Expression analysis - water potential

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Parameters:

.alpha = 0.05
.r = r
.deltam = 2
.minC = 1.5
.maxC = 0.5
.minfc = 0.5
.maxfc = 0.5
.deltam2 = 1

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7.6.981 Vitvi10g00727: * type5 . . . 1777
7.6.982 Vitvi18g00456: * type5 . . . 1778
7.6.983 Vitvi07g01329: * type5 . . . 1779
7.6.984 Vitvi11g01372: * type5 . . . 1780
7.6.985 Vitvi08g00947: * type5 . . . 1781
7.6.986 Vitvi19g02039: * type5 . . . 1782
7.6.987 Vitvi13g00116: * type5 . . . 1783
7.6.988 Vitvi17g00234: * type5 . . . 1784
7.6.989 Vitvi11g00339: * type5 . . . 1785
7.6.990 Vitvi13g01050: * type5 . . . 1787
7.6.991 Vitvi00g01061: * type5 . . . 1788
7.6.992 Vitvi17g00983: * type5 . . . 1789
7.6.993 Vitvi06g00668: type5 . . . 1790
7.6.994 Vitvi18g00888: * type5 . . . 1792
7.6.995 Vitvi07g01916: * type5 . . . 1793
7.6.996 Vitvi16g01407: * type5 . . . 1794
7.6.997 Vitvi10g00209: * type5 . . . 1795
7.6.998 Vitvi18g01299: * type5 . . . 1796
7.6.999 Vitvi05g00276: * type5 . . . 1798
7.6.1000 Vitvi12g00462: * type5 . . . 1799
7.6.1001 Vitvi15g00952: * type5 . . . 1800
7.6.1002 Vitvi12g00208: * type5 . . . 1801
7.6.1003 Vitvi00g00894: * type5 . . . 1802
7.6.1004 Vitvi05g01789: * type5 . . . 1803
7.6.1005 Vitvi01g01173: * type5 . . . 1804
7.6.1006 Vitvi03g00379: * type5 . . . 1805
7.6.1007 Vitvi01g02058: * type5 . . . 1806
7.6.1008 Vitvi15g00739: * type5 . . . 1807
7.6.1009 Vitvi08g01656: * type5 . . . 1808

Appendix **1810**

A Metadata files **1810**
A.1 Project metadata 1810
A.2 Investigation metadata 1811
A.3 Study metadata 1811
A.4 Assay metadata 1812

B SessionInfo **1813**

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2 Project metadata 1810
3 Investigation metadata 1811
4 Study metadata 1811
5 Assay metadata 1812

List of Figures

1 Task

Final document in folder /reports:

```
> fileName(outputFile)
[1] "50_Expression-water-stress_0.05-r-2-1.5-0.5-0.5-0.5-1"
```

2 Information from pISA

Data directory

```
> .inroot
[1] "../../input"
```

Results directory

```
> .oroot
[1] "../../output/50_Expression-water-stress-0.05-r-2-1.5-0.5-0.5-0.5-1"
```

```
project:          _p_VinskaTrta
Investigation:    _I_EnViRoS
Study:            _S_01_Integ
Assay:            _A_01_Desc-R
```

3 Data

Priporočljivo je najprej prebrati phenodata in feature-data, potem pa podatke. To omogoča izbor spremenljivk in vzorcev takoj za tem, ko podatke preberemo.

```
> cat(knit_child(file.path("../doc","10a_Read-Data.Rnw"),quiet=TRUE))
```

Entered 10a-ReadData.Rnw

3.1 Phenodata

Two incomplete lines in original phenodata were manually completed. Sample ids (`ID`) were parsed in Excel to form factors of interest: `variety`,`year` and `day`.

```
> (pfn <- getDesc(.adesc
+     , "Phenodata"))
[1] "Phenodata_20201109.txt"
> dir(file.path(.iroot), pattern = pfn)
[1] "Phenodata_20201109.txt"
> phdata <- read.table(file.path(.iroot, pfn)
+   , header = TRUE
+   , sep = "\t"
+   , stringsAsFactors = FALSE
+   )
> rownames(phdata) <- phdata[,1]
> my.summary(phdata)
```

```
           ID                 Variety            Date     variety
 C18_11d_WS1:  1   Cabernet Volos:134   21.06.2018: 20   C:134
 C18_11d_WS2:  1   Fleurtai      :136   26.06.2019: 20   F:136
 C18_11d_WS3:  1                        7.08.2018 : 20
 C18_11d_WS4:  1                        8.07.2019 : 20
 C18_11d_WW1:  1                        1.08.2018 : 16
 C18_11d_WW2:  1                        18.07.2019: 16
 (Other)    :264                        (Other)   :158
 year          day      treat      rep      project.name
 18:136   34     : 36   WS:135   1   :48   EnViros:270
 19:134   49     : 24   WW:135   2   :48
          20     : 20            3   :48
          22     : 20            4   :48
          67     : 20            NA's:78
          44     : 16
          (Other):134
           species        plant.name   tissue         health.status
 Vitis vinifera:270   grapevine:270       : 78   water stress:134
                                        leaf:192   well watered:136
```

```
 plant.number growth.location growth.conditions
    :78       Udine:270       outside:270
  R1:48
  R2:48
  R3:48
  R4:48
```

```
several leaves ground together and stored at -80oC; an aliquot was received f
```

```
 Metabolites.Order                    Metabolites.File.Name
 2       :  2                                    : 80
 3       :  2        1019Cabernet Volos_6_12_WS1.D:  1
 4       :  2        1019Cabernet Volos_6_12_WS2.D:  1
 5       :  2        1019Cabernet Volos_6_12_WW1.D:  1
 6       :  2        1019Cabernet Volos_6_12_WW2.D:  1
 (Other):180        1019Cabernet Volos_6_21_WS1.D:  1
 NA's    : 80        (Other)                      :185
              Metabolites.File Transcripts.ID
                       : 80            :190
 Cabernet Volos08_07WS:  4      C1_S1   :  1
 Cabernet Volos08_07WW:  4      C1_S2   :  1
 Cabernet Volos08_08WS:  4      C1_S3   :  1
 Cabernet Volos08_08WW:  4      C1_S4   :  1
 Cabernet Volos18_07WS:  4      C1_W1   :  1
 (Other)              :170      (Other):  75
> dim(phdata)
[1] 270  21
> names(phdata)
 [1] "ID"                    "Variety"
 [3] "Date"                  "variety"
 [5] "year"                  "day"
 [7] "treat"                 "rep"
 [9] "project.name"          "species"
[11] "plant.name"            "tissue"
[13] "health.status"         "plant.number"
[15] "growth.location"       "growth.conditions"
[17] "sampling"              "Metabolites.Order"
[19] "Metabolites.File.Name" "Metabolites.File"
[21] "Transcripts.ID"
```

3.2 Declare factor types

In 2018, day 11 is present only for C and day 10 only for F. The two day points coincide and are changed to a common value 11.

```
> for(yr in levels(phdata$year)){
+ cat("\n\nYear:",yr,"\n")
+ print(
+ with(phdata[phdata$year==yr,], ftable(treat,variety,factor(day)))
+ )
+ }
> phdata[phdata$day==10,"day"] <- 11
```

Factors

```
> factors <- colnames(phdata)[4:8]
> factors
[1] "variety" "year"    "day"     "treat"   "rep"
> for (varname in factors)
+ phdata[,varname] <- factor(phdata[,varname])
> #
> # Change the order of levels for treatment
> phdata$treat <- factor(phdata$treat, levels=c("WW","WS"))
> str(phdata[,factors])
'data.frame':        270 obs. of  5 variables:
 $ variety: Factor w/ 2 levels "C","F": 1 1 1 1 1 1 1 1 1 1 ...
 $ year   : Factor w/ 2 levels "18","19": 1 1 1 1 1 1 1 1 1 1 ...
 $ day    : Factor w/ 26 levels "3","11","14",..: 2 2 2 2 2 2 2 2 4 4 ...
 $ treat  : Factor w/ 2 levels "WW","WS": 2 2 2 2 1 1 1 1 2 2 ...
 $ rep    : Factor w/ 4 levels "1","2","3","4": 1 2 3 4 1 2 3 4 1 2 ...
```

Date of sampling might be useful as well

```
> library(lubridate)
Warning: package 'lubridate' was built under R version 4.0.3

Attaching package: 'lubridate'
The following objects are masked from 'package:BiocGenerics':

    intersect, setdiff, union
The following objects are masked from 'package:base':

    date, intersect, setdiff, union
> pdata$date <- as_date(pdata$Date, format="%d.%m.%Y")
Error in h(simpleError(msg, call)): error in evaluating the argument 'x' in se
> table(data.frame(pdata$date,"Count"=1))
Error in data.frame(pdata$date, Count = 1): object 'pdata' not found
```

3.3 Select samples

Check for assay specific sample selection column (assay name)

```
> .aName
[1] "_A_01_Desc-R"
> selectId <- substr(gsub("-",".",.aName),2,nchar(.aName))
> selectId <- .vzorci
Error in eval(expr, envir, enclos): object '.vzorci' not found
> selectId
[1] "A_01_Desc.R"
> #
> if(selectId %in% names(phdata)){
+ pdata <- phdata[!is.na(phdata[,selectId]),]
+ cat("Sample selection column found (", selectId,"),\n",
+ nrow(pdata), "samples will be used.\n")
+ } else {
+ pdata <- phdata
+ cat("No sample selection column found,\n",
+      nrow(pdata), "samples will be used.\n")
+ }
No sample selection column found,
 270 samples will be used.
> dim(pdata)
[1] 270  21
```

Table of sample conditions

```
> head(pdata[,factors])
            variety year day treat rep
C18_11d_WS1       C   18  11    WS   1
C18_11d_WS2       C   18  11    WS   2
C18_11d_WS3       C   18  11    WS   3
C18_11d_WS4       C   18  11    WS   4
C18_11d_WW1       C   18  11    WW   1
C18_11d_WW2       C   18  11    WW   2
> for(yr in levels(pdata$year)){
+ cat("\n\nYear:",yr,"\n")
+ print(
+ with(pdata[pdata$year==yr,], ftable(treat,variety,factor(day)))
+ )
+ }
```

```
Year: 18
                3 11 14 20 28 33 34 39 45 49 52 60 61 67
treat variety
WW    C         1  4  1  5  1  1  4  1  1  4  1  1  4  5
      F         1  4  1  5  1  1  4  1  1  4  1  1  4  5
WS    C         1  4  1  5  1  1  4  1  1  4  1  1  4  5
      F         1  4  1  5  1  1  4  1  1  4  1  1  4  5


Year: 19
                14 22 34 38 43 44 47 48 49 55 56 63 65 69 76
treat variety
WW    C          1  5  5  1  1  4  0  0  4  4  1  1  4  1  1
      F          1  5  5  1  1  4  4  1  0  4  1  1  4  1  1
WS    C          1  5  5  1  1  4  0  0  4  4  1  1  4  1  1
      F          1  5  5  1  1  4  4  1  0  4  1  1  4  1  1
```

```
> my.summary(pdata)
```

```
           ID                  Variety            Date      variety
 C18_11d_WS1:  1   Cabernet Volos:134   21.06.2018: 20   C:134
 C18_11d_WS2:  1   Fleurtai      :136   26.06.2019: 20   F:136
 C18_11d_WS3:  1                        7.08.2018 : 20
 C18_11d_WS4:  1                        8.07.2019 : 20
 C18_11d_WW1:  1                        1.08.2018 : 16
 C18_11d_WW2:  1                        18.07.2019: 16
 (Other)    :264                        (Other)   :158
 year          day       treat       rep       project.name
 18:136   34     : 36   WW:135   1   :48   EnViros:270
 19:134   49     : 24   WS:135   2   :48
          20     : 20            3   :48
          22     : 20            4   :48
          67     : 20            NA's:78
          11     : 16
          (Other):134
           species         plant.name   tissue          health.status
 Vitis vinifera:270   grapevine:270       : 78   water stress:134
                                        leaf:192   well watered:136
```

```
 plant.number growth.location growth.conditions
    :78       Udine:270       outside:270
  R1:48
  R2:48
  R3:48
  R4:48
```

```
several leaves ground together and stored at -80oC; an aliquot was received f
```

```
 Metabolites.Order                    Metabolites.File.Name
 2       :  2                                        : 80
 3       :  2        1019Cabernet Volos_6_12_WS1.D:  1
 4       :  2        1019Cabernet Volos_6_12_WS2.D:  1
 5       :  2        1019Cabernet Volos_6_12_WW1.D:  1
 6       :  2        1019Cabernet Volos_6_12_WW2.D:  1
 (Other):180        1019Cabernet Volos_6_21_WS1.D:  1
 NA's    : 80        (Other)                      :185
              Metabolites.File Transcripts.ID
                     : 80             :190
 Cabernet Volos08_07WS:  4      C1_S1  :  1
 Cabernet Volos08_07WW:  4      C1_S2  :  1
 Cabernet Volos08_08WS:  4      C1_S3  :  1
 Cabernet Volos08_08WW:  4      C1_S4  :  1
 Cabernet Volos18_07WS:  4      C1_W1  :  1
 (Other)              :170      (Other): 75
```

For separate yearly analyses, it will be handy to have two, separate phenodata objects.

```
> dim(pdata)
[1] 270  21
> table(pdata$year)

 18  19
136 134
> pdata18 <- pdata[pdata$year==18,]
> dim(pdata18)
[1] 136  21
> pdata18[1:5,1:6]
                     ID        Variety       Date variety year day
C18_11d_WS1 C18_11d_WS1 Cabernet Volos 12.06.2018       C   18  11
C18_11d_WS2 C18_11d_WS2 Cabernet Volos 12.06.2018       C   18  11
C18_11d_WS3 C18_11d_WS3 Cabernet Volos 12.06.2018       C   18  11
C18_11d_WS4 C18_11d_WS4 Cabernet Volos 12.06.2018       C   18  11
C18_11d_WW1 C18_11d_WW1 Cabernet Volos 12.06.2018       C   18  11
> #
> pdata19 <- pdata[pdata$year==19,]
> dim(pdata19)
[1] 134  21
> pdata19[1:5,1:6]
                     ID        Variety       Date variety year day
C19_22d_WS1 C19_22d_WS1 Cabernet Volos 26.06.2019       C   19  22
C19_22d_WS2 C19_22d_WS2 Cabernet Volos 26.06.2019       C   19  22
C19_22d_WS3 C19_22d_WS3 Cabernet Volos 26.06.2019       C   19  22
C19_22d_WS4 C19_22d_WS4 Cabernet Volos 26.06.2019       C   19  22
C19_22d_WW1 C19_22d_WW1 Cabernet Volos 26.06.2019       C   19  22
```

3.4 Featuredata

```
> (ffn <- getDesc(.adesc,"Featuredata"))
[1] "Transcripts1819-02.txt"
> if(ffn=="") {
+ cat("No feature data declared in the assay metadata file.\\\\")
+ fdata <- NULL
+ }


> fdata <- read.table(file.path(.iroot,ffn)
+     , sep = "\t"
+     , header = TRUE
+     , na.strings = c("", "-","NA")
+     , stringsAsFactors = FALSE
+     , quote = "\"",
+ #    , row.names = 1
+     )
> if(interactive()) my.summary(fdata)
> #"
```

Some genes are listed more than once. Is it OK? Column `geneID` can not be used as row names.

```
> tbl <- table(fdata$geneID)
> tbl[tbl>3]
named integer(0)
> tbl[tbl==3]

Vitvi01g01443 Vitvi03g00845 Vitvi04g02157 Vitvi05g01641 Vitvi06g01689
            3             3             3             3             3
Vitvi07g01861 Vitvi08g01514 Vitvi08g01692 Vitvi08g02189 Vitvi12g01199
            3             3             3             3             3
Vitvi16g00114 Vitvi17g01011 Vitvi19g00061 Vitvi19g01931 Vitvi19g01936
            3             3             3             3             3
Vitvi19g01964
            3
> tbl[tbl==2]

Vitvi00g00711 Vitvi00g00822 Vitvi00g00983 Vitvi00g01149 Vitvi00g01320
            2             2             2             2             2
Vitvi00g01329 Vitvi00g01996 Vitvi00g01999 Vitvi00g02041 Vitvi01g00036
            2             2             2             2             2
Vitvi01g00137 Vitvi01g00165 Vitvi01g00274 Vitvi01g00301 Vitvi01g00348
            2             2             2             2             2
Vitvi01g00373 Vitvi01g00397 Vitvi01g00398 Vitvi01g00417 Vitvi01g00478
            2             2             2             2             2
Vitvi01g00553 Vitvi01g00625 Vitvi01g00681 Vitvi01g00696 Vitvi01g00793
            2             2             2             2             2
Vitvi01g00814 Vitvi01g00828 Vitvi01g00861 Vitvi01g00885 Vitvi01g00993
            2             2             2             2             2
Vitvi01g01351 Vitvi01g01436 Vitvi01g01632 Vitvi01g01645 Vitvi01g01671
            2             2             2             2             2
```

Vitvi01g01773	Vitvi01g01814	Vitvi01g01956	Vitvi01g01982	Vitvi01g02258
2	2	2	2	2
Vitvi01g02269	Vitvi02g00007	Vitvi02g00023	Vitvi02g00085	Vitvi02g00187
2	2	2	2	2
Vitvi02g00220	Vitvi02g00222	Vitvi02g00278	Vitvi02g00380	Vitvi02g00387
2	2	2	2	2
Vitvi02g00485	Vitvi02g00561	Vitvi02g00739	Vitvi02g01143	Vitvi02g01273
2	2	2	2	2
Vitvi02g01365	Vitvi02g01416	Vitvi02g01458	Vitvi02g01751	Vitvi03g00042
2	2	2	2	2
Vitvi03g00059	Vitvi03g00097	Vitvi03g00121	Vitvi03g00167	Vitvi03g00273
2	2	2	2	2
Vitvi03g00278	Vitvi03g00375	Vitvi03g00432	Vitvi03g00442	Vitvi03g00464
2	2	2	2	2
Vitvi03g00521	Vitvi03g00532	Vitvi03g00537	Vitvi03g00541	Vitvi03g00757
2	2	2	2	2
Vitvi03g00785	Vitvi03g00804	Vitvi03g00855	Vitvi03g00900	Vitvi03g00936
2	2	2	2	2
Vitvi03g01059	Vitvi03g01228	Vitvi03g01320	Vitvi04g00092	Vitvi04g00112
2	2	2	2	2
Vitvi04g00113	Vitvi04g00127	Vitvi04g00199	Vitvi04g00205	Vitvi04g00227
2	2	2	2	2
Vitvi04g00279	Vitvi04g00314	Vitvi04g00371	Vitvi04g00450	Vitvi04g00483
2	2	2	2	2
Vitvi04g00520	Vitvi04g00888	Vitvi04g01149	Vitvi04g01257	Vitvi04g01359
2	2	2	2	2
Vitvi04g01462	Vitvi04g01469	Vitvi04g01474	Vitvi04g01560	Vitvi04g01624
2	2	2	2	2
Vitvi04g01633	Vitvi04g01668	Vitvi04g01671	Vitvi04g01694	Vitvi04g01695
2	2	2	2	2
Vitvi04g01709	Vitvi04g01746	Vitvi04g01763	Vitvi04g02022	Vitvi04g02037
2	2	2	2	2
Vitvi04g02038	Vitvi04g02099	Vitvi04g02114	Vitvi04g02185	Vitvi05g00115
2	2	2	2	2
Vitvi05g00132	Vitvi05g00144	Vitvi05g00210	Vitvi05g00239	Vitvi05g00390
2	2	2	2	2
Vitvi05g00409	Vitvi05g00418	Vitvi05g00436	Vitvi05g00443	Vitvi05g00503
2	2	2	2	2
Vitvi05g00541	Vitvi05g00556	Vitvi05g00652	Vitvi05g00737	Vitvi05g00790
2	2	2	2	2
Vitvi05g00953	Vitvi05g00991	Vitvi05g01068	Vitvi05g01130	Vitvi05g01255
2	2	2	2	2
Vitvi05g01369	Vitvi05g01562	Vitvi05g01570	Vitvi05g01603	Vitvi05g01634
2	2	2	2	2
Vitvi05g02135	Vitvi06g00022	Vitvi06g00089	Vitvi06g00200	Vitvi06g00201
2	2	2	2	2
Vitvi06g00212	Vitvi06g00213	Vitvi06g00215	Vitvi06g00243	Vitvi06g00259
2	2	2	2	2
Vitvi06g00319	Vitvi06g00337	Vitvi06g00356	Vitvi06g00365	Vitvi06g00414
2	2	2	2	2
Vitvi06g00439	Vitvi06g00443	Vitvi06g00454	Vitvi06g00472	Vitvi06g00512
2	2	2	2	2
Vitvi06g00525	Vitvi06g00533	Vitvi06g00652	Vitvi06g00668	Vitvi06g00701

2	2	2	2	2
Vitvi06g00789	Vitvi06g01242	Vitvi06g01279	Vitvi06g01469	Vitvi06g01486
2	2	2	2	2
Vitvi06g01604	Vitvi06g01690	Vitvi06g01693	Vitvi06g01718	Vitvi06g01739
2	2	2	2	2
Vitvi06g01836	Vitvi07g00067	Vitvi07g00078	Vitvi07g00080	Vitvi07g00205
2	2	2	2	2
Vitvi07g00316	Vitvi07g00406	Vitvi07g00416	Vitvi07g00464	Vitvi07g00594
2	2	2	2	2
Vitvi07g00630	Vitvi07g00636	Vitvi07g00708	Vitvi07g00908	Vitvi07g00916
2	2	2	2	2
Vitvi07g01028	Vitvi07g01205	Vitvi07g01306	Vitvi07g01340	Vitvi07g01364
2	2	2	2	2
Vitvi07g01402	Vitvi07g01441	Vitvi07g01524	Vitvi07g01569	Vitvi07g01737
2	2	2	2	2
Vitvi07g01749	Vitvi07g01817	Vitvi07g01903	Vitvi07g01937	Vitvi07g01973
2	2	2	2	2
Vitvi07g01983	Vitvi07g01996	Vitvi07g02049	Vitvi07g02102	Vitvi07g02119
2	2	2	2	2
Vitvi07g02123	Vitvi07g02135	Vitvi07g02302	Vitvi07g02394	Vitvi07g02412
2	2	2	2	2
Vitvi07g02447	Vitvi07g02491	Vitvi07g02523	Vitvi07g02528	Vitvi07g02557
2	2	2	2	2
Vitvi07g02631	Vitvi07g02863	Vitvi07g03034	Vitvi07g03040	Vitvi07g03070
2	2	2	2	2
Vitvi07g03110	Vitvi08g00215	Vitvi08g00703	Vitvi08g00740	Vitvi08g00744
2	2	2	2	2
Vitvi08g00799	Vitvi08g00853	Vitvi08g00935	Vitvi08g00961	Vitvi08g00981
2	2	2	2	2
Vitvi08g00983	Vitvi08g00999	Vitvi08g01042	Vitvi08g01082	Vitvi08g01108
2	2	2	2	2
Vitvi08g01206	Vitvi08g01241	Vitvi08g01243	Vitvi08g01302	Vitvi08g01346
2	2	2	2	2
Vitvi08g01376	Vitvi08g01395	Vitvi08g01417	Vitvi08g01506	Vitvi08g01513
2	2	2	2	2
Vitvi08g01519	Vitvi08g01766	Vitvi08g01833	Vitvi08g01864	Vitvi08g01884
2	2	2	2	2
Vitvi08g01931	Vitvi08g01959	Vitvi08g02249	Vitvi08g02367	Vitvi08g02413
2	2	2	2	2
Vitvi09g00067	Vitvi09g00156	Vitvi09g00233	Vitvi09g00239	Vitvi09g00243
2	2	2	2	2
Vitvi09g00249	Vitvi09g00253	Vitvi09g00258	Vitvi09g00277	Vitvi09g00292
2	2	2	2	2
Vitvi09g00297	Vitvi09g00446	Vitvi09g00490	Vitvi09g00653	Vitvi09g00675
2	2	2	2	2
Vitvi09g00816	Vitvi09g00861	Vitvi09g01320	Vitvi09g01500	Vitvi09g01555
2	2	2	2	2
Vitvi09g01556	Vitvi09g01557	Vitvi09g01559	Vitvi09g01930	Vitvi09g01933
2	2	2	2	2
Vitvi09g02012	Vitvi10g00078	Vitvi10g00087	Vitvi10g00125	Vitvi10g00154
2	2	2	2	2
Vitvi10g00219	Vitvi10g00290	Vitvi10g00303	Vitvi10g00316	Vitvi10g00317
2	2	2	2	2

Vitvi10g00336	Vitvi10g00365	Vitvi10g00457	Vitvi10g00554	Vitvi10g00582
2	2	2	2	2
Vitvi10g00605	Vitvi10g00635	Vitvi10g00662	Vitvi10g00663	Vitvi10g00784
2	2	2	2	2
Vitvi10g01029	Vitvi10g01098	Vitvi10g02139	Vitvi10g02141	Vitvi10g02143
2	2	2	2	2
Vitvi10g02151	Vitvi10g02152	Vitvi10g02155	Vitvi10g02157	Vitvi10g02322
2	2	2	2	2
Vitvi10g02324	Vitvi10g02368	Vitvi10g02370	Vitvi10g02408	Vitvi11g00001
2	2	2	2	2
Vitvi11g00068	Vitvi11g00102	Vitvi11g00136	Vitvi11g00137	Vitvi11g00198
2	2	2	2	2
Vitvi11g00270	Vitvi11g00339	Vitvi11g00360	Vitvi11g00480	Vitvi11g00517
2	2	2	2	2
Vitvi11g00597	Vitvi11g00614	Vitvi11g00692	Vitvi11g00724	Vitvi11g00812
2	2	2	2	2
Vitvi11g00865	Vitvi11g01141	Vitvi11g01176	Vitvi12g00021	Vitvi12g00032
2	2	2	2	2
Vitvi12g00089	Vitvi12g00121	Vitvi12g00157	Vitvi12g00220	Vitvi12g00229
2	2	2	2	2
Vitvi12g00284	Vitvi12g00596	Vitvi12g00598	Vitvi12g00606	Vitvi12g00615
2	2	2	2	2
Vitvi12g00628	Vitvi12g00646	Vitvi12g00689	Vitvi12g00691	Vitvi12g00694
2	2	2	2	2
Vitvi12g00837	Vitvi12g01277	Vitvi12g01467	Vitvi12g01780	Vitvi12g01840
2	2	2	2	2
Vitvi12g01863	Vitvi12g01897	Vitvi12g01952	Vitvi12g02074	Vitvi12g02434
2	2	2	2	2
Vitvi12g02435	Vitvi12g02440	Vitvi13g00019	Vitvi13g00031	Vitvi13g00053
2	2	2	2	2
Vitvi13g00095	Vitvi13g00096	Vitvi13g00111	Vitvi13g00149	Vitvi13g00288
2	2	2	2	2
Vitvi13g00328	Vitvi13g00332	Vitvi13g00334	Vitvi13g00344	Vitvi13g00510
2	2	2	2	2
Vitvi13g00627	Vitvi13g00628	Vitvi13g00636	Vitvi13g00637	Vitvi13g00700
2	2	2	2	2
Vitvi13g00744	Vitvi13g01070	Vitvi13g01077	Vitvi13g01233	Vitvi13g01272
2	2	2	2	2
Vitvi13g01327	Vitvi13g01364	Vitvi13g01839	Vitvi13g01854	Vitvi13g02272
2	2	2	2	2
Vitvi14g00020	Vitvi14g00025	Vitvi14g00053	Vitvi14g00160	Vitvi14g00185
2	2	2	2	2
Vitvi14g00237	Vitvi14g00281	Vitvi14g00327	Vitvi14g00380	Vitvi14g00383
2	2	2	2	2
Vitvi14g00397	Vitvi14g00404	Vitvi14g00439	Vitvi14g00484	Vitvi14g00535
2	2	2	2	2
Vitvi14g00562	Vitvi14g00627	Vitvi14g00654	Vitvi14g00658	Vitvi14g00763
2	2	2	2	2
Vitvi14g00841	Vitvi14g01061	Vitvi14g01128	Vitvi14g01280	Vitvi14g01294
2	2	2	2	2
Vitvi14g01321	Vitvi14g01472	Vitvi14g01520	Vitvi14g01596	Vitvi14g01678
2	2	2	2	2
Vitvi14g01746	Vitvi14g01758	Vitvi14g01809	Vitvi14g01983	Vitvi14g02002

2	2	2	2	2
Vitvi14g02027	Vitvi14g02478	Vitvi14g02644	Vitvi14g02869	Vitvi15g00225
2	2	2	2	2
Vitvi15g00526	Vitvi15g00563	Vitvi15g00690	Vitvi15g00827	Vitvi15g00840
2	2	2	2	2
Vitvi15g00878	Vitvi15g00908	Vitvi15g00974	Vitvi15g01077	Vitvi15g01403
2	2	2	2	2
Vitvi15g01468	Vitvi15g01491	Vitvi15g01537	Vitvi15g01539	Vitvi16g00018
2	2	2	2	2
Vitvi16g00048	Vitvi16g00095	Vitvi16g00461	Vitvi16g00796	Vitvi16g00857
2	2	2	2	2
Vitvi16g00935	Vitvi16g00949	Vitvi16g00982	Vitvi16g01025	Vitvi16g01083
2	2	2	2	2
Vitvi16g01089	Vitvi16g01211	Vitvi16g01323	Vitvi16g01326	Vitvi16g01348
2	2	2	2	2
Vitvi16g01358	Vitvi16g01371	Vitvi16g01375	Vitvi16g01391	Vitvi17g00038
2	2	2	2	2
Vitvi17g00161	Vitvi17g00210	Vitvi17g00222	Vitvi17g00225	Vitvi17g00240
2	2	2	2	2
Vitvi17g00253	Vitvi17g00263	Vitvi17g00277	Vitvi17g00287	Vitvi17g00299
2	2	2	2	2
Vitvi17g00428	Vitvi17g00468	Vitvi17g00519	Vitvi17g00548	Vitvi17g00603
2	2	2	2	2
Vitvi17g00614	Vitvi17g00869	Vitvi17g00905	Vitvi17g01148	Vitvi17g01183
2	2	2	2	2
Vitvi17g01348	Vitvi17g01399	Vitvi17g01407	Vitvi18g00056	Vitvi18g00132
2	2	2	2	2
Vitvi18g00177	Vitvi18g00234	Vitvi18g00310	Vitvi18g00358	Vitvi18g00444
2	2	2	2	2
Vitvi18g00507	Vitvi18g00517	Vitvi18g00534	Vitvi18g00579	Vitvi18g00743
2	2	2	2	2
Vitvi18g00762	Vitvi18g00784	Vitvi18g00838	Vitvi18g00909	Vitvi18g00960
2	2	2	2	2
Vitvi18g00966	Vitvi18g01002	Vitvi18g01004	Vitvi18g01019	Vitvi18g01095
2	2	2	2	2
Vitvi18g01103	Vitvi18g01223	Vitvi18g01226	Vitvi18g01242	Vitvi18g01299
2	2	2	2	2
Vitvi18g01309	Vitvi18g01430	Vitvi18g01436	Vitvi18g01634	Vitvi18g01677
2	2	2	2	2
Vitvi18g02066	Vitvi18g02228	Vitvi18g02237	Vitvi18g02378	Vitvi18g03244
2	2	2	2	2
Vitvi19g00015	Vitvi19g00020	Vitvi19g00094	Vitvi19g00138	Vitvi19g00155
2	2	2	2	2
Vitvi19g00197	Vitvi19g00226	Vitvi19g00337	Vitvi19g00339	Vitvi19g00341
2	2	2	2	2
Vitvi19g00353	Vitvi19g00421	Vitvi19g00531	Vitvi19g00539	Vitvi19g00552
2	2	2	2	2
Vitvi19g00602	Vitvi19g00612	Vitvi19g00621	Vitvi19g00675	Vitvi19g00706
2	2	2	2	2
Vitvi19g00745	Vitvi19g00782	Vitvi19g00904	Vitvi19g00928	Vitvi19g01352
2	2	2	2	2
Vitvi19g01464	Vitvi19g01552	Vitvi19g01690	Vitvi19g01692	Vitvi19g01725
2	2	2	2	2

```
Vitvi19g01864 Vitvi19g01933 Vitvi19g01937 Vitvi19g01940 Vitvi19g01952
            2             2             2             2             2
Vitvi19g01957 Vitvi19g01959 Vitvi19g01963 Vitvi19g01965 Vitvi19g01966
            2             2             2             2             2
Vitvi19g01969 Vitvi19g01970 Vitvi19g02001 Vitvi19g02292
            2             2             2             2
```

A glimpse into feature data (or `NULL` if nonexistent)

```
> fdata[1:6,]
  YEAR        geneID BINCODE                            NAME
1 2018 Vitvi15g01736    26.9 misc.glutathione S transferases
2 2018 Vitvi07g02832    35.2            not assigned.unknown
3 2018 Vitvi07g02830    35.2            not assigned.unknown
4 2018 Vitvi07g02812    35.2            not assigned.unknown
5 2018 Vitvi07g02811    35.2            not assigned.unknown
6 2018 Vitvi09g02033    35.2            not assigned.unknown

1                     glutathione S-transferase tau 7 | Chr2:12618111-1261887
2 Disease resistance protein (TIR-NBS-LRR class) family | Chr4:7197325-7201393
3
4                                                                           Ti
5
6   Disease resistance protein (CC-NBS-LRR class) family | Chr1:4145374-414768
> cat(gsub(" \\| "," |\\\n\\\t",fdata$DESCRIPTION[1:6]),sep="\n\n")
glutathione S-transferase tau 7 |
        Chr2:12618111-12618871 REVERSE LENGTH=227 |
        201606

Disease resistance protein (TIR-NBS-LRR class) family |
        Chr4:7197325-7201393 REVERSE LENGTH=1219 |
        201606

NA

Tir-nbs-lrr, resistance protein

NA

Disease resistance protein (CC-NBS-LRR class) family |
        Chr1:4145374-4147680 FORWARD LENGTH=768 |
        201606
> fd <- (apply(fdata[1:6,c(2:5)],1,paste,collapse="\n\t"))
> cat(gsub(" \\| "," |\\\n\\\t",fd[1:6]),sep="\n\n")
Vitvi15g01736
        26.9
        misc.glutathione S transferases
        glutathione S-transferase tau 7 |
        Chr2:12618111-12618871 REVERSE LENGTH=227 |
        201606

Vitvi07g02832
        35.2
```

```
        not assigned.unknown
        Disease resistance protein (TIR-NBS-LRR class) family |
        Chr4:7197325-7201393 REVERSE LENGTH=1219 |
        201606

Vitvi07g02830
        35.2
        not assigned.unknown
        NA

Vitvi07g02812
        35.2
        not assigned.unknown
        Tir-nbs-lrr, resistance protein

Vitvi07g02811
        35.2
        not assigned.unknown
        NA

Vitvi09g02033
        35.2
        not assigned.unknown
        Disease resistance protein (CC-NBS-LRR class) family |
        Chr1:4145374-4147680 FORWARD LENGTH=768 |
        201606

> cat.feature <- function(x,...) {
+ #x <- t(apply(x,1, FUN=function(x) paste(names(x),x,sep=":\t") ))
+ #cat(x)
+ fd <- (apply(x,1,paste,collapse="\n\t"))
+ cat(gsub(" \\| "," |\\\n\\\t",fd),sep="\n\n")
+ }
> cat.feature(fdata[1,2:5])
Vitvi15g01736
        26.9
        misc.glutathione S transferases
        glutathione S-transferase tau 7 |
        Chr2:12618111-12618871 REVERSE LENGTH=227 |
        201606
> cat.feature(fdata[1:2,2:5])
Vitvi15g01736
        26.9
        misc.glutathione S transferases
        glutathione S-transferase tau 7 |
        Chr2:12618111-12618871 REVERSE LENGTH=227 |
        201606

Vitvi07g02832
        35.2
        not assigned.unknown
        Disease resistance protein (TIR-NBS-LRR class) family |
        Chr4:7197325-7201393 REVERSE LENGTH=1219 |
        201606
```

3.5 Transcripts measurements

Normalised transcript measurements for each year are available in two separate files. The first few lines contain factor values and are commented out (by a hash). The first effective line is the table header line with sample ids.

3.5.1 Normalized values

Data for year 2018:

```
> (t18fn <- getDesc(.adesc,"Transcript data 18"))
[1] "/input/Transcripts 2018.txt"
> td  <- read.table(file.path(.aroot,t18fn),
+     header = TRUE,
+     sep = "\t",
+     row.names = 1
+     )
> head(td)
              C18_11d_WS1 C18_11d_WS2 C18_11d_WS3 C18_11d_WS4
Vitvi15g01736   4.6646023    4.109897   4.4482203    4.013955
Vitvi07g02832  -2.4786650   -1.601359  -1.4274193   -2.066419
Vitvi07g02830  -1.8506337   -2.218030  -1.0648492   -1.580992
Vitvi07g02812  -0.5805446   -1.266940  -0.3278837   -1.019113
Vitvi07g02811   2.2762225    1.823447   1.9550503    1.648742
Vitvi09g02033  -1.6901691   -2.218030  -2.6498117   -1.449747
              C18_11d_WW1 C18_11d_WW2 C18_11d_WW3 C18_11d_WW4
Vitvi15g01736    4.717536    4.154237    4.475261    4.466465
Vitvi07g02832   -2.608485   -1.801183   -1.886474   -3.583384
Vitvi07g02830   -1.544354   -1.405255   -1.755229   -1.381750
Vitvi07g02812   -0.858463   -0.434401   -1.234397   -1.047331
Vitvi07g02811    2.086902    2.105707    2.134837    1.908469
Vitvi09g02033   -2.608485   -1.961648   -3.108866   -4.320350
              C18_34d_WS1 C18_34d_WS2 C18_34d_WS3 C18_34d_WS4
Vitvi15g01736    4.400333    4.641164   4.4191231    4.534438
Vitvi07g02832   -5.683146   -2.452000  -4.4274120   -1.876949
Vitvi07g02830   -2.513221   -2.452000  -4.4274120   -2.263972
Vitvi07g02812   -2.875791   -2.693008  -2.5529429   -3.157057
Vitvi07g02811    1.414886    1.409803   0.3970164    1.273993
Vitvi09g02033   -2.513221   -3.345084  -2.1054839   -1.716484
              C18_34d_WW1 C18_34d_WW2 C18_34d_WW3 C18_34d_WW4
Vitvi15g01736    4.924801    5.085690   5.3397350    5.263629
Vitvi07g02832   -2.827859   -3.130016  -4.6322874   -3.196388
Vitvi07g02830   -3.190429   -1.545054  -2.1297871   -3.196388
Vitvi07g02812   -2.827859   -1.182484  -3.4098950   -2.303303
Vitvi07g02811    1.517916    1.357250   0.9626591    1.344985
Vitvi09g02033   -4.412821   -3.130016  -2.3103594   -4.418780
              C18_67d_WS1 C18_67d_WS2 C18_67d_WS3 C18_67d_WS4
Vitvi15g01736  2.05871733   2.2895026   2.9234830    2.575657
Vitvi07g02832 -5.85417200  -4.4786818  -4.4659691   -2.468738
Vitvi07g02830 -2.15373228  -3.2562893  -3.7290035   -2.709746
Vitvi07g02812 -1.21031581  -2.3632045  -2.3504919   -2.999252
Vitvi07g02811  0.02847105   0.5362686   0.9824914    1.231702
Vitvi09g02033 -4.26920950  -3.7417162  -2.5915000   -3.847249
```

```
              C18_67d_WW1 C18_67d_WW2 C18_67d_WW3 C18_67d_WW4
Vitvi15g01736    3.891121    3.040087    4.216897    3.763086
Vitvi07g02832   -2.726982   -4.610965   -2.436913   -3.355855
Vitvi07g02830   -2.726982   -3.873999   -1.493496   -2.075747
Vitvi07g02812   -1.672534   -3.388572   -2.230462   -2.462770
Vitvi07g02811    1.436764    1.552266    1.811015    1.352490
Vitvi09g02033   -2.520531   -2.736495   -3.815424   -2.993285
              F18_10d_WS1 F18_10d_WS2 F18_10d_WS3 F18_10d_WS4
Vitvi15g01736   4.8591409   4.8669435   4.9805904   4.9453953
Vitvi07g02832   2.8881443   2.7032394   2.2757651   2.0553154
Vitvi07g02830   2.8426117   2.4130023   2.2135368   2.0169691
Vitvi07g02812   0.8222302   0.9363895   0.7209384   0.3104447
Vitvi07g02811   3.5853480   3.5007015   3.2965509   3.2141610
Vitvi09g02033   1.0793880   1.0850336   0.6285743   0.8579324
              F18_10d_WW1 F18_10d_WW2 F18_10d_WW3 F18_10d_WW4
Vitvi15g01736    5.705006    4.619238    4.808548    5.276124
Vitvi07g02832    2.747538    3.349854    2.537311    2.621336
Vitvi07g02830    2.287722    3.464855    1.989824    2.321031
Vitvi07g02812    1.073767    1.384521    1.472076    1.016877
Vitvi07g02811    3.818074    4.000053    3.198197    3.501954
Vitvi09g02033    1.073767    1.566041    1.237985    1.268416
              F18_34d_WS1 F18_34d_WS2 F18_34d_WS3 F18_34d_WS4
Vitvi15g01736   4.0647184   3.8504580   5.1418322   4.6269091
Vitvi07g02832   2.2592790   2.1761360   2.3686660   1.2127920
Vitvi07g02830   2.1186455   1.9359657   2.6356368   1.5129655
Vitvi07g02812   0.4316833  -0.6220298  -0.5985972  -0.2055206
Vitvi07g02811   2.9490282   2.7595613   3.1300210   2.4602029
Vitvi09g02033   1.5459405   1.3699329   1.4288835   1.4477479
              F18_34d_WW1 F18_34d_WW2 F18_34d_WW3 F18_34d_WW4
Vitvi15g01736   4.0961725  4.80222138   4.3291524   4.4419027
Vitvi07g02832   1.8816574  1.82887526   1.7895023   1.6490200
Vitvi07g02830   2.1414534  1.62149541   2.1153419   2.1541121
Vitvi07g02812   0.1031253 -0.09471163   0.3053805   0.2855497
Vitvi07g02811   3.0025984  2.73213947   2.8750439   3.0458304
Vitvi09g02033   1.7460934  1.45938991   2.0072243   1.2444445
              F18_67d_WS1 F18_67d_WS2 F18_67d_WS3 F18_67d_WS4
Vitvi15g01736   1.5831276   1.7408584  2.97840555   4.1664059
Vitvi07g02832   1.3093668   1.9241330  2.01456521   2.9813855
Vitvi07g02830   0.8382242   1.4203666  2.18501915   2.8731326
Vitvi07g02812   0.1974739   0.4558154 -0.03878421  -0.0111843
Vitvi07g02811   1.8823168   2.5341865  2.65708760   2.9461961
Vitvi09g02033   1.6066824   1.5040245  1.25520700   0.9986635
              F18_67d_WW1 F18_67d_WW2 F18_67d_WW3 F18_67d_WW4
Vitvi15g01736   3.5580430    3.569471   4.4112089   4.3597440
Vitvi07g02832   2.5563386    2.180583   2.6637430   2.7538173
Vitvi07g02830   2.0265816    2.154972   2.7552617   2.3663511
Vitvi07g02812   0.6773148    0.106805  -0.2413317  -0.1063251
Vitvi07g02811   3.0678390    2.949349   2.9761917   2.9625700
Vitvi09g02033   1.7205680    1.541742   1.6527997   1.3320450
> dim(td)
[1] 16005    48
> t18 <- td
```

```
> (t19fn <- getDesc(.adesc,"Transcript data 19"))
[1] "/input/Transcripts 2019.txt"
> td  <- read.table(file.path(.aroot,t19fn),
+     header = TRUE,
+     sep = "\t",
+     row.names = 1
+     )
> head(td)
```

	C19_22d_WS1	C19_22d_WS2	C19_22d_WS3	C19_22d_WS4
Vitvi15g01736	3.18	3.50	3.19	3.61
Vitvi07g02832	-5.05	-3.02	-0.80	-0.02
Vitvi07g02830	-5.05	-5.35	-2.39	-3.99
Vitvi07g02812	-1.35	-0.95	-0.15	0.26
Vitvi07g02811	2.09	2.29	2.34	2.63
Vitvi09g02033	-5.05	-3.76	-2.39	-2.76
	C19_22d_WW1	C19_22d_WW2	C19_22d_WW3	C19_22d_WW4
Vitvi15g01736	5.42	5.35	4.68	4.92
Vitvi07g02832	-1.36	-2.10	-1.15	-3.81
Vitvi07g02830	-2.28	-1.81	-2.07	-2.59
Vitvi07g02812	-1.36	0.16	-0.29	-0.75
Vitvi07g02811	2.85	3.16	3.09	2.89
Vitvi09g02033	-5.45	-3.68	-1.78	-3.81
	C19_44d_WS1	C19_44d_WS2	C19_44d_WS3	C19_44d_WS4
Vitvi15g01736	5.13	5.19	5.71	5.29
Vitvi07g02832	-3.13	-1.28	-3.18	-2.29
Vitvi07g02830	-3.87	-5.53	-5.50	-2.29
Vitvi07g02812	-0.10	-1.01	-0.29	-0.04
Vitvi07g02811	2.11	1.92	2.40	2.29
Vitvi09g02033	-3.87	-3.95	-2.69	-2.00
	C19_44d_WW1	C19_44d_WW2	C19_44d_WW3	C19_44d_WW4
Vitvi15g01736	6.19	5.62	5.62	6.19
Vitvi07g02832	-5.54	-5.31	-3.73	-1.81
Vitvi07g02830	-3.22	-5.31	-3.73	-2.05
Vitvi07g02812	-0.59	-0.45	-1.07	-0.55
Vitvi07g02811	2.44	2.13	2.08	2.26
Vitvi09g02033	-3.22	-3.72	-3.73	-3.18
	F19_22d_WS1	F19_22d_WS2	F19_22d_WS3	F19_22d_WS4
Vitvi15g01736	3.03	3.93	4.24	2.85
Vitvi07g02832	3.35	3.23	3.02	2.98
Vitvi07g02830	2.28	2.39	1.75	1.35
Vitvi07g02812	2.19	1.04	0.89	1.56
Vitvi07g02811	3.84	3.72	3.01	3.43
Vitvi09g02033	2.70	1.61	1.94	2.47
	F19_22d_WW1	F19_22d_WW2	F19_22d_WW3	F19_22d_WW4
Vitvi15g01736	5.00	4.97	4.47	5.51
Vitvi07g02832	3.18	3.04	2.81	3.05
Vitvi07g02830	2.59	2.07	1.81	2.20
Vitvi07g02812	1.72	1.08	1.42	1.35
Vitvi07g02811	3.79	3.43	3.24	3.33
Vitvi09g02033	2.24	1.90	2.08	1.25
	F19_44d_WS1	F19_44d_WS2	F19_44d_WS3	F19_44d_WS4
Vitvi15g01736	5.84	5.83	4.56	5.23

```
Vitvi07g02832        2.54        3.14        3.01        2.16
Vitvi07g02830        1.13        2.25        2.18        1.90
Vitvi07g02812        0.99        0.84        0.85        0.22
Vitvi07g02811        2.91        3.10        3.18        2.61
Vitvi09g02033        1.21        1.67        2.52        2.21
             F19_44d_WW1 F19_44d_WW2 F19_44d_WW3 F19_44d_WW4
Vitvi15g01736        5.44        6.13        5.96        6.16
Vitvi07g02832        3.84        3.05        3.89        4.02
Vitvi07g02830        2.74        2.79        2.90        2.88
Vitvi07g02812        1.03        0.93        1.49        1.29
Vitvi07g02811        3.32        2.89        3.35        3.26
Vitvi09g02033        1.99        1.14        1.65        1.29
> dim(td)
[1] 15562    32
> t19 <- td

> dim(t18)-dim(t19)
[1] 443  16
```

Data for year 2018 have more genes than data for year 2019.

```
> allNames <- unique(c(rownames(t18),rownames(t19)))
> length(allNames)
[1] 16325
> sum(allNames %in% rownames(t18))
[1] 16005
> sum(allNames %in% rownames(t19))
[1] 15562
> tbl <- table(gene.in.18=allNames %in% rownames(t18),
+              gene.in.19=allNames %in% rownames(t19))
> tbl
          gene.in.19
gene.in.18 FALSE  TRUE
     FALSE     0   320
     TRUE    763 15242
```

We have complete yearly data on 15242 genes. At the meeting on Nov. 19 we decided to use only the genes in the intersection. This will allow us to use the combined set of data.

3.5.2 Keep genes in the intersection

```
> gene.keep <- (allNames %in% rownames(t18))&(allNames %in% rownames(t19))
> sum(gene.keep)
[1] 15242
> t18 <- t18[allNames[gene.keep],]
> t19 <- t19[allNames[gene.keep],]
> all(rownames(t18)==rownames(t19))
[1] TRUE
> dim(t18)
[1] 15242    48
> dim(t19)
[1] 15242    32
```

Order rows of yearly phenodata according to the sequence of samples (columns) in the measurements.

Year 2018

```
> dim(pdata18)
[1] 136  21
> dim(t18)
[1] 15242    48
> pdata18 <- pdata18[colnames(t18),]
> dim(pdata18)
[1] 48 21
> dim(t18)
[1] 15242    48
> pdata18[,4:8]
            variety year day treat rep
C18_11d_WS1       C   18  11    WS   1
C18_11d_WS2       C   18  11    WS   2
C18_11d_WS3       C   18  11    WS   3
C18_11d_WS4       C   18  11    WS   4
C18_11d_WW1       C   18  11    WW   1
C18_11d_WW2       C   18  11    WW   2
C18_11d_WW3       C   18  11    WW   3
C18_11d_WW4       C   18  11    WW   4
C18_34d_WS1       C   18  34    WS   1
C18_34d_WS2       C   18  34    WS   2
C18_34d_WS3       C   18  34    WS   3
C18_34d_WS4       C   18  34    WS   4
C18_34d_WW1       C   18  34    WW   1
C18_34d_WW2       C   18  34    WW   2
C18_34d_WW3       C   18  34    WW   3
C18_34d_WW4       C   18  34    WW   4
C18_67d_WS1       C   18  67    WS   1
C18_67d_WS2       C   18  67    WS   2
C18_67d_WS3       C   18  67    WS   3
C18_67d_WS4       C   18  67    WS   4
C18_67d_WW1       C   18  67    WW   1
C18_67d_WW2       C   18  67    WW   2
```

```
C18_67d_WW3       C   18  67    WW   3
C18_67d_WW4       C   18  67    WW   4
F18_10d_WS1       F   18  11    WS   1
F18_10d_WS2       F   18  11    WS   2
F18_10d_WS3       F   18  11    WS   3
F18_10d_WS4       F   18  11    WS   4
F18_10d_WW1       F   18  11    WW   1
F18_10d_WW2       F   18  11    WW   2
F18_10d_WW3       F   18  11    WW   3
F18_10d_WW4       F   18  11    WW   4
F18_34d_WS1       F   18  34    WS   1
F18_34d_WS2       F   18  34    WS   2
F18_34d_WS3       F   18  34    WS   3
F18_34d_WS4       F   18  34    WS   4
F18_34d_WW1       F   18  34    WW   1
F18_34d_WW2       F   18  34    WW   2
F18_34d_WW3       F   18  34    WW   3
F18_34d_WW4       F   18  34    WW   4
F18_67d_WS1       F   18  67    WS   1
F18_67d_WS2       F   18  67    WS   2
F18_67d_WS3       F   18  67    WS   3
F18_67d_WS4       F   18  67    WS   4
F18_67d_WW1       F   18  67    WW   1
F18_67d_WW2       F   18  67    WW   2
F18_67d_WW3       F   18  67    WW   3
F18_67d_WW4       F   18  67    WW   4
> all(rownames(pdata18)==colnames(t18))
[1] TRUE
```

Get rid of unused factors

```
> str(pdata18[,factors])
'data.frame':        48 obs. of  5 variables:
 $ variety: Factor w/ 2 levels "C","F": 1 1 1 1 1 1 1 1 1 1 ...
 $ year   : Factor w/ 2 levels "18","19": 1 1 1 1 1 1 1 1 1 1 ...
 $ day    : Factor w/ 26 levels "3","11","14",..: 2 2 2 2 2 2 2 2 8 8 ...
 $ treat  : Factor w/ 2 levels "WW","WS": 2 2 2 2 1 1 1 1 2 2 ...
 $ rep    : Factor w/ 4 levels "1","2","3","4": 1 2 3 4 1 2 3 4 1 2 ...
> for (var in factors) pdata18[,var] <- factor(pdata18[,var])
> str(pdata18[,factors])
'data.frame':        48 obs. of  5 variables:
 $ variety: Factor w/ 2 levels "C","F": 1 1 1 1 1 1 1 1 1 1 ...
 $ year   : Factor w/ 1 level "18": 1 1 1 1 1 1 1 1 1 1 ...
 $ day    : Factor w/ 3 levels "11","34","67": 1 1 1 1 1 1 1 1 2 2 ...
 $ treat  : Factor w/ 2 levels "WW","WS": 2 2 2 2 1 1 1 1 2 2 ...
 $ rep    : Factor w/ 4 levels "1","2","3","4": 1 2 3 4 1 2 3 4 1 2 ...
```

Year 2019

```
> dim(pdata19)
[1] 134  21
> dim(t19)
[1] 15242    32
```

```
> pdata19 <- pdata19[colnames(t19),]
> dim(pdata19)
[1] 32 21
> dim(t19)
[1] 15242    32
> pdata19[,4:9]
            variety year day treat rep project.name
C19_22d_WS1       C   19  22    WS   1      EnViros
C19_22d_WS2       C   19  22    WS   2      EnViros
C19_22d_WS3       C   19  22    WS   3      EnViros
C19_22d_WS4       C   19  22    WS   4      EnViros
C19_22d_WW1       C   19  22    WW   1      EnViros
C19_22d_WW2       C   19  22    WW   2      EnViros
C19_22d_WW3       C   19  22    WW   3      EnViros
C19_22d_WW4       C   19  22    WW   4      EnViros
C19_44d_WS1       C   19  44    WS   1      EnViros
C19_44d_WS2       C   19  44    WS   2      EnViros
C19_44d_WS3       C   19  44    WS   3      EnViros
C19_44d_WS4       C   19  44    WS   4      EnViros
C19_44d_WW1       C   19  44    WW   1      EnViros
C19_44d_WW2       C   19  44    WW   2      EnViros
C19_44d_WW3       C   19  44    WW   3      EnViros
C19_44d_WW4       C   19  44    WW   4      EnViros
F19_22d_WS1       F   19  22    WS   1      EnViros
F19_22d_WS2       F   19  22    WS   2      EnViros
F19_22d_WS3       F   19  22    WS   3      EnViros
F19_22d_WS4       F   19  22    WS   4      EnViros
F19_22d_WW1       F   19  22    WW   1      EnViros
F19_22d_WW2       F   19  22    WW   2      EnViros
F19_22d_WW3       F   19  22    WW   3      EnViros
F19_22d_WW4       F   19  22    WW   4      EnViros
F19_44d_WS1       F   19  44    WS   1      EnViros
F19_44d_WS2       F   19  44    WS   2      EnViros
F19_44d_WS3       F   19  44    WS   3      EnViros
F19_44d_WS4       F   19  44    WS   4      EnViros
F19_44d_WW1       F   19  44    WW   1      EnViros
F19_44d_WW2       F   19  44    WW   2      EnViros
F19_44d_WW3       F   19  44    WW   3      EnViros
F19_44d_WW4       F   19  44    WW   4      EnViros
> all(rownames(pdata19)==colnames(t19))
[1] TRUE
```

Get rid of unused factors levels

```
> str(pdata19[,factors])
'data.frame':        32 obs. of  5 variables:
 $ variety: Factor w/ 2 levels "C","F": 1 1 1 1 1 1 1 1 1 1 ...
 $ year   : Factor w/ 2 levels "18","19": 2 2 2 2 2 2 2 2 2 2 ...
 $ day    : Factor w/ 26 levels "3","11","14",..: 5 5 5 5 5 5 5 5 12 12 ...
 $ treat  : Factor w/ 2 levels "WW","WS": 2 2 2 2 1 1 1 1 2 2 ...
 $ rep    : Factor w/ 4 levels "1","2","3","4": 1 2 3 4 1 2 3 4 1 2 ...
```

```
> for (var in factors) pdata19[,var] <- factor(pdata19[,var])
> str(pdata19[,factors])
'data.frame':        32 obs. of  5 variables:
 $ variety: Factor w/ 2 levels "C","F": 1 1 1 1 1 1 1 1 1 1 ...
 $ year   : Factor w/ 1 level "19": 1 1 1 1 1 1 1 1 1 1 ...
 $ day    : Factor w/ 2 levels "22","44": 1 1 1 1 1 1 1 1 2 2 ...
 $ treat  : Factor w/ 2 levels "WW","WS": 2 2 2 2 1 1 1 1 2 2 ...
 $ rep    : Factor w/ 4 levels "1","2","3","4": 1 2 3 4 1 2 3 4 1 2 ...


> t1819 <- data.frame(t18, t19)
> pdata1819 <- rbind(pdata18, pdata19)
> str(pdata1819[,factors])
'data.frame':        80 obs. of  5 variables:
 $ variety: Factor w/ 2 levels "C","F": 1 1 1 1 1 1 1 1 1 1 ...
 $ year   : Factor w/ 2 levels "18","19": 1 1 1 1 1 1 1 1 1 1 ...
 $ day    : Factor w/ 5 levels "11","34","67",..: 1 1 1 1 1 1 1 1 2 2 ...
 $ treat  : Factor w/ 2 levels "WW","WS": 2 2 2 2 1 1 1 1 2 2 ...
 $ rep    : Factor w/ 4 levels "1","2","3","4": 1 2 3 4 1 2 3 4 1 2 ...
> catln("Sample names ",
+ c("different","OK")[1+all(rownames(pdata1819)==colnames(t1819))])
Sample names  OK
```

3.6 Metabolite measurements

Normalised transcript measurements for each year are available in two separate files. The first few lines contains variable names

```
> (mfn18 <- getMeta(.adesc,"Metabolite data 18"))
[1] "/input/Metabolites_2018_raw_data.txt"
> (mfn19 <- getMeta(.adesc,"Metabolite data 19"))
[1] "/input/Metabolites_2019_raw_data.txt"
```

Read the metabolomics data

```
> m18 <- read.table(file.path(.aroot,mfn18),sep="\t",header=TRUE)
> dim(m18)
[1] 96 60
> m19 <- read.table(file.path(.aroot,mfn19),sep="\t",header=TRUE)
> dim(m19)
[1] 96 60
```

Check consistency of column names

```
> ok <- all(colnames(m18)==colnames(m19))
> if(ok) {catln("Column names match")} else {
+    catln("Column names do not match")}
Column names match
>    cbind(names18=colnames(m18),names19=colnames(m19))
      names18                 names19
 [1,] "ID"                    "ID"
 [2,] "Variety"               "Variety"
 [3,] "Date"                  "Date"
 [4,] "Treat"                 "Treat"
 [5,] "Rep"                   "Rep"
 [6,] "Alanine"               "Alanine"
 [7,] "Arabinose"             "Arabinose"
 [8,] "Ascorbic.acid"         "Ascorbic.acid"
 [9,] "Aspartic.acid"         "Aspartic.acid"
[10,] "GABA"                  "GABA"
[11,] "Trans.Caffeic.acid"    "Trans.Caffeic.acid"
[12,] "Catechin"              "Catechin"
[13,] "Citric.acid"           "Citric.acid"
[14,] "Erythronic.acid"       "Erythronic.acid"
[15,] "Ethanolamine"          "Ethanolamine"
[16,] "Fructose"              "Fructose"
[17,] "Fructose.6.phosphate"  "Fructose.6.phosphate"
[18,] "Fumaric.acid"          "Fumaric.acid"
[19,] "Galactinol"            "Galactinol"
[20,] "Galactose"             "Galactose"
[21,] "Gallic.acid"           "Gallic.acid"
[22,] "Gluconic.acid"         "Gluconic.acid"
[23,] "Glucopyranose..H20."   "Glucopyranose..H20."
[24,] "Glucose"               "Glucose"
[25,] "Glutamic.acid"         "Glutamic.acid"
[26,] "Glyceric.acid"         "Glyceric.acid"
```

```
[27,] "Glycine"                "Glycine"
[28,] "Hydroquinone"           "Hydroquinone"
[29,] "Myo.Inostol"            "Myo.Inostol"
[30,] "Isoleucine"             "Isoleucine"
[31,] "Leucine"                "Leucine"
[32,] "Lyxonic.acid"           "Lyxonic.acid"
[33,] "Maleic.acid"            "Maleic.acid"
[34,] "Malic.acid"             "Malic.acid"
[35,] "Malonic.acid"           "Malonic.acid"
[36,] "Mannose.6.phosphate"    "Mannose.6.phosphate"
[37,] "Melibiose"              "Melibiose"
[38,] "Phenylalanine"          "Phenylalanine"
[39,] "Phosphoric.acid"        "Phosphoric.acid"
[40,] "Proline"                "Proline"
[41,] "Putrescine"             "Putrescine"
[42,] "Pyroglutamic.acid"      "Pyroglutamic.acid"
[43,] "Quinic.acid"            "Quinic.acid"
[44,] "X3.caffeoylquinic.acid" "X3.caffeoylquinic.acid"
[45,] "Raffinose"              "Raffinose"
[46,] "Rhamnose"               "Rhamnose"
[47,] "Ribonic.acid"           "Ribonic.acid"
[48,] "Ribose"                 "Ribose"
[49,] "Serine"                 "Serine"
[50,] "Shikimic.acid"          "Shikimic.acid"
[51,] "Succinic.acid"          "Succinic.acid"
[52,] "Sucrose"                "Sucrose"
[53,] "Tartaric.acid"          "Tartaric.acid"
[54,] "Threitol"               "Threitol"
[55,] "Threonic.acid"          "Threonic.acid"
[56,] "Threonolactone"         "Threonolactone"
[57,] "Threonine"              "Threonine"
[58,] "Uracil"                 "Uracil"
[59,] "Valine"                 "Valine"
[60,] "Xylose"                 "Xylose"
```

Use first column as row names

```
> rownames(m18) <- m18[,1]
> rownames(m19) <- m19[,1]
```

Both years together

```
> m1819 <- rbind(m18,m19)
> dim(m1819)
[1] 192  60
> colnames(m1819)[1:7]
[1] "ID"        "Variety"   "Date"      "Treat"     "Rep"
[6] "Alanine"   "Arabinose"
> rownames(m1819) <- m1819[,1]
> head(rownames(m1819))
[1] "C18_11d_WS1" "C18_11d_WS2" "C18_11d_WS3" "C18_11d_WS4"
[5] "C18_11d_WW1" "C18_11d_WW2"
> length(rownames(m1819))
```

```
[1] 192
```

At some point, we will not need the first five descriptive columns.
Intersection of transcriptomics and metabolomics samples

```
> dim(m1819)
[1] 192  60
> dim(t1819)
[1] 15242    80
> head(colnames(t1819))
[1] "C18_11d_WS1" "C18_11d_WS2" "C18_11d_WS3" "C18_11d_WS4"
[5] "C18_11d_WW1" "C18_11d_WW2"
> head(rownames(m1819))
[1] "C18_11d_WS1" "C18_11d_WS2" "C18_11d_WS3" "C18_11d_WS4"
[5] "C18_11d_WW1" "C18_11d_WW2"
> sum(colnames(t1819) %in% rownames(m1819))
[1] 80
> sum(rownames(m1819)%in%colnames(t1819))
[1] 80
> all(sort(colnames(t1819)[(colnames(t1819) %in% rownames(m1819))]) ==
+ sort(rownames(m1819)[(rownames(m1819)%in%colnames(t1819))]))
[1] TRUE

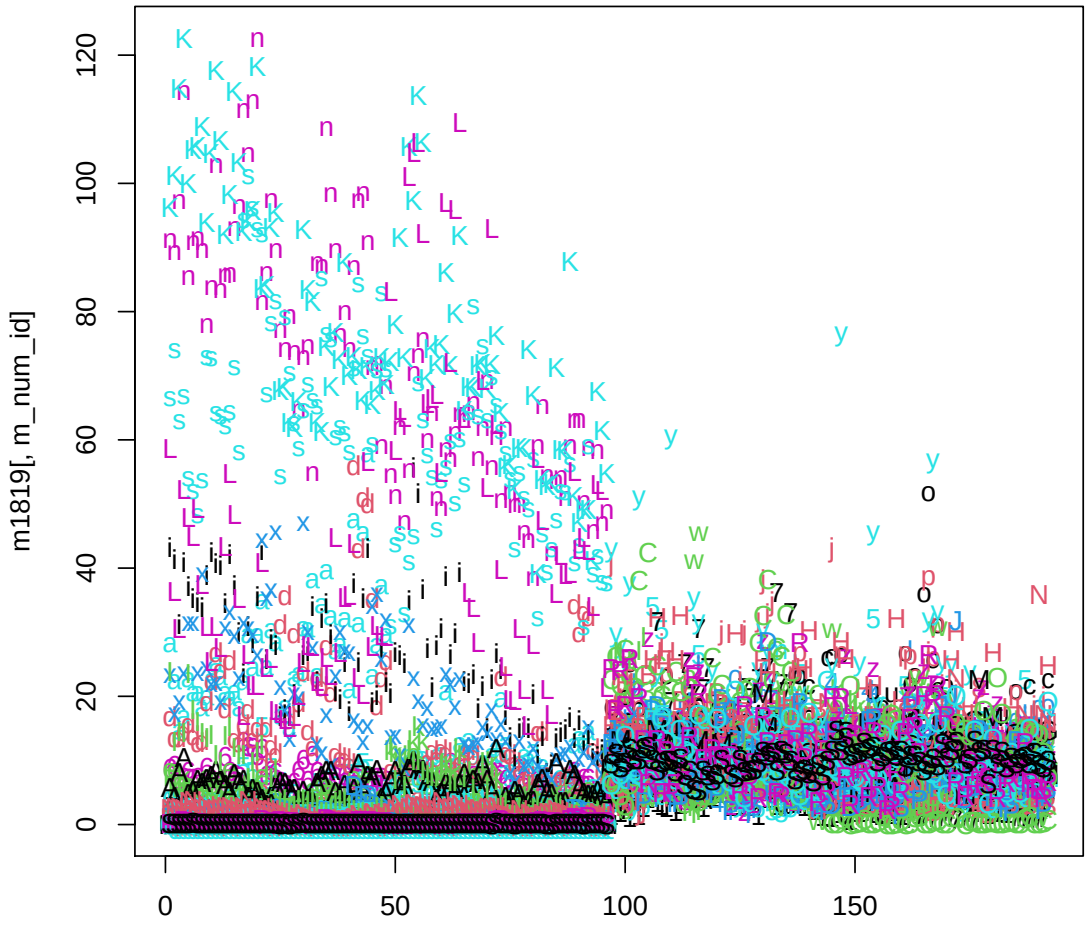

> m_num_id <- 6:ncol(m1819)
> colnames(m1819)[-m_num_id]
[1] "ID"      "Variety" "Date"    "Treat"   "Rep"
```

We end up with 80 samples

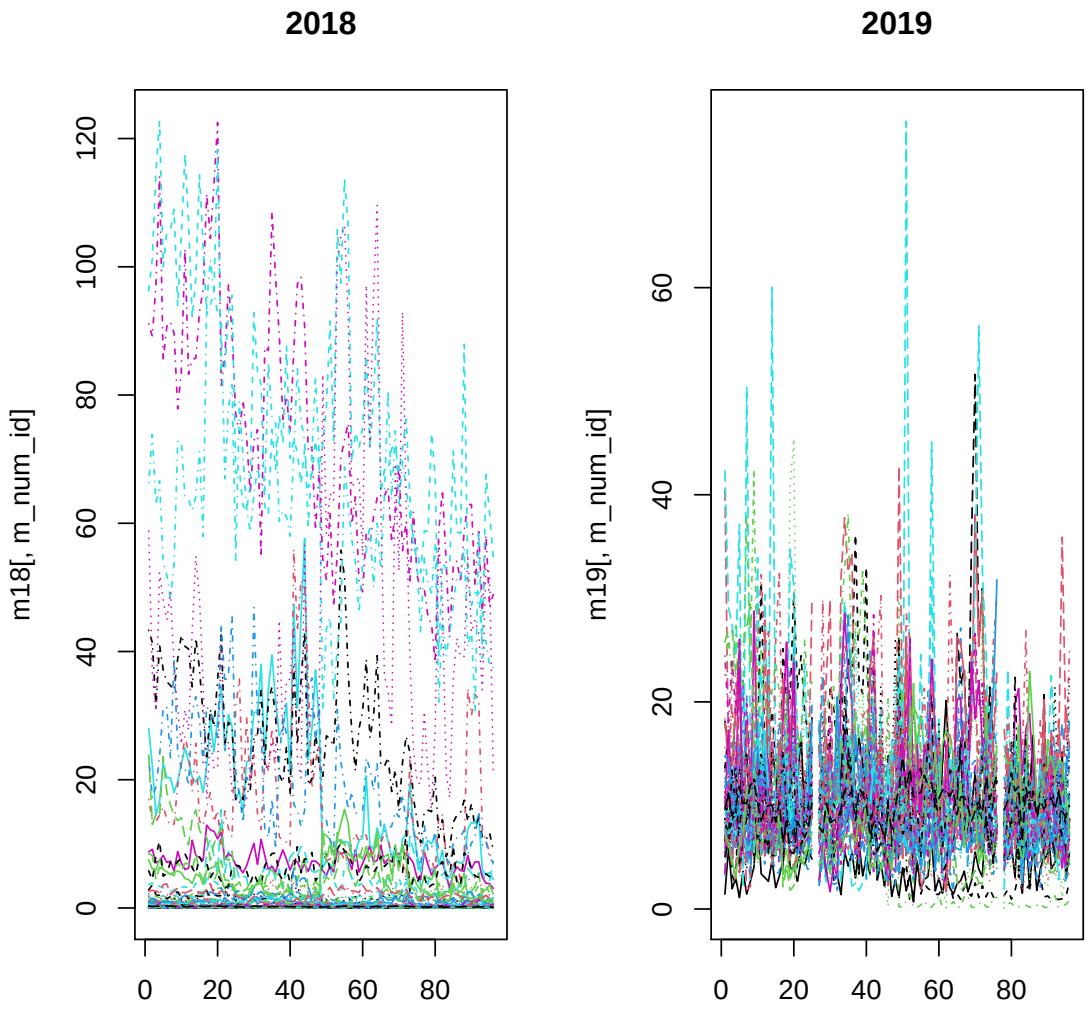
Phenodata for metabolomics data will be prepared when needed from the total phenodata. Selection of needed metabolomics data will be finalized in data analysis scripts.

3.7 Visualize metabolites

```
> matplot(m1819[,m_num_id])
```




```
> par(mfrow=c(1,2))
> matplot(m18[,m_num_id], main="2018", type="l")
> matplot(m19[,m_num_id], main="2019", type="l")
```

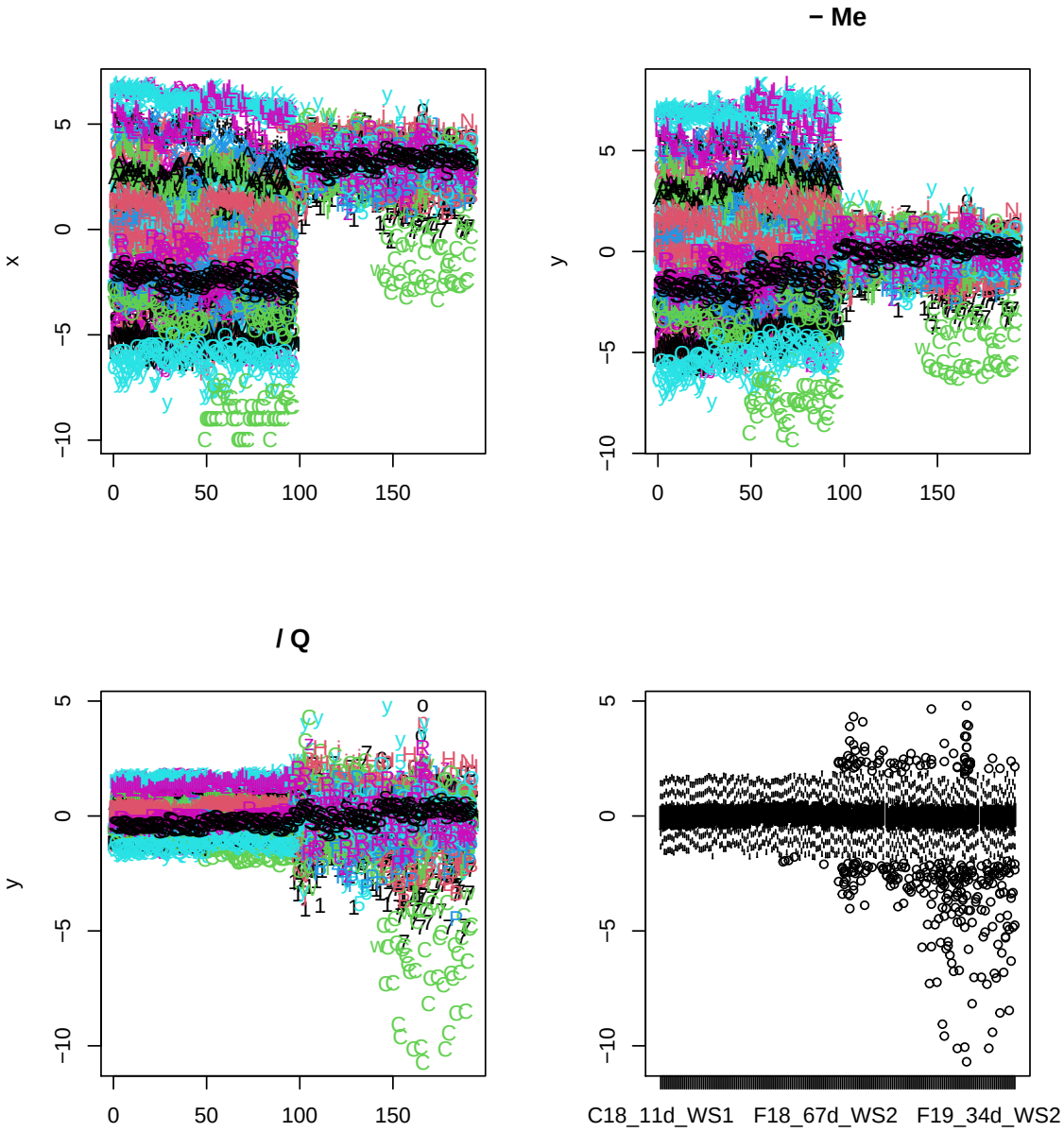


Median standardization of samples

```
> my.parallel <- function(x, m=1:ncol(x), ...){
+ m <- m[m<ncol(x)]
+ par(mar=c(4,8,3,1))
+ xlim <- range(x,na.rm=TRUE)
+ n1 <- nrow(x)
+ plot(0,0,xlim=xlim,ylim=c(n1,1) , type="n", axes=FALSE, ann=FALSE)
+ title(paste(range(m),collapse=":"))
+ axis(1)
+ axis(2,at=1:n1,labels=rownames(x), las=2)
+ box()
+ for(i in m)
+    lines(x[,i],1:n1 , col=i)
+
+ }
> #
> my.parallel(x)
Error in h(simpleError(msg, call)): error in evaluating the argument 'x' in se
```

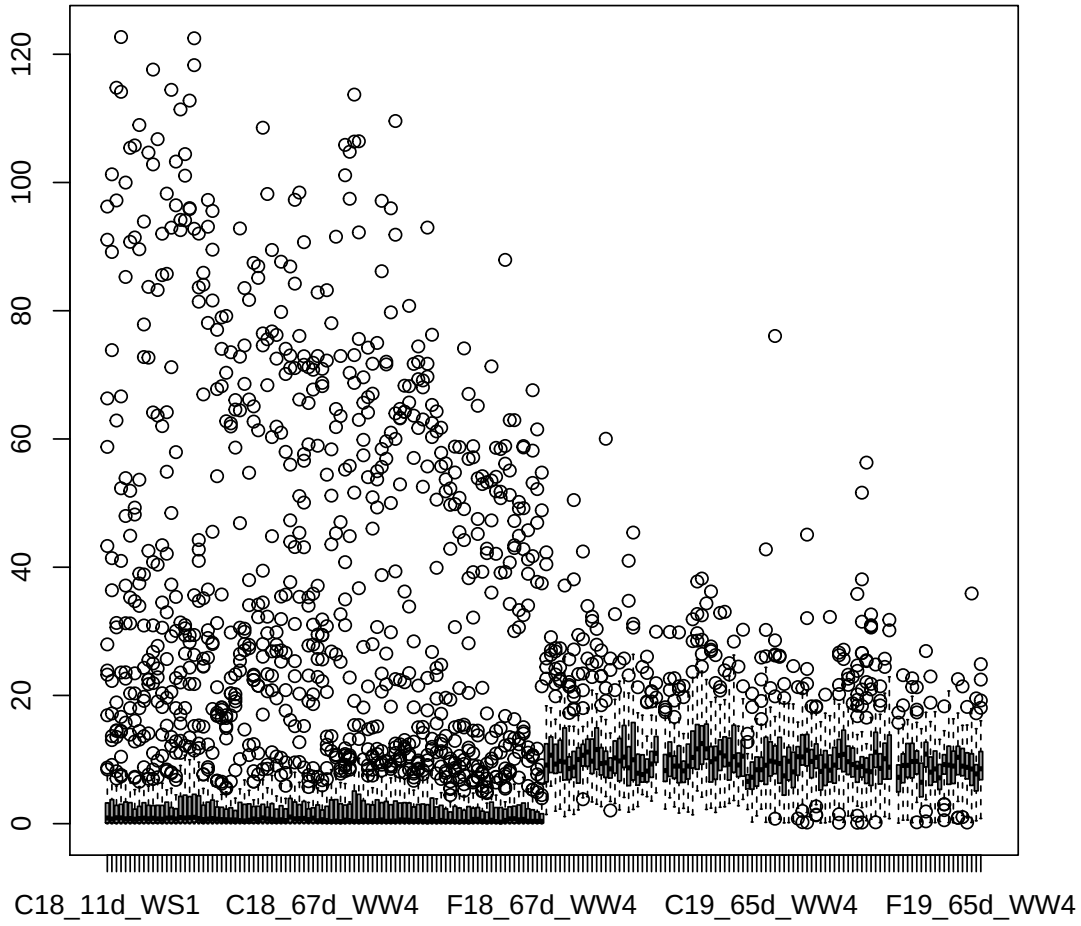
```
> for(k in seq(1,ncol(x),10)) {
+ if(interactive()) windows()
+    my.parallel( x, k:(k+9))
+ }
Error in h(simpleError(msg, call)): error in evaluating the argument 'x' in se

> par(mfrow=c(2,2))
> x <- log2(m1819[,m_num_id])
> matplot(x)
> dim(x)
[1] 192  55
> Me <- apply(x,1,median, na.rm=TRUE)
> Q <- apply(x,1,function(x) diff(quantile(x, probs=c(0.25,0.75), na.rm=TRUE))
> y <- sweep(x,1,Me)
> matplot(y, main="- Me")
> y <- sweep(y,1,Q, "/")
> matplot(y, main="/ Q")
> boxplot(t(y))
```

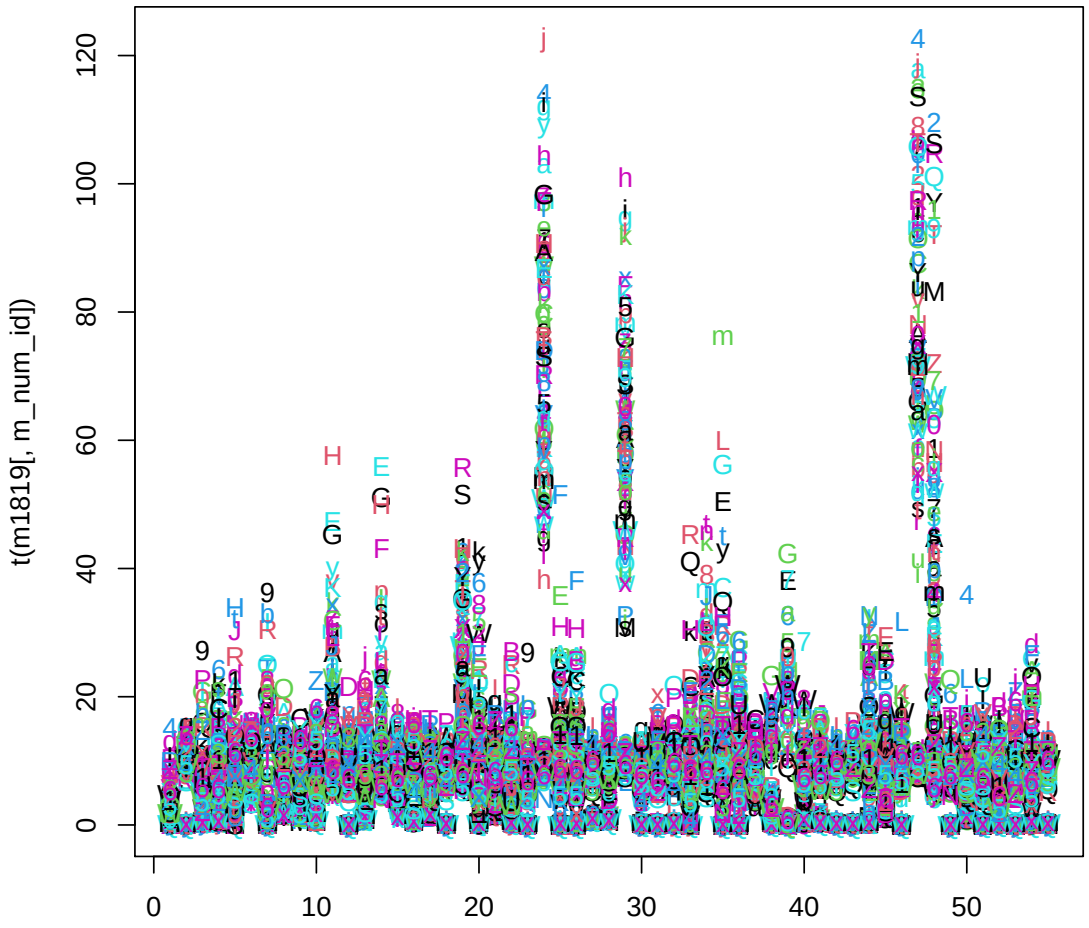


Data are highly skewed with marked differences between years

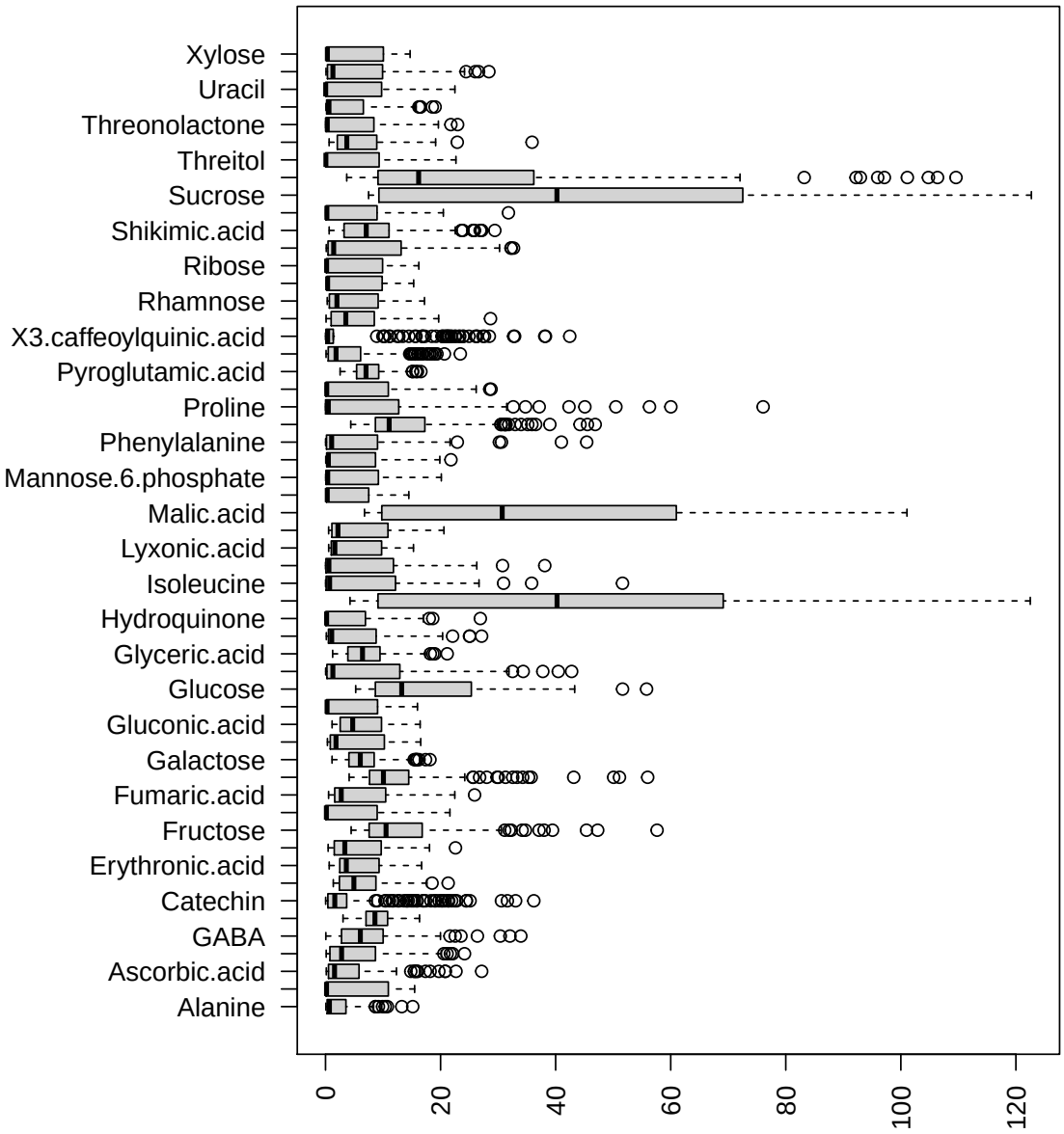
```
> boxplot(t(m1819[,m_num_id]), col=8)
```




```
> matplot(t(m1819[,m_num_id]))
Warning in matplot(t(m1819[, m_num_id])): default 'pch' is smaller than number
```



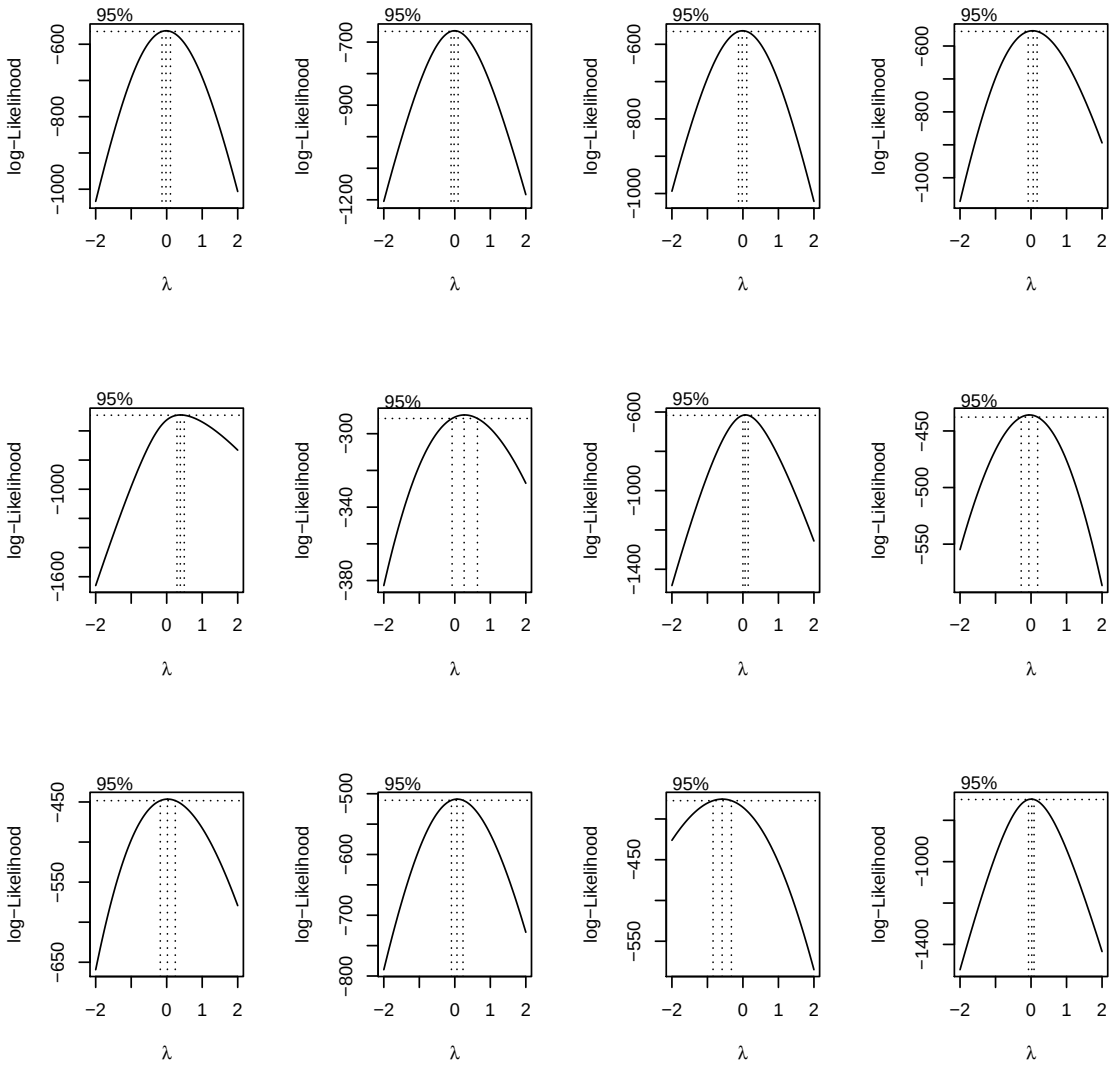

```
> par(mar=c(4,10,3,1))
> boxplot(m1819[,m_num_id], horizontal=TRUE, las=2)
```



Box-Cox transformation

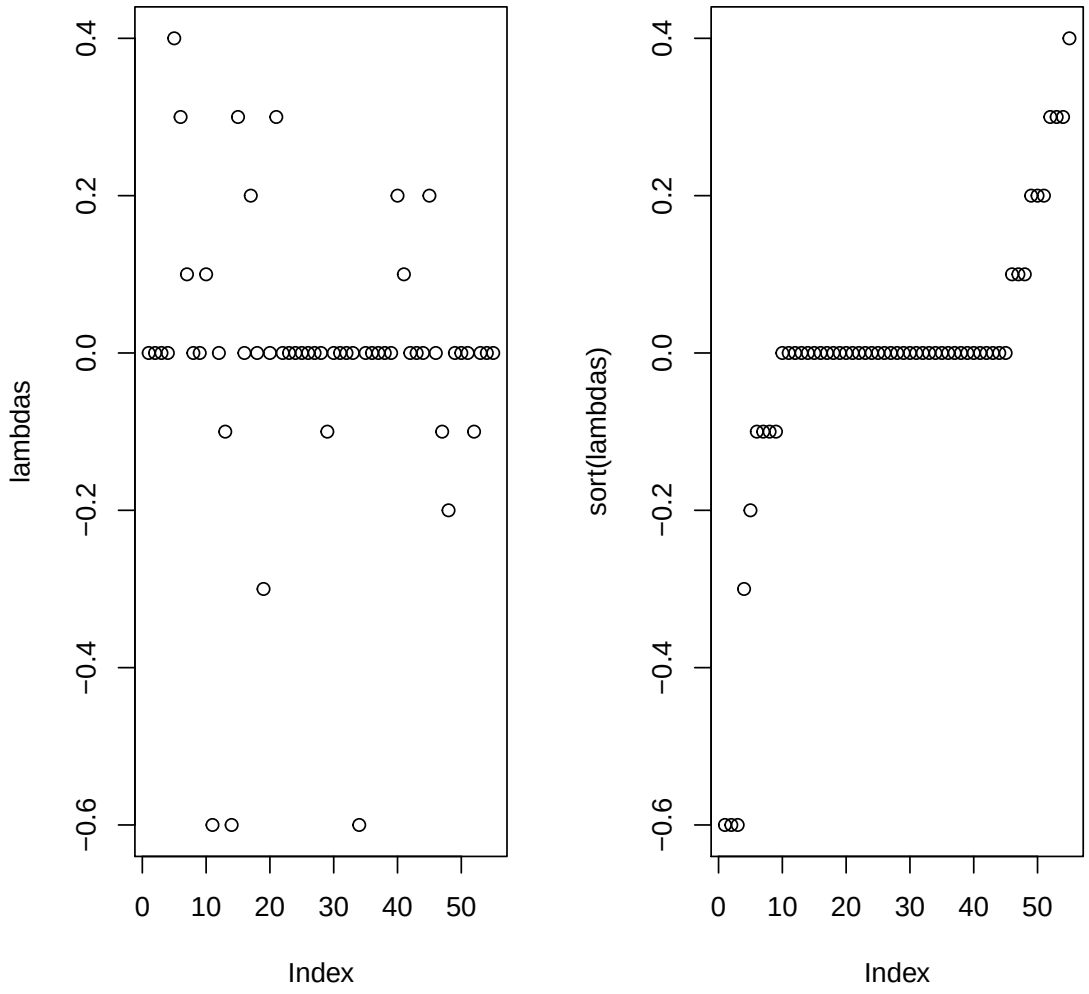
```
> library(MASS)
> par(mfrow=c(3,2))
> my.boxcox <- function(x, plotit=FALSE,...) {
+   require(MASS)
+   bc <- boxcox(x ~1, plotit=plotit, ...)
+   bc$x[which.max(bc$y)]
+   }

> par(mfrow=c(3,4))
> apply(m1819[,m_num_id[1:12] ], 2, my.boxcox , plotit=TRUE)
```



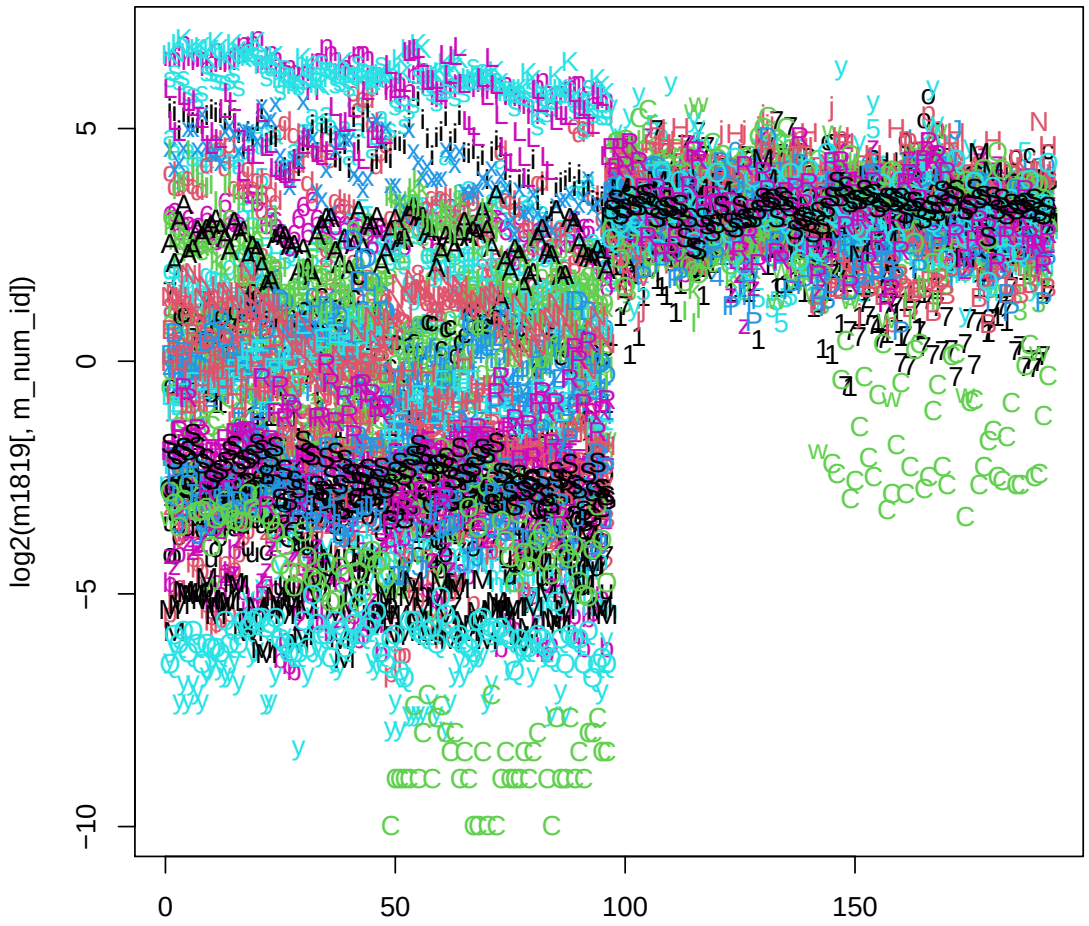

```
      Alanine      Arabinose    Ascorbic.acid
-0.02020202    -0.02020202    -0.02020202
Aspartic.acid           GABA Trans.Caffeic.acid
   0.06060606     0.38383838     0.26262626
     Catechin    Citric.acid  Erythronic.acid
   0.06060606    -0.06060606     0.02020202
Ethanolamine        Fructose Fructose.6.phosphate
   0.06060606    -0.58585859     0.02020202
```

```
> lambdas <- apply(m1819[,m_num_id ], 2, my.boxcox )
> par(mfrow=c(1,2))
> plot(lambdas)
> plot(sort(lambdas))
```



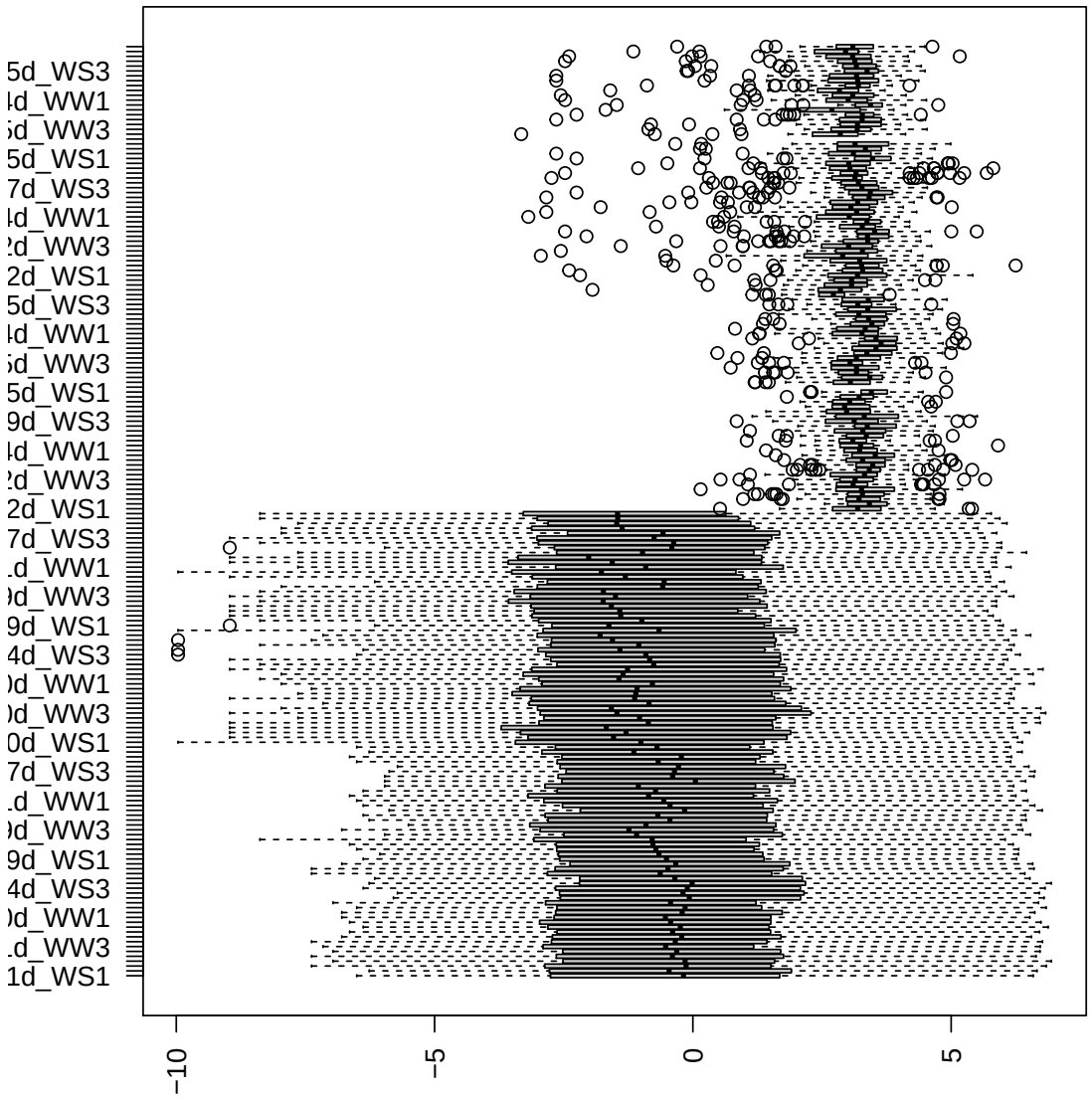
It seems that logarithm is adequate.

```
> matplot(log2(m1819[,m_num_id]))
```



Data are highly skewed with marked differences between years

```
> boxplot(t(log2(m1819[,m_num_id]))
+ , horizontal=TRUE, las=2)
```



3.8 Standardization

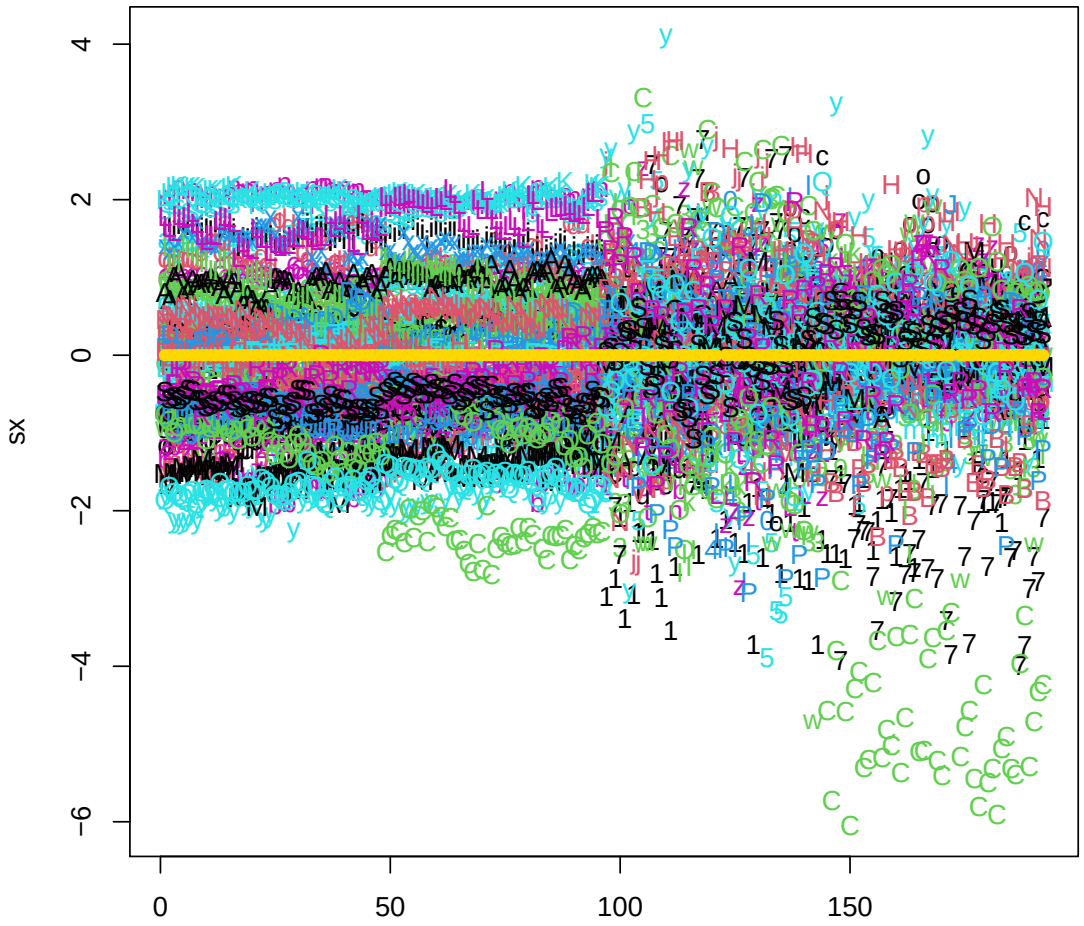
For CCA standardized values are needed

Standardization across samples

```
> x <- t(log2(m1819[,m_num_id]))
> dim(x)
```

```
[1]  55 192
```

```
> sx <- t(scale(x))
> matplot(sx)
> points(1:nrow(sx), apply(sx,1,mean, na.rm=TRUE), col="gold", pch=16)
```

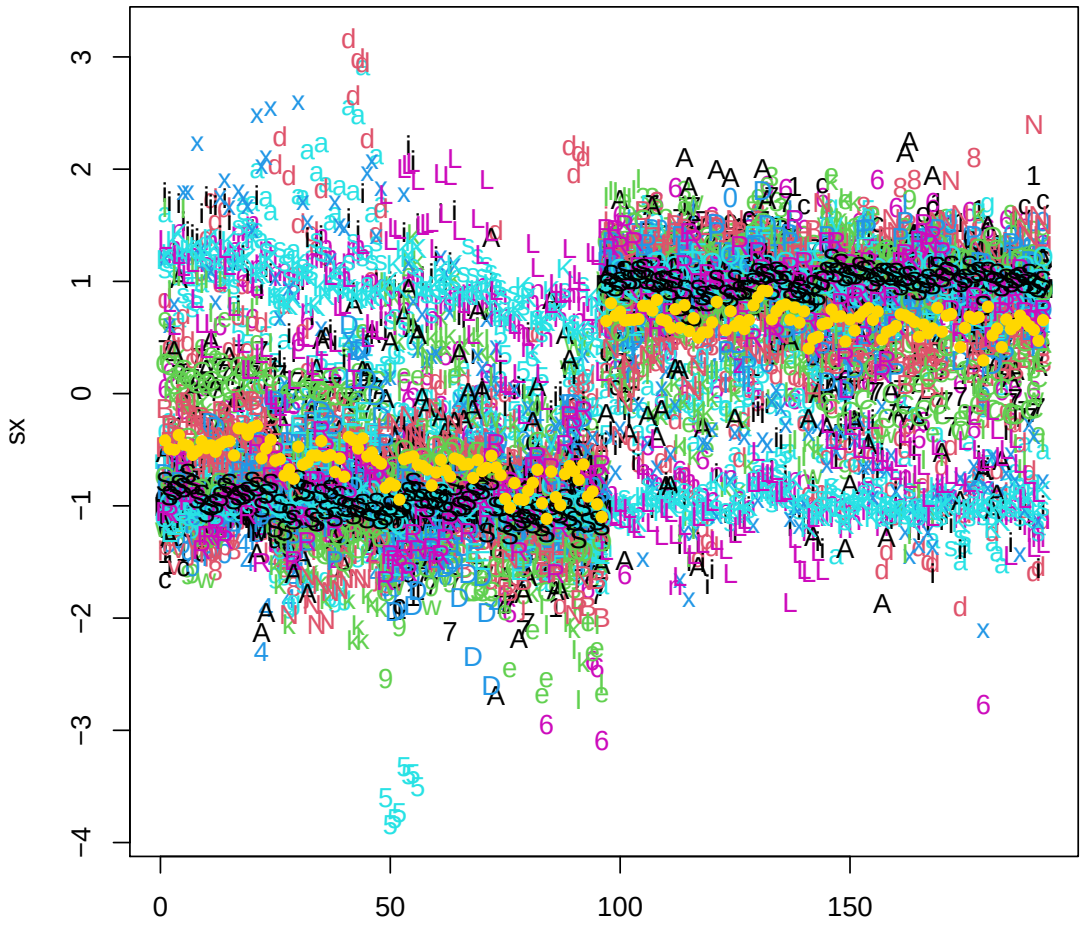



```
> head(apply(sx,1,mean, na.rm=TRUE))
  C18_11d_WS1   C18_11d_WS2   C18_11d_WS3   C18_11d_WS4   C18_11d_WW1
 3.156507e-18  2.714645e-17 -5.391442e-19  2.231091e-17  9.791331e-18
  C18_11d_WW2
-2.039877e-17
```

```
> head(apply(sx,1,sd, na.rm=TRUE))
C18_11d_WS1 C18_11d_WS2 C18_11d_WS3 C18_11d_WS4 C18_11d_WW1
          1           1           1           1           1
C18_11d_WW2
          1
```

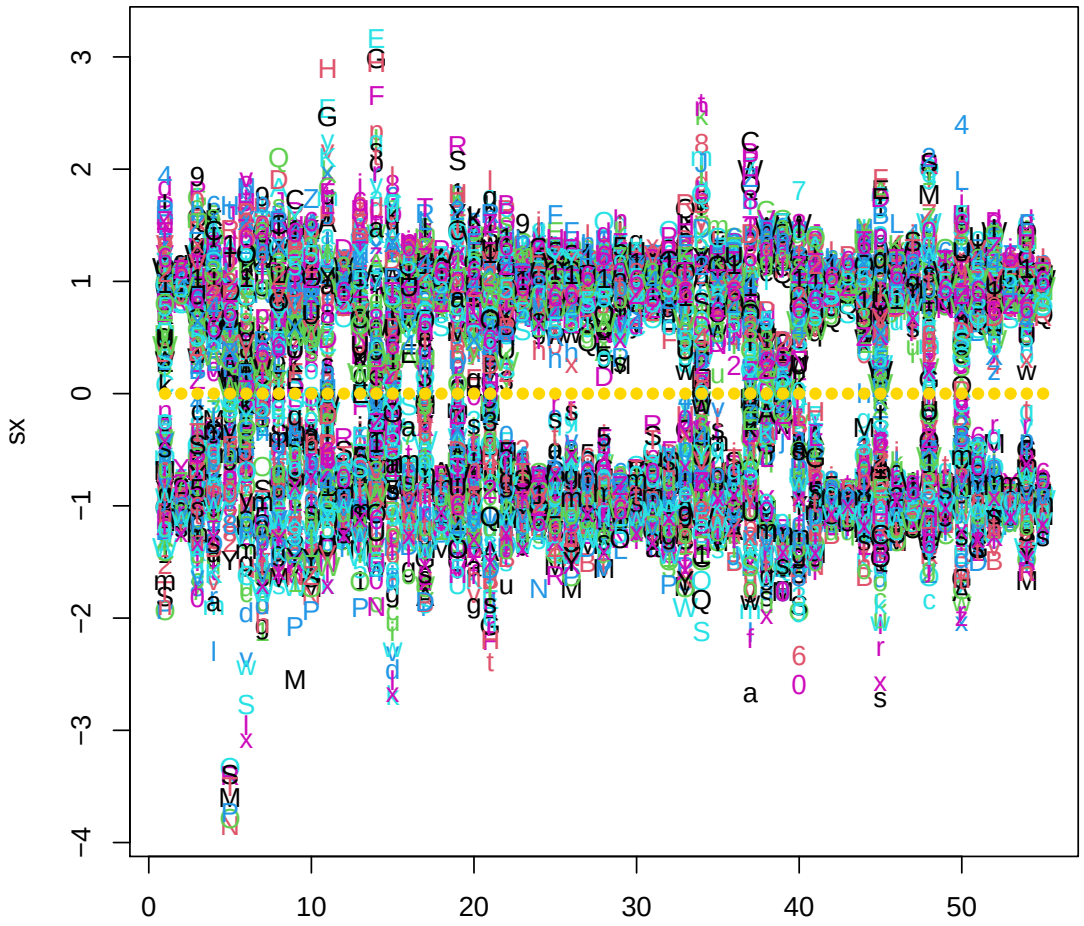
Standardization across variables

```
> x <- log2(m1819[,m_num_id])
> sx <- scale(x)
> matplot(sx)
> points(1:nrow(sx), apply(sx,1,mean, na.rm=TRUE), col="gold", pch=16)
```



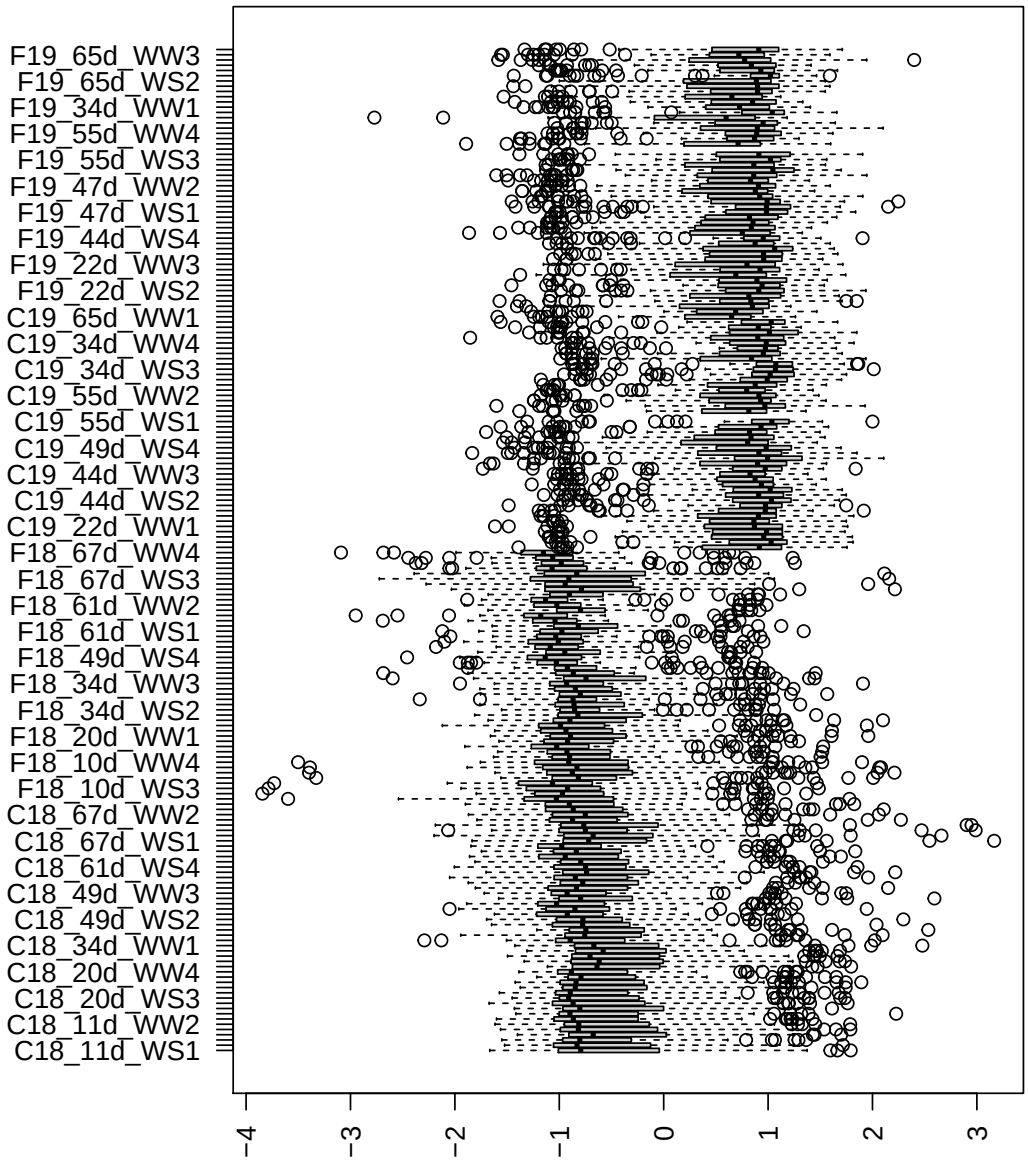

```
> head(apply(sx,2,mean, na.rm=TRUE))
          Alanine         Arabinose      Ascorbic.acid
-3.395835e-18      -1.762114e-17      -2.402592e-17
     Aspartic.acid              GABA Trans.Caffeic.acid
 4.406198e-17      -1.204206e-17       1.468649e-16
> head(apply(sx,2,sd, na.rm=TRUE))
          Alanine         Arabinose      Ascorbic.acid
                1                  1                  1
     Aspartic.acid              GABA Trans.Caffeic.acid
                1                  1                  1


> x <- log2(m1819[,m_num_id])
> sx <- t(scale(x))
> matplot(sx)
Warning in matplot(sx): default 'pch' is smaller than number of columns and he
> points(1:nrow(sx), apply(sx,1,mean, na.rm=TRUE), col="gold", pch=16)
```




```
> head(apply(sx,2,mean, na.rm=TRUE))
C18_11d_WS1 C18_11d_WS2 C18_11d_WS3 C18_11d_WS4 C18_11d_WW1
 -0.4172622  -0.4925258  -0.4993865  -0.3693033  -0.4525290
C18_11d_WW2
 -0.4644972
> head(apply(sx,2,sd, na.rm=TRUE))
C18_11d_WS1 C18_11d_WS2 C18_11d_WS3 C18_11d_WS4 C18_11d_WW1
  0.9061152   0.8297170   0.7423594   0.8131148   0.8619359
C18_11d_WW2
  0.8126080


> par(mar=c(4,10,3,1))
> boxplot(sx, horizontal=TRUE,las=2)
```




```
> sm1819 <- sx
> head(sm1819)
                   C18_11d_WS1 C18_11d_WS2 C18_11d_WS3 C18_11d_WS4
Alanine            -1.42040510  -1.5237244  -0.3221074  -0.2941971
Arabinose          -0.89096253  -0.8768234  -0.9786693  -0.9055979
Ascorbic.acid      -0.48475127  -0.3013277  -0.3439011  -0.0716600
Aspartic.acid      -0.79435180  -1.0652846  -0.9506661  -0.8422994
GABA               -0.79478369  -1.3283418  -1.0815306  -0.9112230
Trans.Caffeic.acid  0.04856765   0.1856718  -0.5986832  -0.4584358
                   C18_11d_WW1 C18_11d_WW2 C18_11d_WW3 C18_11d_WW4
Alanine             -1.4045568  -1.0312407  -0.8260696  -0.9777046
Arabinose           -0.7568413  -0.7921839  -0.9055979  -0.8982160
Ascorbic.acid       -0.5841291  -0.4705092  -0.5050201  -0.4658249
Aspartic.acid       -1.1473972  -1.0508478  -1.2872479  -1.0472819
GABA                -0.8041739  -1.0148328  -0.8827044  -1.2282093
```

```
Trans.Caffeic.acid  -0.1458728  -0.5759619  -0.4884020  -1.1855997
                   C18_20d_WS1 C18_20d_WS2 C18_20d_WS3 C18_20d_WS4
Alanine            -1.30253488  -1.1485305  -0.4301155  -0.4301155
Arabinose          -0.82156681  -0.9093384  -0.9487134  -0.8945735
Ascorbic.acid      -0.40759378  -0.3990459  -0.2193190  -0.3969249
Aspartic.acid      -0.68028375  -1.1419912  -0.7477177  -1.0665004
GABA               -0.55840143  -0.6637706  -0.8598745  -0.8432557
Trans.Caffeic.acid  0.06651981  -0.6147770  -1.0784674  -0.9712290
                   C18_20d_WW1 C18_20d_WW2 C18_20d_WW3 C18_20d_WW4
Alanine             -1.1669862  -1.1745048  -0.7070211 -0.67637466
Arabinose           -0.8733622  -0.9612891  -0.8277002 -0.96988871
Ascorbic.acid       -0.1710309  -0.3976312  -0.3309222 -0.08880282
Aspartic.acid       -0.9979629  -1.0091444  -0.8262651 -1.22149861
GABA                -0.9178608  -0.9071634  -0.5883746 -0.86516407
Trans.Caffeic.acid   0.6097629  -0.1444223  -0.2703104 -0.43635765
                   C18_34d_WS1 C18_34d_WS2 C18_34d_WS3 C18_34d_WS4
Alanine             -0.6524125  -0.7493615  -0.5607169 -0.65060226
Arabinose           -0.8434404  -0.9285614  -0.8803135 -0.90559788
Ascorbic.acid       -0.3934041  -0.3618092  -0.4391011 -0.57954495
Aspartic.acid       -0.5681871  -1.3362907  -1.4955004 -1.23969930
GABA                 0.5383838   0.6785329   0.4481893  0.08421358
Trans.Caffeic.acid   1.2085257   1.0325340   0.9791050  0.67184120
                   C18_34d_WW1 C18_34d_WW2 C18_34d_WW3 C18_34d_WW4
Alanine             -0.4938681  -0.7208561 -0.57357704 -0.17365428
Arabinose           -0.8499066  -1.0407476 -0.92464525 -0.84666098
Ascorbic.acid       -0.8649740  -0.2872844 -0.49847064 -0.57499031
Aspartic.acid       -0.8642301  -2.2922701 -1.90683969 -0.97716973
GABA                 0.9929407   0.1022634  0.51365512 -0.08629024
Trans.Caffeic.acid   0.9342980  -0.3488723 -0.05127649 -0.20189133
                   C18_49d_WS1 C18_49d_WS2 C18_49d_WS3 C18_49d_WS4
Alanine             -0.2726324 -0.35831179 -0.58173446 -0.61190189
Arabinose           -1.0255800 -0.92856138 -0.94871336 -1.00617809
Ascorbic.acid       -0.6890378 -0.72067394 -0.74913040 -0.77756970
Aspartic.acid       -1.4783807 -1.33979505 -1.52418769 -1.82838040
GABA                 0.2730391 -0.05768882  0.01397647 -0.01902277
Trans.Caffeic.acid  -0.7596655 -0.95833043 -1.34574708 -0.80549633
                   C18_49d_WW1 C18_49d_WW2 C18_49d_WW3 C18_49d_WW4
Alanine            -0.78777647  -0.8640990  -0.8123175 -1.01596046
Arabinose          -1.02557995  -0.7674005  -0.9246452 -0.82770022
Ascorbic.acid      -0.63168277  -0.9822666  -1.0052447 -0.84341555
Aspartic.acid      -1.64349297  -1.5802398  -1.4372280 -1.68141186
GABA               -0.89011882  -0.3070515  -0.2091395 -0.03424594
Trans.Caffeic.acid -0.09552259   0.4665606  -0.6970157  0.64777629
                   C18_61d_WS1 C18_61d_WS2 C18_61d_WS3 C18_61d_WS4
Alanine             -0.3989935 -0.48953135  -0.9199530  -0.8991309
Arabinose           -1.0014654 -0.95705493  -0.9698887  -1.0061781
Ascorbic.acid       -0.8649740 -1.07533485  -1.2382552  -1.0429323
Aspartic.acid       -0.5700590 -0.60196936  -0.3984122  -0.5020430
GABA                 0.2573183  0.03096133   0.2921707  -0.1017523
Trans.Caffeic.acid  -0.1502284 -1.07152665  -0.8442359  -1.2882030
                   C18_61d_WW1 C18_61d_WW2 C18_61d_WW3 C18_61d_WW4
Alanine             -0.6973013  -0.7109465  -1.3993516  -1.2173427
Arabinose           -0.8499066  -0.9365057  -0.9169216  -1.0841181
```

Ascorbic.acid	-0.5713676	-0.4823576	-0.8554612	-0.7584837
Aspartic.acid	-0.9913337	-1.3720993	-1.0616491	-1.3328028
GABA	0.1848340	-0.3855115	0.1932726	0.4195016
Trans.Caffeic.acid	-0.4069089	0.1514097	-0.3879618	-1.1184425
	C18_67d_WS1	C18_67d_WS2	C18_67d_WS3	C18_67d_WS4
Alanine	-0.2683969	-0.2996921	-1.0099392	-0.9834577
Arabinose	-1.0511748	-0.9405354	-0.9968055	-0.9528633
Ascorbic.acid	-1.2546783	-0.9234174	-0.9445333	-1.0808826
Aspartic.acid	-0.6752302	-0.7219964	-0.8849168	-0.8531840
GABA	0.4999725	0.4293145	0.5888935	0.5085247
Trans.Caffeic.acid	-0.4596448	-0.5297954	-1.1254938	-0.6948336
	C18_67d_WW1	C18_67d_WW2	C18_67d_WW3	C18_67d_WW4
Alanine	-0.4668387	-0.4710387	-1.1412804	-1.1164723
Arabinose	-0.9876388	-1.0109446	-0.8665250	-0.9786693
Ascorbic.acid	-0.8663435	-1.2546783	-1.4019136	-0.9969523
Aspartic.acid	-1.0472819	-0.7572957	-1.6023971	-1.0592352
GABA	0.2650833	0.1418167	0.1148187	0.1764576
Trans.Caffeic.acid	-1.2192354	-0.4762171	-0.4916597	-0.7092651
	F18_10d_WS1	F18_10d_WS2	F18_10d_WS3	F18_10d_WS4
Alanine	-0.6801339	-0.7855869	-1.9290988	-1.9182512
Arabinose	-1.1325277	-1.0673212	-0.9921970	-1.0784436
Ascorbic.acid	-0.6795006	-0.6763499	-0.5668652	-0.8368111
Aspartic.acid	-0.2260179	-0.5146942	-0.4114244	-0.6291963
GABA	-3.5975121	-3.8432554	-3.7854179	-3.7311978
Trans.Caffeic.acid	-1.1712269	-1.5566942	-0.8241195	-1.2690901
	F18_10d_WW1	F18_10d_WW2	F18_10d_WW3	F18_10d_WW4
Alanine	-1.0189903	-1.11647226	-1.80872651	-1.7554137
Arabinose	-0.8982160	-0.91311277	-0.83080109	-0.9093384
Ascorbic.acid	-0.4550139	-0.59525382	-0.45348288	-0.3399824
Aspartic.acid	-0.3429779	-0.32748229	-0.32433165	-0.2883839
GABA	-3.3285334	-3.39726159	-3.38836674	-3.5016458
Trans.Caffeic.acid	0.1091013	-0.06183566	0.02982272	-0.3442159
	F18_20d_WS1	F18_20d_WS2	F18_20d_WS3	F18_20d_WS4
Alanine	-0.3989935	-0.4367744	-1.3639455	-1.1707356
Arabinose	-1.0511748	-0.9968055	-0.9968055	-0.6679676
Ascorbic.acid	-0.8704679	-0.8677156	-1.0607502	-0.9838834
Aspartic.acid	-0.6151265	-0.5961236	-1.0437330	-0.9611546
GABA	-0.8901188	-0.9636402	-0.8109439	-0.8724295
Trans.Caffeic.acid	-1.0670733	0.1618934	-1.2775696	-0.6335214
	F18_20d_WW1	F18_20d_WW2	F18_20d_WW3	F18_20d_WW4
Alanine	-0.8689990	-0.6915326	-1.1199637	-1.2054012
Arabinose	-1.0728454	-1.0157662	-1.0014654	-0.9246452
Ascorbic.acid	-0.7206739	-0.6879717	-0.8315716	-1.3566288
Aspartic.acid	-0.8019896	-0.8716862	-0.9696531	-0.7143743
GABA	-1.4867876	-1.1085653	-0.6976926	-0.5317253
Trans.Caffeic.acid	-0.1044514	0.3399237	-0.5600763	-0.4463728
	F18_34d_WS1	F18_34d_WS2	F18_34d_WS3	F18_34d_WS4
Alanine	-1.14853050	-1.00100193	-1.1164723	-1.1975502
Arabinose	-1.00146544	-1.01094460	-0.9612891	-0.9285614
Ascorbic.acid	-0.77035196	-0.80594079	-0.8447439	-1.0052447
Aspartic.acid	-0.08906787	-0.47296796	-0.3583326	-0.6157905
GABA	-0.71172267	-0.08786346	-0.4482032	-0.7101077
Trans.Caffeic.acid	0.38304173	-0.64636973	-0.3687437	-0.5260834

	F18_34d_WW1	F18_34d_WW2	F18_34d_WW3	F18_34d_WW4
Alanine	-0.798826516	-0.6763747	-0.9468693	-0.7966027
Arabinose	-0.786547801	-1.0618693	-1.0673212	-0.8597980
Ascorbic.acid	-1.754522307	-1.7216172	-1.6112704	-1.8200162
Aspartic.acid	-0.139533413	-0.3959358	-0.9190598	0.1918374
GABA	-0.832505609	-1.1659845	-0.9086835	-0.7763030
Trans.Caffeic.acid	-0.007332999	-0.0951660	0.1746206	-0.1098216
	F18_49d_WS1	F18_49d_WS2	F18_49d_WS3	F18_49d_WS4
Alanine	-0.8813990	-0.9359801	-0.8689990	-0.6839132
Arabinose	-1.0459286	-1.1016199	-1.0511748	-1.1729203
Ascorbic.acid	-1.2523087	-1.4287209	-1.6685424	-1.3649018
Aspartic.acid	-1.8737376	-0.5322996	-0.9362259	-0.8877828
GABA	0.7166446	0.5230477	0.3452471	-0.3126450
Trans.Caffeic.acid	-0.2820581	-0.6232825	-1.7938439	-1.9520321
	F18_49d_WW1	F18_49d_WW2	F18_49d_WW3	F18_49d_WW4
Alanine	-1.20935940	-1.2054012	-0.9359801	-1.08247037
Arabinose	-1.02064421	-1.1455620	-1.0564878	-0.97425592
Ascorbic.acid	-1.29874782	-0.6455914	-1.1911571	-1.22903904
Aspartic.acid	-0.81750417	-1.1487549	-1.0091444	-0.90130513
GABA	-0.15176956	-0.2414255	0.2016299	0.03950059
Trans.Caffeic.acid	0.03460538	-0.6957063	-1.5433162	-0.96405620
	F18_61d_WS1	F18_61d_WS2	F18_61d_WS3	F18_61d_WS4
Alanine	-1.34929542	-0.93868678	-0.6763747	-0.7309058
Arabinose	-1.23369161	-1.13899393	-1.1016199	-1.1590169
Ascorbic.acid	-1.26906519	-1.31406969	-1.3704714	-1.4888883
Aspartic.acid	-0.21430282	-0.19480061	-0.7851219	-0.9990735
GABA	-0.02029638	0.05699739	0.1523252	-0.5607751
Trans.Caffeic.acid	-0.70269666	-0.52361129	-1.5901101	-2.9498706
	F18_61d_WW1	F18_61d_WW2	F18_61d_WW3	F18_61d_WW4
Alanine	-1.6822688	-1.9075667	-1.2014648	-0.5559537
Arabinose	-1.0898708	-1.1590169	-1.1137095	-1.0109446
Ascorbic.acid	-1.2666470	-1.3270964	-1.2475931	-1.1634985
Aspartic.acid	-0.3489890	-0.8849168	-0.5813898	-0.6058921
GABA	-0.5567099	-0.4547891	-0.1848092	-0.3841255
Trans.Caffeic.acid	-1.4116358	-0.8760588	-1.1559043	-1.2052175
	F18_67d_WS1	F18_67d_WS2	F18_67d_WS3	F18_67d_WS4
Alanine	-1.2335835	-1.11996369	-0.50409137	-0.87641303
Arabinose	-1.1590169	-1.06732124	-1.20985284	-1.13899393
Ascorbic.acid	-1.5124122	-1.74023228	-1.03245310	-1.07717926
Aspartic.acid	-0.5406601	-0.93929677	-1.34862878	-0.87168620
GABA	0.2083702	0.09671283	-0.02981653	0.09527977
Trans.Caffeic.acid	-0.1524087	-0.99816120	-0.53930272	-0.52649560
	F18_67d_WW1	F18_67d_WW2	F18_67d_WW3	F18_67d_WW4
Alanine	-0.68771273	-0.8145911	-0.9120730	-0.4301155
Arabinose	-1.05648778	-1.0957039	-1.1198884	-1.2589760
Ascorbic.acid	-1.44717412	-1.6434274	-1.3931989	-1.3403676
Aspartic.acid	-1.06407077	-0.9600991	-0.9869468	-1.2856130
GABA	0.09272624	-0.1293893	-0.1176987	0.3447692
Trans.Caffeic.acid	-1.74127656	-2.3749262	-2.4456161	-3.0910196
	C19_22d_WS1	C19_22d_WS2	C19_22d_WS3	C19_22d_WS4
Alanine	0.2720501	1.2824603	0.4910994	0.7887854
Arabinose	1.0854730	1.1410463	0.9948382	1.0441785
Ascorbic.acid	0.5077076	1.2996969	0.4546839	0.2179557

Aspartic.acid	1.3002167	1.0138284	1.1871125	1.3693923
GABA	-0.3652211	0.4540044	0.5683581	0.2222463
Trans.Caffeic.acid	-0.9856266	1.0291158	0.2102271	1.5825560
	C19_22d_WW1	C19_22d_WW2	C19_22d_WW3	C19_22d_WW4
Alanine	0.08711792	0.9289745	0.2769671	0.7027119
Arabinose	1.14132150	1.0867292	1.0819988	1.0329153
Ascorbic.acid	0.34494184	0.6917733	0.9890956	0.5804620
Aspartic.acid	1.34162557	0.9135394	1.5509238	1.1114018
GABA	0.64266257	0.4196112	0.1871306	-0.4626375
Trans.Caffeic.acid	-1.61556947	0.1286776	0.2005584	1.4285608
	C19_44d_WS1	C19_44d_WS2	C19_44d_WS3	C19_44d_WS4
Alanine	1.0050069	1.589722	0.8824669	0.8029488
Arabinose	0.9092302	1.045219	0.8819613	1.0608565
Ascorbic.acid	1.7487219	1.213896	1.7487219	1.2801920
Aspartic.acid	1.2843338	1.096224	0.8750735	0.8839919
GABA	0.6856613	1.682973	0.4508374	1.5866186
Trans.Caffeic.acid	0.5475100	-0.466101	0.3607963	1.7095972
	C19_44d_WW1	C19_44d_WW2	C19_44d_WW3	C19_44d_WW4
Alanine	0.7107403	1.1125188	0.5264551	0.8304556
Arabinose	0.9789026	1.0213394	0.9797140	1.0146840
Ascorbic.acid	1.3785054	1.5556943	1.1228496	0.8010254
Aspartic.acid	0.5339921	0.4810936	0.5672792	0.7640104
GABA	0.9245993	0.7243169	0.6443564	0.6443564
Trans.Caffeic.acid	-0.0908902	0.3851661	0.3851661	1.8388831
	C19_49d_WS1	C19_49d_WS2	C19_49d_WS3	C19_49d_WS4
Alanine	1.1079692	1.675464089	0.9633604	1.0067634
Arabinose	1.0791345	1.012816267	0.9252369	0.9817356
Ascorbic.acid	1.2854461	1.809587711	1.5636868	1.5389760
Aspartic.acid	0.7460909	1.178805258	1.0565169	0.6814897
GABA	0.8617421	0.610714821	0.1885628	1.4648404
Trans.Caffeic.acid	-0.6882969	-0.006640693	0.8659242	1.6067934
	C19_49d_WW1	C19_49d_WW2	C19_49d_WW3	C19_49d_WW4
Alanine	0.71074026	1.1125188	1.0460089	1.2458283
Arabinose	0.99717689	1.0124417	0.8214110	0.9321080
Ascorbic.acid	0.90241827	1.2196641	1.3575459	1.3054450
Aspartic.acid	0.31834284	0.5886717	0.4672602	0.2384083
GABA	-0.07535686	0.7774375	0.5169933	0.6246747
Trans.Caffeic.acid	-0.26690844	-0.5856183	0.9473843	1.5784971
	C19_55d_WS1	C19_55d_WS2	C19_55d_WS3	C19_55d_WS4
Alanine	1.13043165	NA	0.7368647	1.3240626
Arabinose	1.00602230	NA	0.9631780	0.9302867
Ascorbic.acid	1.24018846	NA	0.8036164	1.5086137
Aspartic.acid	1.02271128	NA	0.5452540	0.4323224
GABA	0.12780899	NA	0.2139473	0.7509098
Trans.Caffeic.acid	0.04142443	NA	0.8400033	1.3308596
	C19_55d_WW1	C19_55d_WW2	C19_55d_WW3	C19_55d_WW4
Alanine	0.7982590	1.37285782	0.7394250	0.8590999
Arabinose	1.0044974	1.05004056	0.8995193	1.0094331
Ascorbic.acid	0.5606877	0.34246432	1.0371665	0.8126107
Aspartic.acid	0.7681648	1.38403013	0.7178225	0.3695937
GABA	0.2586393	0.05583074	0.2625903	0.2612753
Trans.Caffeic.acid	0.3821308	1.00950745	1.0943552	1.5252216
	C19_34d_WS1	C19_34d_WS2	C19_34d_WS3	C19_34d_WS4

Alanine	0.24694130	1.22934840	1.0223795	1.2124772
Arabinose	1.02861189	0.99795354	1.0978681	1.0697692
Ascorbic.acid	1.23528856	0.98710311	1.1843270	1.2239597
Aspartic.acid	1.59074795	1.67071566	1.2894944	1.1576225
GABA	-0.54863624	0.21948879	0.1726762	-0.6823219
Trans.Caffeic.acid	0.02434738	-0.04495894	0.9624127	1.8518783
	C19_34d_WW1	C19_34d_WW2	C19_34d_WW3	C19_34d_WW4
Alanine	0.7959024	1.3206873	0.8393928	1.1621430
Arabinose	0.9833459	1.0224384	1.0187638	0.9825415
Ascorbic.acid	1.9365717	1.7099495	1.6531531	1.6213218
Aspartic.acid	0.5939251	0.4991472	0.7524648	0.4901751
GABA	-0.5968286	-0.8836893	-0.5587401	-0.5320537
Trans.Caffeic.acid	0.3423869	0.6044133	0.9448722	1.8220911
	C19_65d_WS1	C19_65d_WS2	C19_65d_WS3	C19_65d_WS4
Alanine	0.86981662	1.84944595	0.7419762	1.0656555
Arabinose	1.04521895	0.98495000	0.9097098	1.0195013
Ascorbic.acid	0.97299630	1.11206313	0.6856887	0.9439095
Aspartic.acid	0.85322328	1.30526880	0.5577232	0.8354587
GABA	1.20433121	1.36540008	0.7150083	1.2007751
Trans.Caffeic.acid	-0.03445944	-0.05549566	1.0847800	1.4646504
	C19_65d_WW1	C19_65d_WW2	C19_65d_WW3	C19_65d_WW4
Alanine	0.57960166	1.1992211	0.1542540	0.7520903
Arabinose	0.91257627	0.9516337	0.9516337	0.9998889
Ascorbic.acid	0.29366343	0.6826267	0.1969294	0.5945038
Aspartic.acid	0.64083931	0.2913310	0.4547444	0.5225574
GABA	0.42942294	0.3428547	0.7803355	0.5515722
Trans.Caffeic.acid	0.05840396	0.4894964	1.1884487	1.7482095
	F19_22d_WS1	F19_22d_WS2	F19_22d_WS3	F19_22d_WS4
Alanine	0.08711792	0.9961587	0.4105789	0.8525914
Arabinose	1.13438644	1.1432428	1.0531110	1.1503027
Ascorbic.acid	0.62177779	1.1895916	1.5380609	0.8049083
Aspartic.acid	1.60434969	1.4023739	1.3957151	1.2718004
GABA	0.21255637	0.7219991	0.8669941	0.1028955
Trans.Caffeic.acid	-0.08377750	0.3730062	0.2262719	1.4200051
	F19_22d_WW1	F19_22d_WW2	F19_22d_WW3	F19_22d_WW4
Alanine	-0.25067245	1.1049198	0.48746506	0.7570939
Arabinose	1.10483199	1.0571701	1.13911481	1.1481431
Ascorbic.acid	0.51357764	1.1659735	1.29195938	0.8389273
Aspartic.acid	0.90840960	1.0901997	1.22675356	0.9621851
GABA	-0.07535686	0.1871306	0.07887073	-0.4872417
Trans.Caffeic.acid	0.10543713	0.5475100	0.46005943	1.5231533
	F19_44d_WS1	F19_44d_WS2	F19_44d_WS3	F19_44d_WS4
Alanine	0.8259444	1.36442444	0.4105789	0.7887854
Arabinose	0.9563756	1.06681937	1.0033500	1.0531110
Ascorbic.acid	1.0591295	0.39506053	0.6300897	0.8339895
Aspartic.acid	1.5709259	1.53408190	1.3305144	1.2103491
GABA	1.0629968	1.63329752	0.8199230	1.1475028
Trans.Caffeic.acid	0.1120958	0.09542104	0.7068967	1.9051184
	F19_44d_WW1	F19_44d_WW2	F19_44d_WW3	F19_44d_WW4
Alanine	0.3104650	0.9131409	0.5264551	0.2720501
Arabinose	1.0674767	0.9913054	0.9402066	1.0835816
Ascorbic.acid	0.3399781	1.3168030	1.0202349	0.5289969
Aspartic.acid	0.7535218	0.7825253	0.5820523	0.7671283

GABA	0.2922977	0.8397348	0.4971698	0.5866357
Trans.Caffeic.acid	0.2358574	0.8400033	0.8555830	1.6566622
	F19_47d_WS1	F19_47d_WS2	F19_47d_WS3	F19_47d_WS4
Alanine	0.643819879	0.7265299	0.9328784	0.3730656
Arabinose	0.984549552	0.9116230	0.9627561	1.0794538
Ascorbic.acid	1.115399611	0.7228861	1.1011096	0.3740144
Aspartic.acid	1.477155992	1.3310010	1.4589479	0.9228533
GABA	1.292014347	1.2231993	0.6742929	0.7583604
Trans.Caffeic.acid	0.003724593	-0.3049282	1.2275540	1.3725035
	F19_47d_WW1	F19_47d_WW2	F19_47d_WW3	F19_47d_WW4
Alanine	0.7317161	1.2241998	0.9726240	0.8168353
Arabinose	0.9361769	0.9849500	0.9813321	0.9572320
Ascorbic.acid	0.6560497	0.8189660	0.7945062	1.0390231
Aspartic.acid	1.0408838	1.2011413	0.9541606	0.9278849
GABA	0.5430559	0.2331895	0.8136814	0.3185607
Trans.Caffeic.acid	-0.3982098	-0.2518356	0.8736566	1.7018142
	F19_55d_WS1	F19_55d_WS2	F19_55d_WS3	F19_55d_WS4
Alanine	1.7003494	1.5492019	1.0656555	1.4966108
Arabinose	0.9158957	0.8689514	1.0228041	0.9063406
Ascorbic.acid	0.4589067	0.4132566	0.5892707	0.9831012
Aspartic.acid	1.4023739	0.8633176	0.8401748	0.2913310
GABA	1.2175382	1.1873084	1.0482528	1.0795457
Trans.Caffeic.acid	0.1940951	-0.5026811	1.1038997	1.5560739
	F19_55d_WW1	F19_55d_WW2	F19_55d_WW3	F19_55d_WW4
Alanine	NA	1.52169511	1.1245108	1.3070234
Arabinose	NA	0.80939103	0.9252369	1.0154288
Ascorbic.acid	NA	0.54221849	0.6749130	0.5839986
Aspartic.acid	NA	1.03800586	0.5978411	1.0093469
GABA	NA	1.01689035	0.9091511	0.8908794
Trans.Caffeic.acid	NA	0.09207483	1.2548512	1.6208412
	F19_34d_WS1	F19_34d_WS2	F19_34d_WS3	F19_34d_WS4
Alanine	0.7982590	1.6432584	0.3151241	1.4455128
Arabinose	1.0848435	1.0064027	0.8057164	1.0476367
Ascorbic.acid	0.5661358	0.8642997	0.5327998	1.1518890
Aspartic.acid	1.0621212	1.1758158	1.1823768	0.7629681
GABA	0.2922977	0.3688149	-0.1252694	0.5893444
Trans.Caffeic.acid	-0.3087571	0.1843738	-2.7709424	1.4709739
	F19_34d_WW1	F19_34d_WW2	F19_34d_WW3	F19_34d_WW4
Alanine	0.4910994	1.3318766	0.43059441	0.9799488
Arabinose	0.9861490	0.8855325	0.95422686	1.0601886
Ascorbic.acid	0.8853459	1.1605295	0.70080322	0.6480391
Aspartic.acid	0.5686344	0.6518175	0.34440911	0.4841331
GABA	0.6644284	0.4412663	0.06907130	0.3917591
Trans.Caffeic.acid	0.5503812	0.4511712	0.02434738	1.5478779
	F19_65d_WS1	F19_65d_WS2	F19_65d_WS3	F19_65d_WS4
Alanine	1.1691569	1.54838383	0.9781247	1.0816225
Arabinose	1.0406913	1.10960874	0.9669562	1.0242637
Ascorbic.acid	0.3015962	0.13316265	1.0240327	0.4243959
Aspartic.acid	0.5899885	0.95818365	1.0365627	0.8839919
GABA	0.9511372	0.90352165	1.3277535	0.9911842
Trans.Caffeic.acid	-0.1922971	0.04142443	1.0315578	1.5293538
	F19_65d_WW1	F19_65d_WW2	F19_65d_WW3	F19_65d_WW4
Alanine	1.2280647	1.94458838	0.7767631	1.2137893

```
Arabinose             0.8850242  0.94065190   0.9388677   1.1084197
Ascorbic.acid         0.4958194  0.22090909   0.5057401   0.8487006
Aspartic.acid         1.0962240  0.77537968   0.4531650   0.5873525
GABA                  0.7258587  0.61510148   0.7196751   0.7304676
Trans.Caffeic.acid    0.6324617  0.02434738   1.2751610   1.3898648
```

3.9 Featuredata for metabolites

!!! Rows in featuredata and columns of metabolite data ARE in the same order !!!

```
> (fmfn <- getMeta(.adesc, "Featuredata metabolites"))
[1] "Featuredata_metabolites_210127.txt"
> mfdata <- read.table(file.path(.iroot,fmfn), sep="\t", header=TRUE)
> cbind(rownames(sm1819), make.names(mfdata[,1]), mfdata[,1])
      [,1]                    [,2]
 [1,] "Alanine"               "Alanine"
 [2,] "Arabinose"             "Arabinose"
 [3,] "Ascorbic.acid"         "Ascorbic.acid"
 [4,] "Aspartic.acid"         "Aspartic.acid"
 [5,] "GABA"                  "GABA"
 [6,] "Trans.Caffeic.acid"    "Trans.Caffeic.acid"
 [7,] "Catechin"              "Catechin"
 [8,] "Citric.acid"           "Citric.acid"
 [9,] "Erythronic.acid"       "Erythronic.acid"
[10,] "Ethanolamine"          "Ethanolamine"
[11,] "Fructose"              "Fructose"
[12,] "Fructose.6.phosphate"  "Fructose.6.phosphate"
[13,] "Fumaric.acid"          "Fumaric.acid"
[14,] "Galactinol"            "Galactinol"
[15,] "Galactose"             "Galactose"
[16,] "Gallic.acid"           "Gallic.acid"
[17,] "Gluconic.acid"         "Gluconic.acid"
[18,] "Glucopyranose..H20."   "Glucopyranose..H20."
[19,] "Glucose"               "Glucose"
[20,] "Glutamic.acid"         "Glutamic.acid"
[21,] "Glyceric.acid"         "Glyceric.acid"
[22,] "Glycine"               "Glycine"
[23,] "Hydroquinone"          "Hydroquinone"
[24,] "Myo.Inostol"           "Myo.Inostol"
[25,] "Isoleucine"            "Isoleucine"
[26,] "Leucine"               "Leucine"
[27,] "Lyxonic.acid"          "Lyxonic.acid"
[28,] "Maleic.acid"           "Maleic.acid"
[29,] "Malic.acid"            "Malic.acid"
[30,] "Malonic.acid"          "Malonic.acid"
[31,] "Mannose.6.phosphate"   "Mannose.6.phosphate"
[32,] "Melibiose"             "Melibiose"
[33,] "Phenylalanine"         "Phenylalanine"
[34,] "Phosphoric.acid"       "Phosphoric.acid"
[35,] "Proline"               "Proline"
[36,] "Putrescine"            "Putrescine"
```

```
[37,] "Pyroglutamic.acid"      "Pyroglutamic.acid"
[38,] "Quinic.acid"            "Quinic.acid"
[39,] "X3.caffeoylquinic.acid" "X3.caffeoylquinic.acid"
[40,] "Raffinose"              "Raffinose"
[41,] "Rhamnose"               "Rhamnose"
[42,] "Ribonic.acid"           "Ribonic.acid"
[43,] "Ribose"                 "Ribose"
[44,] "Serine"                 "Serine"
[45,] "Shikimic.acid"          "Shikimic.acid"
[46,] "Succinic.acid"          "Succinic.acid"
[47,] "Sucrose"                "Sucrose"
[48,] "Tartaric.acid"          "Tartaric.acid"
[49,] "Threitol"               "Threitol"
[50,] "Threonic.acid"          "Threonic.acid"
[51,] "Threonolactone"         "Threonolactone"
[52,] "Threonine"              "Threonine"
[53,] "Uracil"                 "Uracil"
[54,] "Valine"                 "Valine"
[55,] "Xylose"                 "Xylose"
      [,3]
 [1,] "Alanine"
 [2,] "Arabinose"
 [3,] "Ascorbic acid"
 [4,] "Aspartic acid"
 [5,] "GABA"
 [6,] "Trans-Caffeic acid"
 [7,] "Catechin"
 [8,] "Citric acid"
 [9,] "Erythronic acid"
[10,] "Ethanolamine"
[11,] "Fructose"
[12,] "Fructose-6-phosphate"
[13,] "Fumaric acid"
[14,] "Galactinol"
[15,] "Galactose"
[16,] "Gallic acid"
[17,] "Gluconic acid"
[18,] "Glucopyranose[-H20]"
[19,] "Glucose"
[20,] "Glutamic acid"
[21,] "Glyceric acid"
[22,] "Glycine"
[23,] "Hydroquinone"
[24,] "Myo-Inostol"
[25,] "Isoleucine"
[26,] "Leucine"
[27,] "Lyxonic acid"
[28,] "Maleic acid"
[29,] "Malic acid"
[30,] "Malonic acid"
[31,] "Mannose-6-phosphate"
[32,] "Melibiose"
[33,] "Phenylalanine"
```

```
[34,] "Phosphoric acid"
[35,] "Proline"
[36,] "Putrescine"
[37,] "Pyroglutamic acid"
[38,] "Quinic acid"
[39,] "3-caffeoylquinic acid"
[40,] "Raffinose"
[41,] "Rhamnose"
[42,] "Ribonic acid"
[43,] "Ribose"
[44,] "Serine"
[45,] "Shikimic acid"
[46,] "Succinic acid"
[47,] "Sucrose"
[48,] "Tartaric acid"
[49,] "Threitol"
[50,] "Threonic acid"
[51,] "Threonolactone"
[52,] "Threonine"
[53,] "Uracil"
[54,] "Valine"
[55,] "Xylose"
```

```
> all(rownames(sm1819)== make.names(mfdata[,1]))
```

```
[1] TRUE
```

```
> rownames(mfdata) <- make.names(mfdata[,1])
> # to be sure, that the fdata rows are in the same order as data
> mfdata <- mfdata[rownames(sm1819),]
> head(mfdata)
```

```
                          Metabolite           Bin
Alanine                      Alanine        5.1001
Arabinose                  Arabinose     10.6.1001
Ascorbic.acid          Ascorbic acid     17.5.1001
Aspartic.acid          Aspartic acid 13.1.1.2.1001
GABA                           GABA       22.1002
Trans.Caffeic.acid Trans-Caffeic acid   16.2.1.1006

Alanine
Arabinose                                                                cell wall
Ascorbic.acid                                                          hormone metabol
Aspartic.acid      amino acid metabolism.synthesis.central amino acid metaboli
GABA                                                                           pol
Trans.Caffeic.acid               secondary metabolism.phenylpropanoids.lignin
```

3.10 Interesting bins

For Canonical Correlation Analysis (CCA) we will need to restrict te number of genes (and metabolites) to those that are of more interest. The Mapman bins of interest are provided in the file (at the investigation layer).

List of bins for metabolite and transcripts:

```
> (bfn <- getMeta(adesc,"Interesting bins"))
[1] "Bin selection.csv"
> bindata <- read.table(file.path(.iroot,bfn), sep="\t", header=TRUE,dec="$")
> head(bindata)
  bin                              description
1 1.2                    PS.photorespiration
2 1.3                        PS.calvin cycle
3 2.1         major CHO metabolism.synthesis
4 2.2       major CHO metabolism.degradation
5 3.1 minor CHO metabolism.raffinose family.
6 3.3          minor CHO metabolism.sugar alcohols
> str(bindata)
'data.frame':   22 obs. of  2 variables:
 $ bin        : chr  "1.2" "1.3" "2.1" "2.2" ...
 $ description: chr  "PS.photorespiration" "PS.calvin cycle" "major CHO metabo
```

At some point, the transcripts and metabolites that correspond to the bins of interest (including the sub-bins) will be selected. Let us try to find them for the first bin:

```
> bindata$bin
 [1] "1.2"   "1.3"   "2.1"   "2.2"   "3.1"   "3.3"   "3.4"   "3.99" "5"
[10] "6"     "8.1"   "10.6" "11"    "12.2" "13.1" "16.1" "16.2" "16.8"
[19] "17.5" "21"    "22"    "23"
> paste0("^",bindata$bin[1])
[1] "^1.2"
> ind <- grep(paste0("^",bindata$bin[1]),fdata$BINCODE)
> ind
 [1]  396   596  1785  1786  1882  1953  2240  2749  2817  2856  6436
[12]  6438  6439  7892  7894  8114  8161  8530  8627  8992  9343 15061
[23] 16469 16736
> fdata[ind,2:3]
              geneID BINCODE
396   Vitvi07g03141   1.2.1
596   Vitvi01g00157 1.2.4.4
1785  Vitvi02g00436   1.2.6
1786  Vitvi02g00437   1.2.6
1882  Vitvi02g00572     1.2
1953  Vitvi02g00680 1.2.4.4
2240  Vitvi03g00154   1.2.6
2749  Vitvi03g01231 1.2.4.4
2817  Vitvi04g00063   1.2.5
2856  Vitvi04g00112 1.2.4.1
6436  Vitvi07g01511   1.2.5
6438  Vitvi07g02608   1.2.5
6439  Vitvi07g02610   1.2.5
7892  Vitvi09g01499   1.2.2
7894  Vitvi09g01500   1.2.2
8114  Vitvi09g00358   1.2.6
8161  Vitvi09g00439   1.2.7
8530  Vitvi10g00078 1.2.4.2
8627  Vitvi10g00223   1.2.1
8992  Vitvi10g00829   1.2.2
9343  Vitvi11g00186 1.2.4.1
15061 Vitvi18g00560   1.2.5
16469 Vitvi19g01352   1.2.2
16736 Vitvi07g02607   1.2.5
```

3.10.1 Genes in bins of interest

```
> intgenes <- sapply(bindata$bin, function(x) fdata$geneID[grep(paste0("^",x),
> str(intgenes)
List of 22
 $ 1.2 : chr [1:24] "Vitvi07g03141" "Vitvi01g00157" "Vitvi02g00436" "Vitvi02g0
 $ 1.3 : chr [1:33] "Vitvi01g00086" "Vitvi01g00360" "Vitvi01g01058" "Vitvi02g0
 $ 2.1 : chr [1:29] "Vitvi02g00250" "Vitvi03g00304" "Vitvi05g00442" "Vitvi05g0
 $ 2.2 : chr [1:53] "Vitvi02g01845" "Vitvi01g00025" "Vitvi01g00052" "Vitvi01g0
 $ 3.1 : chr [1:16] "Vitvi10g02295" "Vitvi00g01259" "Vitvi01g00714" "Vitvi05g0
 $ 3.3 : chr [1:3] "Vitvi11g01277" "Vitvi16g01858" "Vitvi16g00929"
 $ 3.4 : chr [1:6] "Vitvi01g00140" "Vitvi03g00287" "Vitvi07g01777" "Vitvi09g00
 $ 3.99: chr(0)
 $ 5   : chr [1:22] "Vitvi01g00787" "Vitvi04g01402" "Vitvi04g01668" "Vitvi06g0
 $ 6   : chr [1:9] "Vitvi07g03070" "Vitvi00g01243" "Vitvi00g01382" "Vitvi03g00
 $ 8.1 : chr [1:36] "Vitvi07g03070" "Vitvi01g00274" "Vitvi01g00861" "Vitvi01g0
 $ 10.6: chr [1:57] "Vitvi07g02990" "Vitvi01g00593" "Vitvi01g00708" "Vitvi01g0
 $ 11  : chr [1:251] "Vitvi02g01774" "Vitvi07g02896" "Vitvi02g01724" "Vitvi02g
 $ 12.2: chr [1:12] "Vitvi01g00175" "Vitvi05g00403" "Vitvi07g00187" "Vitvi07g0
 $ 13.1: chr [1:134] "Vitvi07g03049" "Vitvi00g00869" "Vitvi02g01749" "Vitvi01g
 $ 16.1: chr [1:83] "Vitvi10g02269" "Vitvi02g00020" "Vitvi02g00034" "Vitvi02g0
 $ 16.2: chr [1:33] "Vitvi07g03081" "Vitvi07g03083" "Vitvi01g02214" "Vitvi01g0
 $ 16.8: chr [1:71] "Vitvi10g02185" "Vitvi01g00556" "Vitvi01g02009" "Vitvi01g0
 $ 17.5: chr [1:53] "Vitvi02g01780" "Vitvi10g02409" "Vitvi01g00481" "Vitvi01g0
 $ 21  : chr [1:134] "Vitvi10g02216" "Vitvi04g02274" "Vitvi01g00023" "Vitvi01g
 $ 22  : chr [1:8] "Vitvi01g00739" "Vitvi01g00789" "Vitvi03g00054" "Vitvi06g01
 $ 23  : chr [1:123] "Vitvi01g00048" "Vitvi01g00115" "Vitvi01g00201" "Vitvi01g

> nn <- t(t(sapply(intgenes,length)))
> nn
     [,1]
1.2    24
1.3    33
2.1    29
2.2    53
3.1    16
3.3     3
3.4     6
3.99    0
5      22
6       9
8.1    36
10.6   57
11    251
12.2   12
13.1  134
16.1   83
16.2   33
16.8   71
17.5   53
21    134
22      8
23    123
```

```
> # unlist(intgenes)
> head(fdata[fdata[,"geneID"]%in% unlist(intgenes),2:3], 10)
           geneID    BINCODE
35  Vitvi02g01774   11.9.4.3
38  Vitvi02g01780     17.5.2
43  Vitvi07g02896     11.1.7
80  Vitvi02g01724   11.9.4.2
103 Vitvi07g02990     10.6.1
126 Vitvi10g02185   16.8.3.1
139 Vitvi07g03081  16.2.1.10
142 Vitvi07g03070        6.3
143 Vitvi07g03070      8.1.9
159 Vitvi07g03049 13.1.6.1.1
> tail(fdata[fdata[,"geneID"]%in% unlist(intgenes),2:3], 10)
             geneID    BINCODE
16883 Vitvi16g01457   16.8.2.1
16886 Vitvi16g01461   16.8.2.1
16887 Vitvi16g01465   16.8.2.1
16888 Vitvi16g01467   16.8.2.1
16890 Vitvi16g01469   16.8.2.1
16891 Vitvi16g01484   16.8.2.1
16897 Vitvi17g00109      23.2
16907 Vitvi18g00124   16.2.1.3
16915 Vitvi18g00759      16.2
16930 Vitvi19g02064 2.2.2.1.2
> length(unique(unlist(intgenes)))
[1] 1183
```

Number of interesting genes: 1183.

3.10.2 Metabolites in bins of interest

```
> intmtbs <- sapply(bindata$bin, function(x) rownames(mfdata)[grep(paste0("^",
> str(intmtbs)
List of 22
 $ 1.2 : chr [1:3] "Glyceric.acid" "Glycine" "Serine"
 $ 1.3 : chr "Fructose.6.phosphate"
 $ 2.1 : chr "Sucrose"
 $ 2.2 : chr [1:2] "Fructose" "Glucose"
 $ 3.1 : chr [1:2] "Galactinol" "Raffinose"
 $ 3.3 : chr "Threitol"
 $ 3.4 : chr "Myo.Inostol"
 $ 3.99: chr [1:3] "Erythronic.acid" "Galactose" "Xylose"
 $ 5   : chr "Alanine"
 $ 6   : chr [1:2] "Citric.acid" "Malic.acid"
 $ 8.1 : chr [1:2] "Fumaric.acid" "Succinic.acid"
 $ 10.6: chr [1:5] "Arabinose" "Melibiose" "Rhamnose" "Ribonic.acid" ...
 $ 11  : chr "Ethanolamine"
 $ 12.2: chr "Glutamic.acid"
 $ 13.1: chr [1:8] "Aspartic.acid" "Isoleucine" "Leucine" "Phenylalanine" ...
 $ 16.1: chr "Hydroquinone"
 $ 16.2: chr [1:4] "Trans.Caffeic.acid" "Gallic.acid" "Quinic.acid" "X3.caffeo
 $ 16.8: chr "Catechin"
 $ 17.5: chr "Ascorbic.acid"
 $ 21  : chr [1:3] "Mannose.6.phosphate" "Pyroglutamic.acid" "Threonic.acid"
 $ 22  : chr [1:2] "GABA" "Putrescine"
 $ 23  : chr "Uracil"
```

```
> nn <- t(t(sapply(intmtbs,length)))
> nn
      [,1]
1.2      3
1.3      1
2.1      1
2.2      2
3.1      2
3.3      1
3.4      1
3.99     3
5        1
6        2
8.1      2
10.6     5
11       1
12.2     1
13.1     8
16.1     1
16.2     4
16.8     1
17.5     1
21       3
22       2
23       1
> # unlist(intmtbs)
> head(mfdata[unlist(intmtbs),2:3], 10)
                            Bin
Glyceric.acid          1.2.1001
Glycine                1.2.1002
Serine                 1.2.1006
Fructose.6.phosphate   1.3.1002
Sucrose              2.1.1.1006
Fructose             2.2.1.1001
Glucose              2.2.1.1002
Galactinol             3.1.1001
Raffinose              3.1.1002
Threitol               3.3.1011
                                                        Description
Glyceric.acid                              PS.photorespiration.glycerate
Glycine                                      PS.photorespiration.glycine
Serine                                        PS.photorespiration.serine
Fructose.6.phosphate                PS.calvin cycle.fructose 6-phosphate
Sucrose                  major CHO metabolism.synthesis.sucrose.sucrose
Fructose               major CHO metabolism.degradation.sucrose.fructose
Glucose                 major CHO metabolism.degradation.sucrose.glucose
Galactinol              minor CHO metabolism.raffinose family.galactinol
Raffinose                minor CHO metabolism.raffinose family.raffinose
Threitol                    minor CHO metabolism.sugar alcohols.threitol
> tail(mfdata[unlist(intmtbs),2:3], 10)
```

```
                                Bin
Quinic.acid            16.2.99.1044
X3.caffeoylquinic.acid 16.2.99.1008
Catechin                16.8.7.1001
Ascorbic.acid             17.5.1001
Mannose.6.phosphate         21.1009
Pyroglutamic.acid           21.1010
Threonic.acid               21.1011
GABA                        22.1002
Putrescine                  22.1003
Uracil                     23.2.1002

Quinic.acid                  secondary metabolism.phenylpropanoids.unspecified
X3.caffeoylquinic.acid secondary metabolism.phenylpropanoids.unspecified.3-caf
Catechin                                secondary metabolism.flavonoids.flavan 3
Ascorbic.acid                                      hormone metabolism.ethyle
Mannose.6.phosphate                                                   redox
Pyroglutamic.acid                                                  redox.p
Threonic.acid                                                         red
GABA                                                          polyamine met
Putrescine                                                polyamine metabolis
Uracil                                                nucleotide metabolism.degrad
```

```
> length(unique(unlist(intmtbs)))
```

```
[1] 47
```

3.11 Created objects overview

```
> #if(!exists("addObject")) {
> addObject <- function(x=NULL,desc="",x0=my.objects){
+ if(is.null(x)) x0 <- data.frame(name="",description="",class="", nrow=NA,ncc
+ nr <- length(x)
+ nc <- ncol(x)
+ if(is.data.frame(x)|is.matrix(x)|is.array(x) ) {
+     nr <- nrow(x)
+     nc <- ncol(x)
+     }
+ if(is.null(nc)) nc <- NA
+ x0 <- rbind(x0,c(deparse(substitute(x)), desc, class(x)[1], nr, nc))
+ x0 <- x0[x0$name!="",]
+ }
+ rownames(x0) <- 1:nrow(x0)
+ return(x0)
+ }
> #}


> (my.objects <- addObject())
  name description class nrow ncol
1                          NA   NA
> (my.objects <- addObject(t18,"Transcripts for 2018"))
  name          description      class  nrow ncol
1  t18 Transcripts for 2018 data.frame 15242   48
> (my.objects <- addObject(t19,"Transcripts for 2019"))
  name          description      class  nrow ncol
1  t18 Transcripts for 2018 data.frame 15242   48
2  t19 Transcripts for 2019 data.frame 15242   32
> (my.objects <- addObject(t1819,"Transcripts for 18/19"))
   name           description      class  nrow ncol
1   t18  Transcripts for 2018 data.frame 15242   48
2   t19  Transcripts for 2019 data.frame 15242   32
3 t1819 Transcripts for 18/19 data.frame 15242   80
> (my.objects <- addObject(pdata18,"Phenodata for 2018"))
     name           description      class  nrow ncol
1     t18  Transcripts for 2018 data.frame 15242   48
2     t19  Transcripts for 2019 data.frame 15242   32
3   t1819 Transcripts for 18/19 data.frame 15242   80
4 pdata18    Phenodata for 2018 data.frame    48   21
> (my.objects <- addObject(pdata19,"Phenodata for 2019"))
     name           description      class  nrow ncol
1     t18  Transcripts for 2018 data.frame 15242   48
2     t19  Transcripts for 2019 data.frame 15242   32
3   t1819 Transcripts for 18/19 data.frame 15242   80
4 pdata18    Phenodata for 2018 data.frame    48   21
5 pdata19    Phenodata for 2019 data.frame    32   21
> (my.objects <- addObject(pdata1819,"Phenodata for 2018/19"))
```

```
       name           description      class  nrow ncol
1       t18  Transcripts for 2018 data.frame 15242   48
2       t19  Transcripts for 2019 data.frame 15242   32
3     t1819 Transcripts for 18/19 data.frame 15242   80
4   pdata18    Phenodata for 2018 data.frame    48   21
5   pdata19    Phenodata for 2019 data.frame    32   21
6 pdata1819 Phenodata for 2018/19 data.frame    80   21
> (my.objects <- addObject(fdata,"Trans. featuredata 18/19"))
       name              description      class  nrow ncol
1       t18     Transcripts for 2018 data.frame 15242   48
2       t19     Transcripts for 2019 data.frame 15242   32
3     t1819    Transcripts for 18/19 data.frame 15242   80
4   pdata18       Phenodata for 2018 data.frame    48   21
5   pdata19       Phenodata for 2019 data.frame    32   21
6 pdata1819    Phenodata for 2018/19 data.frame    80   21
7     fdata Trans. featuredata 18/19 data.frame 16936    5
> (my.objects <- addObject(m18,"Metabolites for 2018"))
       name              description      class  nrow ncol
1       t18     Transcripts for 2018 data.frame 15242   48
2       t19     Transcripts for 2019 data.frame 15242   32
3     t1819    Transcripts for 18/19 data.frame 15242   80
4   pdata18       Phenodata for 2018 data.frame    48   21
5   pdata19       Phenodata for 2019 data.frame    32   21
6 pdata1819    Phenodata for 2018/19 data.frame    80   21
7     fdata Trans. featuredata 18/19 data.frame 16936    5
8       m18     Metabolites for 2018 data.frame    96   60
> (my.objects <- addObject(m19,"Metabolites for 2019"))
       name              description      class  nrow ncol
1       t18     Transcripts for 2018 data.frame 15242   48
2       t19     Transcripts for 2019 data.frame 15242   32
3     t1819    Transcripts for 18/19 data.frame 15242   80
4   pdata18       Phenodata for 2018 data.frame    48   21
5   pdata19       Phenodata for 2019 data.frame    32   21
6 pdata1819    Phenodata for 2018/19 data.frame    80   21
7     fdata Trans. featuredata 18/19 data.frame 16936    5
8       m18     Metabolites for 2018 data.frame    96   60
9       m19     Metabolites for 2019 data.frame    96   60
> (my.objects <- addObject(m1819,"Metabolites for 18/19"))
       name              description      class  nrow ncol
1       t18     Transcripts for 2018 data.frame 15242   48
2       t19     Transcripts for 2019 data.frame 15242   32
3     t1819    Transcripts for 18/19 data.frame 15242   80
4   pdata18       Phenodata for 2018 data.frame    48   21
5   pdata19       Phenodata for 2019 data.frame    32   21
6 pdata1819    Phenodata for 2018/19 data.frame    80   21
7     fdata Trans. featuredata 18/19 data.frame 16936    5
8       m18     Metabolites for 2018 data.frame    96   60
9       m19     Metabolites for 2019 data.frame    96   60
10    m1819    Metabolites for 18/19 data.frame   192   60
> (my.objects <- addObject(sm1819,"Standardized metabolites 18/19"))
```

```
        name                    description      class  nrow ncol
1        t18           Transcripts for 2018 data.frame 15242   48
2        t19           Transcripts for 2019 data.frame 15242   32
3      t1819          Transcripts for 18/19 data.frame 15242   80
4    pdata18             Phenodata for 2018 data.frame    48   21
5    pdata19             Phenodata for 2019 data.frame    32   21
6  pdata1819          Phenodata for 2018/19 data.frame    80   21
7      fdata       Trans. featuredata 18/19 data.frame 16936    5
8        m18           Metabolites for 2018 data.frame    96   60
9        m19           Metabolites for 2019 data.frame    96   60
10     m1819          Metabolites for 18/19 data.frame   192   60
11    sm1819 Standardized metabolites 18/19     matrix    55  192
> (my.objects <- addObject(mfdata,"Metabolites featuredata 18/19"))
        name                    description      class  nrow ncol
1        t18           Transcripts for 2018 data.frame 15242   48
2        t19           Transcripts for 2019 data.frame 15242   32
3      t1819          Transcripts for 18/19 data.frame 15242   80
4    pdata18             Phenodata for 2018 data.frame    48   21
5    pdata19             Phenodata for 2019 data.frame    32   21
6  pdata1819          Phenodata for 2018/19 data.frame    80   21
7      fdata       Trans. featuredata 18/19 data.frame 16936    5
8        m18           Metabolites for 2018 data.frame    96   60
9        m19           Metabolites for 2019 data.frame    96   60
10     m1819          Metabolites for 18/19 data.frame   192   60
11    sm1819 Standardized metabolites 18/19     matrix    55  192
12    mfdata  Metabolites featuredata 18/19 data.frame    55    3
> (my.objects <- addObject(intgenes,"Names of genes in bins"))
        name                    description      class  nrow ncol
1        t18           Transcripts for 2018 data.frame 15242   48
2        t19           Transcripts for 2019 data.frame 15242   32
3      t1819          Transcripts for 18/19 data.frame 15242   80
4    pdata18             Phenodata for 2018 data.frame    48   21
5    pdata19             Phenodata for 2019 data.frame    32   21
6  pdata1819          Phenodata for 2018/19 data.frame    80   21
7      fdata       Trans. featuredata 18/19 data.frame 16936    5
8        m18           Metabolites for 2018 data.frame    96   60
9        m19           Metabolites for 2019 data.frame    96   60
10     m1819          Metabolites for 18/19 data.frame   192   60
11    sm1819 Standardized metabolites 18/19     matrix    55  192
12    mfdata  Metabolites featuredata 18/19 data.frame    55    3
13  intgenes         Names of genes in bins       list    22 <NA>
> (my.objects <- addObject(intmtbs,"Names of metabolites in bins"))
        name                    description      class  nrow ncol
1        t18           Transcripts for 2018 data.frame 15242   48
2        t19           Transcripts for 2019 data.frame 15242   32
3      t1819          Transcripts for 18/19 data.frame 15242   80
4    pdata18             Phenodata for 2018 data.frame    48   21
5    pdata19             Phenodata for 2019 data.frame    32   21
6  pdata1819          Phenodata for 2018/19 data.frame    80   21
7      fdata       Trans. featuredata 18/19 data.frame 16936    5
8        m18           Metabolites for 2018 data.frame    96   60
9        m19           Metabolites for 2019 data.frame    96   60
```

```
10     m1819          Metabolites for 18/19 data.frame   192    60
11    sm1819 Standardized metabolites 18/19     matrix    55   192
12    mfdata  Metabolites featuredata 18/19 data.frame    55     3
13  intgenes         Names of genes in bins       list    22 <NA>
14   intmtbs   Names of metabolites in bins       list    22 <NA>
```

```
> my.objects
        name                    description      class  nrow ncol
1        t18           Transcripts for 2018 data.frame 15242   48
2        t19           Transcripts for 2019 data.frame 15242   32
3      t1819          Transcripts for 18/19 data.frame 15242   80
4    pdata18             Phenodata for 2018 data.frame    48   21
5    pdata19             Phenodata for 2019 data.frame    32   21
6  pdata1819          Phenodata for 2018/19 data.frame    80   21
7      fdata       Trans. featuredata 18/19 data.frame 16936    5
8        m18           Metabolites for 2018 data.frame    96   60
9        m19           Metabolites for 2019 data.frame    96   60
10     m1819          Metabolites for 18/19 data.frame   192   60
11    sm1819 Standardized metabolites 18/19     matrix    55  192
12    mfdata  Metabolites featuredata 18/19 data.frame    55    3
13  intgenes         Names of genes in bins       list    22 <NA>
14   intmtbs   Names of metabolites in bins       list    22 <NA>
```

List of data objects:

```
> my.objects
        name                    description      class  nrow ncol
1        t18           Transcripts for 2018 data.frame 15242   48
2        t19           Transcripts for 2019 data.frame 15242   32
3      t1819          Transcripts for 18/19 data.frame 15242   80
4    pdata18             Phenodata for 2018 data.frame    48   21
5    pdata19             Phenodata for 2019 data.frame    32   21
6  pdata1819          Phenodata for 2018/19 data.frame    80   21
7      fdata       Trans. featuredata 18/19 data.frame 16936    5
8        m18           Metabolites for 2018 data.frame    96   60
9        m19           Metabolites for 2019 data.frame    96   60
10     m1819          Metabolites for 18/19 data.frame   192   60
11    sm1819 Standardized metabolites 18/19     matrix    55  192
12    mfdata  Metabolites featuredata 18/19 data.frame    55    3
13  intgenes         Names of genes in bins       list    22 <NA>
14   intmtbs   Names of metabolites in bins       list    22 <NA>
```

3.12 Data overview

```
> x <- my.objects
> x$name[1]
[1] "t18"
> for(i in 1:nrow(x)){
+ cat("\n\n--------- ", x[i,1],": ",x[i,2], "  ------------------------------
+ print(x[i,])
+ cat("\n")
+ print(head(eval(as.name(x[i,1]))))
+ }


--------- t18: Transcripts for 2018  ------------------------------

  name          description      class  nrow ncol
1  t18 Transcripts for 2018 data.frame 15242   48

              C18_11d_WS1 C18_11d_WS2 C18_11d_WS3 C18_11d_WS4
Vitvi15g01736   4.6646023    4.109897   4.4482203    4.013955
Vitvi07g02832  -2.4786650   -1.601359  -1.4274193   -2.066419
Vitvi07g02830  -1.8506337   -2.218030  -1.0648492   -1.580992
Vitvi07g02812  -0.5805446   -1.266940  -0.3278837   -1.019113
Vitvi07g02811   2.2762225    1.823447   1.9550503    1.648742
Vitvi09g02033  -1.6901691   -2.218030  -2.6498117   -1.449747
              C18_11d_WW1 C18_11d_WW2 C18_11d_WW3 C18_11d_WW4
Vitvi15g01736    4.717536    4.154237    4.475261    4.466465
Vitvi07g02832   -2.608485   -1.801183   -1.886474   -3.583384
Vitvi07g02830   -1.544354   -1.405255   -1.755229   -1.381750
Vitvi07g02812   -0.858463   -0.434401   -1.234397   -1.047331
Vitvi07g02811    2.086902    2.105707    2.134837    1.908469
Vitvi09g02033   -2.608485   -1.961648   -3.108866   -4.320350
              C18_34d_WS1 C18_34d_WS2 C18_34d_WS3 C18_34d_WS4
Vitvi15g01736    4.400333    4.641164   4.4191231    4.534438
Vitvi07g02832   -5.683146   -2.452000  -4.4274120   -1.876949
Vitvi07g02830   -2.513221   -2.452000  -4.4274120   -2.263972
Vitvi07g02812   -2.875791   -2.693008  -2.5529429   -3.157057
Vitvi07g02811    1.414886    1.409803   0.3970164    1.273993
Vitvi09g02033   -2.513221   -3.345084  -2.1054839   -1.716484
              C18_34d_WW1 C18_34d_WW2 C18_34d_WW3 C18_34d_WW4
Vitvi15g01736    4.924801    5.085690   5.3397350    5.263629
Vitvi07g02832   -2.827859   -3.130016  -4.6322874   -3.196388
Vitvi07g02830   -3.190429   -1.545054  -2.1297871   -3.196388
Vitvi07g02812   -2.827859   -1.182484  -3.4098950   -2.303303
Vitvi07g02811    1.517916    1.357250   0.9626591    1.344985
Vitvi09g02033   -4.412821   -3.130016  -2.3103594   -4.418780
              C18_67d_WS1 C18_67d_WS2 C18_67d_WS3 C18_67d_WS4
Vitvi15g01736  2.05871733   2.2895026   2.9234830    2.575657
Vitvi07g02832 -5.85417200  -4.4786818  -4.4659691   -2.468738
Vitvi07g02830 -2.15373228  -3.2562893  -3.7290035   -2.709746
Vitvi07g02812 -1.21031581  -2.3632045  -2.3504919   -2.999252
Vitvi07g02811  0.02847105   0.5362686   0.9824914    1.231702
Vitvi09g02033 -4.26920950  -3.7417162  -2.5915000   -3.847249
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	C18_67d_WW1	C18_67d_WW2	C18_67d_WW3	C18_67d_WW4
Vitvi15g01736	3.891121	3.040087	4.216897	3.763086
Vitvi07g02832	-2.726982	-4.610965	-2.436913	-3.355855
Vitvi07g02830	-2.726982	-3.873999	-1.493496	-2.075747
Vitvi07g02812	-1.672534	-3.388572	-2.230462	-2.462770
Vitvi07g02811	1.436764	1.552266	1.811015	1.352490
Vitvi09g02033	-2.520531	-2.736495	-3.815424	-2.993285
	F18_10d_WS1	F18_10d_WS2	F18_10d_WS3	F18_10d_WS4
Vitvi15g01736	4.8591409	4.8669435	4.9805904	4.9453953
Vitvi07g02832	2.8881443	2.7032394	2.2757651	2.0553154
Vitvi07g02830	2.8426117	2.4130023	2.2135368	2.0169691
Vitvi07g02812	0.8222302	0.9363895	0.7209384	0.3104447
Vitvi07g02811	3.5853480	3.5007015	3.2965509	3.2141610
Vitvi09g02033	1.0793880	1.0850336	0.6285743	0.8579324
	F18_10d_WW1	F18_10d_WW2	F18_10d_WW3	F18_10d_WW4
Vitvi15g01736	5.705006	4.619238	4.808548	5.276124
Vitvi07g02832	2.747538	3.349854	2.537311	2.621336
Vitvi07g02830	2.287722	3.464855	1.989824	2.321031
Vitvi07g02812	1.073767	1.384521	1.472076	1.016877
Vitvi07g02811	3.818074	4.000053	3.198197	3.501954
Vitvi09g02033	1.073767	1.566041	1.237985	1.268416
	F18_34d_WS1	F18_34d_WS2	F18_34d_WS3	F18_34d_WS4
Vitvi15g01736	4.0647184	3.8504580	5.1418322	4.6269091
Vitvi07g02832	2.2592790	2.1761360	2.3686660	1.2127920
Vitvi07g02830	2.1186455	1.9359657	2.6356368	1.5129655
Vitvi07g02812	0.4316833	-0.6220298	-0.5985972	-0.2055206
Vitvi07g02811	2.9490282	2.7595613	3.1300210	2.4602029
Vitvi09g02033	1.5459405	1.3699329	1.4288835	1.4477479
	F18_34d_WW1	F18_34d_WW2	F18_34d_WW3	F18_34d_WW4
Vitvi15g01736	4.0961725	4.80222138	4.3291524	4.4419027
Vitvi07g02832	1.8816574	1.82887526	1.7895023	1.6490200
Vitvi07g02830	2.1414534	1.62149541	2.1153419	2.1541121
Vitvi07g02812	0.1031253	-0.09471163	0.3053805	0.2855497
Vitvi07g02811	3.0025984	2.73213947	2.8750439	3.0458304
Vitvi09g02033	1.7460934	1.45938991	2.0072243	1.2444445
	F18_67d_WS1	F18_67d_WS2	F18_67d_WS3	F18_67d_WS4
Vitvi15g01736	1.5831276	1.7408584	2.97840555	4.1664059
Vitvi07g02832	1.3093668	1.9241330	2.01456521	2.9813855
Vitvi07g02830	0.8382242	1.4203666	2.18501915	2.8731326
Vitvi07g02812	0.1974739	0.4558154	-0.03878421	-0.0111843
Vitvi07g02811	1.8823168	2.5341865	2.65708760	2.9461961
Vitvi09g02033	1.6066824	1.5040245	1.25520700	0.9986635
	F18_67d_WW1	F18_67d_WW2	F18_67d_WW3	F18_67d_WW4
Vitvi15g01736	3.5580430	3.569471	4.4112089	4.3597440
Vitvi07g02832	2.5563386	2.180583	2.6637430	2.7538173
Vitvi07g02830	2.0265816	2.154972	2.7552617	2.3663511
Vitvi07g02812	0.6773148	0.106805	-0.2413317	-0.1063251
Vitvi07g02811	3.0678390	2.949349	2.9761917	2.9625700
Vitvi09g02033	1.7205680	1.541742	1.6527997	1.3320450

--------- t19: Transcripts for 2019 ----------

name	description	class	nrow	ncol
2 t19	Transcripts for 2019 data	data.frame	15242	32

	C19_22d_WS1	C19_22d_WS2	C19_22d_WS3	C19_22d_WS4
Vitvi15g01736	3.18	3.50	3.19	3.61
Vitvi07g02832	-5.05	-3.02	-0.80	-0.02
Vitvi07g02830	-5.05	-5.35	-2.39	-3.99
Vitvi07g02812	-1.35	-0.95	-0.15	0.26
Vitvi07g02811	2.09	2.29	2.34	2.63
Vitvi09g02033	-5.05	-3.76	-2.39	-2.76
	C19_22d_WW1	C19_22d_WW2	C19_22d_WW3	C19_22d_WW4
Vitvi15g01736	5.42	5.35	4.68	4.92
Vitvi07g02832	-1.36	-2.10	-1.15	-3.81
Vitvi07g02830	-2.28	-1.81	-2.07	-2.59
Vitvi07g02812	-1.36	0.16	-0.29	-0.75
Vitvi07g02811	2.85	3.16	3.09	2.89
Vitvi09g02033	-5.45	-3.68	-1.78	-3.81
	C19_44d_WS1	C19_44d_WS2	C19_44d_WS3	C19_44d_WS4
Vitvi15g01736	5.13	5.19	5.71	5.29
Vitvi07g02832	-3.13	-1.28	-3.18	-2.29
Vitvi07g02830	-3.87	-5.53	-5.50	-2.29
Vitvi07g02812	-0.10	-1.01	-0.29	-0.04
Vitvi07g02811	2.11	1.92	2.40	2.29
Vitvi09g02033	-3.87	-3.95	-2.69	-2.00
	C19_44d_WW1	C19_44d_WW2	C19_44d_WW3	C19_44d_WW4
Vitvi15g01736	6.19	5.62	5.62	6.19
Vitvi07g02832	-5.54	-5.31	-3.73	-1.81
Vitvi07g02830	-3.22	-5.31	-3.73	-2.05
Vitvi07g02812	-0.59	-0.45	-1.07	-0.55
Vitvi07g02811	2.44	2.13	2.08	2.26
Vitvi09g02033	-3.22	-3.72	-3.73	-3.18
	F19_22d_WS1	F19_22d_WS2	F19_22d_WS3	F19_22d_WS4
Vitvi15g01736	3.03	3.93	4.24	2.85
Vitvi07g02832	3.35	3.23	3.02	2.98
Vitvi07g02830	2.28	2.39	1.75	1.35
Vitvi07g02812	2.19	1.04	0.89	1.56
Vitvi07g02811	3.84	3.72	3.01	3.43
Vitvi09g02033	2.70	1.61	1.94	2.47
	F19_22d_WW1	F19_22d_WW2	F19_22d_WW3	F19_22d_WW4
Vitvi15g01736	5.00	4.97	4.47	5.51
Vitvi07g02832	3.18	3.04	2.81	3.05
Vitvi07g02830	2.59	2.07	1.81	2.20
Vitvi07g02812	1.72	1.08	1.42	1.35
Vitvi07g02811	3.79	3.43	3.24	3.33
Vitvi09g02033	2.24	1.90	2.08	1.25
	F19_44d_WS1	F19_44d_WS2	F19_44d_WS3	F19_44d_WS4
Vitvi15g01736	5.84	5.83	4.56	5.23
Vitvi07g02832	2.54	3.14	3.01	2.16
Vitvi07g02830	1.13	2.25	2.18	1.90
Vitvi07g02812	0.99	0.84	0.85	0.22
Vitvi07g02811	2.91	3.10	3.18	2.61
Vitvi09g02033	1.21	1.67	2.52	2.21
	F19_44d_WW1	F19_44d_WW2	F19_44d_WW3	F19_44d_WW4

Vitvi15g01736	5.44	6.13	5.96	6.16
Vitvi07g02832	3.84	3.05	3.89	4.02
Vitvi07g02830	2.74	2.79	2.90	2.88
Vitvi07g02812	1.03	0.93	1.49	1.29
Vitvi07g02811	3.32	2.89	3.35	3.26
Vitvi09g02033	1.99	1.14	1.65	1.29

--------- t1819: Transcripts for 18/19 ------------------------------

	name	description	class	nrow	ncol
3	t1819	Transcripts for 18/19	data.frame	15242	80

	C18_11d_WS1	C18_11d_WS2	C18_11d_WS3	C18_11d_WS4
Vitvi15g01736	4.6646023	4.109897	4.4482203	4.013955
Vitvi07g02832	-2.4786650	-1.601359	-1.4274193	-2.066419
Vitvi07g02830	-1.8506337	-2.218030	-1.0648492	-1.580992
Vitvi07g02812	-0.5805446	-1.266940	-0.3278837	-1.019113
Vitvi07g02811	2.2762225	1.823447	1.9550503	1.648742
Vitvi09g02033	-1.6901691	-2.218030	-2.6498117	-1.449747
	C18_11d_WW1	C18_11d_WW2	C18_11d_WW3	C18_11d_WW4
Vitvi15g01736	4.717536	4.154237	4.475261	4.466465
Vitvi07g02832	-2.608485	-1.801183	-1.886474	-3.583384
Vitvi07g02830	-1.544354	-1.405255	-1.755229	-1.381750
Vitvi07g02812	-0.858463	-0.434401	-1.234397	-1.047331
Vitvi07g02811	2.086902	2.105707	2.134837	1.908469
Vitvi09g02033	-2.608485	-1.961648	-3.108866	-4.320350
	C18_34d_WS1	C18_34d_WS2	C18_34d_WS3	C18_34d_WS4
Vitvi15g01736	4.400333	4.641164	4.4191231	4.534438
Vitvi07g02832	-5.683146	-2.452000	-4.4274120	-1.876949
Vitvi07g02830	-2.513221	-2.452000	-4.4274120	-2.263972
Vitvi07g02812	-2.875791	-2.693008	-2.5529429	-3.157057
Vitvi07g02811	1.414886	1.409803	0.3970164	1.273993
Vitvi09g02033	-2.513221	-3.345084	-2.1054839	-1.716484
	C18_34d_WW1	C18_34d_WW2	C18_34d_WW3	C18_34d_WW4
Vitvi15g01736	4.924801	5.085690	5.3397350	5.263629
Vitvi07g02832	-2.827859	-3.130016	-4.6322874	-3.196388
Vitvi07g02830	-3.190429	-1.545054	-2.1297871	-3.196388
Vitvi07g02812	-2.827859	-1.182484	-3.4098950	-2.303303
Vitvi07g02811	1.517916	1.357250	0.9626591	1.344985
Vitvi09g02033	-4.412821	-3.130016	-2.3103594	-4.418780
	C18_67d_WS1	C18_67d_WS2	C18_67d_WS3	C18_67d_WS4
Vitvi15g01736	2.05871733	2.2895026	2.9234830	2.575657
Vitvi07g02832	-5.85417200	-4.4786818	-4.4659691	-2.468738
Vitvi07g02830	-2.15373228	-3.2562893	-3.7290035	-2.709746
Vitvi07g02812	-1.21031581	-2.3632045	-2.3504919	-2.999252
Vitvi07g02811	0.02847105	0.5362686	0.9824914	1.231702
Vitvi09g02033	-4.26920950	-3.7417162	-2.5915000	-3.847249
	C18_67d_WW1	C18_67d_WW2	C18_67d_WW3	C18_67d_WW4
Vitvi15g01736	3.891121	3.040087	4.216897	3.763086
Vitvi07g02832	-2.726982	-4.610965	-2.436913	-3.355855
Vitvi07g02830	-2.726982	-3.873999	-1.493496	-2.075747
Vitvi07g02812	-1.672534	-3.388572	-2.230462	-2.462770

Vitvi07g02811	1.436764	1.552266	1.811015	1.352490
Vitvi09g02033	-2.520531	-2.736495	-3.815424	-2.993285
	F18_10d_WS1	F18_10d_WS2	F18_10d_WS3	F18_10d_WS4
Vitvi15g01736	4.8591409	4.8669435	4.9805904	4.9453953
Vitvi07g02832	2.8881443	2.7032394	2.2757651	2.0553154
Vitvi07g02830	2.8426117	2.4130023	2.2135368	2.0169691
Vitvi07g02812	0.8222302	0.9363895	0.7209384	0.3104447
Vitvi07g02811	3.5853480	3.5007015	3.2965509	3.2141610
Vitvi09g02033	1.0793880	1.0850336	0.6285743	0.8579324
	F18_10d_WW1	F18_10d_WW2	F18_10d_WW3	F18_10d_WW4
Vitvi15g01736	5.705006	4.619238	4.808548	5.276124
Vitvi07g02832	2.747538	3.349854	2.537311	2.621336
Vitvi07g02830	2.287722	3.464855	1.989824	2.321031
Vitvi07g02812	1.073767	1.384521	1.472076	1.016877
Vitvi07g02811	3.818074	4.000053	3.198197	3.501954
Vitvi09g02033	1.073767	1.566041	1.237985	1.268416
	F18_34d_WS1	F18_34d_WS2	F18_34d_WS3	F18_34d_WS4
Vitvi15g01736	4.0647184	3.8504580	5.1418322	4.6269091
Vitvi07g02832	2.2592790	2.1761360	2.3686660	1.2127920
Vitvi07g02830	2.1186455	1.9359657	2.6356368	1.5129655
Vitvi07g02812	0.4316833	-0.6220298	-0.5985972	-0.2055206
Vitvi07g02811	2.9490282	2.7595613	3.1300210	2.4602029
Vitvi09g02033	1.5459405	1.3699329	1.4288835	1.4477479
	F18_34d_WW1	F18_34d_WW2	F18_34d_WW3	F18_34d_WW4
Vitvi15g01736	4.0961725	4.80222138	4.3291524	4.4419027
Vitvi07g02832	1.8816574	1.82887526	1.7895023	1.6490200
Vitvi07g02830	2.1414534	1.62149541	2.1153419	2.1541121
Vitvi07g02812	0.1031253	-0.09471163	0.3053805	0.2855497
Vitvi07g02811	3.0025984	2.73213947	2.8750439	3.0458304
Vitvi09g02033	1.7460934	1.45938991	2.0072243	1.2444445
	F18_67d_WS1	F18_67d_WS2	F18_67d_WS3	F18_67d_WS4
Vitvi15g01736	1.5831276	1.7408584	2.97840555	4.1664059
Vitvi07g02832	1.3093668	1.9241330	2.01456521	2.9813855
Vitvi07g02830	0.8382242	1.4203666	2.18501915	2.8731326
Vitvi07g02812	0.1974739	0.4558154	-0.03878421	-0.0111843
Vitvi07g02811	1.8823168	2.5341865	2.65708760	2.9461961
Vitvi09g02033	1.6066824	1.5040245	1.25520700	0.9986635
	F18_67d_WW1	F18_67d_WW2	F18_67d_WW3	F18_67d_WW4
Vitvi15g01736	3.5580430	3.569471	4.4112089	4.3597440
Vitvi07g02832	2.5563386	2.180583	2.6637430	2.7538173
Vitvi07g02830	2.0265816	2.154972	2.7552617	2.3663511
Vitvi07g02812	0.6773148	0.106805	-0.2413317	-0.1063251
Vitvi07g02811	3.0678390	2.949349	2.9761917	2.9625700
Vitvi09g02033	1.7205680	1.541742	1.6527997	1.3320450
	C19_22d_WS1	C19_22d_WS2	C19_22d_WS3	C19_22d_WS4
Vitvi15g01736	3.18	3.50	3.19	3.61
Vitvi07g02832	-5.05	-3.02	-0.80	-0.02
Vitvi07g02830	-5.05	-5.35	-2.39	-3.99
Vitvi07g02812	-1.35	-0.95	-0.15	0.26
Vitvi07g02811	2.09	2.29	2.34	2.63
Vitvi09g02033	-5.05	-3.76	-2.39	-2.76
	C19_22d_WW1	C19_22d_WW2	C19_22d_WW3	C19_22d_WW4
Vitvi15g01736	5.42	5.35	4.68	4.92

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Vitvi07g02832       -1.36       -2.10       -1.15       -3.81
Vitvi07g02830       -2.28       -1.81       -2.07       -2.59
Vitvi07g02812       -1.36        0.16       -0.29       -0.75
Vitvi07g02811        2.85        3.16        3.09        2.89
Vitvi09g02033       -5.45       -3.68       -1.78       -3.81
               C19_44d_WS1 C19_44d_WS2 C19_44d_WS3 C19_44d_WS4
Vitvi15g01736        5.13        5.19        5.71        5.29
Vitvi07g02832       -3.13       -1.28       -3.18       -2.29
Vitvi07g02830       -3.87       -5.53       -5.50       -2.29
Vitvi07g02812       -0.10       -1.01       -0.29       -0.04
Vitvi07g02811        2.11        1.92        2.40        2.29
Vitvi09g02033       -3.87       -3.95       -2.69       -2.00
               C19_44d_WW1 C19_44d_WW2 C19_44d_WW3 C19_44d_WW4
Vitvi15g01736        6.19        5.62        5.62        6.19
Vitvi07g02832       -5.54       -5.31       -3.73       -1.81
Vitvi07g02830       -3.22       -5.31       -3.73       -2.05
Vitvi07g02812       -0.59       -0.45       -1.07       -0.55
Vitvi07g02811        2.44        2.13        2.08        2.26
Vitvi09g02033       -3.22       -3.72       -3.73       -3.18
               F19_22d_WS1 F19_22d_WS2 F19_22d_WS3 F19_22d_WS4
Vitvi15g01736        3.03        3.93        4.24        2.85
Vitvi07g02832        3.35        3.23        3.02        2.98
Vitvi07g02830        2.28        2.39        1.75        1.35
Vitvi07g02812        2.19        1.04        0.89        1.56
Vitvi07g02811        3.84        3.72        3.01        3.43
Vitvi09g02033        2.70        1.61        1.94        2.47
               F19_22d_WW1 F19_22d_WW2 F19_22d_WW3 F19_22d_WW4
Vitvi15g01736        5.00        4.97        4.47        5.51
Vitvi07g02832        3.18        3.04        2.81        3.05
Vitvi07g02830        2.59        2.07        1.81        2.20
Vitvi07g02812        1.72        1.08        1.42        1.35
Vitvi07g02811        3.79        3.43        3.24        3.33
Vitvi09g02033        2.24        1.90        2.08        1.25
               F19_44d_WS1 F19_44d_WS2 F19_44d_WS3 F19_44d_WS4
Vitvi15g01736        5.84        5.83        4.56        5.23
Vitvi07g02832        2.54        3.14        3.01        2.16
Vitvi07g02830        1.13        2.25        2.18        1.90
Vitvi07g02812        0.99        0.84        0.85        0.22
Vitvi07g02811        2.91        3.10        3.18        2.61
Vitvi09g02033        1.21        1.67        2.52        2.21
               F19_44d_WW1 F19_44d_WW2 F19_44d_WW3 F19_44d_WW4
Vitvi15g01736        5.44        6.13        5.96        6.16
Vitvi07g02832        3.84        3.05        3.89        4.02
Vitvi07g02830        2.74        2.79        2.90        2.88
Vitvi07g02812        1.03        0.93        1.49        1.29
Vitvi07g02811        3.32        2.89        3.35        3.26
Vitvi09g02033        1.99        1.14        1.65        1.29


--------- pdata18: Phenodata for 2018  -------------------------------

     name        description      class nrow ncol
4 pdata18 Phenodata for 2018 data.frame   48   21
```

```
                     ID        Variety       Date variety year day
C18_11d_WS1 C18_11d_WS1 Cabernet Volos 12.06.2018       C   18  11
C18_11d_WS2 C18_11d_WS2 Cabernet Volos 12.06.2018       C   18  11
C18_11d_WS3 C18_11d_WS3 Cabernet Volos 12.06.2018       C   18  11
C18_11d_WS4 C18_11d_WS4 Cabernet Volos 12.06.2018       C   18  11
C18_11d_WW1 C18_11d_WW1 Cabernet Volos 12.06.2018       C   18  11
C18_11d_WW2 C18_11d_WW2 Cabernet Volos 12.06.2018       C   18  11
            treat rep project.name        species plant.name tissue
C18_11d_WS1    WS   1      EnViros Vitis vinifera  grapevine   leaf
C18_11d_WS2    WS   2      EnViros Vitis vinifera  grapevine   leaf
C18_11d_WS3    WS   3      EnViros Vitis vinifera  grapevine   leaf
C18_11d_WS4    WS   4      EnViros Vitis vinifera  grapevine   leaf
C18_11d_WW1    WW   1      EnViros Vitis vinifera  grapevine   leaf
C18_11d_WW2    WW   2      EnViros Vitis vinifera  grapevine   leaf
            health.status plant.number growth.location
C18_11d_WS1  water stress           R1           Udine
C18_11d_WS2  water stress           R2           Udine
C18_11d_WS3  water stress           R3           Udine
C18_11d_WS4  water stress           R4           Udine
C18_11d_WW1  well watered           R1           Udine
C18_11d_WW2  well watered           R2           Udine
            growth.conditions
C18_11d_WS1           outside
C18_11d_WS2           outside
C18_11d_WS3           outside
C18_11d_WS4           outside
C18_11d_WW1           outside
C18_11d_WW2           outside

C18_11d_WS1 several leaves ground together and stored at -80oC; an aliquot was
C18_11d_WS2 several leaves ground together and stored at -80oC; an aliquot was
C18_11d_WS3 several leaves ground together and stored at -80oC; an aliquot was
C18_11d_WS4 several leaves ground together and stored at -80oC; an aliquot was
C18_11d_WW1 several leaves ground together and stored at -80oC; an aliquot was
C18_11d_WW2 several leaves ground together and stored at -80oC; an aliquot was
            Metabolites.Order         Metabolites.File.Name
C18_11d_WS1                 2 1019Cabernet Volos_6_12_WS1.D
C18_11d_WS2                 4 1019Cabernet Volos_6_12_WS2.D
C18_11d_WS3               102 1219Cabernet Volos_6_12_WS3.D
C18_11d_WS4               100 1219Cabernet Volos_6_12_WS4.D
C18_11d_WW1                 6 1019Cabernet Volos_6_12_WW1.D
C18_11d_WW2                 8 1019Cabernet Volos_6_12_WW2.D
               Metabolites.File Transcripts.ID
C18_11d_WS1 Cabernet Volos6_12WS          C1_S1
C18_11d_WS2 Cabernet Volos6_12WS          C1_S2
C18_11d_WS3 Cabernet Volos6_12WS          C1_S3
C18_11d_WS4 Cabernet Volos6_12WS          C1_S4
C18_11d_WW1 Cabernet Volos6_12WW          C1_W1
C18_11d_WW2 Cabernet Volos6_12WW          C1_W2


--------- pdata19: Phenodata for 2019  -------------------------------
```

```
     name        description      class nrow ncol
5 pdata19 Phenodata for 2019 data.frame   32   21

                    ID        Variety       Date variety year day
C19_22d_WS1 C19_22d_WS1 Cabernet Volos 26.06.2019       C   19  22
C19_22d_WS2 C19_22d_WS2 Cabernet Volos 26.06.2019       C   19  22
C19_22d_WS3 C19_22d_WS3 Cabernet Volos 26.06.2019       C   19  22
C19_22d_WS4 C19_22d_WS4 Cabernet Volos 26.06.2019       C   19  22
C19_22d_WW1 C19_22d_WW1 Cabernet Volos 26.06.2019       C   19  22
C19_22d_WW2 C19_22d_WW2 Cabernet Volos 26.06.2019       C   19  22
            treat rep project.name        species plant.name tissue
C19_22d_WS1    WS   1      EnViros Vitis vinifera  grapevine   leaf
C19_22d_WS2    WS   2      EnViros Vitis vinifera  grapevine   leaf
C19_22d_WS3    WS   3      EnViros Vitis vinifera  grapevine   leaf
C19_22d_WS4    WS   4      EnViros Vitis vinifera  grapevine   leaf
C19_22d_WW1    WW   1      EnViros Vitis vinifera  grapevine   leaf
C19_22d_WW2    WW   2      EnViros Vitis vinifera  grapevine   leaf
            health.status plant.number growth.location
C19_22d_WS1  water stress           R1           Udine
C19_22d_WS2  water stress           R2           Udine
C19_22d_WS3  water stress           R3           Udine
C19_22d_WS4  water stress           R4           Udine
C19_22d_WW1  well watered           R1           Udine
C19_22d_WW2  well watered           R2           Udine
            growth.conditions
C19_22d_WS1           outside
C19_22d_WS2           outside
C19_22d_WS3           outside
C19_22d_WS4           outside
C19_22d_WW1           outside
C19_22d_WW2           outside

C19_22d_WS1 several leaves ground together and stored at -80oC; an aliquot was
C19_22d_WS2 several leaves ground together and stored at -80oC; an aliquot was
C19_22d_WS3 several leaves ground together and stored at -80oC; an aliquot was
C19_22d_WS4 several leaves ground together and stored at -80oC; an aliquot was
C19_22d_WW1 several leaves ground together and stored at -80oC; an aliquot was
C19_22d_WW2 several leaves ground together and stored at -80oC; an aliquot was
            Metabolites.Order                 Metabolites.File.Name
C19_22d_WS1                 2 11120Cabernet_Volos_26_06_2019WS_1.D
C19_22d_WS2                27 11120Cabernet_Volos_26_06_2019WS_2.D
C19_22d_WS3                53 11420Cabernet_Volos_26_06_2019WS_3.D
C19_22d_WS4                79 11420Cabernet_Volos_26_06_2019WS_4.D
C19_22d_WW1                 3 11120Cabernet_Volos_26_06_2019WW_1.D
C19_22d_WW2                28 11120Cabernet_Volos_26_06_2019WW_2.D
                Metabolites.File Transcripts.ID
C19_22d_WS1 Cabernet Volos26_06WS           C1S1
C19_22d_WS2 Cabernet Volos26_06WS           C1S2
C19_22d_WS3 Cabernet Volos26_06WS           C1S3
C19_22d_WS4 Cabernet Volos26_06WS           C1S4
C19_22d_WW1 Cabernet Volos26_06WW           C1W1
C19_22d_WW2 Cabernet Volos26_06WW           C1W2
```

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--------- pdata1819: Phenodata for 2018/19  ------------------------------

       name           description      class nrow ncol
6 pdata1819 Phenodata for 2018/19 data.frame   80   21

                    ID        Variety       Date variety year day
C18_11d_WS1 C18_11d_WS1 Cabernet Volos 12.06.2018       C   18  11
C18_11d_WS2 C18_11d_WS2 Cabernet Volos 12.06.2018       C   18  11
C18_11d_WS3 C18_11d_WS3 Cabernet Volos 12.06.2018       C   18  11
C18_11d_WS4 C18_11d_WS4 Cabernet Volos 12.06.2018       C   18  11
C18_11d_WW1 C18_11d_WW1 Cabernet Volos 12.06.2018       C   18  11
C18_11d_WW2 C18_11d_WW2 Cabernet Volos 12.06.2018       C   18  11
            treat rep project.name        species plant.name tissue
C18_11d_WS1    WS   1      EnViros Vitis vinifera  grapevine   leaf
C18_11d_WS2    WS   2      EnViros Vitis vinifera  grapevine   leaf
C18_11d_WS3    WS   3      EnViros Vitis vinifera  grapevine   leaf
C18_11d_WS4    WS   4      EnViros Vitis vinifera  grapevine   leaf
C18_11d_WW1    WW   1      EnViros Vitis vinifera  grapevine   leaf
C18_11d_WW2    WW   2      EnViros Vitis vinifera  grapevine   leaf
            health.status plant.number growth.location
C18_11d_WS1  water stress           R1           Udine
C18_11d_WS2  water stress           R2           Udine
C18_11d_WS3  water stress           R3           Udine
C18_11d_WS4  water stress           R4           Udine
C18_11d_WW1  well watered           R1           Udine
C18_11d_WW2  well watered           R2           Udine
            growth.conditions
C18_11d_WS1           outside
C18_11d_WS2           outside
C18_11d_WS3           outside
C18_11d_WS4           outside
C18_11d_WW1           outside
C18_11d_WW2           outside

C18_11d_WS1 several leaves ground together and stored at -80oC; an aliquot was
C18_11d_WS2 several leaves ground together and stored at -80oC; an aliquot was
C18_11d_WS3 several leaves ground together and stored at -80oC; an aliquot was
C18_11d_WS4 several leaves ground together and stored at -80oC; an aliquot was
C18_11d_WW1 several leaves ground together and stored at -80oC; an aliquot was
C18_11d_WW2 several leaves ground together and stored at -80oC; an aliquot was
            Metabolites.Order         Metabolites.File.Name
C18_11d_WS1                 2 1019Cabernet Volos_6_12_WS1.D
C18_11d_WS2                 4 1019Cabernet Volos_6_12_WS2.D
C18_11d_WS3               102 1219Cabernet Volos_6_12_WS3.D
C18_11d_WS4               100 1219Cabernet Volos_6_12_WS4.D
C18_11d_WW1                 6 1019Cabernet Volos_6_12_WW1.D
C18_11d_WW2                 8 1019Cabernet Volos_6_12_WW2.D
                Metabolites.File Transcripts.ID
C18_11d_WS1 Cabernet Volos6_12WS          C1_S1
C18_11d_WS2 Cabernet Volos6_12WS          C1_S2
C18_11d_WS3 Cabernet Volos6_12WS          C1_S3
```

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C18_11d_WS4 Cabernet Volos6_12WS          C1_S4
C18_11d_WW1 Cabernet Volos6_12WW          C1_W1
C18_11d_WW2 Cabernet Volos6_12WW          C1_W2


--------- fdata: Trans. featuredata 18/19  -------------------------------

   name              description      class  nrow ncol
7 fdata Trans. featuredata 18/19 data.frame 16936    5

  YEAR        geneID BINCODE                              NAME
1 2018 Vitvi15g01736    26.9 misc.glutathione S transferases
2 2018 Vitvi07g02832    35.2            not assigned.unknown
3 2018 Vitvi07g02830    35.2            not assigned.unknown
4 2018 Vitvi07g02812    35.2            not assigned.unknown
5 2018 Vitvi07g02811    35.2            not assigned.unknown
6 2018 Vitvi09g02033    35.2            not assigned.unknown

1                      glutathione S-transferase tau 7 | Chr2:12618111-1261887
2 Disease resistance protein (TIR-NBS-LRR class) family | Chr4:7197325-7201393
3
4                                                                          Ti
5
6   Disease resistance protein (CC-NBS-LRR class) family | Chr1:4145374-414768


--------- m18: Metabolites for 2018  -------------------------------

  name          description      class nrow ncol
8  m18 Metabolites for 2018 data.frame   96   60

                    ID        Variety       Date Treat Rep Alanine
C18_11d_WS1 C18_11d_WS1 Cabernet Volos 12.06.2018    WS   1   0.133
C18_11d_WS2 C18_11d_WS2 Cabernet Volos 12.06.2018    WS   2   0.115
C18_11d_WS3 C18_11d_WS3 Cabernet Volos 12.06.2018    WS   3   0.624
C18_11d_WS4 C18_11d_WS4 Cabernet Volos 12.06.2018    WS   4   0.649
C18_11d_WW1 C18_11d_WW1 Cabernet Volos 12.06.2018    WW   1   0.136
C18_11d_WW2 C18_11d_WW2 Cabernet Volos 12.06.2018    WW   2   0.230
            Arabinose Ascorbic.acid Aspartic.acid  GABA
C18_11d_WS1     0.116         0.885         0.882 1.950
C18_11d_WS2     0.120         1.147         0.613 1.054
C18_11d_WS3     0.094         1.080         0.715 1.401
C18_11d_WS4     0.112         1.587         0.827 1.705
C18_11d_WW1     0.160         0.769         0.549 1.929
C18_11d_WW2     0.147         0.903         0.625 1.513
            Trans.Caffeic.acid Catechin Citric.acid Erythronic.acid
C18_11d_WS1              8.751    2.828       2.236           1.696
C18_11d_WS2              9.164    3.595       2.152           2.039
C18_11d_WS3              7.039    2.059       1.996           1.791
C18_11d_WS4              7.379    1.880       2.619           1.587
C18_11d_WW1              8.197    1.930       2.290           1.999
C18_11d_WW2              7.093    1.419       2.056           1.301
            Ethanolamine Fructose Fructose.6.phosphate Fumaric.acid
```

C18_11d_WS1	1.052	27.962	0.037	0.683
C18_11d_WS2	0.865	22.260	0.035	1.069
C18_11d_WS3	1.335	14.477	0.058	1.907
C18_11d_WS4	0.901	16.651	0.079	2.009
C18_11d_WW1	0.861	22.621	0.033	0.760
C18_11d_WW2	0.805	20.318	0.089	1.094

	Galactinol	Galactose	Gallic.acid	Gluconic.acid
C18_11d_WS1	16.908	8.455	1.002	3.640
C18_11d_WS2	13.660	8.218	0.958	3.911
C18_11d_WS3	13.524	4.445	0.936	3.079
C18_11d_WS4	14.463	6.358	0.905	3.421
C18_11d_WW1	15.754	6.071	1.143	3.133
C18_11d_WW2	13.891	5.467	0.917	2.805

	Glucopyranose..H20.	Glucose	Glutamic.acid	Glyceric.acid
C18_11d_WS1	0.143	43.309	0.491	7.540
C18_11d_WS2	0.155	41.412	0.298	6.082
C18_11d_WS3	0.178	31.305	0.140	5.876
C18_11d_WS4	0.153	40.981	0.202	7.596
C18_11d_WW1	0.169	37.135	0.303	6.008
C18_11d_WW2	0.156	35.269	0.263	5.638

	Glycine	Hydroquinone	Myo.Inostol	Isoleucine	Leucine
C18_11d_WS1	0.742	0.161	91.071	0.055	0.022
C18_11d_WS2	0.727	0.208	89.166	0.054	0.027
C18_11d_WS3	0.913	0.099	97.202	0.072	0.033
C18_11d_WS4	0.742	0.176	114.143	0.150	0.079
C18_11d_WW1	1.031	0.101	85.266	0.146	0.077
C18_11d_WW2	0.847	0.161	90.745	0.096	0.050

	Lyxonic.acid	Maleic.acid	Malic.acid	Malonic.acid
C18_11d_WS1	1.028	1.093	66.326	0.166
C18_11d_WS2	1.187	1.486	73.855	0.140
C18_11d_WS3	1.237	1.108	62.877	0.183
C18_11d_WS4	1.020	1.084	66.638	0.233
C18_11d_WW1	1.205	0.879	53.894	0.156
C18_11d_WW2	1.096	1.202	51.917	0.170

	Mannose.6.phosphate	Melibiose	Phenylalanine
C18_11d_WS1	0.088	0.227	0.095
C18_11d_WS2	0.102	0.204	0.116
C18_11d_WS3	0.134	0.069	0.103
C18_11d_WS4	0.174	0.092	0.203
C18_11d_WW1	0.082	0.178	0.104
C18_11d_WW2	0.198	0.164	0.179

	Phosphoric.acid	Proline	Putrescine	Pyroglutamic.acid
C18_11d_WS1	23.244	0.011	0.054	5.790
C18_11d_WS2	17.190	0.013	0.046	4.354
C18_11d_WS3	18.909	0.006	0.104	8.169
C18_11d_WS4	23.579	0.008	0.111	10.445
C18_11d_WW1	31.264	0.006	0.066	4.966
C18_11d_WW2	31.233	0.008	0.058	5.408

	Quinic.acid	X3.caffeoylquinic.acid	Raffinose	Rhamnose
C18_11d_WS1	1.615	0.677	1.117	0.603
C18_11d_WS2	1.304	0.635	1.544	0.472
C18_11d_WS3	1.254	0.378	0.961	0.516
C18_11d_WS4	1.106	0.423	1.164	0.634

```
C18_11d_WW1       1.985                  0.576     0.870    0.534
C18_11d_WW2       1.513                  0.462     1.001    0.747
           Ribonic.acid Ribose Serine Shikimic.acid Succinic.acid
C18_11d_WS1        0.270  0.151  0.997        23.883         0.139
C18_11d_WS2        0.237  0.152  0.609        13.037         0.133
C18_11d_WS3        0.361  0.162  0.895        14.551         0.089
C18_11d_WS4        0.293  0.154  1.116        14.364         0.106
C18_11d_WW1        0.326  0.164  0.465        23.607         0.140
C18_11d_WW2        0.326  0.164  0.551        18.038         0.119
           Sucrose Tartaric.acid Threitol Threonic.acid
C18_11d_WS1  96.247        58.764    0.025         2.632
C18_11d_WS2 101.273        36.403    0.018         2.741
C18_11d_WS3 114.777        30.620    0.027         2.645
C18_11d_WS4 122.686        52.311    0.033         2.387
C18_11d_WW1  99.984        47.986    0.032         3.639
C18_11d_WW2 105.411        44.912    0.031         3.759
           Threonolactone Threonine Uracil Valine Xylose
C18_11d_WS1          0.145     0.244  0.011  0.267  0.297
C18_11d_WS2          0.121     0.187  0.017  0.259  0.231
C18_11d_WS3          0.086     0.216  0.015  0.360  0.251
C18_11d_WS4          0.129     0.274  0.018  0.684  0.278
C18_11d_WW1          0.160     0.184  0.013  0.582  0.266
C18_11d_WW2          0.334     0.212  0.018  0.319  0.342


--------- m19: Metabolites for 2019  -------------------------------

  name          description      class nrow ncol
9  m19 Metabolites for 2019 data.frame   96   60

                    ID        Variety       Date Treat Rep Alanine
C19_22d_WS1 C19_22d_WS1 Cabernet Volos 26.06.2019    WS   1    1.44
C19_22d_WS2 C19_22d_WS2 Cabernet Volos 26.06.2019    WS   2    5.97
C19_22d_WS3 C19_22d_WS3 Cabernet Volos 26.06.2019    WS   3    1.96
C19_22d_WS4 C19_22d_WS4 Cabernet Volos 26.06.2019    WS   4    2.98
C19_22d_WW1 C19_22d_WW1 Cabernet Volos 26.06.2019    WW   1    1.11
C19_22d_WW2 C19_22d_WW2 Cabernet Volos 26.06.2019    WW   2    3.63
           Arabinose Ascorbic.acid Aspartic.acid  GABA
C19_22d_WS1     13.26          3.60         14.69  3.20
C19_22d_WS2     15.15         11.03         10.00  8.23
C19_22d_WS3     10.67          3.34         12.62  9.39
C19_22d_WS4     12.01          2.39         16.12  6.30
C19_22d_WW1     15.16          2.86         15.53 10.23
C19_22d_WW2     13.30          4.67          8.74  7.91
           Trans.Caffeic.acid Catechin Citric.acid Erythronic.acid
C19_22d_WS1               6.18    13.63        5.35            5.97
C19_22d_WS2              12.17    17.04        6.65            6.24
C19_22d_WS3               9.24     3.24        8.05            5.03
C19_22d_WS4              14.66     2.28        8.26            4.81
C19_22d_WW1               5.00    15.94        8.76            5.13
C19_22d_WW2               8.99     9.05        7.03            4.67
           Ethanolamine Fructose Fructose.6.phosphate Fumaric.acid
C19_22d_WS1         6.68    11.71                5.83         5.54
```

C19_22d_WS2	10.69	12.24	7.71	8.39
C19_22d_WS3	8.34	10.82	8.21	4.05
C19_22d_WS4	5.94	10.75	9.73	11.80
C19_22d_WW1	8.68	14.73	13.54	3.79
C19_22d_WW2	6.65	15.20	21.62	5.53

	Galactinol	Galactose	Gallic.acid	Gluconic.acid
C19_22d_WS1	18.37	12.24	8.35	10.27
C19_22d_WS2	14.63	13.59	6.97	11.45
C19_22d_WS3	19.87	11.75	4.26	9.88
C19_22d_WS4	12.76	12.42	11.59	8.80
C19_22d_WW1	11.17	15.85	8.83	8.55
C19_22d_WW2	12.18	14.85	10.23	7.69

	Glucopyranose..H20.	Glucose	Glutamic.acid	Glyceric.acid
C19_22d_WS1	7.92	11.29	40.46	6.60
C19_22d_WS2	13.10	12.31	14.61	7.73
C19_22d_WS3	10.09	11.09	4.98	9.26
C19_22d_WS4	9.05	11.56	7.01	8.10
C19_22d_WW1	6.55	13.44	22.22	6.49
C19_22d_WW2	8.59	12.87	10.24	5.66

	Glycine	Hydroquinone	Myo.Inostol	Isoleucine	Leucine
C19_22d_WS1	7.71	5.76	9.85	18.14	17.99
C19_22d_WS2	8.66	9.66	10.15	14.90	14.61
C19_22d_WS3	16.27	8.18	9.06	13.60	13.96
C19_22d_WS4	16.39	6.41	9.00	19.76	19.64
C19_22d_WW1	9.61	5.49	9.09	24.93	24.59
C19_22d_WW2	22.09	7.93	8.50	6.72	6.62

	Lyxonic.acid	Maleic.acid	Malic.acid	Malonic.acid
C19_22d_WS1	10.61	10.45	9.97	3.38
C19_22d_WS2	11.95	6.52	9.34	9.58
C19_22d_WS3	9.29	5.28	9.45	7.40
C19_22d_WS4	9.88	10.07	8.48	9.60
C19_22d_WW1	9.79	5.66	10.31	3.53
C19_22d_WW2	10.41	4.09	9.20	7.04

	Mannose.6.phosphate	Melibiose	Phenylalanine
C19_22d_WS1	5.06	6.44	10.84
C19_22d_WS2	6.60	6.69	9.08
C19_22d_WS3	8.72	5.63	15.50
C19_22d_WS4	9.13	4.52	19.50
C19_22d_WW1	10.64	6.69	15.80
C19_22d_WW2	14.61	6.01	7.75

	Phosphoric.acid	Proline	Putrescine	Pyroglutamic.acid
C19_22d_WS1	8.37	42.32	9.77	6.61
C19_22d_WS2	10.42	29.09	17.21	11.75
C19_22d_WS3	8.93	27.38	11.09	12.15
C19_22d_WS4	10.84	24.39	11.07	13.65
C19_22d_WW1	16.18	37.14	26.02	4.01
C19_22d_WW2	17.27	2.09	6.03	6.17

	Quinic.acid	X3.caffeoylquinic.acid	Raffinose	Rhamnose
C19_22d_WS1	15.57	22.62	12.69	8.65
C19_22d_WS2	17.79	26.34	11.81	7.16
C19_22d_WS3	16.01	21.82	12.97	7.92
C19_22d_WS4	13.27	27.36	8.93	7.18
C19_22d_WW1	13.87	23.22	9.27	8.09

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C19_22d_WW2       14.48                  21.36      9.21     7.63
           Ribonic.acid Ribose Serine Shikimic.acid Succinic.acid
C19_22d_WS1         10.72   8.67   7.52         25.77         14.82
C19_22d_WS2         12.01  10.68  10.27         27.03         14.23
C19_22d_WS3          9.29   8.24  23.26         26.88         12.09
C19_22d_WS4          9.88   8.45  22.24         22.56          8.96
C19_22d_WW1          9.90   8.22  10.73         25.90         11.32
C19_22d_WW2         10.44   9.96   7.29         25.63         10.23
           Sucrose Tartaric.acid Threitol Threonic.acid
C19_22d_WS1    9.14          5.49     8.74          6.89
C19_22d_WS2    9.58          7.20     7.03          5.86
C19_22d_WS3    8.30          7.11    13.37          4.25
C19_22d_WS4    9.41          7.89     9.49          2.89
C19_22d_WW1    9.33          6.96     7.26          3.78
C19_22d_WW2    9.51          7.55    12.28          5.13
           Threonolactone Threonine Uracil Valine Xylose
C19_22d_WS1           7.24     11.78   6.22  24.43   9.58
C19_22d_WS2           6.31     13.48   9.03  18.07  11.19
C19_22d_WS3           4.64      9.94   7.75  24.16   8.97
C19_22d_WS4           3.07      7.60  13.93  18.60   9.80
C19_22d_WW1           6.32      7.58   9.59  26.02  11.86
C19_22d_WW2           7.49      7.14   8.35   9.35  10.21


--------- m1819: Metabolites for 18/19  -------------------------------

    name           description      class nrow ncol
10 m1819 Metabolites for 18/19 data.frame  192   60

                    ID        Variety       Date Treat Rep Alanine
C18_11d_WS1 C18_11d_WS1 Cabernet Volos 12.06.2018    WS   1   0.133
C18_11d_WS2 C18_11d_WS2 Cabernet Volos 12.06.2018    WS   2   0.115
C18_11d_WS3 C18_11d_WS3 Cabernet Volos 12.06.2018    WS   3   0.624
C18_11d_WS4 C18_11d_WS4 Cabernet Volos 12.06.2018    WS   4   0.649
C18_11d_WW1 C18_11d_WW1 Cabernet Volos 12.06.2018    WW   1   0.136
C18_11d_WW2 C18_11d_WW2 Cabernet Volos 12.06.2018    WW   2   0.230
           Arabinose Ascorbic.acid Aspartic.acid  GABA
C18_11d_WS1     0.116         0.885         0.882 1.950
C18_11d_WS2     0.120         1.147         0.613 1.054
C18_11d_WS3     0.094         1.080         0.715 1.401
C18_11d_WS4     0.112         1.587         0.827 1.705
C18_11d_WW1     0.160         0.769         0.549 1.929
C18_11d_WW2     0.147         0.903         0.625 1.513
           Trans.Caffeic.acid Catechin Citric.acid Erythronic.acid
C18_11d_WS1              8.751    2.828       2.236           1.696
C18_11d_WS2              9.164    3.595       2.152           2.039
C18_11d_WS3              7.039    2.059       1.996           1.791
C18_11d_WS4              7.379    1.880       2.619           1.587
C18_11d_WW1              8.197    1.930       2.290           1.999
C18_11d_WW2              7.093    1.419       2.056           1.301
           Ethanolamine Fructose Fructose.6.phosphate Fumaric.acid
C18_11d_WS1        1.052   27.962                0.037        0.683
C18_11d_WS2        0.865   22.260                0.035        1.069
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C18_11d_WS3	1.335	14.477	0.058	1.907
C18_11d_WS4	0.901	16.651	0.079	2.009
C18_11d_WW1	0.861	22.621	0.033	0.760
C18_11d_WW2	0.805	20.318	0.089	1.094

	Galactinol	Galactose	Gallic.acid	Gluconic.acid
C18_11d_WS1	16.908	8.455	1.002	3.640
C18_11d_WS2	13.660	8.218	0.958	3.911
C18_11d_WS3	13.524	4.445	0.936	3.079
C18_11d_WS4	14.463	6.358	0.905	3.421
C18_11d_WW1	15.754	6.071	1.143	3.133
C18_11d_WW2	13.891	5.467	0.917	2.805

	Glucopyranose..H20.	Glucose	Glutamic.acid	Glyceric.acid
C18_11d_WS1	0.143	43.309	0.491	7.540
C18_11d_WS2	0.155	41.412	0.298	6.082
C18_11d_WS3	0.178	31.305	0.140	5.876
C18_11d_WS4	0.153	40.981	0.202	7.596
C18_11d_WW1	0.169	37.135	0.303	6.008
C18_11d_WW2	0.156	35.269	0.263	5.638

	Glycine	Hydroquinone	Myo.Inostol	Isoleucine	Leucine
C18_11d_WS1	0.742	0.161	91.071	0.055	0.022
C18_11d_WS2	0.727	0.208	89.166	0.054	0.027
C18_11d_WS3	0.913	0.099	97.202	0.072	0.033
C18_11d_WS4	0.742	0.176	114.143	0.150	0.079
C18_11d_WW1	1.031	0.101	85.266	0.146	0.077
C18_11d_WW2	0.847	0.161	90.745	0.096	0.050

	Lyxonic.acid	Maleic.acid	Malic.acid	Malonic.acid
C18_11d_WS1	1.028	1.093	66.326	0.166
C18_11d_WS2	1.187	1.486	73.855	0.140
C18_11d_WS3	1.237	1.108	62.877	0.183
C18_11d_WS4	1.020	1.084	66.638	0.233
C18_11d_WW1	1.205	0.879	53.894	0.156
C18_11d_WW2	1.096	1.202	51.917	0.170

	Mannose.6.phosphate	Melibiose	Phenylalanine
C18_11d_WS1	0.088	0.227	0.095
C18_11d_WS2	0.102	0.204	0.116
C18_11d_WS3	0.134	0.069	0.103
C18_11d_WS4	0.174	0.092	0.203
C18_11d_WW1	0.082	0.178	0.104
C18_11d_WW2	0.198	0.164	0.179

	Phosphoric.acid	Proline	Putrescine	Pyroglutamic.acid
C18_11d_WS1	23.244	0.011	0.054	5.790
C18_11d_WS2	17.190	0.013	0.046	4.354
C18_11d_WS3	18.909	0.006	0.104	8.169
C18_11d_WS4	23.579	0.008	0.111	10.445
C18_11d_WW1	31.264	0.006	0.066	4.966
C18_11d_WW2	31.233	0.008	0.058	5.408

	Quinic.acid	X3.caffeoylquinic.acid	Raffinose	Rhamnose
C18_11d_WS1	1.615	0.677	1.117	0.603
C18_11d_WS2	1.304	0.635	1.544	0.472
C18_11d_WS3	1.254	0.378	0.961	0.516
C18_11d_WS4	1.106	0.423	1.164	0.634
C18_11d_WW1	1.985	0.576	0.870	0.534
C18_11d_WW2	1.513	0.462	1.001	0.747

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            Ribonic.acid Ribose Serine Shikimic.acid Succinic.acid
C18_11d_WS1        0.270  0.151  0.997        23.883         0.139
C18_11d_WS2        0.237  0.152  0.609        13.037         0.133
C18_11d_WS3        0.361  0.162  0.895        14.551         0.089
C18_11d_WS4        0.293  0.154  1.116        14.364         0.106
C18_11d_WW1        0.326  0.164  0.465        23.607         0.140
C18_11d_WW2        0.326  0.164  0.551        18.038         0.119
            Sucrose Tartaric.acid Threitol Threonic.acid
C18_11d_WS1  96.247        58.764    0.025         2.632
C18_11d_WS2 101.273        36.403    0.018         2.741
C18_11d_WS3 114.777        30.620    0.027         2.645
C18_11d_WS4 122.686        52.311    0.033         2.387
C18_11d_WW1  99.984        47.986    0.032         3.639
C18_11d_WW2 105.411        44.912    0.031         3.759
            Threonolactone Threonine Uracil Valine Xylose
C18_11d_WS1          0.145     0.244  0.011  0.267  0.297
C18_11d_WS2          0.121     0.187  0.017  0.259  0.231
C18_11d_WS3          0.086     0.216  0.015  0.360  0.251
C18_11d_WS4          0.129     0.274  0.018  0.684  0.278
C18_11d_WW1          0.160     0.184  0.013  0.582  0.266
C18_11d_WW2          0.334     0.212  0.018  0.319  0.342


--------- sm1819: Standardized metabolites 18/19  ----------------------------

     name                      description  class nrow ncol
11 sm1819 Standardized metabolites 18/19 matrix   55  192

                  C18_11d_WS1 C18_11d_WS2 C18_11d_WS3 C18_11d_WS4
Alanine           -1.42040510  -1.5237244  -0.3221074  -0.2941971
Arabinose         -0.89096253  -0.8768234  -0.9786693  -0.9055979
Ascorbic.acid     -0.48475127  -0.3013277  -0.3439011  -0.0716600
Aspartic.acid     -0.79435180  -1.0652846  -0.9506661  -0.8422994
GABA              -0.79478369  -1.3283418  -1.0815306  -0.9112230
Trans.Caffeic.acid  0.04856765   0.1856718  -0.5986832  -0.4584358
                  C18_11d_WW1 C18_11d_WW2 C18_11d_WW3 C18_11d_WW4
Alanine            -1.4045568  -1.0312407  -0.8260696  -0.9777046
Arabinose          -0.7568413  -0.7921839  -0.9055979  -0.8982160
Ascorbic.acid      -0.5841291  -0.4705092  -0.5050201  -0.4658249
Aspartic.acid      -1.1473972  -1.0508478  -1.2872479  -1.0472819
GABA               -0.8041739  -1.0148328  -0.8827044  -1.2282093
Trans.Caffeic.acid -0.1458728  -0.5759619  -0.4884020  -1.1855997
                  C18_20d_WS1 C18_20d_WS2 C18_20d_WS3 C18_20d_WS4
Alanine           -1.30253488  -1.1485305  -0.4301155  -0.4301155
Arabinose         -0.82156681  -0.9093384  -0.9487134  -0.8945735
Ascorbic.acid     -0.40759378  -0.3990459  -0.2193190  -0.3969249
Aspartic.acid     -0.68028375  -1.1419912  -0.7477177  -1.0665004
GABA              -0.55840143  -0.6637706  -0.8598745  -0.8432557
Trans.Caffeic.acid  0.06651981  -0.6147770  -1.0784674  -0.9712290
                  C18_20d_WW1 C18_20d_WW2 C18_20d_WW3 C18_20d_WW4
Alanine            -1.1669862  -1.1745048  -0.7070211 -0.67637466
Arabinose          -0.8733622  -0.9612891  -0.8277002 -0.96988871
Ascorbic.acid      -0.1710309  -0.3976312  -0.3309222 -0.08880282
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Aspartic.acid       -0.9979629  -1.0091444  -0.8262651 -1.22149861
GABA                -0.9178608  -0.9071634  -0.5883746 -0.86516407
Trans.Caffeic.acid   0.6097629  -0.1444223  -0.2703104 -0.43635765
                   C18_34d_WS1 C18_34d_WS2 C18_34d_WS3 C18_34d_WS4
Alanine             -0.6524125  -0.7493615  -0.5607169 -0.65060226
Arabinose           -0.8434404  -0.9285614  -0.8803135 -0.90559788
Ascorbic.acid       -0.3934041  -0.3618092  -0.4391011 -0.57954495
Aspartic.acid       -0.5681871  -1.3362907  -1.4955004 -1.23969930
GABA                 0.5383838   0.6785329   0.4481893  0.08421358
Trans.Caffeic.acid   1.2085257   1.0325340   0.9791050  0.67184120
                   C18_34d_WW1 C18_34d_WW2 C18_34d_WW3 C18_34d_WW4
Alanine             -0.4938681  -0.7208561 -0.57357704 -0.17365428
Arabinose           -0.8499066  -1.0407476 -0.92464525 -0.84666098
Ascorbic.acid       -0.8649740  -0.2872844 -0.49847064 -0.57499031
Aspartic.acid       -0.8642301  -2.2922701 -1.90683969 -0.97716973
GABA                 0.9929407   0.1022634  0.51365512 -0.08629024
Trans.Caffeic.acid   0.9342980  -0.3488723 -0.05127649 -0.20189133
                   C18_49d_WS1 C18_49d_WS2 C18_49d_WS3 C18_49d_WS4
Alanine             -0.2726324 -0.35831179 -0.58173446 -0.61190189
Arabinose           -1.0255800 -0.92856138 -0.94871336 -1.00617809
Ascorbic.acid       -0.6890378 -0.72067394 -0.74913040 -0.77756970
Aspartic.acid       -1.4783807 -1.33979505 -1.52418769 -1.82838040
GABA                 0.2730391 -0.05768882  0.01397647 -0.01902277
Trans.Caffeic.acid  -0.7596655 -0.95833043 -1.34574708 -0.80549633
                   C18_49d_WW1 C18_49d_WW2 C18_49d_WW3 C18_49d_WW4
Alanine            -0.78777647  -0.8640990  -0.8123175 -1.01596046
Arabinose          -1.02557995  -0.7674005  -0.9246452 -0.82770022
Ascorbic.acid      -0.63168277  -0.9822666  -1.0052447 -0.84341555
Aspartic.acid      -1.64349297  -1.5802398  -1.4372280 -1.68141186
GABA               -0.89011882  -0.3070515  -0.2091395 -0.03424594
Trans.Caffeic.acid -0.09552259   0.4665606  -0.6970157  0.64777629
                   C18_61d_WS1 C18_61d_WS2 C18_61d_WS3 C18_61d_WS4
Alanine             -0.3989935 -0.48953135  -0.9199530  -0.8991309
Arabinose           -1.0014654 -0.95705493  -0.9698887  -1.0061781
Ascorbic.acid       -0.8649740 -1.07533485  -1.2382552  -1.0429323
Aspartic.acid       -0.5700590 -0.60196936  -0.3984122  -0.5020430
GABA                 0.2573183  0.03096133   0.2921707  -0.1017523
Trans.Caffeic.acid  -0.1502284 -1.07152665  -0.8442359  -1.2882030
                   C18_61d_WW1 C18_61d_WW2 C18_61d_WW3 C18_61d_WW4
Alanine             -0.6973013  -0.7109465  -1.3993516  -1.2173427
Arabinose           -0.8499066  -0.9365057  -0.9169216  -1.0841181
Ascorbic.acid       -0.5713676  -0.4823576  -0.8554612  -0.7584837
Aspartic.acid       -0.9913337  -1.3720993  -1.0616491  -1.3328028
GABA                 0.1848340  -0.3855115   0.1932726   0.4195016
Trans.Caffeic.acid  -0.4069089   0.1514097  -0.3879618  -1.1184425
                   C18_67d_WS1 C18_67d_WS2 C18_67d_WS3 C18_67d_WS4
Alanine             -0.2683969  -0.2996921  -1.0099392  -0.9834577
Arabinose           -1.0511748  -0.9405354  -0.9968055  -0.9528633
Ascorbic.acid       -1.2546783  -0.9234174  -0.9445333  -1.0808826
Aspartic.acid       -0.6752302  -0.7219964  -0.8849168  -0.8531840
GABA                 0.4999725   0.4293145   0.5888935   0.5085247
Trans.Caffeic.acid  -0.4596448  -0.5297954  -1.1254938  -0.6948336
                   C18_67d_WW1 C18_67d_WW2 C18_67d_WW3 C18_67d_WW4
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Alanine             -0.4668387  -0.4710387  -1.1412804  -1.1164723
Arabinose           -0.9876388  -1.0109446  -0.8665250  -0.9786693
Ascorbic.acid       -0.8663435  -1.2546783  -1.4019136  -0.9969523
Aspartic.acid       -1.0472819  -0.7572957  -1.6023971  -1.0592352
GABA                 0.2650833   0.1418167   0.1148187   0.1764576
Trans.Caffeic.acid  -1.2192354  -0.4762171  -0.4916597  -0.7092651
                   F18_10d_WS1 F18_10d_WS2 F18_10d_WS3 F18_10d_WS4
Alanine             -0.6801339  -0.7855869  -1.9290988  -1.9182512
Arabinose           -1.1325277  -1.0673212  -0.9921970  -1.0784436
Ascorbic.acid       -0.6795006  -0.6763499  -0.5668652  -0.8368111
Aspartic.acid       -0.2260179  -0.5146942  -0.4114244  -0.6291963
GABA                -3.5975121  -3.8432554  -3.7854179  -3.7311978
Trans.Caffeic.acid  -1.1712269  -1.5566942  -0.8241195  -1.2690901
                   F18_10d_WW1 F18_10d_WW2 F18_10d_WW3 F18_10d_WW4
Alanine             -1.0189903 -1.11647226 -1.80872651  -1.7554137
Arabinose           -0.8982160 -0.91311277 -0.83080109  -0.9093384
Ascorbic.acid       -0.4550139 -0.59525382 -0.45348288  -0.3399824
Aspartic.acid       -0.3429779 -0.32748229 -0.32433165  -0.2883839
GABA                -3.3285334 -3.39726159 -3.38836674  -3.5016458
Trans.Caffeic.acid   0.1091013 -0.06183566  0.02982272  -0.3442159
                   F18_20d_WS1 F18_20d_WS2 F18_20d_WS3 F18_20d_WS4
Alanine             -0.3989935  -0.4367744  -1.3639455  -1.1707356
Arabinose           -1.0511748  -0.9968055  -0.9968055  -0.6679676
Ascorbic.acid       -0.8704679  -0.8677156  -1.0607502  -0.9838834
Aspartic.acid       -0.6151265  -0.5961236  -1.0437330  -0.9611546
GABA                -0.8901188  -0.9636402  -0.8109439  -0.8724295
Trans.Caffeic.acid  -1.0670733   0.1618934  -1.2775696  -0.6335214
                   F18_20d_WW1 F18_20d_WW2 F18_20d_WW3 F18_20d_WW4
Alanine             -0.8689990  -0.6915326  -1.1199637  -1.2054012
Arabinose           -1.0728454  -1.0157662  -1.0014654  -0.9246452
Ascorbic.acid       -0.7206739  -0.6879717  -0.8315716  -1.3566288
Aspartic.acid       -0.8019896  -0.8716862  -0.9696531  -0.7143743
GABA                -1.4867876  -1.1085653  -0.6976926  -0.5317253
Trans.Caffeic.acid  -0.1044514   0.3399237  -0.5600763  -0.4463728
                   F18_34d_WS1 F18_34d_WS2 F18_34d_WS3 F18_34d_WS4
Alanine            -1.14853050 -1.00100193  -1.1164723  -1.1975502
Arabinose          -1.00146544 -1.01094460  -0.9612891  -0.9285614
Ascorbic.acid      -0.77035196 -0.80594079  -0.8447439  -1.0052447
Aspartic.acid      -0.08906787 -0.47296796  -0.3583326  -0.6157905
GABA               -0.71172267 -0.08786346  -0.4482032  -0.7101077
Trans.Caffeic.acid  0.38304173 -0.64636973  -0.3687437  -0.5260834
                   F18_34d_WW1 F18_34d_WW2 F18_34d_WW3 F18_34d_WW4
Alanine            -0.798826516  -0.6763747  -0.9468693  -0.7966027
Arabinose          -0.786547801  -1.0618693  -1.0673212  -0.8597980
Ascorbic.acid      -1.754522307  -1.7216172  -1.6112704  -1.8200162
Aspartic.acid      -0.139533413  -0.3959358  -0.9190598   0.1918374
GABA               -0.832505609  -1.1659845  -0.9086835  -0.7763030
Trans.Caffeic.acid -0.007332999  -0.0951660   0.1746206  -0.1098216
                   F18_49d_WS1 F18_49d_WS2 F18_49d_WS3 F18_49d_WS4
Alanine             -0.8813990  -0.9359801  -0.8689990  -0.6839132
Arabinose           -1.0459286  -1.1016199  -1.0511748  -1.1729203
Ascorbic.acid       -1.2523087  -1.4287209  -1.6685424  -1.3649018
Aspartic.acid       -1.8737376  -0.5322996  -0.9362259  -0.8877828
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GABA                 0.7166446   0.5230477   0.3452471  -0.3126450
Trans.Caffeic.acid  -0.2820581  -0.6232825  -1.7938439  -1.9520321
                   F18_49d_WW1 F18_49d_WW2 F18_49d_WW3 F18_49d_WW4
Alanine            -1.20935940  -1.2054012  -0.9359801 -1.08247037
Arabinose          -1.02064421  -1.1455620  -1.0564878 -0.97425592
Ascorbic.acid      -1.29874782  -0.6455914  -1.1911571 -1.22903904
Aspartic.acid      -0.81750417  -1.1487549  -1.0091444 -0.90130513
GABA               -0.15176956  -0.2414255   0.2016299  0.03950059
Trans.Caffeic.acid  0.03460538  -0.6957063  -1.5433162 -0.96405620
                   F18_61d_WS1 F18_61d_WS2 F18_61d_WS3 F18_61d_WS4
Alanine            -1.34929542 -0.93868678  -0.6763747  -0.7309058
Arabinose          -1.23369161 -1.13899393  -1.1016199  -1.1590169
Ascorbic.acid      -1.26906519 -1.31406969  -1.3704714  -1.4888883
Aspartic.acid      -0.21430282 -0.19480061  -0.7851219  -0.9990735
GABA               -0.02029638  0.05699739   0.1523252  -0.5607751
Trans.Caffeic.acid -0.70269666 -0.52361129  -1.5901101  -2.9498706
                   F18_61d_WW1 F18_61d_WW2 F18_61d_WW3 F18_61d_WW4
Alanine             -1.6822688  -1.9075667  -1.2014648  -0.5559537
Arabinose           -1.0898708  -1.1590169  -1.1137095  -1.0109446
Ascorbic.acid       -1.2666470  -1.3270964  -1.2475931  -1.1634985
Aspartic.acid       -0.3489890  -0.8849168  -0.5813898  -0.6058921
GABA                -0.5567099  -0.4547891  -0.1848092  -0.3841255
Trans.Caffeic.acid  -1.4116358  -0.8760588  -1.1559043  -1.2052175
                   F18_67d_WS1 F18_67d_WS2 F18_67d_WS3 F18_67d_WS4
Alanine             -1.2335835 -1.11996369 -0.50409137 -0.87641303
Arabinose           -1.1590169 -1.06732124 -1.20985284 -1.13899393
Ascorbic.acid       -1.5124122 -1.74023228 -1.03245310 -1.07717926
Aspartic.acid       -0.5406601 -0.93929677 -1.34862878 -0.87168620
GABA                 0.2083702  0.09671283 -0.02981653  0.09527977
Trans.Caffeic.acid  -0.1524087 -0.99816120 -0.53930272 -0.52649560
                   F18_67d_WW1 F18_67d_WW2 F18_67d_WW3 F18_67d_WW4
Alanine            -0.68771273  -0.8145911  -0.9120730  -0.4301155
Arabinose          -1.05648778  -1.0957039  -1.1198884  -1.2589760
Ascorbic.acid      -1.44717412  -1.6434274  -1.3931989  -1.3403676
Aspartic.acid      -1.06407077  -0.9600991  -0.9869468  -1.2856130
GABA                0.09272624  -0.1293893  -0.1176987   0.3447692
Trans.Caffeic.acid -1.74127656  -2.3749262  -2.4456161  -3.0910196
                   C19_22d_WS1 C19_22d_WS2 C19_22d_WS3 C19_22d_WS4
Alanine              0.2720501   1.2824603   0.4910994   0.7887854
Arabinose            1.0854730   1.1410463   0.9948382   1.0441785
Ascorbic.acid        0.5077076   1.2996969   0.4546839   0.2179557
Aspartic.acid        1.3002167   1.0138284   1.1871125   1.3693923
GABA                -0.3652211   0.4540044   0.5683581   0.2222463
Trans.Caffeic.acid  -0.9856266   1.0291158   0.2102271   1.5825560
                   C19_22d_WW1 C19_22d_WW2 C19_22d_WW3 C19_22d_WW4
Alanine             0.08711792   0.9289745   0.2769671   0.7027119
Arabinose           1.14132150   1.0867292   1.0819988   1.0329153
Ascorbic.acid       0.34494184   0.6917733   0.9890956   0.5804620
Aspartic.acid       1.34162557   0.9135394   1.5509238   1.1114018
GABA                0.64266257   0.4196112   0.1871306  -0.4626375
Trans.Caffeic.acid -1.61556947   0.1286776   0.2005584   1.4285608
                   C19_44d_WS1 C19_44d_WS2 C19_44d_WS3 C19_44d_WS4
Alanine              1.0050069    1.589722   0.8824669   0.8029488
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Arabinose	0.9092302	1.045219	0.8819613	1.0608565
Ascorbic.acid	1.7487219	1.213896	1.7487219	1.2801920
Aspartic.acid	1.2843338	1.096224	0.8750735	0.8839919
GABA	0.6856613	1.682973	0.4508374	1.5866186
Trans.Caffeic.acid	0.5475100	-0.466101	0.3607963	1.7095972
	C19_44d_WW1	C19_44d_WW2	C19_44d_WW3	C19_44d_WW4
Alanine	0.7107403	1.1125188	0.5264551	0.8304556
Arabinose	0.9789026	1.0213394	0.9797140	1.0146840
Ascorbic.acid	1.3785054	1.5556943	1.1228496	0.8010254
Aspartic.acid	0.5339921	0.4810936	0.5672792	0.7640104
GABA	0.9245993	0.7243169	0.6443564	0.6443564
Trans.Caffeic.acid	-0.0908902	0.3851661	0.3851661	1.8388831
	C19_49d_WS1	C19_49d_WS2	C19_49d_WS3	C19_49d_WS4
Alanine	1.1079692	1.675464089	0.9633604	1.0067634
Arabinose	1.0791345	1.012816267	0.9252369	0.9817356
Ascorbic.acid	1.2854461	1.809587711	1.5636868	1.5389760
Aspartic.acid	0.7460909	1.178805258	1.0565169	0.6814897
GABA	0.8617421	0.610714821	0.1885628	1.4648404
Trans.Caffeic.acid	-0.6882969	-0.006640693	0.8659242	1.6067934
	C19_49d_WW1	C19_49d_WW2	C19_49d_WW3	C19_49d_WW4
Alanine	0.71074026	1.1125188	1.0460089	1.2458283
Arabinose	0.99717689	1.0124417	0.8214110	0.9321080
Ascorbic.acid	0.90241827	1.2196641	1.3575459	1.3054450
Aspartic.acid	0.31834284	0.5886717	0.4672602	0.2384083
GABA	-0.07535686	0.7774375	0.5169933	0.6246747
Trans.Caffeic.acid	-0.26690844	-0.5856183	0.9473843	1.5784971
	C19_55d_WS1	C19_55d_WS2	C19_55d_WS3	C19_55d_WS4
Alanine	1.13043165	NA	0.7368647	1.3240626
Arabinose	1.00602230	NA	0.9631780	0.9302867
Ascorbic.acid	1.24018846	NA	0.8036164	1.5086137
Aspartic.acid	1.02271128	NA	0.5452540	0.4323224
GABA	0.12780899	NA	0.2139473	0.7509098
Trans.Caffeic.acid	0.04142443	NA	0.8400033	1.3308596
	C19_55d_WW1	C19_55d_WW2	C19_55d_WW3	C19_55d_WW4
Alanine	0.7982590	1.37285782	0.7394250	0.8590999
Arabinose	1.0044974	1.05004056	0.8995193	1.0094331
Ascorbic.acid	0.5606877	0.34246432	1.0371665	0.8126107
Aspartic.acid	0.7681648	1.38403013	0.7178225	0.3695937
GABA	0.2586393	0.05583074	0.2625903	0.2612753
Trans.Caffeic.acid	0.3821308	1.00950745	1.0943552	1.5252216
	C19_34d_WS1	C19_34d_WS2	C19_34d_WS3	C19_34d_WS4
Alanine	0.24694130	1.22934840	1.0223795	1.2124772
Arabinose	1.02861189	0.99795354	1.0978681	1.0697692
Ascorbic.acid	1.23528856	0.98710311	1.1843270	1.2239597
Aspartic.acid	1.59074795	1.67071566	1.2894944	1.1576225
GABA	-0.54863624	0.21948879	0.1726762	-0.6823219
Trans.Caffeic.acid	0.02434738	-0.04495894	0.9624127	1.8518783
	C19_34d_WW1	C19_34d_WW2	C19_34d_WW3	C19_34d_WW4
Alanine	0.7959024	1.3206873	0.8393928	1.1621430
Arabinose	0.9833459	1.0224384	1.0187638	0.9825415
Ascorbic.acid	1.9365717	1.7099495	1.6531531	1.6213218
Aspartic.acid	0.5939251	0.4991472	0.7524648	0.4901751
GABA	-0.5968286	-0.8836893	-0.5587401	-0.5320537

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Trans.Caffeic.acid   0.3423869   0.6044133   0.9448722   1.8220911
                  C19_65d_WS1 C19_65d_WS2 C19_65d_WS3 C19_65d_WS4
Alanine            0.86981662  1.84944595   0.7419762   1.0656555
Arabinose          1.04521895  0.98495000   0.9097098   1.0195013
Ascorbic.acid      0.97299630  1.11206313   0.6856887   0.9439095
Aspartic.acid      0.85322328  1.30526880   0.5577232   0.8354587
GABA               1.20433121  1.36540008   0.7150083   1.2007751
Trans.Caffeic.acid -0.03445944 -0.05549566   1.0847800   1.4646504
                  C19_65d_WW1 C19_65d_WW2 C19_65d_WW3 C19_65d_WW4
Alanine            0.57960166   1.1992211   0.1542540   0.7520903
Arabinose          0.91257627   0.9516337   0.9516337   0.9998889
Ascorbic.acid      0.29366343   0.6826267   0.1969294   0.5945038
Aspartic.acid      0.64083931   0.2913310   0.4547444   0.5225574
GABA               0.42942294   0.3428547   0.7803355   0.5515722
Trans.Caffeic.acid 0.05840396   0.4894964   1.1884487   1.7482095
                  F19_22d_WS1 F19_22d_WS2 F19_22d_WS3 F19_22d_WS4
Alanine            0.08711792   0.9961587   0.4105789   0.8525914
Arabinose          1.13438644   1.1432428   1.0531110   1.1503027
Ascorbic.acid      0.62177779   1.1895916   1.5380609   0.8049083
Aspartic.acid      1.60434969   1.4023739   1.3957151   1.2718004
GABA               0.21255637   0.7219991   0.8669941   0.1028955
Trans.Caffeic.acid -0.08377750  0.3730062   0.2262719   1.4200051
                  F19_22d_WW1 F19_22d_WW2 F19_22d_WW3 F19_22d_WW4
Alanine           -0.25067245   1.1049198  0.48746506   0.7570939
Arabinose          1.10483199   1.0571701  1.13911481   1.1481431
Ascorbic.acid      0.51357764   1.1659735  1.29195938   0.8389273
Aspartic.acid      0.90840960   1.0901997  1.22675356   0.9621851
GABA              -0.07535686   0.1871306  0.07887073  -0.4872417
Trans.Caffeic.acid 0.10543713   0.5475100  0.46005943   1.5231533
                  F19_44d_WS1 F19_44d_WS2 F19_44d_WS3 F19_44d_WS4
Alanine             0.8259444  1.36442444   0.4105789   0.7887854
Arabinose           0.9563756  1.06681937   1.0033500   1.0531110
Ascorbic.acid       1.0591295  0.39506053   0.6300897   0.8339895
Aspartic.acid       1.5709259  1.53408190   1.3305144   1.2103491
GABA                1.0629968  1.63329752   0.8199230   1.1475028
Trans.Caffeic.acid  0.1120958  0.09542104   0.7068967   1.9051184
                  F19_44d_WW1 F19_44d_WW2 F19_44d_WW3 F19_44d_WW4
Alanine             0.3104650   0.9131409   0.5264551   0.2720501
Arabinose           1.0674767   0.9913054   0.9402066   1.0835816
Ascorbic.acid       0.3399781   1.3168030   1.0202349   0.5289969
Aspartic.acid       0.7535218   0.7825253   0.5820523   0.7671283
GABA                0.2922977   0.8397348   0.4971698   0.5866357
Trans.Caffeic.acid  0.2358574   0.8400033   0.8555830   1.6566622
                  F19_47d_WS1 F19_47d_WS2 F19_47d_WS3 F19_47d_WS4
Alanine           0.643819879   0.7265299   0.9328784   0.3730656
Arabinose         0.984549552   0.9116230   0.9627561   1.0794538
Ascorbic.acid     1.115399611   0.7228861   1.1011096   0.3740144
Aspartic.acid     1.477155992   1.3310010   1.4589479   0.9228533
GABA              1.292014347   1.2231993   0.6742929   0.7583604
Trans.Caffeic.acid 0.003724593 -0.3049282   1.2275540   1.3725035
                  F19_47d_WW1 F19_47d_WW2 F19_47d_WW3 F19_47d_WW4
Alanine             0.7317161   1.2241998   0.9726240   0.8168353
Arabinose           0.9361769   0.9849500   0.9813321   0.9572320
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Ascorbic.acid        0.6560497   0.8189660   0.7945062   1.0390231
Aspartic.acid        1.0408838   1.2011413   0.9541606   0.9278849
GABA                 0.5430559   0.2331895   0.8136814   0.3185607
Trans.Caffeic.acid  -0.3982098  -0.2518356   0.8736566   1.7018142
                   F19_55d_WS1 F19_55d_WS2 F19_55d_WS3 F19_55d_WS4
Alanine              1.7003494   1.5492019   1.0656555   1.4966108
Arabinose            0.9158957   0.8689514   1.0228041   0.9063406
Ascorbic.acid        0.4589067   0.4132566   0.5892707   0.9831012
Aspartic.acid        1.4023739   0.8633176   0.8401748   0.2913310
GABA                 1.2175382   1.1873084   1.0482528   1.0795457
Trans.Caffeic.acid   0.1940951  -0.5026811   1.1038997   1.5560739
                   F19_55d_WW1 F19_55d_WW2 F19_55d_WW3 F19_55d_WW4
Alanine                   NA   1.52169511   1.1245108   1.3070234
Arabinose                 NA   0.80939103   0.9252369   1.0154288
Ascorbic.acid             NA   0.54221849   0.6749130   0.5839986
Aspartic.acid             NA   1.03800586   0.5978411   1.0093469
GABA                      NA   1.01689035   0.9091511   0.8908794
Trans.Caffeic.acid        NA   0.09207483   1.2548512   1.6208412
                   F19_34d_WS1 F19_34d_WS2 F19_34d_WS3 F19_34d_WS4
Alanine              0.7982590   1.6432584   0.3151241   1.4455128
Arabinose            1.0848435   1.0064027   0.8057164   1.0476367
Ascorbic.acid        0.5661358   0.8642997   0.5327998   1.1518890
Aspartic.acid        1.0621212   1.1758158   1.1823768   0.7629681
GABA                 0.2922977   0.3688149  -0.1252694   0.5893444
Trans.Caffeic.acid  -0.3087571   0.1843738  -2.7709424   1.4709739
                   F19_34d_WW1 F19_34d_WW2 F19_34d_WW3 F19_34d_WW4
Alanine              0.4910994   1.3318766  0.43059441   0.9799488
Arabinose            0.9861490   0.8855325  0.95422686   1.0601886
Ascorbic.acid        0.8853459   1.1605295  0.70080322   0.6480391
Aspartic.acid        0.5686344   0.6518175  0.34440911   0.4841331
GABA                 0.6644284   0.4412663  0.06907130   0.3917591
Trans.Caffeic.acid   0.5503812   0.4511712  0.02434738   1.5478779
                   F19_65d_WS1 F19_65d_WS2 F19_65d_WS3 F19_65d_WS4
Alanine              1.1691569  1.54838383   0.9781247   1.0816225
Arabinose            1.0406913  1.10960874   0.9669562   1.0242637
Ascorbic.acid        0.3015962  0.13316265   1.0240327   0.4243959
Aspartic.acid        0.5899885  0.95818365   1.0365627   0.8839919
GABA                 0.9511372  0.90352165   1.3277535   0.9911842
Trans.Caffeic.acid  -0.1922971  0.04142443   1.0315578   1.5293538
                   F19_65d_WW1 F19_65d_WW2 F19_65d_WW3 F19_65d_WW4
Alanine              1.2280647  1.94458838   0.7767631   1.2137893
Arabinose            0.8850242  0.94065190   0.9388677   1.1084197
Ascorbic.acid        0.4958194  0.22090909   0.5057401   0.8487006
Aspartic.acid        1.0962240  0.77537968   0.4531650   0.5873525
GABA                 0.7258587  0.61510148   0.7196751   0.7304676
Trans.Caffeic.acid   0.6324617  0.02434738   1.2751610   1.3898648


--------- mfdata: Metabolites featuredata 18/19  ----------------------------

     name                    description      class nrow ncol
12 mfdata Metabolites featuredata 18/19 data.frame   55    3
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                           Metabolite           Bin
Alanine                       Alanine        5.1001
Arabinose                   Arabinose     10.6.1001
Ascorbic.acid           Ascorbic acid     17.5.1001
Aspartic.acid           Aspartic acid 13.1.1.2.1001
GABA                            GABA       22.1002
Trans.Caffeic.acid Trans-Caffeic acid   16.2.1.1006

Alanine
Arabinose                                                          cell wall
Ascorbic.acid                                                  hormone metabol
Aspartic.acid      amino acid metabolism.synthesis.central amino acid metaboli
GABA                                                                     pol
Trans.Caffeic.acid                secondary metabolism.phenylpropanoids.lignin


--------- intgenes: Names of genes in bins  ------------------------------

       name            description class nrow ncol
13 intgenes Names of genes in bins  list   22 <NA>

$`1.2`
[1] "Vitvi07g03141" "Vitvi01g00157" "Vitvi02g00436" "Vitvi02g00437"
[5] "Vitvi02g00572" "Vitvi02g00680"

$`1.3`
[1] "Vitvi01g00086" "Vitvi01g00360" "Vitvi01g01058" "Vitvi02g00915"
[5] "Vitvi03g00048" "Vitvi03g00097"

$`2.1`
[1] "Vitvi02g00250" "Vitvi03g00304" "Vitvi05g00442" "Vitvi05g01193"
[5] "Vitvi07g00167" "Vitvi07g00544"

$`2.2`
[1] "Vitvi02g01845" "Vitvi01g00025" "Vitvi01g00052" "Vitvi01g00053"
[5] "Vitvi01g00064" "Vitvi01g00681"

$`3.1`
[1] "Vitvi10g02295" "Vitvi00g01259" "Vitvi01g00714" "Vitvi05g00170"
[5] "Vitvi05g00204" "Vitvi07g00431"

$`3.3`
[1] "Vitvi11g01277" "Vitvi16g01858" "Vitvi16g00929"

$`3.4`
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[5] "Vitvi17g00279" "Vitvi18g00994"

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$`6`
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[5] "Vitvi05g00387" "Vitvi05g00388"

$`8.1`
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[5] "Vitvi03g00197" "Vitvi03g00785"

$`10.6`
[1] "Vitvi07g02990" "Vitvi01g00593" "Vitvi01g00708" "Vitvi01g01805"
[5] "Vitvi02g00118" "Vitvi02g00125"

$`11`
[1] "Vitvi02g01774" "Vitvi07g02896" "Vitvi02g01724" "Vitvi02g01739"
[5] "Vitvi07g02982" "Vitvi07g02994"

$`12.2`
[1] "Vitvi01g00175" "Vitvi05g00403" "Vitvi07g00187" "Vitvi07g02204"
[5] "Vitvi08g01586" "Vitvi08g01646"

$`13.1`
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[5] "Vitvi01g00502" "Vitvi01g00536"

$`16.1`
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[5] "Vitvi02g00831" "Vitvi03g00262"

$`16.2`
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[5] "Vitvi02g00283" "Vitvi02g00717"

$`16.8`
[1] "Vitvi10g02185" "Vitvi01g00556" "Vitvi01g02009" "Vitvi01g00557"
[5] "Vitvi01g00558" "Vitvi02g00270"

$`17.5`
[1] "Vitvi02g01780" "Vitvi10g02409" "Vitvi01g00481" "Vitvi01g01671"
[5] "Vitvi02g00032" "Vitvi04g01895"

$`21`
[1] "Vitvi10g02216" "Vitvi04g02274" "Vitvi01g00023" "Vitvi01g01866"
[5] "Vitvi01g01867" "Vitvi01g00133"

$`22`
[1] "Vitvi01g00739" "Vitvi01g00789" "Vitvi03g00054" "Vitvi06g01502"
[5] "Vitvi13g01673" "Vitvi14g01289"

$`23`
[1] "Vitvi01g00048" "Vitvi01g00115" "Vitvi01g00201" "Vitvi01g00421"
[5] "Vitvi01g00483" "Vitvi01g00663"
```

```
--------- intmtbs: Names of metabolites in bins  ----------------------------

      name                   description class nrow ncol
14 intmtbs Names of metabolites in bins  list   22 <NA>

$`1.2`
[1] "Glyceric.acid" "Glycine"       "Serine"

$`1.3`
[1] "Fructose.6.phosphate"

$`2.1`
[1] "Sucrose"

$`2.2`
[1] "Fructose" "Glucose"

$`3.1`
[1] "Galactinol" "Raffinose"

$`3.3`
[1] "Threitol"

$`3.4`
[1] "Myo.Inostol"

$`3.99`
[1] "Erythronic.acid" "Galactose"       "Xylose"

$`5`
[1] "Alanine"

$`6`
[1] "Citric.acid" "Malic.acid"

$`8.1`
[1] "Fumaric.acid"  "Succinic.acid"

$`10.6`
[1] "Arabinose"    "Melibiose"    "Rhamnose"     "Ribonic.acid"
[5] "Ribose"

$`11`
[1] "Ethanolamine"

$`12.2`
[1] "Glutamic.acid"

$`13.1`
[1] "Aspartic.acid" "Isoleucine"    "Leucine"       "Phenylalanine"
```

```
[5] "Proline"        "Shikimic.acid"

$`16.1`
[1] "Hydroquinone"

$`16.2`
[1] "Trans.Caffeic.acid"      "Gallic.acid"
[3] "Quinic.acid"             "X3.caffeoylquinic.acid"

$`16.8`
[1] "Catechin"

$`17.5`
[1] "Ascorbic.acid"

$`21`
[1] "Mannose.6.phosphate" "Pyroglutamic.acid"   "Threonic.acid"

$`22`
[1] "GABA"        "Putrescine"

$`23`
[1] "Uracil"
```

Factor for days within the year

```
> pdata1819$day <- factor(as.character(pdata1819$day))
```

3.13 Water potential

On Dec 12 we decided to include water stress as a prediction factor.
In addition to expression data, we need water stress data.

```
> (wsfn <- getMeta(.adesc, "Water potential data"))
[1] "/input/Stem water potential 2018 2019.txt"
> wpdata <- read.table(file.path(.aroot,wsfn), sep="\t",
+     header=TRUE,
+     row.names=1)
> str(wpdata)
'data.frame':        78 obs. of  5 variables:
 $ variey       : chr  "Cabernet Volos" "Cabernet Volos" "Cabernet Volos" "Cab
 $ date         : chr  "4.06.2018" "15.06.2018" "21.06.2018" "29.06.2018" ...
 $ treatment    : chr  "WW" "WW" "WW" "WW" ...
 $ SWP.mean     : num  -0.34 -0.384 -0.34 -0.2 -0.4 -0.41 -0.455 -0.33 -0.455
 $ SWP.cumulated: num  -0.34 -0.724 -1.064 -1.264 -1.664 ...
```

Tidy factors and dates. Be careful, variety in the header is misspelled:

```
> names(wpdata)
[1] "variey"        "date"          "treatment"     "SWP.mean"
[5] "SWP.cumulated"
> head(wpdata)
                   variey       date treatment SWP.mean SWP.cumulated
C18_3d_WW  Cabernet Volos  4.06.2018        WW   -0.340        -0.340
C18_14d_WW Cabernet Volos 15.06.2018        WW   -0.384        -0.724
C18_20d_WW Cabernet Volos 21.06.2018        WW   -0.340        -1.064
C18_28d_WW Cabernet Volos 29.06.2018        WW   -0.200        -1.264
C18_33d_WW Cabernet Volos  4.07.2018        WW   -0.400        -1.664
C18_39d_WW Cabernet Volos 10.07.2018        WW   -0.410        -2.074
```

```
> X <- wpdata
> X$treat <- factor(X$treatment,levels=c("WW","WS"))
> X$variety <- factor(X$variey)
> # Date of sampling might be useful as well
> require(lubridate)
> X$date <- as_date(X$date, format="%d.%m.%Y")
> X$year <- year(X$date)
> table(data.frame(X$date,"Count"=1))
            Count
X.date       1
  2018-06-04 4
  2018-06-15 4
  2018-06-21 4
  2018-06-29 4
  2018-07-04 4
  2018-07-10 4
  2018-07-16 4
  2018-07-23 4
  2018-07-31 4
  2018-08-07 4
```

```
  2019-06-18 4
  2019-06-26 4
  2019-07-08 4
  2019-07-12 4
  2019-07-17 4
  2019-07-22 2
  2019-07-30 4
  2019-08-06 4
  2019-08-12 4
  2019-08-19 4
```

```
> str(X)
'data.frame':        78 obs. of  8 variables:
 $ variey       : chr  "Cabernet Volos" "Cabernet Volos" "Cabernet Volos" "Cab
 $ date         : Date, format: "2018-06-04" ...
 $ treatment    : chr  "WW" "WW" "WW" "WW" ...
 $ SWP.mean     : num  -0.34 -0.384 -0.34 -0.2 -0.4 -0.41 -0.455 -0.33 -0.455
 $ SWP.cumulated: num  -0.34 -0.724 -1.064 -1.264 -1.664 ...
 $ treat        : Factor w/ 2 levels "WW","WS": 1 1 1 1 1 1 1 1 1 1 ...
 $ variety      : Factor w/ 2 levels "Cabernet Volos",..: 1 1 1 1 1 1 1 1 1 1
 $ year         : num  2018 2018 2018 2018 2018 ...
```

Order by date

```
> X <- X[order(X$date),]
```

```
> wpdata <- X
```

Tidy dates ...

```
> table(wpdata$date,wpdata$variety)
```

```
            Cabernet Volos Fleurtai
  2018-06-04              2        2
  2018-06-15              2        2
  2018-06-21              2        2
  2018-06-29              2        2
  2018-07-04              2        2
  2018-07-10              2        2
  2018-07-16              2        2
  2018-07-23              2        2
  2018-07-31              2        2
  2018-08-07              2        2
  2019-06-18              2        2
  2019-06-26              2        2
  2019-07-08              2        2
  2019-07-12              2        2
  2019-07-17              2        2
  2019-07-22              0        2
  2019-07-30              2        2
  2019-08-06              2        2
  2019-08-12              2        2
  2019-08-19              2        2
```

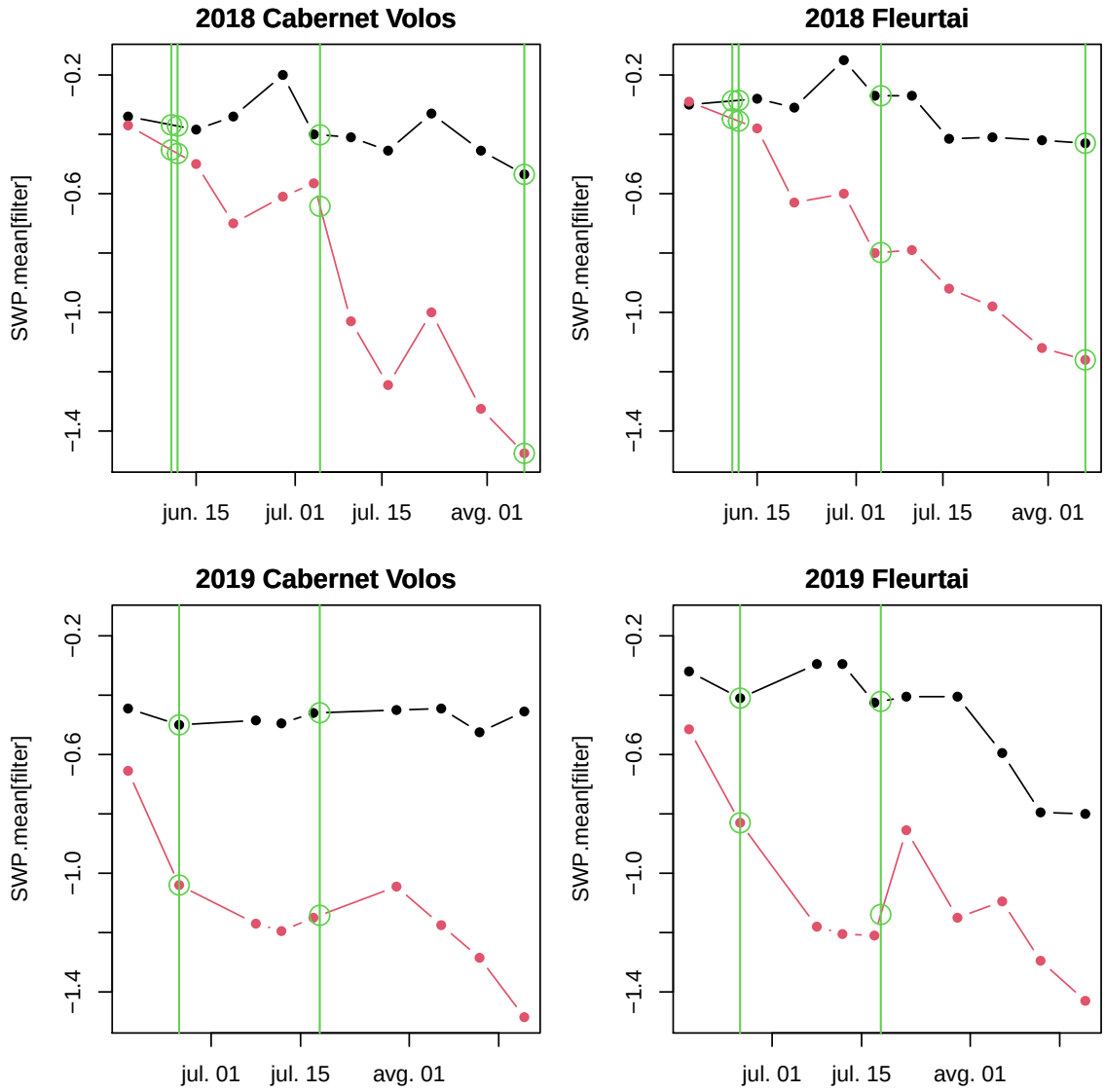
```
> table(pdata1819$date)
```

```
< table of extent 0 >
> pdata1819$date <- as_date(pdata1819$Date, format="%d.%m.%Y")
> table(pdata1819$date)

2018-06-11 2018-06-12 2018-07-05 2018-08-07 2019-06-26 2019-07-18
         8          8         16         16         16         16
> pdata1819$Year <- factor(paste0("20",pdata1819$year))
```

Water potential and transcriptomics are not measured at the same dates. We will interpolate the water potential to matching dates.

```
> wpas <- NULL
> par(mfrow=c(2,2),mar=c(3,4,2,1))
> for( yr in unique(wpdata$year)){
+ for (vari in levels(wpdata$variety)) {
+   with(wpdata, {
+     filter <- (wpdata$year==yr) & (variety== vari)
+     plot(date[filter], SWP.mean[filter], type="n",ylim=range(SWP.mean))
+     for(tr in levels(treat)){
+     select <- filter & (treat %in% tr)
+     lines(date[select],SWP.mean[select],type="b",pch=16,col=treat[select])
+     title(paste(yr,vari))
+     unidata <- unique(pdata1819$date[pdata1819$Year==yr])
+     abline(v=unidata, col=3)
+     wpa <- (approx(date[select],SWP.mean[select],unidata))
+ #    print(data.frame(wpa))
+ #    if(is.null(wpas)) wpas <- data.frame(wpa) else
+     wpas <<- rbind(wpas,data.frame(wpa,yr,
+     variety=substr(vari,1,1),
+     treat=tr))
+     points(wpa,col=3,cex=2)
+     }
+     })
+   }
+ }
```




```
> colnames(wpas)[1:2] <- c("date","swp")
> #rownames(wpas) <- wpas[,1]
> #,by.x=c("date","variety","treat"),by.y=c("date","variety","treat"))
```

@

Order water potential data by date

```
> diff(wpas$date)
Time differences in days
 [1]  23  33 -57   1  23  33 -57   1  23  33 -57   1  23  33 -57 380
[17]  22 -22  22 -22  22 -22  22
> wpas <- wpas[order(wpas$date),]
> diff(wpas$date)
Time differences in days
 [1]   0   0   0   1   0   0   0  23   0   0   0  33   0   0   0 323
[17]   0   0   0  22   0   0   0
```

Convert treatment and variety into factors

```
> (wpas$treat <- factor(wpas$treat, levels=c("WW","WS")))
 [1] WW WS WW WS WW WS WW WS WW WS WW WS WW WS WW WS WW WS WW WS WW WS
[23] WW WS
Levels: WW WS
```

```
> (wpas$variety <- factor(wpas$variety))
 [1] C C F F C C F F C C F F C C F F C C F F C C F F
Levels: C F

> with(wpas,ftable(yr,variety,treat,date))
                  date 2018-06-11 2018-06-12 2018-07-05 2018-08-07 2019-06-26
yr   variety treat
2018 C       WW                 1          1          1          1          0
             WS                 1          1          1          1          0
     F       WW                 1          1          1          1          0
             WS                 1          1          1          1          0
2019 C       WW                 0          0          0          0          1
             WS                 0          0          0          0          1
     F       WW                 0          0          0          0          1
             WS                 0          0          0          0          1
```

Check date consistency

```
> all(pdata1819$date %in% wpas$date)
[1] TRUE
```

Add interpolated WP values to measured date to phenodata.

```
> mapdate <- match(pdata1819$date,wpas$date)
> pdata1819w <- pdata1819
> pdata1819w$swp <- wpas[mapdate,c("swp")]
> dim(pdata1819w)
[1] 80 24
> head(pdata1819w)
                      ID        Variety       Date variety year day
C18_11d_WS1 C18_11d_WS1 Cabernet Volos 12.06.2018       C   18  11
C18_11d_WS2 C18_11d_WS2 Cabernet Volos 12.06.2018       C   18  11
C18_11d_WS3 C18_11d_WS3 Cabernet Volos 12.06.2018       C   18  11
C18_11d_WS4 C18_11d_WS4 Cabernet Volos 12.06.2018       C   18  11
C18_11d_WW1 C18_11d_WW1 Cabernet Volos 12.06.2018       C   18  11
C18_11d_WW2 C18_11d_WW2 Cabernet Volos 12.06.2018       C   18  11
            treat rep project.name        species plant.name tissue
C18_11d_WS1    WS   1      EnViros Vitis vinifera  grapevine   leaf
C18_11d_WS2    WS   2      EnViros Vitis vinifera  grapevine   leaf
C18_11d_WS3    WS   3      EnViros Vitis vinifera  grapevine   leaf
C18_11d_WS4    WS   4      EnViros Vitis vinifera  grapevine   leaf
C18_11d_WW1    WW   1      EnViros Vitis vinifera  grapevine   leaf
C18_11d_WW2    WW   2      EnViros Vitis vinifera  grapevine   leaf
            health.status plant.number growth.location
C18_11d_WS1  water stress           R1           Udine
C18_11d_WS2  water stress           R2           Udine
C18_11d_WS3  water stress           R3           Udine
C18_11d_WS4  water stress           R4           Udine
C18_11d_WW1  well watered           R1           Udine
C18_11d_WW2  well watered           R2           Udine
            growth.conditions
C18_11d_WS1           outside
C18_11d_WS2           outside
```

```
C18_11d_WS3           outside
C18_11d_WS4           outside
C18_11d_WW1           outside
C18_11d_WW2           outside

C18_11d_WS1 several leaves ground together and stored at -80oC; an aliquot was
C18_11d_WS2 several leaves ground together and stored at -80oC; an aliquot was
C18_11d_WS3 several leaves ground together and stored at -80oC; an aliquot was
C18_11d_WS4 several leaves ground together and stored at -80oC; an aliquot was
C18_11d_WW1 several leaves ground together and stored at -80oC; an aliquot was
C18_11d_WW2 several leaves ground together and stored at -80oC; an aliquot was
            Metabolites.Order         Metabolites.File.Name
C18_11d_WS1                 2 1019Cabernet Volos_6_12_WS1.D
C18_11d_WS2                 4 1019Cabernet Volos_6_12_WS2.D
C18_11d_WS3               102 1219Cabernet Volos_6_12_WS3.D
C18_11d_WS4               100 1219Cabernet Volos_6_12_WS4.D
C18_11d_WW1                 6 1019Cabernet Volos_6_12_WW1.D
C18_11d_WW2                 8 1019Cabernet Volos_6_12_WW2.D
               Metabolites.File Transcripts.ID       date Year
C18_11d_WS1 Cabernet Volos6_12WS          C1_S1 2018-06-12 2018
C18_11d_WS2 Cabernet Volos6_12WS          C1_S2 2018-06-12 2018
C18_11d_WS3 Cabernet Volos6_12WS          C1_S3 2018-06-12 2018
C18_11d_WS4 Cabernet Volos6_12WS          C1_S4 2018-06-12 2018
C18_11d_WW1 Cabernet Volos6_12WW          C1_W1 2018-06-12 2018
C18_11d_WW2 Cabernet Volos6_12WW          C1_W2 2018-06-12 2018
               swp
C18_11d_WS1 -0.372
C18_11d_WS2 -0.372
C18_11d_WS3 -0.372
C18_11d_WS4 -0.372
C18_11d_WW1 -0.372
C18_11d_WW2 -0.372
```

```
> all(colnames(t1819)==rownames(pdata1819w))
[1] TRUE
```

One plot:

```
> t1819[1,]
              C18_11d_WS1 C18_11d_WS2 C18_11d_WS3 C18_11d_WS4
Vitvi15g01736    4.664602    4.109897     4.44822    4.013955
              C18_11d_WW1 C18_11d_WW2 C18_11d_WW3 C18_11d_WW4
Vitvi15g01736    4.717536    4.154237    4.475261    4.466465
              C18_34d_WS1 C18_34d_WS2 C18_34d_WS3 C18_34d_WS4
Vitvi15g01736    4.400333    4.641164    4.419123    4.534438
              C18_34d_WW1 C18_34d_WW2 C18_34d_WW3 C18_34d_WW4
Vitvi15g01736    4.924801     5.08569    5.339735    5.263629
              C18_67d_WS1 C18_67d_WS2 C18_67d_WS3 C18_67d_WS4
Vitvi15g01736    2.058717    2.289503    2.923483    2.575657
              C18_67d_WW1 C18_67d_WW2 C18_67d_WW3 C18_67d_WW4
Vitvi15g01736    3.891121    3.040087    4.216897    3.763086
              F18_10d_WS1 F18_10d_WS2 F18_10d_WS3 F18_10d_WS4
```

```
Vitvi15g01736    4.859141    4.866943     4.98059    4.945395
              F18_10d_WW1 F18_10d_WW2 F18_10d_WW3 F18_10d_WW4
Vitvi15g01736    5.705006    4.619238    4.808548    5.276124
              F18_34d_WS1 F18_34d_WS2 F18_34d_WS3 F18_34d_WS4
Vitvi15g01736    4.064718    3.850458    5.141832    4.626909
              F18_34d_WW1 F18_34d_WW2 F18_34d_WW3 F18_34d_WW4
Vitvi15g01736    4.096173    4.802221    4.329152    4.441903
              F18_67d_WS1 F18_67d_WS2 F18_67d_WS3 F18_67d_WS4
Vitvi15g01736    1.583128    1.740858    2.978406    4.166406
              F18_67d_WW1 F18_67d_WW2 F18_67d_WW3 F18_67d_WW4
Vitvi15g01736    3.558043    3.569471    4.411209    4.359744
              C19_22d_WS1 C19_22d_WS2 C19_22d_WS3 C19_22d_WS4
Vitvi15g01736        3.18         3.5        3.19        3.61
              C19_22d_WW1 C19_22d_WW2 C19_22d_WW3 C19_22d_WW4
Vitvi15g01736        5.42        5.35        4.68        4.92
              C19_44d_WS1 C19_44d_WS2 C19_44d_WS3 C19_44d_WS4
Vitvi15g01736        5.13        5.19        5.71        5.29
              C19_44d_WW1 C19_44d_WW2 C19_44d_WW3 C19_44d_WW4
Vitvi15g01736        6.19        5.62        5.62        6.19
              F19_22d_WS1 F19_22d_WS2 F19_22d_WS3 F19_22d_WS4
Vitvi15g01736        3.03        3.93        4.24        2.85
              F19_22d_WW1 F19_22d_WW2 F19_22d_WW3 F19_22d_WW4
Vitvi15g01736           5        4.97        4.47        5.51
              F19_44d_WS1 F19_44d_WS2 F19_44d_WS3 F19_44d_WS4
Vitvi15g01736        5.84        5.83        4.56        5.23
              F19_44d_WW1 F19_44d_WW2 F19_44d_WW3 F19_44d_WW4
Vitvi15g01736        5.44        6.13        5.96        6.16
> (varname <- rownames(t1819)[1])
[1] "Vitvi15g01736"

> .testing <- !TRUE
> pd <- pdata1819w
> par(mfrow=c(2,2),mar=c(3,4,2,1))
> (varname <- rownames(t1819)[1])
[1] "Vitvi15g01736"
> (yr <- unique(pd$year)[1])
[1] 18
Levels: 18 19
> (vari  <-  levels(pd$variety)[1])
[1] "C"
> for( yr in unique(pd$year)){
+ for (vari in levels(pd$variety)) {
+     filter <- (pd$year %in% yr) & (pd$variety %in% vari)
+     print(filter)
+     print(pd$date[filter])
+ (    y <- unlist(t1819[varname,]))
+   with(pd, {
+     plot(pd$swp[filter], y[filter],
+        type="p",
+        bg=pd$treat[filter],
+        pch=21,
```

```
+         cex=1,
+         col="white",
+         xlim=range(pd$swp)
+         )
+      for(i in 1:length(levels(treat))){
+      tr <- levels(pd$treat)[i]
+      select <- filter & (pd$treat %in% tr)
+      fit <- lm(y[select]~pd$swp[select])
+      print(fit)
+      abline(fit,col=i)
+ #     lines(date[select],swp[select],type="b",pch=16,col=treat[select])
+      title(paste(varname, yr, vari))
+      }
+      })
+    }
+ }
 [1]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
[12]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
[23]  TRUE  TRUE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[34] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[45] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[56] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[67] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[78] FALSE FALSE FALSE
 [1] "2018-06-12" "2018-06-12" "2018-06-12" "2018-06-12" "2018-06-12"
 [6] "2018-06-12" "2018-06-12" "2018-06-12" "2018-07-05" "2018-07-05"
[11] "2018-07-05" "2018-07-05" "2018-07-05" "2018-07-05" "2018-07-05"
[16] "2018-07-05" "2018-08-07" "2018-08-07" "2018-08-07" "2018-08-07"
[21] "2018-08-07" "2018-08-07" "2018-08-07" "2018-08-07"

Call:
lm(formula = y[select] ~ pd$swp[select])

Coefficients:
   (Intercept)  pd$swp[select]
         7.219           6.359


Call:
lm(formula = y[select] ~ pd$swp[select])

Coefficients:
   (Intercept)  pd$swp[select]
         9.226          12.539

 [1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[12] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[23] FALSE FALSE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
[34]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
[45]  TRUE  TRUE  TRUE  TRUE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[56] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[67] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[78] FALSE FALSE FALSE
```

```
 [1] "2018-06-11" "2018-06-11" "2018-06-11" "2018-06-11" "2018-06-11"
 [6] "2018-06-11" "2018-06-11" "2018-06-11" "2018-07-05" "2018-07-05"
[11] "2018-07-05" "2018-07-05" "2018-07-05" "2018-07-05" "2018-07-05"
[16] "2018-07-05" "2018-08-07" "2018-08-07" "2018-08-07" "2018-08-07"
[21] "2018-08-07" "2018-08-07" "2018-08-07" "2018-08-07"

Call:
lm(formula = y[select] ~ pd$swp[select])

Coefficients:
   (Intercept)  pd$swp[select]
         7.011           5.778


Call:
lm(formula = y[select] ~ pd$swp[select])

Coefficients:
   (Intercept)  pd$swp[select]
         9.935          13.685

 [1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[12] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[23] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[34] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[45] FALSE FALSE FALSE FALSE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
[56]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE FALSE FALSE
[67] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[78] FALSE FALSE FALSE
 [1] "2019-06-26" "2019-06-26" "2019-06-26" "2019-06-26" "2019-06-26"
 [6] "2019-06-26" "2019-06-26" "2019-06-26" "2019-07-18" "2019-07-18"
[11] "2019-07-18" "2019-07-18" "2019-07-18" "2019-07-18" "2019-07-18"
[16] "2019-07-18"

Call:
lm(formula = y[select] ~ pd$swp[select])

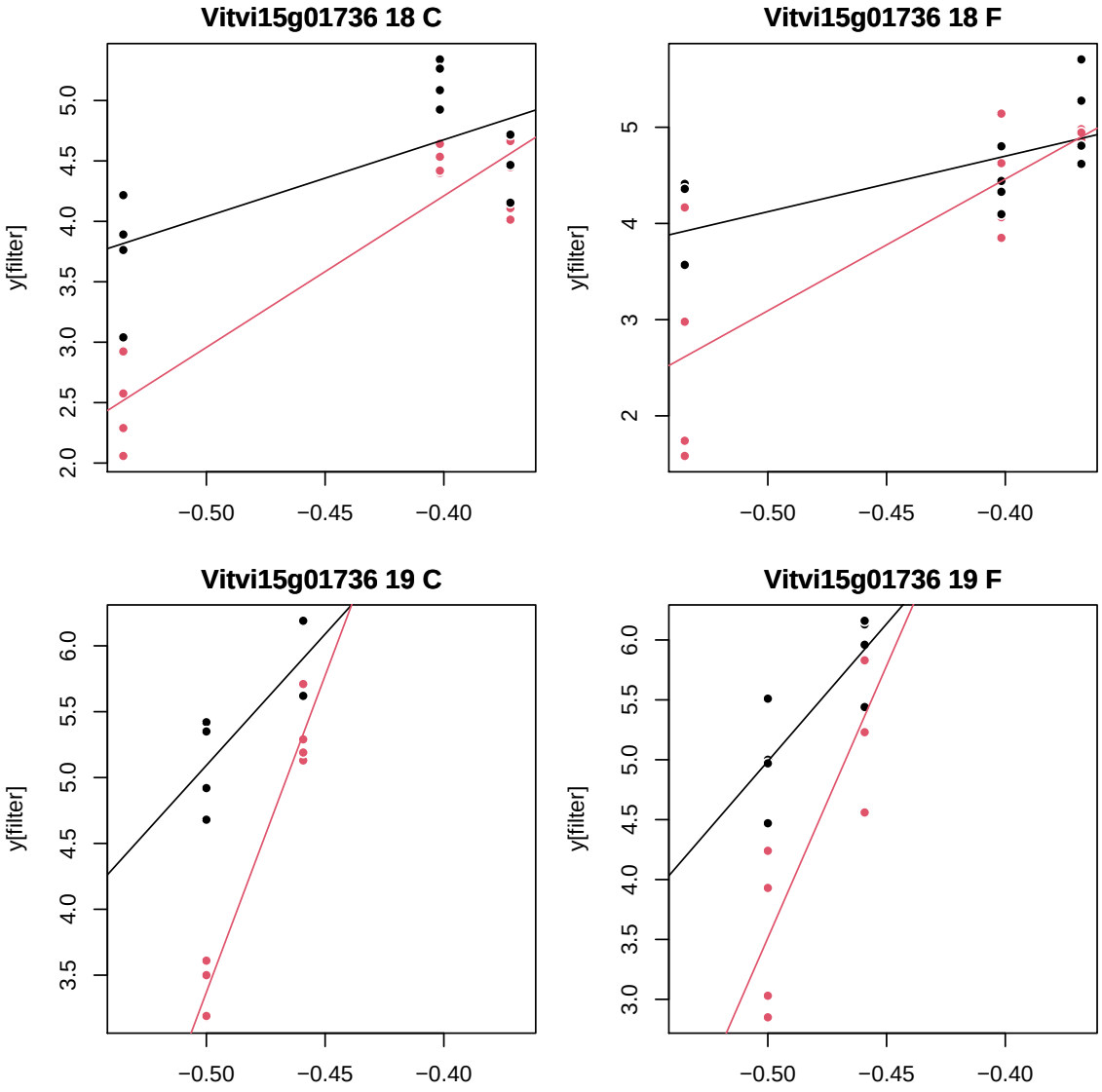
Coefficients:
   (Intercept)  pd$swp[select]
         15.06           19.93


Call:
lm(formula = y[select] ~ pd$swp[select])

Coefficients:
   (Intercept)  pd$swp[select]
         27.41           48.08

 [1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[12] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[23] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[34] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
```

```
[45] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[56] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE  TRUE  TRUE
[67]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
[78]  TRUE  TRUE  TRUE
 [1] "2019-06-26" "2019-06-26" "2019-06-26" "2019-06-26" "2019-06-26"
 [6] "2019-06-26" "2019-06-26" "2019-06-26" "2019-07-18" "2019-07-18"
[11] "2019-07-18" "2019-07-18" "2019-07-18" "2019-07-18" "2019-07-18"
[16] "2019-07-18"
```




```
Call:
lm(formula = y[select] ~ pd$swp[select])

Coefficients:
   (Intercept)  pd$swp[select]
         16.45           22.93


Call:
lm(formula = y[select] ~ pd$swp[select])

Coefficients:
```

```
   (Intercept)  pd$swp[select]
         26.23           45.44
> .testing <- FALSE
```

4 Expression and water poential analysis

```
> varname <- rownames(t1819)[10]
> pd <- pdata1819
> (y <- unlist(t1819[varname,]))
C18_11d_WS1 C18_11d_WS2 C18_11d_WS3 C18_11d_WS4 C18_11d_WW1
   4.088427    3.961216    4.127170    3.916955    4.472212
C18_11d_WW2 C18_11d_WW3 C18_11d_WW4 C18_34d_WS1 C18_34d_WS2
   4.309540    4.212060    4.154032    4.086692    3.914995
C18_34d_WS3 C18_34d_WS4 C18_34d_WW1 C18_34d_WW2 C18_34d_WW3
   4.065776    4.081348    4.313965    4.041339    4.318997
C18_34d_WW4 C18_67d_WS1 C18_67d_WS2 C18_67d_WS3 C18_67d_WS4
   4.238240    4.441597    4.248104    4.242540    3.969094
C18_67d_WW1 C18_67d_WW2 C18_67d_WW3 C18_67d_WW4 F18_10d_WS1
   4.160356    4.676748    4.467201    4.359372    4.102511
F18_10d_WS2 F18_10d_WS3 F18_10d_WS4 F18_10d_WW1 F18_10d_WW2
   4.307786    4.261419    4.248699    4.239323    4.289799
F18_10d_WW3 F18_10d_WW4 F18_34d_WS1 F18_34d_WS2 F18_34d_WS3
   4.620659    4.532309    4.114948    4.149386    4.350818
F18_34d_WS4 F18_34d_WW1 F18_34d_WW2 F18_34d_WW3 F18_34d_WW4
   4.075166    4.239367    4.109161    4.460006    4.507653
F18_67d_WS1 F18_67d_WS2 F18_67d_WS3 F18_67d_WS4 F18_67d_WW1
   4.443768    4.392282    4.258226    4.311732    4.659167
F18_67d_WW2 F18_67d_WW3 F18_67d_WW4 C19_22d_WS1 C19_22d_WS2
   4.584738    4.404701    4.488189    5.160000    5.040000
C19_22d_WS3 C19_22d_WS4 C19_22d_WW1 C19_22d_WW2 C19_22d_WW3
   4.950000    4.920000    5.060000    4.710000    5.410000
C19_22d_WW4 C19_44d_WS1 C19_44d_WS2 C19_44d_WS3 C19_44d_WS4
   5.070000    4.420000    4.480000    4.490000    4.570000
C19_44d_WW1 C19_44d_WW2 C19_44d_WW3 C19_44d_WW4 F19_22d_WS1
   4.930000    5.000000    4.820000    4.770000    5.560000
F19_22d_WS2 F19_22d_WS3 F19_22d_WS4 F19_22d_WW1 F19_22d_WW2
   5.150000    5.130000    5.690000    5.060000    5.160000
F19_22d_WW3 F19_22d_WW4 F19_44d_WS1 F19_44d_WS2 F19_44d_WS3
   5.250000    4.940000    4.710000    4.320000    4.910000
F19_44d_WS4 F19_44d_WW1 F19_44d_WW2 F19_44d_WW3 F19_44d_WW4
   4.540000    5.030000    4.700000    4.820000    4.720000
> means <- tapply(y,pd[,c("date","treat","variety")],mean,na.rm=TRUE)
> means
, , variety = C

            treat
date               WW       WS
  2018-06-11       NA       NA
  2018-06-12 4.286961 4.023442
  2018-07-05 4.228135 4.037203
  2018-08-07 4.415919 4.225334
```

```
  2019-06-26 5.062500 5.017500
  2019-07-18 4.880000 4.490000

, , variety = F

           treat
date              WW       WS
  2018-06-11 4.420523 4.230104
  2018-06-12       NA       NA
  2018-07-05 4.329047 4.172579
  2018-08-07 4.534199 4.351502
  2019-06-26 5.102500 5.382500
  2019-07-18 4.817500 4.620000
> tfilter <- wpas$treat %in% "WW"
> vfilter <- wpas$variety %in% "C"
> (swp <- wpas$swp[as.character(wpas$date) %in% dimnames(means)[[1]]])
 [1] -0.3680000 -0.4527273 -0.2872727 -0.3472727 -0.3720000 -0.4645455
 [7] -0.2854545 -0.3554545 -0.4016667 -0.6425000 -0.2700000 -0.7983333
[13] -0.5350000 -1.4750000 -0.4300000 -1.1600000 -0.5000000 -1.0400000
[19] -0.4100000 -0.8300000 -0.4592308 -1.1419231 -0.4210000 -1.1390000

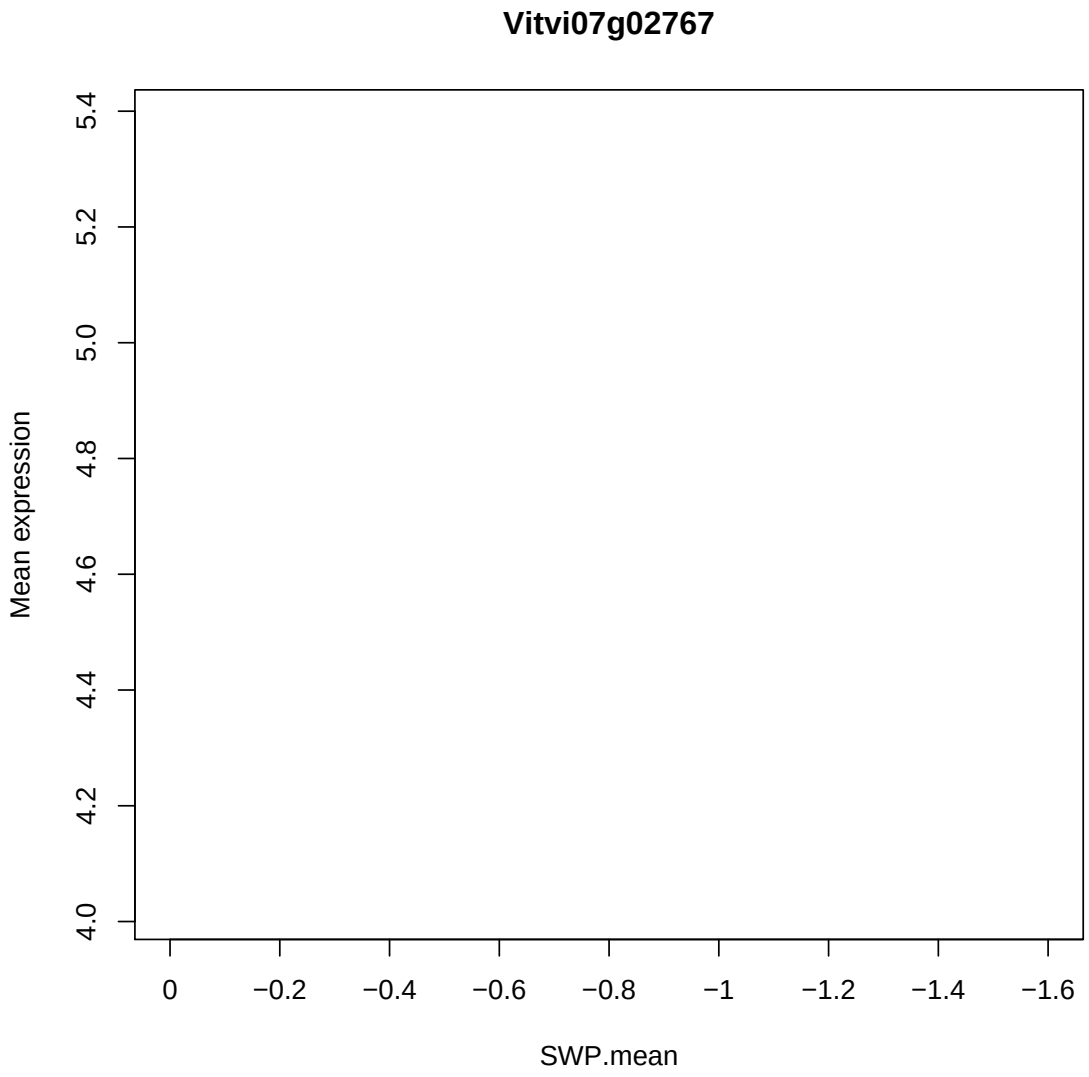

> varname <- rownames(t1819)[10]
> #varname <- rownames(t1819)[runif(1,1,10000)]
> (y <- unlist(t1819[varname,]))
C18_11d_WS1 C18_11d_WS2 C18_11d_WS3 C18_11d_WS4 C18_11d_WW1
   4.088427    3.961216    4.127170    3.916955    4.472212
C18_11d_WW2 C18_11d_WW3 C18_11d_WW4 C18_34d_WS1 C18_34d_WS2
   4.309540    4.212060    4.154032    4.086692    3.914995
C18_34d_WS3 C18_34d_WS4 C18_34d_WW1 C18_34d_WW2 C18_34d_WW3
   4.065776    4.081348    4.313965    4.041339    4.318997
C18_34d_WW4 C18_67d_WS1 C18_67d_WS2 C18_67d_WS3 C18_67d_WS4
   4.238240    4.441597    4.248104    4.242540    3.969094
C18_67d_WW1 C18_67d_WW2 C18_67d_WW3 C18_67d_WW4 F18_10d_WS1
   4.160356    4.676748    4.467201    4.359372    4.102511
F18_10d_WS2 F18_10d_WS3 F18_10d_WS4 F18_10d_WW1 F18_10d_WW2
   4.307786    4.261419    4.248699    4.239323    4.289799
F18_10d_WW3 F18_10d_WW4 F18_34d_WS1 F18_34d_WS2 F18_34d_WS3
   4.620659    4.532309    4.114948    4.149386    4.350818
F18_34d_WS4 F18_34d_WW1 F18_34d_WW2 F18_34d_WW3 F18_34d_WW4
   4.075166    4.239367    4.109161    4.460006    4.507653
F18_67d_WS1 F18_67d_WS2 F18_67d_WS3 F18_67d_WS4 F18_67d_WW1
   4.443768    4.392282    4.258226    4.311732    4.659167
F18_67d_WW2 F18_67d_WW3 F18_67d_WW4 C19_22d_WS1 C19_22d_WS2
   4.584738    4.404701    4.488189    5.160000    5.040000
C19_22d_WS3 C19_22d_WS4 C19_22d_WW1 C19_22d_WW2 C19_22d_WW3
   4.950000    4.920000    5.060000    4.710000    5.410000
C19_22d_WW4 C19_44d_WS1 C19_44d_WS2 C19_44d_WS3 C19_44d_WS4
   5.070000    4.420000    4.480000    4.490000    4.570000
C19_44d_WW1 C19_44d_WW2 C19_44d_WW3 C19_44d_WW4 F19_22d_WS1
   4.930000    5.000000    4.820000    4.770000    5.560000
F19_22d_WS2 F19_22d_WS3 F19_22d_WS4 F19_22d_WW1 F19_22d_WW2
   5.150000    5.130000    5.690000    5.060000    5.160000
```

```
F19_22d_WW3 F19_22d_WW4 F19_44d_WS1 F19_44d_WS2 F19_44d_WS3
   5.250000    4.940000    4.710000    4.320000    4.910000
F19_44d_WS4 F19_44d_WW1 F19_44d_WW2 F19_44d_WW3 F19_44d_WW4
   4.540000    5.030000    4.700000    4.820000    4.720000
> means <- tapply(y,pd[,c("date","treat","variety")],mean,na.rm=TRUE)
> swps <- tapply(pd$swp,pd[,c("date","treat","variety")],unique)
Error in tapply(pd$swp, pd[, c("date", "treat", "variety")], unique): argument
> means
, , variety = C

            treat
date                WW       WS
  2018-06-11        NA       NA
  2018-06-12 4.286961 4.023442
  2018-07-05 4.228135 4.037203
  2018-08-07 4.415919 4.225334
  2019-06-26 5.062500 5.017500
  2019-07-18 4.880000 4.490000

, , variety = F

            treat
date                WW       WS
  2018-06-11 4.420523 4.230104
  2018-06-12        NA       NA
  2018-07-05 4.329047 4.172579
  2018-08-07 4.534199 4.351502
  2019-06-26 5.102500 5.382500
  2019-07-18 4.817500 4.620000
> ylim <- range(means, na.rm=TRUE)
> xlim <- c(min(wpas$swp,-1.6,na.rm=TRUE), max(wpas$swp,0, na.rm=TRUE))
> vlvls <- unique(wpas$variety)
> tlvls <- rev(unique(wpas$treat))
> cols <- c(4,2)
> pchs <- c(16,16)
> plot(1,1, #wpas$swp[tfilter & vfilter], means[,"WS",vlvls[i]],
+       ylim=ylim,
+       xlim=-rev(xlim),
+       xlab = "SWP.mean",
+       ylab = "Mean expression",
+       type="n",
+       axes=FALSE
+       )
> axis(2)
> box()
> axis(1,at=seq(0,2,0.2),labels=-(seq(0,2,0.2)))
> title(varname)
```



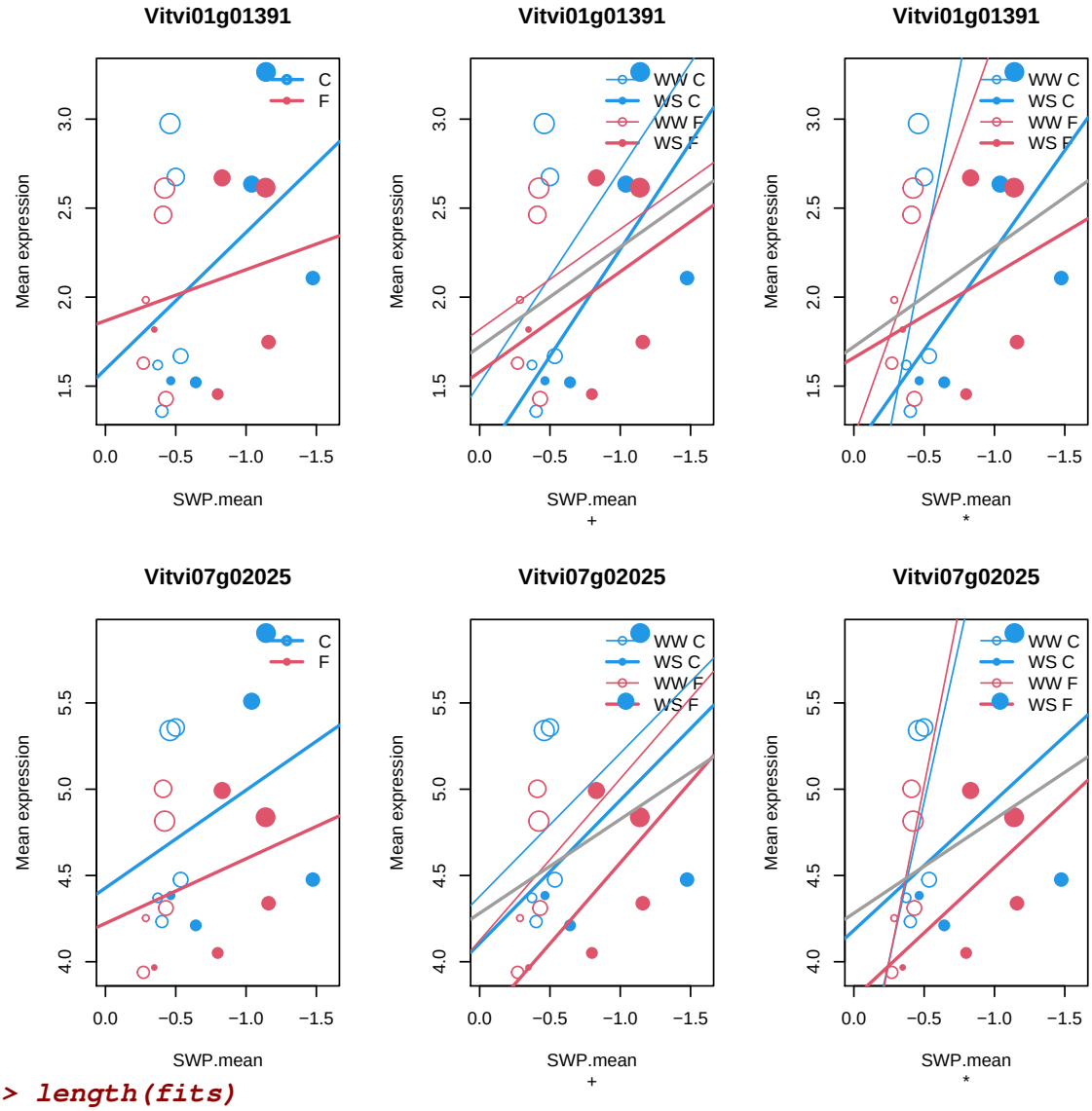

```
> legend("topright", bty="n", pch=pchs, col=cols,legend <- vlvls)
Error in as.graphicsAnnot(legend): argument "legend" is missing, with no defau
> #
> for(i in 1:length(vlvls)){
+ for( j in 1:length(tlvls)){
+ tfilter <- wpas$treat %in% tlvls[j]
+ vfilter <- wpas$variety %in% vlvls[i]
+ yy <- means[as.character(wpa$date),tlvls[j],vlvls[i]]
+ wpa <- wpas[tfilter & vfilter,]
+ all(wpa$date==names(yy))
+ points(-wpa$swp, yy,
+        col = cols[j],
+        pch = pchs[j]
+        )
+        }
+
+ }
Error in eval(expr, envir, enclos): object 'wpa' not found
```

4.1 Expression vs water potential

```
> plot.ewp <- function(varname,cols=c(4,2),pchs=c(1,16),lwd=c(1,2,1,2)
+      ,model=c("*"), verbose=FALSE, exprs=t1819, pd=pdata1819,ylim=NULL, cex=
+ if(verbose) print(varname)
+ (y <- unlist(exprs[varname,]))
+ means <- tapply(y,pd[,c("date","treat","variety")],mean,na.rm=TRUE)
+ #print(means)
+ swps <- tapply(wpas$swp,wpas[,c("date","treat","variety")],function(x) x[1])
+ #print(swps)
+ if(is.null(ylim)) ylim <- range(means, na.rm=TRUE)
+ xlim <- c(min(wpas$swp,-1.6,na.rm=TRUE), max(wpas$swp,0, na.rm=TRUE))
+ vlvls <- levels(wpas$variety)
+ tlvls <- levels(wpas$treat)
+ #cols <- c(4,2)
+ #pchs <- c(1,16)
+ plot(1,1, #wpas$swp[tfilter & vfilter], means[,"WS",vlvls[i]],
+       ylim=ylim,
+       xlim=rev(xlim),
+       xlab = "SWP.mean",
+       ylab = "Mean expression",
+       type="n",
+       axes=TRUE
+       )
+ title(varname,model)
+ if(model=="") {
+ legend("topright", bty="n", pch=pchs, col=rep(cols,each=1),lwd=c(2,2),
+        legend= vlvls)
+ } else {
+ legend("topright", bty="n", pch=pchs, col=rep(cols,each=2),lwd=lwd,
+        legend= outer(tlvls,vlvls,paste))
+        }
+ #
+ allx <- NULL
+ ally <- NULL
+ fits <- list(name=varname)
+ for(i in 1:length(vlvls)){
+ #for( j in 1:length(tlvls)){
+ #tfilter <- wpas$treat %in% tlvls[j]
+ vfilter <- wpas$variety %in% vlvls[i]
+ wpa <- wpas[vfilter,]
+ means[,,vlvls[i]]
+ mns <- melt(means[,,vlvls[i]])
+ mns
+ wp <- melt(swps[,,vlvls[i]])
+ wp
+ all(wpa$date==dimnames(mns)$date)
+ yy <- mns[,"value"]
+ xx <- wp[,"value"]
+ #print(cbind(xx,yy))
+ if(is.null(cex)) cex <- 0.5+as.numeric(mns$date)/3
+ points(xx , yy,
+       col = cols[i],
```

```
+       pch = pchs[as.numeric(mns$treat)]
+      , cex=cex
+       )
+ #      }
+   xx <- xx
+   if(model=="") fit <- lm(yy~xx)
+   if(model=="+") fit <- lm(yy~xx+mns$treat)
+   if(model=="*") fit <- lm(yy~xx*mns$treat)
+   if(verbose) print(summary(fit))
+   coef <- fit$coefficients
+ #  print(coef)
+   if(length(coef)<3) coef[3] <- 0
+   if(length(coef)<4) coef[4] <- 0
+   abline(coef[1:2], col=cols[i],lwd=1)
+   abline(coef[1:2]+coef[3:4],col=cols[i],lwd=2,lty=1)
+   ally <- c(ally,yy)
+   allx <- c(allx,xx)
+   fits[[vlvls[i]]] <- fit
+ }
+ fit <- lm(ally~allx)
+ fits[["all"]] <- fit
+ fits[["r"]] <- cor(ally,allx,use="complete")
+ if(verbose) print(summary(fit))
+ if(all) abline(fit$coefficients,lwd=2,col=8)
+ #points(-swps,means,cex=1.5)
+ invisible(fits)
+ }


> par(mfrow=c(2,3))
> #
> varname <- rownames(t1819)[10]
> varname
[1] "Vitvi07g02767"
> varnames <- c("Vitvi03g01254")
> set.seed(1234)
> for(vari in 1:2){
+ varname <- rownames(t1819)[runif(1,1,10000)]
+ plot.ewp(varname,model="",all=FALSE)
+ plot.ewp(varname,model="+")
+ fits <- plot.ewp(varname,model="*")
+ }
```




```
> length(fits)
[1] 5
> names(fits)
[1] "name" "C"    "F"    "all"  "r"
```

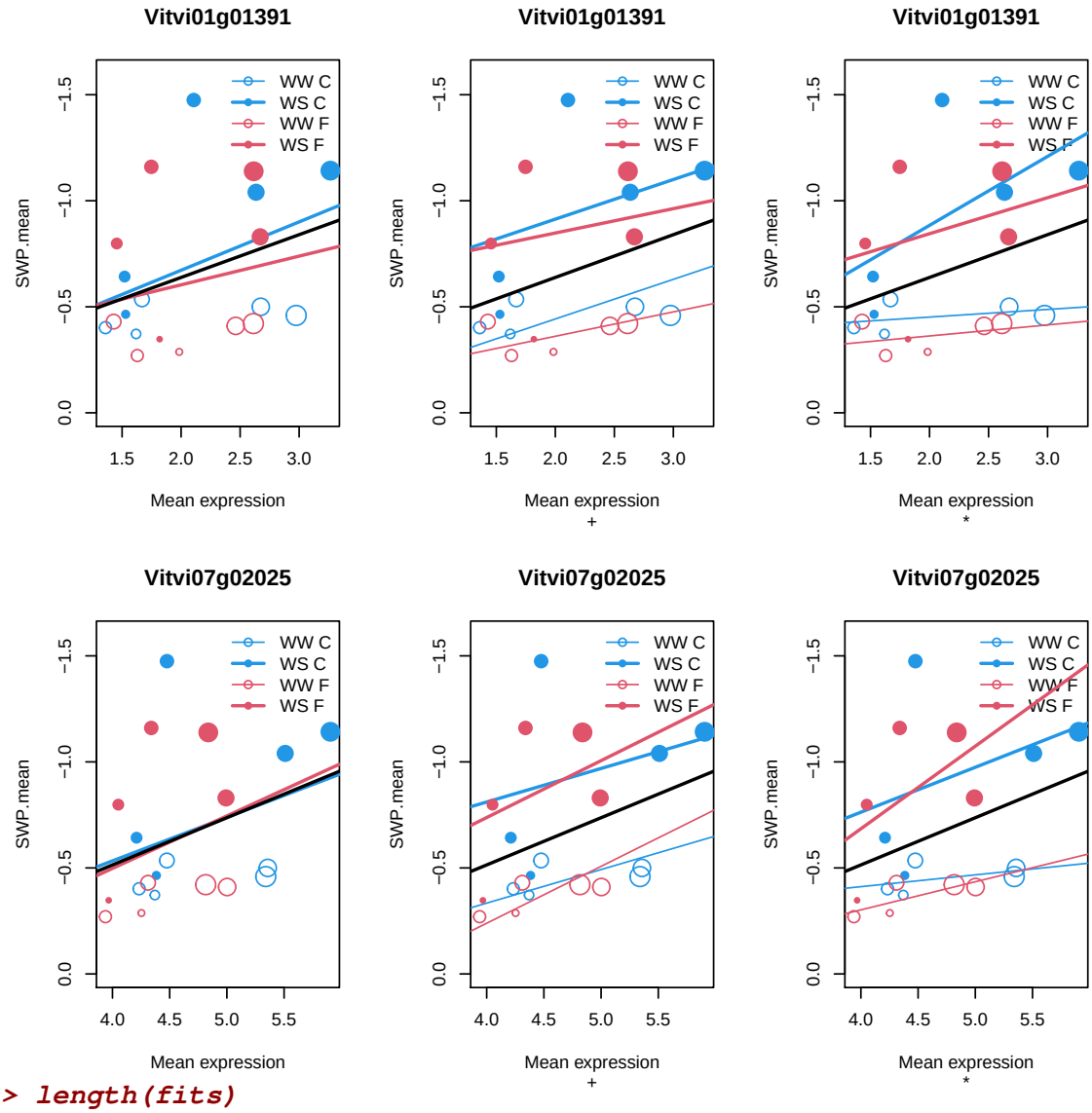
4.2 Water potential vs Expression

```
> require(reshape2)
> plot.wpe <- function(varname,cols=c(4,2),pchs=c(1,16),lwd=c(1,2,1,2)
+       ,model=c("*"),  exprs=t1819, pd=pdata1819, verbose=FALSE){
+ if(verbose) print(varname)
+ (y <- unlist(exprs[varname,]))
+ means <- tapply(y,pd[,c("date","treat","variety")],mean,na.rm=TRUE)
+ means
+ swps <- tapply(wpas$swp,wpas[,c("date","treat","variety")],function(x) x[1])
+ swps
+ ylim <- range(means, na.rm=TRUE)
+ xlim <- c(min(wpas$swp,-1.6,na.rm=TRUE), max(wpas$swp,0, na.rm=TRUE))
+ vlvls <- levels(wpas$variety)
+ tlvls <- levels(wpas$treat)
```

```
+ #cols <- c(4,2)
+ #pchs <- c(1,16)
+ plot(1,1, #wpas$swp[tfilter & vfilter], means[,"WS",vlvls[i]],
+       xlim=ylim,
+       ylim=rev(xlim),
+       ylab = "SWP.mean",
+       xlab = "Mean expression",
+       type="n",
+       axes=TRUE
+       )
+
+ title(varname, model)
+ legend("topright", bty="n", pch=pchs, col=rep(cols,each=2),lwd=lwd,
+        legend= outer(tlvls,vlvls,paste))
+ #
+ ally <- NULL
+ allx <- NULL
+ fits <- list(name=varname)
+ for(i in 1:length(vlvls)){
+ #for( j in 1:length(tlvls)){
+ #tfilter <- wpas$treat %in% tlvls[j]
+ vfilter <- wpas$variety %in% vlvls[i]
+ wpa <- wpas[vfilter,]
+ means[,,vlvls[i]]
+ mns <- melt(means[,,vlvls[i]])
+ wp <- melt(swps[,,vlvls[i]])
+ wp
+ all(wpa$date==dimnames(mns)$date)
+ yy <- mns[,"value"]
+ xx <- wp[,"value"]
+ points(yy, xx,
+       col = cols[i],
+       pch = pchs[as.numeric(mns$treat)]
+      , cex=0.5+as.numeric(mns$date)/3
+       )
+ #      }
+   xx <- xx
+   if(model=="" ) fit <- lm(xx~yy)
+   if(model=="+") fit <- lm(xx~yy+mns$treat)
+   if(model=="*") fit <- lm(xx~yy*mns$treat)
+ #
+   if(verbose) print(summary(fit))
+   coef <- fit$coefficients
+   if(length(coef)<3) coef[3] <- 0
+   if(length(coef)<4) coef[4] <- 0
+   abline(coef[1:2], col=cols[i],lwd=1)
+   abline(coef[1:2]+coef[3:4],col=cols[i],lwd=2)
+   ally <- c(ally,yy)
+   allx <- c(allx,xx)
+   fits[[vlvls[i]]] <- fit
+ }
+ fit <- lm(allx~ally)
+ fits[["all"]] <- fit
```

```
+ fits[["r"]] <- cor(ally,allx,use="complete")
+ if (verbose) print(summary(fit))
+ abline(fit$coefficients,lwd=2)
+ #points(-swps,means,cex=1.5)
+ invisible(fits)
+ }


> par(mfrow=c(2,3))
> #
> #varname <- rownames(t1819)[10]
> varname <- c("Vitvi03g01254")
> set.seed(1234)
> for(vari in 1:2){
+ varname <- rownames(t1819)[runif(1,1,10000)]
+ plot.wpe(varname,model="")
+ plot.wpe(varname,model="+")
+ fits <- plot.wpe(varname,model="*")
+ }
```

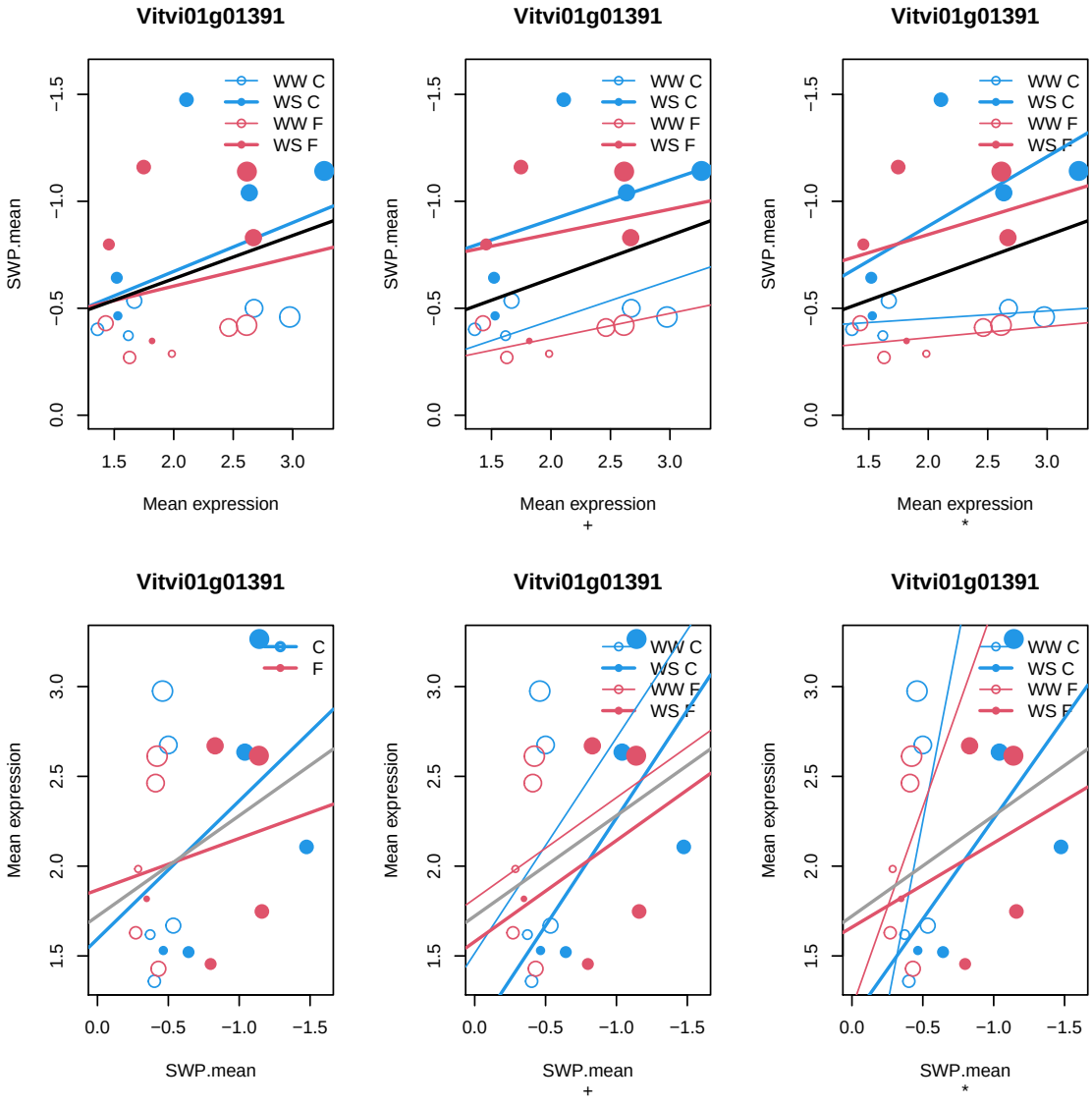



```
> length(fits)
[1] 5
```

```
> names(fits)
[1] "name" "C"    "F"    "all"  "r"

> testvar <- "Vitvi01g01391"

> par(mfrow=c(2,3))
> #
> #varname <- rownames(t1819)[10]
> varnames <- c("Vitvi03g01254")
> set.seed(1234)
> varname <- rownames(t1819)[runif(1,1,10000)]
> plot.wpe(varname,model="")
> plot.wpe(varname,model="+")
> plot.wpe(varname,model="*")
> fits <- plot.ewp(varname,model="")
> plot.ewp(varname,model="+")
> plot.ewp(varname,model="*")
```




```
> fits
```

```
$name
[1] "Vitvi01g01391"

$C

Call:
lm(formula = yy ~ xx)

Coefficients:
(Intercept)           xx
     1.5950      -0.7686


$F

Call:
lm(formula = yy ~ xx)

Coefficients:
(Intercept)           xx
     1.8673      -0.2872


$all

Call:
lm(formula = ally ~ allx)

Coefficients:
(Intercept)         allx
     1.7218      -0.5594


$r
[1] -0.3359093

> varname
[1] "Vitvi01g01391"
> pd <- pdata1819
> (y <- unlist(t1819[varname,]))
C18_11d_WS1 C18_11d_WS2 C18_11d_WS3 C18_11d_WS4 C18_11d_WW1
  1.5776032   1.4525081   1.5639675   1.5265365   1.5687083
C18_11d_WW2 C18_11d_WW3 C18_11d_WW4 C18_34d_WS1 C18_34d_WS2
  1.5729410   1.3865447   1.9464369   1.7347063   1.2654132
C18_34d_WS3 C18_34d_WS4 C18_34d_WW1 C18_34d_WW2 C18_34d_WW3
  1.4874714   1.5978309   1.4698219   0.8040958   1.3141315
C18_34d_WW4 C18_67d_WS1 C18_67d_WS2 C18_67d_WS3 C18_67d_WS4
  1.8480061   2.4172910   2.2355638   2.1438253   1.6317226
C18_67d_WW1 C18_67d_WW2 C18_67d_WW3 C18_67d_WW4 F18_10d_WS1
  1.6332742   1.9178152   1.4992723   1.6246928   1.7805825
F18_10d_WS2 F18_10d_WS3 F18_10d_WS4 F18_10d_WW1 F18_10d_WW2
  1.8735295   1.9142822   1.7035168   2.0980960   2.1052765
```

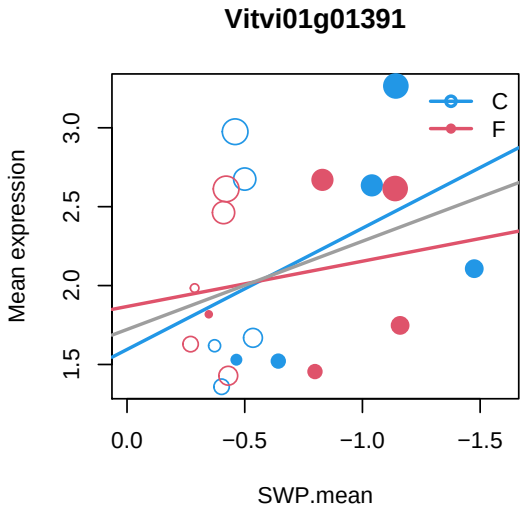
```
F18_10d_WW3 F18_10d_WW4 F18_34d_WS1 F18_34d_WS2 F18_34d_WS3
  1.9447357   1.7887485   1.5892246   1.3699329   1.4469174
F18_34d_WS4 F18_34d_WW1 F18_34d_WW2 F18_34d_WW3 F18_34d_WW4
  1.4139991   1.5153857   1.4749029   1.9144891   1.6107161
F18_67d_WS1 F18_67d_WS2 F18_67d_WS3 F18_67d_WS4 F18_67d_WW1
  1.9483340   1.6580581   1.9058175   1.4784712   1.4242818
F18_67d_WW2 F18_67d_WW3 F18_67d_WW4 C19_22d_WS1 C19_22d_WS2
  1.3742853   1.4653761   1.4504864   2.8000000   2.6400000
C19_22d_WS3 C19_22d_WS4 C19_22d_WW1 C19_22d_WW2 C19_22d_WW3
  2.2900000   2.8100000   2.5900000   2.7900000   2.7500000
C19_22d_WW4 C19_44d_WS1 C19_44d_WS2 C19_44d_WS3 C19_44d_WS4
  2.5700000   2.9400000   3.3900000   3.3900000   3.3400000
C19_44d_WW1 C19_44d_WW2 C19_44d_WW3 C19_44d_WW4 F19_22d_WS1
  2.6900000   3.1600000   3.1200000   2.9300000   2.5900000
F19_22d_WS2 F19_22d_WS3 F19_22d_WS4 F19_22d_WW1 F19_22d_WW2
  2.9200000   2.8600000   2.3100000   2.4100000   2.1600000
F19_22d_WW3 F19_22d_WW4 F19_44d_WS1 F19_44d_WS2 F19_44d_WS3
  2.7200000   2.5600000   2.4800000   2.6400000   2.8200000
F19_44d_WS4 F19_44d_WW1 F19_44d_WW2 F19_44d_WW3 F19_44d_WW4
  2.5200000   2.6300000   2.5300000   2.6400000   2.6500000
> means <- tapply(y,pd[,c("date","treat","variety")],mean,na.rm=TRUE)
> means
, , variety = C

            treat
date               WW       WS
  2018-06-11       NA       NA
  2018-06-12 1.618658 1.530154
  2018-07-05 1.359014 1.521355
  2018-08-07 1.668764 2.107101
  2019-06-26 2.675000 2.635000
  2019-07-18 2.975000 3.265000

, , variety = F

            treat
date               WW       WS
  2018-06-11 1.984214 1.817978
  2018-06-12       NA       NA
  2018-07-05 1.628873 1.455019
  2018-08-07 1.428607 1.747670
  2019-06-26 2.462500 2.670000
  2019-07-18 2.612500 2.615000
> par(mfrow=c(2,2))
> plot.ewp(varname,model="")
> usr <- par("usr")
> for(i in 1:2){
+   par(usr=usr)
+   wpa$swp
+   ( yy <- as.vector( ( means[as.character(wpa$date), ,vlvls[i]]) ) )
+   xx <- -rep(wpa$swp, length(tlvls))[!is.na(yy)]
+   yy <- yy[!is.na(yy)]
```

```
+    plot(xx, yy, pch=16, col=cols[i], xlim=-xlim, ylim=ylim)
+    fit <- lm(yy ~ xx)
+    abline(fit, col=cols[i])
+    }
Error in eval(expr, envir, enclos): object 'wpa' not found
```



5 Linear models for water potential

```
> library(limma)
Warning: package 'limma' was built under R version 4.0.3

Attaching package: 'limma'
The following object is masked from 'package:BiocGenerics':

    plotMA
```

```
> exprs <- t1819
> pd <- pdata1819w
```

We will use models on average expressions across replicates.

```
> varname <- testvar
> (y <- unlist(t1819[varname,]))
```

```
C18_11d_WS1 C18_11d_WS2 C18_11d_WS3 C18_11d_WS4 C18_11d_WW1
  1.5776032   1.4525081   1.5639675   1.5265365   1.5687083
C18_11d_WW2 C18_11d_WW3 C18_11d_WW4 C18_34d_WS1 C18_34d_WS2
  1.5729410   1.3865447   1.9464369   1.7347063   1.2654132
C18_34d_WS3 C18_34d_WS4 C18_34d_WW1 C18_34d_WW2 C18_34d_WW3
  1.4874714   1.5978309   1.4698219   0.8040958   1.3141315
C18_34d_WW4 C18_67d_WS1 C18_67d_WS2 C18_67d_WS3 C18_67d_WS4
  1.8480061   2.4172910   2.2355638   2.1438253   1.6317226
C18_67d_WW1 C18_67d_WW2 C18_67d_WW3 C18_67d_WW4 F18_10d_WS1
  1.6332742   1.9178152   1.4992723   1.6246928   1.7805825
F18_10d_WS2 F18_10d_WS3 F18_10d_WS4 F18_10d_WW1 F18_10d_WW2
  1.8735295   1.9142822   1.7035168   2.0980960   2.1052765
F18_10d_WW3 F18_10d_WW4 F18_34d_WS1 F18_34d_WS2 F18_34d_WS3
  1.9447357   1.7887485   1.5892246   1.3699329   1.4469174
F18_34d_WS4 F18_34d_WW1 F18_34d_WW2 F18_34d_WW3 F18_34d_WW4
  1.4139991   1.5153857   1.4749029   1.9144891   1.6107161
F18_67d_WS1 F18_67d_WS2 F18_67d_WS3 F18_67d_WS4 F18_67d_WW1
  1.9483340   1.6580581   1.9058175   1.4784712   1.4242818
F18_67d_WW2 F18_67d_WW3 F18_67d_WW4 C19_22d_WS1 C19_22d_WS2
  1.3742853   1.4653761   1.4504864   2.8000000   2.6400000
C19_22d_WS3 C19_22d_WS4 C19_22d_WW1 C19_22d_WW2 C19_22d_WW3
  2.2900000   2.8100000   2.5900000   2.7900000   2.7500000
C19_22d_WW4 C19_44d_WS1 C19_44d_WS2 C19_44d_WS3 C19_44d_WS4
  2.5700000   2.9400000   3.3900000   3.3900000   3.3400000
C19_44d_WW1 C19_44d_WW2 C19_44d_WW3 C19_44d_WW4 F19_22d_WS1
  2.6900000   3.1600000   3.1200000   2.9300000   2.5900000
F19_22d_WS2 F19_22d_WS3 F19_22d_WS4 F19_22d_WW1 F19_22d_WW2
  2.9200000   2.8600000   2.3100000   2.4100000   2.1600000
F19_22d_WW3 F19_22d_WW4 F19_44d_WS1 F19_44d_WS2 F19_44d_WS3
  2.7200000   2.5600000   2.4800000   2.6400000   2.8200000
F19_44d_WS4 F19_44d_WW1 F19_44d_WW2 F19_44d_WW3 F19_44d_WW4
  2.5200000   2.6300000   2.5300000   2.6400000   2.6500000
```

```
> means <- tapply(y,pd[,c("date","treat","variety")],mean,na.rm=TRUE)
> means
```

```
, , variety = C

            treat
date               WW       WS
  2018-06-11       NA       NA
  2018-06-12 1.618658 1.530154
  2018-07-05 1.359014 1.521355
  2018-08-07 1.668764 2.107101
  2019-06-26 2.675000 2.635000
  2019-07-18 2.975000 3.265000

, , variety = F
```

```
           treat
date              WW       WS
  2018-06-11 1.984214 1.817978
  2018-06-12       NA       NA
  2018-07-05 1.628873 1.455019
  2018-08-07 1.428607 1.747670
  2019-06-26 2.462500 2.670000
  2019-07-18 2.612500 2.615000
```

```
> swps <- tapply(wpas$swp,wpas[,c("date","treat","variety")],function(x) x[1])
> swps
```

```
, , variety = C

           treat
date                 WW         WS
  2018-06-11 -0.3680000 -0.4527273
  2018-06-12 -0.3720000 -0.4645455
  2018-07-05 -0.4016667 -0.6425000
  2018-08-07 -0.5350000 -1.4750000
  2019-06-26 -0.5000000 -1.0400000
  2019-07-18 -0.4592308 -1.1419231

, , variety = F

           treat
date                 WW         WS
  2018-06-11 -0.2872727 -0.3472727
  2018-06-12 -0.2854545 -0.3554545
  2018-07-05 -0.2700000 -0.7983333
  2018-08-07 -0.4300000 -1.1600000
  2019-06-26 -0.4100000 -0.8300000
  2019-07-18 -0.4210000 -1.1390000
```

Small phenodata

```
> exp <- unlist(as.data.frame(means))
> swp <- unlist(as.data.frame(swps))
> treat <- factor(substr(names(swp),1,2),levels=levels(wpas$treat))
> variety <- factor(substr(names(swp),4,4))
> sday <- as.numeric(substr(names(swp),5,5))
> pd1 <- data.frame(swp,treat,variety,sday=sday,date=dimnames(swps)[[1]],
+       row.names=names(swp))
>
> str(pd1)
'data.frame':        24 obs. of  5 variables:
 $ swp    : num  -0.368 -0.372 -0.402 -0.535 -0.5 ...
 $ treat  : Factor w/ 2 levels "WW","WS": 1 1 1 1 1 1 2 2 2 2 ...
 $ variety: Factor w/ 2 levels "C","F": 1 1 1 1 1 1 1 1 1 1 ...
 $ sday   : num  1 2 3 4 5 6 1 2 3 4 ...
 $ date   : chr  "2018-06-11" "2018-06-12" "2018-07-05" "2018-08-07" ...
```

5.1 Interpolated water potential data

```
> pd1
```

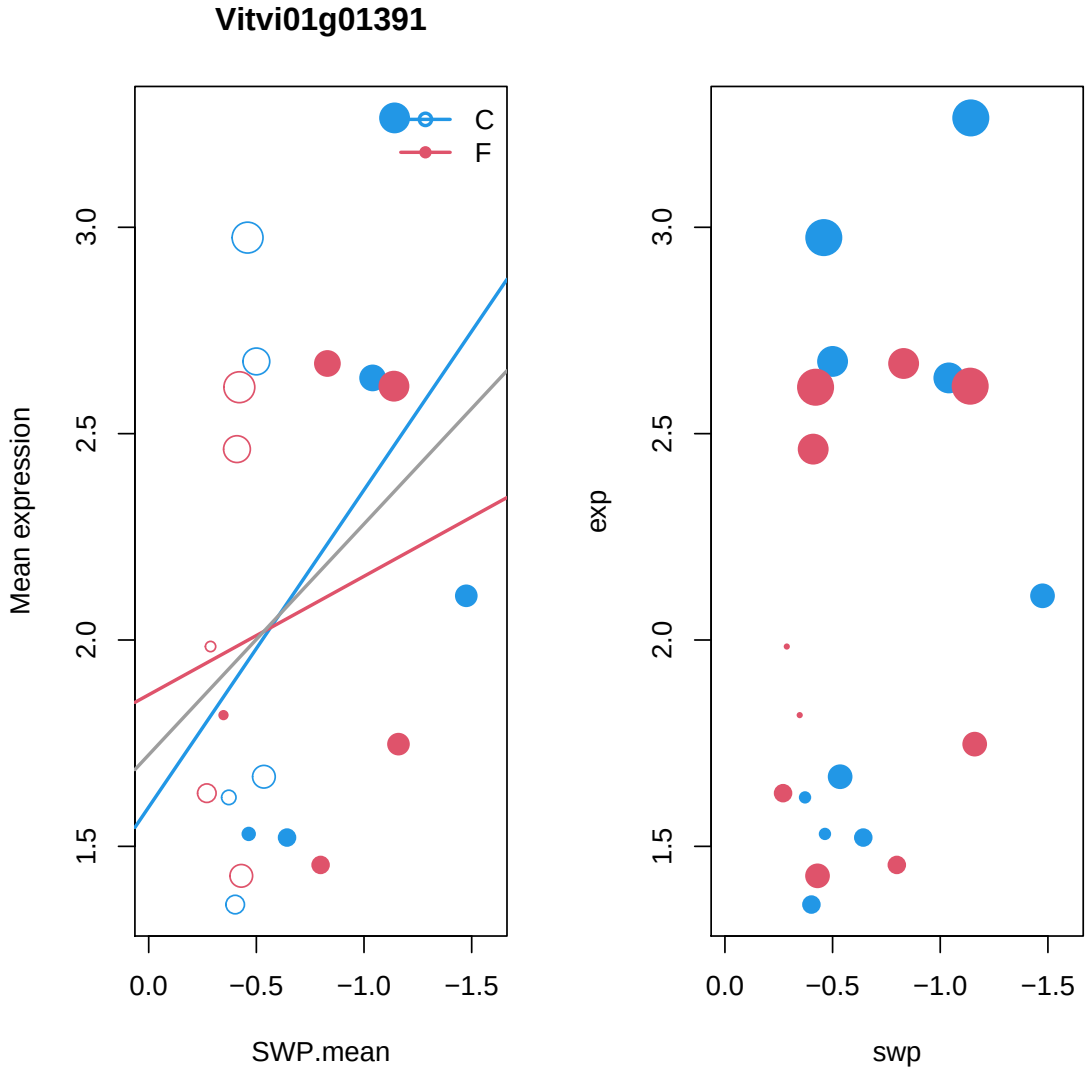
```
              swp treat variety sday       date
WW.C1 -0.3680000    WW       C    1 2018-06-11
WW.C2 -0.3720000    WW       C    2 2018-06-12
WW.C3 -0.4016667    WW       C    3 2018-07-05
WW.C4 -0.5350000    WW       C    4 2018-08-07
WW.C5 -0.5000000    WW       C    5 2019-06-26
WW.C6 -0.4592308    WW       C    6 2019-07-18
WS.C1 -0.4527273    WS       C    1 2018-06-11
WS.C2 -0.4645455    WS       C    2 2018-06-12
WS.C3 -0.6425000    WS       C    3 2018-07-05
WS.C4 -1.4750000    WS       C    4 2018-08-07
WS.C5 -1.0400000    WS       C    5 2019-06-26
WS.C6 -1.1419231    WS       C    6 2019-07-18
WW.F1 -0.2872727    WW       F    1 2018-06-11
WW.F2 -0.2854545    WW       F    2 2018-06-12
WW.F3 -0.2700000    WW       F    3 2018-07-05
WW.F4 -0.4300000    WW       F    4 2018-08-07
WW.F5 -0.4100000    WW       F    5 2019-06-26
WW.F6 -0.4210000    WW       F    6 2019-07-18
WS.F1 -0.3472727    WS       F    1 2018-06-11
WS.F2 -0.3554545    WS       F    2 2018-06-12
WS.F3 -0.7983333    WS       F    3 2018-07-05
WS.F4 -1.1600000    WS       F    4 2018-08-07
WS.F5 -0.8300000    WS       F    5 2019-06-26
WS.F6 -1.1390000    WS       F    6 2019-07-18
```

```
> my.write.table(pd1,file=file.path(.oroot,"swp-interpolated.txt"),
+   label="Interpolated swp data, considered as phenodata when swp is used."
+   )
```

Object: pd1
Label: Interpolated swp data, considered as phenodata when swp is used.
File :
../../output/50_Expression-water-stress-0.05-r-2-1.5-0.5-0.5-0.5-1/swp-interpolated.txt

Graphical test, check the points positions

```
> par(mfrow=c(1,2))
> plot.ewp(varname, model="")
> plot(swp,exp,xlim=c(0,-1.6),pch=16, col=6-as.numeric(variety)*2,cex=sday/2)
```



Aggregated expressions

```
> FUN <- function(x) unlist(as.data.frame(tapply(unlist(x),pd[,c("date","treat
> FUN(exprs[1,])
   WW.C1    WW.C2    WW.C3    WW.C4    WW.C5    WW.C6    WS.C1
      NA 4.453375 5.153464 3.727798 5.092500 5.905000       NA
   WS.C2    WS.C3    WS.C4    WS.C5    WS.C6    WW.F1    WW.F2
4.309168 4.498764 2.461840 3.370000 5.330000 5.102229       NA
   WW.F3    WW.F4    WW.F5    WW.F6    WS.F1    WS.F2    WS.F3
4.417362 3.974617 4.987500 5.922500 4.913018       NA 4.420979
   WS.F4    WS.F5    WS.F6
2.617199 3.512500 5.365000
> expr <- t(apply(exprs,1, FUN=FUN))
> dim(expr)
```

```
[1] 15242    24
```

```
> str(expr)
```

```
 num [1:15242, 1:24] NA NA NA NA NA NA NA NA NA NA ...
 - attr(*, "dimnames")=List of 2
  ..$ : chr [1:15242] "Vitvi15g01736" "Vitvi07g02832" "Vitvi07g02830" "Vitvi07
  ..$ : chr [1:24] "WW.C1" "WW.C2" "WW.C3" "WW.C4" ...
```

```
> filter <- apply(expr,2,function(x) !all(is.na(x)))
> expr <- expr[,filter]
> pd1 <- pd1[filter,]
> dim(expr)
```

```
[1] 15242    20
```

```
> dim(pd1)
```

```
[1] 20  5
```

```
> str(expr)
```

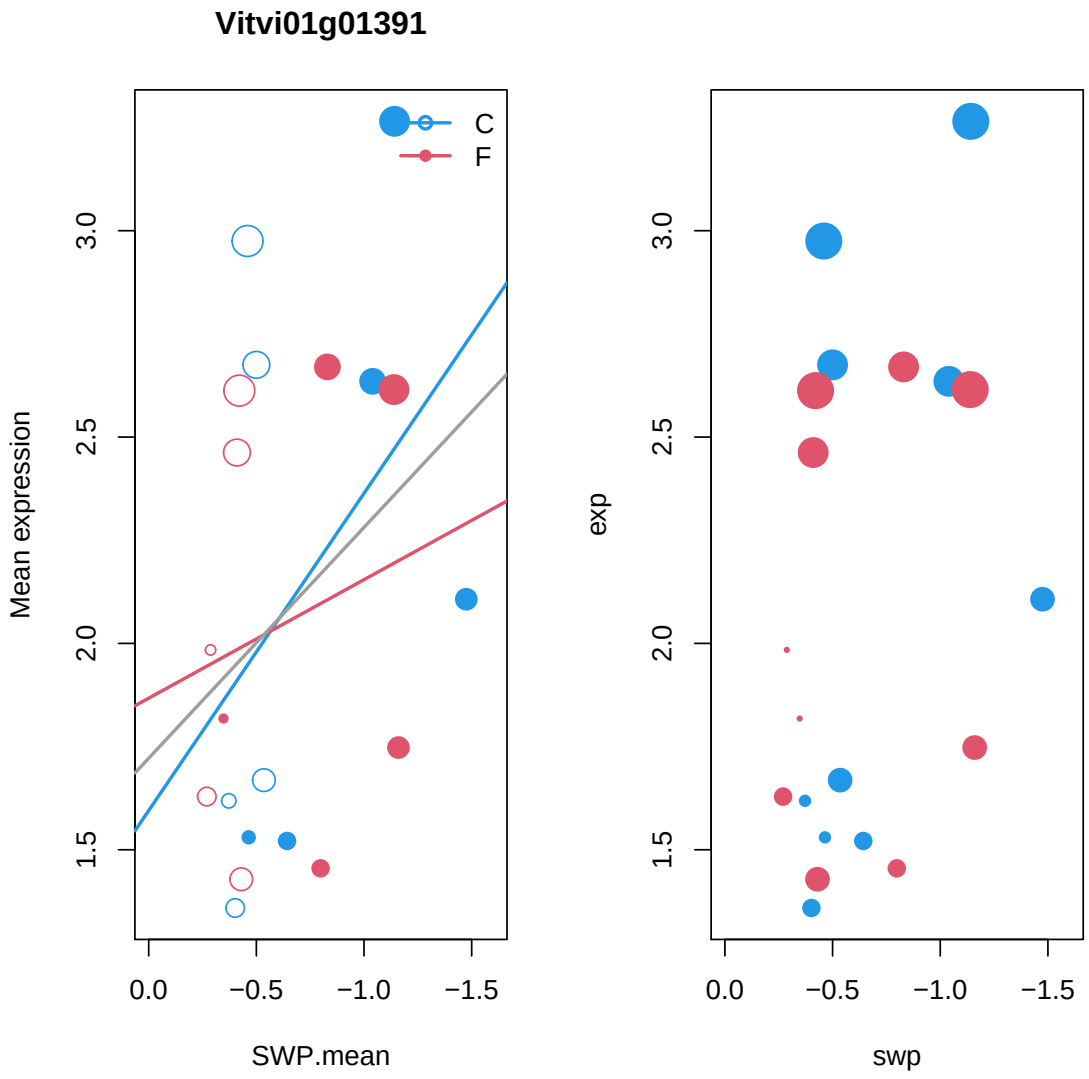
```
 num [1:15242, 1:20] 4.453 -2.47 -1.522 -0.894 2.059 ...
 - attr(*, "dimnames")=List of 2
  ..$ : chr [1:15242] "Vitvi15g01736" "Vitvi07g02832" "Vitvi07g02830" "Vitvi07
  ..$ : chr [1:20] "WW.C2" "WW.C3" "WW.C4" "WW.C5" ...
```

```
> str(pd1)
```

```
'data.frame':        20 obs. of  5 variables:
 $ swp    : num  -0.372 -0.402 -0.535 -0.5 -0.459 ...
 $ treat  : Factor w/ 2 levels "WW","WS": 1 1 1 1 1 2 2 2 2 2 ...
 $ variety: Factor w/ 2 levels "C","F": 1 1 1 1 1 1 1 1 1 1 ...
 $ sday   : num  2 3 4 5 6 2 3 4 5 6 ...
 $ date   : chr  "2018-06-12" "2018-07-05" "2018-08-07" "2019-06-26" ...
```

Check regressions

```
> varname <- testvar
> par(mfrow=c(1,2))
> fits <- plot.ewp(varname, model="")
> plot(swp,exp,xlim=c(0,-1.6),pch=16, col=6-as.numeric(variety)*2,cex=sday/2)
```




```
> lapply(fits[2:4],function(x) x$coefficients)
$C
(Intercept)          xx
  1.5950412  -0.7685916

$F
(Intercept)          xx
  1.8672599  -0.2871816

$all
(Intercept)        allx
  1.7217725  -0.5593981
> fitc <- lm(expr[varname,]~pd1$swp*pd1$variety)$coefficients
> fitc[c(1,2)]
(Intercept)     pd1$swp
  1.5950412  -0.7685916
> fitf <- c(fitc[1]+fitc[3],fitc[2]+fitc[4])
> fitf
(Intercept)     pd1$swp
  1.8672599  -0.2871816
```

```
> fitc <- fitc[c(1,2)]
> fita <- lm(expr[varname,]~pd1$swp)$coefficients
> fita
```

```
(Intercept)     pd1$swp
  1.7217725  -0.5593981
```

Looks ok.

```
> all(colnames(expr)==rownames(pd1))
```

```
[1] TRUE
```

Replace expressions and phenodata with the reduced ones.

```
> .exprs <- exprs
> .pd <- pd
```

```
> exprs <- expr
> pd <- pd1
> swp <- pd$swp
> all(colnames(exprs)==rownames(pd))
```

```
[1] TRUE
```

```
> cat(knit_child(file.path("../doc/","50a_limma-fit-swp.Rnw"),quiet=TRUE))
```

```
> testvar <- "Vitvi01g01391"
```

5.2 Overall Model

Simple model with water potential for all data:

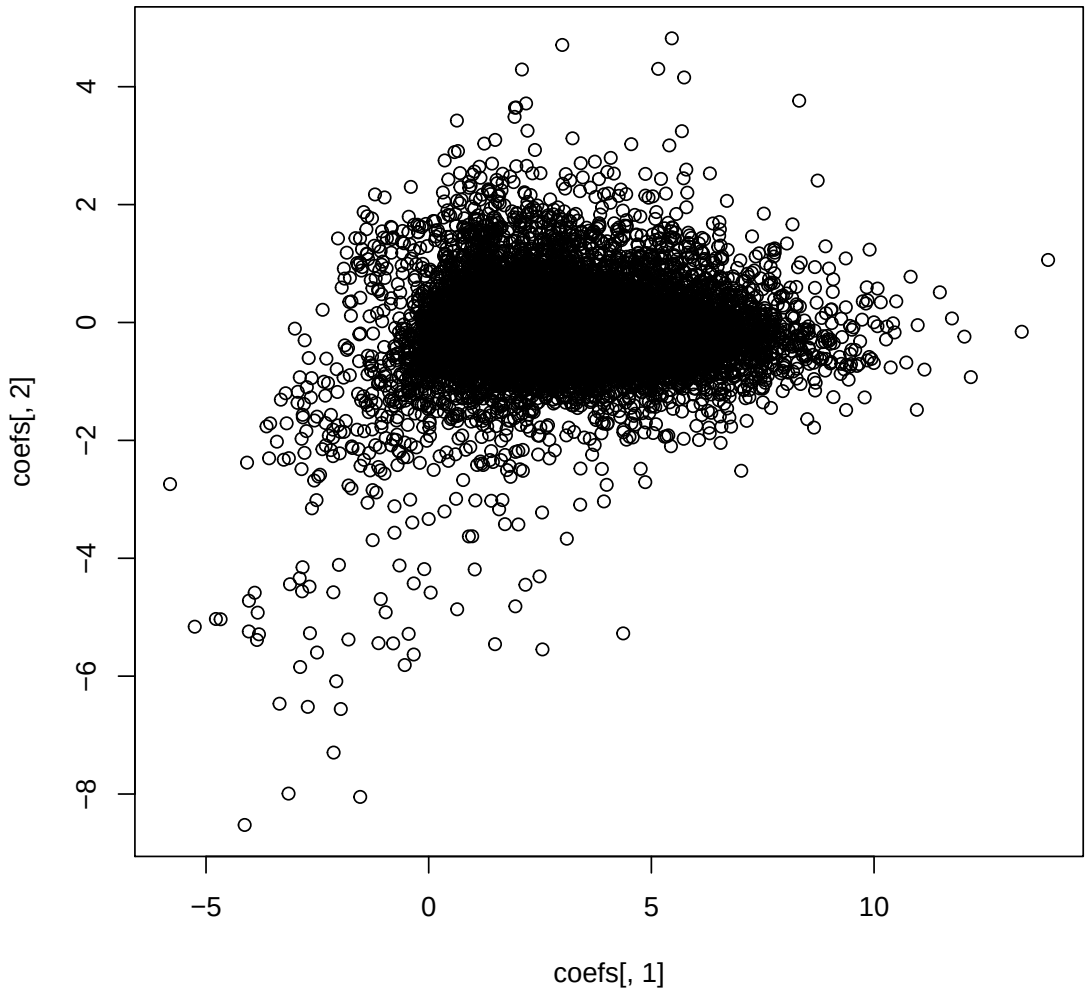
```
> design1 <- with(pd, model.matrix(~ swp))
> #design1[,2] <- (-design1[,2])
> head(design1)
  (Intercept)        swp
1           1 -0.3720000
2           1 -0.4016667
3           1 -0.5350000
4           1 -0.5000000
5           1 -0.4592308
6           1 -0.4645455
> tail(design1)
   (Intercept)        swp
15           1 -0.4210000
16           1 -0.3472727
17           1 -0.7983333
18           1 -1.1600000
19           1 -0.8300000
20           1 -1.1390000
```

Linear model

```
> fit1 <- lmFit(exprs, design1)
> fit1[testvar,]$coefficients
              (Intercept)        swp
Vitvi01g01391    1.721772 -0.5593981
> fit1 <- eBayes(fit1)
> fit1[testvar,]$coefficients
              (Intercept)        swp
Vitvi01g01391    1.721772 -0.5593981
> head(fit1[1:6,]$coefficients)
              (Intercept)       swp
Vitvi15g01736  5.42287213 1.4417521
Vitvi07g02832  0.79297631 1.4868377
Vitvi07g02830  1.05522190 2.1023461
Vitvi07g02812  0.02875199 0.5715781
Vitvi07g02811  3.02521622 0.8198777
Vitvi09g02033 -0.13442101 0.9949253
> fit <- fit1
> fit[testvar,]$coef
              (Intercept)        swp
Vitvi01g01391    1.721772 -0.5593981
```

Models for each variety

```
> coefs <- fit1$coefficients
> plot(coefs[,1],coefs[,2])
```




```
> dim(coefs[abs(coefs[,2])>2,])
[1] 252   2
```

Top table

```
> which <- 2
>   tt <- topTable(fit1,coef=which, number=Inf)
>   head(tt)
                  logFC    AveExpr         t      P.Value
Vitvi16g01985 -5.241765 -0.5987979 -7.927163 7.223317e-08
Vitvi05g01740 -1.942843  2.4651929 -6.647068 1.145780e-06
Vitvi17g00152 -4.152022 -0.1074944 -6.643733 1.154385e-06
Vitvi05g00011  4.156807  3.0078249  6.335044 2.321195e-06
Vitvi17g01086 -1.698436  5.0044446 -6.317734 2.414762e-06
Vitvi07g01395 -1.403819  4.1341533 -6.181798 3.297561e-06
                 adj.P.Val        B
Vitvi16g01985 0.001100978 7.653204
Vitvi05g01740 0.005865048 5.322334
Vitvi17g00152 0.005865048 5.315906
Vitvi05g00011 0.007278732 4.713350
Vitvi17g01086 0.007278732 4.679118
Vitvi07g01395 0.007278732 4.408716
```

5.3 Models for variety

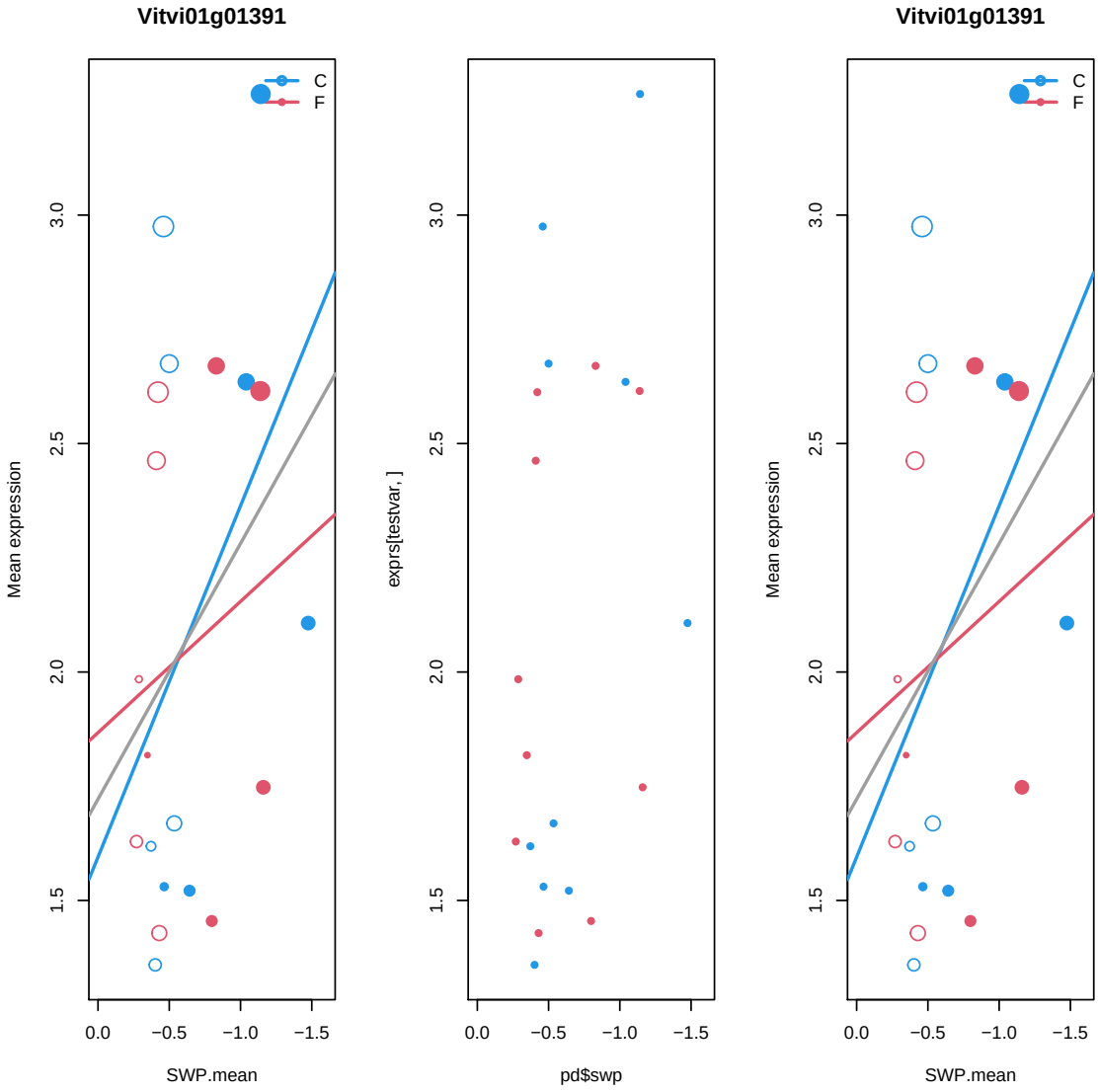
Model with water potential by variety (slopes are of interest).

```
> design2 <- with(pd, model.matrix(~ swp*variety))
> head(design2)
  (Intercept)        swp varietyF swp:varietyF
1           1 -0.3720000        0            0
2           1 -0.4016667        0            0
3           1 -0.5350000        0            0
4           1 -0.5000000        0            0
5           1 -0.4592308        0            0
6           1 -0.4645455        0            0
> tail(design2)
   (Intercept)        swp varietyF swp:varietyF
15           1 -0.4210000        1   -0.4210000
16           1 -0.3472727        1   -0.3472727
17           1 -0.7983333        1   -0.7983333
18           1 -1.1600000        1   -1.1600000
19           1 -0.8300000        1   -0.8300000
20           1 -1.1390000        1   -1.1390000
```

Linear model

```
> fit2 <- lmFit(exprs, design2)
> fit2[testvar,]$coefficients
              (Intercept)        swp  varietyF swp:varietyF
Vitvi01g01391    1.595041 -0.7685916 0.2722187    0.4814101


> varname <- testvar
> par(mfrow=c(1,3))
> p <- plot.ewp(varname,model="")
> plot(pd$swp,exprs[testvar,],  xlim=c(0,-1.6),
+    ,pch=16, col=6-as.numeric(pd$variety)*2,cex=pd$day/2)
> c(p$C$coef[2],p$F$coef[2])
        xx         xx
-0.7685916 -0.2871816
> fit2$coef[testvar,]
 (Intercept)          swp     varietyF swp:varietyF
   1.5950412   -0.7685916    0.2722187    0.4814101
> p <- plot.ewp(varname,model="", exprs=exprs, pd=pd)
```




```
> #
> fit2 <- eBayes(fit2)
> fit2[testvar,]$coefficients
             (Intercept)        swp  varietyF swp:varietyF
Vitvi01g01391    1.595041 -0.7685916 0.2722187    0.4814101
> head(fit2[1:6,]$coefficients)
             (Intercept)          swp   varietyF
Vitvi15g01736    5.550751  1.593545190 -0.2500355
Vitvi07g02832   -2.634115  0.508155686  5.4166972
Vitvi07g02830   -1.750650  1.548036562  4.3321685
Vitvi07g02812   -1.381363 -0.009794742  2.3030352
Vitvi07g02811    2.236177  0.566269561  1.2588734
Vitvi09g02033   -2.842837  0.419564483  4.1984533
             swp:varietyF
Vitvi15g01736  -0.31758915
Vitvi07g02832  -0.25109586
Vitvi07g02830  -0.90607176
Vitvi07g02812   0.40349136
Vitvi07g02811   0.02240192
Vitvi09g02033  -0.76028515
```

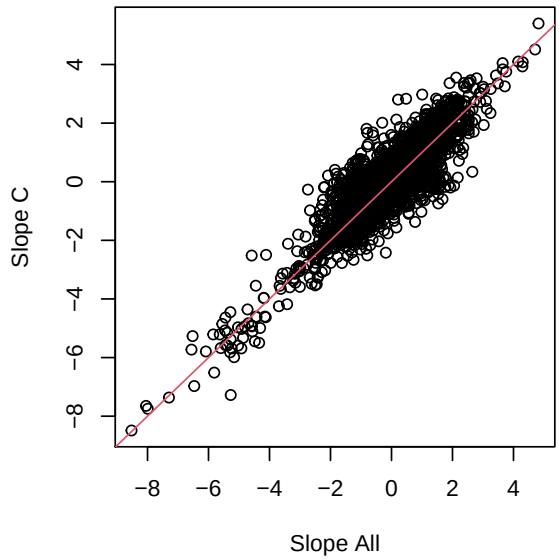
For comparison, here is the beginning of coefficients for overall model.

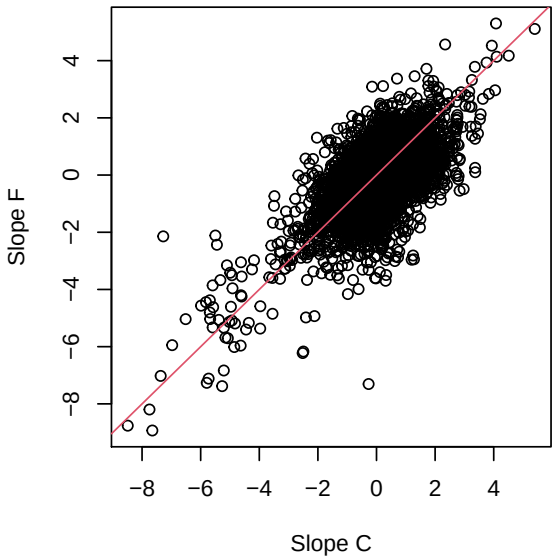
```
> head(fit1[1:6,]$coefficients)
              (Intercept)       swp
Vitvi15g01736  5.42287213 1.4417521
Vitvi07g02832  0.79297631 1.4868377
Vitvi07g02830  1.05522190 2.1023461
Vitvi07g02812  0.02875199 0.5715781
Vitvi07g02811  3.02521622 0.8198777
Vitvi09g02033 -0.13442101 0.9949253

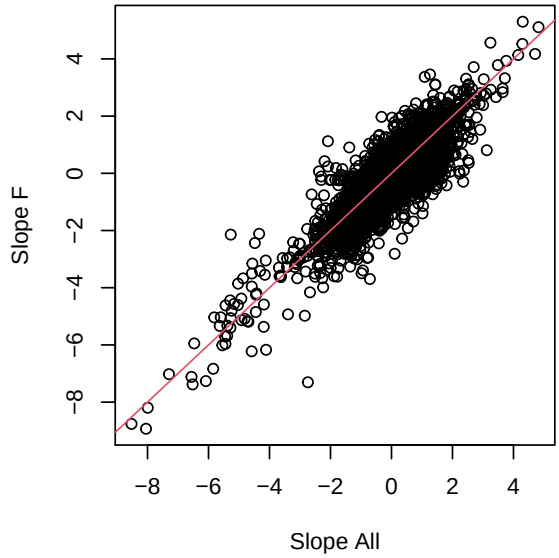

> fita[2]
   pd1$swp
-0.5593981
> fit1[testvar,]$coefficients[2]
[1] -0.5593981
> fitc[2]
   pd1$swp
-0.7685916
> fit2[testvar,]$coefficients[2]
[1] -0.7685916
> fitf[2]
   pd1$swp
-0.2871816
> fit2[testvar,]$coefficients[2]+fit2[testvar,]$coefficients[4]
[1] -0.2871816
```

Plots of coefficients

```
> oldpar <- par(mfrow=c(2,2), mar=c(4,4,1,1))
> coefs1 <- fit1$coefficients
> coefs2 <- fit2$coefficients
> plot(coefs1[,2],coefs2[,2], xlab="Slope All",ylab="Slope C")
> abline(c(0,1),col=2)
> cf24 <- coefs2[,2] + coefs2[,4]
> plot(coefs2[,2], cf24, xlab="Slope C",ylab="Slope F")
> abline(c(0,1),col=2)
> plot(coefs1[,2], cf24, xlab="Slope All",ylab="Slope F")
> abline(c(0,1),col=2)
> par(oldpar)
```







5.4 Mean expressions

```
> my.predict <- function(fit, x=1){
+ cf <- fit$coefficients
+ mc <- cf%*%c(1,x,0,0)
+ mf <- cf%*%c(1,x,1,x)
+ return(data.frame(mc=mc,mf=mf))
+ }
> fit2$coefficients[1:2,]
```

```
                (Intercept)       swp   varietyF swp:varietyF
Vitvi15g01736     5.550751 1.5935452 -0.2500355   -0.3175892
Vitvi07g02832    -2.634115 0.5081557  5.4166972   -0.2510959
```

```
> my.predict(fit2)[1:2,]
```

```
                      mc       mf
Vitvi15g01736  7.144296 6.576671
Vitvi07g02832 -2.125959 3.039642
```

```
> my.predict(fit2)[testvar,]
```

```
                       mc       mf
Vitvi01g01391 0.8264496 1.580078
```

```
> ma <- fit1$coefficients%*%c(1,mean(swp))
> macf <- data.frame(ma=ma,my.predict(fit2, x=mean(swp)))
> head(macf)
```

```
                       ma        mc        mf
Vitvi15g01736  4.4767407  4.505007 4.4633851
Vitvi07g02832 -0.1827419 -2.967585 2.6138903
Vitvi07g02830 -0.3244159 -2.766529 2.1602371
Vitvi07g02812 -0.3463388 -1.374935 0.6633139
Vitvi07g02811  2.4871819  1.864570 3.1087423
Vitvi09g02033 -0.7873280 -3.118171 1.5792098
```

```
> macf[testvar,]
```

```
                    ma      mc       mf
Vitvi01g01391 2.08887 2.09942 2.055719
```

Another way is using a separate model for varieties. It will provide opportunity to test the differences between varieties:

```
> design3 <- with(pd, model.matrix(~ 0+variety))
> head(design3)
```

```
  varietyC varietyF
1        1        0
2        1        0
3        1        0
4        1        0
5        1        0
6        1        0
```

```
> tail(design3)
```

```
   varietyC varietyF
15        0        1
16        0        1
17        0        1
18        0        1
19        0        1
20        0        1
```

```
> fit3 <- lmFit(exprs, design3)
> fit3[testvar,]$coefficients
```

```
              varietyC varietyF
Vitvi01g01391 2.135505 2.042236
```

```
> mswps <- with(pd, aggregate(swp, list(variety), mean) )$x
> my.predict(fit2, mswps[1])[testvar,1]
```

```
[1] 2.135505
```

```
> my.predict(fit2, mswps[2])[testvar,2]
```

```
[1] 2.042236
```

Object `fit3` holds mean expressins for varieties.

5.4.1 Plots of variety coefficients

I will try to set the variety slopes compared to slope of complete data
For comparison, here is the beginning of coefficients for overall model.

```
> head(fit1[1:6,]$coefficients)
```

```
              (Intercept)       swp
Vitvi15g01736  5.42287213 1.4417521
Vitvi07g02832  0.79297631 1.4868377
Vitvi07g02830  1.05522190 2.1023461
Vitvi07g02812  0.02875199 0.5715781
Vitvi07g02811  3.02521622 0.8198777
Vitvi09g02033 -0.13442101 0.9949253
```

Extract slopes

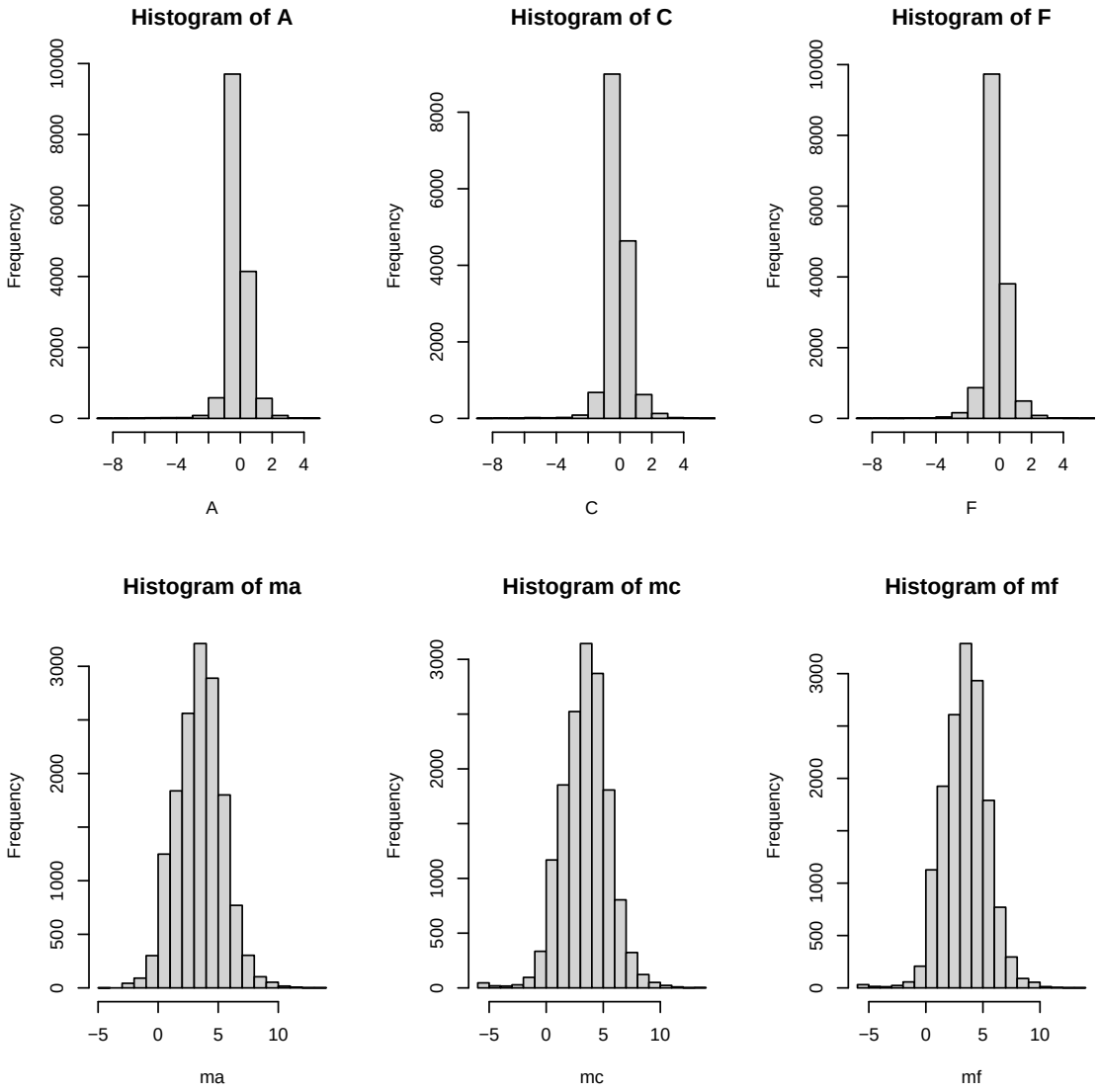
```
> A <- fit1$coefficients[,2]
> C <- fit2$coefficients[,2]
> F <- fit2$coefficients[,2]+fit2$coefficients[,4]
> ma <- macf[,"ma"]
> mc <- fit3$coefficients[,1]
> mf <- fit3$coefficients[,2]
> coefs <- data.frame(A,C,F,ma,mc,mf)
> head(coefs)
```

```
                       A            C          F          ma
Vitvi15g01736 1.4417521  1.593545190  1.2759560  4.4767407
Vitvi07g02832 1.4868377  0.508155686  0.2570598 -0.1827419
Vitvi07g02830 2.1023461  1.548036562  0.6419648 -0.3244159
Vitvi07g02812 0.5715781 -0.009794742  0.3936966 -0.3463388
Vitvi07g02811 0.8198777  0.566269561  0.5886715  2.4871819
Vitvi09g02033 0.9949253  0.419564483 -0.3407207 -0.7873280
                      mc        mf
Vitvi15g01736  4.430191 4.5232904
Vitvi07g02832 -2.991443 2.6259591
Vitvi07g02830 -2.839209 2.1903769
Vitvi07g02812 -1.374475 0.6817977
Vitvi07g02811  1.837984 3.1363800
Vitvi09g02033 -3.137869 1.5632132
```

```
> ca <- C-A
> fa <- F-A
> fc <- F-C
> coefs <- data.frame(mc,mf,C,F)
> head(coefs)
```

```
                      mc        mf            C          F
Vitvi15g01736  4.430191 4.5232904  1.593545190  1.2759560
Vitvi07g02832 -2.991443 2.6259591  0.508155686  0.2570598
Vitvi07g02830 -2.839209 2.1903769  1.548036562  0.6419648
Vitvi07g02812 -1.374475 0.6817977 -0.009794742  0.3936966
Vitvi07g02811  1.837984 3.1363800  0.566269561  0.5886715
Vitvi09g02033 -3.137869 1.5632132  0.419564483 -0.3407207
```

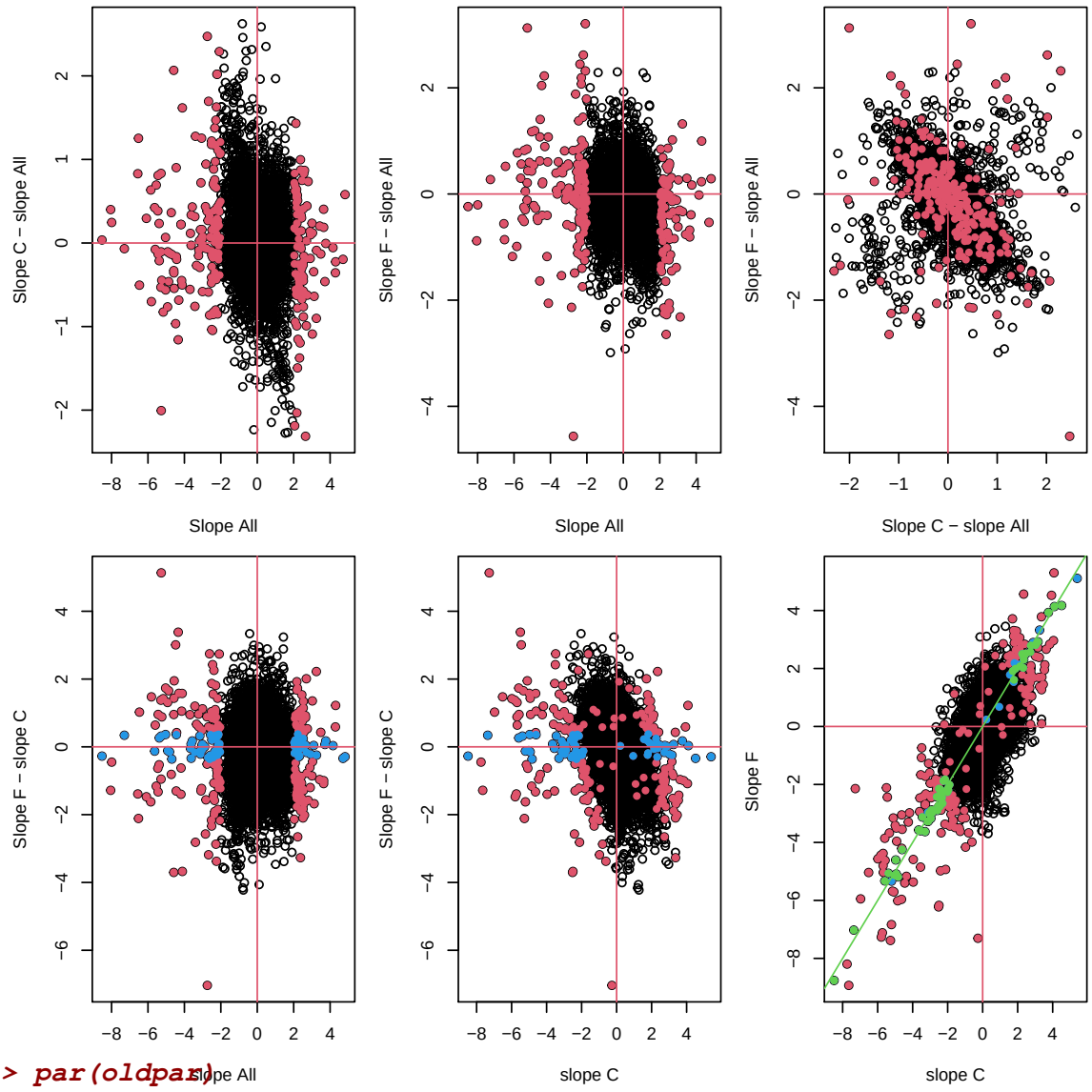
```
> par(mfrow=c(2,3))
> hist(A,xlim=range(c(A,C,F)))
> hist(C,xlim=range(c(A,C,F)))
> hist(F,xlim=range(c(A,C,F)))
> hist(ma)
> hist(mc)
> hist(mf)
```



5.4.2 Types by effects

```
> delta <- 2
> large_abs_A <- abs(A)> delta
> small_fc <- abs(fc) < delta/5
> small_ca <- abs(ca) < delta/5
> oldpar <- par(mfrow=c(2,3), mar=c(4,4,1,1))
> plot(A,ca, xlab="Slope All",ylab="Slope C - slope All")
> points(A[large_abs_A],ca[large_abs_A],col=2,pch=16)
> abline(h=0,v=0,col=2)
> plot(A,fa, xlab="Slope All",ylab="Slope F - slope All")
```

```
> points(A[large_abs_A],fa[large_abs_A],col=2,pch=16)
> abline(h=0,v=0,col=2)
> plot(ca,fa, xlab="Slope C - slope All",ylab="Slope F - slope All")
> points(ca[large_abs_A],fa[large_abs_A],col=2,pch=16)
> abline(h=0,v=0,col=2)
> #
> plot(A,fc, xlab="slope All",ylab="Slope F - slope C")
> points(A[large_abs_A],fc[large_abs_A],col=2,pch=16)
> points(A[large_abs_A&small_fc],fc[large_abs_A&small_fc],col=4,pch=16)
> abline(h=0,v=0,col=2)
> #
> plot(C,fc, xlab="slope C",ylab="Slope F - slope C")
> points(C[large_abs_A],fc[large_abs_A],col=2,pch=16)
> points(C[large_abs_A&small_fc],fc[large_abs_A&small_fc],col=4,pch=16)
> abline(h=0,v=0,col=2)
> #
> plot(C,F, xlab="slope C",ylab="Slope F ")
> points(C[large_abs_A],F[large_abs_A],col=2,pch=16)
> points(C[large_abs_A&small_fc],F[large_abs_A&small_fc],col=4,pch=16)
> type1 <- large_abs_A&small_fc&small_ca
> points(
+    C[type1],
+    F[type1],
+    col=3,pch=16)
>
> abline(h=0,v=0,col=2)
> abline(c(0,1),col=3)
```




```
> par(oldpar)
```

6 Situation types and Type selection criteria

Boundaries:
minX X at least ... (>)
maxX X at most ... (<)
deltaxy difference of mean x-y treshold (<)

```
> .deltam      # <- 2
.deltam
    "2"
> .minC        # <-  2
.minC
"1.5"
> .maxC        # <- 0.5
.maxC
"0.5"
> .minfc       # <- 1
.minfc
 "0.5"
> .maxfc       # <- 0.5
.maxfc
 "0.5"
> .deltam2     # <- .deltam/2
.deltam2
     "1"
```

6.1 Types

Type1

```
> # type1 <- (large_abs_C|large_abs_F) & small_fc & (abs(mc-mf)<deltam)
```

Absolute slope C or F larger than 1.5 with difference of slopes smaller than 0.5 and difference of means below 2.

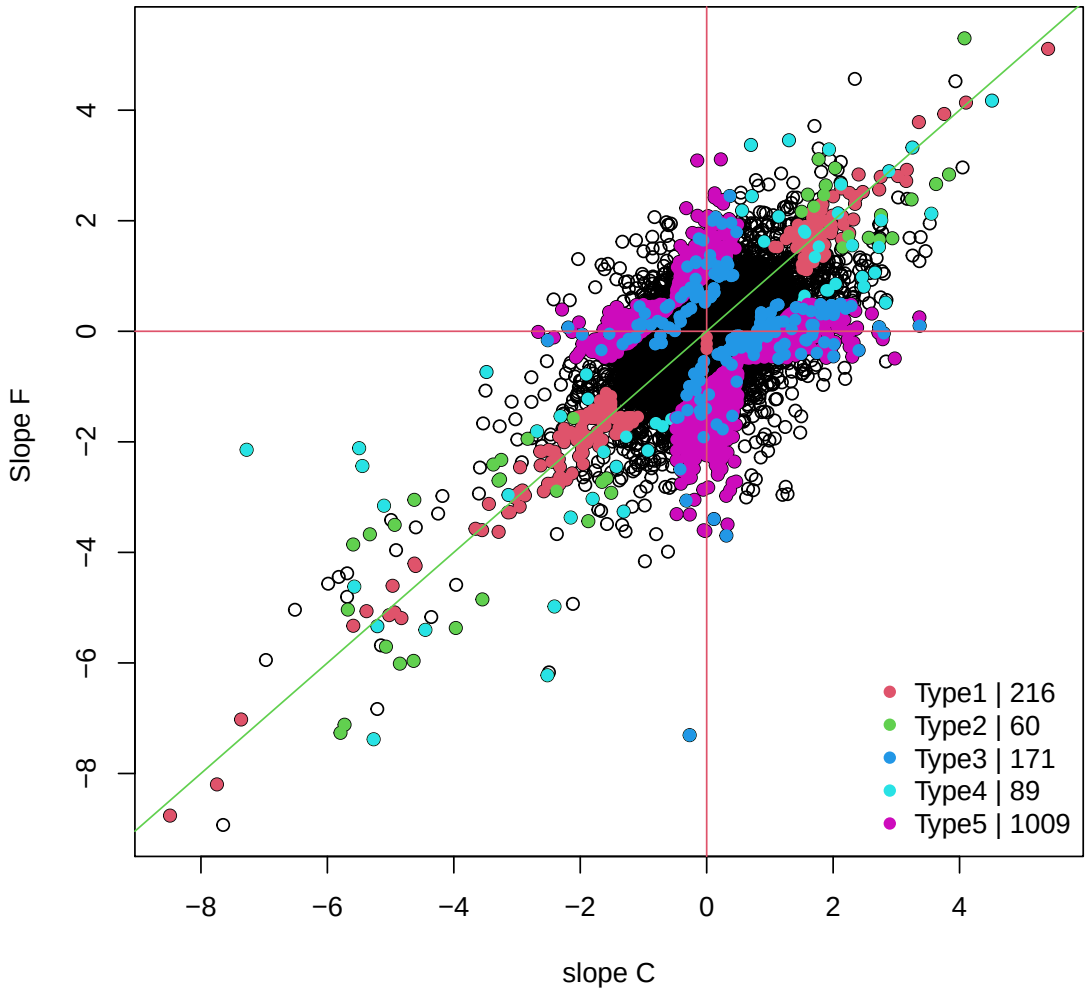
Type2

```
> #type2 <- (large_abs_C & large_abs_F) & (abs(fc) > minfc)&(abs(mc-mf)>deltam
> #type2 <- type2 & ( (C*F >0) )
```

Both slopes C and F larger than 1.5 , both positive or negative, with difference of slopes larger than 0.5 and difference of means above 1.

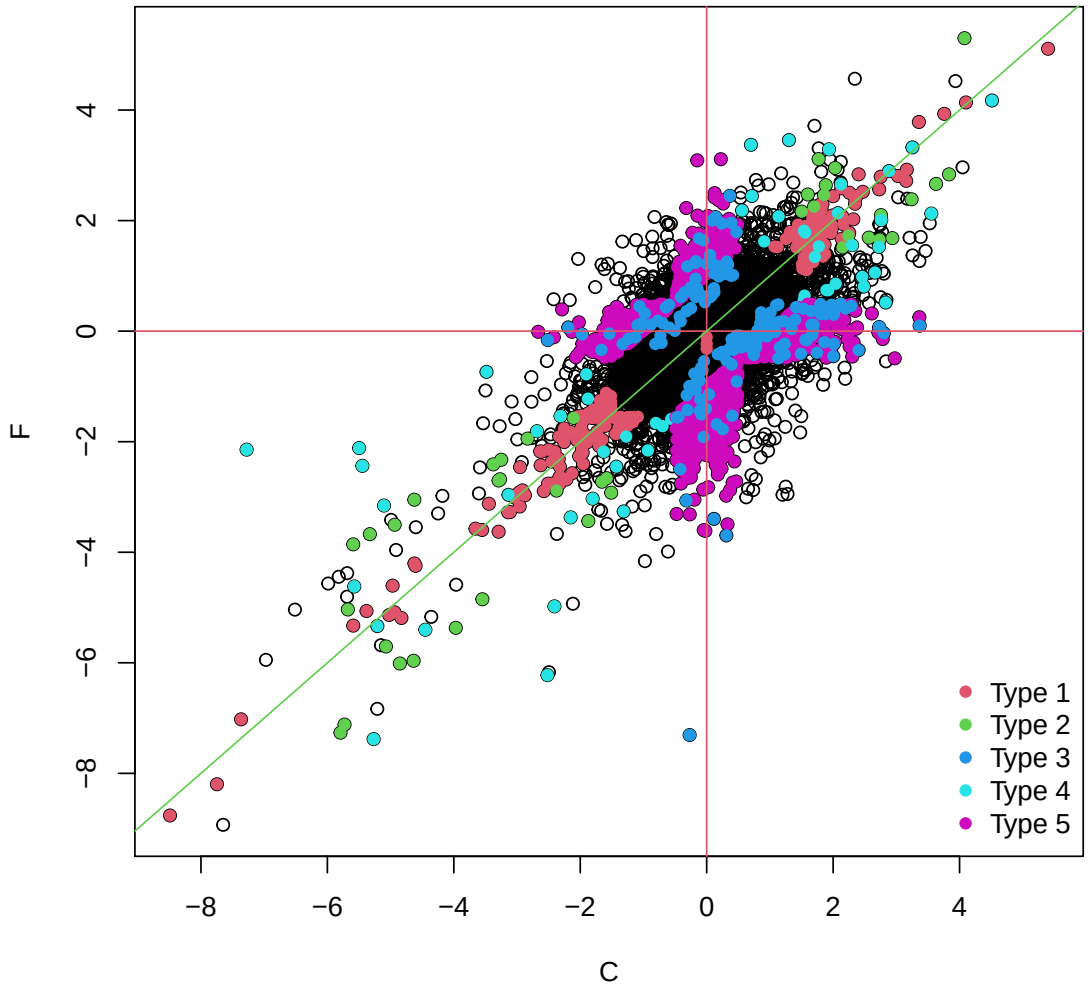
```
> #
> delta <- 2
> #
> deltam <- .deltam #2
> deltam2 <- .deltam2 # delta mean for type 2
> minC <- .minC   # 2       # slope C larger
> maxC <- .maxC     # slope C smaller
> minF <- minC    # slope F larger
> maxF <- maxC    # slope F smaller
> minA <- minC    # slope A larger
> minfc <- .minfc # 1      # difference F - C larger
> minfc5 <- as.numeric(minfc)*2 # difference for F - C larger for type 5
> maxfc <- .maxfc    # difference F - C smaller
> maxca <- maxfc  # difference C - A smaller
> maxfa <- maxfc  # difference F - A smaller
> #
> large_abs_A <- abs(A)> minA
> large_abs_C <- abs(C)> minC
> large_abs_F <- abs(F)> minF
> #
> small_fc <- abs(fc) < maxfc
> small_ca <- abs(ca) < maxca
> small_fa <- abs(fa) < maxfa
> plot(C,F, xlab="slope C",ylab="Slope F ")
> #points(C[large_abs_A],F[large_abs_A],col=2,pch=16)
> #
> type10 <- large_abs_A & small_fc & small_ca
> type1 <- (large_abs_C|large_abs_F) & small_fc & (abs(mc-mf)<deltam)
> table(type10,type1)
       type1
type10  FALSE  TRUE
  FALSE 15019    49
  TRUE      7   167
> points(
+    C[type1],
+    F[type1],
+    col=2, pch=16)
> #
```

```
> type2 <- (large_abs_C & large_abs_F) & (abs(fc) > minfc)&(abs(mc-mf)>deltam2
> type2 <- type2 & ( (C*F >0) )
> points(
+    C[type2],
+    F[type2],
+    col=3,pch=16)
> #
> type30 <- ((abs(C)<maxC)|(abs(F)<maxF)) & (abs(fc)> minfc)
> type3 <- ((abs(C)<maxC)|(abs(F)<maxF)) & (abs(fc)> minfc)&(abs(mc-mf)>deltam
> table(type3,type30)
       type30
type3   FALSE  TRUE
  FALSE 11471  3600
  TRUE      0   171
> points(
+    C[type3],
+    F[type3],
+    col=4,pch=16)
> #
> type4 <- (large_abs_C|large_abs_F)&(abs(mc-mf)>deltam)&(C*F>0)
> points(
+    C[type4],
+    F[type4],
+    col=5,pch=16)
> #
> type5 <- ((abs(C)<maxC)|(abs(F)<maxF)) & (abs(fc)> minfc5)&(abs(mc-mf)<delta
> points(
+    C[type5],
+    F[type5],
+    col=6,pch=16)
>
> table(type3,type5)
       type5
type3   FALSE  TRUE
  FALSE 14062  1009
  TRUE    171     0
> points(
+    C[type3],
+    F[type3],
+    col=4,pch=16)
> # type 3 is a subset of type5, type3 & large mean difference
>
> #
> abline(h=0,v=0,col=2)
> abline(c(0,1),col=3)
> types <- data.frame(type1,type2,type3,type4,type5)
> nt <- apply(types,2,sum)
> legend("bottomright",pch=rep(16,5),col=2:6,legend=paste0("Type",1:5," | ",nt
```




```
> head(types)
              type1 type2 type3 type4 type5
Vitvi15g01736  TRUE FALSE FALSE FALSE FALSE
Vitvi07g02832 FALSE FALSE FALSE FALSE FALSE
Vitvi07g02830 FALSE FALSE FALSE  TRUE FALSE
Vitvi07g02812 FALSE FALSE FALSE FALSE FALSE
Vitvi07g02811 FALSE FALSE FALSE FALSE FALSE
Vitvi09g02033 FALSE FALSE  TRUE FALSE FALSE
> plot.types <- function(x=C, y=F, type=types,title,...){
+ xlab <- deparse(substitute(x))
+ ylab <- deparse(substitute(y))
+
+ plot(x,y, xlab=xlab,ylab=ylab)
+ m <- ncol(type)
+ sek <- c(1,2,4,5,3)
+ for( i in sek){
+ points(
+    x[types[,i]],
+    y[types[,i]],
```

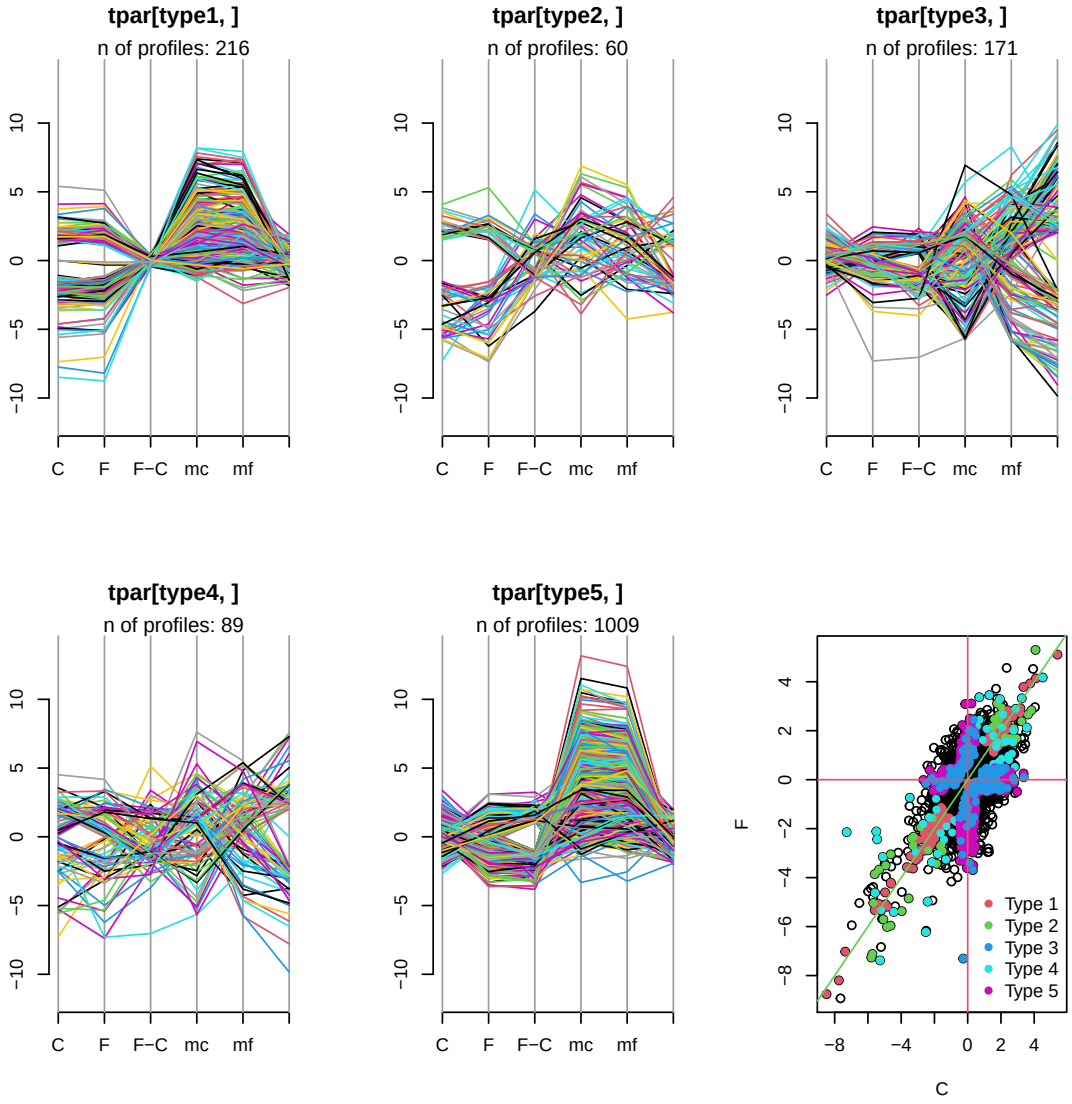
```
+     col=i+1,pch=16)
+     }
+     abline(h=0,v=0,col=2)
+ abline(c(0,1),col=3)
+ if(!missing(title)) title(title)
+ legend("bottomright",pch=rep(16,m),col=1+(1:m),legend=paste("Type",1:m),bty=
+ }
> plot.types()
```



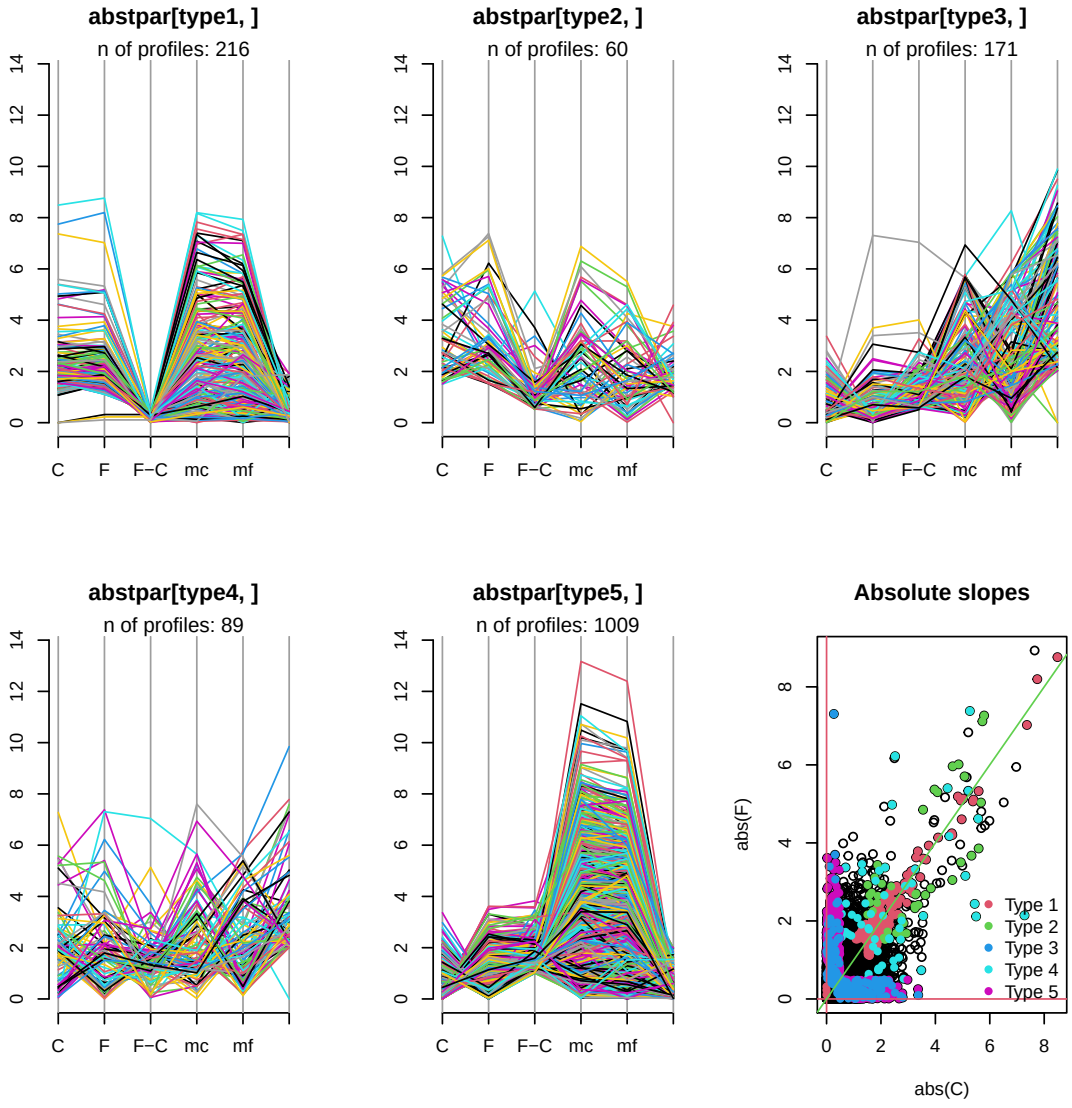

```
> x <- coefs[type1,]
> ylim <- range(x)
> my.parallelplot <- function(x, ylim = range(x), title,  ...){
+ if(missing(title)) title <- deparse(substitute(x))
+ m <- ncol(x)
+ plot(0,0, type = "n"
+      , xlim = c(1,m)
+      , ylim = ylim
+      , axes = FALSE
+      , ann=FALSE
+      )
```

```
+ title(title)
+ mtext(paste("n of profiles:", nrow(x)),cex=0.75)
+ axis(2)
+ axis(1, at=1:m,labels=gsub("\\.\\.\\.","-",colnames(x)),cex=0.9,xpd=TRUE)
+ abline(v=1:m,col=8)
+ x$col <- 1:nrow(x)
+ apply(x,1,function(y) lines(1:m,y[-(m+1)],col=y[m+1]))
+ invisible(nrow(x))
+ }
> if(interactive()) my.parallelplot(coefs[type1,])

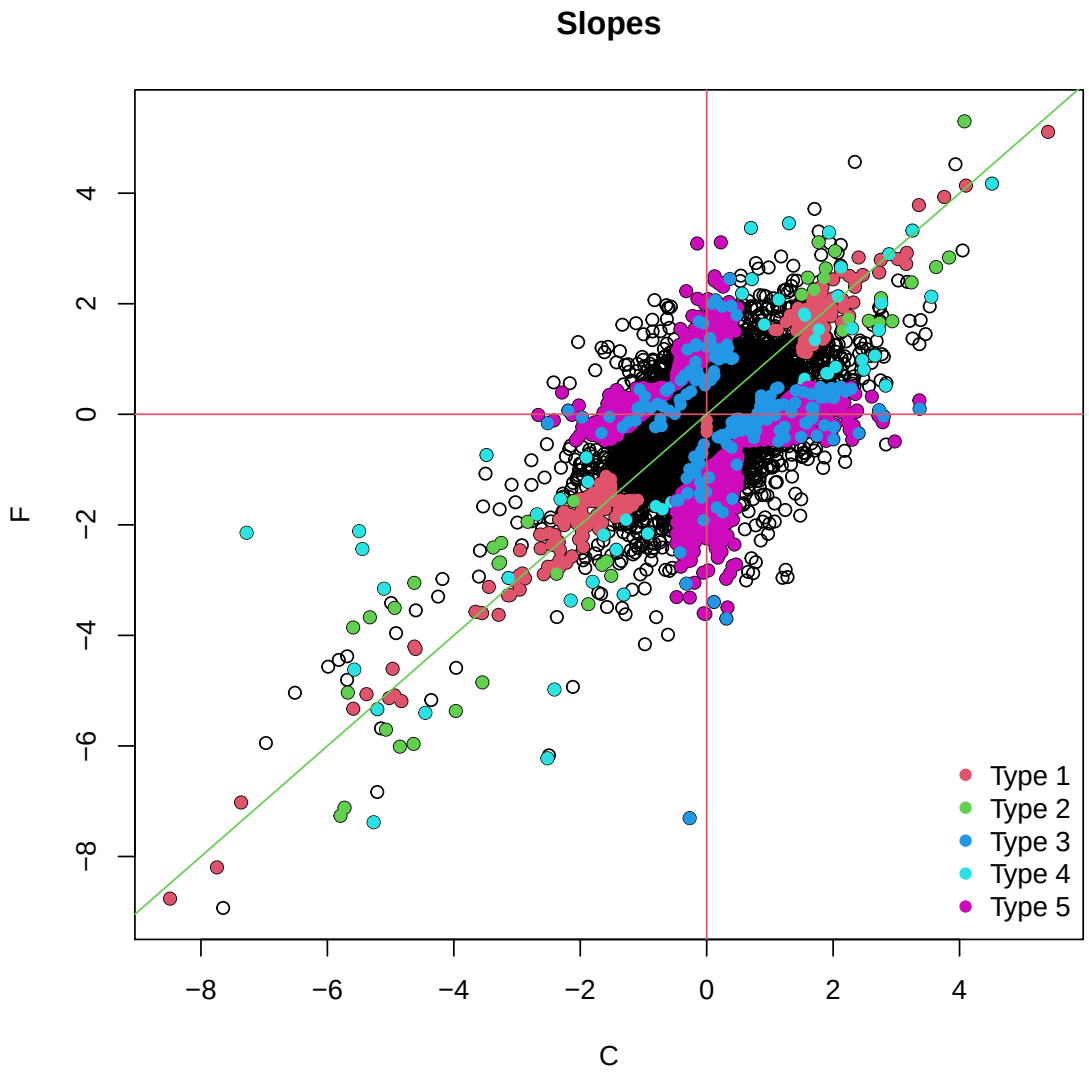
> par(mfrow=c(2,3))
> tpar <- data.frame(C,F,F-C,mc,mf,mf-mc)
> ylim <- range(tpar)
> my.parallelplot(tpar[type1,], ylim=ylim)
> my.parallelplot(tpar[type2,], ylim=ylim)
> my.parallelplot(tpar[type3,], ylim=ylim)
> my.parallelplot(tpar[type4,], ylim=ylim)
> my.parallelplot(tpar[type5,], ylim=ylim)
> plot.types()
```



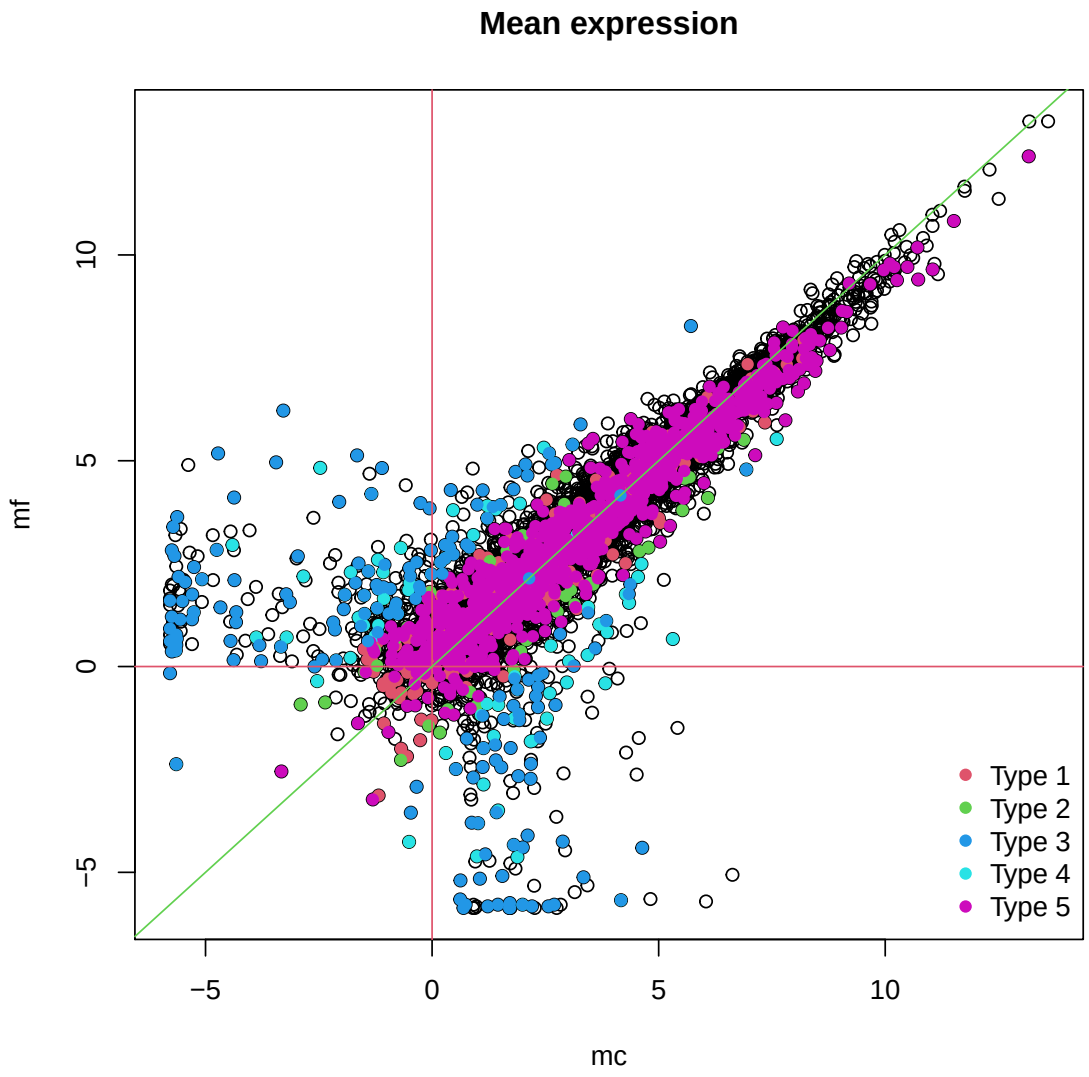
```
> par(mfrow=c(2,3))
> tpar <- data.frame(C,F,F-C,mc,mf,mf-mc)
> abstpar <- abs(tpar)
> ylim <- range(abstpar)
> my.parallelplot(abstpar[type1,], ylim=ylim)
> my.parallelplot(abstpar[type2,], ylim=ylim)
> my.parallelplot(abstpar[type3,], ylim=ylim)
> my.parallelplot(abstpar[type4,], ylim=ylim)
> my.parallelplot(abstpar[type5,], ylim=ylim)
> plot.types(abs(C),abs(F),title="Absolute slopes")
```



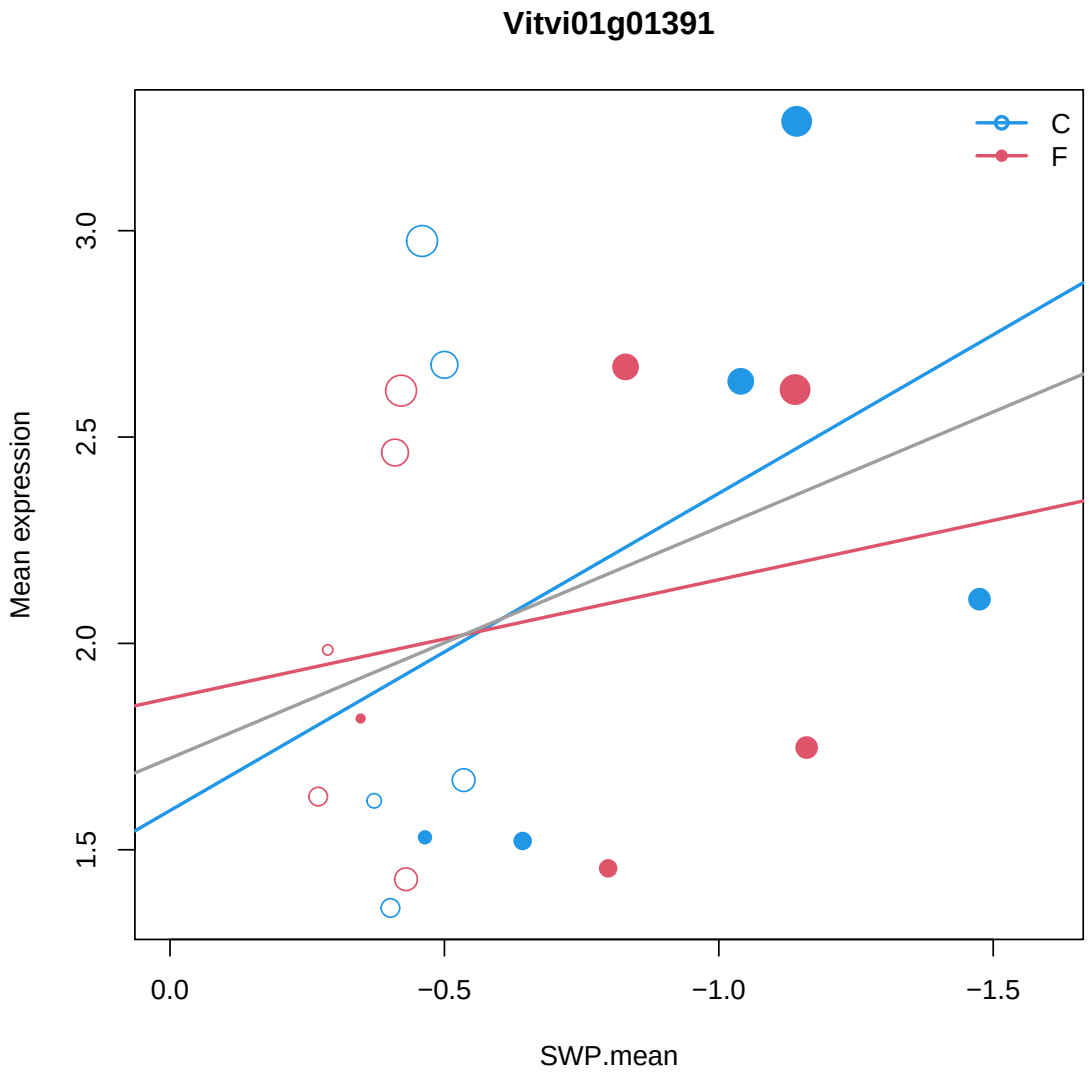

```
> plot.types(C,F,title="Slopes")
```




```
> plot.types(mc,mf,title="Mean expression")
```

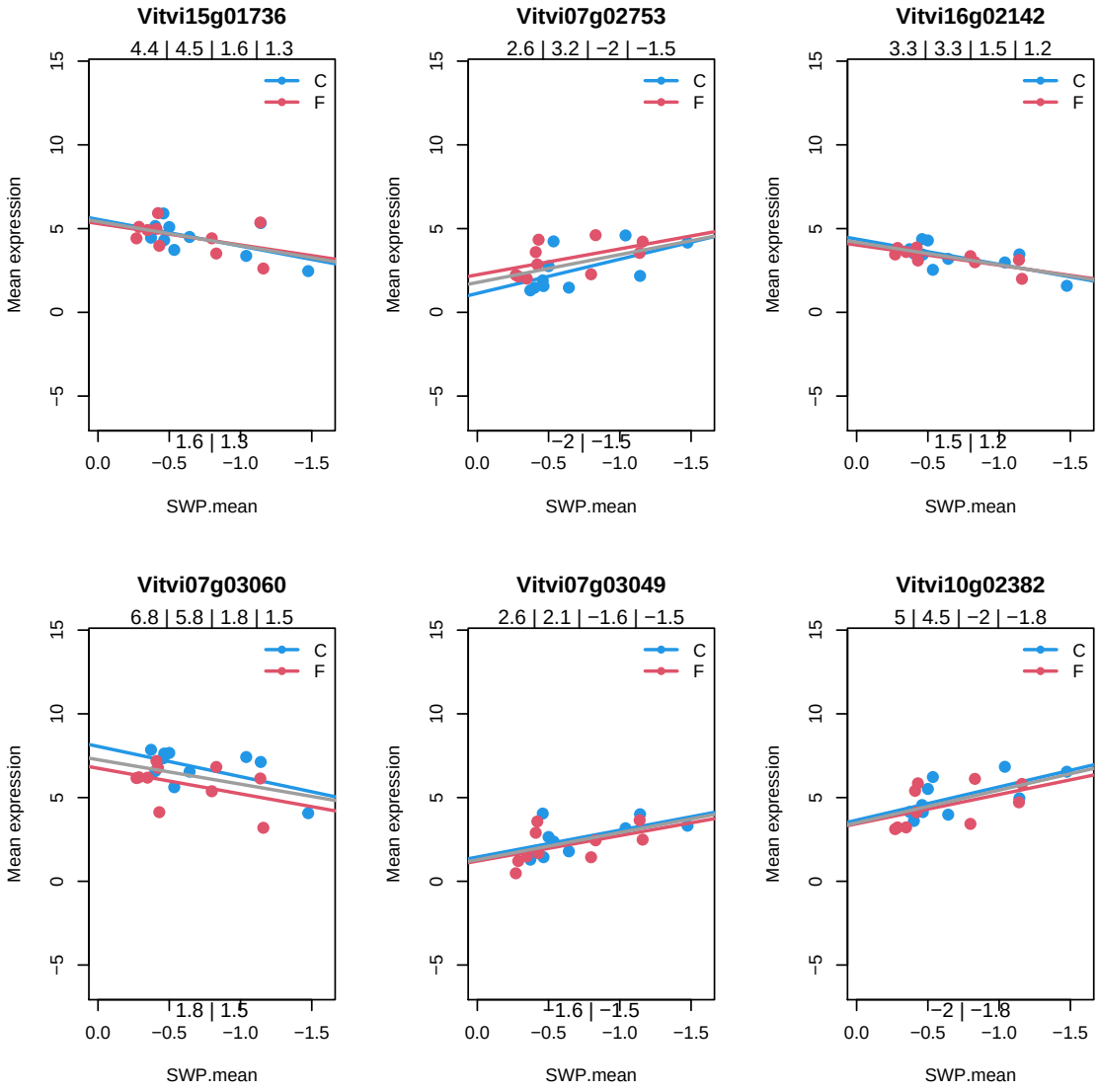



```
> varname <- testvar
> plot.ewp(varname,model="", exprs=exprs, pd=pd)
```

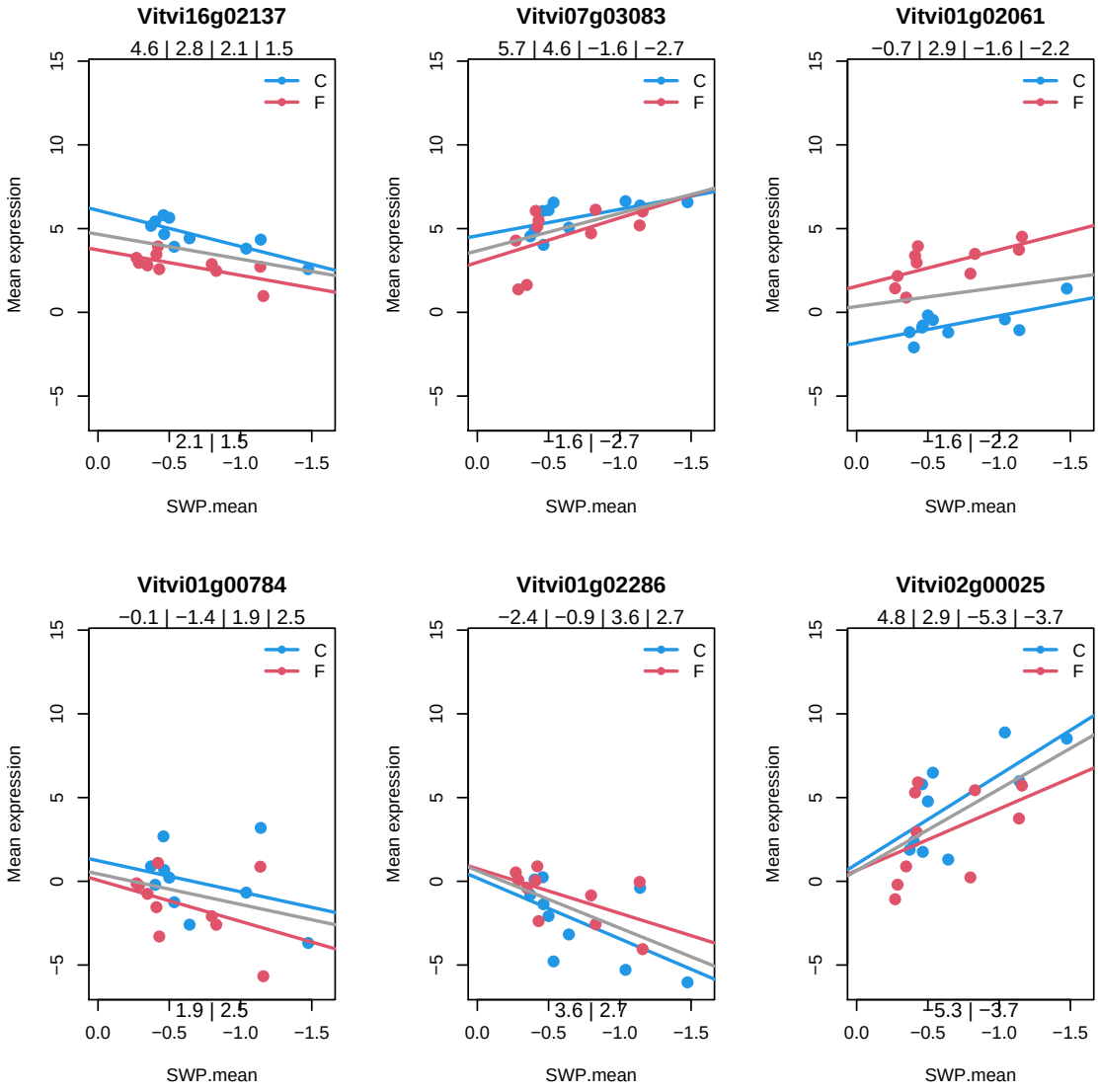



```
> apply(data.frame(type1,type2,type3,type4, type5),2,sum)
type1 type2 type3 type4 type5
  216    60   171    89  1009

> par(mfrow=c(2,3))
> filt <- type1
> print(sum(filt))
[1] 216
> for(i in 1:min(sum(filt),6)){
+ varname <- rownames(exprs)[filt][i]
+ p <- plot.ewp(varname,model="", exprs=exprs, pd=pd, ylim=range(exprs)
+       , cex= 1.5
+       , pch = c(16,16)
+       )
+ mtext(paste(round(coefs[varname,],1),collapse=" | "),cex=0.75)
+ mtext(paste(round(c(p$C$coefficients[2],p$F$coefficients[2]),1)
+ ,collapse=" | "),1,cex=0.75)
+ }
```



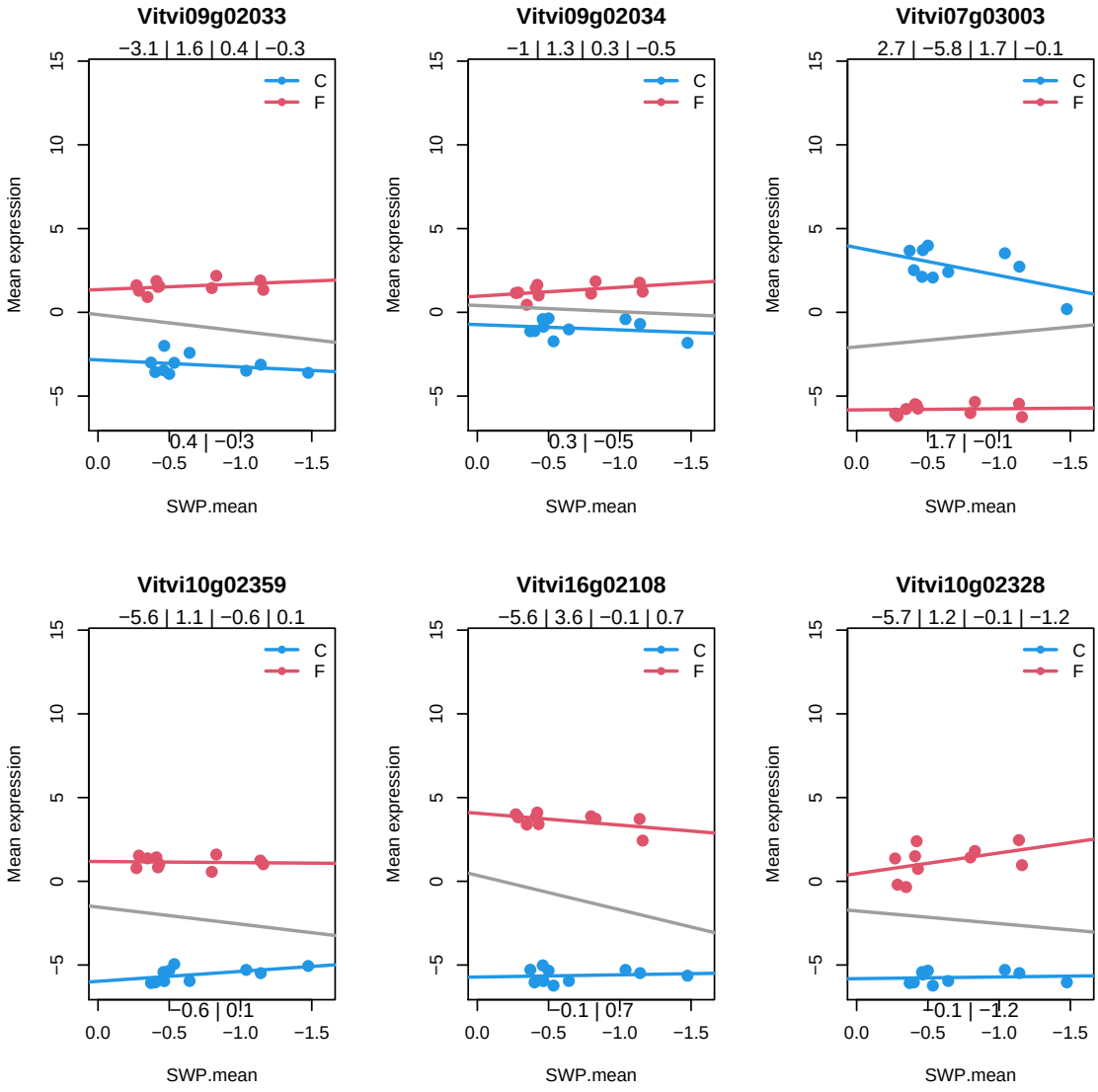

```
> par(mfrow=c(2,3))
> filt <- type2
> print(sum(filt))
[1] 60
> for(i in 1:min(sum(filt),6)){
+ varname <- rownames(exprs)[filt][i]
+ p <- plot.ewp(varname,model="", exprs=exprs, pd=pd, ylim=range(exprs)
+       , cex= 1.5
+       , pch = c(16,16)
+       )
+ mtext(paste(round(coefs[varname,],1),collapse=" | "),cex=0.75)
+ mtext(paste(round(c(p$C$coefficients[2],p$F$coefficients[2]),1)
+ ,collapse=" | "),1,cex=0.75)
+ }
```




```
> par(mfrow=c(2,3))
> filt <- type3
> print(sum(filt))
```

```
[1] 171
```

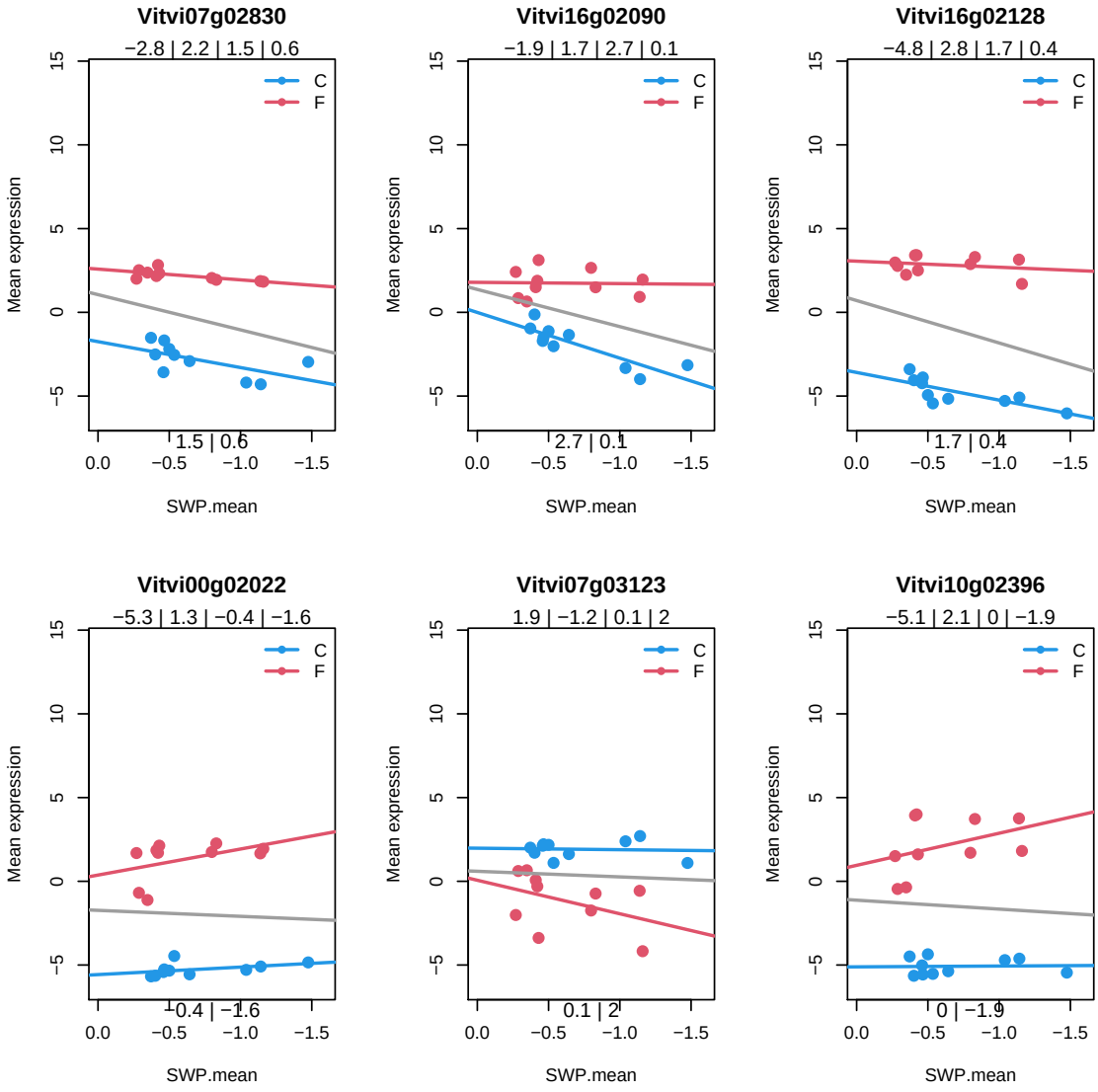
```
> for(i in 1:min(sum(filt),6)){
+ varname <- rownames(exprs)[filt][i]
+ p <- plot.ewp(varname,model="", exprs=exprs, pd=pd, ylim=range(exprs)
+       , cex= 1.5
+       , pch = c(16,16)
+       )
+ mtext(paste(round(coefs[varname,],1),collapse=" | "),cex=0.75)
+ mtext(paste(round(c(p$C$coefficients[2],p$F$coefficients[2]),1)
+ ,collapse=" | "),1,cex=0.75)
+ }
```



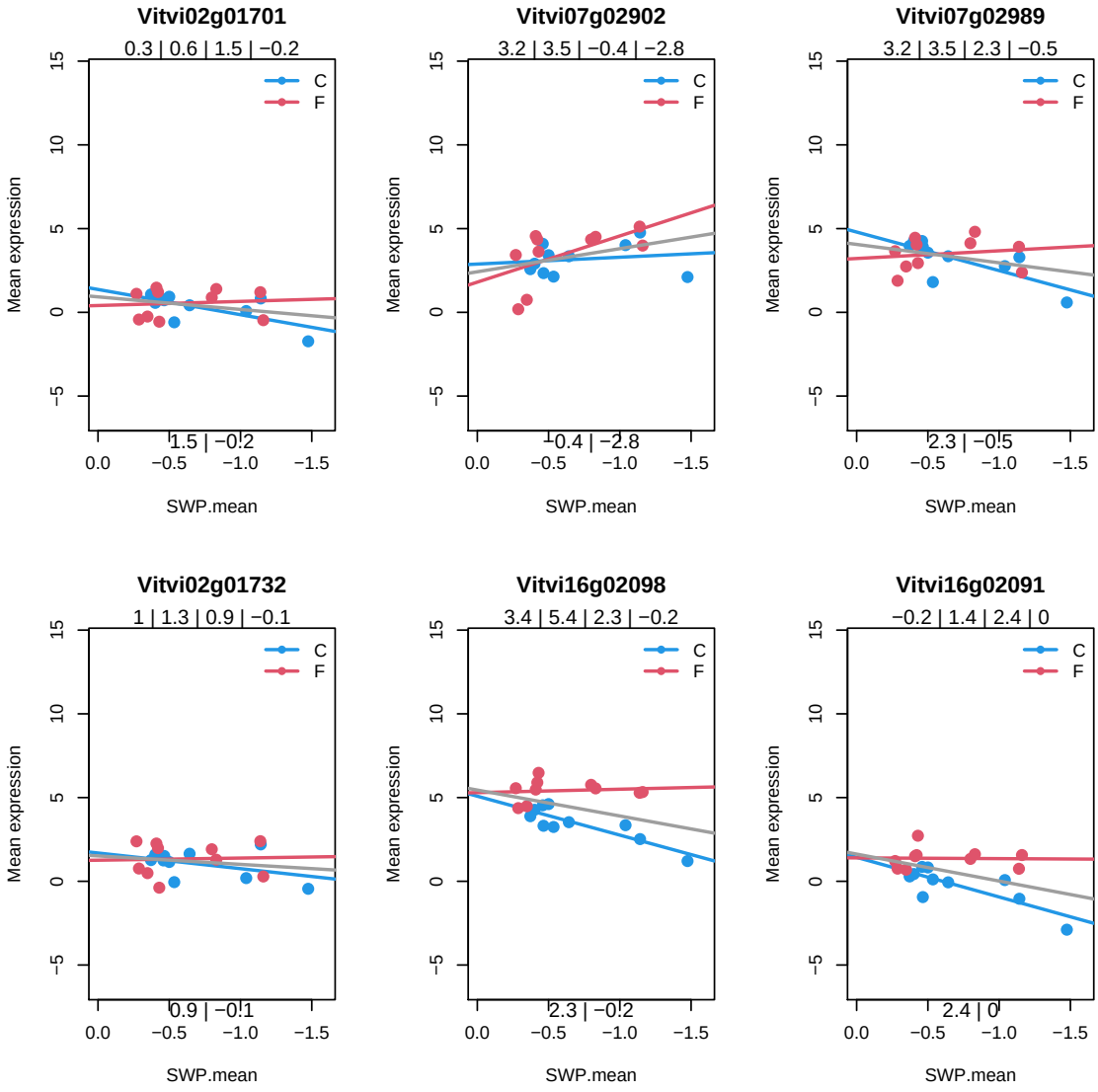

```
> par(mfrow=c(2,3))
> filt <- type4
> print(sum(filt))
```

```
[1] 89
```

```
> for(i in 1:min(sum(filt),6)){
+ varname <- rownames(exprs)[filt][i]
+ p <- plot.ewp(varname,model="", exprs=exprs, pd=pd, ylim=range(exprs)
+       , cex= 1.5
+       , pch = c(16,16)
+       )
+ mtext(paste(round(coefs[varname,],1),collapse=" | "),cex=0.75)
+ mtext(paste(round(c(p$C$coefficients[2],p$F$coefficients[2]),1)
+ ,collapse=" | "),1,cex=0.75)
+ }
```




```
> par(mfrow=c(2,3))
> filt <- type5
> print(sum(filt))
[1] 1009
> for(i in 1:min(sum(filt),6)){
+ varname <- rownames(exprs)[filt][i]
+ p <- plot.ewp(varname,model="", exprs=exprs, pd=pd, ylim=range(exprs)
+       , cex= 1.5
+       , pch = c(16,16)
+       )
+ mtext(paste(round(coefs[varname,],1),collapse=" | "),cex=0.75)
+ mtext(paste(round(c(p$C$coefficients[2],p$F$coefficients[2]),1)
+ ,collapse=" | "),1,cex=0.75)
+ }
```




```
> which <- 2
>   tt <- topTable(fit,coef=which, number=Inf)
>   head(tt)
                   logFC    AveExpr         t      P.Value
Vitvi16g01985 -5.241765 -0.5987979 -7.927163 7.223317e-08
Vitvi05g01740 -1.942843  2.4651929 -6.647068 1.145780e-06
Vitvi17g00152 -4.152022 -0.1074944 -6.643733 1.154385e-06
Vitvi05g00011  4.156807  3.0078249  6.335044 2.321195e-06
Vitvi17g01086 -1.698436  5.0044446 -6.317734 2.414762e-06
Vitvi07g01395 -1.403819  4.1341533 -6.181798 3.297561e-06
                 adj.P.Val        B
Vitvi16g01985 0.001100978 7.653204
Vitvi05g01740 0.005865048 5.322334
Vitvi17g00152 0.005865048 5.315906
Vitvi05g00011 0.007278732 4.713350
Vitvi17g01086 0.007278732 4.679118
Vitvi07g01395 0.007278732 4.408716
```

6.1.1 Export output files

Export fit in a form:

```
> fit <- fit2
> fitfn <- "lm-fit-swpXvariety-statistics.txt"
>
> write.fit(head(fit),file="", adjust="BH")
```

```
                A        Coef.(Intercept)        Coef.swp        Coef.varietyF
Vitvi15g01736         4.47674068175         5.55075053709523         1.5935451902
Vitvi07g02832        -0.1827419310625        -2.63411470430457         0.508155
Vitvi07g02830        -0.3244159185          -1.75065019963238         1.548036561
Vitvi07g02812        -0.3463388427625        -1.38136290124246        -0.00979
Vitvi07g02811         2.4871819448375         2.23617701208318         0.5662695
Vitvi09g02033        -0.78732802375          -2.84283707706586         0.4195644
```

```
> write.fit(fit,file=file.path(.oroot,fitfn), adjust="BH")
```

Export top table

```
> ttfn <- "TopTable.txt"
> tt <- topTable(fit, number=Inf)
```

Removing intercept from test coefficients

```
> tt$type <- ""
> types <- types[rownames(tt),]
> all(rownames(tt)==rownames(types))
```

[1] TRUE

```
> #ind <- sapply(rownames(tt),FUN=function(x) match(x,rownames(types)))
> for(i in 1:ncol(types)) tt$type[types[,i]] <- colnames(types)[i]
> ind <- sapply(rownames(tt),FUN=function(x) match(x,fdata$geneID))
> ttext <- data.frame(tt,fdata[ind,2:5] )
> my.write.table(ttext,file=file.path(.oroot,ttfn))
```

Warning in write.table(x, file = file, col.names = col.names, sep = sep, : appending column names to file Object: ttext
Label:
File :
../../output/50_Expression-water-stress-0.05-r-2-1.5-0.5-0.5-0.5-1/TopTable.txt

```
> .topn <- 100
> topn <- .topn
```

7 Types by significance of contrasts

Starting point is fit2

Model with water potential by variety.

```
> design2 <- with(pd, model.matrix(~ swp*variety))
> head(design2)
  (Intercept)        swp varietyF swp:varietyF
1           1 -0.3720000        0            0
2           1 -0.4016667        0            0
3           1 -0.5350000        0            0
4           1 -0.5000000        0            0
5           1 -0.4592308        0            0
6           1 -0.4645455        0            0
> tail(design2)
   (Intercept)        swp varietyF swp:varietyF
15           1 -0.4210000        1   -0.4210000
16           1 -0.3472727        1   -0.3472727
17           1 -0.7983333        1   -0.7983333
18           1 -1.1600000        1   -1.1600000
19           1 -0.8300000        1   -0.8300000
20           1 -1.1390000        1   -1.1390000
```

Linear model

```
> fit2 <- lmFit(exprs, design2)
> fit2[testvar,]$coefficients
              (Intercept)        swp  varietyF swp:varietyF
Vitvi01g01391    1.595041 -0.7685916 0.2722187    0.4814101


> design3 <- with(pd, model.matrix(~ 0+variety))
> head(design3)
  varietyC varietyF
1        1        0
2        1        0
3        1        0
4        1        0
5        1        0
6        1        0
> tail(design3)
   varietyC varietyF
15        0        1
16        0        1
17        0        1
18        0        1
19        0        1
20        0        1
> fit3 <- lmFit(exprs, design3)
> fit3[testvar,]$coefficients
              varietyC varietyF
Vitvi01g01391 2.135505 2.042236
```

Combine design2 and design3: Replace interceps with means in coefficients and standard deviations

```
> fit4 <- fit2
> fit4$coefficients[,1] <- fit3$coefficients[,1]
> fit4$coefficients[,3] <- fit3$coefficients[,2]
> fit4$stdev.unscaled[,1] <- fit3$stdev.unscaled[,1]
> fit4$stdev.unscaled[,3] <- fit3$stdev.unscaled[,2]
> dimnames(fit4$coefficients)[[2]] <- c("mc","c1","mf","f1.c1")
> fit4[testvar,]$coefficients
                    mc         c1       mf     f1.c1
Vitvi01g01391 2.135505 -0.7685916 2.042236 0.4814101
> fit2[testvar,]$coefficients
              (Intercept)        swp  varietyF swp:varietyF
Vitvi01g01391    1.595041 -0.7685916 0.2722187    0.4814101
> fit3[testvar,]$coefficients
              varietyC varietyF
Vitvi01g01391 2.135505 2.042236


> fit4<- eBayes(fit4)
> head(fit4)
An object of class "MArrayLM"
$coefficients
                     mc           c1        mf        f1.c1
Vitvi15g01736  4.430191  1.593545190 4.5232904 -0.31758915
Vitvi07g02832 -2.991443  0.508155686 2.6259591 -0.25109586
Vitvi07g02830 -2.839209  1.548036562 2.1903769 -0.90607176
Vitvi07g02812 -1.374475 -0.009794742 0.6817977  0.40349136
Vitvi07g02811  1.837984  0.566269561 3.1363800  0.02240192
Vitvi09g02033 -3.137869  0.419564483 1.5632132 -0.76028515

$rank
[1] 4

$assign
[1] 0 1 2 3

$qr
$qr
  (Intercept)         swp   varietyF swp:varietyF
1  -4.4721360  2.93478215 -2.2360680   1.36240911
2   0.2236068 -1.54891442 -0.3031114  -0.50167273
3   0.2236068  0.04473752  2.2154285  -1.44373971
4   0.2236068  0.06733399  0.1816105   0.76367769
5   0.2236068  0.09365515  0.1805019   0.08777677
15 more rows ...

$qraux
[1] 1.223607 1.130819 1.182562 1.066939

$pivot
[1] 1 2 3 4
```

```
$tol
[1] 1e-07

$rank
[1] 4


$df.residual
[1] 16 16 16 16 16 16

$sigma
Vitvi15g01736 Vitvi07g02832 Vitvi07g02830 Vitvi07g02812
    0.8941832     0.7681327     0.5921856     0.8558602
Vitvi07g02811 Vitvi09g02033
    0.5294628     0.4728364

$cov.coefficients
             (Intercept)        swp   varietyF swp:varietyF
(Intercept)    0.4827337  0.5442848 -0.4827337   -0.5442848
swp            0.5442848  0.7740261 -0.5442848   -0.7740261
varietyF      -0.4827337 -0.5442848  0.9319295    1.1174059
swp:varietyF  -0.5442848 -0.7740261  1.1174059    1.7146670

$stdev.unscaled
              (Intercept)       swp  varietyF swp:varietyF
Vitvi15g01736   0.3162278 0.8797875 0.3162278     1.309453
Vitvi07g02832   0.3162278 0.8797875 0.3162278     1.309453
Vitvi07g02830   0.3162278 0.8797875 0.3162278     1.309453
Vitvi07g02812   0.3162278 0.8797875 0.3162278     1.309453
Vitvi07g02811   0.3162278 0.8797875 0.3162278     1.309453
Vitvi09g02033   0.3162278 0.8797875 0.3162278     1.309453

$pivot
[1] 1 2 3 4

$Amean
Vitvi15g01736 Vitvi07g02832 Vitvi07g02830 Vitvi07g02812
    4.4767407    -0.1827419    -0.3244159    -0.3463388
Vitvi07g02811 Vitvi09g02033
    2.4871819    -0.7873280

$method
[1] "ls"

$design
  (Intercept)        swp varietyF swp:varietyF
1           1 -0.3720000        0            0
2           1 -0.4016667        0            0
3           1 -0.5350000        0            0
4           1 -0.5000000        0            0
5           1 -0.4592308        0            0
15 more rows ...
```

```
$df.prior
[1] 5.442291

$s2.prior
[1] 0.240232

$var.prior
[1] 66.60227703 10.07260620 66.60227703  0.04162642

$proportion
[1] 0.01

$s2.post
Vitvi15g01736 Vitvi07g02832 Vitvi07g02830 Vitvi07g02812
    0.6575990     0.5012458     0.3226499     0.6075545
Vitvi07g02811 Vitvi09g02033
    0.2701533     0.2278022

$t
                      mc         c1        mf       f1.c1
Vitvi15g01736  17.275947  2.2336032 17.638998 -0.29908538
Vitvi07g02832 -13.361504  0.8158186 11.729043 -0.27084716
Vitvi07g02830 -15.806350  3.0976880 12.194194 -1.21816734
Vitvi07g02812  -5.576277 -0.0142831  2.766068  0.39532267
Vitvi07g02811  11.182439  1.2383410 19.081984  0.03291472
Vitvi09g02033 -20.790067  0.9991759 10.357126 -1.21648751

$df.total
[1] 21.44229 21.44229 21.44229 21.44229 21.44229 21.44229

$p.value
                         mc          c1           mf
Vitvi15g01736 4.582548e-14 0.036281328 3.017391e-14
Vitvi07g02832 7.201069e-12 0.423574363 8.525719e-11
Vitvi07g02830 2.699108e-13 0.005361432 4.109529e-11
Vitvi07g02812 1.447097e-05 0.988736185 1.143671e-02
Vitvi07g02811 2.066890e-10 0.228976529 6.157627e-15
Vitvi09g02033 1.072274e-15 0.328852510 8.363470e-10
                   f1.c1
Vitvi15g01736 0.7677545
Vitvi07g02832 0.7890987
Vitvi07g02830 0.2363952
Vitvi07g02812 0.6965102
Vitvi07g02811 0.9740471
Vitvi09g02033 0.2370210

$lods
              (Intercept)       swp  varietyF swp:varietyF
Vitvi15g01736    22.24850 -3.752633 22.674807    -4.606008
Vitvi07g02832    17.06898 -5.596946 14.528954    -4.606206
Vitvi07g02830    20.43614 -2.117771 15.279322    -4.589886
Vitvi07g02812     2.18499 -5.915023 -4.428434    -4.605189
```

```
Vitvi07g02811    13.61819 -5.197139 24.293108    -4.607100
Vitvi09g02033    26.06635 -5.441685 12.180326    -4.589930

$F
[1] 2254.10642  247.98545  418.69222   43.13726 1749.02568
[6]  607.83918

$F.p.value
[1] 8.457058e-28 1.282015e-17 5.163533e-20 5.858488e-10
[5] 1.273489e-26 9.935192e-22
> fit4[testvar,]
An object of class "MArrayLM"
$coefficients
                    mc         c1       mf     f1.c1
Vitvi01g01391 2.135505 -0.7685916 2.042236 0.4814101

$rank
[1] 4

$assign
[1] 0 1 2 3

$qr
$qr
  (Intercept)         swp   varietyF swp:varietyF
1  -4.4721360  2.93478215 -2.2360680   1.36240911
2   0.2236068 -1.54891442 -0.3031114  -0.50167273
3   0.2236068  0.04473752  2.2154285  -1.44373971
4   0.2236068  0.06733399  0.1816105   0.76367769
5   0.2236068  0.09365515  0.1805019   0.08777677
15 more rows ...

$qraux
[1] 1.223607 1.130819 1.182562 1.066939

$pivot
[1] 1 2 3 4

$tol
[1] 1e-07

$rank
[1] 4


$df.residual
[1] 16

$sigma
Vitvi01g01391
    0.5999568

$cov.coefficients
```

```
             (Intercept)        swp   varietyF swp:varietyF
(Intercept)    0.4827337  0.5442848 -0.4827337   -0.5442848
swp            0.5442848  0.7740261 -0.5442848   -0.7740261
varietyF      -0.4827337 -0.5442848  0.9319295    1.1174059
swp:varietyF  -0.5442848 -0.7740261  1.1174059    1.7146670

$stdev.unscaled
              (Intercept)       swp  varietyF swp:varietyF
Vitvi01g01391   0.3162278 0.8797875 0.3162278     1.309453

$pivot
[1] 1 2 3 4

$Amean
Vitvi01g01391
      2.08887

$method
[1] "ls"

$design
  (Intercept)        swp varietyF swp:varietyF
1           1 -0.3720000        0            0
2           1 -0.4016667        0            0
3           1 -0.5350000        0            0
4           1 -0.5000000        0            0
5           1 -0.4592308        0            0
15 more rows ...

$df.prior
[1] 5.442291

$s2.prior
[1] 0.240232

$var.prior
[1] 66.60227703 10.07260620 66.60227703  0.04162642

$proportion
[1] 0.01

$s2.post
Vitvi01g01391
    0.3295629

$t
                    mc        c1       mf     f1.c1
Vitvi01g01391 11.76336 -1.521769 11.24959 0.6404071

$df.total
[1] 21.44229

$p.value
```

```
                        mc        c1           mf     f1.c1
Vitvi01g01391 8.072923e-11 0.1426785 1.850714e-10 0.5286929

$lods
              (Intercept)       swp varietyF swp:varietyF
Vitvi01g01391    14.58507 -4.850464 13.73182    -4.602121

$F
[1] 1143.211

$F.p.value
[1] 1.193144e-24


> tt <- topTable(fit4,2,number=Inf)
> tt[testvar,]
                   logFC AveExpr         t   P.Value
Vitvi01g01391 -0.7685916 2.08887 -1.521769 0.1426785
              adj.P.Val         B
Vitvi01g01391 0.6681823 -4.850464
```

With difference of means

```
> fit4 <- fit2
> fit4$coefficients[,1] <- fit3$coefficients[,1]
> fit4$coefficients[,3] <- fit3$coefficients[,2]-fit3$coefficients[,1]
> fit4$stdev.unscaled[,1] <- fit3$stdev.unscaled[,1]
> fit4$stdev.unscaled[,3] <- apply(fit3$stdev.unscaled[,1:2], 1
+       , function(x) sqrt(sum(x^2 )) )
> dimnames(fit4$coefficients)[[2]] <- c("mc","c","mf.mc","f.c")
> fit4[testvar,]$coefficients
                     mc          c       mf.mc       f.c
Vitvi01g01391 2.135505 -0.7685916 -0.09326836 0.4814101
> fit3[testvar,]$stdev.unscaled
               varietyC  varietyF
Vitvi01g01391 0.3162278 0.3162278
> fit4[testvar,]$stdev.unscaled
              (Intercept)       swp  varietyF swp:varietyF
Vitvi01g01391   0.3162278 0.8797875 0.4472136     1.309453
> #
> fit2[testvar,]$coefficients
              (Intercept)        swp  varietyF swp:varietyF
Vitvi01g01391    1.595041 -0.7685916 0.2722187    0.4814101
> fit3[testvar,]$coefficients
              varietyC varietyF
Vitvi01g01391 2.135505 2.042236


> fit4<- eBayes(fit4)
> head(fit4)
```

```
An object of class "MArrayLM"
$coefficients
                     mc            c      mf.mc         f.c
Vitvi15g01736  4.430191  1.593545190 0.09309953 -0.31758915
Vitvi07g02832 -2.991443  0.508155686 5.61740208 -0.25109586
Vitvi07g02830 -2.839209  1.548036562 5.02958569 -0.90607176
Vitvi07g02812 -1.374475 -0.009794742 2.05627305  0.40349136
Vitvi07g02811  1.837984  0.566269561 1.29839620  0.02240192
Vitvi09g02033 -3.137869  0.419564483 4.70108235 -0.76028515

$rank
[1] 4

$assign
[1] 0 1 2 3

$qr
$qr
  (Intercept)         swp   varietyF swp:varietyF
1  -4.4721360  2.93478215 -2.2360680   1.36240911
2   0.2236068 -1.54891442 -0.3031114  -0.50167273
3   0.2236068  0.04473752  2.2154285  -1.44373971
4   0.2236068  0.06733399  0.1816105   0.76367769
5   0.2236068  0.09365515  0.1805019   0.08777677
15 more rows ...

$qraux
[1] 1.223607 1.130819 1.182562 1.066939

$pivot
[1] 1 2 3 4

$tol
[1] 1e-07

$rank
[1] 4


$df.residual
[1] 16 16 16 16 16 16

$sigma
Vitvi15g01736 Vitvi07g02832 Vitvi07g02830 Vitvi07g02812
    0.8941832     0.7681327     0.5921856     0.8558602
Vitvi07g02811 Vitvi09g02033
    0.5294628     0.4728364

$cov.coefficients
             (Intercept)        swp   varietyF swp:varietyF
(Intercept)    0.4827337  0.5442848 -0.4827337   -0.5442848
swp            0.5442848  0.7740261 -0.5442848   -0.7740261
varietyF      -0.4827337 -0.5442848  0.9319295    1.1174059
```

```
swp:varietyF  -0.5442848 -0.7740261  1.1174059    1.7146670

$stdev.unscaled
              (Intercept)       swp  varietyF swp:varietyF
Vitvi15g01736   0.3162278 0.8797875 0.4472136     1.309453
Vitvi07g02832   0.3162278 0.8797875 0.4472136     1.309453
Vitvi07g02830   0.3162278 0.8797875 0.4472136     1.309453
Vitvi07g02812   0.3162278 0.8797875 0.4472136     1.309453
Vitvi07g02811   0.3162278 0.8797875 0.4472136     1.309453
Vitvi09g02033   0.3162278 0.8797875 0.4472136     1.309453

$pivot
[1] 1 2 3 4

$Amean
Vitvi15g01736 Vitvi07g02832 Vitvi07g02830 Vitvi07g02812
    4.4767407    -0.1827419    -0.3244159    -0.3463388
Vitvi07g02811 Vitvi09g02033
    2.4871819    -0.7873280

$method
[1] "ls"

$design
  (Intercept)        swp varietyF swp:varietyF
1           1 -0.3720000        0            0
2           1 -0.4016667        0            0
3           1 -0.5350000        0            0
4           1 -0.5000000        0            0
5           1 -0.4592308        0            0
15 more rows ...

$df.prior
[1] 5.442291

$s2.prior
[1] 0.240232

$var.prior
[1] 66.60227703 10.07260620 66.60227703  0.04162642

$proportion
[1] 0.01

$s2.post
Vitvi15g01736 Vitvi07g02832 Vitvi07g02830 Vitvi07g02812
    0.6575990     0.5012458     0.3226499     0.6075545
Vitvi07g02811 Vitvi09g02033
    0.2701533     0.2278022

$t
                      mc          c      mf.mc         f.c
Vitvi15g01736  17.275947  2.2336032  0.2567154 -0.29908538
```

```
Vitvi07g02832 -13.361504  0.8158186 17.7416959 -0.27084716
Vitvi07g02830 -15.806350  3.0976880 19.7993745 -1.21816734
Vitvi07g02812  -5.576277 -0.0142831  5.8989290  0.39532267
Vitvi07g02811  11.182439  1.2383410  5.5858219  0.03291472
Vitvi09g02033 -20.790067  0.9991759 22.0243909 -1.21648751

$df.total
[1] 21.44229 21.44229 21.44229 21.44229 21.44229 21.44229

$p.value
                         mc           c        mf.mc
Vitvi15g01736 4.582548e-14 0.036281328 7.998456e-01
Vitvi07g02832 7.201069e-12 0.423574363 2.684665e-14
Vitvi07g02830 2.699108e-13 0.005361432 2.906795e-15
Vitvi07g02812 1.447097e-05 0.988736185 6.838803e-06
Vitvi07g02811 2.066890e-10 0.228976529 1.415145e-05
Vitvi09g02033 1.072274e-15 0.328852510 3.282724e-16
                     f.c
Vitvi15g01736 0.7677545
Vitvi07g02832 0.7890987
Vitvi07g02830 0.2363952
Vitvi07g02812 0.6965102
Vitvi07g02811 0.9740471
Vitvi09g02033 0.2370210

$lods
              (Intercept)       swp  varietyF swp:varietyF
Vitvi15g01736    22.24850 -3.752633 -7.466375    -4.606008
Vitvi07g02832    17.06898 -5.596946 22.901410    -4.606206
Vitvi07g02830    20.43614 -2.117771 25.106813    -4.589886
Vitvi07g02812     2.18499 -5.915023  3.264972    -4.605189
Vitvi07g02811    13.61819 -5.197139  2.529137    -4.607100
Vitvi09g02033    26.06635 -5.441685 27.247330    -4.589930

$F
[1] 602.7271 384.9793 557.1593  43.1426 512.2023 699.0823

$F.p.value
[1] 1.086743e-21 1.253785e-19 2.503334e-21 5.851652e-10
[5] 6.109721e-21 2.247742e-22
> fit4[testvar,]
An object of class "MArrayLM"
$coefficients
                     mc          c       mf.mc       f.c
Vitvi01g01391 2.135505 -0.7685916 -0.09326836 0.4814101

$rank
[1] 4

$assign
[1] 0 1 2 3

$qr
```

```
$qr
  (Intercept)         swp   varietyF swp:varietyF
1  -4.4721360  2.93478215 -2.2360680   1.36240911
2   0.2236068 -1.54891442 -0.3031114  -0.50167273
3   0.2236068  0.04473752  2.2154285  -1.44373971
4   0.2236068  0.06733399  0.1816105   0.76367769
5   0.2236068  0.09365515  0.1805019   0.08777677
15 more rows ...

$qraux
[1] 1.223607 1.130819 1.182562 1.066939

$pivot
[1] 1 2 3 4

$tol
[1] 1e-07

$rank
[1] 4


$df.residual
[1] 16

$sigma
Vitvi01g01391
    0.5999568

$cov.coefficients
             (Intercept)        swp   varietyF swp:varietyF
(Intercept)    0.4827337  0.5442848 -0.4827337   -0.5442848
swp            0.5442848  0.7740261 -0.5442848   -0.7740261
varietyF      -0.4827337 -0.5442848  0.9319295    1.1174059
swp:varietyF  -0.5442848 -0.7740261  1.1174059    1.7146670

$stdev.unscaled
              (Intercept)       swp  varietyF swp:varietyF
Vitvi01g01391   0.3162278 0.8797875 0.4472136     1.309453

$pivot
[1] 1 2 3 4

$Amean
Vitvi01g01391
      2.08887

$method
[1] "ls"

$design
  (Intercept)        swp varietyF swp:varietyF
1           1 -0.3720000        0            0
```

```
2           1 -0.4016667        0            0
3           1 -0.5350000        0            0
4           1 -0.5000000        0            0
5           1 -0.4592308        0            0
15 more rows ...

$df.prior
[1] 5.442291

$s2.prior
[1] 0.240232

$var.prior
[1] 66.60227703 10.07260620 66.60227703  0.04162642

$proportion
[1] 0.01

$s2.post
Vitvi01g01391
    0.3295629

$t
                    mc         c      mf.mc       f.c
Vitvi01g01391 11.76336 -1.521769 -0.3632873 0.6404071

$df.total
[1] 21.44229

$p.value
                         mc         c     mf.mc       f.c
Vitvi01g01391 8.072923e-11 0.1426785 0.7199473 0.5286929

$lods
              (Intercept)       swp varietyF swp:varietyF
Vitvi01g01391    14.58507 -4.850464 -7.43206    -4.602121

$F
[1] 373.4584

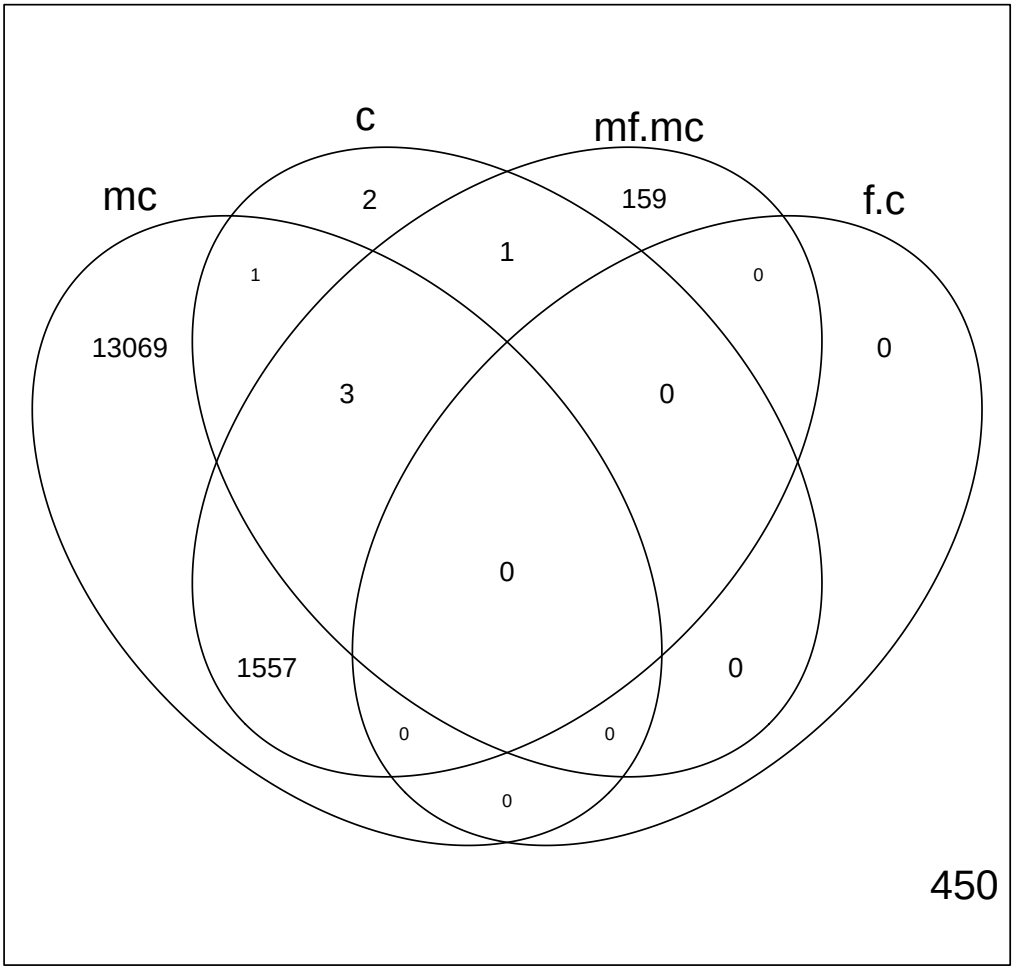
$F.p.value
[1] 1.728022e-19


> fit4[testvar,]$coef
                    mc         c       mf.mc       f.c
Vitvi01g01391 2.135505 -0.7685916 -0.09326836 0.4814101
> fit4[testvar,]$p.value
                         mc         c     mf.mc       f.c
Vitvi01g01391 8.072923e-11 0.1426785 0.7199473 0.5286929
> #
> tt.mc <- topTable(fit4,1,number=Inf, sort.by="none", confint=TRUE)
> all(rownames(fit4)==rownames(tt.mc))
```

```
[1] TRUE
> tt.mc[testvar,]
                 logFC     CI.L     CI.R AveExpr        t
Vitvi01g01391 2.135505 1.758448 2.512561 2.08887 11.76336
                 P.Value    adj.P.Val        B
Vitvi01g01391 8.072923e-11 1.060206e-10 14.58507
> alpha <- as.numeric(.alpha)
> with(tt.mc, table(p=P.Value < alpha, adj.p=adj.P.Val < alpha))
       adj.p
p       FALSE  TRUE
  FALSE   605     0
  TRUE      7 14630
> #
> tt.c <- topTable(fit4,2,number=Inf, sort.by="none", confint=TRUE)
> tt.c[testvar,]
                  logFC      CI.L      CI.R AveExpr
Vitvi01g01391 -0.7685916 -1.817613 0.2804301 2.08887
                     t   P.Value adj.P.Val         B
Vitvi01g01391 -1.521769 0.1426785 0.6681823 -4.850464
> with(tt.c, table(p=P.Value < alpha, adj.p=adj.P.Val < alpha))
       adj.p
p       FALSE  TRUE
  FALSE 13748     0
  TRUE   1487     7
> #
> tt.mf.mc <- topTable(fit4,3,number=Inf, sort.by="none", confint=TRUE)
> tt.mf.mc[testvar,]
                   logFC       CI.L      CI.R AveExpr
Vitvi01g01391 -0.09326836 -0.6265071 0.4399704 2.08887
                      t   P.Value adj.P.Val        B
Vitvi01g01391 -0.3632873 0.7199473 0.9142513 -7.43206
> with(tt.mf.mc, table(p=P.Value < alpha, adj.p=adj.P.Val < alpha))
       adj.p
p       FALSE  TRUE
  FALSE 12053     0
  TRUE   1469  1720
> #
> tt.f.c <- topTable(fit4,4,number=Inf, sort.by="none", confint=TRUE)
> tt.f.c[testvar,]
                  logFC      CI.L     CI.R AveExpr
Vitvi01g01391 0.4814101 -1.079927 2.042747 2.08887
                     t   P.Value adj.P.Val         B
Vitvi01g01391 0.6404071 0.5286929 0.9999488 -4.602121
> with(tt.f.c, table(p=P.Value < alpha, adj.p=adj.P.Val < alpha))
       adj.p
p       FALSE
  FALSE 15083
  TRUE    159
```

7.0.1 Write fit

```
> fit4fn <- "lm-fit-means-swpXvariety-statistics.txt"
> fit <- fit4
> decide0 <- decideTests(fit,lfc=0 )
> vennDiagram(decide0)
```




```
> #ind <- sapply(rownames(fit),FUN=function(x) match(x,fdata$geneID))
> ind <- match(rownames(fit),fdata$geneID)
> df4 <- as.data.frame(fit)
> write.fit(fit,file="../doc/tmp2.txt", adjust="BH")
> df4 <-  read.table("../doc/tmp2.txt")
> colnames(df4)
 [1] "A"                 "Coef.mc"
 [3] "Coef.c"            "Coef.mf.mc"
 [5] "Coef.f.c"          "t.mc"
 [7] "t.c"               "t.mf.mc"
 [9] "t.f.c"             "P.value.mc"
[11] "P.value.c"         "P.value.mf.mc"
[13] "P.value.f.c"       "P.value.adj.mc"
[15] "P.value.adj.c"     "P.value.adj.mf.mc"
[17] "P.value.adj.f.c"   "F"
[19] "F.p.value"
```

```
> Koef.f <- df4$Coef.f.c+df4$Coef.c
> ins <- grep("t.",colnames(df4))[1]
> df4 <- data.frame(df4[,1:(ins-1)],Koef.f,df4[,ins:ncol(df4)])
> df4$type <- ""
> types <- types[rownames(df4),]
> all(rownames(df4)==rownames(types))
[1] TRUE
> #ind <- sapply(rownames(tt),FUN=function(x) match(x,rownames(types)))
> for(i in 1:ncol(types)) {
+       df4$type[types[,i]] <- paste(df4$type[types[,i]], colnames(types)[i],
+       print(table(df4$type))
+       }

       |type1
 15026    216

       |type1 |type2
 14966    216     60

       |type1 |type2 |type3
 14795    216     60    171

                  |type1       |type2 |type2|type4
       14760          216          40           20
      |type3 |type3|type4       |type4
         137           34          35

                  |type1       |type2 |type2|type4
       13751          216          40           20
      |type3 |type3|type4       |type4       |type5
         137           34          35         1009
> df4$type <- gsub("^\\|","", df4$type)
>
> # Mark interesting genes:
> stat4 <- data.frame(df4,fdata[ind,2:5] )
> pc <- stat4[,"P.value.c"]
> pfc <- stat4[,"P.value.f.c"]
> inc <- c("","*")[(pc < alpha)+1]
> incf <- c("","+")[((pc > alpha)&(pfc < alpha))+1]
> df4$interestingC <- inc
> df4$interestingFC <- incf
> #
> stat4 <- data.frame(df4,fdata[ind,2:5] )
> table(stat4$interestingC,stat4$interestingFC)

            +
    13700    48
  *  1494     0
```

Some genes are classified into two types:

```
> t(t(table(df4$type)))
```

```
                [,1]
               13751
type1            216
type2             40
type2|type4       20
type3            137
type3|type4       34
type4             35
type5           1009
```

```
> xtable(table(Count=df4$type), auto=TRUE, caption="Table of types.")
```

	Count
	13751
type1	216
type2	40
type2|type4	20
type3	137
type3|type4	34
type4	35
type5	1009

Table 1: Table of types.

Genes from interesting bins are marked by '*' (for significant slope C) and '+' (for significant difference in slopes).

```
> my.write.table(stat4,file=file.path(.oroot,fit4fn),
+ label="WP x variety model statistics, types and gene annotation")
```

Warning in write.table(x, file = file, col.names = col.names, sep = sep, : appending column names to file Object: stat4
Label: WP x variety model statistics, types and gene annotation
File :
../../output/50_Expression-water-stress-0.05-r-2-1.5-0.5-0.5-0.5-1/lm-fit-means-swpXvariety-statistics.txt

Comparison with effects.
Large abs slope C

```
> alpha
[1] 0.05
> indp <- (tt.c$P.Value < alpha)
> sum(indp)
[1] 1494
> table(rownames(tt.c)[indp]%in%rownames(tt.c)[large_abs_C])

FALSE  TRUE
  954   540
> table(indp,large_abs_C)
       large_abs_C
indp    FALSE  TRUE
  FALSE 13626   122
  TRUE    954   540
```

Small difference of slopes

```
> alpha
[1] 0.05
> indp <- (tt.f.c$P.Value > alpha)
> sum(indp)
[1] 15083
> table(rownames(tt.c)[indp]%in%rownames(tt.c)[small_fc])

FALSE  TRUE
 4606 10477
> table(indp,small_fc)
       small_fc
indp    FALSE  TRUE
  FALSE   159     0
  TRUE   4606 10477
```

Large difference of mean expressions

```
> alpha
[1] 0.05
> range(tt.mf.mc$P.Value)
[1] 1.063003e-25 9.999648e-01
> indp <- (tt.mf.mc$P.Value < alpha)
> sum(indp)
[1] 3189
> table(rownames(tt.c)[indp]%in%rownames(tt.c)[(abs(mc-mf)<deltam)])

FALSE  TRUE
  406  2783
> table(indp,large.diff.means=(abs(mc-mf)<deltam))
       large.diff.means
indp    FALSE  TRUE
  FALSE     7 12046
  TRUE    406  2783
```

7.1 Genes in types

Plots of situation for genes in determined types. Significance can be checked in individual plots.

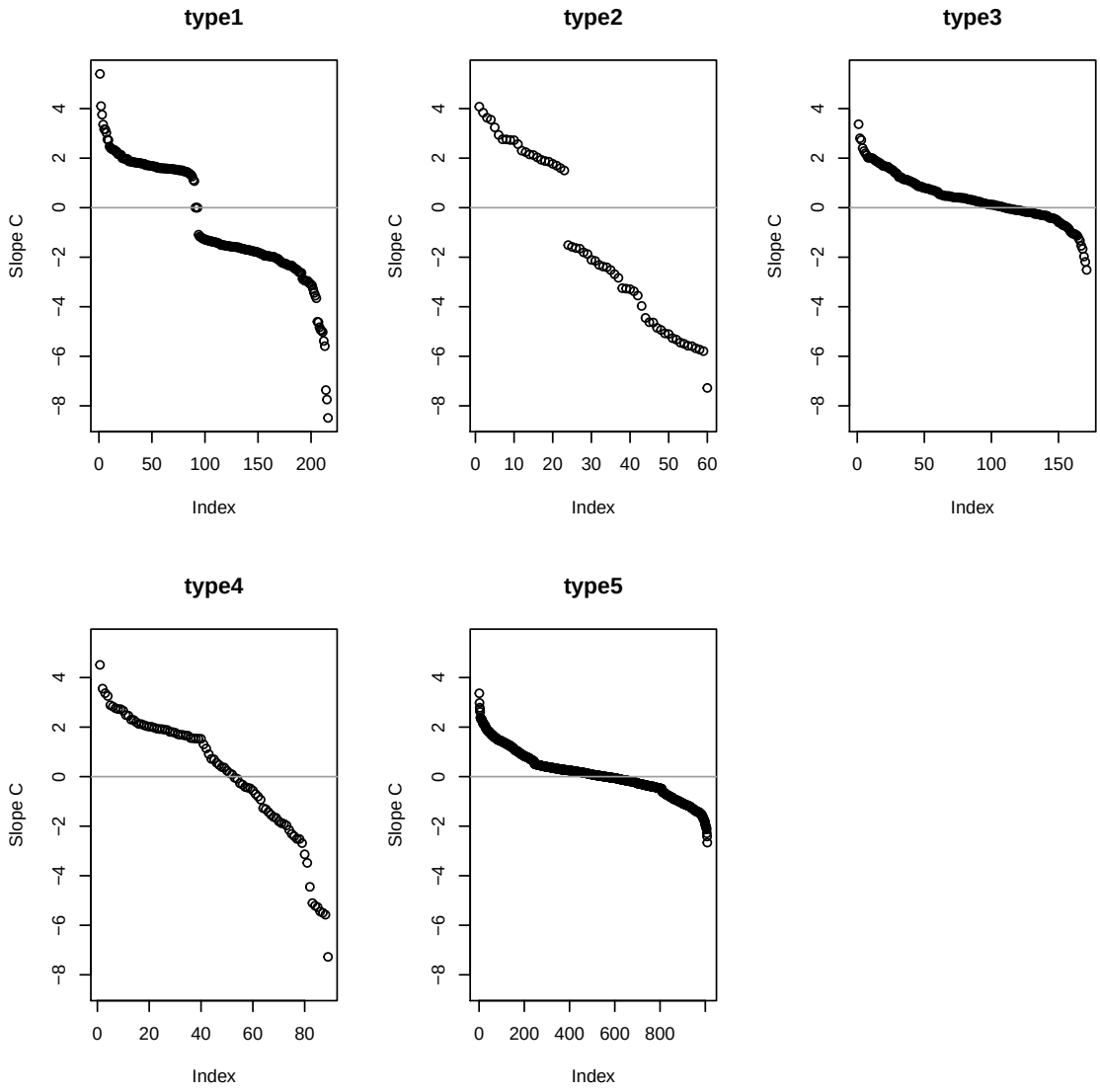
Figures caption:

Mean expression (E) and mean water potential (WP). C (blue) and all F (red). Gray line (if present) is regression of all data, regardles of treatment and variety.

Order stat4 by swp

```
> ordr <- rev(order(stat4$Coef.c))
> stat4 <- stat4[ordr,]
> types <- types[rownames(stat4),]
> all(rownames(stat4)==rownames(types))
[1] TRUE

> par(mfrow=c(2,3))
> ylim <- range(stat4[,"Coef.c"])
> for(i in 1:ncol(types)){
+ varnames <- rownames(stat4)[types[,i]]
+ plot(stat4[varnames,"Coef.c"], ylab="Slope C",
+   ,ylim=ylim, main=colnames(types)[i])
+   abline(h=0,col=8)
+ }
```




```
> # Report for selected genes
> out <- ""
> (cname <- "")
```

```
[1] ""
```

```
> colnames(stat4)
```

```
 [1] "A"                  "Coef.mc"
 [3] "Coef.c"             "Coef.mf.mc"
 [5] "Coef.f.c"           "Koef.f"
 [7] "t.mc"               "t.c"
 [9] "t.mf.mc"            "t.f.c"
[11] "P.value.mc"         "P.value.c"
[13] "P.value.mf.mc"      "P.value.f.c"
[15] "P.value.adj.mc"     "P.value.adj.c"
[17] "P.value.adj.mf.mc" "P.value.adj.f.c"
[19] "F"                  "F.p.value"
[21] "type"               "interestingC"
[23] "interestingFC"      "geneID"
[25] "BINCODE"            "NAME"
[27] "DESCRIPTION"
```

```
> tipi <- sort(unique(stat4$type))[-1]
> i <- 1
> for(i in 1:ncol(types)){
+ out <- paste(out,"
+ \\clearpage
+ \\subsection{",colnames(types)[i],"}\\")
+ varnames <- rownames(stat4)[types[,i]]
+ varname <- varnames[2]
+ for(varname in varnames)
+  out <- paste(out,knit_child(file.path("../doc/","50aa_one-gene-plots.Rnw"),
+ }
```

7.2 type1

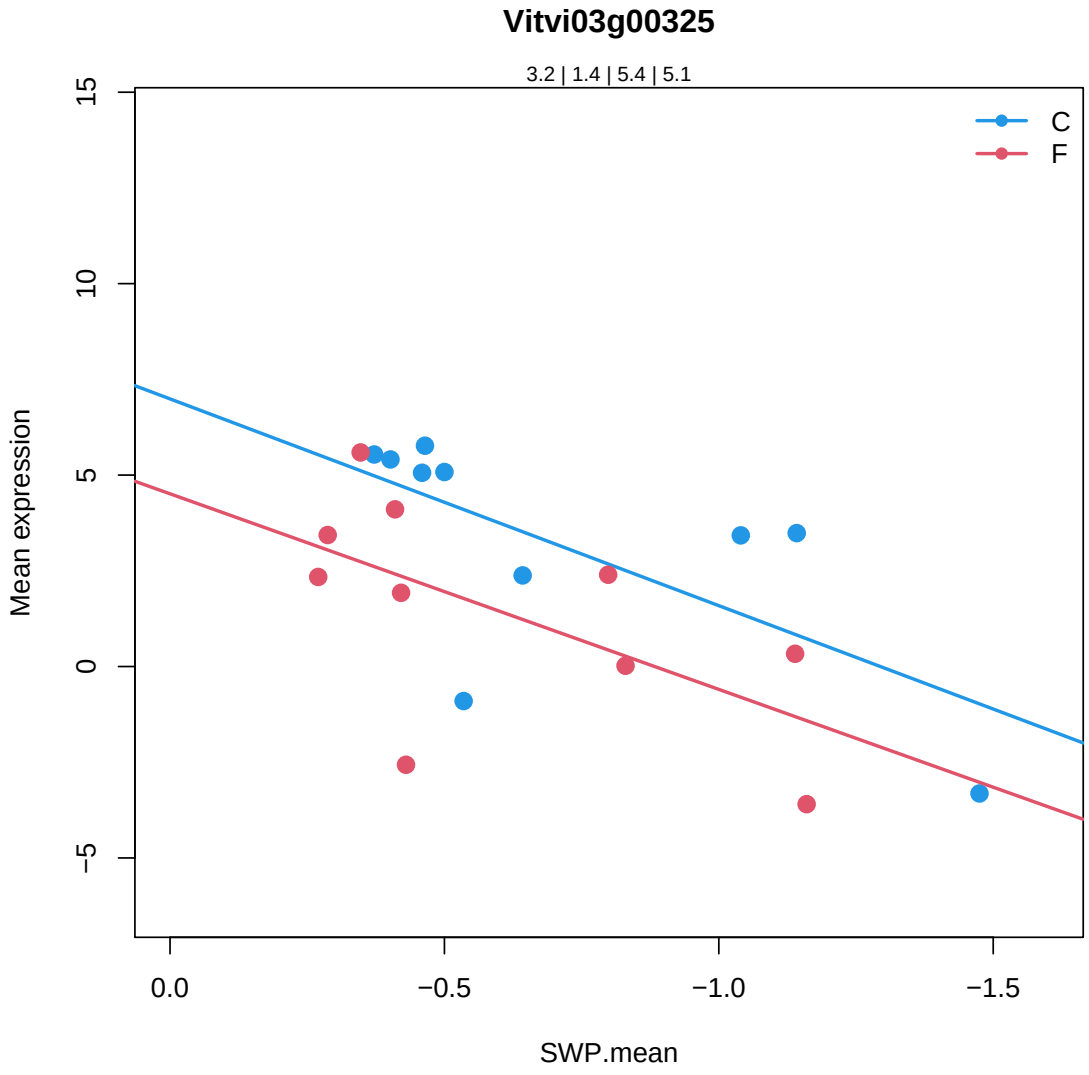
7.2.1 Vitvi03g00325: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00325
        27.3.25
        RNA.regulation of transcription.MYB domain transcription factor family
        RAD-like 1 |
        Chr4:18271457-18271857 REVERSE LENGTH=100 |
        201606
```

Coefficients for Vitvi03g00325.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.192321	9.103982e-05	***	0.0001006038	***
SlopeC	5.400429	0.008080928	**	0.2851146	
MeanF-MeanC	-1.794048	0.06988085	.	0.2960684	
SlopeF-SlopeC	-0.2916254	0.9166302		0.9999488	



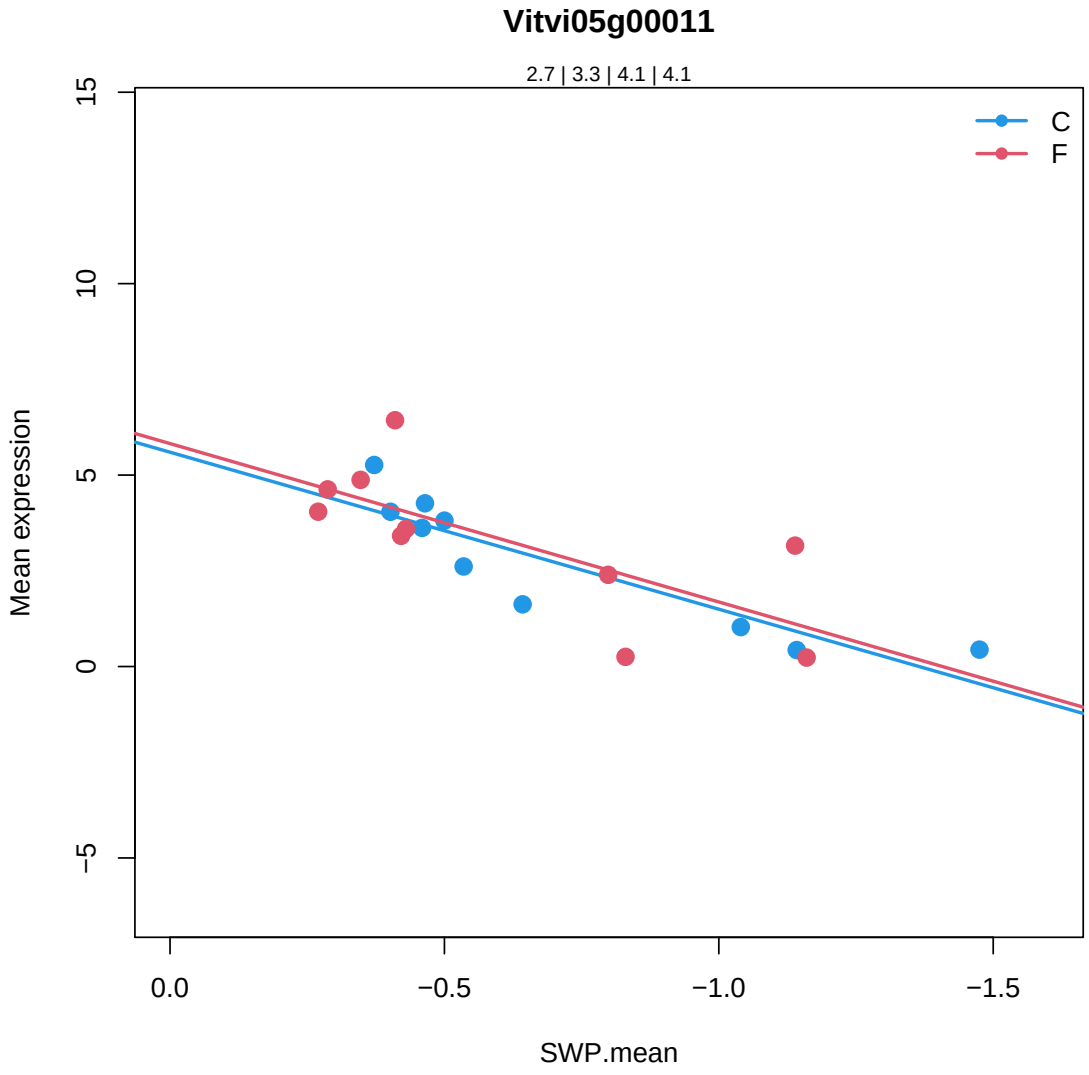
7.2.2 Vitvi05g00011: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00011
        35.2
        not assigned.unknown
        Pollen Ole e 1 allergen and extensin family protein |
        Chr3:5676904-5677788 FORWARD LENGTH=180 |
        201606
```

Coefficients for Vitvi05g00011.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.71363	3.60489e-08	***	4.329163e-08	***
SlopeC	4.101024	0.0001755321	***	0.07644173	.
MeanF-MeanC	0.5883901	0.2148664		0.5622308	
SlopeF-SlopeC	0.03610049	0.978881		0.9999488	



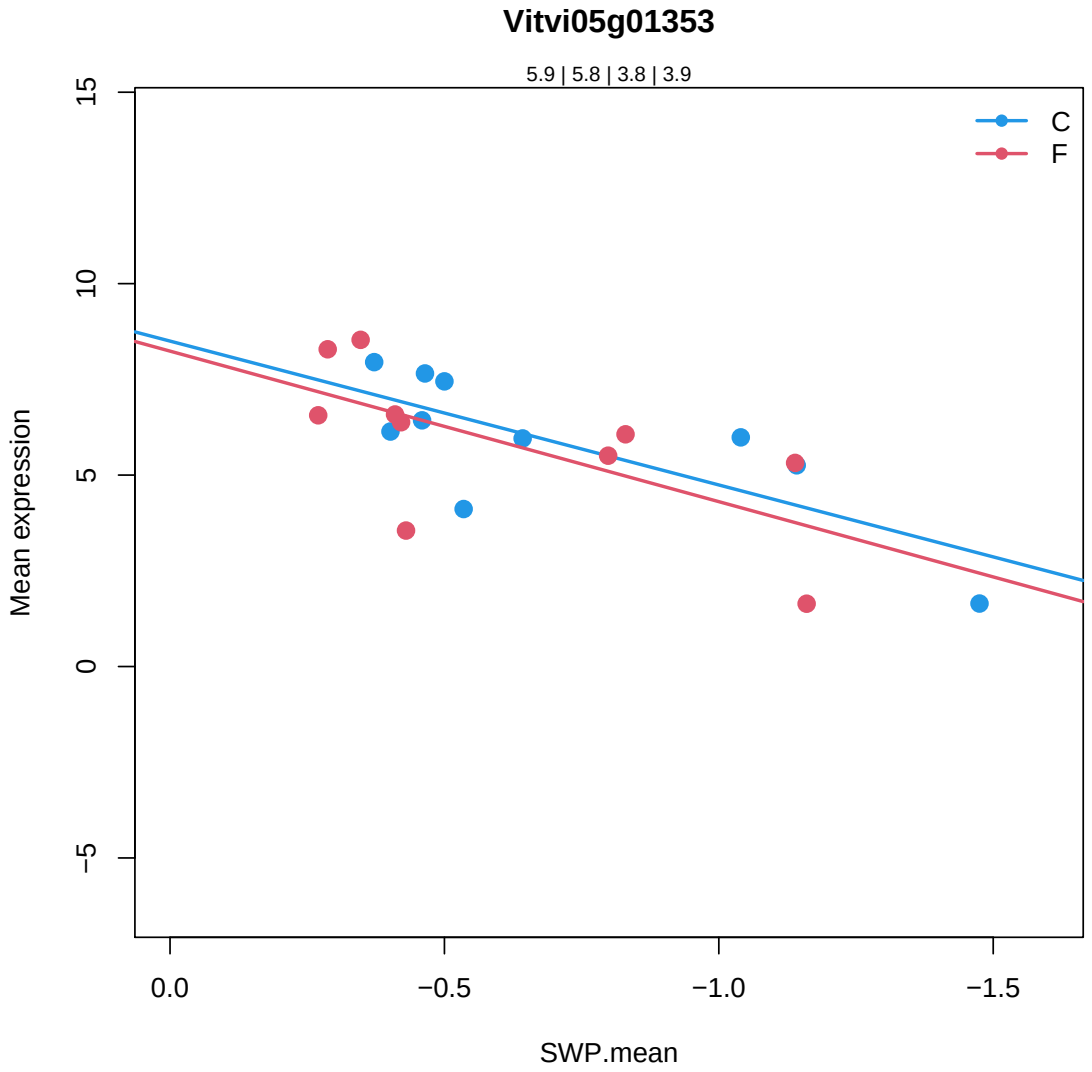
7.2.3 Vitvi05g01353: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01353
        10.8.1
        cell wall.pectinesterases.PME
        pectin methylesterase 61 |
        Chr3:21803015-21805098 REVERSE LENGTH=529 |
        201606
```

Coefficients for Vitvi05g01353.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.857325	2.084874e-12	***	2.936936e-12	***
SlopeC	3.757248	0.003467502	**	0.2238297	
MeanF-MeanC	-0.01519937	0.9793892		0.994731	
SlopeF-SlopeC	0.1744137	0.9193632		0.9999488	



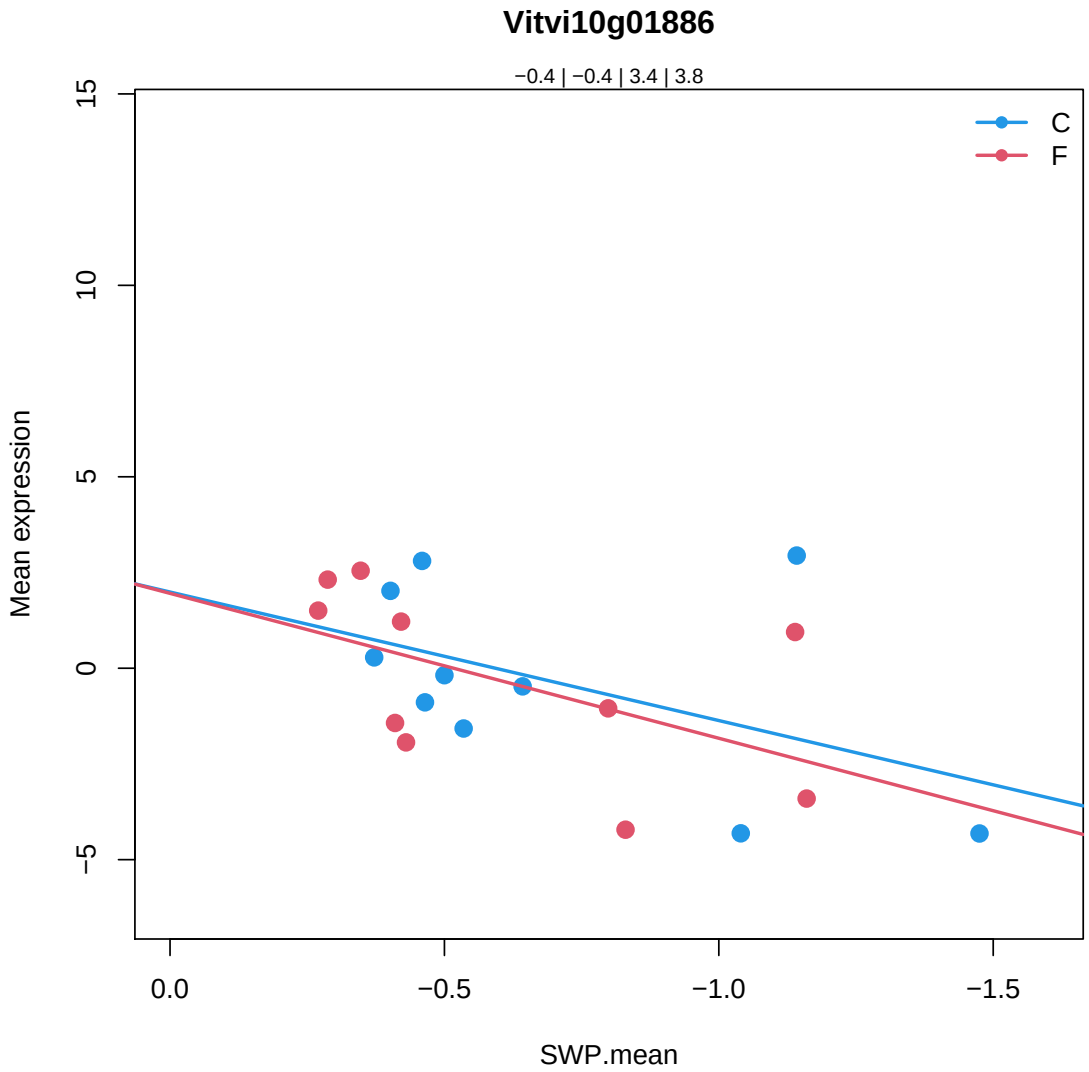
7.2.4 Vitvi10g01886: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g01886
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi10g01886.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	−0.3703529	0.5581725		0.5640192	
SlopeC	3.356612	0.06592693	.	0.5539461	
MeanF−MeanC	0.01931686	0.9826998		0.9957601	
SlopeF−SlopeC	0.4277199	0.8697865		0.9999488	



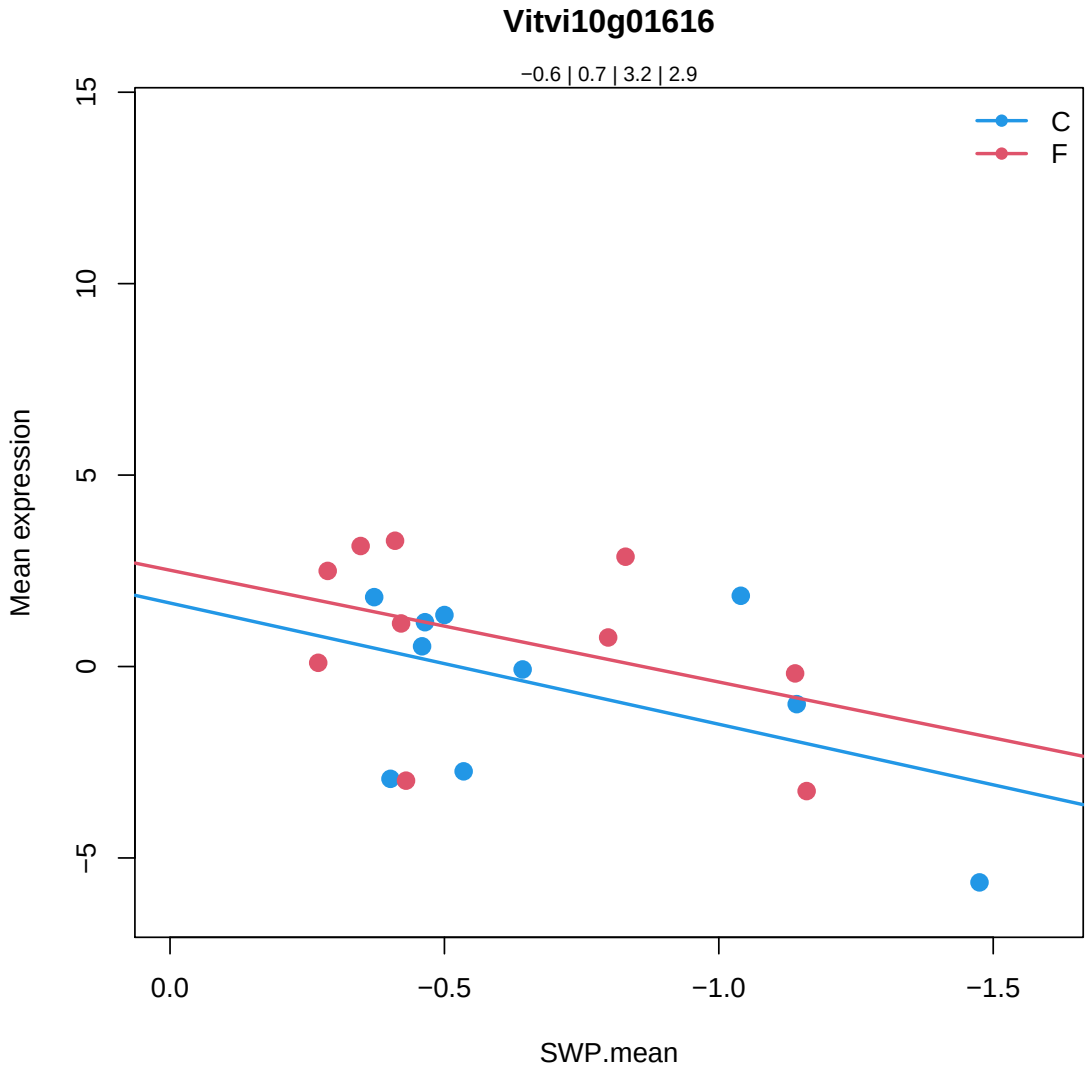
7.2.5 Vitvi10g01616: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g01616
        35.2
        not assigned.unknown
        Stigma-specific Stig1 family protein |
        Chr1:4026195-4026617 REVERSE LENGTH=140 |
        201606
```

Coefficients for Vitvi10g01616.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.5679815	0.3801571		0.3862388	
SlopeC	3.165031	0.08679714	.	0.5916646	
MeanF-MeanC	1.30418	0.1601766		0.4837762	
SlopeF-SlopeC	-0.2446635	0.9265967		0.9999488	



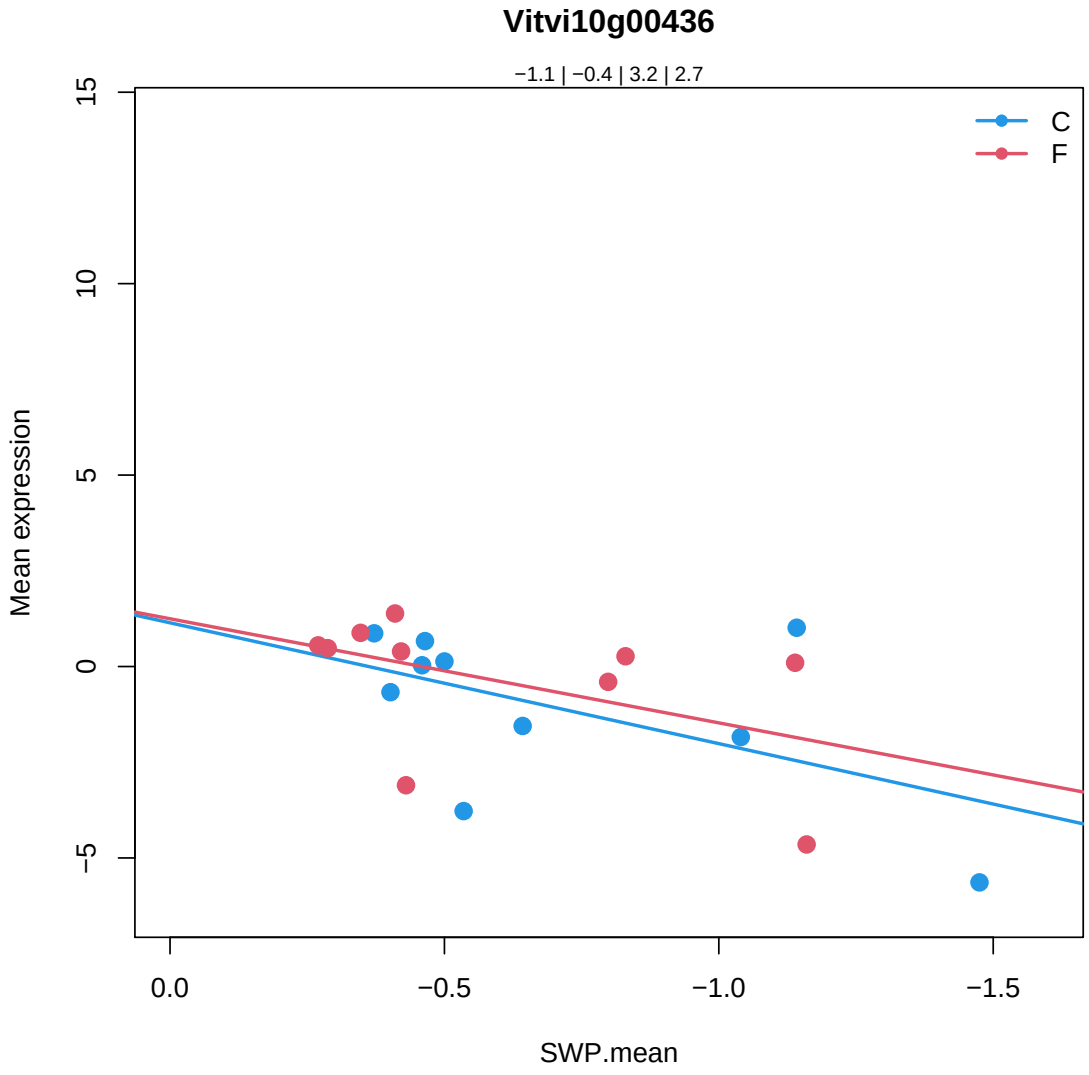
7.2.6 Vitvi10g00436: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00436
        3.8.2
        minor CHO metabolism.galactose.alpha-galactosidases
        Melibiase family protein |
        Chr3:20882886-20885745 FORWARD LENGTH=437 |
        201606
```

Coefficients for Vitvi10g00436.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.077179	0.04821491	*	0.05022154	.
SlopeC	3.15566	0.03841712	*	0.4670907	
MeanF-MeanC	0.6675279	0.3688215		0.724094	
SlopeF-SlopeC	-0.4366108	0.8394522		0.9999488	



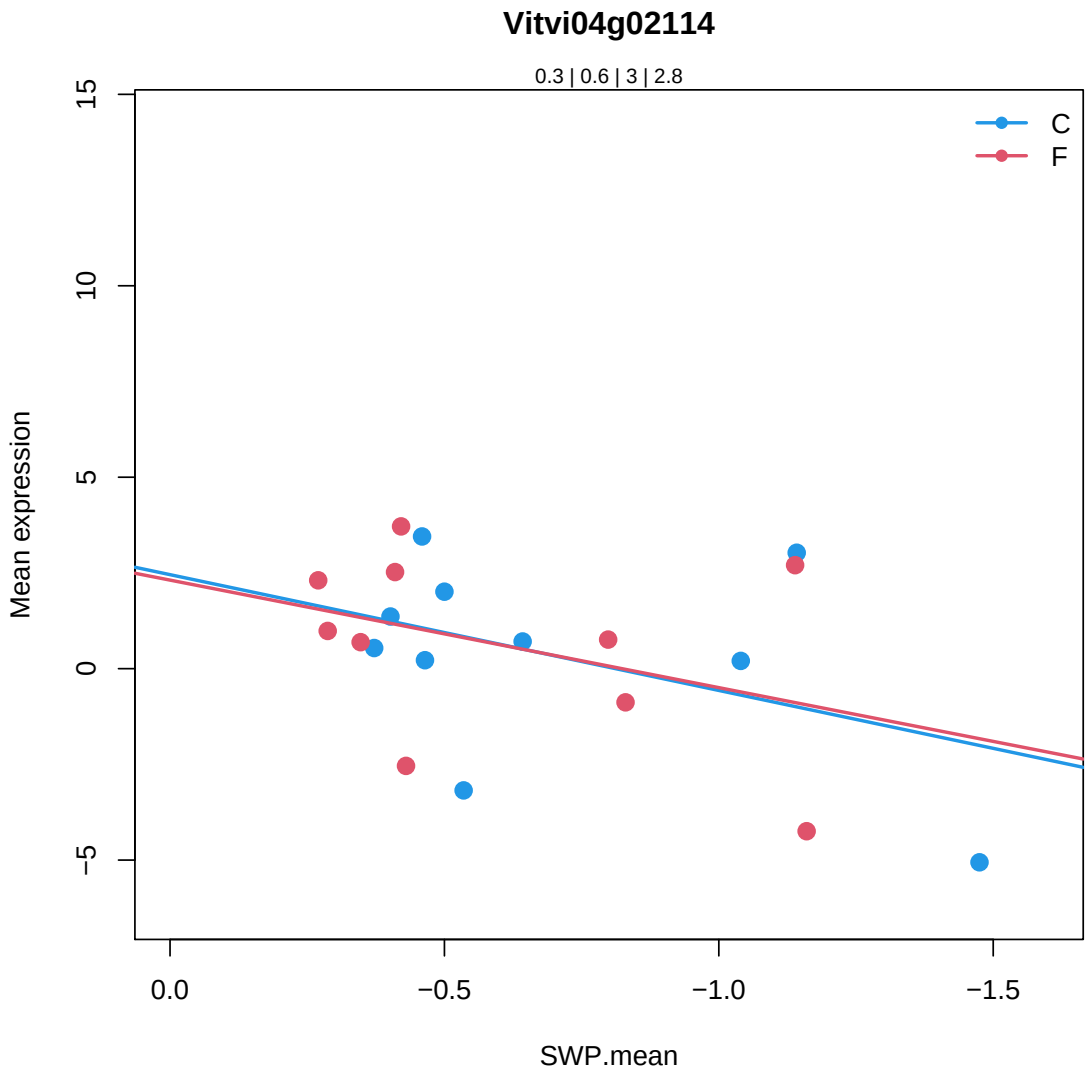
7.2.7 Vitvi04g02114: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
Vitvi04g02114
        35.2
        not assigned.unknown
        S-adenosyl-L-methionine-dependent methyltransferases superfamily prote
        Chr5:1232122-1233888 FORWARD LENGTH=401 |
        201606

Vitvi04g02114
        17.8.1.1.7
        hormone metabolism.salicylic acid.synthesis-degradation.synthesis.meth
        S-adenosyl-L-methionine-dependent methyltransferases superfamily prote
        Chr5:1232122-1233888 FORWARD LENGTH=401 |
        201606
```

Coefficients for Vitvi04g02114.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3284336	0.6354879		0.6405731	
SlopeC	3.024528	0.1260986		0.6471837	
MeanF-MeanC	0.2730671	0.7801191		0.9373729	
SlopeF-SlopeC	-0.2163602	0.9397313		0.9999488	


Vitvi04g02114
0.3 | 0.6 | 3 | 2.8
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

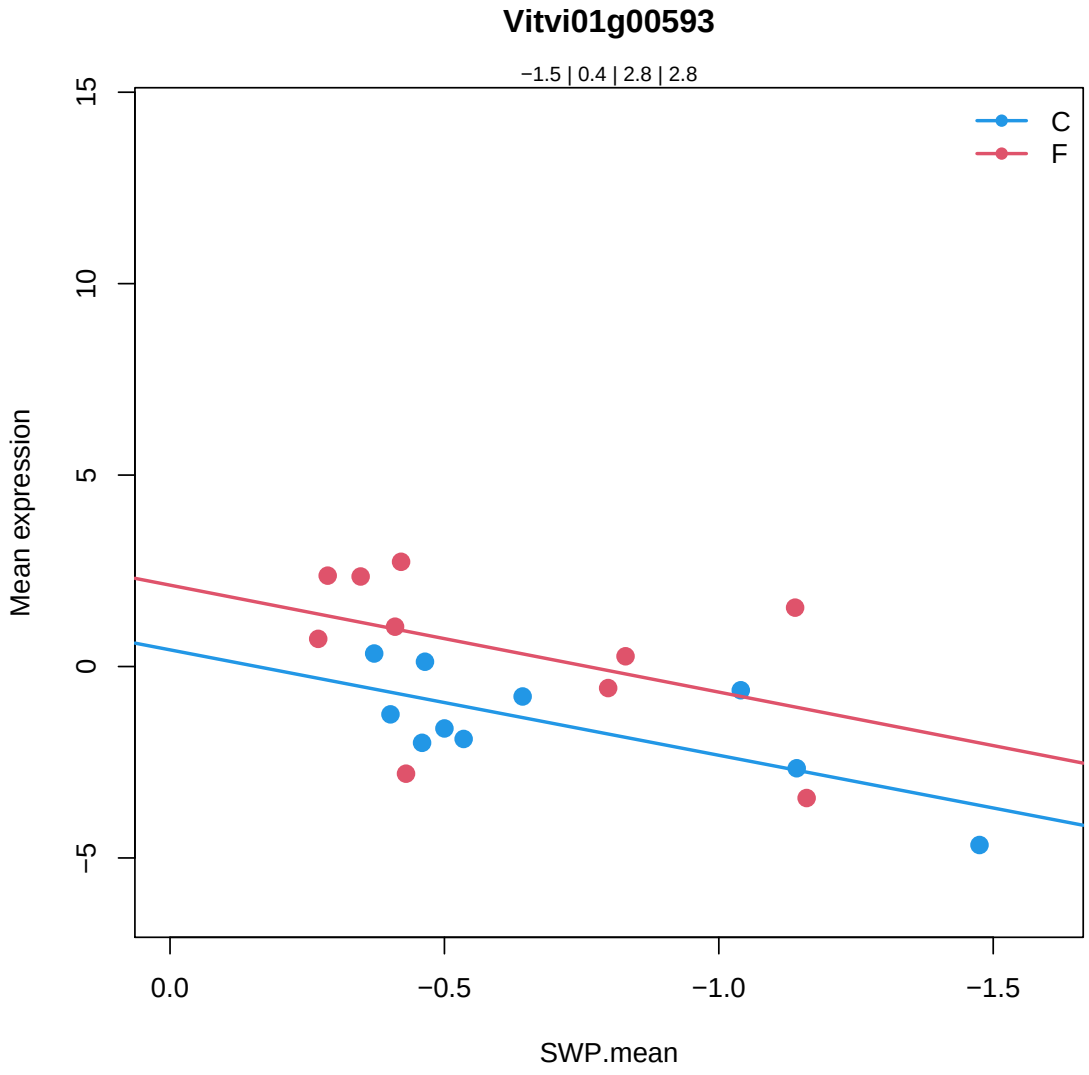
7.2.8 Vitvi01g00593: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00593
        10.6.3
        cell wall.degradation.pectate lyases and polygalacturonases
        Pectate lyase family protein |
        Chr1:25401660-25403165 FORWARD LENGTH=408 |
        201606
```

Coefficients for Vitvi01g00593.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.500933	0.003006862	**	0.003221834	**
SlopeC	2.753643	0.03843906	*	0.4670907	
MeanF-MeanC	1.923883	0.006245072	**	0.0535965	.
SlopeF-SlopeC	0.04027117	0.9829088		0.9999488	



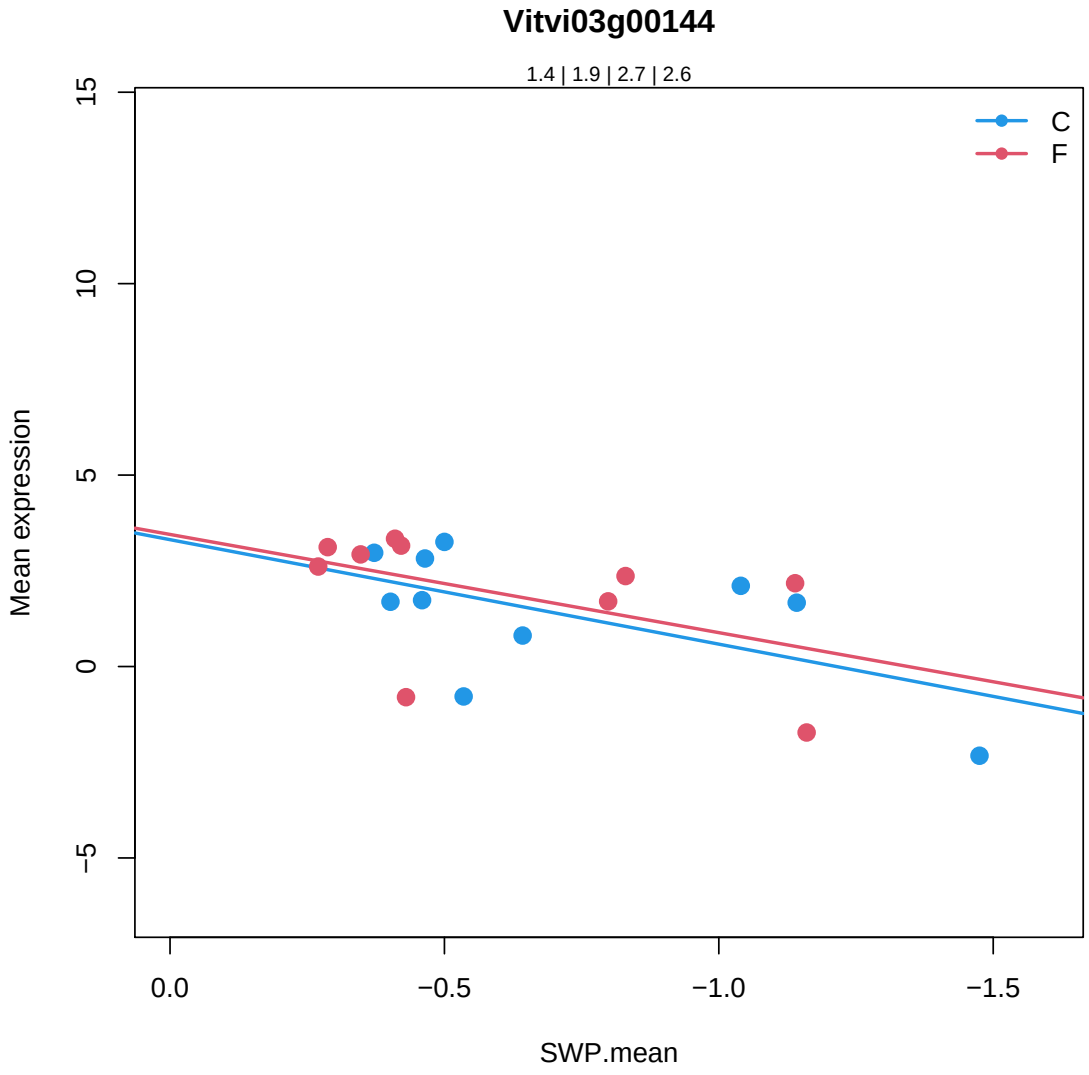
7.2.9 Vitvi03g00144: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00144
        29.4.1.56
        protein.postranslational modification.kinase.receptor like cytoplasmat
        Protein kinase superfamily protein |
        Chr4:16676234-16677962 FORWARD LENGTH=448 |
        201606
```

Coefficients for Vitvi03g00144.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.394192	0.003904502	**	0.004175431	**
SlopeC	2.728777	0.03328153	*	0.4433084	
MeanF-MeanC	0.4924859	0.4281192		0.7634182	
SlopeF-SlopeC	-0.1638066	0.9277451		0.9999488	



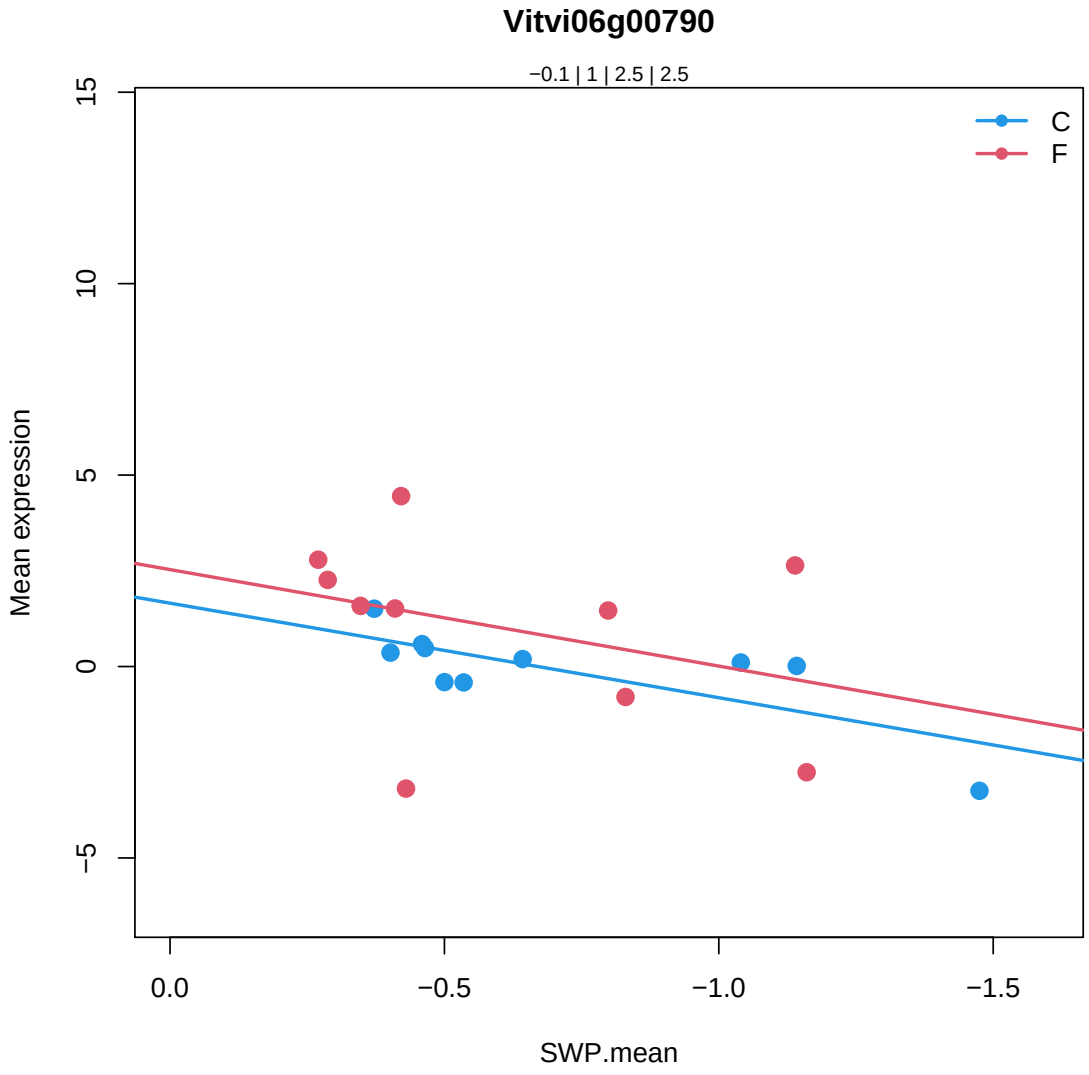
7.2.10 Vitvi06g00790: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00790
        10.7
        cell wall.modification
        expansin A8 |
        Chr2:16949121-16950472 REVERSE LENGTH=253 |
        201606
```

Coefficients for Vitvi06g00790.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.08166594	0.8741388		0.8769003	
SlopeC	2.469095	0.09581708	.	0.6064284	
MeanF-MeanC	1.077543	0.1493144		0.4655993	
SlopeF-SlopeC	0.05143393	0.9807731		0.9999488	



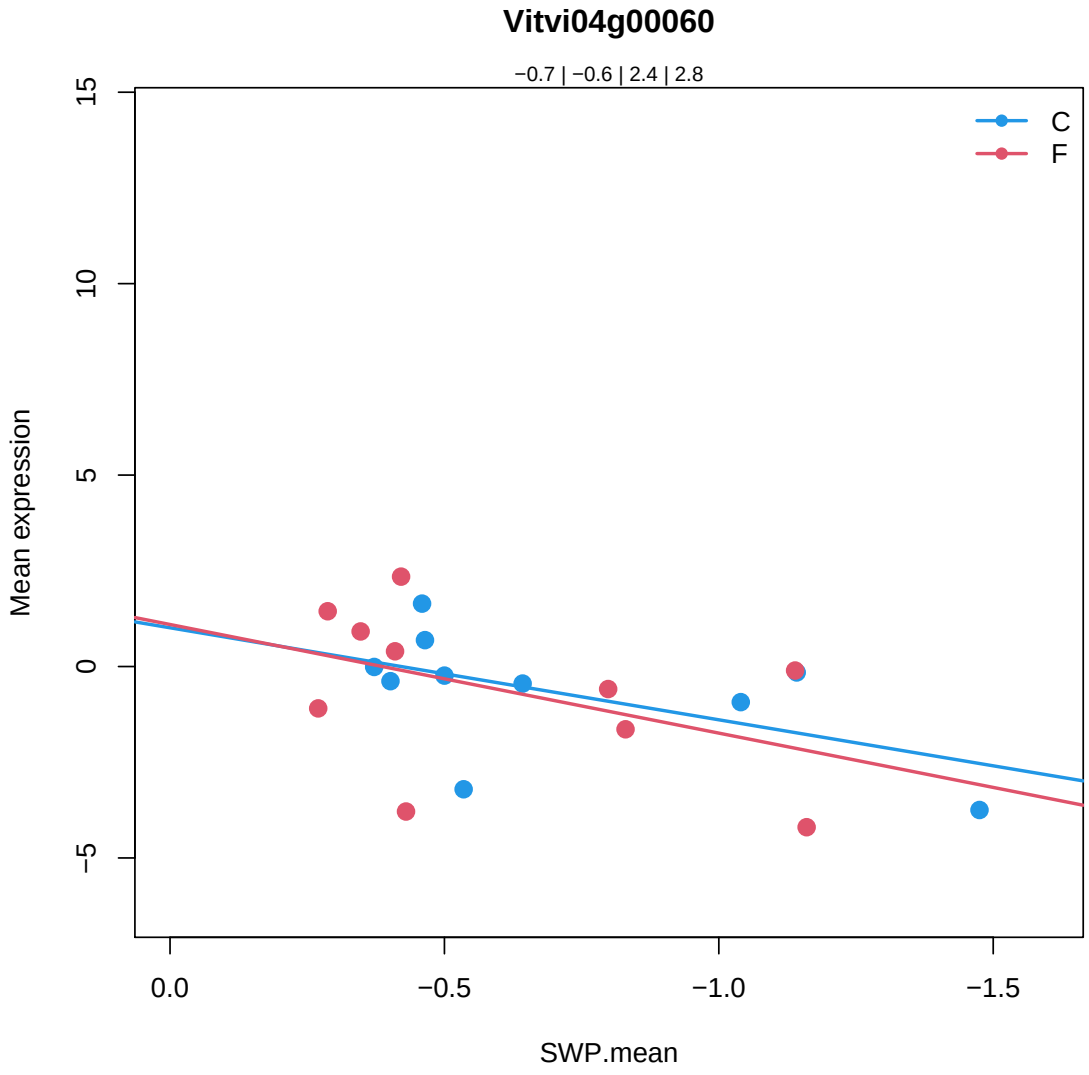
7.2.11 Vitvi04g00060: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00060
        29.4
        protein.postranslational modification
        Protein phosphatase 2C family protein |
        Chr5:9085512-9087372 REVERSE LENGTH=331 |
        201606
```

Coefficients for Vitvi04g00060.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.6784558	0.1755229		0.1802533	
SlopeC	2.403369	0.0886092	.	0.5943767	
MeanF-MeanC	0.04771275	0.9451034		0.9857335	
SlopeF-SlopeC	0.4336031	0.8308518		0.9999488	



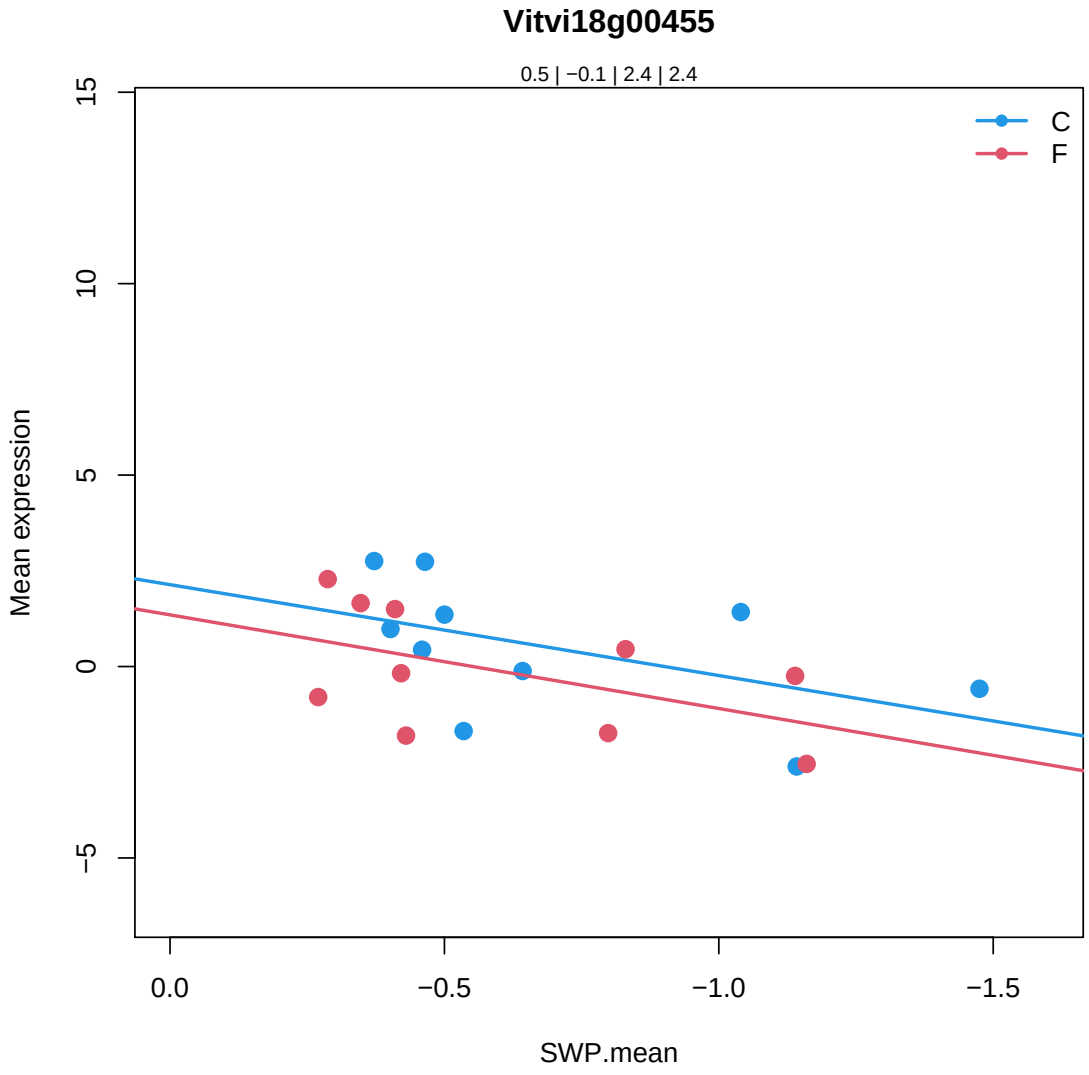
7.2.12 Vitvi18g00455: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00455
        26.7
        misc.oxidases - copper, flavone etc
        Cupredoxin superfamily protein |
        Chr1:27188287-27189093 FORWARD LENGTH=181 |
        201606
```

Coefficients for Vitvi18g00455.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4689391	0.2851456		0.2906956	
SlopeC	2.373306	0.059008	.	0.5387954	
MeanF-MeanC	-0.6103592	0.3242723		0.6848408	
SlopeF-SlopeC	0.07233783	0.9678037		0.9999488	



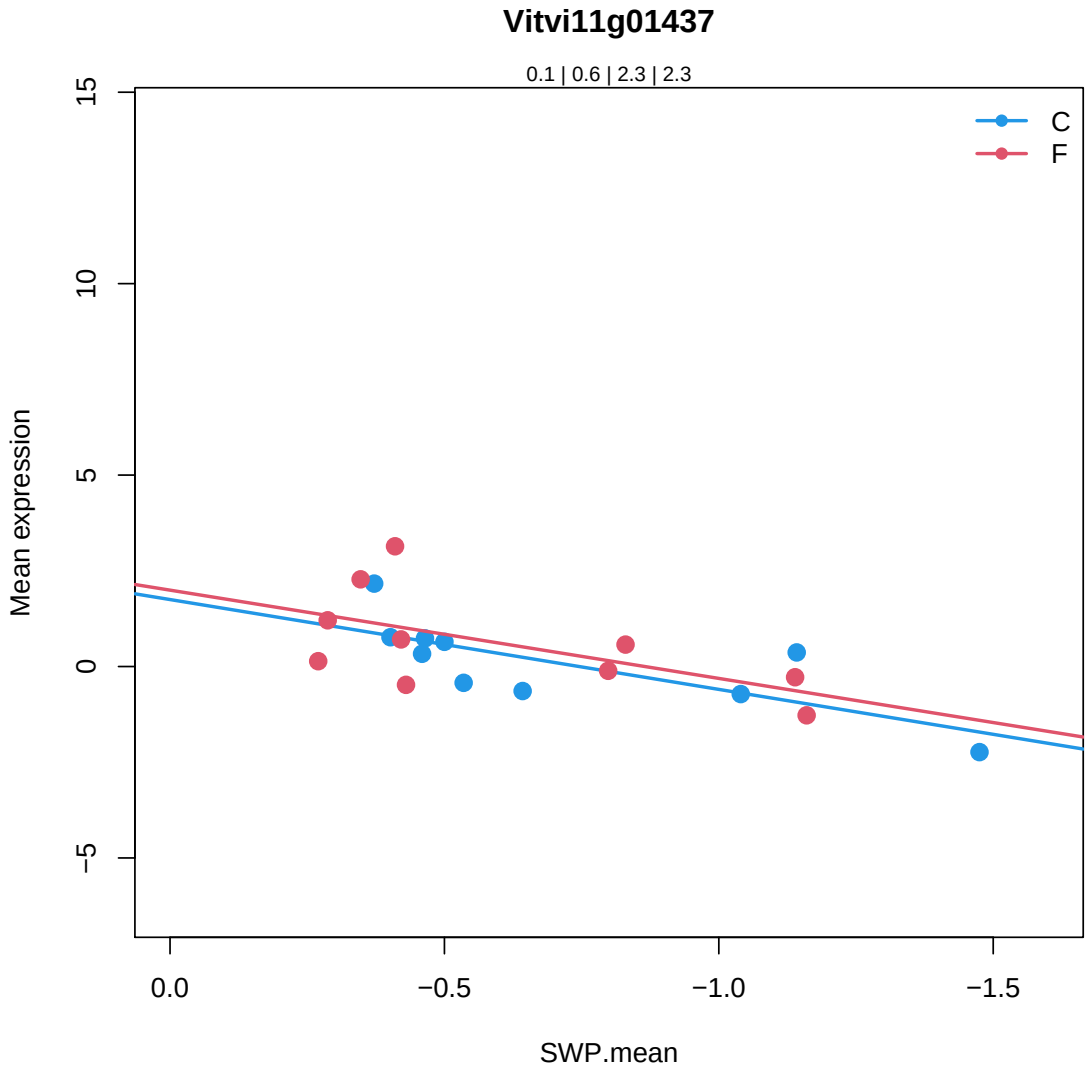
7.2.13 Vitvi11g01437: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g01437
        26.12
        misc.peroxidases
        peroxidase superfamily protein |
        Chr2:17296986-17298690 REVERSE LENGTH=328 |
        201606
```

Coefficients for Vitvi11g01437.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.09876858	0.7280102		0.7325278	
SlopeC	2.346685	0.006578595	**	0.2702721	
MeanF-MeanC	0.4910265	0.2288586		0.5816886	
SlopeF-SlopeC	-0.04140832	0.9718717		0.9999488	



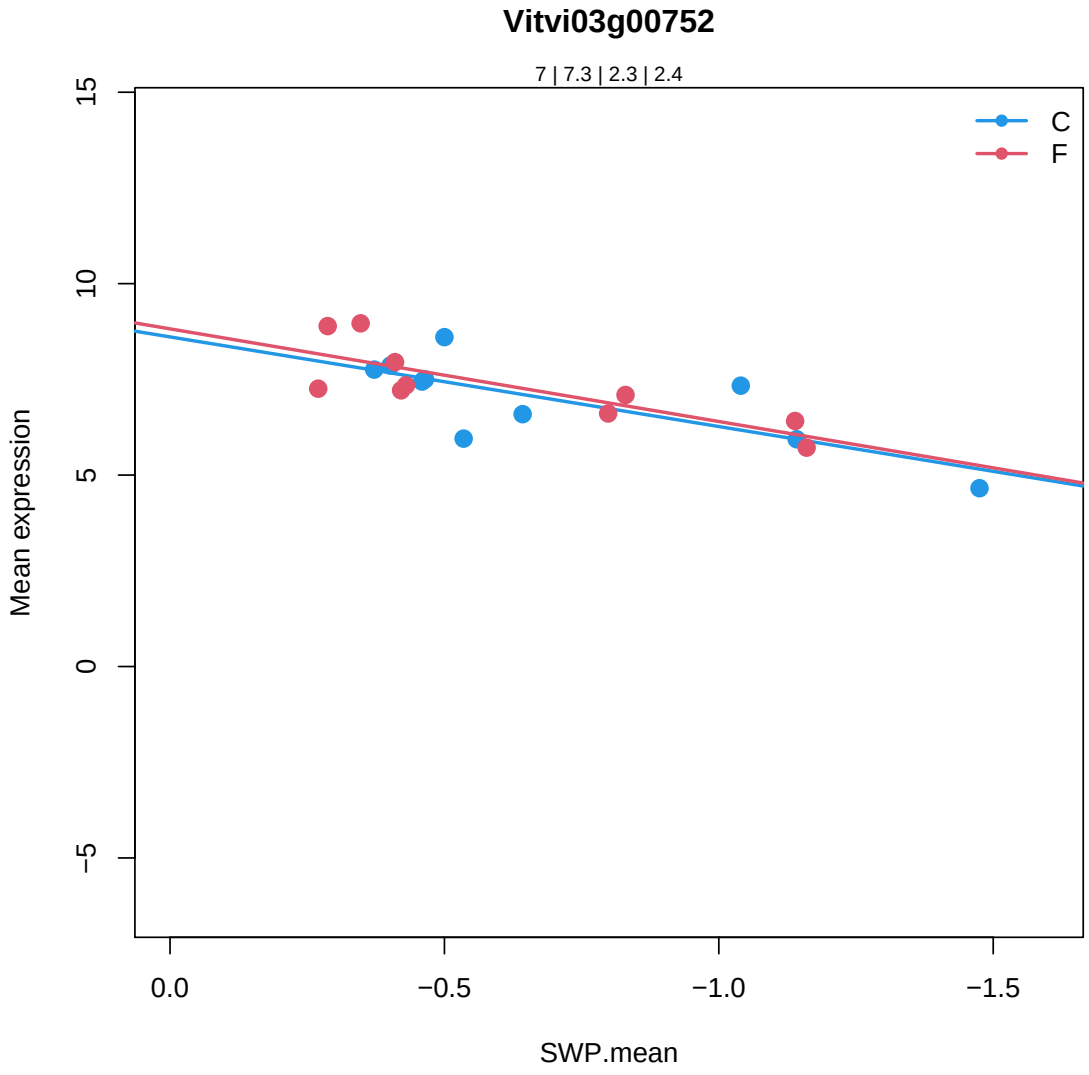
7.2.14 Vitvi03g00752: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00752
        20.1.7.1
        stress.biotic.PR-proteins.PR1 (antifungal)
        pathogenesis-related protein 1 |
        Chr2:6241944-6242429 REVERSE LENGTH=161 |
        201606
```

Coefficients for Vitvi03g00752.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.962961	9.923214e-20	***	4.751795e-19	***
SlopeC	2.340669	0.000749668	***	0.1076608	
MeanF-MeanC	0.3817999	0.2211937		0.5723025	
SlopeF-SlopeC	0.07947066	0.929457		0.9999488	



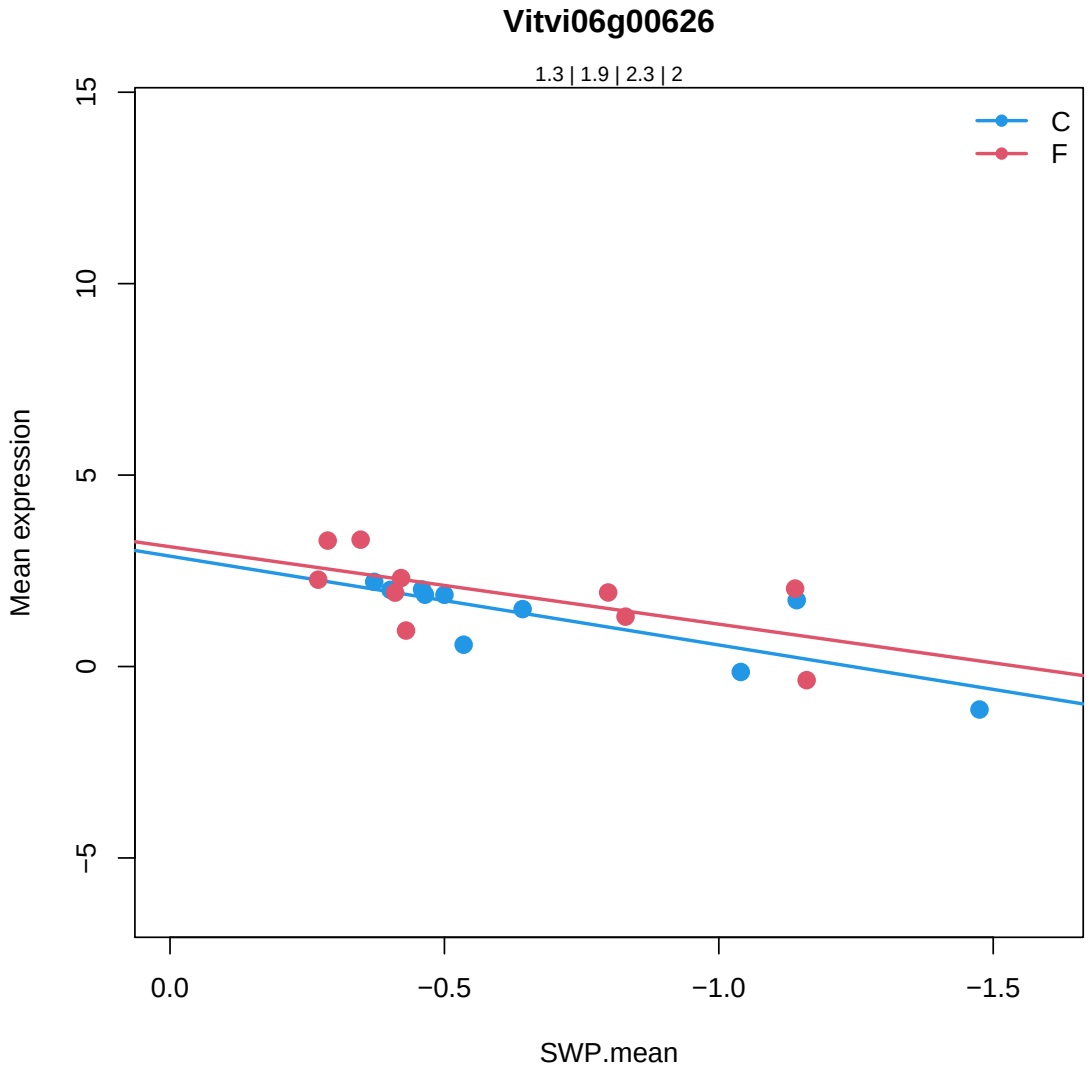
7.2.15 Vitvi06g00626: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00626
        30.2.8.2
        signalling.receptor kinases.leucine rich repeat VIII.type 2
        Protein kinase superfamily protein |
        Chr3:2750285-2751674 FORWARD LENGTH=305 |
        201606
```

Coefficients for Vitvi06g00626.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.250849	2.584959e-05	***	2.88983e-05	***
SlopeC	2.319803	0.00183732	**	0.160246	
MeanF-MeanC	0.6455885	0.06500153	.	0.2823463	
SlopeF-SlopeC	-0.297086	0.7627901		0.9999488	



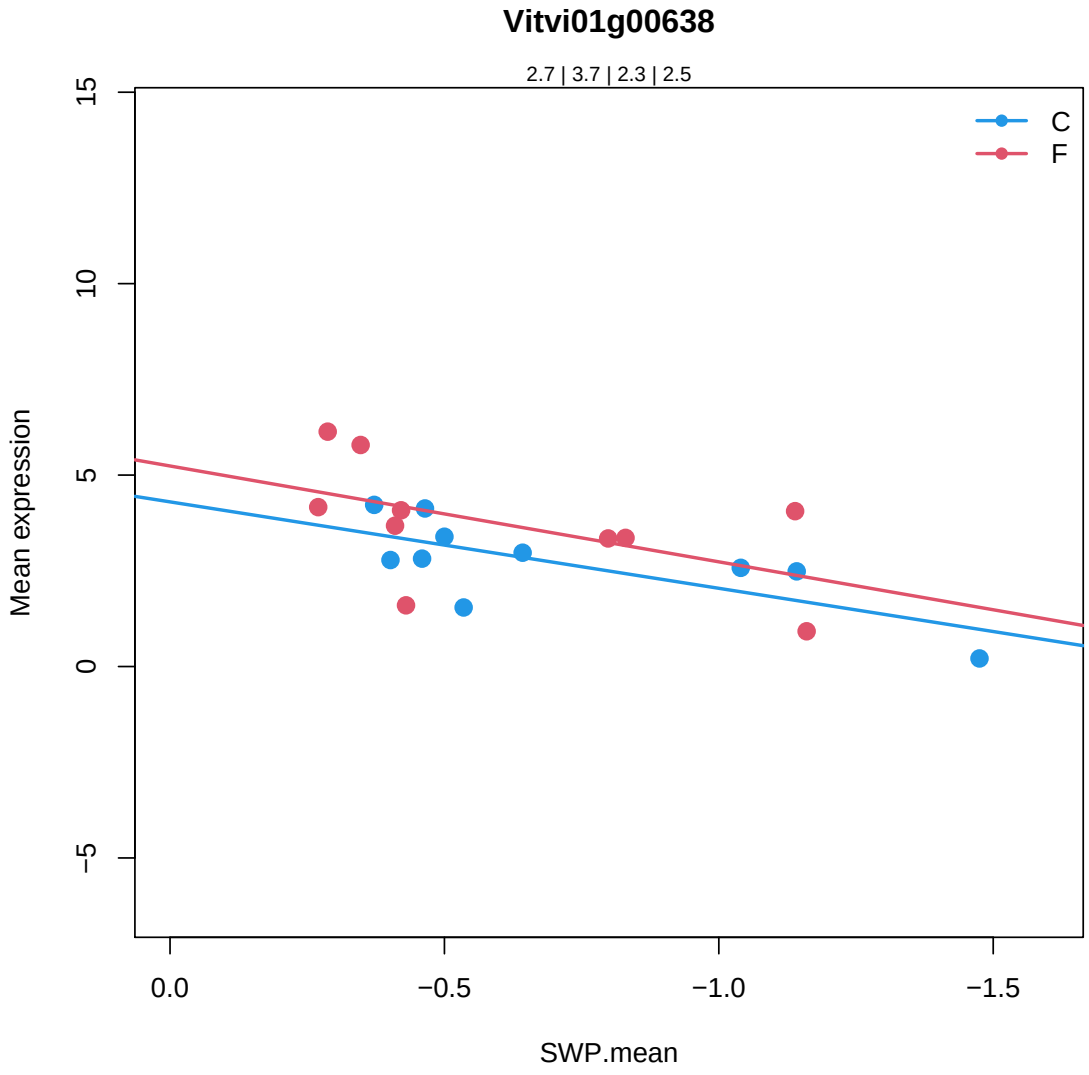
7.2.16 Vitvi01g00638: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00638
        35.2
        not assigned.unknown
        DUF868 family protein (DUF868) |
        Chr4:7480896-7481753 FORWARD LENGTH=285 |
        201606
```

Coefficients for Vitvi01g00638.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.712506	5.204179e-08	***	6.219877e-08	***
SlopeC	2.257332	0.0235059	*	0.3983963	
MeanF-MeanC	0.9995699	0.04541677	*	0.2251195	
SlopeF-SlopeC	0.2461278	0.8598843		0.9999488	



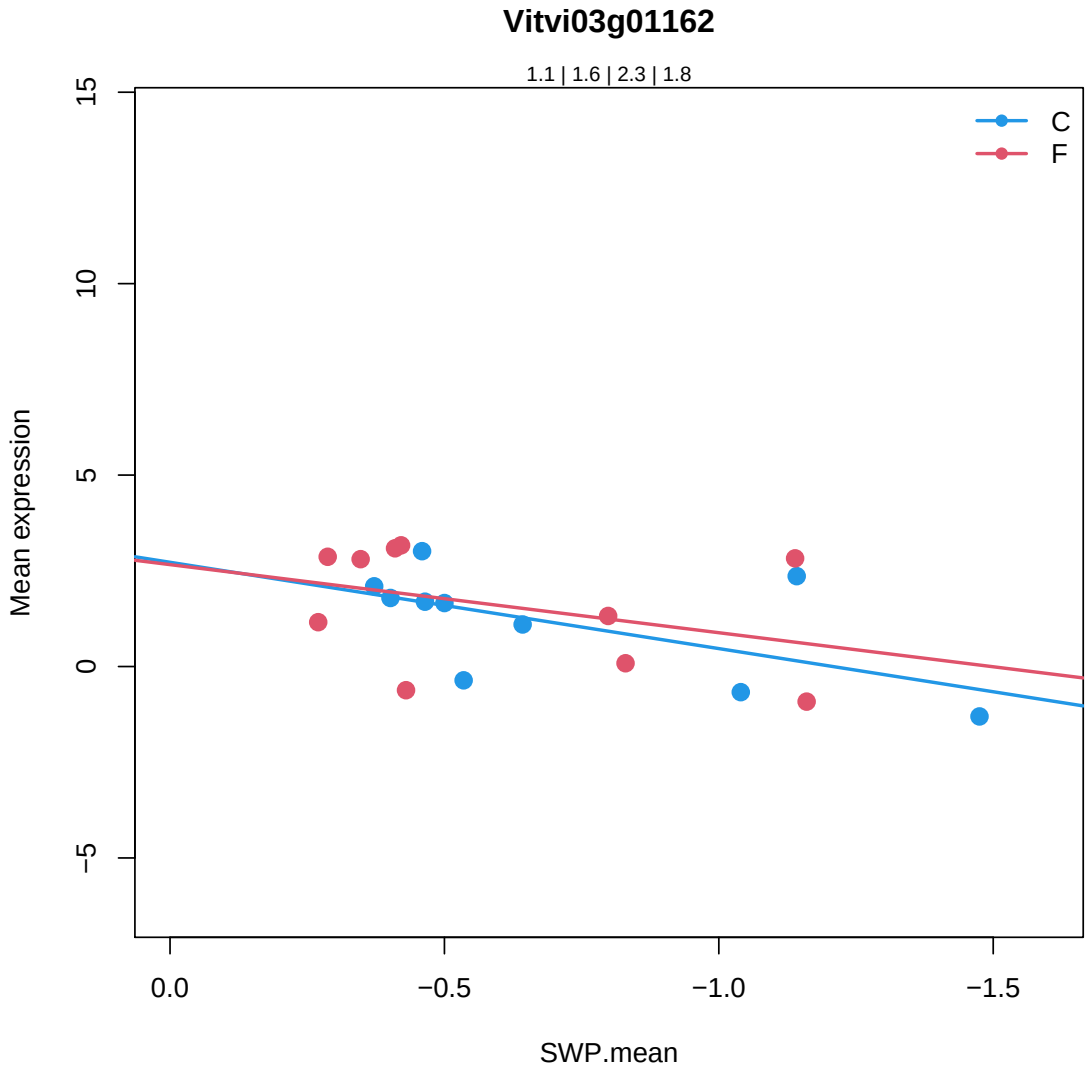
7.2.17 Vitvi03g01162: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g01162
        26.2
        misc.UDP glucosyl and glucoronyl transferases
        UDP-glucosyl transferase 85A3 |
        Chr1:7900522-7902332 REVERSE LENGTH=488 |
        201606
```

Coefficients for Vitvi03g01162.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.137076	0.008329468	**	0.008839838	**
SlopeC	2.254074	0.0506402	.	0.5104439	
MeanF-MeanC	0.4403571	0.4348589		0.7674876	
SlopeF-SlopeC	-0.4754753	0.7719849		0.9999488	



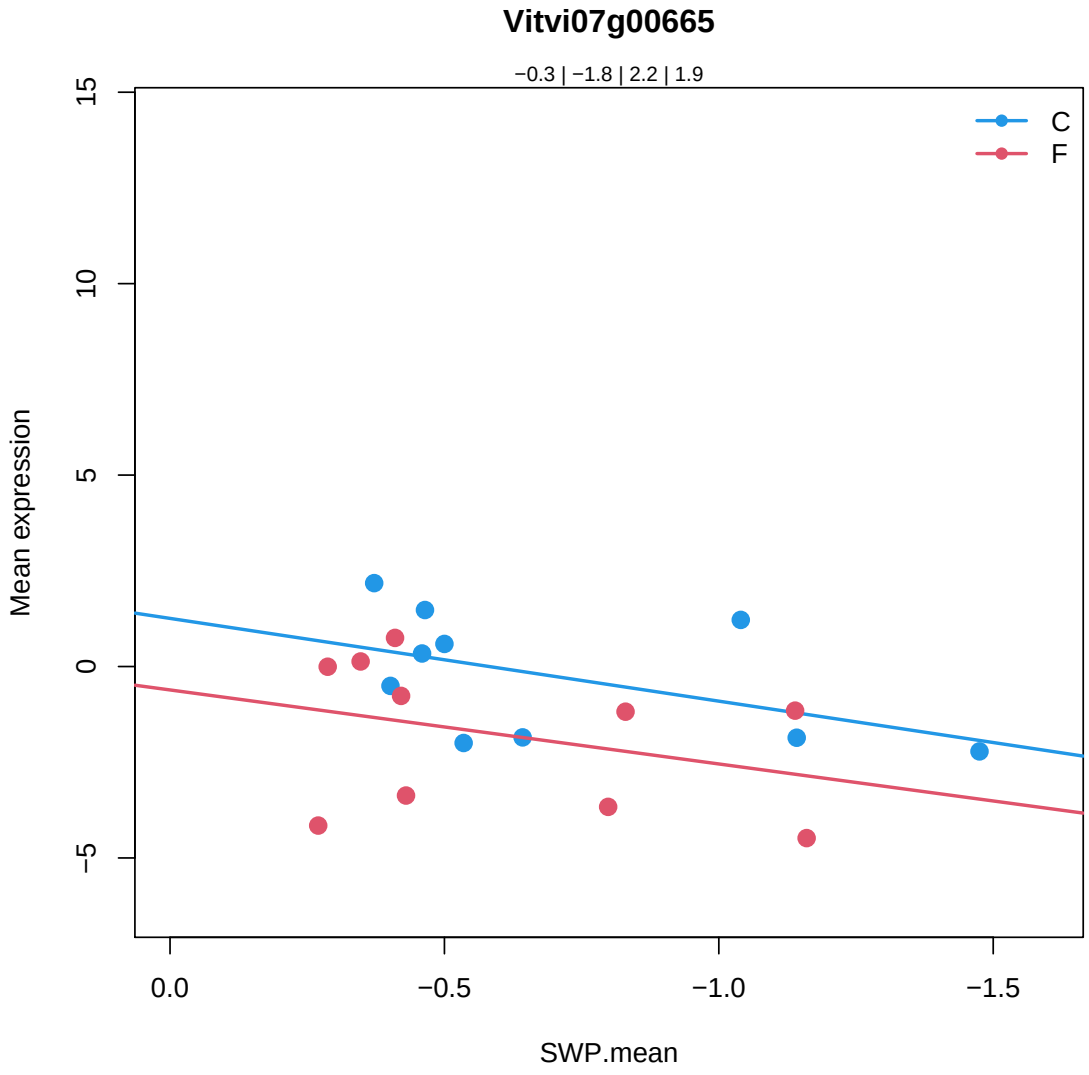
7.2.18 Vitvi07g00665: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g00665
        10.2.1
        cell wall.cellulose synthesis.cellulose synthase
        cellulose synthase A4 |
        Chr5:17714713-17719564 FORWARD LENGTH=1078 |
        201606
```

Coefficients for Vitvi07g00665.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.26307	0.5897013		0.5950498	
SlopeC	2.161511	0.1205218		0.6393992	
MeanF-MeanC	-1.52667	0.03531195	*	0.188458	
SlopeF-SlopeC	-0.228278	0.9097275		0.9999488	



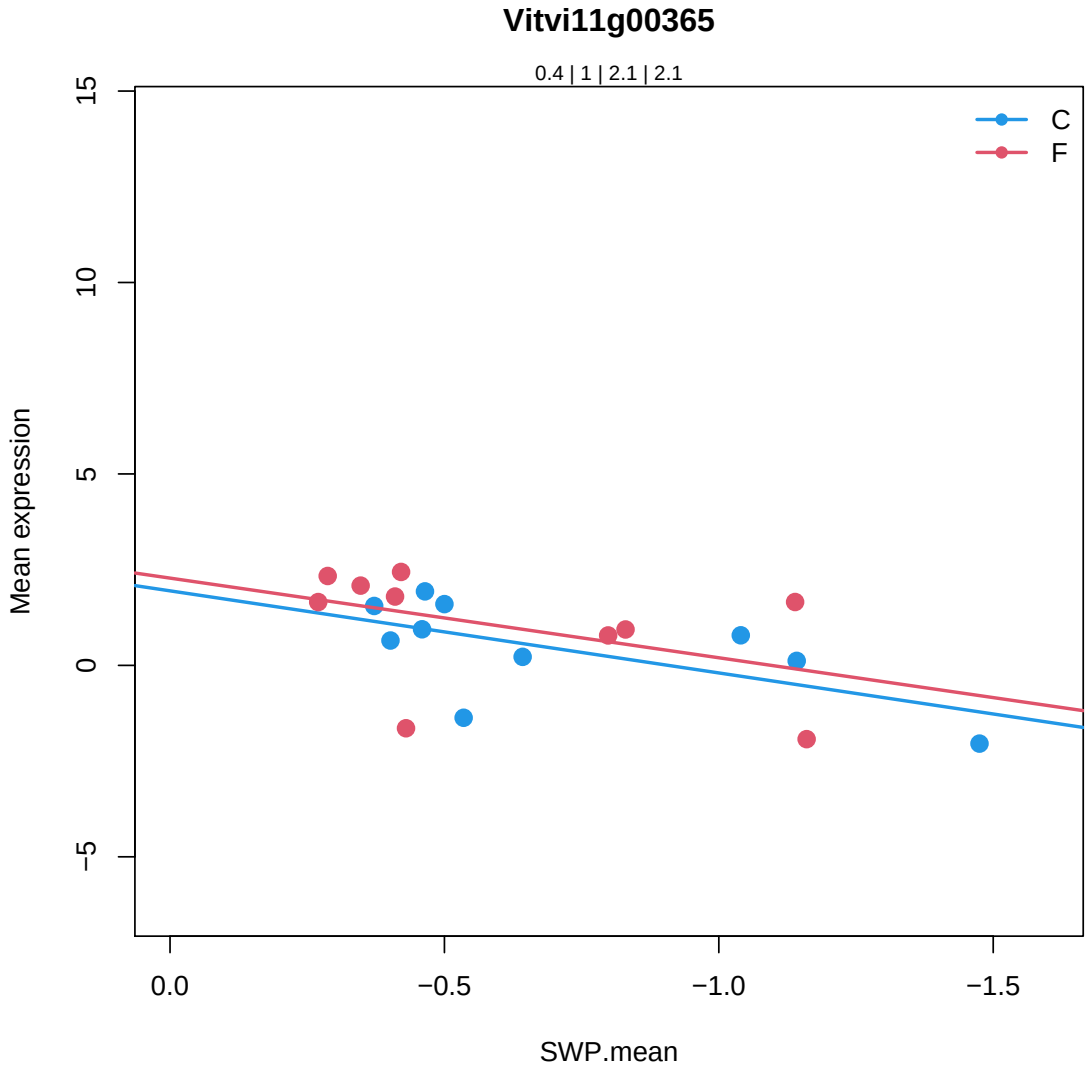
7.2.19 Vitvi11g00365: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00365
        15.2
        metal handling.binding, chelation and storage
        [Sotub12g009040.1.1]: Metal ion binding protein [Sotub12g009040.1.1]:
        [stNIB-v1_0017795]
```

Coefficients for Vitvi11g00365.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4387756	0.2354167		0.2407718	
SlopeC	2.144061	0.04362538	*	0.4850023	
MeanF-MeanC	0.5724837	0.2724907		0.6360341	
SlopeF-SlopeC	-0.06396351	0.9661169		0.9999488	



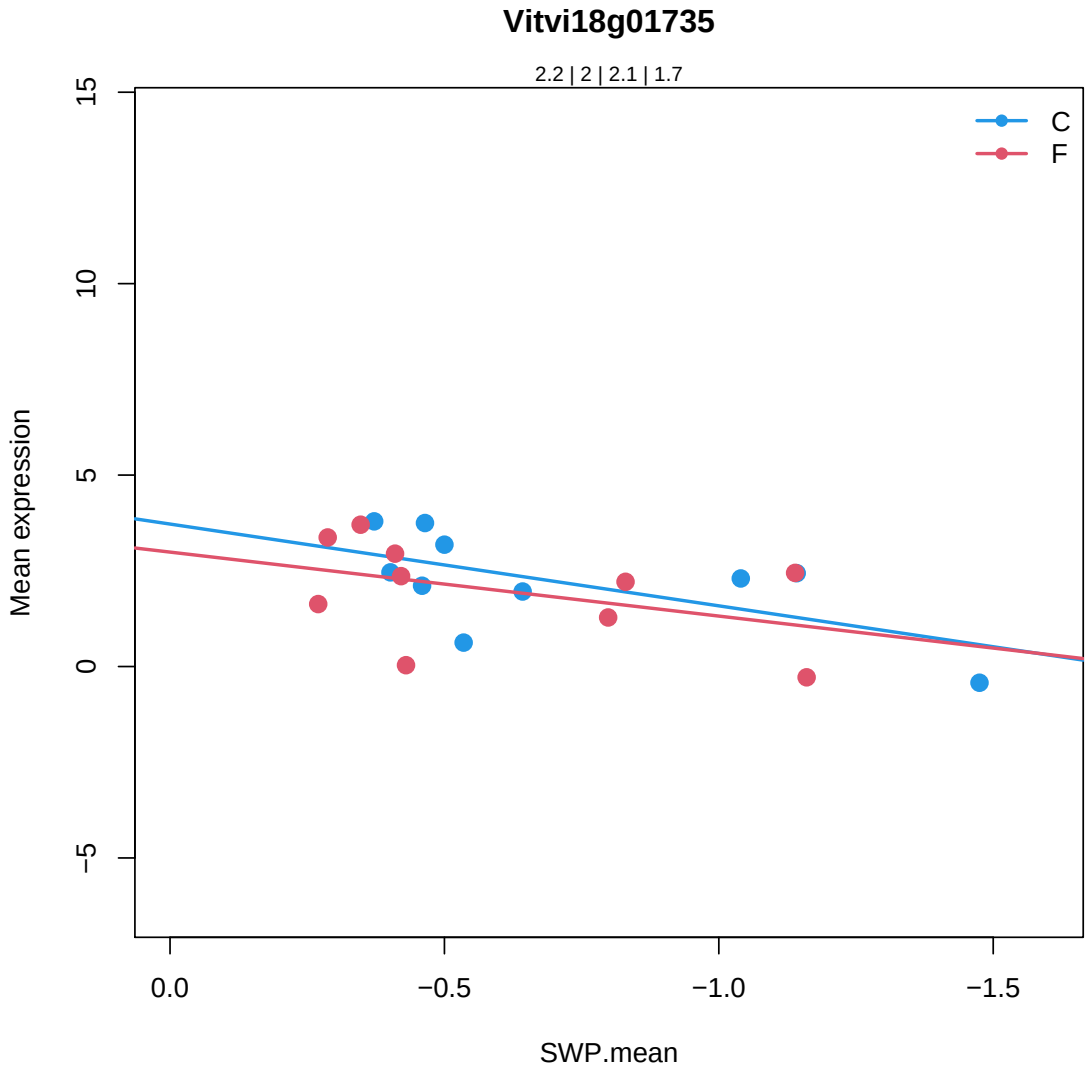
7.2.20 Vitvi18g01735: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g01735
        35.2
        not assigned.unknown
        hypothetical protein |
        Chr1:8025503-8026060 REVERSE LENGTH=185 |
        201606
```

Coefficients for Vitvi18g01735.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.218754	1.174506e-06	***	1.353635e-06	***
SlopeC	2.136215	0.03083978	*	0.4322019	
MeanF-MeanC	-0.2484138	0.6024201		0.8612137	
SlopeF-SlopeC	-0.4651096	0.7385773		0.9999488	



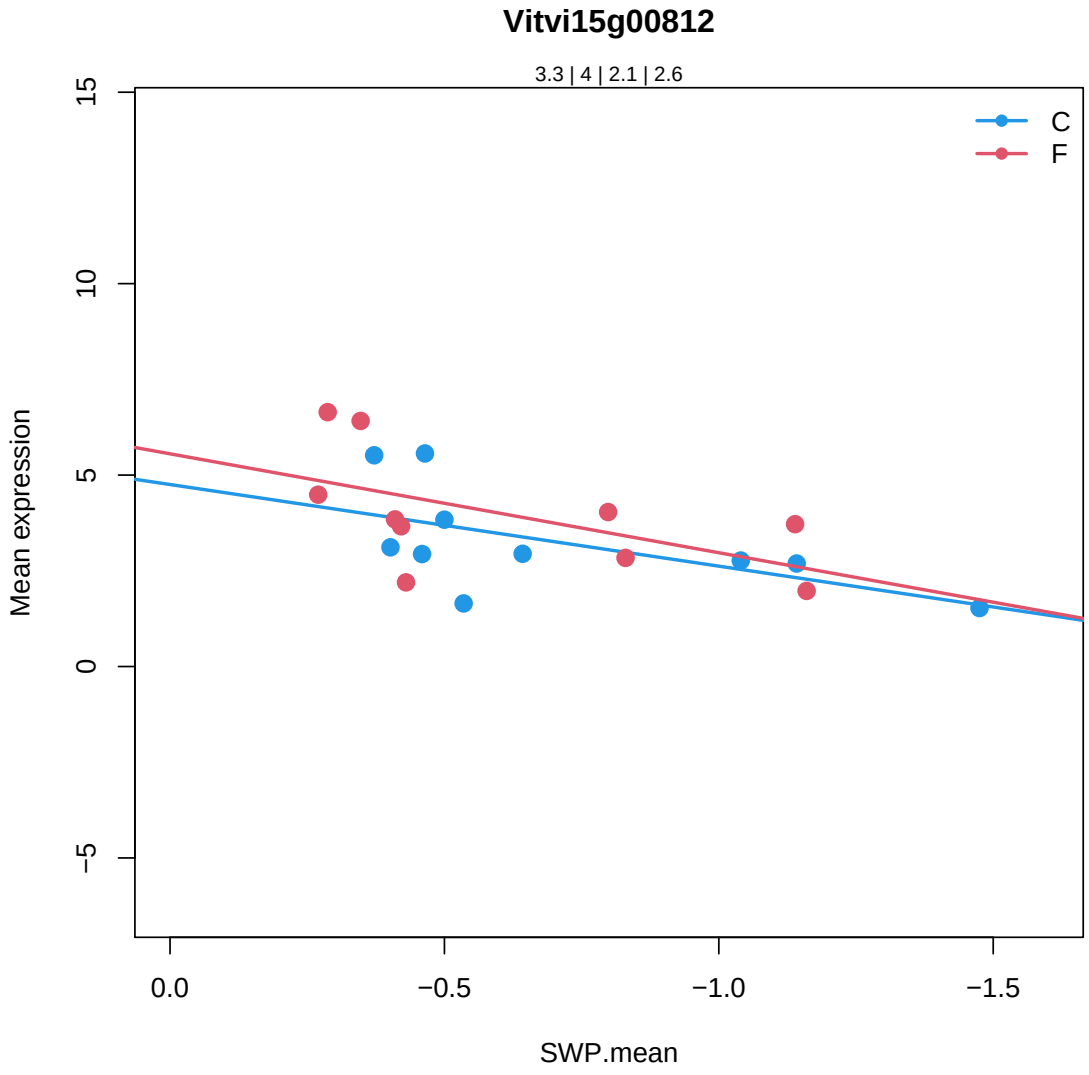
7.2.21 Vitvi15g00812: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g00812
        26.7
        misc.oxidases - copper, flavone etc
        Oxidoreductase%2C zinc-binding dehydrogenase family protein |
        Chr1:8398245-8399656 REVERSE LENGTH=386 |
        201606
```

Coefficients for Vitvi15g00812.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.254347	8.246706e-09	***	1.008798e-08	***
SlopeC	2.132014	0.04382603	*	0.4861691	
MeanF-MeanC	0.7269828	0.1652003		0.4931388	
SlopeF-SlopeC	0.4515342	0.7634678		0.9999488	



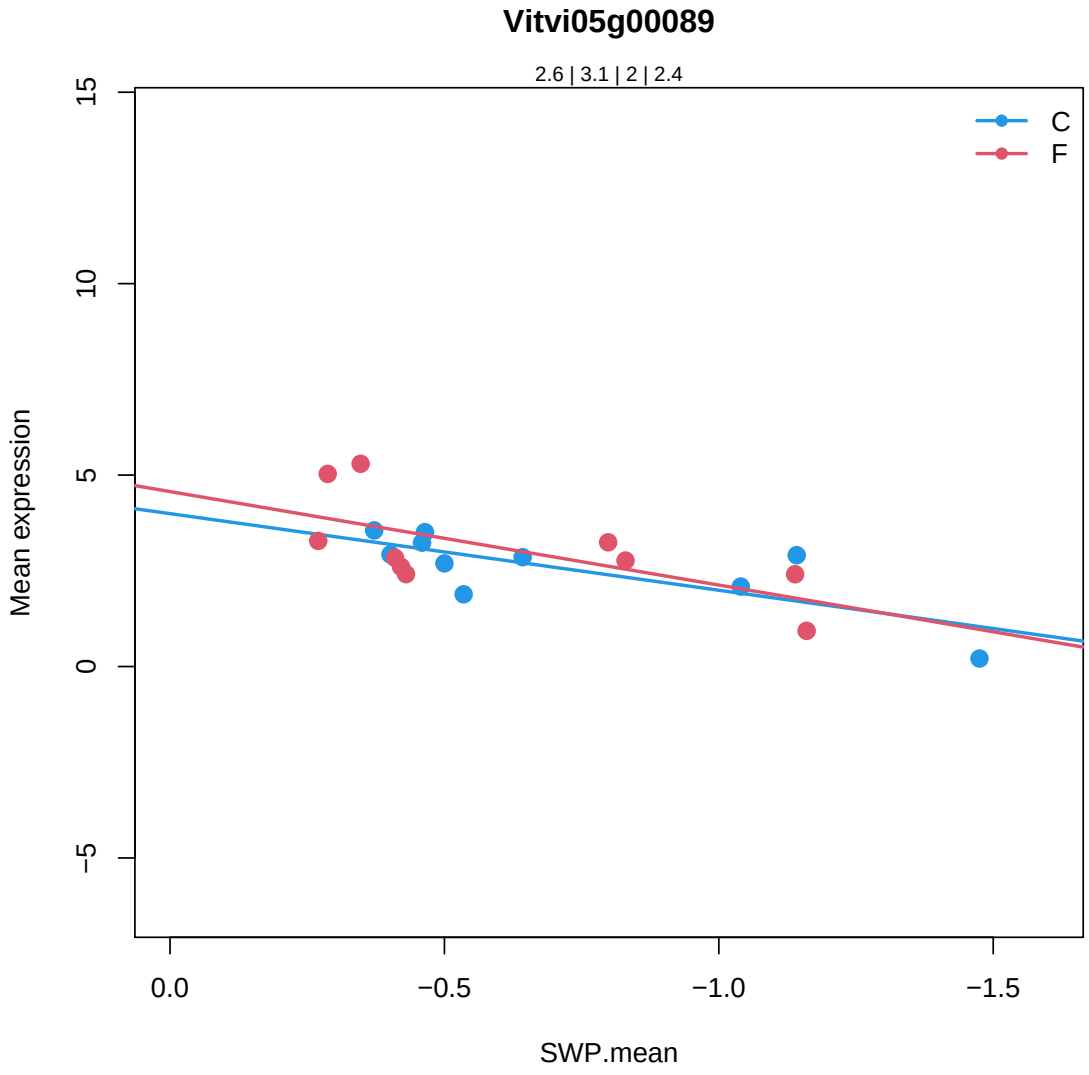
7.2.22 Vitvi05g00089: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00089
        10.6.2
        cell wall.degradation.mannan-xylose-arabinose-fucose
        beta-xylosidase 1 |
        Chr5:20012179-20016659 REVERSE LENGTH=774 |
        201606
```

Coefficients for Vitvi05g00089.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.58641	8.431286e-10	***	1.065498e-09	***
SlopeC	2.000394	0.008881079	**	0.2903326	
MeanF-MeanC	0.4950349	0.1754928		0.507769	
SlopeF-SlopeC	0.4406078	0.6744241		0.9999488	



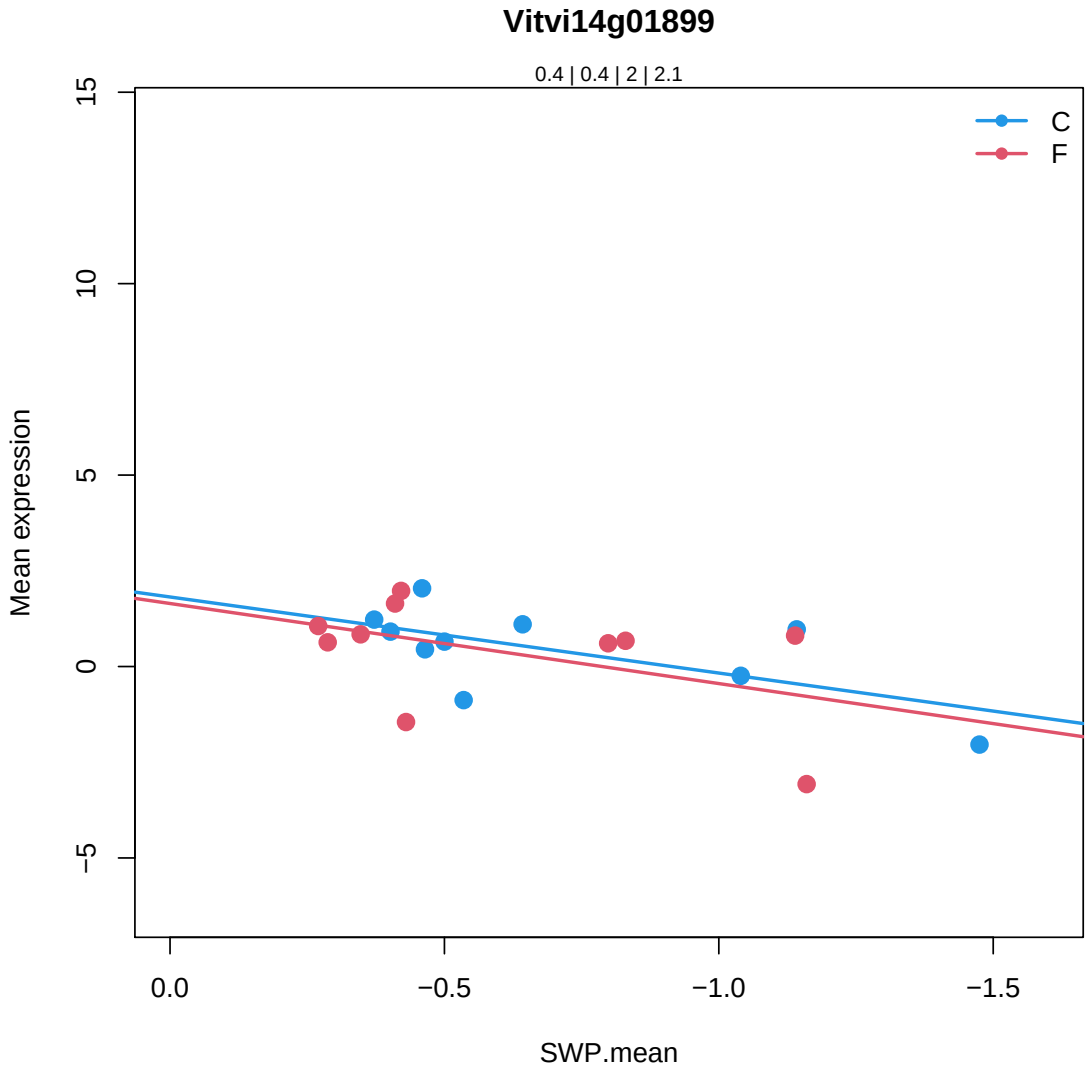
7.2.23 Vitvi14g01899: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01899
        17.2.2
        hormone metabolism.auxin.signal transduction
        Auxin efflux carrier family protein |
        Chr5:4892159-4893937 REVERSE LENGTH=367 |
        201606
```

Coefficients for Vitvi14g01899.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4192037	0.228612		0.2339222	
SlopeC	1.986801	0.04665072	*	0.4955054	
MeanF-MeanC	-0.04772652	0.9214517		0.9796658	
SlopeF-SlopeC	0.1041887	0.9413919		0.9999488	



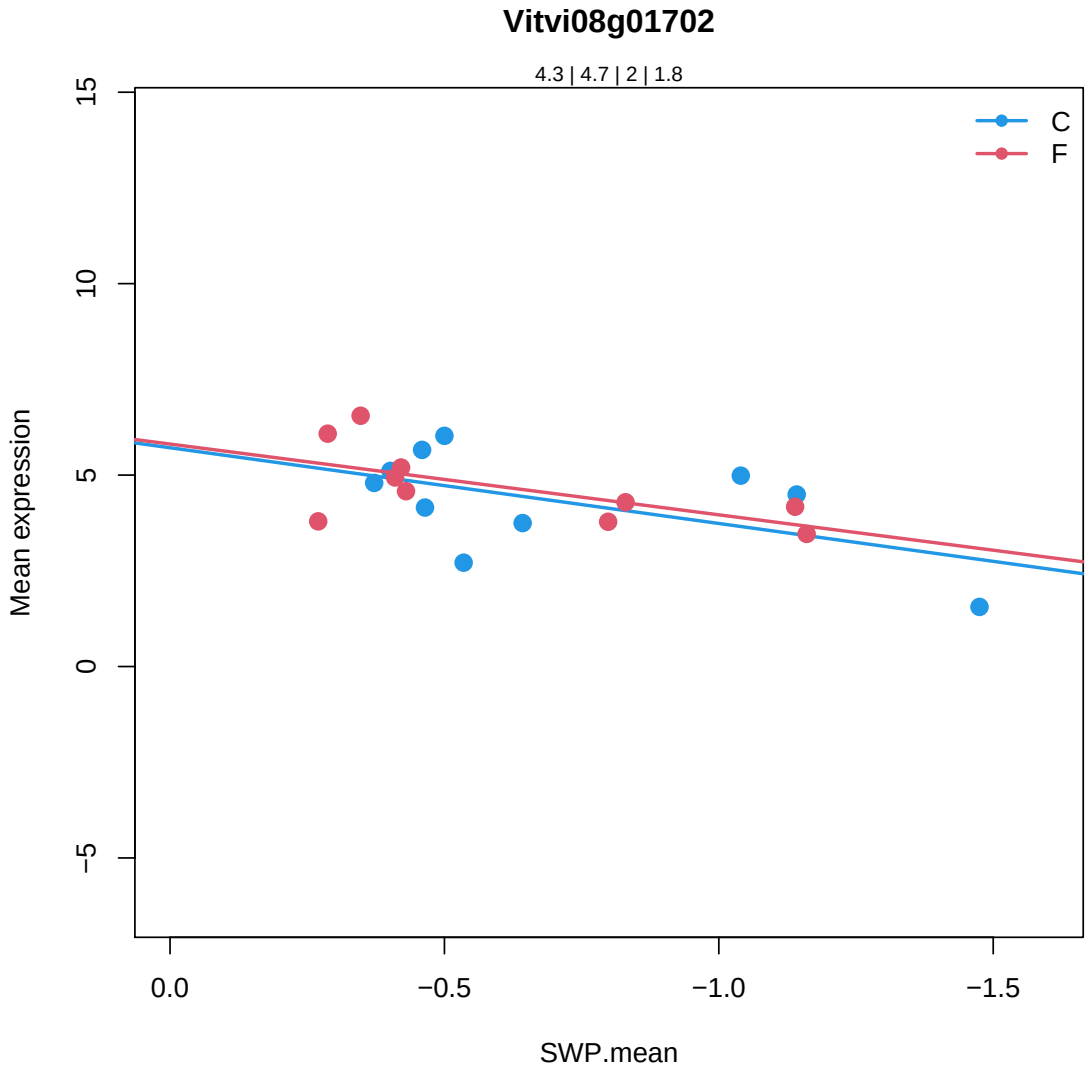
7.2.24 Vitvi08g01702: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01702
        26.4.1
        misc.beta 1,3 glucan hydrolases.glucan endo-1,3-beta-glucosidase
        beta-1%2C3-glucanase 3 |
        Chr3:21181916-21183045 REVERSE LENGTH=341 |
        201606
```

Coefficients for Vitvi08g01702.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.323019	1.105145e-12	***	1.581358e-12	***
SlopeC	1.977921	0.02447287	*	0.4039715	
MeanF-MeanC	0.3611676	0.3943046		0.7416431	
SlopeF-SlopeC	-0.1292418	0.9163785		0.9999488	



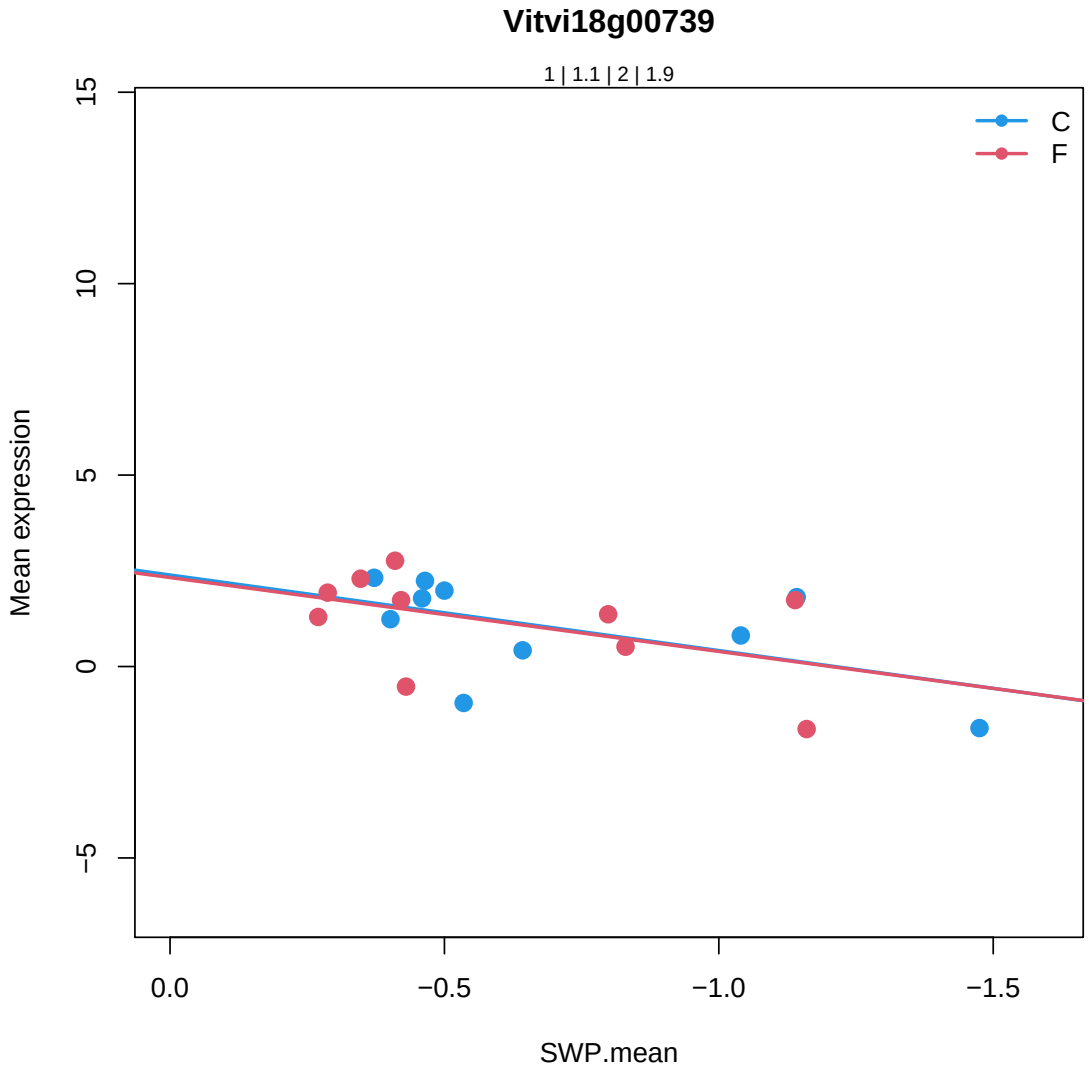
7.2.25 Vitvi18g00739: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00739
        35.2
        not assigned.unknown
        Serine/threonine-protein kinase WNK (With No Lysine)-like protein |
        Chr1:22139282-22141585 FORWARD LENGTH=386 |
        201606
```

Coefficients for Vitvi18g00739.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.00389	0.007775717	**	0.008257906	**
SlopeC	1.973629	0.05021318	.	0.5104439	
MeanF-MeanC	0.143076	0.7701454		0.9333211	
SlopeF-SlopeC	-0.04316739	0.9759574		0.9999488	



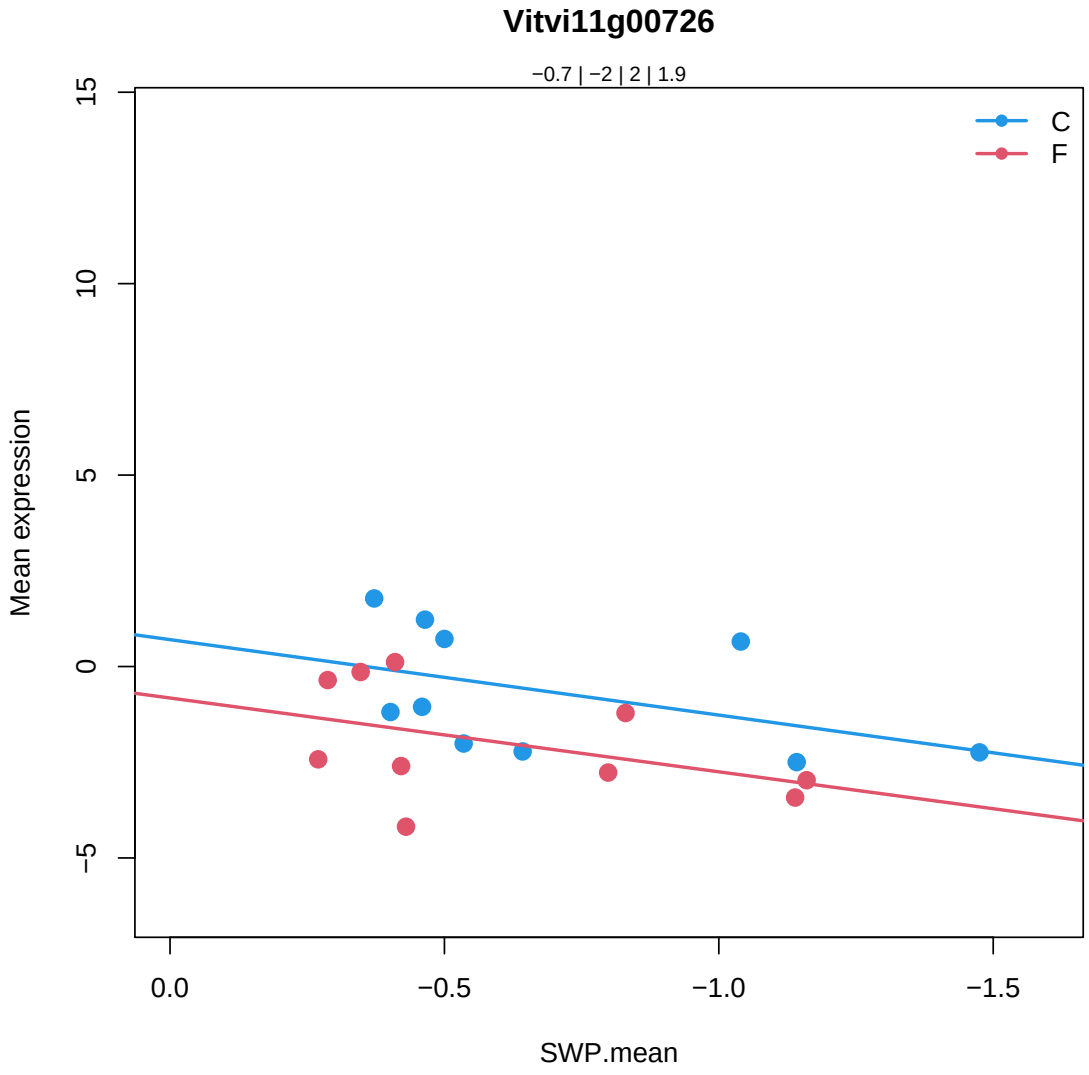
7.2.26 Vitvi11g00726: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00726
        10.2.1
        cell wall.cellulose synthesis.cellulose synthase
        Cellulose synthase family protein |
        Chr5:5736859-5741407 REVERSE LENGTH=1026 |
        201606
```

Coefficients for Vitvi11g00726.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.6836656	0.1103692		0.114012	
SlopeC	1.970264	0.0988823	.	0.6110181	
MeanF-MeanC	-1.313174	0.03419632	*	0.1847644	
SlopeF-SlopeC	-0.04289516	0.9801009		0.9999488	



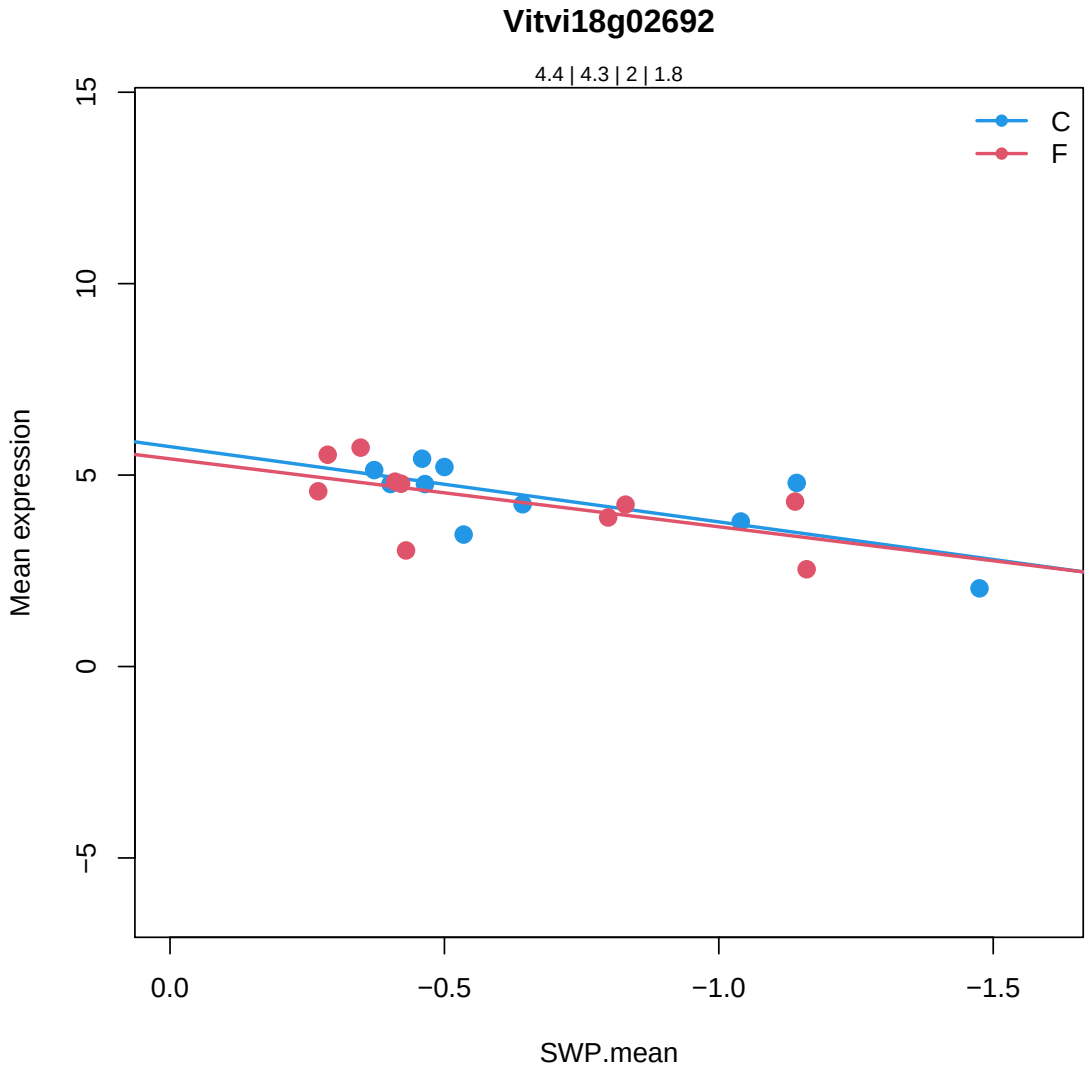
7.2.27 Vitvi18g02692: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02692
        33.1
        development.storage proteins
        phospholipase A 2A |
        Chr2:11293912-11295708 REVERSE LENGTH=407 |
        201606
```

Coefficients for Vitvi18g02692.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.360617	7.812961e-15	***	1.320527e-14	***
SlopeC	1.964537	0.00593268	**	0.2647742	
MeanF-MeanC	-0.01807404	0.9564322		0.9900128	
SlopeF-SlopeC	-0.1900203	0.8445492		0.9999488	



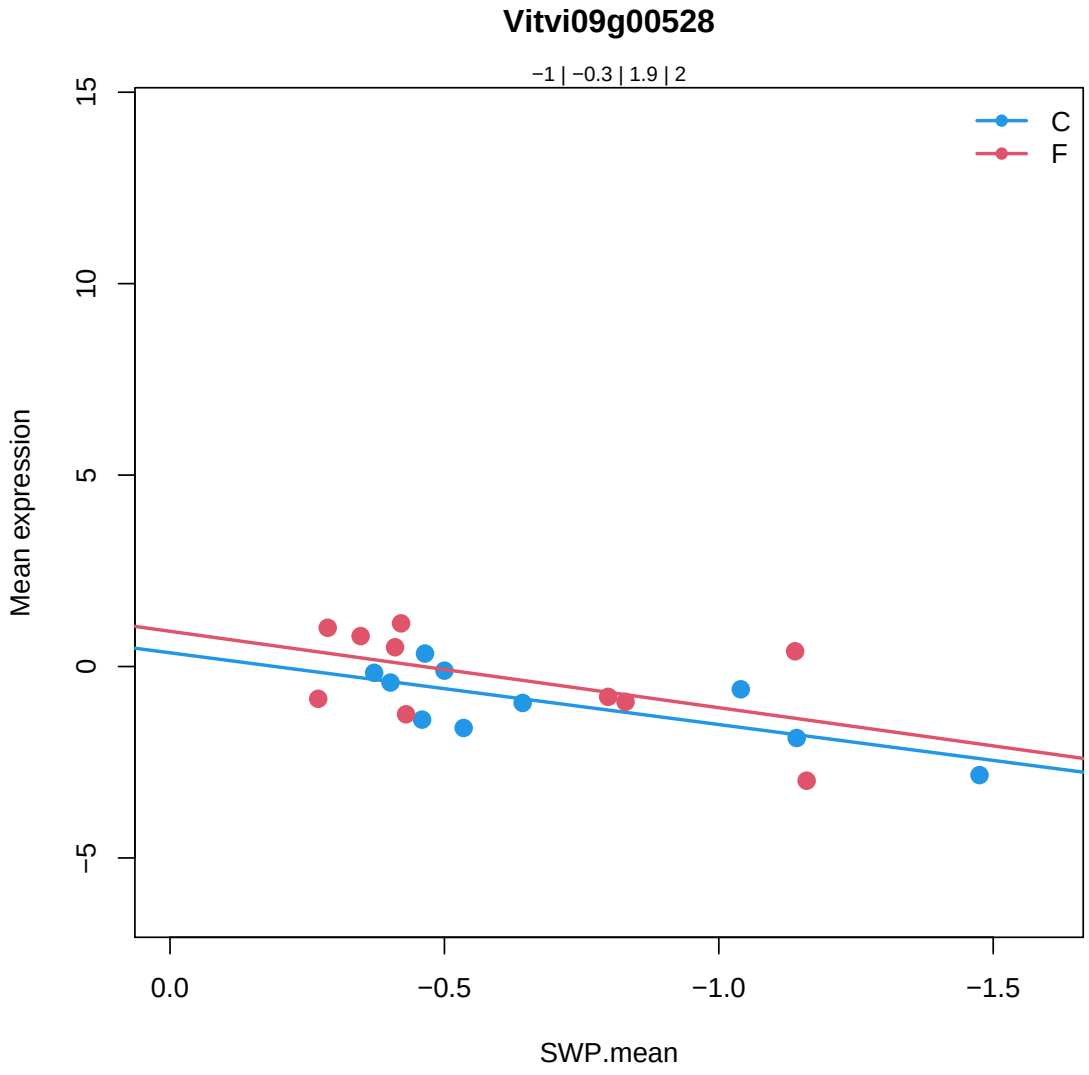
7.2.28 Vitvi09g00528: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00528
        27.4
        RNA.RNA binding
        Ran BP2/NZF zinc finger-like superfamily protein |
        Chr3:5315437-5316048 FORWARD LENGTH=164 |
        201606
```

Coefficients for Vitvi09g00528.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.9593925	0.002052068	**	0.002206067	**
SlopeC	1.873686	0.02239027	*	0.3929231	
MeanF-MeanC	0.6639333	0.1006213		0.3655074	
SlopeF-SlopeC	0.1219435	0.9152932		0.9999488	



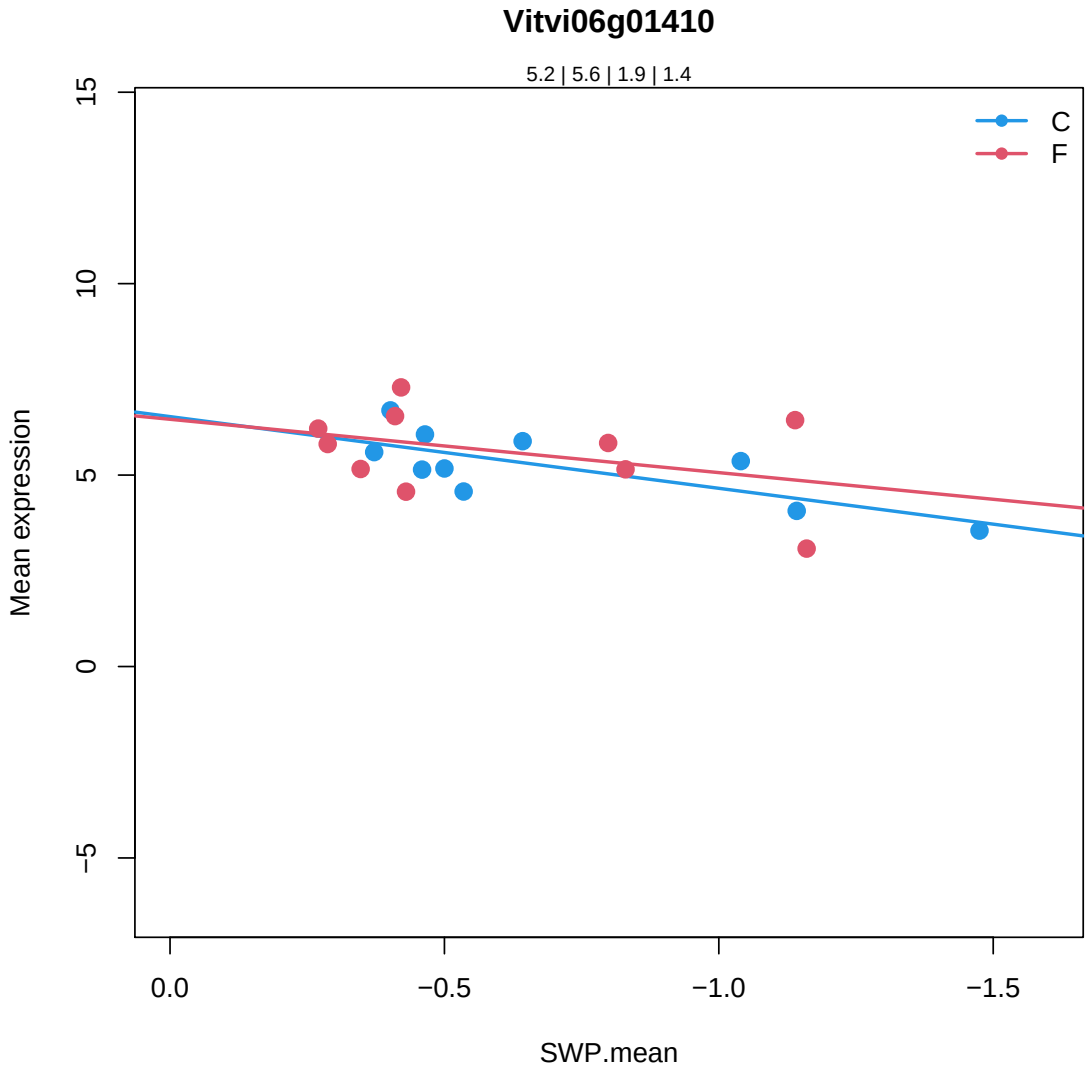
7.2.29 Vitvi06g01410: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01410
        35.2
        not assigned.unknown
        Stress responsive A/B Barrel Domain-containing protein |
        Chr5:7502709-7503137 FORWARD LENGTH=111 |
        201606
```

Coefficients for Vitvi06g01410.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.210105	4.426778e-15	***	7.713839e-15	***
SlopeC	1.872423	0.02035627	*	0.3769378	
MeanF-MeanC	0.3982189	0.306225		0.6693361	
SlopeF-SlopeC	-0.4794743	0.6707493		0.9999488	



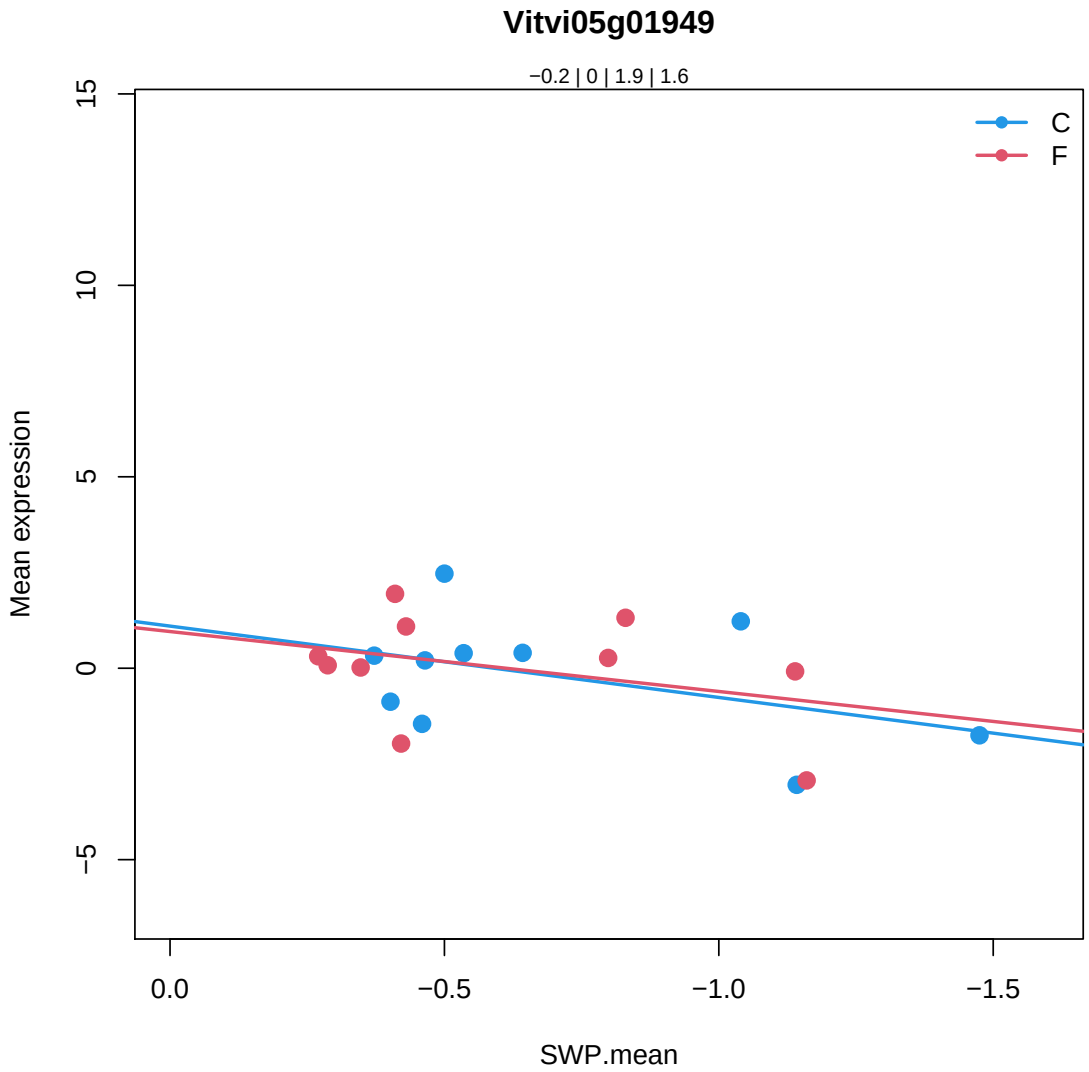
7.2.30 Vitvi05g01949: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01949
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi05g01949.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.210327	0.6149165		0.6202063	
SlopeC	1.863721	0.1185711		0.6360742	
MeanF-MeanC	0.2148942	0.7158808		0.9126186	
SlopeF-SlopeC	-0.2986706	0.8626698		0.9999488	



7.2.31 Vitvi19g01964: * type1

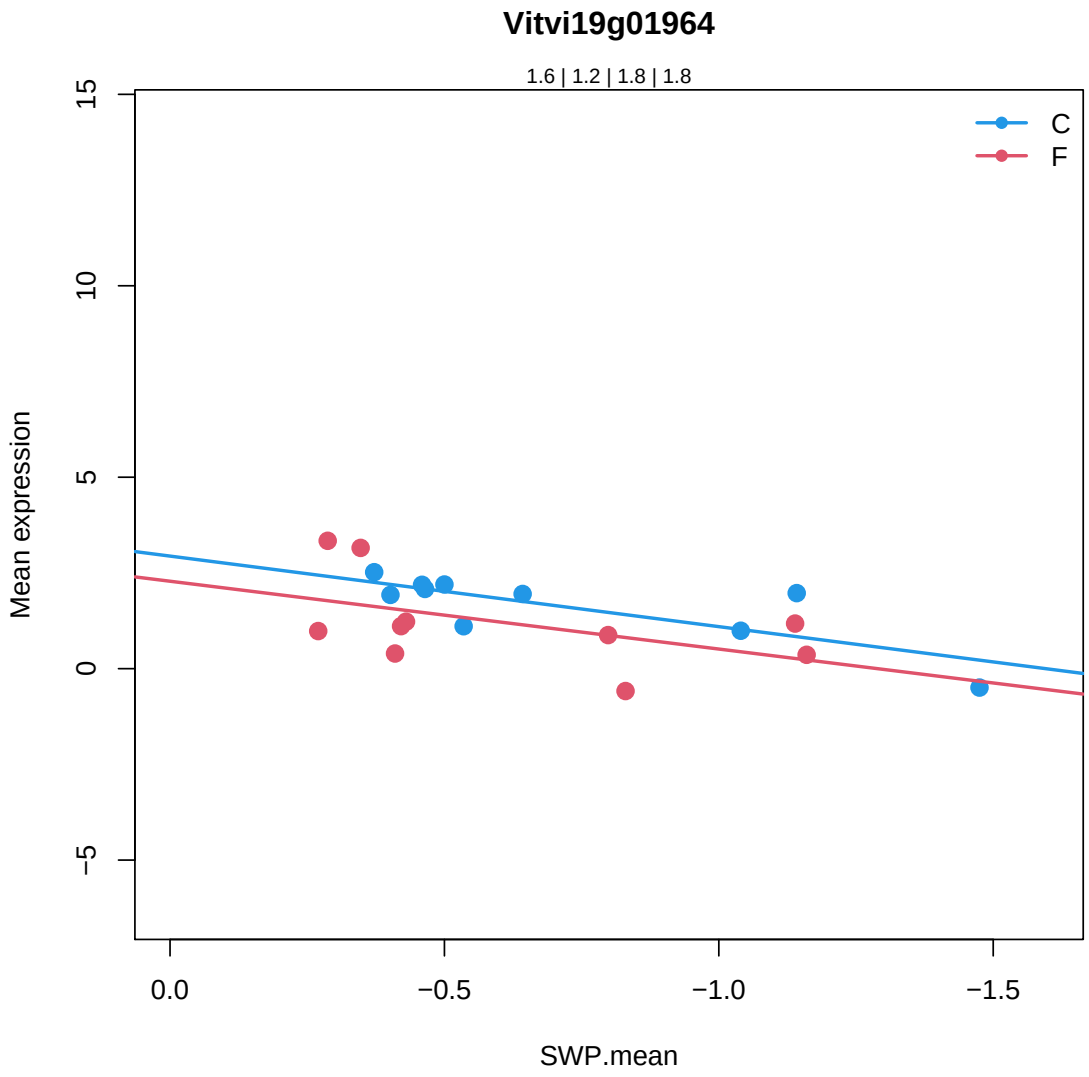
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
Vitvi19g01964
        29.4
        protein.postranslational modification
        S-locus lectin protein kinase family protein |
        Chr4:13666281-13669202 FORWARD LENGTH=829 |
        201606

Vitvi19g01964
        35.2
        not assigned.unknown
        S-locus lectin protein kinase family protein |
        Chr4:13666281-13669202 FORWARD LENGTH=829 |
        201606

Vitvi19g01964
        30.2.24
        signalling.receptor kinases.S-locus glycoprotein like
        S-locus lectin protein kinase family protein |
        Chr4:13666281-13669202 FORWARD LENGTH=829 |
        201606
```

Coefficients for Vitvi19g01964.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.64409	1.835565e-06	***	2.106436e-06	***
SlopeC	1.842262	0.01622166	*	0.3486596	
MeanF-MeanC	-0.4402879	0.233247		0.5881143	
SlopeF-SlopeC	-0.07120019	0.946614		0.9999488	


Vitvi19g01964
1.6 | 1.2 | 1.8 | 1.8
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

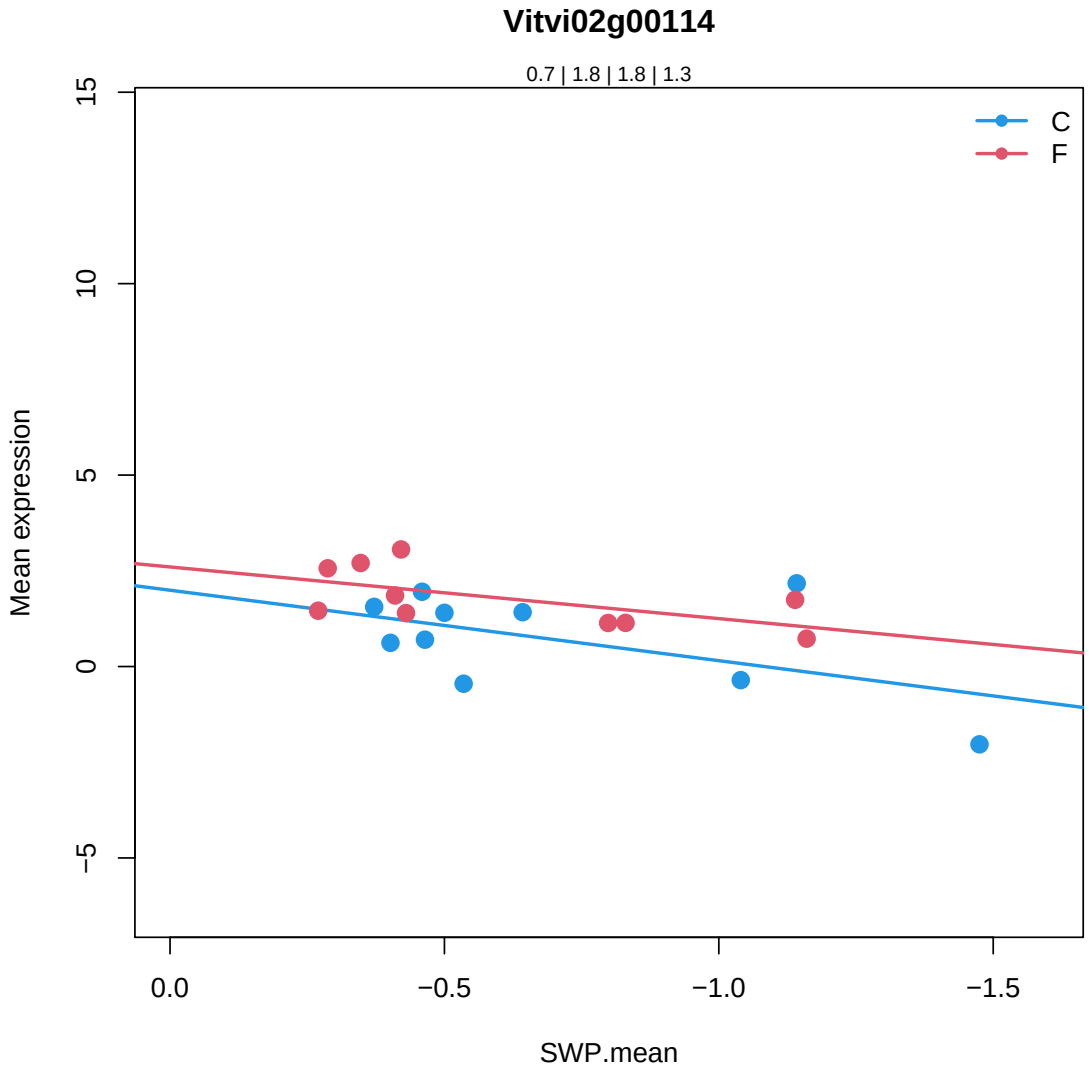
7.2.32 Vitvi02g00114: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00114
        27.3.32
        RNA.regulation of transcription.WRKY domain transcription factor famil
        WRKY family transcription factor |
        Chr4:12392666-12393739 REVERSE LENGTH=324 |
        201606
```

Coefficients for Vitvi02g00114.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6986666	0.01716135	*	0.01807569	*
SlopeC	1.839945	0.0231704	*	0.3983963	
MeanF-MeanC	1.079523	0.01006937	*	0.07647104	.
SlopeF-SlopeC	-0.4907263	0.6656208		0.9999488	



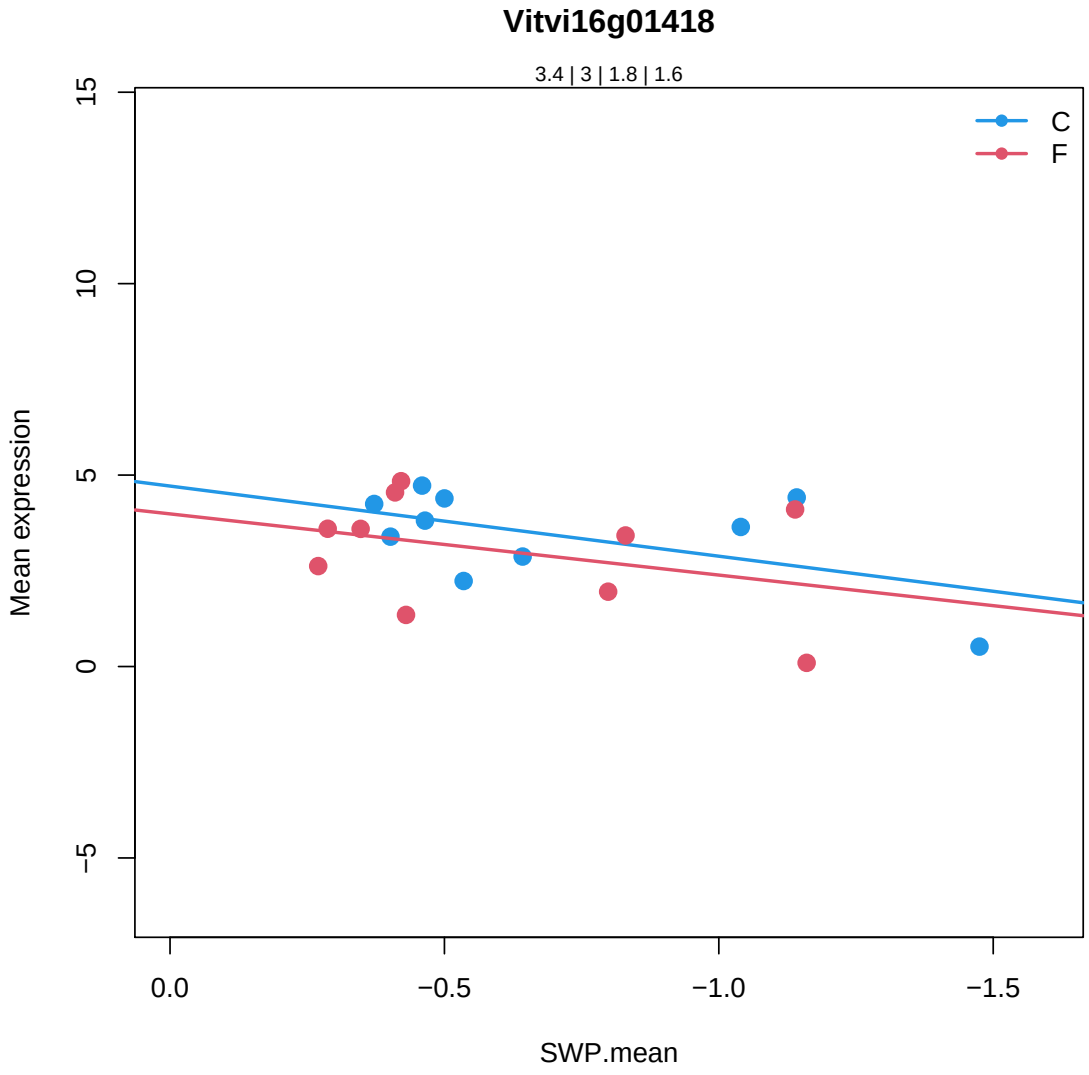
7.2.33 Vitvi16g01418: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01418
        10.8.1
        cell wall.pectinesterases.PME
        Plant invertase/pectin methylesterase inhibitor superfamily |
        Chr3:18249840-18253647 FORWARD LENGTH=598 |
        201606
```

Coefficients for Vitvi16g01418.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.4248	5.790718e-09	***	7.120784e-09	***
SlopeC	1.831717	0.08845111	.	0.5943767	
MeanF-MeanC	-0.4121328	0.4381749		0.7700124	
SlopeF-SlopeC	-0.2337712	0.8797968		0.9999488	



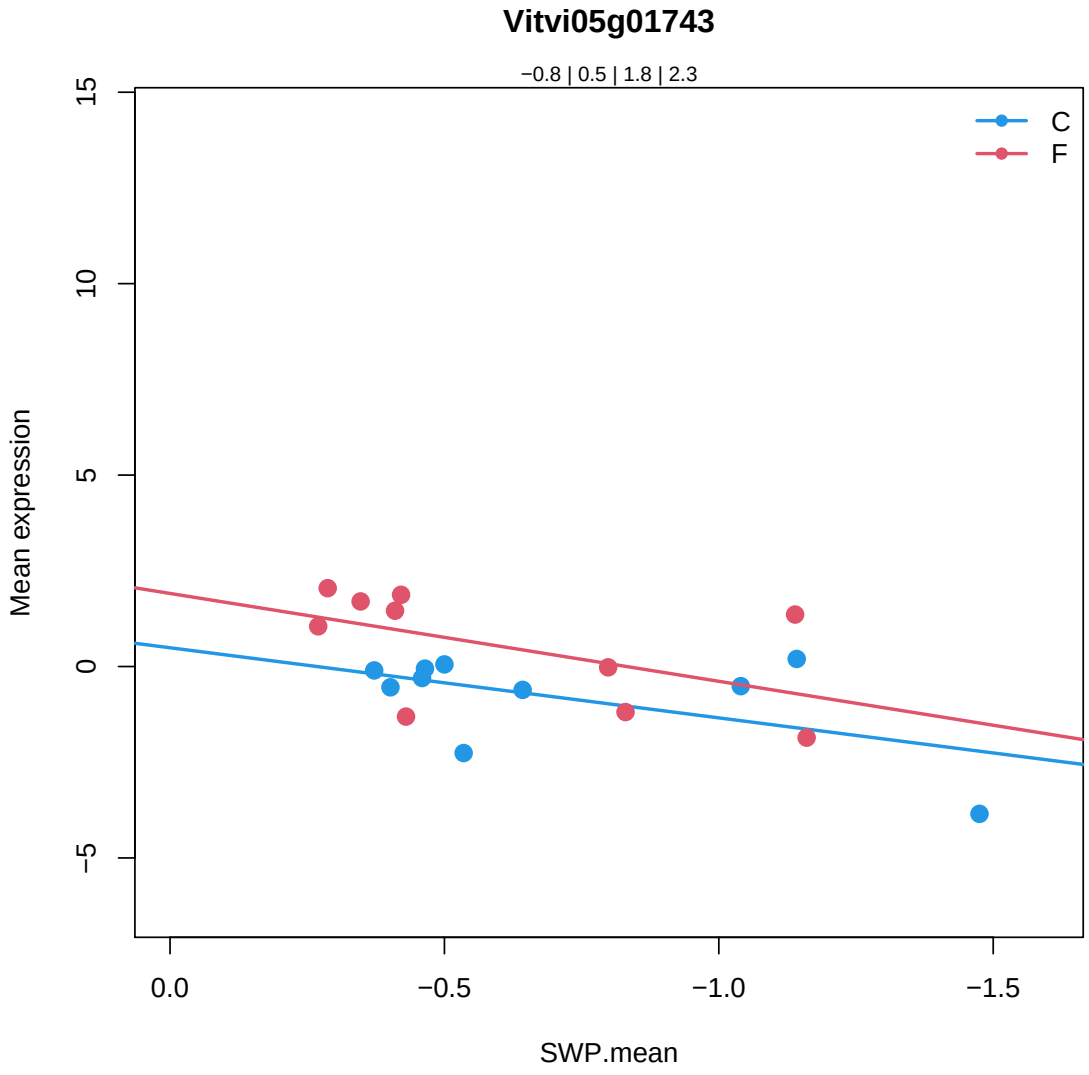
7.2.34 Vitvi05g01743: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01743
        35.2
        not assigned.unknown
        hypothetical protein |
        Chr3:2156930-2157624 FORWARD LENGTH=187 |
        201606
```

Coefficients for Vitvi05g01743.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.797796	0.03105648	*	0.03249333	*
SlopeC	1.831631	0.07034412	.	0.5604792	
MeanF-MeanC	1.308384	0.01397497	*	0.0970417	.
SlopeF-SlopeC	0.4631932	0.7493807		0.9999488	



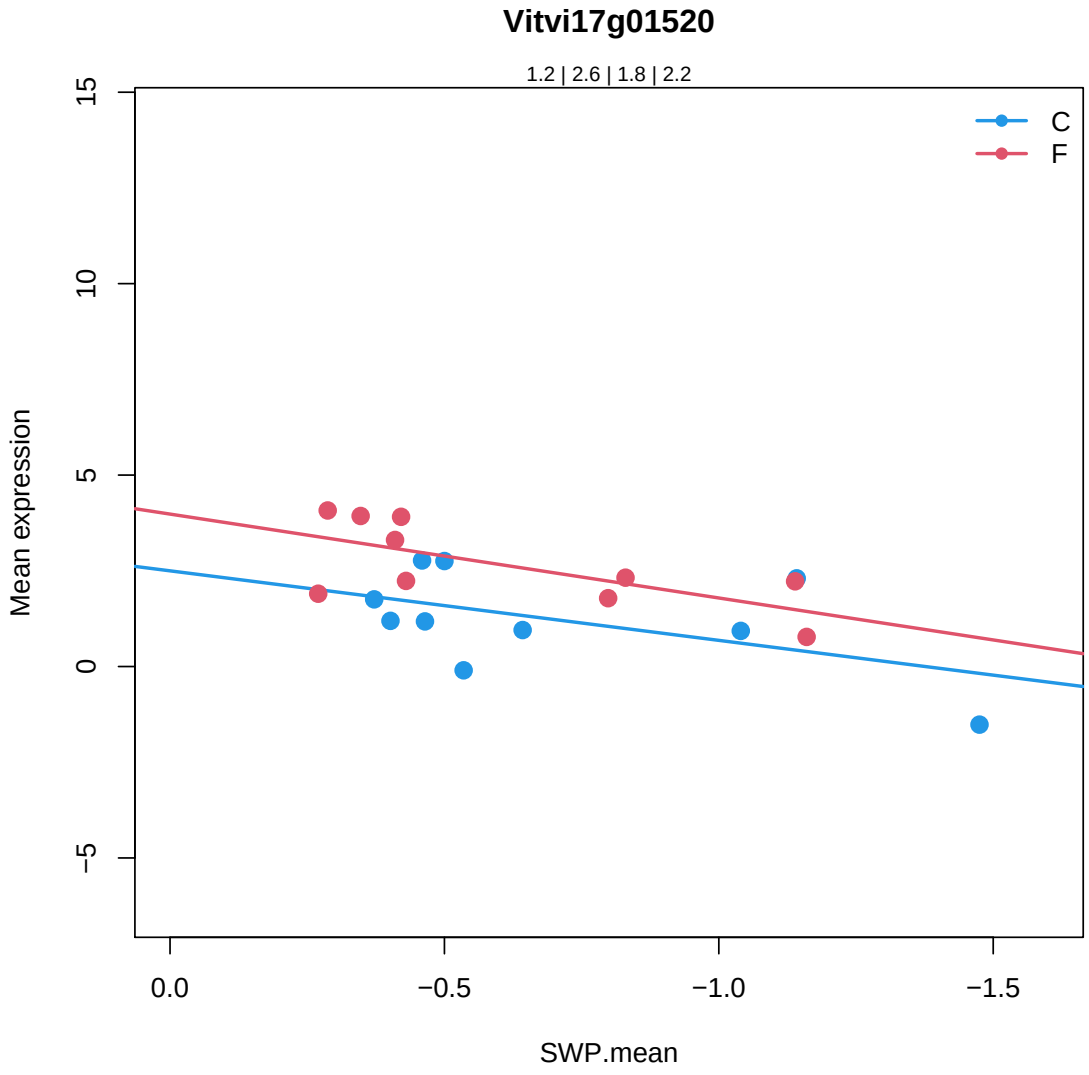
7.2.35 Vitvi17g01520: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g01520
        20.1.7.1
        stress.biotic.PR-proteins.PR1 (antifungal)
        alpha/beta-Hydrolases superfamily protein |
        Chr3:17755553-17757292 REVERSE LENGTH=515 |
        201606
```

Coefficients for Vitvi17g01520.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.221775	0.0004318051	***	0.0004709533	***
SlopeC	1.815974	0.03731855	*	0.4620709	
MeanF-MeanC	1.424372	0.002485011	**	0.02626667	*
SlopeF-SlopeC	0.3752235	0.7609075		0.9999488	



7.2.36 Vitvi05g00953: type1

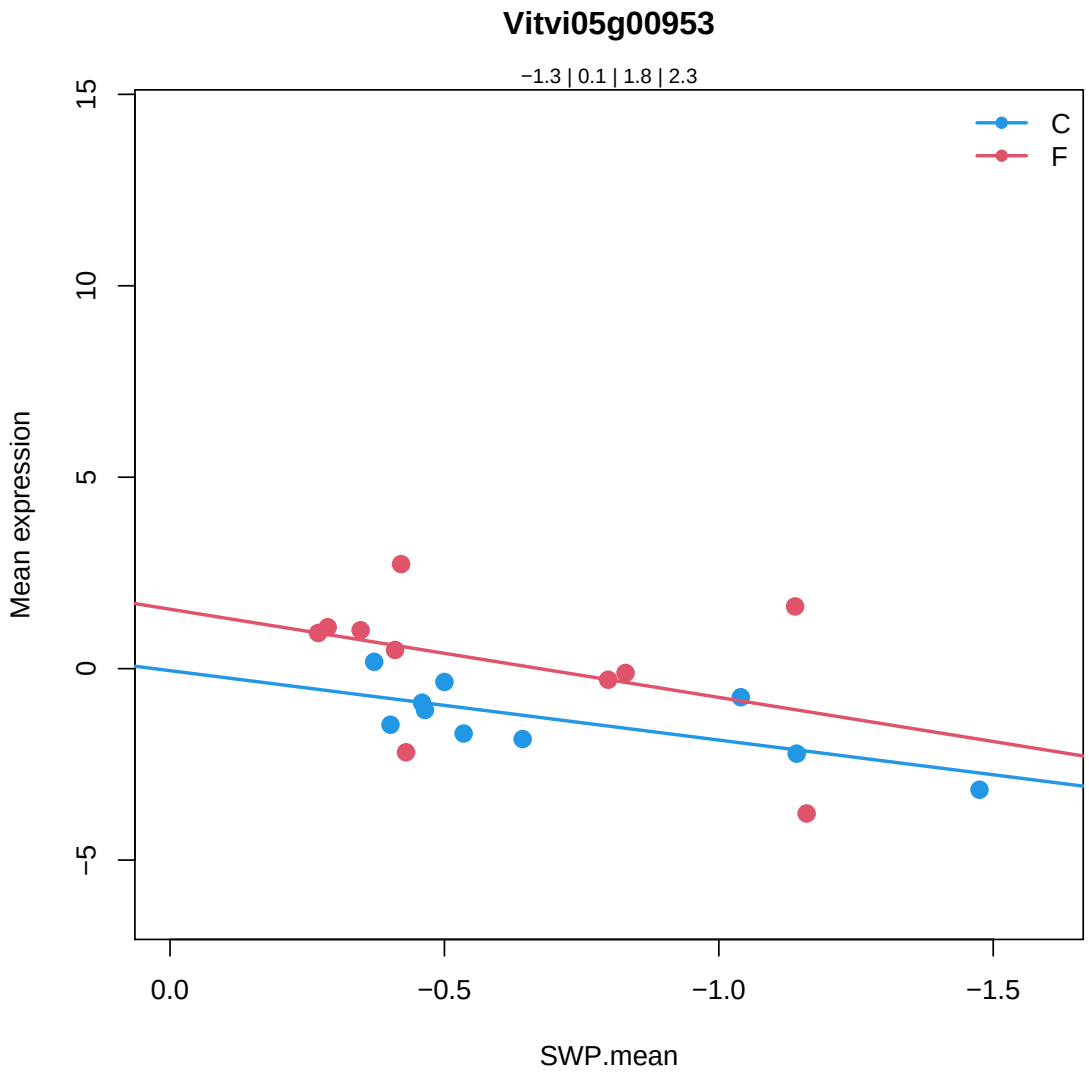
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00953
        35.2
        not assigned.unknown
        Pectin lyase-like superfamily protein |
        Chr3:2212973-2214614 REVERSE LENGTH=383 |
        201606

Vitvi05g00953
        10.6.3
        cell wall.degradation.pectate lyases and polygalacturonases
        Pectin lyase-like superfamily protein |
        Chr3:2212973-2214614 REVERSE LENGTH=383 |
        201606
```

Coefficients for Vitvi05g00953.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.327067	0.002475979	**	0.002656732	**
SlopeC	1.81224	0.1070398		0.6223948	
MeanF-MeanC	1.475956	0.01340097	*	0.09434534	.
SlopeF-SlopeC	0.4911137	0.7623402		0.9999488	


Vitvi05g00953
−1.3 | 0.1 | 1.8 | 2.3
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

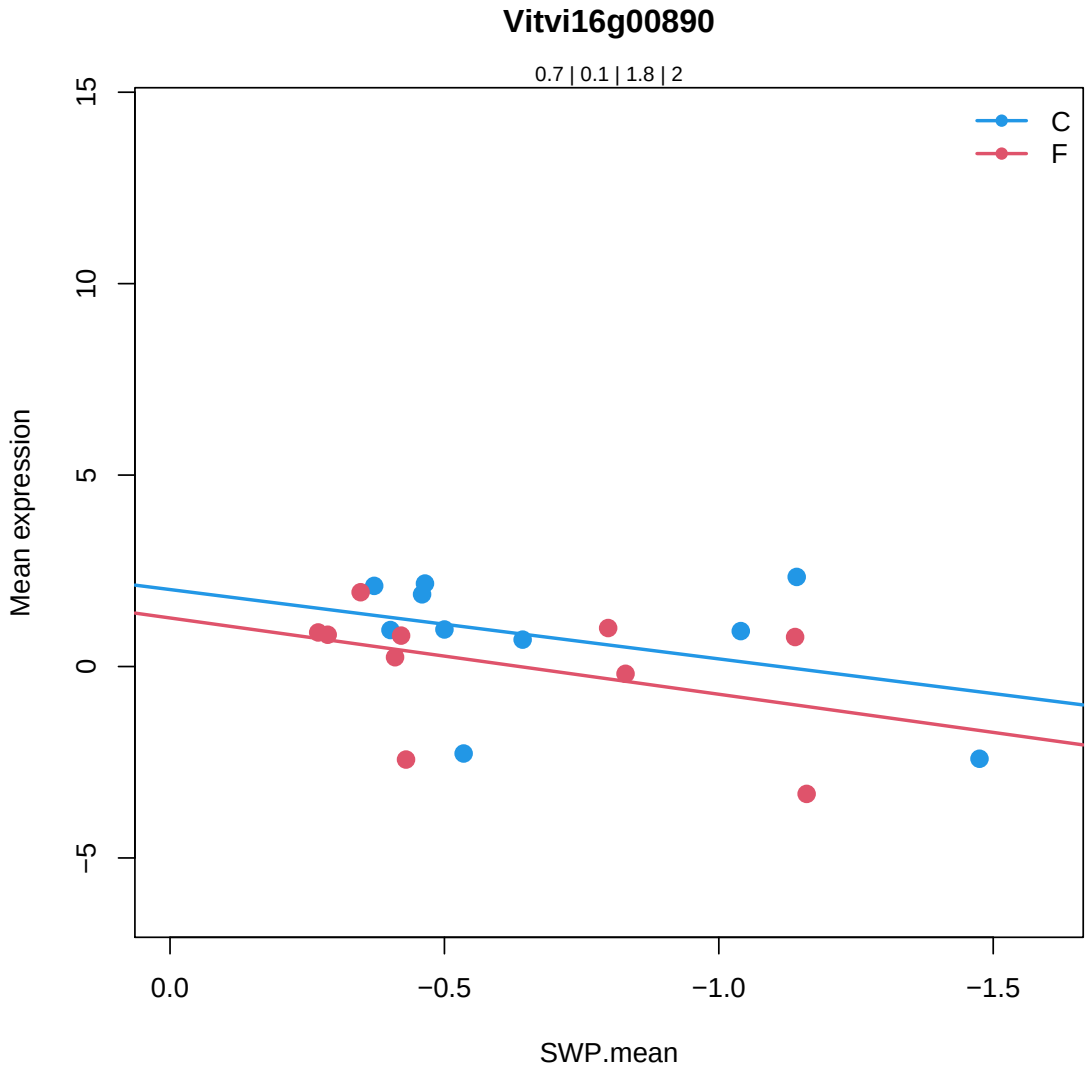
7.2.37 Vitvi16g00890: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g00890
        17.6.1.11
        hormone metabolism.gibberelin.synthesis-degradation.GA20 oxidase
        2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protei
        Chr4:12991325-12992409 REVERSE LENGTH=297 |
        201606
```

Coefficients for Vitvi16g00890.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.7365445	0.1196838		0.1235253	
SlopeC	1.811372	0.1663686		0.6963267	
MeanF-MeanC	-0.6827218	0.2999173		0.6662078	
SlopeF-SlopeC	0.1812594	0.9241587		0.9999488	



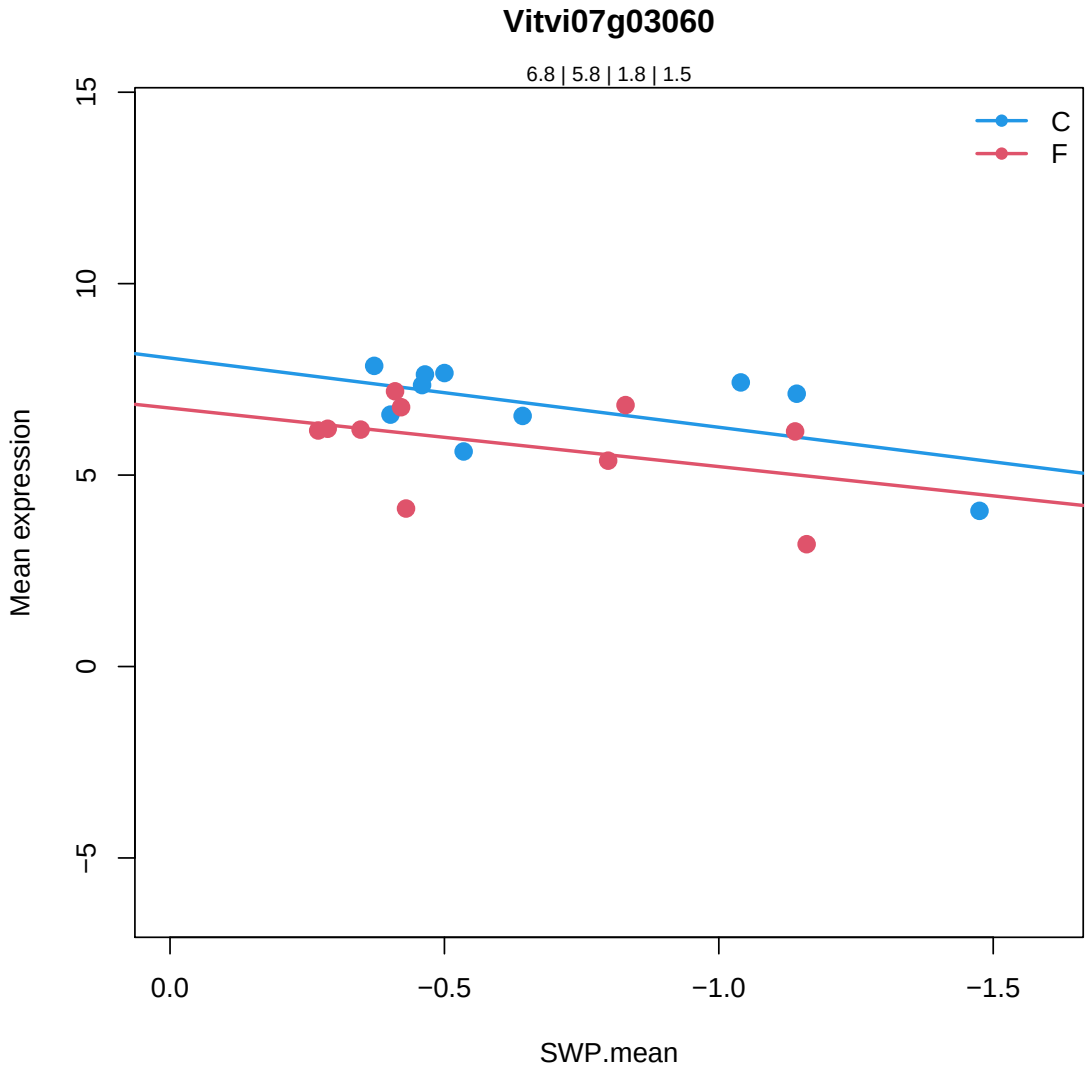
7.2.38 Vitvi07g03060: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g03060
        35.2
        not assigned.unknown
        xyloglucan endotransglucosylase/hydrolase 7 |
        Chr4:17775703-17777372 REVERSE LENGTH=293 |
        201606
```

Coefficients for Vitvi07g03060.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.784736	4.977596e-16	***	9.696896e-16	***
SlopeC	1.806511	0.05116526	.	0.5115585	
MeanF-MeanC	-0.9661227	0.04110897	*	0.2102067	
SlopeF-SlopeC	-0.2781636	0.8328067		0.9999488	



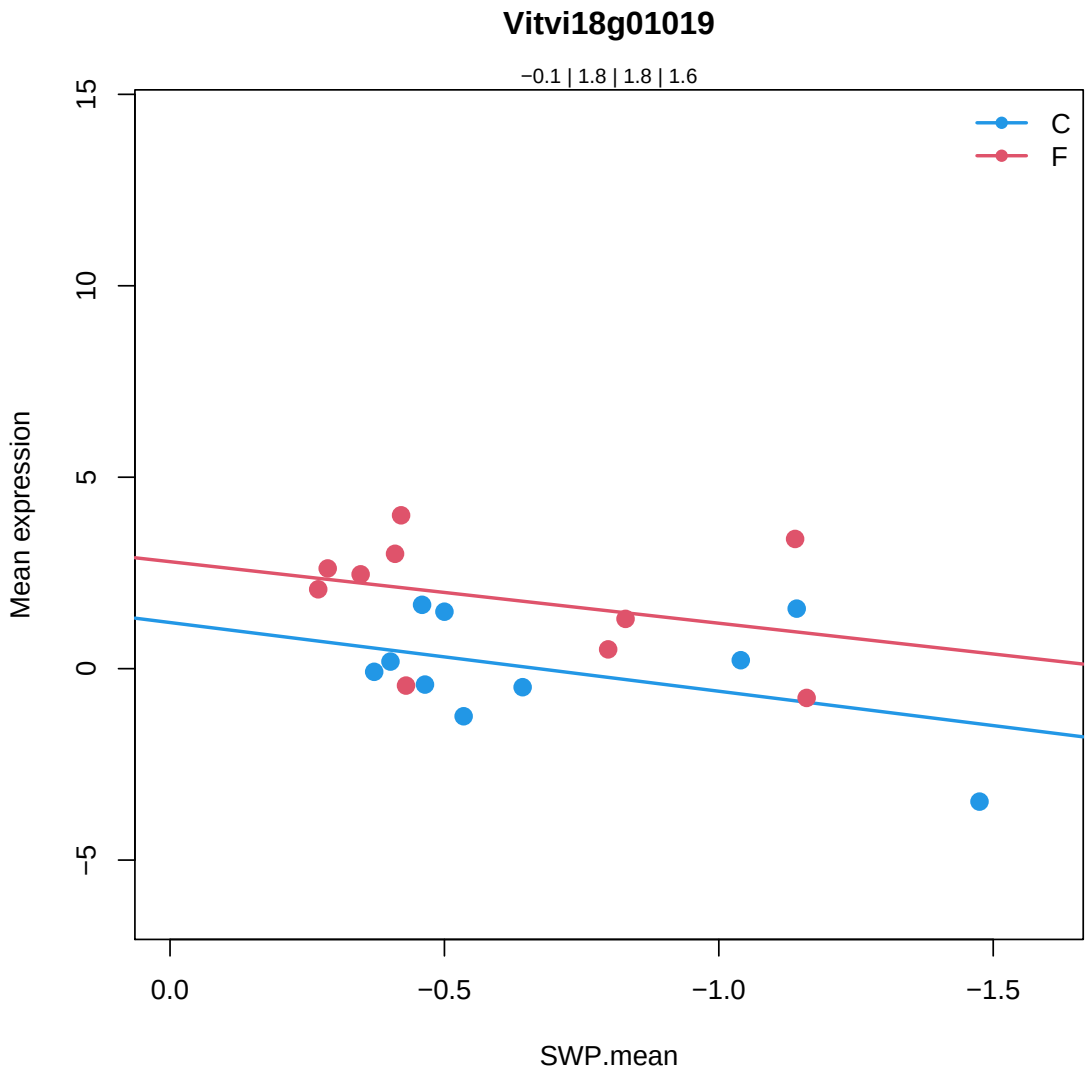
7.2.39 Vitvi18g01019: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
Vitvi18g01019
        17.4.1
        hormone metabolism.cytokinin.synthesis-degradation
        cytokinin oxidase 5 |
        Chr1:28315248-28318064 REVERSE LENGTH=540 |
        201606

Vitvi18g01019
        35.2
        not assigned.unknown
        cytokinin oxidase 5 |
        Chr1:28315248-28318064 REVERSE LENGTH=540 |
        201606
```

Coefficients for Vitvi18g01019.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.05724541	0.8950899		0.8975041	
SlopeC	1.79425	0.1473439		0.6736918	
MeanF-MeanC	1.871392	0.005526883	**	0.04935017	*
SlopeF-SlopeC	-0.1871561	0.9170727		0.9999488	


Vitvi18g01019
−0.1 | 1.8 | 1.8 | 1.6
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

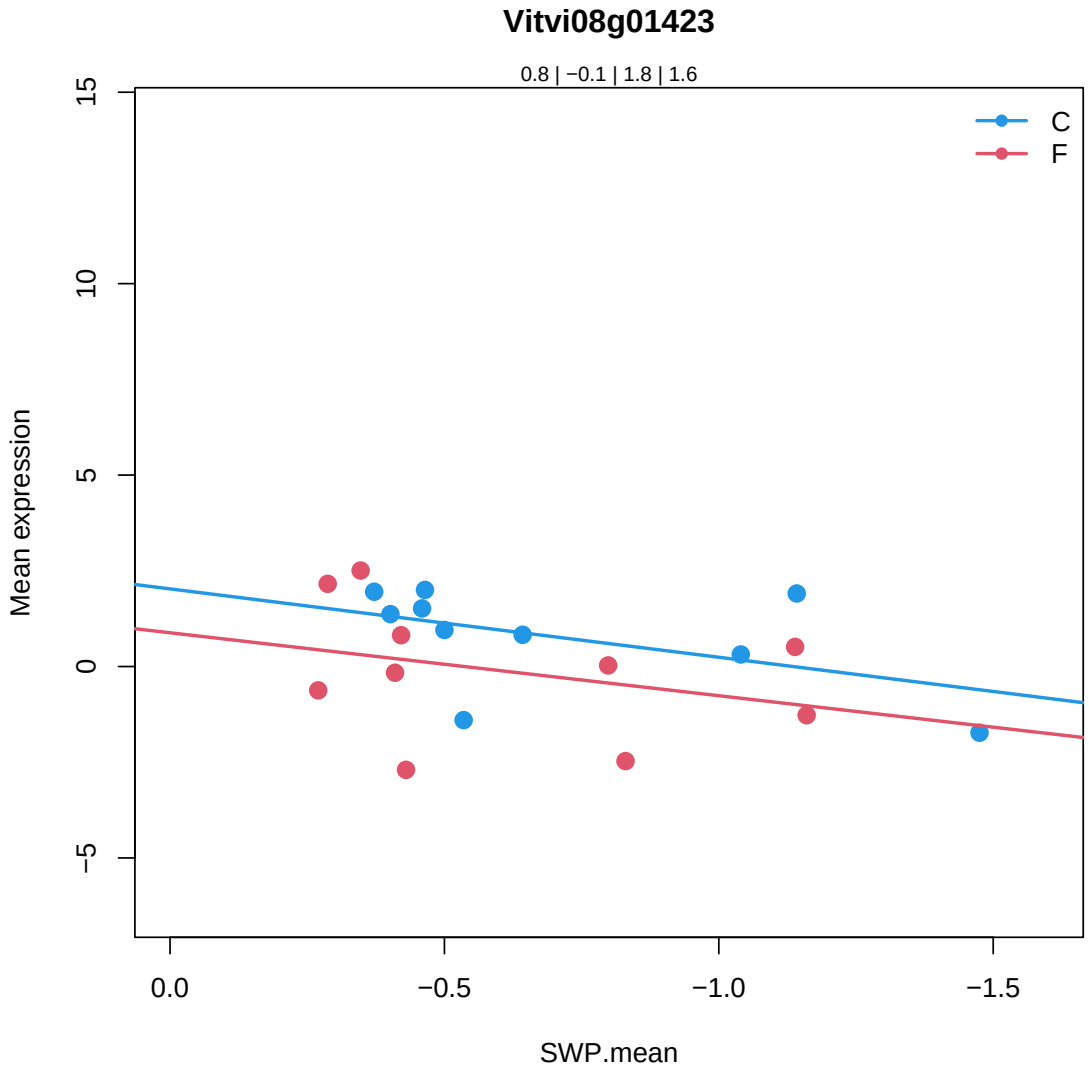
7.2.40 Vitvi08g01423: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01423
        33.99
        development.unspecified
        Transducin/WD40 repeat-like superfamily protein |
        Chr1:4395114-4396154 REVERSE LENGTH=346 |
        201606
```

Coefficients for Vitvi08g01423.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.7717173	0.07992995	.	0.08284322	.
SlopeC	1.786032	0.1408532		0.6676582	
MeanF-MeanC	-0.8919507	0.1476043		0.462538	
SlopeF-SlopeC	-0.1420339	0.9356415		0.9999488	



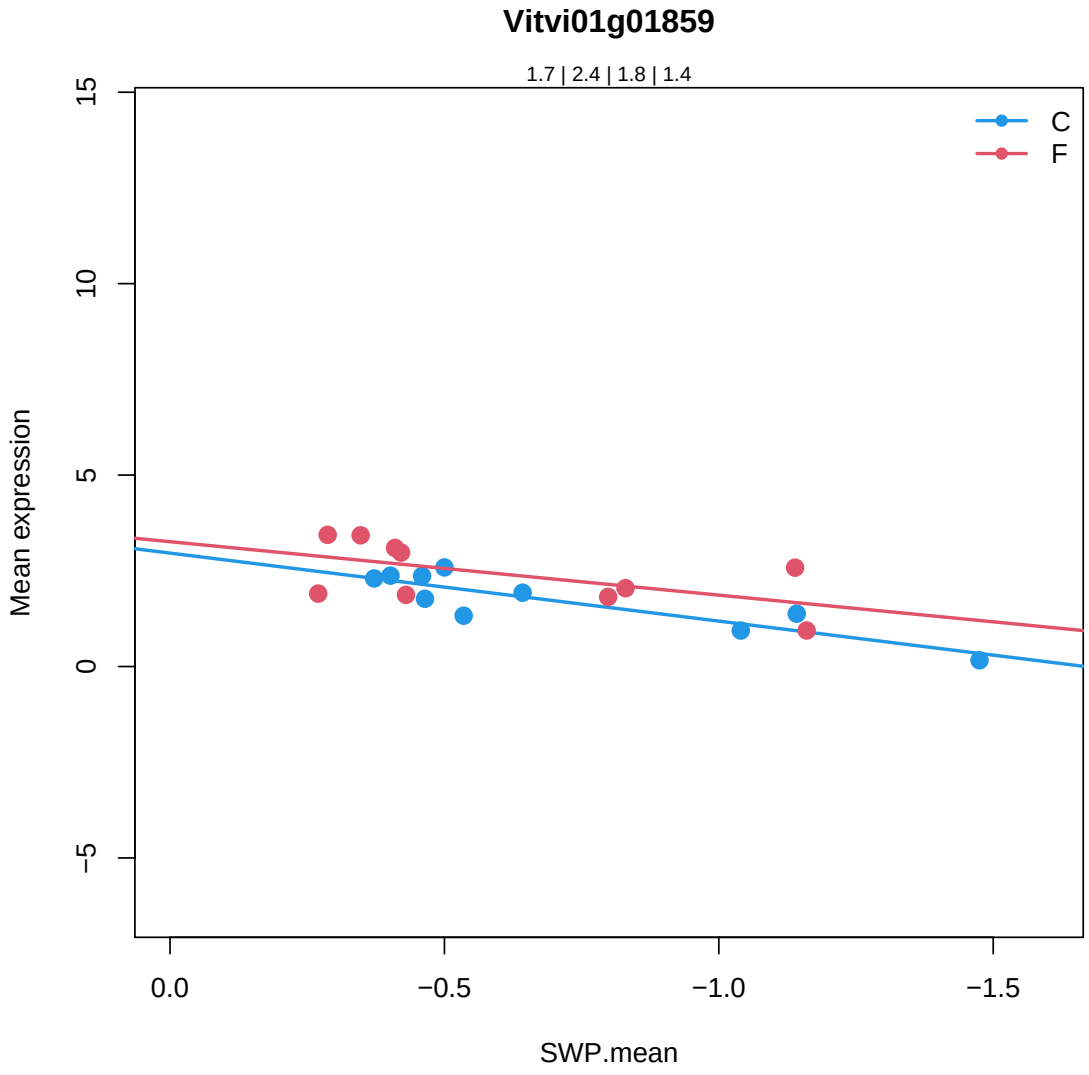
7.2.41 Vitvi01g01859: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01859
        34.3
        transport.amino acids
        cationic amino acid transporter 5 |
        Chr2:14744175-14745884 REVERSE LENGTH=569 |
        201606
```

Coefficients for Vitvi01g01859.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.713228	2.218647e-09	***	2.765733e-09	***
SlopeC	1.776255	0.001440988	**	0.1479249	
MeanF-MeanC	0.6967432	0.01012655	*	0.07671412	.
SlopeF-SlopeC	-0.3812887	0.6035584		0.9999488	



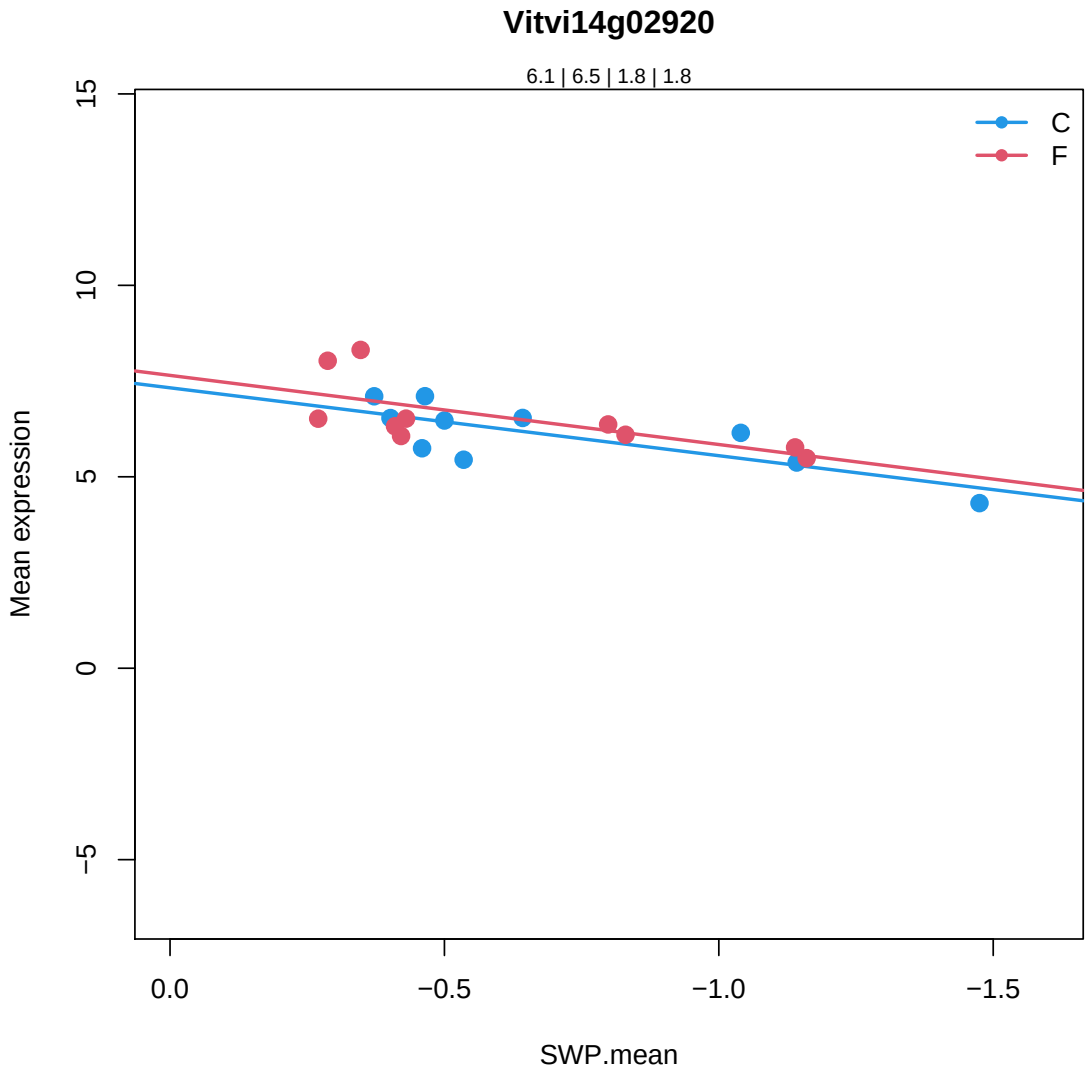
7.2.42 Vitvi14g02920: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g02920
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi14g02920.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.076921	2.414801e-19	***	1.009224e-18	***
SlopeC	1.773165	0.00361041	**	0.2248659	
MeanF-MeanC	0.471545	0.1018388		0.3683906	
SlopeF-SlopeC	0.0325679	0.9682127		0.9999488	



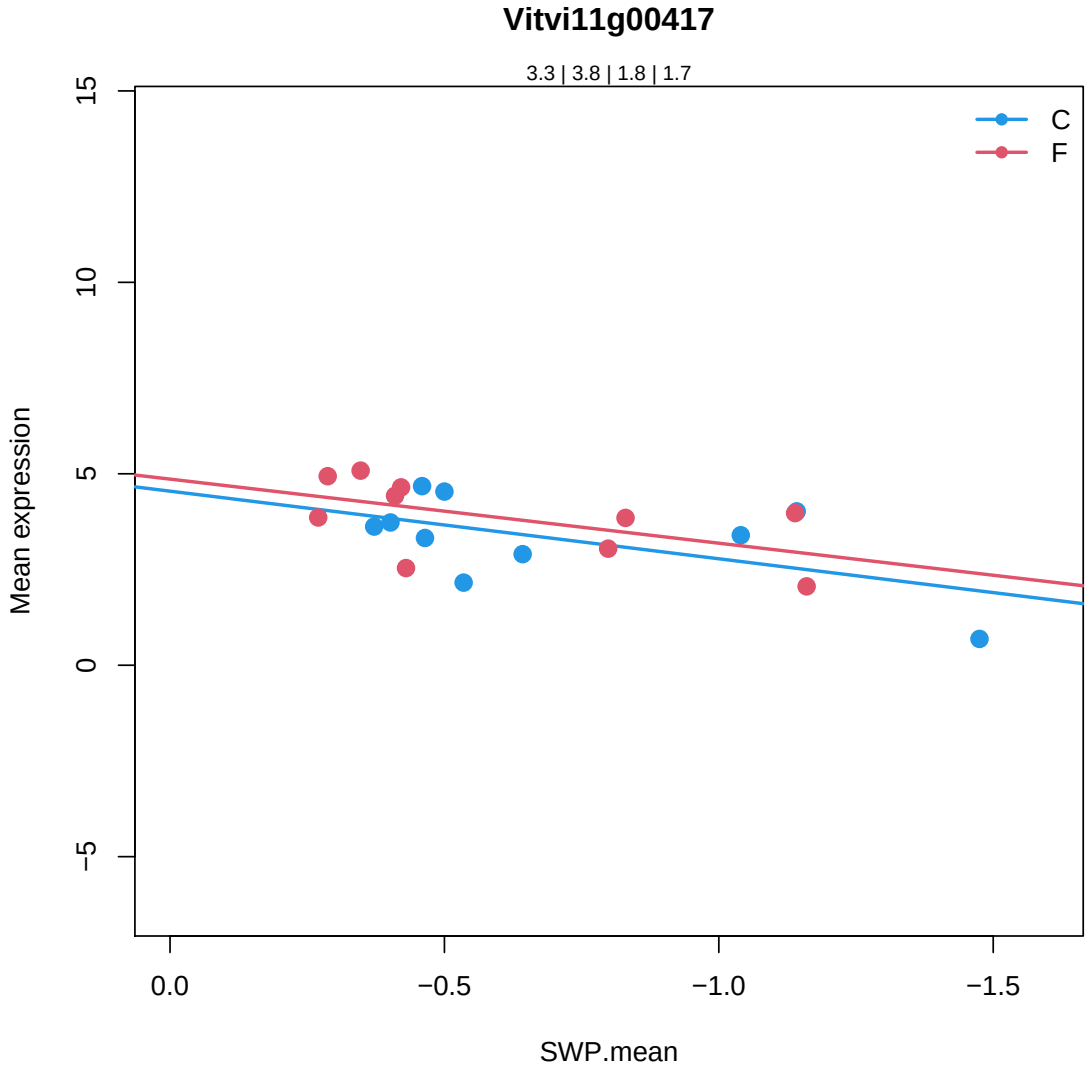
7.2.43 Vitvi11g00417: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00417
        35.2
        not assigned.unknown
        Blight-associated protein P12 (Fragment) IPR007112 Expansin 45, endogl
```

Coefficients for Vitvi11g00417.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.304206	5.030692e-11	***	6.663001e-11	***
SlopeC	1.766152	0.03041745	*	0.4320841	
MeanF-MeanC	0.5367591	0.1800678		0.5148802	
SlopeF-SlopeC	-0.09280912	0.9355396		0.9999488	



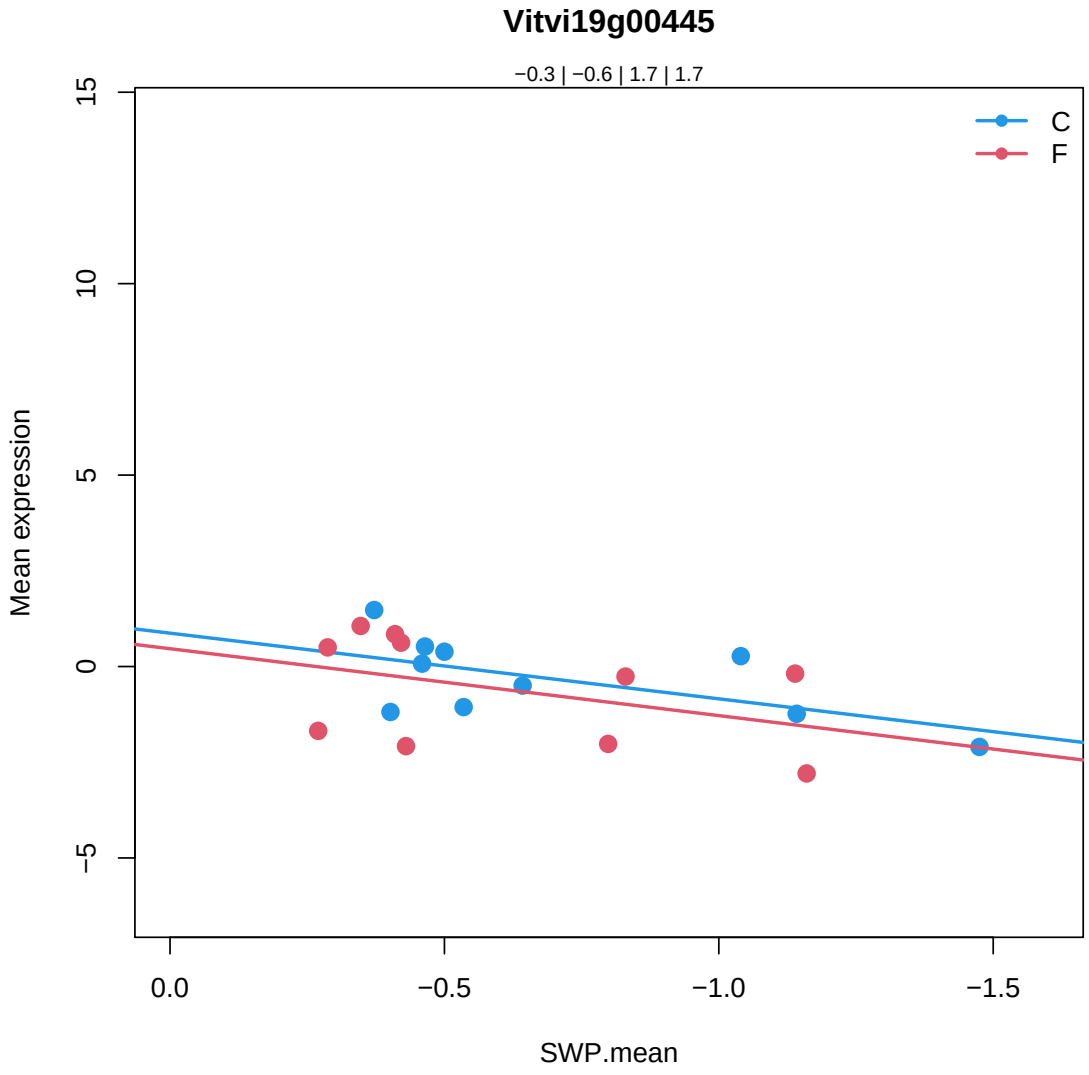
7.2.44 Vitvi19g00445: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g00445
        26.19
        misc.plastocyanin-like
        early nodulin-like protein 9 |
        Chr3:7186754-7187453 REVERSE LENGTH=203 |
        201606
```

Coefficients for Vitvi19g00445.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.3349494	0.3131867		0.3189624	
SlopeC	1.714973	0.07085602	.	0.5619081	
MeanF-MeanC	-0.2646416	0.5699285		0.8461686	
SlopeF-SlopeC	0.03205397	0.9811773		0.9999488	



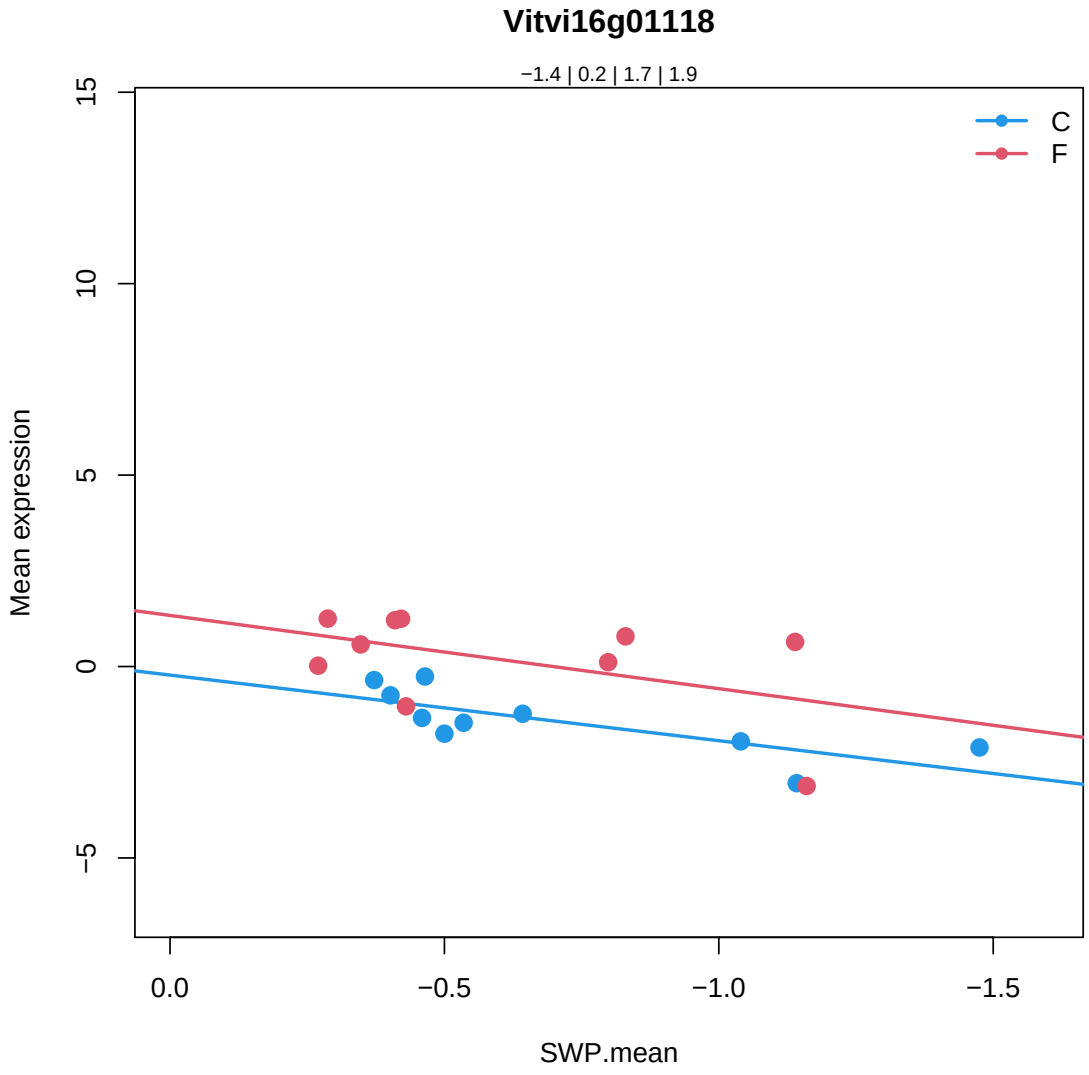
7.2.45 Vitvi16g01118: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01118
        31.1
        cell.organisation
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi16g01118.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.428624	4.13253e-05	***	4.599681e-05	***
SlopeC	1.71423	0.03784566	*	0.4650681	
MeanF-MeanC	1.597388	0.0005472244	***	0.007561917	**
SlopeF-SlopeC	0.1988921	0.8646378		0.9999488	



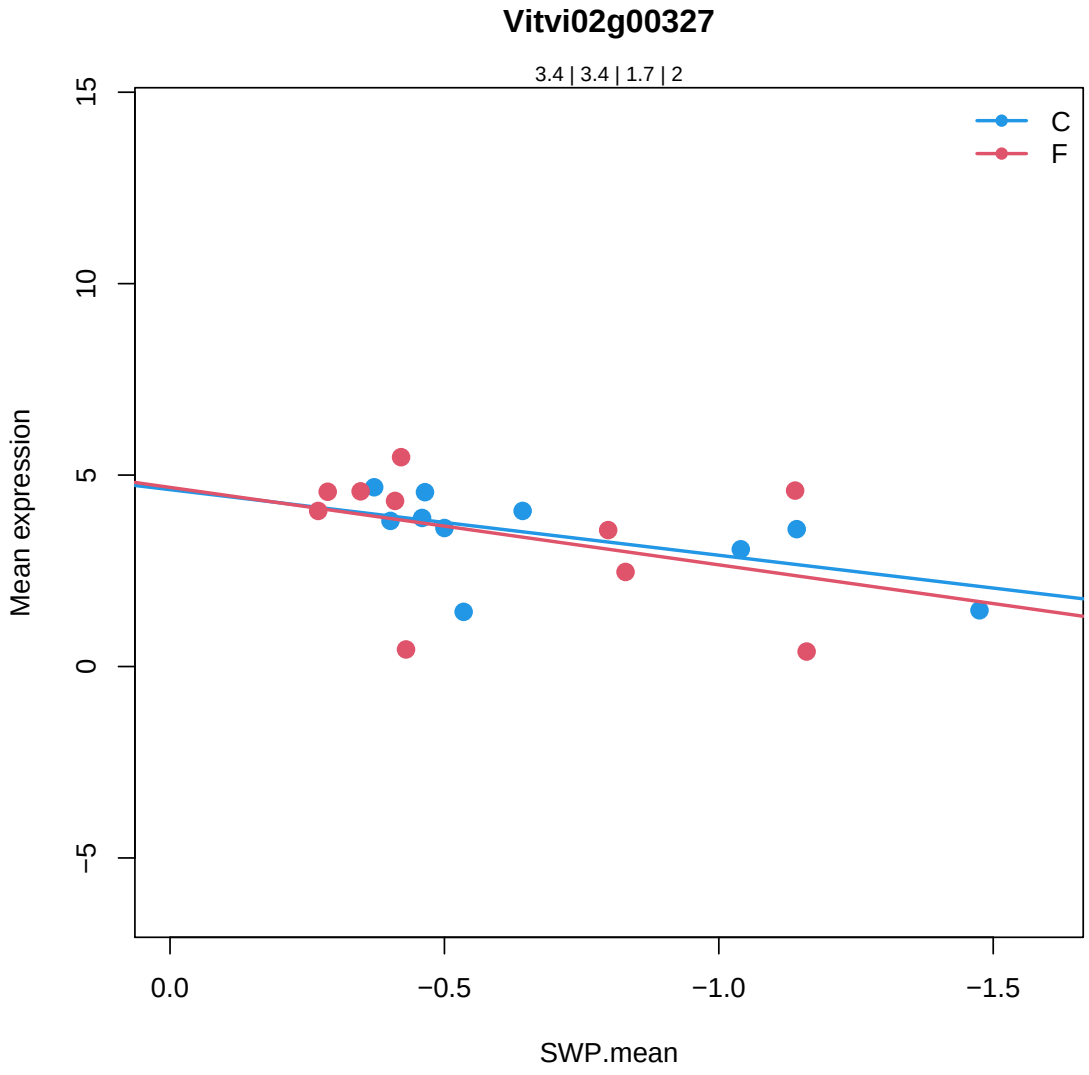
7.2.46 Vitvi02g00327: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00327
        31.1
        cell.organisation
        tubulin beta 8 |
        Chr5:8042962-8044528 FORWARD LENGTH=449 |
        201606
```

Coefficients for Vitvi02g00327.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.414548	1.831356e-08	***	2.218e-08	***
SlopeC	1.713415	0.1320727		0.6544384	
MeanF-MeanC	0.03133804	0.9555981		0.9897544	
SlopeF-SlopeC	0.3093124	0.8511772		0.9999488	



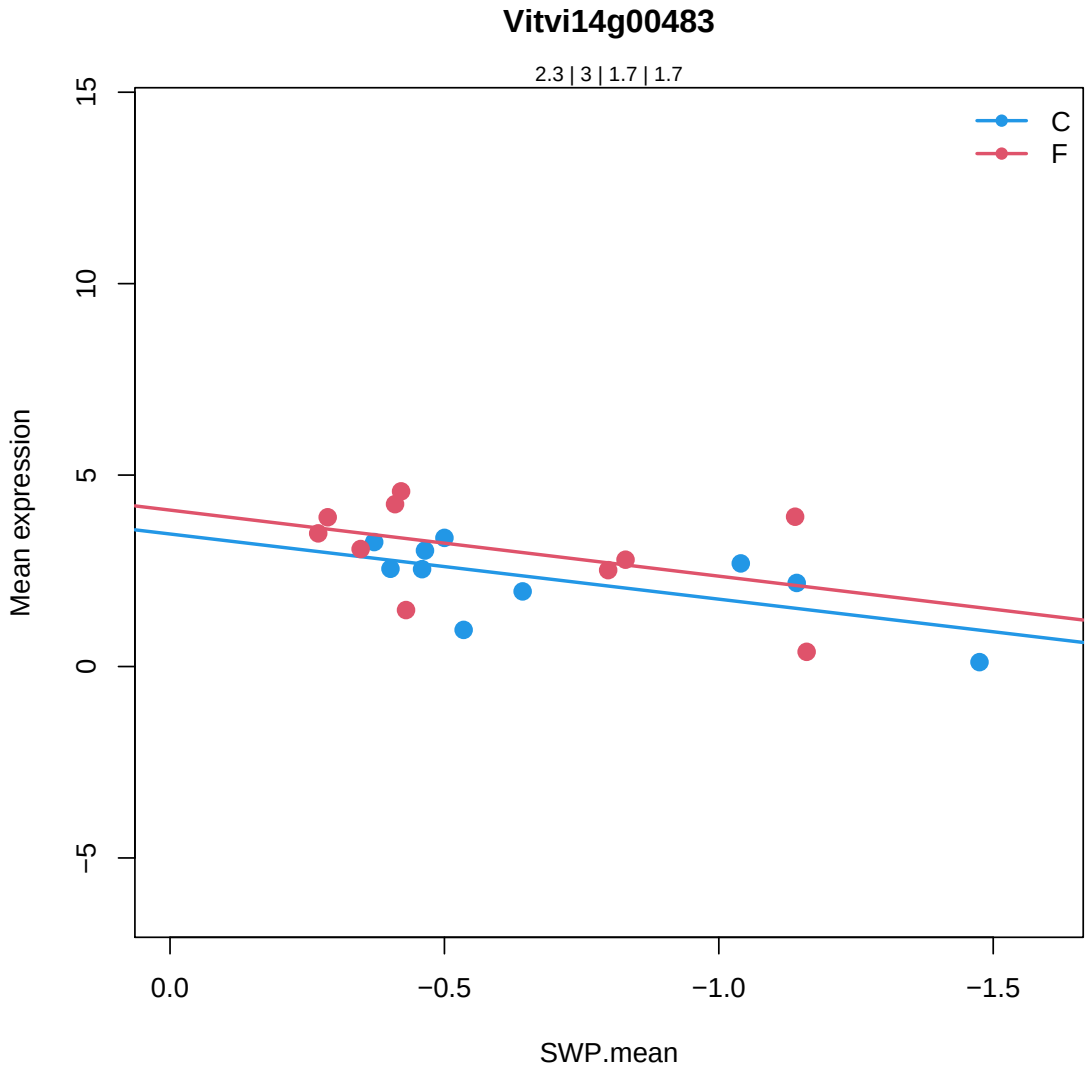
7.2.47 Vitvi14g00483: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g00483
        27.3.40
        RNA.regulation of transcription.AUX/IAA family
        AUX/IAA transcriptional regulator family protein |
        Chr5:17550465-17551206 FORWARD LENGTH=186 |
        201606
```

Coefficients for Vitvi14g00483.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.264275	1.777948e-07	***	2.094727e-07	***
SlopeC	1.702212	0.05369344	.	0.519002	
MeanF-MeanC	0.7694255	0.08347577	.	0.3271632	
SlopeF-SlopeC	0.02318897	0.9852646		0.9999488	



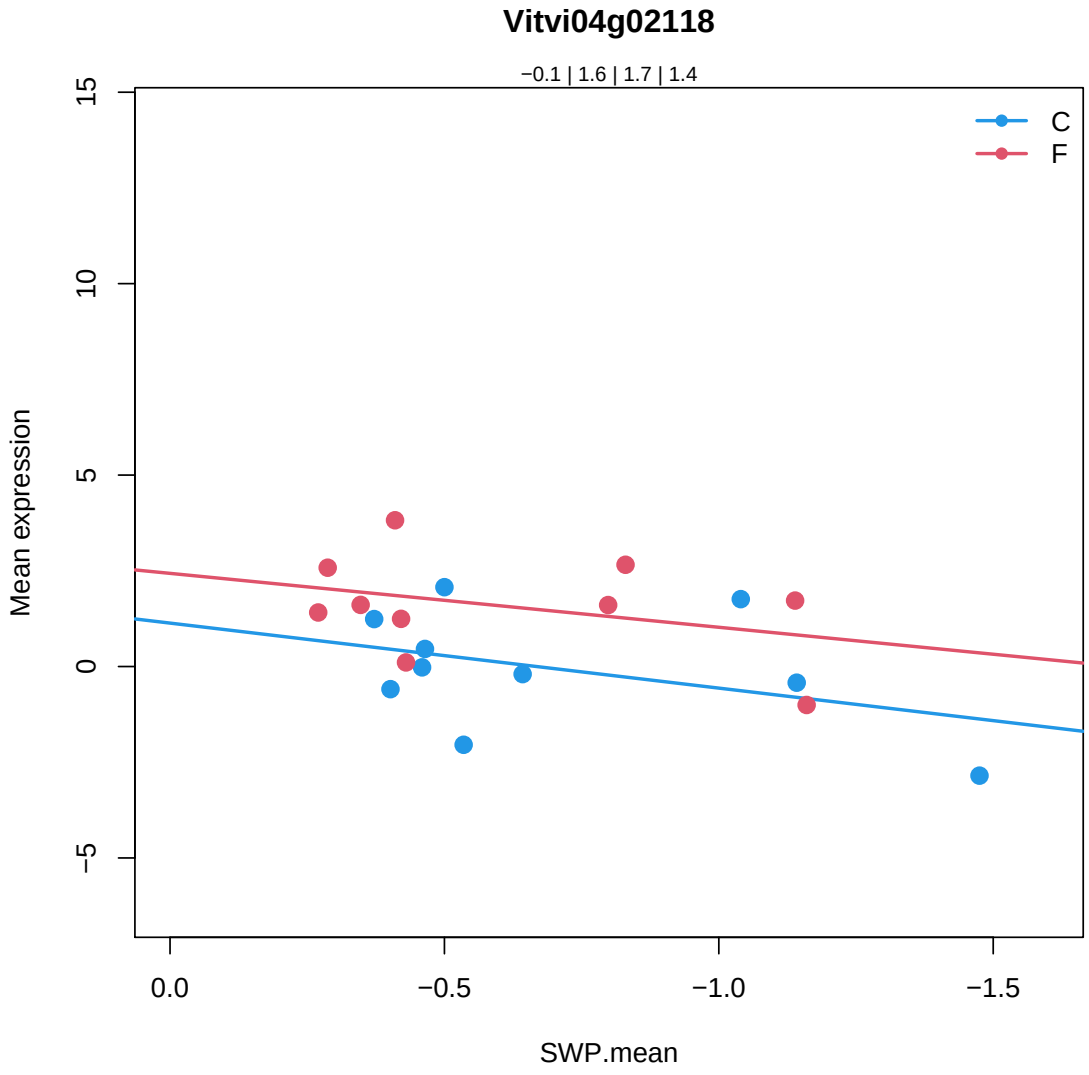
7.2.48 Vitvi04g02118: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g02118
        17.8.1.1.7
        hormone metabolism.salicylic acid.synthesis-degradation.synthesis.meth
        S-adenosyl-L-methionine-dependent methyltransferases superfamily prote
        Chr3:3614544-3617137 FORWARD LENGTH=379 |
        201606
```

Coefficients for Vitvi04g02118.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.05986017	0.8812865		0.8837798	
SlopeC	1.698116	0.1379482		0.6650191	
MeanF-MeanC	1.635175	0.008085224	**	0.06489467	.
SlopeF-SlopeC	-0.2899153	0.8613533		0.9999488	



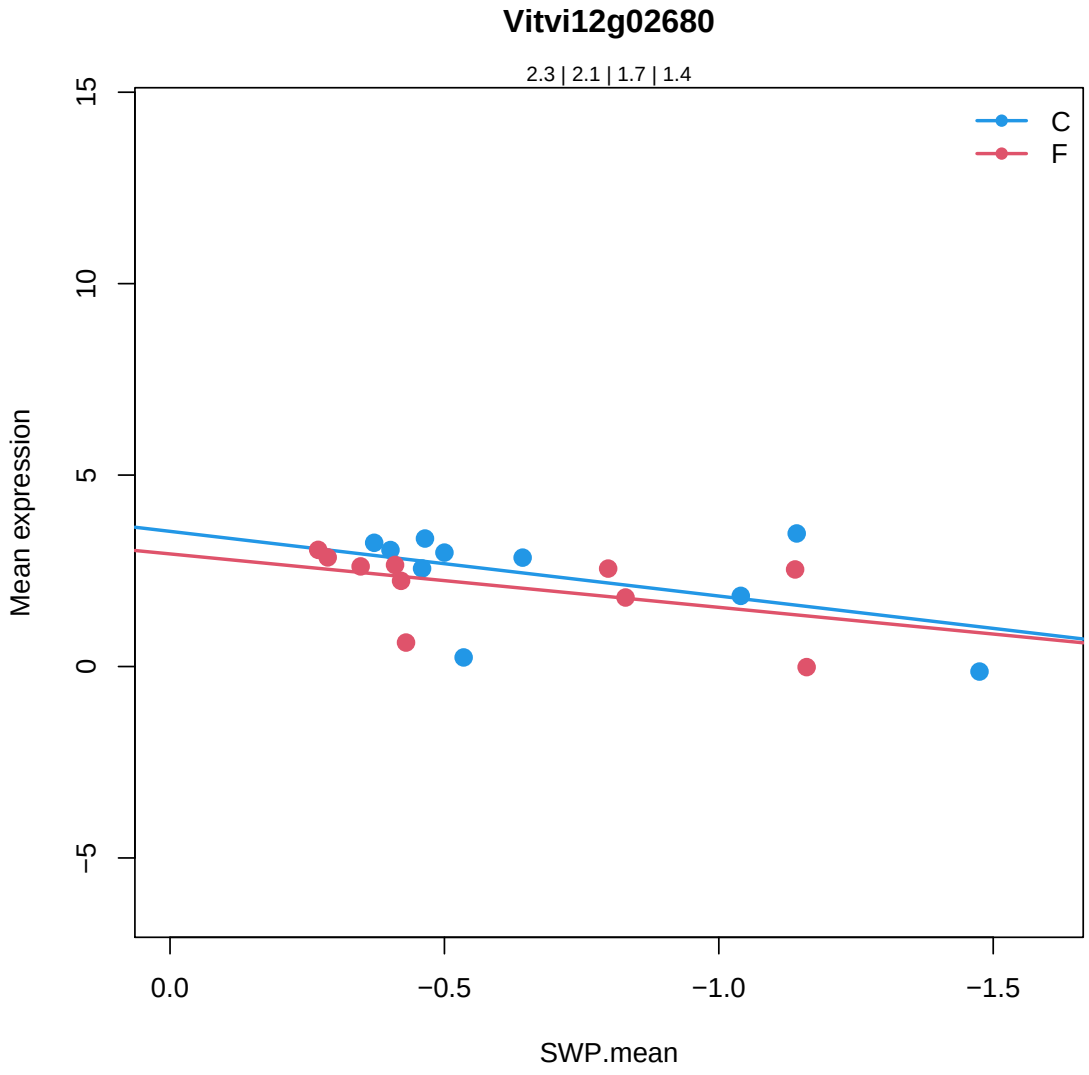
7.2.49 Vitvi12g02680: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02680
        27.3.46
        RNA.regulation of transcription.DNA methyltransferases
        methyltransferase 1 |
        Chr5:19932501-19938186 FORWARD LENGTH=1534 |
        201606
```

Coefficients for Vitvi12g02680.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.342038	1.296457e-07	***	1.533969e-07	***
SlopeC	1.689152	0.05857295	.	0.5384614	
MeanF-MeanC	-0.2513567	0.5647468		0.8419894	
SlopeF-SlopeC	-0.2938427	0.8175822		0.9999488	



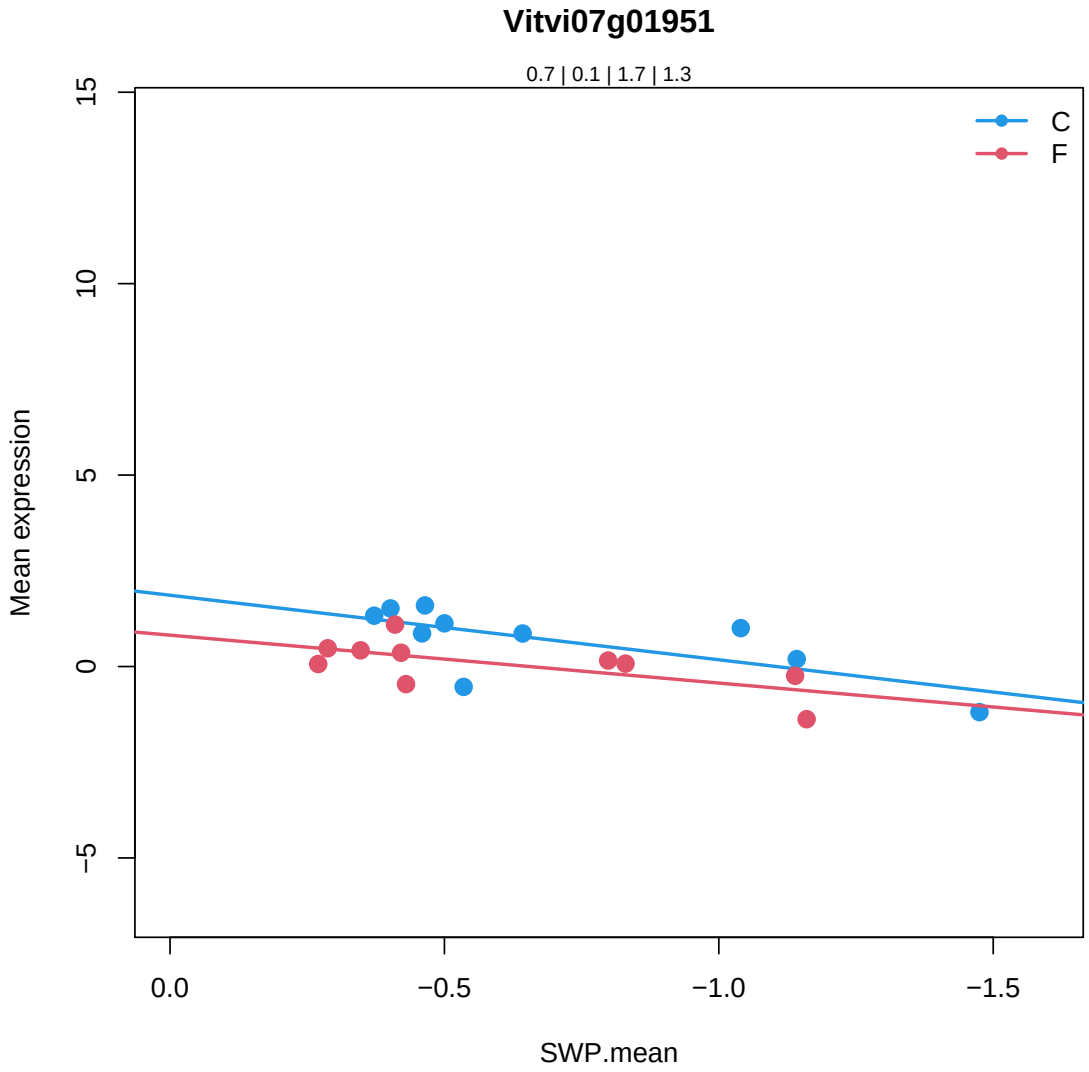
7.2.50 Vitvi07g01951: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01951
        35.2
        not assigned.unknown
        SAUR-like auxin-responsive protein family |
        Chr5:21772107-21772535 FORWARD LENGTH=142 |
        201606
```

Coefficients for Vitvi07g01951.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6767413	0.001494154	**	0.00161254	**
SlopeC	1.685263	0.003692717	**	0.2260417	
MeanF-MeanC	-0.619724	0.02801824	*	0.1613961	
SlopeF-SlopeC	-0.4345027	0.5784109		0.9999488	



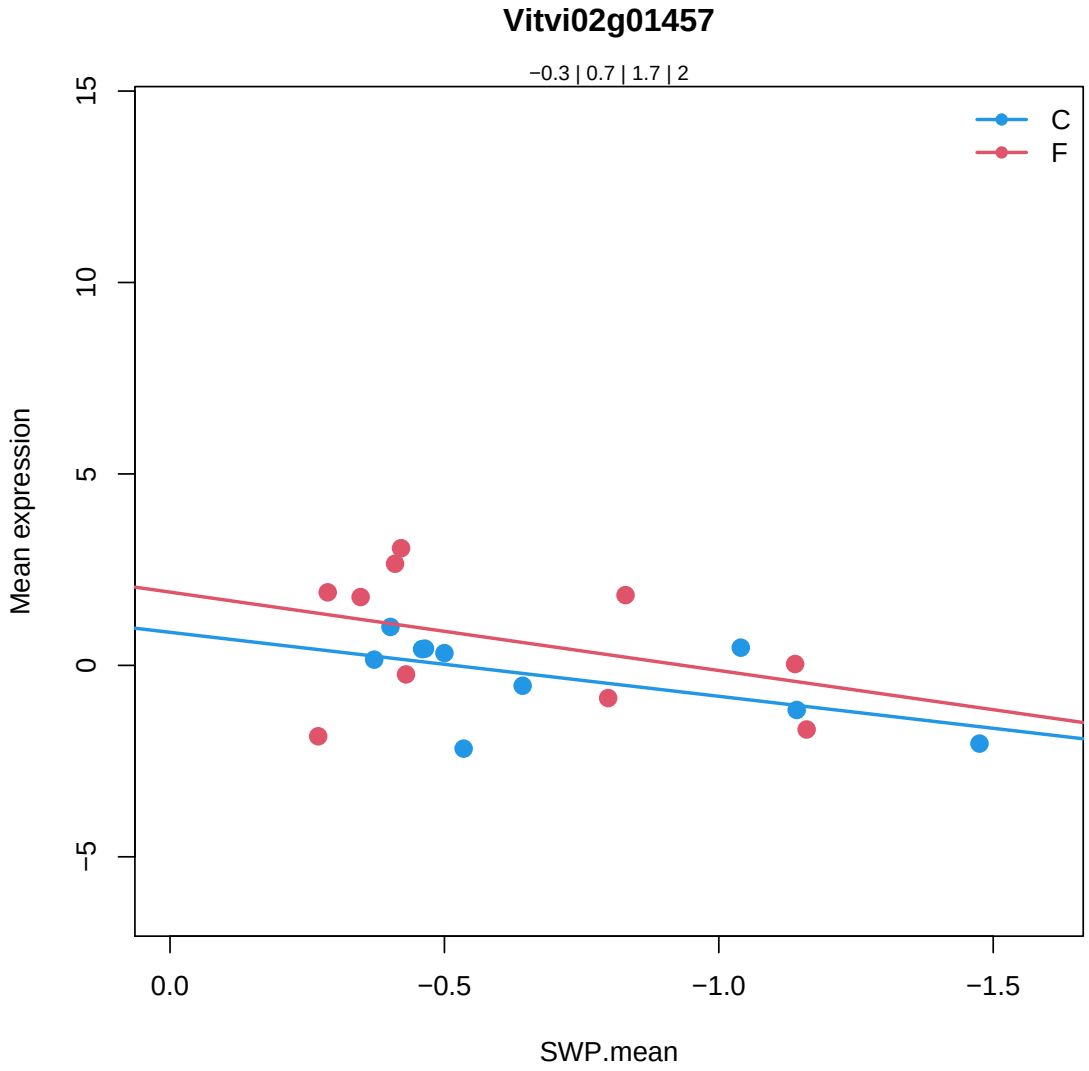
7.2.51 Vitvi02g01457: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g01457
        35.2
        not assigned.unknown
        [Sotub08g023330.1.1]: Cytochrome b [Sotub08g023340.1.1]: Unknown Prote
        [stNIB-v1_0012210]
```

Coefficients for Vitvi02g01457.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.3118384	0.4402904		0.446471	
SlopeC	1.671346	0.1444288		0.6693663	
MeanF-MeanC	0.9776932	0.09561947	.	0.3555579	
SlopeF-SlopeC	0.3760593	0.8210411		0.9999488	



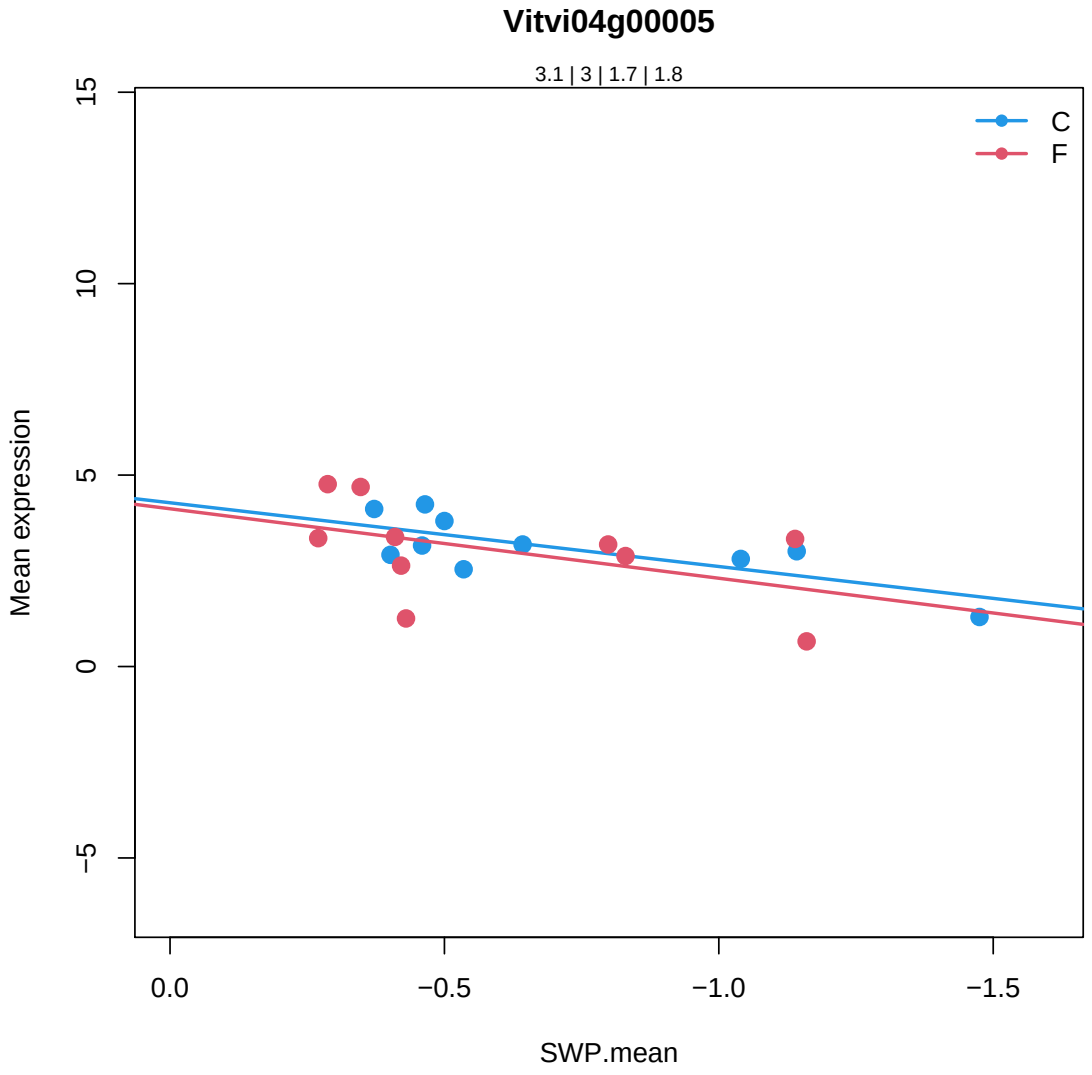
7.2.52 Vitvi04g00005: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00005
        35.2
        not assigned.unknown
        Avr9/Cf-9 rapidly elicited protein |
        Chr1:19407559-19408185 REVERSE LENGTH=208 |
        201606
```

Coefficients for Vitvi04g00005.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.106576	1.349803e-10	***	1.757985e-10	***
SlopeC	1.664904	0.03855333	*	0.4674859	
MeanF-MeanC	-0.09244316	0.8120131		0.9478302	
SlopeF-SlopeC	0.1496865	0.8953137		0.9999488	



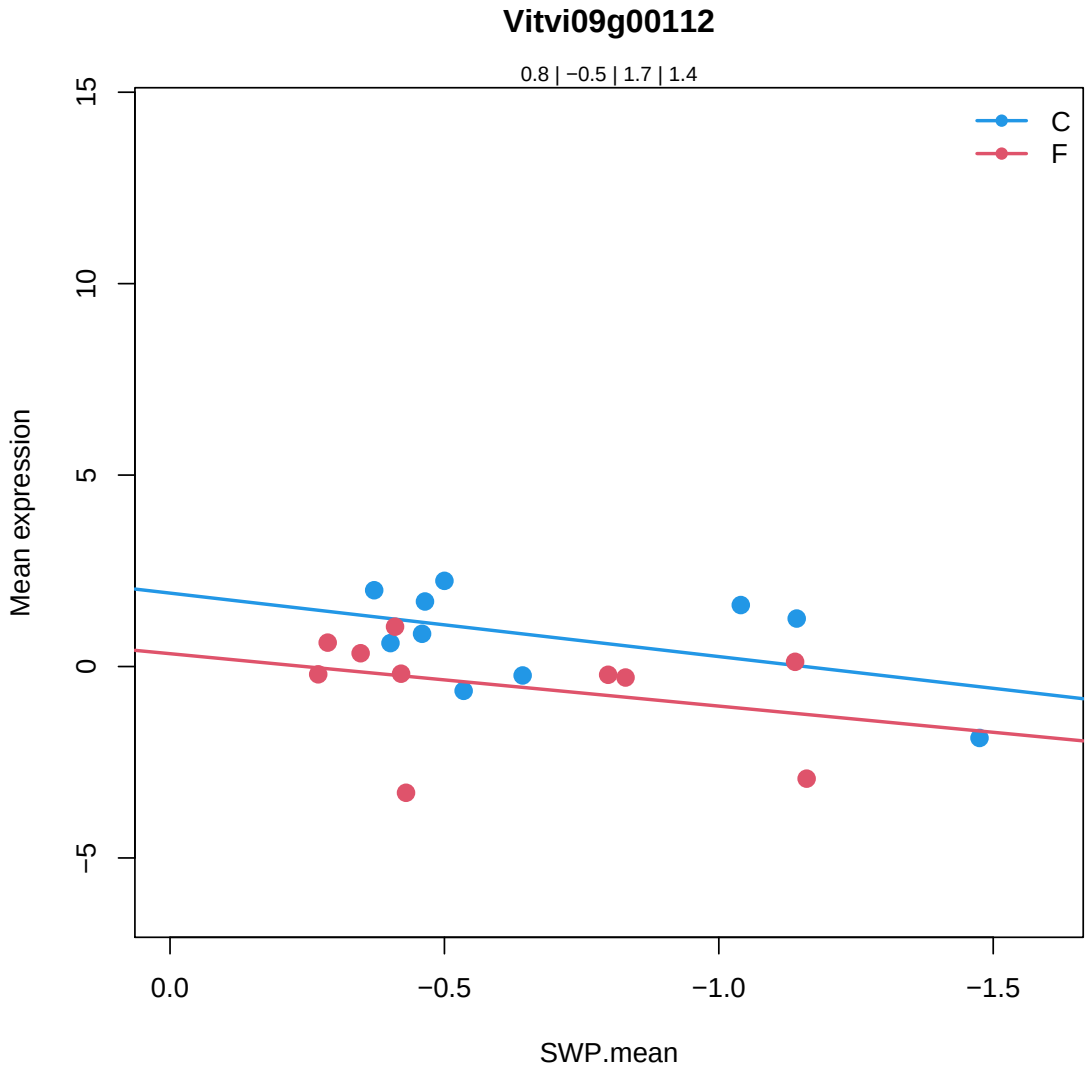
7.2.53 Vitvi09g00112: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00112
        27.3.25
        RNA.regulation of transcription.MYB domain transcription factor family
        myb domain protein 7 |
        Chr2:7255669-7256550 REVERSE LENGTH=269 |
        201606
```

Coefficients for Vitvi09g00112.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.7516576	0.05699717	.	0.05927208	.
SlopeC	1.657835	0.1254089		0.6460361	
MeanF-MeanC	-1.250463	0.02744369	*	0.1591483	
SlopeF-SlopeC	-0.2890606	0.853559		0.9999488	



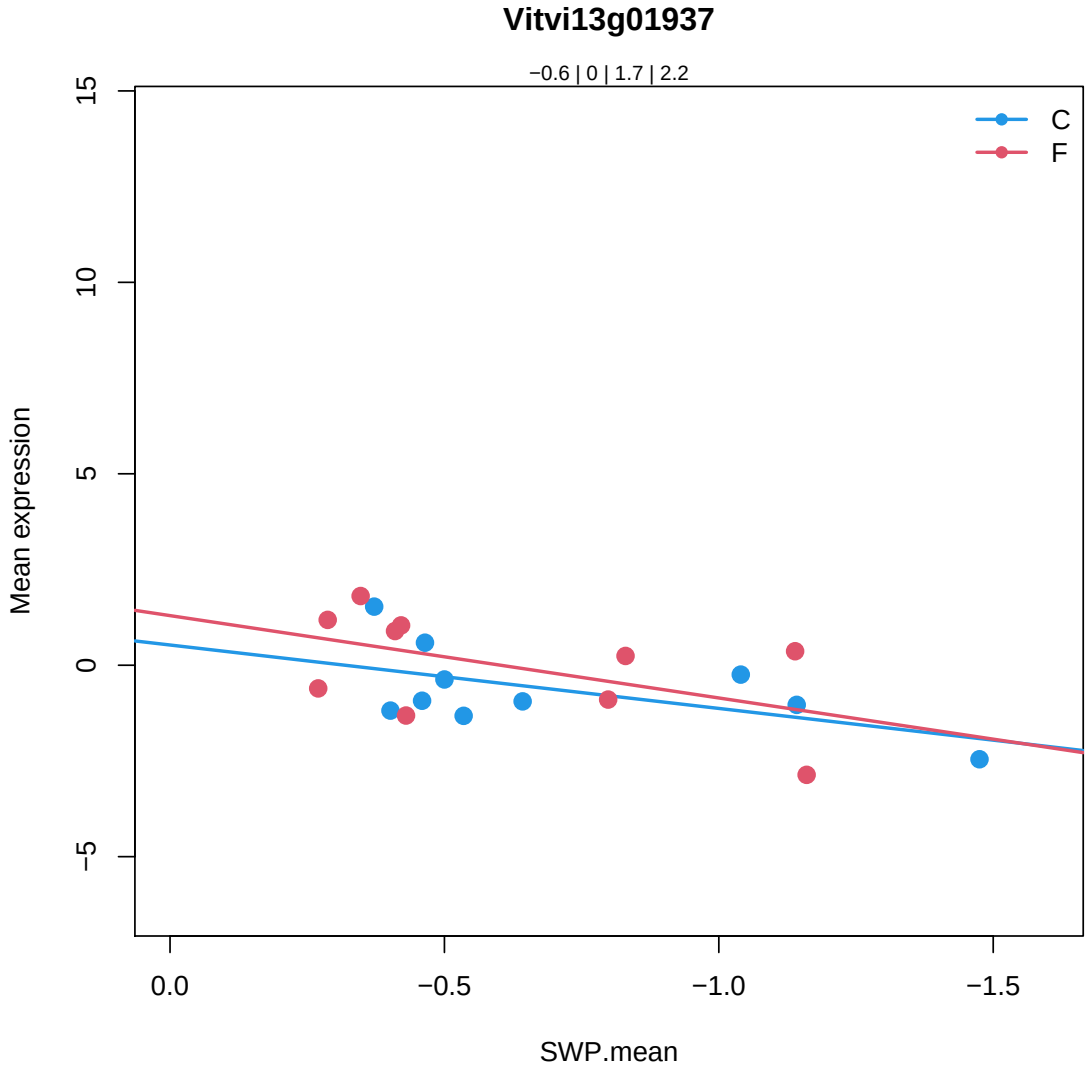
7.2.54 Vitvi13g01937: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g01937
        35.2
        not assigned.unknown
        Unknown Protein IPR007750 Protein of unknown function DUF674
```

Coefficients for Vitvi13g01937.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.63701	0.05704208	.	0.05931473	.
SlopeC	1.656786	0.07373898	.	0.5667824	
MeanF-MeanC	0.6221561	0.1790991		0.5136084	
SlopeF-SlopeC	0.4941654	0.710037		0.9999488	



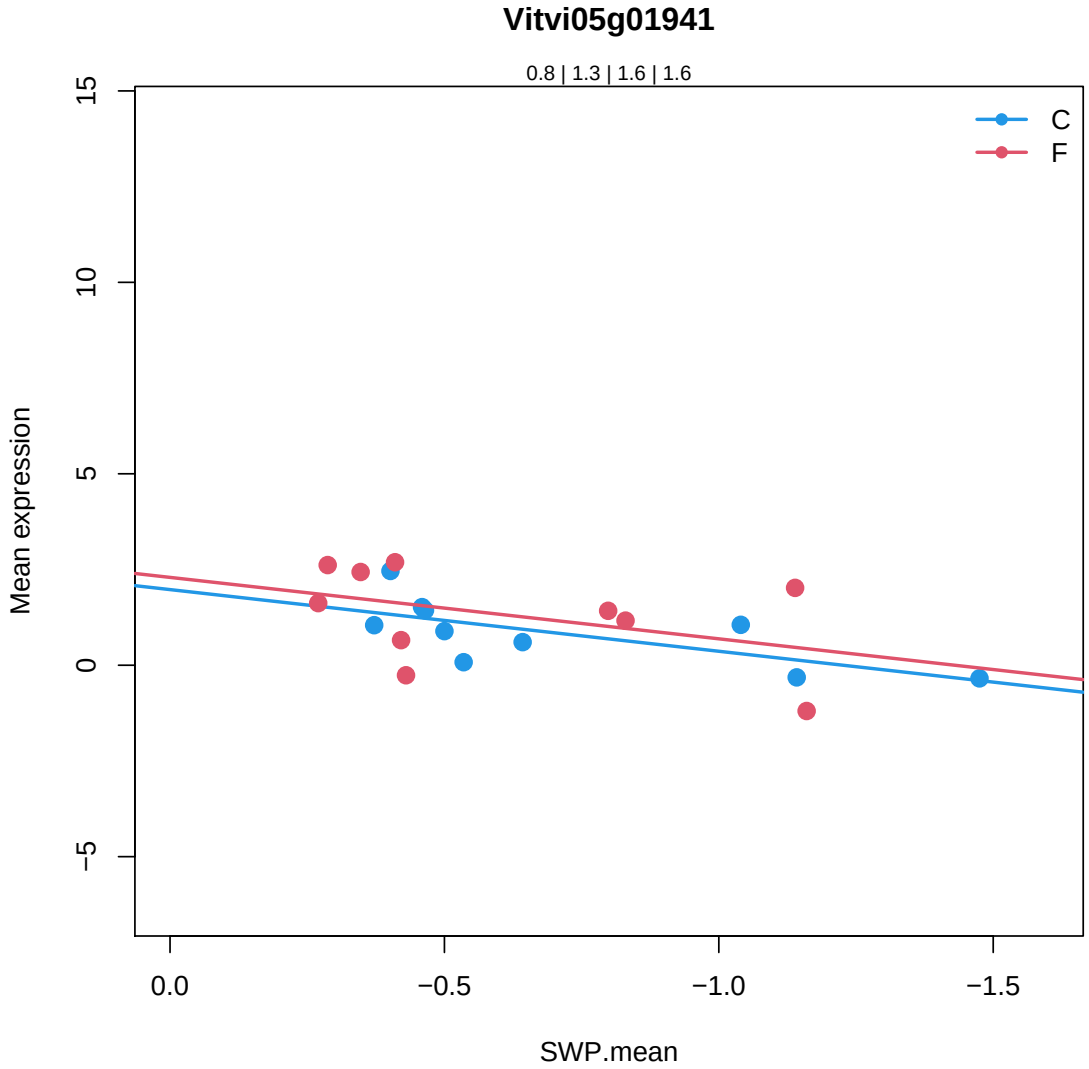
7.2.55 Vitvi05g01941: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01941
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi05g01941.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8425615	0.006591407	**	0.007009923	**
SlopeC	1.610657	0.05101669	.	0.5112402	
MeanF-MeanC	0.4738833	0.244605		0.6040618	
SlopeF-SlopeC	-0.006193255	0.9957886		0.9999488	



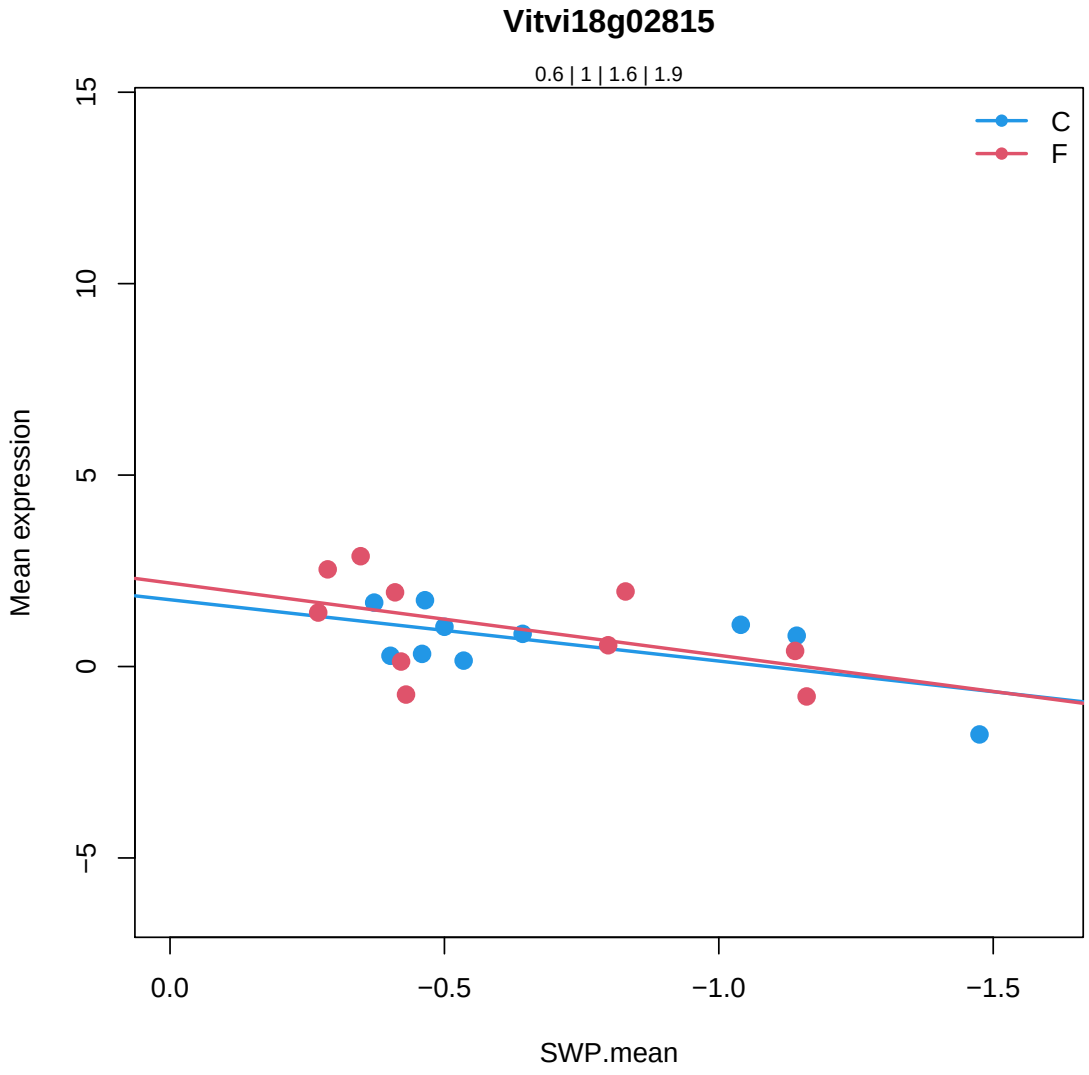
7.2.56 Vitvi18g02815: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02815
        26.28
        misc.GDSL-motif lipase
        GDSL-like Lipase/Acylhydrolase superfamily protein |
        Chr1:28499179-28500943 FORWARD LENGTH=364 |
        201606
```

Coefficients for Vitvi18g02815.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6177167	0.04754848	*	0.04954091	*
SlopeC	1.601233	0.06332287	.	0.5471512	
MeanF-MeanC	0.412581	0.3319344		0.6913562	
SlopeF-SlopeC	0.2861639	0.8163246		0.9999488	



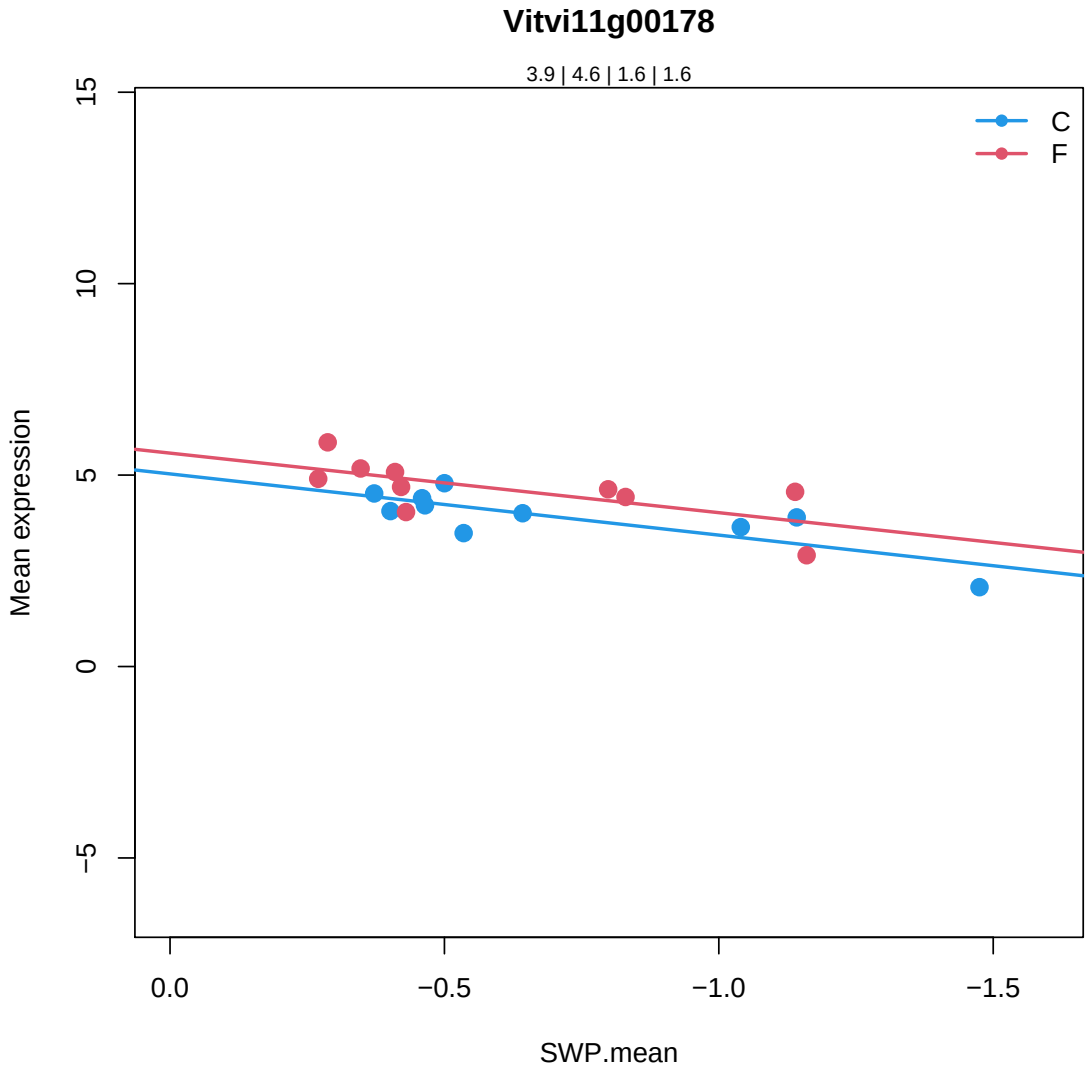
7.2.57 Vitvi11g00178: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00178
        26.3.2
        misc.gluco-, galacto- and mannosidases.beta-galactosidase
        beta galactosidase 1 |
        Chr3:4511192-4515756 FORWARD LENGTH=847 |
        201606
```

Coefficients for Vitvi11g00178.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.906544	1.002399e-16	***	2.179849e-16	***
SlopeC	1.598496	0.002452883	**	0.1888224	
MeanF-MeanC	0.7193079	0.006164221	**	0.05307237	.
SlopeF-SlopeC	-0.04327093	0.9508202		0.9999488	



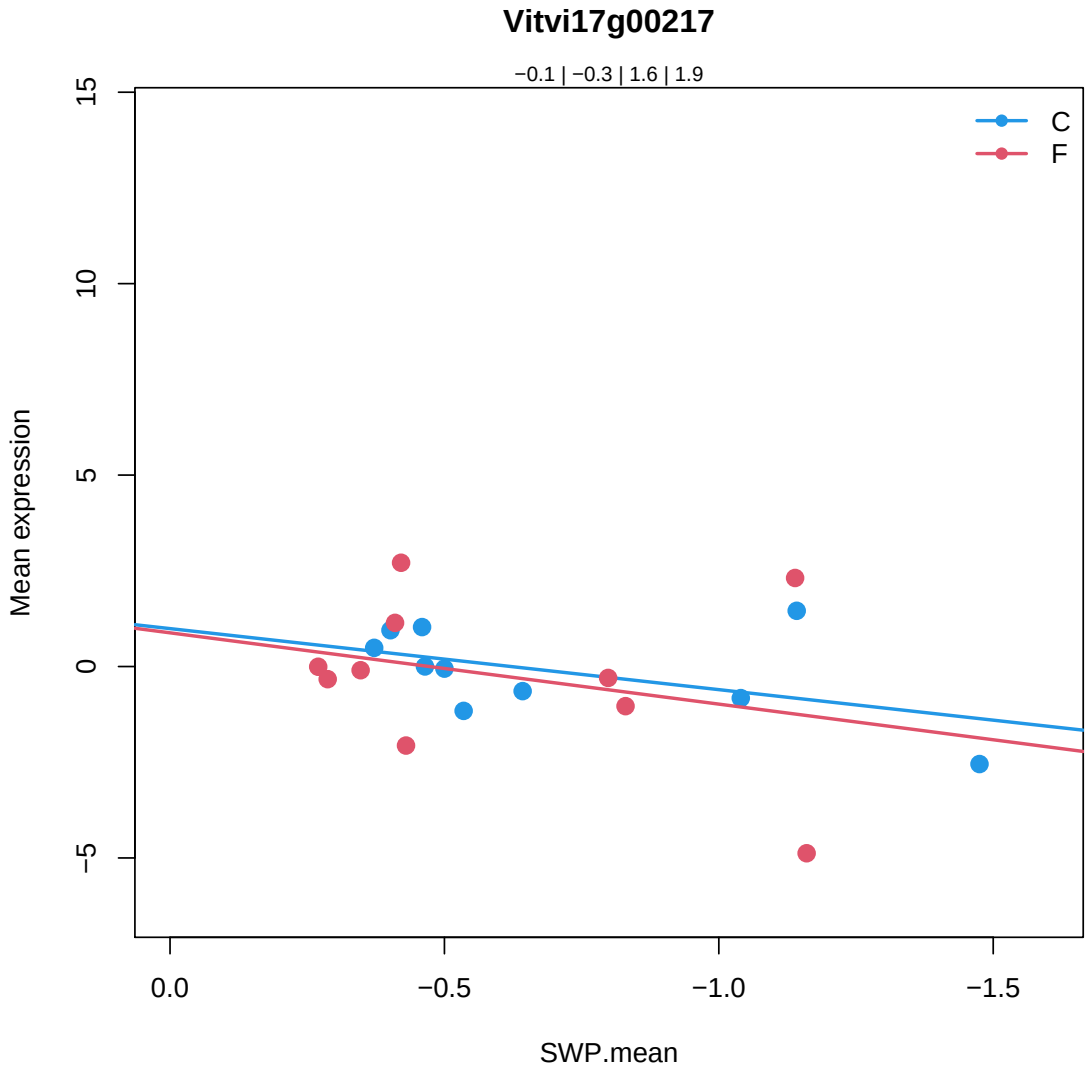
7.2.58 Vitvi17g00217: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00217
        20.1.7.5
        stress.biotic.PR-proteins.PR5 (thaumatin-like proteins)
        Pathogenesis-related thaumatin superfamily protein |
        Chr1:6277024-6278005 REVERSE LENGTH=243 |
        201606
```

Coefficients for Vitvi17g00217.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.1308321	0.7892083		0.7932678	
SlopeC	1.59409	0.2487794		0.7601216	
MeanF-MeanC	-0.1237943	0.8579752		0.962554	
SlopeF-SlopeC	0.267747	0.8948189		0.9999488	



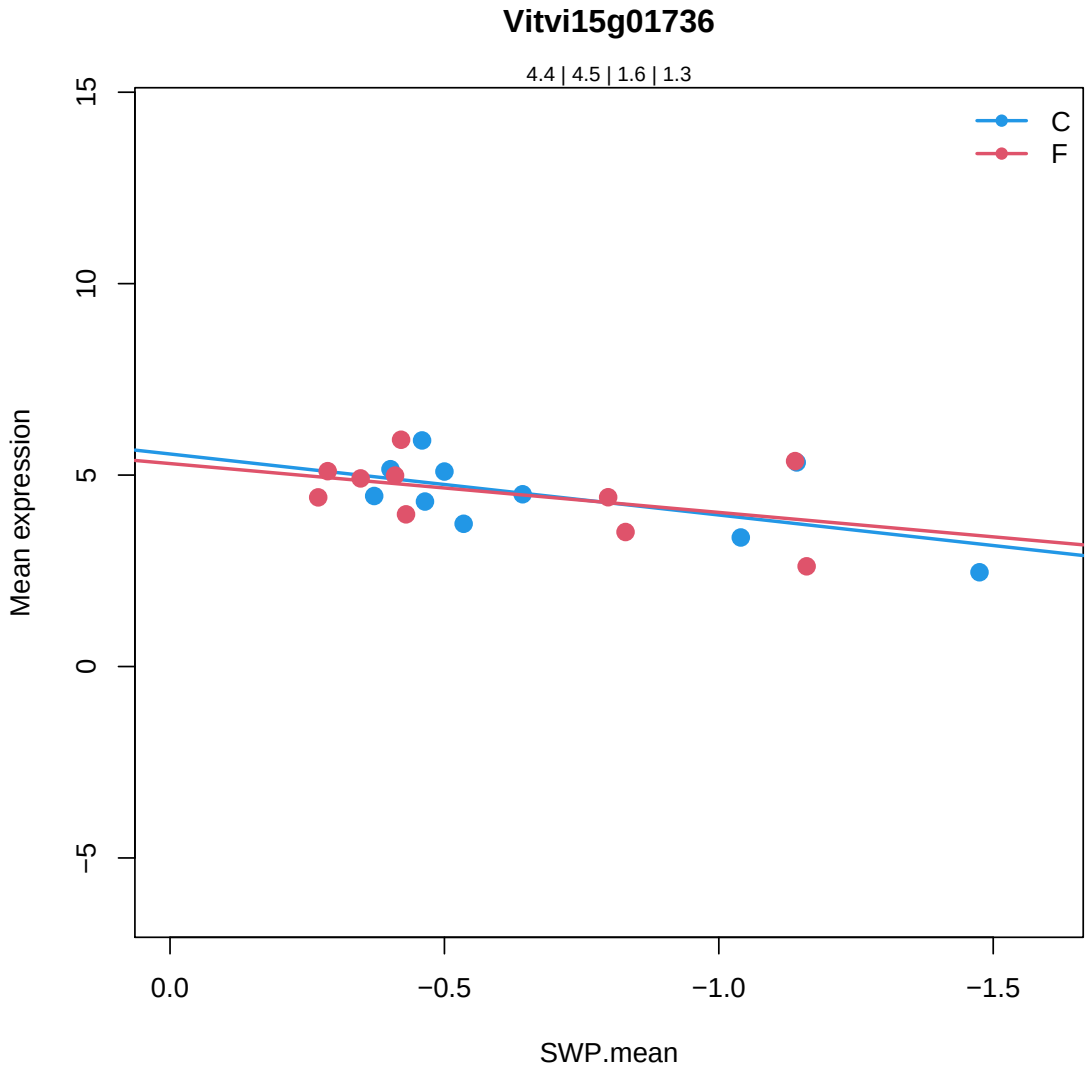
7.2.59 Vitvi15g01736: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g01736
        26.9
        misc.glutathione S transferases
        glutathione S-transferase tau 7 |
        Chr2:12618111-12618871 REVERSE LENGTH=227 |
        201606
```

Coefficients for Vitvi15g01736.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.430191	4.582548e-14	***	7.229811e-14	***
SlopeC	1.593545	0.03628133	*	0.4574028	
MeanF-MeanC	0.09309953	0.7998456		0.9439603	
SlopeF-SlopeC	-0.3175892	0.7677545		0.9999488	



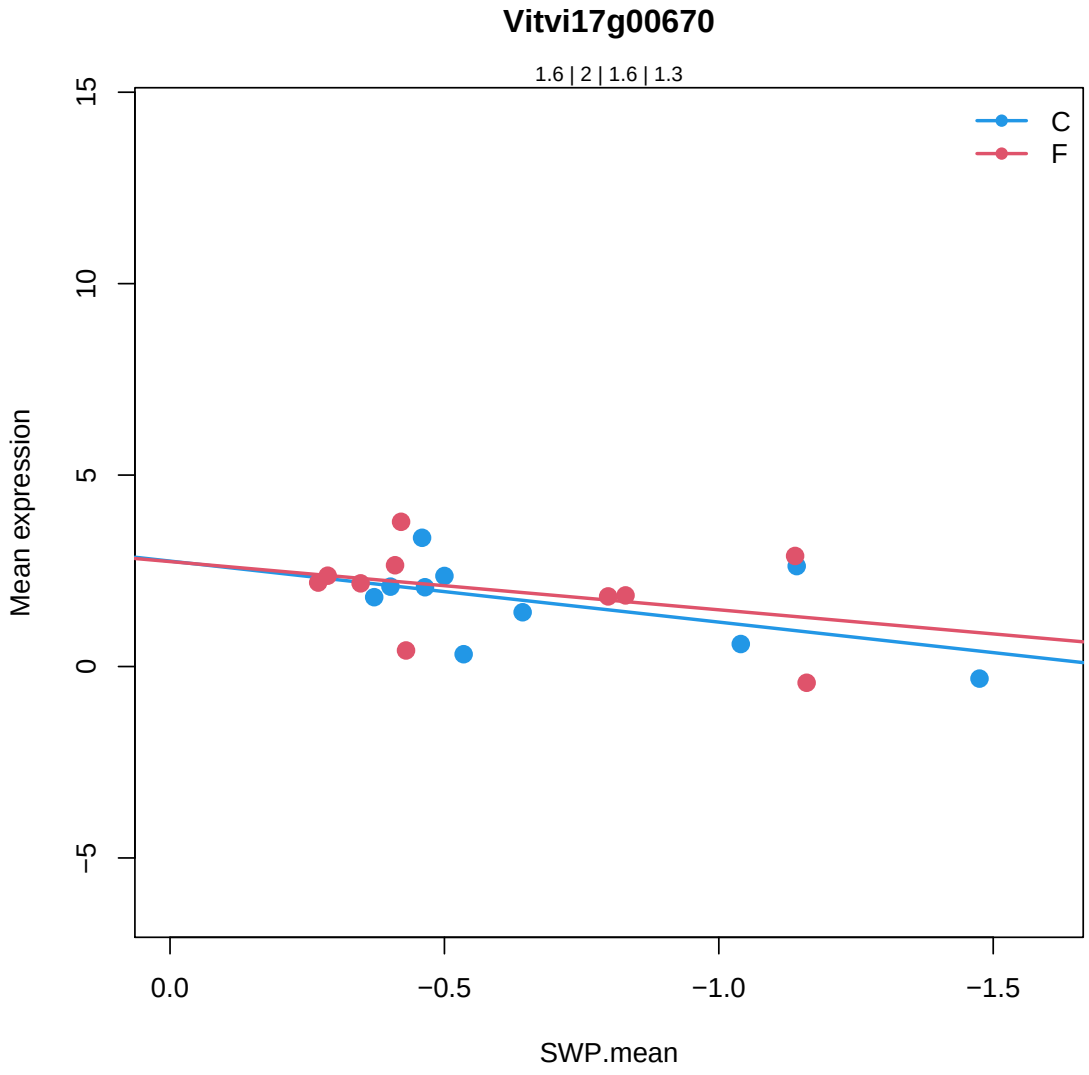
7.2.60 Vitvi17g00670: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00670
        27.3.11
        RNA.regulation of transcription.C2H2 zinc finger family
        C2H2-like zinc finger protein |
        Chr1:9193735-9195102 FORWARD LENGTH=455 |
        201606
```

Coefficients for Vitvi17g00670.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.632701	3.302526e-05	***	3.683922e-05	***
SlopeC	1.593544	0.08066537	.	0.5763978	
MeanF-MeanC	0.3405621	0.4492281		0.7774651	
SlopeF-SlopeC	-0.3342479	0.798583		0.9999488	



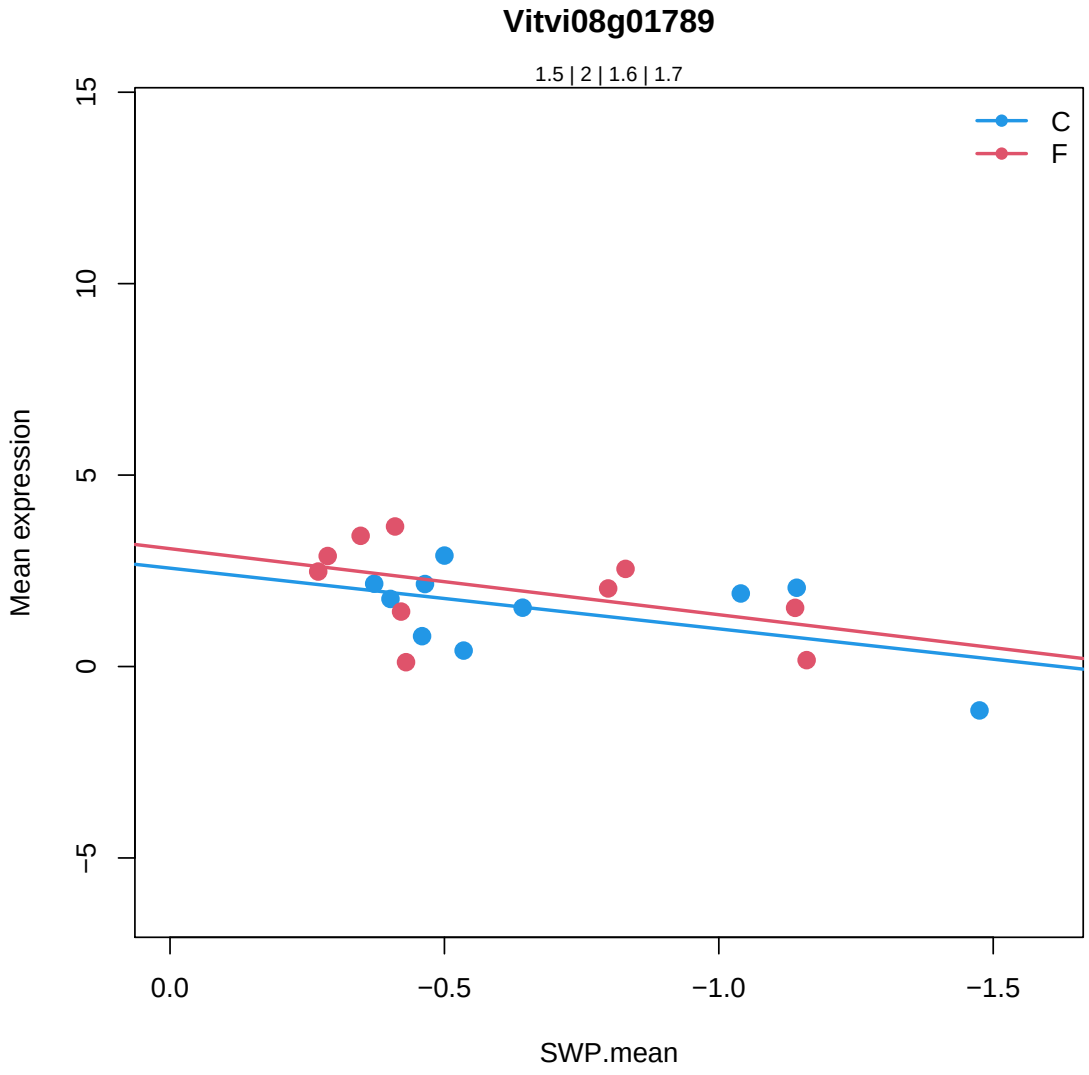
7.2.61 Vitvi08g01789: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01789
        26.3.5
        misc.gluco-, galacto- and mannosidases.glycosyl hydrolase family 5
        alpha/beta-Hydrolases superfamily protein |
        Chr3:1033788-1034591 FORWARD LENGTH=267 |
        201606
```

Coefficients for Vitvi08g01789.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.454261	0.0001135931	***	0.0001253265	***
SlopeC	1.58514	0.07890384	.	0.5748584	
MeanF-MeanC	0.5729973	0.2033962		0.5476211	
SlopeF-SlopeC	0.1388354	0.9145543		0.9999488	



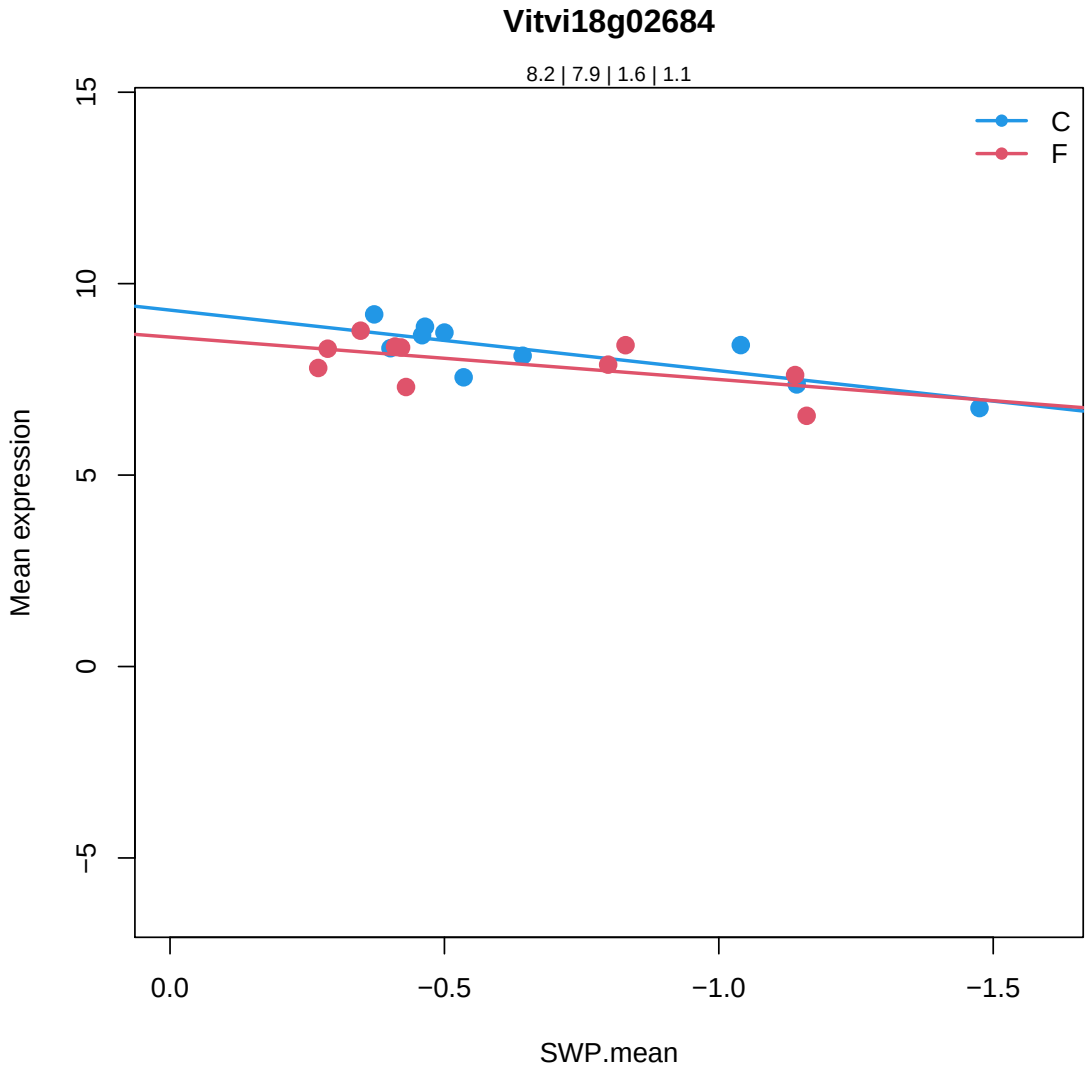
7.2.62 Vitvi18g02684: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02684
        35.2
        not assigned.unknown
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi18g02684.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	8.19425	1.142172e-23	***	3.817759e-22	***
SlopeC	1.584538	0.002251962	**	0.1816214	
MeanF-MeanC	-0.2647429	0.2670226		0.629212	
SlopeF-SlopeC	-0.4763518	0.4912711		0.9999488	



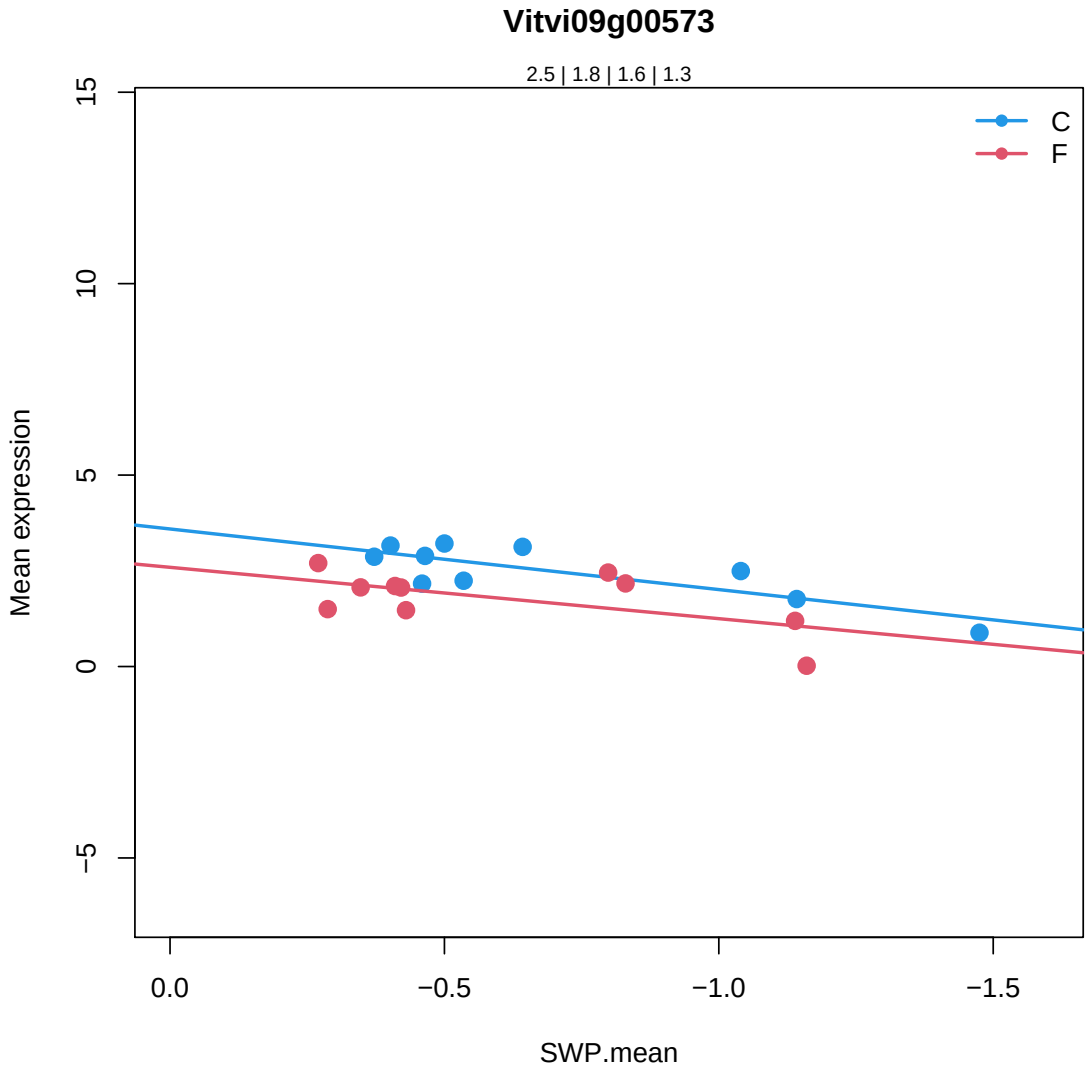
7.2.63 Vitvi09g00573: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00573
        26.4.1
        misc.beta 1,3 glucan hydrolases.glucan endo-1,3-beta-glucosidase
        plant natriuretic peptide A |
        Chr2:8091032-8091644 REVERSE LENGTH=130 |
        201606
```

Coefficients for Vitvi09g00573.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.47956	1.939154e-12	***	2.737481e-12	***
SlopeC	1.583014	0.003495044	**	0.2238297	
MeanF-MeanC	-0.7056667	0.008894757	**	0.06970379	.
SlopeF-SlopeC	-0.2418998	0.7395005		0.9999488	



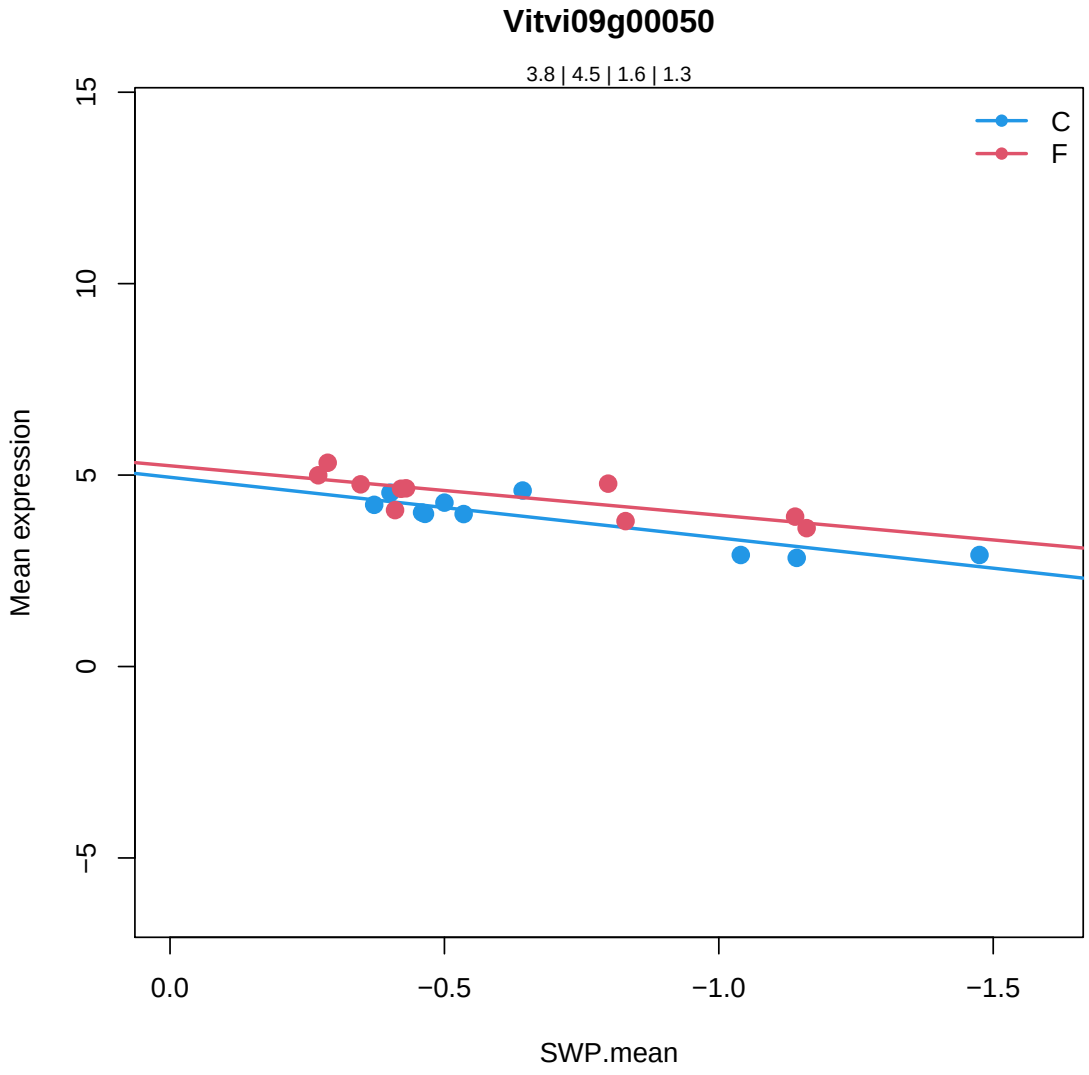
7.2.64 Vitvi09g00050: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00050
        17.2.3
        hormone metabolism.auxin.induced-regulated-responsive-activated
        Dormancy/auxin associated family protein |
        Chr1:20182683-20183242 FORWARD LENGTH=123 |
        201606
```

Coefficients for Vitvi09g00050.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.829218	3.779339e-19	***	1.486573e-18	***
SlopeC	1.58268	0.0001747403	***	0.07644173	.
MeanF-MeanC	0.6266748	0.001944776	**	0.02158943	*
SlopeF-SlopeC	-0.2915633	0.5808		0.9999488	



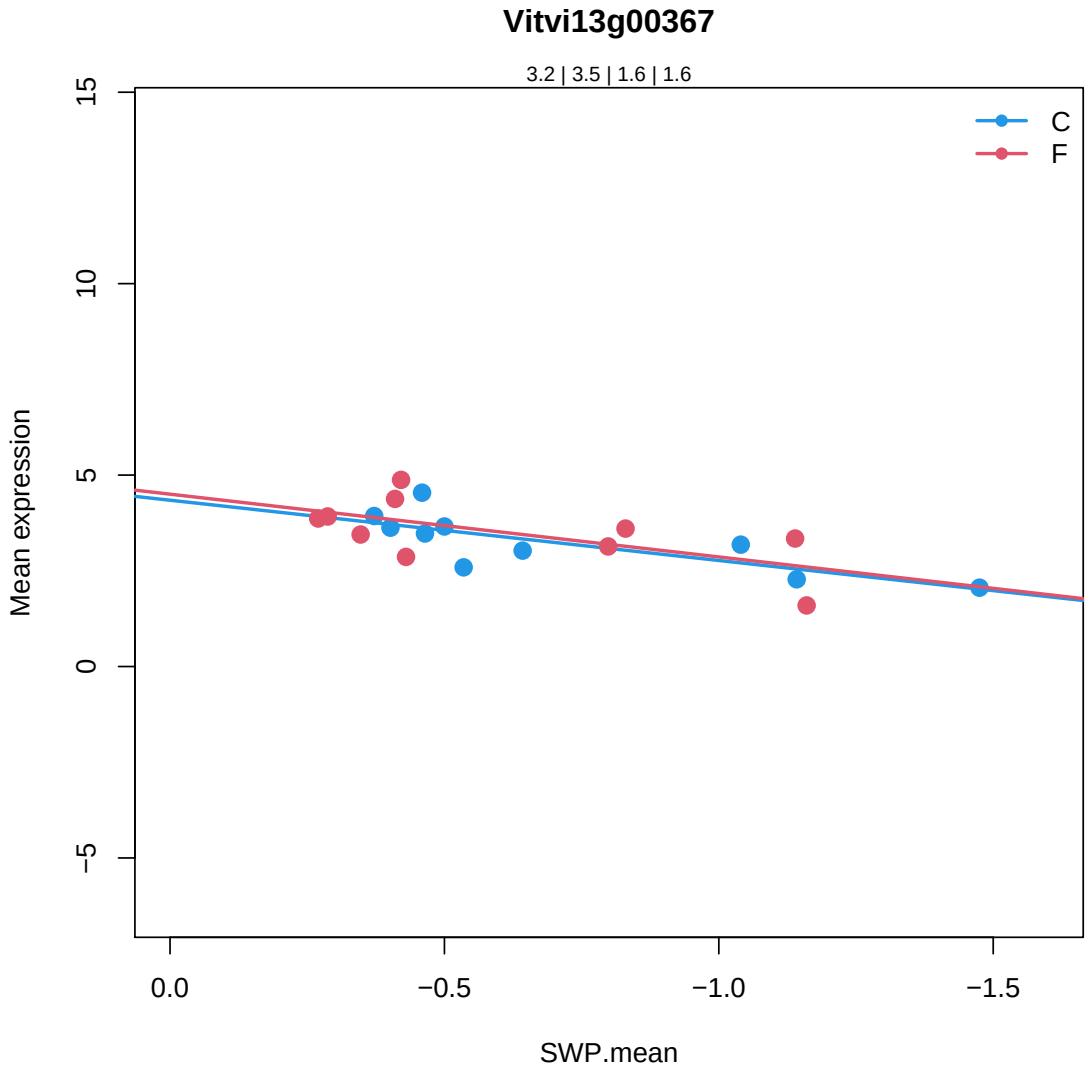
7.2.65 Vitvi13g00367: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00367
        34.13
        transport.peptides and oligopeptides
        Major facilitator superfamily protein |
        Chr2:15864396-15866408 REVERSE LENGTH=575 |
        201606
```

Coefficients for Vitvi13g00367.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.236374	6.230874e-14	***	9.720674e-14	***
SlopeC	1.574206	0.007123992	**	0.2775469	
MeanF-MeanC	0.2659487	0.3338965		0.6930751	
SlopeF-SlopeC	0.06562819	0.9343734		0.9999488	



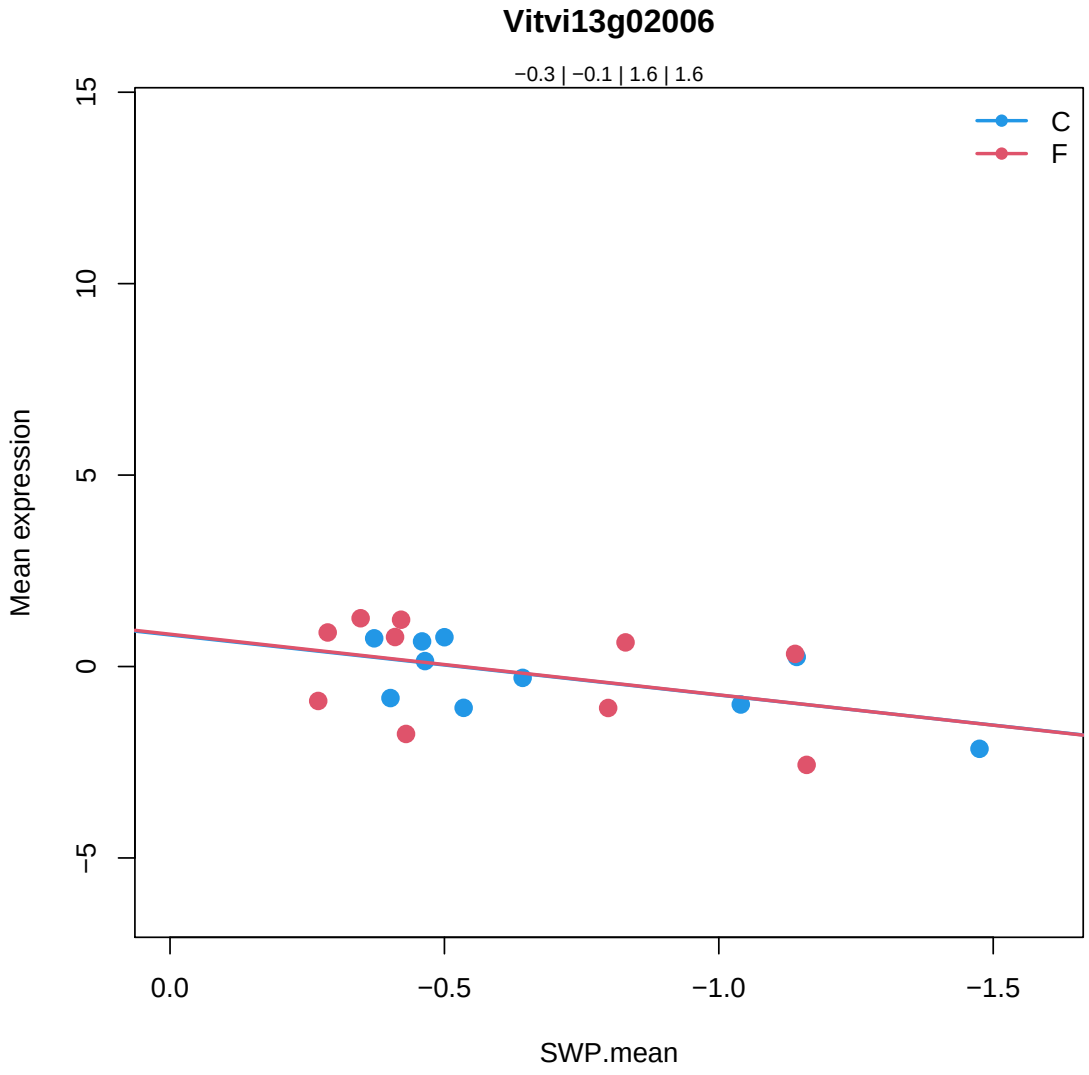
7.2.66 Vitvi13g02006: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g02006
        35.2
        not assigned.unknown
        Subtilisin-like serine endopeptidase family protein |
        Chr5:23858951-23862087 REVERSE LENGTH=741 |
        201606
```

Coefficients for Vitvi13g02006.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.2793474	0.3746988		0.3807694	
SlopeC	1.569977	0.08097243	.	0.5764511	
MeanF-MeanC	0.1582498	0.7200428		0.9142513	
SlopeF-SlopeC	0.01502227	0.990715		0.9999488	



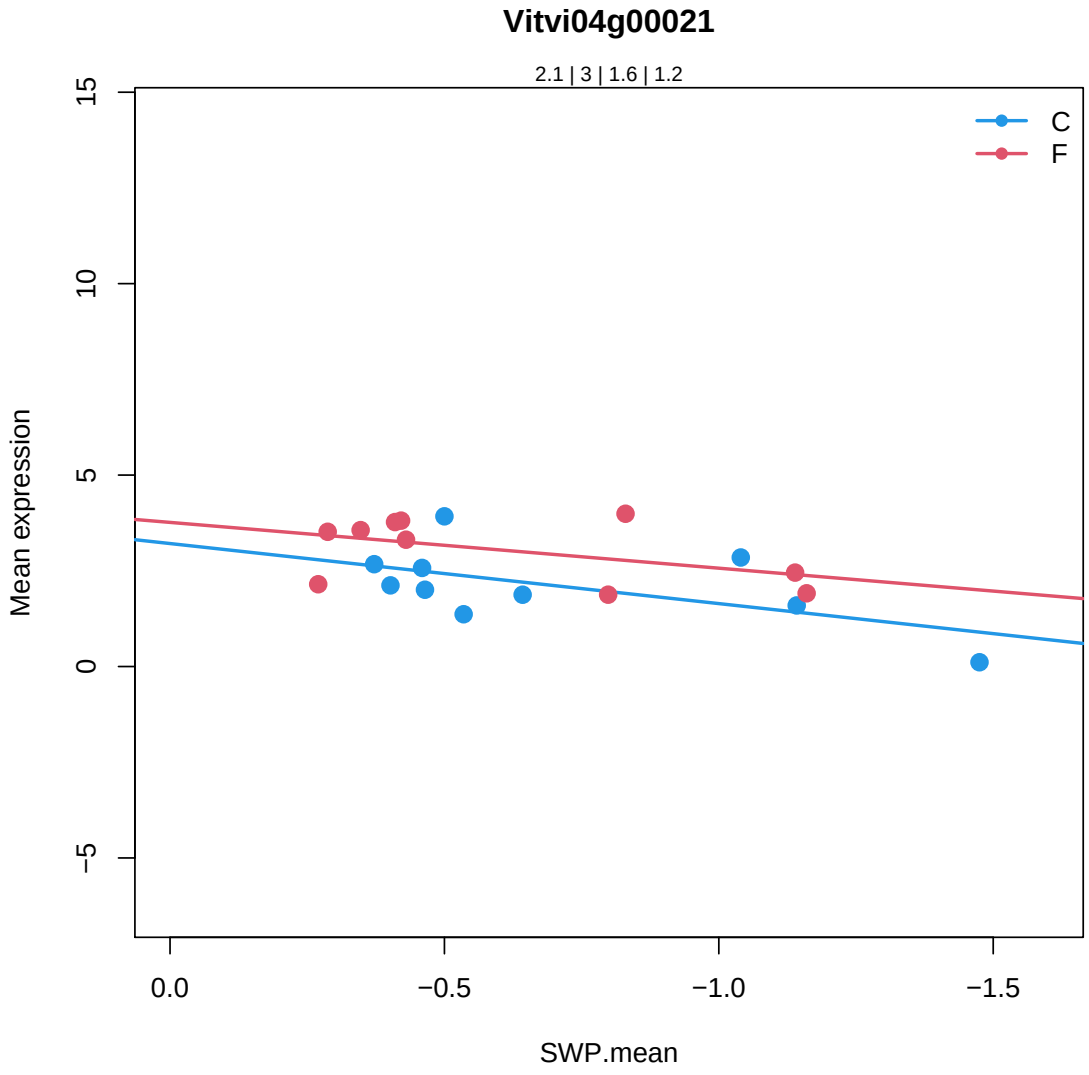
7.2.67 Vitvi04g00021: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00021
        30.2.11
        signalling.receptor kinases.leucine rich repeat XI
        kinase family with leucine-rich repeat domain-containing protein |
        Chr5:9050880-9053978 FORWARD LENGTH=1005 |
        201606
```

Coefficients for Vitvi04g00021.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.108913	1.365488e-08	***	1.659445e-08	***
SlopeC	1.56852	0.02775129	*	0.4237571	
MeanF-MeanC	0.9265657	0.01202077	*	0.08708205	.
SlopeF-SlopeC	-0.3727809	0.7098633		0.9999488	



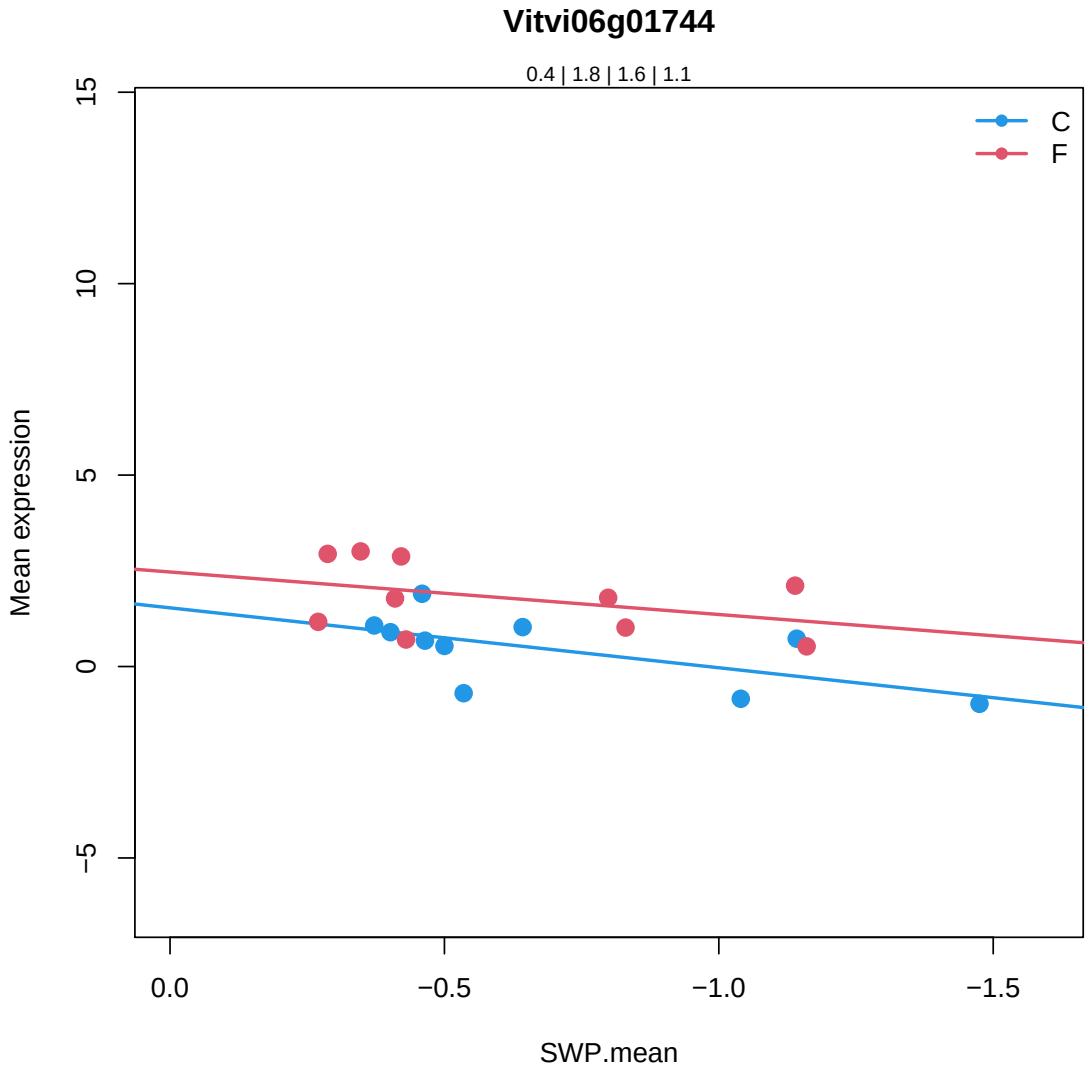
7.2.68 Vitvi06g01744: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01744
        35.2
        not assigned.unknown
        UDP-glucosyl transferase 71C4 |
        Chr1:2225963-2227402 FORWARD LENGTH=479 |
        201606
```

Coefficients for Vitvi06g01744.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4323643	0.09166084	.	0.09488553	.
SlopeC	1.564877	0.0317634	*	0.4343406	
MeanF-MeanC	1.36013	0.0007474462	***	0.009804282	**
SlopeF-SlopeC	-0.4548831	0.658184		0.9999488	



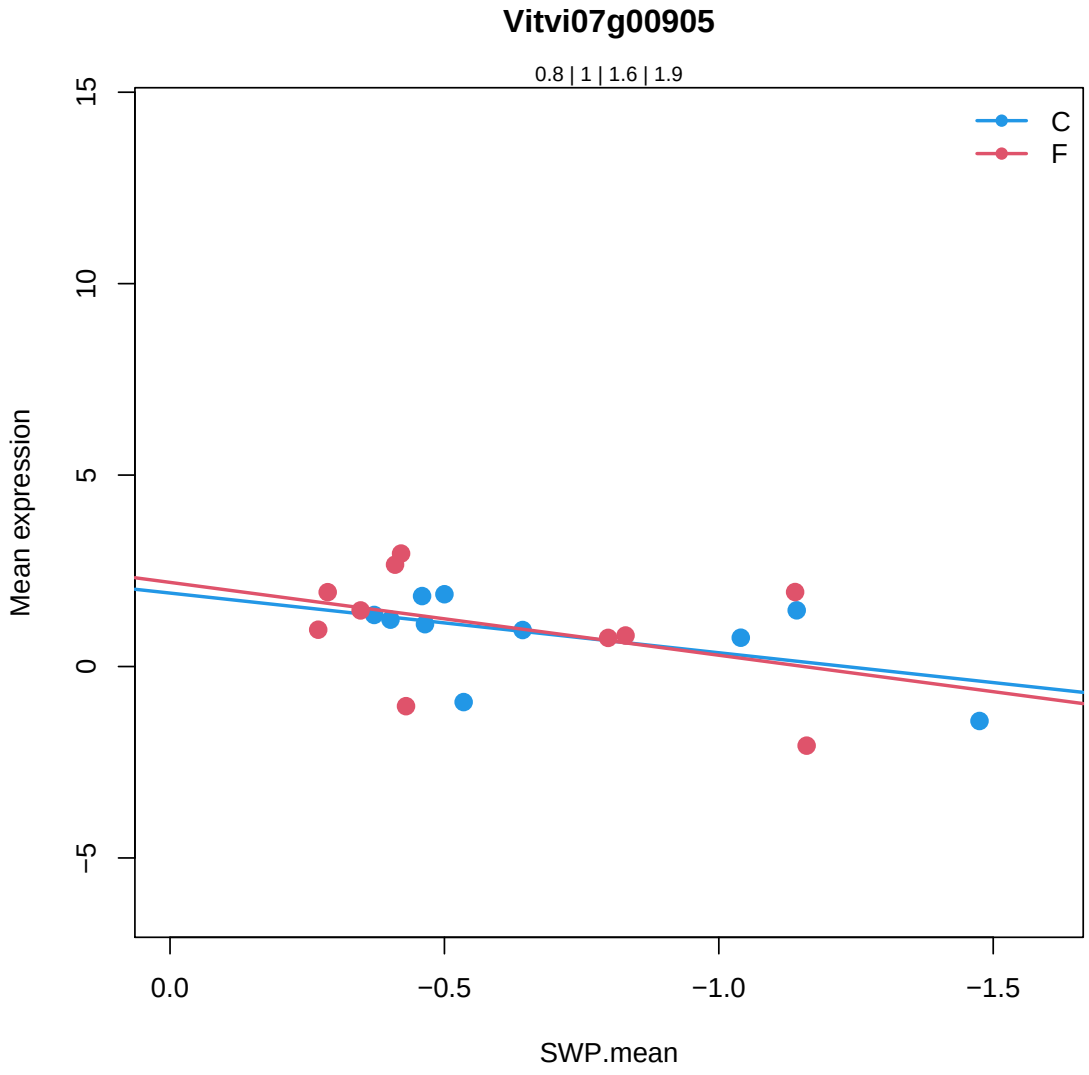
7.2.69 Vitvi07g00905: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g00905
        30.11
        signalling.light
        Phototropic-responsive NPH3 family protein |
        Chr5:19786881-19789003 FORWARD LENGTH=614 |
        201606
```

Coefficients for Vitvi07g00905.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8223898	0.03249897	*	0.03398623	*
SlopeC	1.558654	0.1339875		0.6579374	
MeanF-MeanC	0.2153674	0.6762392		0.8951087	
SlopeF-SlopeC	0.343932	0.8195743		0.9999488	



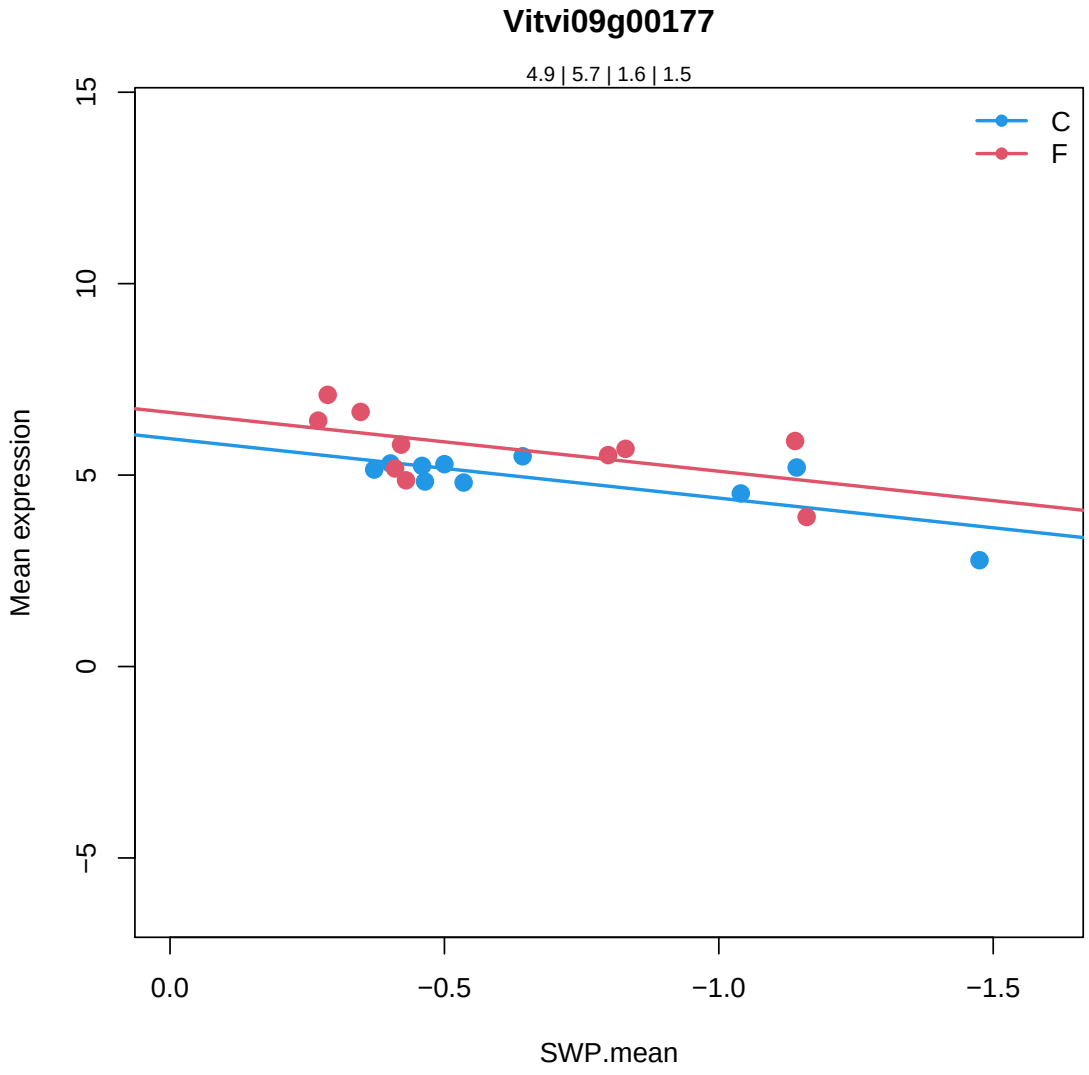
7.2.70 Vitvi09g00177: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00177
        26.3.2
        misc.gluco-, galacto- and mannosidases.beta-galactosidase
        beta galactosidase 1 |
        Chr3:4511192-4515756 FORWARD LENGTH=847 |
        201606
```

Coefficients for Vitvi09g00177.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.859533	6.509885e-17	***	1.462398e-16	***
SlopeC	1.551235	0.01231335	*	0.3235864	
MeanF-MeanC	0.8403859	0.008201953	**	0.0656932	.
SlopeF-SlopeC	-0.01689556	0.9842278		0.9999488	



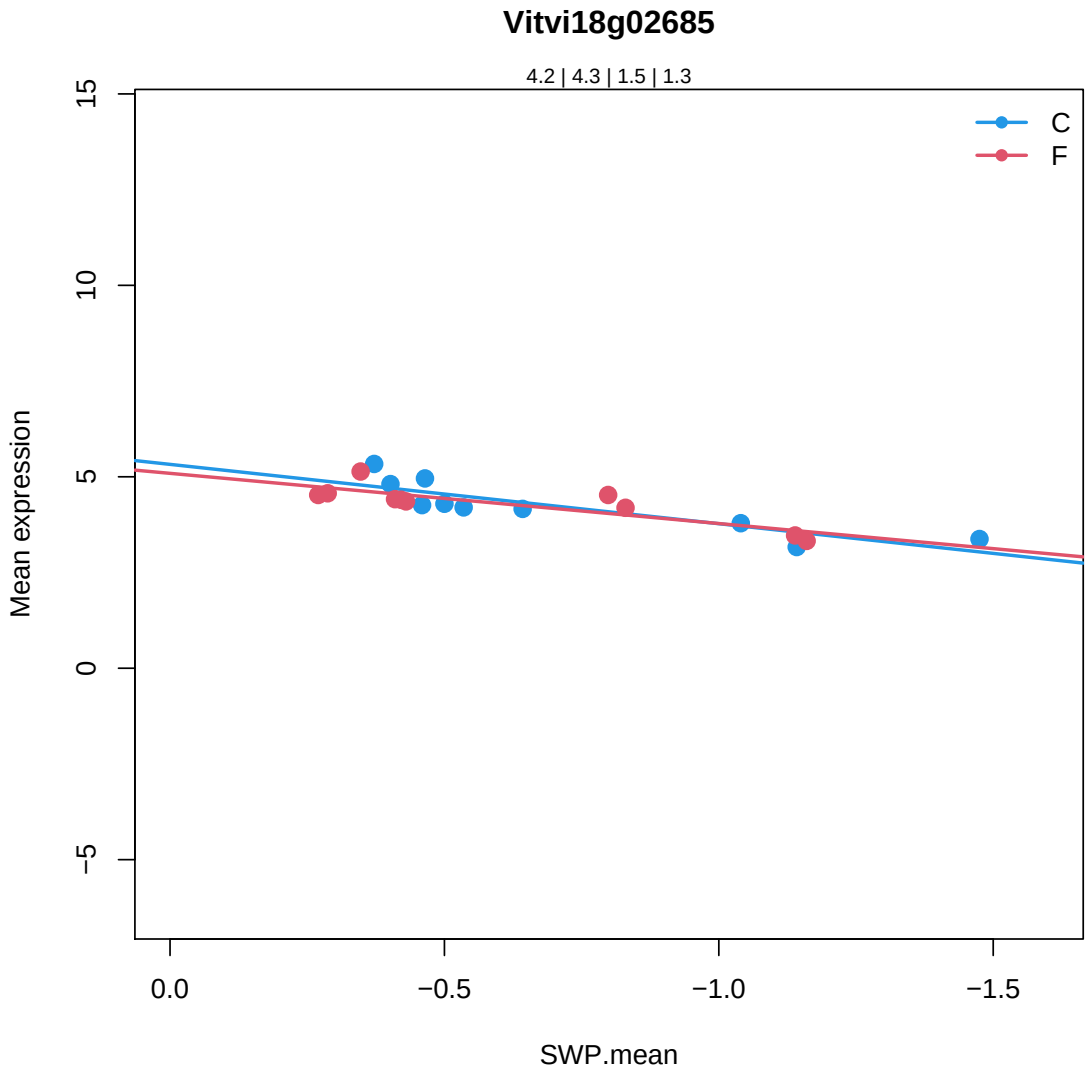
7.2.71 Vitvi18g02685: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02685
        35.2
        not assigned.unknown
        Calmodulin IPR011992 EF-Hand type
```

Coefficients for Vitvi18g02685.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.234483	1.764956e-20	***	1.125584e-19	***
SlopeC	1.549599	0.0001341873	***	0.07644173	.
MeanF-MeanC	0.05642384	0.7428452		0.9241305	
SlopeF-SlopeC	-0.2385602	0.636144		0.9999488	



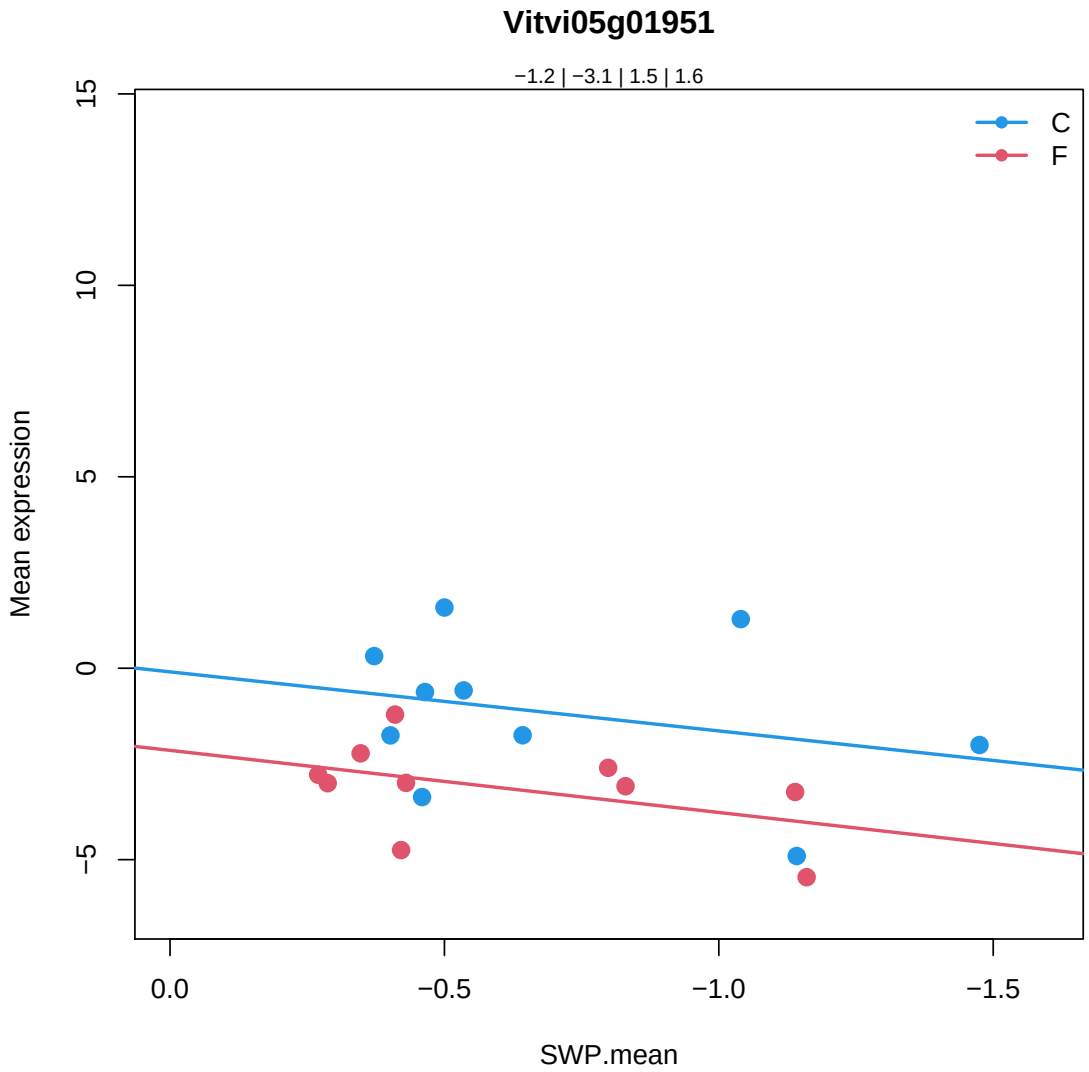
7.2.72 Vitvi05g01951: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01951
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi05g01951.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.180023	0.01749749	*	0.01842337	*
SlopeC	1.542255	0.2396463		0.7540013	
MeanF-MeanC	-1.953694	0.006503444	**	0.05528837	.
SlopeF-SlopeC	0.07982944	0.9668383		0.9999488	



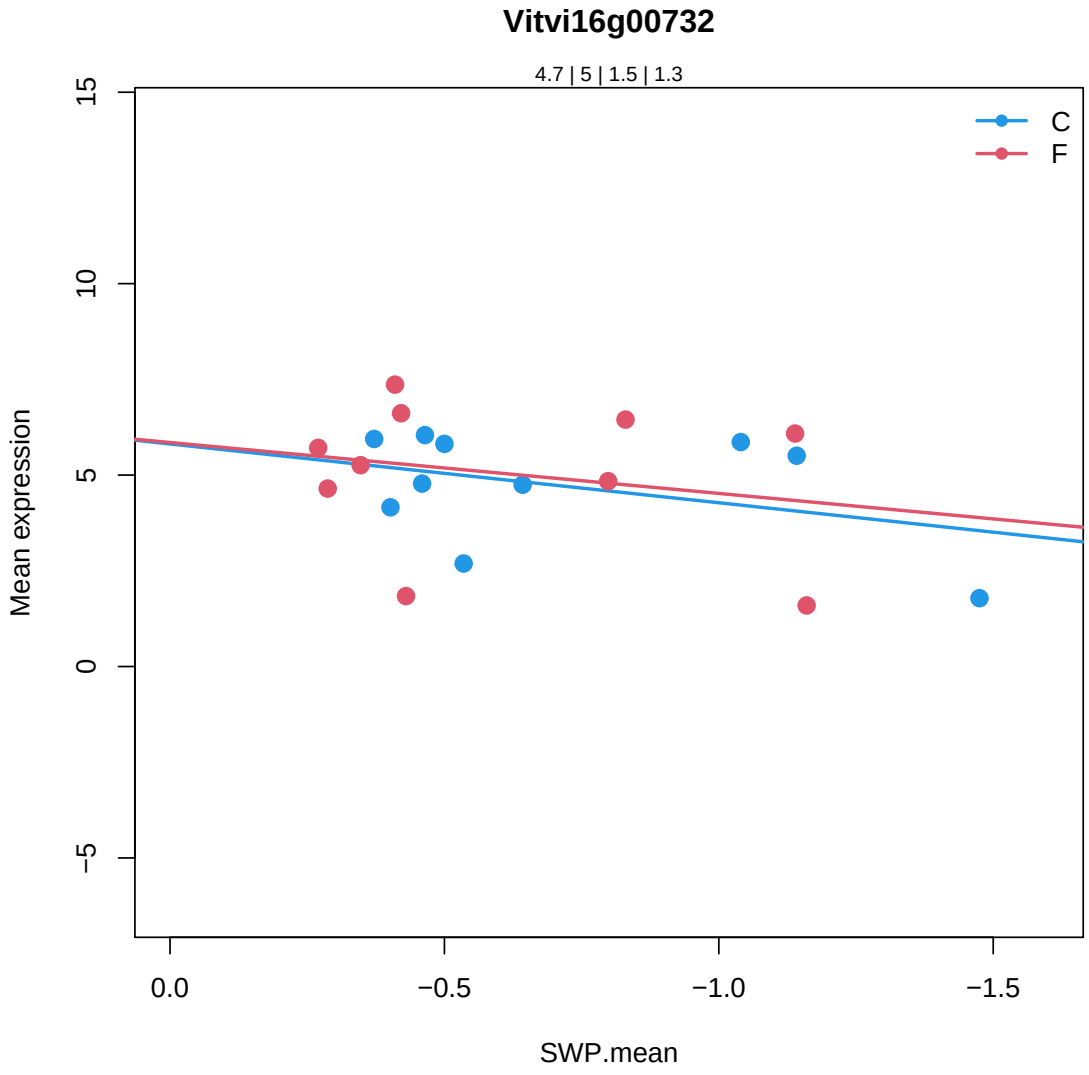
7.2.73 Vitvi16g00732: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g00732
        26.18
        misc.invertase/pectin methylesterase inhibitor family protein
        Plant invertase/pectin methylesterase inhibitor superfamily protein |
        Chr5:25040699-25041310 FORWARD LENGTH=203 |
        201606
```

Coefficients for Vitvi16g00732.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.732783	2.068892e-09	***	2.581584e-09	***
SlopeC	1.535914	0.2634437		0.7701943	
MeanF-MeanC	0.3076609	0.6554149		0.8844988	
SlopeF-SlopeC	-0.2059225	0.9185678		0.9999488	



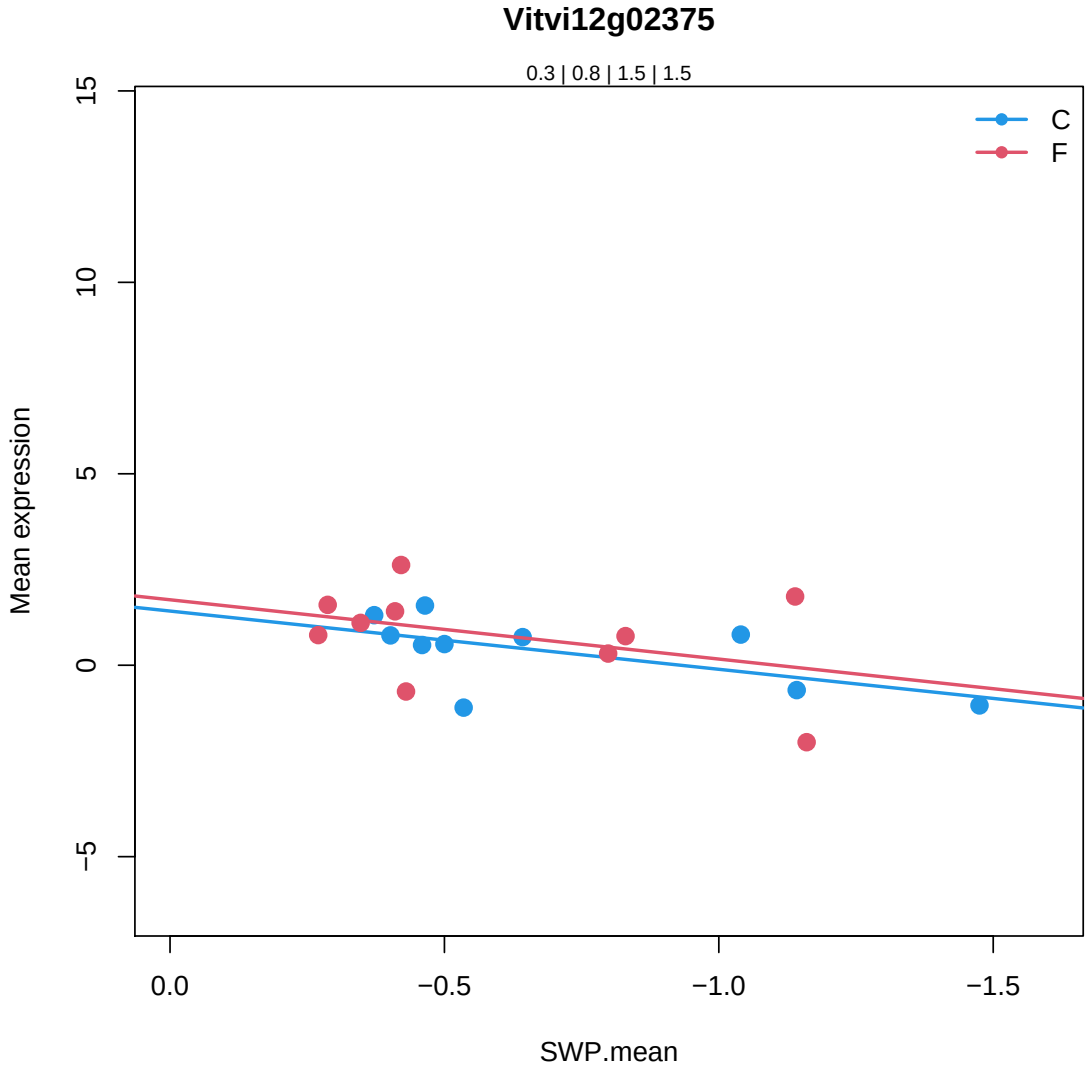
7.2.74 Vitvi12g02375: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02375
        26.10
        misc.cytochrome P450
        NA
```

Coefficients for Vitvi12g02375.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3451721	0.2655183		0.27094	
SlopeC	1.521239	0.08415782	.	0.5841227	
MeanF-MeanC	0.4204667	0.3357121		0.695595	
SlopeF-SlopeC	0.02693553	0.9830096		0.9999488	



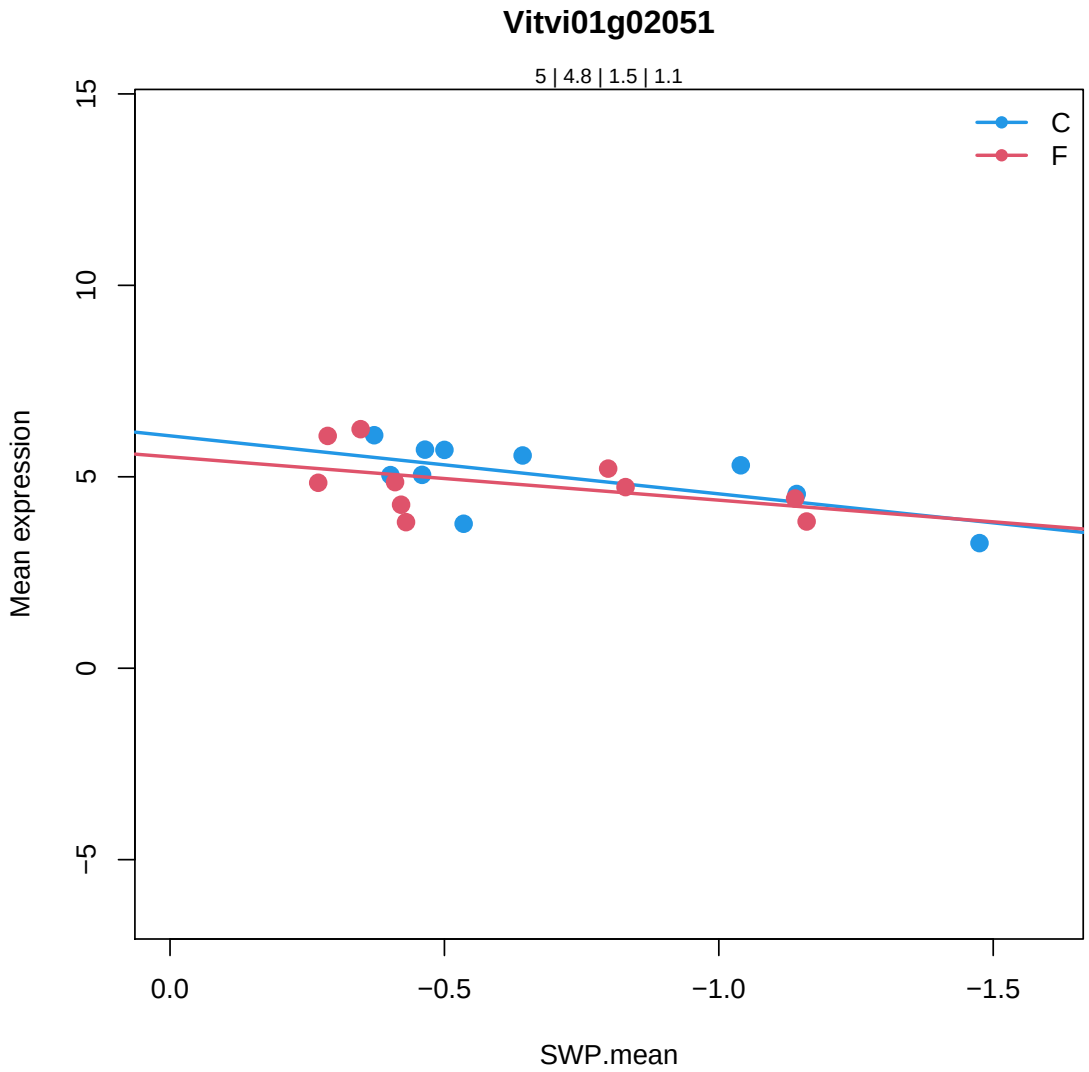
7.2.75 Vitvi01g02051: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g02051
        35.1
        not assigned.no ontology
        NA
```

Coefficients for Vitvi01g02051.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.003793	1.827053e-16	***	3.798525e-16	***
SlopeC	1.515294	0.02214125	*	0.3928719	
MeanF-MeanC	-0.1730718	0.5851719		0.8542425	
SlopeF-SlopeC	-0.3848945	0.6779938		0.9999488	



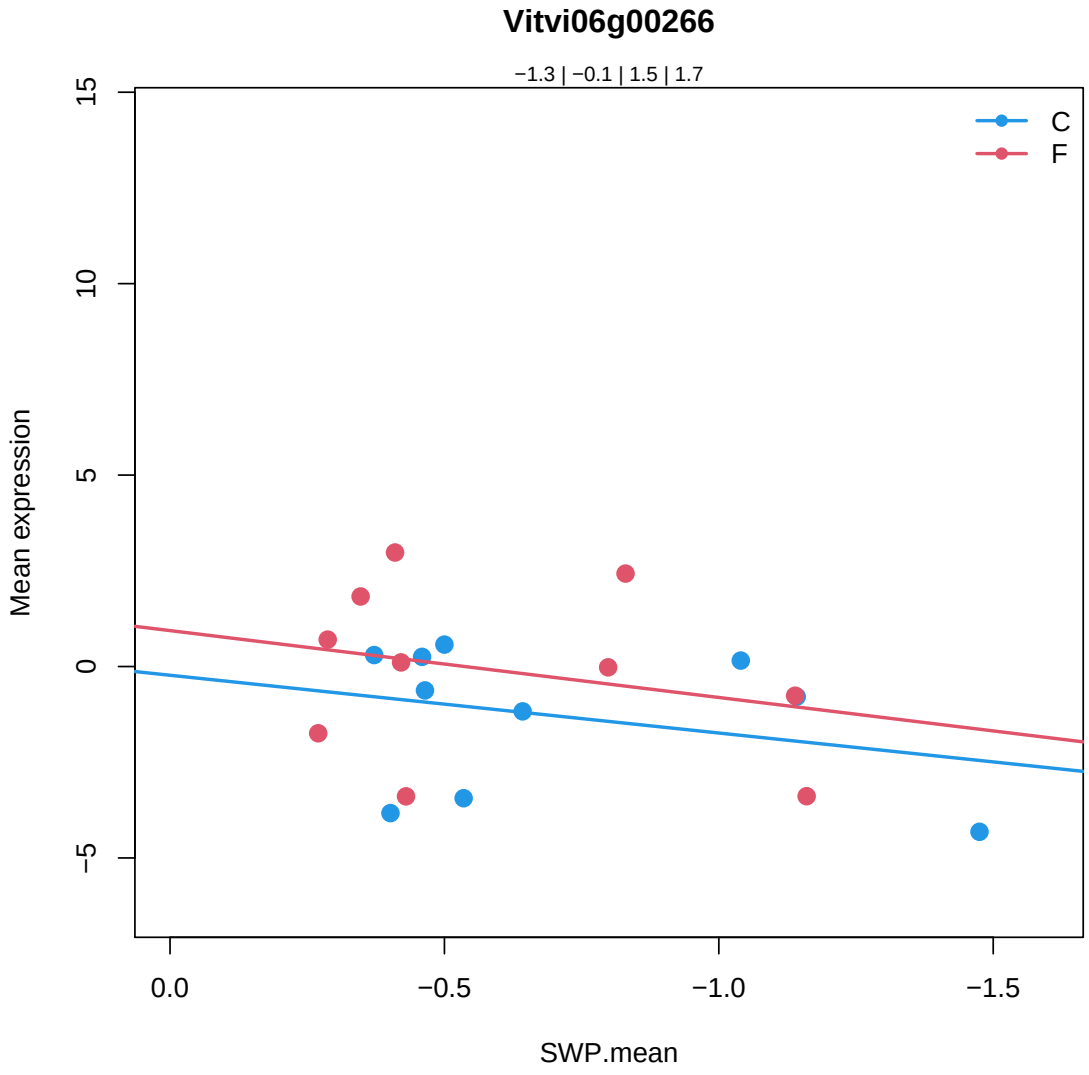
7.2.76 Vitvi06g00266: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00266
        26.2
        misc.UDP glucosyl and glucoronyl transferases
        glycosyltransferase family protein 2 |
        Chr5:24402329-24405521 REVERSE LENGTH=932 |
        201606
```

Coefficients for Vitvi06g00266.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.288917	0.03647398	*	0.03810132	*
SlopeC	1.508771	0.358335		0.8183149	
MeanF-MeanC	1.162776	0.1690658		0.4980482	
SlopeF-SlopeC	0.2379273	0.9216986		0.9999488	



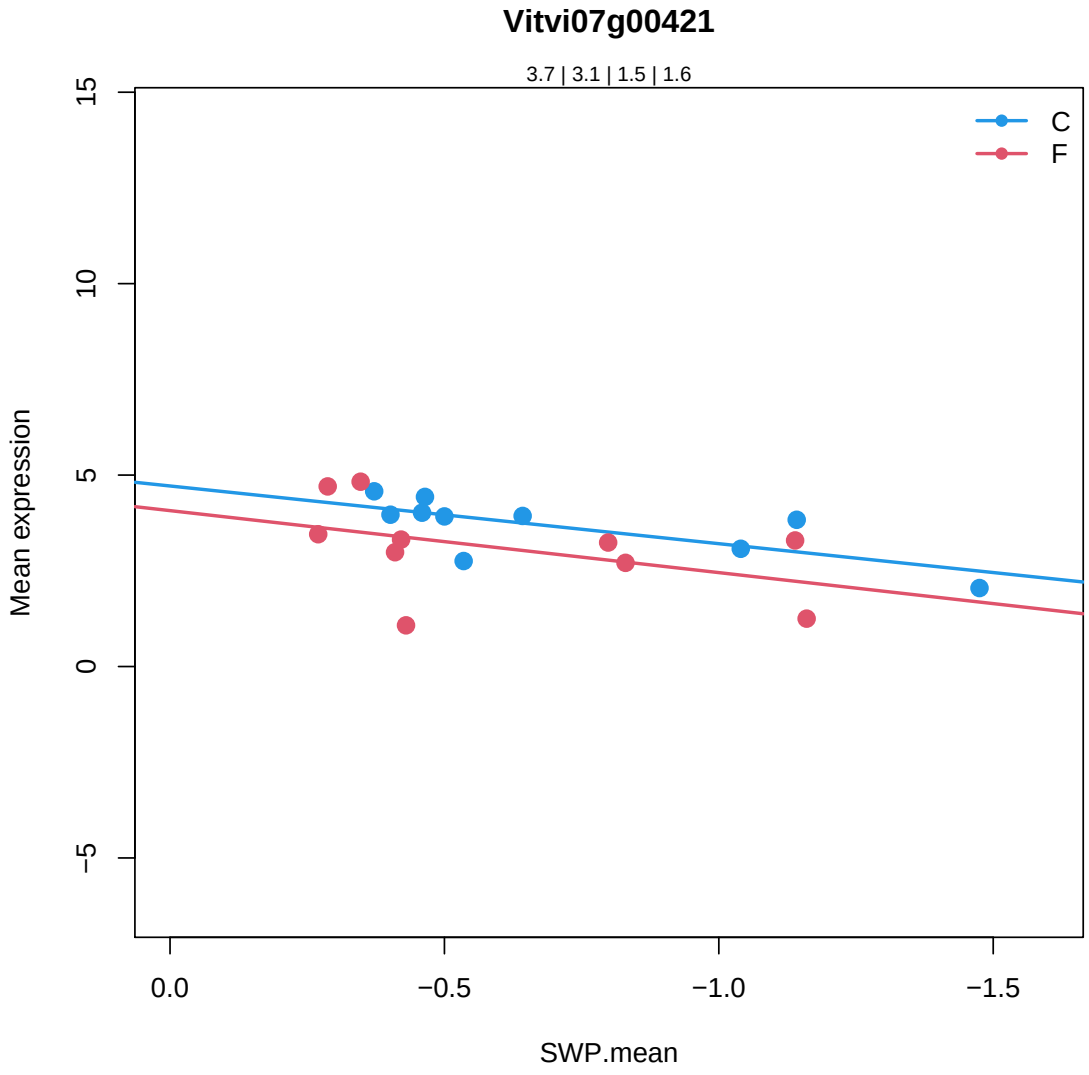
7.2.77 Vitvi07g00421: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g00421
        27.3.32
        RNA.regulation of transcription.WRKY domain transcription factor famil
        WRKY DNA-binding protein 35 |
        Chr2:14693839-14696378 REVERSE LENGTH=427 |
        201606
```

Coefficients for Vitvi07g00421.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.655355	2.946396e-12	***	4.122357e-12	***
SlopeC	1.507519	0.0502646	.	0.5104439	
MeanF-MeanC	-0.5703813	0.1372131		0.4433753	
SlopeF-SlopeC	0.1115172	0.9188421		0.9999488	



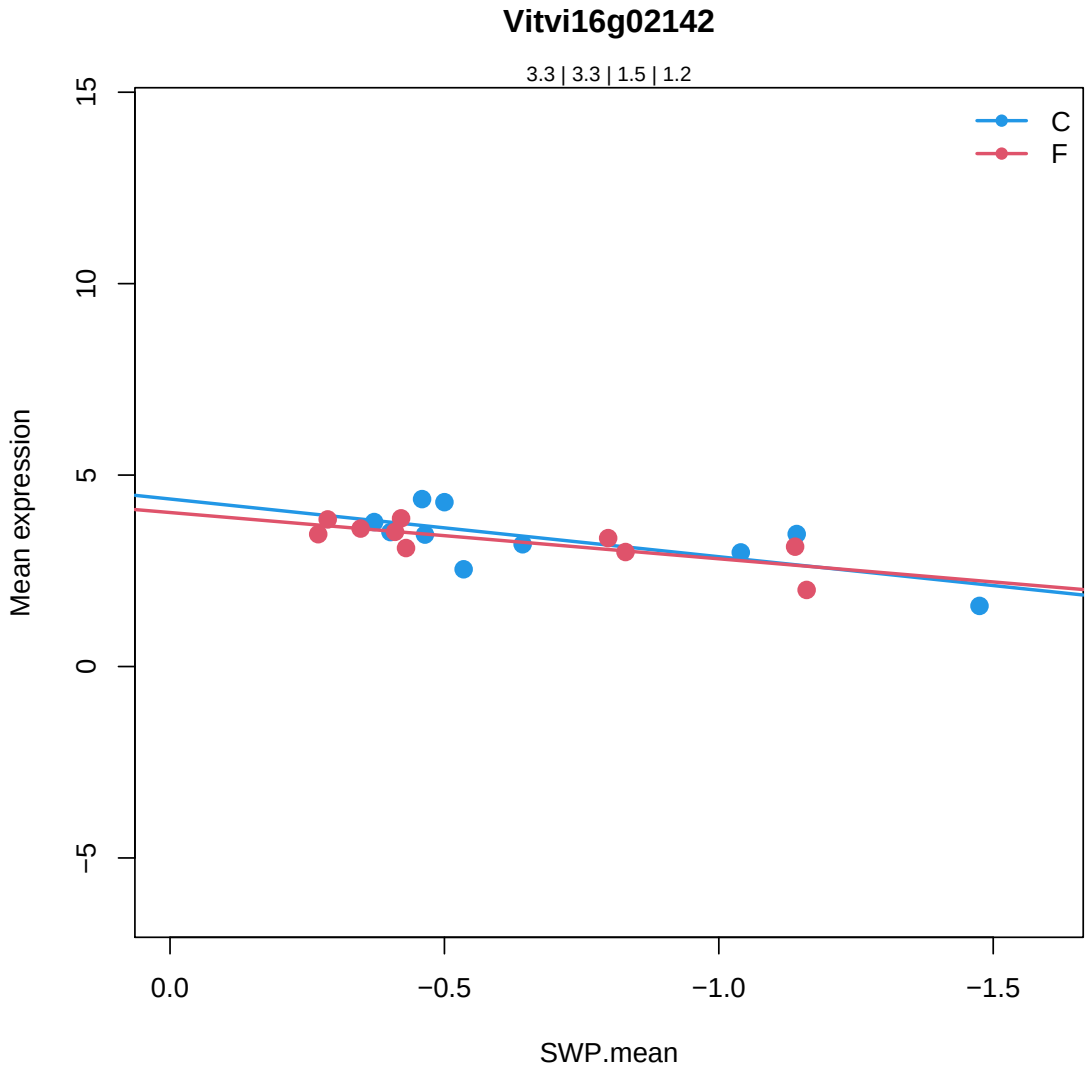
7.2.78 Vitvi16g02142: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g02142
        35.2
        not assigned.unknown
        PR5-like receptor kinase |
        Chr5:15293325-15295838 REVERSE LENGTH=665 |
        201606
```

Coefficients for Vitvi16g02142.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.315001	1.289912e-15	***	2.382554e-15	***
SlopeC	1.50696	0.002857826	**	0.2035467	
MeanF-MeanC	-0.02948725	0.8980992		0.973376	
SlopeF-SlopeC	-0.2983955	0.6587387		0.9999488	



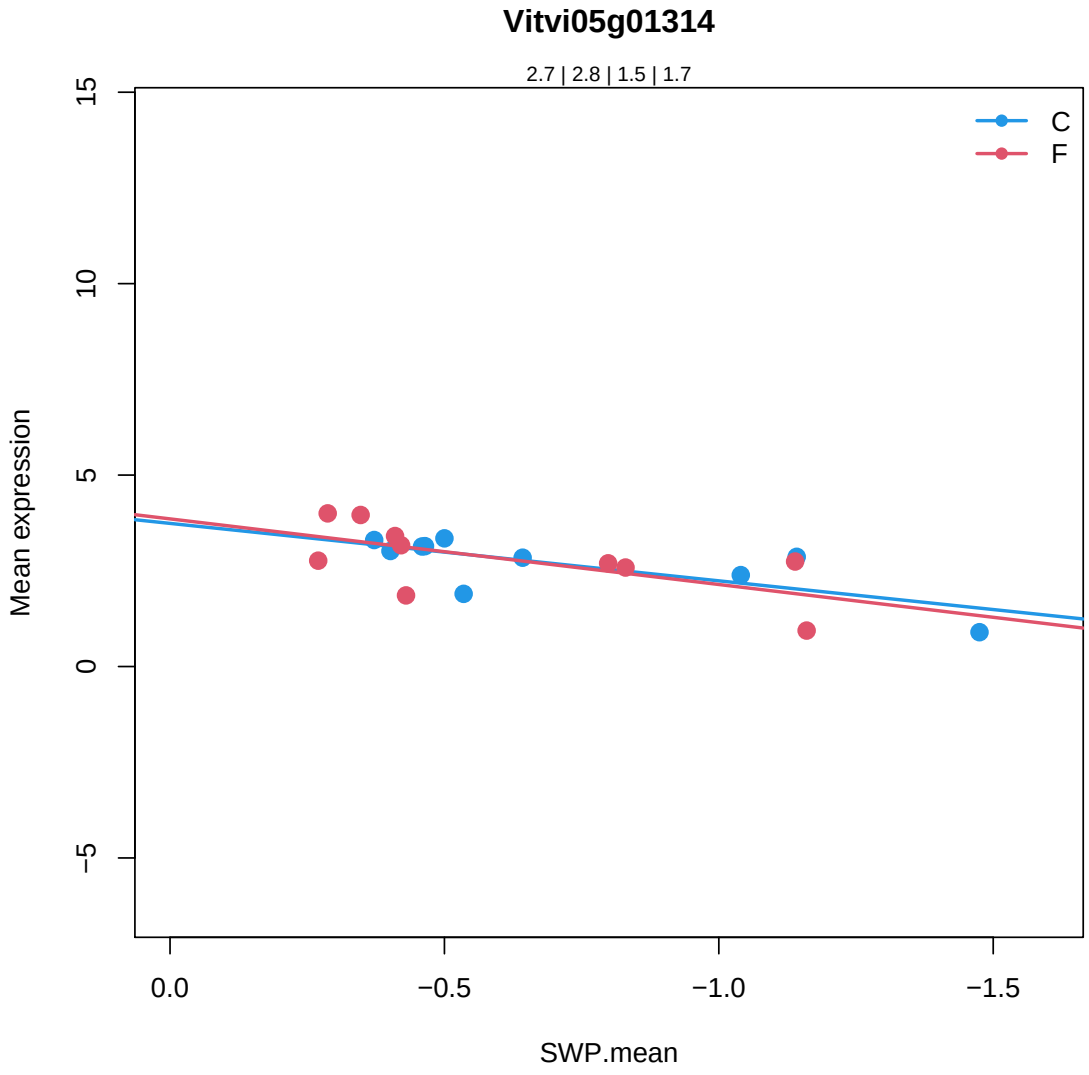
7.2.79 Vitvi05g01314: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01314
        35.2
        not assigned.unknown
        dCTP pyrophosphatase-like protein |
        Chr3:9213236-9214144 FORWARD LENGTH=141 |
        201606
```

Coefficients for Vitvi05g01314.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.683525	4.76701e-12	***	6.593354e-12	***
SlopeC	1.500077	0.01205259	*	0.3229093	
MeanF-MeanC	0.1280583	0.6497156		0.8819884	
SlopeF-SlopeC	0.2136234	0.7955011		0.9999488	



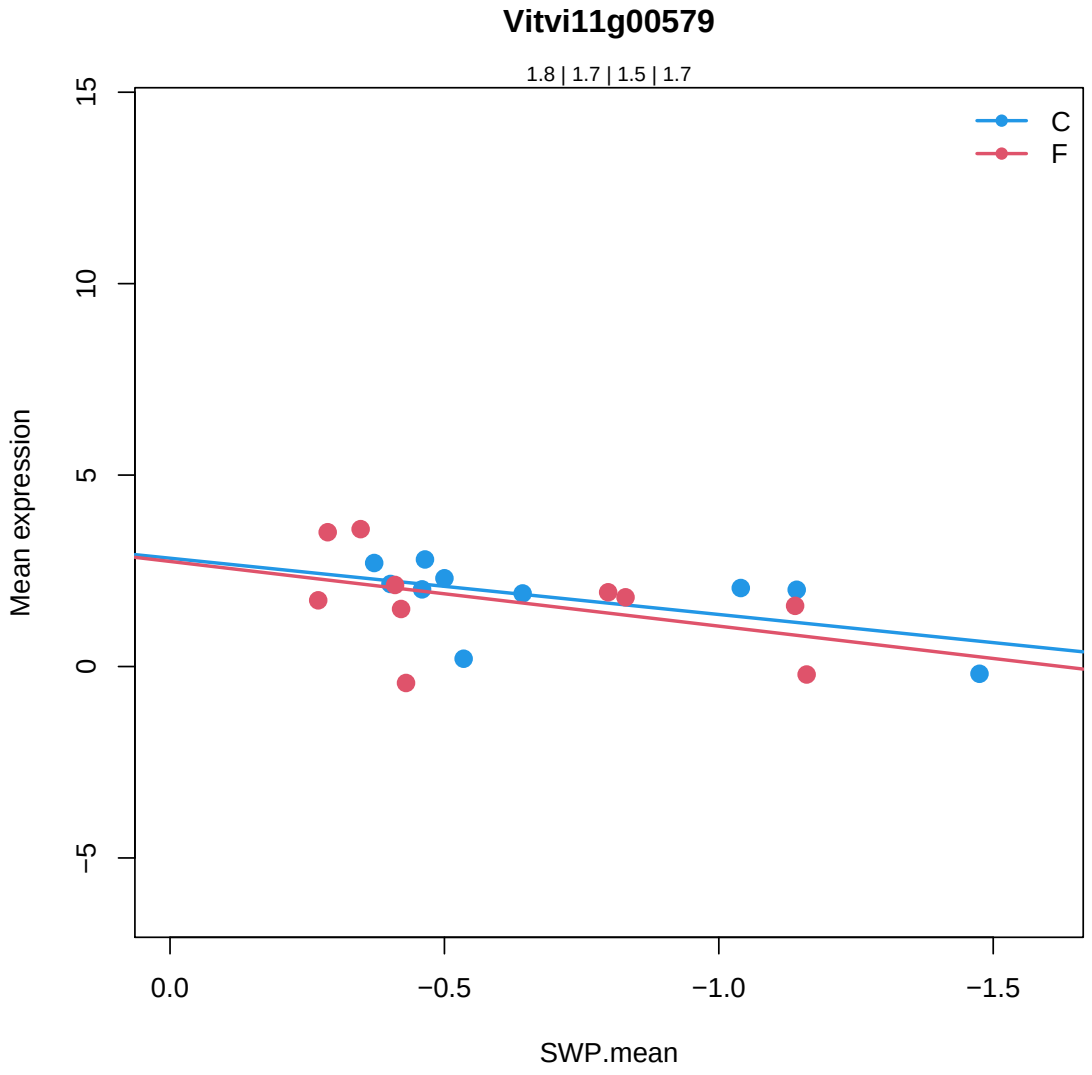
7.2.80 Vitvi11g00579: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00579
        30.3
        signalling.calcium
        calcium-binding EF hand family protein |
        Chr4:15501134-15503321 FORWARD LENGTH=498 |
        201606
```

Coefficients for Vitvi11g00579.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.795264	6.384216e-06	***	7.237502e-06	***
SlopeC	1.469687	0.09538147	.	0.6054995	
MeanF-MeanC	-0.08033232	0.8529609		0.960757	
SlopeF-SlopeC	0.2197738	0.8625071		0.9999488	



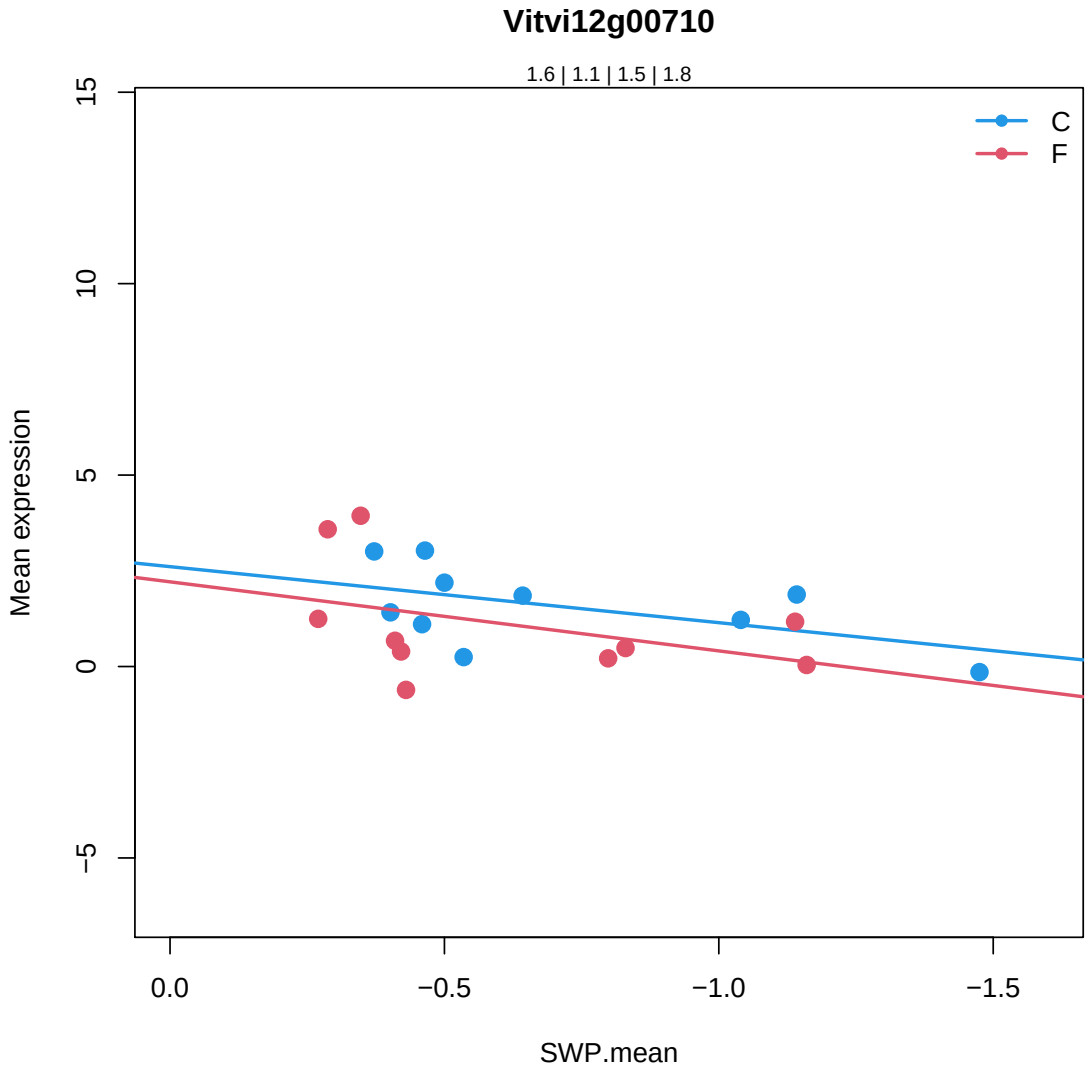
7.2.81 Vitvi12g00710: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00710
        35.1
        not assigned.no ontology
        HXXXD-type acyl-transferase family protein |
        Chr5:16431448-16433086 FORWARD LENGTH=457 |
        201606
```

Coefficients for Vitvi12g00710.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.579266	0.0001401601	***	0.0001543361	***
SlopeC	1.463347	0.1383624		0.6650191	
MeanF-MeanC	-0.4665462	0.345083		0.7046831	
SlopeF-SlopeC	0.3407302	0.8119916		0.9999488	



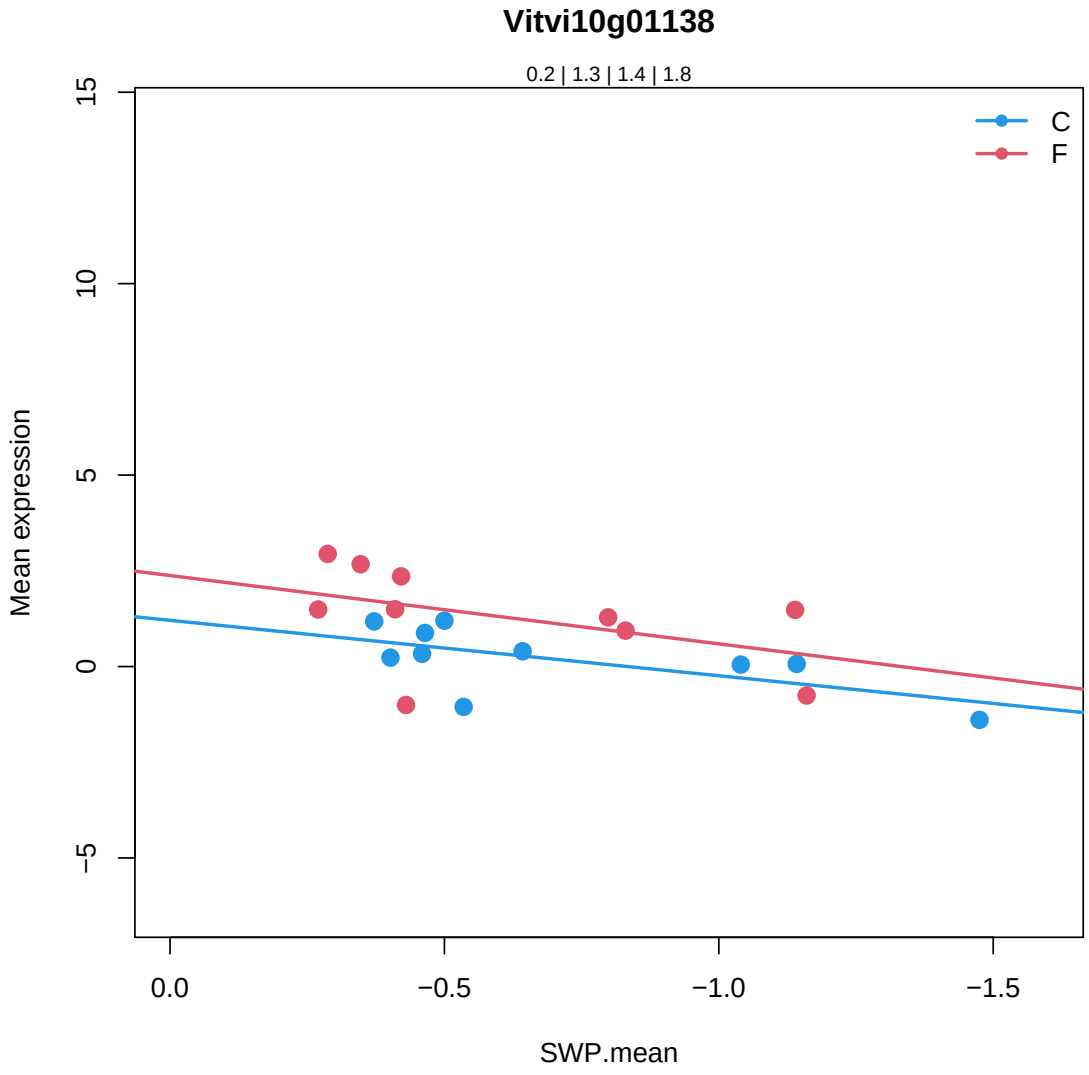
7.2.82 Vitvi10g01138: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g01138
        26.10
        misc.cytochrome P450
        cytochrome P450%2C family 71%2C subfamily B%2C polypeptide 34 |
        Chr3:9639199-9640866 REVERSE LENGTH=500 |
        201606
```

Coefficients for Vitvi10g01138.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1886069	0.5137493		0.5198544	
SlopeC	1.447452	0.08092438	.	0.5764511	
MeanF-MeanC	1.100601	0.01212643	*	0.08768291	.
SlopeF-SlopeC	0.3368975	0.7772886		0.9999488	



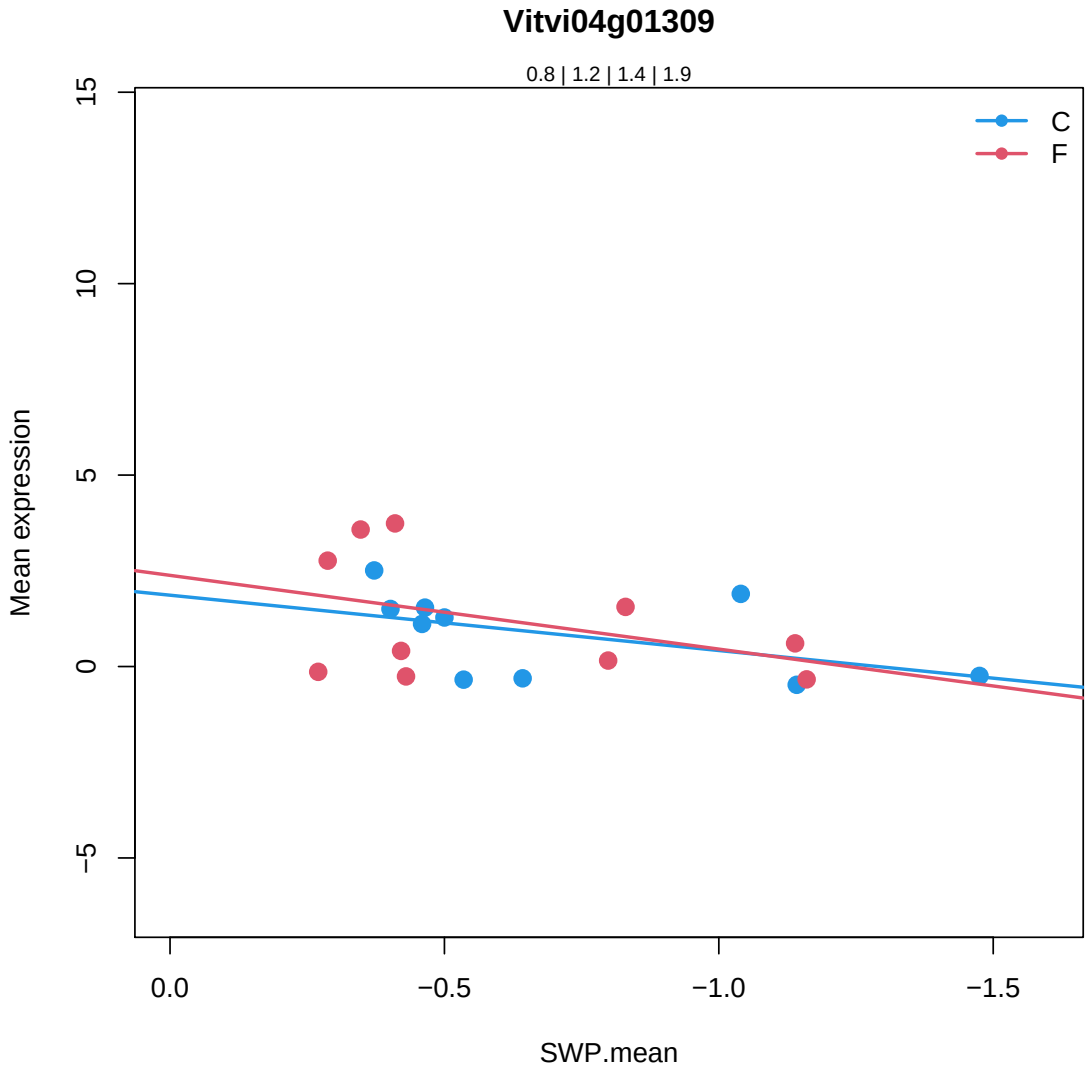
7.2.83 Vitvi04g01309: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01309
        27.3.25
        RNA.regulation of transcription.MYB domain transcription factor family
        RAD-like 6 |
        Chr1:28244463-28245453 REVERSE LENGTH=97 |
        201606
```

Coefficients for Vitvi04g01309.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8465924	0.02994507	*	0.03134342	*
SlopeC	1.444642	0.1682215		0.6980212	
MeanF-MeanC	0.3606213	0.4912335		0.8011134	
SlopeF-SlopeC	0.481058	0.7527578		0.9999488	



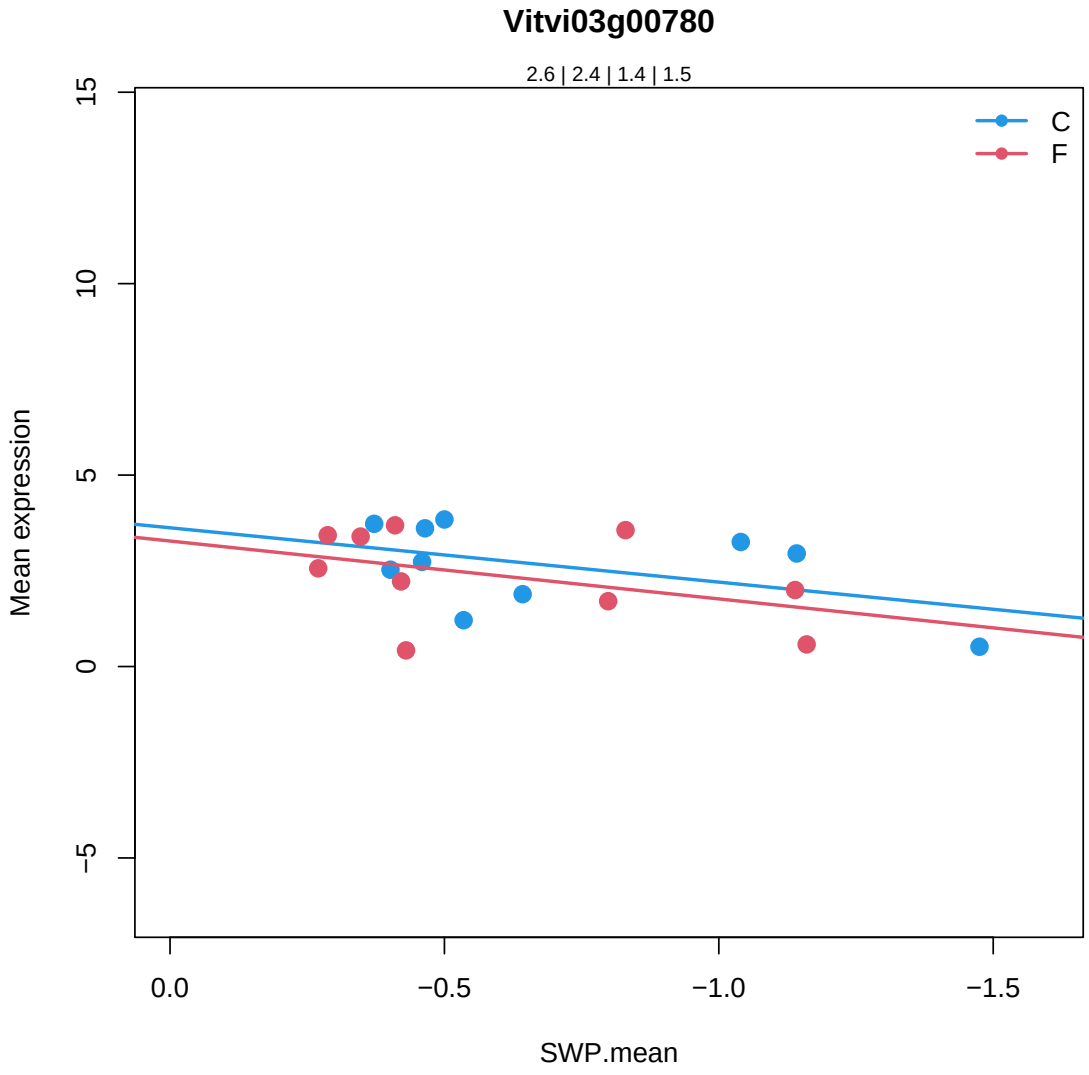
7.2.84 Vitvi03g00780: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00780
        17.3.1.2.99
        hormone metabolism.brassinosteroid.synthesis-degradation.sterols.other
        FAD/NAD(P)-binding oxidoreductase family protein |
        Chr1:21714094-21717246 REVERSE LENGTH=531 |
        201606
```

Coefficients for Vitvi03g00780.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.625734	2.565608e-08	***	3.09375e-08	***
SlopeC	1.418833	0.1130047		0.6290529	
MeanF-MeanC	-0.2696277	0.5432267		0.8299692	
SlopeF-SlopeC	0.09293993	0.9426974		0.9999488	



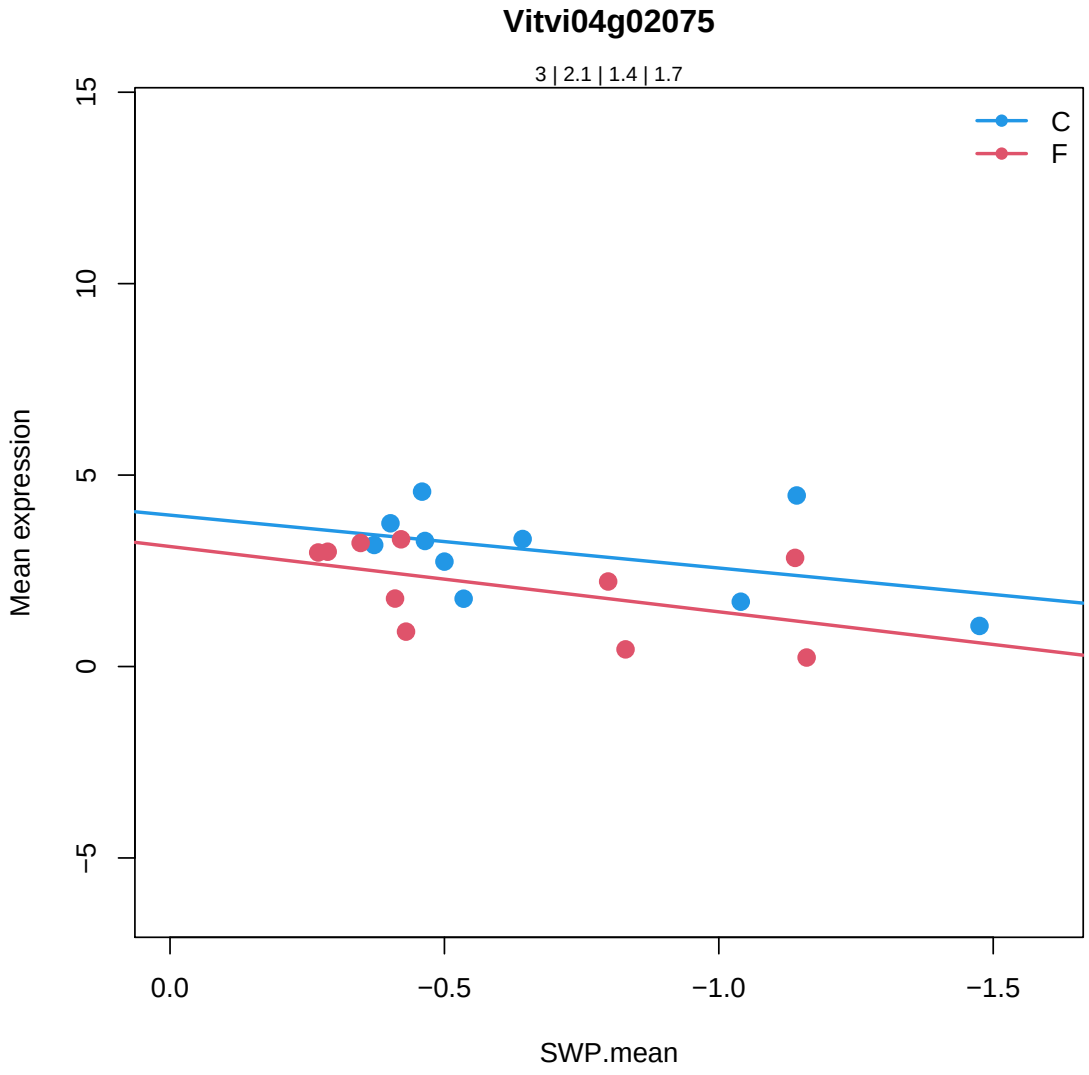
7.2.85 Vitvi04g02075: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g02075
        35.2
        not assigned.unknown
        SAUR-like auxin-responsive protein family |
        Chr4:16596860-16597144 FORWARD LENGTH=94 |
        201606
```

Coefficients for Vitvi04g02075.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.982272	3.381984e-09	***	4.192615e-09	***
SlopeC	1.381268	0.1255774		0.6460361	
MeanF-MeanC	-0.8871479	0.05672474	.	0.2592499	
SlopeF-SlopeC	0.324337	0.8038447		0.9999488	



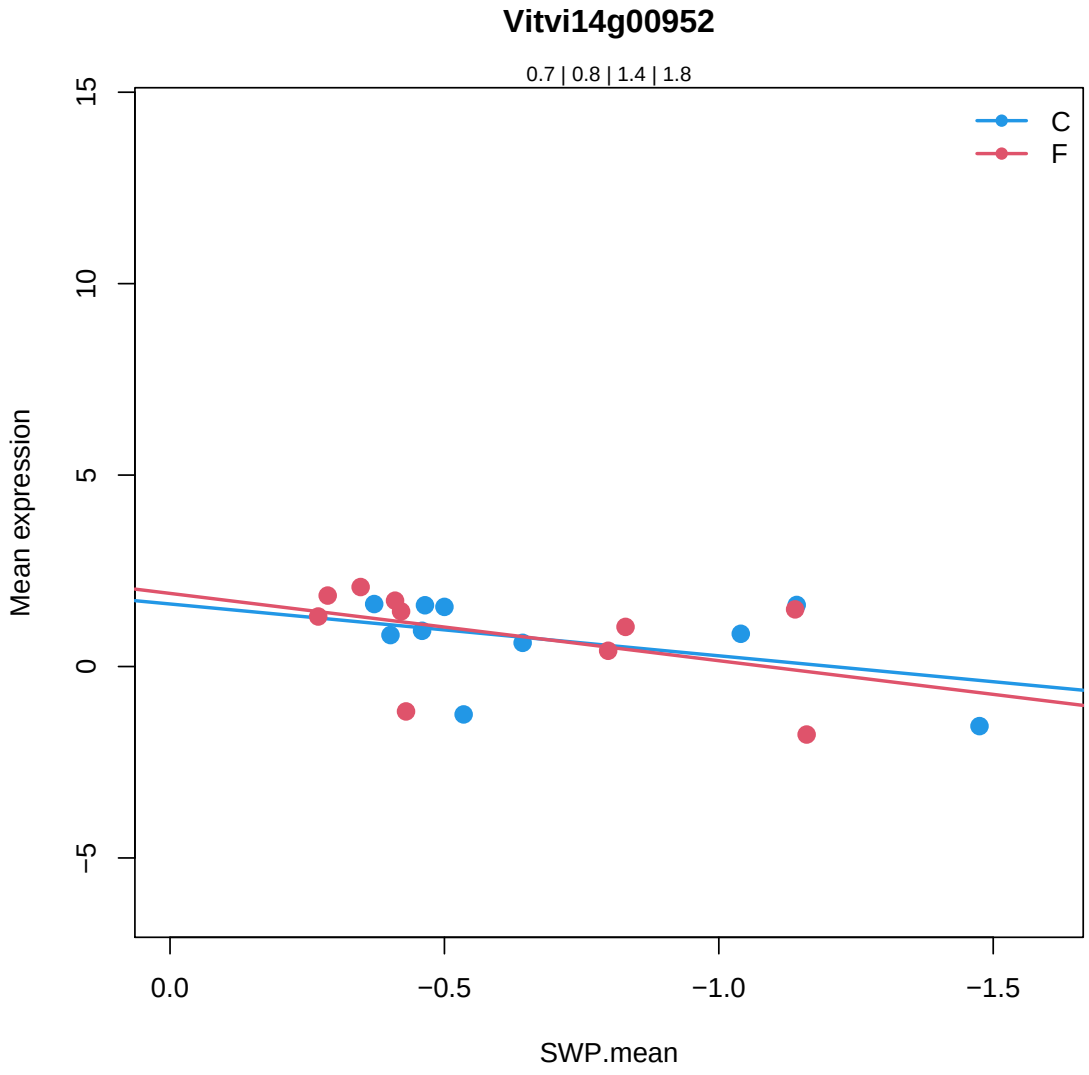
7.2.86 Vitvi14g00952: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g00952
        29.4.1.56
        protein.postranslational modification.kinase.receptor like cytoplasmat
        Protein kinase superfamily protein |
        Chr5:15008433-15011025 REVERSE LENGTH=552 |
        201606
```

Coefficients for Vitvi14g00952.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6814394	0.05116172	.	0.05326186	.
SlopeC	1.35337	0.1548672		0.6857741	
MeanF-MeanC	0.1569735	0.7397964		0.9225159	
SlopeF-SlopeC	0.404242	0.7701399		0.9999488	



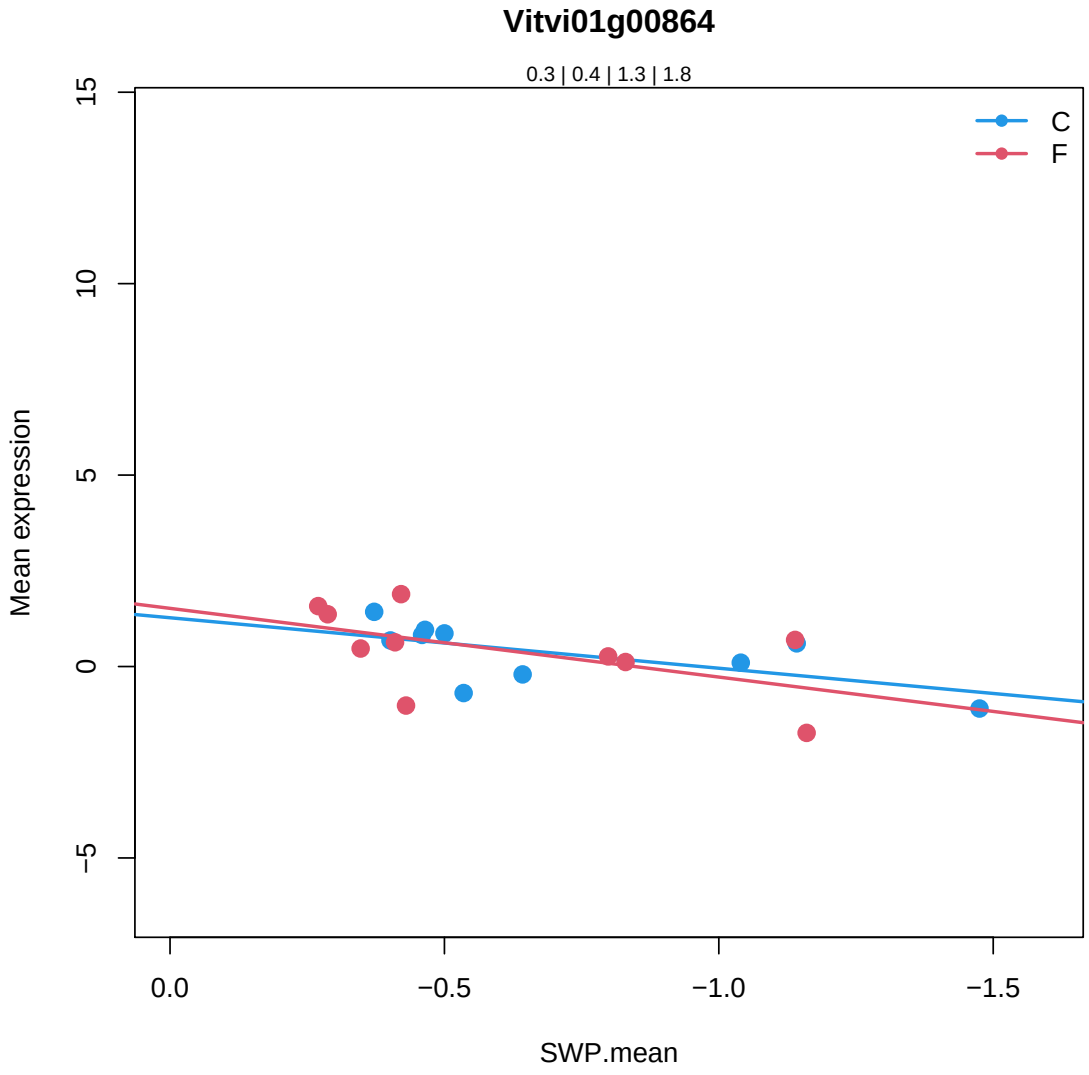
7.2.87 Vitvi01g00864: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00864
        35.2
        not assigned.unknown
        ARM repeat superfamily protein |
        Chr1:9455669-9457917 REVERSE LENGTH=625 |
        201606
```

Coefficients for Vitvi01g00864.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3465441	0.1694328		0.1740929	
SlopeC	1.317957	0.06516508	.	0.5524172	
MeanF-MeanC	0.07912716	0.8205966		0.9503527	
SlopeF-SlopeC	0.4763593	0.6416797		0.9999488	



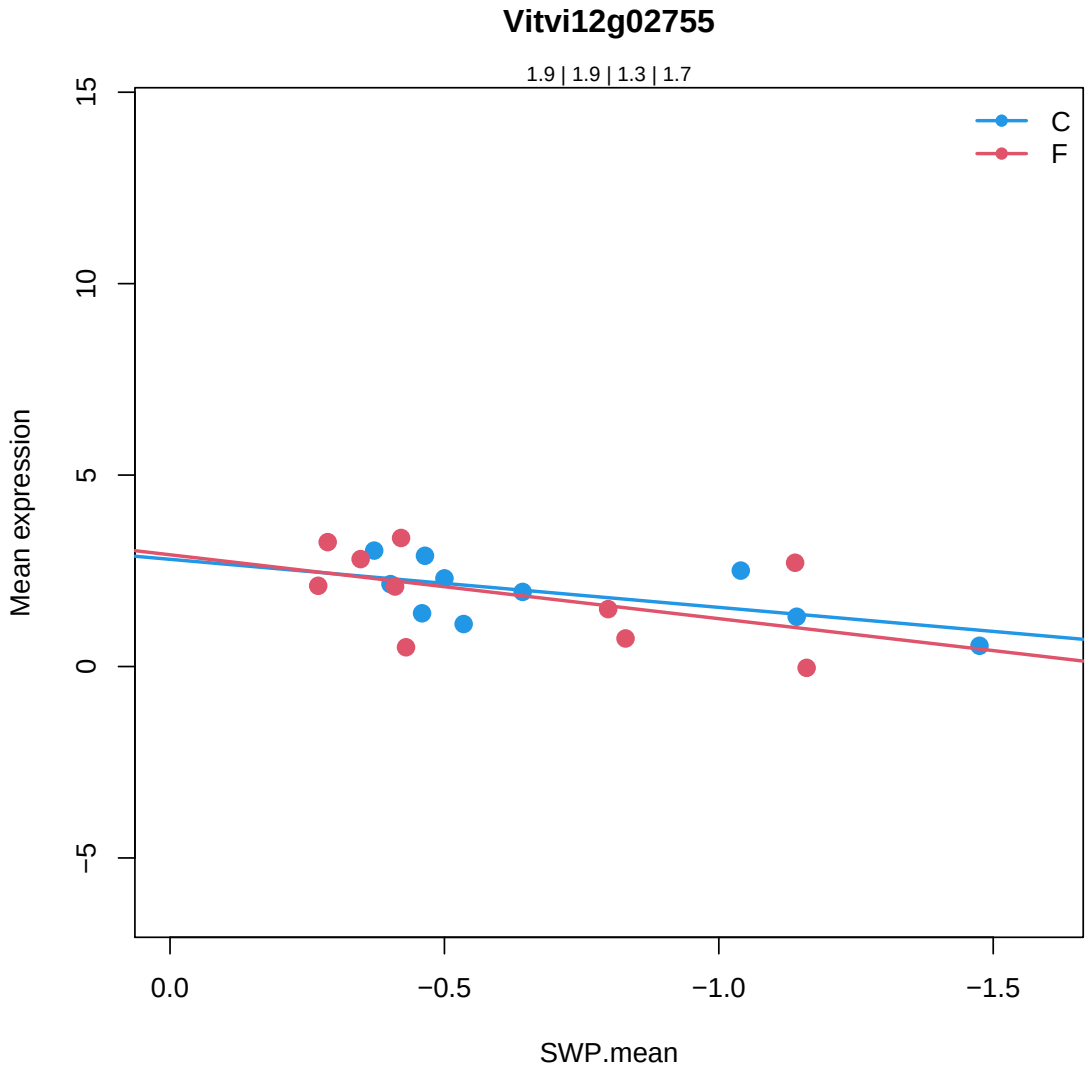
7.2.88 Vitvi12g02755: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02755
        35.2
        not assigned.unknown
        Polyketide cyclase/dehydrase and lipid transport superfamily protein |
        Chr5:20234771-20236135 REVERSE LENGTH=242 |
        201606
```

Coefficients for Vitvi12g02755.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.917028	3.354134e-07	***	3.919027e-07	***
SlopeC	1.255384	0.1021259		0.6138959	
MeanF-MeanC	-0.01514054	0.9680551		0.9925468	
SlopeF-SlopeC	0.4131881	0.7094099		0.9999488	



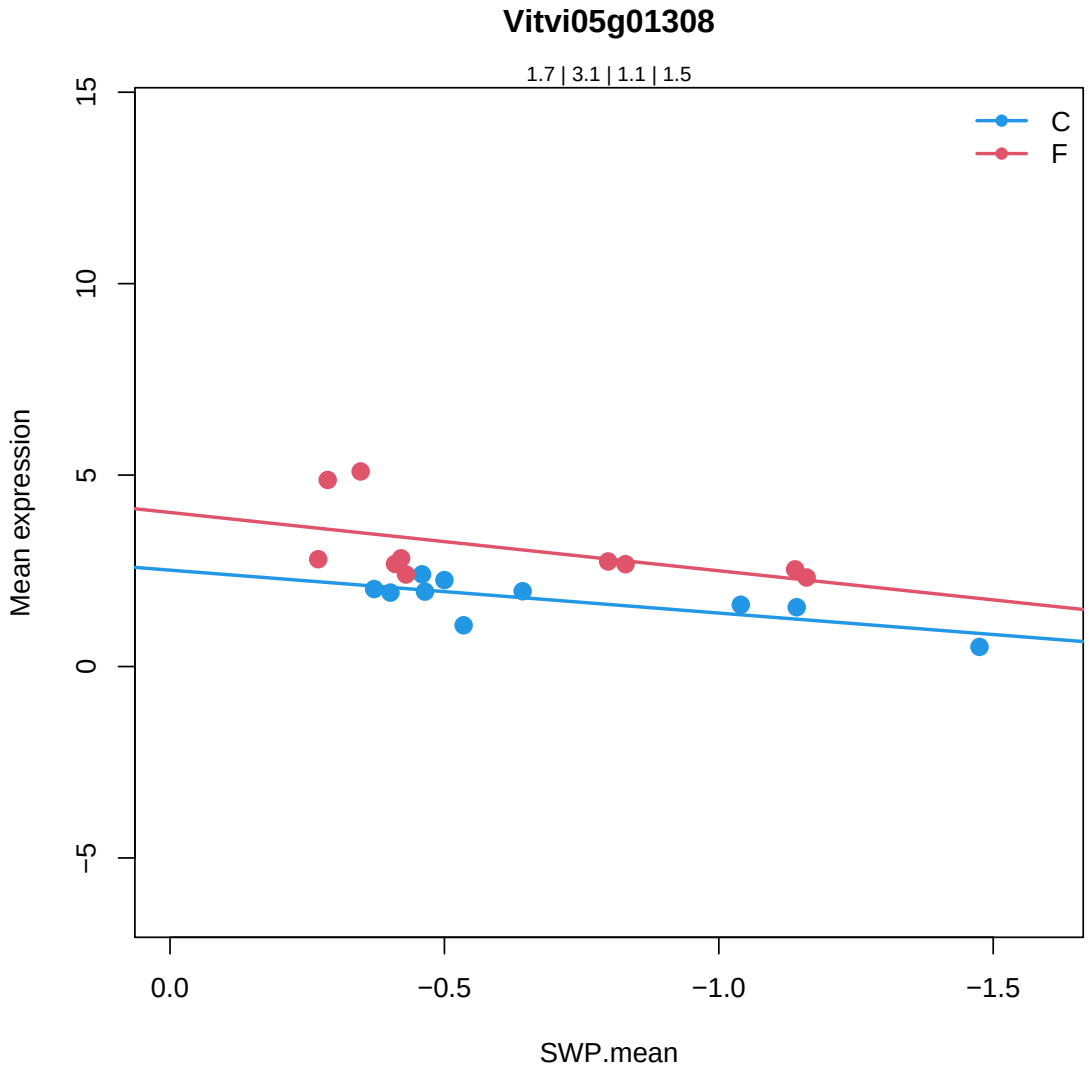
7.2.89 Vitvi05g01308: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01308
        30.5
        signalling.G-proteins
        Immunoglobulin E-set superfamily protein |
        Chr3:2514175-2515544 FORWARD LENGTH=240 |
        201606
```

Coefficients for Vitvi05g01308.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.728964	3.932462e-08	***	4.71586e-08	***
SlopeC	1.121079	0.0665859	.	0.5548906	
MeanF-MeanC	1.366588	0.000135811	***	0.002333744	**
SlopeF-SlopeC	0.4013877	0.6466699		0.9999488	



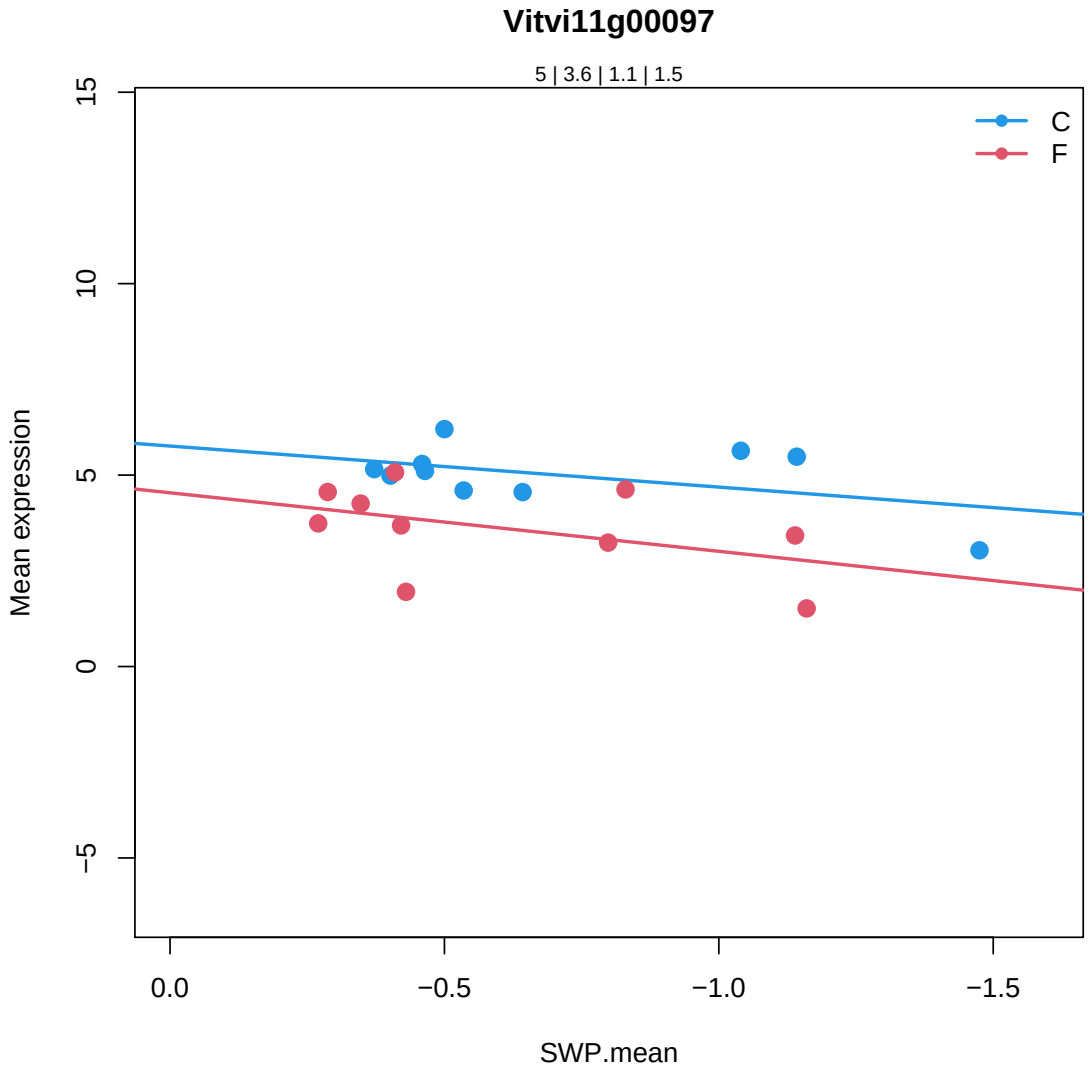
7.2.90 Vitvi11g00097: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00097
        27.3.25
        RNA.regulation of transcription.MYB domain transcription factor family
        Duplicated homeodomain-like superfamily protein |
        Chr5:13726807-13727729 FORWARD LENGTH=258 |
        201606
```

Coefficients for Vitvi11g00097.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.004513	1.064788e-14	***	1.775074e-14	***
SlopeC	1.072321	0.1669975		0.6971721	
MeanF-MeanC	-1.398392	0.00138924	**	0.01641457	*
SlopeF-SlopeC	0.4559302	0.6868592		0.9999488	



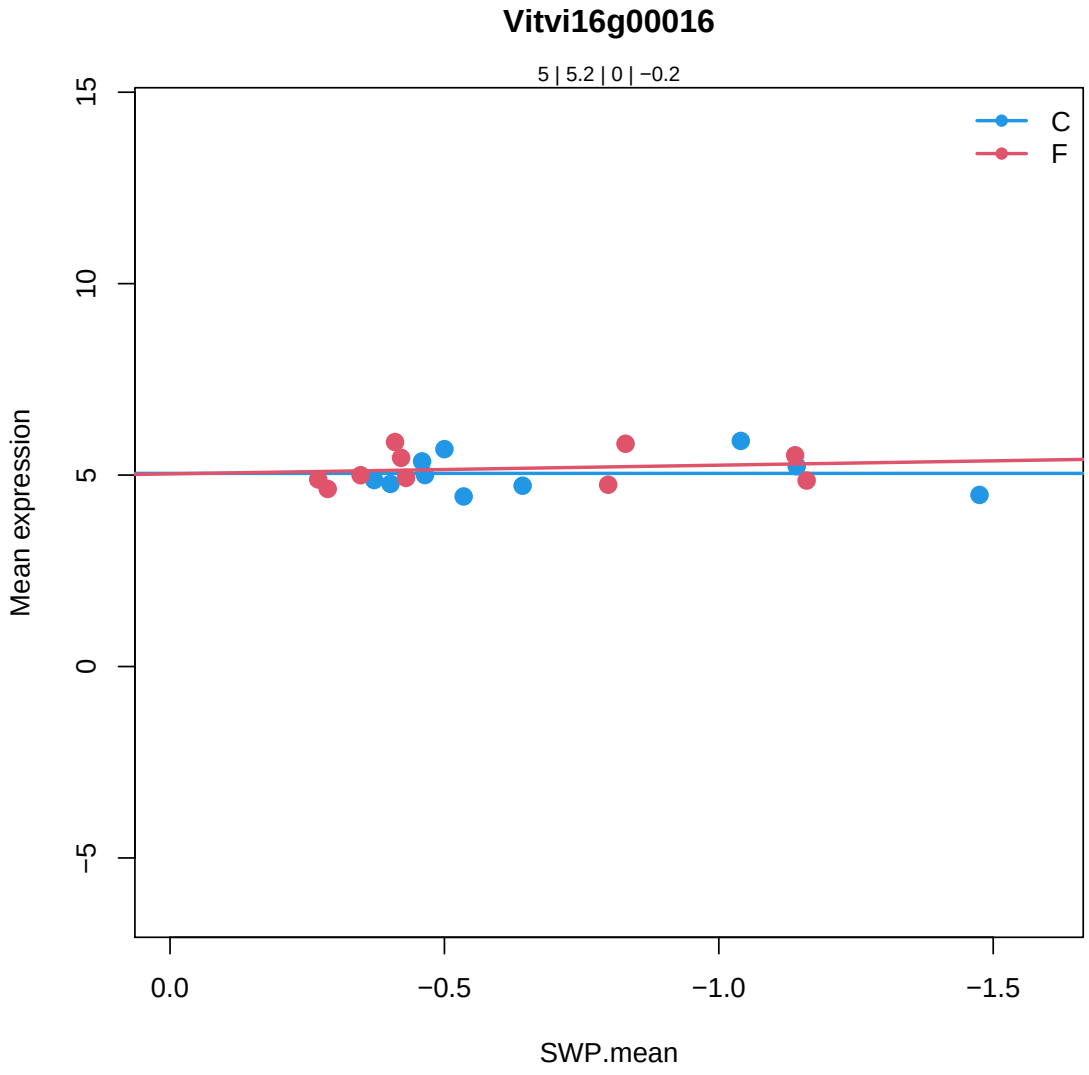
7.2.91 Vitvi16g00016: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g00016
        35.2
        not assigned.unknown
        hypothetical protein |
        Chr1:9835122-9835842 REVERSE LENGTH=123 |
        201606
```

Coefficients for Vitvi16g00016.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.044148	1.119238e-19	***	5.240991e-19	***
SlopeC	7.788995e-05	0.9998586		0.9998964	
MeanF-MeanC	0.1258619	0.5745221		0.8492524	
SlopeF-SlopeC	-0.2264954	0.7294618		0.9999488	



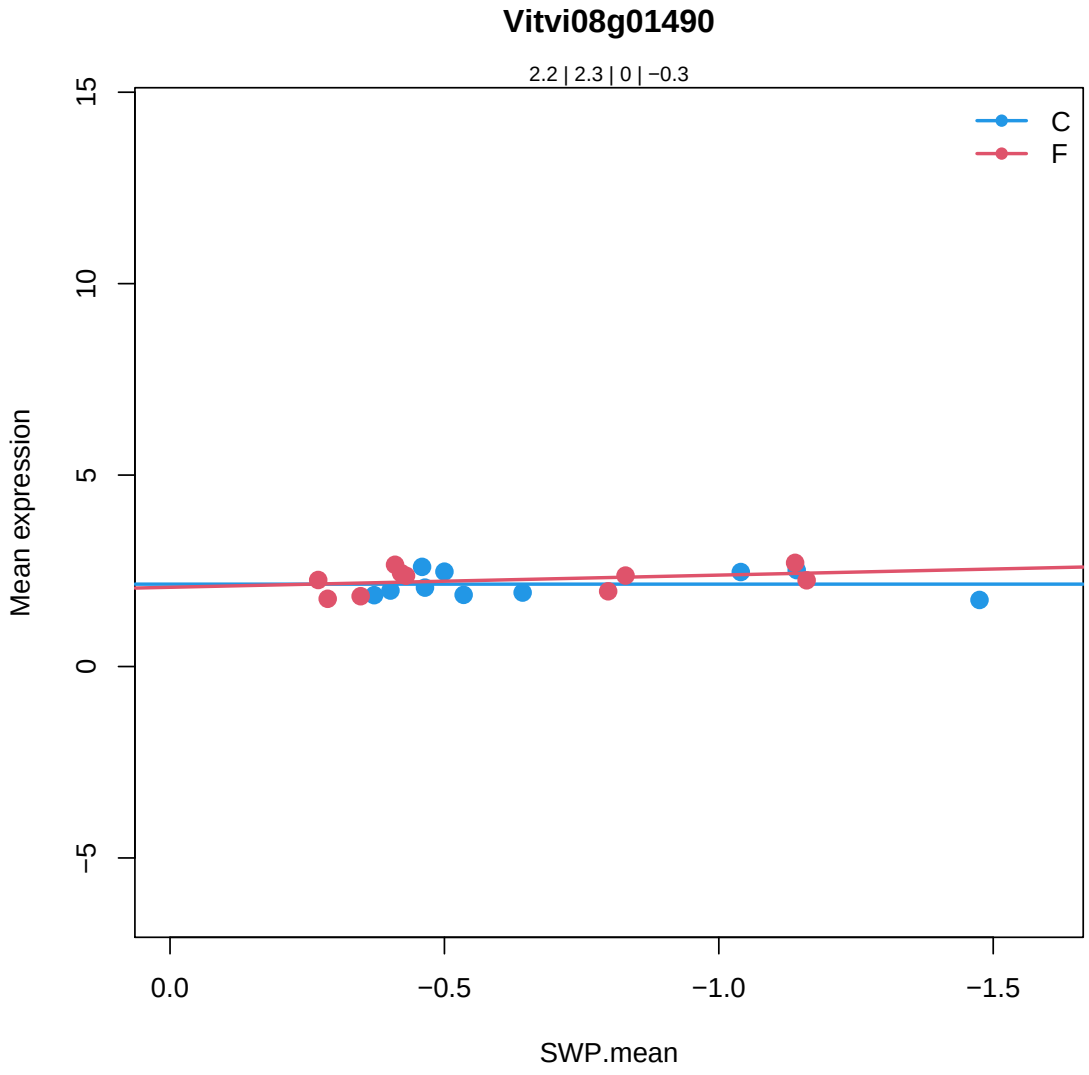
7.2.92 Vitvi08g01490: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01490
        23.2.1.2
        nucleotide metabolism.degradation.pyrimidine.uridine nucleosidase
        uridine-ribohydrolase 1 |
        Chr2:15224692-15226633 REVERSE LENGTH=336 |
        201606
```

Coefficients for Vitvi08g01490.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.151318	2.15851e-14	***	3.501118e-14	***
SlopeC	-4.385765e-05	0.9998964		0.9998964	
MeanF-MeanC	0.1118183	0.5168101		0.816402	
SlopeF-SlopeC	-0.3180126	0.5287951		0.9999488	



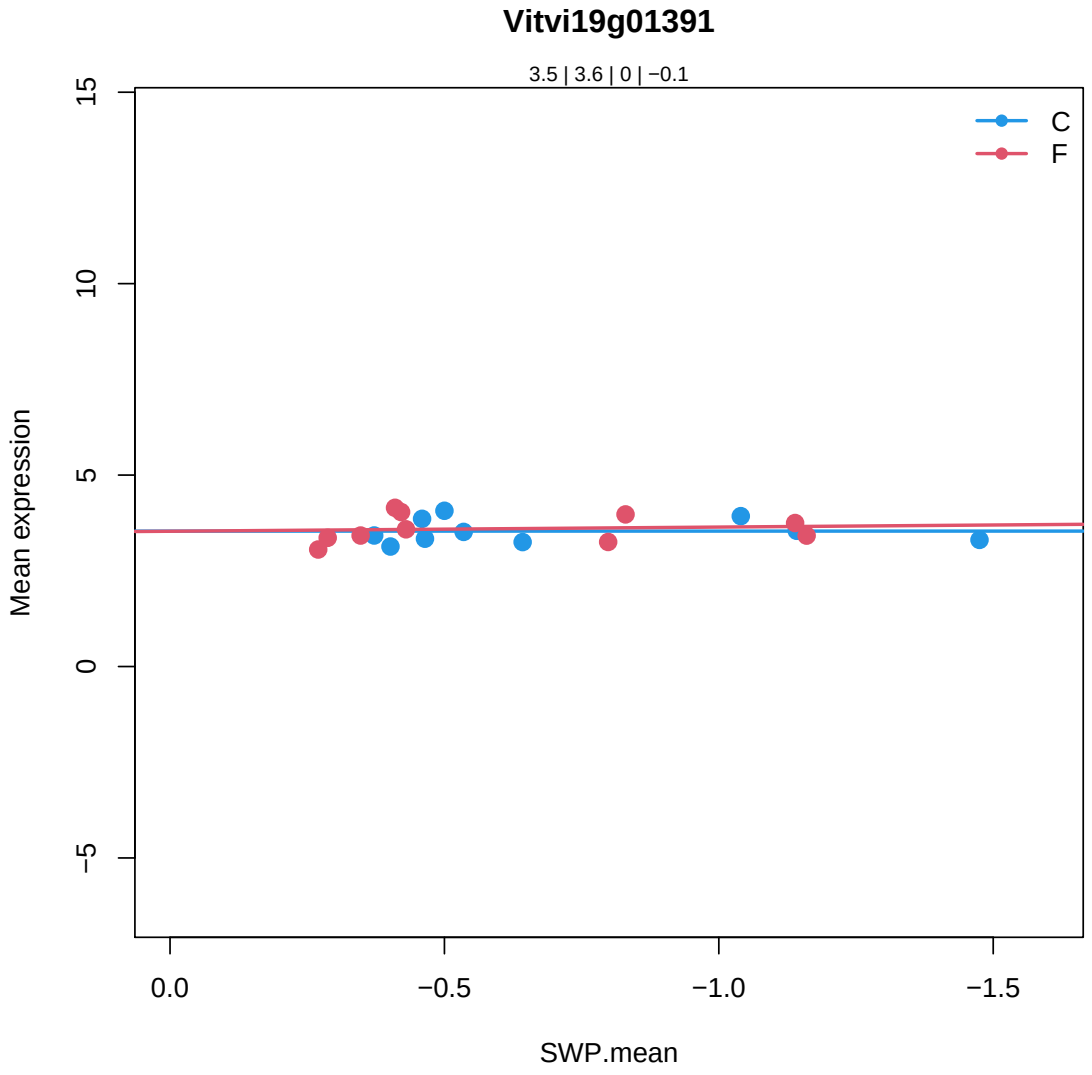
7.2.93 Vitvi19g01391: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g01391
        35.2
        not assigned.unknown
        Ribosomal protein L18ae family |
        Chr1:19984908-19985960 REVERSE LENGTH=153 |
        201606
```

Coefficients for Vitvi19g01391.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.536443	1.918373e-18	***	6.090364e-18	***
SlopeC	-8.840028e-05	0.9998001		0.9998964	
MeanF-MeanC	0.06284276	0.7263763		0.9169873	
SlopeF-SlopeC	-0.108777	0.8359528		0.9999488	



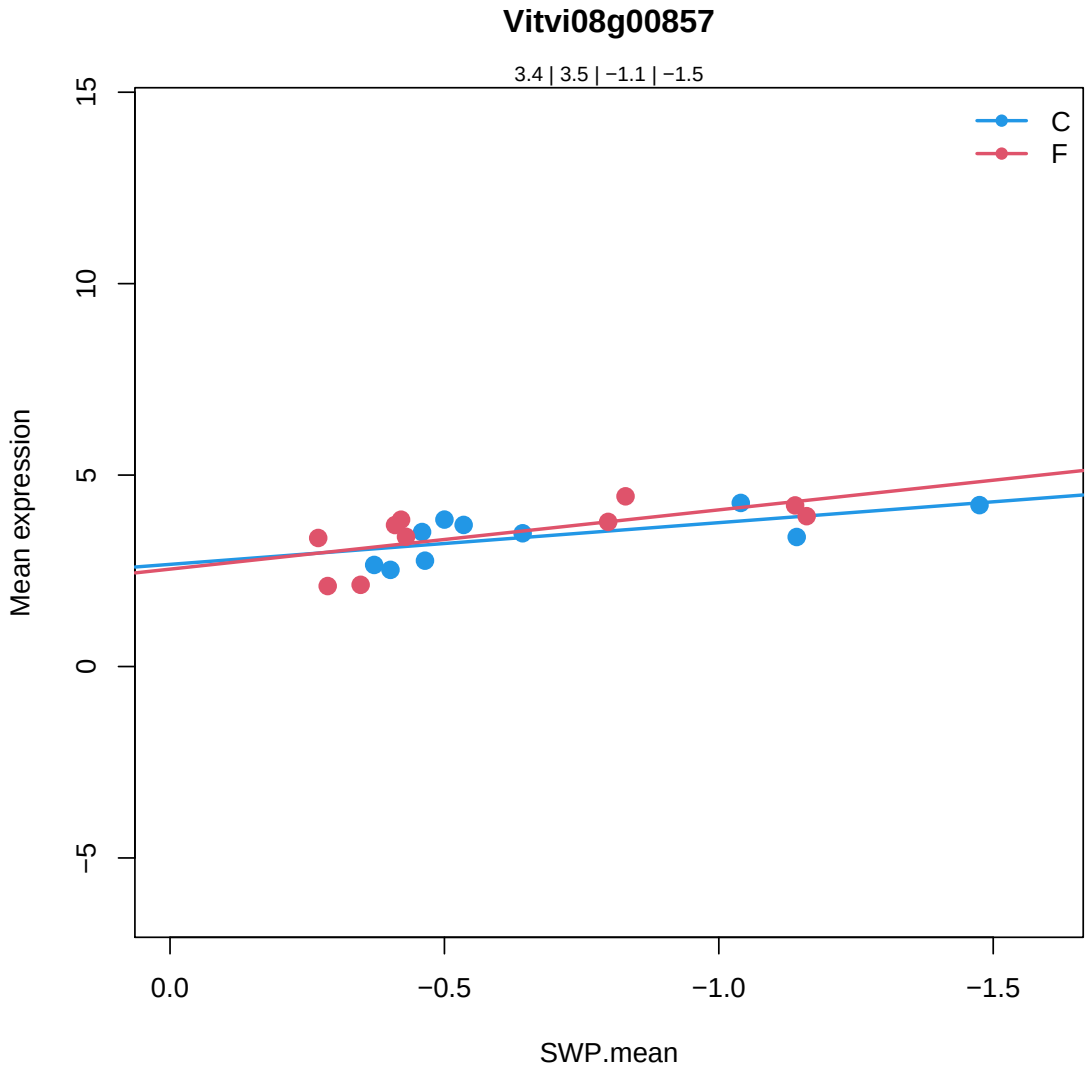
7.2.94 Vitvi08g00857: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g00857
        35.2
        not assigned.unknown
        RING/U-box superfamily protein |
        Chr3:3413068-3413613 REVERSE LENGTH=181 |
        201606
```

Coefficients for Vitvi08g00857.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.433887	2.386415e-15	***	4.286322e-15	***
SlopeC	-1.08926	0.03297358	*	0.4417082	
MeanF-MeanC	0.05274916	0.8301412		0.9526501	
SlopeF-SlopeC	-0.4590712	0.5254875		0.9999488	



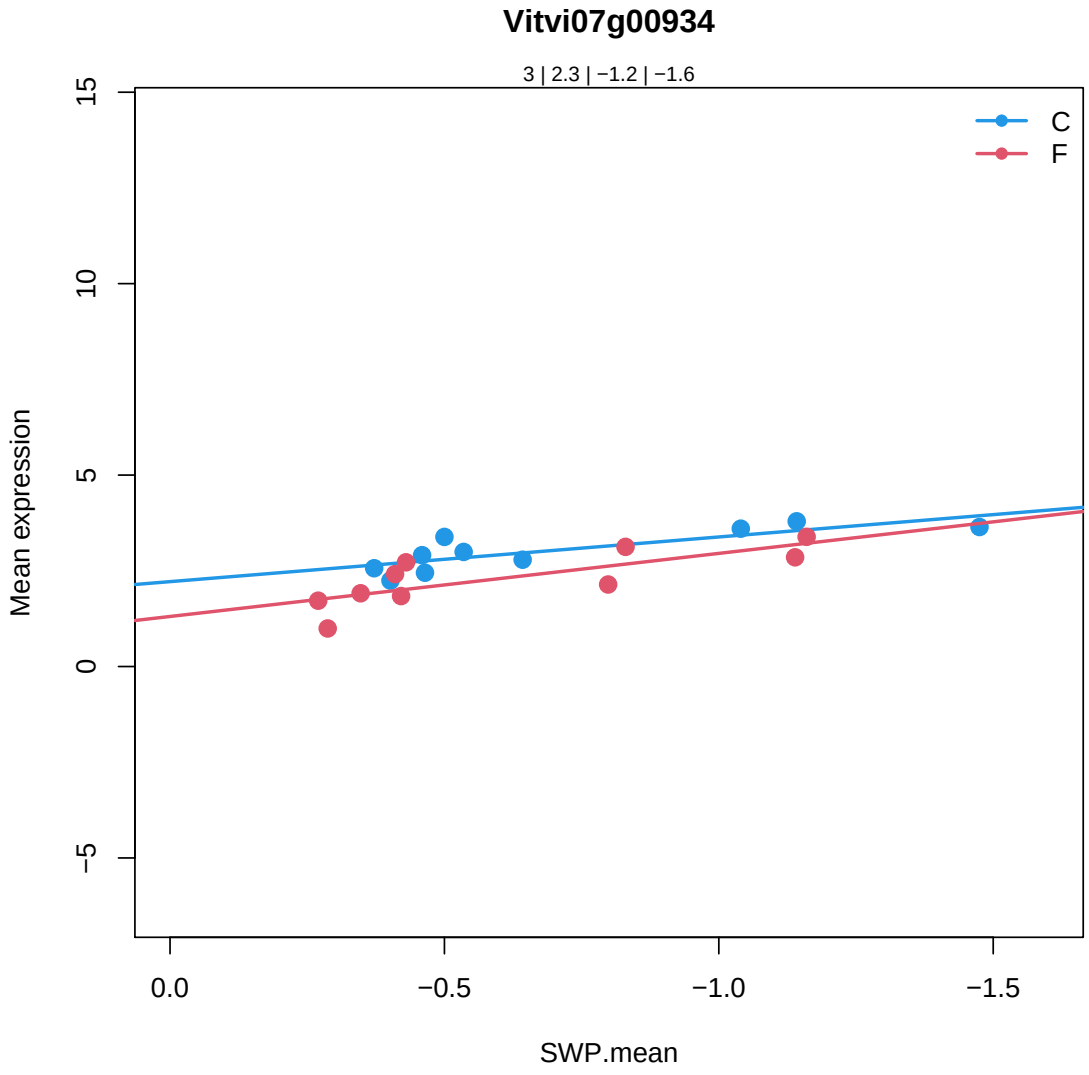
7.2.95 Vitvi07g00934: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g00934
        35.2
        not assigned.unknown
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi07g00934.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.037176	3.481848e-16	***	6.948197e-16	***
SlopeC	-1.16672	0.006235914	**	0.2647742	
MeanF-MeanC	-0.7264405	0.001248858	**	0.01503561	*
SlopeF-SlopeC	-0.4809399	0.4102702		0.9999488	



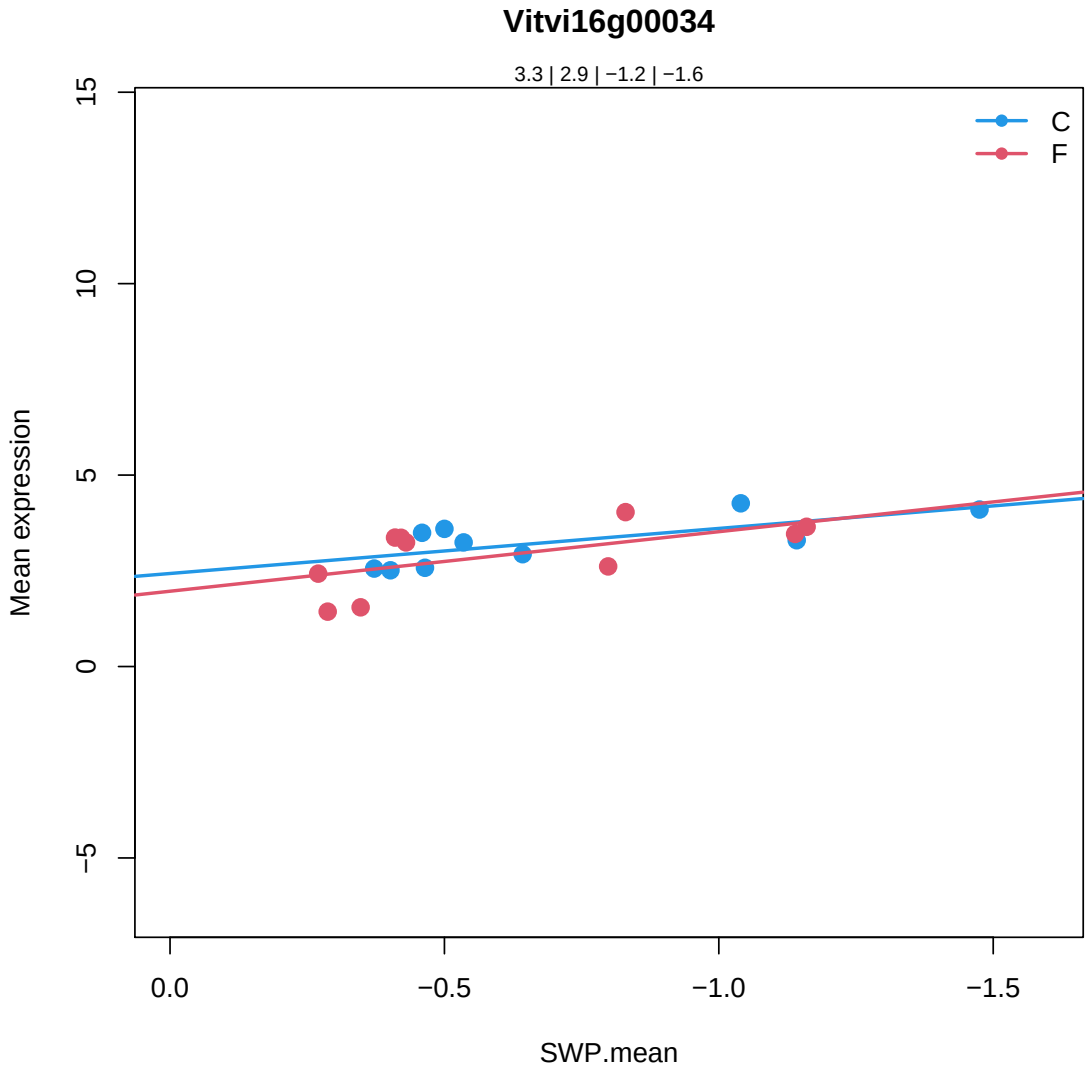
7.2.96 Vitvi16g00034: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g00034
        34.99
        transport.misc
        Major facilitator superfamily protein |
        Chr1:24109752-24111165 FORWARD LENGTH=442 |
        201606
```

Coefficients for Vitvi16g00034.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.25725	3.617753e-14	***	5.75713e-14	***
SlopeC	-1.176826	0.03362483	*	0.4433084	
MeanF-MeanC	-0.3437019	0.2059661		0.550148	
SlopeF-SlopeC	-0.3782124	0.6289896		0.9999488	



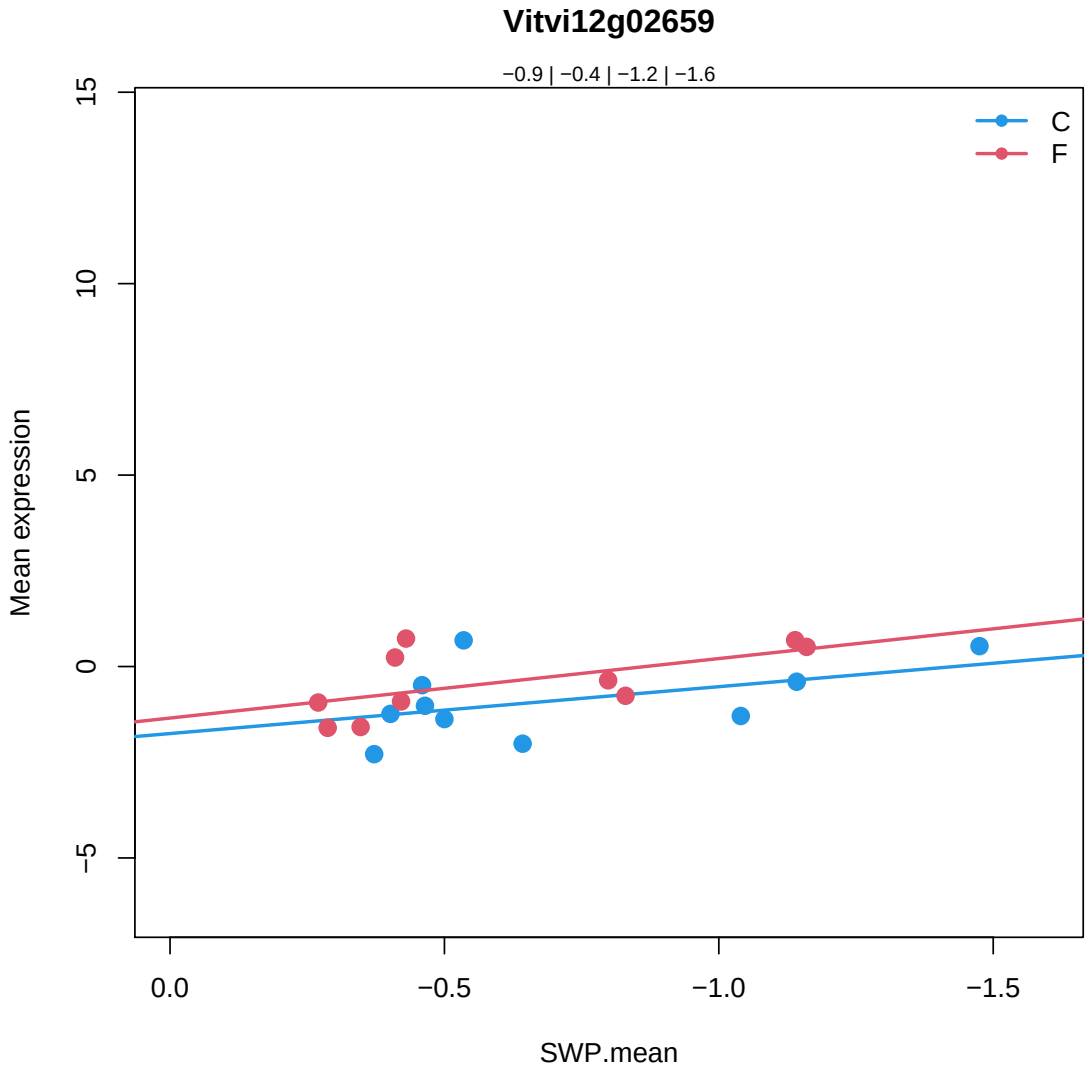
7.2.97 Vitvi12g02659: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02659
        33.1
        development.storage proteins
        RmlC-like cupins superfamily protein |
        Chr1:2404300-2405863 REVERSE LENGTH=356 |
        201606
```

Coefficients for Vitvi12g02659.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	−0.8903097	0.001420755	**	0.001534085	**
SlopeC	−1.224612	0.08438042	.	0.5848879	
MeanF−MeanC	0.4908415	0.167988		0.4965043	
SlopeF−SlopeC	−0.3289884	0.7471009		0.9999488	



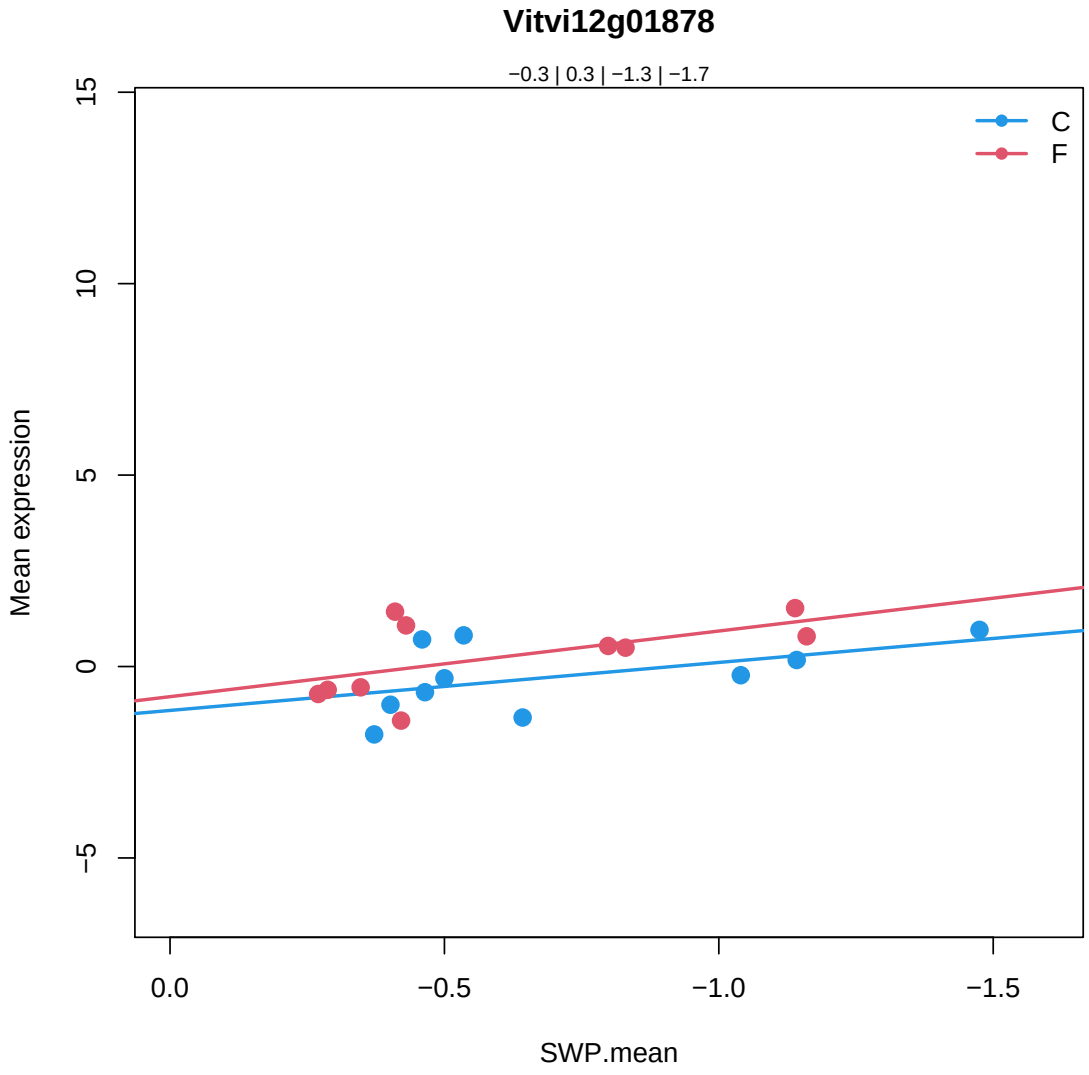
7.2.98 Vitvi12g01878: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g01878
        35.2
        not assigned.unknown
        RmlC-like cupins superfamily protein |
        Chr1:2404300-2405863 REVERSE LENGTH=356 |
        201606
```

Coefficients for Vitvi12g01878.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.2661147	0.2965848		0.3022967	
SlopeC	-1.253066	0.08422197	.	0.5843019	
MeanF-MeanC	0.5229317	0.1516884		0.469258	
SlopeF-SlopeC	-0.4615107	0.6585985		0.9999488	



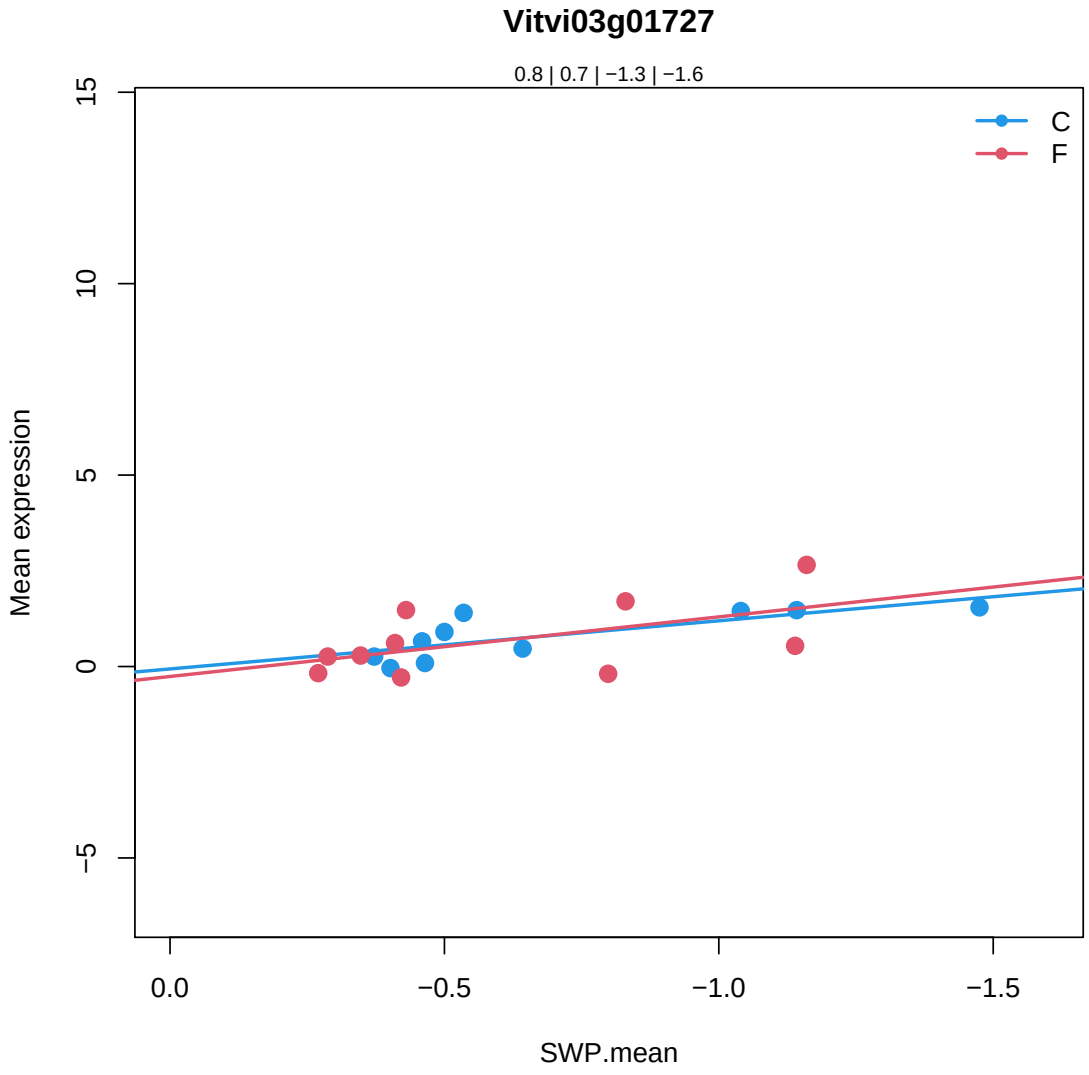
7.2.99 Vitvi03g01727: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g01727
        17.1.3
        hormone metabolism.abscisic acid.induced-regulated-responsive-activate
        HVA22 homologue A |
        Chr1:28008109-28009156 REVERSE LENGTH=177 |
        201606
```

Coefficients for Vitvi03g01727.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8209294	0.0004568991	***	0.0004980017	***
SlopeC	-1.256935	0.03334747	*	0.4433084	
MeanF-MeanC	-0.1327742	0.6413008		0.8777751	
SlopeF-SlopeC	-0.3002579	0.7187048		0.9999488	



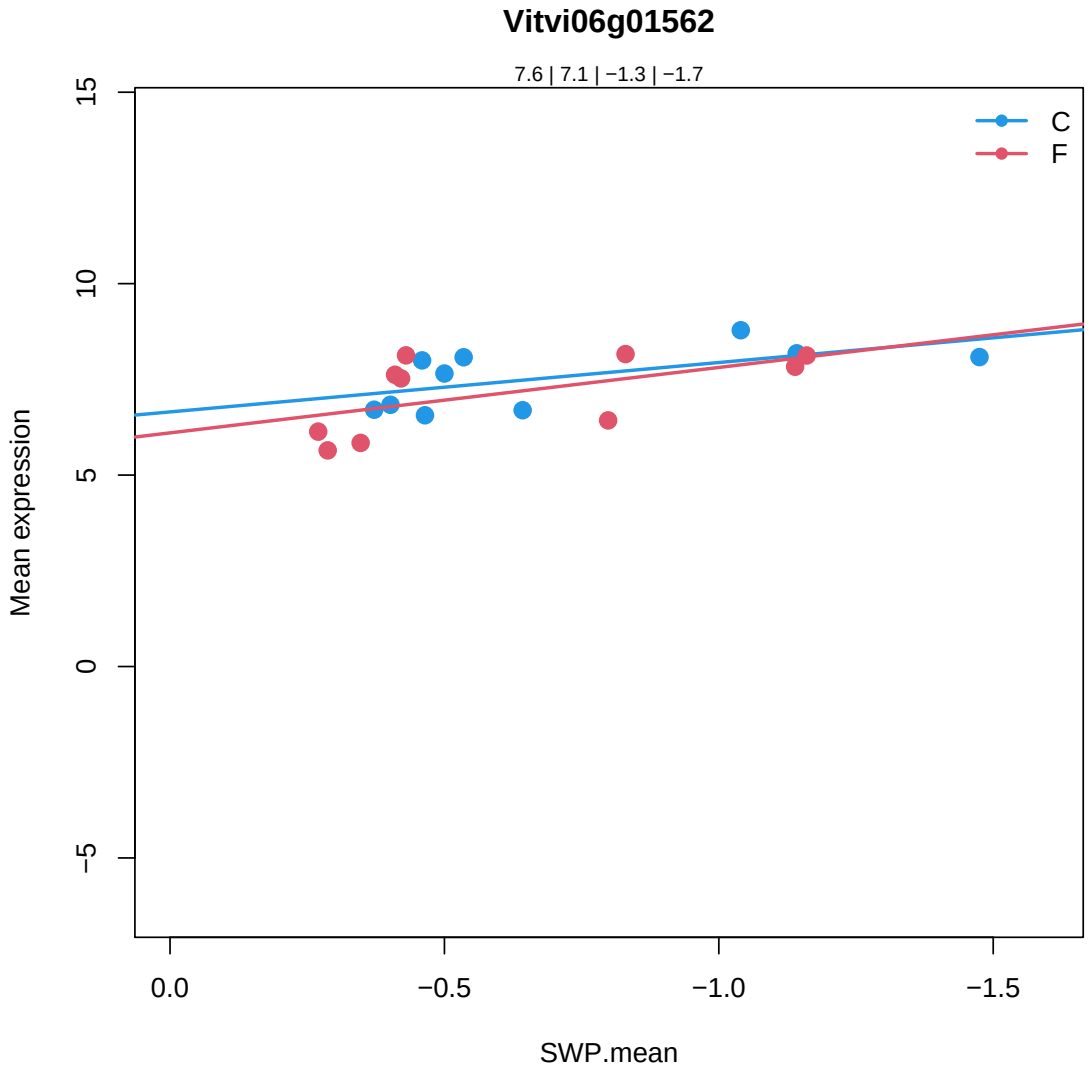
7.2.100 Vitvi06g01562: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01562
        20.2.1
        stress.abiotic.heat
        DNAJ homologue 3 |
        Chr3:15869115-15871059 REVERSE LENGTH=420 |
        201606
```

Coefficients for Vitvi06g01562.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.556709	5.440189e-20	***	2.842625e-19	***
SlopeC	-1.289769	0.05263446	.	0.5144558	
MeanF-MeanC	-0.4134006	0.2095786		0.5540716	
SlopeF-SlopeC	-0.4180297	0.6595469		0.9999488	



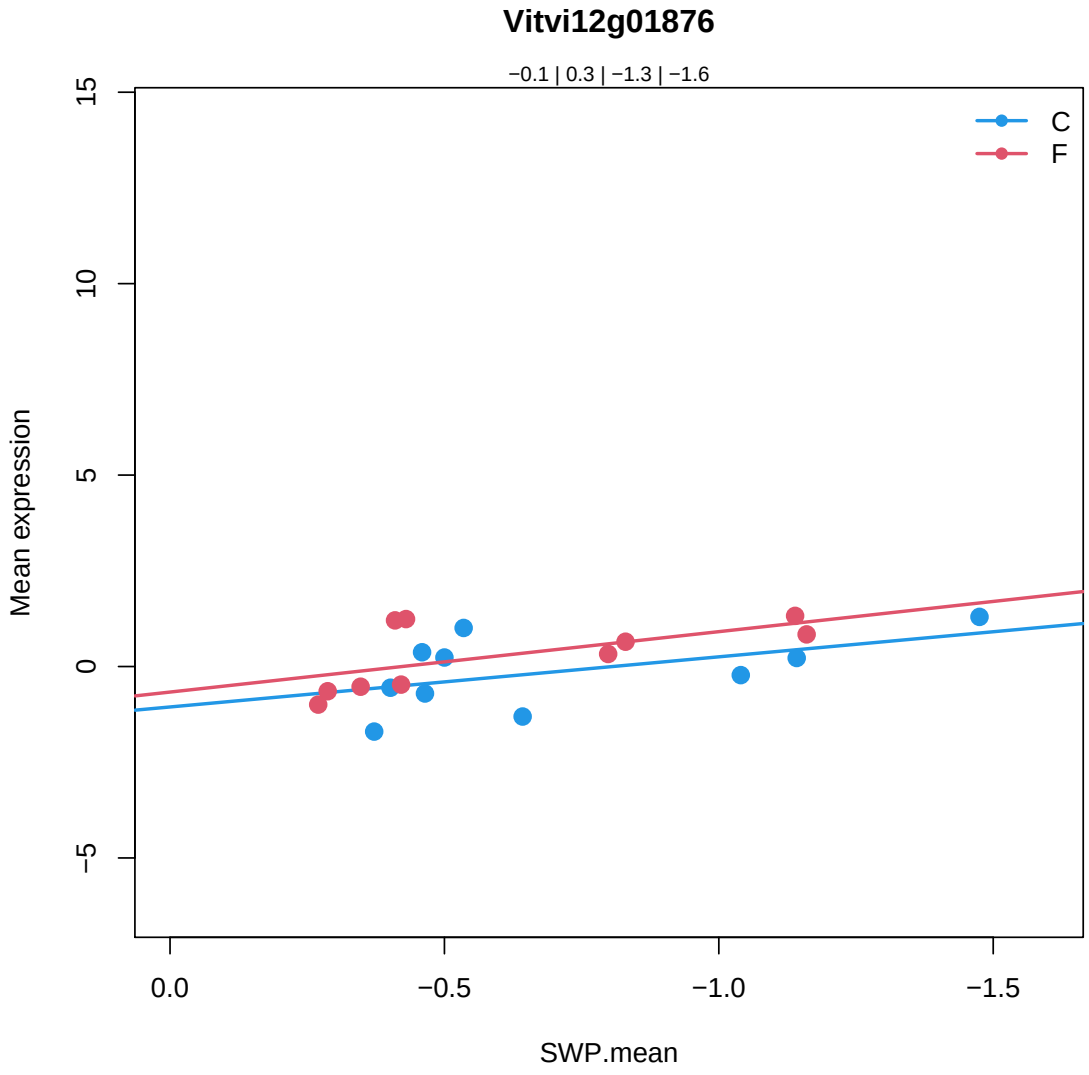
7.2.101 Vitvi12g01876: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g01876
        33.1
        development.storage proteins
        RmlC-like cupins superfamily protein |
        Chr1:2404300-2405863 REVERSE LENGTH=356 |
        201606
```

Coefficients for Vitvi12g01876.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.1356184	0.5669346		0.5727592	
SlopeC	-1.309394	0.05625572	.	0.5302719	
MeanF-MeanC	0.4295061	0.2066185		0.5512875	
SlopeF-SlopeC	-0.2685781	0.7835767		0.9999488	



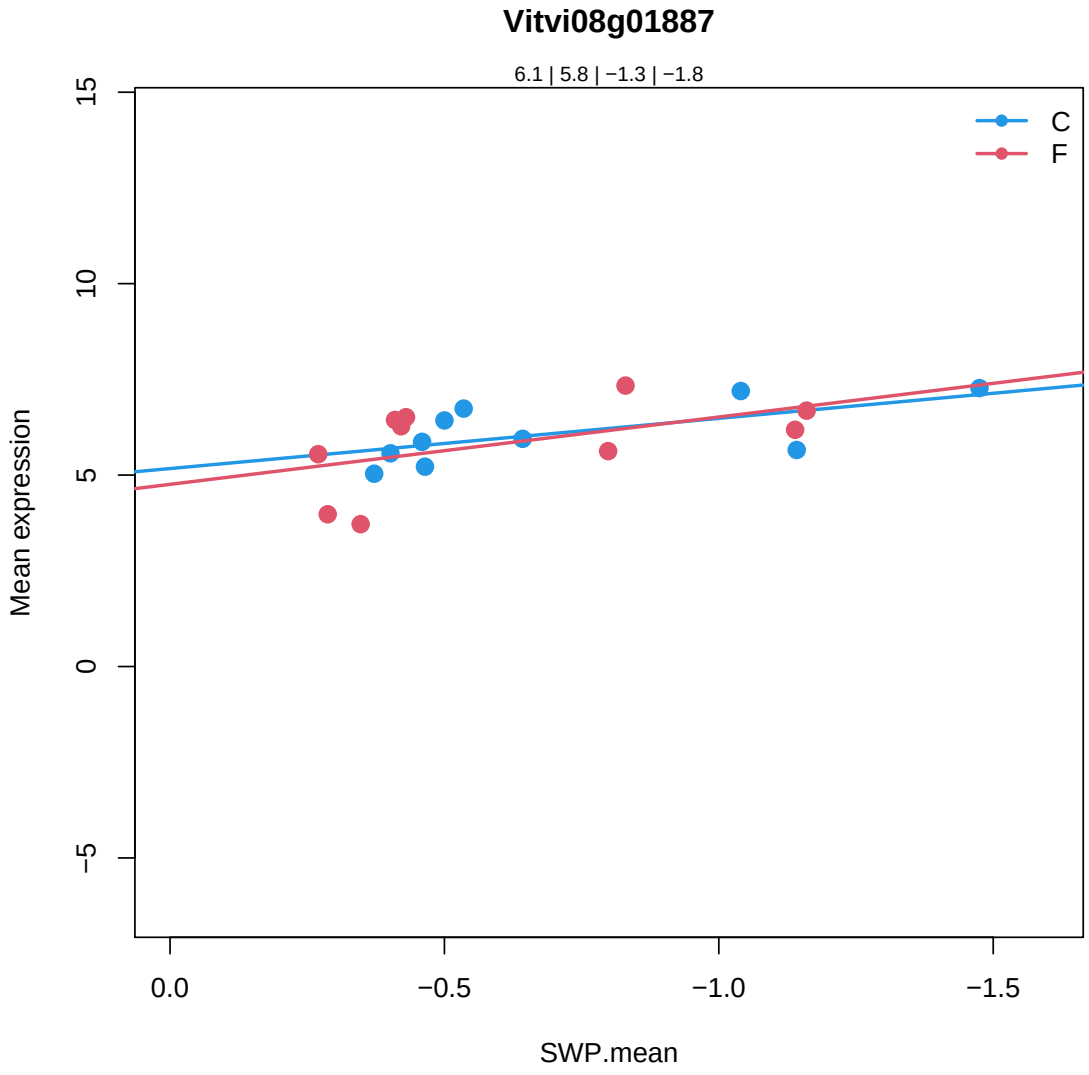
7.2.102 Vitvi08g01887: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01887
        35.2
        not assigned.unknown
        Remorin family protein |
        Chr2:17471119-17472519 REVERSE LENGTH=274 |
        201606
```

Coefficients for Vitvi08g01887.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.092284	4.484759e-17	***	1.037437e-16	***
SlopeC	-1.310628	0.07442267	.	0.5682824	
MeanF-MeanC	-0.2627953	0.4674664		0.7876703	
SlopeF-SlopeC	-0.4483446	0.6707454		0.9999488	



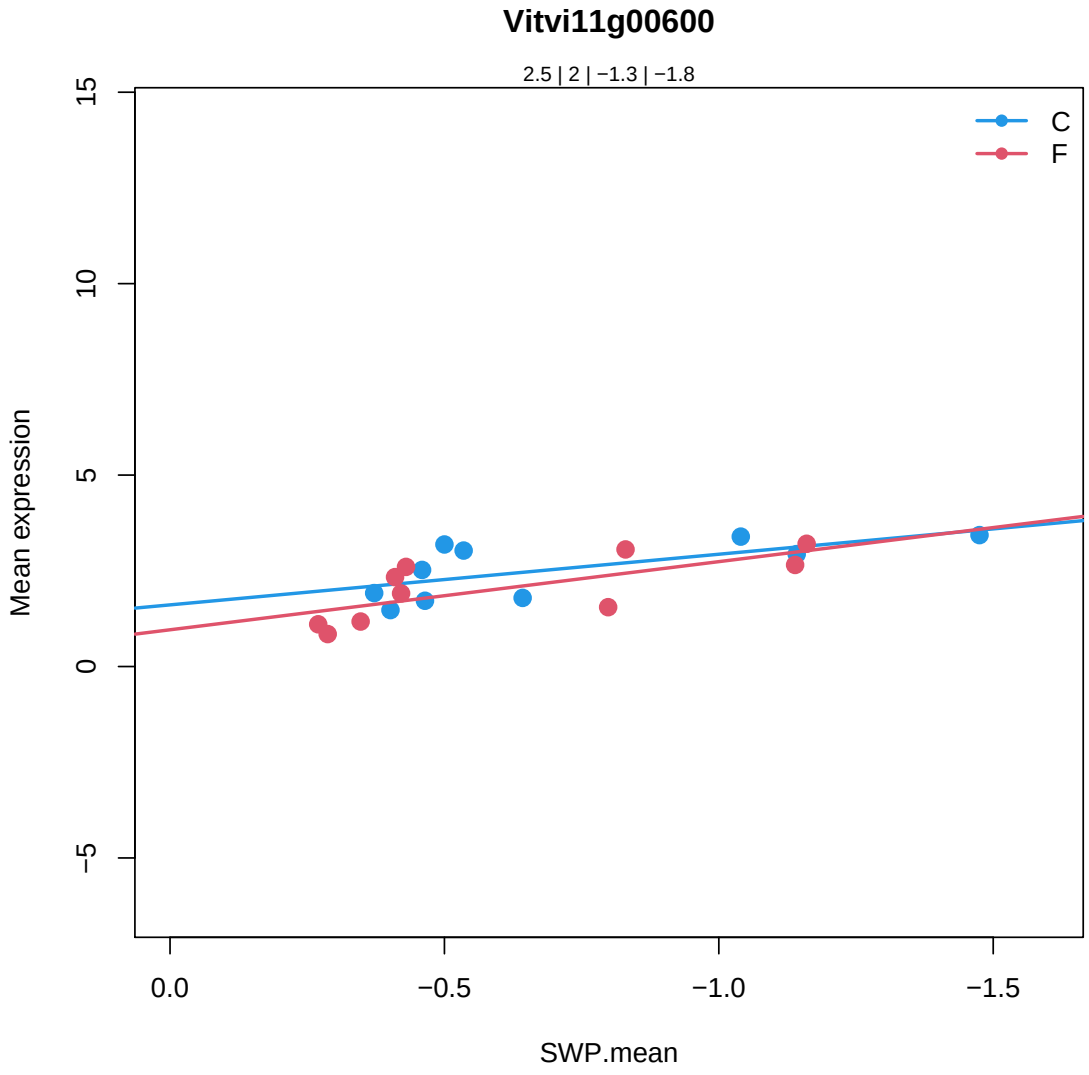
7.2.103 Vitvi11g00600: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00600
        29.4.1
        protein.postranslational modification.kinase
        kinase superfamily with octicosapeptide/Phox/Bem1p domain-containing p
        Chr3:17280430-17284857 REVERSE LENGTH=1155 |
        201606
```

Coefficients for Vitvi11g00600.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.539925	3.820091e-12	***	5.309185e-12	***
SlopeC	-1.32255	0.01713142	*	0.3546065	
MeanF-MeanC	-0.4962363	0.06993603	.	0.2961014	
SlopeF-SlopeC	-0.4572286	0.5546237		0.9999488	



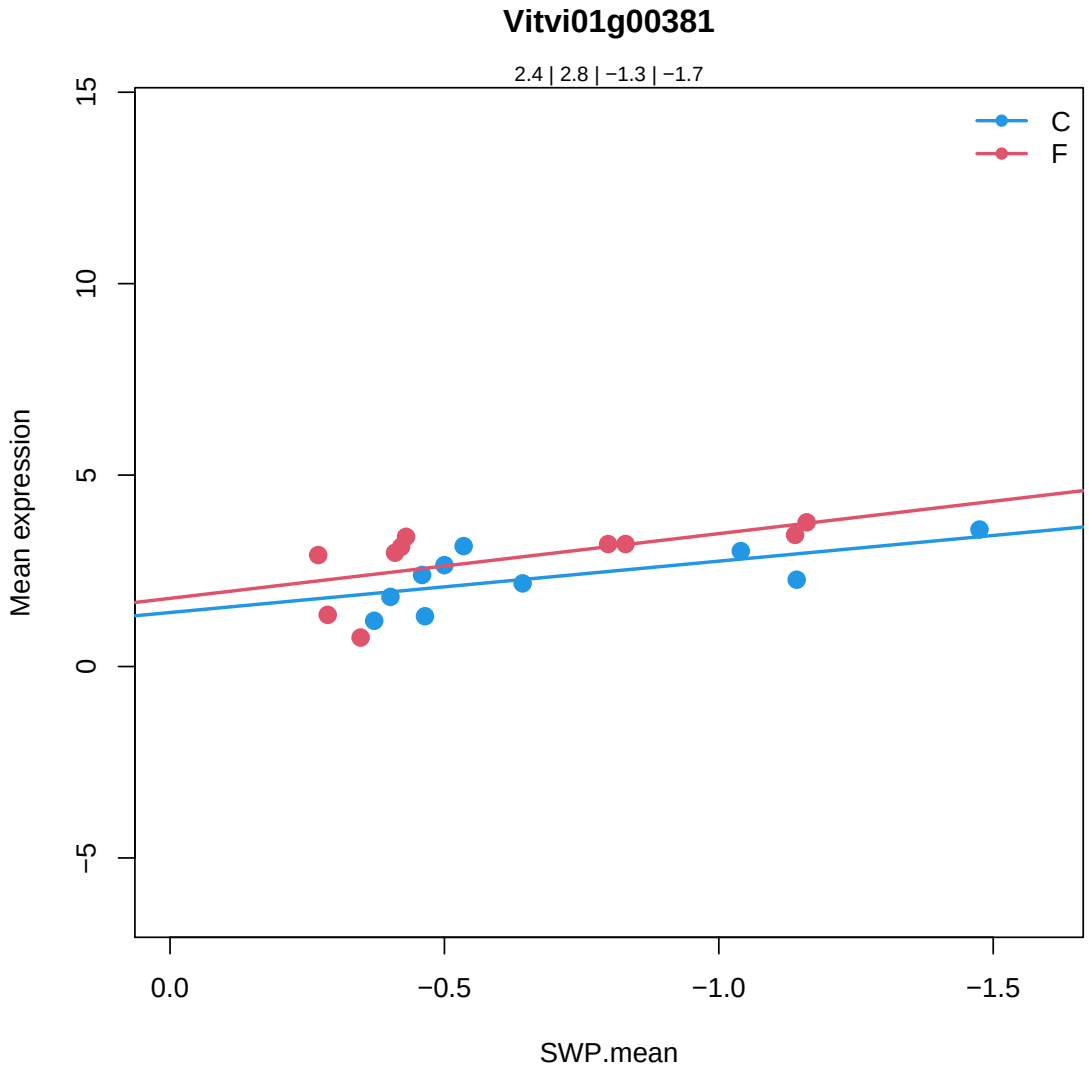
7.2.104 Vitvi01g00381: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00381
        29.5.11.4.2
        protein.degradation.ubiquitin.E3.RING
        RING/FYVE/PHD zinc finger superfamily protein |
        Chr2:142610-143809 REVERSE LENGTH=259 |
        201606
```

Coefficients for Vitvi01g00381.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.353922	2.686253e-10	***	3.455762e-10	***
SlopeC	-1.341719	0.03443939	*	0.444078	
MeanF-MeanC	0.4562126	0.1454344		0.4594471	
SlopeF-SlopeC	-0.3488876	0.6970381		0.9999488	



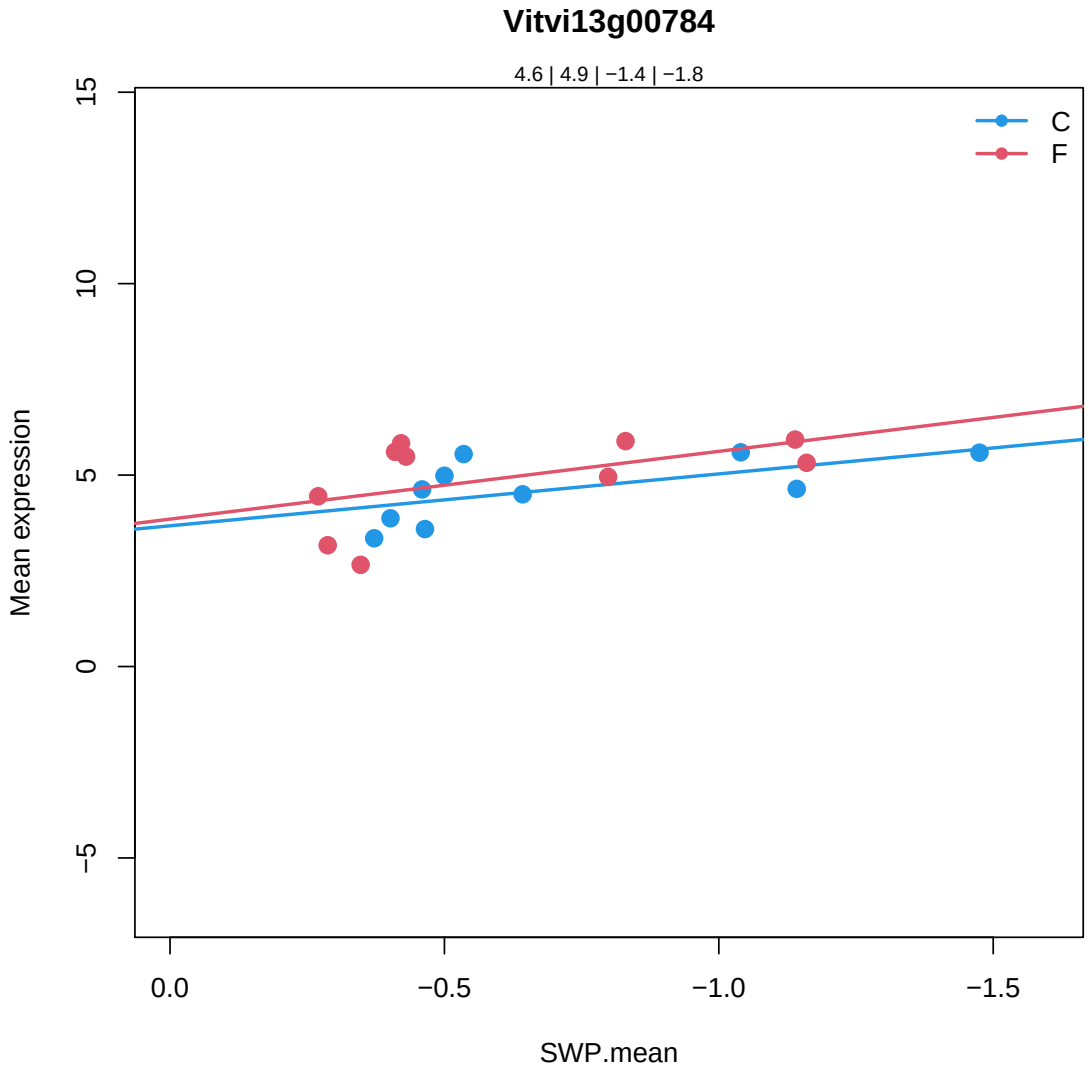
7.2.105 Vitvi13g00784: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00784
        34.16
        transport.ABC transporters and multidrug resistance systems
        pleiotropic drug resistance 6 |
        Chr2:15257583-15263627 FORWARD LENGTH=1453 |
        201606
```

Coefficients for Vitvi13g00784.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.628324	1.615091e-14	***	2.647581e-14	***
SlopeC	-1.355593	0.06886842	.	0.5574314	
MeanF-MeanC	0.2998051	0.4138202		0.7531281	
SlopeF-SlopeC	-0.4145343	0.6978076		0.9999488	



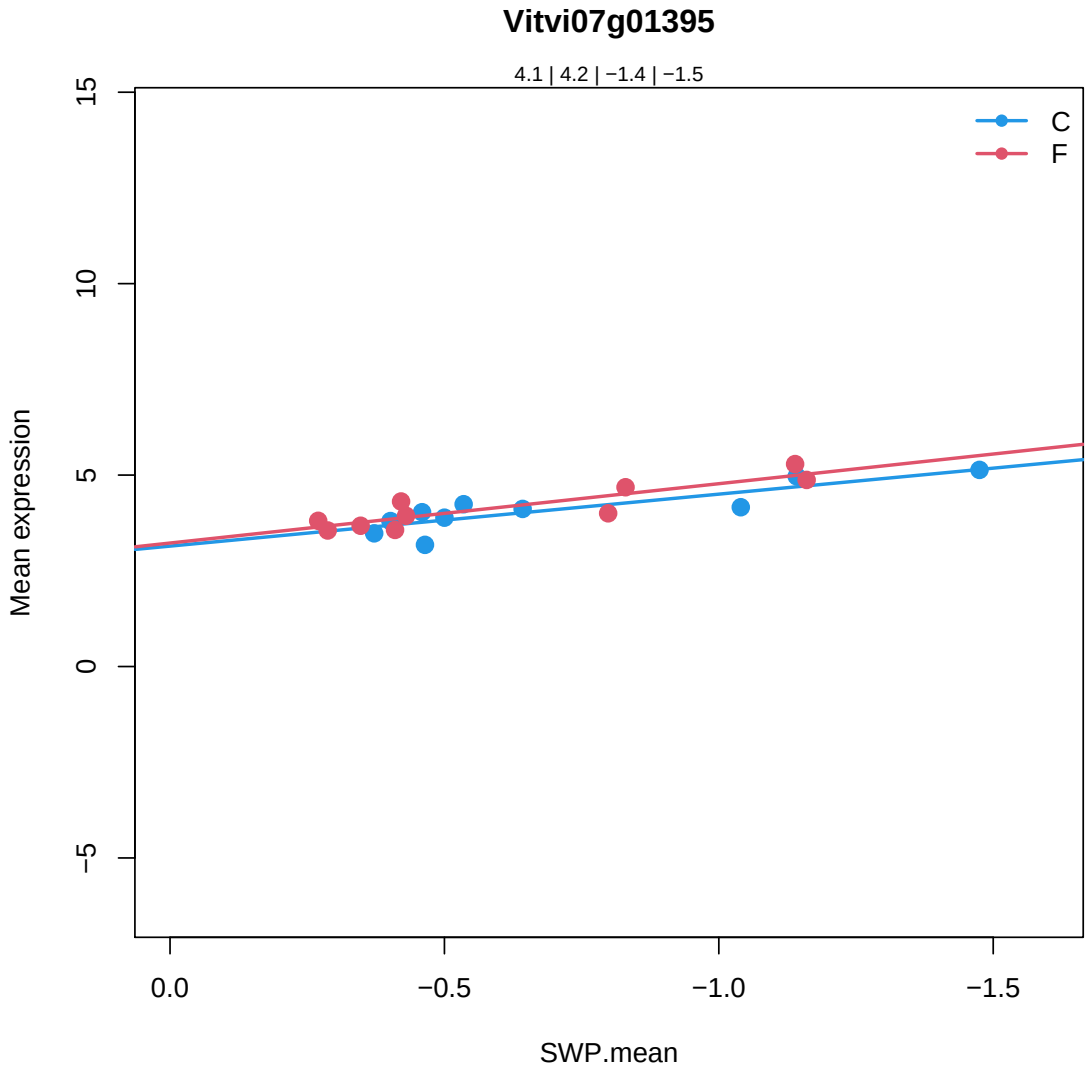
7.2.106 Vitvi07g01395: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01395
        26.2
        misc.UDP glucosyl and glucoronyl transferases
        UDP-glucosyl transferase 85A2 |
        Chr1:7895068-7897527 REVERSE LENGTH=481 |
        201606
```

Coefficients for Vitvi07g01395.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.098973	1.390377e-20	***	9.307042e-20	***
SlopeC	-1.357018	0.0003476217	***	0.09461517	.
MeanF-MeanC	0.07036105	0.6693211		0.892233	
SlopeF-SlopeC	-0.1929631	0.6890673		0.9999488	



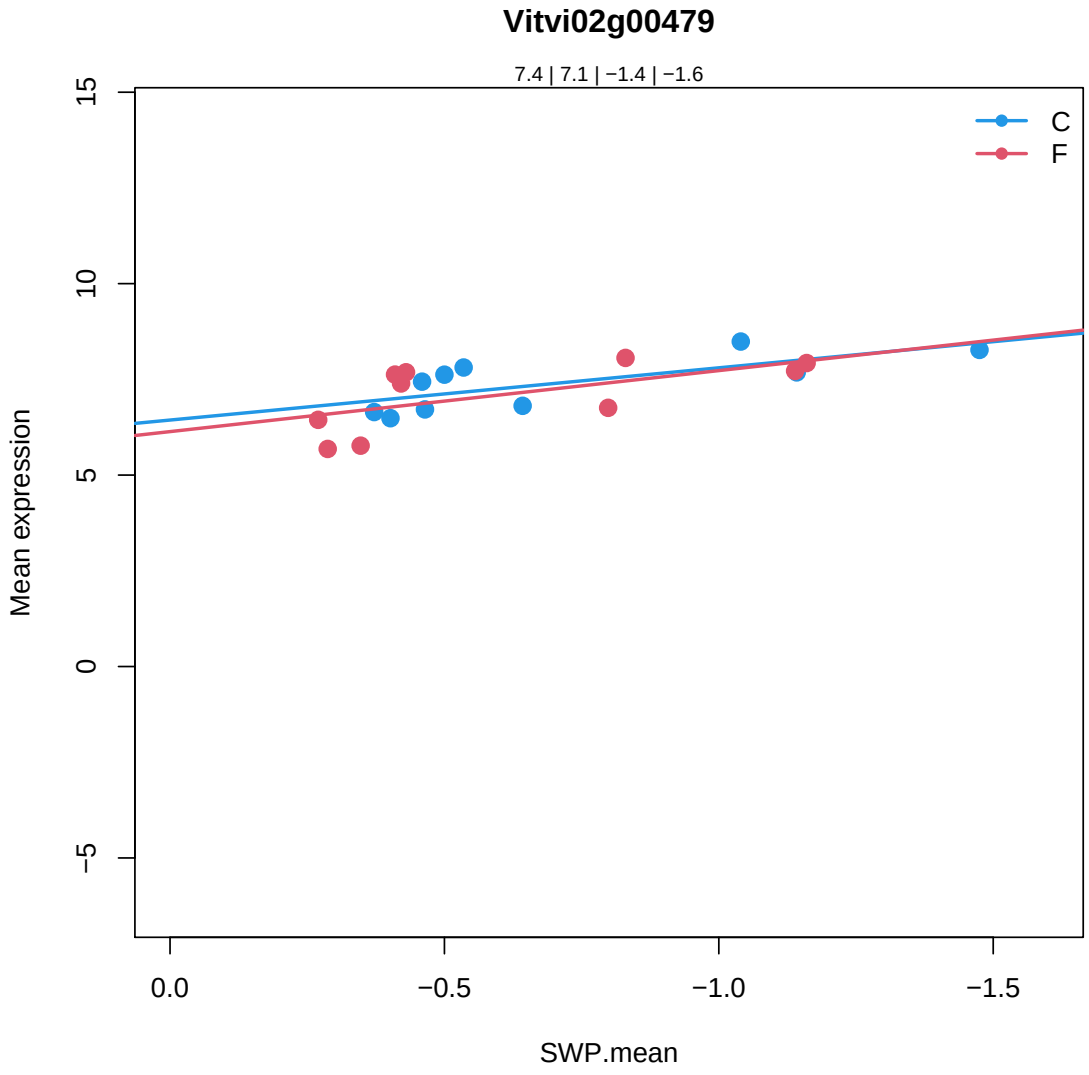
7.2.107 Vitvi02g00479: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00479
        35.1.40
        not assigned.no ontology.glycine rich proteins
        glycine-rich protein |
        Chr4:11944050-11945565 REVERSE LENGTH=356 |
        201606
```

Coefficients for Vitvi02g00479.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.396619	2.052347e-21	***	2.003963e-20	***
SlopeC	-1.364266	0.01694217	*	0.3536249	
MeanF-MeanC	-0.2907691	0.2896869		0.6552023	
SlopeF-SlopeC	-0.2291237	0.7729633		0.9999488	



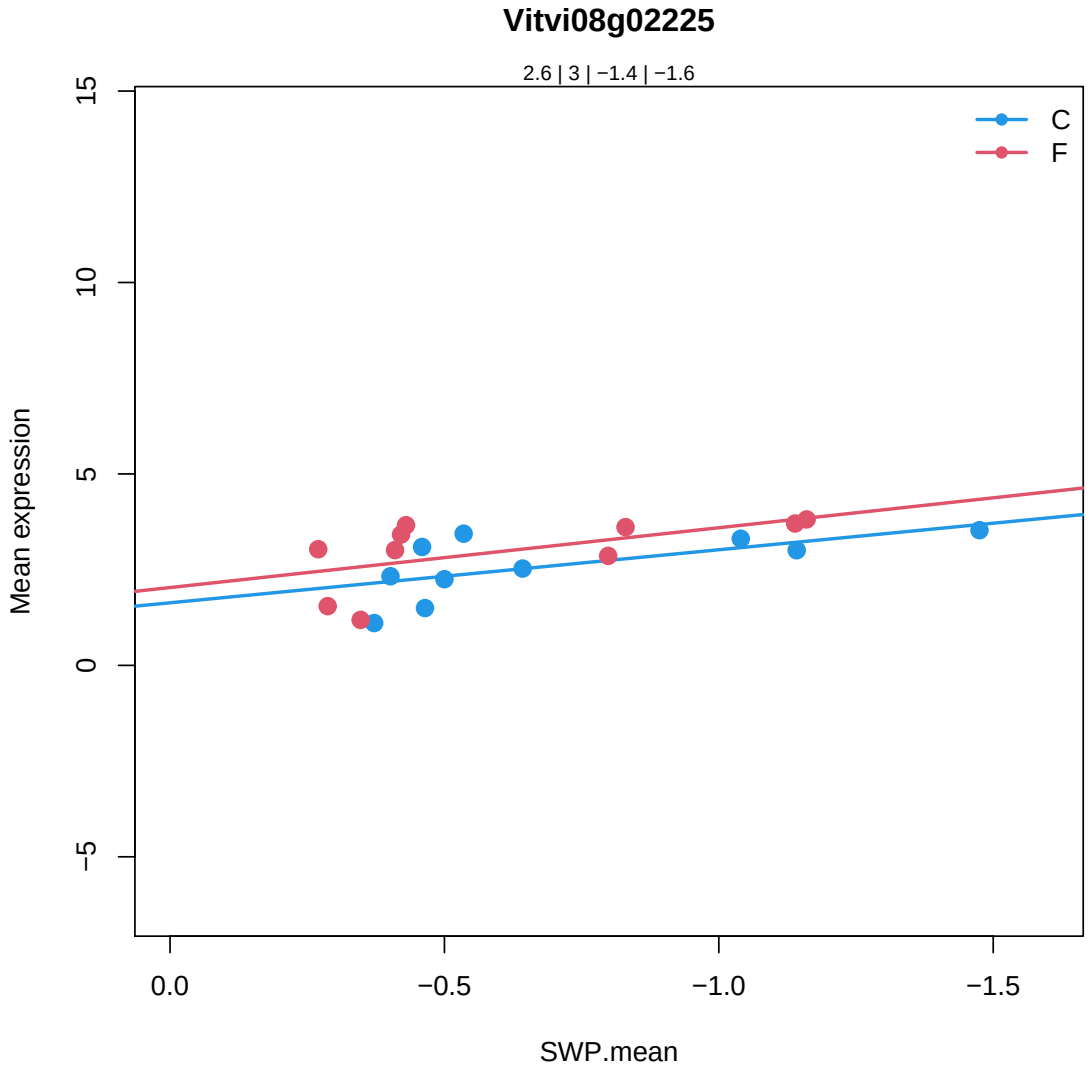
7.2.108 Vitvi08g02225: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g02225
        35.2
        not assigned.unknown
        [Sotub09g012710.1.1]: Unknown Protein [Sotub09g012710.1.1]: Unknown Pr
        [stNIB-v1_0001331]
```

Coefficients for Vitvi08g02225.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.608389	4.555546e-11	***	6.044714e-11	***
SlopeC	-1.385499	0.03056749	*	0.4321285	
MeanF-MeanC	0.3758626	0.2299304		0.5834191	
SlopeF-SlopeC	-0.1769986	0.8443383		0.9999488	



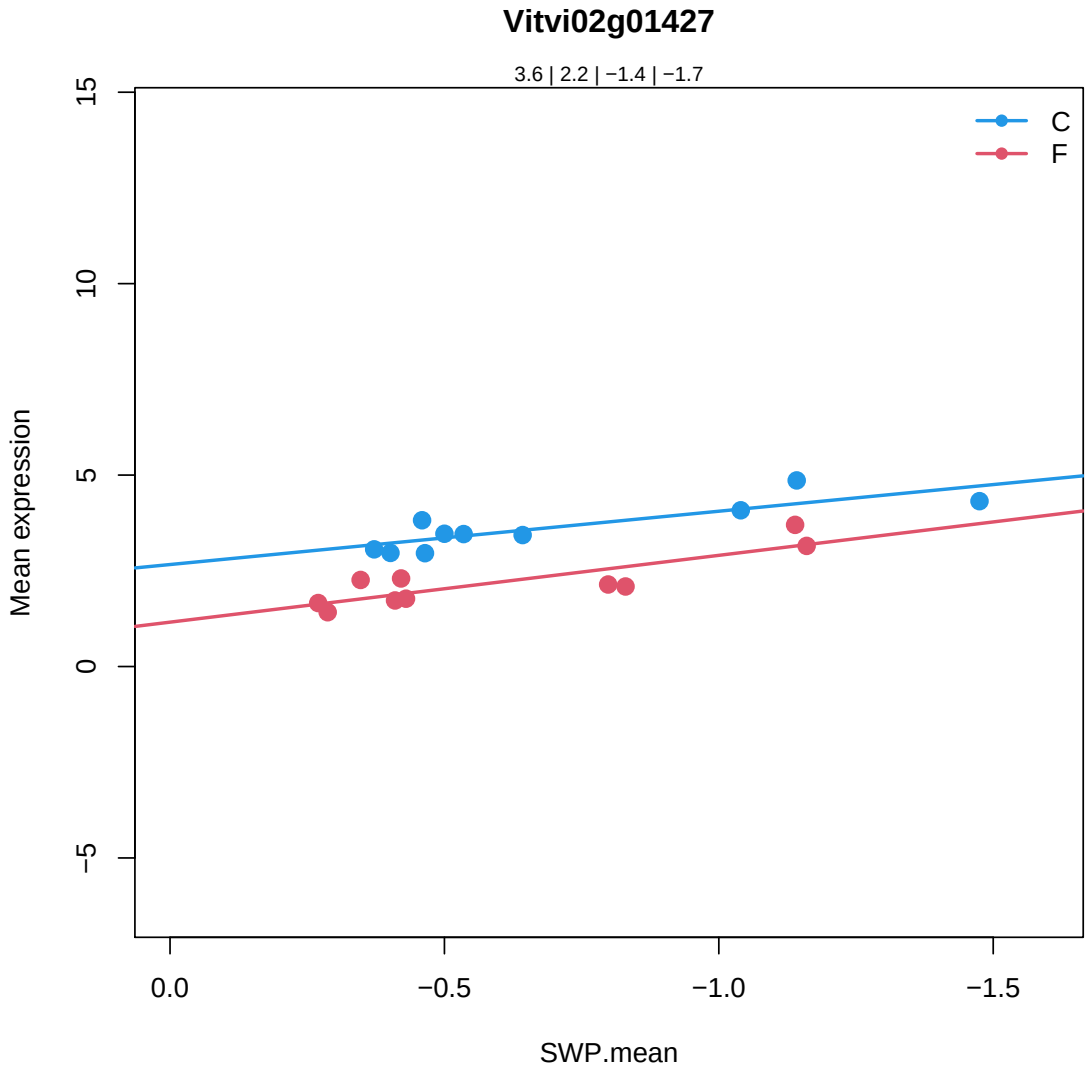
7.2.109 Vitvi02g01427: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g01427
        26.10
        misc.cytochrome P450
        cytochrome P450%2C family 706%2C subfamily A%2C polypeptide 4 |
        Chr4:7308016-7309692 REVERSE LENGTH=516 |
        201606
```

Coefficients for Vitvi02g01427.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.642495	2.019881e-18	***	6.37017e-18	***
SlopeC	-1.392242	0.0008651745	***	0.1184327	
MeanF-MeanC	-1.420987	1.149488e-07	***	4.574544e-06	***
SlopeF-SlopeC	-0.3530263	0.5170181		0.9999488	



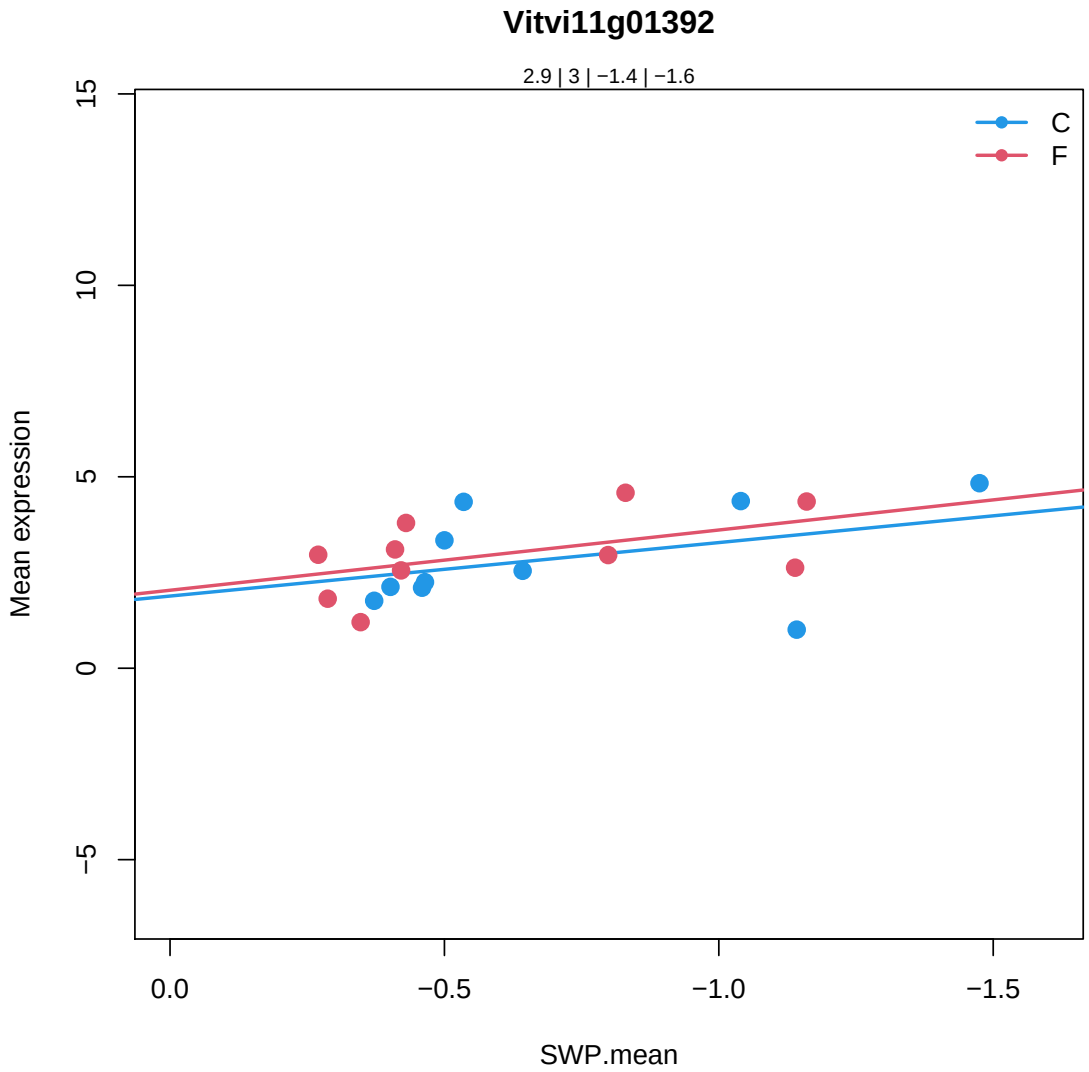
7.2.110 Vitvi11g01392: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g01392
        30.10
        signalling.phosphorelay
        NA
```

Coefficients for Vitvi11g01392.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.867044	7.063474e-09	***	8.66421e-09	***
SlopeC	-1.397001	0.1225777		0.6442513	
MeanF-MeanC	0.1280502	0.7747072		0.9355874	
SlopeF-SlopeC	-0.1768015	0.8925552		0.9999488	



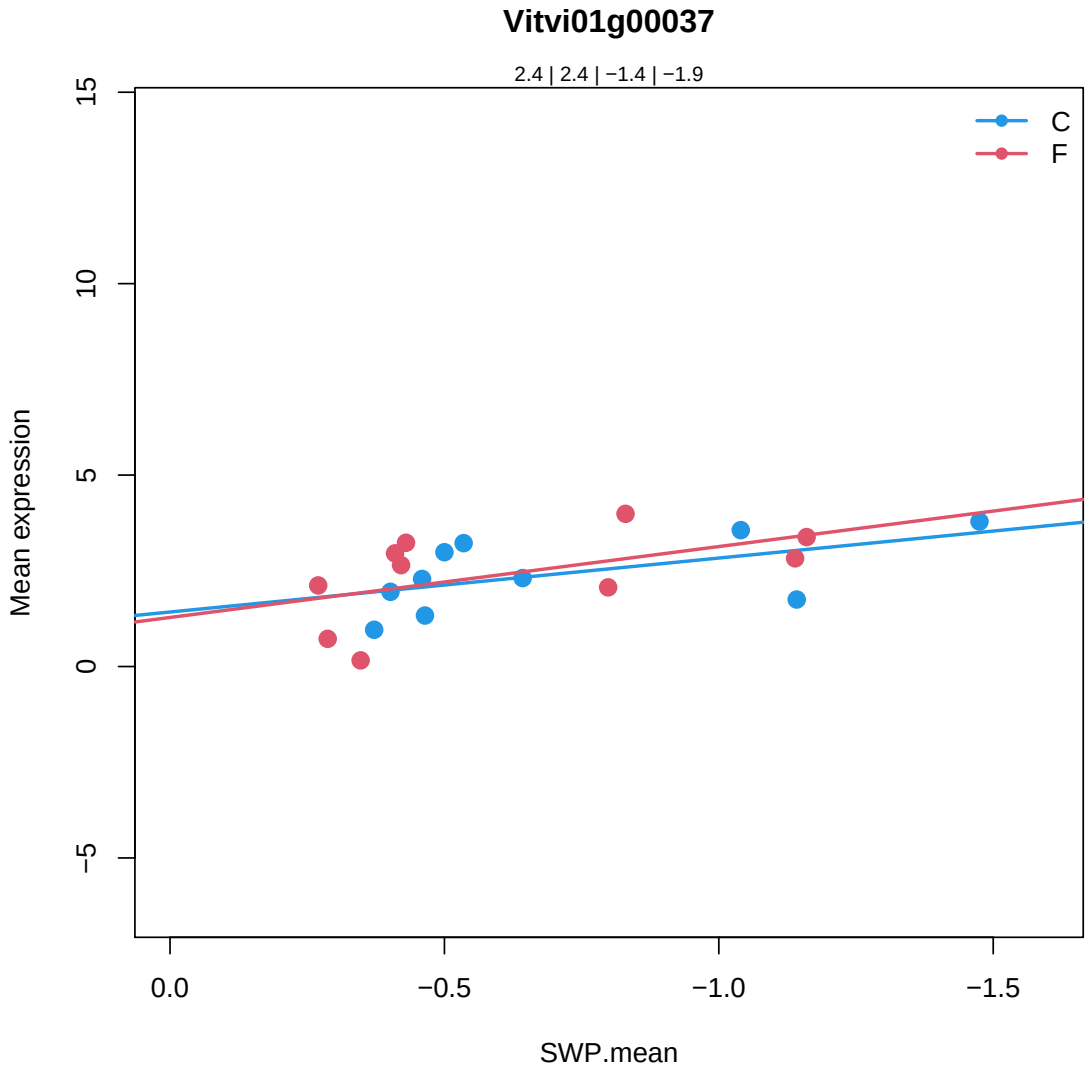
7.2.111 Vitvi01g00037: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00037
        35.2
        not assigned.unknown
        ABI five binding protein 2 |
        Chr1:4713969-4715158 FORWARD LENGTH=348 |
        201606
```

Coefficients for Vitvi01g00037.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.414563	1.341453e-08	***	1.630887e-08	***
SlopeC	-1.409016	0.07748119	.	0.5717559	
MeanF-MeanC	-0.004961904	0.9898685		0.9970642	
SlopeF-SlopeC	-0.4431473	0.6990273		0.9999488	



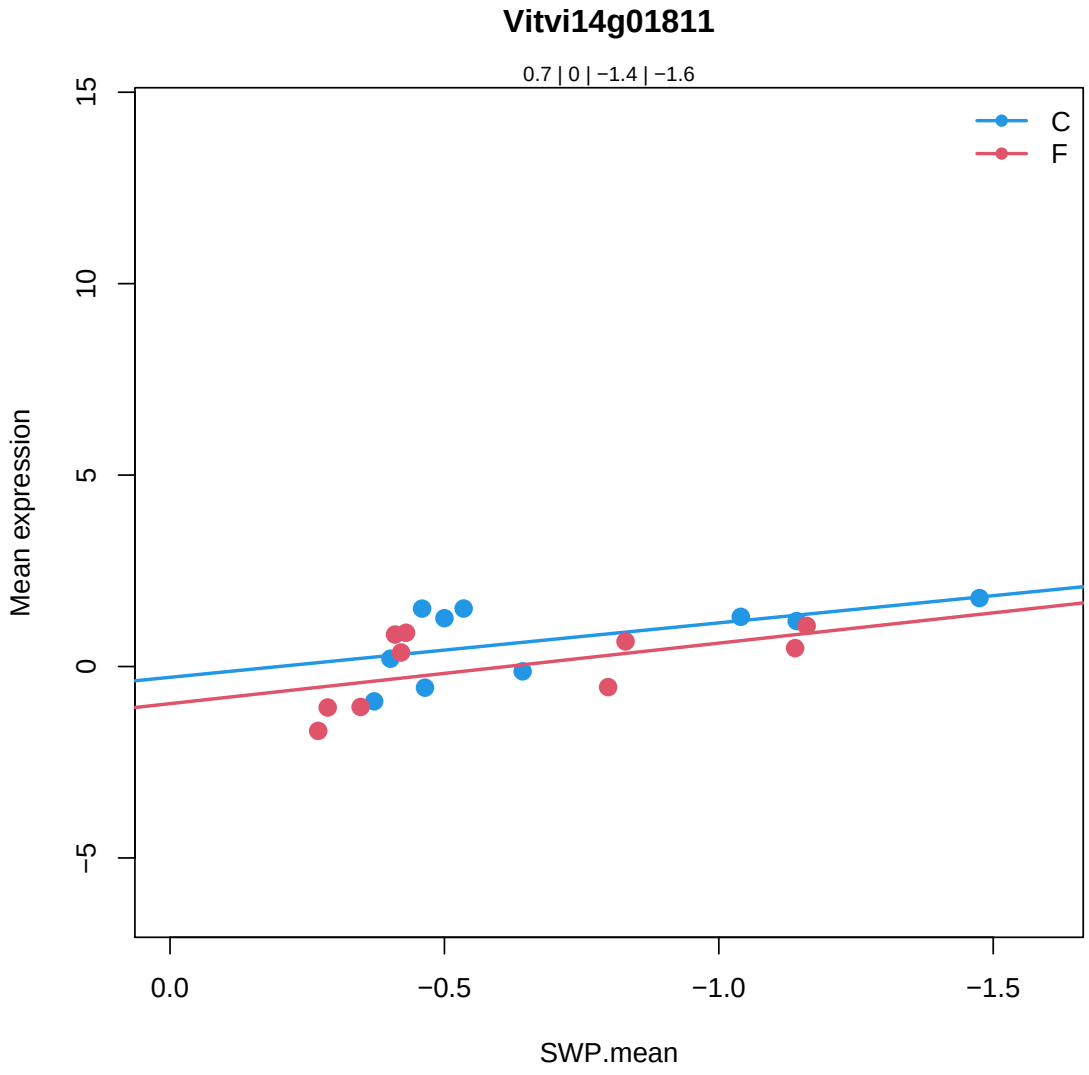
7.2.112 Vitvi14g01811: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01811
        35.2
        not assigned.unknown
        TRICHOME BIREFRINGENCE-LIKE 22 |
        Chr3:10471960-10473735 REVERSE LENGTH=414 |
        201606
```

Coefficients for Vitvi14g01811.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.7176293	0.008845858	**	0.009383295	**
SlopeC	-1.42152	0.05275518	.	0.5144558	
MeanF-MeanC	-0.7244294	0.0522048	.	0.2462722	
SlopeF-SlopeC	-0.159325	0.8787397		0.9999488	



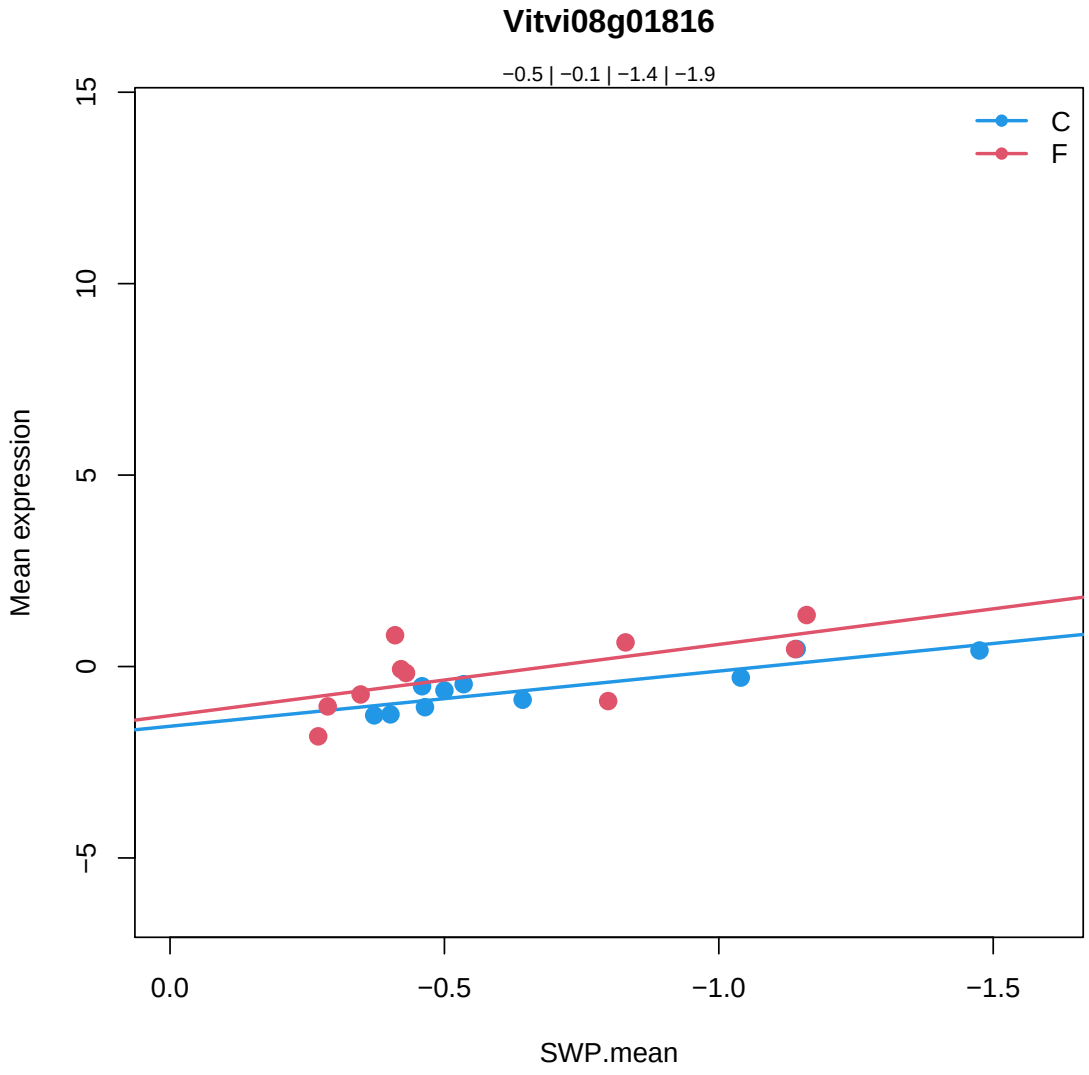
7.2.113 Vitvi08g01816: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01816
        35.1.12
        not assigned.no ontology.pumilio/Puf RNA-binding domain-containing pro
        pumilio 12 |
        Chr5:22881721-22883842 FORWARD LENGTH=596 |
        201606
```

Coefficients for Vitvi08g01816.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	−0.5471354	0.006347134	**	0.006751554	**
SlopeC	−1.441226	0.009171907	**	0.2905571	
MeanF−MeanC	0.3979652	0.1344258		0.438365	
SlopeF−SlopeC	−0.4174685	0.5830683		0.9999488	



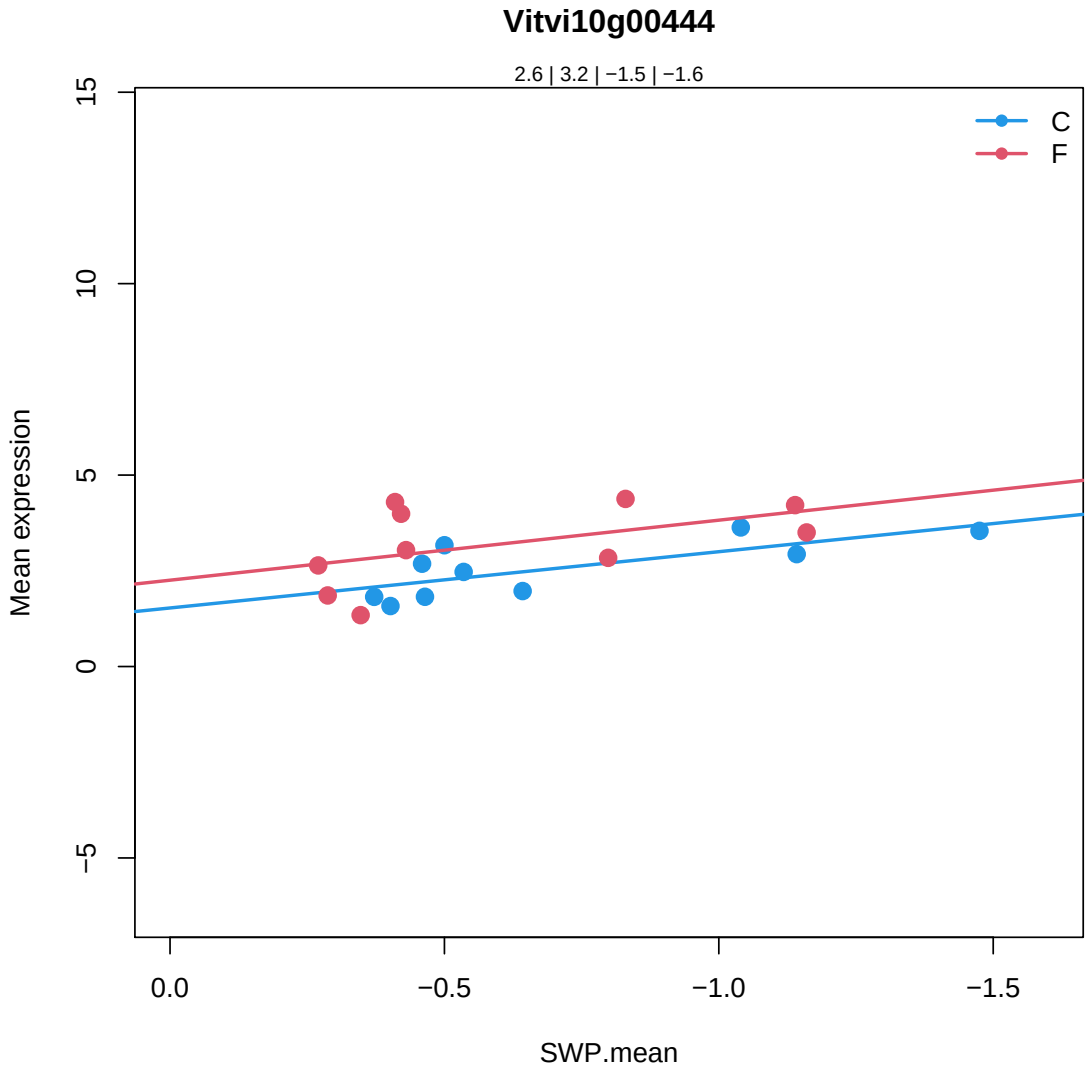
7.2.114 Vitvi10g00444: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00444
        27.3.8
        RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family
        DOF zinc finger protein 1 |
        Chr1:19174266-19174850 FORWARD LENGTH=194 |
        201606
```

Coefficients for Vitvi10g00444.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.562525	1.68952e-10	***	2.19219e-10	***
SlopeC	-1.469644	0.02961247	*	0.4299803	
MeanF-MeanC	0.646972	0.0562449	.	0.2580935	
SlopeF-SlopeC	-0.09792533	0.917876		0.9999488	



7.2.115 Vitvi03g00845: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

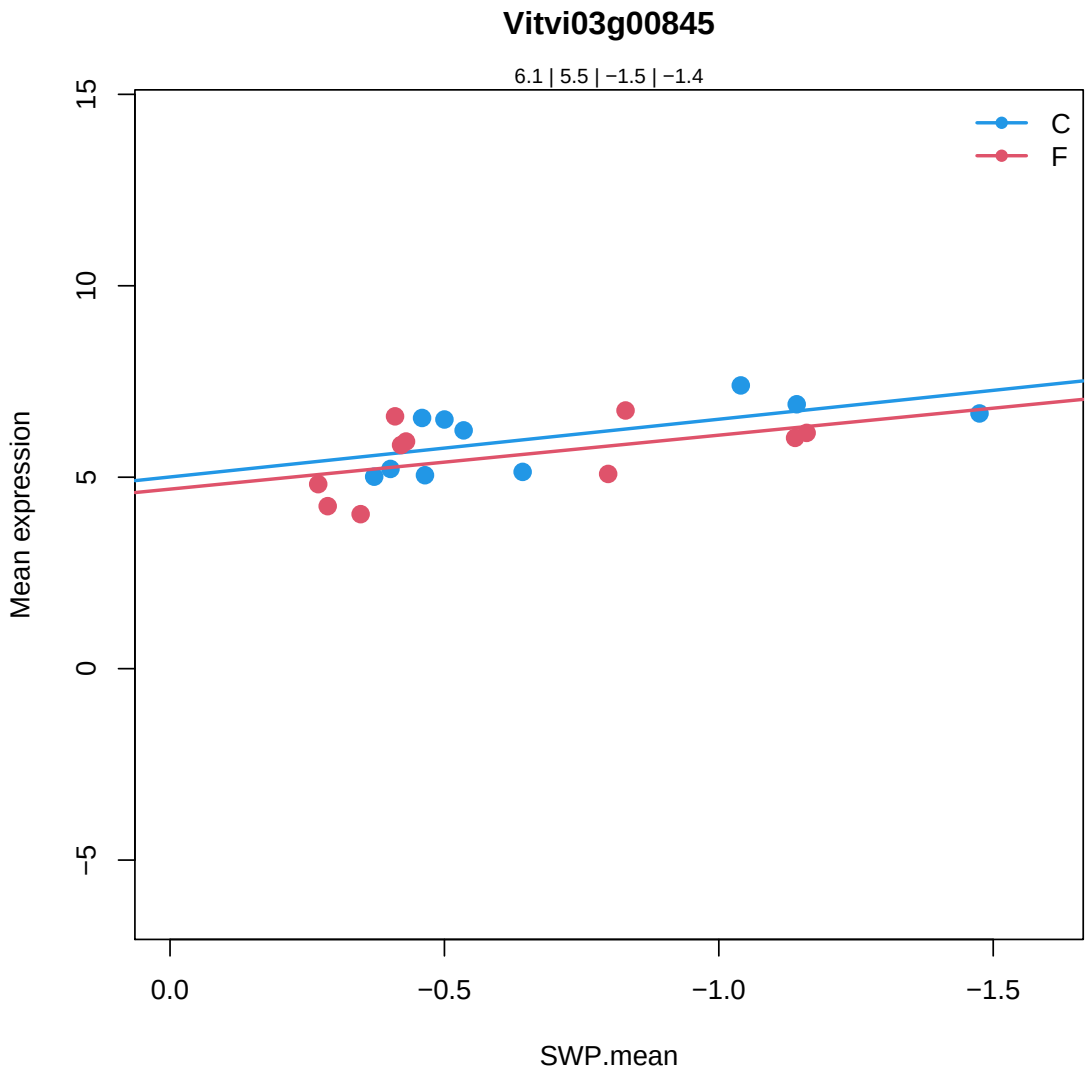
```
Vitvi03g00845
        29.6
        protein.folding
        mitochondrial HSO70 2 |
        Chr5:2975721-2978508 FORWARD LENGTH=682 |
        201606

Vitvi03g00845
        20.2.1
        stress.abiotic.heat
        mitochondrial HSO70 2 |
        Chr5:2975721-2978508 FORWARD LENGTH=682 |
        201606

Vitvi03g00845
        35.2
        not assigned.unknown
        mitochondrial HSO70 2 |
        Chr5:2975721-2978508 FORWARD LENGTH=682 |
        201606
```

Coefficients for Vitvi03g00845.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.066659	7.857574e-18	***	2.123872e-17	***
SlopeC	-1.508056	0.02802278	*	0.426079	
MeanF-MeanC	-0.5194915	0.1249078		0.4183355	
SlopeF-SlopeC	0.09892301	0.9182476		0.9999488	


Vitvi03g00845
6.1 | 5.5 | −1.5 | −1.4
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

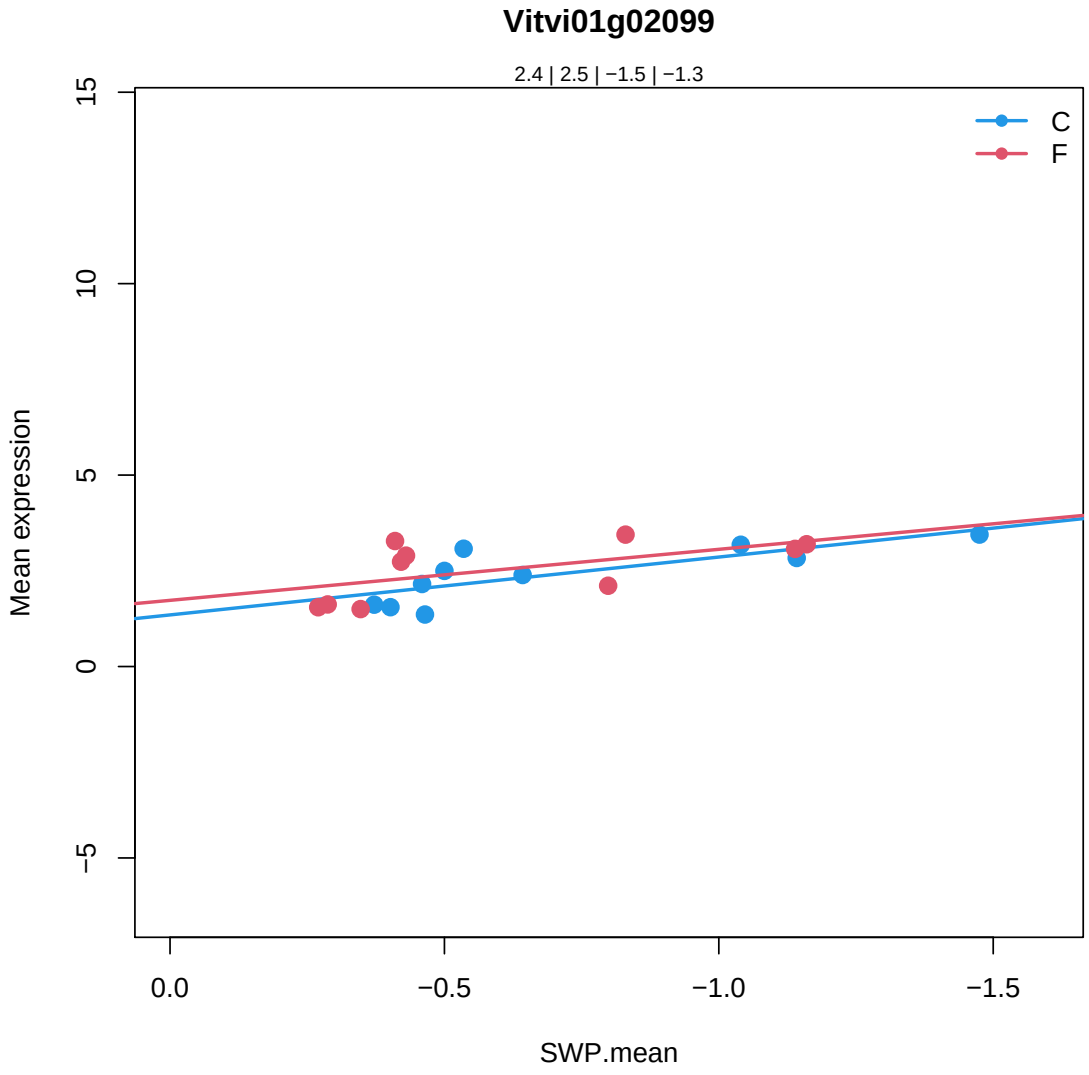
7.2.116 Vitvi01g02099: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g02099
        29.5.11.4.2
        protein.degradation.ubiquitin.E3.RING
        glycosyltransferase family protein (DUF23) |
        Chr1:9449812-9451539 REVERSE LENGTH=575 |
        201606
```

Coefficients for Vitvi01g02099.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.410227	4.484603e-12	***	6.208948e-12	***
SlopeC	-1.51117	0.005508617	**	0.2577627	
MeanF-MeanC	0.1298453	0.6072669		0.8620981	
SlopeF-SlopeC	0.1782757	0.8090889		0.9999488	



7.2.117 Vitvi03g00432: * type1

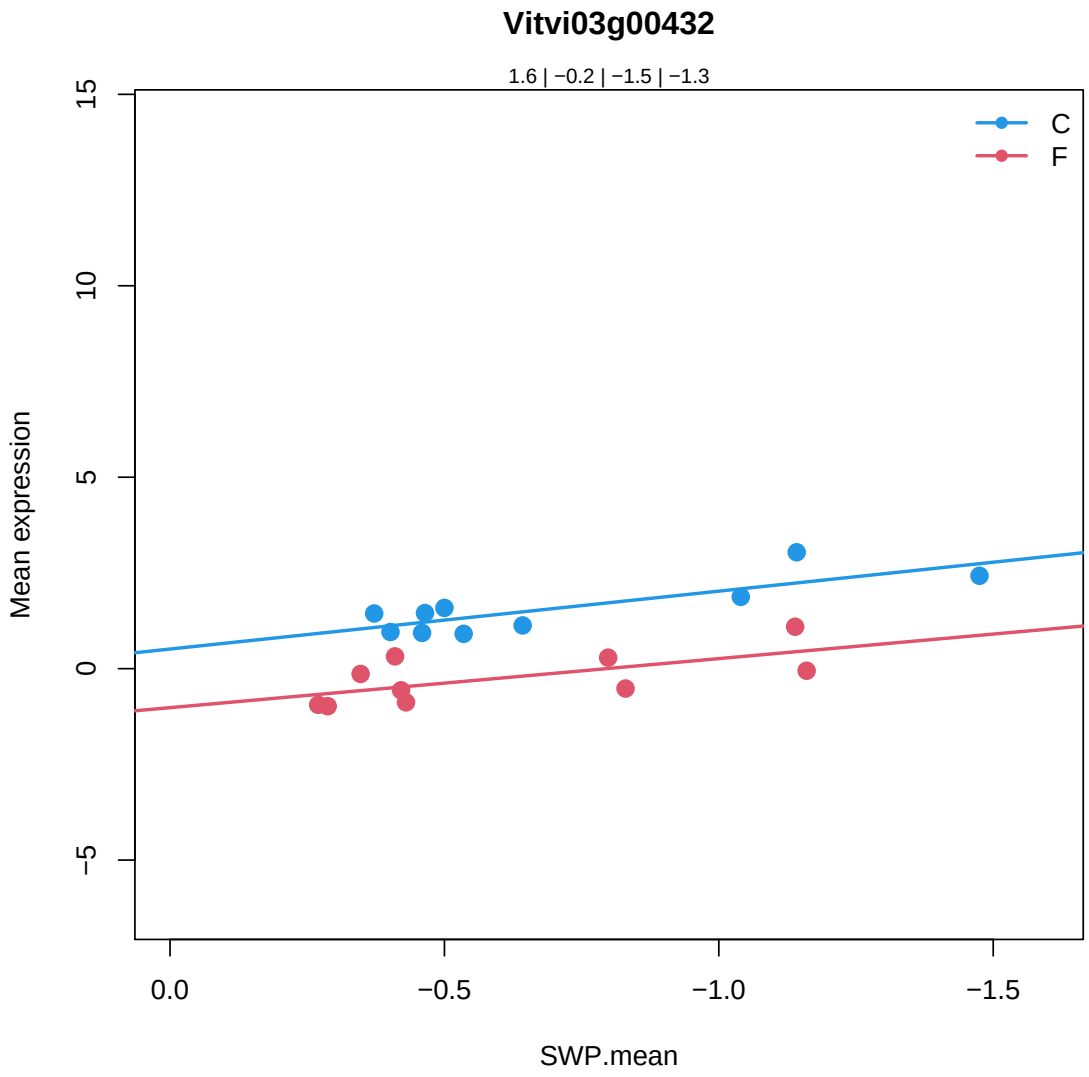
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00432
        21.2
        redox.ascorbate and glutathione
        2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protei
        Chr3:6554004-6554987 REVERSE LENGTH=278 |
        201606

Vitvi03g00432
        26.8
        misc.nitrilases, nitrile lyases, berberine bridge enzymes, reticuline
        2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protei
        Chr3:6554004-6554987 REVERSE LENGTH=278 |
        201606
```

Coefficients for Vitvi03g00432.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.575091	1.062316e-09	***	1.338499e-09	***
SlopeC	-1.511848	0.001957741	**	0.1673186	
MeanF-MeanC	-1.813218	3.728598e-08	***	1.681399e-06	***
SlopeF-SlopeC	0.230625	0.7213458		0.9999488	


Vitvi03g00432
1.6 | −0.2 | −1.5 | −1.3
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

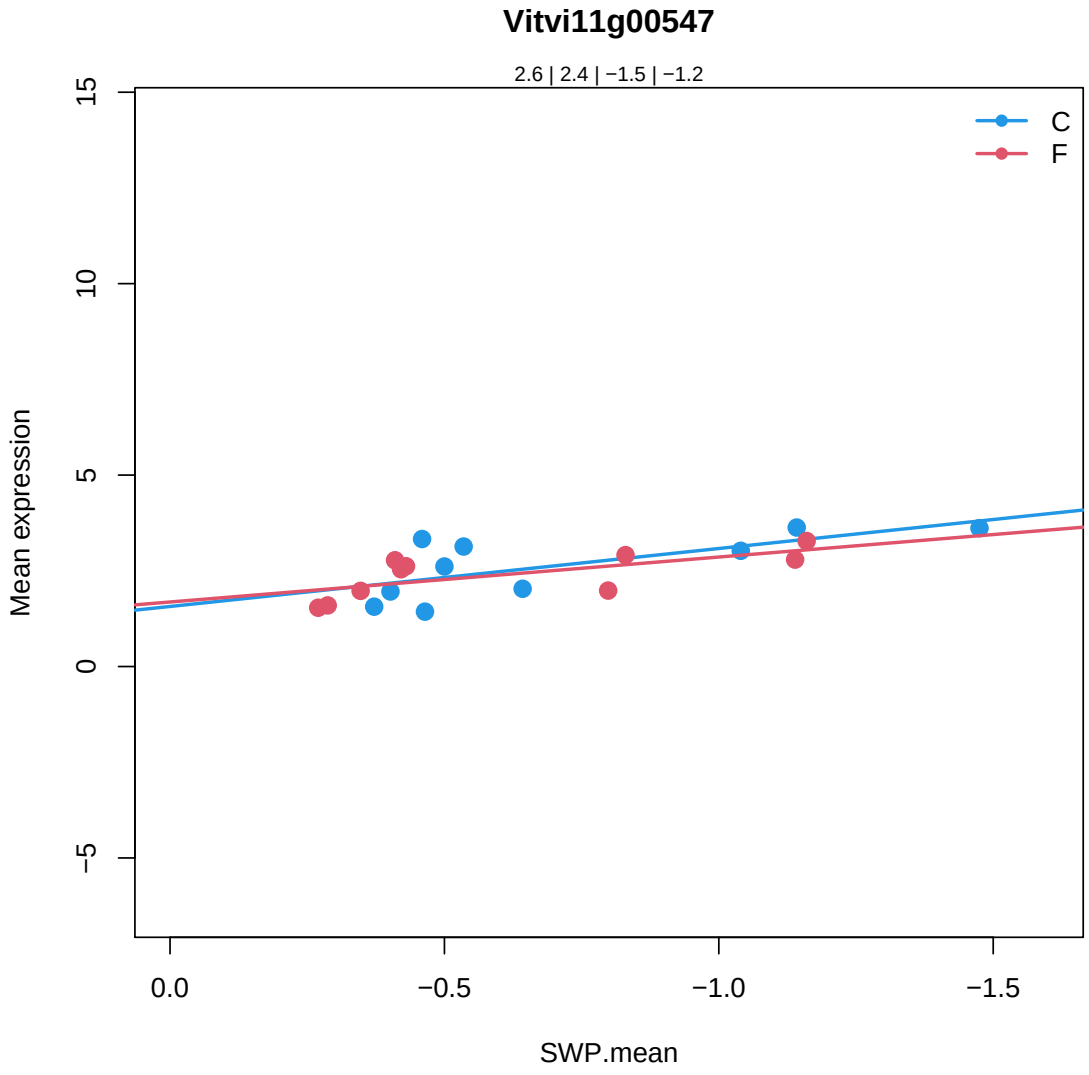
7.2.118 Vitvi11g00547: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00547
        30.3
        signalling.calcium
        Calcium-dependent lipid-binding (CaLB domain) family protein |
        Chr1:1625098-1628940 FORWARD LENGTH=560 |
        201606
```

Coefficients for Vitvi11g00547.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.632836	4.518668e-13	***	6.635216e-13	***
SlopeC	-1.514086	0.004394116	**	0.2399107	
MeanF-MeanC	-0.2323474	0.347272		0.7068069	
SlopeF-SlopeC	0.3399814	0.6359192		0.9999488	



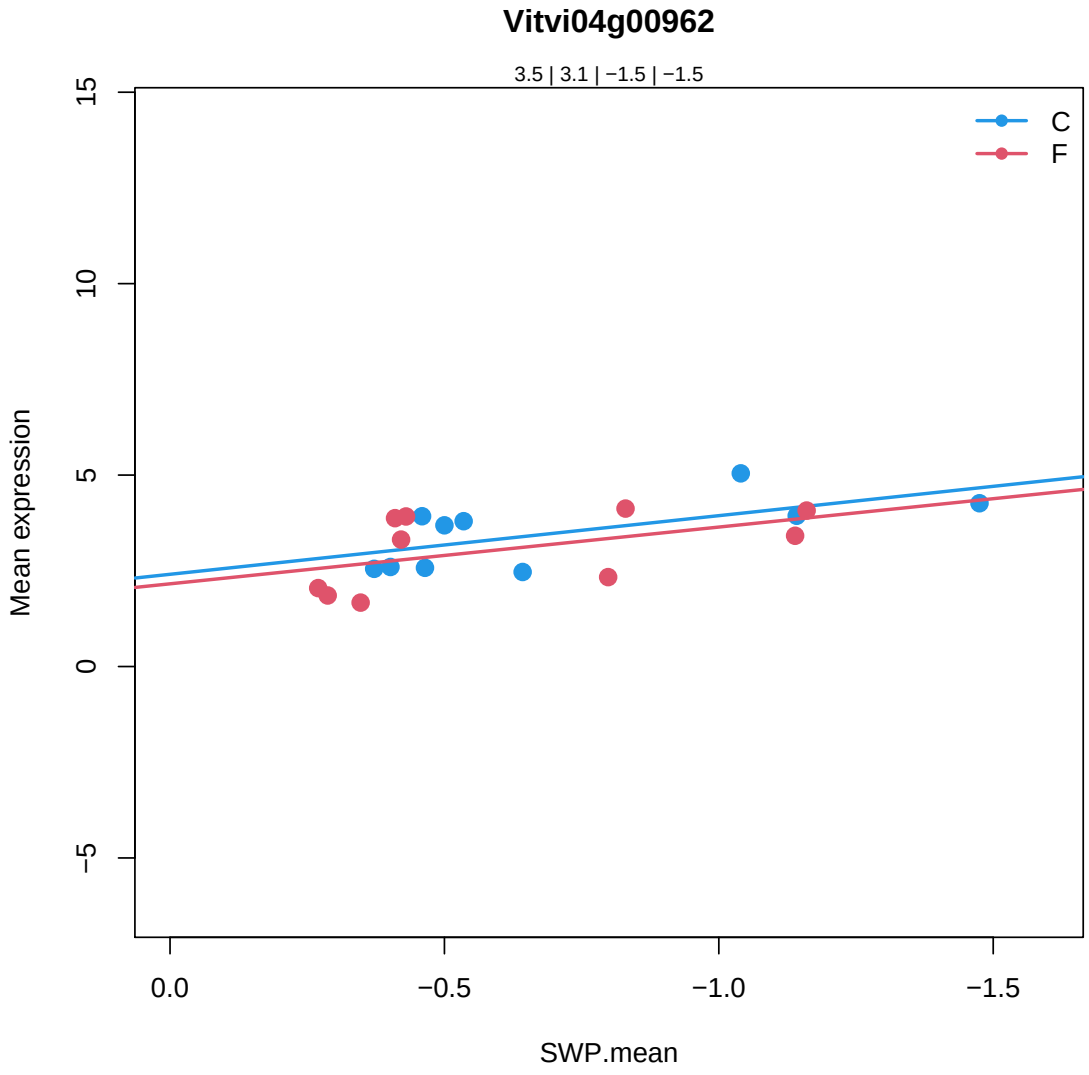
7.2.119 Vitvi04g00962: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00962
        35.2
        not assigned.unknown
        hikeshi-like protein |
        Chr1:24600356-24601027 REVERSE LENGTH=190 |
        201606
```

Coefficients for Vitvi04g00962.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.485224	8.556232e-13	***	1.233463e-12	***
SlopeC	-1.531557	0.02812359	*	0.4263731	
MeanF-MeanC	-0.4222037	0.2152382		0.5627205	
SlopeF-SlopeC	0.0494308	0.9597476		0.9999488	



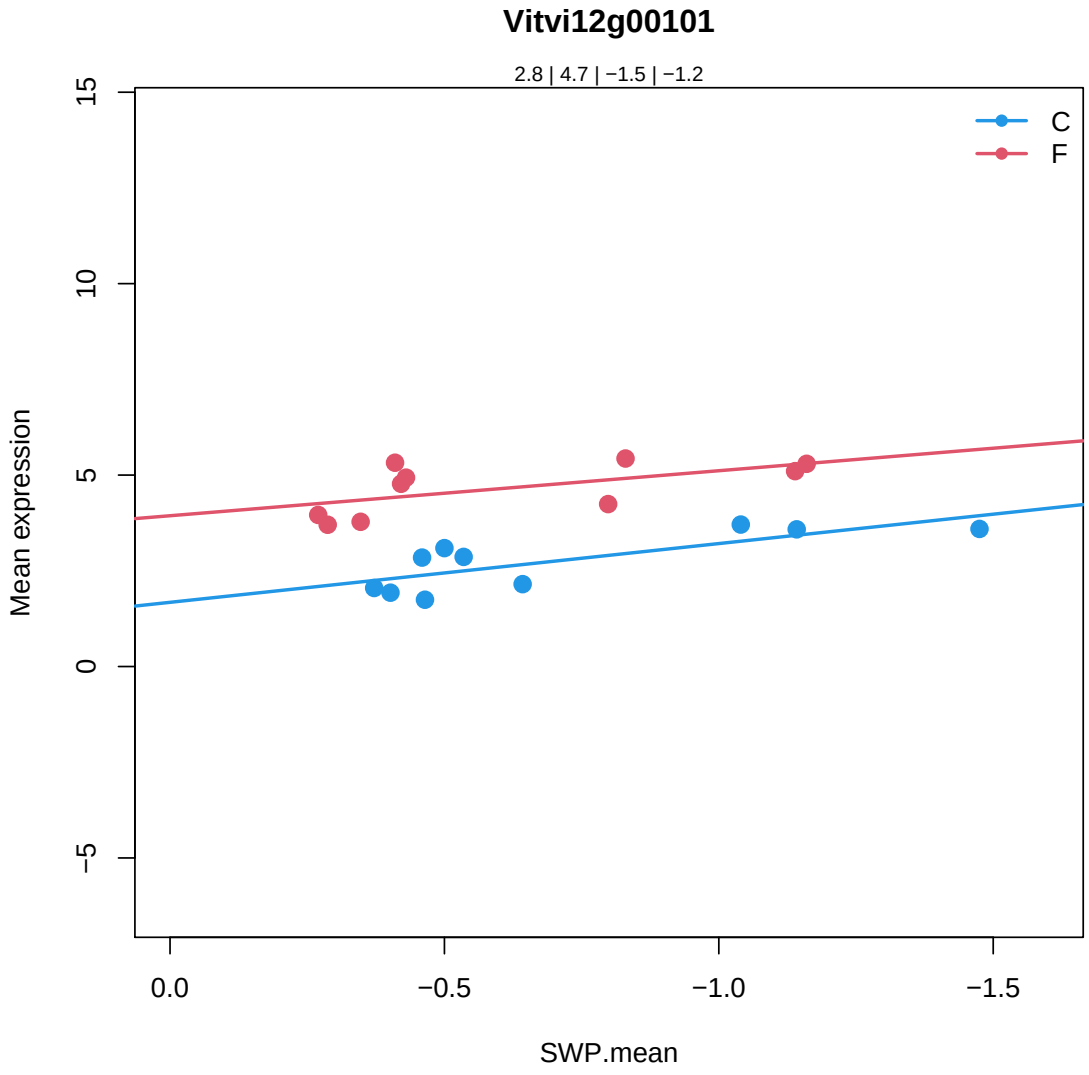
7.2.120 Vitvi12g00101: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00101
        34.16
        transport.ABC transporters and multidrug resistance systems
        MATE efflux family protein |
        Chr3:21819124-21821288 FORWARD LENGTH=507 |
        201606
```

Coefficients for Vitvi12g00101.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.755737	9.506814e-14	***	1.462779e-13	***
SlopeC	-1.534671	0.003082809	**	0.2103859	
MeanF-MeanC	1.898405	5.628455e-08	***	2.451112e-06	***
SlopeF-SlopeC	0.359012	0.6056038		0.9999488	



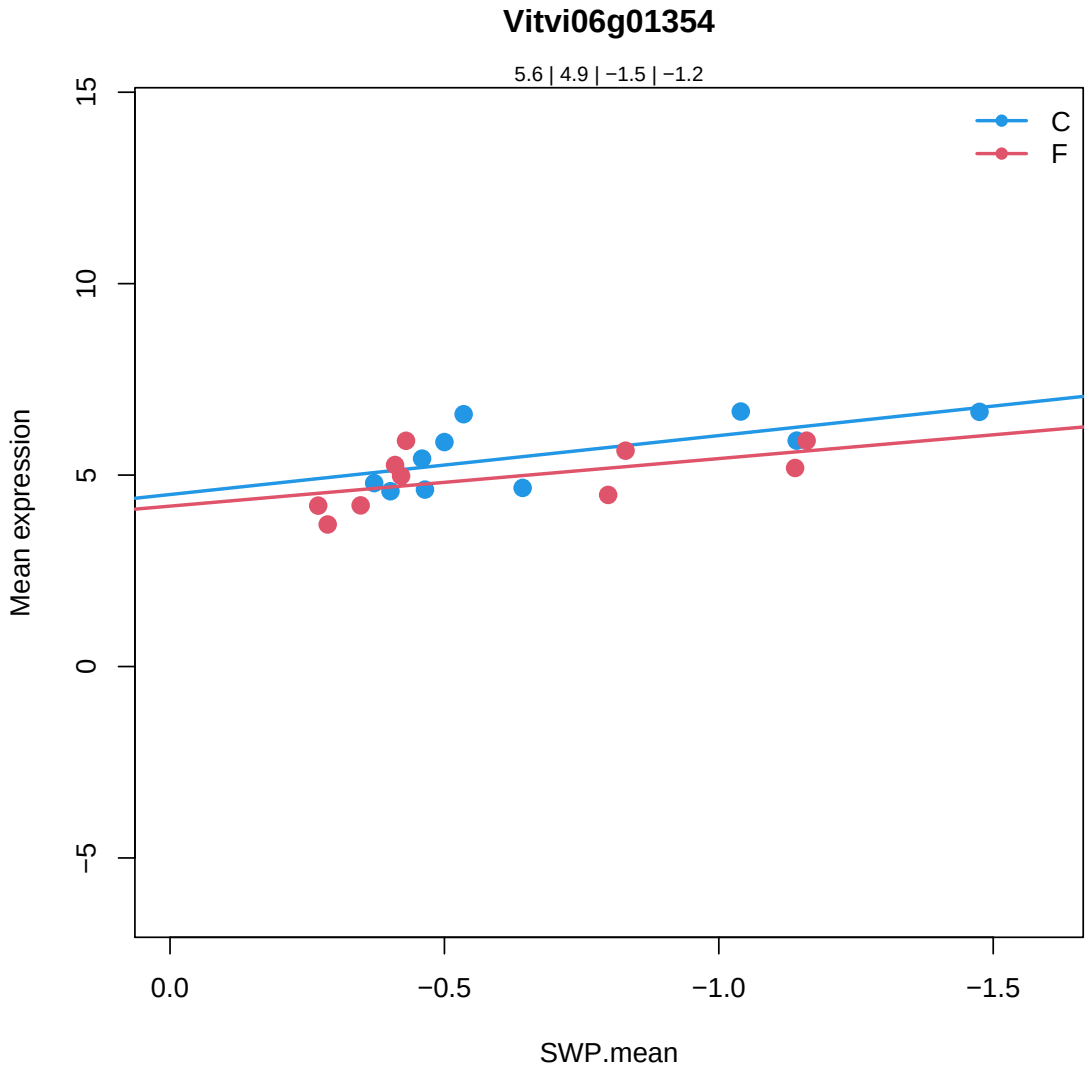
7.2.121 Vitvi06g01354: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01354
        31.5.1
        cell.cell death.plants
        Pheophorbide a oxygenase family protein with Rieske 2Fe-2S domain-cont
        Chr3:16383858-16386204 FORWARD LENGTH=537 |
        201606
```

Coefficients for Vitvi06g01354.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.574733	3.314337e-18	***	9.858923e-18	***
SlopeC	-1.539195	0.01245439	*	0.3261682	
MeanF-MeanC	-0.6289323	0.03947009	*	0.2046966	
SlopeF-SlopeC	0.2973165	0.7267595		0.9999488	



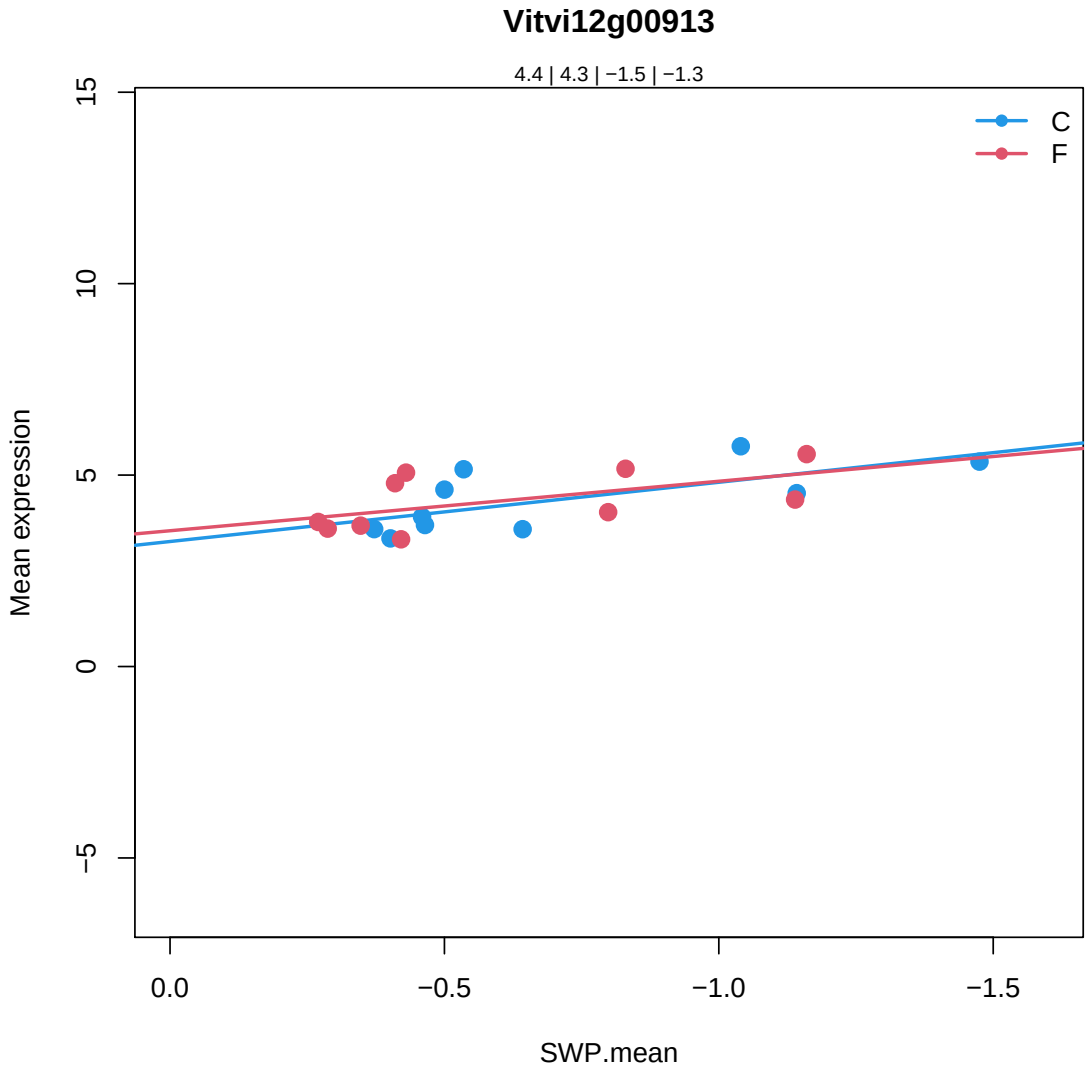
7.2.122 Vitvi12g00913: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00913
        27.1.1
        RNA.processing.splicing
        serine/arginine-rich splicing factor-like protein%2C putative |
        Chr5:25681849-25683553 REVERSE LENGTH=303 |
        201606
```

Coefficients for Vitvi12g00913.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.352667	2.795362e-16	***	5.644811e-16	***
SlopeC	-1.547135	0.00977034	**	0.3009465	
MeanF-MeanC	-0.01933659	0.9450567		0.9857335	
SlopeF-SlopeC	0.2545257	0.7569603		0.9999488	



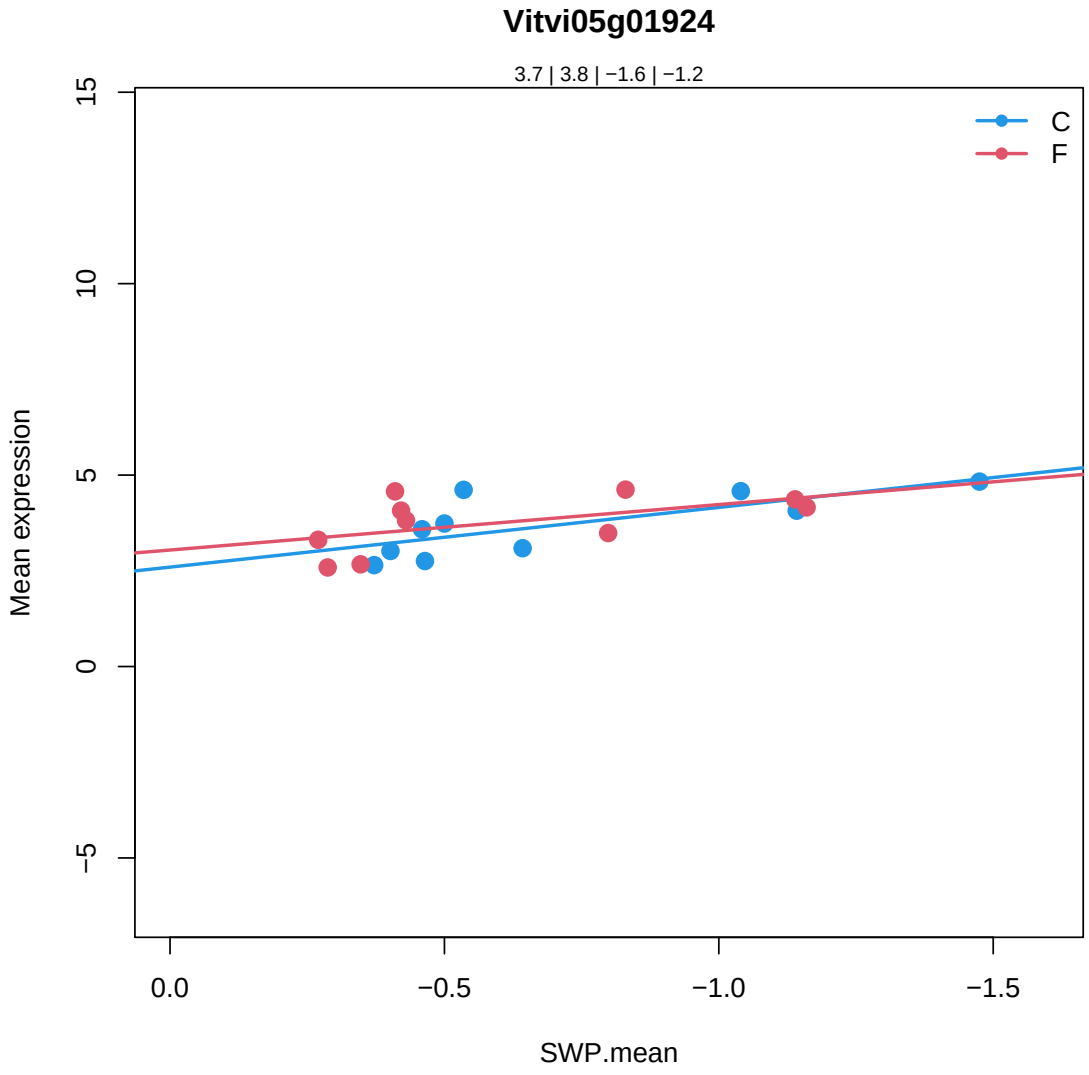
7.2.123 Vitvi05g01924: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01924
        17.5.1
        hormone metabolism.ethylene.synthesis-degradation
        2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protei
        Chr1:842895-844158 REVERSE LENGTH=379 |
        201606
```

Coefficients for Vitvi05g01924.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.692352	2.735716e-15	***	4.878646e-15	***
SlopeC	-1.559202	0.006502964	**	0.2686129	
MeanF-MeanC	0.07347336	0.7826008		0.9384607	
SlopeF-SlopeC	0.372102	0.633784		0.9999488	



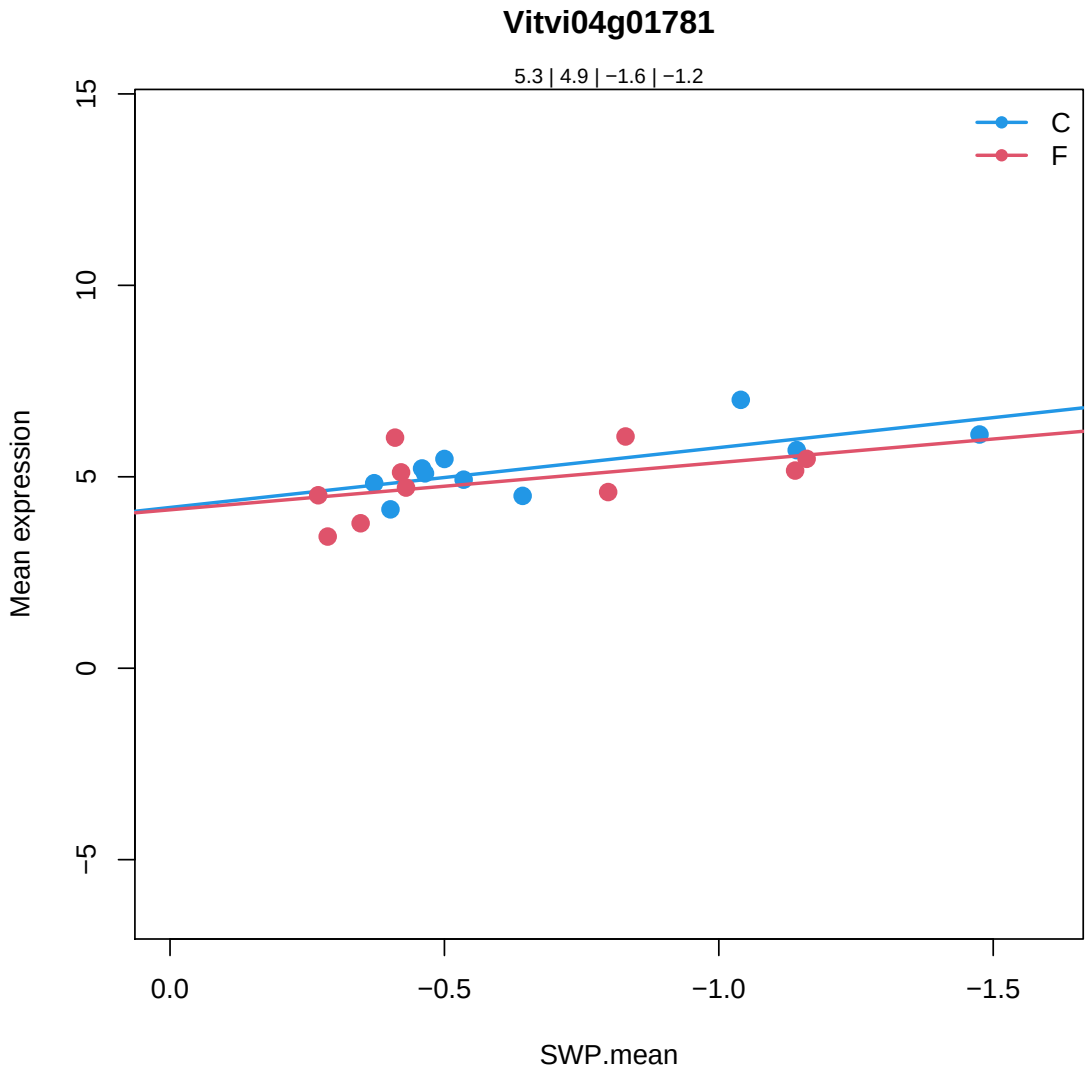
7.2.124 Vitvi04g01781: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01781
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi04g01781.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.298749	1.71787e-17	***	4.311506e-17	***
SlopeC	-1.56403	0.0134099	*	0.3305597	
MeanF-MeanC	-0.410543	0.1783045		0.5127769	
SlopeF-SlopeC	0.3309496	0.7053918		0.9999488	



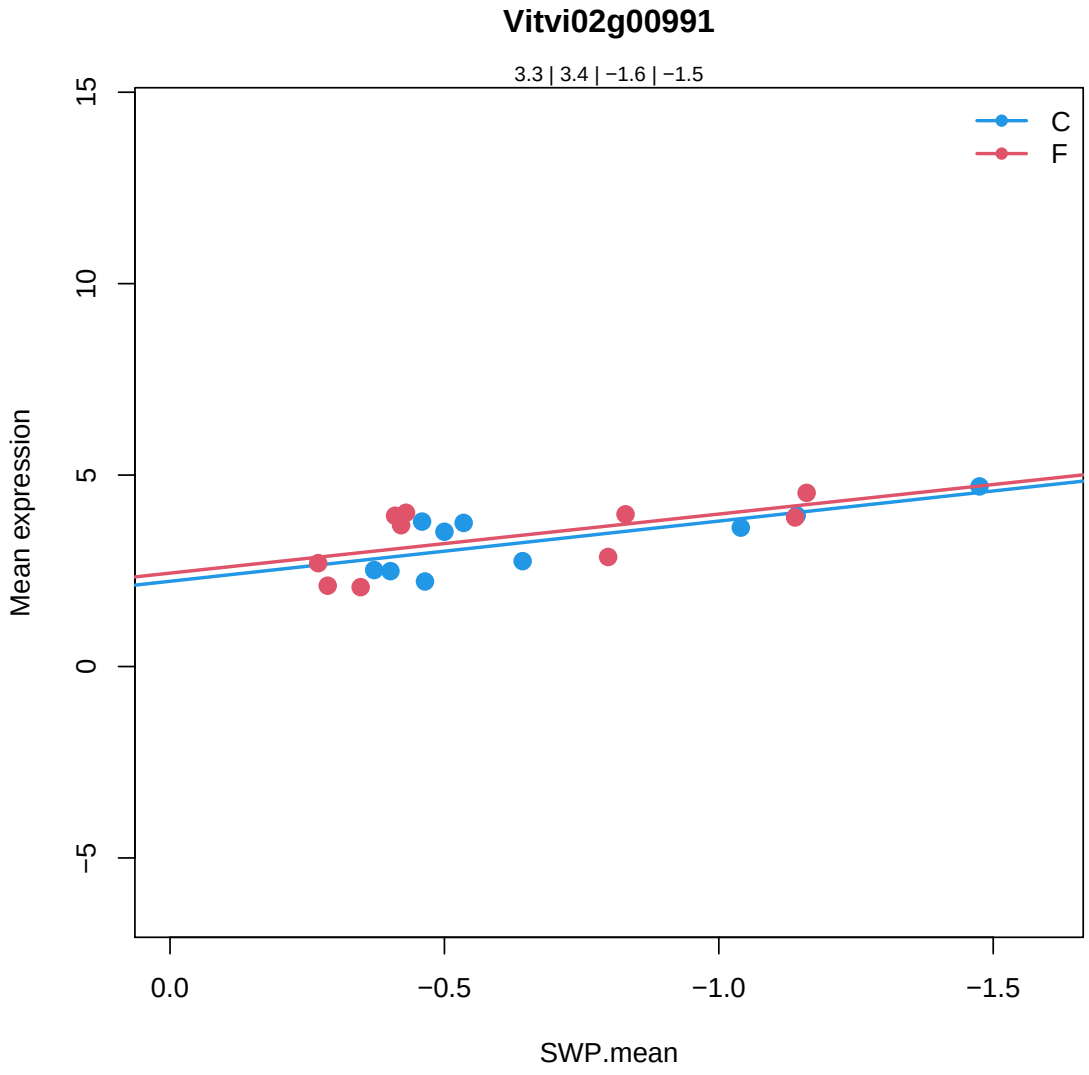
7.2.125 Vitvi02g00991: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00991
        35.2
        not assigned.unknown
        UDP-Glycosyltransferase superfamily protein |
        Chr2:15417618-15419108 REVERSE LENGTH=496 |
        201606
```

Coefficients for Vitvi02g00991.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.33156	5.382133e-14	***	8.43976e-14	***
SlopeC	-1.572287	0.008310277	**	0.2862911	
MeanF-MeanC	0.04742068	0.8646699		0.964386	
SlopeF-SlopeC	0.02977909	0.9708319		0.9999488	



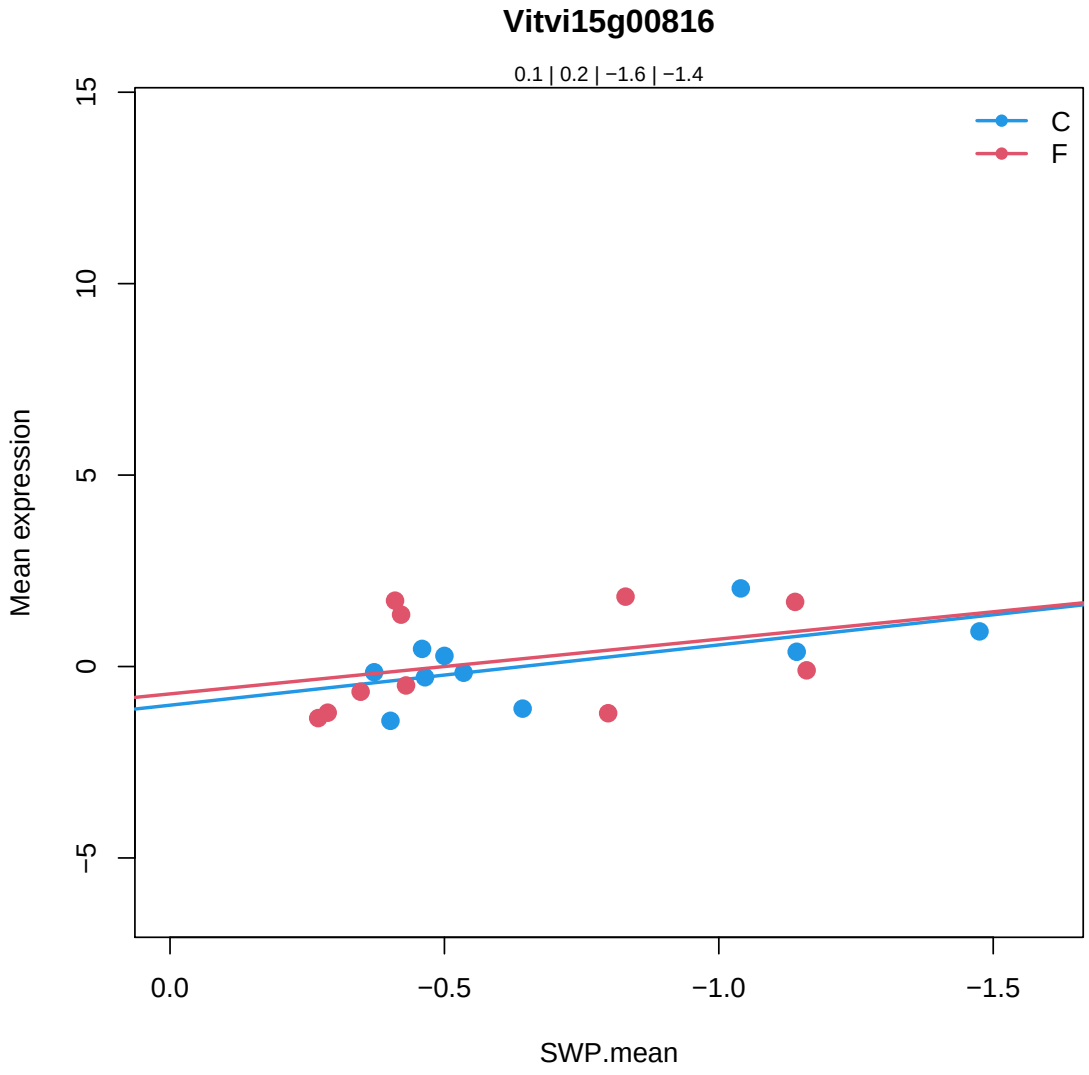
7.2.126 Vitvi15g00816: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g00816
        35.2
        not assigned.unknown
        FASCICLIN-like arabinogalactan protein 8 |
        Chr2:18742797-18744059 REVERSE LENGTH=420 |
        201606
```

Coefficients for Vitvi15g00816.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.09682662	0.7589199		0.7633774	
SlopeC	-1.574329	0.08327988	.	0.5813429	
MeanF-MeanC	0.05920581	0.89434		0.9721746	
SlopeF-SlopeC	0.1447743	0.9116766		0.9999488	



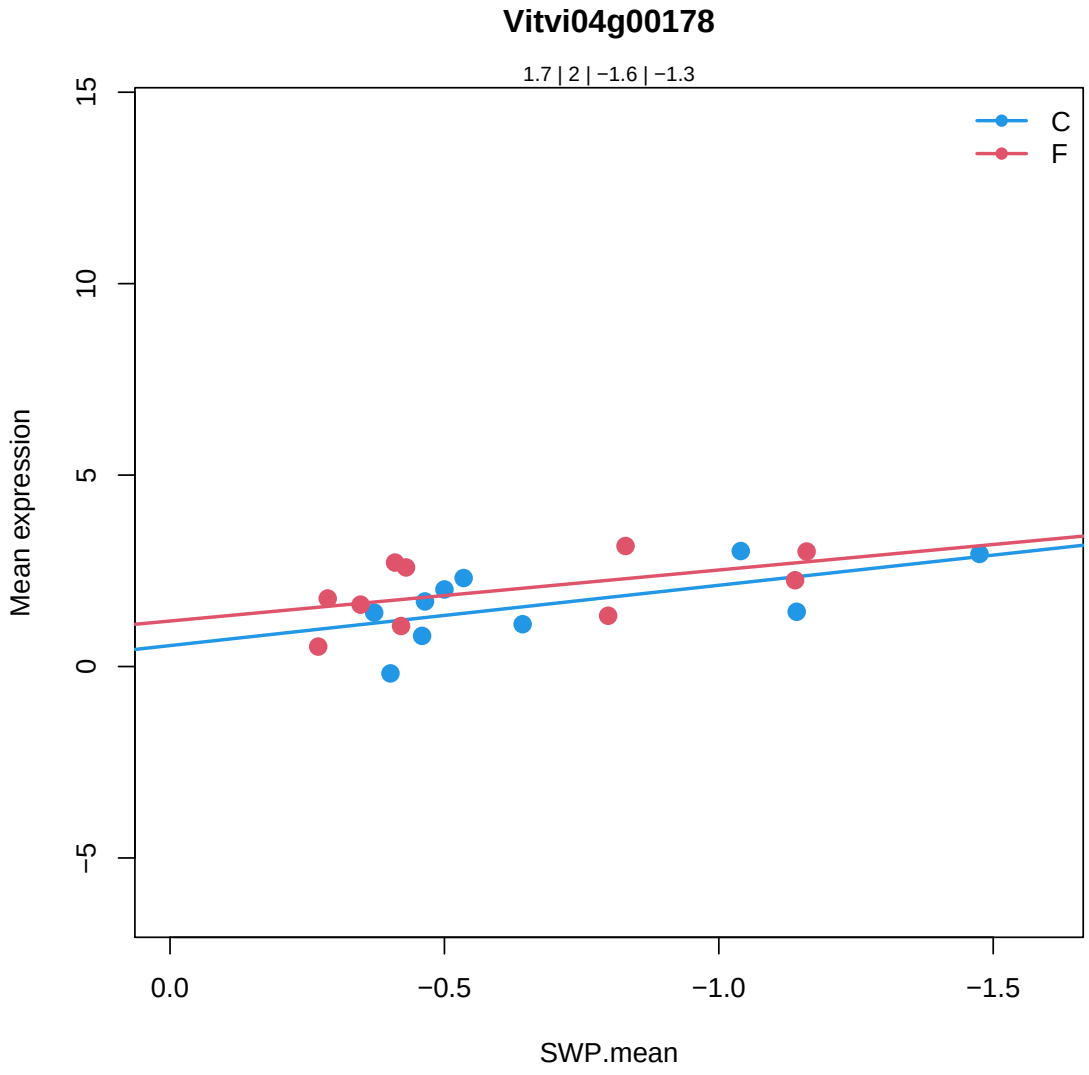
7.2.127 Vitvi04g00178: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00178
        26.3.5
        misc.gluco-, galacto- and mannosidases.glycosyl hydrolase family 5
        alpha/beta-Hydrolases superfamily protein |
        Chr4:16000282-16001450 FORWARD LENGTH=218 |
        201606
```

Coefficients for Vitvi04g00178.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.654019	5.082719e-07	***	5.91335e-07	***
SlopeC	-1.575118	0.02462149	*	0.4057089	
MeanF-MeanC	0.3461239	0.3076938		0.6711319	
SlopeF-SlopeC	0.2428666	0.8046557		0.9999488	



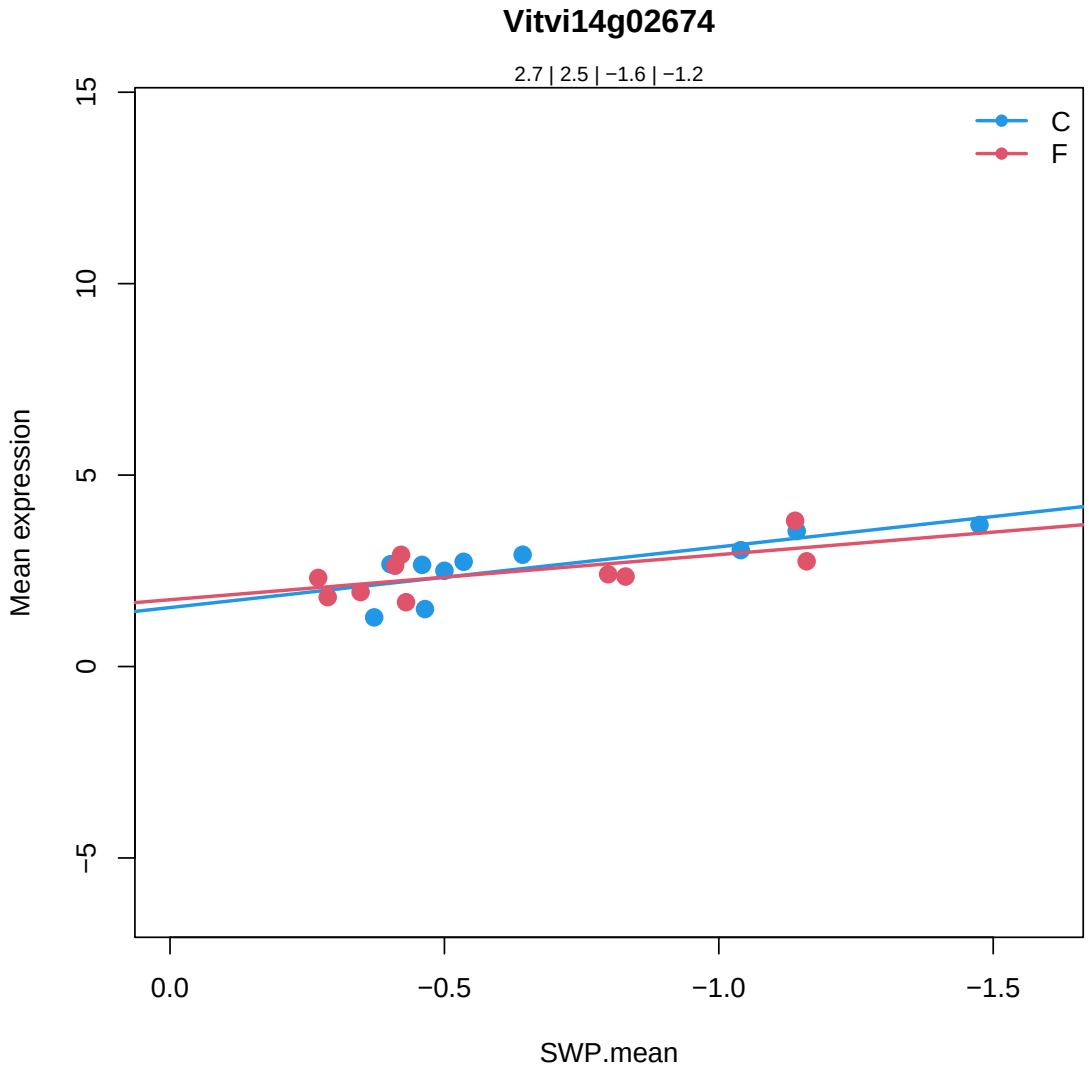
7.2.128 Vitvi14g02674: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g02674
        27.3.50
        RNA.regulation of transcription.general transcription
        RNA-directed DNA polymerase (reverse transcriptase)-related family pro
        Chr3:8789309-8790907 FORWARD LENGTH=532 |
        201606
```

Coefficients for Vitvi14g02674.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.654027	8.609237e-14	***	1.328023e-13	***
SlopeC	-1.58514	0.00166598	**	0.1556102	
MeanF-MeanC	-0.1927377	0.3995015		0.7442687	
SlopeF-SlopeC	0.4082367	0.5405994		0.9999488	



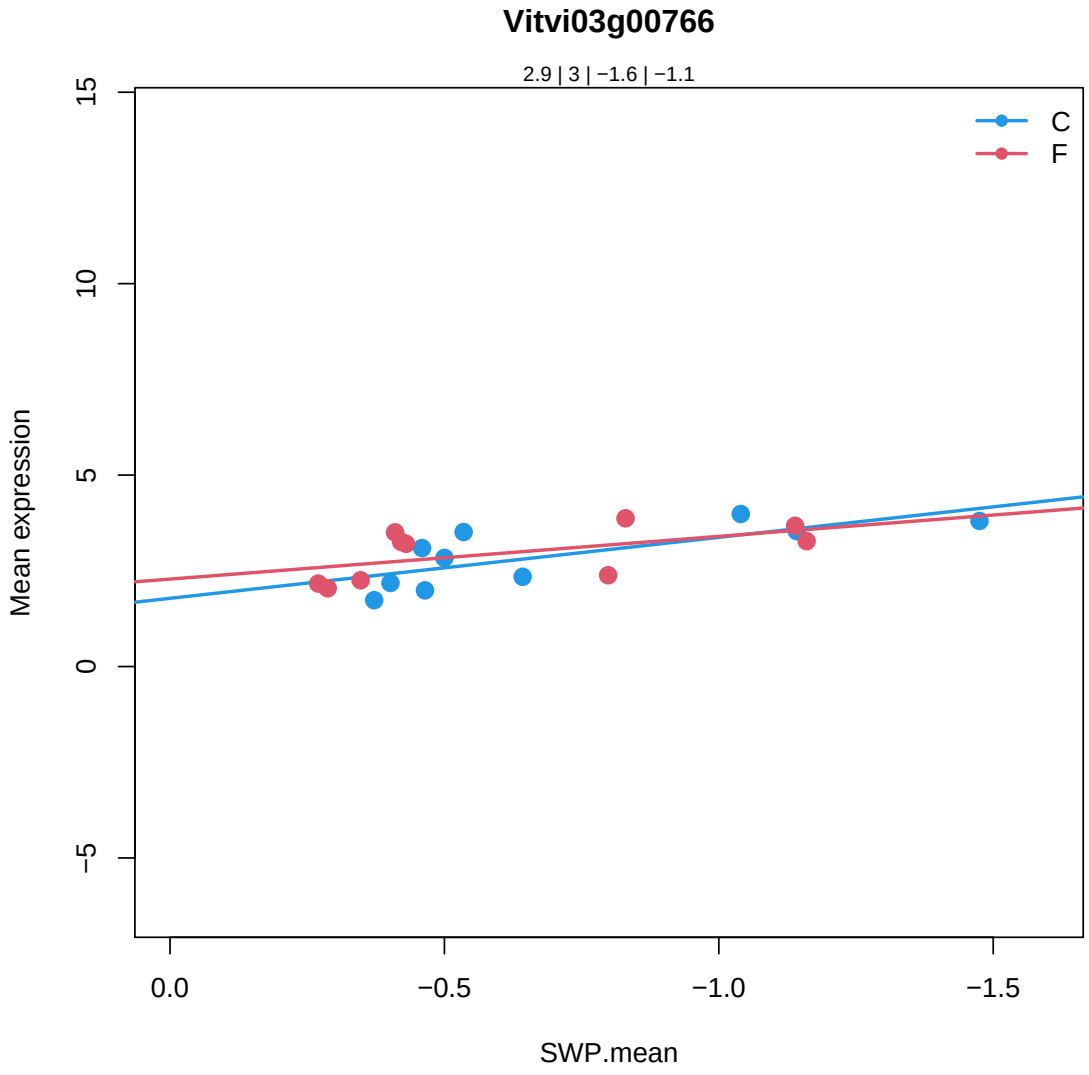
7.2.129 Vitvi03g00766: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00766
        35.1
        not assigned.no ontology
        CBS domain protein (DUF21) |
        Chr2:6182362-6184648 REVERSE LENGTH=423 |
        201606
```

Coefficients for Vitvi03g00766.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.900922	1.3203e-13	***	2.007983e-13	***
SlopeC	-1.592341	0.003913092	**	0.2293975	
MeanF-MeanC	0.06199901	0.8067811		0.9464295	
SlopeF-SlopeC	0.4766948	0.522444		0.9999488	



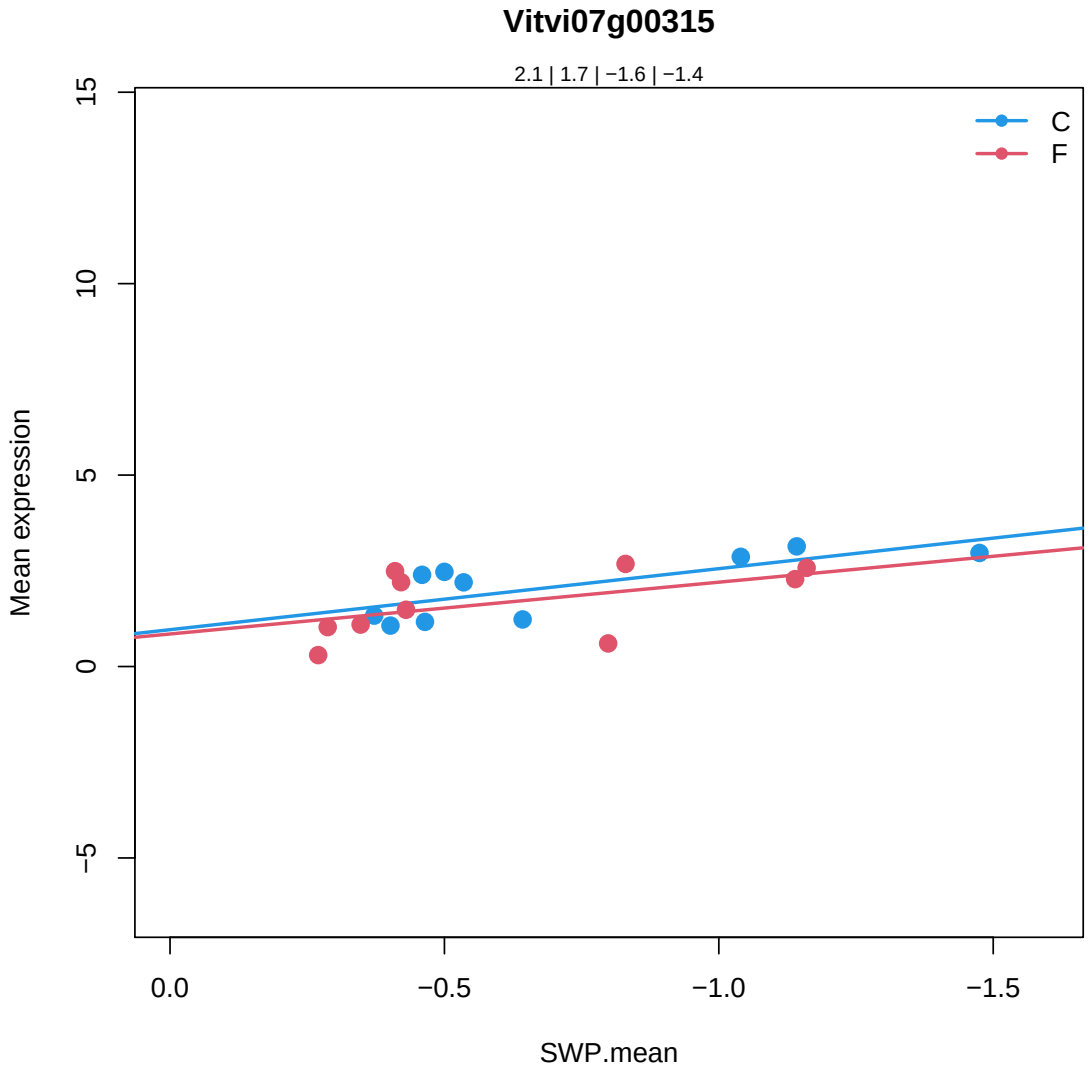
7.2.130 Vitvi07g00315: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g00315
        28.1
        DNA.synthesis/chromatin structure
        zinc finger (CCCH type) helicase family protein |
        Chr2:19545828-19550871 REVERSE LENGTH=1015 |
        201606
```

Coefficients for Vitvi07g00315.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.082814	1.151928e-09	***	1.45009e-09	***
SlopeC	-1.593846	0.01063253	*	0.3110577	
MeanF-MeanC	-0.4088765	0.1722101		0.5024667	
SlopeF-SlopeC	0.2412863	0.7786519		0.9999488	



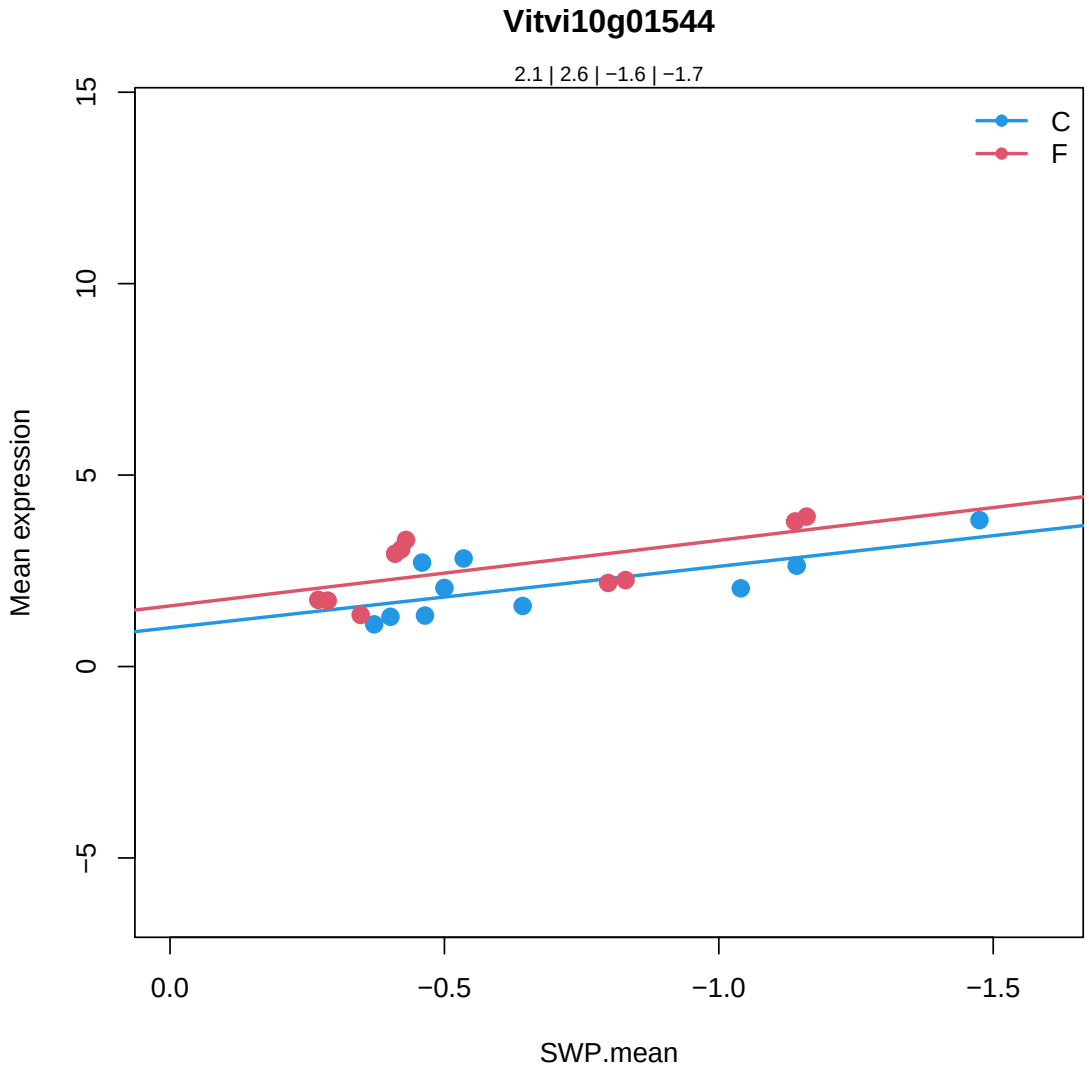
7.2.131 Vitvi10g01544: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g01544
        35.2
        not assigned.unknown
        E3 ubiquitin-protein ligase |
        Chr3:6965671-6967102 FORWARD LENGTH=425 |
        201606
```

Coefficients for Vitvi10g01544.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.140199	6.191029e-10	***	7.865179e-10	***
SlopeC	-1.602621	0.009802541	**	0.3011737	
MeanF-MeanC	0.4864314	0.1050379		0.3758187	
SlopeF-SlopeC	-0.1098173	0.8973909		0.9999488	



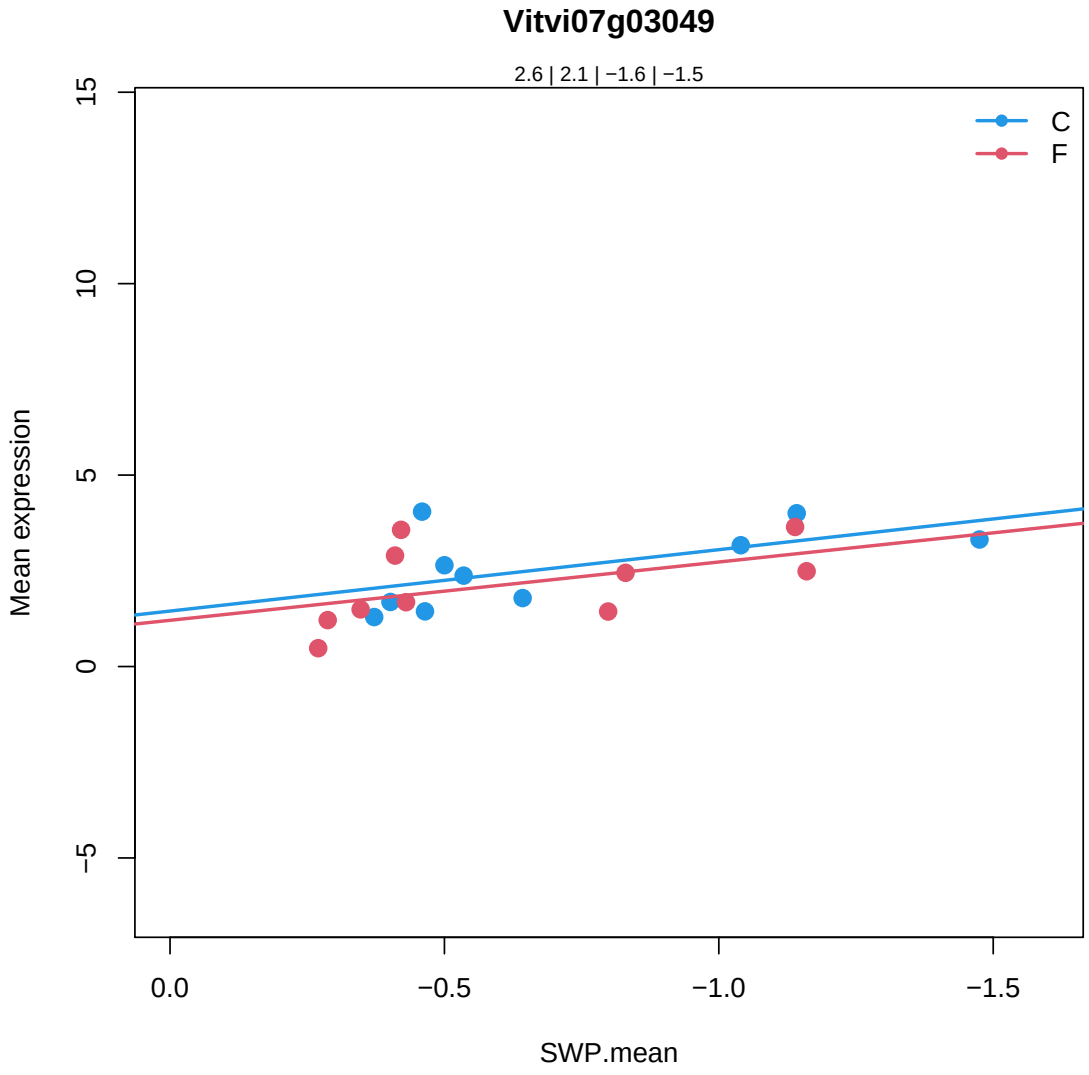
7.2.132 Vitvi07g03049: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g03049
        13.1.6.1.1
        amino acid metabolism.synthesis.aromatic aa.chorismate.3-deoxy-D-arabi
        3-deoxy-D-arabino-heptulosonate 7-phosphate synthase 1 |
        Chr4:18539654-18541832 FORWARD LENGTH=525 |
        201606
```

Coefficients for Vitvi07g03049.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.575644	2.315396e-09	***	2.884451e-09	***
SlopeC	-1.603605	0.03976744	*	0.4708616	
MeanF-MeanC	-0.4410604	0.2491464		0.6091793	
SlopeF-SlopeC	0.08108974	0.9413972		0.9999488	



7.2.133 Vitvi17g00287: * type1

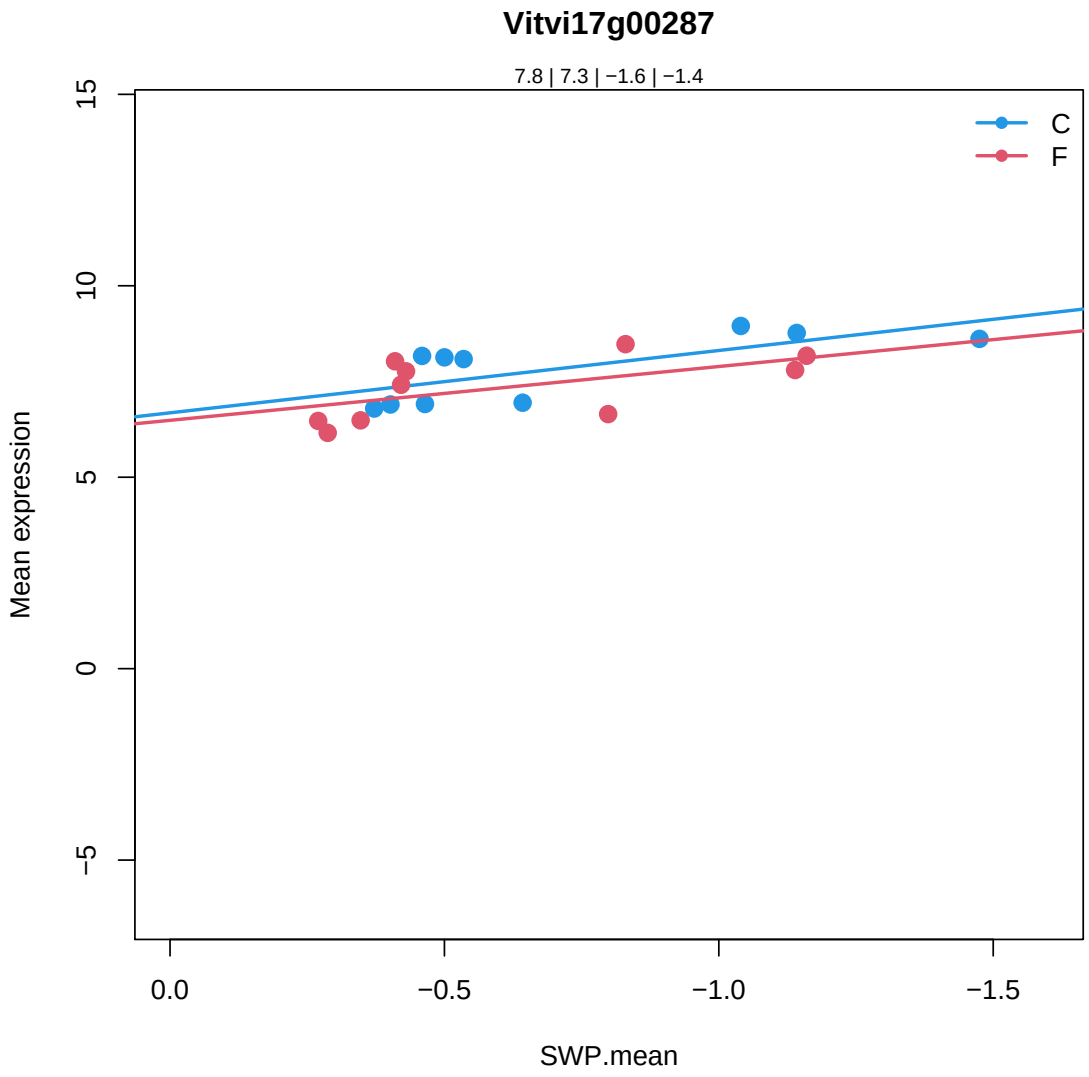
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00287
        29.6
        protein.folding
        chloroplast heat shock protein 70-1 |
        Chr4:12590094-12593437 FORWARD LENGTH=718 |
        201606

Vitvi17g00287
        20.2.1
        stress.abiotic.heat
        chloroplast heat shock protein 70-1 |
        Chr4:12590094-12593437 FORWARD LENGTH=718 |
        201606
```

Coefficients for Vitvi17g00287.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.826385	1.972115e-21	***	1.93679e-20	***
SlopeC	-1.628149	0.007961231	**	0.2832315	
MeanF-MeanC	-0.4846599	0.1010527		0.3663761	
SlopeF-SlopeC	0.2227912	0.7904987		0.9999488	


Vitvi17g00287
7.8 | 7.3 | −1.6 | −1.4
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

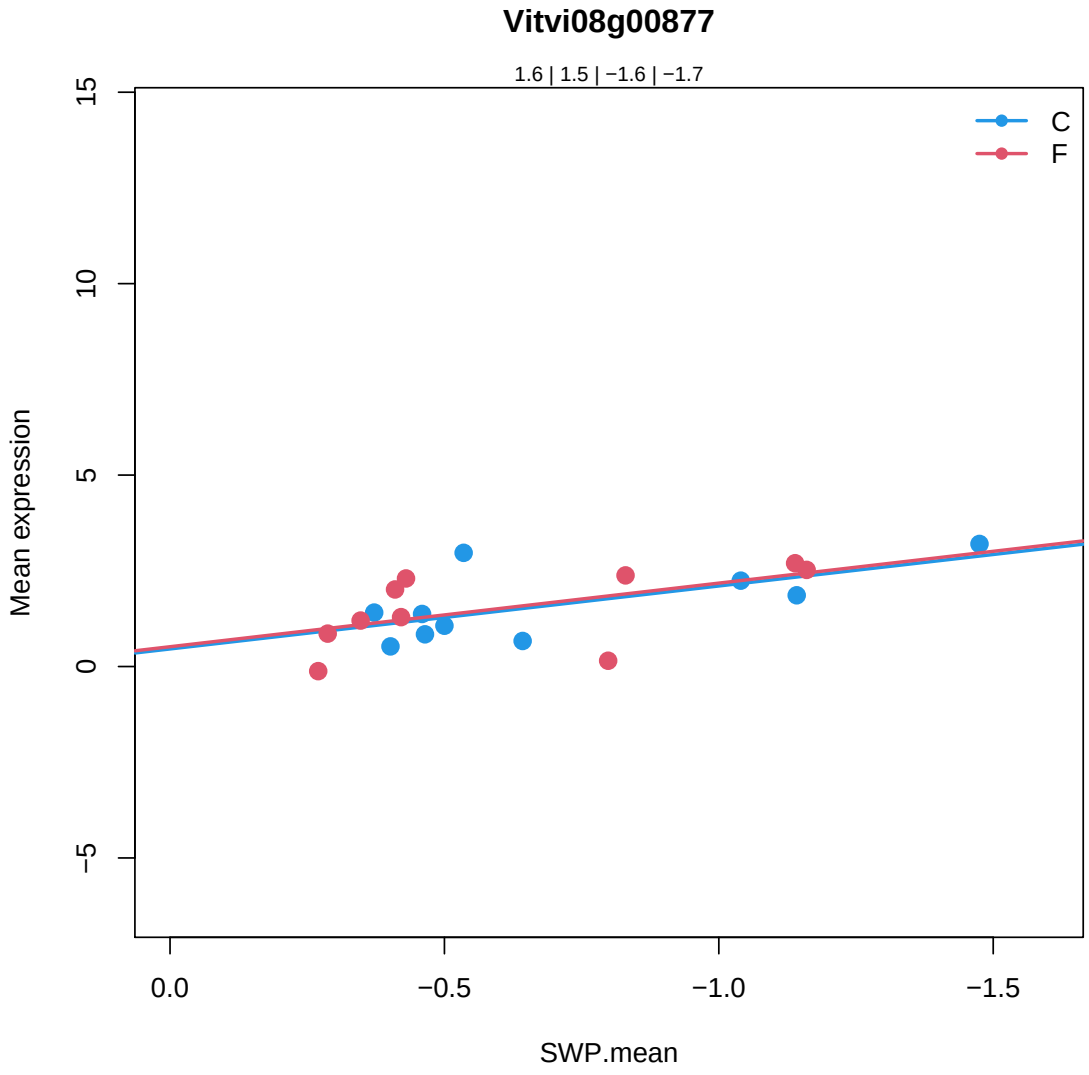
7.2.134 Vitvi08g00877: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g00877
        10.6.2
        cell wall.degradation.mannan-xylose-arabinose-fucose
        Glycosyl hydrolase superfamily protein |
        Chr5:361189-362867 REVERSE LENGTH=448 |
        201606
```

Coefficients for Vitvi08g00877.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.615209	8.009752e-07	***	9.266386e-07	***
SlopeC	-1.645206	0.0202006	*	0.3764029	
MeanF-MeanC	-0.08594045	0.7990073		0.9437748	
SlopeF-SlopeC	-0.01592818	0.9871305		0.9999488	



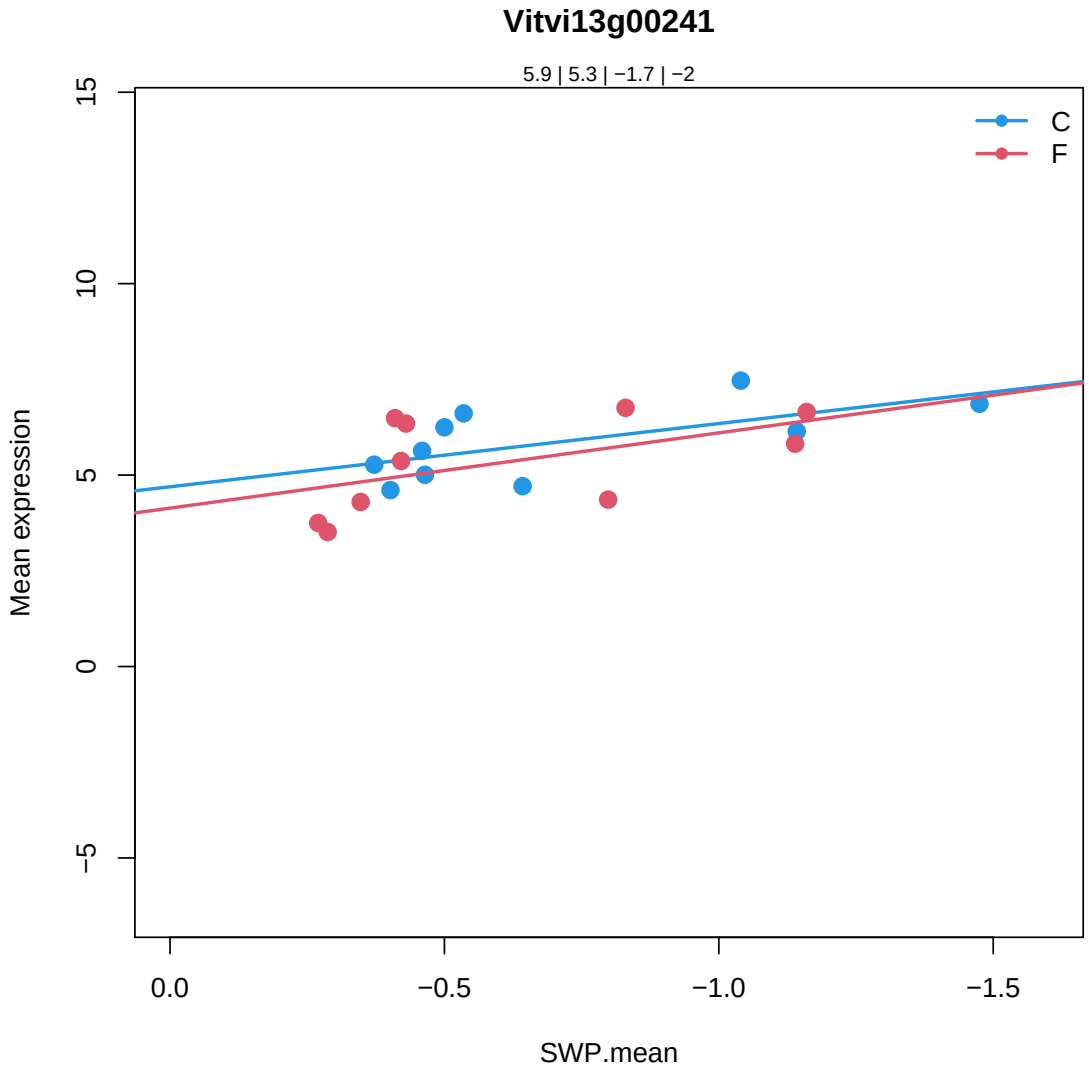
7.2.135 Vitvi13g00241: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00241
        21.2.1
        redox.ascorbate and glutathione.ascorbate
        dehydroascorbate reductase 2 |
        Chr1:28250255-28251237 REVERSE LENGTH=213 |
        201606
```

Coefficients for Vitvi13g00241.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.855599	6.807616e-16	***	1.302557e-15	***
SlopeC	-1.65169	0.04266318	*	0.48214	
MeanF-MeanC	-0.5209892	0.1951408		0.5362063	
SlopeF-SlopeC	-0.3134823	0.7860909		0.9999488	



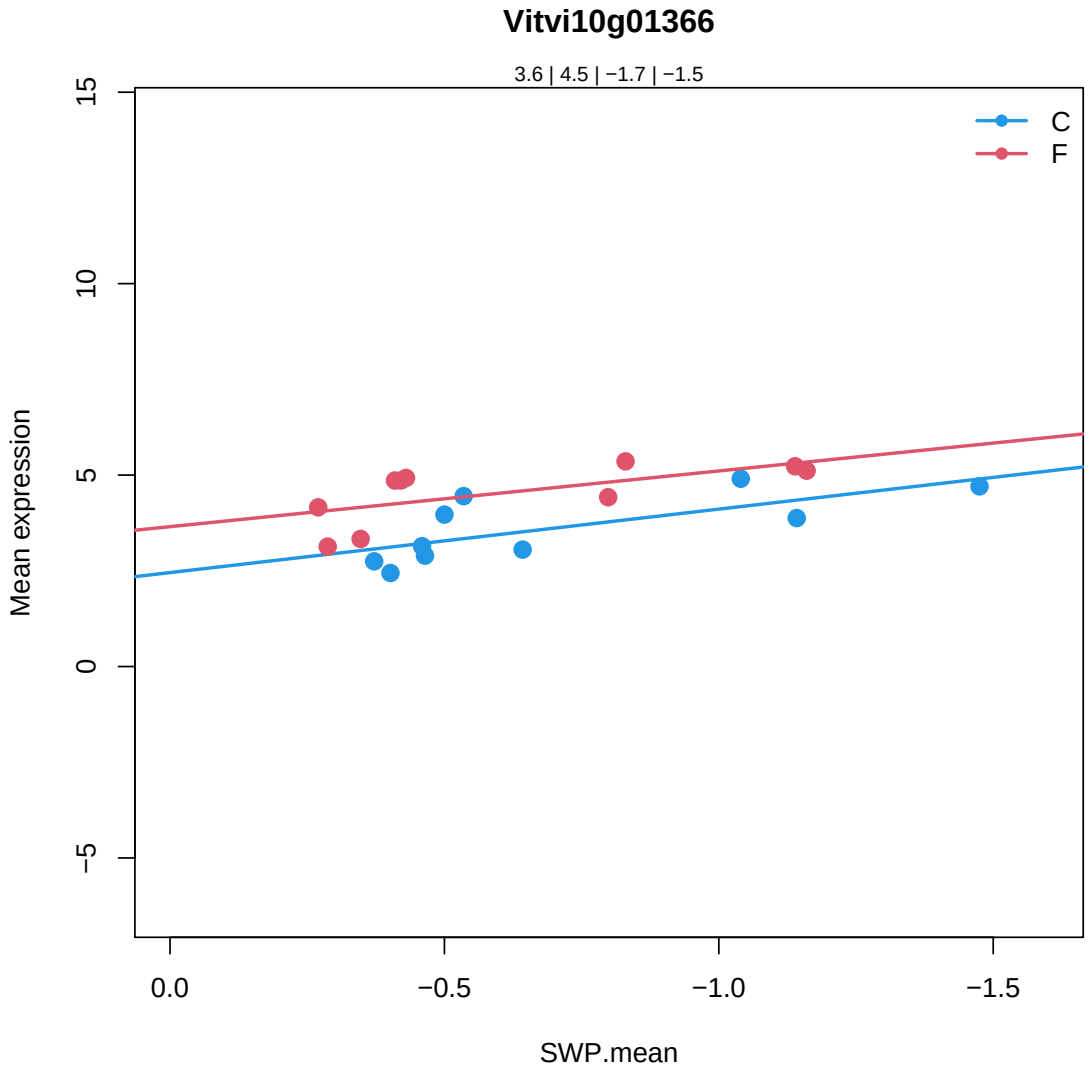
7.2.136 Vitvi10g01366: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g01366
        16.2
        secondary metabolism.phenylpropanoids
        nicotinamidase 2 |
        Chr5:7826005-7826601 REVERSE LENGTH=198 |
        201606
```

Coefficients for Vitvi10g01366.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.618555	7.525381e-15	***	1.274607e-14	***
SlopeC	-1.657775	0.00519472	**	0.2562392	
MeanF-MeanC	0.9203104	0.002653097	**	0.0277356	*
SlopeF-SlopeC	0.2025806	0.8008114		0.9999488	



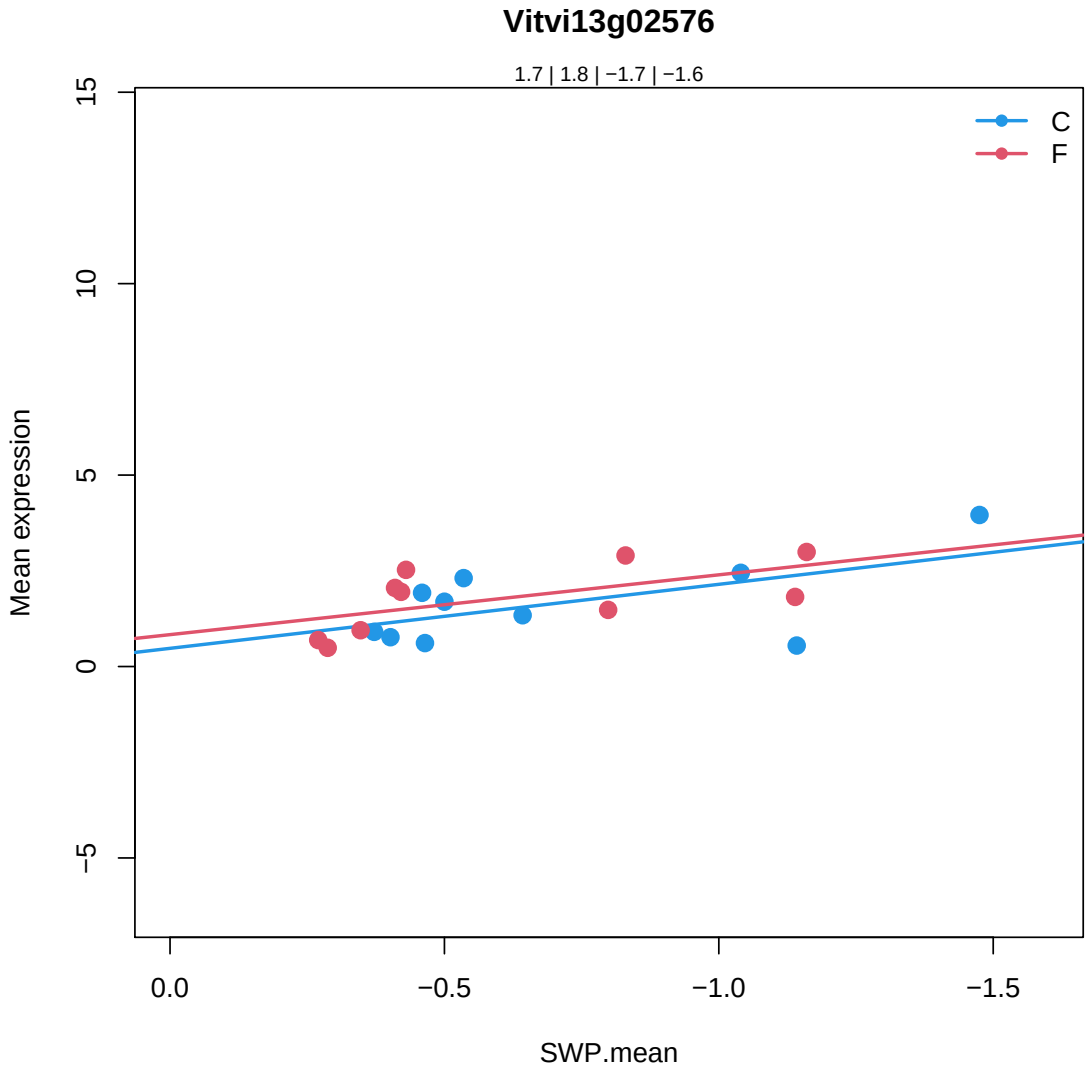
7.2.137 Vitvi13g02576: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g02576
        35.2
        not assigned.unknown
        oxidoreductase/transition metal ion-binding protein |
        Chr2:13580600-13580962 FORWARD LENGTH=120 |
        201606
```

Coefficients for Vitvi13g02576.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.650056	7.486693e-07	***	8.667845e-07	***
SlopeC	−1.671749	0.02029366	*	0.3768116	
MeanF−MeanC	0.1341797	0.6961594		0.9046669	
SlopeF−SlopeC	0.1094618	0.9132158		0.9999488	



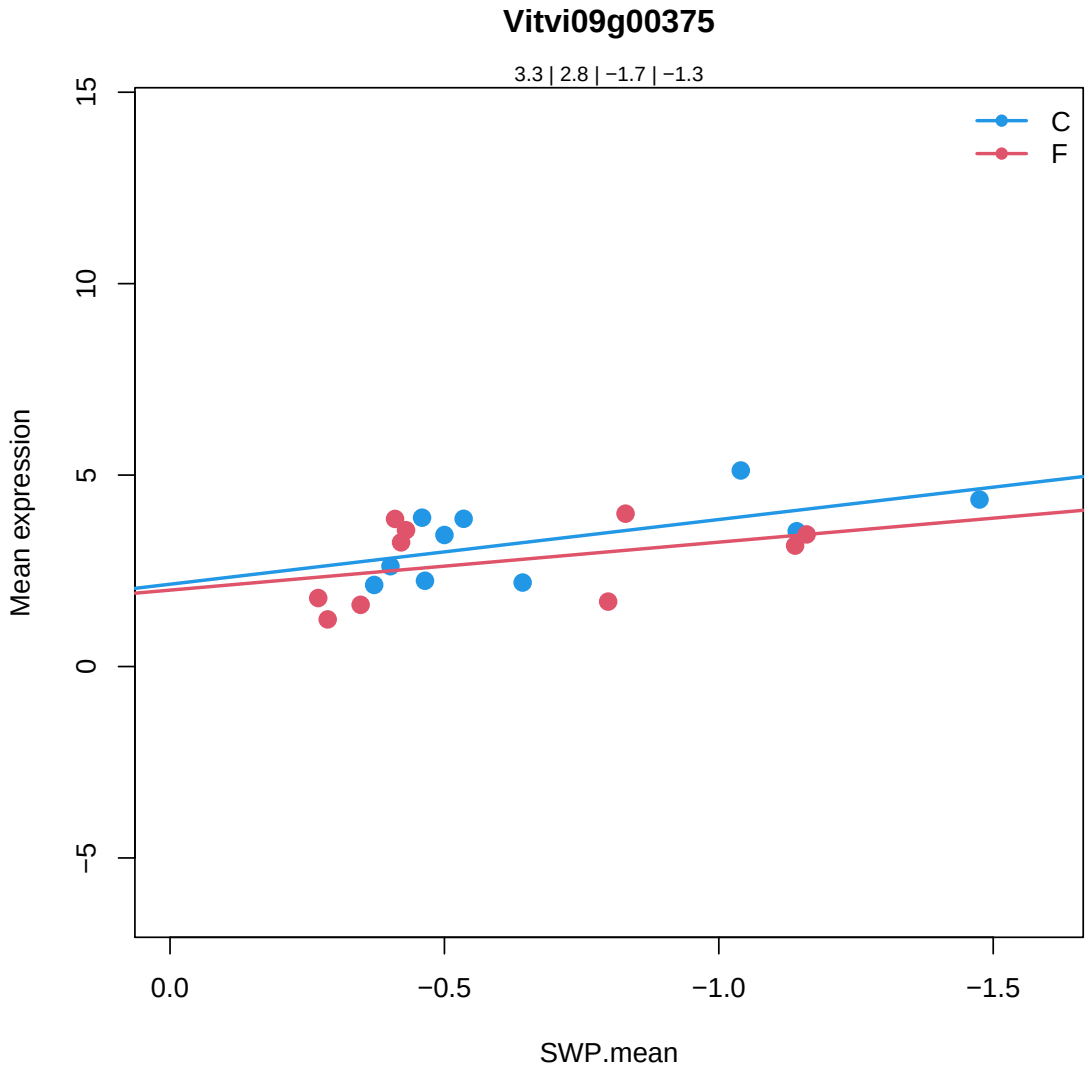
7.2.138 Vitvi09g00375: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00375
        18
        Co-factor and vitamine metabolism
        pyridoxine biosynthesis 1.2 |
        Chr3:5444121-5445065 REVERSE LENGTH=314 |
        201606
```

Coefficients for Vitvi09g00375.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.337637	2.515381e-11	***	3.376139e-11	***
SlopeC	-1.689545	0.03313431	*	0.4430116	
MeanF-MeanC	-0.5792549	0.139207		0.4466932	
SlopeF-SlopeC	0.4365358	0.6965334		0.9999488	



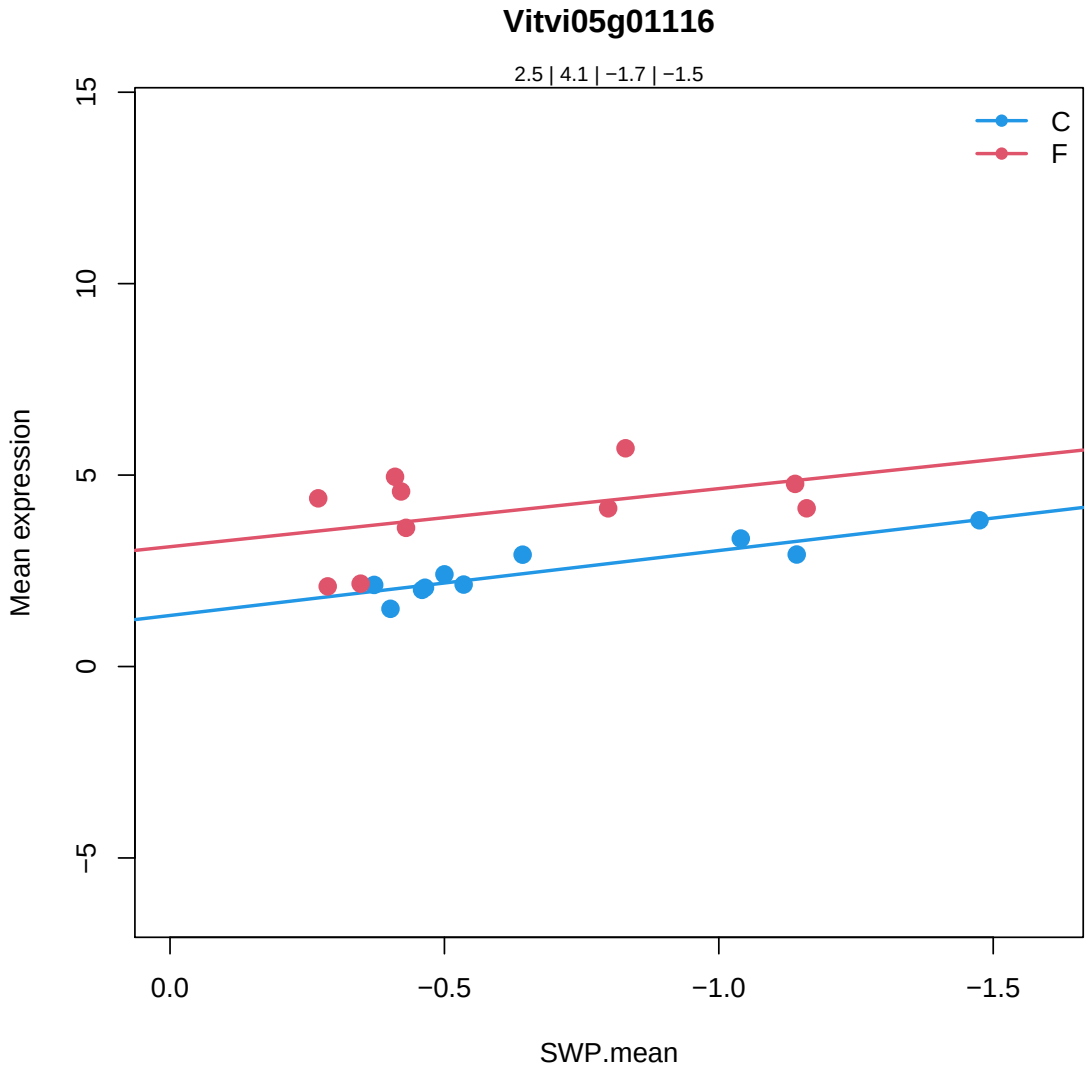
7.2.139 Vitvi05g01116: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01116
        11.1.11
        lipid metabolism.FA synthesis and FA elongation.fatty acid elongase
        HXXXD-type acyl-transferase family protein |
        Chr4:12660929-12662537 FORWARD LENGTH=421 |
        201606
```

Coefficients for Vitvi05g01116.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.52539	3.801912e-10	***	4.865962e-10	***
SlopeC	-1.695659	0.01616485	*	0.3486596	
MeanF-MeanC	1.527811	0.0001382594	***	0.002365151	**
SlopeF-SlopeC	0.1786811	0.8550996		0.9999488	



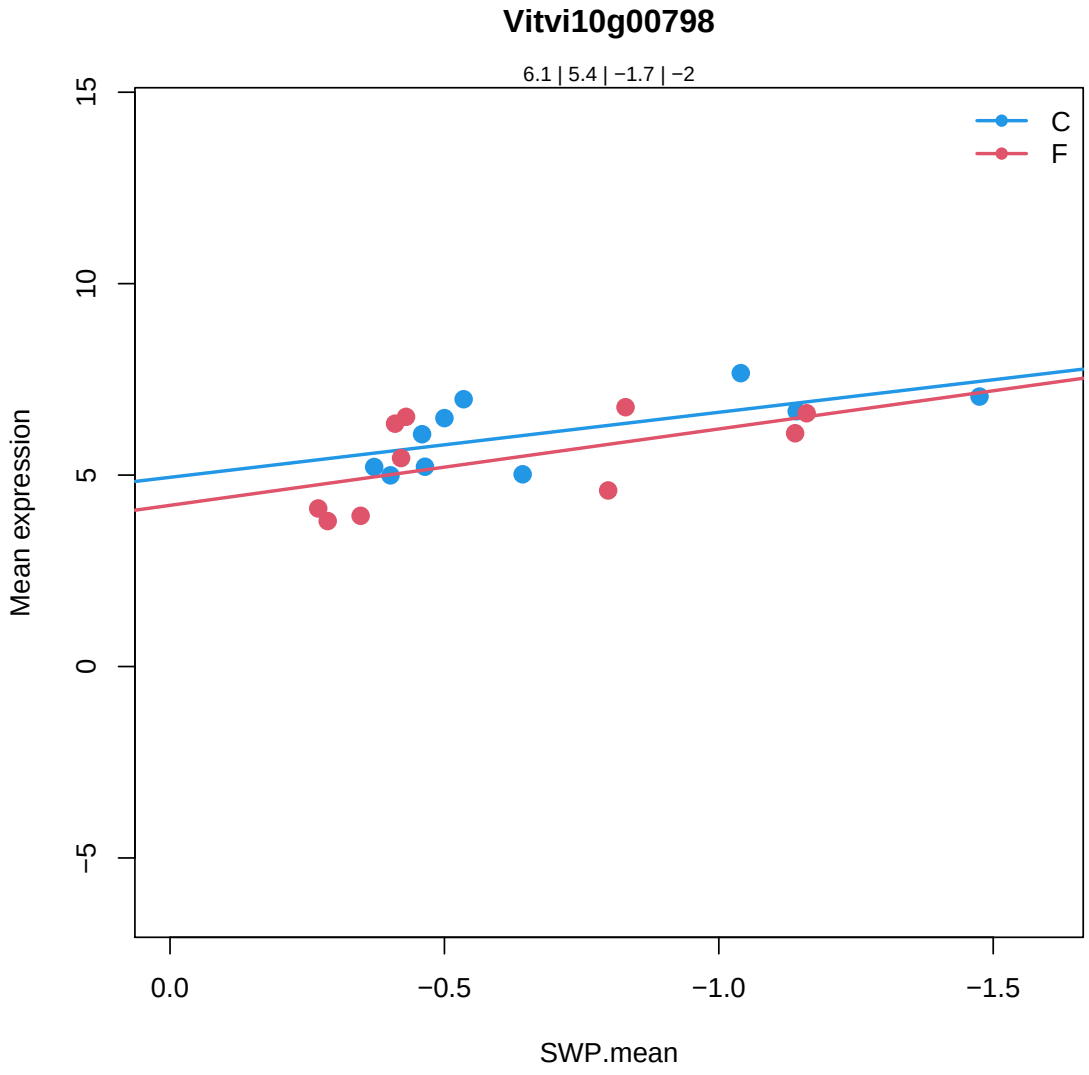
7.2.140 Vitvi10g00798: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00798
        29.5.11.4.3.3
        protein.degradation.ubiquitin.E3.SCF.cullin
        SGS domain-containing protein |
        Chr1:10546794-10548072 REVERSE LENGTH=229 |
        201606
```

Coefficients for Vitvi10g00798.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.135884	1.006157e-16	***	2.18615e-16	***
SlopeC	-1.69829	0.03024769	*	0.4320841	
MeanF-MeanC	-0.7109646	0.06946186	.	0.2947488	
SlopeF-SlopeC	-0.296639	0.7879845		0.9999488	



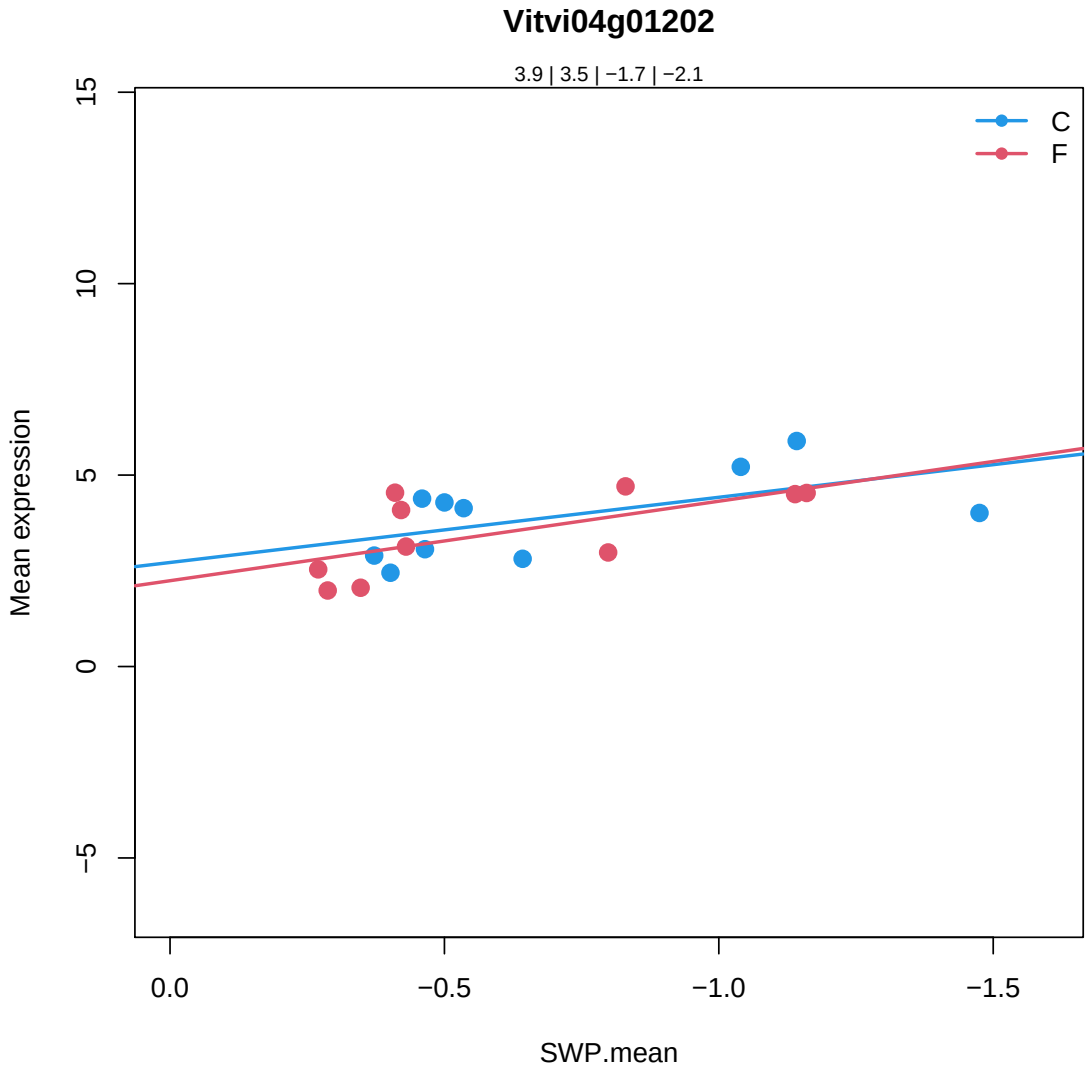
7.2.141 Vitvi04g01202: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01202
        27.1.20
        RNA.processing.degradation dicer
        dicer-like 2 |
        Chr3:768020-774525 REVERSE LENGTH=1374 |
        201606
```

Coefficients for Vitvi04g01202.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.914467	8.449722e-13	***	1.218339e-12	***
SlopeC	-1.702794	0.02948553	*	0.4299803	
MeanF-MeanC	-0.4084844	0.2831982		0.6485007	
SlopeF-SlopeC	-0.3731589	0.7346169		0.9999488	



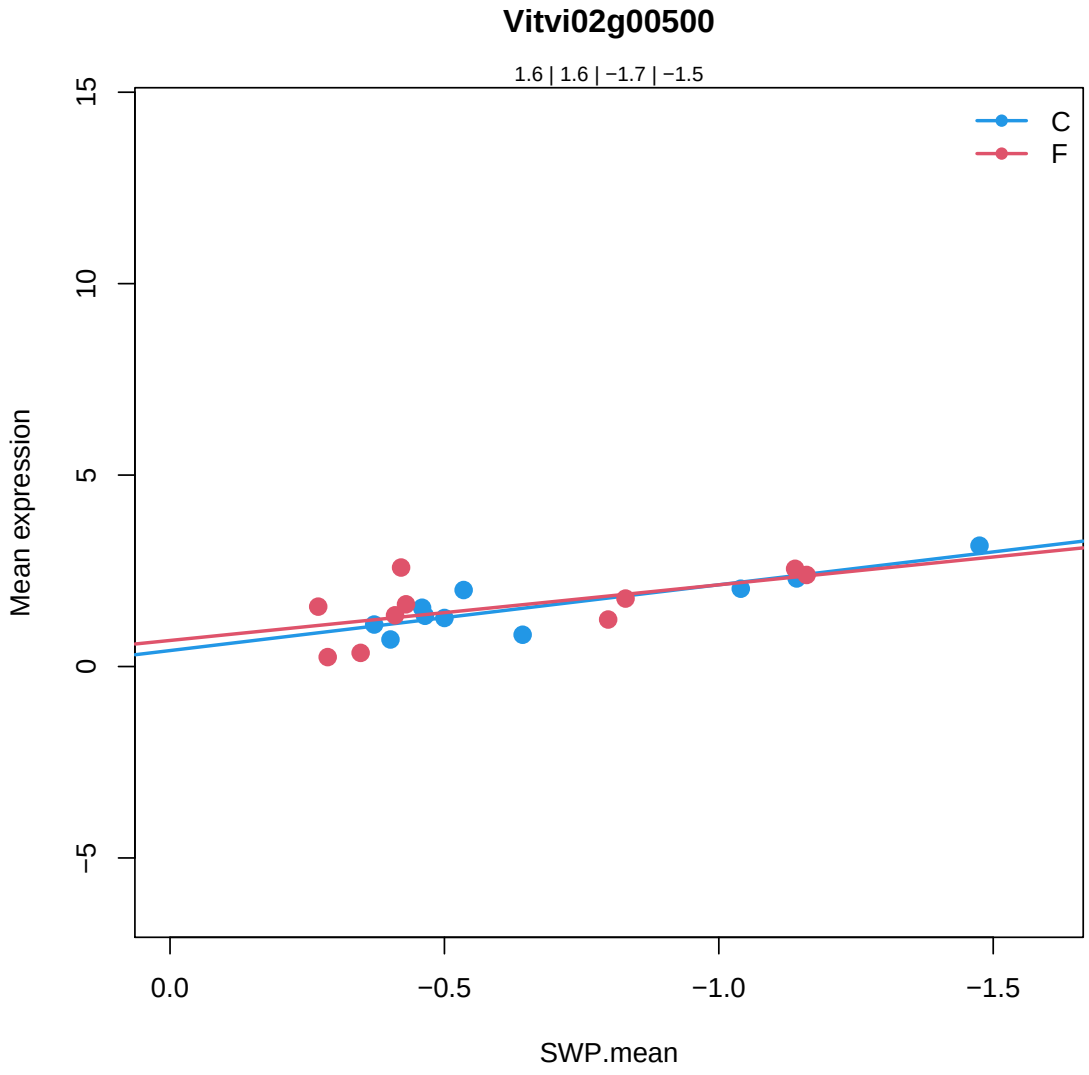
7.2.142 Vitvi02g00500: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00500
        35.2
        not assigned.unknown
        Plant invertase/pectin methylesterase inhibitor superfamily protein |
        Chr5:25040699-25041310 FORWARD LENGTH=203 |
        201606
```

Coefficients for Vitvi02g00500.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.62457	4.970831e-09	***	6.127409e-09	***
SlopeC	-1.71789	0.001806131	**	0.160246	
MeanF-MeanC	-0.05871081	0.8131117		0.9482333	
SlopeF-SlopeC	0.2645399	0.7162486		0.9999488	



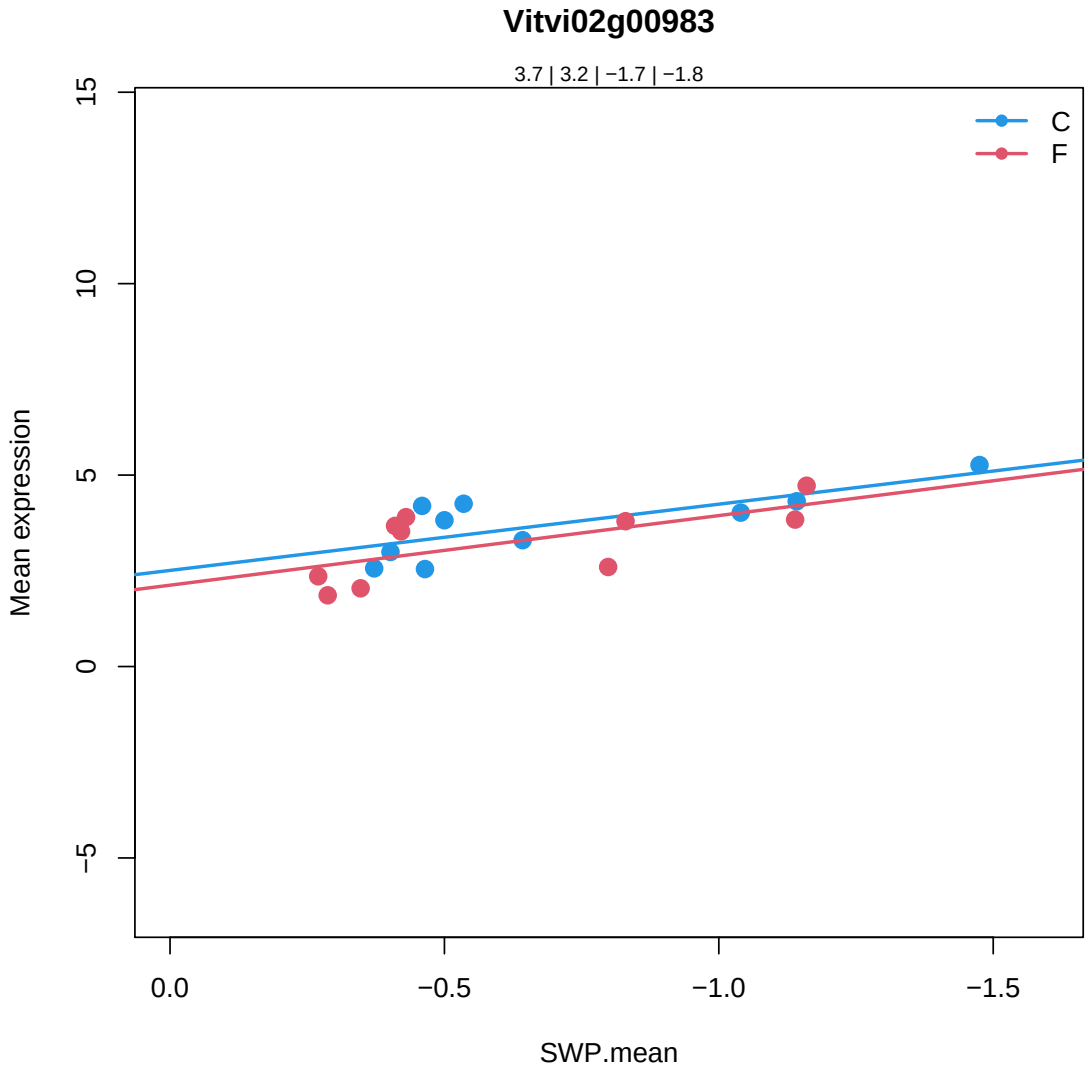
7.2.143 Vitvi02g00983: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00983
        35.2
        not assigned.unknown
        UDP-Glycosyltransferase superfamily protein |
        Chr2:15417618-15419108 REVERSE LENGTH=496 |
        201606
```

Coefficients for Vitvi02g00983.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.726364	1.280806e-14	***	2.117818e-14	***
SlopeC	-1.730352	0.005692474	**	0.2614474	
MeanF-MeanC	-0.4946906	0.0984271	.	0.3613261	
SlopeF-SlopeC	-0.08771546	0.9176478		0.9999488	



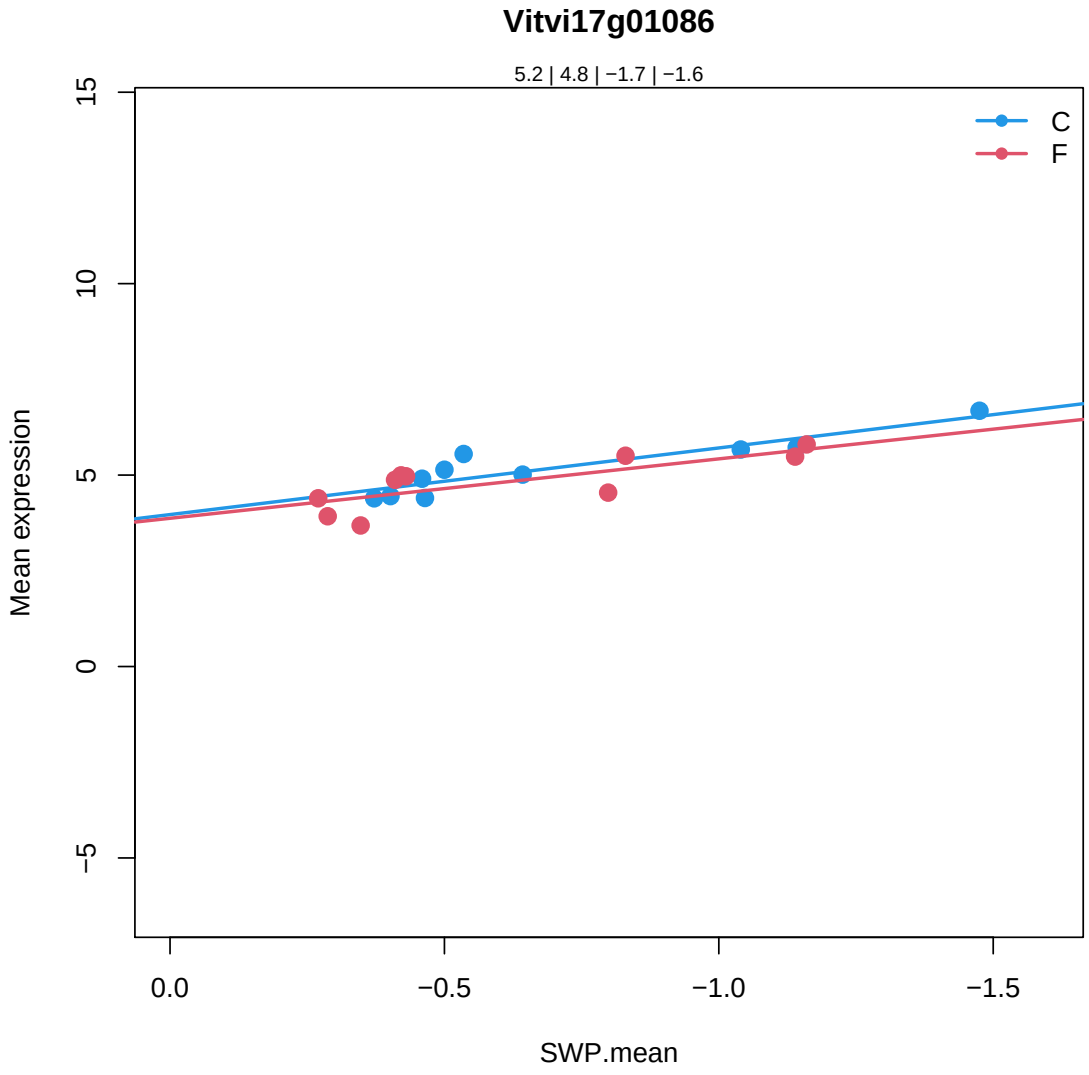
7.2.144 Vitvi17g01086: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g01086
        13.1.1.1.1
        amino acid metabolism.synthesis.central amino acid metabolism.GABA.glu
        glutamate decarboxylase |
        Chr5:5711141-5714839 FORWARD LENGTH=502 |
        201606
```

Coefficients for Vitvi17g01086.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.192026	2.69292e-21	***	2.468827e-20	***
SlopeC	-1.740421	0.0001322915	***	0.07644173	.
MeanF-MeanC	-0.3751626	0.06188059	.	0.2742611	
SlopeF-SlopeC	0.1882582	0.7389244		0.9999488	



7.2.145 Vitvi16g00982: * type1

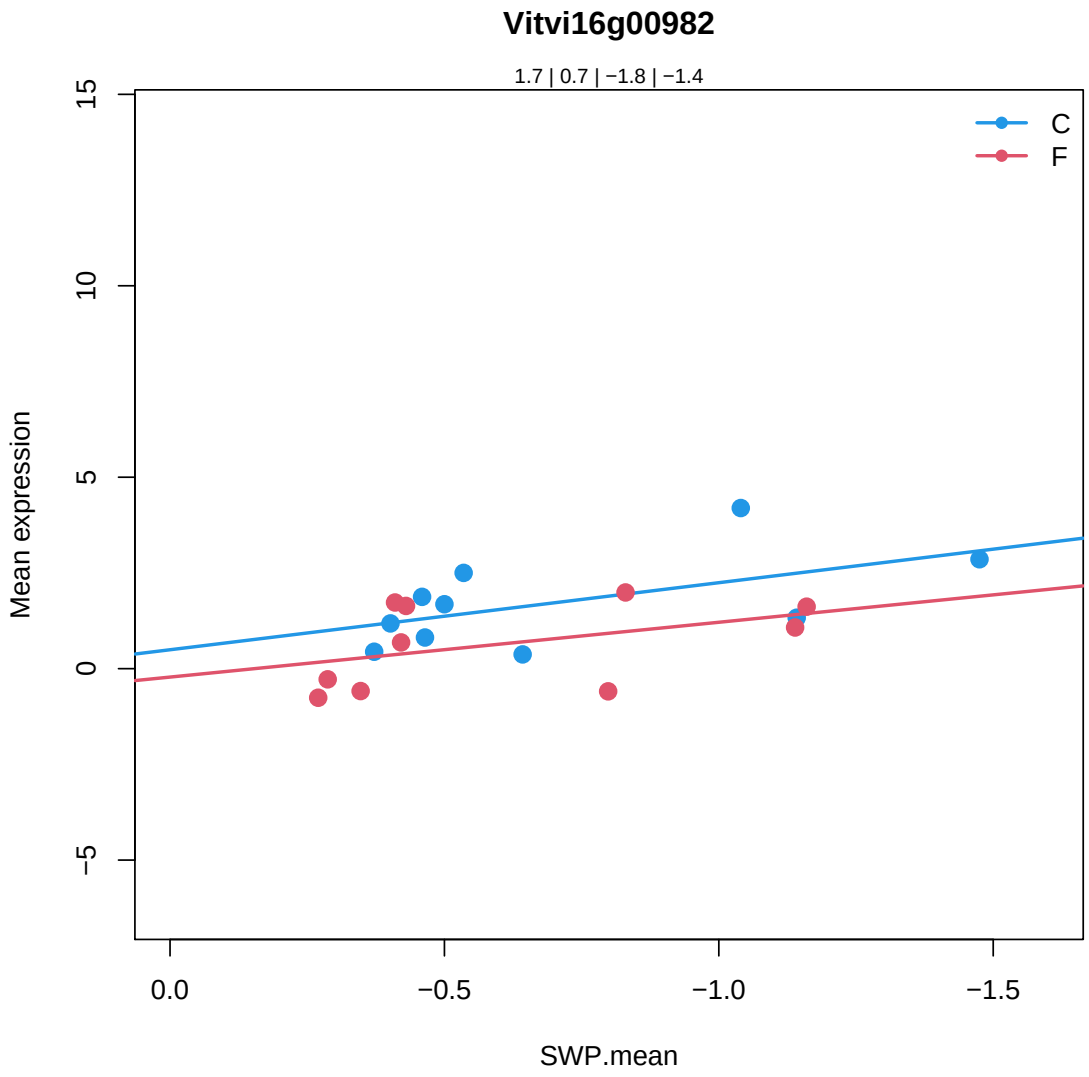
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g00982
        20.2.1
        stress.abiotic.heat
        heat shock factor 4 |
        Chr4:17440660-17441706 FORWARD LENGTH=284 |
        201606

Vitvi16g00982
        27.3.23
        RNA.regulation of transcription.heat-shock transcription factor family
        heat shock factor 4 |
        Chr4:17440660-17441706 FORWARD LENGTH=284 |
        201606
```

Coefficients for Vitvi16g00982.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.724872	8.428279e-06	***	9.534202e-06	***
SlopeC	-1.751151	0.04586852	*	0.4926906	
MeanF-MeanC	-1.073212	0.01824505	*	0.1178352	
SlopeF-SlopeC	0.319471	0.7974924		0.9999488	


Vitvi16g00982
1.7 | 0.7 | −1.8 | −1.4
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

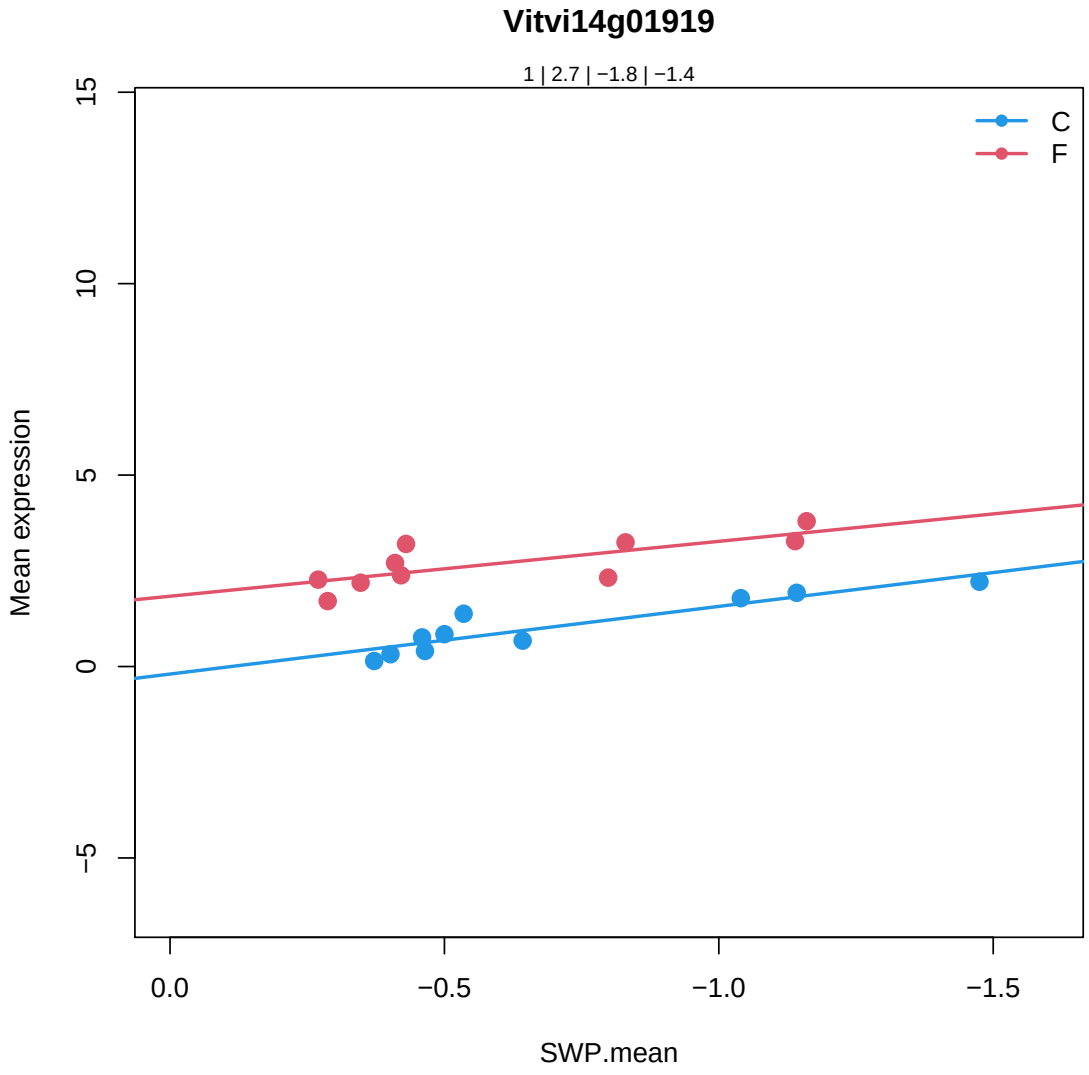
7.2.146 Vitvi14g01919: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01919
        35.2
        not assigned.unknown
        3-dehydroquinate synthase |
        Chr3:10793126-10795304 REVERSE LENGTH=422 |
        201606
```

Coefficients for Vitvi14g01919.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.045312	6.751507e-08	***	8.041452e-08	***
SlopeC	-1.767111	7.61116e-05	***	0.07644173	.
MeanF-MeanC	1.663539	9.349791e-09	***	4.687813e-07	***
SlopeF-SlopeC	0.333937	0.5423894		0.9999488	



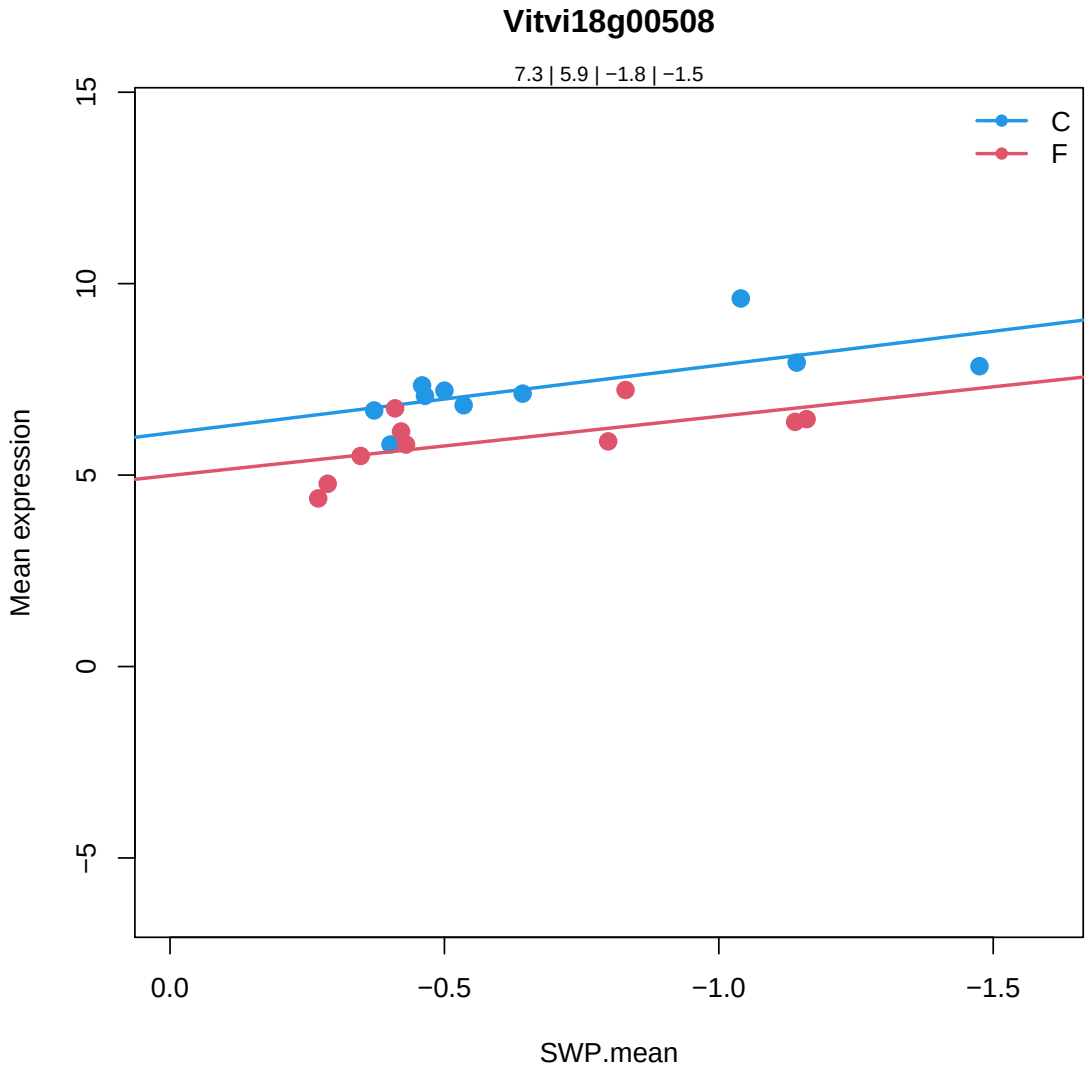
7.2.147 Vitvi18g00508: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00508
        9.8
        mitochondrial electron transport / ATP synthesis.uncoupling protein
        uncoupling protein 5 |
        Chr2:9563531-9564472 REVERSE LENGTH=313 |
        201606
```

Coefficients for Vitvi18g00508.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.344885	6.22014e-20	***	3.185732e-19	***
SlopeC	-1.770808	0.008851147	**	0.2903326	
MeanF-MeanC	-1.415514	0.0001756439	***	0.002897364	**
SlopeF-SlopeC	0.2259134	0.8074009		0.9999488	



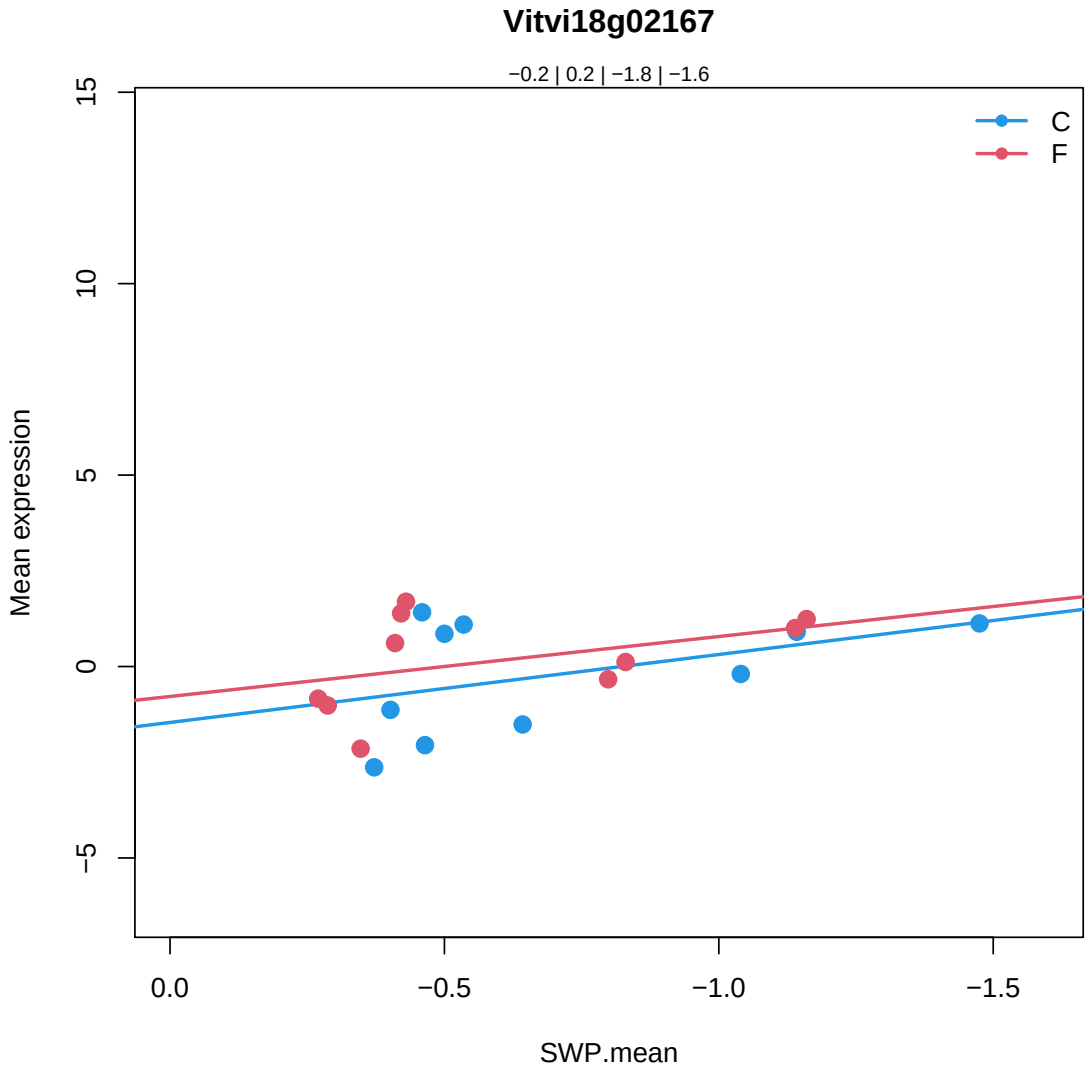
7.2.148 Vitvi18g02167: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02167
        17.1.1.1.12
        hormone metabolism.abscisic acid.synthesis-degradation.synthesis.absci
        aldehyde oxidase 1 |
        Chr5:7116783-7122338 FORWARD LENGTH=1368 |
        201606
```

Coefficients for Vitvi18g02167.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.2128345	0.5677555		0.5735505	
SlopeC	-1.774895	0.09629287	.	0.6067366	
MeanF-MeanC	0.3844787	0.4665734		0.7876703	
SlopeF-SlopeC	0.2086531	0.8920053		0.9999488	



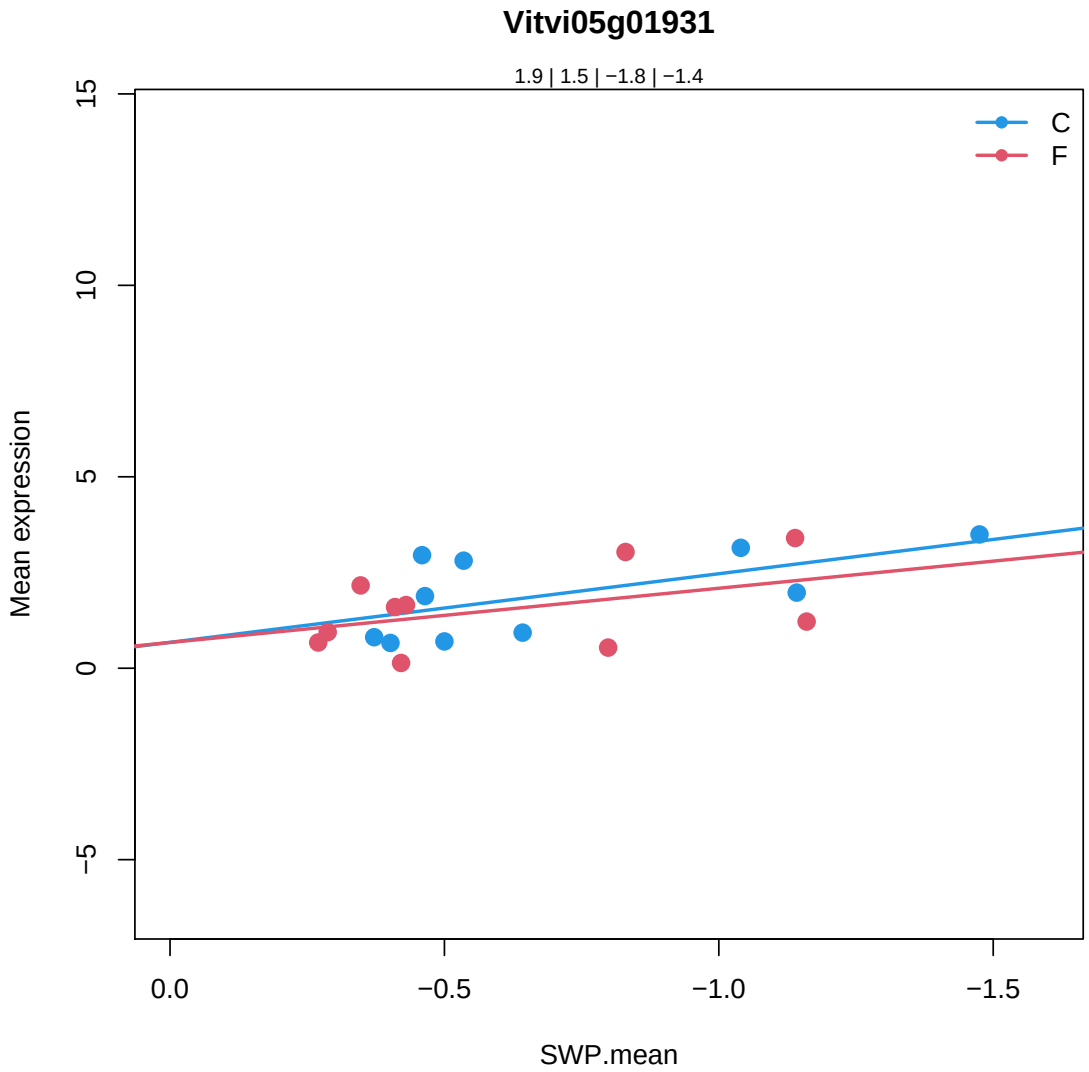
7.2.149 Vitvi05g01931: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01931
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi05g01931.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.935812	5.915734e-07	***	6.872532e-07	***
SlopeC	-1.79156	0.02990746	*	0.4304569	
MeanF-MeanC	-0.4005626	0.3177162		0.6790186	
SlopeF-SlopeC	0.3751086	0.7467065		0.9999488	



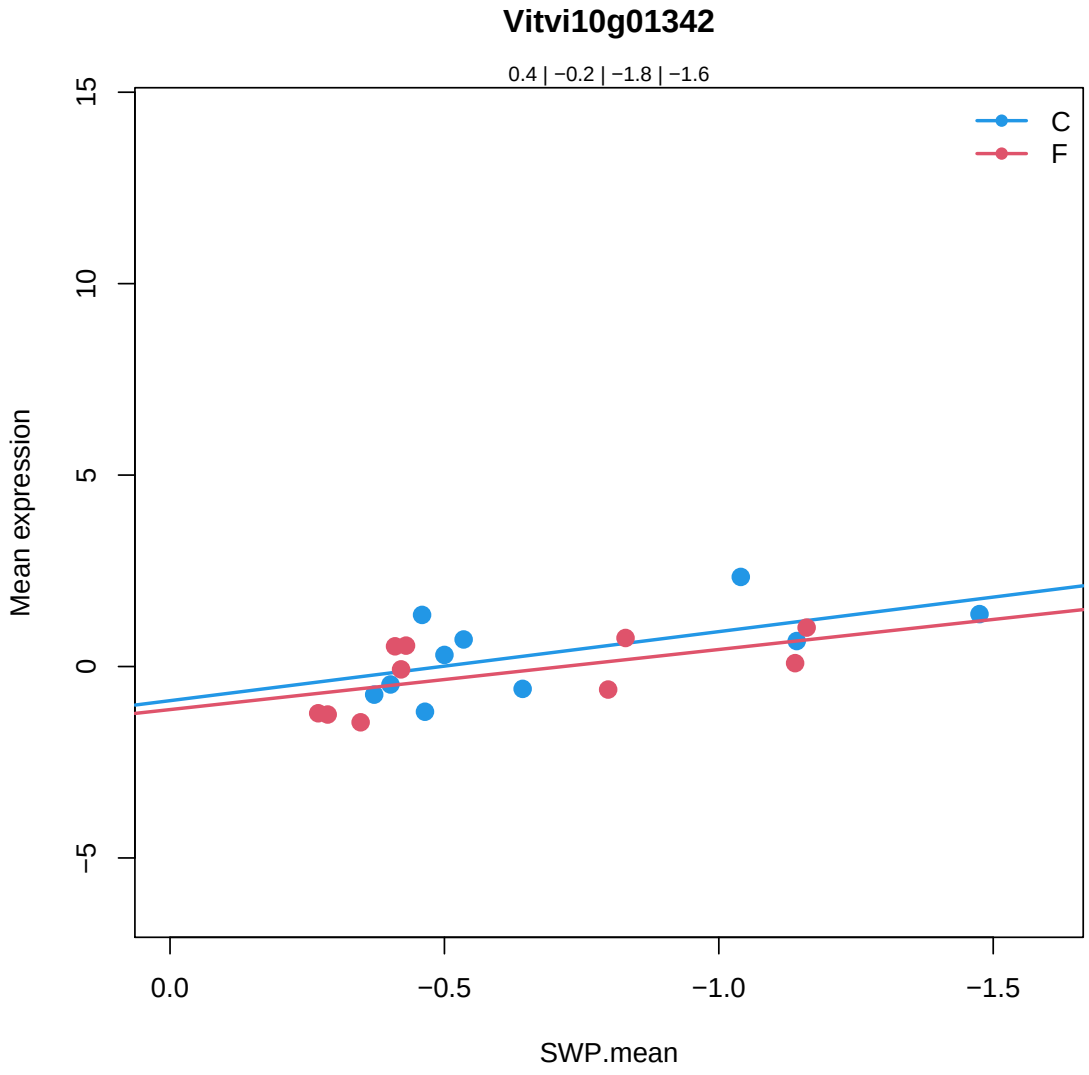
7.2.150 Vitvi10g01342: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g01342
        27.3.36
        RNA.regulation of transcription.argonaute transcription factor family
        Argonaute family protein |
        Chr1:11181777-11185112 FORWARD LENGTH=1014 |
        201606
```

Coefficients for Vitvi10g01342.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3761012	0.144305		0.1485645	
SlopeC	−1.802985	0.0161523	*	0.3486596	
MeanF−MeanC	−0.5447118	0.1353421		0.4400114	
SlopeF−SlopeC	0.2340175	0.8220433		0.9999488	



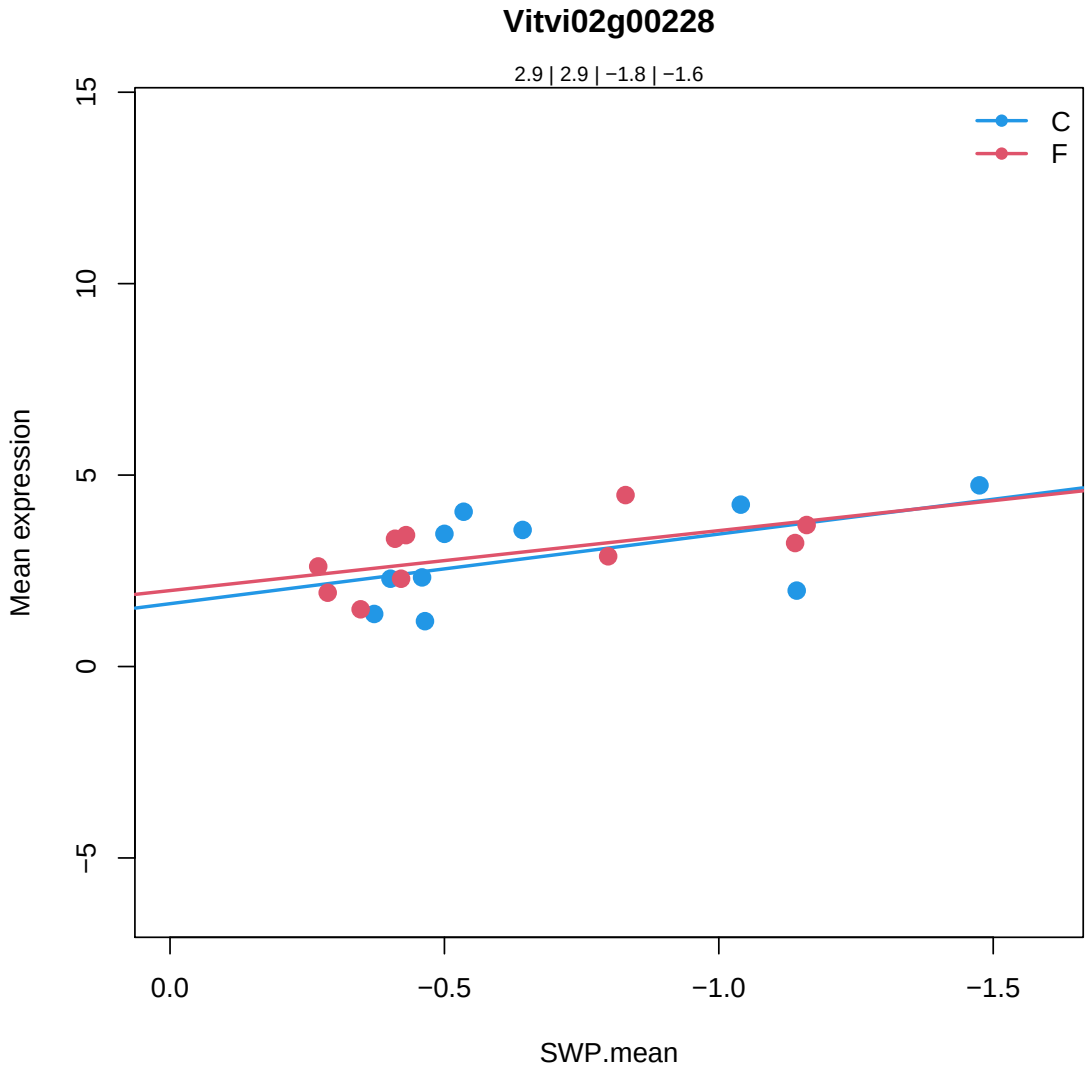
7.2.151 Vitvi02g00228: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00228
        27.3.35
        RNA.regulation of transcription.bZIP transcription factor family
        homeobox 7 |
        Chr2:19165777-19166773 REVERSE LENGTH=258 |
        201606
```

Coefficients for Vitvi02g00228.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.91942	3.526112e-10	***	4.517906e-10	***
SlopeC	-1.818326	0.02386796	*	0.3984616	
MeanF-MeanC	0.01795977	0.9627522		0.9915437	
SlopeF-SlopeC	0.2522321	0.8228588		0.9999488	



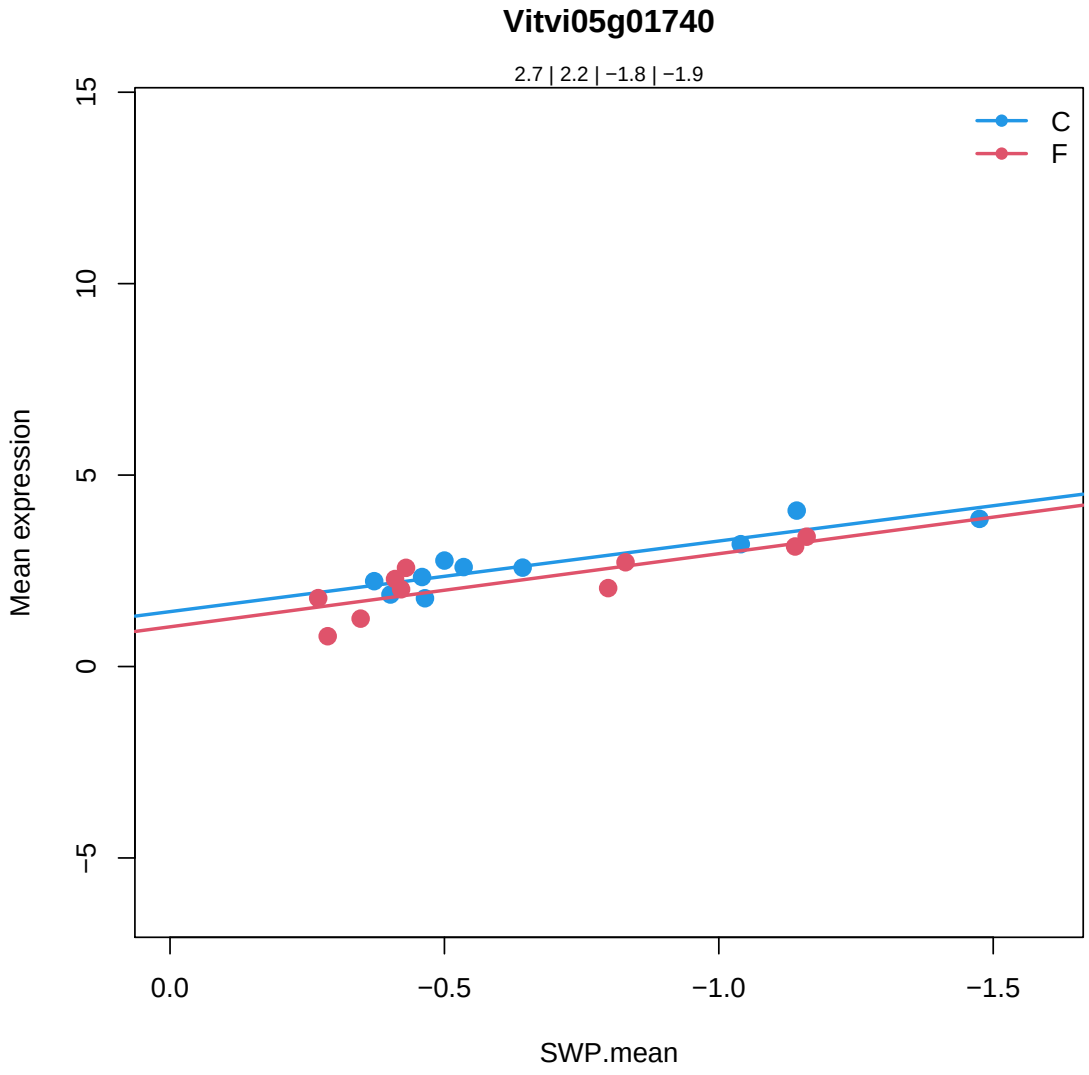
7.2.152 Vitvi05g01740: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01740
        16.8.2
        secondary metabolism.flavonoids.chalcones
        NAD(P)-linked oxidoreductase superfamily protein |
        Chr1:22071410-22073067 REVERSE LENGTH=326 |
        201606
```

Coefficients for Vitvi05g01740.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.730013	4.118221e-15	***	7.20665e-15	***
SlopeC	-1.844095	0.0001091579	***	0.07644173	.
MeanF-MeanC	-0.5296411	0.01417235	*	0.09792158	.
SlopeF-SlopeC	-0.06541604	0.9113725		0.9999488	



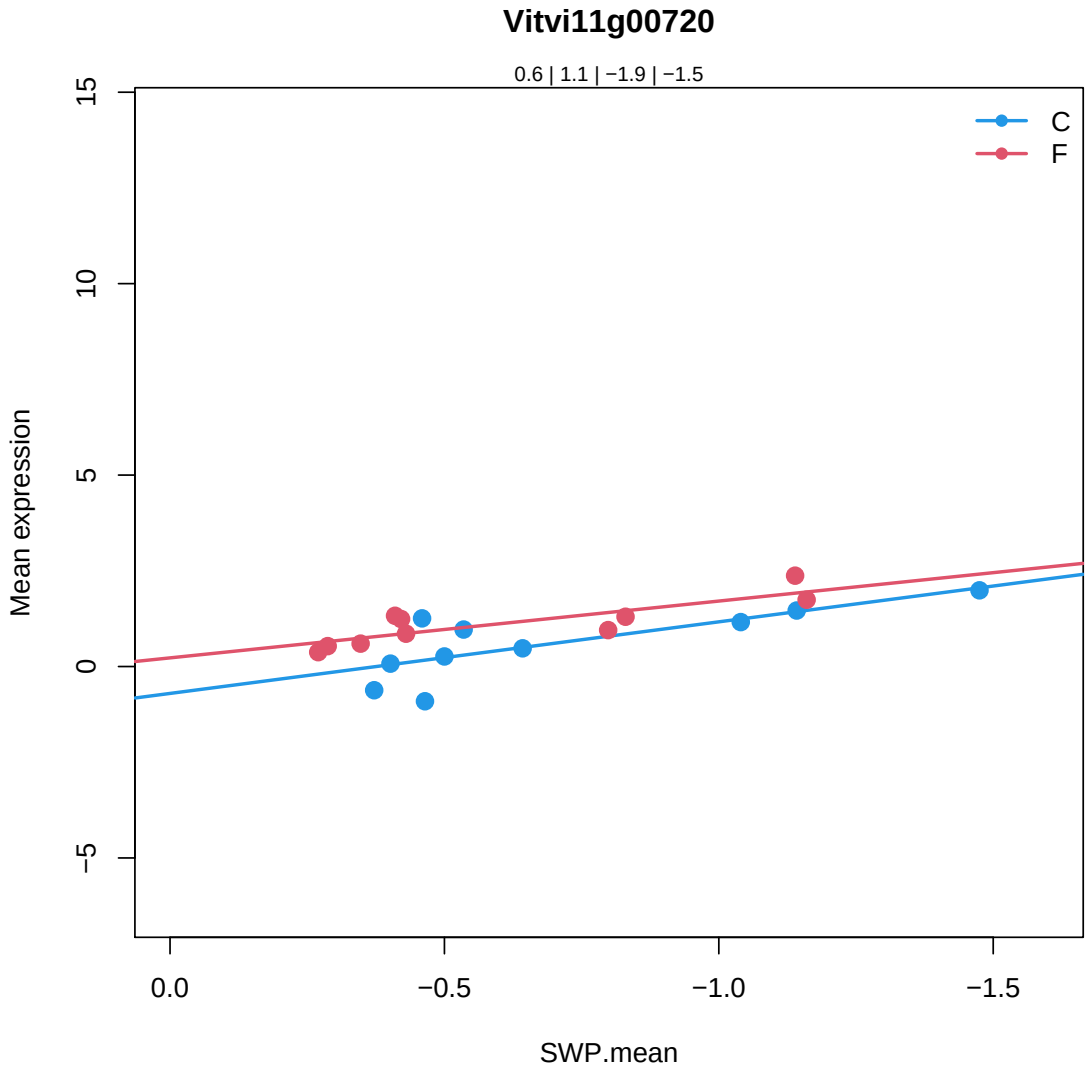
7.2.153 Vitvi11g00720: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00720
        16.2.1.4
        secondary metabolism.phenylpropanoids.lignin biosynthesis.HCT
        hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase |
        Chr5:19836654-19838092 REVERSE LENGTH=433 |
        201606
```

Coefficients for Vitvi11g00720.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6120572	0.0009528719	***	0.001032317	**
SlopeC	−1.869816	0.0003856001	***	0.09467692	.
MeanF−MeanC	0.5173539	0.03242582	*	0.1784782	
SlopeF−SlopeC	0.3861115	0.5659556		0.9999488	



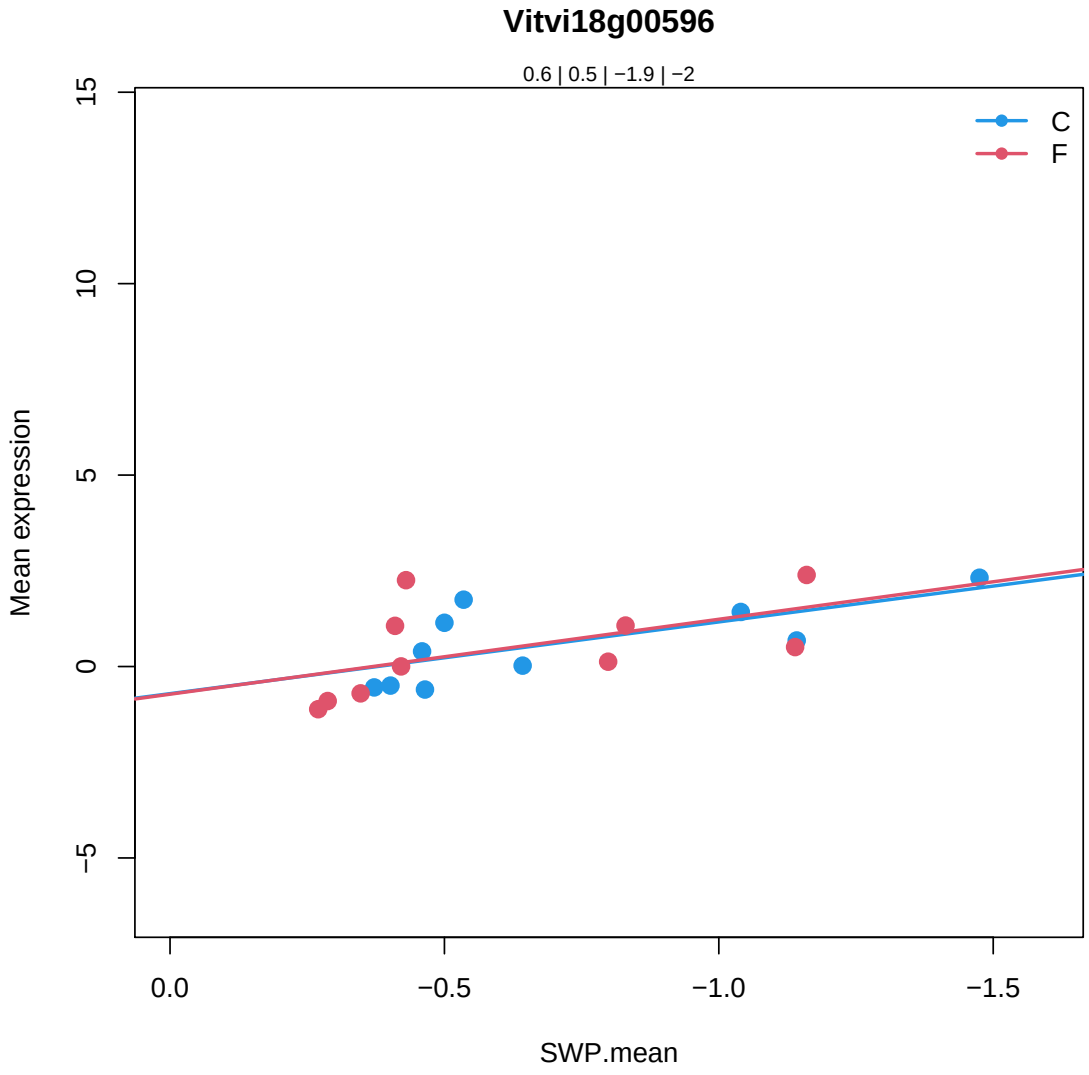
7.2.154 Vitvi18g00596: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00596
        35.2
        not assigned.unknown
        tubulin alpha-6 chain |
        Chr1:18520144-18521600 REVERSE LENGTH=209 |
        201606
```

Coefficients for Vitvi18g00596.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6083869	0.03667248	*	0.03830343	*
SlopeC	−1.872526	0.02219784	*	0.3929231	
MeanF−MeanC	−0.1388005	0.7227382		0.9149482	
SlopeF−SlopeC	−0.08545914	0.9404426		0.9999488	



7.2.155 Vitvi08g02189: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

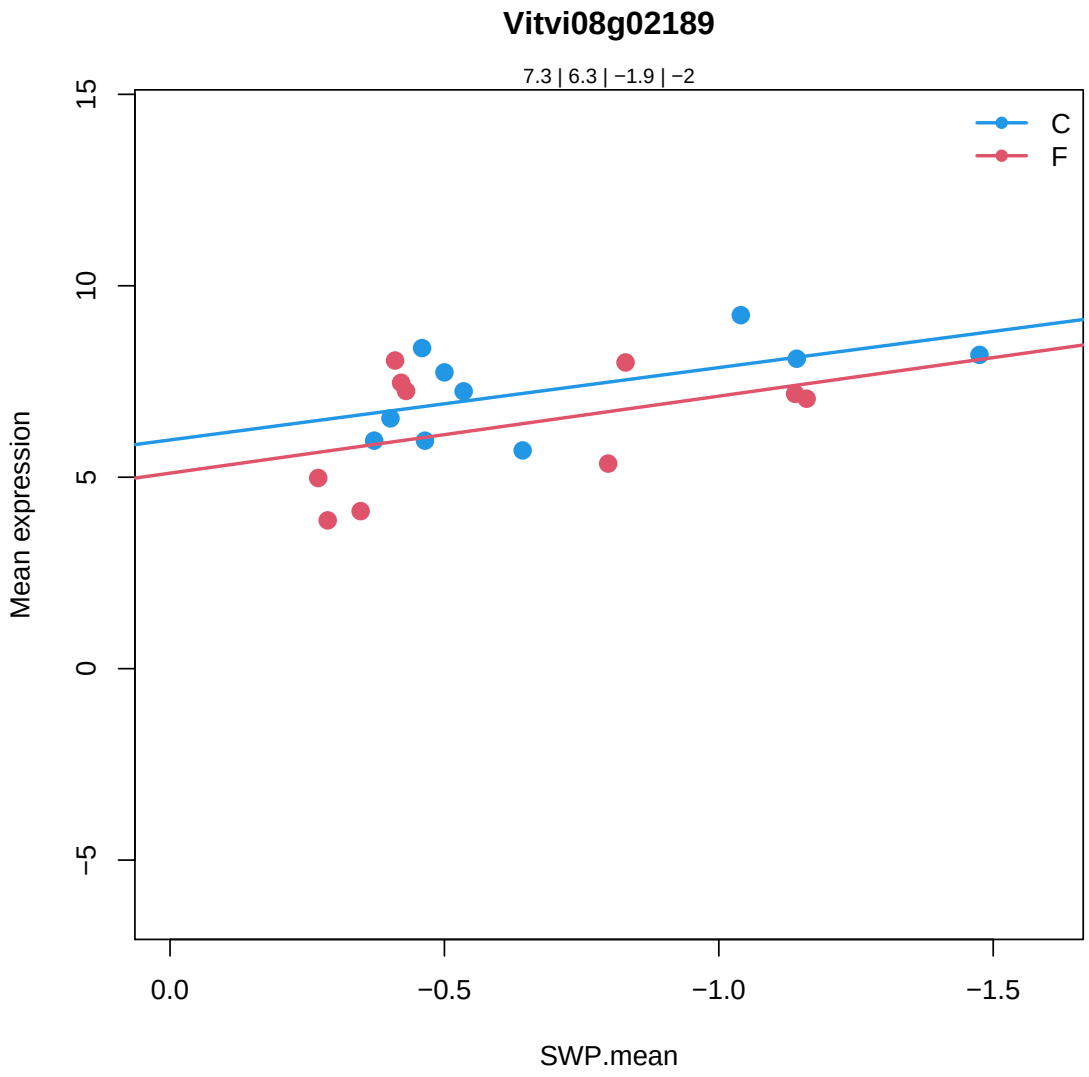
```
Vitvi08g02189
        35.2
        not assigned.unknown
        heat shock cognate protein 70-1 |
        Chr5:554055-556334 REVERSE LENGTH=651 |
        201606

Vitvi08g02189
        29.6
        protein.folding
        heat shock cognate protein 70-1 |
        Chr5:554055-556334 REVERSE LENGTH=651 |
        201606

Vitvi08g02189
        20.2.1
        stress.abiotic.heat
        heat shock cognate protein 70-1 |
        Chr5:554055-556334 REVERSE LENGTH=651 |
        201606
```

Coefficients for Vitvi08g02189.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.302125	2.297086e-15	***	4.135623e-15	***
SlopeC	-1.890543	0.07608554	.	0.5694531	
MeanF-MeanC	-0.9706519	0.07339059	.	0.3042207	
SlopeF-SlopeC	-0.1210553	0.9368313		0.9999488	


Vitvi08g02189
7.3 | 6.3 | −1.9 | −2
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

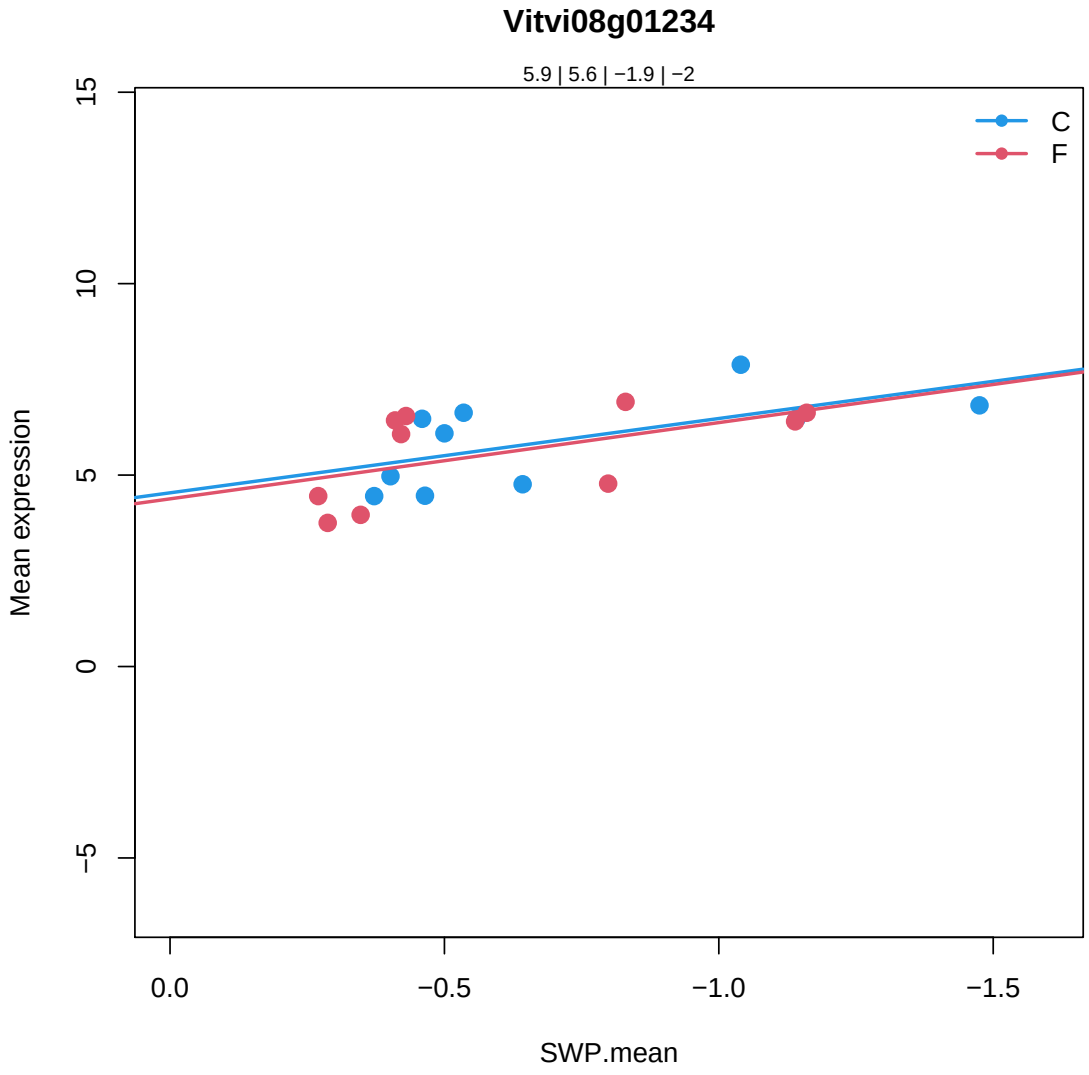
7.2.156 Vitvi08g01234: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01234
        35.1.3
        not assigned.no ontology.armadillo/beta-catenin repeat family protein
        Fes1A |
        Chr3:2871710-2873109 FORWARD LENGTH=327 |
        201606
```

Coefficients for Vitvi08g01234.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.90145	1.529707e-15	***	2.79868e-15	***
SlopeC	-1.940814	0.02472301	*	0.4060648	
MeanF-MeanC	-0.3092112	0.4572898		0.7825787	
SlopeF-SlopeC	-0.05059603	0.9666479		0.9999488	



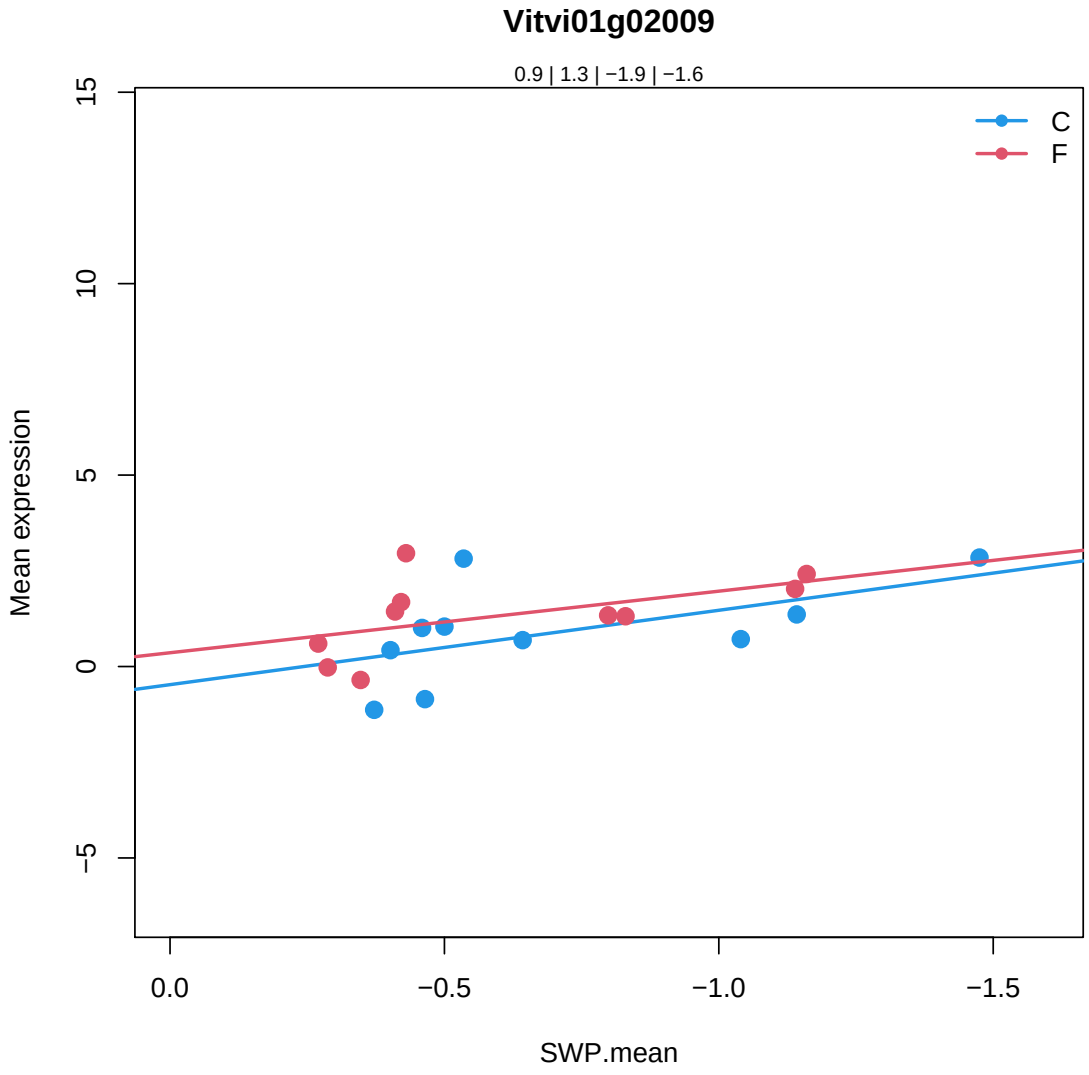
7.2.157 Vitvi01g02009: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g02009
        16.8.2
        secondary metabolism.flavonoids.chalcones
        NAD(P)-linked oxidoreductase superfamily protein |
        Chr1:22071410-22073067 REVERSE LENGTH=326 |
        201606
```

Coefficients for Vitvi01g02009.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8920748	0.006206541	**	0.006605229	**
SlopeC	-1.942709	0.02693091	*	0.4184311	
MeanF-MeanC	0.4474214	0.2938199		0.6604339	
SlopeF-SlopeC	0.3343367	0.7862208		0.9999488	



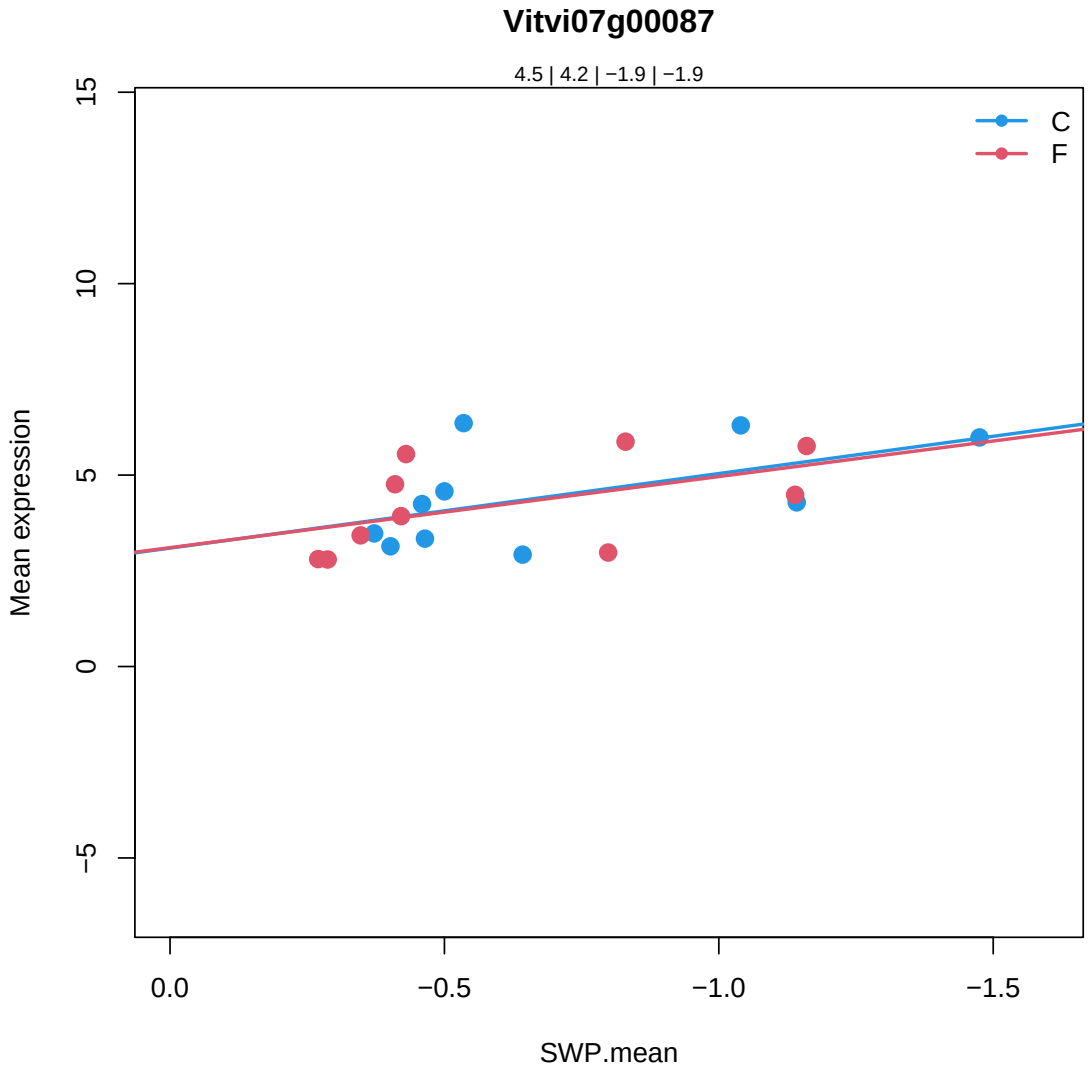
7.2.158 Vitvi07g00087: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g00087
        35.1
        not assigned.no ontology
        Bax inhibitor-1 family protein |
        Chr1:730148-731379 FORWARD LENGTH=247 |
        201606
```

Coefficients for Vitvi07g00087.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.461907	3.187147e-12	***	4.45021e-12	***
SlopeC	-1.946211	0.04011329	*	0.472859	
MeanF-MeanC	-0.2263095	0.6222682		0.8698761	
SlopeF-SlopeC	0.08953531	0.9467777		0.9999488	



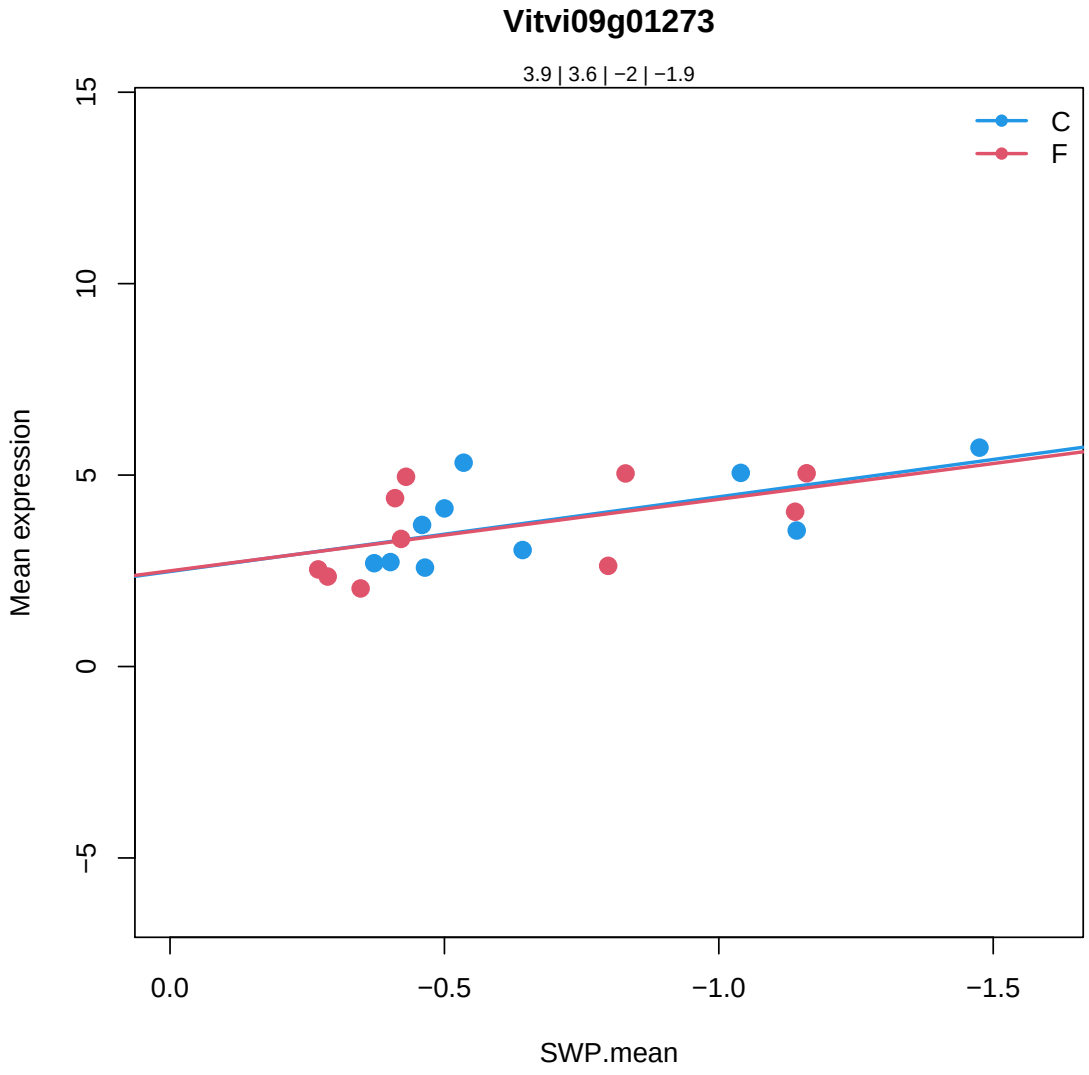
7.2.159 Vitvi09g01273: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g01273
        35.2
        not assigned.unknown
        ATP-dependent DNA helicase |
        Chr4:14990523-14992855 FORWARD LENGTH=589 |
        201606
```

Coefficients for Vitvi09g01273.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.852927	7.081238e-12	***	9.740297e-12	***
SlopeC	-1.951126	0.02373849	*	0.3983963	
MeanF-MeanC	-0.2157831	0.6018321		0.8611337	
SlopeF-SlopeC	0.08240906	0.9455691		0.9999488	



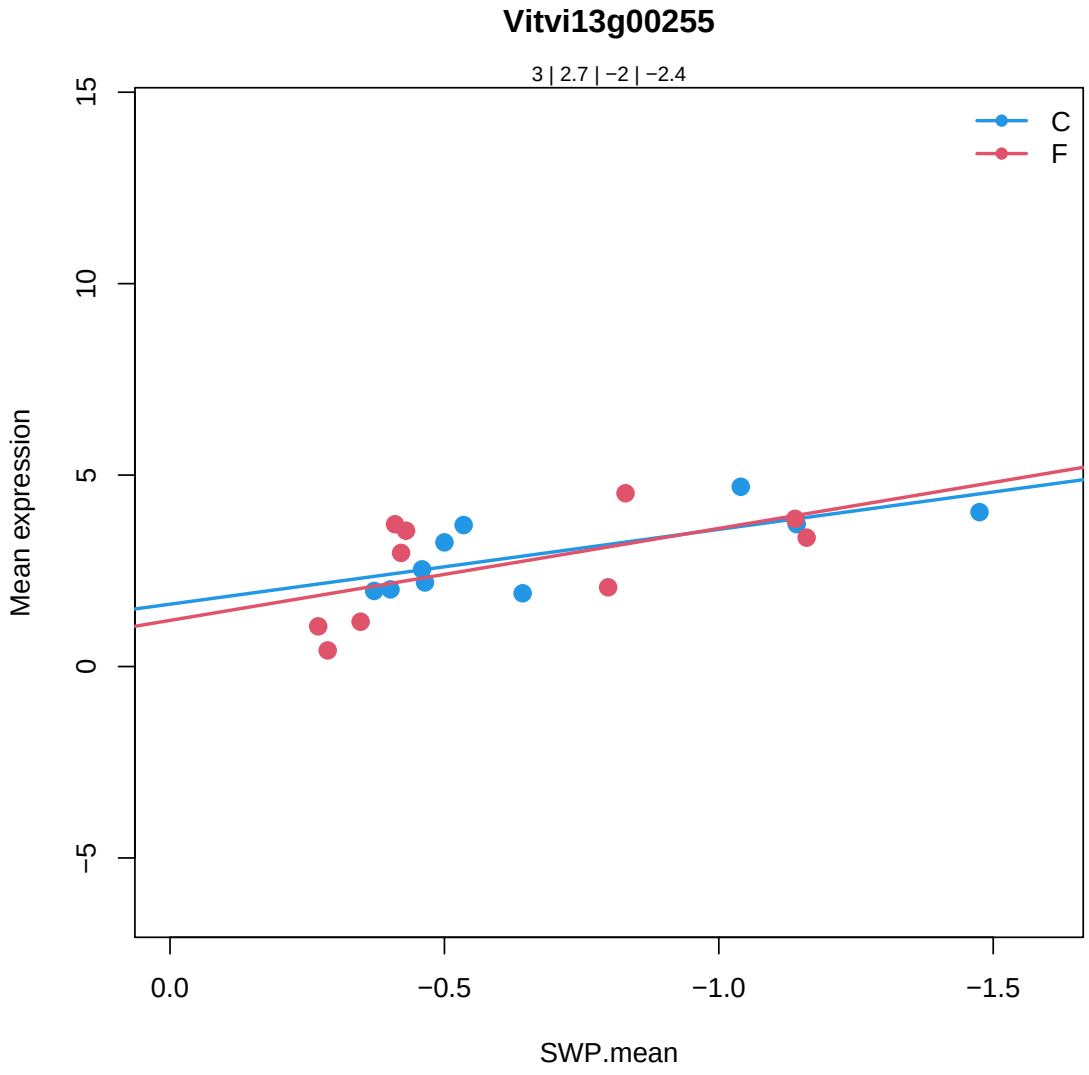
7.2.160 Vitvi13g00255: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00255
        34.19.2
        transport.major intrinsic proteins.TIP
        tonoplast intrinsic protein 1%3B3 |
        Chr4:625092-625850 REVERSE LENGTH=252 |
        201606
```

Coefficients for Vitvi13g00255.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.001449	4.678443e-10	***	5.969264e-10	***
SlopeC	-1.953979	0.02047822	*	0.3769674	
MeanF-MeanC	-0.3328085	0.4109846		0.7515148	
SlopeF-SlopeC	-0.4483182	0.7034636		0.9999488	



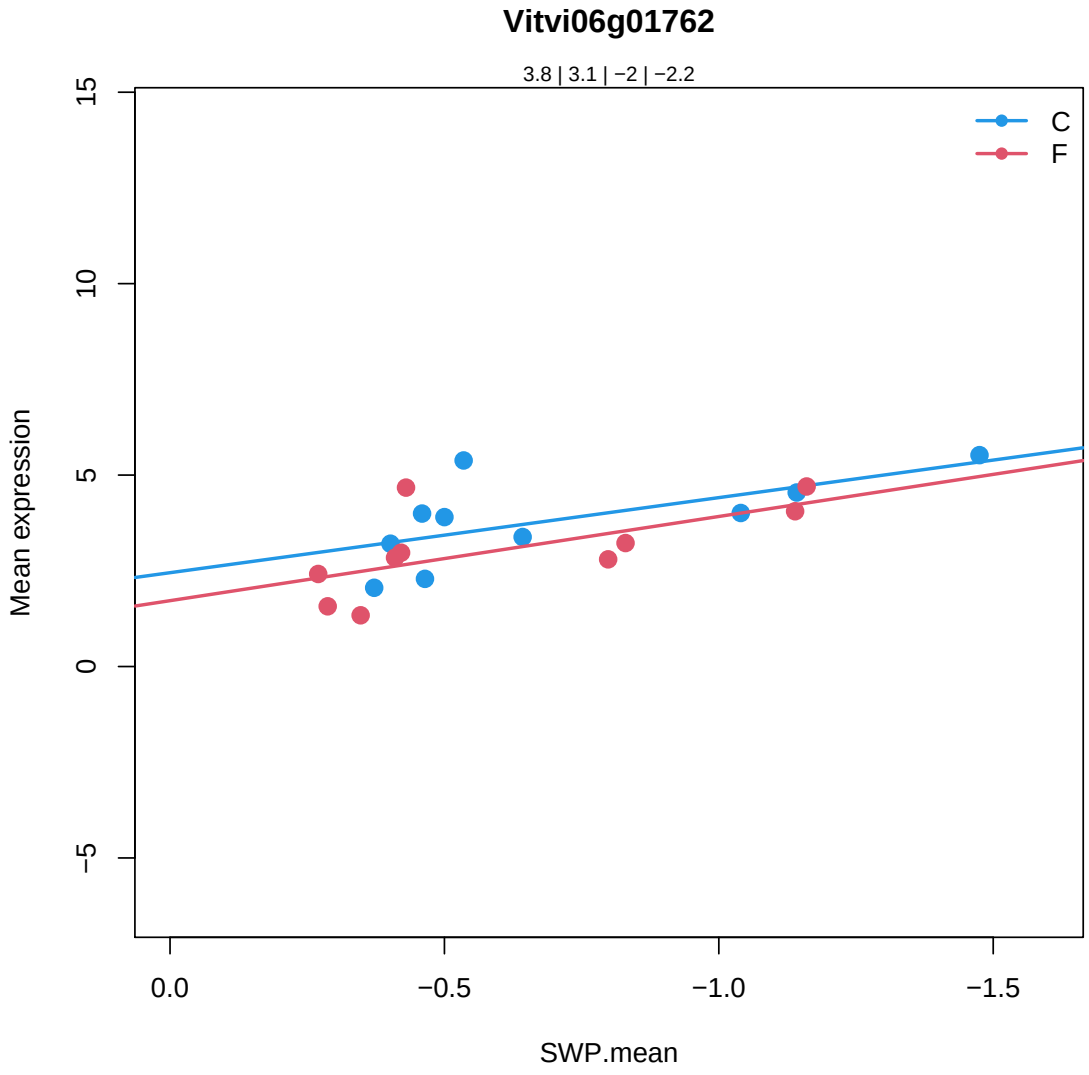
7.2.161 Vitvi06g01762: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01762
        26.2
        misc.UDP glucosyl and glucoronyl transferases
        UDP-Glycosyltransferase superfamily protein |
        Chr2:12872200-12873691 FORWARD LENGTH=454 |
        201606
```

Coefficients for Vitvi06g01762.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.829051	1.707816e-12	***	2.417397e-12	***
SlopeC	-1.96081	0.0148532	*	0.3368935	
MeanF-MeanC	-0.7695267	0.05330879	.	0.2493196	
SlopeF-SlopeC	-0.2379683	0.8310348		0.9999488	



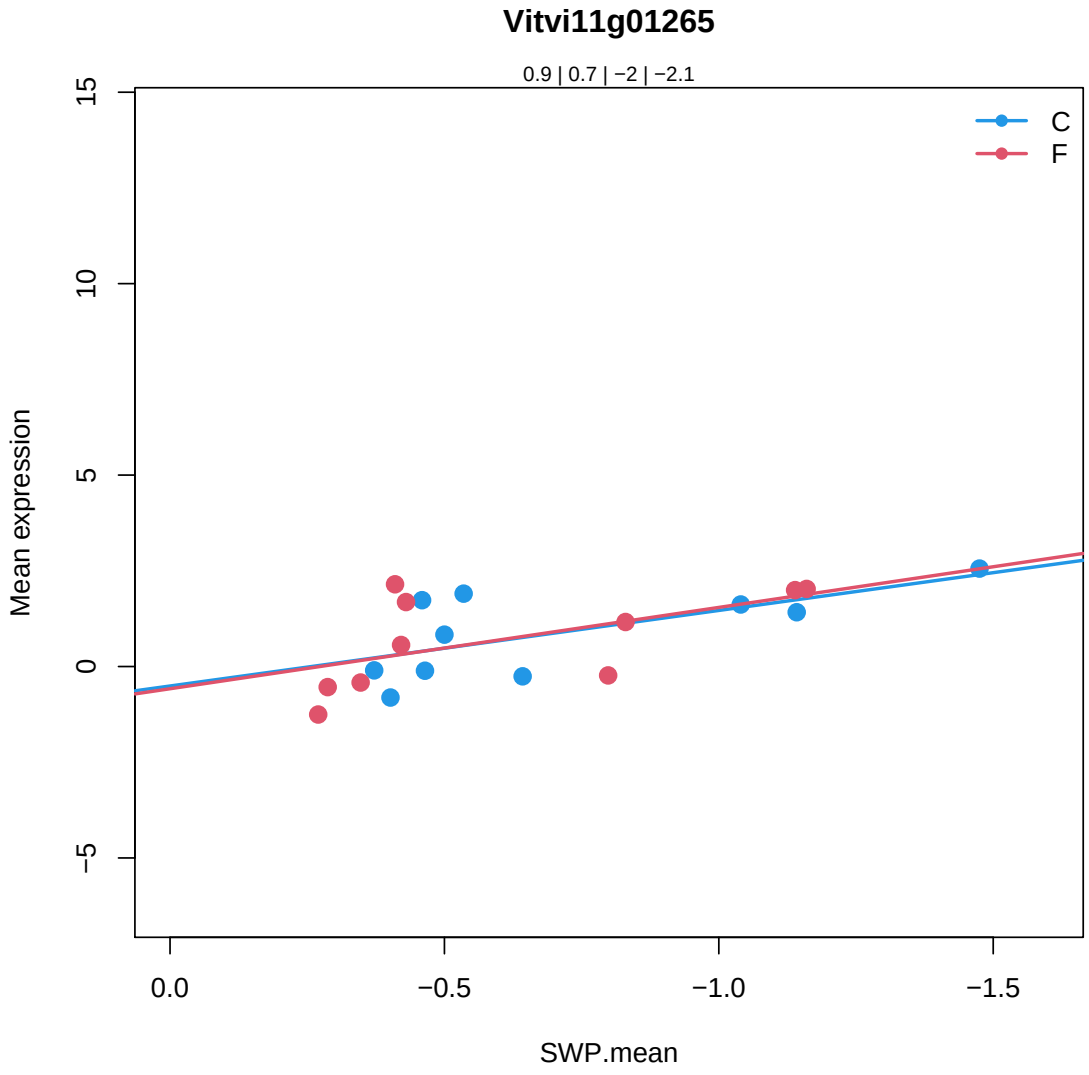
7.2.162 Vitvi11g01265: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g01265
        10.6.2
        cell wall.degradation.mannan-xylose-arabinose-fucose
        xyloglucan endotransglycosylase 6 |
        Chr4:13128694-13129715 FORWARD LENGTH=286 |
        201606
```

Coefficients for Vitvi11g01265.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8786255	0.00530675	**	0.005654745	**
SlopeC	−1.973338	0.02040242	*	0.3769378	
MeanF−MeanC	−0.1651298	0.6842467		0.89854	
SlopeF−SlopeC	−0.1505334	0.8990682		0.9999488	



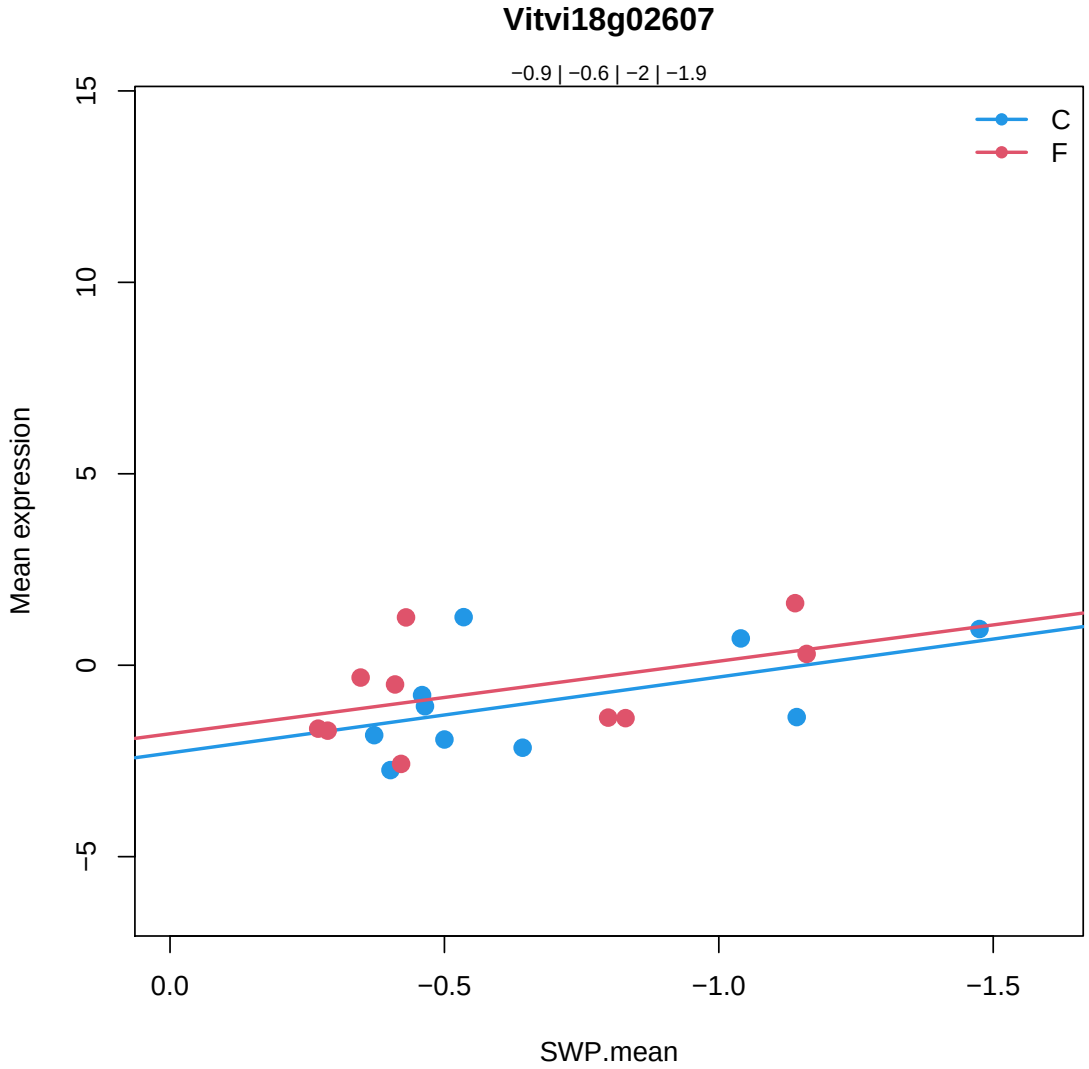
7.2.163 Vitvi18g02607: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02607
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi18g02607.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	−0.8967429	0.01911297	*	0.02010211	*
SlopeC	−1.98267	0.0567301	.	0.5329089	
MeanF−MeanC	0.2611649	0.6070969		0.8620618	
SlopeF−SlopeC	0.08735273	0.9530133		0.9999488	



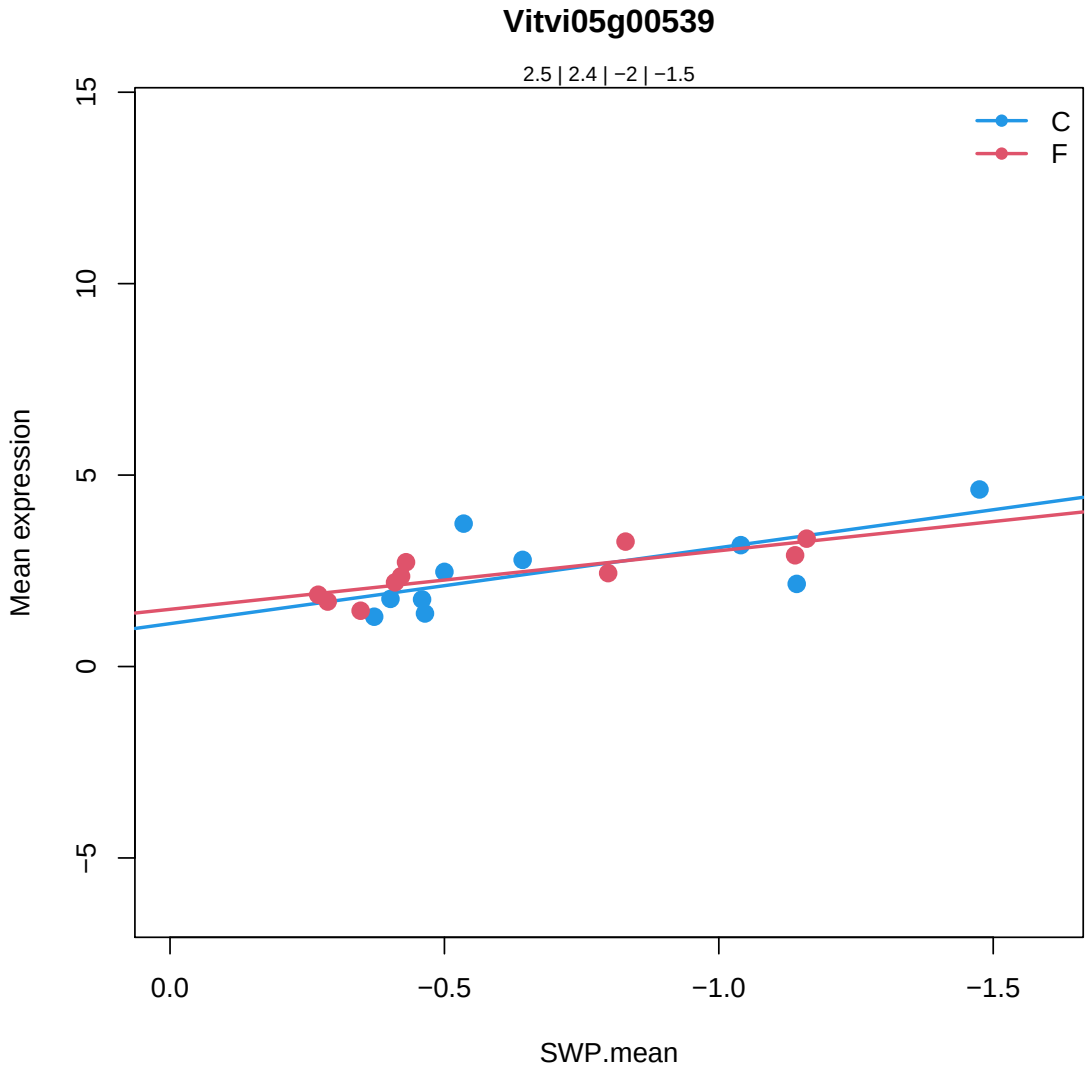
7.2.164 Vitvi05g00539: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00539
        13.1.3.4.12
        amino acid metabolism.synthesis.aspartate family.methionine.homocystei
        homocysteine methyltransferase 2 |
        Chr3:23370575-23371974 REVERSE LENGTH=293 |
        201606
```

Coefficients for Vitvi05g00539.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.514555	1.026531e-11	***	1.399873e-11	***
SlopeC	-1.983181	0.001236499	**	0.1365704	
MeanF-MeanC	-0.08927246	0.7451312		0.9250114	
SlopeF-SlopeC	0.4546535	0.57277		0.9999488	



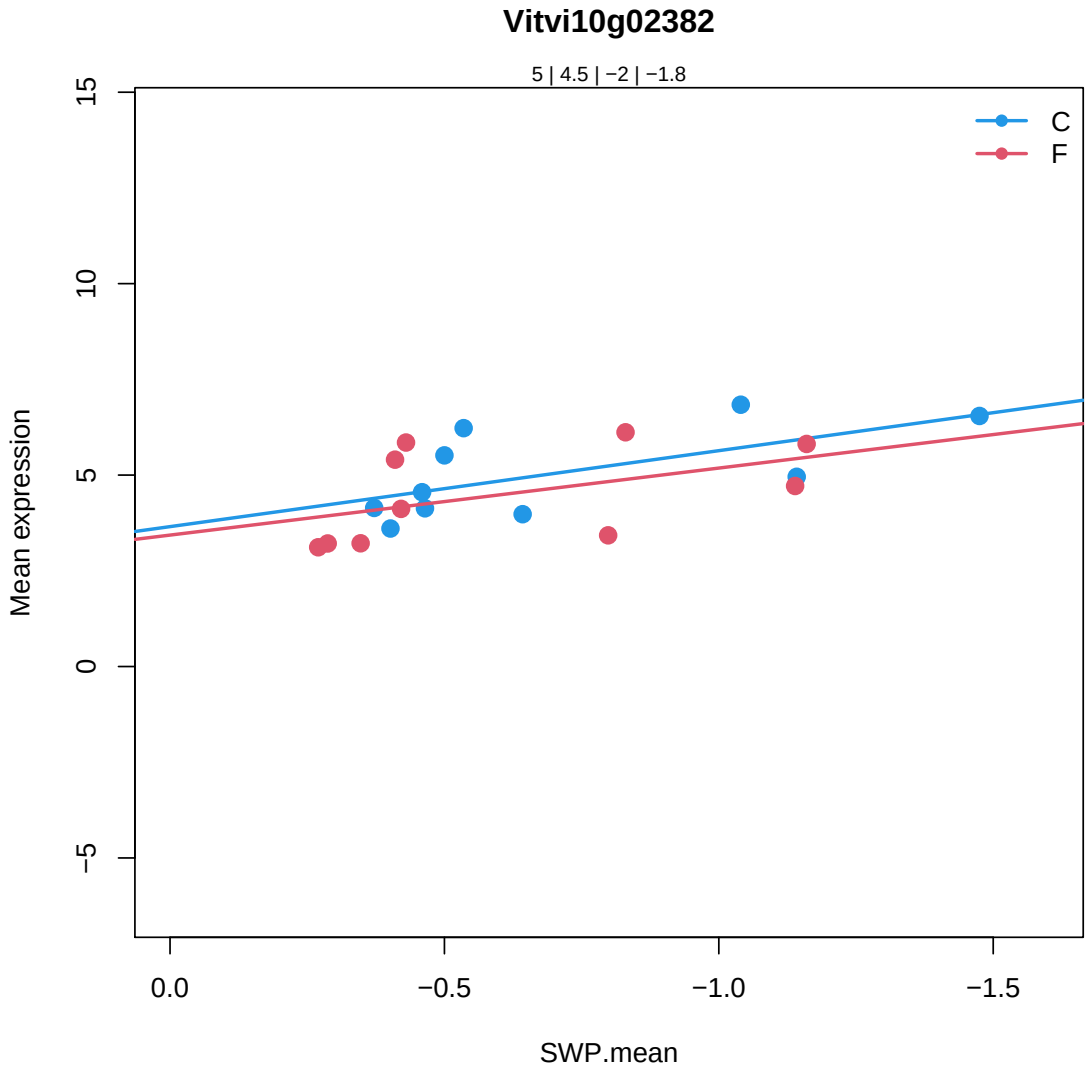
7.2.165 Vitvi10g02382: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g02382
        20.2.1
        stress.abiotic.heat
        Aldolase-type TIM barrel family protein |
        Chr4:11340492-11341732 FORWARD LENGTH=286 |
        201606
```

Coefficients for Vitvi10g02382.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.048511	5.62629e-14	***	8.804509e-14	***
SlopeC	-1.983972	0.02471352	*	0.4060648	
MeanF-MeanC	-0.5497127	0.2018712		0.5452933	
SlopeF-SlopeC	0.2334417	0.8503601		0.9999488	



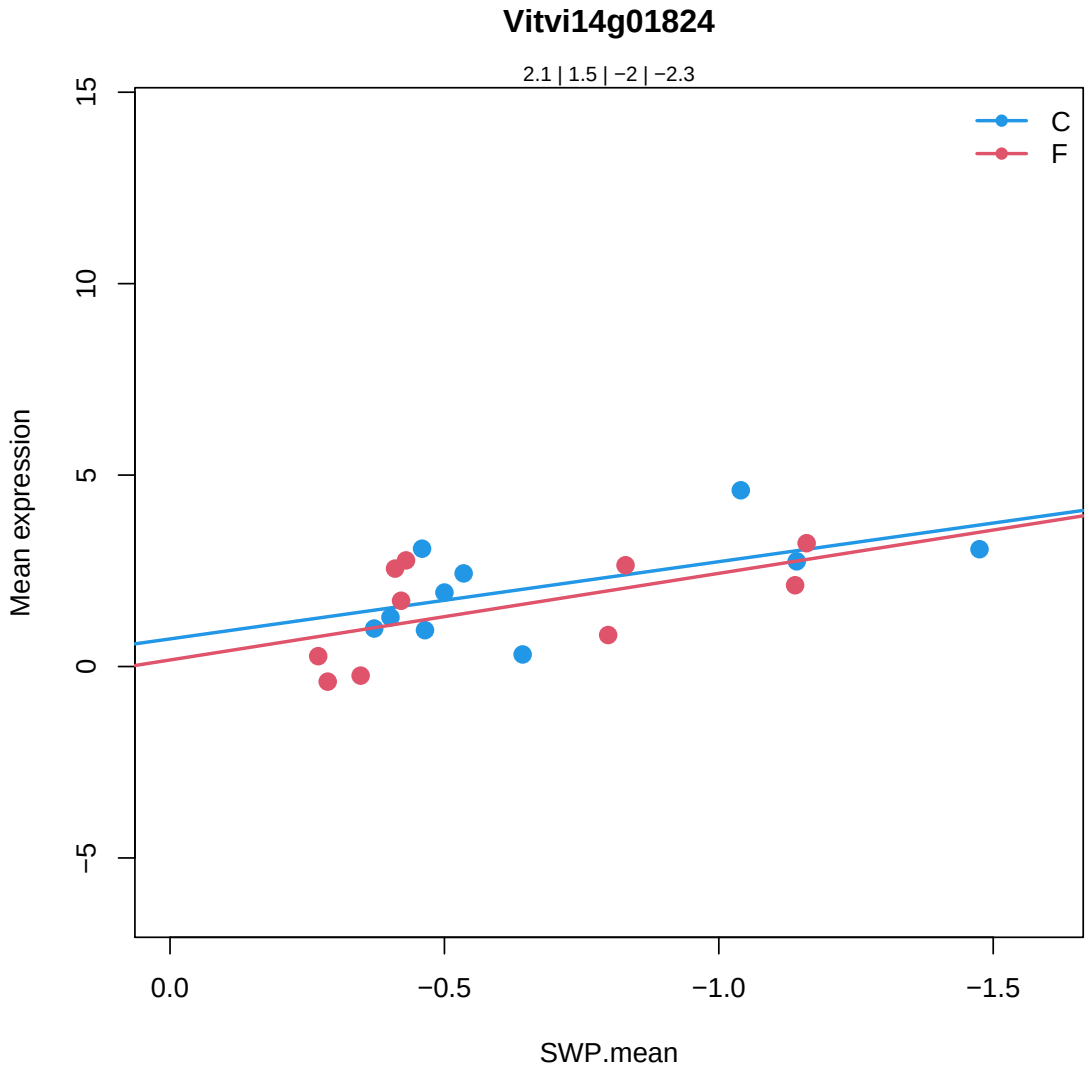
7.2.166 Vitvi14g01824: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01824
        27.3.11
        RNA.regulation of transcription.C2H2 zinc finger family
        zinc finger (AN1-like) family protein |
        Chr3:10520585-10521223 FORWARD LENGTH=186 |
        201606
```

Coefficients for Vitvi14g01824.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.139654	1.058859e-06	***	1.222014e-06	***
SlopeC	-2.017435	0.03297887	*	0.4417082	
MeanF-MeanC	-0.5902321	0.2034348		0.5476211	
SlopeF-SlopeC	-0.2450116	0.8542036		0.9999488	



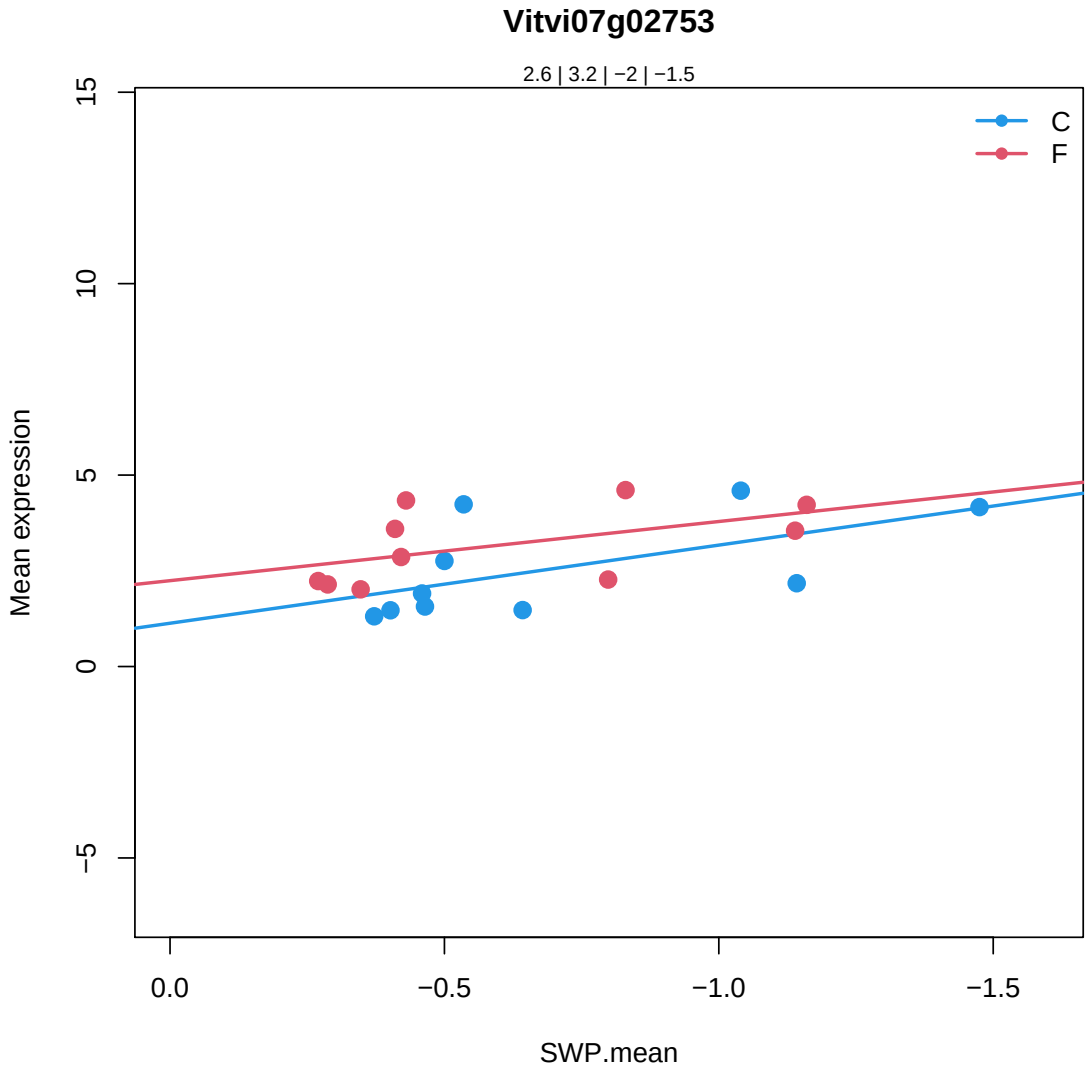
7.2.167 Vitvi07g02753: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g02753
        35.2
        not assigned.unknown
        amino acid-ligase |
        Chr3:2263806-2264576 REVERSE LENGTH=199 |
        201606
```

Coefficients for Vitvi07g02753.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.56519	1.008754e-08	***	1.231315e-08	***
SlopeC	-2.040545	0.01765684	*	0.3571759	
MeanF-MeanC	0.6181004	0.1402064		0.448595	
SlopeF-SlopeC	0.4955967	0.6790587		0.9999488	



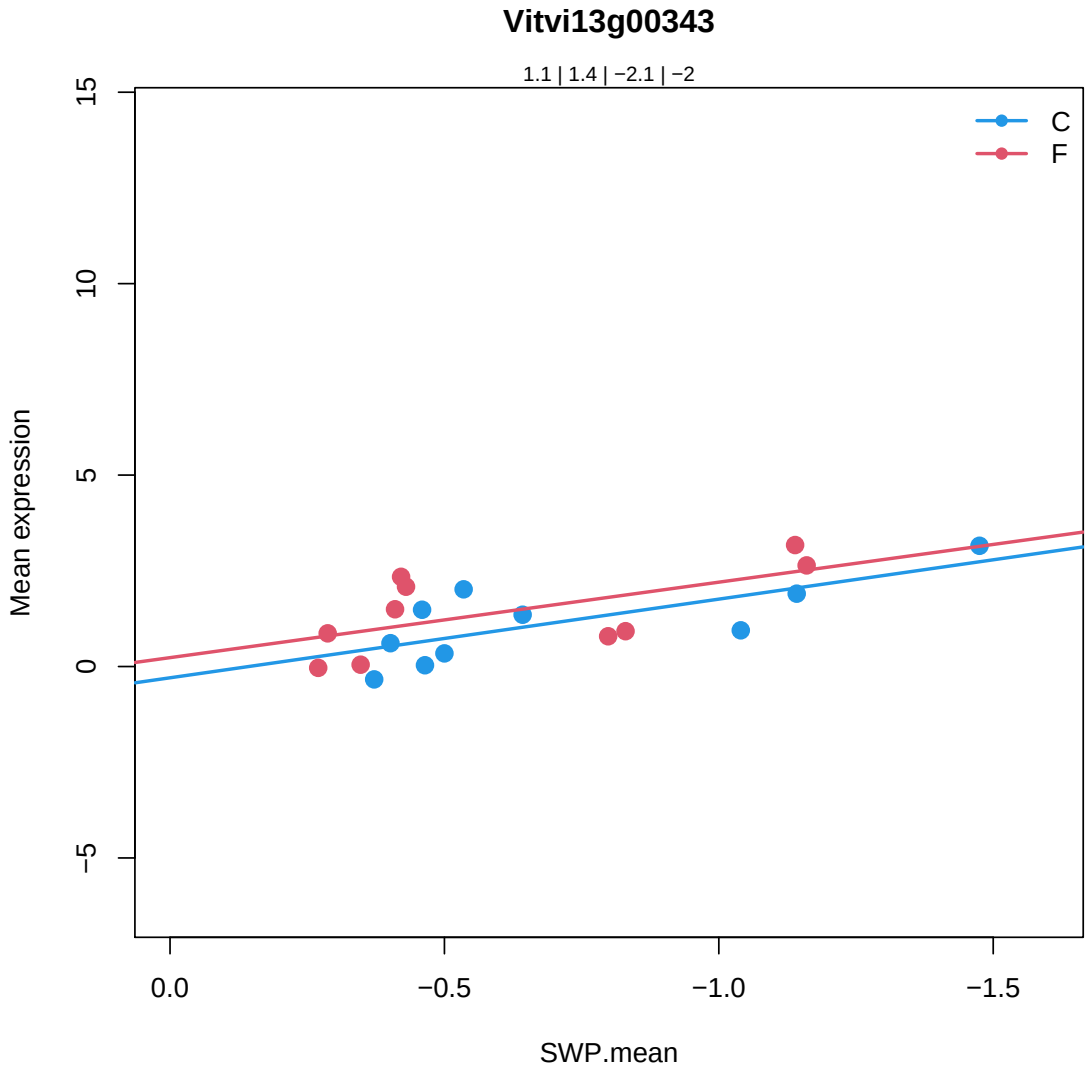
7.2.168 Vitvi13g00343: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00343
        35.2
        not assigned.unknown
        NAD(P)-binding Rossmann-fold superfamily protein |
        Chr2:12582523-12583954 FORWARD LENGTH=322 |
        201606
```

Coefficients for Vitvi13g00343.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.14993	9.794303e-05	***	0.0001081225	***
SlopeC	-2.05435	0.005803521	**	0.2626746	
MeanF-MeanC	0.2827783	0.4159279		0.7545314	
SlopeF-SlopeC	0.08342333	0.9341639		0.9999488	



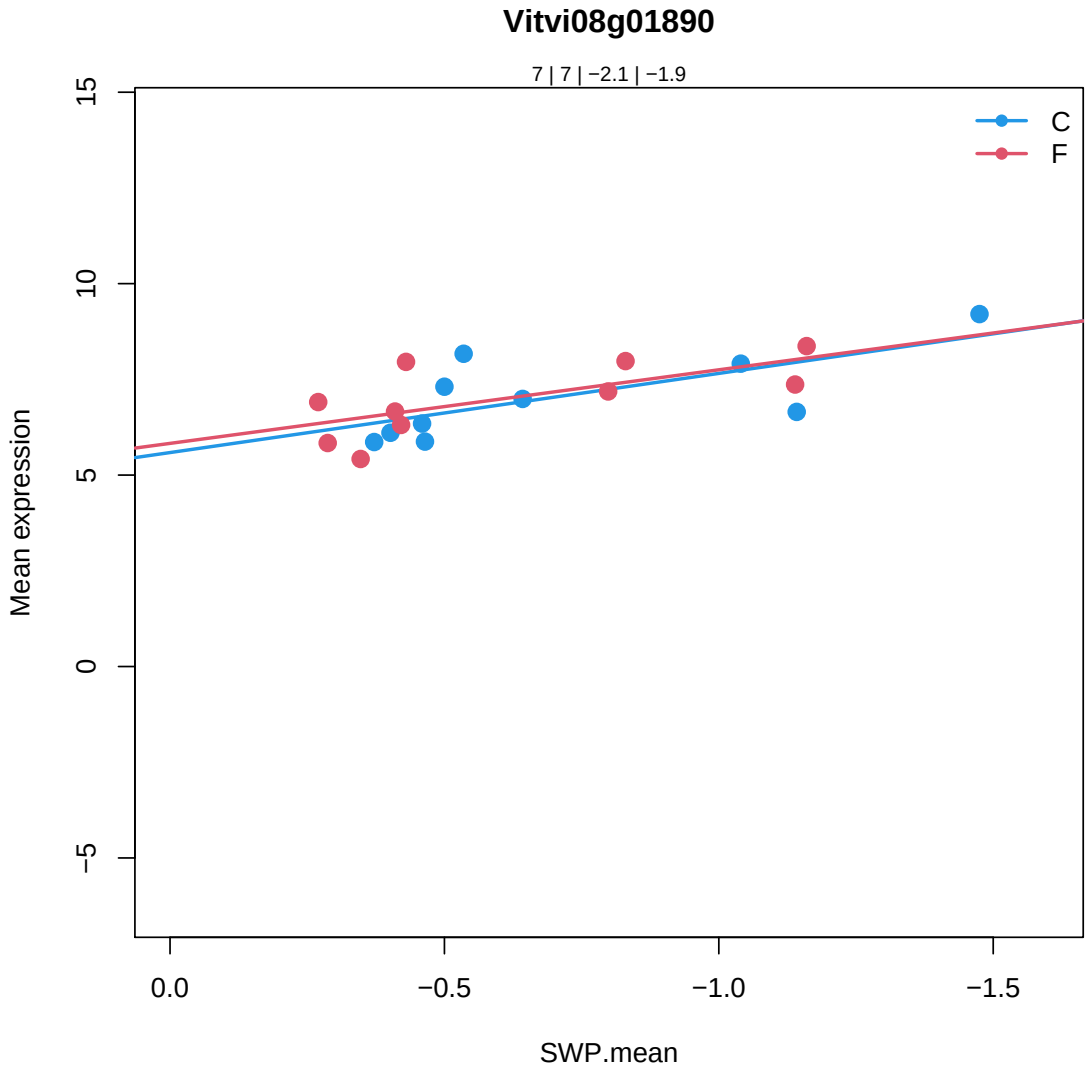
7.2.169 Vitvi08g01890: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01890
        3.1.2.2
        minor CHO metabolism.raffinose family.raffinose synthases.putative
        seed imbibition 2 |
        Chr3:21288982-21292694 REVERSE LENGTH=773 |
        201606
```

Coefficients for Vitvi08g01890.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.041681	3.209318e-19	***	1.28999e-18	***
SlopeC	-2.067362	0.003819954	**	0.2269459	
MeanF-MeanC	-0.04310173	0.8954217		0.9727746	
SlopeF-SlopeC	0.1452297	0.8797751		0.9999488	



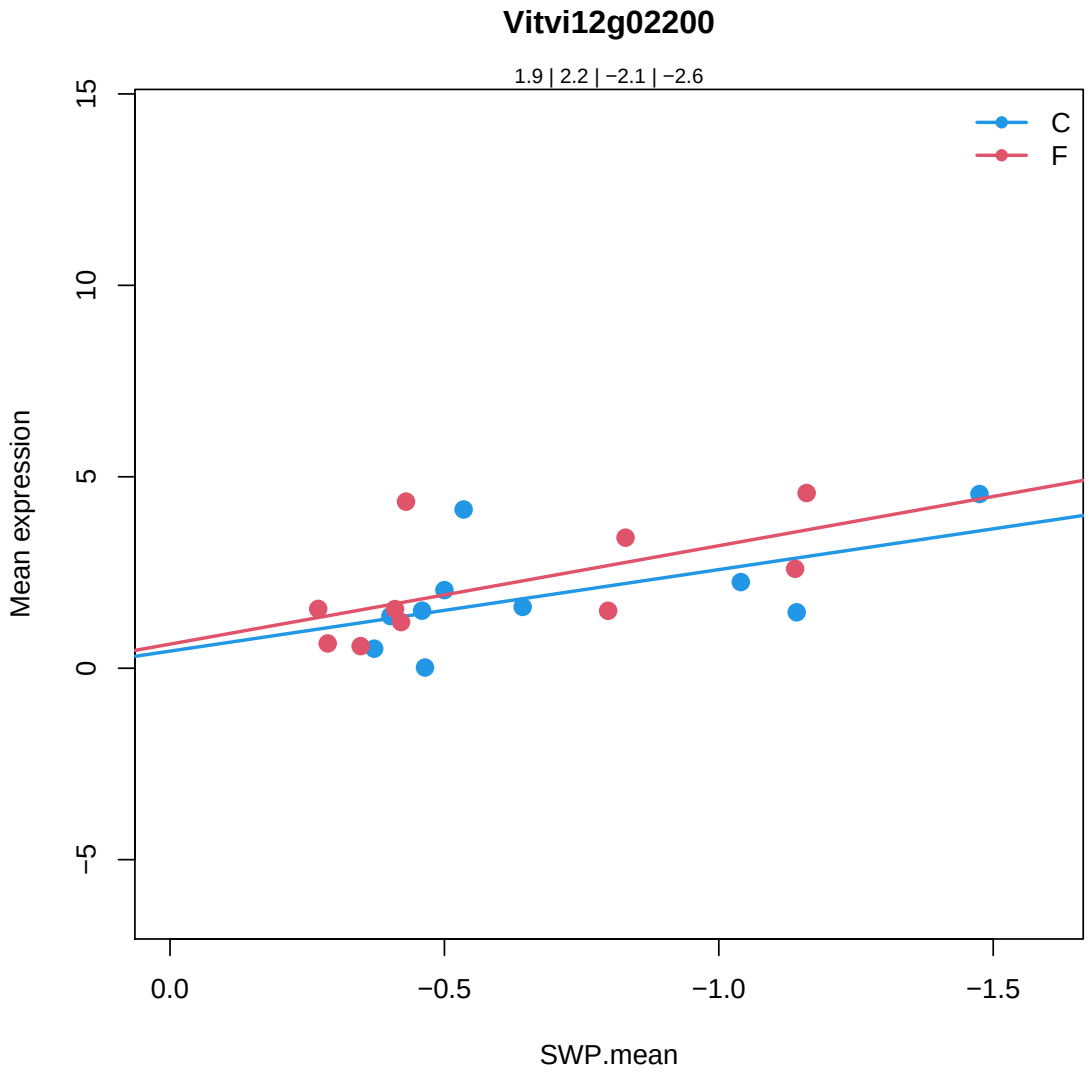
7.2.170 Vitvi12g02200: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02200
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi12g02200.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.943816	1.461434e-05	***	1.644167e-05	***
SlopeC	-2.128876	0.039425	*	0.4699262	
MeanF-MeanC	0.251856	0.6149148		0.8669553	
SlopeF-SlopeC	-0.4414103	0.7628773		0.9999488	



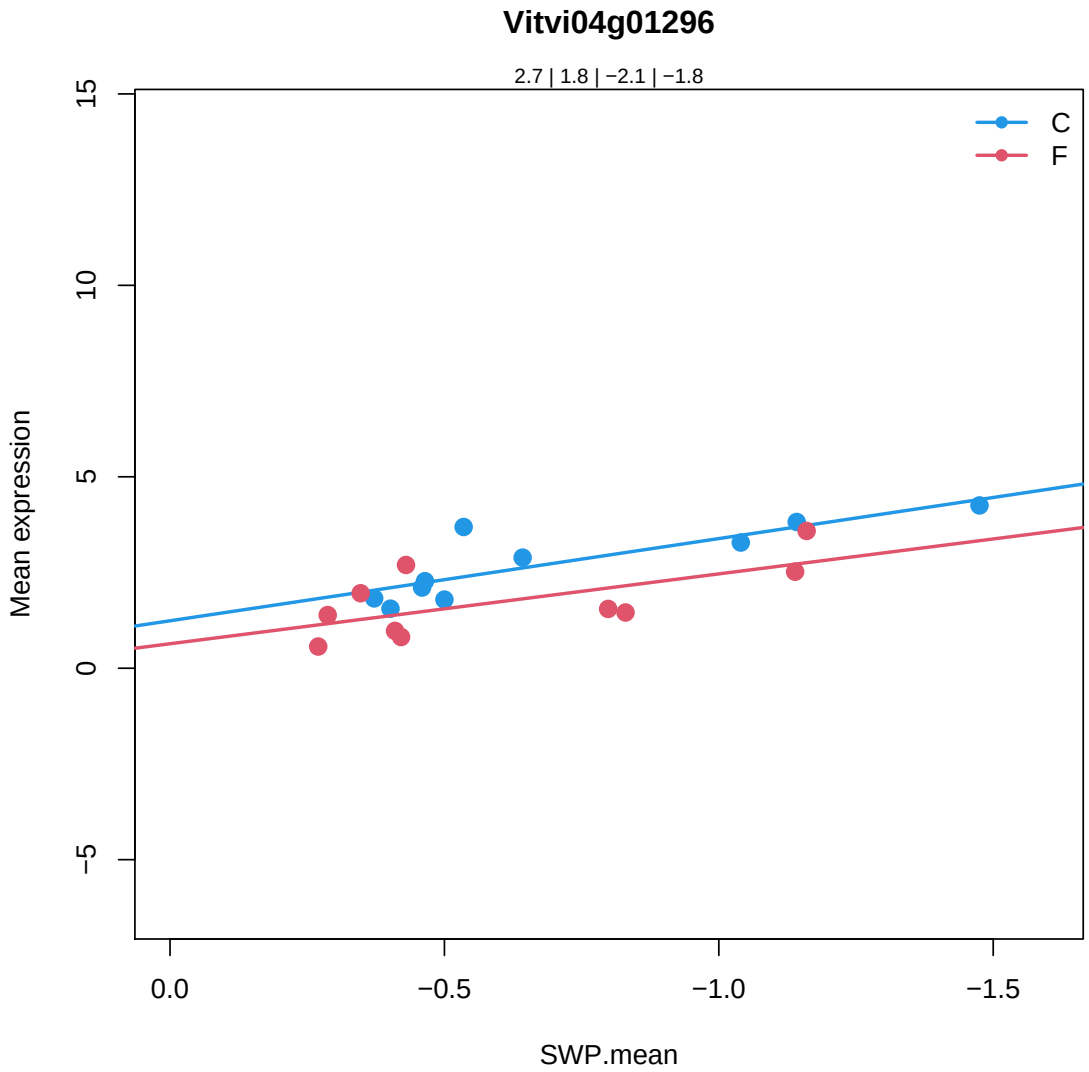
7.2.171 Vitvi04g01296: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01296
        35.1
        not assigned.no ontology
        NA
```

Coefficients for Vitvi04g01296.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.74839	2.964505e-12	***	4.146934e-12	***
SlopeC	-2.146713	0.0007482566	***	0.1076608	
MeanF-MeanC	-0.9975088	0.001680168	**	0.01919724	*
SlopeF-SlopeC	0.3222407	0.6959423		0.9999488	



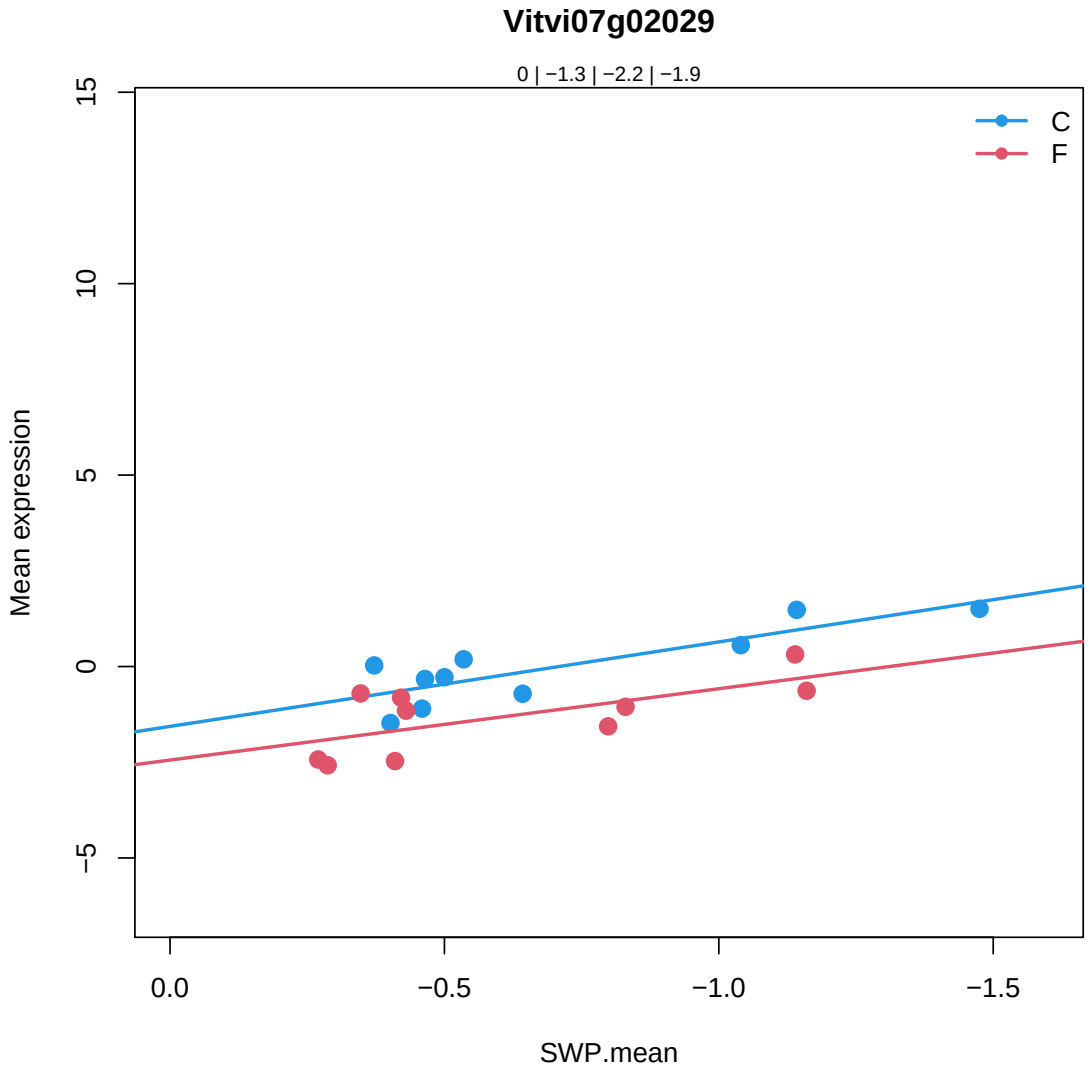
7.2.172 Vitvi07g02029: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g02029
        26.12
        misc.peroxidases
        Peroxidase superfamily protein |
        Chr4:16084856-16086105 FORWARD LENGTH=325 |
        201606
```

Coefficients for Vitvi07g02029.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.01301875	0.9478156		0.9489362	
SlopeC	-2.206244	0.0005793016	***	0.1005065	
MeanF-MeanC	-1.295242	0.00012824	***	0.002228774	**
SlopeF-SlopeC	0.3426853	0.6779806		0.9999488	



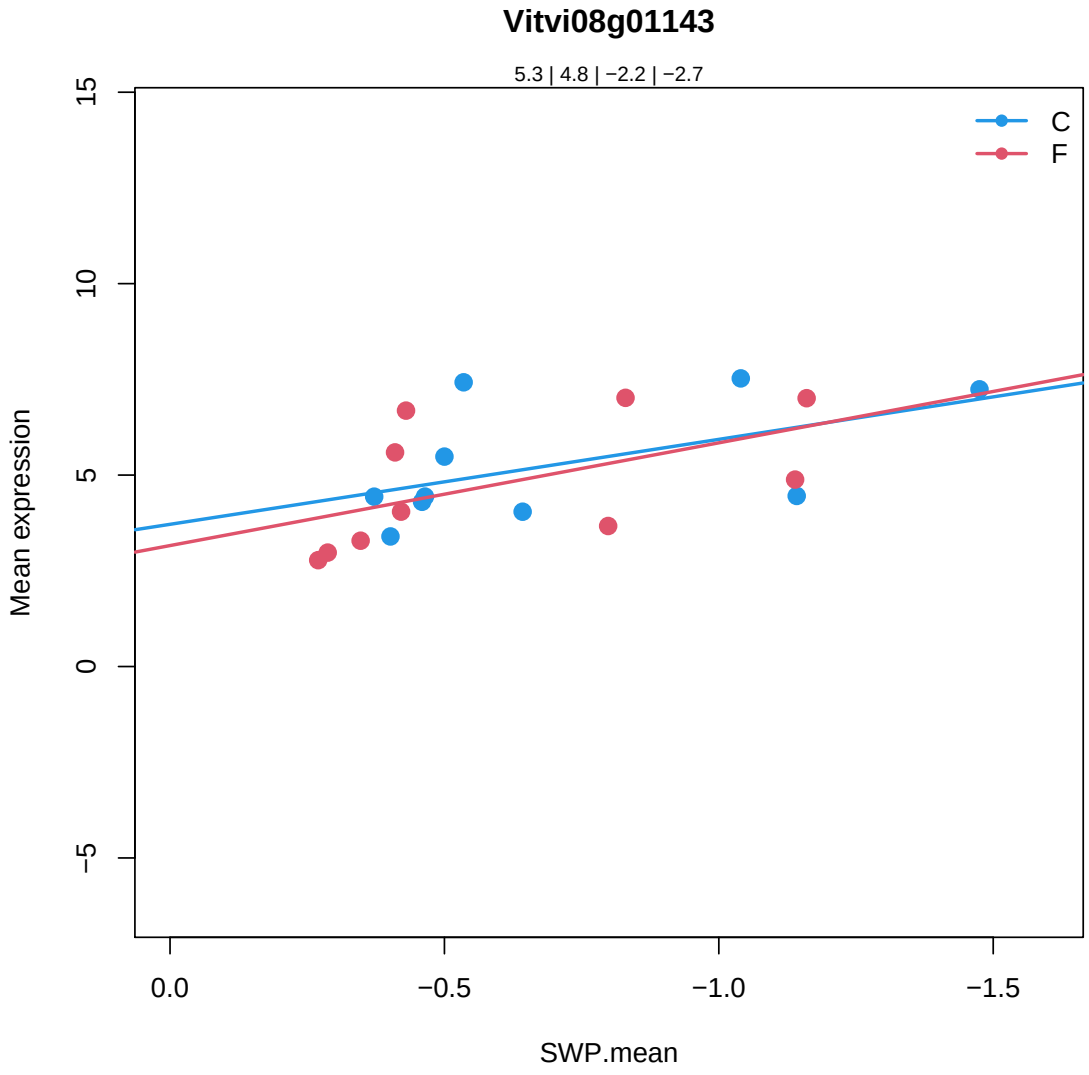
7.2.173 Vitvi08g01143: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01143
        21.2.1
        redox.ascorbate and glutathione.ascorbate
        ascorbate peroxidase 2 |
        Chr3:2956301-2958163 FORWARD LENGTH=251 |
        201606
```

Coefficients for Vitvi08g01143.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.274202	9.724664e-12	***	1.328047e-11	***
SlopeC	-2.218766	0.05960803	.	0.5395912	
MeanF-MeanC	-0.4804745	0.4061604		0.7482679	
SlopeF-SlopeC	-0.4643908	0.7823844		0.9999488	



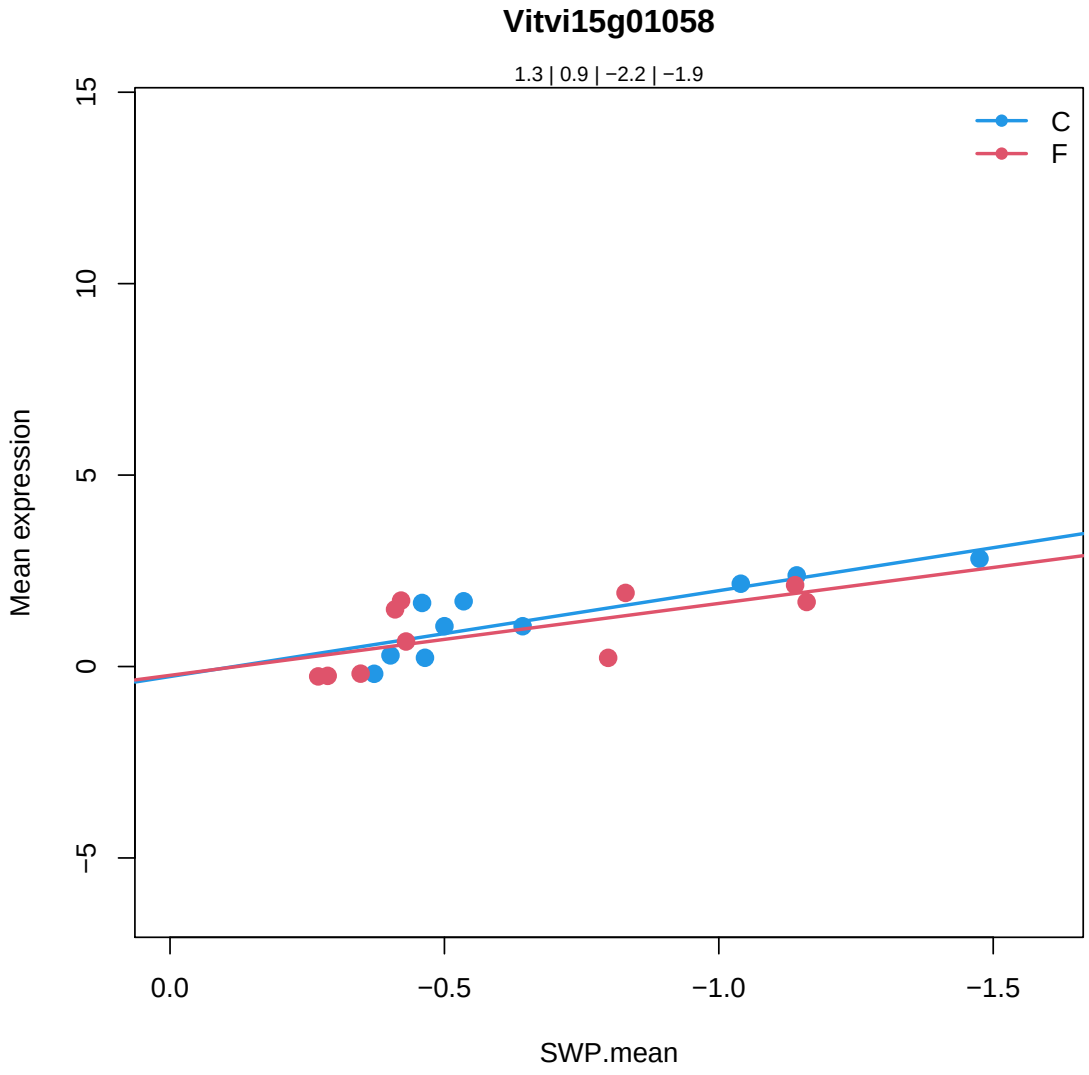
7.2.174 Vitvi15g01058: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g01058
        34.99
        transport.misc
        receptor-like protein kinase 4 |
        Chr4:148958-151496 FORWARD LENGTH=818 |
        201606
```

Coefficients for Vitvi15g01058.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.315457	1.50292e-06	***	1.727695e-06	***
SlopeC	-2.243262	0.0005907899	***	0.1005065	
MeanF-MeanC	-0.4016553	0.1705762		0.5001776	
SlopeF-SlopeC	0.3650419	0.6642526		0.9999488	



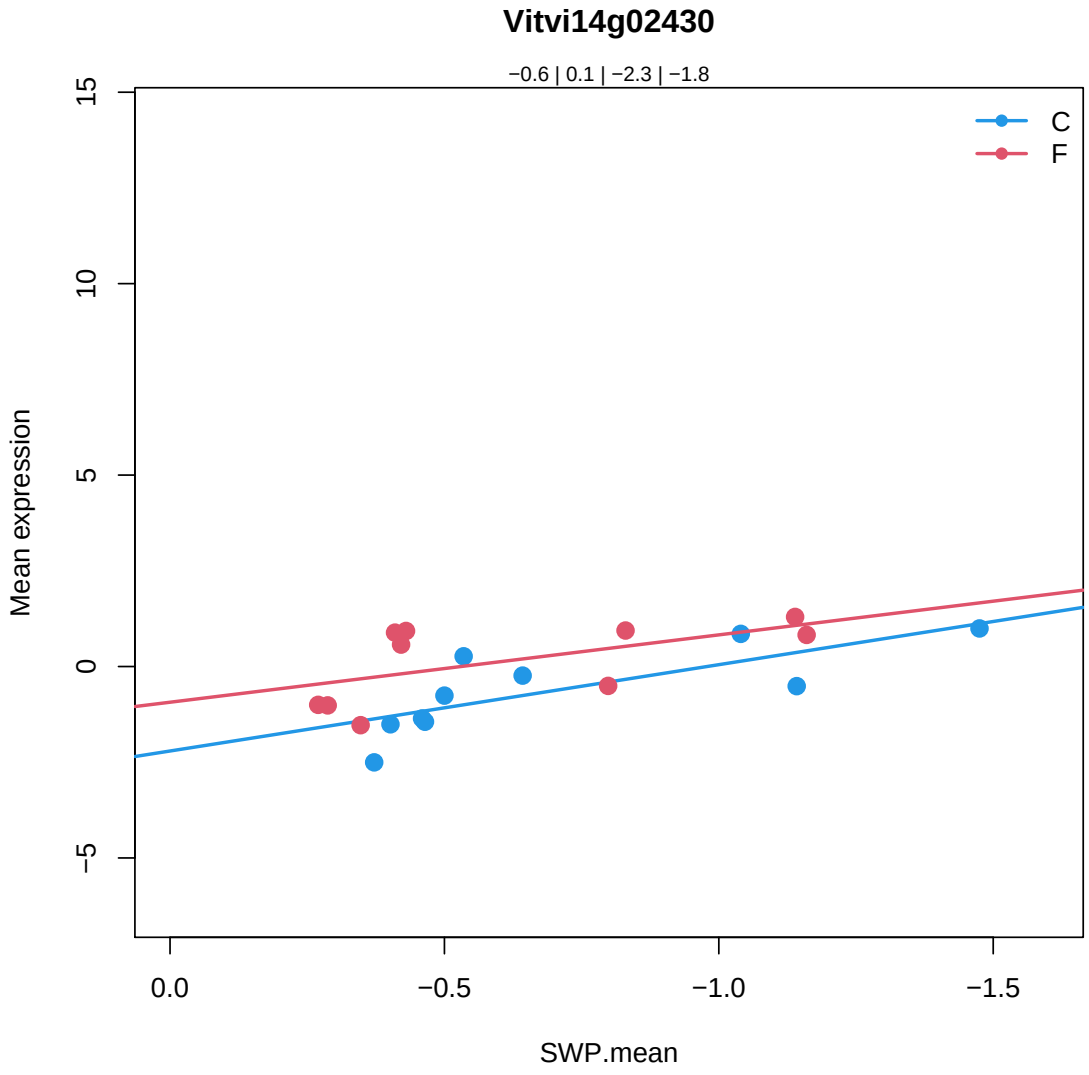
7.2.175 Vitvi14g02430: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g02430
        27.3.25
        RNA.regulation of transcription.MYB domain transcription factor family
        myb domain protein 43 |
        Chr5:5438291-5440214 FORWARD LENGTH=327 |
        201606
```

Coefficients for Vitvi14g02430.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.6209638	0.01722476	*	0.01813997	*
SlopeC	-2.254746	0.002837264	**	0.2035467	
MeanF-MeanC	0.7600814	0.03620843	*	0.1914287	
SlopeF-SlopeC	0.4955903	0.6238294		0.9999488	



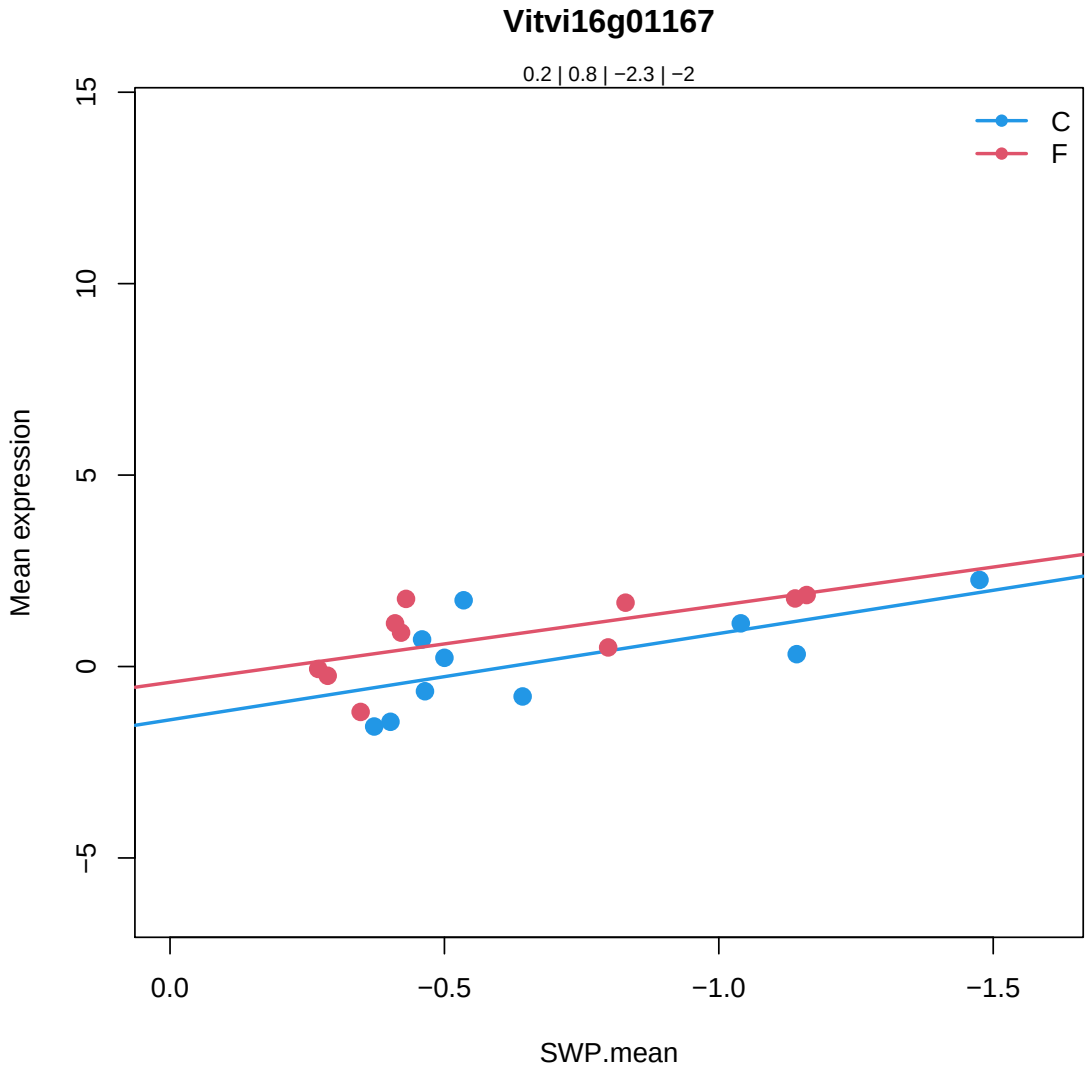
7.2.176 Vitvi16g01167: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01167
        30.2.24
        signalling.receptor kinases.S-locus glycoprotein like
        Protein kinase superfamily protein |
        Chr5:8139334-8142391 REVERSE LENGTH=872 |
        201606
```

Coefficients for Vitvi16g01167.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1937513	0.4781553		0.4843841	
SlopeC	−2.254897	0.006418653	**	0.2665752	
MeanF−MeanC	0.6160093	0.1192124		0.4059508	
SlopeF−SlopeC	0.2474672	0.8259004		0.9999488	



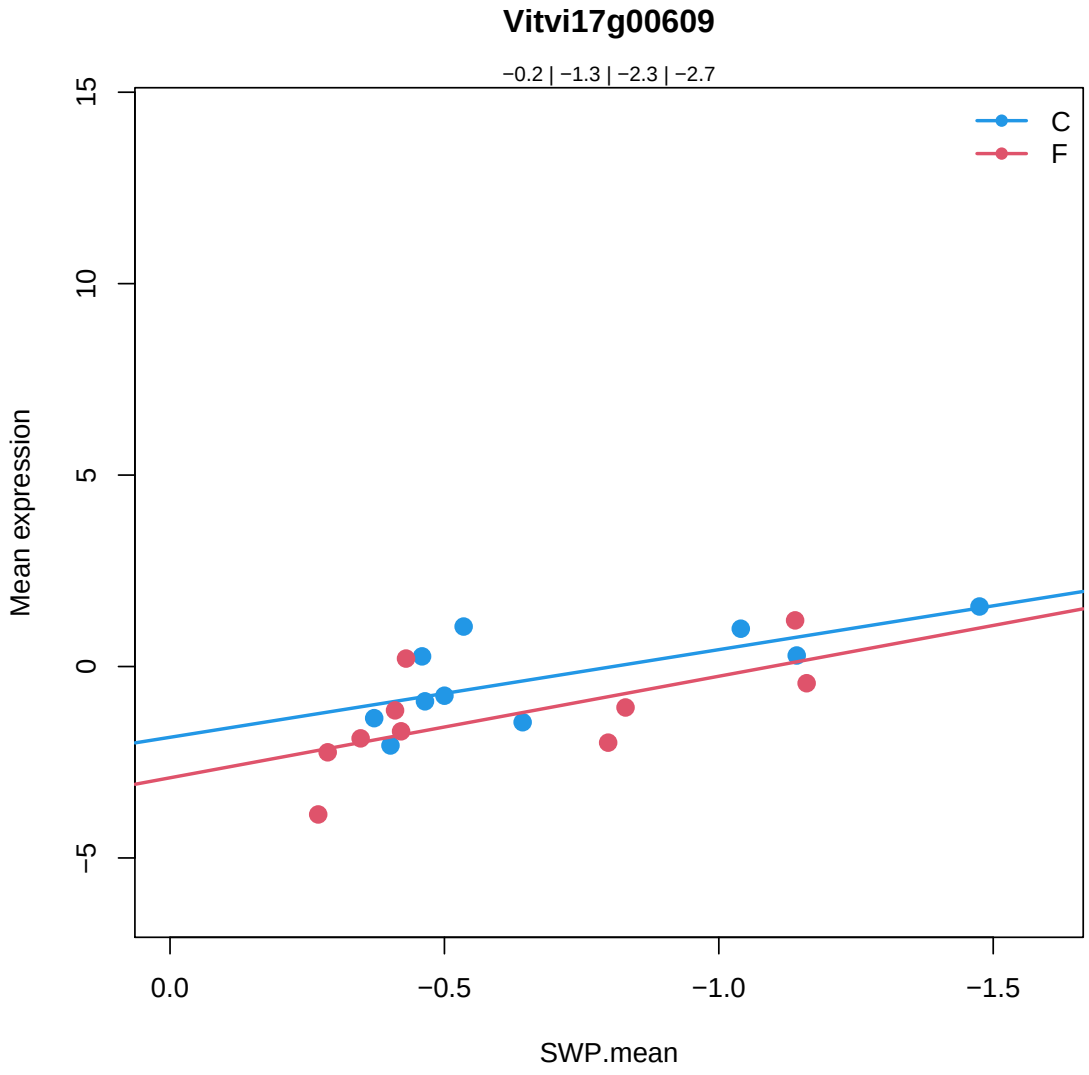
7.2.177 Vitvi17g00609: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00609
        26.28
        misc.GDSL-motif lipase
        GDSL-like Lipase/Acylhydrolase superfamily protein |
        Chr1:27988150-27989765 REVERSE LENGTH=366 |
        201606
```

Coefficients for Vitvi17g00609.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.238655	0.426092		0.4321596	
SlopeC	-2.289082	0.01066502	*	0.3111585	
MeanF-MeanC	-1.051499	0.01938865	*	0.1233396	
SlopeF-SlopeC	-0.3631281	0.7684787		0.9999488	



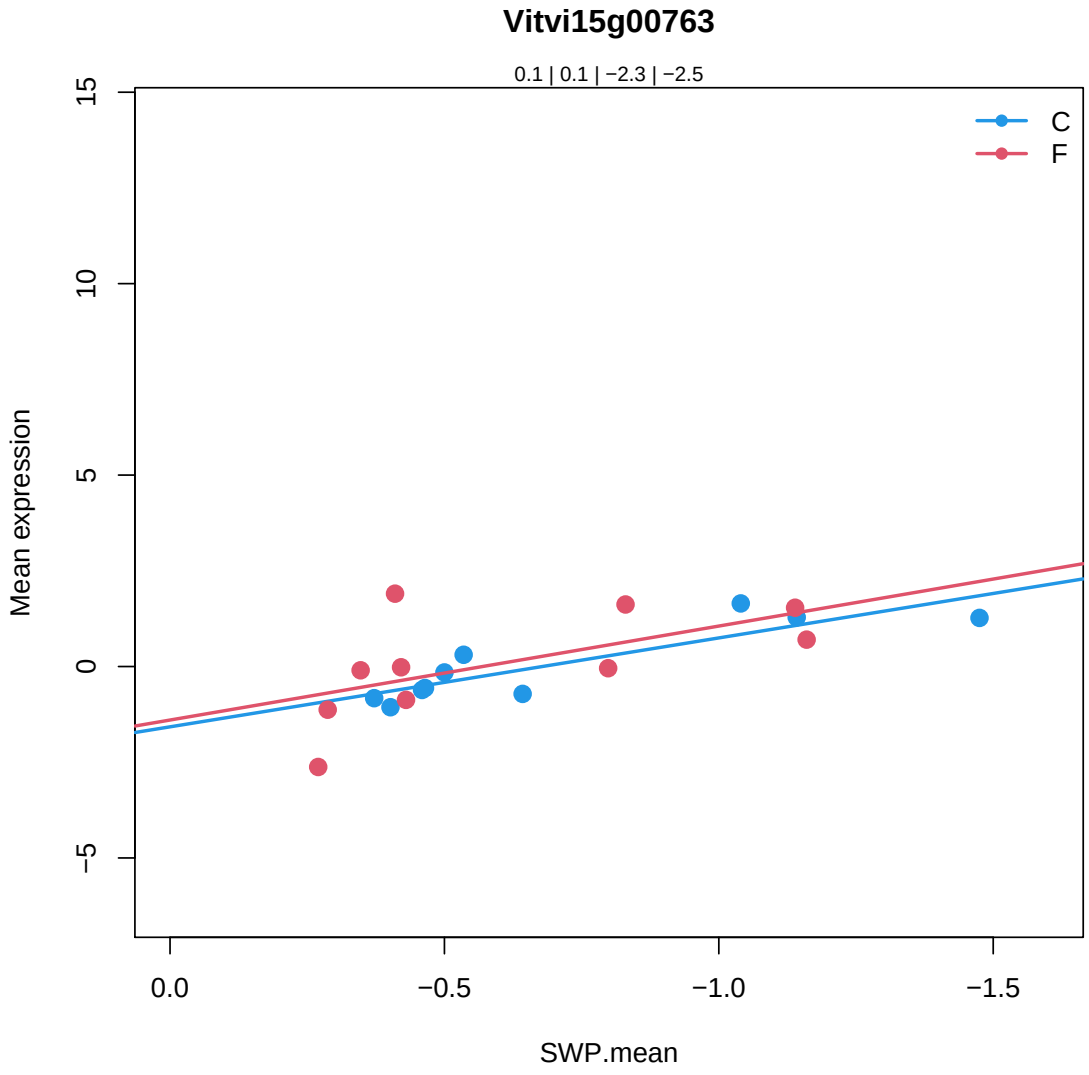
7.2.178 Vitvi15g00763: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g00763
        29.5.1
        protein.degradation.subtilases
        subtilase family protein |
        Chr1:310332-313011 FORWARD LENGTH=774 |
        201606
```

Coefficients for Vitvi15g00763.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.05752024	0.8295751		0.8329633	
SlopeC	-2.321806	0.00462461	**	0.2436609	
MeanF-MeanC	0.03992714	0.9158251		0.9772612	
SlopeF-SlopeC	-0.1323801	0.9047383		0.9999488	



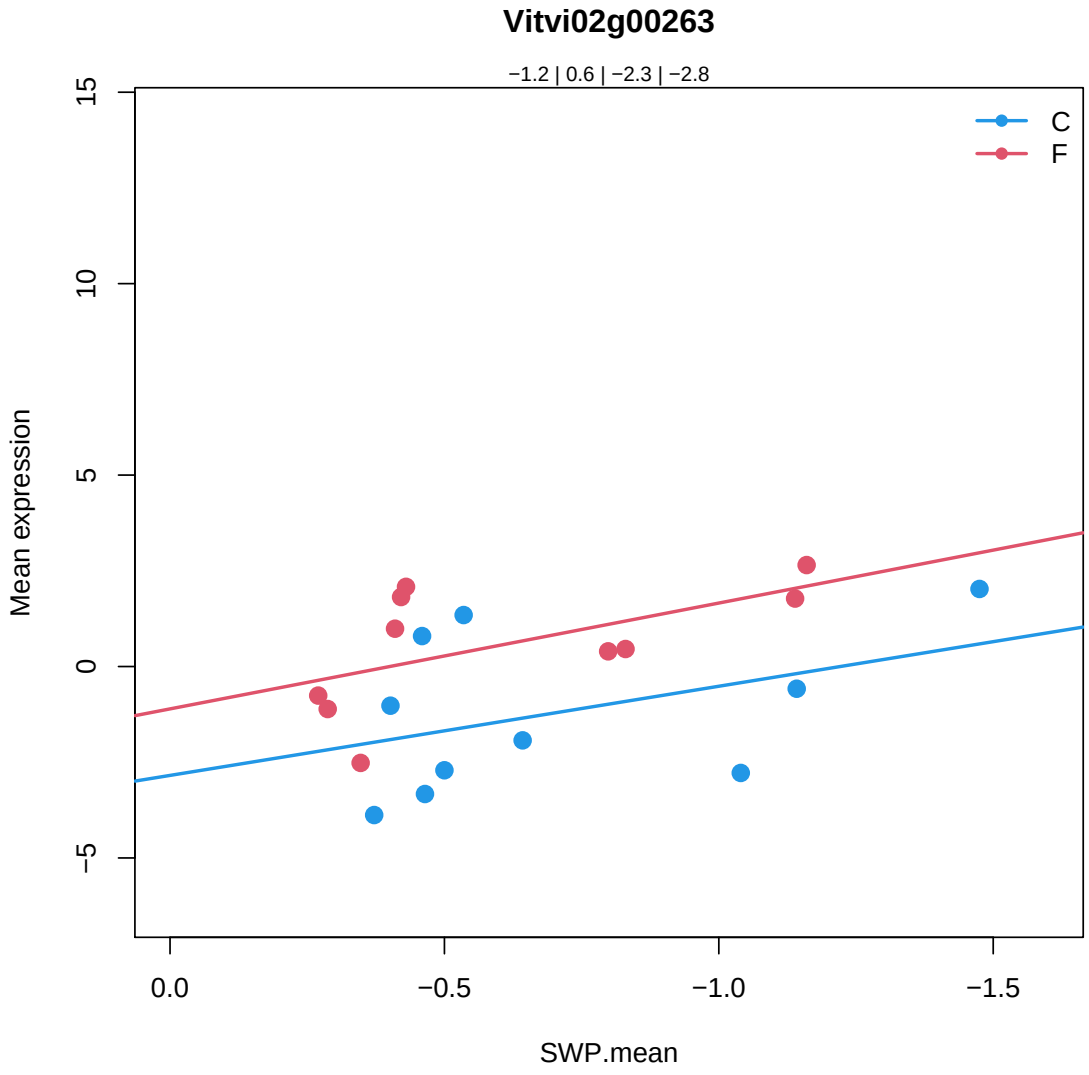
7.2.179 Vitvi02g00263: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00263
        26.6
        misc.O-methyl transferases
        O-methyltransferase 1 |
        Chr5:21982075-21984167 FORWARD LENGTH=363 |
        201606
```

Coefficients for Vitvi02g00263.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.206661	0.01891324	*	0.0198948	*
SlopeC	-2.328381	0.09249281	.	0.6008919	
MeanF-MeanC	1.784135	0.01466739	*	0.1004817	
SlopeF-SlopeC	-0.4357503	0.826854		0.9999488	



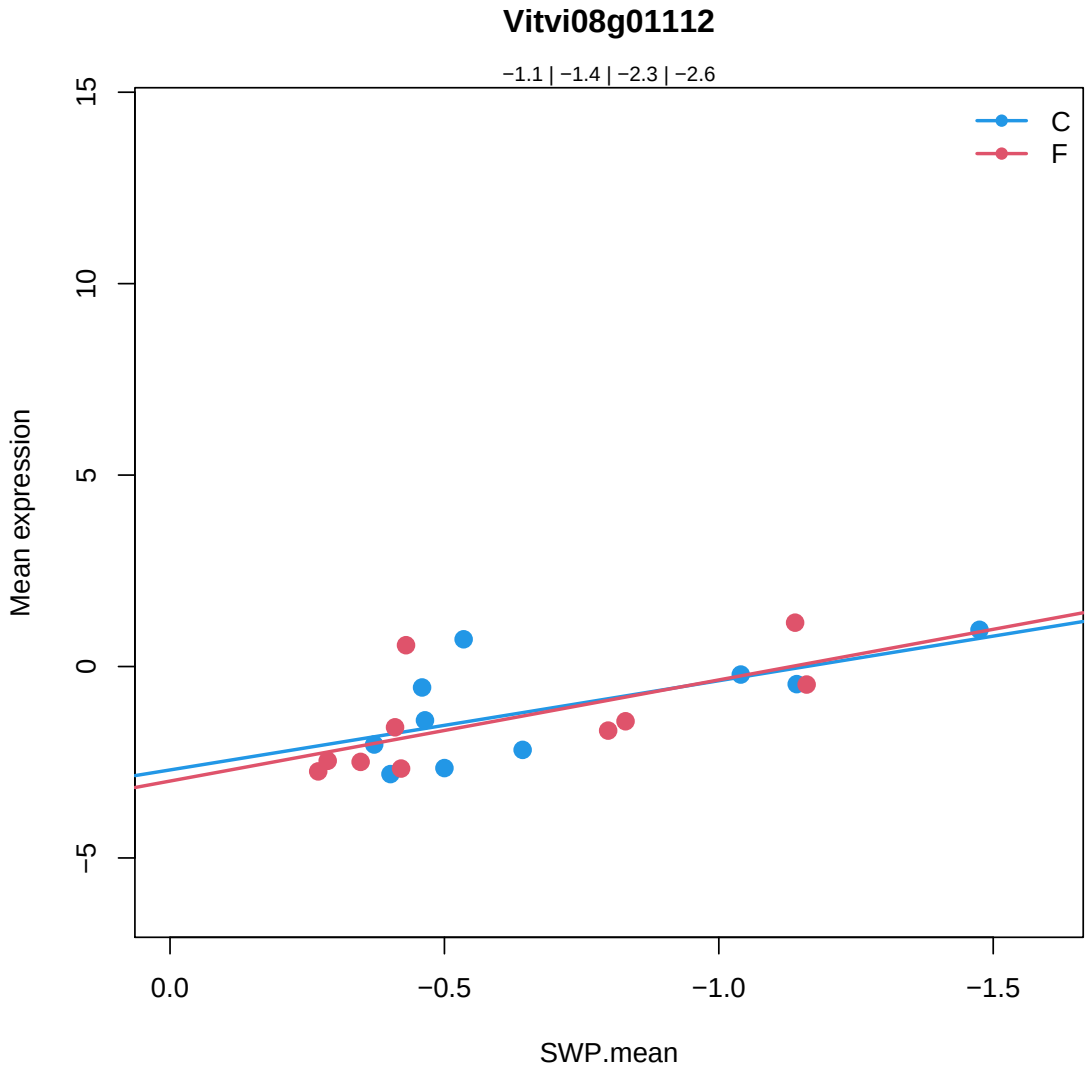
7.2.180 Vitvi08g01112: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01112
        34.16
        transport.ABC transporters and multidrug resistance systems
        ABC-2 type transporter family protein |
        Chr2:15673555-15675822 REVERSE LENGTH=755 |
        201606
```

Coefficients for Vitvi08g01112.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.062956	0.002339767	**	0.002512698	**
SlopeC	-2.329875	0.01271304	*	0.3273178	
MeanF-MeanC	-0.3189805	0.471925		0.7897762	
SlopeF-SlopeC	-0.3120123	0.8090679		0.9999488	



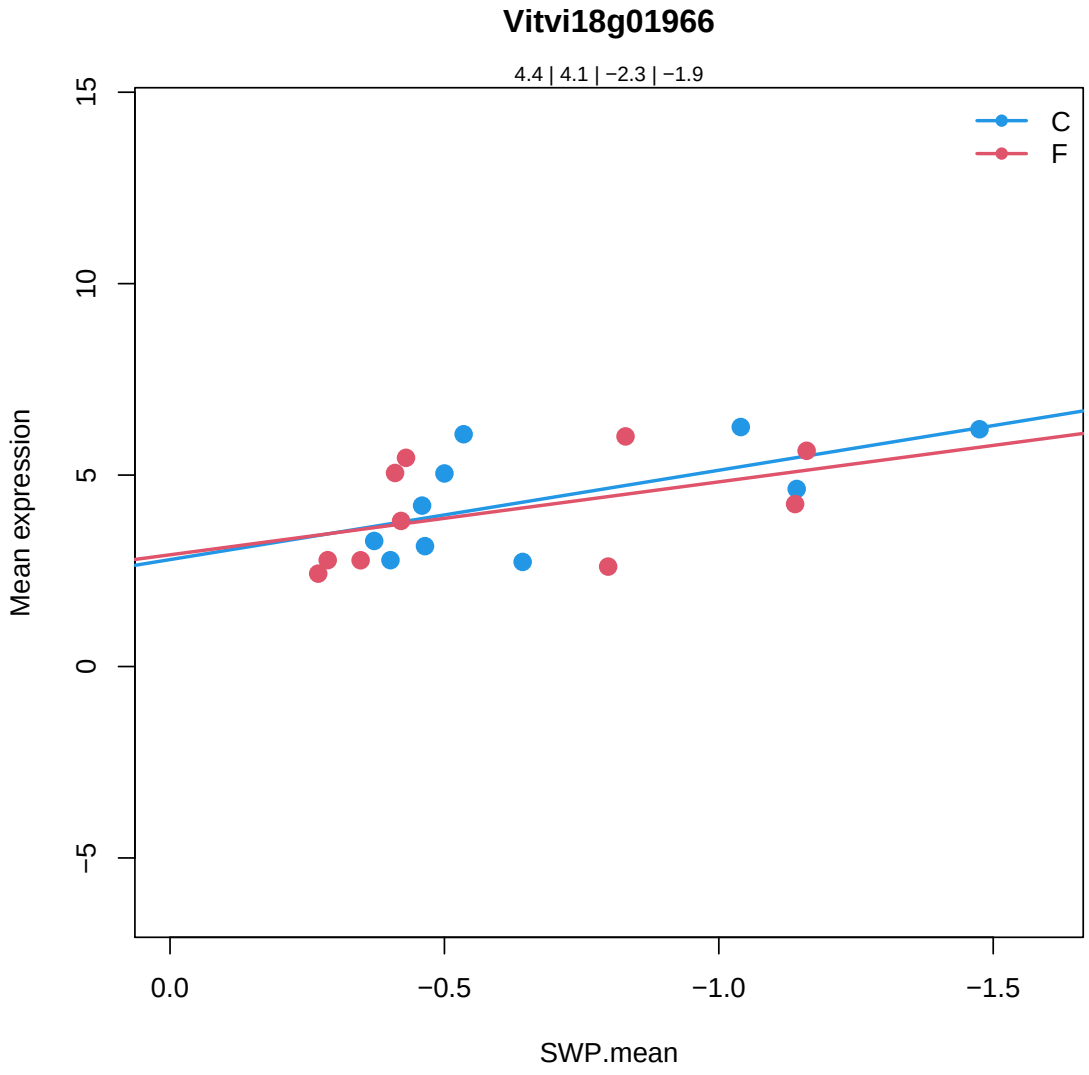
7.2.181 Vitvi18g01966: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g01966
        35.1
        not assigned.no ontology
        T-complex protein 11 |
        Chr1:8118049-8121854 FORWARD LENGTH=1020 |
        201606
```

Coefficients for Vitvi18g01966.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.433318	1.802502e-11	***	2.433242e-11	***
SlopeC	-2.333415	0.02502935	*	0.4079655	
MeanF-MeanC	-0.3550498	0.4785471		0.7941132	
SlopeF-SlopeC	0.4288107	0.768948		0.9999488	



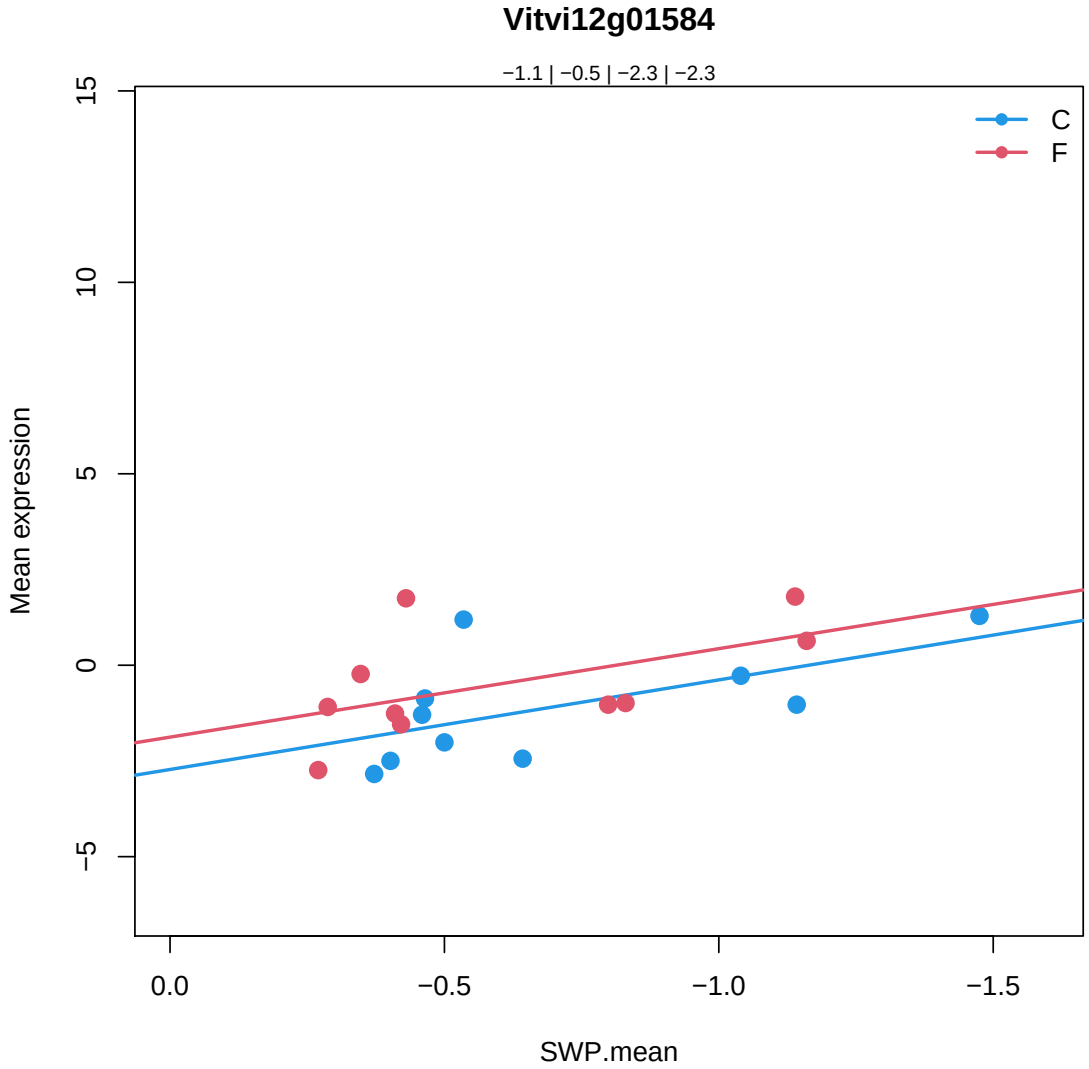
7.2.182 Vitvi12g01584: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g01584
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi12g01584.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.07798	0.006247541	**	0.006647006	**
SlopeC	-2.340025	0.02750159	*	0.4233169	
MeanF-MeanC	0.6075684	0.240133		0.5976418	
SlopeF-SlopeC	0.02913283	0.9843975		0.9999488	



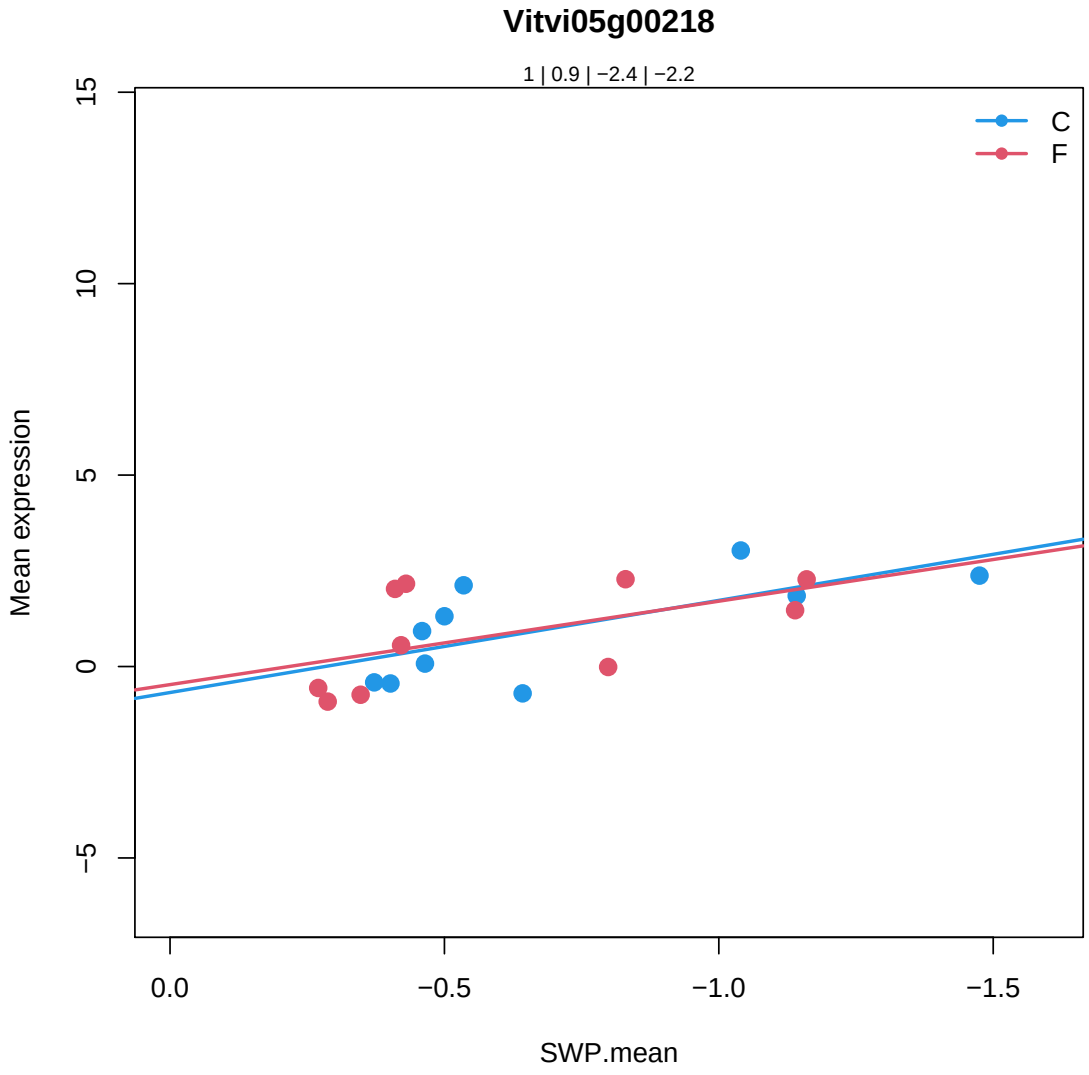
7.2.183 Vitvi05g00218: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00218
        34.9
        transport.metabolite transporters at the mitochondrial membrane
        Mitochondrial substrate carrier family protein |
        Chr5:5087822-5089677 FORWARD LENGTH=316 |
        201606
```

Coefficients for Vitvi05g00218.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.01281	0.003695211	**	0.003952449	**
SlopeC	-2.406759	0.01103064	*	0.3143947	
MeanF-MeanC	-0.1584336	0.7221519		0.914736	
SlopeF-SlopeC	0.2287034	0.8606836		0.9999488	



7.2.184 Vitvi06g00443: * type1

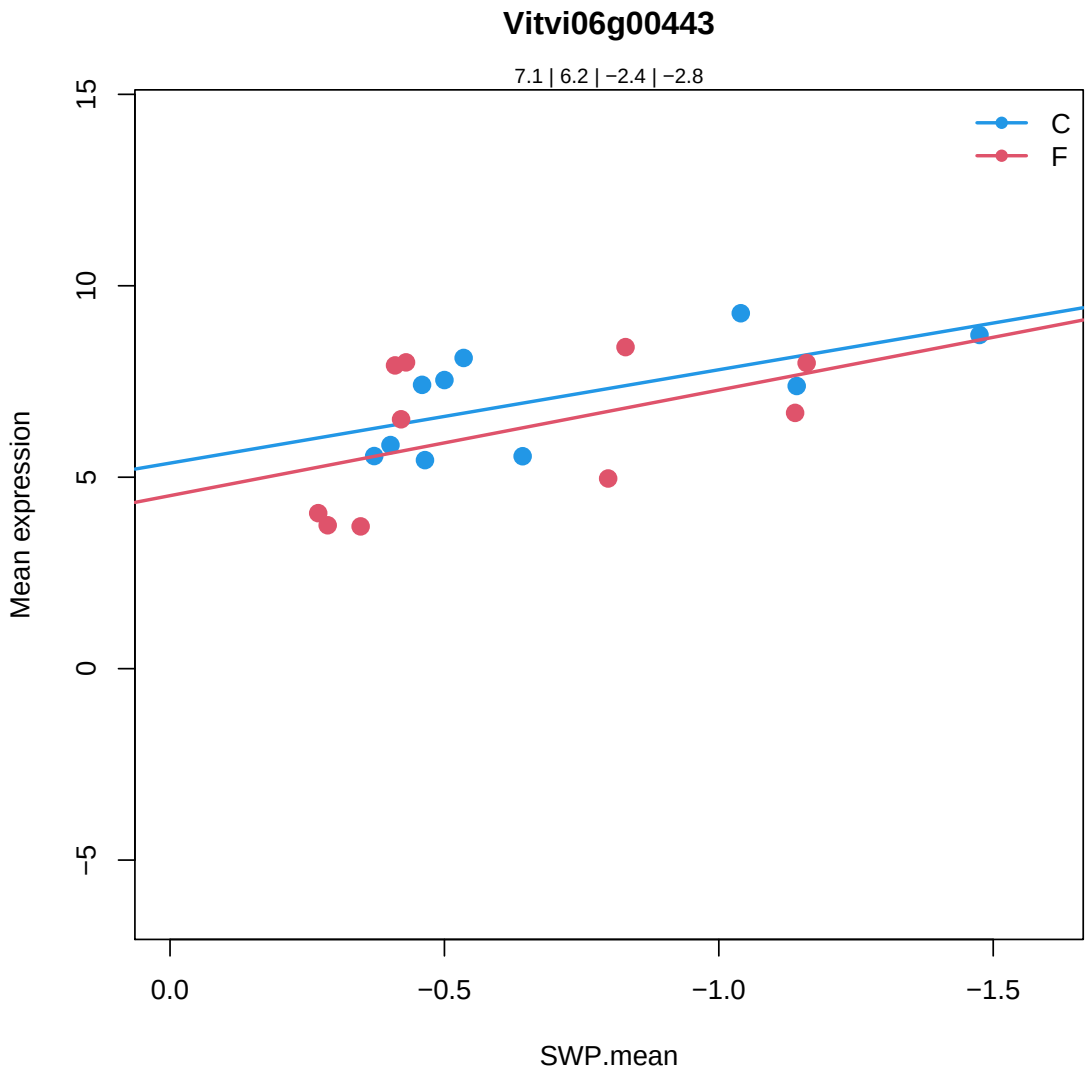
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00443
        29.6
        protein.folding
        heat shock cognate protein 70-1 |
        Chr5:554055-556334 REVERSE LENGTH=651 |
        201606

Vitvi06g00443
        20.2.1
        stress.abiotic.heat
        heat shock cognate protein 70-1 |
        Chr5:554055-556334 REVERSE LENGTH=651 |
        201606
```

Coefficients for Vitvi06g00443.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.083015	4.877361e-14	***	7.675863e-14	***
SlopeC	-2.438983	0.0447607	*	0.4901168	
MeanF-MeanC	-0.885021	0.1427101		0.4537312	
SlopeF-SlopeC	-0.3183393	0.8534745		0.9999488	


Vitvi06g00443
7.1 | 6.2 | −2.4 | −2.8
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

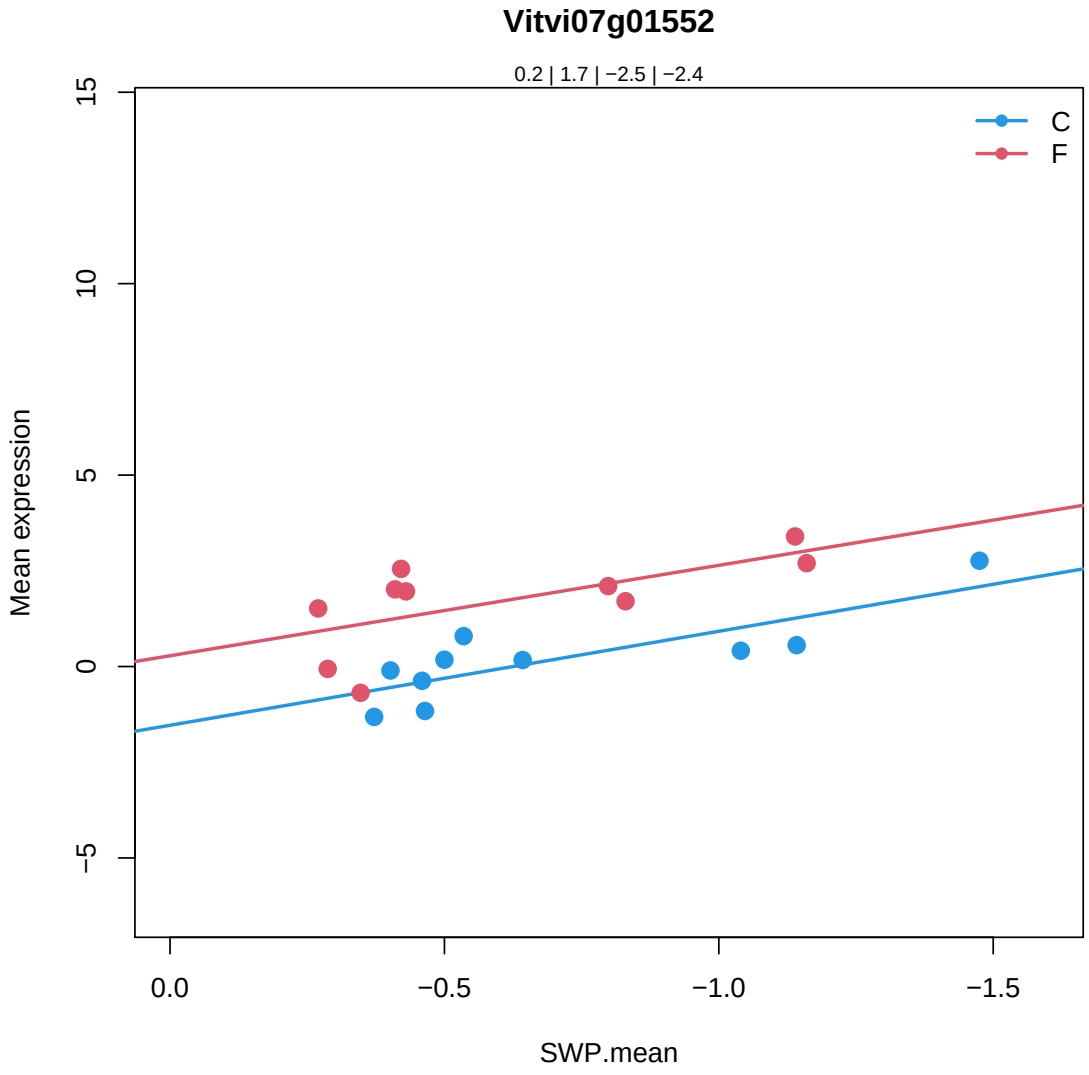
7.2.185 Vitvi07g01552: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01552
        35.2
        not assigned.unknown
        basic leucine-zipper 6 |
        Chr2:9732601-9733284 REVERSE LENGTH=227 |
        201606
```

Coefficients for Vitvi07g01552.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1917637	0.4448755		0.4510305	
SlopeC	-2.454713	0.001716853	**	0.1571259	
MeanF-MeanC	1.528104	0.0002476447	***	0.003915614	**
SlopeF-SlopeC	0.09286943	0.9283139		0.9999488	



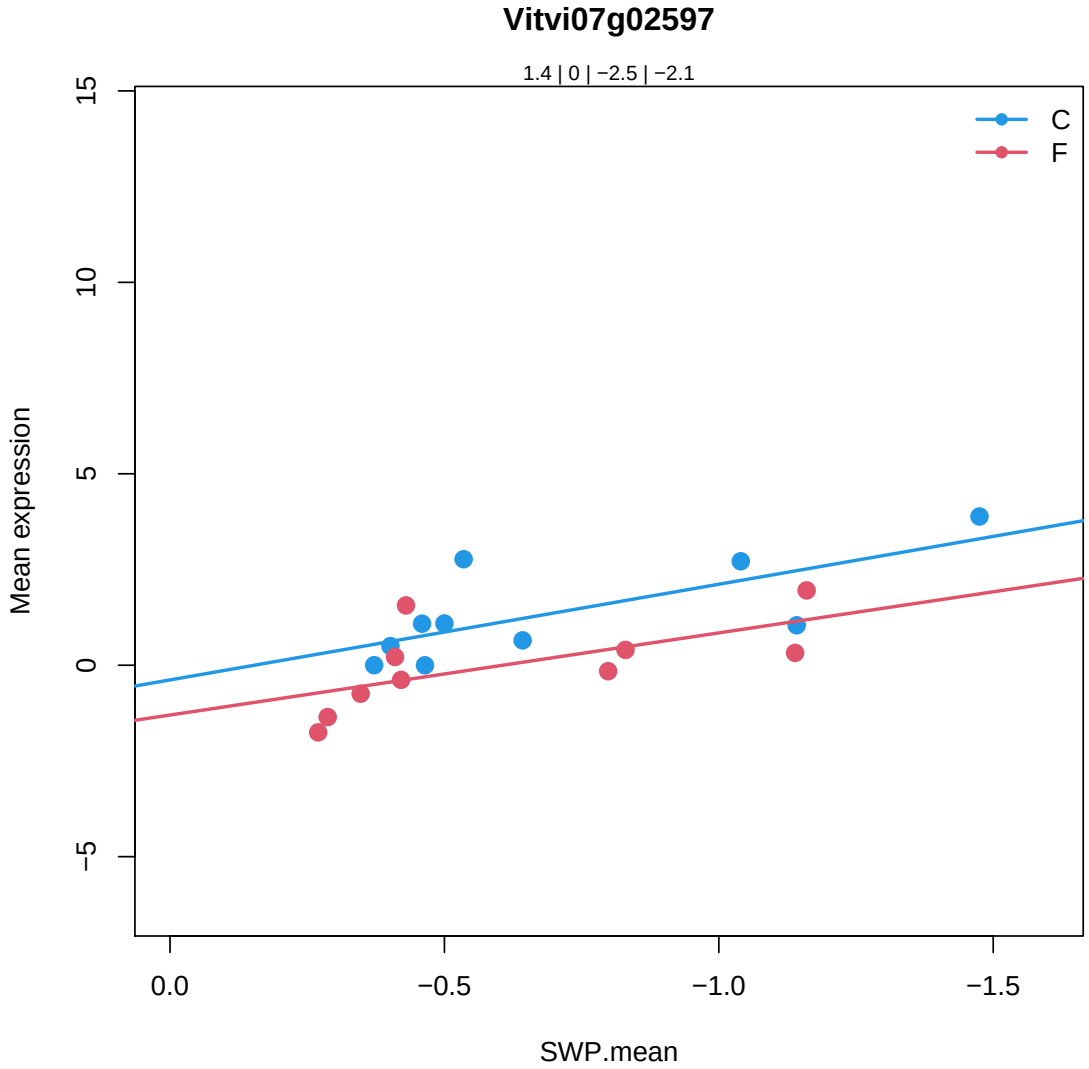
7.2.186 Vitvi07g02597: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g02597
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi07g02597.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.373304	5.182407e-05	***	5.755629e-05	***
SlopeC	-2.498658	0.00339104	**	0.2208813	
MeanF-MeanC	-1.366992	0.001871035	**	0.02090306	*
SlopeF-SlopeC	0.3531685	0.7574547		0.9999488	



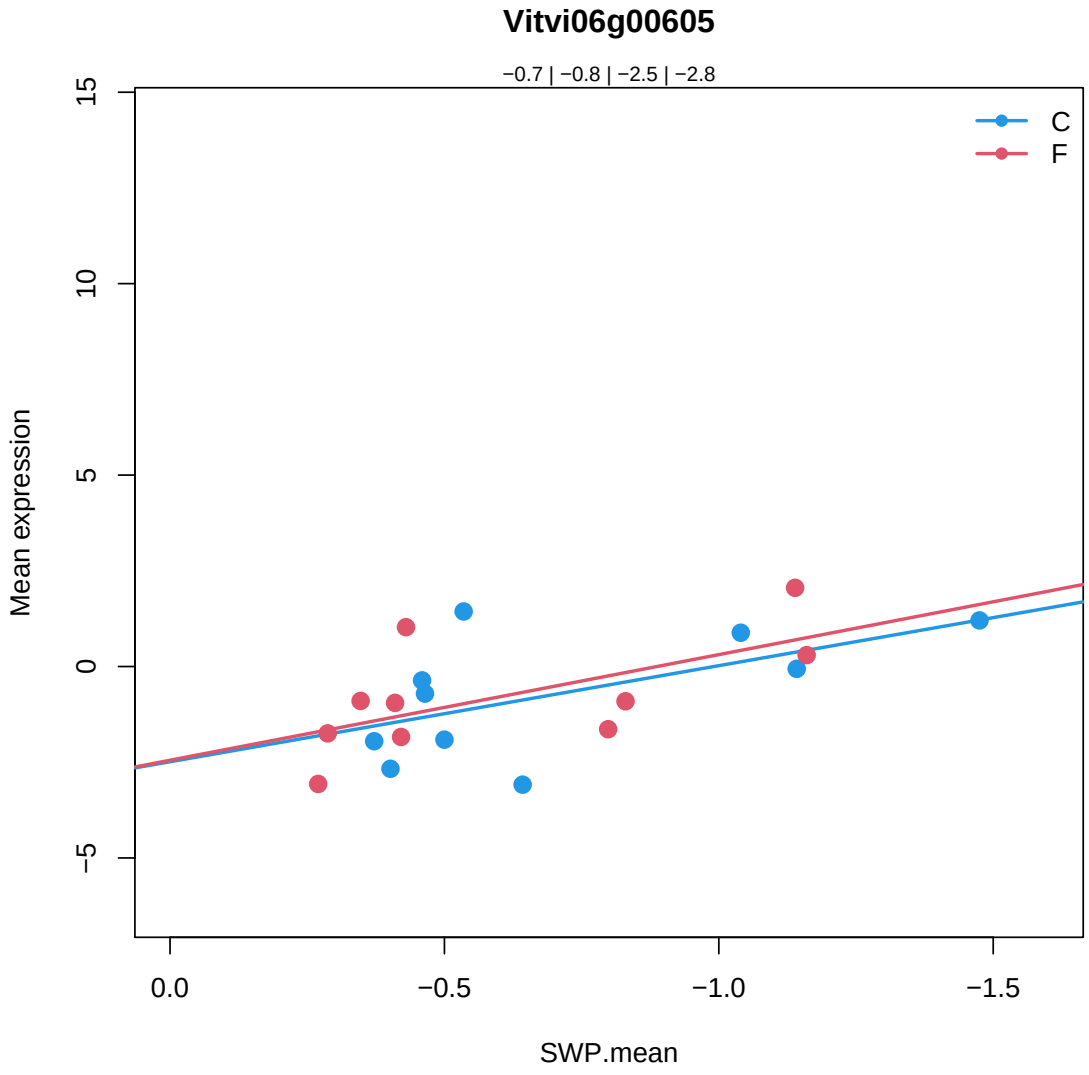
7.2.187 Vitvi06g00605: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00605
        26.10
        misc.cytochrome P450
        cytochrome P450%2C family 86%2C subfamily A%2C polypeptide 1 |
        Chr5:23765999-23767997 REVERSE LENGTH=513 |
        201606
```

Coefficients for Vitvi06g00605.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.7223887	0.06446106	.	0.06695622	.
SlopeC	-2.509662	0.02374058	*	0.3983963	
MeanF-MeanC	-0.04468309	0.9328475		0.981995	
SlopeF-SlopeC	-0.2491978	0.872519		0.9999488	



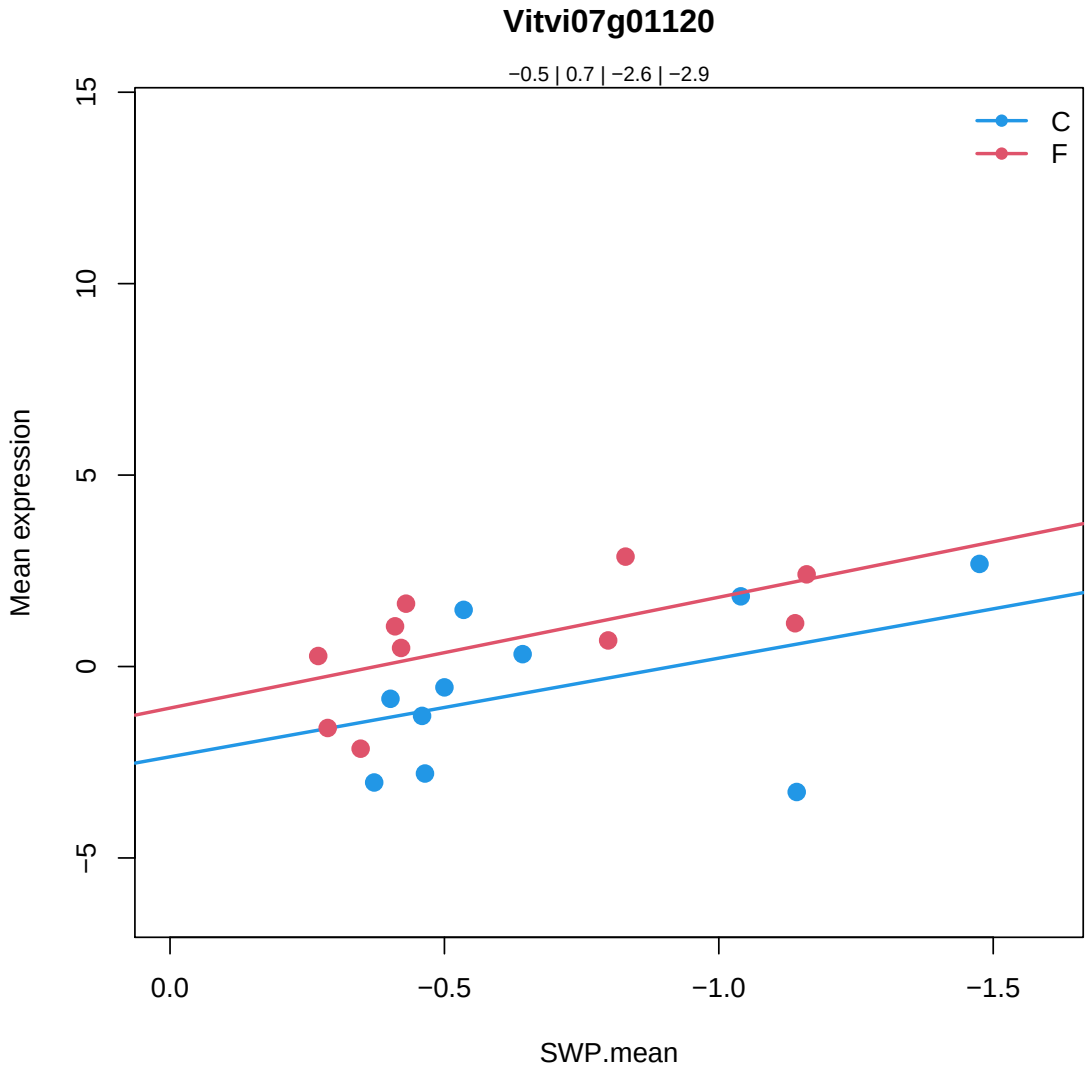
7.2.188 Vitvi07g01120: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01120
        35.2
        not assigned.unknown
        nuclear transport factor 2/RNA recognition motif protein |
        Chr3:2307289-2308326 REVERSE LENGTH=293 |
        201606
```

Coefficients for Vitvi07g01120.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	−0.5464727	0.2536031		0.2590069	
SlopeC	−2.576419	0.05972457	.	0.5396099	
MeanF−MeanC	1.225249	0.07667075	.	0.3124641	
SlopeF−SlopeC	−0.318679	0.8703226		0.9999488	



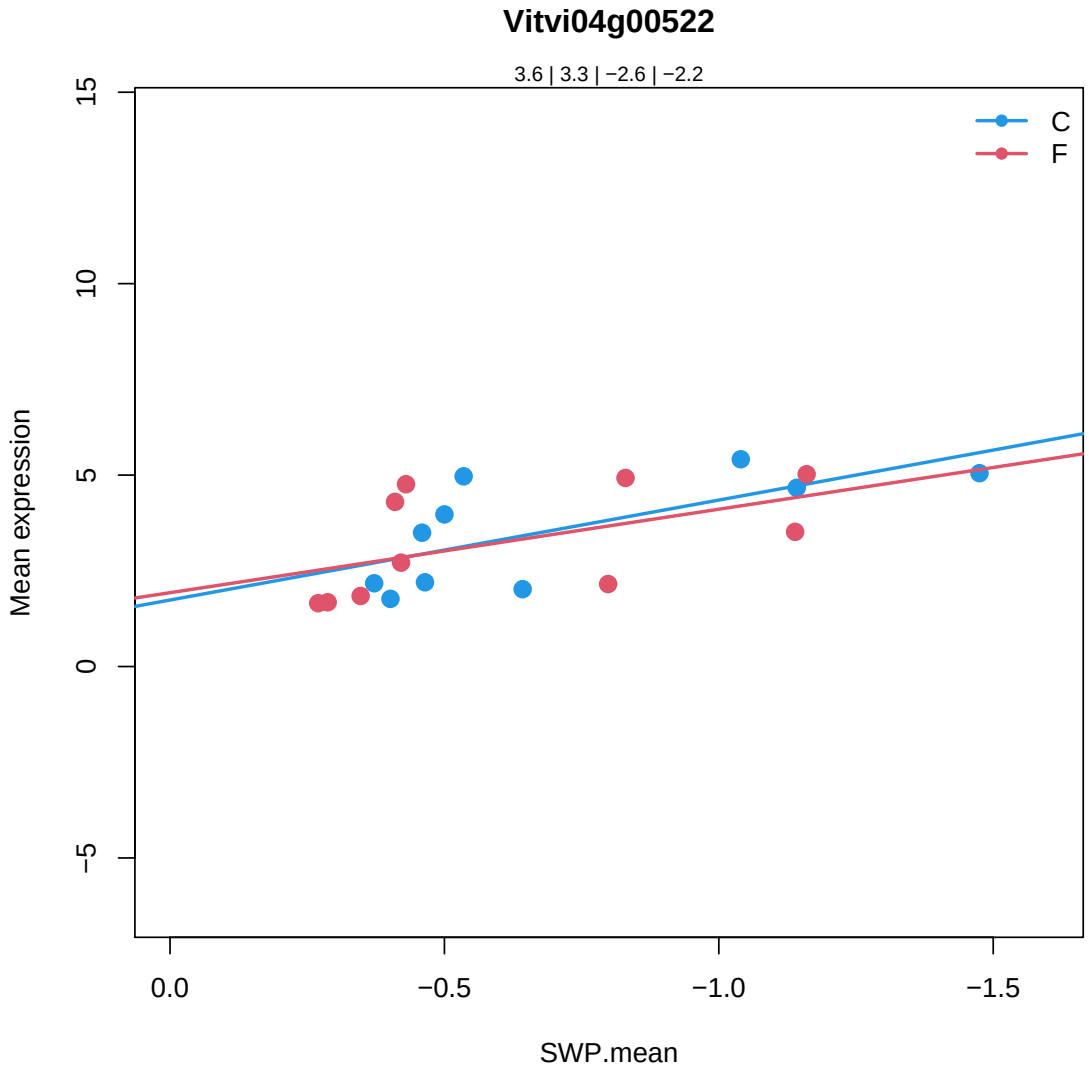
7.2.189 Vitvi04g00522: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00522
        20.2.1
        stress.abiotic.heat
        casein lytic proteinase B4 |
        Chr2:10697877-10701998 REVERSE LENGTH=964 |
        201606
```

Coefficients for Vitvi04g00522.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.572372	4.357544e-10	***	5.565884e-10	***
SlopeC	-2.610525	0.01012679	*	0.3042563	
MeanF-MeanC	-0.3157466	0.5093765		0.812391	
SlopeF-SlopeC	0.4302342	0.7578561		0.9999488	



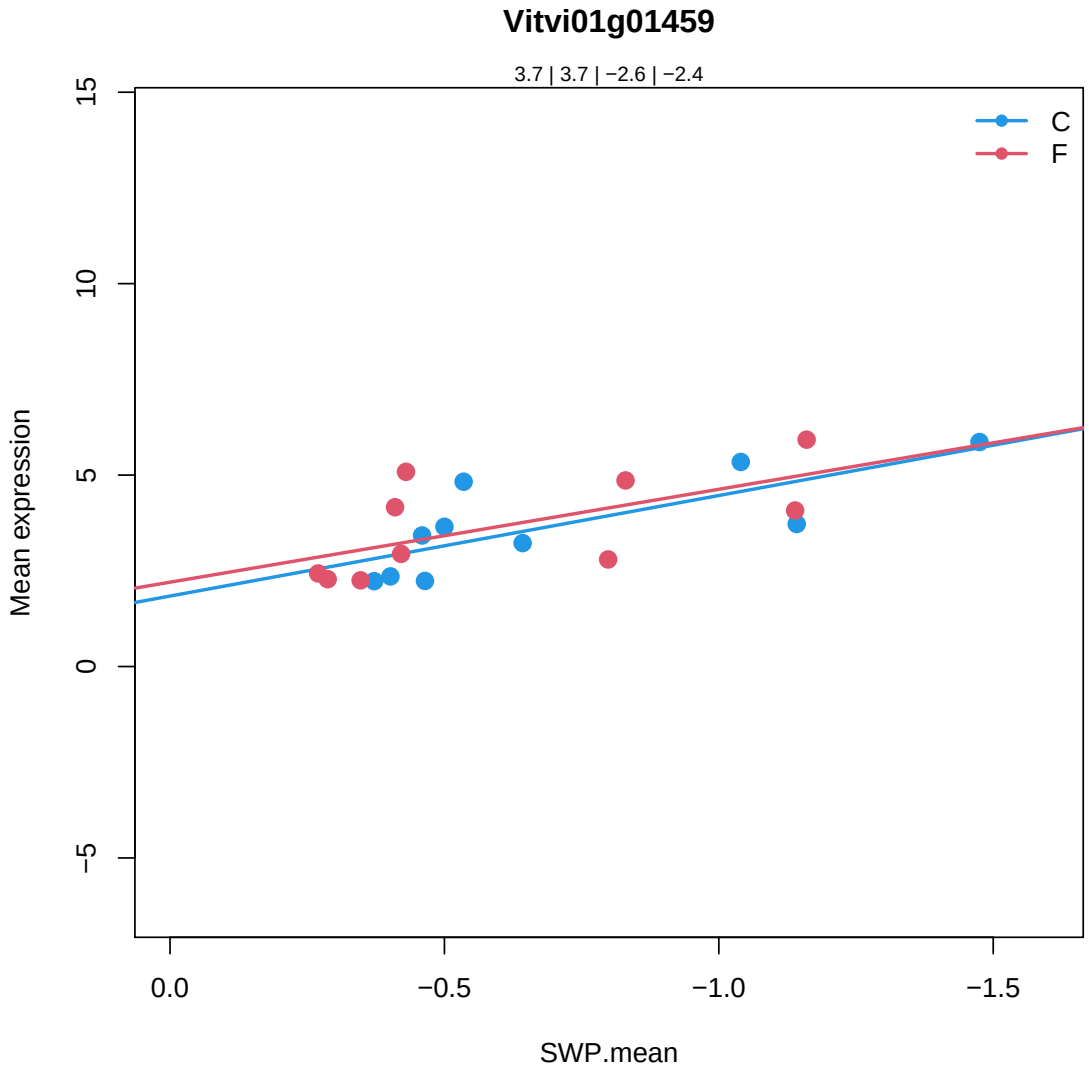
7.2.190 Vitvi01g01459: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01459
        17.1.3
        hormone metabolism.abscisic acid.induced-regulated-responsive-activate
        GRAM domain family protein |
        Chr5:4207081-4207812 FORWARD LENGTH=213 |
        201606
```

Coefficients for Vitvi01g01459.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.686915	1.001241e-11	***	1.366363e-11	***
SlopeC	-2.625931	0.002885634	**	0.2045713	
MeanF-MeanC	-0.006086896	0.9879085		0.9967265	
SlopeF-SlopeC	0.1996119	0.8652634		0.9999488	



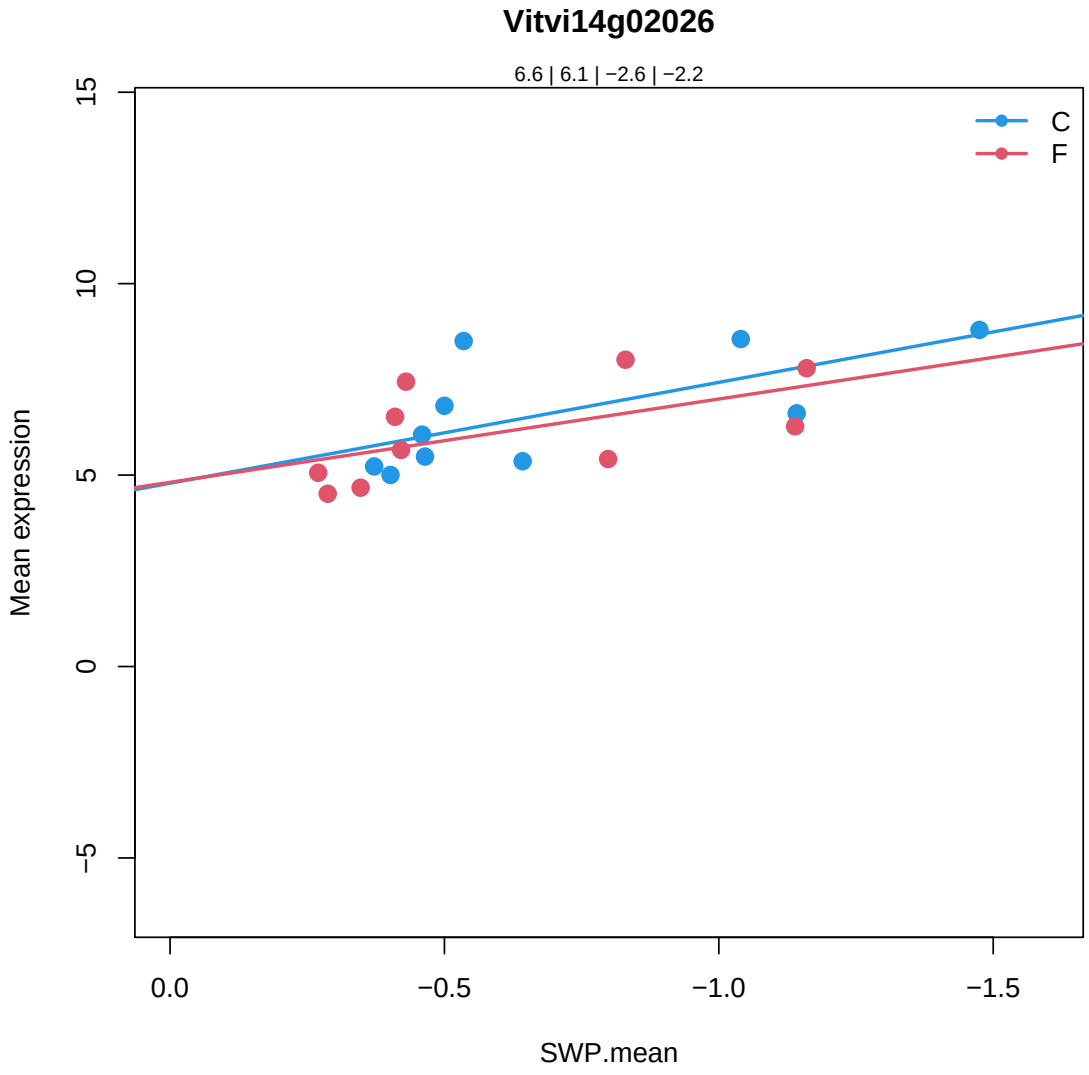
7.2.191 Vitvi14g02026: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g02026
        20.2.1
        stress.abiotic.heat
        casein lytic proteinase B3 |
        Chr5:5014399-5018255 REVERSE LENGTH=968 |
        201606
```

Coefficients for Vitvi14g02026.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.639492	1.082566e-15	***	2.018406e-15	***
SlopeC	-2.634207	0.007307227	**	0.2775469	
MeanF-MeanC	-0.5036664	0.2773301		0.6412508	
SlopeF-SlopeC	0.4582077	0.7324697		0.9999488	



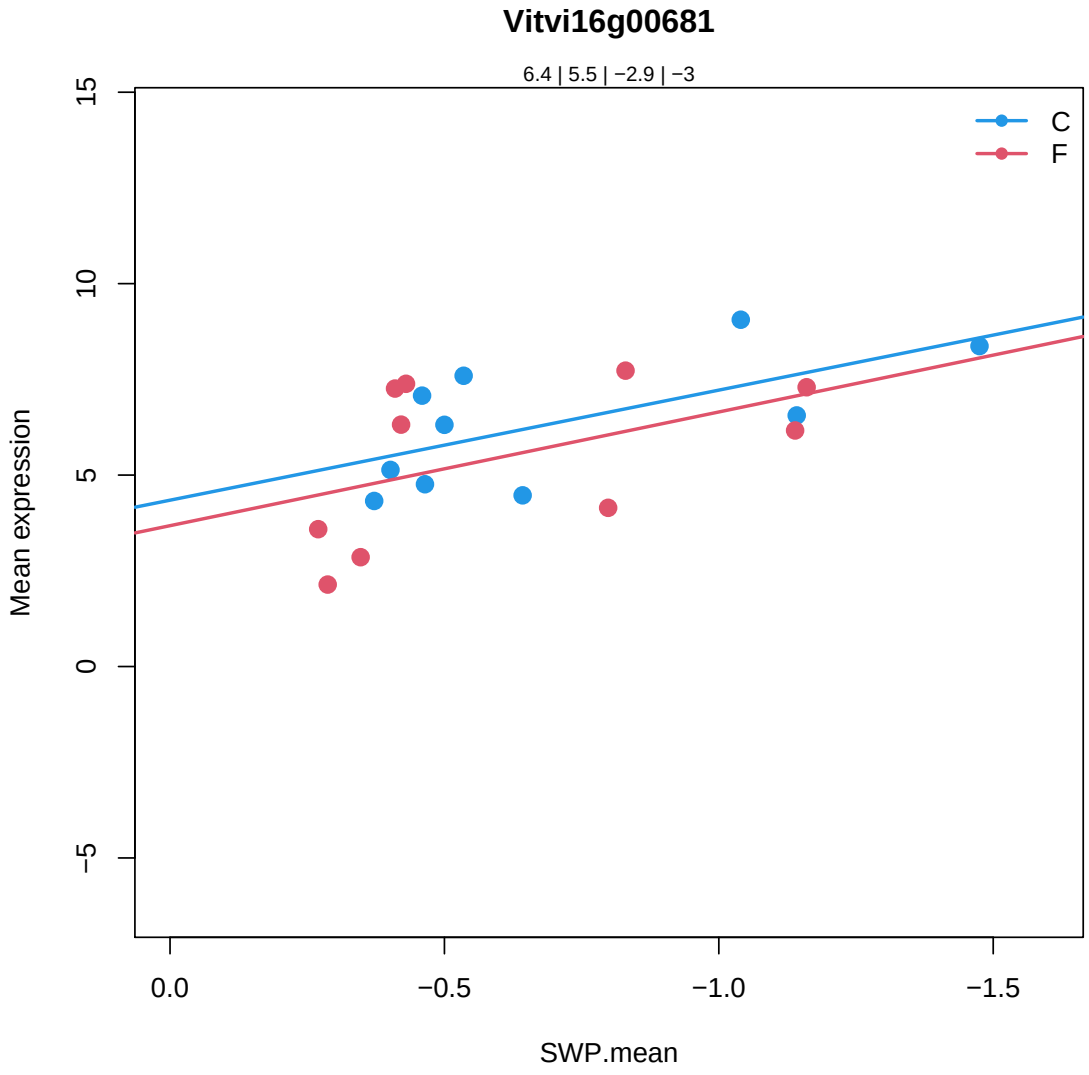
7.2.192 Vitvi16g00681: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g00681
        20.2.1
        stress.abiotic.heat
        mitochondrion-localized small heat shock protein 23.6 |
        Chr4:12917089-12917858 FORWARD LENGTH=210 |
        201606
```

Coefficients for Vitvi16g00681.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.365536	4.303294e-12	***	5.964428e-12	***
SlopeC	-2.874618	0.03674623	*	0.4602035	
MeanF-MeanC	-0.8780277	0.1947686		0.5358599	
SlopeF-SlopeC	-0.09509428	0.9609728		0.9999488	



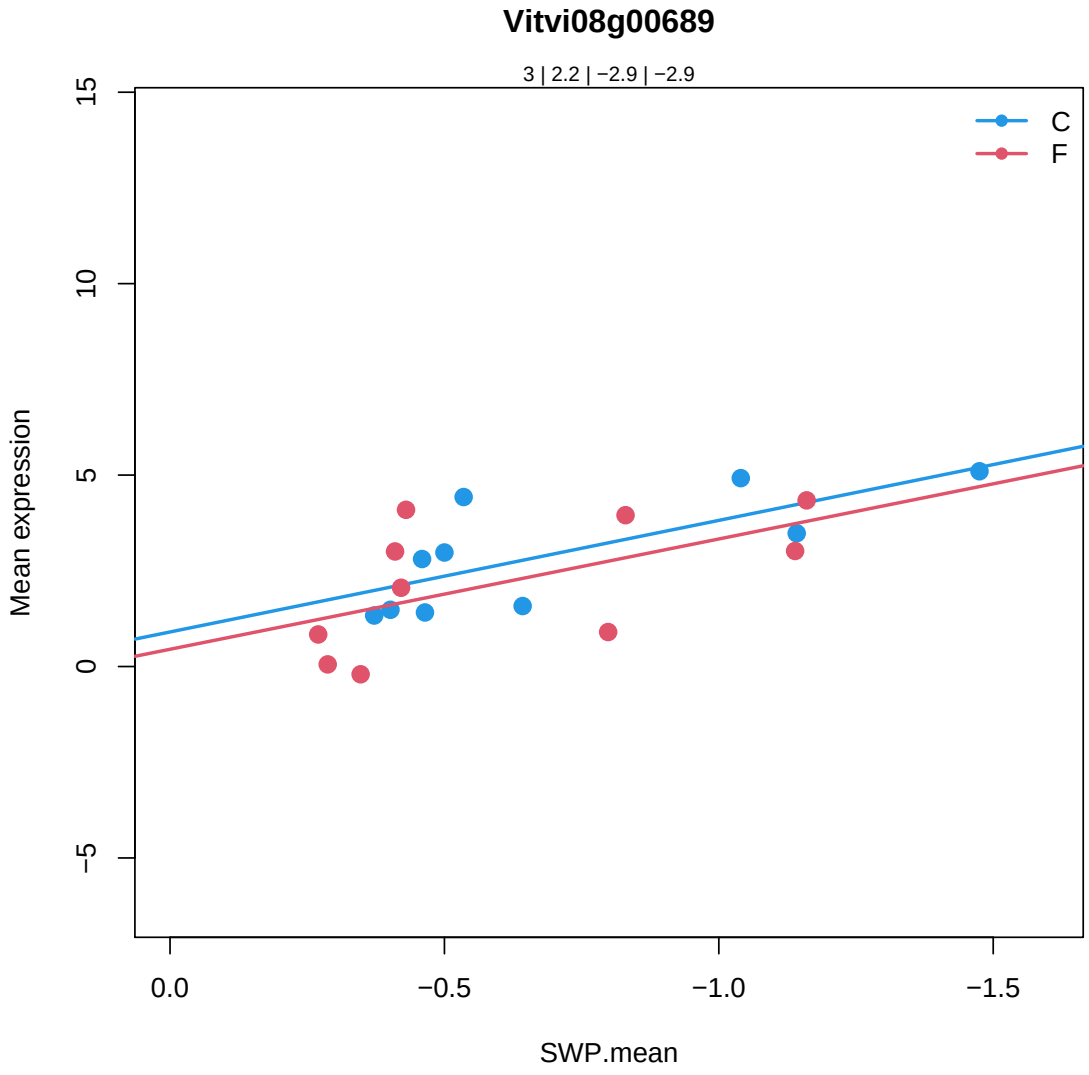
7.2.193 Vitvi08g00689: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g00689
        20.2.1
        stress.abiotic.heat
        DNAJ heat shock N-terminal domain-containing protein |
        Chr3:2737589-2740265 FORWARD LENGTH=572 |
        201606
```

Coefficients for Vitvi08g00689.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.951604	5.060499e-08	***	6.049579e-08	***
SlopeC	-2.914322	0.008477063	**	0.2890546	
MeanF-MeanC	-0.7461071	0.1588471		0.4815329	
SlopeF-SlopeC	0.03394978	0.9821109		0.9999488	



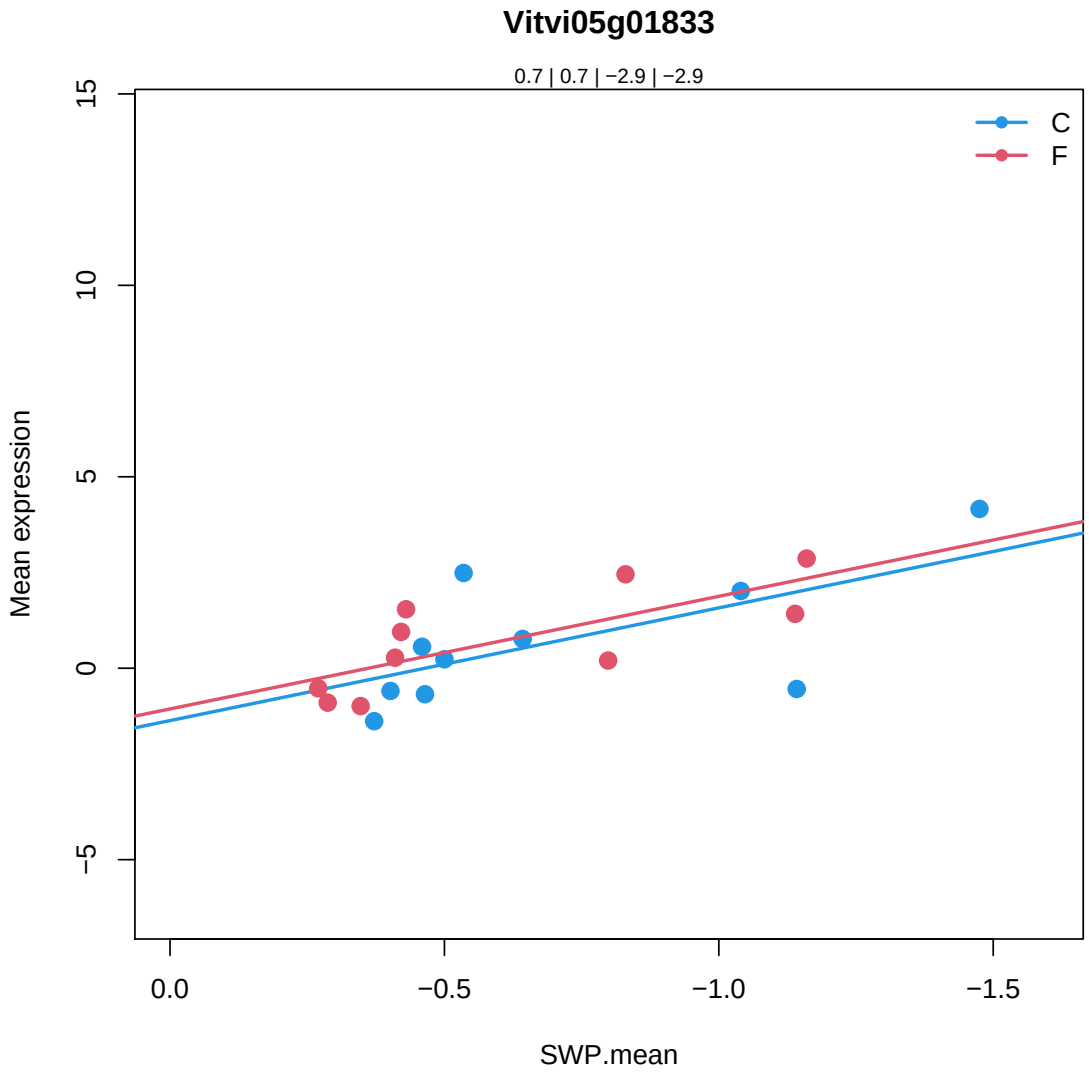
7.2.194 Vitvi05g01833: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01833
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi05g01833.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.7023488	0.0473538	*	0.04934819	*
SlopeC	-2.943432	0.004540305	**	0.2419697	
MeanF-MeanC	0.02632047	0.9560566		0.9899375	
SlopeF-SlopeC	0.002075687	0.9988158		0.9999488	



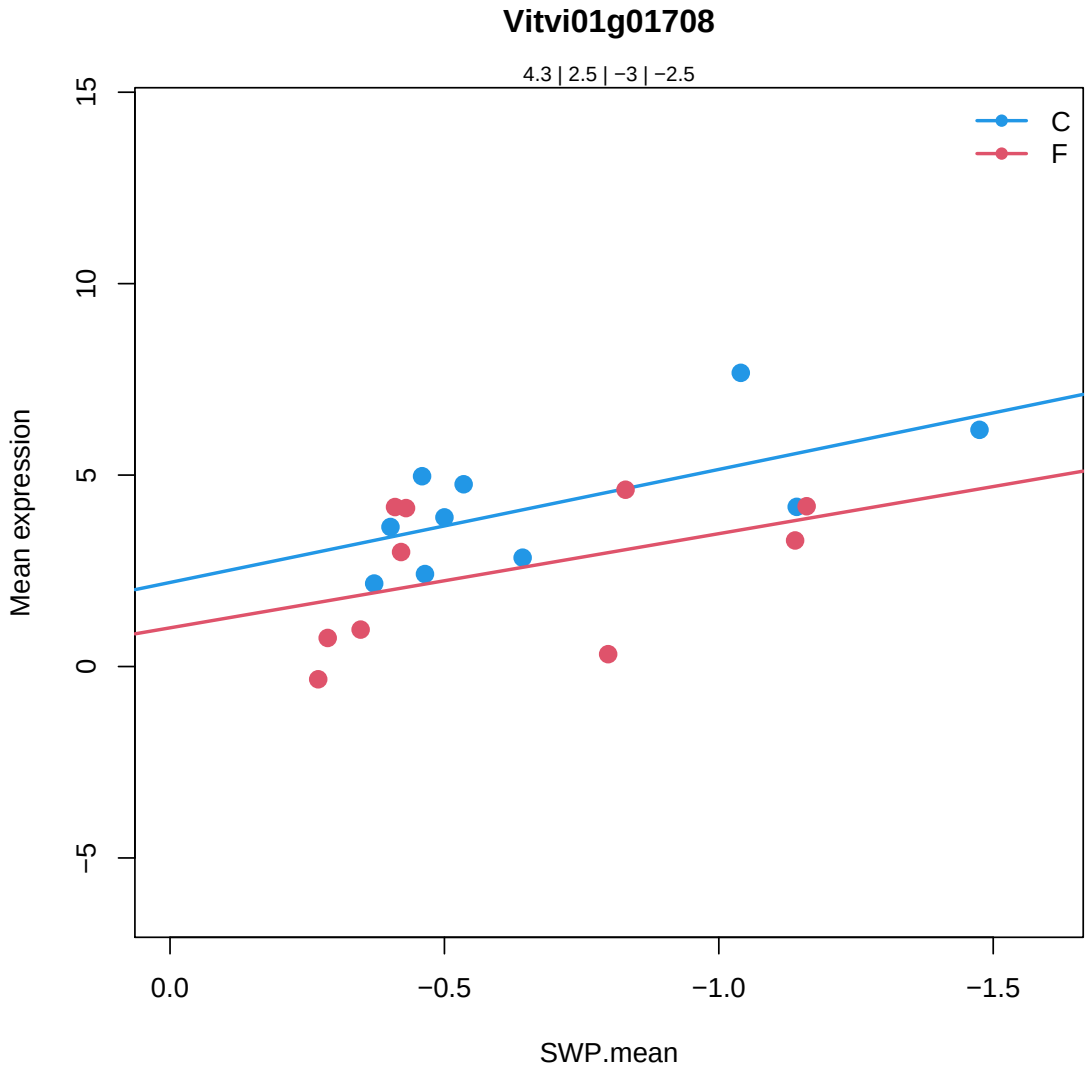
7.2.195 Vitvi01g01708: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01708
        20.2.1
        stress.abiotic.heat
        BCL-2-associated athanogene 5 |
        Chr1:4076334-4076981 FORWARD LENGTH=215 |
        201606
```

Coefficients for Vitvi01g01708.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.271601	2.851353e-09	***	3.543732e-09	***
SlopeC	-2.952446	0.02543851	*	0.4079655	
MeanF-MeanC	-1.762888	0.01009625	*	0.07663695	.
SlopeF-SlopeC	0.4926336	0.7902962		0.9999488	



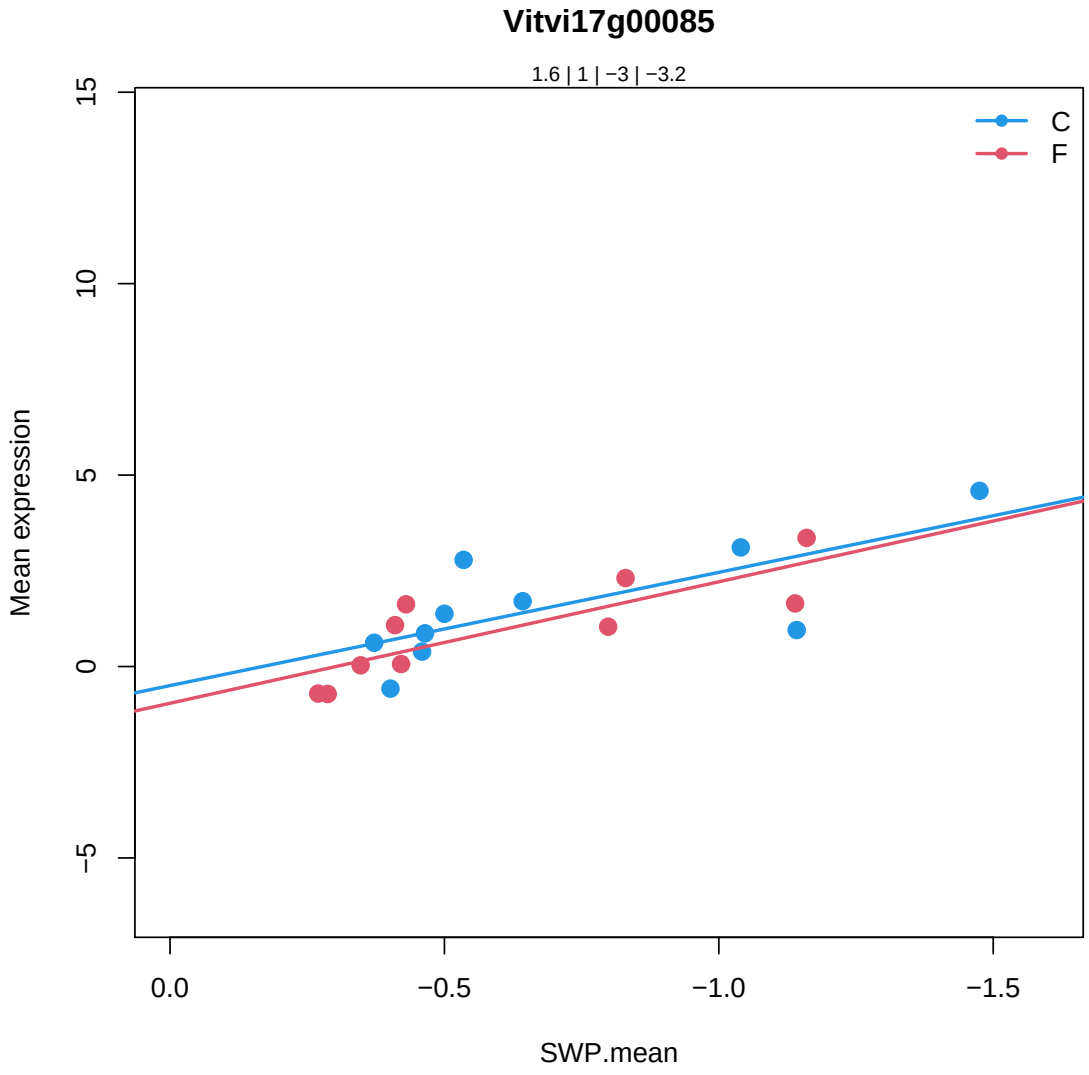
7.2.196 Vitvi17g00085: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00085
        17.1.3
        hormone metabolism.abscisic acid.induced-regulated-responsive-activate
        HVA22 homologue D |
        Chr4:12828237-12829019 FORWARD LENGTH=135 |
        201606
```

Coefficients for Vitvi17g00085.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.581834	8.293491e-06	***	9.383817e-06	***
SlopeC	-2.957952	0.0007828248	***	0.1097382	
MeanF-MeanC	-0.608472	0.1283374		0.4255208	
SlopeF-SlopeC	-0.2145244	0.8507385		0.9999488	



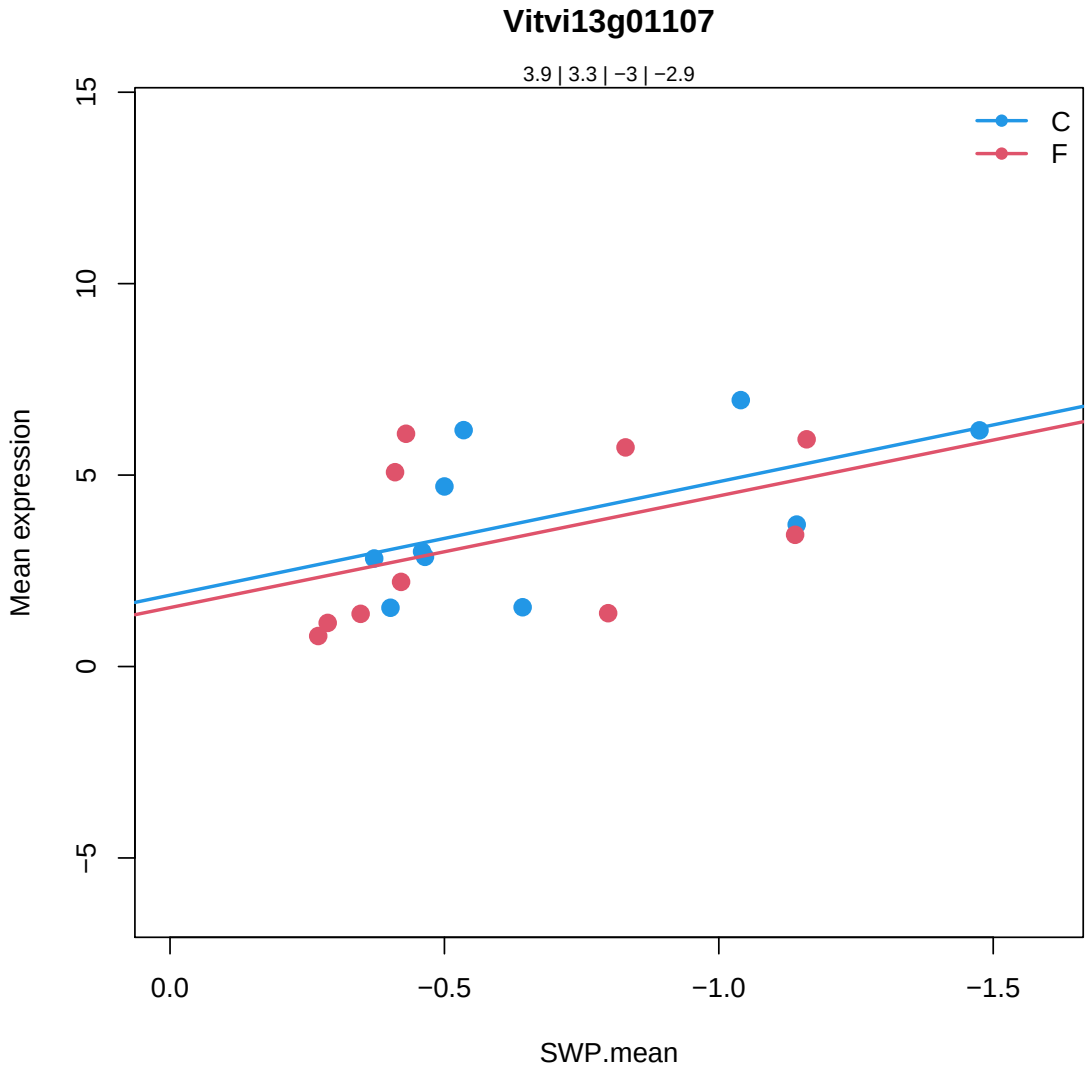
7.2.197 Vitvi13g01107: type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g01107
        35.2
        not assigned.unknown
        HSP20-like chaperones superfamily protein |
        Chr3:951885-953490 FORWARD LENGTH=150 |
        201606
```

Coefficients for Vitvi13g01107.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.94795	1.781634e-07	***	2.098907e-07	***
SlopeC	-2.964306	0.05399201	.	0.5205226	
MeanF-MeanC	-0.6315872	0.4022459		0.7465943	
SlopeF-SlopeC	0.04693335	0.9828977		0.9999488	



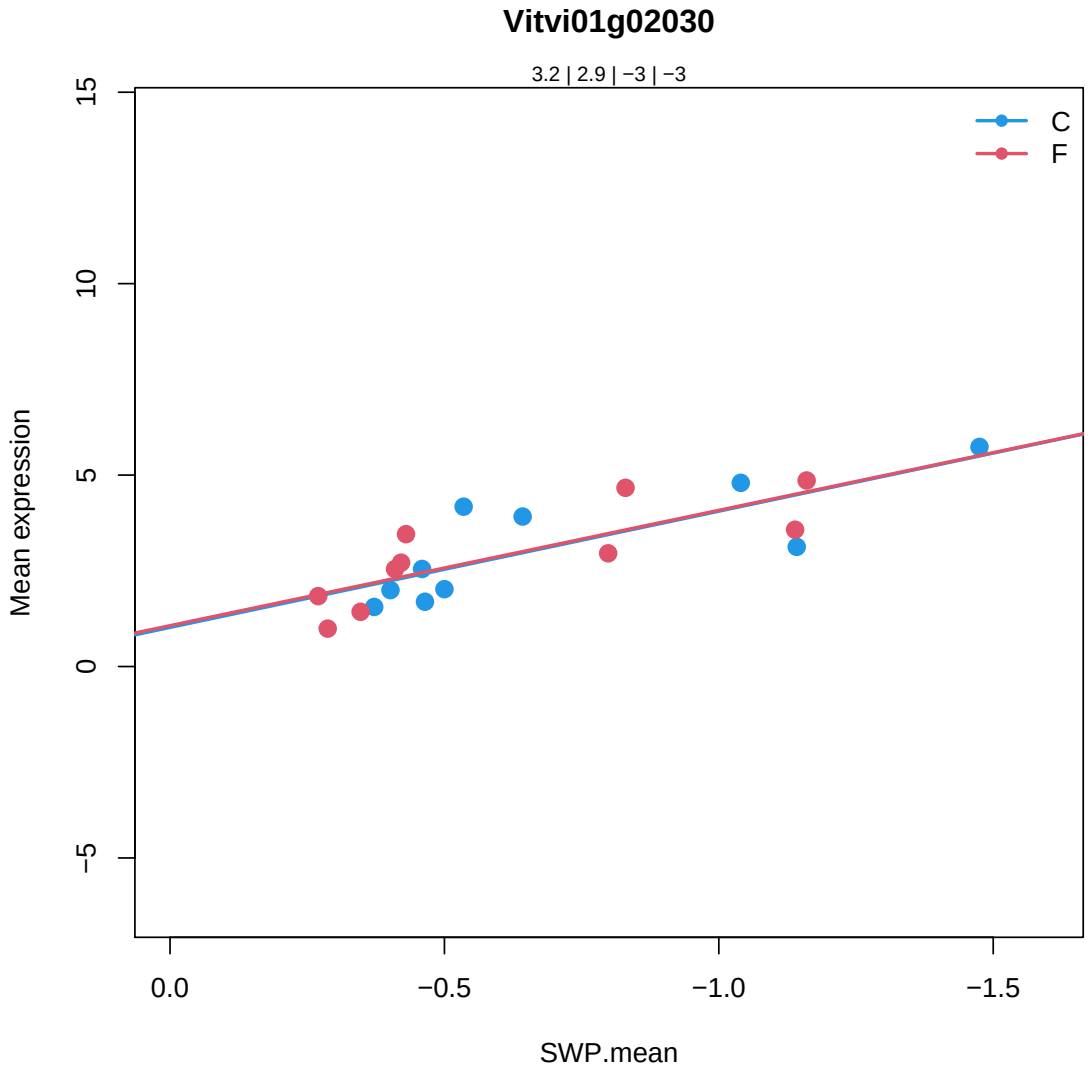
7.2.198 Vitvi01g02030: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g02030
        29.5.11.4.2
        protein.degradation.ubiquitin.E3.RING
        RING/U-box superfamily protein |
        Chr1:25442486-25442887 FORWARD LENGTH=133 |
        201606
```

Coefficients for Vitvi01g02030.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.155968	1.931528e-11	***	2.603728e-11	***
SlopeC	-3.035038	0.0002471739	***	0.08263916	.
MeanF-MeanC	-0.2534253	0.4789676		0.7941132	
SlopeF-SlopeC	0.02234586	0.9828888		0.9999488	



7.2.199 Vitvi13g01839: * type1

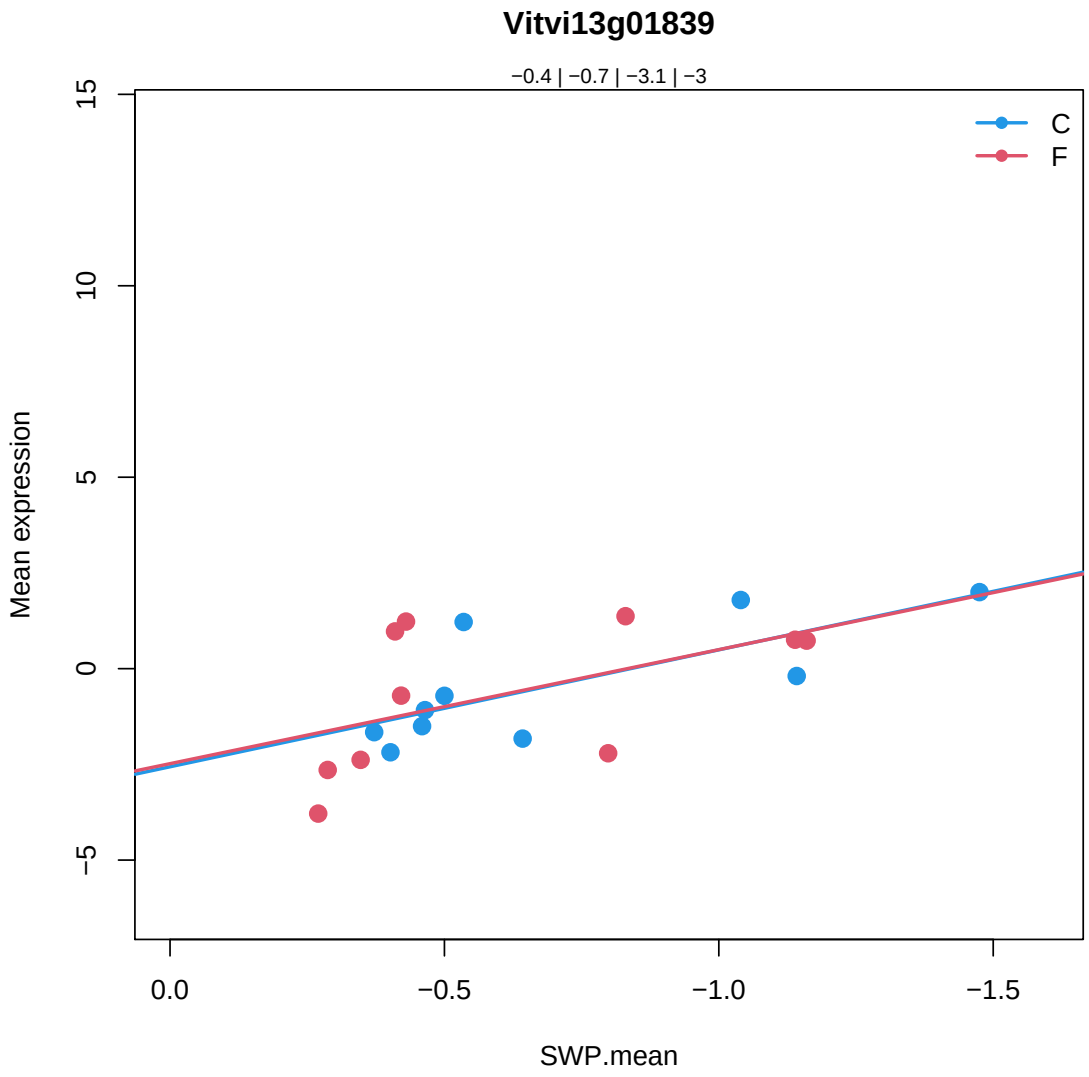
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g01839
        26.21
        misc.protease inhibitor/seed storage/lipid transfer protein (LTP) fami
        Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin
        Chr2:18305418-18306202 REVERSE LENGTH=205 |
        201606

Vitvi13g01839
        11.6
        lipid metabolism.lipid transfer proteins etc
        Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin
        Chr2:18305418-18306202 REVERSE LENGTH=205 |
        201606
```

Coefficients for Vitvi13g01839.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.4151178	0.3157402		0.321477	
SlopeC	-3.054071	0.01277848	*	0.3284478	
MeanF-MeanC	-0.2519902	0.6636665		0.8886547	
SlopeF-SlopeC	0.07550815	0.9644251		0.9999488	


Vitvi13g01839
−0.4 | −0.7 | −3.1 | −3
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

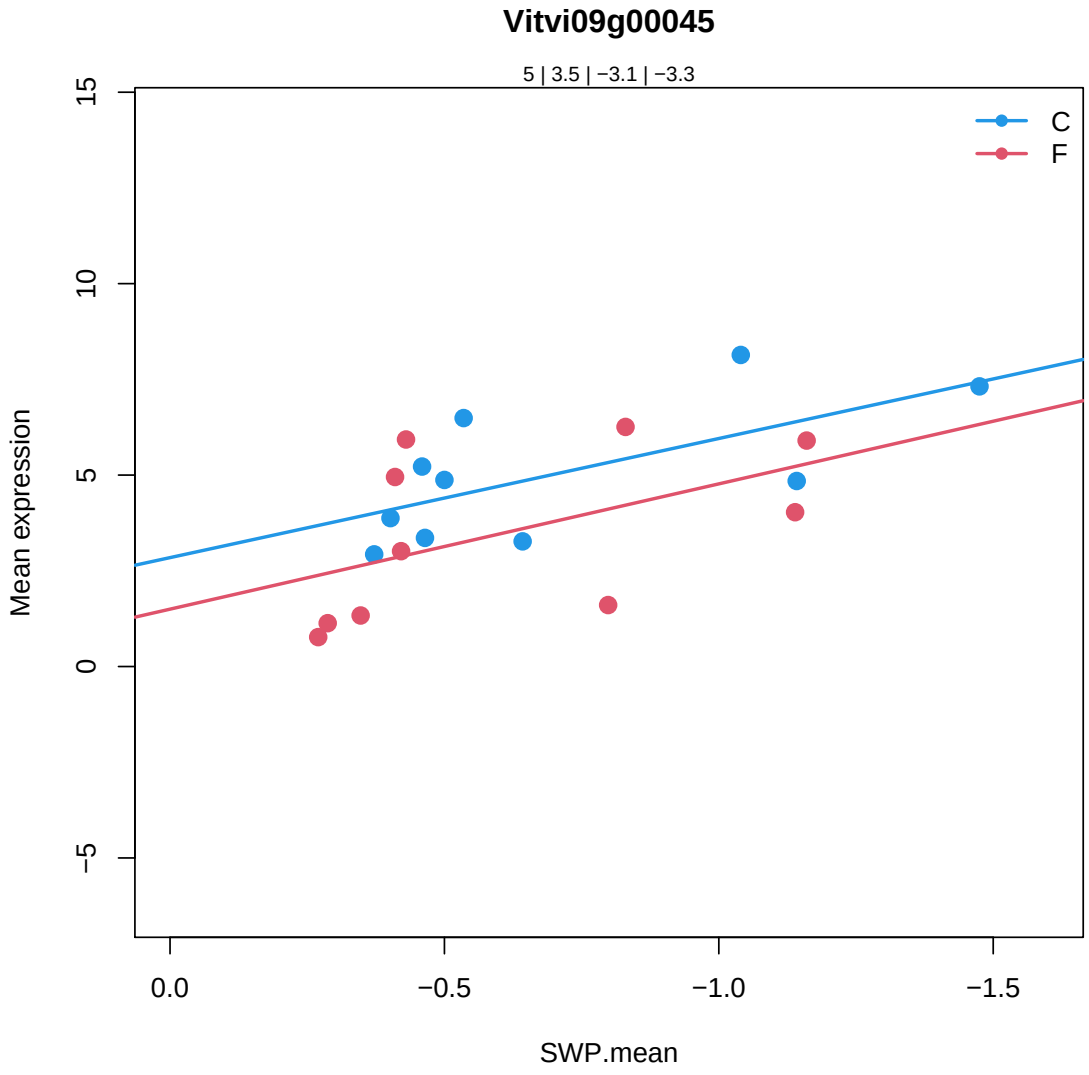
7.2.200 Vitvi09g00045: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00045
        20.2.1
        stress.abiotic.heat
        HSP20-like chaperones superfamily protein |
        Chr1:20179558-20180122 REVERSE LENGTH=155 |
        201606
```

Coefficients for Vitvi09g00045.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.031606	6.76044e-10	***	8.576166e-10	***
SlopeC	-3.111025	0.02970244	*	0.4299803	
MeanF-MeanC	-1.539846	0.03378118	*	0.1831436	
SlopeF-SlopeC	-0.1609299	0.9362353		0.9999488	



7.2.201 Vitvi06g00533: * type1

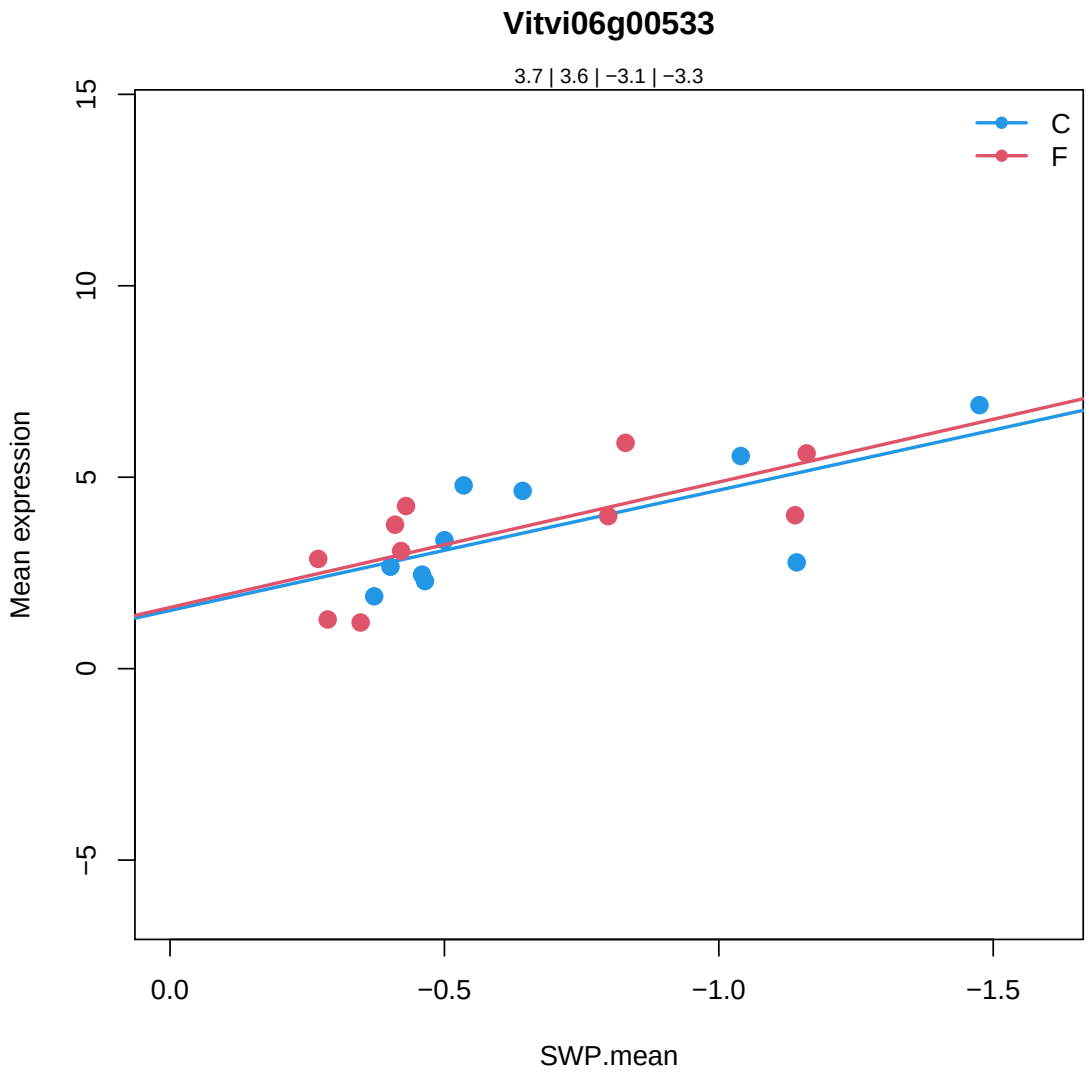
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00533
        29.4
        protein.postranslational modification
        highly ABA-induced PP2C protein 3 |
        Chr2:12608855-12610124 FORWARD LENGTH=362 |
        201606

Vitvi06g00533
        17.1.2
        hormone metabolism.abscisic acid.signal transduction
        highly ABA-induced PP2C protein 3 |
        Chr2:12608855-12610124 FORWARD LENGTH=362 |
        201606
```

Coefficients for Vitvi06g00533.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.728735	1.948614e-10	***	2.522359e-10	***
SlopeC	-3.141484	0.002657744	**	0.1966472	
MeanF-MeanC	-0.1342722	0.7778878		0.9365376	
SlopeF-SlopeC	-0.1347465	0.9229198		0.9999488	


Vitvi06g00533
3.7 | 3.6 | −3.1 | −3.3
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

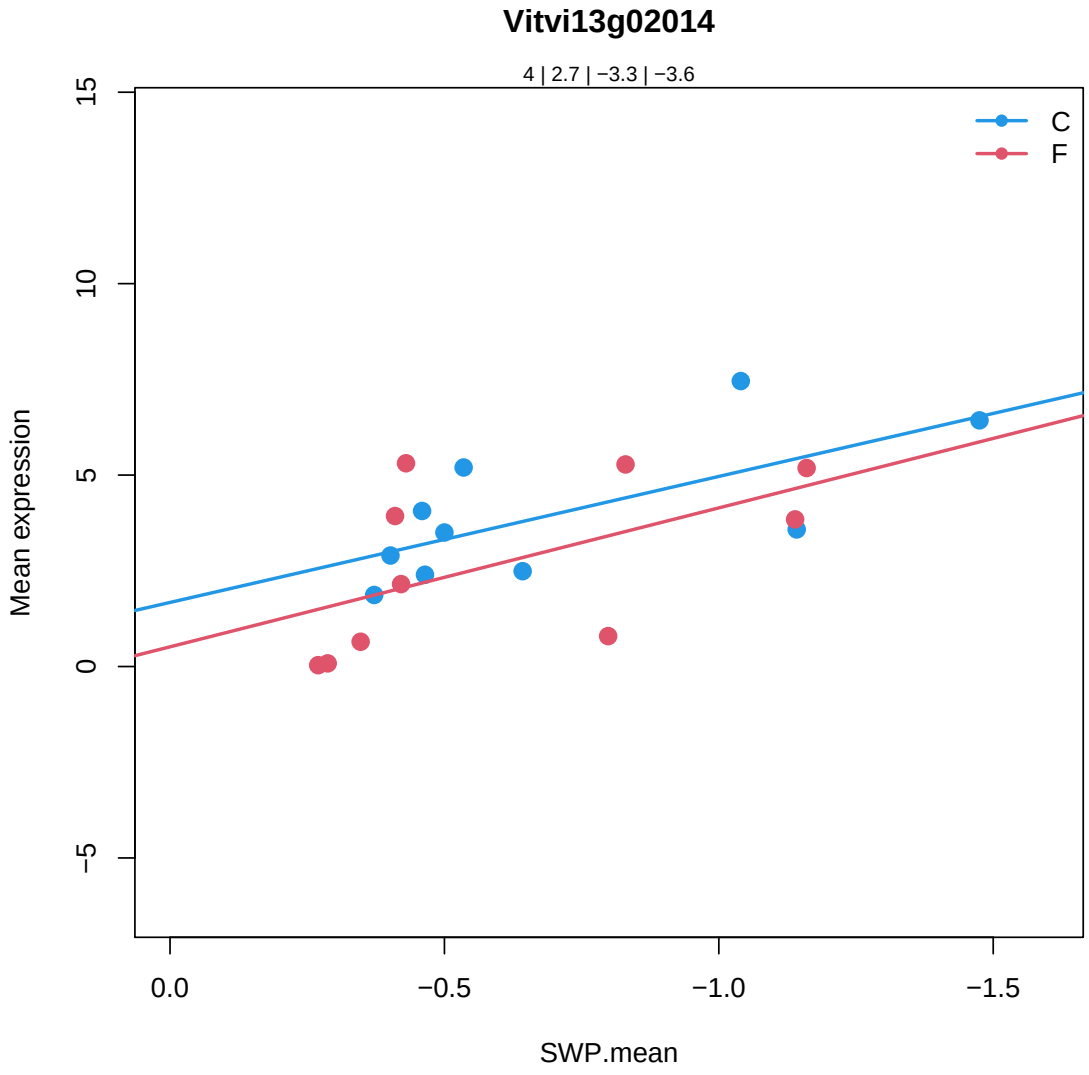
7.2.202 Vitvi13g02014: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g02014
        20.2.1
        stress.abiotic.heat
        heat shock protein 18.2 |
        Chr5:24062632-24063117 FORWARD LENGTH=161 |
        201606
```

Coefficients for Vitvi13g02014.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.987802	3.089219e-08	***	3.715155e-08	***
SlopeC	-3.29079	0.02078355	*	0.378927	
MeanF-MeanC	-1.26242	0.07326951	.	0.3040495	
SlopeF-SlopeC	-0.3375916	0.8650362		0.9999488	



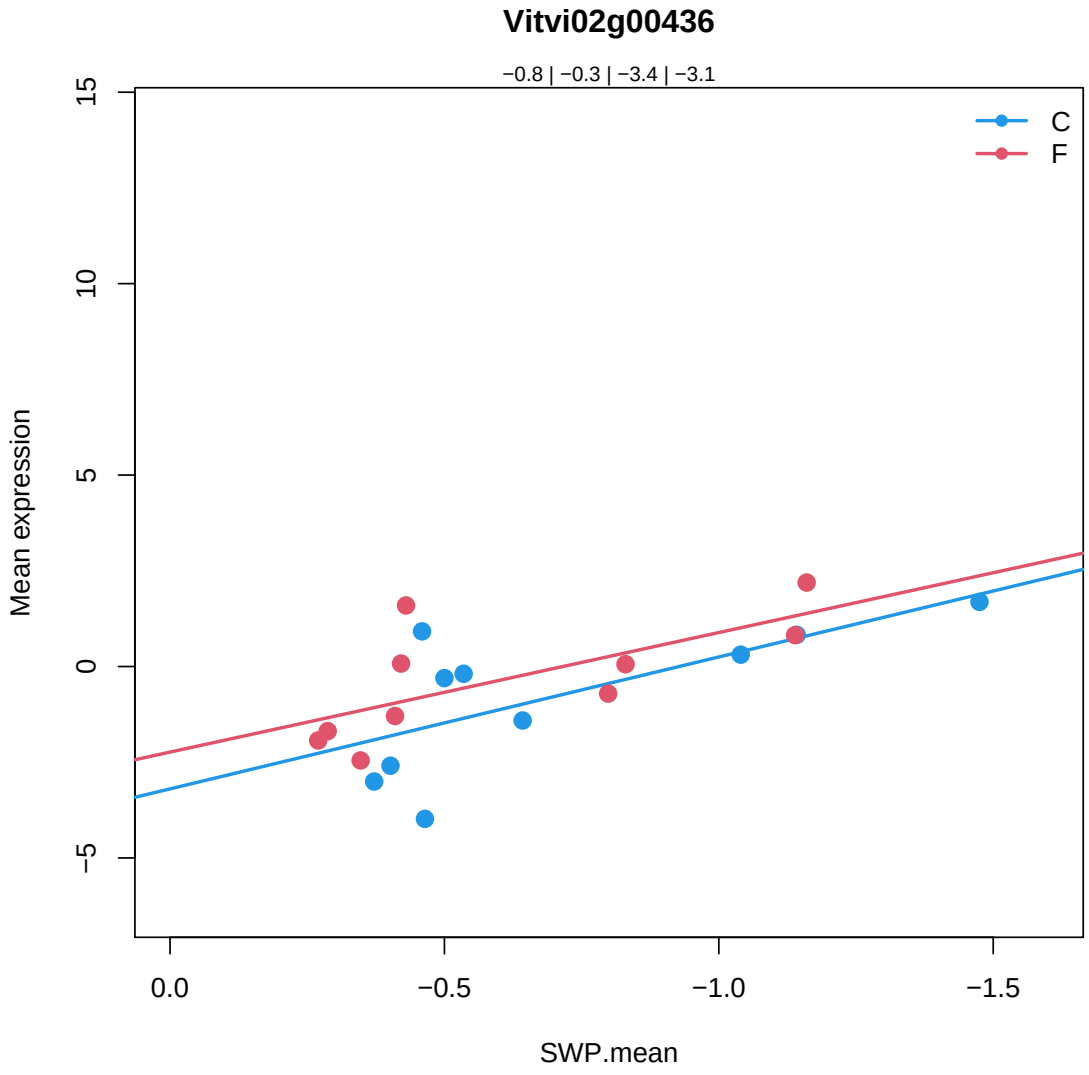
7.2.203 Vitvi02g00436: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00436
        1.2.6
        PS.photorespiration.hydroxypyruvate reductase
        D-isomer specific 2-hydroxyacid dehydrogenase family protein |
        Chr1:4274649-4275831 FORWARD LENGTH=323 |
        201606
```

Coefficients for Vitvi02g00436.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.7732662	0.04915228	*	0.05118742	.
SlopeC	-3.44536	0.003042667	**	0.2098476	
MeanF-MeanC	0.4405752	0.4100686		0.7507664	
SlopeF-SlopeC	0.3224828	0.8356227		0.9999488	



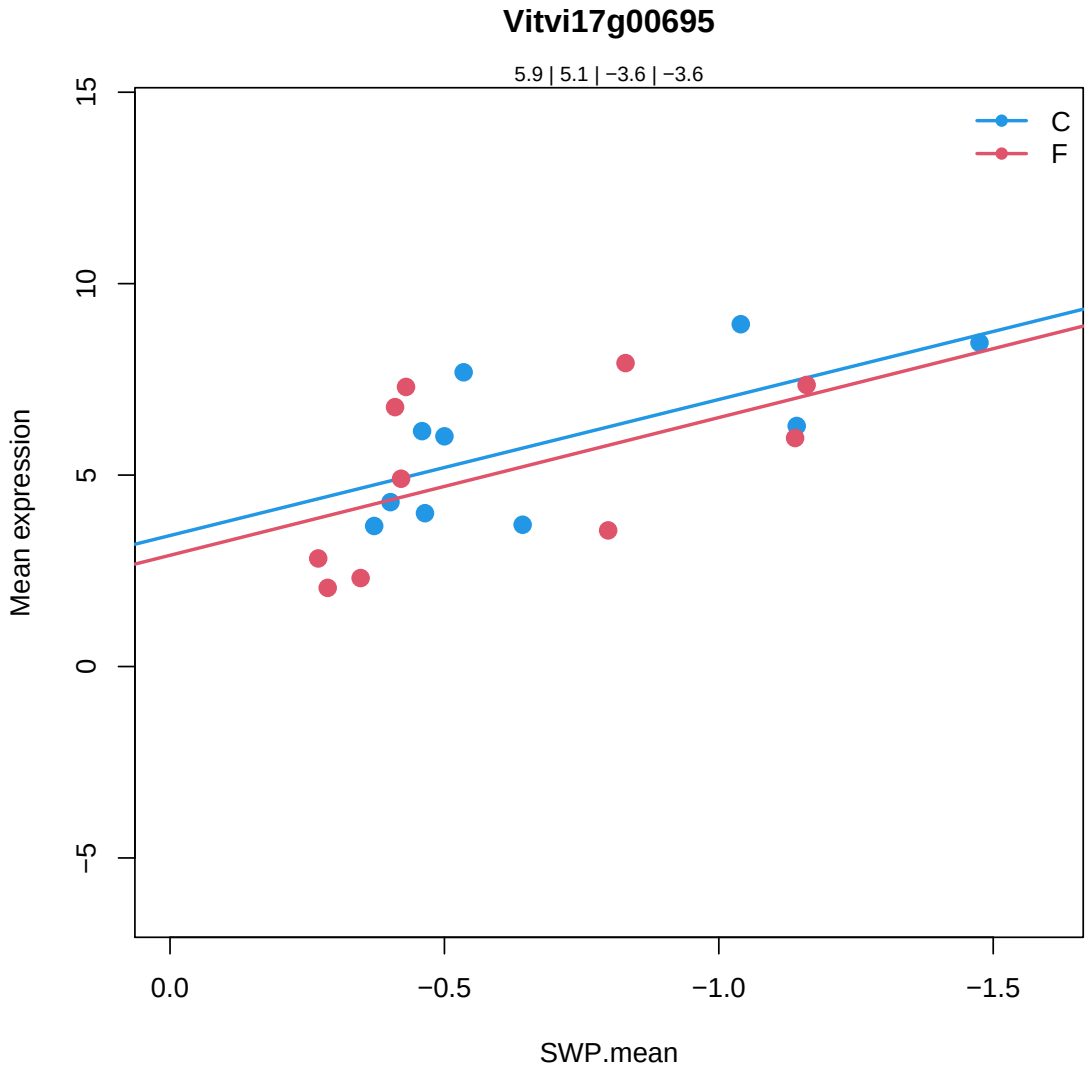
7.2.204 Vitvi17g00695: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00695
        20.2.1
        stress.abiotic.heat
        heat shock protein 101 |
        Chr1:27936715-27939862 REVERSE LENGTH=911 |
        201606
```

Coefficients for Vitvi17g00695.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.919457	5.917164e-11	***	7.808607e-11	***
SlopeC	-3.552929	0.01728155	*	0.3551322	
MeanF-MeanC	-0.822455	0.252864		0.6127344	
SlopeF-SlopeC	-0.04441921	0.9829086		0.9999488	



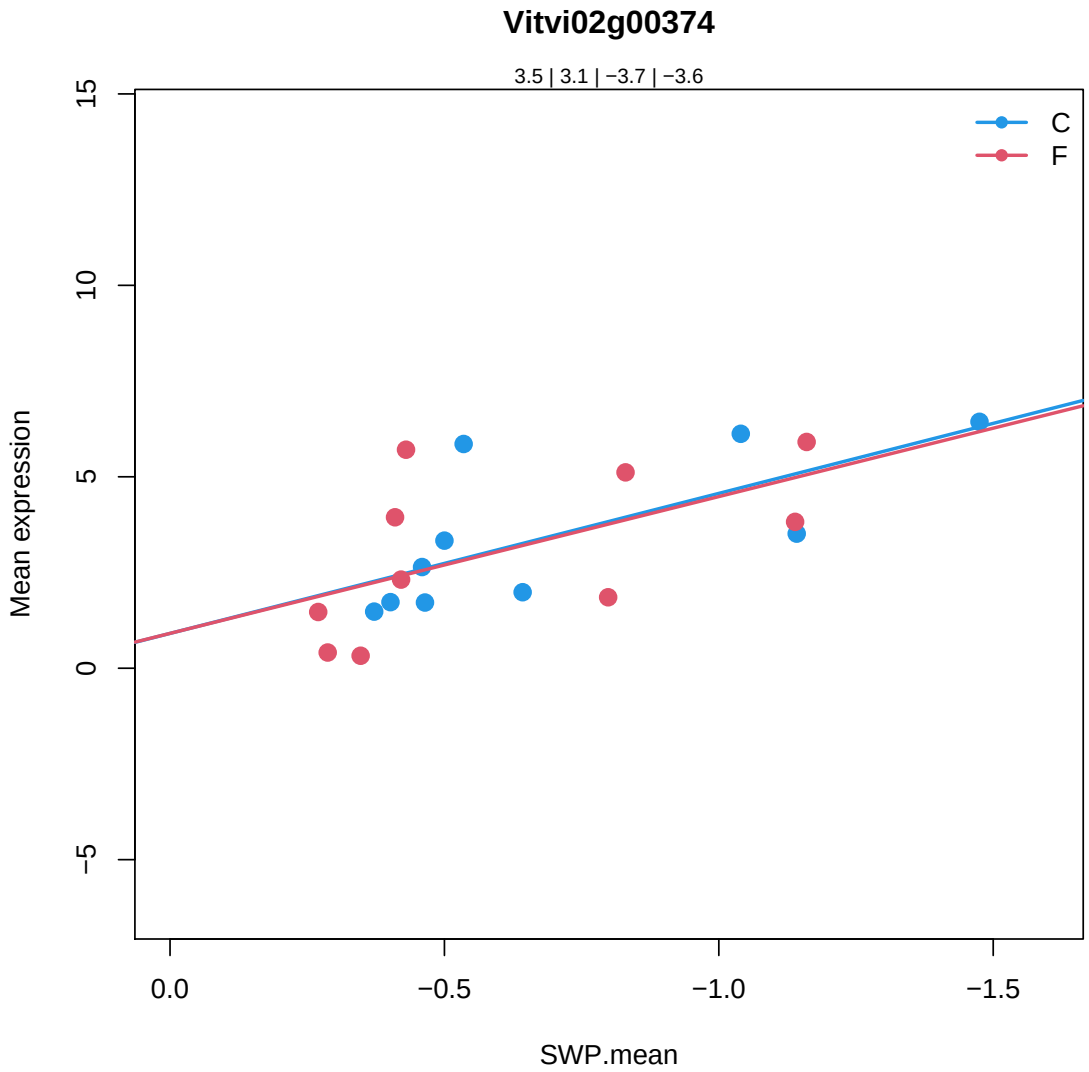
7.2.205 Vitvi02g00374: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00374
        29.5.11
        protein.degradation.ubiquitin
        UBX domain-containing protein IPR001012 UBX
```

Coefficients for Vitvi02g00374.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.480907	1.548508e-07	***	1.828223e-07	***
SlopeC	-3.65719	0.008877934	**	0.2903326	
MeanF-MeanC	-0.3940523	0.548229		0.832362	
SlopeF-SlopeC	0.08429943	0.96486		0.9999488	



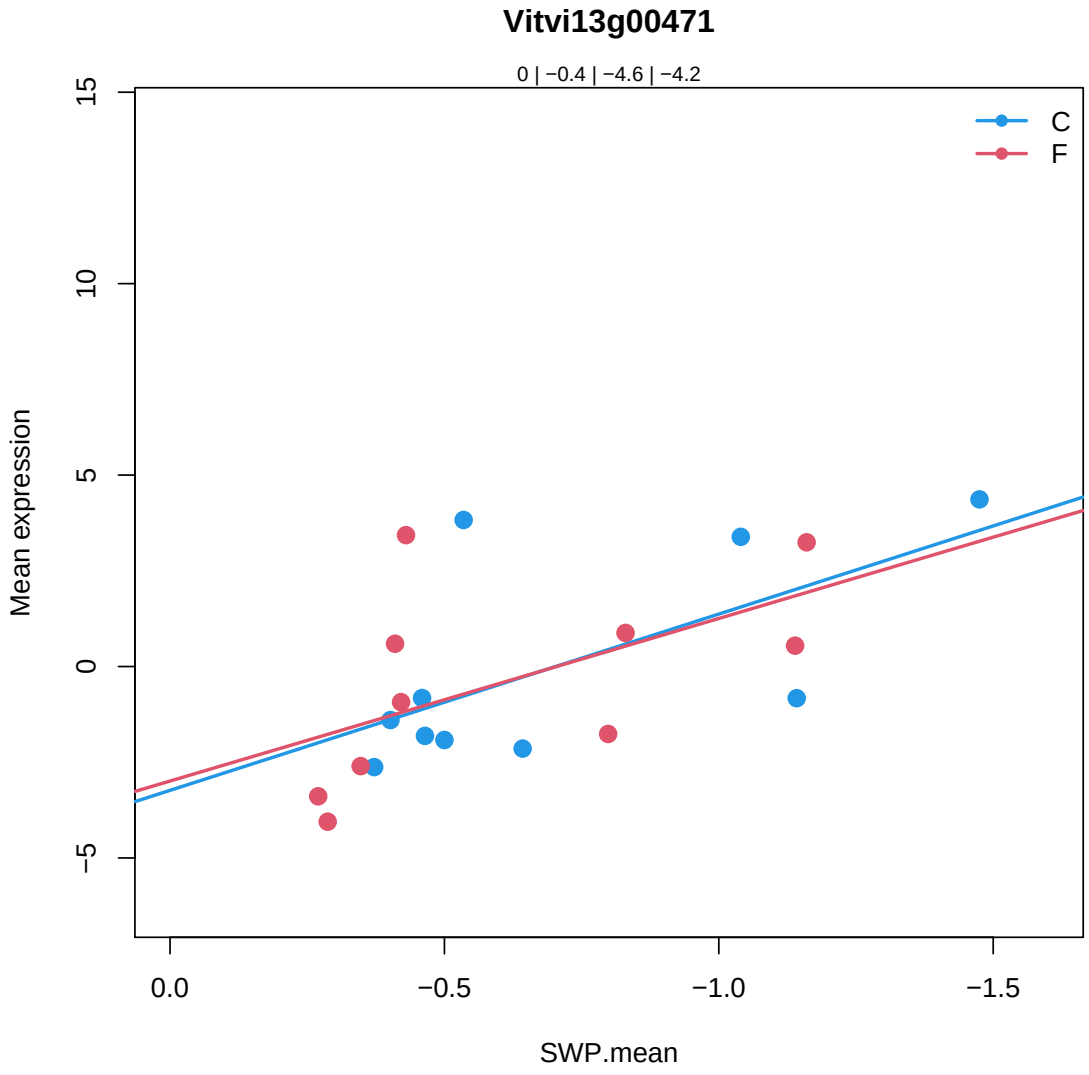
7.2.206 Vitvi13g00471: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00471
        20.2.1
        stress.abiotic.heat
        heat shock protein 18.2 |
        Chr5:24062632-24063117 FORWARD LENGTH=161 |
        201606
```

Coefficients for Vitvi13g00471.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.00289999	0.9963119		0.9965734	
SlopeC	-4.604229	0.01421304	*	0.3359386	
MeanF-MeanC	-0.4070974	0.6471743		0.8804711	
SlopeF-SlopeC	0.3580492	0.8904042		0.9999488	



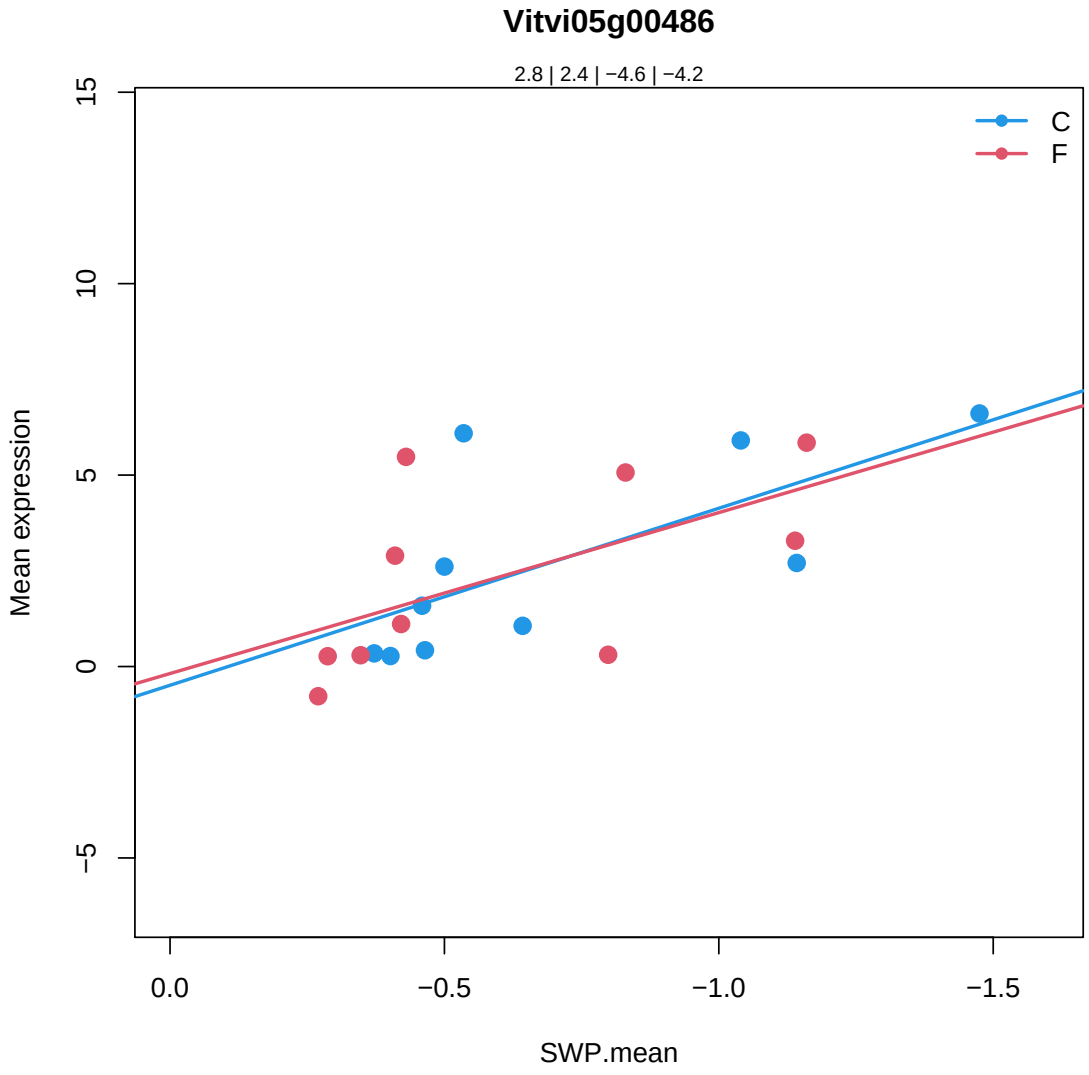
7.2.207 Vitvi05g00486: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00486
        20.2.1
        stress.abiotic.heat
        heat-shock protein 70T-2 |
        Chr2:13651720-13653411 REVERSE LENGTH=563 |
        201606
```

Coefficients for Vitvi05g00486.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.761098	6.57414e-05	***	7.285905e-05	***
SlopeC	-4.622837	0.007179199	**	0.2775469	
MeanF-MeanC	-0.3837781	0.6324297		0.8748606	
SlopeF-SlopeC	0.4200715	0.8577626		0.9999488	



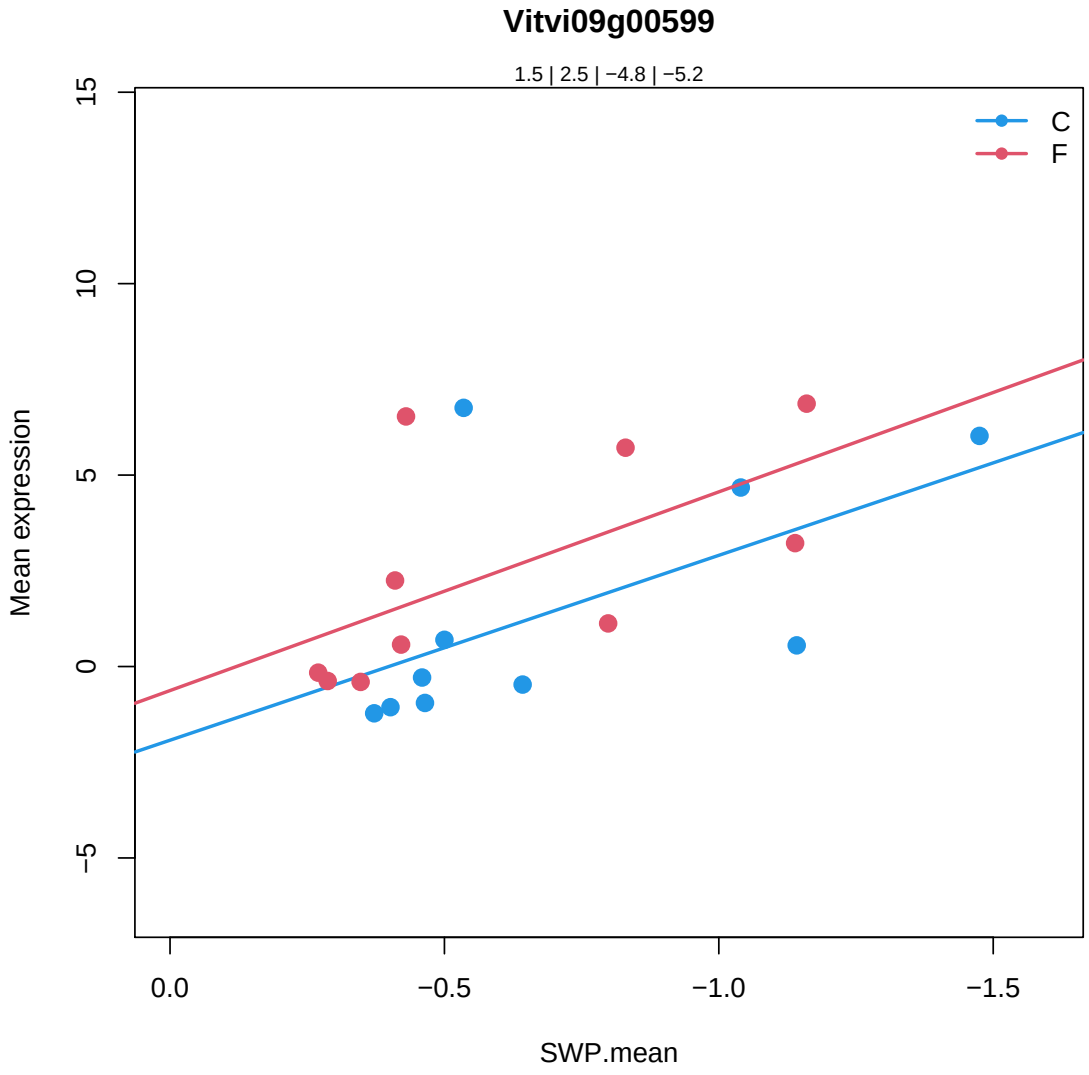
7.2.208 Vitvi09g00599: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00599
        20.2.1
        stress.abiotic.heat
        HSP20-like chaperones superfamily protein |
        Chr1:19574783-19575766 REVERSE LENGTH=232 |
        201606
```

Coefficients for Vitvi09g00599.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.470814	0.04748063	*	0.0494736	*
SlopeC	-4.828826	0.02144893	*	0.386893	
MeanF-MeanC	1.063106	0.294488		0.661003	
SlopeF-SlopeC	-0.3605426	0.9021035		0.9999488	



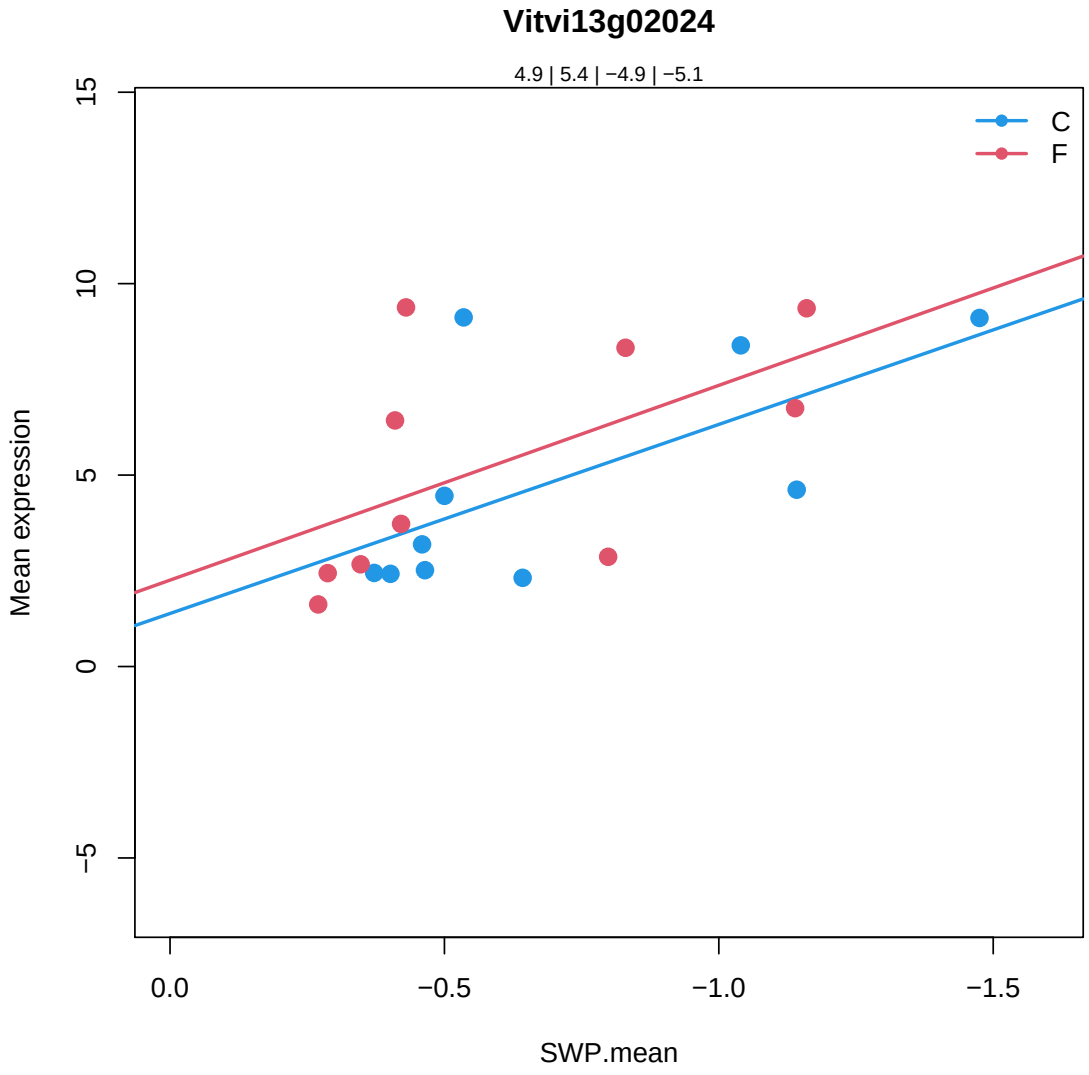
7.2.209 Vitvi13g02024: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g02024
        26.2
        misc.UDP glucosyl and glucoronyl transferases
        heat shock protein 18.2 |
        Chr5:24062632-24063117 FORWARD LENGTH=161 |
        201606
```

Coefficients for Vitvi13g02024.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.85719	4.650855e-07	***	5.414217e-07	***
SlopeC	-4.938026	0.01671165	*	0.3523917	
MeanF-MeanC	0.4983951	0.6115774		0.8646381	
SlopeF-SlopeC	-0.1483944	0.9586909		0.9999488	



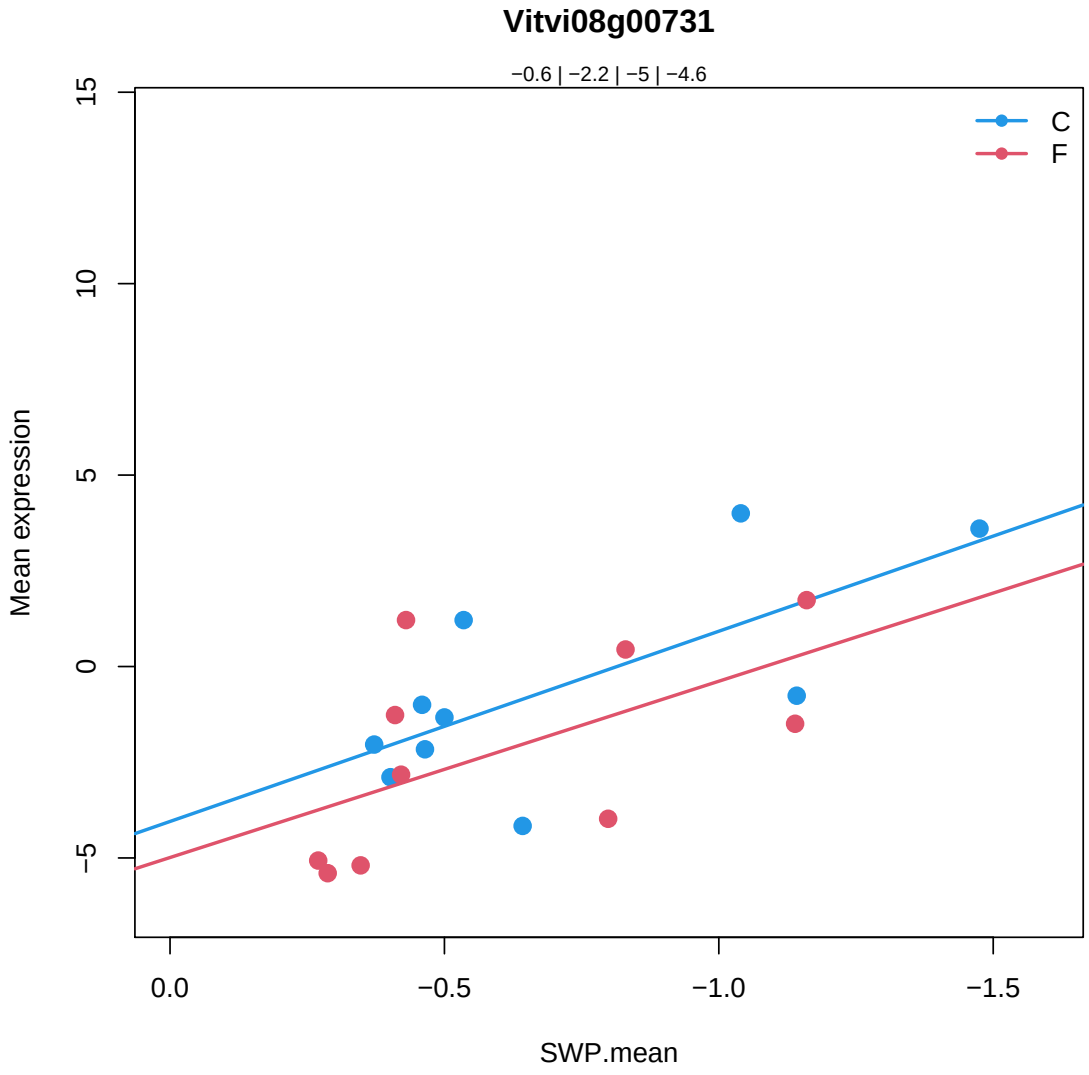
7.2.210 Vitvi08g00731: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g00731
        20.2.1
        stress.abiotic.heat
        HSP20-like chaperones superfamily protein |
        Chr1:19980510-19980983 FORWARD LENGTH=157 |
        201606
```

Coefficients for Vitvi08g00731.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.5532469	0.3709281		0.3770381	
SlopeC	-4.968213	0.007536943	**	0.2777732	
MeanF-MeanC	-1.630057	0.07041397	.	0.2973667	
SlopeF-SlopeC	0.3636611	0.8860073		0.9999488	



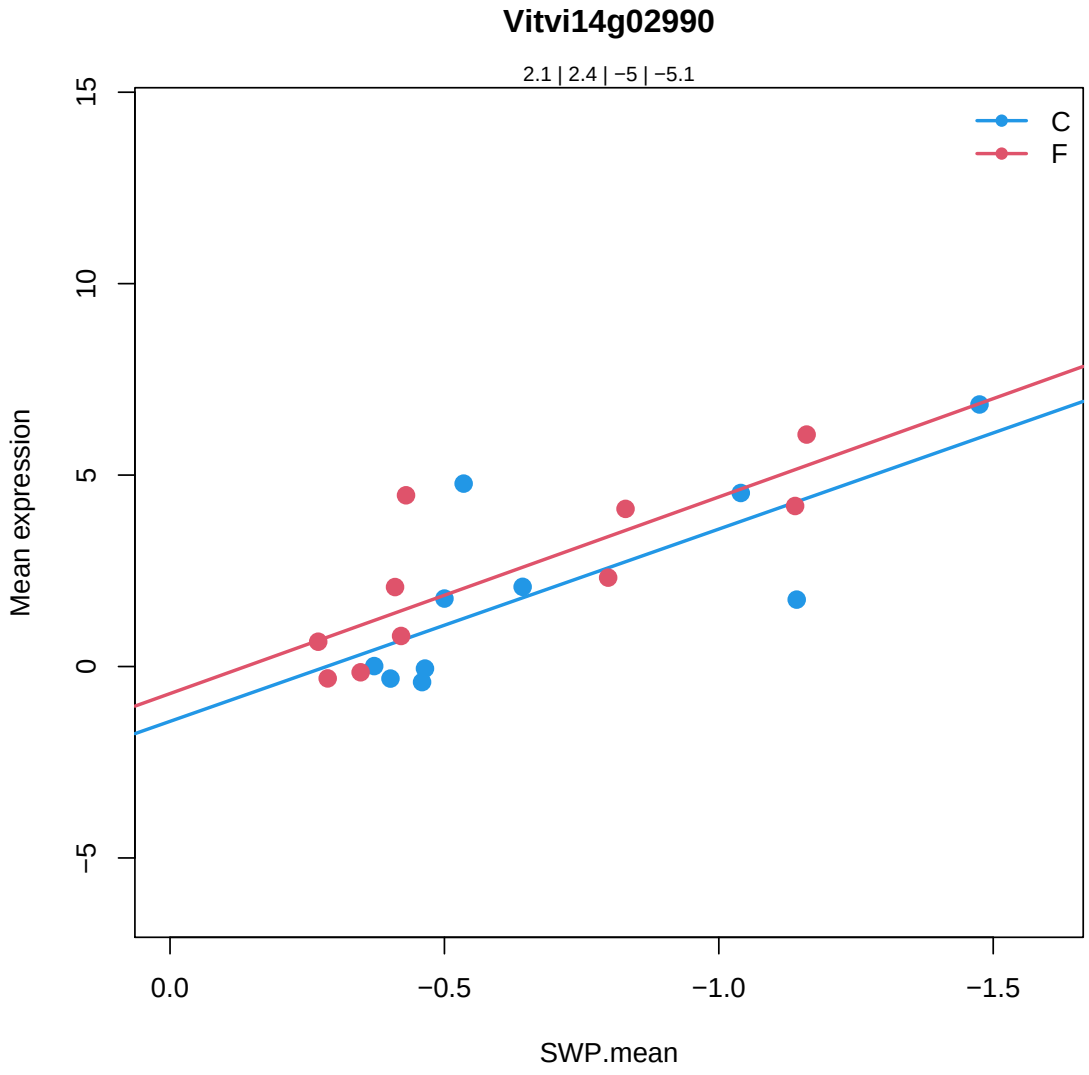
7.2.211 Vitvi14g02990: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g02990
        35.2
        not assigned.unknown
        hypothetical protein |
        Chr3:10061633-10062481 FORWARD LENGTH=282 |
        201606
```

Coefficients for Vitvi14g02990.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.099223	9.197532e-05	***	0.0001016303	***
SlopeC	-5.022153	0.0004647919	***	0.1005065	
MeanF-MeanC	0.3227609	0.6073488		0.8620981	
SlopeF-SlopeC	-0.1129527	0.9508756		0.9999488	



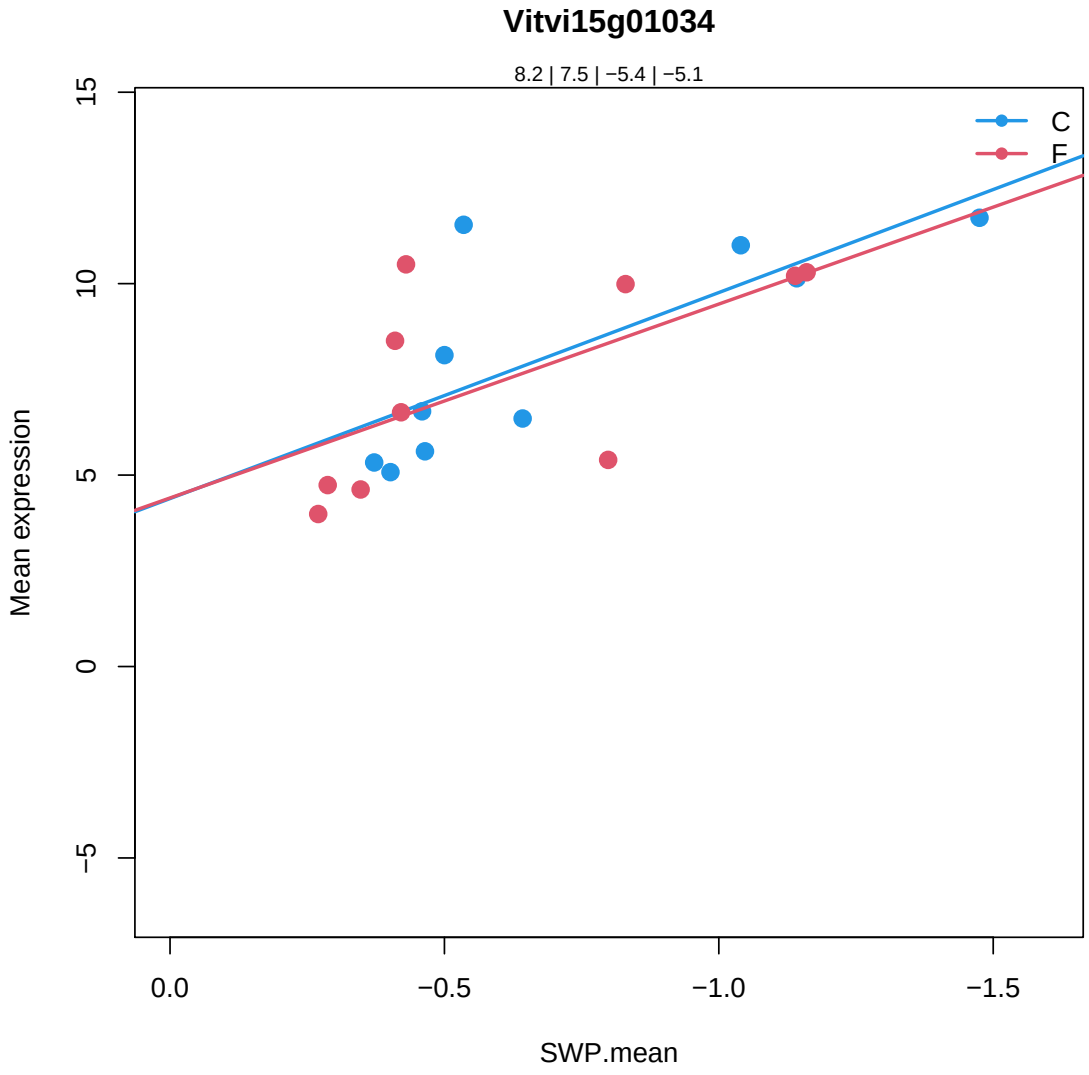
7.2.212 Vitvi15g01034: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g01034
        20.2.1
        stress.abiotic.heat
        BCL-2-associated athanogene 6 |
        Chr2:18986586-18989827 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi15g01034.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	8.170016	1.181955e-12	***	1.687937e-12	***
SlopeC	-5.38071	0.002228703	**	0.1816214	
MeanF-MeanC	-0.6819577	0.3963123		0.7423612	
SlopeF-SlopeC	0.316925	0.8920127		0.9999488	



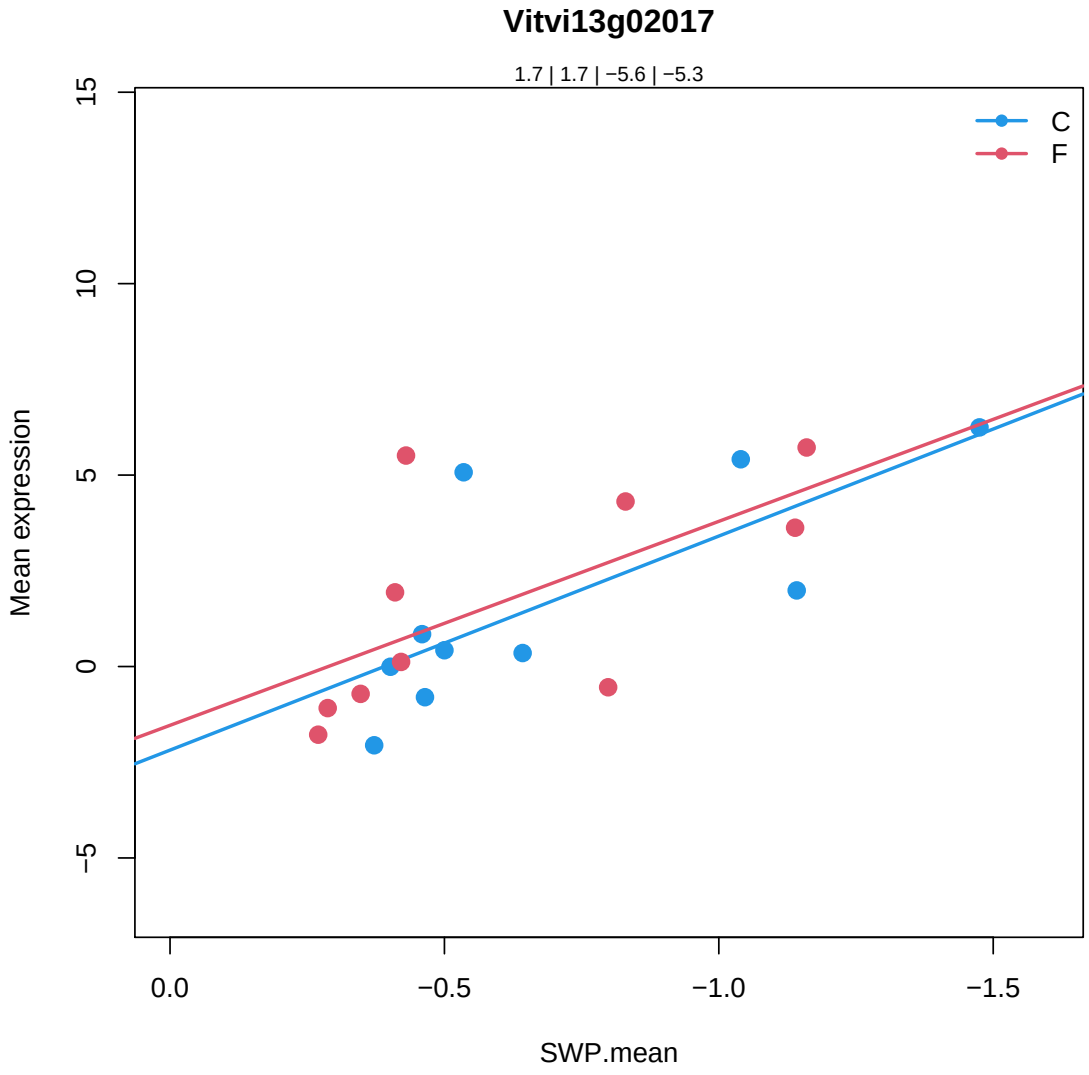
7.2.213 Vitvi13g02017: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g02017
        20.2.1
        stress.abiotic.heat
        heat shock protein 18.2 |
        Chr5:24062632-24063117 FORWARD LENGTH=161 |
        201606
```

Coefficients for Vitvi13g02017.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.747598	0.008703427	**	0.009234138	**
SlopeC	-5.59067	0.003192727	**	0.2103859	
MeanF-MeanC	-0.03771032	0.9652737		0.9919971	
SlopeF-SlopeC	0.2632103	0.9173508		0.9999488	



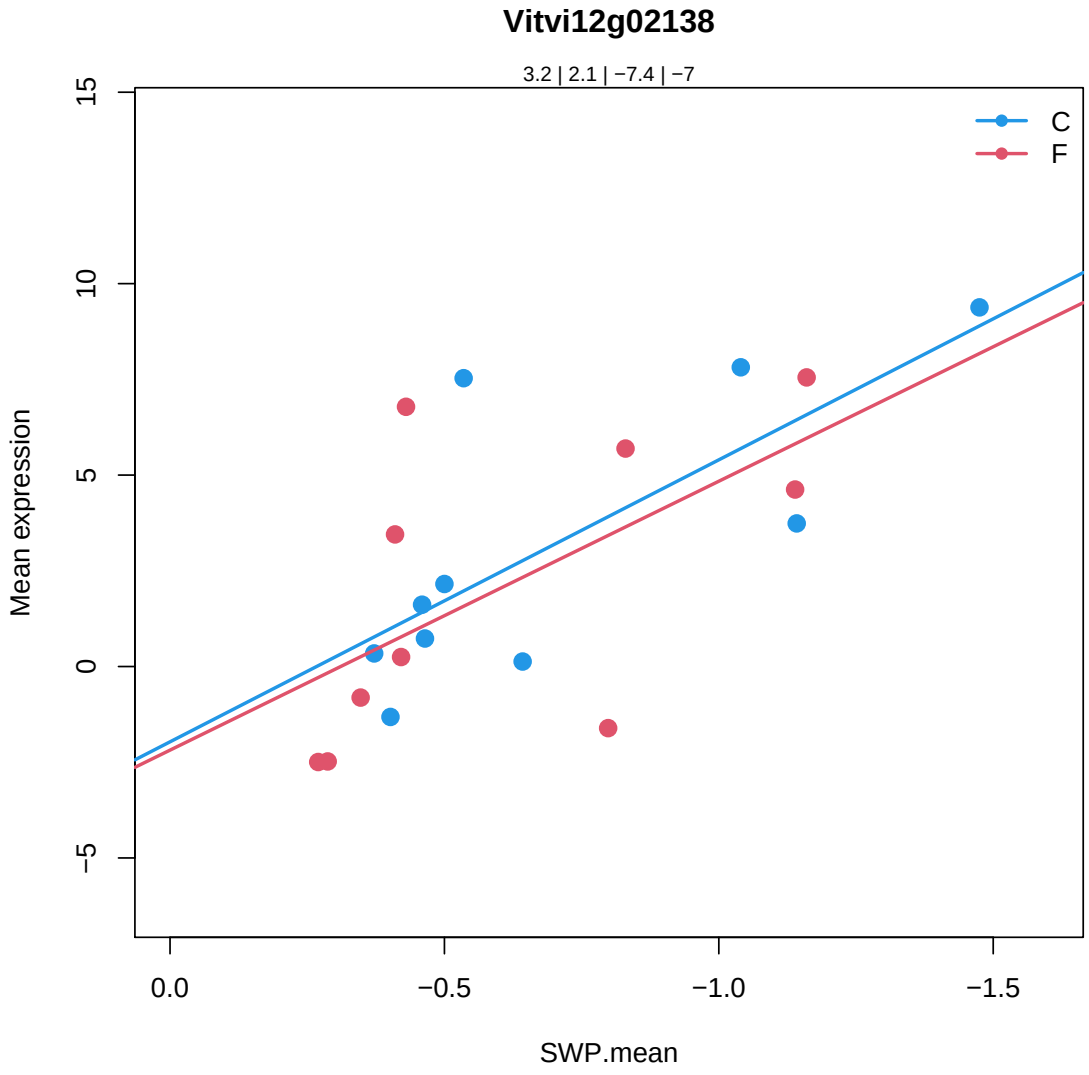
7.2.214 Vitvi12g02138: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02138
        20.2.1
        stress.abiotic.heat
        HSP20-like chaperones superfamily protein |
        Chr4:6370537-6371124 FORWARD LENGTH=195 |
        201606
```

Coefficients for Vitvi12g02138.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.21186	0.0008015218	***	0.0008698943	***
SlopeC	−7.364735	0.004094778	**	0.2328828	
MeanF−MeanC	−1.11679	0.3484371		0.7079025	
SlopeF−SlopeC	0.3417037	0.9211381		0.9999488	



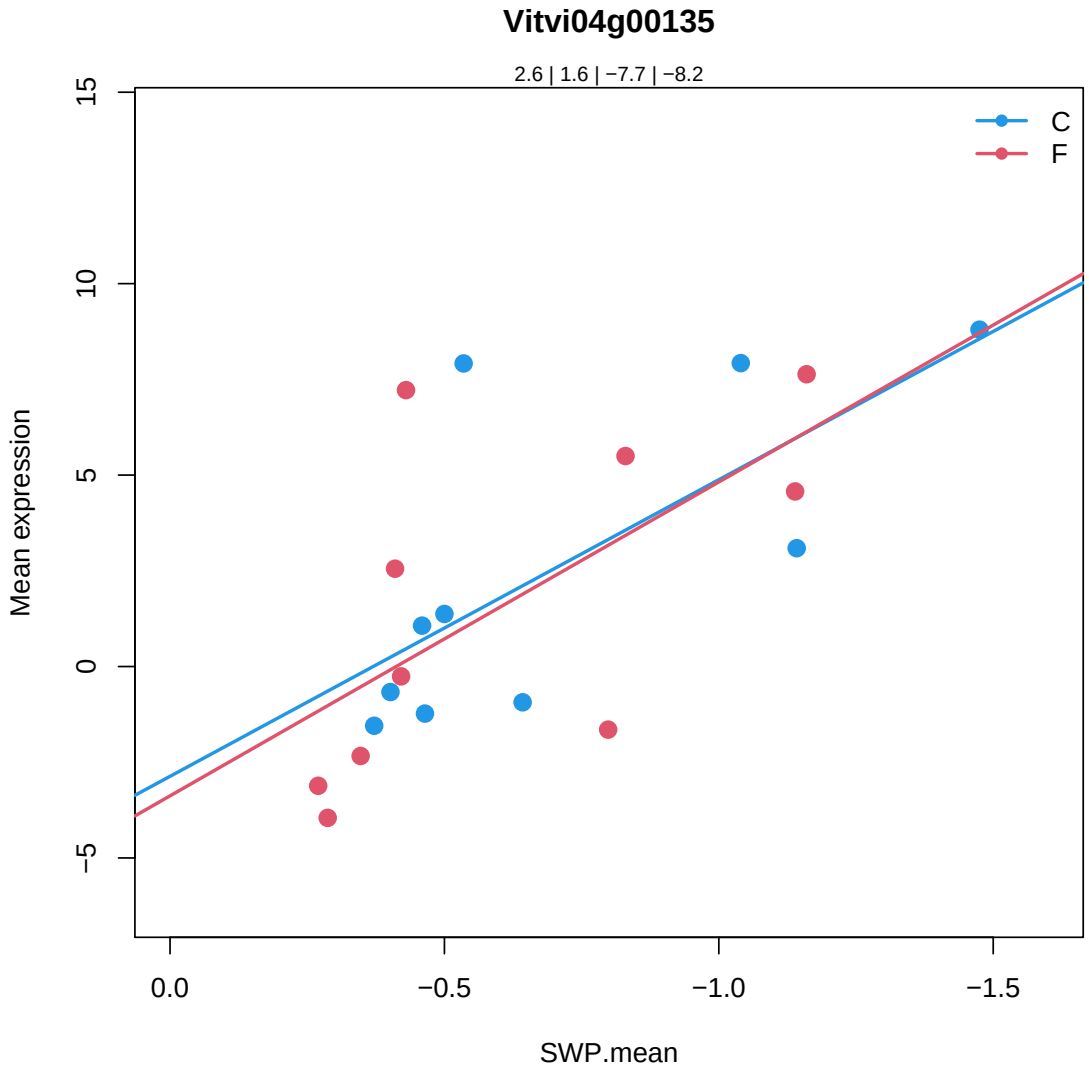
7.2.215 Vitvi04g00135: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00135
        20.2.1
        stress.abiotic.heat
        17.6 kDa class II heat shock protein |
        Chr5:3882409-3882876 REVERSE LENGTH=155 |
        201606
```

Coefficients for Vitvi04g00135.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.578927	0.01060559	*	0.01122885	*
SlopeC	-7.746727	0.006376148	**	0.2661465	
MeanF-MeanC	-0.9622751	0.4681276		0.7878981	
SlopeF-SlopeC	-0.4507473	0.9070348		0.9999488	



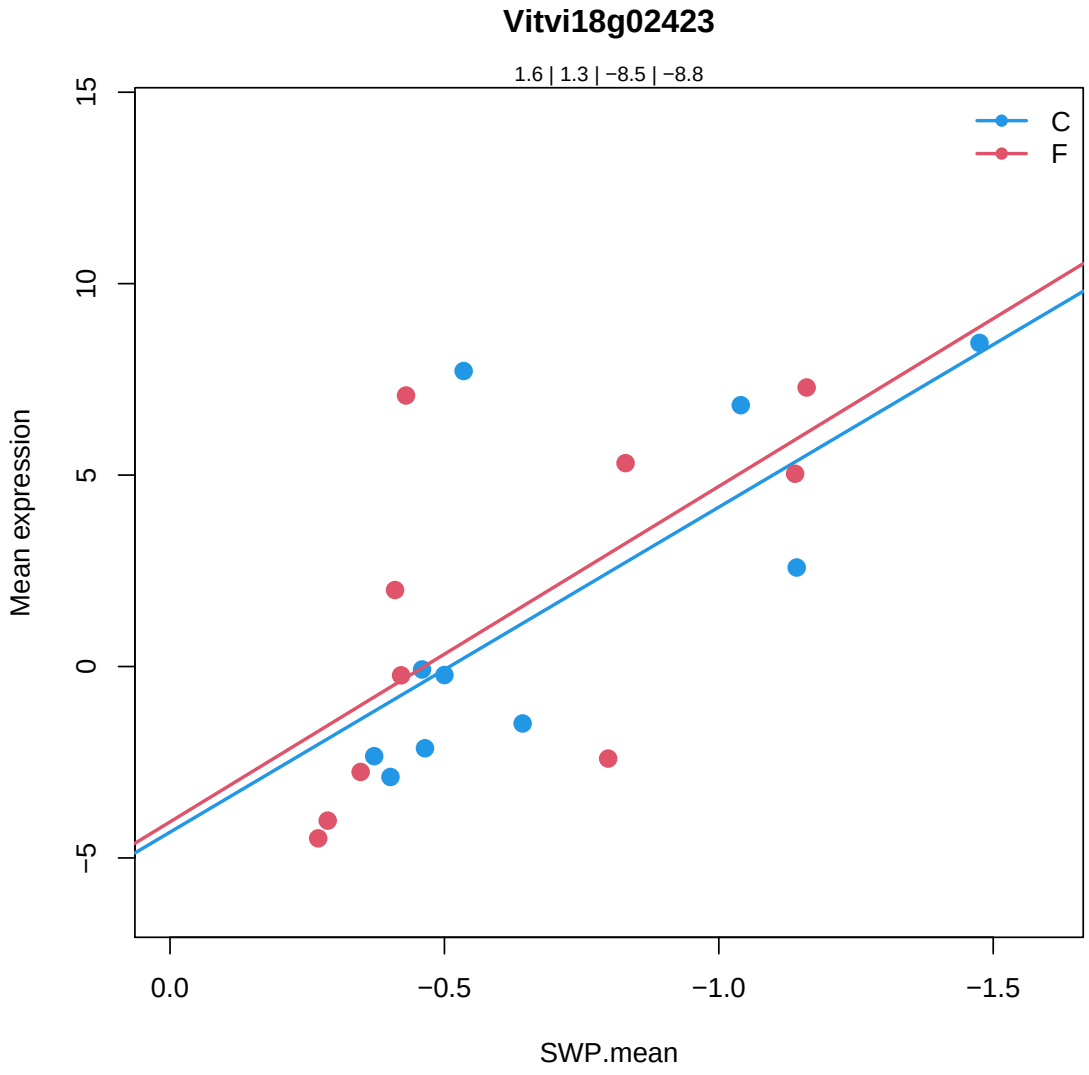
7.2.216 Vitvi18g02423: * type1

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02423
        35.2
        not assigned.unknown
        HSP20-like chaperones superfamily protein |
        Chr4:6370537-6371124 FORWARD LENGTH=195 |
        201606
```

Coefficients for Vitvi18g02423.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.643122	0.1022202		0.1056729	
SlopeC	-8.488894	0.004528886	**	0.2419697	
MeanF-MeanC	-0.3621322	0.7927368		0.9414753	
SlopeF-SlopeC	-0.2732159	0.9459792		0.9999488	



7.3 type2

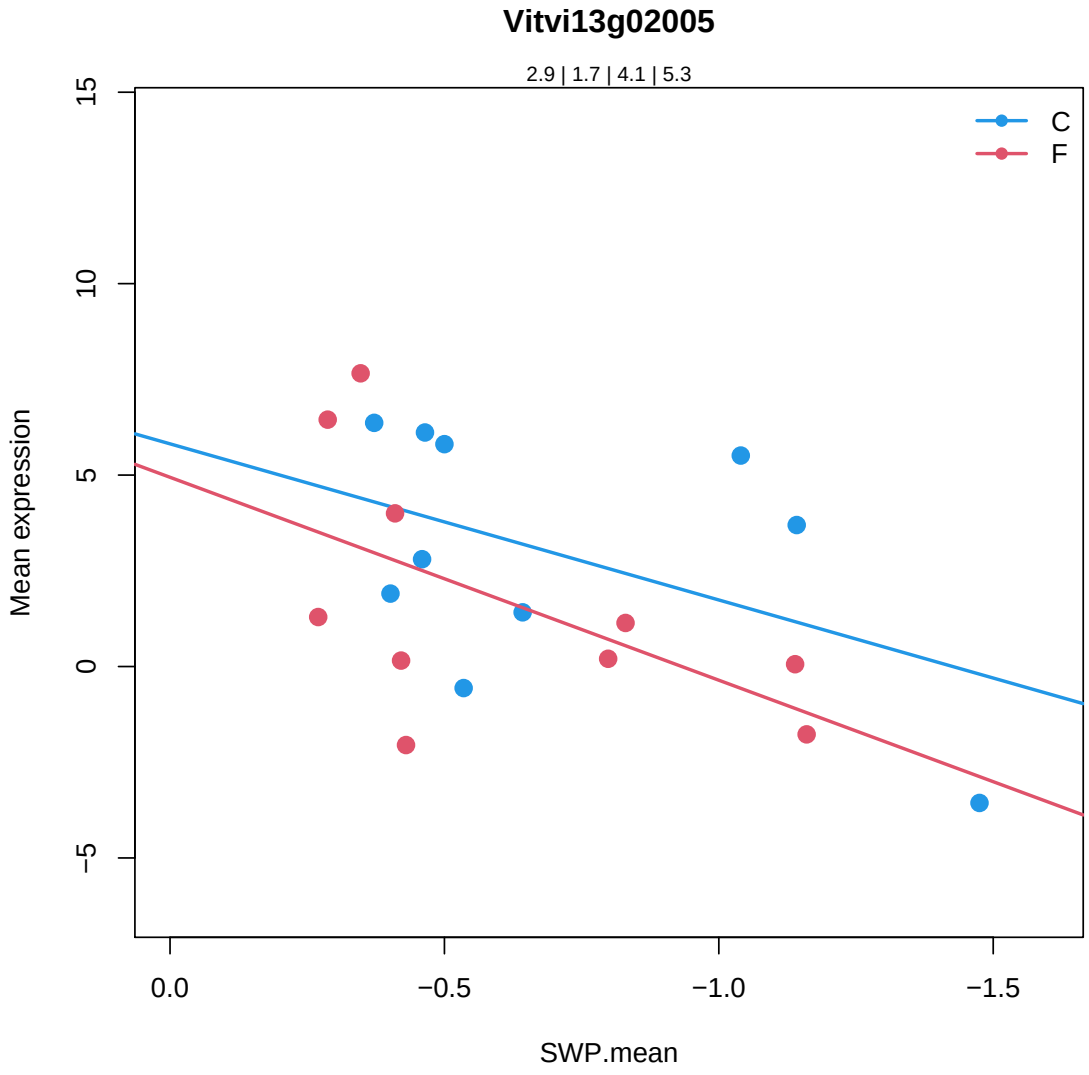
7.3.1 Vitvi13g02005: type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g02005
        29.5.1
        protein.degradation.subtilases
        Subtilisin-like serine endopeptidase family protein |
        Chr5:23755787-23758600 FORWARD LENGTH=710 |
        201606
```

Coefficients for Vitvi13g02005.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.948421	0.001571115	**	0.001694639	**
SlopeC	4.07808	0.08613381	.	0.5889741	
MeanF-MeanC	-1.235611	0.2955399		0.6617627	
SlopeF-SlopeC	1.221977	0.7207826		0.9999488	



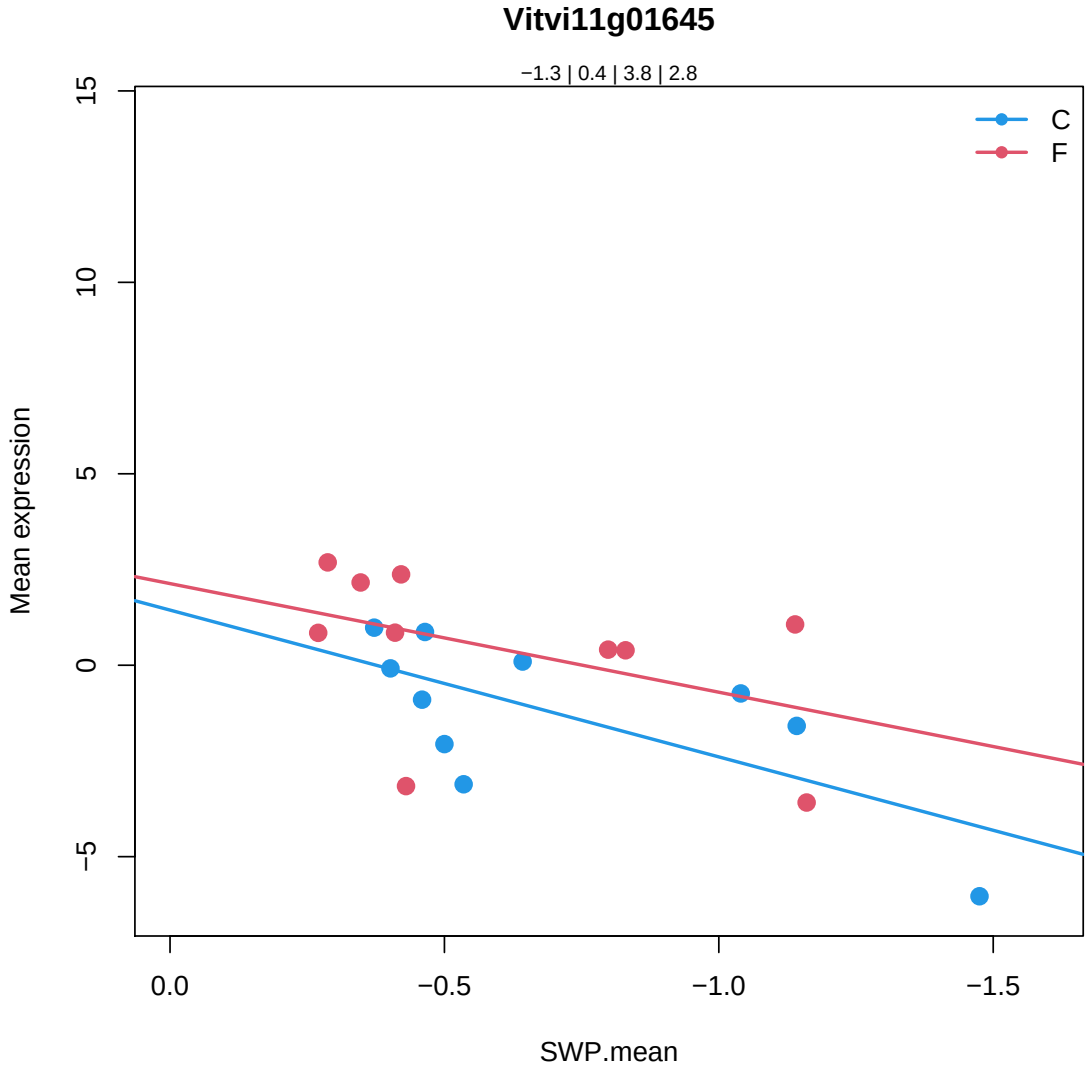
7.3.2 Vitvi11g01645: * type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g01645
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi11g01645.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.256387	0.0220056	*	0.02311893	*
SlopeC	3.833904	0.01301173	*	0.3305597	
MeanF-MeanC	1.659781	0.03113549	*	0.1738341	
SlopeF-SlopeC	-0.9971111	0.6408022		0.9999488	



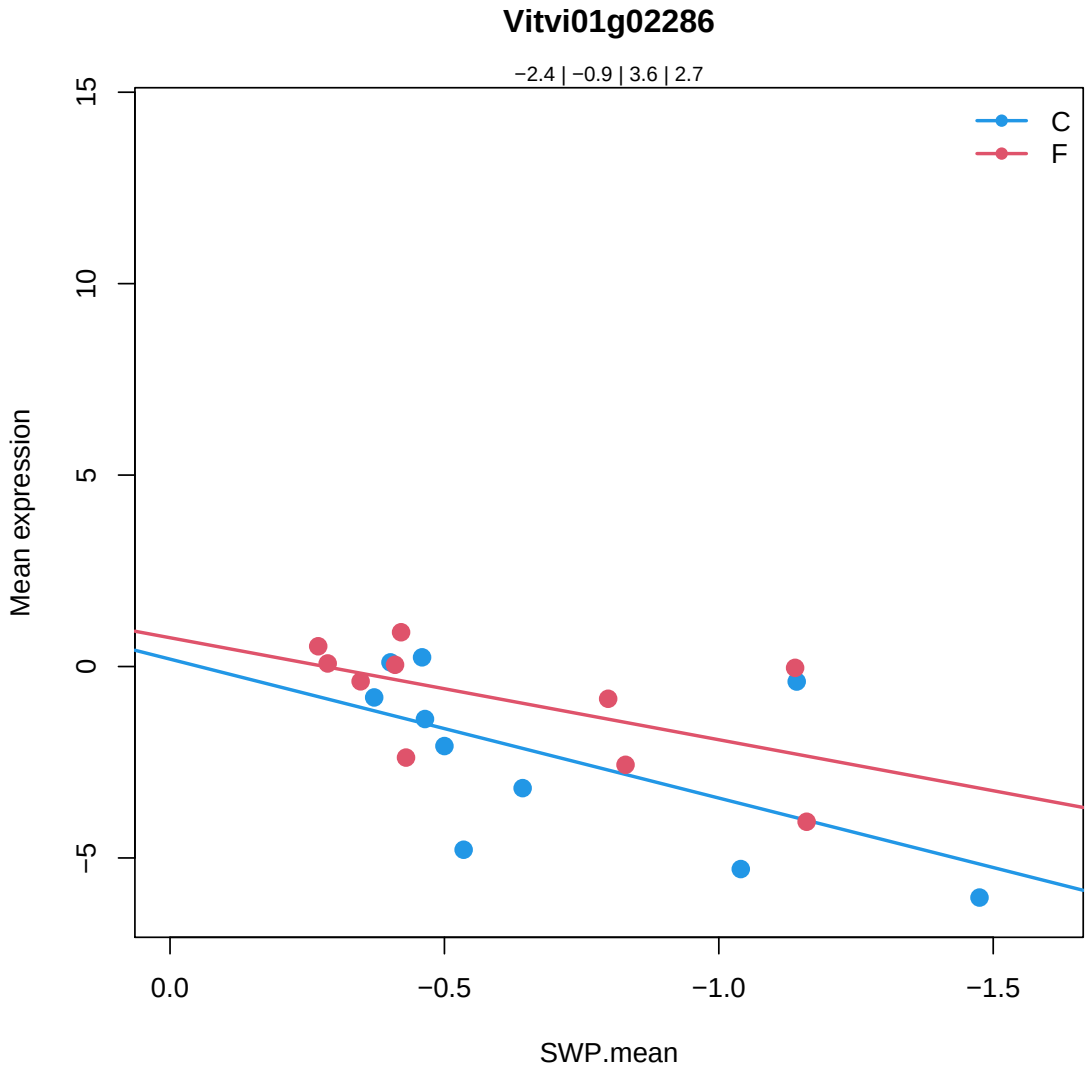
7.3.3 Vitvi01g02286: * type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g02286
        17.2.3
        hormone metabolism.auxin.induced-regulated-responsive-activated
        SAUR-like auxin-responsive protein family |
        Chr5:20644780-20645331 FORWARD LENGTH=183 |
        201606
```

Coefficients for Vitvi01g02286.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-2.35875	6.3206e-05	***	7.006952e-05	***
SlopeC	3.628699	0.01215037	*	0.3229093	
MeanF-MeanC	1.487141	0.03823163	*	0.1999748	
SlopeF-SlopeC	-0.9648213	0.6295866		0.9999488	



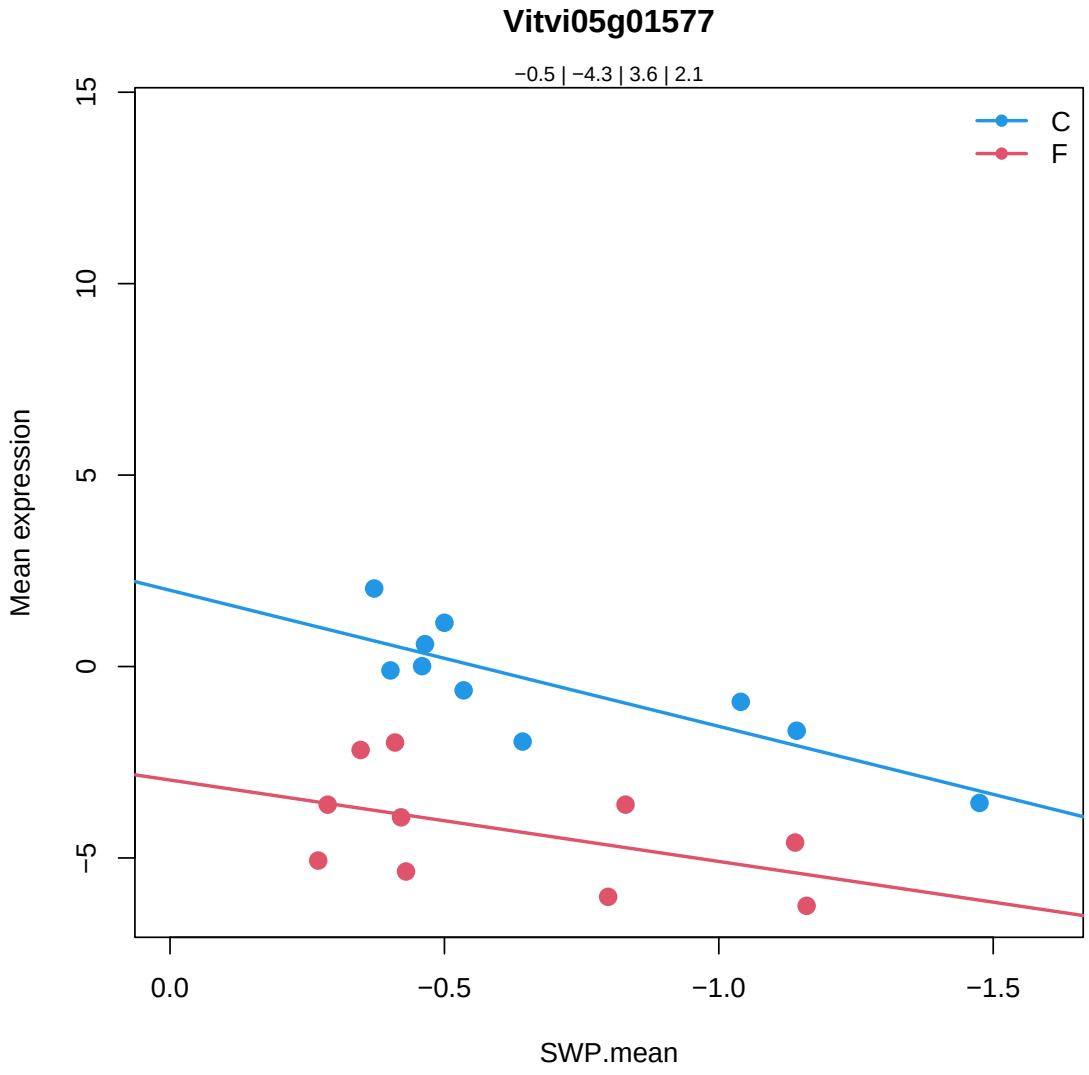
7.3.4 Vitvi05g01577: * type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01577
        20.1.7.3
        stress.biotic.PR-proteins.PR3/4/8/11 (chitinases and chitin binding pr
        homolog of carrot EP3-3 chitinase |
        Chr3:20145935-20147034 FORWARD LENGTH=273 |
        201606
```

Coefficients for Vitvi05g01577.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.5075609	0.1396409		0.1438405	
SlopeC	3.553568	0.0008792532	***	0.118598	
MeanF-MeanC	-3.752991	6.802344e-08	***	2.920601e-06	***
SlopeF-SlopeC	-1.42671	0.3093121		0.9999488	



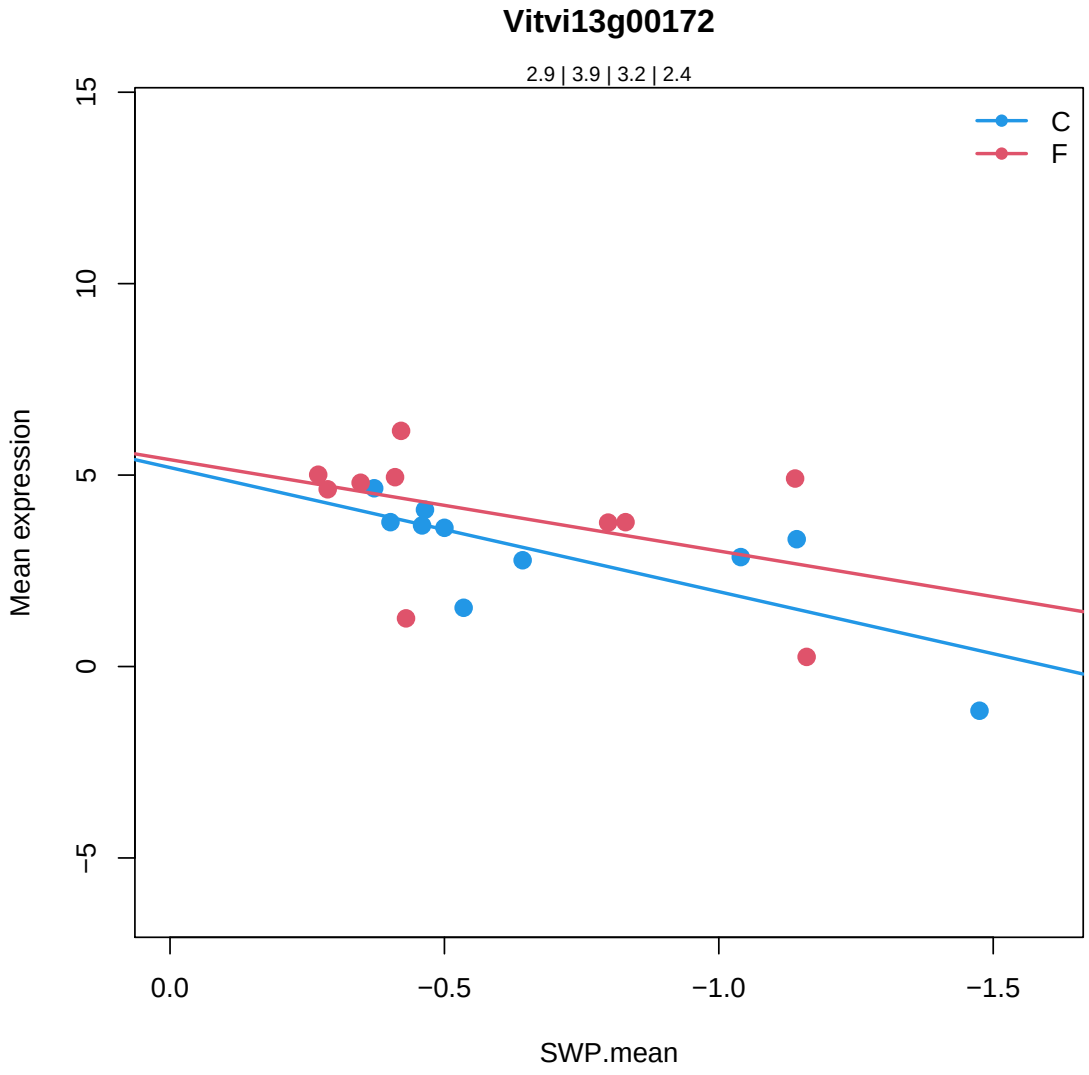
7.3.5 Vitvi13g00172: * type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00172
        10.7
        cell wall.modification
        expansin A8 |
        Chr2:16949121-16950472 REVERSE LENGTH=253 |
        201606
```

Coefficients for Vitvi13g00172.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.916449	5.190381e-07	***	6.037224e-07	***
SlopeC	3.240978	0.01020129	*	0.3054776	
MeanF-MeanC	1.032131	0.09184968	.	0.3470433	
SlopeF-SlopeC	-0.8556393	0.6224147		0.9999488	



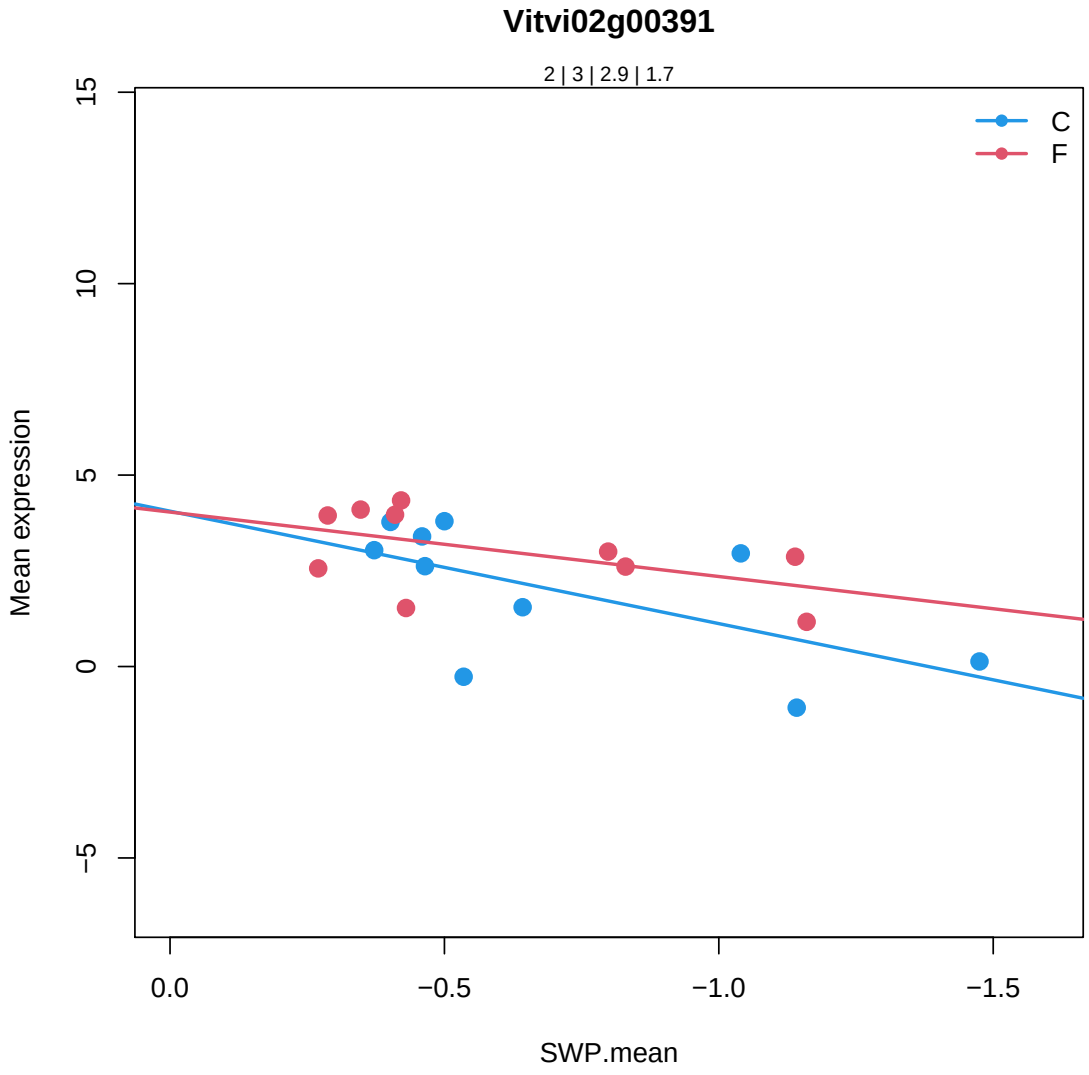
7.3.6 Vitvi02g00391: * type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00391
        20.1.7.5
        stress.biotic.PR-proteins.PR5 (thaumatin-like proteins)
        osmotin 34 |
        Chr4:7025127-7026113 REVERSE LENGTH=244 |
        201606
```

Coefficients for Vitvi02g00391.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.992013	1.280131e-05	***	1.441791e-05	***
SlopeC	2.936439	0.00699603	**	0.2775469	
MeanF-MeanC	1.016364	0.05486513	.	0.253872	
SlopeF-SlopeC	-1.253394	0.4018436		0.9999488	



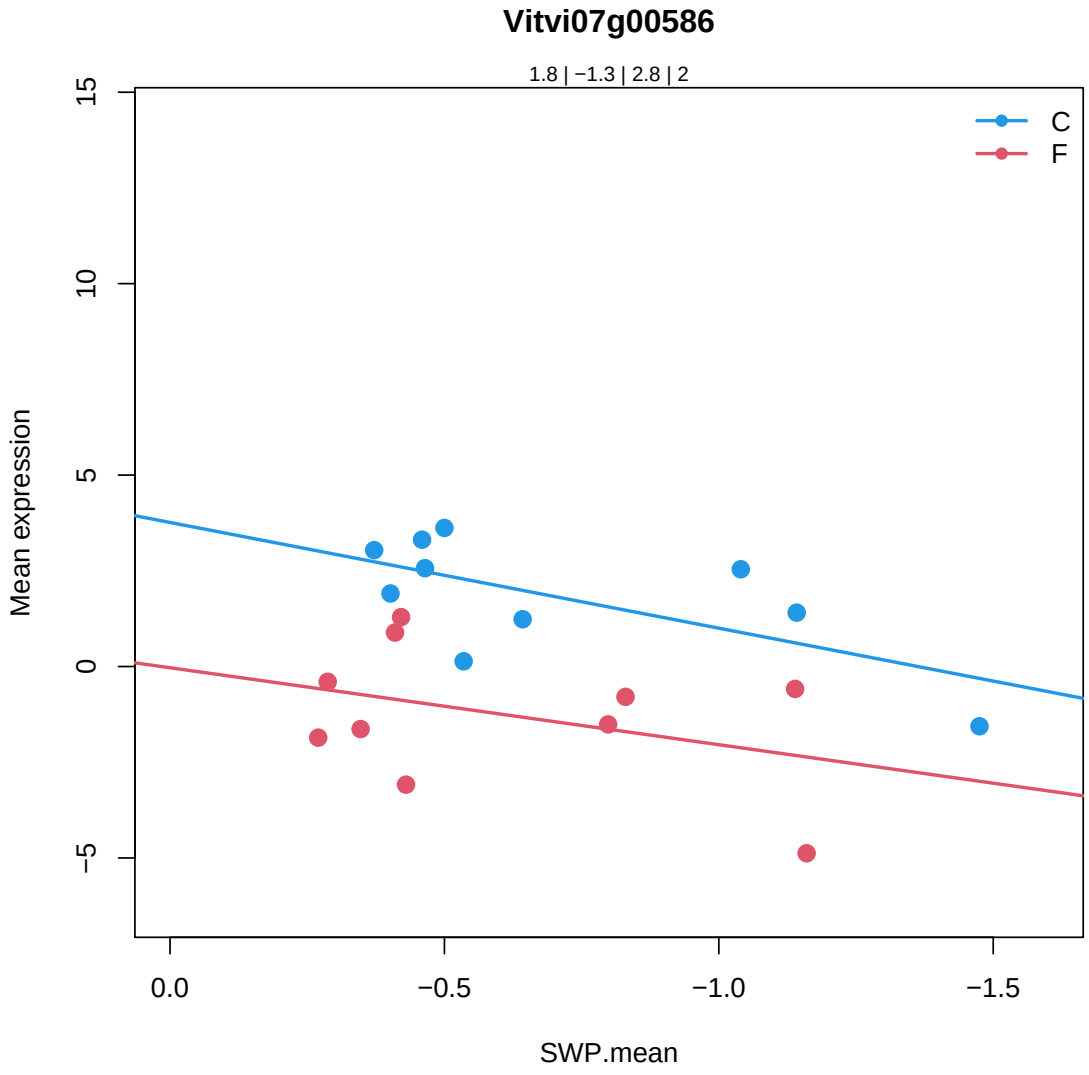
7.3.7 Vitvi07g00586: * type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g00586
        29.5.4
        protein.degradation.aspartate protease
        Eukaryotic aspartyl protease family protein |
        Chr2:966506-967891 REVERSE LENGTH=461 |
        201606
```

Coefficients for Vitvi07g00586.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.820575	0.0003499595	***	0.0003821523	***
SlopeC	2.761208	0.03074027	*	0.4322019	
MeanF-MeanC	-3.07708	4.782582e-05	***	0.0009503821	***
SlopeF-SlopeC	-0.7514262	0.6766004		0.9999488	



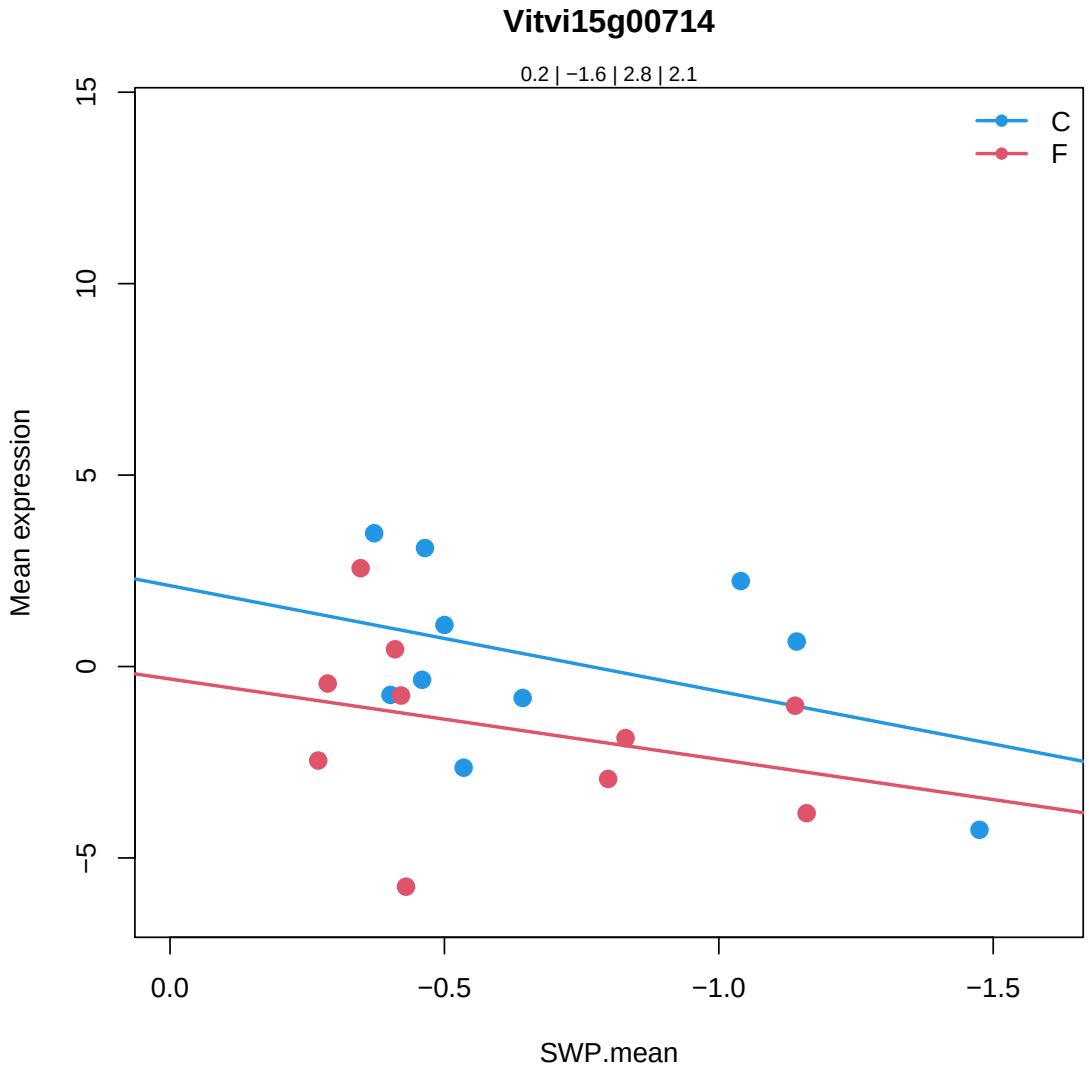
7.3.8 Vitvi15g00714: type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g00714
        26.21
        misc.protease inhibitor/seed storage/lipid transfer protein (LTP) fami
        Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin
        Chr4:69433-69819 REVERSE LENGTH=128 |
        201606
```

Coefficients for Vitvi15g00714.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1724214	0.7927213		0.7967463	
SlopeC	2.757195	0.1407973		0.6676582	
MeanF-MeanC	-1.777328	0.06572122	.	0.2846357	
SlopeF-SlopeC	-0.6577505	0.8086901		0.9999488	



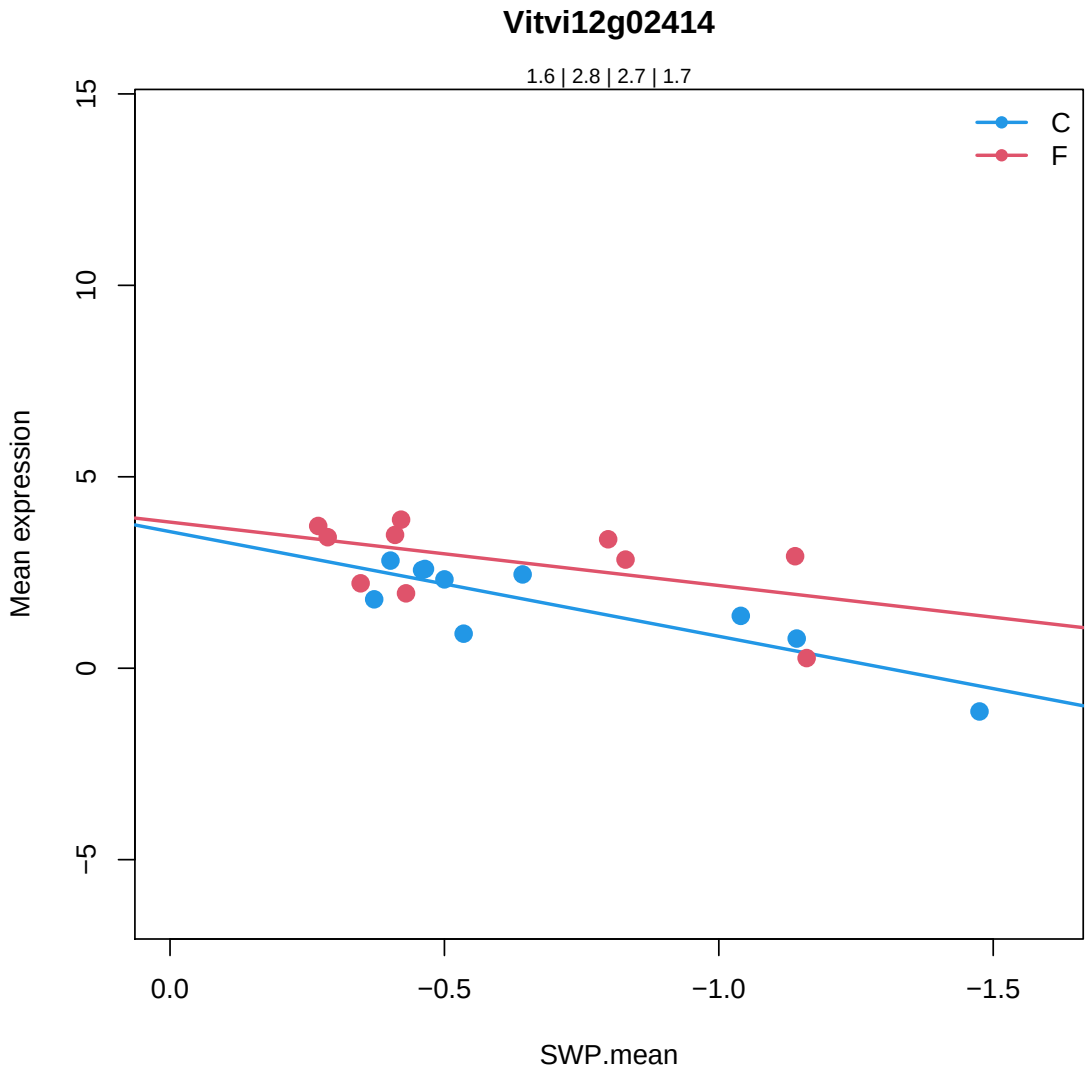
7.3.9 Vitvi12g02414: * type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02414
        35.2
        not assigned.unknown
        Genomic DNA chromosome 3 P1 clone MSD21
```

Coefficients for Vitvi12g02414.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.645198	1.000115e-06	***	1.155267e-06	***
SlopeC	2.733097	0.0005824794	***	0.1005065	
MeanF-MeanC	1.161642	0.002828531	**	0.02929549	*
SlopeF-SlopeC	-1.077144	0.2976229		0.9999488	



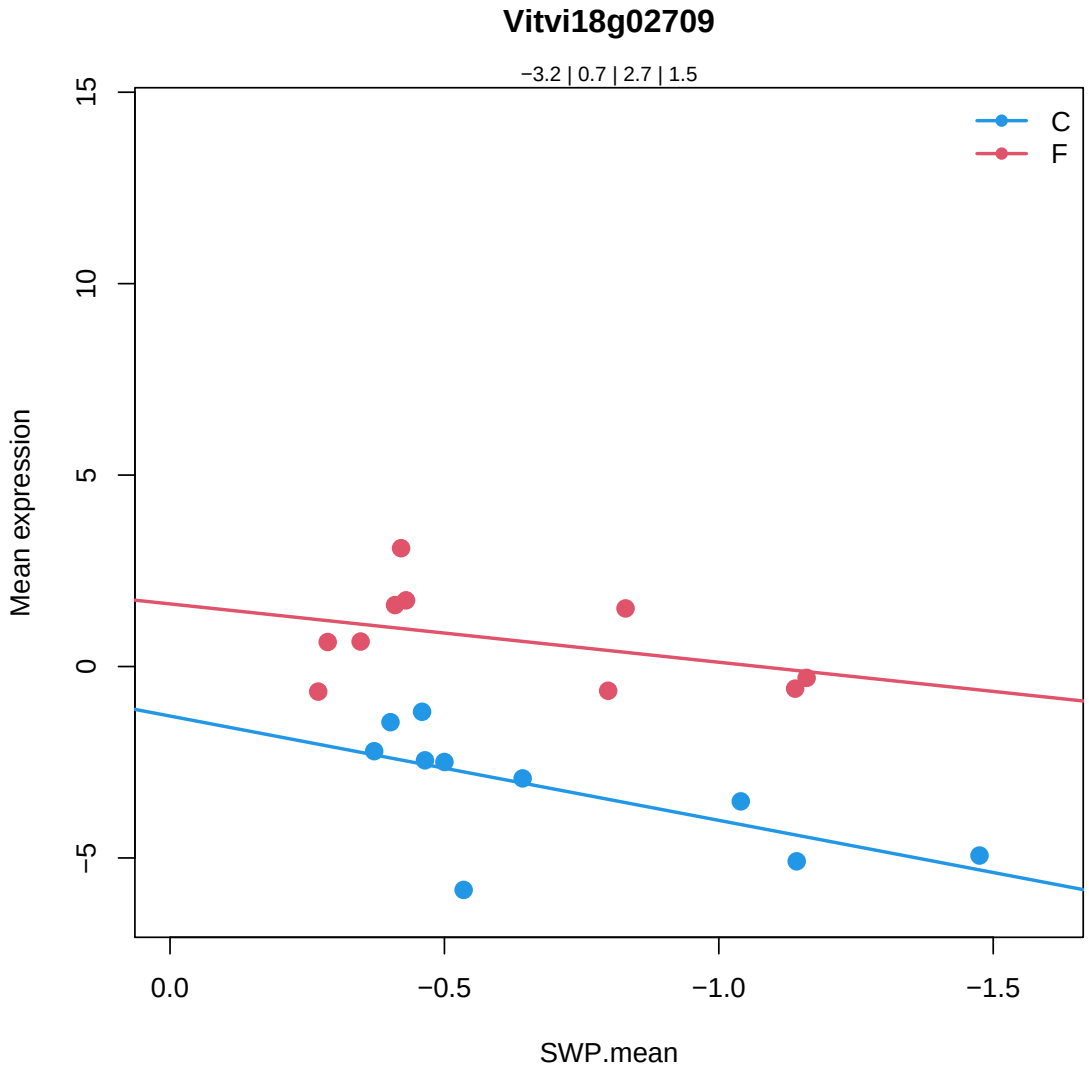
7.3.10 Vitvi18g02709: * type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02709
        35.1.40
        not assigned.no ontology.glycine rich proteins
        Cupredoxin superfamily protein |
        Chr2:6873666-6874701 REVERSE LENGTH=257 |
        201606
```

Coefficients for Vitvi18g02709.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-3.209467	8.027118e-09	***	9.824888e-09	***
SlopeC	2.724042	0.01110047	*	0.3143947	
MeanF-MeanC	3.91652	9.423432e-08	***	3.871481e-06	***
SlopeF-SlopeC	-1.199916	0.4198128		0.9999488	



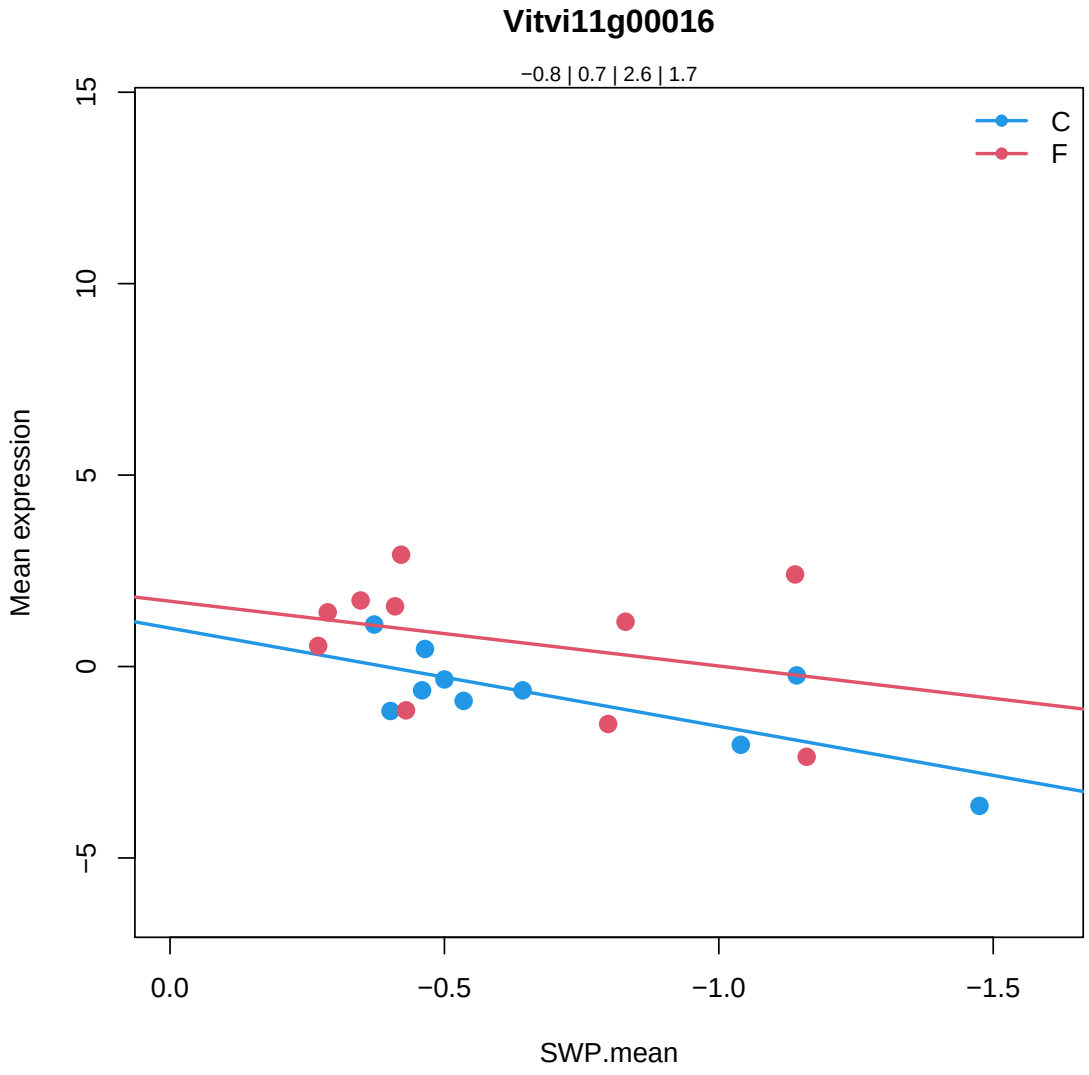
7.3.11 Vitvi11g00016: * type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00016
        35.2
        not assigned.unknown
        Plant invertase/pectin methylesterase inhibitor superfamily |
        Chr5:7076971-7079077 REVERSE LENGTH=538 |
        201606
```

Coefficients for Vitvi11g00016.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.8004064	0.0548222	.	0.05704143	.
SlopeC	2.564374	0.02908345	*	0.4288878	
MeanF-MeanC	1.474787	0.01493928	*	0.1015631	
SlopeF-SlopeC	-0.8725008	0.5983658		0.9999488	



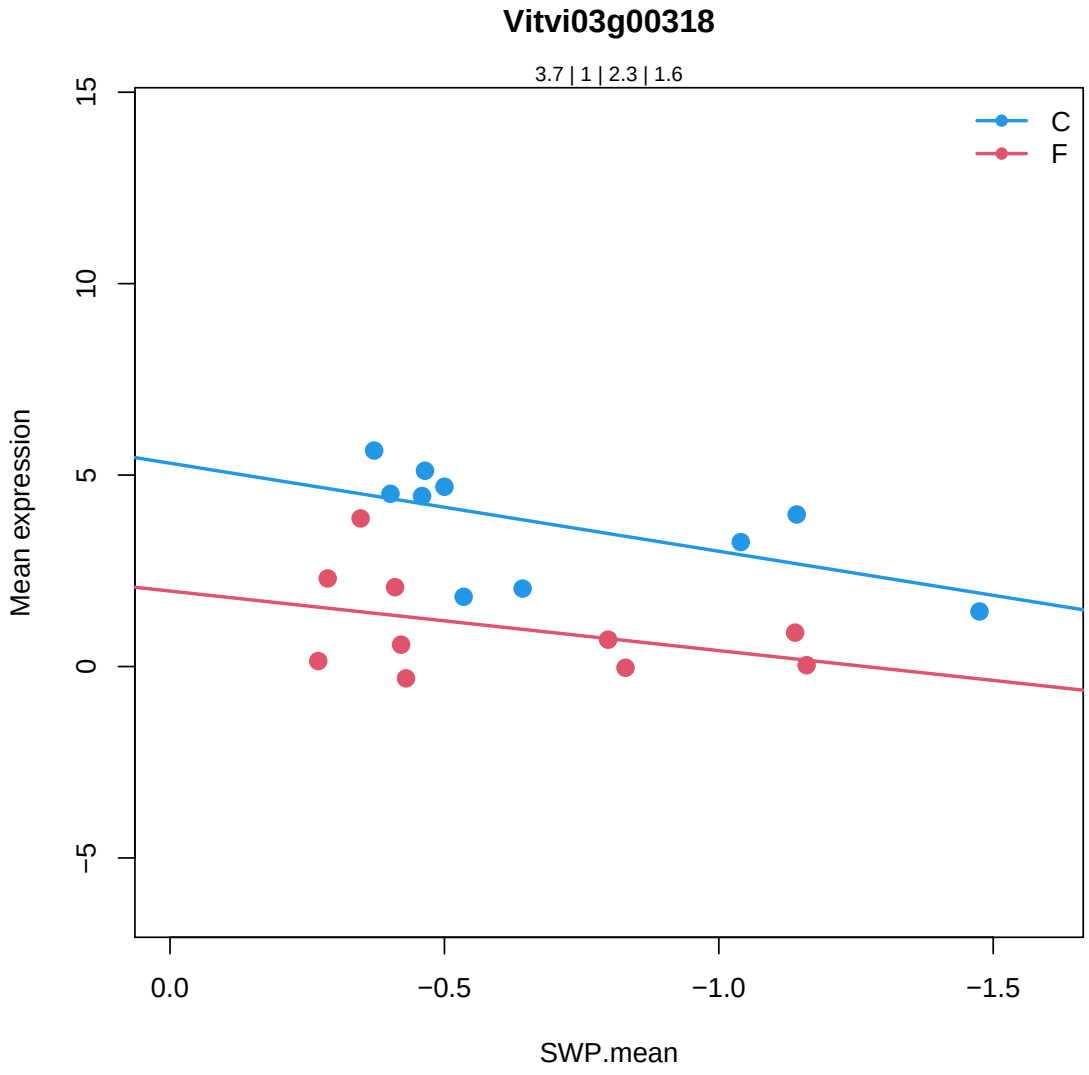
7.3.12 Vitvi03g00318: * type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00318
        27.3.25
        RNA.regulation of transcription.MYB domain transcription factor family
        RAD-like 6 |
        Chr1:28245073-28245453 REVERSE LENGTH=126 |
        201606
```

Coefficients for Vitvi03g00318.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.692558	8.664173e-10	***	1.094475e-09	***
SlopeC	2.300824	0.03059091	*	0.4321285	
MeanF-MeanC	-2.669643	2.876014e-05	***	0.0006253381	***
SlopeF-SlopeC	-0.7449947	0.6196467		0.9999488	



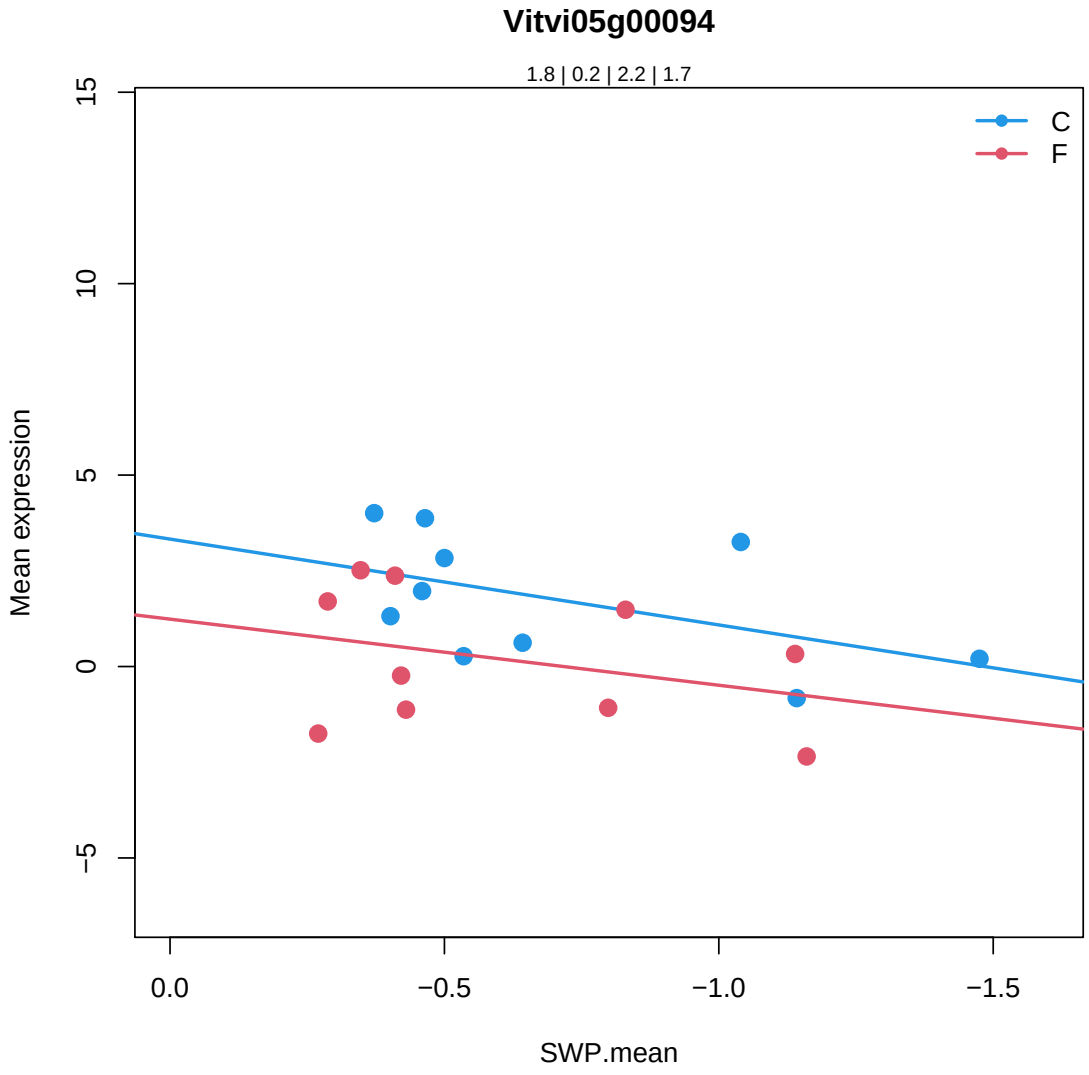
7.3.13 Vitvi05g00094: type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00094
        20.1.7.3
        stress.biotic.PR-proteins.PR3/4/8/11 (chitinases and chitin binding pr
        Chitinase family protein |
        Chr1:1766833-1768117 REVERSE LENGTH=321 |
        201606
```

Coefficients for Vitvi05g00094.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.75152	0.0009882148	***	0.001070151	**
SlopeC	2.242017	0.09374752	.	0.6028633	
MeanF-MeanC	-1.566073	0.02500179	*	0.1486222	
SlopeF-SlopeC	-0.5159695	0.7888473		0.9999488	



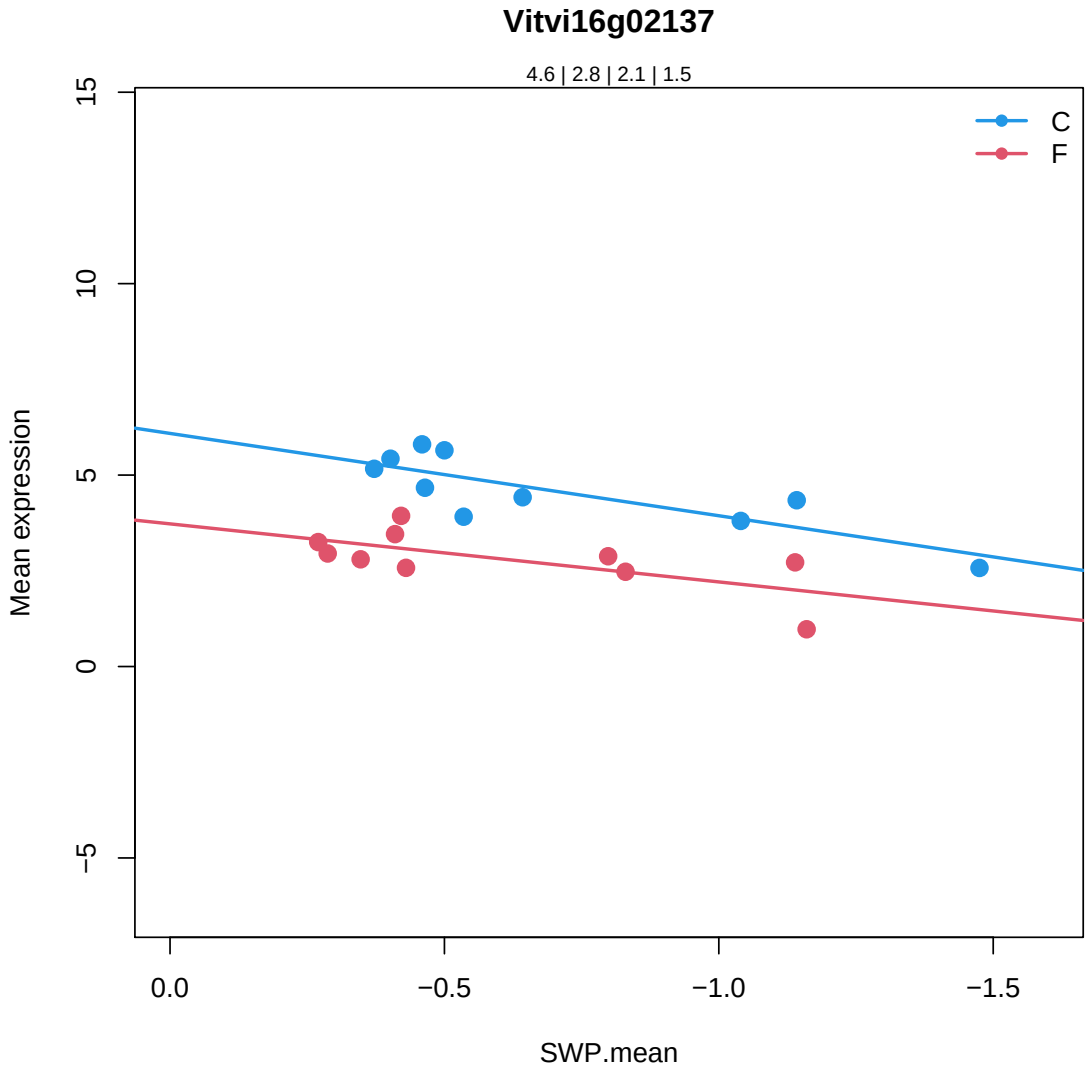
7.3.14 Vitvi16g02137: * type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g02137
        35.2
        not assigned.unknown
        PR5-like receptor kinase |
        Chr5:15293325-15295838 REVERSE LENGTH=665 |
        201606
```

Coefficients for Vitvi16g02137.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.576307	2.446722e-17	***	5.954484e-17	***
SlopeC	2.149758	0.0003725907	***	0.09467692	.
MeanF-MeanC	-1.774357	8.117334e-07	***	2.701199e-05	***
SlopeF-SlopeC	-0.6336356	0.4129181		0.9999488	



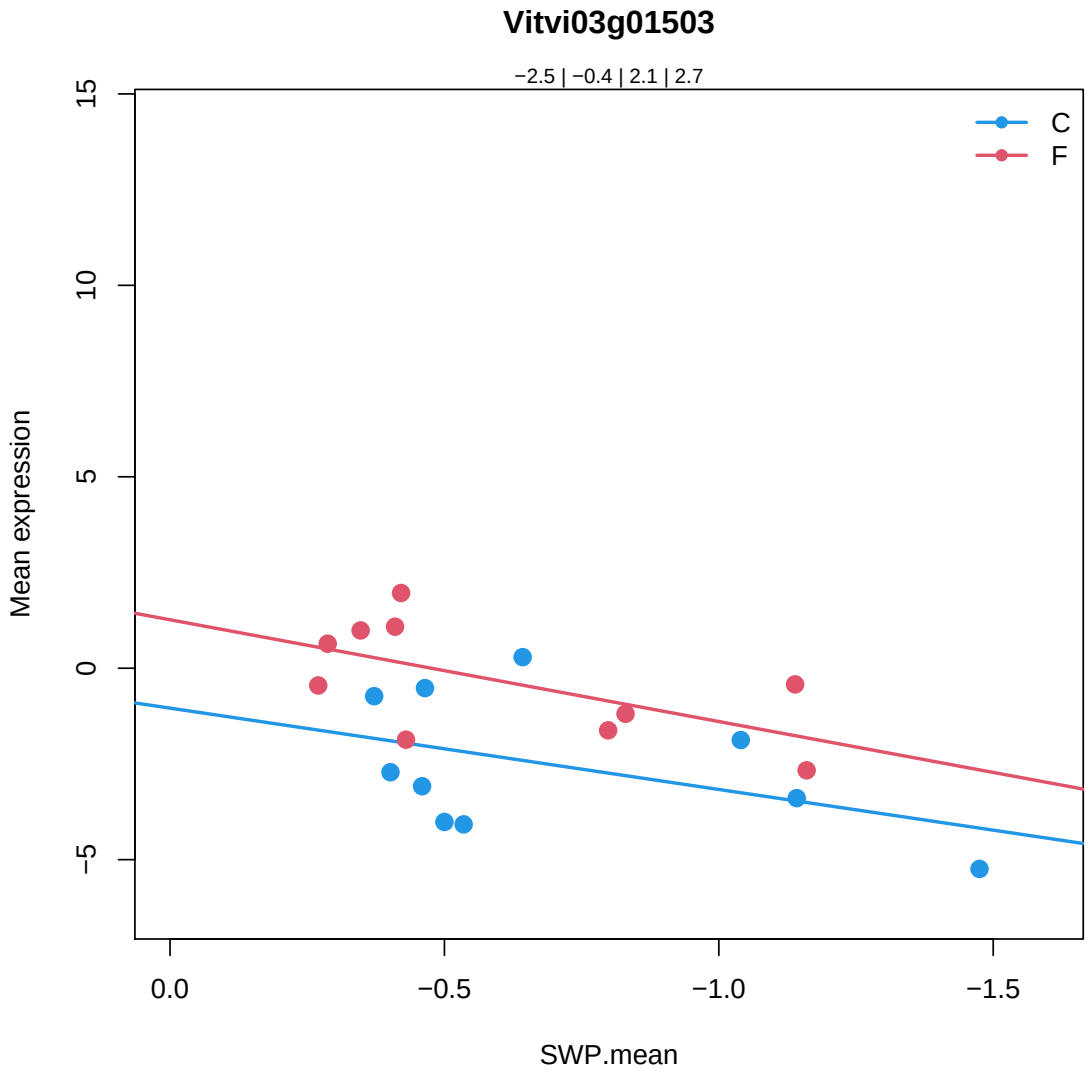
7.3.15 Vitvi03g01503: type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g01503
        35.2
        not assigned.unknown
        Organ-specific protein S2
```

Coefficients for Vitvi03g01503.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	−2.536121	4.151528e−06	***	4.725735e−06	***
SlopeC	2.124611	0.07938146	.	0.5748584	
MeanF−MeanC	2.181984	0.00122855	**	0.01484977	*
SlopeF−SlopeC	0.5331686	0.7591512		0.9999488	



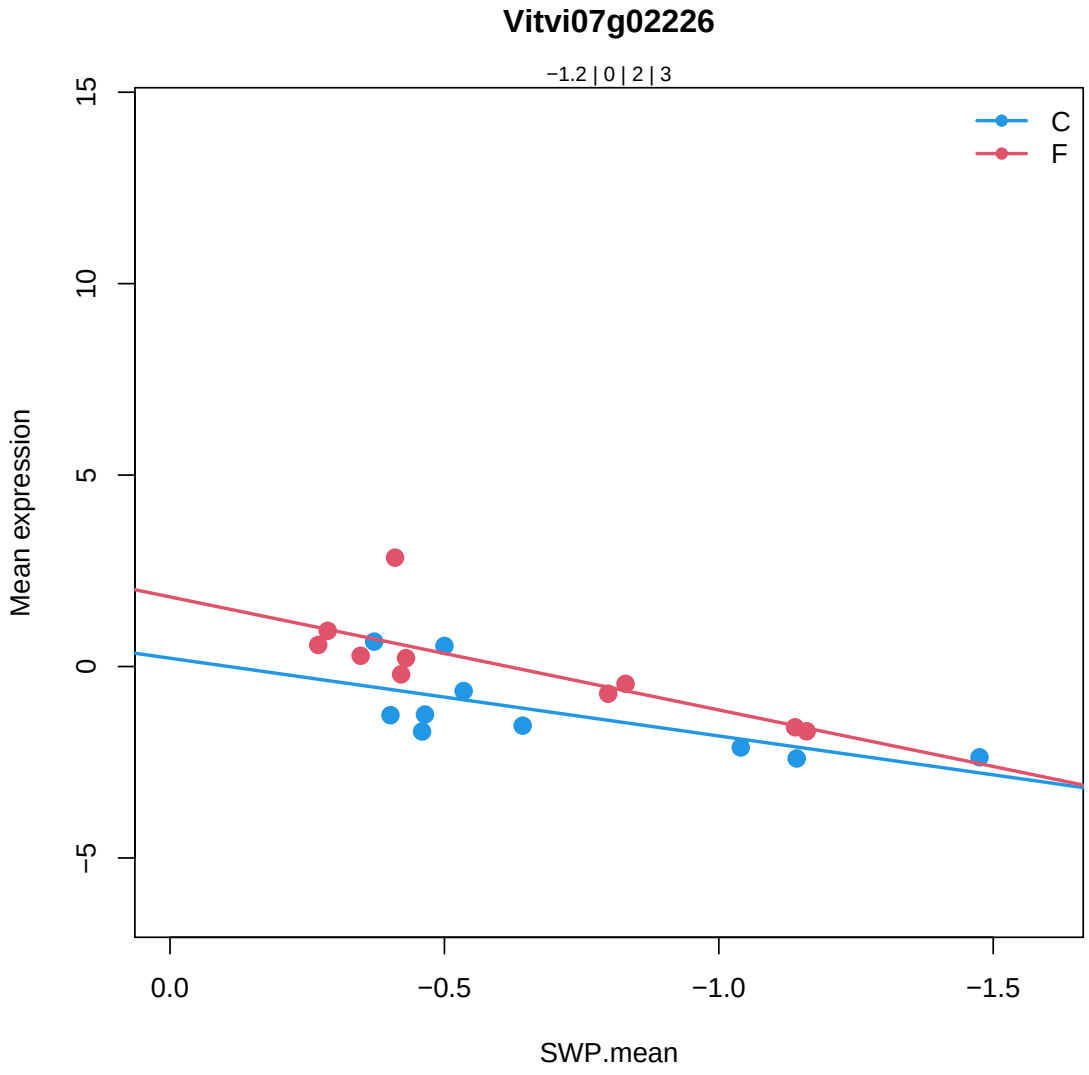
7.3.16 Vitvi07g02226: * type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g02226
        10.6.3
        cell wall.degradation.pectate lyases and polygalacturonases
        Pectin lyase-like superfamily protein |
        Chr3:9777025-9780267 FORWARD LENGTH=470 |
        201606
```

Coefficients for Vitvi07g02226.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.210898	6.960267e-05	***	7.708231e-05	***
SlopeC	2.030632	0.007339062	**	0.2775732	
MeanF-MeanC	1.22983	0.001946382	**	0.02159152	*
SlopeF-SlopeC	0.9218452	0.3764086		0.9999488	



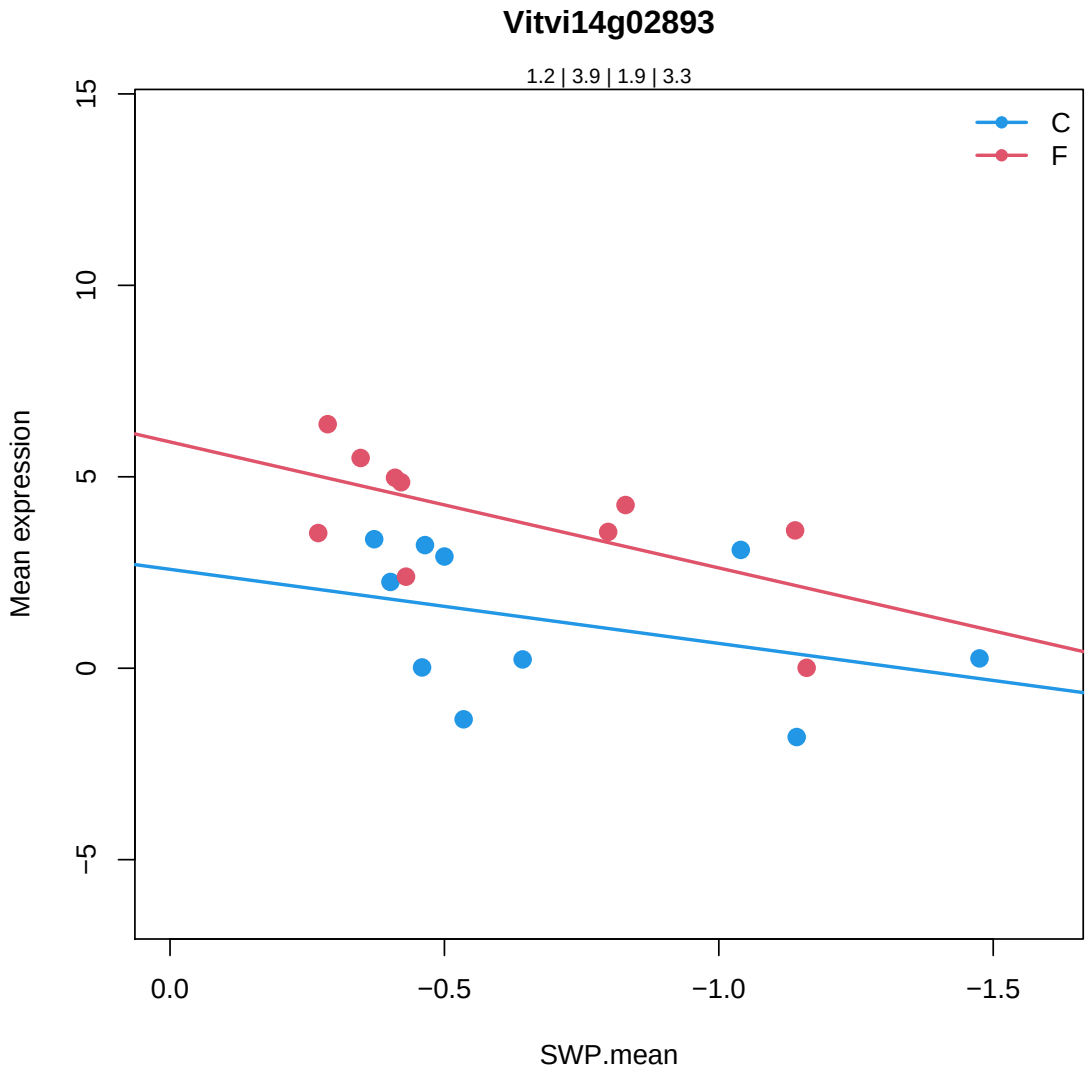
7.3.17 Vitvi14g02893: type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g02893
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi14g02893.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.221987	0.017794	*	0.01873169	*
SlopeC	1.934911	0.1585324		0.6889929	
MeanF-MeanC	2.683206	0.0006505913	***	0.008798857	**
SlopeF-SlopeC	1.355003	0.4992098		0.9999488	



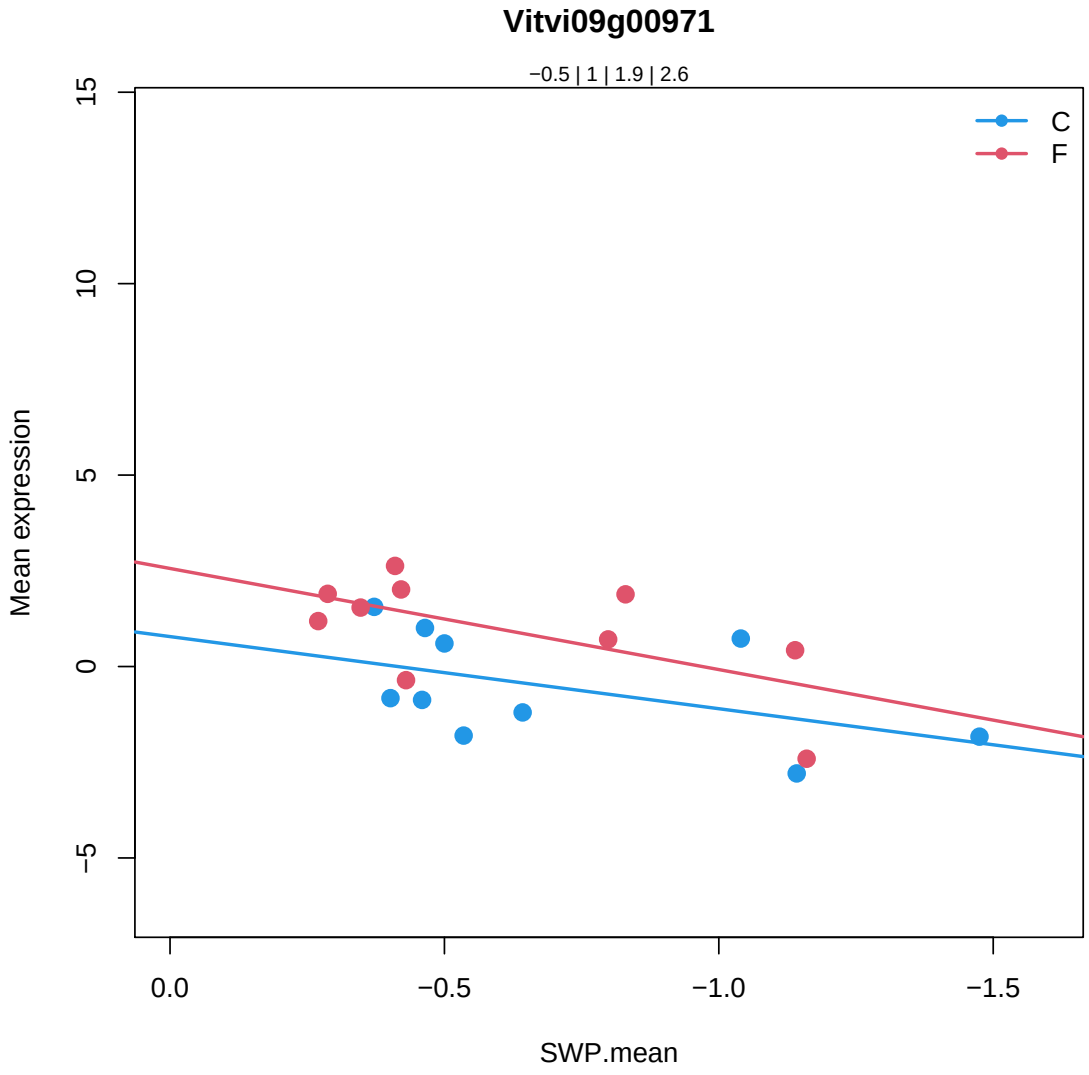
7.3.18 Vitvi09g00971: type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00971
        34.19.3
        transport.major intrinsic proteins.NIP
        NOD26-like intrinsic protein 6%3B1 |
        Chr1:30350640-30352015 REVERSE LENGTH=305 |
        201606
```

Coefficients for Vitvi09g00971.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.5429204	0.1436317		0.1479012	
SlopeC	1.883775	0.071919	.	0.5630621	
MeanF-MeanC	1.494678	0.007449359	**	0.06123152	.
SlopeF-SlopeC	0.7567378	0.6146061		0.9999488	



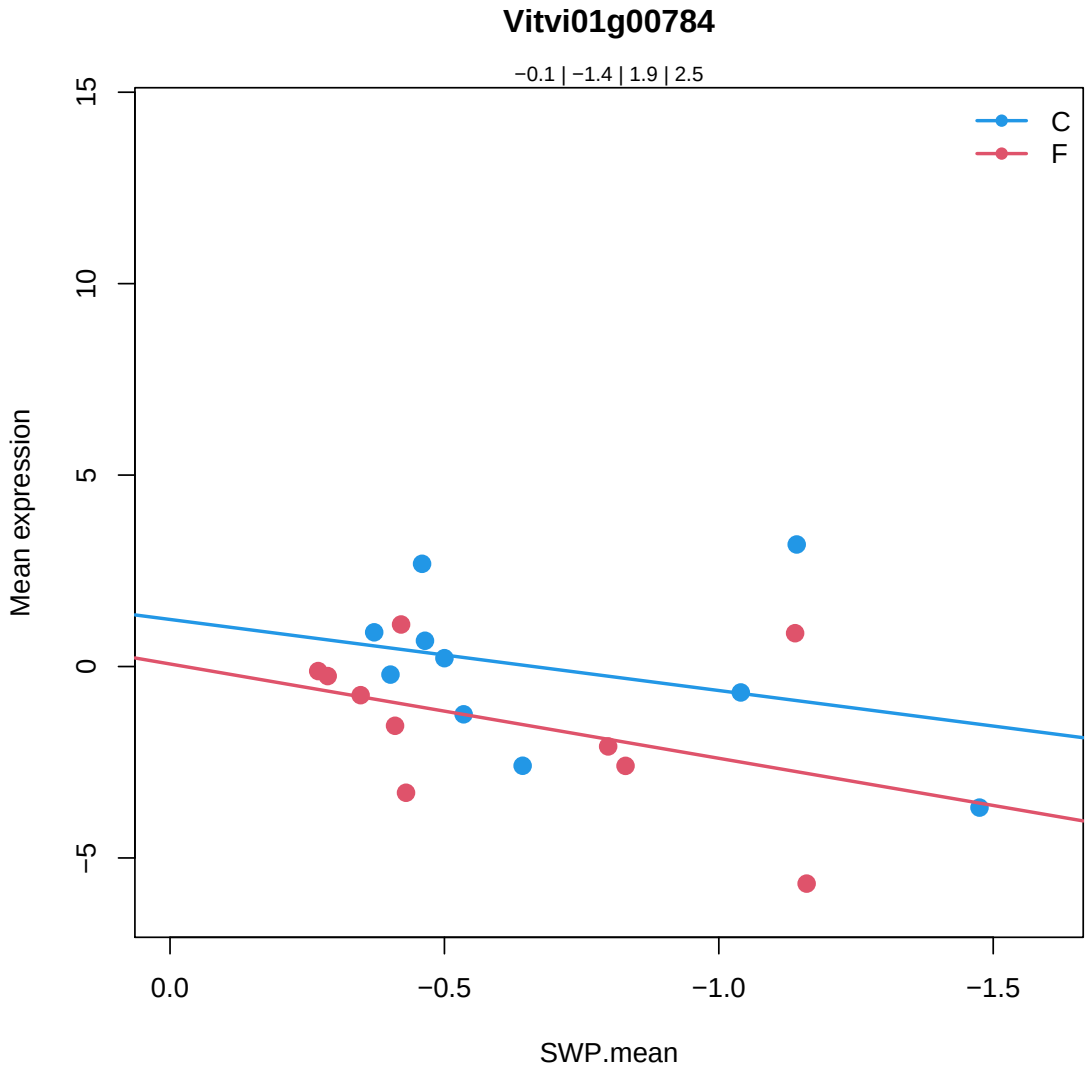
7.3.19 Vitvi01g00784: type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00784
        10.7
        cell wall.modification
        xyloglucan:xyloglucosyl transferase 33 |
        Chr1:3479257-3480957 REVERSE LENGTH=310 |
        201606
```

Coefficients for Vitvi01g00784.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.07603549	0.8952843		0.89764	
SlopeC	1.85592	0.2554205		0.7656086	
MeanF-MeanC	-1.358668	0.1069009		0.3801643	
SlopeF-SlopeC	0.6076206	0.7995979		0.9999488	



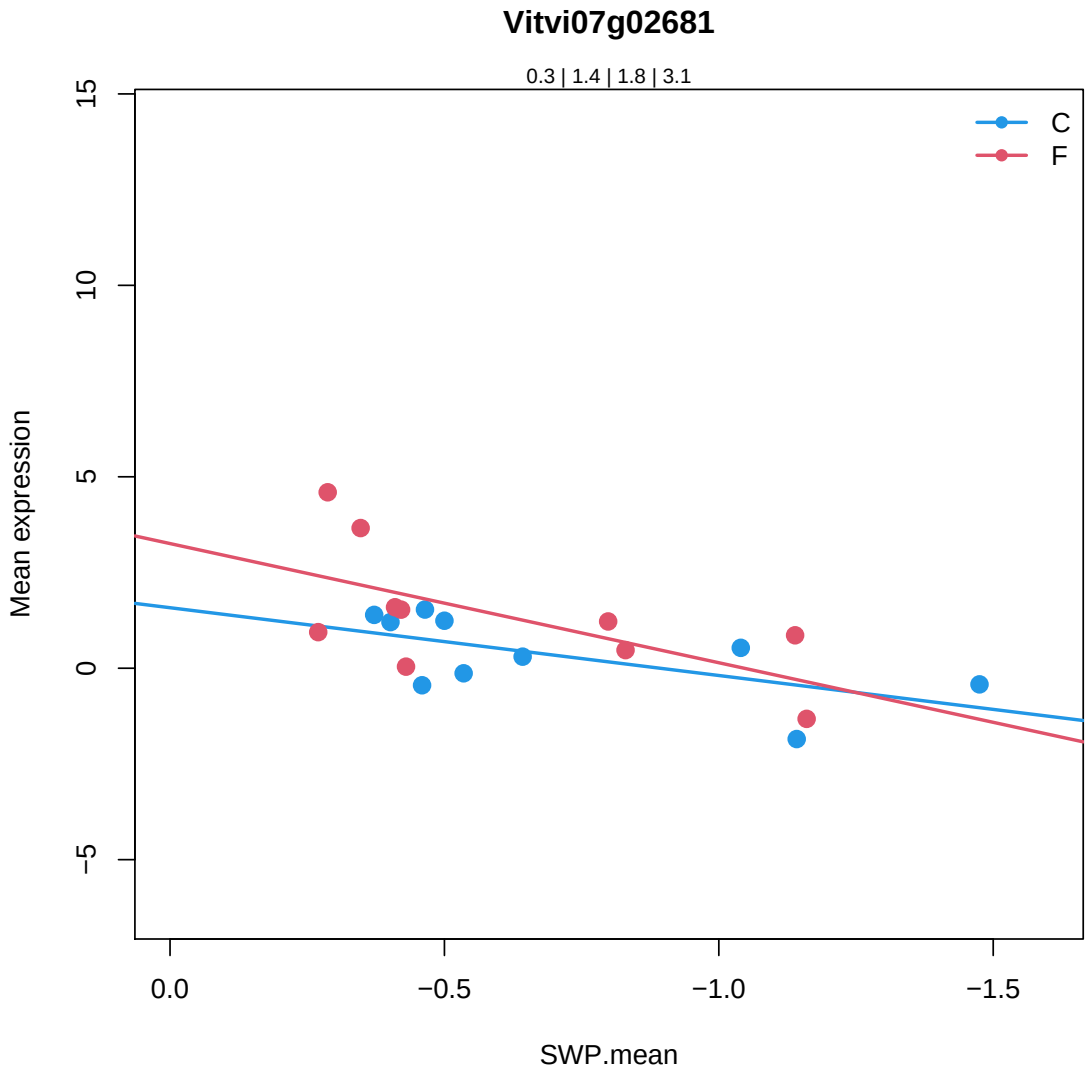
7.3.20 Vitvi07g02681: type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g02681
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi07g02681.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3353629	0.3204223		0.3261789	
SlopeC	1.770583	0.06691152	.	0.5548906	
MeanF-MeanC	1.023932	0.03922308	*	0.2038273	
SlopeF-SlopeC	1.342068	0.3365688		0.9999488	



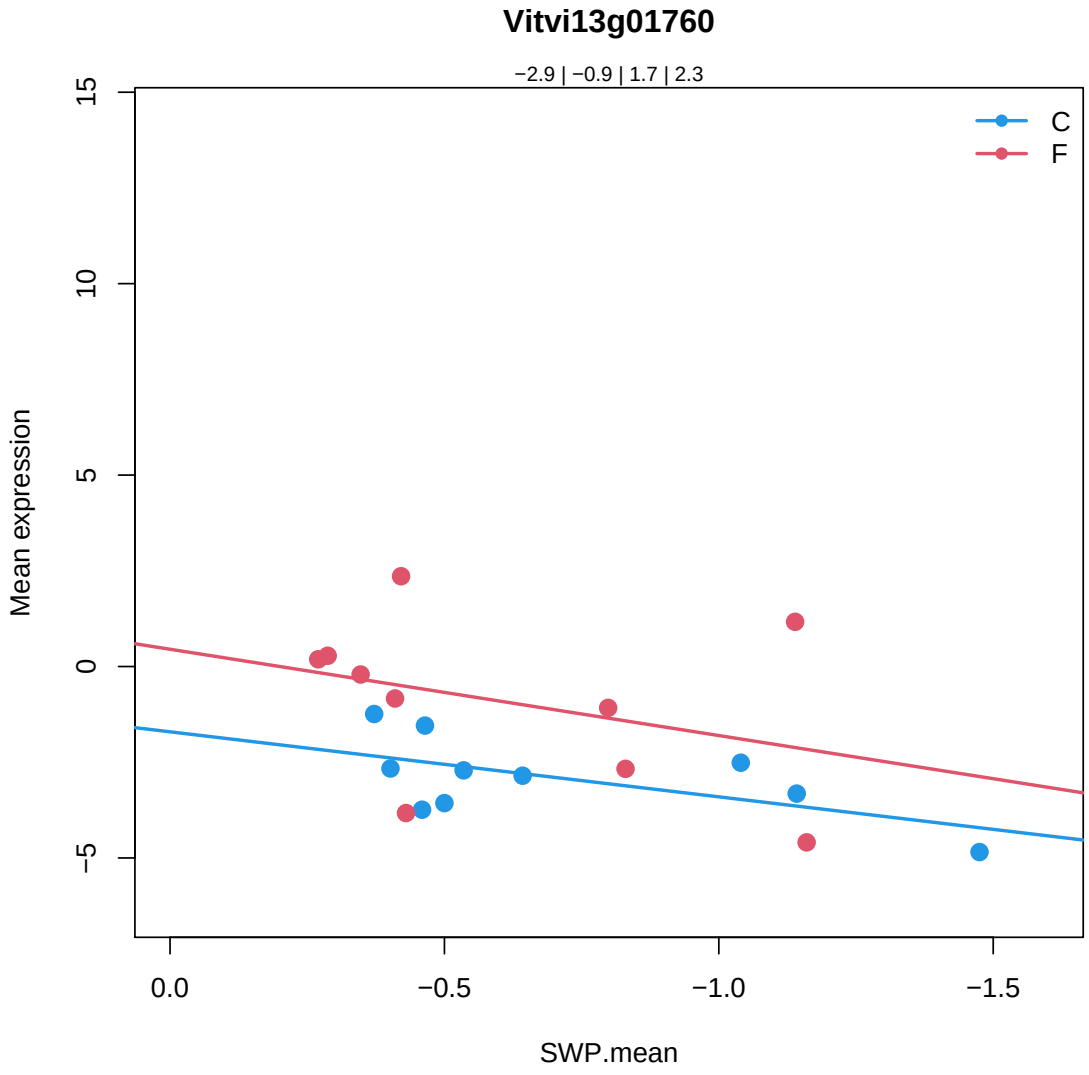
7.3.21 Vitvi13g01760: type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g01760
        35.2
        not assigned.unknown
        Leucine-rich repeat (LRR) family protein |
        Chr3:7280930-7282027 FORWARD LENGTH=365 |
        201606
```

Coefficients for Vitvi13g01760.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-2.899762	2.749233e-06	***	3.140979e-06	***
SlopeC	1.698164	0.1988836		0.7265417	
MeanF-MeanC	1.977597	0.00616659	**	0.05307237	.
SlopeF-SlopeC	0.5558194	0.7734422		0.9999488	



7.3.22 Vitvi19g00094: type2

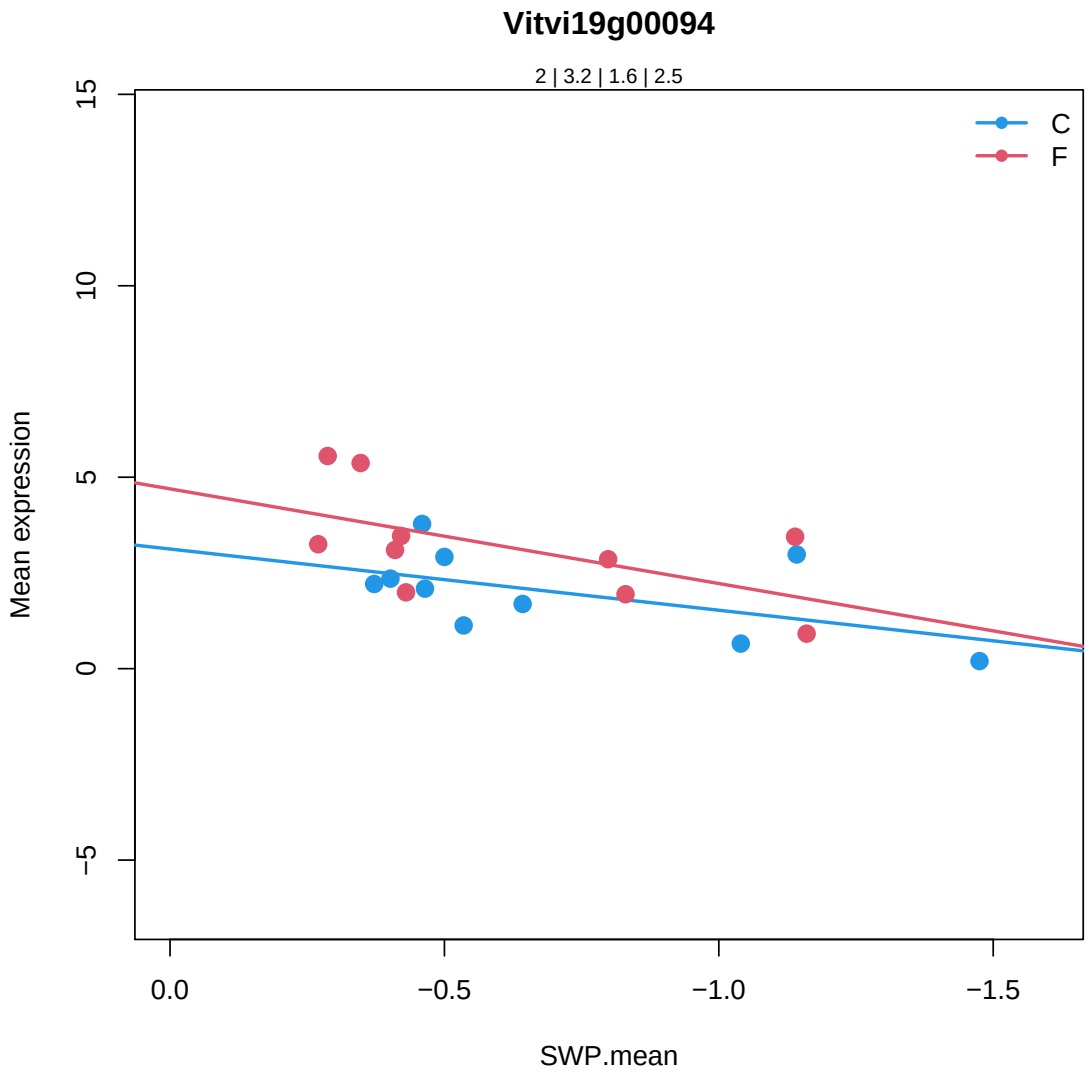
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g00094
        20.1.7
        stress.biotic.PR-proteins
        pathogenesis-related family protein |
        Chr1:29621447-29622431 REVERSE LENGTH=238 |
        201606

Vitvi19g00094
        35.2
        not assigned.unknown
        pathogenesis-related family protein |
        Chr1:29621447-29622431 REVERSE LENGTH=238 |
        201606
```

Coefficients for Vitvi19g00094.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.000287	2.504844e-06	***	2.864343e-06	***
SlopeC	1.598781	0.08255374	.	0.5797186	
MeanF-MeanC	1.188635	0.01437332	*	0.09904078	.
SlopeF-SlopeC	0.8735558	0.5108944		0.9999488	


Vitvi19g00094
2 | 3.2 | 1.6 | 2.5
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

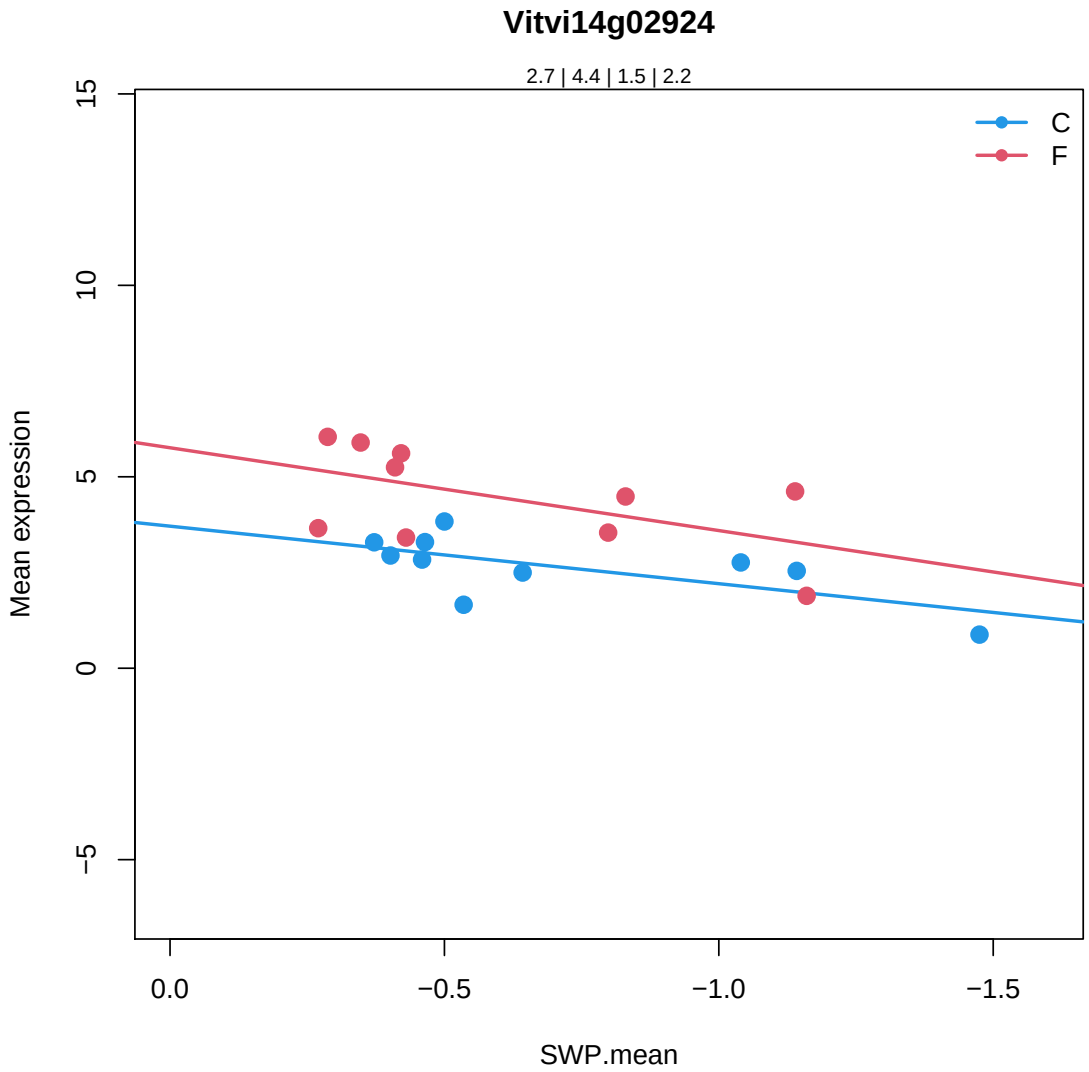
7.3.23 Vitvi14g02924: type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g02924
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi14g02924.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.65358	2.158855e-09	***	2.692518e-09	***
SlopeC	1.502144	0.05850777	.	0.5384614	
MeanF-MeanC	1.786688	0.0001229555	***	0.002154124	**
SlopeF-SlopeC	0.660274	0.5612348		0.9999488	



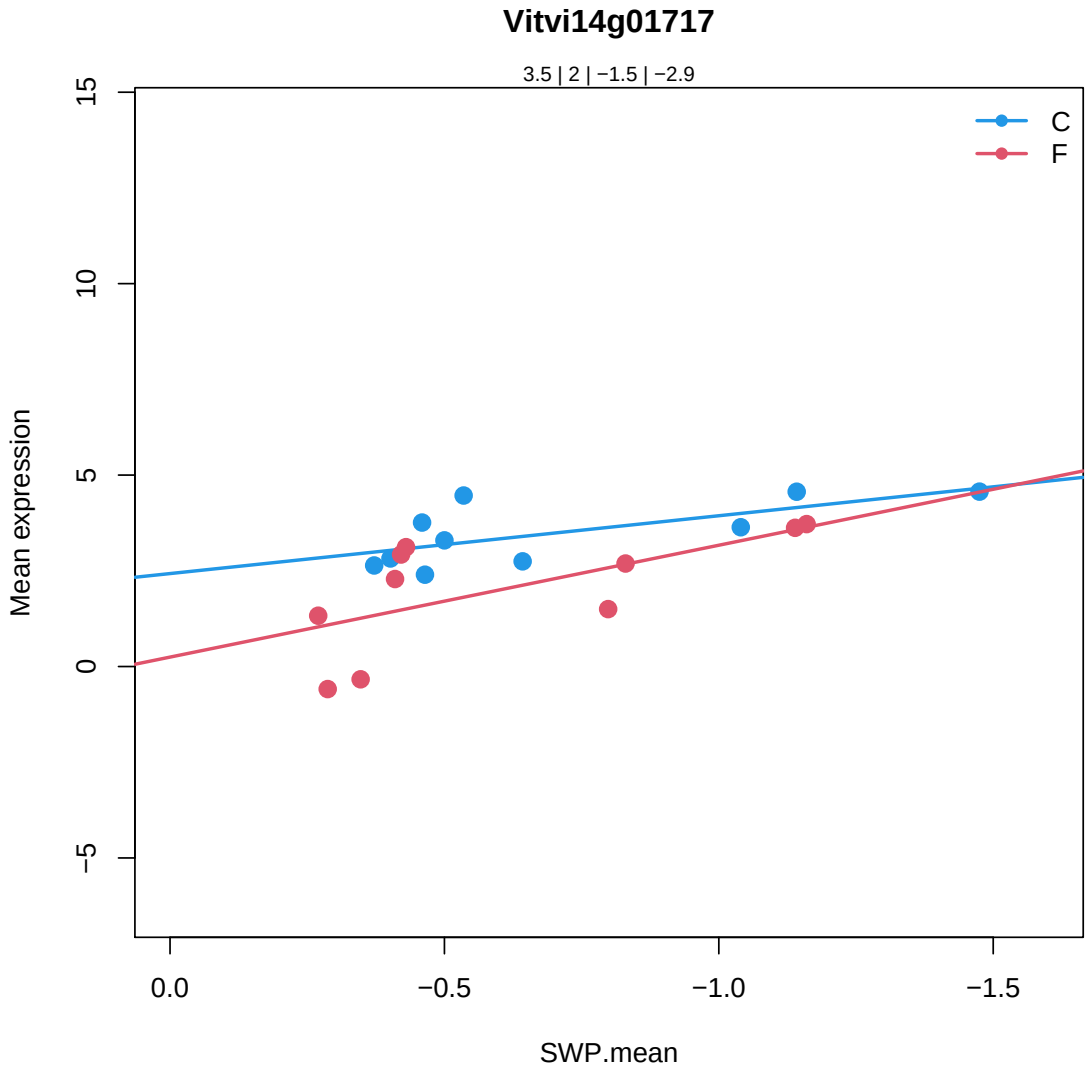
7.3.24 Vitvi14g01717: type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01717
        3.1.2.2
        minor CHO metabolism.raffinose family.raffinose synthases.putative
        Raffinose synthase family protein |
        Chr5:16161720-16165085 FORWARD LENGTH=783 |
        201606
```

Coefficients for Vitvi14g01717.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.48977	2.551646e-11	***	3.423608e-11	***
SlopeC	-1.510356	0.06495838	.	0.5518928	
MeanF-MeanC	-1.463541	0.001266488	**	0.01523584	*
SlopeF-SlopeC	-1.411876	0.2350381		0.9999488	



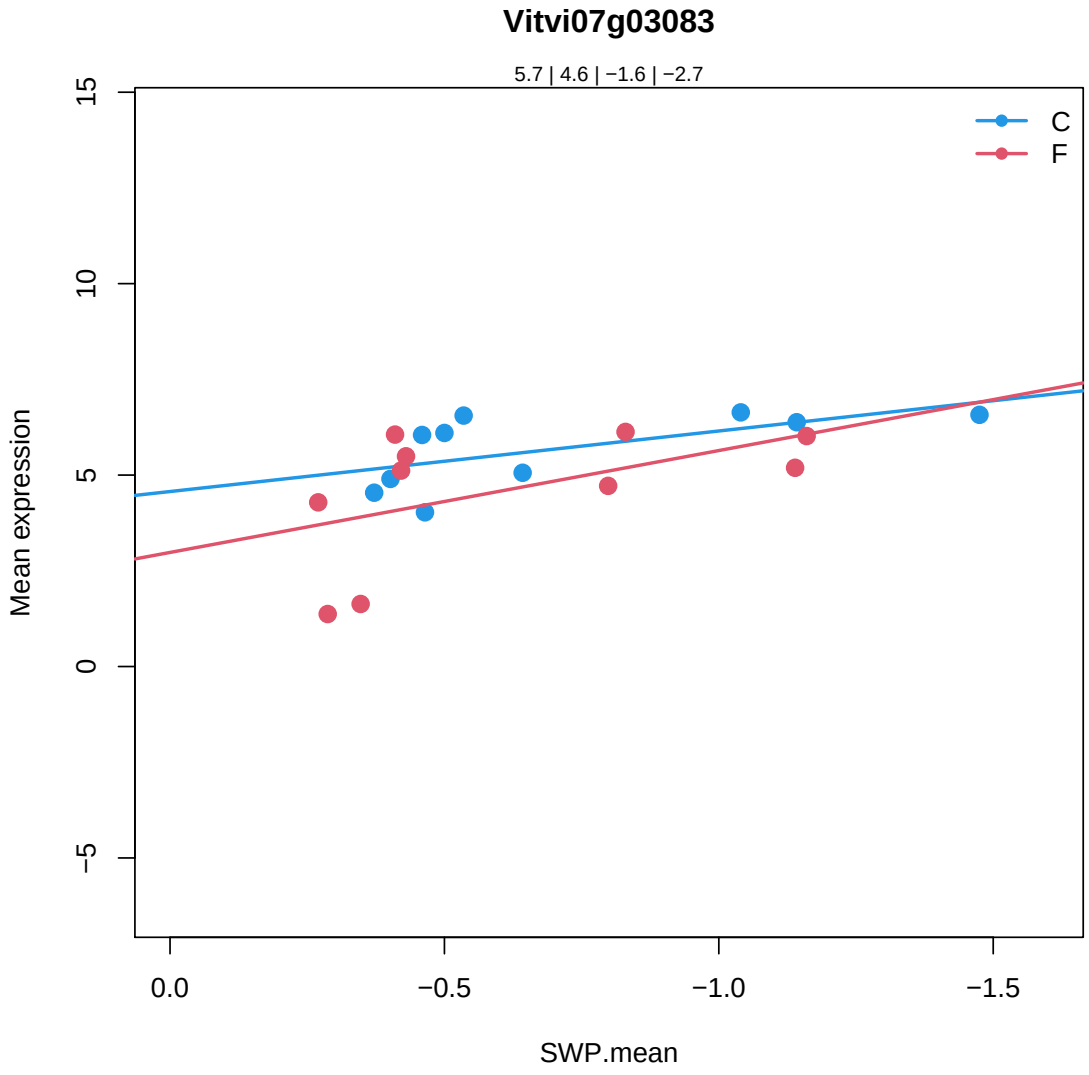
7.3.25 Vitvi07g03083: type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g03083
        16.2.1.10
        secondary metabolism.phenylpropanoids.lignin biosynthesis.CAD
        cinnamyl alcohol dehydrogenase 7 |
        Chr4:17852670-17854302 FORWARD LENGTH=357 |
        201606
```

Coefficients for Vitvi07g03083.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.681929	1.478938e-13	***	2.242536e-13	***
SlopeC	-1.581192	0.1177783		0.6341652	
MeanF-MeanC	-1.080877	0.03958276	*	0.204845	
SlopeF-SlopeC	-1.079921	0.4626984		0.9999488	



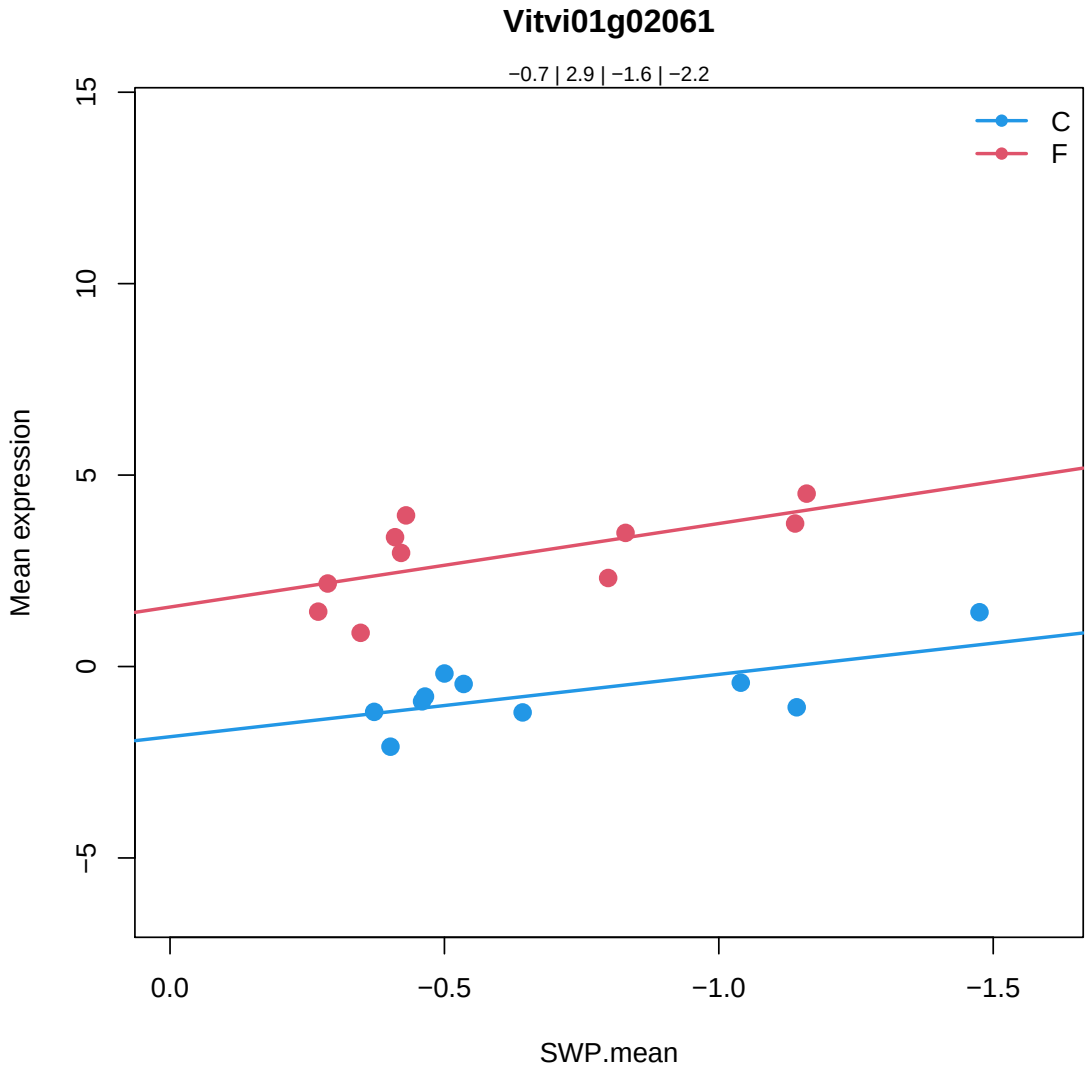
7.3.26 Vitvi01g02061: * type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g02061
        35.1.26
        not assigned.no ontology.DC1 domain containing protein
        DC1 domain-containing protein |
        Chr1:22261978-22264243 FORWARD LENGTH=578 |
        201606
```

Coefficients for Vitvi01g02061.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.6880274	0.009278023	**	0.009836925	**
SlopeC	-1.628569	0.02384104	*	0.3984486	
MeanF-MeanC	3.570542	6.641649e-10	***	4.033148e-08	***
SlopeF-SlopeC	-0.5520575	0.5853545		0.9999488	



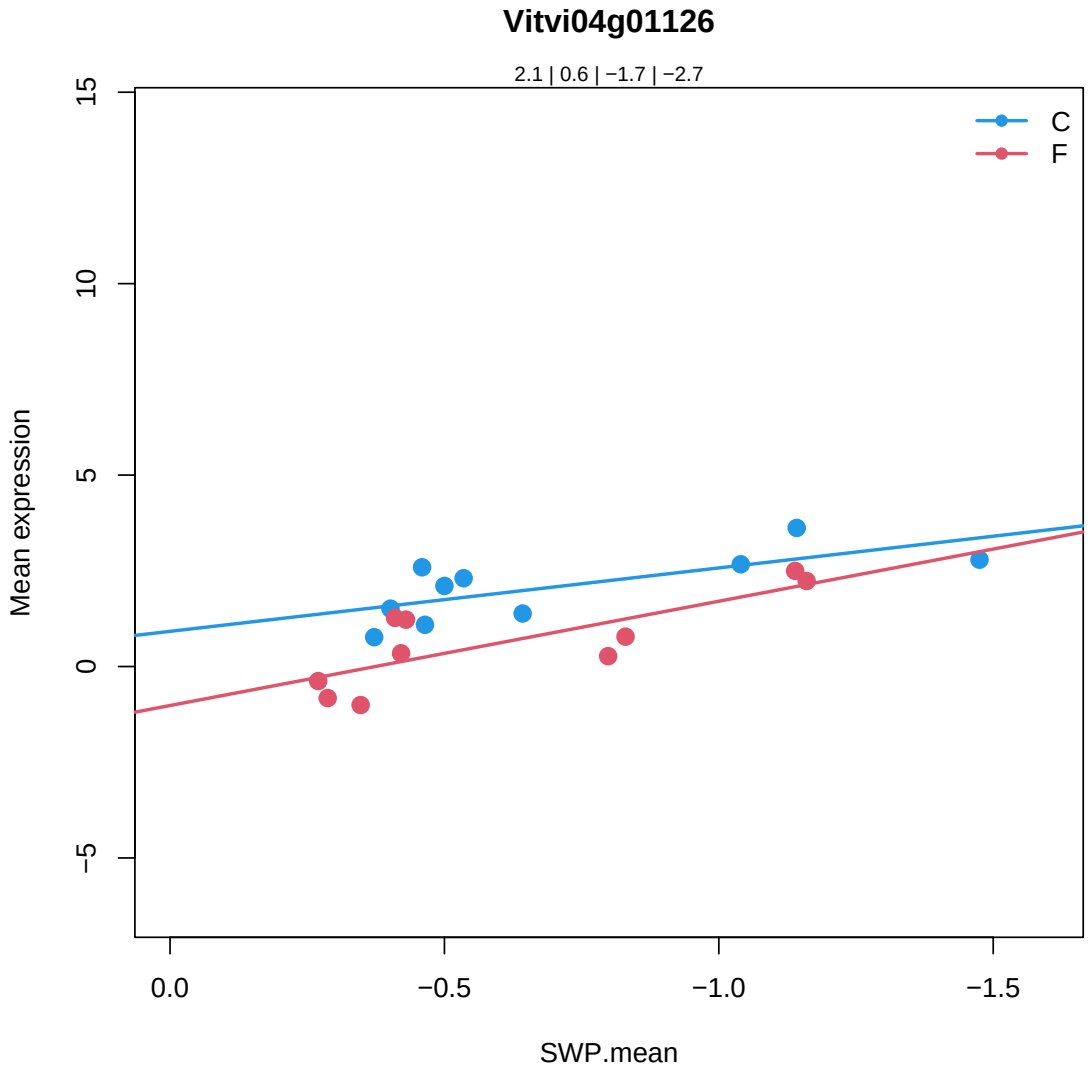
7.3.27 Vitvi04g01126: * type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01126
        35.2
        not assigned.unknown
        transmembrane protein |
        Chr5:14191711-14193654 REVERSE LENGTH=295 |
        201606
```

Coefficients for Vitvi04g01126.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.083353	2.456297e-09	***	3.058482e-09	***
SlopeC	-1.656076	0.01093921	*	0.3141738	
MeanF-MeanC	-1.442417	9.732007e-05	***	0.001768001	**
SlopeF-SlopeC	-1.068136	0.2404919		0.9999488	



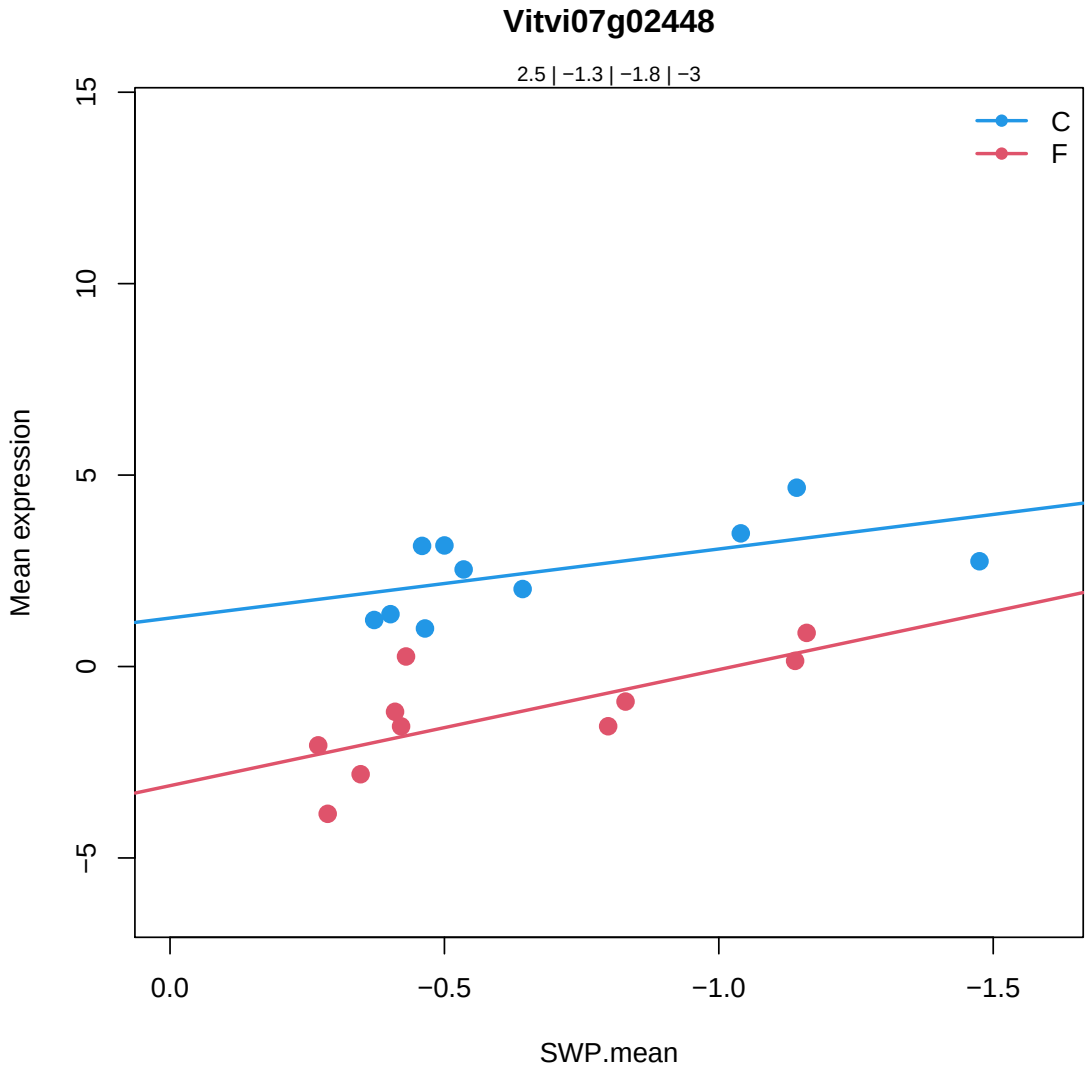
7.3.28 Vitvi07g02448: * type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g02448
        26.2
        misc.UDP glucosyl and glucoronyl transferases
        Uridine diphosphate glycosyltransferase 74E2 |
        Chr1:1703196-1704639 REVERSE LENGTH=453 |
        201606
```

Coefficients for Vitvi07g02448.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.534319	1.823511e-08	***	2.209025e-08	***
SlopeC	-1.803435	0.03725763	*	0.4620709	
MeanF-MeanC	-3.799573	6.720516e-09	***	3.41447e-07	***
SlopeF-SlopeC	-1.227884	0.3209972		0.9999488	



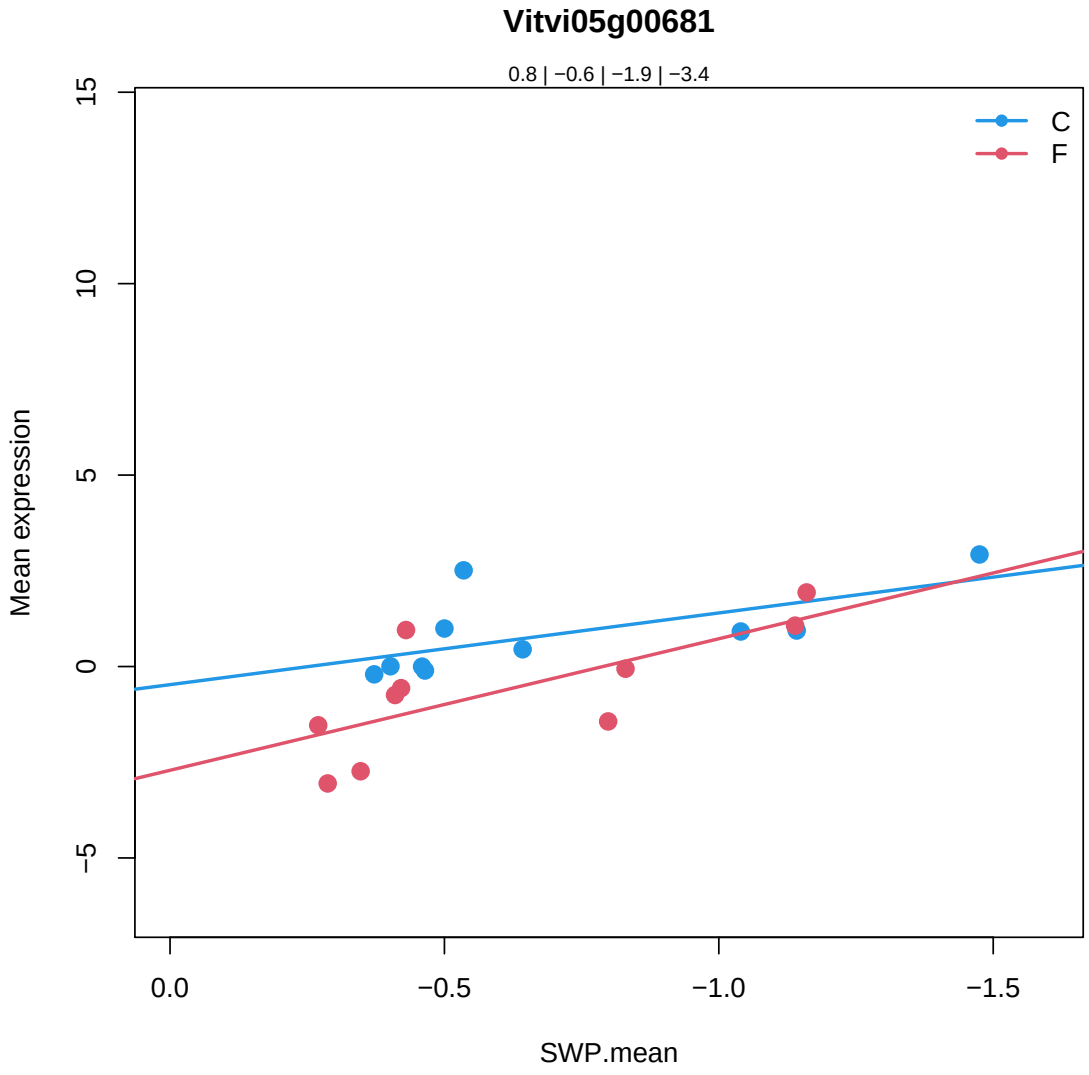
7.3.29 Vitvi05g00681: * type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00681
        10.2.1
        cell wall.cellulose synthesis.cellulose synthase
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi05g00681.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8430558	0.009925451	**	0.01051311	*
SlopeC	−1.872315	0.03446689	*	0.444078	
MeanF−MeanC	−1.460116	0.002266089	**	0.02434089	*
SlopeF−SlopeC	−1.563097	0.218861		0.9999488	



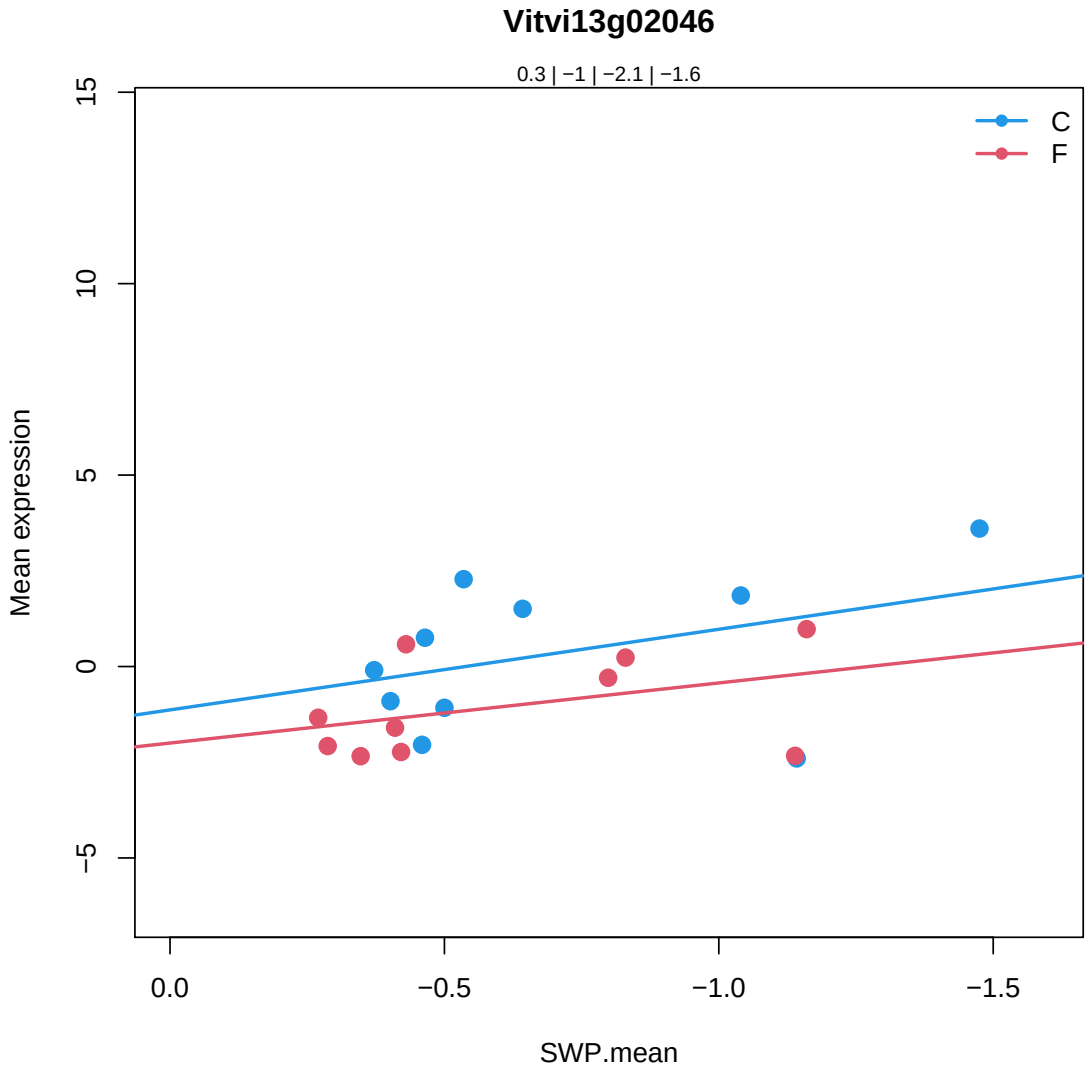
7.3.30 Vitvi13g02046: type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g02046
        35.2
        not assigned.unknown
        Low temperature and salt responsive protein family |
        Chr3:1756195-1756494 REVERSE LENGTH=54 |
        201606
```

Coefficients for Vitvi13g02046.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3474452	0.4477327		0.4538367	
SlopeC	−2.106085	0.10648		0.6211132	
MeanF−MeanC	−1.389891	0.039901	*	0.2059503	
SlopeF−SlopeC	0.5362332	0.7759191		0.9999488	



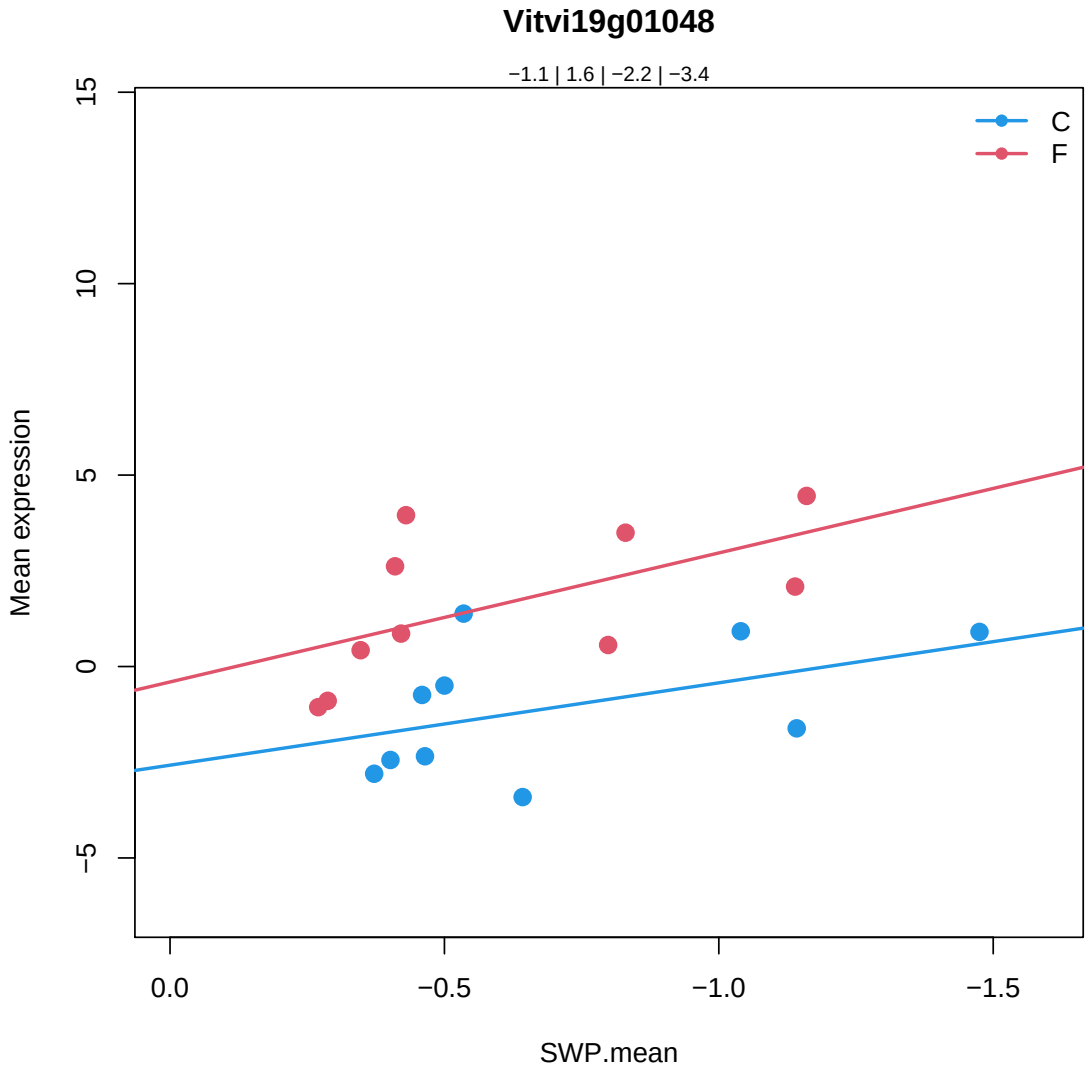
7.3.31 Vitvi19g01048: type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g01048
        26.9
        misc.glutathione S transferases
        glutathione S-transferase TAU 25 |
        Chr1:5872208-5872958 FORWARD LENGTH=221 |
        201606
```

Coefficients for Vitvi19g01048.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.064541	0.02951157	*	0.03089603	*
SlopeC	-2.150775	0.1048283		0.6181019	
MeanF-MeanC	2.714192	0.0003836245	***	0.005633145	**
SlopeF-SlopeC	-1.218795	0.5258973		0.9999488	



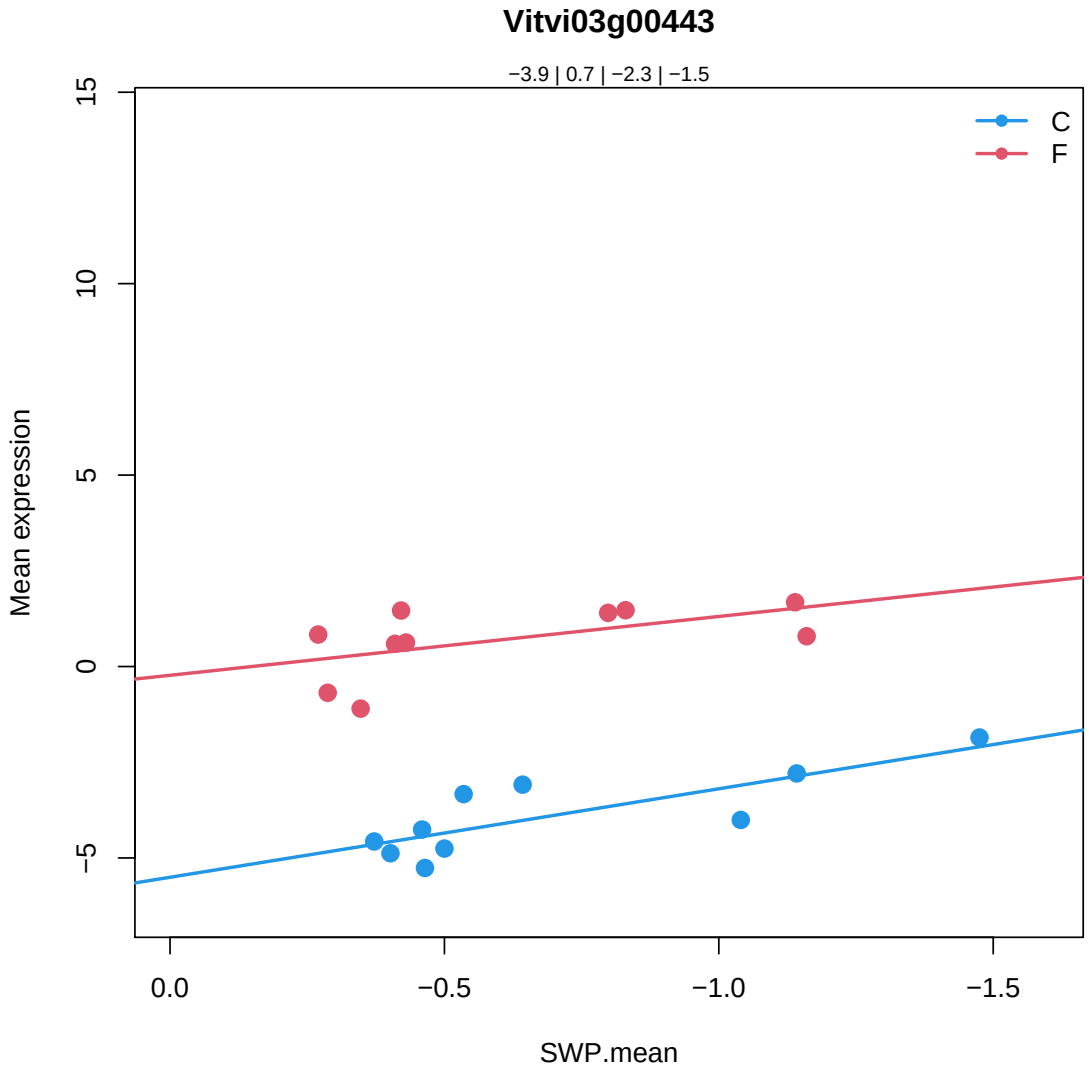
7.3.32 Vitvi03g00443: * type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00443
        26.8
        misc.nitrilases, nitrile lyases, berberine bridge enzymes, reticuline
        acetone-cyanohydrin lyase |
        Chr2:10042681-10043686 REVERSE LENGTH=187 |
        201606
```

Coefficients for Vitvi03g00443.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-3.879575	2.657365e-14	***	4.276136e-14	***
SlopeC	-2.311521	0.001013174	**	0.1271346	
MeanF-MeanC	4.586549	9.379116e-13	***	8.360029e-11	***
SlopeF-SlopeC	0.7750986	0.401223		0.9999488	



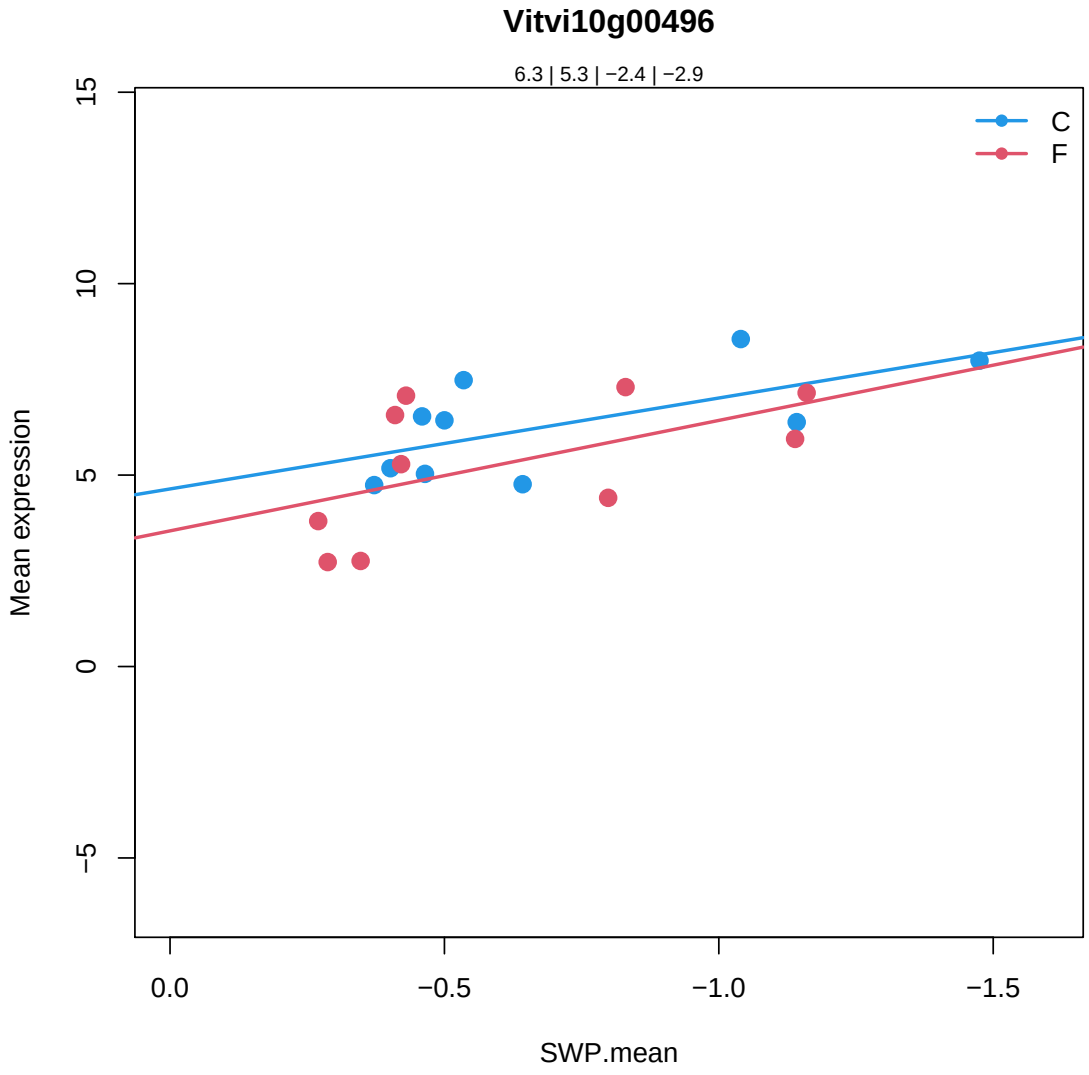
7.3.33 Vitvi10g00496: * type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00496
        20.2.1
        stress.abiotic.heat
        DNAJ heat shock family protein |
        Chr2:8848353-8849815 REVERSE LENGTH=337 |
        201606
```

Coefficients for Vitvi10g00496.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.307557	1.015293e-13	***	1.558732e-13	***
SlopeC	-2.37507	0.03527843	*	0.449641	
MeanF-MeanC	-1.007003	0.07458251	.	0.3074175	
SlopeF-SlopeC	-0.5100529	0.7489109		0.9999488	



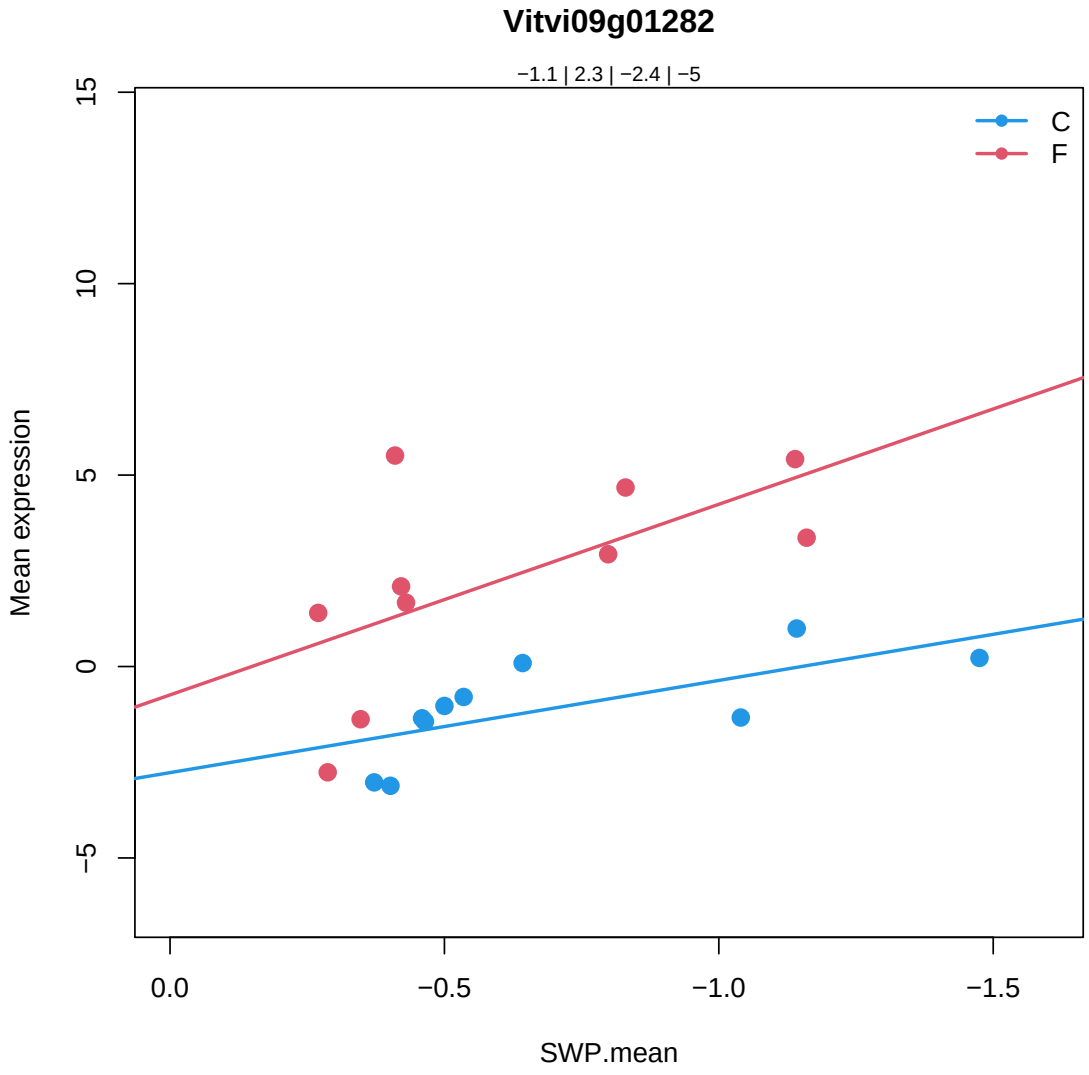
7.3.34 Vitvi09g01282: type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g01282
        26.13
        misc.acid and other phosphatases
        HAD superfamily%2C subfamily IIIB acid phosphatase |
        Chr4:12901736-12902882 REVERSE LENGTH=260 |
        201606
```

Coefficients for Vitvi09g01282.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	−1.078226	0.03754027	*	0.03919906	*
SlopeC	−2.408129	0.08927348	.	0.5953805	
MeanF−MeanC	3.37008	7.180676e−05	***	0.001351208	**
SlopeF−SlopeC	−2.570707	0.2154002		0.9999488	



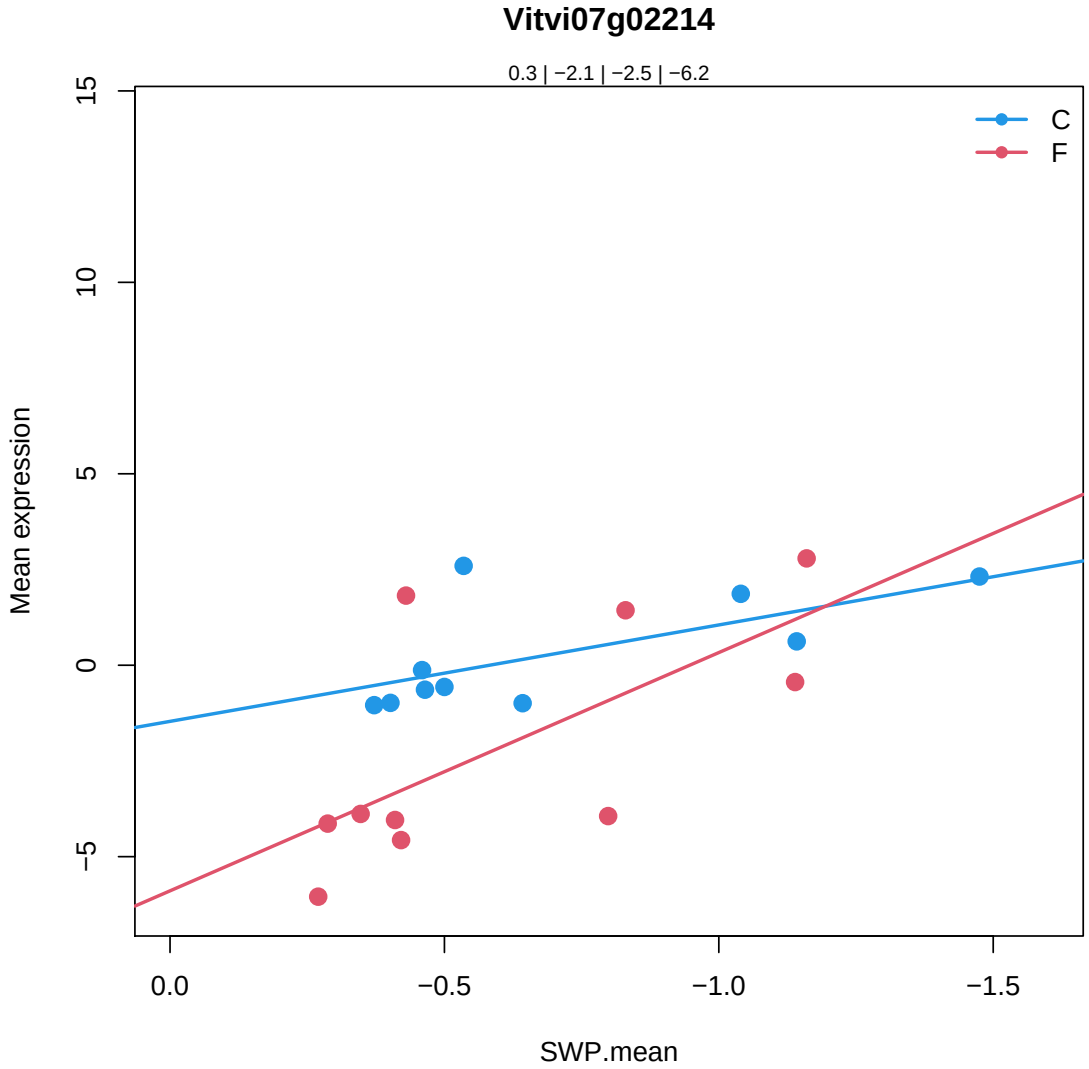
7.3.35 Vitvi07g02214: type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g02214
        35.2
        not assigned.unknown
        GATA transcription factor 22 IPR000679 Zinc finger, GATA-type
```

Coefficients for Vitvi07g02214.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3045917	0.5752195		0.5808597	
SlopeC	−2.518808	0.1052292		0.619507	
MeanF−MeanC	−2.405858	0.004444061	**	0.04150513	*
SlopeF−SlopeC	−3.70436	0.1091801		0.9999488	



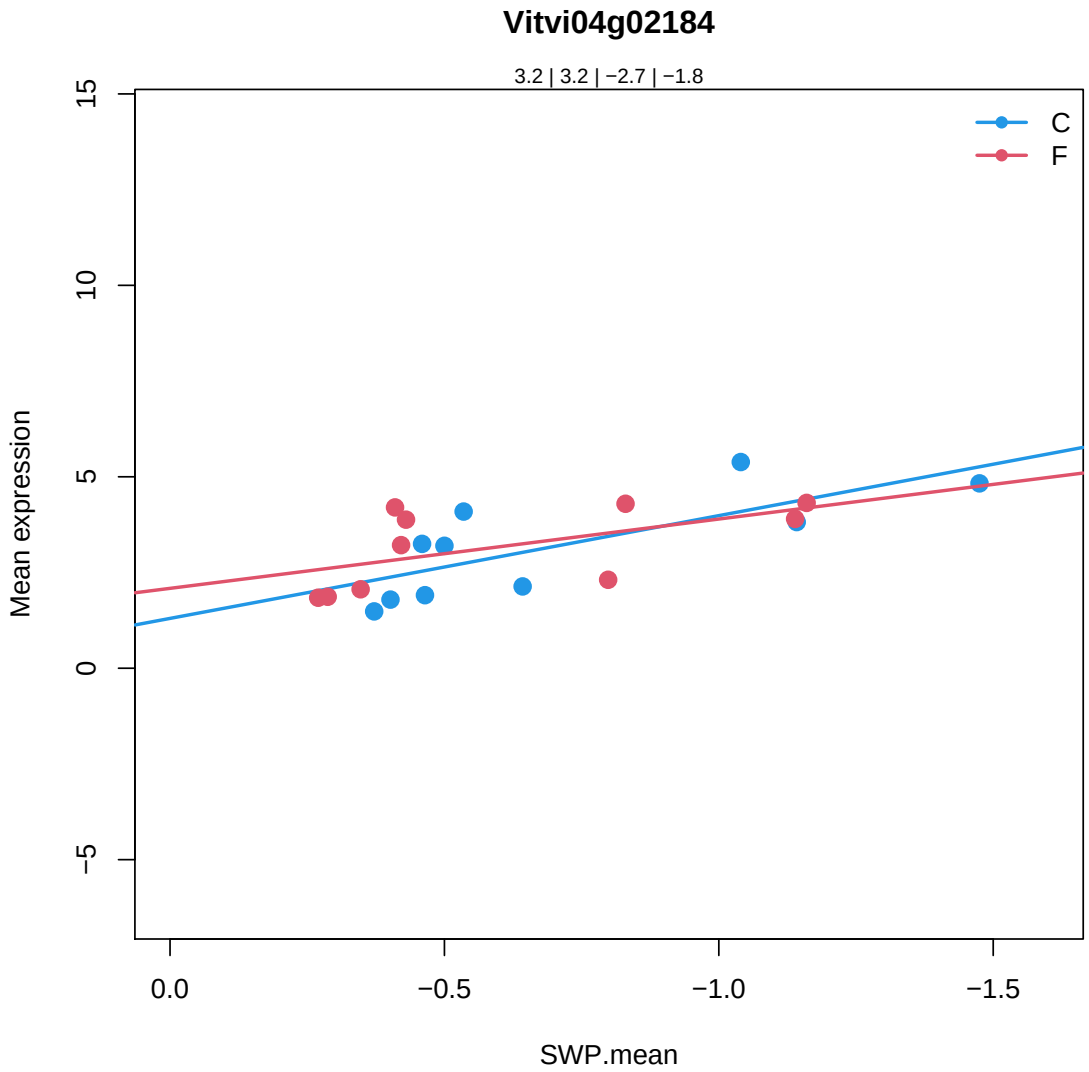
7.3.36 Vitvi04g02184: * type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g02184
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi04g02184.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.188648	4.960672e-11	***	6.572546e-11	***
SlopeC	-2.684272	0.001446058	**	0.1479249	
MeanF-MeanC	4.405018e-05	0.999907		0.9999648	
SlopeF-SlopeC	0.8740834	0.4329252		0.9999488	



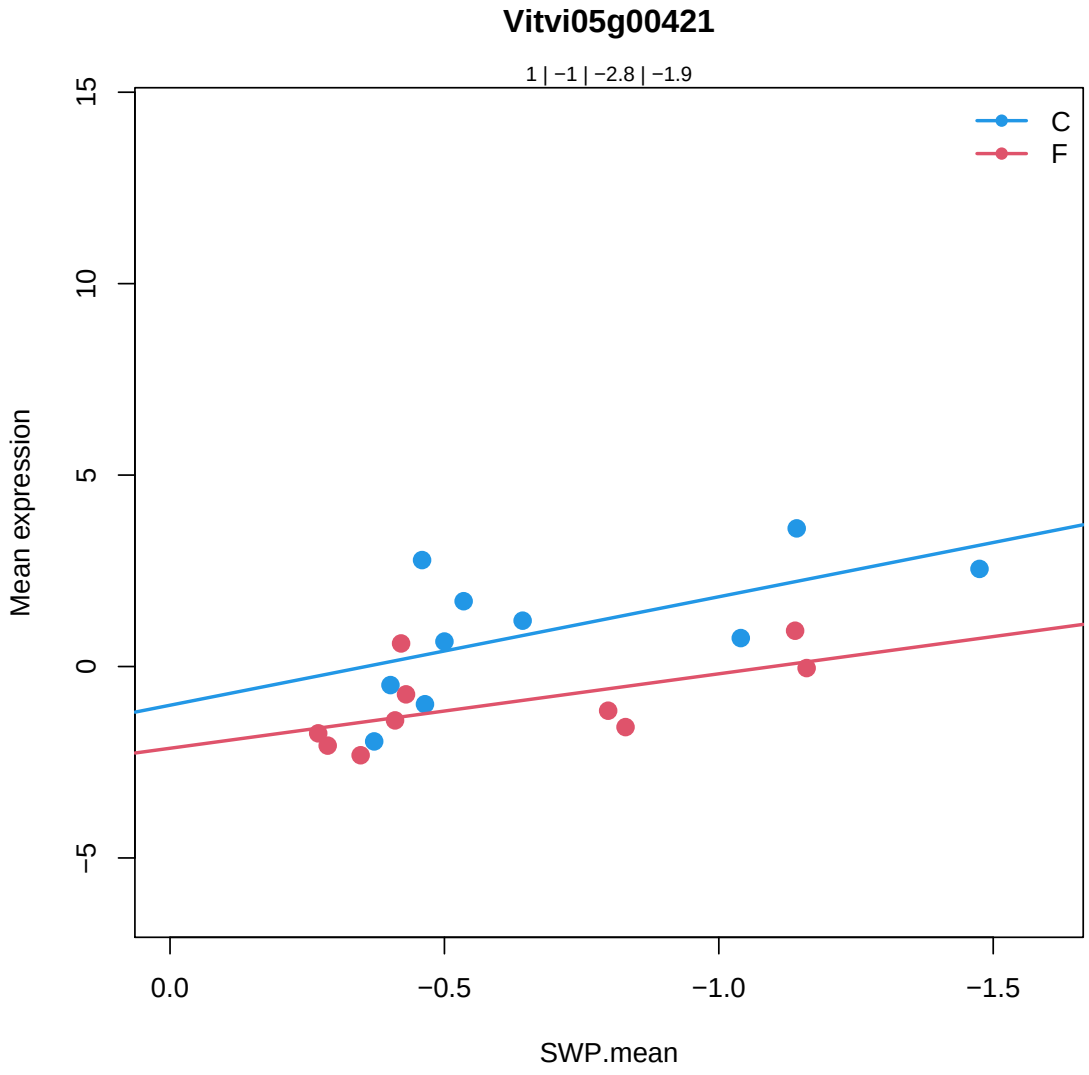
7.3.37 Vitvi05g00421: * type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00421
        17.4.1
        hormone metabolism.cytokinin.synthesis-degradation
        isopentenyltransferase 5 |
        Chr5:6362389-6363381 REVERSE LENGTH=330 |
        201606
```

Coefficients for Vitvi05g00421.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.9809172	0.01036541	*	0.01097607	*
SlopeC	−2.832505	0.008139059	**	0.2851324	
MeanF−MeanC	−1.931301	0.0007771899	***	0.01010745	*
SlopeF−SlopeC	0.8876307	0.5456677		0.9999488	



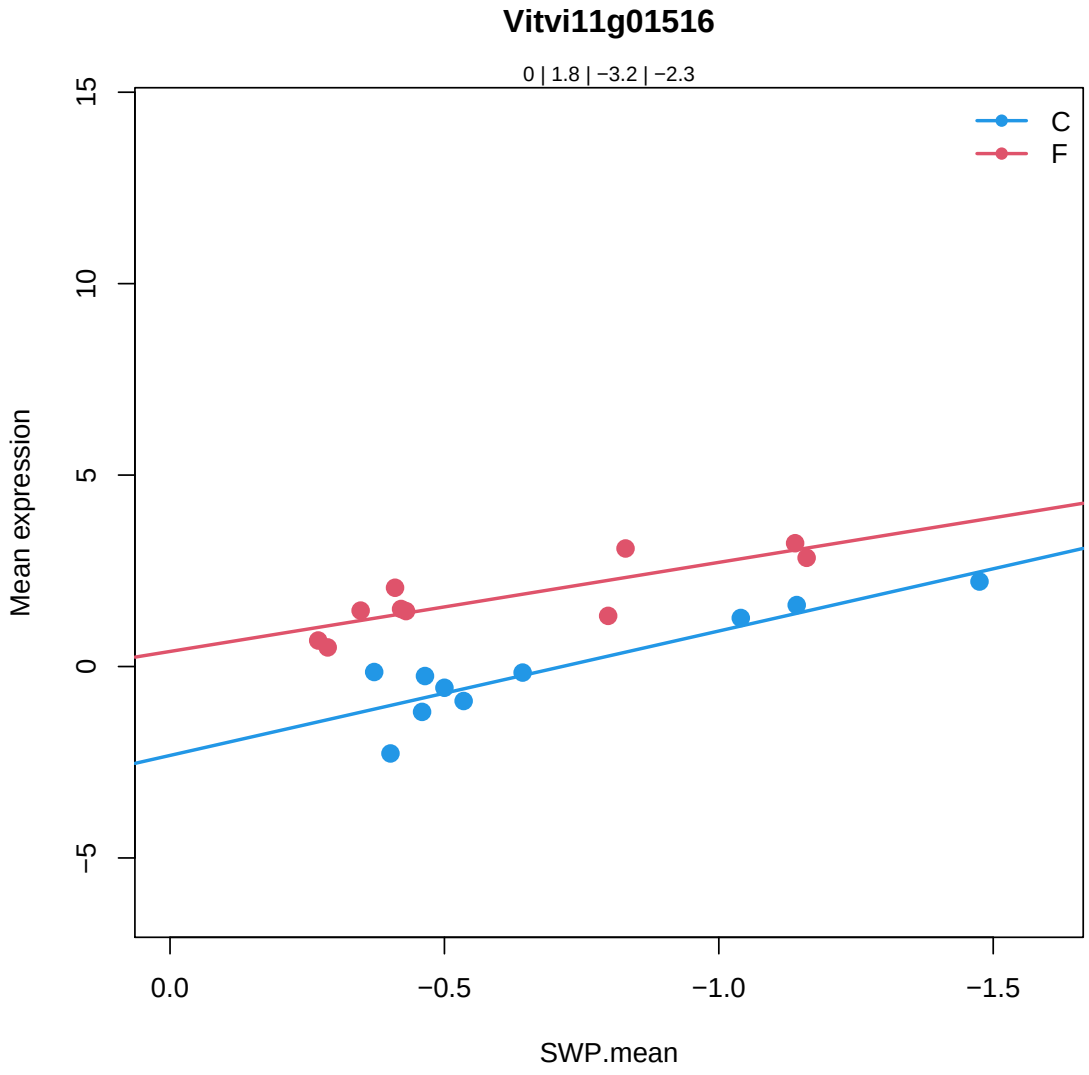
7.3.38 Vitvi11g01516: * type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g01516
        29.5.5
        protein.degradation.serine protease
        serine carboxypeptidase-like 29 |
        Chr4:15003474-15006017 FORWARD LENGTH=479 |
        201606
```

Coefficients for Vitvi11g01516.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.03709564	0.840428		0.8435271	
SlopeC	-3.24962	2.102715e-06	***	0.01365018	*
MeanF-MeanC	1.848123	3.942282e-07	***	1.417176e-05	***
SlopeF-SlopeC	0.9230391	0.2339817		0.9999488	



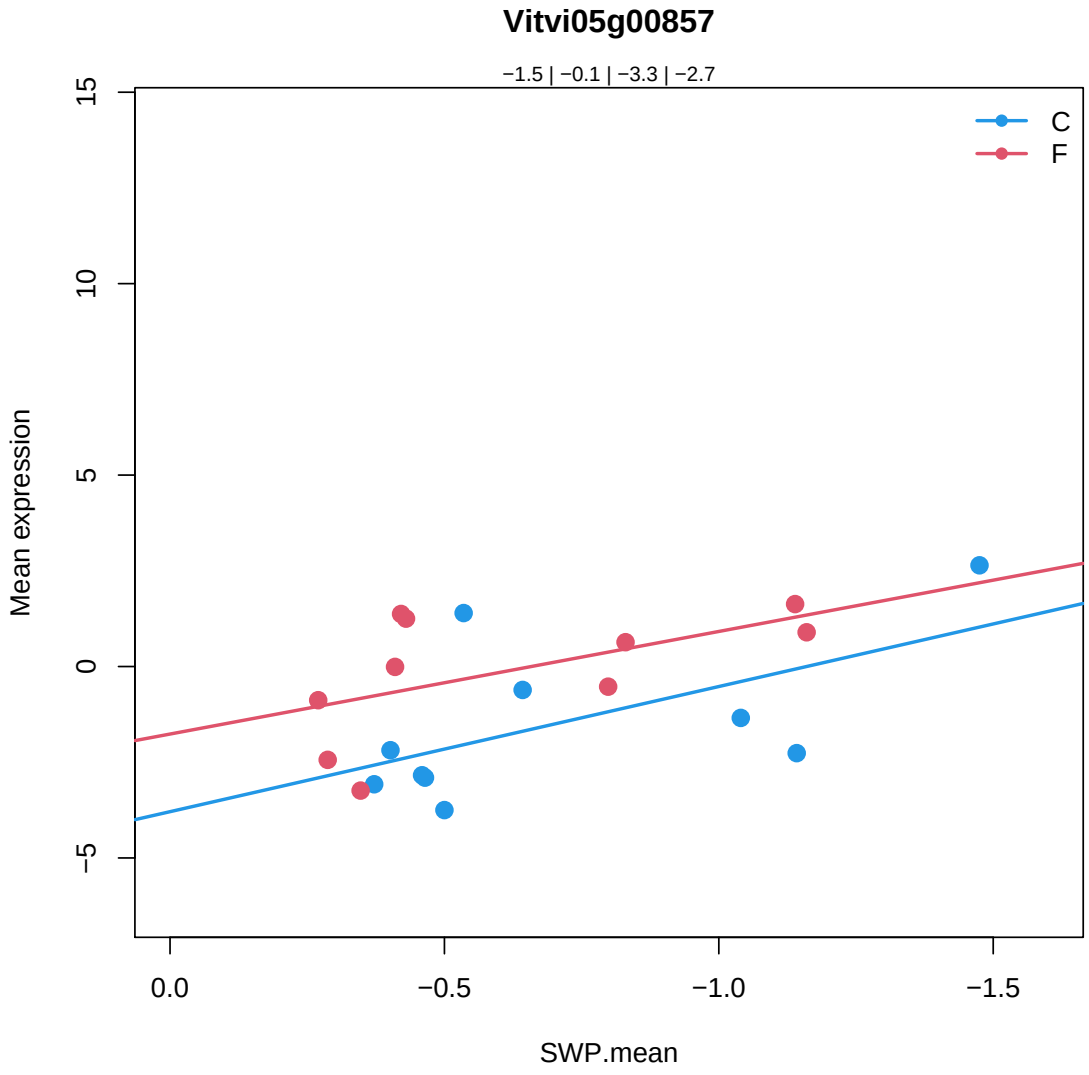
7.3.39 Vitvi05g00857: * type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00857
        34.99
        transport.misc
        AWPM-19-like family protein |
        Chr1:1245070-1245888 FORWARD LENGTH=186 |
        201606
```

Coefficients for Vitvi05g00857.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.493231	0.003146049	**	0.003369788	**
SlopeC	-3.268603	0.01595194	*	0.3483374	
MeanF-MeanC	1.361971	0.04355944	*	0.2186479	
SlopeF-SlopeC	0.5892431	0.754362		0.9999488	



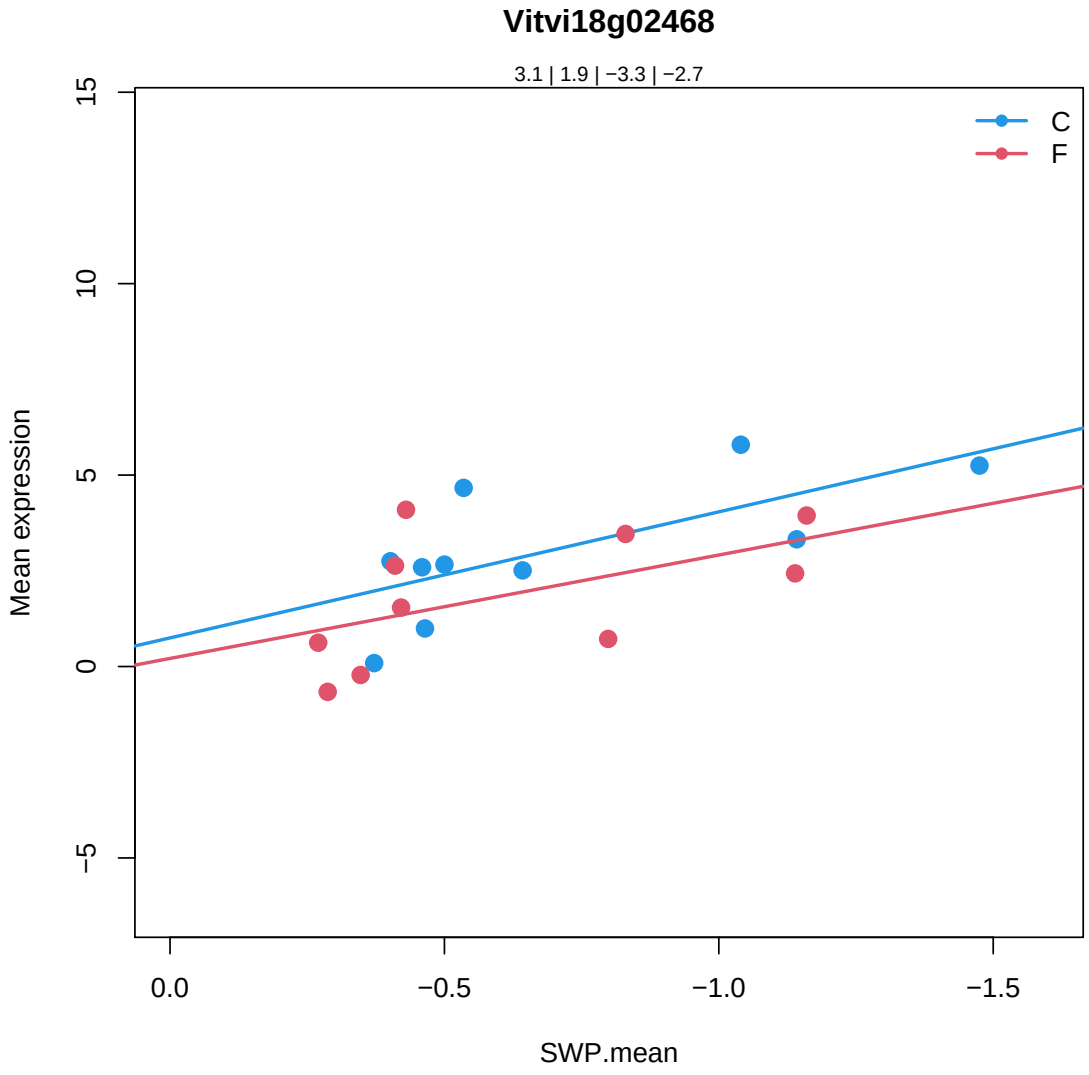
7.3.40 Vitvi18g02468: * type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02468
        30.3
        signalling.calcium
        calmodulin like 37 |
        Chr5:16942758-16943315 REVERSE LENGTH=185 |
        201606
```

Coefficients for Vitvi18g02468.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.062446	1.604581e-07	***	1.892812e-07	***
SlopeC	-3.292034	0.007741766	**	0.280858	
MeanF-MeanC	-1.205656	0.04612069	*	0.2274849	
SlopeF-SlopeC	0.5903653	0.7267852		0.9999488	



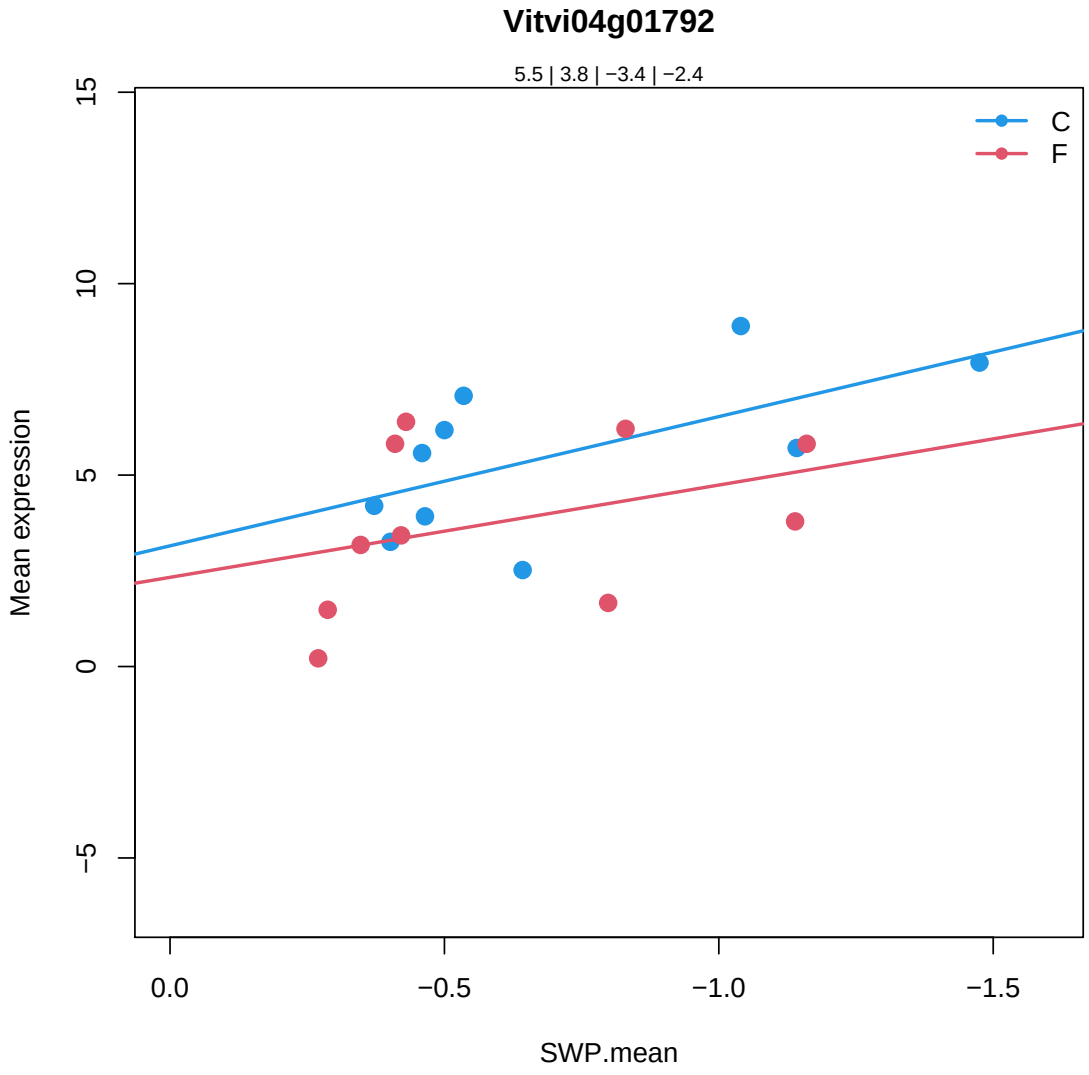
7.3.41 Vitvi04g01792: * type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01792
        29.2.2.3.3
        protein.synthesis.ribosome biogenesis.pre-rRNA processing and modifica
        17.6 kDa class II heat shock protein |
        Chr5:3882409-3882876 REVERSE LENGTH=155 |
        201606
```

Coefficients for Vitvi04g01792.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.525374	1.099806e-09	***	1.385049e-09	***
SlopeC	-3.37508	0.03583257	*	0.4530652	
MeanF-MeanC	-1.727532	0.03469007	*	0.1865724	
SlopeF-SlopeC	0.9644771	0.6714896		0.9999488	



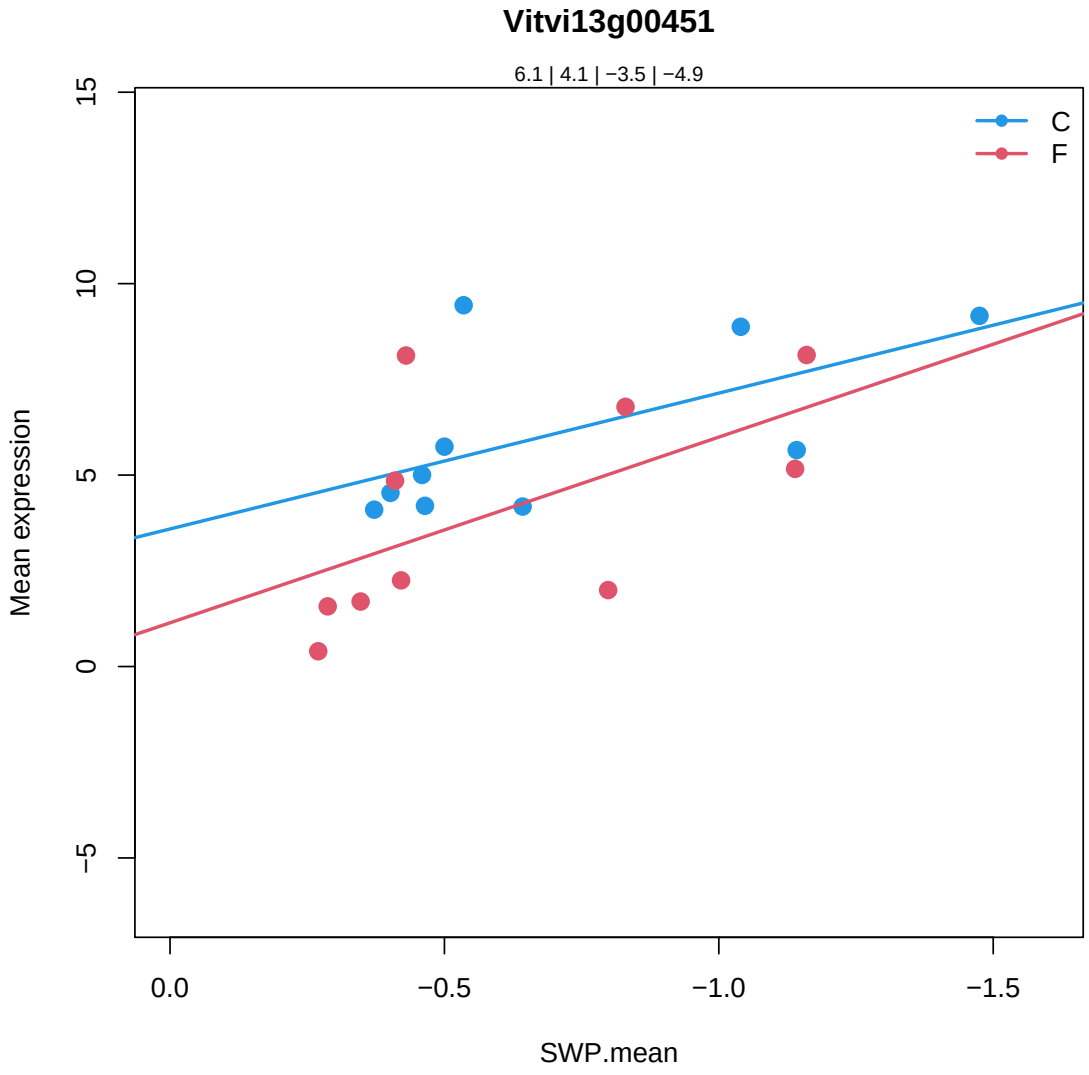
7.3.42 Vitvi13g00451: * type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00451
        20.2.1
        stress.abiotic.heat
        heat shock protein 18.2 |
        Chr5:24062632-24063117 FORWARD LENGTH=161 |
        201606
```

Coefficients for Vitvi13g00451.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.08702	1.42437e-09	***	1.78744e-09	***
SlopeC	-3.548031	0.04710944	*	0.4986403	
MeanF-MeanC	-1.990168	0.02999342	*	0.1689493	
SlopeF-SlopeC	-1.302419	0.60872		0.9999488	



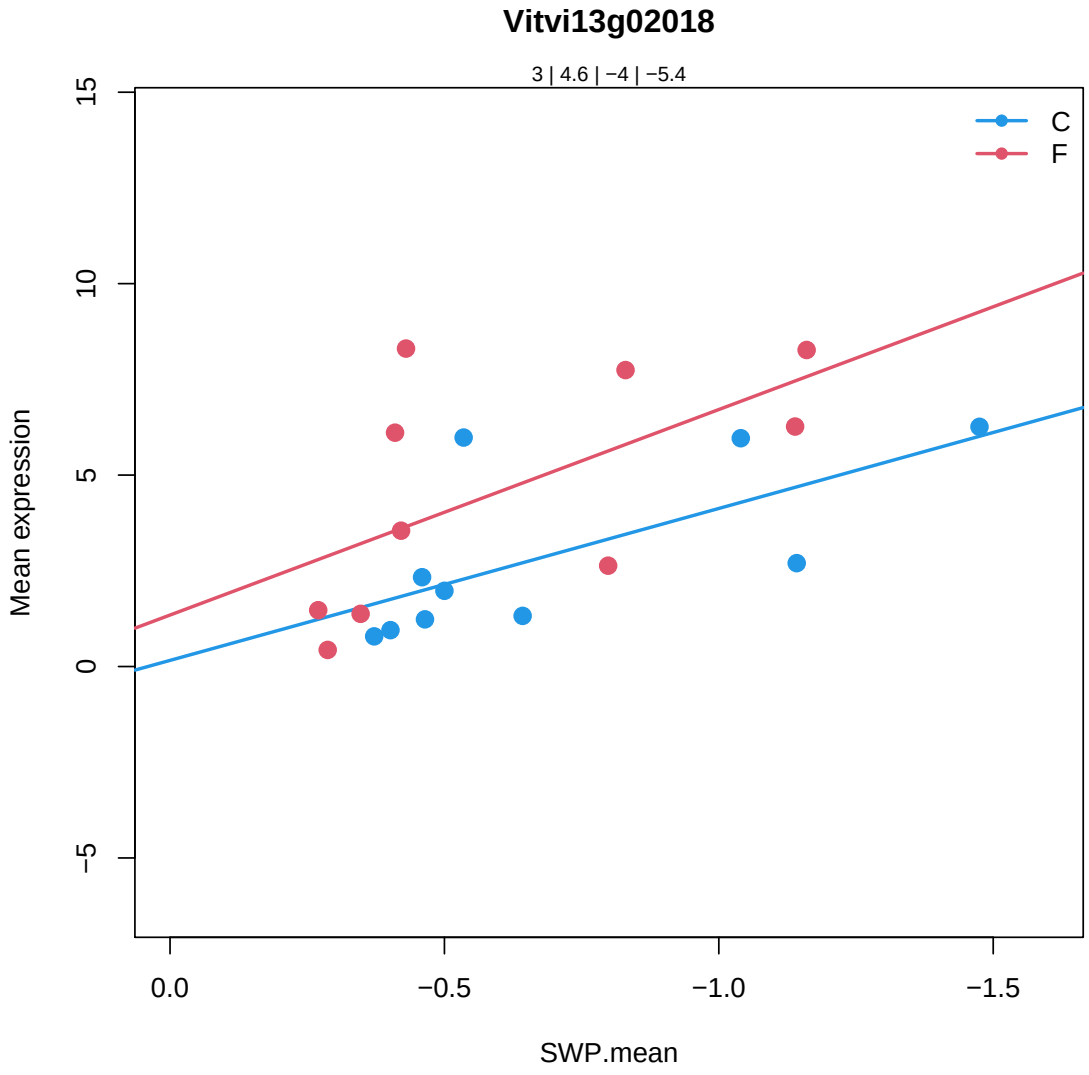
7.3.43 Vitvi13g02018: * type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g02018
        20.2.1
        stress.abiotic.heat
        heat shock protein 18.2 |
        Chr5:24062632-24063117 FORWARD LENGTH=161 |
        201606
```

Coefficients for Vitvi13g02018.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.950521	8.38613e-05	***	9.27519e-05	***
SlopeC	-3.968203	0.02917498	*	0.4292327	
MeanF-MeanC	1.664414	0.06710013	.	0.2880958	
SlopeF-SlopeC	-1.399499	0.5853876		0.9999488	



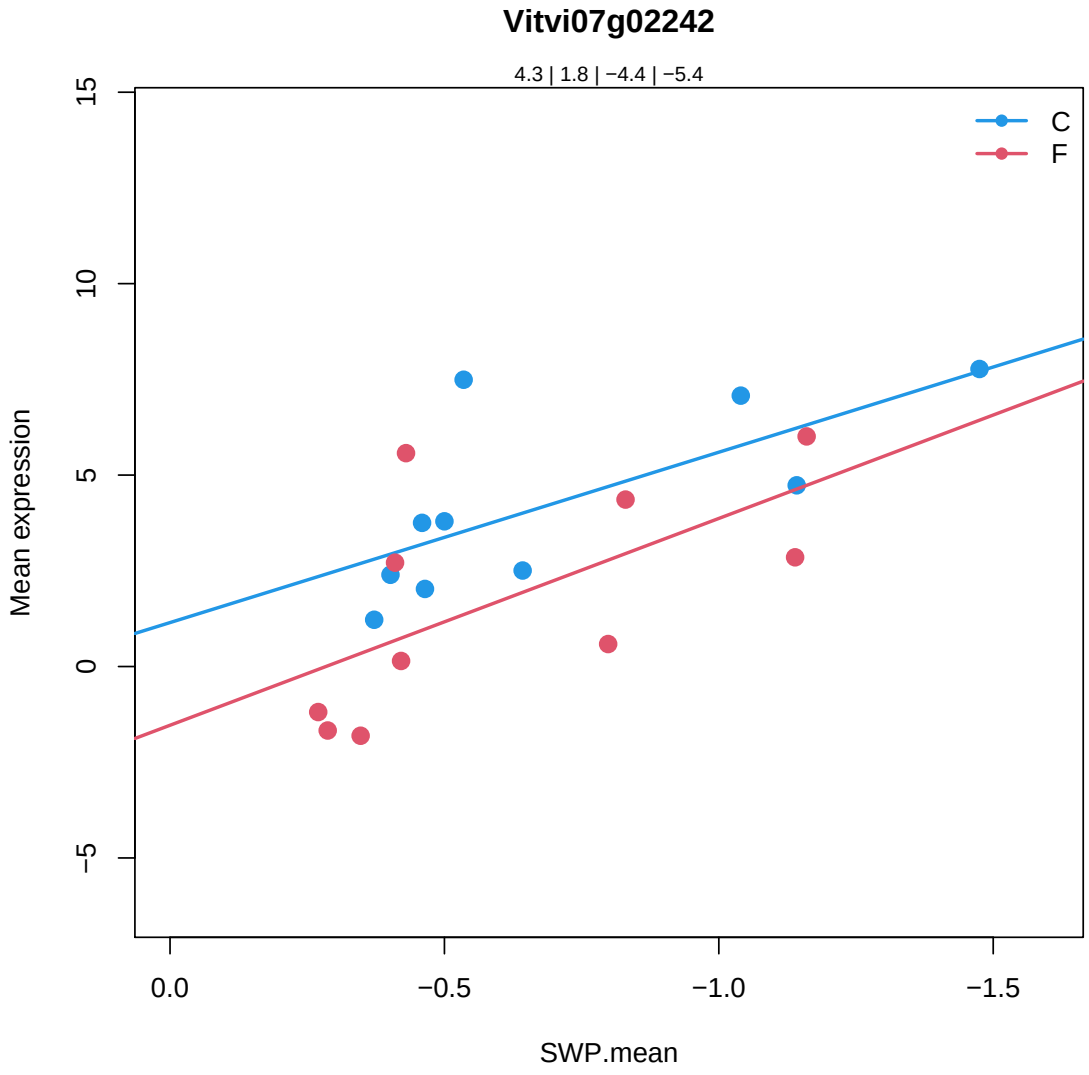
7.3.44 Vitvi07g02242: * type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g02242
        3.1.1.1
        minor CHO metabolism.raffinose family.galactinol synthases.known
        galactinol synthase 1 |
        Chr2:19369049-19370372 REVERSE LENGTH=344 |
        201606
```

Coefficients for Vitvi07g02242.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.276297	3.725657e-07	***	4.348787e-07	***
SlopeC	-4.449677	0.01340344	*	0.3305597	
MeanF-MeanC	-2.519255	0.00668982	**	0.05649099	.
SlopeF-SlopeC	-0.9519606	0.7022784		0.9999488	



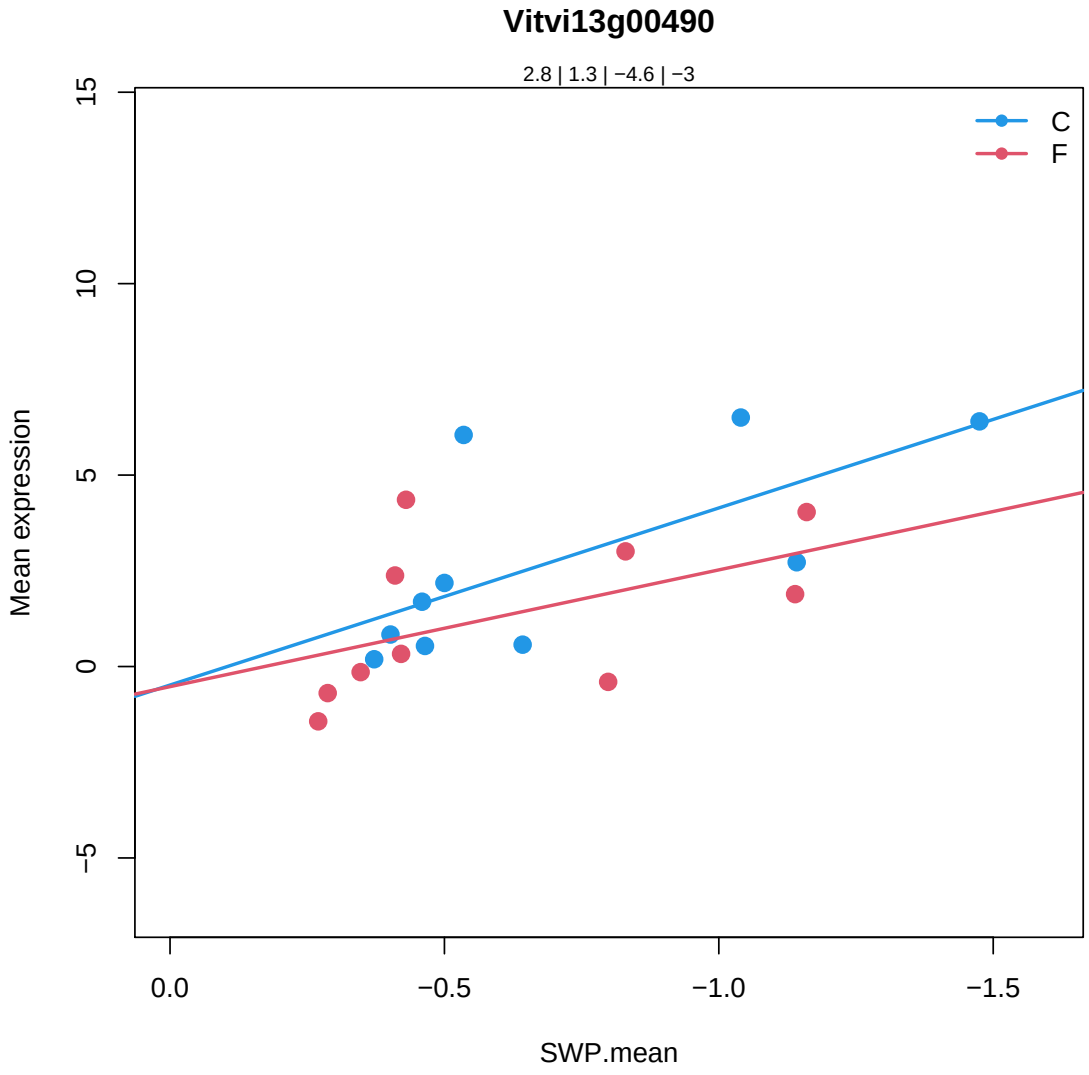
7.3.45 Vitvi13g00490: * type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00490
        20.2.1
        stress.abiotic.heat
        heat shock protein 18.2 |
        Chr5:24062632-24063117 FORWARD LENGTH=161 |
        201606
```

Coefficients for Vitvi13g00490.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.768364	3.965659e-05	***	4.415558e-05	***
SlopeC	-4.624813	0.005434675	**	0.2577627	
MeanF-MeanC	-1.436279	0.07249786	.	0.3024112	
SlopeF-SlopeC	1.575339	0.486818		0.9999488	



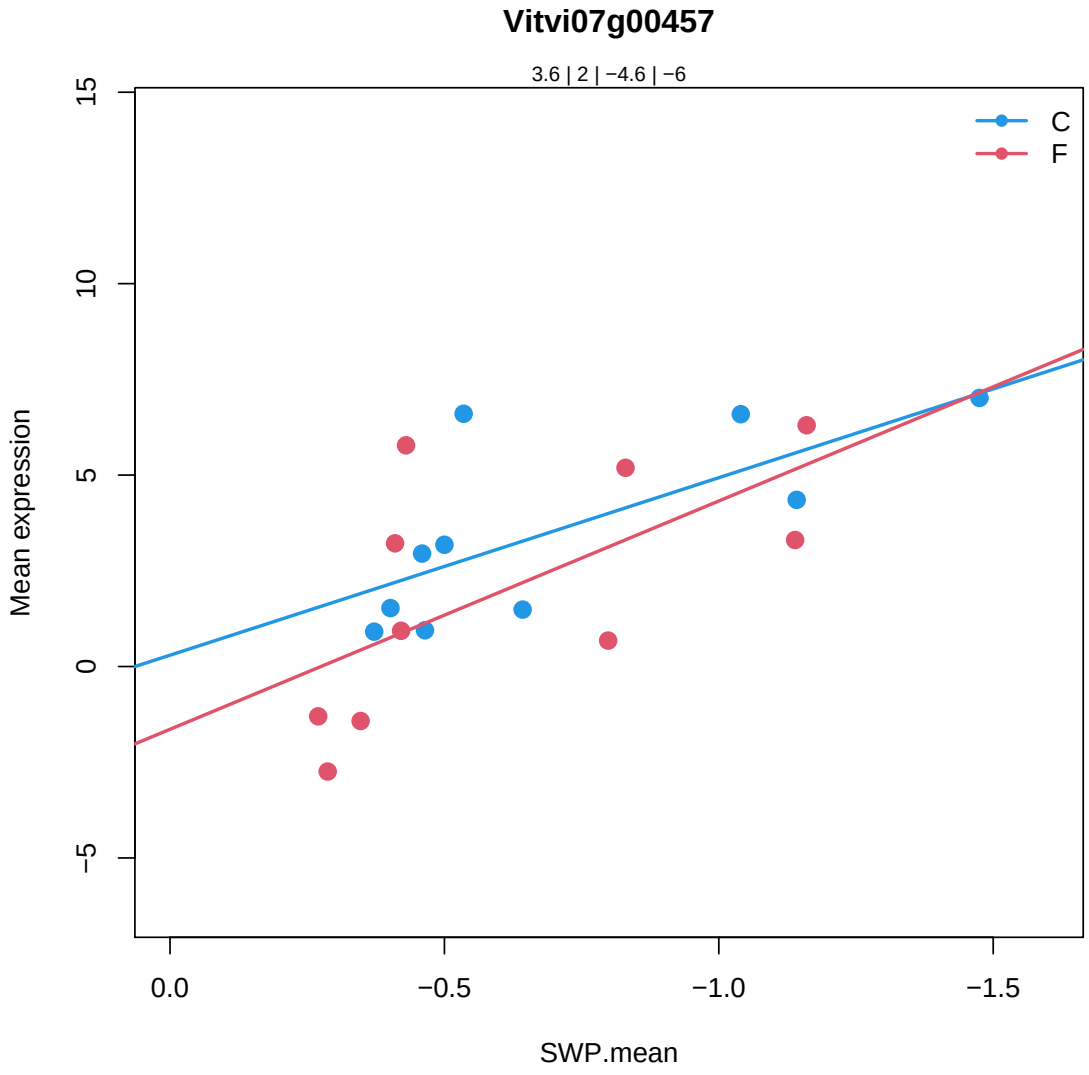
7.3.46 Vitvi07g00457: * type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g00457
        3.1.1.1
        minor CHO metabolism.raffinose family.galactinol synthases.known
        galactinol synthase 1 |
        Chr2:19369049-19370372 REVERSE LENGTH=344 |
        201606
```

Coefficients for Vitvi07g00457.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.555754	1.102899e-05	***	1.244477e-05	***
SlopeC	-4.635979	0.01424512	*	0.3359386	
MeanF-MeanC	-1.562377	0.09116898	.	0.3456204	
SlopeF-SlopeC	-1.327112	0.6131283		0.9999488	



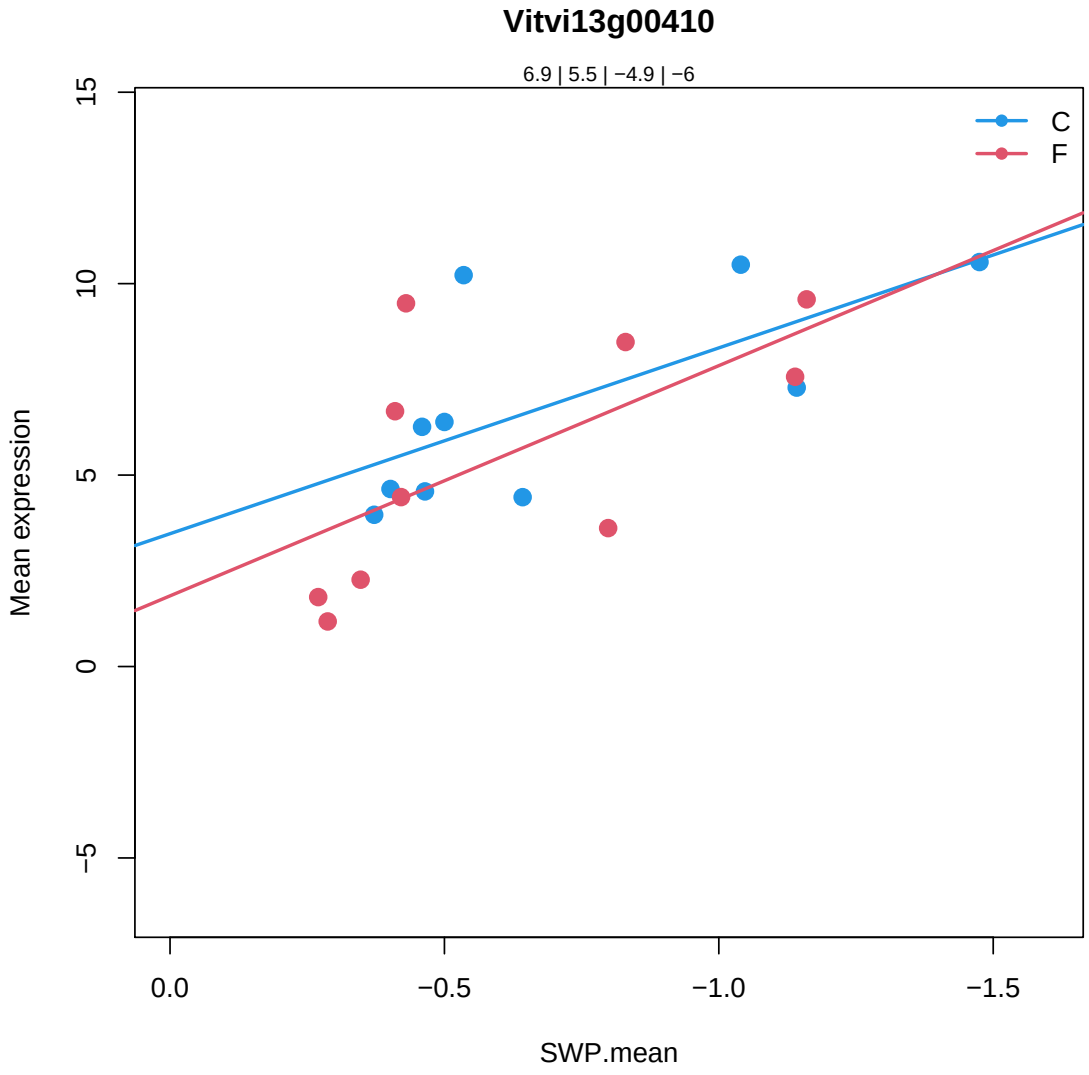
7.3.47 Vitvi13g00410: * type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00410
        35.2
        not assigned.unknown
        heat shock protein 18.2 |
        Chr5:24062632-24063117 FORWARD LENGTH=161 |
        201606
```

Coefficients for Vitvi13g00410.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.880973	5.561548e-10	***	7.077067e-10	***
SlopeC	-4.853089	0.01369382	*	0.3344891	
MeanF-MeanC	-1.372646	0.1496748		0.4660558	
SlopeF-SlopeC	-1.160051	0.6705588		0.9999488	



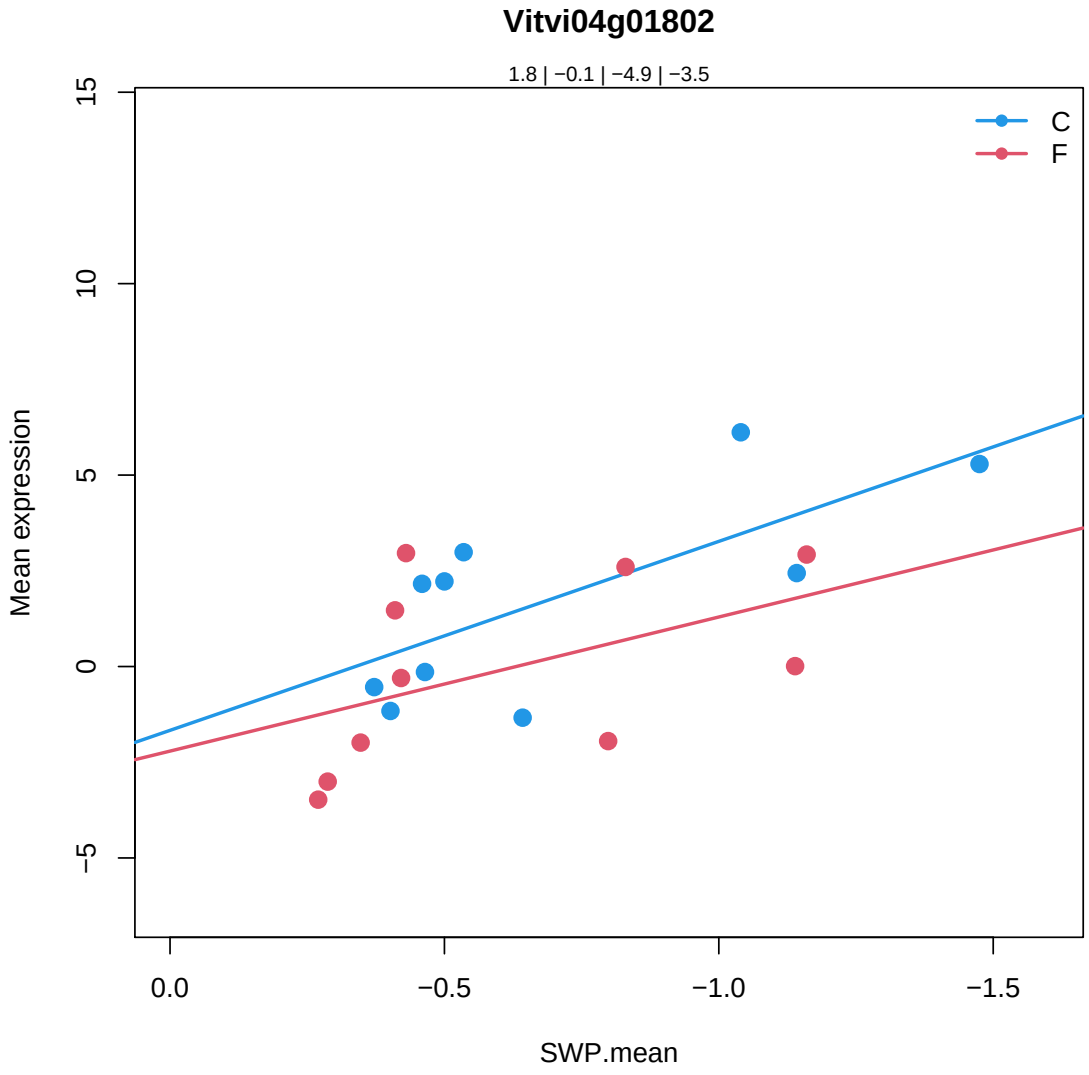
7.3.48 Vitvi04g01802: * type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01802
        20.2.1
        stress.abiotic.heat
        17.6 kDa class II heat shock protein |
        Chr5:3882409-3882876 REVERSE LENGTH=155 |
        201606
```

Coefficients for Vitvi04g01802.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.803501	0.00537385	**	0.005725846	**
SlopeC	-4.935441	0.00604259	**	0.2647742	
MeanF-MeanC	-1.879083	0.03283183	*	0.179723	
SlopeF-SlopeC	1.433256	0.5585218		0.9999488	



7.3.49 Vitvi11g00724: * type2

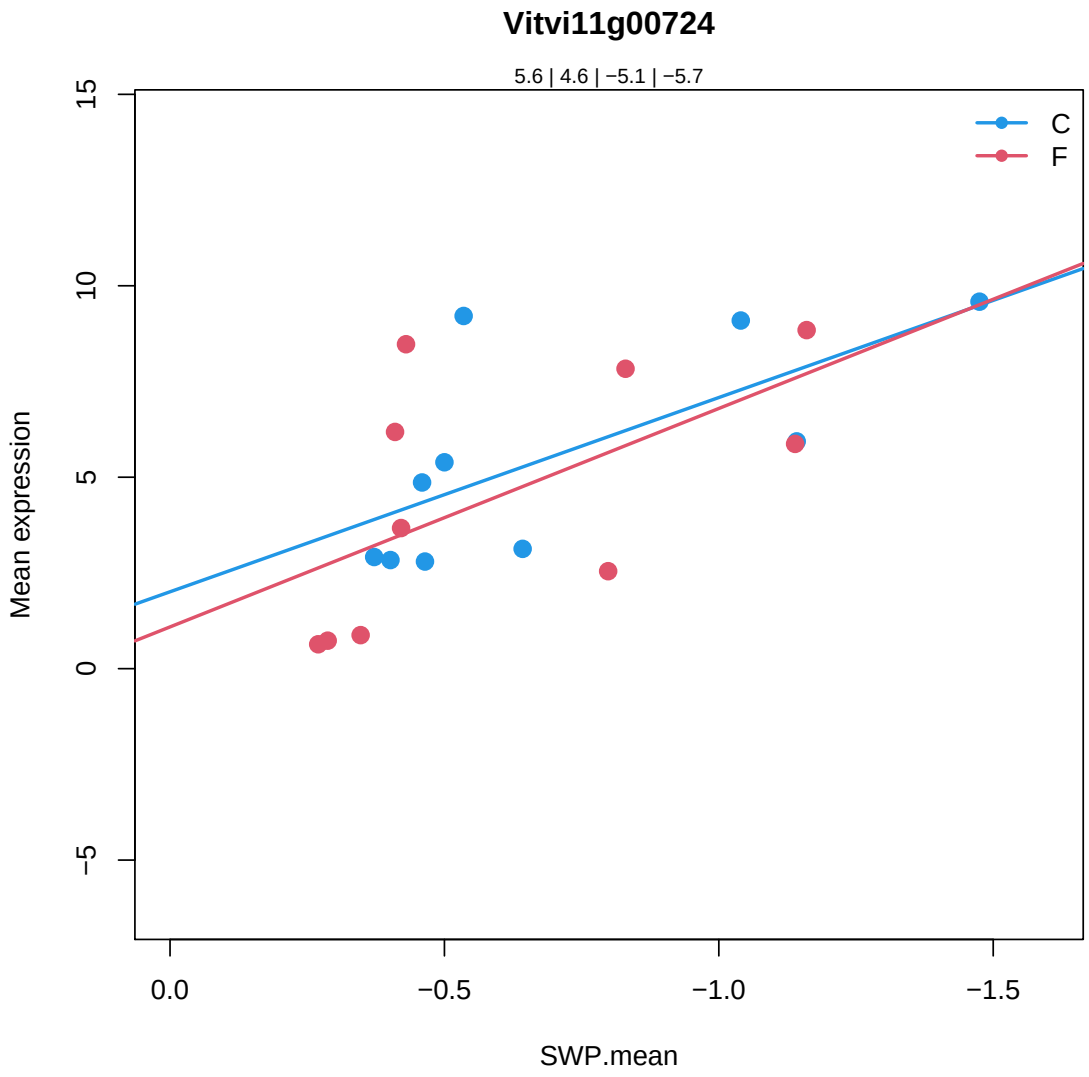
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00724
        20.2.1
        stress.abiotic.heat
        heat shock protein 70B |
        Chr1:5502386-5504326 REVERSE LENGTH=646 |
        201606

Vitvi11g00724
        29.6
        protein.folding
        heat shock protein 70B |
        Chr1:5502386-5504326 REVERSE LENGTH=646 |
        201606
```

Coefficients for Vitvi11g00724.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.57538	5.63319e-08	***	6.726816e-08	***
SlopeC	-5.073527	0.01469064	*	0.3359386	
MeanF-MeanC	-1.009405	0.3105058		0.6744662	
SlopeF-SlopeC	-0.6317686	0.8263893		0.9999488	


Vitvi11g00724
5.6 | 4.6 | −5.1 | −5.7
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

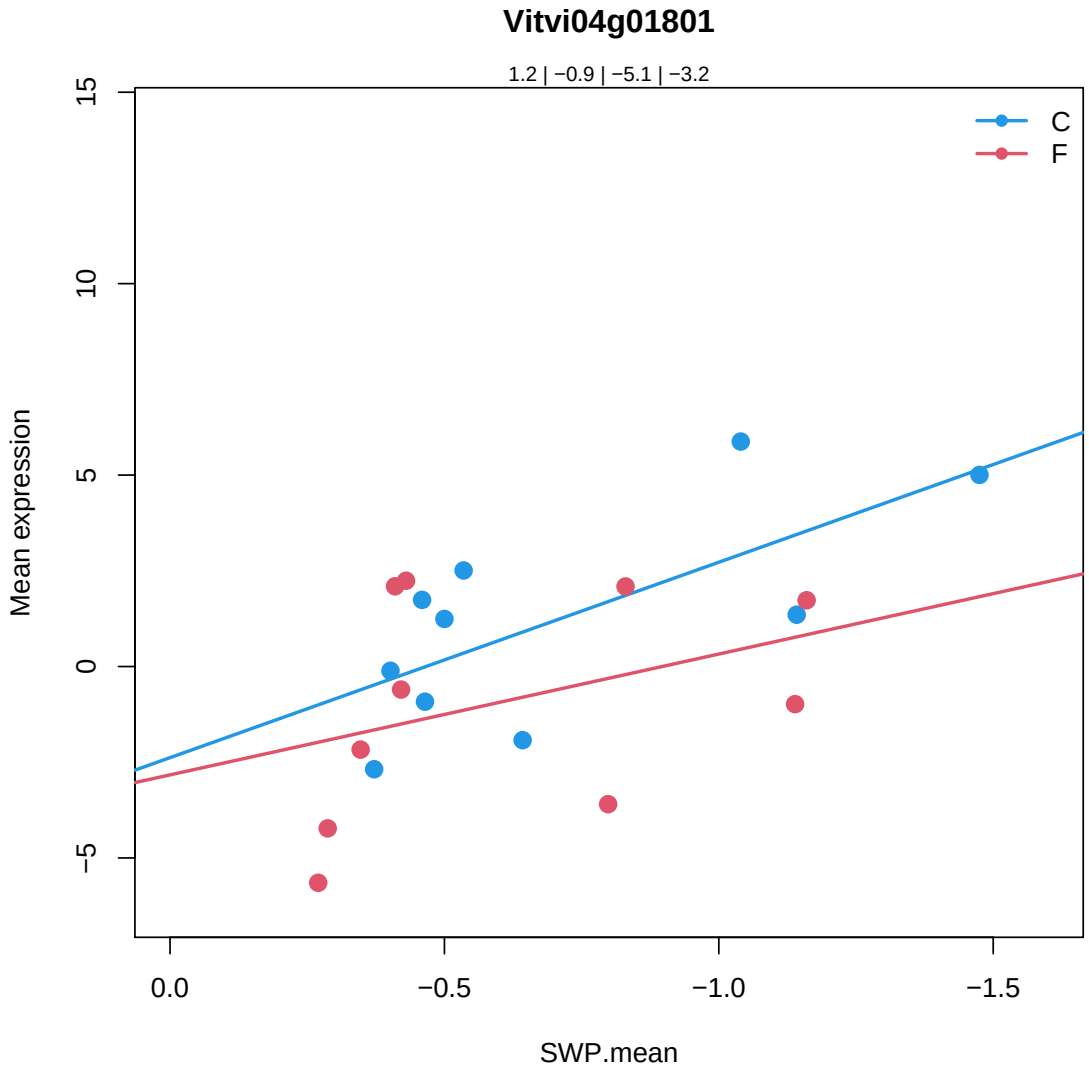
7.3.50 Vitvi04g01801: * type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01801
        20.2.1
        stress.abiotic.heat
        17.6 kDa class II heat shock protein |
        Chr5:3882409-3882876 REVERSE LENGTH=155 |
        201606
```

Coefficients for Vitvi04g01801.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.208586	0.09664858	.	0.09995371	.
SlopeC	-5.104125	0.01523524	*	0.3393703	
MeanF-MeanC	-2.115849	0.04303485	*	0.2168388	
SlopeF-SlopeC	1.948595	0.5059525		0.9999488	



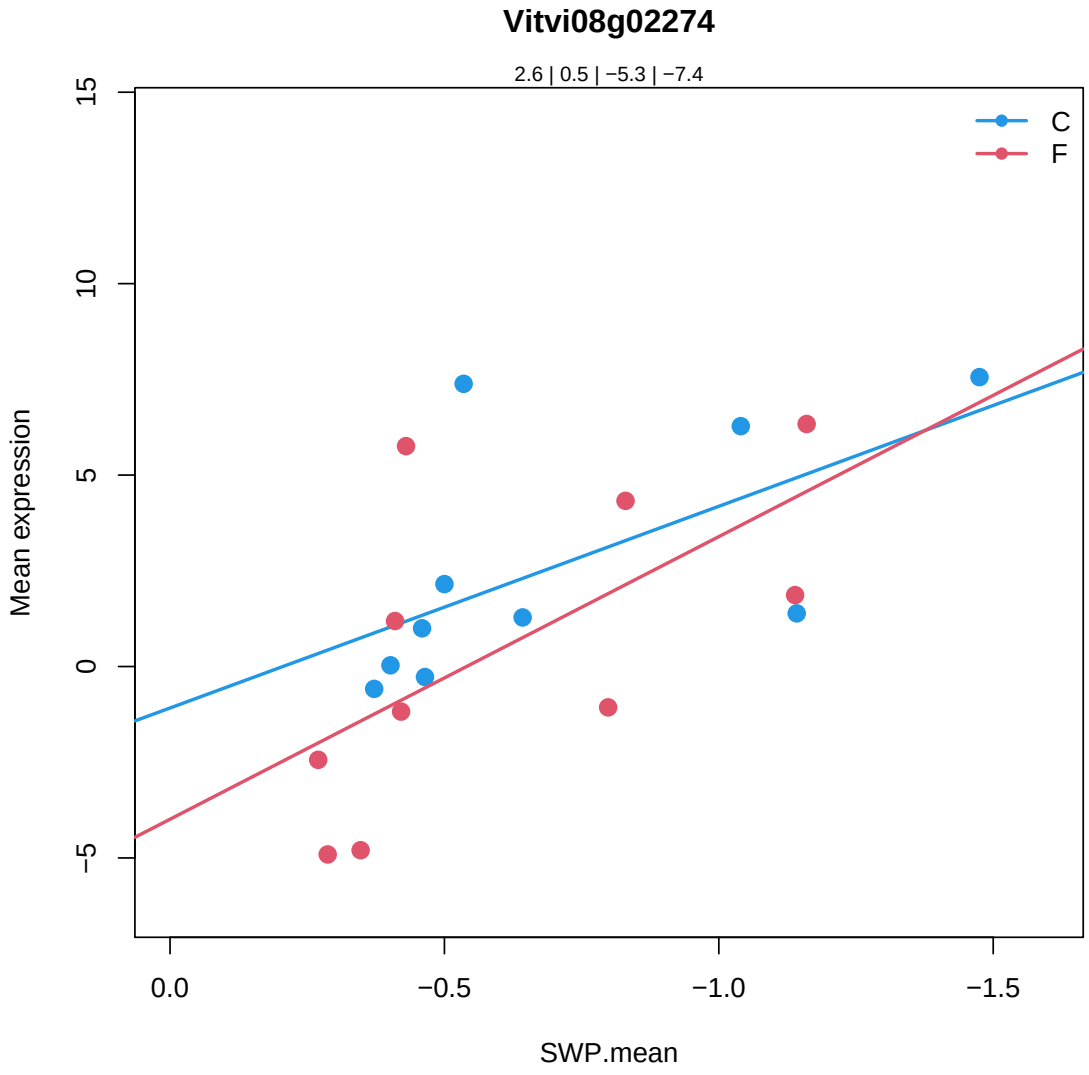
7.3.51 Vitvi08g02274: * type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g02274
        35.2
        not assigned.unknown
        plant/protein |
        Chr3:3091225-3091674 REVERSE LENGTH=149 |
        201606
```

Coefficients for Vitvi08g02274.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.621184	0.004851113	**	0.005175743	**
SlopeC	−5.267913	0.03371344	*	0.4433084	
MeanF−MeanC	−2.113039	0.08753536	.	0.337434	
SlopeF−SlopeC	−2.113051	0.5473344		0.9999488	



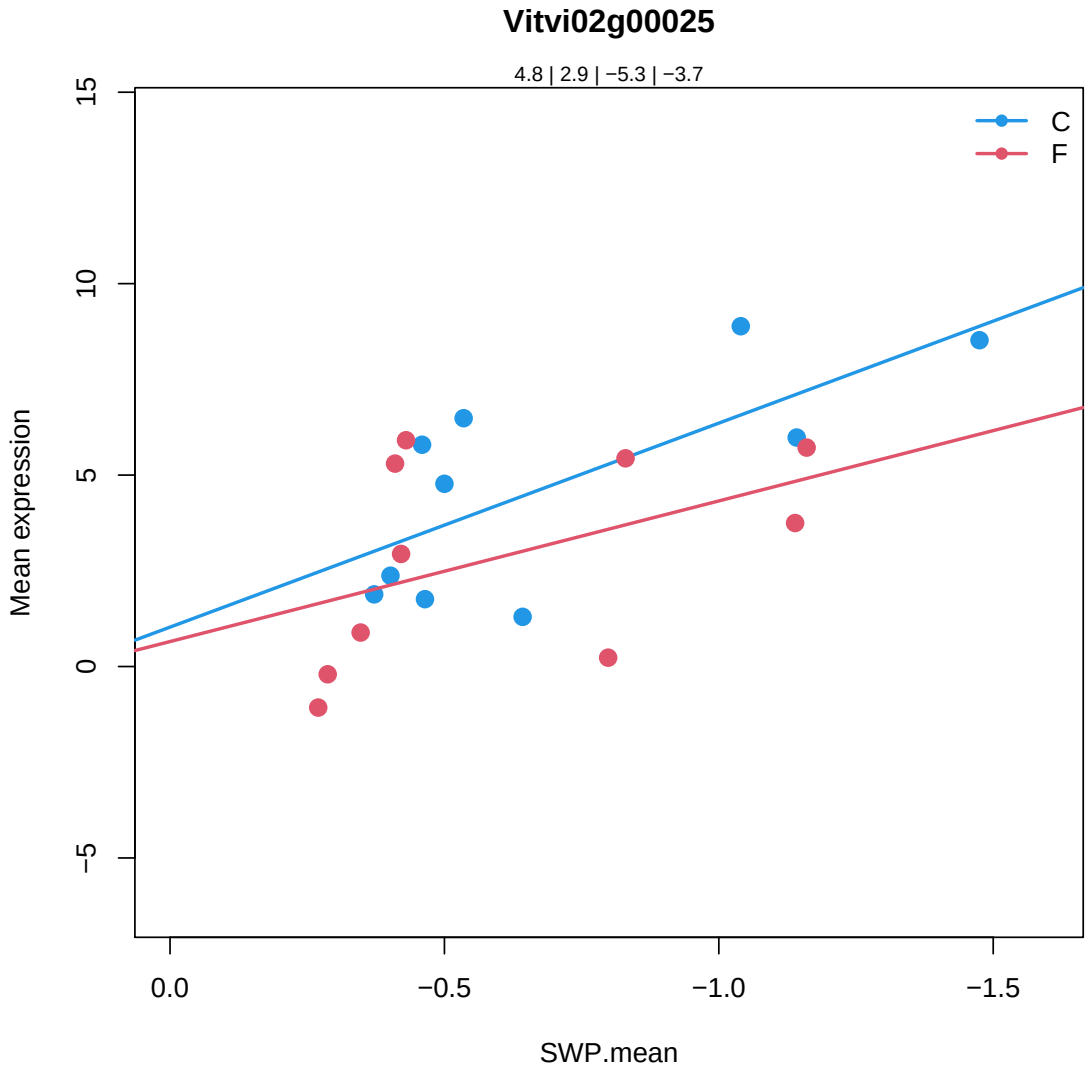
7.3.52 Vitvi02g00025: * type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00025
        20.2.1
        stress.abiotic.heat
        heat shock-like protein |
        Chr5:21352557-21355147 FORWARD LENGTH=700 |
        201606
```

Coefficients for Vitvi02g00025.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.775282	2.294969e-07	***	2.694701e-07	***
SlopeC	-5.328021	0.00701325	**	0.2775469	
MeanF-MeanC	-1.885708	0.05012567	.	0.2392782	
SlopeF-SlopeC	1.655038	0.5403657		0.9999488	



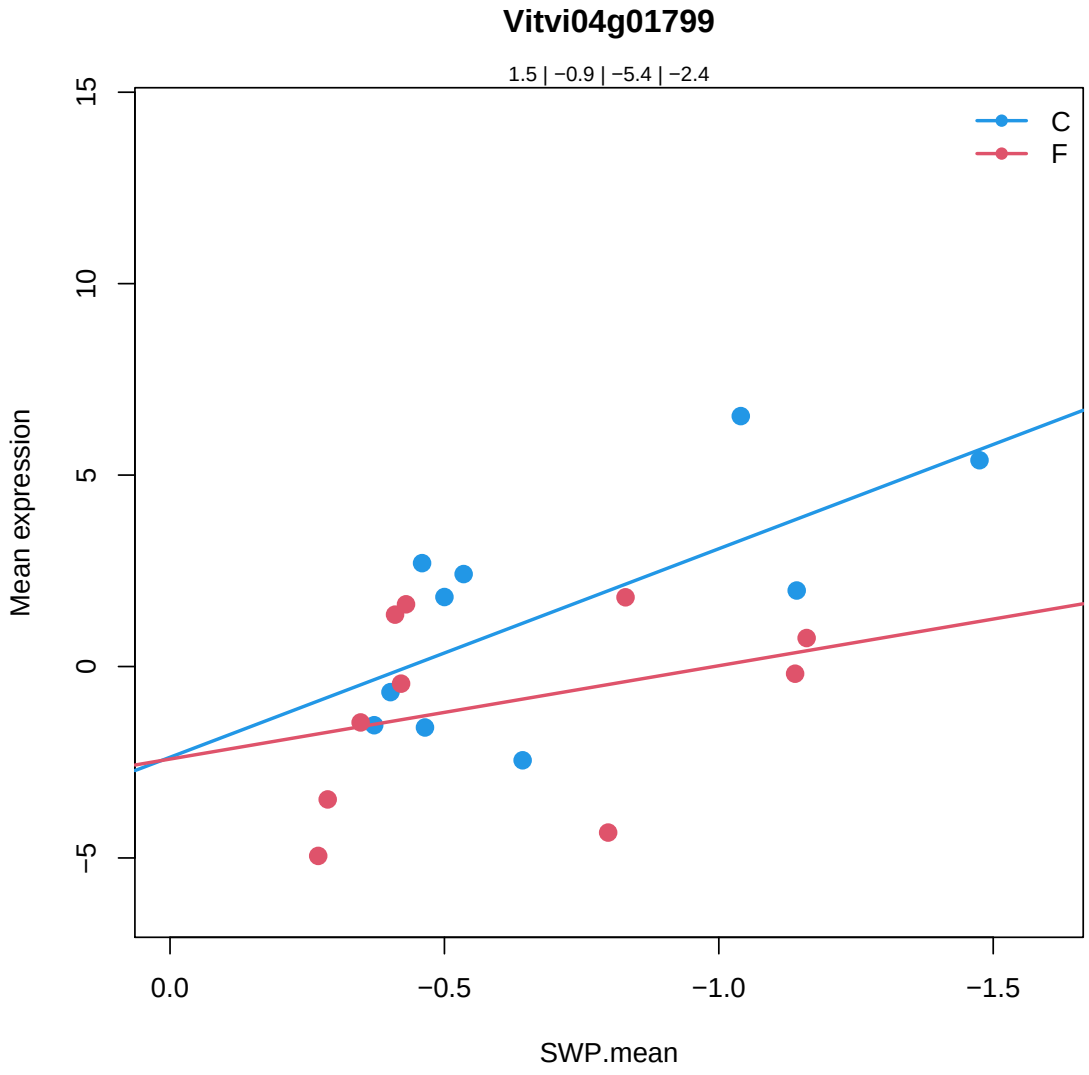
7.3.53 Vitvi04g01799: * type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01799
        20.2.1
        stress.abiotic.heat
        17.6 kDa class II heat shock protein |
        Chr5:3882409-3882876 REVERSE LENGTH=155 |
        201606
```

Coefficients for Vitvi04g01799.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.459784	0.04054411	*	0.04232114	*
SlopeC	-5.446372	0.008008975	**	0.2832315	
MeanF-MeanC	-2.391652	0.01948465	*	0.1236922	
SlopeF-SlopeC	3.008905	0.2899314		0.9999488	



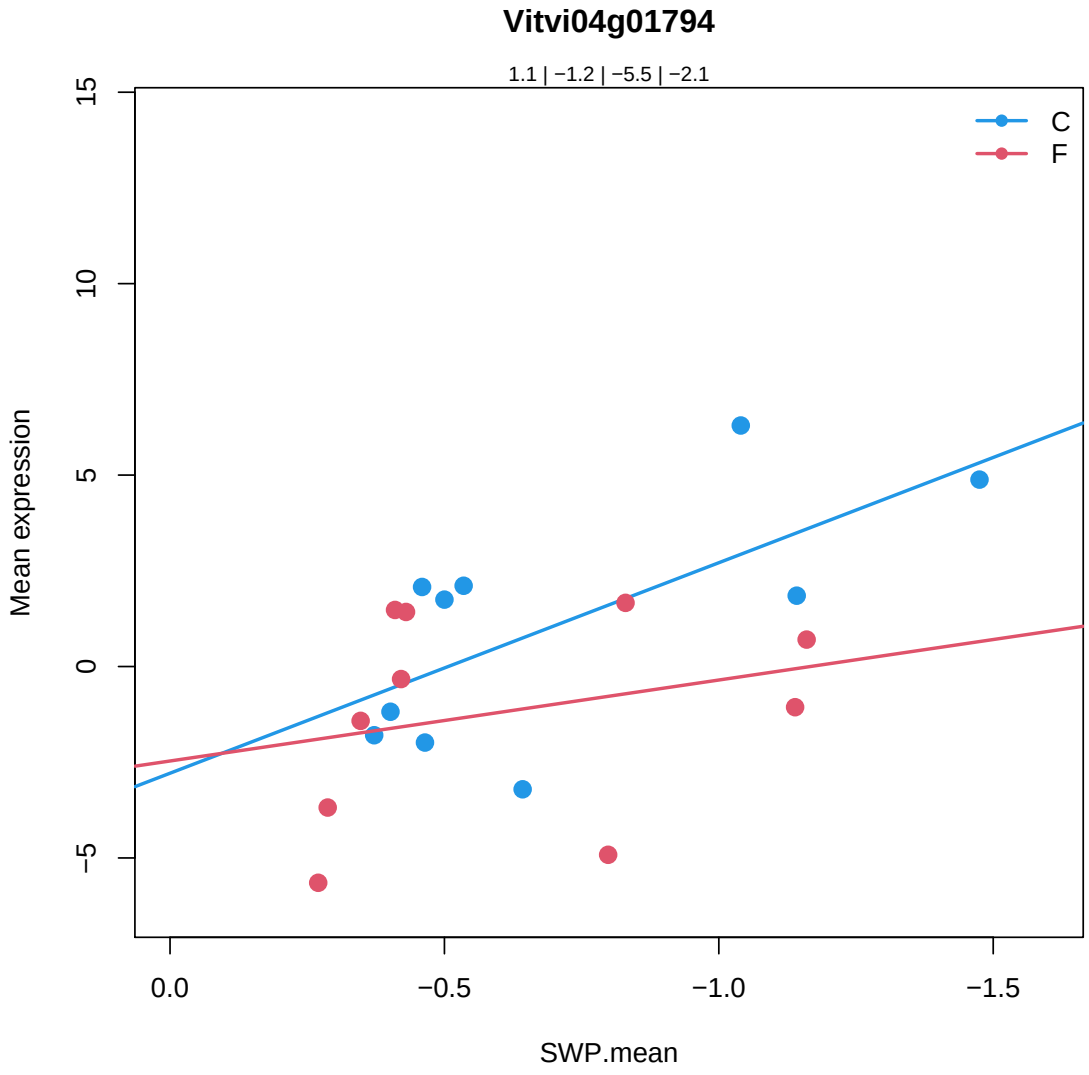
7.3.54 Vitvi04g01794: * type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01794
        20.2.1
        stress.abiotic.heat
        17.6 kDa class II heat shock protein |
        Chr5:3882409-3882876 REVERSE LENGTH=155 |
        201606
```

Coefficients for Vitvi04g01794.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.079134	0.1462899		0.1505876	
SlopeC	-5.497568	0.01158549	*	0.318473	
MeanF-MeanC	-2.25819	0.03651267	*	0.192703	
SlopeF-SlopeC	3.382727	0.2663928		0.9999488	



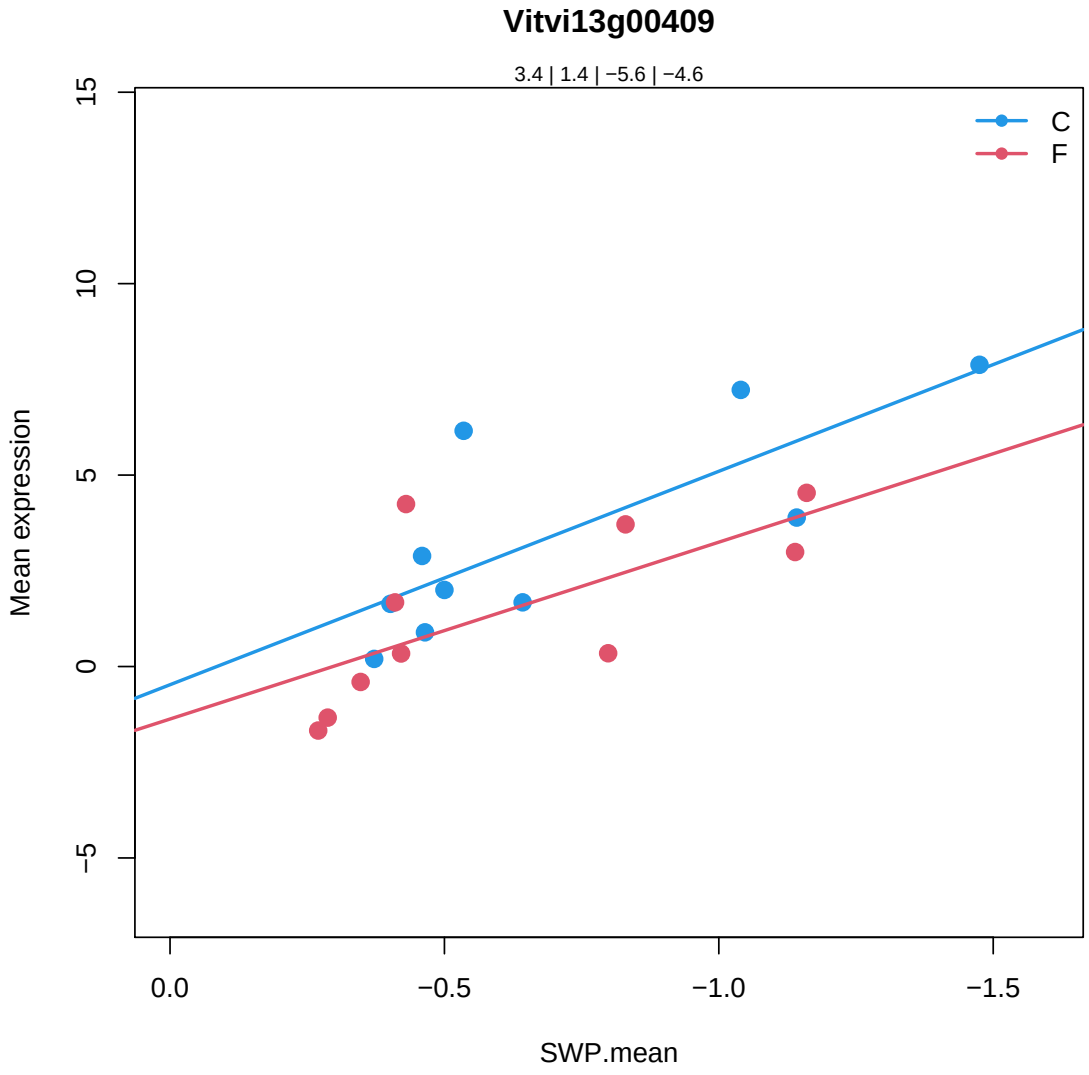
7.3.55 Vitvi13g00409: * type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00409
        35.2
        not assigned.unknown
        heat shock protein 18.2 |
        Chr5:24062632-24063117 FORWARD LENGTH=161 |
        201606
```

Coefficients for Vitvi13g00409.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.444287	7.91282e-07	***	9.154942e-07	***
SlopeC	-5.574561	0.0006440829	***	0.1015345	
MeanF-MeanC	-2.001179	0.01018303	*	0.0770272	.
SlopeF-SlopeC	0.9551048	0.650661		0.9999488	



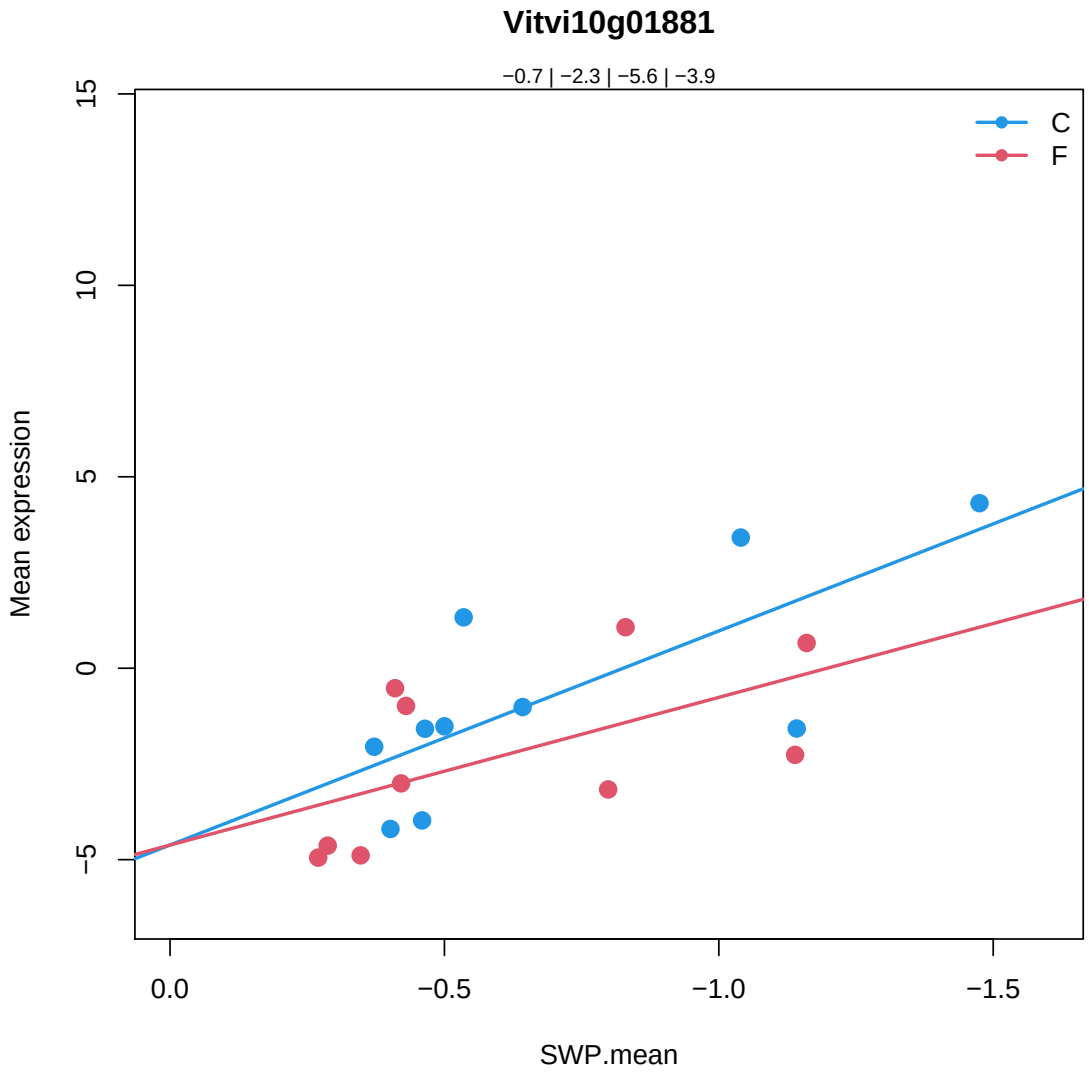
7.3.56 Vitvi10g01881: * type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g01881
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi10g01881.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	−0.6859056	0.2218556		0.2272071	
SlopeC	−5.591522	0.00133436	**	0.1432275	
MeanF−MeanC	−1.582313	0.05253977	.	0.2472403	
SlopeF−SlopeC	1.734231	0.4507249		0.9999488	



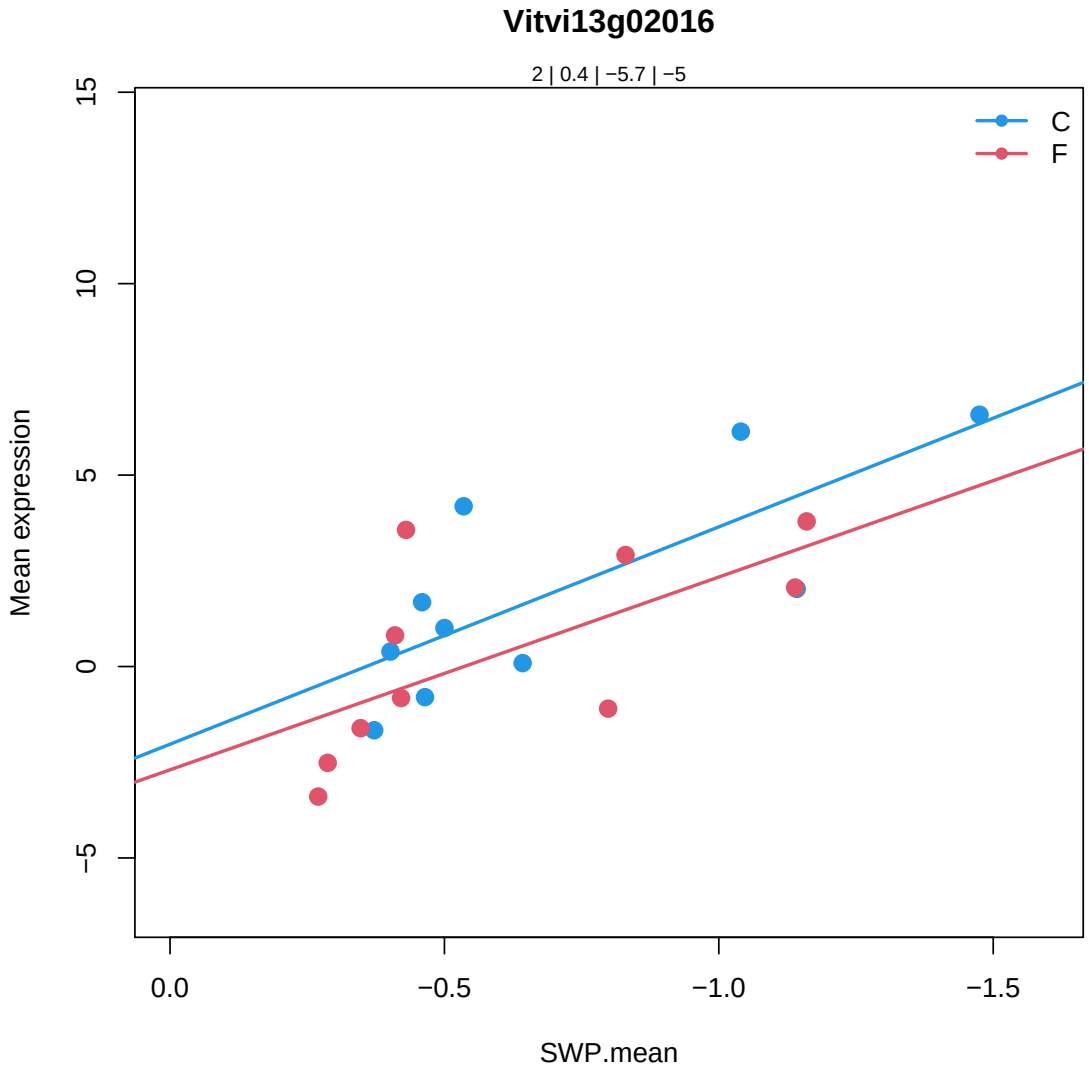
7.3.57 Vitvi13g02016: * type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g02016
        20.2.1
        stress.abiotic.heat
        HSP20-like chaperones superfamily protein |
        Chr1:19980510-19980983 FORWARD LENGTH=157 |
        201606
```

Coefficients for Vitvi13g02016.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.962441	0.001860074	**	0.002001642	**
SlopeC	-5.676271	0.001329333	**	0.1432275	
MeanF-MeanC	-1.5925	0.05433262	.	0.2525382	
SlopeF-SlopeC	0.6414647	0.7821337		0.9999488	



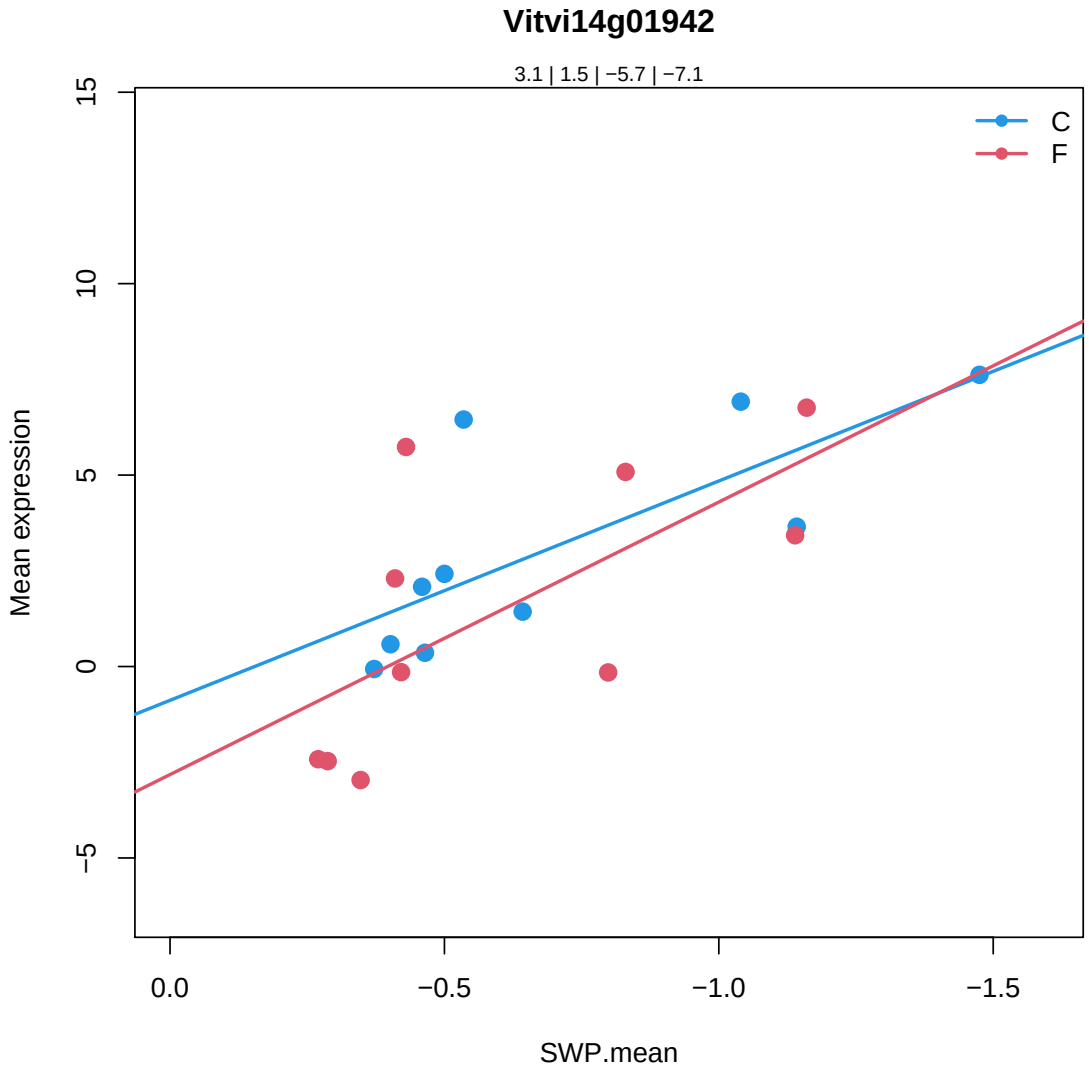
7.3.58 Vitvi14g01942: * type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01942
        29.5.7
        protein.degradation.metalloprotease
        FTSH protease 6 |
        Chr5:4951071-4952777 REVERSE LENGTH=514 |
        201606
```

Coefficients for Vitvi14g01942.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.144964	0.0001381096	***	0.0001521111	***
SlopeC	−5.728533	0.00627106	**	0.2647742	
MeanF−MeanC	−1.630516	0.1042469		0.373954	
SlopeF−SlopeC	−1.388999	0.6266054		0.9999488	



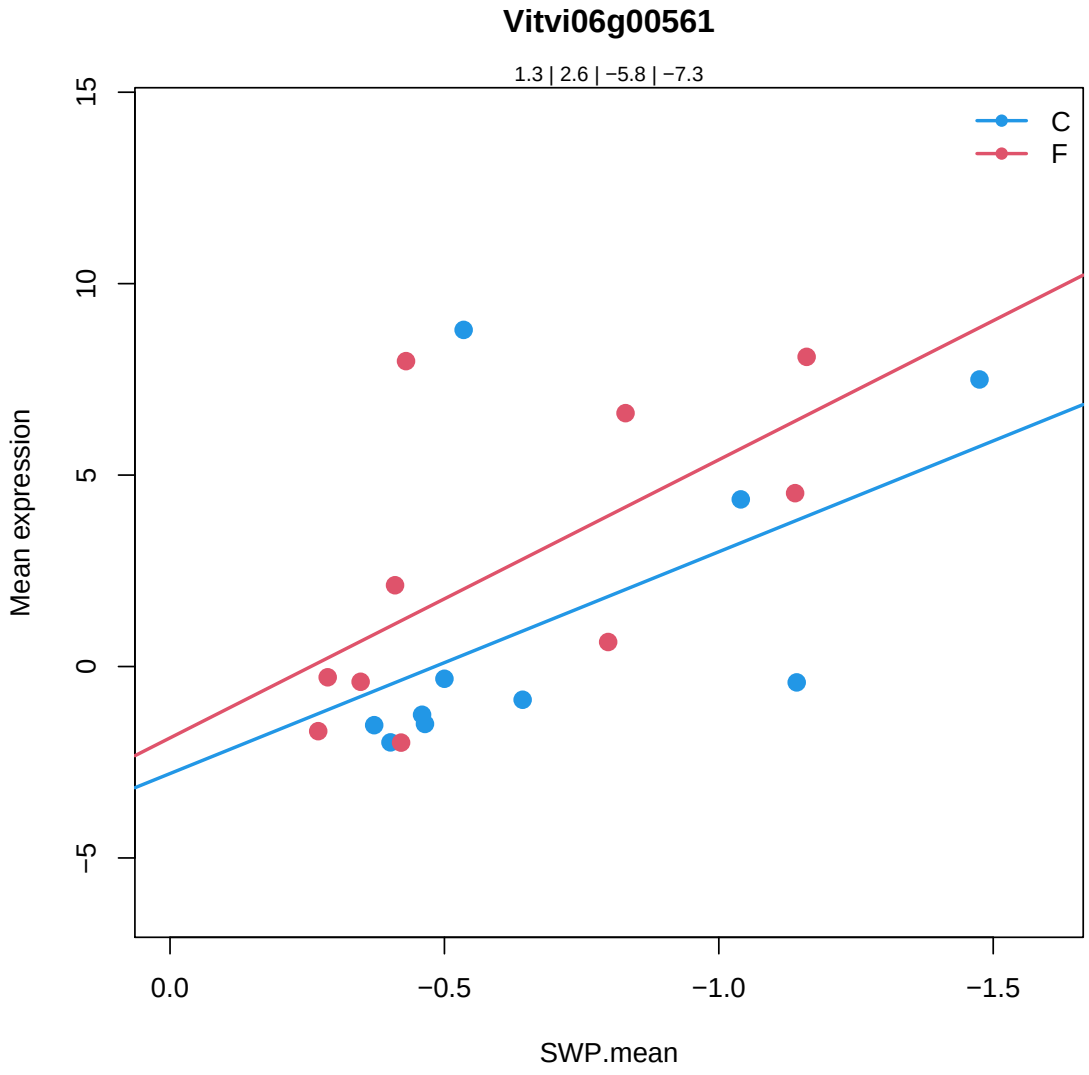
7.3.59 Vitvi06g00561: * type2

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00561
        35.2
        not assigned.unknown
        HSP20-like chaperones superfamily protein |
        Chr2:12633279-12633740 REVERSE LENGTH=153 |
        201606
```

Coefficients for Vitvi06g00561.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.277783	0.1875177		0.1923899	
SlopeC	-5.792331	0.03745657	*	0.4626524	
MeanF-MeanC	1.283774	0.3442368		0.7038982	
SlopeF-SlopeC	-1.47236	0.7085305		0.9999488	



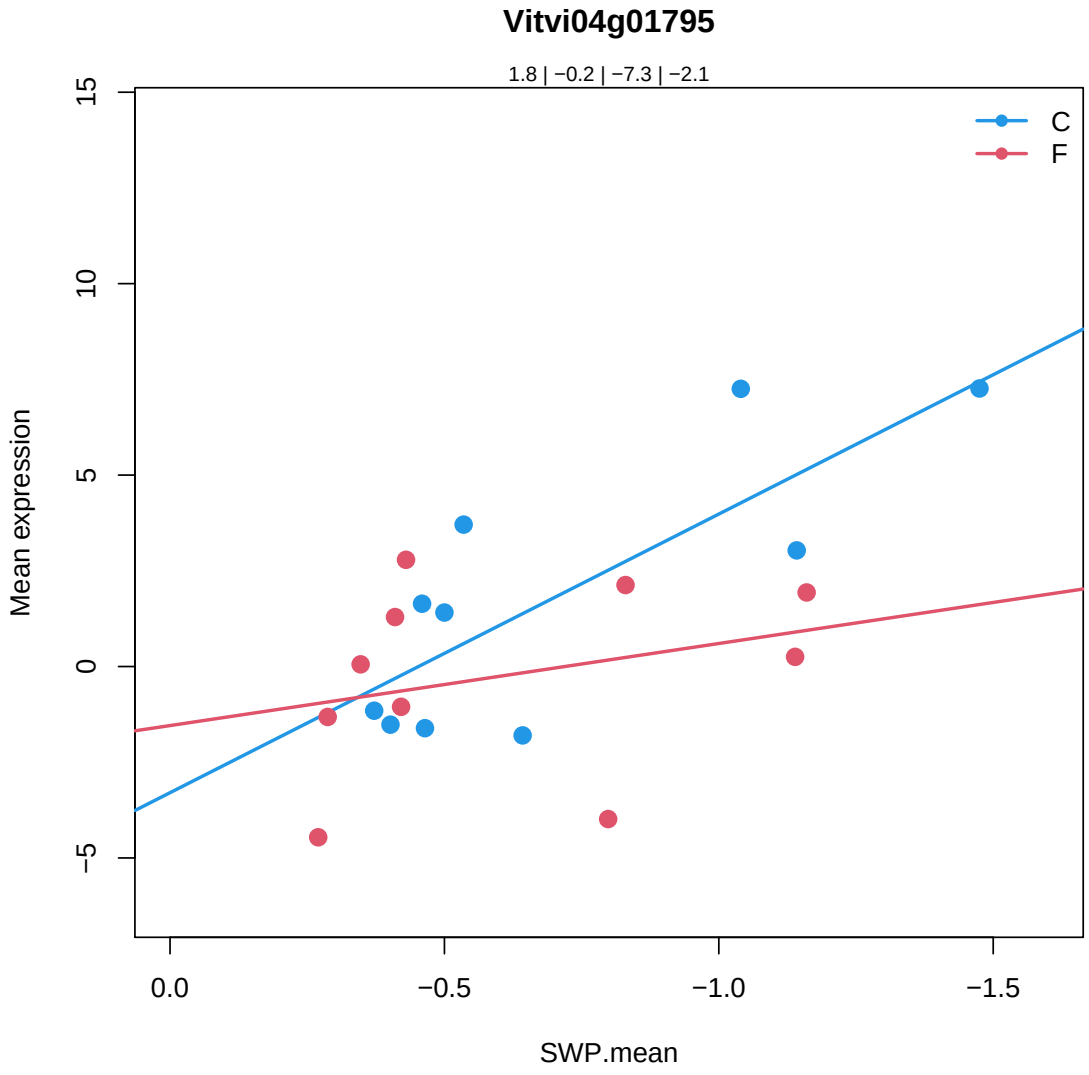
7.3.60 Vitvi04g01795: * type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01795
        35.2
        not assigned.unknown
        17.6 kDa class II heat shock protein |
        Chr5:3882409-3882876 REVERSE LENGTH=155 |
        201606
```

Coefficients for Vitvi04g01795.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.821988	0.01144052	*	0.01210359	*
SlopeC	−7.277261	0.0006740302	***	0.1037734	
MeanF−MeanC	−2.058336	0.03814072	*	0.1995898	
SlopeF−SlopeC	5.133591	0.07347637	.	0.9999488	



7.4 type3

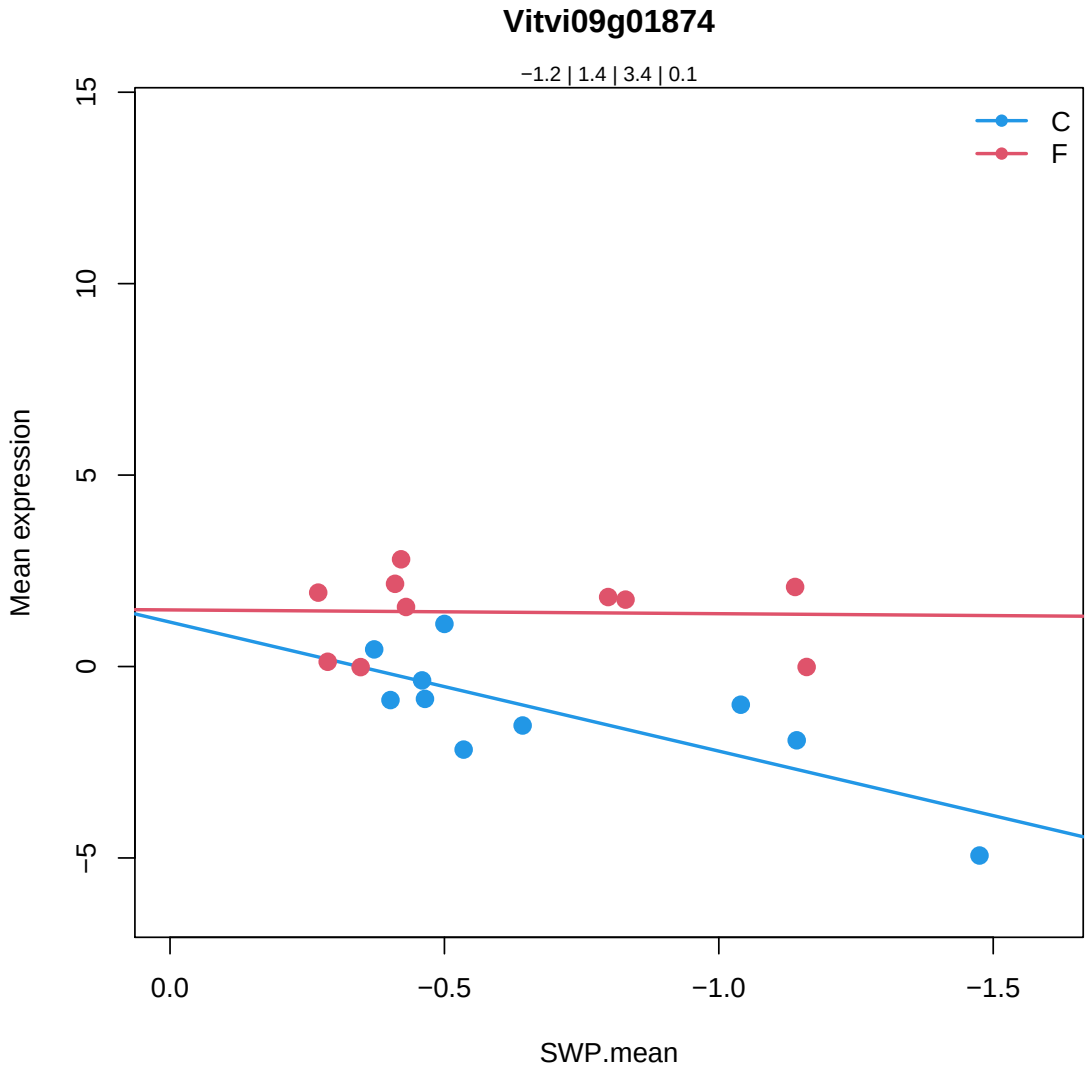
7.4.1 Vitvi09g01874: * type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g01874
        35.2
        not assigned.unknown
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606
```

Coefficients for Vitvi09g01874.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.209693	0.0007634725	***	0.0008287763	***
SlopeC	3.369133	0.0007557867	***	0.1076608	
MeanF-MeanC	2.627733	5.179869e-06	***	0.0001389992	***
SlopeF-SlopeC	-3.270373	0.01811727	*	0.9999488	



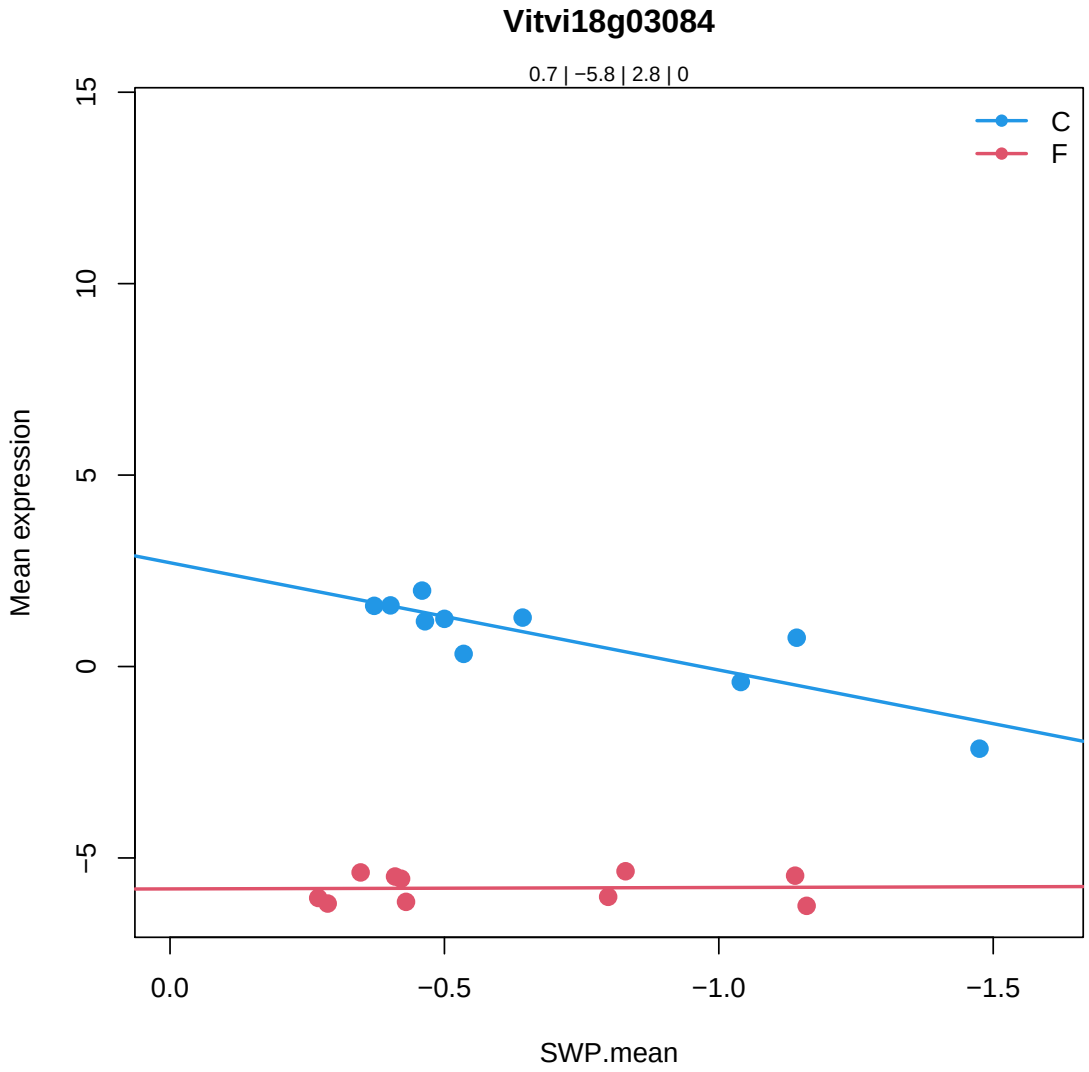
7.4.2 Vitvi18g03084: * type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g03084
        30.2.25
        signalling.receptor kinases.wall associated kinase
        Protein kinase family protein |
        Chr3:9241725-9243113 FORWARD LENGTH=433 |
        201606
```

Coefficients for Vitvi18g03084.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.7399658	0.0002141846	***	0.0002349817	***
SlopeC	2.801771	4.827114e-06	***	0.01839372	*
MeanF-MeanC	-6.526298	2.769532e-18	***	6.920199e-16	***
SlopeF-SlopeC	-2.838533	0.0004720067	***	0.9999488	



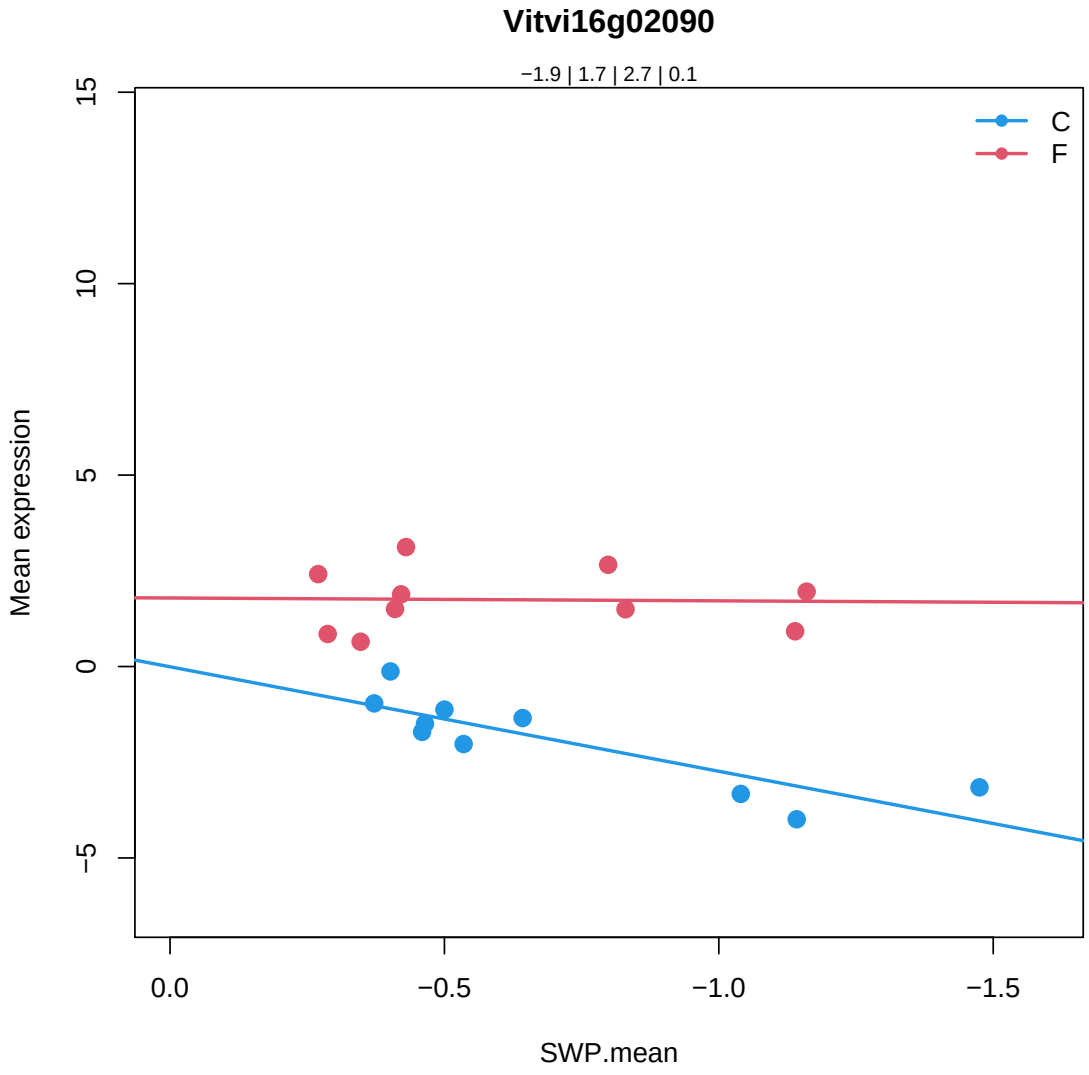
7.4.3 Vitvi16g02090: * type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g02090
        35.2
        not assigned.unknown
        PR5-like receptor kinase |
        Chr5:15293325-15295838 REVERSE LENGTH=665 |
        201606
```

Coefficients for Vitvi16g02090.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.926199	2.28078e-08	***	2.753775e-08	***
SlopeC	2.729033	0.0002614243	***	0.08298279	.
MeanF-MeanC	3.670552	1.144627e-10	***	7.8943e-09	***
SlopeF-SlopeC	-2.654757	0.009425042	**	0.9999488	



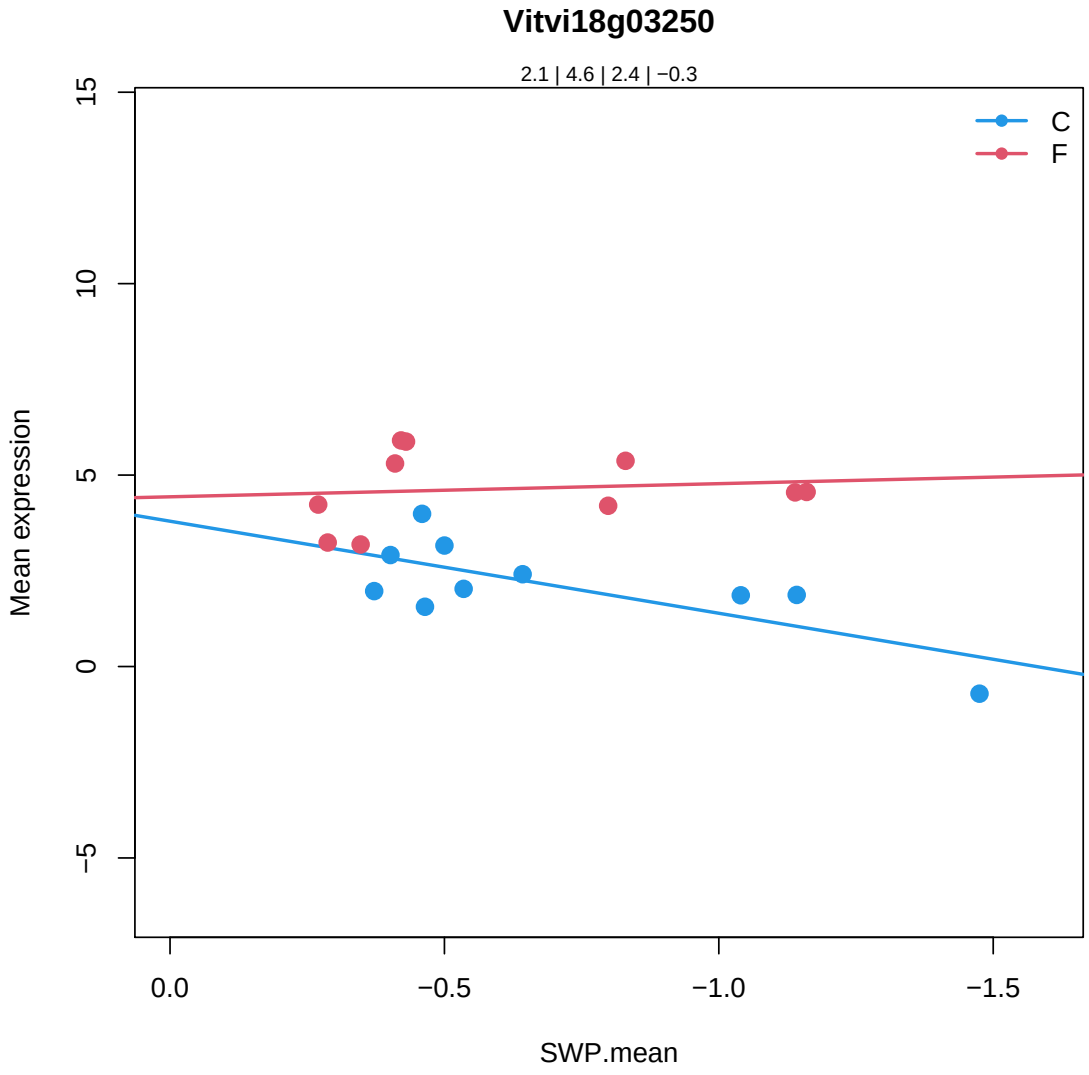
7.4.4 Vitvi18g03250: * type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g03250
        26.10
        misc.cytochrome P450
        cytochrome P450%2C family 714%2C subfamily A%2C polypeptide 1 |
        Chr5:8567674-8570260 REVERSE LENGTH=532 |
        201606
```

Coefficients for Vitvi18g03250.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.104769	1.319663e-07	***	1.560942e-07	***
SlopeC	2.403889	0.004635983	**	0.2436609	
MeanF-MeanC	2.536661	1.526731e-06	***	4.778322e-05	***
SlopeF-SlopeC	-2.746937	0.02414396	*	0.9999488	



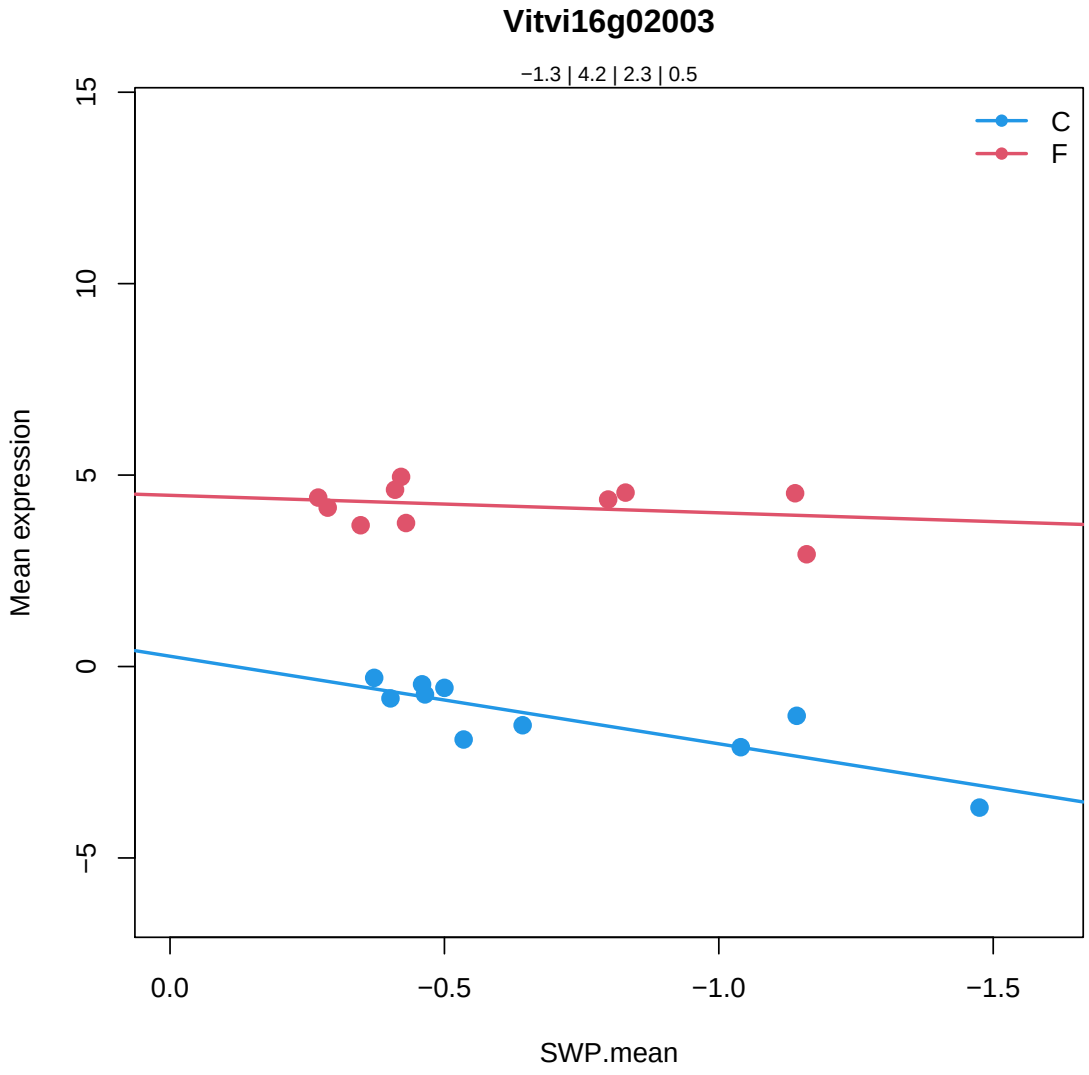
7.4.5 Vitvi16g02003: * type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g02003
        35.2
        not assigned.unknown
        PR5-like receptor kinase |
        Chr5:15293325-15295838 REVERSE LENGTH=665 |
        201606
```

Coefficients for Vitvi16g02003.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.339973	2.33912e-07	***	2.745485e-07	***
SlopeC	2.2875	0.000164243	***	0.07644173	.
MeanF-MeanC	5.532948	4.544274e-16	***	7.214982e-14	***
SlopeF-SlopeC	-1.830222	0.02298766	*	0.9999488	



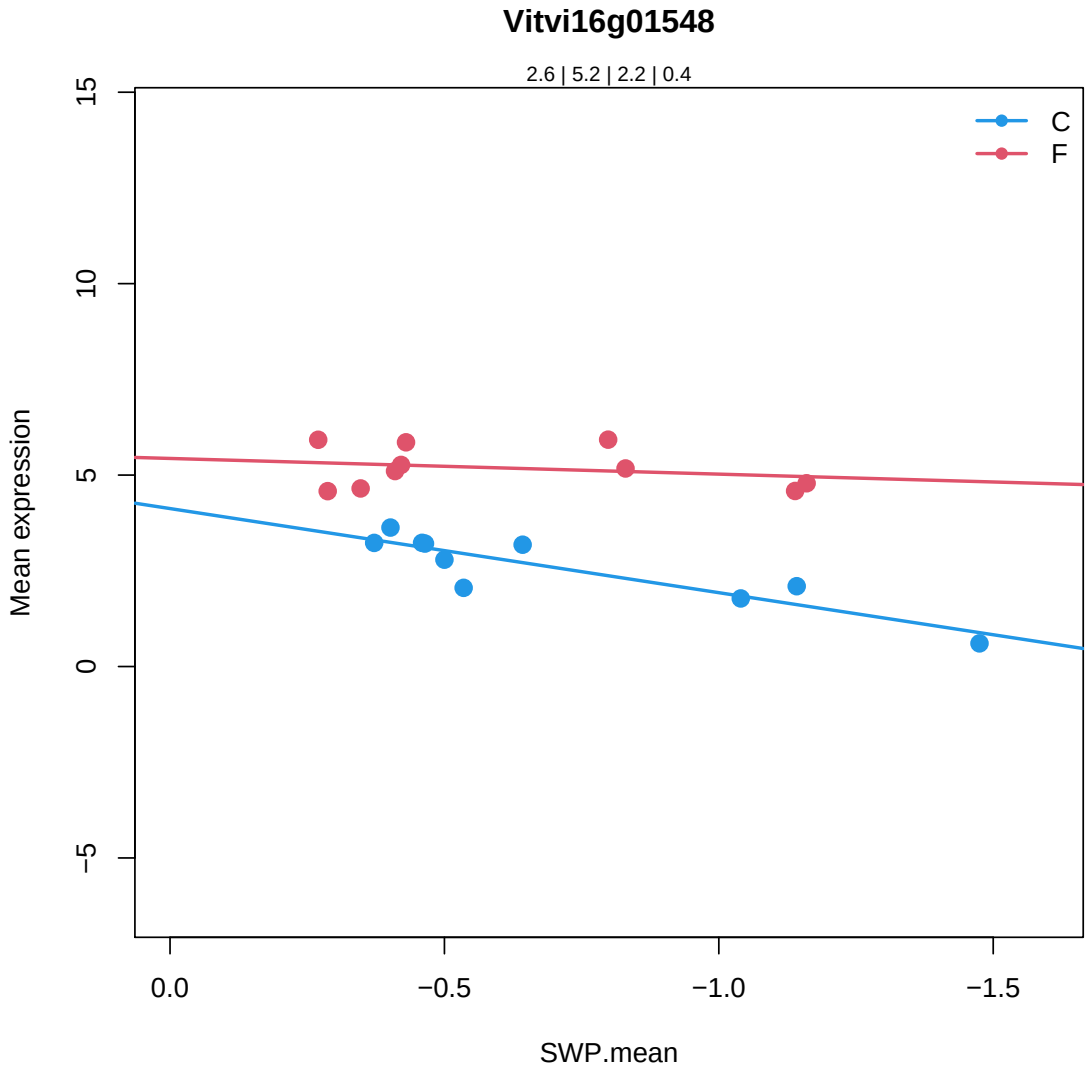
7.4.6 Vitvi16g01548: * type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01548
        35.2
        not assigned.unknown
        dihydroflavonol 4-reductase |
        Chr5:17164296-17165864 REVERSE LENGTH=382 |
        201606
```

Coefficients for Vitvi16g01548.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.580398	1.607866e-13	***	2.431742e-13	***
SlopeC	2.196869	6.152636e-05	***	0.07213729	.
MeanF-MeanC	2.60436	1.084352e-10	***	7.546893e-09	***
SlopeF-SlopeC	-1.787469	0.0128491	*	0.9999488	



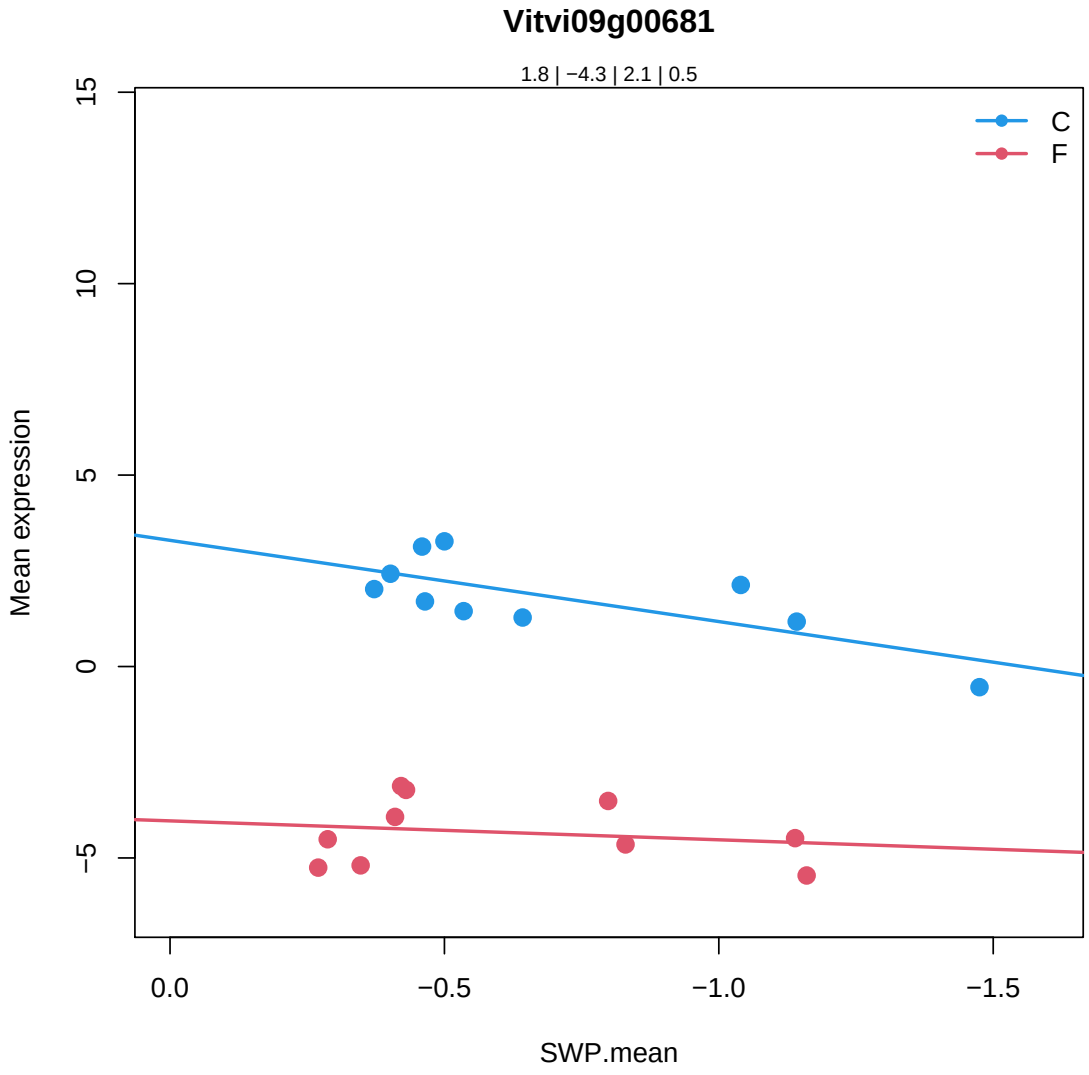
7.4.7 Vitvi09g00681: * type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00681
        20.1.2
        stress.biotic.receptors
        receptor like protein 1 |
        Chr1:2270633-2274654 FORWARD LENGTH=913 |
        201606
```

Coefficients for Vitvi09g00681.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.80362	2.175092e-07	***	2.556307e-07	***
SlopeC	2.121009	0.004715187	**	0.2454895	
MeanF-MeanC	-6.136671	2.131152e-14	***	2.537736e-12	***
SlopeF-SlopeC	-1.626761	0.1188241		0.9999488	



7.4.8 Vitvi12g00606: * type3 | type4

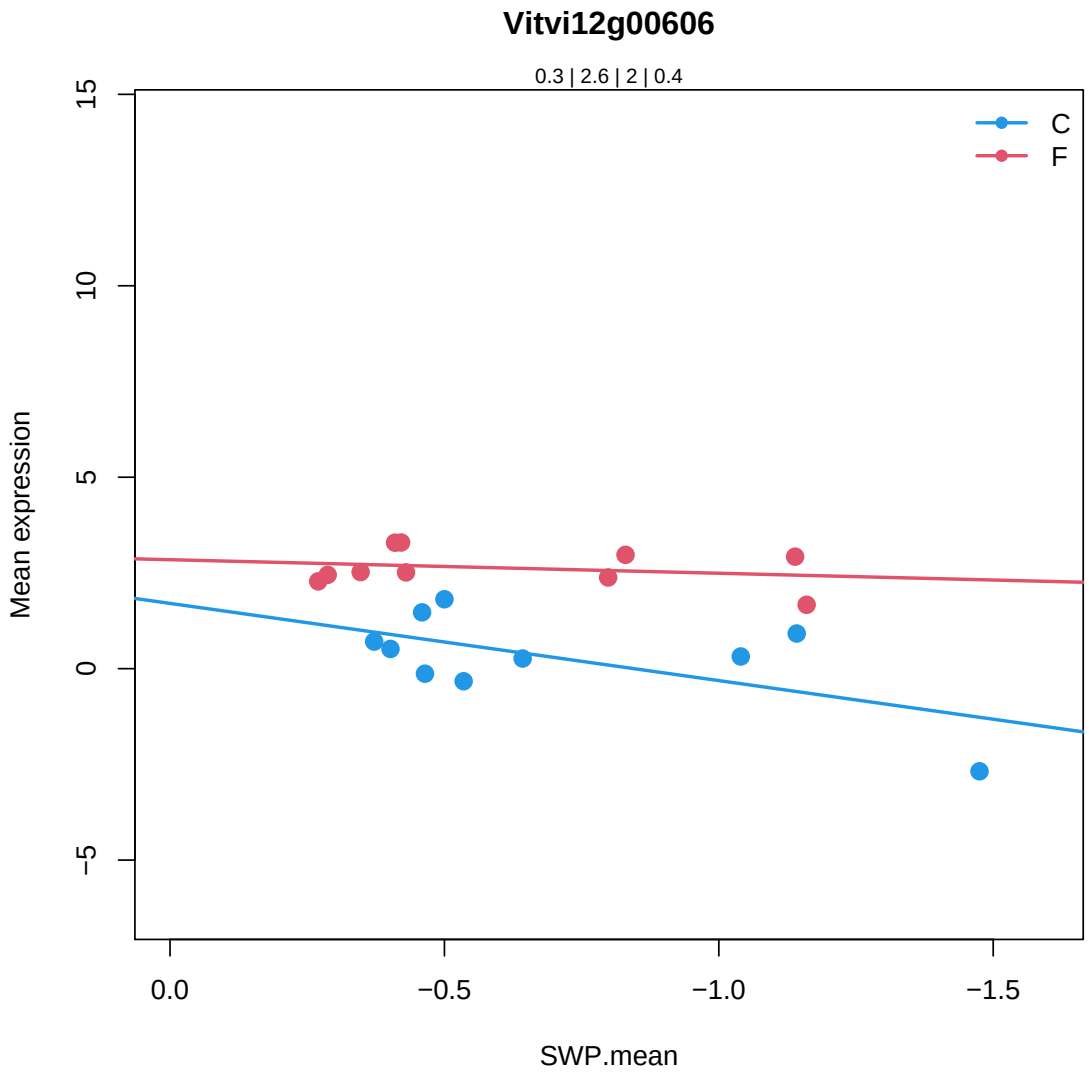
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00606
        29.4
        protein.postranslational modification
        G-type lectin S-receptor-like Serine/Threonine-kinase |
        Chr4:1419278-1422828 REVERSE LENGTH=1010 |
        201606

Vitvi12g00606
        30.2.24
        signalling.receptor kinases.S-locus glycoprotein like
        G-type lectin S-receptor-like Serine/Threonine-kinase |
        Chr4:1419278-1422828 REVERSE LENGTH=1010 |
        201606
```

Coefficients for Vitvi12g00606.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.2862625	0.2372891		0.2426379	
SlopeC	2.016467	0.005608764	**	0.2614336	
MeanF-MeanC	2.343448	5.354432e-07	***	1.871841e-05	***
SlopeF-SlopeC	-1.662881	0.1025429		0.9999488	


Vitvi12g00606
0.3 | 2.6 | 2 | 0.4
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

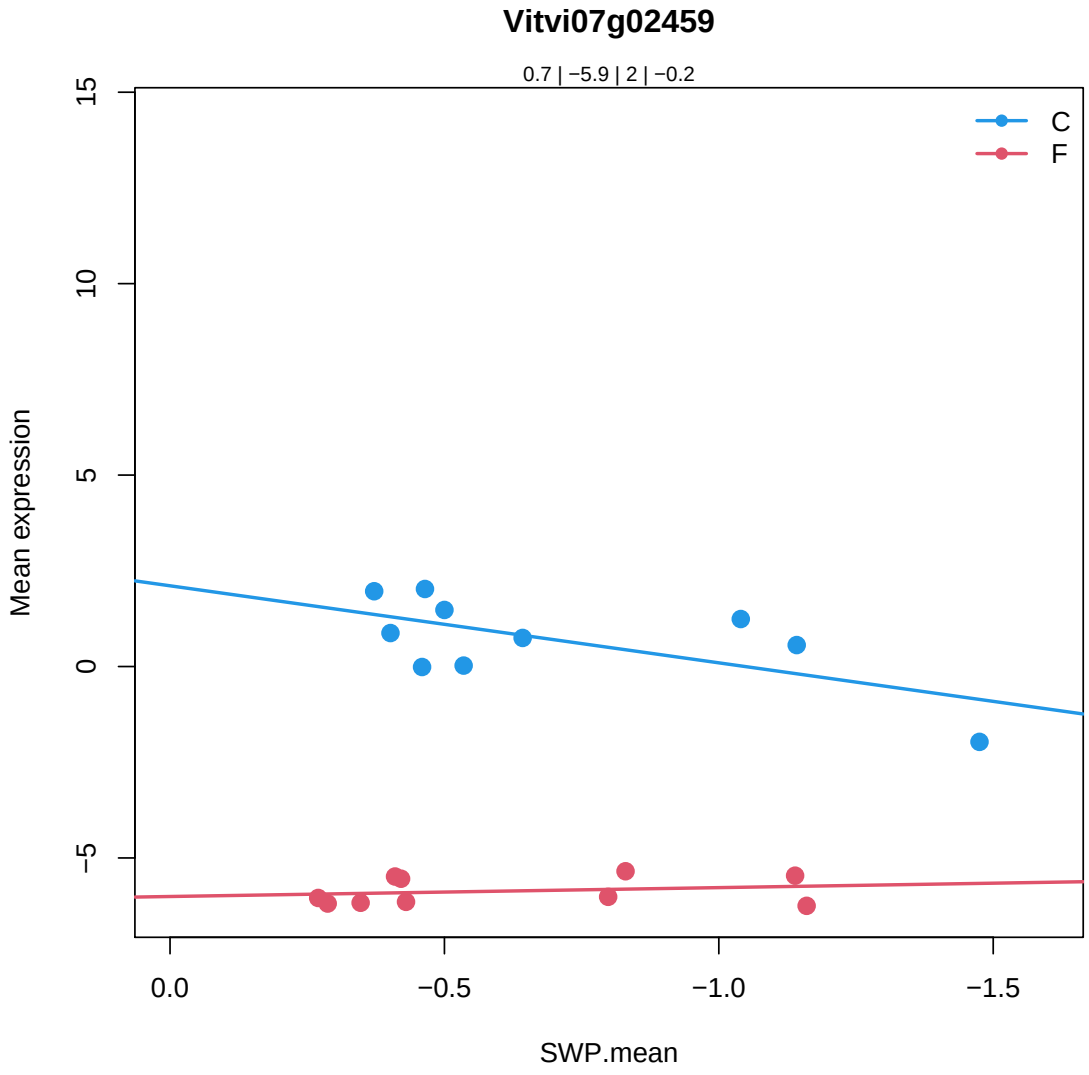
7.4.9 Vitvi07g02459: * type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g02459
        35.2
        not assigned.unknown
        Ankyrin repeat family protein |
        Chr5:1349781-1352525 REVERSE LENGTH=625 |
        201606
```

Coefficients for Vitvi07g02459.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6932742	0.003485594	**	0.003730073	**
SlopeC	2.012497	0.002490803	**	0.1896965	
MeanF-MeanC	-6.558855	3.497533e-16	***	5.611515e-14	***
SlopeF-SlopeC	-2.244575	0.01782121	*	0.9999488	



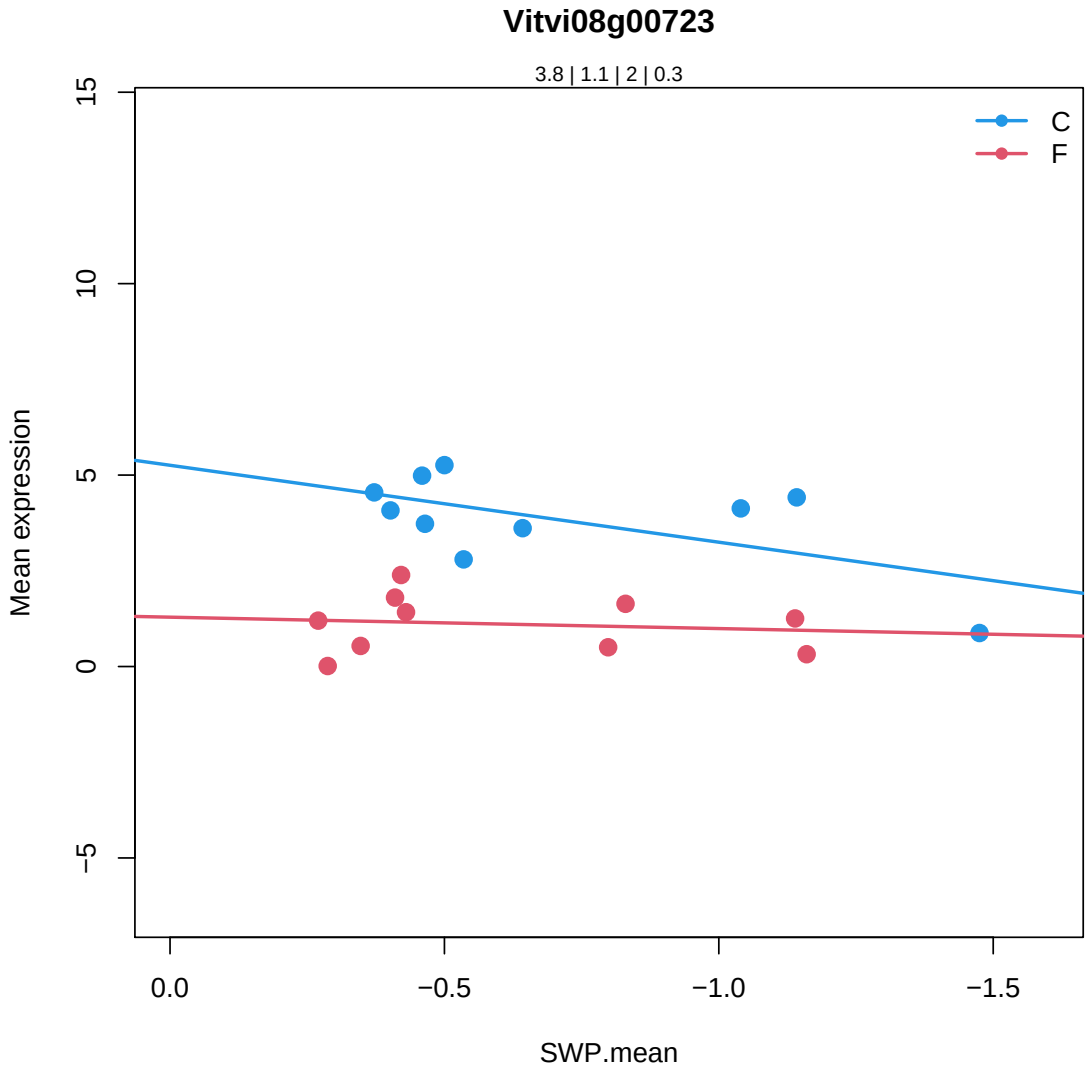
7.4.10 Vitvi08g00723: * type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g00723
        34.5
        transport.ammonium
        ammonium transporter 2 |
        Chr2:16039672-16042291 REVERSE LENGTH=475 |
        201606
```

Coefficients for Vitvi08g00723.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.8431	1.699178e-12	***	2.40584e-12	***
SlopeC	2.009066	0.01311545	*	0.3305597	
MeanF-MeanC	-2.73582	3.419843e-07	***	1.241077e-05	***
SlopeF-SlopeC	-1.711553	0.1362029		0.9999488	



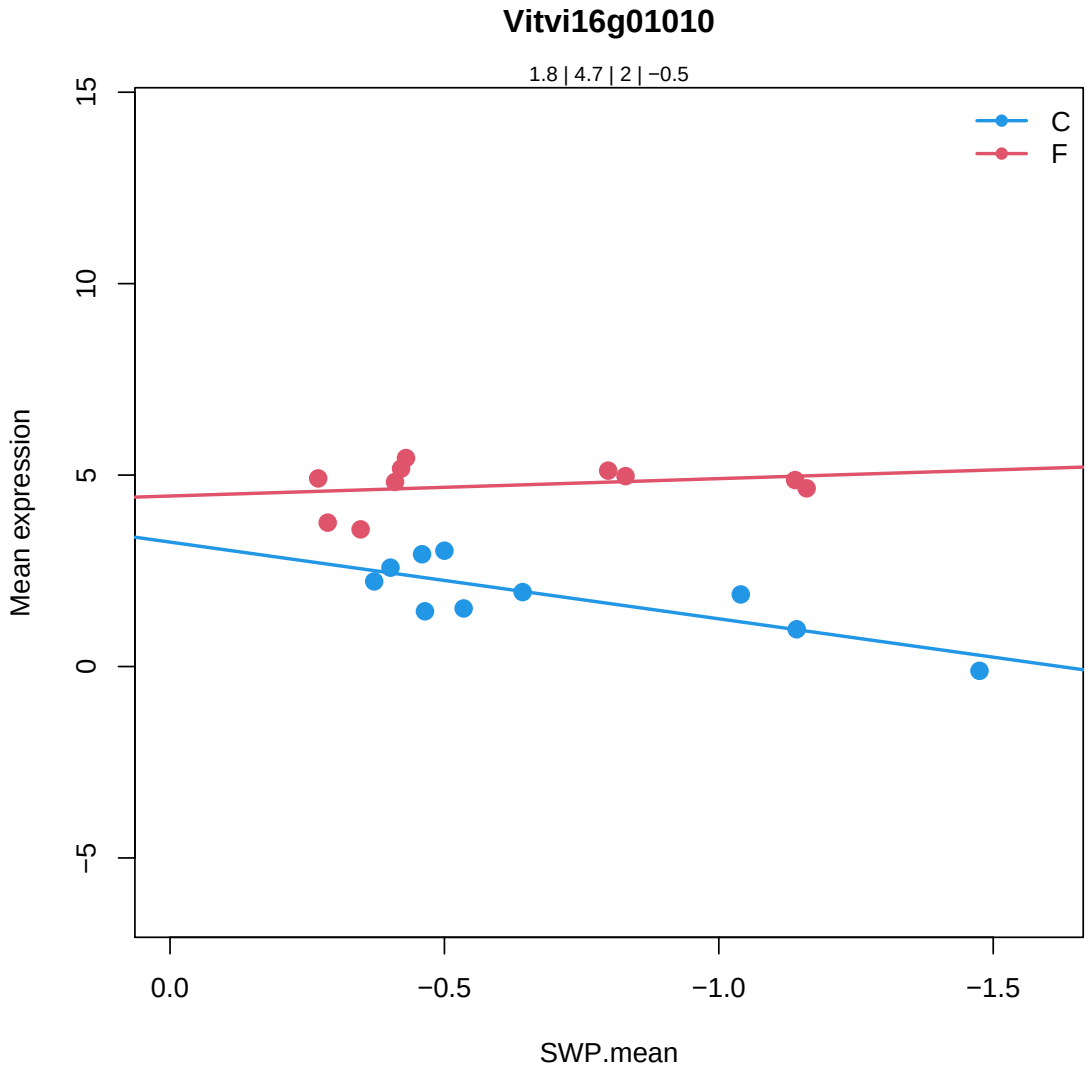
7.4.11 Vitvi16g01010: * type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01010
        35.2
        not assigned.unknown
        suppressor of npr1-1 constitutive 4 |
        Chr1:24997491-25001961 REVERSE LENGTH=1101 |
        201606
```

Coefficients for Vitvi16g01010.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.840664	1.600078e-09	***	2.004306e-09	***
SlopeC	2.003371	0.00078477	***	0.1097382	
MeanF-MeanC	2.889029	2.424297e-10	***	1.585886e-08	***
SlopeF-SlopeC	-2.457307	0.004028662	**	0.9999488	



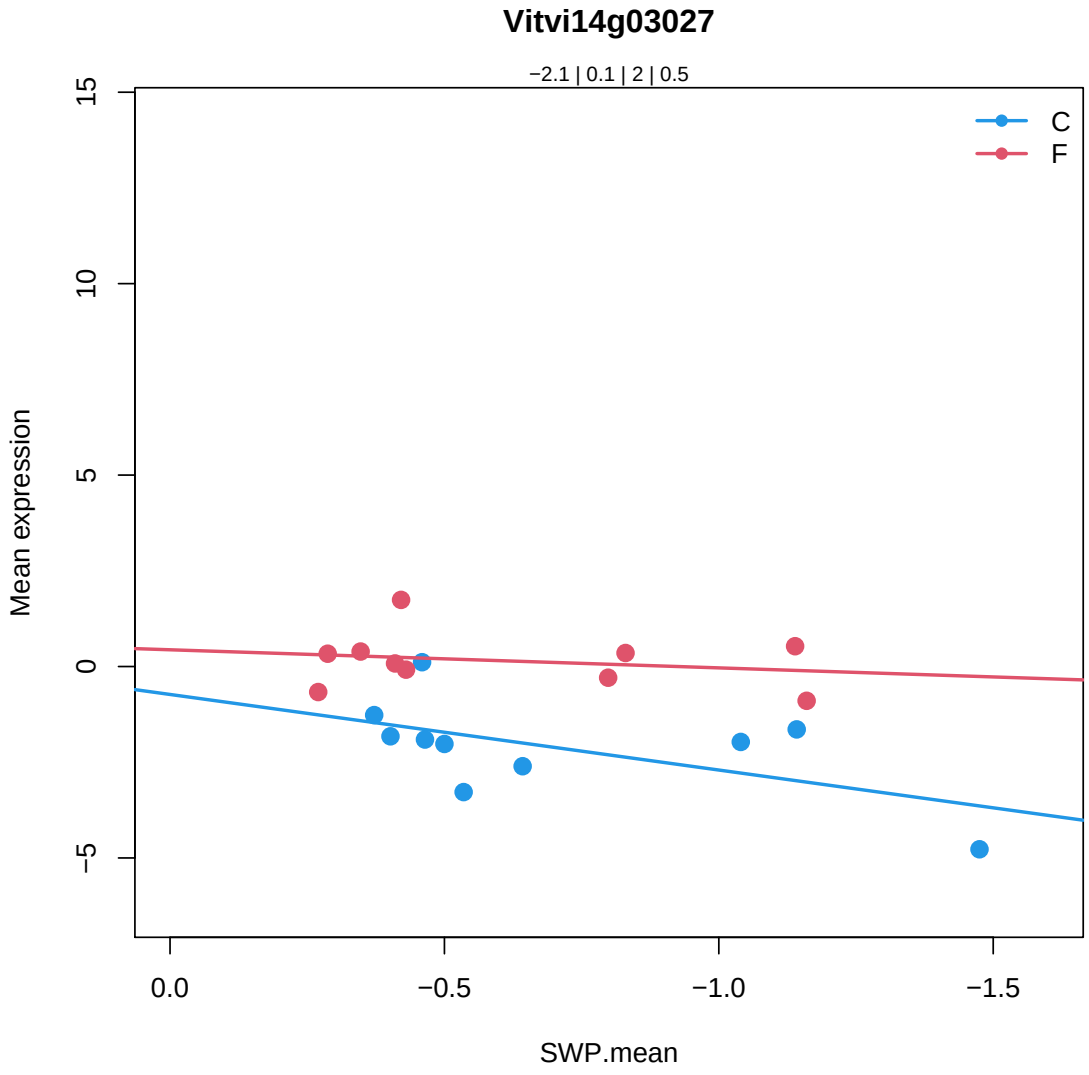
7.4.12 Vitvi14g03027: * type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g03027
        35.2
        not assigned.unknown
        transmembrane protein |
        Chr1:8425981-8427045 REVERSE LENGTH=354 |
        201606
```

Coefficients for Vitvi14g03027.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-2.117932	9.501523e-08	***	1.12825e-07	***
SlopeC	1.973808	0.01542005	*	0.3393703	
MeanF-MeanC	2.267038	6.121502e-06	***	0.000160592	***
SlopeF-SlopeC	-1.501193	0.1926976		0.9999488	



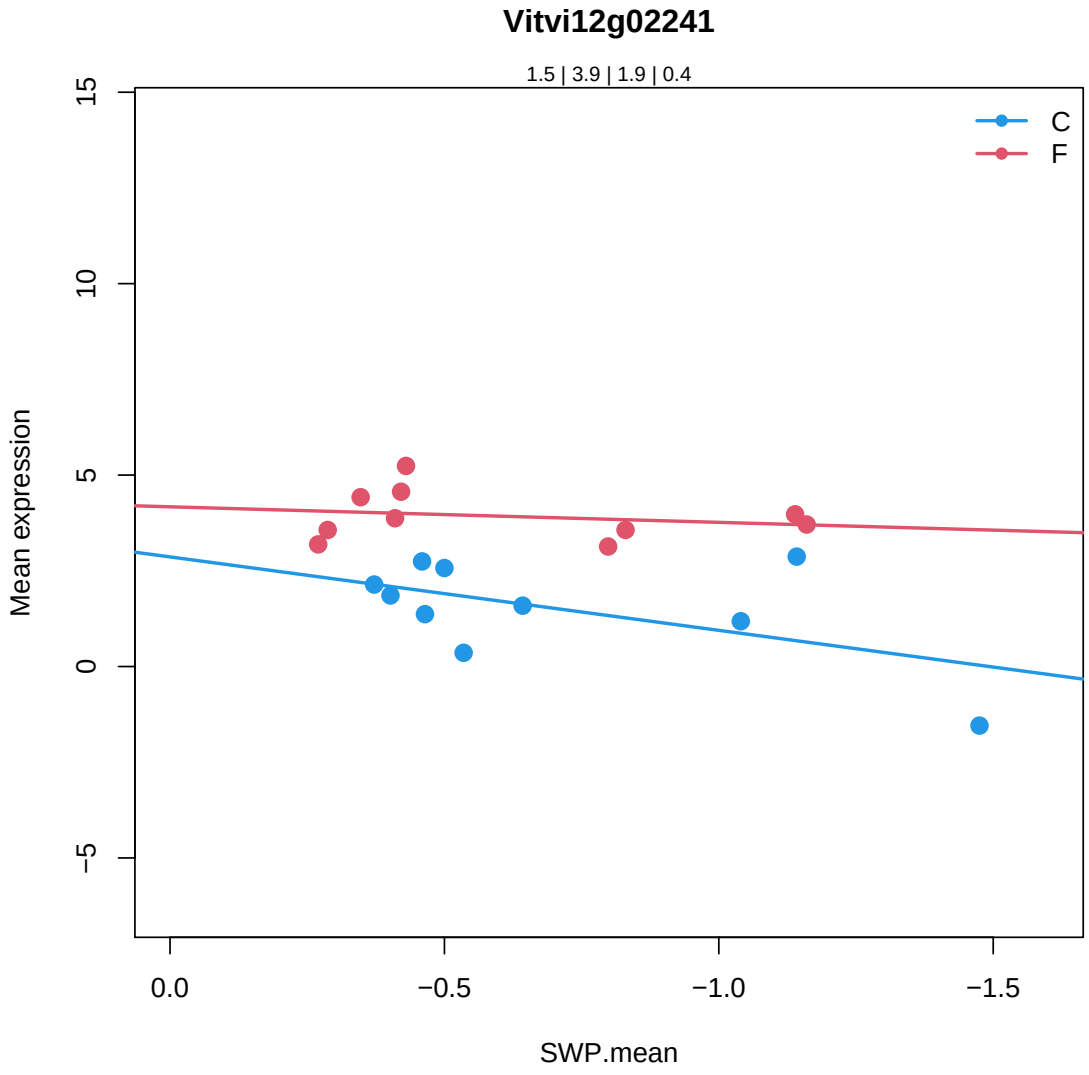
7.4.13 Vitvi12g02241: * type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02241
        26.6
        misc.O-methyl transferases
        O-methyltransferase family protein |
        Chr4:16730989-16732808 REVERSE LENGTH=382 |
        201606
```

Coefficients for Vitvi12g02241.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.513909	1.593673e-05	***	1.791222e-05	***
SlopeC	1.917744	0.01970617	*	0.374907	
MeanF-MeanC	2.40998	3.204087e-06	***	9.094357e-05	***
SlopeF-SlopeC	-1.511665	0.195969		0.9999488	



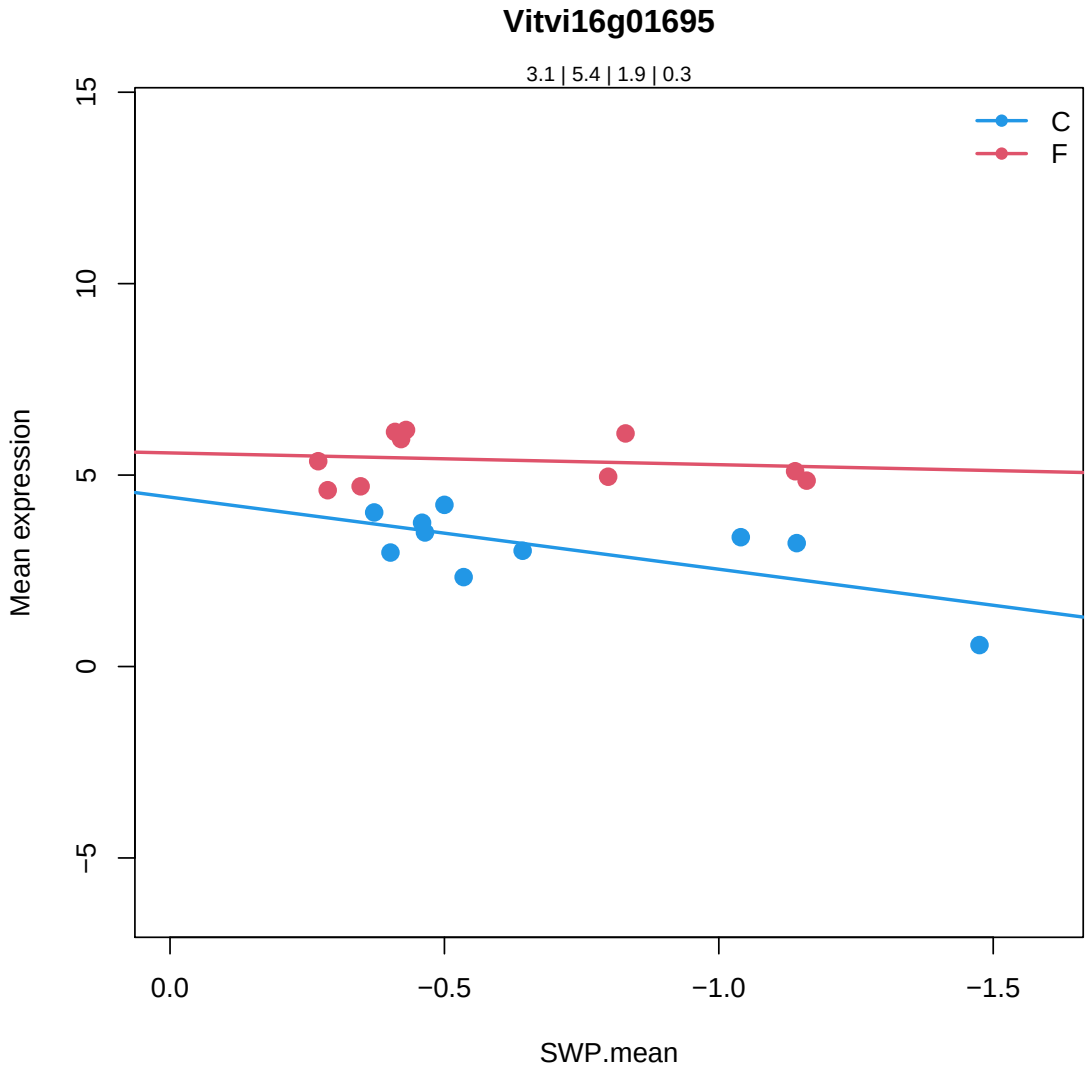
7.4.14 Vitvi16g01695: * type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01695
        35.2
        not assigned.unknown
        receptor like protein 6 |
        Chr1:17183550-17186534 REVERSE LENGTH=994 |
        201606
```

Coefficients for Vitvi16g01695.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.099689	1.944845e-12	***	2.745261e-12	***
SlopeC	1.88261	0.005080912	**	0.2530826	
MeanF-MeanC	2.292059	2.105269e-07	***	7.903575e-06	***
SlopeF-SlopeC	-1.575394	0.09360147	.	0.9999488	



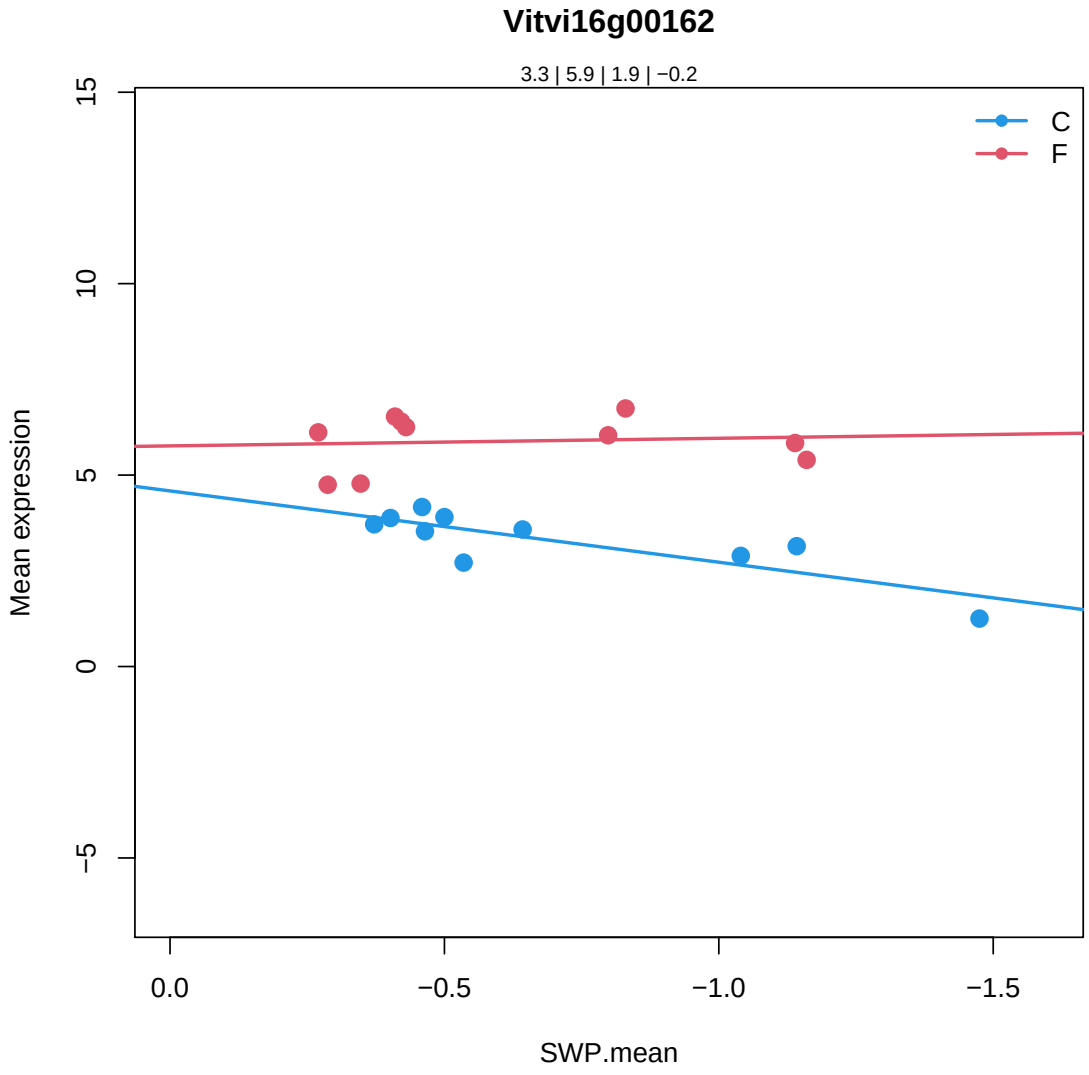
7.4.15 Vitvi16g00162: * type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g00162
        35.2
        not assigned.unknown
        NB-ARC domain-containing disease resistance protein |
        Chr4:13633953-13636736 REVERSE LENGTH=927 |
        201606
```

Coefficients for Vitvi16g00162.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.27686	4.140595e-14	***	6.560389e-14	***
SlopeC	1.862536	0.00186088	**	0.160246	
MeanF-MeanC	2.606492	2.387076e-09	***	1.285647e-07	***
SlopeF-SlopeC	-2.06133	0.01522443	*	0.9999488	



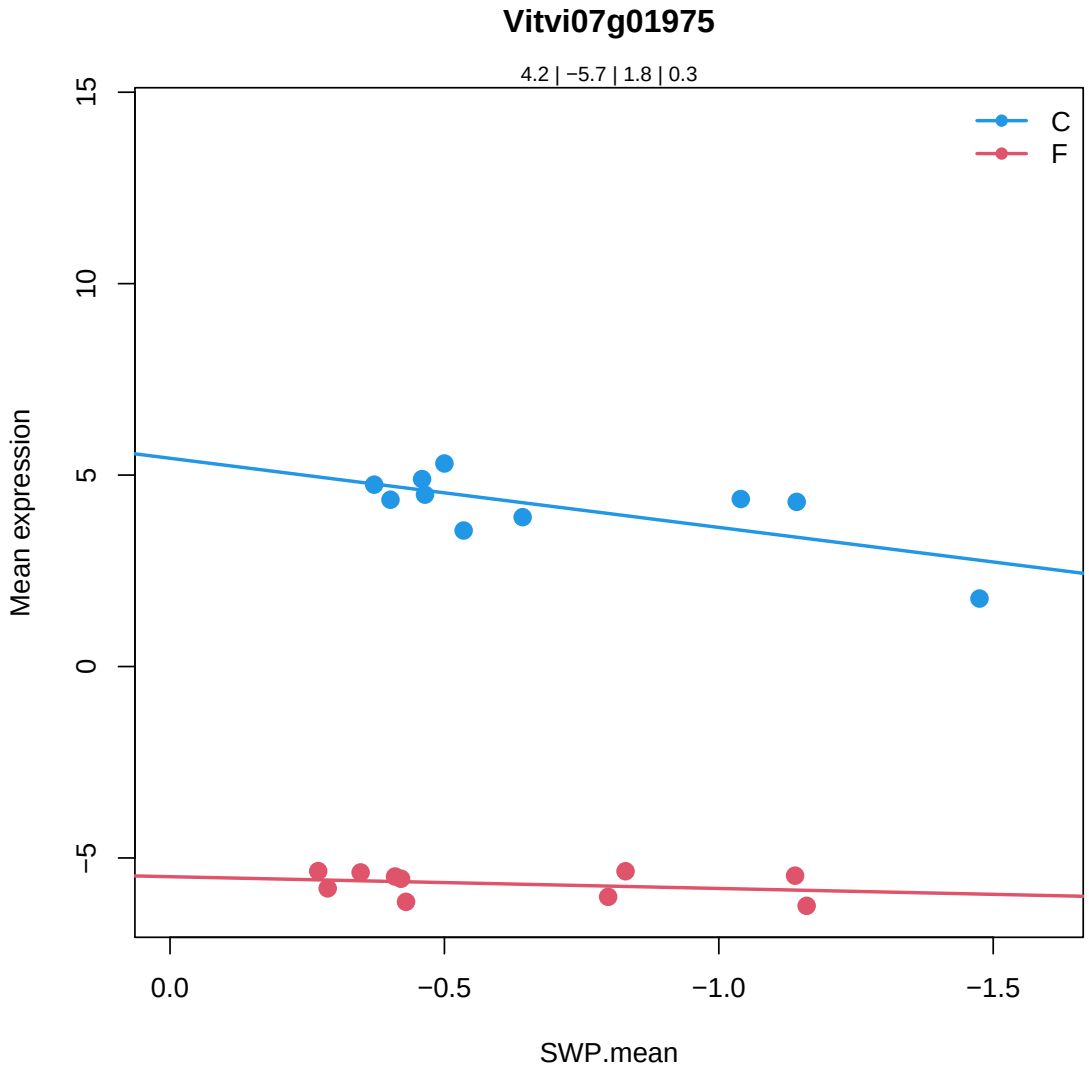
7.4.16 Vitvi07g01975: * type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01975
        35.2
        not assigned.unknown
        ammonium transporter 2 |
        Chr2:16039672-16042291 REVERSE LENGTH=475 |
        201606
```

Coefficients for Vitvi07g01975.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.169379	6.951417e-17	***	1.554254e-16	***
SlopeC	1.805957	0.001302019	**	0.1417527	
MeanF-MeanC	-9.845904	1.491184e-21	***	9.882012e-19	***
SlopeF-SlopeC	-1.498707	0.05160997	.	0.9999488	



7.4.17 Vitvi12g02434: * type3 | type4

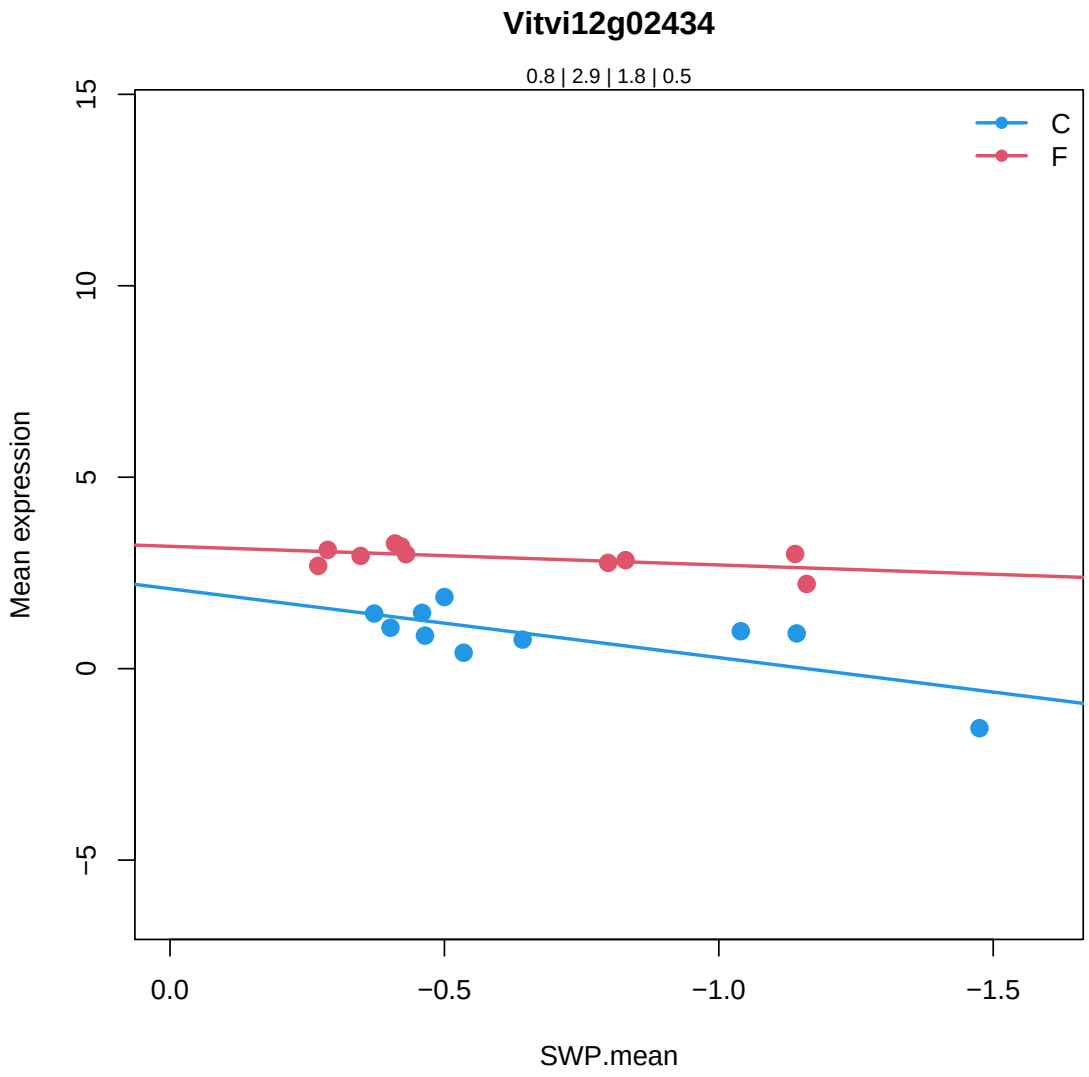
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02434
        29.4
        protein.postranslational modification
        G-type lectin S-receptor-like Serine/Threonine-kinase |
        Chr4:1419278-1422828 REVERSE LENGTH=1010 |
        201606

Vitvi12g02434
        30.2.24
        signalling.receptor kinases.S-locus glycoprotein like
        G-type lectin S-receptor-like Serine/Threonine-kinase |
        Chr4:1419278-1422828 REVERSE LENGTH=1010 |
        201606
```

Coefficients for Vitvi12g02434.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8214444	4.165707e-05	***	4.635592e-05	***
SlopeC	1.798958	0.0005749267	***	0.1005065	
MeanF-MeanC	2.077066	7.184554e-09	***	3.638105e-07	***
SlopeF-SlopeC	-1.311562	0.06099283	.	0.9999488	


Vitvi12g02434
0.8 | 2.9 | 1.8 | 0.5
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

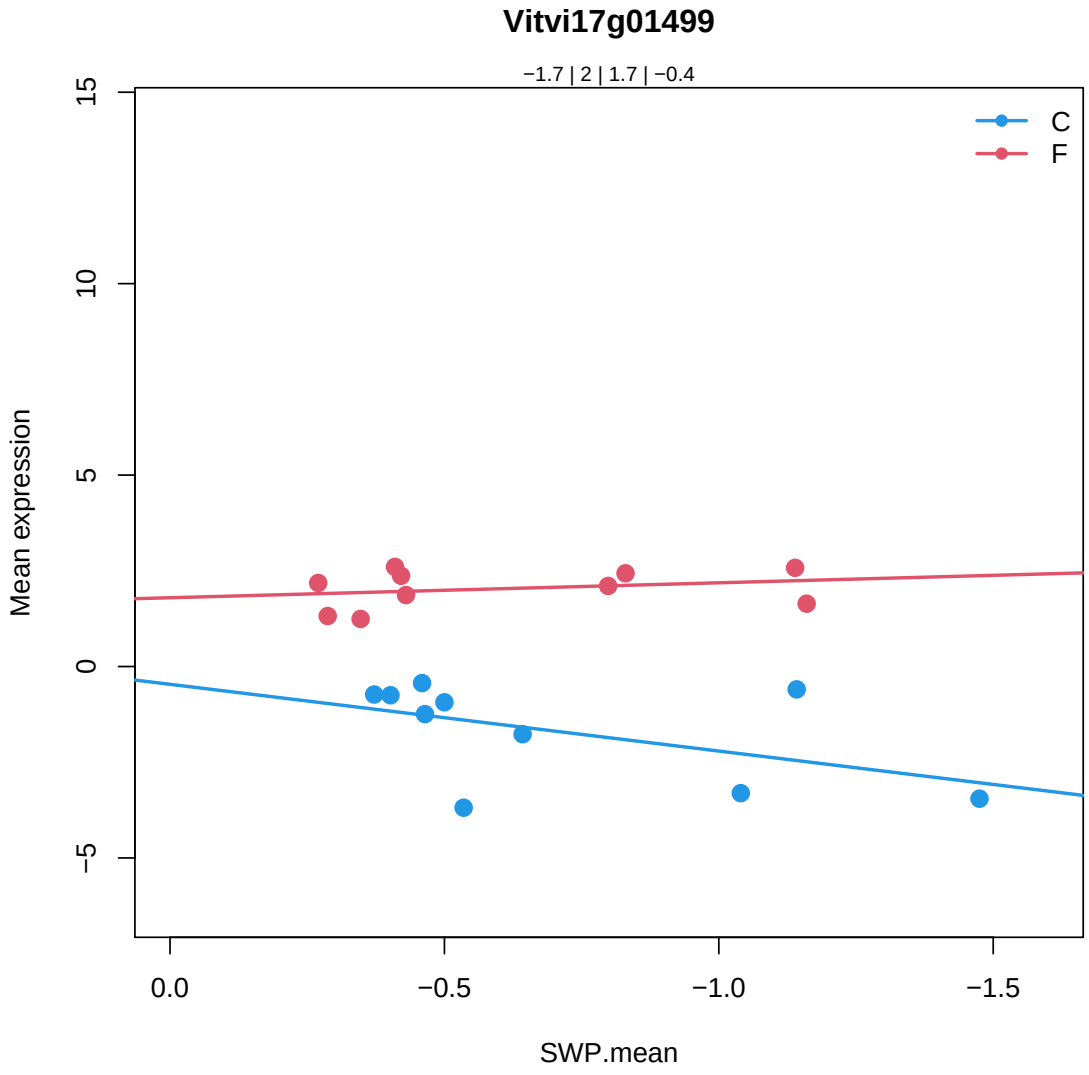
7.4.18 Vitvi17g01499: * type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g01499
        26.2
        misc.UDP glucosyl and glucoronyl transferases
        UDP-Glycosyltransferase superfamily protein |
        Chr3:368840-370484 REVERSE LENGTH=464 |
        201606
```

Coefficients for Vitvi17g01499.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.690499	1.763896e-06	***	2.024953e-06	***
SlopeC	1.743445	0.02511451	*	0.4079655	
MeanF-MeanC	3.724487	1.268641e-09	***	7.215157e-08	***
SlopeF-SlopeC	-2.133583	0.06070084	.	0.9999488	



7.4.19 Vitvi09g00253: * type3 | type4

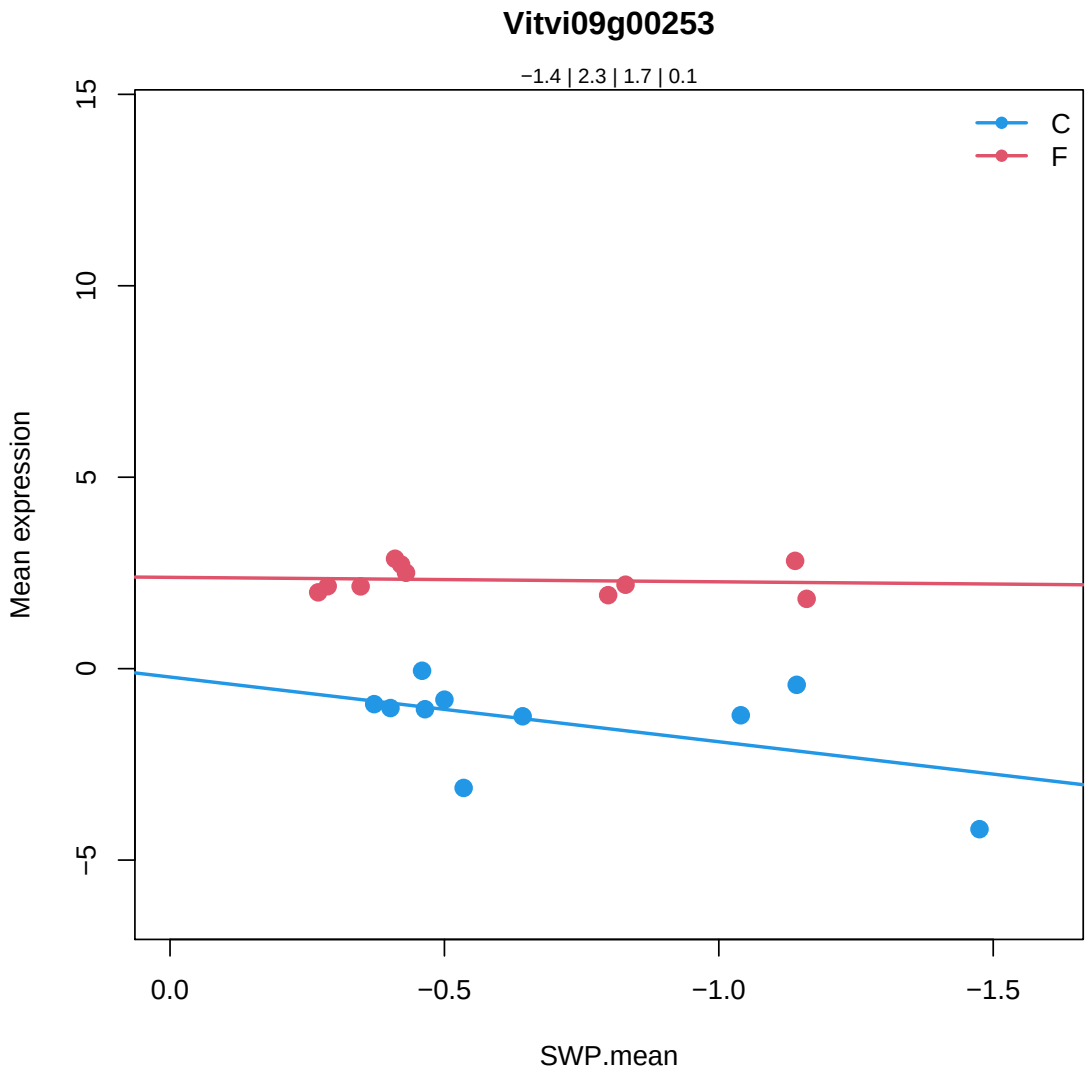
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00253
        29.4
        protein.postranslational modification
        Leucine-rich repeat transmembrane protein kinase protein |
        Chr4:14665802-14669438 REVERSE LENGTH=876 |
        201606

Vitvi09g00253
        30.2.1
        signalling.receptor kinases.leucine rich repeat I
        Leucine-rich repeat transmembrane protein kinase protein |
        Chr4:14665802-14669438 REVERSE LENGTH=876 |
        201606
```

Coefficients for Vitvi09g00253.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.407384	1.22789e-05	***	1.383771e-05	***
SlopeC	1.690283	0.02356607	*	0.3983963	
MeanF-MeanC	3.721139	5.921833e-10	***	3.639539e-08	***
SlopeF-SlopeC	-1.574086	0.1418375		0.9999488	


Vitvi09g00253
−1.4 | 2.3 | 1.7 | 0.1
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

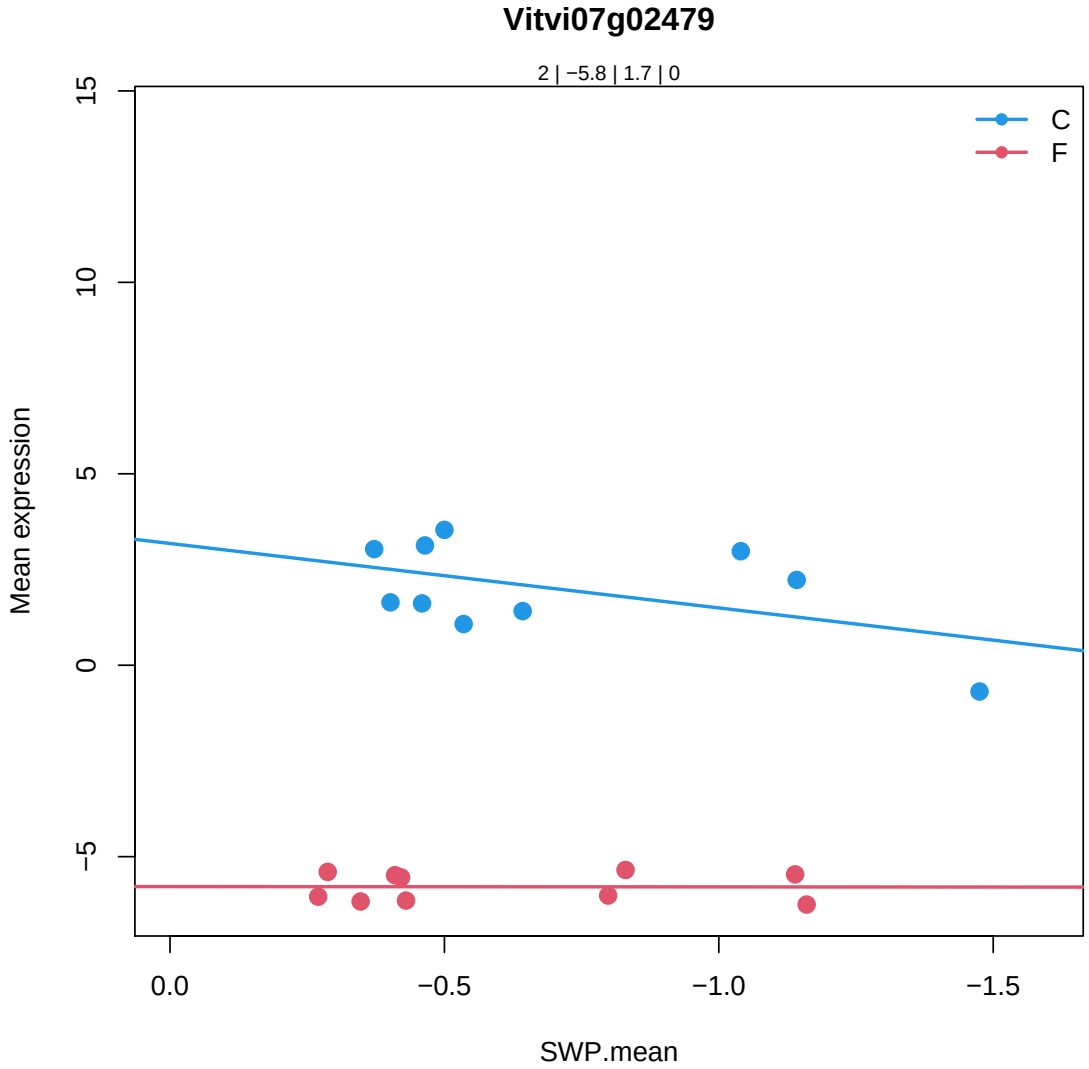
7.4.20 Vitvi07g02479: * type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g02479
        35.2
        not assigned.unknown
        Serine_threonine-protein phosphatase 6 regulatory ankyrin repeat subun
```

Coefficients for Vitvi07g02479.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.996167	6.687837e-08	***	7.966241e-08	***
SlopeC	1.683394	0.02375949	*	0.3983963	
MeanF-MeanC	-7.7825	2.962028e-16	***	4.961235e-14	***
SlopeF-SlopeC	-1.67543	0.1182497		0.9999488	



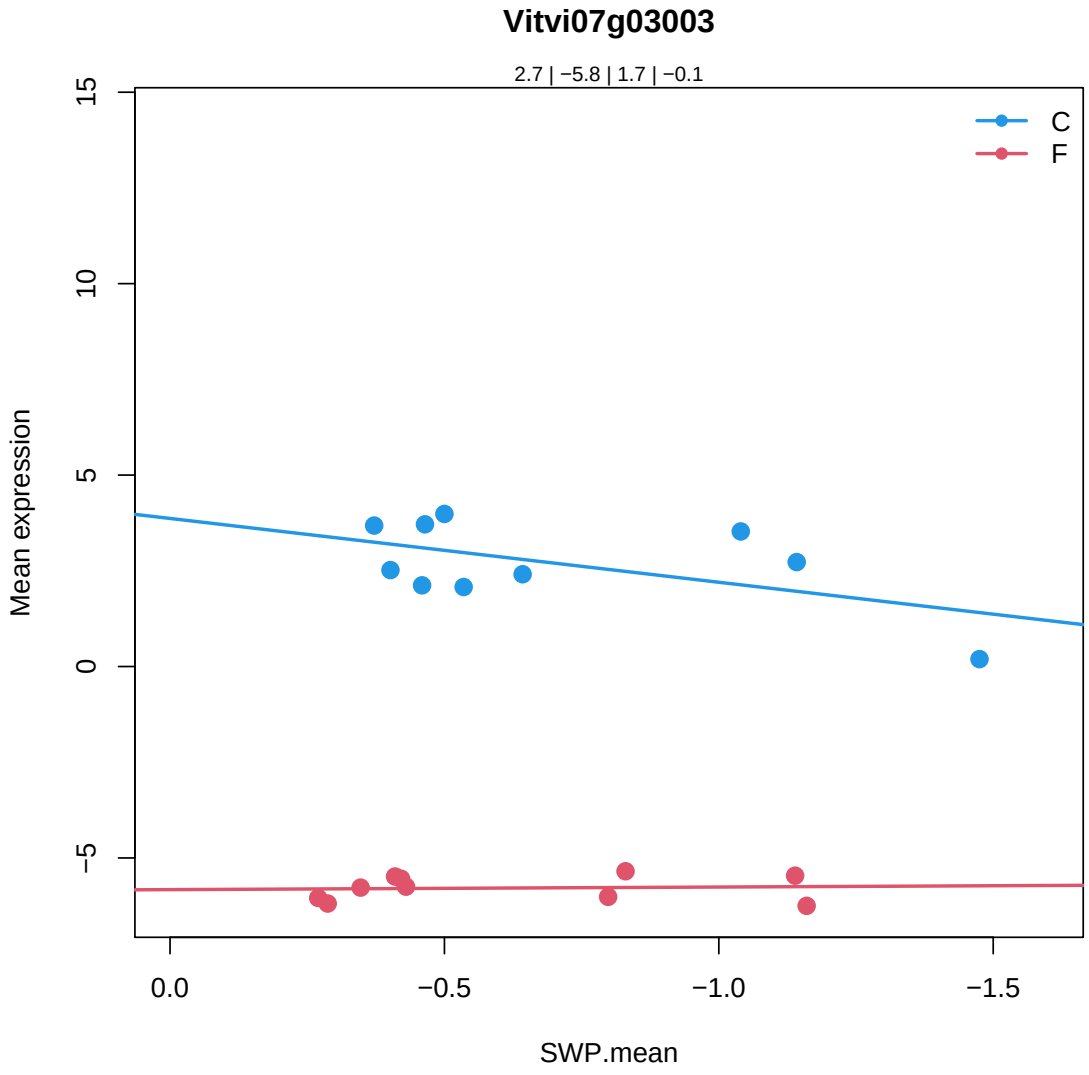
7.4.21 Vitvi07g03003: * type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g03003
        31.1
        cell.organisation
        Ankyrin repeat family protein |
        Chr3:6424135-6426471 REVERSE LENGTH=653 |
        201606
```

Coefficients for Vitvi07g03003.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.695259	2.950611e-11	***	3.947789e-11	***
SlopeC	1.666543	0.01164374	*	0.318473	
MeanF-MeanC	-8.481592	3.014671e-18	***	7.411229e-16	***
SlopeF-SlopeC	-1.734139	0.0671711	.	0.9999488	



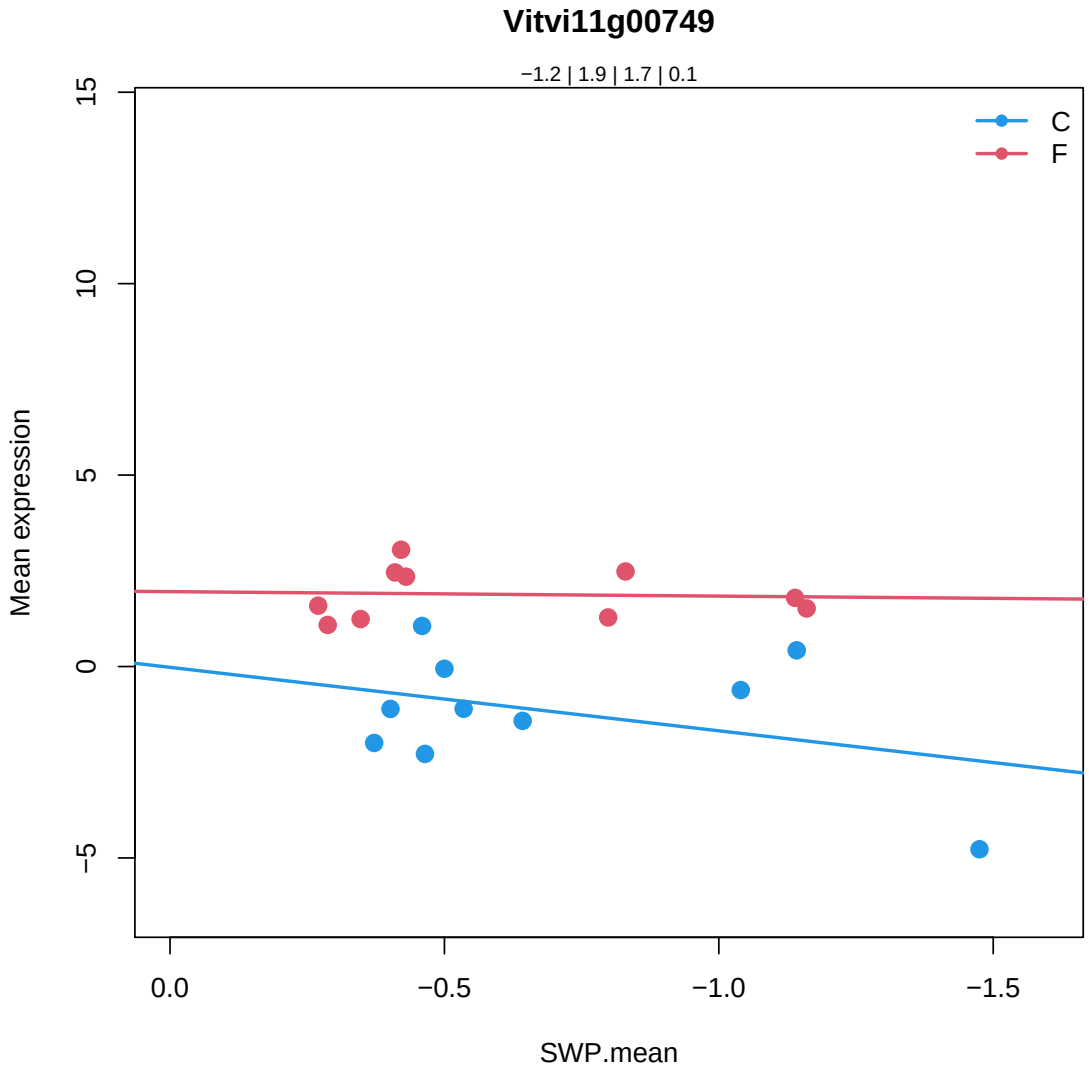
7.4.22 Vitvi11g00749: type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00749
        30.2.12
        signalling.receptor kinases.leucine rich repeat XII
        kinase family with leucine-rich repeat domain-containing protein |
        Chr1:13220940-13224386 FORWARD LENGTH=1120 |
        201606
```

Coefficients for Vitvi11g00749.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.187309	0.002453198	**	0.002632658	**
SlopeC	1.657462	0.09954394	.	0.6110181	
MeanF-MeanC	3.071475	2.889466e-06	***	8.264173e-05	***
SlopeF-SlopeC	-1.540859	0.2941879		0.9999488	



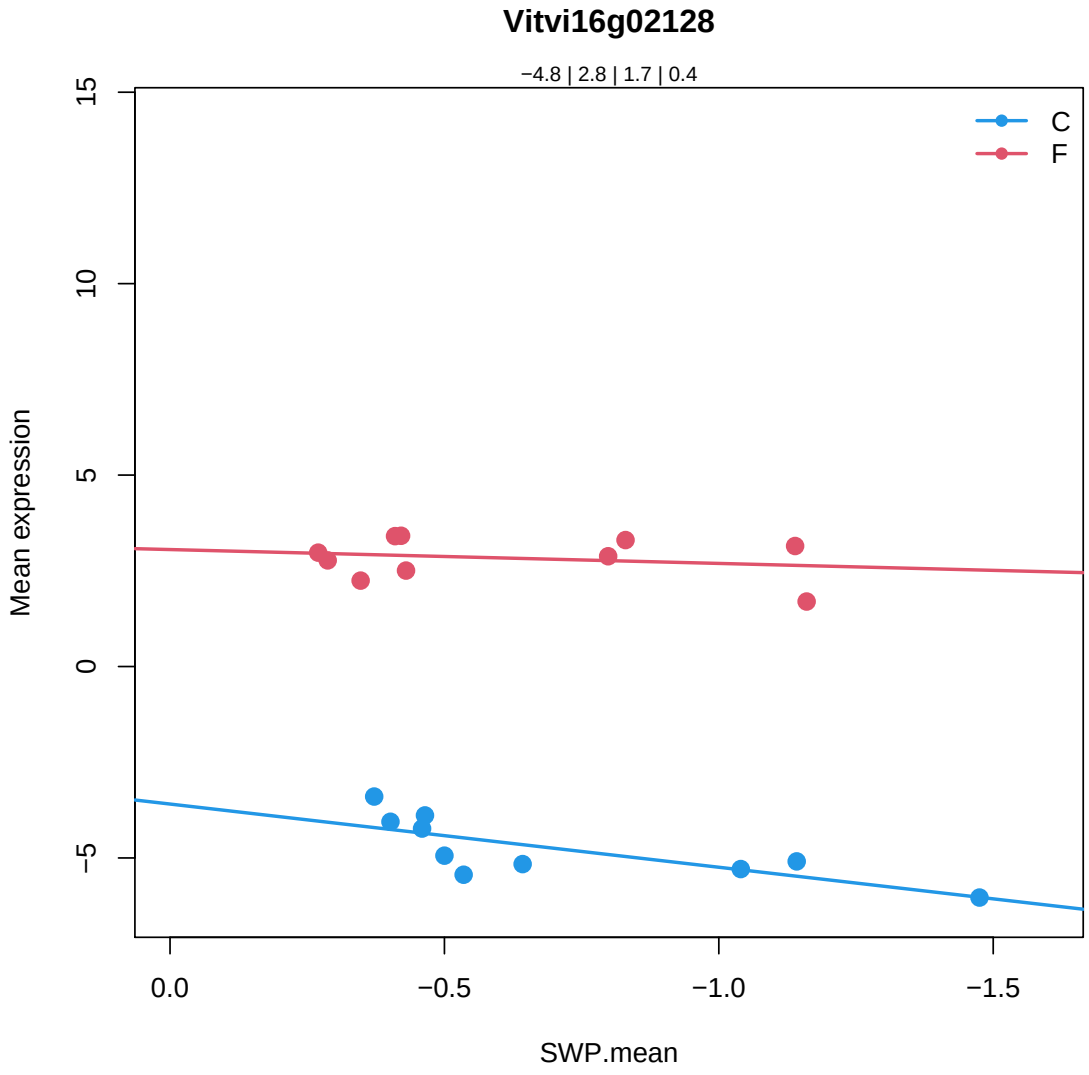
7.4.23 Vitvi16g02128: * type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g02128
        35.2
        not assigned.unknown
        PR5-like receptor kinase |
        Chr5:15293325-15295838 REVERSE LENGTH=665 |
        201606
```

Coefficients for Vitvi16g02128.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-4.752626	3.621096e-18	***	1.065291e-17	***
SlopeC	1.650819	0.002533182	**	0.1902008	
MeanF-MeanC	7.586807	2.867599e-19	***	8.405375e-17	***
SlopeF-SlopeC	-1.288502	0.08722927	.	0.9999488	



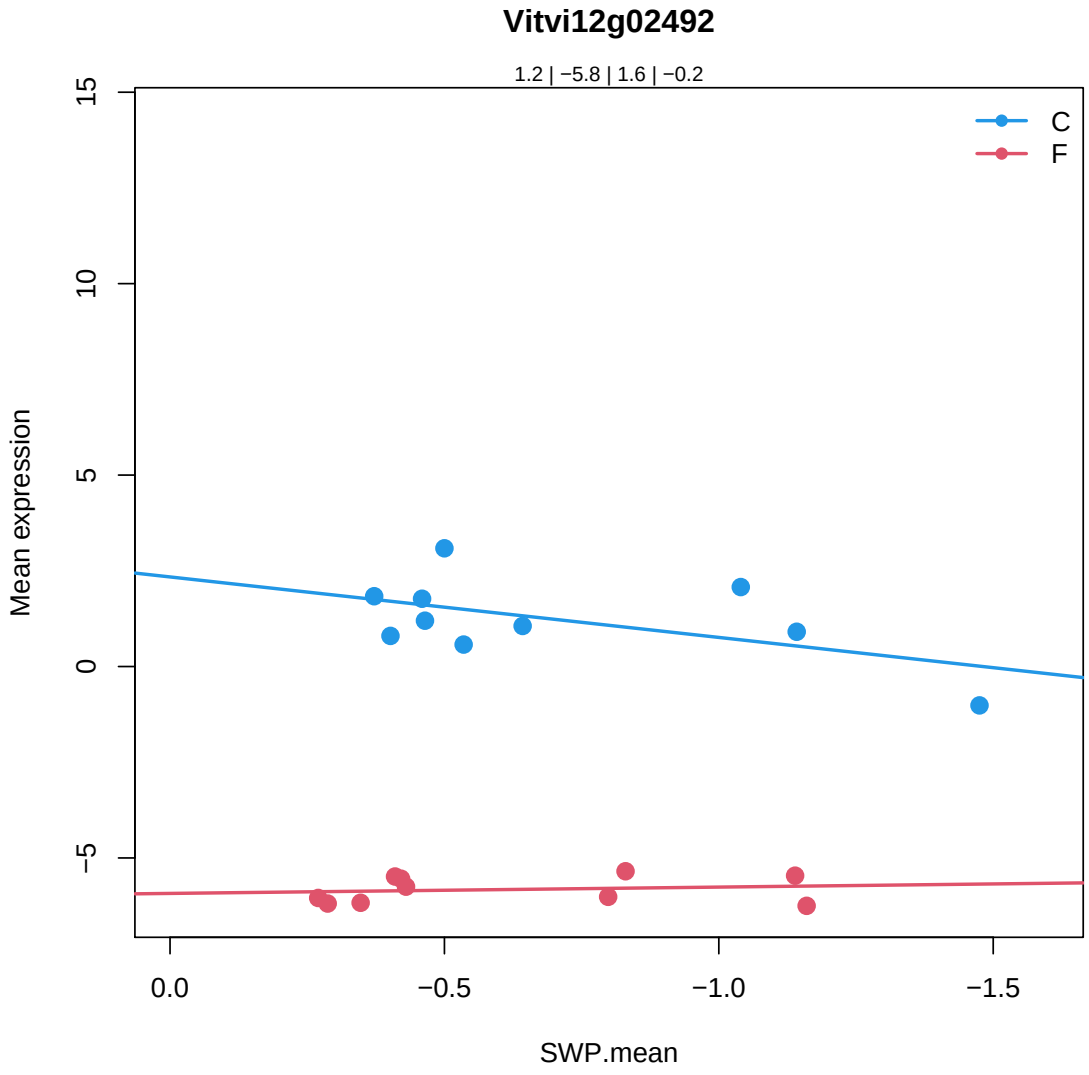
7.4.24 Vitvi12g02492: * type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02492
        30.2.12
        signalling.receptor kinases.leucine rich repeat XII
        receptor like protein 22 |
        Chr2:13853897-13855666 REVERSE LENGTH=589 |
        201606
```

Coefficients for Vitvi12g02492.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.228831	9.368109e-06	***	1.058714e-05	***
SlopeC	1.579994	0.01438592	*	0.3359386	
MeanF-MeanC	-7.054787	9.455527e-17	***	1.736399e-14	***
SlopeF-SlopeC	-1.745248	0.06109156	.	0.9999488	



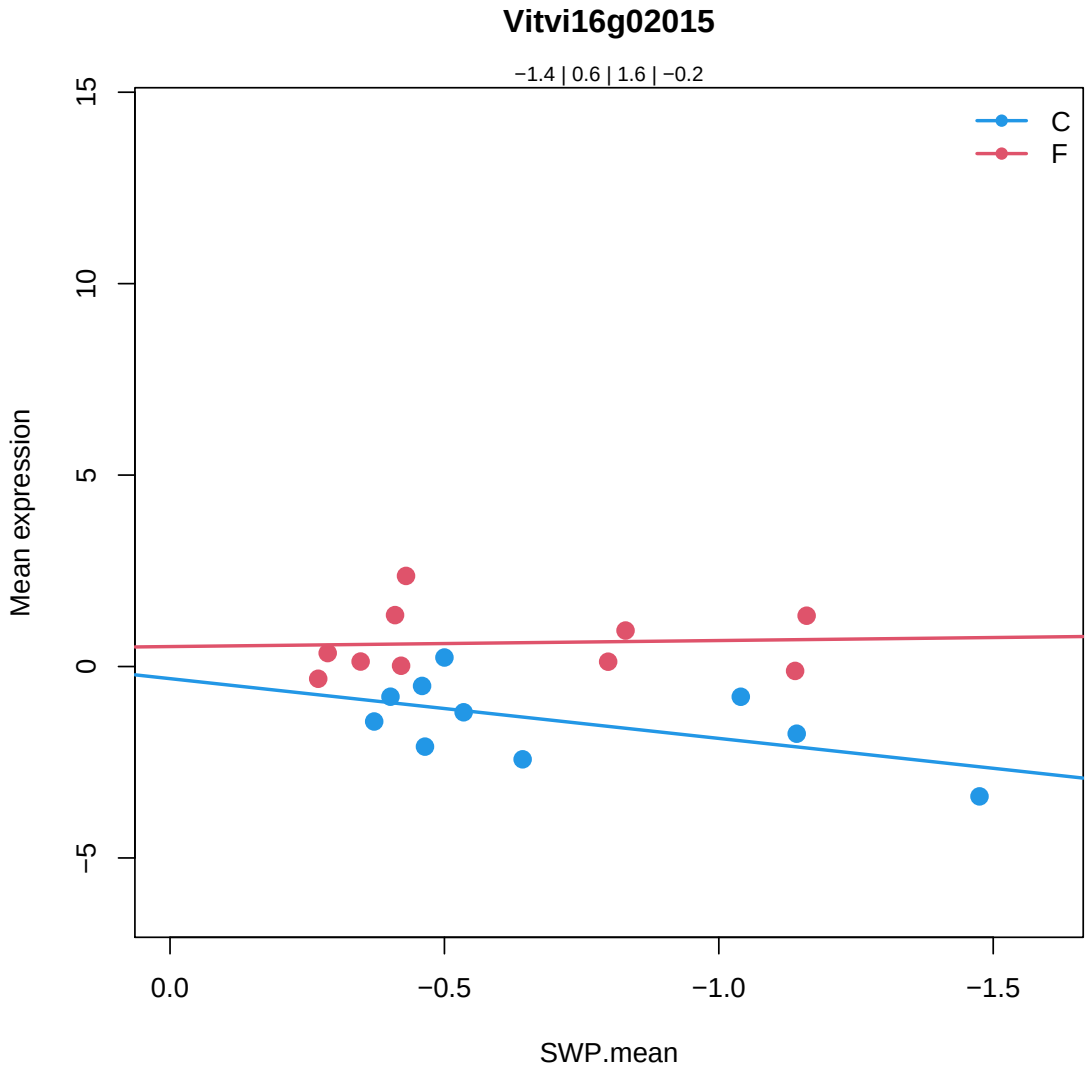
7.4.25 Vitvi16g02015: * type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g02015
        35.2
        not assigned.unknown
        PR5-like receptor kinase |
        Chr5:15293325-15295838 REVERSE LENGTH=665 |
        201606
```

Coefficients for Vitvi16g02015.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.41461	2.01347e-05	***	2.257729e-05	***
SlopeC	1.561065	0.04258379	*	0.48214	
MeanF-MeanC	2.031392	1.653779e-05	***	0.0003908047	***
SlopeF-SlopeC	-1.71816	0.1254976		0.9999488	



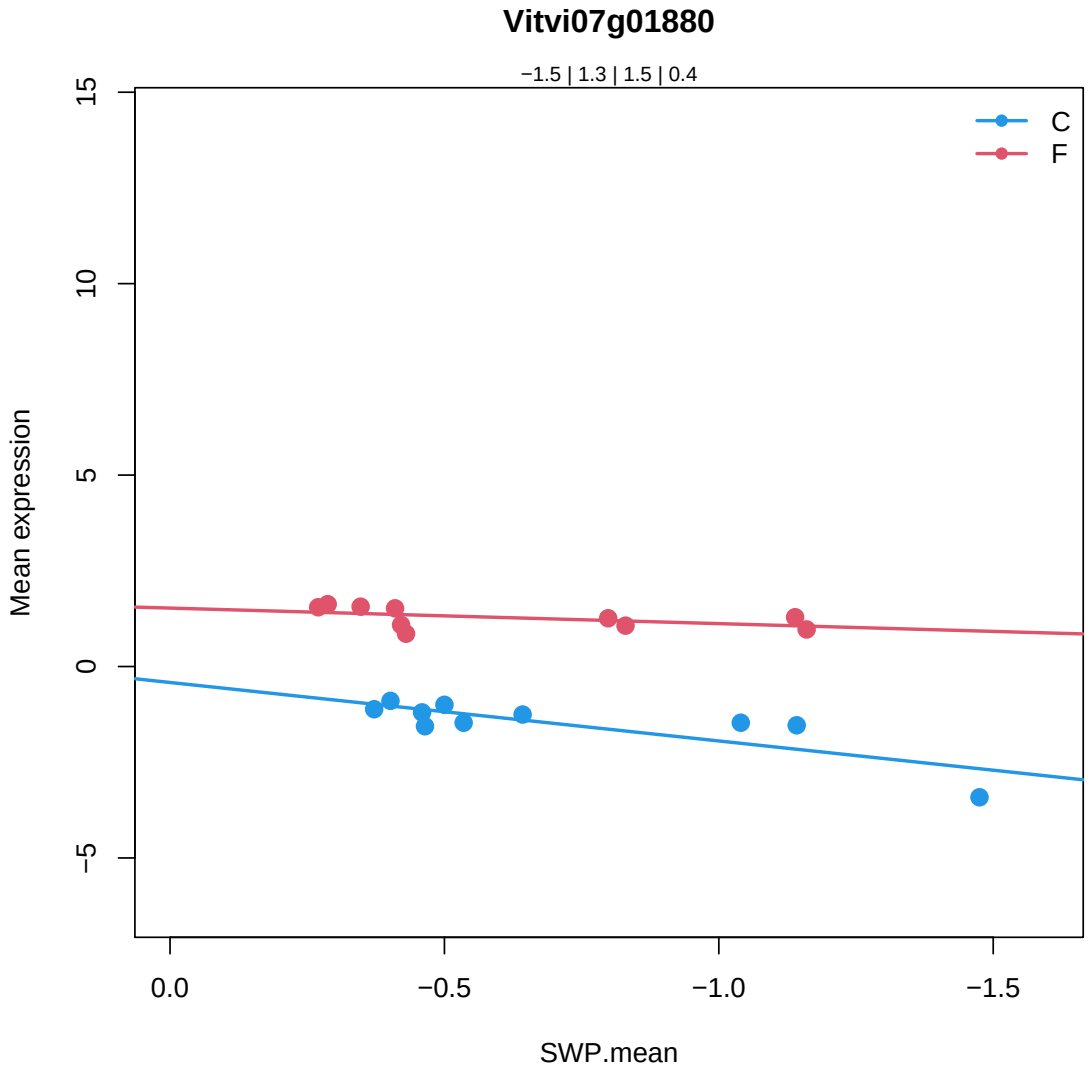
7.4.26 Vitvi07g01880: * type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01880
        29.2.1.2.2.3
        protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L3
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi07g01880.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.491084	7.084737e-11	***	9.323568e-11	***
SlopeC	1.527266	0.0002627845	***	0.08298279	.
MeanF-MeanC	2.769697	3.688811e-13	***	3.627411e-11	***
SlopeF-SlopeC	-1.121594	0.04294883	*	0.9999488	



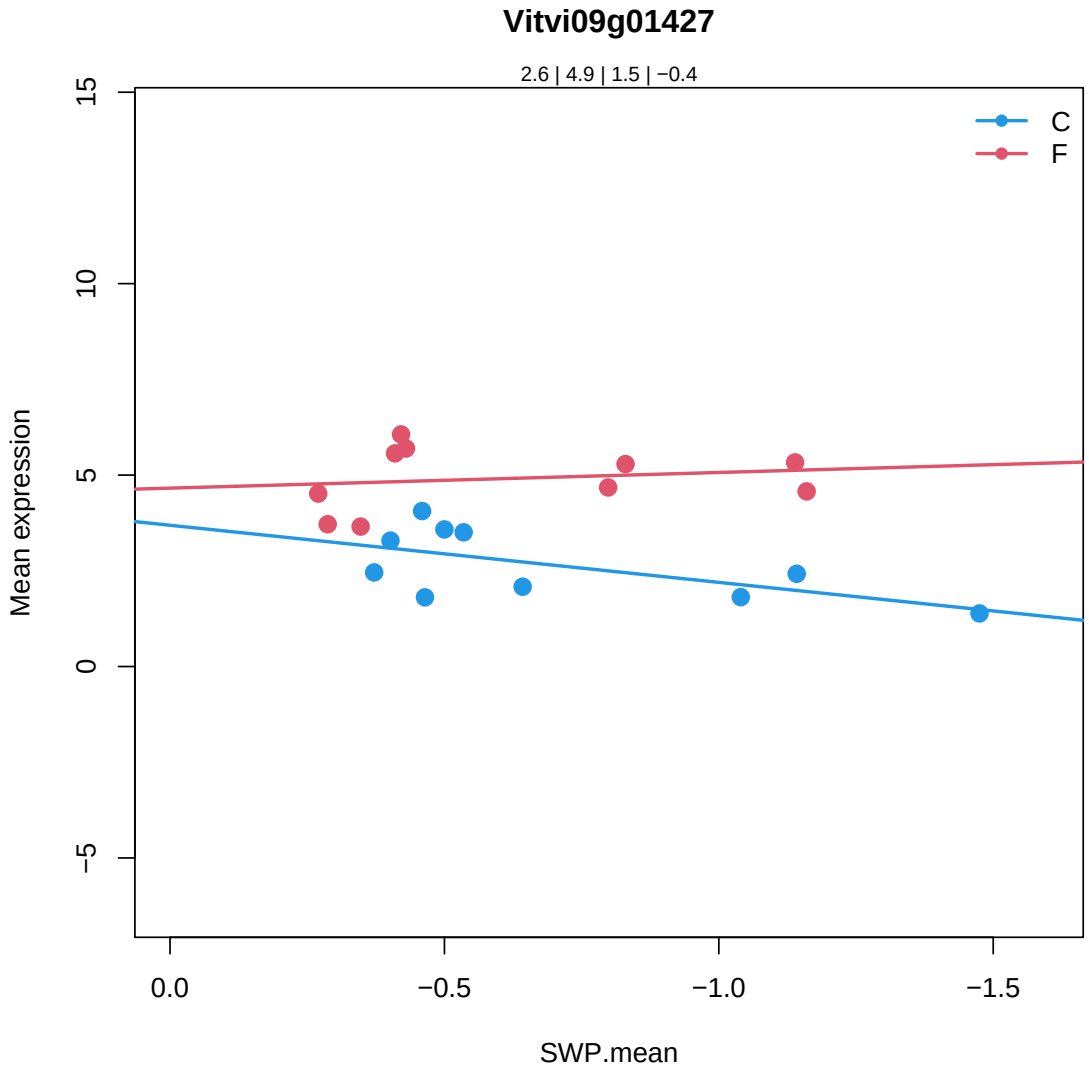
7.4.27 Vitvi09g01427: * type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g01427
        16.1.5
        secondary metabolism.isoprenoids.terpenoids
        lupeol synthase 2 |
        Chr1:29696722-29701024 FORWARD LENGTH=763 |
        201606
```

Coefficients for Vitvi09g01427.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.640377	1.670713e-10	***	2.168157e-10	***
SlopeC	1.49161	0.03178072	*	0.4343406	
MeanF-MeanC	2.267754	7.710756e-07	***	2.577354e-05	***
SlopeF-SlopeC	-1.90059	0.06232887	.	0.9999488	



7.4.28 Vitvi12g00615: * type3

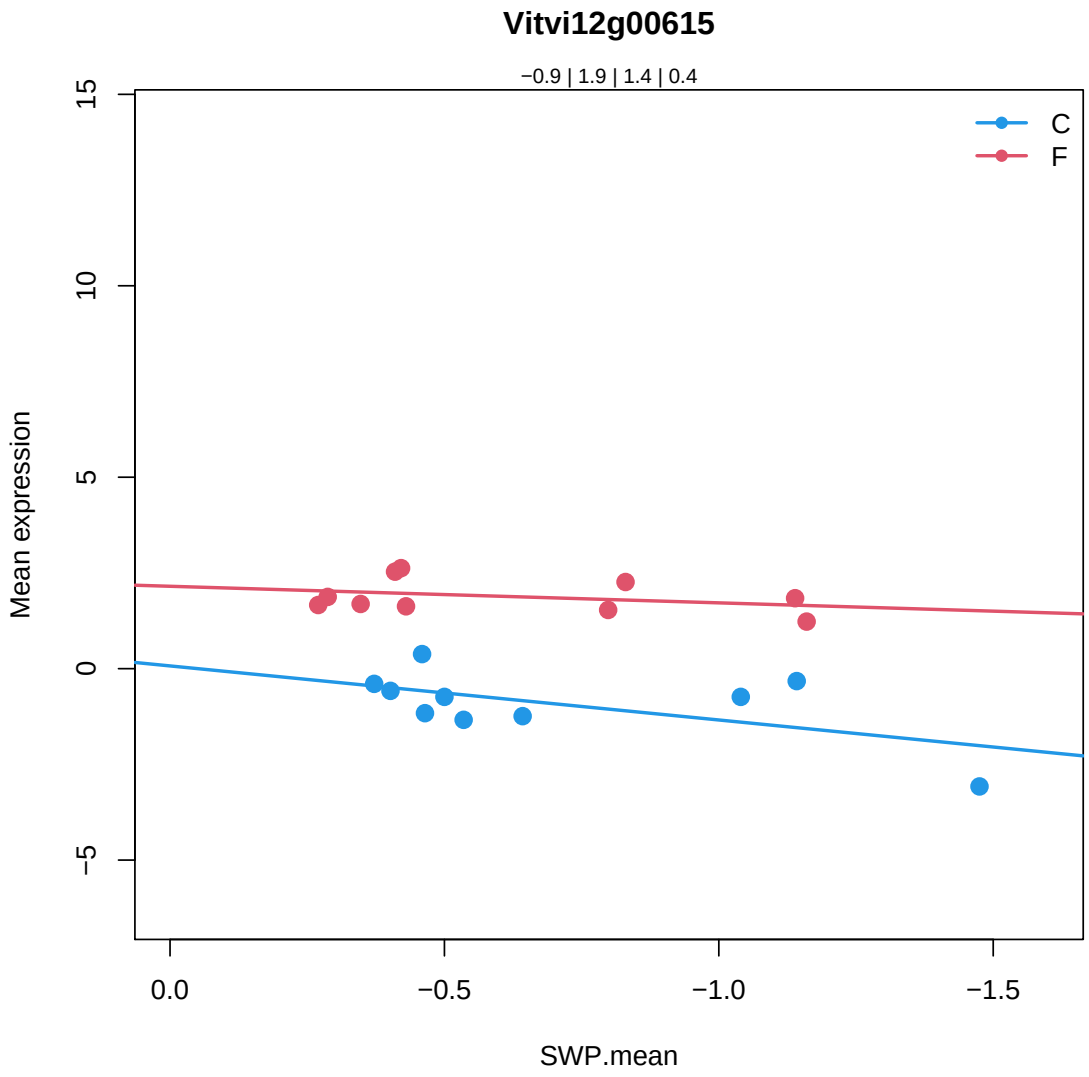
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00615
        29.4
        protein.postranslational modification
        G-type lectin S-receptor-like Serine/Threonine-kinase |
        Chr4:1419278-1422828 REVERSE LENGTH=1010 |
        201606

Vitvi12g00615
        30.2.24
        signalling.receptor kinases.S-locus glycoprotein like
        G-type lectin S-receptor-like Serine/Threonine-kinase |
        Chr4:1419278-1422828 REVERSE LENGTH=1010 |
        201606
```

Coefficients for Vitvi12g00615.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.9215172	8.711577e-05	***	9.630248e-05	***
SlopeC	1.411899	0.01468082	*	0.3359386	
MeanF-MeanC	2.808987	7.923962e-10	***	4.699495e-08	***
SlopeF-SlopeC	-0.9790786	0.2296063		0.9999488	


Vitvi12g00615
−0.9 | 1.9 | 1.4 | 0.4
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

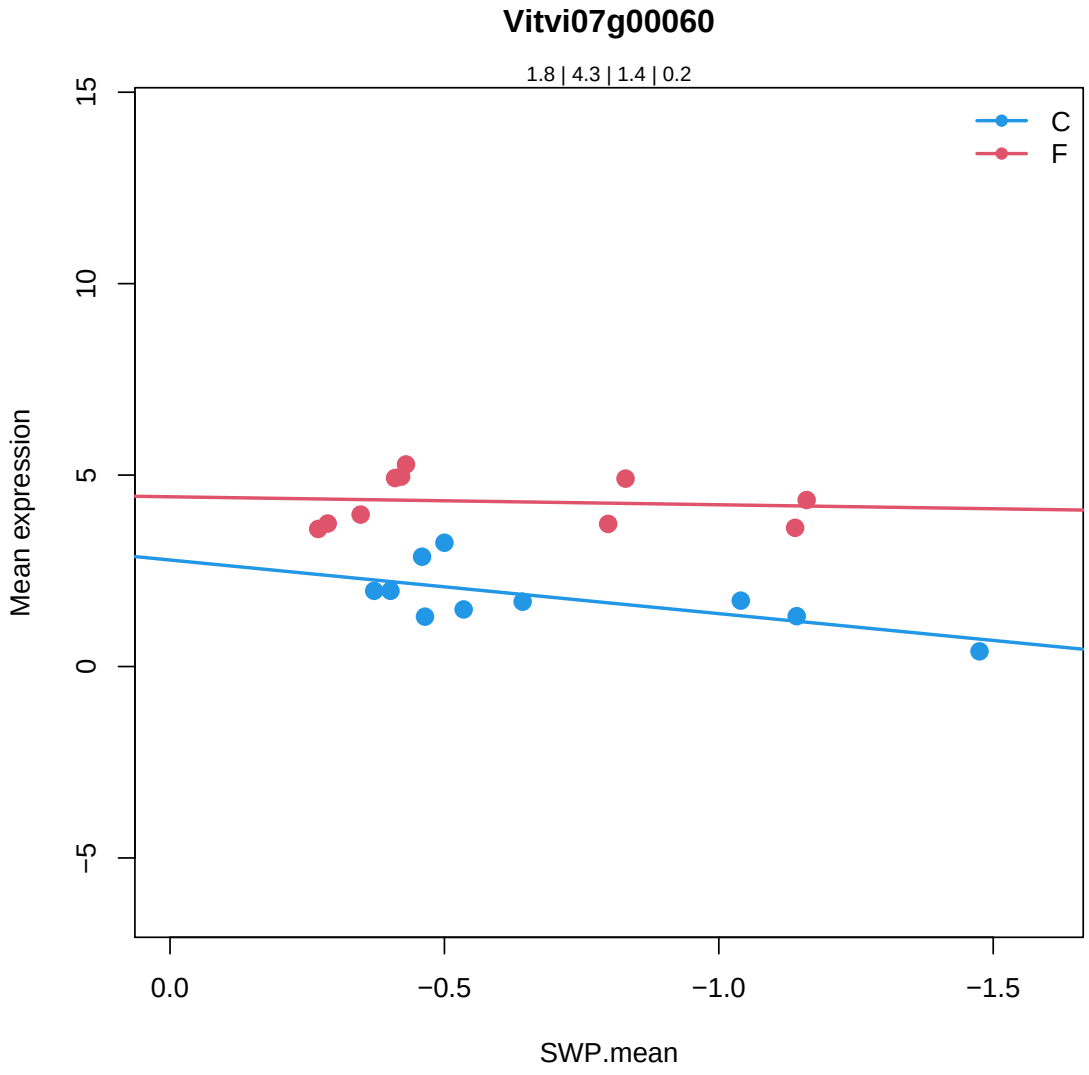
7.4.29 Vitvi07g00060: * type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g00060
        35.2
        not assigned.unknown
        Ubiquitin-conjugating enzyme/RWD-like protein |
        Chr2:16225777-16226772 FORWARD LENGTH=331 |
        201606
```

Coefficients for Vitvi07g00060.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.797056	8.679692e-09	***	1.061253e-08	***
SlopeC	1.400516	0.01885436	*	0.3679617	
MeanF-MeanC	2.508855	1.082839e-08	***	5.358644e-07	***
SlopeF-SlopeC	-1.192193	0.1607068		0.9999488	



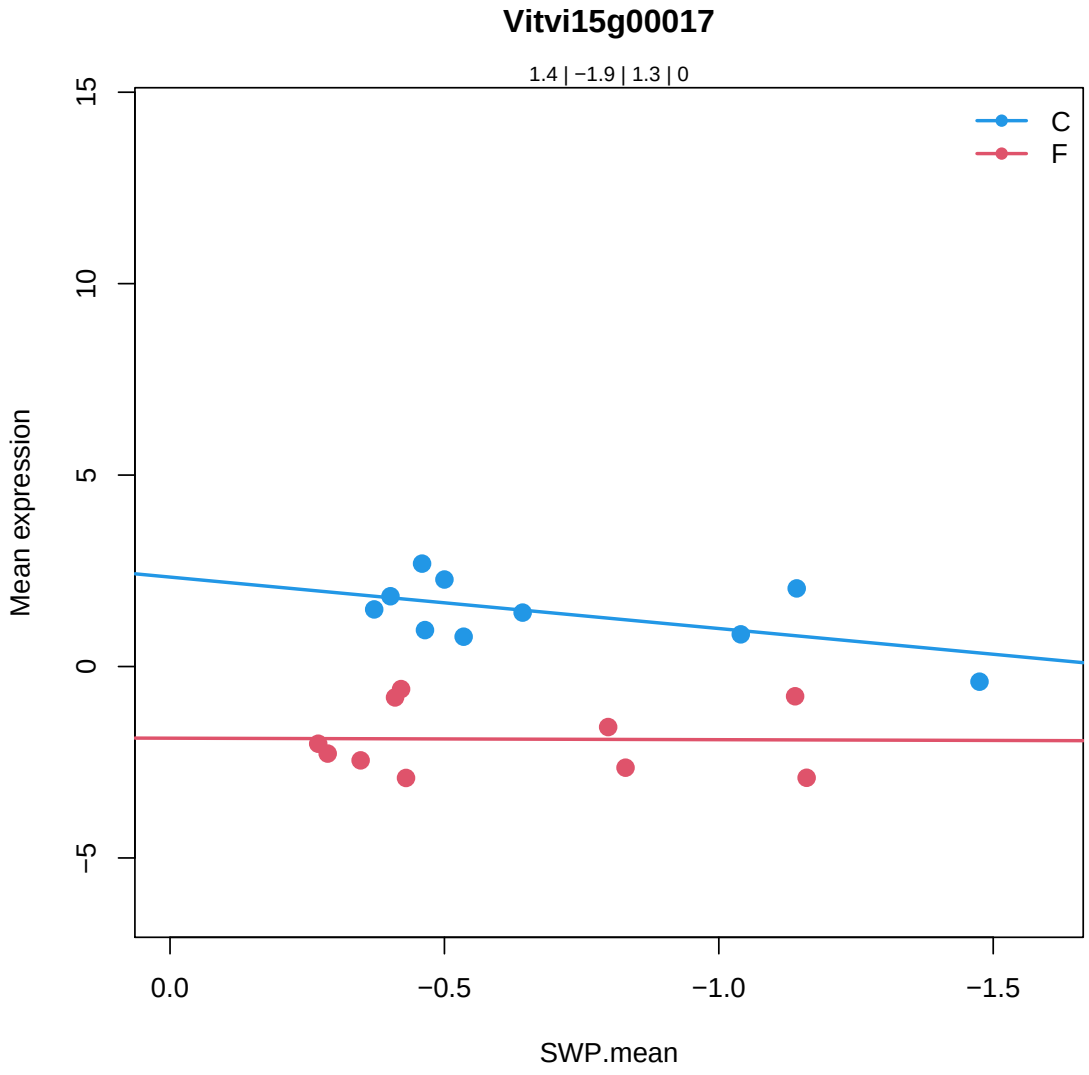
7.4.30 Vitvi15g00017: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g00017
        35.2
        not assigned.unknown
        NB-ARC domain-containing disease resistance protein |
        Chr3:4857940-4861104 FORWARD LENGTH=1054 |
        201606
```

Coefficients for Vitvi15g00017.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.390779	1.520535e-05	***	1.710027e-05	***
SlopeC	1.343637	0.06706753	.	0.5552652	
MeanF-MeanC	-3.286505	5.811022e-09	***	2.972201e-07	***
SlopeF-SlopeC	-1.304475	0.2218154		0.9999488	



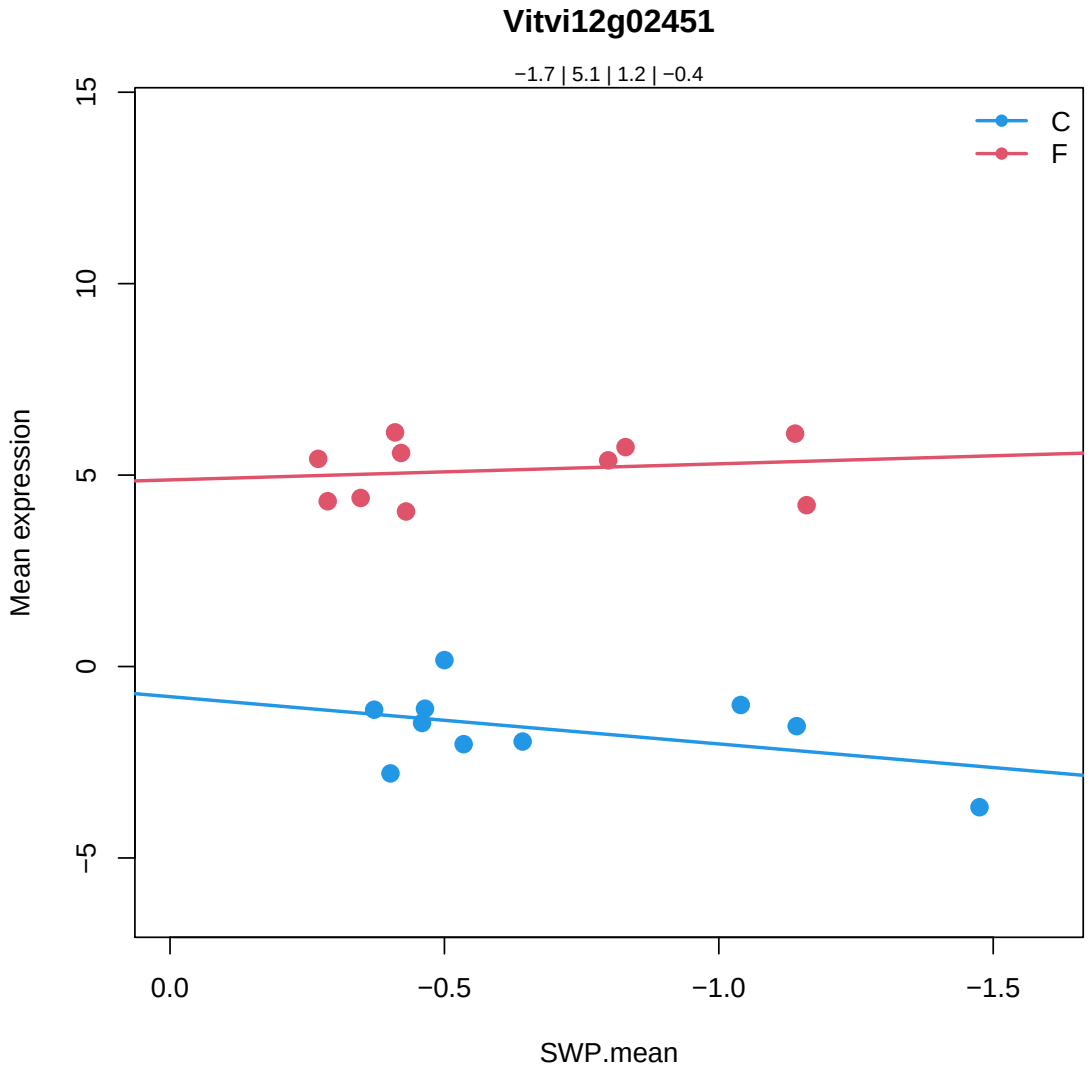
7.4.31 Vitvi12g02451: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02451
        16.8.1.21
        secondary metabolism.flavonoids.anthocyanins.anthocyanin 5-aromatic ac
        HXXXD-type acyl-transferase family protein |
        Chr1:1009542-1010951 REVERSE LENGTH=469 |
        201606
```

Coefficients for Vitvi12g02451.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.655451	2.884365e-06	***	3.294626e-06	***
SlopeC	1.234009	0.1071191		0.6223948	
MeanF-MeanC	6.785157	1.620031e-14	***	2.019201e-12	***
SlopeF-SlopeC	-1.654182	0.1444542		0.9999488	



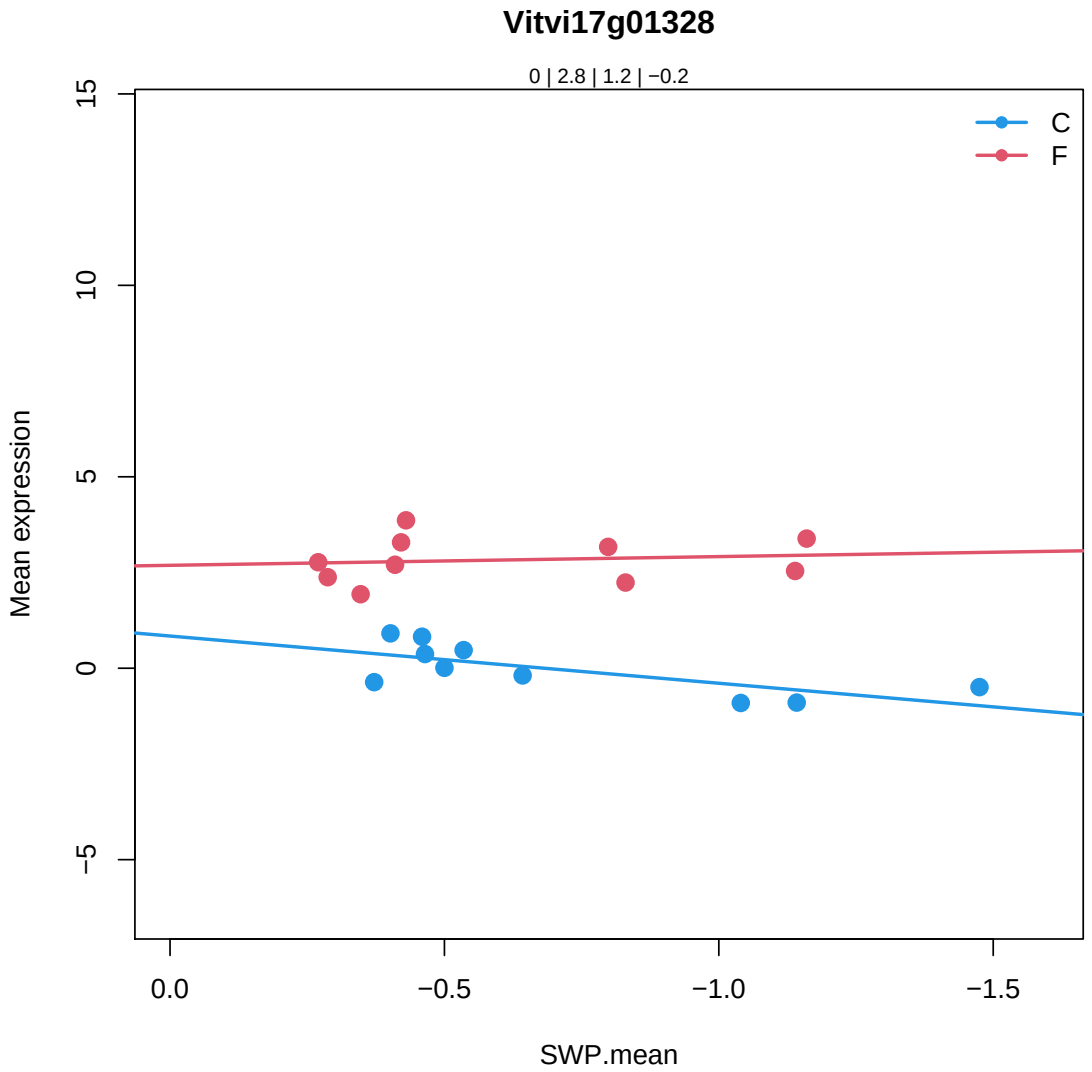
7.4.32 Vitvi17g01328: * type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g01328
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi17g01328.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.02650758	0.8790298		0.8816908	
SlopeC	1.233294	0.01745139	*	0.3551322	
MeanF-MeanC	2.852842	8.627588e-11	***	6.144939e-09	***
SlopeF-SlopeC	-1.460876	0.05279348	.	0.9999488	



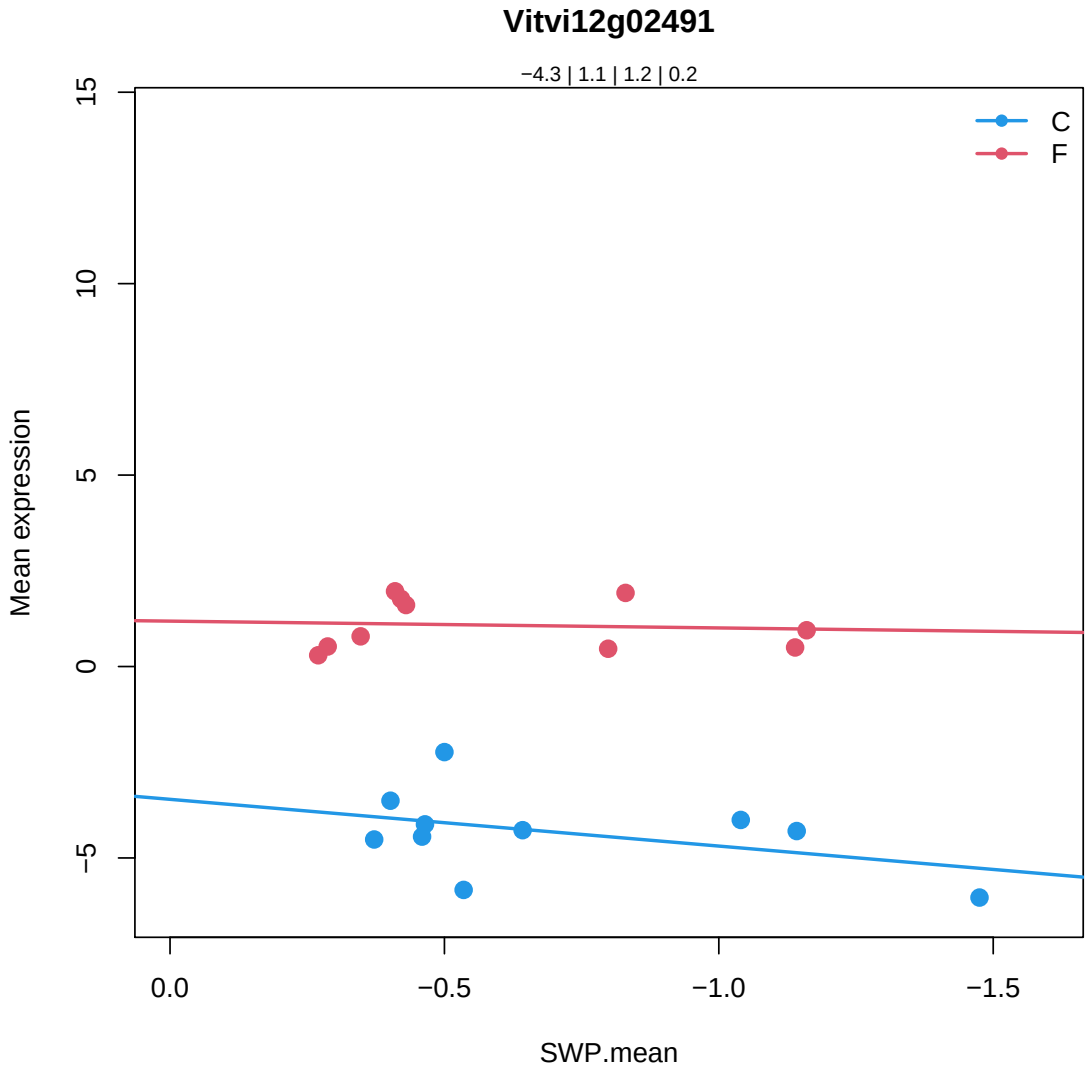
7.4.33 Vitvi12g02491: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02491
        30.2.12
        signalling.receptor kinases.leucine rich repeat XII
        receptor like protein 6 |
        Chr1:17183550-17186534 REVERSE LENGTH=994 |
        201606
```

Coefficients for Vitvi12g02491.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-4.327187	5.817118e-14	***	9.090067e-14	***
SlopeC	1.220752	0.09780238	.	0.6084506	
MeanF-MeanC	5.404248	6.868441e-13	***	6.374487e-11	***
SlopeF-SlopeC	-1.042901	0.331487		0.9999488	



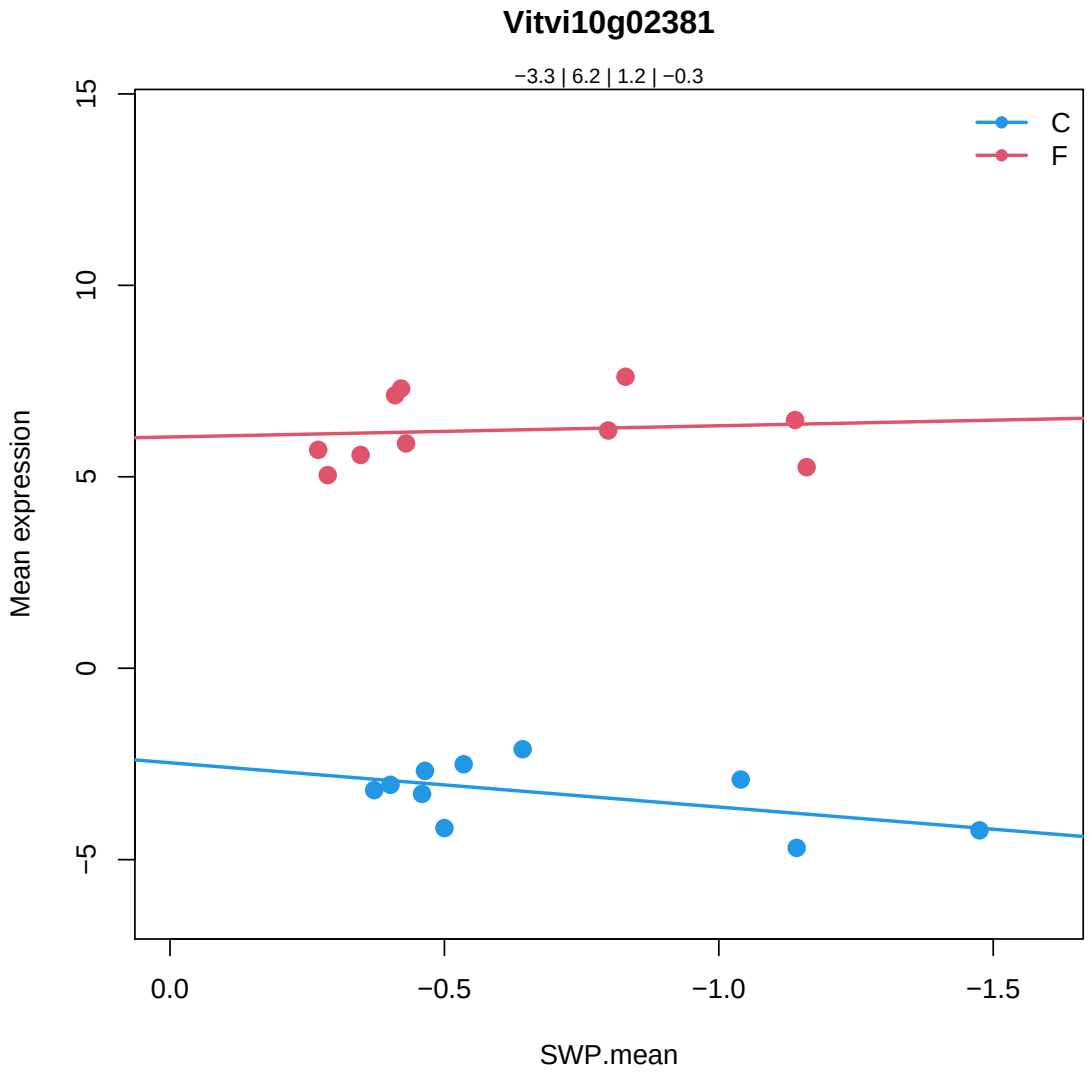
7.4.34 Vitvi10g02381: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g02381
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi10g02381.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-3.282562	6.75514e-12	***	9.297619e-12	***
SlopeC	1.156847	0.1039412		0.6157294	
MeanF-MeanC	9.500513	3.451249e-18	***	8.219364e-16	***
SlopeF-SlopeC	-1.44987	0.1671388		0.9999488	



7.4.35 Vitvi10g02155: * type3

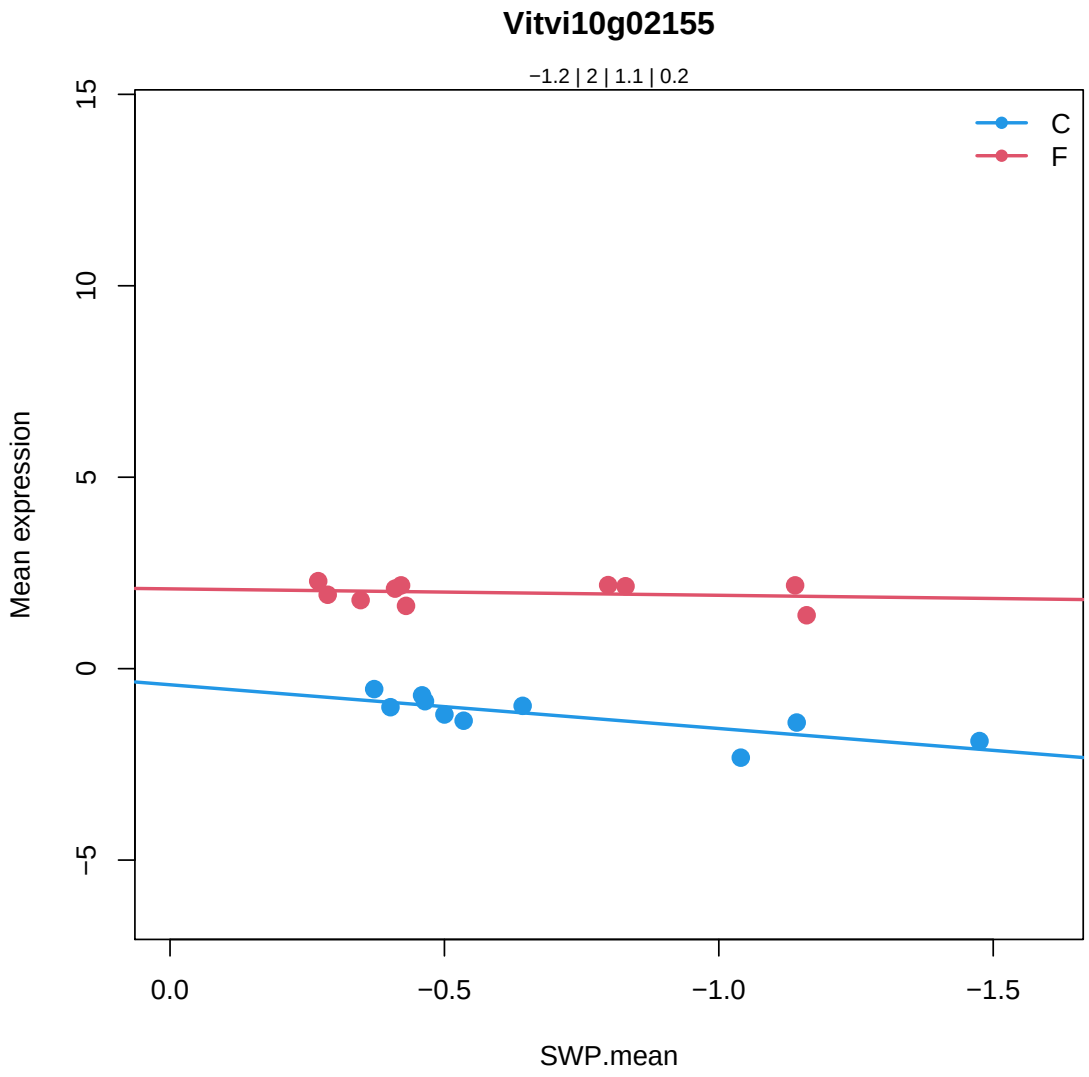
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g02155
        29.4
        protein.postranslational modification
        S-locus lectin protein kinase family protein |
        Chr1:3841286-3844284 FORWARD LENGTH=845 |
        201606

Vitvi10g02155
        30.2.24
        signalling.receptor kinases.S-locus glycoprotein like
        S-locus lectin protein kinase family protein |
        Chr1:3841286-3844284 FORWARD LENGTH=845 |
        201606
```

Coefficients for Vitvi10g02155.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.224278	9.970009e-10	***	1.256826e-09	***
SlopeC	1.142074	0.002407175	**	0.1862445	
MeanF-MeanC	3.205734	6.790304e-15	***	8.771001e-13	***
SlopeF-SlopeC	-0.9741702	0.0617809	.	0.9999488	


Vitvi10g02155
−1.2 | 2 | 1.1 | 0.2
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

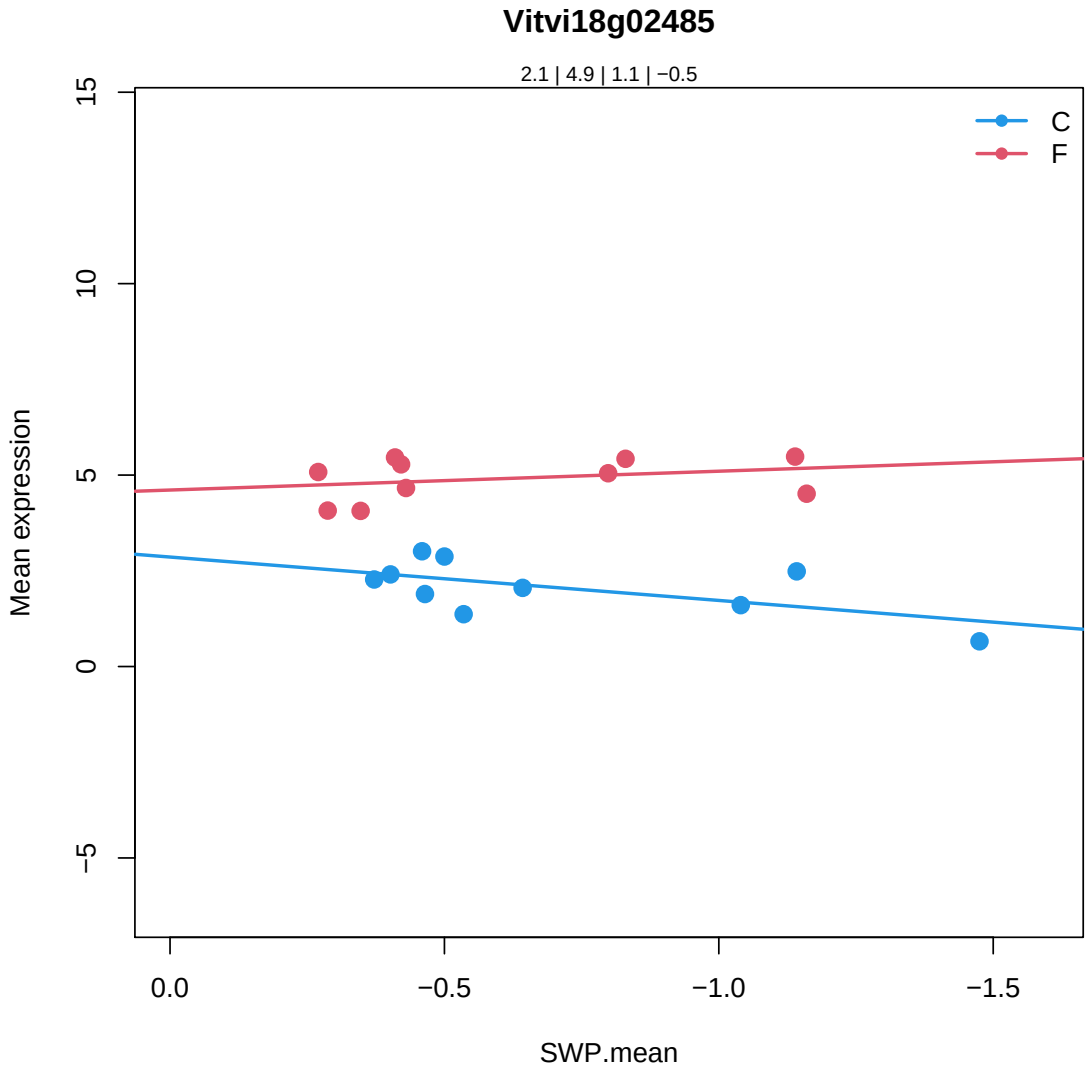
7.4.36 Vitvi18g02485: * type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02485
        17.7.1.5
        hormone metabolism.jasmonate.synthesis-degradation.12-oxophytodienoate
        12-oxophytodienoate reductase 2 |
        Chr1:28778976-28780355 FORWARD LENGTH=374 |
        201606
```

Coefficients for Vitvi18g02485.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.062013	9.401842e-11	***	1.231548e-10	***
SlopeC	1.13339	0.0312388	*	0.4322019	
MeanF-MeanC	2.84682	1.470283e-10	***	9.915952e-09	***
SlopeF-SlopeC	-1.625173	0.03726078	*	0.9999488	



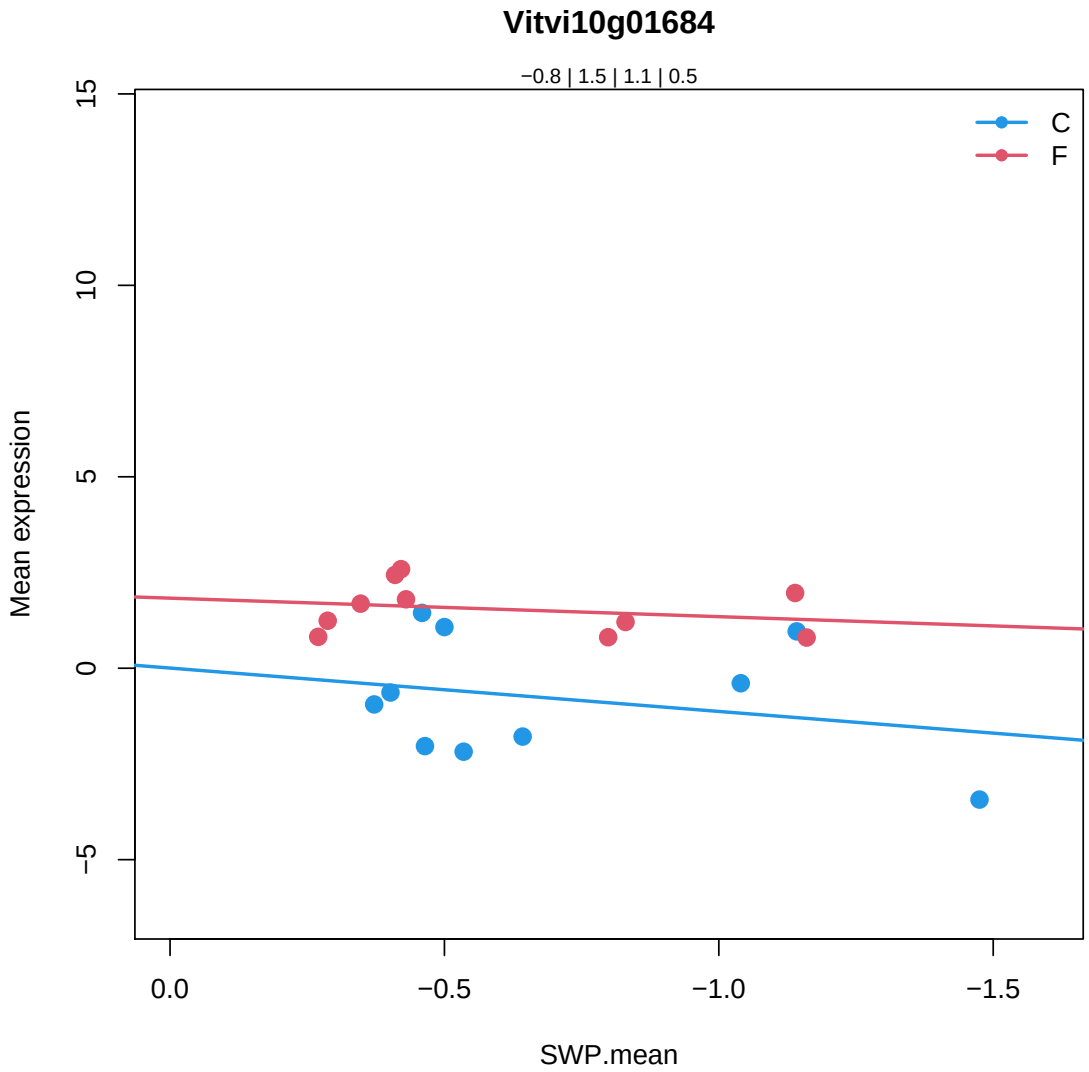
7.4.37 Vitvi10g01684: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g01684
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi10g01684.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	−0.7921471	0.03504116	*	0.03661964	*
SlopeC	1.132955	0.2600657		0.7683507	
MeanF−MeanC	2.327525	0.0001231869	***	0.002155701	**
SlopeF−SlopeC	−0.6497282	0.6602557		0.9999488	



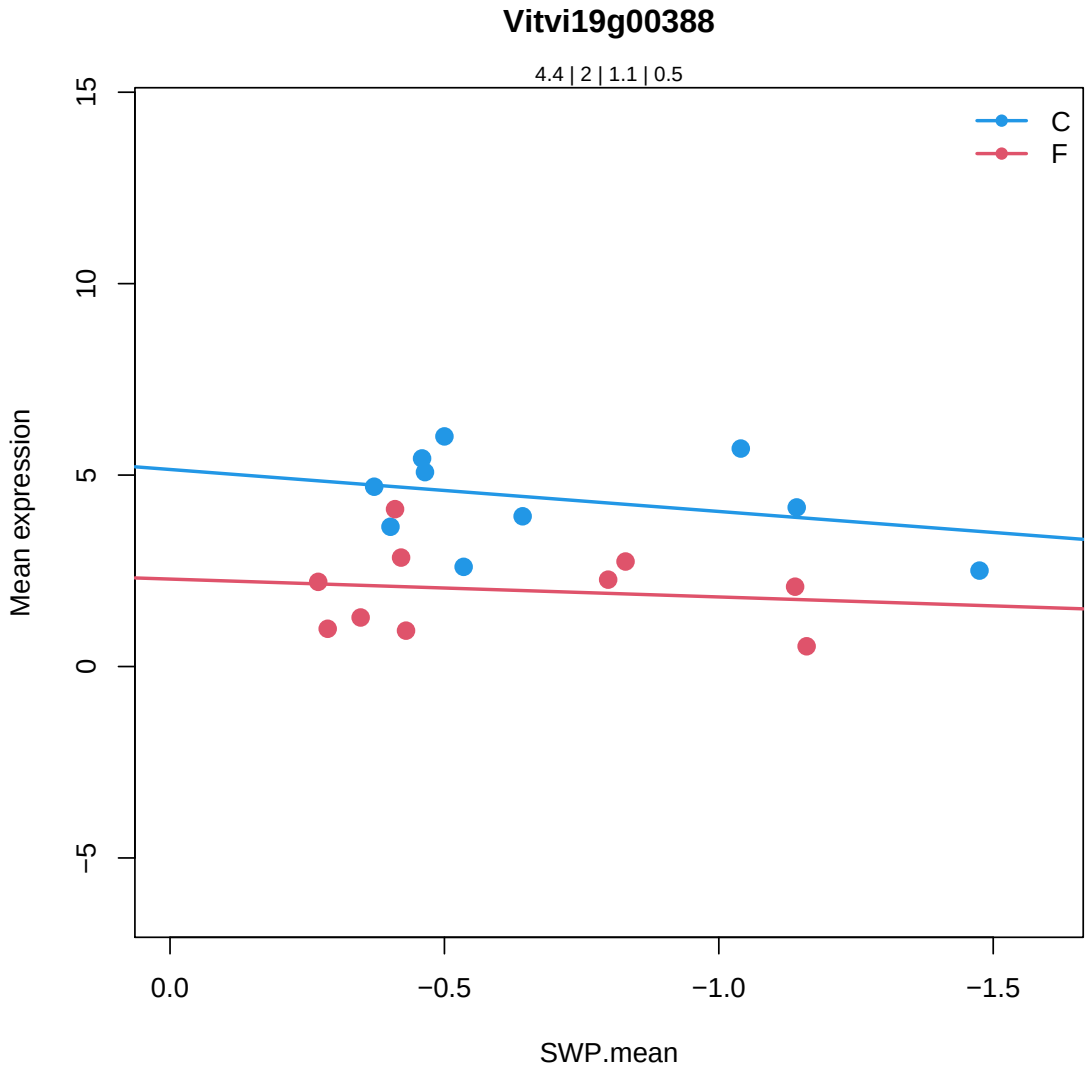
7.4.38 Vitvi19g00388: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g00388
        16.1.5
        secondary metabolism.isoprenoids.terpenoids
        terpene synthase 21 |
        Chr5:8092969-8095128 FORWARD LENGTH=545 |
        201606
```

Coefficients for Vitvi19g00388.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.374877	9.839223e-12	***	1.343331e-11	***
SlopeC	1.096454	0.2492748		0.760332	
MeanF-MeanC	-2.375559	5.049045e-05	***	0.000991721	***
SlopeF-SlopeC	-0.6295435	0.6523777		0.9999488	



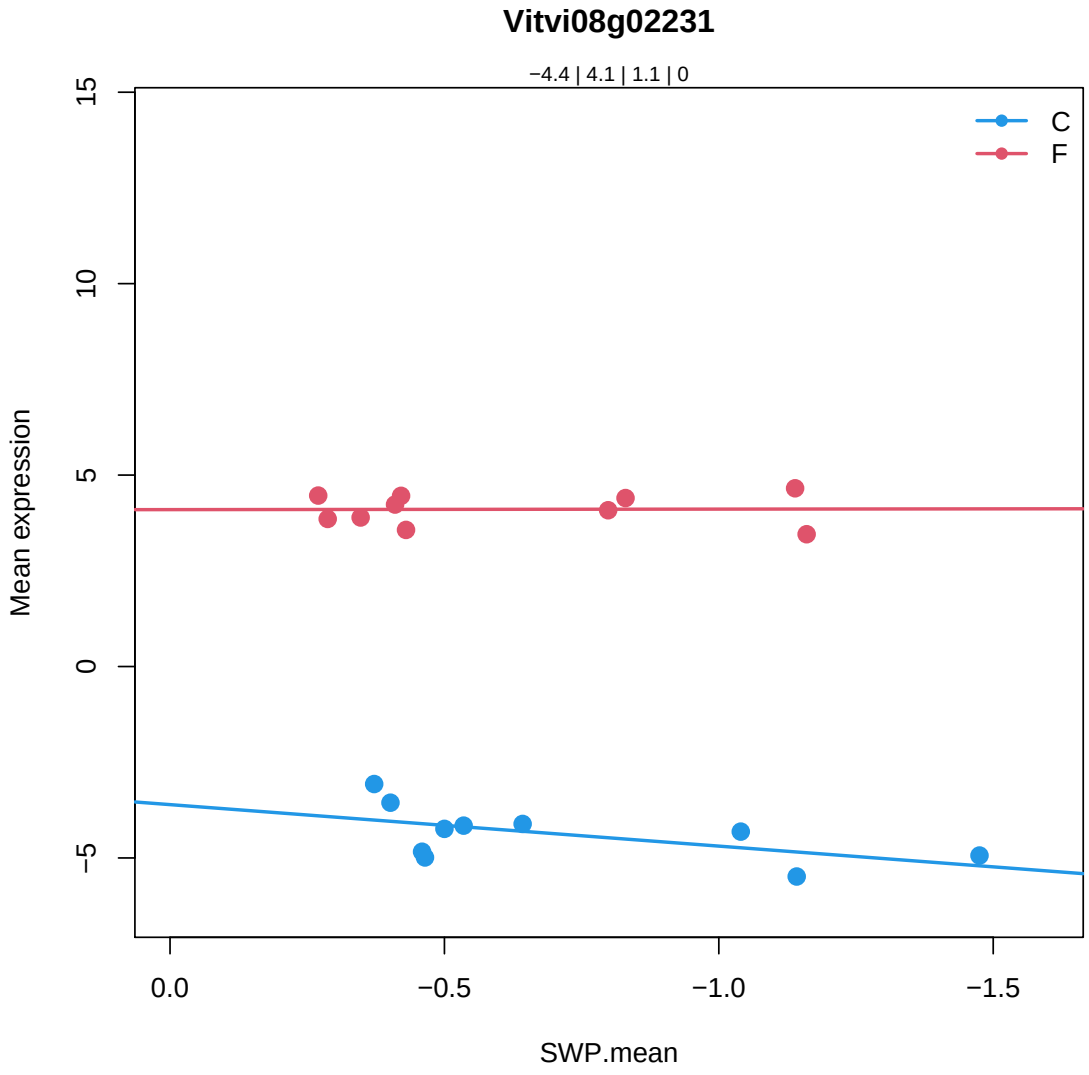
7.4.39 Vitvi08g02231: * type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g02231
        1.3.7
        PS.calvin cycle.FBPase
        high cyclic electron flow 1 |
        Chr3:20016951-2018527 FORWARD LENGTH=417 |
        201606
```

Coefficients for Vitvi08g02231.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-4.369236	8.352797e-18	***	2.245781e-17	***
SlopeC	1.083398	0.02879223	*	0.4275443	
MeanF-MeanC	8.475029	1.103454e-20	***	5.425435e-18	***
SlopeF-SlopeC	-1.096231	0.1257159		0.9999488	



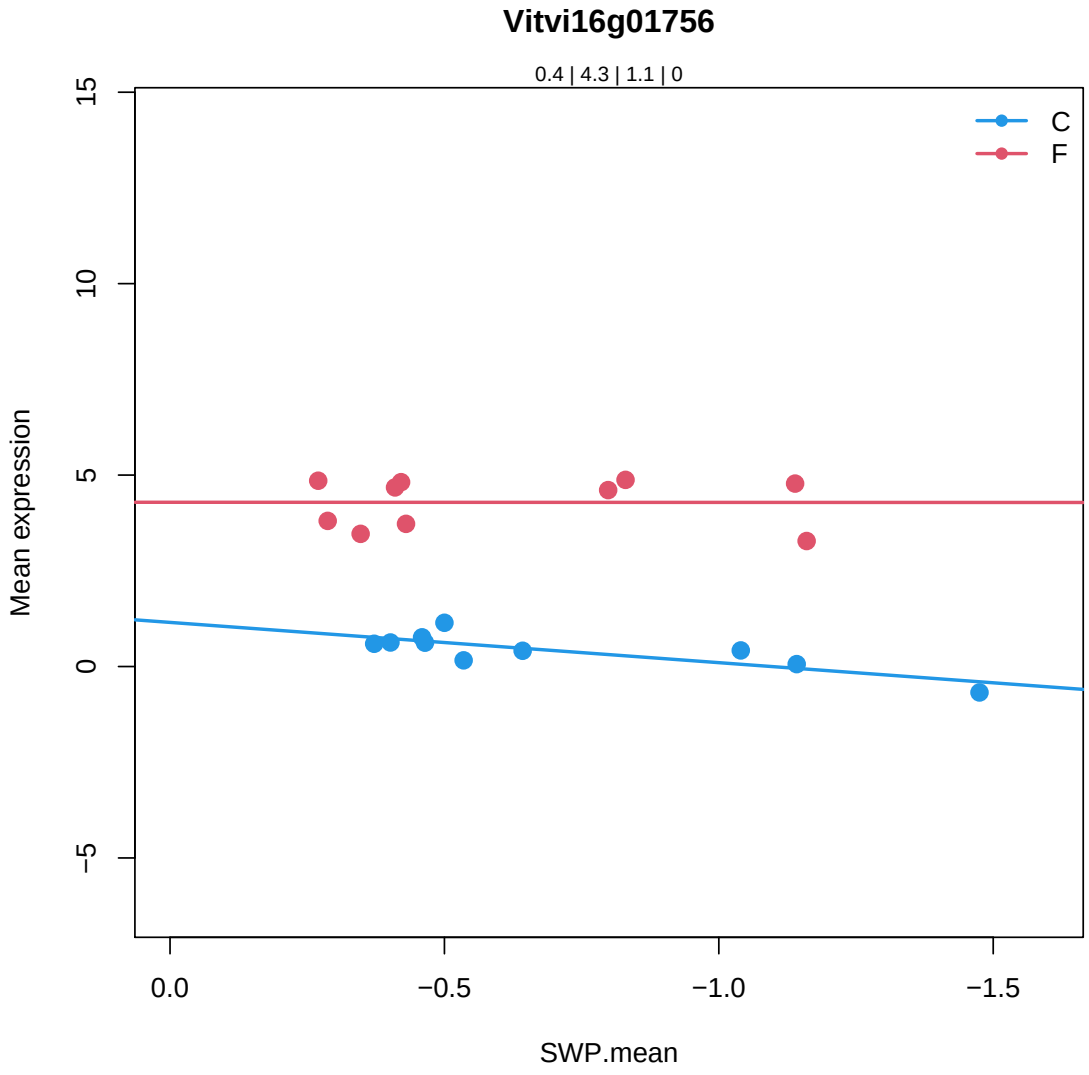
7.4.40 Vitvi16g01756: * type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01756
        20.1.2.1
        stress.biotic.receptors.CC-NBS-LRR
        NB-ARC domain-containing disease resistance protein |
        Chr3:4857940-4861104 FORWARD LENGTH=1054 |
        201606
```

Coefficients for Vitvi16g01756.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4126079	0.01939715	*	0.0203996	*
SlopeC	1.051572	0.03057608	*	0.4321285	
MeanF-MeanC	3.875102	8.16547e-14	***	8.703363e-12	***
SlopeF-SlopeC	-1.048555	0.1355052		0.9999488	



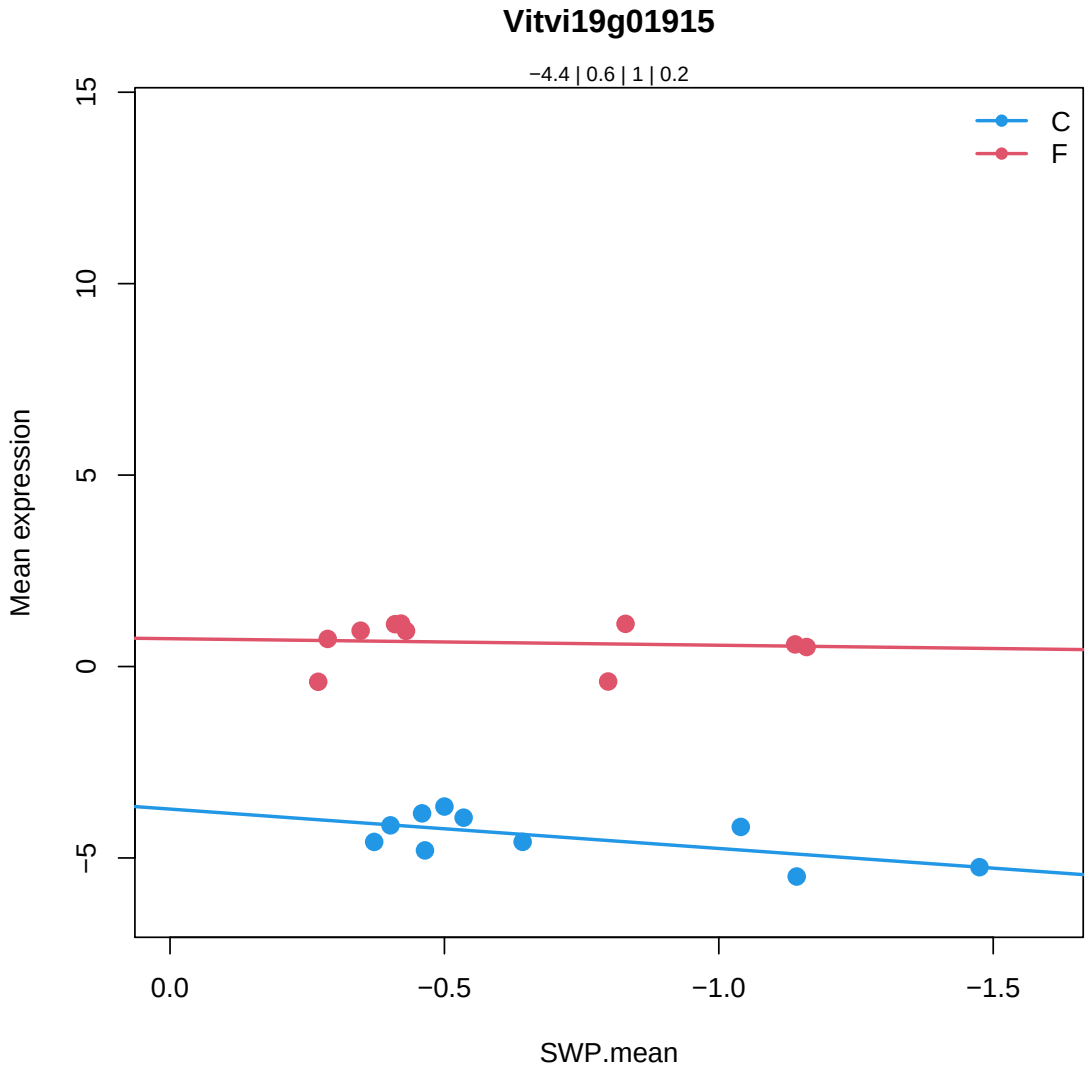
7.4.41 Vitvi19g01915: * type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g01915
        35.2
        not assigned.unknown
        transmembrane protein%2C putative (DUF594) |
        Chr5:18426296-18428929 REVERSE LENGTH=877 |
        201606
```

Coefficients for Vitvi19g01915.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-4.447013	9.287273e-18	***	2.467003e-17	***
SlopeC	1.028429	0.04097007	*	0.477587	
MeanF-MeanC	5.069224	8.005183e-16	***	1.193587e-13	***
SlopeF-SlopeC	-0.8577339	0.2362057		0.9999488	



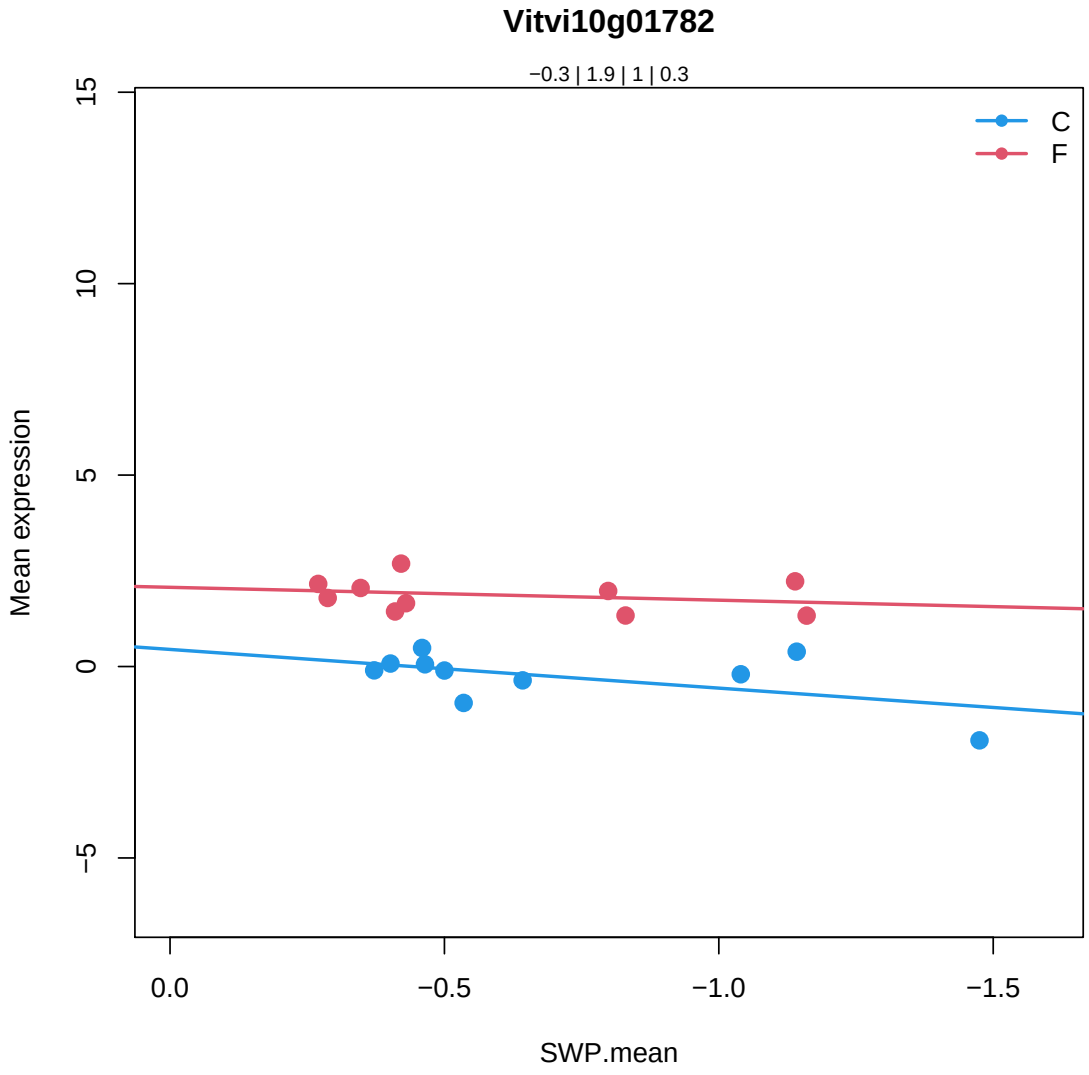
7.4.42 Vitvi10g01782: * type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g01782
        30.1.1
        signalling.in sugar and nutrient physiology.misc
        glutamate receptor 2.9 |
        Chr2:12501092-12504912 REVERSE LENGTH=940 |
        201606
```

Coefficients for Vitvi10g01782.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.2642536	0.1325344		0.1366495	
SlopeC	1.01045	0.0431868	*	0.48214	
MeanF-MeanC	2.127978	1.189535e-08	***	5.848673e-07	***
SlopeF-SlopeC	-0.6742042	0.3460658		0.9999488	



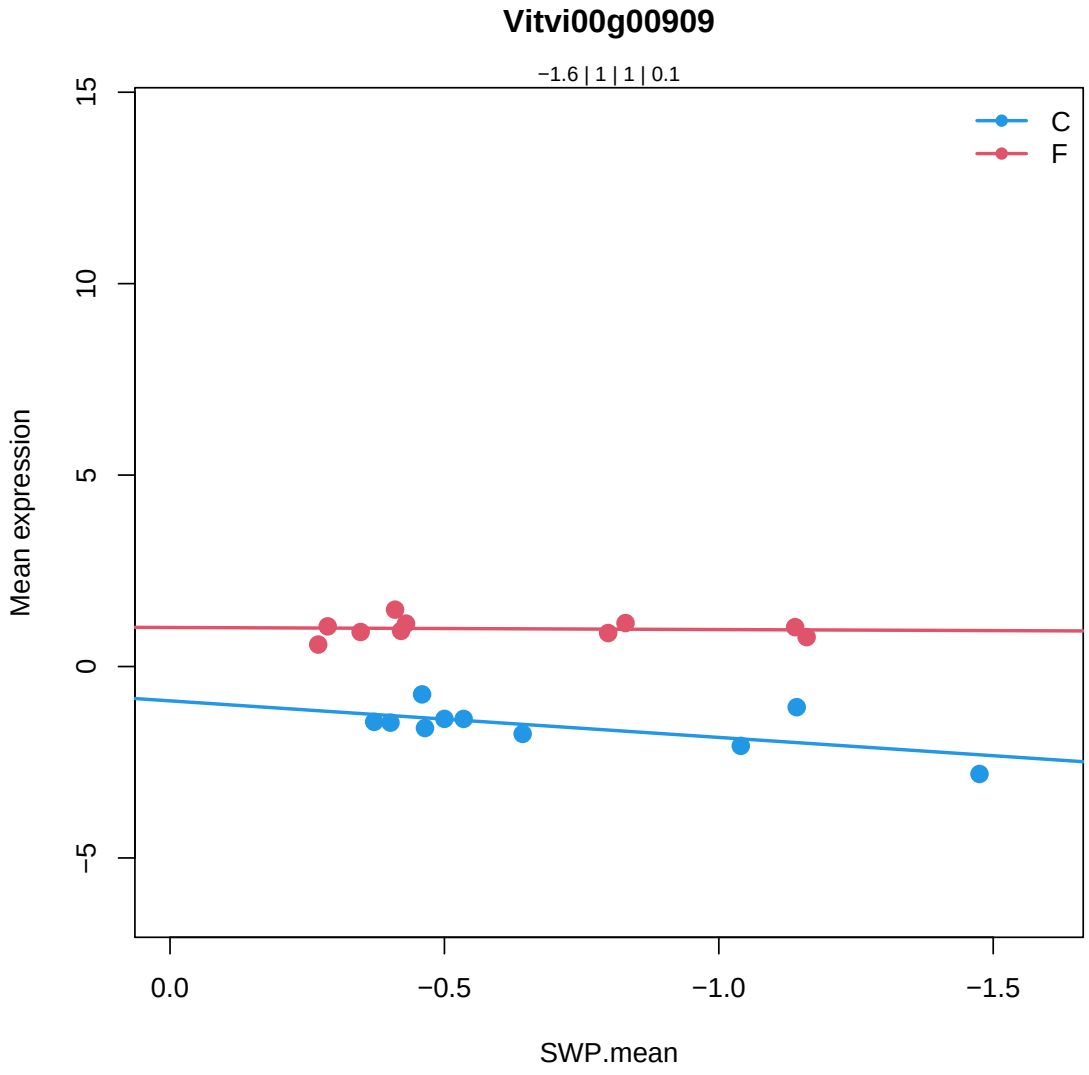
7.4.43 Vitvi00g00909: * type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi00g00909
        35.2
        not assigned.unknown
        S-domain-1 13 |
        Chr1:3817725-3820752 REVERSE LENGTH=830 |
        201606
```

Coefficients for Vitvi00g00909.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.568455	4.214786e-11	***	5.598412e-11	***
SlopeC	0.9551037	0.0143183	*	0.3359386	
MeanF-MeanC	2.554812	2.816519e-12	***	2.398289e-10	***
SlopeF-SlopeC	-0.9007427	0.1057256		0.9999488	



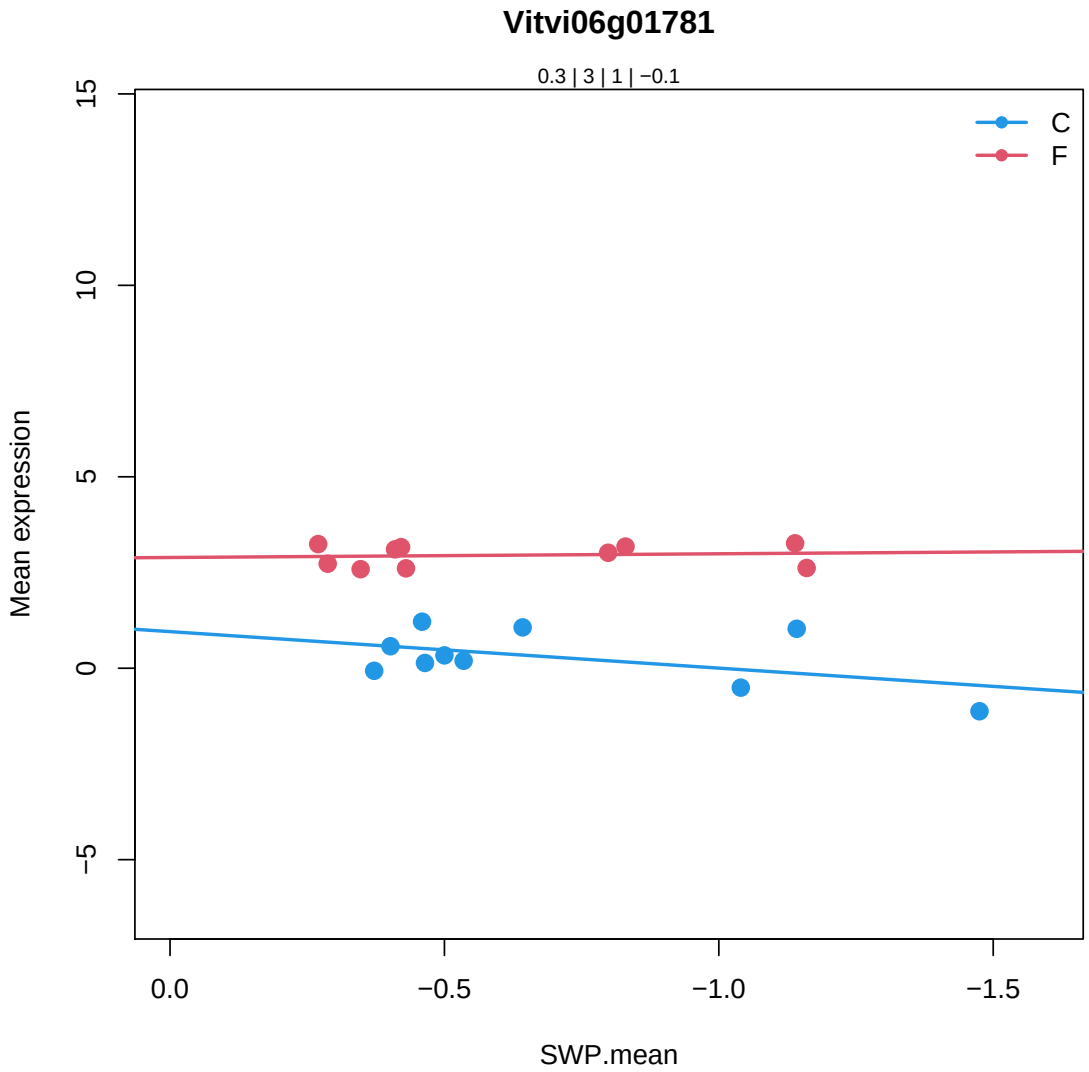
7.4.44 Vitvi06g01781: * type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01781
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi06g01781.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.2854014	0.09493677	.	0.09822334	.
SlopeC	0.9534047	0.04794865	*	0.5005708	
MeanF-MeanC	2.665455	1.158902e-10	***	7.956748e-09	***
SlopeF-SlopeC	-1.049892	0.1352856		0.9999488	



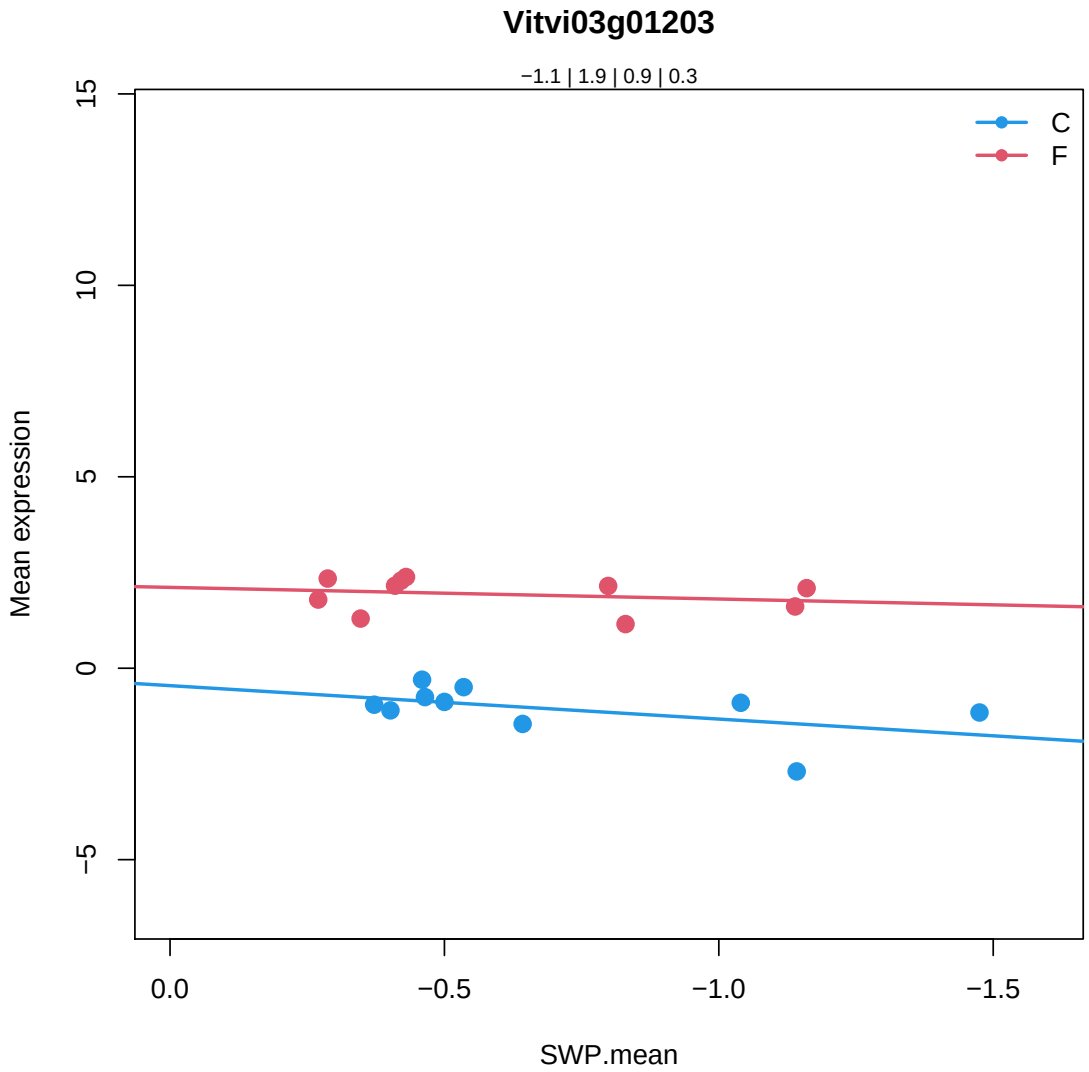
7.4.45 Vitvi03g01203: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g01203
        20.1.7
        stress.biotic.PR-proteins
        NA
```

Coefficients for Vitvi03g01203.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.069156	1.912096e-06	***	2.193104e-06	***
SlopeC	0.8730637	0.07152071	.	0.5630621	
MeanF-MeanC	2.995445	1.645966e-11	***	1.286555e-09	***
SlopeF-SlopeC	-0.5689925	0.4155755		0.9999488	



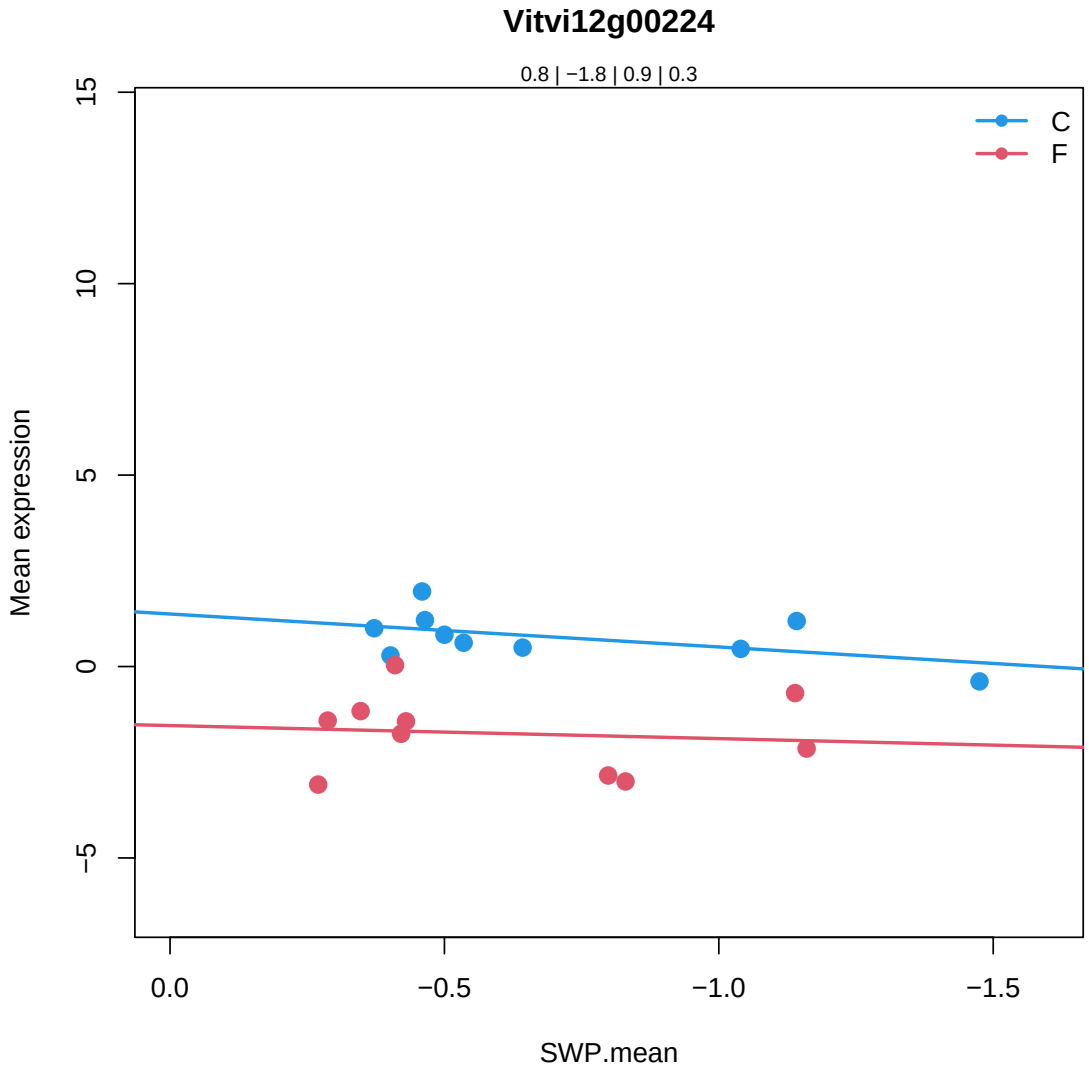
7.4.46 Vitvi12g00224: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00224
        30.3
        signalling.calcium
        sodium/calcium exchanger family protein / calcium-binding EF hand fami
        Chr1:19844790-19847533 FORWARD LENGTH=585 |
        201606
```

Coefficients for Vitvi12g00224.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.7663387	0.005773139	**	0.006147421	**
SlopeC	0.861183	0.2289851		0.7480049	
MeanF-MeanC	-2.516537	4.494446e-07	***	1.593124e-05	***
SlopeF-SlopeC	-0.5208545	0.6199535		0.9999488	



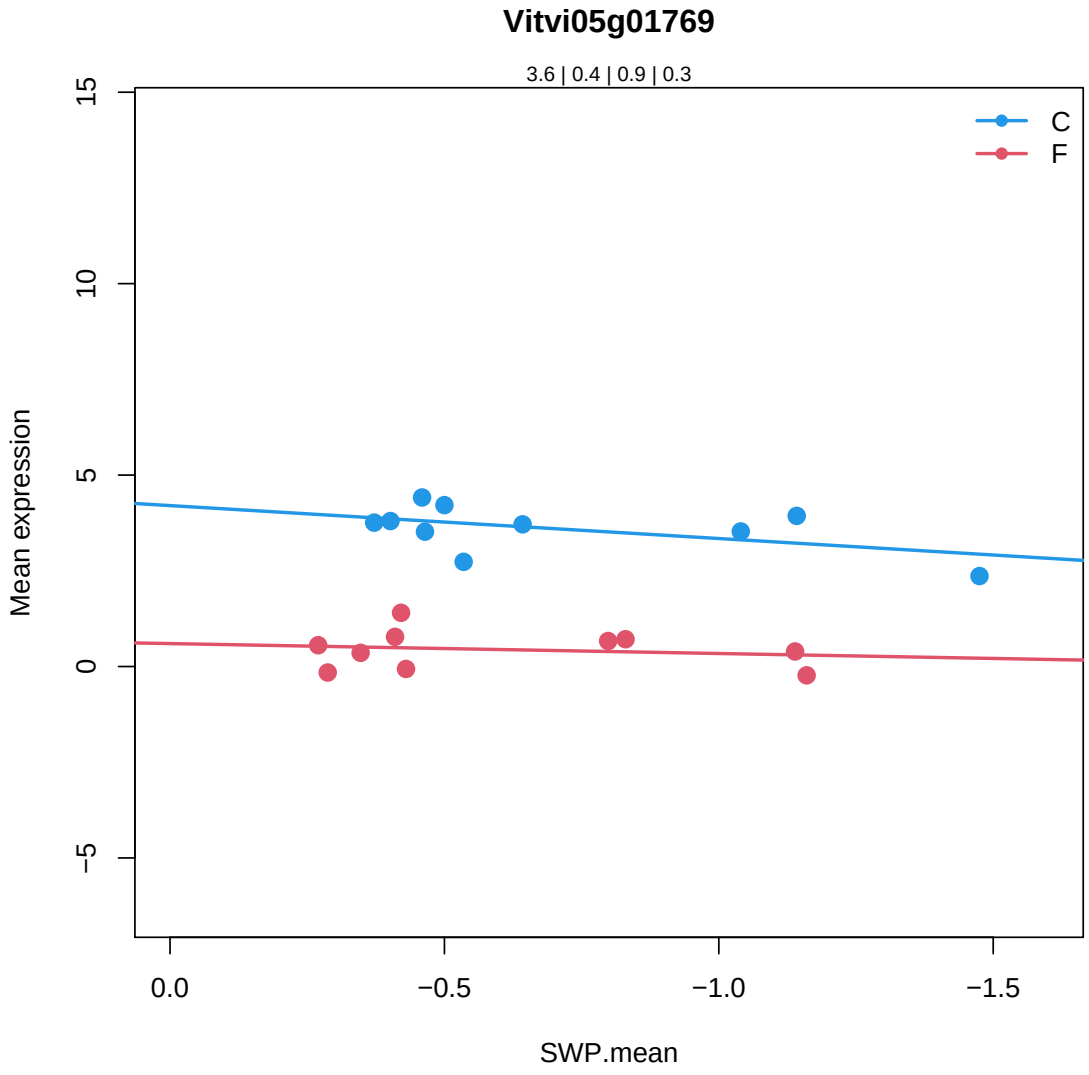
7.4.47 Vitvi05g01769: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01769
        33.99
        development.unspecified
        NAD(P)-binding Rossmann-fold superfamily protein |
        Chr4:12565219-12566474 FORWARD LENGTH=388 |
        201606
```

Coefficients for Vitvi05g01769.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.598108	5.821804e-16	***	1.122813e-15	***
SlopeC	0.8599829	0.07964345	.	0.5748584	
MeanF-MeanC	-3.156922	8.003238e-12	***	6.558353e-10	***
SlopeF-SlopeC	-0.6013267	0.3969066		0.9999488	



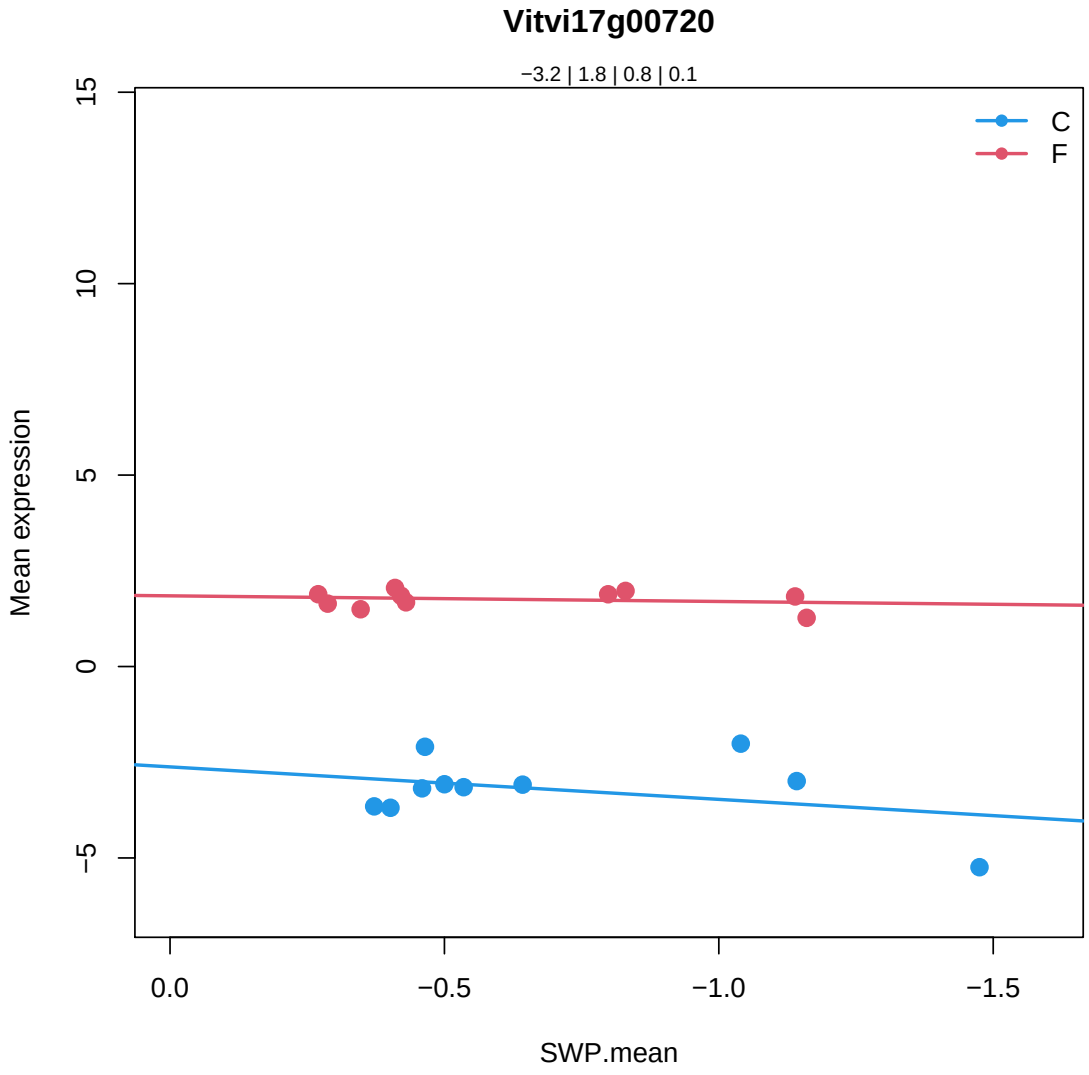
7.4.48 Vitvi17g00720: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00720
        27.1.2
        RNA.processing.RNA helicase
        RPA70-kDa subunit B |
        Chr5:2572107-2574879 FORWARD LENGTH=604 |
        201606
```

Coefficients for Vitvi17g00720.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-3.218369	1.163452e-13	***	1.777778e-13	***
SlopeC	0.8485391	0.132765		0.654787	
MeanF-MeanC	4.974902	1.95339e-14	***	2.362982e-12	***
SlopeF-SlopeC	-0.7012975	0.3951432		0.9999488	



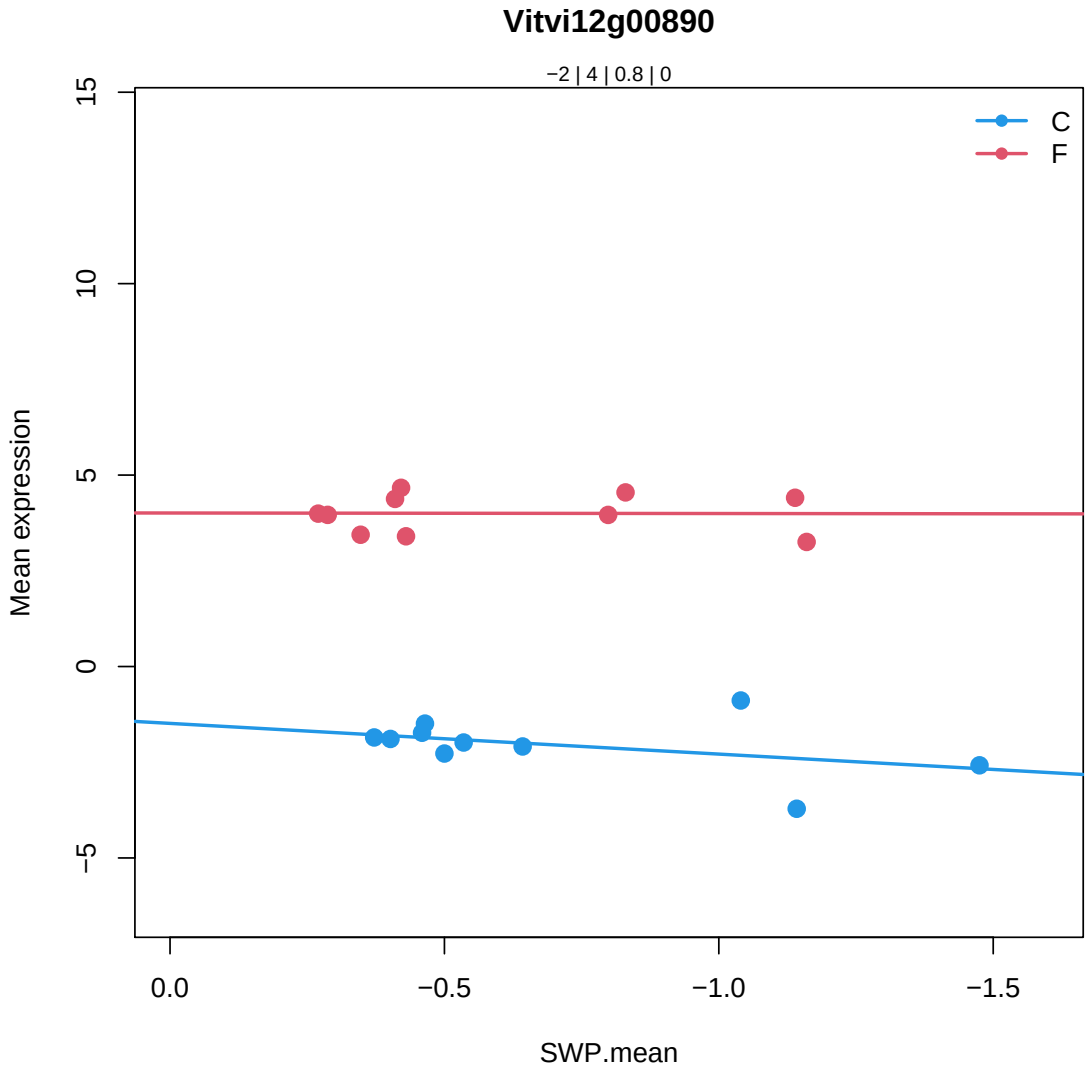
7.4.49 Vitvi12g00890: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00890
        20.1.2.2
        stress.biotic.receptors.TIR-NBS-LRR
        disease resistance protein (TIR-NBS-LRR class) |
        Chr5:5822999-5827153 FORWARD LENGTH=1295 |
        201606
```

Coefficients for Vitvi12g00890.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-2.0495	3.811956e-10	***	4.878407e-10	***
SlopeC	0.8021031	0.1427618		0.6681823	
MeanF-MeanC	6.050493	1.969616e-16	***	3.373134e-14	***
SlopeF-SlopeC	-0.7886223	0.3260888		0.9999488	



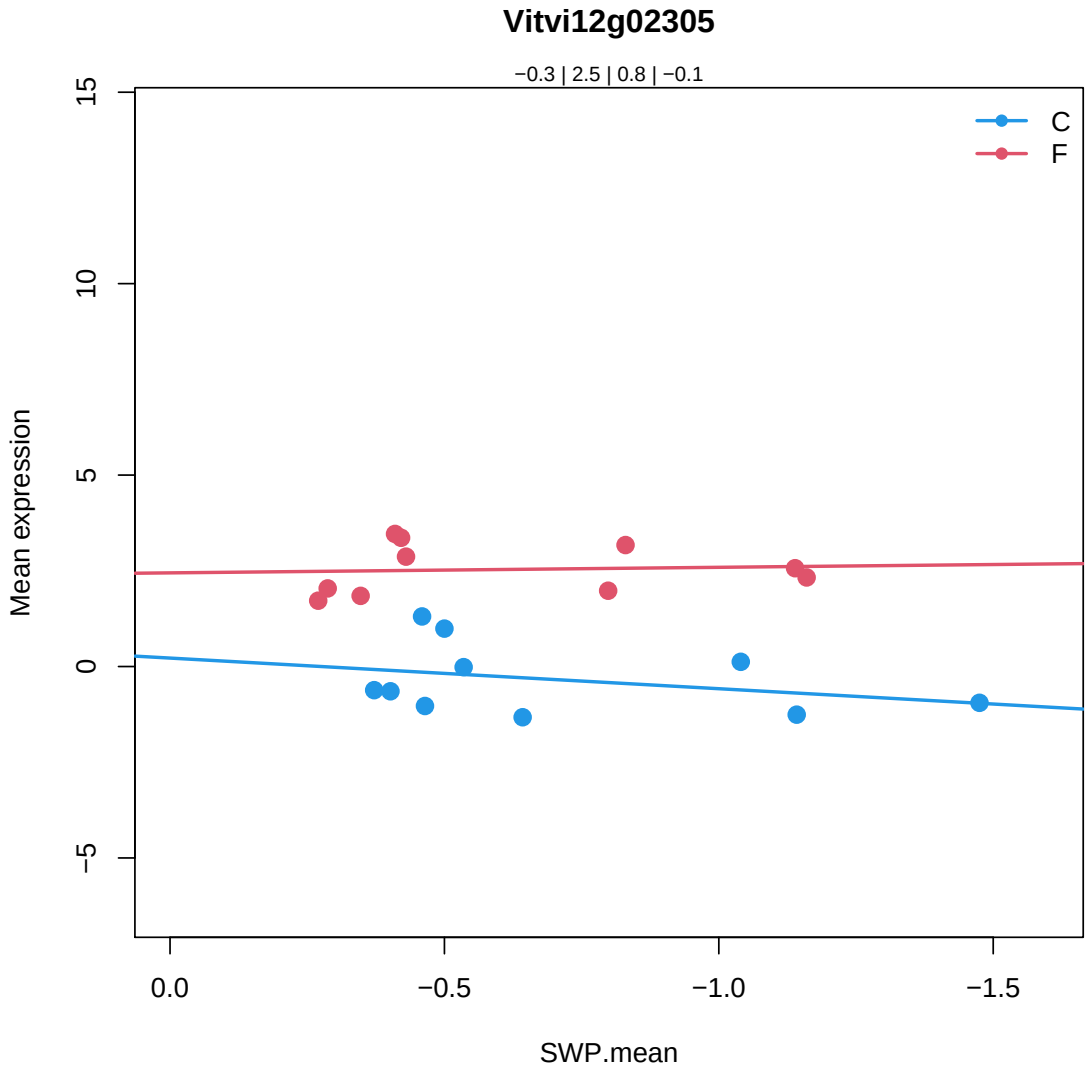
7.4.50 Vitvi12g02305: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02305
        29.4.1
        protein.postranslational modification.kinase
        S-locus lectin protein kinase family protein |
        Chr2:8293789-8296275 FORWARD LENGTH=828 |
        201606
```

Coefficients for Vitvi12g02305.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.3422799	0.1606106		0.1651505	
SlopeC	0.7999182	0.2354089		0.7519022	
MeanF-MeanC	2.876762	1.992221e-08	***	9.489195e-07	***
SlopeF-SlopeC	-0.9449434	0.3433747		0.9999488	



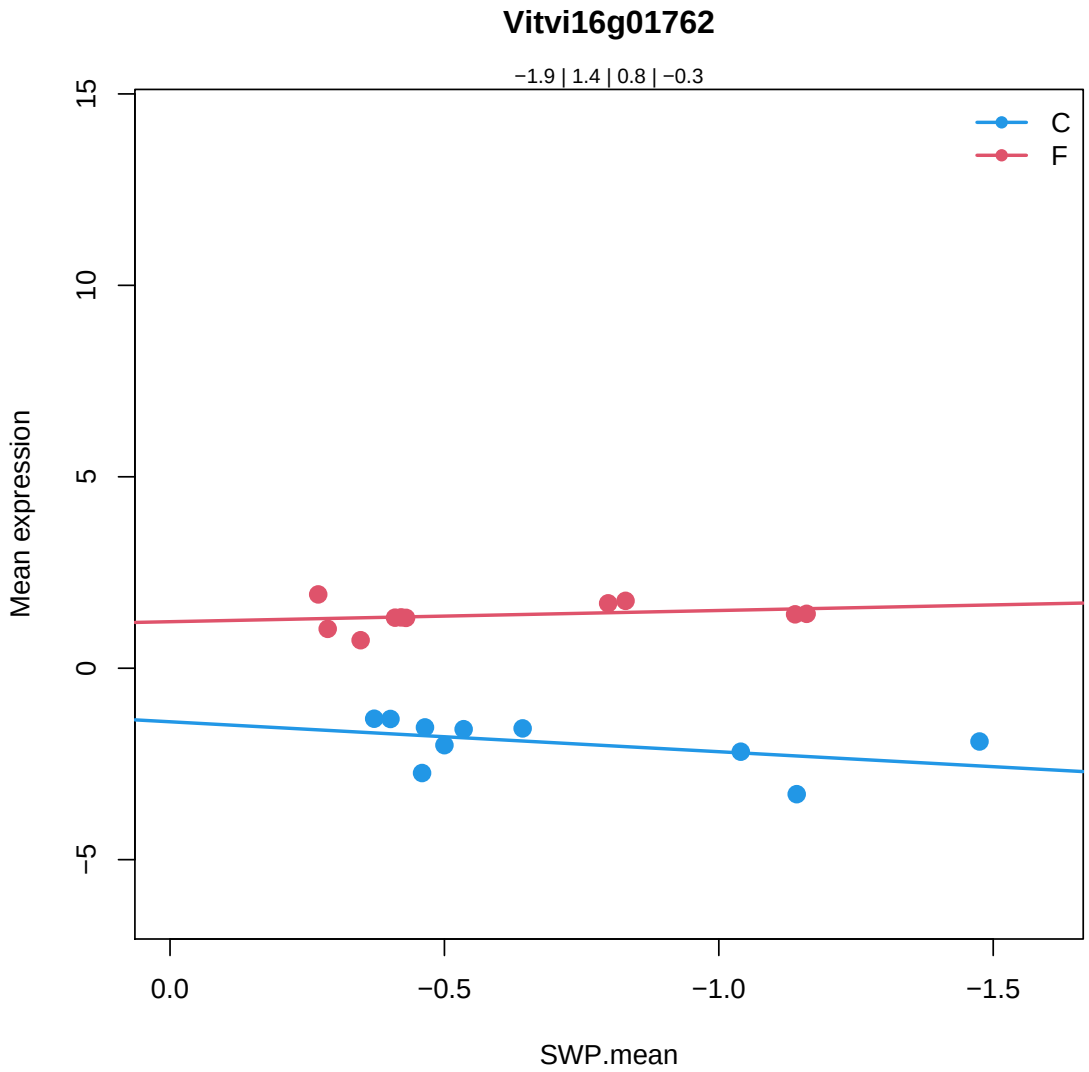
7.4.51 Vitvi16g01762: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01762
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi16g01762.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.948574	2.626243e-11	***	3.521837e-11	***
SlopeC	0.7816522	0.08589085	.	0.5889741	
MeanF-MeanC	3.341787	6.303147e-13	***	5.894023e-11	***
SlopeF-SlopeC	-1.074305	0.1109652		0.9999488	



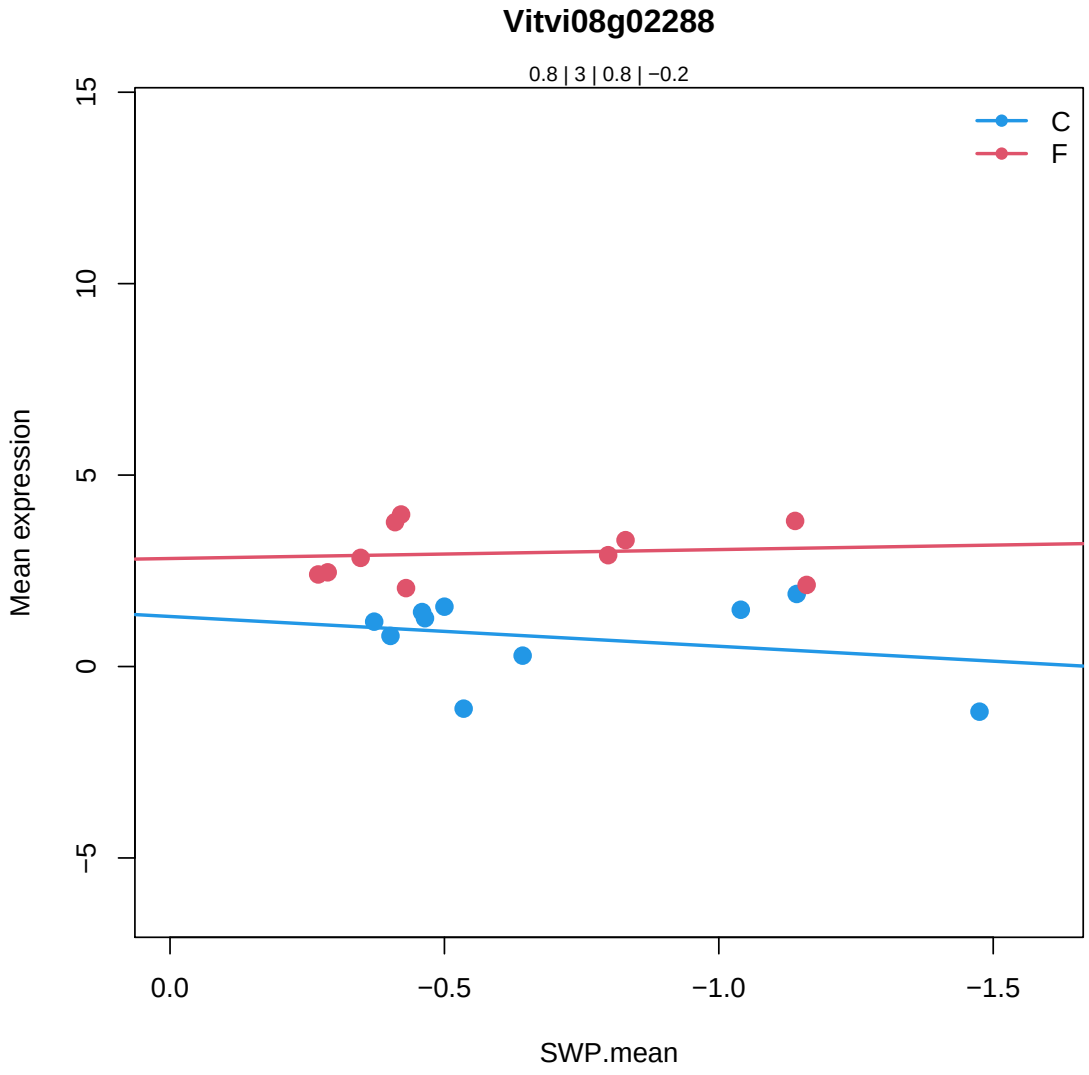
7.4.52 Vitvi08g02288: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g02288
        26.2
        misc.UDP glucosyl and glucoronyl transferases
        UDP-Glycosyltransferase superfamily protein |
        Chr2:15415227-15416717 REVERSE LENGTH=496 |
        201606
```

Coefficients for Vitvi08g02288.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.7597769	0.01067766	*	0.01130436	*
SlopeC	0.7784241	0.3145507		0.7945612	
MeanF-MeanC	2.203336	1.000257e-05	***	0.0002528345	***
SlopeF-SlopeC	-1.012031	0.3783293		0.9999488	



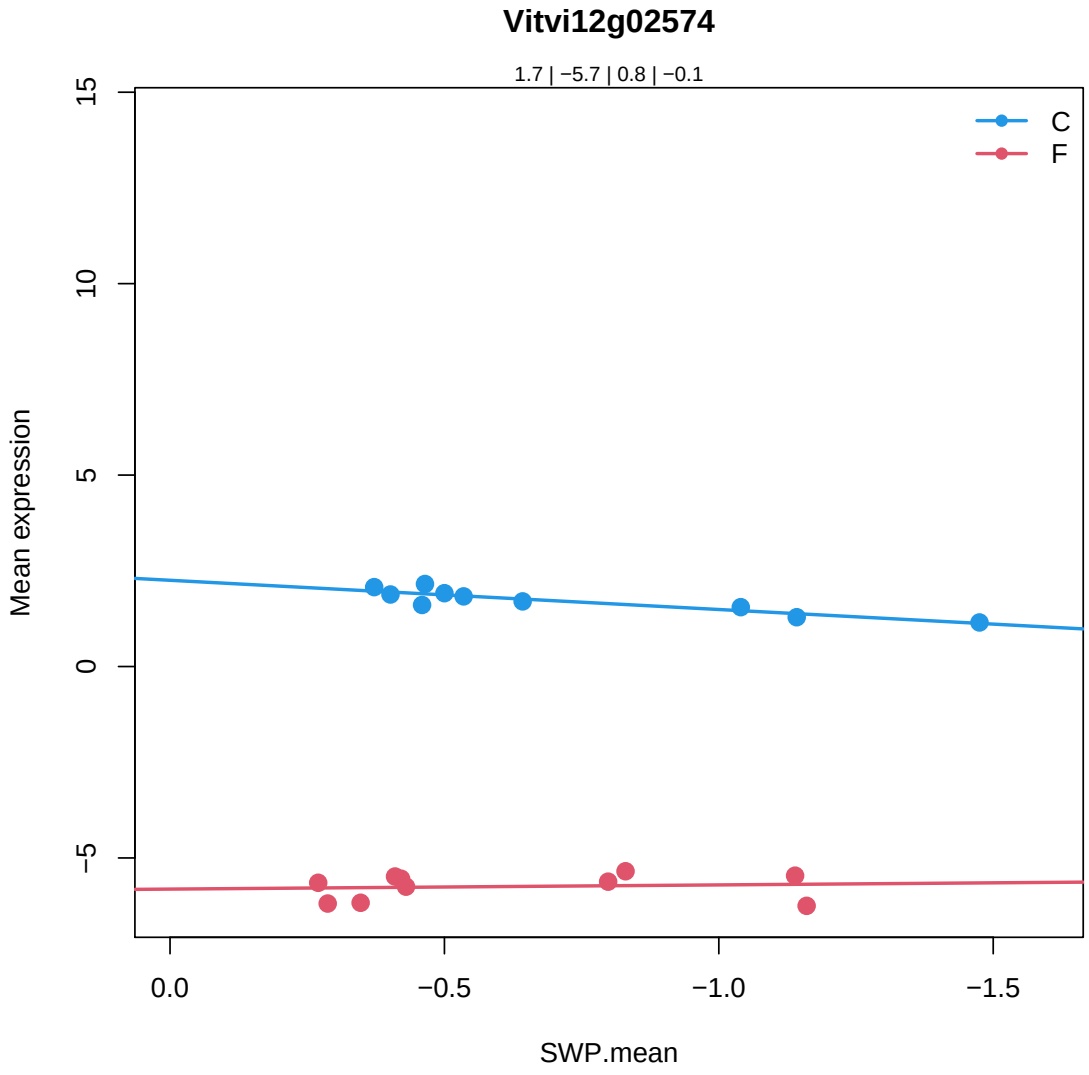
7.4.53 Vitvi12g02574: * type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02574
        12.2.1.2
        N-metabolism.ammonia metabolism.glutamate synthase.NADH dependent
        NADH-dependent glutamate synthase 1 |
        Chr5:21700518-21709629 FORWARD LENGTH=2208 |
        201606
```

Coefficients for Vitvi12g02574.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.715258	2.38061e-13	***	3.562618e-13	***
SlopeC	0.7631201	0.01872167	*	0.3670688	
MeanF-MeanC	-7.461966	1.72012e-23	***	3.745438e-20	***
SlopeF-SlopeC	-0.8723763	0.06390125	.	0.9999488	



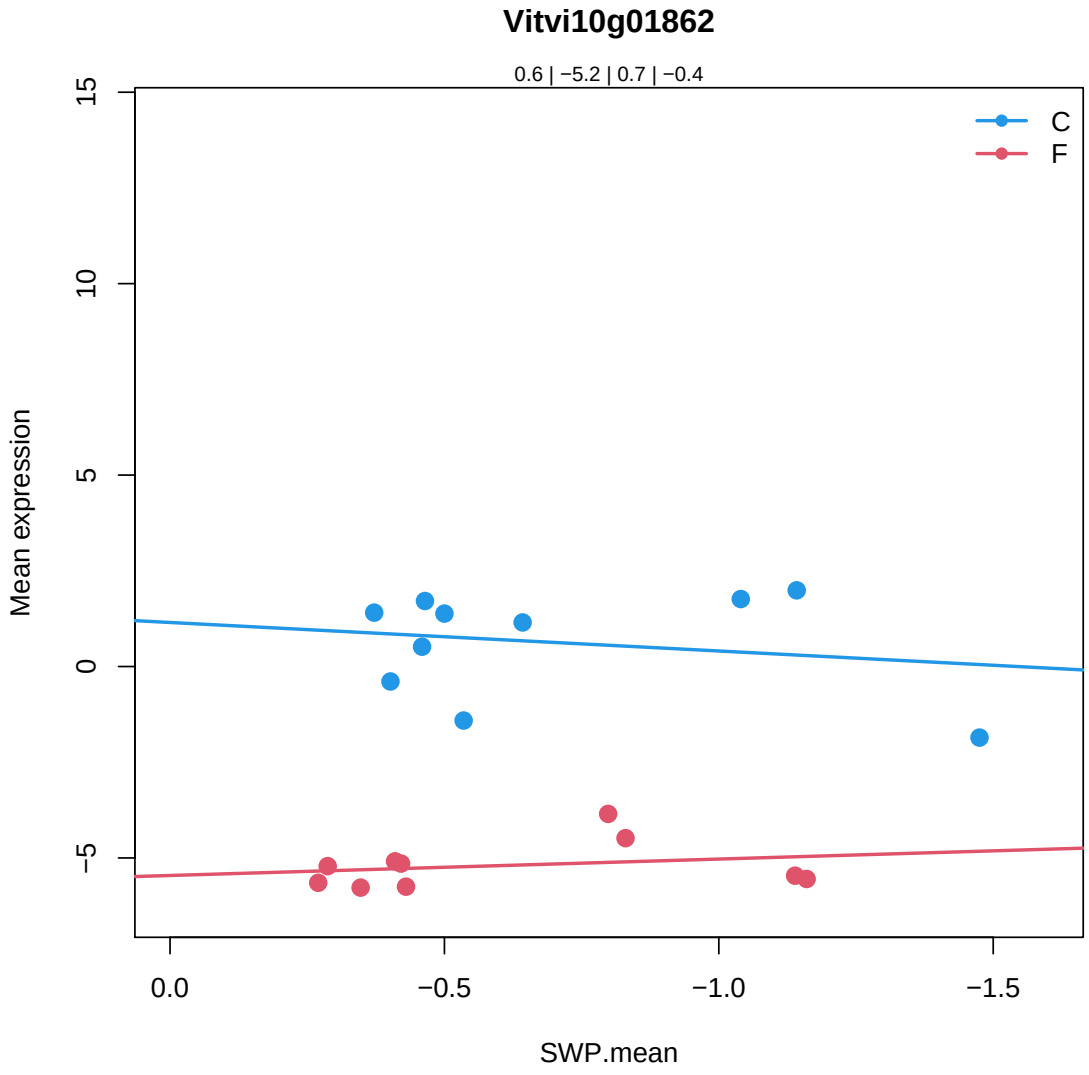
7.4.54 Vitvi10g01862: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g01862
        16.1.5
        secondary metabolism.isoprenoids.terpenoids
        Terpenoid cyclases family protein |
        Chr1:29684558-29688673 REVERSE LENGTH=759 |
        201606
```

Coefficients for Vitvi10g01862.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6263385	0.0577119	.	0.05999896	.
SlopeC	0.7447214	0.4009091		0.835066	
MeanF-MeanC	-5.822896	9.330016e-12	***	7.604711e-10	***
SlopeF-SlopeC	-1.173754	0.3742103		0.9999488	



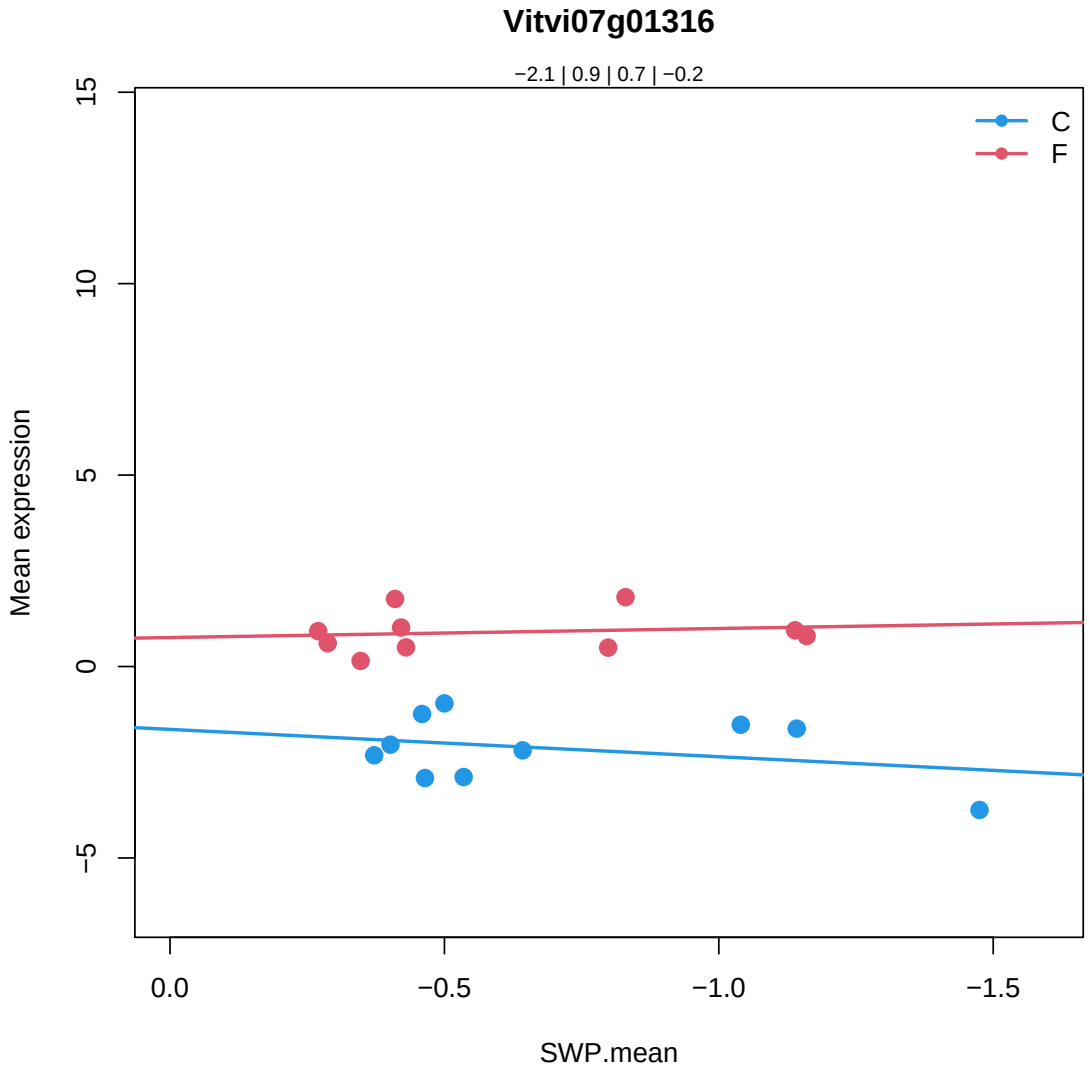
7.4.55 Vitvi07g01316: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01316
        35.2
        not assigned.unknown
        Disease resistance protein (CC-NBS-LRR class) family |
        Chr5:26715845-26717901 REVERSE LENGTH=591 |
        201606
```

Coefficients for Vitvi07g01316.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-2.144129	1.493231e-09	***	1.872158e-09	***
SlopeC	0.7132768	0.243604		0.7565475	
MeanF-MeanC	3.044584	1.38895e-09	***	7.726415e-08	***
SlopeF-SlopeC	-0.9493738	0.2955315		0.9999488	



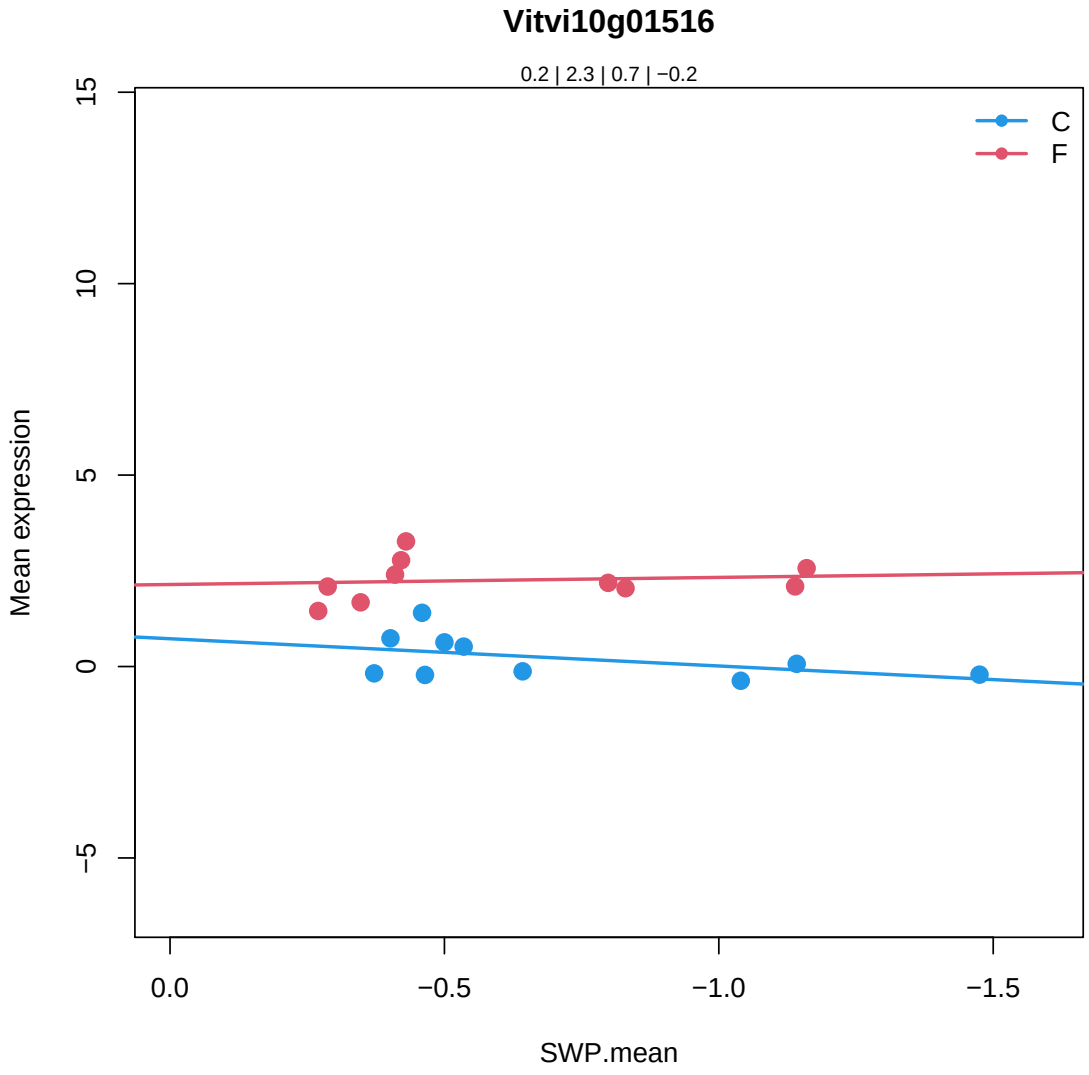
7.4.56 Vitvi10g01516: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g01516
        29.4.1
        protein.postranslational modification.kinase
        S-locus lectin protein kinase family protein |
        Chr2:8293789-8296275 FORWARD LENGTH=828 |
        201606
```

Coefficients for Vitvi10g01516.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.2251199	0.1950886		0.2000364	
SlopeC	0.7115362	0.1432593		0.6683681	
MeanF-MeanC	2.029835	2.470742e-08	***	1.148142e-06	***
SlopeF-SlopeC	-0.8969151	0.211867		0.9999488	



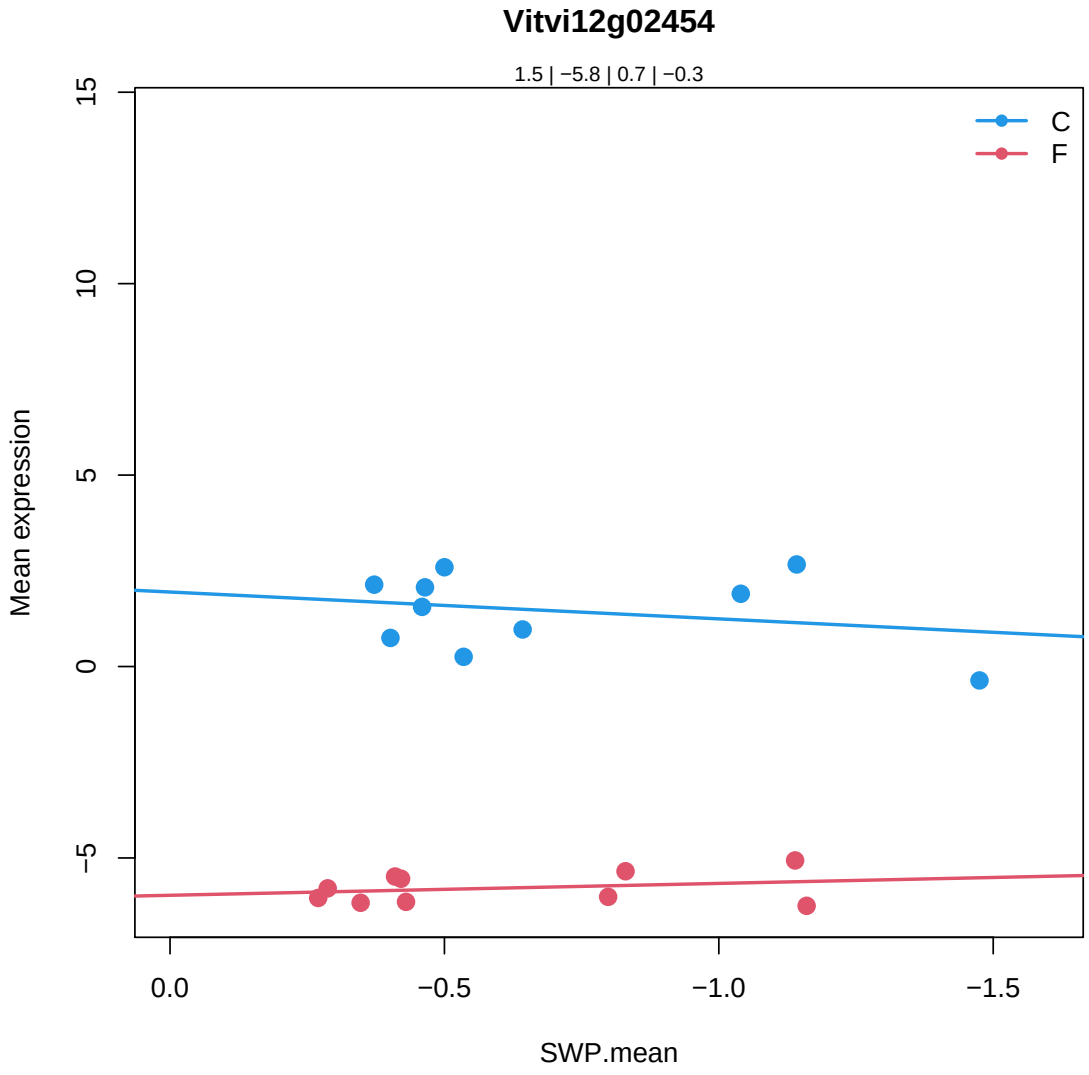
7.4.57 Vitvi12g02454: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02454
        16.8.1.21
        secondary metabolism.flavonoids.anthocyanins.anthocyanin 5-aromatic ac
        HXXXD-type acyl-transferase family protein |
        Chr1:1009542-1010951 REVERSE LENGTH=469 |
        201606
```

Coefficients for Vitvi12g02454.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.45233	2.652875e-06	***	3.031801e-06	***
SlopeC	0.7013162	0.2852786		0.7782707	
MeanF-MeanC	-7.238537	2.656374e-16	***	4.498717e-14	***
SlopeF-SlopeC	-1.011435	0.3000955		0.9999488	



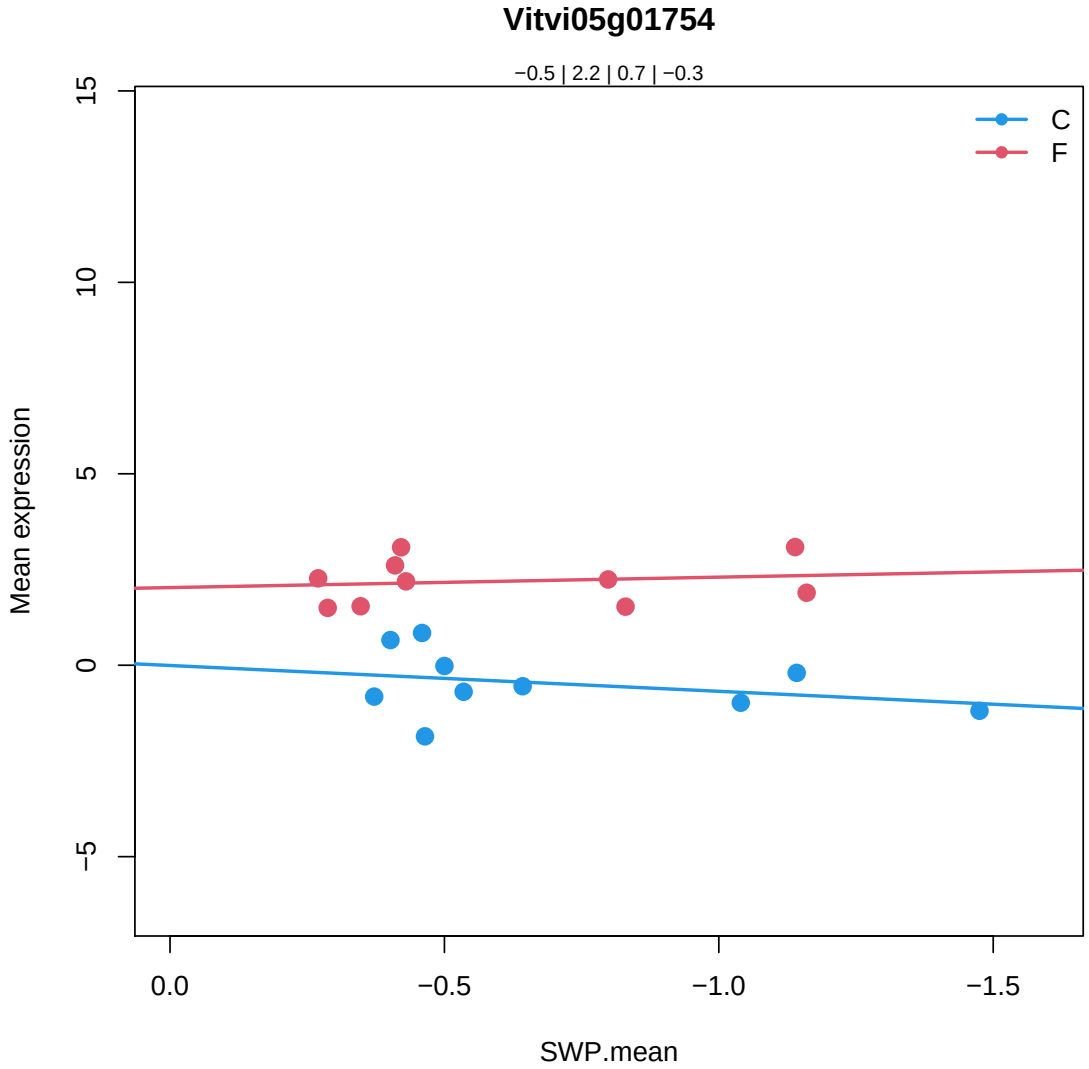
7.4.58 Vitvi05g01754: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01754
        35.2
        not assigned.unknown
        Major allergen Mal d 1 IPR000916 Bet v I allergen
```

Coefficients for Vitvi05g01754.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.481004	0.03669385	*	0.03832312	*
SlopeC	0.6742206	0.2740239		0.7746054	
MeanF-MeanC	2.674313	1.56981e-08	***	7.595885e-07	***
SlopeF-SlopeC	-0.9464936	0.3014605		0.9999488	



7.4.59 Vitvi09g00243: type3

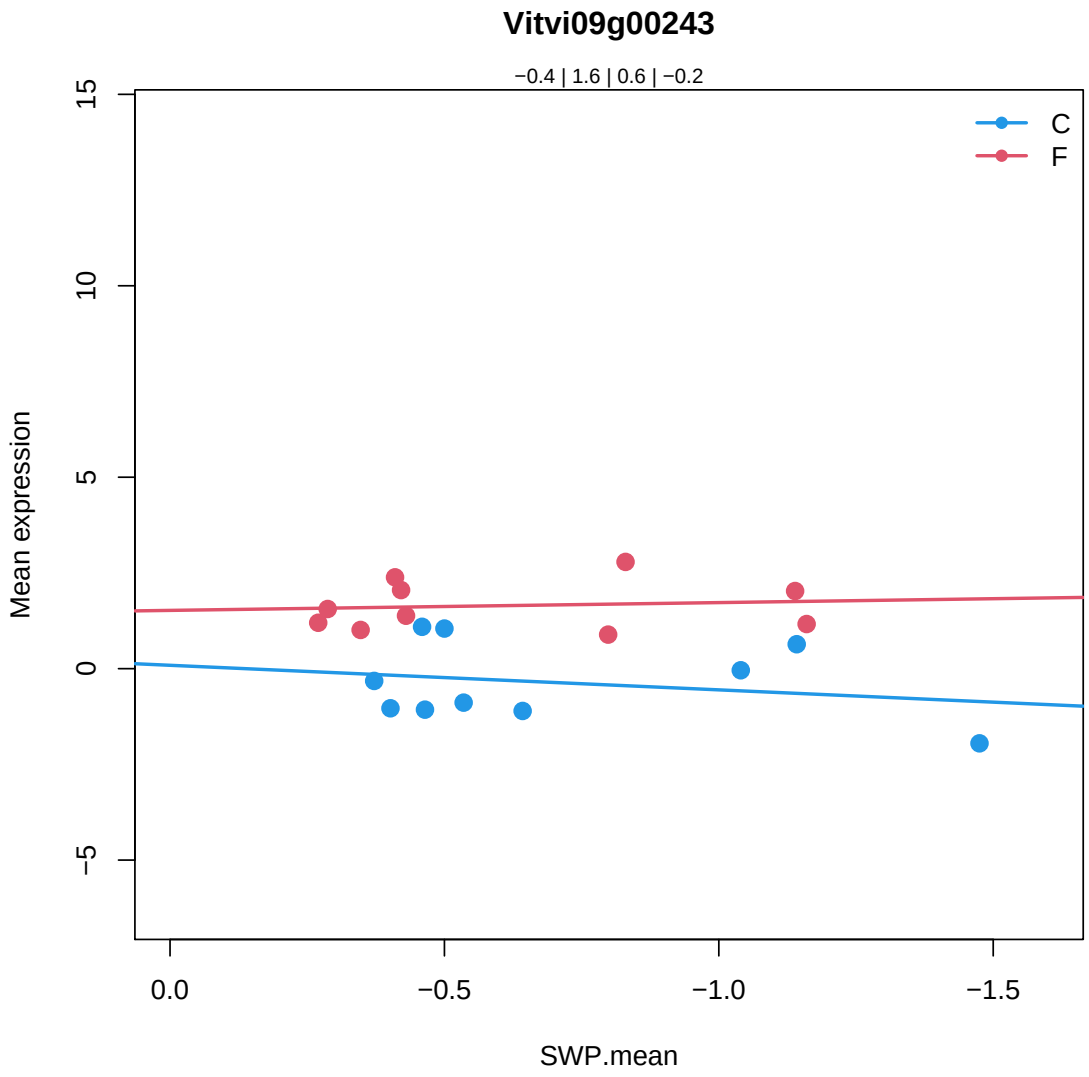
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00243
        29.4
        protein.postranslational modification
        Leucine-rich repeat transmembrane protein kinase protein |
        Chr4:14666179-14669438 REVERSE LENGTH=732 |
        201606

Vitvi09g00243
        30.2.1
        signalling.receptor kinases.leucine rich repeat I
        Leucine-rich repeat transmembrane protein kinase protein |
        Chr4:14666179-14669438 REVERSE LENGTH=732 |
        201606
```

Coefficients for Vitvi09g00243.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.363607	0.1675273		0.1721931	
SlopeC	0.6418738	0.3747674		0.8249251	
MeanF-MeanC	2.009195	1.428137e-05	***	0.0003461114	***
SlopeF-SlopeC	-0.8453834	0.4312835		0.9999488	


Vitvi09g00243
−0.4 | 1.6 | 0.6 | −0.2
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

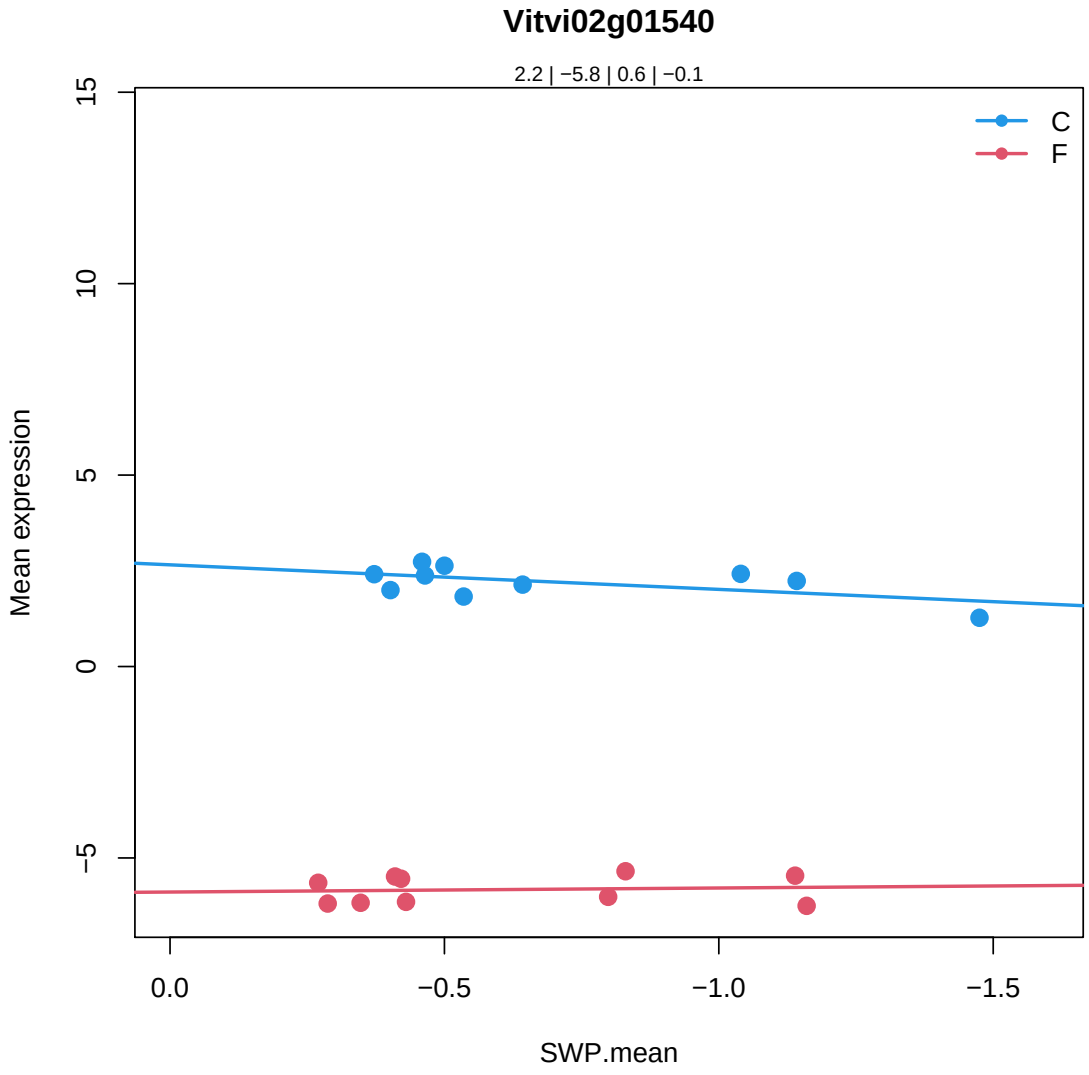
7.4.60 Vitvi02g01540: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g01540
        35.2
        not assigned.unknown
        putative acyl-coenzyme A oxidase |
        Chr3:2115589-2116825 REVERSE LENGTH=187 |
        201606
```

Coefficients for Vitvi02g01540.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.204748	5.645367e-14	***	8.833455e-14	***
SlopeC	0.6413852	0.08795971	.	0.5932372	
MeanF-MeanC	-8.030705	1.614533e-22	***	1.447572e-19	***
SlopeF-SlopeC	-0.7470045	0.1761303		0.9999488	



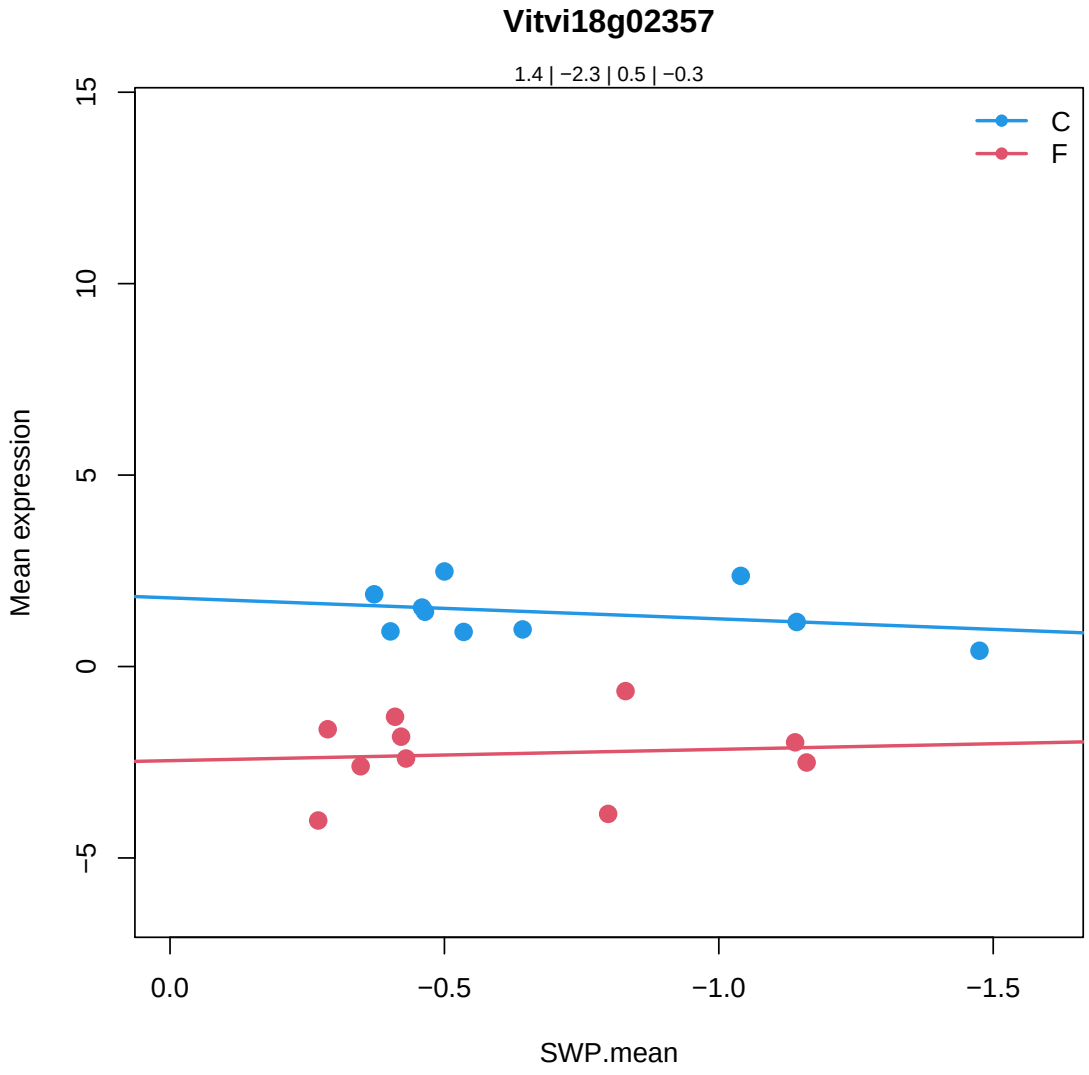
7.4.61 Vitvi18g02357: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02357
        35.2
        not assigned.unknown
        disease resistance protein (TIR-NBS-LRR class) |
        Chr5:5822999-5827153 FORWARD LENGTH=1295 |
        201606
```

Coefficients for Vitvi18g02357.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.407074	2.513138e-05	***	2.810982e-05	***
SlopeC	0.5475821	0.4630792		0.8604478	
MeanF-MeanC	-3.686375	1.891169e-09	***	1.036878e-07	***
SlopeF-SlopeC	-0.8421445	0.4485147		0.9999488	



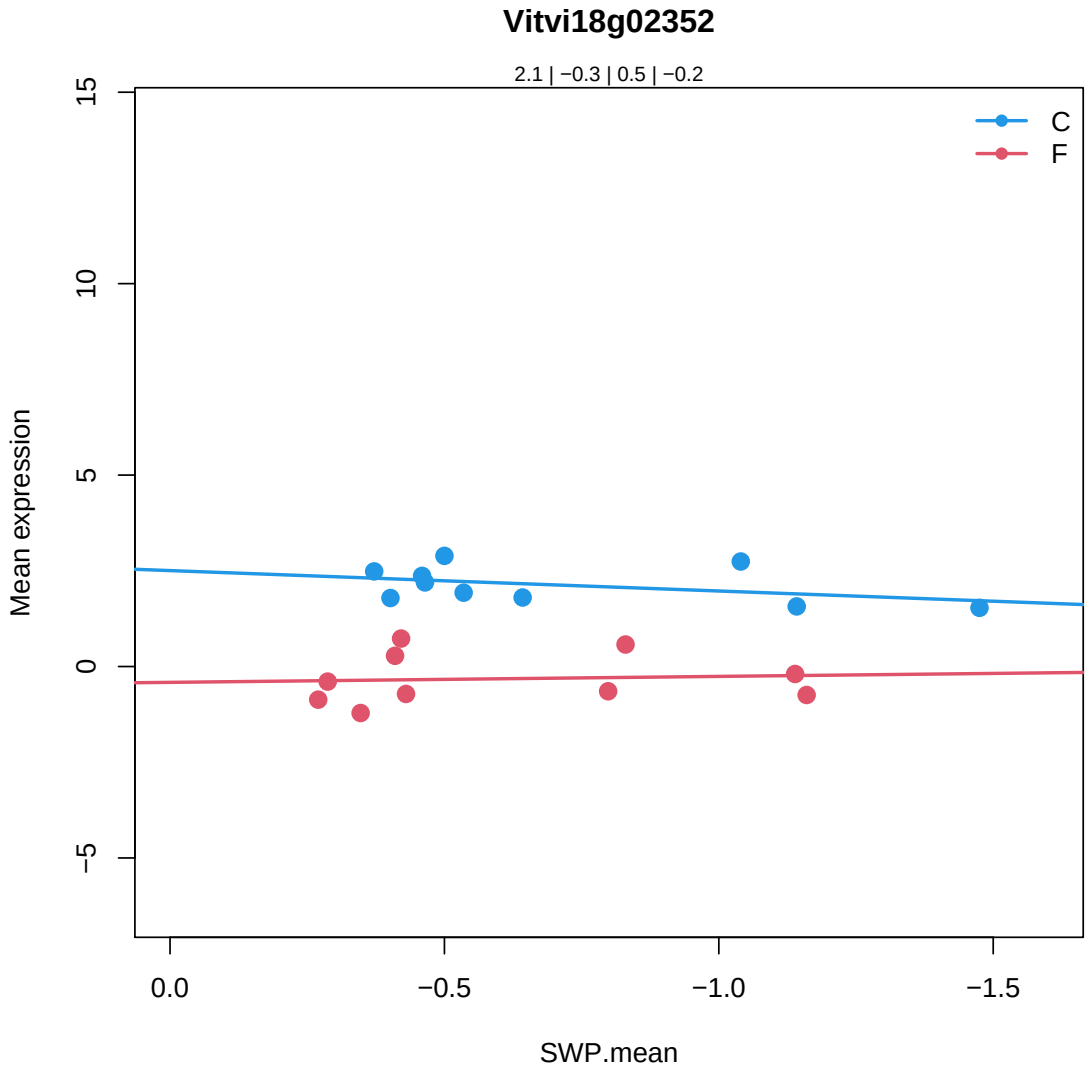
7.4.62 Vitvi18g02352: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02352
        20.1.2.2
        stress.biotic.receptors.TIR-NBS-LRR
        Disease resistance protein (TIR-NBS-LRR class) family |
        Chr5:14568141-14571907 REVERSE LENGTH=1125 |
        201606
```

Coefficients for Vitvi18g02352.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.13041	6.001855e-11	***	7.919685e-11	***
SlopeC	0.5332623	0.2942162		0.7823247	
MeanF-MeanC	-2.449533	2.611196e-09	***	1.396486e-07	***
SlopeF-SlopeC	-0.6889797	0.361014		0.9999488	



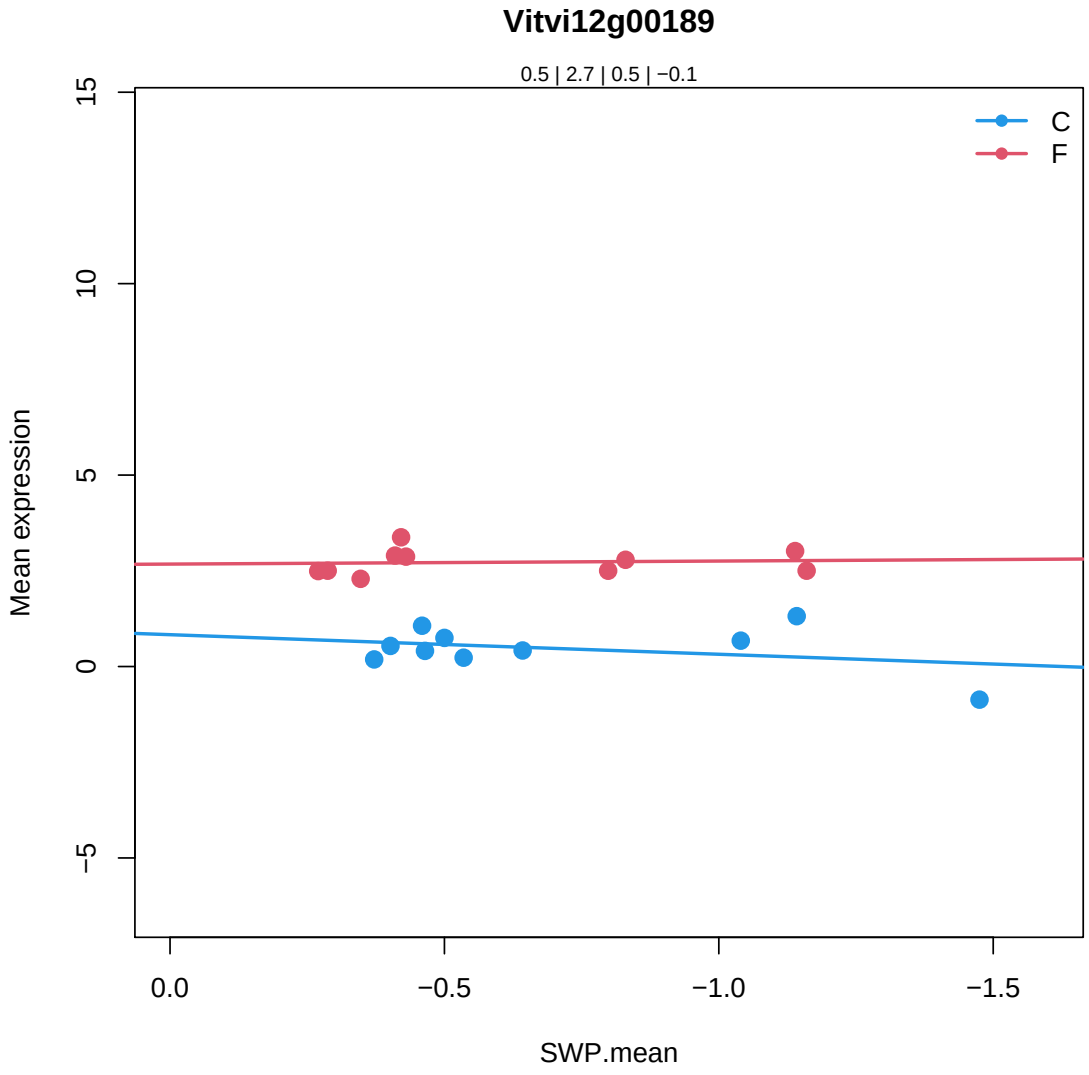
7.4.63 Vitvi12g00189: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00189
        18.3
        Co-factor and vitamine metabolism.riboflavin
        chloroplast ribosomal protein S4 |
        ChrC:45223-45828 REVERSE LENGTH=201 |
        201606
```

Coefficients for Vitvi12g00189.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4717706	0.005605186	**	0.005970248	**
SlopeC	0.5109577	0.2438255		0.7565938	
MeanF-MeanC	2.251601	7.909235e-10	***	4.699495e-08	***
SlopeF-SlopeC	-0.5901015	0.3627651		0.9999488	



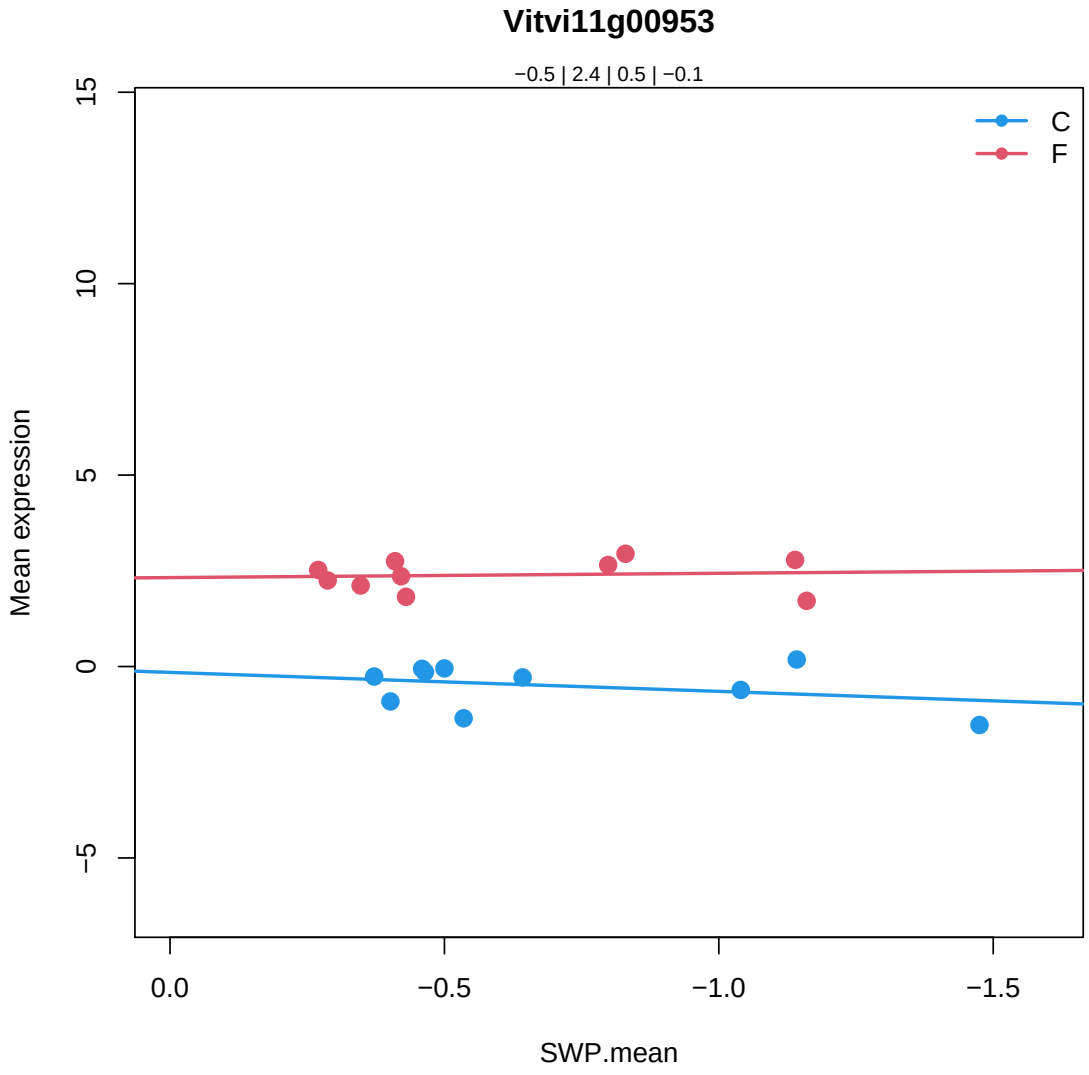
7.4.64 Vitvi11g00953: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00953
        29.2.3
        protein.synthesis.initiation
        Trimeric LpxA-like enzyme |
        Chr2:14746340-14748532 FORWARD LENGTH=730 |
        201606
```

Coefficients for Vitvi11g00953.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.5021509	0.005208738	**	0.005553413	**
SlopeC	0.4950328	0.2826555		0.7773135	
MeanF-MeanC	2.893199	1.987626e-11	***	1.530071e-09	***
SlopeF-SlopeC	-0.6075274	0.3736076		0.9999488	



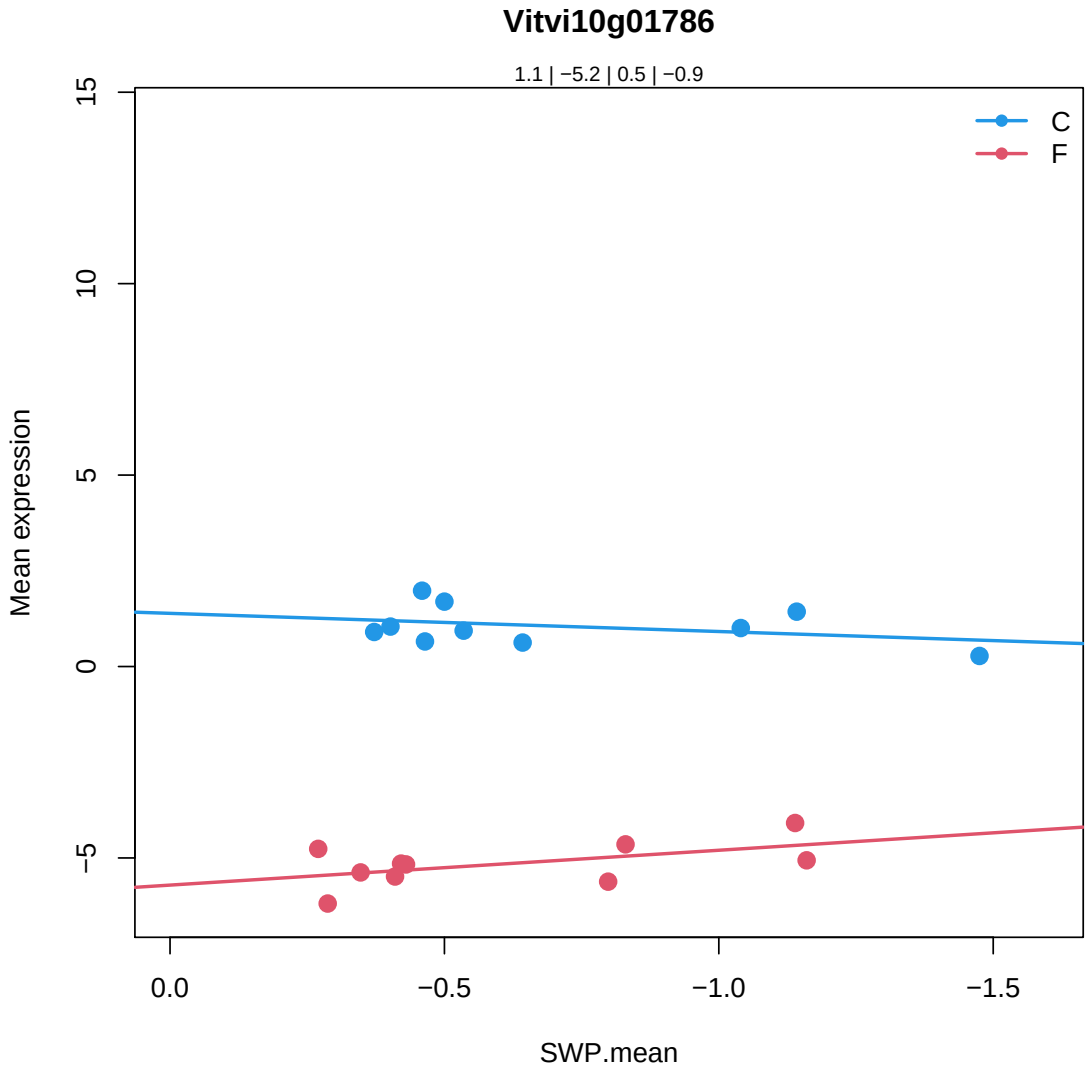
7.4.65 Vitvi10g01786: + type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g01786
        35.2
        not assigned.unknown
        glutamate receptor 2.9 |
        Chr2:12501092-12504912 REVERSE LENGTH=940 |
        201606
```

Coefficients for Vitvi10g01786.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.054962	1.528935e-06	***	1.757336e-06	***
SlopeC	0.4742976	0.3009198		0.7855144	
MeanF-MeanC	-6.209645	3.820353e-18	***	8.958434e-16	***
SlopeF-SlopeC	-1.384343	0.04982324	*	0.9999488	



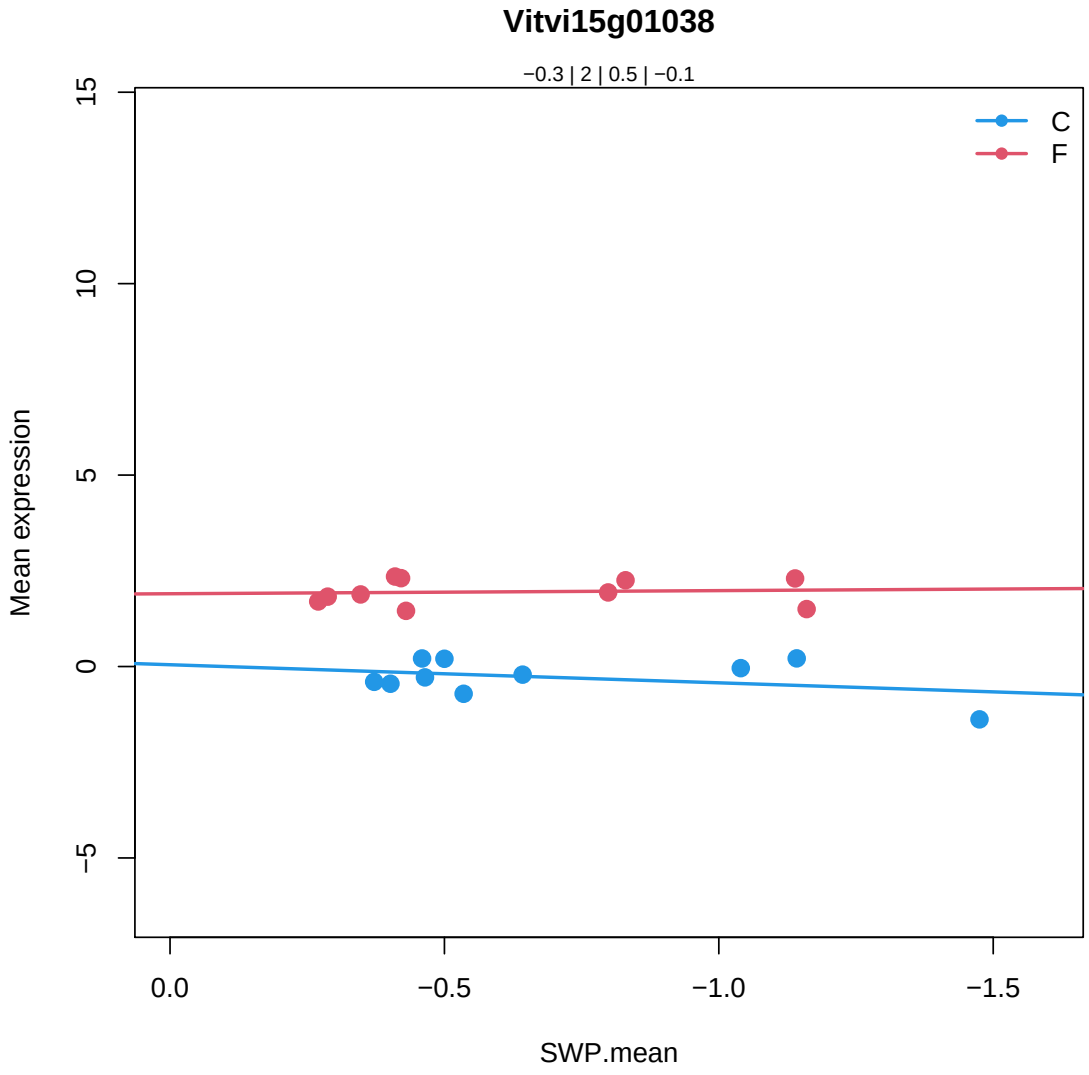
7.4.66 Vitvi15g01038: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g01038
        35.2
        not assigned.unknown
        chitinase A |
        Chr5:8143805-8145153 REVERSE LENGTH=302 |
        201606
```

Coefficients for Vitvi15g01038.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.2856267	0.05542222	.	0.05765787	.
SlopeC	0.4725446	0.2414942		0.7548923	
MeanF-MeanC	2.236081	1.963708e-10	***	1.30134e-08	***
SlopeF-SlopeC	-0.5538995	0.3533634		0.9999488	



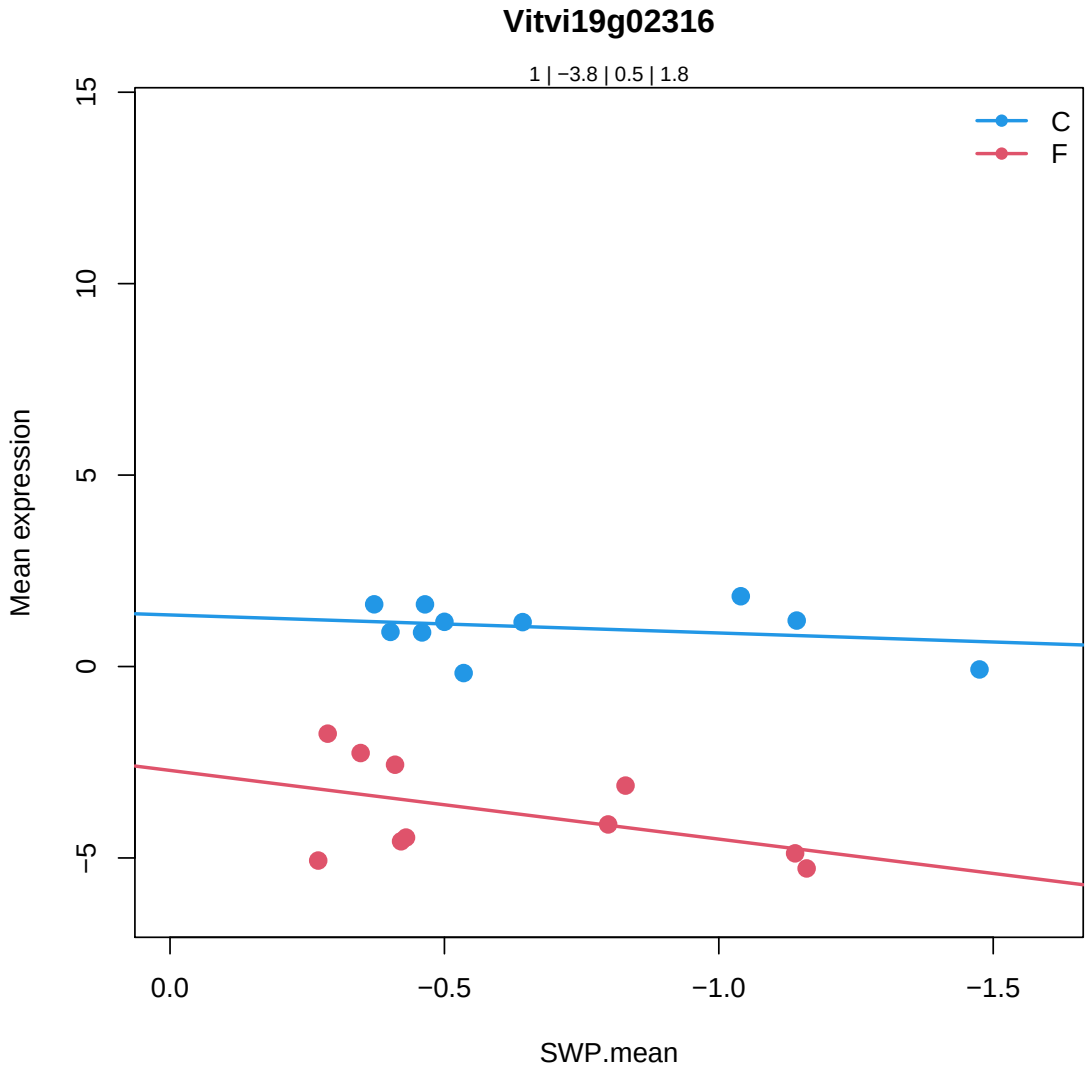
7.4.67 Vitvi19g02316: type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g02316
        35.2
        not assigned.unknown
        Disease resistance protein (CC-NBS-LRR class) family |
        Chr1:4145011-4147680 FORWARD LENGTH=889 |
        201606
```

Coefficients for Vitvi19g02316.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.015579	0.001366712	**	0.001476046	**
SlopeC	0.4709163	0.5464691		0.8857058	
MeanF-MeanC	-4.822373	3.259702e-11	***	2.400211e-09	***
SlopeF-SlopeC	1.323198	0.2600661		0.9999488	



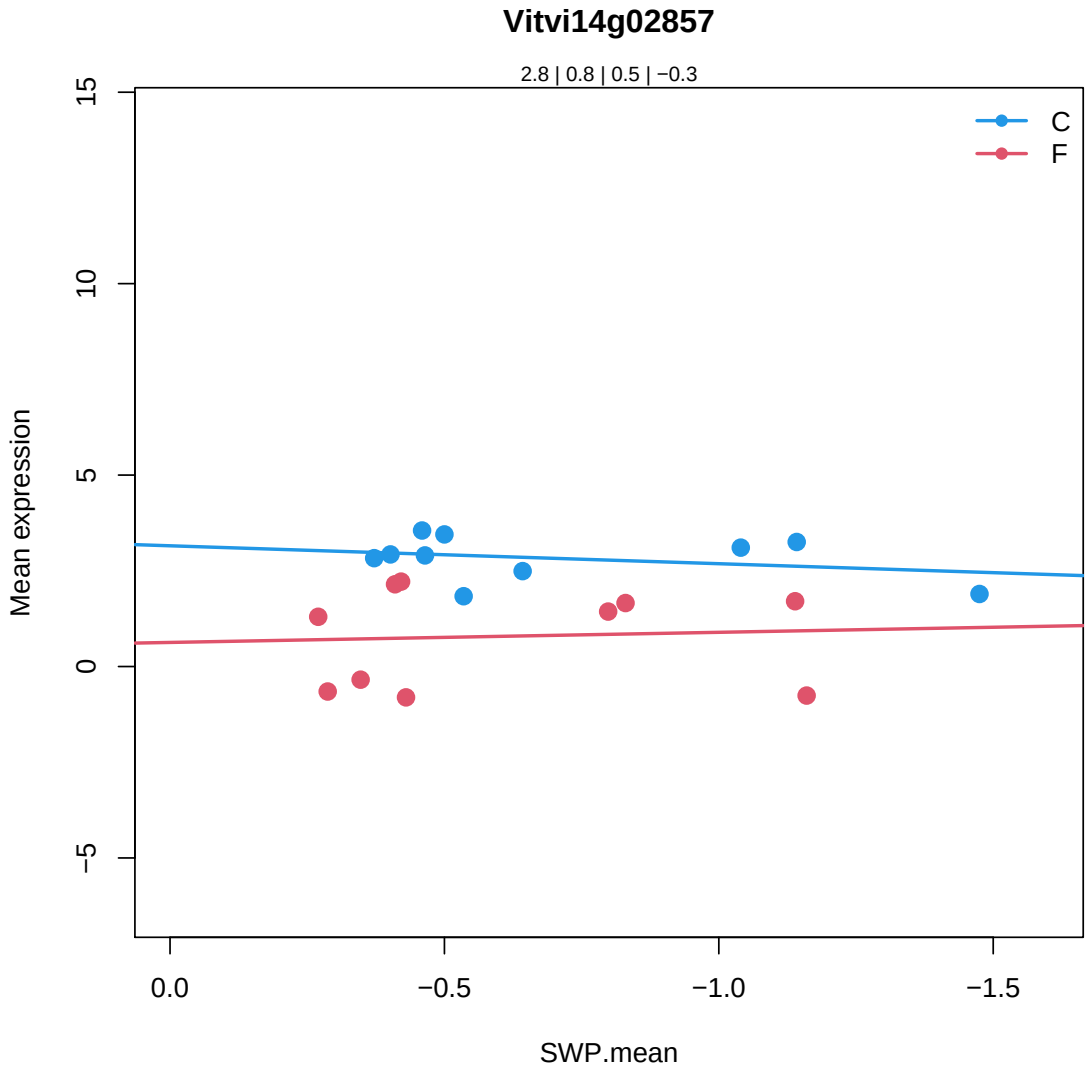
7.4.68 Vitvi14g02857: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g02857
        26.6
        misc.O-methyl transferases
        S-adenosyl-L-methionine-dependent methyltransferases superfamily prote
        Chr1:5204625-5205912 FORWARD LENGTH=351 |
        201606
```

Coefficients for Vitvi14g02857.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.82408	3.234582e-09	***	4.014126e-09	***
SlopeC	0.4682665	0.5732071		0.8925427	
MeanF-MeanC	-2.03398	7.382951e-05	***	0.001384752	**
SlopeF-SlopeC	-0.7325813	0.5539195		0.9999488	



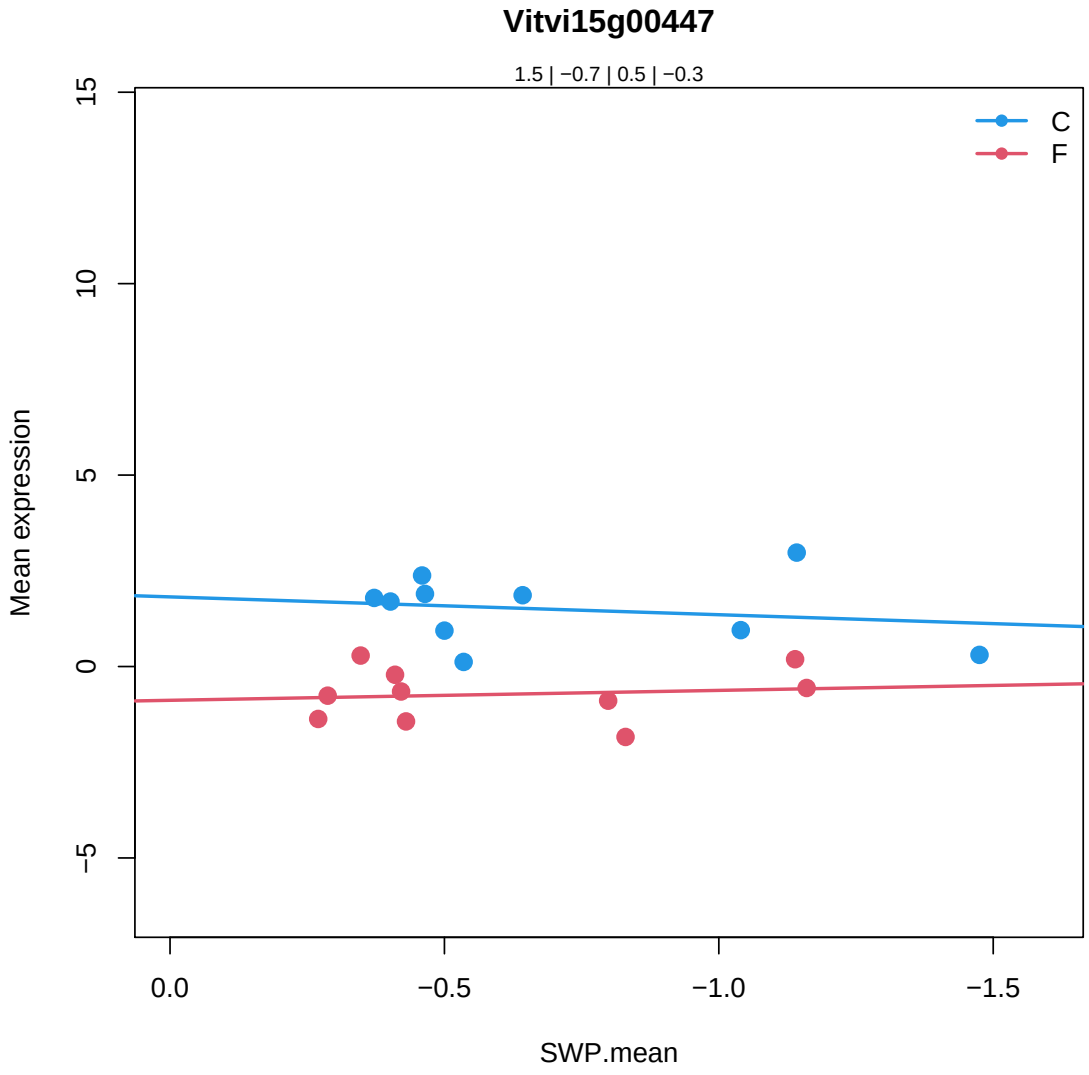
7.4.69 Vitvi15g00447: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g00447
        35.1
        not assigned.no ontology
        Haloacid dehalogenase-like hydrolase (HAD) superfamily protein |
        Chr2:16194639-16195995 REVERSE LENGTH=244 |
        201606
```

Coefficients for Vitvi15g00447.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.491034	3.863569e-06	***	4.401235e-06	***
SlopeC	0.465704	0.49746		0.8696279	
MeanF-MeanC	-2.216072	1.904599e-06	***	5.748494e-05	***
SlopeF-SlopeC	-0.7245698	0.4783875		0.9999488	



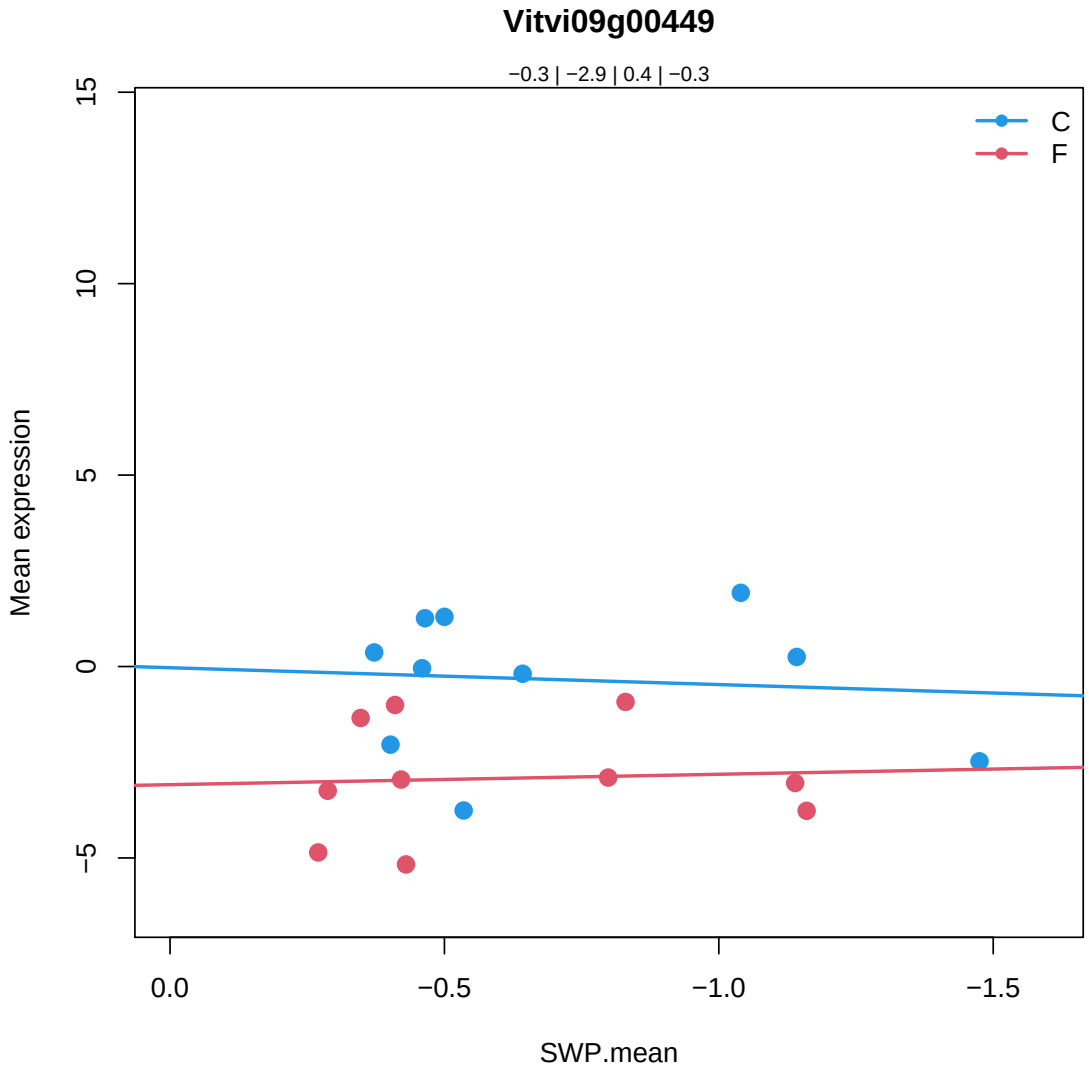
7.4.70 Vitvi09g00449: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00449
        16.5.1.1.1.11
        secondary metabolism.sulfur-containing.glucosinolates.synthesis.alipha
        2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protei
        Chr1:19669216-19670321 FORWARD LENGTH=317 |
        201606
```

Coefficients for Vitvi09g00449.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.3408835	0.4931141		0.4992723	
SlopeC	0.4404241	0.7492138		0.9470665	
MeanF-MeanC	-2.579913	0.00119807	**	0.01455058	*
SlopeF-SlopeC	-0.7120246	0.7284725		0.9999488	



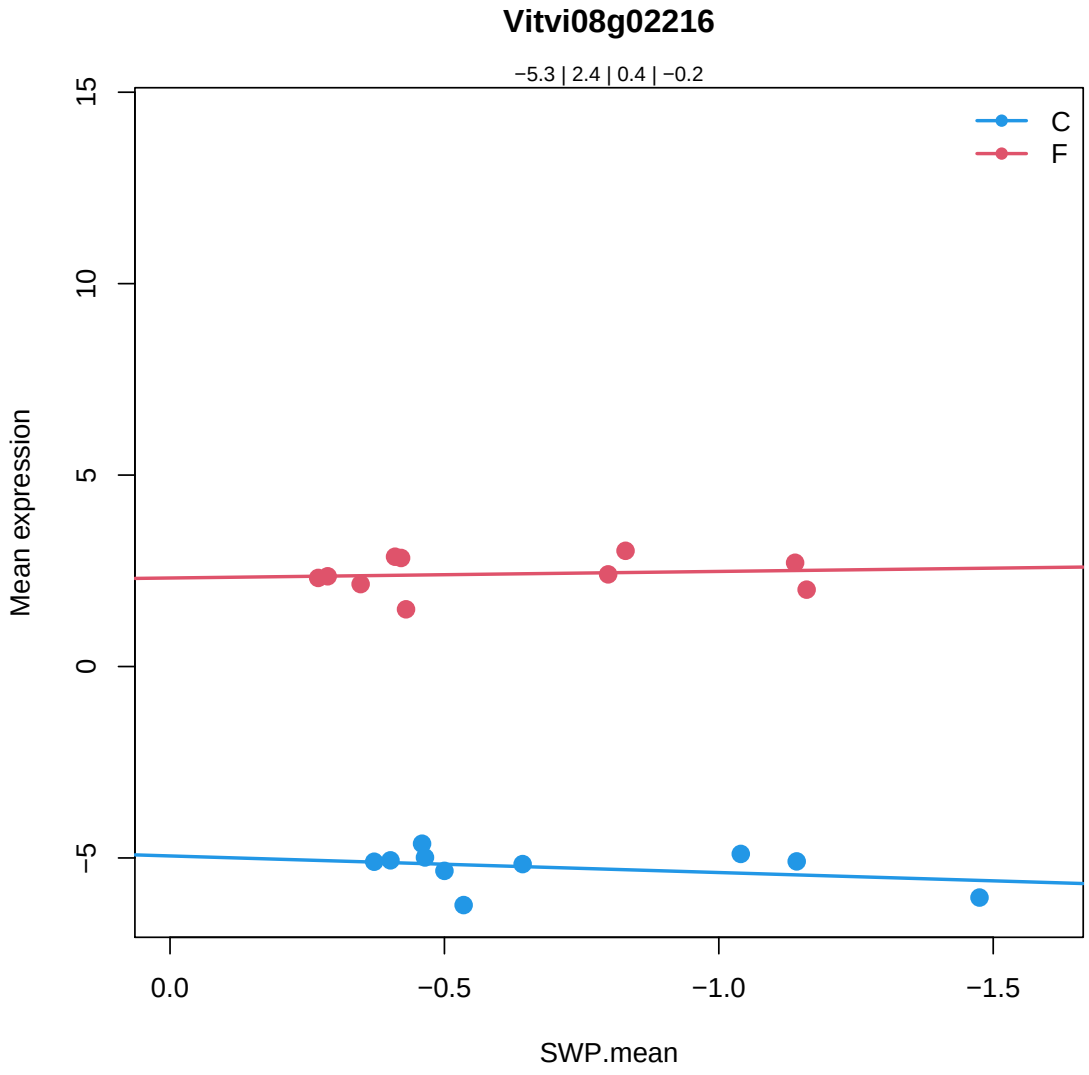
7.4.71 Vitvi08g02216: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g02216
        35.2
        not assigned.unknown
        lectin protein kinase family protein |
        Chr1:12503450-12505939 FORWARD LENGTH=829 |
        201606
```

Coefficients for Vitvi08g02216.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.252424	4.797931e-20	***	2.562325e-19	***
SlopeC	0.4331962	0.3297671		0.8007475	
MeanF-MeanC	7.669036	2.448307e-20	***	9.329275e-18	***
SlopeF-SlopeC	-0.6046646	0.3600822		0.9999488	



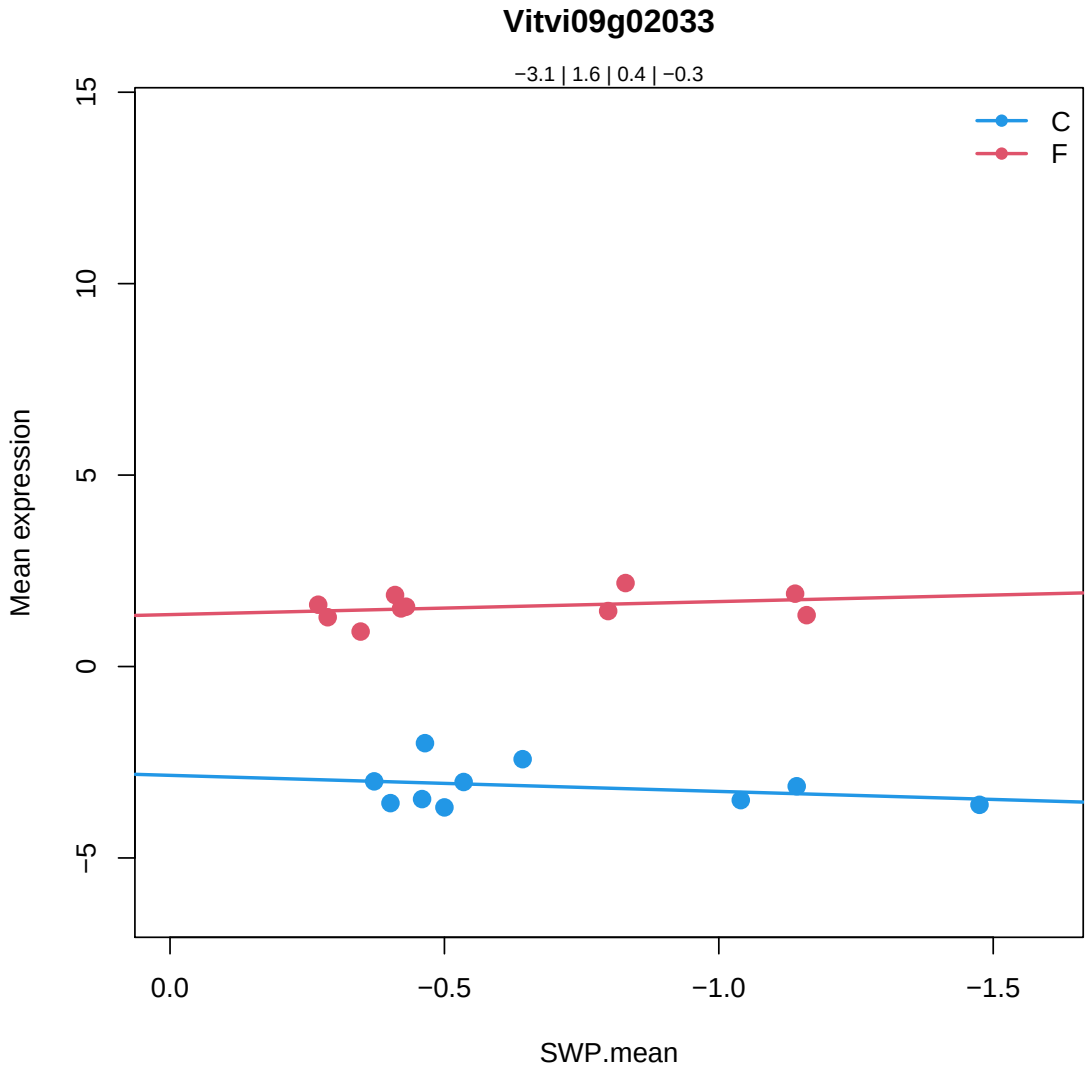
7.4.72 Vitvi09g02033: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g02033
        35.2
        not assigned.unknown
        Disease resistance protein (CC-NBS-LRR class) family |
        Chr1:4145374-4147680 FORWARD LENGTH=768 |
        201606
```

Coefficients for Vitvi09g02033.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-3.137869	1.072274e-15	***	1.999706e-15	***
SlopeC	0.4195645	0.3288525		0.8006793	
MeanF-MeanC	4.701082	3.282724e-16	***	5.380137e-14	***
SlopeF-SlopeC	-0.7602852	0.237021		0.9999488	



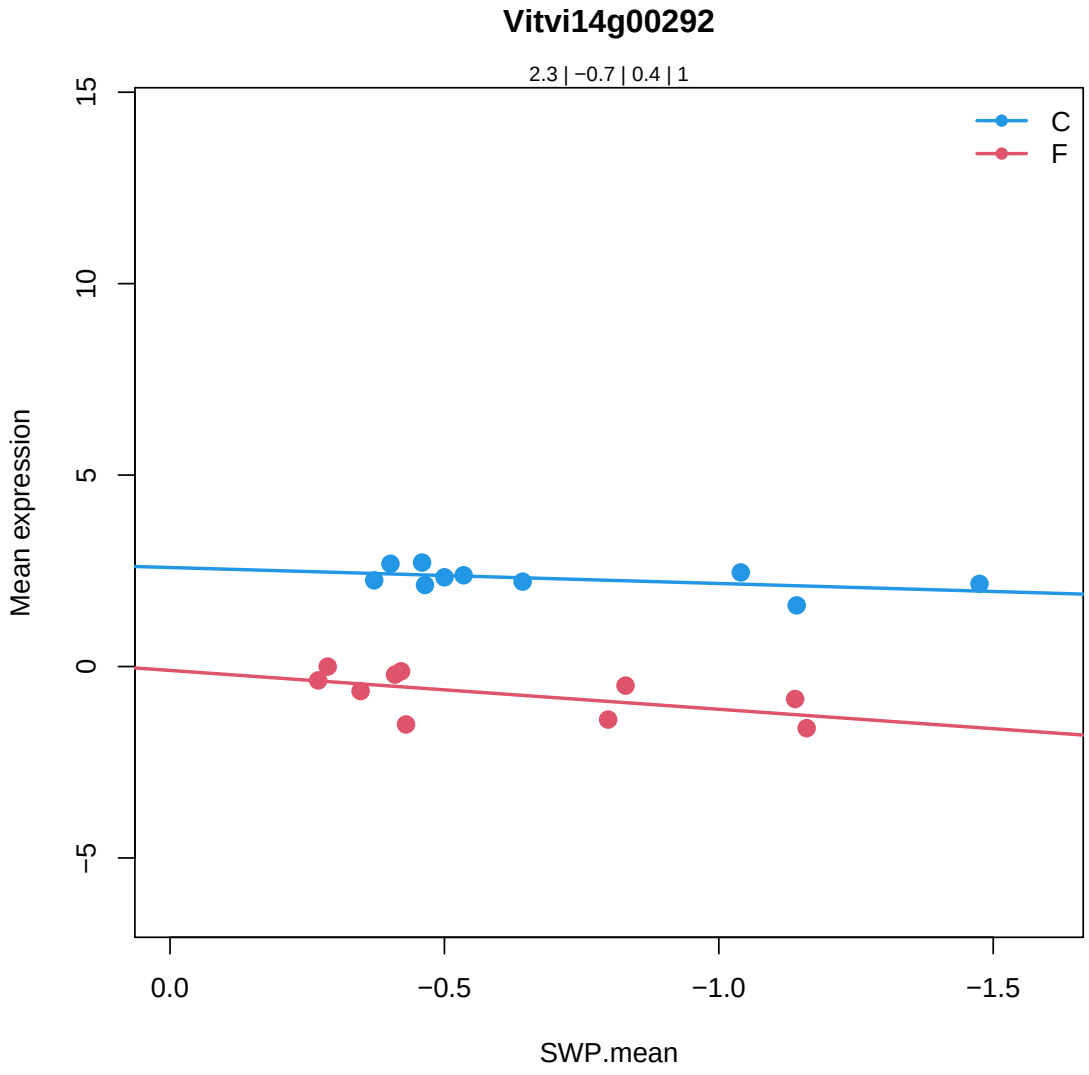
7.4.73 Vitvi14g00292: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g00292
        35.2
        not assigned.unknown
        NB-ARC domain-containing disease resistance protein |
        Chr4:13620977-13623934 REVERSE LENGTH=985 |
        201606
```

Coefficients for Vitvi14g00292.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.292092	1.009057e-13	***	1.549314e-13	***
SlopeC	0.417061	0.2894582		0.7810093	
MeanF-MeanC	-3.011858	4.340757e-13	***	4.241142e-11	***
SlopeF-SlopeC	0.597024	0.3078057		0.9999488	



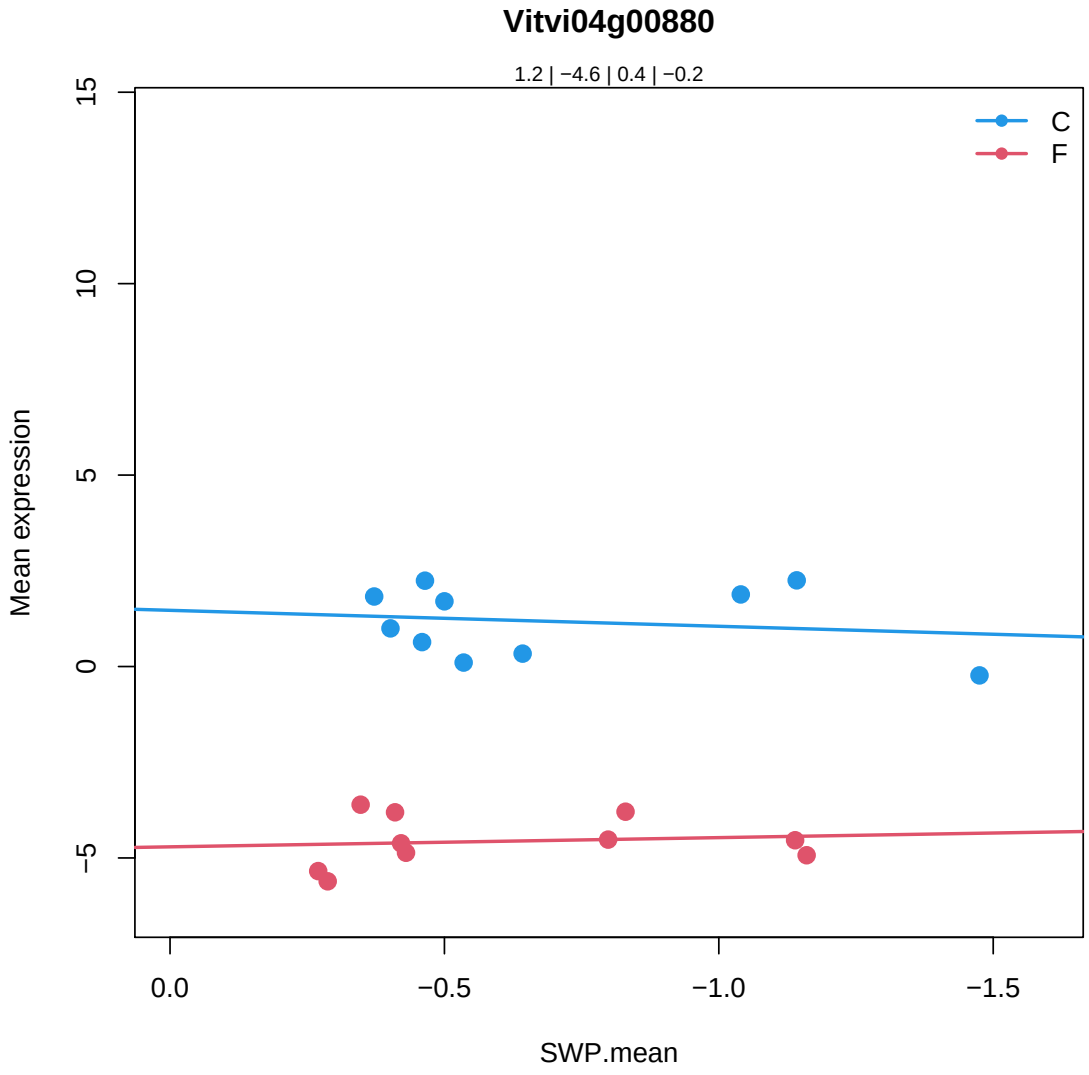
7.4.74 Vitvi04g00880: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00880
        26.9
        misc.glutathione S transferases
        glutathione S-transferase F11 |
        Chr3:735071-735877 FORWARD LENGTH=214 |
        201606
```

Coefficients for Vitvi04g00880.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.174587	8.50636e-05	***	9.405437e-05	***
SlopeC	0.4162185	0.5449479		0.8854168	
MeanF-MeanC	-5.737718	9.234523e-14	***	9.707076e-12	***
SlopeF-SlopeC	-0.6565215	0.5213969		0.9999488	



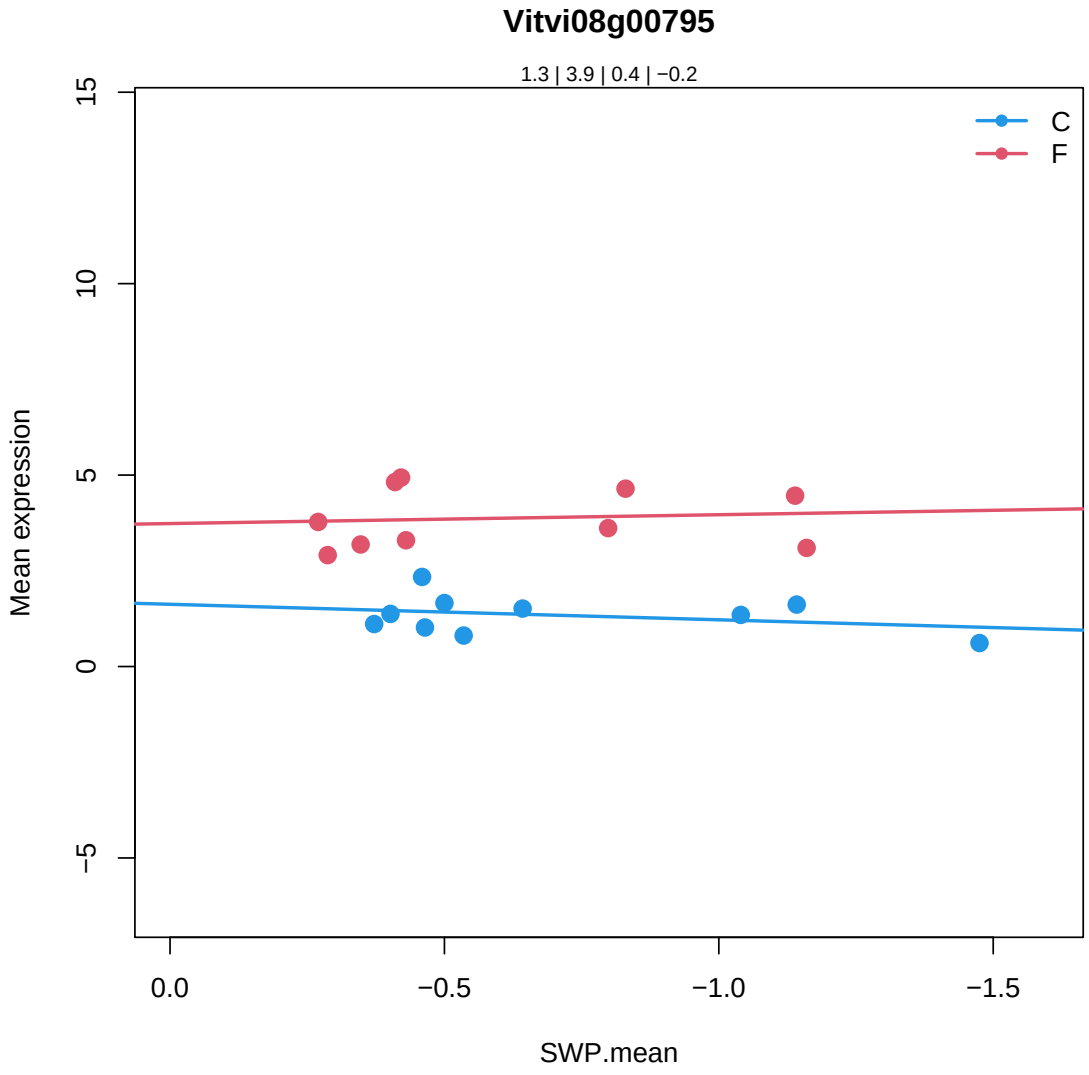
7.4.75 Vitvi08g00795: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g00795
        34.12
        transport.metal
        iron regulated 1 |
        Chr2:16104292-16105930 FORWARD LENGTH=379 |
        201606
```

Coefficients for Vitvi08g00795.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.340088	1.12549e-06	***	1.298027e-06	***
SlopeC	0.4054471	0.4742574		0.8622843	
MeanF-MeanC	2.534255	1.075366e-08	***	5.339e-07	***
SlopeF-SlopeC	-0.6361485	0.4509523		0.9999488	



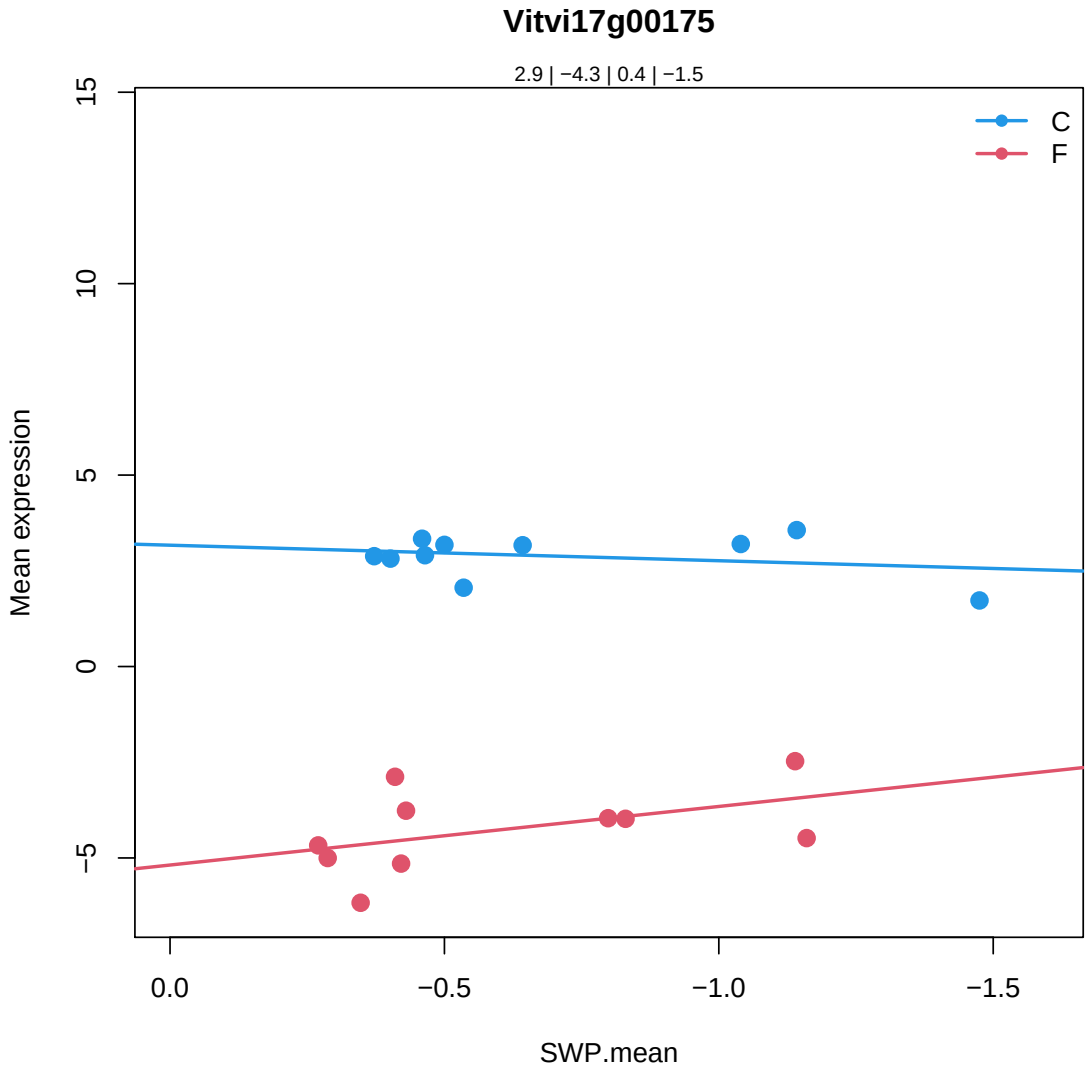
7.4.76 Vitvi17g00175: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00175
        30.2.25
        signalling.receptor kinases.wall associated kinase
        wall associated kinase 5 |
        Chr1:7429980-7432346 FORWARD LENGTH=733 |
        201606
```

Coefficients for Vitvi17g00175.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.883592	5.172864e-11	***	6.845355e-11	***
SlopeC	0.4052957	0.5492078		0.8871925	
MeanF-MeanC	-7.136685	8.065835e-16	***	1.193587e-13	***
SlopeF-SlopeC	-1.935313	0.06406735	.	0.9999488	



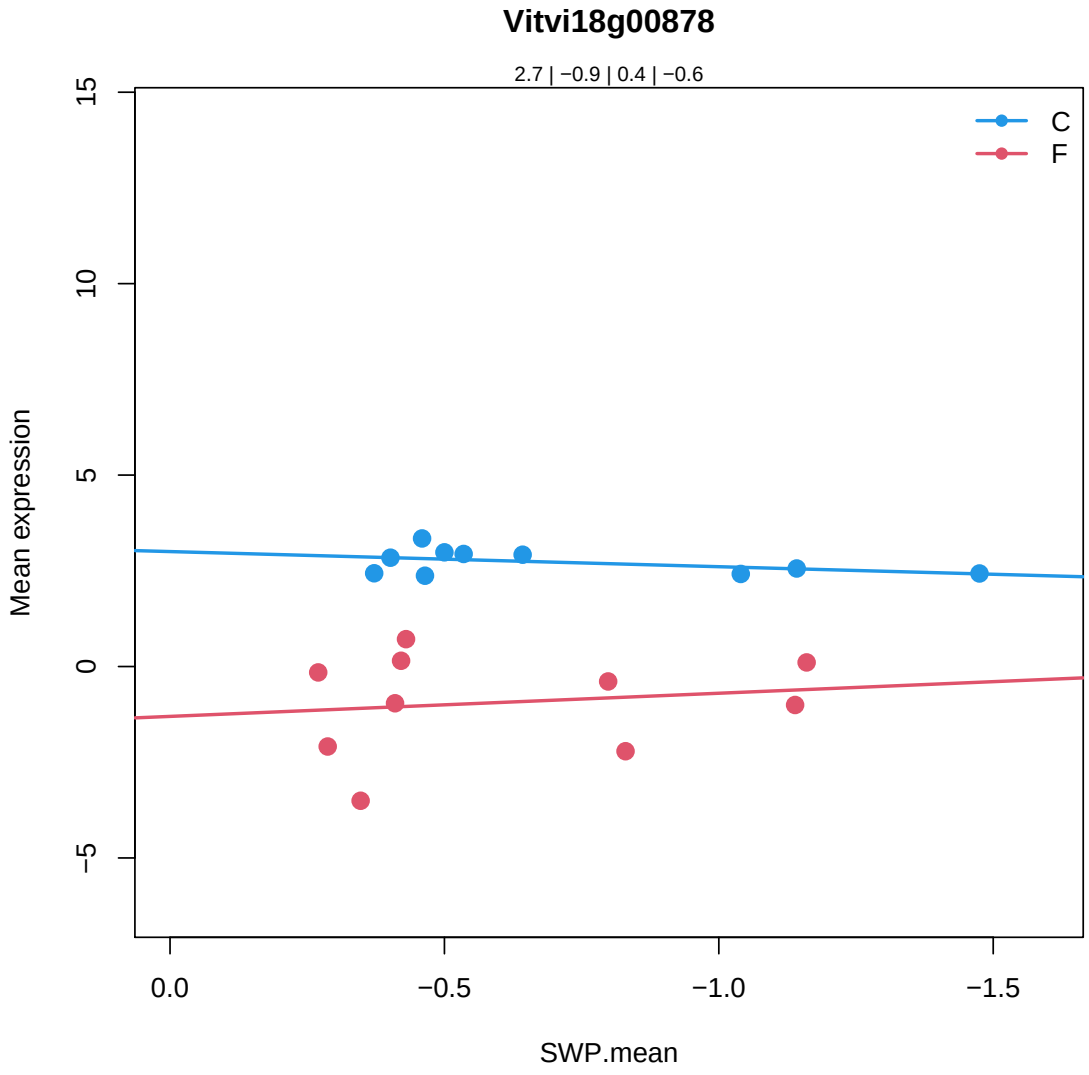
7.4.77 Vitvi18g00878: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00878
        26.10
        misc.cytochrome P450
        cytochrome P450%2C family 82%2C subfamily C%2C polypeptide 4 |
        Chr4:15452040-15453966 FORWARD LENGTH=524 |
        201606
```

Coefficients for Vitvi18g00878.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.724363	3.048733e-09	***	3.785029e-09	***
SlopeC	0.3950882	0.6207516		0.9092346	
MeanF-MeanC	-3.65896	7.494057e-09	***	3.769783e-07	***
SlopeF-SlopeC	-1.000008	0.4026699		0.9999488	



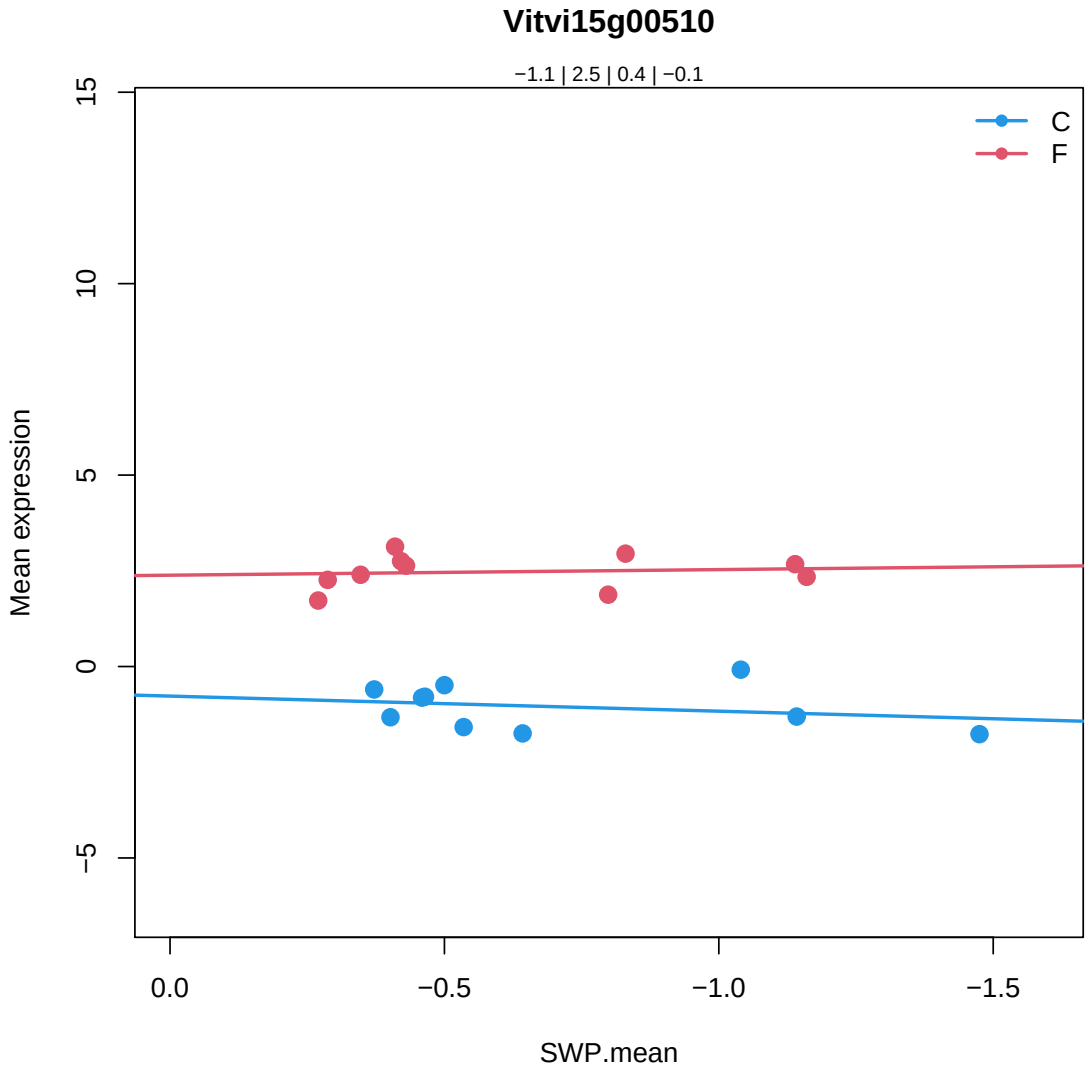
7.4.78 Vitvi15g00510: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g00510
        16.5.1.1.1.11
        secondary metabolism.sulfur-containing.glucosinolates.synthesis.alipha
        senescence-related gene 1 |
        Chr1:5820258-5821741 FORWARD LENGTH=358 |
        201606
```

Coefficients for Vitvi15g00510.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.050028	2.480227e-06	***	2.837258e-06	***
SlopeC	0.3941475	0.4015109		0.8352435	
MeanF-MeanC	3.523845	7.070508e-13	***	6.492089e-11	***
SlopeF-SlopeC	-0.5403209	0.4391315		0.9999488	



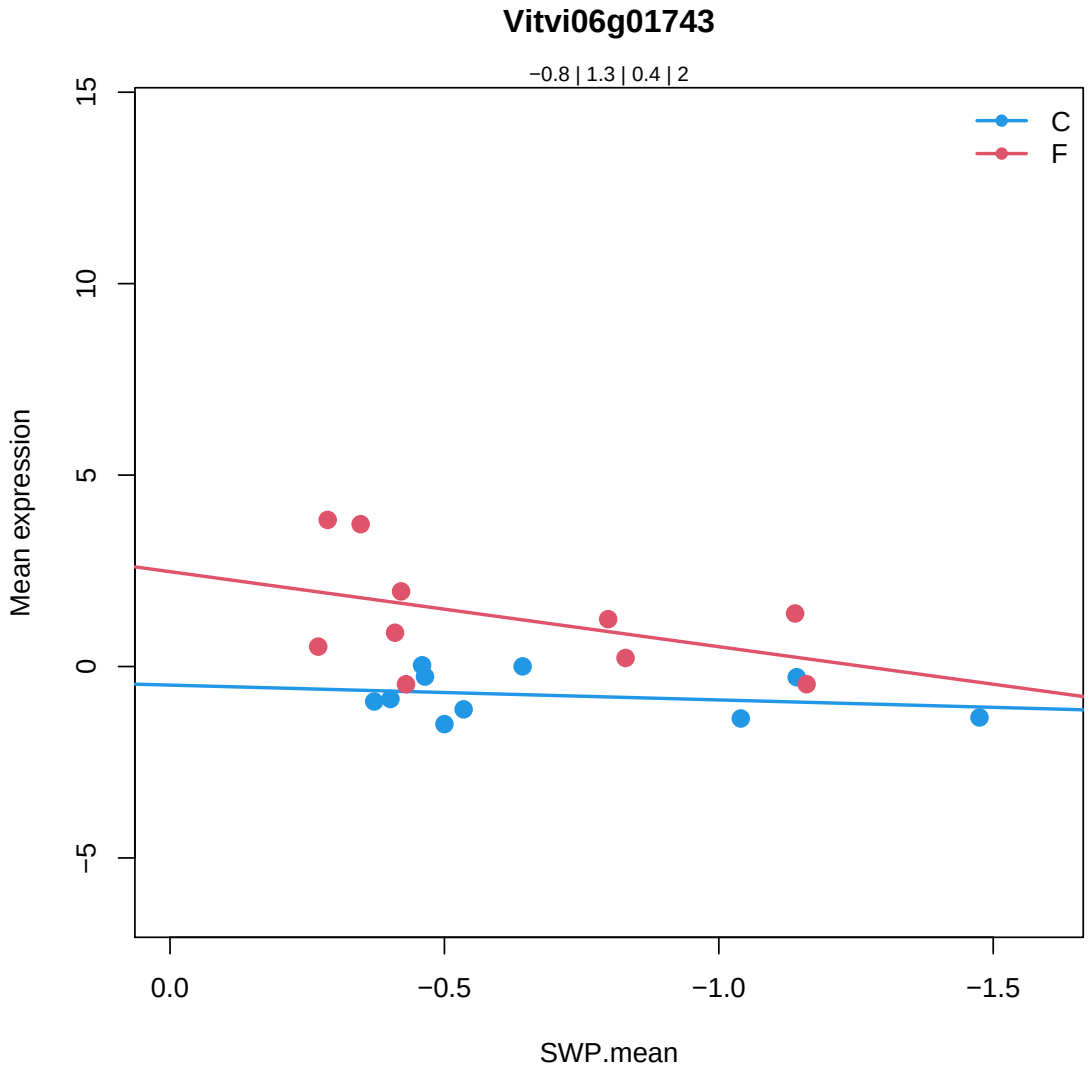
7.4.79 Vitvi06g01743: type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01743
        35.2
        not assigned.unknown
        UDP-glucosyl transferase 71C4 |
        Chr1:2225963-2227402 FORWARD LENGTH=479 |
        201606
```

Coefficients for Vitvi06g01743.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.7579229	0.02425504	*	0.02545585	*
SlopeC	0.3874884	0.6604477		0.9219292	
MeanF-MeanC	2.040905	0.0001421972	***	0.002421403	**
SlopeF-SlopeC	1.572361	0.2377642		0.9999488	



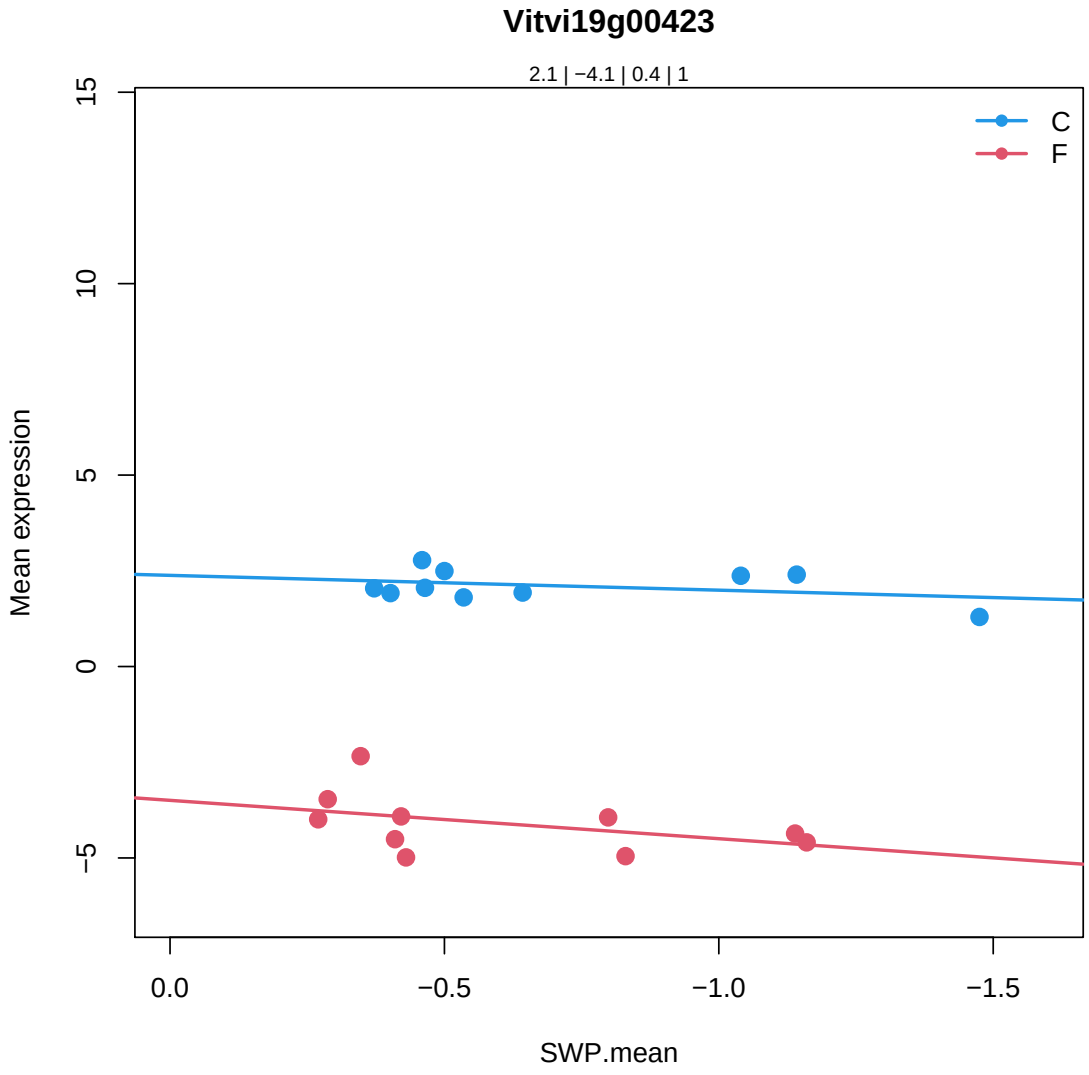
7.4.80 Vitvi19g00423: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g00423
        31.1
        cell.organisation
        ankyrin repeat family protein |
        Chr1:914222-916222 REVERSE LENGTH=616 |
        201606
```

Coefficients for Vitvi19g00423.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.108583	1.187907e-10	***	1.549912e-10	***
SlopeC	0.3867001	0.4558144		0.8579805	
MeanF-MeanC	-6.214375	5.518305e-17	***	1.051375e-14	***
SlopeF-SlopeC	0.6148745	0.4260505		0.9999488	



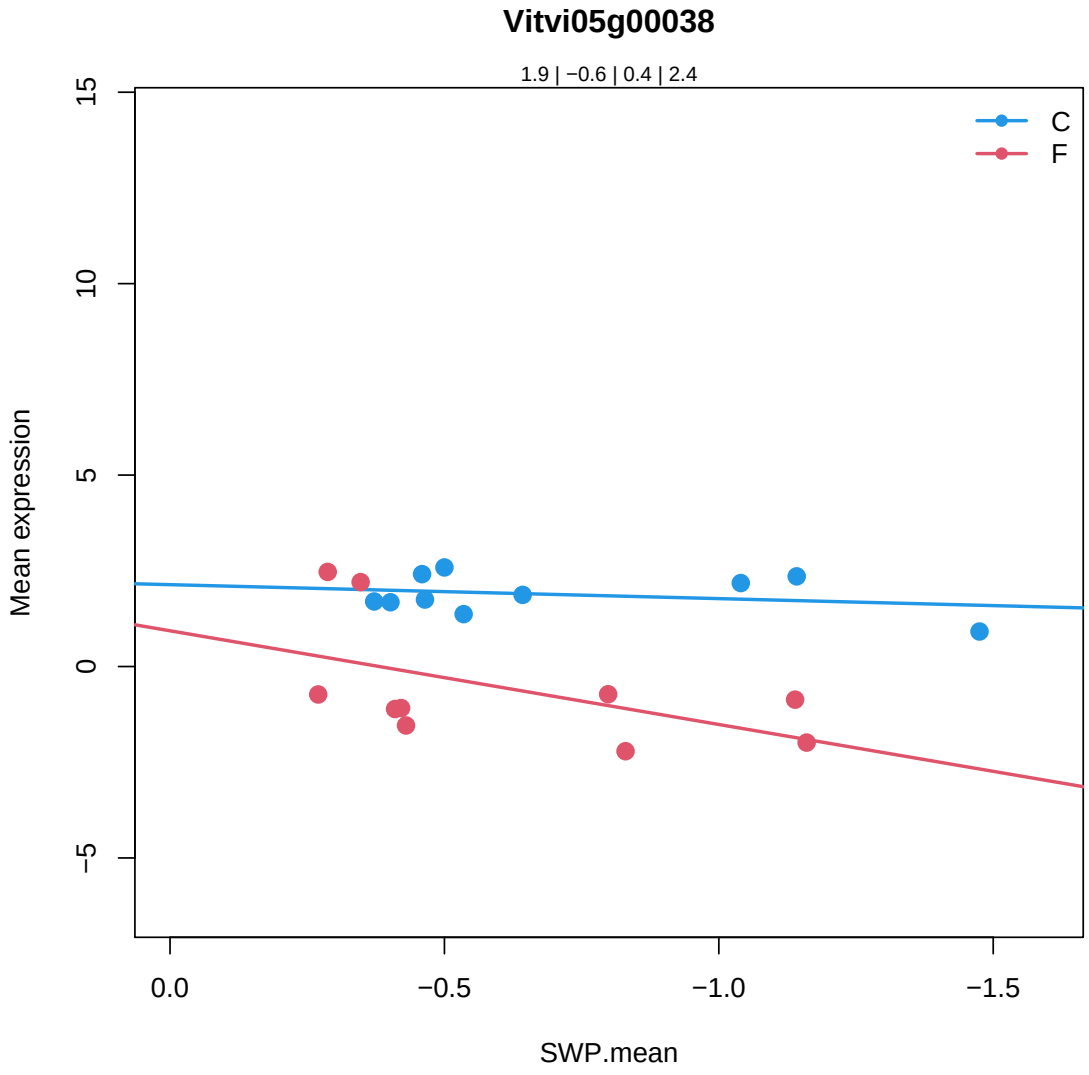
7.4.81 Vitvi05g00038: type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00038
        26.3.5
        misc.gluco-, galacto- and mannosidases.glycosyl hydrolase family 5
        alpha/beta-Hydrolases superfamily protein |
        Chr4:1035722-1037403 FORWARD LENGTH=324 |
        201606
```

Coefficients for Vitvi05g00038.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.881532	4.363251e-06	***	4.964146e-06	***
SlopeC	0.3647677	0.6752848		0.9252688	
MeanF-MeanC	-2.439425	1.40955e-05	***	0.0003437499	***
SlopeF-SlopeC	2.082283	0.1179377		0.9999488	



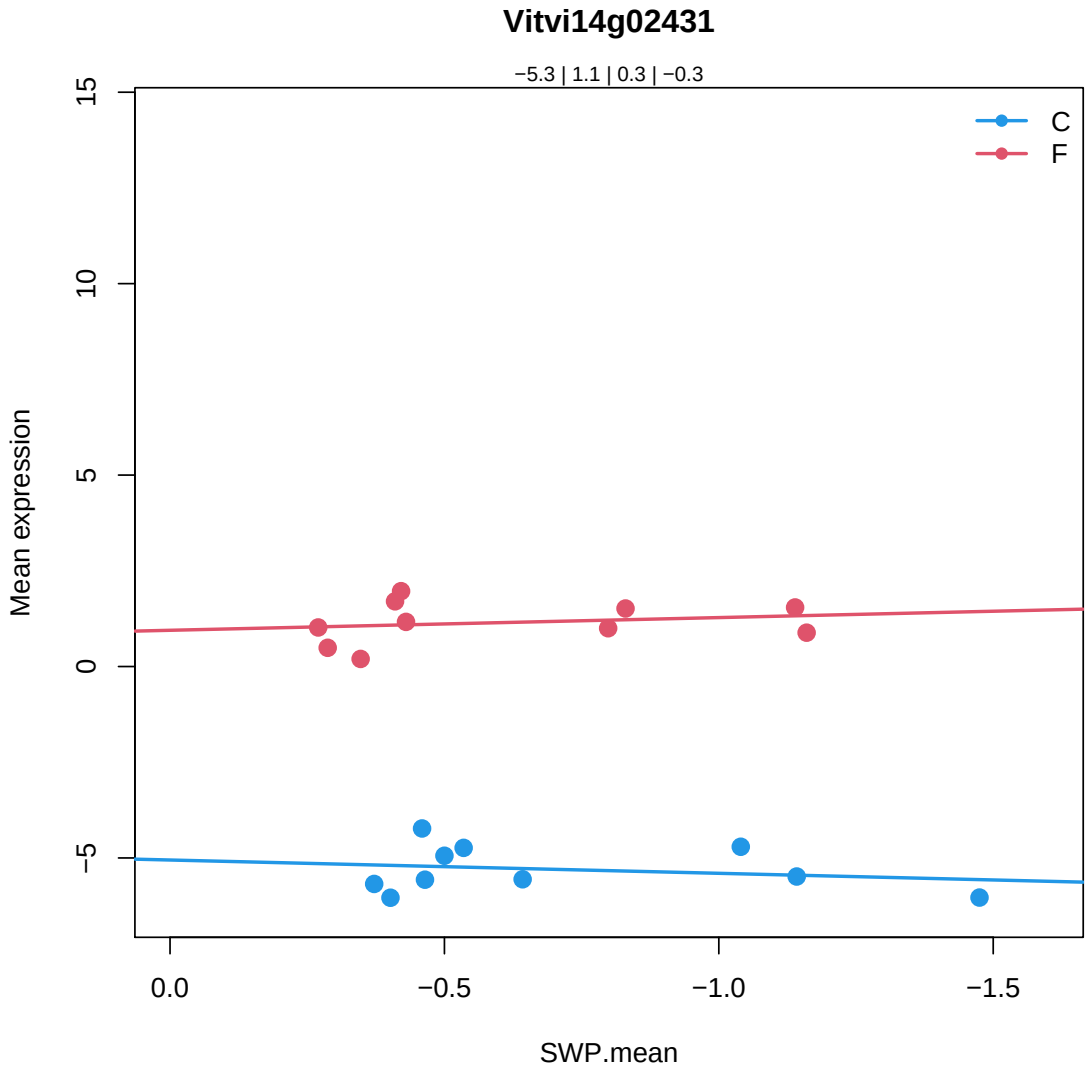
7.4.82 Vitvi14g02431: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g02431
        35.2
        not assigned.unknown
        proline-rich family protein |
        Chr3:2746014-2748326 FORWARD LENGTH=541 |
        201606
```

Coefficients for Vitvi14g02431.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.297885	9.851675e-19	***	3.401115e-18	***
SlopeC	0.3475746	0.4994736		0.8698903	
MeanF-MeanC	6.446191	2.26784e-17	***	4.735126e-15	***
SlopeF-SlopeC	-0.6795796	0.3768597		0.9999488	



7.4.83 Vitvi16g00461: type3

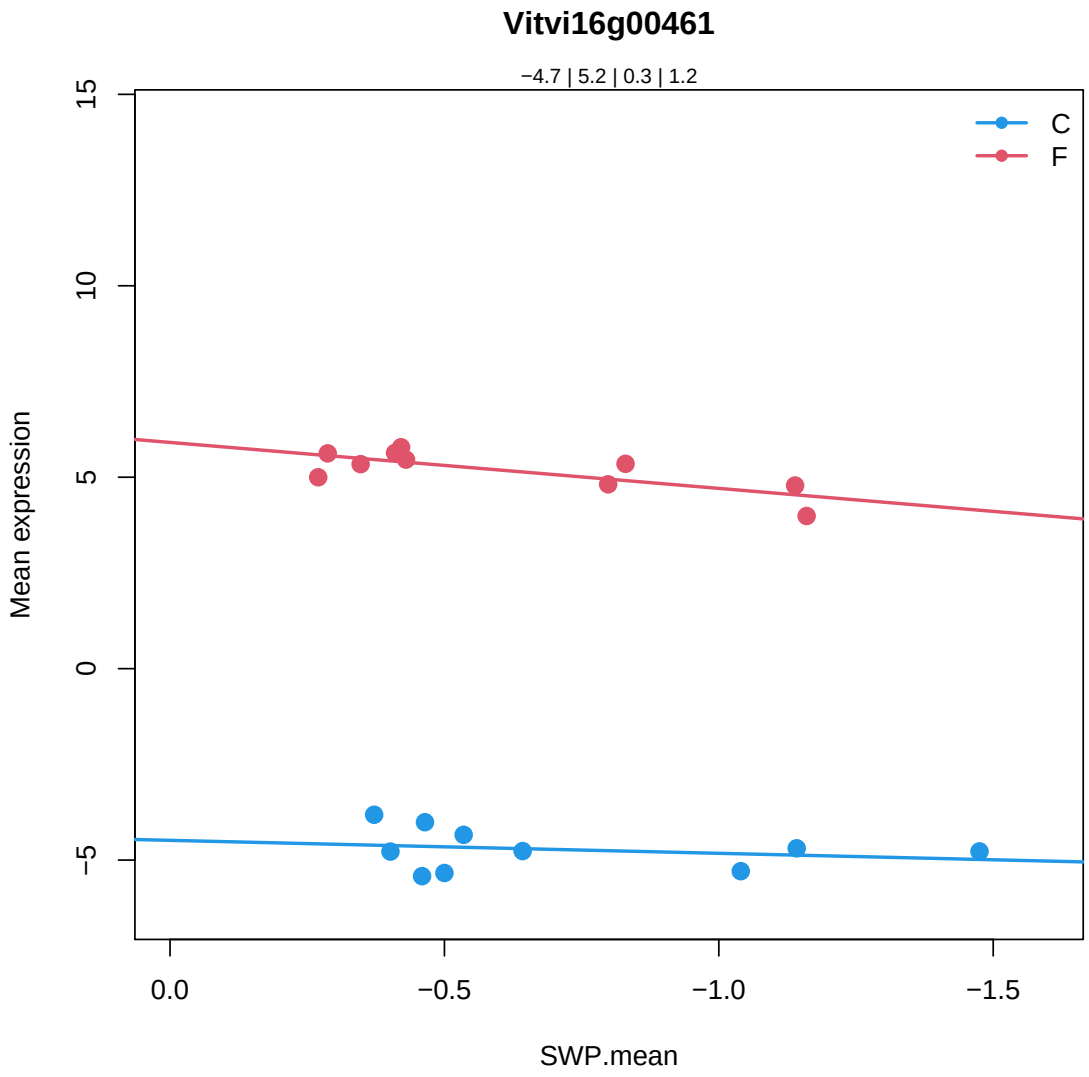
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g00461
        20.1.2
        stress.biotic.receptors
        receptor like protein 6 |
        Chr1:17183550-17186534 REVERSE LENGTH=994 |
        201606

Vitvi16g00461
        30.2.99
        signalling.receptor kinases.misc
        receptor like protein 6 |
        Chr1:17183550-17186534 REVERSE LENGTH=994 |
        201606
```

Coefficients for Vitvi16g00461.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-4.722292	2.494196e-19	***	1.037569e-18	***
SlopeC	0.3383841	0.4318552		0.8481624	
MeanF-MeanC	9.899645	6.085779e-23	***	7.701512e-20	***
SlopeF-SlopeC	0.8621788	0.1844285		0.9999488	


Vitvi16g00461
−4.7 | 5.2 | 0.3 | 1.2
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

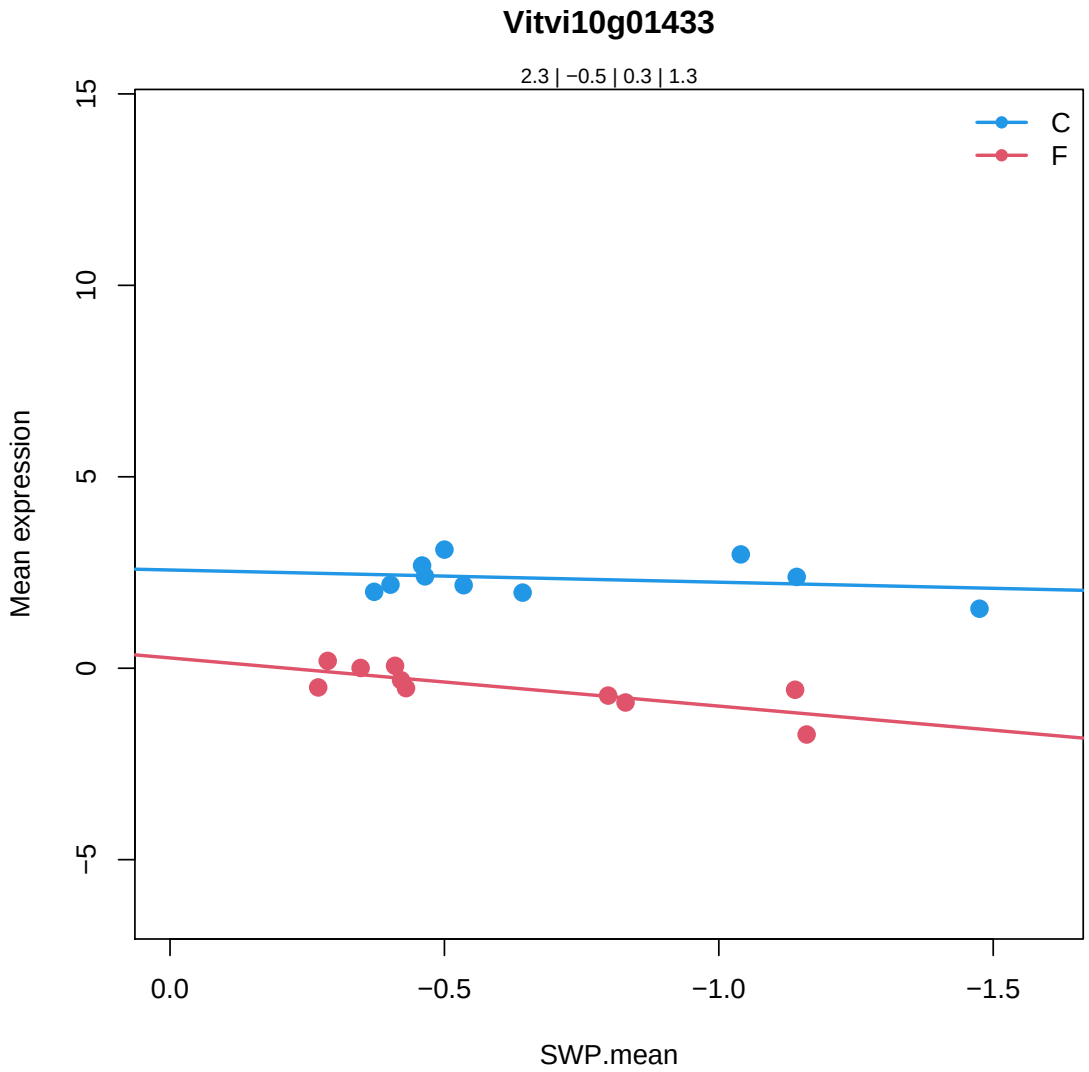
7.4.84 Vitvi10g01433: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g01433
        35.2
        not assigned.unknown
        Cc-nbs-lrr, resistance protein
```

Coefficients for Vitvi10g01433.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.341082	1.16306e-13	***	1.777357e-13	***
SlopeC	0.319163	0.4279343		0.8478579	
MeanF-MeanC	-2.838822	2.40963e-12	***	2.063347e-10	***
SlopeF-SlopeC	0.9389207	0.124867		0.9999488	



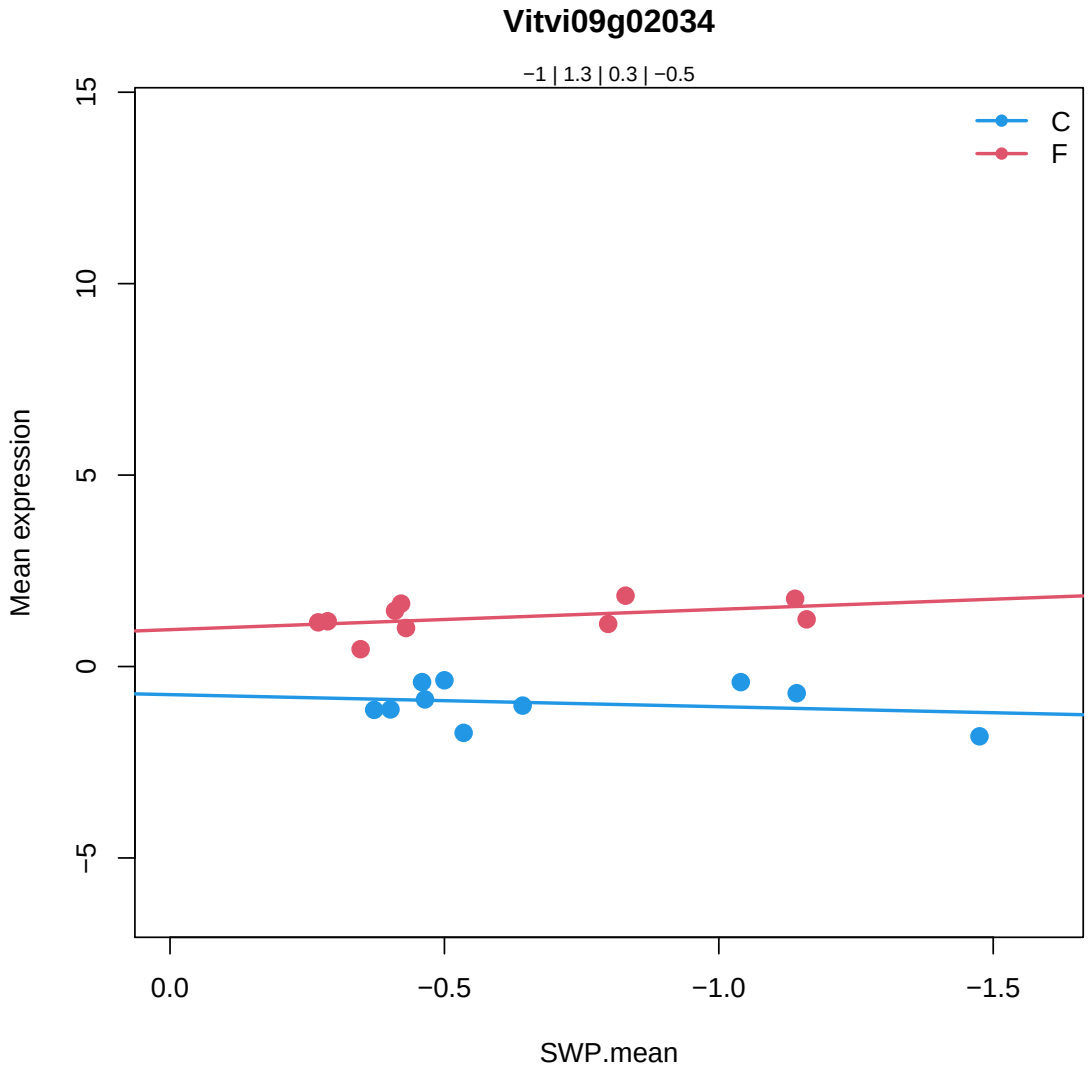
7.4.85 Vitvi09g02034: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g02034
        35.2
        not assigned.unknown
        Disease resistance protein (CC-NBS-LRR class) family |
        Chr5:25283252-25286002 REVERSE LENGTH=888 |
        201606
```

Coefficients for Vitvi09g02034.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.9561502	2.494946e-06	***	2.853667e-06	***
SlopeC	0.3149011	0.4610207		0.8603302	
MeanF-MeanC	2.241888	6.381769e-10	***	3.890837e-08	***
SlopeF-SlopeC	-0.8453521	0.1898639		0.9999488	



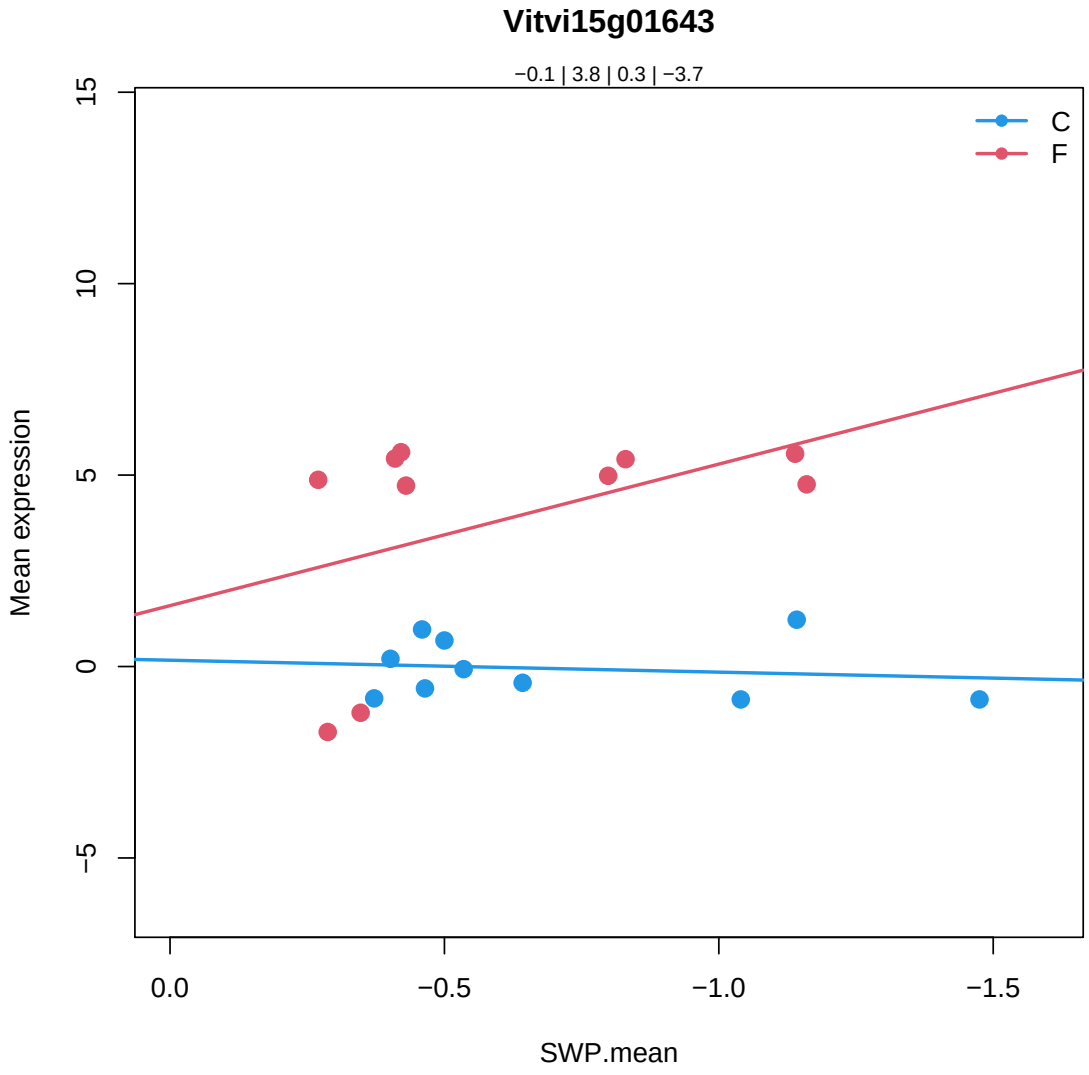
7.4.86 Vitvi15g01643: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g01643
        16.8.1.12
        secondary metabolism.flavonoids.anthocyanins.anthocyanidin 3-O-glucosy
        UDP-Glycosyltransferase superfamily protein |
        Chr2:9593012-9594424 FORWARD LENGTH=470 |
        201606
```

Coefficients for Vitvi15g01643.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.05461697	0.9210385		0.922673	
SlopeC	0.3115766	0.8389936		0.9693055	
MeanF-MeanC	3.897101	4.895259e-05	***	0.0009663134	***
SlopeF-SlopeC	-4.007713	0.08969632	.	0.9999488	



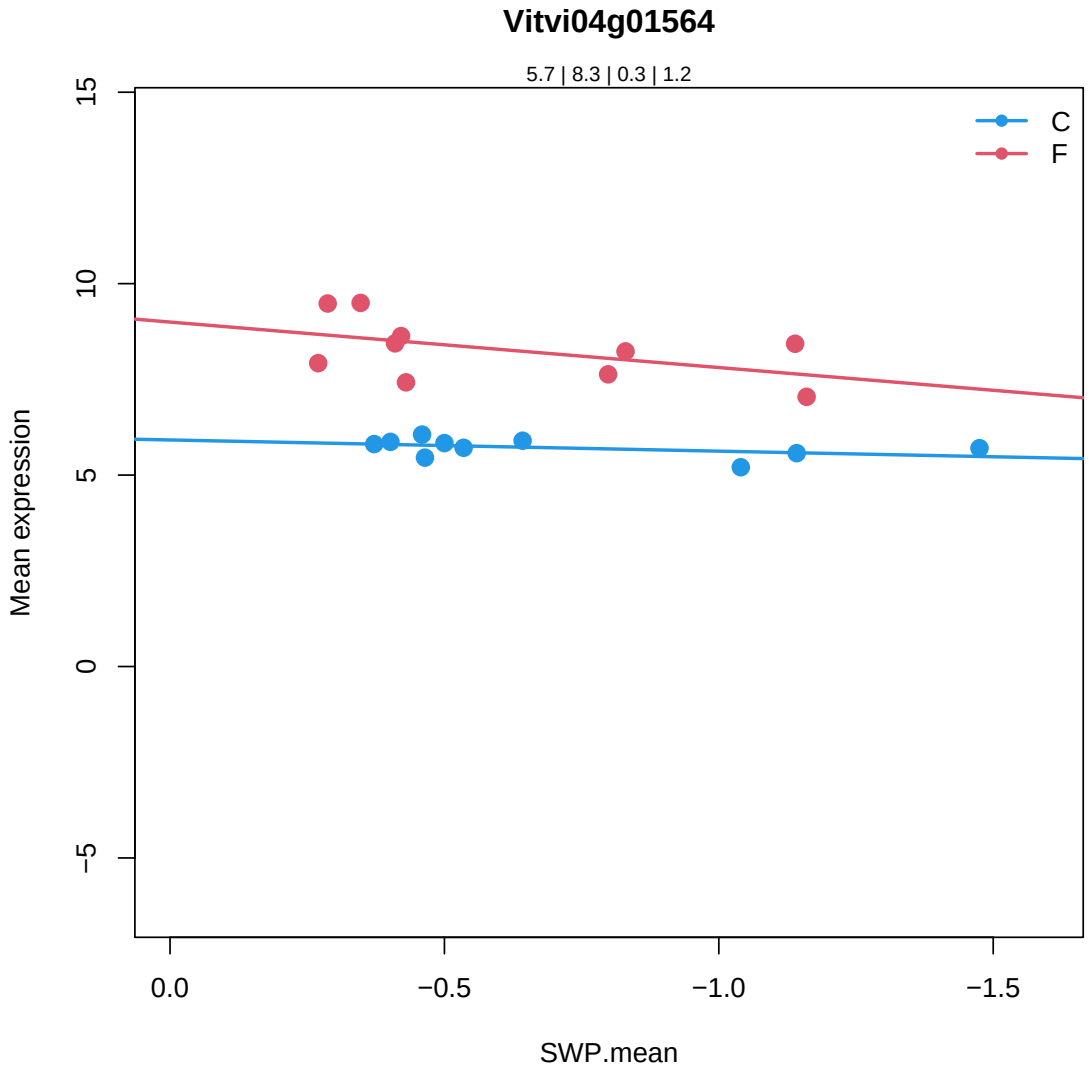
7.4.87 Vitvi04g01564: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01564
        21.6
        redox.dismutases and catalases
        catalase 2 |
        Chr4:16700937-16702955 REVERSE LENGTH=492 |
        201606
```

Coefficients for Vitvi04g01564.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.711654	4.527077e-20	***	2.436834e-19	***
SlopeC	0.2922377	0.5415533		0.8844269	
MeanF-MeanC	2.56113	4.670918e-10	***	2.941906e-08	***
SlopeF-SlopeC	0.8958716	0.2149973		0.9999488	



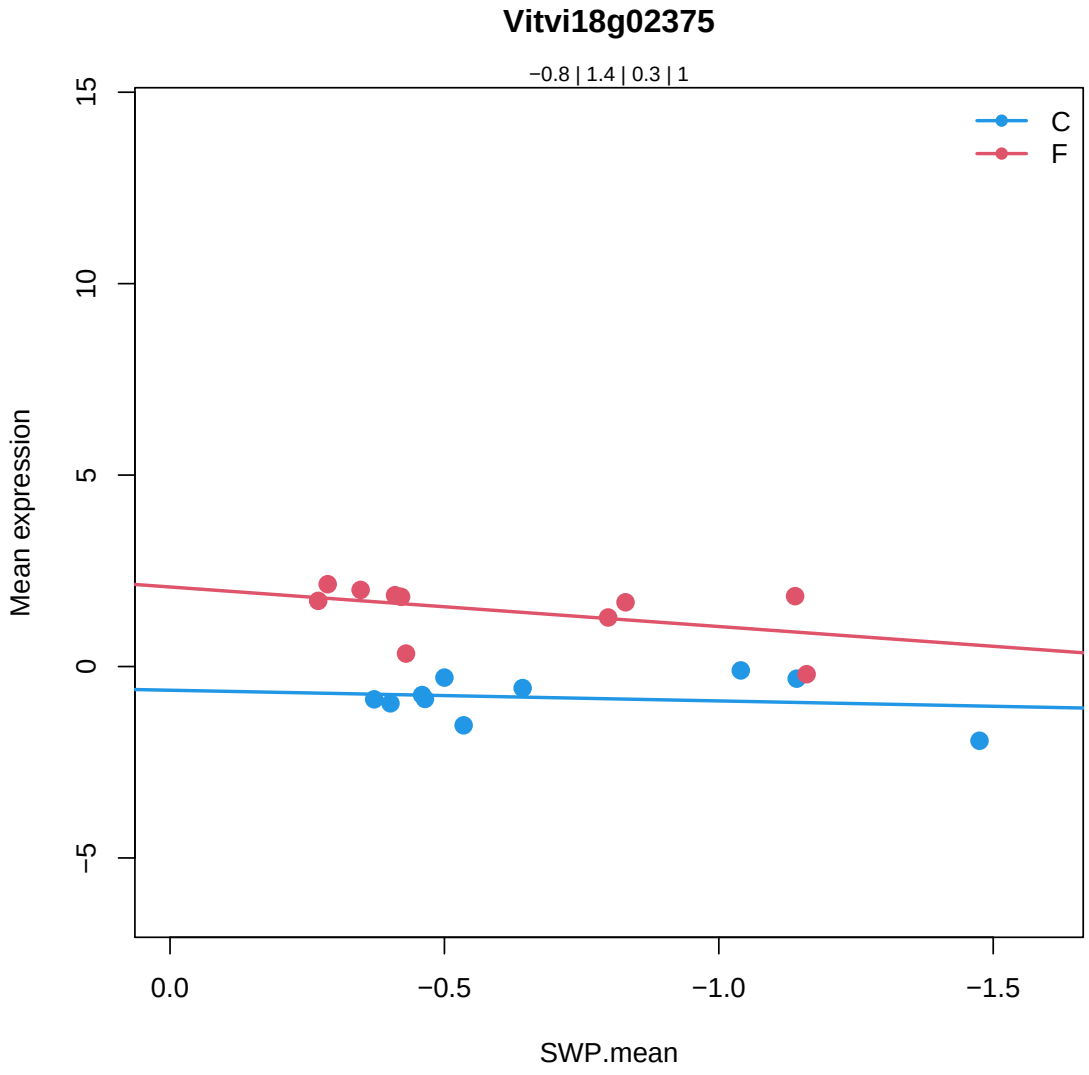
7.4.88 Vitvi18g02375: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02375
        20.1.2.2
        stress.biotic.receptors.TIR-NBS-LRR
        disease resistance protein (TIR-NBS-LRR class) |
        Chr5:5822999-5827153 FORWARD LENGTH=1294 |
        201606
```

Coefficients for Vitvi18g02375.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.8159101	0.000452161	***	0.0004929431	***
SlopeC	0.2794751	0.6157693		0.9075408	
MeanF-MeanC	2.263943	5.611324e-08	***	2.450653e-06	***
SlopeF-SlopeC	0.7533646	0.3666132		0.9999488	



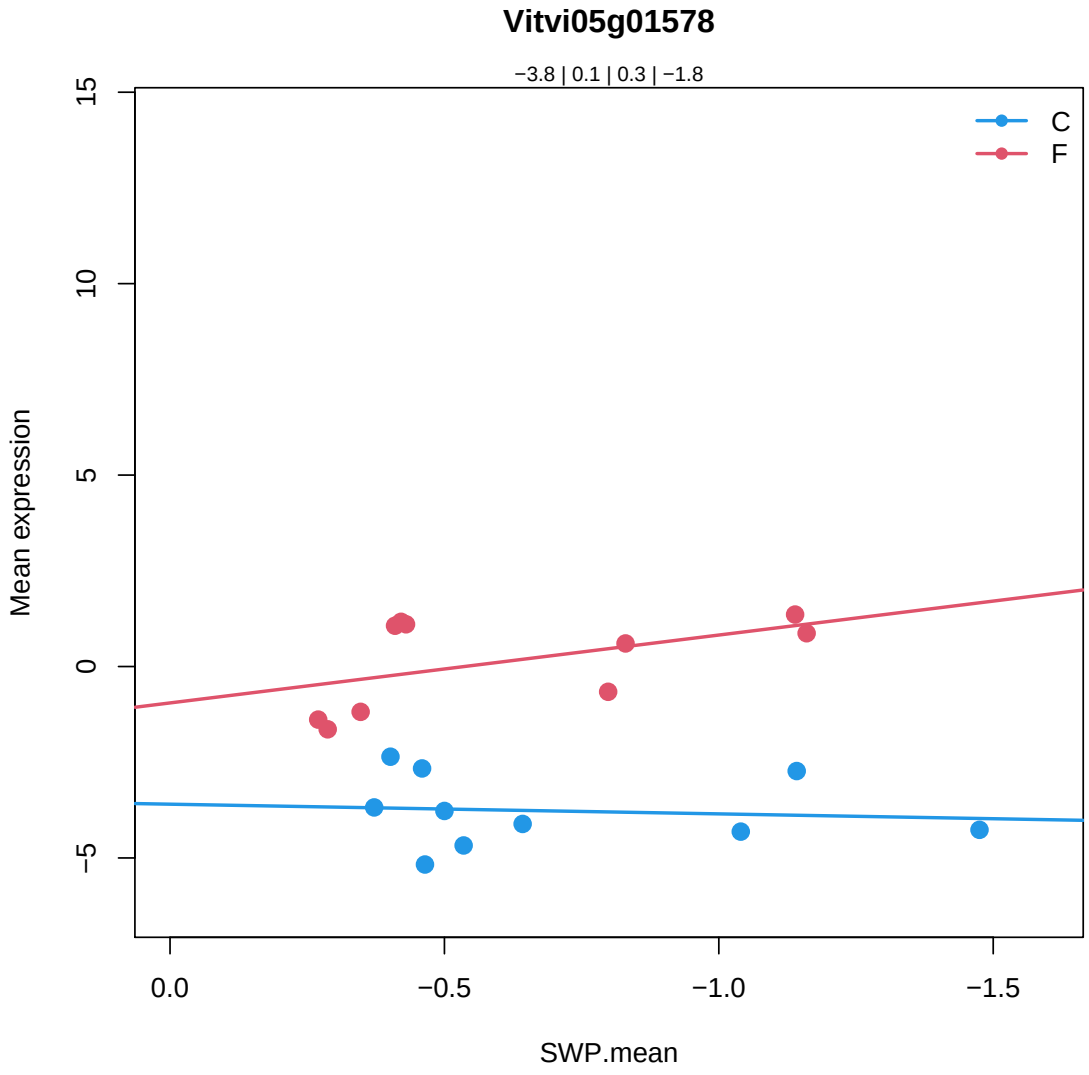
7.4.89 Vitvi05g01578: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01578
        35.2
        not assigned.unknown
        homolog of carrot EP3-3 chitinase |
        Chr3:20145935-20147034 FORWARD LENGTH=273 |
        201606
```

Coefficients for Vitvi05g01578.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-3.773614	1.602428e-11	***	2.168121e-11	***
SlopeC	0.2532287	0.7602289		0.9479775	
MeanF-MeanC	3.902919	4.915293e-09	***	2.531044e-07	***
SlopeF-SlopeC	-2.026263	0.1111117		0.9999488	



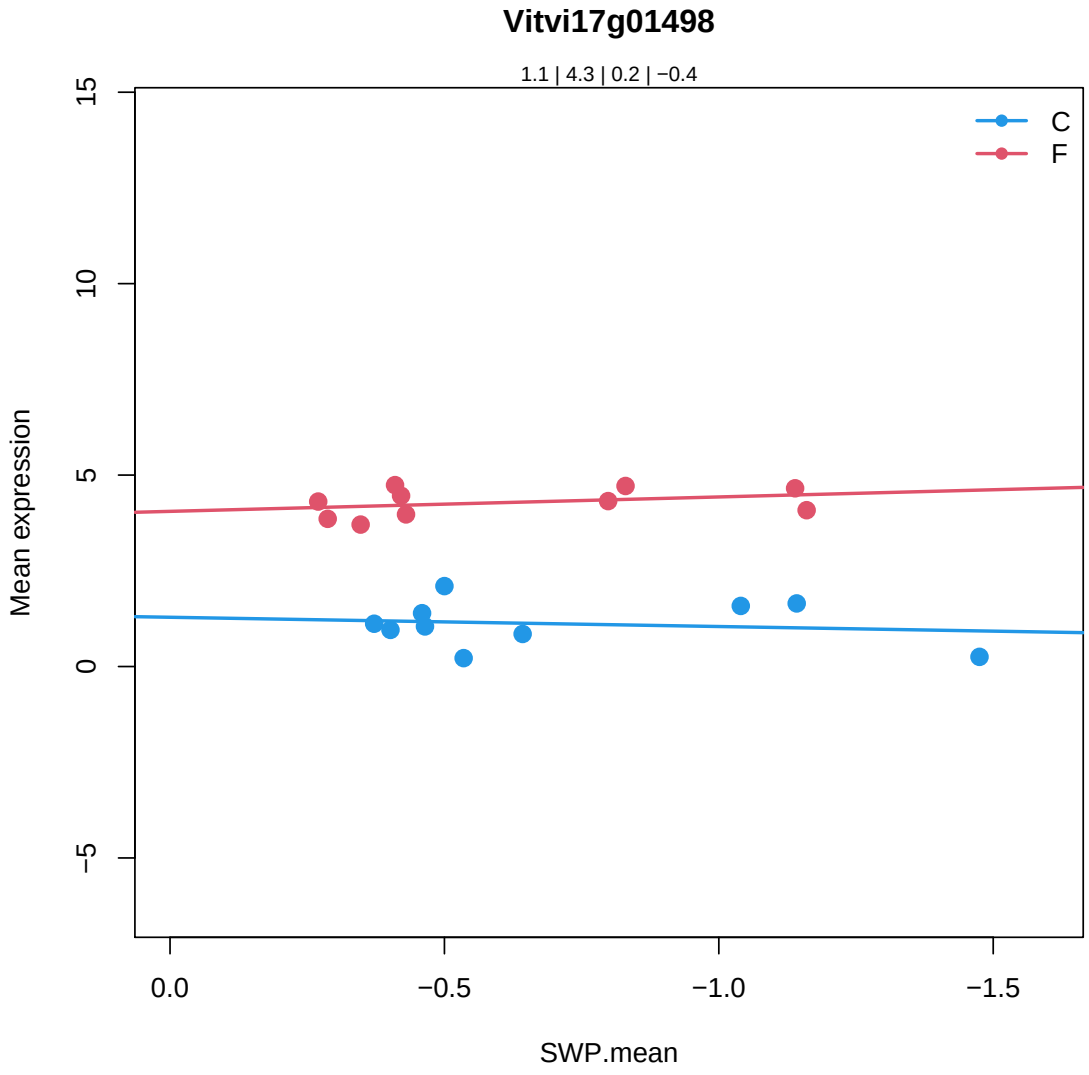
7.4.90 Vitvi17g01498: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g01498
        35.2
        not assigned.unknown
        UDP-Glycosyltransferase superfamily protein |
        Chr3:368840-370484 REVERSE LENGTH=464 |
        201606
```

Coefficients for Vitvi17g01498.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.116419	6.122047e-07	***	7.108421e-07	***
SlopeC	0.2417754	0.5927262		0.9005224	
MeanF-MeanC	3.165145	2.984236e-12	***	2.526985e-10	***
SlopeF-SlopeC	-0.6183683	0.3611582		0.9999488	



7.4.91 Vitvi11g00865: type3 | type4

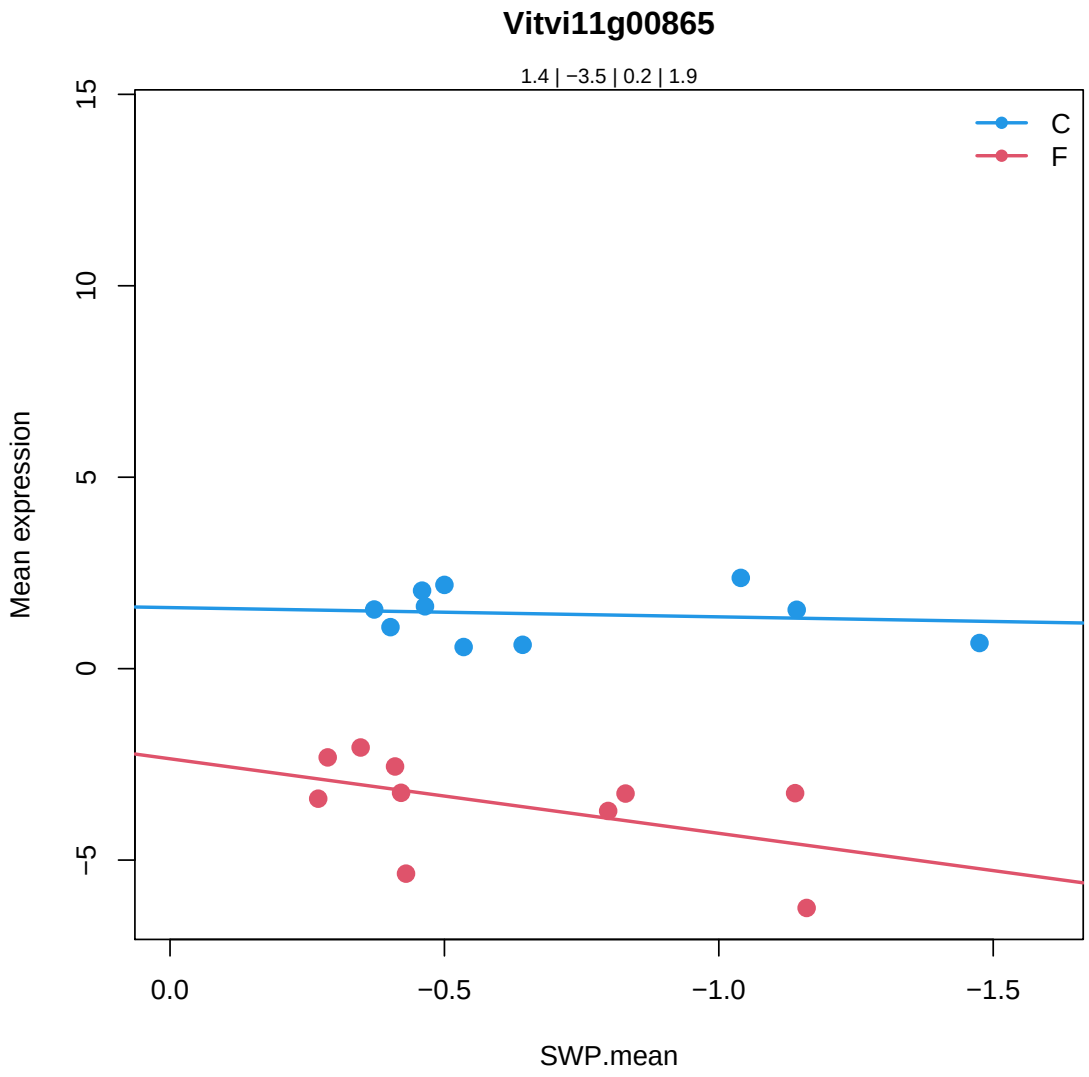
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00865
        20
        stress
        Ankyrin repeat family protein |
        Chr5:1354240-1356754 REVERSE LENGTH=669 |
        201606

Vitvi11g00865
        19.99
        tetrapyrrole synthesis.unspecified
        Ankyrin repeat family protein |
        Chr5:1354240-1356754 REVERSE LENGTH=669 |
        201606
```

Coefficients for Vitvi11g00865.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.424545	4.543505e-05	***	5.050843e-05	***
SlopeC	0.241433	0.7594168		0.9479775	
MeanF-MeanC	-4.965309	2.386458e-11	***	1.774361e-09	***
SlopeF-SlopeC	1.705682	0.1554573		0.9999488	


Vitvi11g00865
1.4 | −3.5 | 0.2 | 1.9
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

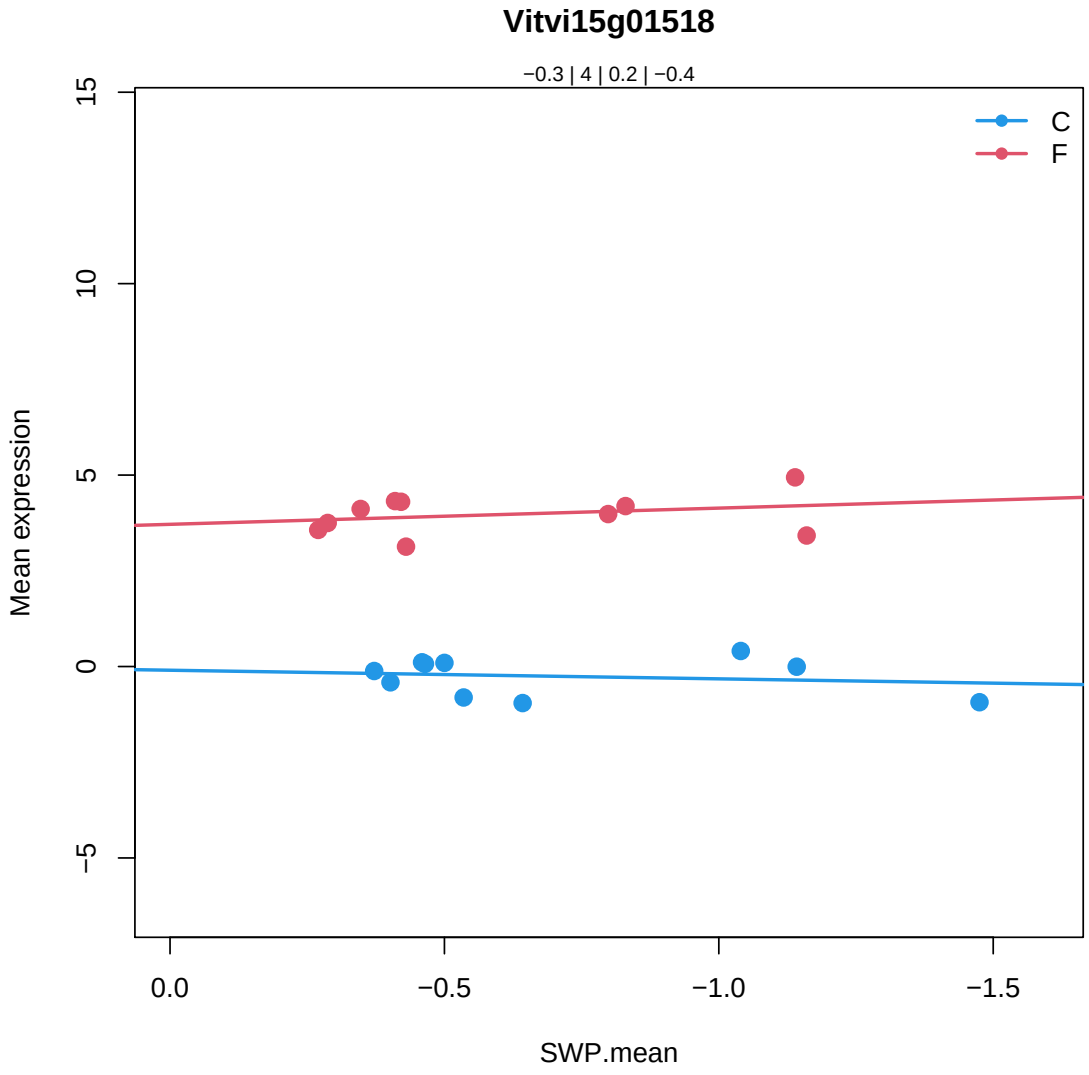
7.4.92 Vitvi15g01518: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g01518
        35.2
        not assigned.unknown
        cytochrome P450%2C family 76%2C subfamily C%2C polypeptide 4 |
        Chr2:18773541-18775654 REVERSE LENGTH=511 |
        201606
```

Coefficients for Vitvi15g01518.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.2552639	0.1310599		0.1351383	
SlopeC	0.2250984	0.6238153		0.9099454	
MeanF-MeanC	4.227029	1.310937e-14	***	1.665108e-12	***
SlopeF-SlopeC	-0.6486406	0.3460733		0.9999488	



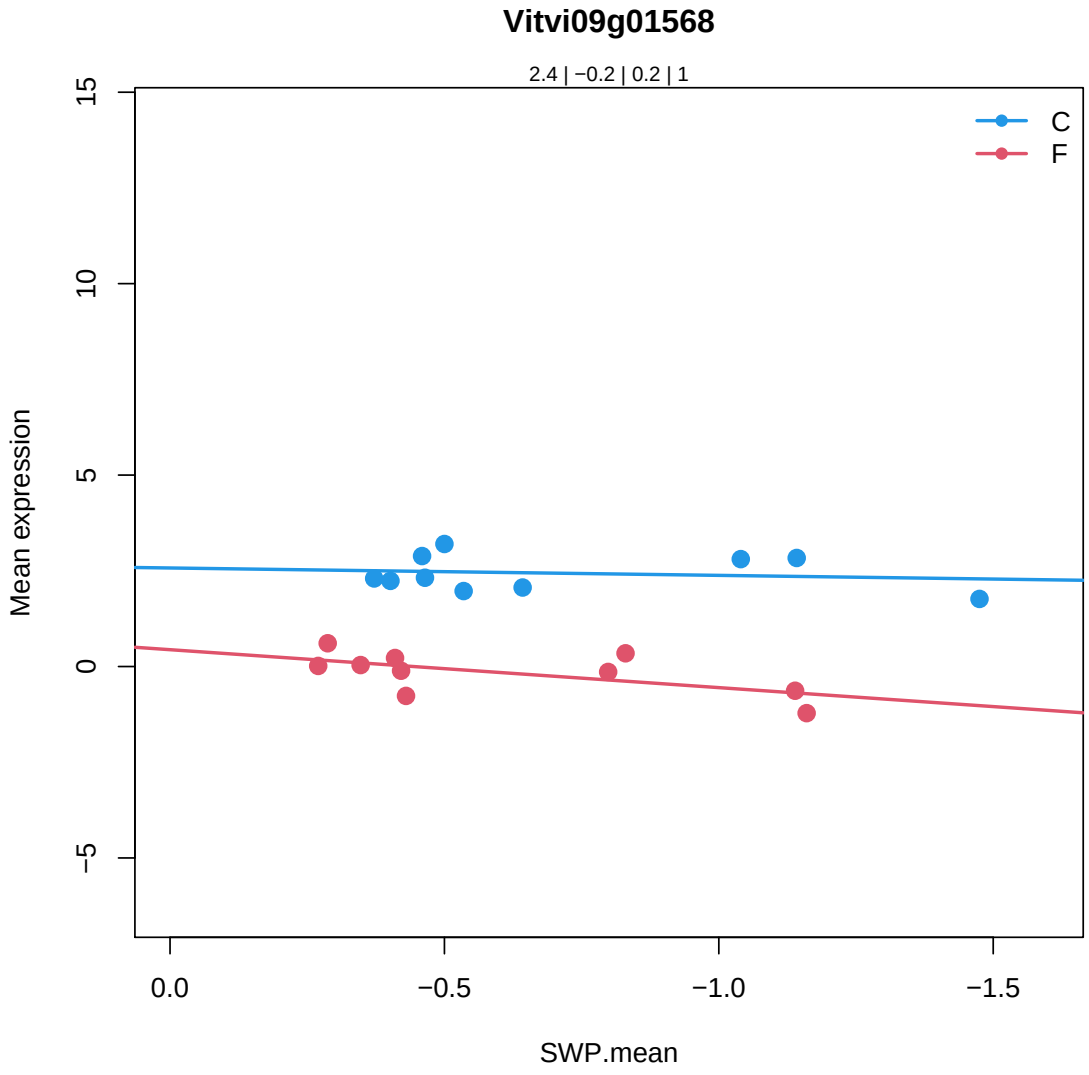
7.4.93 Vitvi09g01568: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g01568
        35.2
        not assigned.unknown
        Disease resistance protein (CC-NBS-LRR class) family |
        Chr5:25283252-25286002 REVERSE LENGTH=888 |
        201606
```

Coefficients for Vitvi09g01568.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.437894	2.000817e-13	***	3.008726e-13	***
SlopeC	0.1927476	0.652963		0.919485	
MeanF-MeanC	-2.602079	4.676273e-11	***	3.426719e-09	***
SlopeF-SlopeC	0.7978776	0.2182953		0.9999488	



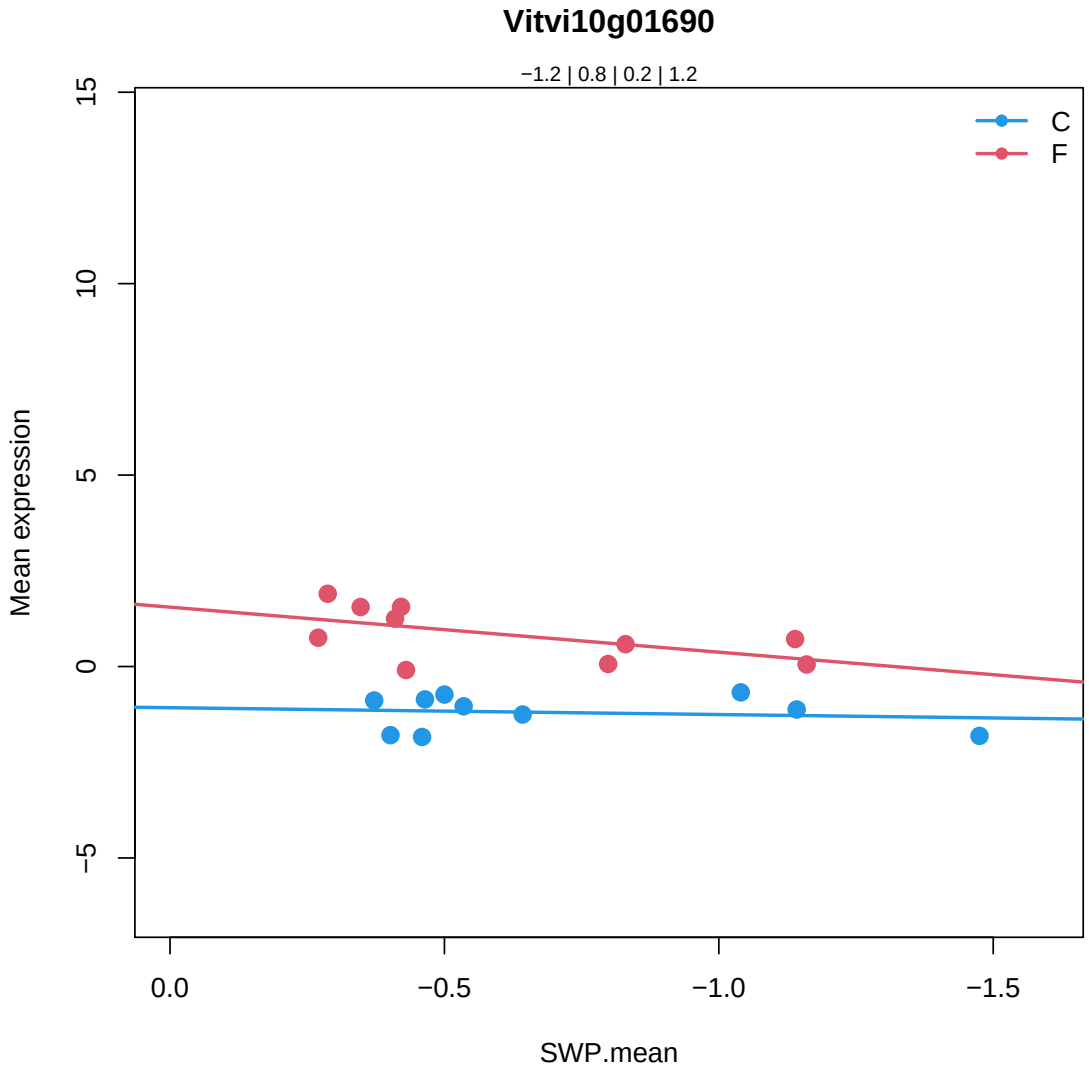
7.4.94 Vitvi10g01690: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g01690
        34.15
        transport.potassium
        Outward rectifying potassium channel protein |
        Chr5:22531718-22532893 FORWARD LENGTH=363 |
        201606
```

Coefficients for Vitvi10g01690.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.201545	4.83426e-07	***	5.626006e-07	***
SlopeC	0.1783541	0.7091412		0.9346979	
MeanF-MeanC	2.035534	2.674266e-08	***	1.231455e-06	***
SlopeF-SlopeC	0.9974776	0.1698717		0.9999488	



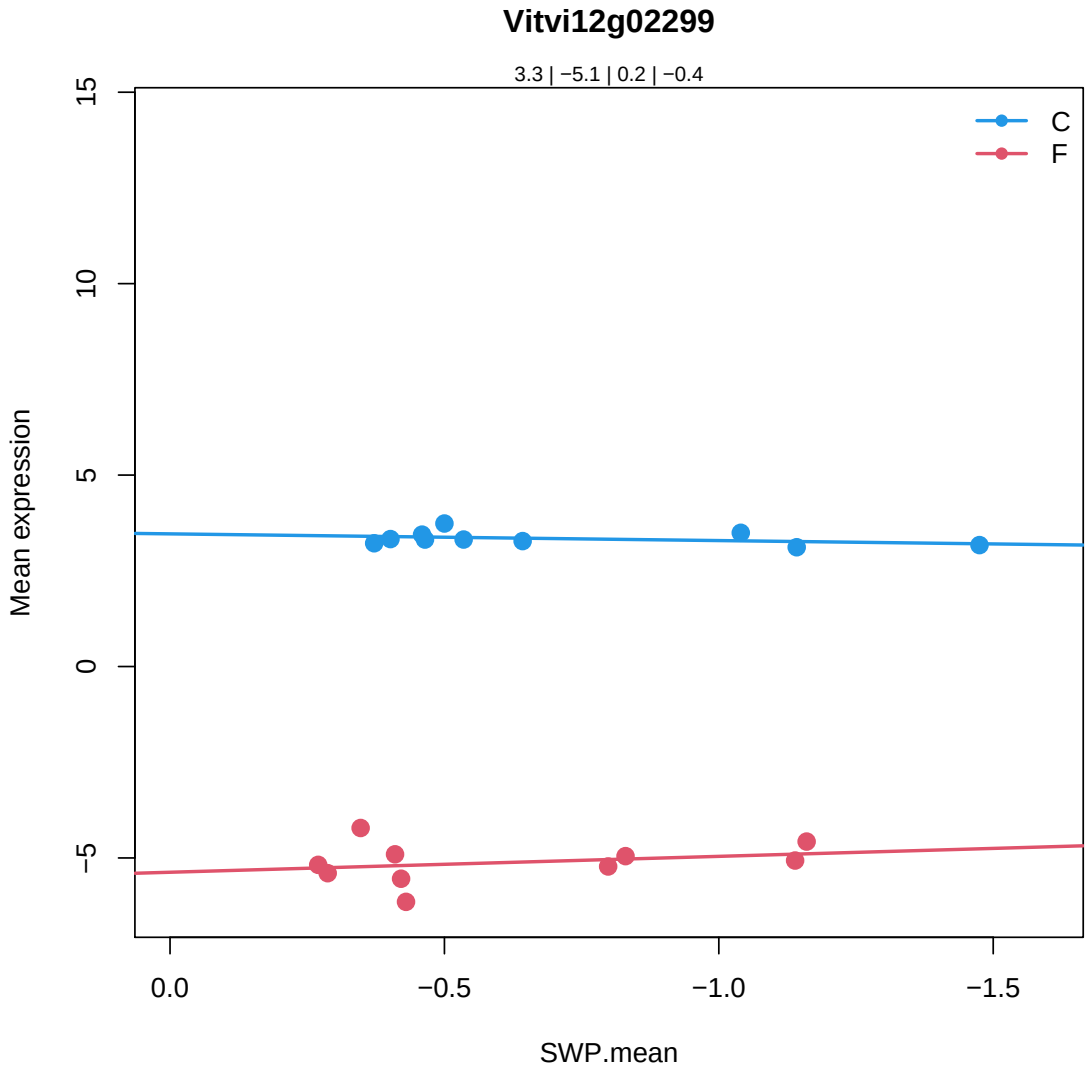
7.4.95 Vitvi12g02299: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02299
        27.1.2
        RNA.processing.RNA helicase
        Replication factor-A protein 1-like protein |
        Chr5:24549682-24552641 REVERSE LENGTH=629 |
        201606
```

Coefficients for Vitvi12g02299.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.341335	2.807135e-17	***	6.747571e-17	***
SlopeC	0.1751199	0.6449803		0.9168025	
MeanF-MeanC	-8.461733	1.340734e-22	***	1.362365e-19	***
SlopeF-SlopeC	-0.5902386	0.3017046		0.9999488	



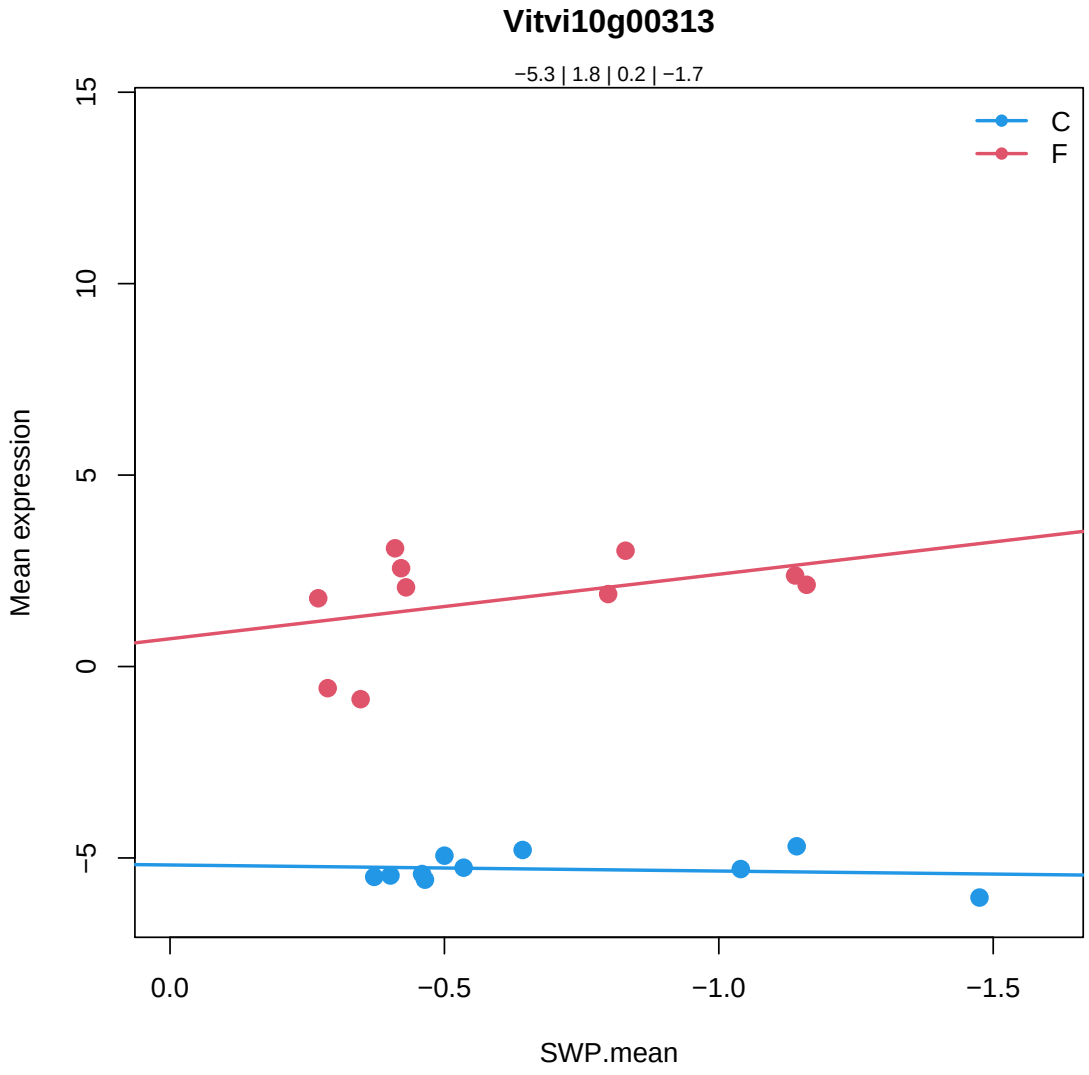
7.4.96 Vitvi10g00313: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00313
        29.5.11.4.2
        protein.degradation.ubiquitin.E3.RING
        plant U-box 8 |
        Chr4:11356143-11357267 REVERSE LENGTH=374 |
        201606
```

Coefficients for Vitvi10g00313.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.2947	6.44878e-15	***	1.098975e-14	***
SlopeC	0.1580878	0.8400291		0.9694858	
MeanF-MeanC	7.046217	2.205385e-14	***	2.605774e-12	***
SlopeF-SlopeC	-1.843471	0.12405		0.9999488	



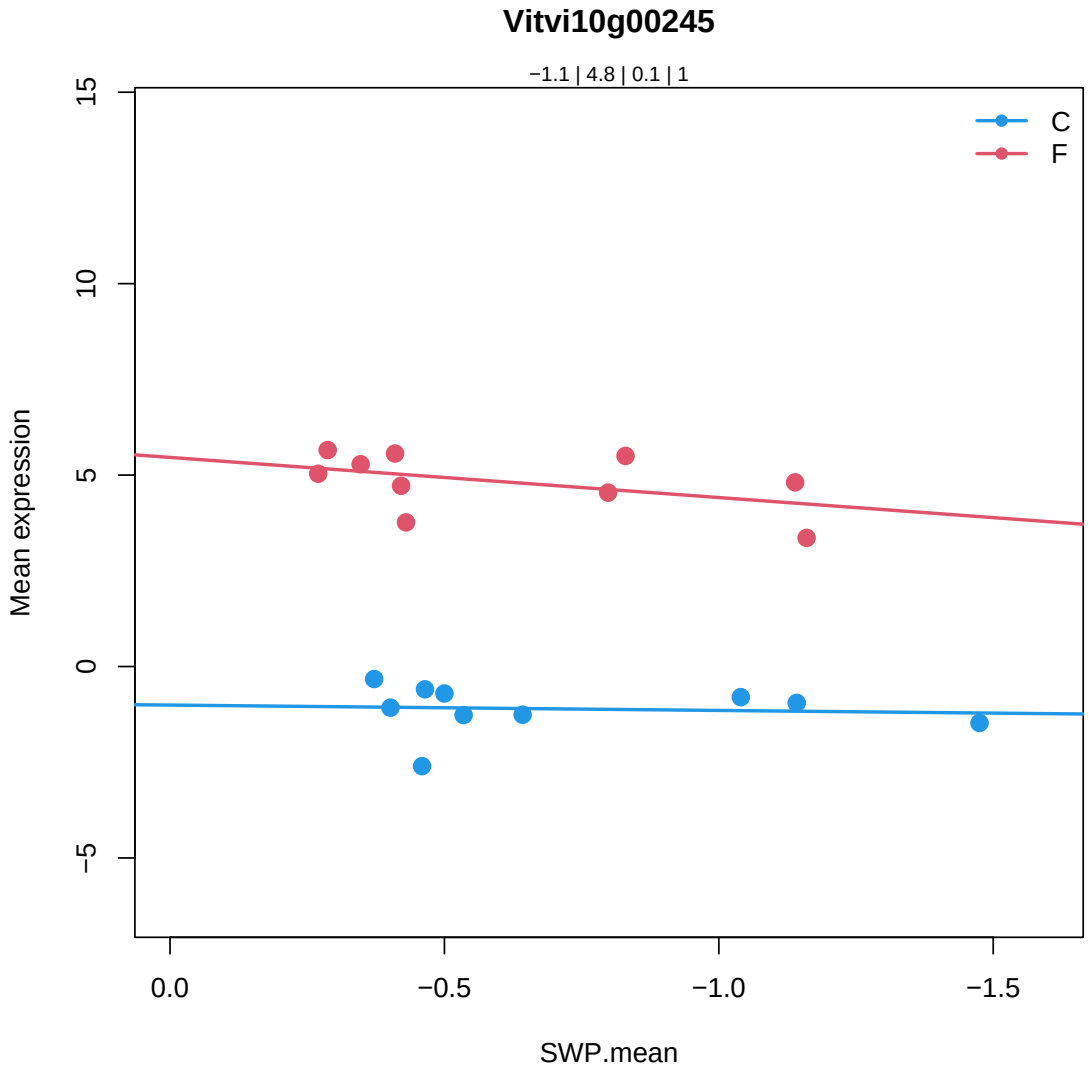
7.4.97 Vitvi10g00245: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00245
        34.12
        transport.metal
        Heavy metal transport/detoxification superfamily protein |
        Chr4:9255062-9255955 FORWARD LENGTH=261 |
        201606
```

Coefficients for Vitvi10g00245.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.105623	2.189343e-05	***	2.452412e-05	***
SlopeC	0.1403099	0.80778		0.9578587	
MeanF-MeanC	5.928422	1.466645e-15	***	2.089216e-13	***
SlopeF-SlopeC	0.9081239	0.2960244		0.9999488	



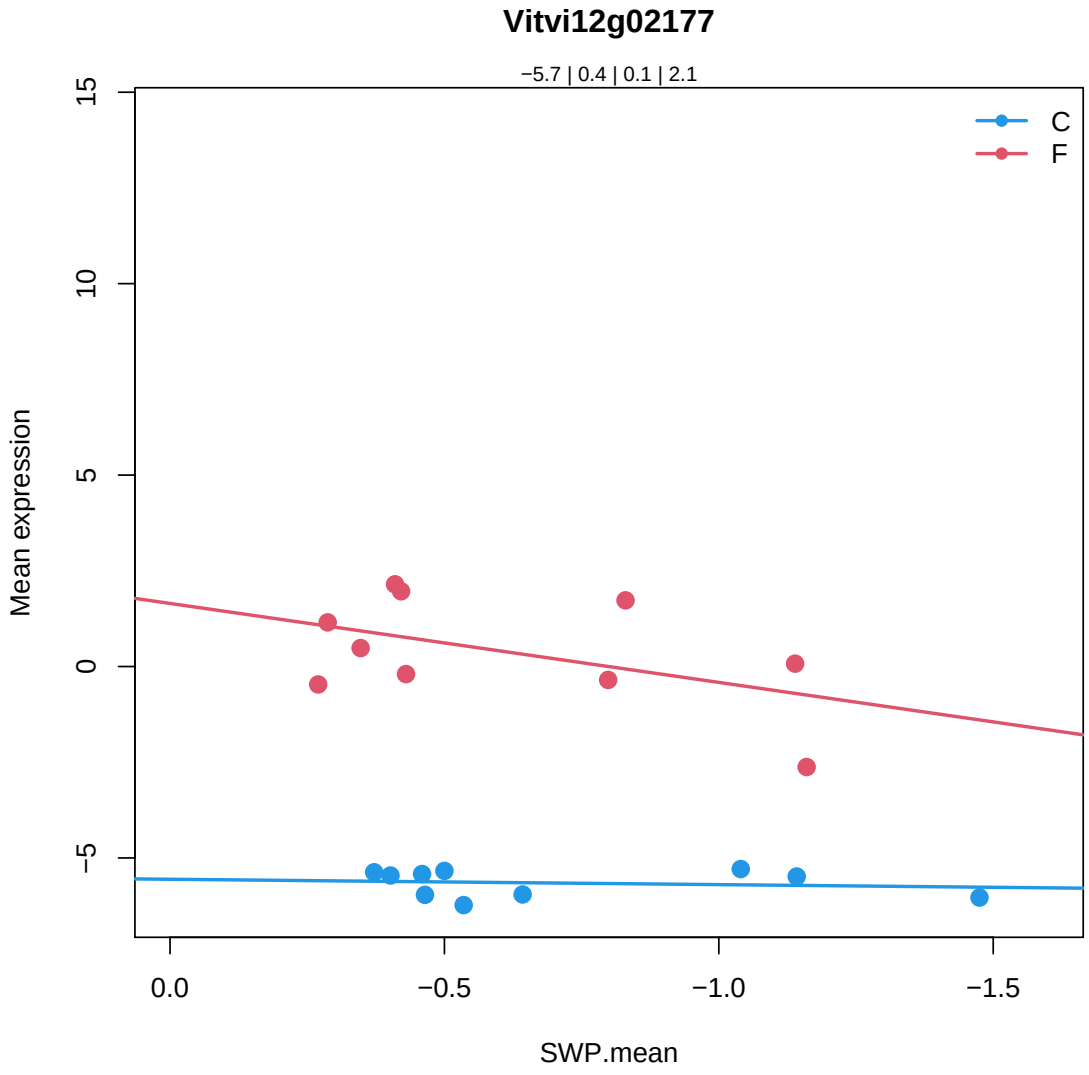
7.4.98 Vitvi12g02177: type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02177
        16.1.5
        secondary metabolism.isoprenoids.terpenoids
        terpene synthase 21 |
        Chr5:8092969-8095128 FORWARD LENGTH=545 |
        201606
```

Coefficients for Vitvi12g02177.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.654707	1.734801e-15	***	3.157989e-15	***
SlopeC	0.1400847	0.8582087		0.9733541	
MeanF-MeanC	6.045631	4.807264e-13	***	4.608322e-11	***
SlopeF-SlopeC	1.922026	0.1100849		0.9999488	



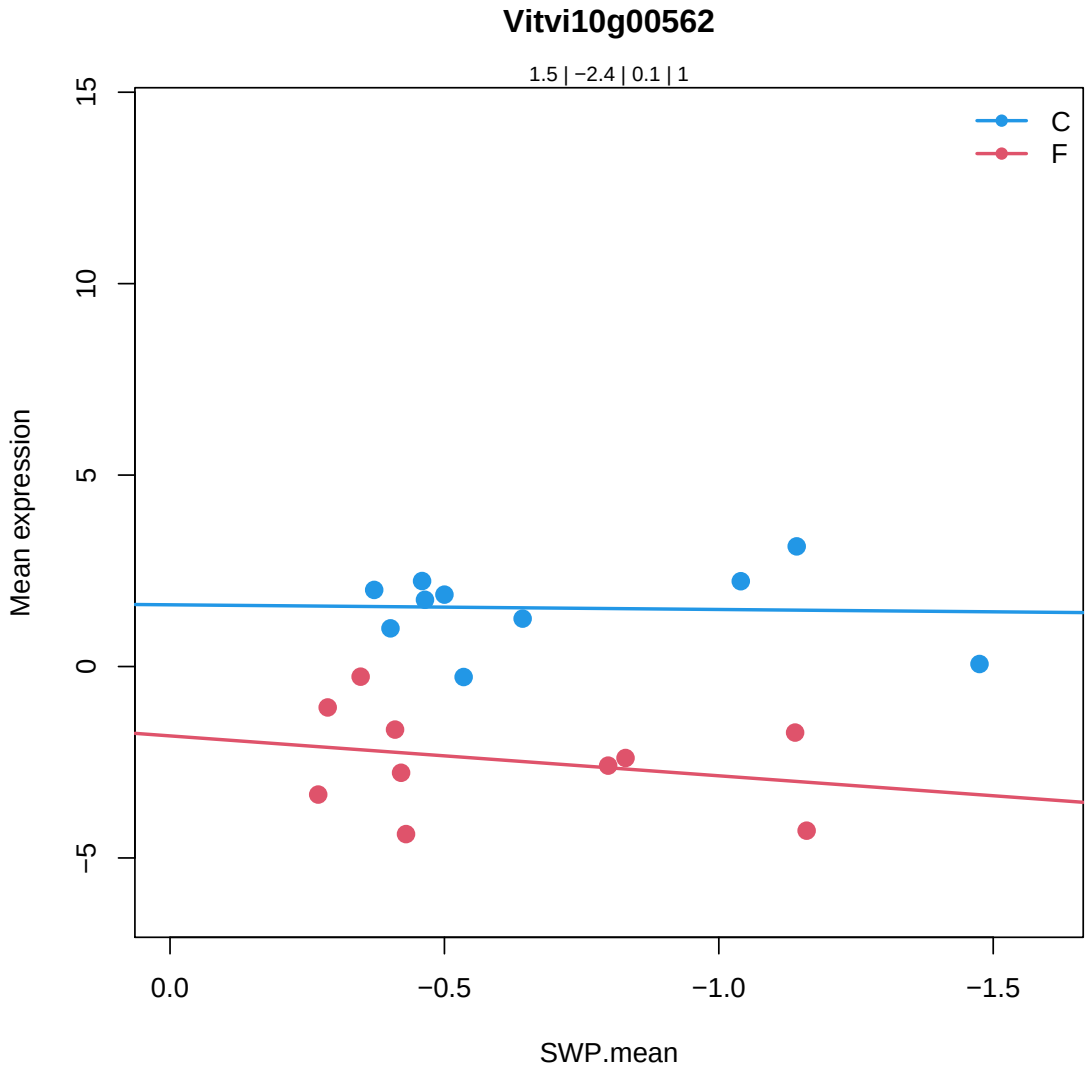
7.4.99 Vitvi10g00562: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00562
        35.1.41
        not assigned.no ontology.hydroxyproline rich proteins
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr4:10231439-10234534 FORWARD LENGTH=642 |
        201606
```

Coefficients for Vitvi10g00562.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.525685	0.0002361897	***	0.0002589744	***
SlopeC	0.1219441	0.9004682		0.9825248	
MeanF-MeanC	-3.972657	5.664188e-08	***	2.459645e-06	***
SlopeF-SlopeC	0.9200333	0.5279688		0.9999488	



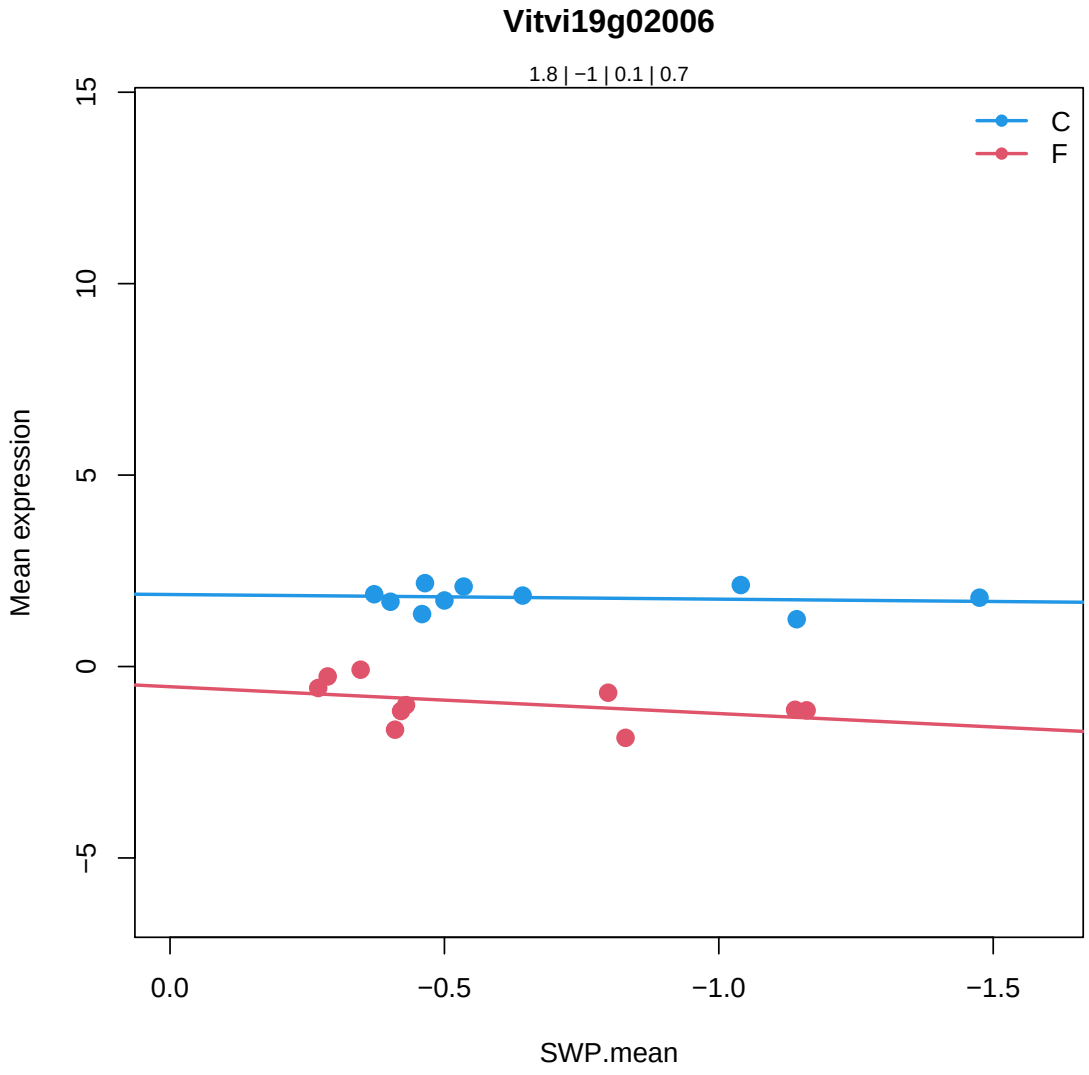
7.4.100 Vitvi19g02006: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g02006
        35.2
        not assigned.unknown
        DNAse I-like superfamily protein |
        Chr1:16528880-16531065 REVERSE LENGTH=626 |
        201606
```

Coefficients for Vitvi19g02006.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.795294	3.167513e-11	***	4.231679e-11	***
SlopeC	0.1215598	0.7663917		0.9497688	
MeanF-MeanC	-2.74995	6.901356e-12	***	5.685971e-10	***
SlopeF-SlopeC	0.5796105	0.3458208		0.9999488	



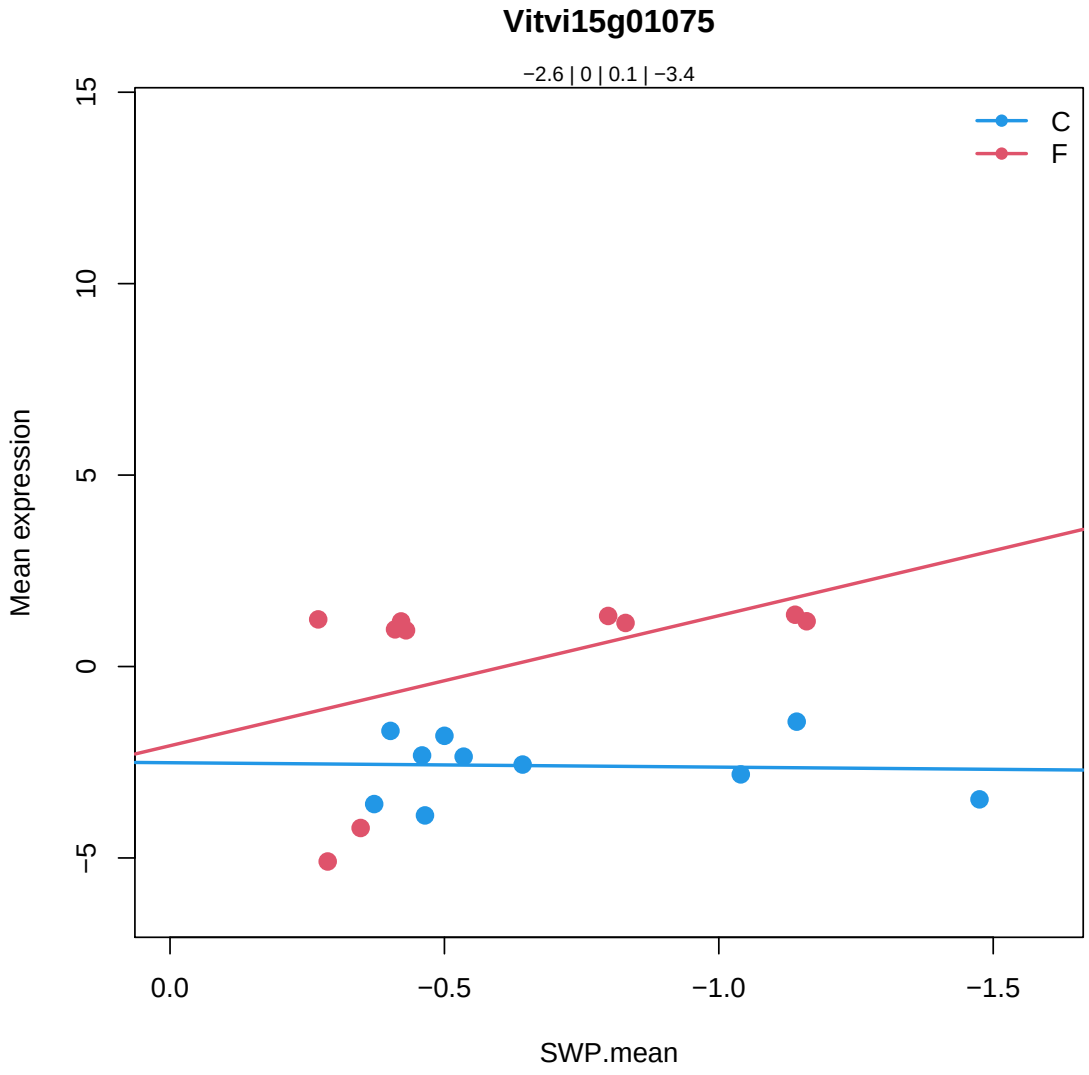
7.4.101 Vitvi15g01075: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g01075
        16.8.1.12
        secondary metabolism.flavonoids.anthocyanins.anthocyanidin 3-O-glucosy
        UDP-Glycosyltransferase superfamily protein |
        Chr2:9593012-9594424 FORWARD LENGTH=470 |
        201606
```

Coefficients for Vitvi15g01075.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-2.593823	2.386606e-05	***	2.671022e-05	***
SlopeC	0.1146464	0.9328867		0.988165	
MeanF-MeanC	2.594459	0.001032986	**	0.01287389	*
SlopeF-SlopeC	-3.510991	0.09385012	.	0.9999488	



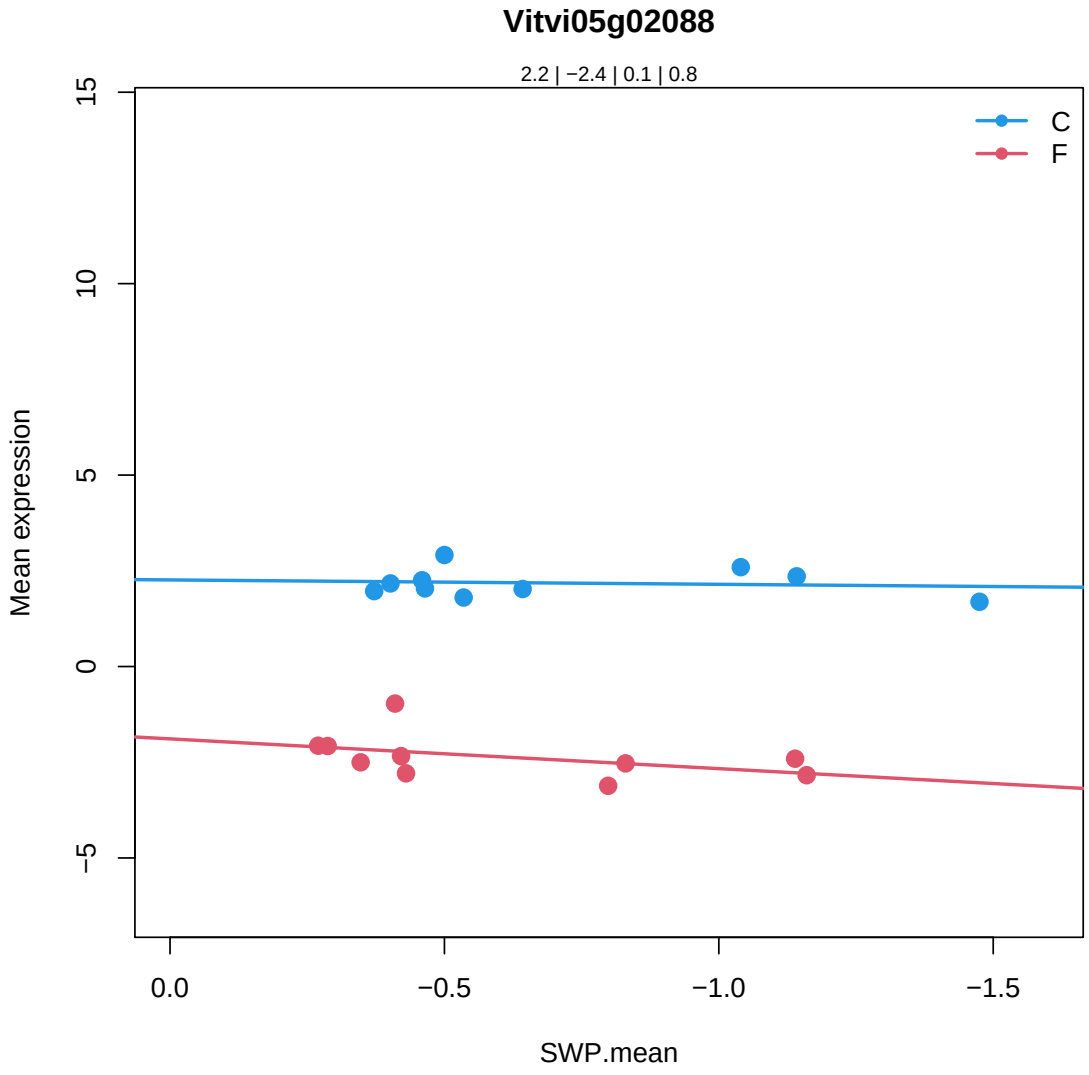
7.4.102 Vitvi05g02088: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g02088
        35.2
        not assigned.unknown
        Ankyrin repeat family protein |
        Chr1:2386275-2387986 REVERSE LENGTH=543 |
        201606
```

Coefficients for Vitvi05g02088.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.180989	2.000373e-12	***	2.822597e-12	***
SlopeC	0.1146372	0.7899726		0.9536338	
MeanF-MeanC	-4.544651	8.447674e-16	***	1.238072e-13	***
SlopeF-SlopeC	0.6625091	0.3066699		0.9999488	



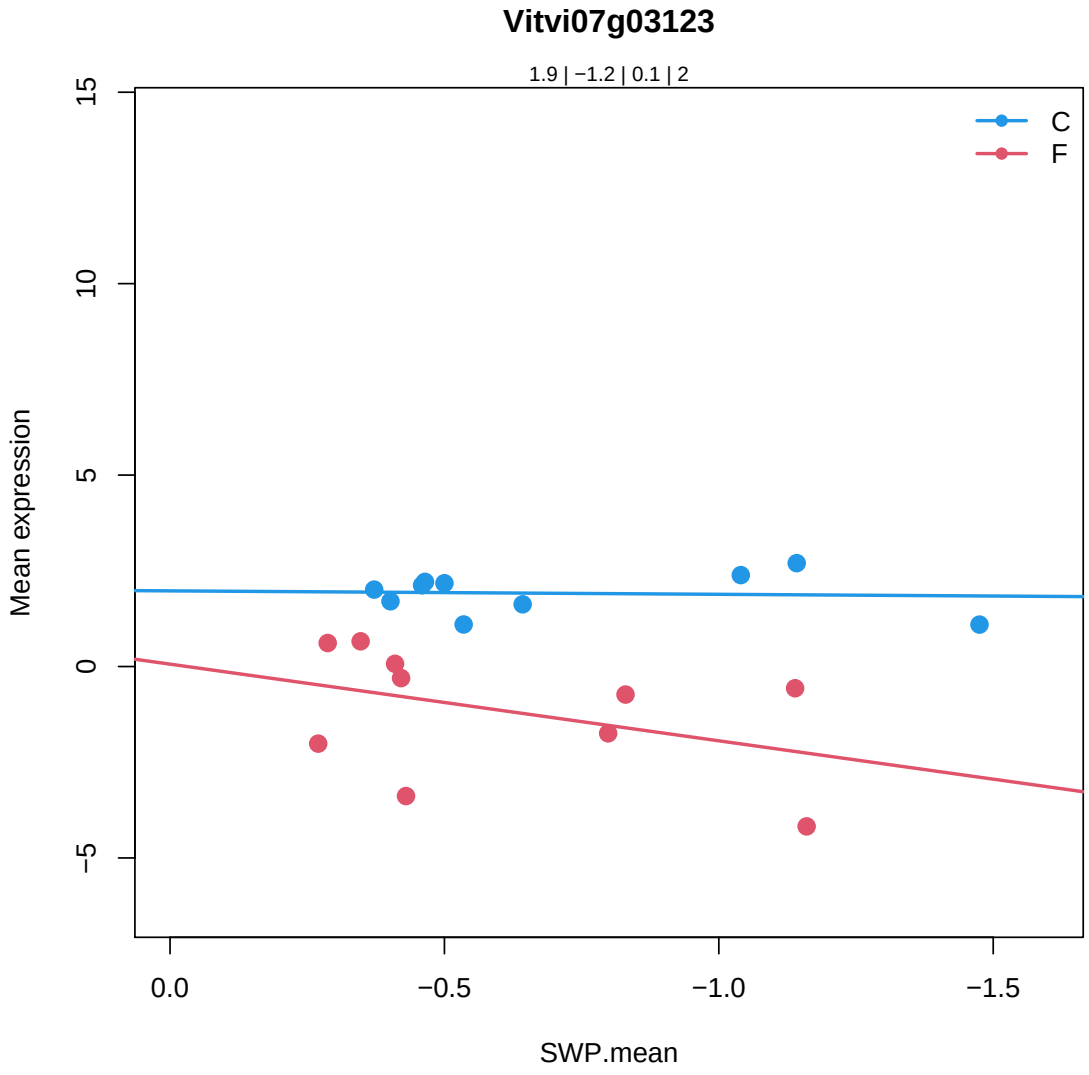
7.4.103 Vitvi07g03123: type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g03123
        31.1
        cell.organisation
        tubulin alpha-5 |
        Chr5:6687212-6688926 FORWARD LENGTH=450 |
        201606
```

Coefficients for Vitvi07g03123.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.912632	1.0113e-05	***	1.14188e-05	***
SlopeC	0.0898298	0.9238393		0.9860755	
MeanF-MeanC	-3.070558	1.72904e-06	***	5.302623e-05	***
SlopeF-SlopeC	1.912759	0.1806418		0.9999488	



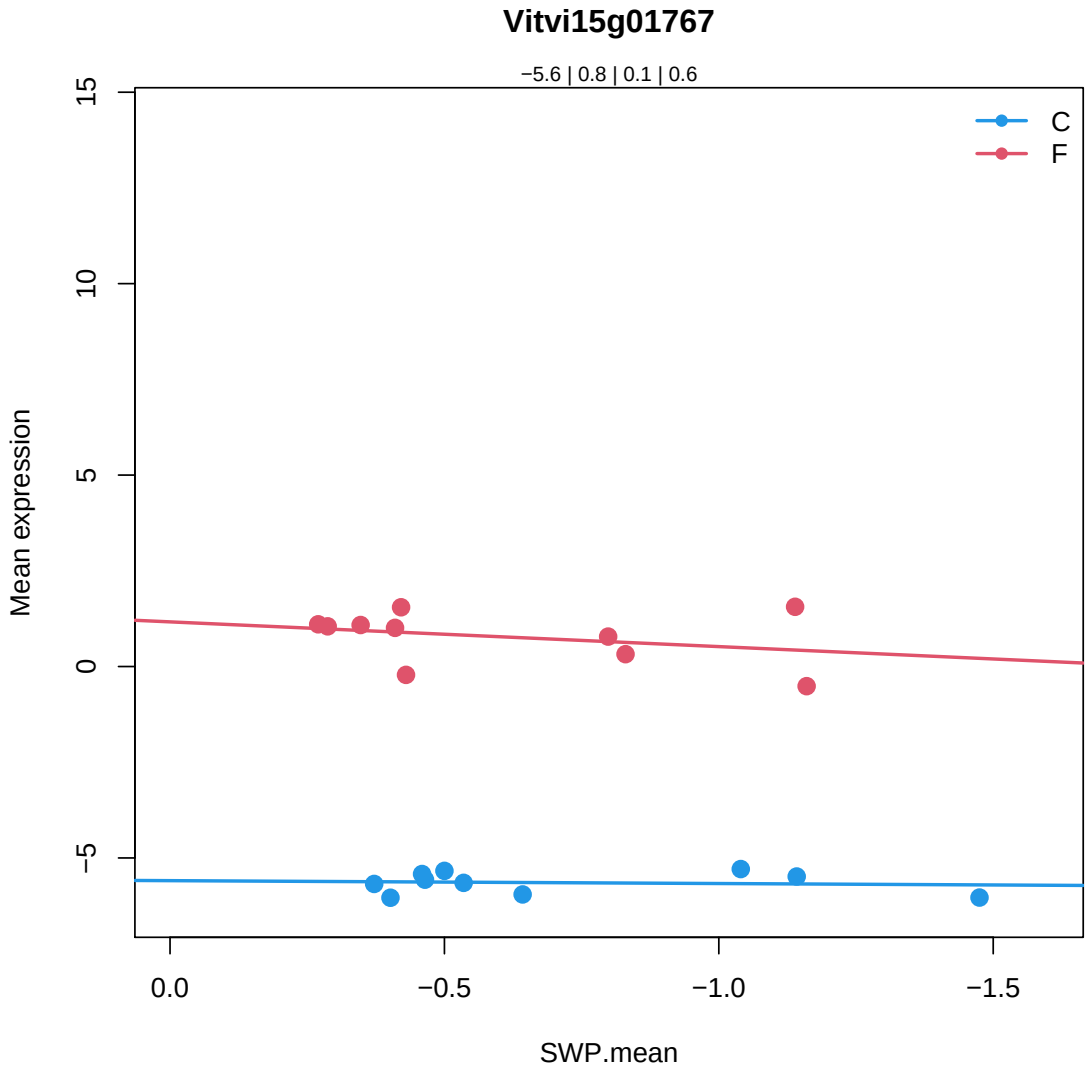
7.4.104 Vitvi15g01767: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g01767
        27.3.4
        RNA.regulation of transcription.auxin response transcription factor fa
        auxin response factor 6 |
        Chr1:10686125-10690036 REVERSE LENGTH=935 |
        201606
```

Coefficients for Vitvi15g01767.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.645642	4.168893e-20	***	2.270178e-19	***
SlopeC	0.07502912	0.8730036		0.9762394	
MeanF-MeanC	6.418102	4.061077e-18	***	9.378627e-16	***
SlopeF-SlopeC	0.570769	0.4174469		0.9999488	



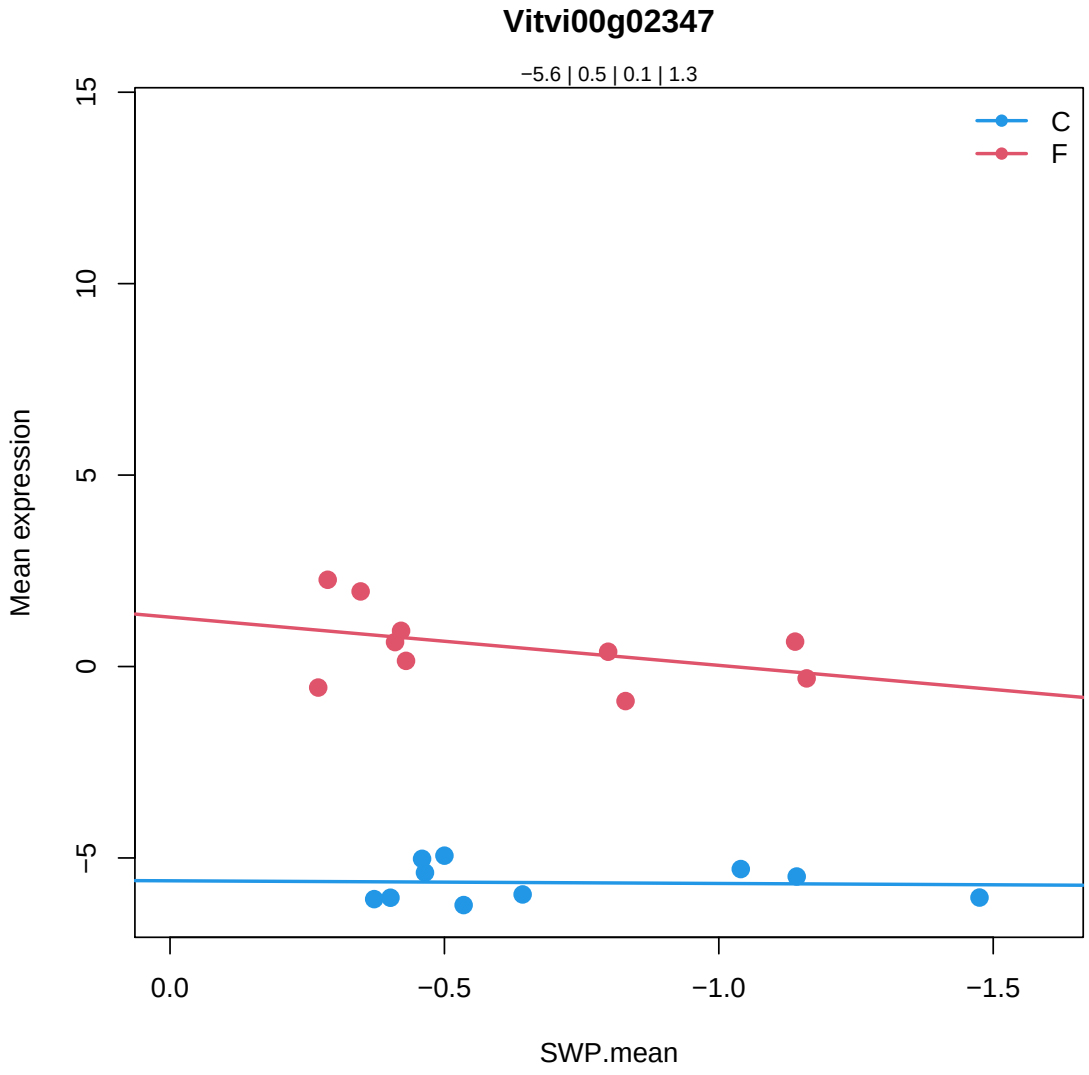
7.4.105 Vitvi00g02347: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi00g02347
        35.2
        not assigned.unknown
        S-locus lectin protein kinase family protein |
        Chr1:3810372-3813053 FORWARD LENGTH=748 |
        201606
```

Coefficients for Vitvi00g02347.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.645391	2.520357e-17	***	6.120006e-17	***
SlopeC	0.06949314	0.9131709		0.9839968	
MeanF-MeanC	6.167235	5.084148e-15	***	6.680395e-13	***
SlopeF-SlopeC	1.189664	0.2180264		0.9999488	



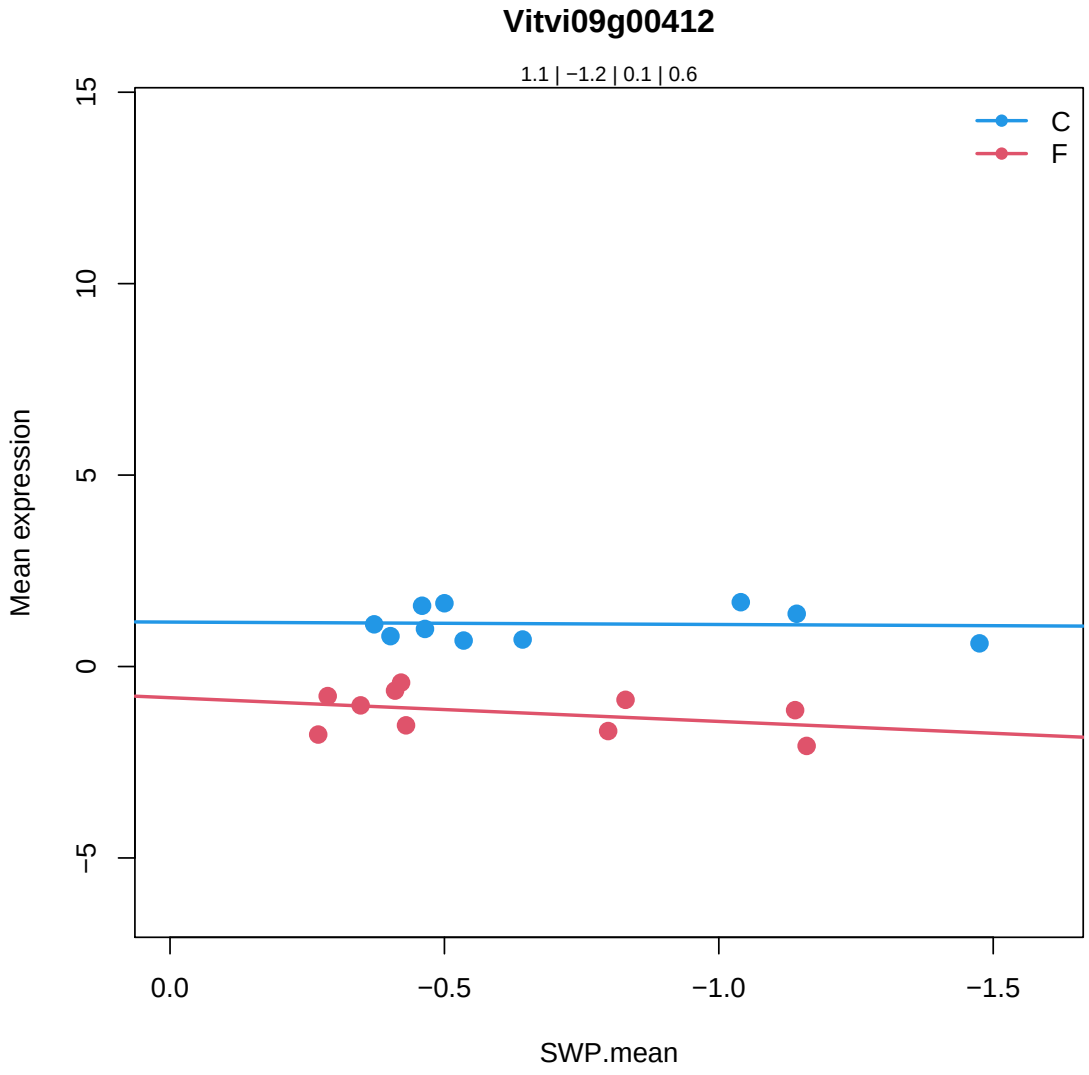
7.4.106 Vitvi09g00412: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00412
        20.1.2.1
        stress.biotic.receptors.CC-NBS-LRR
        LRR and NB-ARC domains-containing disease resistance protein |
        Chr1:4174875-4177559 REVERSE LENGTH=894 |
        201606
```

Coefficients for Vitvi09g00412.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.116178	4.313658e-07	***	5.027049e-07	***
SlopeC	0.06277971	0.8866095		0.9791994	
MeanF-MeanC	-2.30824	7.274389e-10	***	4.348088e-08	***
SlopeF-SlopeC	0.5571793	0.3990486		0.9999488	



7.4.107 Vitvi11g00001: type3

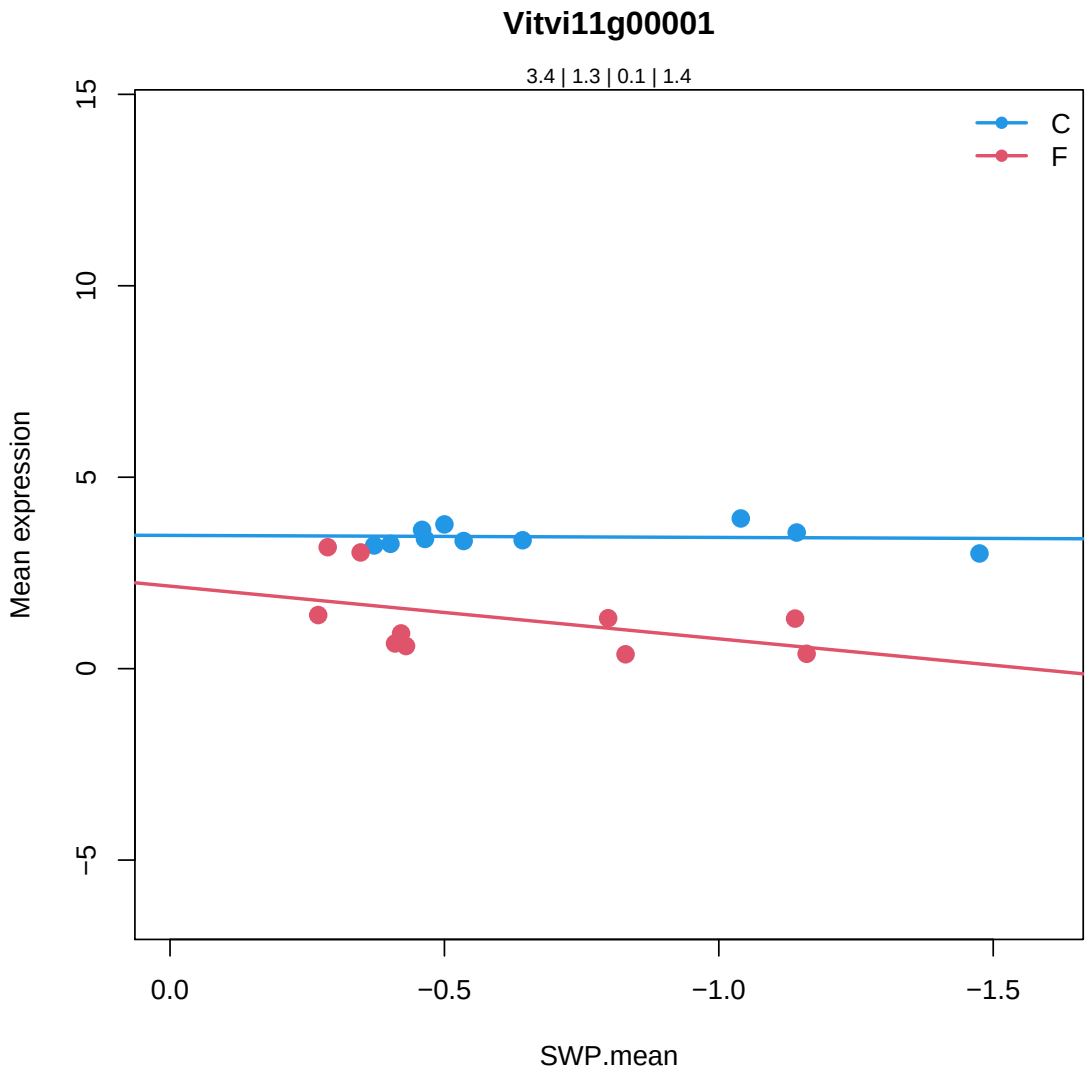
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00001
        11.10.2
        lipid metabolism.glycolipid synthesis.DGDG synthase
        digalactosyl diacylglycerol deficient 2 |
        Chr4:238154-240019 REVERSE LENGTH=473 |
        201606

Vitvi11g00001
        35.2
        not assigned.unknown
        digalactosyl diacylglycerol deficient 2 |
        Chr4:238154-240019 REVERSE LENGTH=473 |
        201606
```

Coefficients for Vitvi11g00001.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.442962	1.035011e-13	***	1.587566e-13	***
SlopeC	0.05303929	0.927675		0.9869214	
MeanF-MeanC	-2.126774	3.428407e-07	***	1.24123e-05	***
SlopeF-SlopeC	1.323482	0.1382439		0.9999488	


Vitvi11g00001
3.4 | 1.3 | 0.1 | 1.4
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

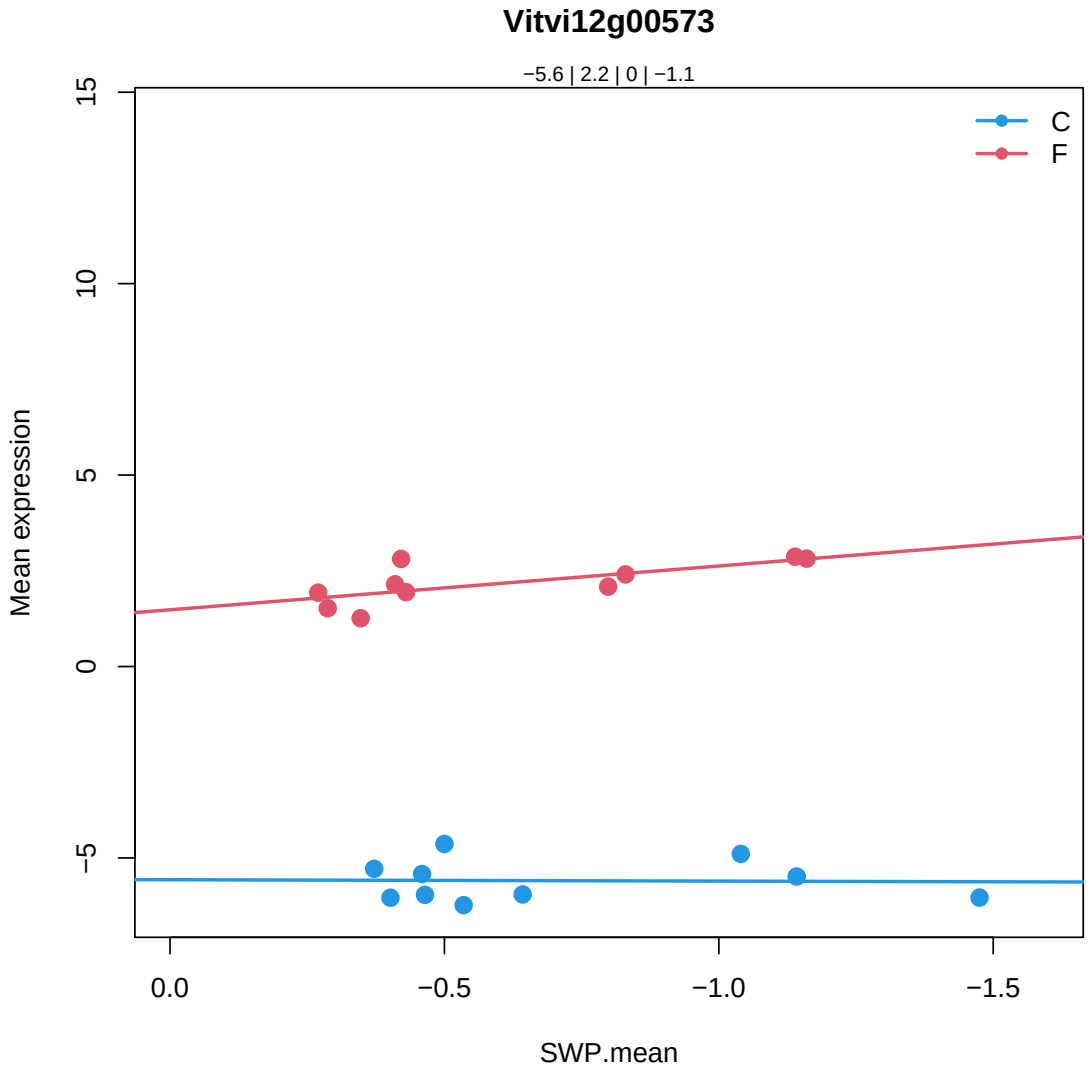
7.4.108 Vitvi12g00573: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00573
        16.1.5
        secondary metabolism.isoprenoids.terpenoids
        Terpenoid cyclases/Protein prenyltransferases superfamily protein |
        Chr3:9430805-9433844 FORWARD LENGTH=598 |
        201606
```

Coefficients for Vitvi12g00573.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.593941	1.355898e-20	***	9.122575e-20	***
SlopeC	0.0353512	0.9360889		0.9889957	
MeanF-MeanC	7.77276	1.966886e-20	***	8.102506e-18	***
SlopeF-SlopeC	-1.179046	0.08305281	.	0.9999488	



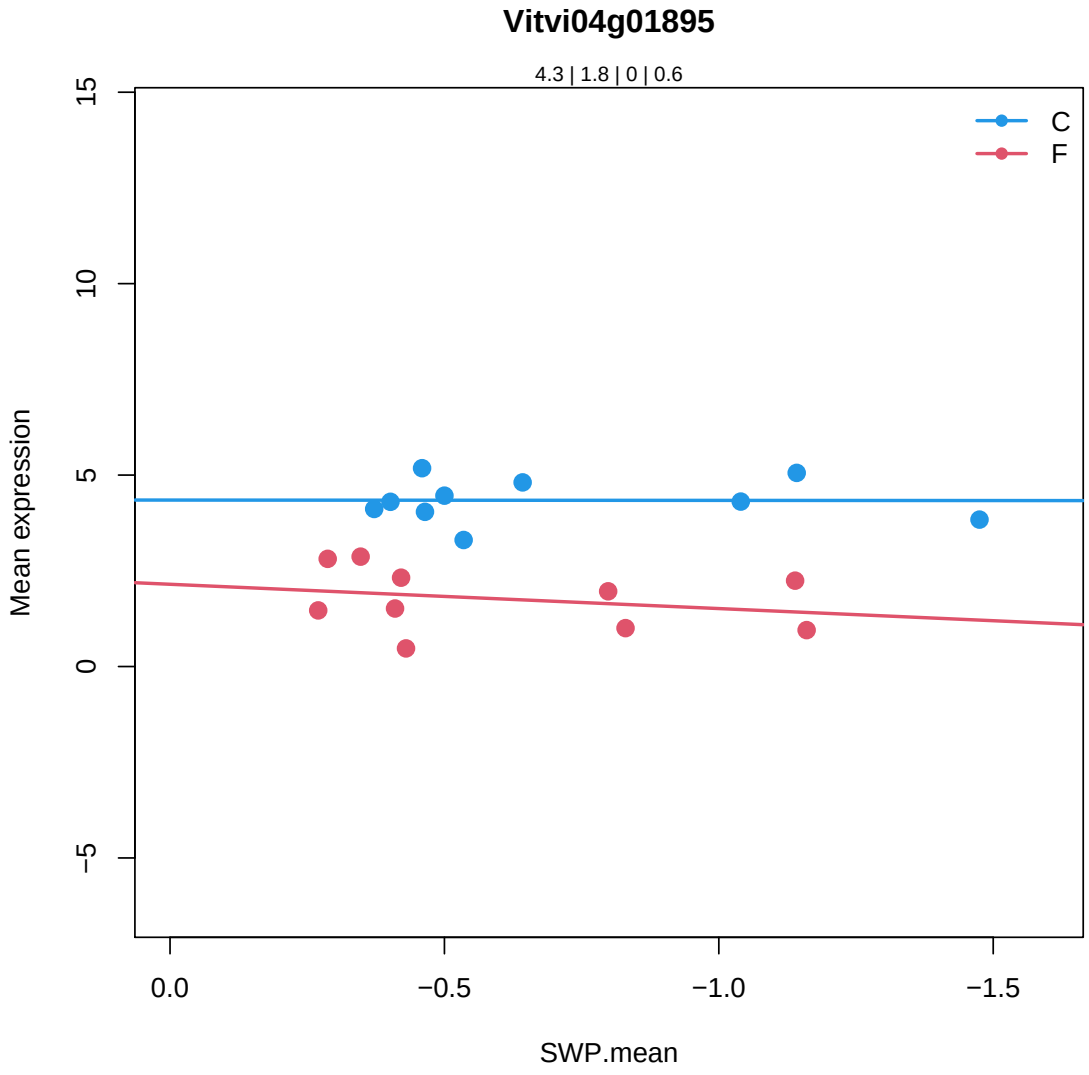
7.4.109 Vitvi04g01895: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01895
        17.5.2
        hormone metabolism.ethylene.signal transduction
        PPPDE thiol peptidase family protein |
        Chr4:15464905-15469204 FORWARD LENGTH=680 |
        201606
```

Coefficients for Vitvi04g01895.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.341404	1.665437e-15	***	3.038616e-15	***
SlopeC	0.008270129	0.9890131		0.9983274	
MeanF-MeanC	-2.579973	2.362103e-08	***	1.104392e-06	***
SlopeF-SlopeC	0.6261308	0.4861564		0.9999488	



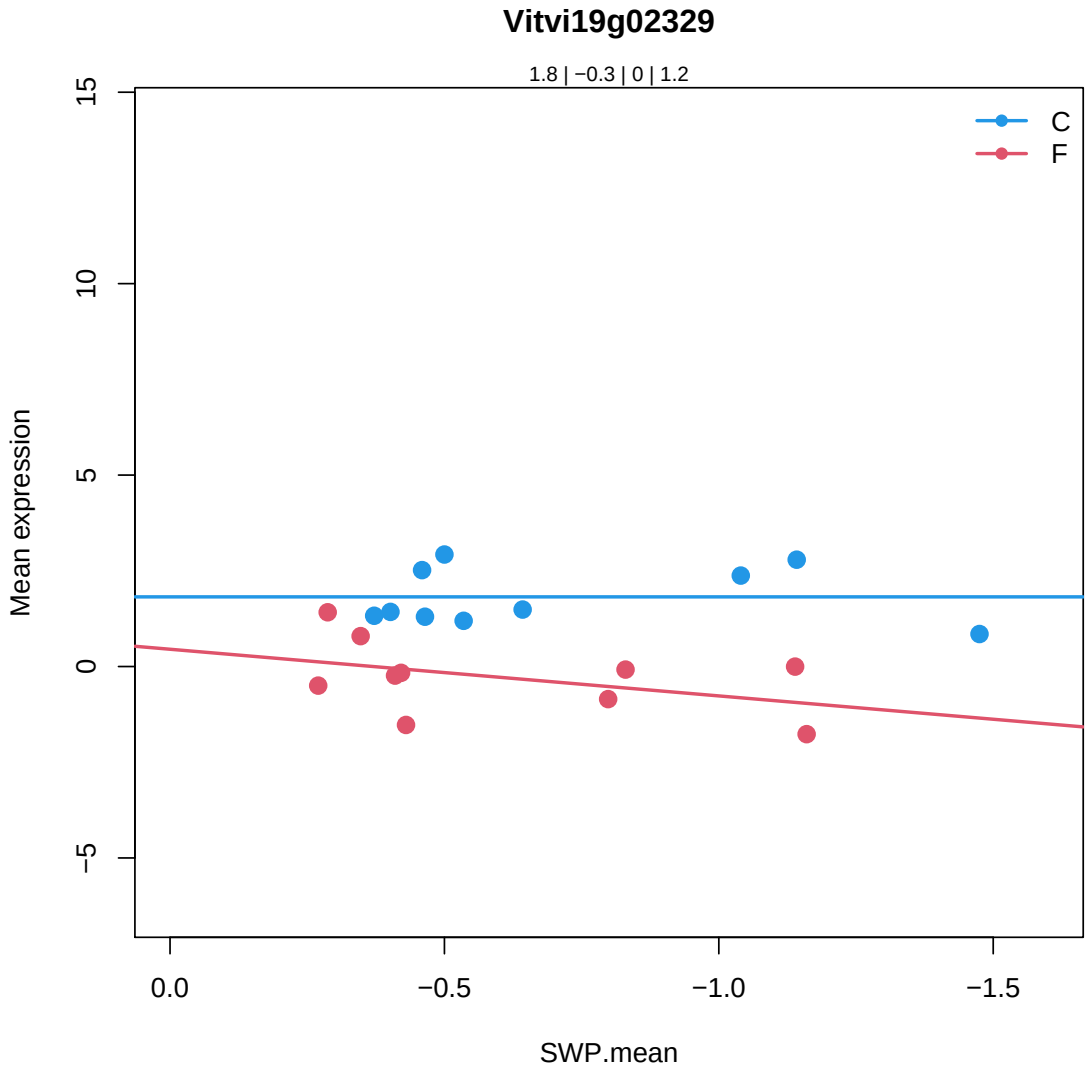
7.4.110 Vitvi19g02329: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g02329
        26.3.5
        misc.gluco-, galacto- and mannosidases.glycosyl hydrolase family 5
        NB-ARC domain-containing disease resistance protein |
        Chr3:4857940-4861104 FORWARD LENGTH=1054 |
        201606
```

Coefficients for Vitvi19g02329.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.818909	2.689727e-07	***	3.15142e-07	***
SlopeC	0.0001976475	0.9997733		0.9998964	
MeanF-MeanC	-2.110744	4.96342e-06	***	0.0001341356	***
SlopeF-SlopeC	1.21853	0.2468431		0.9999488	



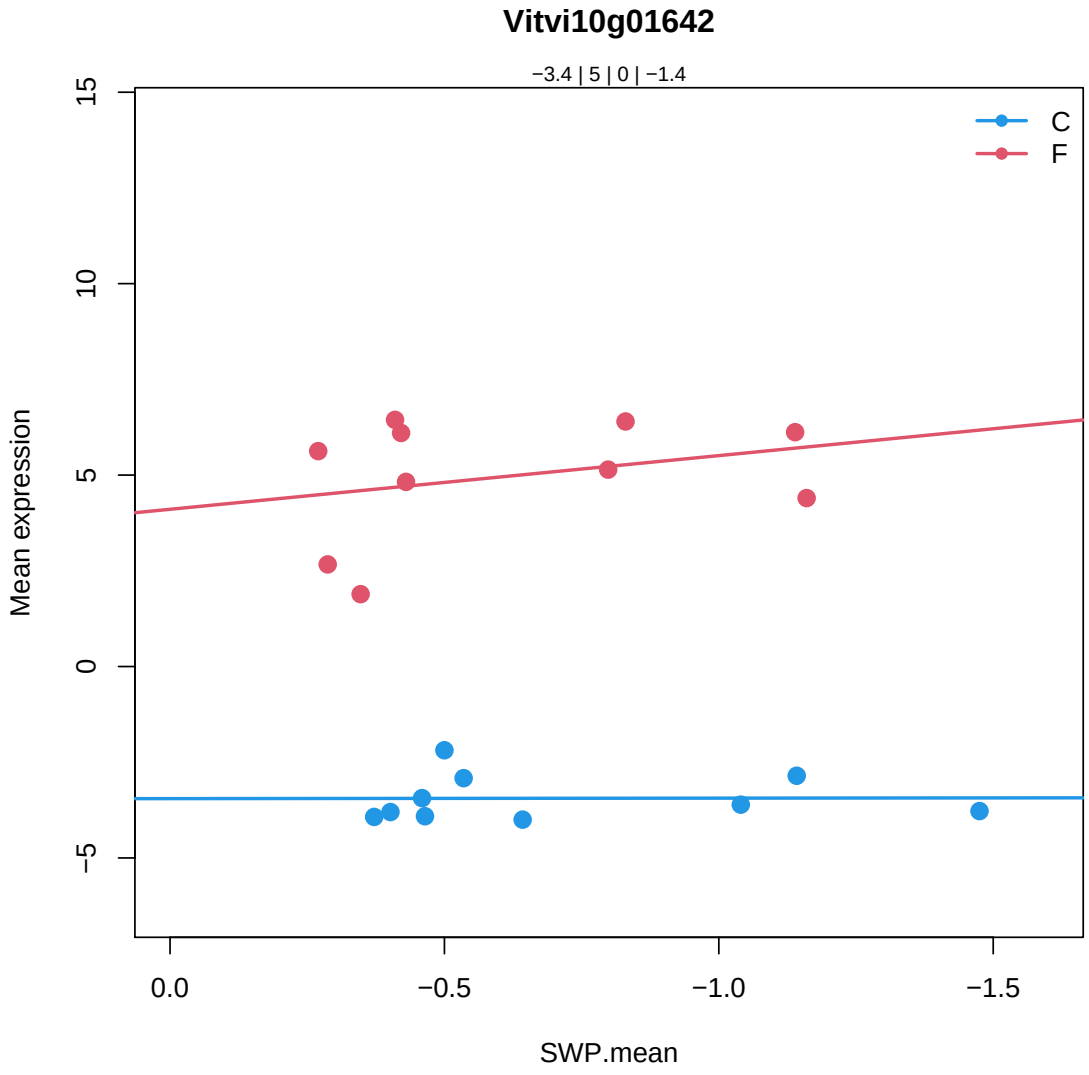
7.4.111 Vitvi10g01642: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g01642
        35.2
        not assigned.unknown
        senescence regulator (Protein of unknown function%2C DUF584) |
        Chr1:3945852-3946457 FORWARD LENGTH=201 |
        201606
```

Coefficients for Vitvi10g01642.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-3.441614	1.297633e-09	***	1.631084e-09	***
SlopeC	-0.01243179	0.9896517		0.9983274	
MeanF-MeanC	8.402486	3.756324e-14	***	4.179116e-12	***
SlopeF-SlopeC	-1.389259	0.3354931		0.9999488	



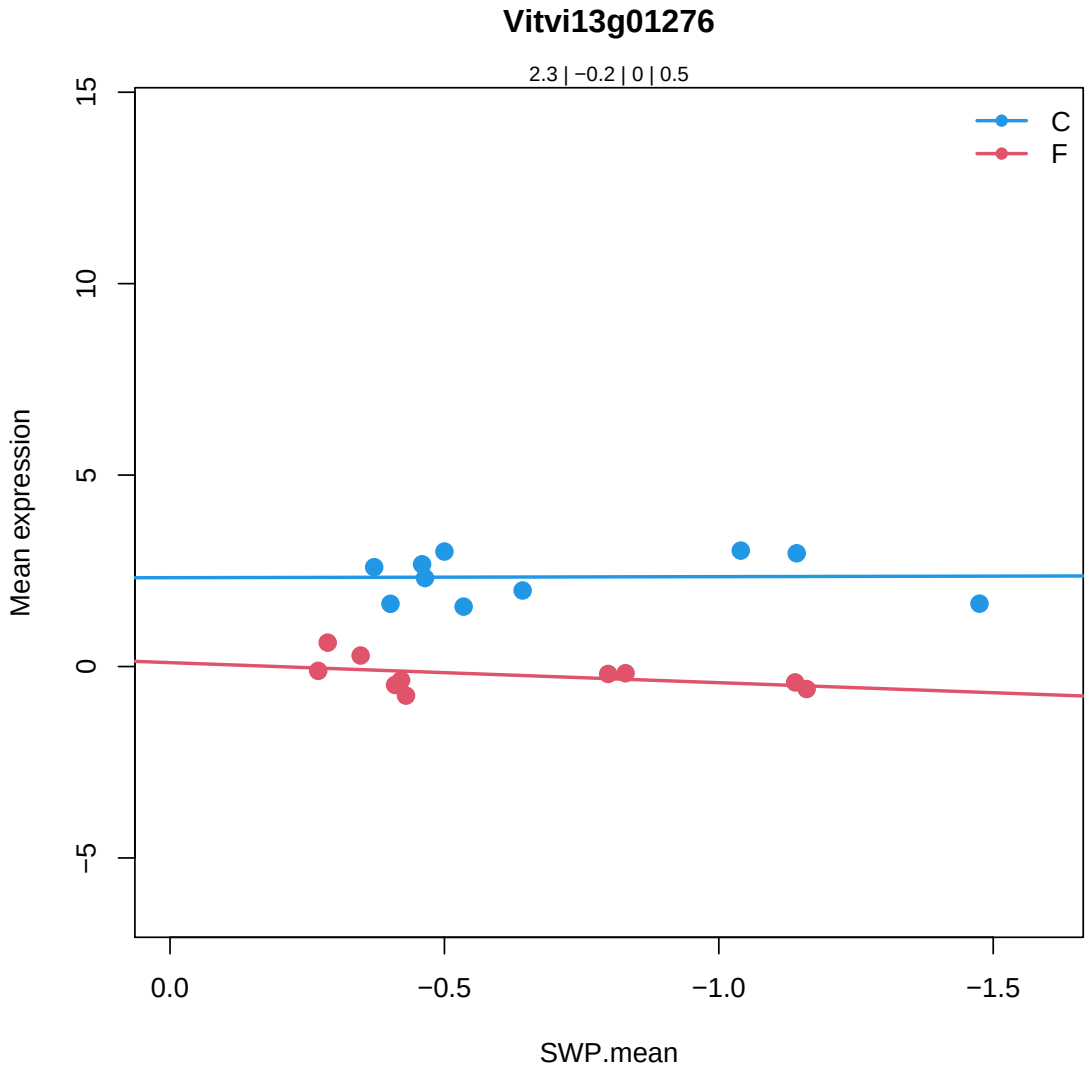
7.4.112 Vitvi13g01276: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g01276
        20.1.2.1
        stress.biotic.receptors.CC-NBS-LRR
        NB-ARC domain-containing disease resistance protein |
        Chr3:4857940-4861104 FORWARD LENGTH=1054 |
        201606
```

Coefficients for Vitvi13g01276.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.339188	1.900236e-12	***	2.683286e-12	***
SlopeC	-0.02691208	0.953351		0.9925445	
MeanF-MeanC	-2.556826	2.521551e-10	***	1.642457e-08	***
SlopeF-SlopeC	0.5507127	0.4247292		0.9999488	



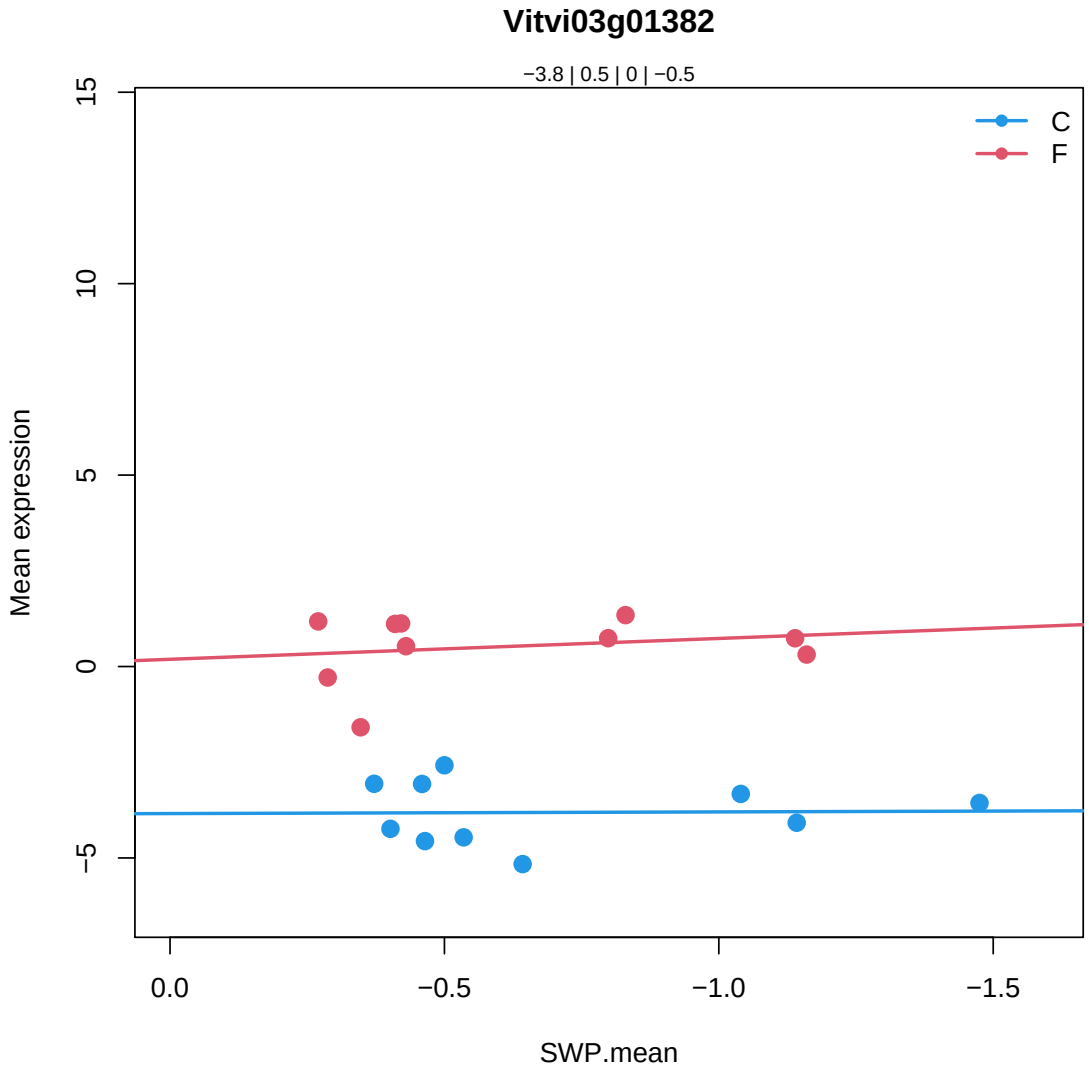
7.4.113 Vitvi03g01382: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g01382
        35.2
        not assigned.unknown
        NB-ARC domain-containing disease resistance protein |
        Chr3:17130739-17133246 REVERSE LENGTH=835 |
        201606
```

Coefficients for Vitvi03g01382.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-3.810353	8.712992e-13	***	1.255112e-12	***
SlopeC	-0.04335667	0.9519888		0.9925445	
MeanF-MeanC	4.330659	5.823213e-11	***	4.206513e-09	***
SlopeF-SlopeC	-0.5007456	0.6411963		0.9999488	



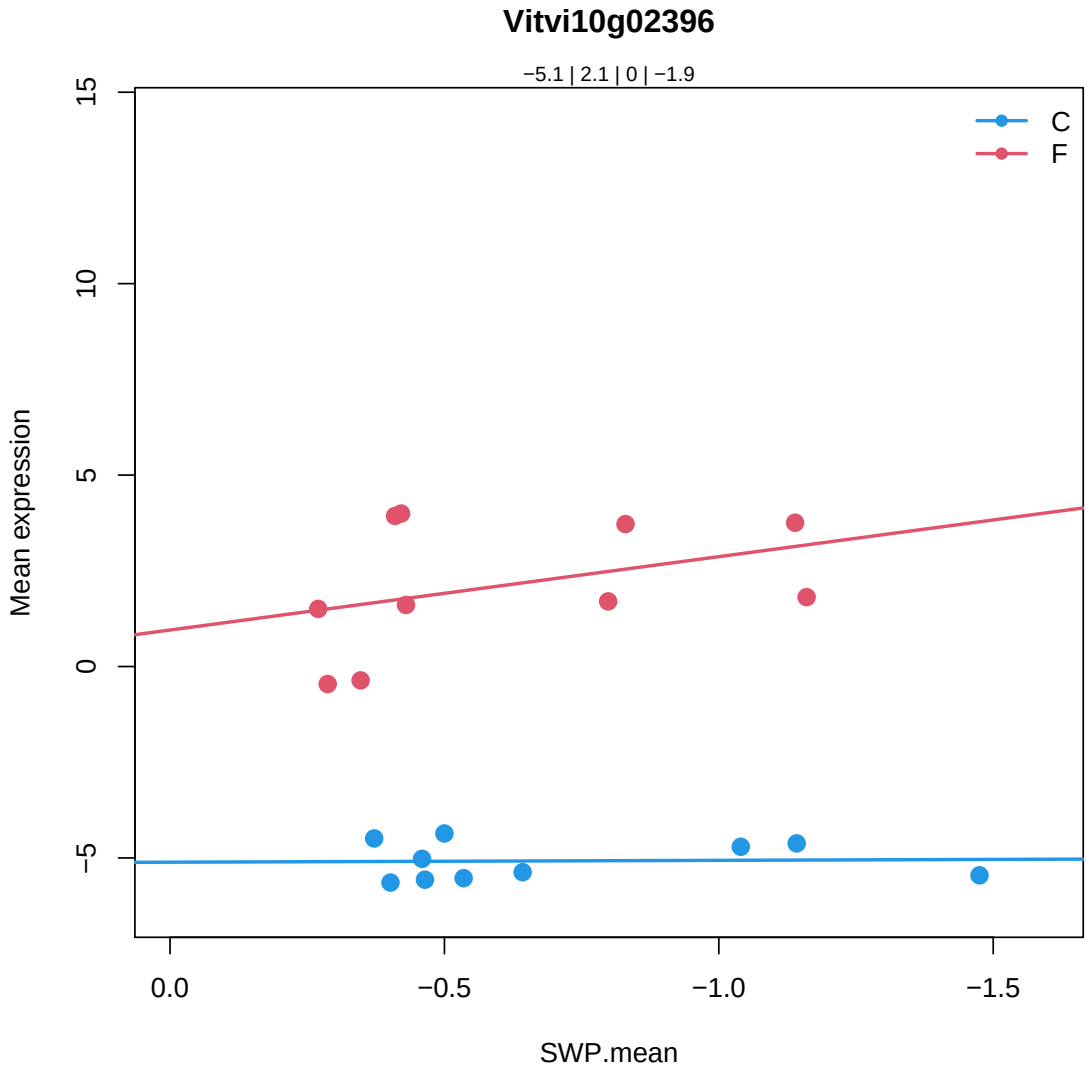
7.4.114 Vitvi10g02396: type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g02396
        14.2
        S-assimilation.APR
        APS reductase 1 |
        Chr4:2325069-2326718 FORWARD LENGTH=465 |
        201606
```

Coefficients for Vitvi10g02396.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.076664	1.036555e-12	***	1.485024e-12	***
SlopeC	-0.04830116	0.9602008		0.9937458	
MeanF-MeanC	7.197329	9.873187e-13	***	8.749251e-11	***
SlopeF-SlopeC	-1.867763	0.2034859		0.9999488	



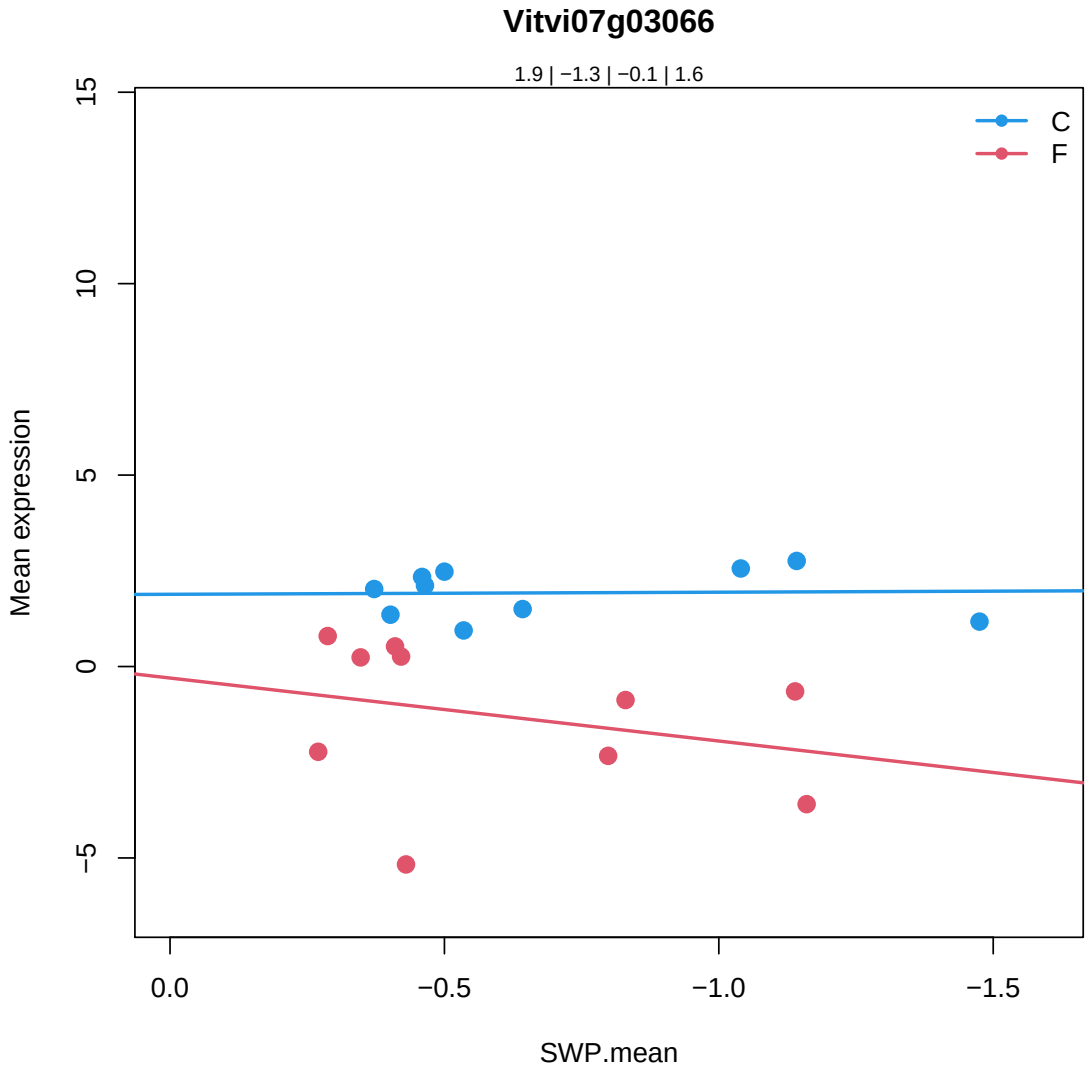
7.4.115 Vitvi07g03066: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g03066
        35.2
        not assigned.unknown
        tubulin alpha-5 |
        Chr5:6687212-6688926 FORWARD LENGTH=450 |
        201606
```

Coefficients for Vitvi07g03066.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.924411	0.0001445351	***	0.0001590961	***
SlopeC	-0.0543839	0.9630928		0.9939741	
MeanF-MeanC	-3.22752	1.874679e-05	***	0.0004355772	***
SlopeF-SlopeC	1.698955	0.3367385		0.9999488	



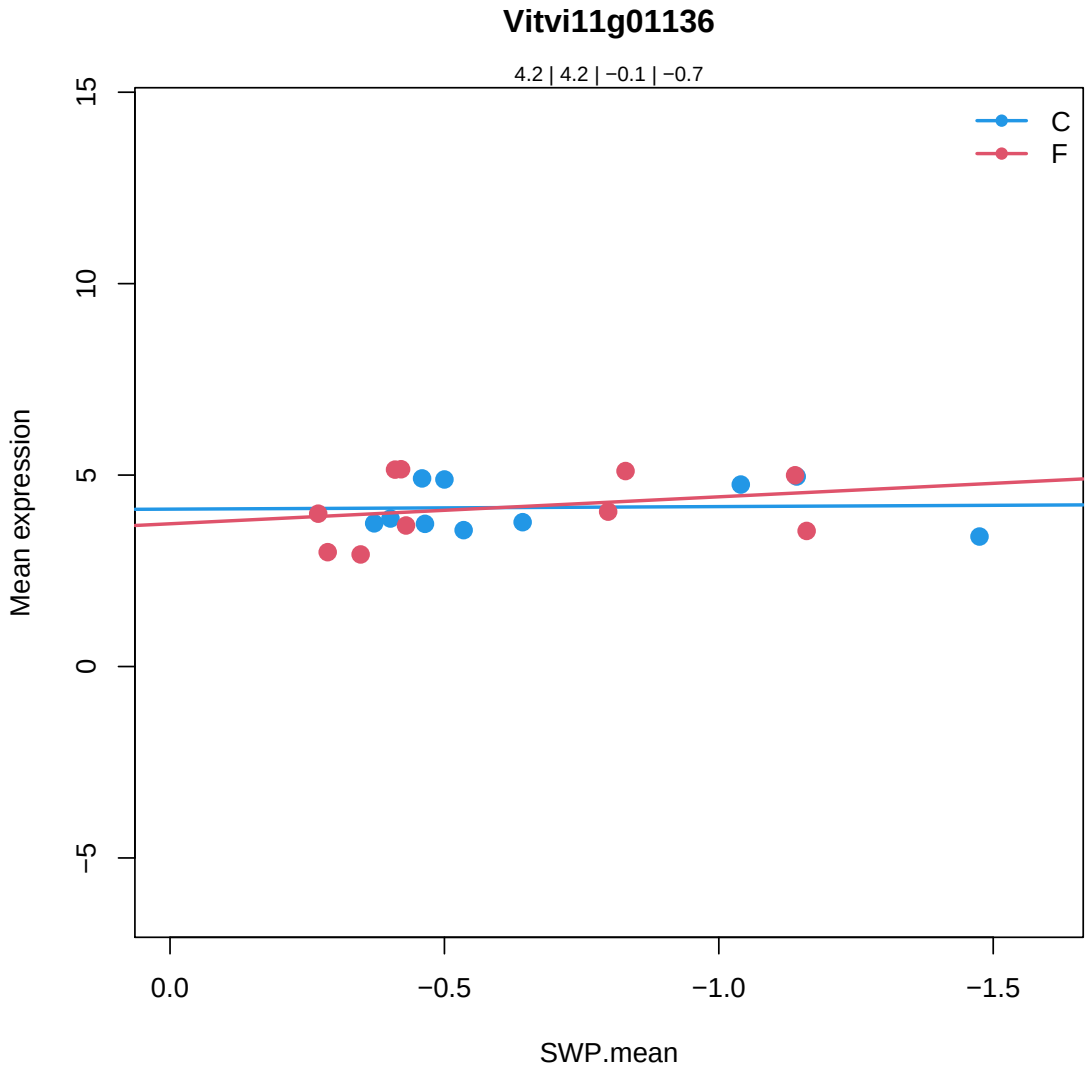
7.4.116 Vitvi11g01136: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g01136
        30.5
        signalling.G-proteins
        Ypt/Rab-GAP domain of gyp1p superfamily protein |
        Chr4:14658088-14660370 FORWARD LENGTH=703 |
        201606
```

Coefficients for Vitvi11g01136.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.156966	2.119973e-14	***	3.442642e-14	***
SlopeC	-0.06670208	0.9185037		0.9851716	
MeanF-MeanC	-4.762838e-05	0.9998853		0.9999648	
SlopeF-SlopeC	-0.6375405	0.5132309		0.9999488	



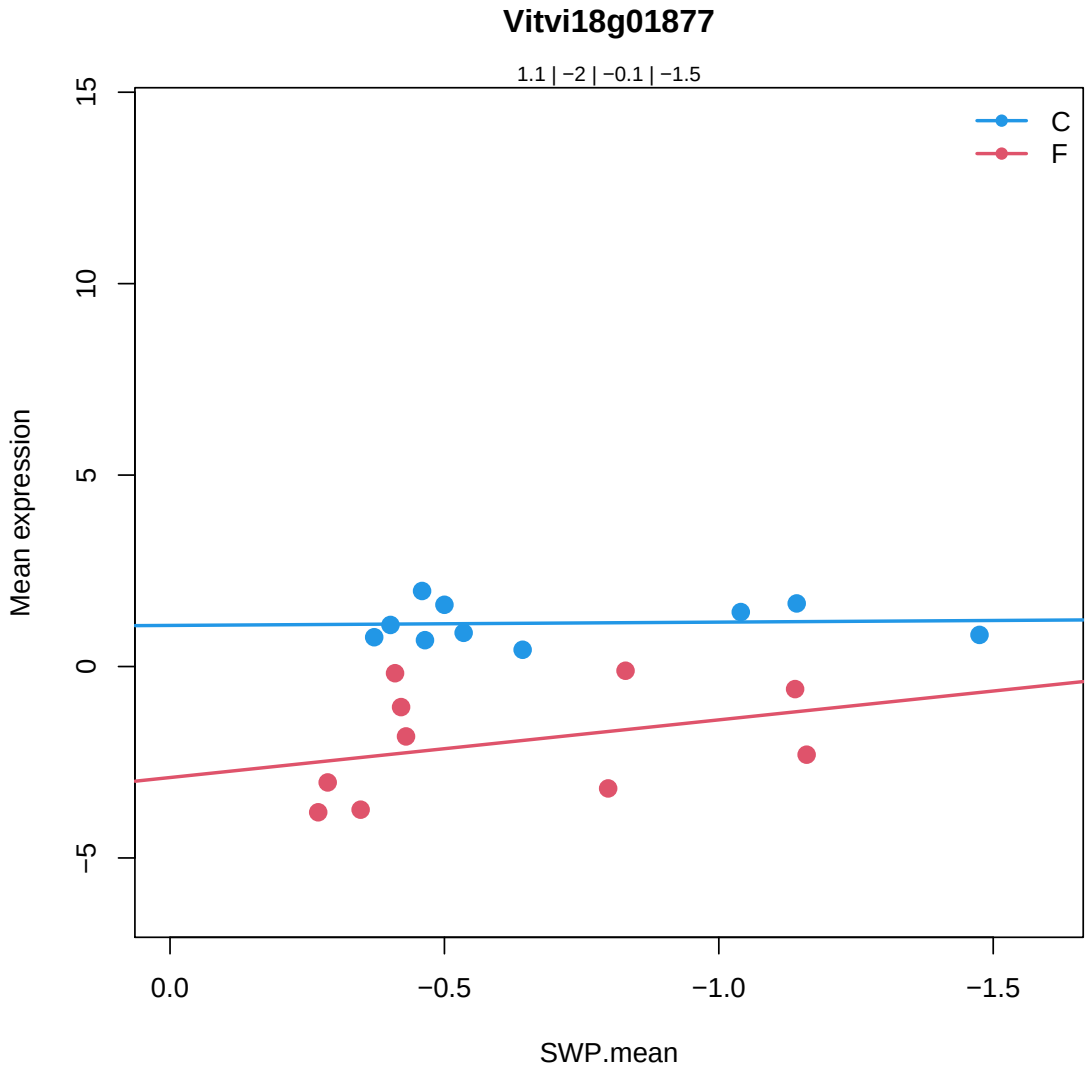
7.4.117 Vitvi18g01877: type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g01877
        20.1.2.2
        stress.biotic.receptors.TIR-NBS-LRR
        Disease resistance protein (TIR-NBS-LRR class) family |
        Chr5:14568141-14571907 REVERSE LENGTH=1125 |
        201606
```

Coefficients for Vitvi18g01877.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.133662	0.001197745	**	0.001295489	**
SlopeC	-0.08588147	0.9200083		0.9853314	
MeanF-MeanC	-3.115832	3.373809e-07	***	1.227294e-05	***
SlopeF-SlopeC	-1.420387	0.2713186		0.9999488	



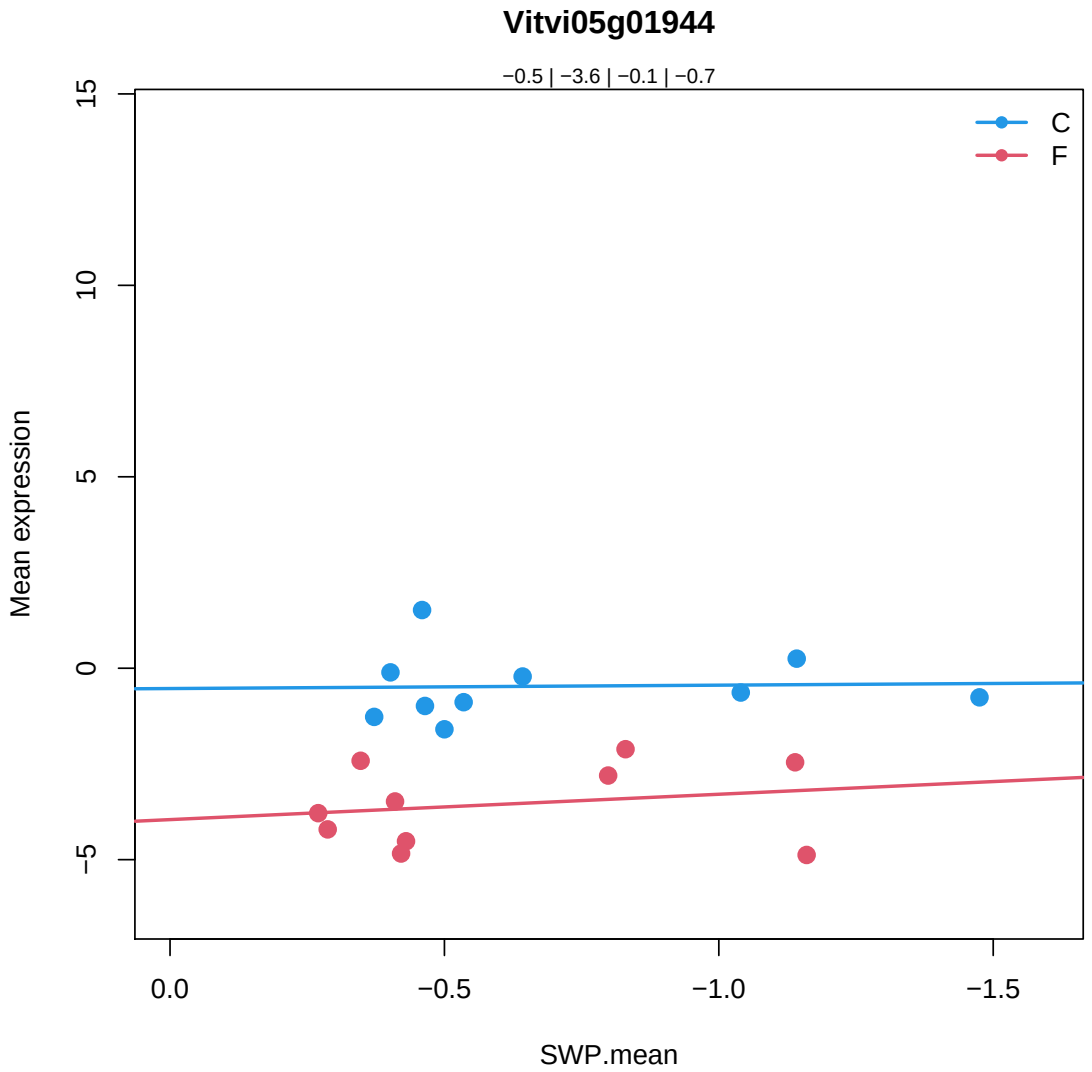
7.4.118 Vitvi05g01944: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01944
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi05g01944.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.4689322	0.1193905		0.1232392	
SlopeC	-0.08787982	0.9140078		0.9841969	
MeanF-MeanC	-3.081605	1.844868e-07	***	7.065196e-06	***
SlopeF-SlopeC	-0.574188	0.6363228		0.9999488	



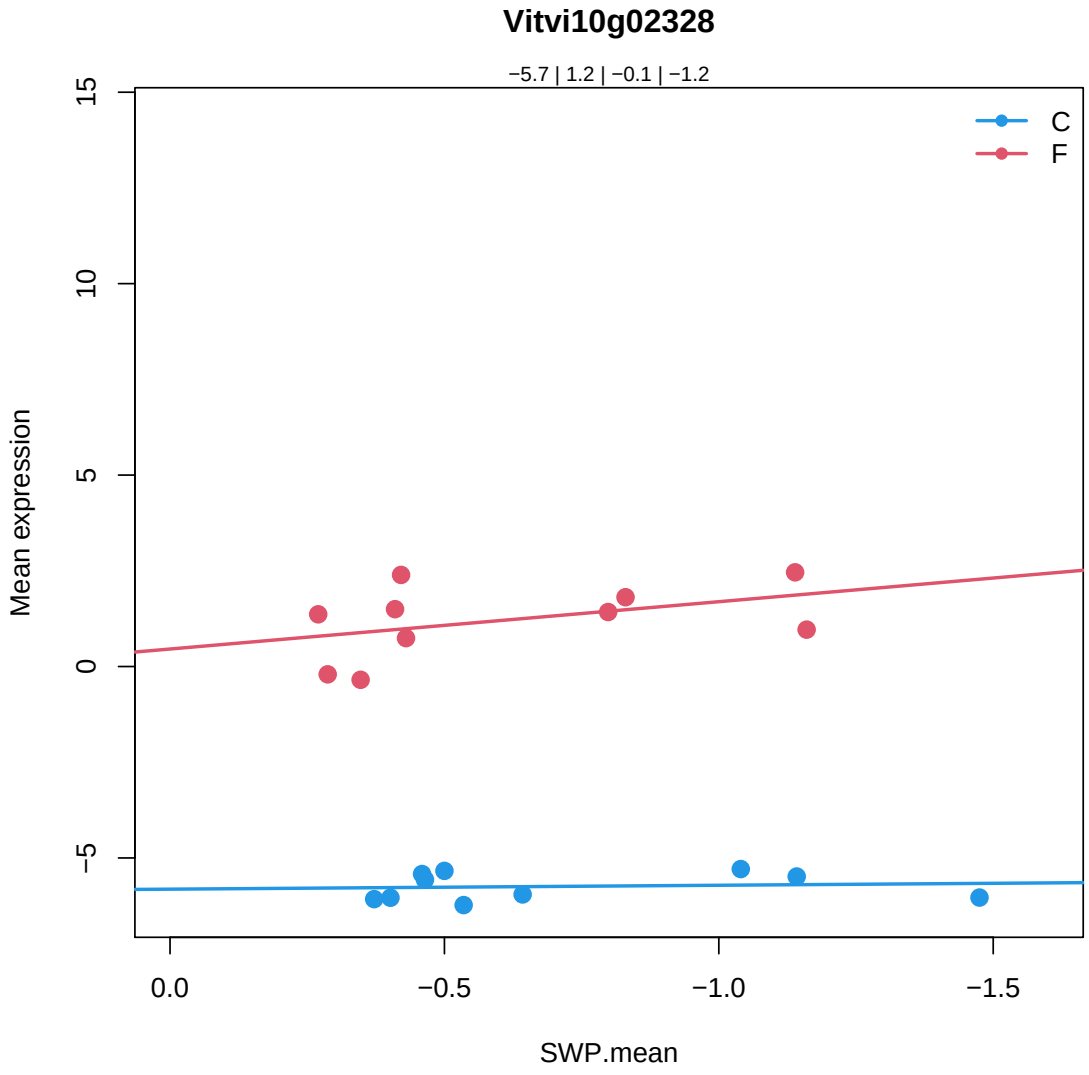
7.4.119 Vitvi10g02328: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g02328
        35.2
        not assigned.unknown
        B-box type zinc finger family protein |
        Chr4:13675853-13676616 FORWARD LENGTH=223 |
        201606
```

Coefficients for Vitvi10g02328.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.743315	2.15372e-18	***	6.743426e-18	***
SlopeC	-0.1021136	0.8593585		0.9737381	
MeanF-MeanC	6.953263	5.463107e-17	***	1.051375e-14	***
SlopeF-SlopeC	-1.134082	0.1948572		0.9999488	



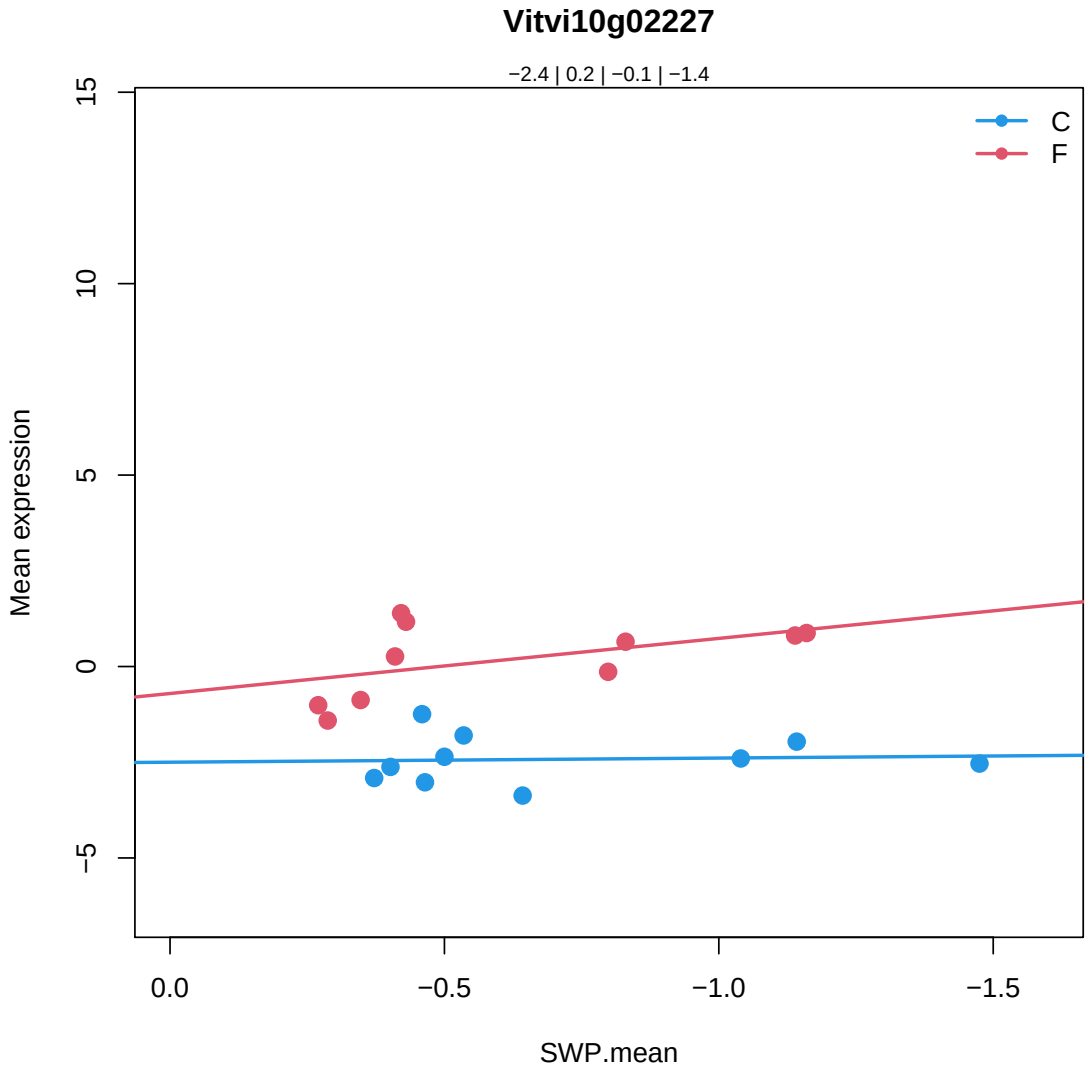
7.4.120 Vitvi10g02227: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g02227
        30.2.17
        signalling.receptor kinases.DUF 26
        Receptor-like protein kinase-related family protein |
        Chr3:7771065-7772137 FORWARD LENGTH=252 |
        201606
```

Coefficients for Vitvi10g02227.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-2.423304	6.172705e-10	***	7.843632e-10	***
SlopeC	-0.1082359	0.8673084		0.9757404	
MeanF-MeanC	2.595396	7.441044e-08	***	3.150455e-06	***
SlopeF-SlopeC	-1.330957	0.1766957		0.9999488	



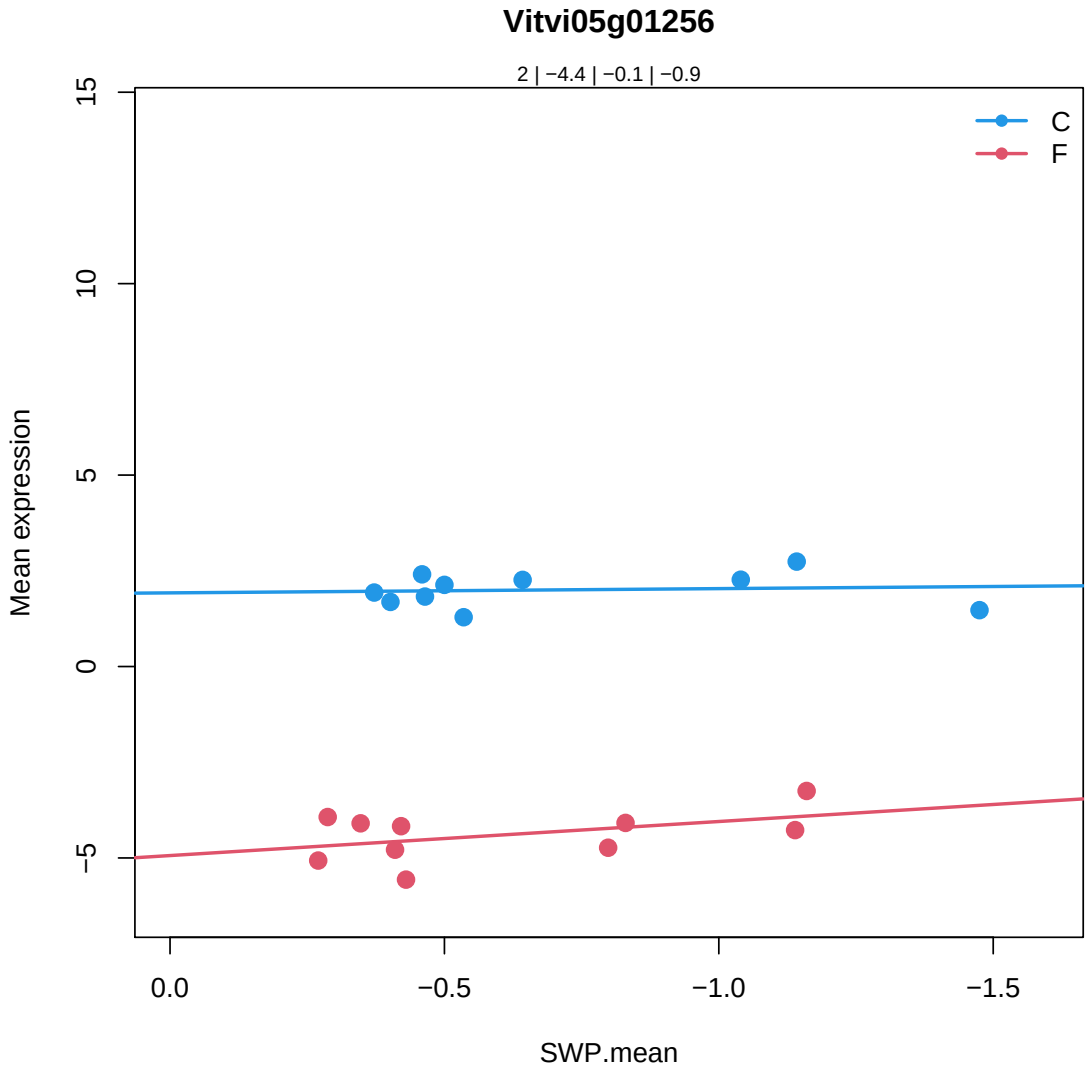
7.4.121 Vitvi05g01256: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01256
        35.2
        not assigned.unknown
        putative recombination initiation defect 1 |
        Chr4:8178330-8183515 FORWARD LENGTH=1330 |
        201606
```

Coefficients for Vitvi05g01256.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.001451	6.940822e-11	***	9.134964e-11	***
SlopeC	-0.110715	0.8158342		0.9600047	
MeanF-MeanC	-6.397203	5.618949e-18	***	1.276116e-15	***
SlopeF-SlopeC	-0.7789144	0.2773861		0.9999488	



7.4.122 Vitvi08g02249: type3

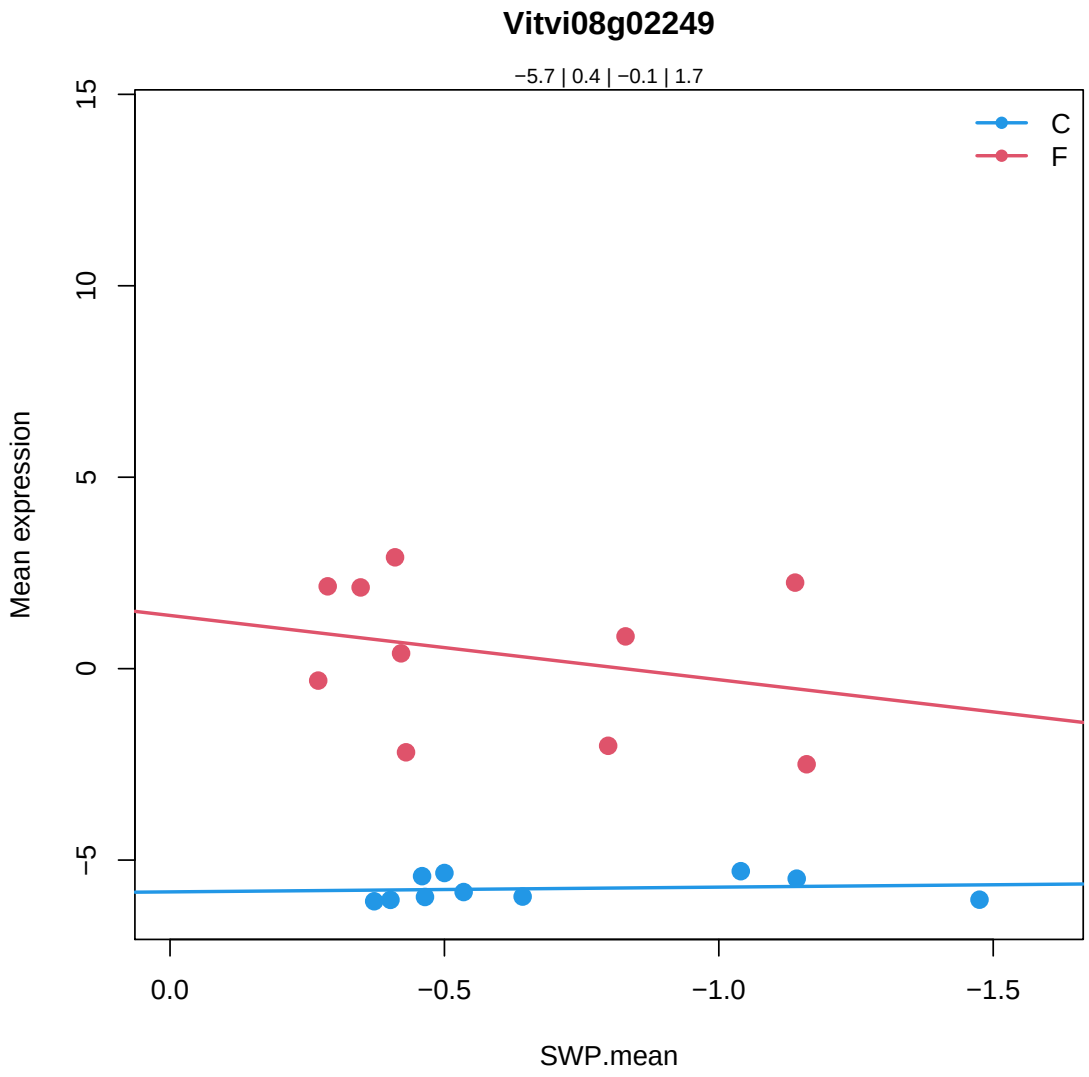
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g02249
        29.5
        protein.degradation
        Eukaryotic aspartyl protease family protein |
        Chr3:19465644-19467053 REVERSE LENGTH=469 |
        201606

Vitvi08g02249
        35.2
        not assigned.unknown
        Eukaryotic aspartyl protease family protein |
        Chr3:19465644-19467053 REVERSE LENGTH=469 |
        201606
```

Coefficients for Vitvi08g02249.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.743315	3.296028e-12	***	4.598028e-12	***
SlopeC	-0.1237221	0.9152126		0.9842726	
MeanF-MeanC	6.109273	6.937645e-10	***	4.179588e-08	***
SlopeF-SlopeC	1.802499	0.3033914		0.9999488	


Vitvi08g02249
−5.7 | 0.4 | −0.1 | 1.7
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

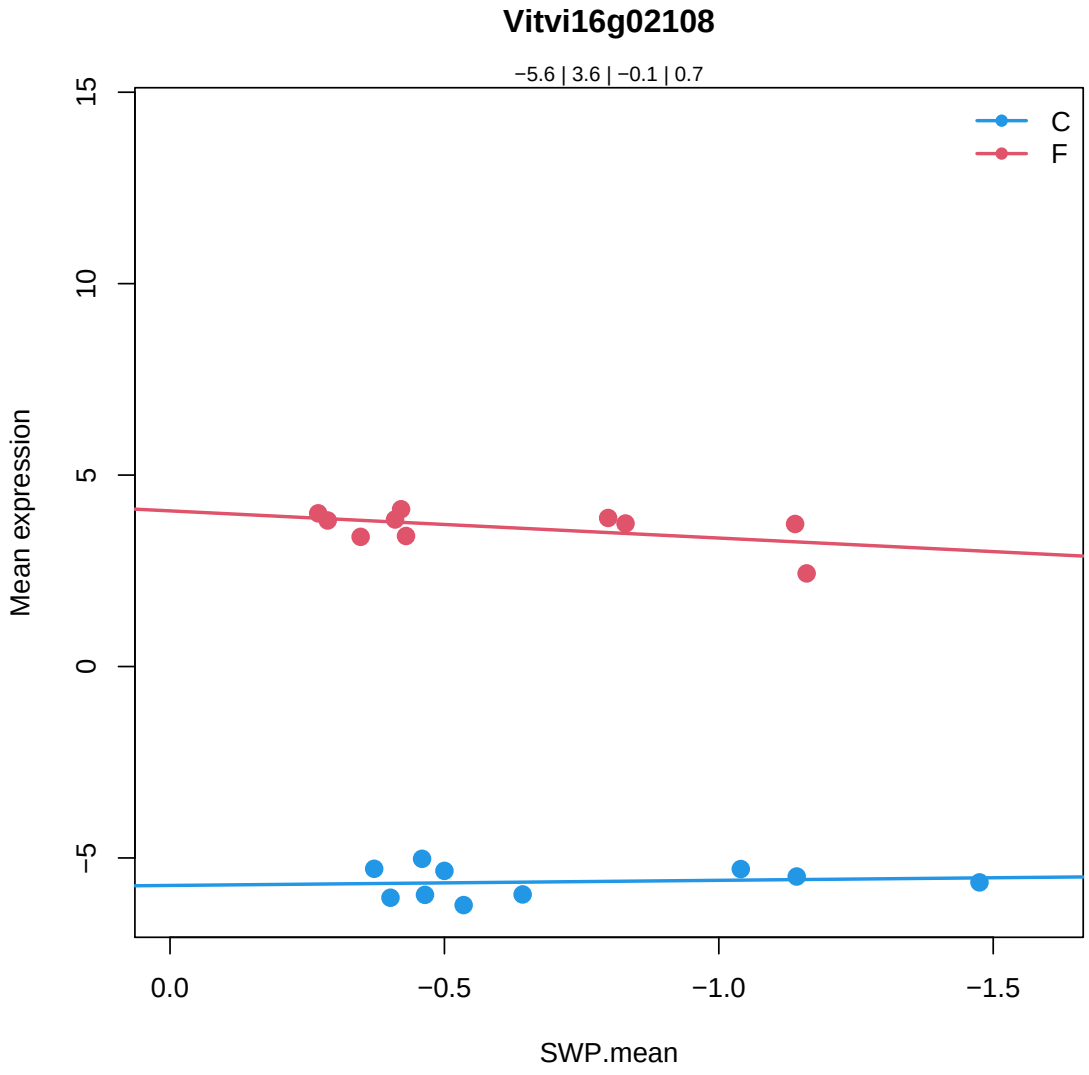
7.4.123 Vitvi16g02108: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g02108
        35.2
        not assigned.unknown
        PR5-like receptor kinase |
        Chr5:15293122-15295838 REVERSE LENGTH=672 |
        201606
```

Coefficients for Vitvi16g02108.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.624317	1.351418e-21	***	1.448545e-20	***
SlopeC	-0.1338112	0.7366805		0.9430092	
MeanF-MeanC	9.257013	5.415291e-23	***	7.503624e-20	***
SlopeF-SlopeC	0.8429268	0.1638138		0.9999488	



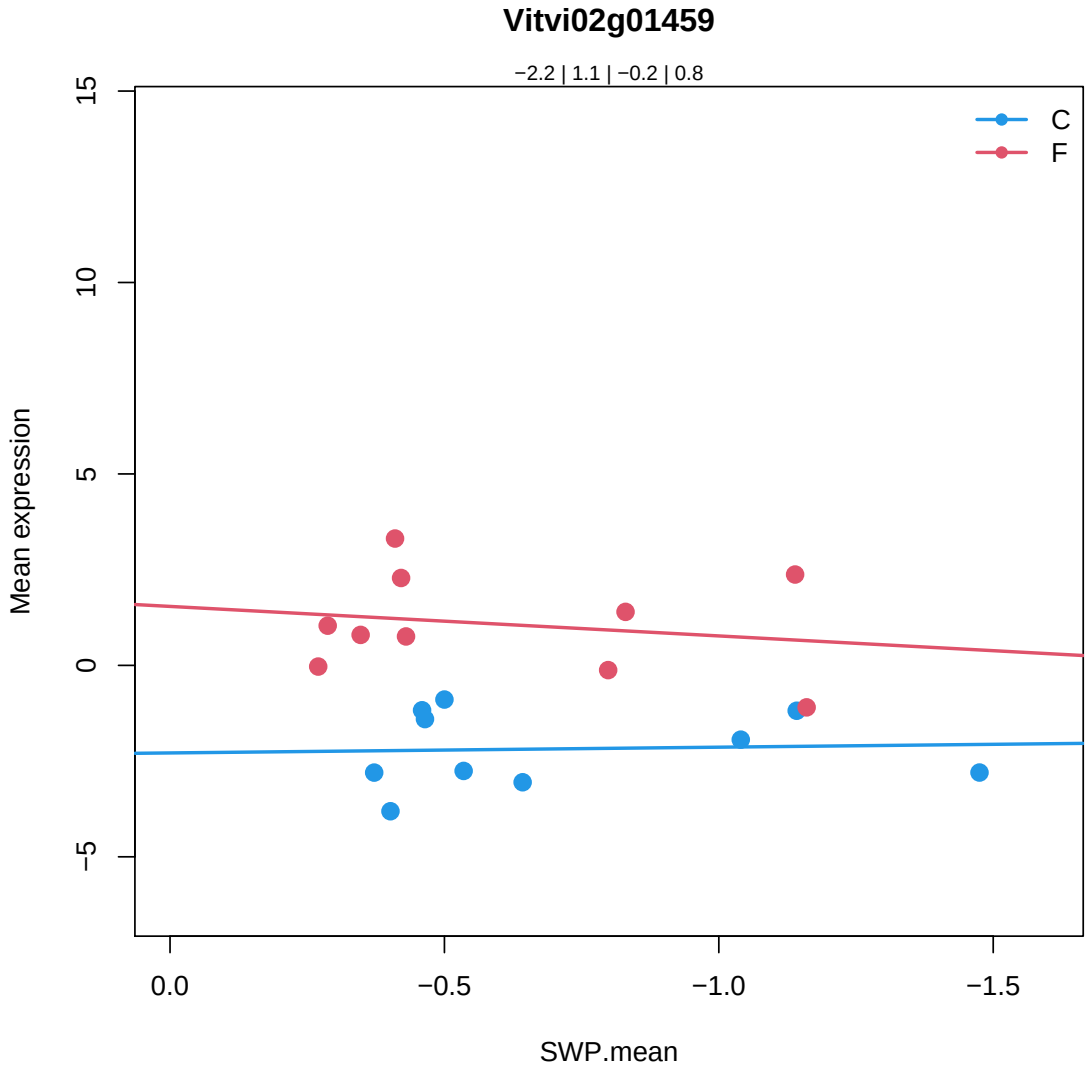
7.4.124 Vitvi02g01459: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g01459
        35.2
        not assigned.unknown
        [Sotub08g023330.1.1]: Cytochrome b [Sotub08g023340.1.1]: Unknown Prote
        [stNIB-v1_0012210]
```

Coefficients for Vitvi02g01459.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-2.181328	2.445539e-06	***	2.797787e-06	***
SlopeC	-0.1500046	0.8767469		0.9764303	
MeanF-MeanC	3.25143	1.13799e-06	***	3.638867e-05	***
SlopeF-SlopeC	0.9207425	0.52431		0.9999488	



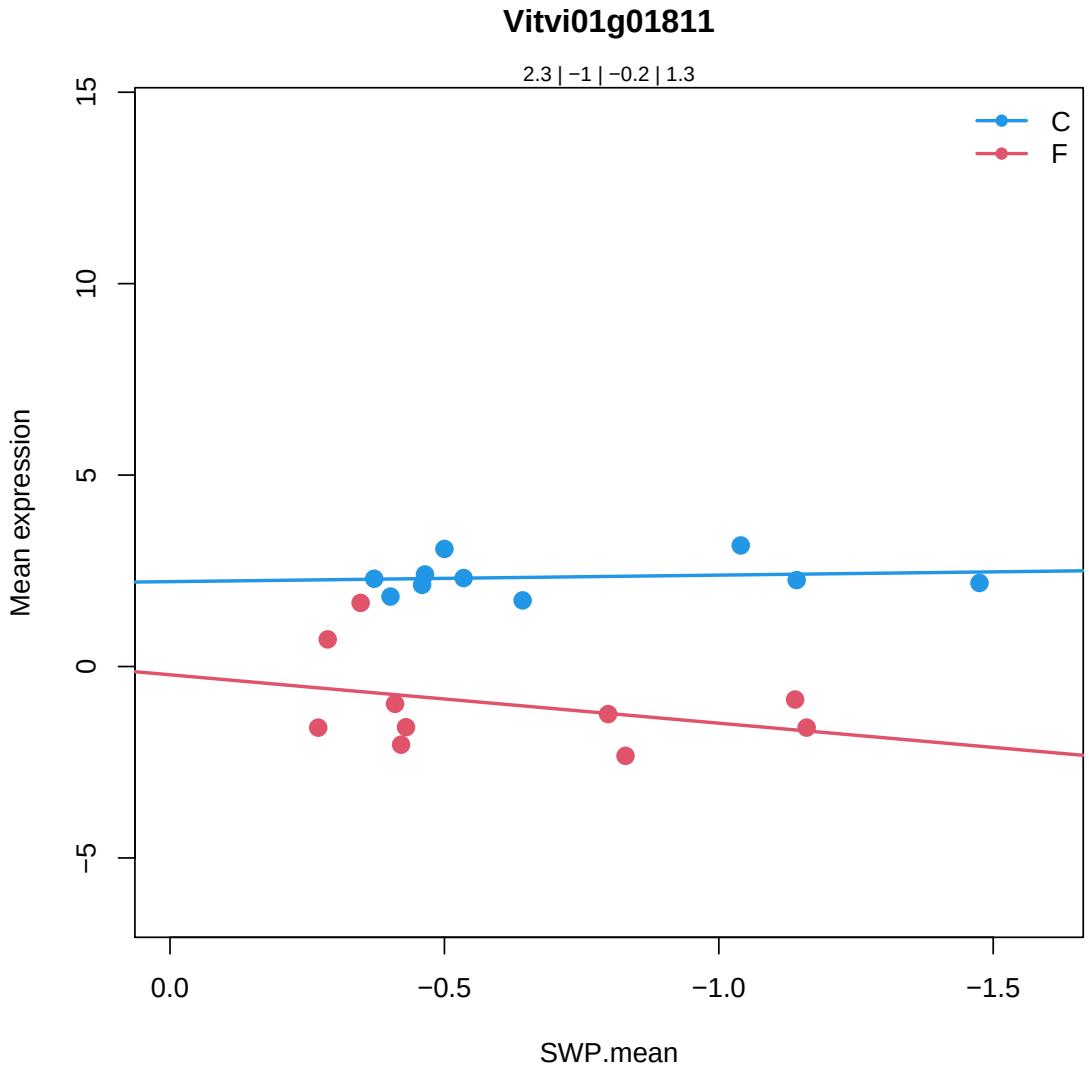
7.4.125 Vitvi01g01811: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01811
        35.2
        not assigned.unknown
        heparan-alpha-glucosaminide N-acetyltransferase-like protein (DUF1624)
        Chr5:19392408-19394689 FORWARD LENGTH=403 |
        201606
```

Coefficients for Vitvi01g01811.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.336578	1.790596e-08	***	2.169669e-08	***
SlopeC	-0.1698524	0.822491		0.9640425	
MeanF-MeanC	-3.322936	1.629062e-08	***	7.857644e-07	***
SlopeF-SlopeC	1.433989	0.2113931		0.9999488	



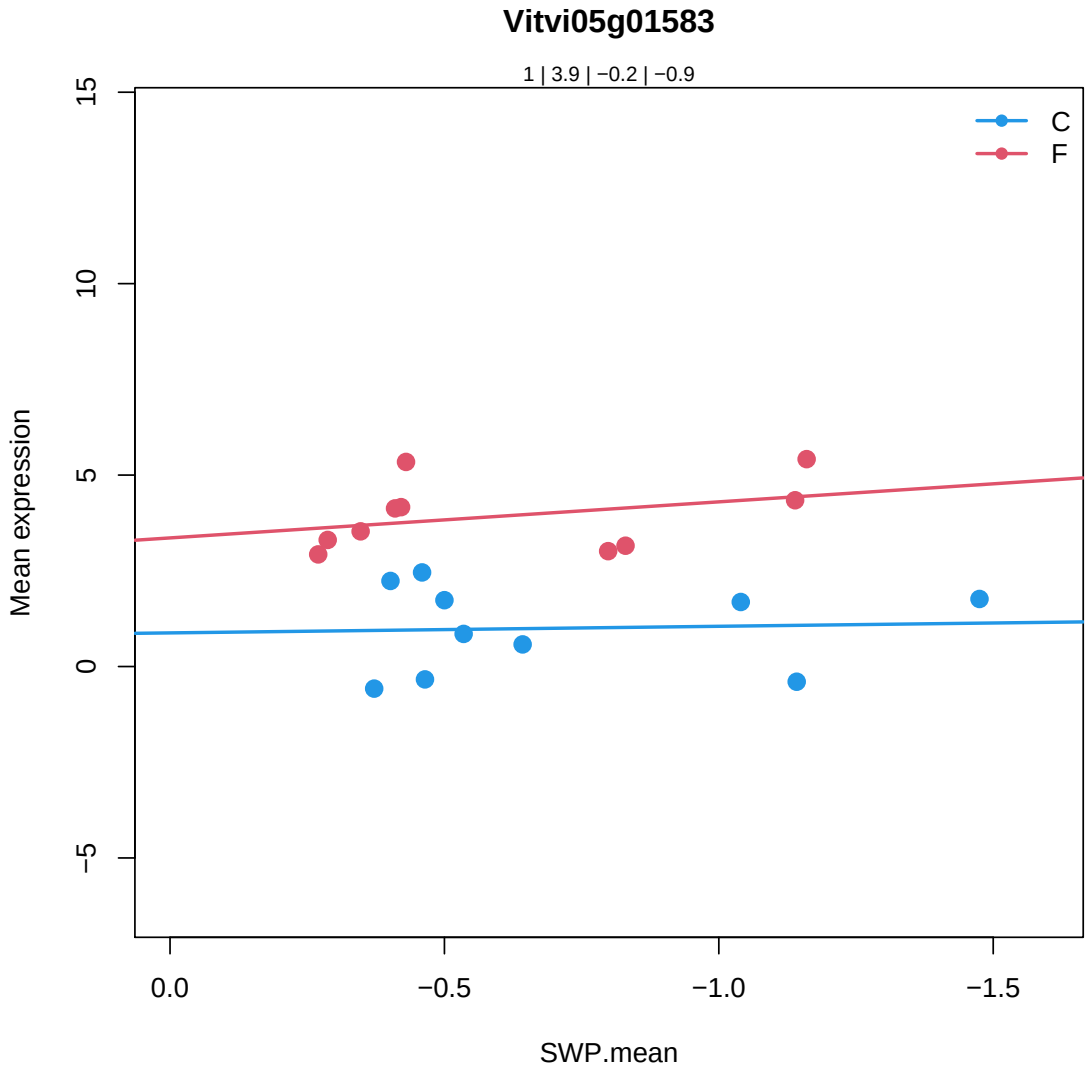
7.4.126 Vitvi05g01583: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01583
        35.2
        not assigned.unknown
        homolog of carrot EP3-3 chitinase |
        Chr3:20145935-20147034 FORWARD LENGTH=273 |
        201606
```

Coefficients for Vitvi05g01583.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.999109	0.003214568	**	0.003442212	**
SlopeC	-0.1723941	0.8389707		0.9693055	
MeanF-MeanC	2.933626	7.446069e-07	***	2.499845e-05	***
SlopeF-SlopeC	-0.7694163	0.543858		0.9999488	



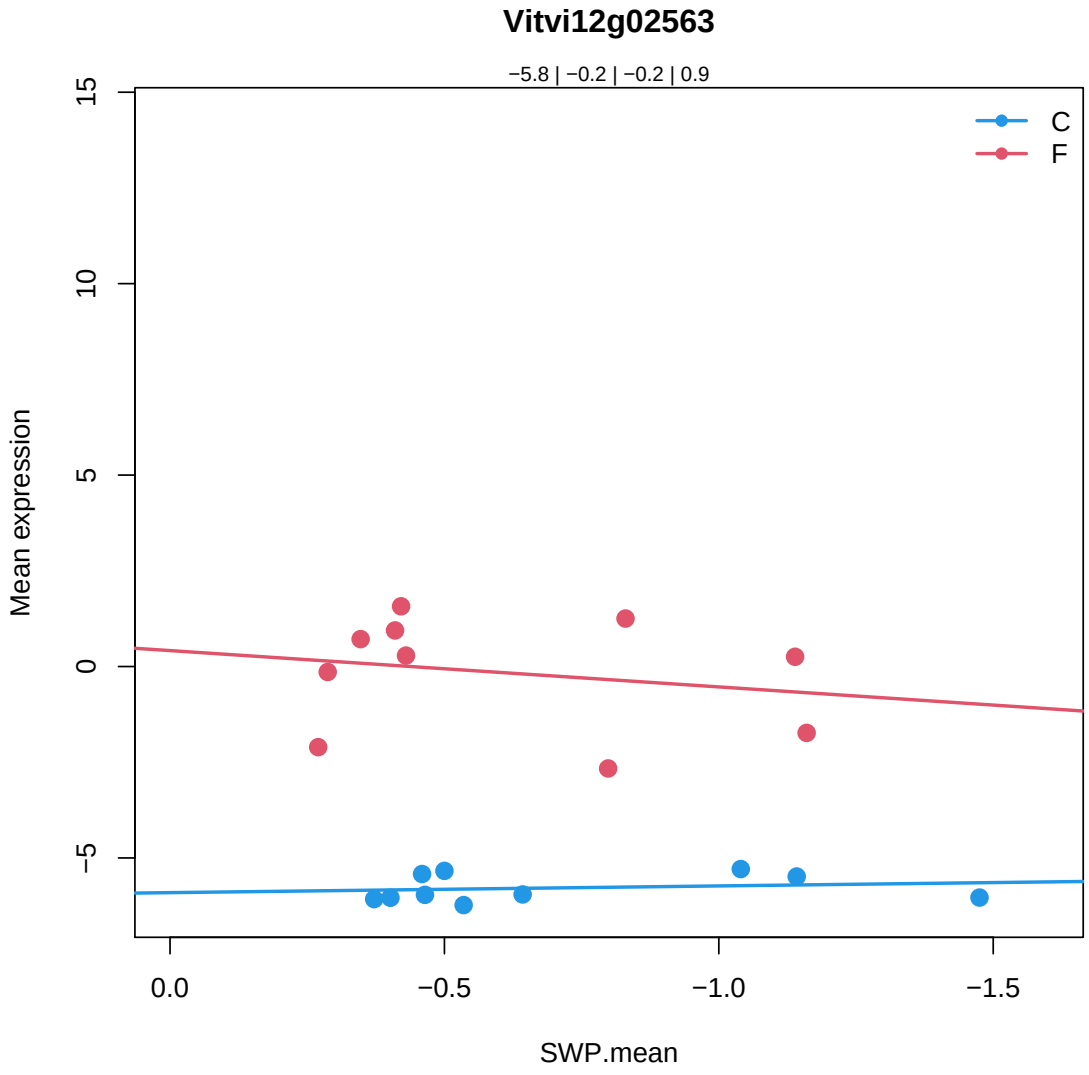
7.4.127 Vitvi12g02563: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02563
        35.2
        not assigned.unknown
        Peroxidase superfamily protein |
        Chr5:25659551-25660946 REVERSE LENGTH=328 |
        201606
```

Coefficients for Vitvi12g02563.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.782939	1.37936e-14	***	2.273133e-14	***
SlopeC	-0.175305	0.8435181		0.9700368	
MeanF-MeanC	5.620778	2.202456e-11	***	1.653686e-09	***
SlopeF-SlopeC	1.123919	0.3989503		0.9999488	



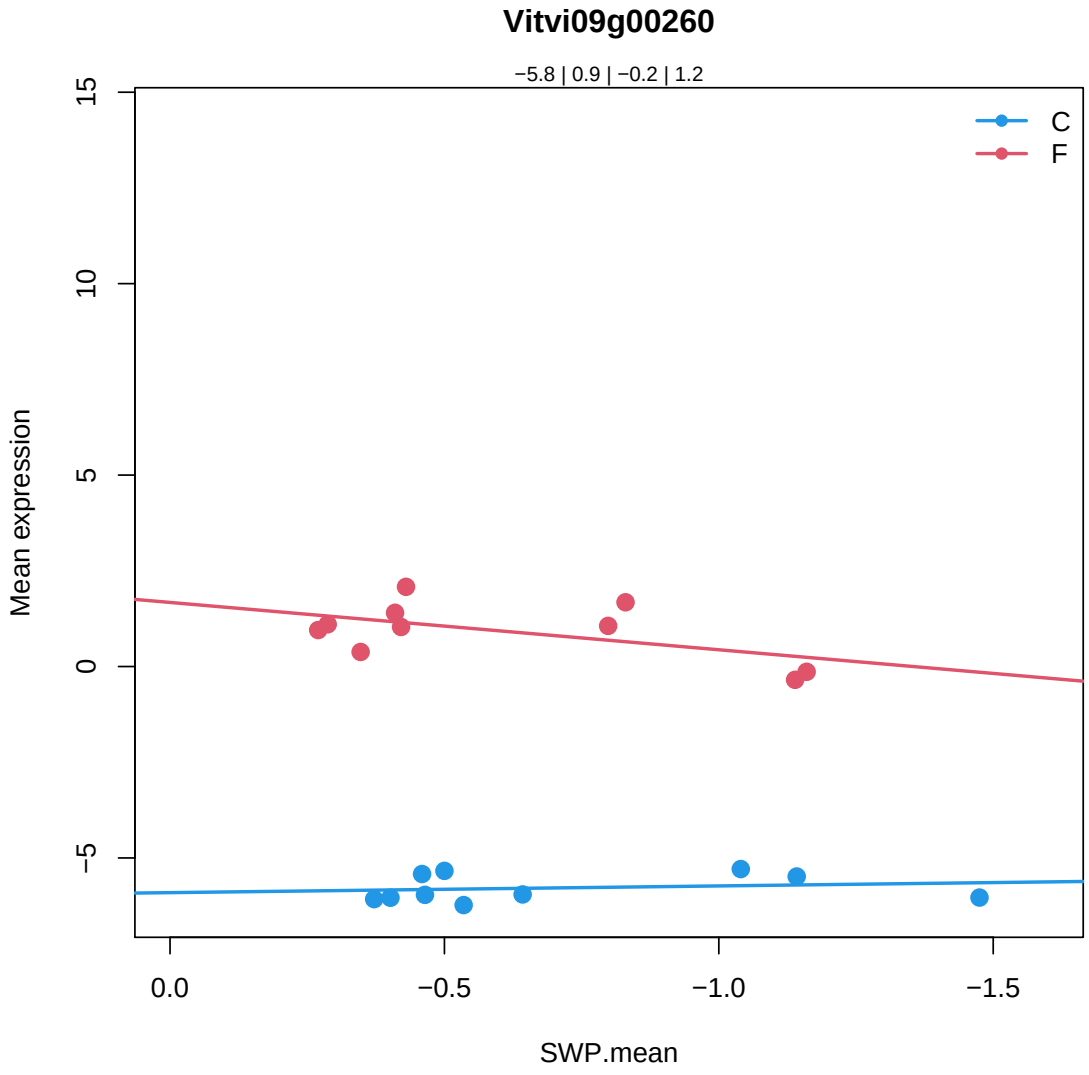
7.4.128 Vitvi09g00260: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00260
        35.2
        not assigned.unknown
        root hair specific 16 |
        Chr4:14385631-14389524 FORWARD LENGTH=911 |
        201606
```

Coefficients for Vitvi09g00260.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.782939	2.796541e-20	***	1.639624e-19	***
SlopeC	-0.175305	0.7105724		0.935038	
MeanF-MeanC	6.703427	1.820469e-18	***	4.624598e-16	***
SlopeF-SlopeC	1.411262	0.05450845	.	0.9999488	



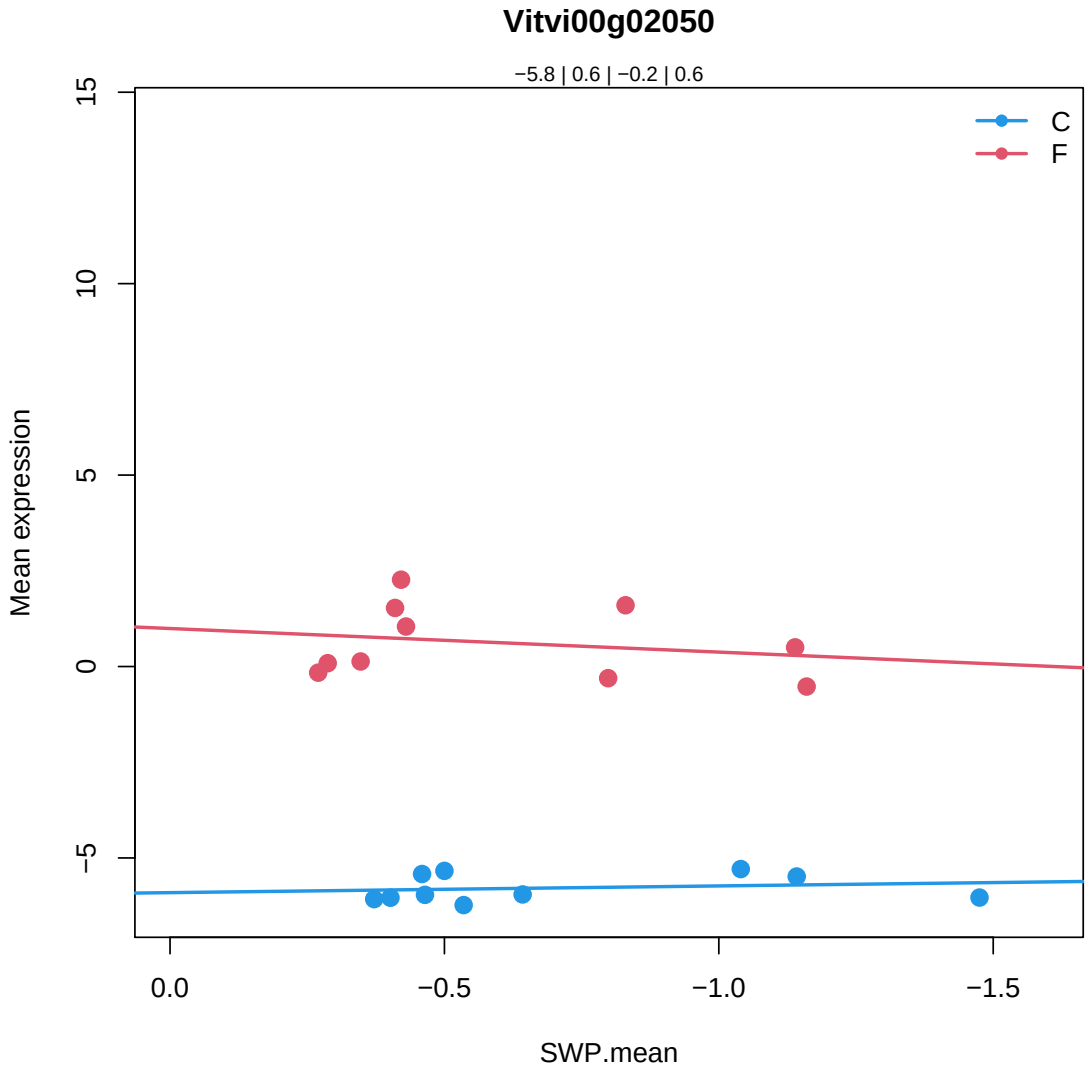
7.4.129 Vitvi00g02050: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi00g02050
        35.2
        not assigned.unknown
        white-brown complex-like protein |
        Chr1:6142870-6145894 FORWARD LENGTH=703 |
        201606
```

Coefficients for Vitvi00g02050.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.782939	5.701001e-18	***	1.591614e-17	***
SlopeC	-0.175305	0.7732186		0.9513135	
MeanF-MeanC	6.400031	9.078429e-16	***	1.317842e-13	***
SlopeF-SlopeC	0.7909815	0.3861325		0.9999488	



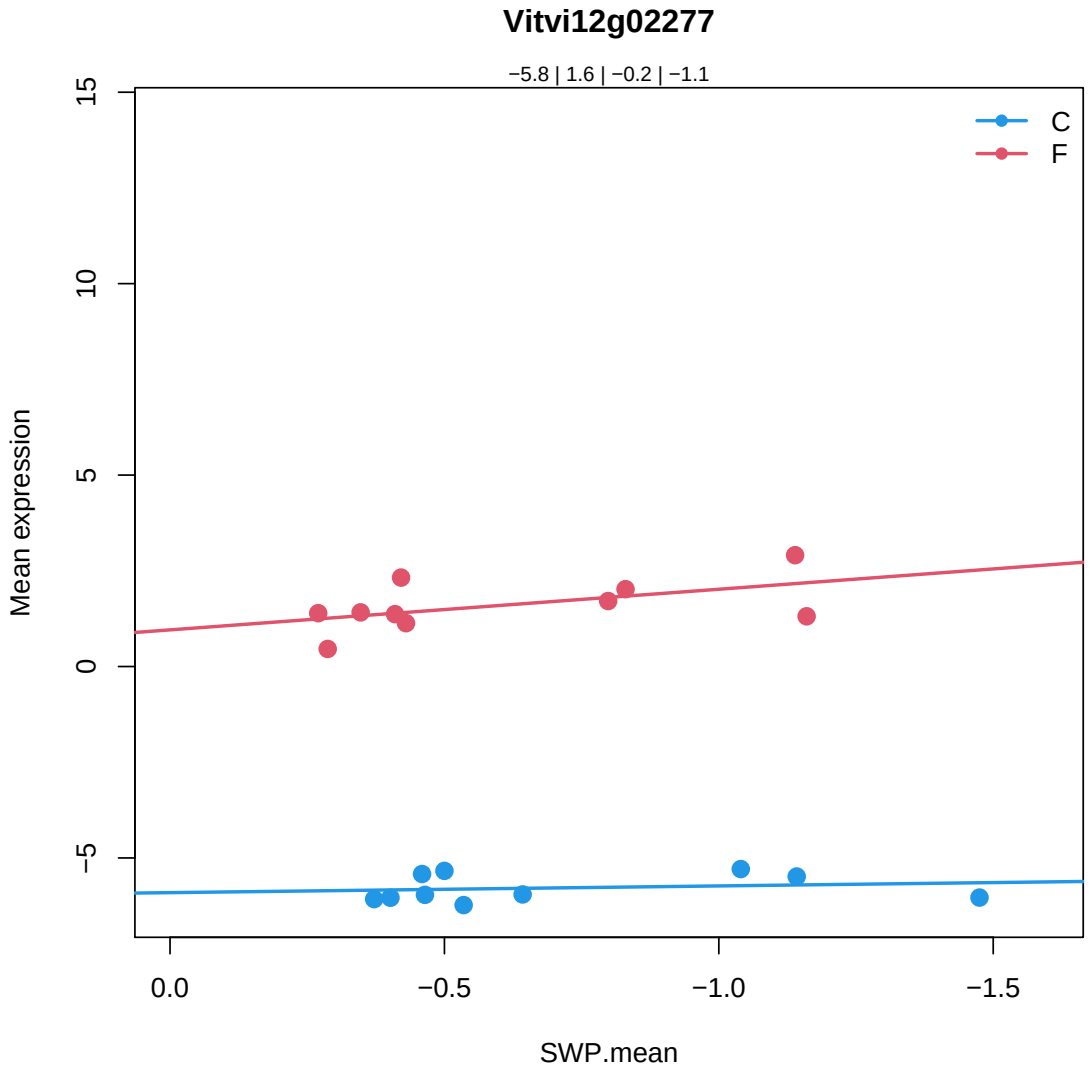
7.4.130 Vitvi12g02277: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02277
        26.6
        misc.O-methyl transferases
        O-methyltransferase family protein |
        Chr4:16730989-16732808 REVERSE LENGTH=382 |
        201606
```

Coefficients for Vitvi12g02277.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.782939	8.296975e-21	***	6.147909e-20	***
SlopeC	-0.175305	0.6943143		0.9312515	
MeanF-MeanC	7.386632	7.098532e-20	***	2.412759e-17	***
SlopeF-SlopeC	-0.8857104	0.1903979		0.9999488	



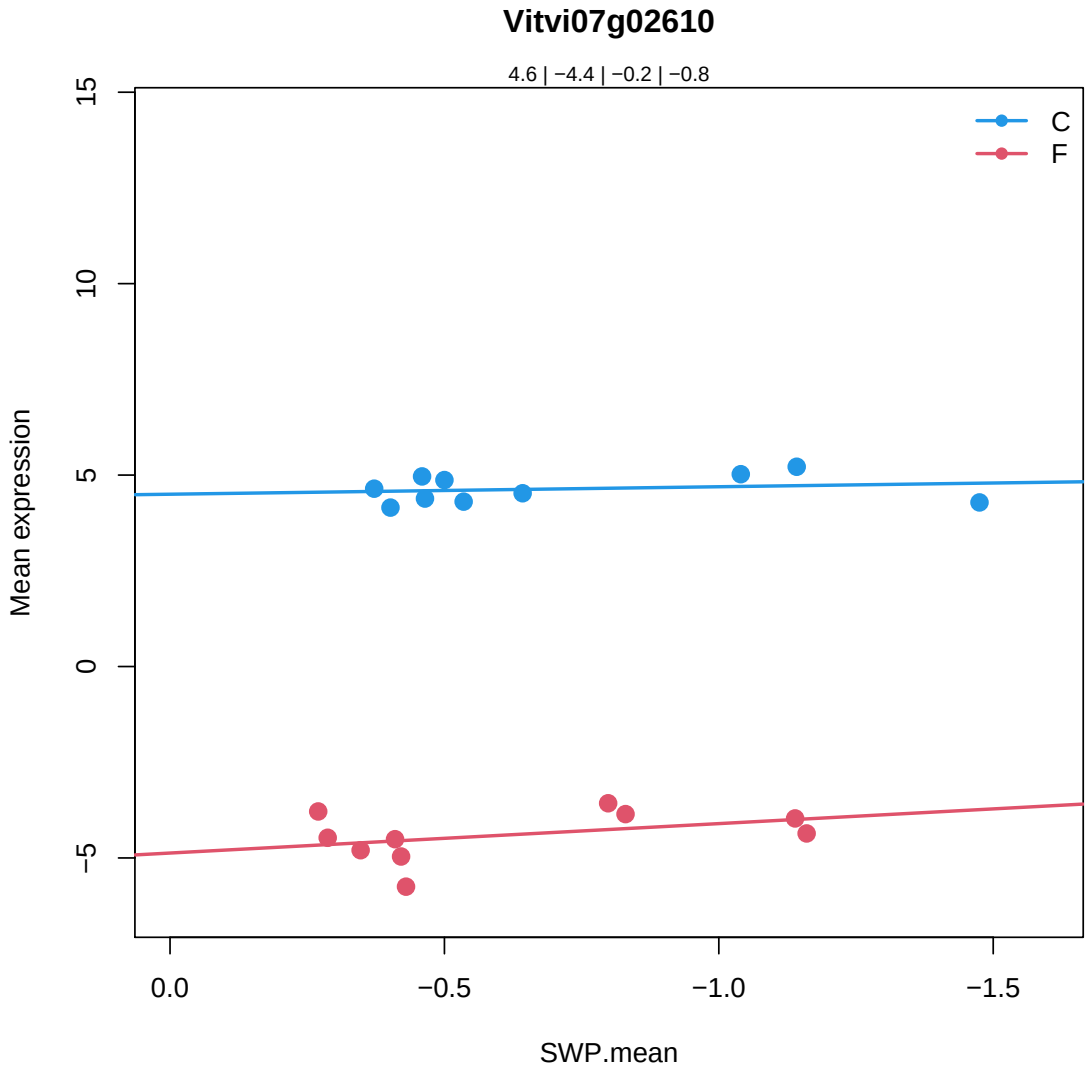
7.4.131 Vitvi07g02610: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g02610
        1.2.5
        PS.photorespiration.serine hydroxymethyltransferase
        serine hydroxymethyltransferase 2 |
        Chr5:9418299-9421725 FORWARD LENGTH=517 |
        201606
```

Coefficients for Vitvi07g02610.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.637405	1.581562e-18	***	5.136202e-18	***
SlopeC	-0.1950476	0.6710919		0.9241164	
MeanF-MeanC	-9.040767	1.838372e-21	***	1.120819e-18	***
SlopeF-SlopeC	-0.5736965	0.4042537		0.9999488	



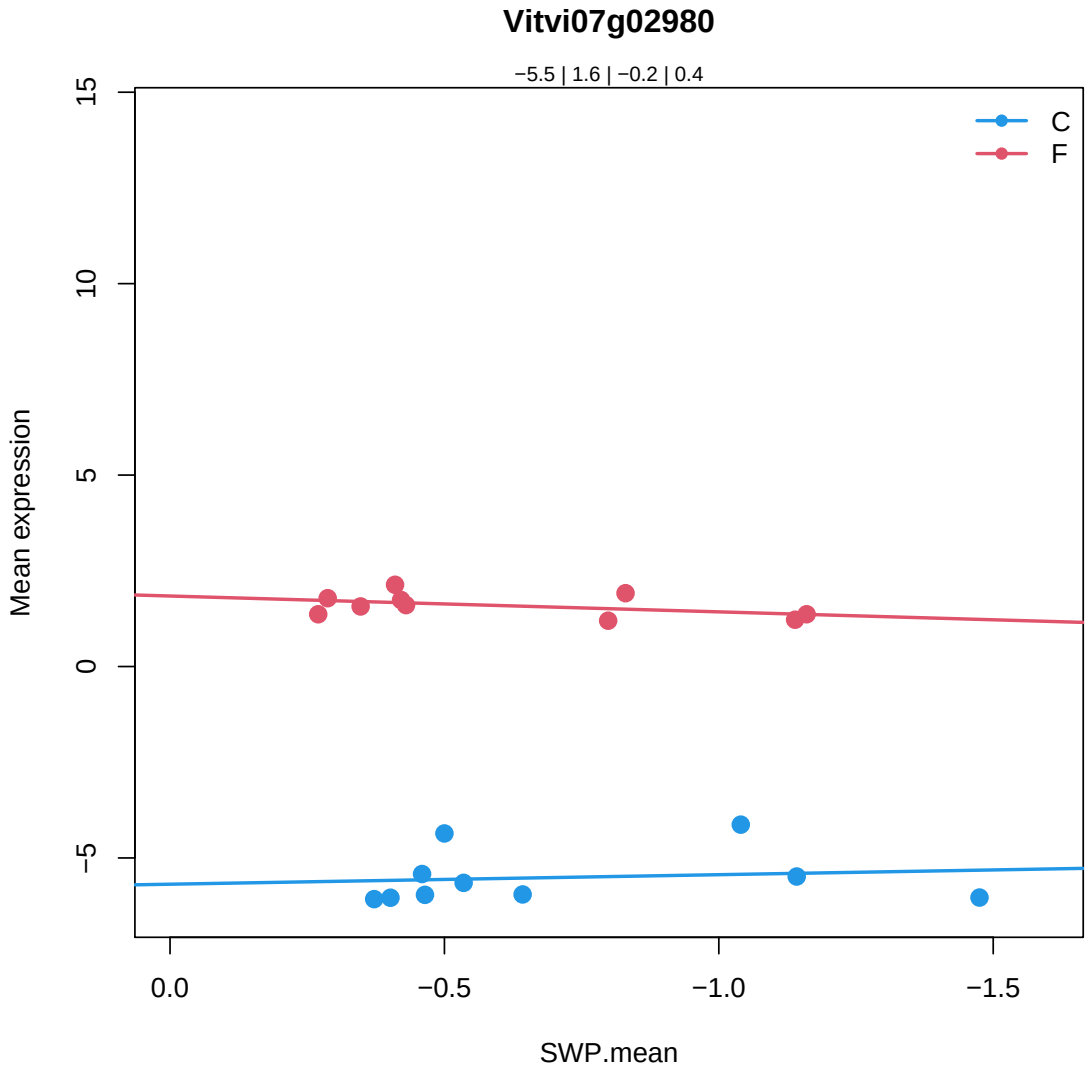
7.4.132 Vitvi07g02980: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g02980
        31.4
        cell.vesicle transport
        syntaxin of plants 51 |
        Chr1:5555183-5556340 REVERSE LENGTH=232 |
        201606
```

Coefficients for Vitvi07g02980.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.511141	1.543888e-19	***	6.87064e-19	***
SlopeC	-0.248419	0.6114235		0.9065647	
MeanF-MeanC	7.100373	1.090434e-18	***	2.915858e-16	***
SlopeF-SlopeC	0.662695	0.3657246		0.9999488	



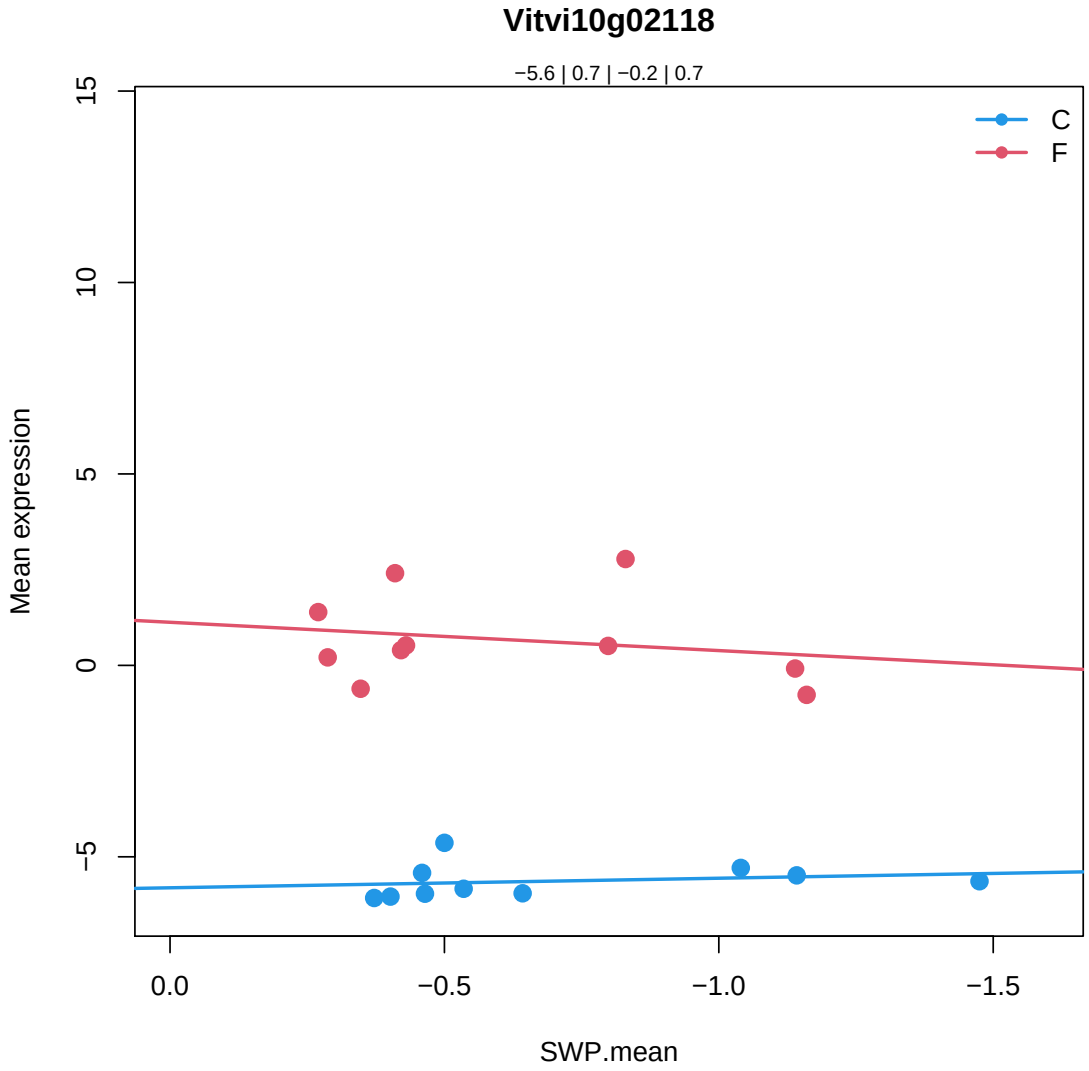
7.4.133 Vitvi10g02118: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g02118
        35.2
        not assigned.unknown
        [Sotub12g030120.1.1]: Ankyrin repeat family protein-like [Sotub05g0194
        [stNIB-v1_0002762]
```

Coefficients for Vitvi10g02118.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.633441	6.682918e-16	***	1.27934e-15	***
SlopeC	-0.2499543	0.7376838		0.9430092	
MeanF-MeanC	6.308418	7.588484e-14	***	8.203098e-12	***
SlopeF-SlopeC	0.9894694	0.3768534		0.9999488	



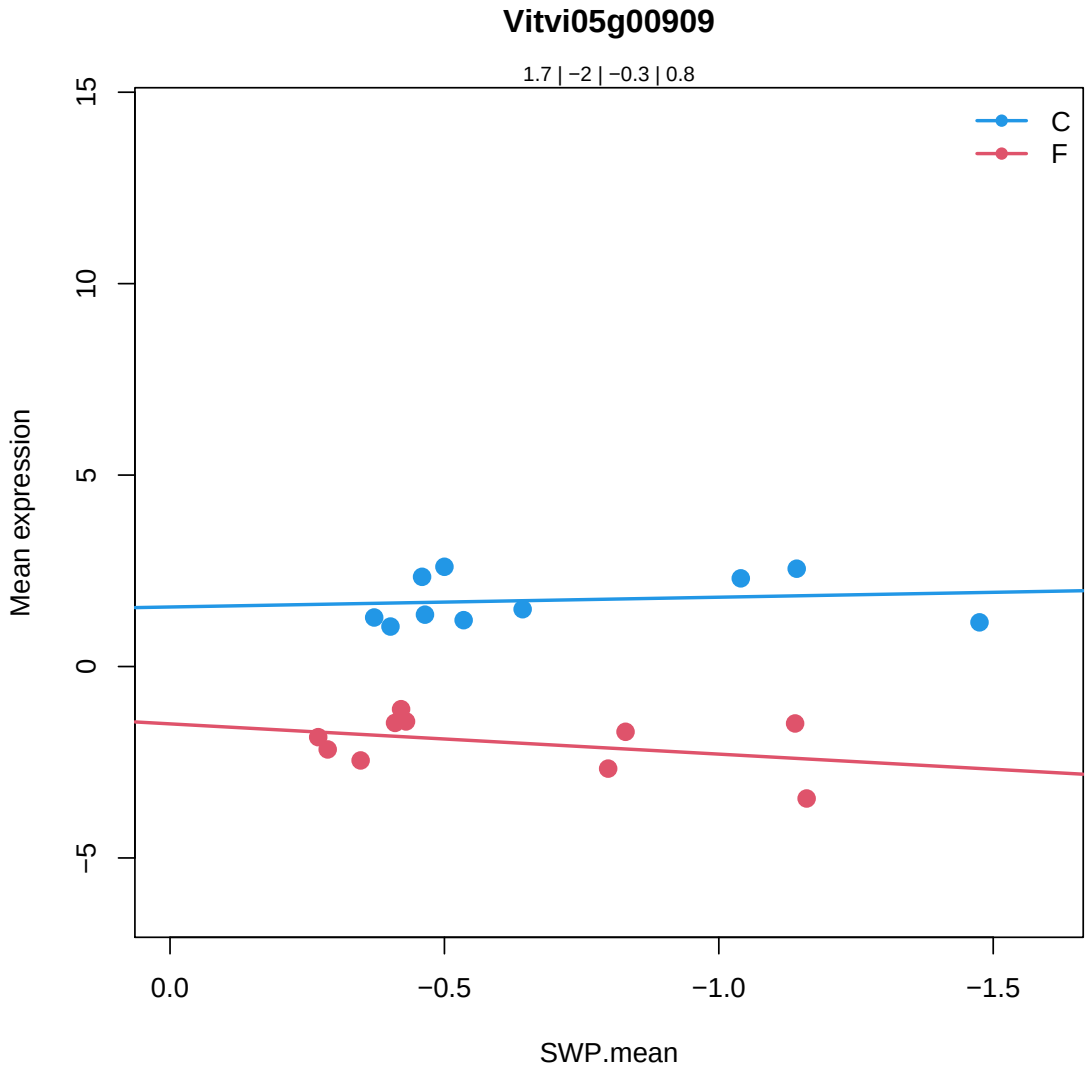
7.4.134 Vitvi05g00909: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00909
        20.1.2.2
        stress.biotic.receptors.TIR-NBS-LRR
        disease resistance protein (TIR-NBS-LRR class) |
        Chr5:5822999-5827153 FORWARD LENGTH=1295 |
        201606
```

Coefficients for Vitvi05g00909.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.734407	2.101861e-08	***	2.540165e-08	***
SlopeC	-0.2554092	0.6531717		0.919605	
MeanF-MeanC	-3.713598	1.157191e-11	***	9.234507e-10	***
SlopeF-SlopeC	1.045479	0.2235796		0.9999488	



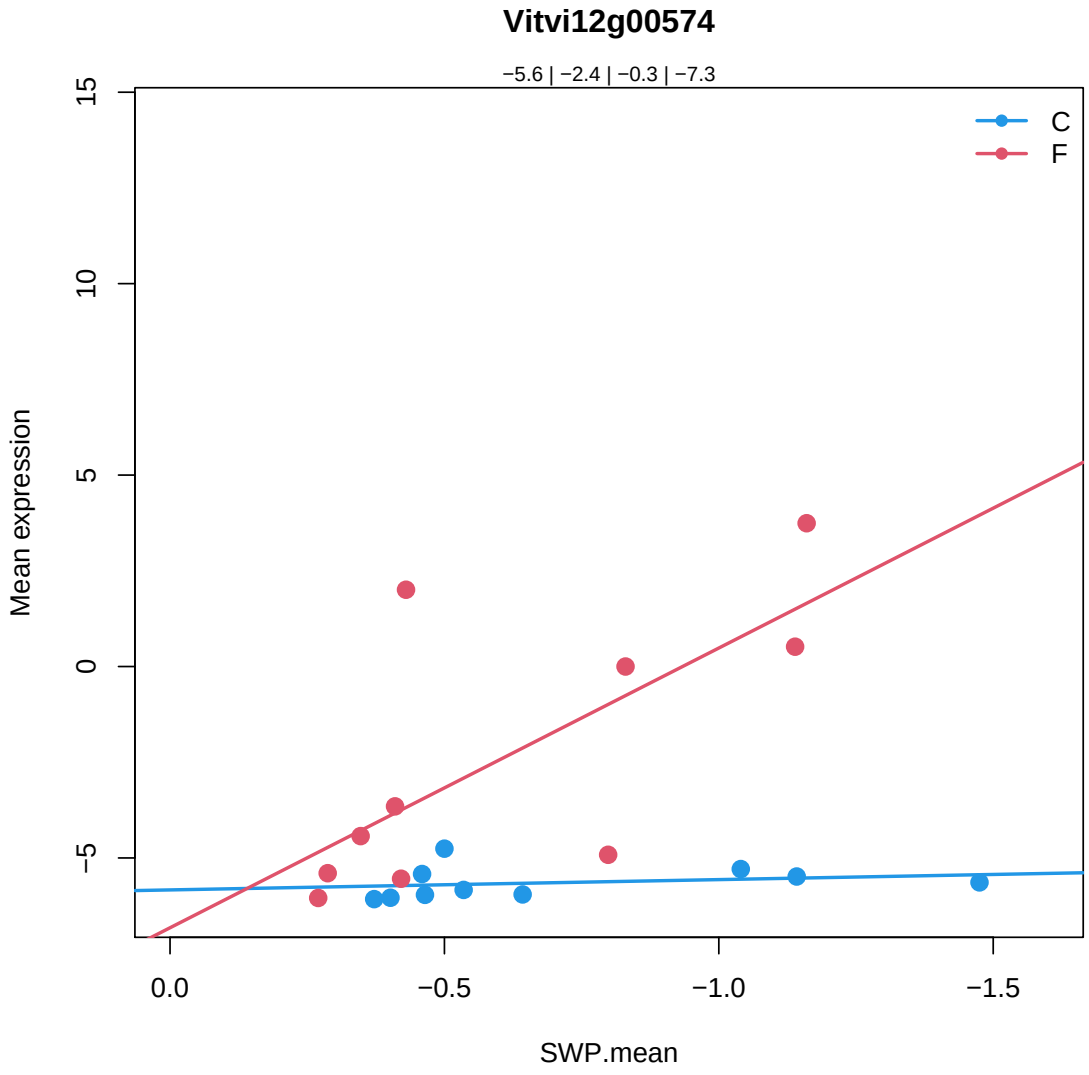
7.4.135 Vitvi12g00574: + type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00574
        16.1.5
        secondary metabolism.isoprenoids.terpenoids
        terpene synthase-like sequence-1%2C8-cineole |
        Chr3:9447545-9450316 FORWARD LENGTH=600 |
        201606
```

Coefficients for Vitvi12g00574.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.645691	6.169158e-10	***	7.839779e-10	***
SlopeC	-0.2692201	0.8584264		0.9734036	
MeanF-MeanC	3.273791	0.0002909881	***	0.004497484	**
SlopeF-SlopeC	-7.036961	0.004526106	**	0.9999488	



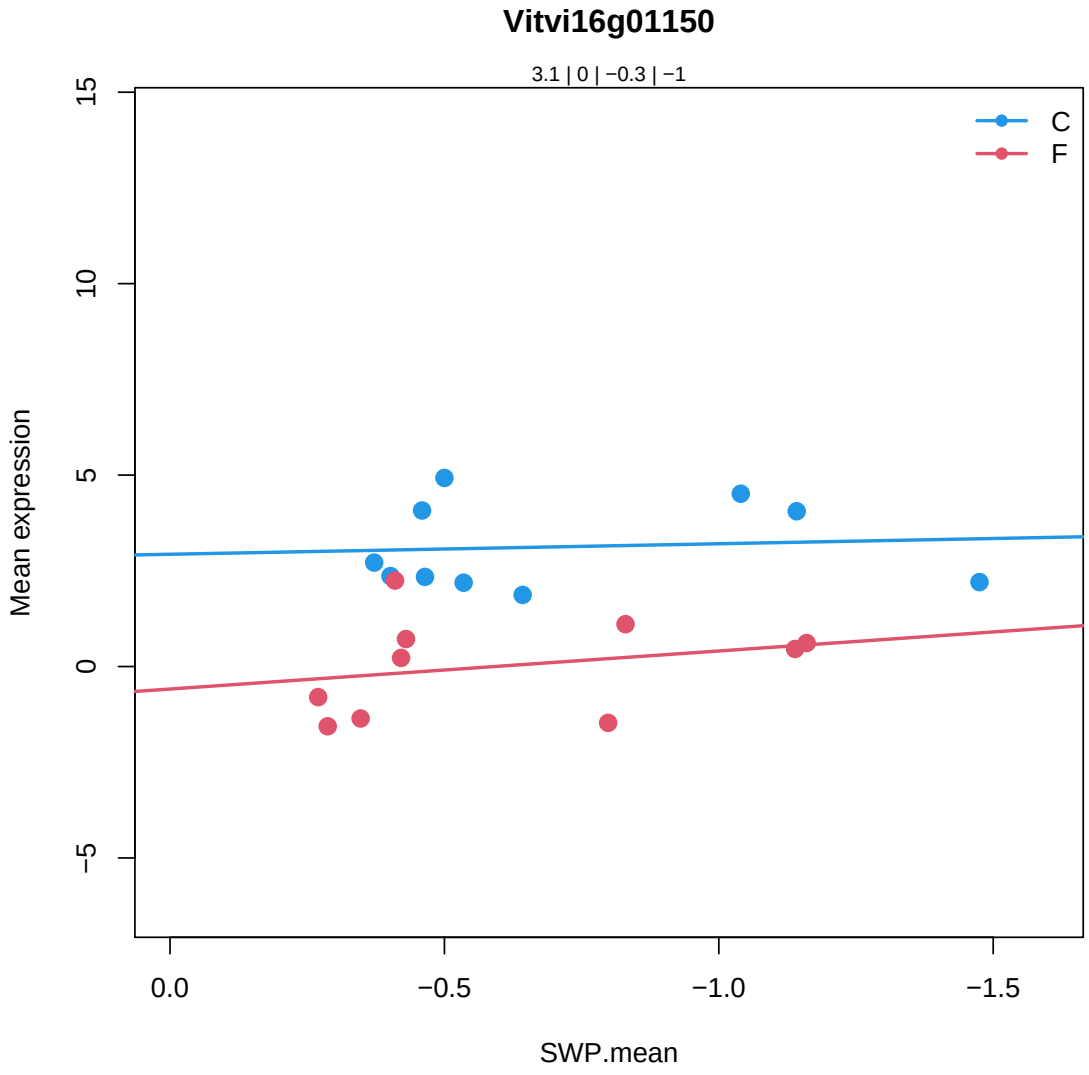
7.4.136 Vitvi16g01150: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01150
        35.2
        not assigned.unknown
        UDP-glucosyl transferase 88A1 |
        Chr3:5619355-5620833 REVERSE LENGTH=462 |
        201606
```

Coefficients for Vitvi16g01150.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.124938	1.127124e-08	***	1.37371e-08	***
SlopeC	-0.2741166	0.780935		0.9528017	
MeanF-MeanC	-3.107337	2.862501e-06	***	8.232121e-05	***
SlopeF-SlopeC	-0.7199466	0.6242786		0.9999488	



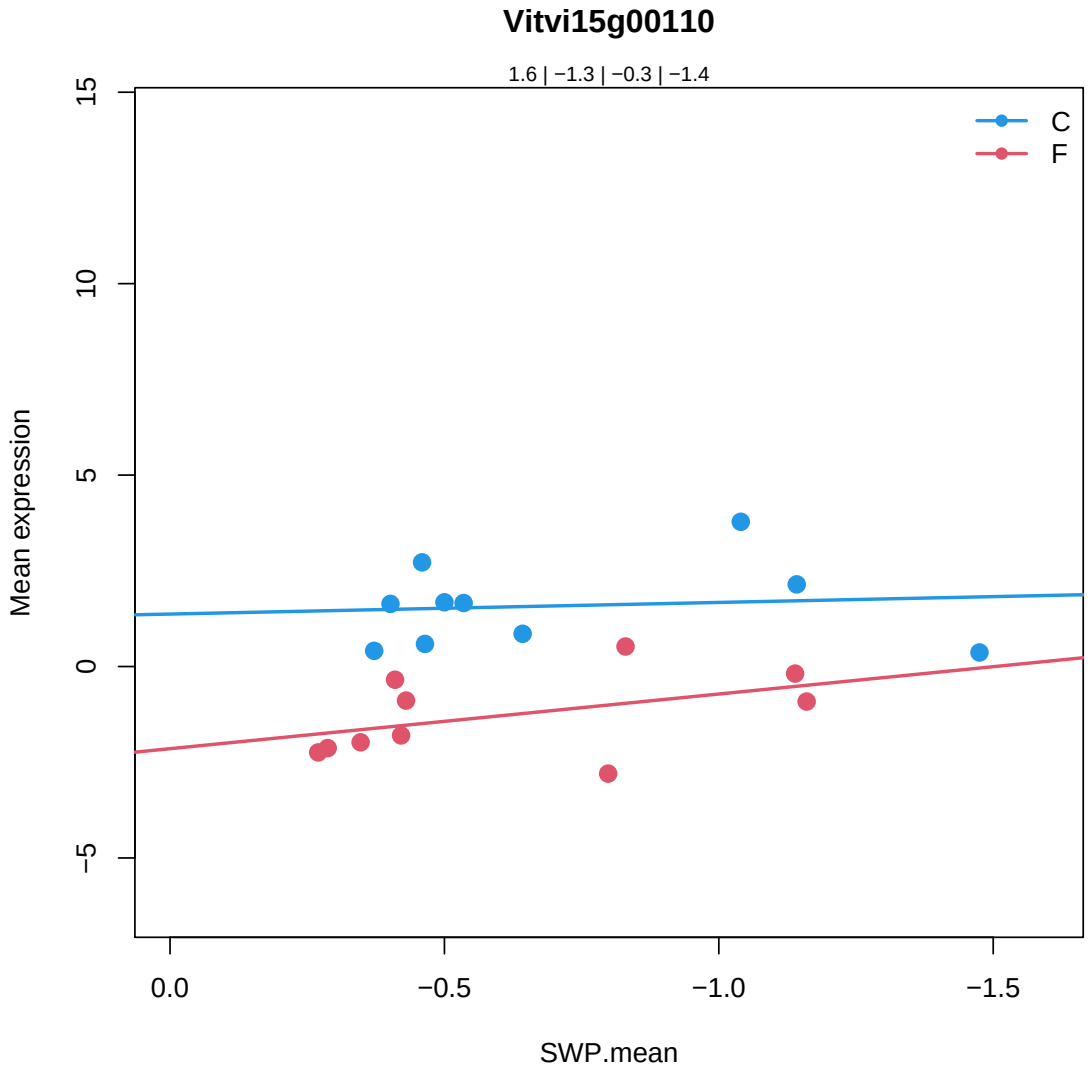
7.4.137 Vitvi15g00110: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g00110
        35.2
        not assigned.unknown
        Pentatricopeptide repeat (PPR) superfamily protein |
        Chr4:14962617-14964995 REVERSE LENGTH=792 |
        201606
```

Coefficients for Vitvi15g00110.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.58373	3.827328e-05	***	4.26309e-05	***
SlopeC	-0.3035374	0.7255101		0.9394623	
MeanF-MeanC	-2.859953	1.41705e-06	***	4.481054e-05	***
SlopeF-SlopeC	-1.124079	0.385905		0.9999488	



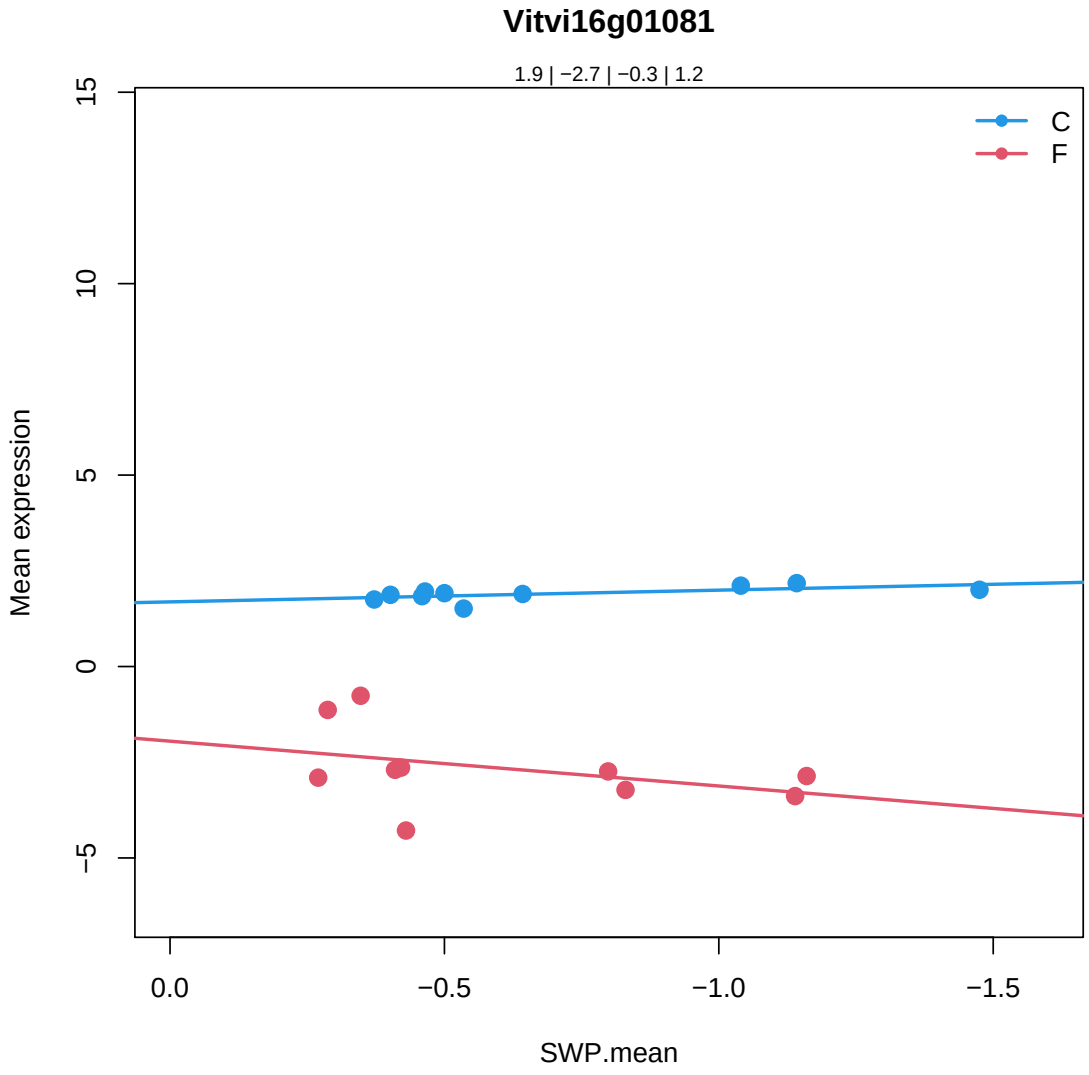
7.4.138 Vitvi16g01081: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01081
        35.1
        not assigned.no ontology
        Ribosomal protein L31 |
        Chr1:28272163-28272687 FORWARD LENGTH=144 |
        201606
```

Coefficients for Vitvi16g01081.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.903497	9.543851e-09	***	1.165511e-08	***
SlopeC	-0.3059787	0.6076322		0.9048393	
MeanF-MeanC	-4.566578	5.138006e-13	***	4.894593e-11	***
SlopeF-SlopeC	1.476801	0.1055467		0.9999488	



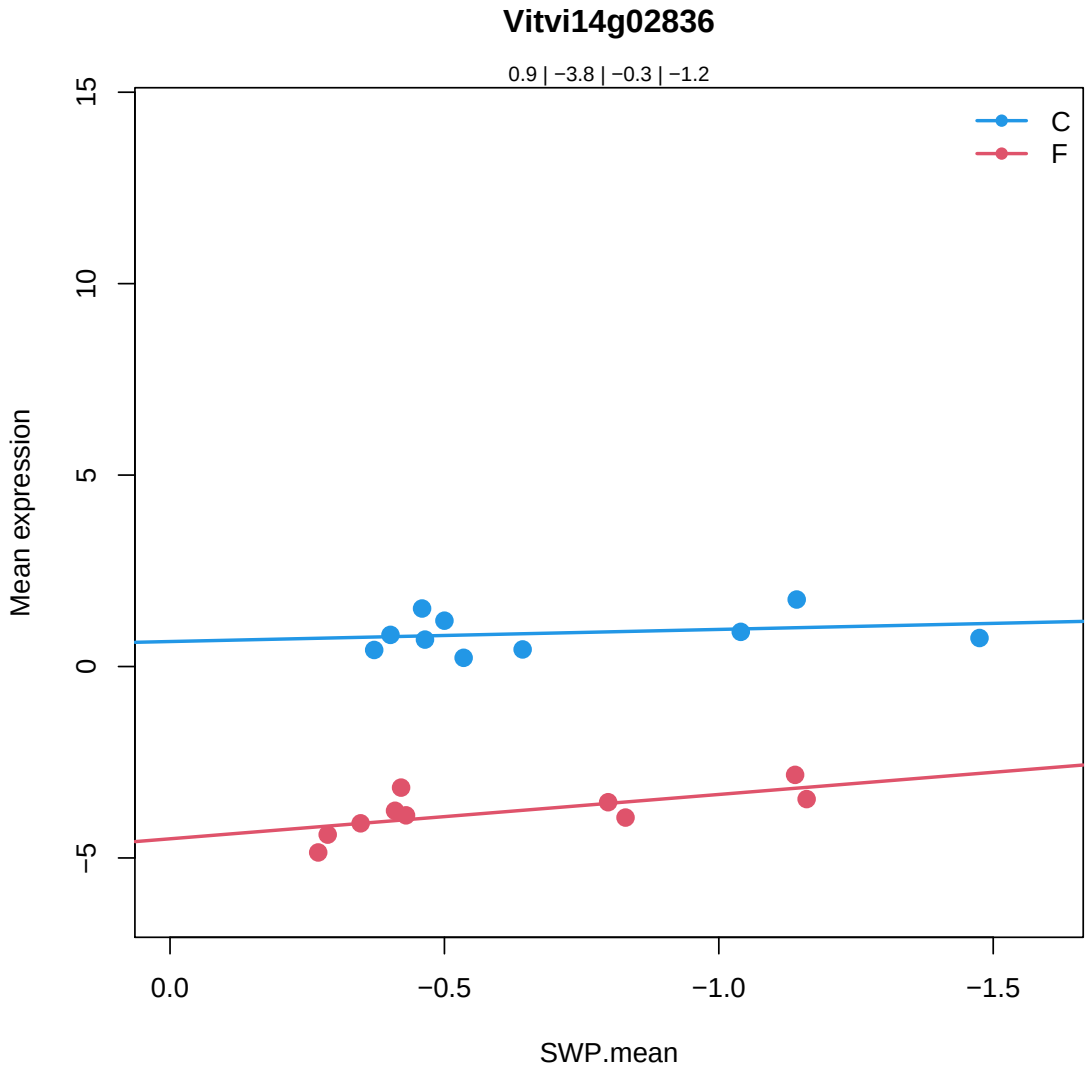
7.4.139 Vitvi14g02836: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g02836
        35.2
        not assigned.unknown
        leukocyte receptor cluster-like protein |
        Chr4:9313721-9315554 FORWARD LENGTH=252 |
        201606
```

Coefficients for Vitvi14g02836.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8747762	9.987641e-06	***	1.127809e-05	***
SlopeC	-0.316434	0.4639449		0.8605531	
MeanF-MeanC	-4.668963	4.690574e-16	***	7.295279e-14	***
SlopeF-SlopeC	-0.8417265	0.1966118		0.9999488	



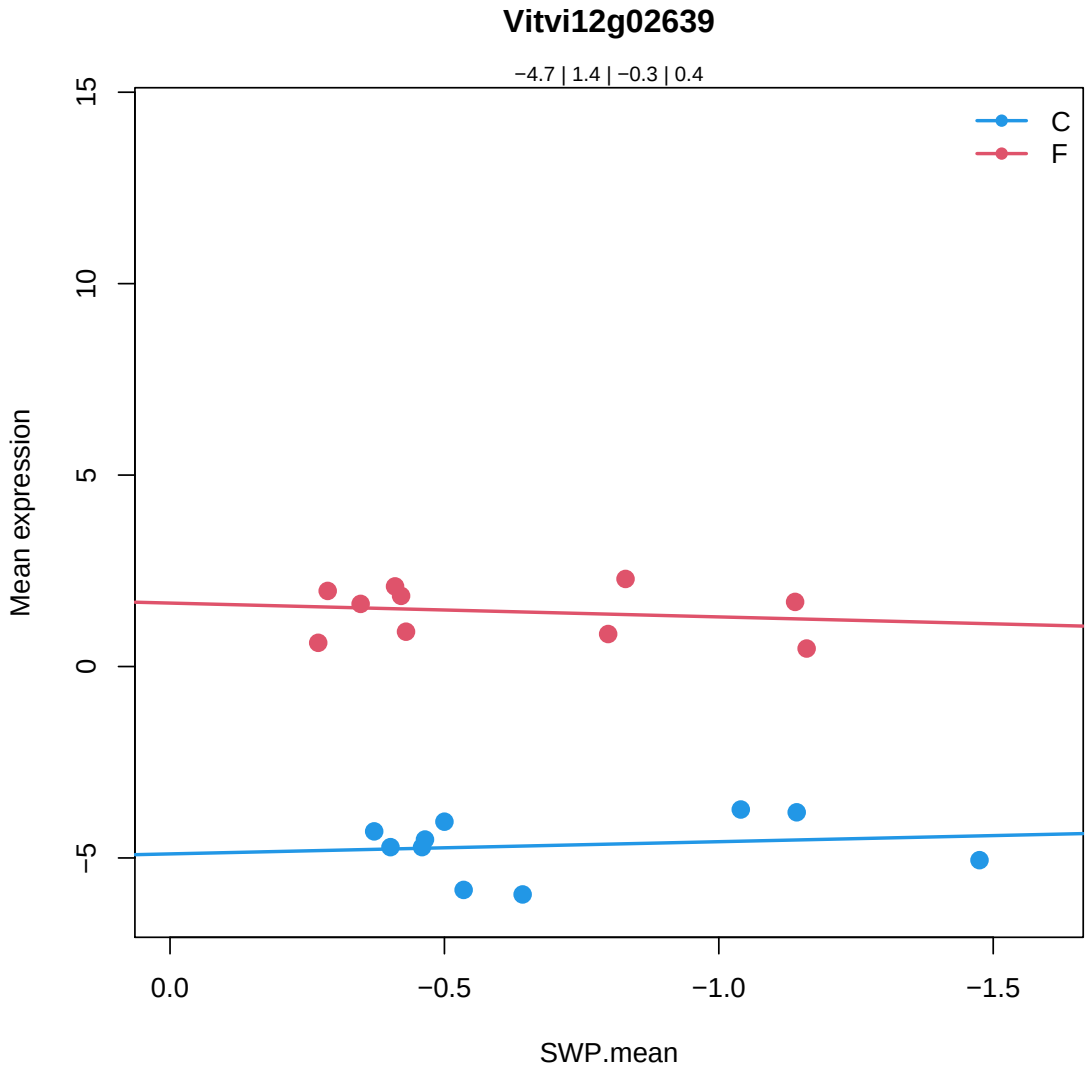
7.4.140 Vitvi12g02639: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02639
        20.1.2.2
        stress.biotic.receptors.TIR-NBS-LRR
        Disease resistance protein (TIR-NBS-LRR class) family |
        Chr4:7197325-7201393 REVERSE LENGTH=1219 |
        201606
```

Coefficients for Vitvi12g02639.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-4.670053	6.412297e-16	***	1.230315e-15	***
SlopeC	-0.3186462	0.6064537		0.9047128	
MeanF-MeanC	6.10689	3.180341e-15	***	4.23452e-13	***
SlopeF-SlopeC	0.6798038	0.46175		0.9999488	



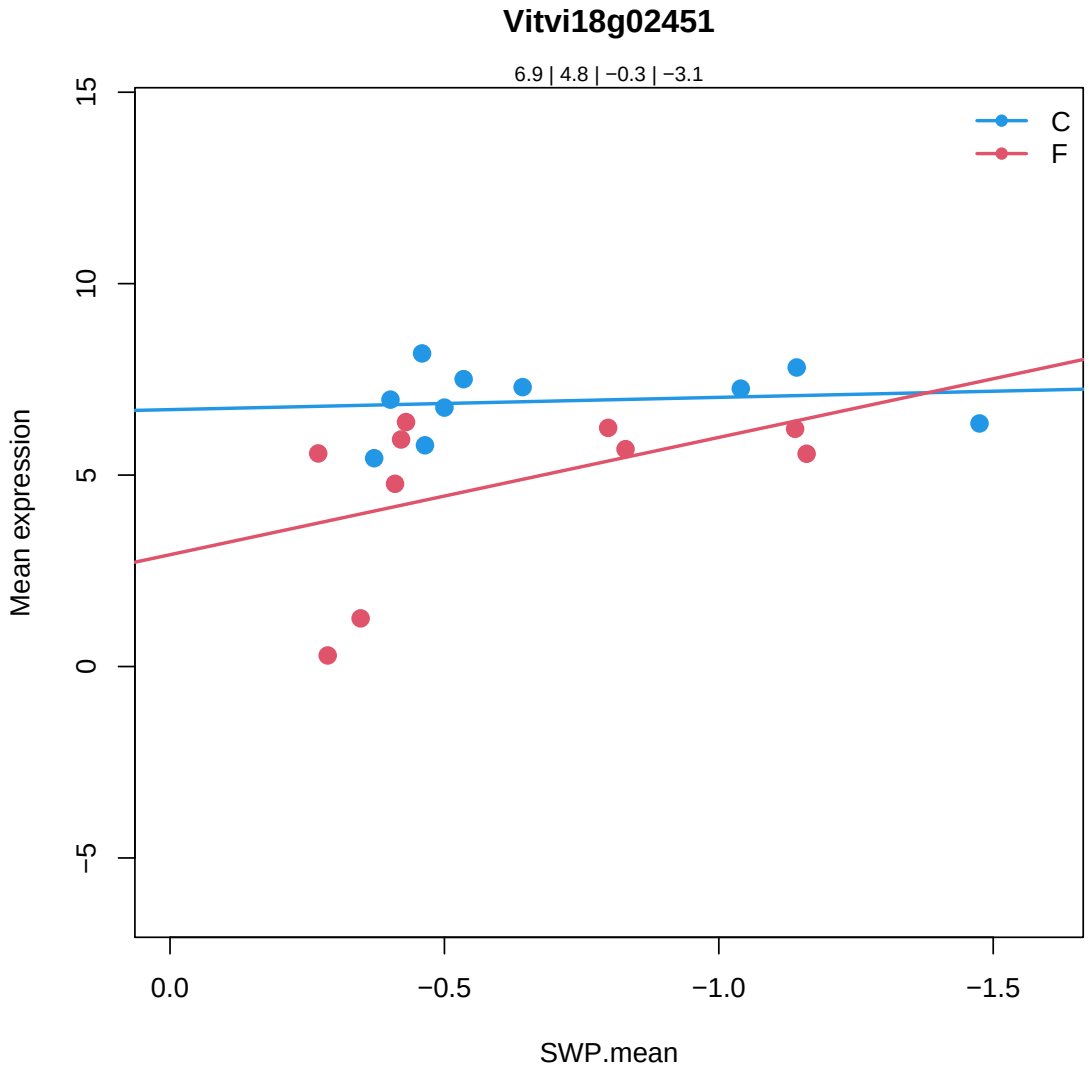
7.4.141 Vitvi18g02451: type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02451
        16.1.5
        secondary metabolism.isoprenoids.terpenoids
        terpene synthase 21 |
        Chr5:8092969-8095128 FORWARD LENGTH=545 |
        201606
```

Coefficients for Vitvi18g02451.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.934609	2.33132e-13	***	3.491597e-13	***
SlopeC	-0.3205063	0.7938969		0.9552081	
MeanF-MeanC	-2.147399	0.00214966	**	0.02330378	*
SlopeF-SlopeC	-2.742855	0.1428692		0.9999488	



7.4.142 Vitvi09g01930: type3

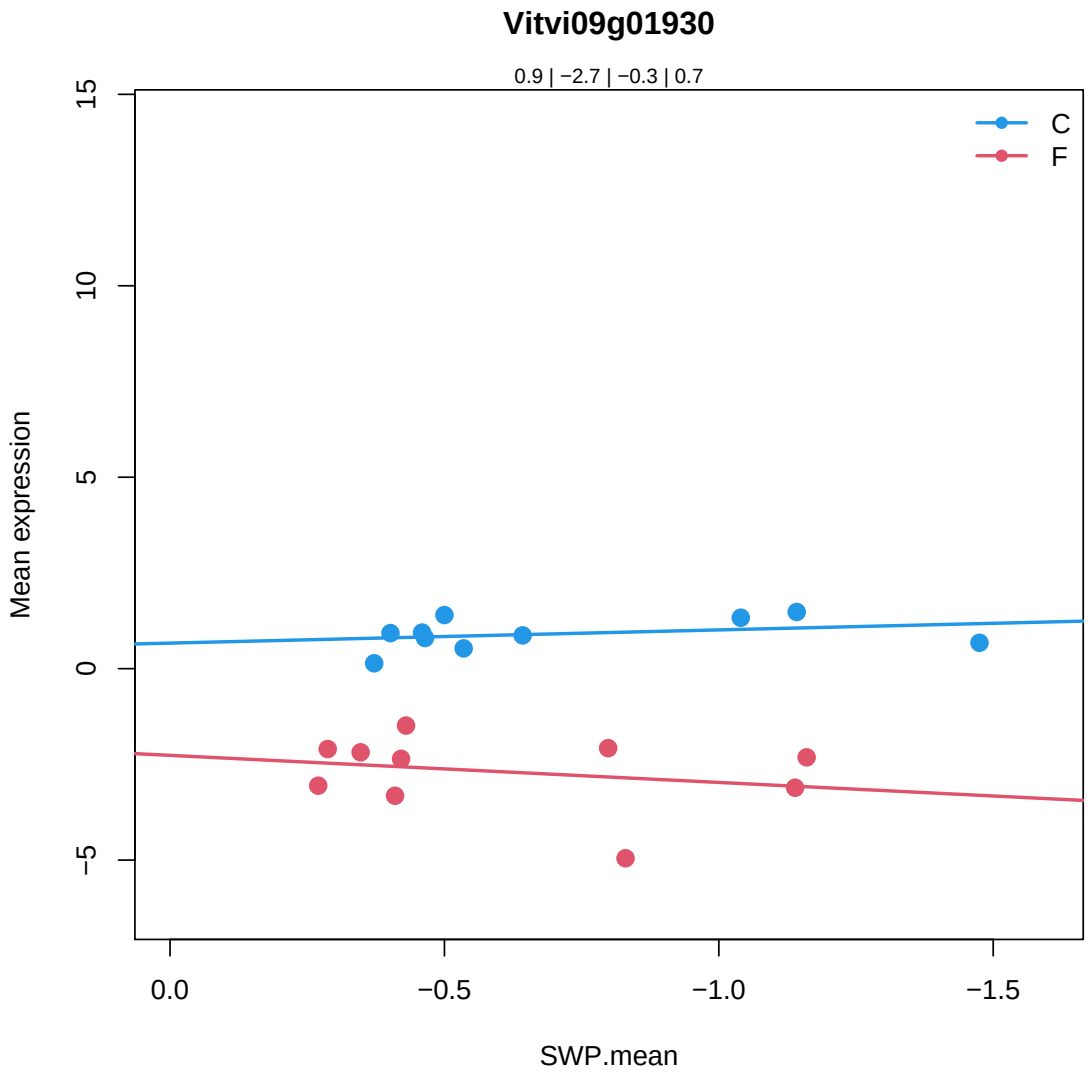
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g01930
        29.2.1.2.2.7
        protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L7
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606

Vitvi09g01930
        20.1.2
        stress.biotic.receptors
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606
```

Coefficients for Vitvi09g01930.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.9094944	0.0005236805	***	0.0005699349	***
SlopeC	-0.3447382	0.5844654		0.8963999	
MeanF-MeanC	-3.605352	1.392337e-10	***	9.432003e-09	***
SlopeF-SlopeC	1.051695	0.2676335		0.9999488	


Vitvi09g01930
0.9 | −2.7 | −0.3 | 0.7
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

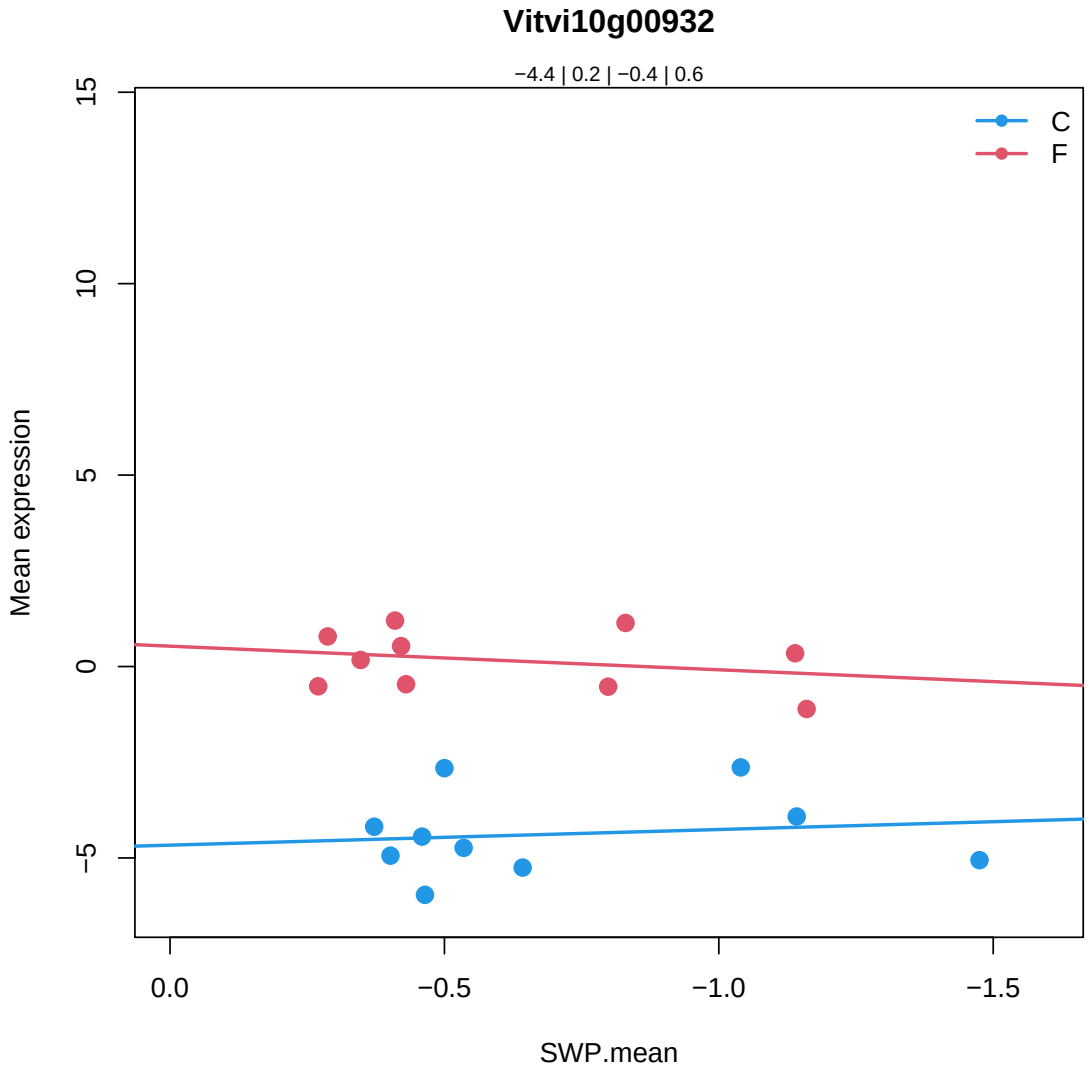
7.4.143 Vitvi10g00932: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00932
        30.2.12
        signalling.receptor kinases.leucine rich repeat XII
        Leucine-rich receptor-like protein kinase family protein |
        Chr2:11208367-11213895 REVERSE LENGTH=976 |
        201606
```

Coefficients for Vitvi10g00932.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-4.378537	3.058643e-13	***	4.544286e-13	***
SlopeC	-0.4084059	0.6038814		0.9046943	
MeanF-MeanC	4.534266	1.228068e-10	***	8.393817e-09	***
SlopeF-SlopeC	1.024973	0.3844253		0.9999488	



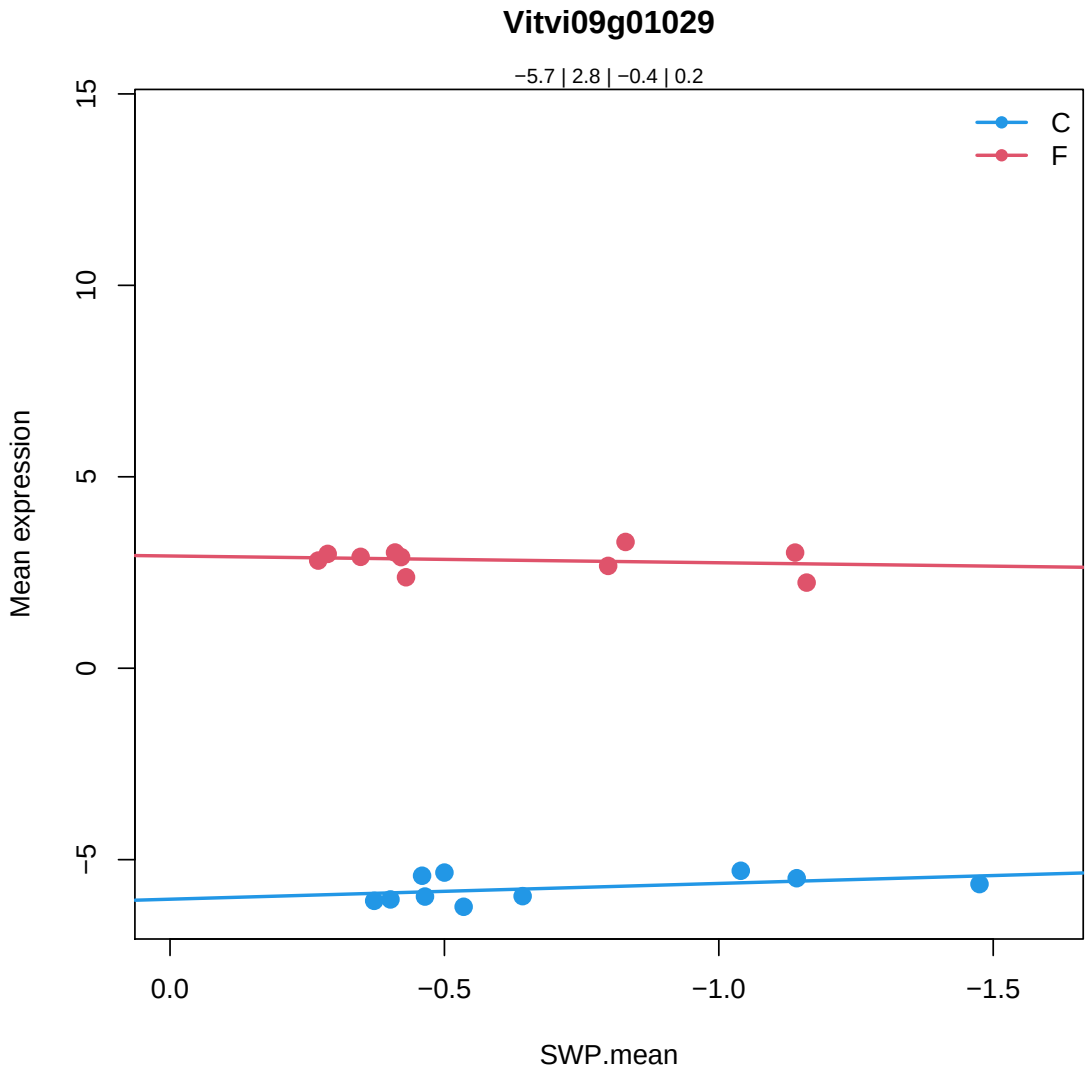
7.4.144 Vitvi09g01029: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g01029
        35.2
        not assigned.unknown
        F-box family protein IPR001810 Cyclin-like F-box
```

Coefficients for Vitvi09g01029.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.743315	2.38997e-23	***	6.259093e-22	***
SlopeC	-0.4120206	0.2275175		0.7470763	
MeanF-MeanC	8.566668	7.69953e-24	***	2.933906e-20	***
SlopeF-SlopeC	0.5891659	0.2456761		0.9999488	



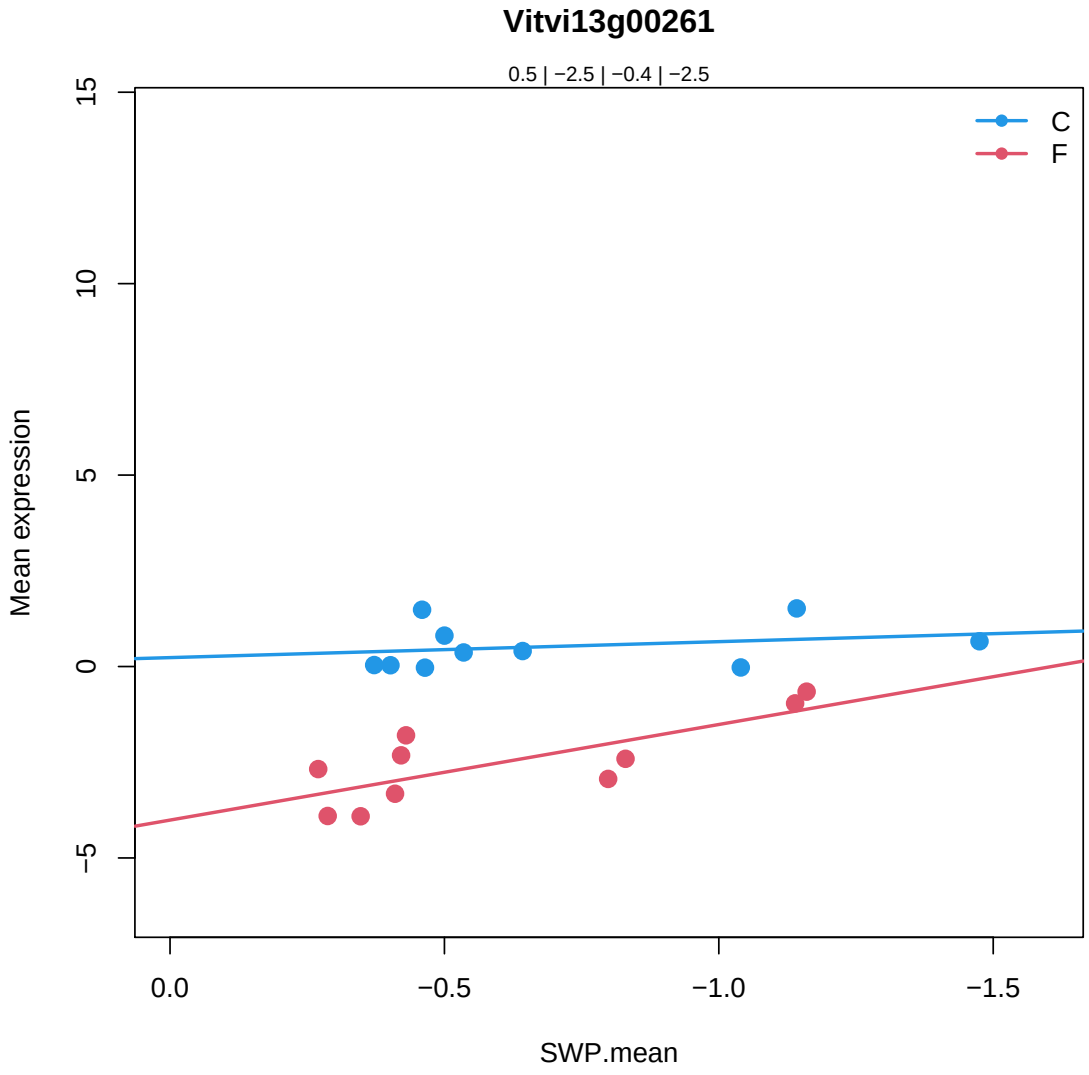
7.4.145 Vitvi13g00261: + type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00261
        35.2
        not assigned.unknown
        PIF / Ping-Pong family of plant transposase |
        Chr3:20518518-20520690 FORWARD LENGTH=406 |
        201606
```

Coefficients for Vitvi13g00261.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.5253927	0.0164883	*	0.01737758	*
SlopeC	−0.4169403	0.4660837		0.8618199	
MeanF−MeanC	−3.015297	5.911452e−10	***	3.639539e−08	***
SlopeF−SlopeC	−2.079326	0.02120173	*	0.9999488	



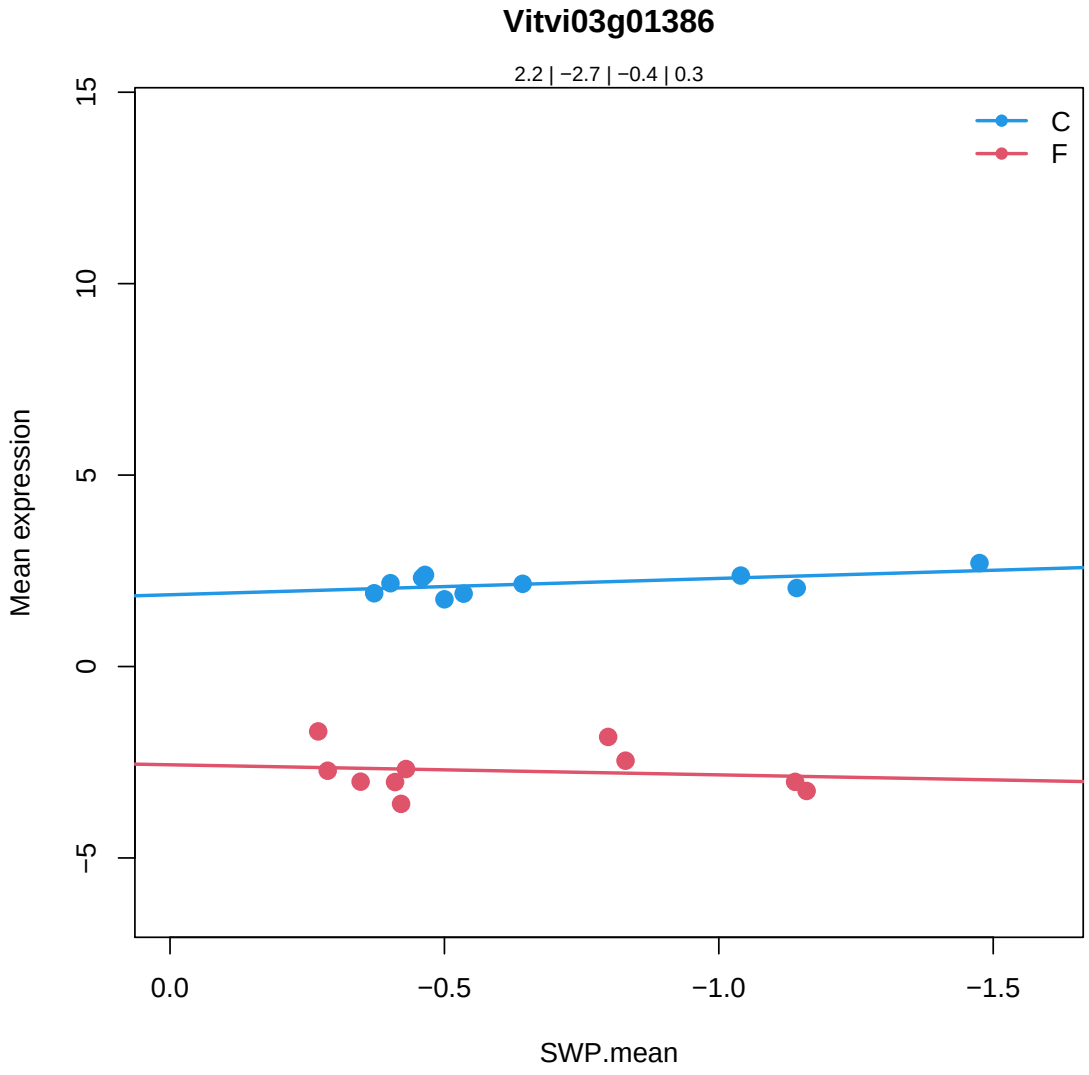
7.4.146 Vitvi03g01386: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g01386
        20.1.2.1
        stress.biotic.receptors.CC-NBS-LRR
        Disease resistance protein (CC-NBS-LRR class) family |
        Chr1:21828398-21831713 FORWARD LENGTH=1049 |
        201606
```

Coefficients for Vitvi03g01386.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.174408	1.744863e-12	***	2.468462e-12	***
SlopeC	-0.426629	0.3219785		0.797271	
MeanF-MeanC	-4.901399	1.452618e-16	***	2.54492e-14	***
SlopeF-SlopeC	0.6899416	0.282868		0.9999488	



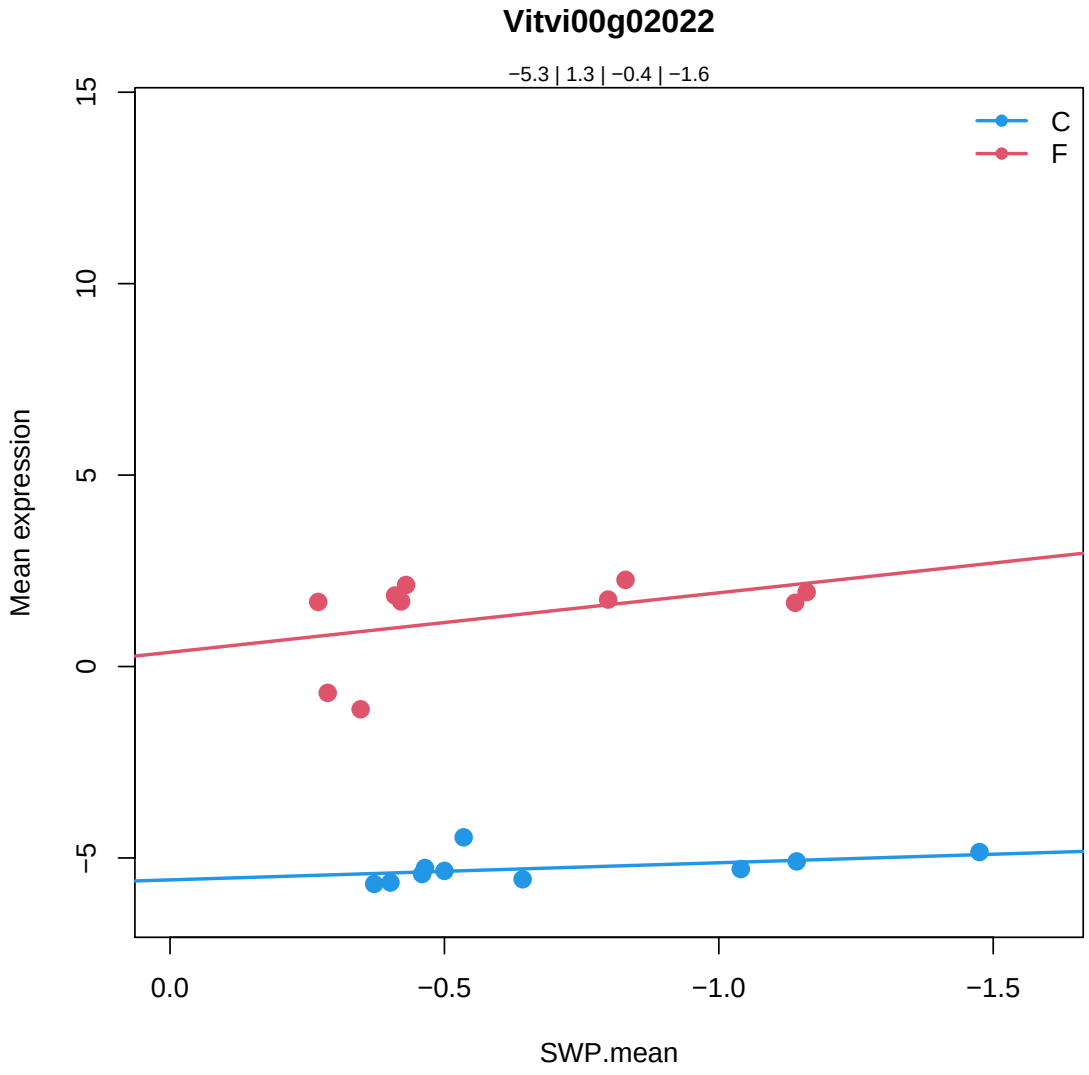
7.4.147 Vitvi00g02022: type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi00g02022
        17.1.2
        hormone metabolism.abscisic acid.signal transduction
        GCR2-like 1 |
        Chr5:26086129-26087304 REVERSE LENGTH=311 |
        201606
```

Coefficients for Vitvi00g02022.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.25859	4.249314e-16	***	8.367965e-16	***
SlopeC	-0.446971	0.5134631		0.8711742	
MeanF-MeanC	6.577033	5.234018e-15	***	6.818539e-13	***
SlopeF-SlopeC	-1.107401	0.2809345		0.9999488	



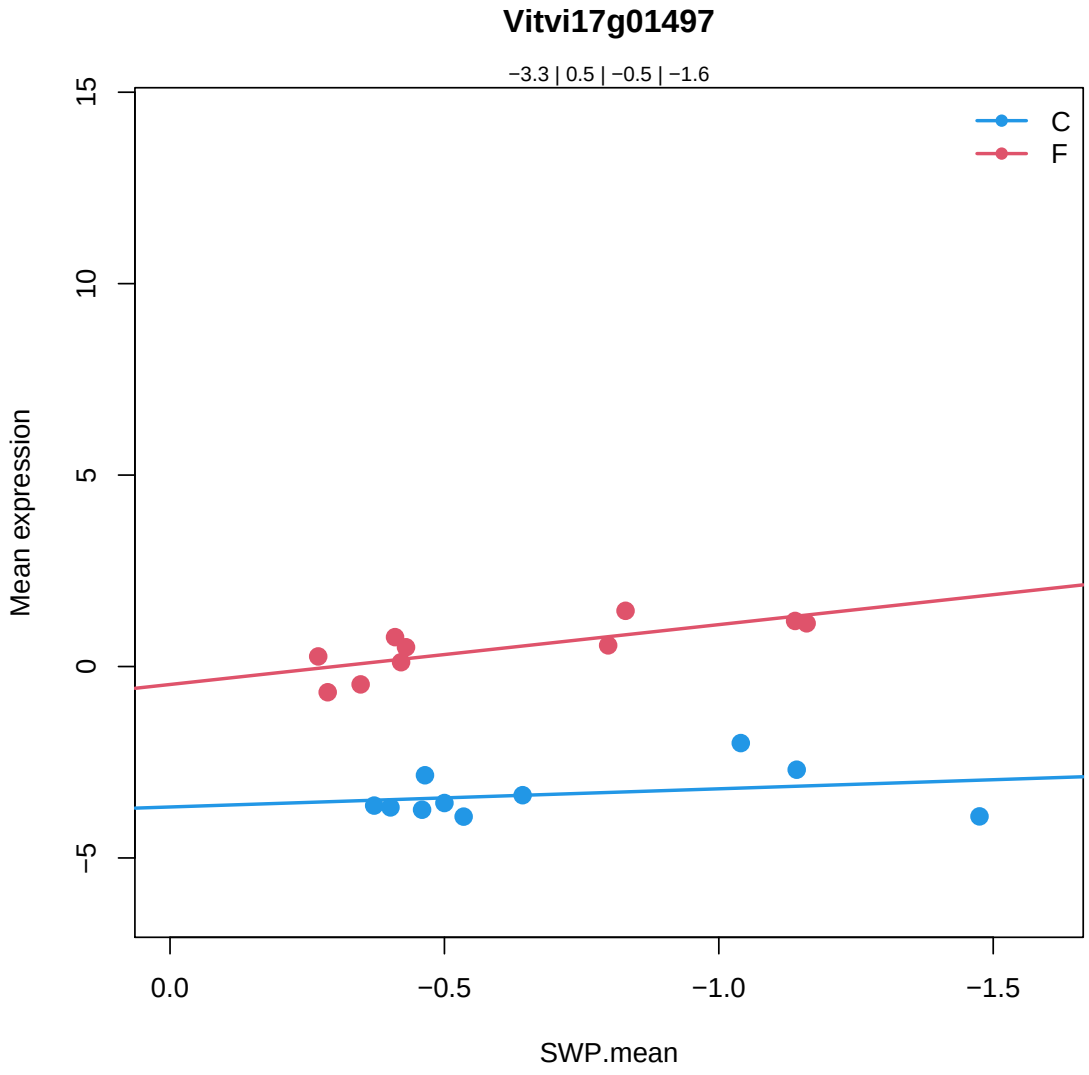
7.4.148 Vitvi17g01497: type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g01497
        26.2
        misc.UDP glucosyl and glucoronyl transferases
        UDP-Glycosyltransferase superfamily protein |
        Chr3:368840-370484 REVERSE LENGTH=464 |
        201606
```

Coefficients for Vitvi17g01497.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-3.334798	4.342005e-15	***	7.574779e-15	***
SlopeC	-0.4744792	0.331881		0.801141	
MeanF-MeanC	3.817918	3.025e-13	***	3.053447e-11	***
SlopeF-SlopeC	-1.089142	0.1403554		0.9999488	



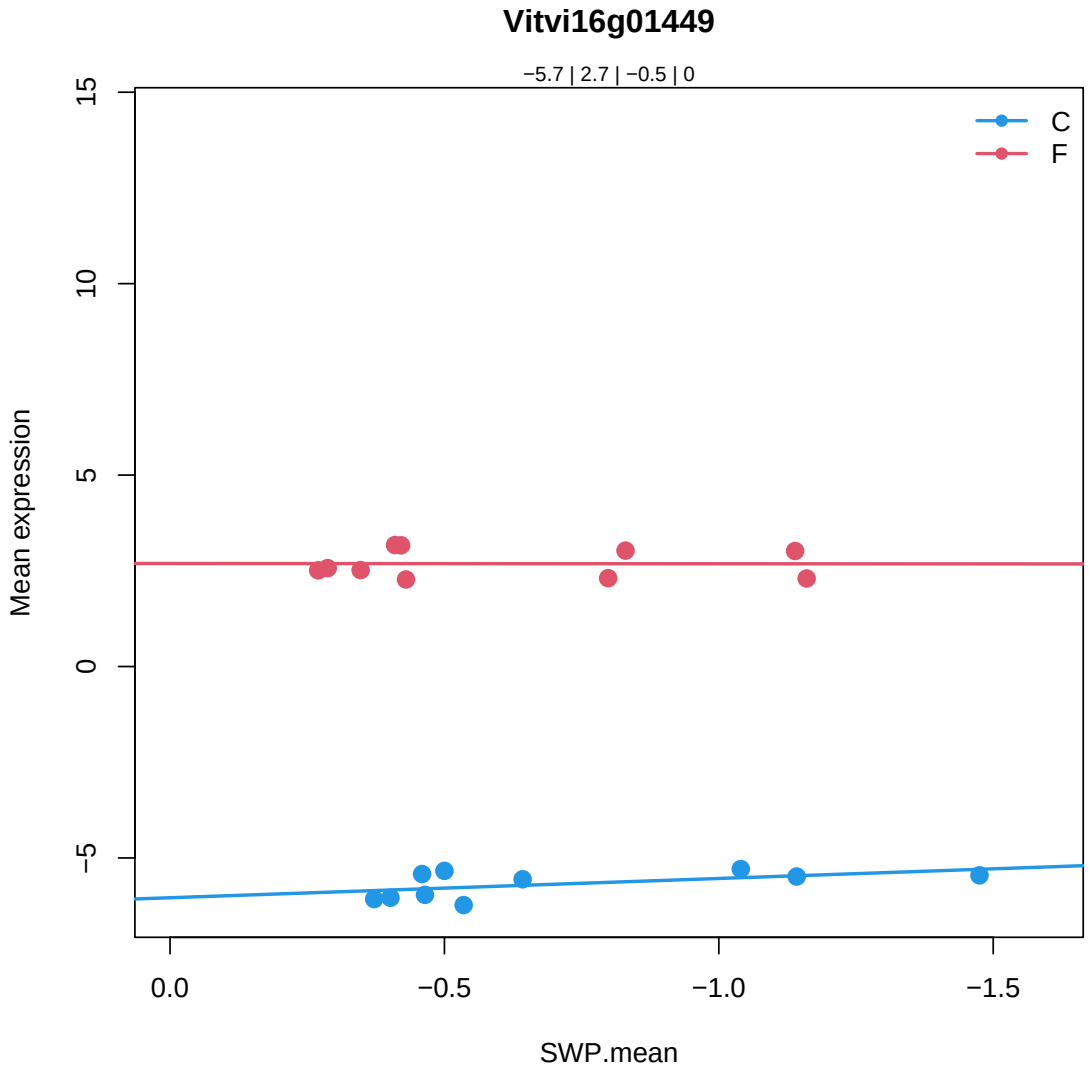
7.4.149 Vitvi16g01449: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01449
        27.3.25
        RNA.regulation of transcription.MYB domain transcription factor family
        myb domain protein 93 |
        Chr1:12709128-12710423 FORWARD LENGTH=365 |
        201606
```

Coefficients for Vitvi16g01449.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.685266	7.359657e-23	***	1.472125e-21	***
SlopeC	-0.5034745	0.1602782		0.6890054	
MeanF-MeanC	8.371372	3.122279e-23	***	5.287753e-20	***
SlopeF-SlopeC	0.5096698	0.333551		0.9999488	



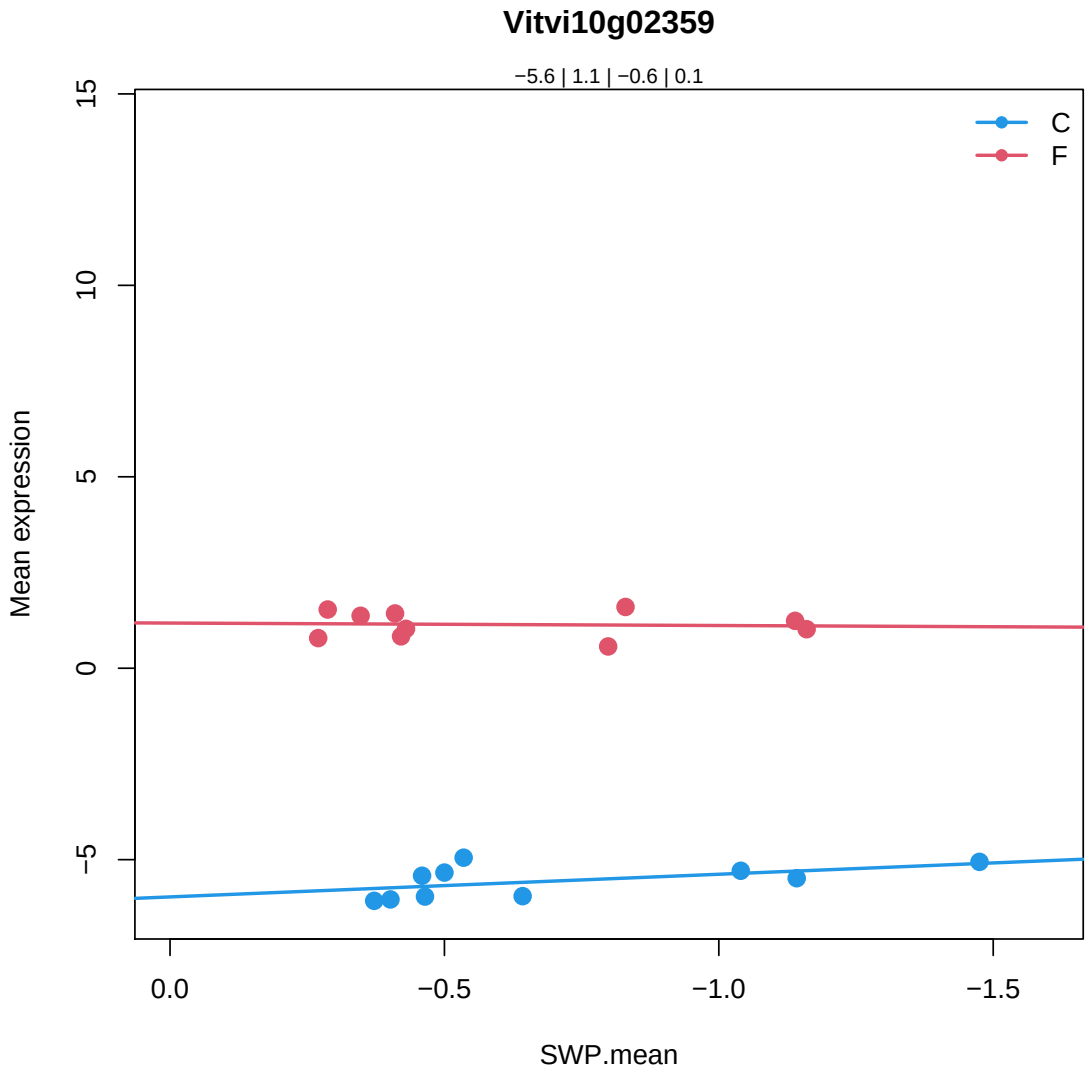
7.4.150 Vitvi10g02359: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g02359
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi10g02359.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.557034	2.244379e-22	***	3.559711e-21	***
SlopeC	-0.5918692	0.1115026		0.6258604	
MeanF-MeanC	6.697526	6.625561e-21	***	3.482303e-18	***
SlopeF-SlopeC	0.6561161	0.2297345		0.9999488	



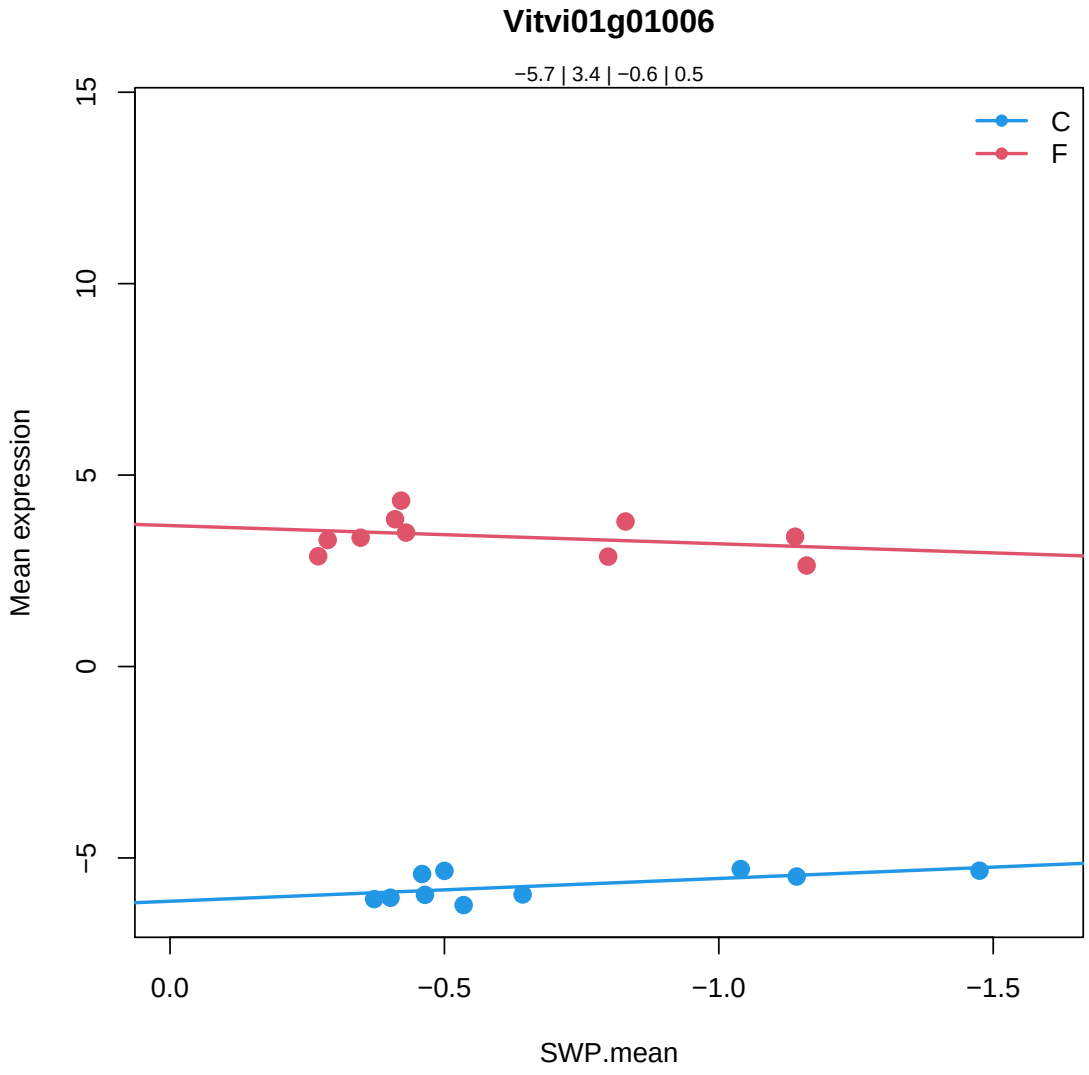
7.4.151 Vitvi01g01006: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01006
        35.2
        not assigned.unknown
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606
```

Coefficients for Vitvi01g01006.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.712755	8.273396e-22	***	9.813471e-21	***
SlopeC	-0.594586	0.141829		0.6676582	
MeanF-MeanC	9.104039	6.568669e-23	***	7.701512e-20	***
SlopeF-SlopeC	1.070103	0.07900839	.	0.9999488	



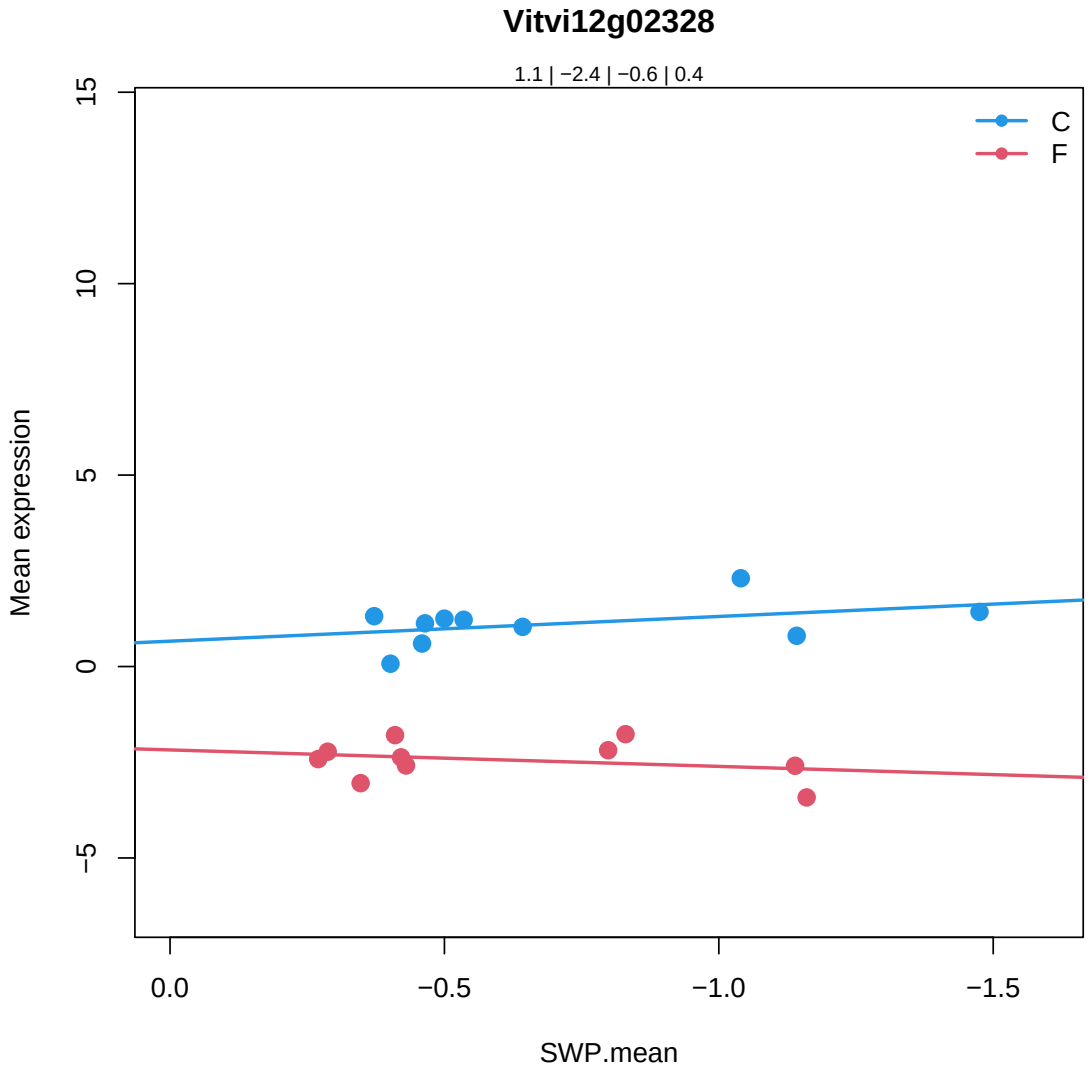
7.4.152 Vitvi12g02328: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02328
        35.2
        not assigned.unknown
        Ankyrin repeat family protein |
        Chr4:1524199-1527133 REVERSE LENGTH=751 |
        201606
```

Coefficients for Vitvi12g02328.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.115688	1.152208e-06	***	1.328137e-06	***
SlopeC	-0.645458	0.1786171		0.7108306	
MeanF-MeanC	-3.556267	6.900606e-13	***	6.374487e-11	***
SlopeF-SlopeC	1.075452	0.1341766		0.9999488	



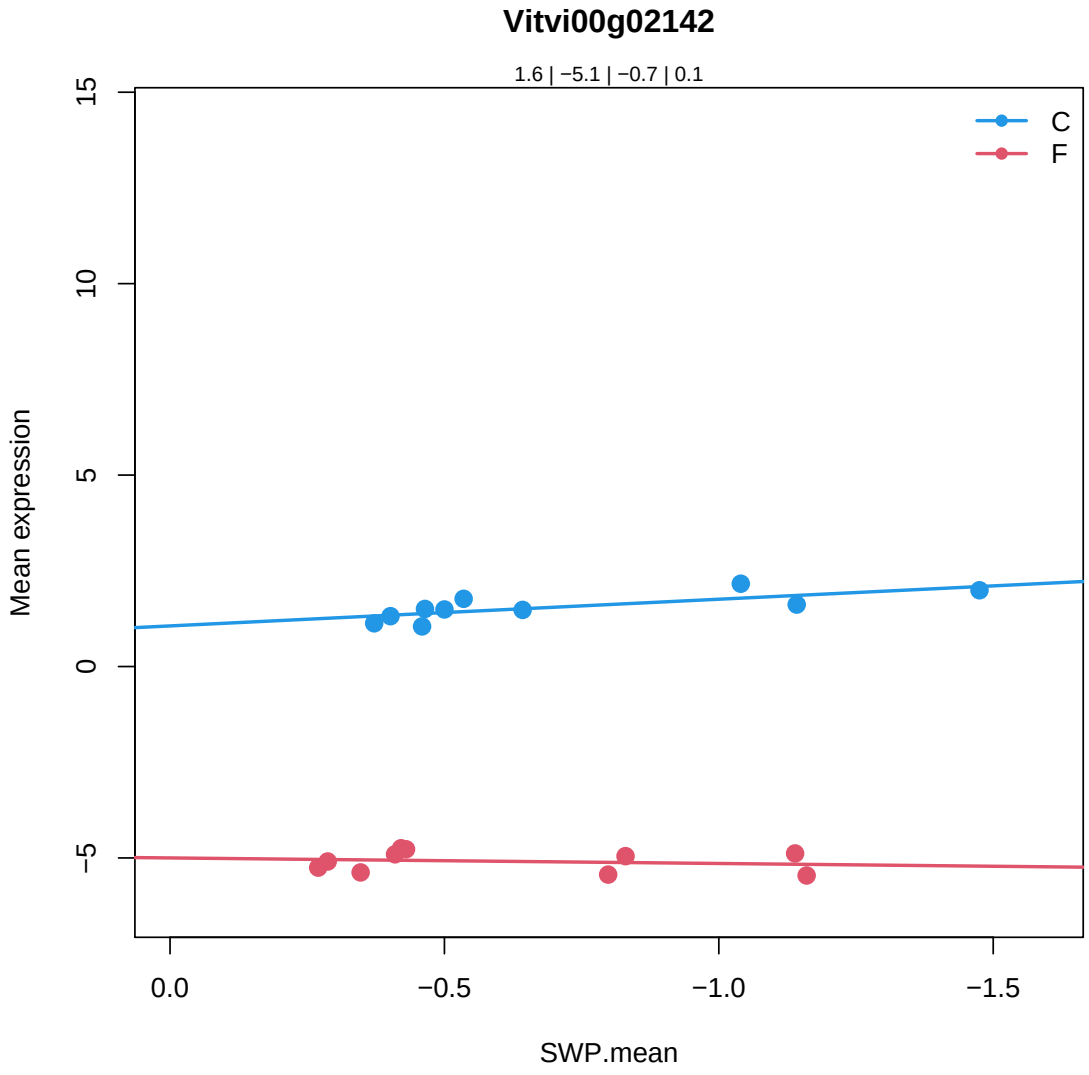
7.4.153 Vitvi00g02142: * type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi00g02142
        35.2
        not assigned.unknown
        Thioredoxin superfamily protein |
        Chr5:26344097-26346057 REVERSE LENGTH=275 |
        201606
```

Coefficients for Vitvi00g02142.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.550321	1.487197e-12	***	2.112174e-12	***
SlopeC	-0.6971163	0.02886707	*	0.4275918	
MeanF-MeanC	-6.638005	1.739453e-22	***	1.47293e-19	***
SlopeF-SlopeC	0.8422066	0.07076574	.	0.9999488	



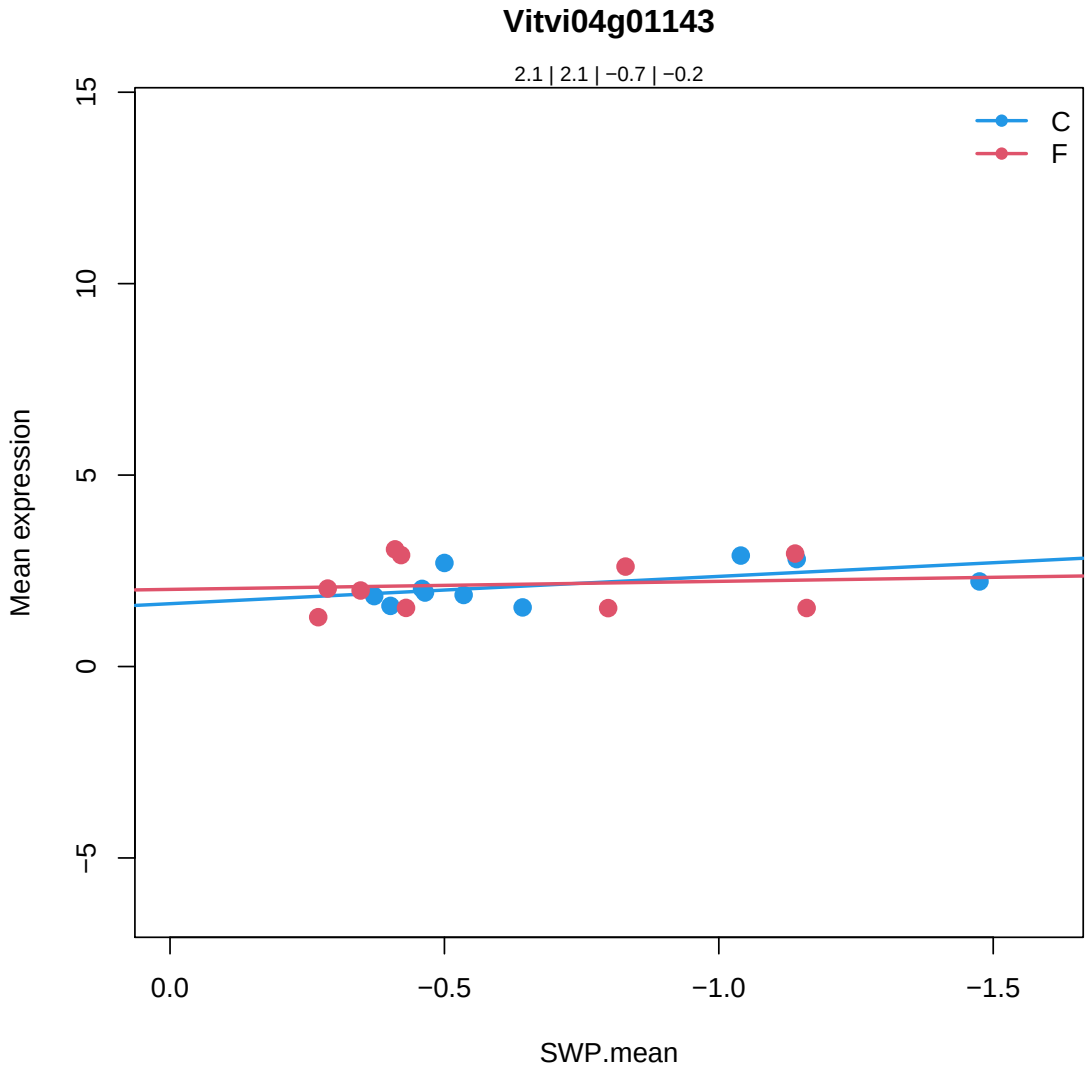
7.4.154 Vitvi04g01143: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01143
        30.2
        signalling.receptor kinases
        Leucine-rich repeat (LRR) family protein |
        Chr1:24286943-24289105 FORWARD LENGTH=720 |
        201606
```

Coefficients for Vitvi04g01143.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.142228	7.258799e-11	***	9.55181e-11	***
SlopeC	-0.713225	0.171214		0.7015862	
MeanF-MeanC	7.854292e-05	0.9997581		0.9999648	
SlopeF-SlopeC	0.5026672	0.5097682		0.9999488	



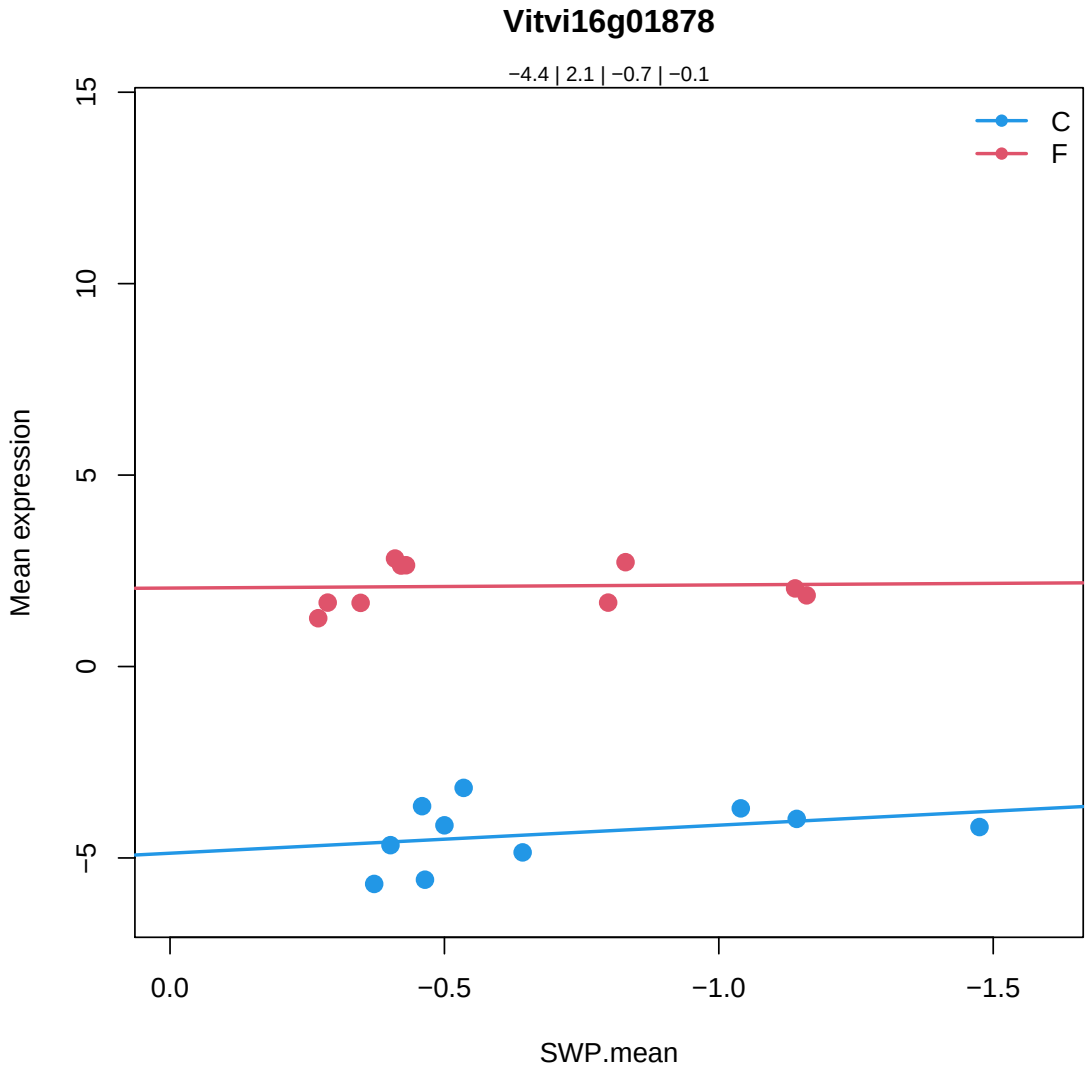
7.4.155 Vitvi16g01878: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01878
        20.1.2
        stress.biotic.receptors
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606
```

Coefficients for Vitvi16g01878.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-4.361077	1.19789e-15	***	2.222008e-15	***
SlopeC	-0.7326619	0.2252582		0.7450109	
MeanF-MeanC	6.459833	4.634794e-16	***	7.282838e-14	***
SlopeF-SlopeC	0.6505336	0.4644259		0.9999488	



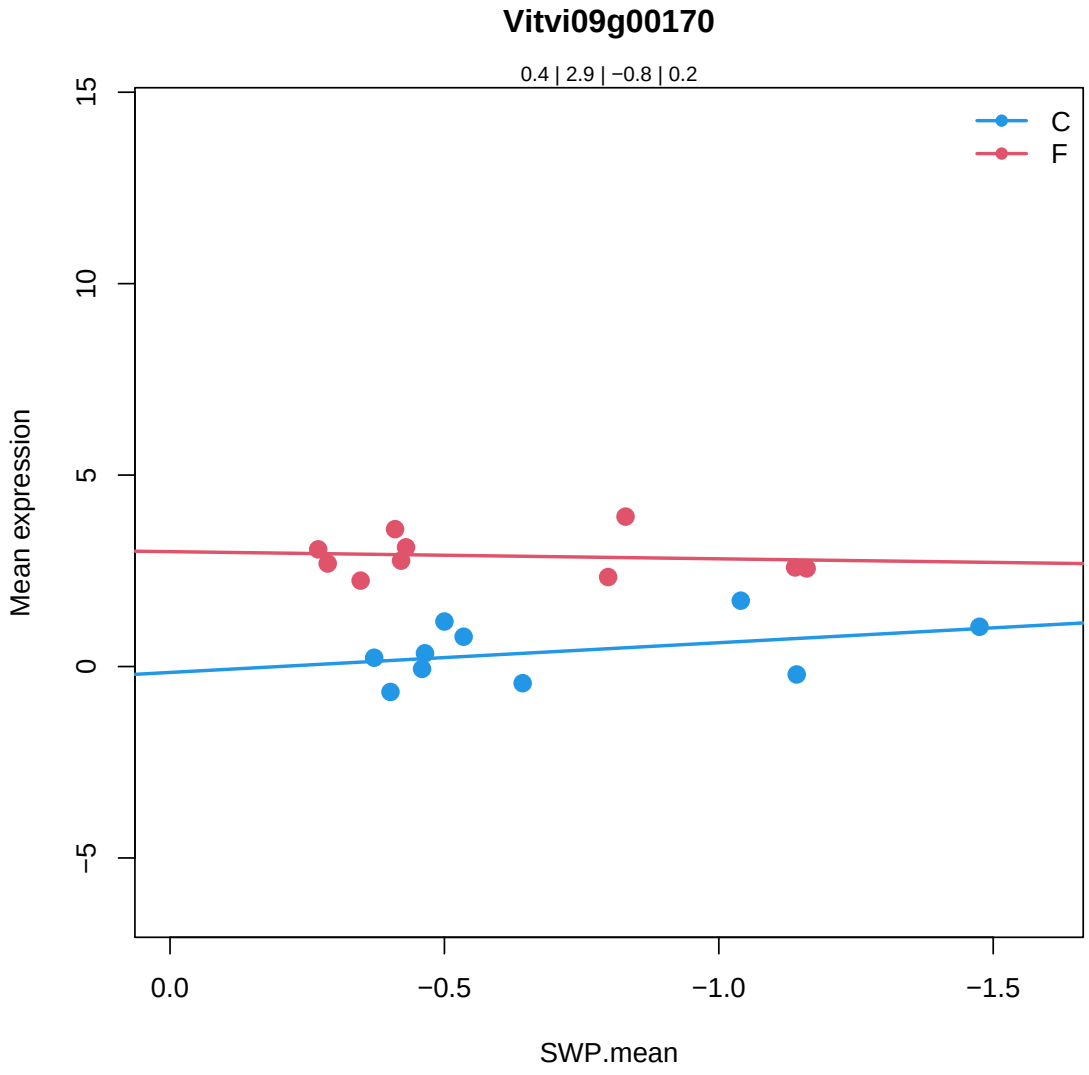
7.4.156 Vitvi09g00170: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00170
        26.16
        misc.myrosinases-lectin-jacalin
        F-box/RNI-like superfamily protein |
        Chr3:15824938-15826391 REVERSE LENGTH=427 |
        201606
```

Coefficients for Vitvi09g00170.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.391508	0.06125161	.	0.0636529	.
SlopeC	-0.7766092	0.1733654		0.7056946	
MeanF-MeanC	2.494406	1.200884e-08	***	5.885492e-07	***
SlopeF-SlopeC	0.9634186	0.2533338		0.9999488	



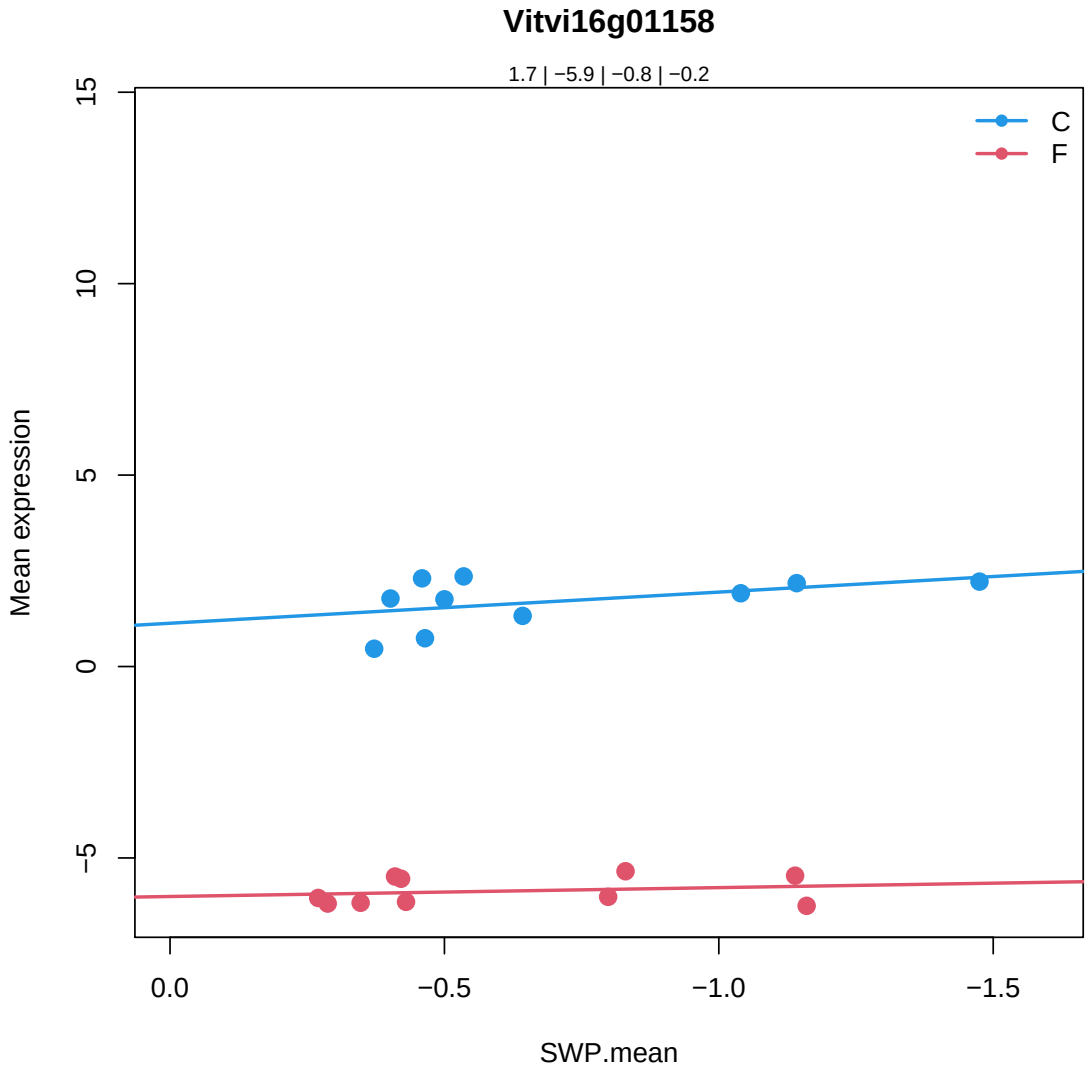
7.4.157 Vitvi16g01158: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01158
        35.2
        not assigned.unknown
        PR5-like receptor kinase |
        Chr5:15293122-15295838 REVERSE LENGTH=672 |
        201606
```

Coefficients for Vitvi16g01158.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.701951	5.15729e-10	***	6.567585e-10	***
SlopeC	-0.813624	0.08152114	.	0.5779075	
MeanF-MeanC	-7.567532	5.421649e-20	***	1.921785e-17	***
SlopeF-SlopeC	0.5815453	0.3897895		0.9999488	



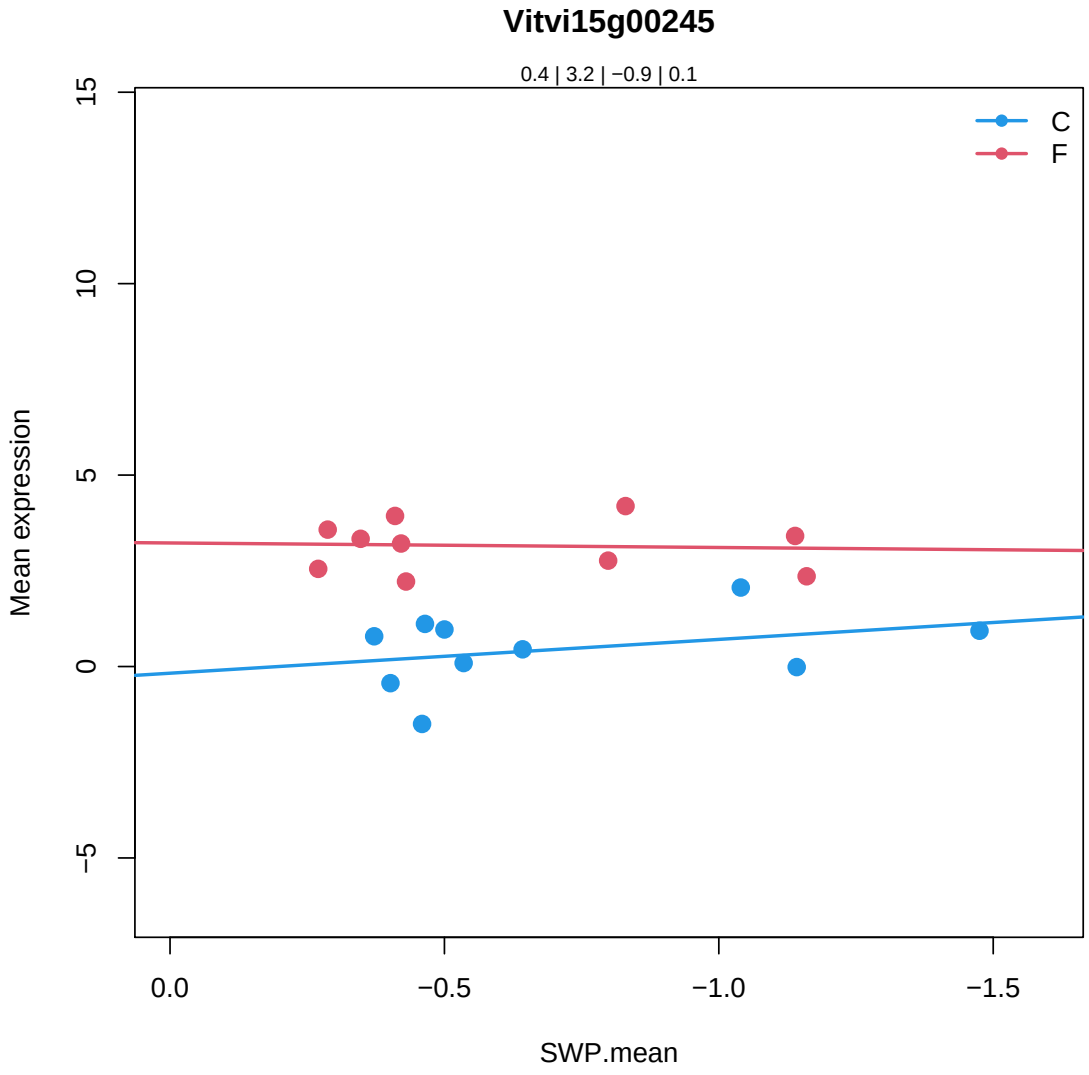
7.4.158 Vitvi15g00245: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g00245
        20.1.2.2
        stress.biotic.receptors.TIR-NBS-LRR
        disease resistance protein (TIR-NBS-LRR class) |
        Chr5:5822999-5827153 FORWARD LENGTH=1295 |
        201606
```

Coefficients for Vitvi15g00245.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4456436	0.08275899	.	0.08575205	.
SlopeC	-0.8828349	0.2087882		0.7320795	
MeanF-MeanC	2.709153	1.018959e-07	***	4.152665e-06	***
SlopeF-SlopeC	1.000898	0.3345948		0.9999488	



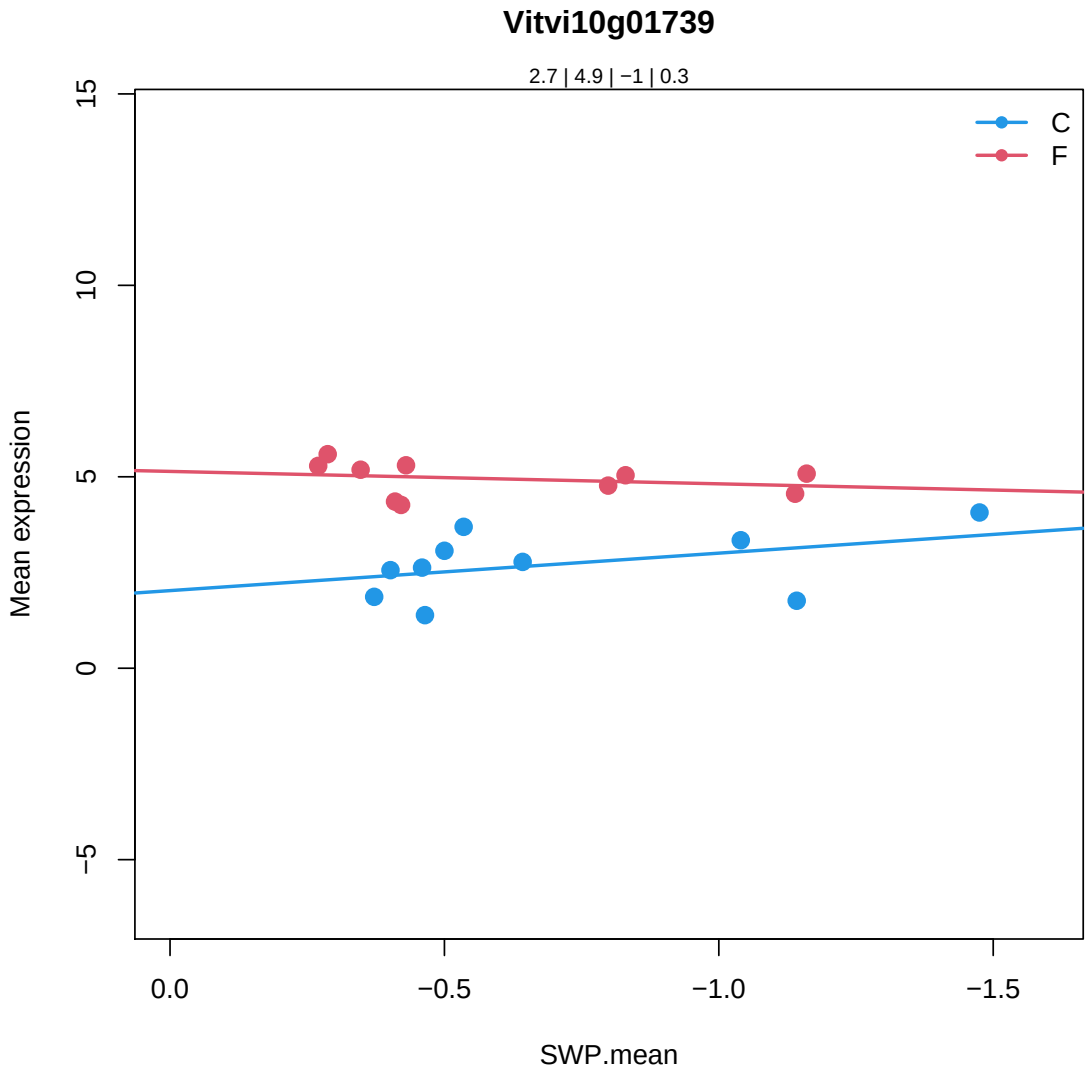
7.4.159 Vitvi10g01739: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g01739
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi10g01739.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.714859	4.496605e-12	***	6.225001e-12	***
SlopeC	-0.9783917	0.09034051	.	0.5961693	
MeanF-MeanC	2.227631	7.953729e-08	***	3.33969e-06	***
SlopeF-SlopeC	1.302982	0.1271647		0.9999488	



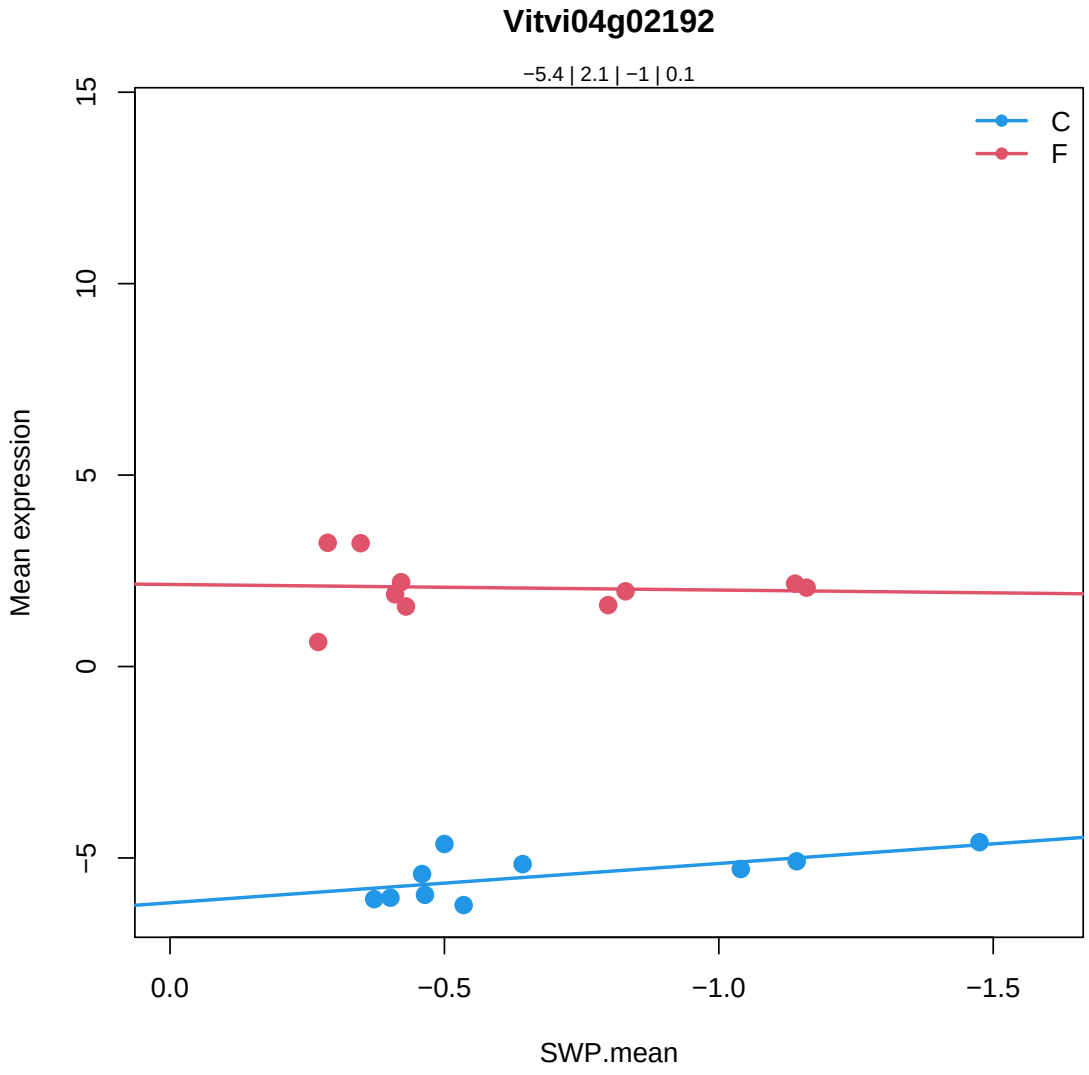
7.4.160 Vitvi04g02192: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g02192
        16.4.1
        secondary metabolism.N misc.alkaloid-like
        Calcium-dependent phosphotriesterase superfamily protein |
        Chr3:19086548-19087909 FORWARD LENGTH=371 |
        201606
```

Coefficients for Vitvi04g02192.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.449157	3.37321e-18	***	1.001646e-17	***
SlopeC	-1.026036	0.07682635	.	0.5706566	
MeanF-MeanC	7.503254	5.887175e-18	***	1.300468e-15	***
SlopeF-SlopeC	1.171818	0.1681586		0.9999488	



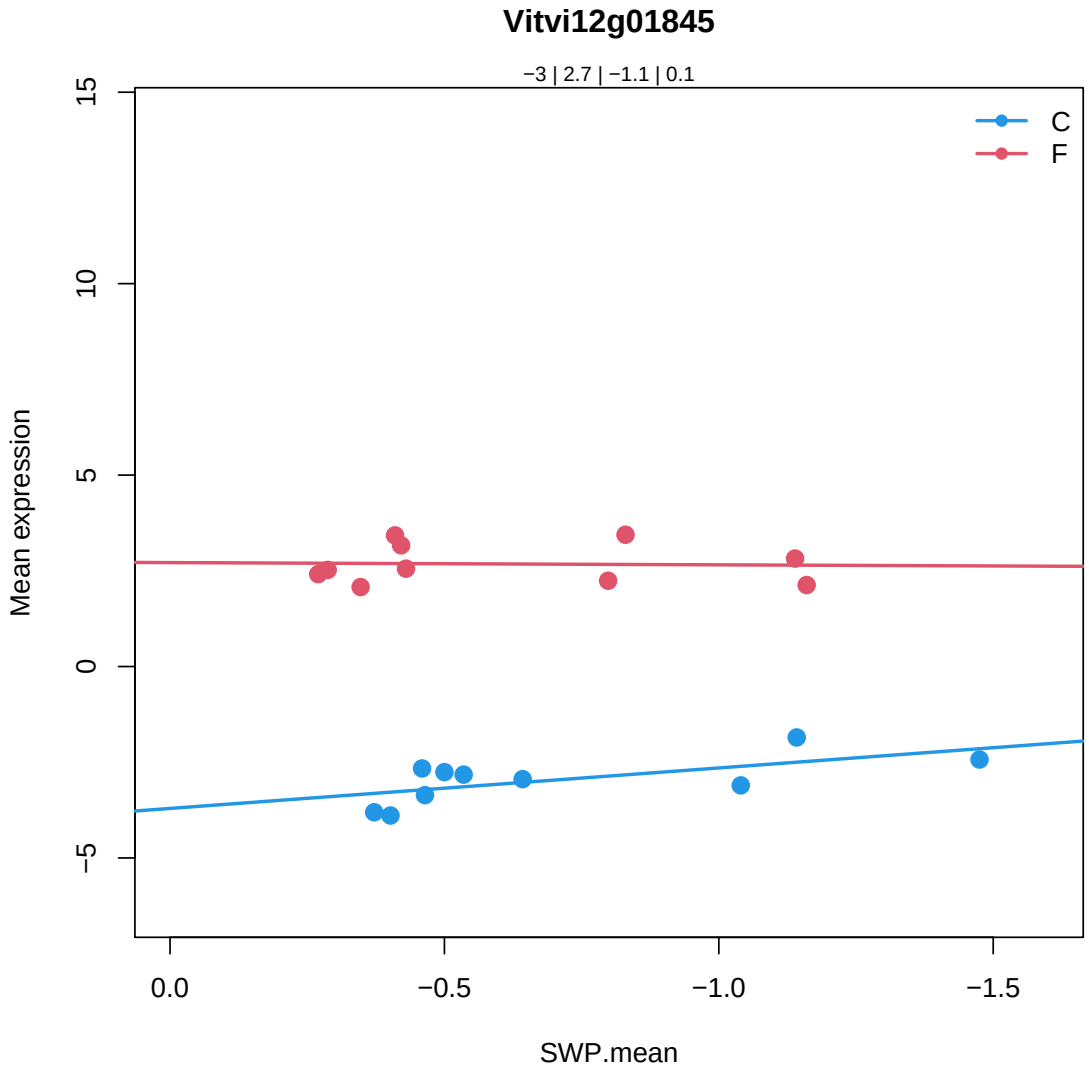
7.4.161 Vitvi12g01845: * type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g01845
        20.1.2.1
        stress.biotic.receptors.CC-NBS-LRR
        NB-ARC domain-containing disease resistance protein |
        Chr3:4857940-4861104 FORWARD LENGTH=1054 |
        201606
```

Coefficients for Vitvi12g01845.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-2.963099	1.512192e-14	***	2.483978e-14	***
SlopeC	-1.057327	0.02894713	*	0.4283614	
MeanF-MeanC	5.641784	3.409841e-17	***	6.838525e-15	***
SlopeF-SlopeC	1.115801	0.1114708		0.9999488	



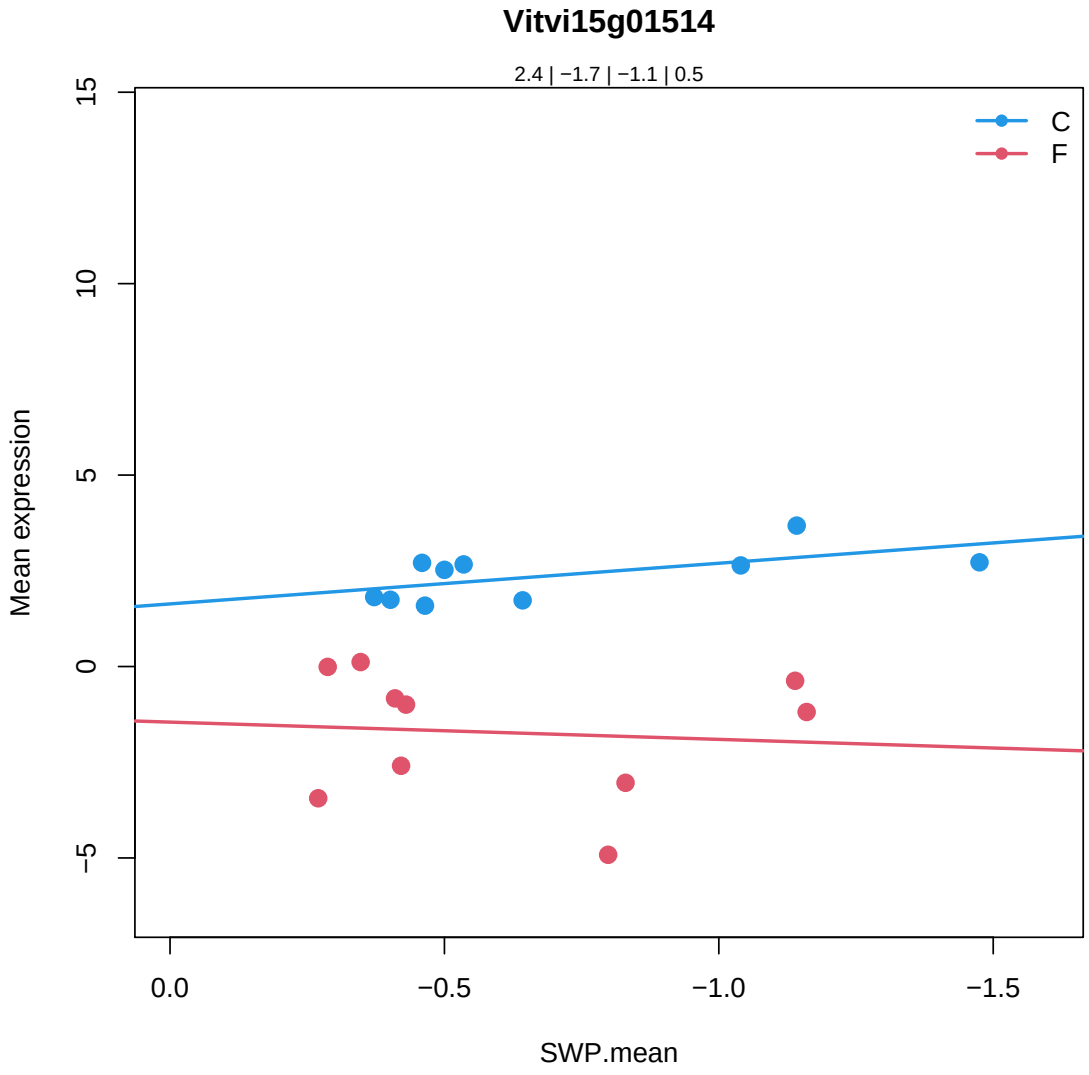
7.4.162 Vitvi15g01514: type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g01514
        35.2
        not assigned.unknown
        cytochrome P450%2C family 76%2C subfamily C%2C polypeptide 1 |
        Chr2:18776391-18778354 REVERSE LENGTH=512 |
        201606
```

Coefficients for Vitvi15g01514.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.381574	1.79077e-06	***	2.05565e-06	***
SlopeC	-1.06173	0.3100232		0.7925436	
MeanF-MeanC	-4.108615	8.428322e-08	***	3.509959e-06	***
SlopeF-SlopeC	1.512169	0.330839		0.9999488	



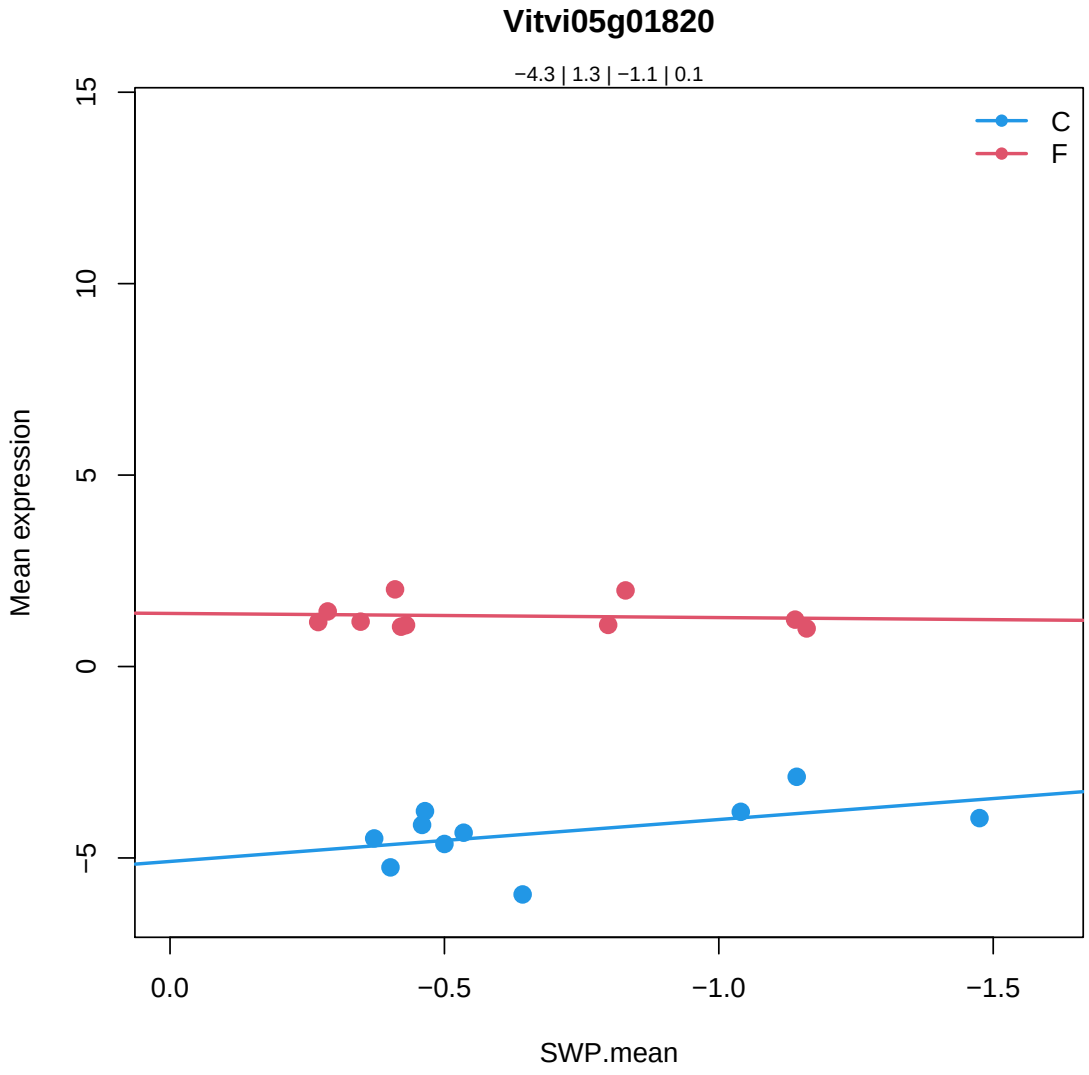
7.4.163 Vitvi05g01820: * type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01820
        35.2
        not assigned.unknown
        RNA-directed DNA polymerase (reverse transcriptase)-related family pro
        Chr3:8789309-8790907 FORWARD LENGTH=532 |
        201606
```

Coefficients for Vitvi05g01820.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-4.321537	1.221516e-16	***	2.614202e-16	***
SlopeC	-1.095343	0.04724099	*	0.4993392	
MeanF-MeanC	5.641628	6.341921e-16	***	9.570649e-14	***
SlopeF-SlopeC	1.203532	0.1348108		0.9999488	



7.4.164 Vitvi07g01569: * type3

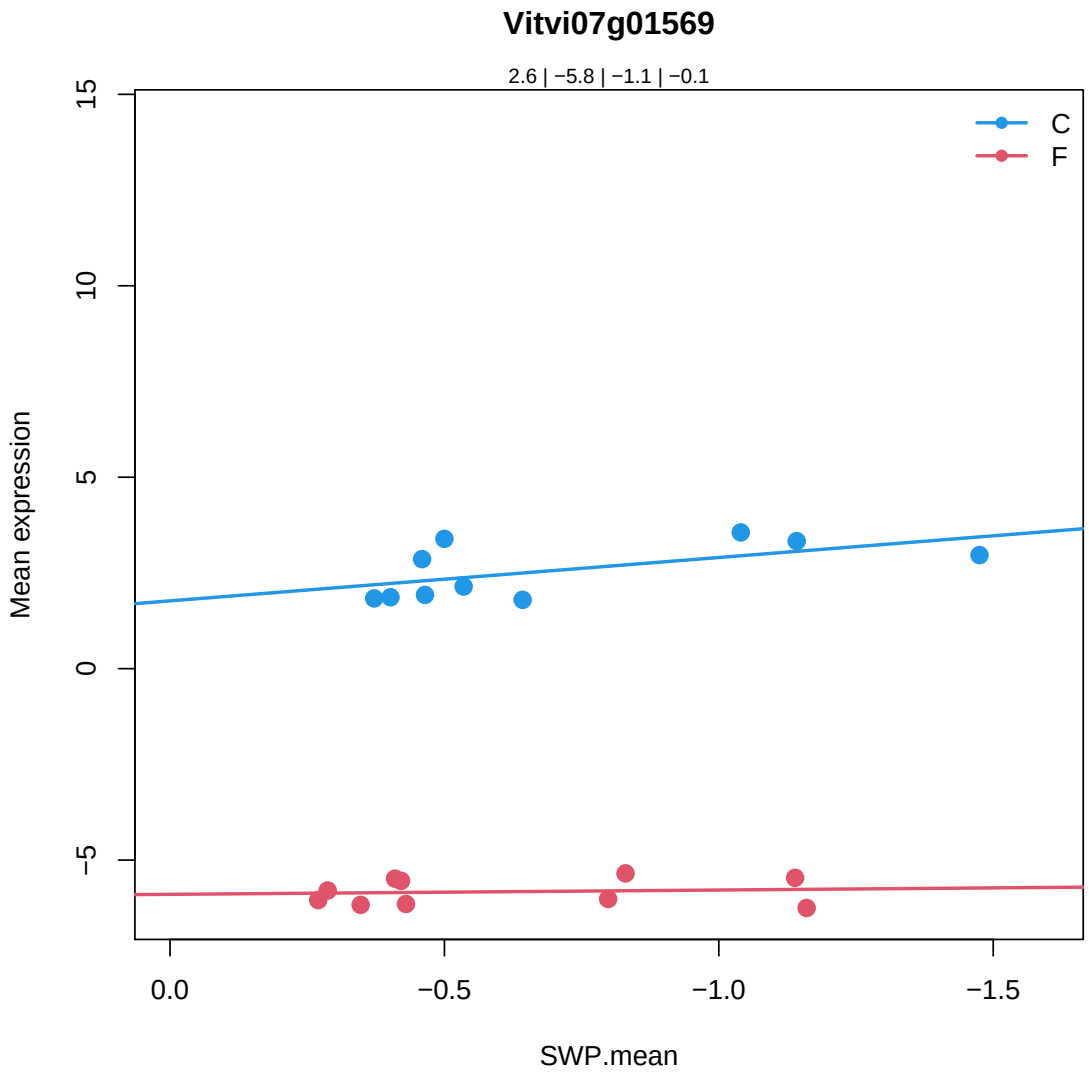
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01569
        26.24
        misc.GCN5-related N-acetyltransferase
        N-acetyl-l-glutamate synthase 1 |
        Chr2:9749988-9752737 FORWARD LENGTH=609 |
        201606

Vitvi07g01569
        35.2
        not assigned.unknown
        N-acetyl-l-glutamate synthase 1 |
        Chr2:9749988-9752737 FORWARD LENGTH=609 |
        201606
```

Coefficients for Vitvi07g01569.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.566733	1.653028e-13	***	2.497319e-13	***
SlopeC	-1.132495	0.01769768	*	0.3571759	
MeanF-MeanC	-8.39269	4.961717e-21	***	2.800981e-18	***
SlopeF-SlopeC	1.020438	0.1344627		0.9999488	


Vitvi07g01569
2.6 | −5.8 | −1.1 | −0.1
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

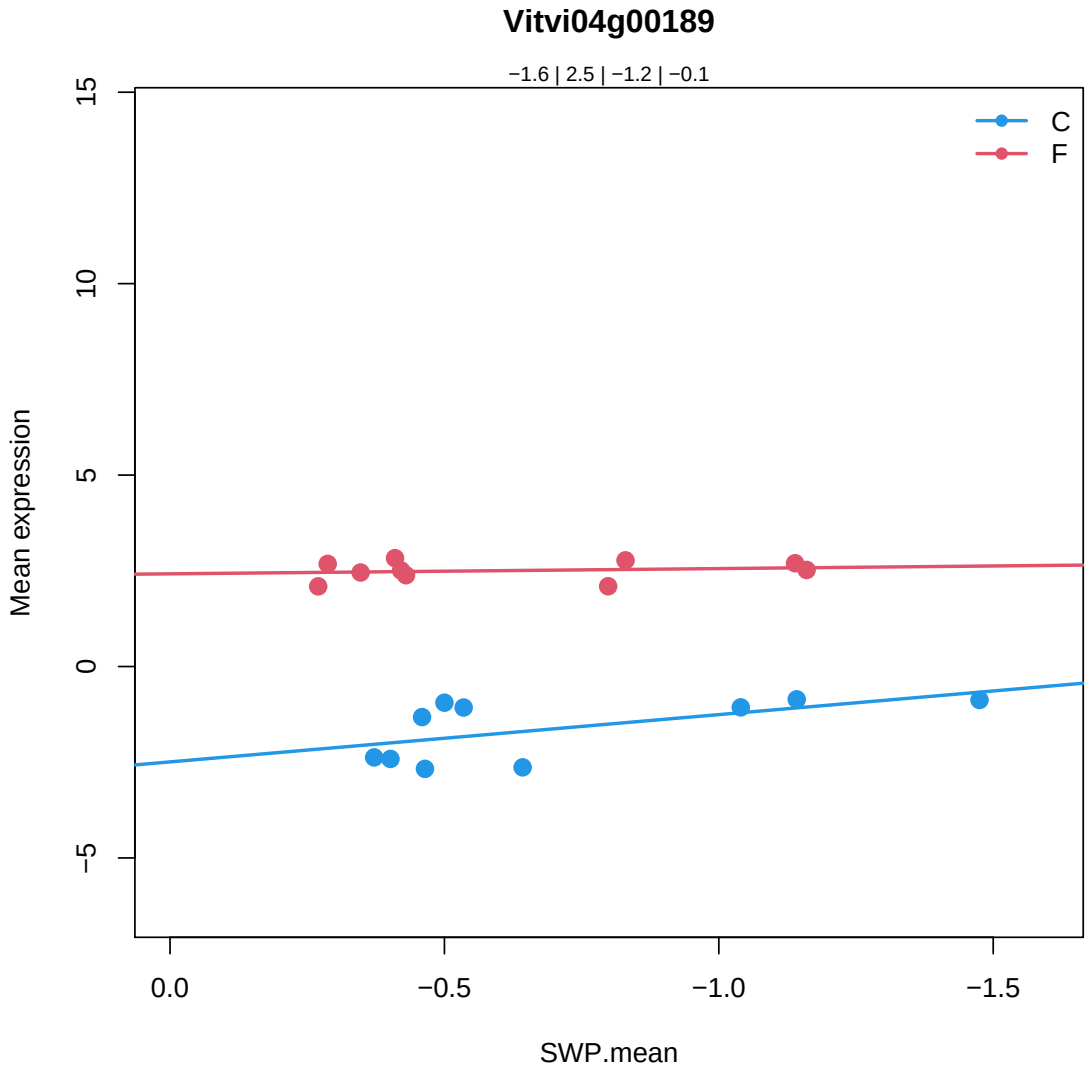
7.4.165 Vitvi04g00189: * type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00189
        28.2
        DNA.repair
        sterile alpha motif (SAM) domain-containing protein |
        Chr2:18827761-18830505 REVERSE LENGTH=631 |
        201606
```

Coefficients for Vitvi04g00189.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.622777	1.322004e-09	***	1.661169e-09	***
SlopeC	-1.235233	0.01153378	*	0.318473	
MeanF-MeanC	4.126921	1.686347e-14	***	2.072846e-12	***
SlopeF-SlopeC	1.098512	0.1134135		0.9999488	



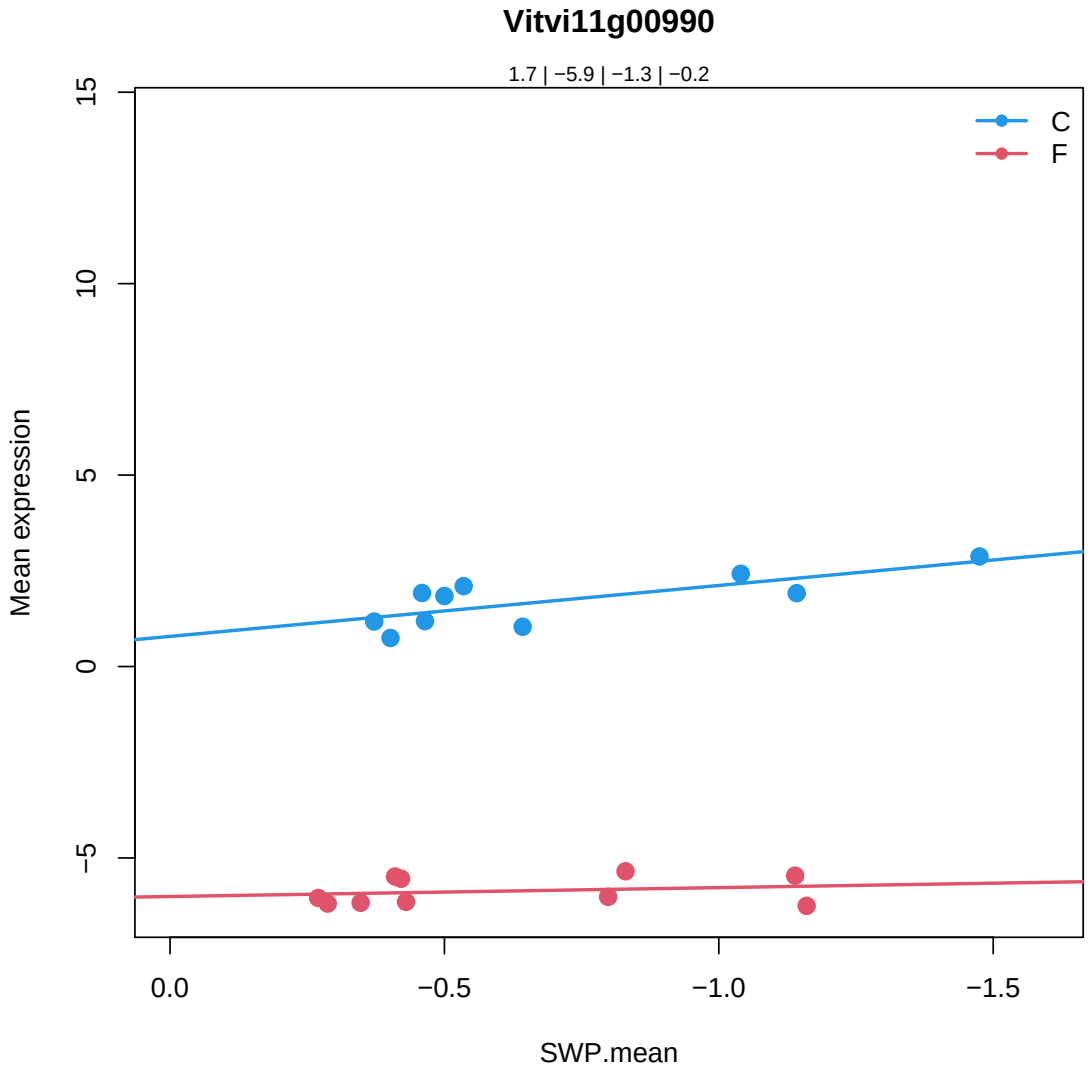
7.4.166 Vitvi11g00990: * type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00990
        35.2
        not assigned.unknown
        RING/U-box superfamily protein |
        Chr2:8093469-8094452 FORWARD LENGTH=181 |
        201606
```

Coefficients for Vitvi11g00990.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.721796	3.353624e-11	***	4.473259e-11	***
SlopeC	-1.330176	0.002501574	**	0.1896965	
MeanF-MeanC	-7.587376	2.924031e-21	***	1.714157e-18	***
SlopeF-SlopeC	1.098097	0.07117897	.	0.9999488	



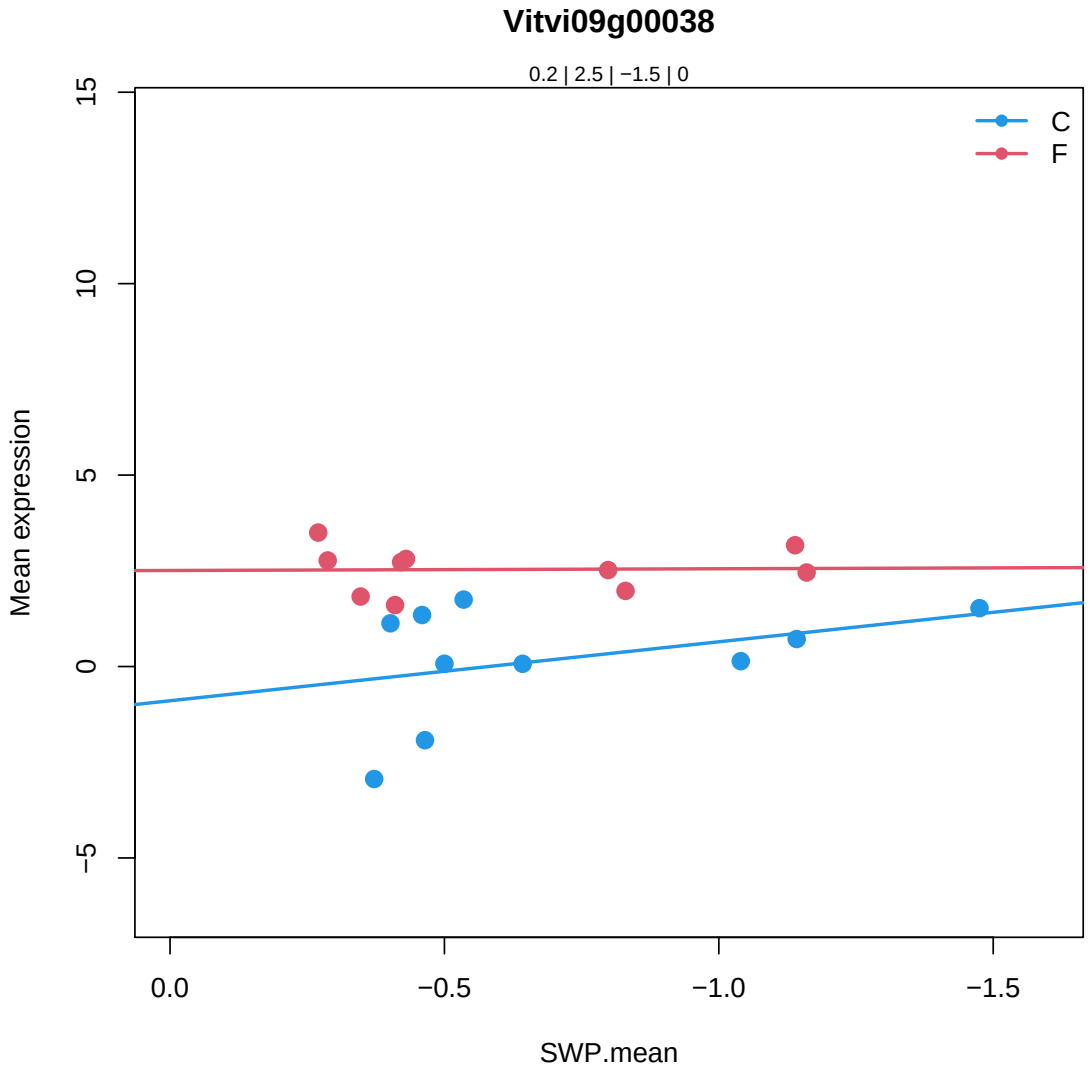
7.4.167 Vitvi09g00038: type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00038
        26.28
        misc.GDSL-motif lipase
        GDSL lipase 1 |
        Chr5:16418920-16420400 FORWARD LENGTH=374 |
        201606
```

Coefficients for Vitvi09g00038.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1883609	0.5662382		0.5720935	
SlopeC	-1.539814	0.1013475		0.6135572	
MeanF-MeanC	2.347224	4.113761e-05	***	0.0008326951	***
SlopeF-SlopeC	1.494714	0.2765741		0.9999488	



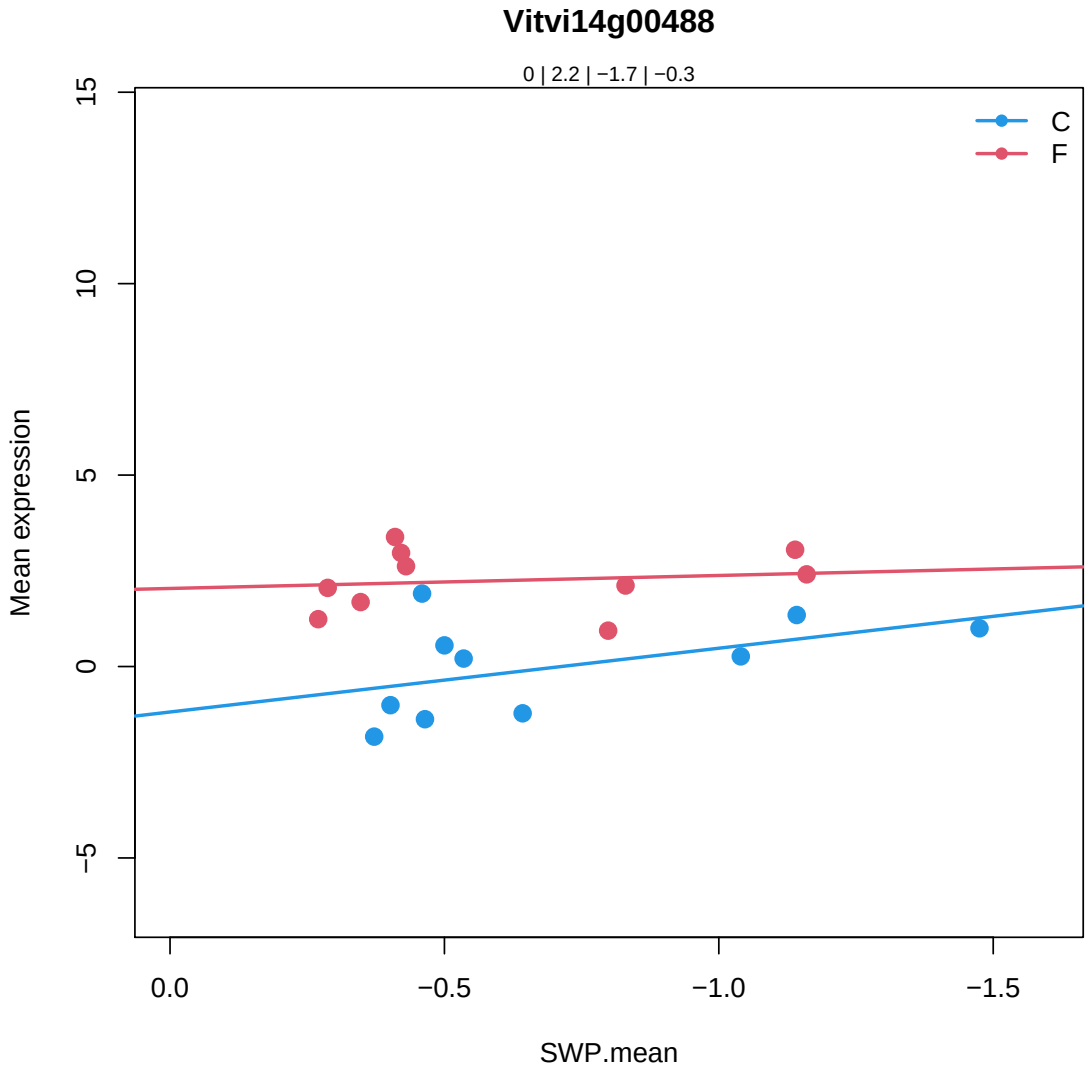
7.4.168 Vitvi14g00488: type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g00488
        20.1.7
        stress.biotic.PR-proteins
        pathogenesis-related 4 |
        Chr3:1285691-1286531 REVERSE LENGTH=212 |
        201606
```

Coefficients for Vitvi14g00488.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.01658827	0.954802		0.9555543	
SlopeC	-1.665567	0.0507581	.	0.5104439	
MeanF-MeanC	2.2616	1.619289e-05	***	0.0003838445	***
SlopeF-SlopeC	1.326057	0.2805442		0.9999488	



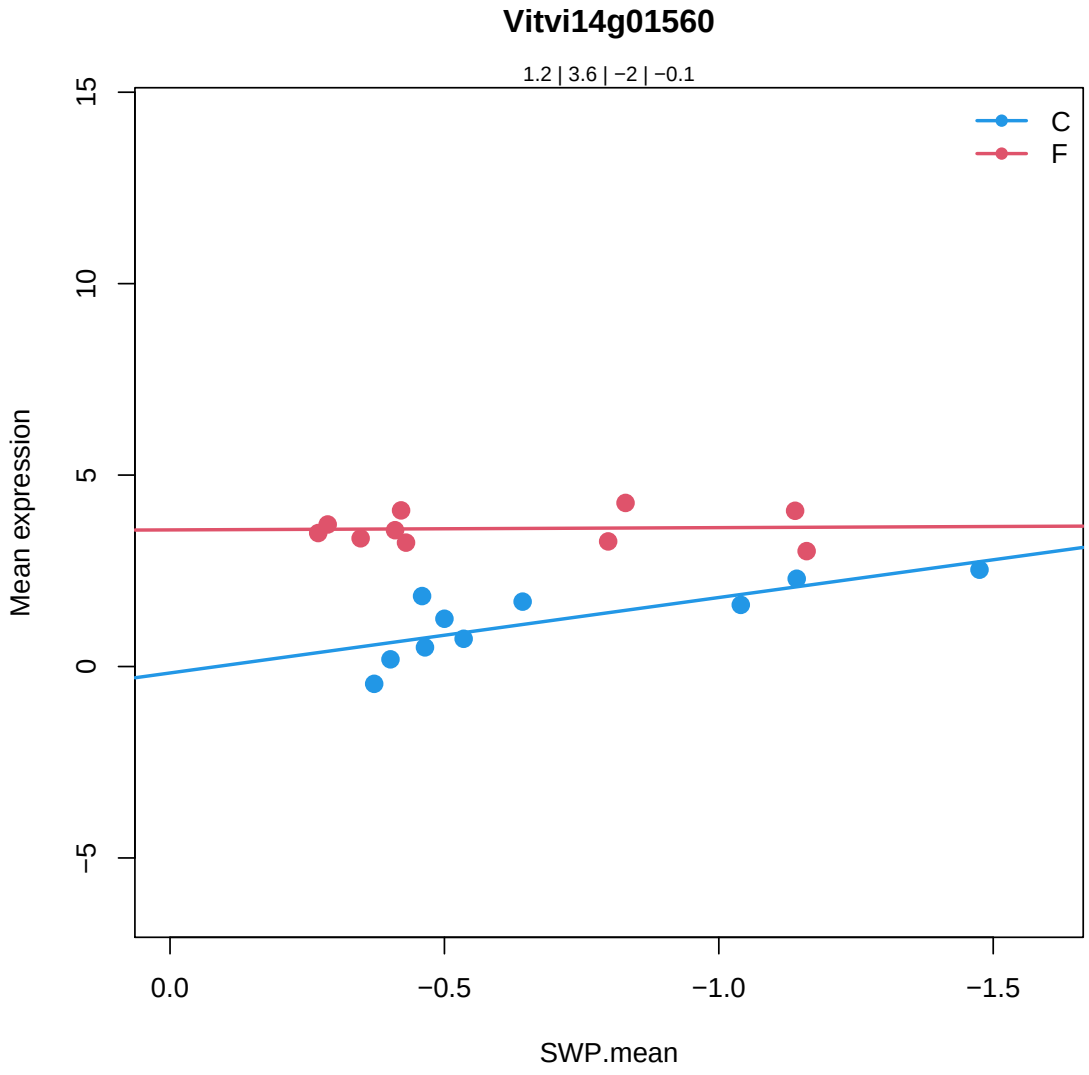
7.4.169 Vitvi14g01560: * type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01560
        34.18
        transport.unspecified anions
        chloride channel B |
        Chr3:10024147-10026921 FORWARD LENGTH=780 |
        201606
```

Coefficients for Vitvi14g01560.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.217239	3.697346e-07	***	4.316072e-07	***
SlopeC	-1.971048	0.0003913296	***	0.09467692	.
MeanF-MeanC	2.386564	1.581577e-09	***	8.765963e-08	***
SlopeF-SlopeC	1.911944	0.01226789	*	0.9999488	



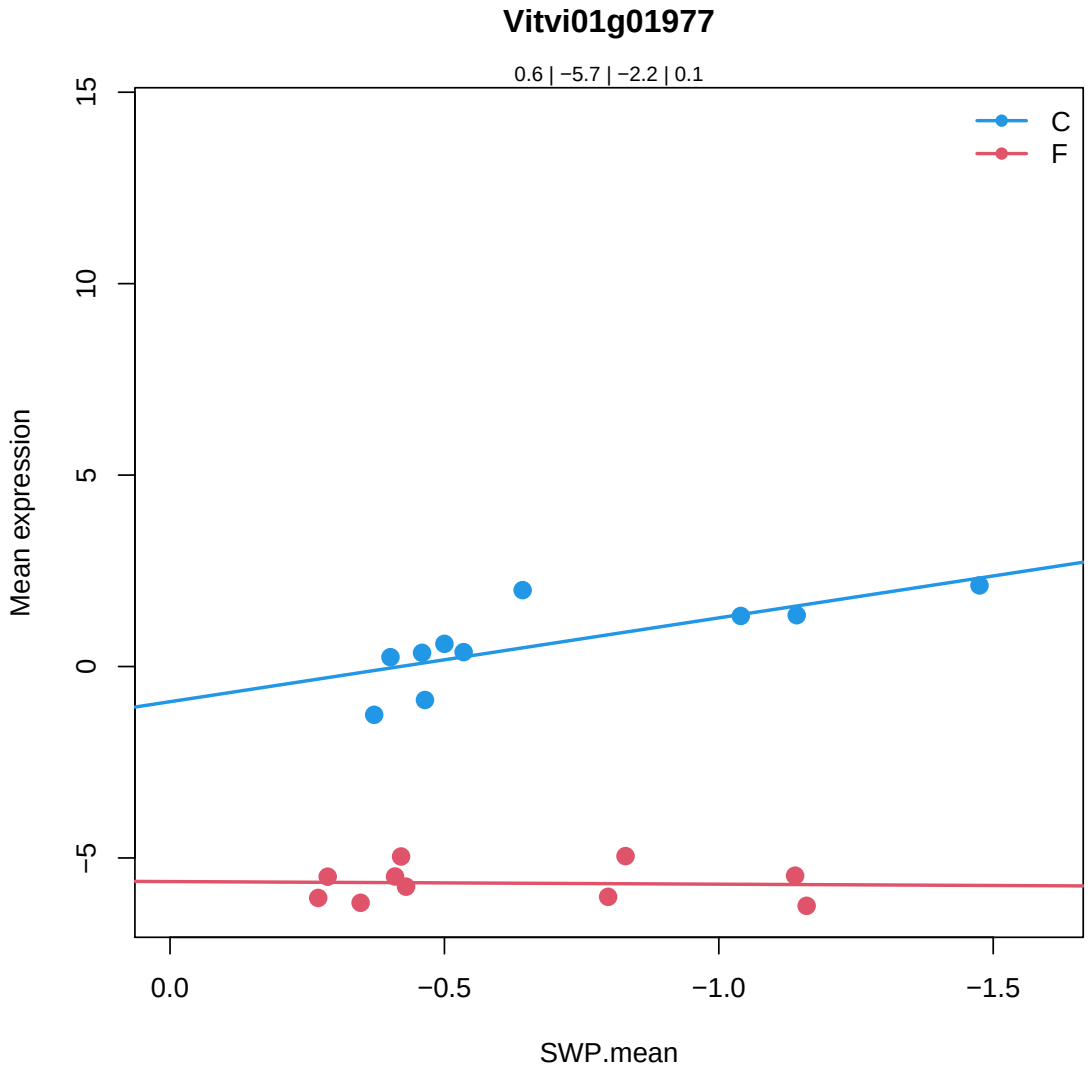
7.4.170 Vitvi01g01977: * type3

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01977
        20.1
        stress.biotic
        Polyketide cyclase/dehydrase and lipid transport superfamily protein |
        Chr1:8198788-8199359 FORWARD LENGTH=148 |
        201606
```

Coefficients for Vitvi01g01977.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6206962	0.004645355	**	0.004958298	**
SlopeC	−2.189318	0.0006200866	***	0.1005065	
MeanF−MeanC	−6.278969	1.930905e−16	***	3.344415e−14	***
SlopeF−SlopeC	2.257369	0.01121402	*	0.9999488	



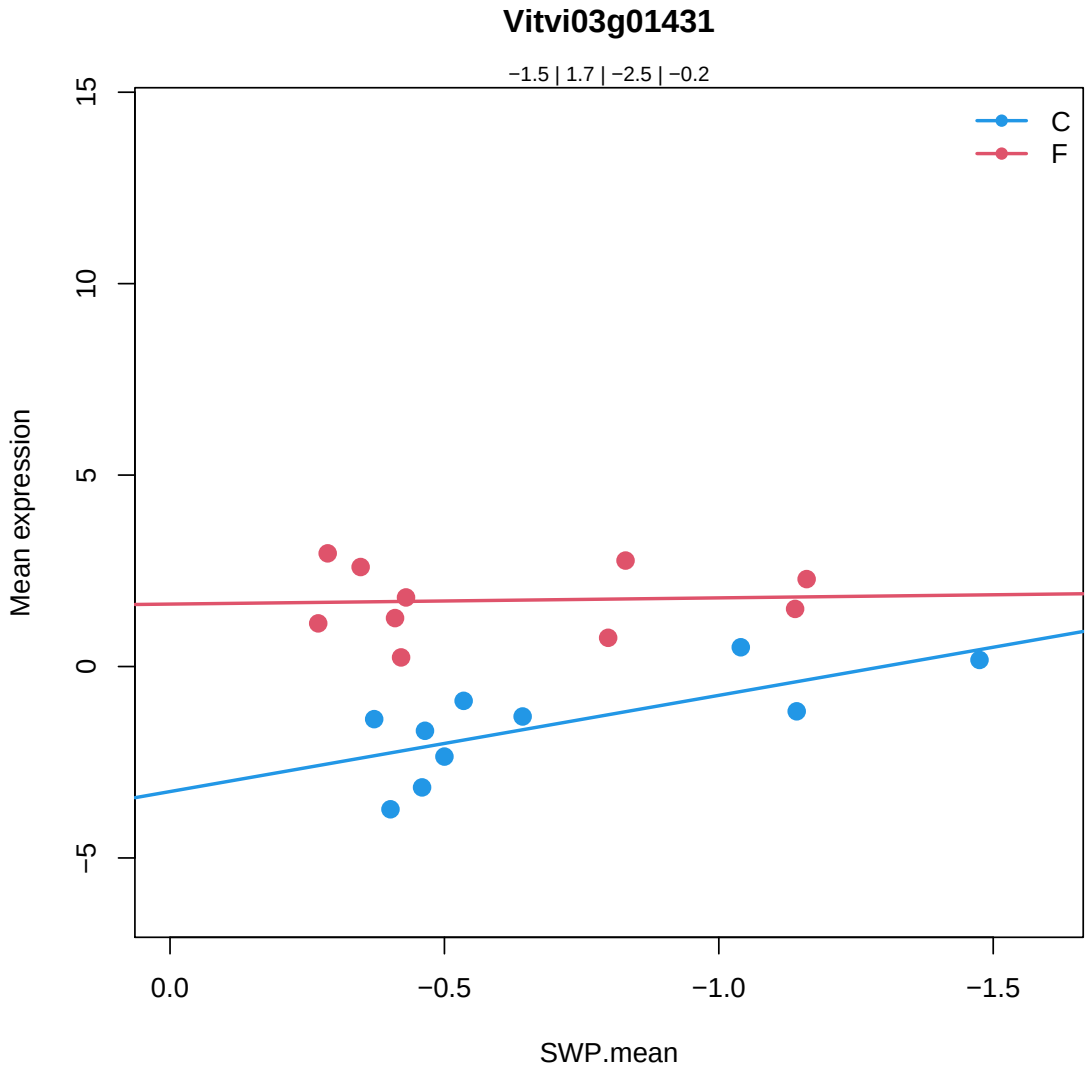
7.4.171 Vitvi03g01431: * type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g01431
        26.7
        misc.oxidases - copper, flavone etc
        flavin-dependent monooxygenase 1 |
        Chr1:6650656-6653053 REVERSE LENGTH=530 |
        201606
```

Coefficients for Vitvi03g01431.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.498922	2.078617e-05	***	2.330265e-05	***
SlopeC	-2.513015	0.003608732	**	0.2248659	
MeanF-MeanC	3.228153	4.224193e-08	***	1.877118e-06	***
SlopeF-SlopeC	2.351136	0.05238461	.	0.9999488	



7.5 type4

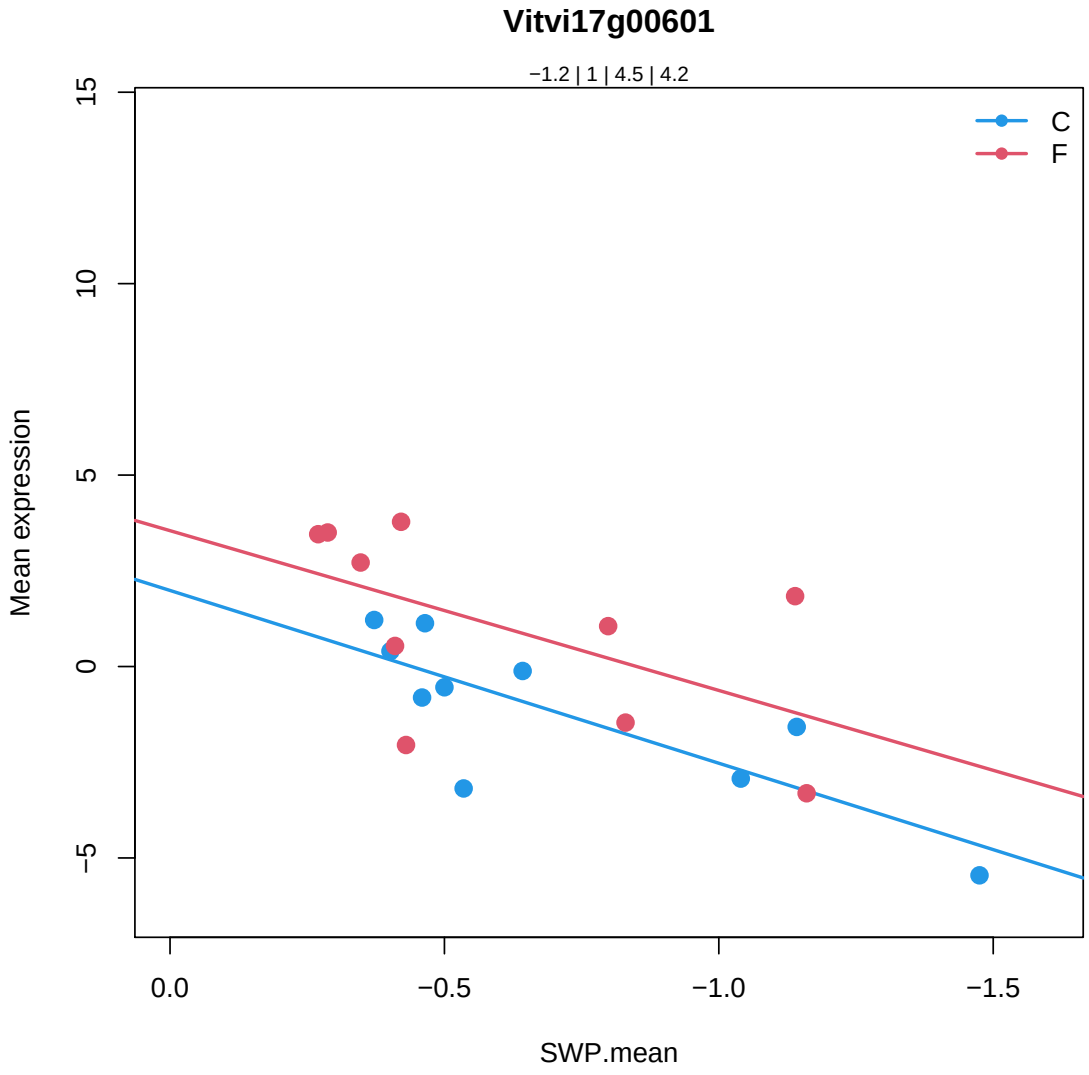
7.5.1 Vitvi17g00601: * type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00601
        17.6.3
        hormone metabolism.gibberelin.induced-regulated-responsive-activated
        Gibberellin-regulated family protein |
        Chr1:28053378-28053893 FORWARD LENGTH=101 |
        201606
```

Coefficients for Vitvi17g00601.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.186615	0.02892715	*	0.03029669	*
SlopeC	4.512791	0.004217337	**	0.2376222	
MeanF-MeanC	2.192138	0.005867102	**	0.05151288	.
SlopeF-SlopeC	-0.3397197	0.8729075		0.9999488	



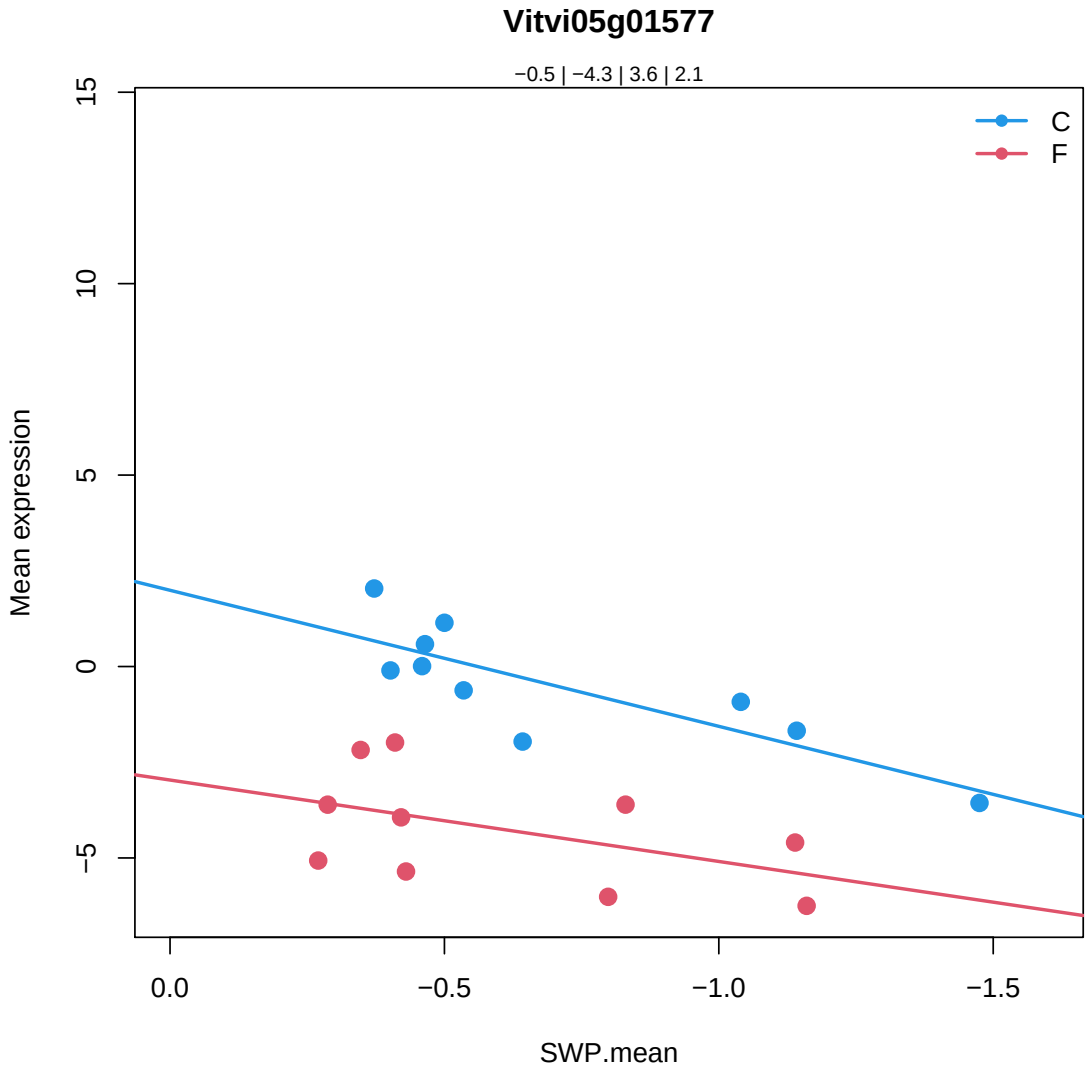
7.5.2 Vitvi05g01577: * type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01577
        20.1.7.3
        stress.biotic.PR-proteins.PR3/4/8/11 (chitinases and chitin binding pr
        homolog of carrot EP3-3 chitinase |
        Chr3:20145935-20147034 FORWARD LENGTH=273 |
        201606
```

Coefficients for Vitvi05g01577.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.5075609	0.1396409		0.1438405	
SlopeC	3.553568	0.0008792532	***	0.118598	
MeanF-MeanC	-3.752991	6.802344e-08	***	2.920601e-06	***
SlopeF-SlopeC	-1.42671	0.3093121		0.9999488	



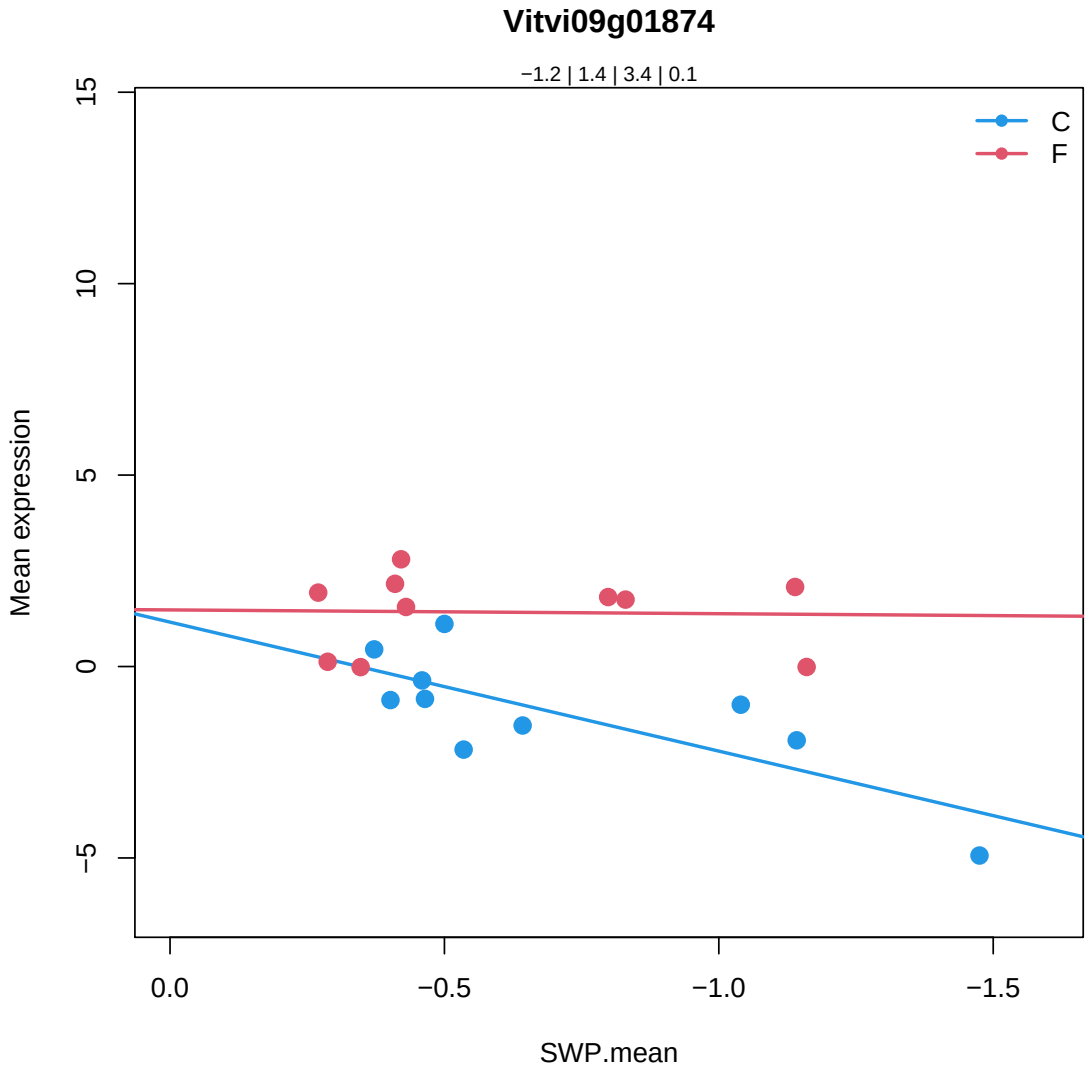
7.5.3 Vitvi09g01874: * type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g01874
        35.2
        not assigned.unknown
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606
```

Coefficients for Vitvi09g01874.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.209693	0.0007634725	***	0.0008287763	***
SlopeC	3.369133	0.0007557867	***	0.1076608	
MeanF-MeanC	2.627733	5.179869e-06	***	0.0001389992	***
SlopeF-SlopeC	-3.270373	0.01811727	*	0.9999488	



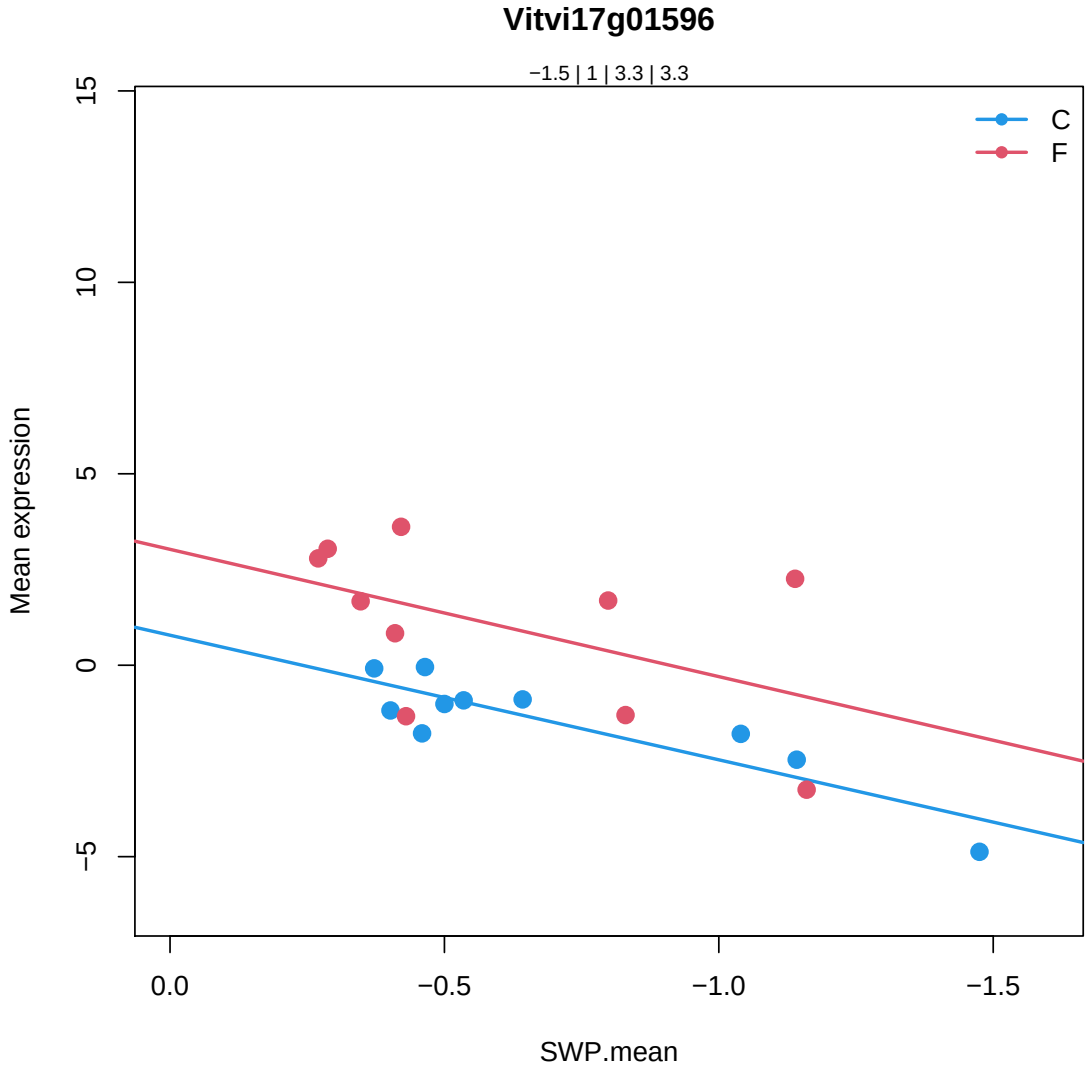
7.5.4 Vitvi17g01596: * type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g01596
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi17g01596.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.504888	0.00196087	**	0.002109513	**
SlopeC	3.254213	0.01212222	*	0.3229093	
MeanF-MeanC	2.506095	0.0004361519	***	0.006295291	**
SlopeF-SlopeC	0.07011039	0.9687282		0.9999488	



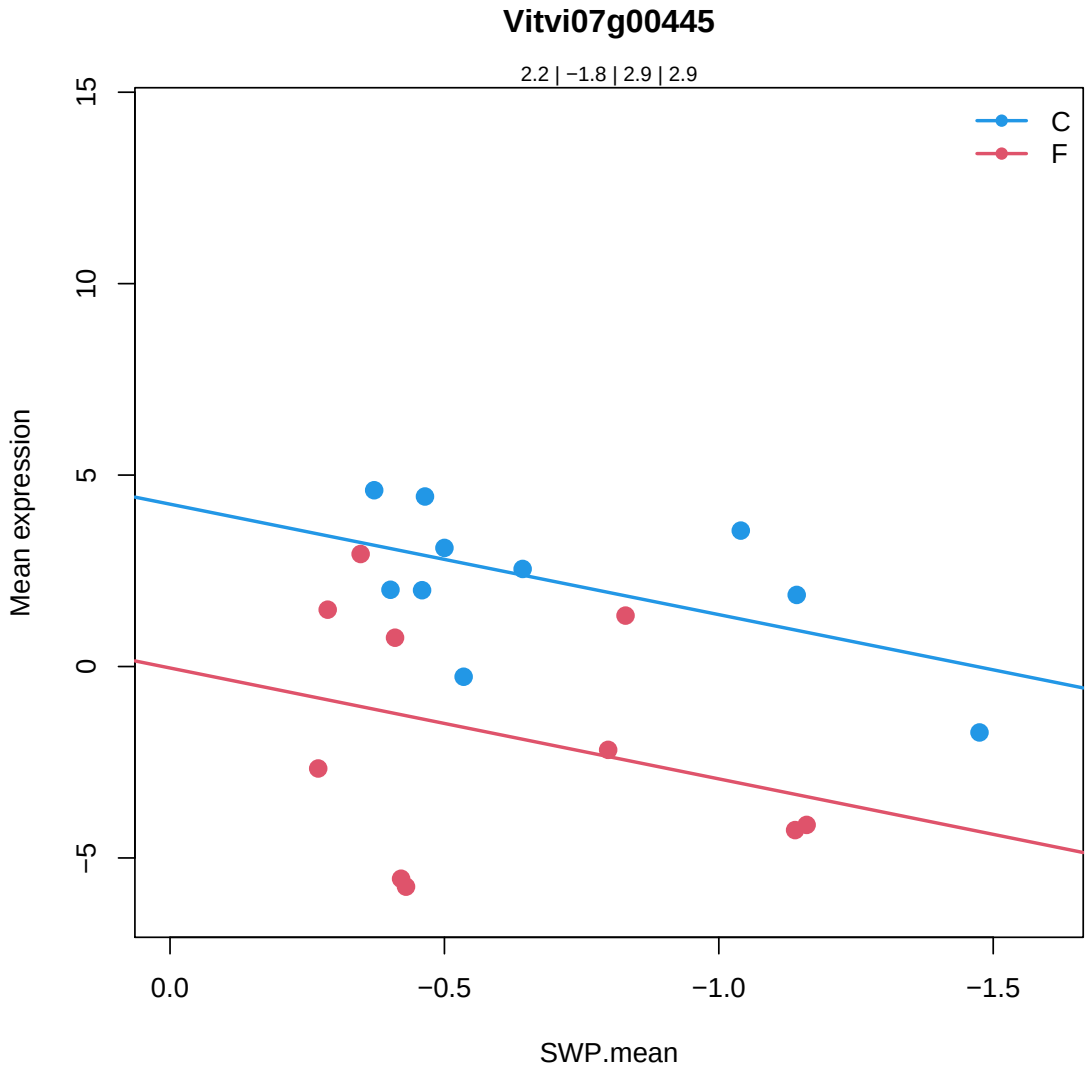
7.5.5 Vitvi07g00445: type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g00445
        11.1.9
        lipid metabolism.FA synthesis and FA elongation.long chain fatty acid
        AMP-dependent synthetase and ligase family protein |
        Chr2:19393835-19397616 FORWARD LENGTH=660 |
        201606
```

Coefficients for Vitvi07g00445.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.211746	0.005213937	**	0.005558566	**
SlopeC	2.884577	0.1593951		0.6889929	
MeanF-MeanC	-4.015337	0.0006405182	***	0.008670318	**
SlopeF-SlopeC	0.01163635	0.9968841		0.9999488	



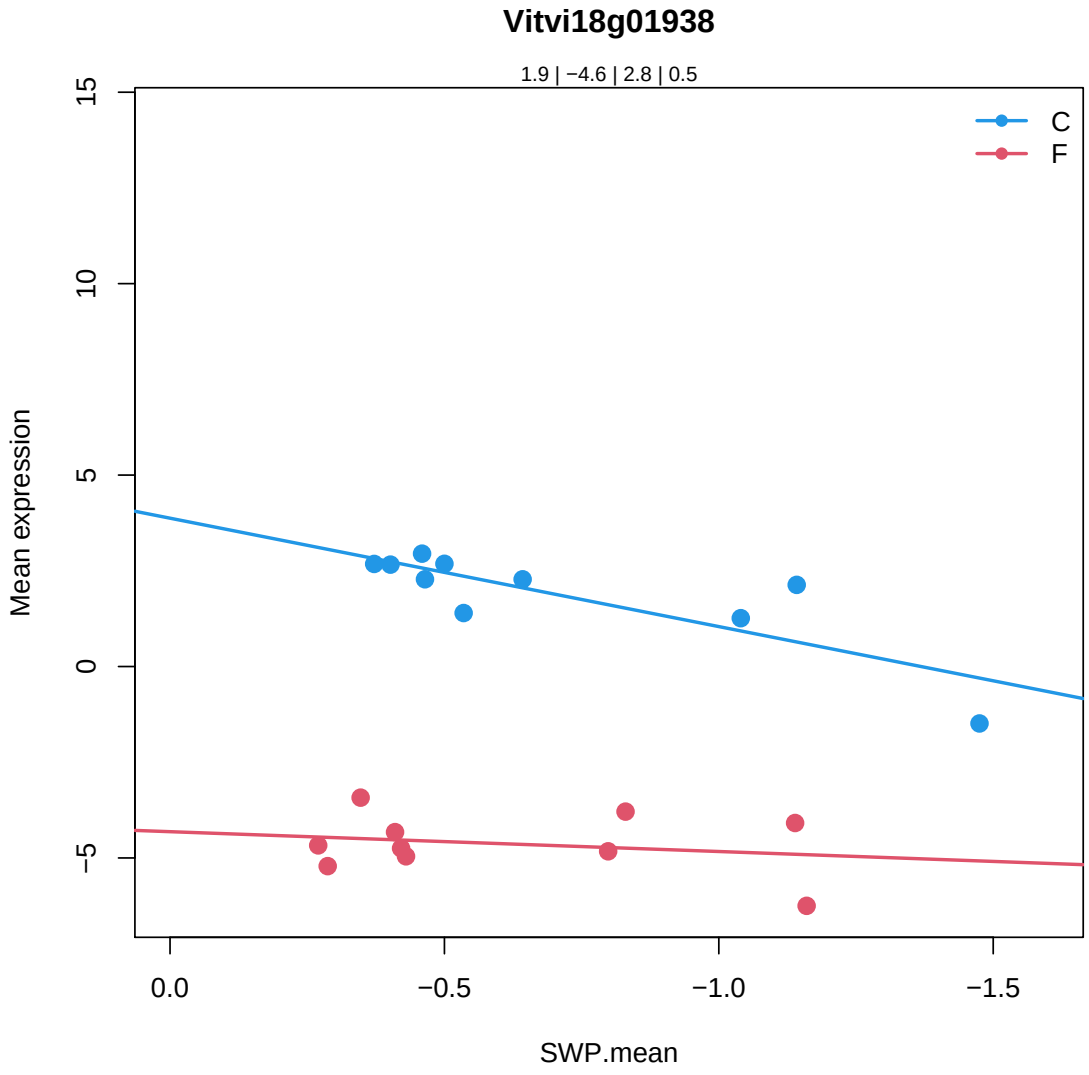
7.5.6 Vitvi18g01938: * type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g01938
        30.2.25
        signalling.receptor kinases.wall associated kinase
        wall associated kinase 3 |
        Chr1:7434303-7436702 FORWARD LENGTH=741 |
        201606
```

Coefficients for Vitvi18g01938.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.88307	6.297909e-08	***	7.509993e-08	***
SlopeC	2.831106	0.0002667732	***	0.08298279	.
MeanF-MeanC	-6.512595	3.19492e-15	***	4.23452e-13	***
SlopeF-SlopeC	-2.313519	0.02603853	*	0.9999488	



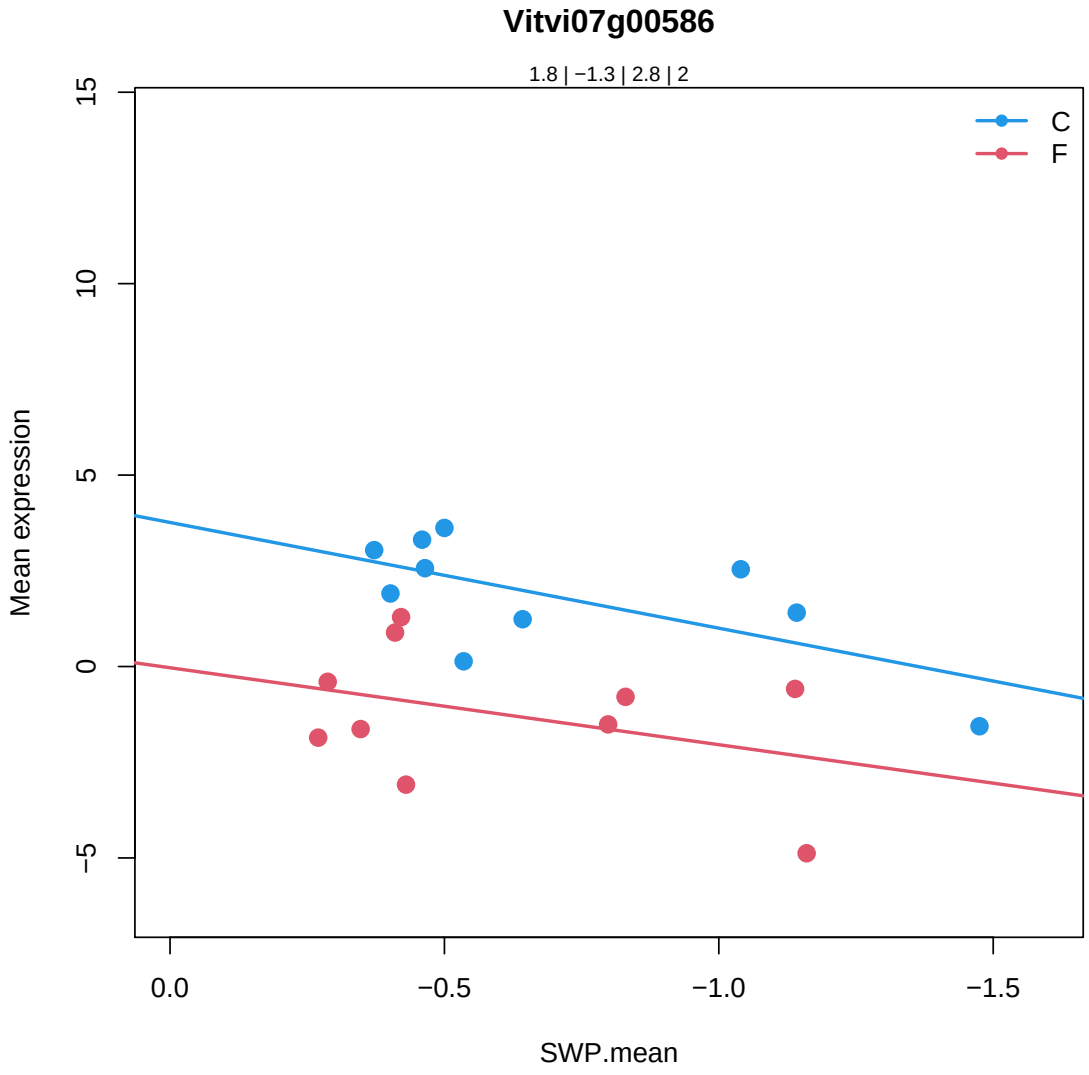
7.5.7 Vitvi07g00586: * type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g00586
        29.5.4
        protein.degradation.aspartate protease
        Eukaryotic aspartyl protease family protein |
        Chr2:966506-967891 REVERSE LENGTH=461 |
        201606
```

Coefficients for Vitvi07g00586.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.820575	0.0003499595	***	0.0003821523	***
SlopeC	2.761208	0.03074027	*	0.4322019	
MeanF-MeanC	-3.07708	4.782582e-05	***	0.0009503821	***
SlopeF-SlopeC	-0.7514262	0.6766004		0.9999488	



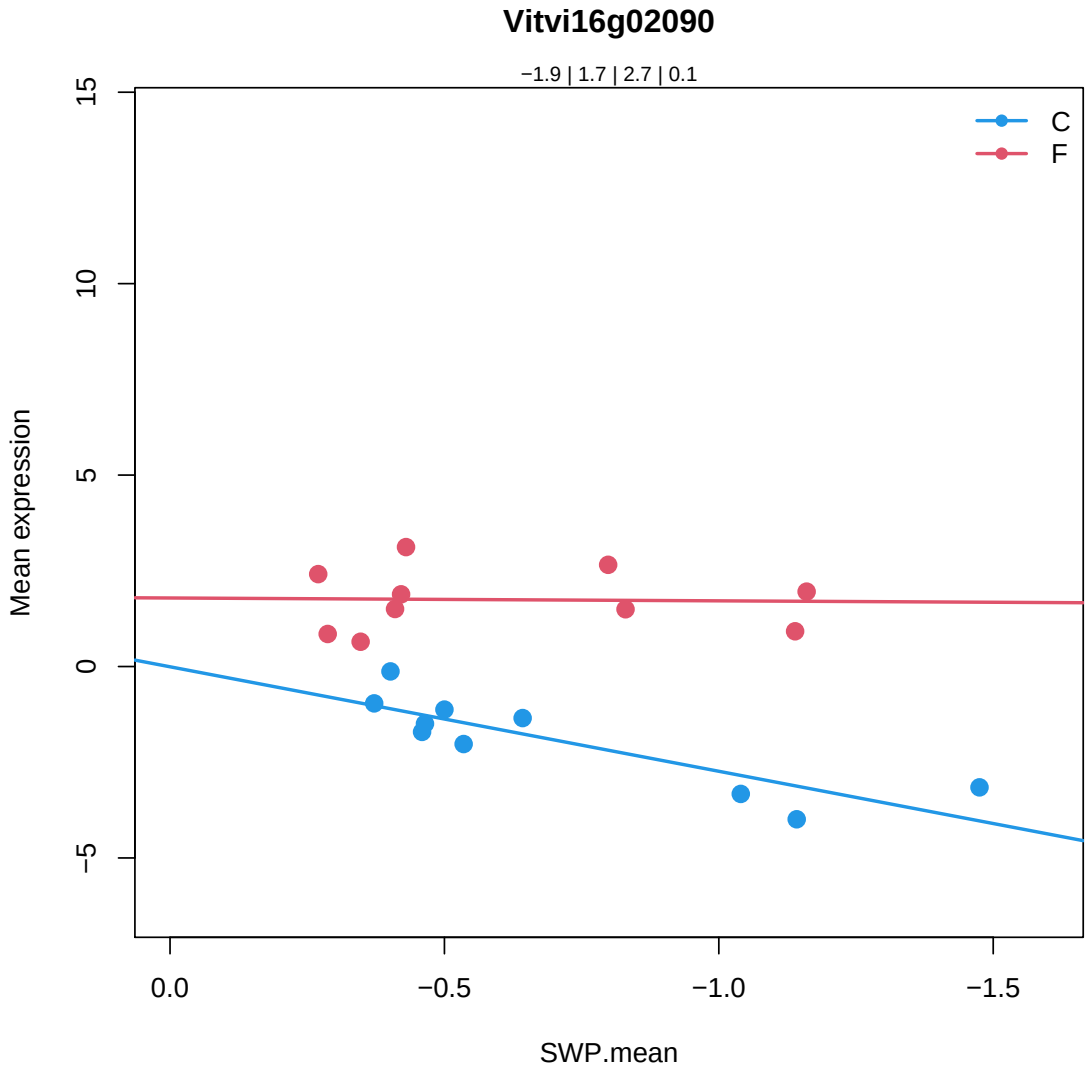
7.5.8 Vitvi16g02090: * type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g02090
        35.2
        not assigned.unknown
        PR5-like receptor kinase |
        Chr5:15293325-15295838 REVERSE LENGTH=665 |
        201606
```

Coefficients for Vitvi16g02090.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.926199	2.28078e-08	***	2.753775e-08	***
SlopeC	2.729033	0.0002614243	***	0.08298279	.
MeanF-MeanC	3.670552	1.144627e-10	***	7.8943e-09	***
SlopeF-SlopeC	-2.654757	0.009425042	**	0.9999488	



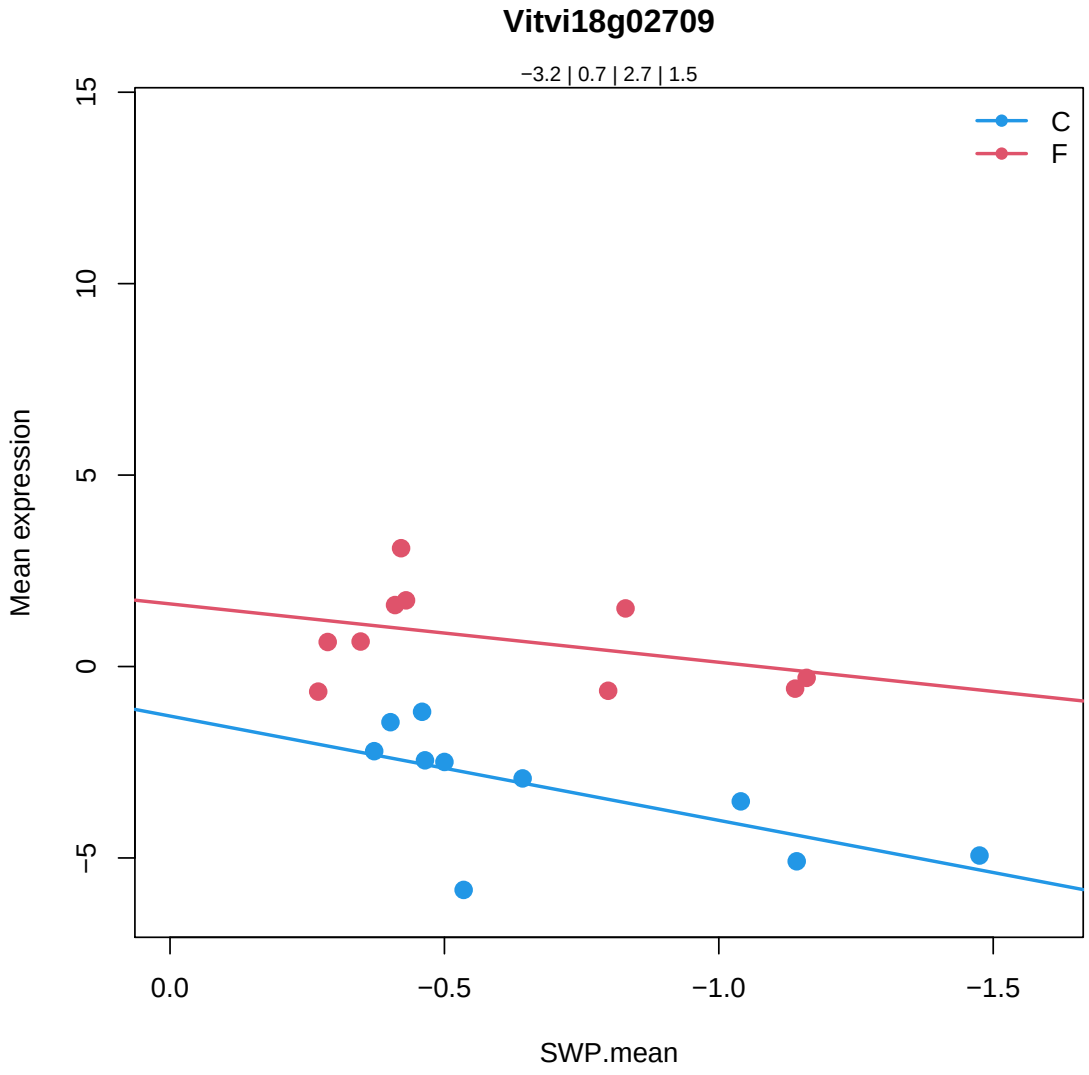
7.5.9 Vitvi18g02709: * type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02709
        35.1.40
        not assigned.no ontology.glycine rich proteins
        Cupredoxin superfamily protein |
        Chr2:6873666-6874701 REVERSE LENGTH=257 |
        201606
```

Coefficients for Vitvi18g02709.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-3.209467	8.027118e-09	***	9.824888e-09	***
SlopeC	2.724042	0.01110047	*	0.3143947	
MeanF-MeanC	3.91652	9.423432e-08	***	3.871481e-06	***
SlopeF-SlopeC	-1.199916	0.4198128		0.9999488	



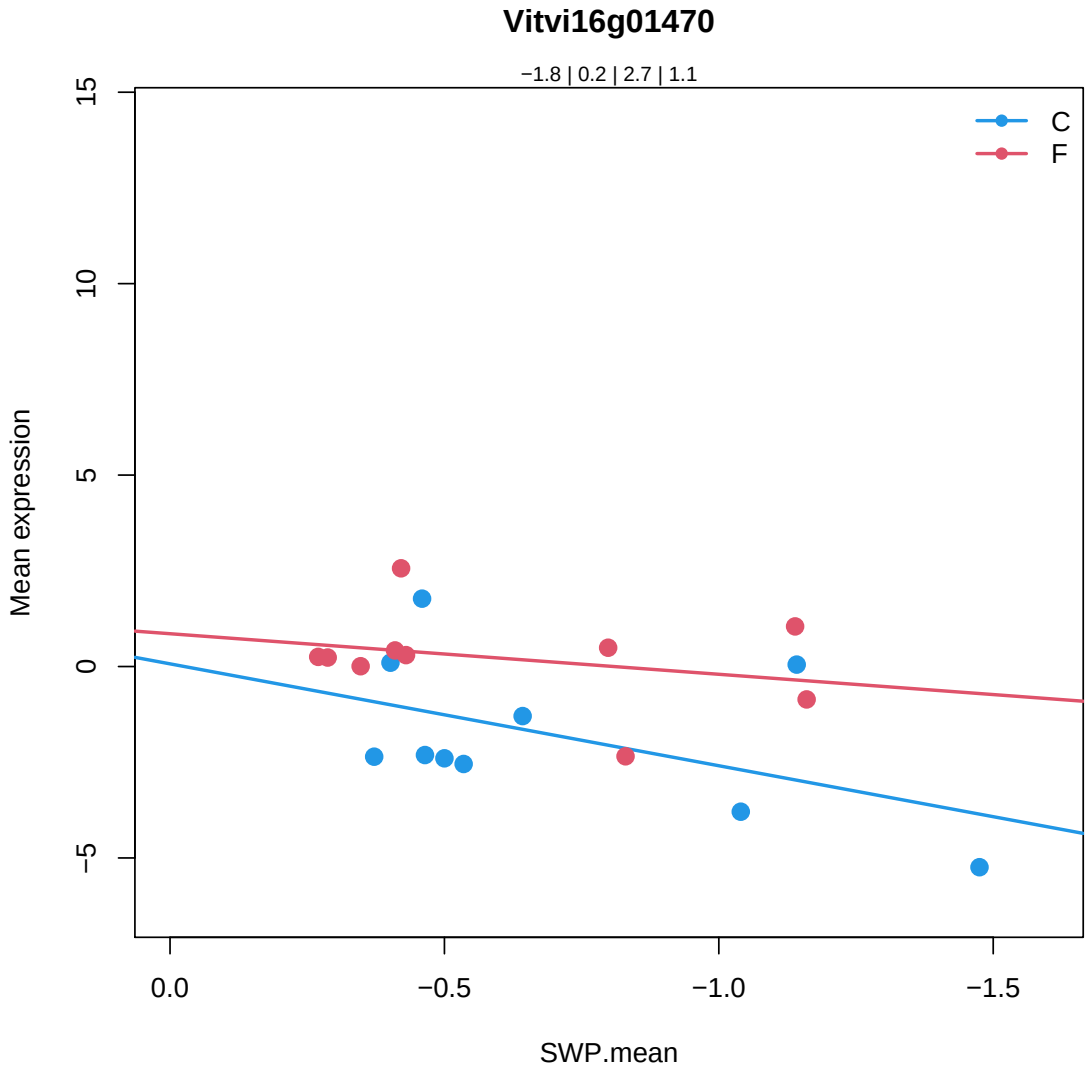
7.5.10 Vitvi16g01470: * type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01470
        35.2
        not assigned.unknown
        Chalcone and stilbene synthase family protein |
        Chr5:4488762-4490035 FORWARD LENGTH=395 |
        201606
```

Coefficients for Vitvi16g01470.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.801762	0.0005550164	***	0.0006037799	***
SlopeC	2.661094	0.04304173	*	0.48214	
MeanF-MeanC	2.012758	0.004222528	**	0.03986124	*
SlopeF-SlopeC	-1.601562	0.3941009		0.9999488	



7.5.11 Vitvi09g00258: * type4

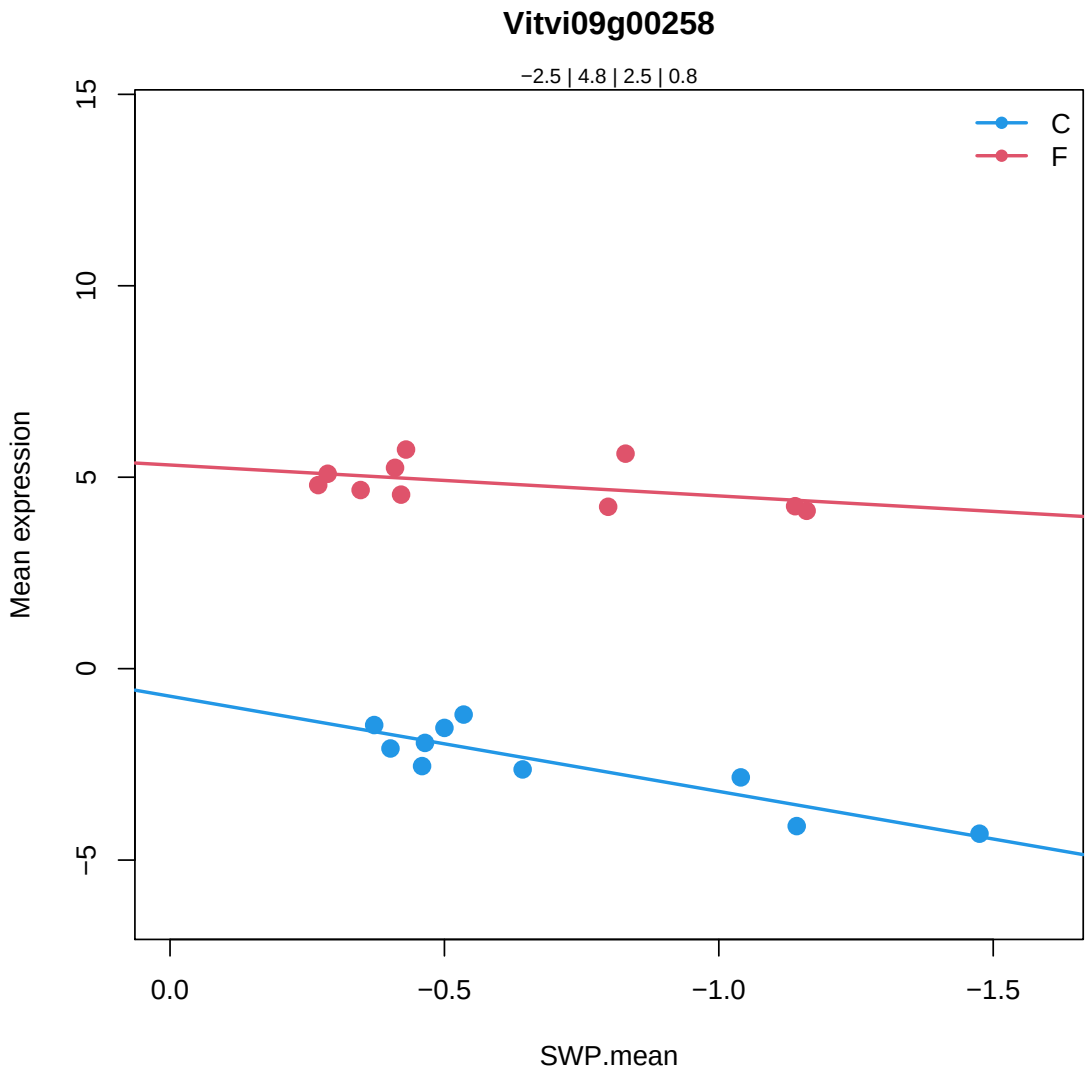
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00258
        30.2.1
        signalling.receptor kinases.leucine rich repeat I
        root hair specific 6 |
        Chr1:19270193-19274122 REVERSE LENGTH=890 |
        201606

Vitvi09g00258
        29.4
        protein.postranslational modification
        root hair specific 6 |
        Chr1:19270193-19274122 REVERSE LENGTH=890 |
        201606
```

Coefficients for Vitvi09g00258.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-2.468524	6.812044e-13	***	9.893204e-13	***
SlopeC	2.485974	1.903022e-05	***	0.04768143	*
MeanF-MeanC	7.295481	1.887833e-19	***	5.860462e-17	***
SlopeF-SlopeC	-1.678231	0.02167859	*	0.9999488	


Vitvi09g00258
−2.5 | 4.8 | 2.5 | 0.8
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

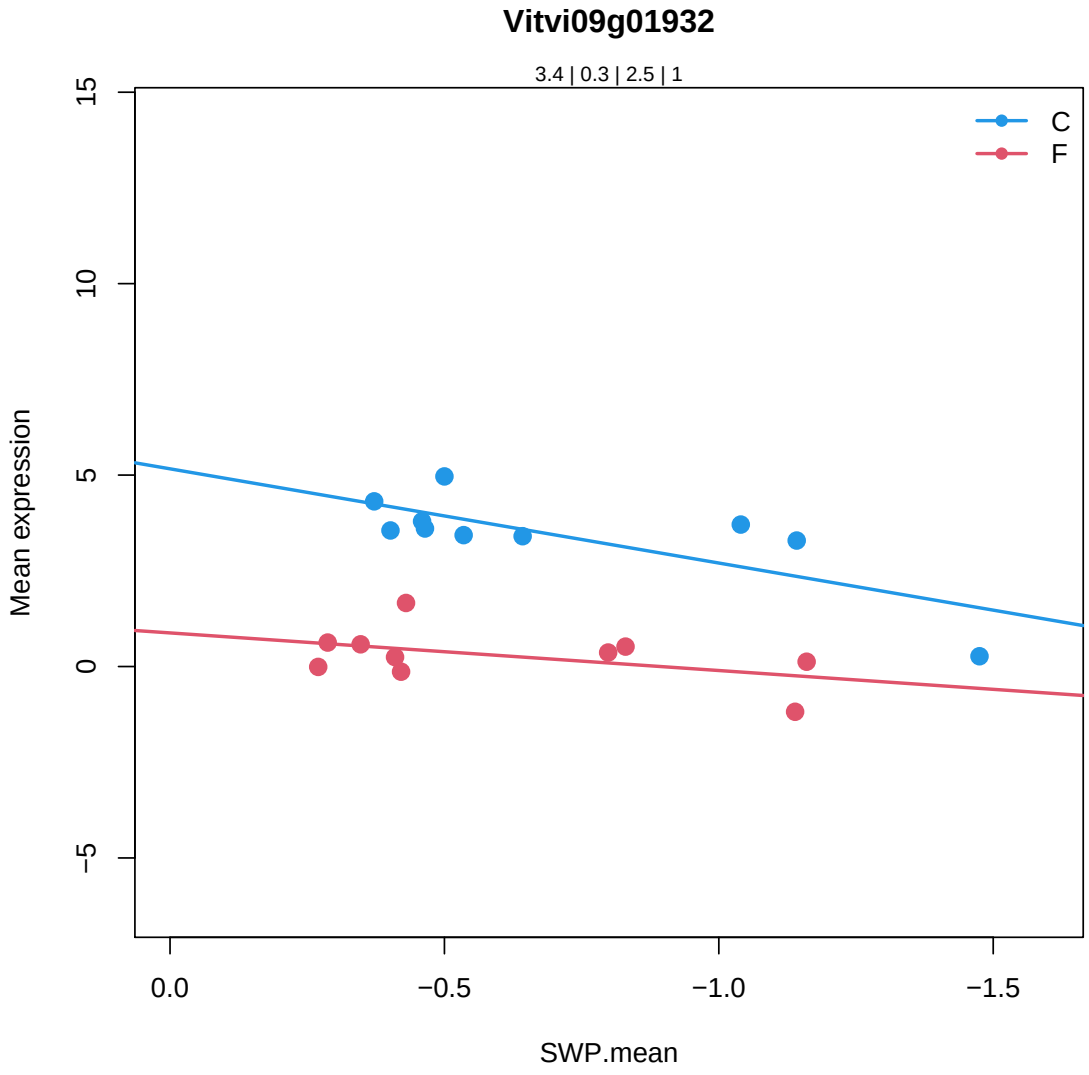
7.5.12 Vitvi09g01932: * type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g01932
        20.1.2
        stress.biotic.receptors
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606
```

Coefficients for Vitvi09g01932.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.433029	3.782626e-13	***	5.580756e-13	***
SlopeC	2.460612	0.000623382	***	0.1005065	
MeanF-MeanC	-3.153777	1.327157e-09	***	7.464401e-08	***
SlopeF-SlopeC	-1.478196	0.120754		0.9999488	



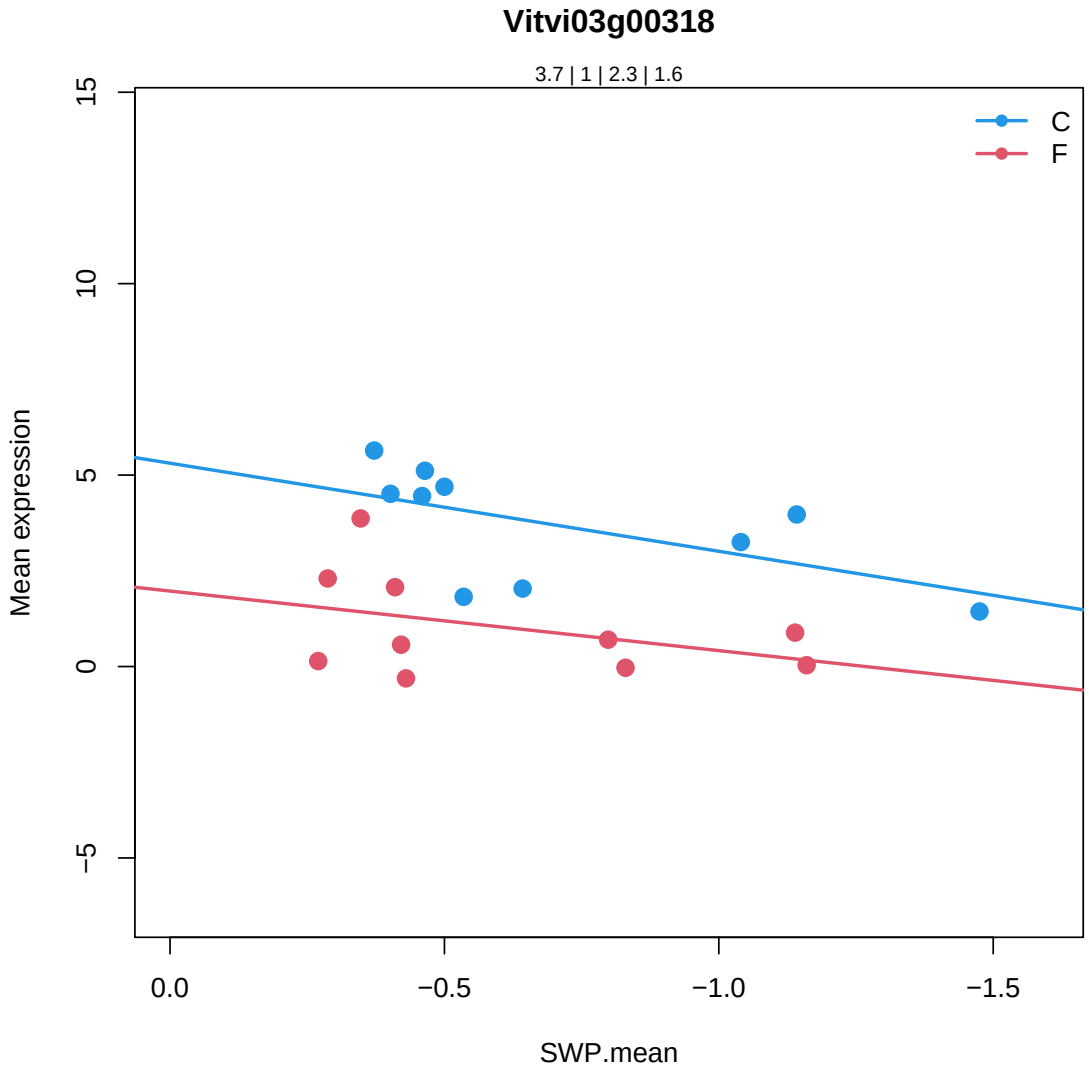
7.5.13 Vitvi03g00318: * type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00318
        27.3.25
        RNA.regulation of transcription.MYB domain transcription factor family
        RAD-like 6 |
        Chr1:28245073-28245453 REVERSE LENGTH=126 |
        201606
```

Coefficients for Vitvi03g00318.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.692558	8.664173e-10	***	1.094475e-09	***
SlopeC	2.300824	0.03059091	*	0.4321285	
MeanF-MeanC	-2.669643	2.876014e-05	***	0.0006253381	***
SlopeF-SlopeC	-0.7449947	0.6196467		0.9999488	



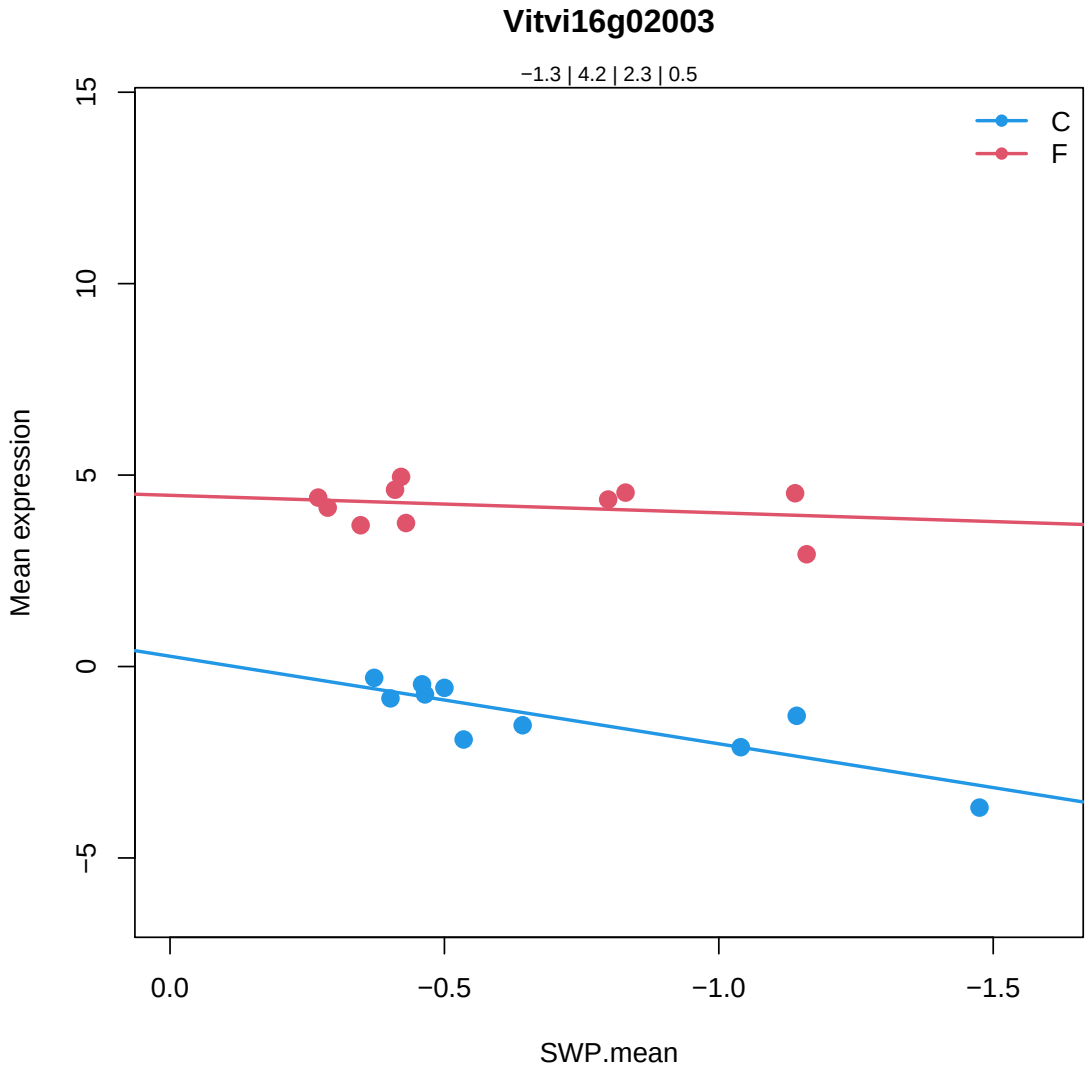
7.5.14 Vitvi16g02003: * type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g02003
        35.2
        not assigned.unknown
        PR5-like receptor kinase |
        Chr5:15293325-15295838 REVERSE LENGTH=665 |
        201606
```

Coefficients for Vitvi16g02003.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.339973	2.33912e-07	***	2.745485e-07	***
SlopeC	2.2875	0.000164243	***	0.07644173	.
MeanF-MeanC	5.532948	4.544274e-16	***	7.214982e-14	***
SlopeF-SlopeC	-1.830222	0.02298766	*	0.9999488	



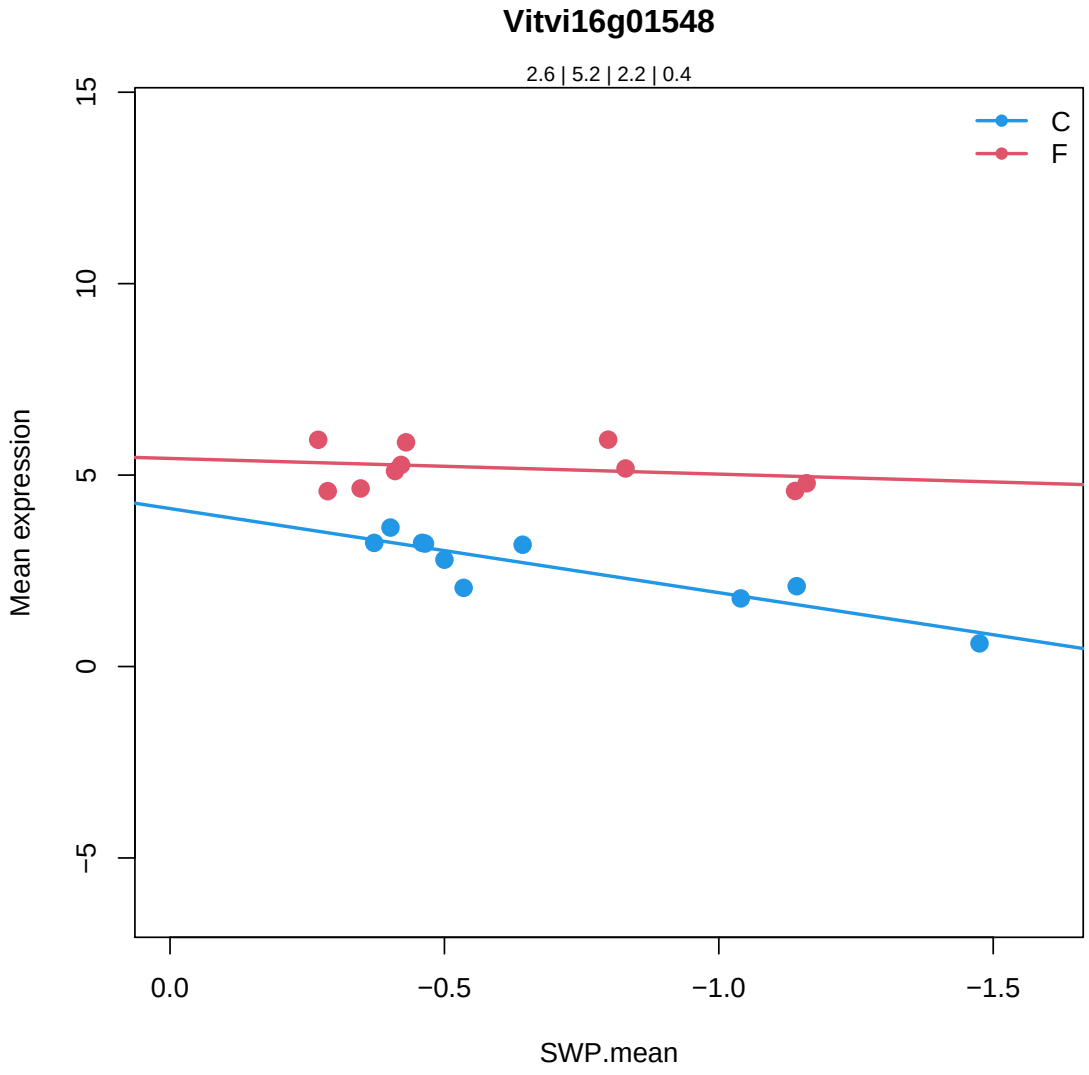
7.5.15 Vitvi16g01548: * type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01548
        35.2
        not assigned.unknown
        dihydroflavonol 4-reductase |
        Chr5:17164296-17165864 REVERSE LENGTH=382 |
        201606
```

Coefficients for Vitvi16g01548.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.580398	1.607866e-13	***	2.431742e-13	***
SlopeC	2.196869	6.152636e-05	***	0.07213729	.
MeanF-MeanC	2.60436	1.084352e-10	***	7.546893e-09	***
SlopeF-SlopeC	-1.787469	0.0128491	*	0.9999488	



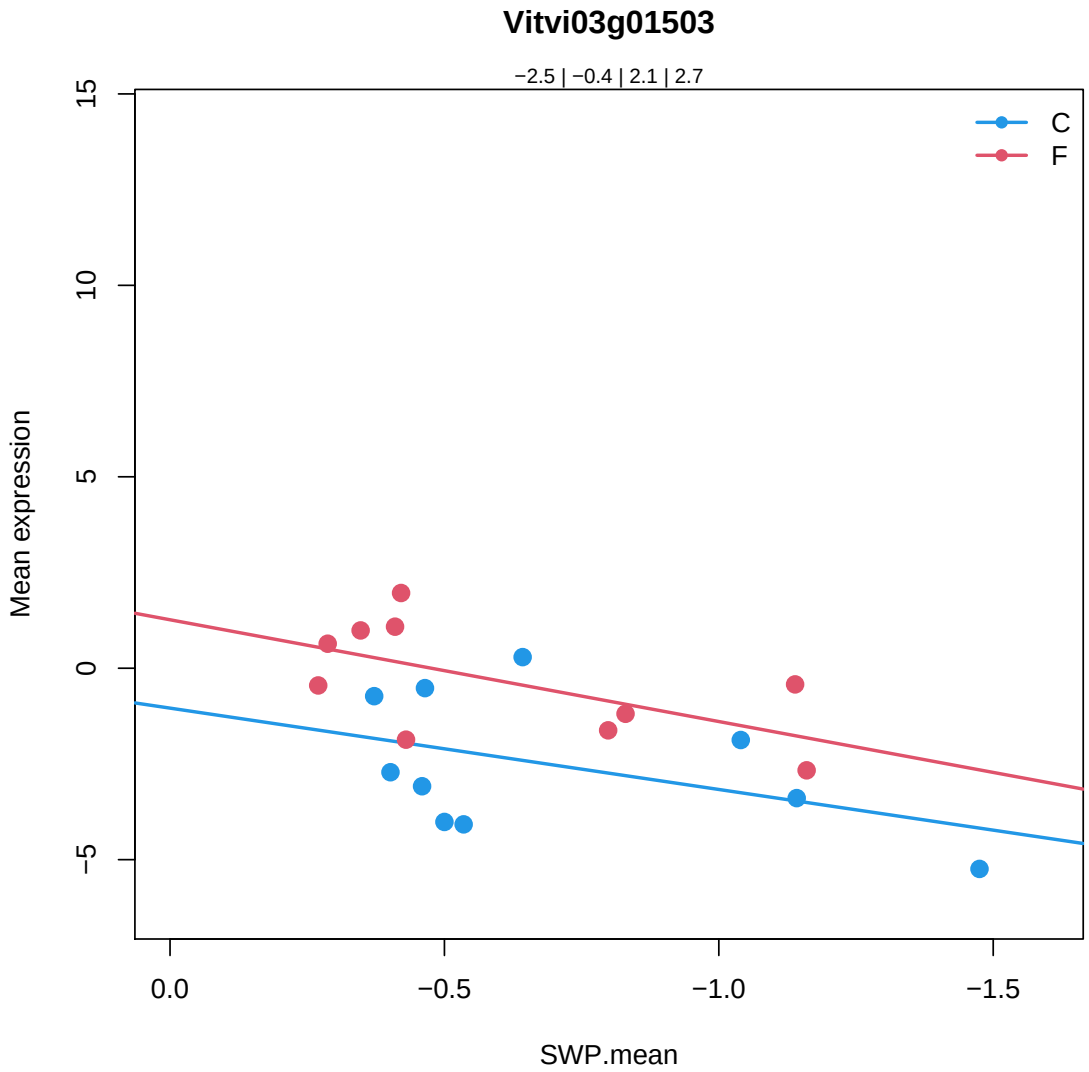
7.5.16 Vitvi03g01503: type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g01503
        35.2
        not assigned.unknown
        Organ-specific protein S2
```

Coefficients for Vitvi03g01503.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-2.536121	4.151528e-06	***	4.725735e-06	***
SlopeC	2.124611	0.07938146	.	0.5748584	
MeanF-MeanC	2.181984	0.00122855	**	0.01484977	*
SlopeF-SlopeC	0.5331686	0.7591512		0.9999488	



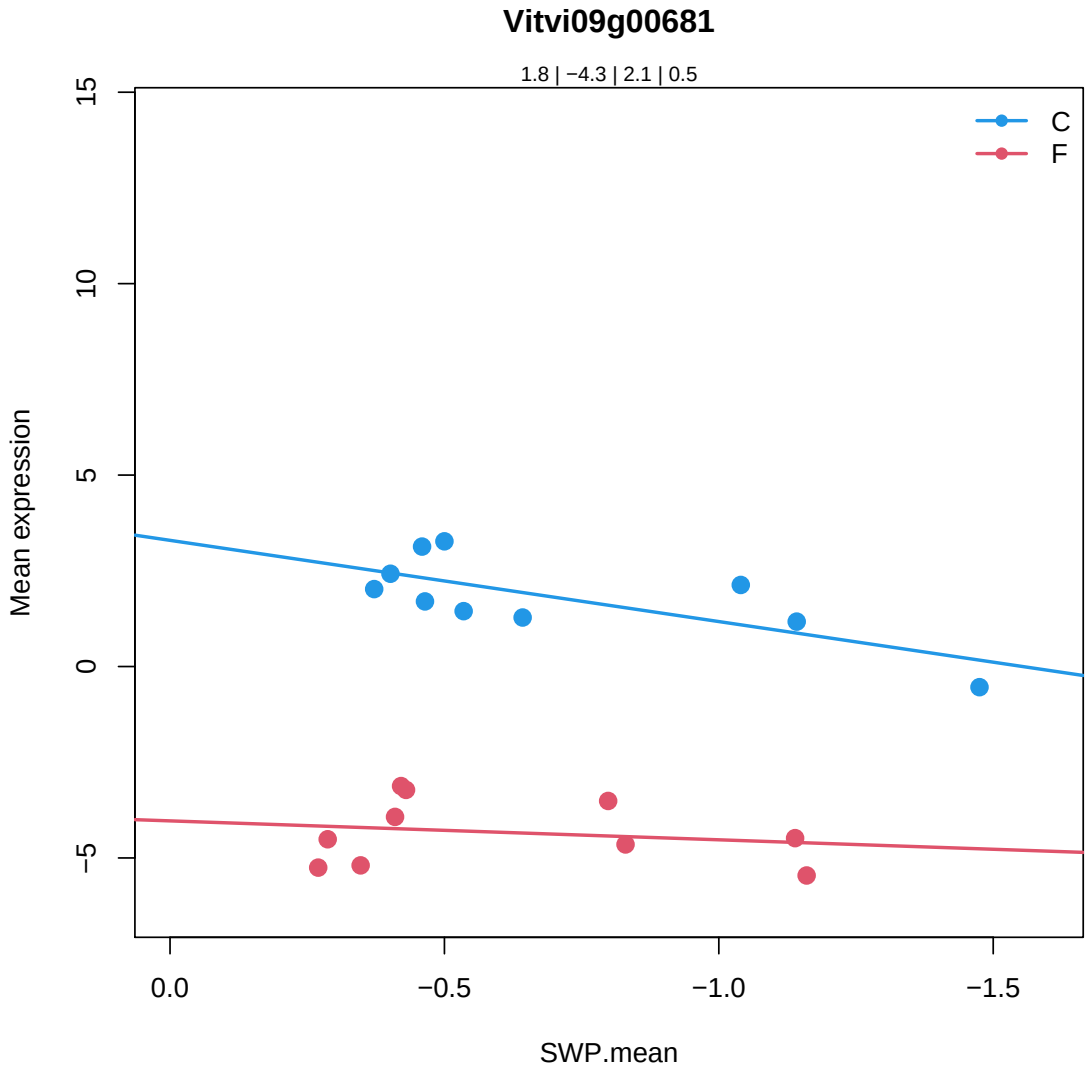
7.5.17 Vitvi09g00681: * type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00681
        20.1.2
        stress.biotic.receptors
        receptor like protein 1 |
        Chr1:2270633-2274654 FORWARD LENGTH=913 |
        201606
```

Coefficients for Vitvi09g00681.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.80362	2.175092e-07	***	2.556307e-07	***
SlopeC	2.121009	0.004715187	**	0.2454895	
MeanF-MeanC	-6.136671	2.131152e-14	***	2.537736e-12	***
SlopeF-SlopeC	-1.626761	0.1188241		0.9999488	



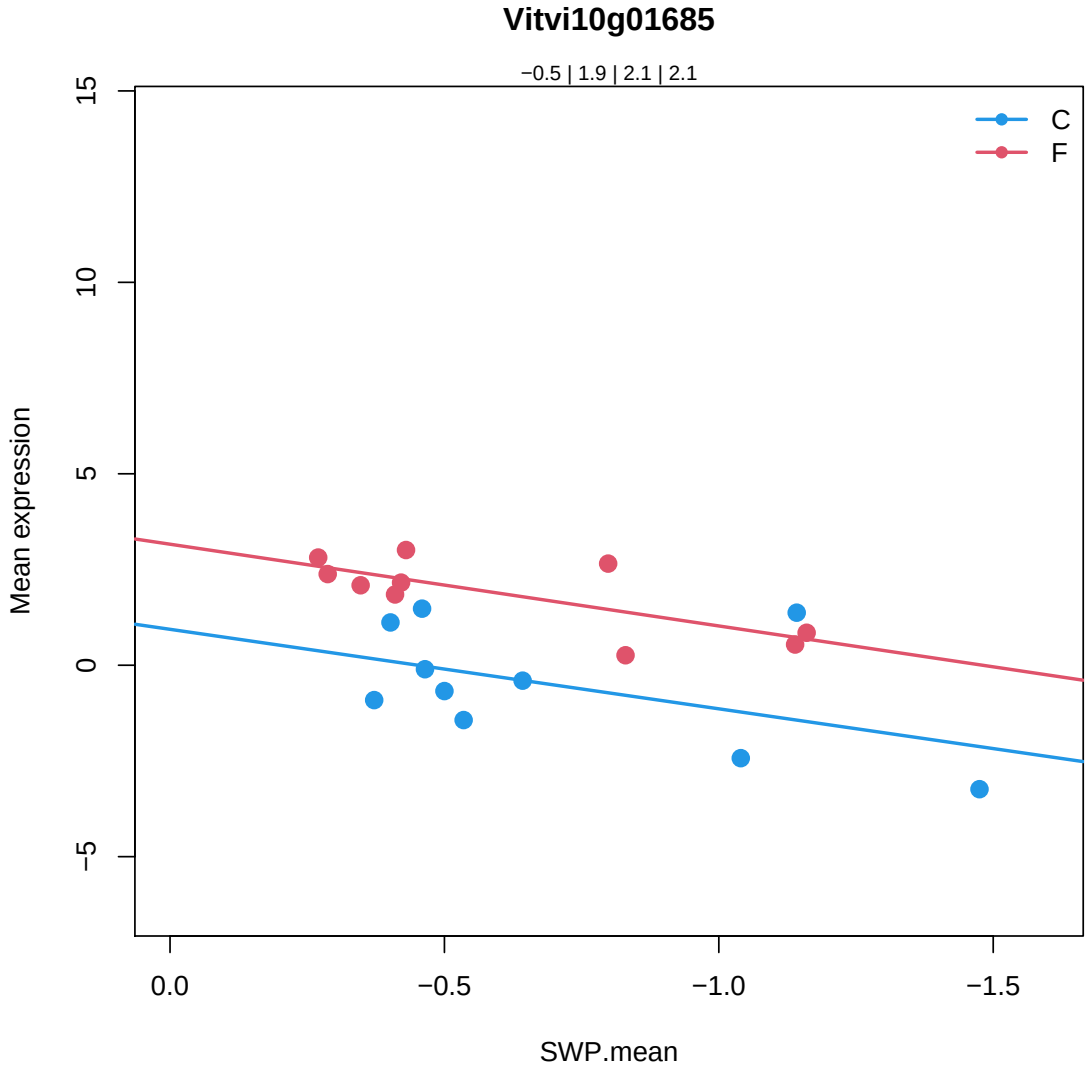
7.5.18 Vitvi10g01685: * type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g01685
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi10g01685.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.5224823	0.1171482		0.1209328	
SlopeC	2.076279	0.02951921	*	0.4299803	
MeanF-MeanC	2.382122	3.023132e-05	***	0.0006517479	***
SlopeF-SlopeC	0.05856843	0.9651568		0.9999488	



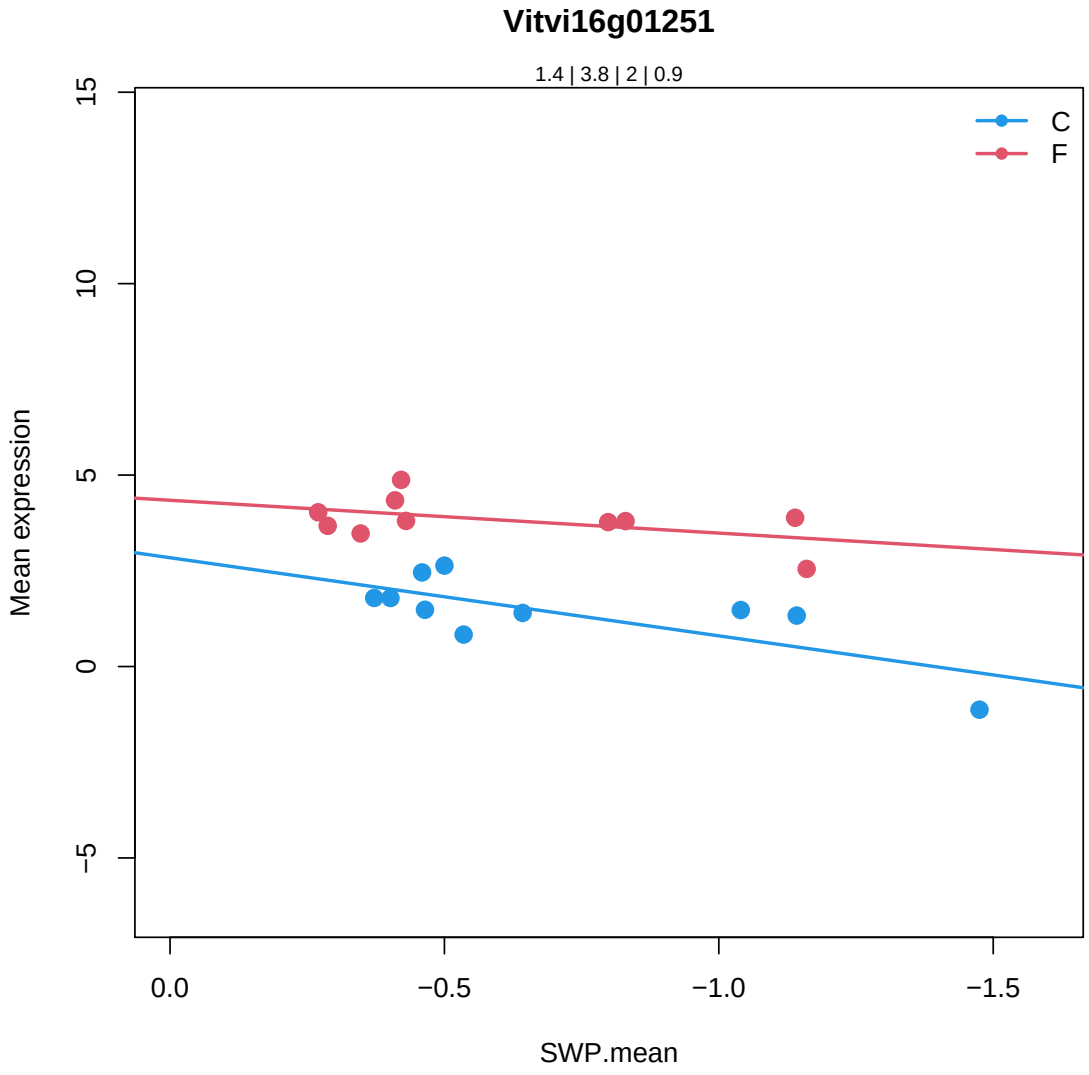
7.5.19 Vitvi16g01251: * type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01251
        35.2
        not assigned.unknown
        PR5-like receptor kinase |
        Chr5:15293325-15295838 REVERSE LENGTH=665 |
        201606
```

Coefficients for Vitvi16g01251.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.406554	3.194893e-07	***	3.734972e-07	***
SlopeC	2.040488	0.001029046	**	0.1273773	
MeanF-MeanC	2.413194	1.372374e-08	***	6.661697e-07	***
SlopeF-SlopeC	-1.182968	0.1538897		0.9999488	



7.5.20 Vitvi12g00606: * type3 | type4

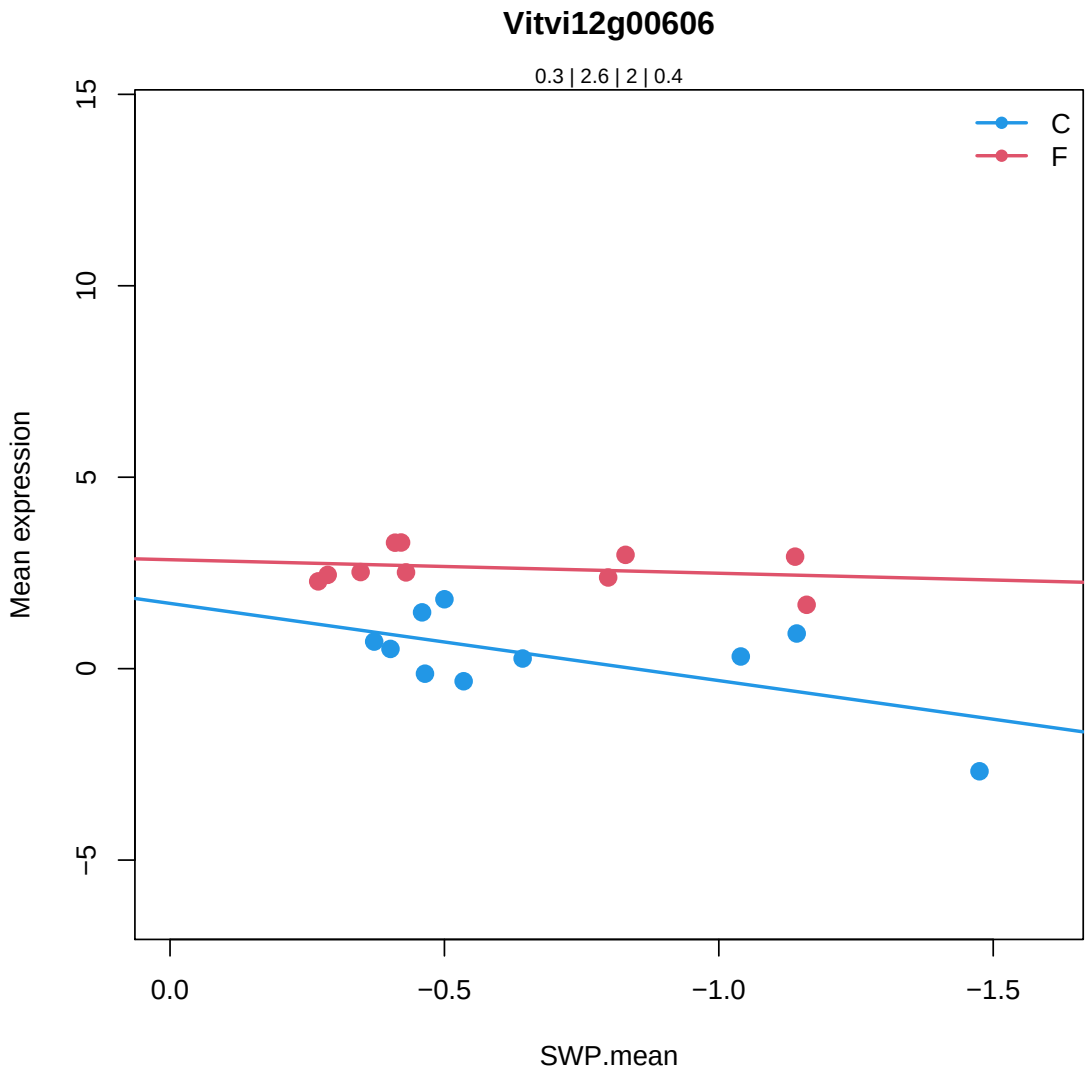
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00606
        29.4
        protein.postranslational modification
        G-type lectin S-receptor-like Serine/Threonine-kinase |
        Chr4:1419278-1422828 REVERSE LENGTH=1010 |
        201606

Vitvi12g00606
        30.2.24
        signalling.receptor kinases.S-locus glycoprotein like
        G-type lectin S-receptor-like Serine/Threonine-kinase |
        Chr4:1419278-1422828 REVERSE LENGTH=1010 |
        201606
```

Coefficients for Vitvi12g00606.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.2862625	0.2372891		0.2426379	
SlopeC	2.016467	0.005608764	**	0.2614336	
MeanF-MeanC	2.343448	5.354432e-07	***	1.871841e-05	***
SlopeF-SlopeC	-1.662881	0.1025429		0.9999488	


Vitvi12g00606
0.3 | 2.6 | 2 | 0.4
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

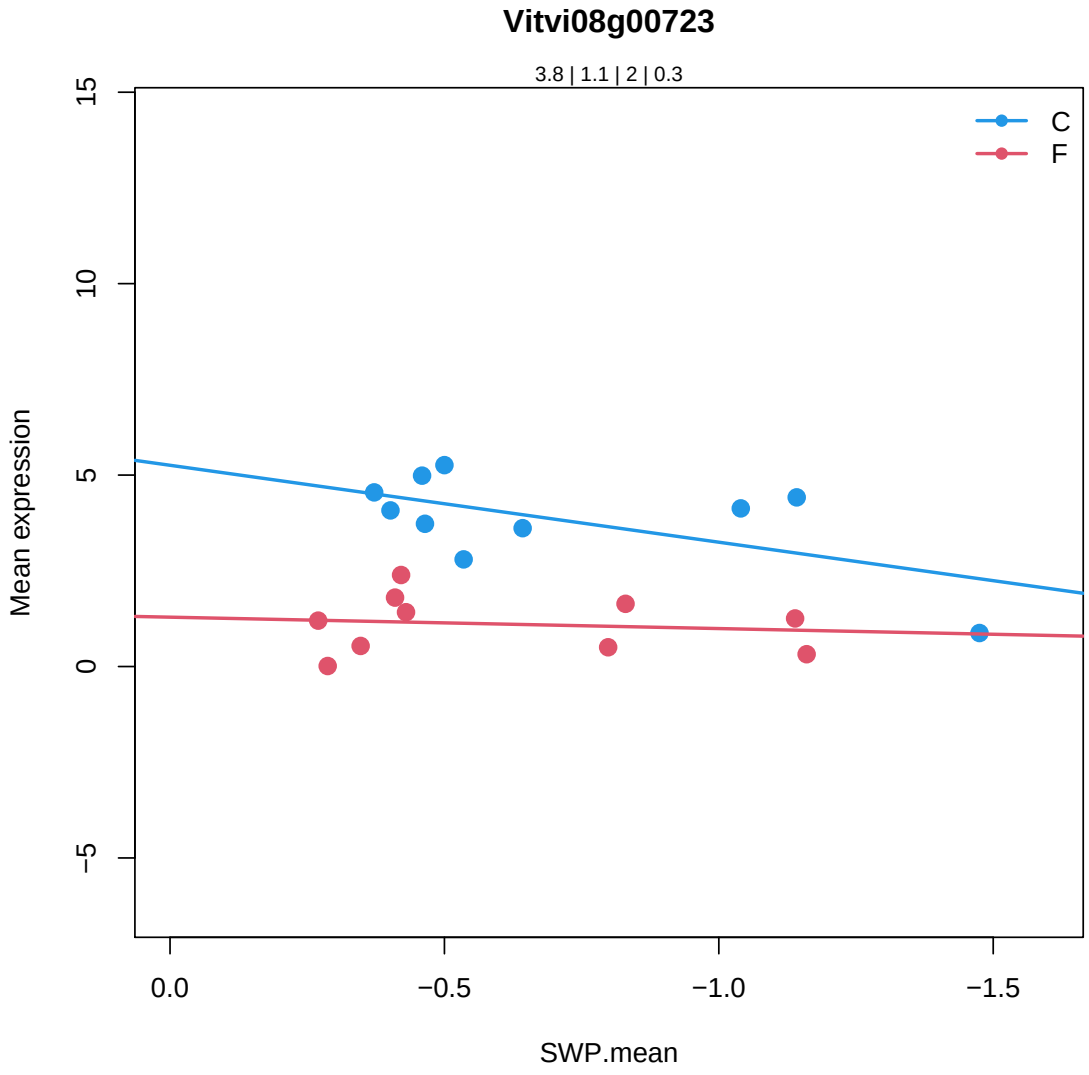
7.5.21 Vitvi08g00723: * type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g00723
        34.5
        transport.ammonium
        ammonium transporter 2 |
        Chr2:16039672-16042291 REVERSE LENGTH=475 |
        201606
```

Coefficients for Vitvi08g00723.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.8431	1.699178e-12	***	2.40584e-12	***
SlopeC	2.009066	0.01311545	*	0.3305597	
MeanF-MeanC	-2.73582	3.419843e-07	***	1.241077e-05	***
SlopeF-SlopeC	-1.711553	0.1362029		0.9999488	



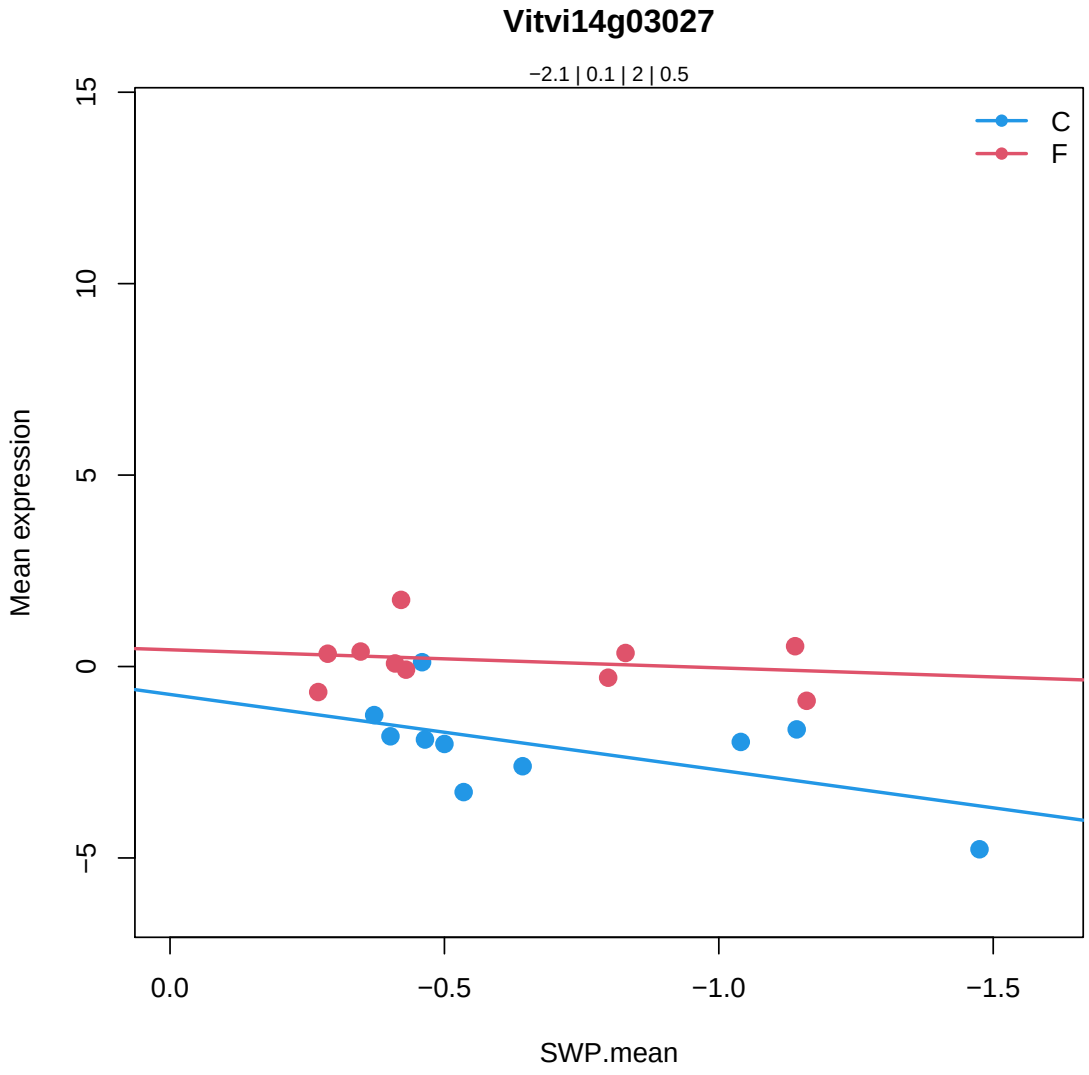
7.5.22 Vitvi14g03027: * type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g03027
        35.2
        not assigned.unknown
        transmembrane protein |
        Chr1:8425981-8427045 REVERSE LENGTH=354 |
        201606
```

Coefficients for Vitvi14g03027.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-2.117932	9.501523e-08	***	1.12825e-07	***
SlopeC	1.973808	0.01542005	*	0.3393703	
MeanF-MeanC	2.267038	6.121502e-06	***	0.000160592	***
SlopeF-SlopeC	-1.501193	0.1926976		0.9999488	



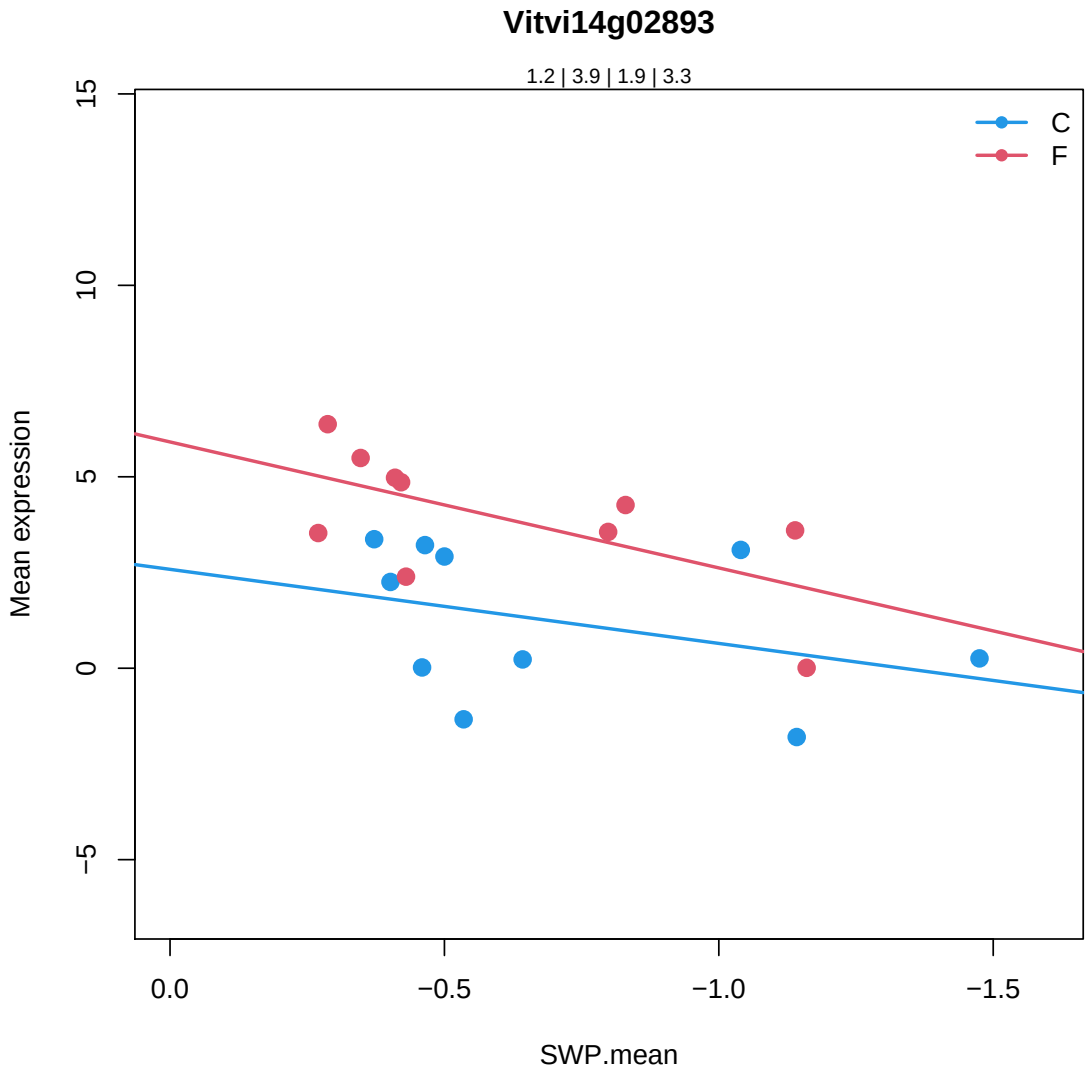
7.5.23 Vitvi14g02893: type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g02893
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi14g02893.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.221987	0.017794	*	0.01873169	*
SlopeC	1.934911	0.1585324		0.6889929	
MeanF-MeanC	2.683206	0.0006505913	***	0.008798857	**
SlopeF-SlopeC	1.355003	0.4992098		0.9999488	



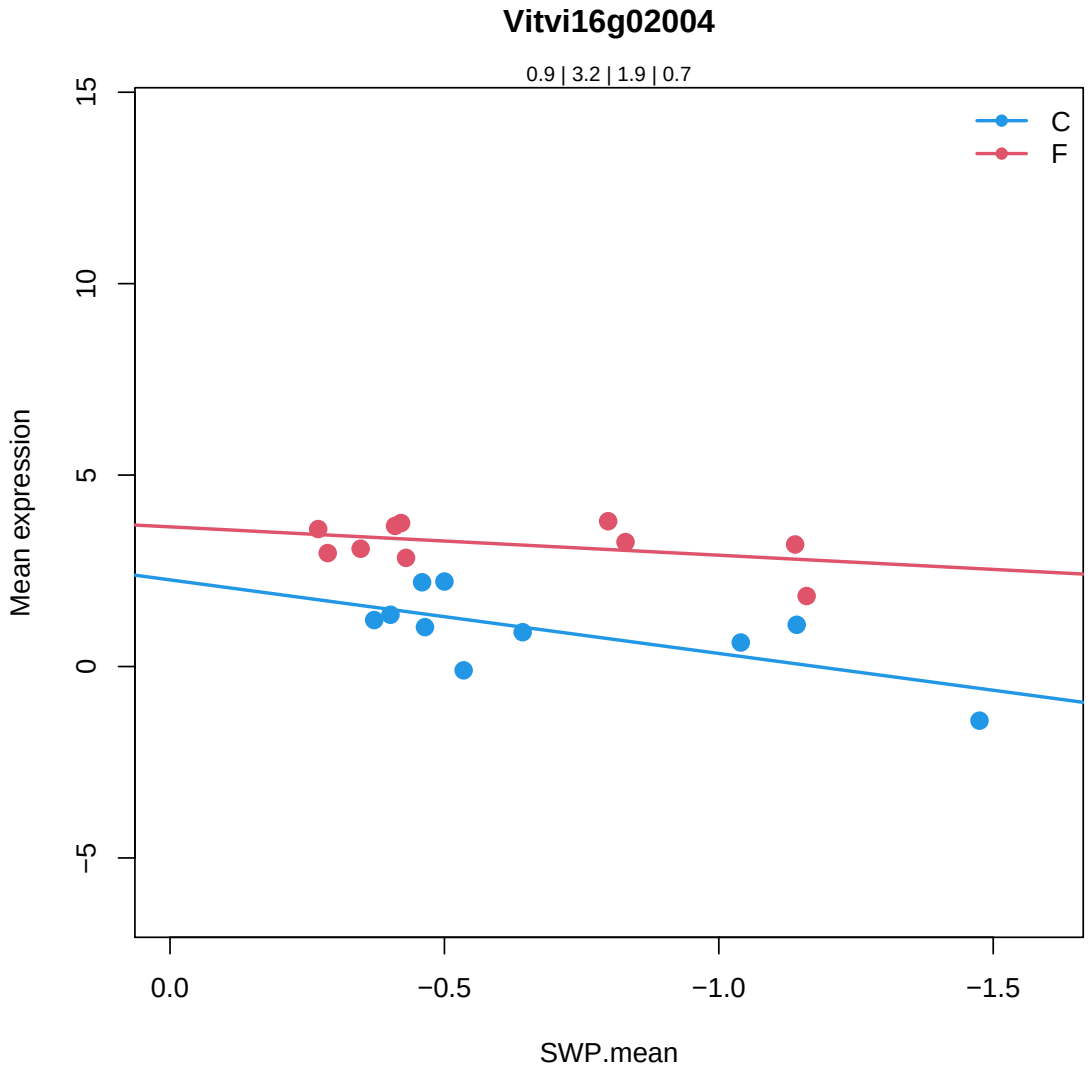
7.5.24 Vitvi16g02004: * type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g02004
        35.2
        not assigned.unknown
        Protein kinase superfamily protein |
        Chr1:24961634-24963941 REVERSE LENGTH=663 |
        201606
```

Coefficients for Vitvi16g02004.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.9113851	0.0002464427	***	0.0002700417	***
SlopeC	1.921524	0.003150659	**	0.2103859	
MeanF-MeanC	2.284602	1.120093e-07	***	4.480959e-06	***
SlopeF-SlopeC	-1.180849	0.1839705		0.9999488	



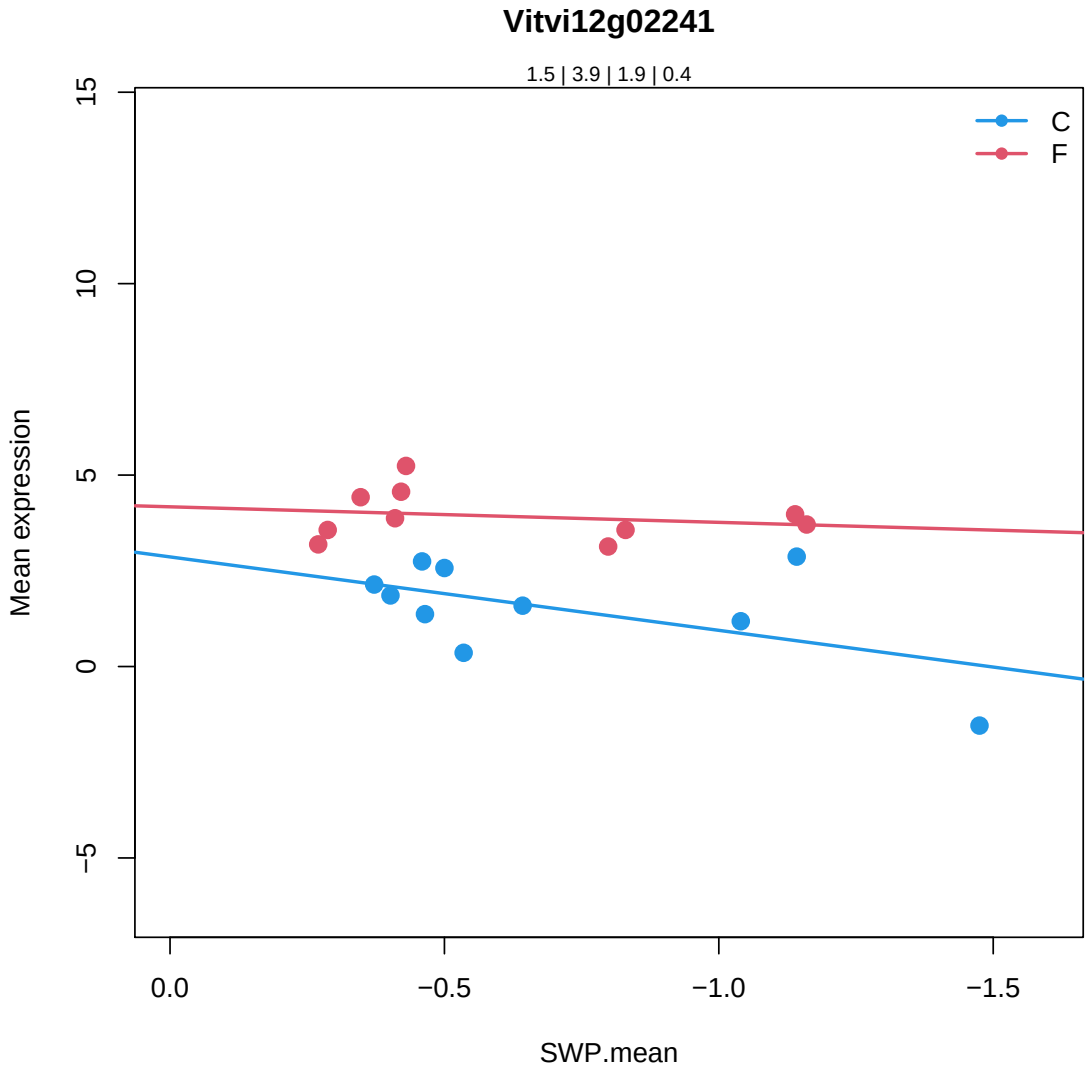
7.5.25 Vitvi12g02241: * type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02241
        26.6
        misc.O-methyl transferases
        O-methyltransferase family protein |
        Chr4:16730989-16732808 REVERSE LENGTH=382 |
        201606
```

Coefficients for Vitvi12g02241.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.513909	1.593673e-05	***	1.791222e-05	***
SlopeC	1.917744	0.01970617	*	0.374907	
MeanF-MeanC	2.40998	3.204087e-06	***	9.094357e-05	***
SlopeF-SlopeC	-1.511665	0.195969		0.9999488	



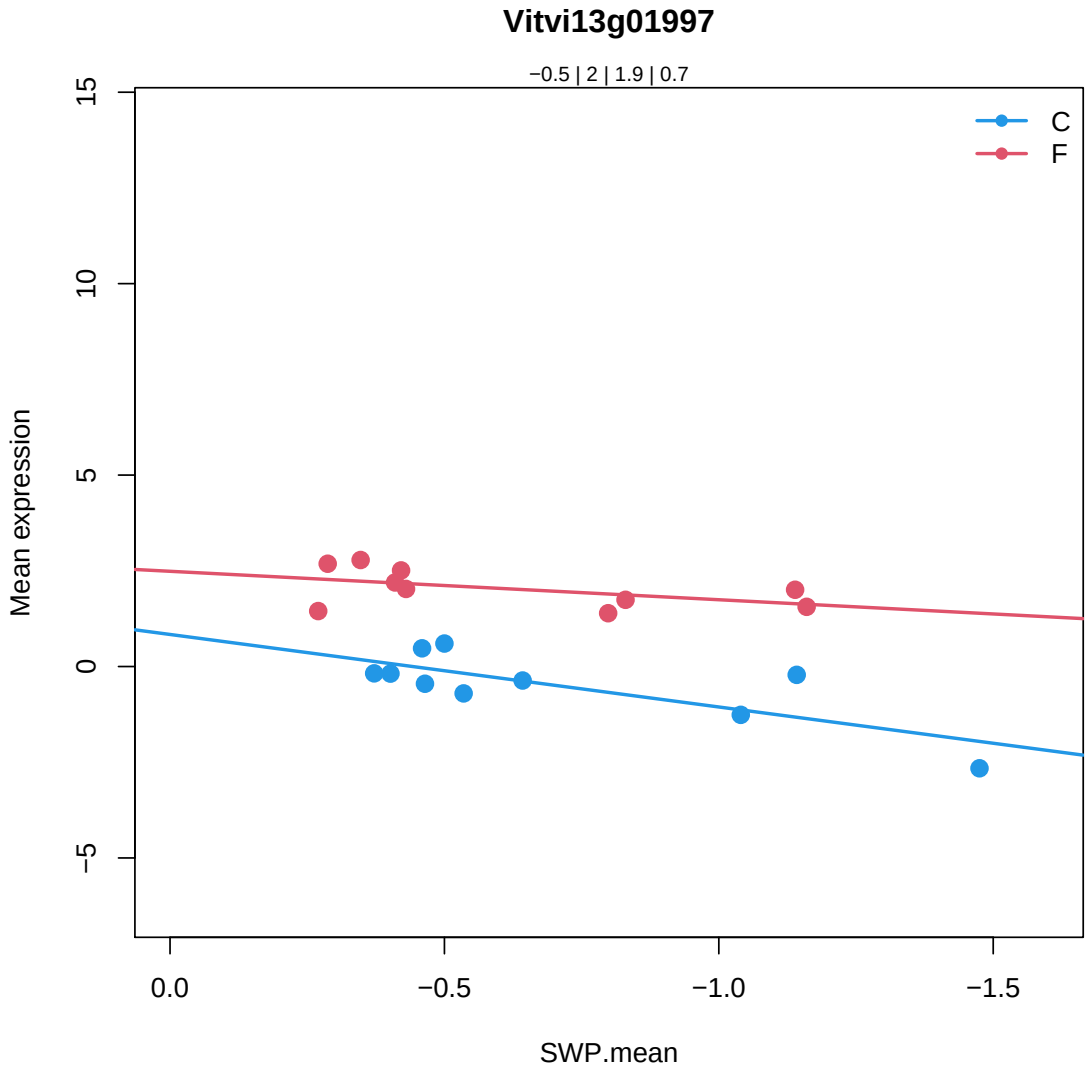
7.5.26 Vitvi13g01997: * type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g01997
        26.8
        misc.nitrilases, nitrile lyases, berberine bridge enzymes, reticuline
        NAD(P)-binding Rossmann-fold superfamily protein |
        Chr2:12586509-12587684 FORWARD LENGTH=245 |
        201606
```

Coefficients for Vitvi13g01997.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.4945913	0.007974908	**	0.008466501	**
SlopeC	1.894216	0.0005889995	***	0.1005065	
MeanF-MeanC	2.528975	5.726677e-10	***	3.562694e-08	***
SlopeF-SlopeC	-1.151737	0.1145477		0.9999488	



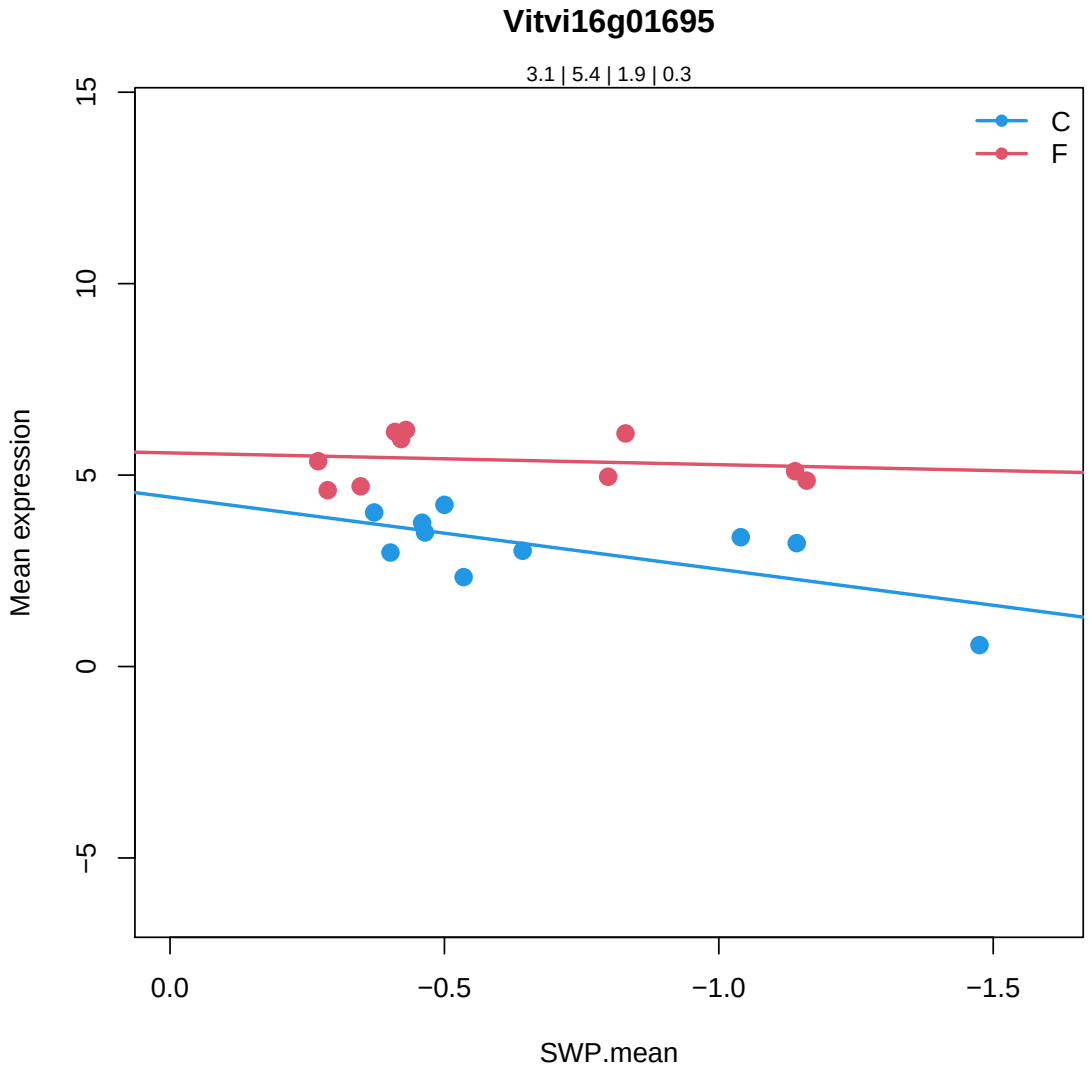
7.5.27 Vitvi16g01695: * type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01695
        35.2
        not assigned.unknown
        receptor like protein 6 |
        Chr1:17183550-17186534 REVERSE LENGTH=994 |
        201606
```

Coefficients for Vitvi16g01695.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.099689	1.944845e-12	***	2.745261e-12	***
SlopeC	1.88261	0.005080912	**	0.2530826	
MeanF-MeanC	2.292059	2.105269e-07	***	7.903575e-06	***
SlopeF-SlopeC	-1.575394	0.09360147	.	0.9999488	



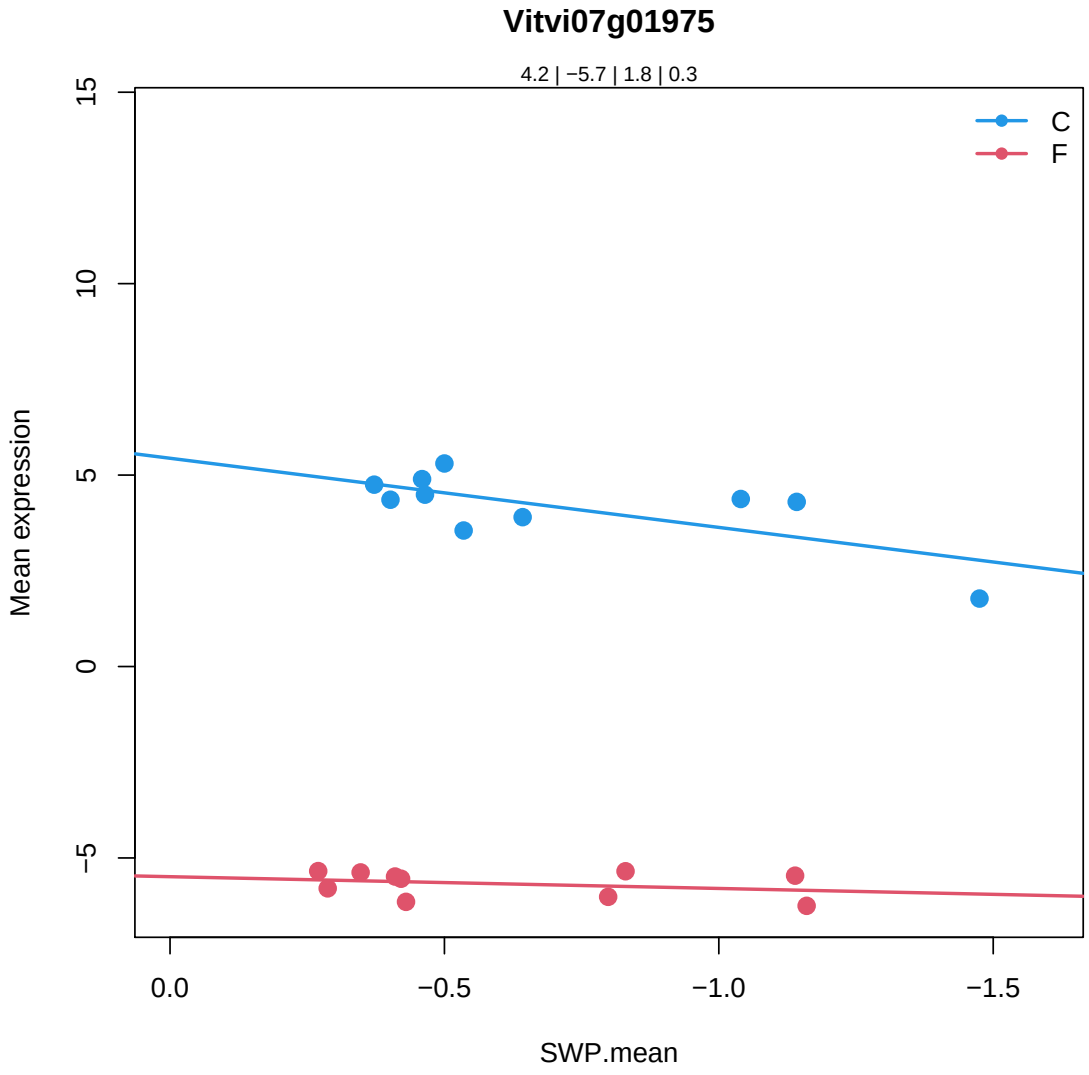
7.5.28 Vitvi07g01975: * type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01975
        35.2
        not assigned.unknown
        ammonium transporter 2 |
        Chr2:16039672-16042291 REVERSE LENGTH=475 |
        201606
```

Coefficients for Vitvi07g01975.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.169379	6.951417e-17	***	1.554254e-16	***
SlopeC	1.805957	0.001302019	**	0.1417527	
MeanF-MeanC	-9.845904	1.491184e-21	***	9.882012e-19	***
SlopeF-SlopeC	-1.498707	0.05160997	.	0.9999488	



7.5.29 Vitvi12g02434: * type3 | type4

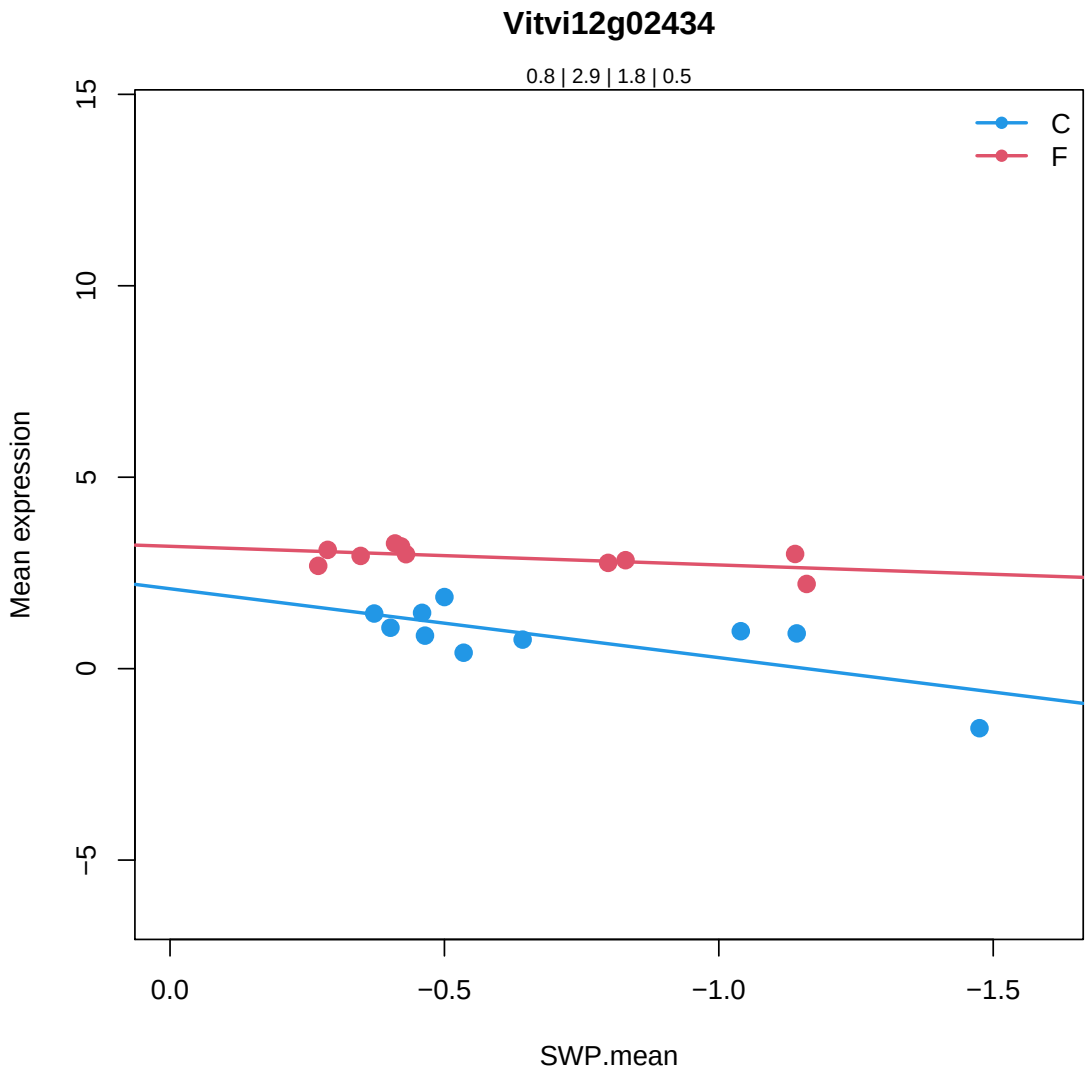
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02434
        29.4
        protein.postranslational modification
        G-type lectin S-receptor-like Serine/Threonine-kinase |
        Chr4:1419278-1422828 REVERSE LENGTH=1010 |
        201606

Vitvi12g02434
        30.2.24
        signalling.receptor kinases.S-locus glycoprotein like
        G-type lectin S-receptor-like Serine/Threonine-kinase |
        Chr4:1419278-1422828 REVERSE LENGTH=1010 |
        201606
```

Coefficients for Vitvi12g02434.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8214444	4.165707e-05	***	4.635592e-05	***
SlopeC	1.798958	0.0005749267	***	0.1005065	
MeanF-MeanC	2.077066	7.184554e-09	***	3.638105e-07	***
SlopeF-SlopeC	-1.311562	0.06099283	.	0.9999488	


Vitvi12g02434
0.8 | 2.9 | 1.8 | 0.5
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

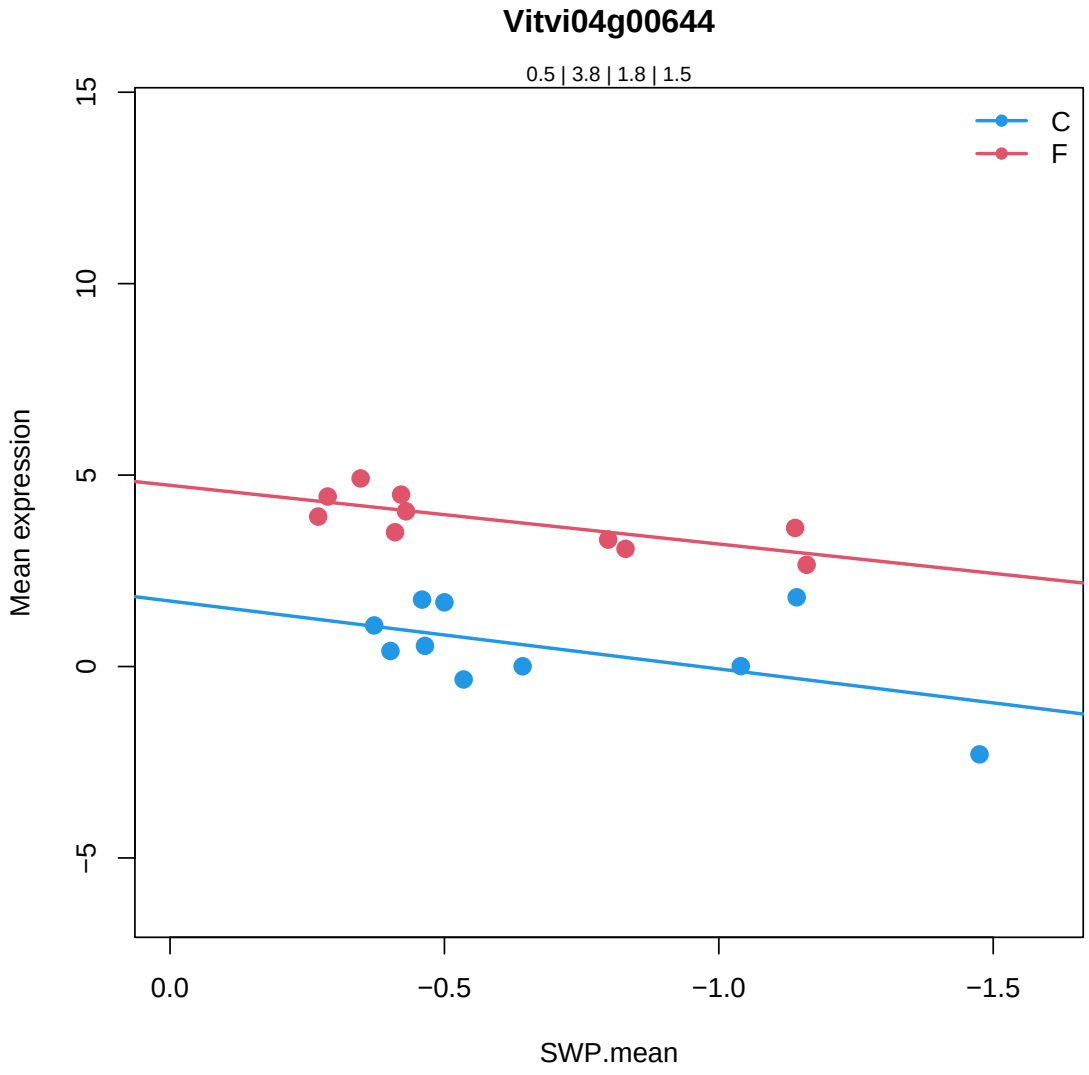
7.5.30 Vitvi04g00644: * type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00644
        27.3.99
        RNA.regulation of transcription.unclassified
        Eukaryotic aspartyl protease family protein |
        Chr5:3403331-3405331 REVERSE LENGTH=474 |
        201606
```

Coefficients for Vitvi04g00644.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4634607	0.07445566	.	0.07723768	.
SlopeC	1.773287	0.01733481	*	0.3551322	
MeanF-MeanC	3.335309	3.590415e-09	***	1.887073e-07	***
SlopeF-SlopeC	-0.240009	0.8168131		0.9999488	

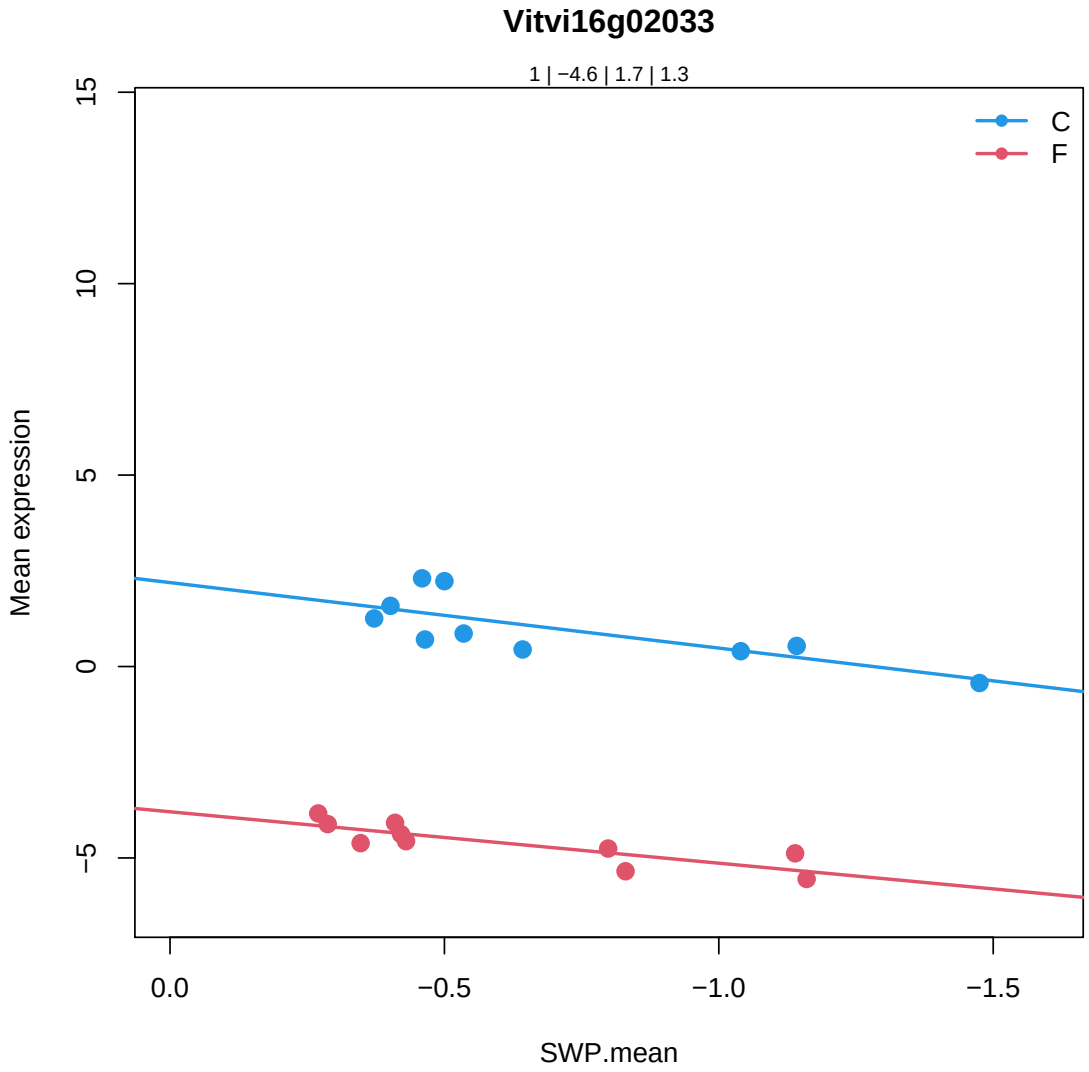


7.5.31 Vitvi16g02033: * type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
Vitvi16g02033
        35.2
        not assigned.unknown
        PR5-like receptor kinase |
        Chr5:15293325-15295838 REVERSE LENGTH=665 |
        201606
```

Coefficients for Vitvi16g02033.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.9889555	1.720114e-06	***	1.975137e-06	***
SlopeC	1.710997	0.0005617774	***	0.1005065	
MeanF-MeanC	-5.601053	1.00955e-17	***	2.167263e-15	***
SlopeF-SlopeC	-0.3682916	0.564525		0.9999488	



7.5.32 Vitvi09g00253: * type3 | type4

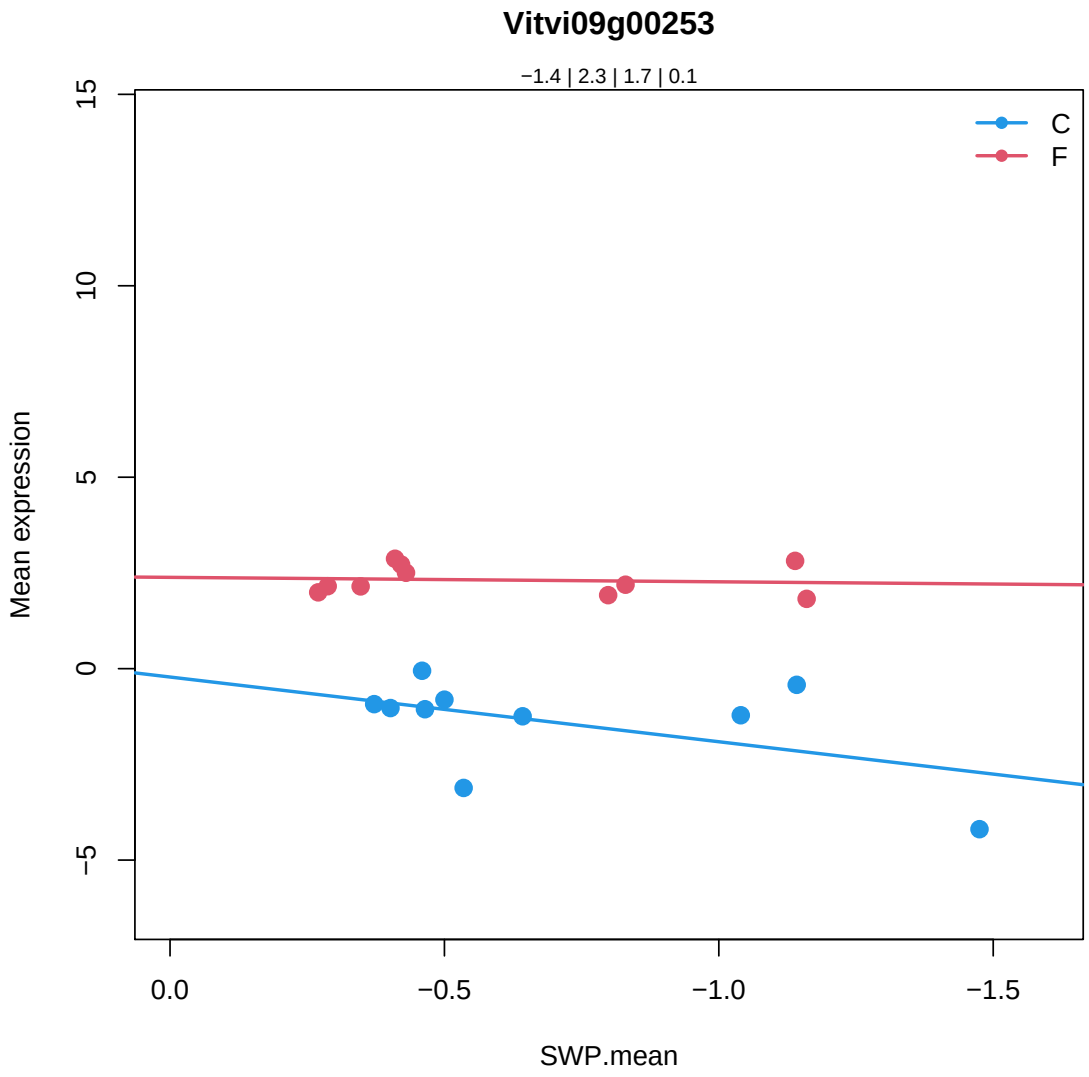
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00253
        29.4
        protein.postranslational modification
        Leucine-rich repeat transmembrane protein kinase protein |
        Chr4:14665802-14669438 REVERSE LENGTH=876 |
        201606

Vitvi09g00253
        30.2.1
        signalling.receptor kinases.leucine rich repeat I
        Leucine-rich repeat transmembrane protein kinase protein |
        Chr4:14665802-14669438 REVERSE LENGTH=876 |
        201606
```

Coefficients for Vitvi09g00253.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.407384	1.22789e-05	***	1.383771e-05	***
SlopeC	1.690283	0.02356607	*	0.3983963	
MeanF-MeanC	3.721139	5.921833e-10	***	3.639539e-08	***
SlopeF-SlopeC	-1.574086	0.1418375		0.9999488	


Vitvi09g00253
−1.4 | 2.3 | 1.7 | 0.1
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

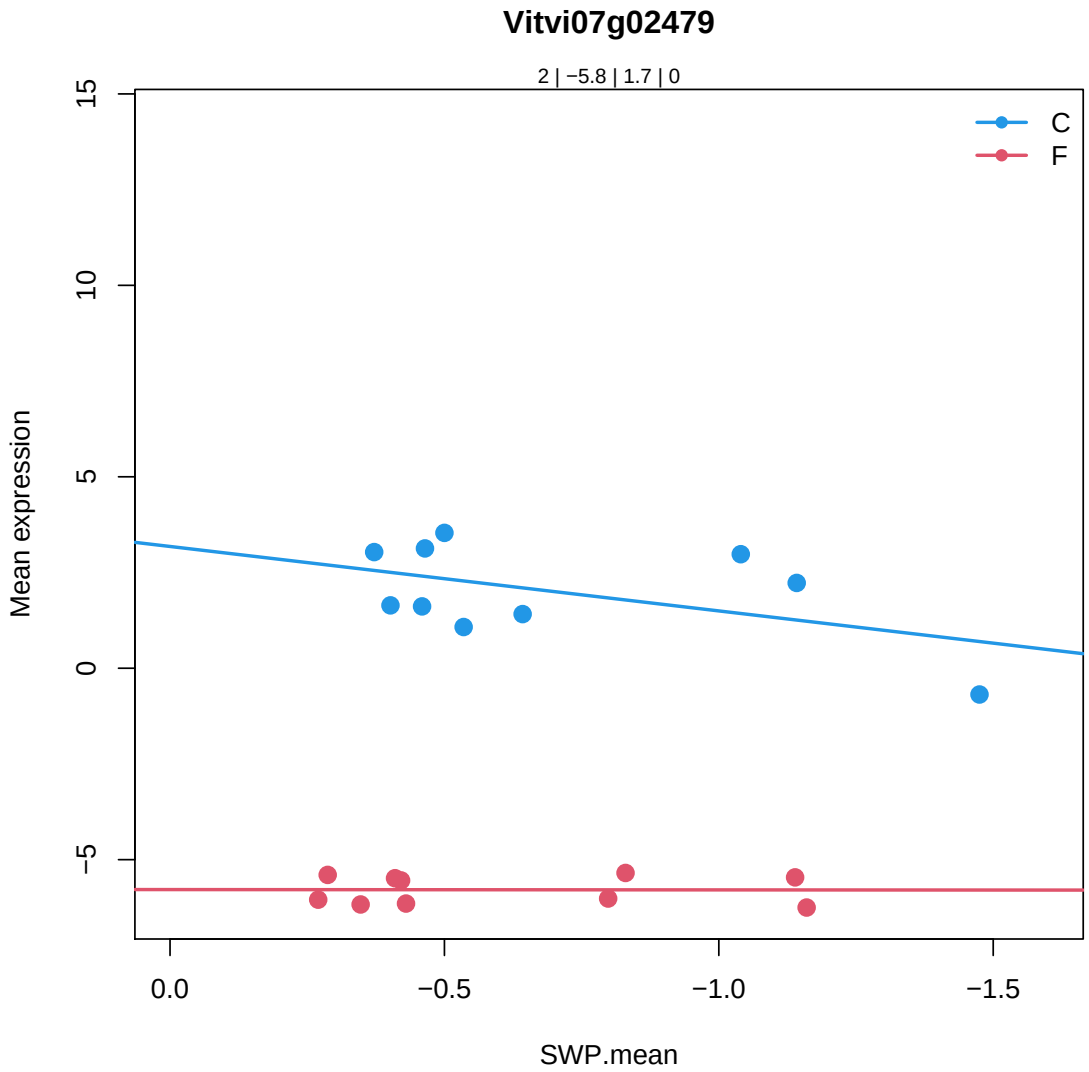
7.5.33 Vitvi07g02479: * type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g02479
        35.2
        not assigned.unknown
        Serine_threonine-protein phosphatase 6 regulatory ankyrin repeat subun
```

Coefficients for Vitvi07g02479.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.996167	6.687837e-08	***	7.966241e-08	***
SlopeC	1.683394	0.02375949	*	0.3983963	
MeanF-MeanC	-7.7825	2.962028e-16	***	4.961235e-14	***
SlopeF-SlopeC	-1.67543	0.1182497		0.9999488	



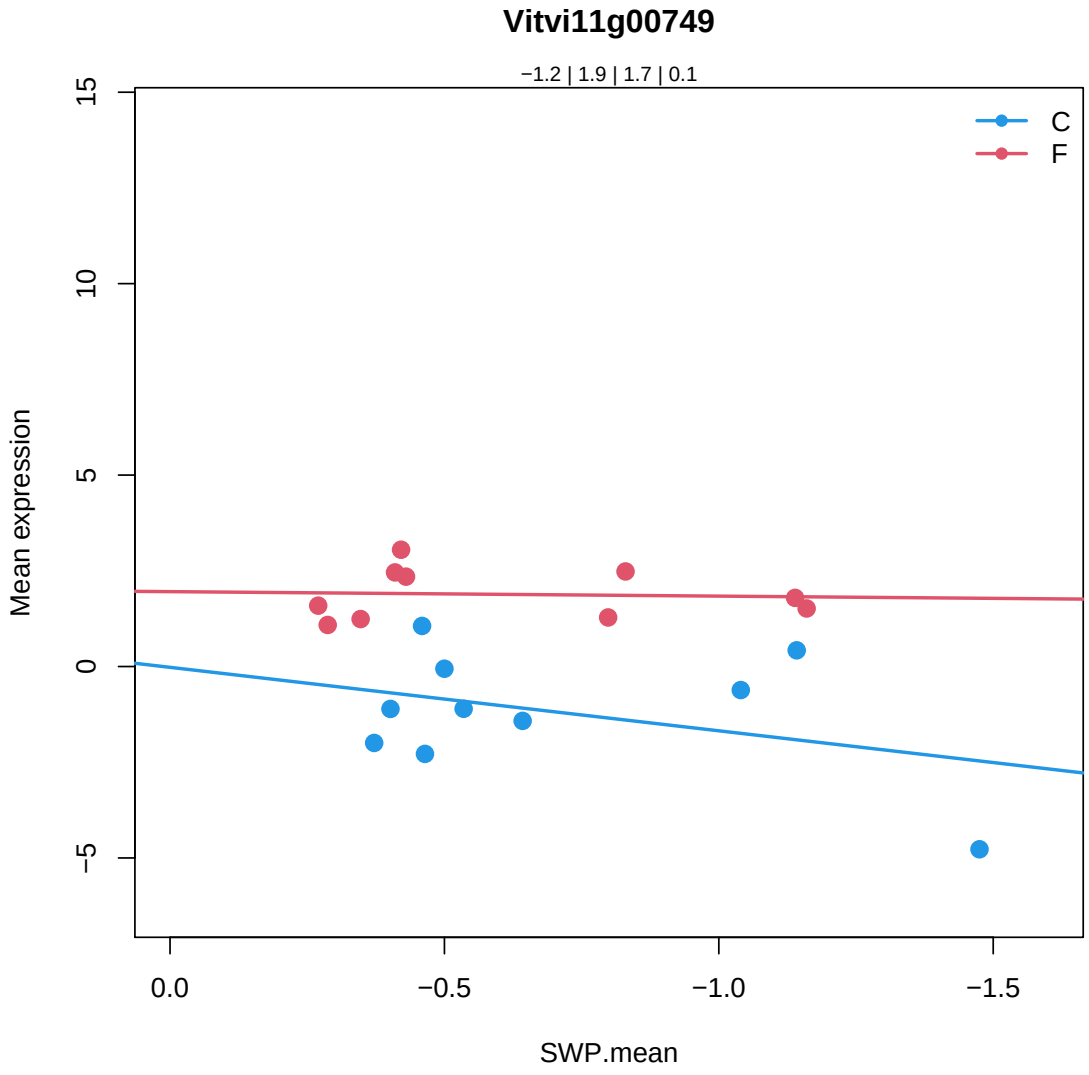
7.5.34 Vitvi11g00749: type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00749
        30.2.12
        signalling.receptor kinases.leucine rich repeat XII
        kinase family with leucine-rich repeat domain-containing protein |
        Chr1:13220940-13224386 FORWARD LENGTH=1120 |
        201606
```

Coefficients for Vitvi11g00749.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.187309	0.002453198	**	0.002632658	**
SlopeC	1.657462	0.09954394	.	0.6110181	
MeanF-MeanC	3.071475	2.889466e-06	***	8.264173e-05	***
SlopeF-SlopeC	-1.540859	0.2941879		0.9999488	



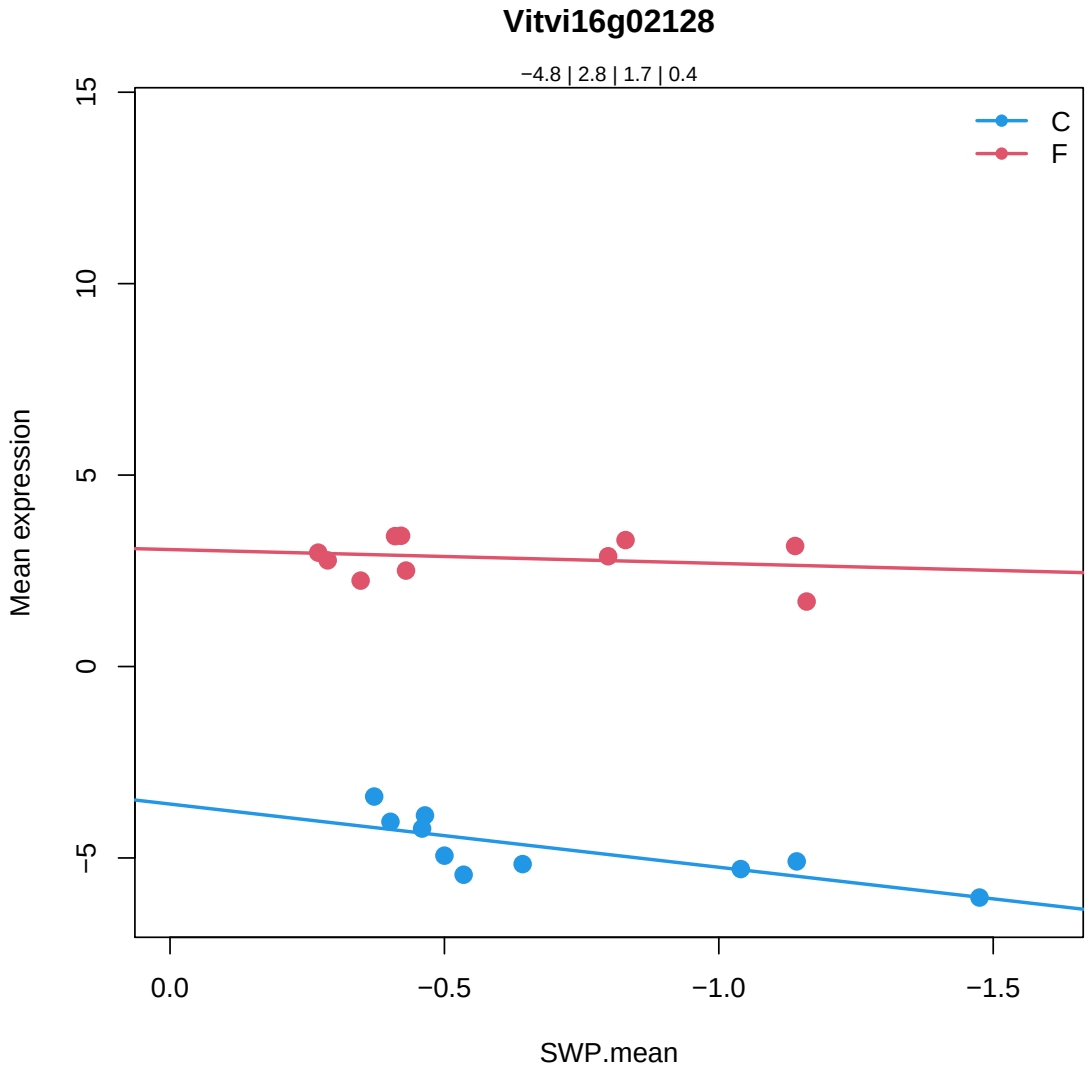
7.5.35 Vitvi16g02128: * type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g02128
        35.2
        not assigned.unknown
        PR5-like receptor kinase |
        Chr5:15293325-15295838 REVERSE LENGTH=665 |
        201606
```

Coefficients for Vitvi16g02128.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-4.752626	3.621096e-18	***	1.065291e-17	***
SlopeC	1.650819	0.002533182	**	0.1902008	
MeanF-MeanC	7.586807	2.867599e-19	***	8.405375e-17	***
SlopeF-SlopeC	-1.288502	0.08722927	.	0.9999488	



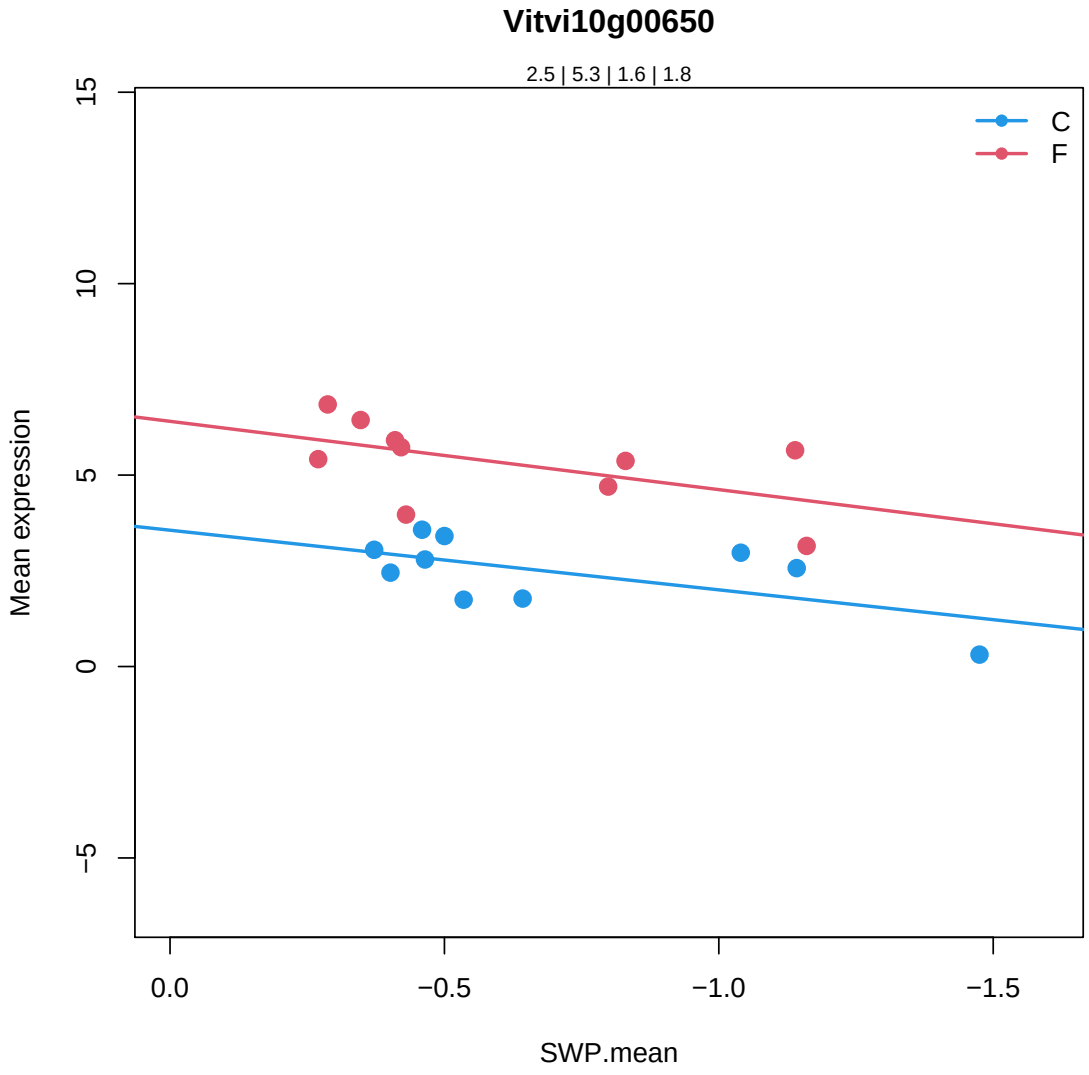
7.5.36 Vitvi10g00650: * type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00650
        30.2.8.2
        signalling.receptor kinases.leucine rich repeat VIII.type 2
        Leucine-rich repeat transmembrane protein kinase |
        Chr1:2359817-2363859 REVERSE LENGTH=801 |
        201606
```

Coefficients for Vitvi10g00650.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.464913	3.775848e-09	***	4.66987e-09	***
SlopeC	1.557723	0.04212555	*	0.4812642	
MeanF-MeanC	2.852172	1.1026e-07	***	4.434256e-06	***
SlopeF-SlopeC	0.2259447	0.835169		0.9999488	



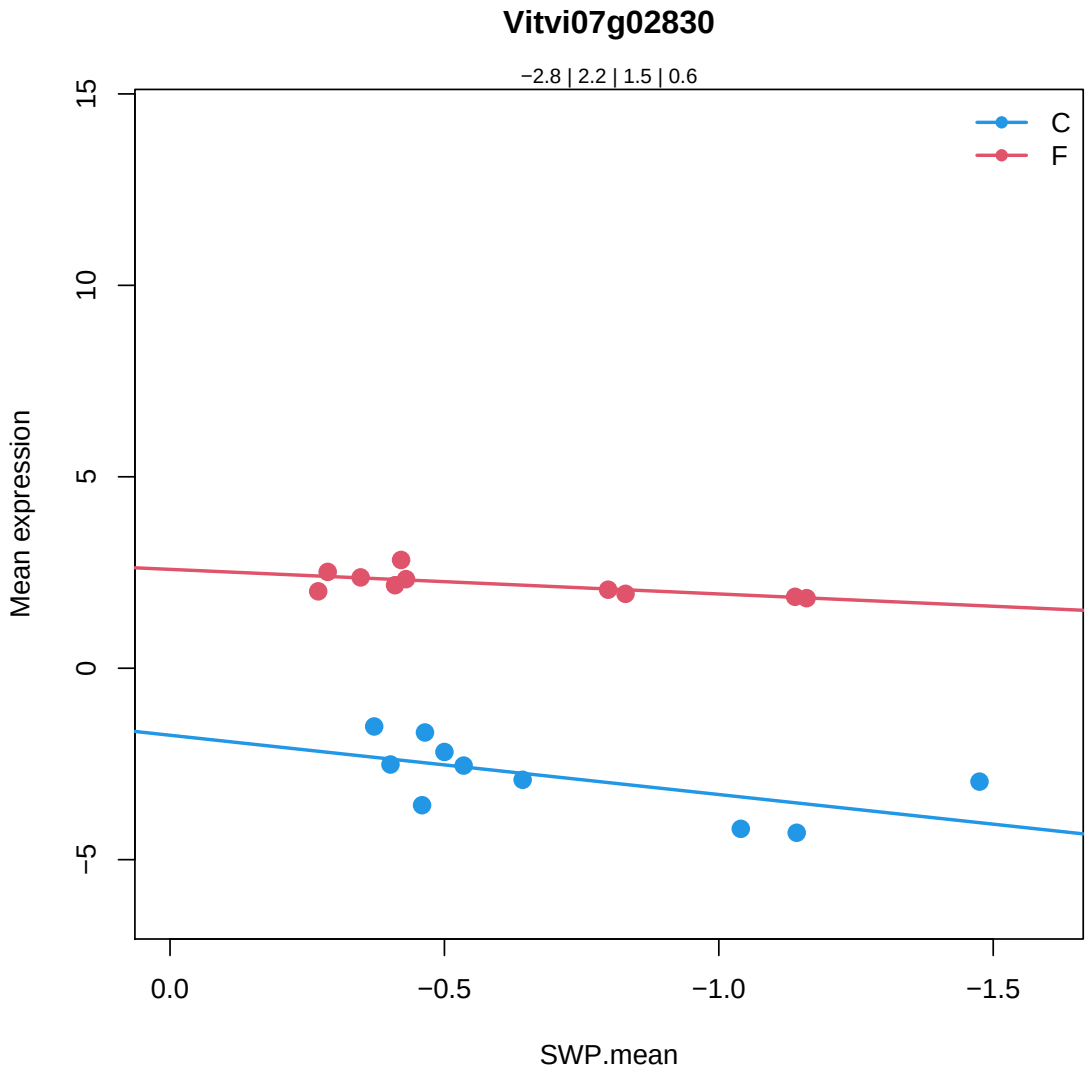
7.5.37 Vitvi07g02830: * type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g02830
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi07g02830.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-2.839209	2.699108e-13	***	4.025816e-13	***
SlopeC	1.548037	0.005361432	**	0.2577627	
MeanF-MeanC	5.029586	2.906795e-15	***	3.955836e-13	***
SlopeF-SlopeC	-0.9060718	0.2363952		0.9999488	



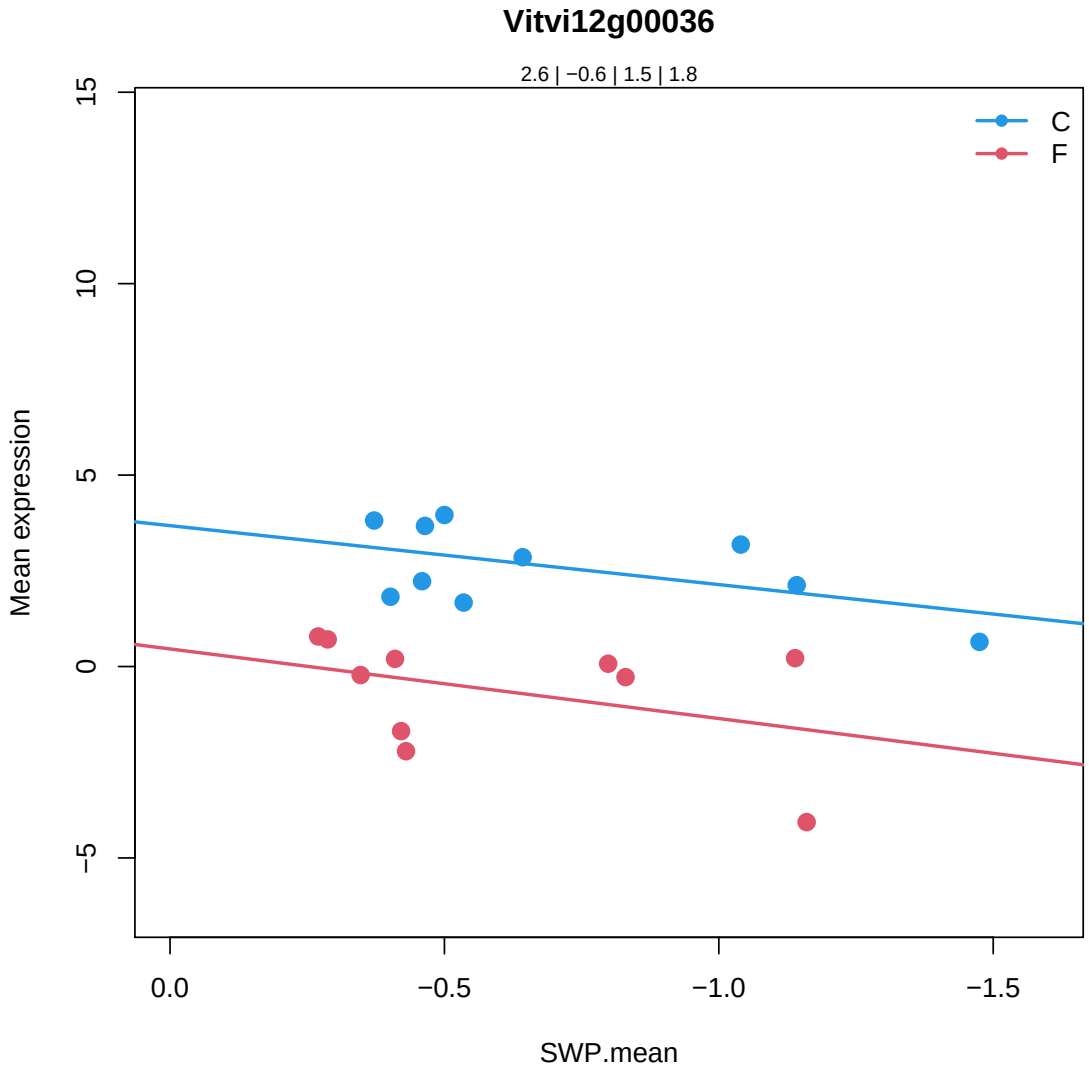
7.5.38 Vitvi12g00036: type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00036
        11.3
        lipid metabolism.phospholipid synthesis
        glycerol-3-phosphate acyltransferase 1 |
        Chr1:1994170-1996067 REVERSE LENGTH=585 |
        201606
```

Coefficients for Vitvi12g00036.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.596959	2.662307e-07	***	3.119533e-07	***
SlopeC	1.53938	0.1313064		0.6540431	
MeanF-MeanC	-3.245096	1.721806e-06	***	5.291083e-05	***
SlopeF-SlopeC	0.2776615	0.8509929		0.9999488	



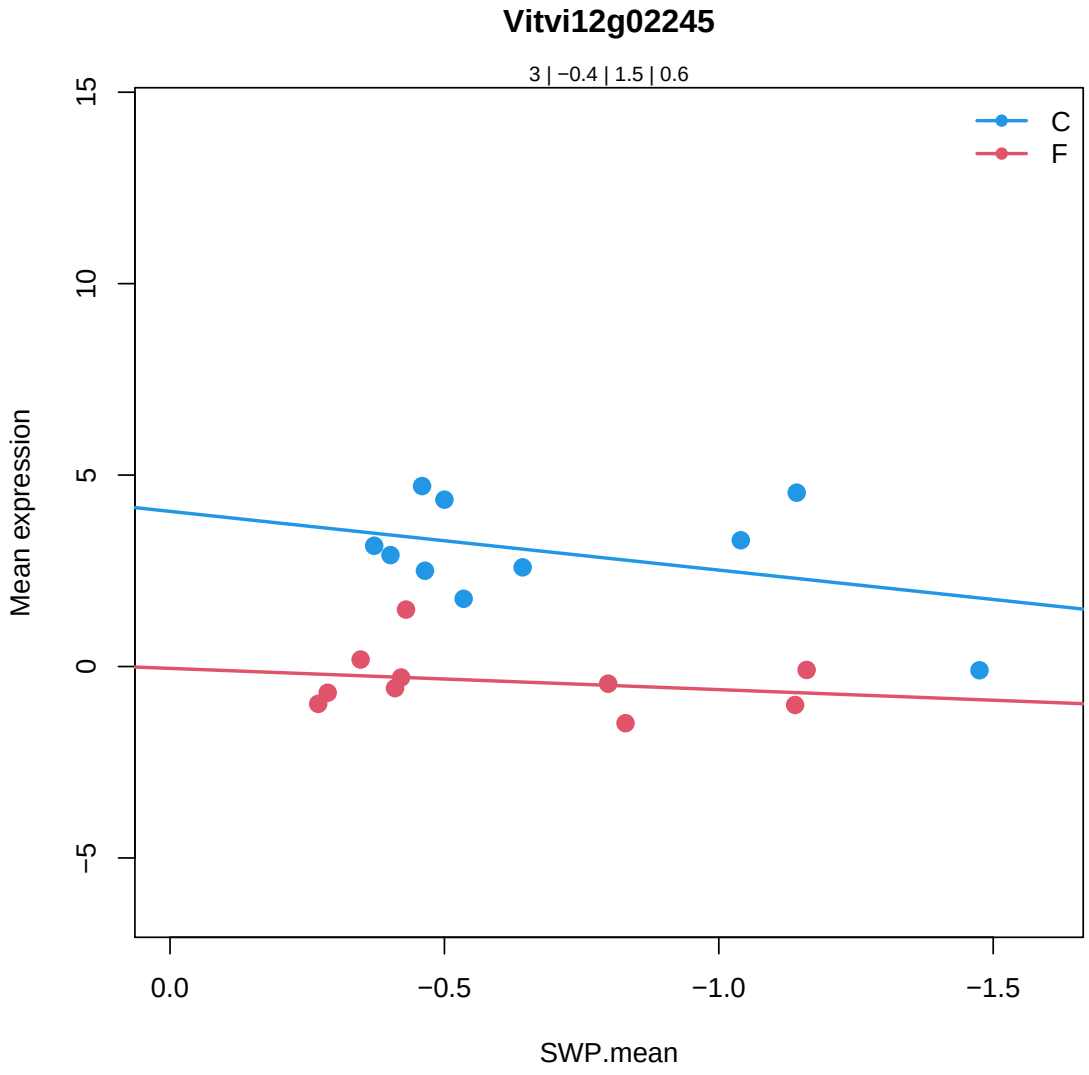
7.5.39 Vitvi12g02245: type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02245
        26.6
        misc.O-methyl transferases
        O-methyltransferase family protein |
        Chr4:16730989-16732808 REVERSE LENGTH=382 |
        201606
```

Coefficients for Vitvi12g02245.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.973277	7.660899e-09	***	9.382677e-09	***
SlopeC	1.534084	0.1047146		0.6180159	
MeanF-MeanC	-3.359933	3.051465e-07	***	1.12344e-05	***
SlopeF-SlopeC	-0.9798485	0.4750741		0.9999488	



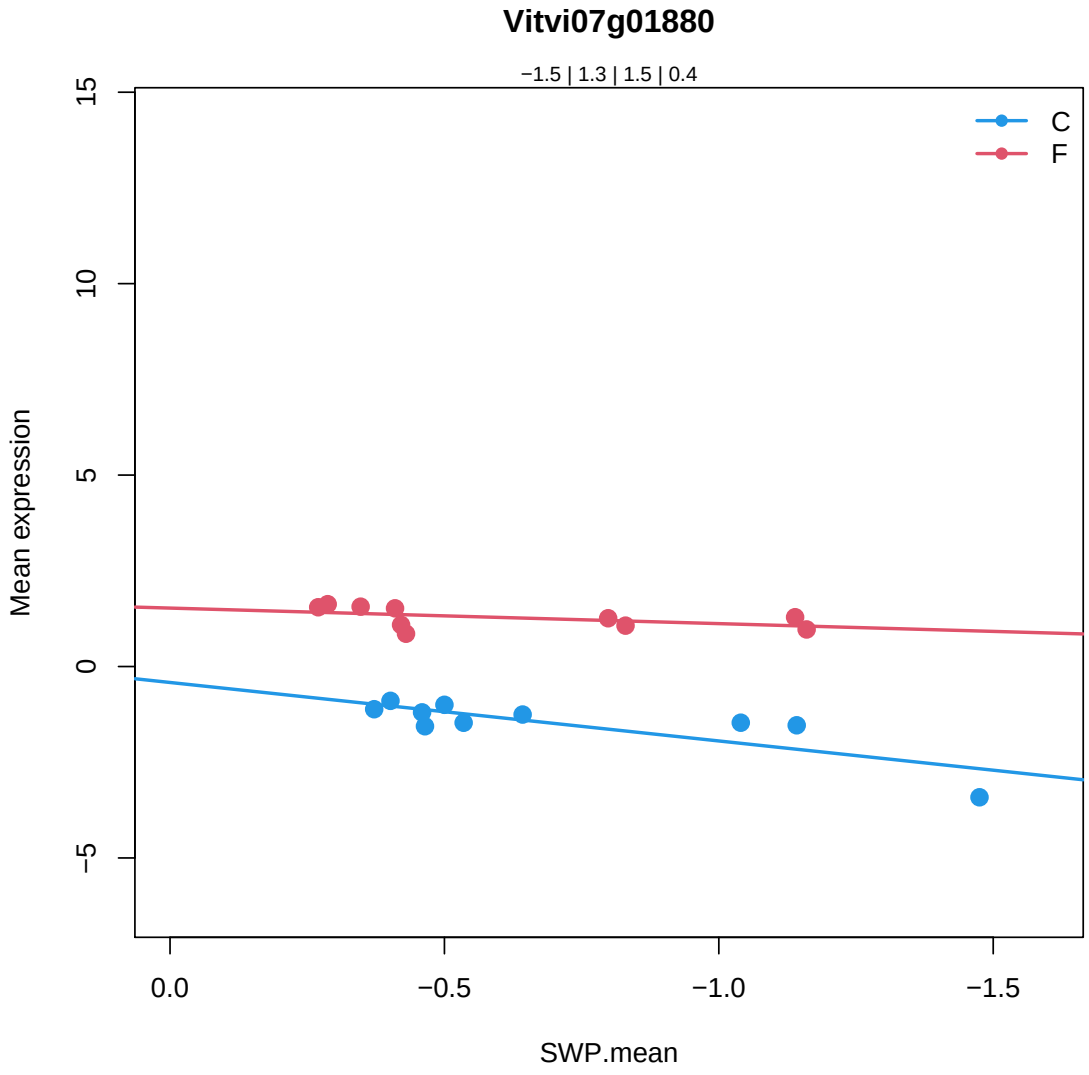
7.5.40 Vitvi07g01880: * type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01880
        29.2.1.2.2.3
        protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L3
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi07g01880.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.491084	7.084737e-11	***	9.323568e-11	***
SlopeC	1.527266	0.0002627845	***	0.08298279	.
MeanF-MeanC	2.769697	3.688811e-13	***	3.627411e-11	***
SlopeF-SlopeC	-1.121594	0.04294883	*	0.9999488	



7.5.41 Vitvi14g01809: type4

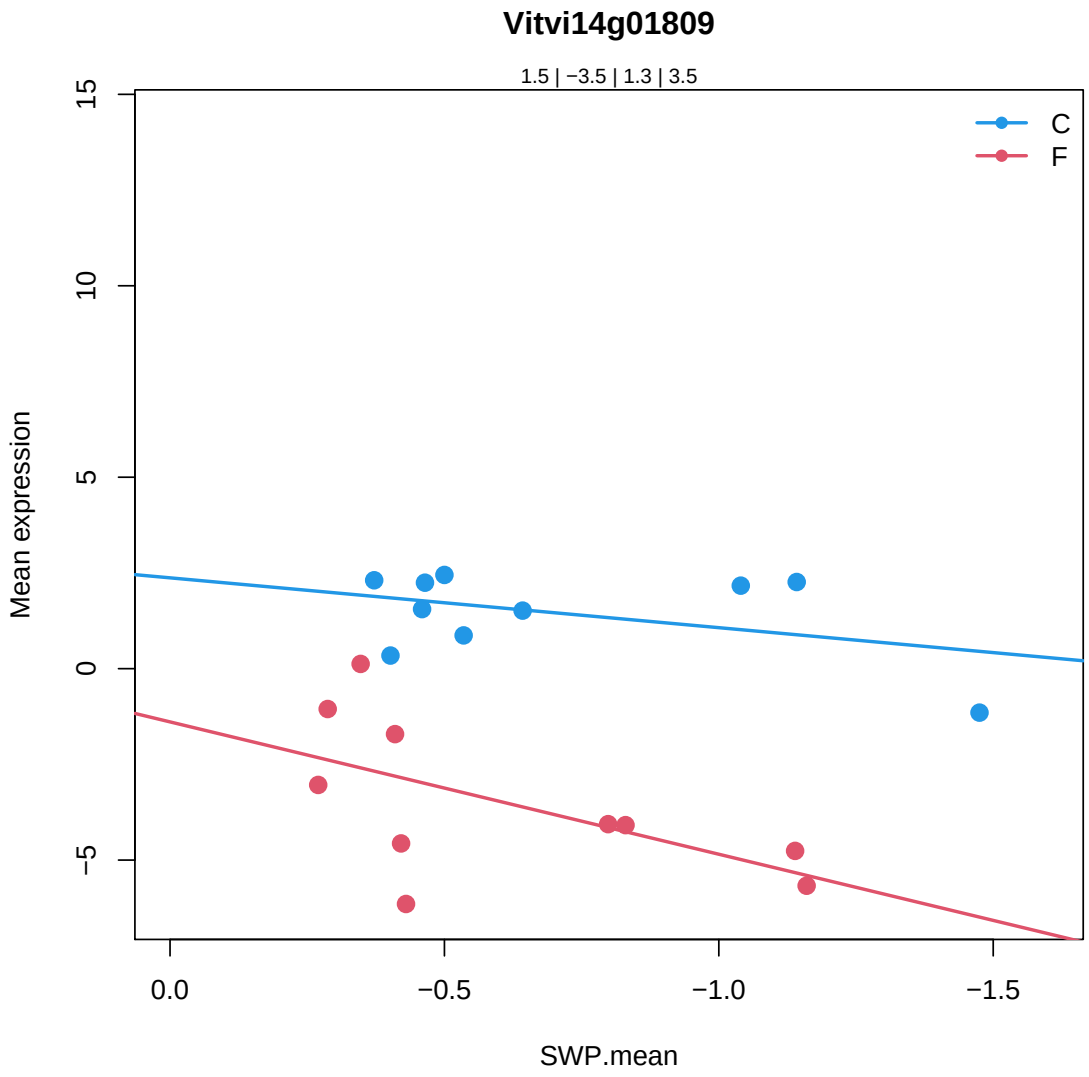
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01809
        26.14
        misc.oxygenases
        Peroxidase superfamily protein |
        Chr3:159689-162726 REVERSE LENGTH=639 |
        201606

Vitvi14g01809
        35.2
        not assigned.unknown
        Peroxidase superfamily protein |
        Chr3:159689-162726 REVERSE LENGTH=639 |
        201606
```

Coefficients for Vitvi14g01809.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.456259	0.001813832	**	0.001952569	**
SlopeC	1.301701	0.265568		0.7701943	
MeanF-MeanC	-4.953091	2.328898e-08	***	1.092217e-06	***
SlopeF-SlopeC	2.154381	0.2172755		0.9999488	


Vitvi14g01809
1.5 | −3.5 | 1.3 | 3.5
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

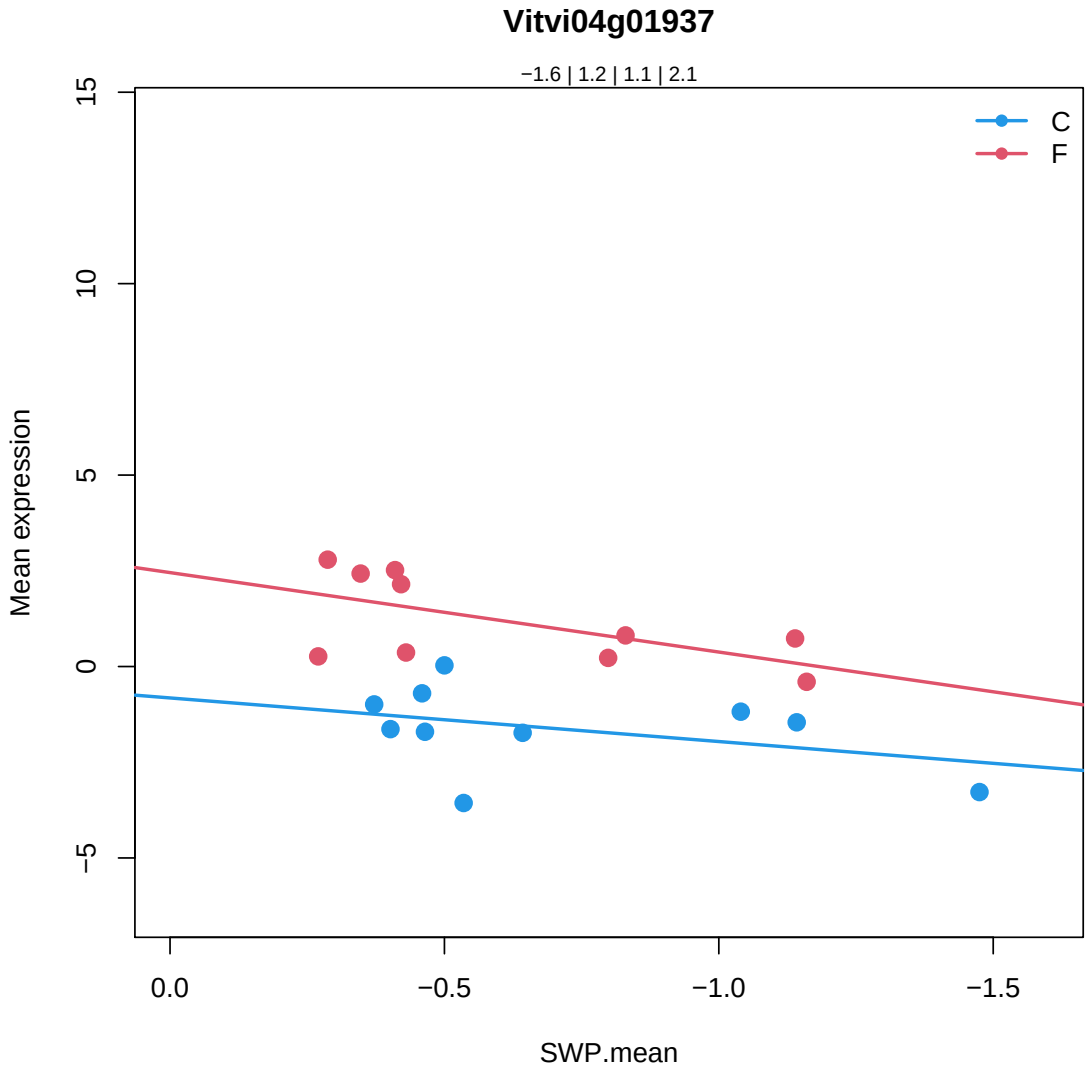
7.5.42 Vitvi04g01937: type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01937
        27.3.99
        RNA.regulation of transcription.unclassified
        Eukaryotic aspartyl protease family protein |
        Chr5:3403331-3405331 REVERSE LENGTH=474 |
        201606
```

Coefficients for Vitvi04g01937.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.621219	1.342132e-05	***	1.510841e-05	***
SlopeC	1.13847	0.1712478		0.7015862	
MeanF-MeanC	2.809877	7.652417e-07	***	2.563476e-05	***
SlopeF-SlopeC	0.9367621	0.4424164		0.9999488	



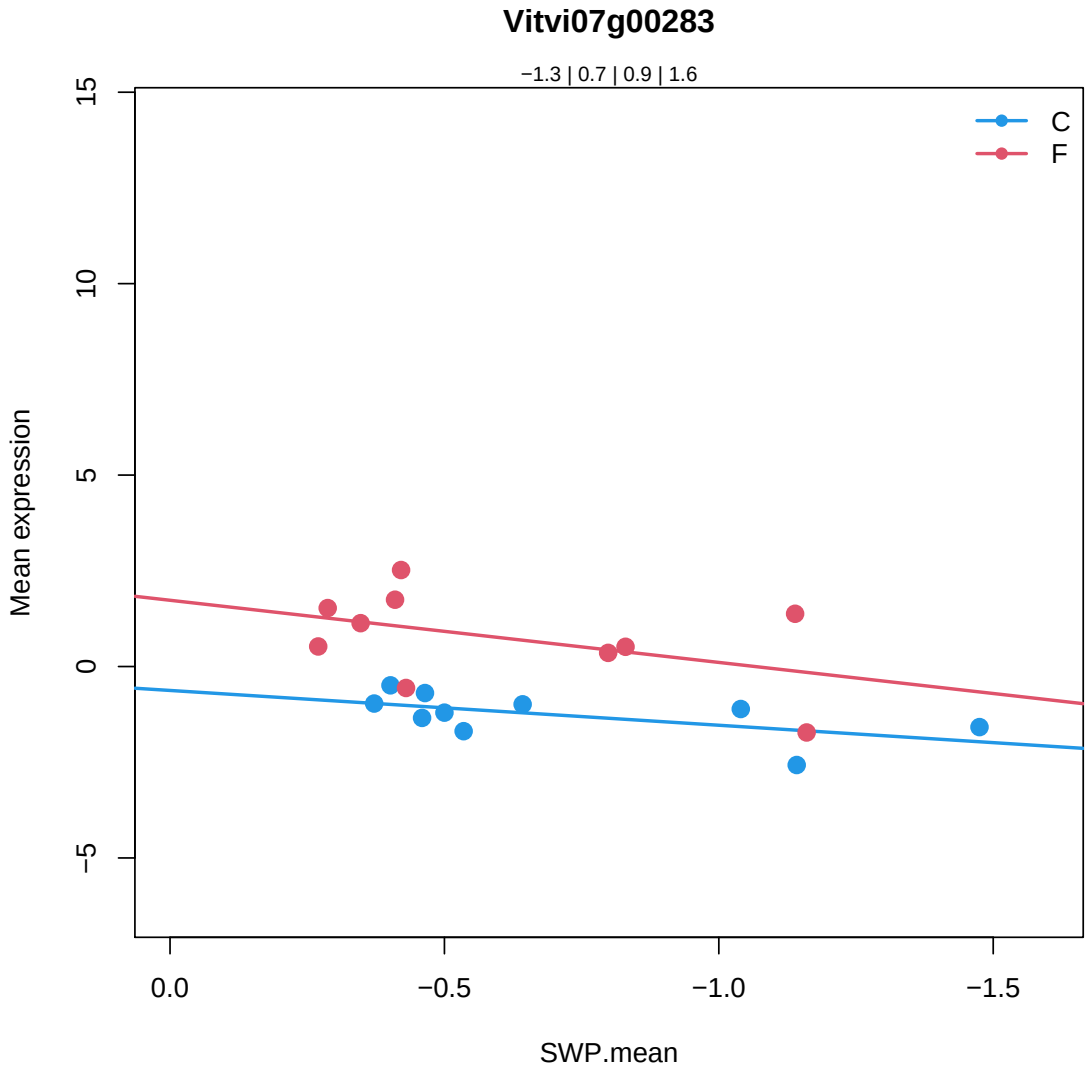
7.5.43 Vitvi07g00283: type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g00283
        26.9
        misc.glutathione S transferases
        glutathione S-transferase phi 8 |
        Chr2:19558213-19559266 FORWARD LENGTH=263 |
        201606
```

Coefficients for Vitvi07g00283.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.264137	6.185009e-05	***	6.858133e-05	***
SlopeC	0.9084089	0.2136027		0.7371282	
MeanF-MeanC	2.005367	1.480113e-05	***	0.0003552736	***
SlopeF-SlopeC	0.7148398	0.5052139		0.9999488	



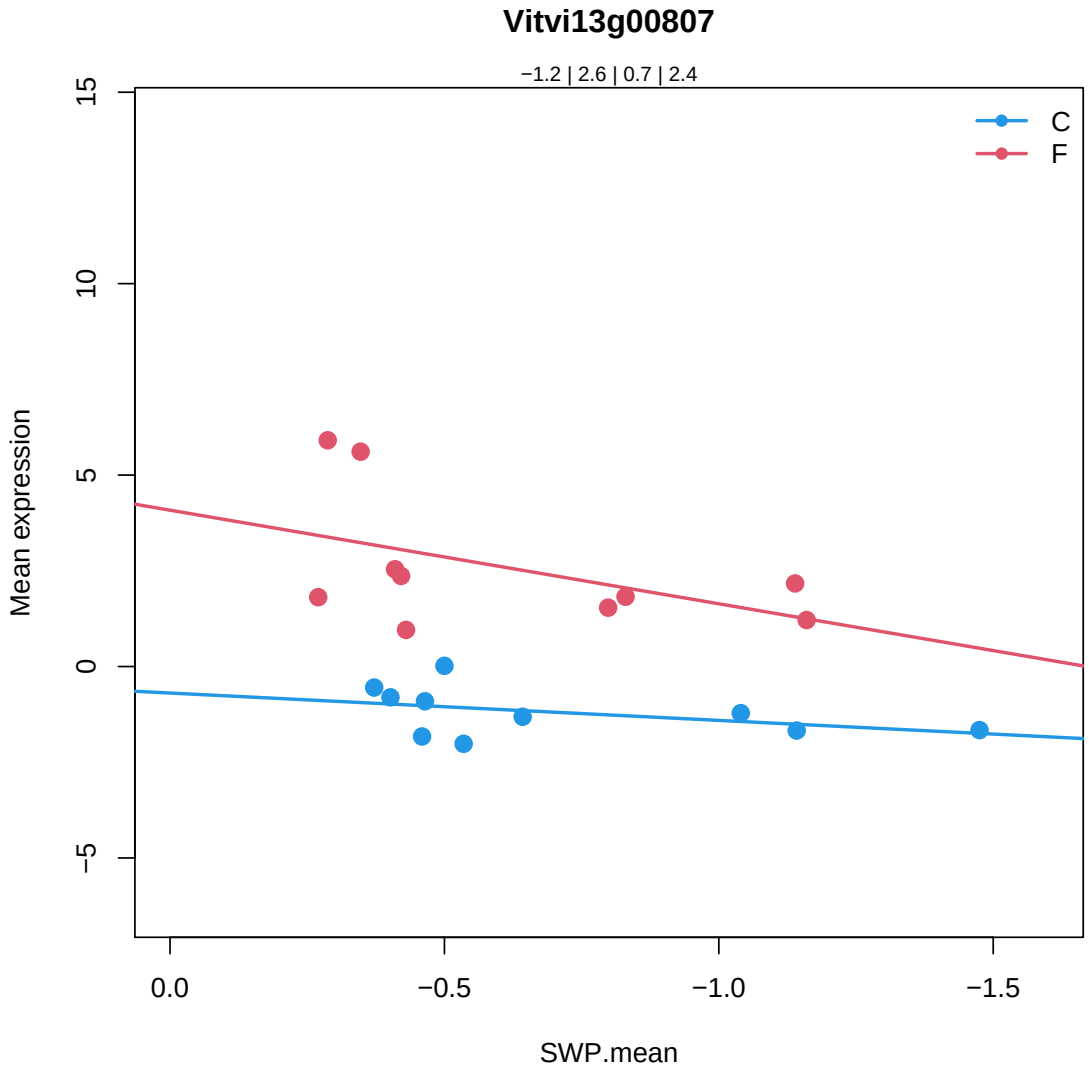
7.5.44 Vitvi13g00807: type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00807
        35.2
        not assigned.unknown
        Ankyrin repeat family protein |
        Chr5:1354240-1356754 REVERSE LENGTH=669 |
        201606
```

Coefficients for Vitvi13g00807.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.195329	0.00214581	**	0.002306193	**
SlopeC	0.7145515	0.4617959		0.8604478	
MeanF-MeanC	3.788788	1.033391e-07	***	4.200254e-06	***
SlopeF-SlopeC	1.730151	0.2360724		0.9999488	



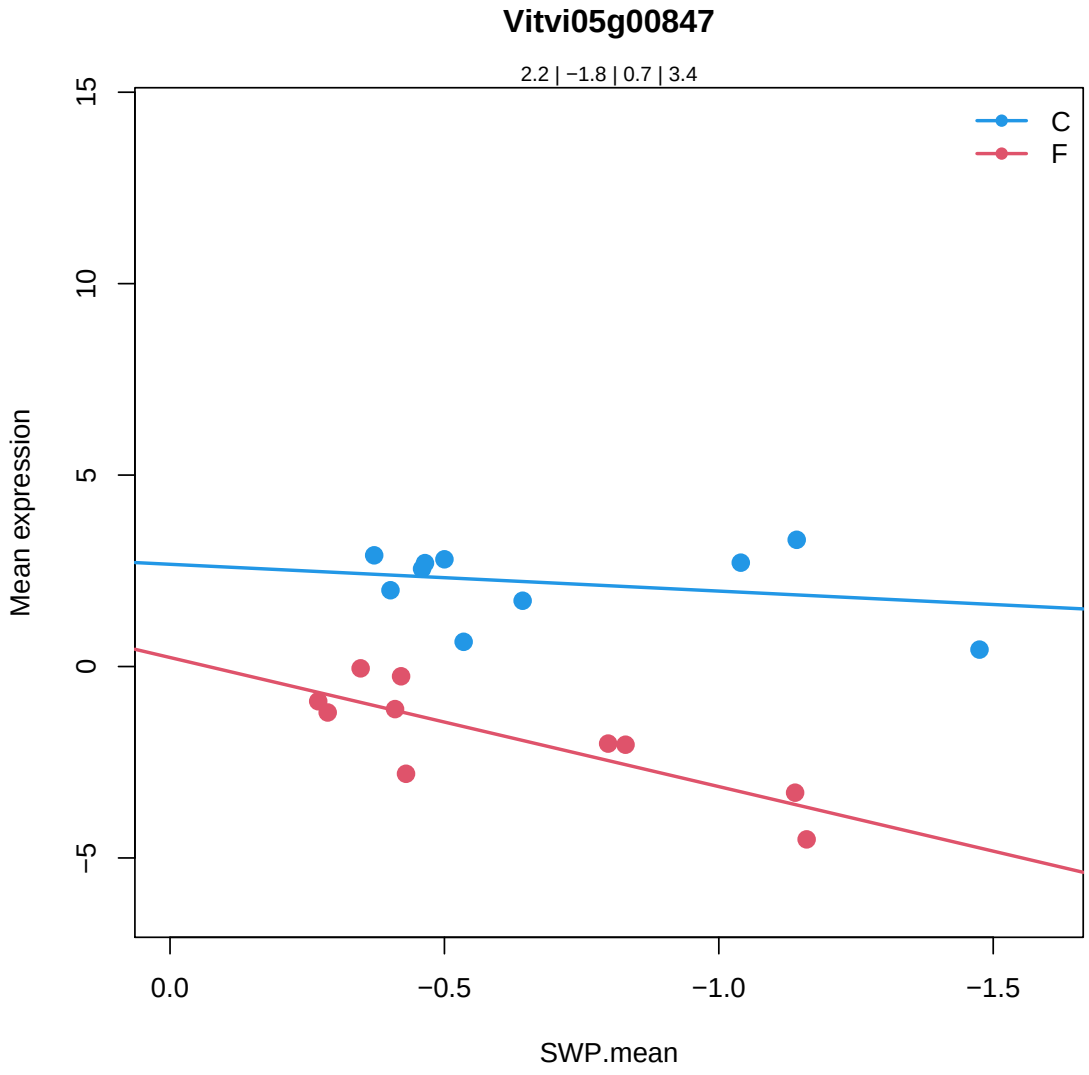
7.5.45 Vitvi05g00847: + type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00847
        30.3
        signalling.calcium
        Calcium-binding EF-hand family protein |
        Chr4:7810215-7810679 FORWARD LENGTH=154 |
        201606
```

Coefficients for Vitvi05g00847.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.177676	4.164641e-08	***	4.991151e-08	***
SlopeC	0.7001947	0.3501821		0.8124192	
MeanF-MeanC	-3.99674	4.445221e-10	***	2.821747e-08	***
SlopeF-SlopeC	2.671128	0.02304466	*	0.9999488	



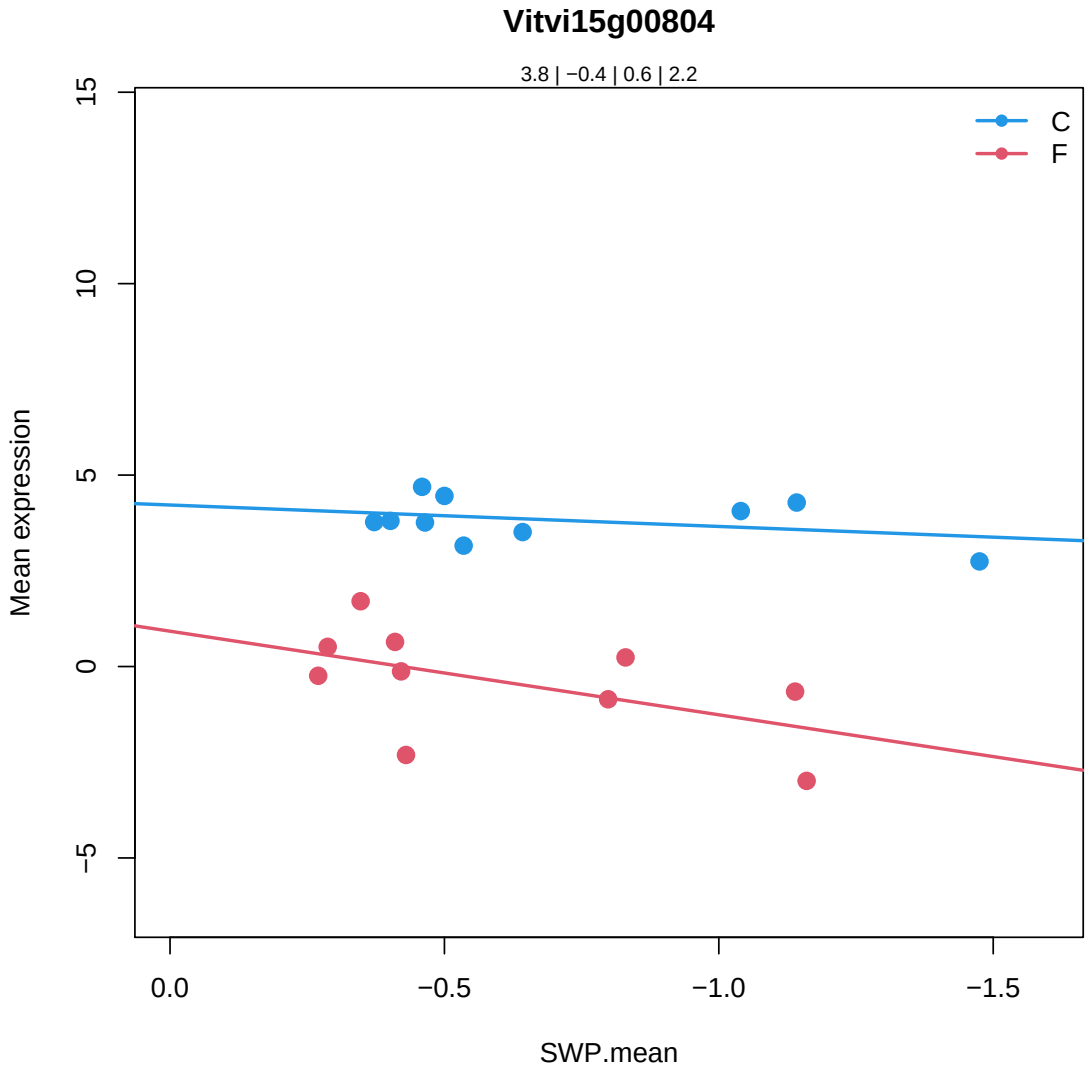
7.5.46 Vitvi15g00804: type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g00804
        26.10
        misc.cytochrome P450
        cytochrome P450%2C family 76%2C subfamily C%2C polypeptide 2 |
        Chr2:18779935-18781922 REVERSE LENGTH=512 |
        201606
```

Coefficients for Vitvi15g00804.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.824202	3.801638e-12	***	5.28402e-12	***
SlopeC	0.5598445	0.4752488		0.8622843	
MeanF-MeanC	-4.23207	3.864461e-10	***	2.464524e-08	***
SlopeF-SlopeC	1.623612	0.1711245		0.9999488	



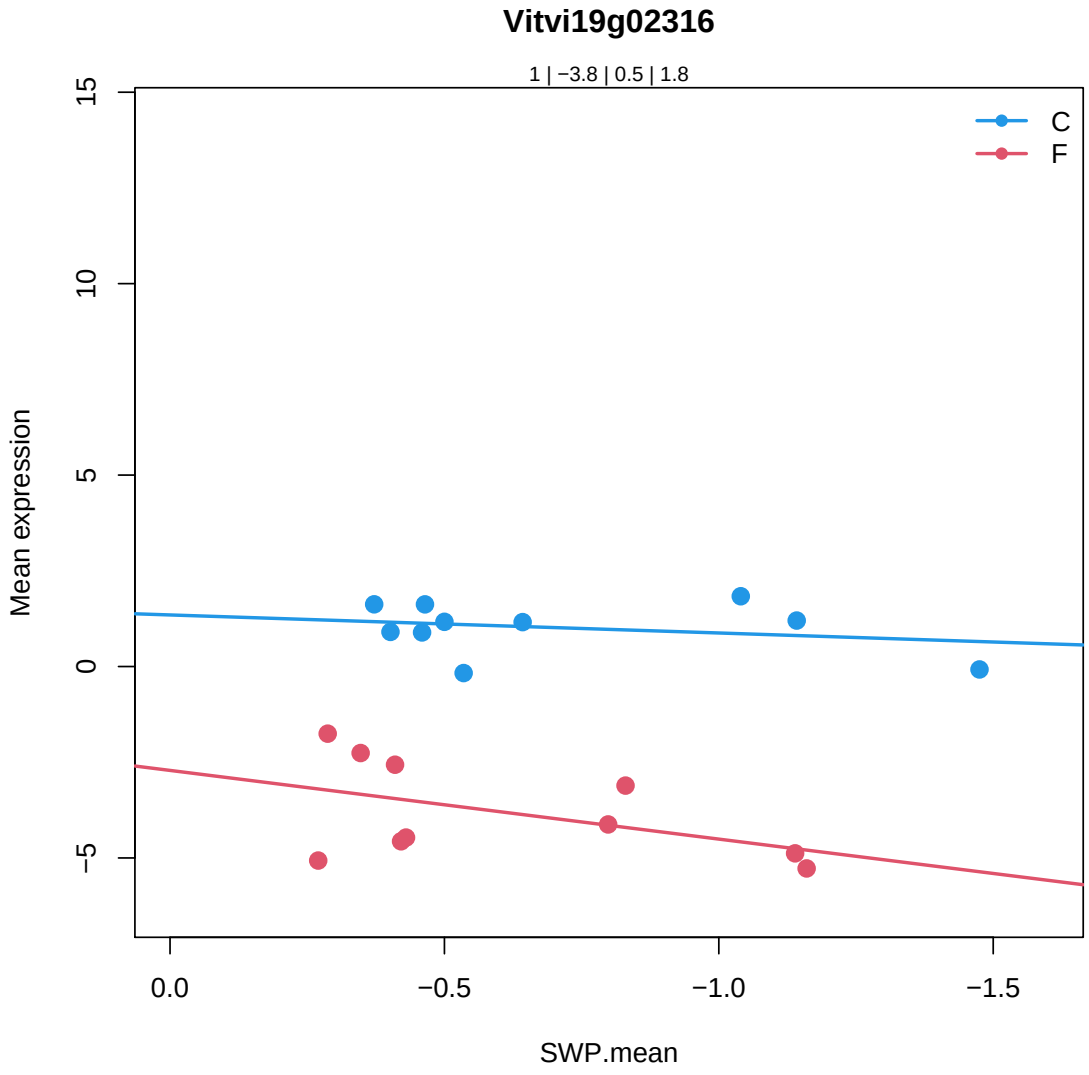
7.5.47 Vitvi19g02316: type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g02316
        35.2
        not assigned.unknown
        Disease resistance protein (CC-NBS-LRR class) family |
        Chr1:4145011-4147680 FORWARD LENGTH=889 |
        201606
```

Coefficients for Vitvi19g02316.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.015579	0.001366712	**	0.001476046	**
SlopeC	0.4709163	0.5464691		0.8857058	
MeanF-MeanC	-4.822373	3.259702e-11	***	2.400211e-09	***
SlopeF-SlopeC	1.323198	0.2600661		0.9999488	



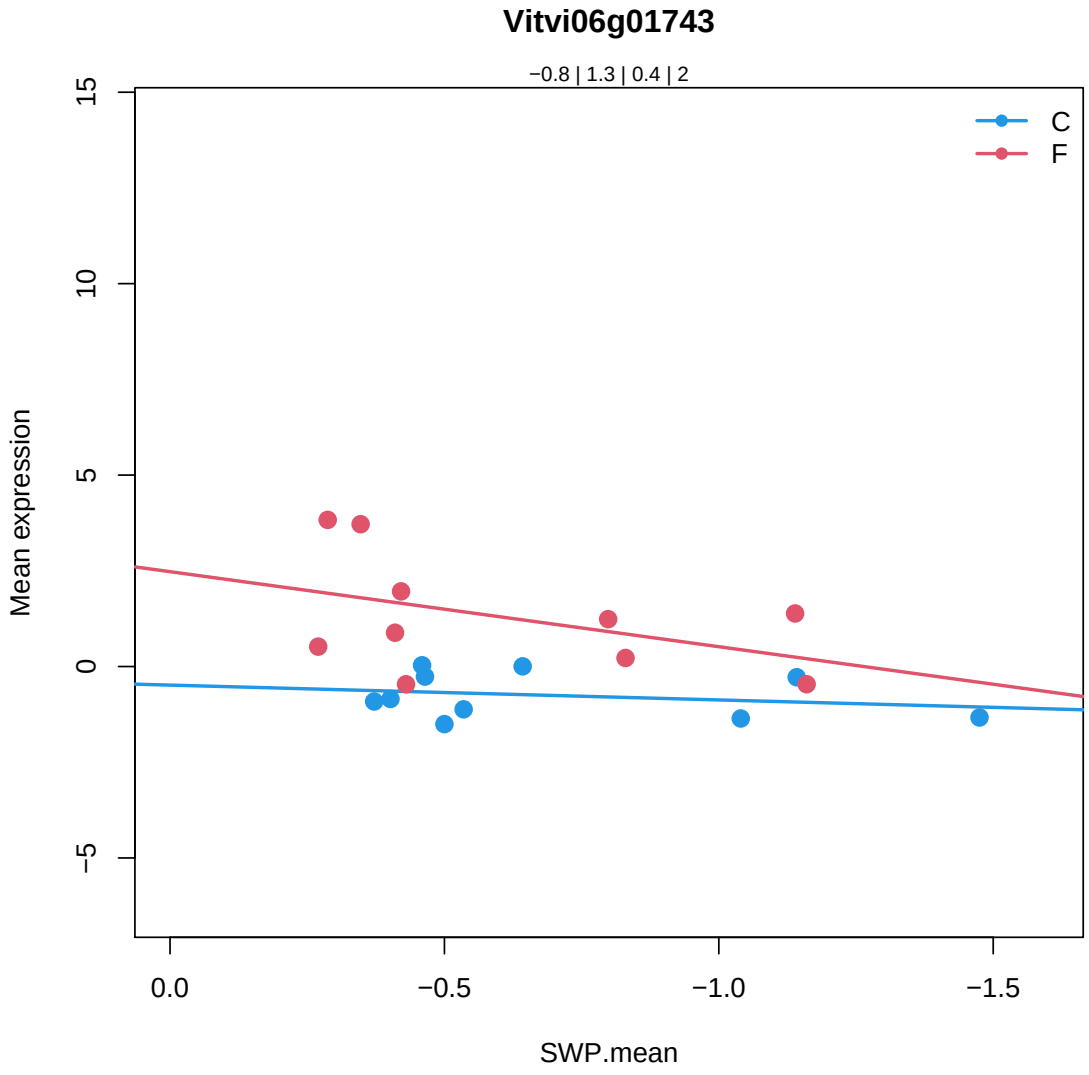
7.5.48 Vitvi06g01743: type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01743
        35.2
        not assigned.unknown
        UDP-glucosyl transferase 71C4 |
        Chr1:2225963-2227402 FORWARD LENGTH=479 |
        201606
```

Coefficients for Vitvi06g01743.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.7579229	0.02425504	*	0.02545585	*
SlopeC	0.3874884	0.6604477		0.9219292	
MeanF-MeanC	2.040905	0.0001421972	***	0.002421403	**
SlopeF-SlopeC	1.572361	0.2377642		0.9999488	



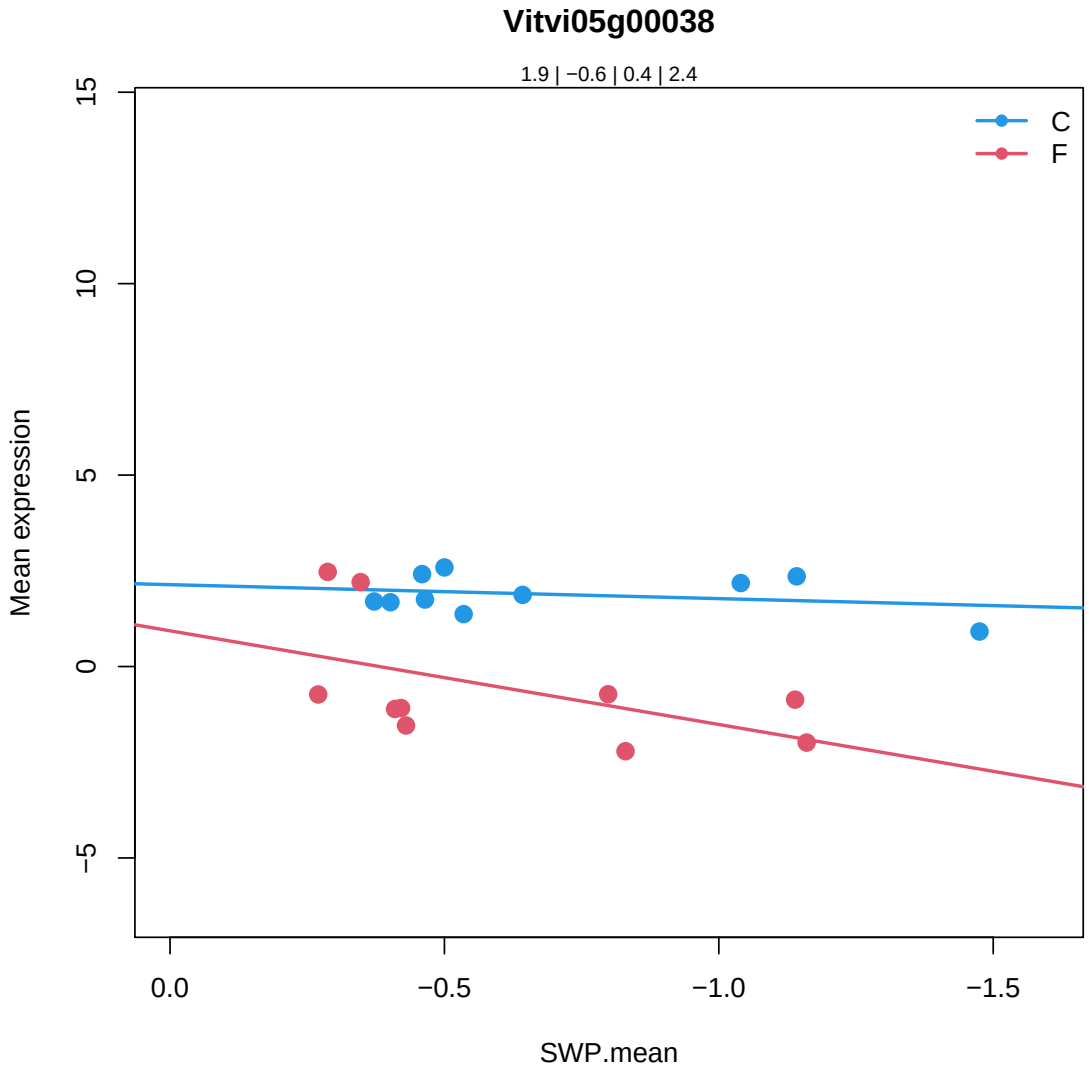
7.5.49 Vitvi05g00038: type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00038
        26.3.5
        misc.gluco-, galacto- and mannosidases.glycosyl hydrolase family 5
        alpha/beta-Hydrolases superfamily protein |
        Chr4:1035722-1037403 FORWARD LENGTH=324 |
        201606
```

Coefficients for Vitvi05g00038.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.881532	4.363251e-06	***	4.964146e-06	***
SlopeC	0.3647677	0.6752848		0.9252688	
MeanF-MeanC	-2.439425	1.40955e-05	***	0.0003437499	***
SlopeF-SlopeC	2.082283	0.1179377		0.9999488	



7.5.50 Vitvi11g00865: type3 | type4

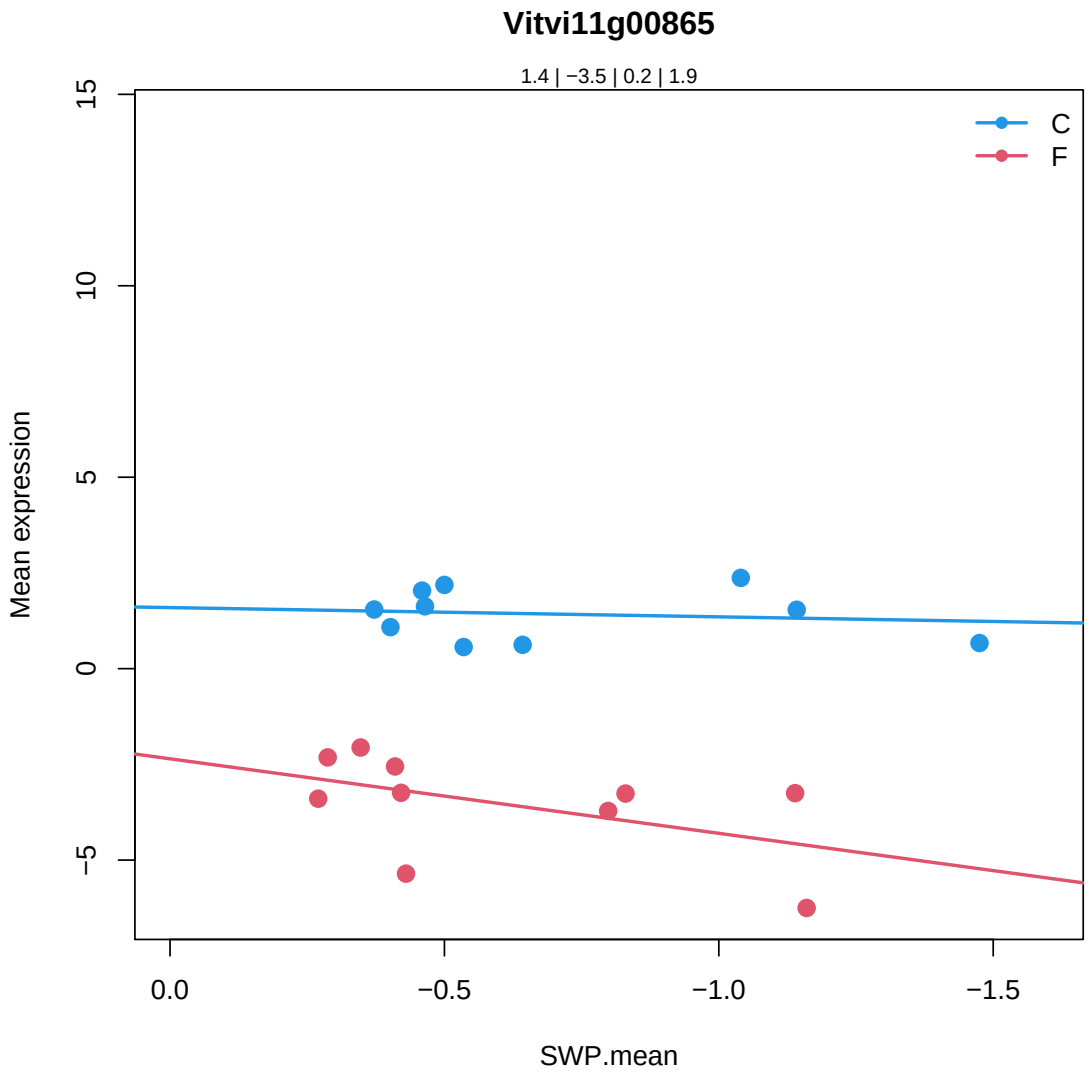
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00865
        20
        stress
        Ankyrin repeat family protein |
        Chr5:1354240-1356754 REVERSE LENGTH=669 |
        201606

Vitvi11g00865
        19.99
        tetrapyrrole synthesis.unspecified
        Ankyrin repeat family protein |
        Chr5:1354240-1356754 REVERSE LENGTH=669 |
        201606
```

Coefficients for Vitvi11g00865.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.424545	4.543505e-05	***	5.050843e-05	***
SlopeC	0.241433	0.7594168		0.9479775	
MeanF-MeanC	-4.965309	2.386458e-11	***	1.774361e-09	***
SlopeF-SlopeC	1.705682	0.1554573		0.9999488	


Vitvi11g00865
1.4 | −3.5 | 0.2 | 1.9
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

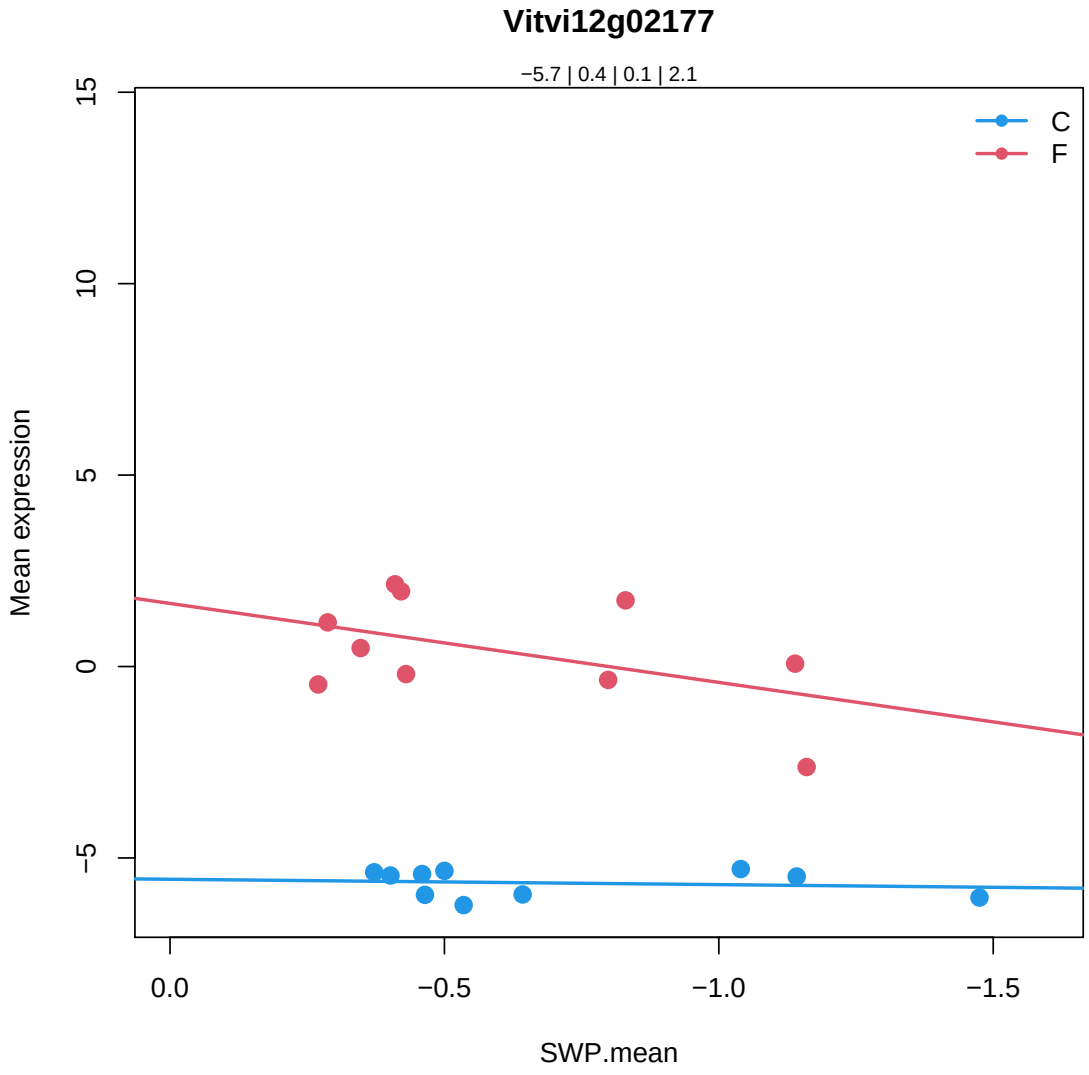
7.5.51 Vitvi12g02177: type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02177
        16.1.5
        secondary metabolism.isoprenoids.terpenoids
        terpene synthase 21 |
        Chr5:8092969-8095128 FORWARD LENGTH=545 |
        201606
```

Coefficients for Vitvi12g02177.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.654707	1.734801e-15	***	3.157989e-15	***
SlopeC	0.1400847	0.8582087		0.9733541	
MeanF-MeanC	6.045631	4.807264e-13	***	4.608322e-11	***
SlopeF-SlopeC	1.922026	0.1100849		0.9999488	



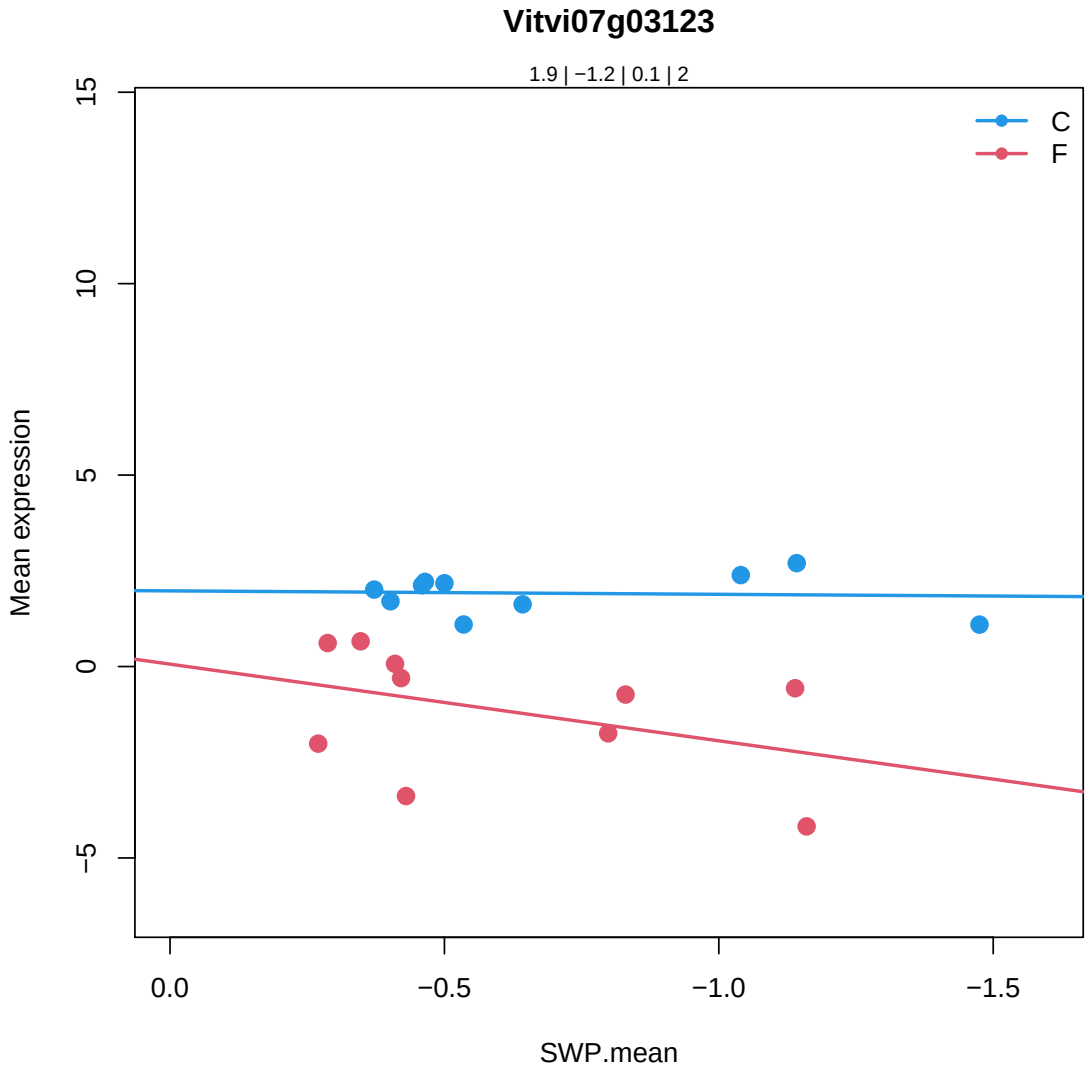
7.5.52 Vitvi07g03123: type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g03123
        31.1
        cell.organisation
        tubulin alpha-5 |
        Chr5:6687212-6688926 FORWARD LENGTH=450 |
        201606
```

Coefficients for Vitvi07g03123.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.912632	1.0113e-05	***	1.14188e-05	***
SlopeC	0.0898298	0.9238393		0.9860755	
MeanF-MeanC	-3.070558	1.72904e-06	***	5.302623e-05	***
SlopeF-SlopeC	1.912759	0.1806418		0.9999488	



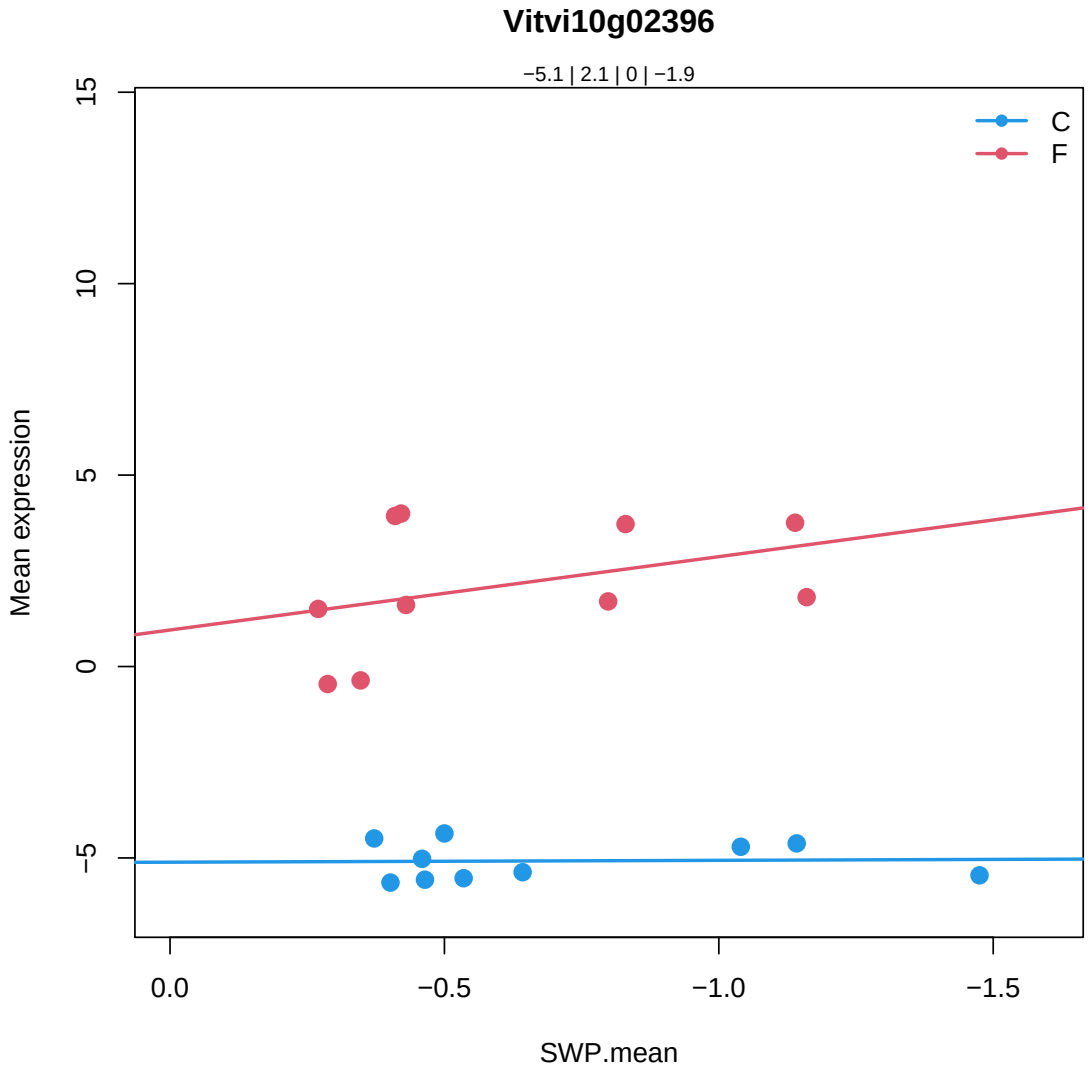
7.5.53 Vitvi10g02396: type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g02396
        14.2
        S-assimilation.APR
        APS reductase 1 |
        Chr4:2325069-2326718 FORWARD LENGTH=465 |
        201606
```

Coefficients for Vitvi10g02396.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.076664	1.036555e-12	***	1.485024e-12	***
SlopeC	-0.04830116	0.9602008		0.9937458	
MeanF-MeanC	7.197329	9.873187e-13	***	8.749251e-11	***
SlopeF-SlopeC	-1.867763	0.2034859		0.9999488	



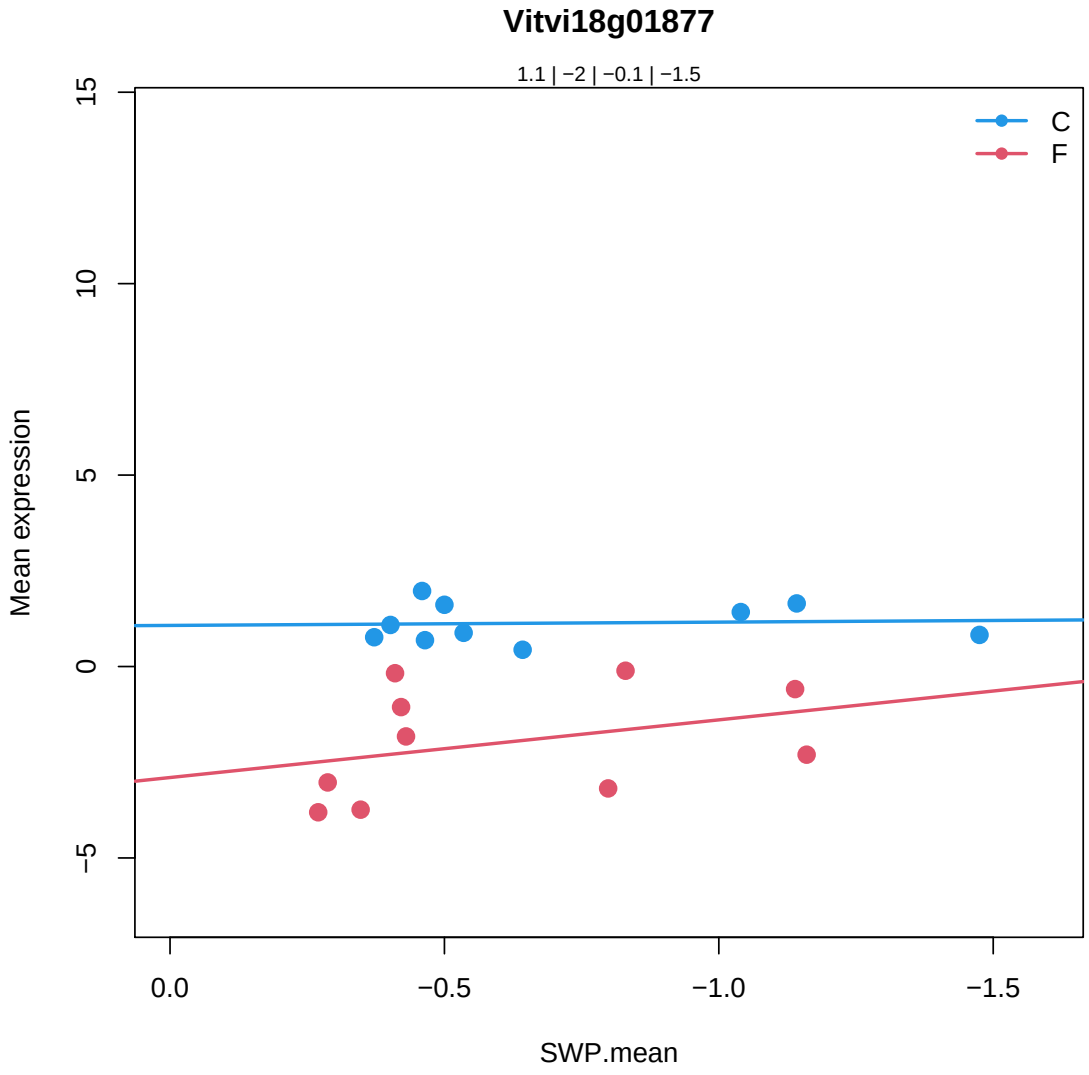
7.5.54 Vitvi18g01877: type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g01877
        20.1.2.2
        stress.biotic.receptors.TIR-NBS-LRR
        Disease resistance protein (TIR-NBS-LRR class) family |
        Chr5:14568141-14571907 REVERSE LENGTH=1125 |
        201606
```

Coefficients for Vitvi18g01877.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.133662	0.001197745	**	0.001295489	**
SlopeC	-0.08588147	0.9200083		0.9853314	
MeanF-MeanC	-3.115832	3.373809e-07	***	1.227294e-05	***
SlopeF-SlopeC	-1.420387	0.2713186		0.9999488	



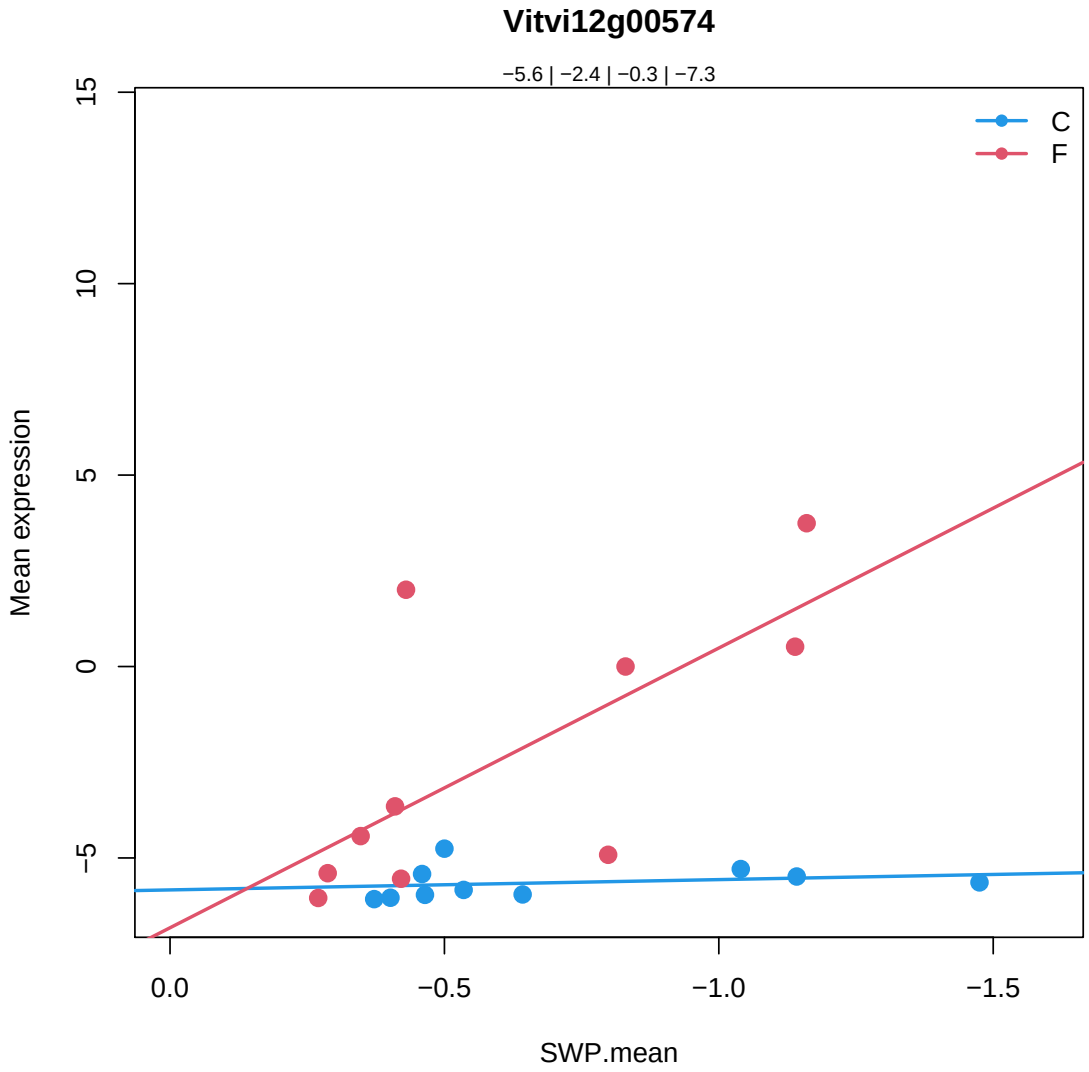
7.5.55 Vitvi12g00574: + type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00574
        16.1.5
        secondary metabolism.isoprenoids.terpenoids
        terpene synthase-like sequence-1%2C8-cineole |
        Chr3:9447545-9450316 FORWARD LENGTH=600 |
        201606
```

Coefficients for Vitvi12g00574.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.645691	6.169158e-10	***	7.839779e-10	***
SlopeC	-0.2692201	0.8584264		0.9734036	
MeanF-MeanC	3.273791	0.0002909881	***	0.004497484	**
SlopeF-SlopeC	-7.036961	0.004526106	**	0.9999488	



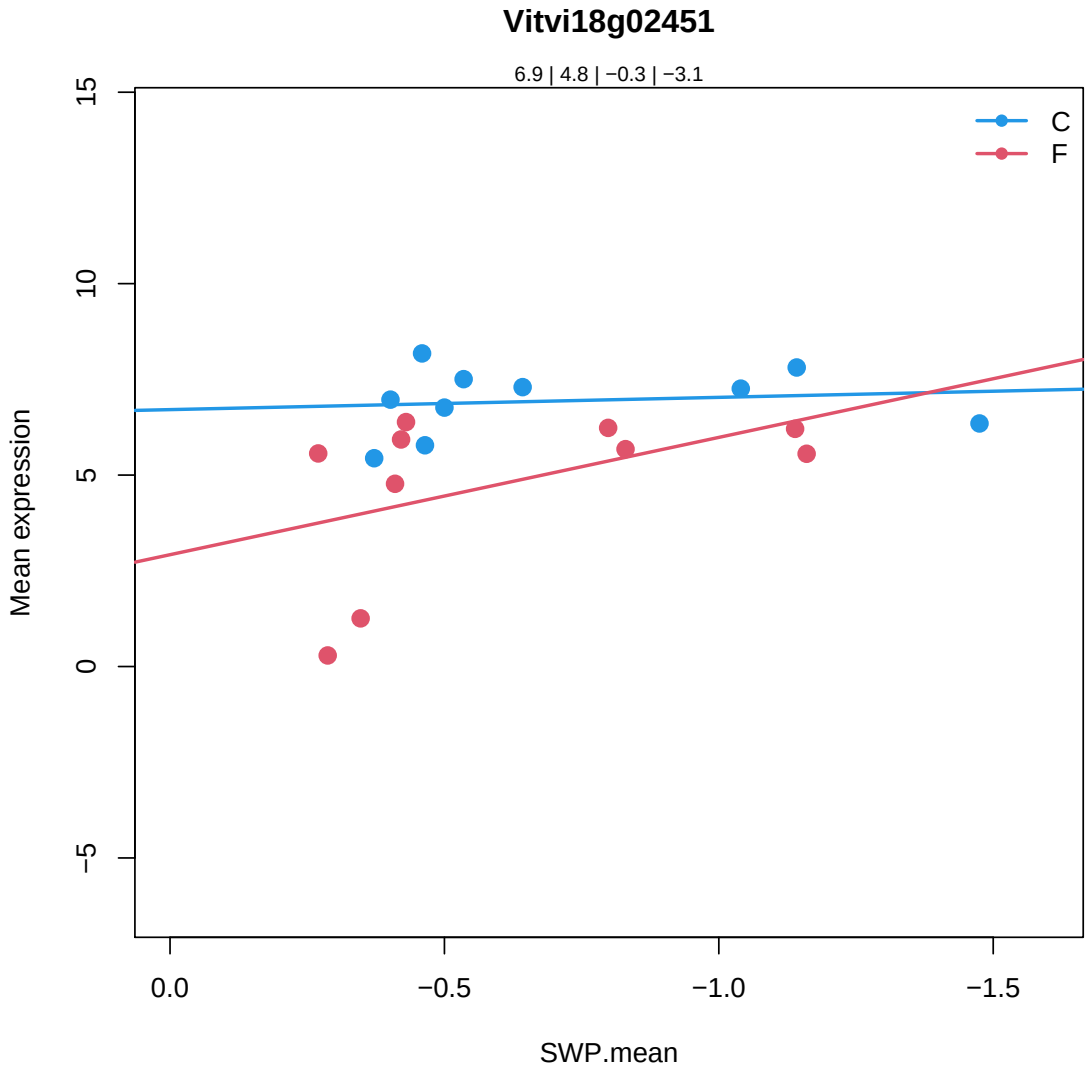
7.5.56 Vitvi18g02451: type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02451
        16.1.5
        secondary metabolism.isoprenoids.terpenoids
        terpene synthase 21 |
        Chr5:8092969-8095128 FORWARD LENGTH=545 |
        201606
```

Coefficients for Vitvi18g02451.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.934609	2.33132e-13	***	3.491597e-13	***
SlopeC	-0.3205063	0.7938969		0.9552081	
MeanF-MeanC	-2.147399	0.00214966	**	0.02330378	*
SlopeF-SlopeC	-2.742855	0.1428692		0.9999488	



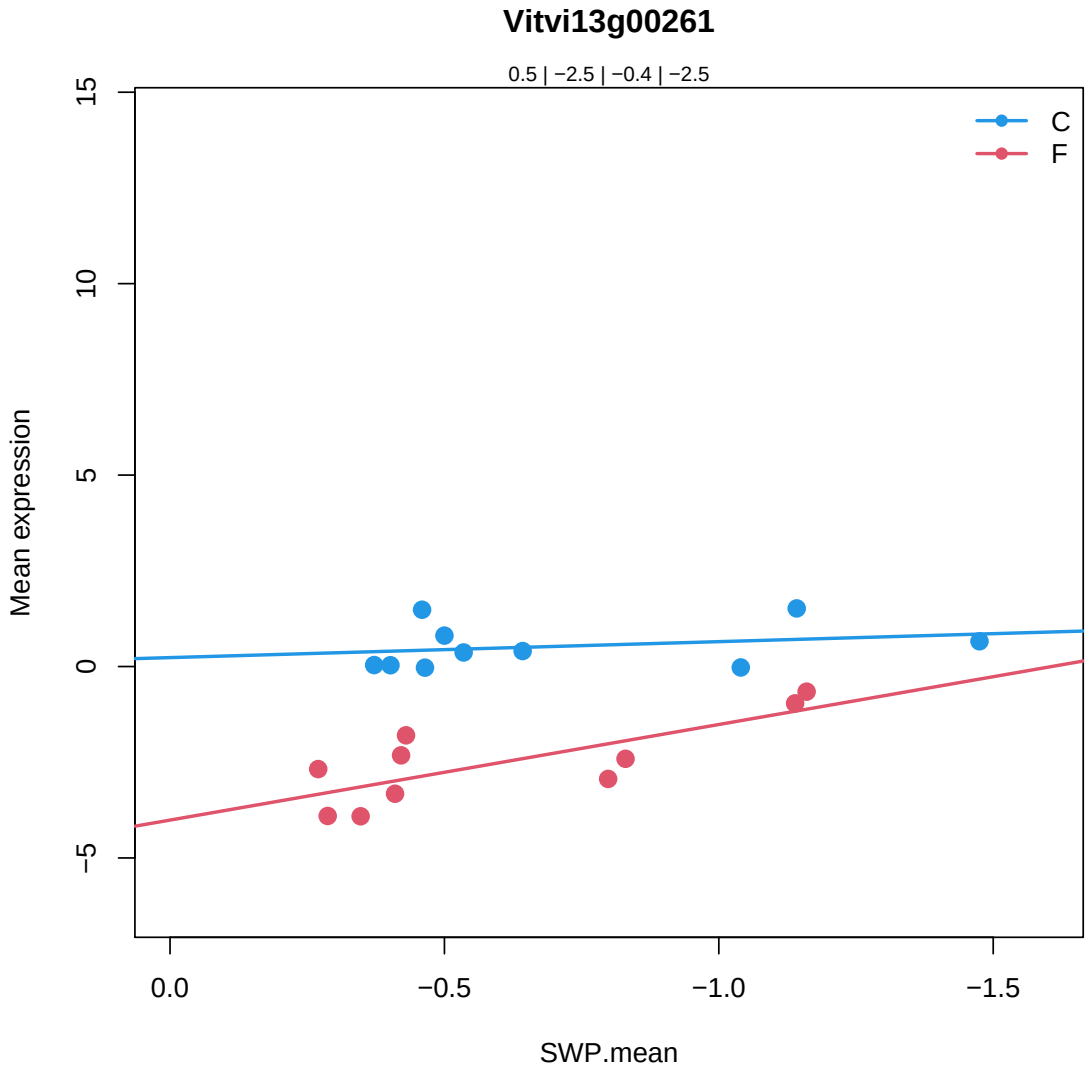
7.5.57 Vitvi13g00261: + type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00261
        35.2
        not assigned.unknown
        PIF / Ping-Pong family of plant transposase |
        Chr3:20518518-20520690 FORWARD LENGTH=406 |
        201606
```

Coefficients for Vitvi13g00261.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.5253927	0.0164883	*	0.01737758	*
SlopeC	-0.4169403	0.4660837		0.8618199	
MeanF-MeanC	-3.015297	5.911452e-10	***	3.639539e-08	***
SlopeF-SlopeC	-2.079326	0.02120173	*	0.9999488	



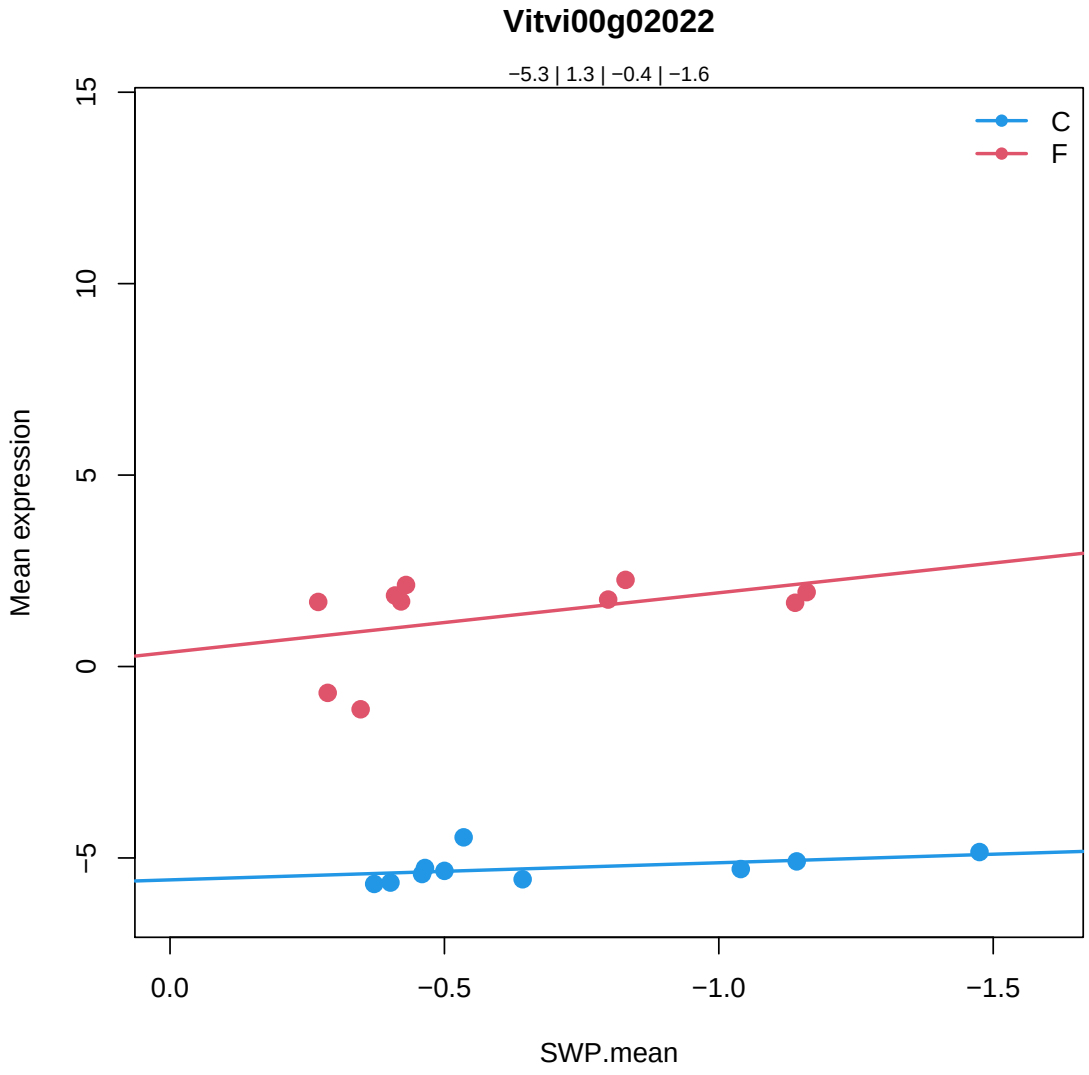
7.5.58 Vitvi00g02022: type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi00g02022
        17.1.2
        hormone metabolism.abscisic acid.signal transduction
        GCR2-like 1 |
        Chr5:26086129-26087304 REVERSE LENGTH=311 |
        201606
```

Coefficients for Vitvi00g02022.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.25859	4.249314e-16	***	8.367965e-16	***
SlopeC	-0.446971	0.5134631		0.8711742	
MeanF-MeanC	6.577033	5.234018e-15	***	6.818539e-13	***
SlopeF-SlopeC	-1.107401	0.2809345		0.9999488	



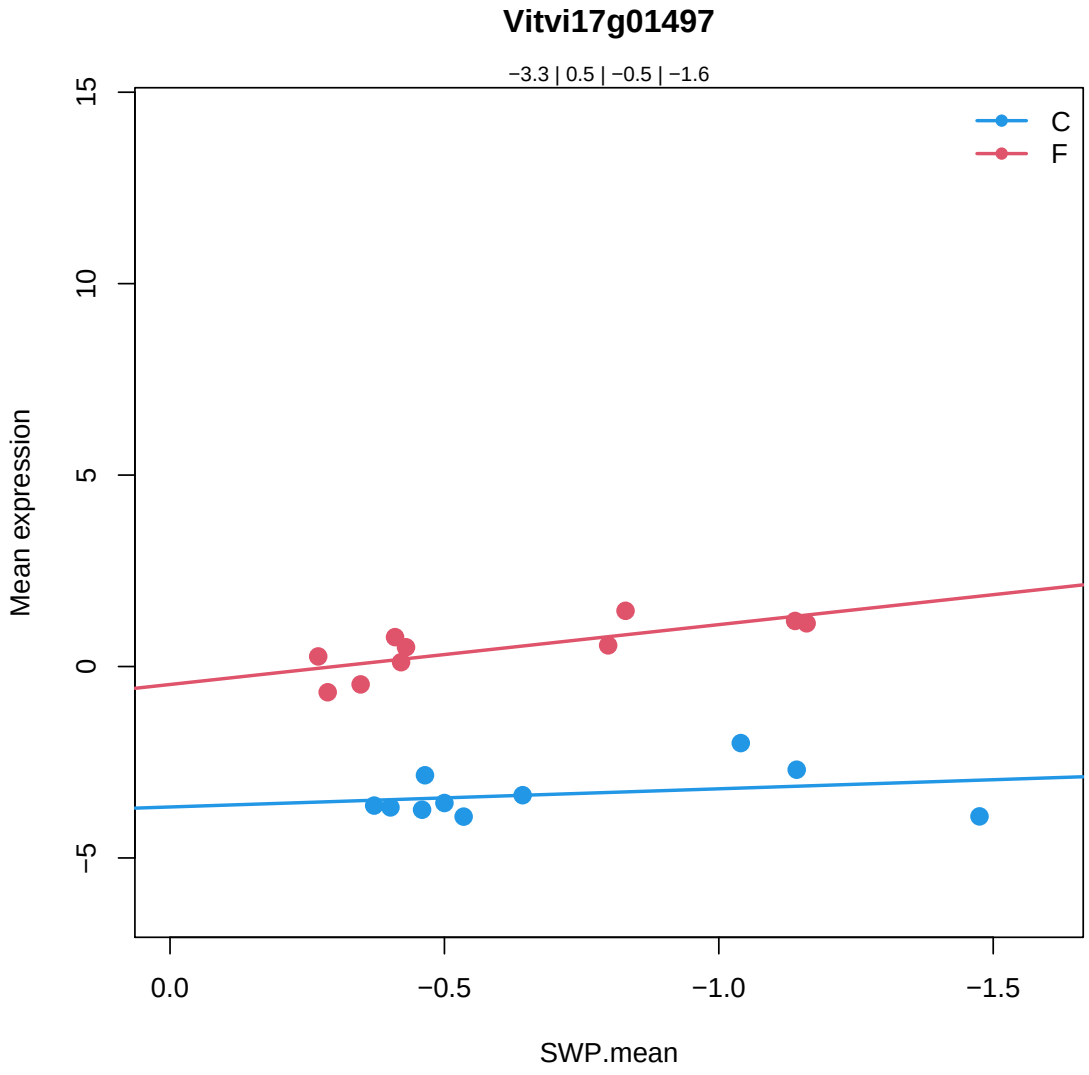
7.5.59 Vitvi17g01497: type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g01497
        26.2
        misc.UDP glucosyl and glucoronyl transferases
        UDP-Glycosyltransferase superfamily protein |
        Chr3:368840-370484 REVERSE LENGTH=464 |
        201606
```

Coefficients for Vitvi17g01497.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-3.334798	4.342005e-15	***	7.574779e-15	***
SlopeC	-0.4744792	0.331881		0.801141	
MeanF-MeanC	3.817918	3.025e-13	***	3.053447e-11	***
SlopeF-SlopeC	-1.089142	0.1403554		0.9999488	



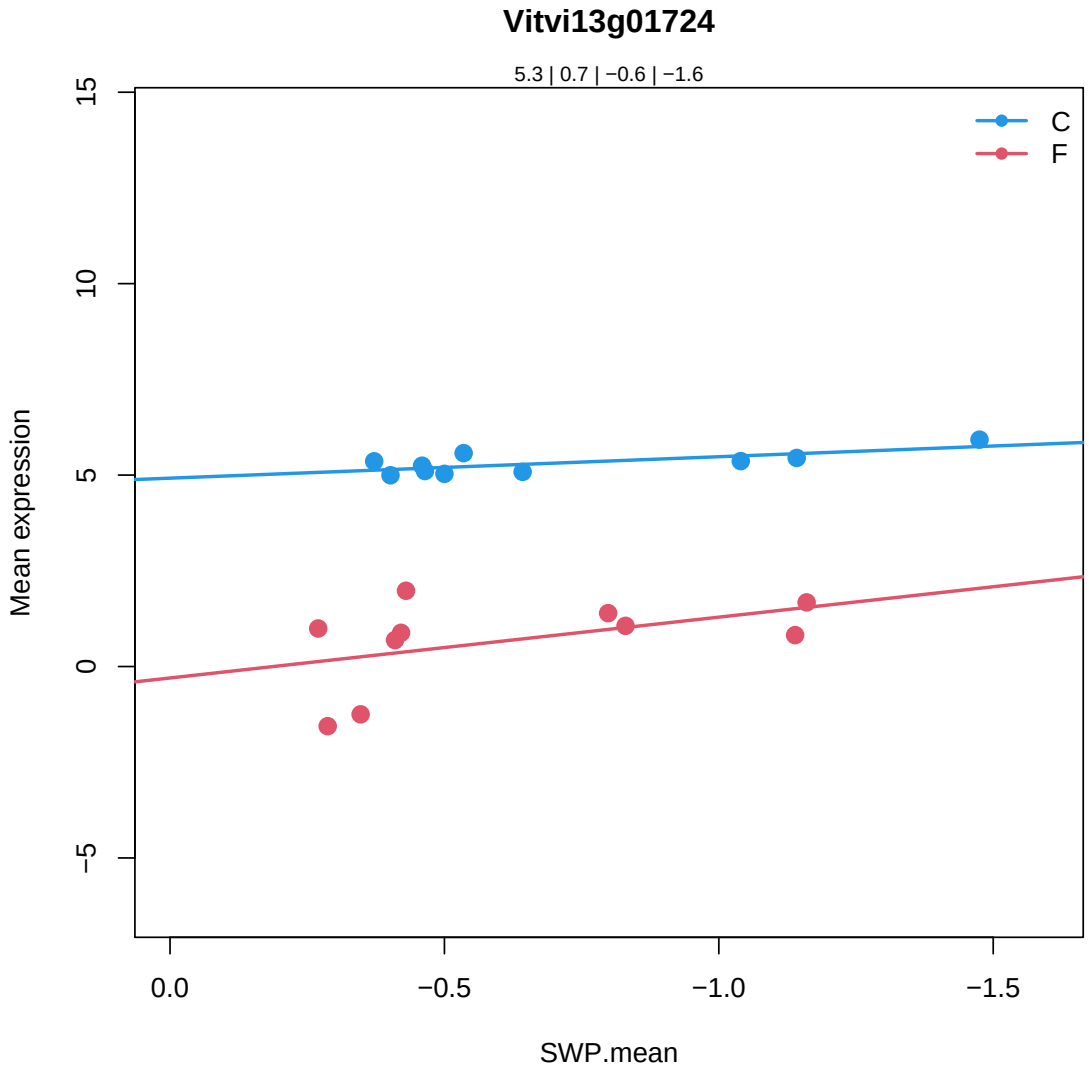
7.5.60 Vitvi13g01724: type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g01724
        17.1.1.1.10
        hormone metabolism.abscisic acid.synthesis-degradation.synthesis.9-cis
        carotenoid cleavage dioxygenase 1 |
        Chr3:23452940-23455896 FORWARD LENGTH=538 |
        201606
```

Coefficients for Vitvi13g01724.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.313104	1.065947e-16	***	2.305544e-16	***
SlopeC	-0.5600995	0.3879137		0.8295407	
MeanF-MeanC	-4.644629	1.740046e-12	***	1.506919e-10	***
SlopeF-SlopeC	-1.02838	0.2890149		0.9999488	



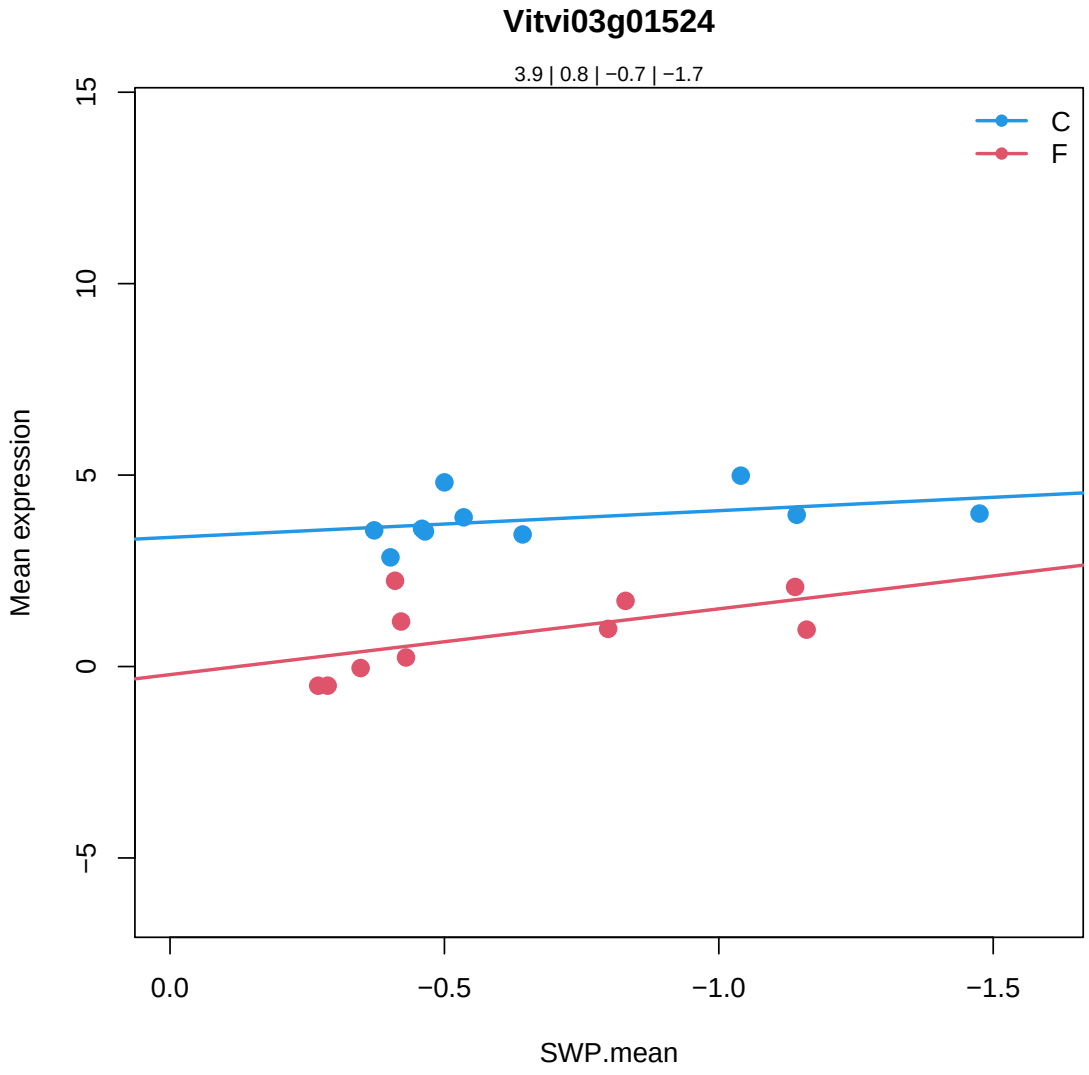
7.5.61 Vitvi03g01524: type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g01524
        26.10
        misc.cytochrome P450
        cytochrome P450%2C family 82%2C subfamily C%2C polypeptide 2 |
        Chr4:15462408-15464358 FORWARD LENGTH=523 |
        201606
```

Coefficients for Vitvi03g01524.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.863115	3.164956e-14	***	5.057161e-14	***
SlopeC	-0.6979398	0.2657481		0.7701943	
MeanF-MeanC	-3.028344	2.438519e-09	***	1.308729e-07	***
SlopeF-SlopeC	-1.020488	0.2740226		0.9999488	



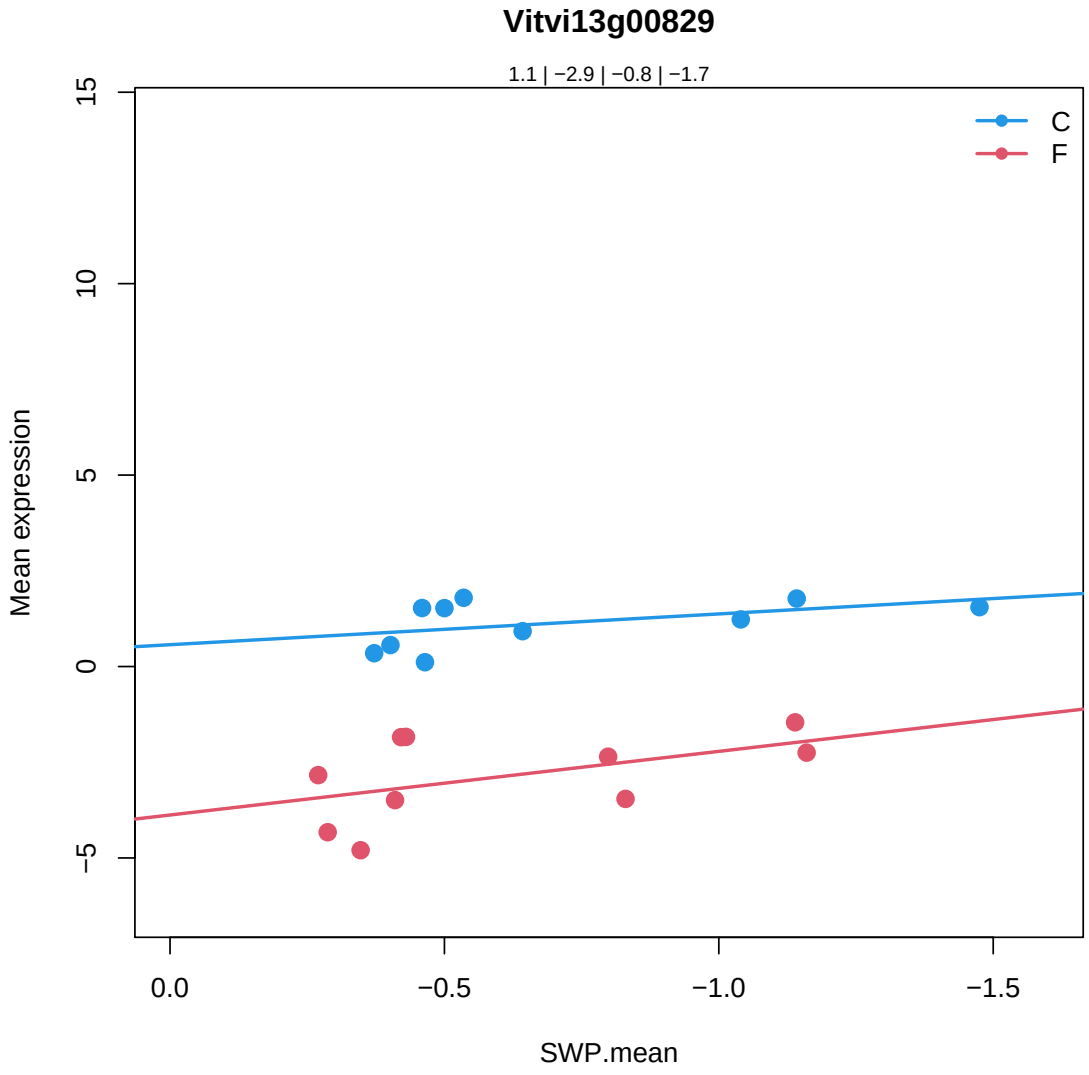
7.5.62 Vitvi13g00829: type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00829
        26.28
        misc.GDSL-motif lipase
        GDSL-like Lipase/Acylhydrolase superfamily protein |
        Chr5:915650-918326 FORWARD LENGTH=359 |
        201606
```

Coefficients for Vitvi13g00829.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.134556	0.0001034462	***	0.0001141728	***
SlopeC	-0.8037133	0.2398442		0.7540013	
MeanF-MeanC	-4.000103	7.183617e-11	***	5.140502e-09	***
SlopeF-SlopeC	-0.8582677	0.3953278		0.9999488	



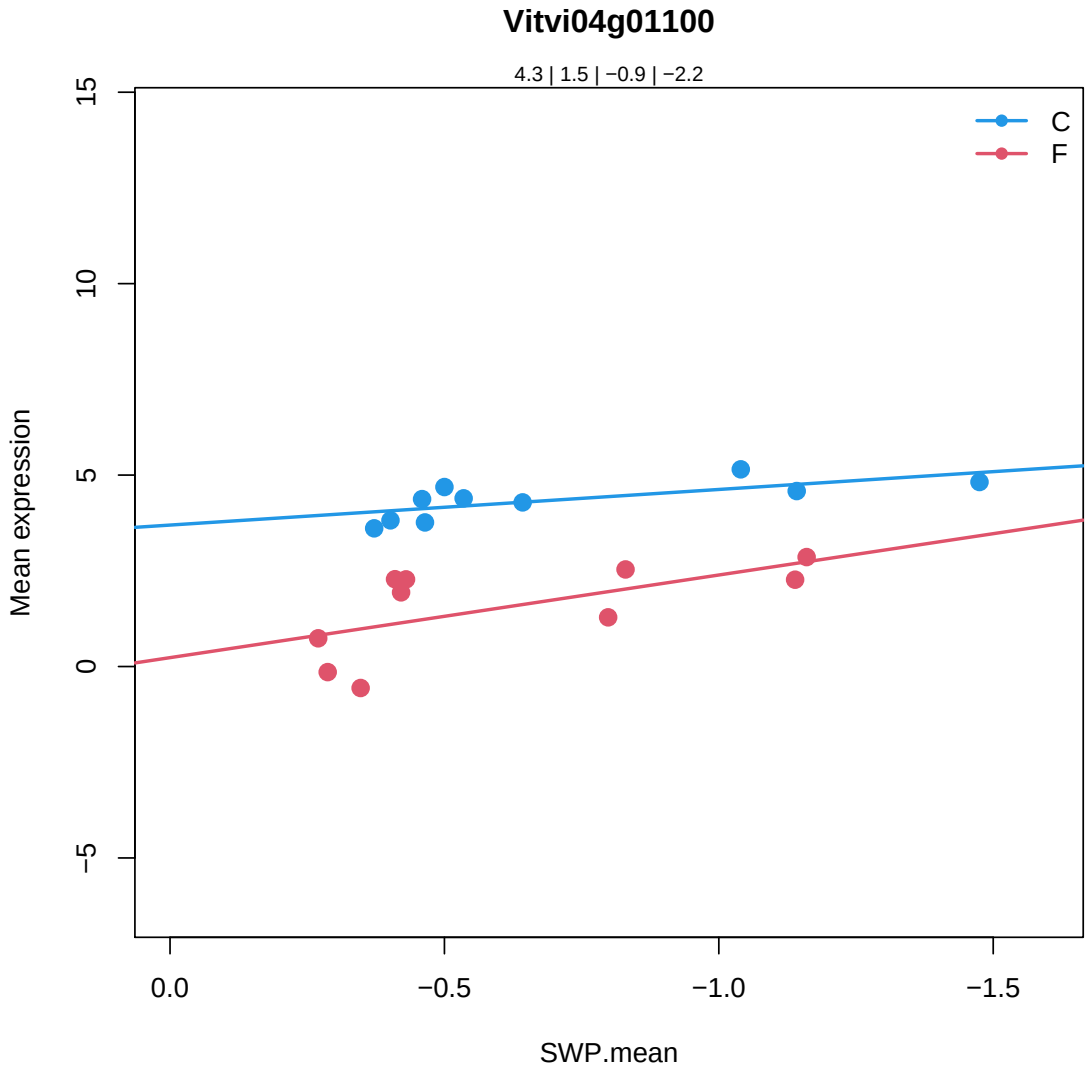
7.5.63 Vitvi04g01100: type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01100
        31.1
        cell.organisation
        phloem protein 2-B1 |
        Chr2:590393-591595 REVERSE LENGTH=336 |
        201606
```

Coefficients for Vitvi04g01100.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.348044	1.905579e-15	***	3.458543e-15	***
SlopeC	-0.9302426	0.1347228		0.6596656	
MeanF-MeanC	-2.801248	6.673827e-09	***	3.402089e-07	***
SlopeF-SlopeC	-1.228185	0.1821518		0.9999488	



7.5.64 Vitvi14g01128: type4

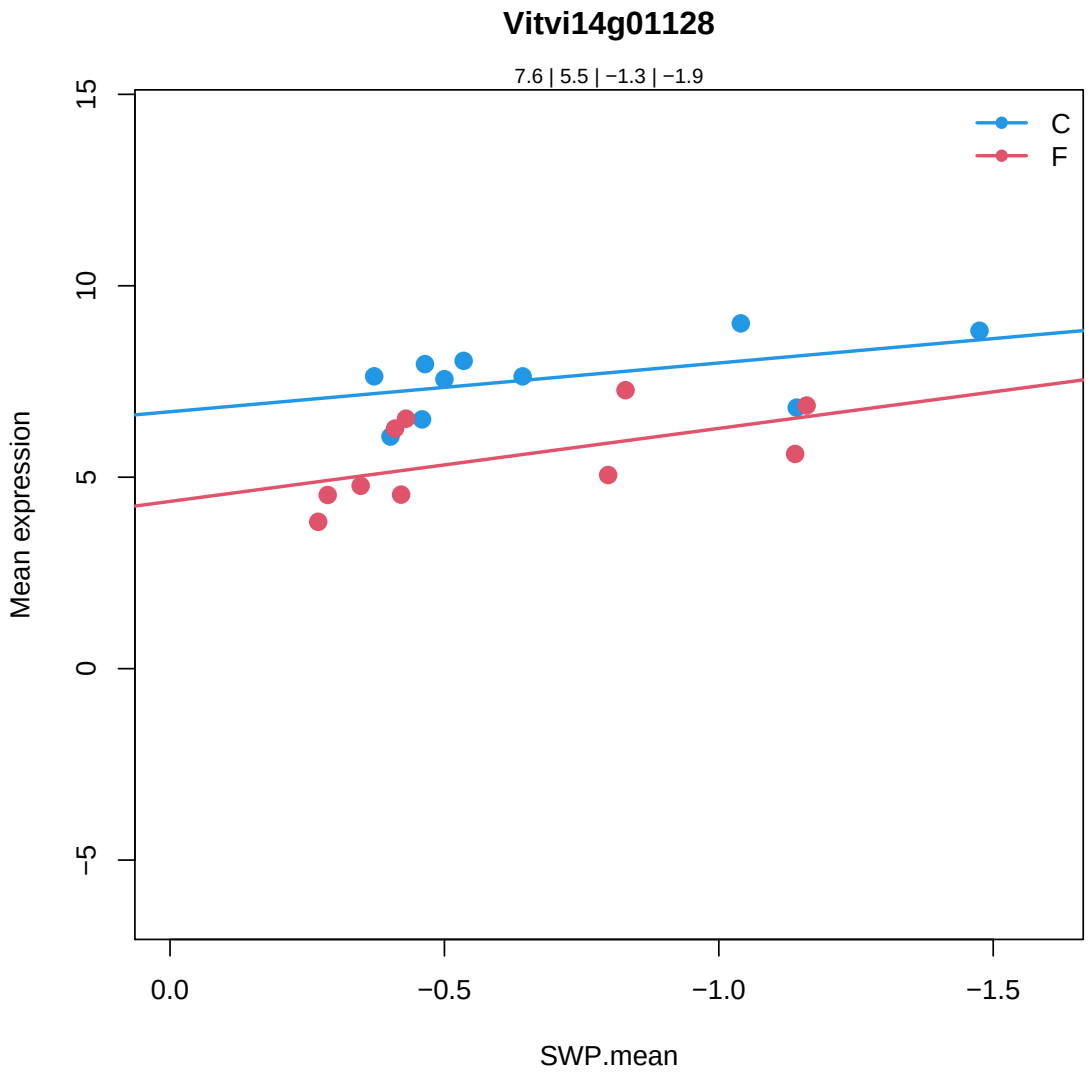
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01128
        26.21
        misc.protease inhibitor/seed storage/lipid transfer protein (LTP) fami
        Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin
        Chr3:6267102-6267392 FORWARD LENGTH=96 |
        201606

Vitvi14g01128
        11.6
        lipid metabolism.lipid transfer proteins etc
        Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin
        Chr3:6267102-6267392 FORWARD LENGTH=96 |
        201606
```

Coefficients for Vitvi14g01128.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.605298	1.655195e-18	***	5.34955e-18	***
SlopeC	-1.2737	0.1015743		0.6135572	
MeanF-MeanC	-2.075585	1.796388e-05	***	0.0004222686	***
SlopeF-SlopeC	-0.6333015	0.5736211		0.9999488	


Vitvi14g01128
7.6 | 5.5 | −1.3 | −1.9
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

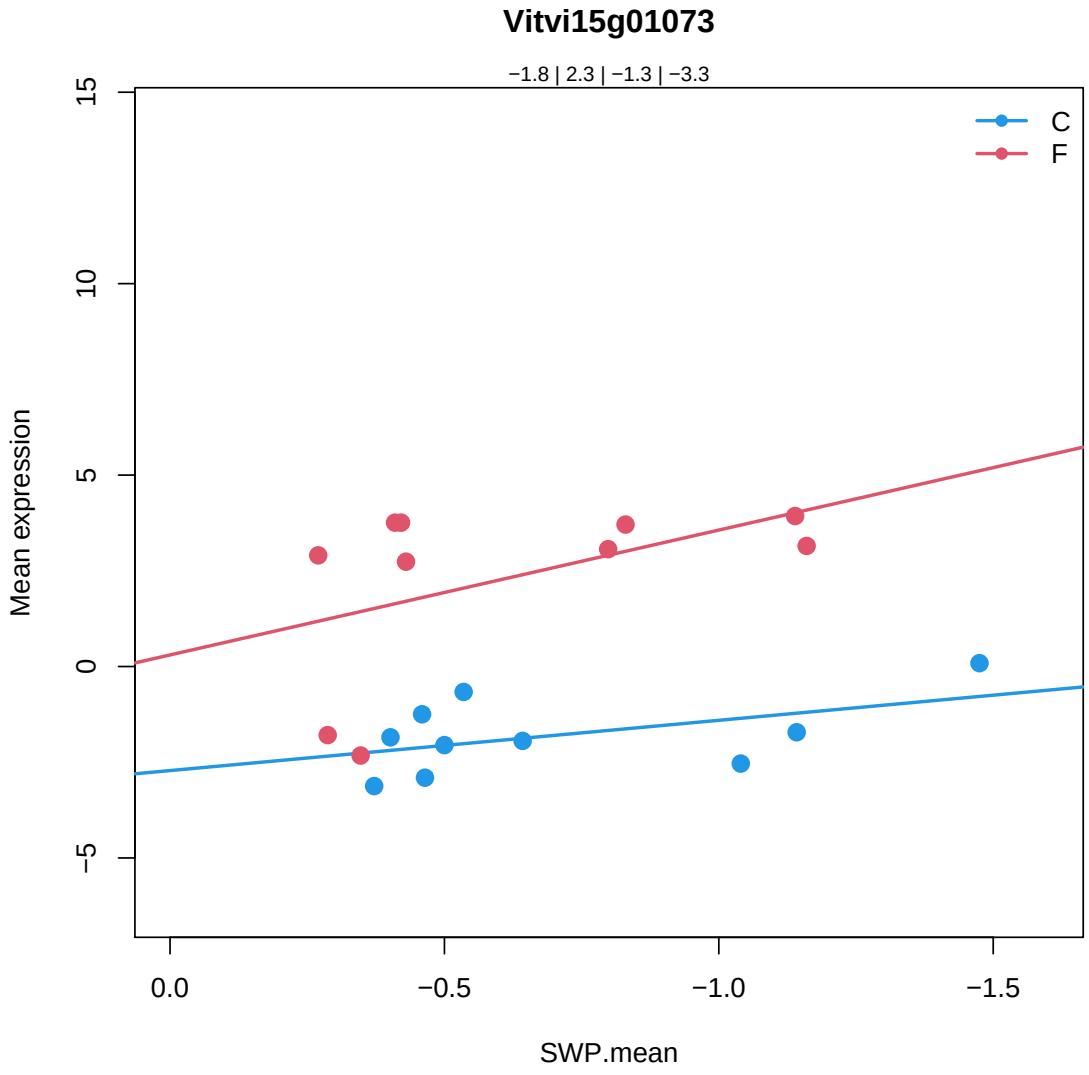
7.5.65 Vitvi15g01073: type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g01073
        16.8.1.12
        secondary metabolism.flavonoids.anthocyanins.anthocyanidin 3-O-glucosy
        UDP-Glycosyltransferase superfamily protein |
        Chr2:9593012-9594424 FORWARD LENGTH=470 |
        201606
```

Coefficients for Vitvi15g01073.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.794704	0.0007996753	***	0.000867952	***
SlopeC	-1.312703	0.316654		0.7963375	
MeanF-MeanC	4.084005	2.895334e-06	***	8.264173e-05	***
SlopeF-SlopeC	-1.948958	0.317825		0.9999488	



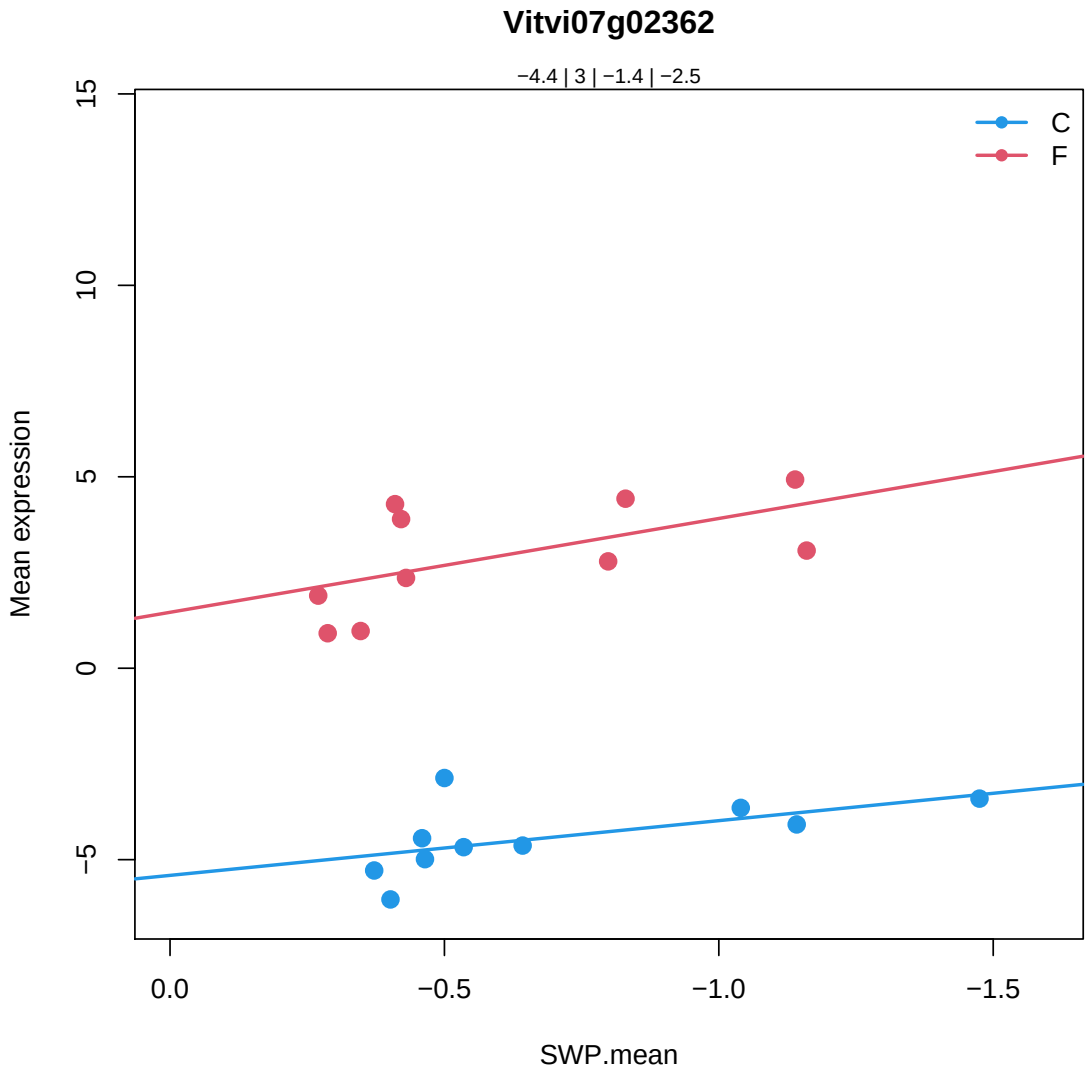
7.5.66 Vitvi07g02362: type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g02362
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi07g02362.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-4.405545	7.862665e-13	***	1.136489e-12	***
SlopeC	-1.429156	0.09515211	.	0.6053158	
MeanF-MeanC	7.359295	2.860697e-14	***	3.303238e-12	***
SlopeF-SlopeC	-1.021377	0.4111096		0.9999488	



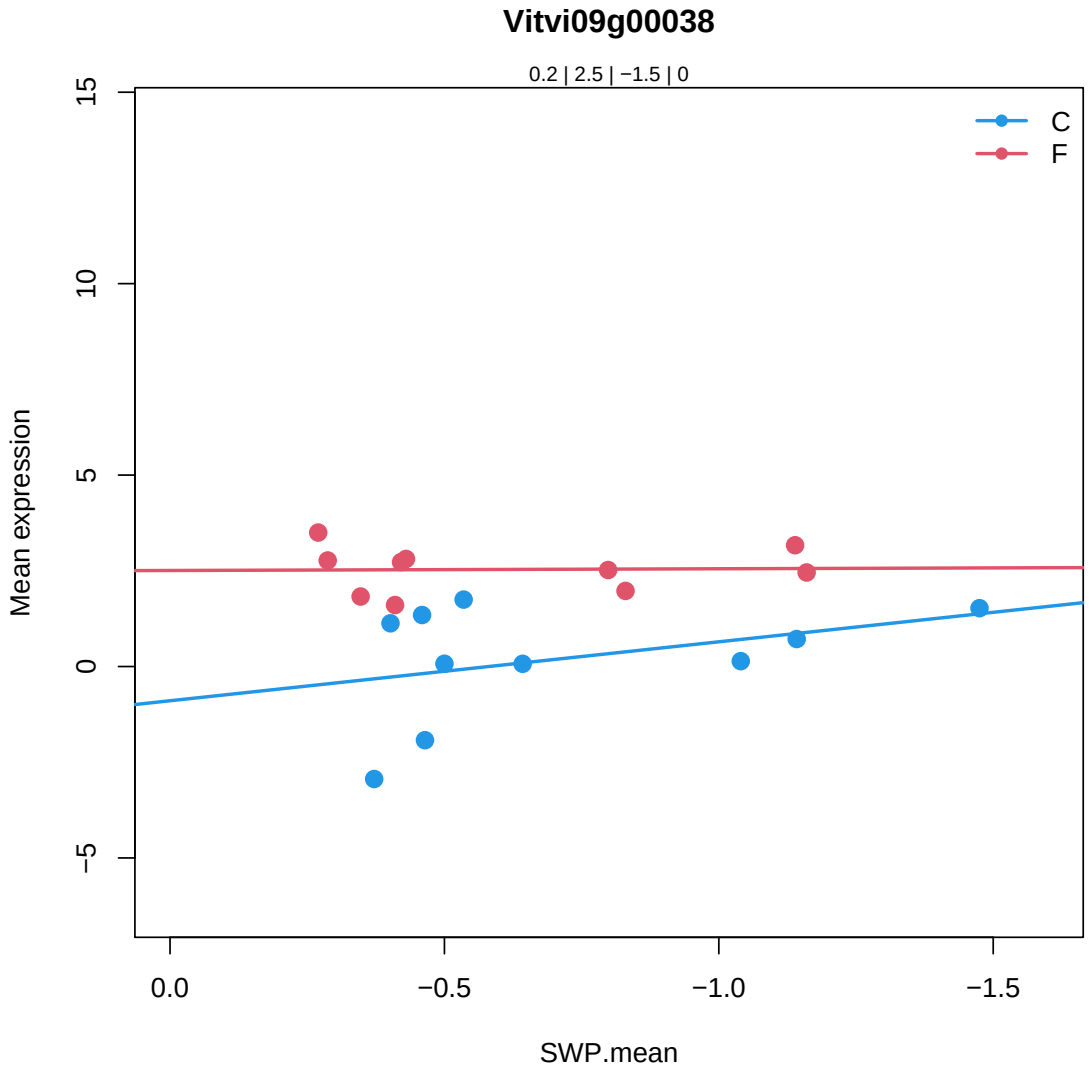
7.5.67 Vitvi09g00038: type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00038
        26.28
        misc.GDSL-motif lipase
        GDSL lipase 1 |
        Chr5:16418920-16420400 FORWARD LENGTH=374 |
        201606
```

Coefficients for Vitvi09g00038.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1883609	0.5662382		0.5720935	
SlopeC	-1.539814	0.1013475		0.6135572	
MeanF-MeanC	2.347224	4.113761e-05	***	0.0008326951	***
SlopeF-SlopeC	1.494714	0.2765741		0.9999488	



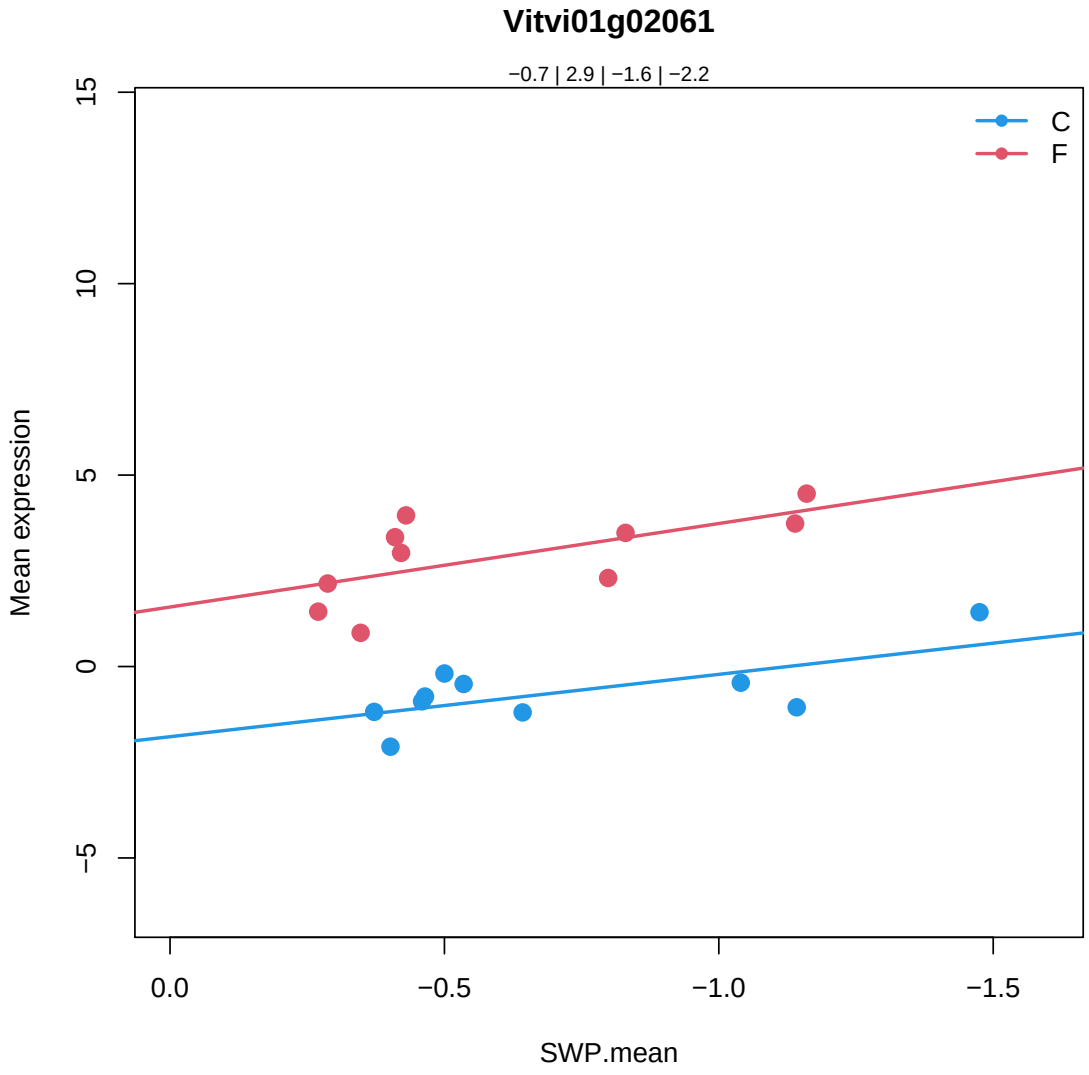
7.5.68 Vitvi01g02061: * type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g02061
        35.1.26
        not assigned.no ontology.DC1 domain containing protein
        DC1 domain-containing protein |
        Chr1:22261978-22264243 FORWARD LENGTH=578 |
        201606
```

Coefficients for Vitvi01g02061.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.6880274	0.009278023	**	0.009836925	**
SlopeC	-1.628569	0.02384104	*	0.3984486	
MeanF-MeanC	3.570542	6.641649e-10	***	4.033148e-08	***
SlopeF-SlopeC	-0.5520575	0.5853545		0.9999488	



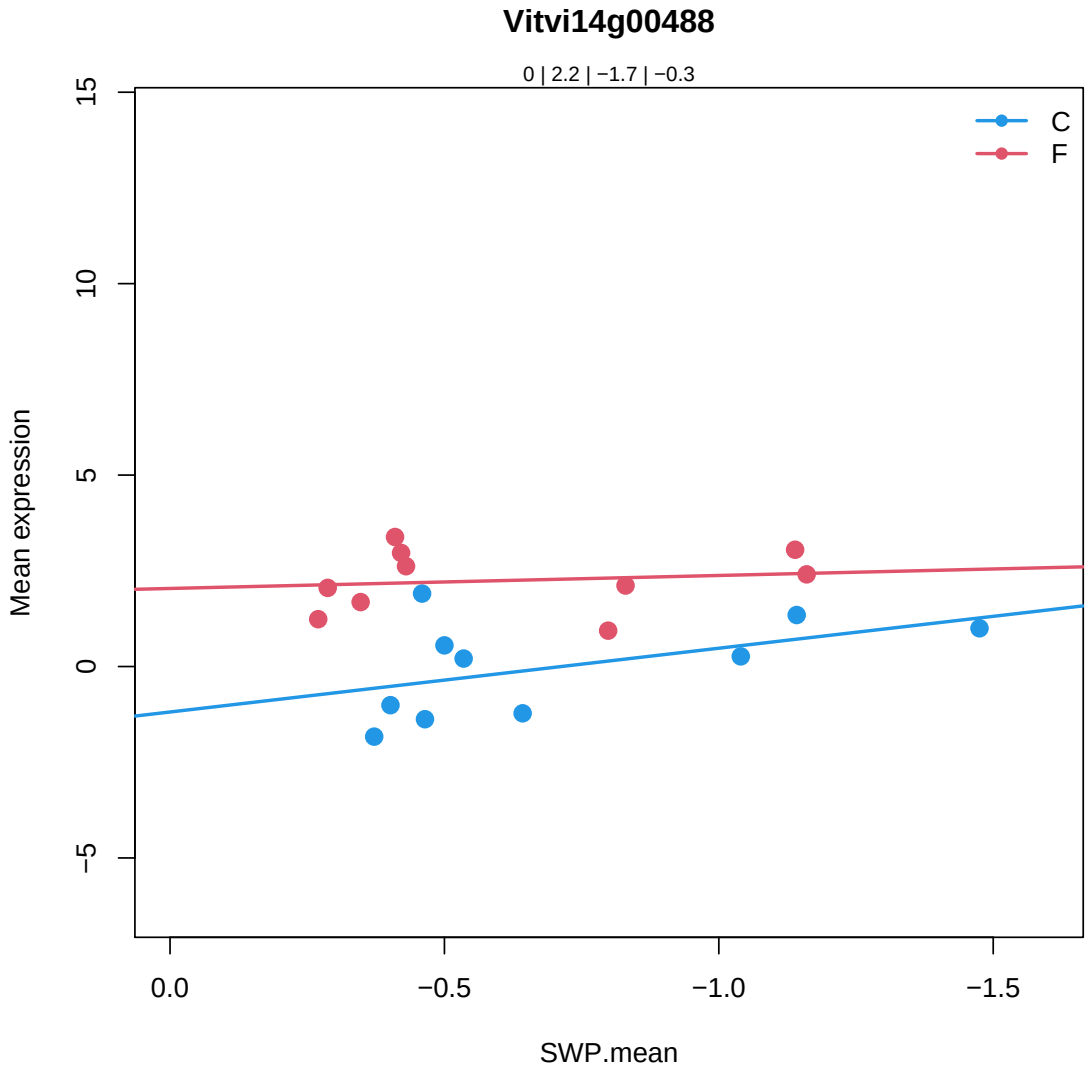
7.5.69 Vitvi14g00488: type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g00488
        20.1.7
        stress.biotic.PR-proteins
        pathogenesis-related 4 |
        Chr3:1285691-1286531 REVERSE LENGTH=212 |
        201606
```

Coefficients for Vitvi14g00488.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.01658827	0.954802		0.9555543	
SlopeC	-1.665567	0.0507581	.	0.5104439	
MeanF-MeanC	2.2616	1.619289e-05	***	0.0003838445	***
SlopeF-SlopeC	1.326057	0.2805442		0.9999488	



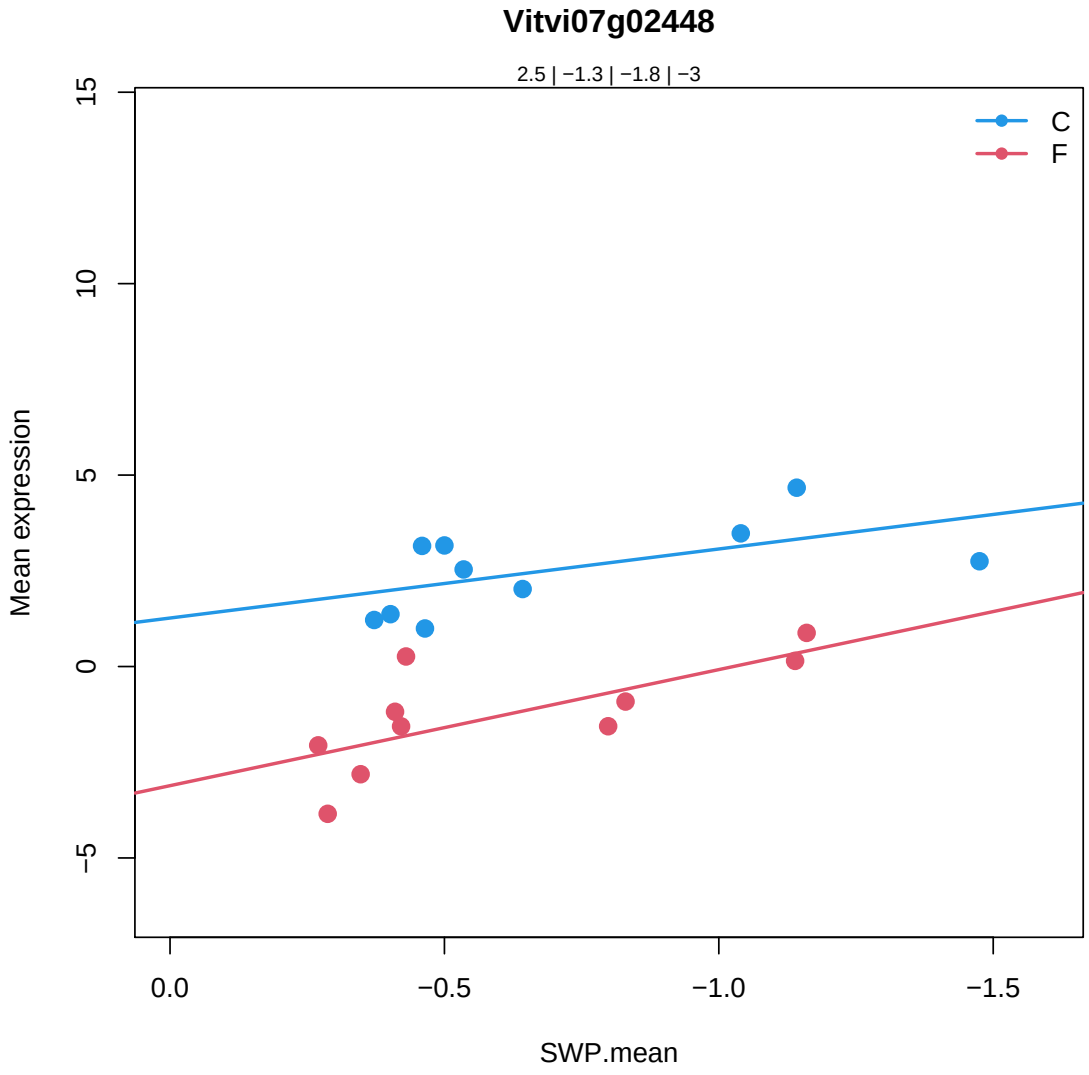
7.5.70 Vitvi07g02448: * type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g02448
        26.2
        misc.UDP glucosyl and glucoronyl transferases
        Uridine diphosphate glycosyltransferase 74E2 |
        Chr1:1703196-1704639 REVERSE LENGTH=453 |
        201606
```

Coefficients for Vitvi07g02448.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.534319	1.823511e-08	***	2.209025e-08	***
SlopeC	-1.803435	0.03725763	*	0.4620709	
MeanF-MeanC	-3.799573	6.720516e-09	***	3.41447e-07	***
SlopeF-SlopeC	-1.227884	0.3209972		0.9999488	



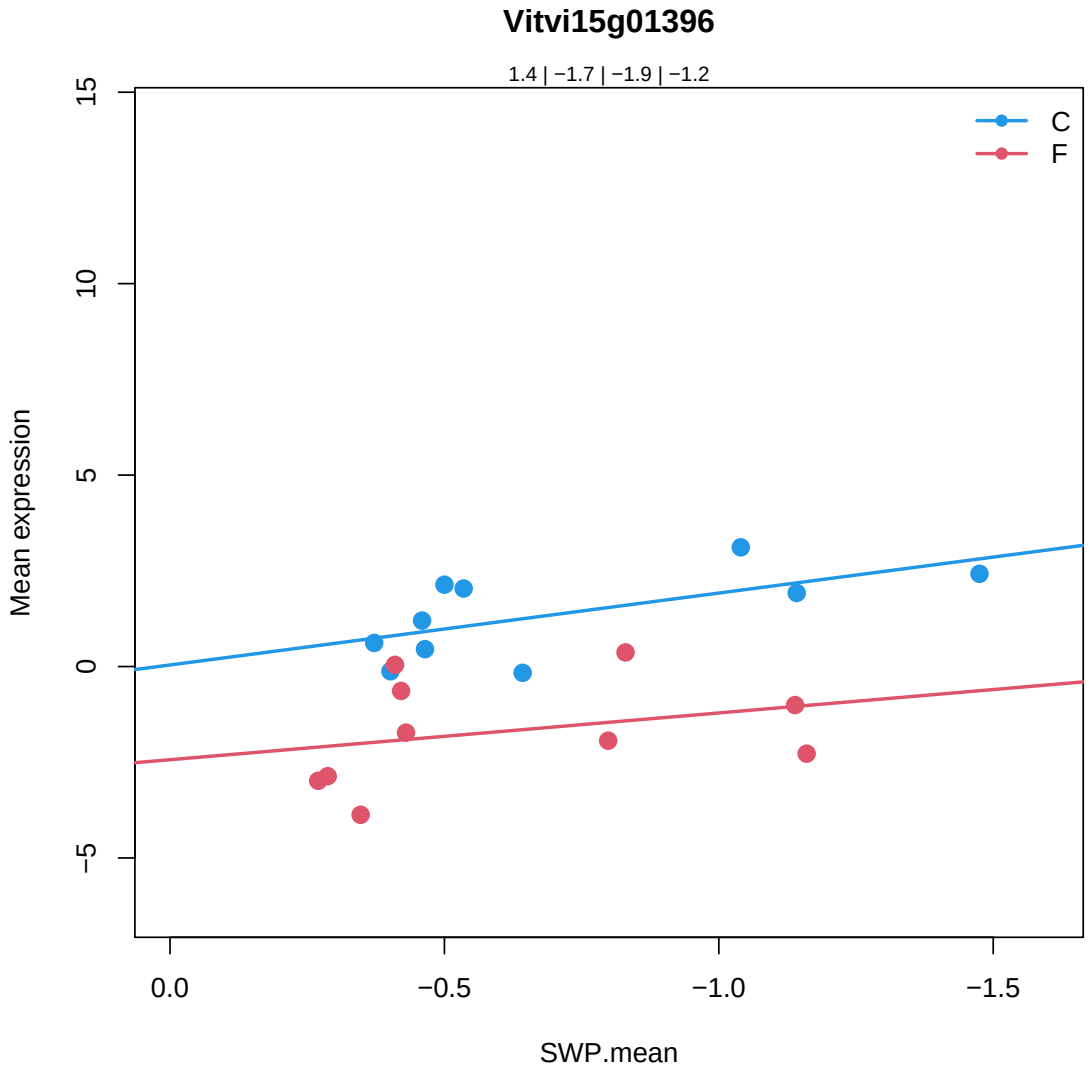
7.5.71 Vitvi15g01396: type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g01396
        35.2
        not assigned.unknown
        cation exchanger 9 |
        Chr3:4661143-4663074 REVERSE LENGTH=643 |
        201606
```

Coefficients for Vitvi15g01396.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.361299	0.000500317	***	0.0005447801	***
SlopeC	−1.878113	0.0549002	.	0.5230463	
MeanF−MeanC	−3.051023	1.790801e−06	***	5.449958e−05	***
SlopeF−SlopeC	0.6565928	0.638243		0.9999488	



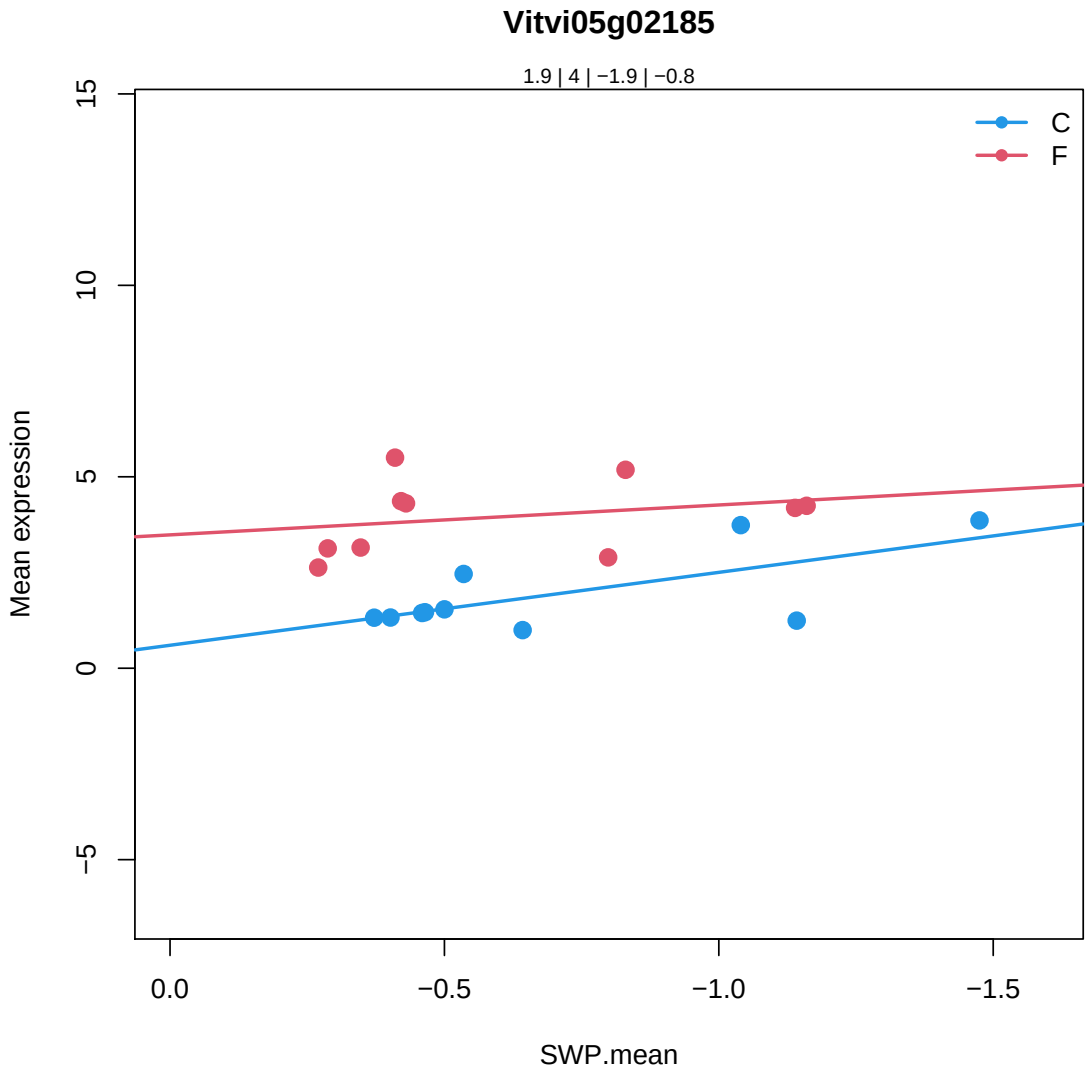
7.5.72 Vitvi05g02185: * type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g02185
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi05g02185.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.938307	2.171468e-07	***	2.552245e-07	***
SlopeC	-1.903955	0.0153545	*	0.3393703	
MeanF-MeanC	2.020325	1.737192e-05	***	0.000409247	***
SlopeF-SlopeC	1.123199	0.3081246		0.9999488	



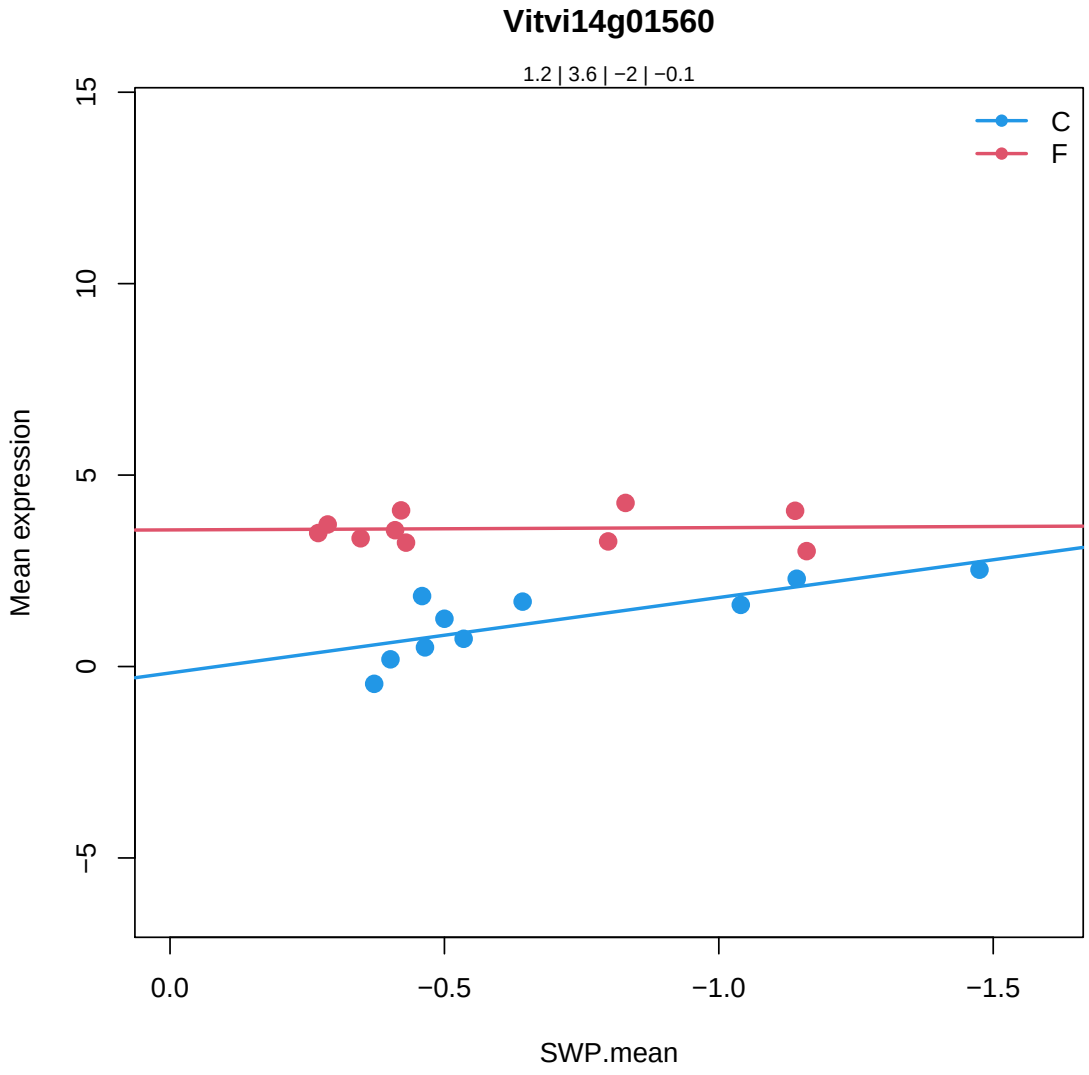
7.5.73 Vitvi14g01560: * type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01560
        34.18
        transport.unspecified anions
        chloride channel B |
        Chr3:10024147-10026921 FORWARD LENGTH=780 |
        201606
```

Coefficients for Vitvi14g01560.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.217239	3.697346e-07	***	4.316072e-07	***
SlopeC	-1.971048	0.0003913296	***	0.09467692	.
MeanF-MeanC	2.386564	1.581577e-09	***	8.765963e-08	***
SlopeF-SlopeC	1.911944	0.01226789	*	0.9999488	



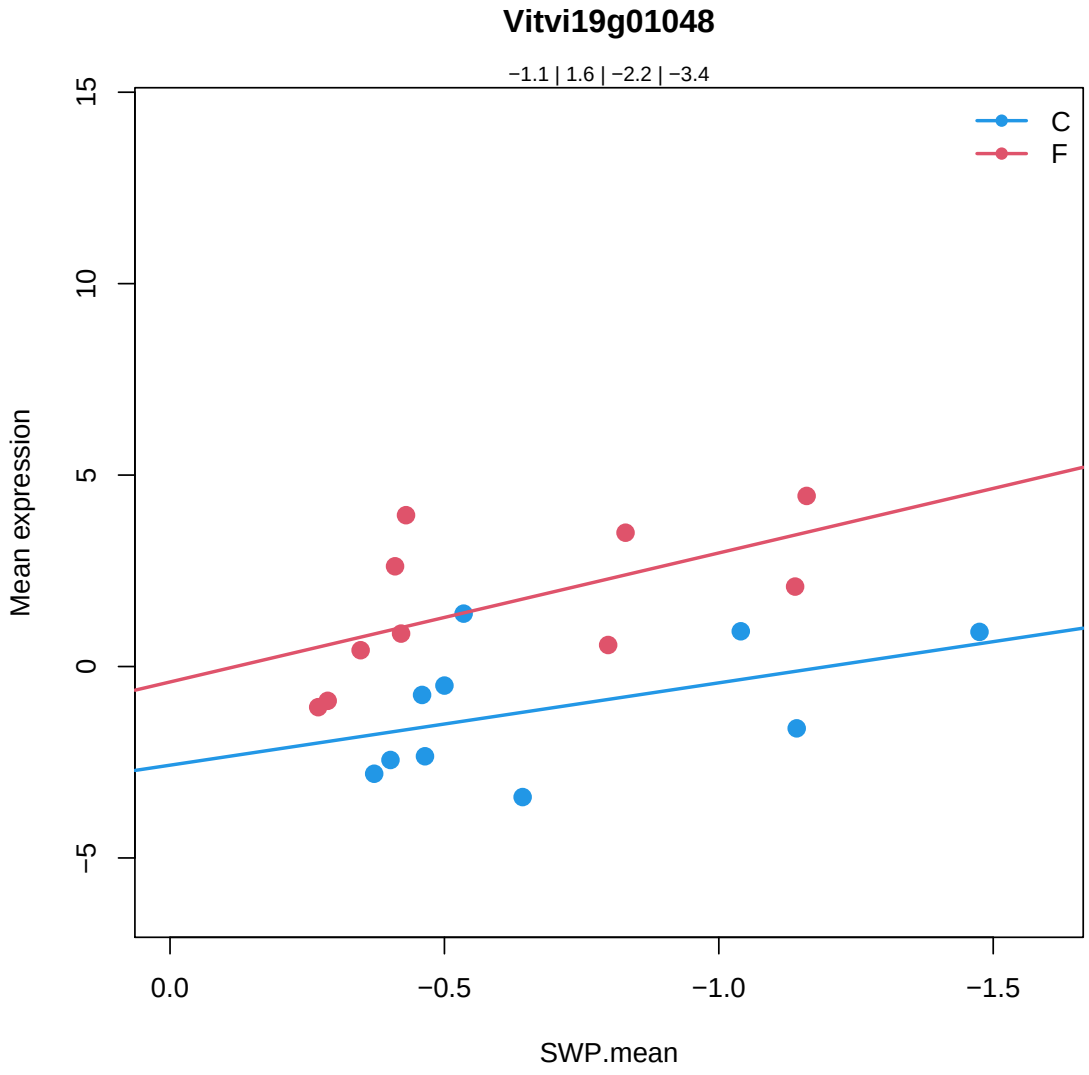
7.5.74 Vitvi19g01048: type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g01048
        26.9
        misc.glutathione S transferases
        glutathione S-transferase TAU 25 |
        Chr1:5872208-5872958 FORWARD LENGTH=221 |
        201606
```

Coefficients for Vitvi19g01048.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.064541	0.02951157	*	0.03089603	*
SlopeC	-2.150775	0.1048283		0.6181019	
MeanF-MeanC	2.714192	0.0003836245	***	0.005633145	**
SlopeF-SlopeC	-1.218795	0.5258973		0.9999488	



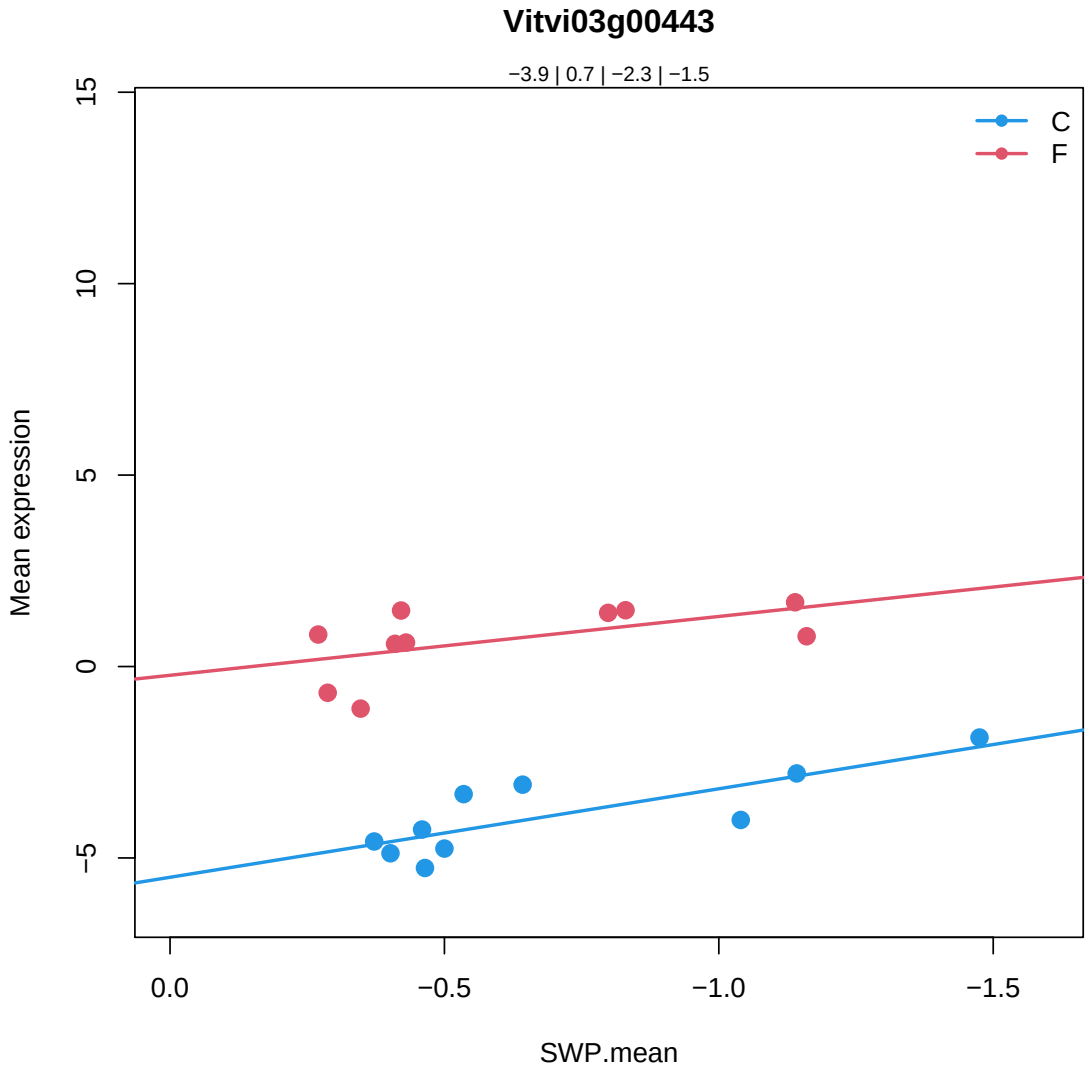
7.5.75 Vitvi03g00443: * type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00443
        26.8
        misc.nitrilases, nitrile lyases, berberine bridge enzymes, reticuline
        acetone-cyanohydrin lyase |
        Chr2:10042681-10043686 REVERSE LENGTH=187 |
        201606
```

Coefficients for Vitvi03g00443.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-3.879575	2.657365e-14	***	4.276136e-14	***
SlopeC	-2.311521	0.001013174	**	0.1271346	
MeanF-MeanC	4.586549	9.379116e-13	***	8.360029e-11	***
SlopeF-SlopeC	0.7750986	0.401223		0.9999488	



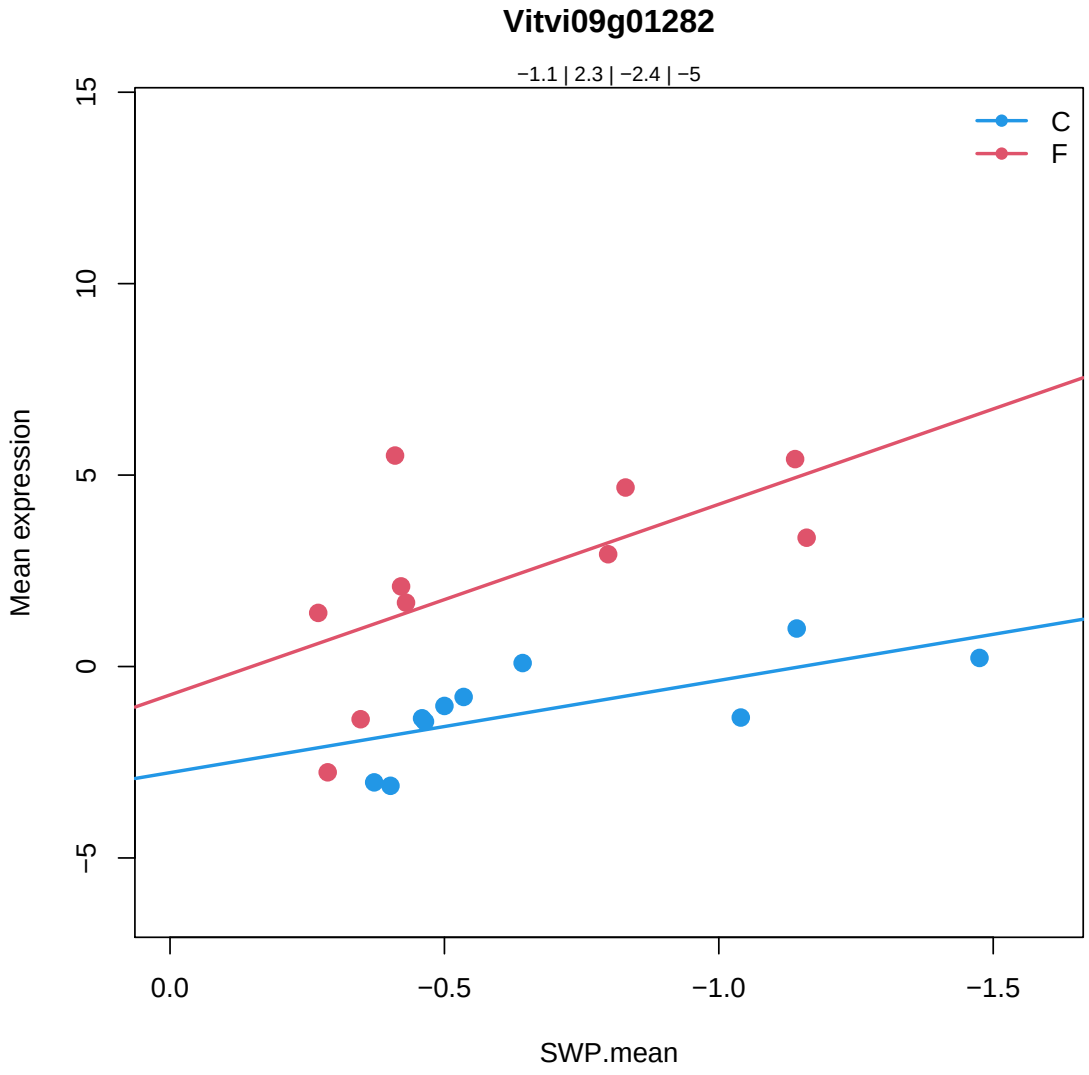
7.5.76 Vitvi09g01282: type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g01282
        26.13
        misc.acid and other phosphatases
        HAD superfamily%2C subfamily IIIB acid phosphatase |
        Chr4:12901736-12902882 REVERSE LENGTH=260 |
        201606
```

Coefficients for Vitvi09g01282.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	−1.078226	0.03754027	*	0.03919906	*
SlopeC	−2.408129	0.08927348	.	0.5953805	
MeanF−MeanC	3.37008	7.180676e−05	***	0.001351208	**
SlopeF−SlopeC	−2.570707	0.2154002		0.9999488	



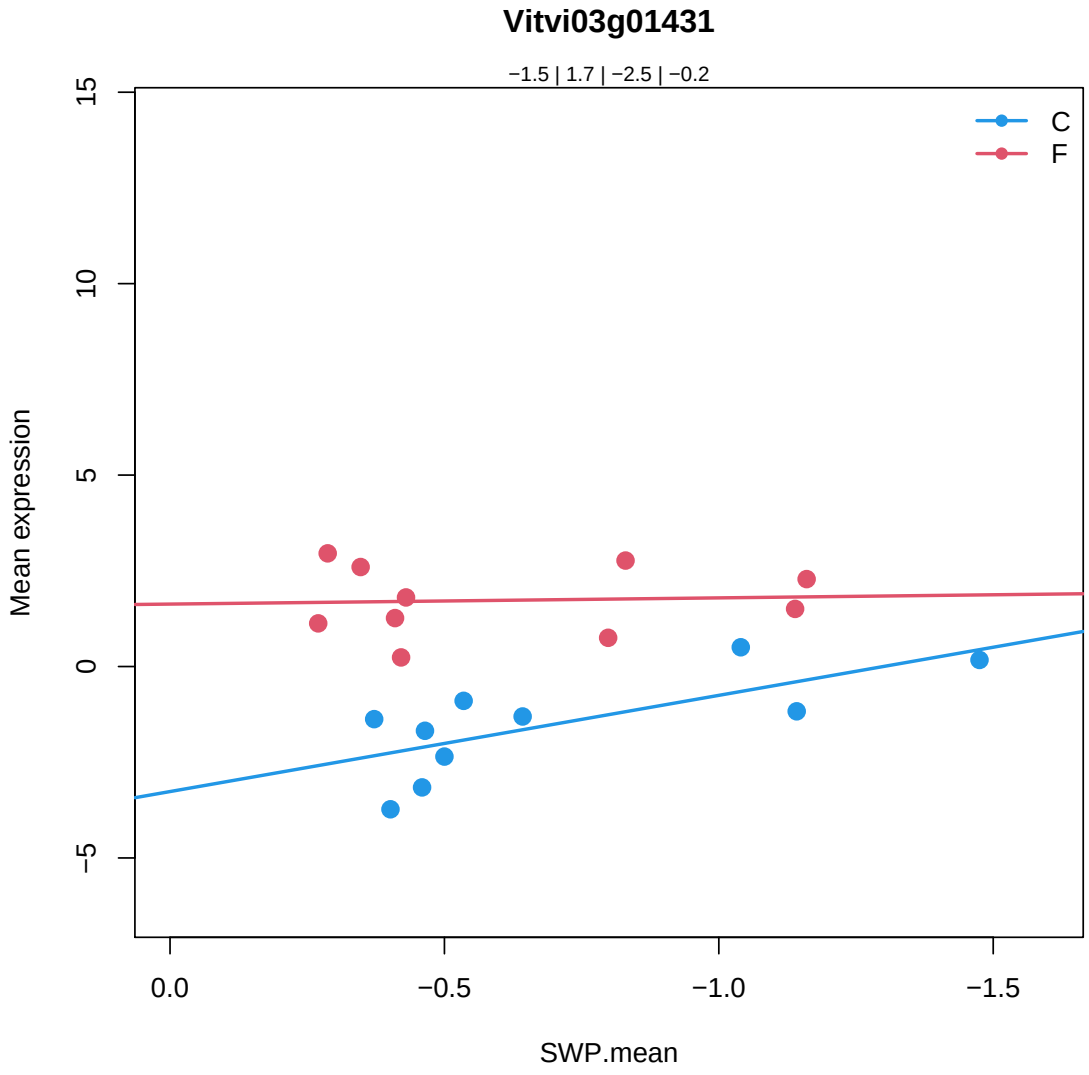
7.5.77 Vitvi03g01431: * type3 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g01431
        26.7
        misc.oxidases - copper, flavone etc
        flavin-dependent monooxygenase 1 |
        Chr1:6650656-6653053 REVERSE LENGTH=530 |
        201606
```

Coefficients for Vitvi03g01431.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.498922	2.078617e-05	***	2.330265e-05	***
SlopeC	-2.513015	0.003608732	**	0.2248659	
MeanF-MeanC	3.228153	4.224193e-08	***	1.877118e-06	***
SlopeF-SlopeC	2.351136	0.05238461	.	0.9999488	



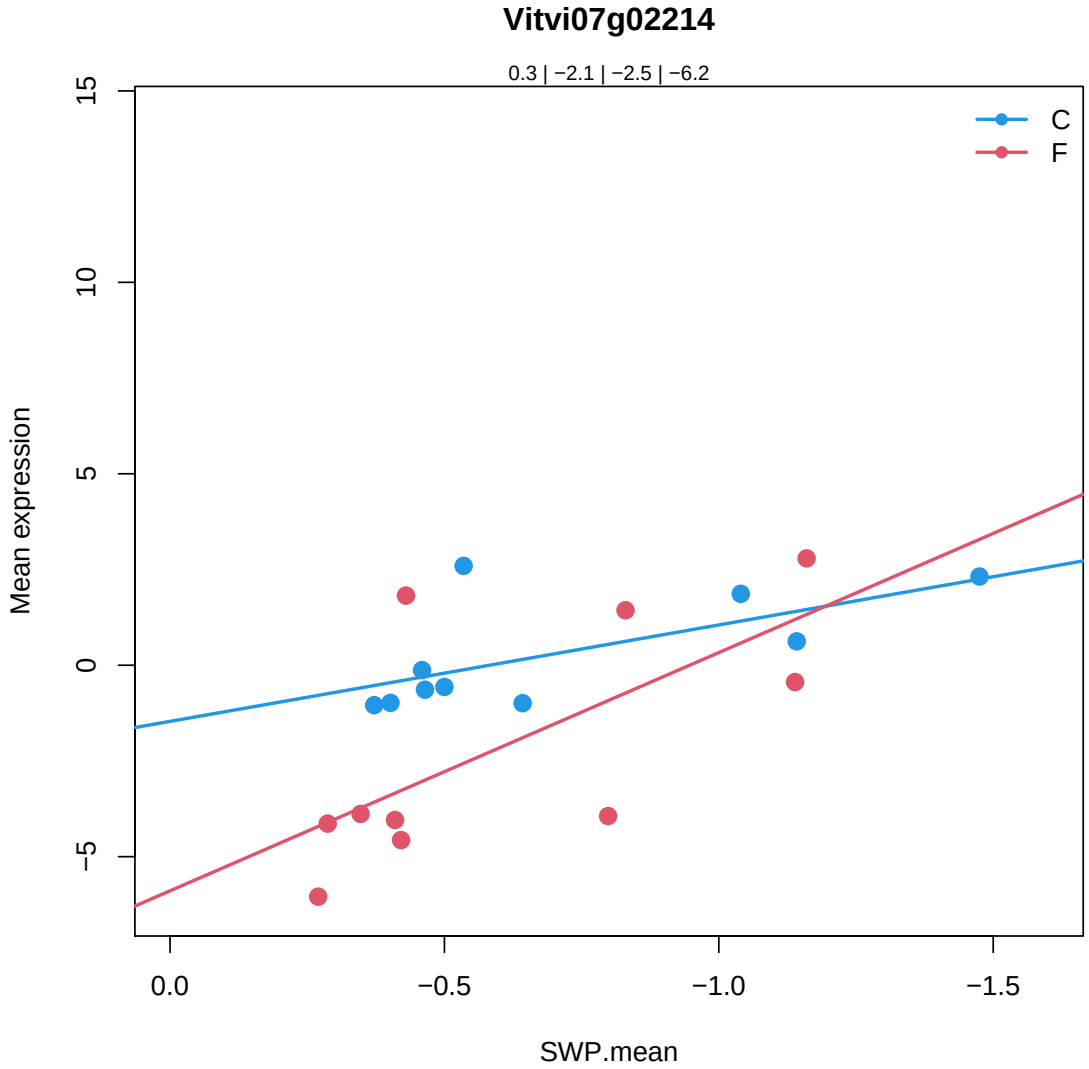
7.5.78 Vitvi07g02214: type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g02214
        35.2
        not assigned.unknown
        GATA transcription factor 22 IPR000679 Zinc finger, GATA-type
```

Coefficients for Vitvi07g02214.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3045917	0.5752195		0.5808597	
SlopeC	−2.518808	0.1052292		0.619507	
MeanF−MeanC	−2.405858	0.004444061	**	0.04150513	*
SlopeF−SlopeC	−3.70436	0.1091801		0.9999488	



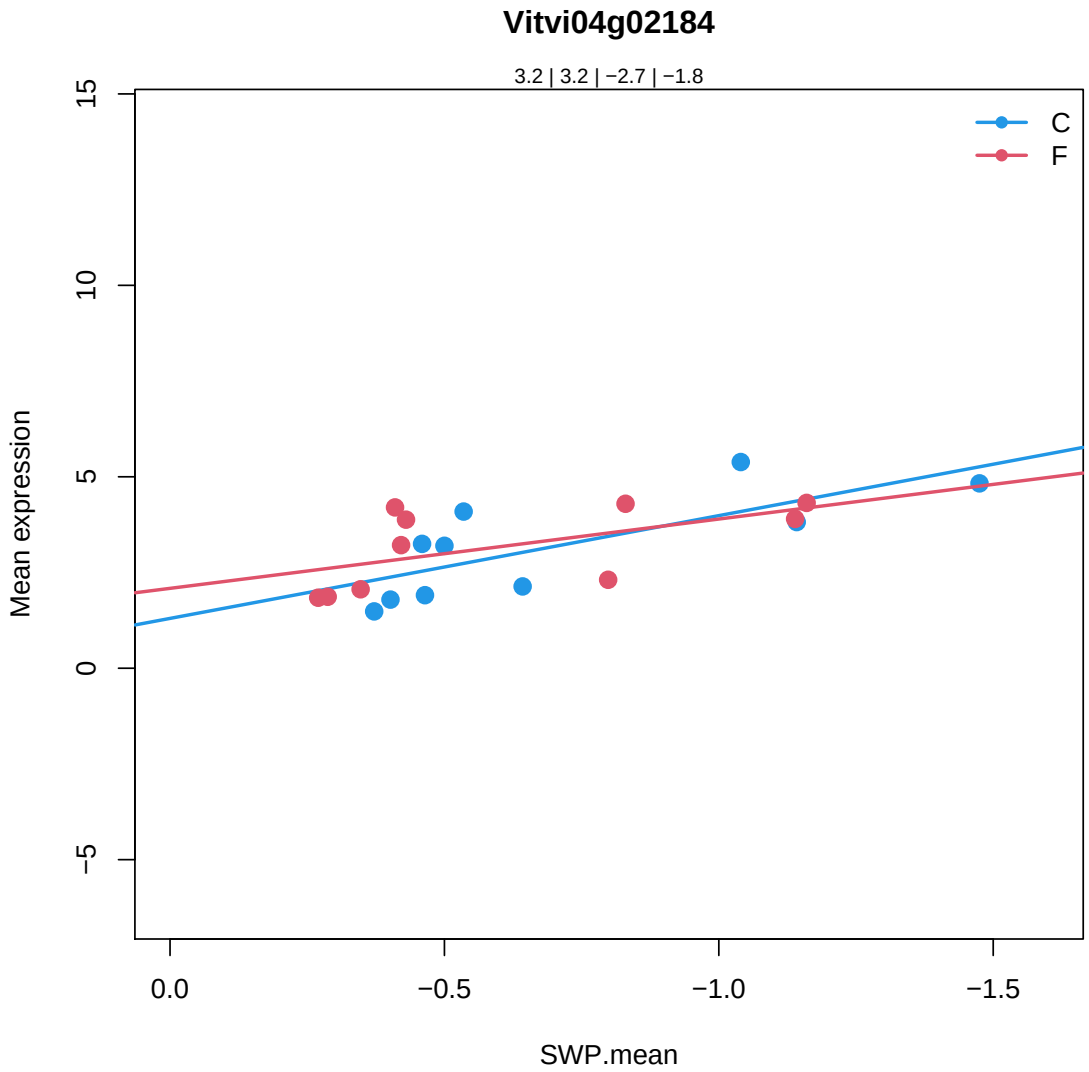
7.5.79 Vitvi04g02184: * type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g02184
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi04g02184.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.188648	4.960672e-11	***	6.572546e-11	***
SlopeC	-2.684272	0.001446058	**	0.1479249	
MeanF-MeanC	4.405018e-05	0.999907		0.9999648	
SlopeF-SlopeC	0.8740834	0.4329252		0.9999488	



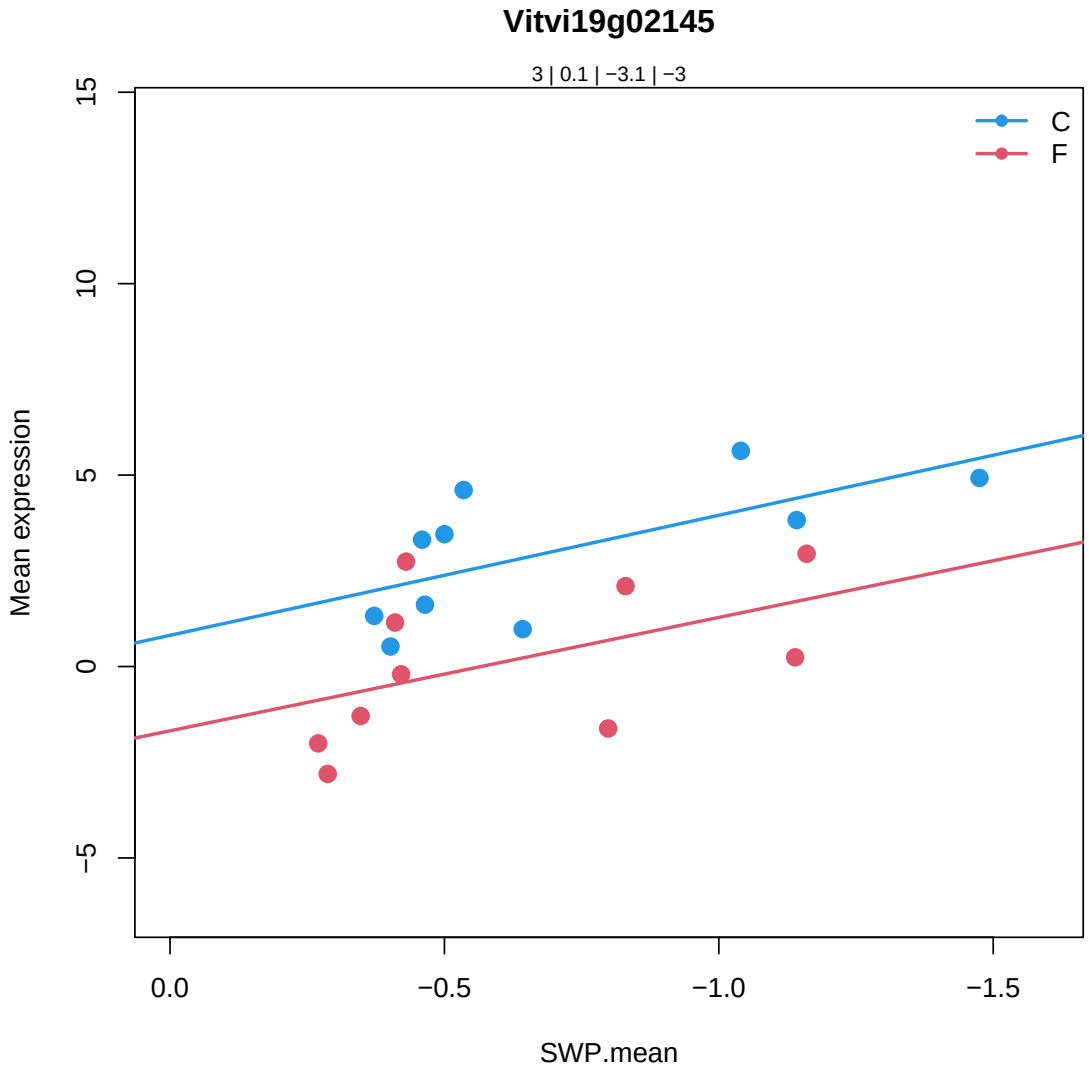
7.5.80 Vitvi19g02145: * type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g02145
        26.9
        misc.glutathione S transferases
        glutathione S-transferase TAU 25 |
        Chr1:5872208-5872958 FORWARD LENGTH=221 |
        201606
```

Coefficients for Vitvi19g02145.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.020018	1.808191e-06	***	2.075492e-06	***
SlopeC	-3.135408	0.02447993	*	0.4039715	
MeanF-MeanC	-2.894891	0.0002419684	***	0.003857827	**
SlopeF-SlopeC	0.1742035	0.9288624		0.9999488	



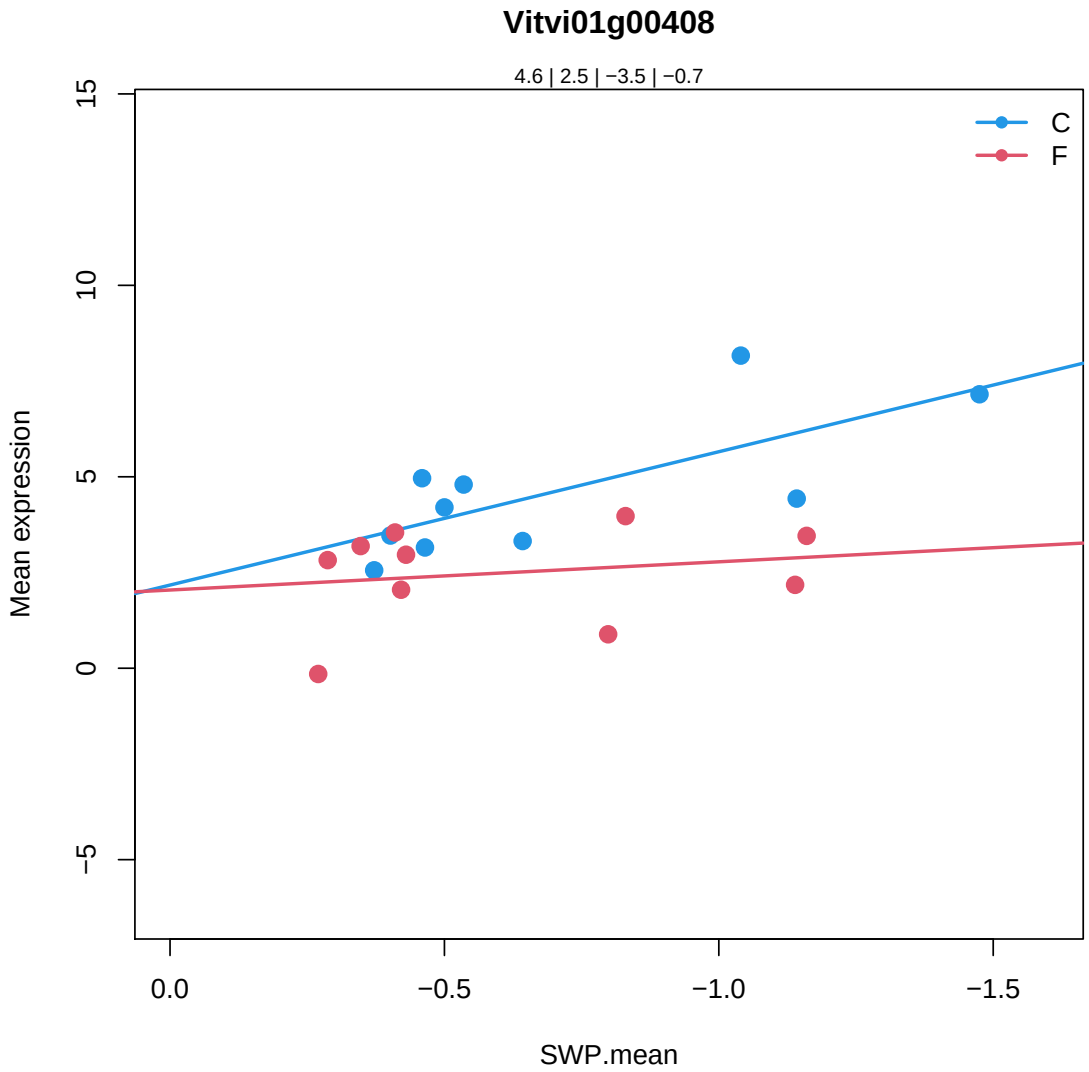
7.5.81 Vitvi01g00408: * type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00408
        20.2.1
        stress.abiotic.heat
        Chaperone protein dnaJ IPR001623 Heat shock protein DnaJ, N-terminal
```

Coefficients for Vitvi01g00408.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.620739	2.147964e-11	***	2.890884e-11	***
SlopeC	-3.482485	0.002526958	**	0.1902008	
MeanF-MeanC	-2.129225	0.0004797738	***	0.006808857	**
SlopeF-SlopeC	2.745564	0.08420911	.	0.9999488	



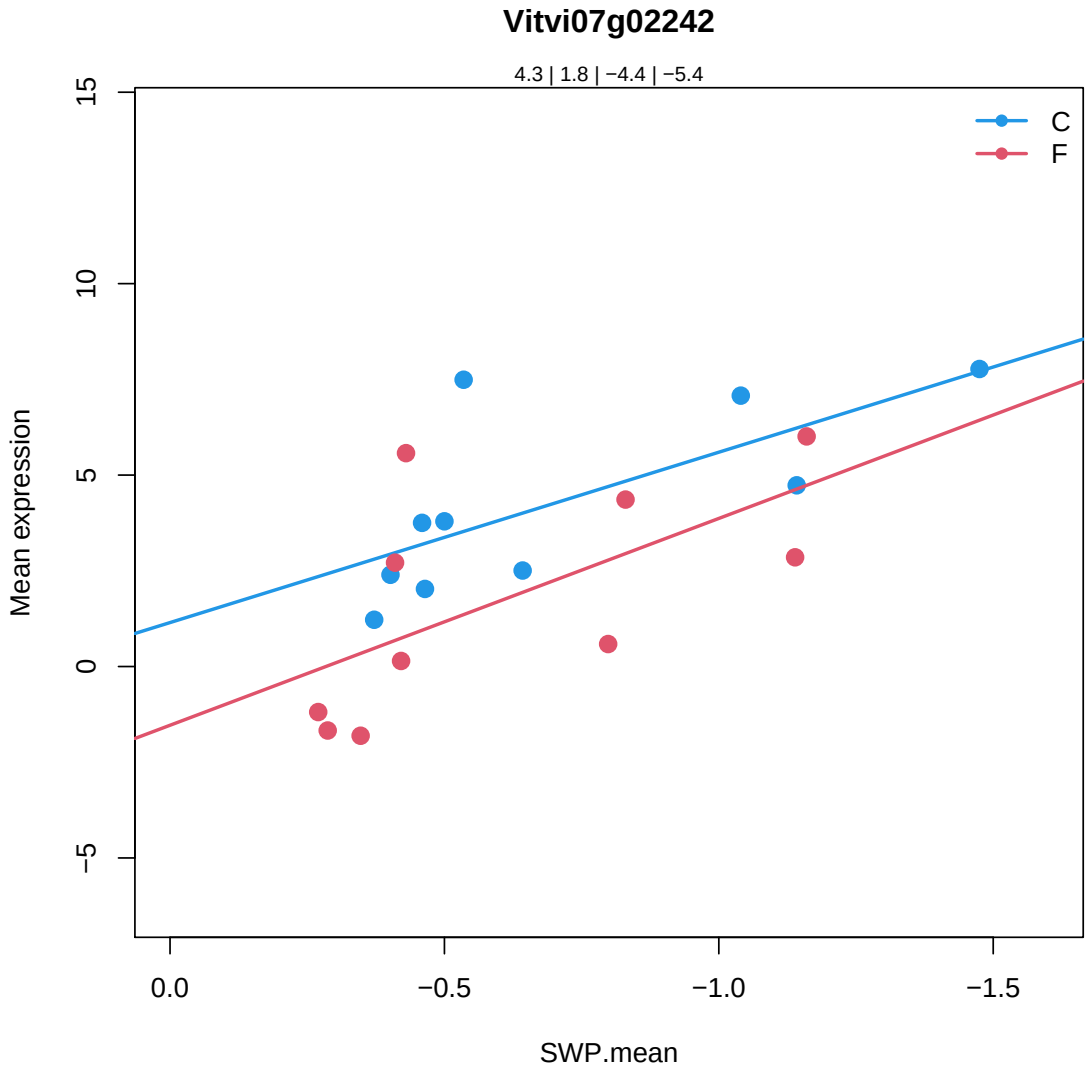
7.5.82 Vitvi07g02242: * type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g02242
        3.1.1.1
        minor CHO metabolism.raffinose family.galactinol synthases.known
        galactinol synthase 1 |
        Chr2:19369049-19370372 REVERSE LENGTH=344 |
        201606
```

Coefficients for Vitvi07g02242.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.276297	3.725657e-07	***	4.348787e-07	***
SlopeC	-4.449677	0.01340344	*	0.3305597	
MeanF-MeanC	-2.519255	0.00668982	**	0.05649099	.
SlopeF-SlopeC	-0.9519606	0.7022784		0.9999488	



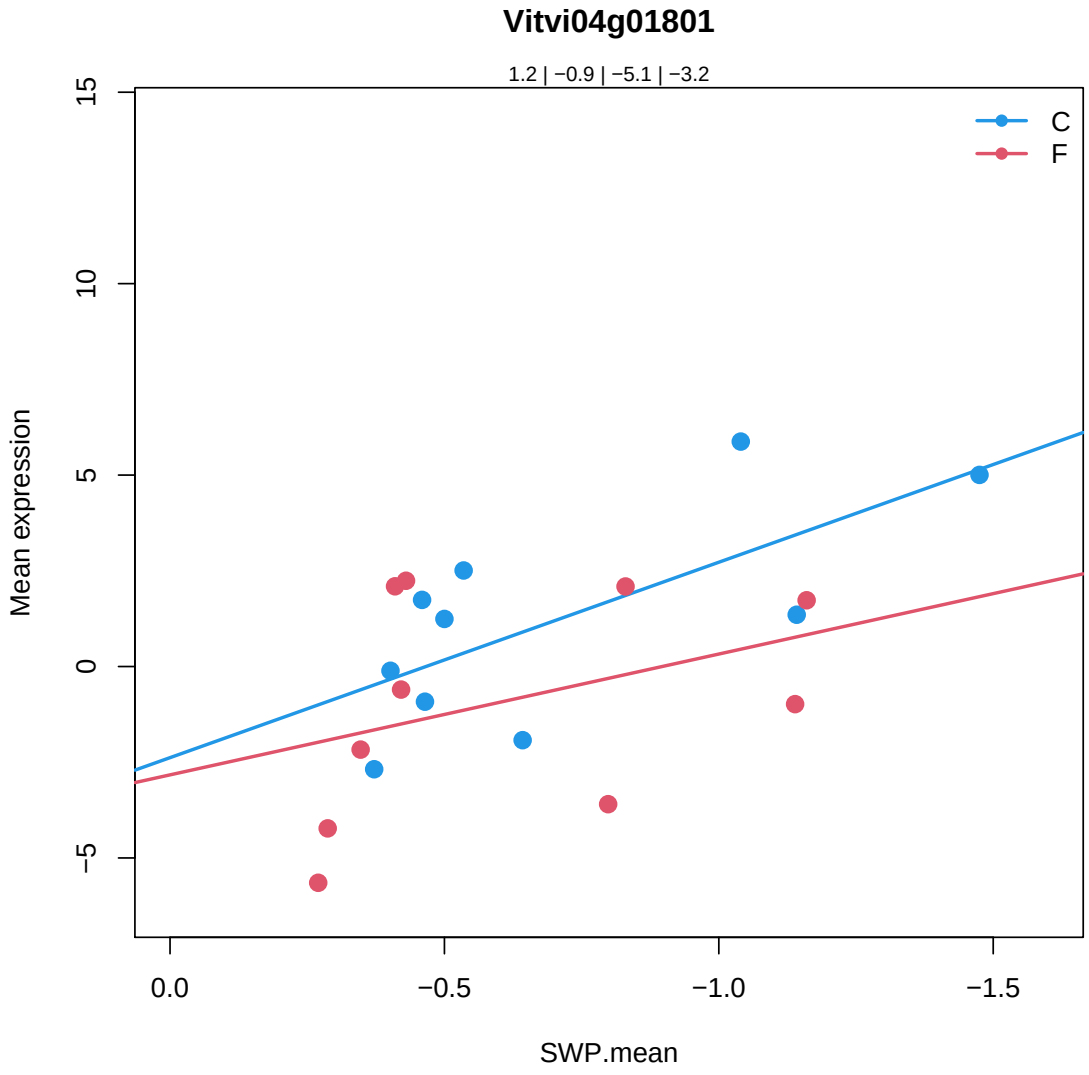
7.5.83 Vitvi04g01801: * type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01801
        20.2.1
        stress.abiotic.heat
        17.6 kDa class II heat shock protein |
        Chr5:3882409-3882876 REVERSE LENGTH=155 |
        201606
```

Coefficients for Vitvi04g01801.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.208586	0.09664858	.	0.09995371	.
SlopeC	-5.104125	0.01523524	*	0.3393703	
MeanF-MeanC	-2.115849	0.04303485	*	0.2168388	
SlopeF-SlopeC	1.948595	0.5059525		0.9999488	



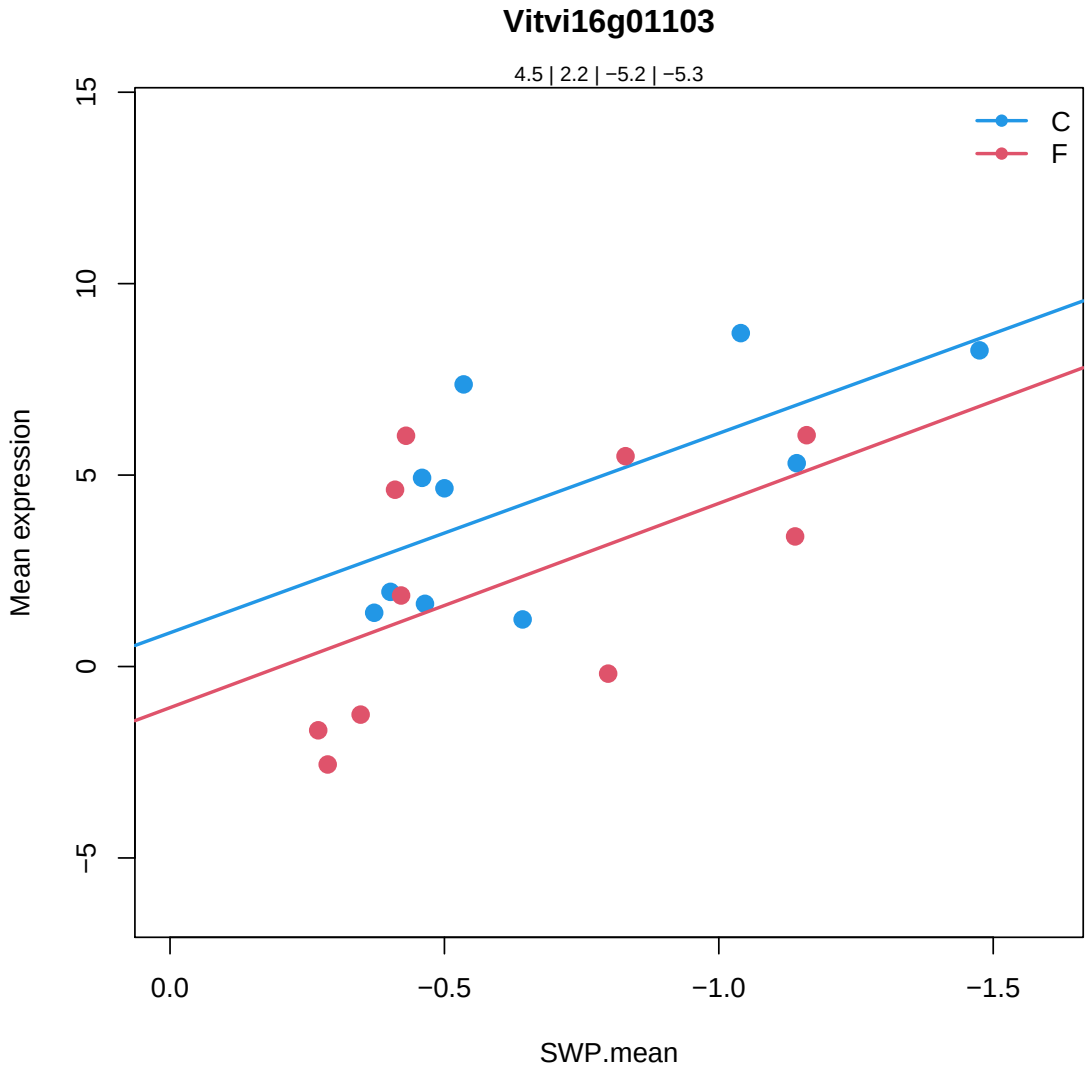
7.5.84 Vitvi16g01103: * type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01103
        20.2.1
        stress.abiotic.heat
        heat shock-like protein |
        Chr5:21352557-21355147 FORWARD LENGTH=700 |
        201606
```

Coefficients for Vitvi16g01103.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.544681	3.332247e-06	***	3.801939e-06	***
SlopeC	-5.209495	0.01806874	*	0.3612388	
MeanF-MeanC	-2.368196	0.03229181	*	0.1781367	
SlopeF-SlopeC	-0.1260899	0.9671792		0.9999488	



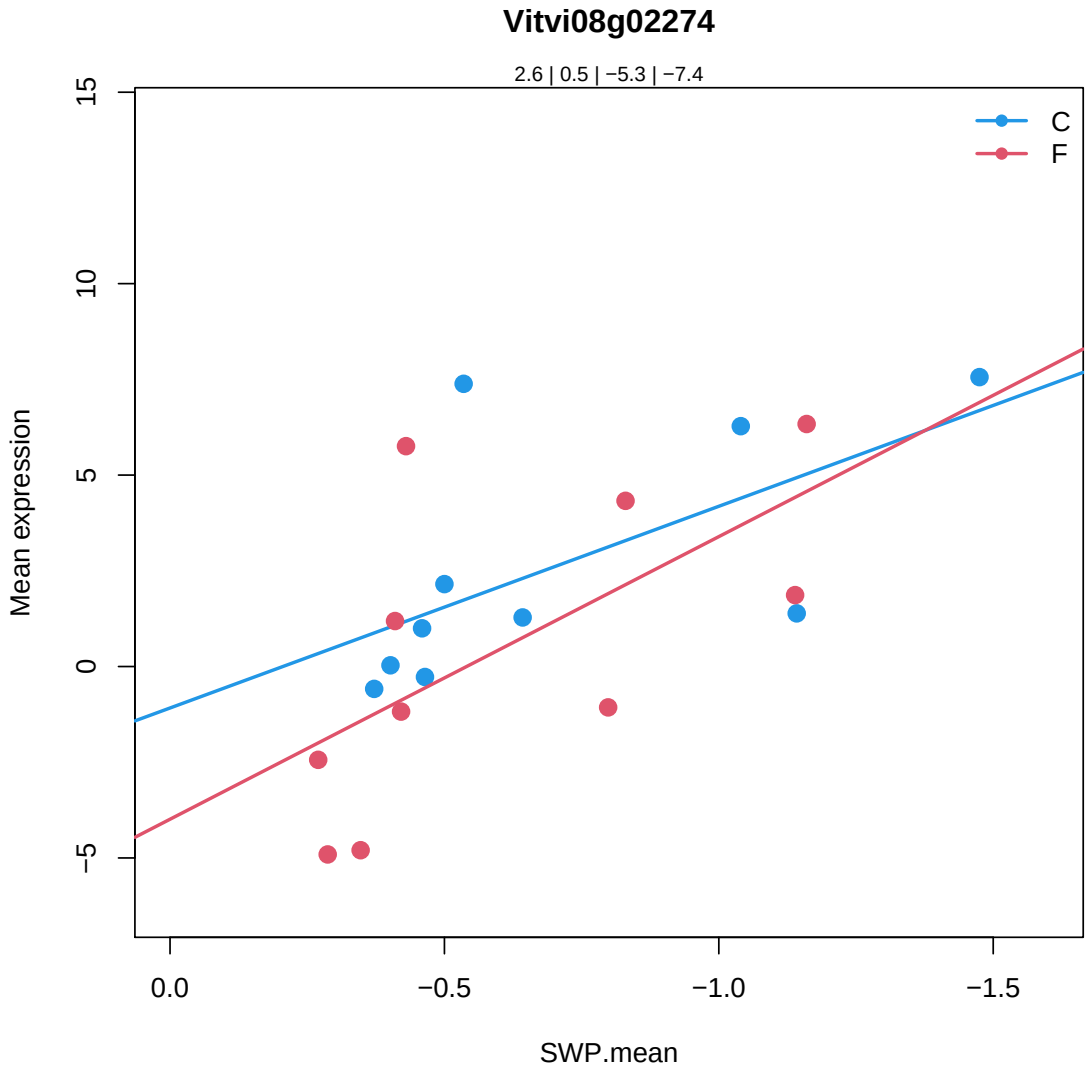
7.5.85 Vitvi08g02274: * type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g02274
        35.2
        not assigned.unknown
        plant/protein |
        Chr3:3091225-3091674 REVERSE LENGTH=149 |
        201606
```

Coefficients for Vitvi08g02274.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.621184	0.004851113	**	0.005175743	**
SlopeC	-5.267913	0.03371344	*	0.4433084	
MeanF-MeanC	-2.113039	0.08753536	.	0.337434	
SlopeF-SlopeC	-2.113051	0.5473344		0.9999488	



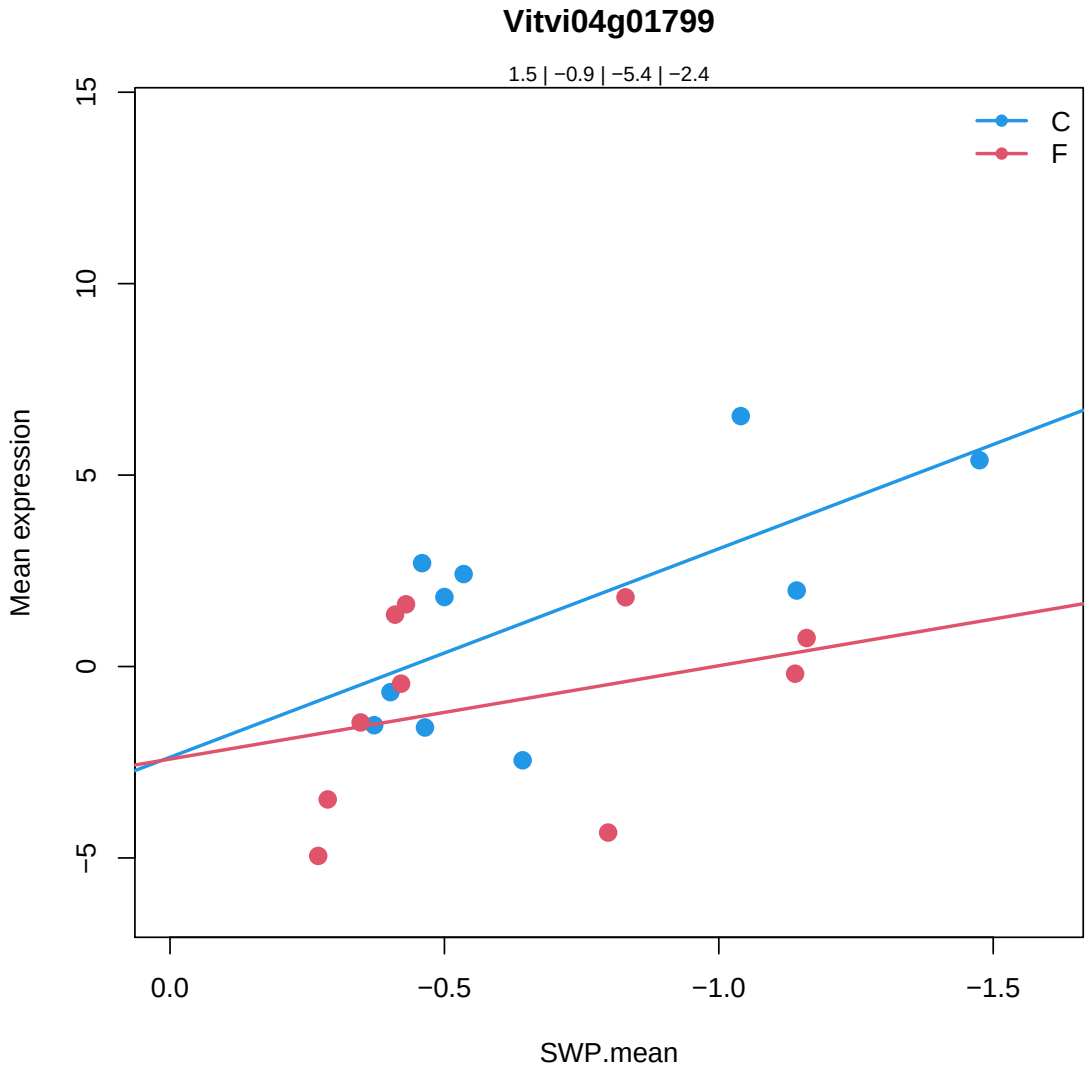
7.5.86 Vitvi04g01799: * type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01799
        20.2.1
        stress.abiotic.heat
        17.6 kDa class II heat shock protein |
        Chr5:3882409-3882876 REVERSE LENGTH=155 |
        201606
```

Coefficients for Vitvi04g01799.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.459784	0.04054411	*	0.04232114	*
SlopeC	-5.446372	0.008008975	**	0.2832315	
MeanF-MeanC	-2.391652	0.01948465	*	0.1236922	
SlopeF-SlopeC	3.008905	0.2899314		0.9999488	



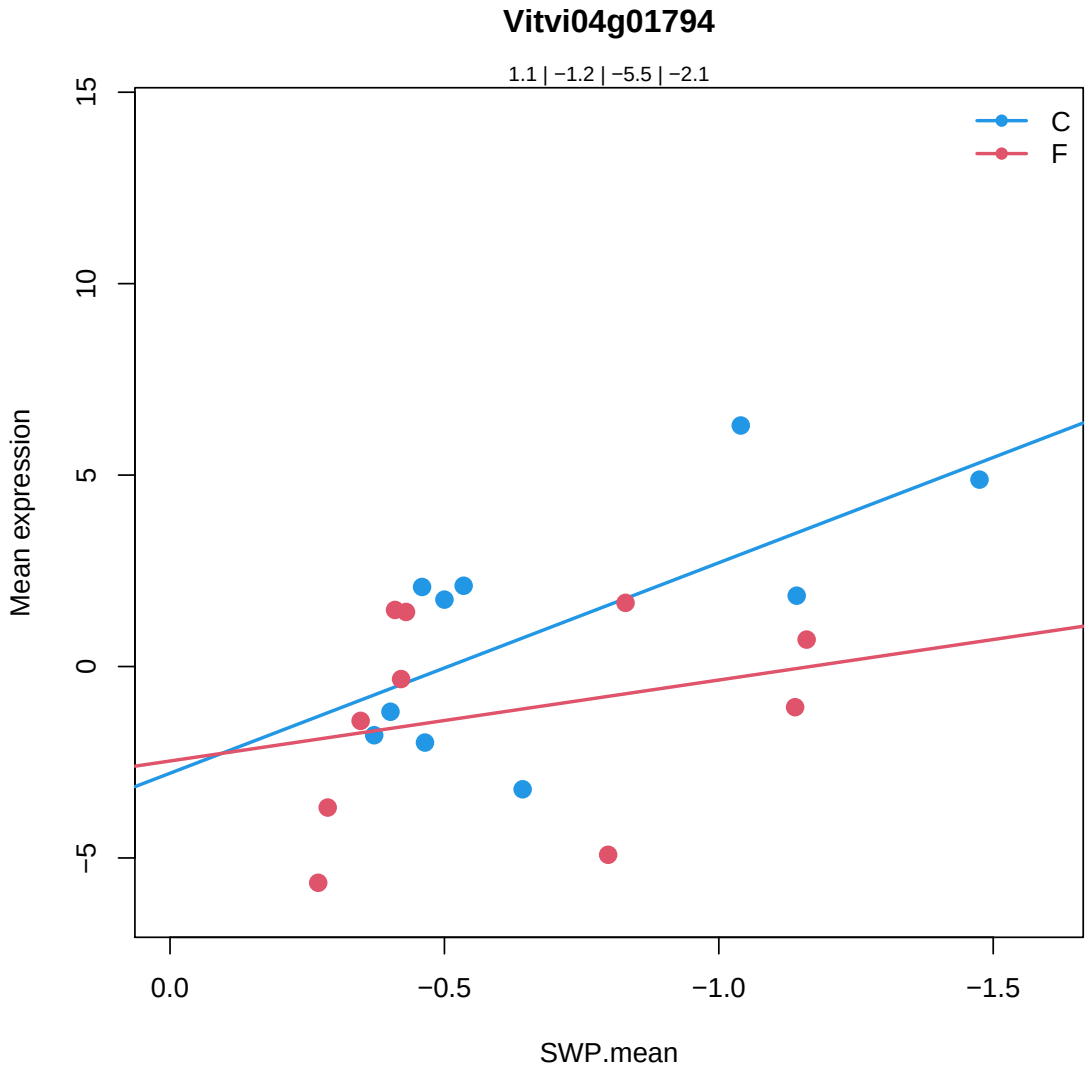
7.5.87 Vitvi04g01794: * type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01794
        20.2.1
        stress.abiotic.heat
        17.6 kDa class II heat shock protein |
        Chr5:3882409-3882876 REVERSE LENGTH=155 |
        201606
```

Coefficients for Vitvi04g01794.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.079134	0.1462899		0.1505876	
SlopeC	-5.497568	0.01158549	*	0.318473	
MeanF-MeanC	-2.25819	0.03651267	*	0.192703	
SlopeF-SlopeC	3.382727	0.2663928		0.9999488	



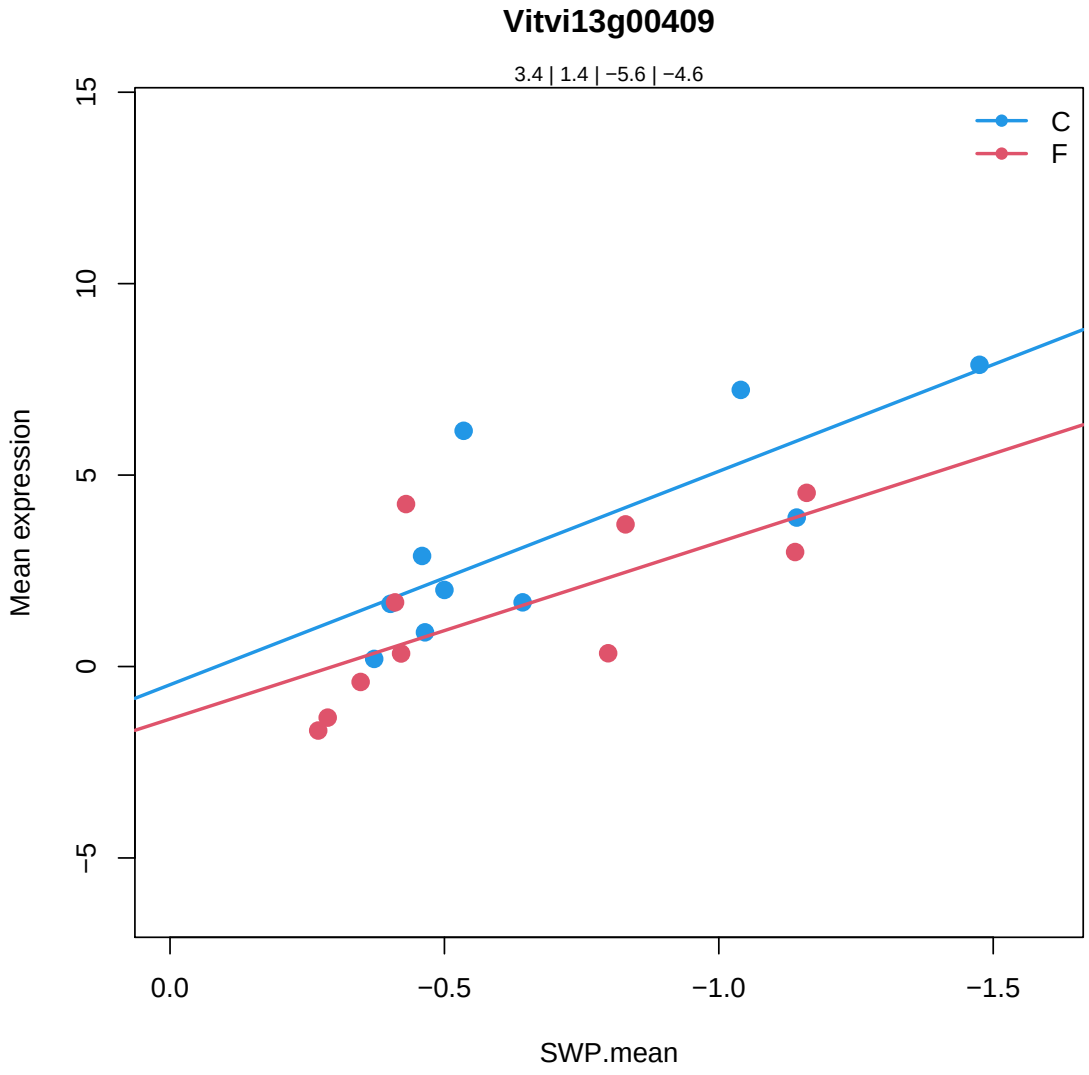
7.5.88 Vitvi13g00409: * type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00409
        35.2
        not assigned.unknown
        heat shock protein 18.2 |
        Chr5:24062632-24063117 FORWARD LENGTH=161 |
        201606
```

Coefficients for Vitvi13g00409.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.444287	7.91282e-07	***	9.154942e-07	***
SlopeC	-5.574561	0.0006440829	***	0.1015345	
MeanF-MeanC	-2.001179	0.01018303	*	0.0770272	.
SlopeF-SlopeC	0.9551048	0.650661		0.9999488	



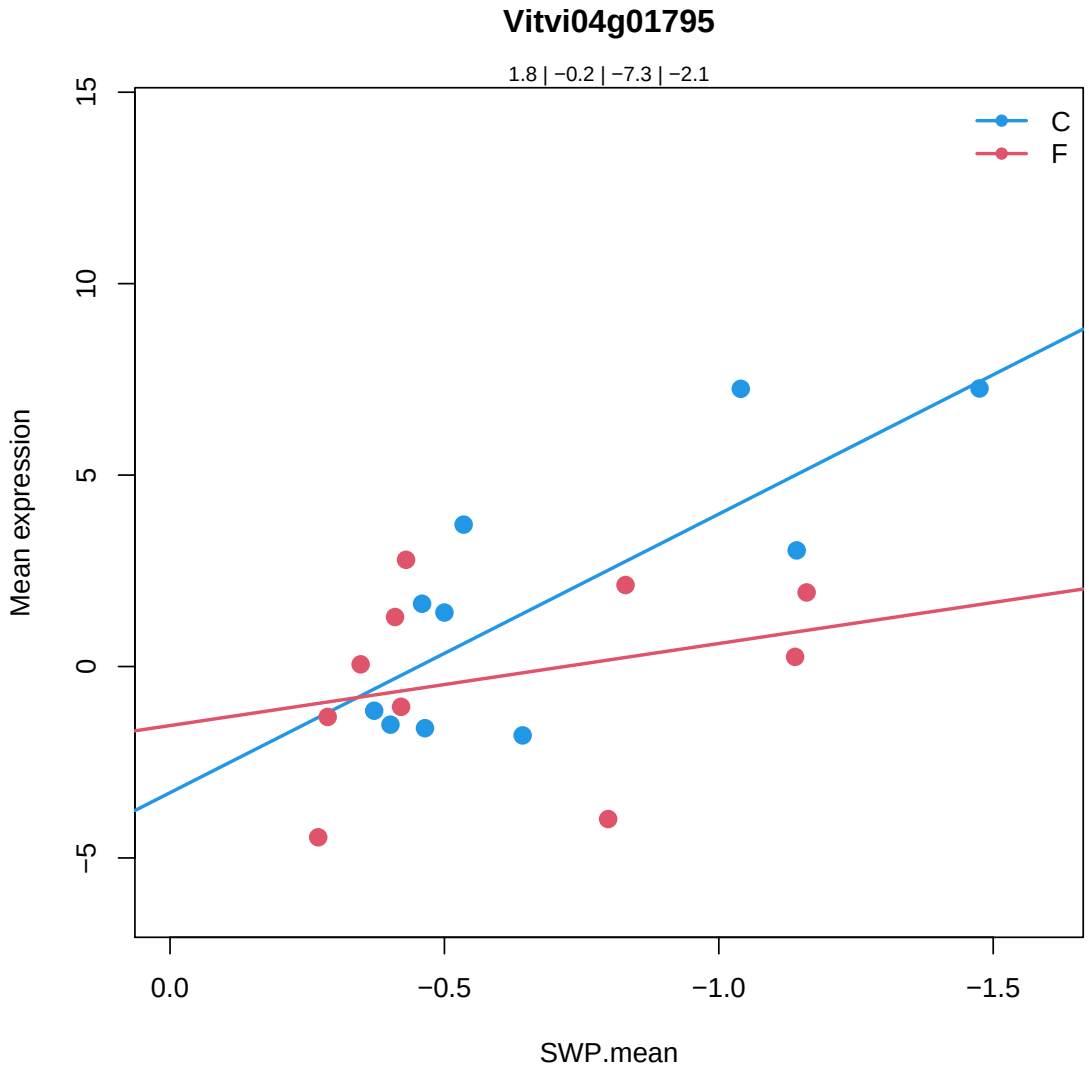
7.5.89 Vitvi04g01795: * type2 | type4

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01795
        35.2
        not assigned.unknown
        17.6 kDa class II heat shock protein |
        Chr5:3882409-3882876 REVERSE LENGTH=155 |
        201606
```

Coefficients for Vitvi04g01795.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.821988	0.01144052	*	0.01210359	*
SlopeC	−7.277261	0.0006740302	***	0.1037734	
MeanF−MeanC	−2.058336	0.03814072	*	0.1995898	
SlopeF−SlopeC	5.133591	0.07347637	.	0.9999488	



7.6 type5

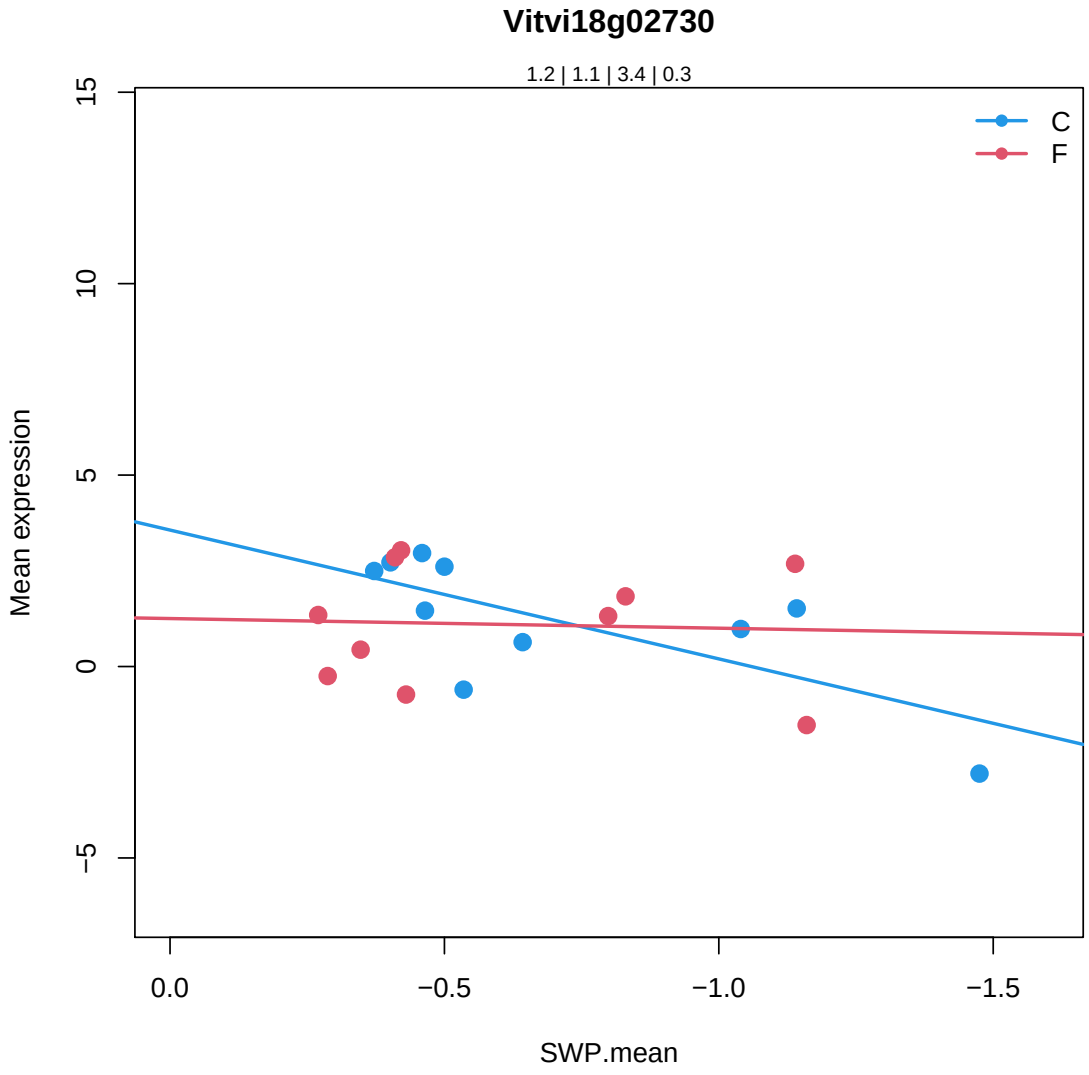
7.6.1 Vitvi18g02730: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02730
        35.2
        not assigned.unknown
        calcium uniporter (DUF607) |
        Chr5:17062507-17063934 FORWARD LENGTH=293 |
        201606
```

Coefficients for Vitvi18g02730.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.197709	0.009522617	**	0.01009064	*
SlopeC	3.364707	0.008940607	**	0.2903326	
MeanF-MeanC	-0.09823464	0.8703899		0.9660555	
SlopeF-SlopeC	-3.112693	0.08808841	.	0.9999488	



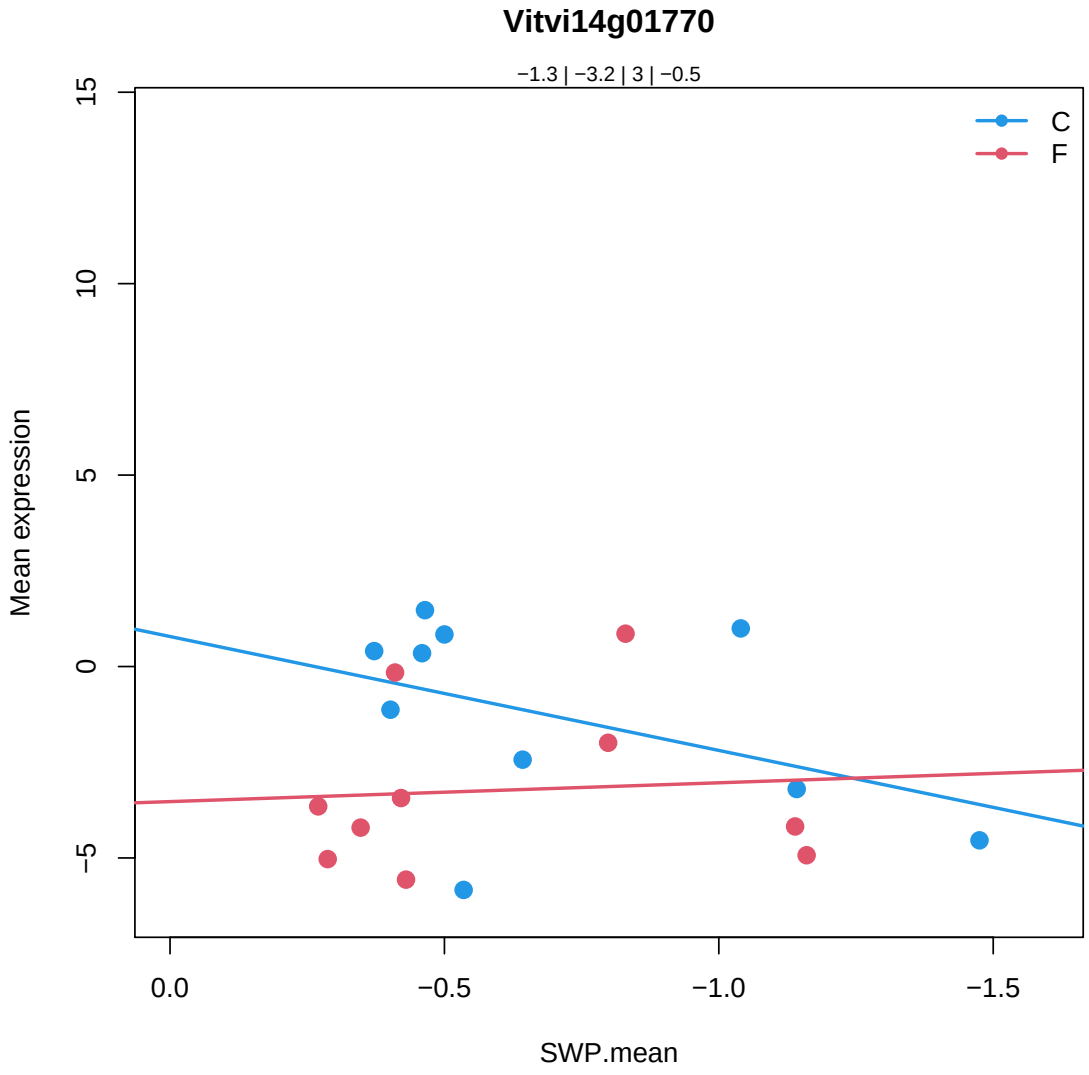
7.6.2 Vitvi14g01770: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01770
        28.99
        DNA.unspecified
        Exonuclease family protein |
        Chr3:10389609-10391544 FORWARD LENGTH=357 |
        201606
```

Coefficients for Vitvi14g01770.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	−1.308148	0.05623463	.	0.05849108	.
SlopeC	2.974912	0.113551		0.6305081	
MeanF−MeanC	−1.920874	0.04814758	*	0.2335663	
SlopeF−SlopeC	−3.466655	0.2102088		0.9999488	



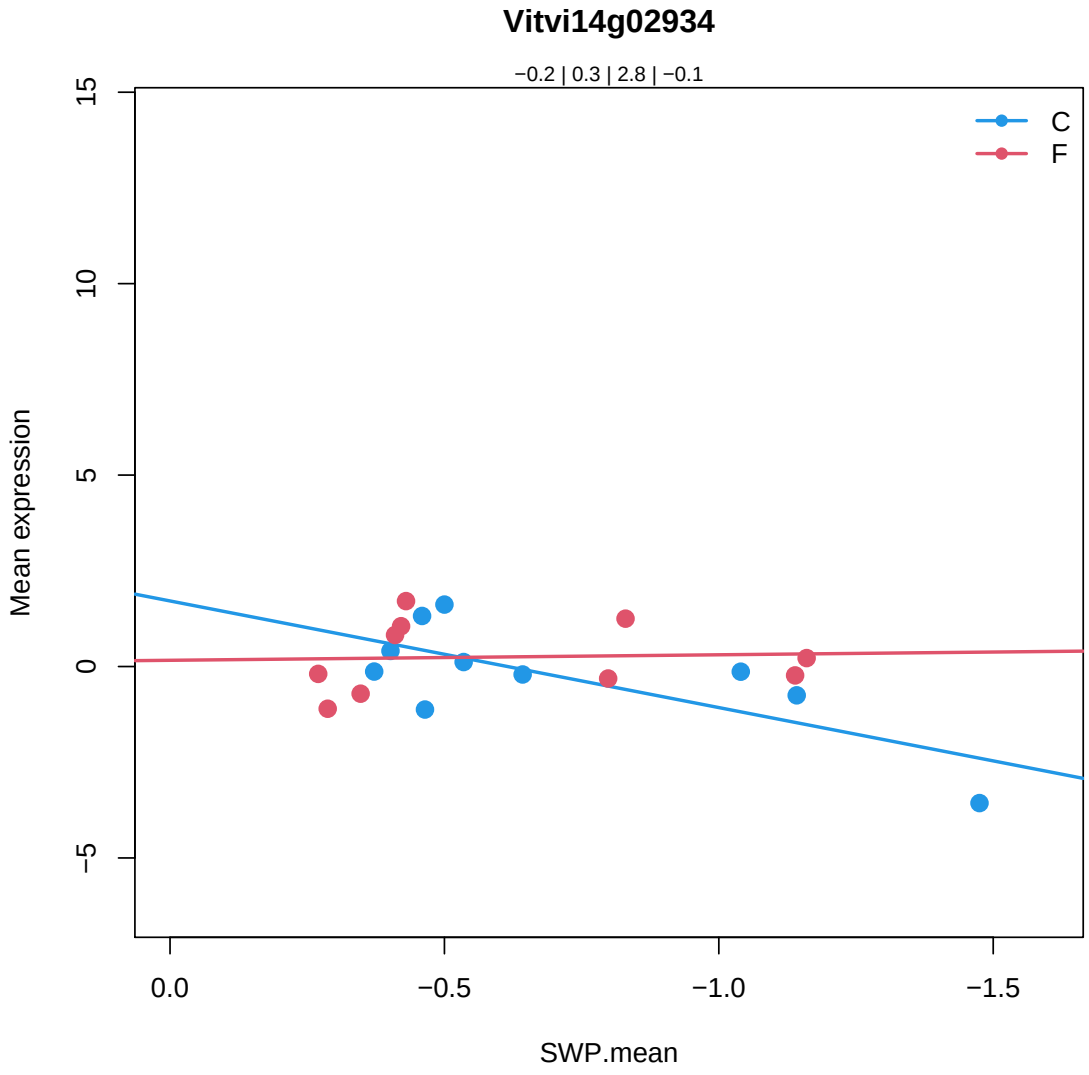
7.6.3 Vitvi14g02934: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g02934
        34.16
        transport.ABC transporters and multidrug resistance systems
        transporter associated with antigen processing protein 2 |
        Chr5:15625660-15629621 FORWARD LENGTH=644 |
        201606
```

Coefficients for Vitvi14g02934.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.2456549	0.3984604		0.4045922	
SlopeC	2.784639	0.002032099	**	0.1701827	
MeanF-MeanC	0.4958826	0.2321044		0.5863973	
SlopeF-SlopeC	-2.928269	0.02149545	*	0.9999488	



7.6.4 Vitvi10g00663: * type5

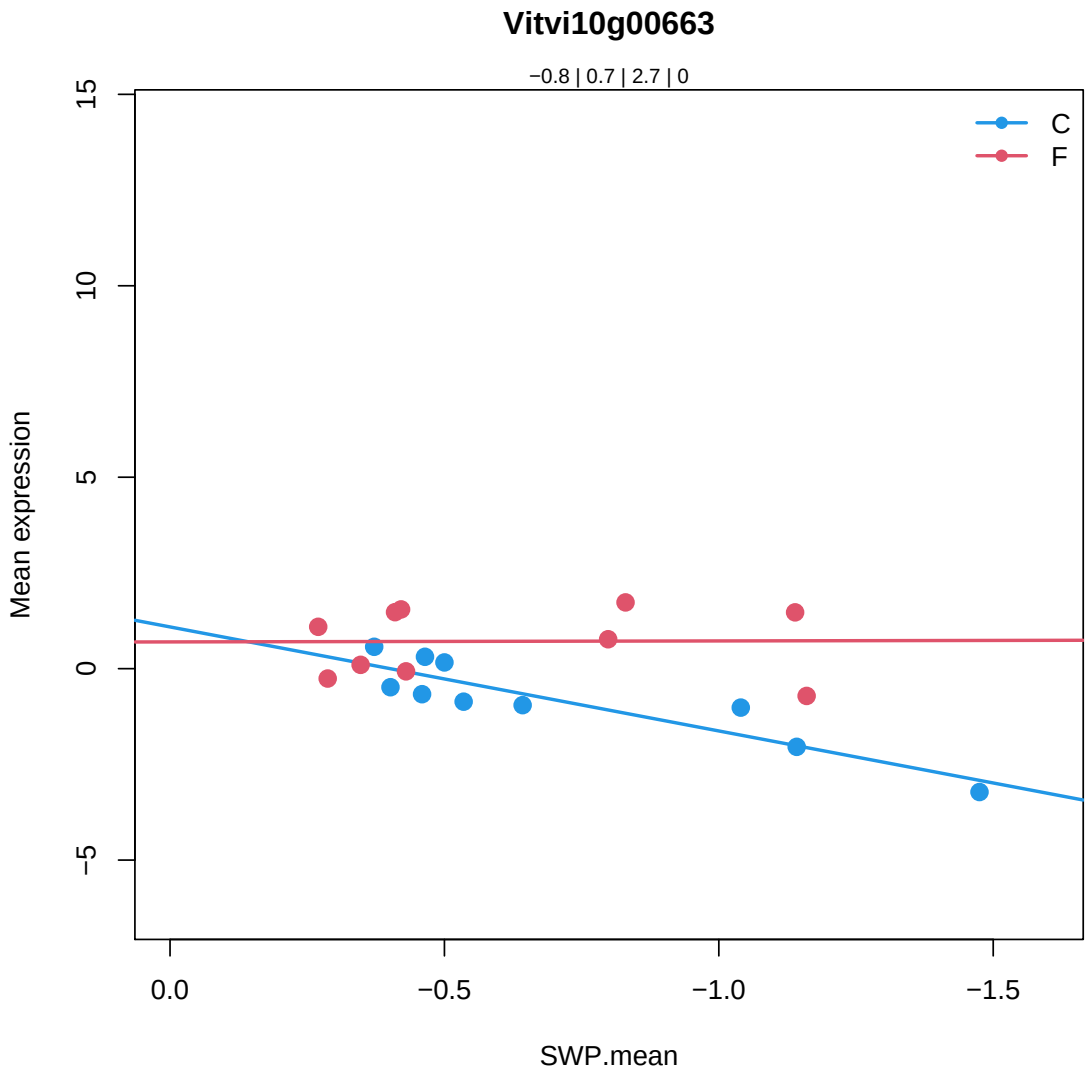
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00663
        33.99
        development.unspecified
        K-box region and MADS-box transcription factor family protein |
        Chr3:21739150-21741766 FORWARD LENGTH=241 |
        201606

Vitvi10g00663
        27.3.24
        RNA.regulation of transcription.MADS box transcription factor family
        K-box region and MADS-box transcription factor family protein |
        Chr3:21739150-21741766 FORWARD LENGTH=241 |
        201606
```

Coefficients for Vitvi10g00663.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.8209171	0.001213348	**	0.001311992	**
SlopeC	2.716708	0.0002212026	***	0.08109226	.
MeanF-MeanC	1.534975	6.737202e-05	***	0.001277494	**
SlopeF-SlopeC	-2.742007	0.00662921	**	0.9999488	


Vitvi10g00663
−0.8 | 0.7 | 2.7 | 0
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

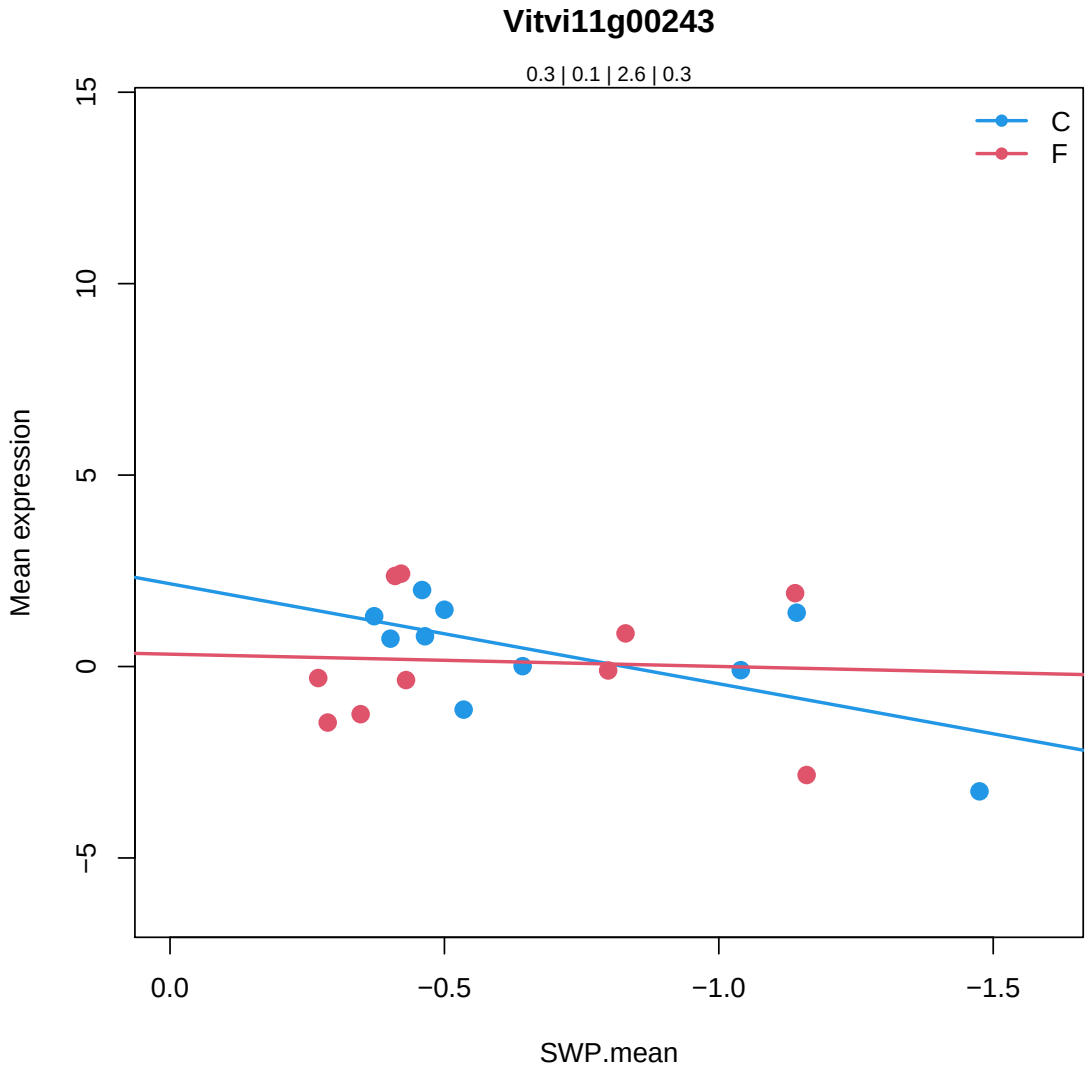
7.6.5 Vitvi11g00243: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00243
        10.5.3
        cell wall.cell wall proteins.LRR
        Leucine-rich repeat (LRR) family protein |
        Chr4:14418826-14420073 FORWARD LENGTH=415 |
        201606
```

Coefficients for Vitvi11g00243.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3244235	0.4712635		0.4774978	
SlopeC	2.612418	0.04557967	*	0.4926906	
MeanF-MeanC	-0.1974358	0.7553592		0.9285435	
SlopeF-SlopeC	-2.292601	0.2242025		0.9999488	



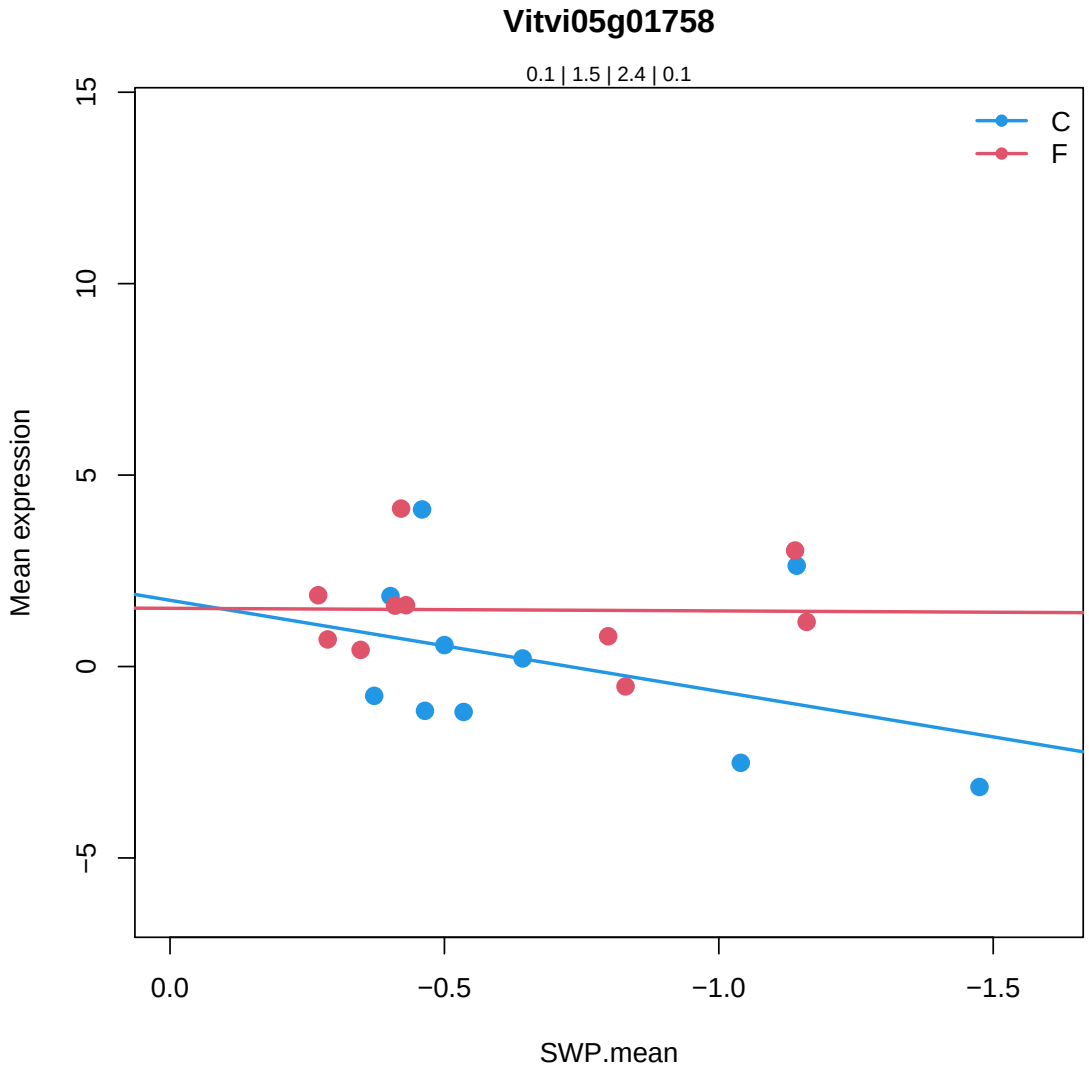
7.6.6 Vitvi05g01758: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01758
        35.2
        not assigned.unknown
        MLP-like protein 423 |
        Chr1:8500653-8501458 REVERSE LENGTH=155 |
        201606
```

Coefficients for Vitvi05g01758.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.0573489	0.9123565		0.914276	
SlopeC	2.378762	0.1113767		0.6258604	
MeanF-MeanC	1.421246	0.06415951	.	0.2806081	
SlopeF-SlopeC	-2.310635	0.2905474		0.9999488	



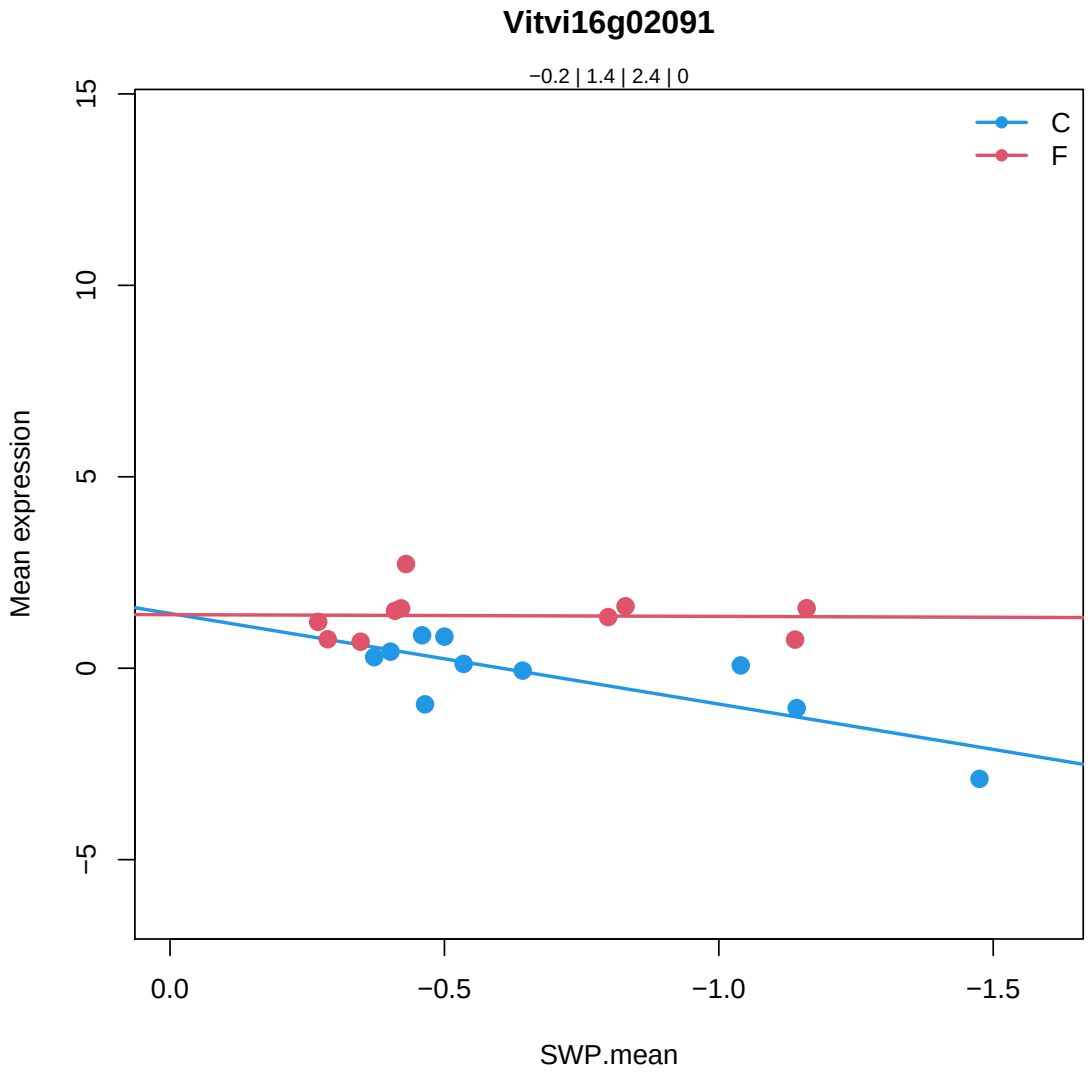
7.6.7 Vitvi16g02091: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g02091
        35.2
        not assigned.unknown
        Receptor-like protein kinase
```

Coefficients for Vitvi16g02091.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	−0.2346616	0.2592422		0.2646775	
SlopeC	2.366765	0.0003865785	***	0.09467692	.
MeanF−MeanC	1.605684	1.346083e−05	***	0.0003309194	***
SlopeF−SlopeC	−2.321945	0.01135478	*	0.9999488	



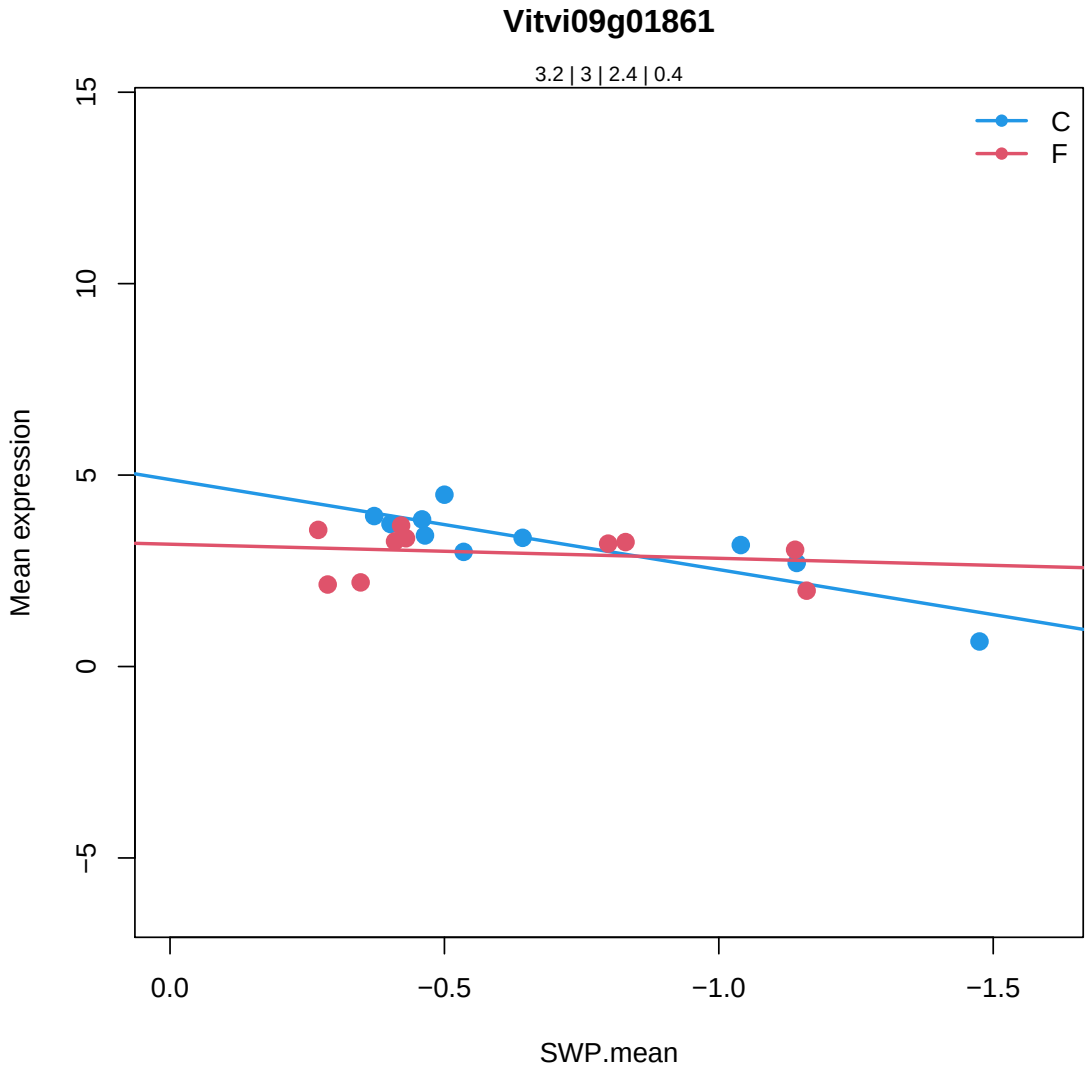
7.6.8 Vitvi09g01861: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g01861
        35.2
        not assigned.unknown
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606
```

Coefficients for Vitvi09g01861.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.229087	3.258075e-14	***	5.201589e-14	***
SlopeC	2.350915	0.000148304	***	0.07644173	.
MeanF-MeanC	-0.2591712	0.3297596		0.6893699	
SlopeF-SlopeC	-1.983011	0.01633076	*	0.9999488	



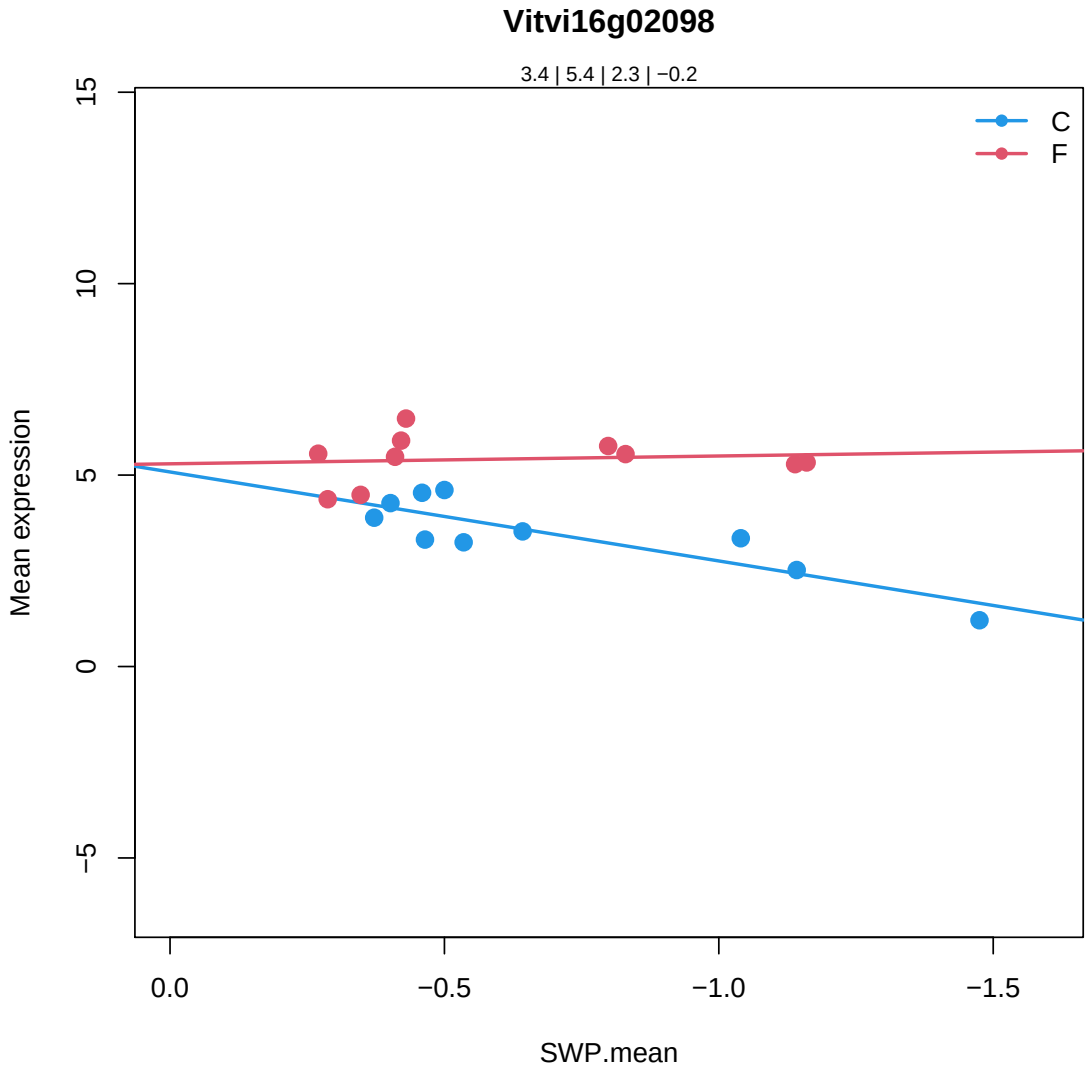
7.6.9 Vitvi16g02098: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g02098
        35.2
        not assigned.unknown
        PR5-like receptor kinase |
        Chr5:15293325-15295838 REVERSE LENGTH=665 |
        201606
```

Coefficients for Vitvi16g02098.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.446831	7.658968e-15	***	1.295793e-14	***
SlopeC	2.32385	0.000156973	***	0.07644173	.
MeanF-MeanC	1.97166	1.502738e-07	***	5.828175e-06	***
SlopeF-SlopeC	-2.527587	0.003019792	**	0.9999488	



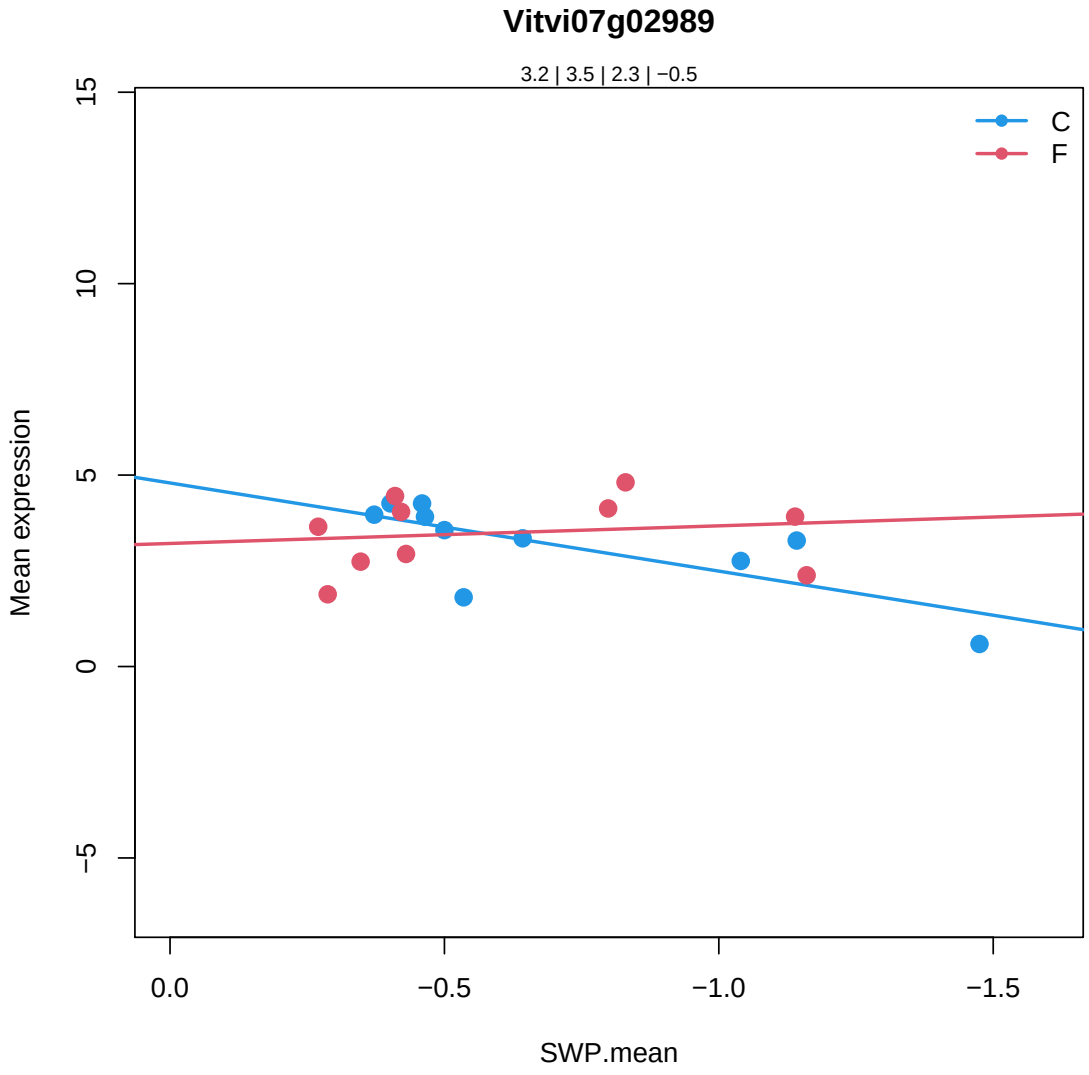
7.6.10 Vitvi07g02989: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g02989
        29.7
        protein.glycosylation
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi07g02989.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.174867	5.288199e-11	***	6.993122e-11	***
SlopeC	2.302397	0.004902096	**	0.2503311	
MeanF-MeanC	0.3194933	0.4013746		0.7457035	
SlopeF-SlopeC	-2.762497	0.01936364	*	0.9999488	



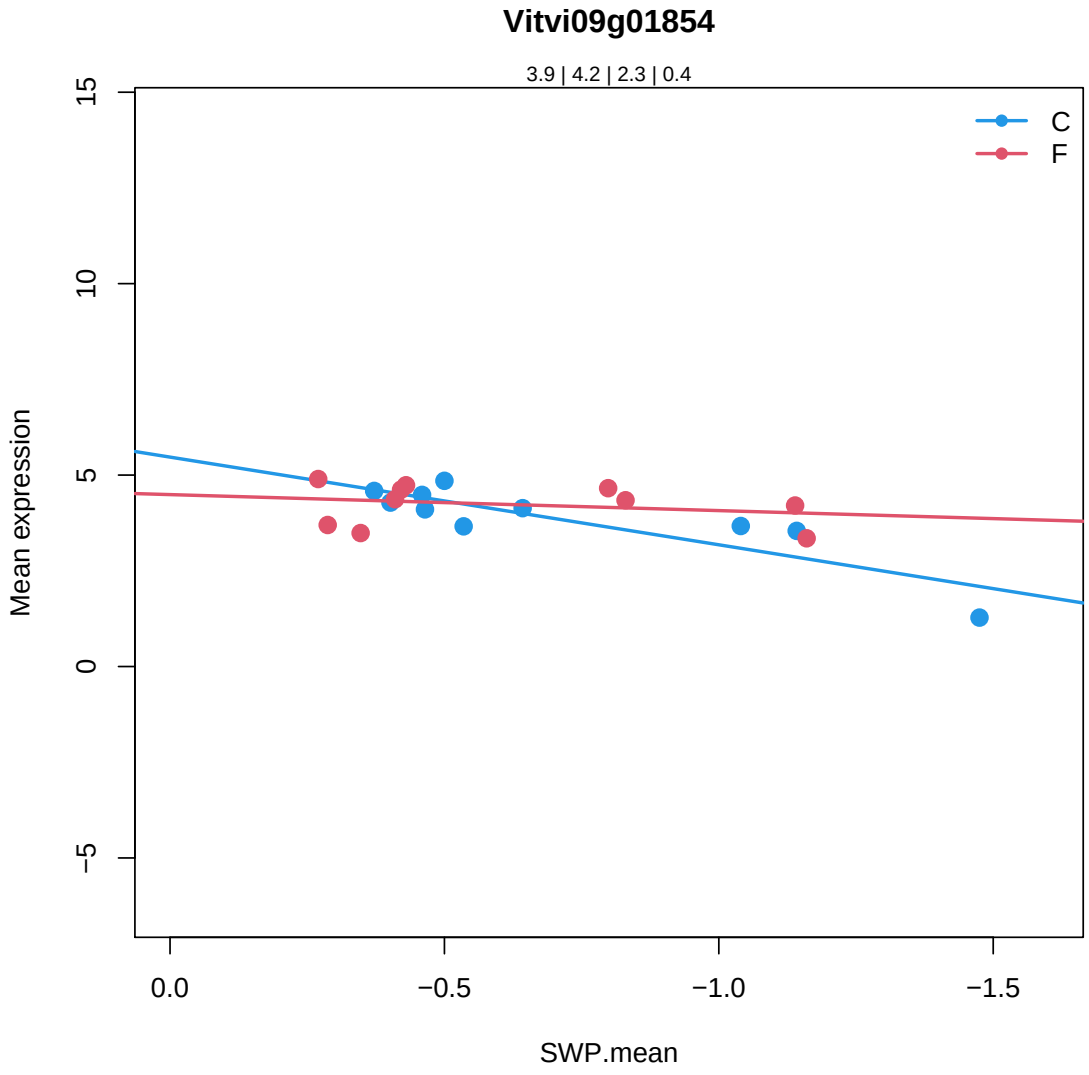
7.6.11 Vitvi09g01854: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g01854
        35.2
        not assigned.unknown
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606
```

Coefficients for Vitvi09g01854.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.859152	1.450528e-16	***	3.061333e-16	***
SlopeC	2.28969	7.414771e-05	***	0.07644173	.
MeanF-MeanC	0.3765295	0.1285355		0.4259921	
SlopeF-SlopeC	-1.871842	0.01373577	*	0.9999488	



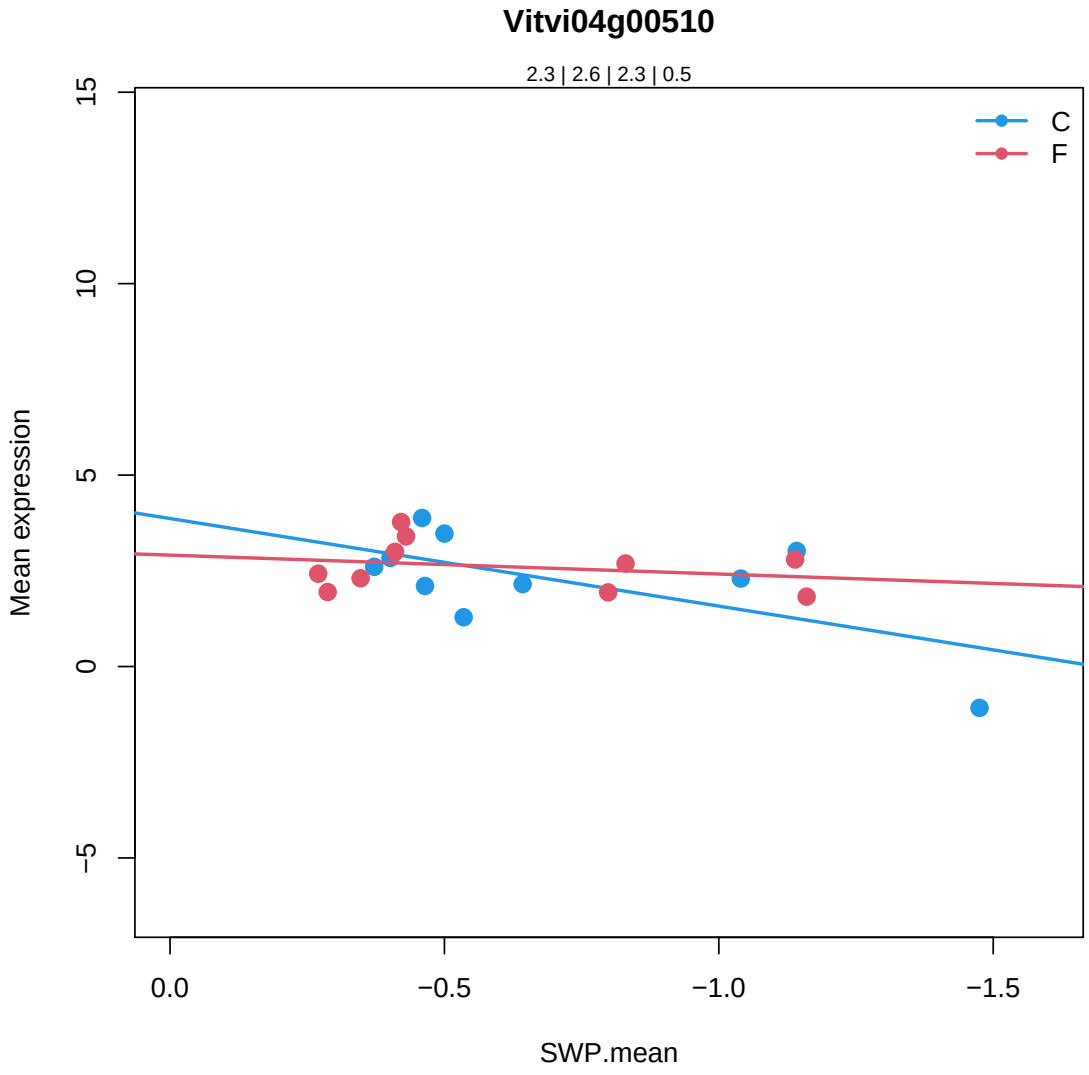
7.6.12 Vitvi04g00510: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00510
        27.3.32
        RNA.regulation of transcription.WRKY domain transcription factor famil
        WRKY DNA-binding protein 18 |
        Chr4:15383879-15384812 FORWARD LENGTH=245 |
        201606
```

Coefficients for Vitvi04g00510.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.256808	2.981701e-08	***	3.588117e-08	***
SlopeC	2.287168	0.005696268	**	0.2614474	
MeanF-MeanC	0.3518458	0.3629519		0.7208951	
SlopeF-SlopeC	-1.794392	0.1200508		0.9999488	



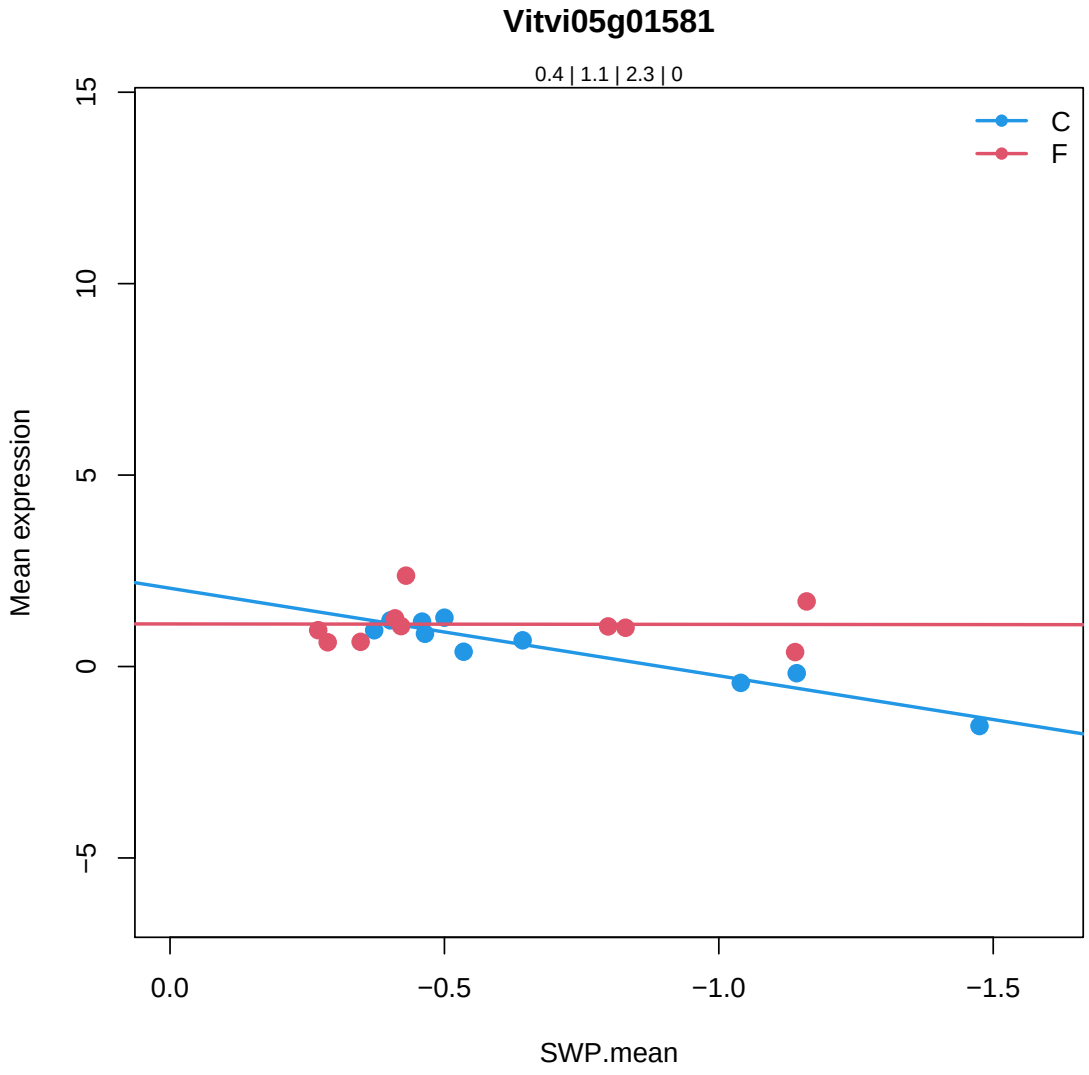
7.6.13 Vitvi05g01581: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01581
        20.1.7.3
        stress.biotic.PR-proteins.PR3/4/8/11 (chitinases and chitin binding pr
        homolog of carrot EP3-3 chitinase |
        Chr3:20145935-20147034 FORWARD LENGTH=273 |
        201606
```

Coefficients for Vitvi05g01581.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4368721	0.009024529	**	0.009570157	**
SlopeC	2.2861	2.189805e-05	***	0.04768143	*
MeanF-MeanC	0.6679842	0.005283957	**	0.04768388	*
SlopeF-SlopeC	-2.274535	0.001603921	**	0.9999488	



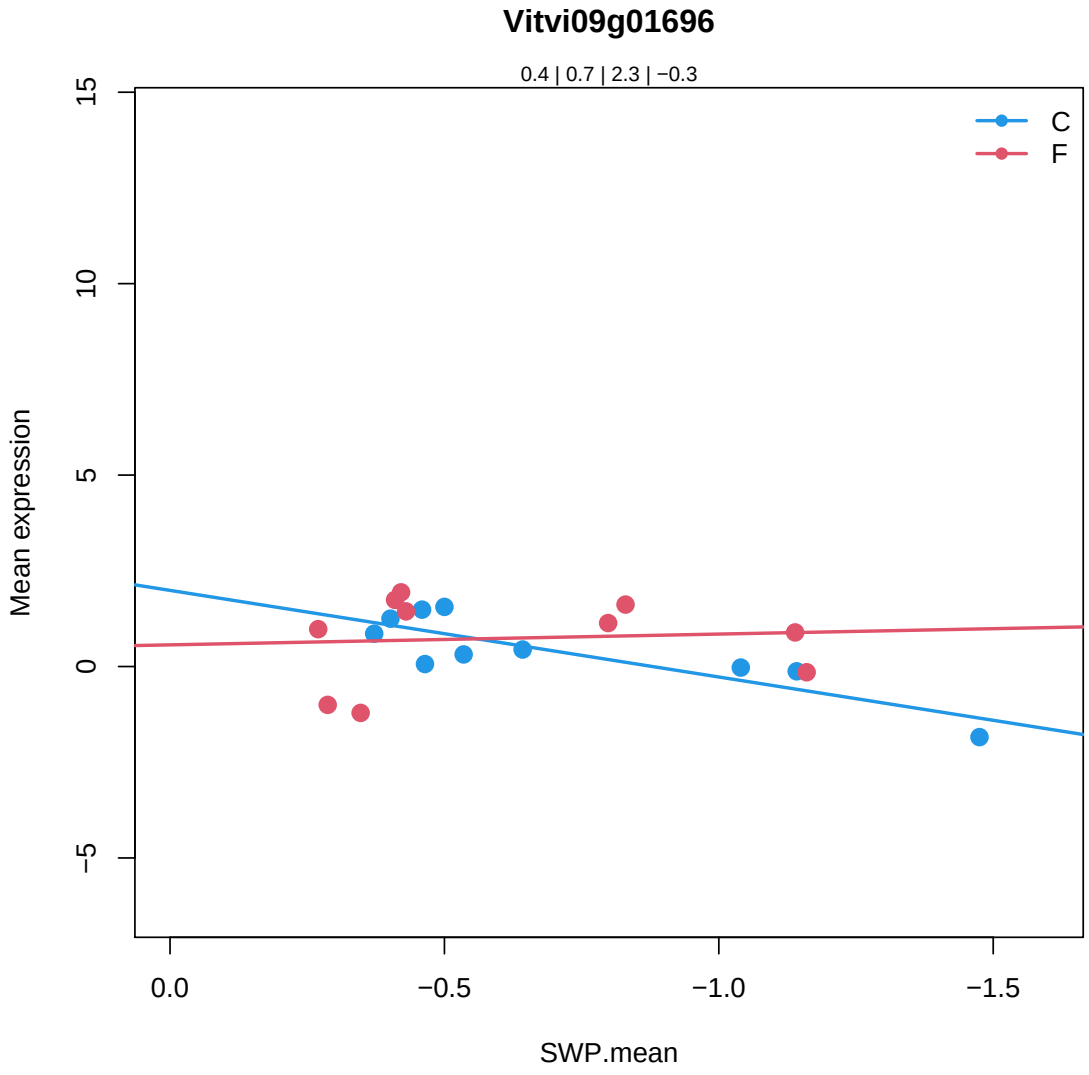
7.6.14 Vitvi09g01696: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g01696
        20.1.2
        stress.biotic.receptors
        receptor like protein 1 |
        Chr1:2270633-2274654 FORWARD LENGTH=913 |
        201606
```

Coefficients for Vitvi09g01696.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3976992	0.1502863		0.15467	
SlopeC	2.261964	0.005987002	**	0.2647742	
MeanF-MeanC	0.3394621	0.3778739		0.7294269	
SlopeF-SlopeC	-2.543567	0.03129144	*	0.9999488	



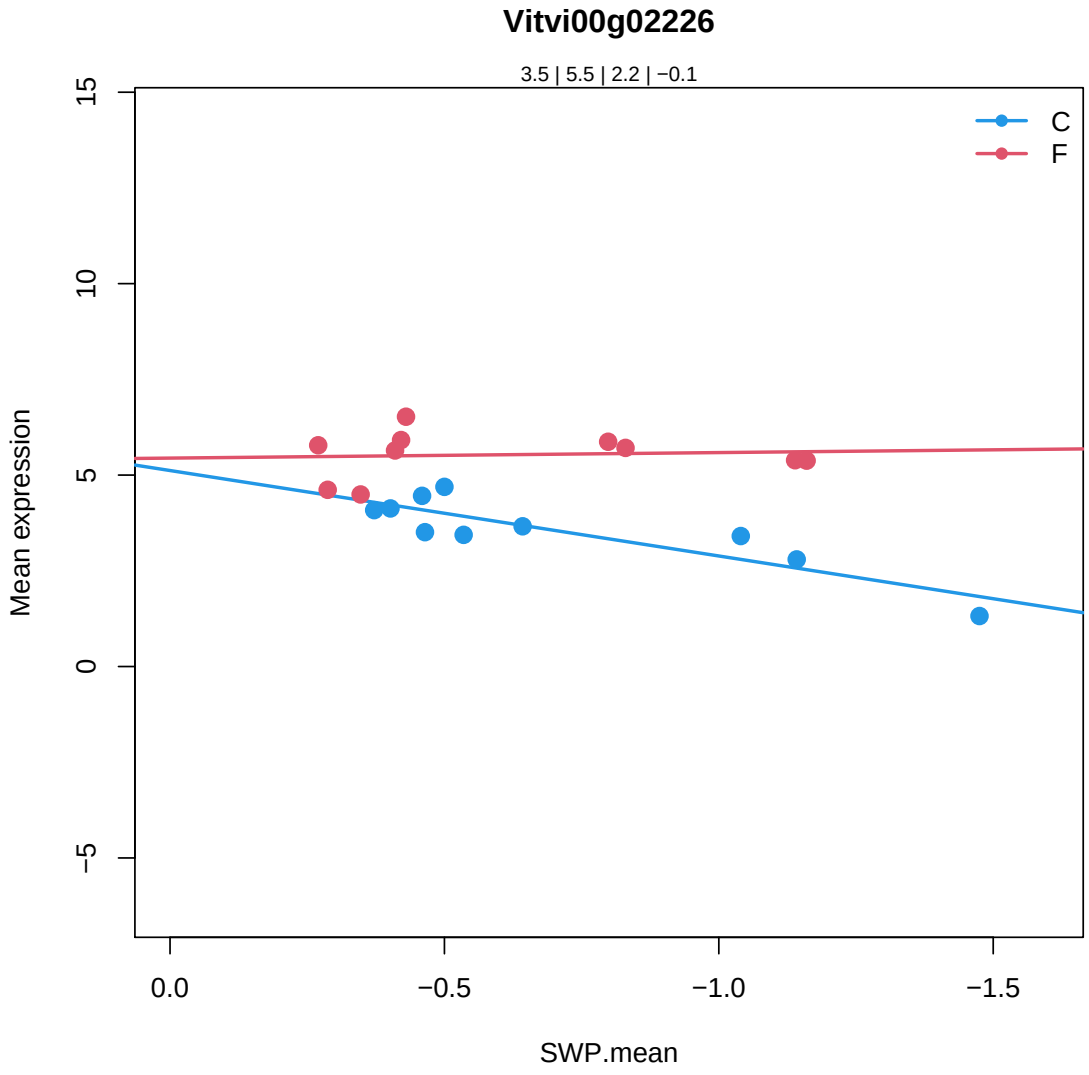
7.6.15 Vitvi00g02226: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi00g02226
        35.2
        not assigned.unknown
        PR5-like receptor kinase |
        Chr5:15293325-15295838 REVERSE LENGTH=665 |
        201606
```

Coefficients for Vitvi00g02226.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.549584	1.613386e-15	***	2.94647e-15	***
SlopeC	2.231859	0.0001456927	***	0.07644173	.
MeanF-MeanC	1.981757	6.472083e-08	***	2.794547e-06	***
SlopeF-SlopeC	-2.375927	0.003388446	**	0.9999488	



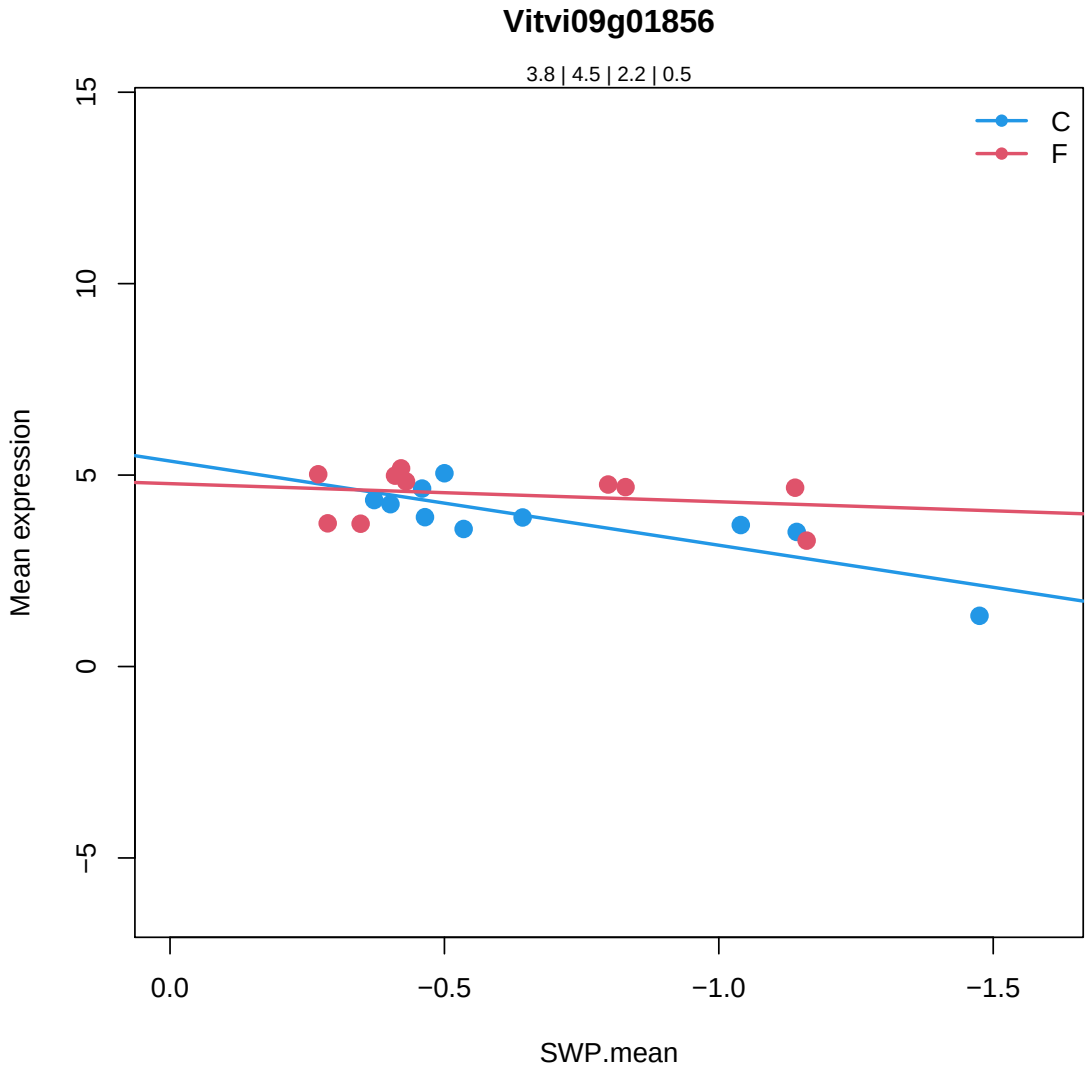
7.6.16 Vitvi09g01856: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g01856
        20.1.2
        stress.biotic.receptors
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606
```

Coefficients for Vitvi09g01856.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.820257	2.049205e-15	***	3.707299e-15	***
SlopeC	2.197973	0.0004216347	***	0.09737206	.
MeanF-MeanC	0.6678597	0.02104969	*	0.1306881	
SlopeF-SlopeC	-1.725148	0.03917642	*	0.9999488	



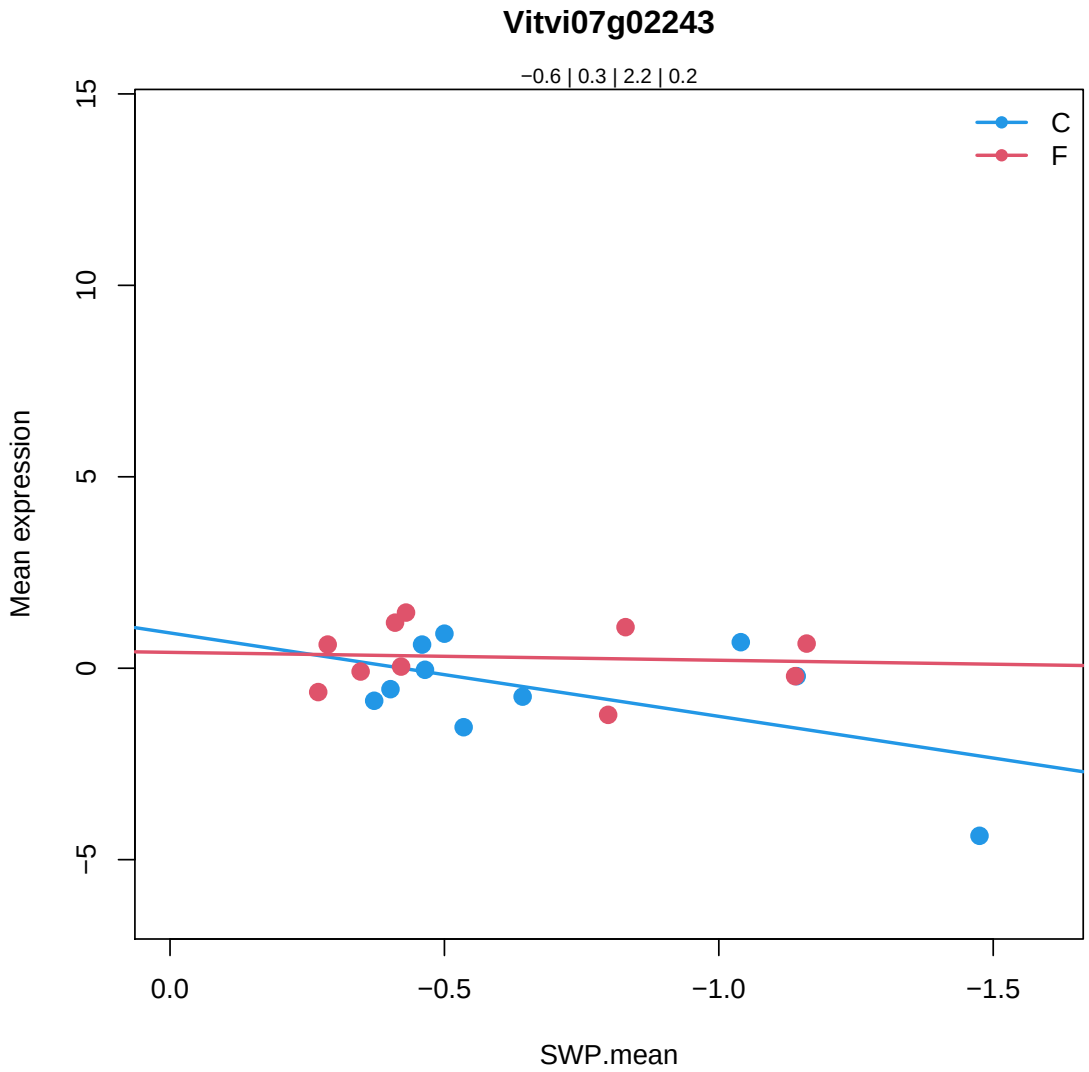
7.6.17 Vitvi07g02243: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g02243
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi07g02243.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	−0.6105923	0.07473414	.	0.07752128	.
SlopeC	2.177967	0.02545229	*	0.4079655	
MeanF−MeanC	0.8990698	0.0643251	.	0.2808113	
SlopeF−SlopeC	−1.971339	0.1586438		0.9999488	



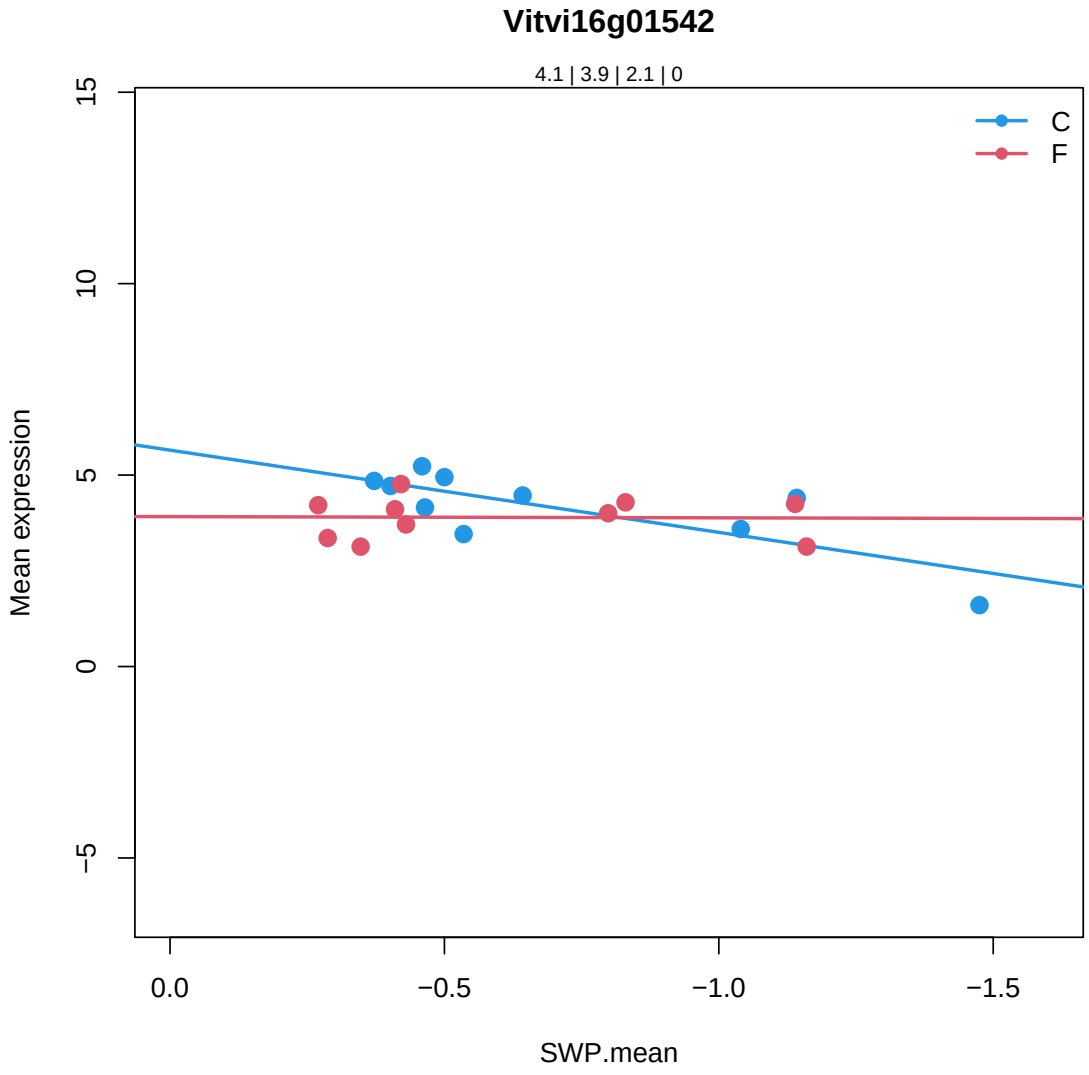
7.6.18 Vitvi16g01542: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01542
        35.2
        not assigned.unknown
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606
```

Coefficients for Vitvi16g01542.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.141452	6.308257e-16	***	1.211421e-15	***
SlopeC	2.146633	0.0006675167	***	0.1037734	
MeanF-MeanC	-0.2460853	0.3799787		0.7316365	
SlopeF-SlopeC	-2.115503	0.01542334	*	0.9999488	



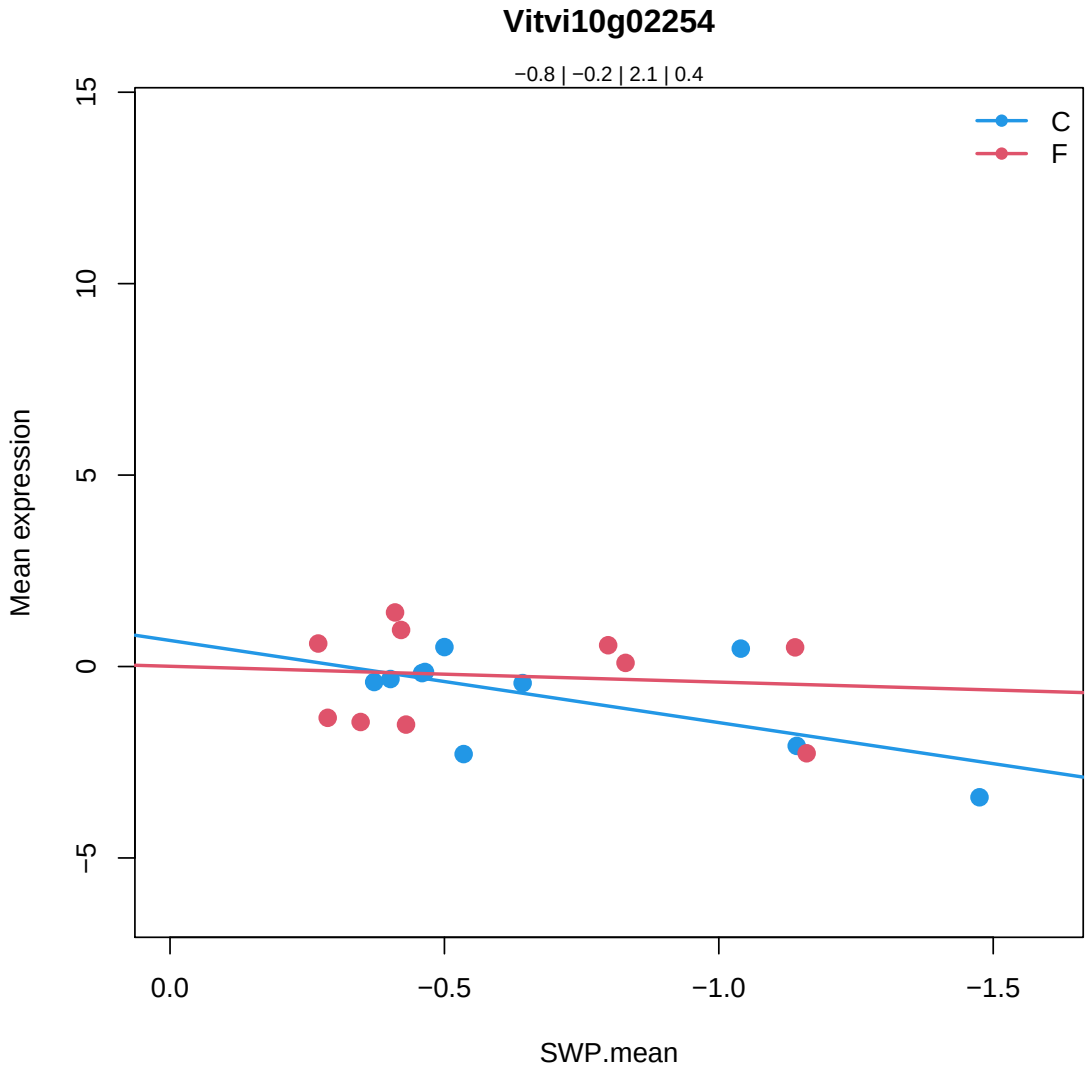
7.6.19 Vitvi10g02254: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g02254
        35.2
        not assigned.unknown
        basic helix-loop-helix (bHLH) DNA-binding superfamily protein |
        Chr4:11215259-11216212 FORWARD LENGTH=190 |
        201606
```

Coefficients for Vitvi10g02254.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.828063	0.02437447	*	0.02557767	*
SlopeC	2.144833	0.03471706	*	0.4457939	
MeanF-MeanC	0.5827176	0.241291		0.5990445	
SlopeF-SlopeC	-1.731657	0.2345692		0.9999488	



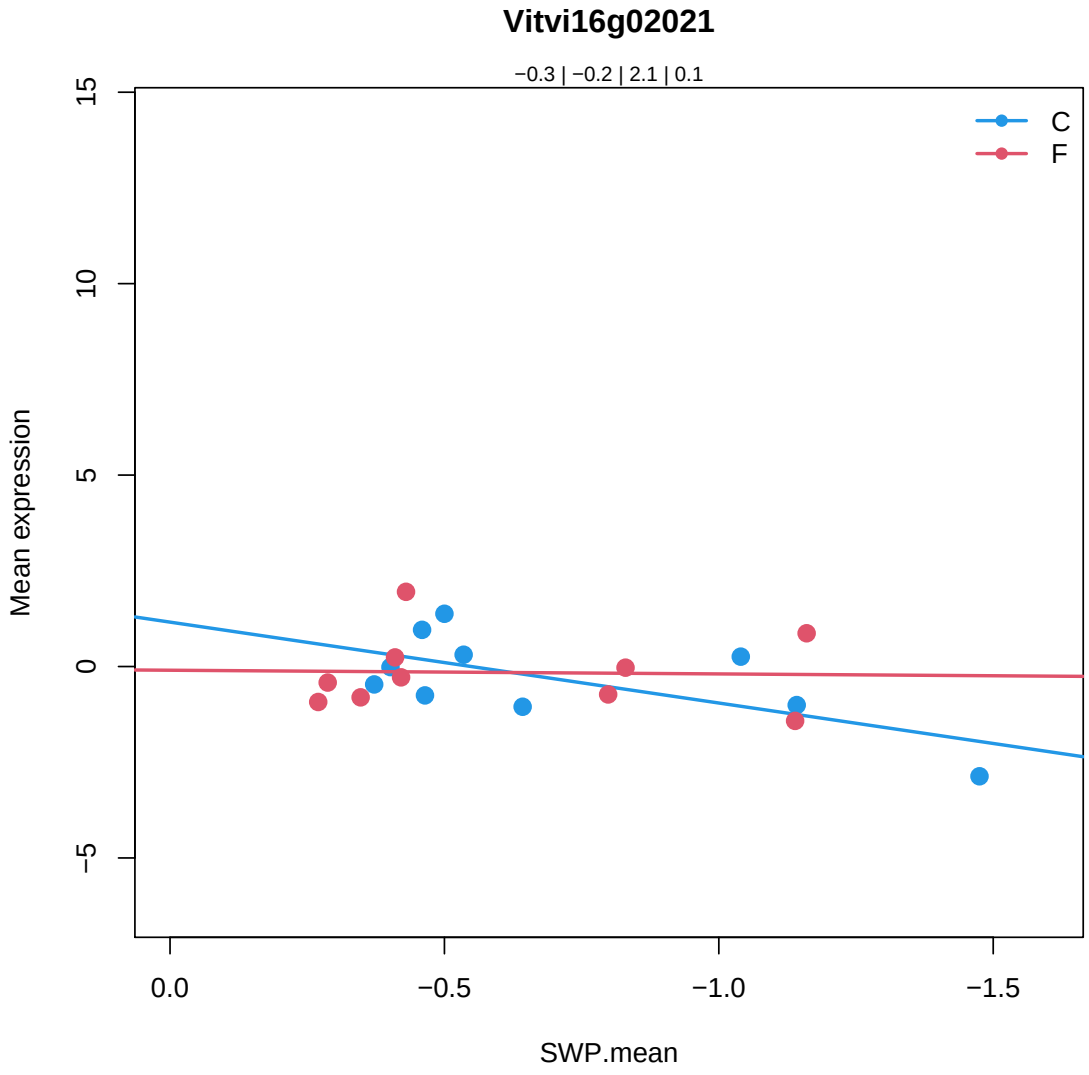
7.6.20 Vitvi16g02021: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g02021
        35.2
        not assigned.unknown
        PR5-like receptor kinase |
        Chr5:15293325-15295838 REVERSE LENGTH=665 |
        201606
```

Coefficients for Vitvi16g02021.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.3262667	0.262738		0.2681208	
SlopeC	2.113053	0.01394122	*	0.3359386	
MeanF-MeanC	0.1706188	0.6748503		0.8949163	
SlopeF-SlopeC	-2.016905	0.1003787		0.9999488	



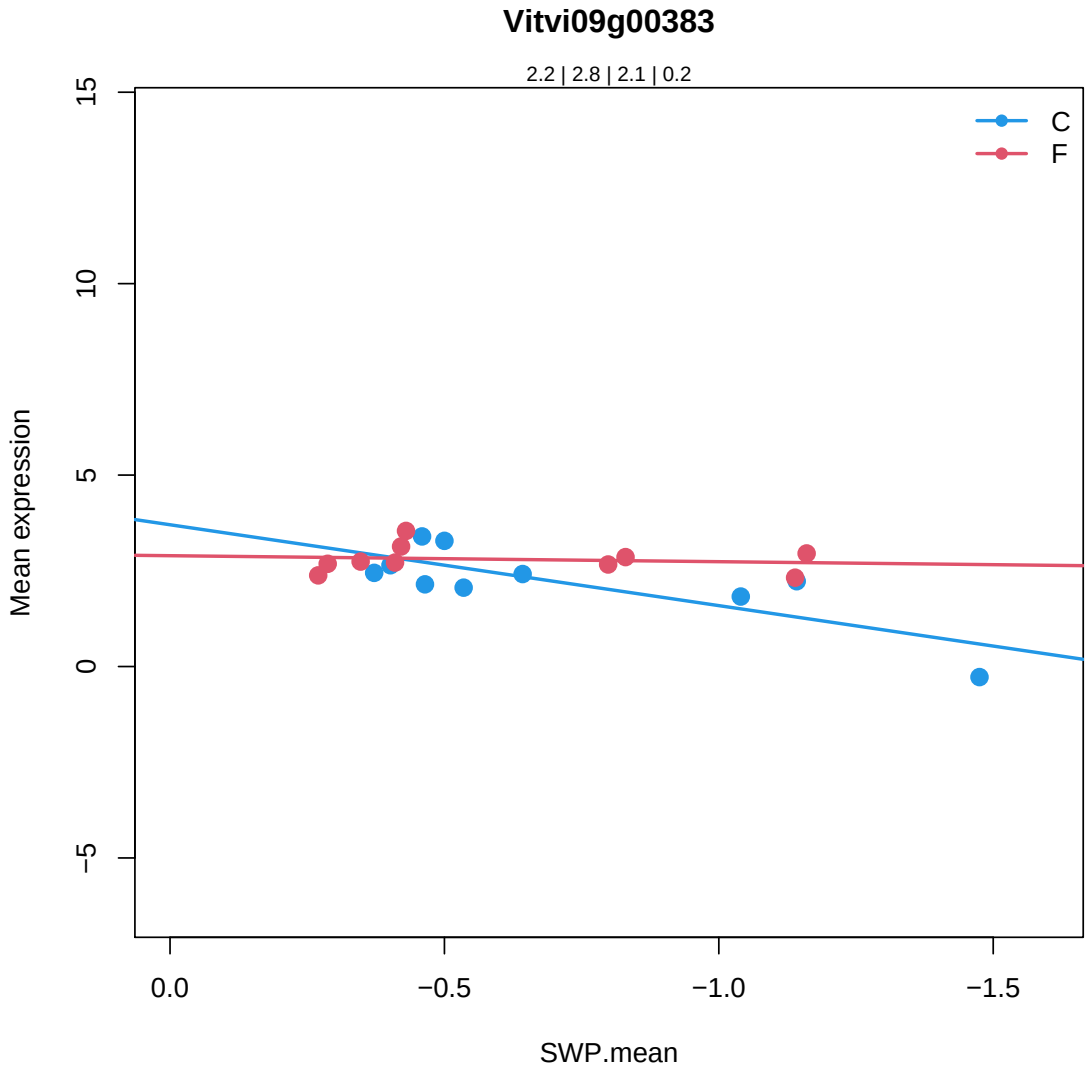
7.6.21 Vitvi09g00383: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00383
        30.3
        signalling.calcium
        calmodulin-binding family protein |
        Chr4:15944604-15946736 REVERSE LENGTH=526 |
        201606
```

Coefficients for Vitvi09g00383.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.217043	6.67746e-12	***	9.193194e-12	***
SlopeC	2.112195	0.0001500368	***	0.07644173	.
MeanF-MeanC	0.5820295	0.02103902	*	0.1306881	
SlopeF-SlopeC	-1.955973	0.009293644	**	0.9999488	



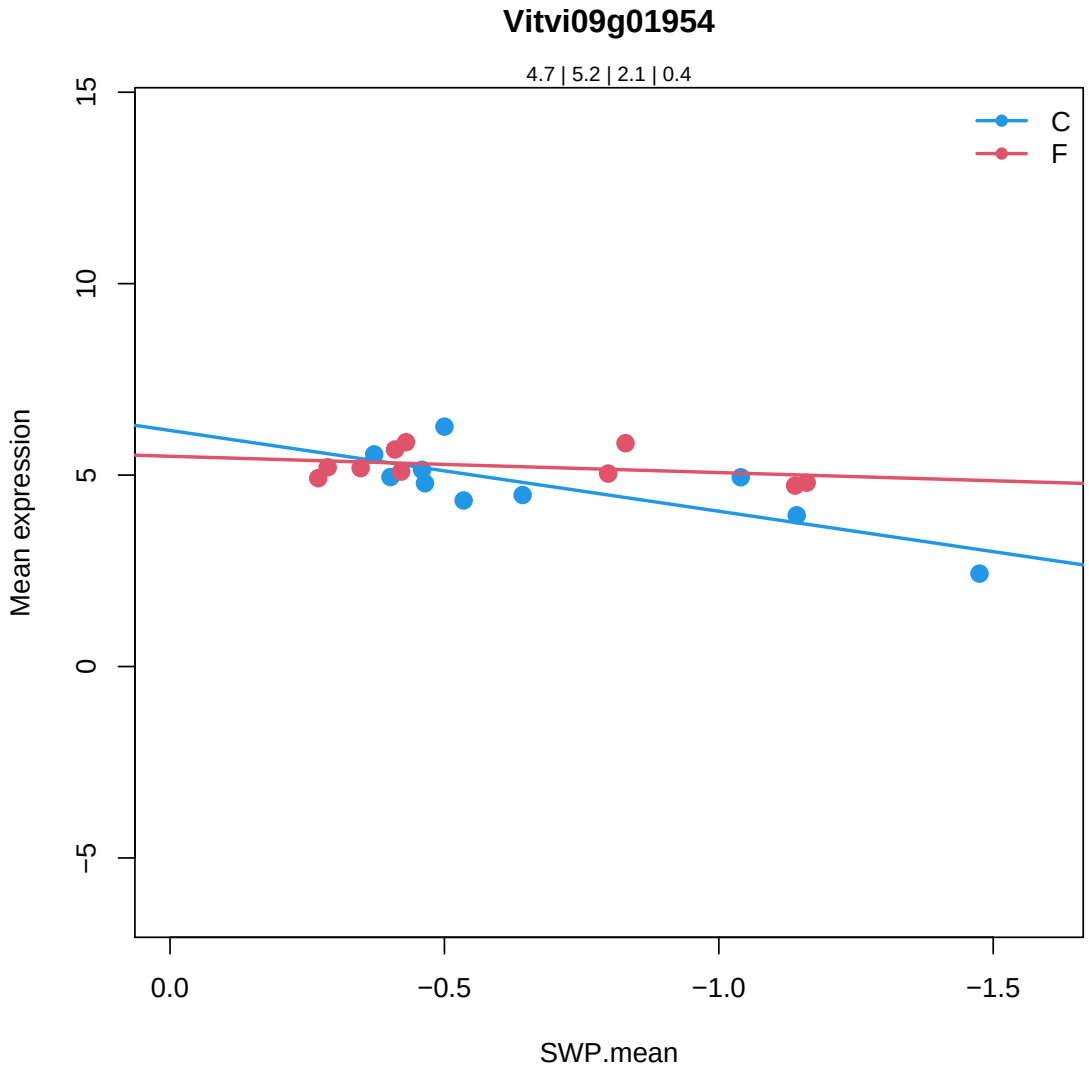
7.6.22 Vitvi09g01954: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g01954
        35.2
        not assigned.unknown
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606
```

Coefficients for Vitvi09g01954.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.681168	3.736863e-18	***	1.09386e-17	***
SlopeC	2.11011	0.0002234533	***	0.08109226	.
MeanF-MeanC	0.550509	0.03343409	*	0.1820659	
SlopeF-SlopeC	-1.683463	0.02701861	*	0.9999488	



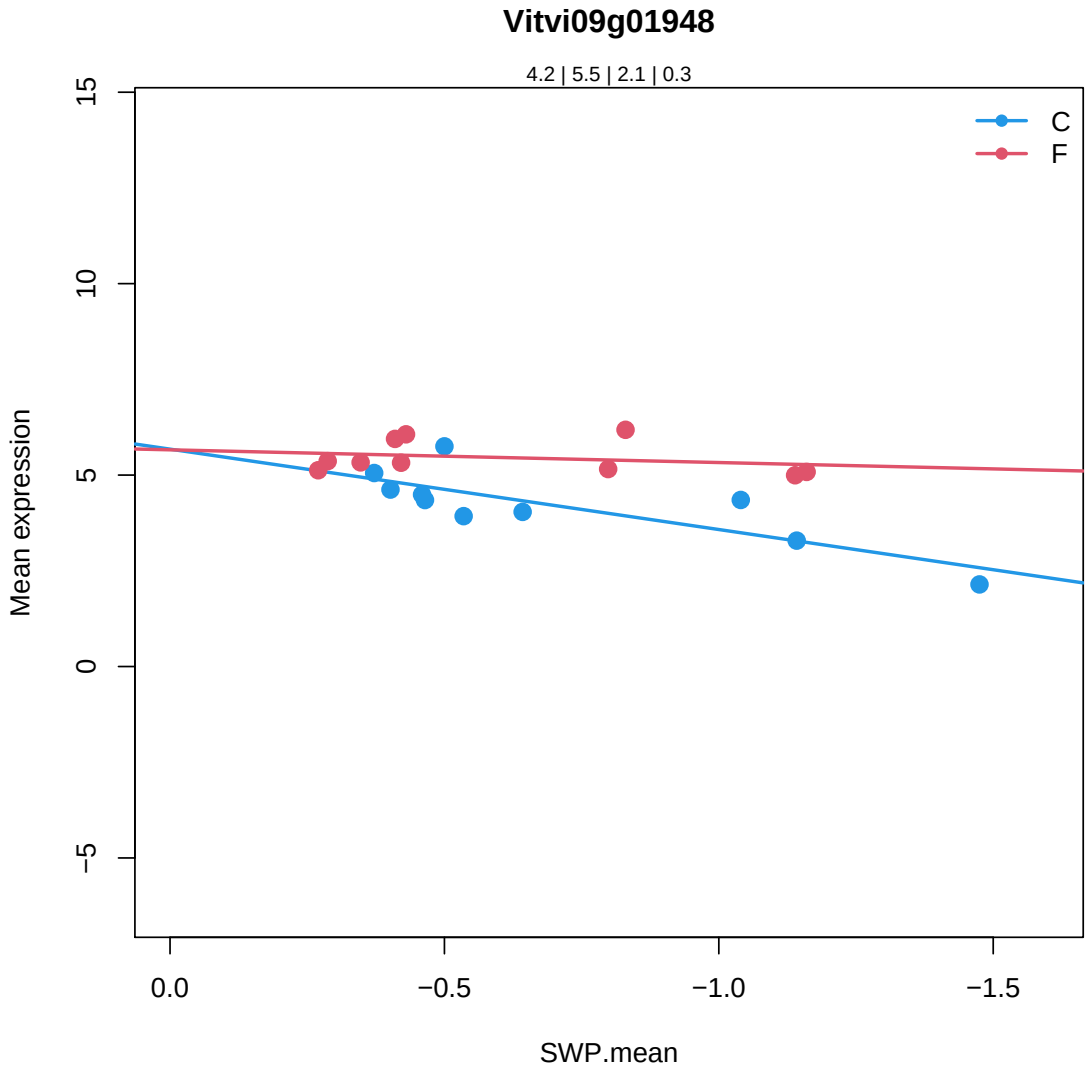
7.6.23 Vitvi09g01948: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g01948
        35.2
        not assigned.unknown
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606
```

Coefficients for Vitvi09g01948.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.200998	1.598364e-17	***	4.037499e-17	***
SlopeC	2.099137	0.0001557553	***	0.07644173	.
MeanF-MeanC	1.256068	2.246776e-05	***	0.0005036082	***
SlopeF-SlopeC	-1.766936	0.01695143	*	0.9999488	



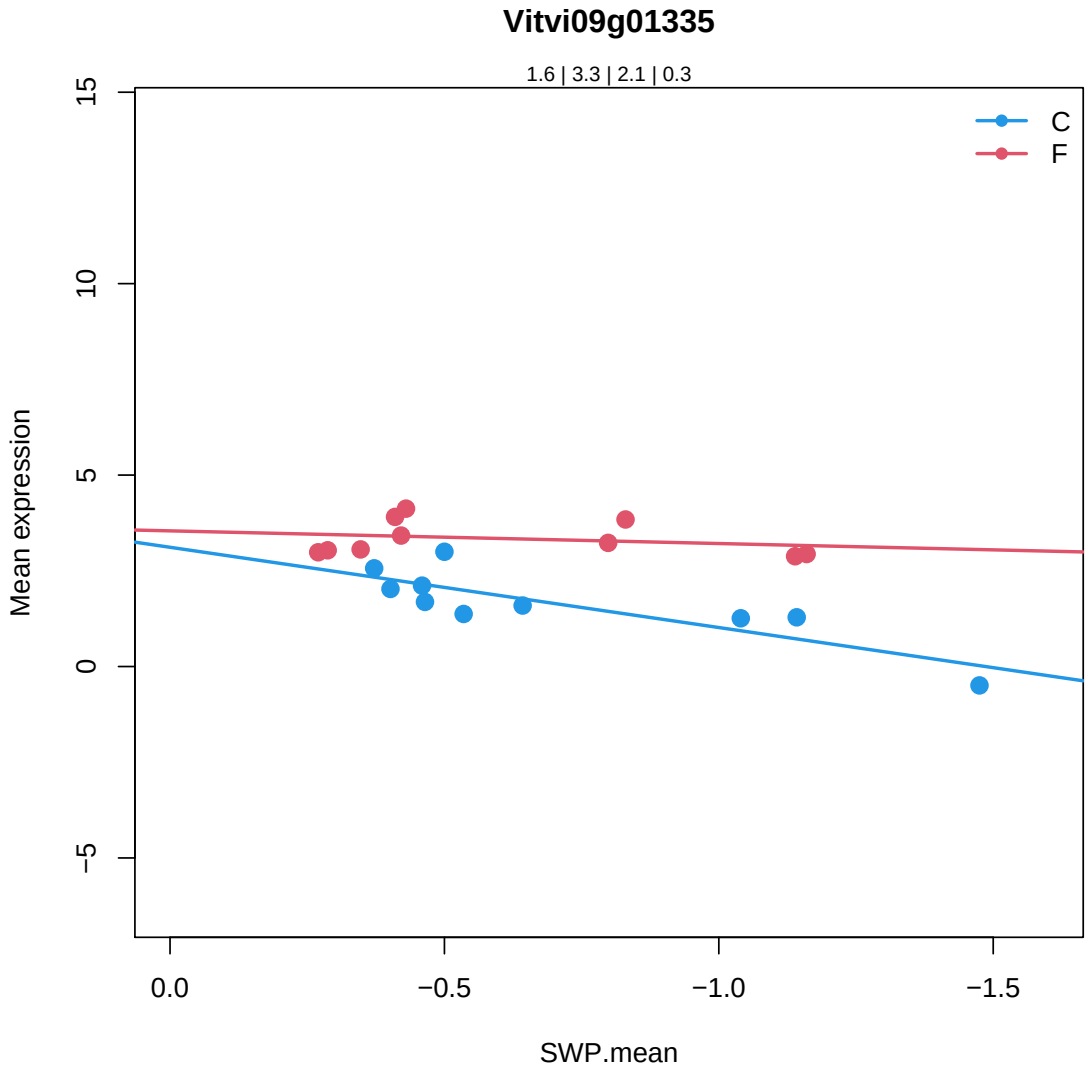
7.6.24 Vitvi09g01335: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g01335
        35.2
        not assigned.unknown
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606
```

Coefficients for Vitvi09g01335.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.640402	8.137972e-10	***	1.029284e-09	***
SlopeC	2.095882	9.96398e-05	***	0.07644173	.
MeanF-MeanC	1.701105	1.598465e-07	***	6.152474e-06	***
SlopeF-SlopeC	-1.765299	0.01338604	*	0.9999488	



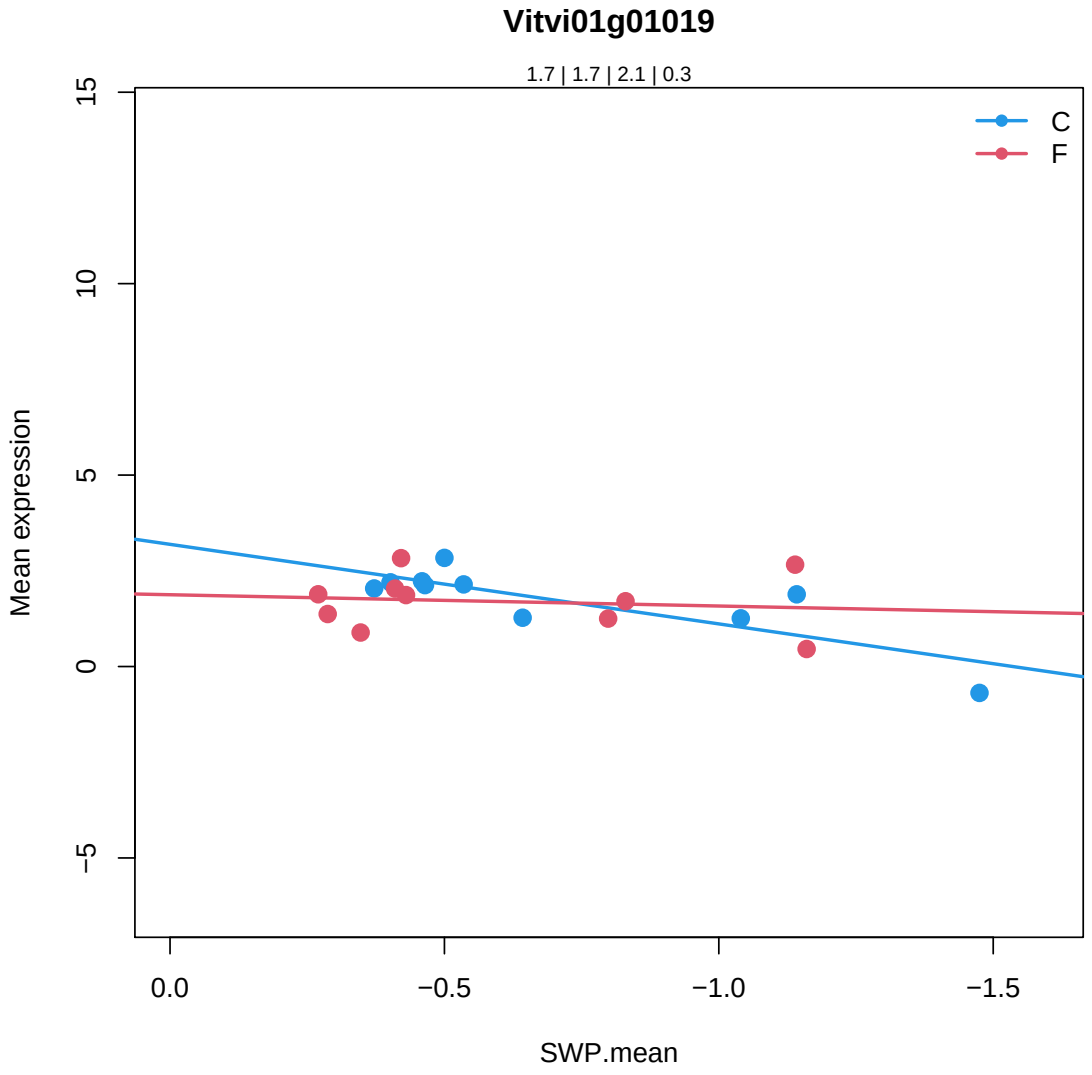
7.6.25 Vitvi01g01019: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01019
        34.3
        transport.amino acids
        Transmembrane amino acid transporter family protein |
        Chr3:10984245-10985767 REVERSE LENGTH=405 |
        201606
```

Coefficients for Vitvi01g01019.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.729811	2.773842e-08	***	3.340884e-08	***
SlopeC	2.077916	0.001434278	**	0.1479249	
MeanF-MeanC	-0.03480933	0.9052082		0.974982	
SlopeF-SlopeC	-1.783326	0.04692402	*	0.9999488	



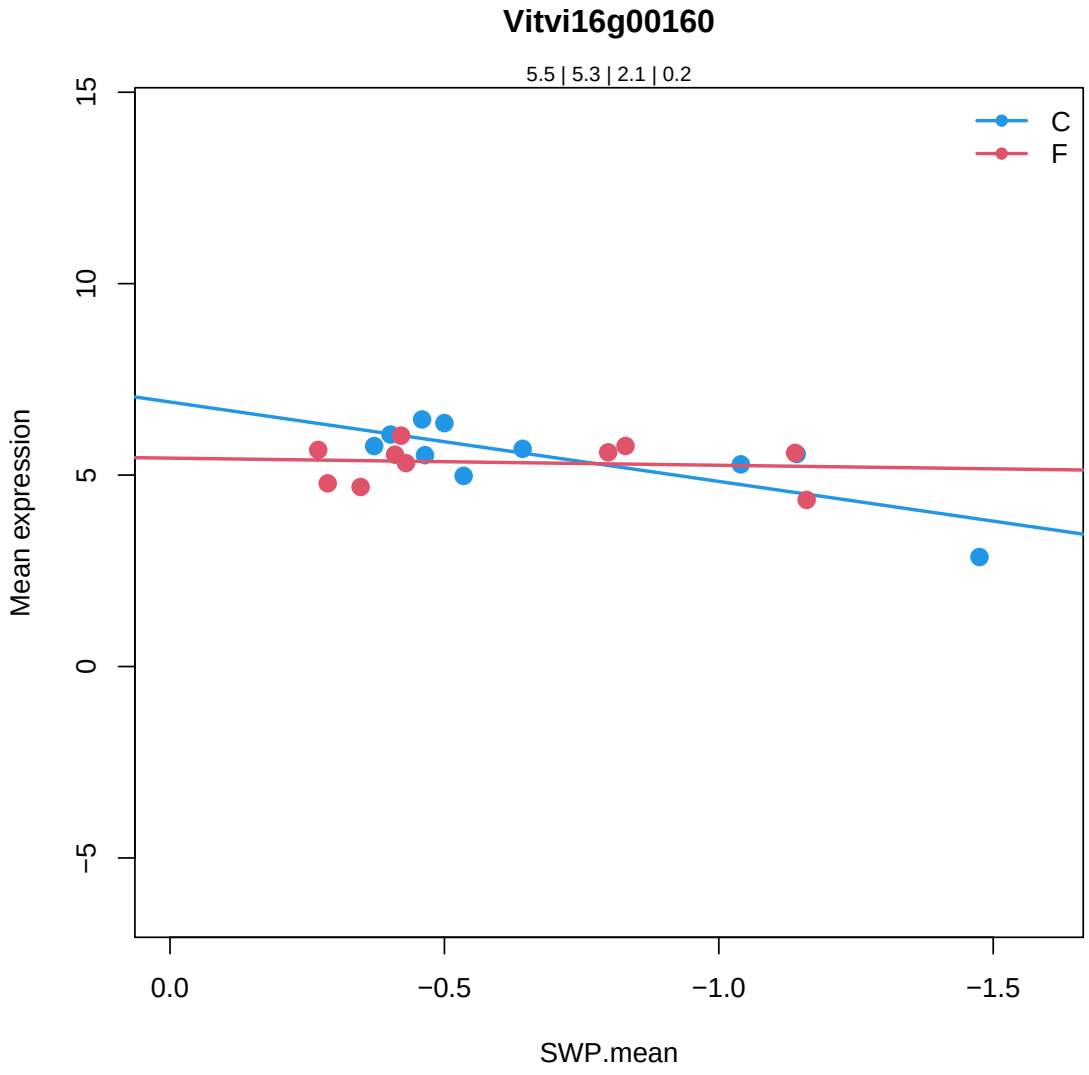
7.6.26 Vitvi16g00160: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g00160
        35.2
        not assigned.unknown
        Sulfite exporter TauE/SafE family protein |
        Chr2:10977174-10979677 FORWARD LENGTH=476 |
        201606
```

Coefficients for Vitvi16g00160.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.450037	1.225169e-18	***	4.117755e-18	***
SlopeC	2.073752	0.0007209777	***	0.1076608	
MeanF-MeanC	-0.1209822	0.6554347		0.8844988	
SlopeF-SlopeC	-1.887619	0.02492933	*	0.9999488	



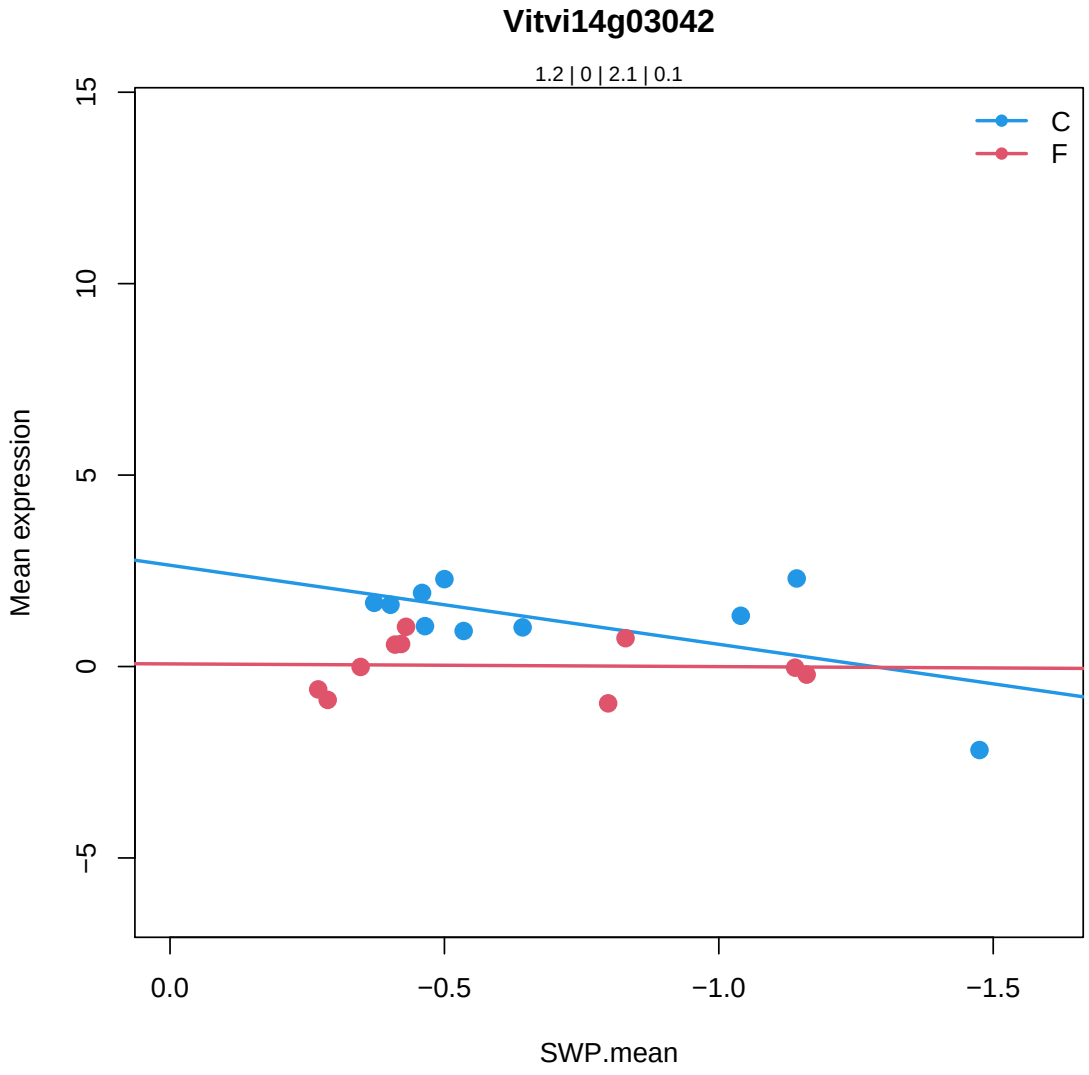
7.6.27 Vitvi14g03042: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g03042
        29.5.9
        protein.degradation.AAA type
        AAA-ATPase 1 |
        Chr5:16020218-16021762 REVERSE LENGTH=514 |
        201606
```

Coefficients for Vitvi14g03042.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.192857	0.0001858375	***	0.0002041173	***
SlopeC	2.064825	0.01053067	*	0.3096058	
MeanF-MeanC	-1.167728	0.005112284	**	0.04654805	*
SlopeF-SlopeC	-1.994307	0.08294194	.	0.9999488	



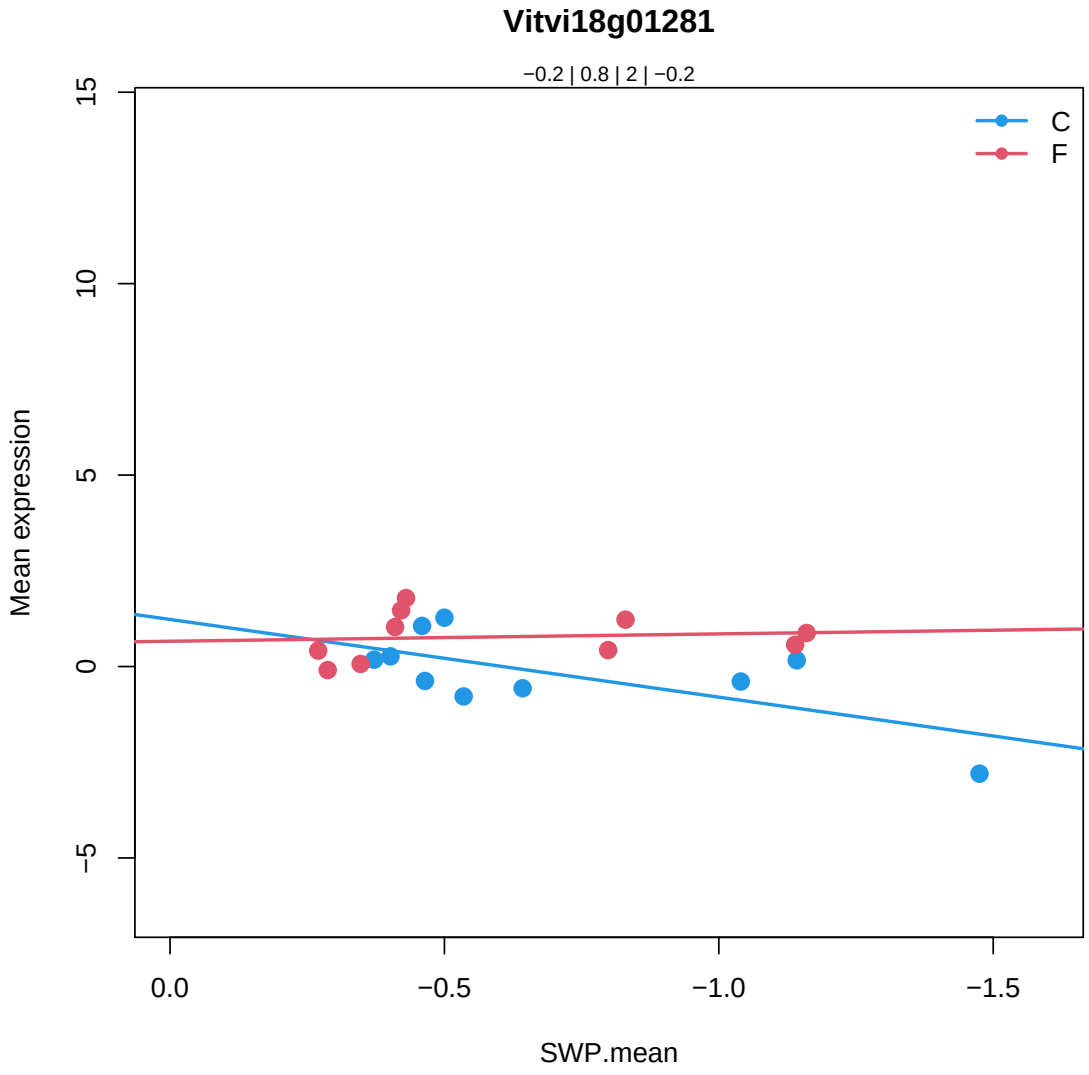
7.6.28 Vitvi18g01281: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g01281
        29.4
        protein.postranslational modification
        receptor-like protein kinase 1 |
        Chr5:24498467-24501494 REVERSE LENGTH=832 |
        201606
```

Coefficients for Vitvi18g01281.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.1976097	0.3888288		0.3949176	
SlopeC	2.029457	0.003785477	**	0.2269459	
MeanF-MeanC	0.9745386	0.005751961	**	0.05076513	.
SlopeF-SlopeC	-2.221749	0.02619175	*	0.9999488	



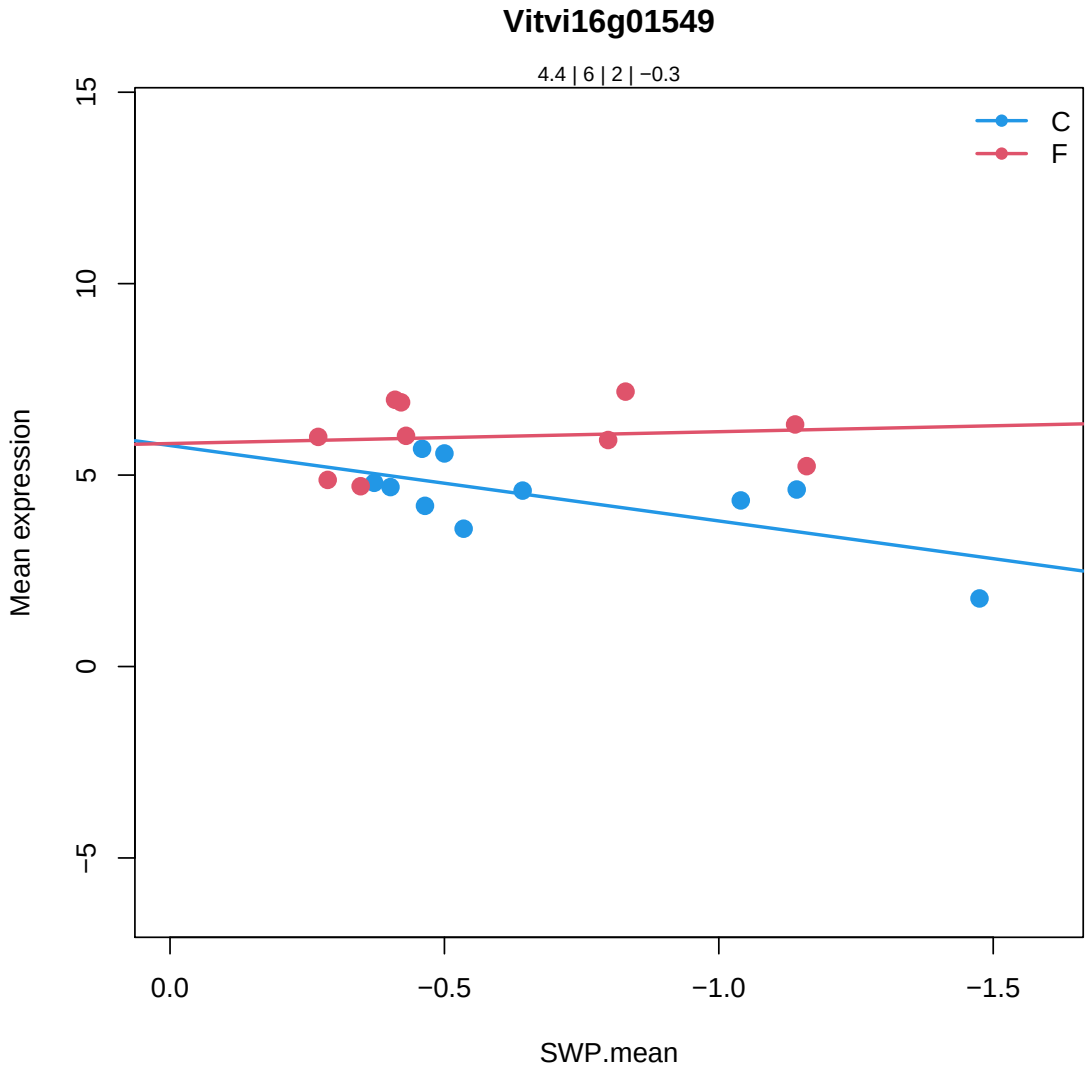
7.6.29 Vitvi16g01549: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01549
        35.2
        not assigned.unknown
        receptor like protein 34 |
        Chr3:3450988-3453672 REVERSE LENGTH=894 |
        201606
```

Coefficients for Vitvi16g01549.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.386477	4.739072e-14	***	7.467481e-14	***
SlopeC	1.969869	0.01098639	*	0.3141738	
MeanF-MeanC	1.62591	0.0001789125	***	0.002941731	**
SlopeF-SlopeC	-2.278492	0.0419335	*	0.9999488	



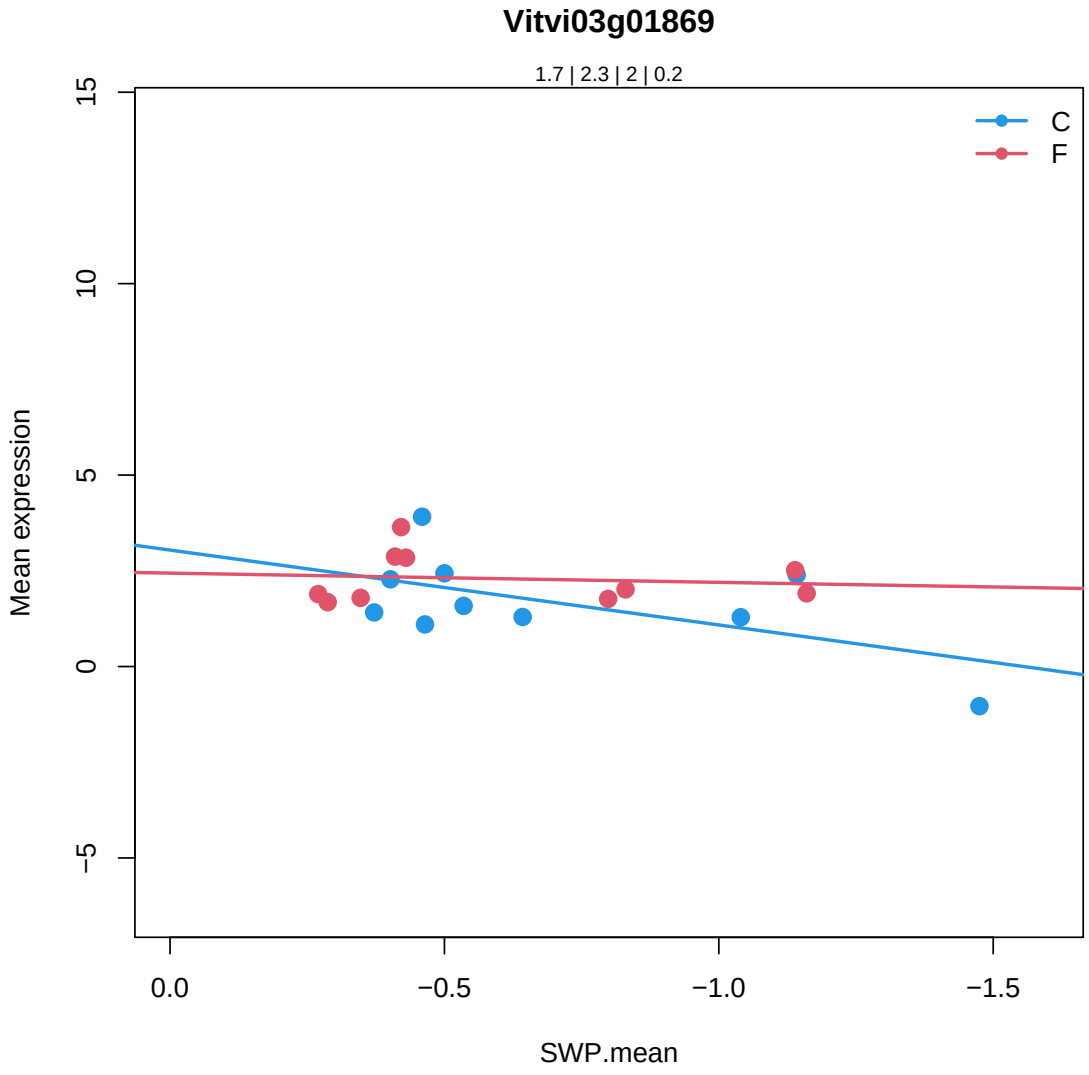
7.6.30 Vitvi03g01869: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g01869
        35.2
        not assigned.unknown
        UDP-Glycosyltransferase superfamily protein |
        Chr3:7667099-7668556 FORWARD LENGTH=485 |
        201606
```

Coefficients for Vitvi03g01869.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.665901	2.266382e-06	***	2.594967e-06	***
SlopeC	1.955673	0.0134462	*	0.3305597	
MeanF-MeanC	0.6263891	0.1041064		0.3738902	
SlopeF-SlopeC	-1.714757	0.1271766		0.9999488	



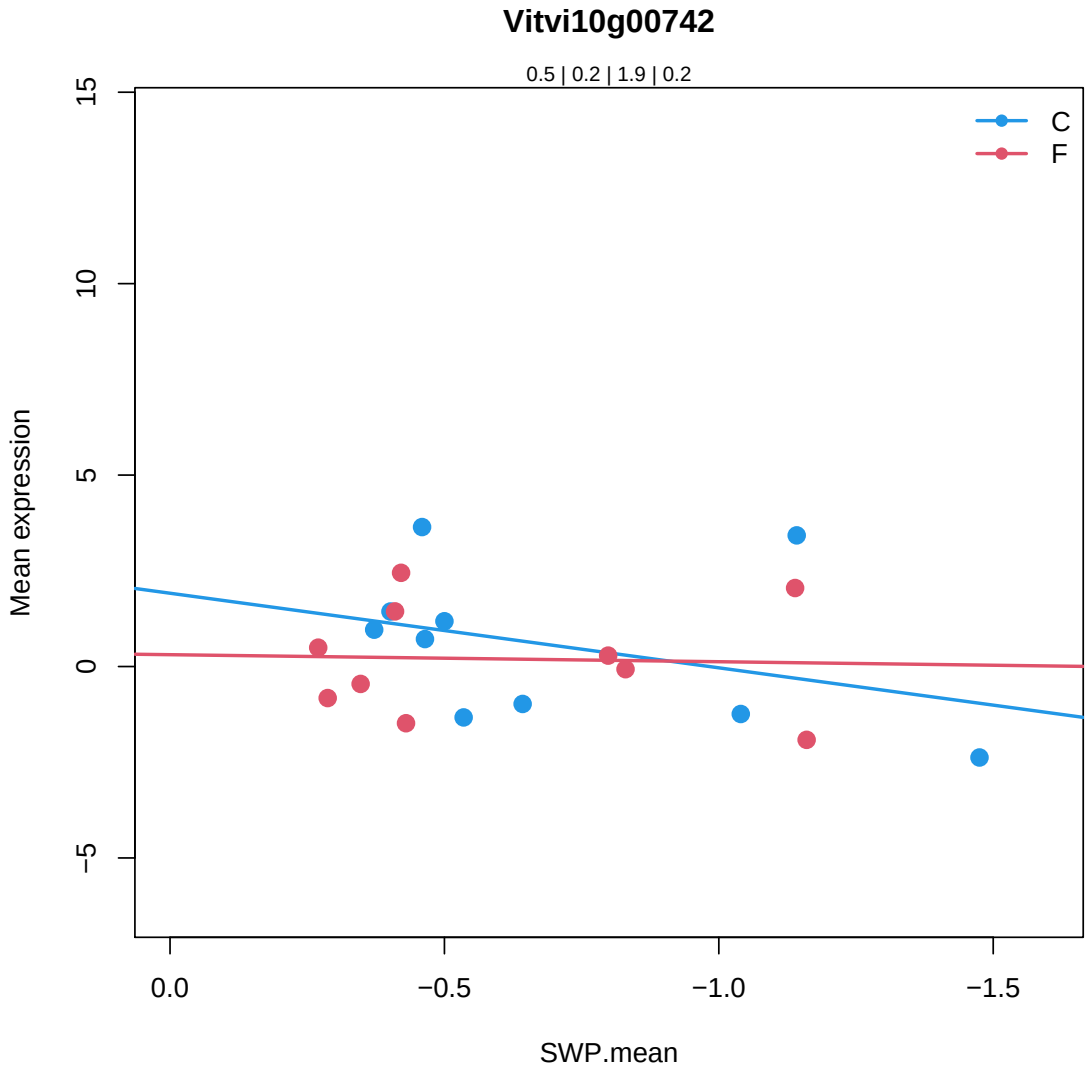
7.6.31 Vitvi10g00742: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00742
        30.2.12
        signalling.receptor kinases.leucine rich repeat XII
        Leucine-rich receptor-like protein kinase family protein |
        Chr5:18791802-18795407 FORWARD LENGTH=1173 |
        201606
```

Coefficients for Vitvi10g00742.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.5441057	0.2822085		0.2877205	
SlopeC	1.948621	0.1699894		0.7004125	
MeanF-MeanC	-0.3471976	0.6237392		0.8706267	
SlopeF-SlopeC	-1.765154	0.39703		0.9999488	



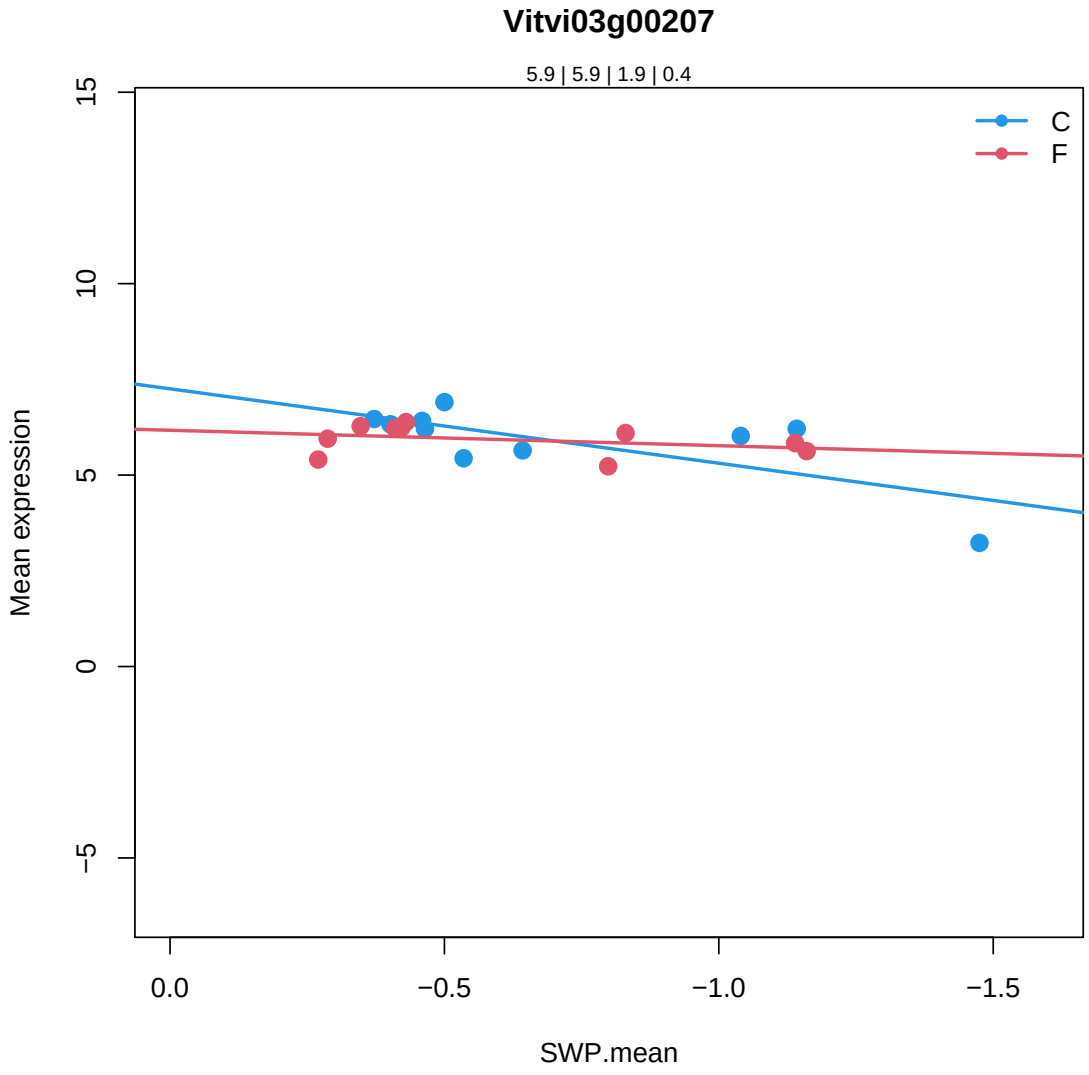
7.6.32 Vitvi03g00207: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00207
        27.3.27
        RNA.regulation of transcription.NAC domain transcription factor family
        NAC domain containing protein 36 |
        Chr2:7407123-7408120 FORWARD LENGTH=276 |
        201606
```

Coefficients for Vitvi03g00207.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.88632	1.010976e-19	***	4.827475e-19	***
SlopeC	1.942965	0.0008966901	***	0.1188465	
MeanF-MeanC	0.03886058	0.8809396		0.9689711	
SlopeF-SlopeC	-1.540484	0.05256793	.	0.9999488	



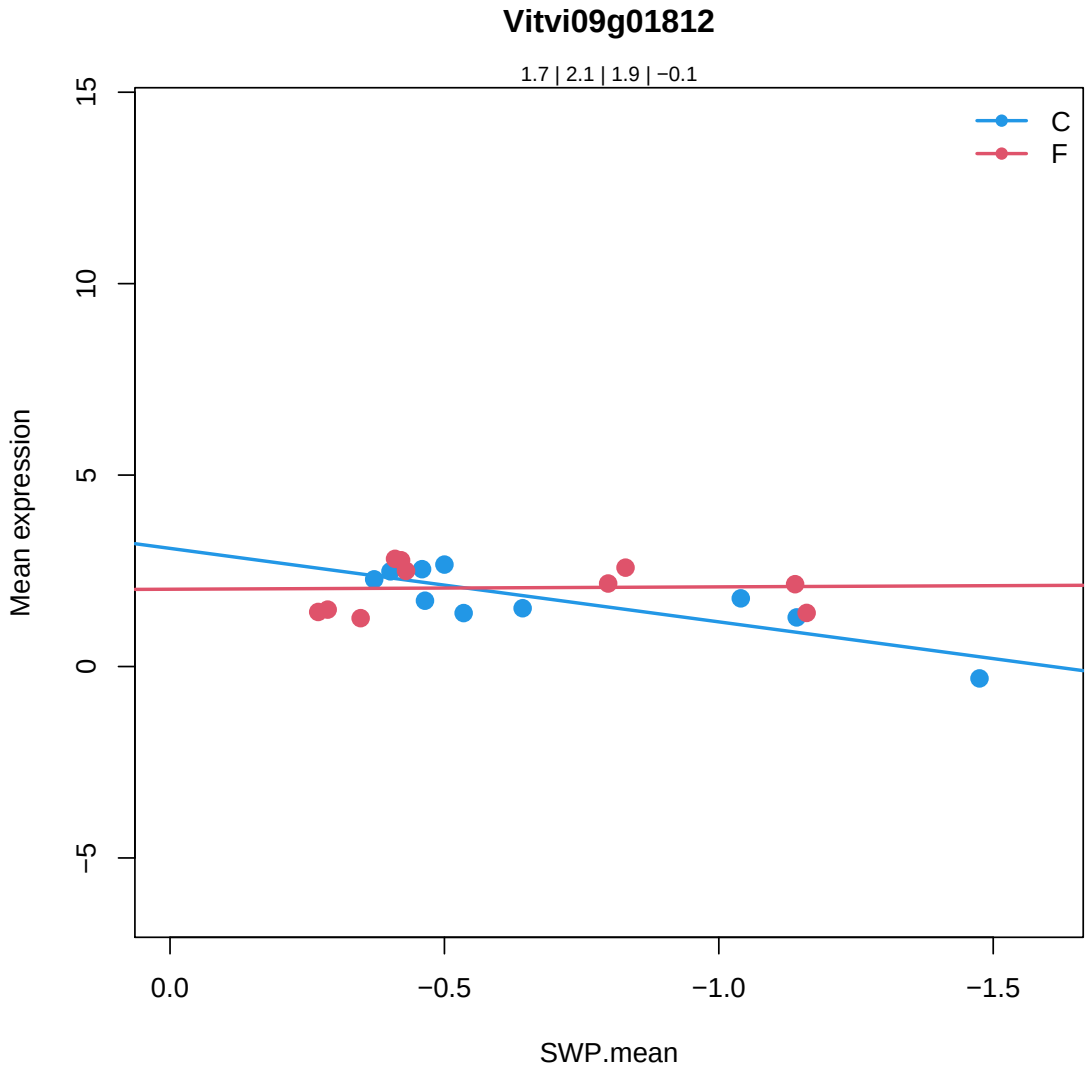
7.6.33 Vitvi09g01812: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g01812
        20.1.2
        stress.biotic.receptors
        receptor like protein 1 |
        Chr1:2270633-2274654 FORWARD LENGTH=913 |
        201606
```

Coefficients for Vitvi09g01812.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.735602	2.578953e-09	***	3.209111e-09	***
SlopeC	1.919239	0.0008702575	***	0.1184327	
MeanF-MeanC	0.3203048	0.21809		0.567451	
SlopeF-SlopeC	-1.980952	0.01385965	*	0.9999488	



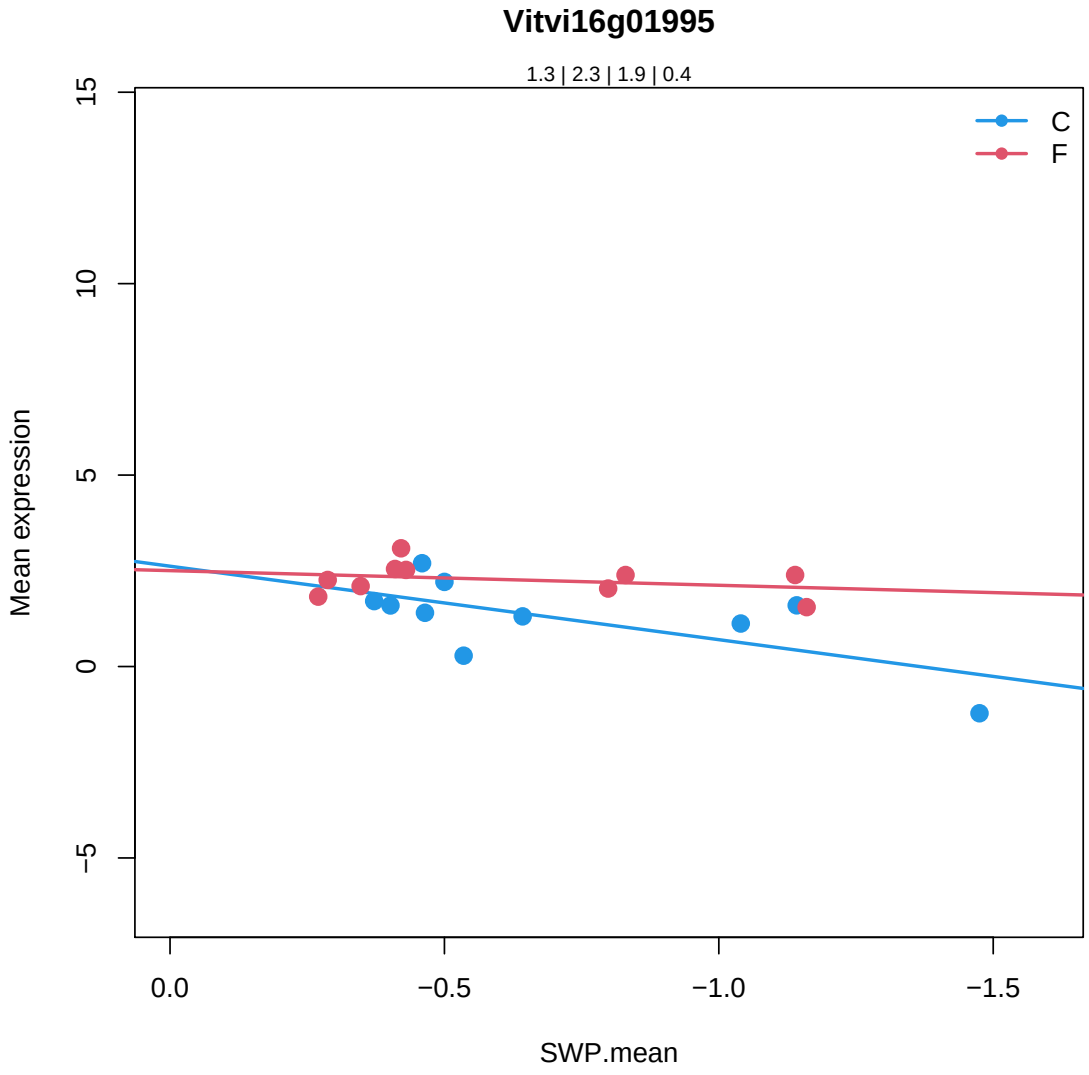
7.6.34 Vitvi16g01995: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01995
        35.2
        not assigned.unknown
        PR5-like receptor kinase |
        Chr5:15293325-15295838 REVERSE LENGTH=665 |
        201606
```

Coefficients for Vitvi16g01995.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.270518	2.436594e-06	***	2.787971e-06	***
SlopeC	1.918908	0.002355775	**	0.1841371	
MeanF-MeanC	1.000552	0.001907489	**	0.02124687	*
SlopeF-SlopeC	-1.536769	0.07734706	.	0.9999488	



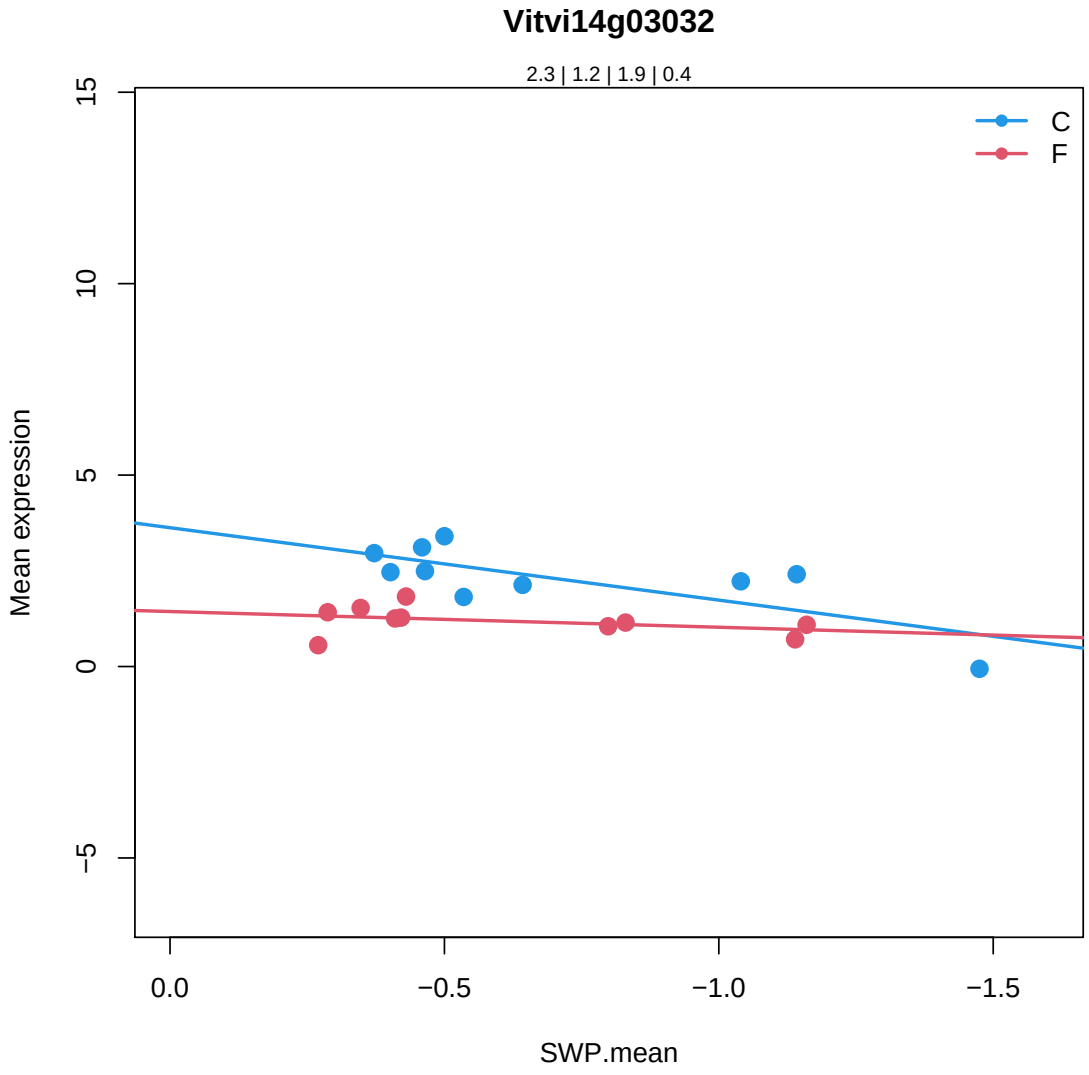
7.6.35 Vitvi14g03032: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g03032
        35.2
        not assigned.unknown
        senescence-associated gene 101 |
        Chr5:4828754-4830769 FORWARD LENGTH=537 |
        201606
```

Coefficients for Vitvi14g03032.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.295758	4.137197e-12	***	5.741001e-12	***
SlopeC	1.890992	0.0005292593	***	0.1005065	
MeanF-MeanC	-1.109618	0.00011621	***	0.002052459	**
SlopeF-SlopeC	-1.481025	0.04379561	*	0.9999488	



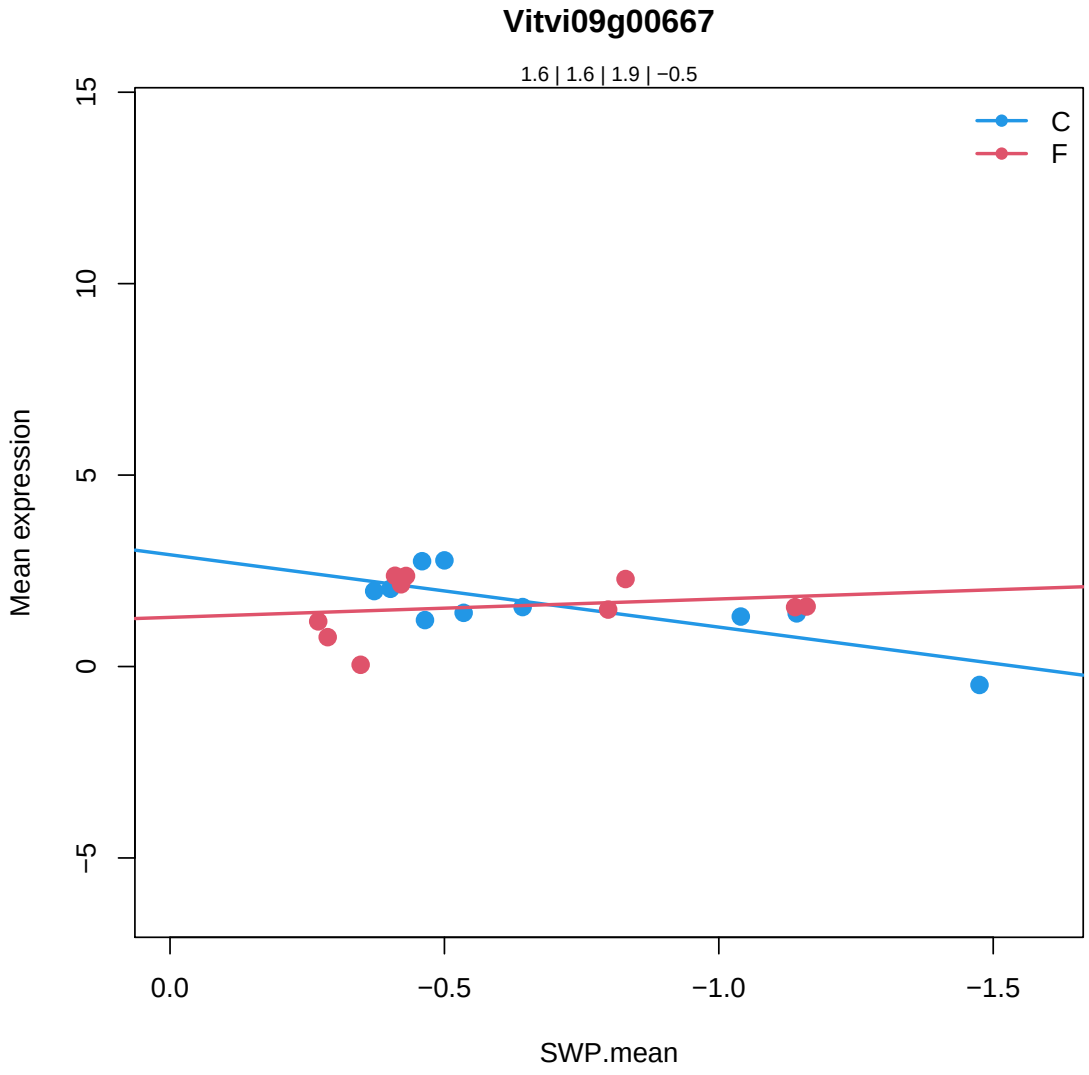
7.6.36 Vitvi09g00667: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00667
        20.1.2
        stress.biotic.receptors
        receptor like protein 1 |
        Chr1:2270633-2274654 FORWARD LENGTH=913 |
        201606
```

Coefficients for Vitvi09g00667.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.590052	1.599417e-07	***	1.887013e-07	***
SlopeC	1.889958	0.003763512	**	0.2269459	
MeanF-MeanC	-0.01386751	0.9630231		0.9915927	
SlopeF-SlopeC	-2.370296	0.01217728	*	0.9999488	



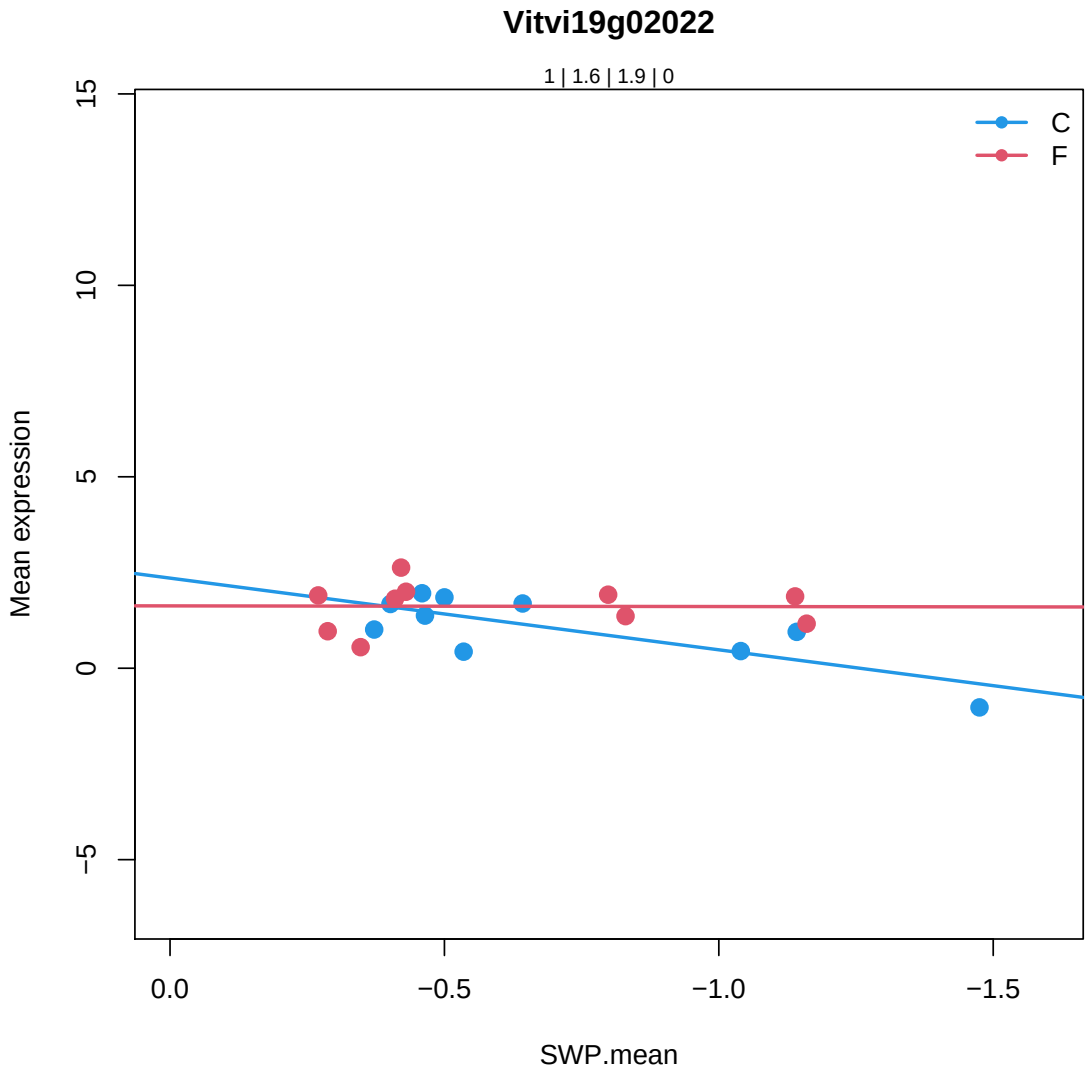
7.6.37 Vitvi19g02022: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g02022
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi19g02022.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.036599	1.540848e-05	***	1.732488e-05	***
SlopeC	1.872573	0.001628496	**	0.1556102	
MeanF-MeanC	0.5810322	0.03893743	*	0.2029373	
SlopeF-SlopeC	-1.855836	0.02557959	*	0.9999488	



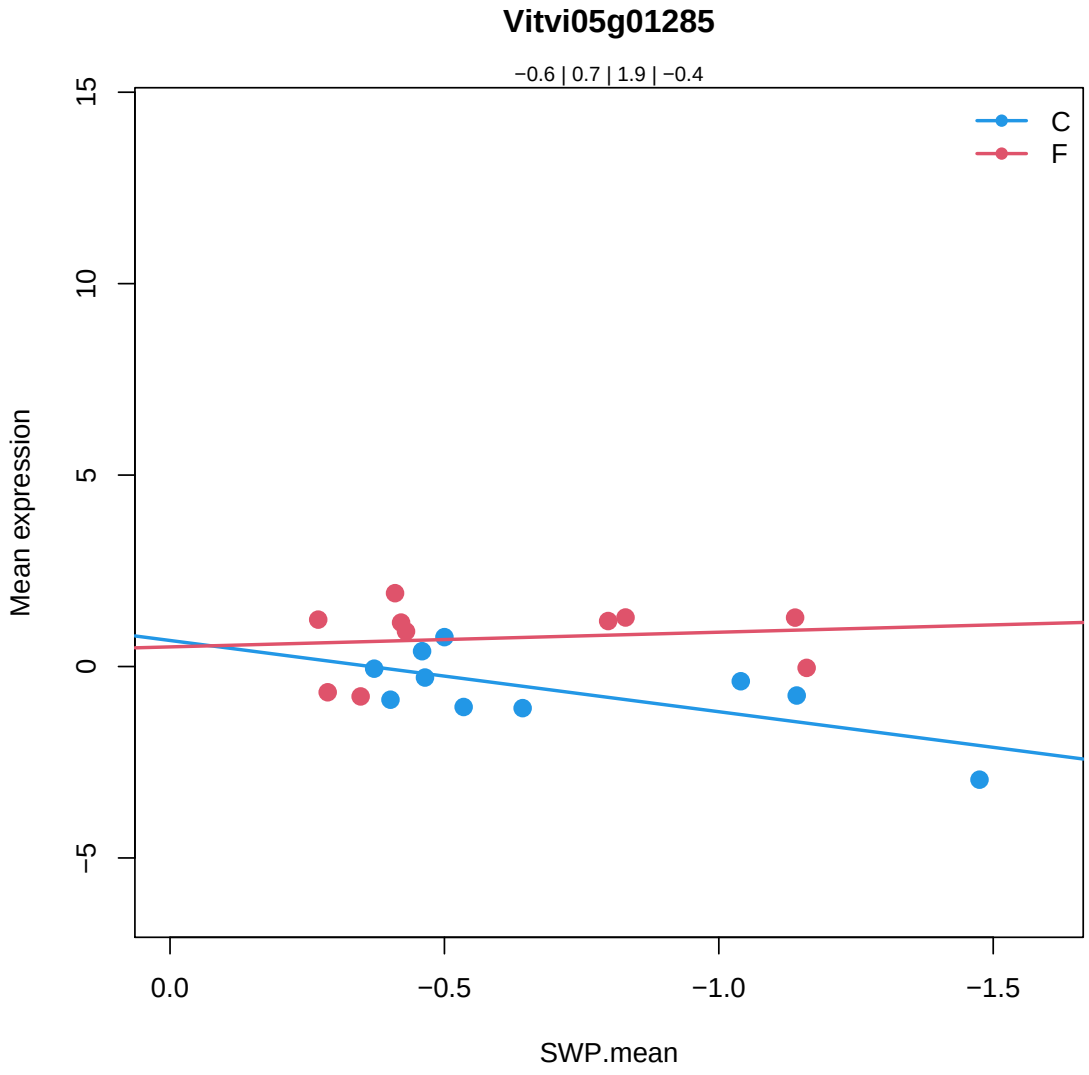
7.6.38 Vitvi05g01285: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01285
        35.2
        not assigned.unknown
        indole-3-acetate beta-D-glucosyltransferase |
        Chr4:8877877-8879301 REVERSE LENGTH=474 |
        201606
```

Coefficients for Vitvi05g01285.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.6285472	0.02067477	*	0.02173275	*
SlopeC	1.860691	0.01455316	*	0.3359386	
MeanF-MeanC	1.374557	0.0008738596	***	0.01117397	*
SlopeF-SlopeC	-2.244205	0.04275548	*	0.9999488	



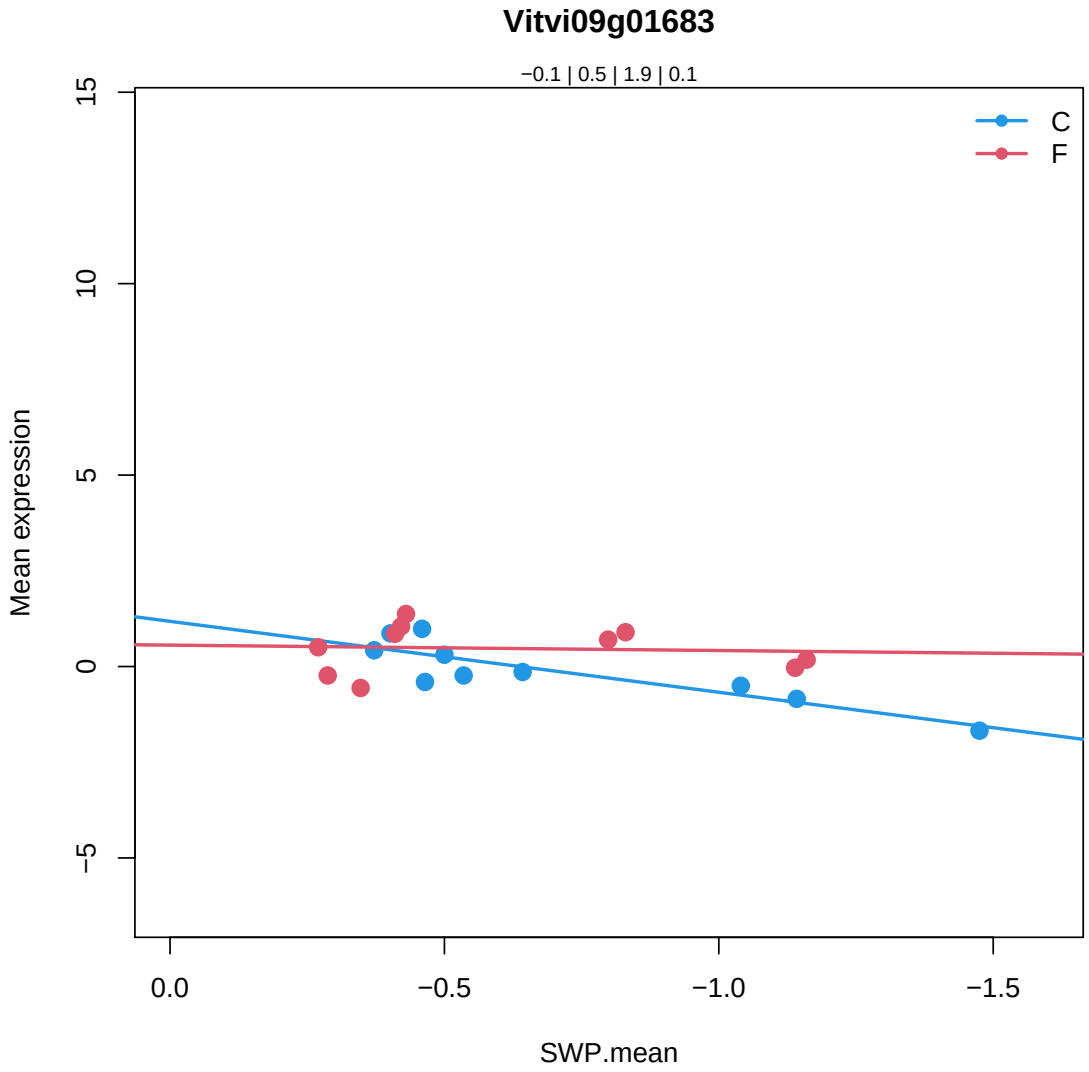
7.6.39 Vitvi09g01683: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g01683
        20.1.2
        stress.biotic.receptors
        receptor like protein 1 |
        Chr1:2270633-2274654 FORWARD LENGTH=913 |
        201606
```

Coefficients for Vitvi09g01683.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.1223697	0.47724		0.483489	
SlopeC	1.852284	0.0007332136	***	0.1076608	
MeanF-MeanC	0.5951364	0.02114283	*	0.1311596	
SlopeF-SlopeC	-1.710913	0.02331123	*	0.9999488	



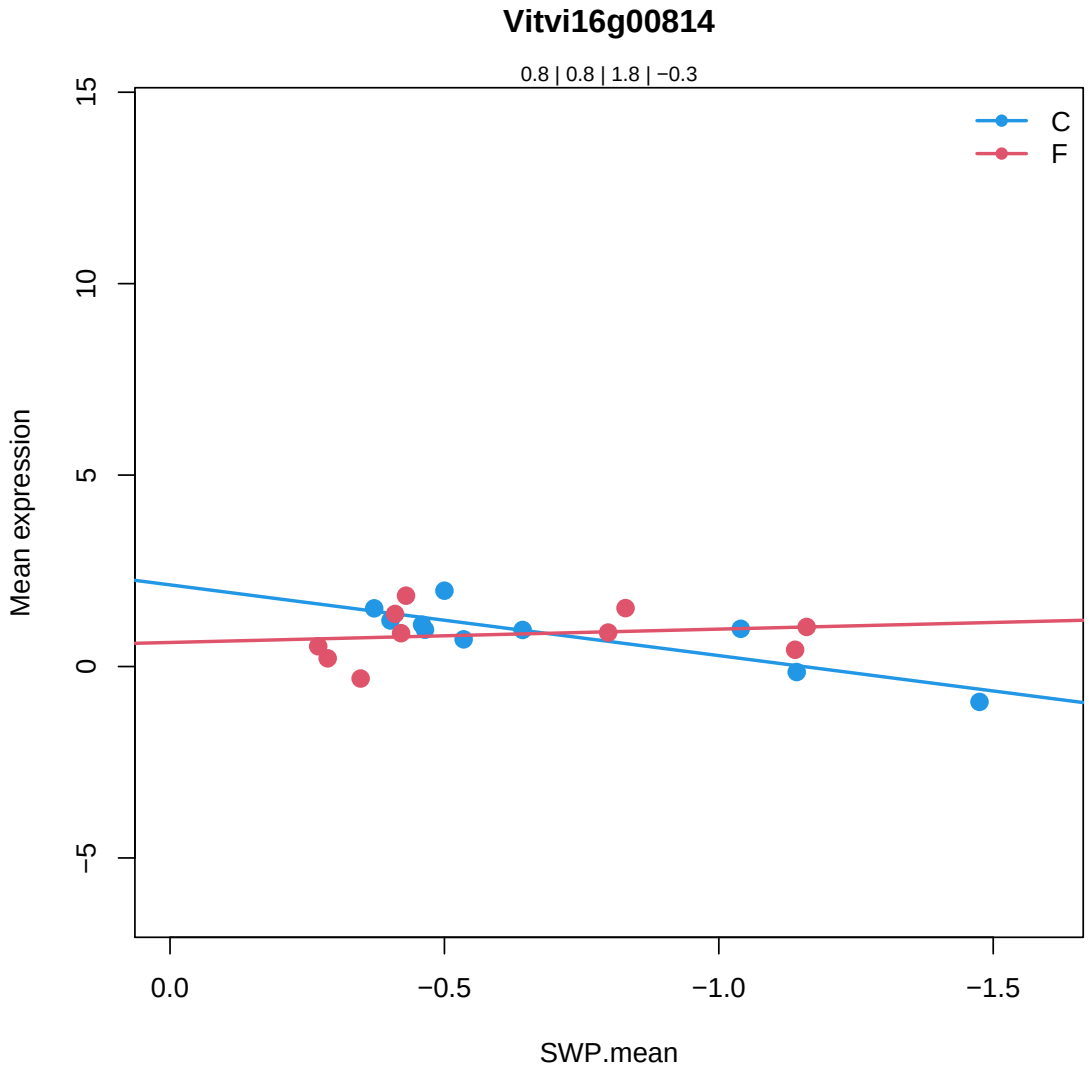
7.6.40 Vitvi16g00814: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g00814
        35.2
        not assigned.unknown
        Protein kinase superfamily protein |
        Chr1:24961634-24963941 REVERSE LENGTH=666 |
        201606
```

Coefficients for Vitvi16g00814.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8334508	0.0001093319	***	0.0001206427	***
SlopeC	1.847189	0.001108435	**	0.1330296	
MeanF-MeanC	0.006900955	0.978186		0.994504	
SlopeF-SlopeC	-2.195694	0.006624803	**	0.9999488	



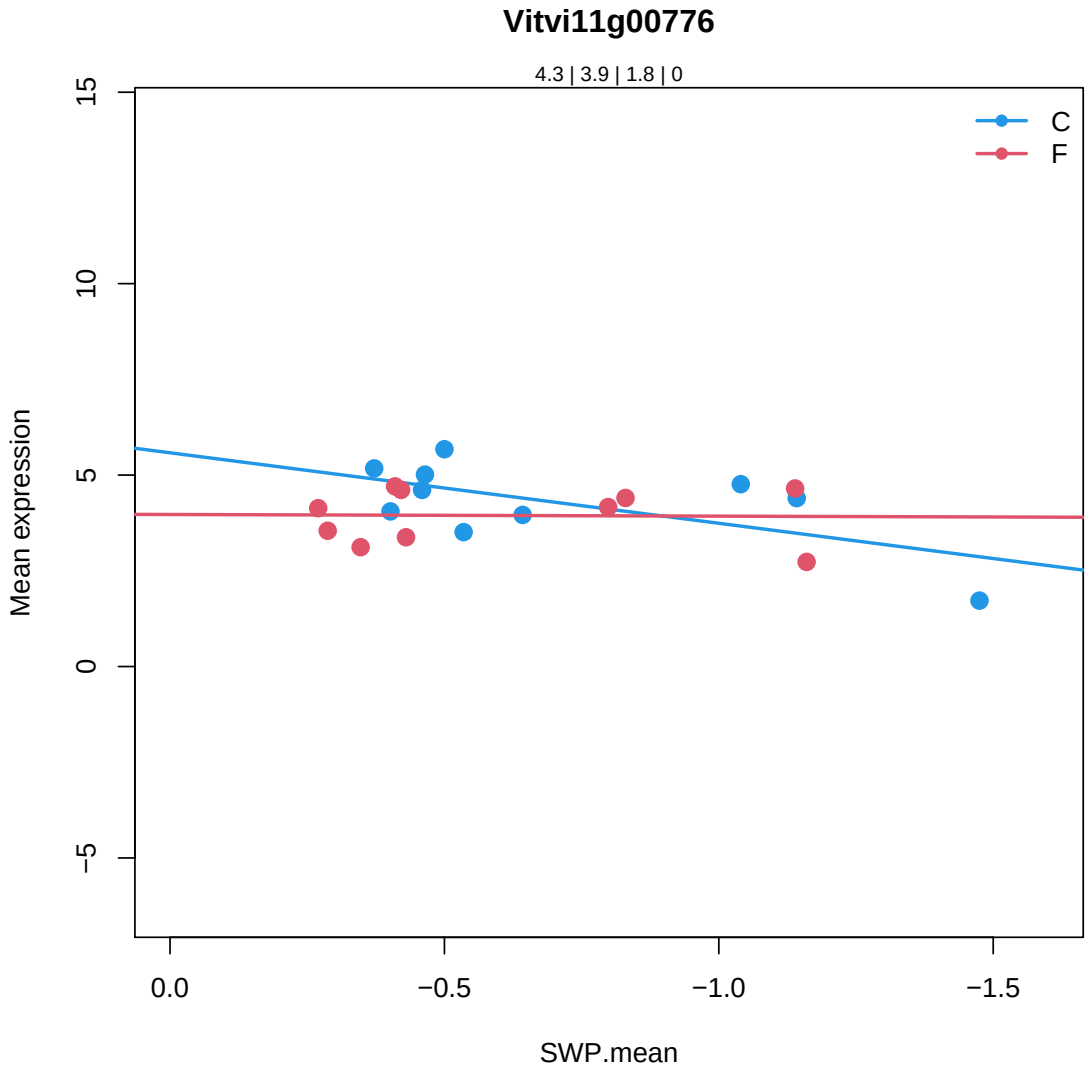
7.6.41 Vitvi11g00776: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00776
        35.2
        not assigned.unknown
        Leucine-rich repeat receptor-like protein kinase family protein |
        Chr4:5637467-5640496 REVERSE LENGTH=1009 |
        201606
```

Coefficients for Vitvi11g00776.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.287529	2.271583e-14	***	3.679434e-14	***
SlopeC	1.840896	0.01157168	*	0.318473	
MeanF-MeanC	-0.3434326	0.3222382		0.6828918	
SlopeF-SlopeC	-1.79792	0.08407379	.	0.9999488	



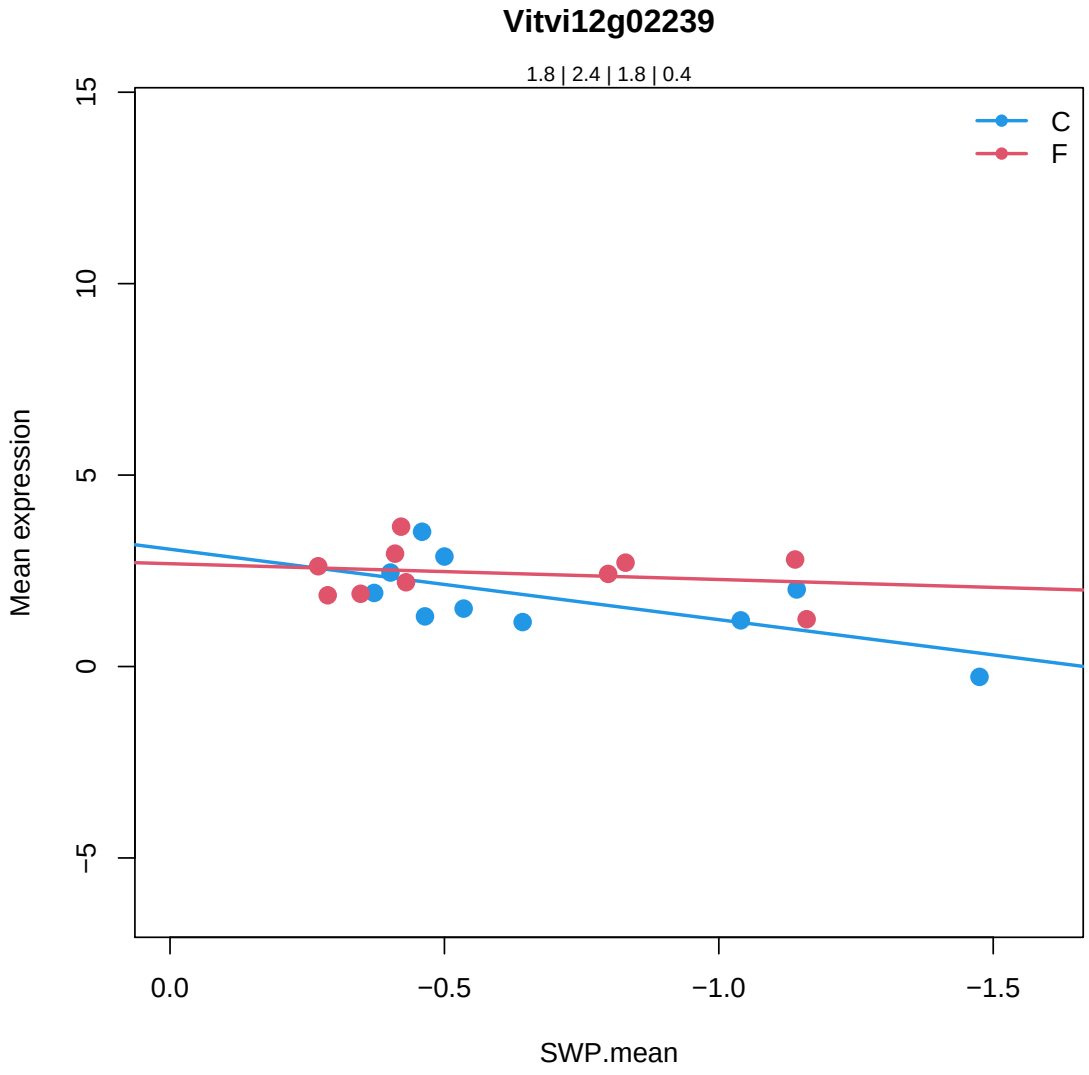
7.6.42 Vitvi12g02239: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02239
        30.2.12
        signalling.receptor kinases.leucine rich repeat XII
        Leucine-rich repeat protein kinase family protein |
        Chr3:17527611-17530748 FORWARD LENGTH=1010 |
        201606
```

Coefficients for Vitvi12g02239.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.769829	9.049211e-08	***	1.07496e-07	***
SlopeC	1.839386	0.007638483	**	0.2791441	
MeanF-MeanC	0.6643175	0.04853306	*	0.2346894	
SlopeF-SlopeC	-1.426784	0.1395736		0.9999488	



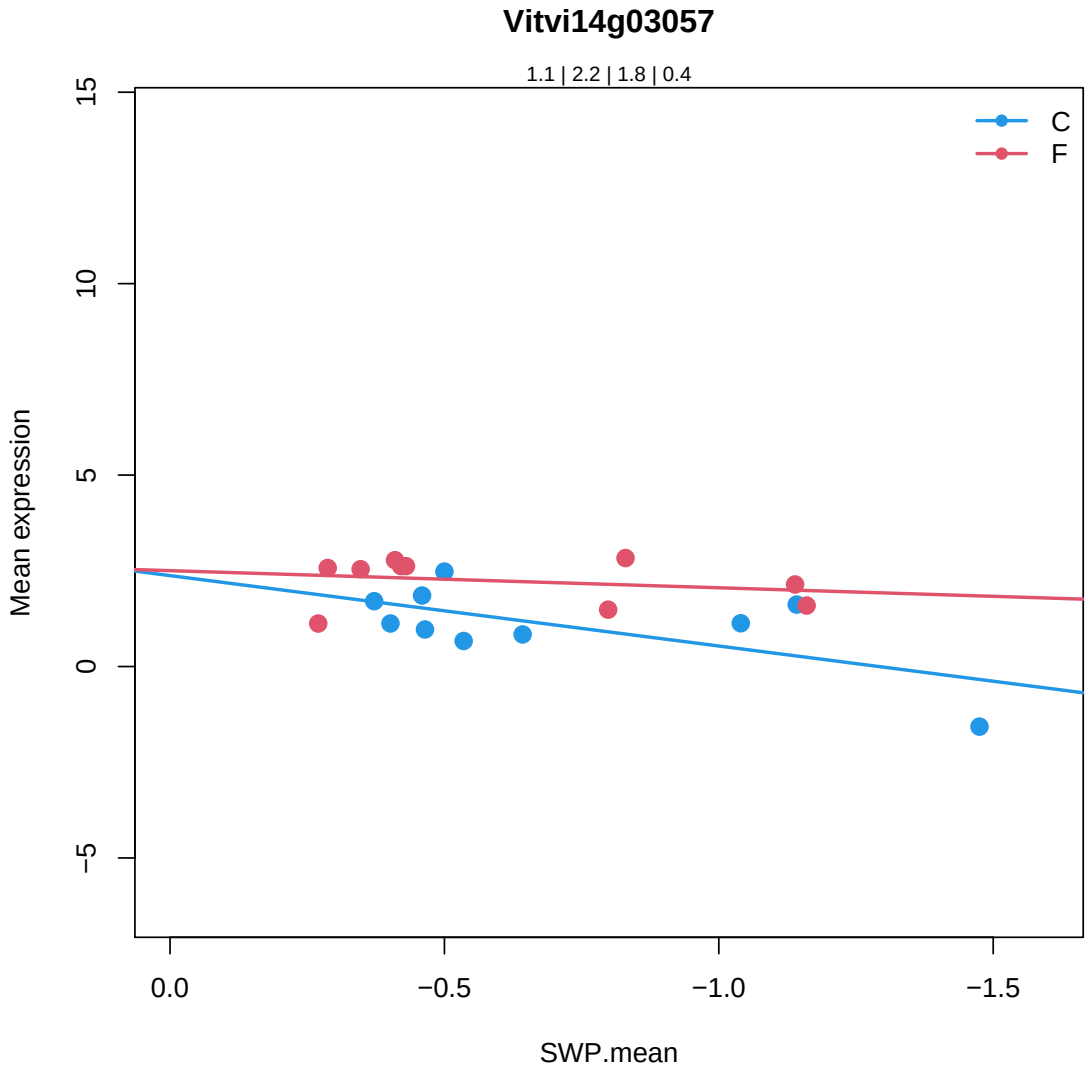
7.6.43 Vitvi14g03057: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g03057
        35.2
        not assigned.unknown
        Leucine-rich repeat receptor-like protein kinase family protein |
        Chr4:5637467-5640496 REVERSE LENGTH=1009 |
        201606
```

Coefficients for Vitvi14g03057.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.081444	7.919614e-05	***	8.76176e-05	***
SlopeC	1.839061	0.007193766	**	0.2775469	
MeanF-MeanC	1.149688	0.001446577	**	0.01693451	*
SlopeF-SlopeC	-1.391957	0.1455251		0.9999488	



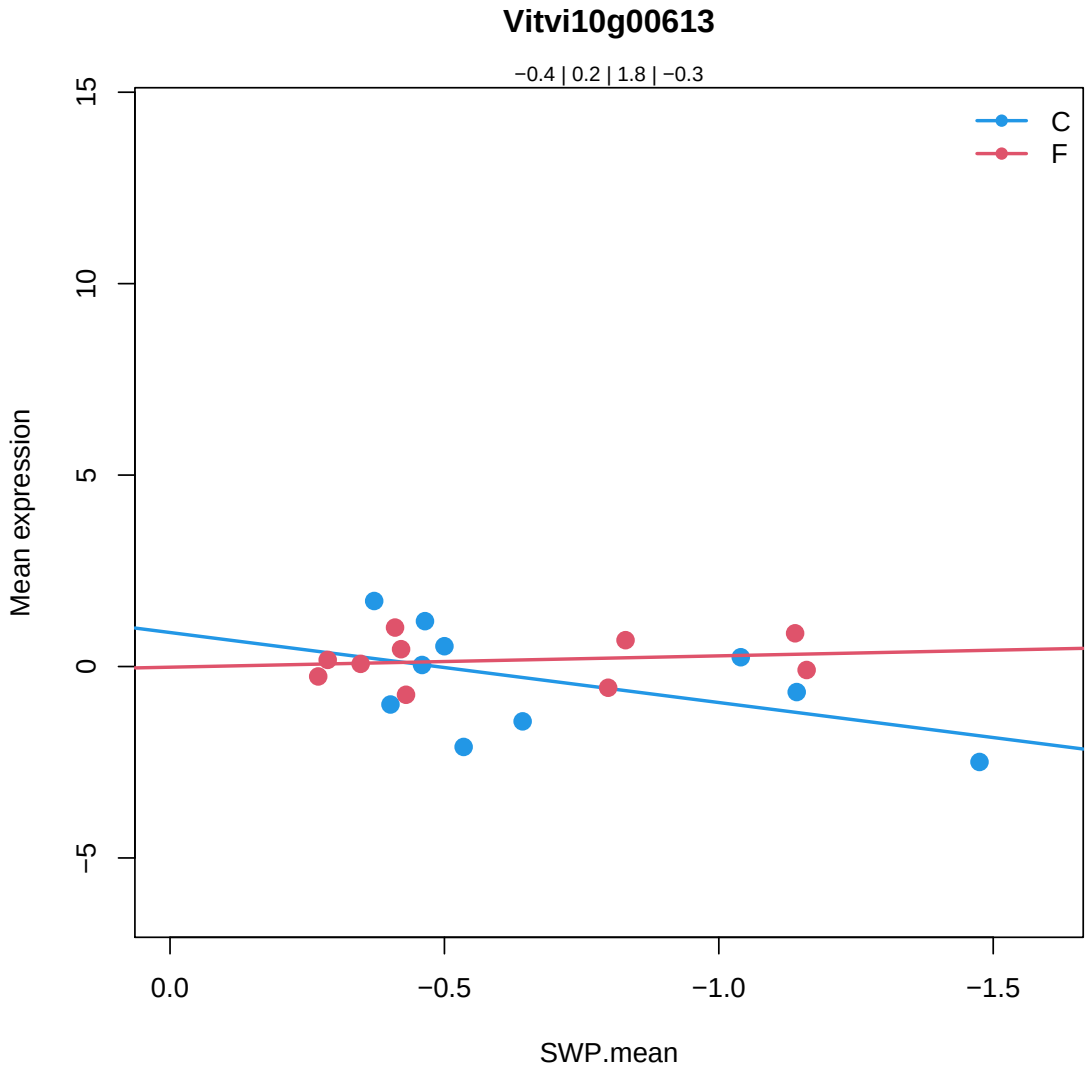
7.6.44 Vitvi10g00613: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00613
        10.2.1
        cell wall.cellulose synthesis.cellulose synthase
        cellulose synthase family protein |
        Chr4:10312846-10316719 REVERSE LENGTH=985 |
        201606
```

Coefficients for Vitvi10g00613.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.3978763	0.1750966		0.1798519	
SlopeC	1.828719	0.03047437	*	0.4320841	
MeanF-MeanC	0.5603847	0.1767898		0.5101322	
SlopeF-SlopeC	-2.124476	0.08458891	.	0.9999488	



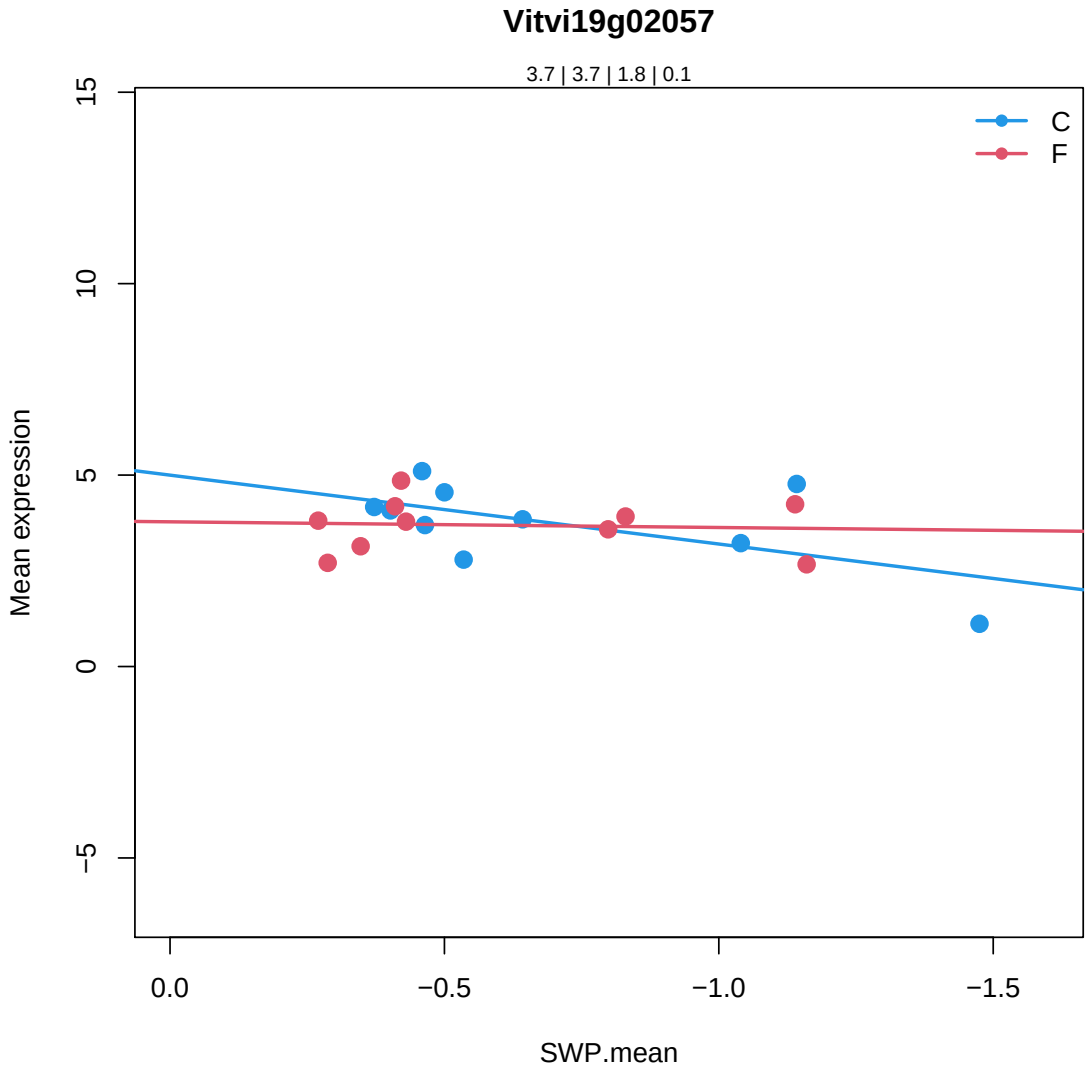
7.6.45 Vitvi19g02057: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g02057
        34.12
        transport.metal
        zinc transporter 11 precursor |
        Chr1:20906161-20907225 FORWARD LENGTH=326 |
        201606
```

Coefficients for Vitvi19g02057.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.733292	7.842978e-13	***	1.133858e-12	***
SlopeC	1.799119	0.01677207	*	0.3523917	
MeanF-MeanC	-0.04448852	0.900763		0.9740639	
SlopeF-SlopeC	-1.650978	0.1243958		0.9999488	



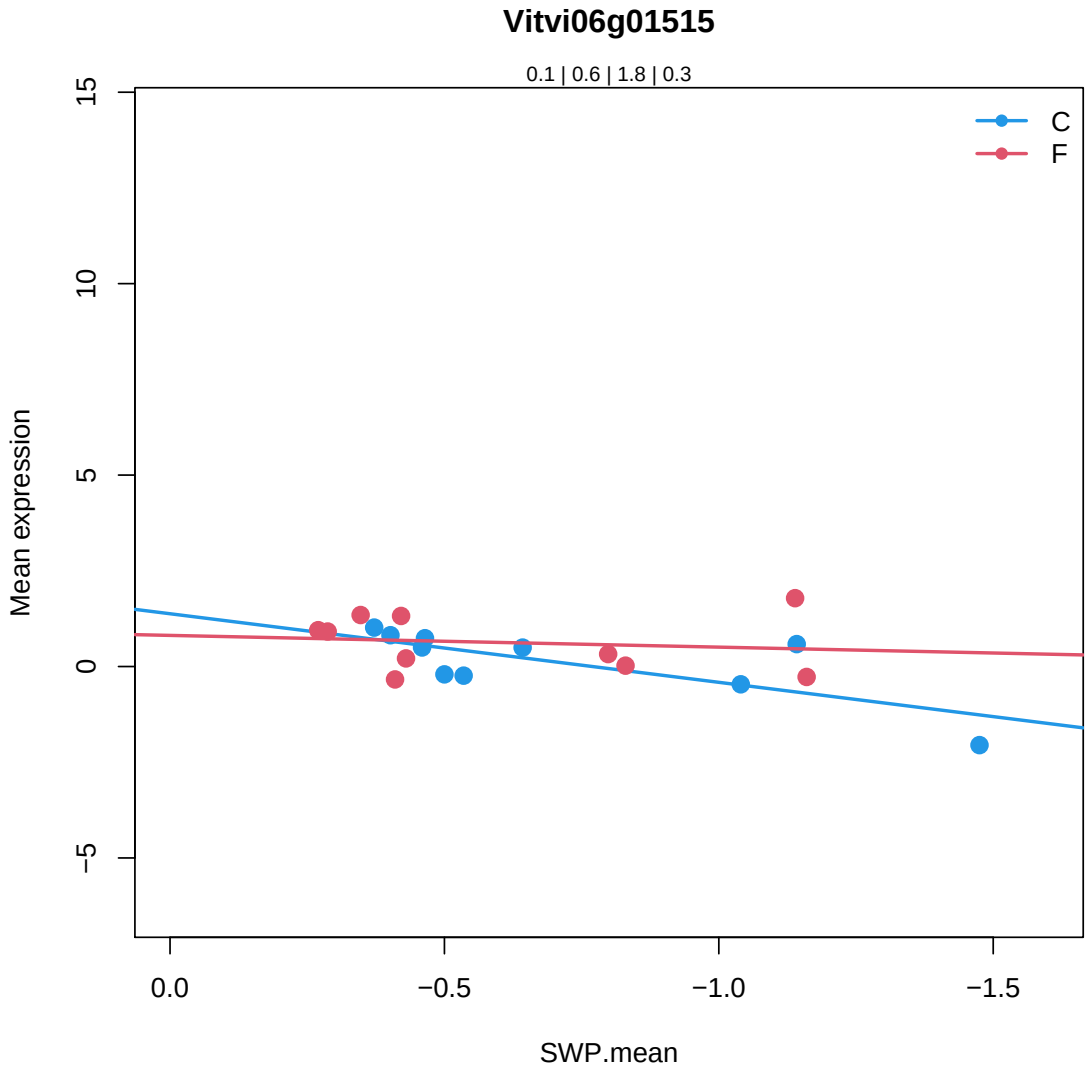
7.6.46 Vitvi06g01515: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01515
        27.3.27
        RNA.regulation of transcription.NAC domain transcription factor family
        NAC domain containing protein 90 |
        Chr5:7408924-7410038 REVERSE LENGTH=235 |
        201606
```

Coefficients for Vitvi06g01515.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1188095	0.5768337		0.5824125	
SlopeC	1.791011	0.005711978	**	0.2614474	
MeanF-MeanC	0.5072372	0.1015759		0.3678357	
SlopeF-SlopeC	-1.484489	0.1017305		0.9999488	



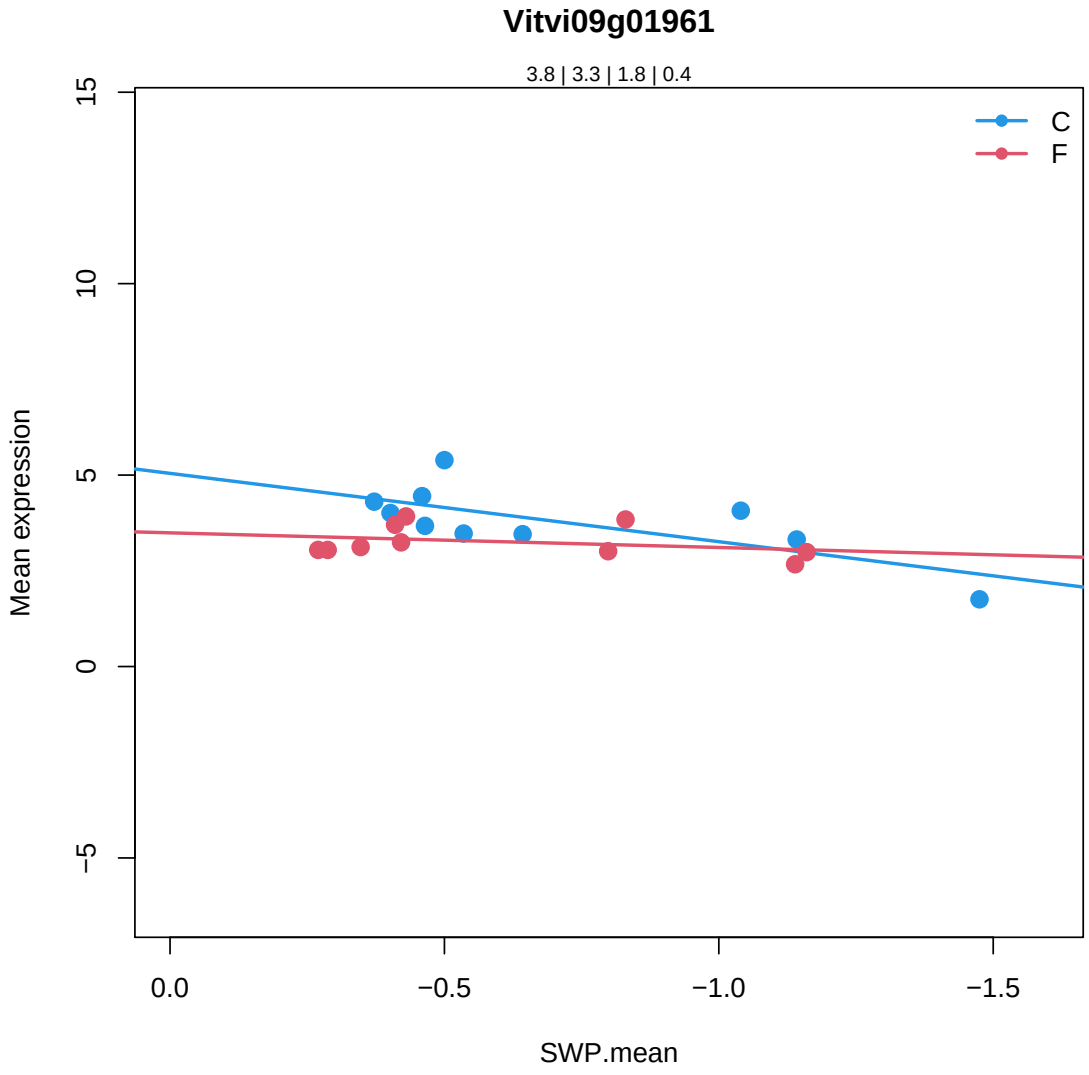
7.6.47 Vitvi09g01961: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g01961
        35.2
        not assigned.unknown
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606
```

Coefficients for Vitvi09g01961.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.790167	4.732846e-16	***	9.254399e-16	***
SlopeC	1.784379	0.001418026	**	0.1479249	
MeanF-MeanC	-0.5316294	0.04347181	*	0.2183187	
SlopeF-SlopeC	-1.402013	0.06658066	.	0.9999488	



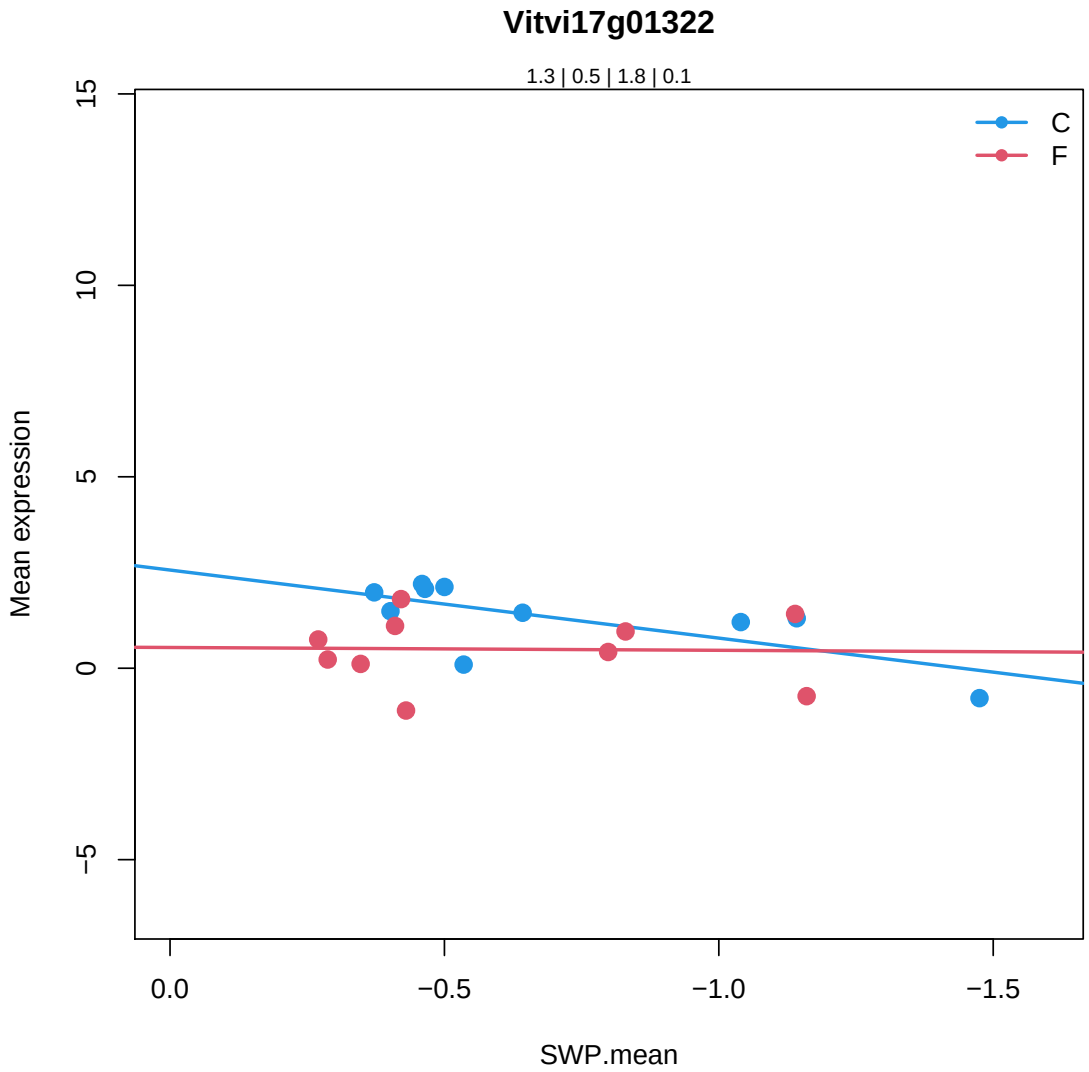
7.6.48 Vitvi17g01322: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g01322
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi17g01322.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.313881	2.698796e-05	***	3.015766e-05	***
SlopeC	1.777495	0.01718838	*	0.3549937	
MeanF-MeanC	-0.8171579	0.0292802	*	0.1663141	
SlopeF-SlopeC	-1.70372	0.1108135		0.9999488	



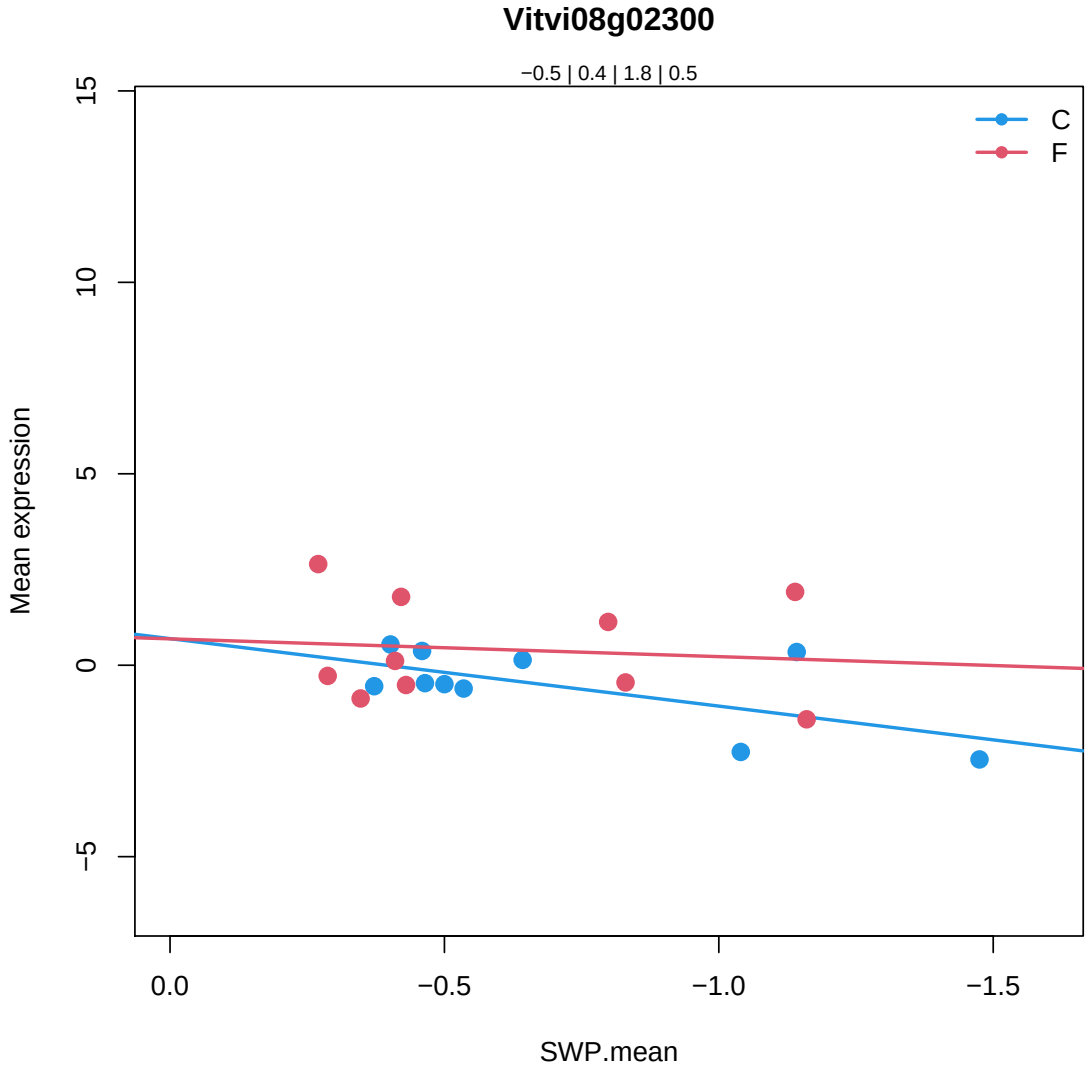
7.6.49 Vitvi08g02300: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g02300
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi08g02300.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	−0.5448287	0.1162978		0.1200712	
SlopeC	1.762531	0.07054354	.	0.5607758	
MeanF−MeanC	0.9504926	0.05616735	.	0.25794	
SlopeF−SlopeC	−1.298304	0.3567596		0.9999488	



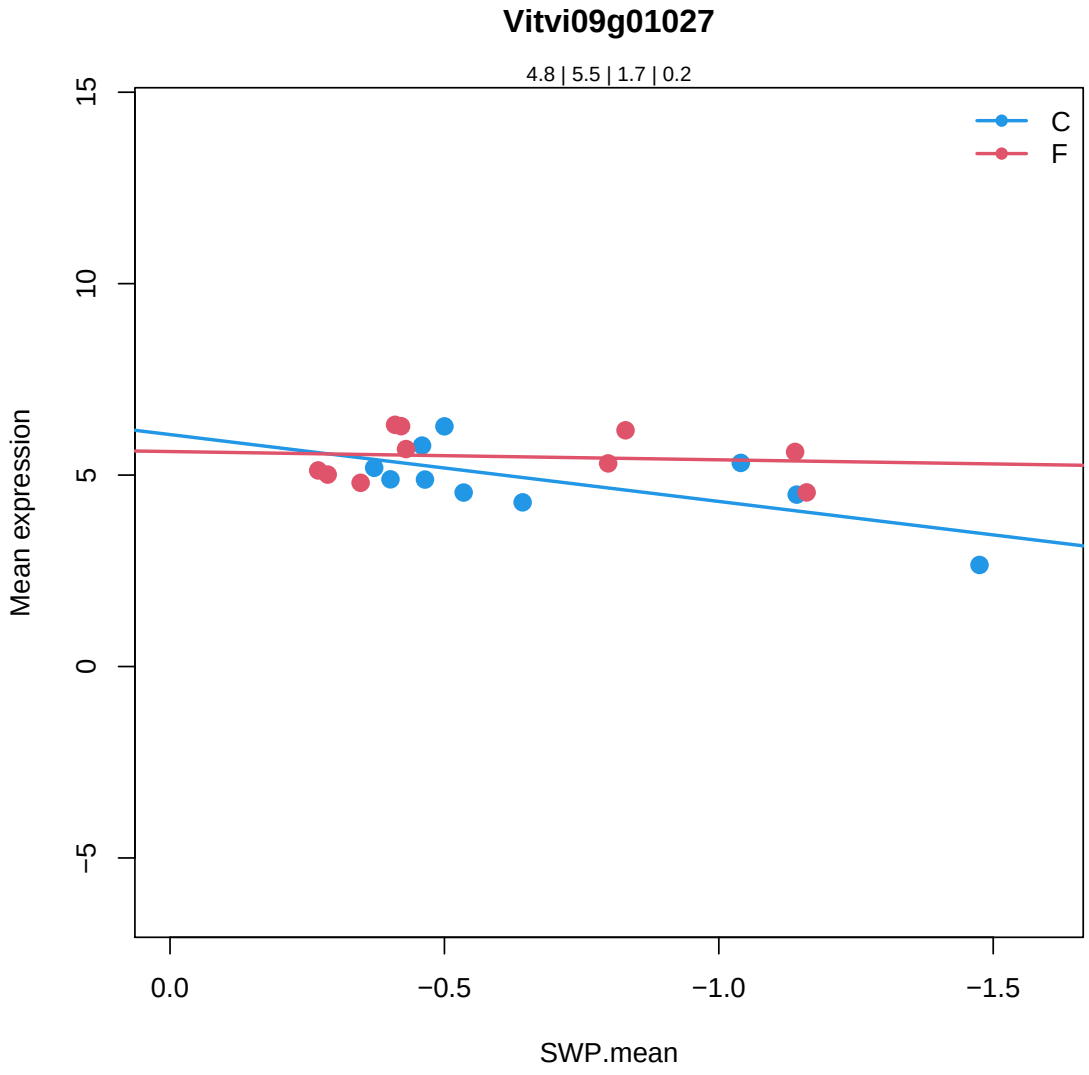
7.6.50 Vitvi09g01027: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g01027
        20.1.2
        stress.biotic.receptors
        receptor like protein 1 |
        Chr1:2270633-2274654 FORWARD LENGTH=913 |
        201606
```

Coefficients for Vitvi09g01027.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.829567	1.354224e-16	***	2.874802e-16	***
SlopeC	1.746818	0.006890348	**	0.2771047	
MeanF-MeanC	0.6532721	0.03897438	*	0.2030237	
SlopeF-SlopeC	-1.531076	0.09263291	.	0.9999488	



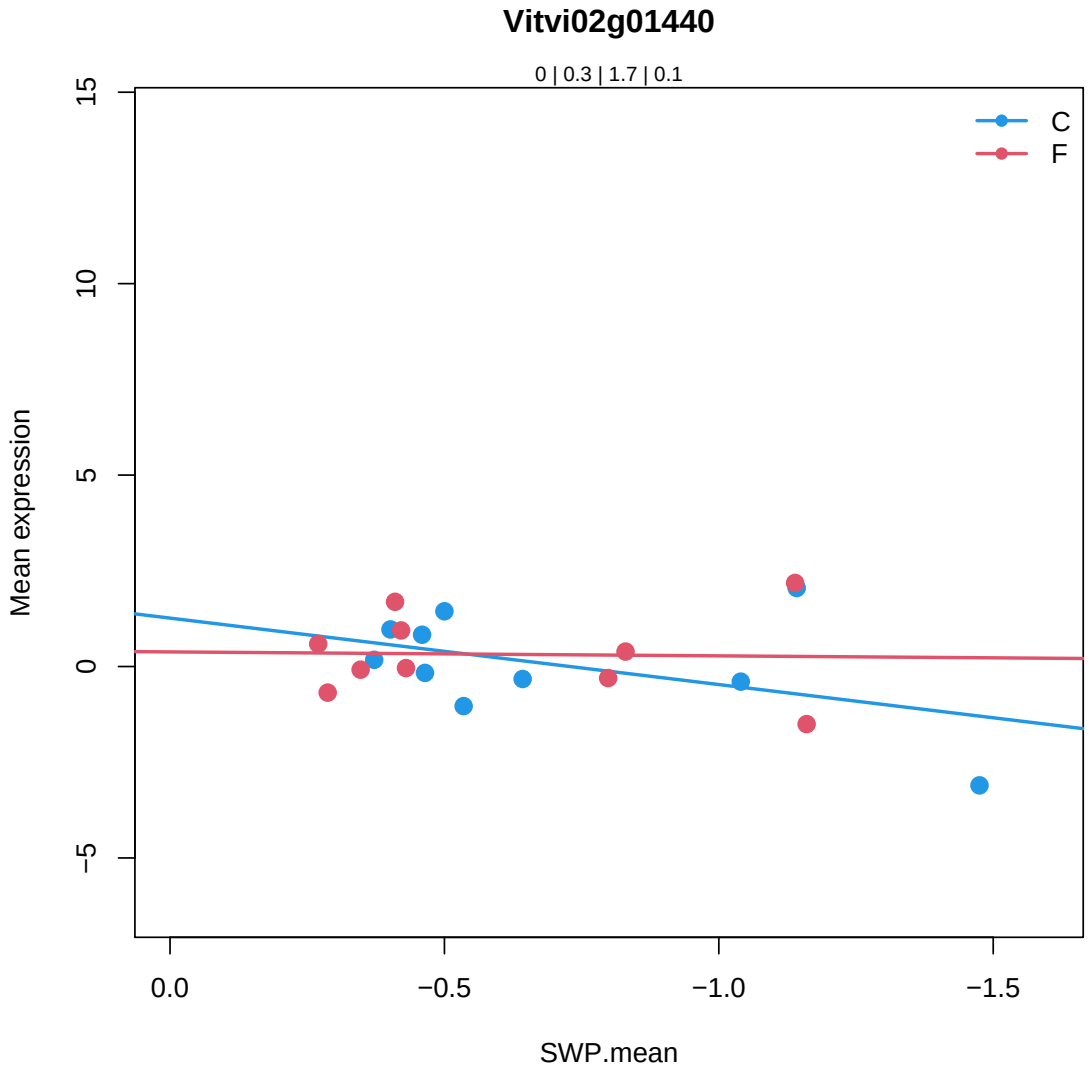
7.6.51 Vitvi02g01440: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g01440
        35.2
        not assigned.unknown
        Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin
        Chr2:18626377-18626781 FORWARD LENGTH=134 |
        201606
```

Coefficients for Vitvi02g01440.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.04392201	0.9029072		0.9050448	
SlopeC	1.734924	0.09395993	.	0.6031557	
MeanF-MeanC	0.2744689	0.5910713		0.8571096	
SlopeF-SlopeC	-1.631996	0.2802773		0.9999488	



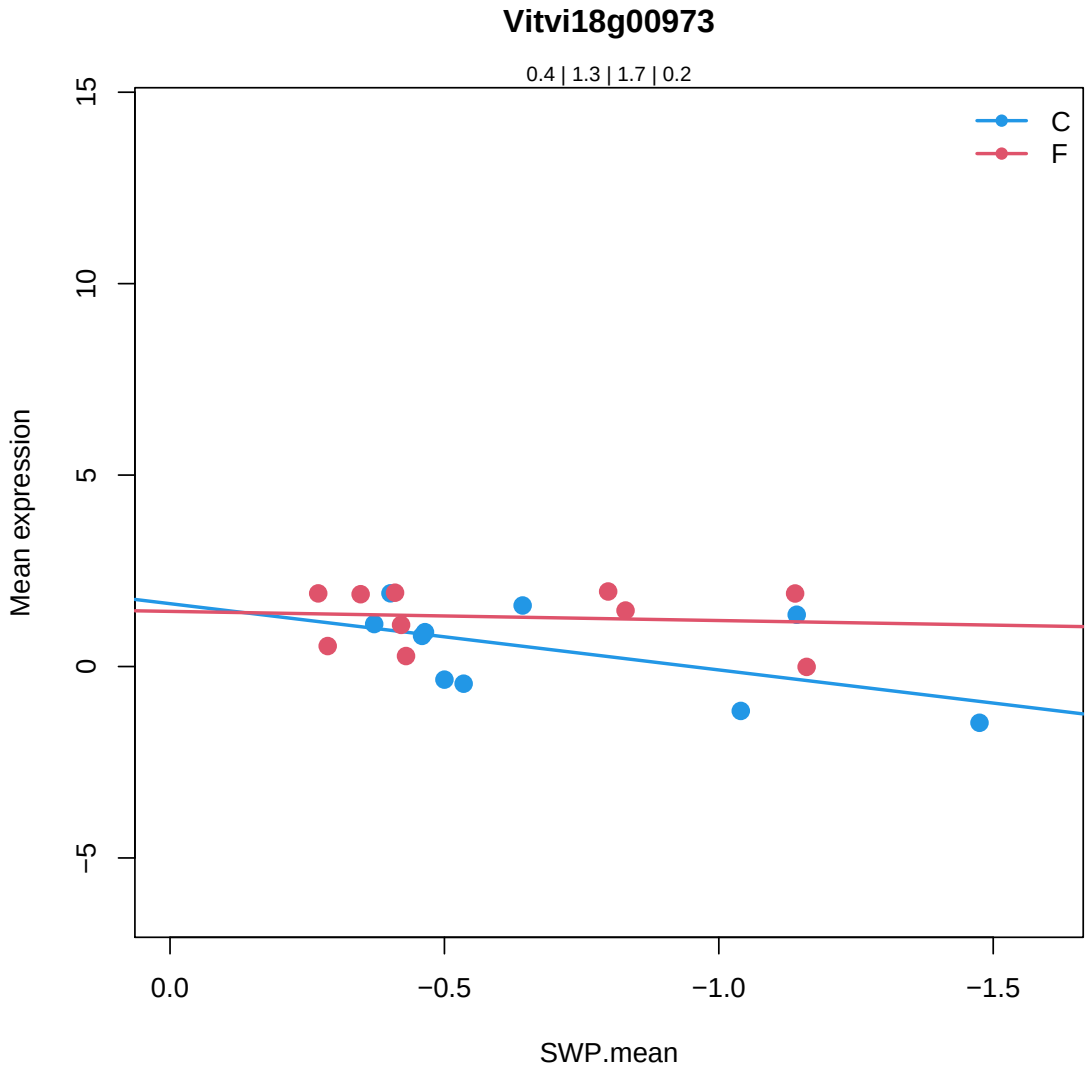
7.6.52 Vitvi18g00973: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00973
        27.3.25
        RNA.regulation of transcription.MYB domain transcription factor family
        RAD-like 1 |
        Chr4:18271457-18271857 REVERSE LENGTH=100 |
        201606
```

Coefficients for Vitvi18g00973.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4243761	0.1283994		0.1324309	
SlopeC	1.730751	0.03038041	*	0.4320841	
MeanF-MeanC	0.8696495	0.03213576	*	0.1776605	
SlopeF-SlopeC	-1.491567	0.1935135		0.9999488	



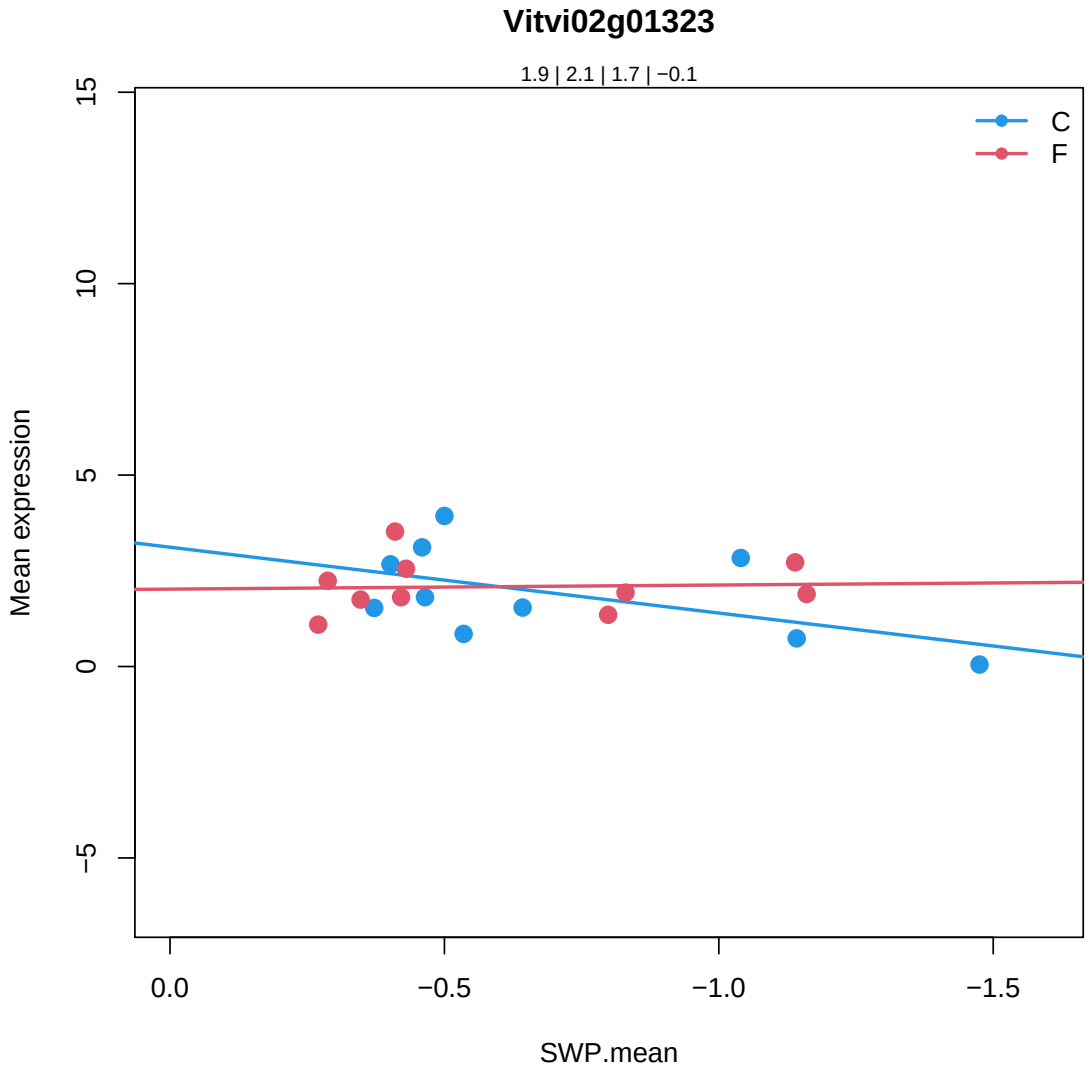
7.6.53 Vitvi02g01323: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g01323
        35.2
        not assigned.unknown
        Disease resistance-responsive (dirigent-like protein) family protein |
        Chr4:12339152-12339715 REVERSE LENGTH=187 |
        201606
```

Coefficients for Vitvi02g01323.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.906896	4.051085e-07	***	4.724664e-07	***
SlopeC	1.719627	0.03007728	*	0.4312902	
MeanF-MeanC	0.1795444	0.6380716		0.8771974	
SlopeF-SlopeC	-1.826547	0.111901		0.9999488	



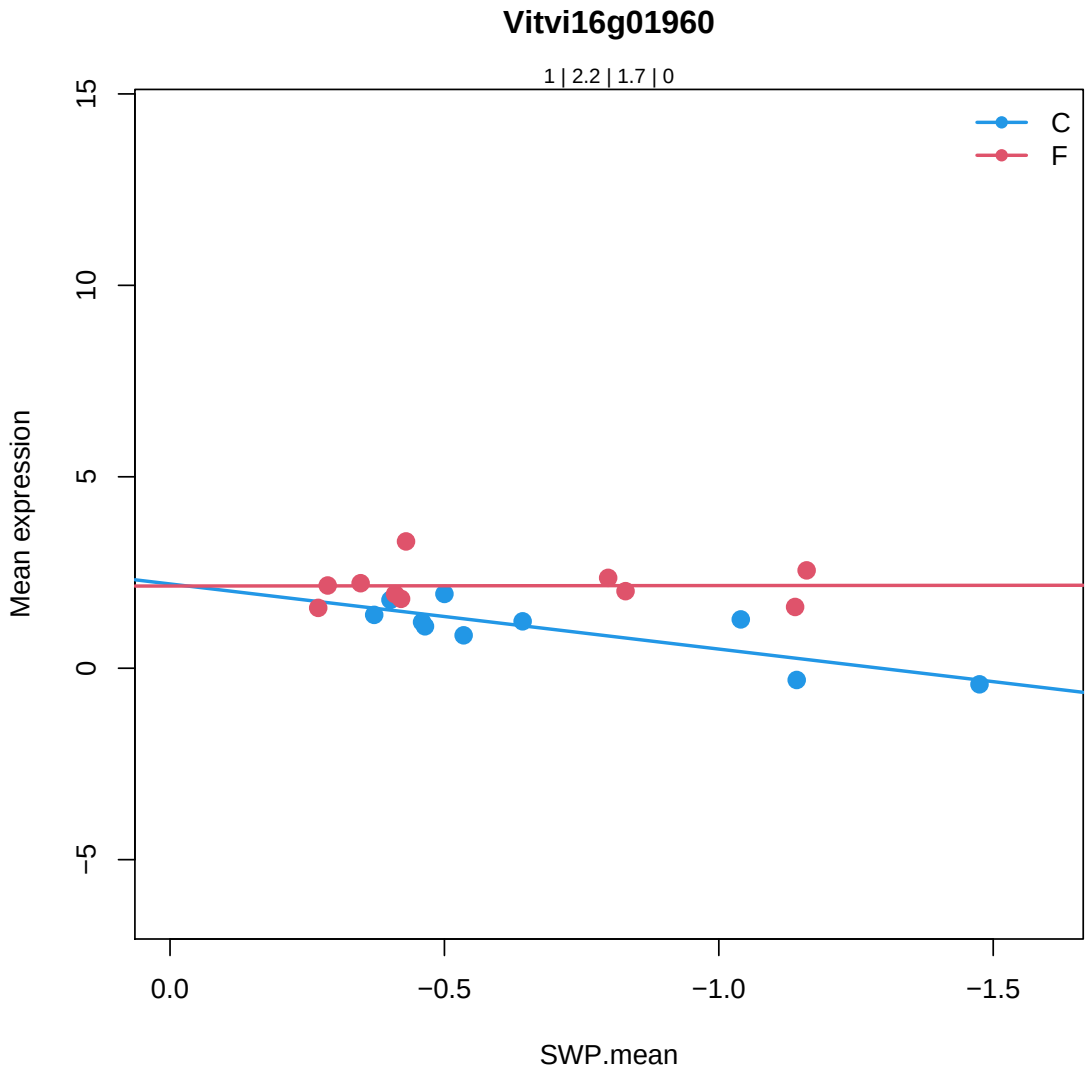
7.6.54 Vitvi16g01960: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01960
        30.2.24
        signalling.receptor kinases.S-locus glycoprotein like
        NA
```

Coefficients for Vitvi16g01960.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.004778	2.984788e-06	***	3.408056e-06	***
SlopeC	1.701228	0.0009907854	***	0.1271346	
MeanF-MeanC	1.149623	4.831542e-05	***	0.0009563943	***
SlopeF-SlopeC	-1.713058	0.0173612	*	0.9999488	



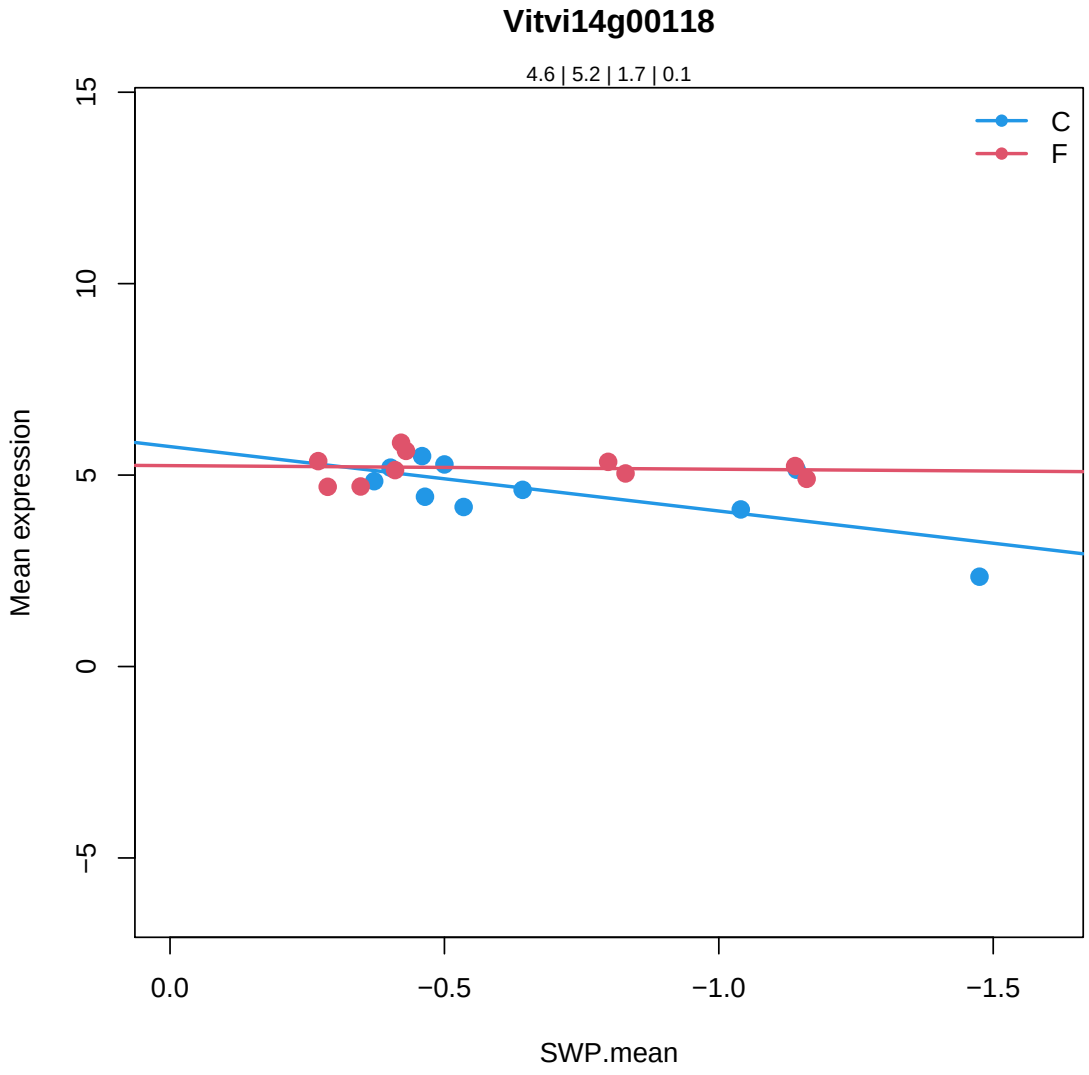
7.6.55 Vitvi14g00118: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g00118
        30.3
        signalling.calcium
        Calmodulin-binding protein |
        Chr4:13125224-13127765 FORWARD LENGTH=601 |
        201606
```

Coefficients for Vitvi14g00118.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.561031	7.78368e-18	***	2.105019e-17	***
SlopeC	1.682527	0.002089582	**	0.1730947	
MeanF-MeanC	0.628127	0.01769459	*	0.1151092	
SlopeF-SlopeC	-1.588436	0.03738332	*	0.9999488	



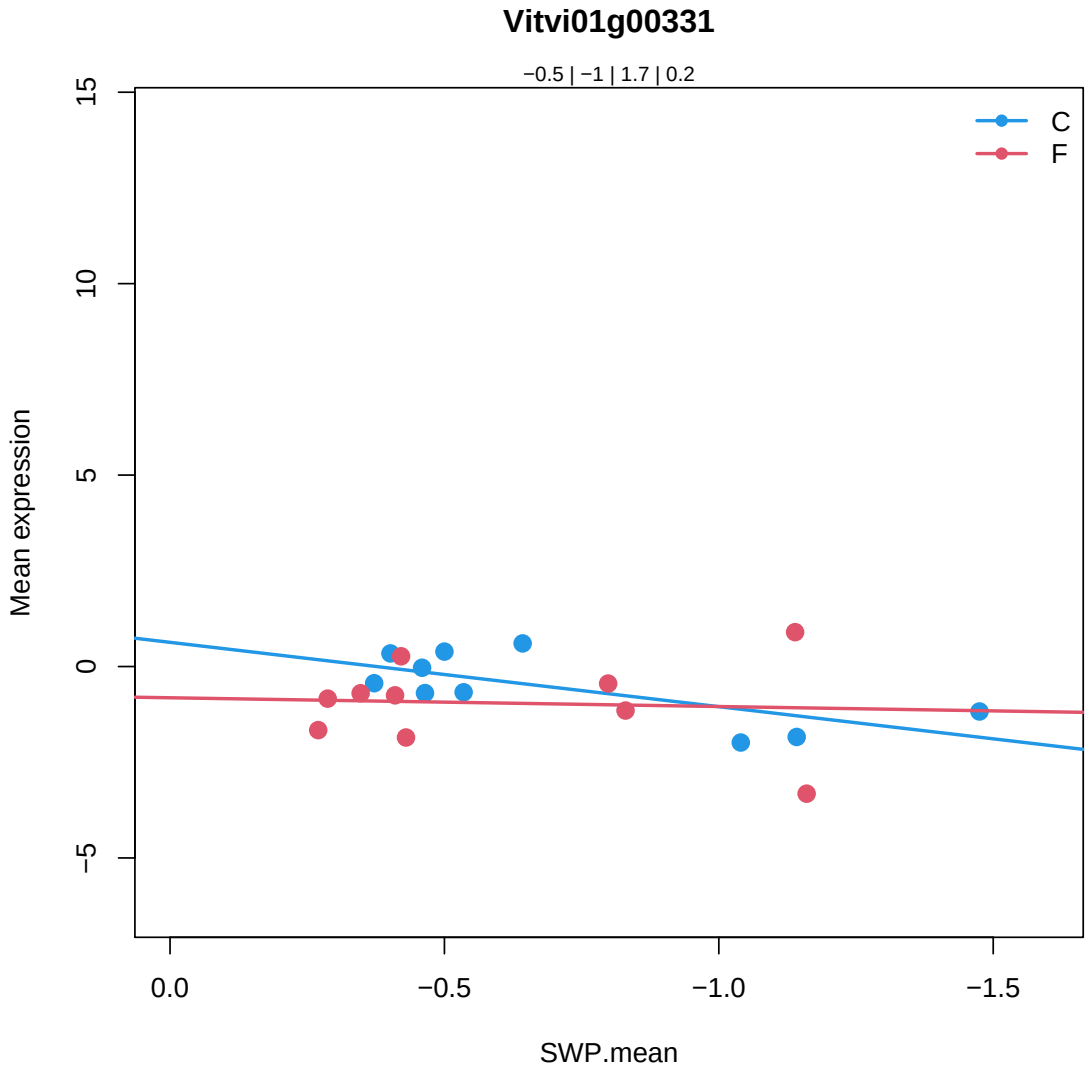
7.6.56 Vitvi01g00331: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00331
        31
        cell
        Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin
        Chr3:6267102-6267392 FORWARD LENGTH=96 |
        201606
```

Coefficients for Vitvi01g00331.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.5498868	0.06614128	.	0.06866404	.
SlopeC	1.679967	0.04526234	*	0.4920745	
MeanF-MeanC	-0.4057805	0.3236257		0.6841474	
SlopeF-SlopeC	-1.451365	0.2305183		0.9999488	



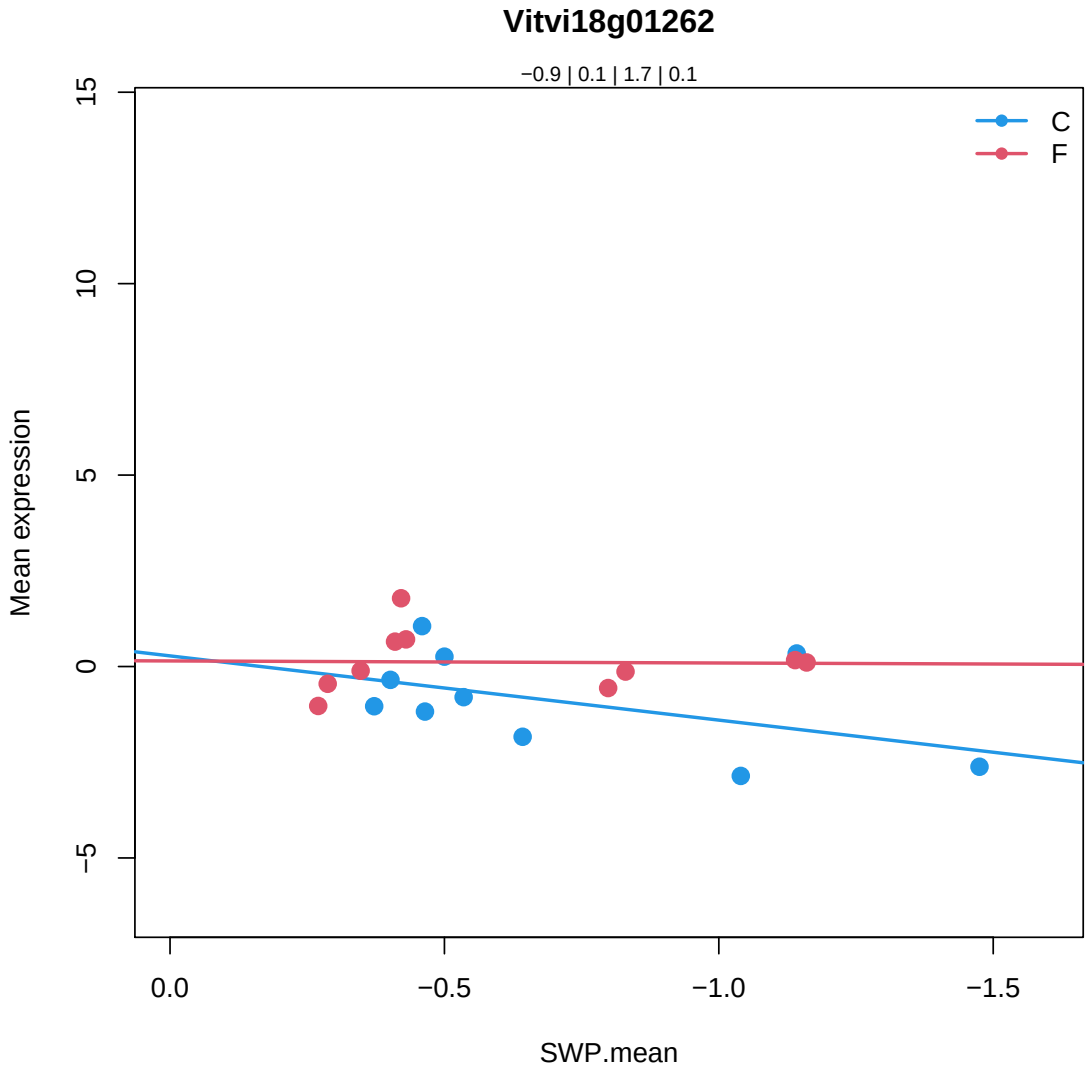
7.6.57 Vitvi18g01262: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g01262
        30.2.12
        signalling.receptor kinases.leucine rich repeat XII
        Leucine-rich repeat protein kinase family protein |
        Chr3:17527611-17530748 FORWARD LENGTH=1010 |
        201606
```

Coefficients for Vitvi18g01262.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.902123	0.005227458	**	0.005572202	**
SlopeC	1.678005	0.04986674	*	0.5091026	
MeanF-MeanC	1.014862	0.02184095	*	0.1343421	
SlopeF-SlopeC	-1.624447	0.1905261		0.9999488	



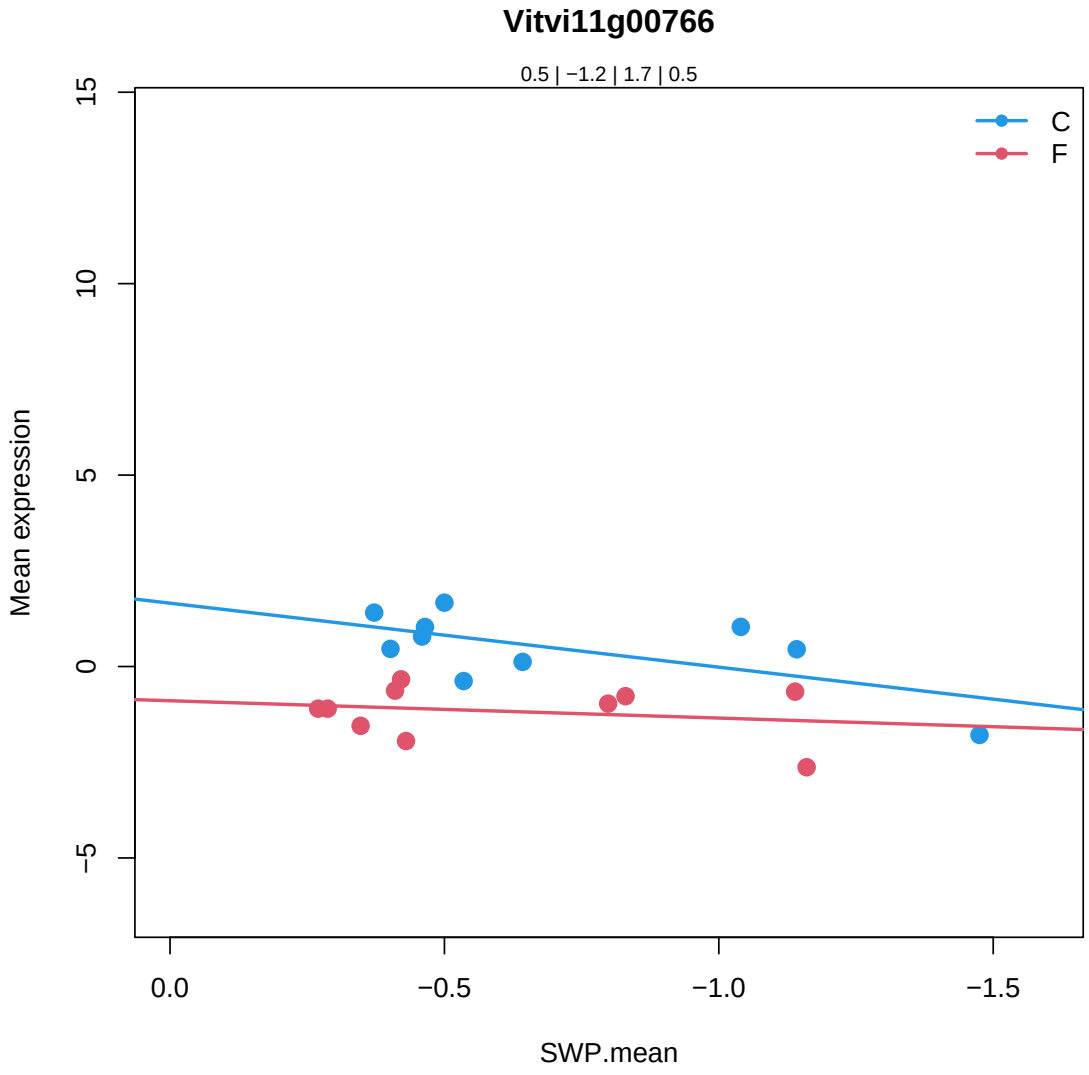
7.6.58 Vitvi11g00766: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00766
        30.2.12
        signalling.receptor kinases.leucine rich repeat XII
        kinase family with leucine-rich repeat domain-containing protein |
        Chr1:13220940-13224386 FORWARD LENGTH=1120 |
        201606
```

Coefficients for Vitvi11g00766.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.479062	0.04456731	*	0.04647612	*
SlopeC	1.67106	0.01401099	*	0.3359386	
MeanF-MeanC	-1.648529	3.581314e-05	***	0.000745199	***
SlopeF-SlopeC	-1.219236	0.2035843		0.9999488	



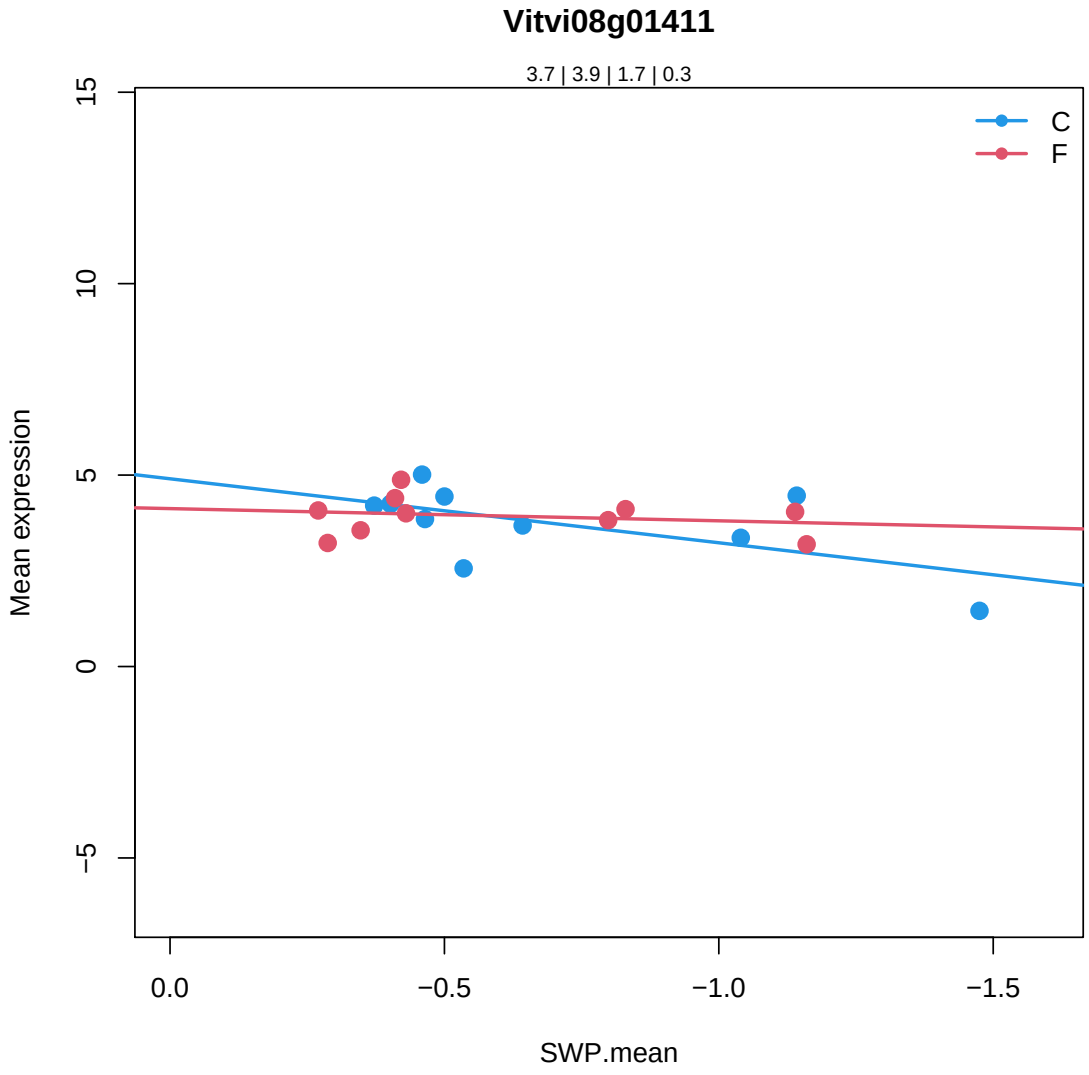
7.6.59 Vitvi08g01411: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01411
        29.5
        protein.degradation
        alpha/beta-Hydrolases superfamily protein |
        Chr2:10334622-10336579 FORWARD LENGTH=434 |
        201606
```

Coefficients for Vitvi08g01411.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.728044	3.958472e-14	***	6.282282e-14	***
SlopeC	1.670923	0.01051156	*	0.3096058	
MeanF-MeanC	0.2020717	0.5118939		0.8136412	
SlopeF-SlopeC	-1.352307	0.1420107		0.9999488	



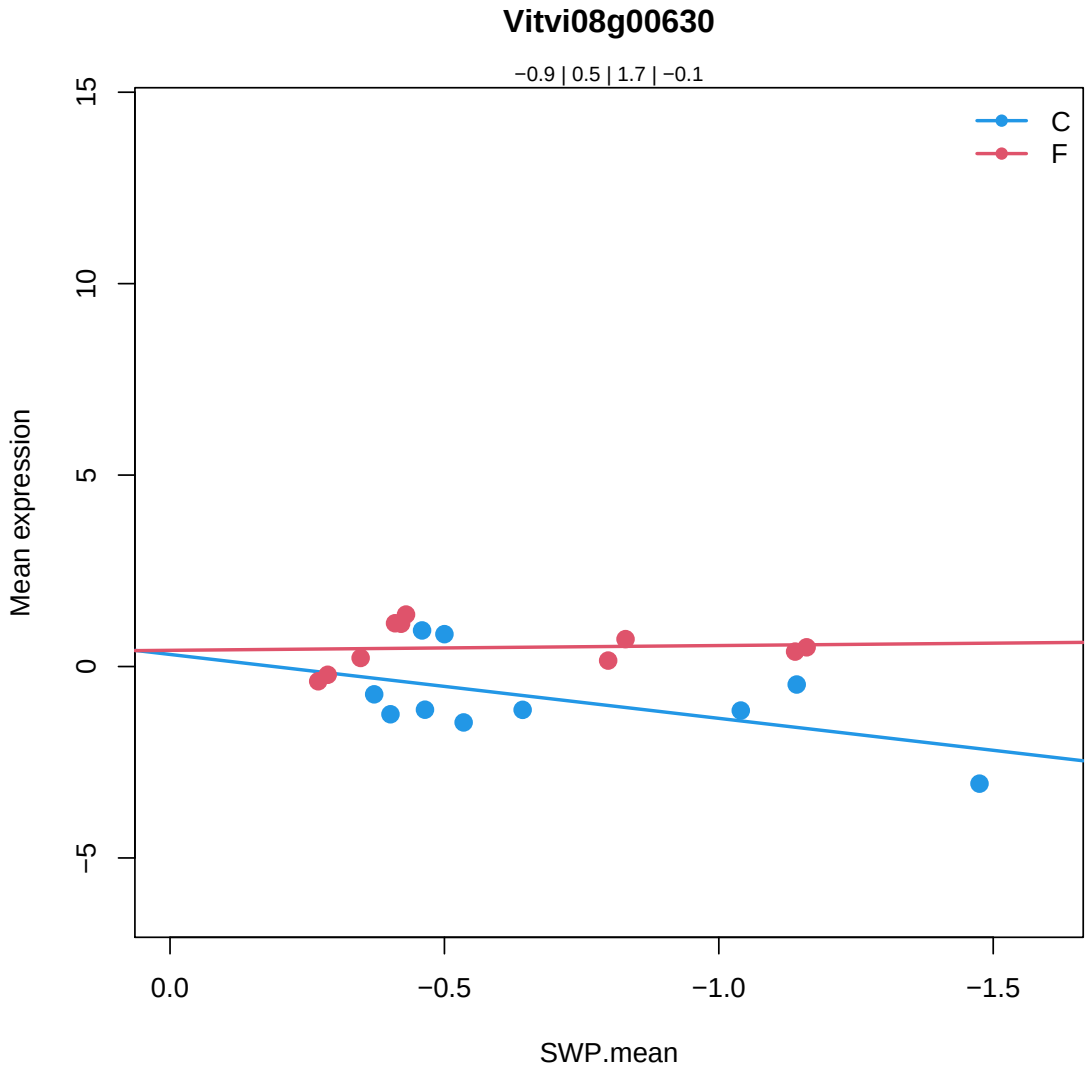
7.6.60 Vitvi08g00630: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g00630
        35.2
        not assigned.unknown
        E3 ubiquitin-protein ligase PUB24-like protein |
        Chr3:3736578-3738208 REVERSE LENGTH=456 |
        201606
```

Coefficients for Vitvi08g00630.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.8585846	0.001922776	**	0.002068677	**
SlopeC	1.668838	0.0220346	*	0.3914352	
MeanF-MeanC	1.357437	0.0007080838	***	0.009384875	**
SlopeF-SlopeC	-1.793805	0.08877097	.	0.9999488	



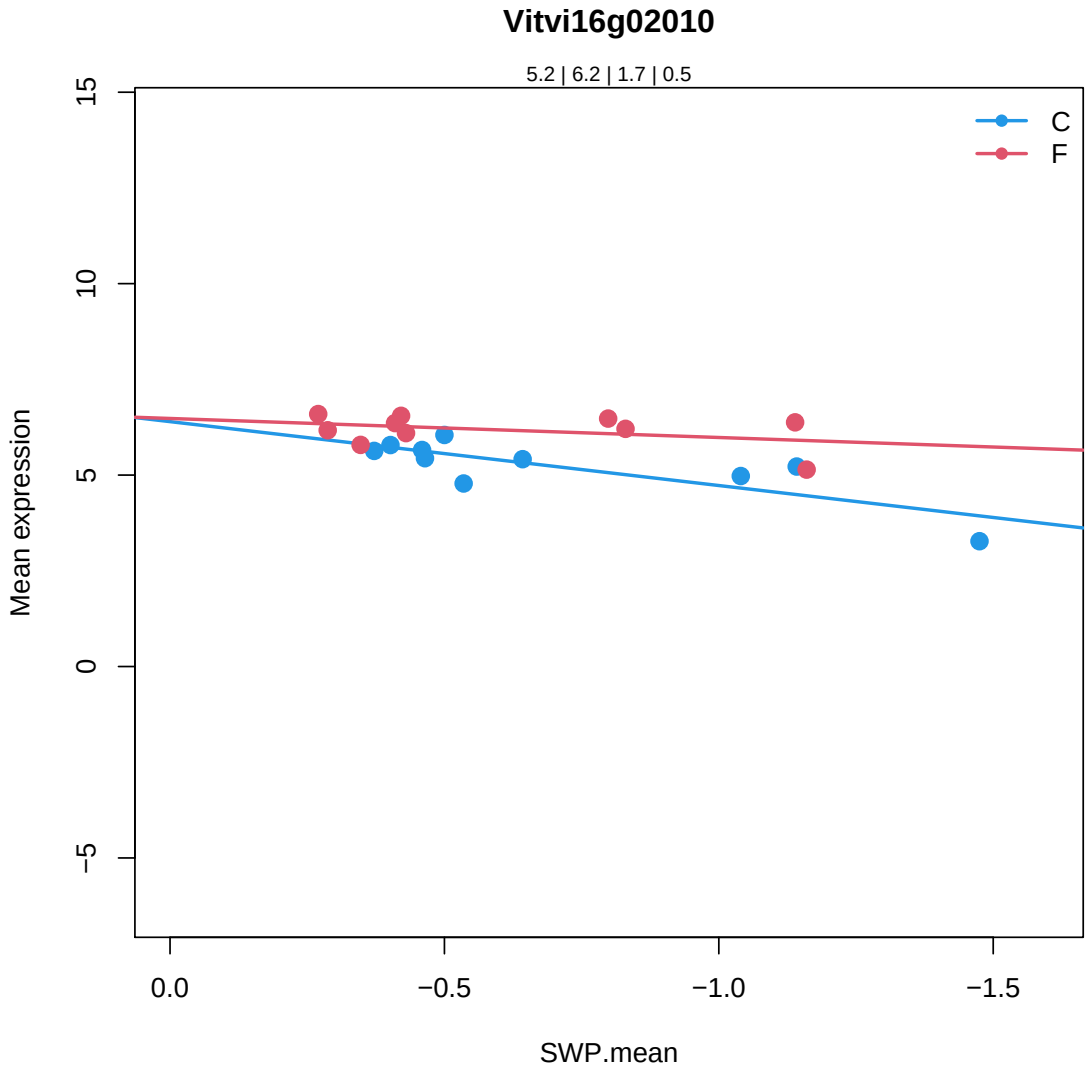
7.6.61 Vitvi16g02010: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g02010
        29.5.11.4.2
        protein.degradation.ubiquitin.E3.RING
        Protein kinase superfamily protein |
        Chr1:24965410-24967432 REVERSE LENGTH=609 |
        201606
```

Coefficients for Vitvi16g02010.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.222345	1.552625e-20	***	1.013495e-19	***
SlopeC	1.668473	0.0005237736	***	0.1005065	
MeanF-MeanC	0.9532332	0.0001547785	***	0.002583936	**
SlopeF-SlopeC	-1.171397	0.06793874	.	0.9999488	



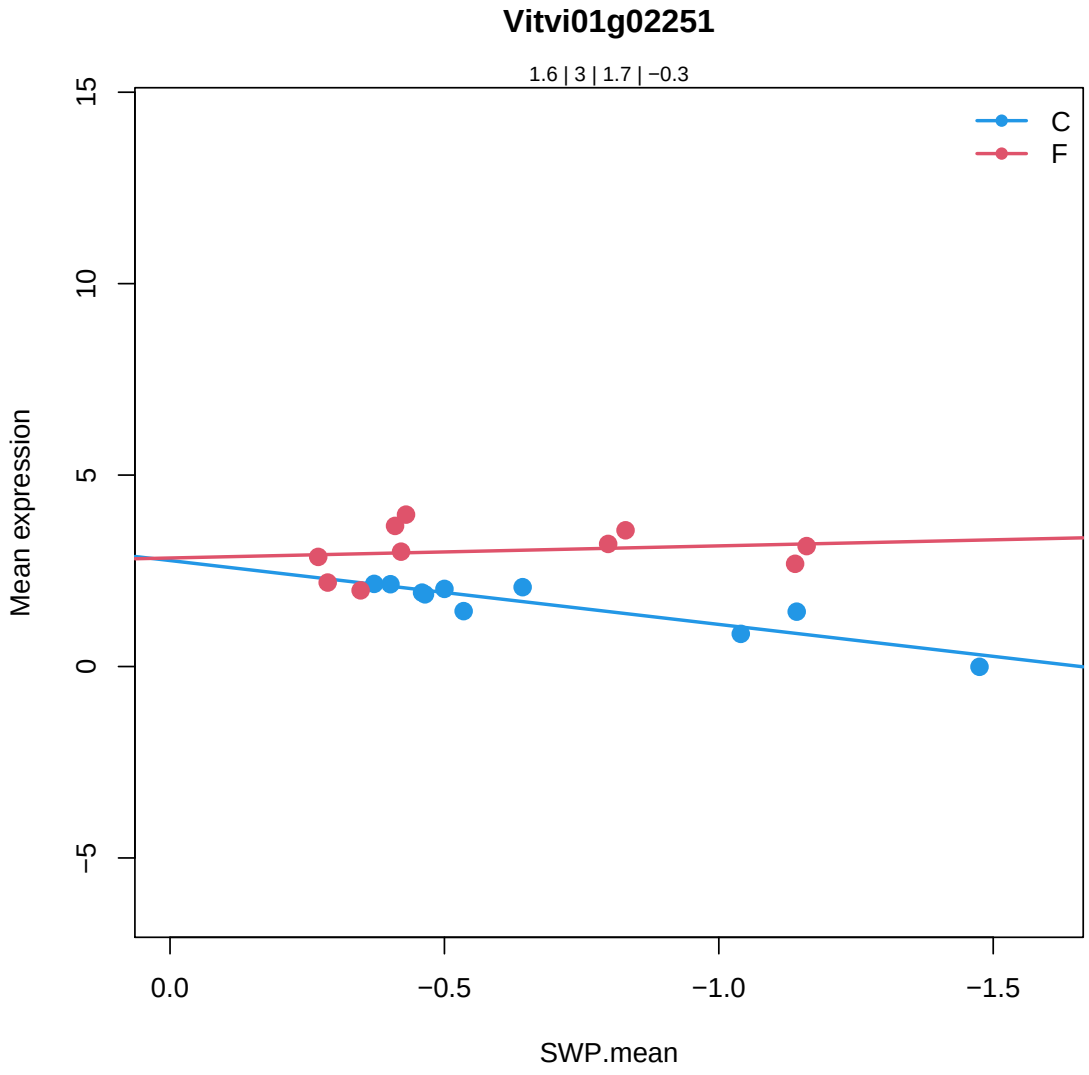
7.6.62 Vitvi01g02251: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g02251
        35.2
        not assigned.unknown
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606
```

Coefficients for Vitvi01g02251.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.594571	1.864711e-09	***	2.33043e-09	***
SlopeC	1.66785	0.001222641	**	0.1365704	
MeanF-MeanC	1.432543	2.793651e-06	***	8.079855e-05	***
SlopeF-SlopeC	-1.98467	0.007088398	**	0.9999488	



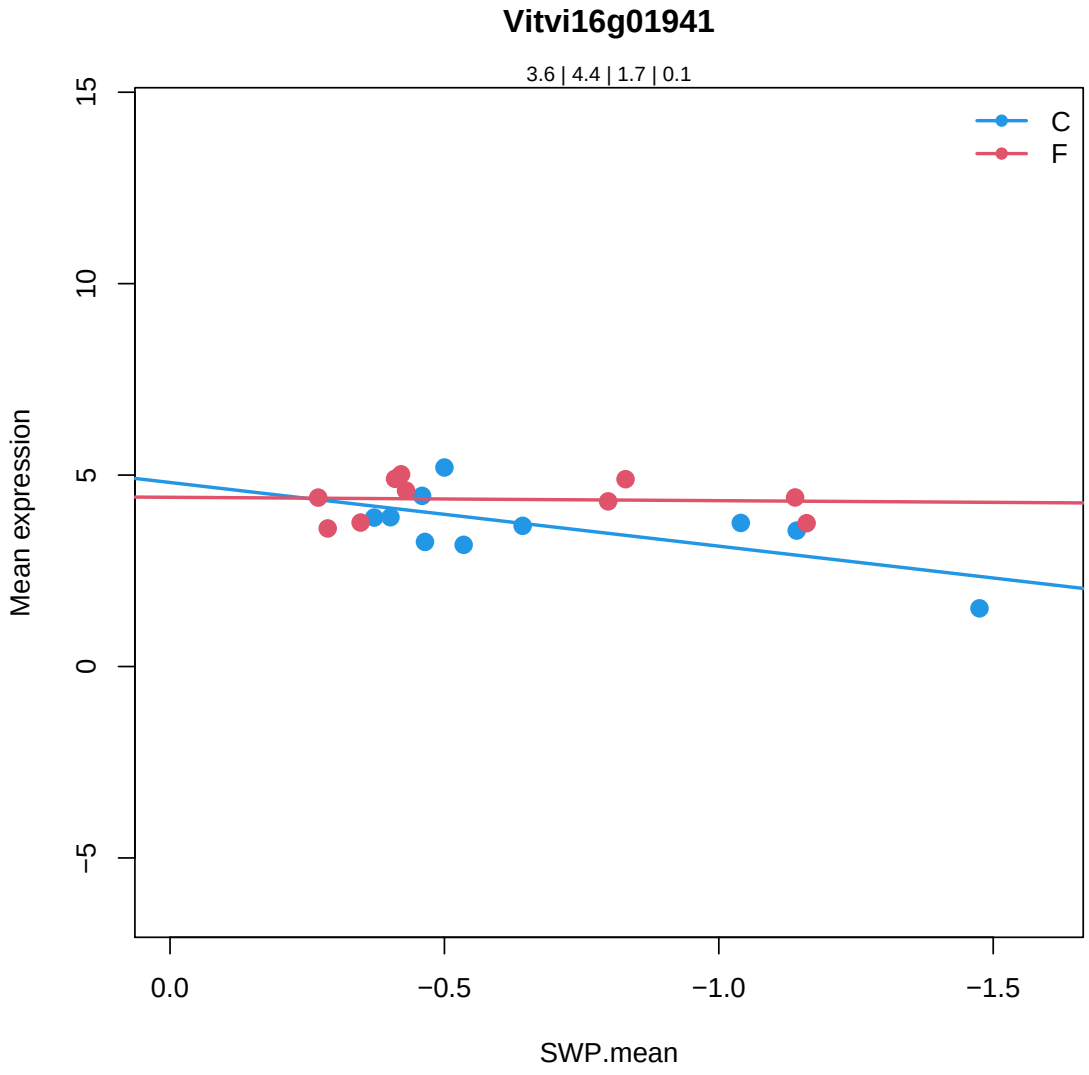
7.6.63 Vitvi16g01941: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01941
        35.2
        not assigned.unknown
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606
```

Coefficients for Vitvi16g01941.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.637016	1.05734e-14	***	1.763237e-14	***
SlopeC	1.662818	0.005942228	**	0.2647742	
MeanF-MeanC	0.7289679	0.01537784	*	0.1036334	
SlopeF-SlopeC	-1.574477	0.06533589	.	0.9999488	



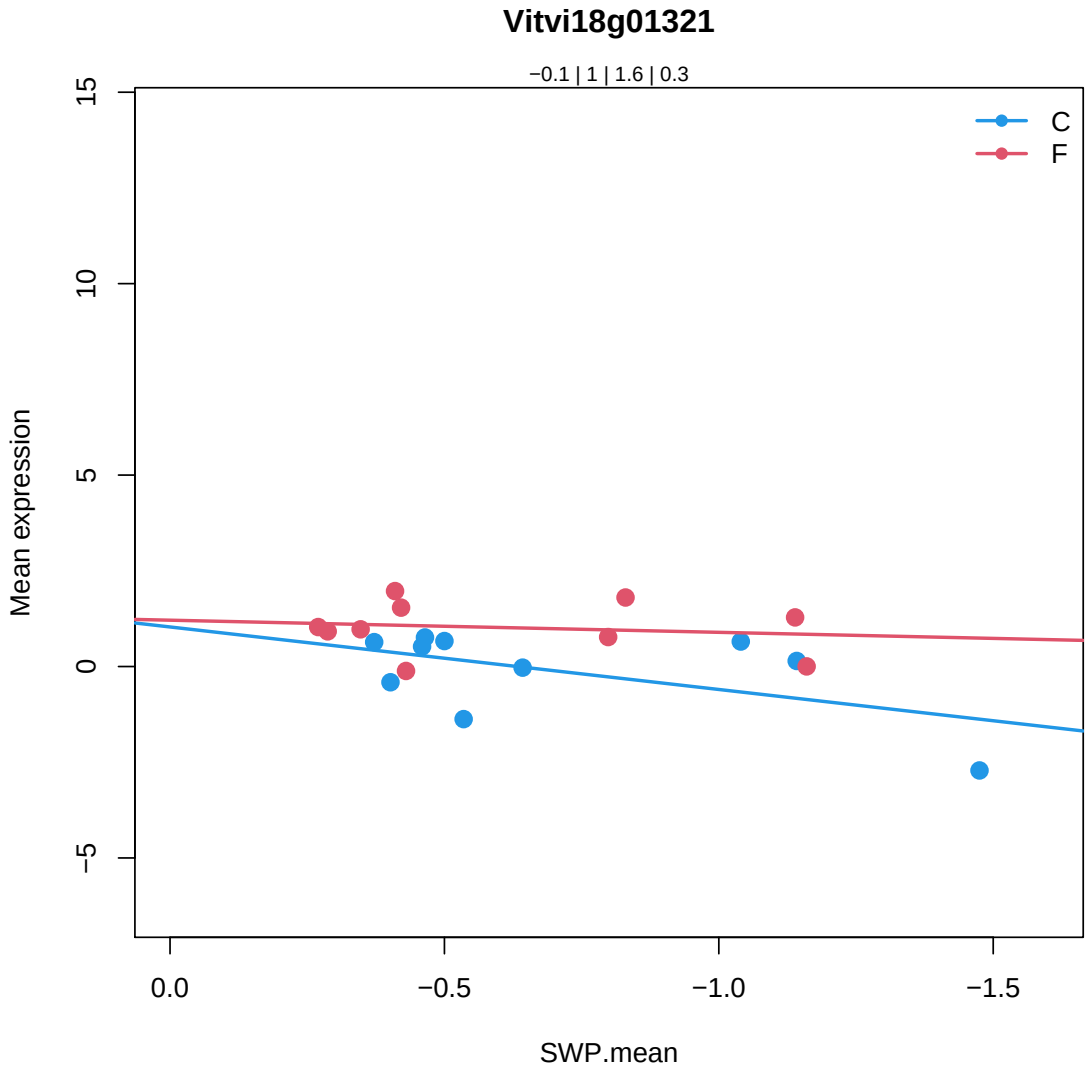
7.6.64 Vitvi18g01321: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g01321
        33.99
        development.unspecified
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi18g01321.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.1149328	0.650885		0.6558333	
SlopeC	1.632696	0.02881099	*	0.4275443	
MeanF-MeanC	1.131846	0.004265536	**	0.04015769	*
SlopeF-SlopeC	-1.315766	0.2180917		0.9999488	



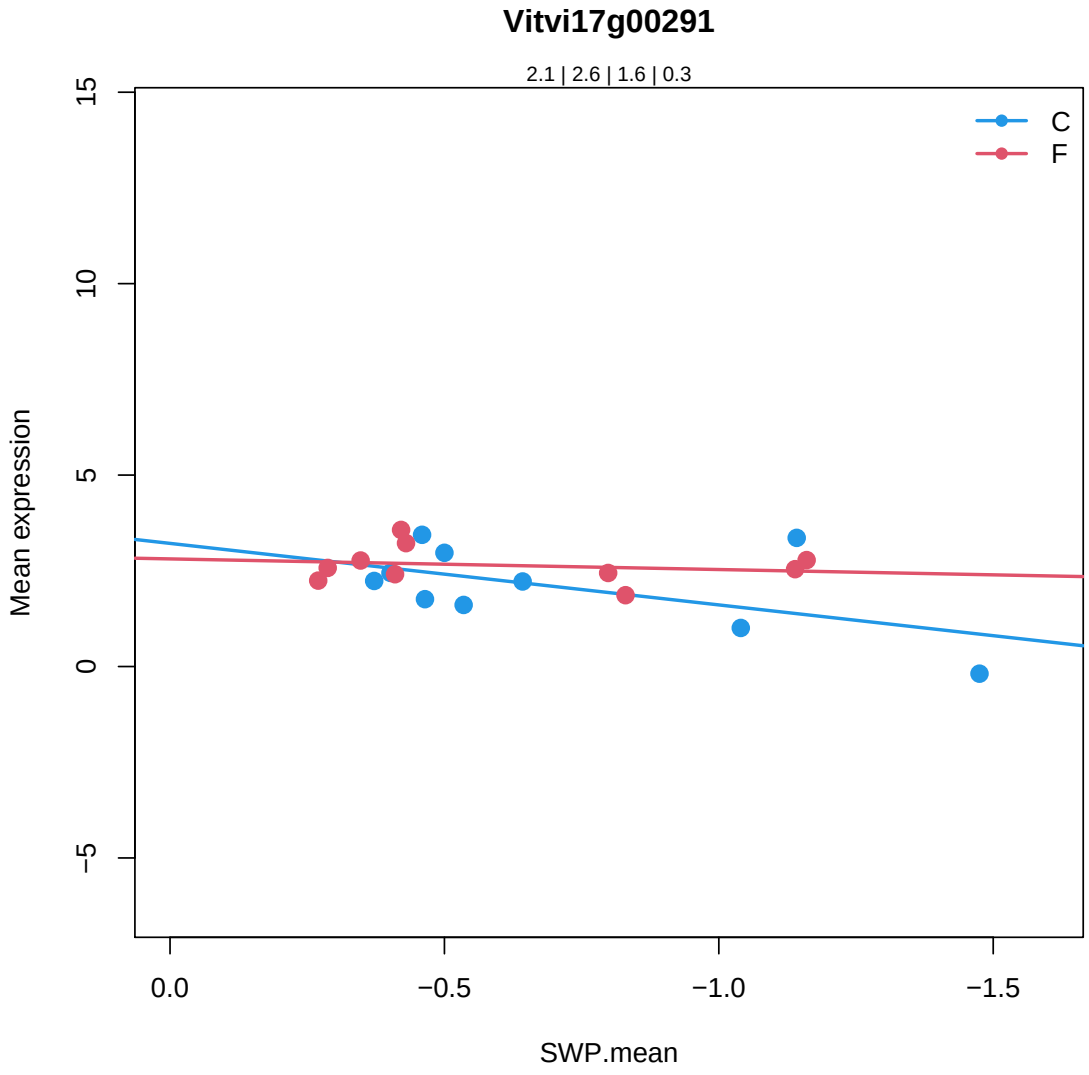
7.6.65 Vitvi17g00291: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00291
        30.3
        signalling.calcium
        Calmodulin binding protein-like protein |
        Chr1:27745761-27749178 REVERSE LENGTH=451 |
        201606
```

Coefficients for Vitvi17g00291.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.085829	7.012054e-09	***	8.602521e-09	***
SlopeC	1.606842	0.01877163	*	0.3672878	
MeanF-MeanC	0.5556075	0.09809392	.	0.3606907	
SlopeF-SlopeC	-1.32927	0.1719655		0.9999488	



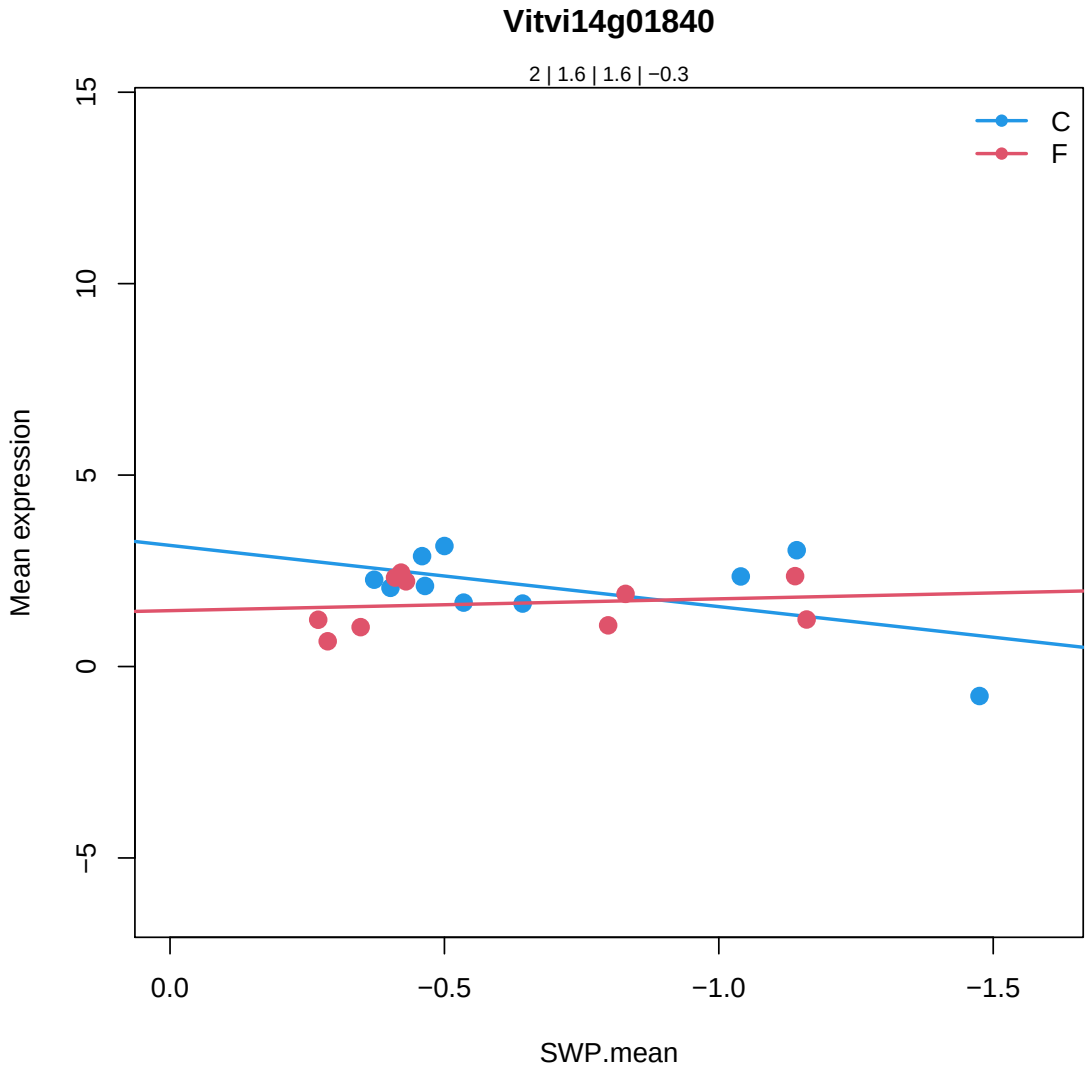
7.6.66 Vitvi14g01840: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01840
        35.2
        not assigned.unknown
        P-loop containing nucleoside triphosphate hydrolases superfamily prote
        Chr3:10722437-10723870 FORWARD LENGTH=438 |
        201606
```

Coefficients for Vitvi14g01840.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.038915	4.668906e-08	***	5.588023e-08	***
SlopeC	1.59901	0.03069674	*	0.4322019	
MeanF-MeanC	-0.3919823	0.2769102		0.6407765	
SlopeF-SlopeC	-1.90788	0.07746042	.	0.9999488	



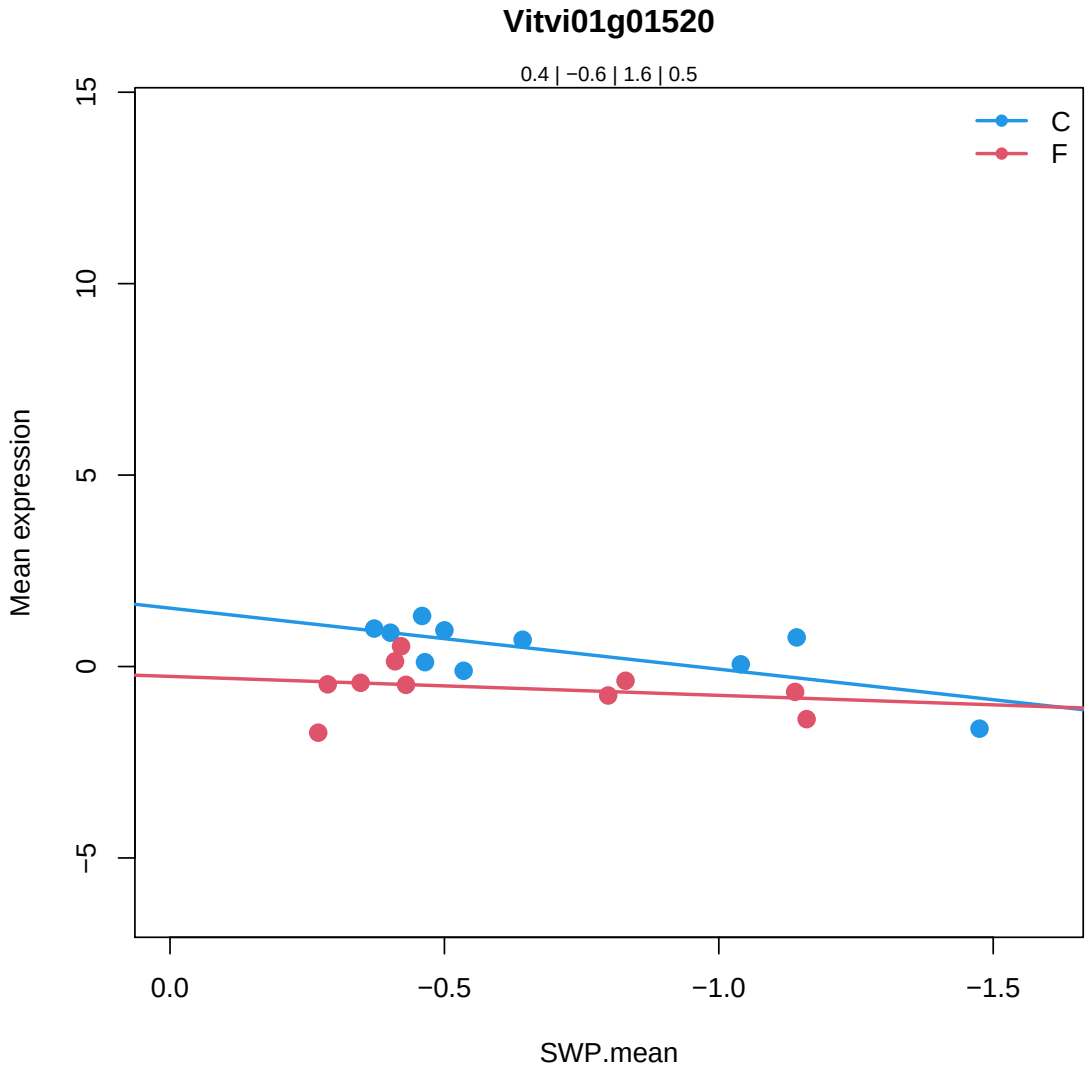
7.6.67 Vitvi01g01520: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01520
        35.2
        not assigned.unknown
        HXXXD-type acyl-transferase family protein |
        Chr3:9519741-9521069 FORWARD LENGTH=442 |
        201606
```

Coefficients for Vitvi01g01520.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4033867	0.04994232	*	0.05200662	.
SlopeC	1.5941	0.007517301	**	0.2777732	
MeanF-MeanC	-0.9633581	0.002041678	**	0.02237186	*
SlopeF-SlopeC	-1.09904	0.1857964		0.9999488	



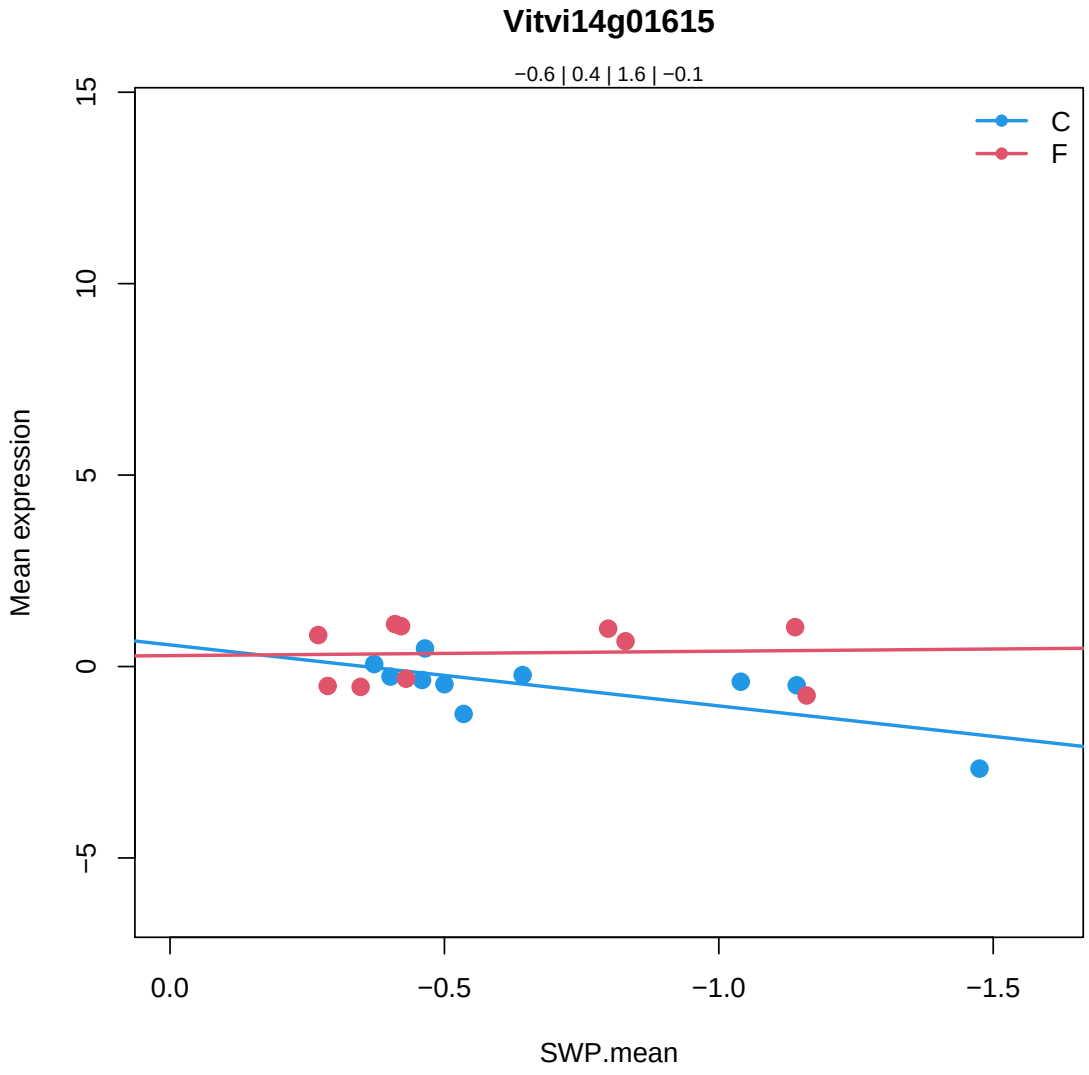
7.6.68 Vitvi14g01615: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01615
        27.3.25
        RNA.regulation of transcription.MYB domain transcription factor family
        myb domain protein 63 |
        Chr1:29786509-29787589 FORWARD LENGTH=327 |
        201606
```

Coefficients for Vitvi14g01615.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	−0.5559626	0.01792939	*	0.01887161	*
SlopeC	1.593458	0.01512027	*	0.3384188	
MeanF−MeanC	0.9101389	0.007240515	**	0.0599131	.
SlopeF−SlopeC	−1.708661	0.07060673	.	0.9999488	



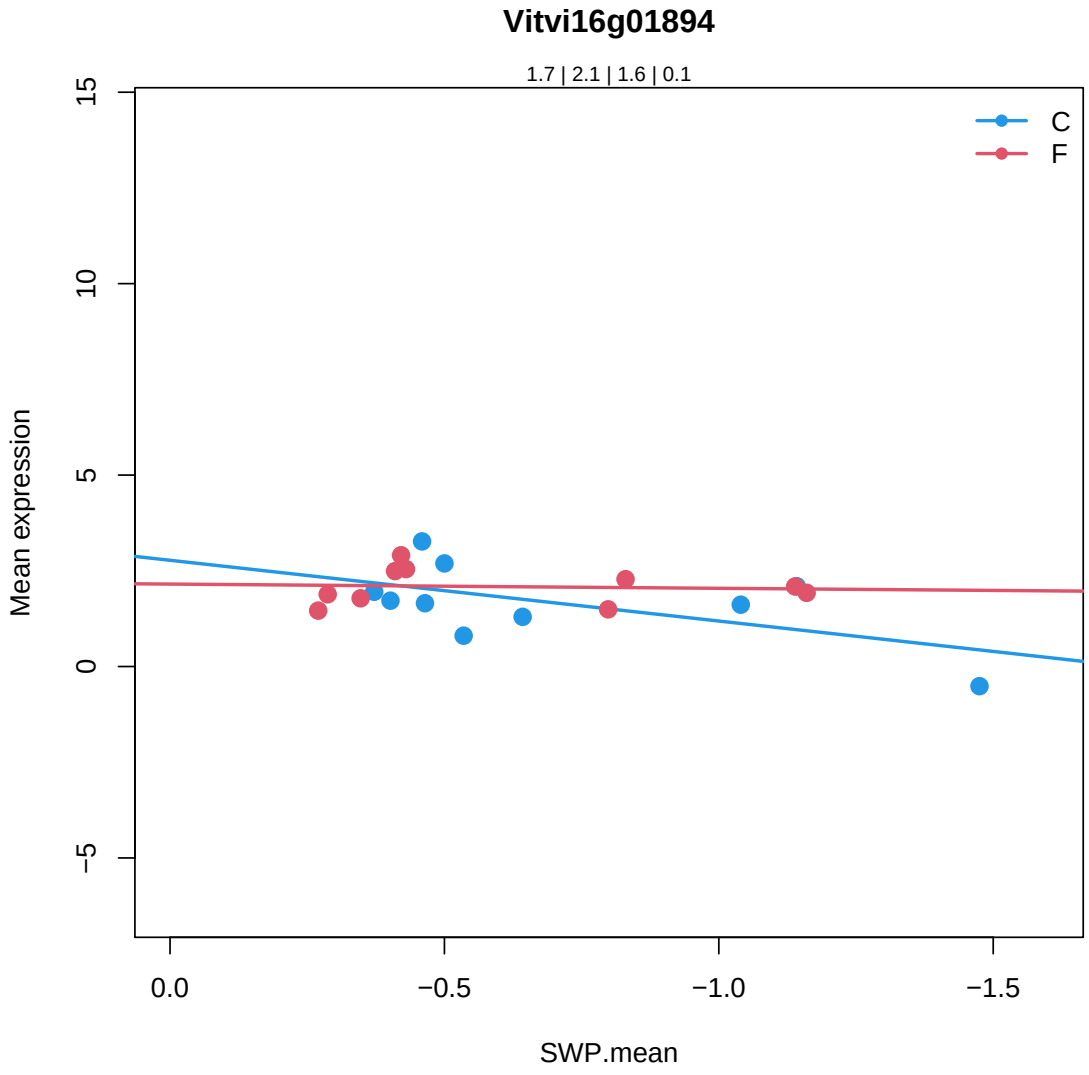
7.6.69 Vitvi16g01894: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01894
        35.2
        not assigned.unknown
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606
```

Coefficients for Vitvi16g01894.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.658707	9.421405e-08	***	1.118824e-07	***
SlopeC	1.586504	0.01318089	*	0.3305597	
MeanF-MeanC	0.4269438	0.1668968		0.4954895	
SlopeF-SlopeC	-1.47633	0.1055658		0.9999488	



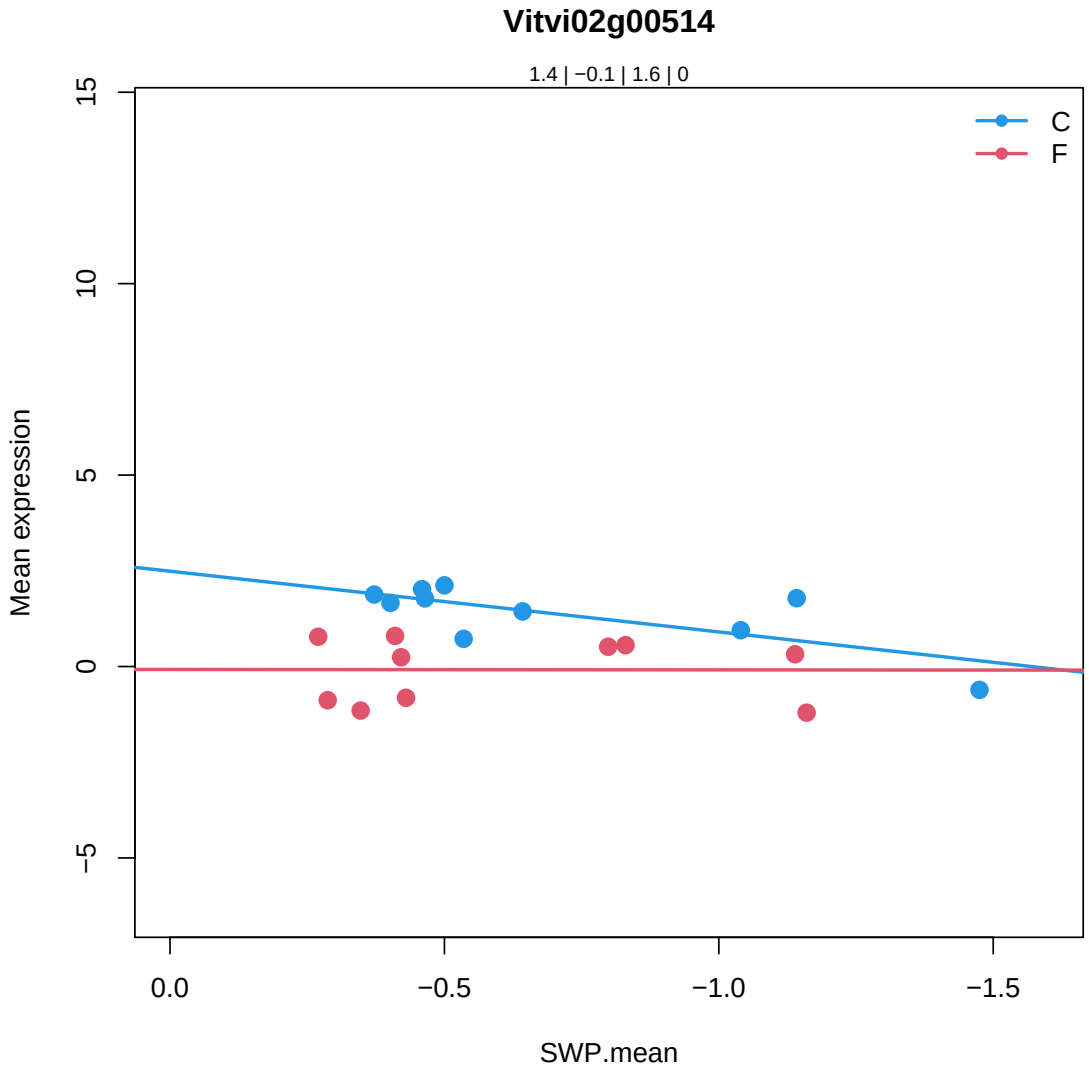
7.6.70 Vitvi02g00514: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00514
        3.2.2
        minor CHO metabolism.trehalose.TPP
        Haloacid dehalogenase-like hydrolase (HAD) superfamily protein |
        Chr4:7365480-7367346 REVERSE LENGTH=368 |
        201606
```

Coefficients for Vitvi02g00514.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.374201	3.098048e-06	***	3.536053e-06	***
SlopeC	1.585843	0.01689594	*	0.3532619	
MeanF-MeanC	-1.458001	0.0001202433	***	0.002114546	**
SlopeF-SlopeC	-1.575343	0.0981852	.	0.9999488	



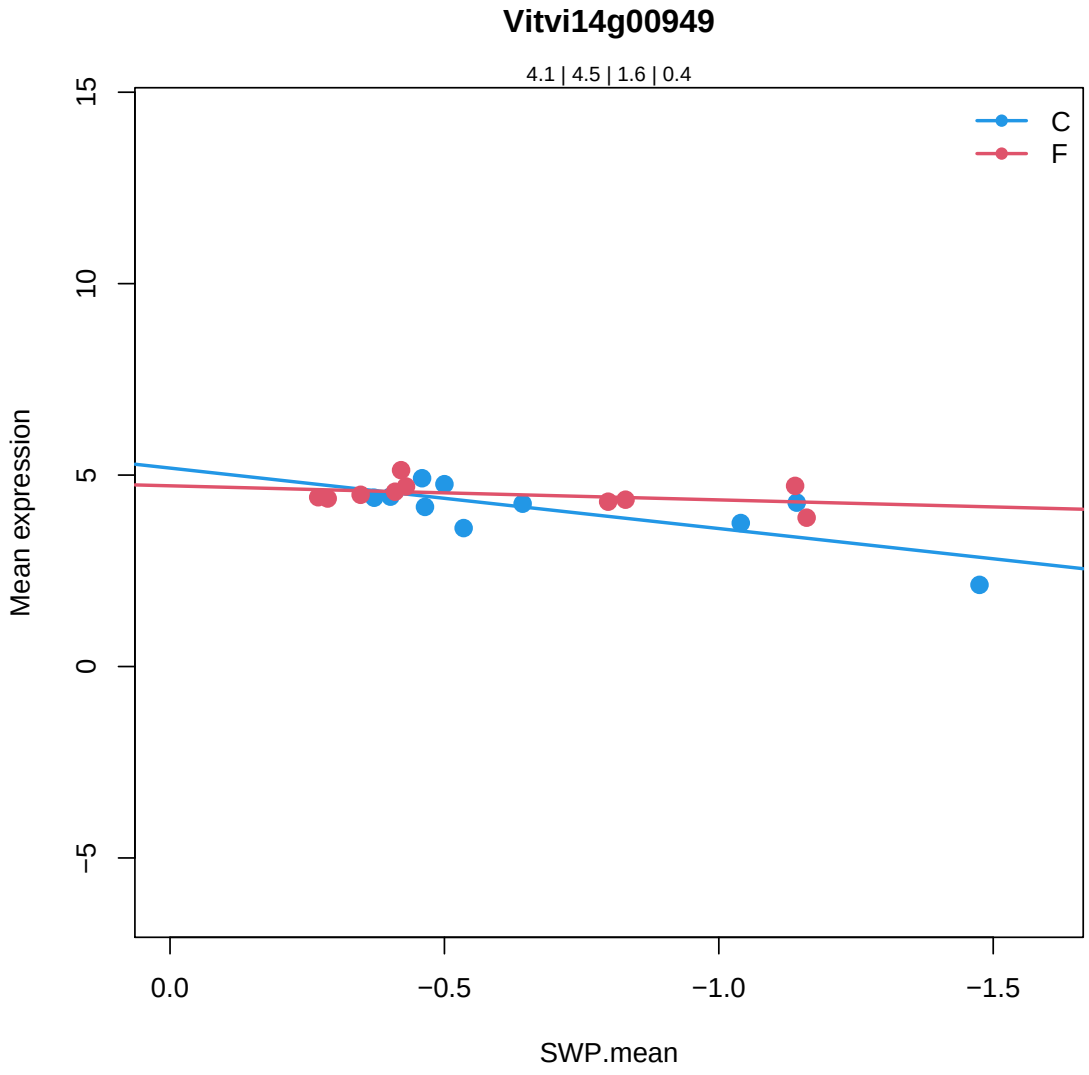
7.6.71 Vitvi14g00949: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g00949
        35.2
        not assigned.unknown
        calmodulin like 23 |
        Chr1:24770856-24771329 REVERSE LENGTH=157 |
        201606
```

Coefficients for Vitvi14g00949.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.072086	1.981153e-18	***	6.263582e-18	***
SlopeC	1.579131	0.000748817	***	0.1076608	
MeanF-MeanC	0.4234804	0.05052196	.	0.2405337	
SlopeF-SlopeC	-1.211273	0.05561633	.	0.9999488	



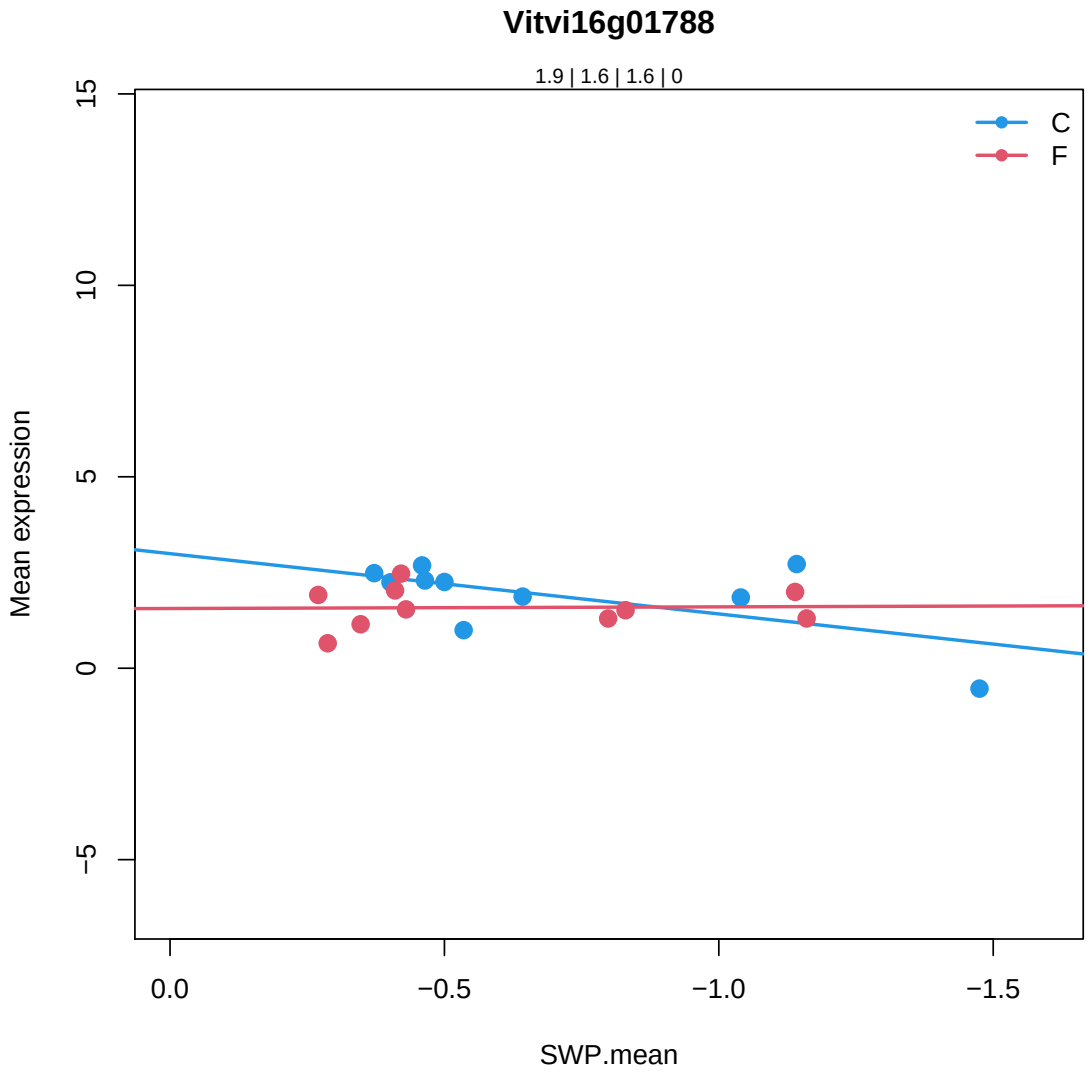
7.6.72 Vitvi16g01788: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01788
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi16g01788.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.885587	9.388171e-09	***	1.146683e-08	***
SlopeC	1.574766	0.01296574	*	0.3305597	
MeanF-MeanC	-0.2997653	0.321492		0.6821915	
SlopeF-SlopeC	-1.61773	0.07513063	.	0.9999488	



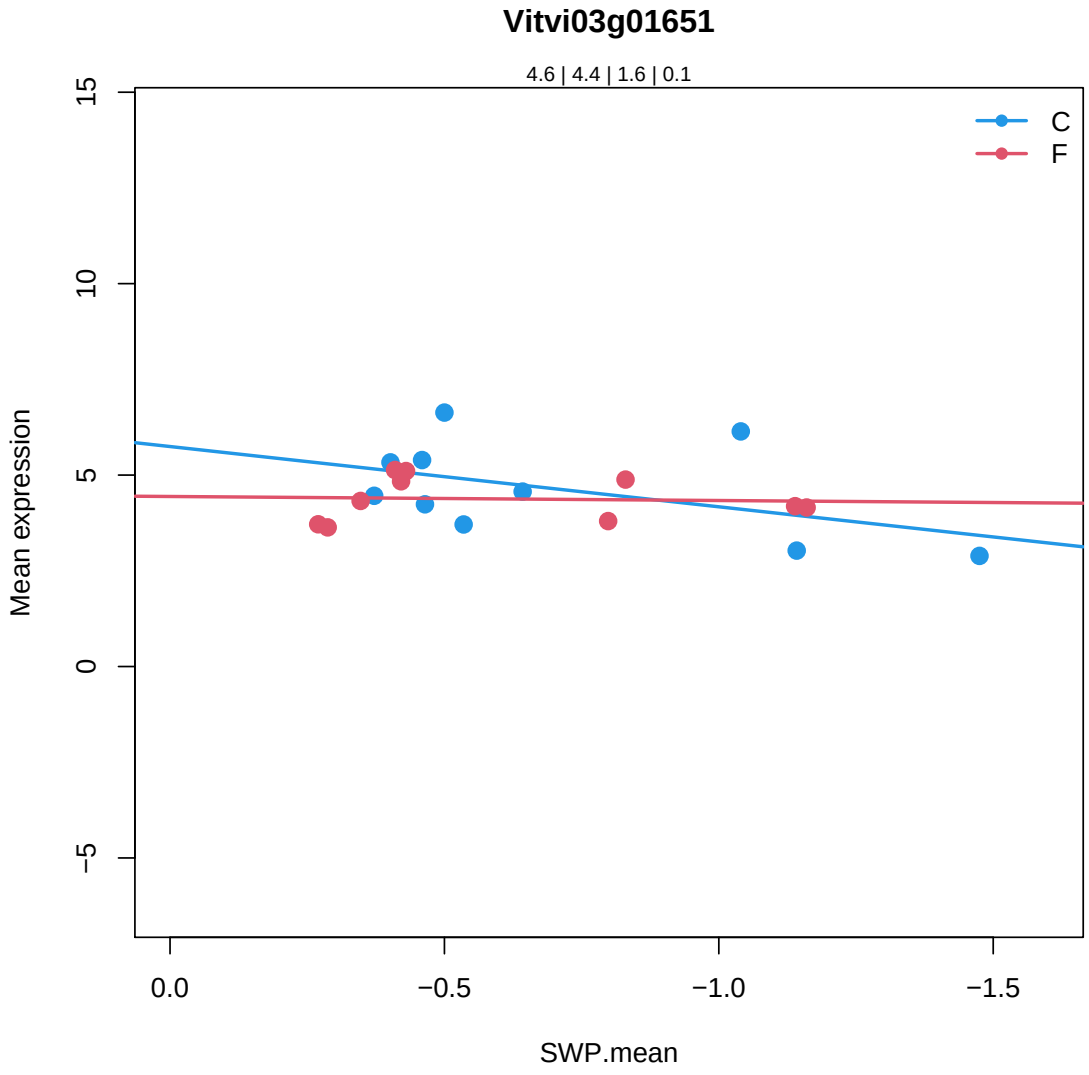
7.6.73 Vitvi03g01651: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g01651
        20.1.7.1
        stress.biotic.PR-proteins.PR1 (antifungal)
        basic pathogenesis-related protein 1 |
        Chr2:6225703-6226188 REVERSE LENGTH=161 |
        201606
```

Coefficients for Vitvi03g01651.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.638698	3.559958e-14	***	5.669894e-14	***
SlopeC	1.574002	0.04456876	*	0.4893928	
MeanF-MeanC	-0.2618371	0.492513		0.8020175	
SlopeF-SlopeC	-1.468926	0.1949533		0.9999488	



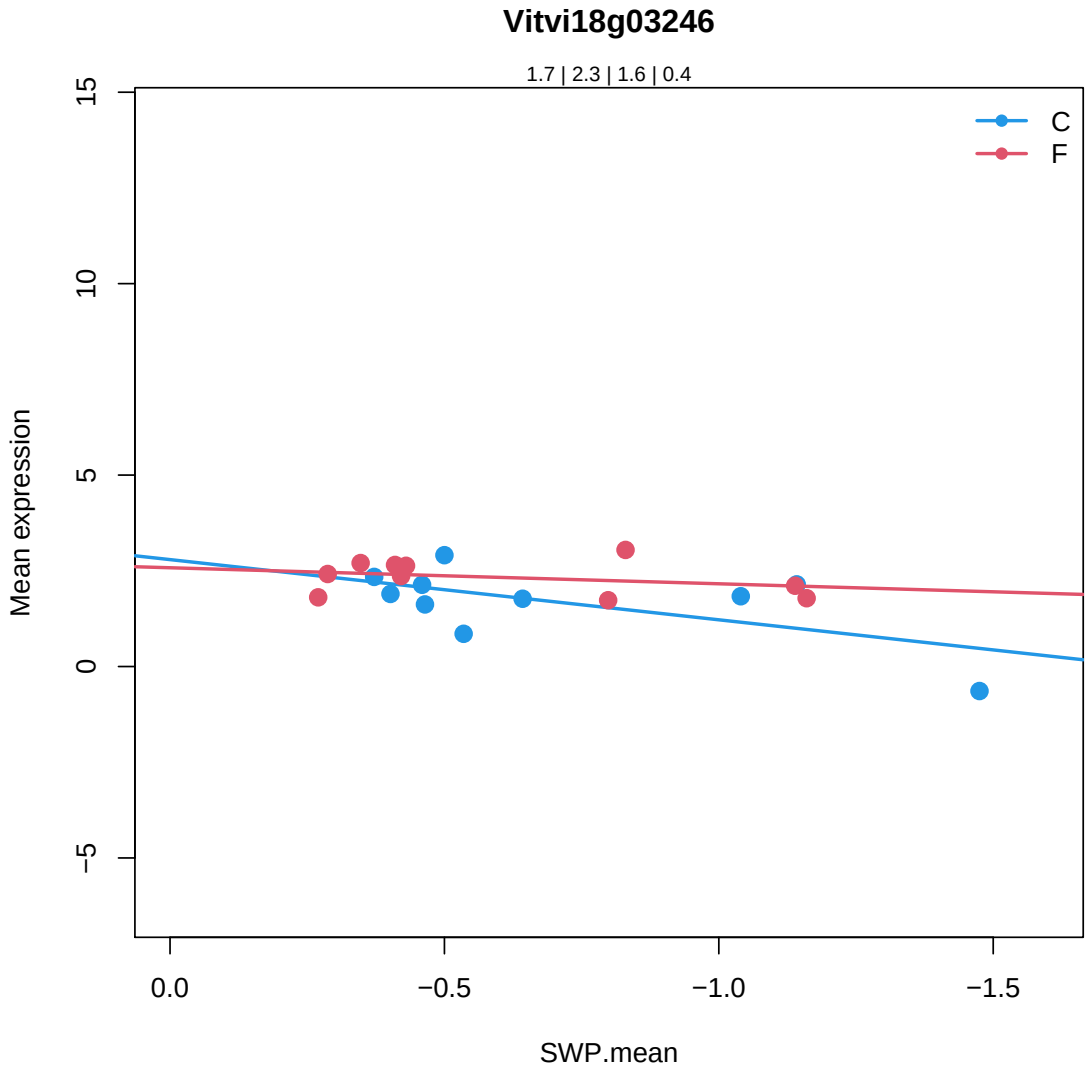
7.6.74 Vitvi18g03246: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g03246
        30.2.12
        signalling.receptor kinases.leucine rich repeat XII
        receptor like protein 6 |
        Chr1:17183550-17186534 REVERSE LENGTH=994 |
        201606
```

Coefficients for Vitvi18g03246.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.686416	2.199991e-08	***	2.657283e-08	***
SlopeC	1.572368	0.008889031	**	0.2903326	
MeanF-MeanC	0.6376899	0.03185468	*	0.176556	
SlopeF-SlopeC	-1.153825	0.1703506		0.9999488	



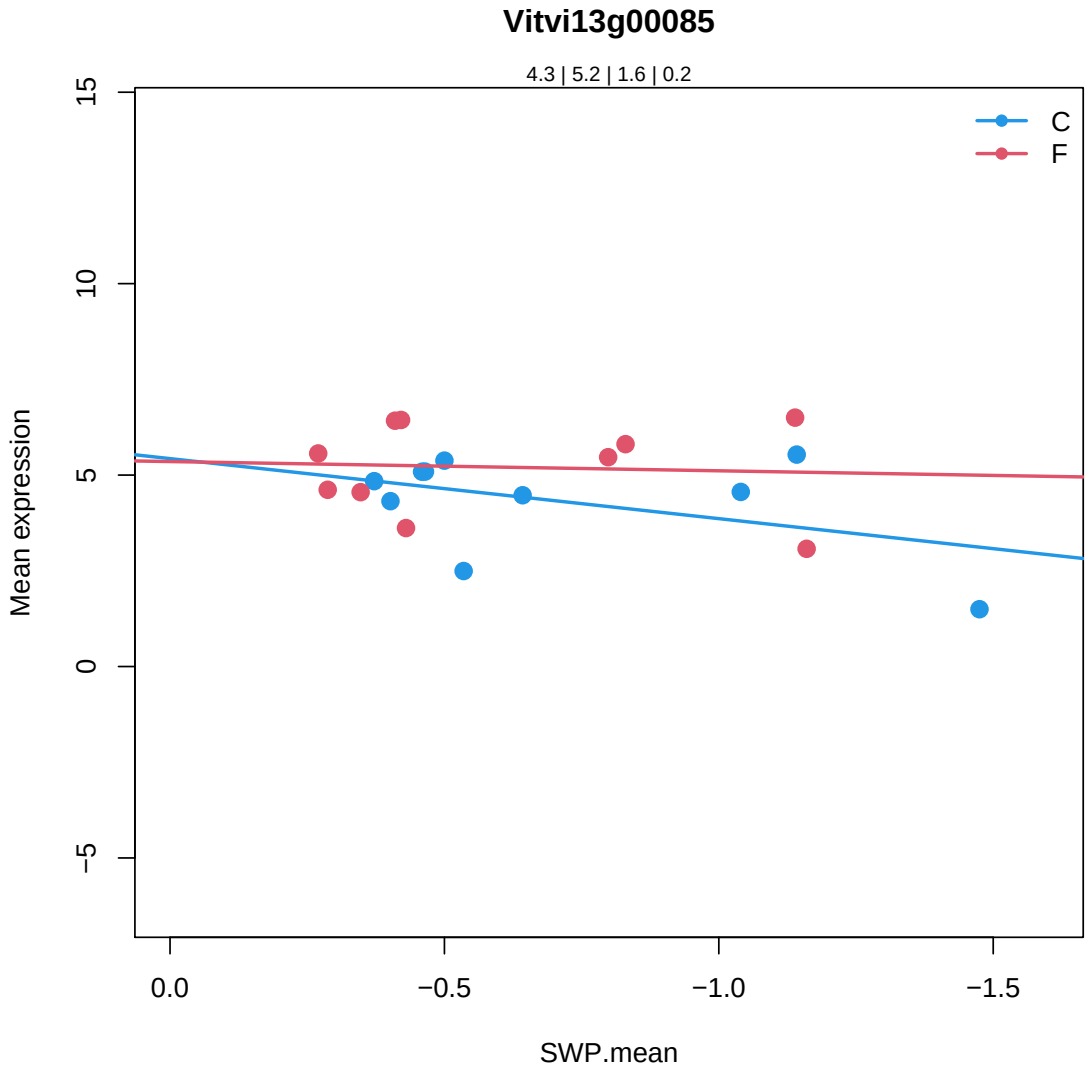
7.6.75 Vitvi13g00085: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00085
        27.3.37
        RNA.regulation of transcription.lateral organ boundaries gene family (
        LOB domain-containing protein 21 |
        Chr3:3475036-3475533 FORWARD LENGTH=165 |
        201606
```

Coefficients for Vitvi13g00085.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.327386	3.542528e-11	***	4.720273e-11	***
SlopeC	1.567726	0.1241348		0.6455347	
MeanF-MeanC	0.8784706	0.09193566	.	0.3472821	
SlopeF-SlopeC	-1.32646	0.3730393		0.9999488	



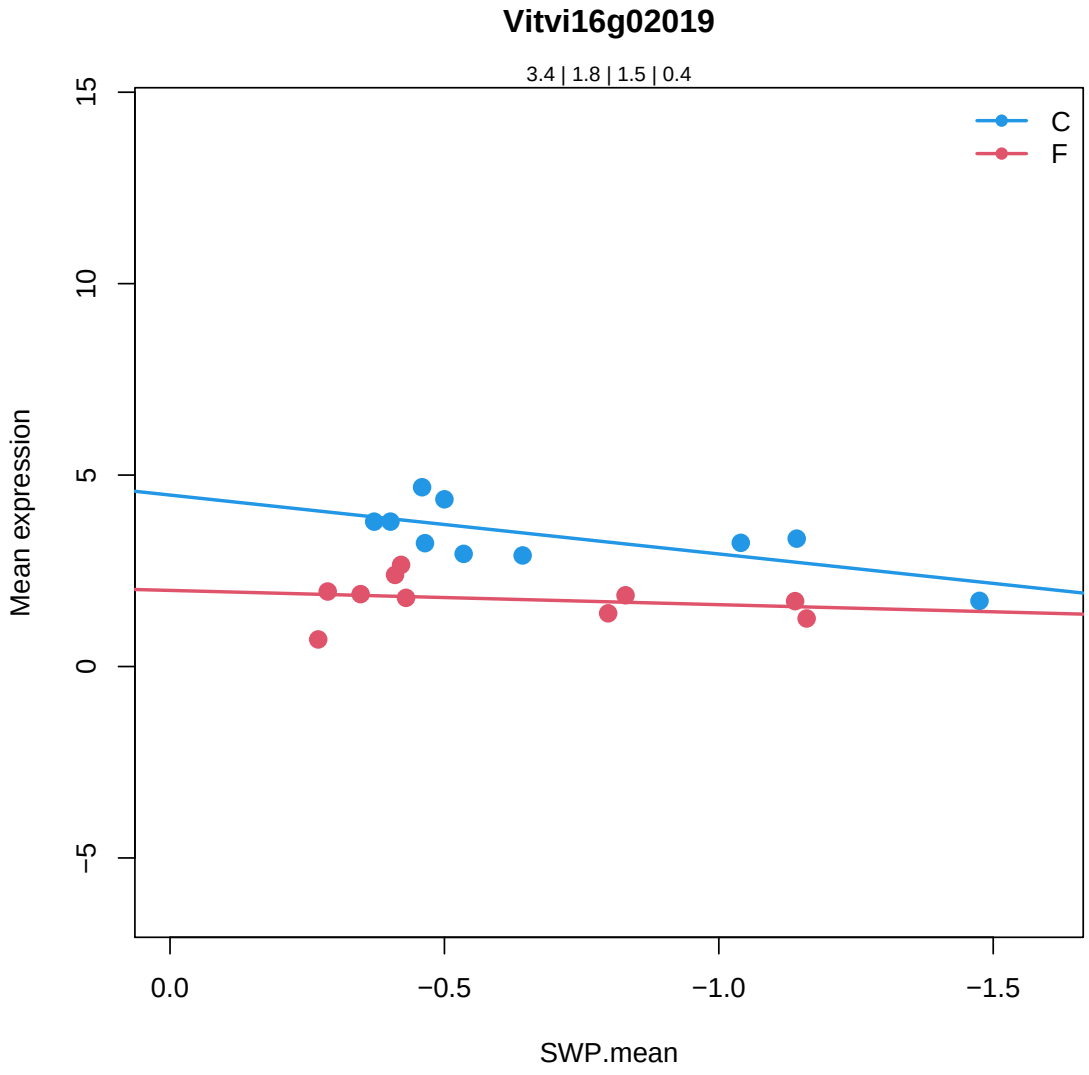
7.6.76 Vitvi16g02019: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g02019
        35.2
        not assigned.unknown
        PR5-like receptor kinase |
        Chr5:15293325-15295838 REVERSE LENGTH=665 |
        201606
```

Coefficients for Vitvi16g02019.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.39667	9.859704e-15	***	1.649633e-14	***
SlopeC	1.537975	0.006208008	**	0.2647742	
MeanF-MeanC	-1.635778	2.45203e-06	***	7.201126e-05	***
SlopeF-SlopeC	-1.165723	0.1369239		0.9999488	



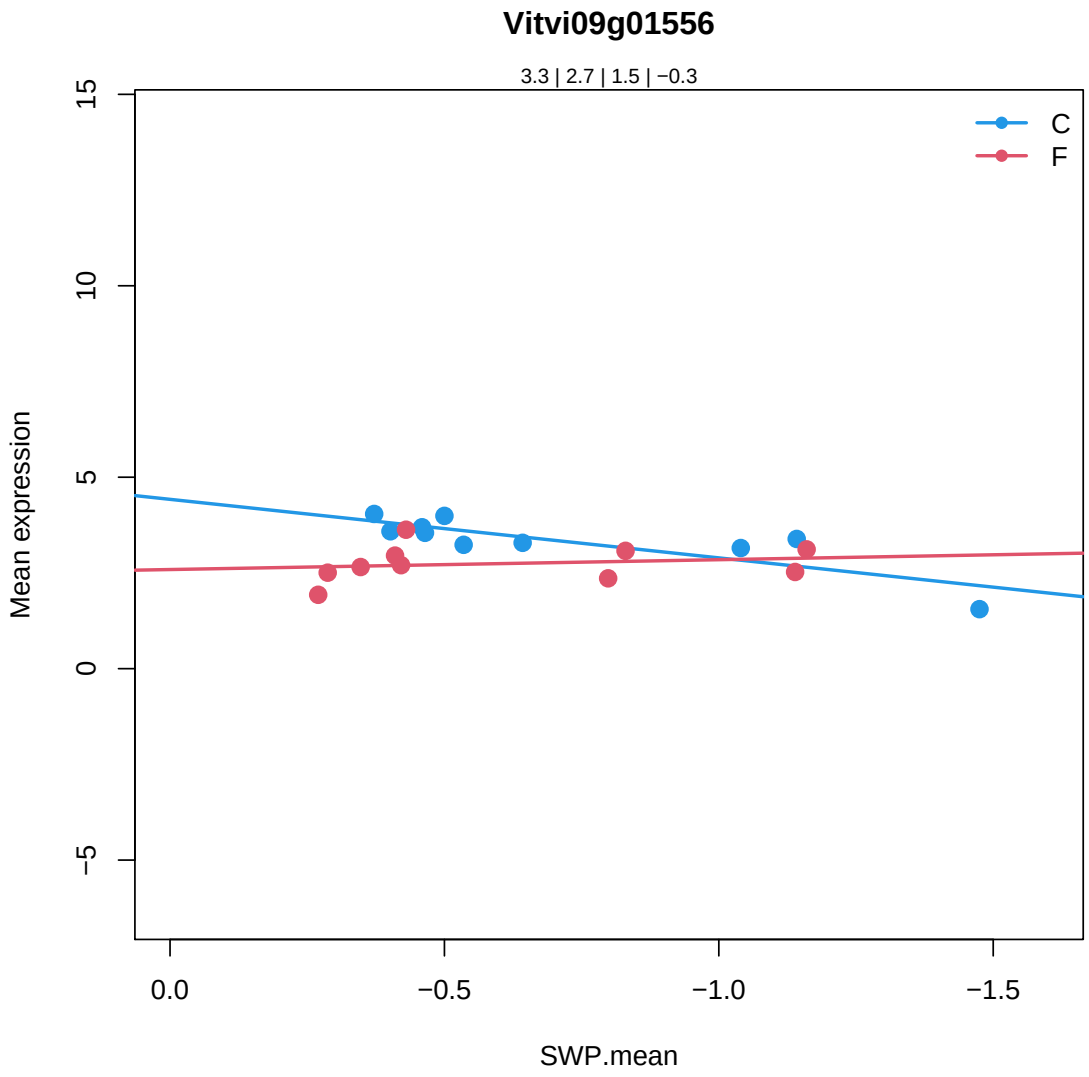
7.6.77 Vitvi09g01556: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
Vitvi09g01556
        29.4
        protein.postranslational modification
        Leucine-rich repeat transmembrane protein kinase protein |
        Chr4:14666179-14669438 REVERSE LENGTH=732 |
        201606

Vitvi09g01556
        30.2.1
        signalling.receptor kinases.leucine rich repeat I
        Leucine-rich repeat transmembrane protein kinase protein |
        Chr4:14666179-14669438 REVERSE LENGTH=732 |
        201606
```

Coefficients for Vitvi09g01556.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.346932	1.550798e-16	***	3.258065e-16	***
SlopeC	1.52868	0.001147058	**	0.1350583	
MeanF-MeanC	-0.6019676	0.008353883	**	0.06656032	.
SlopeF-SlopeC	-1.78573	0.0076567	**	0.9999488	


Vitvi09g01556
3.3 | 2.7 | 1.5 | −0.3
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

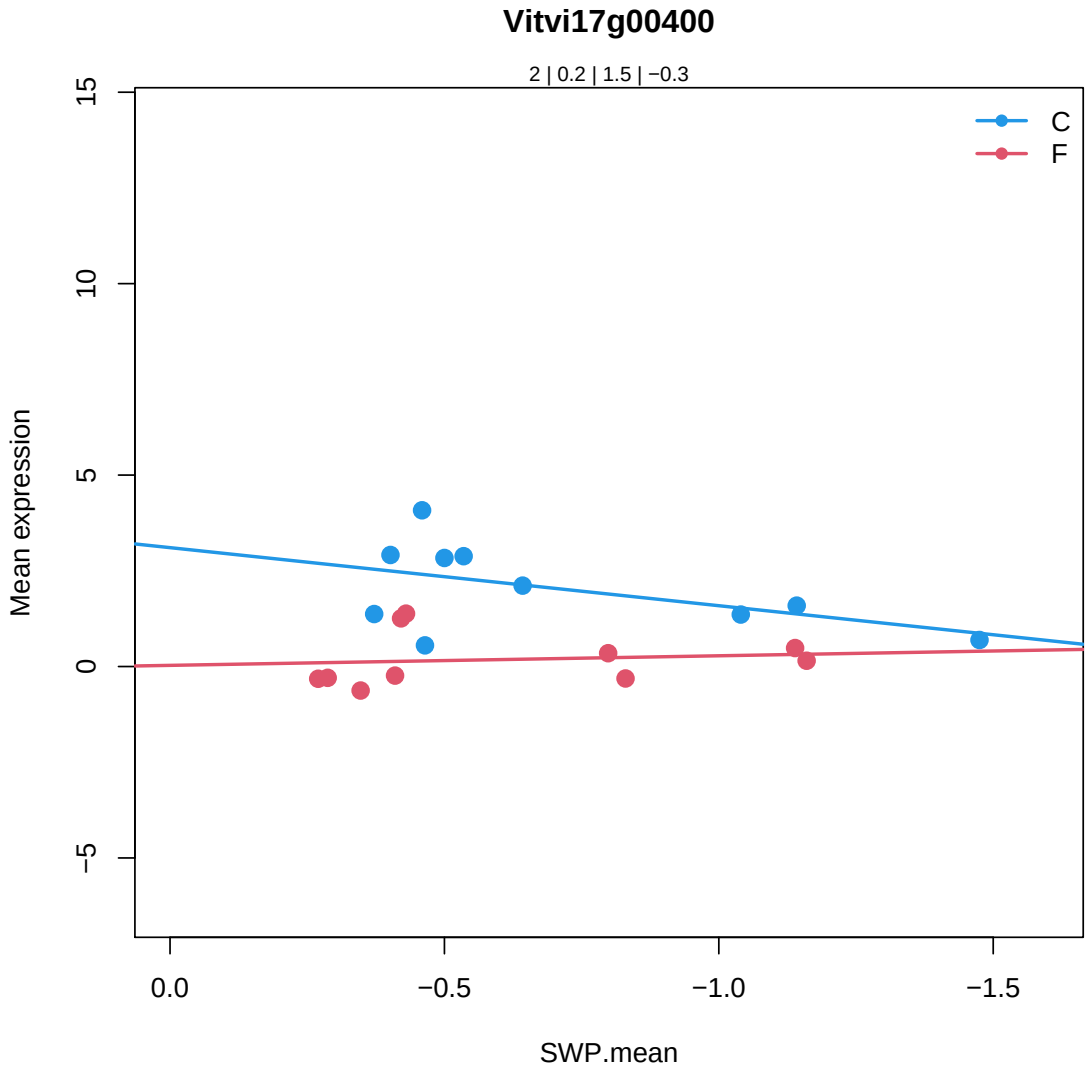
7.6.78 Vitvi17g00400: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00400
        30.2.25
        signalling.receptor kinases.wall associated kinase
        Wall-associated kinase family protein |
        Chr1:26228703-26231339 REVERSE LENGTH=792 |
        201606
```

Coefficients for Vitvi17g00400.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.038537	7.219069e-08	***	8.594317e-08	***
SlopeC	1.516381	0.04429824	*	0.4885628	
MeanF-MeanC	-1.855852	4.008841e-05	***	0.000815791	***
SlopeF-SlopeC	-1.766717	0.108939		0.9999488	



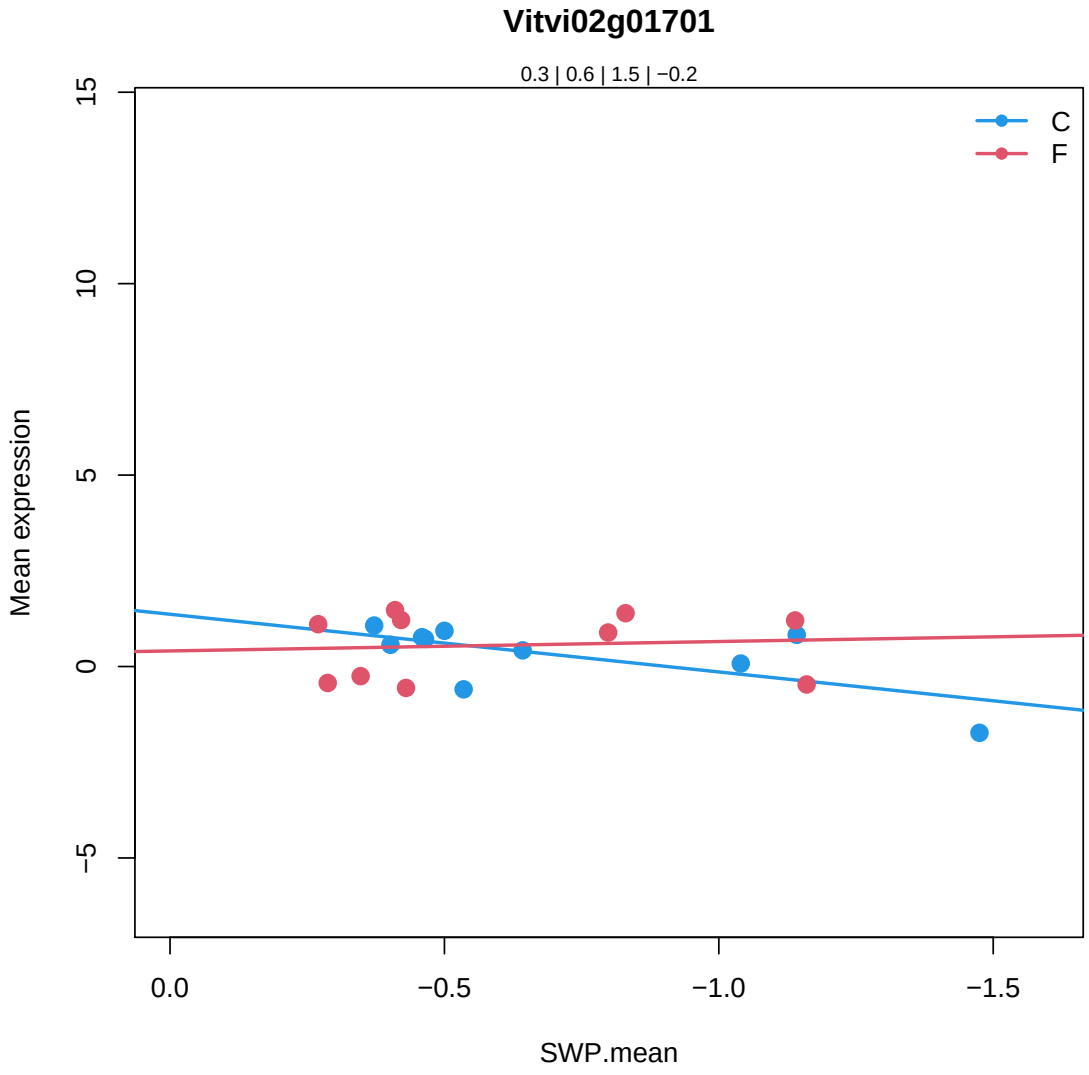
7.6.79 Vitvi02g01701: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g01701
        3.2.2
        minor CHO metabolism.trehalose.TPP
        Haloacid dehalogenase-like hydrolase (HAD) superfamily protein |
        Chr4:7365480-7367346 REVERSE LENGTH=368 |
        201606
```

Coefficients for Vitvi02g01701.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3054623	0.2060418		0.2111537	
SlopeC	1.506429	0.03081765	*	0.4322019	
MeanF-MeanC	0.2509056	0.4570458		0.7825787	
SlopeF-SlopeC	-1.752282	0.0848874	.	0.9999488	



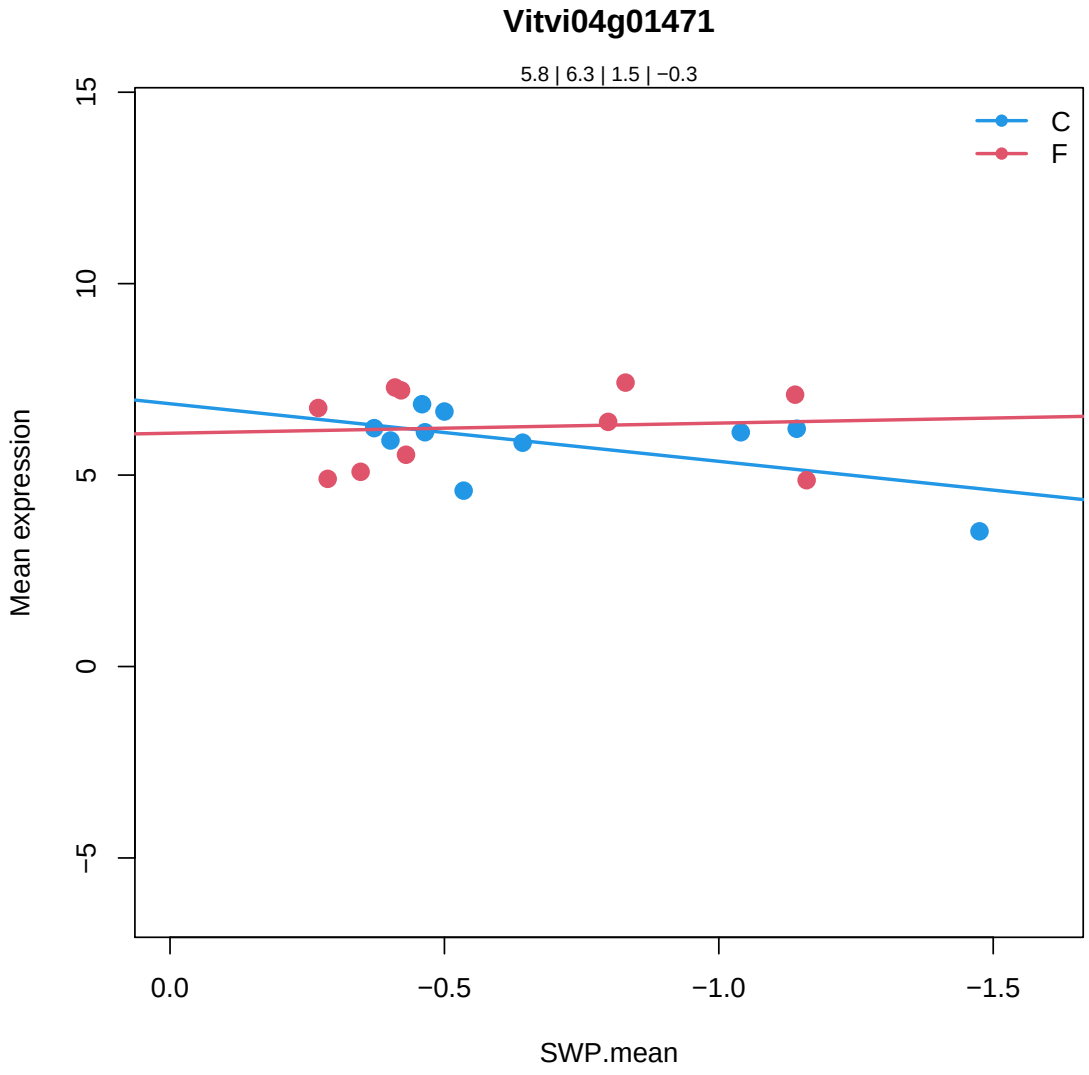
7.6.80 Vitvi04g01471: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01471
        20.1.7.5
        stress.biotic.PR-proteins.PR5 (thaumatin-like proteins)
        Pathogenesis-related thaumatin superfamily protein |
        Chr4:18066448-18067984 REVERSE LENGTH=345 |
        201606
```

Coefficients for Vitvi04g01471.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.805325	1.505798e-15	***	2.758911e-15	***
SlopeC	1.504108	0.07038356	.	0.5604944	
MeanF-MeanC	0.4486499	0.2761825		0.639993	
SlopeF-SlopeC	-1.768985	0.1469854		0.9999488	



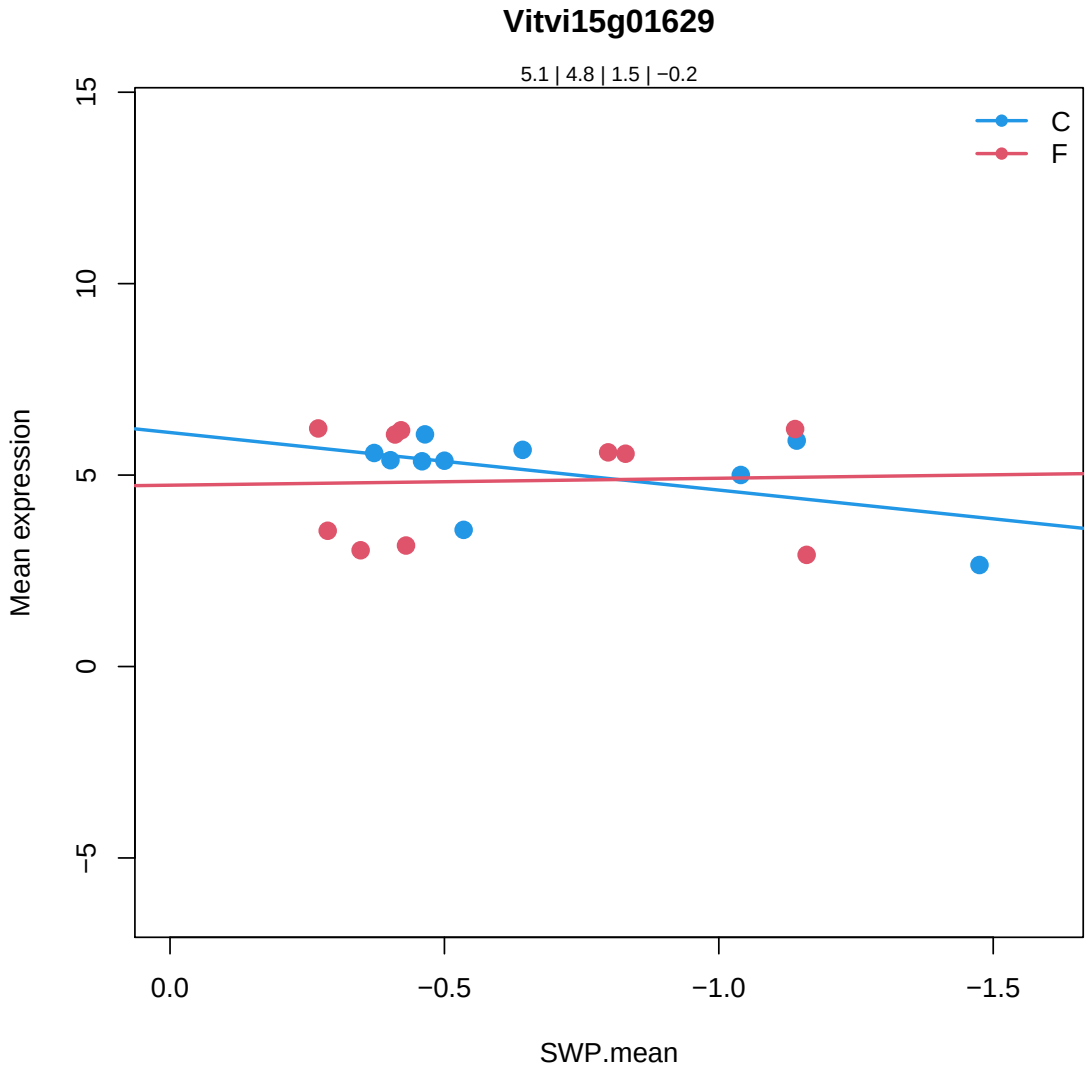
7.6.81 Vitvi15g01629: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g01629
        35.2
        not assigned.unknown
        hypothetical protein |
        Chr5:16711437-16711742 FORWARD LENGTH=101 |
        201606
```

Coefficients for Vitvi15g01629.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.054472	3.607818e-12	***	5.021951e-12	***
SlopeC	1.503307	0.1532979		0.684281	
MeanF-MeanC	-0.2085631	0.69017		0.9013534	
SlopeF-SlopeC	-1.684587	0.2773504		0.9999488	



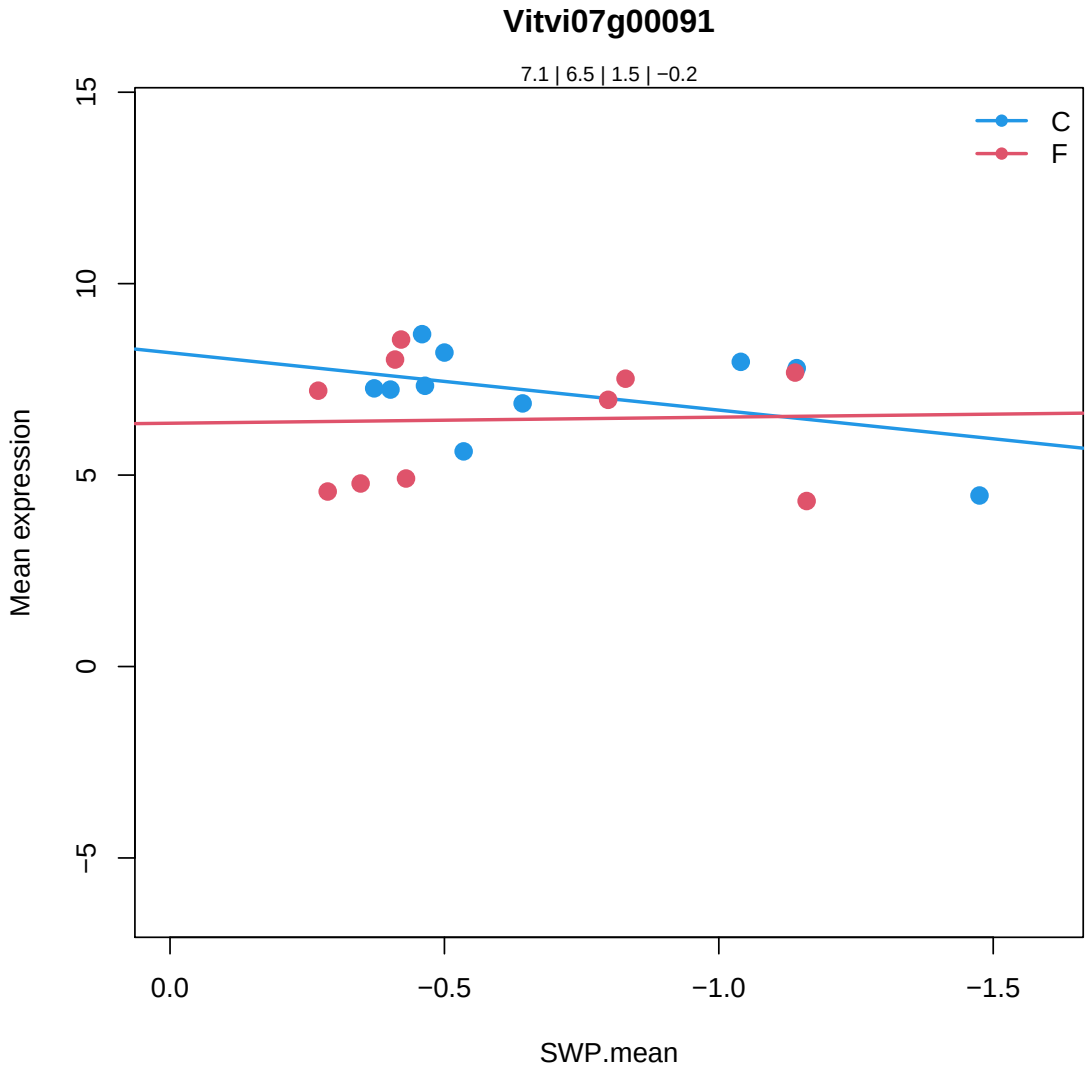
7.6.82 Vitvi07g00091: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g00091
        34.6
        transport.sulphate
        sulfate transporter 3%3B1 |
        Chr3:19251503-19255677 REVERSE LENGTH=658 |
        201606
```

Coefficients for Vitvi07g00091.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.14173	3.93284e-14	***	6.242253e-14	***
SlopeC	1.498238	0.2031781		0.7293041	
MeanF-MeanC	-0.6911558	0.2465711		0.6064606	
SlopeF-SlopeC	-1.656511	0.3403827		0.9999488	



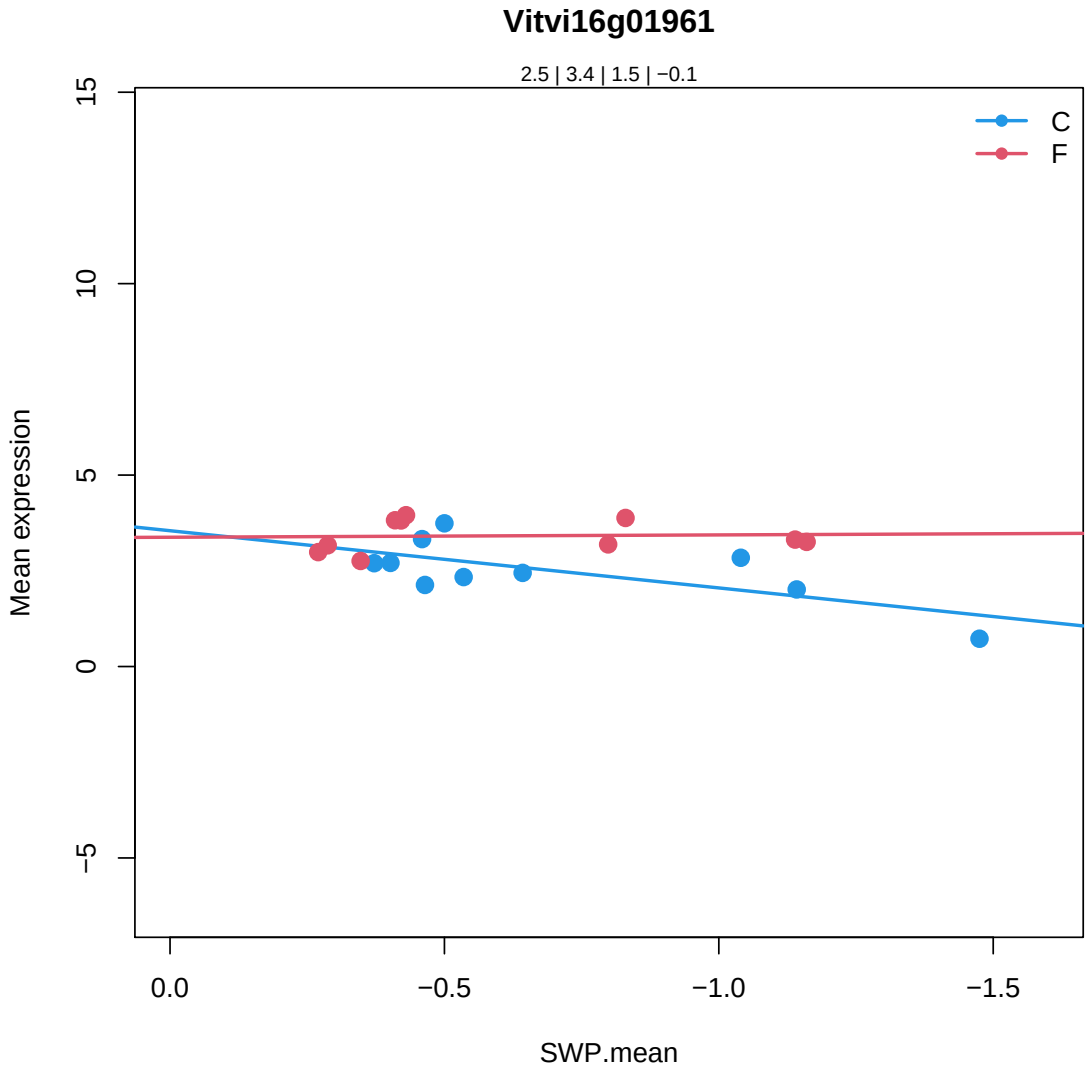
7.6.83 Vitvi16g01961: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01961
        30.2.24
        signalling.receptor kinases.S-locus glycoprotein like
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606
```

Coefficients for Vitvi16g01961.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.496139	8.150453e-13	***	1.176636e-12	***
SlopeC	1.494468	0.004067862	**	0.2328828	
MeanF-MeanC	0.917519	0.0008297517	***	0.01072695	*
SlopeF-SlopeC	-1.555261	0.03515065	*	0.9999488	



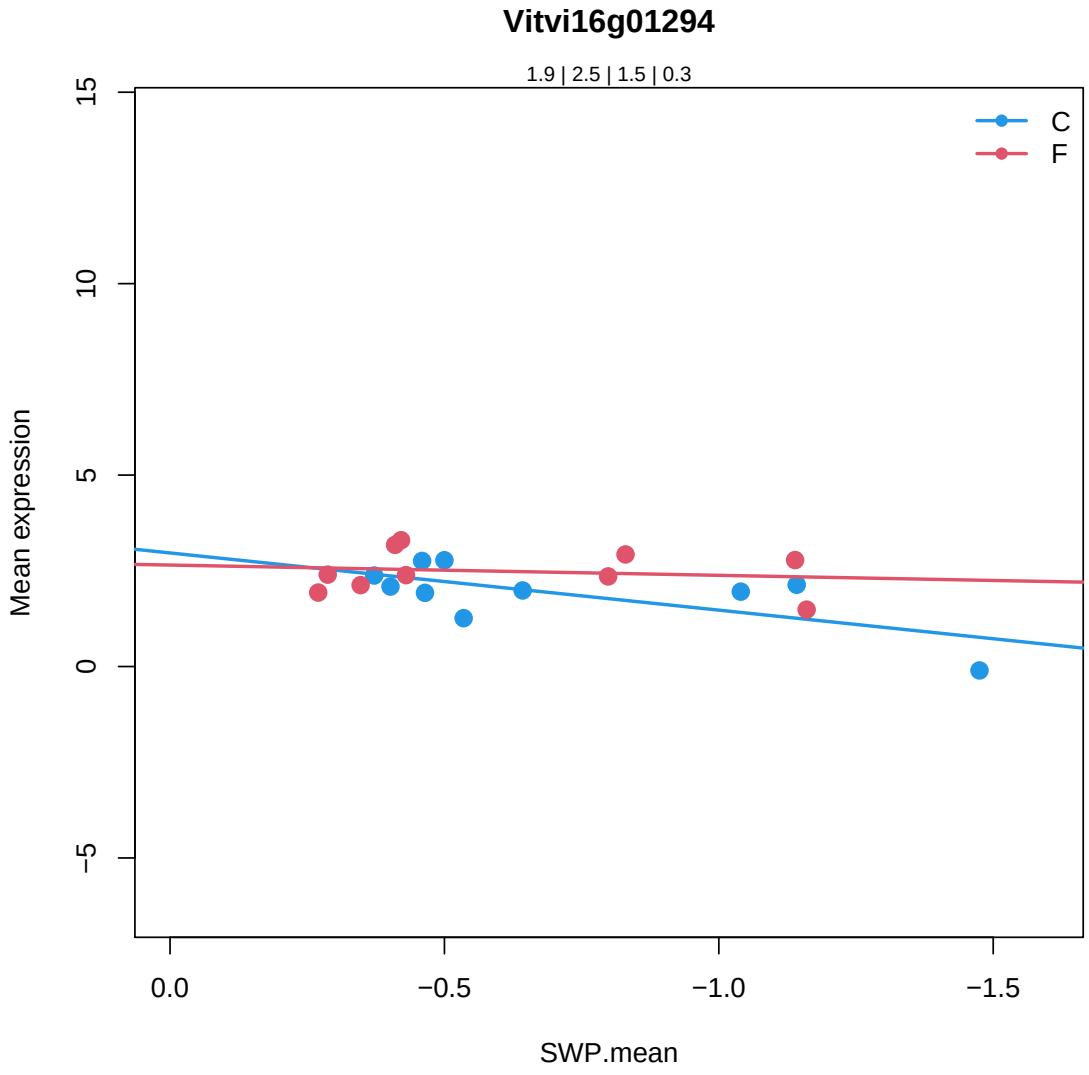
7.6.84 Vitvi16g01294: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01294
        29.5.11.4.2
        protein.degradation.ubiquitin.E3.RING
        Protein kinase family protein |
        Chr5:15280643-15282709 REVERSE LENGTH=620 |
        201606
```

Coefficients for Vitvi16g01294.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.915808	1.001568e-09	***	1.262479e-09	***
SlopeC	1.493879	0.008963217	**	0.2903326	
MeanF-MeanC	0.5706354	0.04226747	*	0.2140335	
SlopeF-SlopeC	-1.22552	0.1278236		0.9999488	



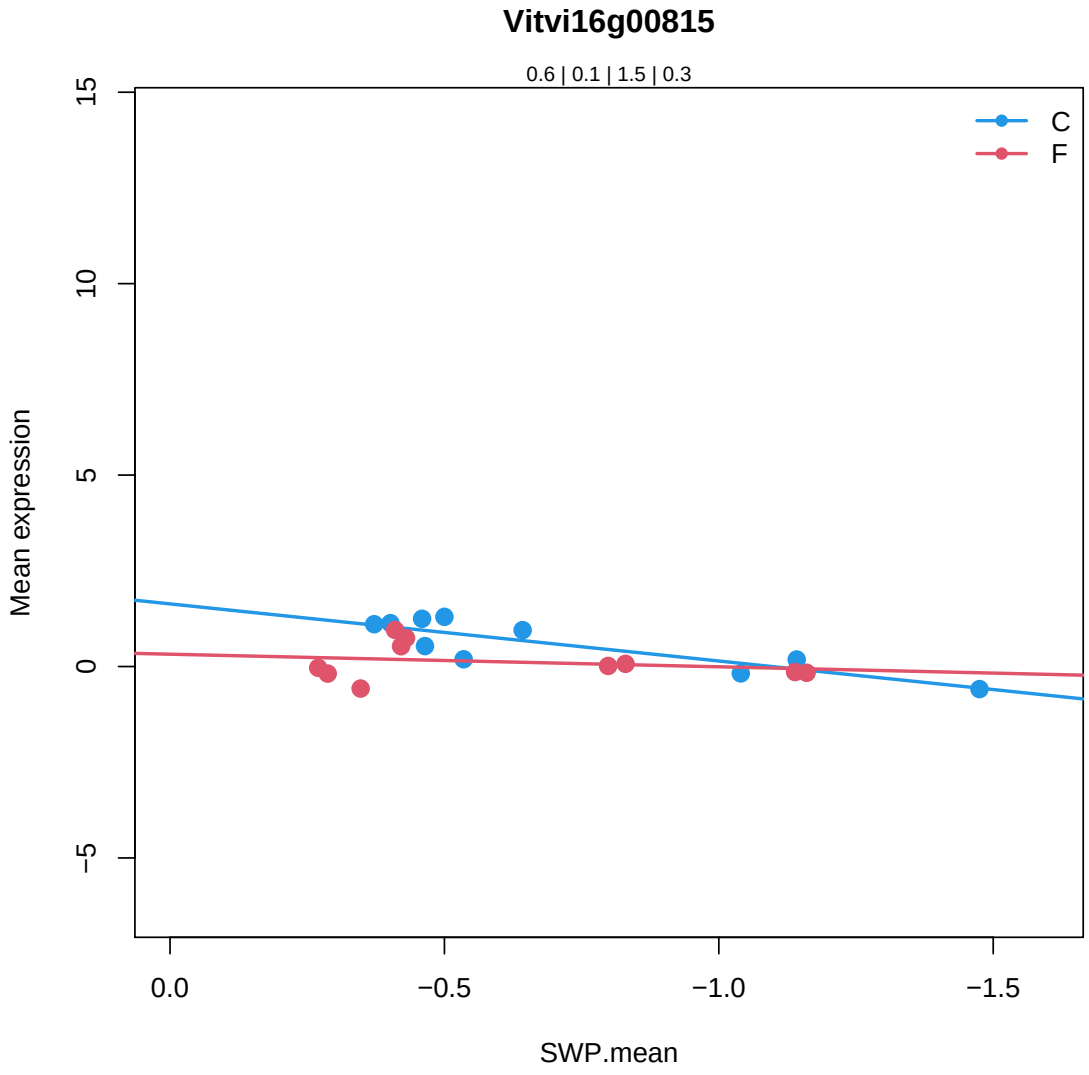
7.6.85 Vitvi16g00815: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g00815
        35.2
        not assigned.unknown
        PR5-like receptor kinase |
        Chr5:15293325-15295838 REVERSE LENGTH=665 |
        201606
```

Coefficients for Vitvi16g00815.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.5867581	0.0004280692	***	0.000466979	***
SlopeC	1.491975	0.001013885	**	0.1271346	
MeanF-MeanC	-0.4659128	0.02931808	*	0.1663141	
SlopeF-SlopeC	-1.162975	0.0594056	.	0.9999488	



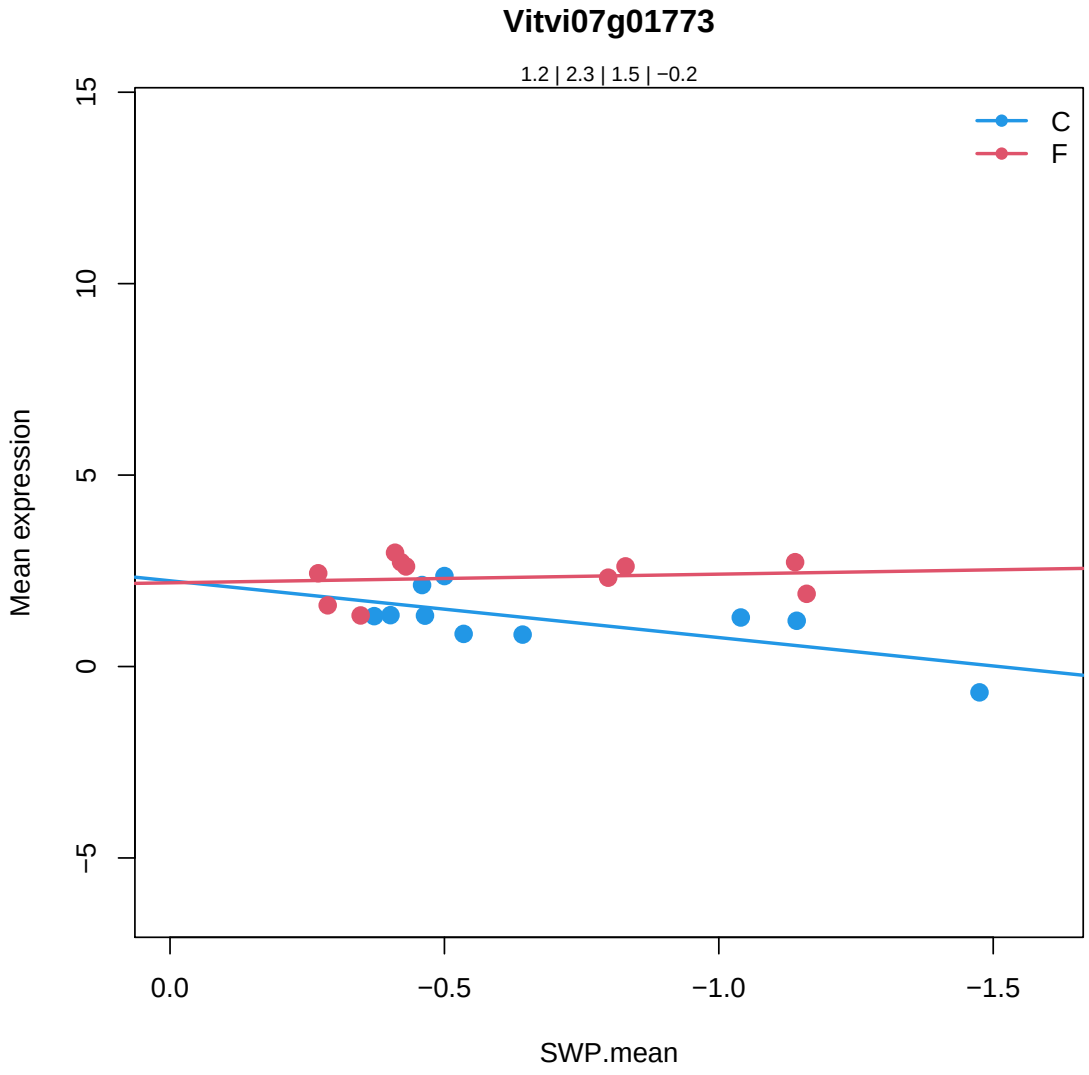
7.6.86 Vitvi07g01773: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01773
        26.3.5
        misc.gluco-, galacto- and mannosidases.glycosyl hydrolase family 5
        P-loop containing nucleoside triphosphate hydrolases superfamily prote
        Chr3:18784993-18786248 REVERSE LENGTH=312 |
        201606
```

Coefficients for Vitvi07g01773.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.196096	1.42681e-06	***	1.640821e-06	***
SlopeC	1.482639	0.007771155	**	0.280858	
MeanF-MeanC	1.127587	0.000243031	***	0.003866679	**
SlopeF-SlopeC	-1.709281	0.03330959	*	0.9999488	



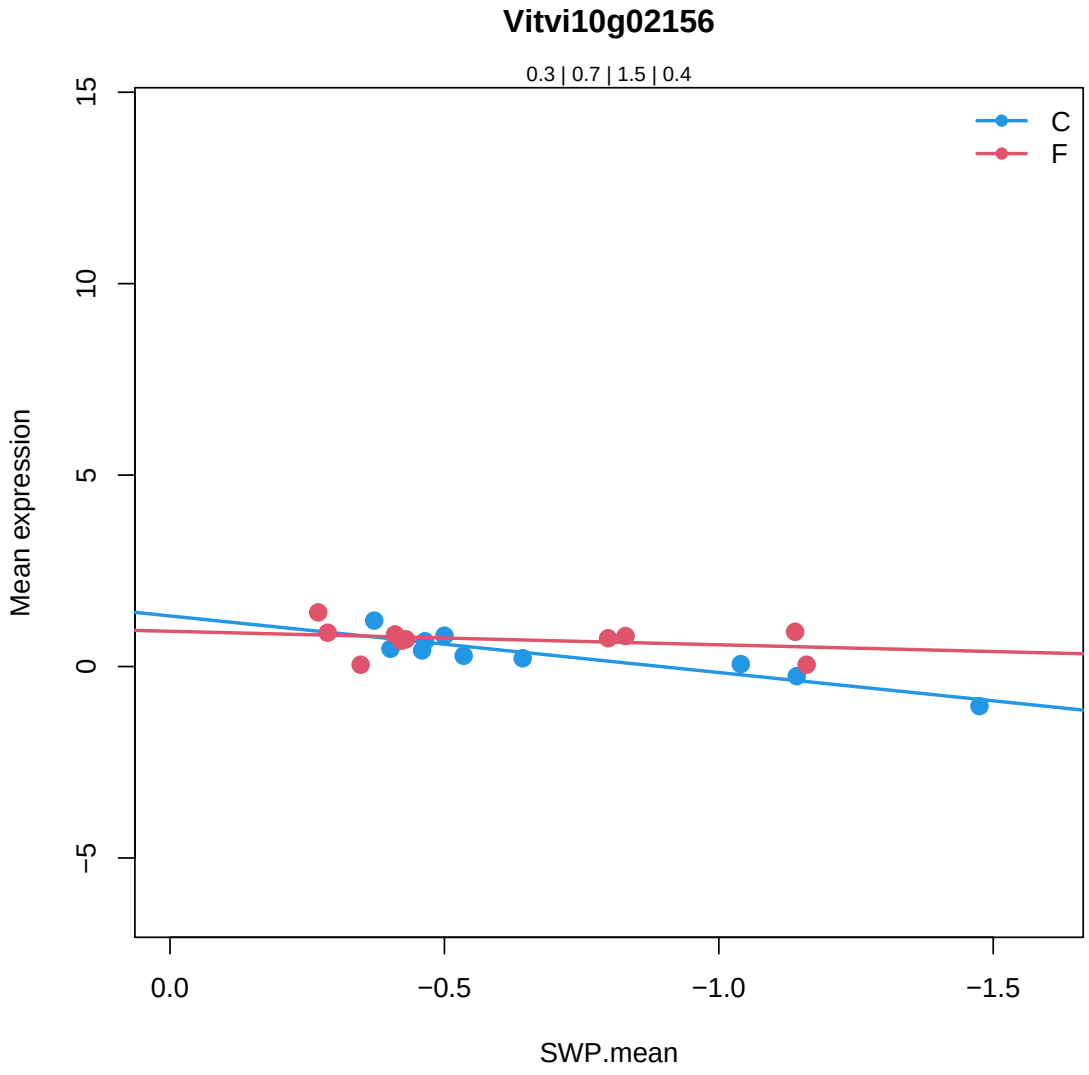
7.6.87 Vitvi10g02156: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g02156
        35.2
        not assigned.unknown
        Copia-like polyprotein/retrotransposon |
        Chr1:12402283-12403209 FORWARD LENGTH=308 |
        201606
```

Coefficients for Vitvi10g02156.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.2818628	0.03120038	*	0.03264165	*
SlopeC	1.477534	0.0002736205	***	0.08341047	.
MeanF-MeanC	0.4232631	0.02302767	*	0.1399473	
SlopeF-SlopeC	-1.124535	0.03720268	*	0.9999488	



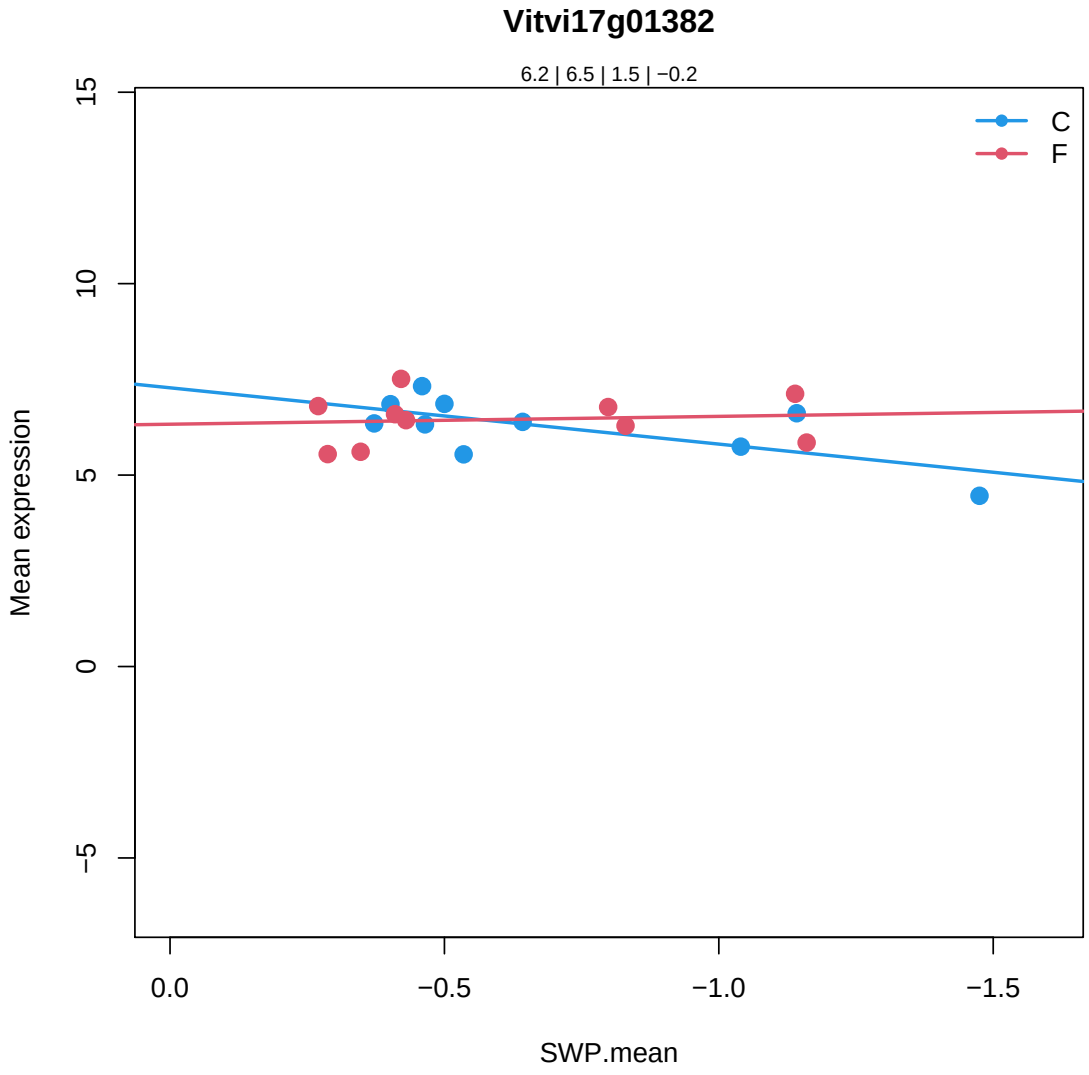
7.6.88 Vitvi17g01382: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g01382
        35.2
        not assigned.unknown
        glutathione S-transferase tau 7 |
        Chr2:12618111-12618871 REVERSE LENGTH=227 |
        201606
```

Coefficients for Vitvi17g01382.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.245463	1.486165e-19	***	6.650655e-19	***
SlopeC	1.470506	0.01331844	*	0.3305597	
MeanF-MeanC	0.2075883	0.4618337		0.7848846	
SlopeF-SlopeC	-1.6754	0.05119355	.	0.9999488	



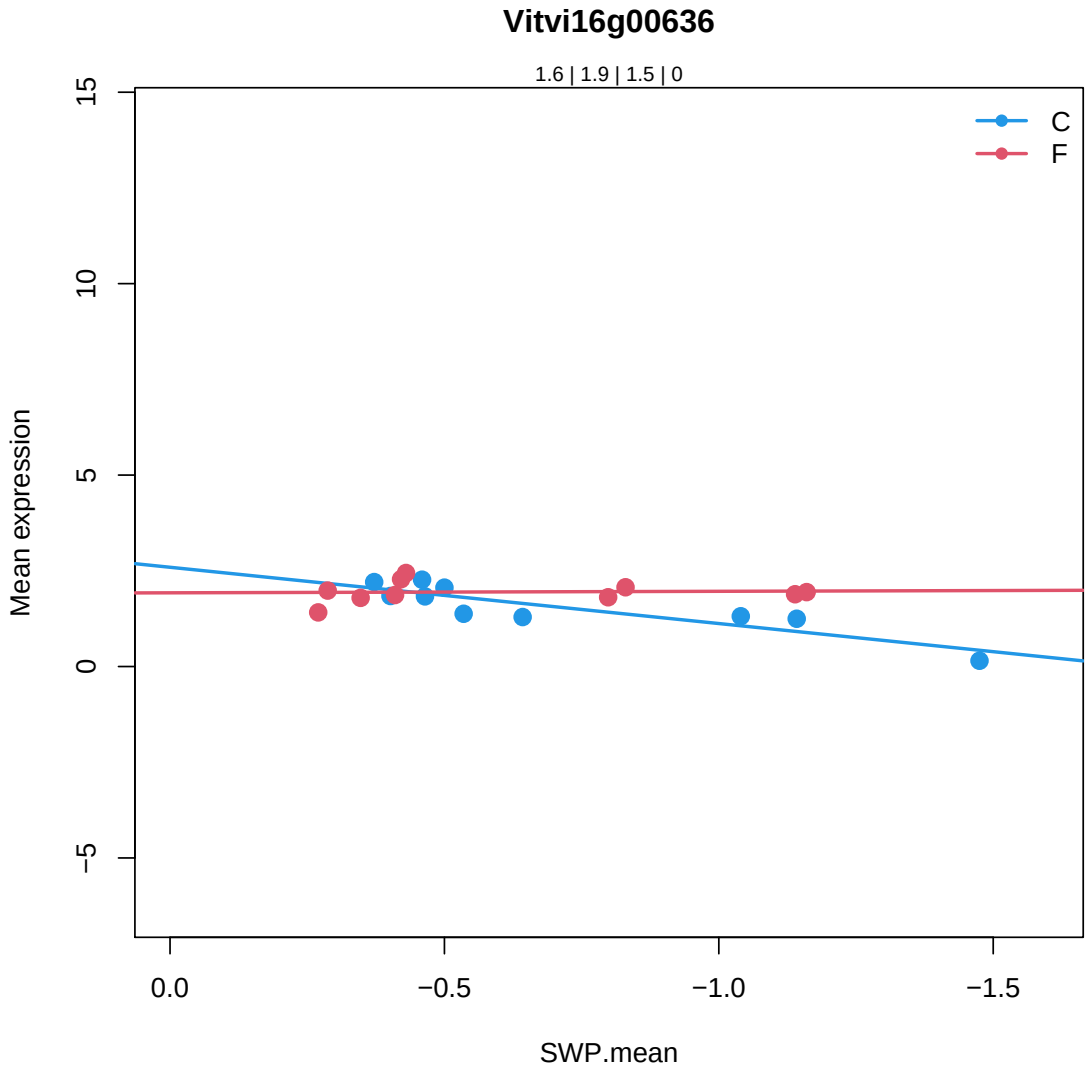
7.6.89 Vitvi16g00636: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g00636
        35.2
        not assigned.unknown
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606
```

Coefficients for Vitvi16g00636.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.558723	4.742435e-12	***	6.560554e-12	***
SlopeC	1.469682	0.0001382542	***	0.07644173	.
MeanF-MeanC	0.3902008	0.02463273	*	0.1468905	
SlopeF-SlopeC	-1.508811	0.00430676	**	0.9999488	



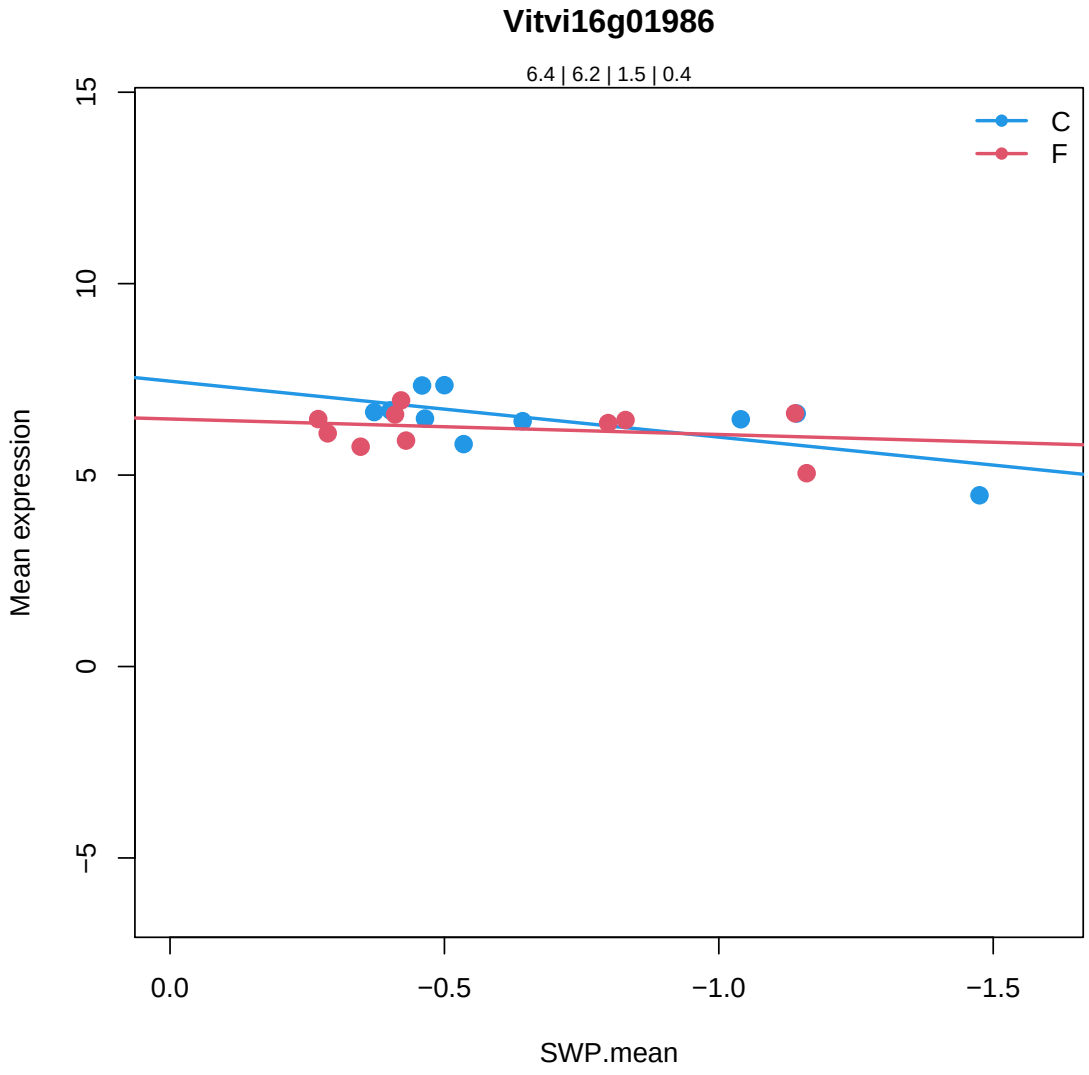
7.6.90 Vitvi16g01986: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01986
        35.2
        not assigned.unknown
        PR5-like receptor kinase |
        Chr5:15293325-15295838 REVERSE LENGTH=665 |
        201606
```

Coefficients for Vitvi16g01986.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.425295	1.672773e-20	***	1.076707e-19	***
SlopeC	1.461204	0.008627167	**	0.2903326	
MeanF-MeanC	-0.2069842	0.429344		0.7640469	
SlopeF-SlopeC	-1.056444	0.1745792		0.9999488	



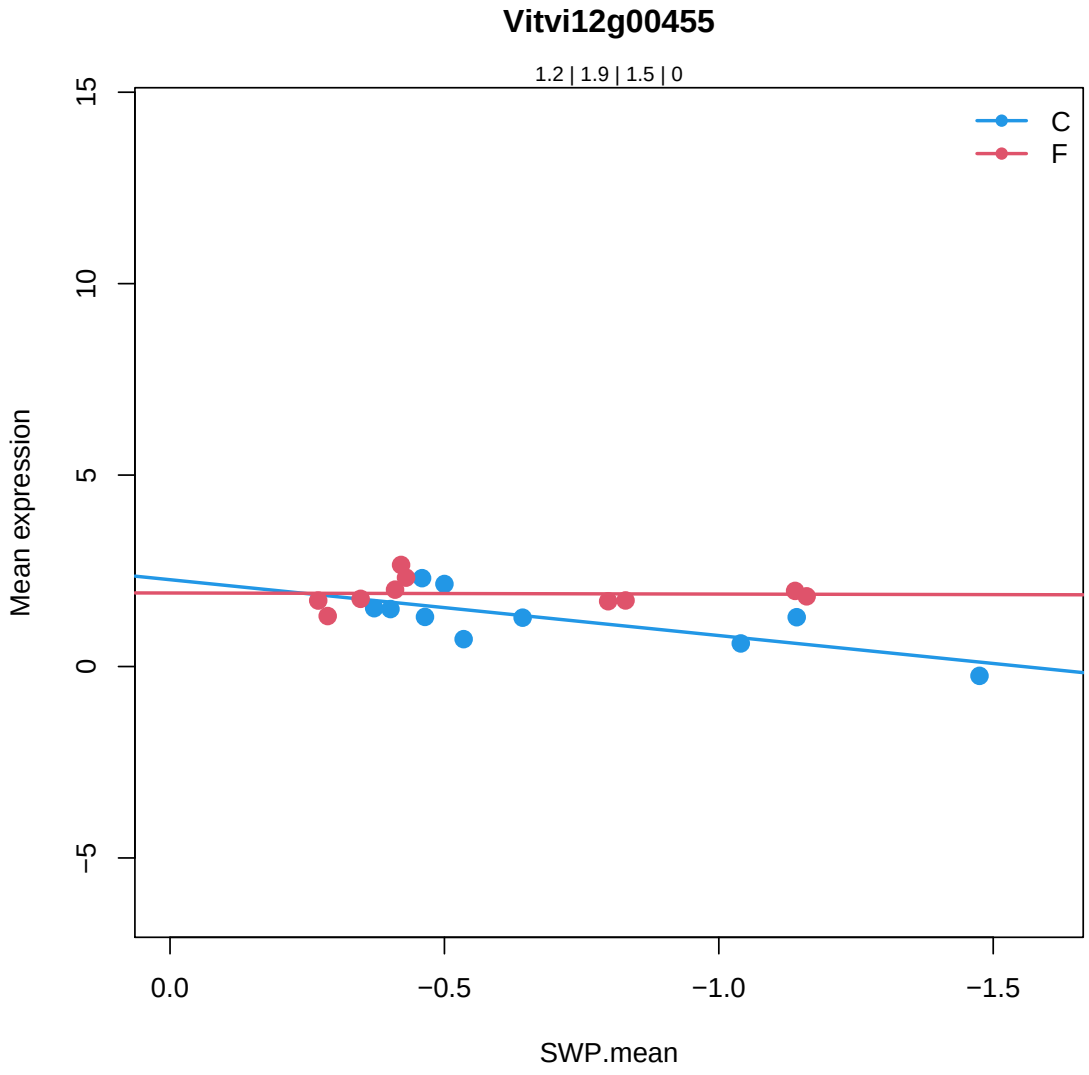
7.6.91 Vitvi12g00455: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00455
        35.2
        not assigned.unknown
        hypothetical protein |
        Chr1:4062625-4063305 REVERSE LENGTH=226 |
        201606
```

Coefficients for Vitvi12g00455.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.241728	3.842803e-08	***	4.609428e-08	***
SlopeC	1.45888	0.002049178	**	0.1706753	
MeanF-MeanC	0.6610518	0.005019808	**	0.04593086	*
SlopeF-SlopeC	-1.431183	0.0308271	*	0.9999488	



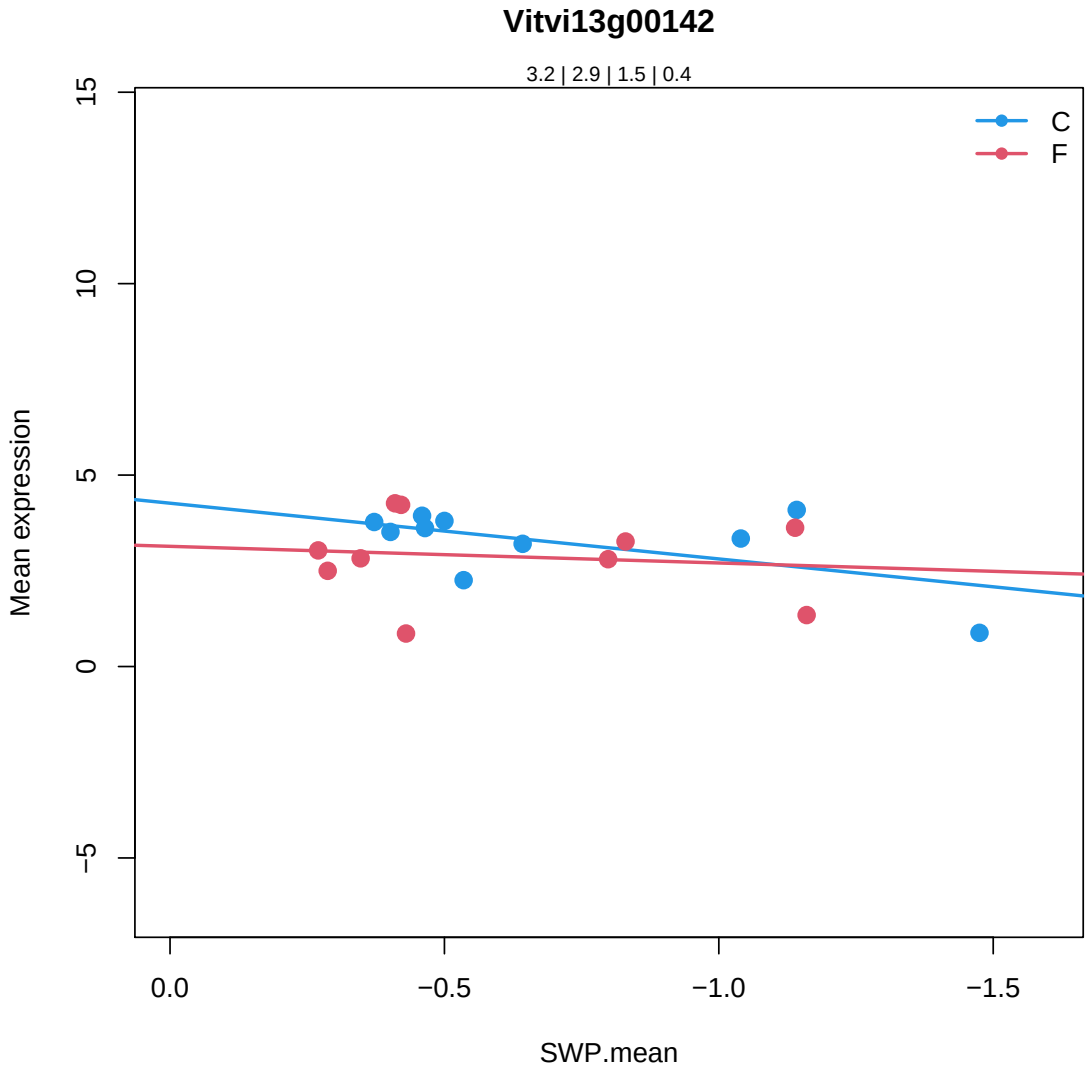
7.6.92 Vitvi13g00142: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00142
        34.13
        transport.peptides and oligopeptides
        Major facilitator superfamily protein |
        Chr2:16897123-16901171 FORWARD LENGTH=583 |
        201606
```

Coefficients for Vitvi13g00142.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.241739	2.023741e-10	***	2.617384e-10	***
SlopeC	1.455522	0.0848574	.	0.5861394	
MeanF-MeanC	-0.3676924	0.3792139		0.7307959	
SlopeF-SlopeC	-1.020401	0.4041657		0.9999488	



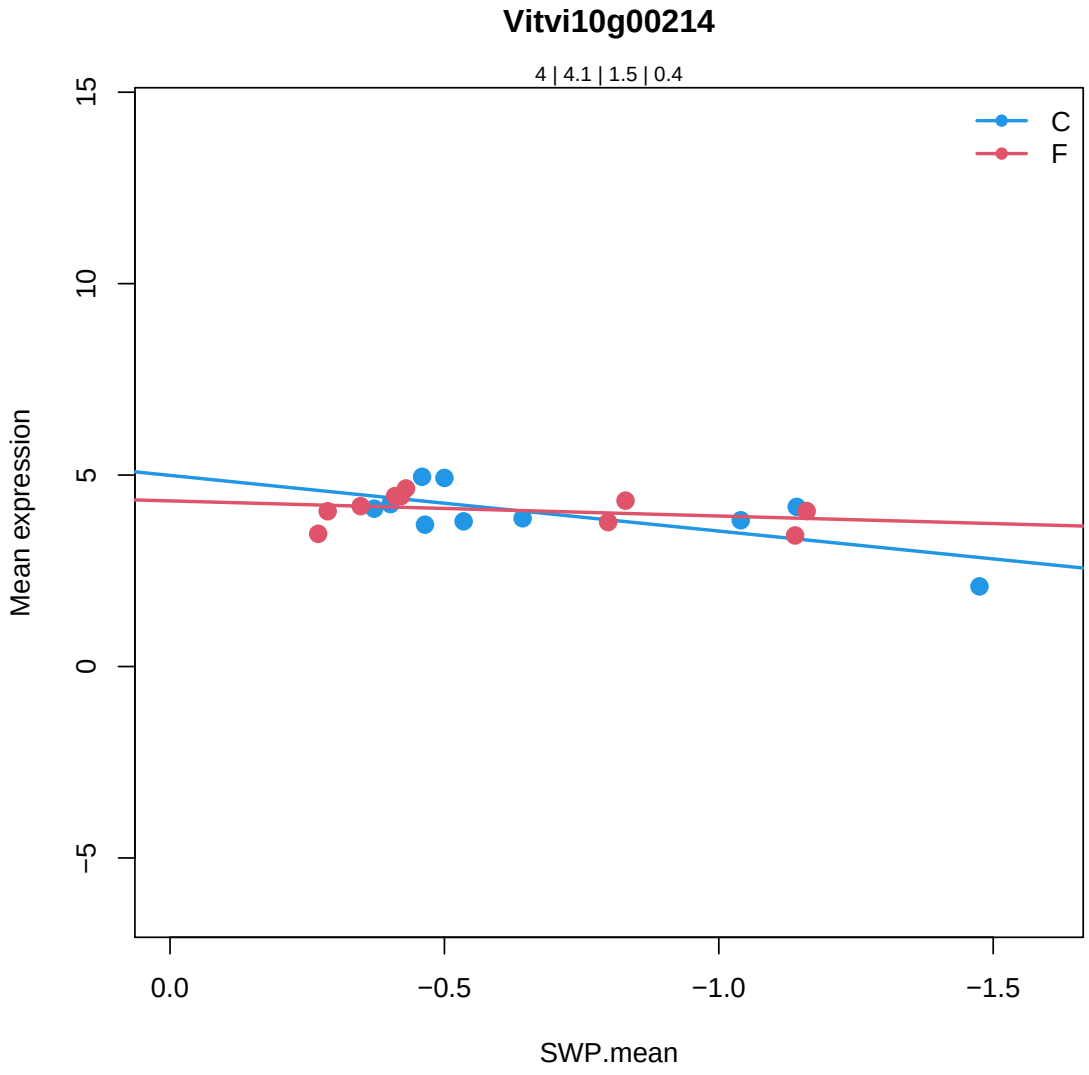
7.6.93 Vitvi10g00214: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00214
        29.5.11.4.2
        protein.degradation.ubiquitin.E3.RING
        RING domain ligase2 |
        Chr5:4648355-4650563 REVERSE LENGTH=468 |
        201606
```

Coefficients for Vitvi10g00214.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.969313	3.92746e-17	***	9.206759e-17	***
SlopeC	1.454166	0.004087419	**	0.2328828	
MeanF-MeanC	0.115584	0.6203719		0.8688513	
SlopeF-SlopeC	-1.059395	0.1302963		0.9999488	



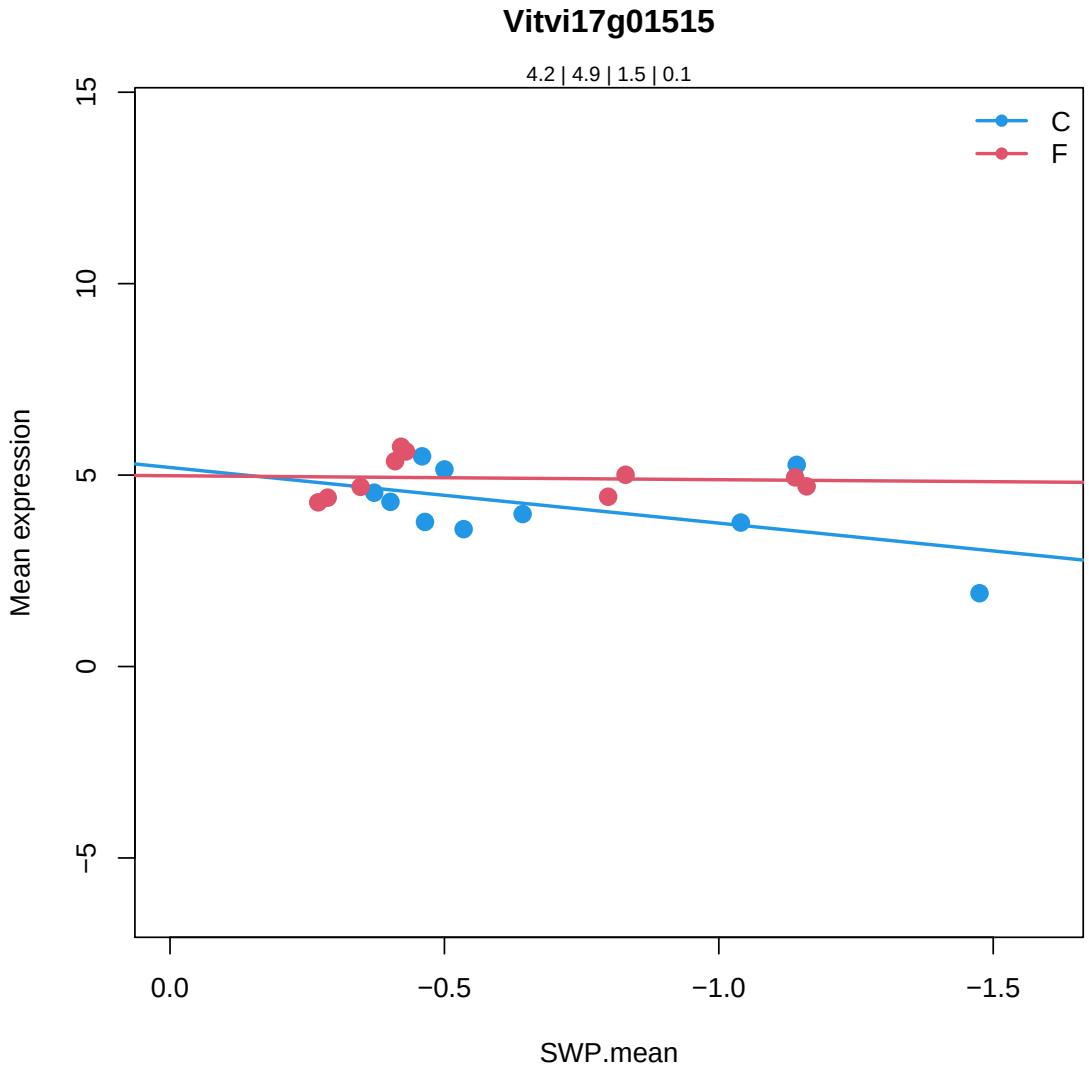
7.6.94 Vitvi17g01515: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g01515
        35.2
        not assigned.unknown
        alpha/beta-Hydrolases superfamily protein |
        Chr3:17755553-17757692 REVERSE LENGTH=623 |
        201606
```

Coefficients for Vitvi17g01515.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.176393	9.957558e-15	***	1.664726e-14	***
SlopeC	1.452703	0.0296525	*	0.4299803	
MeanF-MeanC	0.7434088	0.02868424	*	0.1640545	
SlopeF-SlopeC	-1.34923	0.1604663		0.9999488	



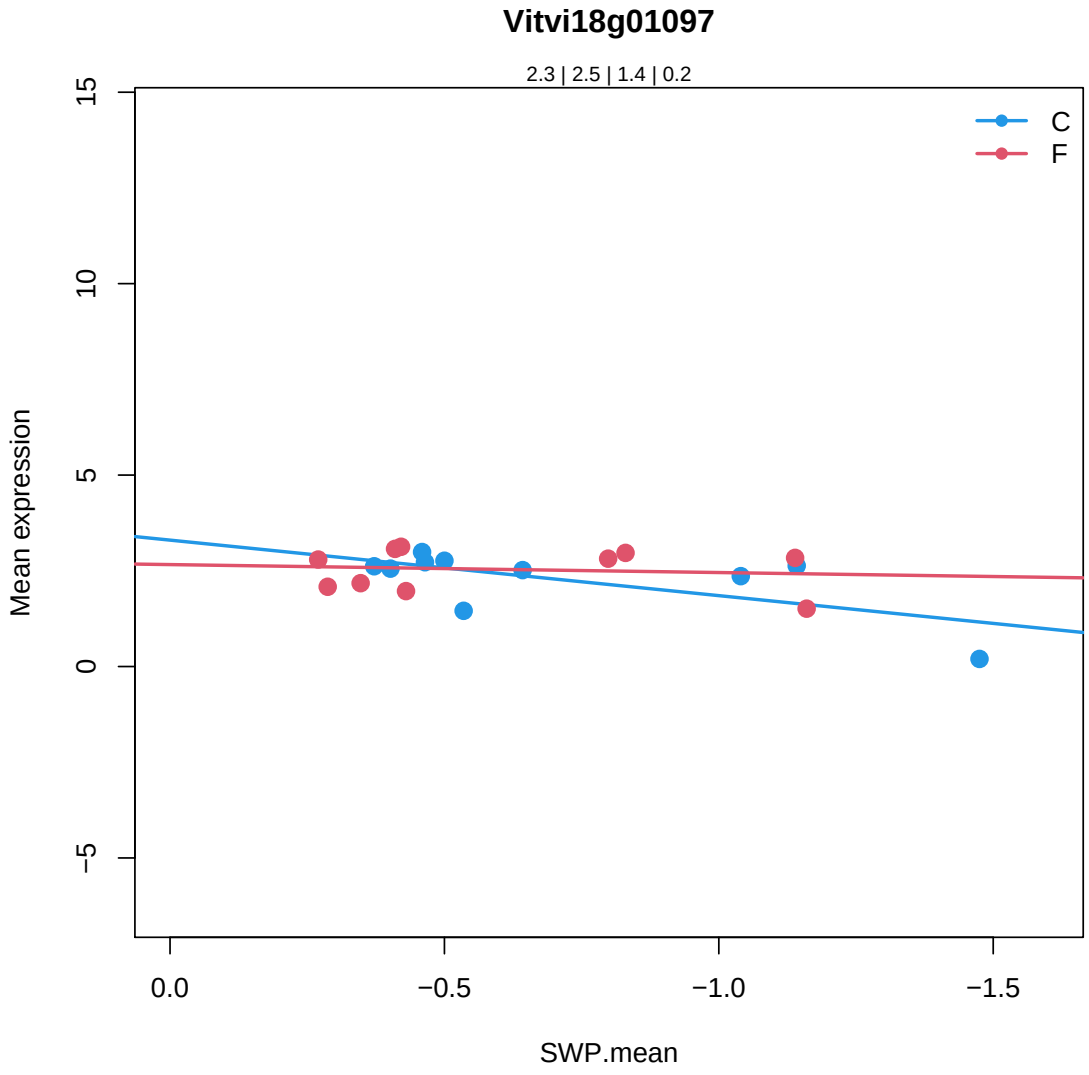
7.6.95 Vitvi18g01097: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g01097
        13.2.3.5.1
        amino acid metabolism.degradation.aspartate family.lysine.lysine decar
        Putative lysine decarboxylase family protein |
        Chr3:19812977-19815430 REVERSE LENGTH=215 |
        201606
```

Coefficients for Vitvi18g01097.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.281344	4.859661e-11	***	6.440393e-11	***
SlopeC	1.449988	0.01156494	*	0.318473	
MeanF-MeanC	0.254263	0.3514588		0.7100922	
SlopeF-SlopeC	-1.242316	0.1266028		0.9999488	



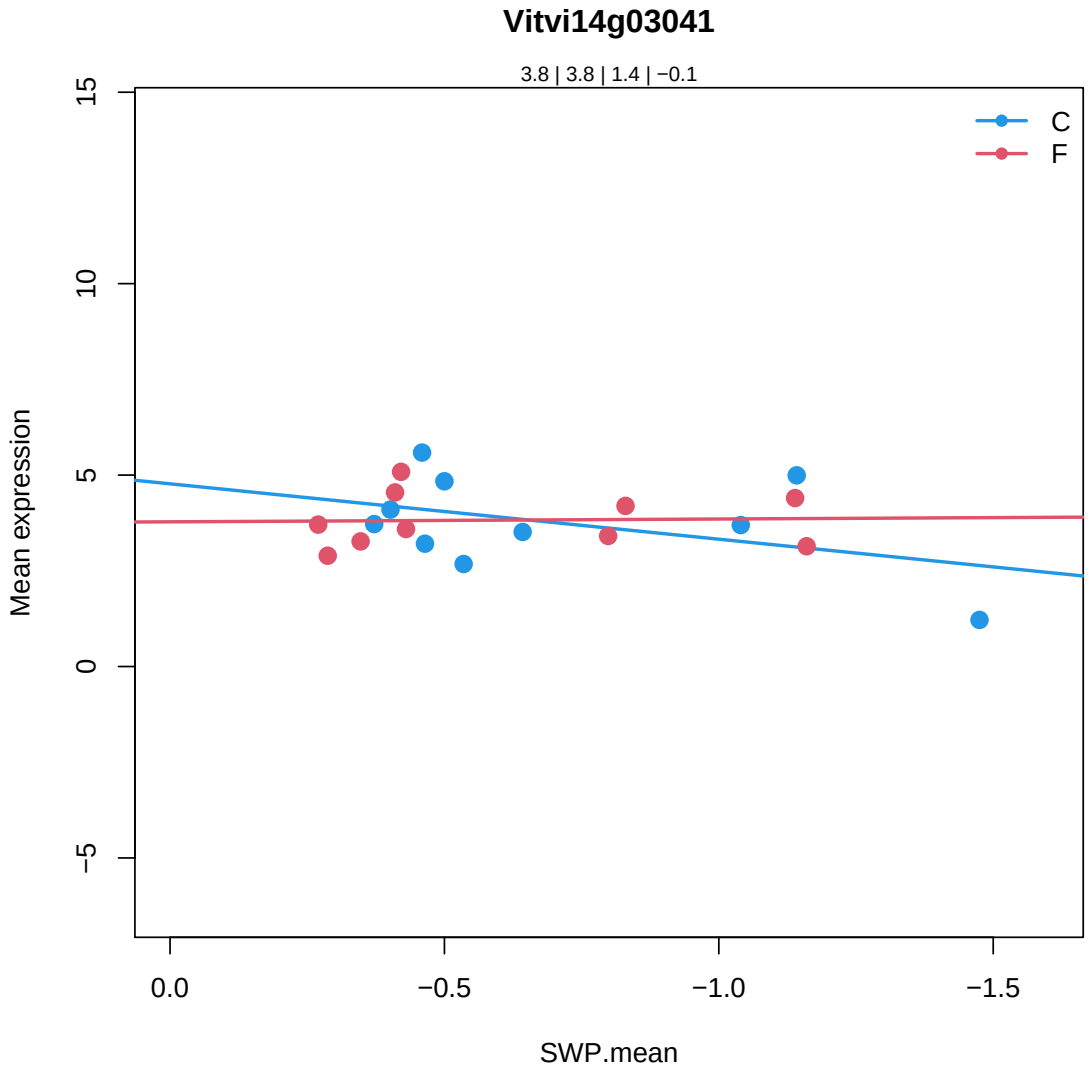
7.6.96 Vitvi14g03041: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g03041
        29.5.9
        protein.degradation.AAA type
        AAA-ATPase 1 |
        Chr5:16020218-16021762 REVERSE LENGTH=514 |
        201606
```

Coefficients for Vitvi14g03041.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.754716	8.410124e-12	***	1.15328e-11	***
SlopeC	1.446365	0.08039426	.	0.5759705	
MeanF-MeanC	0.06898646	0.864899		0.9643899	
SlopeF-SlopeC	-1.519724	0.2089123		0.9999488	



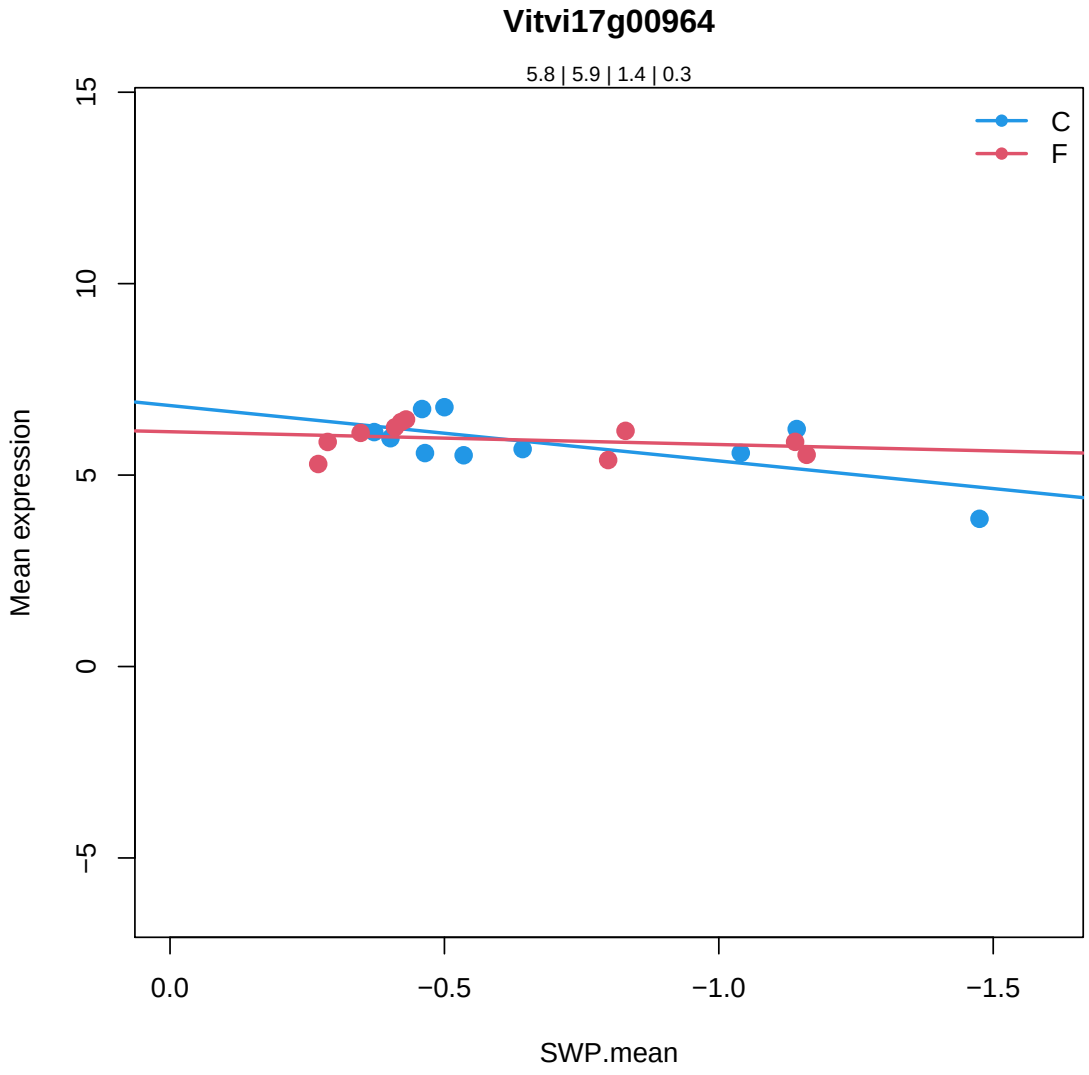
7.6.97 Vitvi17g00964: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00964
        30.2.11
        signalling.receptor kinases.leucine rich repeat XI
        Leucine-rich repeat protein kinase family protein |
        Chr2:13554920-13556845 FORWARD LENGTH=641 |
        201606
```

Coefficients for Vitvi17g00964.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.799194	2.916485e-20	***	1.69345e-19	***
SlopeC	1.445571	0.005507368	**	0.2577627	
MeanF-MeanC	0.1292269	0.5929107		0.8574279	
SlopeF-SlopeC	-1.111556	0.1254875		0.9999488	



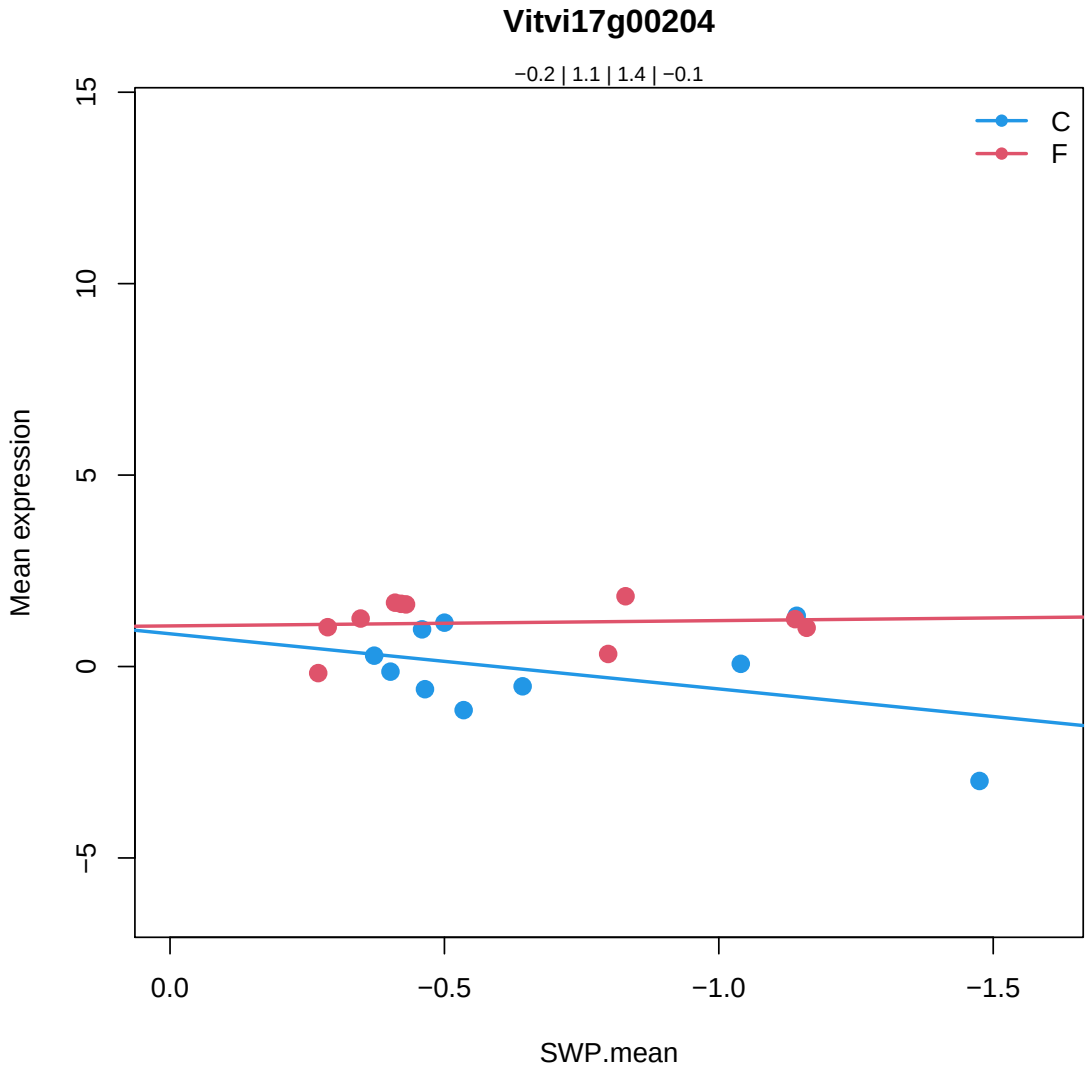
7.6.98 Vitvi17g00204: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00204
        35.2
        not assigned.unknown
        Leucine-rich repeat receptor-like protein kinase family protein |
        Chr4:5637467-5640496 REVERSE LENGTH=1009 |
        201606
```

Coefficients for Vitvi17g00204.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.1578332	0.5808721		0.5862958	
SlopeC	1.440379	0.07981691	.	0.5748584	
MeanF-MeanC	1.302509	0.003574812	**	0.0351985	*
SlopeF-SlopeC	-1.578961	0.1897105		0.9999488	



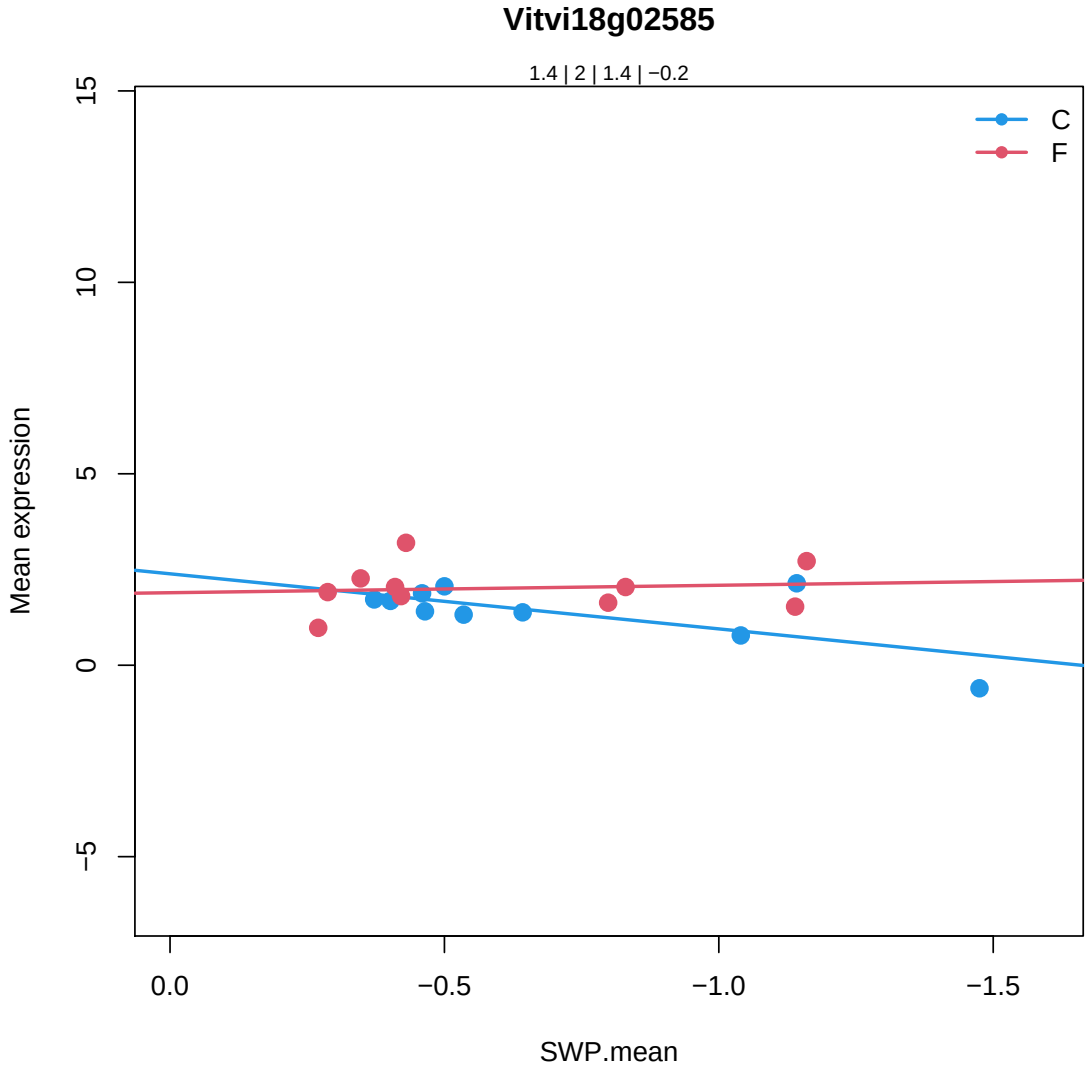
7.6.99 Vitvi18g02585: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02585
        35.2
        not assigned.unknown
        Avr9_Cf-9 rapidly elicited protein 75
```

Coefficients for Vitvi18g02585.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.375953	3.868982e-07	***	4.5147e-07	***
SlopeC	1.438235	0.01323695	*	0.3305597	
MeanF-MeanC	0.6361428	0.02841165	*	0.1632305	
SlopeF-SlopeC	-1.632692	0.05175106	.	0.9999488	



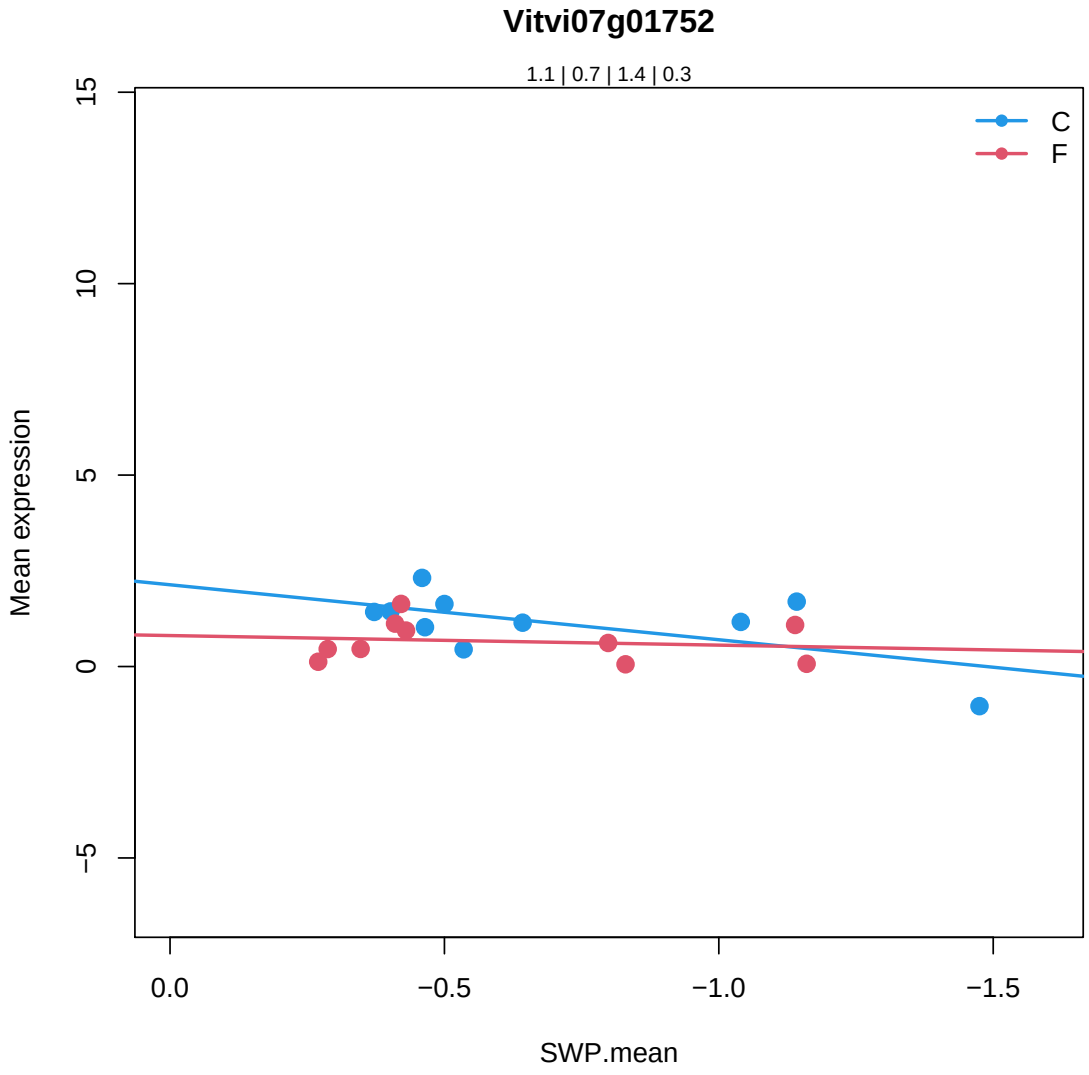
7.6.100 Vitvi07g01752: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01752
        28.1
        DNA.synthesis/chromatin structure
        centrin2 |
        Chr3:18674421-18675502 FORWARD LENGTH=169 |
        201606
```

Coefficients for Vitvi07g01752.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.125539	1.119778e-05	***	1.263241e-05	***
SlopeC	1.435711	0.01629334	*	0.3487964	
MeanF-MeanC	-0.4693303	0.1081483		0.3831244	
SlopeF-SlopeC	-1.185486	0.1625488		0.9999488	



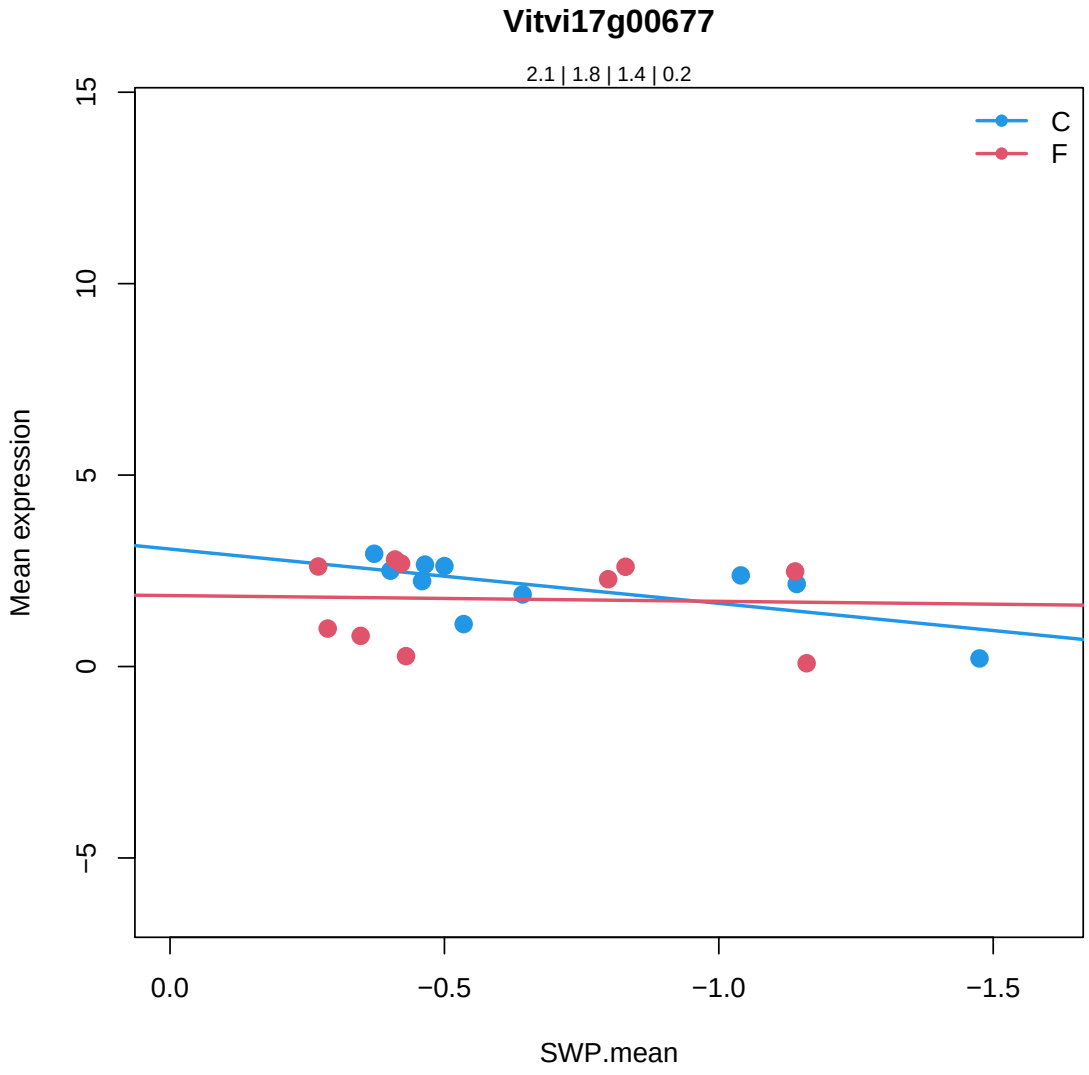
7.6.101 Vitvi17g00677: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00677
        27.3.99
        RNA.regulation of transcription.unclassified
        Remorin family protein |
        Chr5:24643625-24644725 REVERSE LENGTH=240 |
        201606
```

Coefficients for Vitvi17g00677.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.069892	1.350163e-07	***	1.596648e-07	***
SlopeC	1.418872	0.07179225	.	0.5630621	
MeanF-MeanC	-0.3087279	0.4264246		0.7622334	
SlopeF-SlopeC	-1.268678	0.2677432		0.9999488	



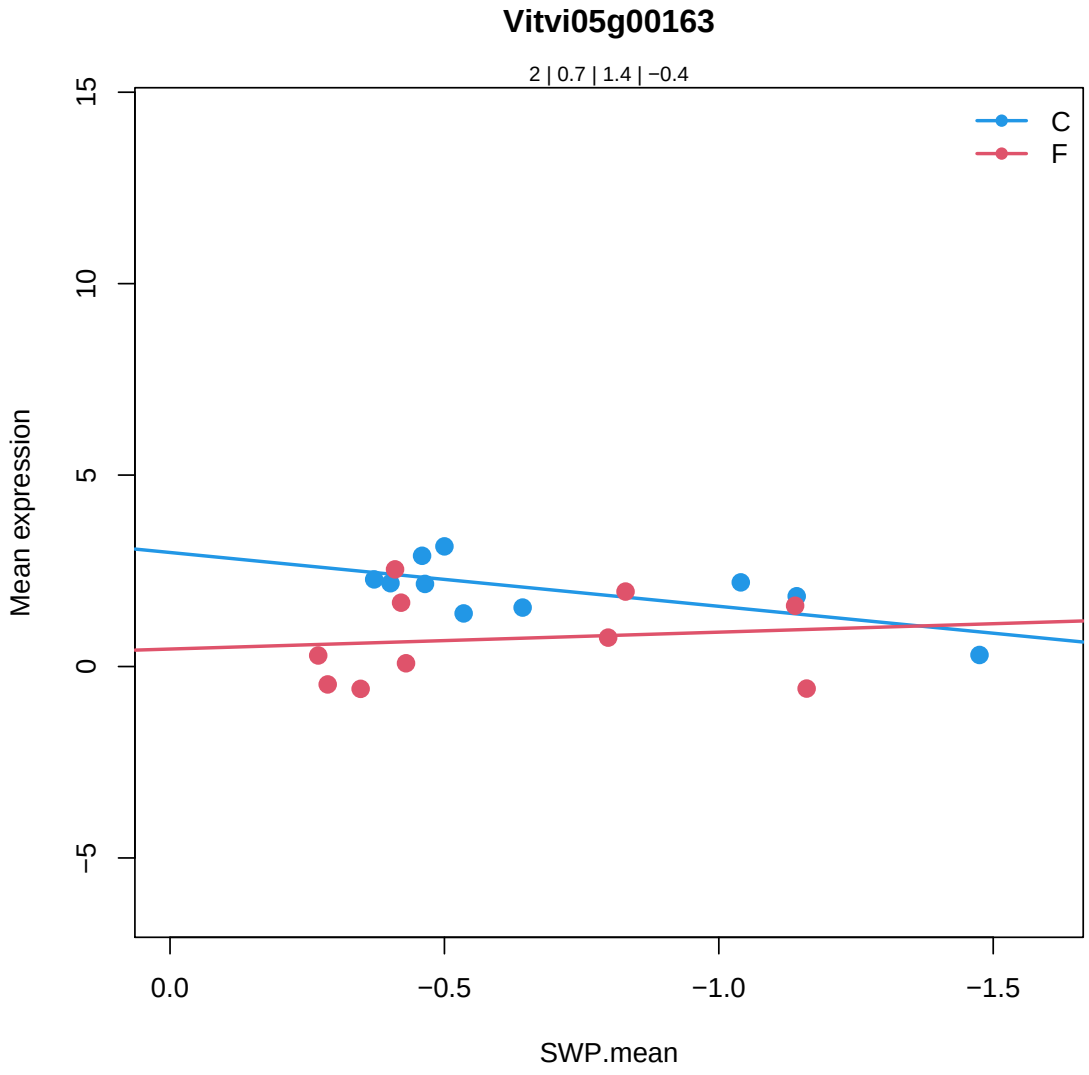
7.6.102 Vitvi05g00163: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00163
        17.6.1.13
        hormone metabolism.gibberelin.synthesis-degradation.GA2 oxidase
        gibberellin 2-oxidase 6 |
        Chr1:486964-489116 FORWARD LENGTH=265 |
        201606
```

Coefficients for Vitvi05g00163.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.989793	3.426797e-07	***	4.003314e-07	***
SlopeC	1.405586	0.07971648	.	0.5748584	
MeanF-MeanC	-1.264749	0.00370322	**	0.03618236	*
SlopeF-SlopeC	-1.846737	0.1190109		0.9999488	



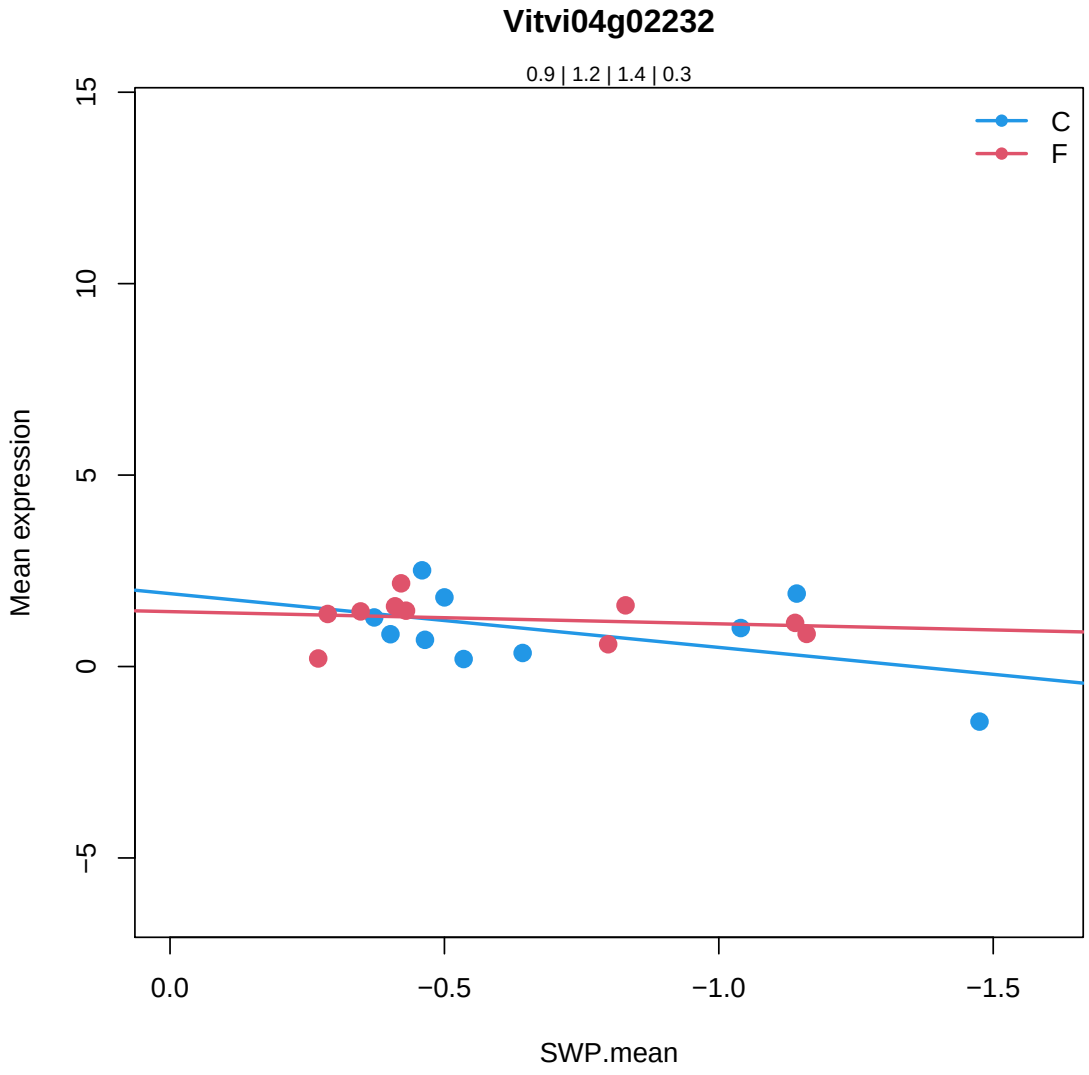
7.6.103 Vitvi04g02232: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g02232
        35.2
        not assigned.unknown
        receptor-like protein kinase 1 |
        Chr5:24498467-24501494 REVERSE LENGTH=832 |
        201606
```

Coefficients for Vitvi04g02232.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.9159042	0.0009995197	***	0.001082316	**
SlopeC	1.404581	0.04787159	*	0.5004518	
MeanF-MeanC	0.3235241	0.352248		0.7107724	
SlopeF-SlopeC	-1.085888	0.2877954		0.9999488	



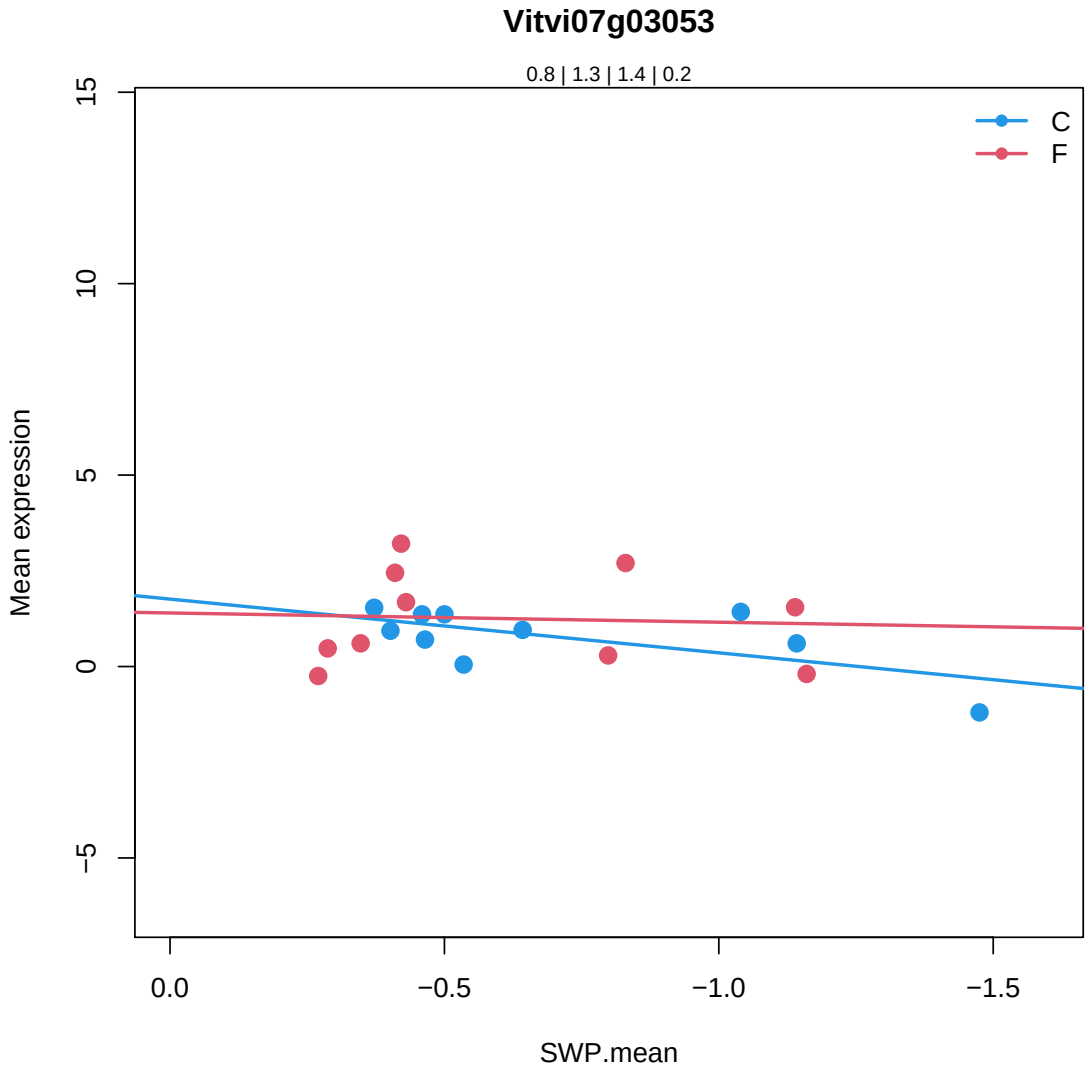
7.6.104 Vitvi07g03053: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g03053
        34.16
        transport.ABC transporters and multidrug resistance systems
        white-brown complex-like protein |
        Chr1:6142870-6145894 FORWARD LENGTH=703 |
        201606
```

Coefficients for Vitvi07g03053.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.7739521	0.01613784	*	0.01701176	*
SlopeC	1.403057	0.1032907		0.6146329	
MeanF-MeanC	0.4775553	0.2671179		0.6292752	
SlopeF-SlopeC	-1.161908	0.3543114		0.9999488	



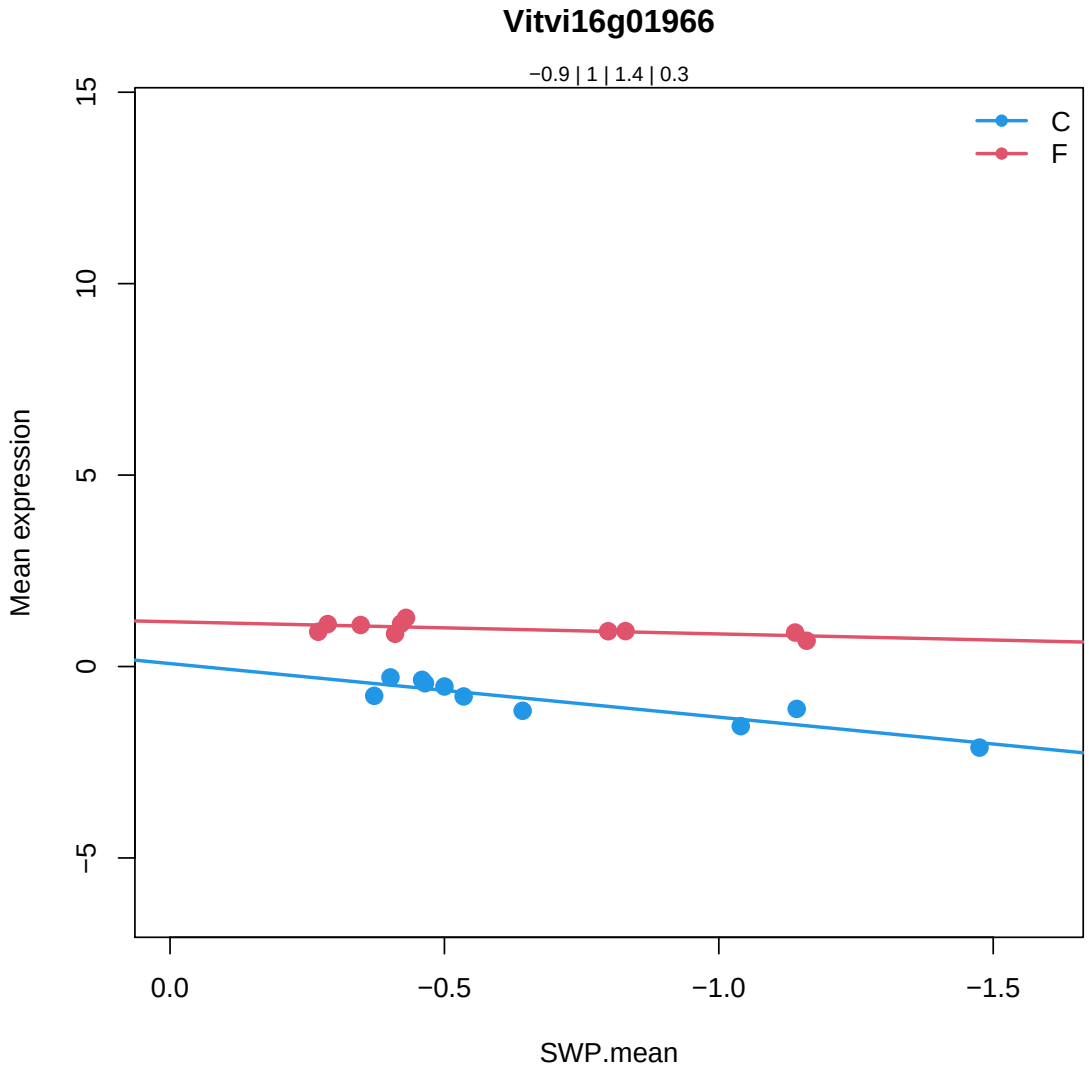
7.6.105 Vitvi16g01966: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01966
        30.2.24
        signalling.receptor kinases.S-locus glycoprotein like
        Protein kinase superfamily protein |
        Chr5:8139334-8141839 REVERSE LENGTH=745 |
        201606
```

Coefficients for Vitvi16g01966.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.9078716	5.194948e-09	***	6.396429e-09	***
SlopeC	1.399935	3.701481e-05	***	0.05641797	.
MeanF-MeanC	1.883144	4.428493e-12	***	3.708741e-10	***
SlopeF-SlopeC	-1.081662	0.01361739	*	0.9999488	



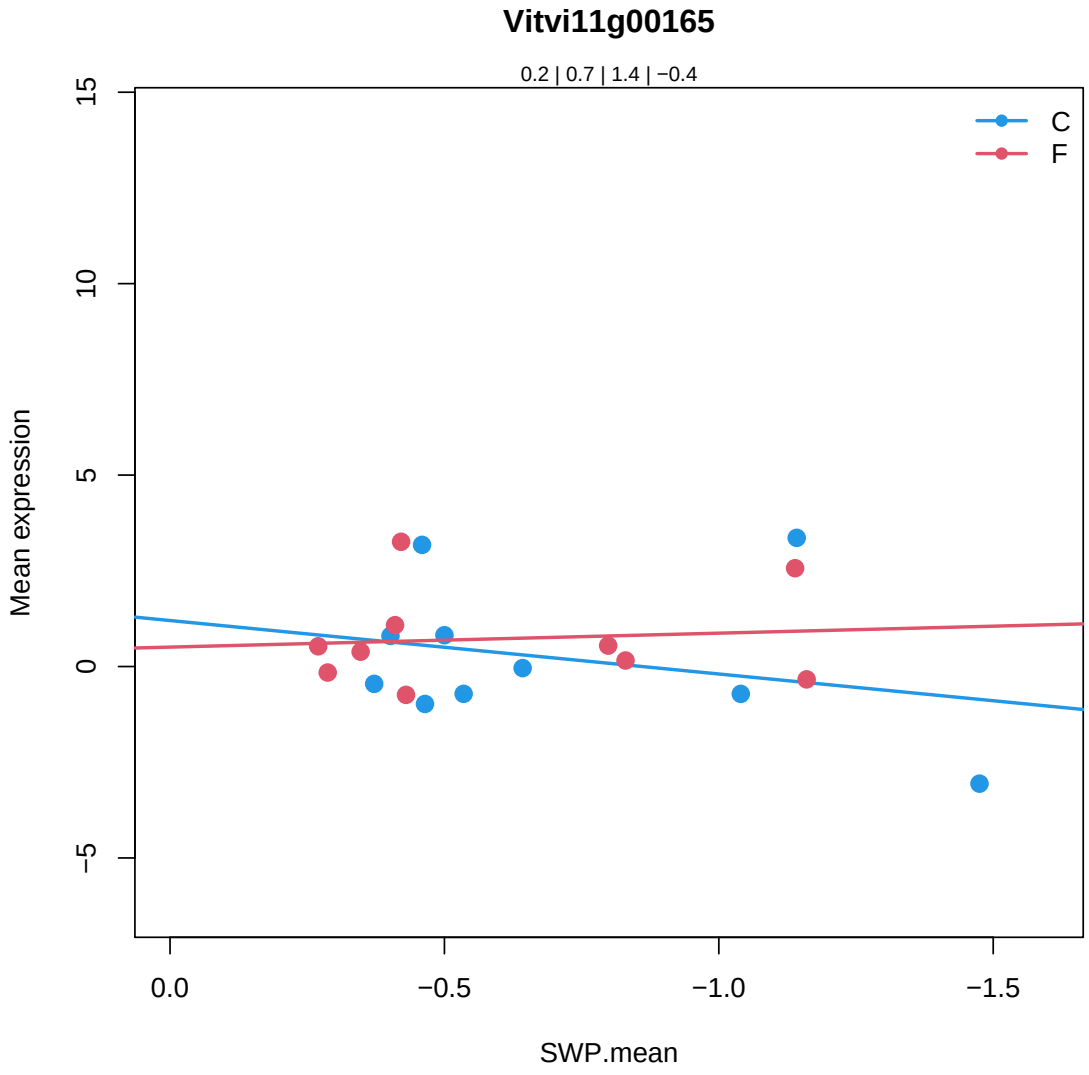
7.6.106 Vitvi11g00165: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00165
        27.3.6
        RNA.regulation of transcription.basic helix-loop-helix family (bHLH)
        basic helix-loop-helix (bHLH) DNA-binding family protein |
        Chr5:23038703-23041410 REVERSE LENGTH=525 |
        201606
```

Coefficients for Vitvi11g00165.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.2193624	0.6437599		0.6487826	
SlopeC	1.396301	0.295124		0.7828803	
MeanF-MeanC	0.5094593	0.4495239		0.7776356	
SlopeF-SlopeC	-1.760691	0.3733498		0.9999488	



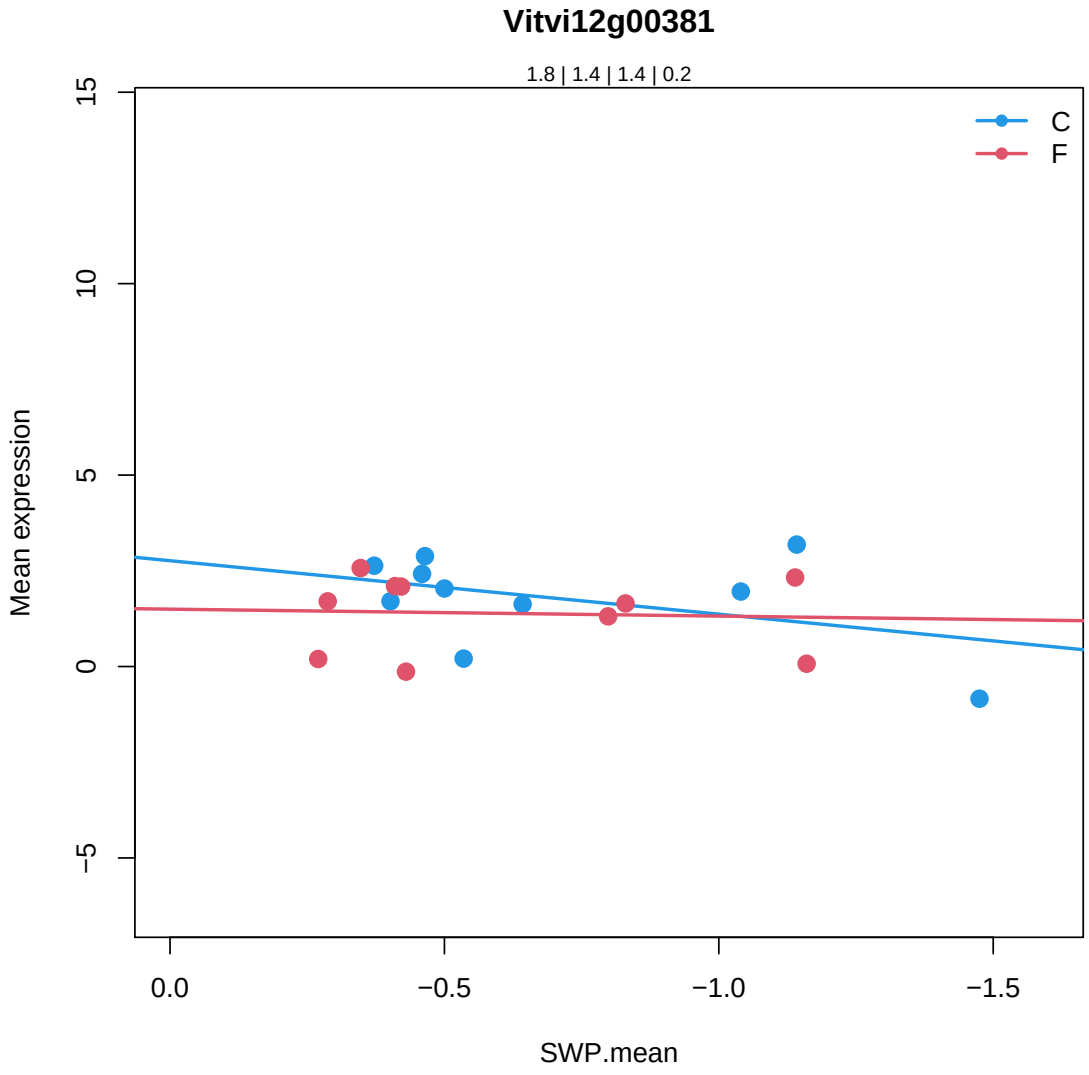
7.6.107 Vitvi12g00381: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00381
        14.2
        S-assimilation.APR
        APS reductase 3 |
        Chr4:11657284-11658973 REVERSE LENGTH=458 |
        201606
```

Coefficients for Vitvi12g00381.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.781504	1.273567e-05	***	1.434504e-05	***
SlopeC	1.396148	0.1273408		0.6480866	
MeanF-MeanC	-0.3937019	0.3886548		0.7373509	
SlopeF-SlopeC	-1.214828	0.3640933		0.9999488	



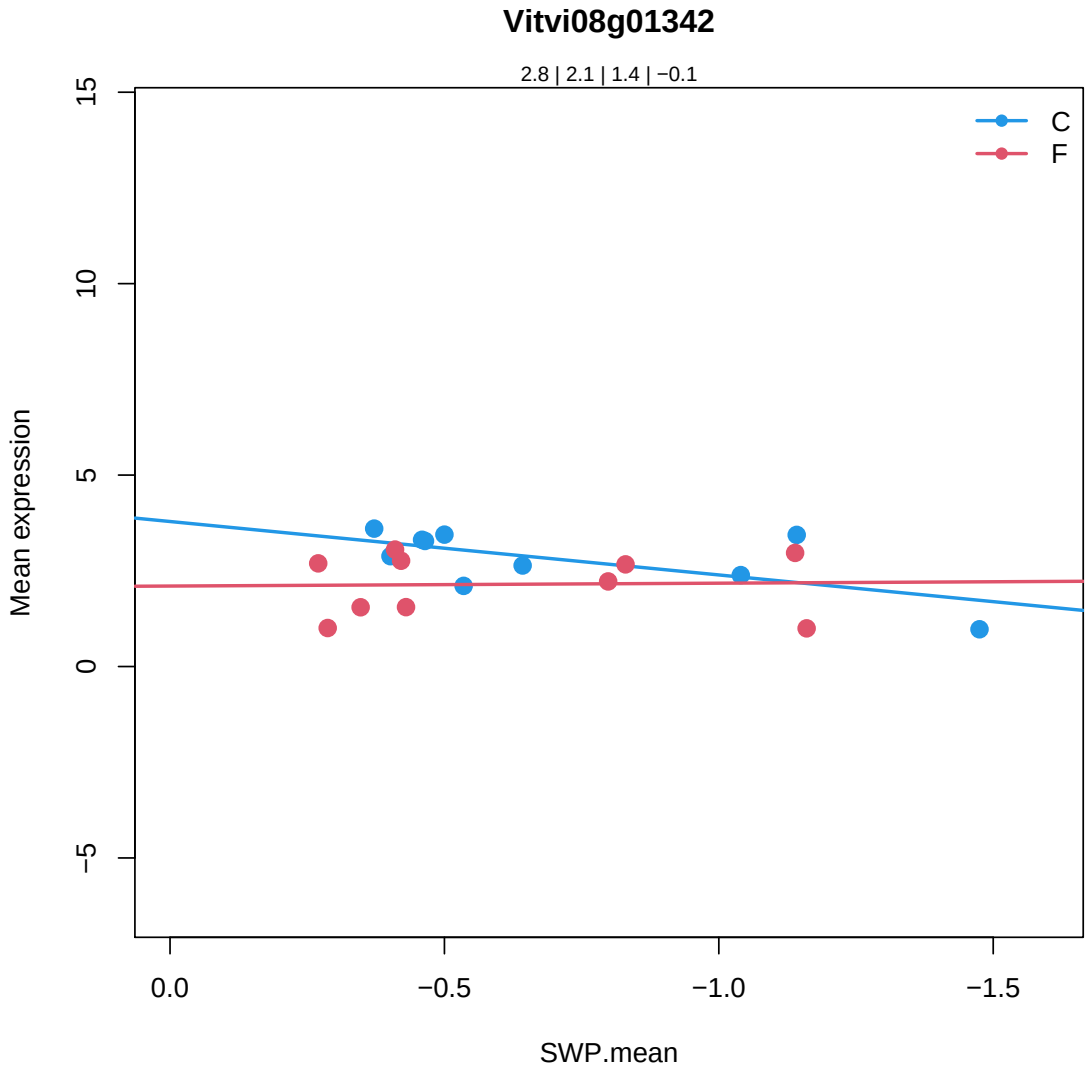
7.6.108 Vitvi08g01342: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01342
        35.2
        not assigned.unknown
        glycerol-3-phosphate acyltransferase 6 |
        Chr2:15952816-15955364 REVERSE LENGTH=501 |
        201606
```

Coefficients for Vitvi08g01342.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.805967	2.062439e-11	***	2.777496e-11	***
SlopeC	1.395468	0.0342961	*	0.4436999	
MeanF-MeanC	-0.6590582	0.04769539	*	0.2321115	
SlopeF-SlopeC	-1.470131	0.1242063		0.9999488	



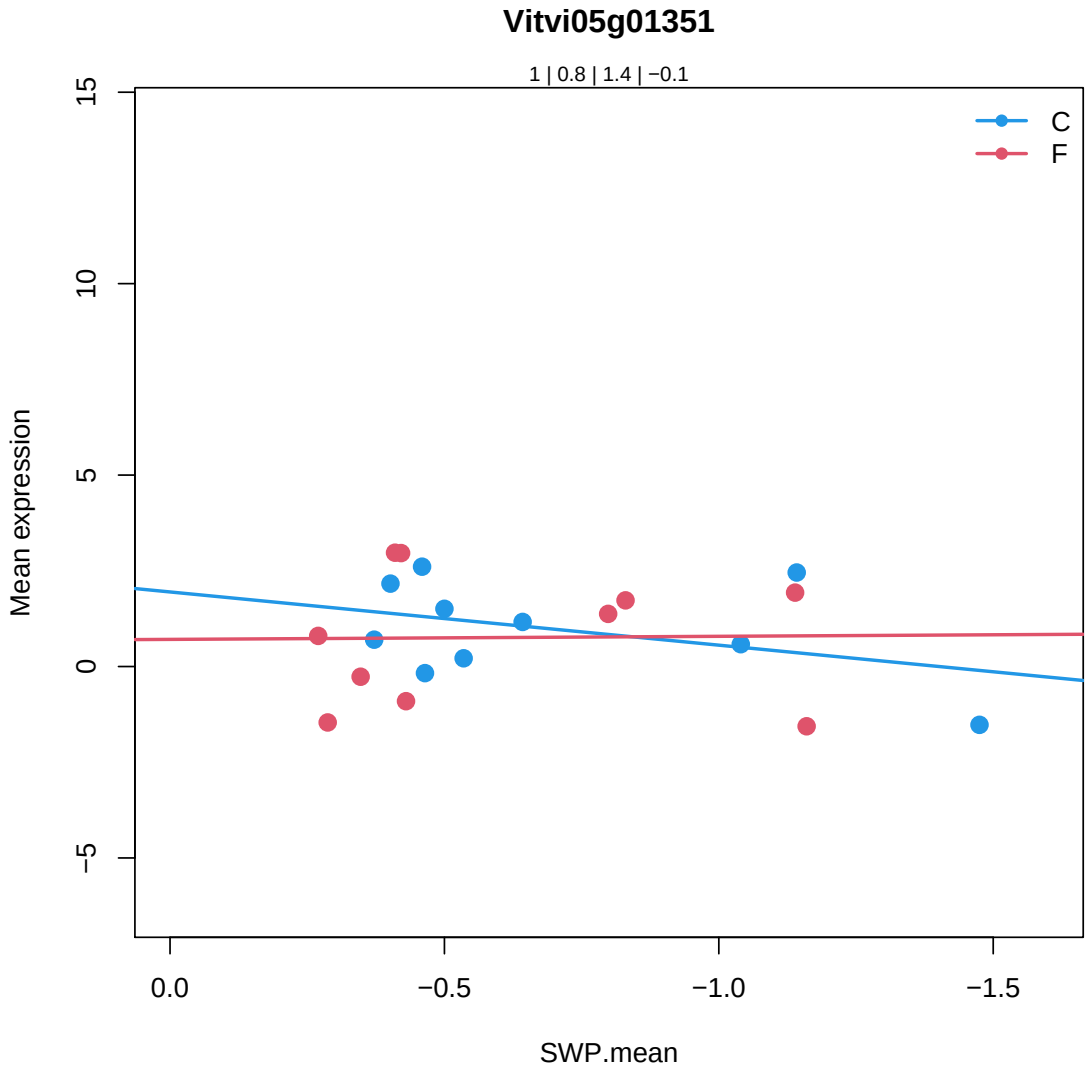
7.6.109 Vitvi05g01351: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01351
        34.3
        transport.amino acids
        Transmembrane amino acid transporter family protein |
        Chr5:5501044-5502856 REVERSE LENGTH=426 |
        201606
```

Coefficients for Vitvi05g01351.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.9700983	0.03606625	*	0.03768315	*
SlopeC	1.389607	0.262209		0.7700616	
MeanF-MeanC	-0.2128785	0.7319541		0.918522	
SlopeF-SlopeC	-1.469707	0.4222142		0.9999488	



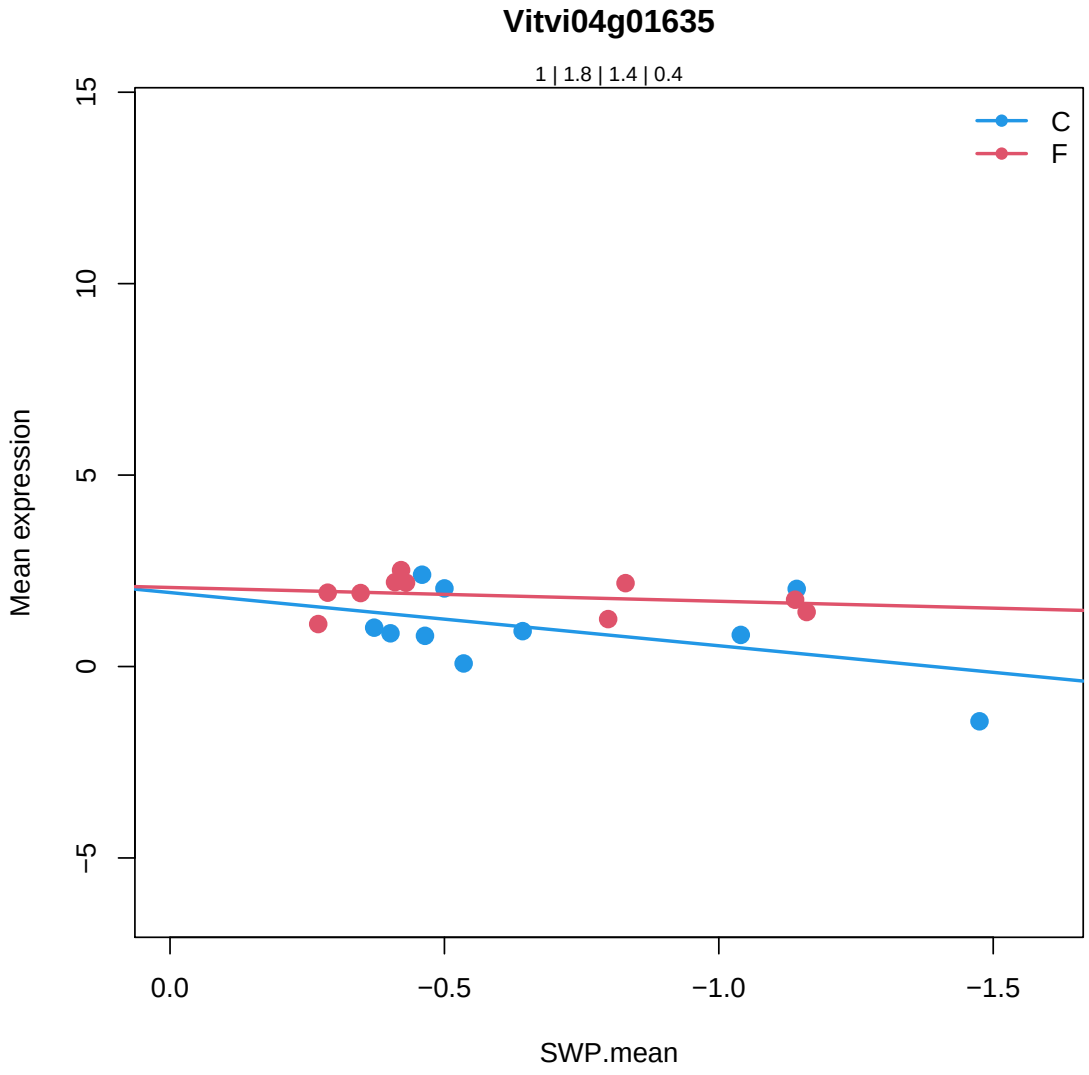
7.6.110 Vitvi04g01635: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01635
        35.2
        not assigned.unknown
        receptor-like protein kinase 1 |
        Chr5:24498467-24501494 REVERSE LENGTH=832 |
        201606
```

Coefficients for Vitvi04g01635.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.9545568	0.0004716728	***	0.0005139207	***
SlopeC	1.389382	0.04268247	*	0.48214	
MeanF-MeanC	0.8903566	0.01277721	*	0.09121794	.
SlopeF-SlopeC	-1.029594	0.2952514		0.9999488	



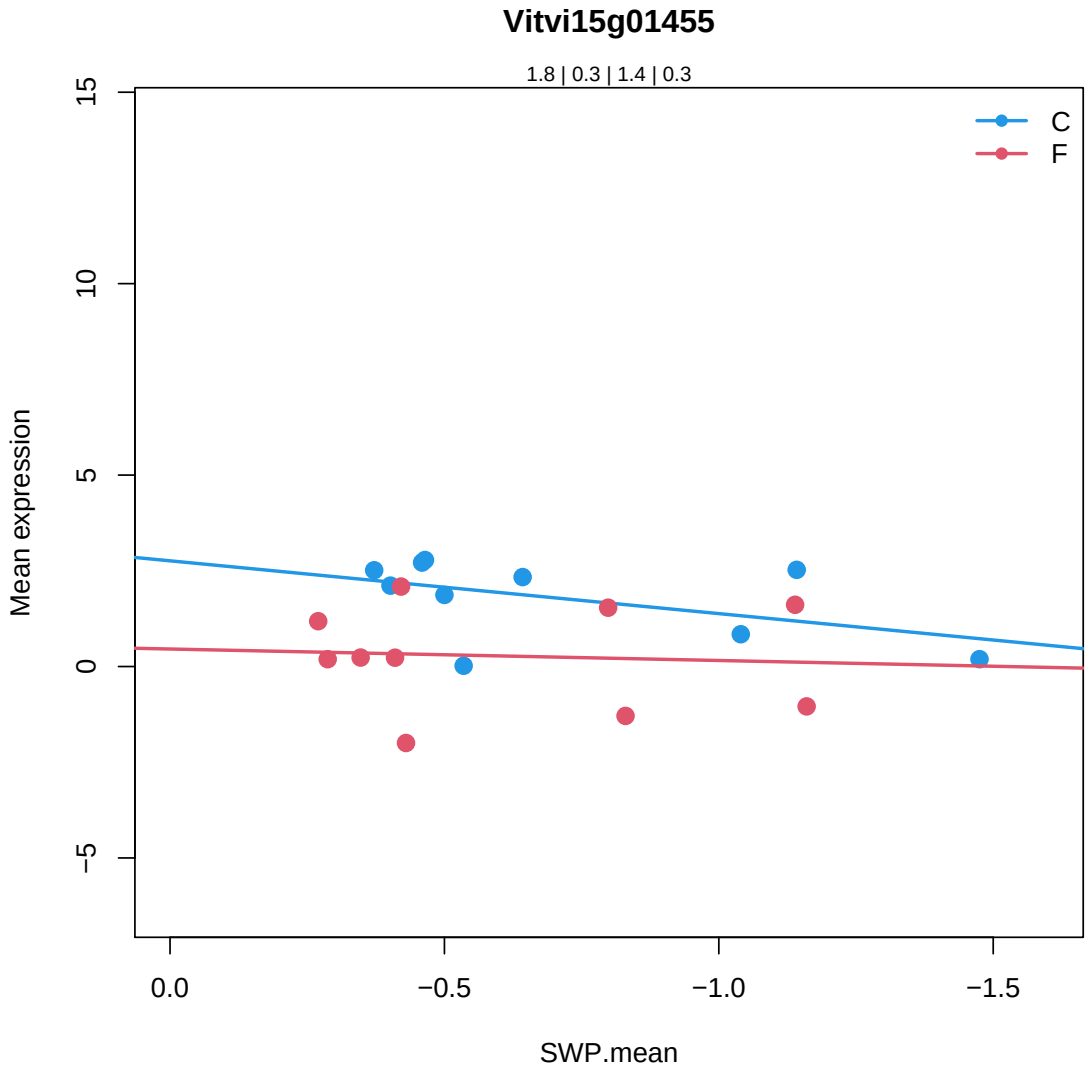
7.6.111 Vitvi15g01455: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g01455
        35.2
        not assigned.unknown
        hypothetical protein |
        Chr3:19546446-19546868 REVERSE LENGTH=140 |
        201606
```

Coefficients for Vitvi15g01455.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.790851	3.572198e-05	***	3.982113e-05	***
SlopeC	1.378529	0.1652076		0.6962465	
MeanF-MeanC	-1.516298	0.005222029	**	0.04726494	*
SlopeF-SlopeC	-1.078362	0.4583753		0.9999488	



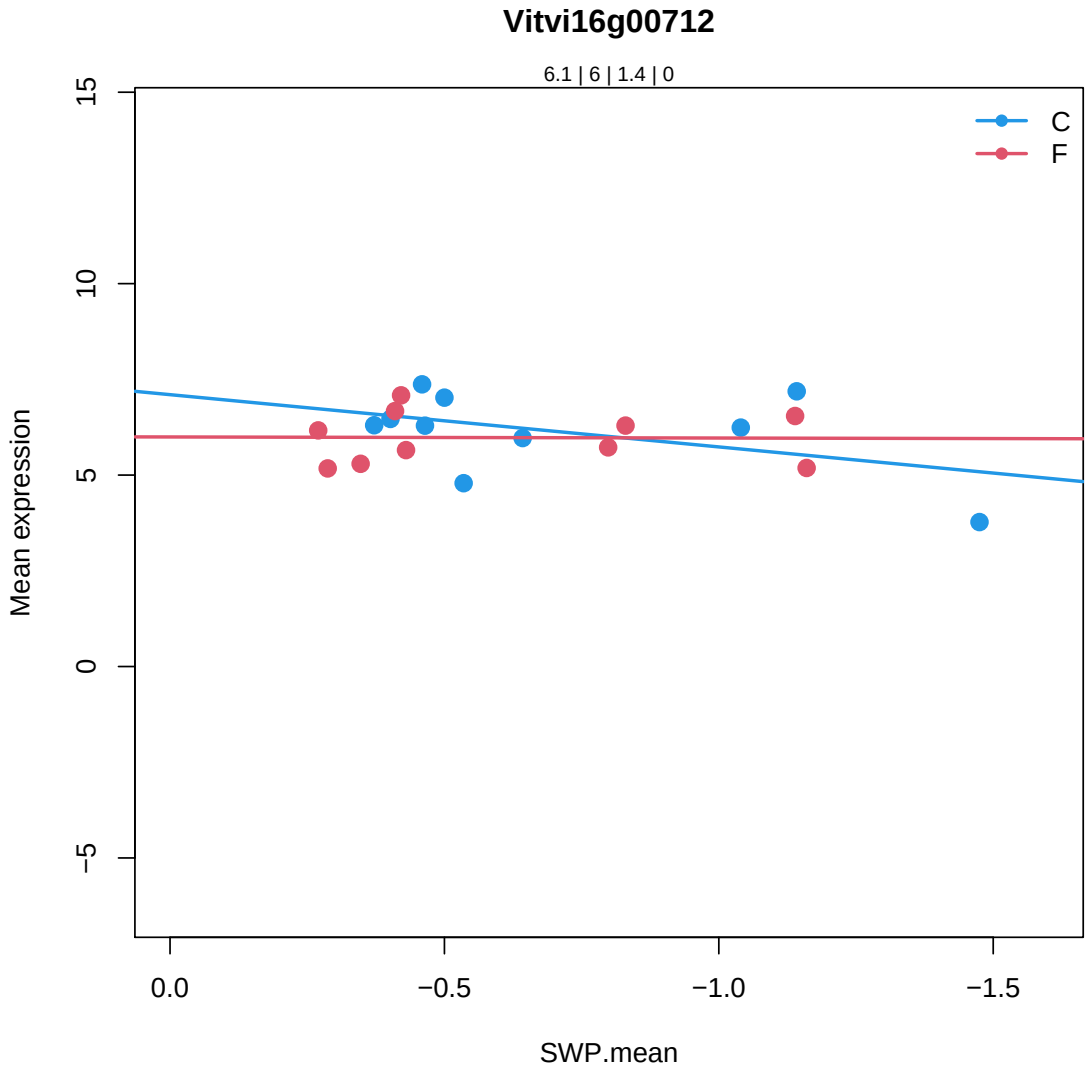
7.6.112 Vitvi16g00712: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g00712
        3.2.2
        minor CHO metabolism.trehalose.TPP
        Haloacid dehalogenase-like hydrolase (HAD) superfamily protein |
        Chr5:20902266-20904292 FORWARD LENGTH=385 |
        201606
```

Coefficients for Vitvi16g00712.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.140583	5.362024e-17	***	1.22329e-16	***
SlopeC	1.364708	0.0681563	.	0.5569429	
MeanF-MeanC	-0.1618507	0.6585469		0.8862262	
SlopeF-SlopeC	-1.336617	0.2198141		0.9999488	



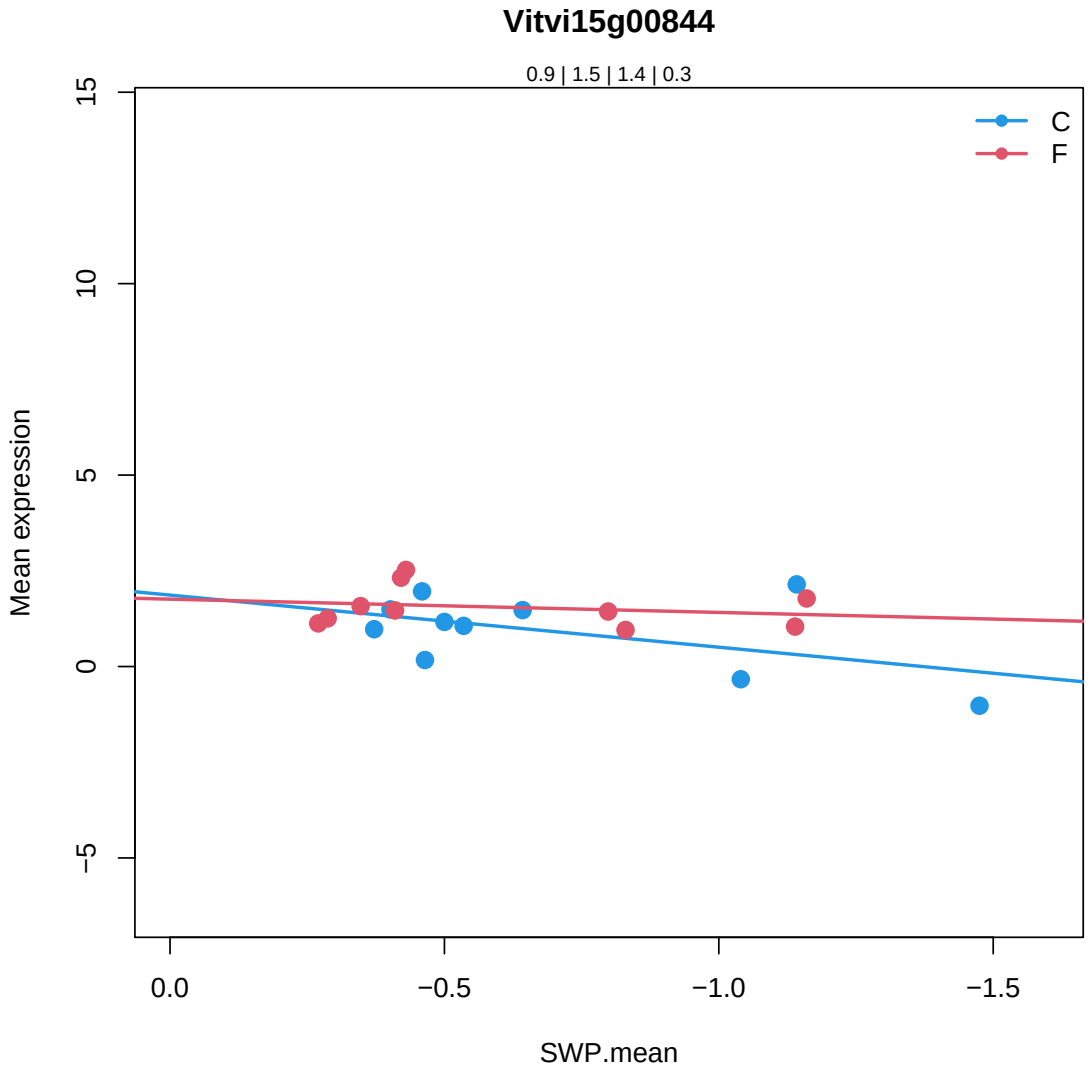
7.6.113 Vitvi15g00844: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g00844
        35.2
        not assigned.unknown
        BON association protein 2 |
        Chr2:18847125-18847748 REVERSE LENGTH=207 |
        201606
```

Coefficients for Vitvi15g00844.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.9085873	0.0004840805	***	0.0005272513	***
SlopeC	1.360291	0.038047	*	0.465793	
MeanF-MeanC	0.6393328	0.05342568	.	0.2495606	
SlopeF-SlopeC	-1.013662	0.280634		0.9999488	



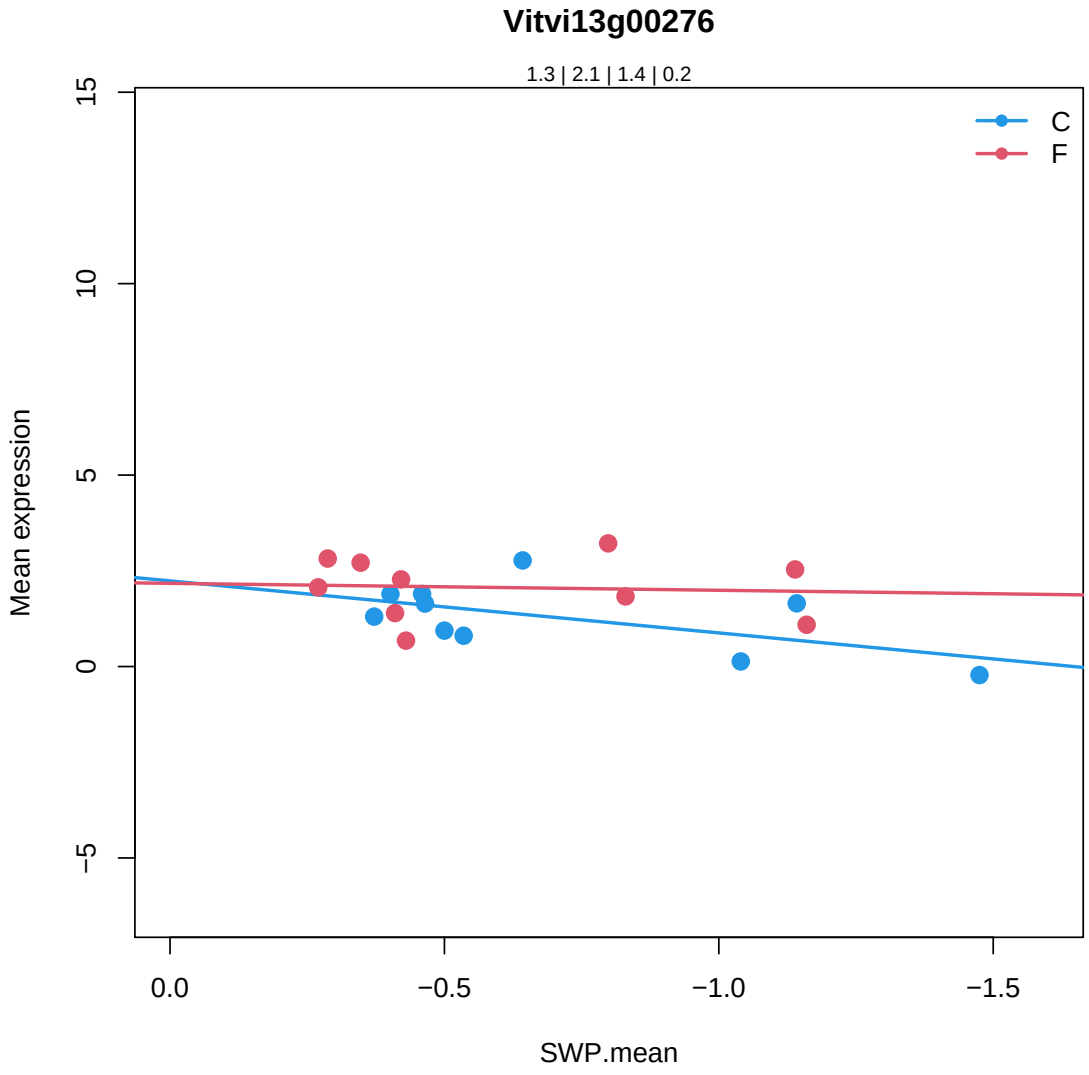
7.6.114 Vitvi13g00276: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00276
        28.1.3.2.4
        DNA.synthesis/chromatin structure.histone.core.H4
        Histone superfamily protein |
        Chr5:24146352-24146663 REVERSE LENGTH=103 |
        201606
```

Coefficients for Vitvi13g00276.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.280912	2.134314e-05	***	2.391473e-05	***
SlopeC	1.358059	0.05153793	.	0.513159	
MeanF-MeanC	0.7809075	0.0294854	*	0.1670693	
SlopeF-SlopeC	-1.176933	0.2430001		0.9999488	



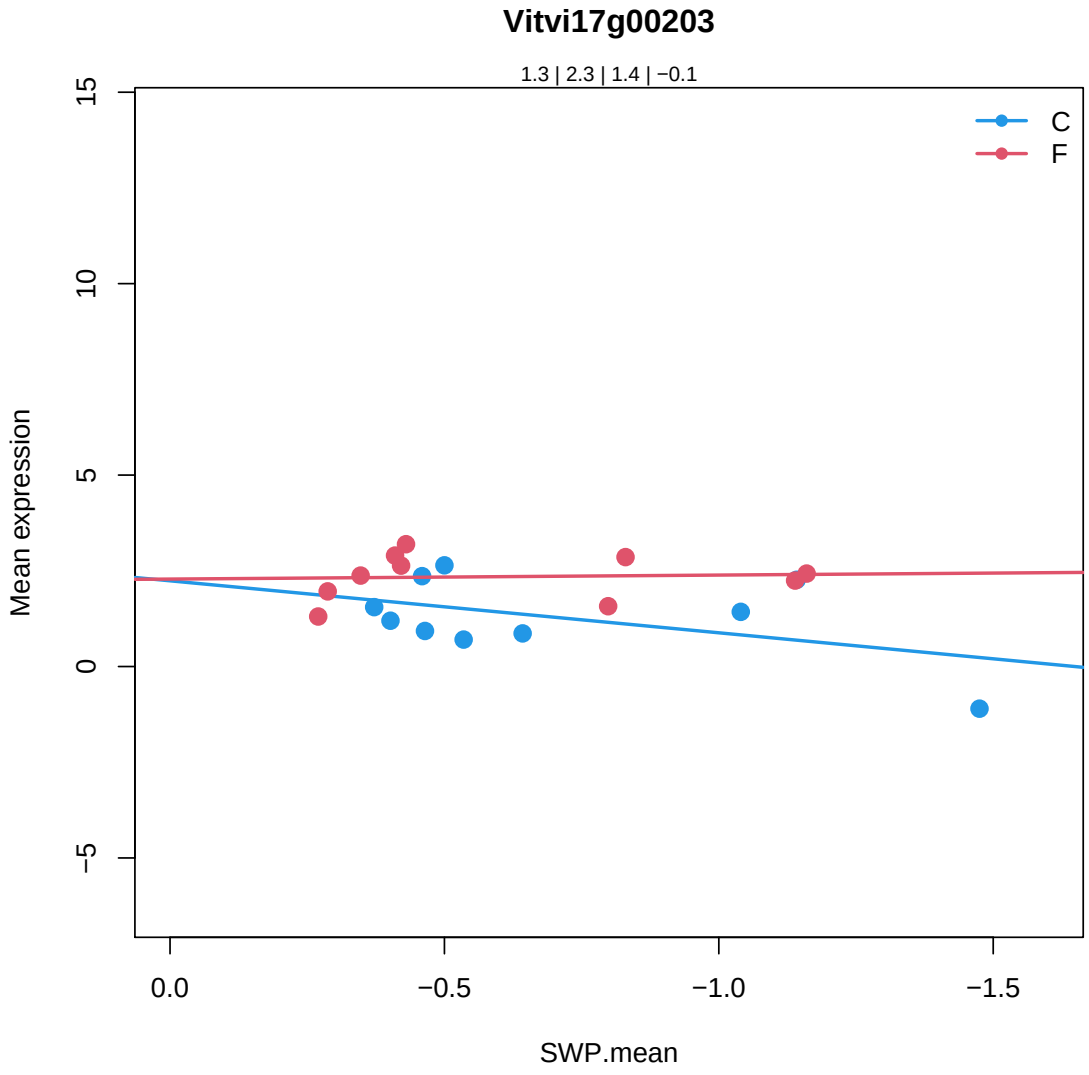
7.6.115 Vitvi17g00203: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00203
        35.2
        not assigned.unknown
        Leucine-rich repeat receptor-like protein kinase family protein |
        Chr4:5637467-5640496 REVERSE LENGTH=1009 |
        201606
```

Coefficients for Vitvi17g00203.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.283781	2.684796e-05	***	3.000562e-05	***
SlopeC	1.35785	0.05604484	.	0.5289384	
MeanF-MeanC	1.063653	0.005174533	**	0.04691864	*
SlopeF-SlopeC	-1.462133	0.1583888		0.9999488	



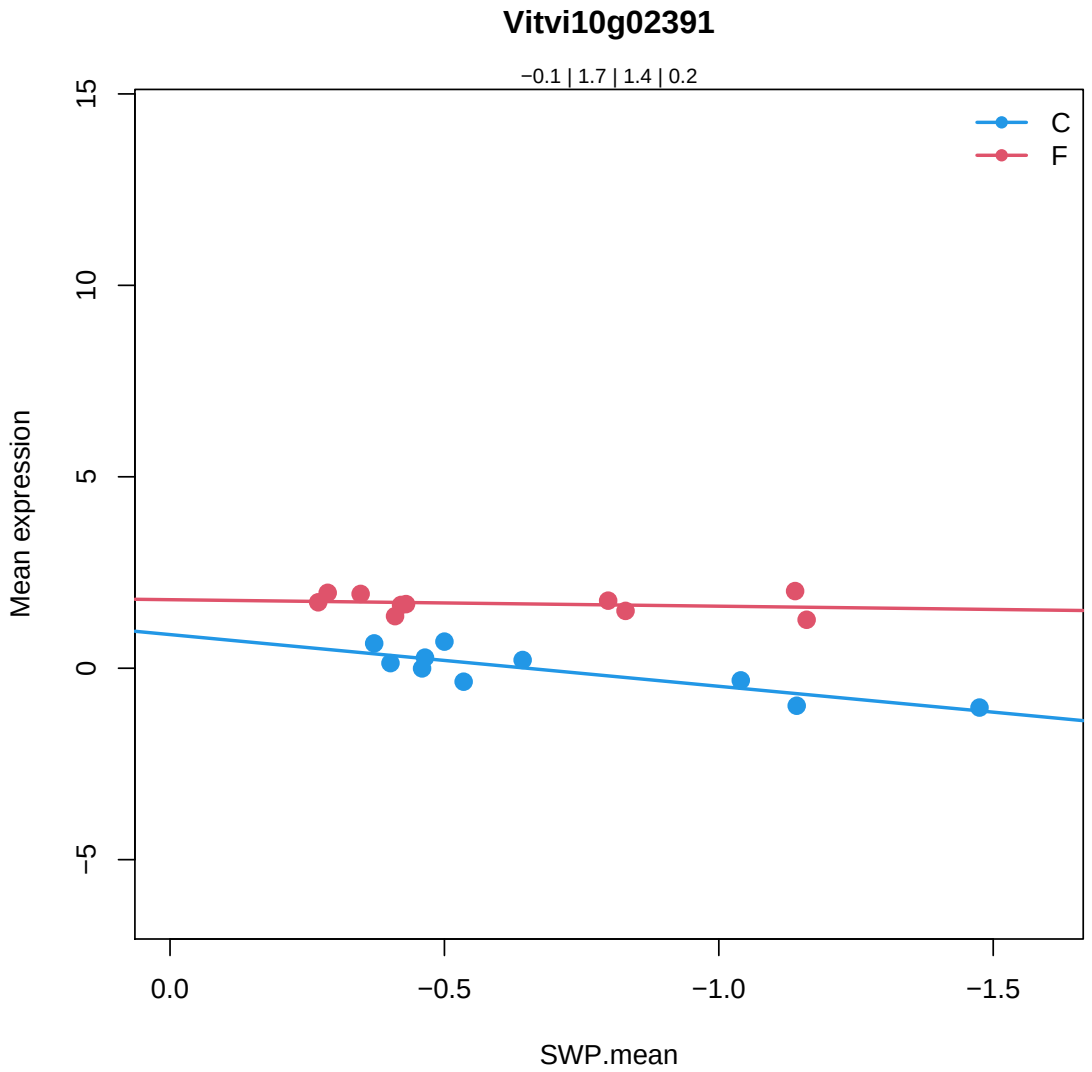
7.6.116 Vitvi10g02391: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g02391
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi10g02391.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.07135229	0.5341921		0.5401457	
SlopeC	1.35047	0.0003059234	***	0.08967085	.
MeanF-MeanC	1.757536	2.77682e-10	***	1.793402e-08	***
SlopeF-SlopeC	-1.180772	0.0195039	*	0.9999488	



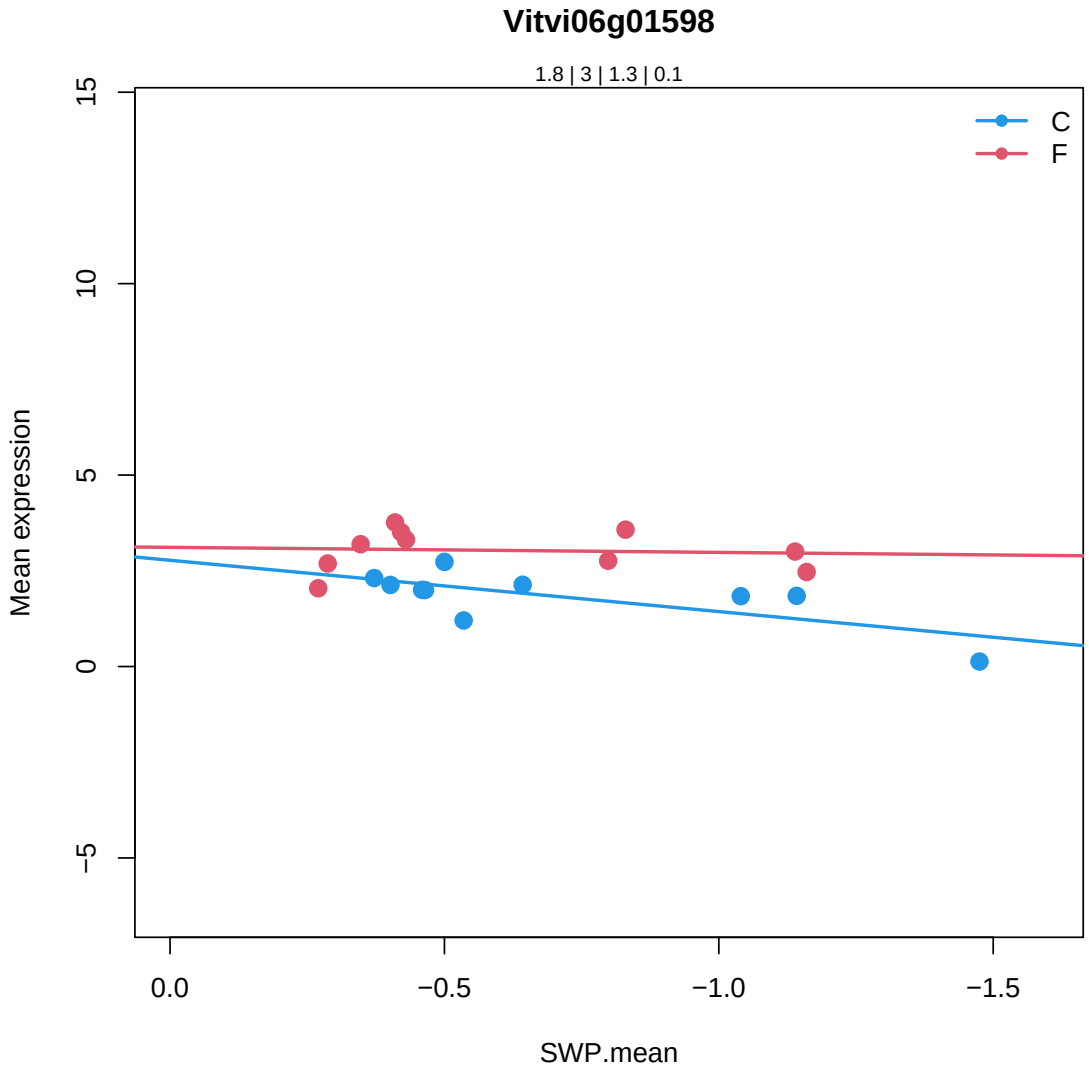
7.6.117 Vitvi06g01598: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01598
        35.2
        not assigned.unknown
        Disease resistance-responsive (dirigent-like protein) family protein |
        Chr1:21536188-21536745 FORWARD LENGTH=185 |
        201606
```

Coefficients for Vitvi06g01598.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.832576	3.980857e-10	***	5.092423e-10	***
SlopeC	1.339956	0.009773555	**	0.3009465	
MeanF-MeanC	1.199604	5.733041e-05	***	0.00111033	**
SlopeF-SlopeC	-1.207872	0.1003057		0.9999488	



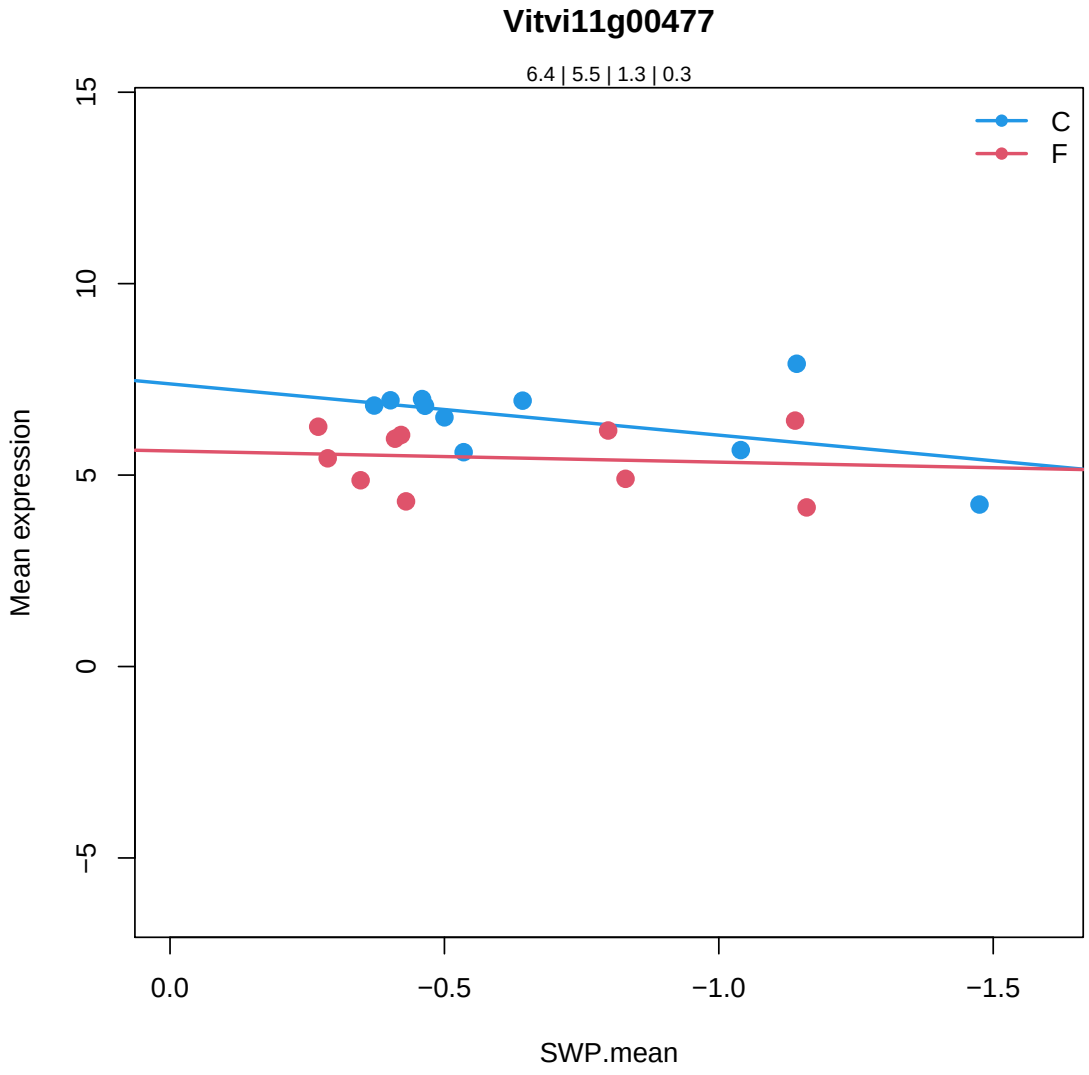
7.6.118 Vitvi11g00477: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00477
        35.1.27
        not assigned.no ontology.tetratricopeptide repeat (TPR)
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr5:6814093-6815171 FORWARD LENGTH=290 |
        201606
```

Coefficients for Vitvi11g00477.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.440243	3.342485e-17	***	7.926895e-17	***
SlopeC	1.338776	0.07995106	.	0.5748584	
MeanF-MeanC	-0.9882613	0.01419923	*	0.09806283	.
SlopeF-SlopeC	-1.046803	0.3450045		0.9999488	



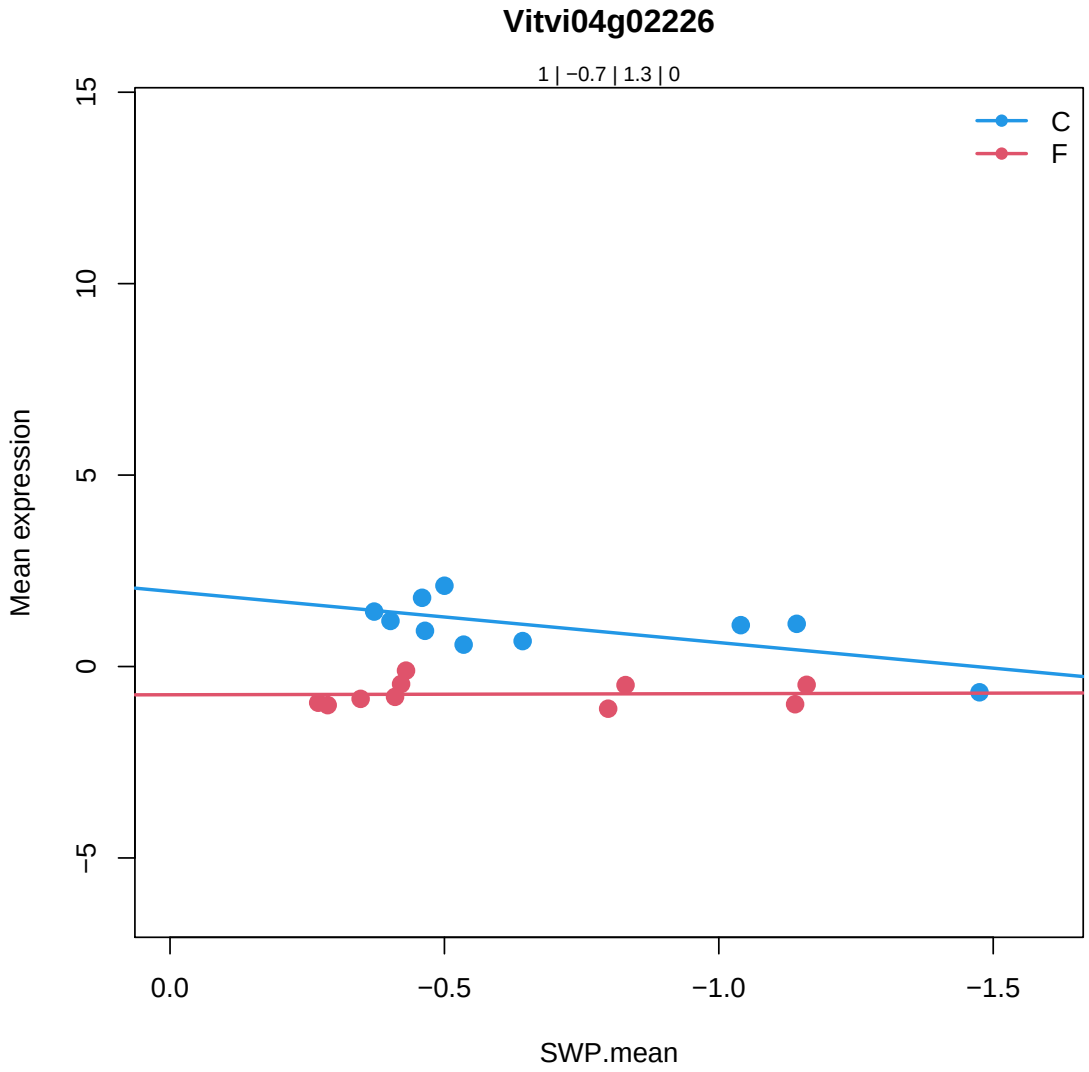
7.6.119 Vitvi04g02226: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g02226
        35.2
        not assigned.unknown
        receptor-like protein kinase 1 |
        Chr5:24498467-24501494 REVERSE LENGTH=832 |
        201606
```

Coefficients for Vitvi04g02226.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.021976	1.38508e-06	***	1.593794e-06	***
SlopeC	1.336214	0.0052874	**	0.2574116	
MeanF-MeanC	-1.742557	7.658478e-08	***	3.233532e-06	***
SlopeF-SlopeC	-1.364572	0.04494877	*	0.9999488	



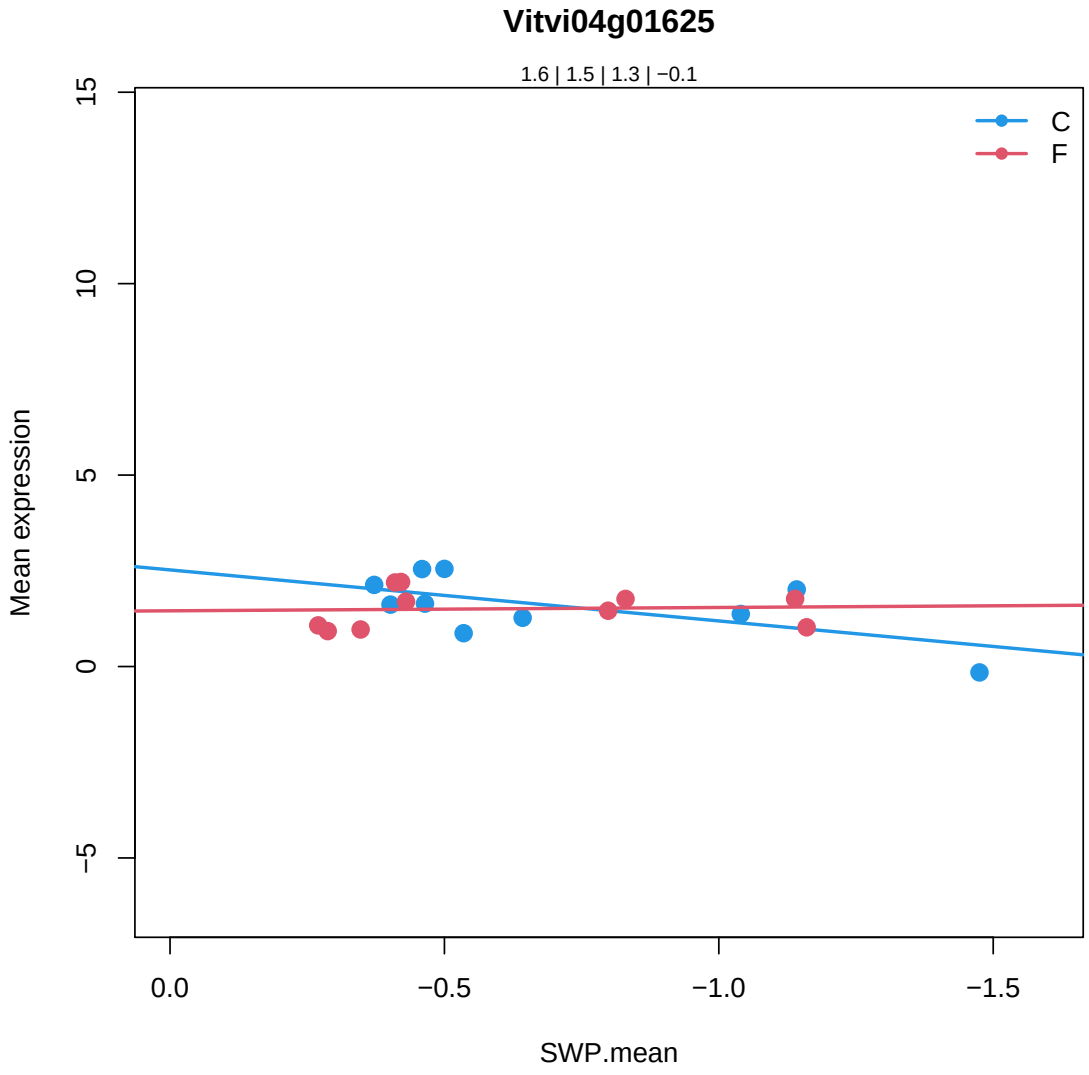
7.6.120 Vitvi04g01625: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01625
        29.4
        protein.postranslational modification
        receptor-like protein kinase 1 |
        Chr5:24498467-24501494 REVERSE LENGTH=832 |
        201606
```

Coefficients for Vitvi04g01625.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.585884	1.947957e-08	***	2.356783e-08	***
SlopeC	1.332748	0.01609918	*	0.3486596	
MeanF-MeanC	-0.07804405	0.7663457		0.9321541	
SlopeF-SlopeC	-1.41966	0.07524103	.	0.9999488	



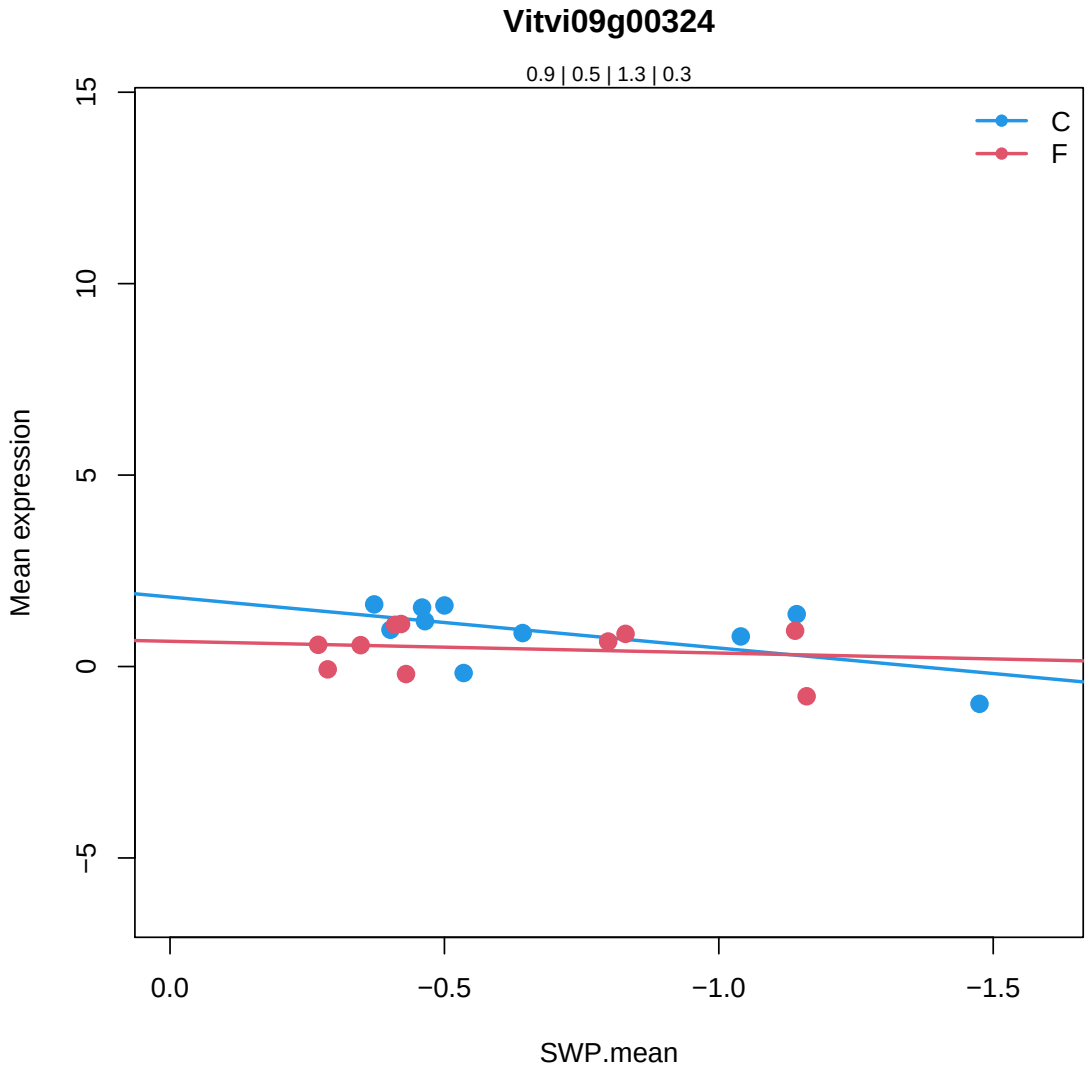
7.6.121 Vitvi09g00324: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00324
        35.2
        not assigned.unknown
        transmembrane protein |
        Chr1:19417666-19419591 FORWARD LENGTH=319 |
        201606
```

Coefficients for Vitvi09g00324.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8783748	0.0002795186	***	0.000305955	***
SlopeC	1.332098	0.02762061	*	0.4233169	
MeanF-MeanC	-0.4068222	0.1700171		0.4994027	
SlopeF-SlopeC	-1.02503	0.2350349		0.9999488	



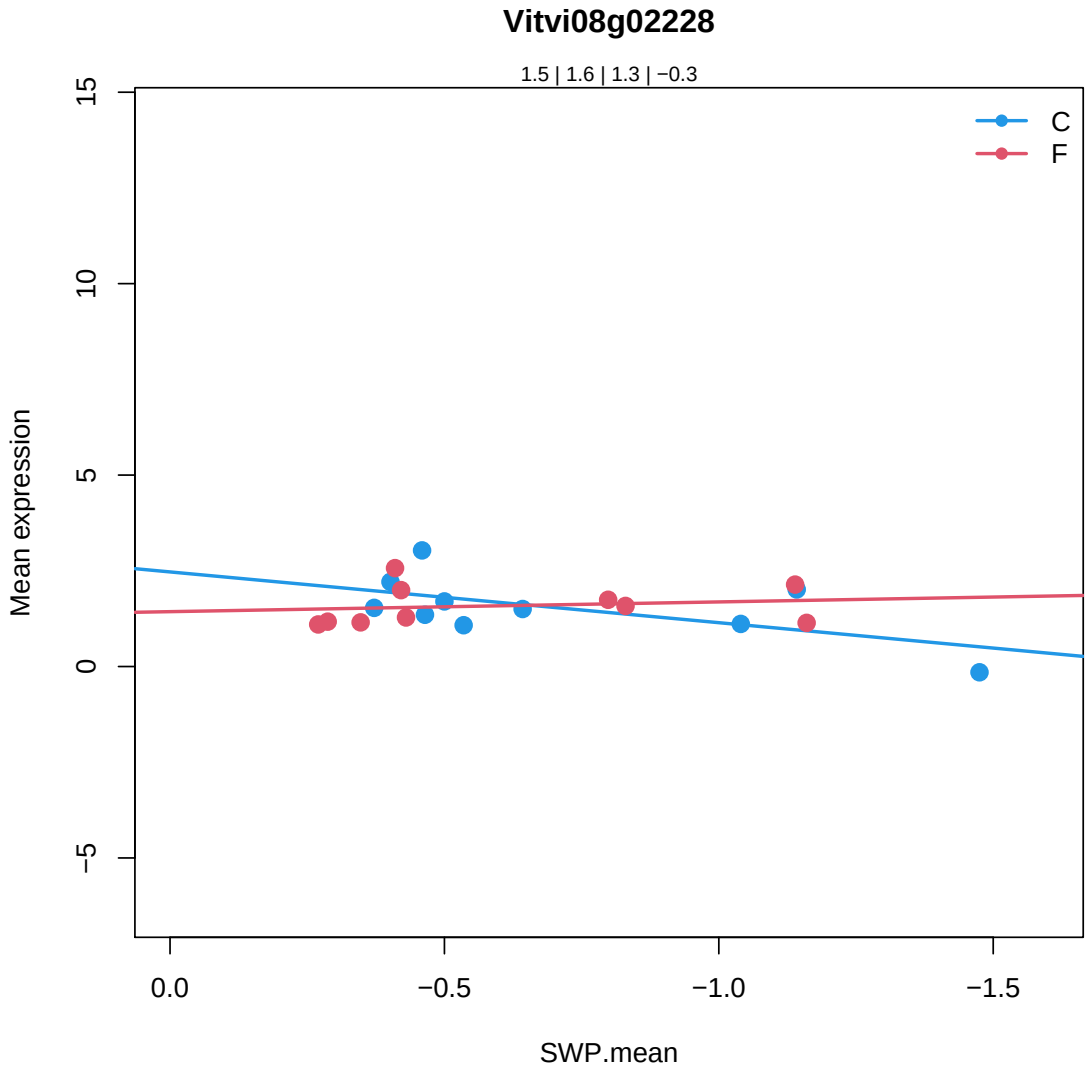
7.6.122 Vitvi08g02228: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g02228
        26.9
        misc.glutathione S transferases
        glutathione S-transferase tau 7 |
        Chr2:12618111-12618871 REVERSE LENGTH=227 |
        201606
```

Coefficients for Vitvi08g02228.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.538064	4.729542e-08	***	5.659262e-08	***
SlopeC	1.325955	0.01882887	*	0.3679354	
MeanF-MeanC	0.04943836	0.8538923		0.9609451	
SlopeF-SlopeC	-1.580456	0.05440027	.	0.9999488	



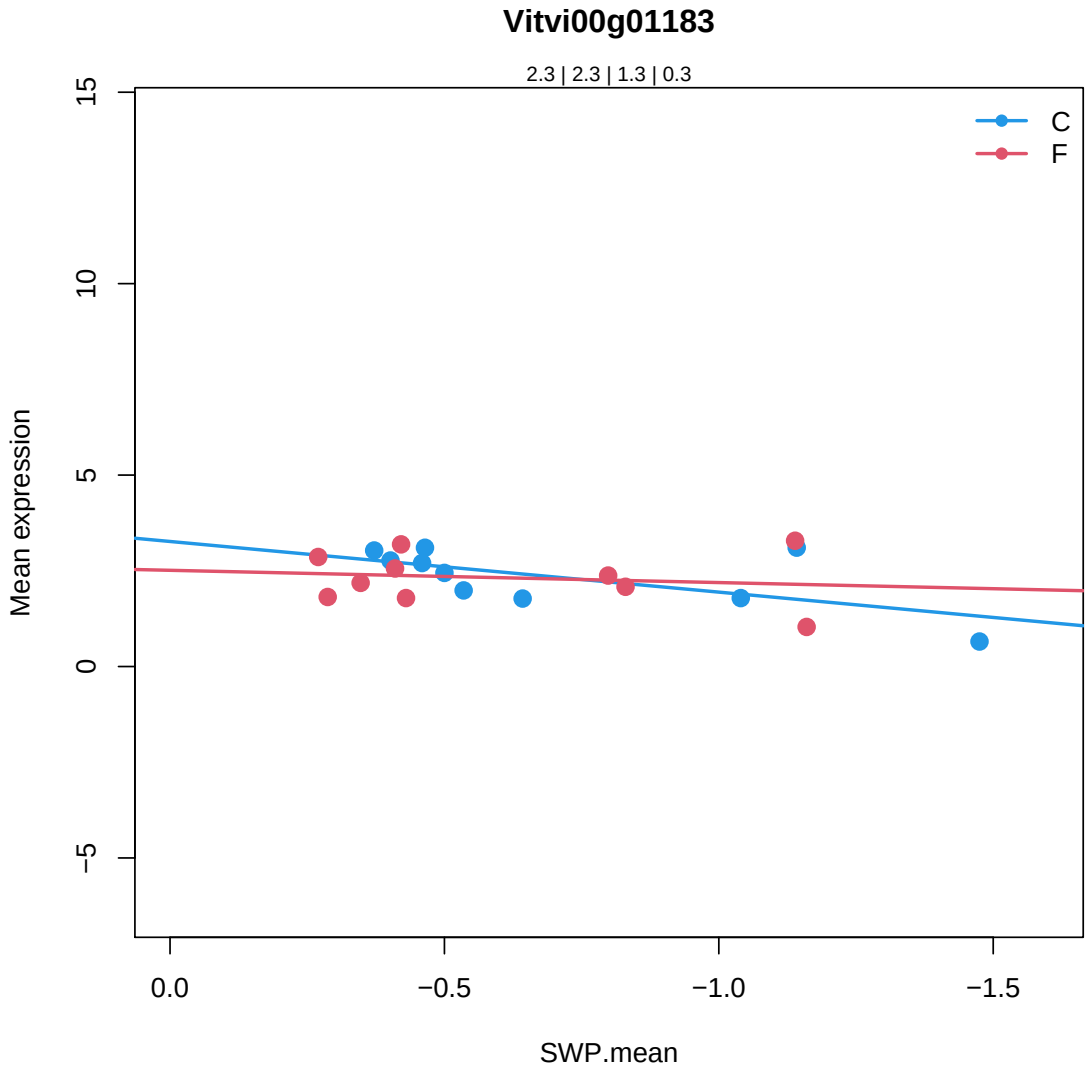
7.6.123 Vitvi00g01183: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi00g01183
        35.2
        not assigned.unknown
        Copper amine oxidase family protein |
        Chr1:23258253-23261772 REVERSE LENGTH=712 |
        201606
```

Coefficients for Vitvi00g01183.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.335456	1.18865e-10	***	1.550749e-10	***
SlopeC	1.322569	0.02870224	*	0.4275443	
MeanF-MeanC	-0.01788023	0.950843		0.987972	
SlopeF-SlopeC	-1.002067	0.2455767		0.9999488	



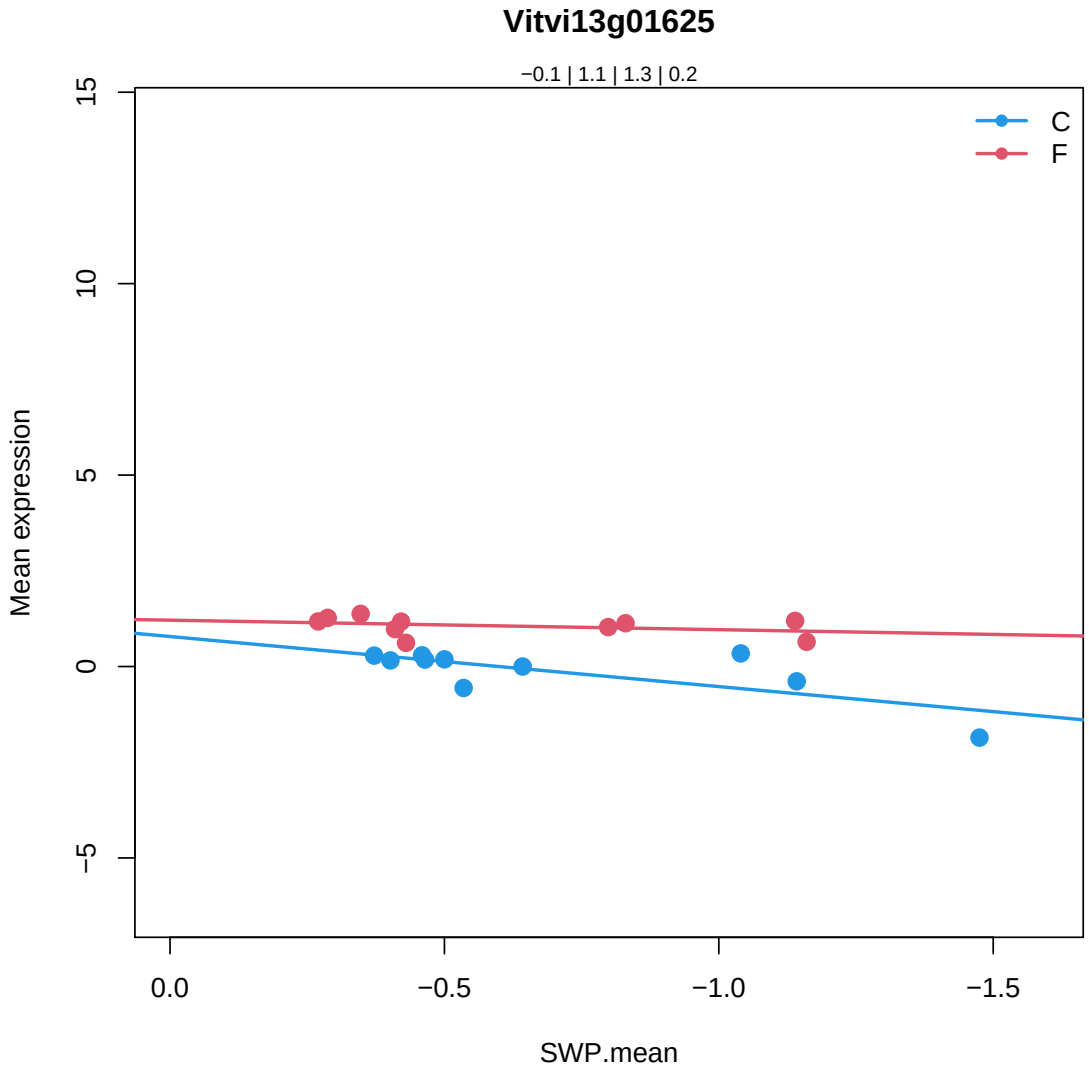
7.6.124 Vitvi13g01625: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g01625
        35.2
        not assigned.unknown
        Excinuclease ABC%2C C subunit%2C N-terminal |
        Chr5:17347567-17348379 FORWARD LENGTH=170 |
        201606
```

Coefficients for Vitvi13g01625.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.1357281	0.3133878		0.3191459	
SlopeC	1.307058	0.001748404	**	0.158626	
MeanF-MeanC	1.194811	2.060054e-06	***	6.132684e-05	***
SlopeF-SlopeC	-1.058976	0.06497371	.	0.9999488	



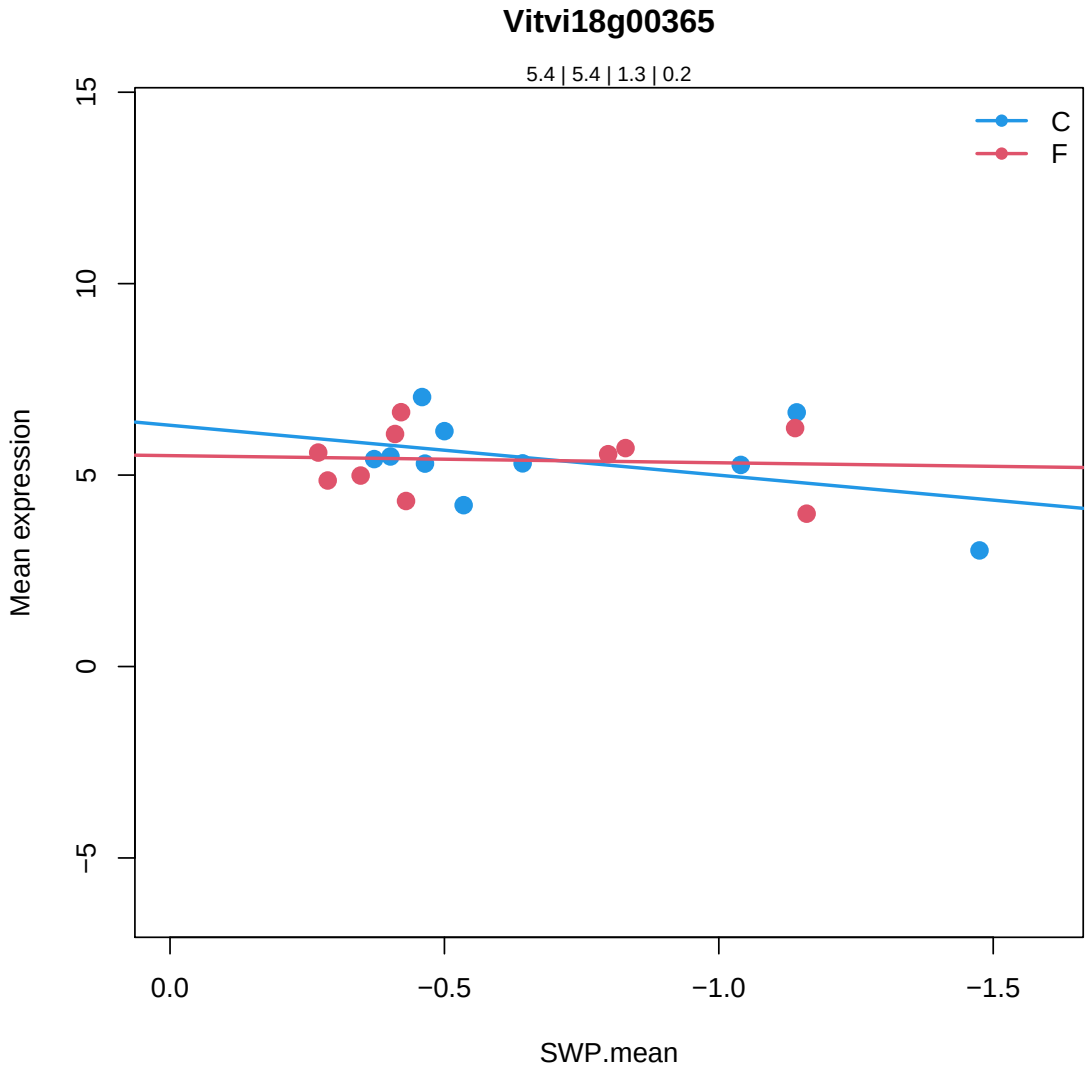
7.6.125 Vitvi18g00365: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00365
        34.6
        transport.sulphate
        sulfate transporter 1%3B1 |
        Chr4:5500480-5505982 FORWARD LENGTH=649 |
        201606
```

Coefficients for Vitvi18g00365.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.384121	7.221721e-15	***	1.224671e-14	***
SlopeC	1.303545	0.1140173		0.6311525	
MeanF-MeanC	0.01007881	0.9802384		0.9949434	
SlopeF-SlopeC	-1.116927	0.3534494		0.9999488	



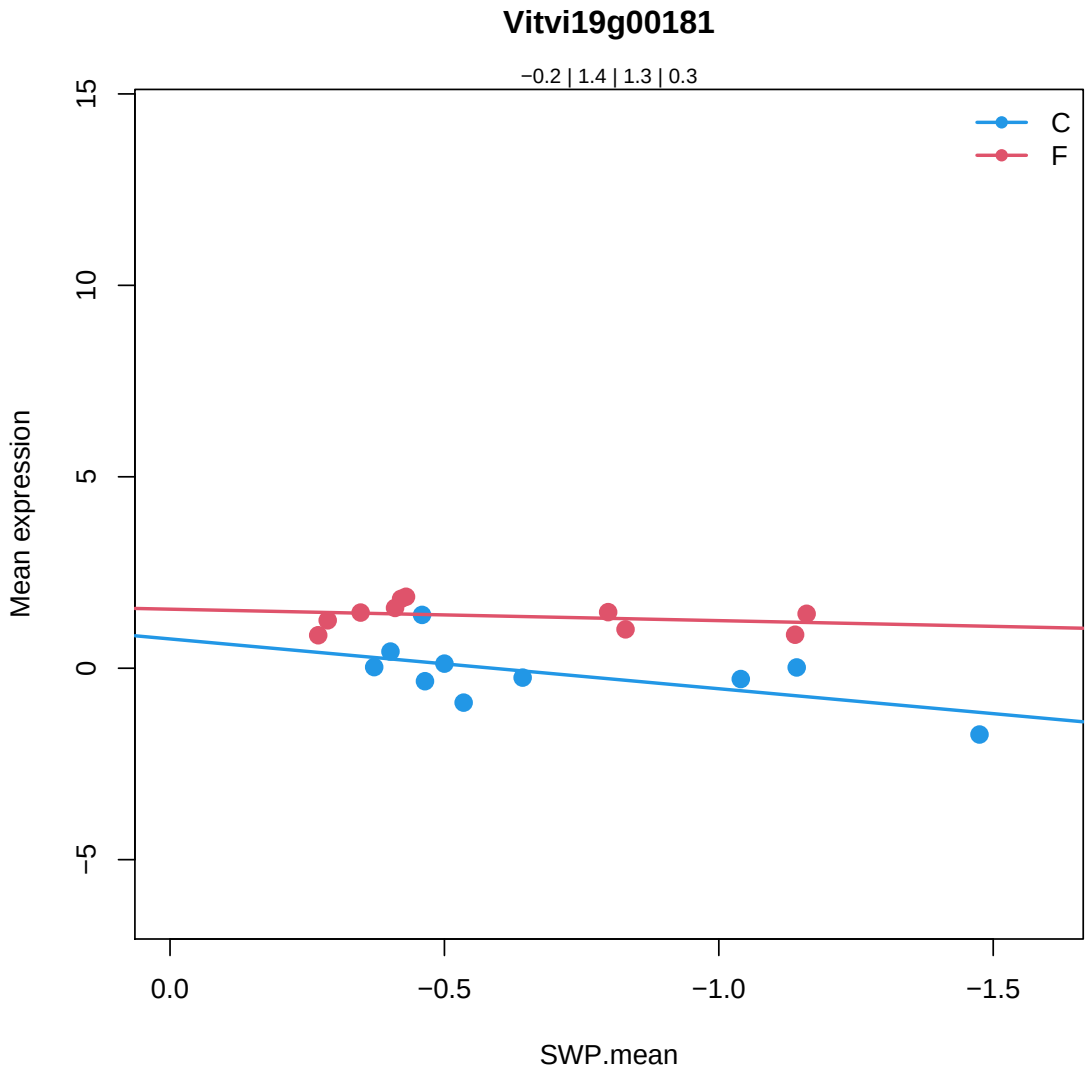
7.6.126 Vitvi19g00181: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g00181
        35.1
        not assigned.no ontology
        NA
```

Coefficients for Vitvi19g00181.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	−0.1500634	0.3854678		0.3916084	
SlopeC	1.300793	0.01158366	*	0.318473	
MeanF−MeanC	1.509599	2.724759e−06	***	7.910623e−05	***
SlopeF−SlopeC	−1.001836	0.167586		0.9999488	



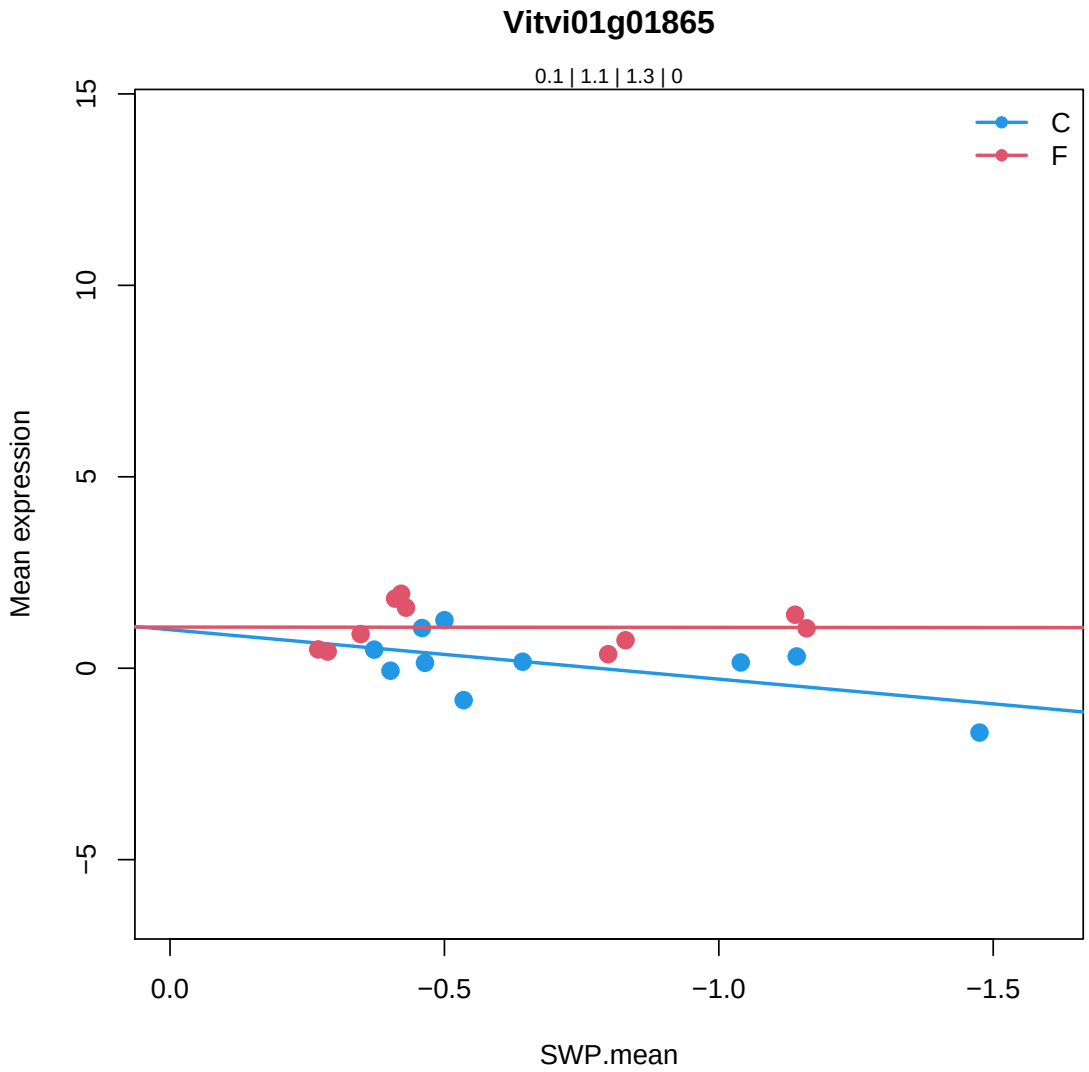
7.6.127 Vitvi01g01865: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01865
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi01g01865.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.098011	0.6321544		0.6372551	
SlopeC	1.290993	0.03163096	*	0.4333479	
MeanF-MeanC	0.971925	0.002607541	**	0.02733435	*
SlopeF-SlopeC	-1.283344	0.1392562		0.9999488	



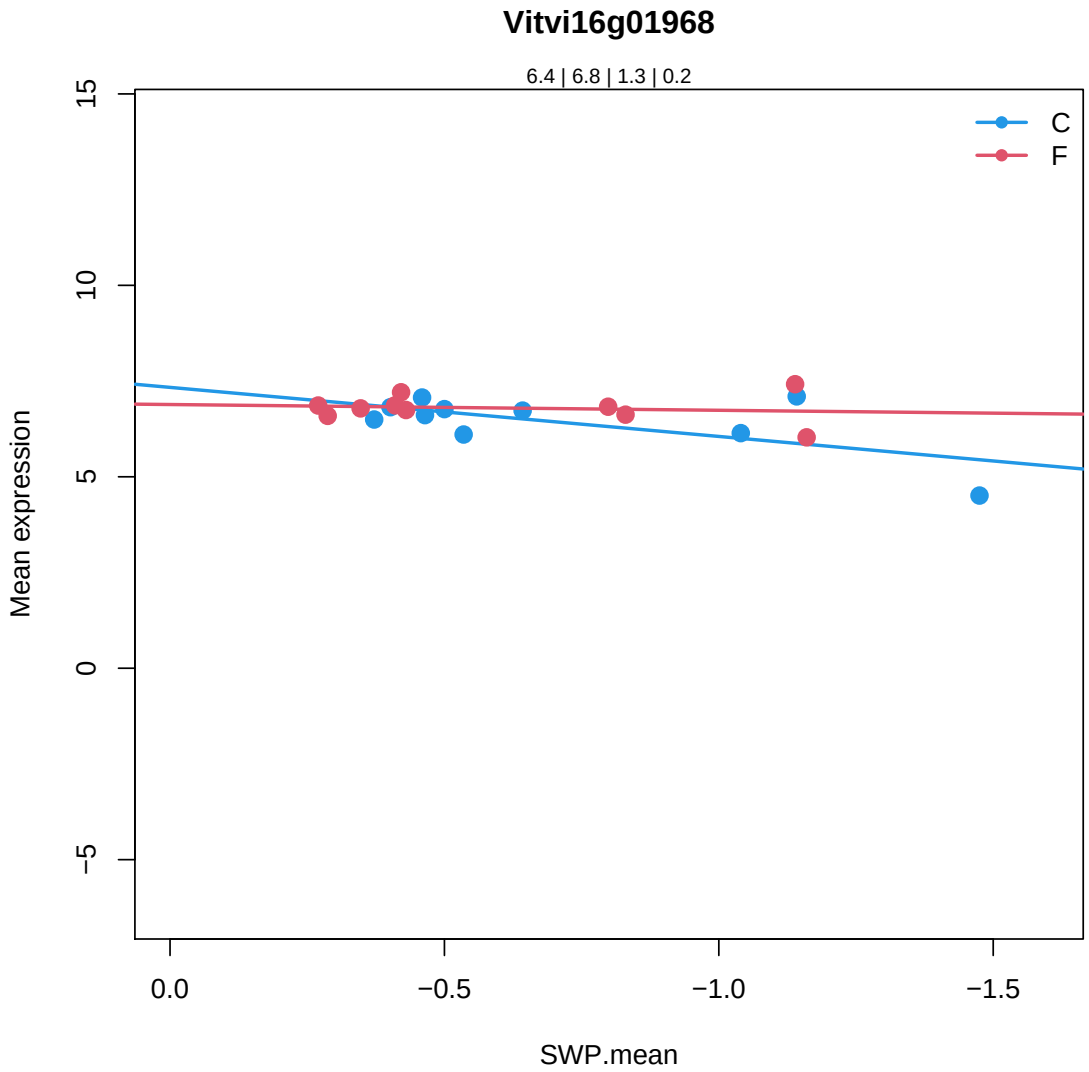
7.6.128 Vitvi16g01968: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01968
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi16g01968.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.434235	1.164578e-21	***	1.288134e-20	***
SlopeC	1.281377	0.009010845	**	0.2903326	
MeanF-MeanC	0.3612914	0.1258382		0.4198829	
SlopeF-SlopeC	-1.131178	0.1029854		0.9999488	



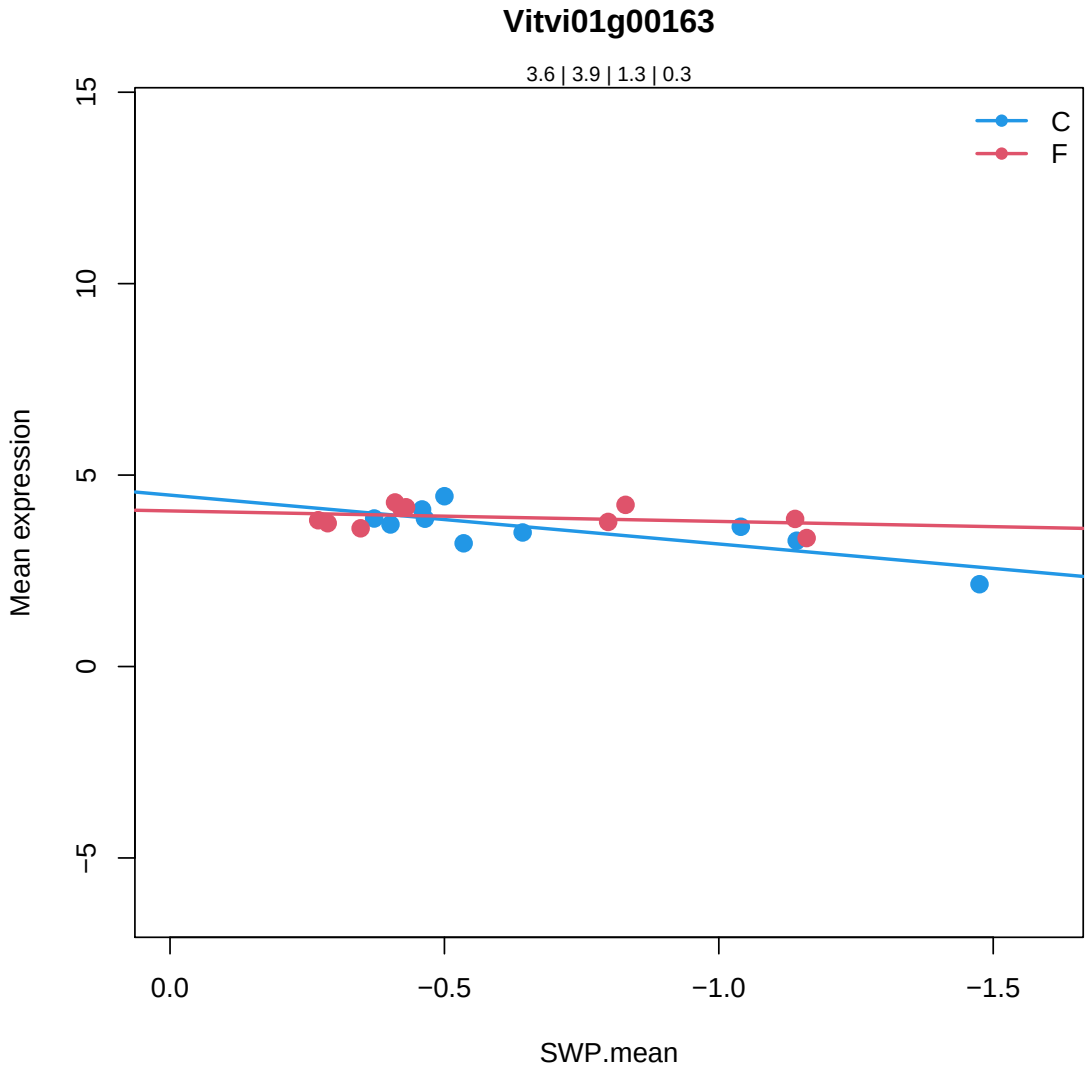
7.6.129 Vitvi01g00163: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00163
        29.2.1.2.2.536
        protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L36A
        transmembrane protein |
        Chr5:7795409-7796310 REVERSE LENGTH=271 |
        201606
```

Coefficients for Vitvi01g00163.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.578817	1.708706e-18	***	5.496856e-18	***
SlopeC	1.276165	0.001503274	**	0.1516502	
MeanF-MeanC	0.3179431	0.08883692	.	0.340352	
SlopeF-SlopeC	-1.002142	0.06841895	.	0.9999488	



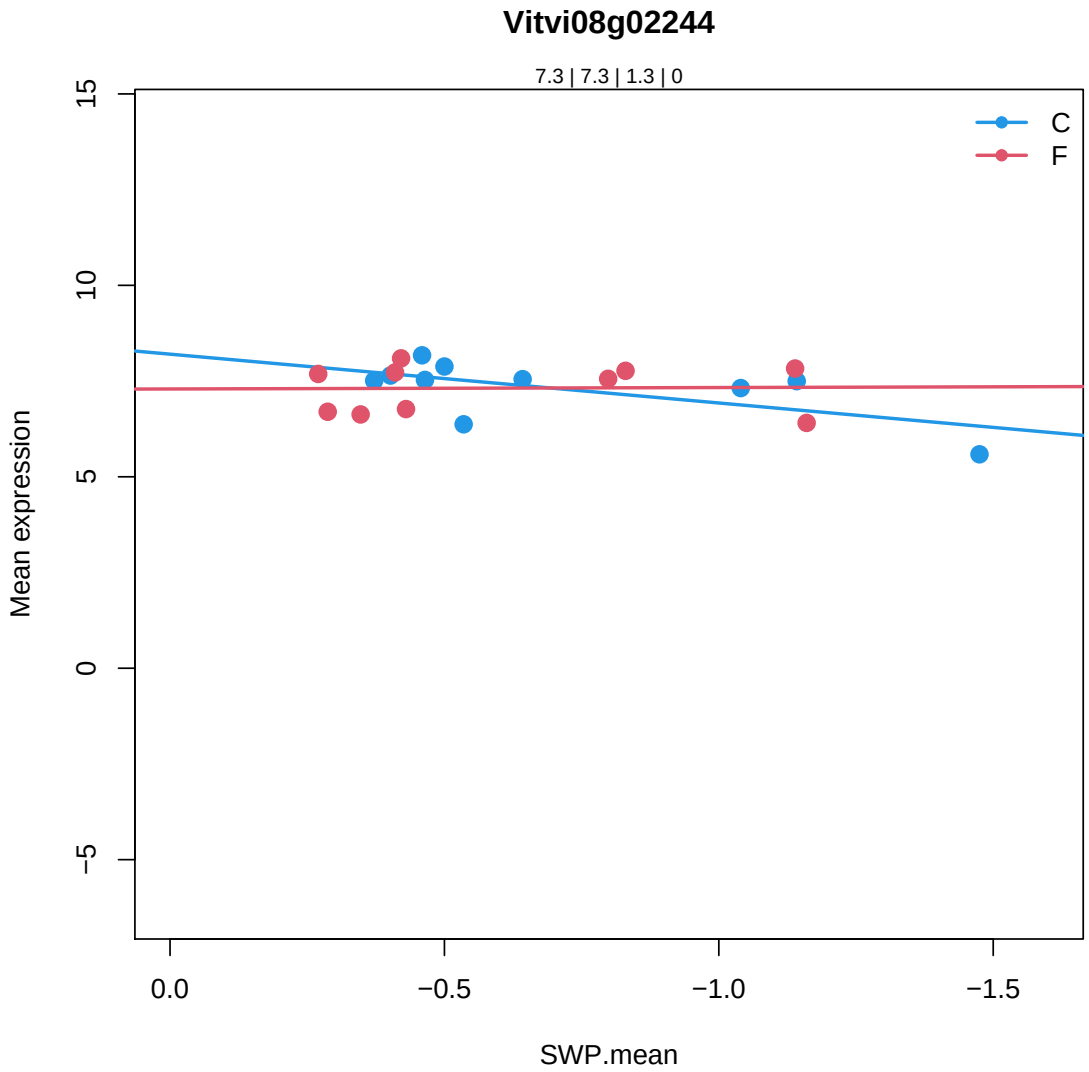
7.6.130 Vitvi08g02244: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g02244
        27.3.62
        RNA.regulation of transcription.nucleosome/chromatin assembly factor g
        NA
```

Coefficients for Vitvi08g02244.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.305923	3.219331e-21	***	2.859501e-20	***
SlopeC	1.275192	0.02561548	*	0.4084008	
MeanF-MeanC	0.01001943	0.9707669		0.9933672	
SlopeF-SlopeC	-1.312542	0.1117118		0.9999488	



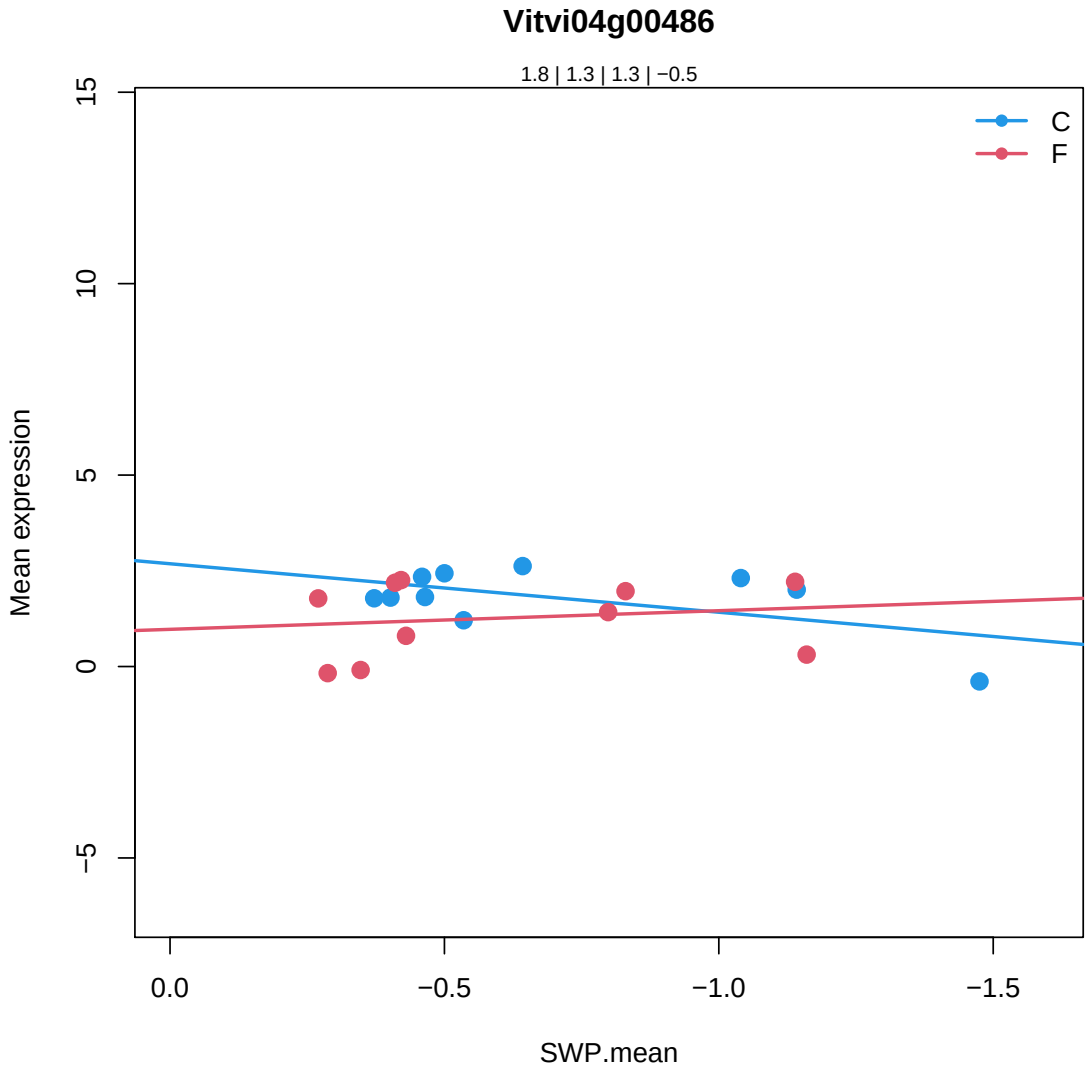
7.6.131 Vitvi04g00486: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00486
        35.2
        not assigned.unknown
        structural maintenance of chromosomes flexible hinge domain protein |
        Chr3:3718529-3721123 FORWARD LENGTH=702 |
        201606
```

Coefficients for Vitvi04g00486.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.793367	6.742475e-07	***	7.817496e-07	***
SlopeC	1.266444	0.09277173	.	0.6012018	
MeanF-MeanC	-0.526113	0.164905		0.4926463	
SlopeF-SlopeC	-1.753168	0.1163497		0.9999488	



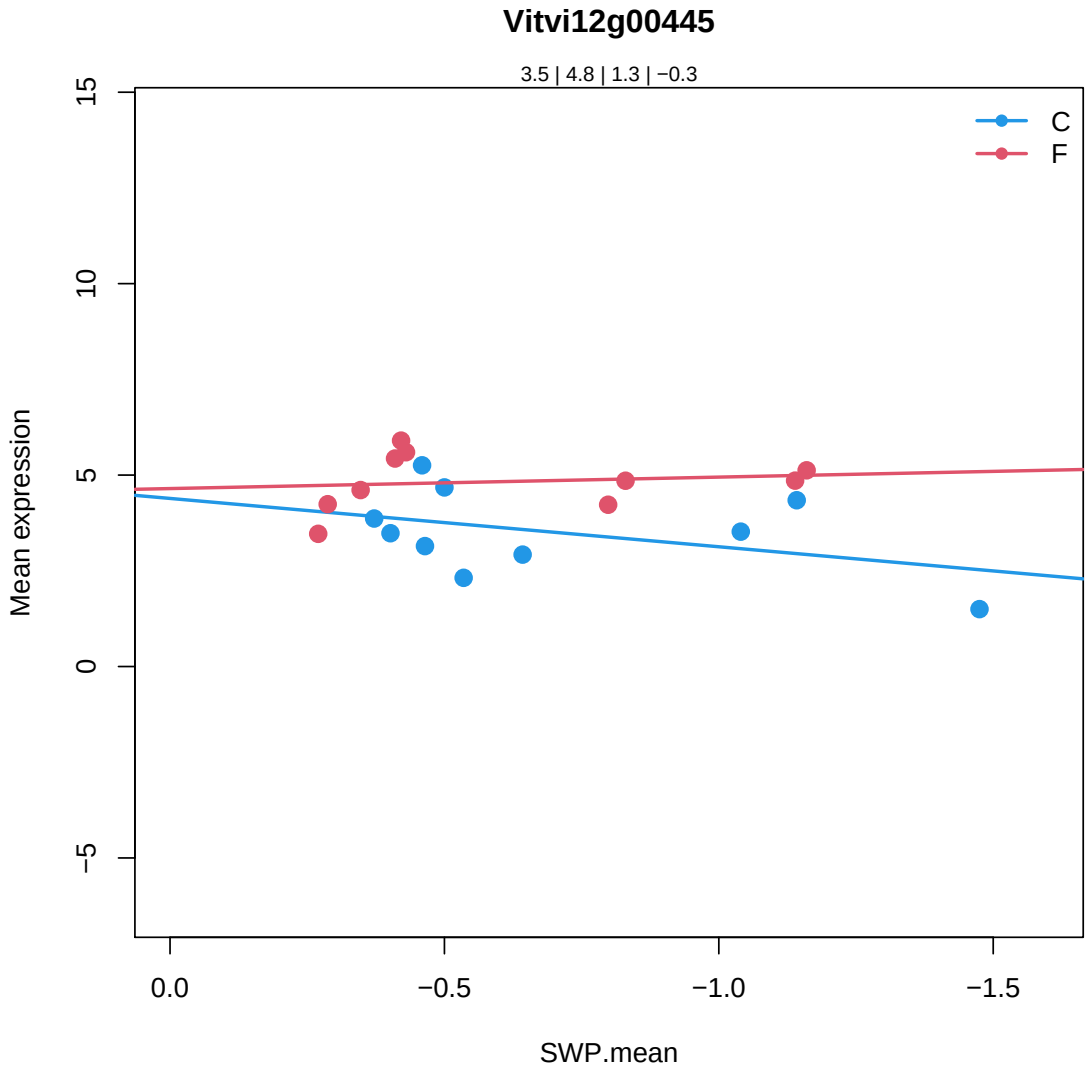
7.6.132 Vitvi12g00445: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00445
        17.5.1.2
        hormone metabolism.ethylene.synthesis-degradation.1-aminocyclopropane-
        ethylene-forming enzyme |
        Chr1:1431419-1432695 REVERSE LENGTH=323 |
        201606
```

Coefficients for Vitvi12g00445.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.502585	9.332759e-12	***	1.27567e-11	***
SlopeC	1.262311	0.1021448		0.6138959	
MeanF-MeanC	1.327419	0.001927278	**	0.02141077	*
SlopeF-SlopeC	-1.561651	0.1701624		0.9999488	



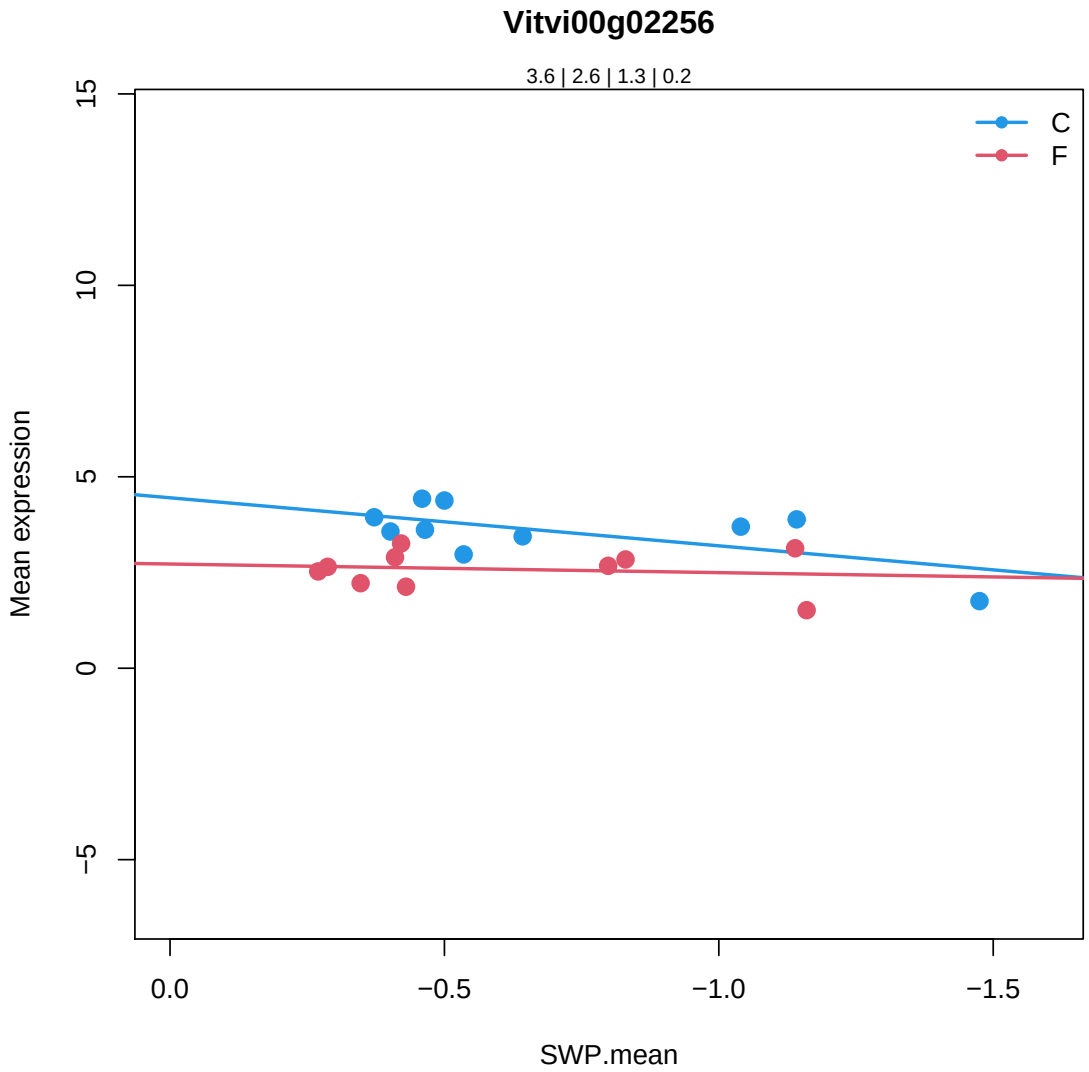
7.6.133 Vitvi00g02256: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi00g02256
        35.2
        not assigned.unknown
        Receptor-like protein kinase
```

Coefficients for Vitvi00g02256.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.569283	2.871852e-15	***	5.108866e-15	***
SlopeC	1.254562	0.02046235	*	0.3769674	
MeanF-MeanC	-0.9849266	0.0008684383	***	0.01111397	*
SlopeF-SlopeC	-1.029921	0.1816498		0.9999488	



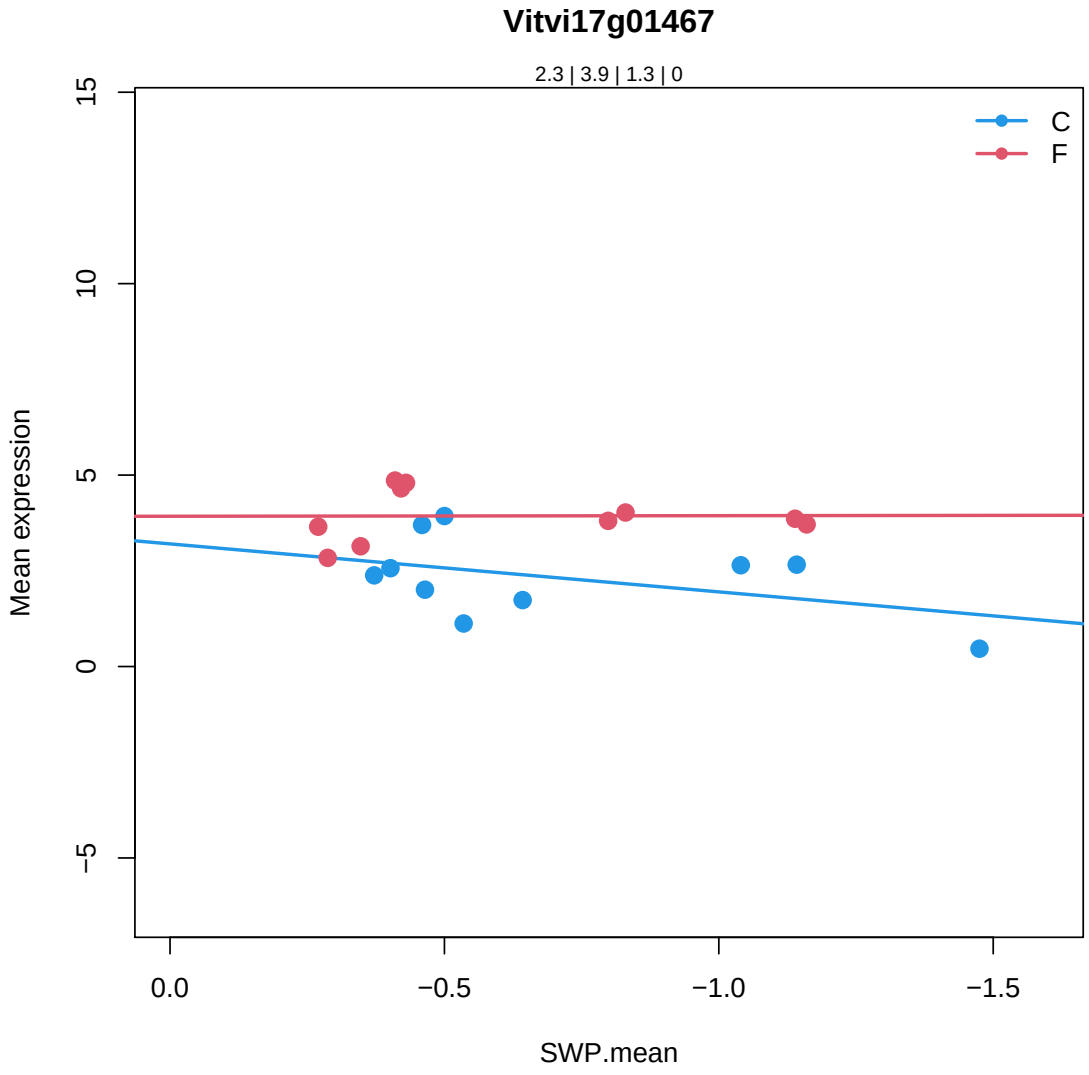
7.6.134 Vitvi17g01467: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g01467
        26.9
        misc.glutathione S transferases
        glutathione S-transferase tau 9 |
        Chr5:25088775-25089566 REVERSE LENGTH=240 |
        201606
```

Coefficients for Vitvi17g01467.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.32119	6.043356e-09	***	7.424862e-09	***
SlopeC	1.253316	0.08637096	.	0.5895505	
MeanF-MeanC	1.612464	0.0001669149	***	0.002762341	**
SlopeF-SlopeC	-1.268367	0.2349236		0.9999488	



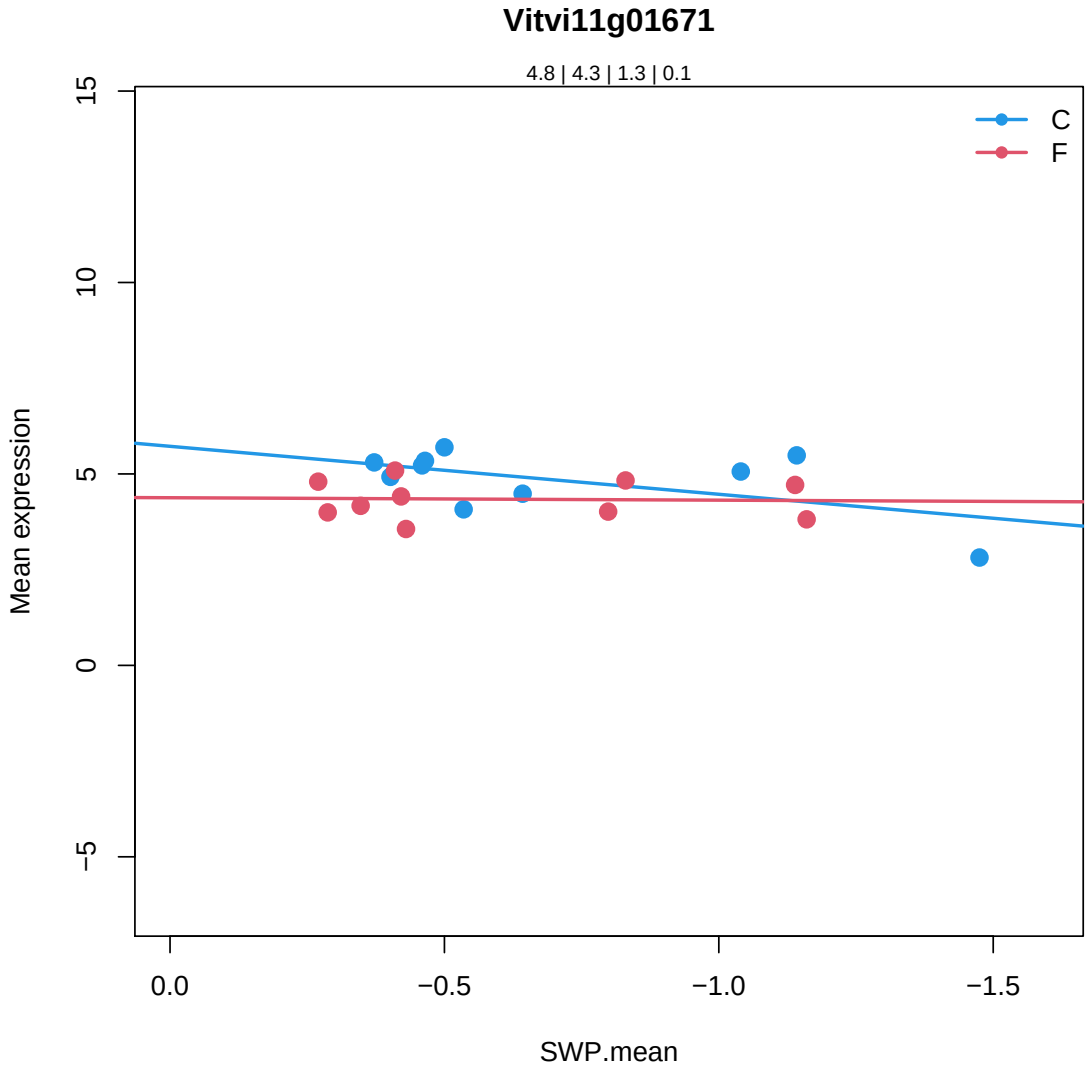
7.6.135 Vitvi11g01671: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g01671
        35.1
        not assigned.no ontology
        [Sotub07g008080.1.1]: UPF0497 membrane protein 13 [Sotub07g008080.1.1]
        [stNIB-v1_0009389]
```

Coefficients for Vitvi11g01671.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.840579	2.885715e-17	***	6.922264e-17	***
SlopeC	1.252473	0.03130779	*	0.4322019	
MeanF-MeanC	-0.5010761	0.08379066	.	0.327849	
SlopeF-SlopeC	-1.188869	0.1562337		0.9999488	



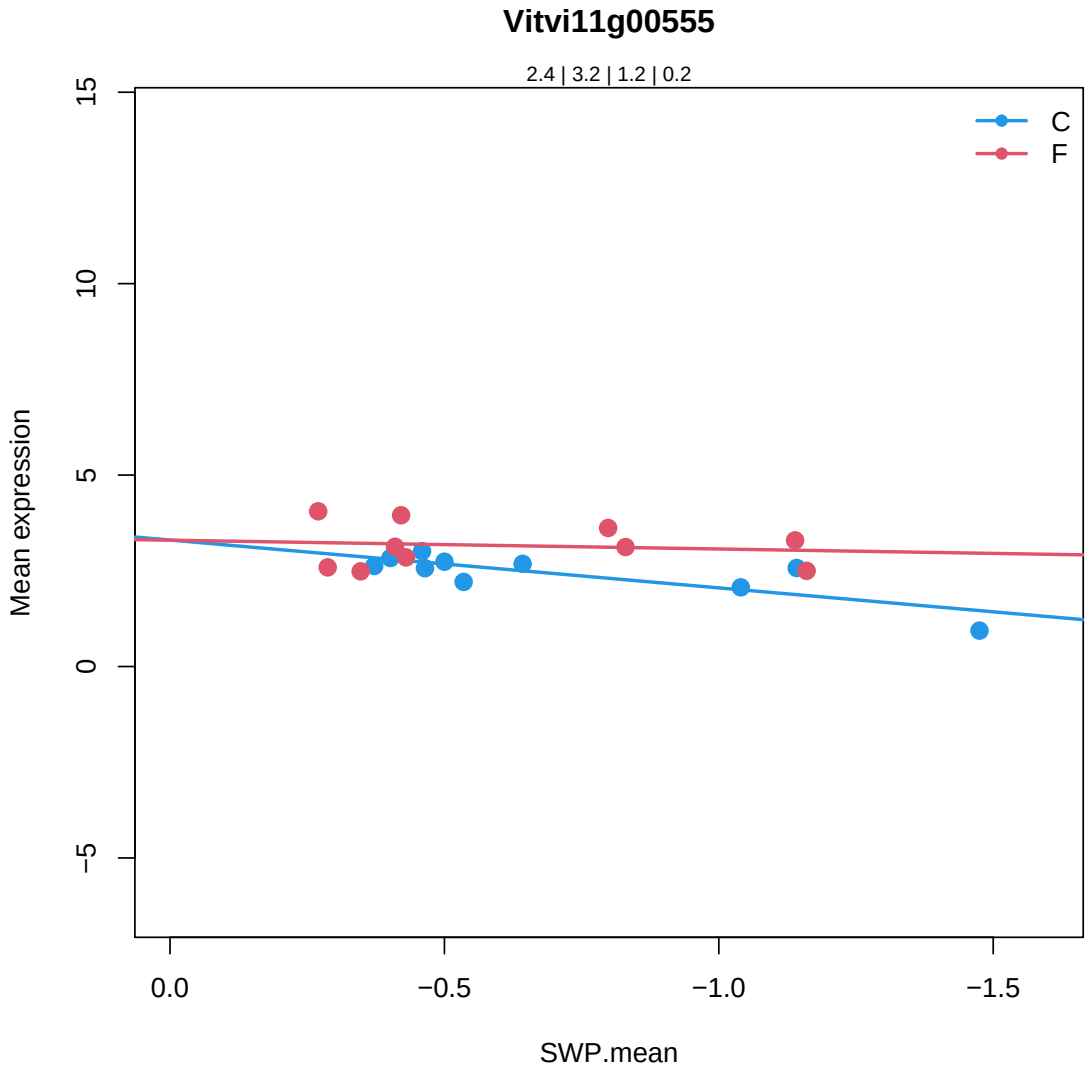
7.6.136 Vitvi11g00555: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00555
        11.10.1
        lipid metabolism.glycolipid synthesis.MGDG synthase
        monogalactosyldiacylglycerol synthase type C |
        Chr2:4743388-4746214 FORWARD LENGTH=372 |
        201606
```

Coefficients for Vitvi11g00555.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.424612	4.817302e-13	***	7.060805e-13	***
SlopeC	1.249284	0.009618251	**	0.2991865	
MeanF-MeanC	0.7342933	0.003444731	**	0.03413822	*
SlopeF-SlopeC	-1.019464	0.1337172		0.9999488	



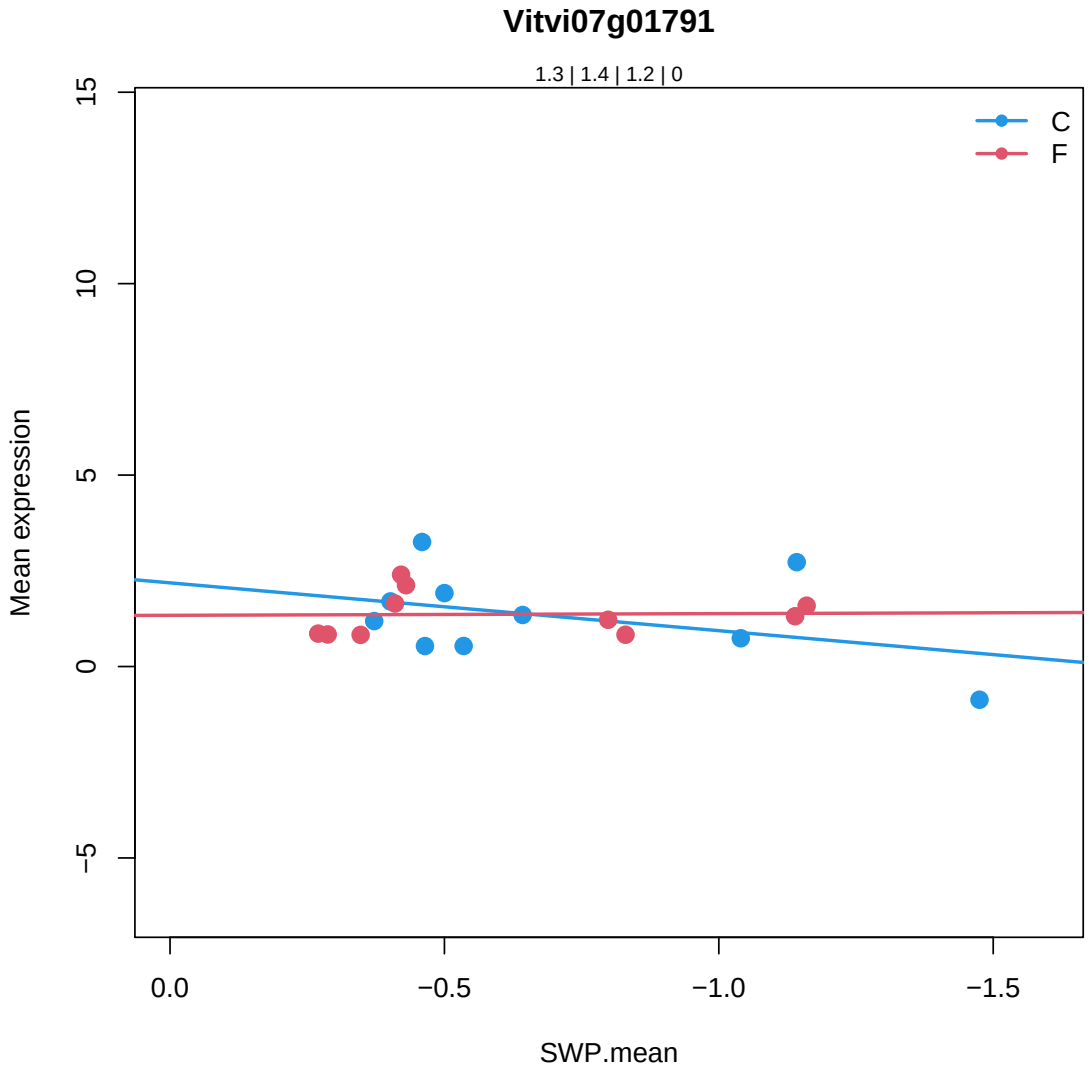
7.6.137 Vitvi07g01791: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01791
        21.2.1
        redox.ascorbate and glutathione.ascorbate
        Cupredoxin superfamily protein |
        Chr4:18479453-18481184 FORWARD LENGTH=474 |
        201606
```

Coefficients for Vitvi07g01791.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.306854	5.956485e-05	***	6.606661e-05	***
SlopeC	1.249253	0.1016		0.6135572	
MeanF-MeanC	0.05732736	0.8787226		0.9686965	
SlopeF-SlopeC	-1.292991	0.2472497		0.9999488	



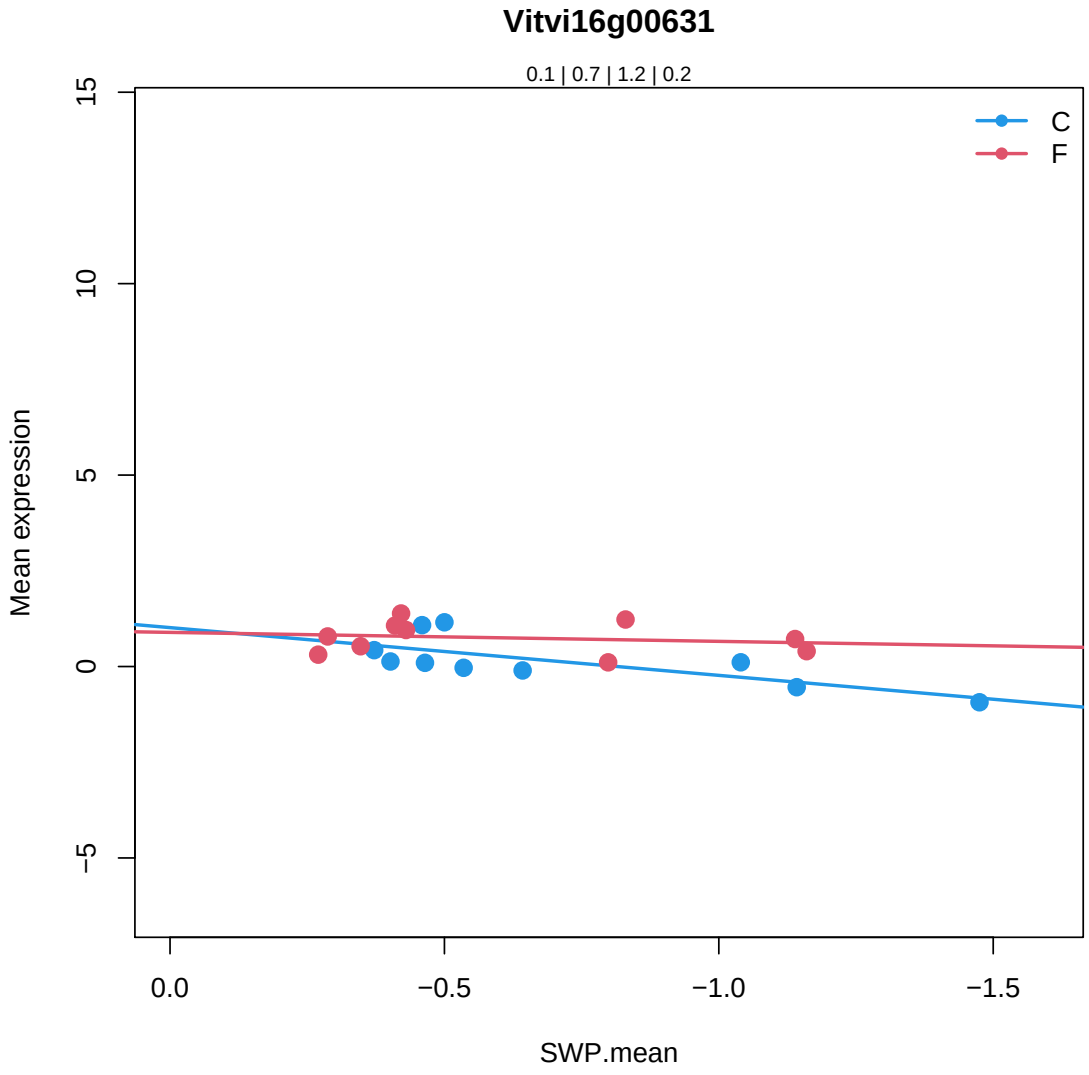
7.6.138 Vitvi16g00631: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g00631
        35.2
        not assigned.unknown
        Leucine-rich repeat protein kinase family protein |
        Chr3:20899403-20902390 REVERSE LENGTH=964 |
        201606
```

Coefficients for Vitvi16g00631.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.138975	0.3479599		0.3539275	
SlopeC	1.246727	0.005405643	**	0.2577627	
MeanF-MeanC	0.6096795	0.007087853	**	0.0589057	.
SlopeF-SlopeC	-1.012186	0.105946		0.9999488	



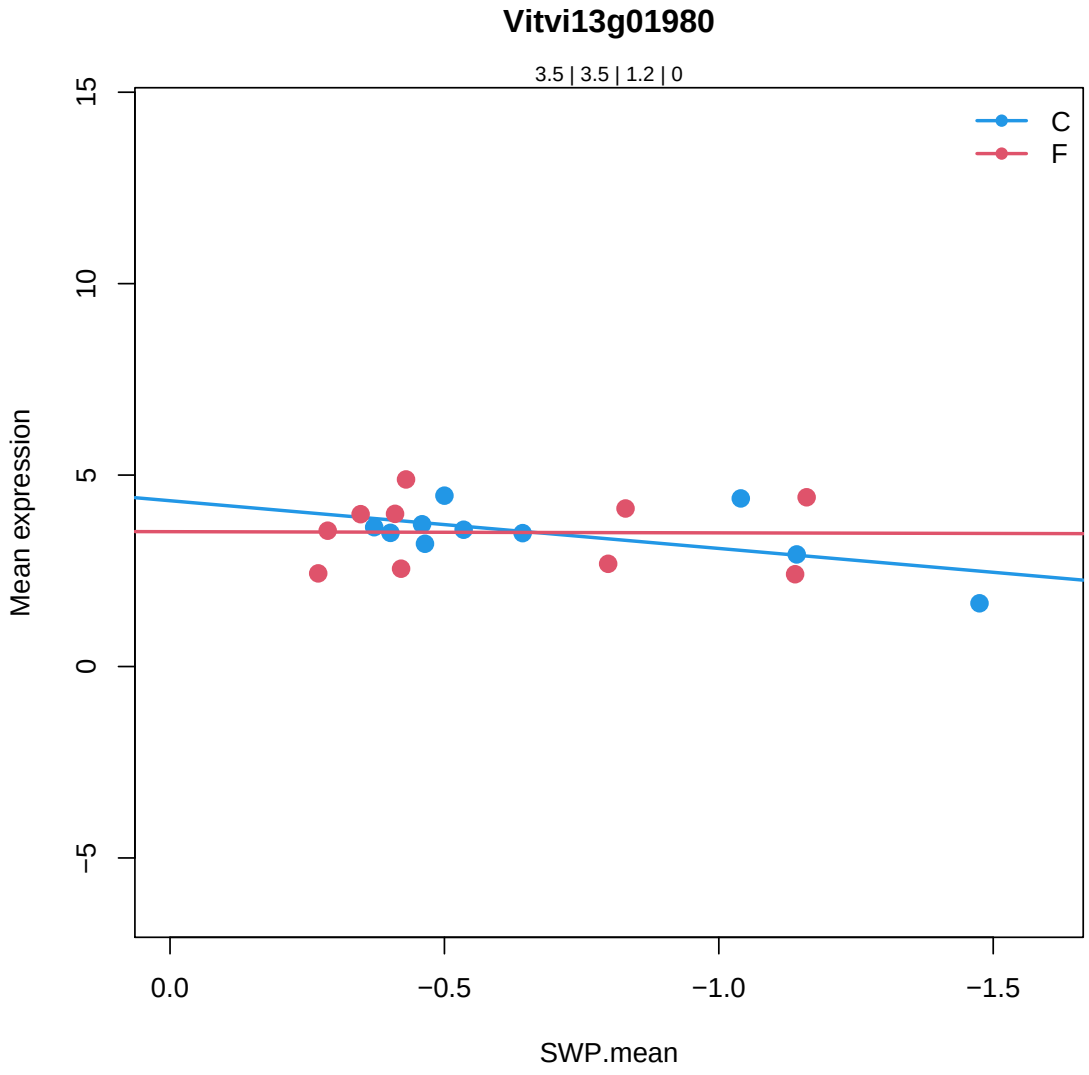
7.6.139 Vitvi13g01980: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g01980
        35.2
        not assigned.unknown
        Cysteine/Histidine-rich C1 domain family protein |
        Chr2:6980450-6981939 FORWARD LENGTH=243 |
        201606
```

Coefficients for Vitvi13g01980.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.453811	1.801507e-12	***	2.547178e-12	***
SlopeC	1.246487	0.07640034	.	0.5694531	
MeanF-MeanC	0.04881365	0.8872899		0.9704865	
SlopeF-SlopeC	-1.215722	0.2357151		0.9999488	



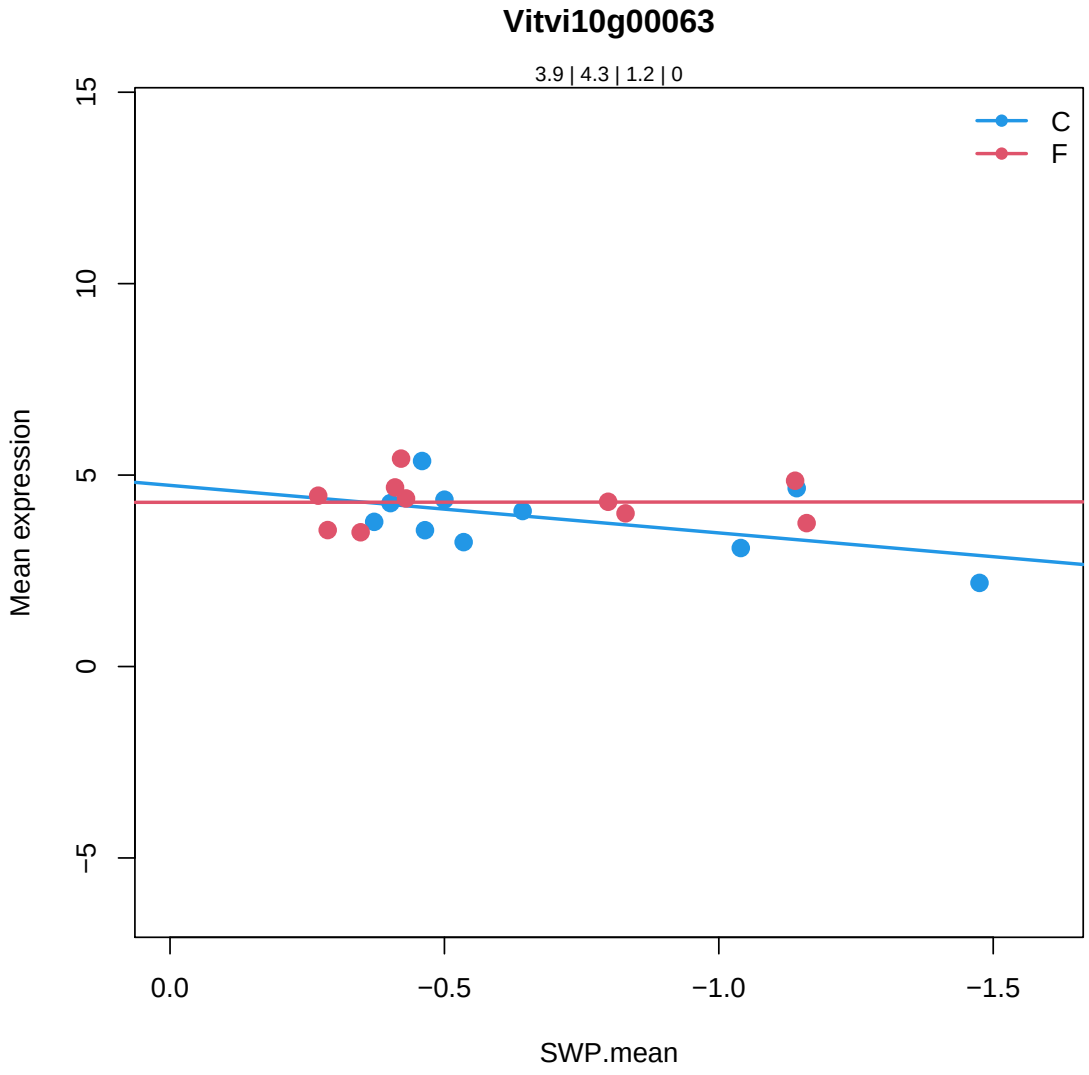
7.6.140 Vitvi10g00063: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00063
        27.3.32
        RNA.regulation of transcription.WRKY domain transcription factor famil
        WRKY DNA-binding protein 31 |
        Chr4:11691381-11694234 REVERSE LENGTH=538 |
        201606
```

Coefficients for Vitvi10g00063.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.857831	2.052041e-14	***	3.334102e-14	***
SlopeC	1.241679	0.04969305	*	0.5087769	
MeanF-MeanC	0.4350666	0.1660556		0.4945328	
SlopeF-SlopeC	-1.248967	0.1741266		0.9999488	



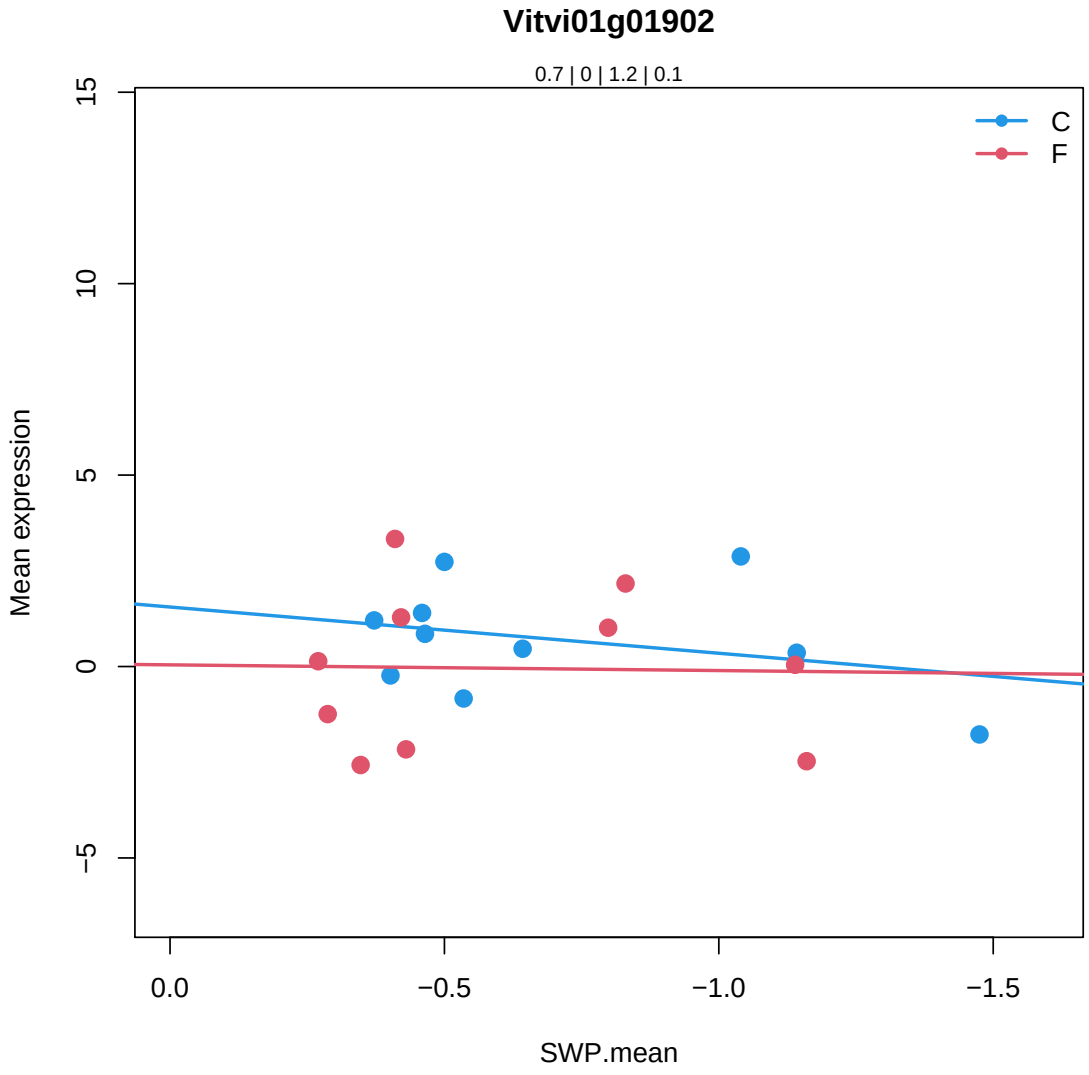
7.6.141 Vitvi01g01902: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01902
        35.2
        not assigned.unknown
        RING-H2 finger A2A |
        Chr1:5193703-5194170 REVERSE LENGTH=155 |
        201606
```

Coefficients for Vitvi01g01902.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.7047541	0.1820556		0.1868739	
SlopeC	1.207583	0.4050313		0.836381	
MeanF-MeanC	-0.7520743	0.3096033		0.6733695	
SlopeF-SlopeC	-1.058653	0.6219462		0.9999488	



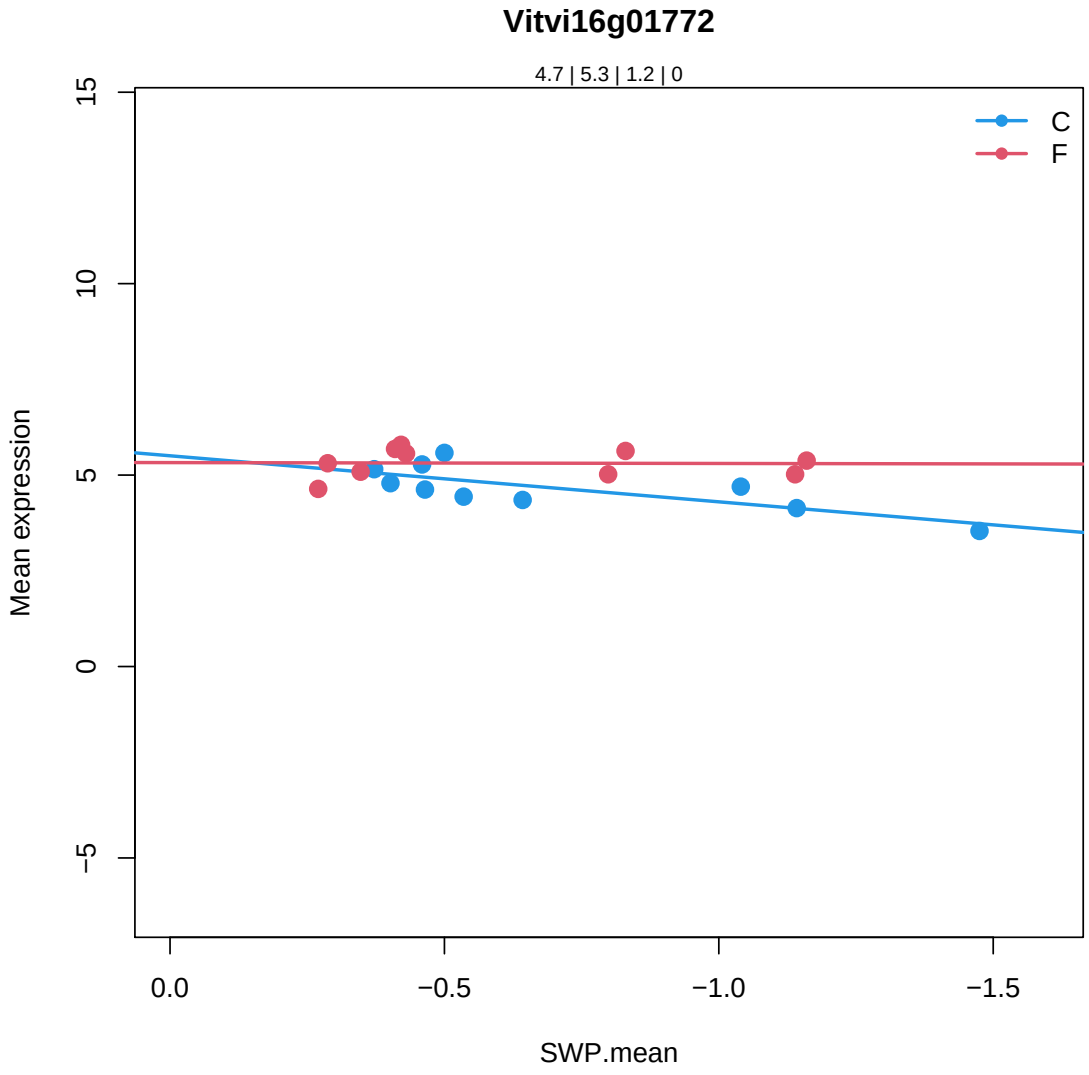
7.6.142 Vitvi16g01772: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01772
        20.1.2
        stress.biotic.receptors
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606
```

Coefficients for Vitvi16g01772.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.658307	2.127549e-20	***	1.312021e-19	***
SlopeC	1.203085	0.00379709	**	0.2269459	
MeanF-MeanC	0.6537352	0.002239087	**	0.02406782	*
SlopeF-SlopeC	-1.18044	0.0440328	*	0.9999488	



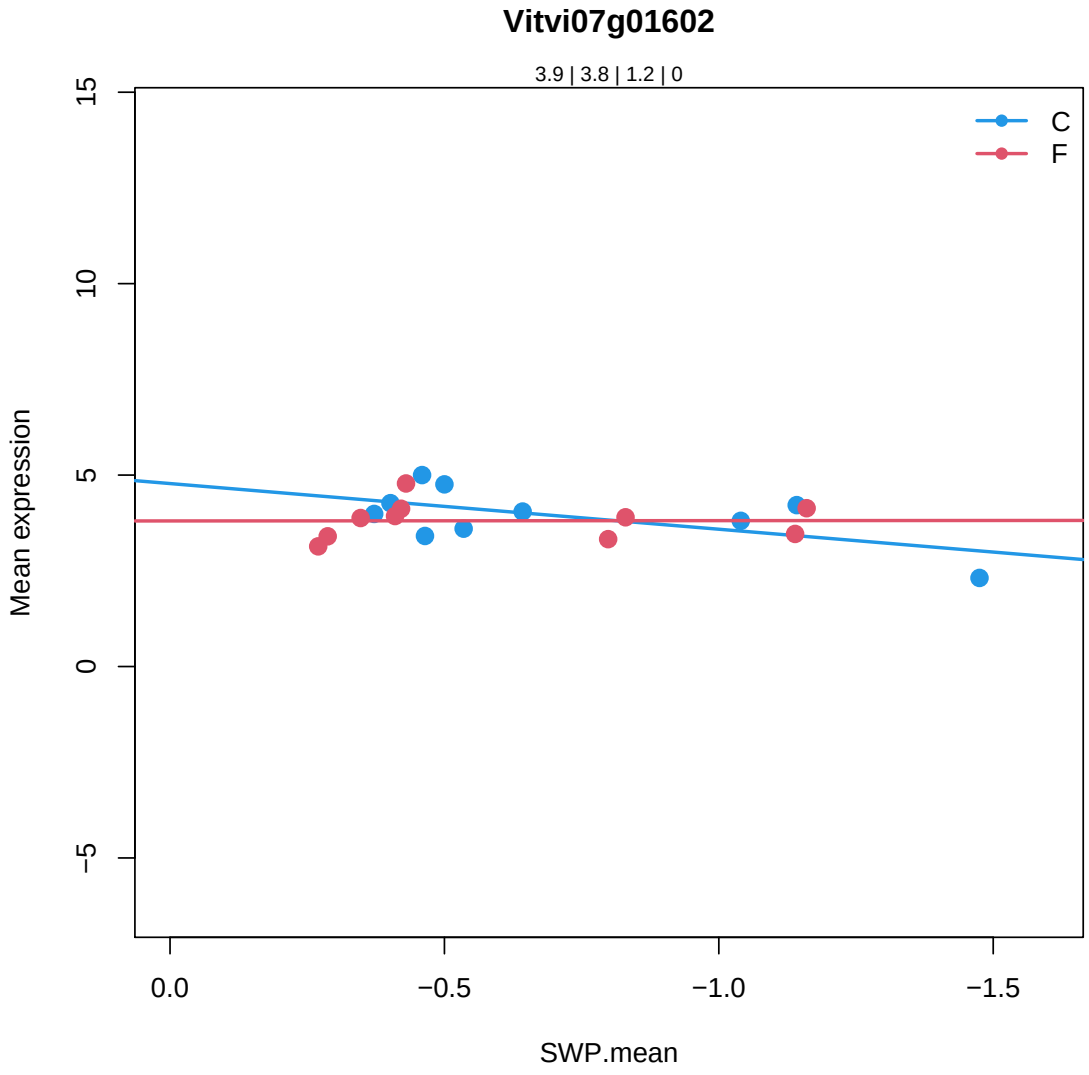
7.6.143 Vitvi07g01602: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01602
        35.2
        not assigned.unknown
        zinc-finger protein 1 |
        Chr5:26919142-26919879 REVERSE LENGTH=245 |
        201606
```

Coefficients for Vitvi07g01602.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.939952	2.41728e-16	***	4.936251e-16	***
SlopeC	1.192797	0.02382236	*	0.3984486	
MeanF-MeanC	-0.1330677	0.5989302		0.8604564	
SlopeF-SlopeC	-1.200395	0.1146006		0.9999488	



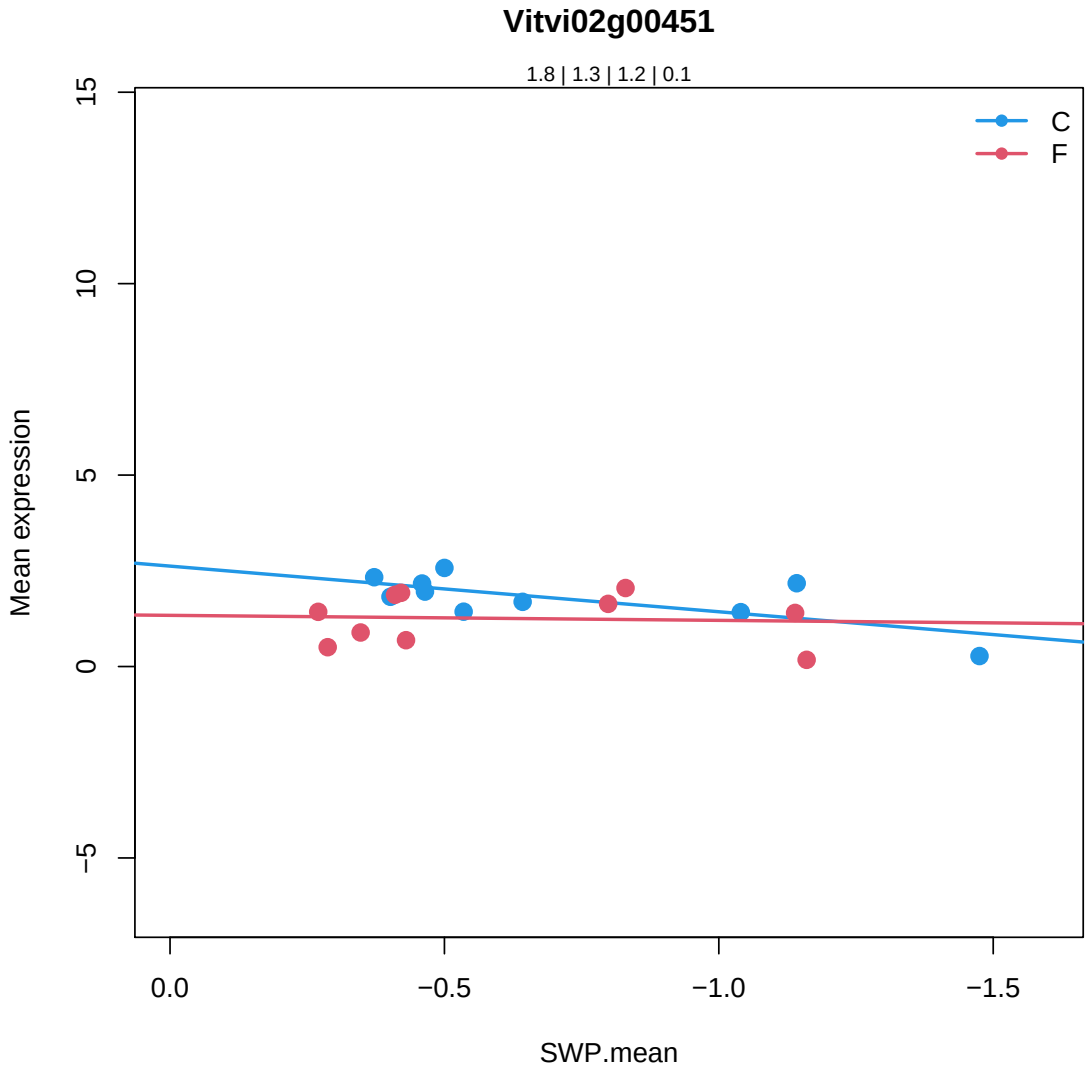
7.6.144 Vitvi02g00451: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00451
        34.9
        transport.metabolite transporters at the mitochondrial membrane
        C4-dicarboxylate transporter/malic acid transport protein |
        Chr1:4257427-4259249 REVERSE LENGTH=556 |
        201606
```

Coefficients for Vitvi02g00451.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.784251	2.228333e-09	***	2.777353e-09	***
SlopeC	1.192142	0.02814141	*	0.4263731	
MeanF-MeanC	-0.5274845	0.0528428	.	0.2480536	
SlopeF-SlopeC	-1.061184	0.1734156		0.9999488	



7.6.145 Vitvi09g00233: type5

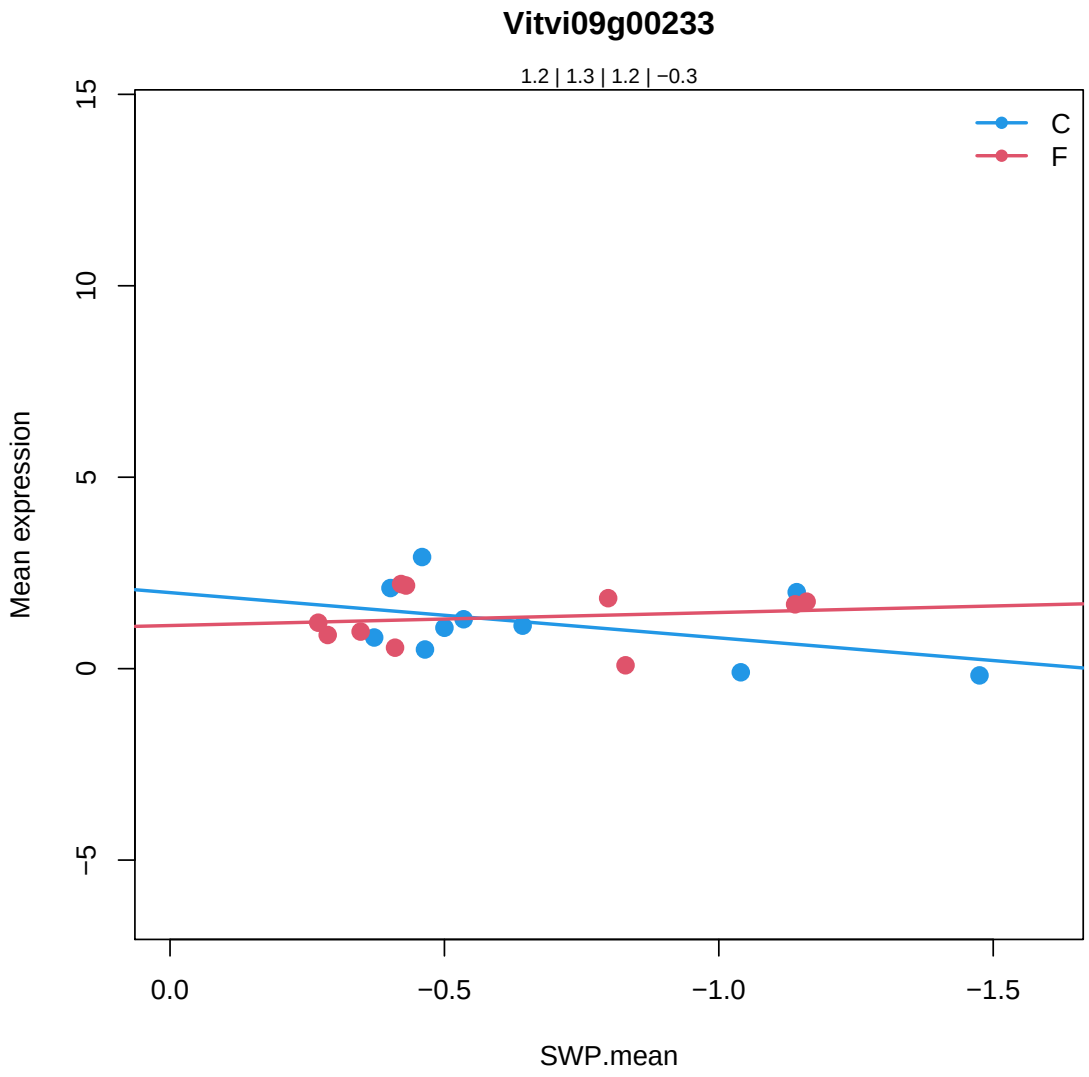
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00233
        30.2.1
        signalling.receptor kinases.leucine rich repeat I
        Leucine-rich repeat transmembrane protein kinase protein |
        Chr2:8344759-8348431 REVERSE LENGTH=877 |
        201606

Vitvi09g00233
        29.4
        protein.postranslational modification
        Leucine-rich repeat transmembrane protein kinase protein |
        Chr2:8344759-8348431 REVERSE LENGTH=877 |
        201606
```

Coefficients for Vitvi09g00233.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.153999	9.771132e-05	***	0.0001078745	***
SlopeC	1.182958	0.0929837	.	0.6013509	
MeanF-MeanC	0.179352	0.6053789		0.8617574	
SlopeF-SlopeC	-1.523618	0.1427573		0.9999488	


Vitvi09g00233
1.2 | 1.3 | 1.2 | −0.3
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

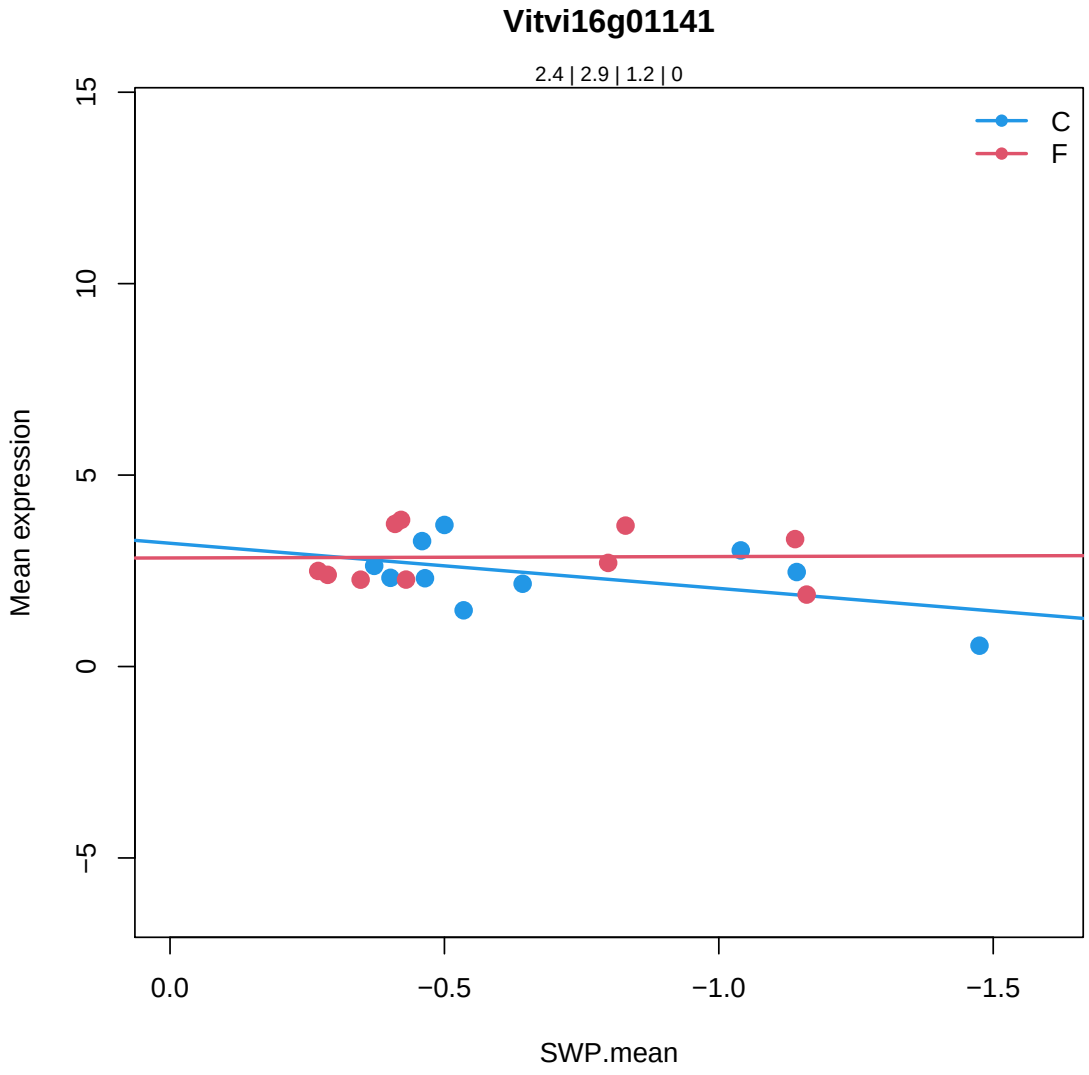
7.6.146 Vitvi16g01141: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01141
        35.2
        not assigned.unknown
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606
```

Coefficients for Vitvi16g01141.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.389662	8.369175e-10	***	1.057999e-09	***
SlopeC	1.179609	0.08002217	.	0.5749981	
MeanF-MeanC	0.4679096	0.1660102		0.4945328	
SlopeF-SlopeC	-1.215838	0.2168068		0.9999488	



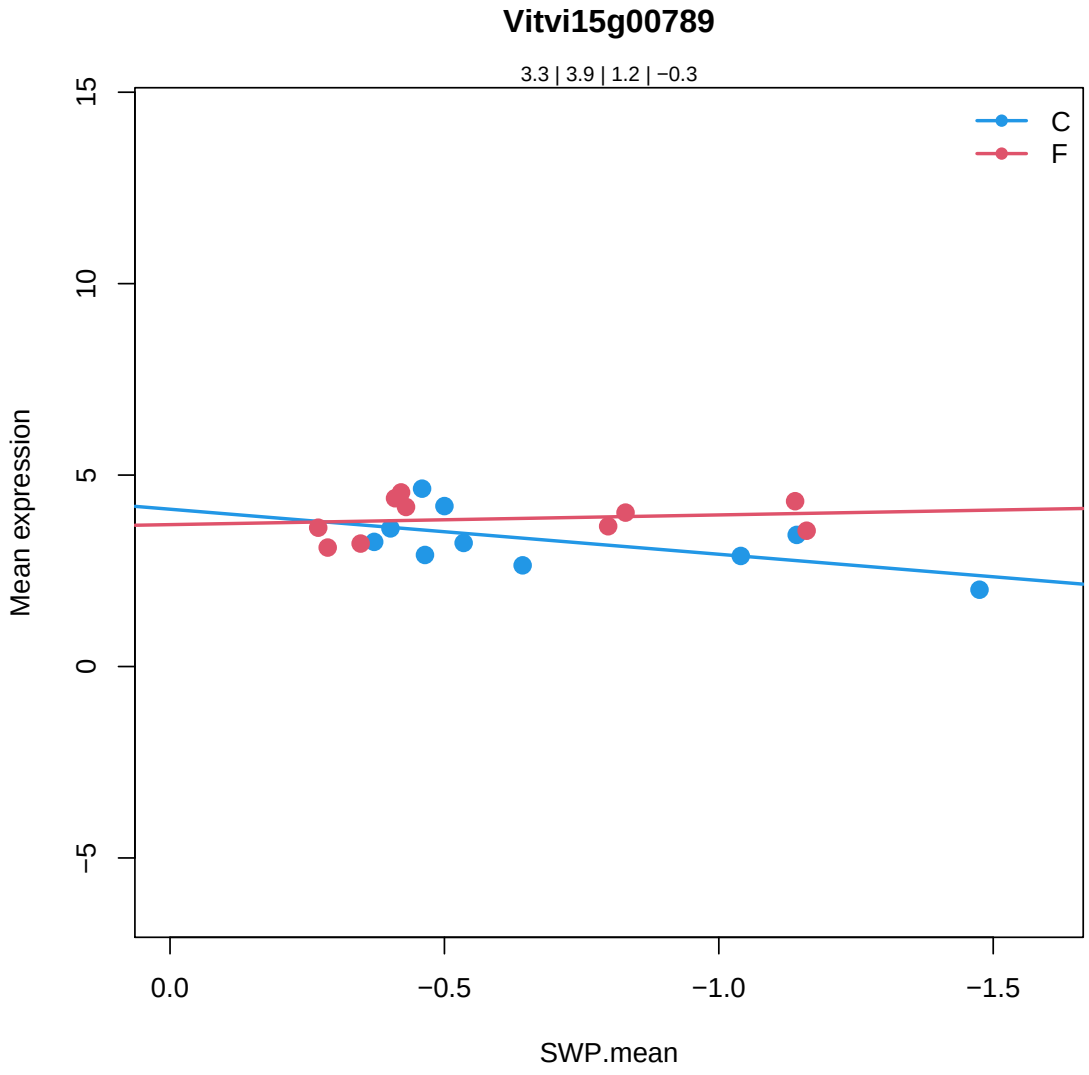
7.6.147 Vitvi15g00789: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g00789
        26.3.5
        misc.gluco-, galacto- and mannosidases.glycosyl hydrolase family 5
        alpha/beta-Hydrolases superfamily protein |
        Chr2:18789799-18790788 FORWARD LENGTH=329 |
        201606
```

Coefficients for Vitvi15g00789.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.281118	1.376717e-14	***	2.269269e-14	***
SlopeC	1.176291	0.02763164	*	0.4233169	
MeanF-MeanC	0.5790078	0.03236116	*	0.1782612	
SlopeF-SlopeC	-1.429398	0.06702405	.	0.9999488	



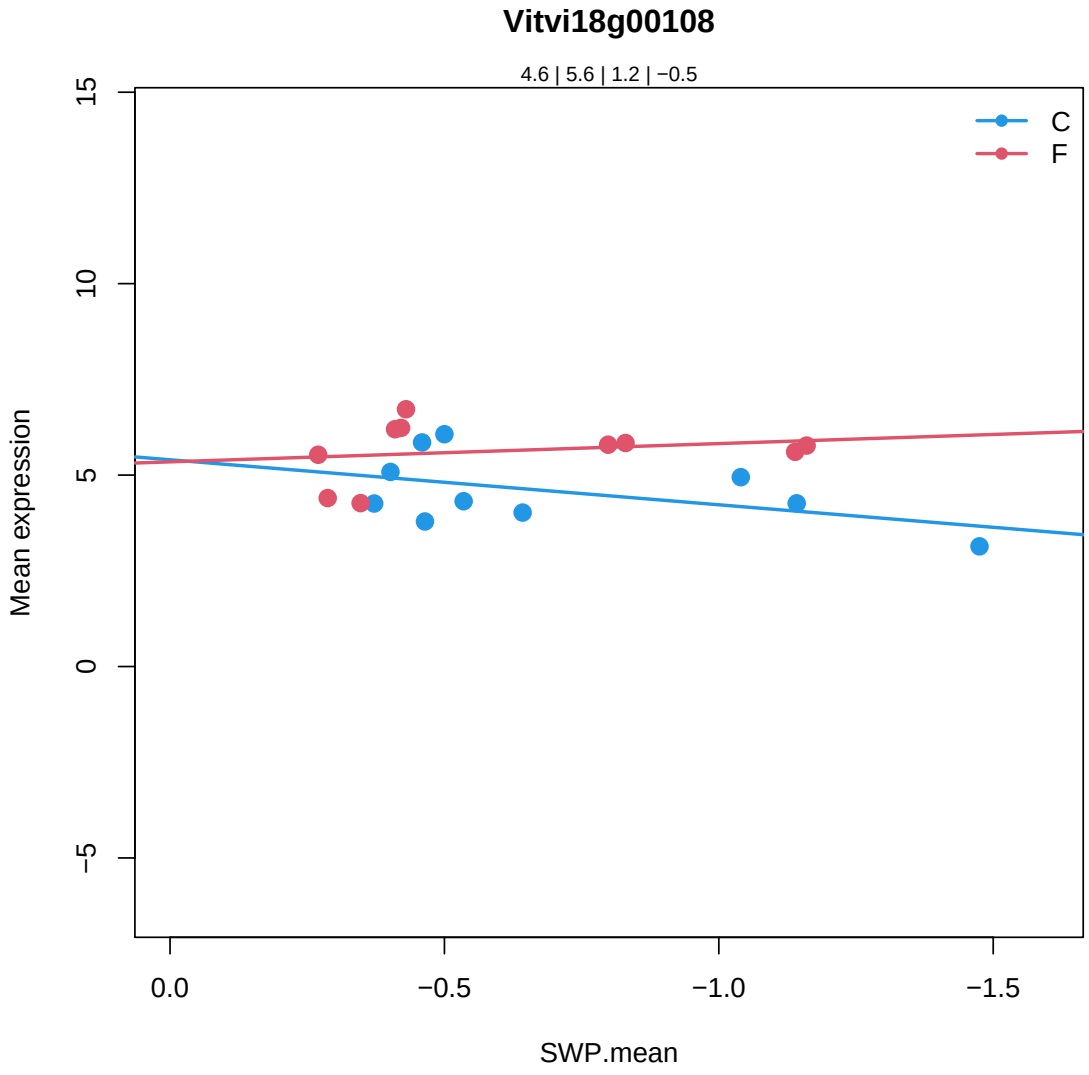
7.6.148 Vitvi18g00108: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00108
        26.10
        misc.cytochrome P450
        cytochrome P450%2C family 87%2C subfamily A%2C polypeptide 2 |
        Chr1:4342462-4343980 FORWARD LENGTH=366 |
        201606
```

Coefficients for Vitvi18g00108.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.572942	5.292129e-15	***	9.137135e-15	***
SlopeC	1.1758	0.08980316	.	0.5953805	
MeanF-MeanC	1.06266	0.004649624	**	0.04321315	*
SlopeF-SlopeC	-1.652723	0.1078758		0.9999488	



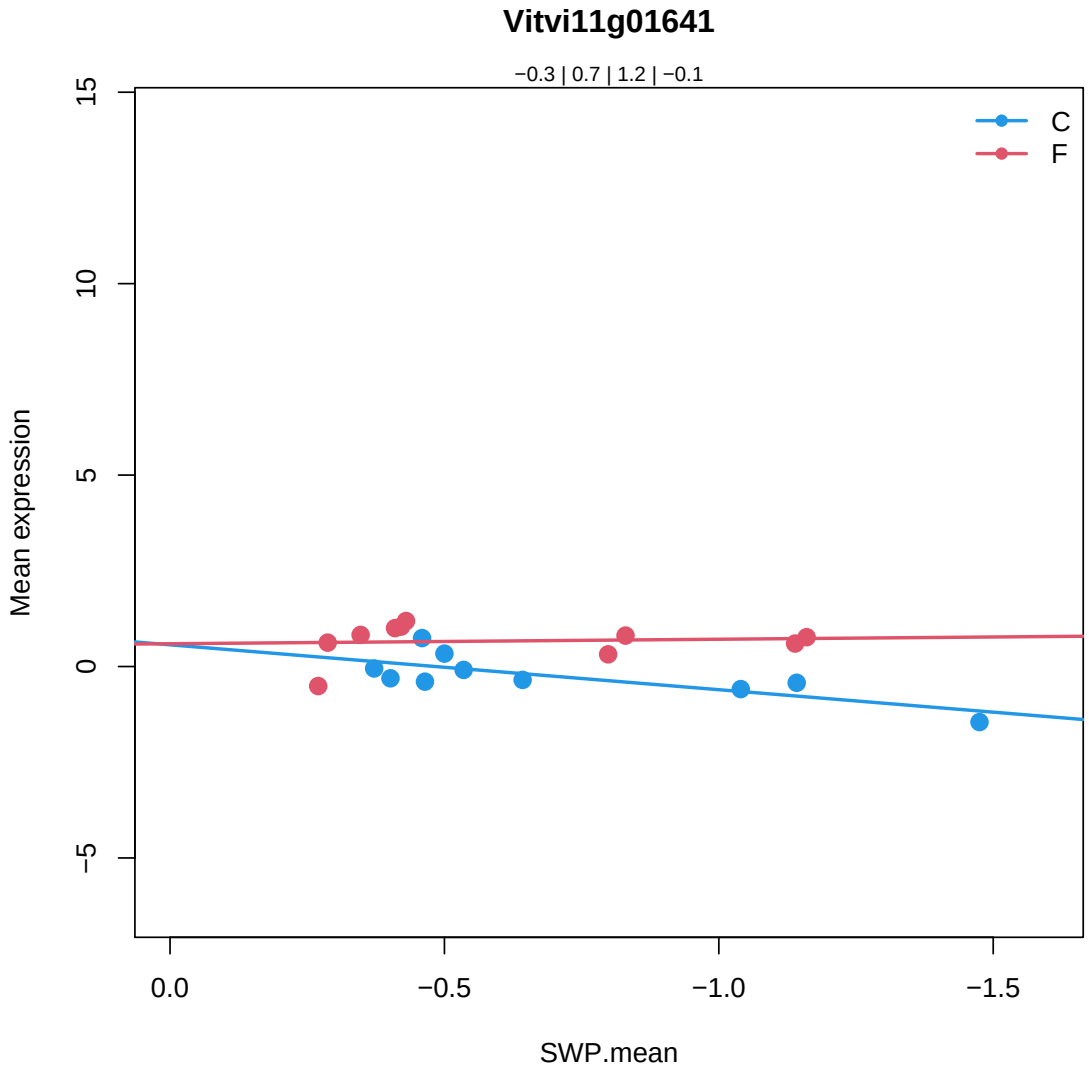
7.6.149 Vitvi11g01641: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g01641
        30.2.12
        signalling.receptor kinases.leucine rich repeat XII
        EF-TU receptor |
        Chr5:6922497-6925679 FORWARD LENGTH=1031 |
        201606
```

Coefficients for Vitvi11g01641.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.2578324	0.09360759	.	0.09686129	.
SlopeC	1.172355	0.00909194	**	0.2903326	
MeanF-MeanC	0.9242348	0.0002133608	***	0.003444963	**
SlopeF-SlopeC	-1.289937	0.045837	*	0.9999488	



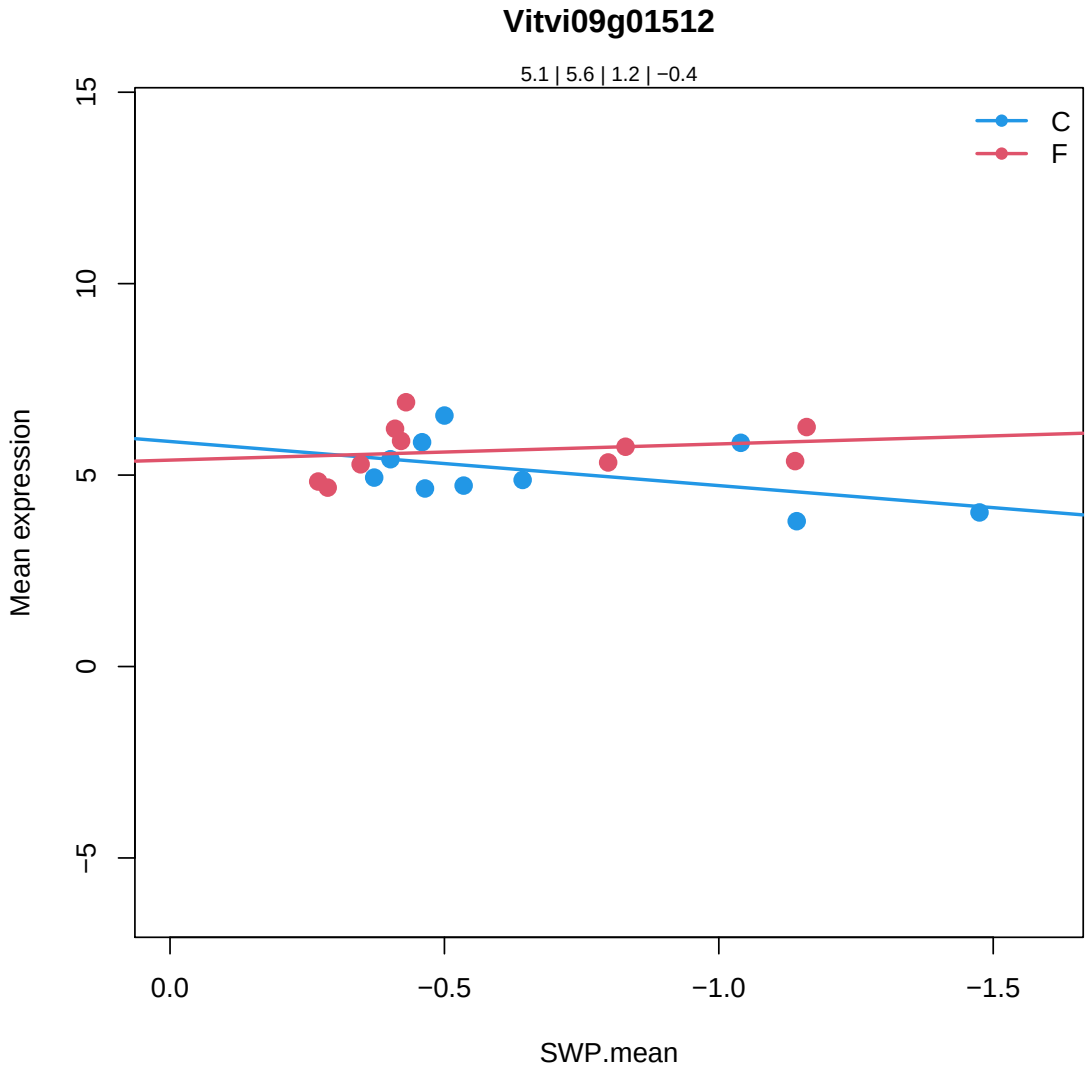
7.6.150 Vitvi09g01512: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g01512
        35.2
        not assigned.unknown
        germin 3 |
        Chr5:6975315-6975950 REVERSE LENGTH=211 |
        201606
```

Coefficients for Vitvi09g01512.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.066968	1.178889e-16	***	2.53008e-16	***
SlopeC	1.152248	0.07208585	.	0.5630621	
MeanF-MeanC	0.5807945	0.07433118	.	0.3068021	
SlopeF-SlopeC	-1.574348	0.09677392	.	0.9999488	



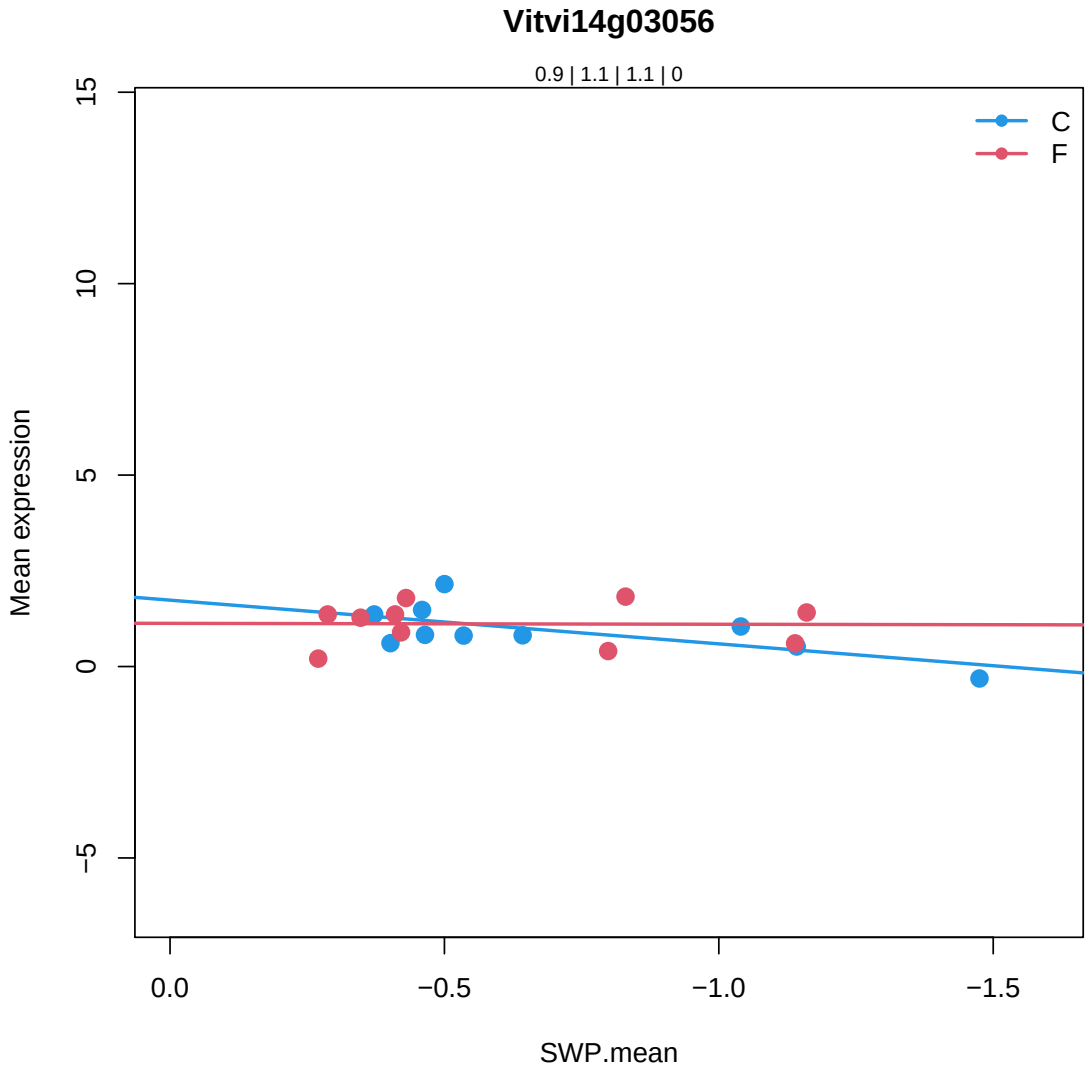
7.6.151 Vitvi14g03056: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g03056
        35.2
        not assigned.unknown
        Leucine-rich repeat receptor-like protein kinase family protein |
        Chr4:5637467-5640496 REVERSE LENGTH=1009 |
        201606
```

Coefficients for Vitvi14g03056.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.9304593	2.047126e-05	***	2.29513e-05	***
SlopeC	1.141703	0.02586304	*	0.4105308	
MeanF-MeanC	0.1821974	0.4604413		0.7842268	
SlopeF-SlopeC	-1.118305	0.1297544		0.9999488	



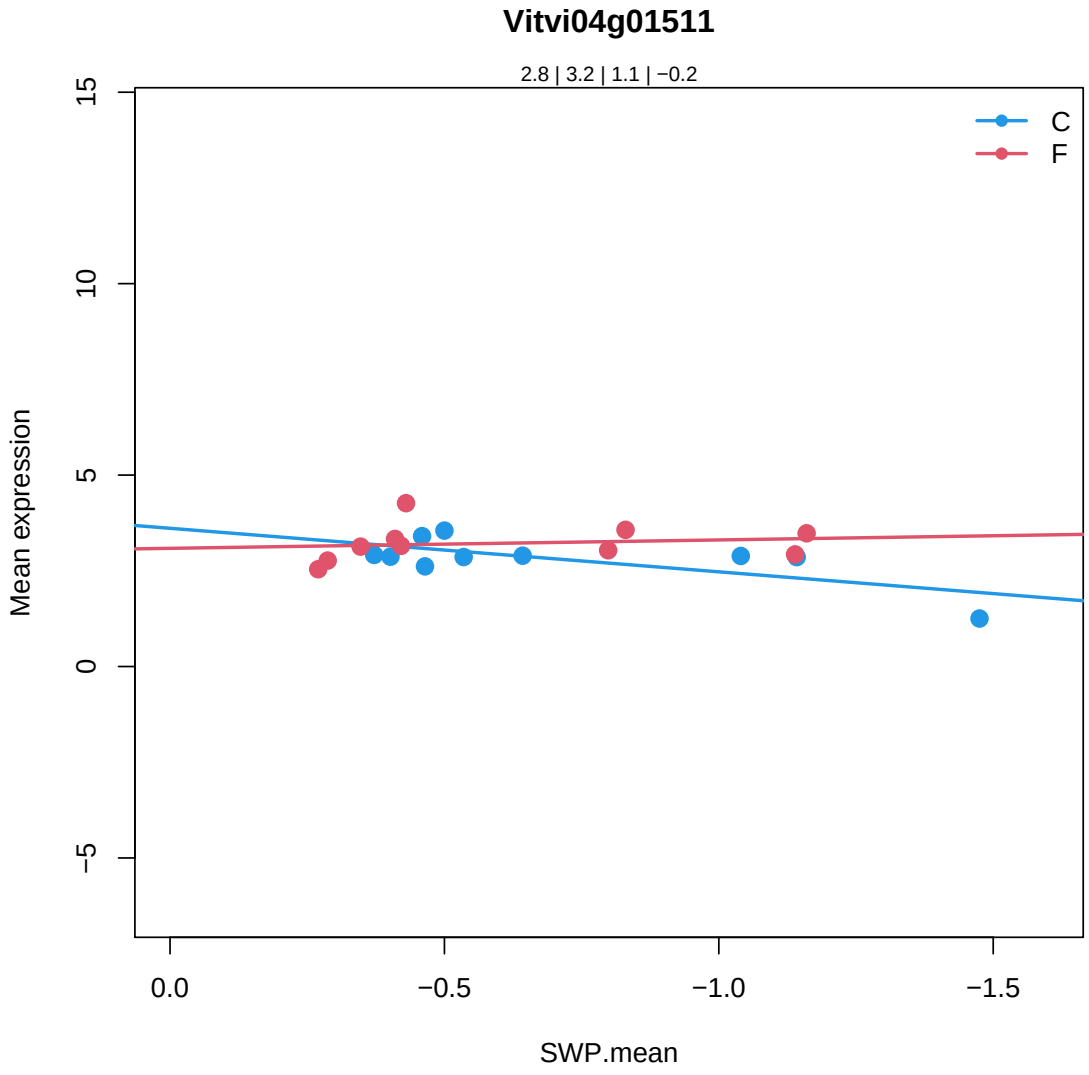
7.6.152 Vitvi04g01511: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01511
        35.2
        not assigned.unknown
        NAC domain containing protein 36 |
        Chr2:7407123-7408120 FORWARD LENGTH=276 |
        201606
```

Coefficients for Vitvi04g01511.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.810575	1.489511e-14	***	2.448568e-14	***
SlopeC	1.137279	0.01459268	*	0.3359386	
MeanF-MeanC	0.4096464	0.07338146	.	0.3042207	
SlopeF-SlopeC	-1.356108	0.04503661	*	0.9999488	



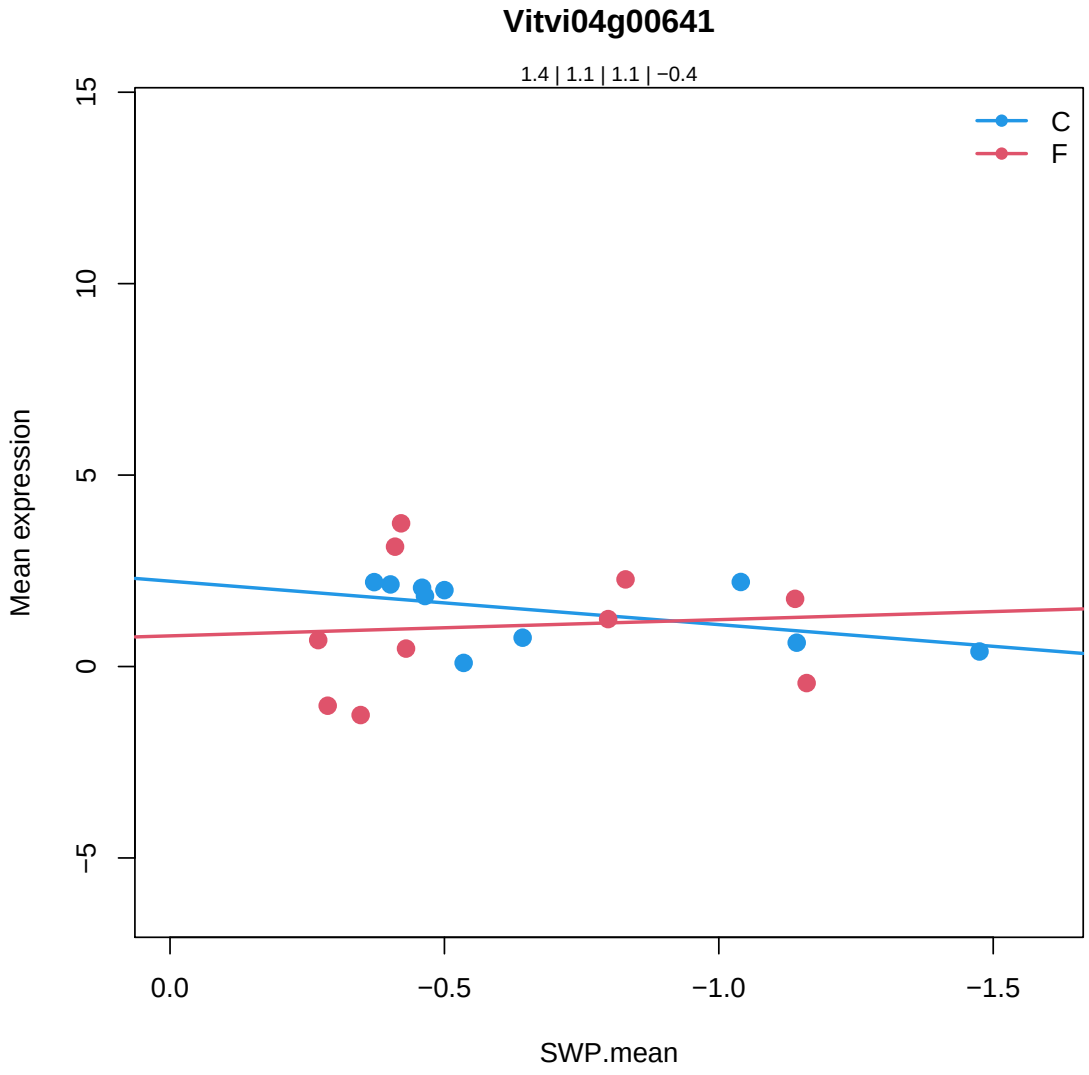
7.6.153 Vitvi04g00641: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00641
        27.3.99
        RNA.regulation of transcription.unclassified
        Eukaryotic aspartyl protease family protein |
        Chr5:3403331-3405331 REVERSE LENGTH=474 |
        201606
```

Coefficients for Vitvi04g00641.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.431058	0.001274906	**	0.001377676	**
SlopeC	1.134245	0.3028577		0.7878153	
MeanF-MeanC	-0.3726915	0.5022871		0.8077506	
SlopeF-SlopeC	-1.557792	0.340841		0.9999488	



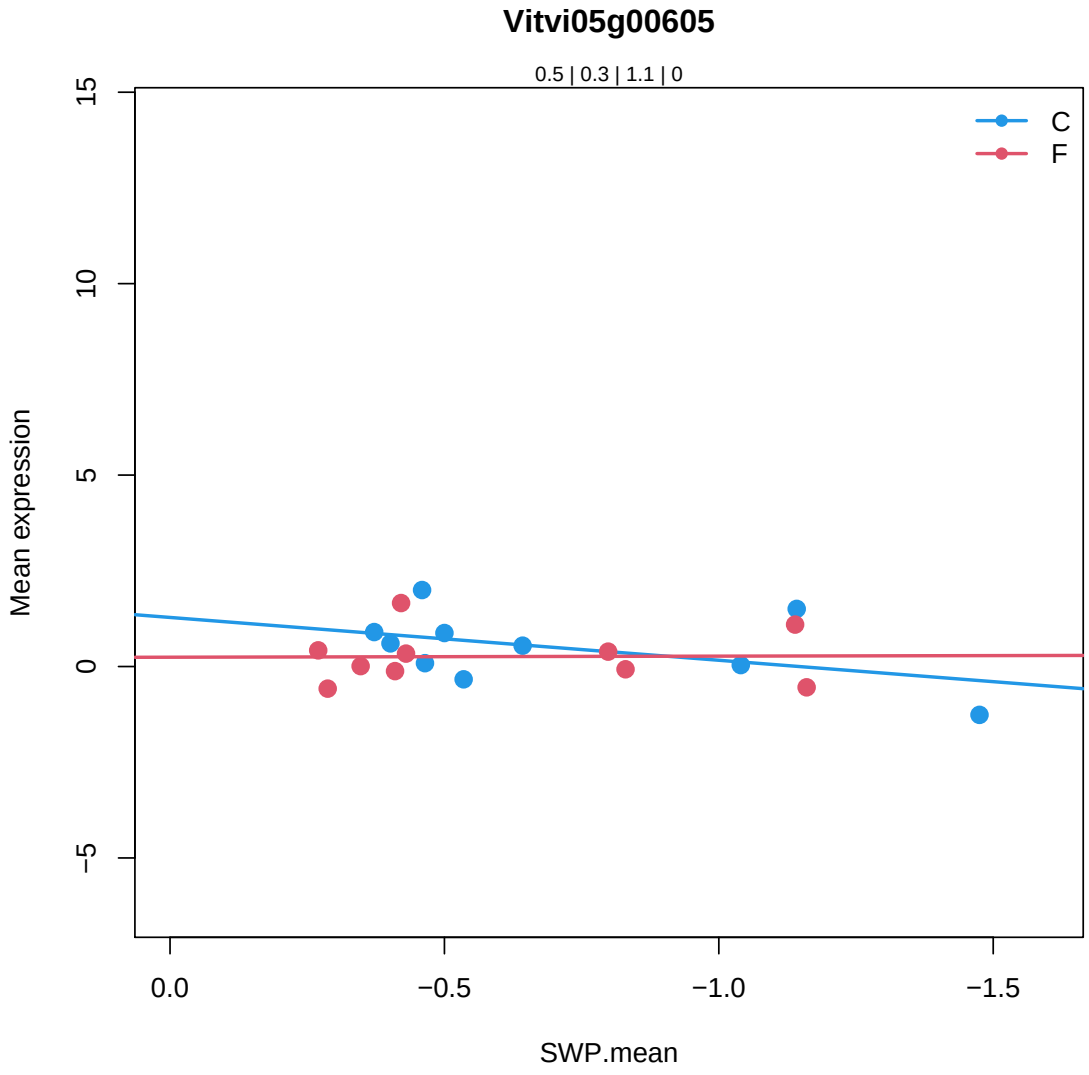
7.6.154 Vitvi05g00605: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00605
        30.3
        signalling.calcium
        calmodulin 8 |
        Chr4:8397800-8398695 FORWARD LENGTH=121 |
        201606
```

Coefficients for Vitvi05g00605.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4952409	0.04675441	*	0.04873022	*
SlopeC	1.118037	0.1012669		0.6135572	
MeanF-MeanC	-0.2355964	0.4854565		0.7977697	
SlopeF-SlopeC	-1.145998	0.2512285		0.9999488	



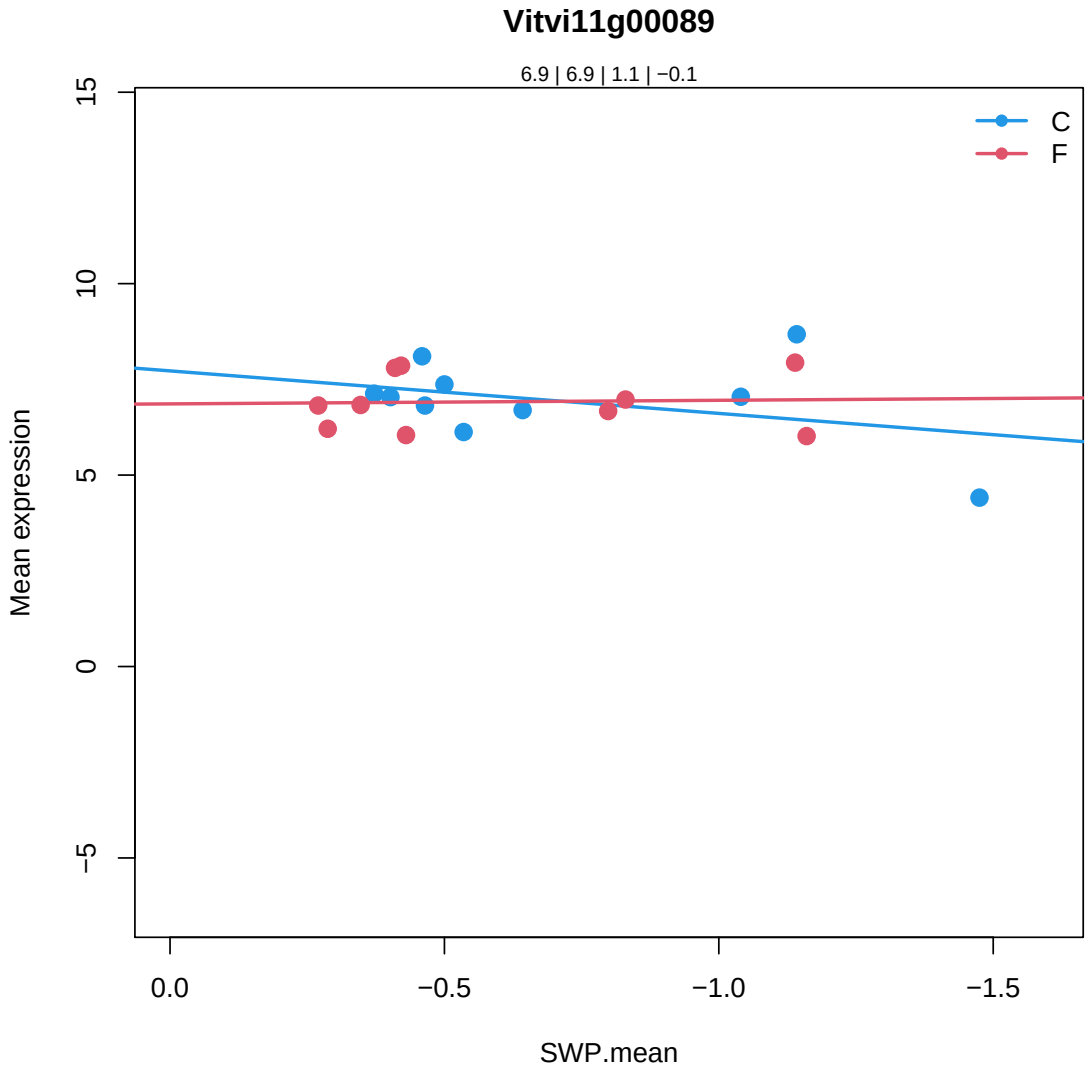
7.6.155 Vitvi11g00089: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00089
        35.2
        not assigned.unknown
        germin 3 |
        Chr5:6975315-6975950 REVERSE LENGTH=211 |
        201606
```

Coefficients for Vitvi11g00089.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.940375	2.079636e-17	***	5.142409e-17	***
SlopeC	1.110072	0.1623773		0.6917183	
MeanF-MeanC	-0.02424436	0.9510044		0.987972	
SlopeF-SlopeC	-1.203617	0.3035794		0.9999488	



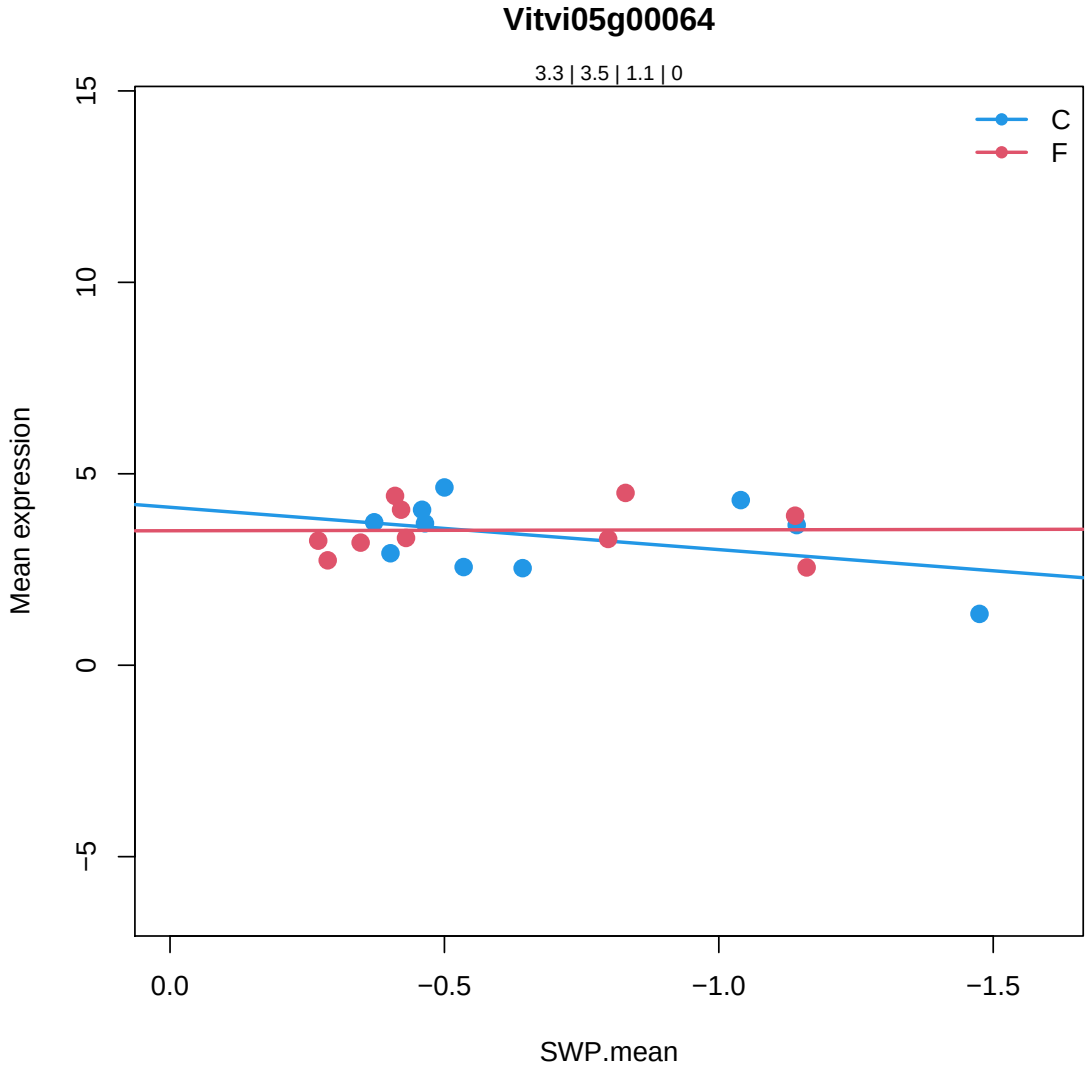
7.6.156 Vitvi05g00064: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00064
        35.2
        not assigned.unknown
        Heavy-metal associated domain protein IPR006121 Heavy metal transport_
```

Coefficients for Vitvi05g00064.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.347822	4.169479e-12	***	5.783691e-12	***
SlopeC	1.10561	0.1173629		0.6341652	
MeanF-MeanC	0.1782371	0.6101337		0.8639593	
SlopeF-SlopeC	-1.1285	0.2755478		0.9999488	



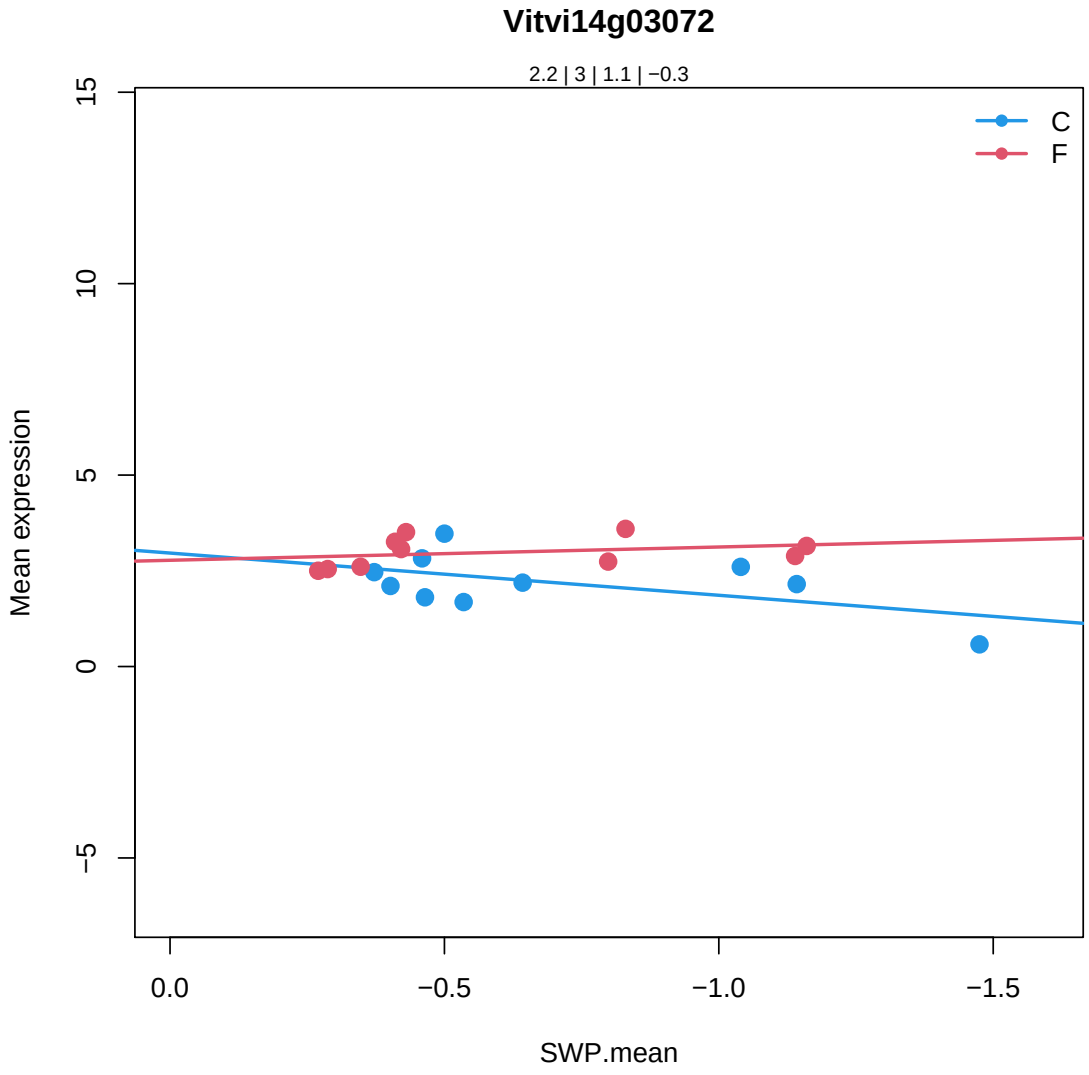
7.6.157 Vitvi14g03072: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g03072
        35.2
        not assigned.unknown
        Leucine-rich repeat receptor-like protein kinase family protein |
        Chr4:5637467-5640496 REVERSE LENGTH=1009 |
        201606
```

Coefficients for Vitvi14g03072.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.187882	1.728867e-11	***	2.335702e-11	***
SlopeC	1.102712	0.03076822	*	0.4322019	
MeanF-MeanC	0.7979875	0.003406508	**	0.03389164	*
SlopeF-SlopeC	-1.449372	0.05364229	.	0.9999488	



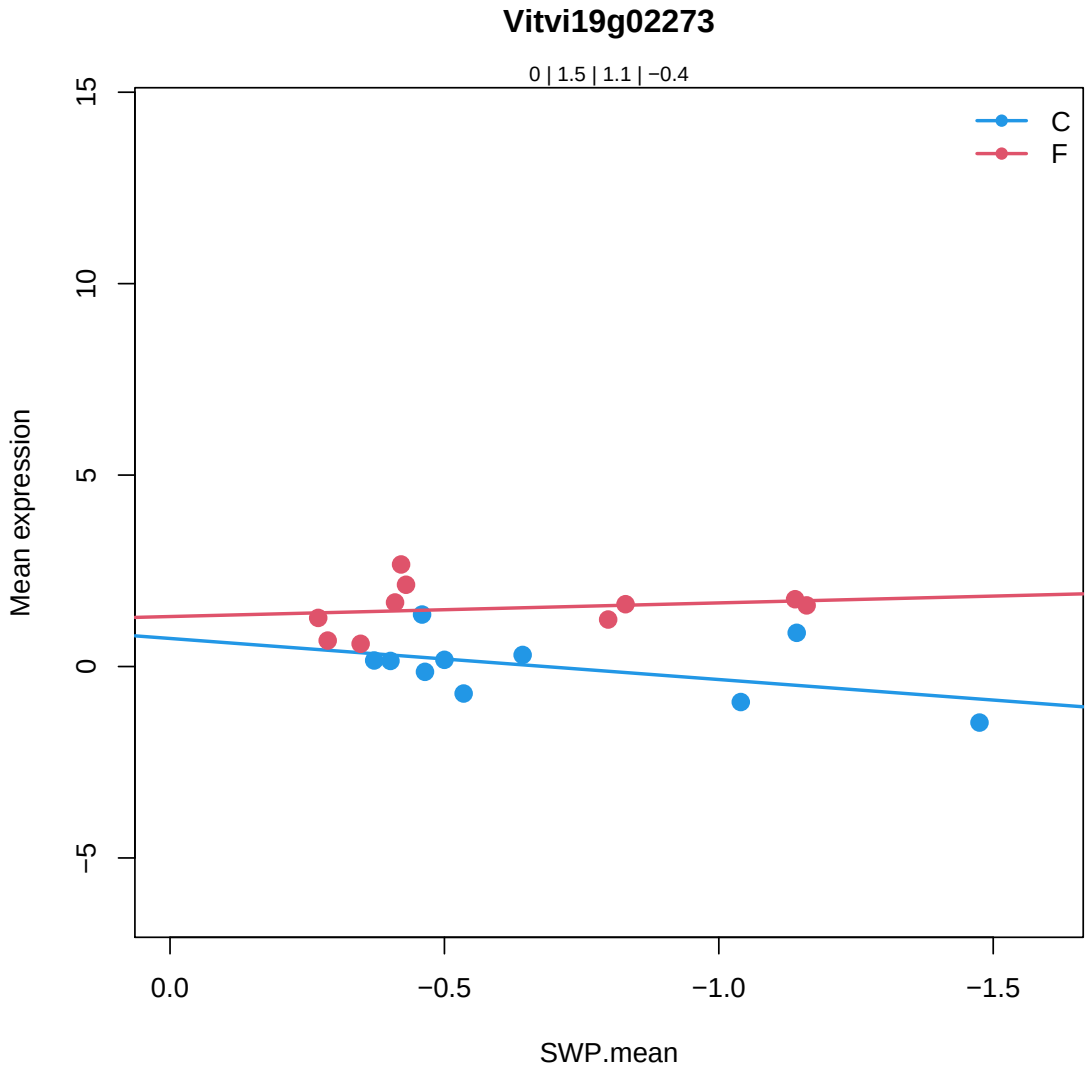
7.6.158 Vitvi19g02273: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g02273
        27.3.27
        RNA.regulation of transcription.NAC domain transcription factor family
        NAC (No Apical Meristem) domain transcriptional regulator superfamily
        Chr3:4109417-4110648 FORWARD LENGTH=303 |
        201606
```

Coefficients for Vitvi19g02273.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.0218323	0.9183094		0.9199995	
SlopeC	1.072494	0.08081368	.	0.5763978	
MeanF-MeanC	1.544091	3.597609e-05	***	0.0007467006	***
SlopeF-SlopeC	-1.428718	0.1155775		0.9999488	



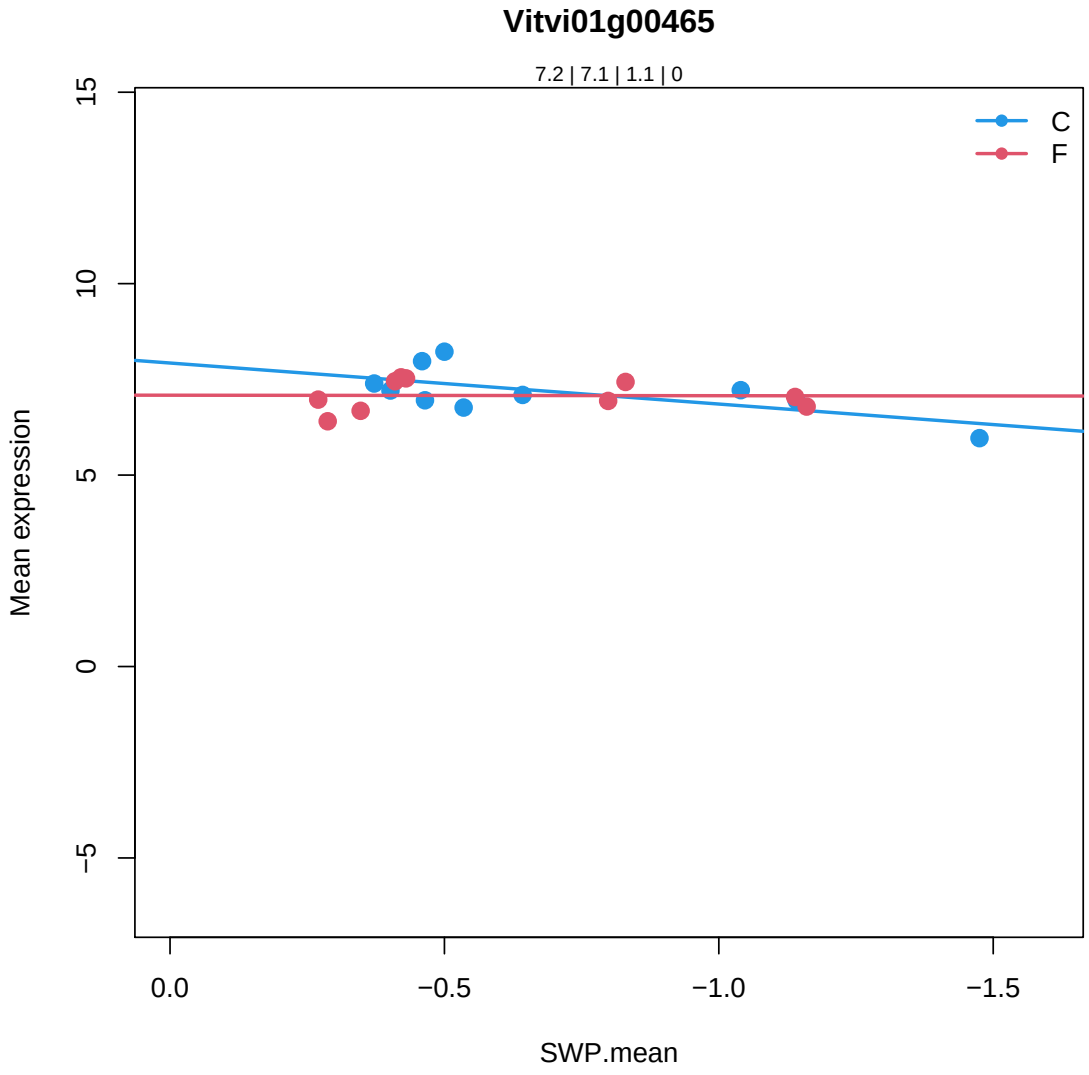
7.6.159 Vitvi01g00465: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00465
        35.1
        not assigned.no ontology
        PLANT CADMIUM RESISTANCE 2 |
        Chr1:5128591-5129458 REVERSE LENGTH=152 |
        201606
```

Coefficients for Vitvi01g00465.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.173162	2.502556e-23	***	6.421542e-22	***
SlopeC	1.071557	0.01723769	*	0.3551322	
MeanF-MeanC	-0.09506329	0.6568551		0.8855638	
SlopeF-SlopeC	-1.058668	0.1010389		0.9999488	



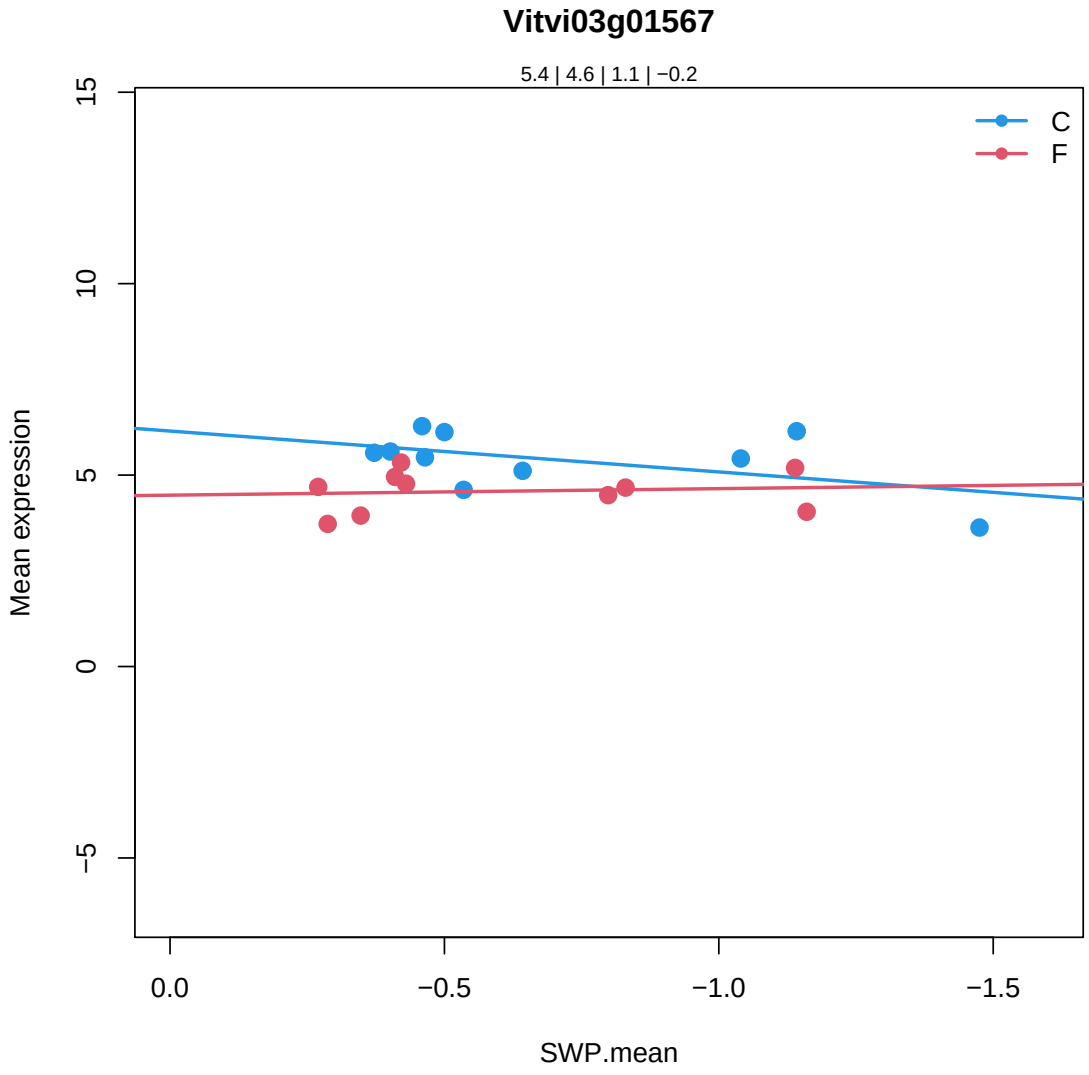
7.6.160 Vitvi03g01567: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g01567
        35.1
        not assigned.no ontology
        PLAC8 family protein |
        Chr3:6333048-6333948 REVERSE LENGTH=184 |
        201606
```

Coefficients for Vitvi03g01567.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.39927	2.78554e-18	***	8.439119e-18	***
SlopeC	1.067886	0.06182326	.	0.5446524	
MeanF-MeanC	-0.8205354	0.007055824	**	0.05870237	.
SlopeF-SlopeC	-1.238272	0.1393591		0.9999488	



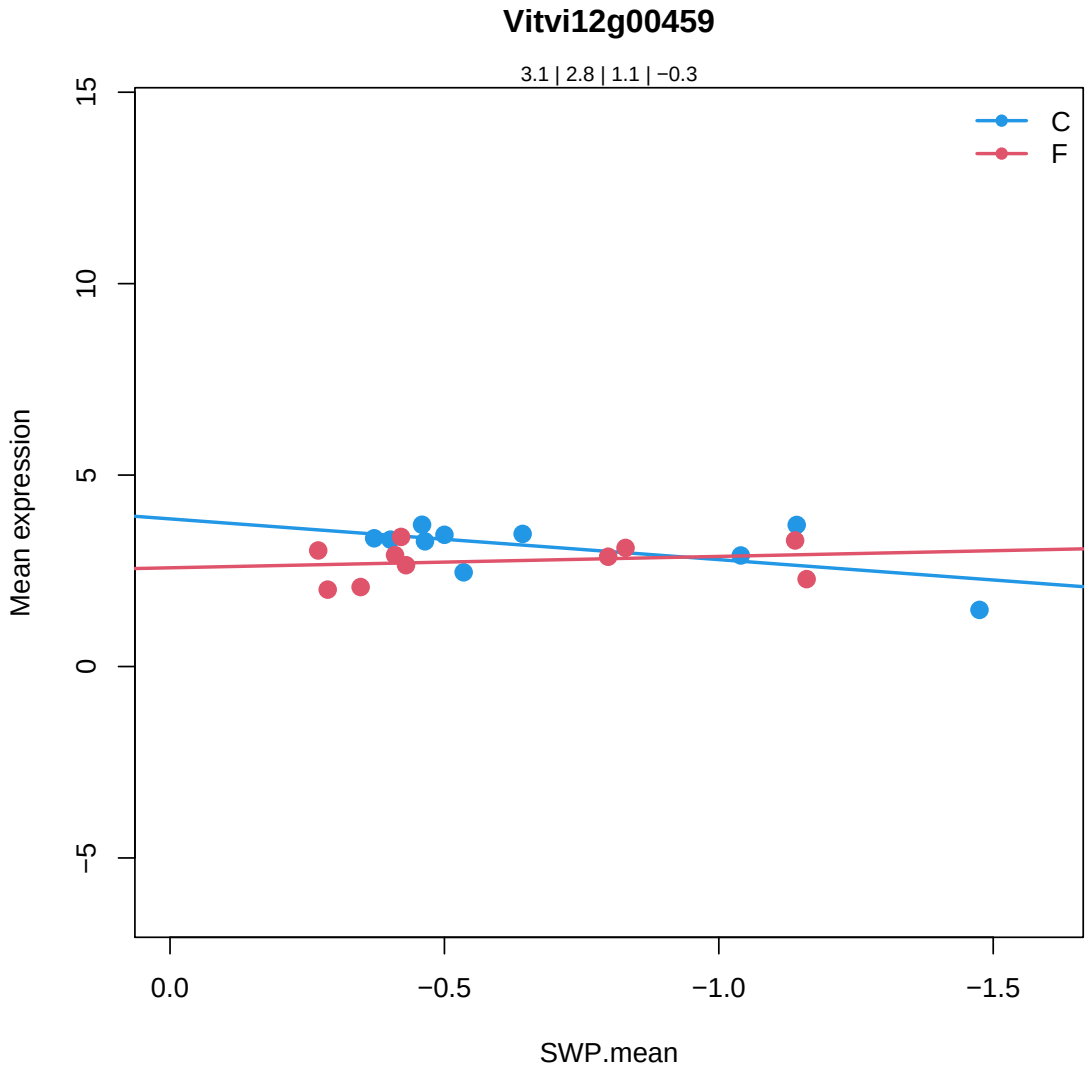
7.6.161 Vitvi12g00459: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00459
        35.1
        not assigned.no ontology
        transferases%2C transferring glycosyl groups |
        Chr2:1590341-1592667 REVERSE LENGTH=460 |
        201606
```

Coefficients for Vitvi12g00459.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.107542	1.258373e-14	***	2.082079e-14	***
SlopeC	1.063977	0.03384457	*	0.4433084	
MeanF-MeanC	-0.3480669	0.1590786		0.4818855	
SlopeF-SlopeC	-1.361565	0.0644845	.	0.9999488	



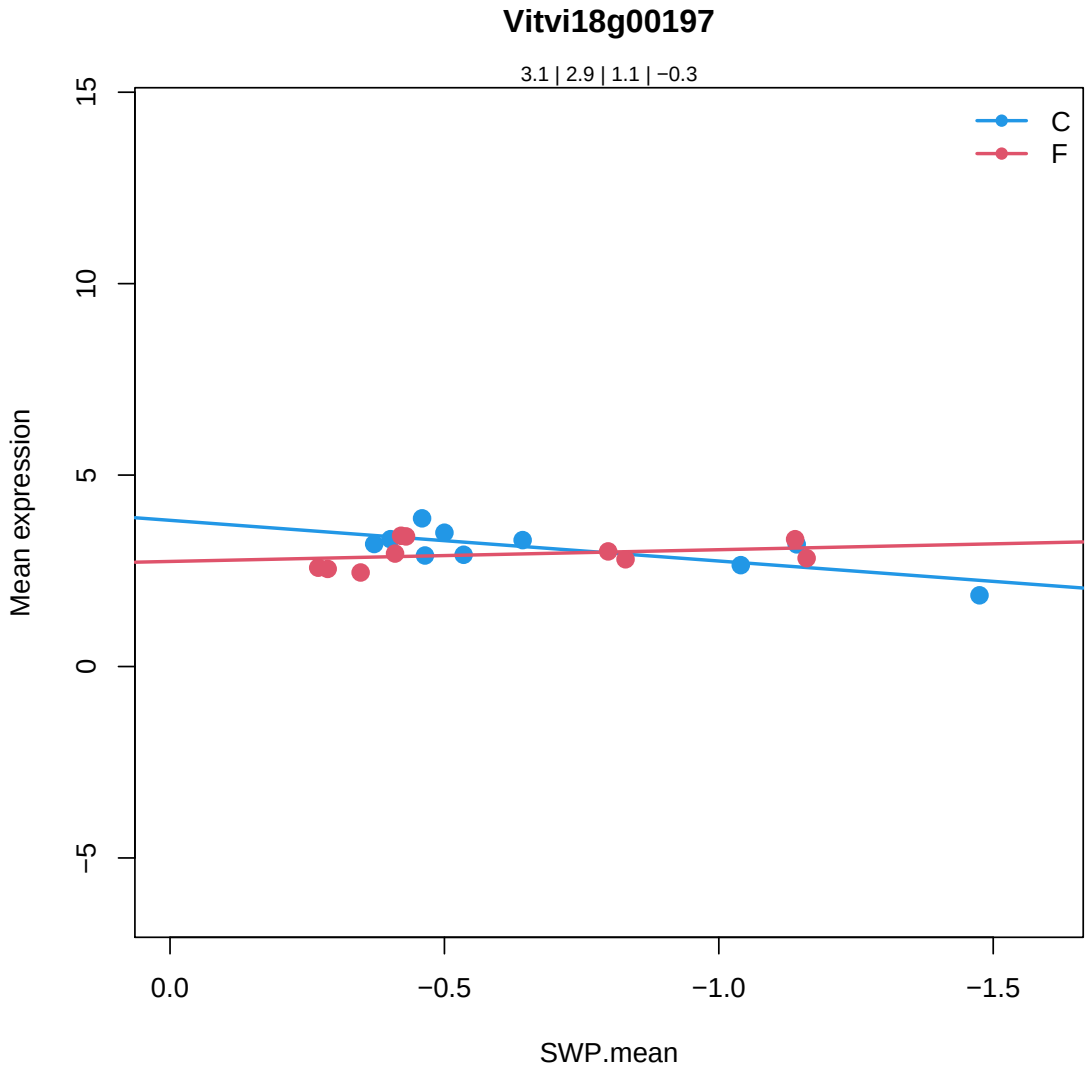
7.6.162 Vitvi18g00197: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00197
        30.2.25
        signalling.receptor kinases.wall associated kinase
        cell wall-associated kinase |
        Chr1:7439512-7441892 FORWARD LENGTH=735 |
        201606
```

Coefficients for Vitvi18g00197.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.070672	6.266222e-17	***	1.412866e-16	***
SlopeC	1.062898	0.007211103	**	0.2775469	
MeanF-MeanC	-0.1396938	0.4510447		0.778837	
SlopeF-SlopeC	-1.369316	0.01767425	*	0.9999488	



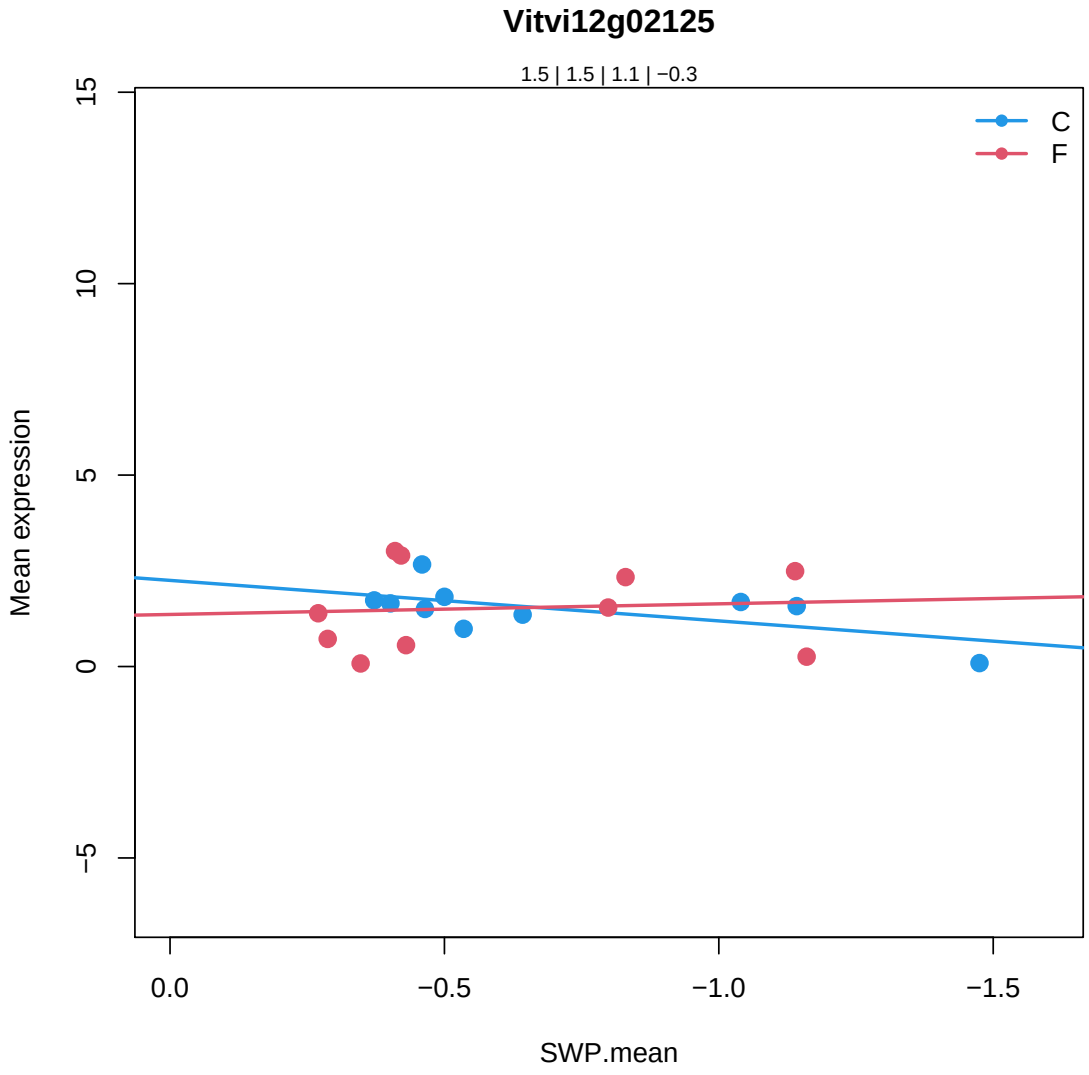
7.6.163 Vitvi12g02125: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02125
        34.13
        transport.peptides and oligopeptides
        Major facilitator superfamily protein |
        Chr1:12127712-12130327 REVERSE LENGTH=601 |
        201606
```

Coefficients for Vitvi12g02125.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.505433	9.333226e-06	***	1.054928e-05	***
SlopeC	1.057994	0.1598396		0.6889929	
MeanF-MeanC	0.02321941	0.9504533		0.9878929	
SlopeF-SlopeC	-1.335629	0.2301634		0.9999488	



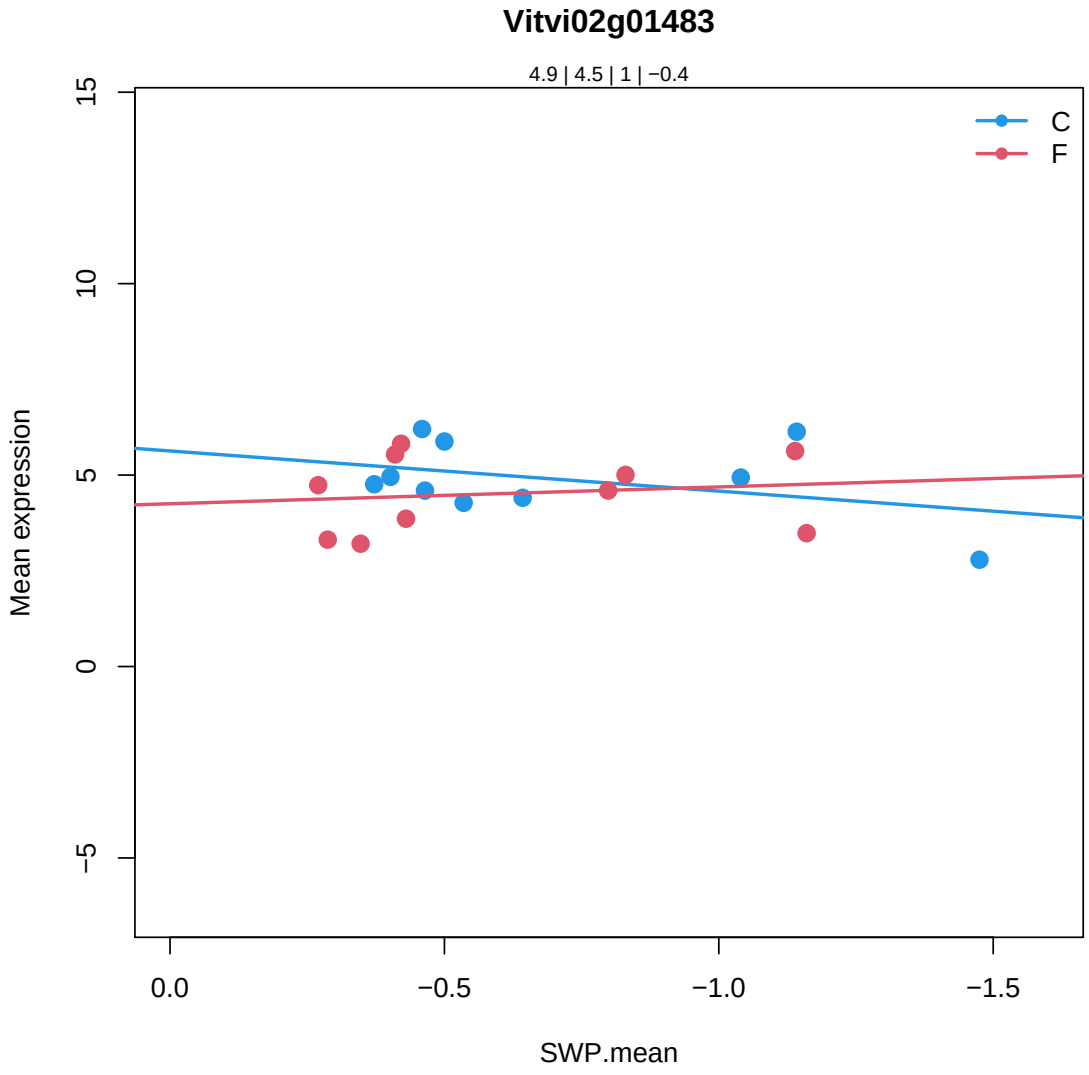
7.6.164 Vitvi02g01483: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g01483
        28.1
        DNA.synthesis/chromatin structure
        myo-inositol polyphosphate 5-phosphatase 2 |
        Chr4:9991492-9994099 REVERSE LENGTH=581 |
        201606
```

Coefficients for Vitvi02g01483.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.892658	7.1738e-14	***	1.114267e-13	***
SlopeC	1.04799	0.2071822		0.7302381	
MeanF-MeanC	-0.3740519	0.3712552		0.7253777	
SlopeF-SlopeC	-1.486944	0.2284098		0.9999488	



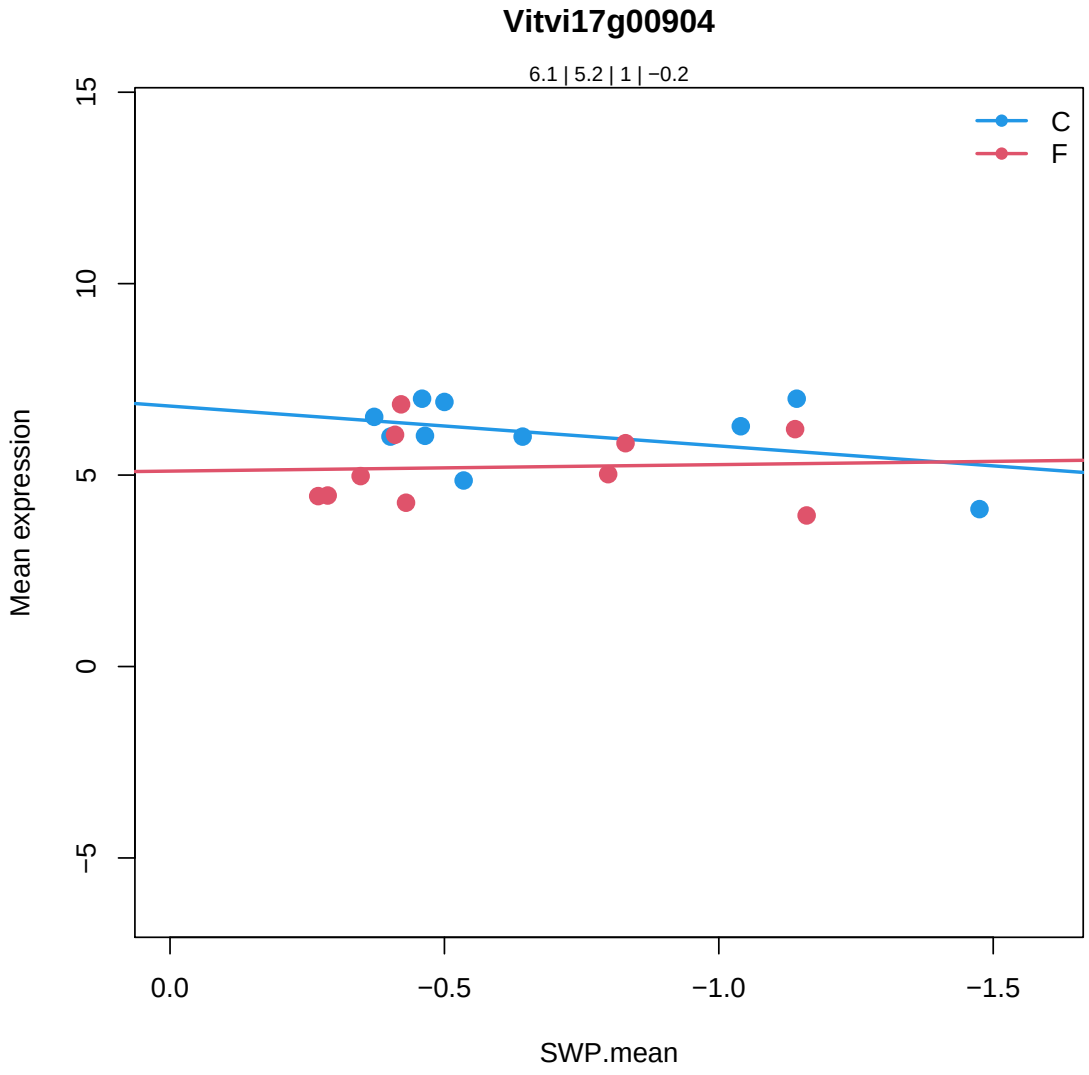
7.6.165 Vitvi17g00904: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00904
        15.1
        metal handling.acquisition
        ferric reduction oxidase 8 |
        Chr5:20415832-20418582 FORWARD LENGTH=728 |
        201606
```

Coefficients for Vitvi17g00904.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.070015	3.316645e-16	***	6.636416e-16	***
SlopeC	1.041051	0.1888843		0.7197362	
MeanF-MeanC	-0.8631611	0.03782888	*	0.1984129	
SlopeF-SlopeC	-1.210481	0.300875		0.9999488	



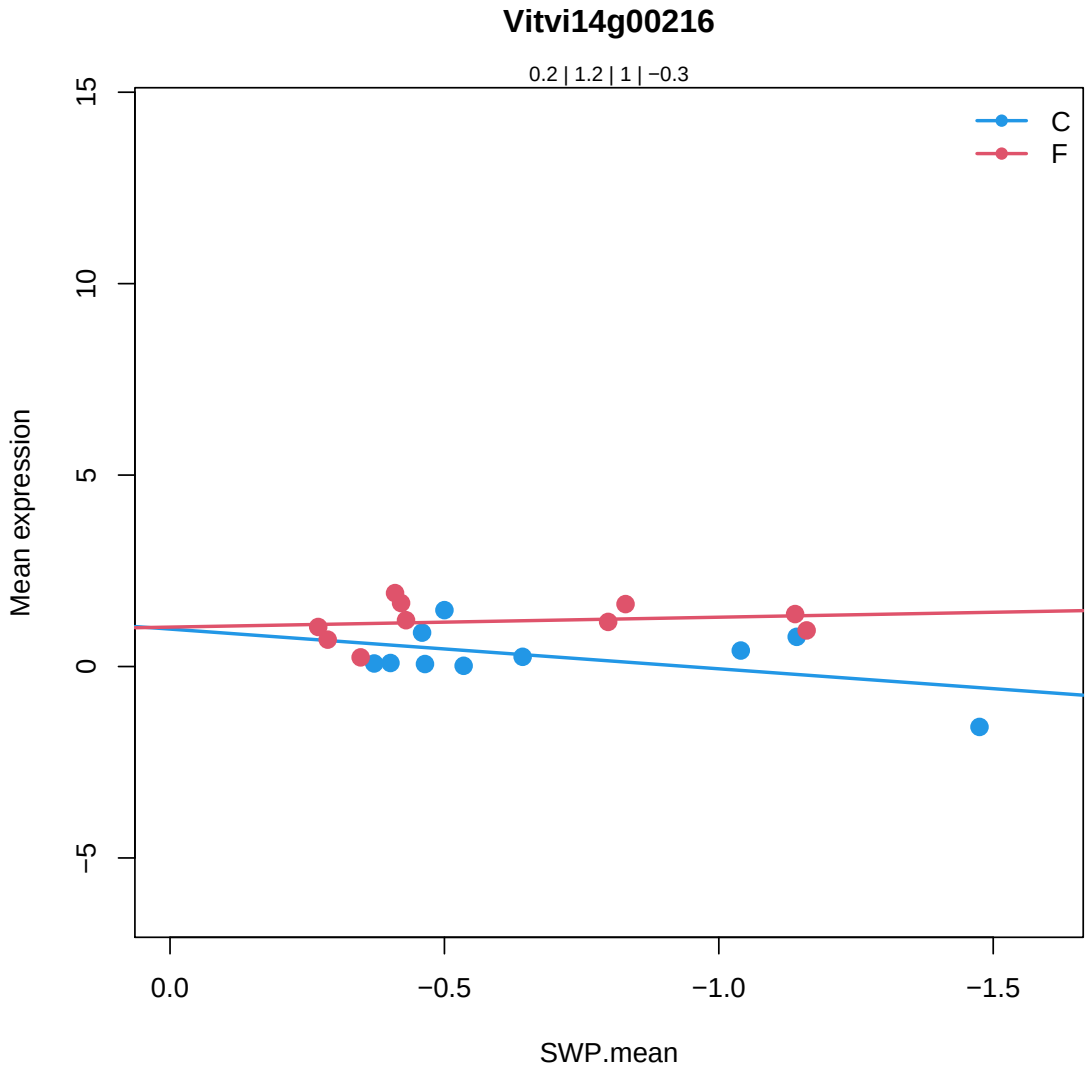
7.6.166 Vitvi14g00216: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g00216
        29.2.2.3.3
        protein.synthesis.ribosome biogenesis.pre-rRNA processing and modifica
        S-adenosyl-L-methionine-dependent methyltransferase |
        Chr3:1546585-1547976 REVERSE LENGTH=463 |
        201606
```

Coefficients for Vitvi14g00216.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.2480844	0.2052861		0.2104076	
SlopeC	1.037444	0.0626849	.	0.5471512	
MeanF-MeanC	0.938472	0.00211149	**	0.02297168	*
SlopeF-SlopeC	-1.296069	0.1139072		0.9999488	



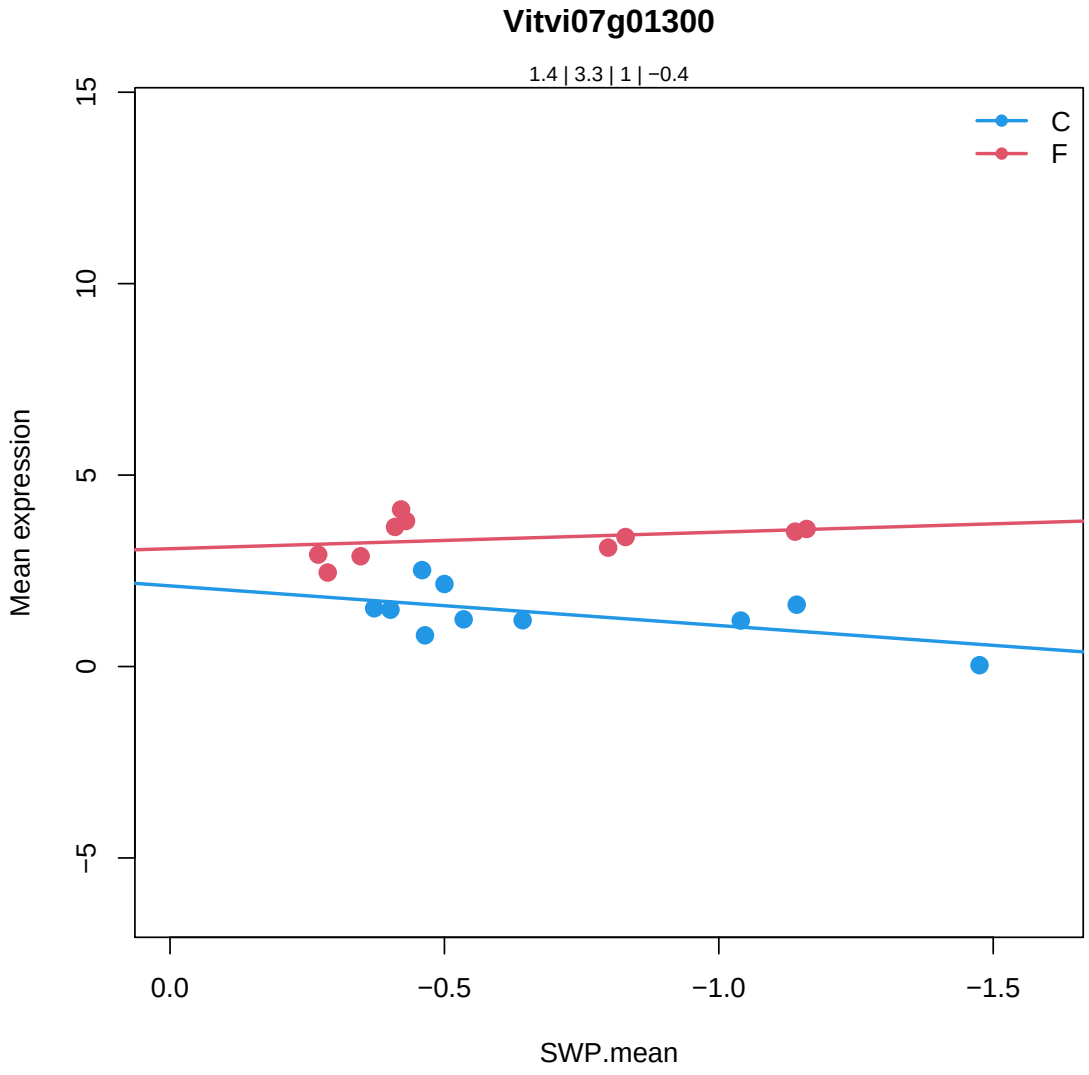
7.6.167 Vitvi07g01300: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01300
        26.8
        misc.nitrilases, nitrile lyases, berberine bridge enzymes, reticuline
        methyl esterase 1 |
        Chr2:10047462-10049248 REVERSE LENGTH=263 |
        201606
```

Coefficients for Vitvi07g01300.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.378154	5.187386e-08	***	6.200293e-08	***
SlopeC	1.03572	0.03867464	*	0.468212	
MeanF-MeanC	1.962676	4.623615e-08	***	2.036796e-06	***
SlopeF-SlopeC	-1.469136	0.04779462	*	0.9999488	



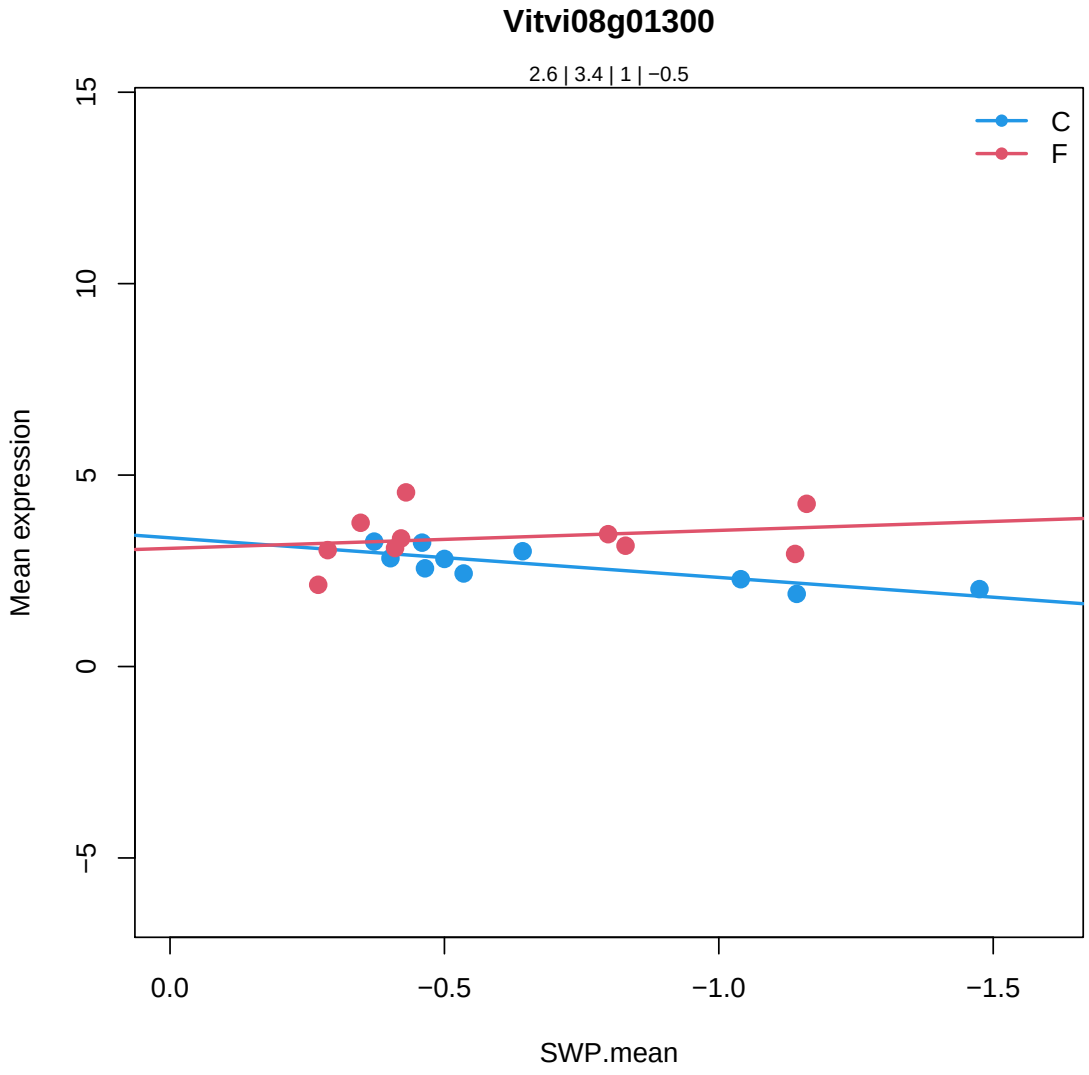
7.6.168 Vitvi08g01300: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01300
        30.1.1
        signalling.in sugar and nutrient physiology.misc
        PAR1 protein |
        Chr3:20014032-20015299 REVERSE LENGTH=183 |
        201606
```

Coefficients for Vitvi08g01300.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.633932	2.942471e-13	***	4.376808e-13	***
SlopeC	1.034343	0.03721453	*	0.4620709	
MeanF-MeanC	0.7377122	0.005129053	**	0.04664501	*
SlopeF-SlopeC	-1.503536	0.04142051	*	0.9999488	



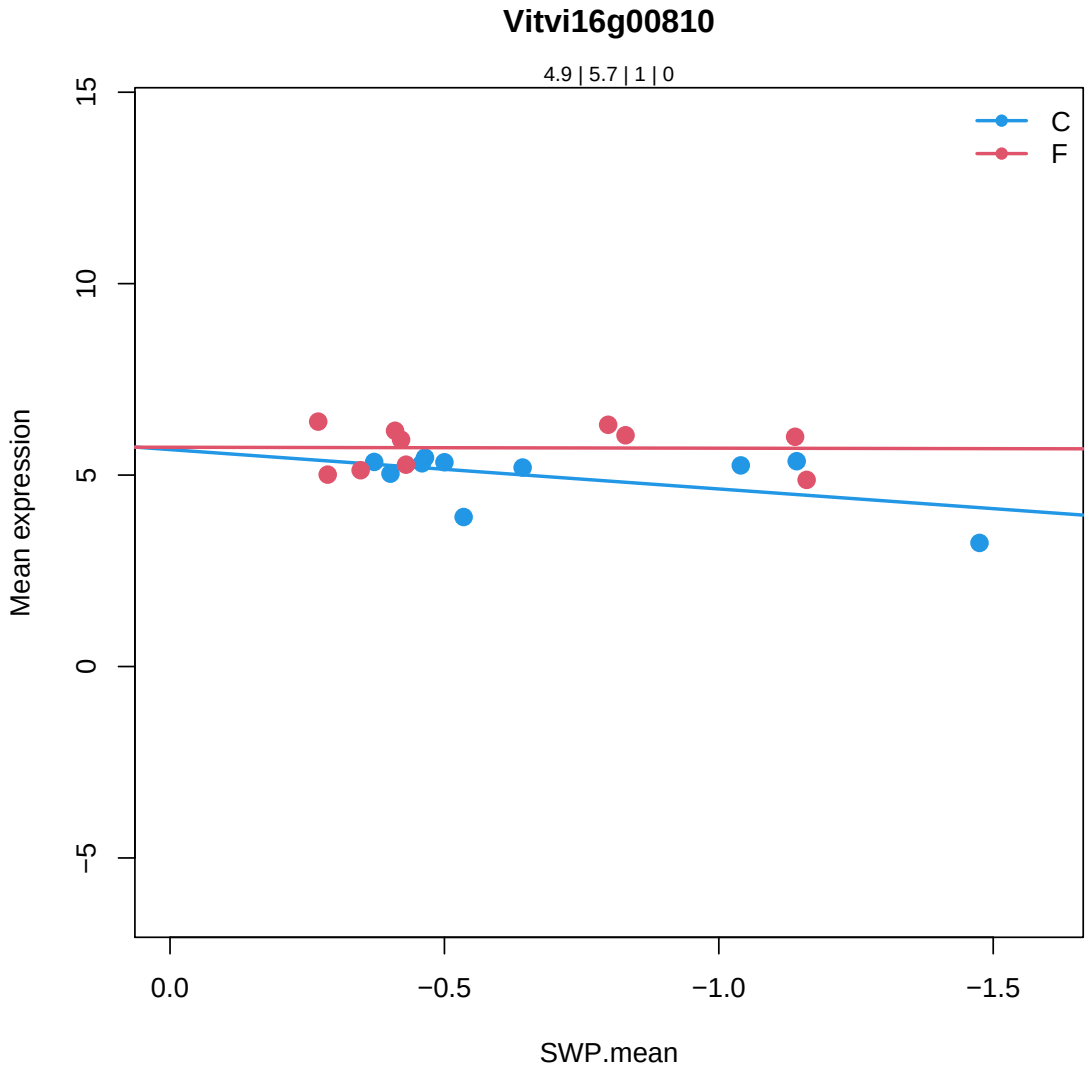
7.6.169 Vitvi16g00810: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g00810
        35.2
        not assigned.unknown
        Protein kinase superfamily protein |
        Chr1:24961634-24963941 REVERSE LENGTH=663 |
        201606
```

Coefficients for Vitvi16g00810.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.942253	1.496776e-17	***	3.80041e-17	***
SlopeC	1.027809	0.06941765	.	0.5582027	
MeanF-MeanC	0.7693895	0.01024916	*	0.07734272	.
SlopeF-SlopeC	-1.003507	0.2234036		0.9999488	



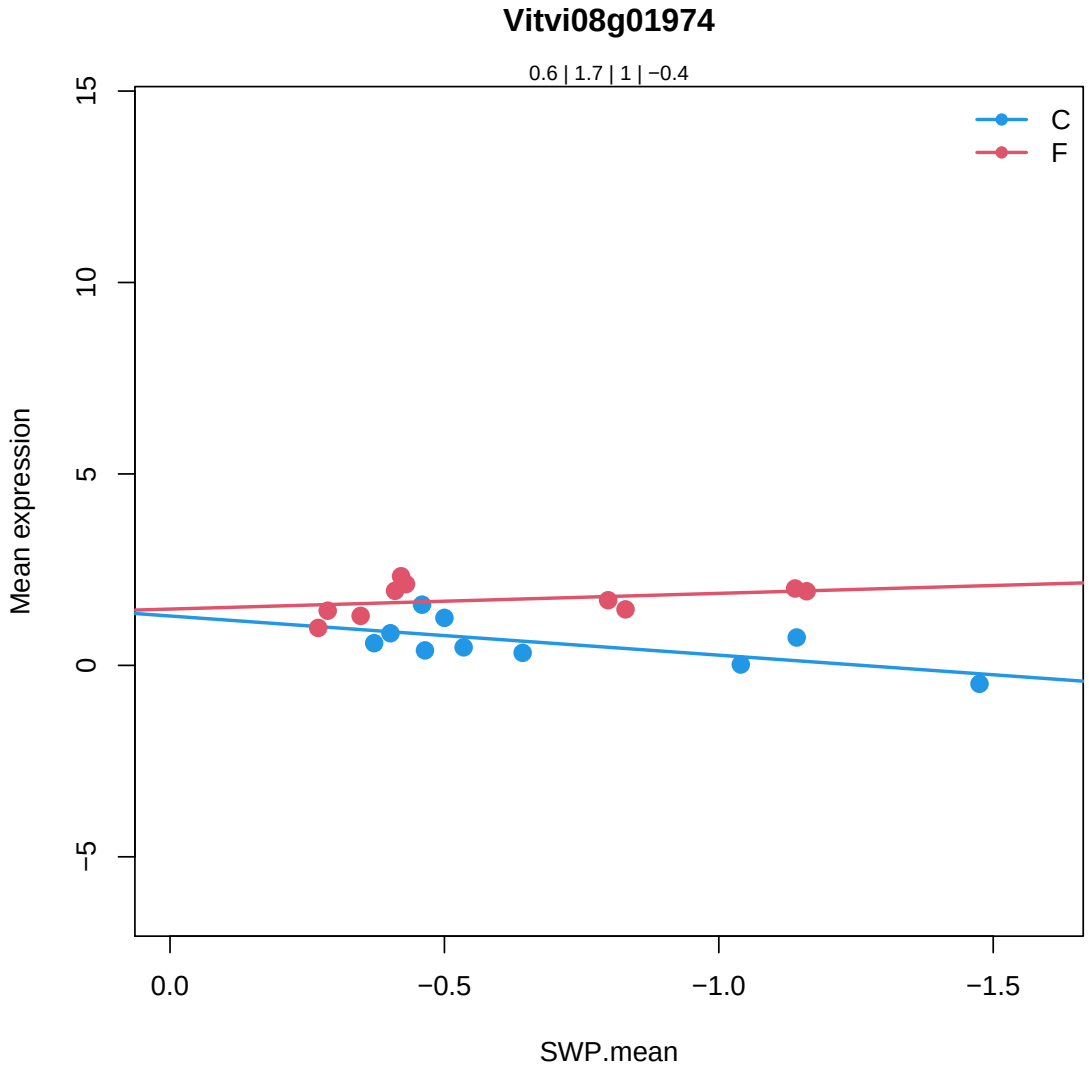
7.6.170 Vitvi08g01974: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01974
        35.2
        not assigned.unknown
        [Sotub10g018190.1.1]: Unknown Protein [Sotub10g018190.1.1]: Unknown Pr
        [stNIB-v1_0012744]
```

Coefficients for Vitvi08g01974.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.5700647	0.0007020877	***	0.0007627929	***
SlopeC	1.0229	0.01846127	*	0.3653003	
MeanF-MeanC	1.150264	1.242824e-05	***	0.0003075181	***
SlopeF-SlopeC	-1.433484	0.02548362	*	0.9999488	



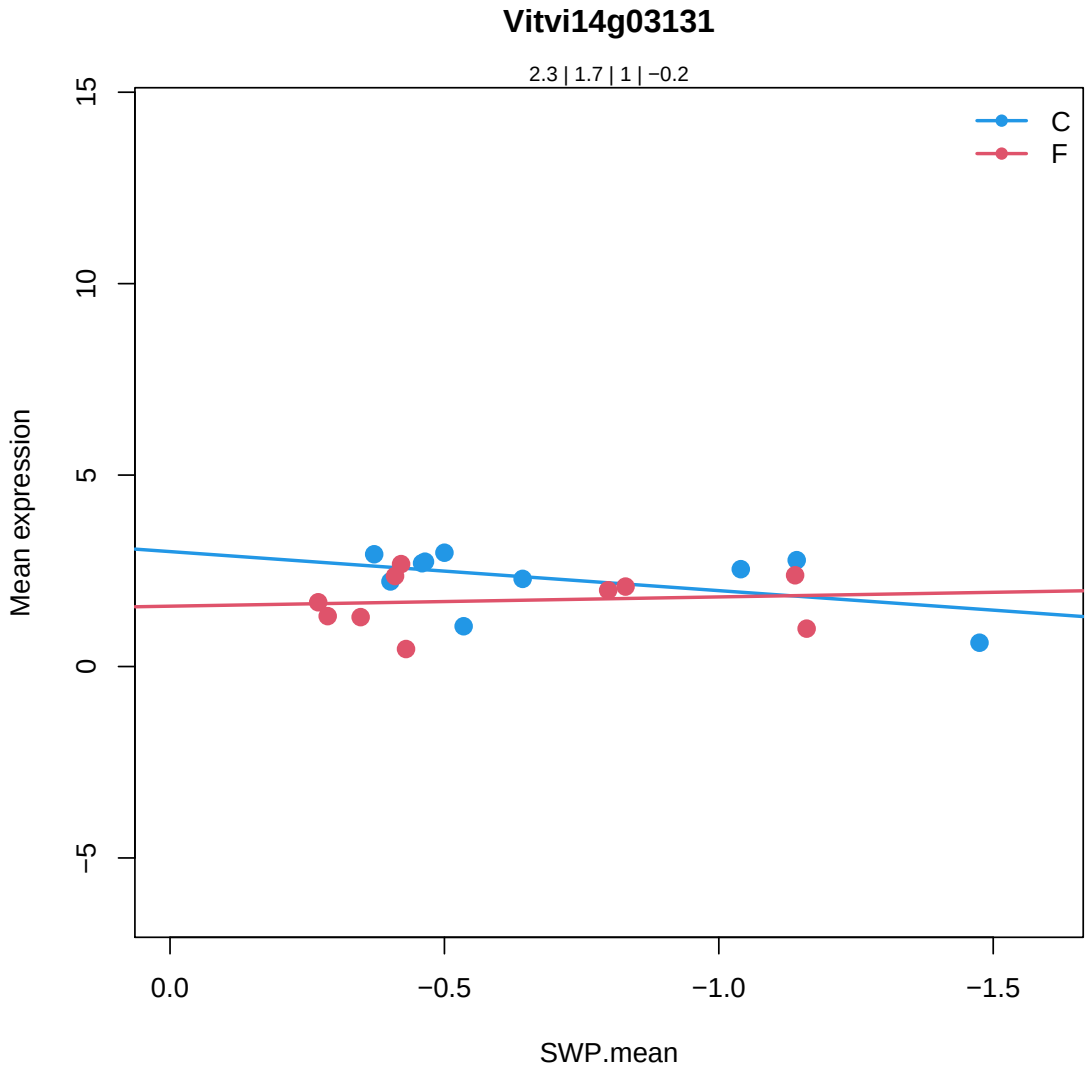
7.6.171 Vitvi14g03131: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g03131
        35.2
        not assigned.unknown
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606
```

Coefficients for Vitvi14g03131.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.284338	6.980034e-10	***	8.848111e-10	***
SlopeC	1.019539	0.1078156		0.6223948	
MeanF-MeanC	-0.5614375	0.08304906	.	0.3265825	
SlopeF-SlopeC	-1.261174	0.1773559		0.9999488	



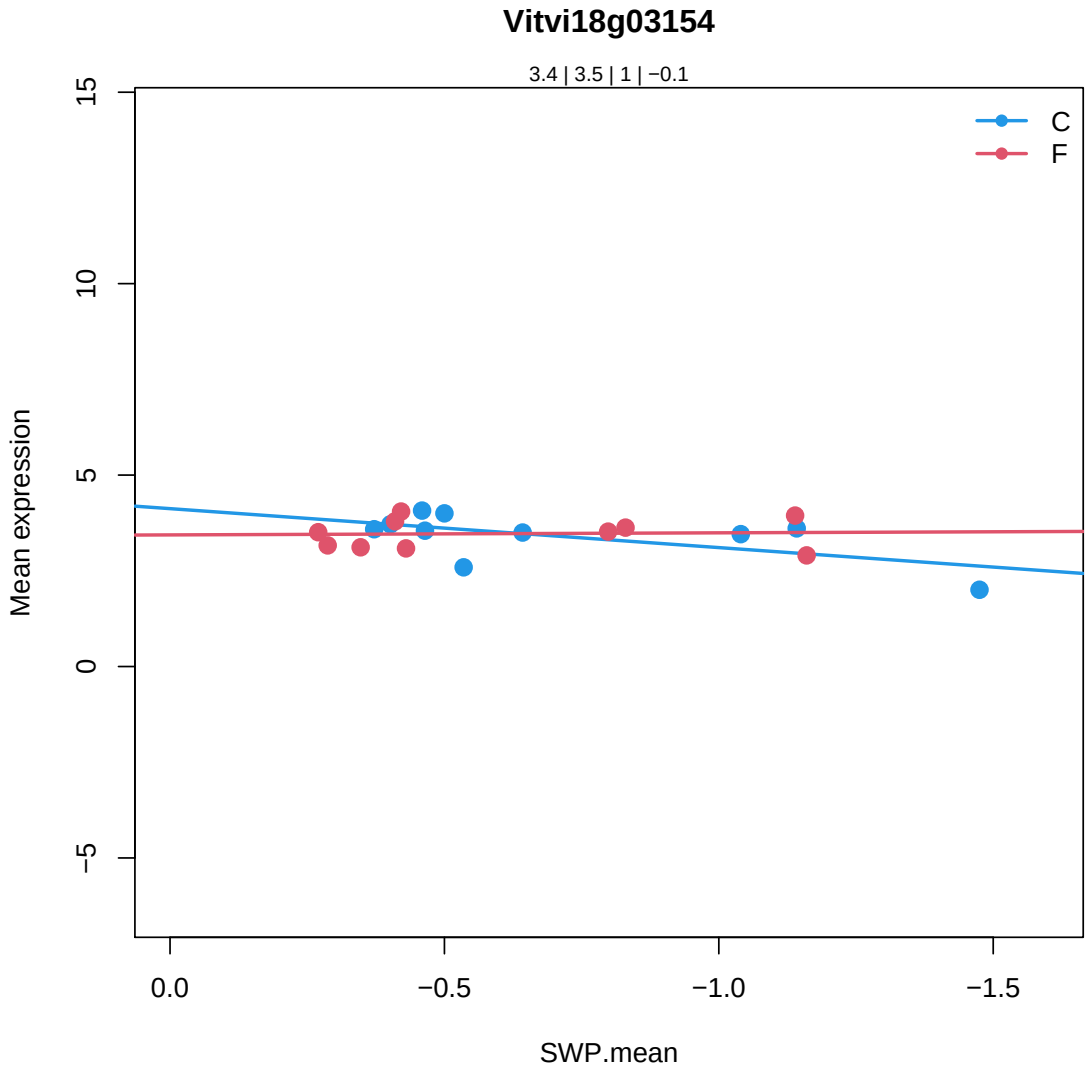
7.6.172 Vitvi18g03154: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g03154
        35.1
        not assigned.no ontology
        Gag-Pol-related retrotransposon family protein |
        Chr3:7363921-7365138 FORWARD LENGTH=405 |
        201606
```

Coefficients for Vitvi18g03154.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.407957	2.371909e-16	***	4.8501e-16	***
SlopeC	1.017218	0.02551558	*	0.4079655	
MeanF-MeanC	0.06254895	0.7743133		0.9355874	
SlopeF-SlopeC	-1.071478	0.1038094		0.9999488	



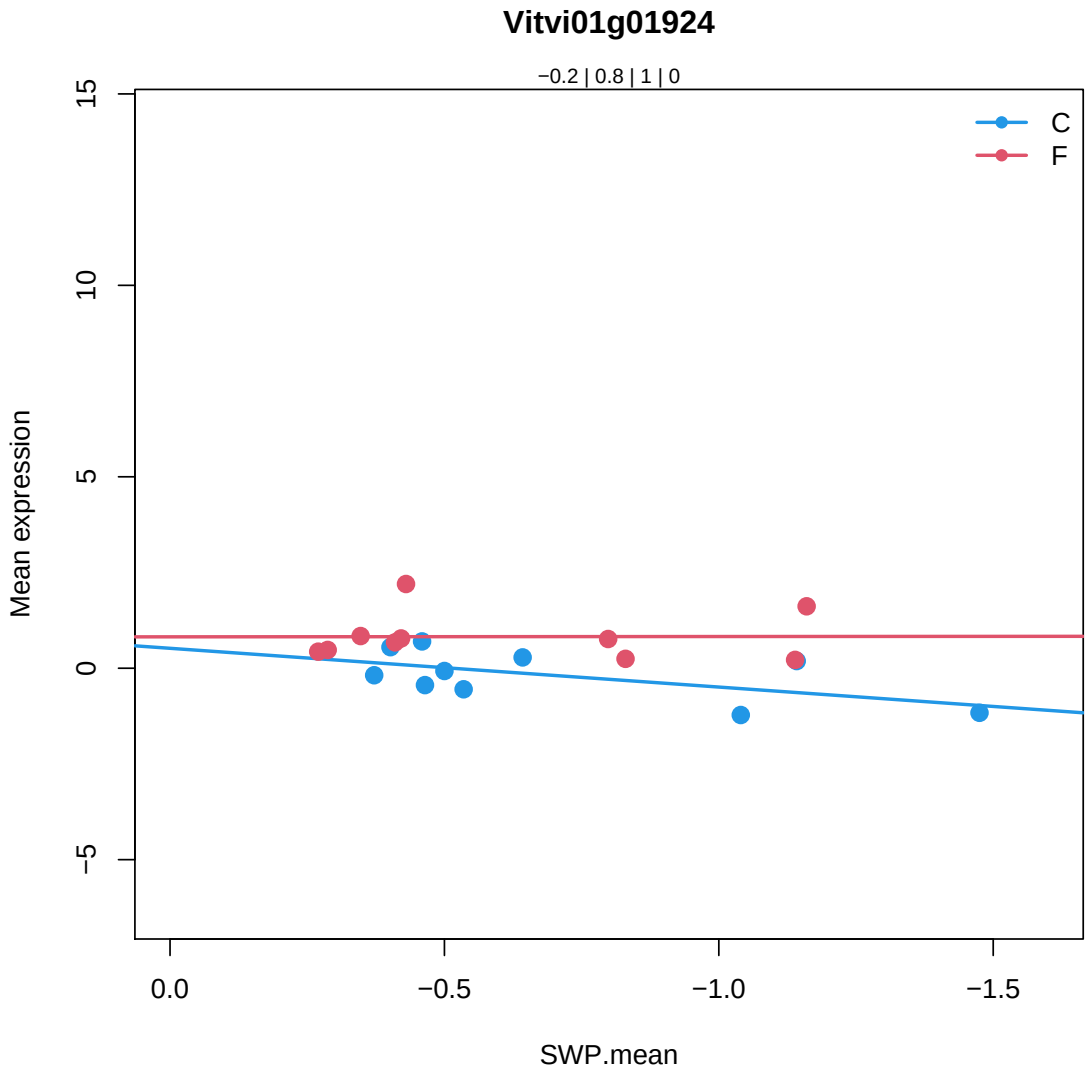
7.6.173 Vitvi01g01924: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01924
        35.2
        not assigned.unknown
        Protein IDA
```

Coefficients for Vitvi01g01924.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	−0.1914909	0.3152675		0.3210173	
SlopeC	1.012496	0.06383187	.	0.5471512	
MeanF−MeanC	1.016005	0.0008846062	***	0.01127355	*
SlopeF−SlopeC	−1.020193	0.1997656		0.9999488	



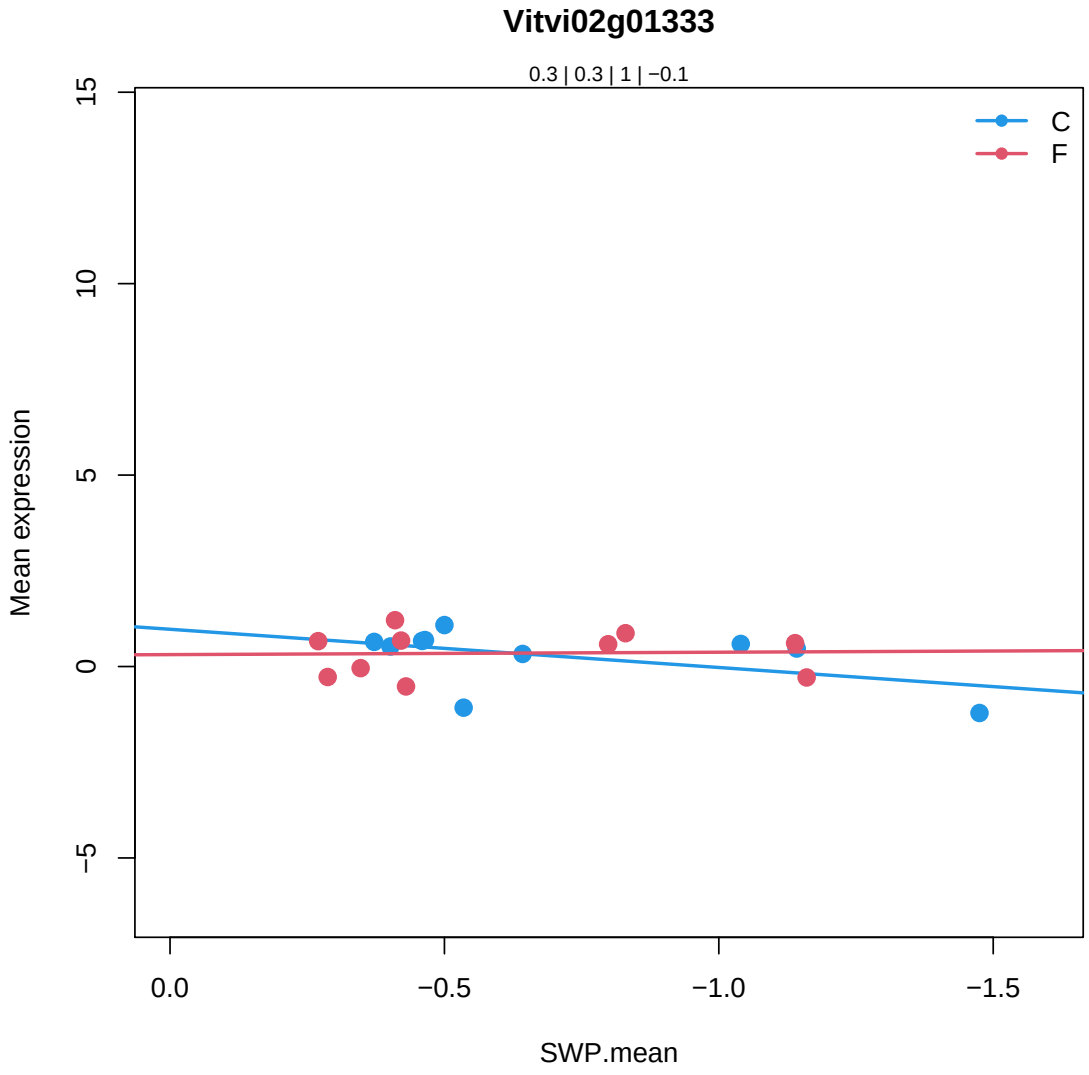
7.6.174 Vitvi02g01333: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g01333
        34.1.1.4
        transport.p- and v-ATPases.H+-transporting two-sector ATPase.subunit E
        vacuolar H+-ATPase subunit E isoform 3 |
        Chr1:23828914-23830002 REVERSE LENGTH=192 |
        201606
```

Coefficients for Vitvi02g01333.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.2707012	0.1859377		0.1907946	
SlopeC	0.9983877	0.08409107	.	0.5839253	
MeanF-MeanC	0.07827092	0.7826237		0.9384607	
SlopeF-SlopeC	-1.061022	0.2096083		0.9999488	



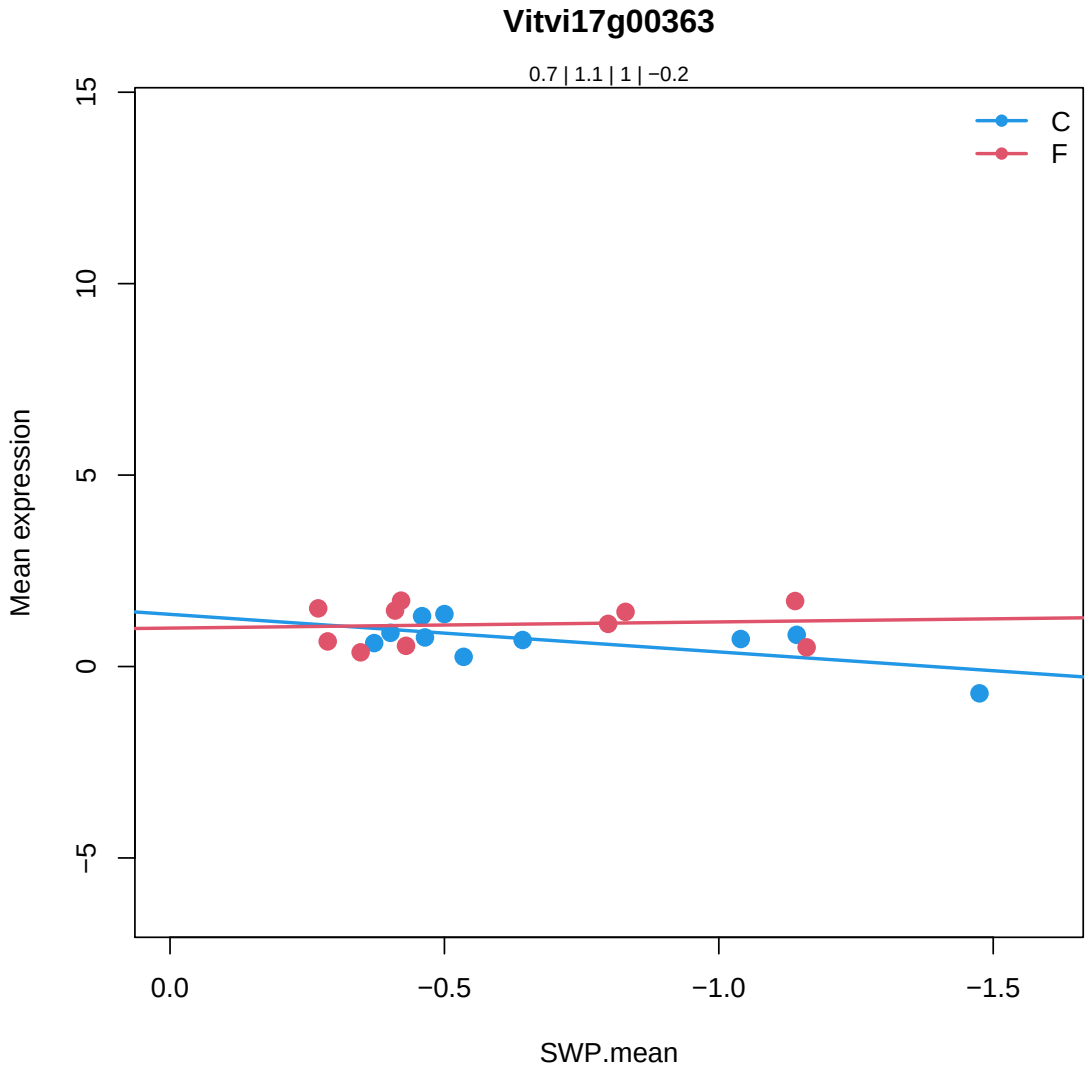
7.6.175 Vitvi17g00363: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00363
        35.2
        not assigned.unknown
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi17g00363.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6723738	0.0004452242	***	0.0004854849	***
SlopeC	0.9817758	0.04101571	*	0.477587	
MeanF-MeanC	0.4295419	0.07499487	.	0.3080226	
SlopeF-SlopeC	-1.143122	0.1034182		0.9999488	



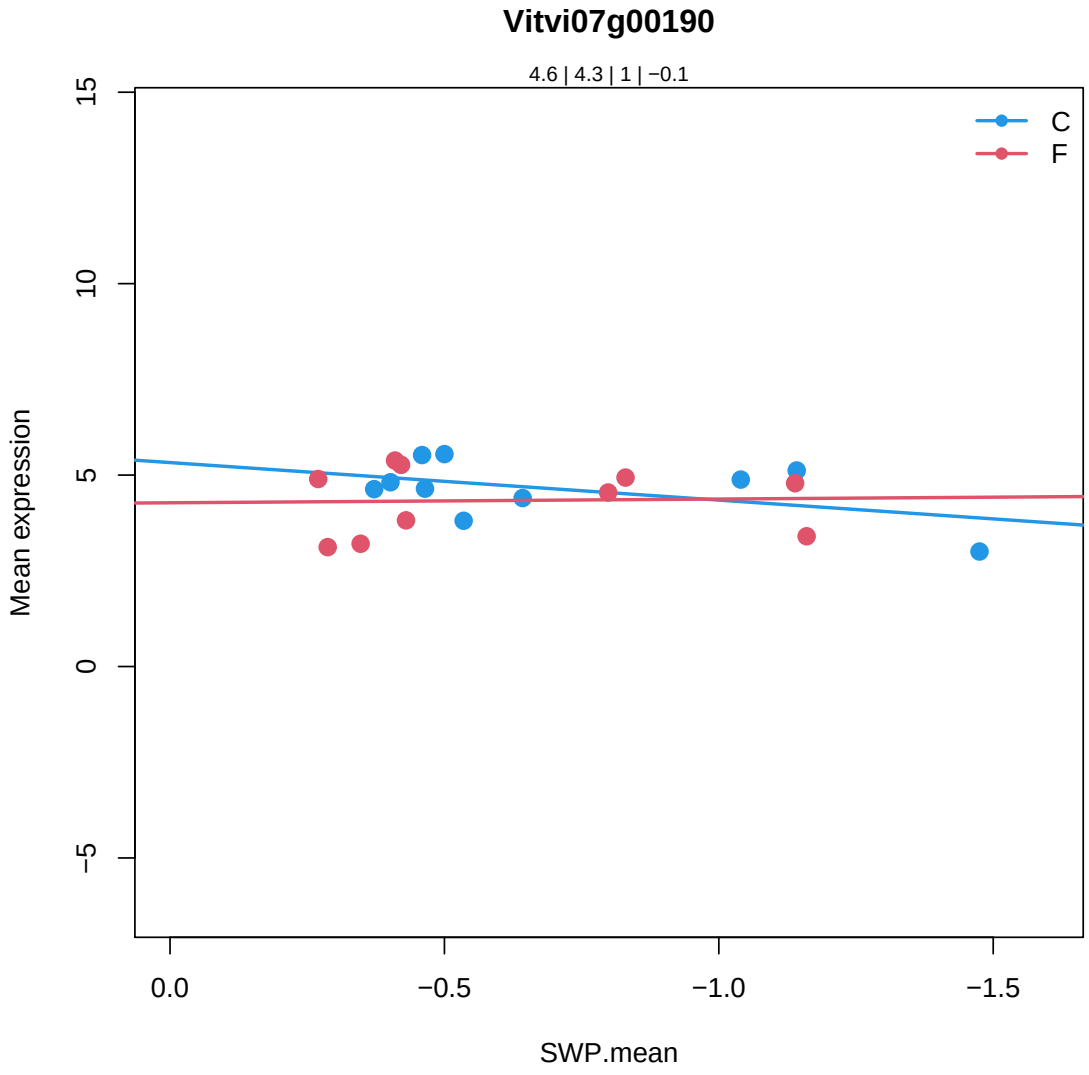
7.6.176 Vitvi07g00190: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g00190
        35.1
        not assigned.no ontology
        oxidoreductase%2C 2OG-Fe(II) oxygenase family protein |
        Chr4:1306658-1310699 FORWARD LENGTH=569 |
        201606
```

Coefficients for Vitvi07g00190.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.637235	4.171377e-15	***	7.293809e-15	***
SlopeC	0.9805244	0.1538627		0.6851709	
MeanF-MeanC	-0.3016654	0.3808589		0.7323138	
SlopeF-SlopeC	-1.078047	0.2869377		0.9999488	



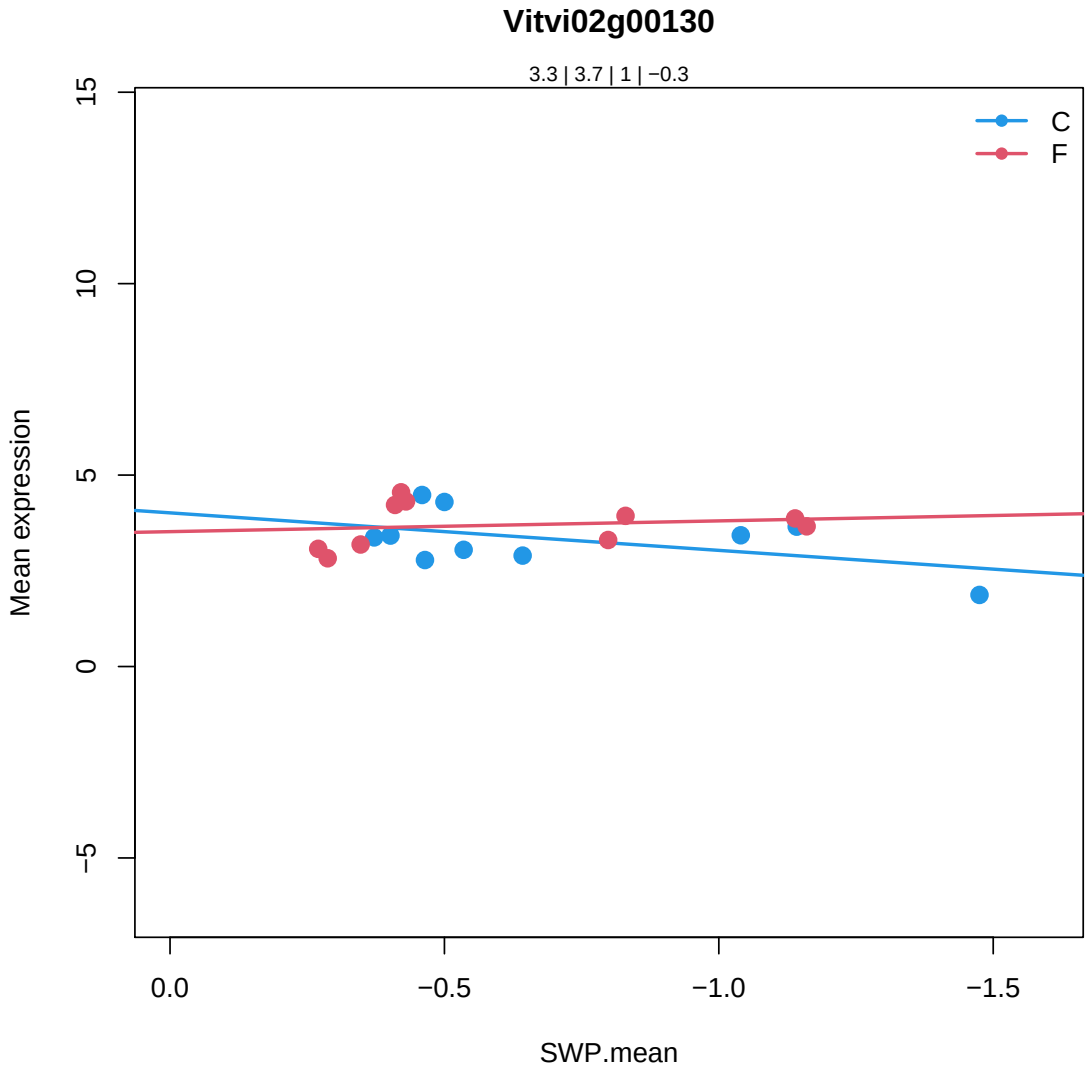
7.6.177 Vitvi02g00130: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00130
        29.5.11.4.2
        protein.degradation.ubiquitin.E3.RING
        RING/U-box superfamily protein |
        Chr5:21529022-21533008 FORWARD LENGTH=382 |
        201606
```

Coefficients for Vitvi02g00130.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.32446	5.5407e-14	***	8.675914e-14	***
SlopeC	0.9798245	0.08386863	.	0.5829118	
MeanF-MeanC	0.3692299	0.193006		0.5334977	
SlopeF-SlopeC	-1.261001	0.1316153		0.9999488	



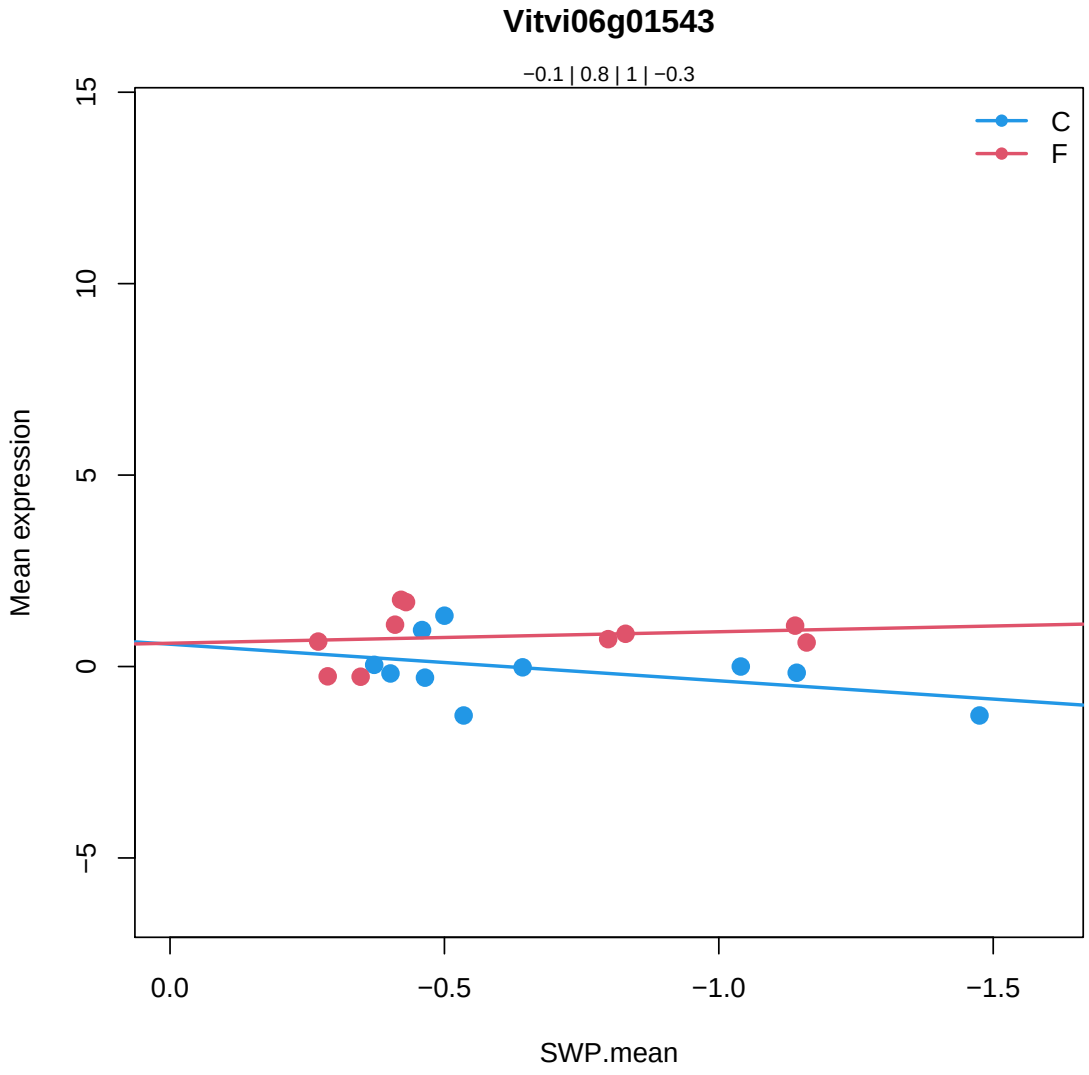
7.6.178 Vitvi06g01543: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01543
        35.2
        not assigned.unknown
        hypothetical protein |
        Chr5:1912895-1913263 FORWARD LENGTH=122 |
        201606
```

Coefficients for Vitvi06g01543.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.08909211	0.6866755		0.6913931	
SlopeC	0.9553275	0.1296781		0.6520375	
MeanF-MeanC	0.8801153	0.009330554	**	0.07215439	.
SlopeF-SlopeC	-1.254988	0.1785021		0.9999488	



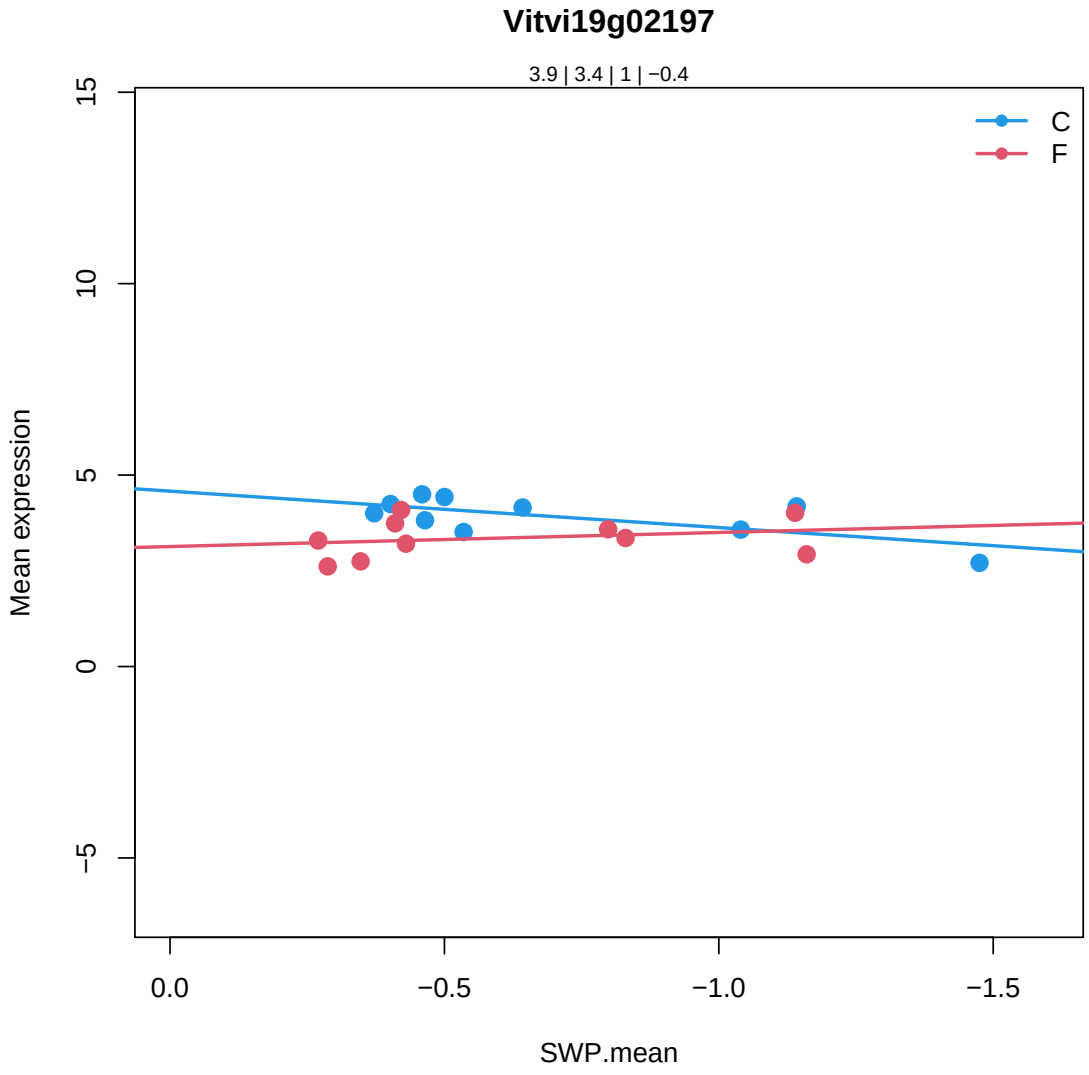
7.6.179 Vitvi19g02197: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g02197
        26.9
        misc.glutathione S transferases
        glutathione S-transferase TAU 25 |
        Chr1:5872208-5872958 FORWARD LENGTH=221 |
        201606
```

Coefficients for Vitvi19g02197.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.912405	1.123868e-17	***	2.926703e-17	***
SlopeC	0.9500499	0.03414188	*	0.4433084	
MeanF-MeanC	-0.5551209	0.01651046	*	0.1092242	
SlopeF-SlopeC	-1.317636	0.04691241	*	0.9999488	



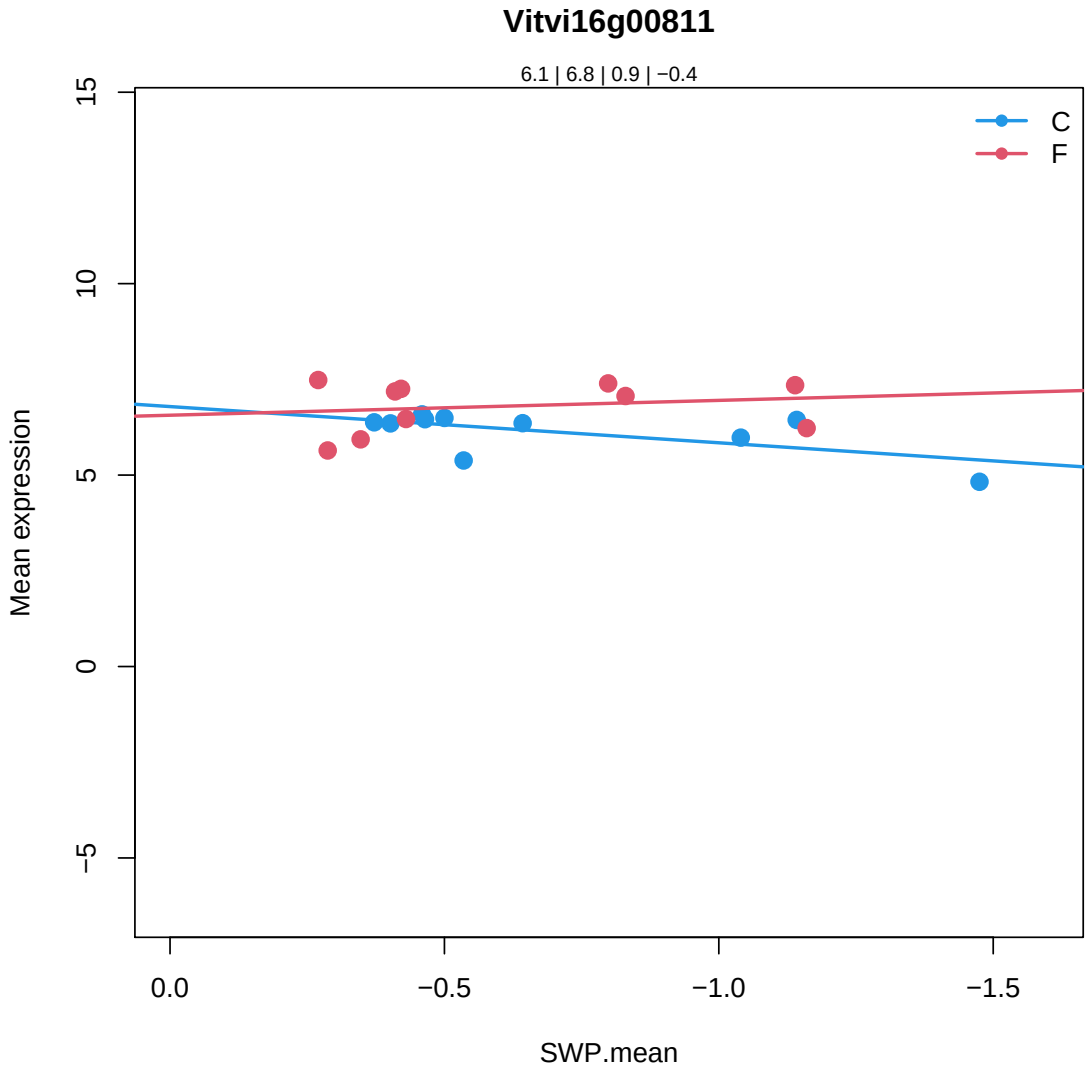
7.6.180 Vitvi16g00811: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g00811
        35.2
        not assigned.unknown
        PR5-like receptor kinase |
        Chr5:15293325-15295838 REVERSE LENGTH=665 |
        201606
```

Coefficients for Vitvi16g00811.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.12423	4.460681e-20	***	2.406273e-19	***
SlopeC	0.9457417	0.07466501	.	0.5682824	
MeanF-MeanC	0.675128	0.01544214	*	0.1038699	
SlopeF-SlopeC	-1.333079	0.090184	.	0.9999488	



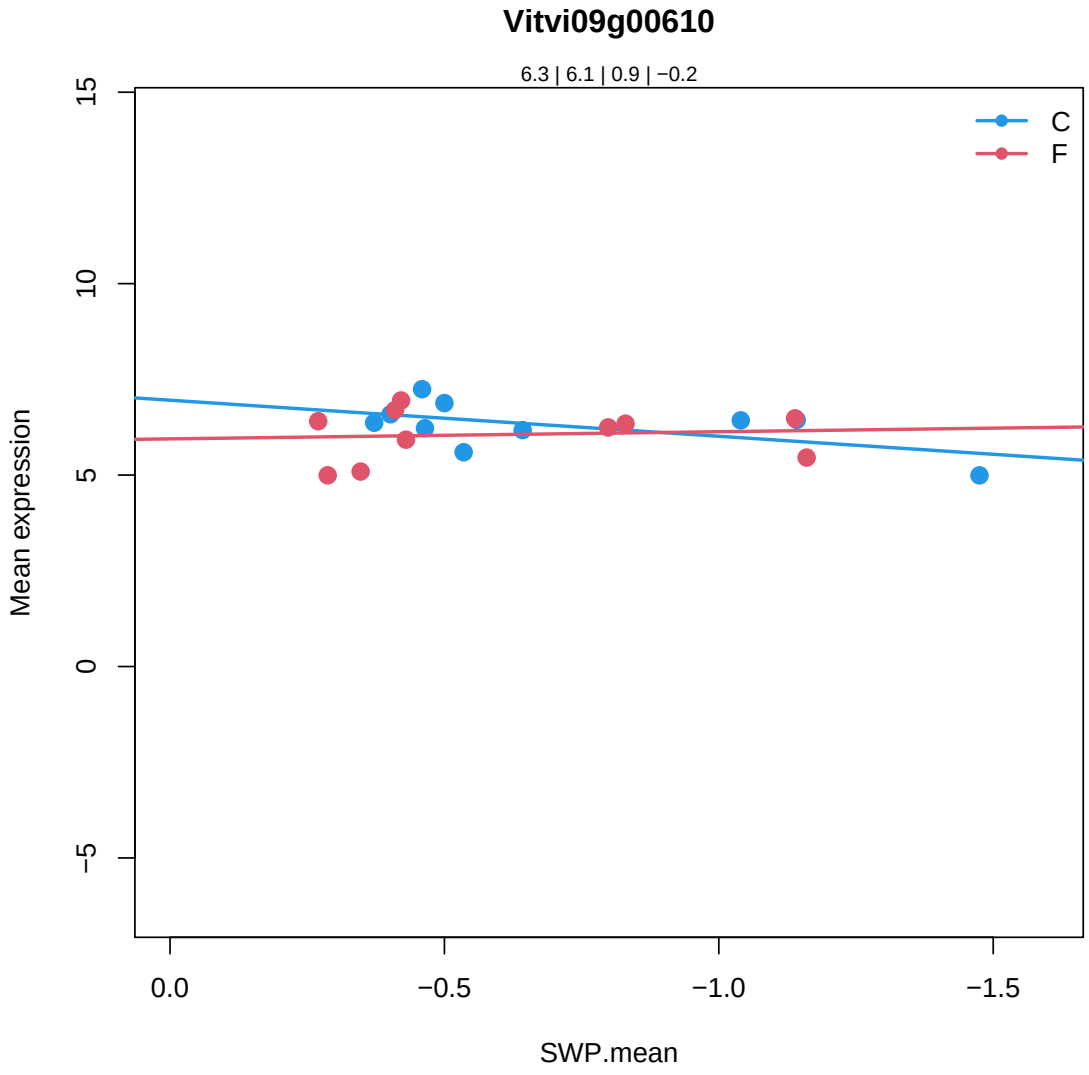
7.6.181 Vitvi09g00610: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00610
        35.2
        not assigned.unknown
        LURP-one-like protein (DUF567) |
        Chr3:5348054-5349178 REVERSE LENGTH=220 |
        201606
```

Coefficients for Vitvi09g00610.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.29333	6.854403e-20	***	3.460577e-19	***
SlopeC	0.9414813	0.08950798	.	0.5953805	
MeanF-MeanC	-0.234381	0.3933955		0.7408135	
SlopeF-SlopeC	-1.128013	0.1666564		0.9999488	



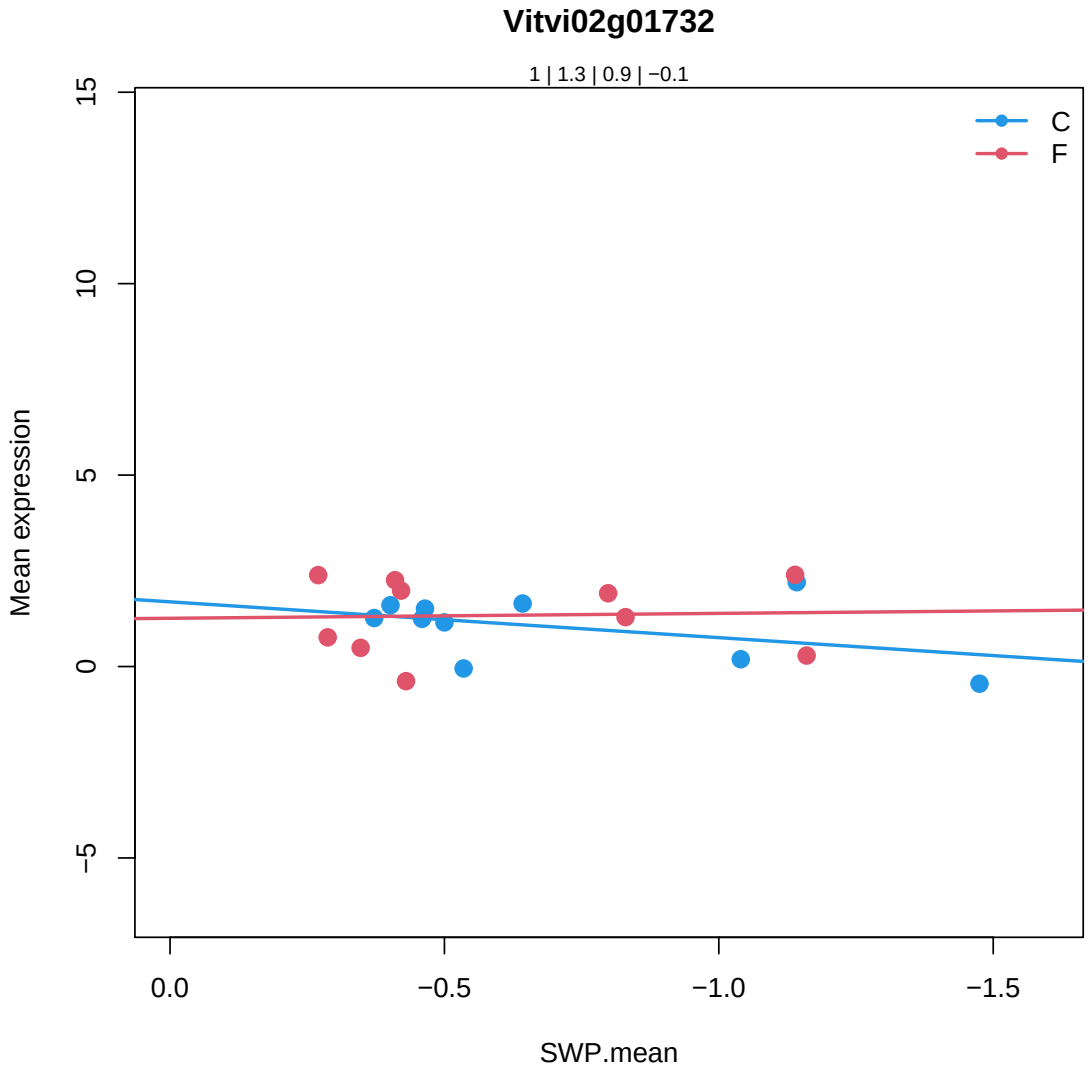
7.6.182 Vitvi02g01732: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g01732
        26.2
        misc.UDP glucosyl and glucoronyl transferases
        myb domain protein 66 |
        Chr5:4763656-4764738 REVERSE LENGTH=203 |
        201606
```

Coefficients for Vitvi02g01732.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.031532	0.0009524218	***	0.001031903	**
SlopeC	0.9351093	0.2258295		0.7454275	
MeanF-MeanC	0.3060078	0.4308898		0.7654572	
SlopeF-SlopeC	-1.062943	0.3515081		0.9999488	



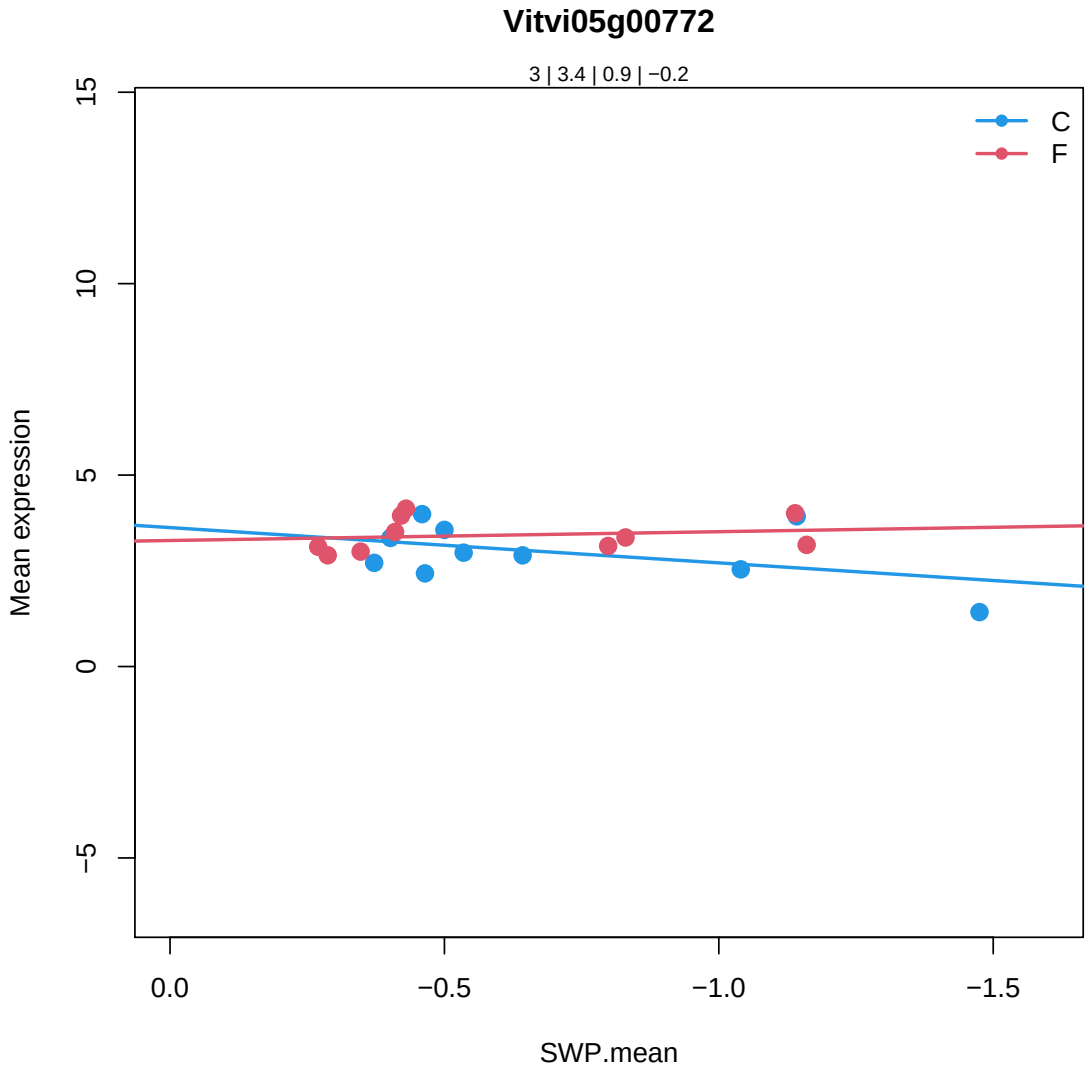
7.6.183 Vitvi05g00772: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00772
        29.4
        protein.postranslational modification
        Protein phosphatase 2C family protein |
        Chr3:8355257-8356381 REVERSE LENGTH=260 |
        201606
```

Coefficients for Vitvi05g00772.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.980419	1.786597e-13	***	2.694836e-13	***
SlopeC	0.9208777	0.08721096	.	0.5928945	
MeanF-MeanC	0.4507369	0.09876774	.	0.3620534	
SlopeF-SlopeC	-1.150913	0.1469152		0.9999488	



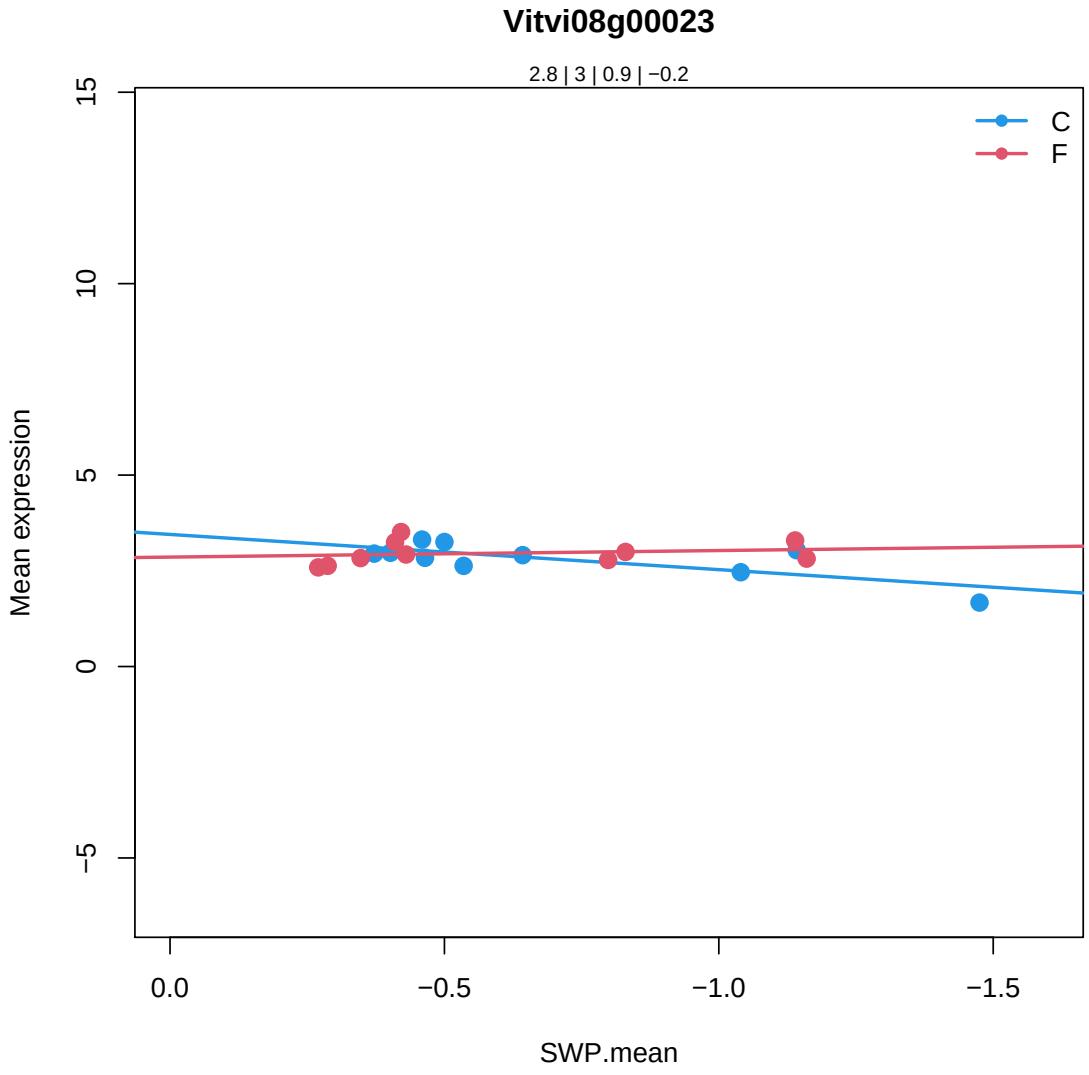
7.6.184 Vitvi08g00023: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g00023
        33.2
        development.late embryogenesis abundant
        Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein fam
        Chr3:20065731-20066438 FORWARD LENGTH=235 |
        201606
```

Coefficients for Vitvi08g00023.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.803269	7.545913e-17	***	1.674892e-16	***
SlopeC	0.9190857	0.0109058	*	0.3141738	
MeanF-MeanC	0.1588698	0.3537917		0.7117863	
SlopeF-SlopeC	-1.090278	0.03720804	*	0.9999488	



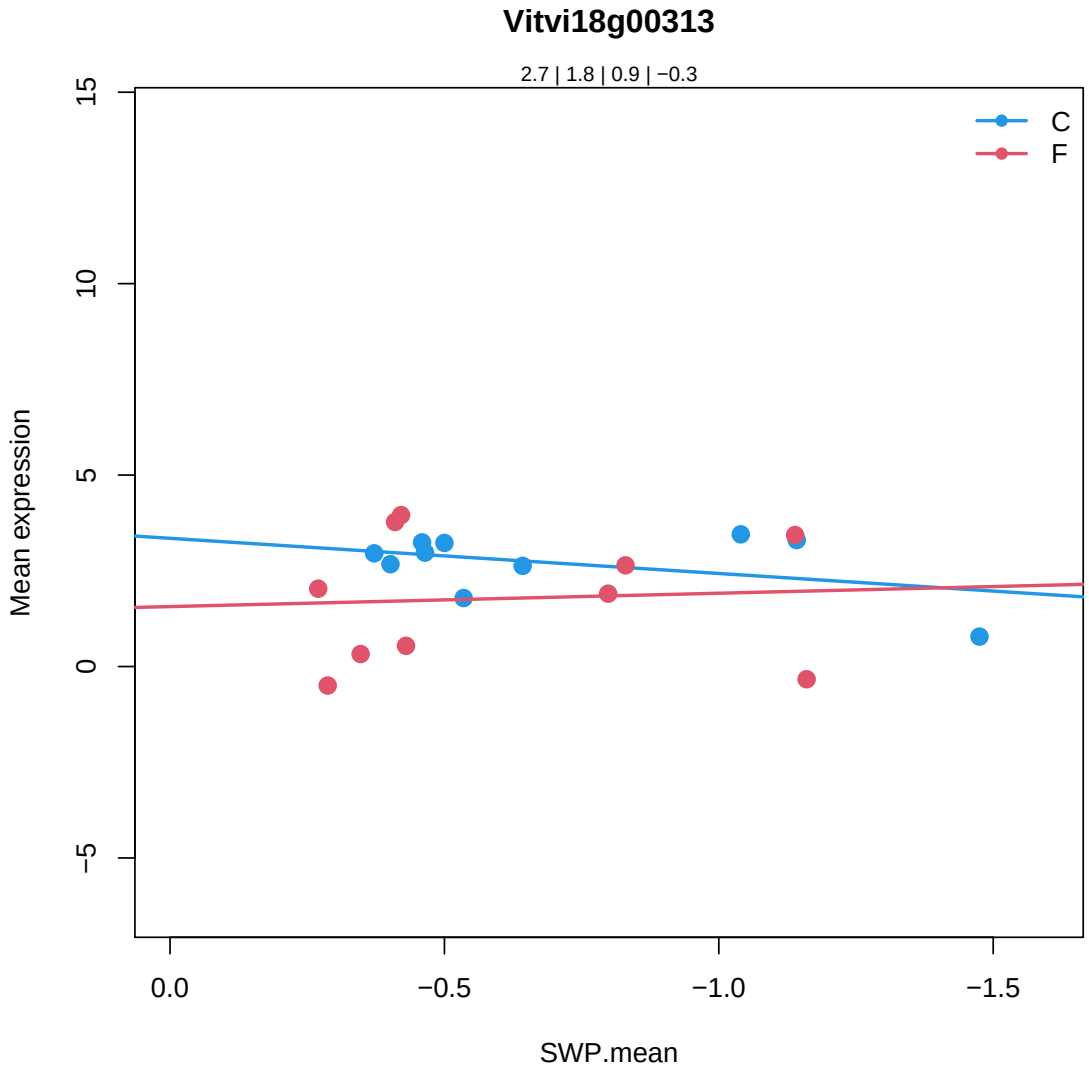
7.6.185 Vitvi18g00313: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00313
        17.2.3
        hormone metabolism.auxin.induced-regulated-responsive-activated
        O-fucosyltransferase family protein |
        Chr2:216980-220057 FORWARD LENGTH=529 |
        201606
```

Coefficients for Vitvi18g00313.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.702495	5.617919e-07	***	6.529037e-07	***
SlopeC	0.9183462	0.400987		0.835066	
MeanF-MeanC	-0.9247154	0.1040898		0.3738902	
SlopeF-SlopeC	-1.267313	0.4356194		0.9999488	



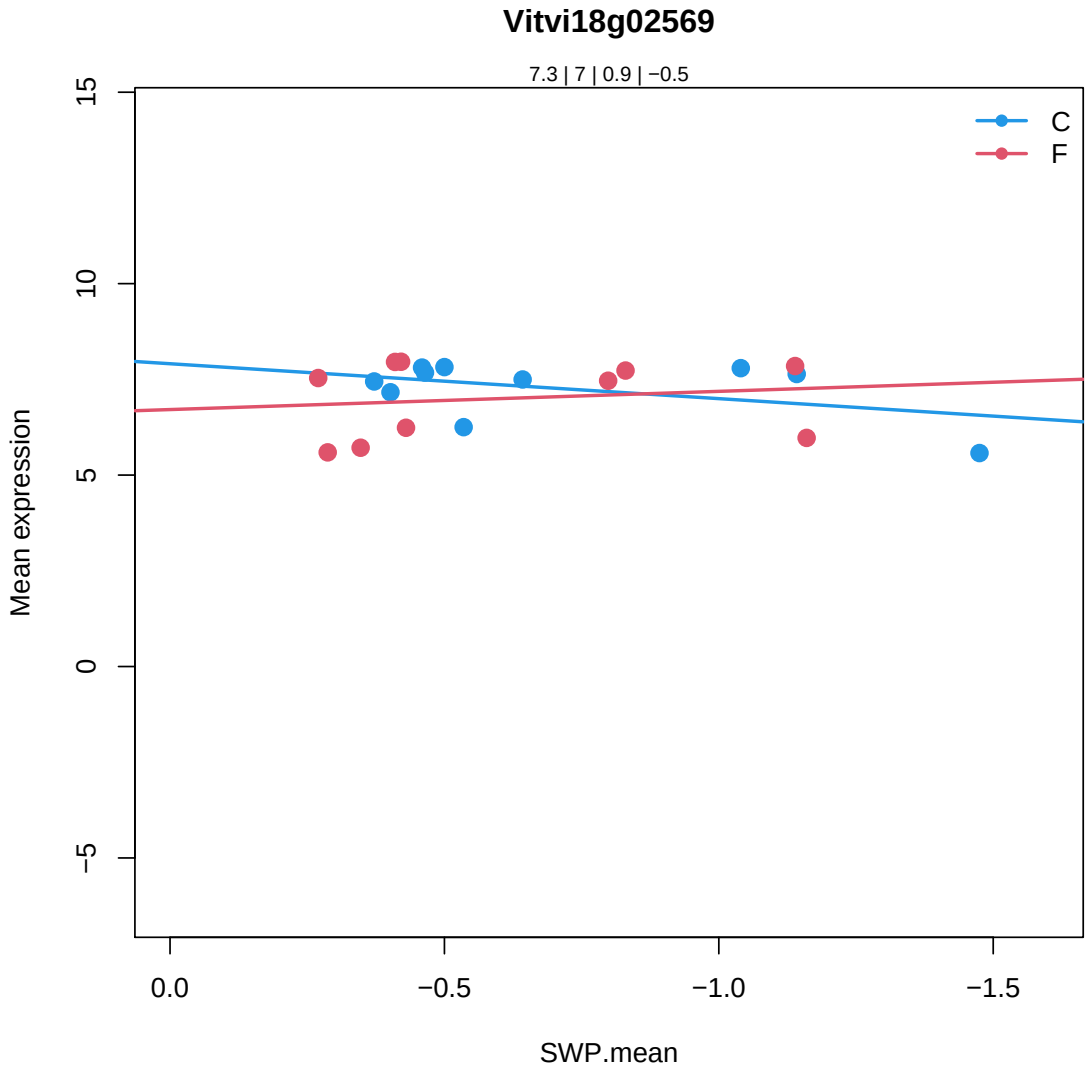
7.6.186 Vitvi18g02569: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02569
        33.99
        development.unspecified
        senescence-associated family protein%2C putative (DUF581) |
        Chr1:29338787-29339491 FORWARD LENGTH=162 |
        201606
```

Coefficients for Vitvi18g02569.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.266803	1.658218e-18	***	5.357924e-18	***
SlopeC	0.9117223	0.2137275		0.7371282	
MeanF-MeanC	-0.2661879	0.4697007		0.7887163	
SlopeF-SlopeC	-1.387278	0.204045		0.9999488	



7.6.187 Vitvi01g00036: type5

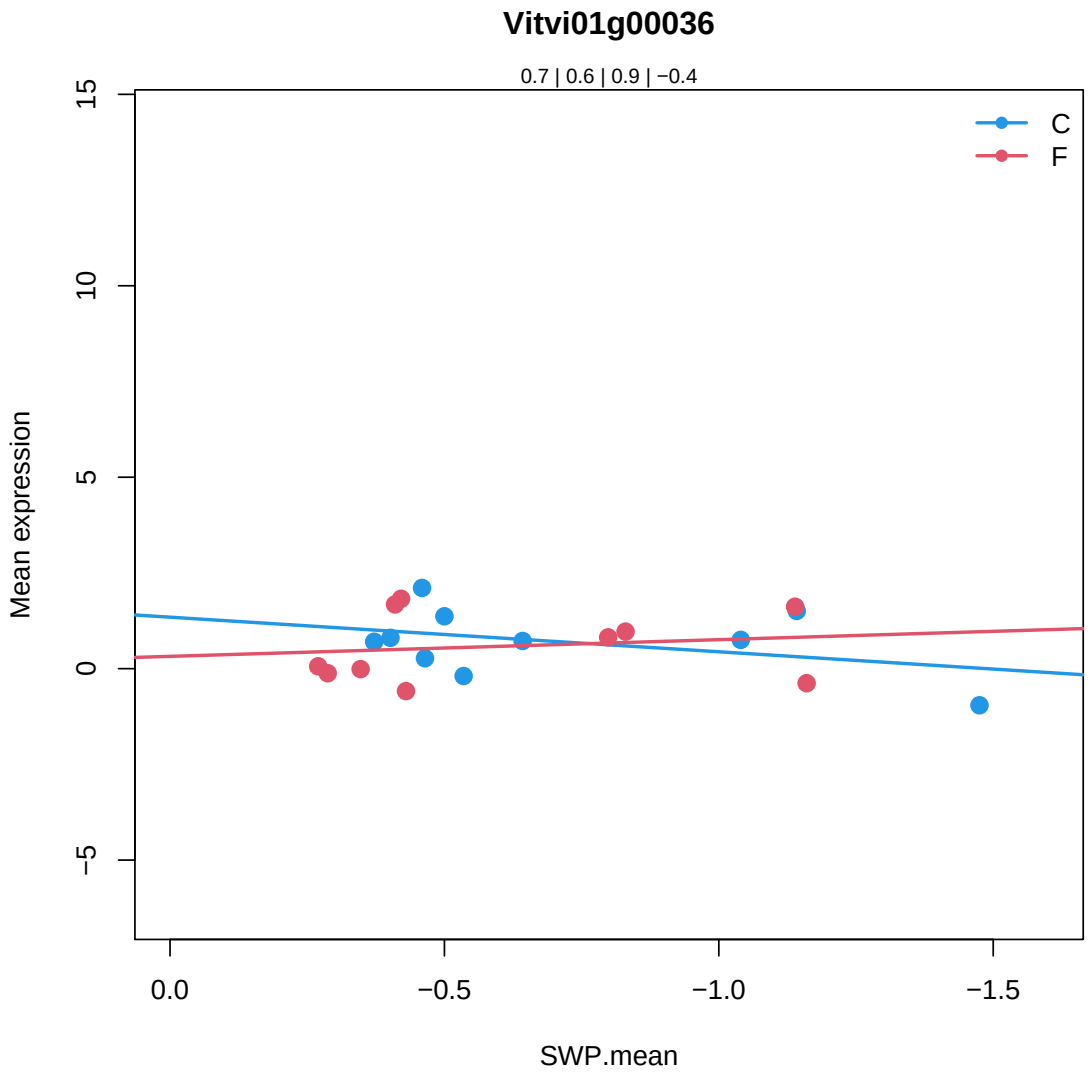
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00036
        35.2
        not assigned.unknown
        Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM
        Chr5:24543988-24546027 FORWARD LENGTH=459 |
        201606

Vitvi01g00036
        29.3.1
        protein.targeting.nucleus
        Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM
        Chr5:24543988-24546027 FORWARD LENGTH=459 |
        201606
```

Coefficients for Vitvi01g00036.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.7087097	0.01200716	*	0.0126969	*
SlopeC	0.9035124	0.2220726		0.741278	
MeanF-MeanC	-0.1221796	0.7412162		0.9232463	
SlopeF-SlopeC	-1.339458	0.2238392		0.9999488	


Vitvi01g00036
0.7 | 0.6 | 0.9 | −0.4
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

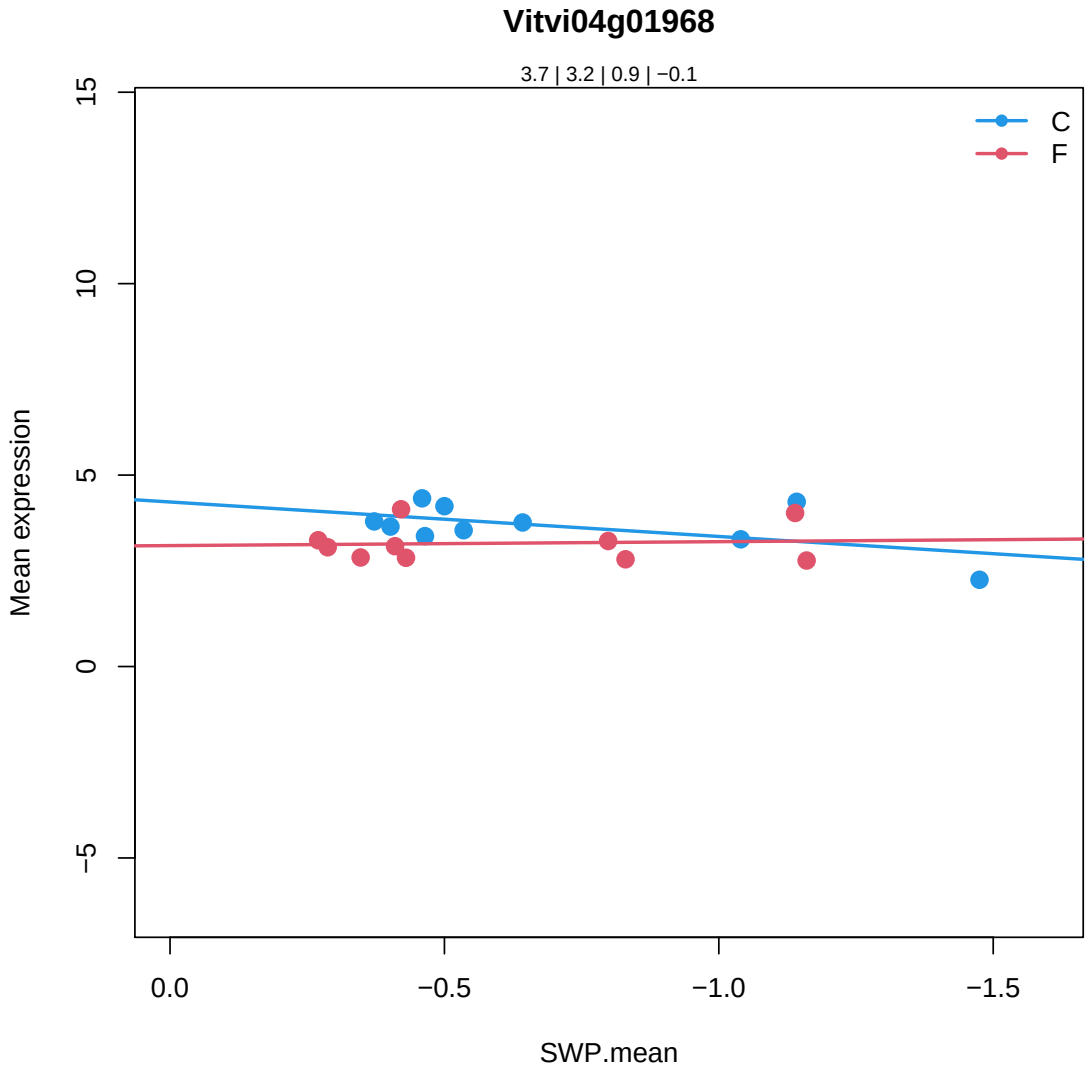
7.6.188 Vitvi04g01968: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01968
        30.1.1
        signalling.in sugar and nutrient physiology.misc
        glutamate receptor 2.2 |
        Chr2:10522783-10525840 REVERSE LENGTH=920 |
        201606
```

Coefficients for Vitvi04g01968.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.664099	2.318267e-16	***	4.746142e-16	***
SlopeC	0.9004802	0.06084155	.	0.5422759	
MeanF-MeanC	-0.4433699	0.06871618	.	0.2928893	
SlopeF-SlopeC	-1.003133	0.1531631		0.9999488	



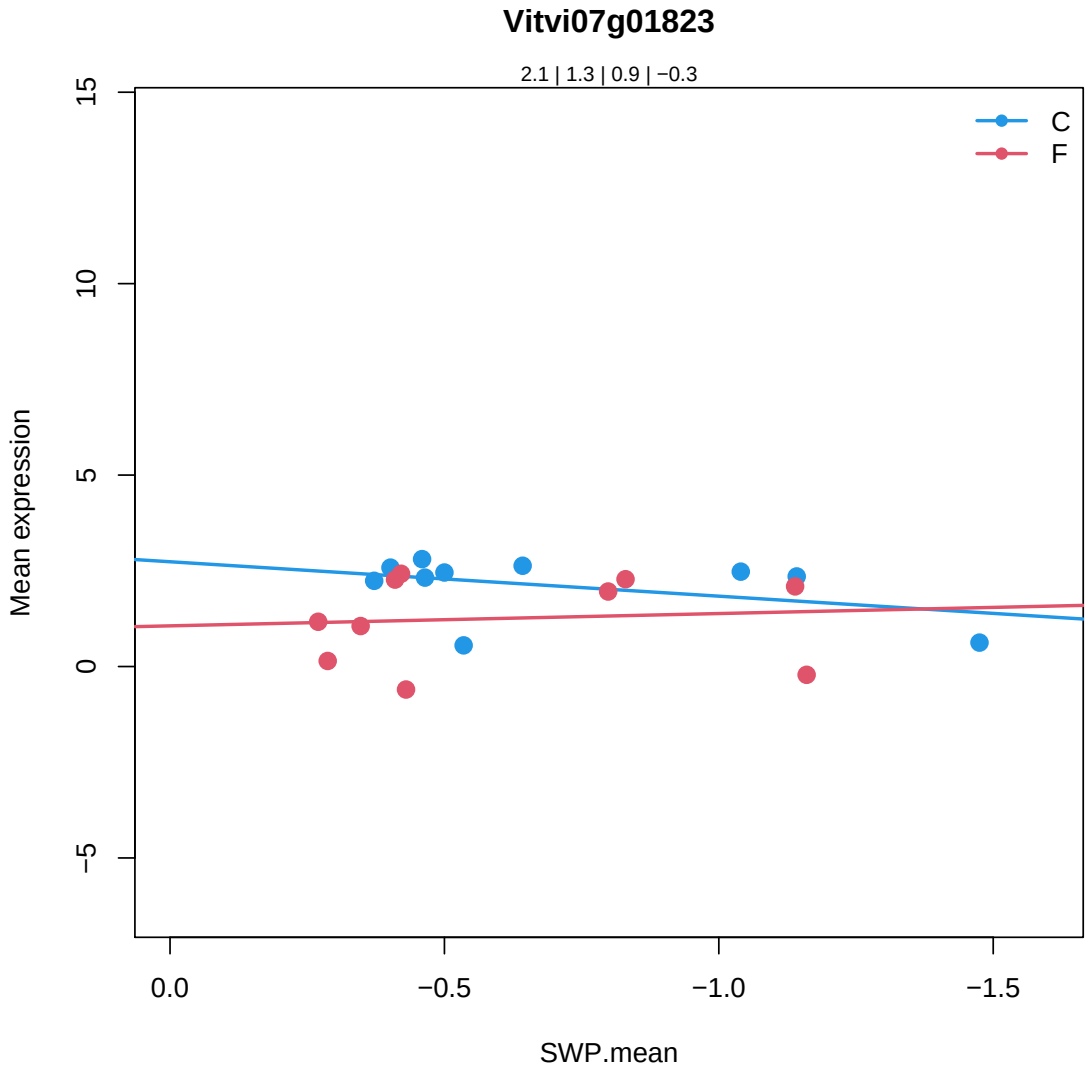
7.6.189 Vitvi07g01823: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01823
        27.3.15
        RNA.regulation of transcription.CCAAT box binding factor family, HAP3
        nuclear factor Y%2C subunit B3 |
        Chr4:8344663-8345148 FORWARD LENGTH=161 |
        201606
```

Coefficients for Vitvi07g01823.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.10419	2.856596e-07	***	3.344361e-07	***
SlopeC	0.8989831	0.2727312		0.7744696	
MeanF-MeanC	-0.8463822	0.04920077	*	0.2361962	
SlopeF-SlopeC	-1.220368	0.3159946		0.9999488	



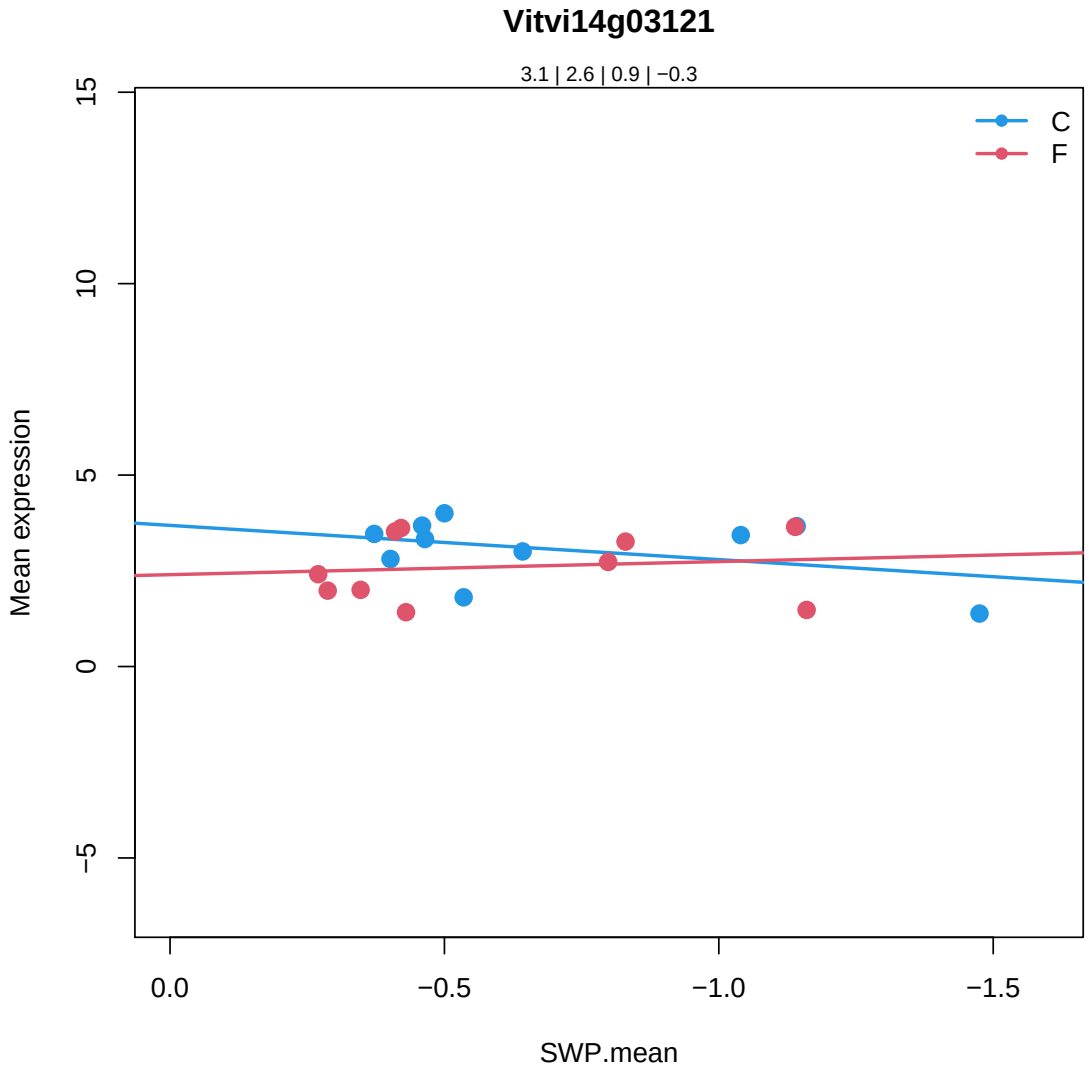
7.6.190 Vitvi14g03121: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g03121
        35.2
        not assigned.unknown
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606
```

Coefficients for Vitvi14g03121.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.057734	4.122142e-11	***	5.479174e-11	***
SlopeC	0.893609	0.213974		0.7372044	
MeanF-MeanC	-0.450344	0.2177877		0.5668579	
SlopeF-SlopeC	-1.235633	0.2471239		0.9999488	



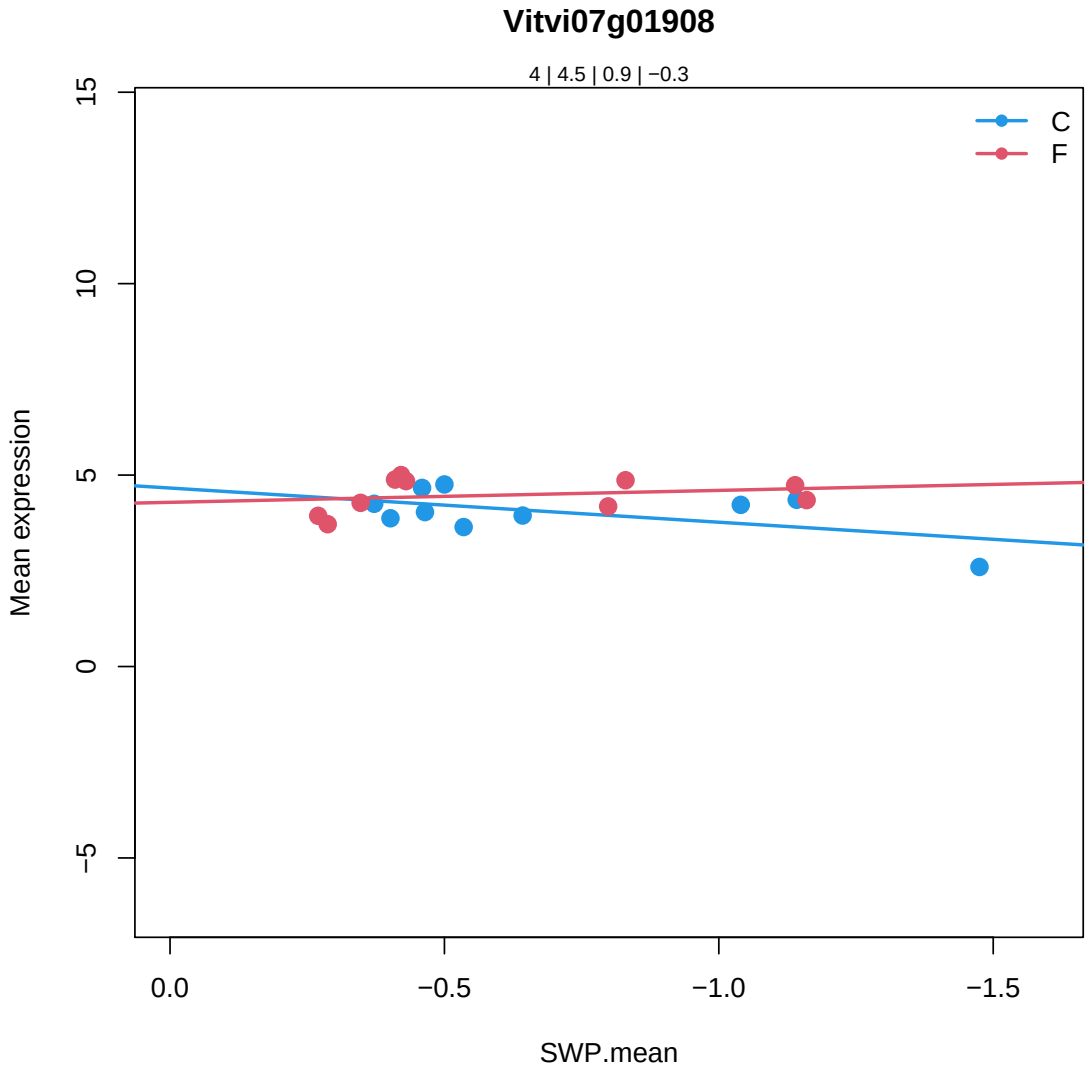
7.6.191 Vitvi07g01908: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01908
        20.1.7.1
        stress.biotic.PR-proteins.PR1 (antifungal)
        alpha/beta-Hydrolases superfamily protein |
        Chr3:19431566-19434292 FORWARD LENGTH=541 |
        201606
```

Coefficients for Vitvi07g01908.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.033881	1.46375e-17	***	3.725864e-17	***
SlopeC	0.8929569	0.05421466	.	0.5209838	
MeanF-MeanC	0.4441001	0.05917652	.	0.2654236	
SlopeF-SlopeC	-1.204537	0.07876189	.	0.9999488	



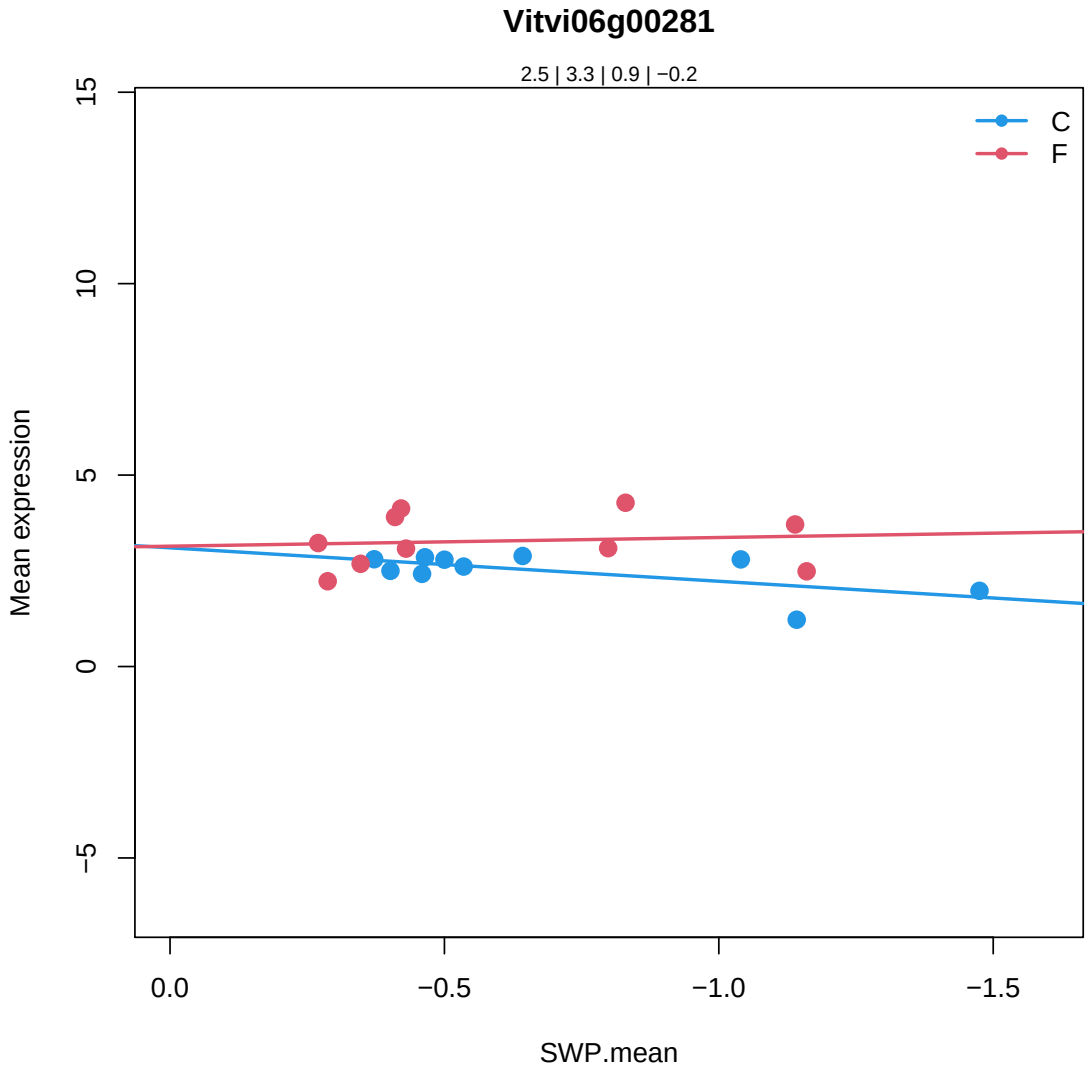
7.6.192 Vitvi06g00281: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00281
        34.19.1
        transport.major intrinsic proteins.PIP
        plasma membrane intrinsic protein 2 |
        Chr2:15613624-15614920 REVERSE LENGTH=328 |
        201606
```

Coefficients for Vitvi06g00281.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.485847	5.301356e-12	***	7.31781e-12	***
SlopeC	0.8736793	0.1007684		0.6125964	
MeanF-MeanC	0.7952427	0.005704437	**	0.05040408	.
SlopeF-SlopeC	-1.100412	0.1611789		0.9999488	



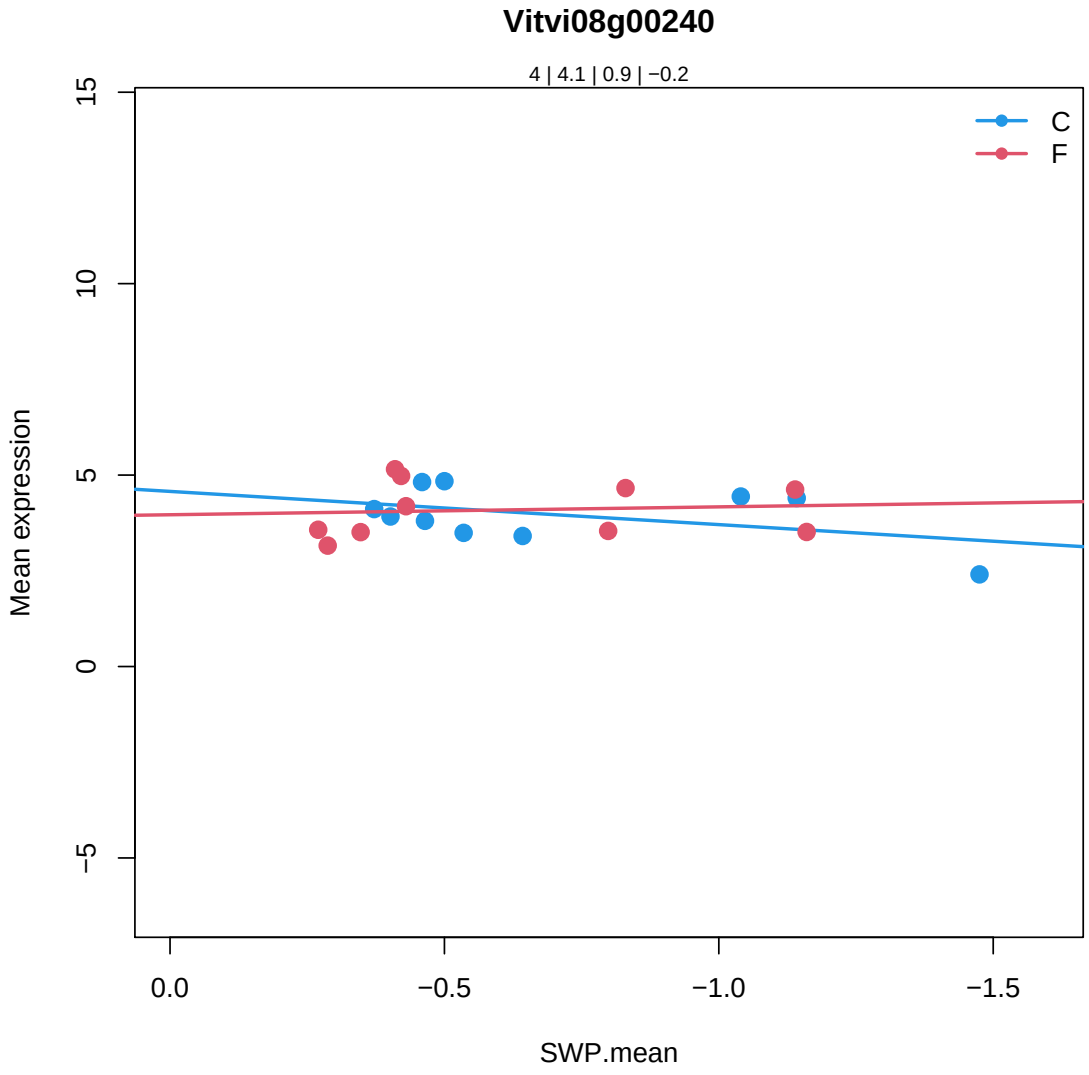
7.6.193 Vitvi08g00240: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g00240
        10.5.1.1
        cell wall.cell wall proteins.AGPs.AGP
        FASCICLIN-like arabinogalactan protein 17 precursor |
        Chr5:1952939-1955047 FORWARD LENGTH=458 |
        201606
```

Coefficients for Vitvi08g00240.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.963801	1.164125e-14	***	1.932853e-14	***
SlopeC	0.8673092	0.16034		0.6890054	
MeanF-MeanC	0.125555	0.6828606		0.8979782	
SlopeF-SlopeC	-1.073216	0.2397893		0.9999488	



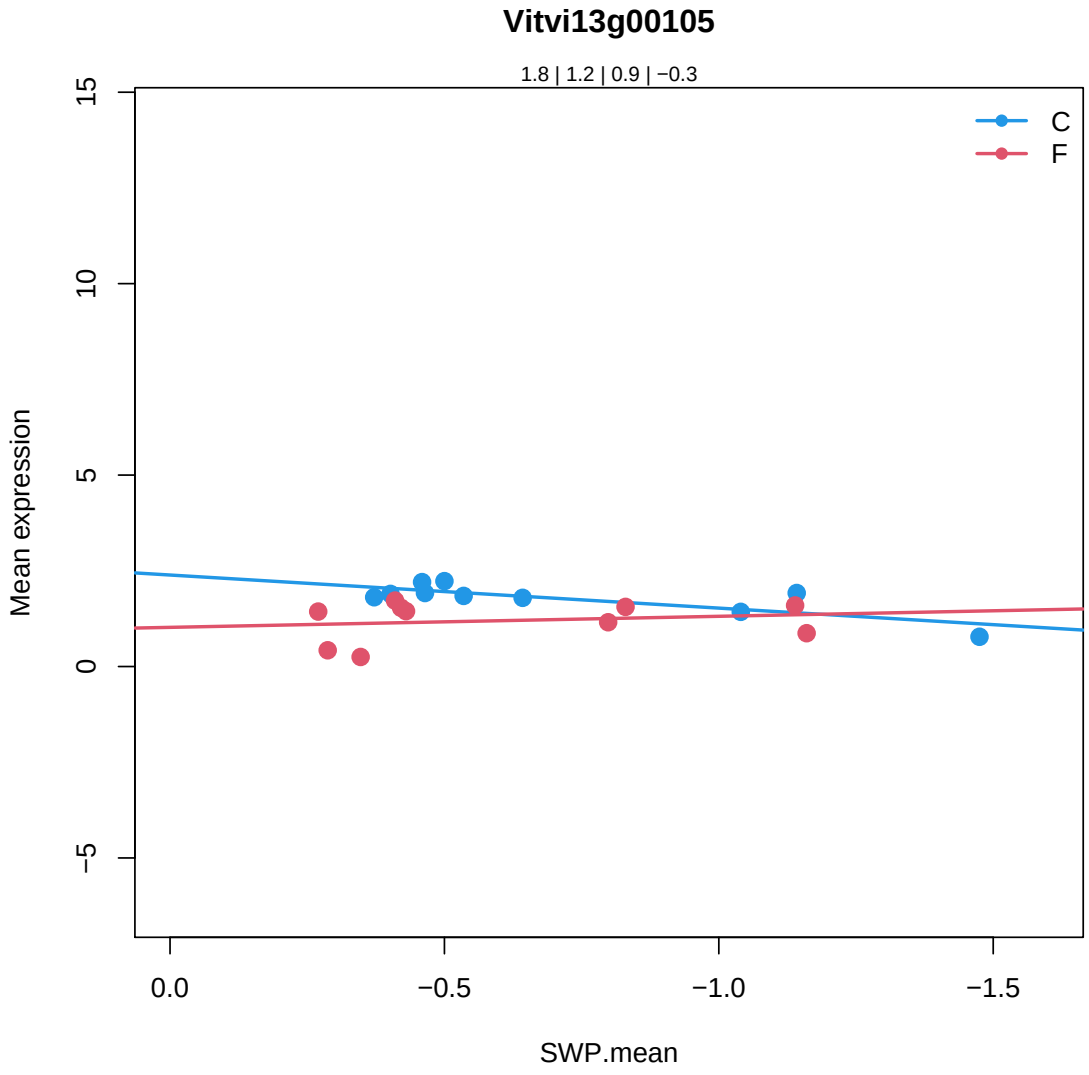
7.6.194 Vitvi13g00105: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00105
        26.13
        misc.acid and other phosphatases
        histidine acid phosphatase family protein |
        Chr1:3205817-3208444 FORWARD LENGTH=487 |
        201606
```

Coefficients for Vitvi13g00105.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.782157	1.920066e-11	***	2.588964e-11	***
SlopeC	0.8641853	0.03790562	*	0.4651621	
MeanF-MeanC	-0.5834415	0.00773481	**	0.06294392	.
SlopeF-SlopeC	-1.152755	0.06033458	.	0.9999488	



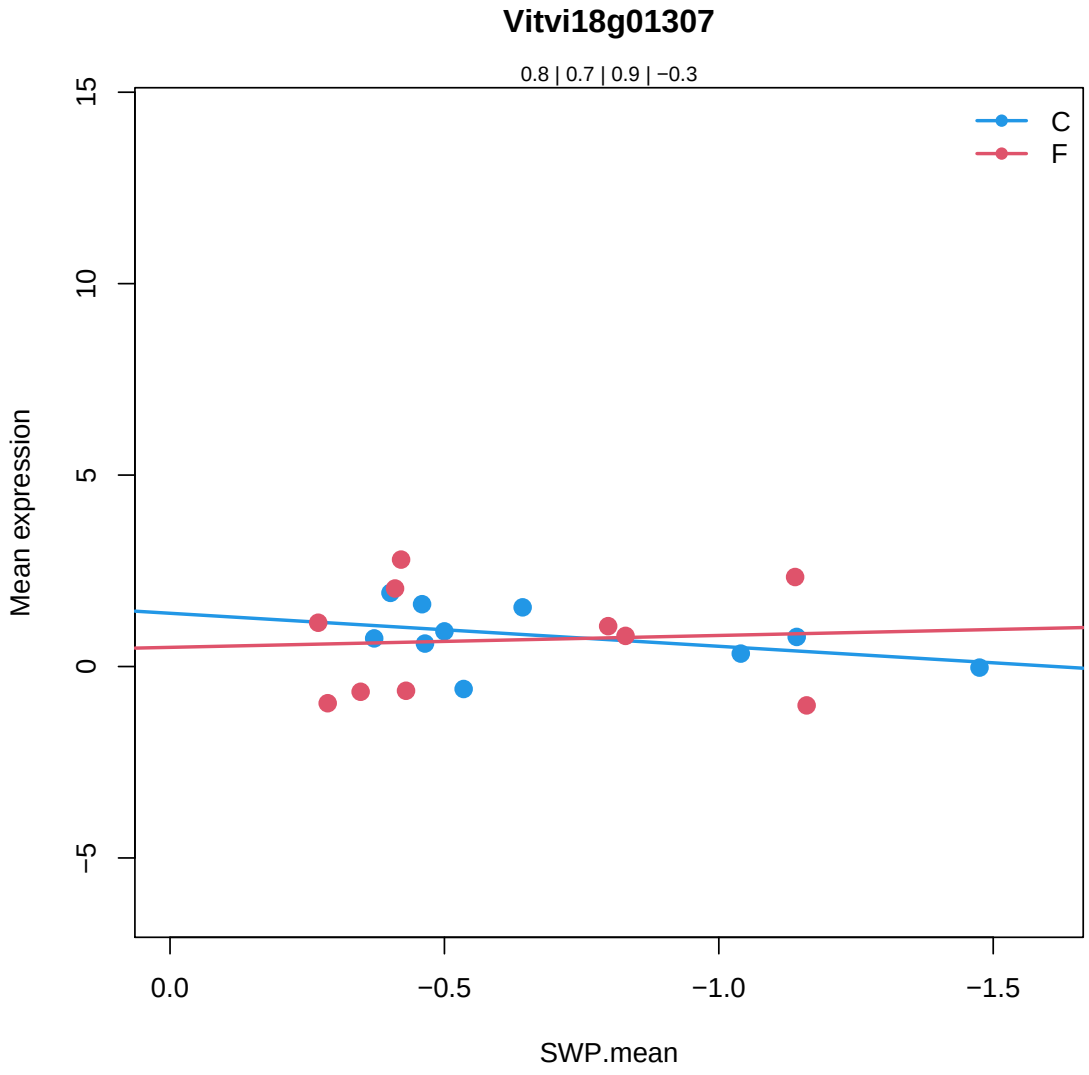
7.6.195 Vitvi18g01307: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g01307
        33.99
        development.unspecified
        Vacuolar iron transporter (VIT) family protein |
        Chr3:15565332-15565928 FORWARD LENGTH=198 |
        201606
```

Coefficients for Vitvi18g01307.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.7841882	0.0291659	*	0.03054044	*
SlopeC	0.8622408	0.3658338		0.8202312	
MeanF-MeanC	-0.09444994	0.8440688		0.9586416	
SlopeF-SlopeC	-1.172896	0.4077877		0.9999488	



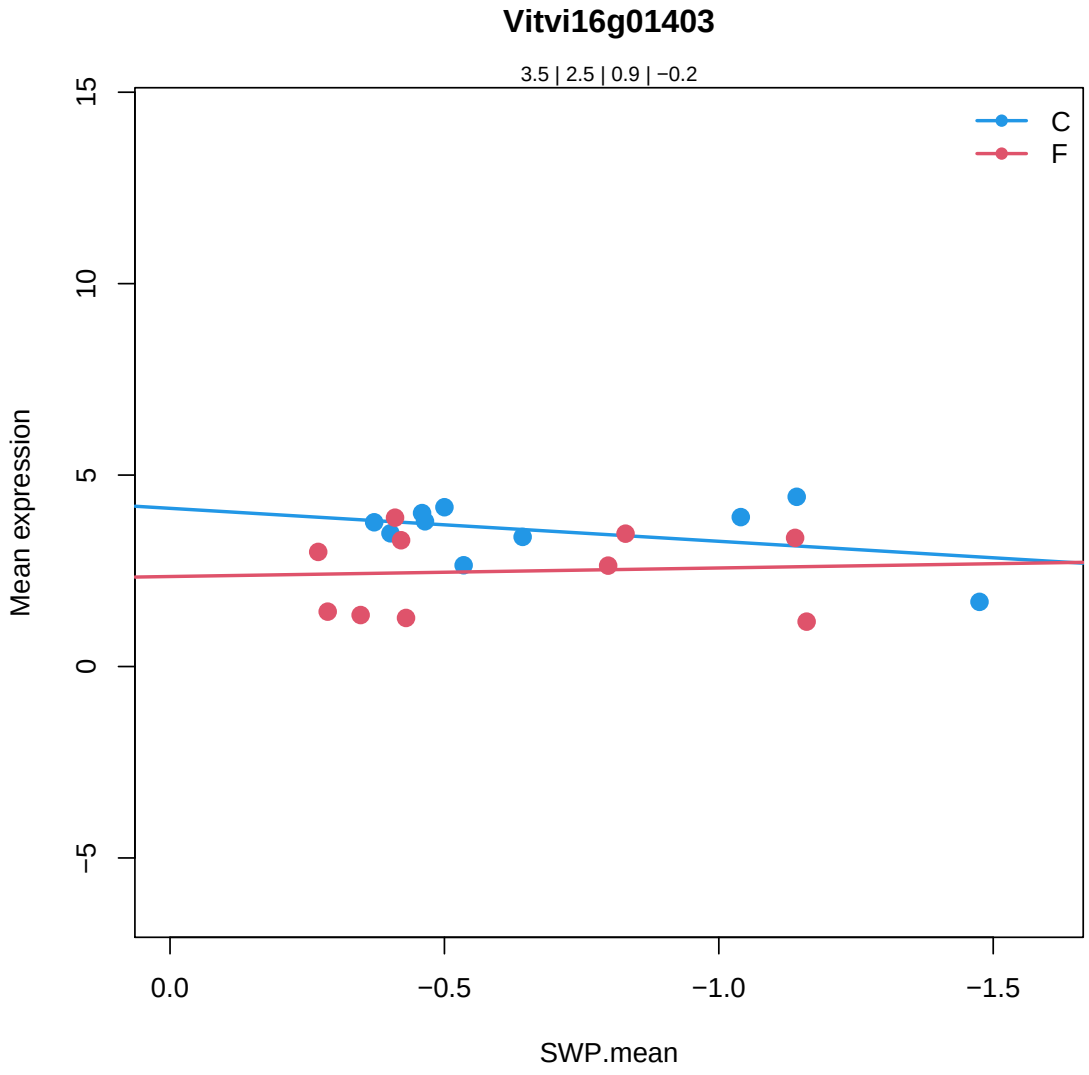
7.6.196 Vitvi16g01403: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01403
        35.2
        not assigned.unknown
        Ribonuclease P protein subunit P38-like protein |
        Chr5:21499899-21502235 FORWARD LENGTH=720 |
        201606
```

Coefficients for Vitvi16g01403.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.525908	1.824487e-11	***	2.462266e-11	***
SlopeC	0.8608531	0.2763647		0.7754618	
MeanF-MeanC	-1.039865	0.01467607	*	0.1004817	
SlopeF-SlopeC	-1.083835	0.355258		0.9999488	



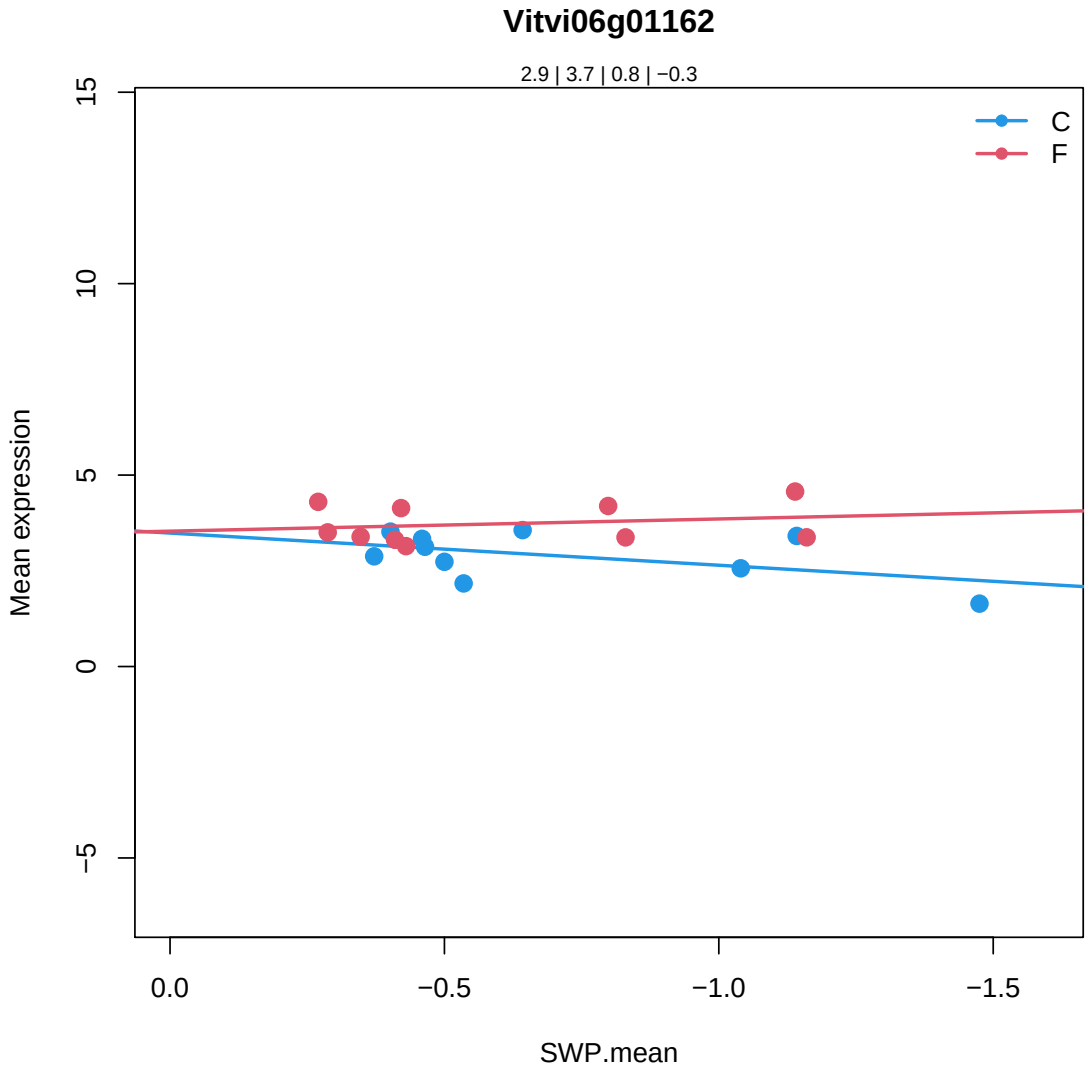
7.6.197 Vitvi06g01162: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01162
        35.2
        not assigned.unknown
        Putative methyltransferase family protein |
        Chr2:11434317-11436078 REVERSE LENGTH=209 |
        201606
```

Coefficients for Vitvi06g01162.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.894859	6.413212e-14	***	9.997972e-14	***
SlopeC	0.8397289	0.09072416	.	0.5978459	
MeanF-MeanC	0.8343965	0.002276813	**	0.02443208	*
SlopeF-SlopeC	-1.158191	0.1152954		0.9999488	



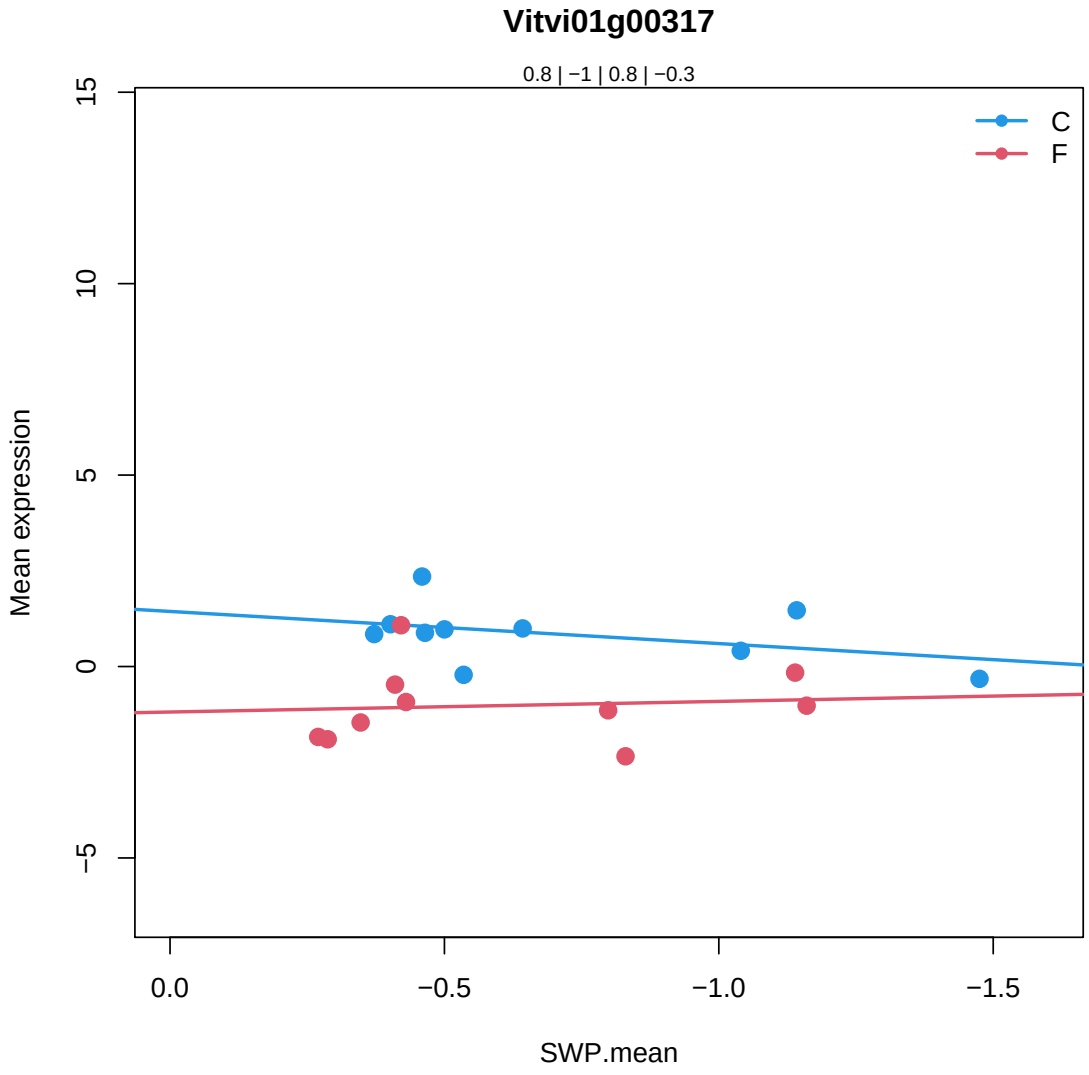
7.6.198 Vitvi01g00317: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00317
        35.2
        not assigned.unknown
        Core-2/I-branching beta-1%2C6-N-acetylglucosaminyltransferase family p
        Chr1:25642838-25645484 FORWARD LENGTH=408 |
        201606
```

Coefficients for Vitvi01g00317.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8484523	0.003757058	**	0.004018038	**
SlopeC	0.8389534	0.2607375		0.7688128	
MeanF-MeanC	-1.867983	4.903258e-05	***	0.0009663134	***
SlopeF-SlopeC	-1.11622	0.3132888		0.9999488	



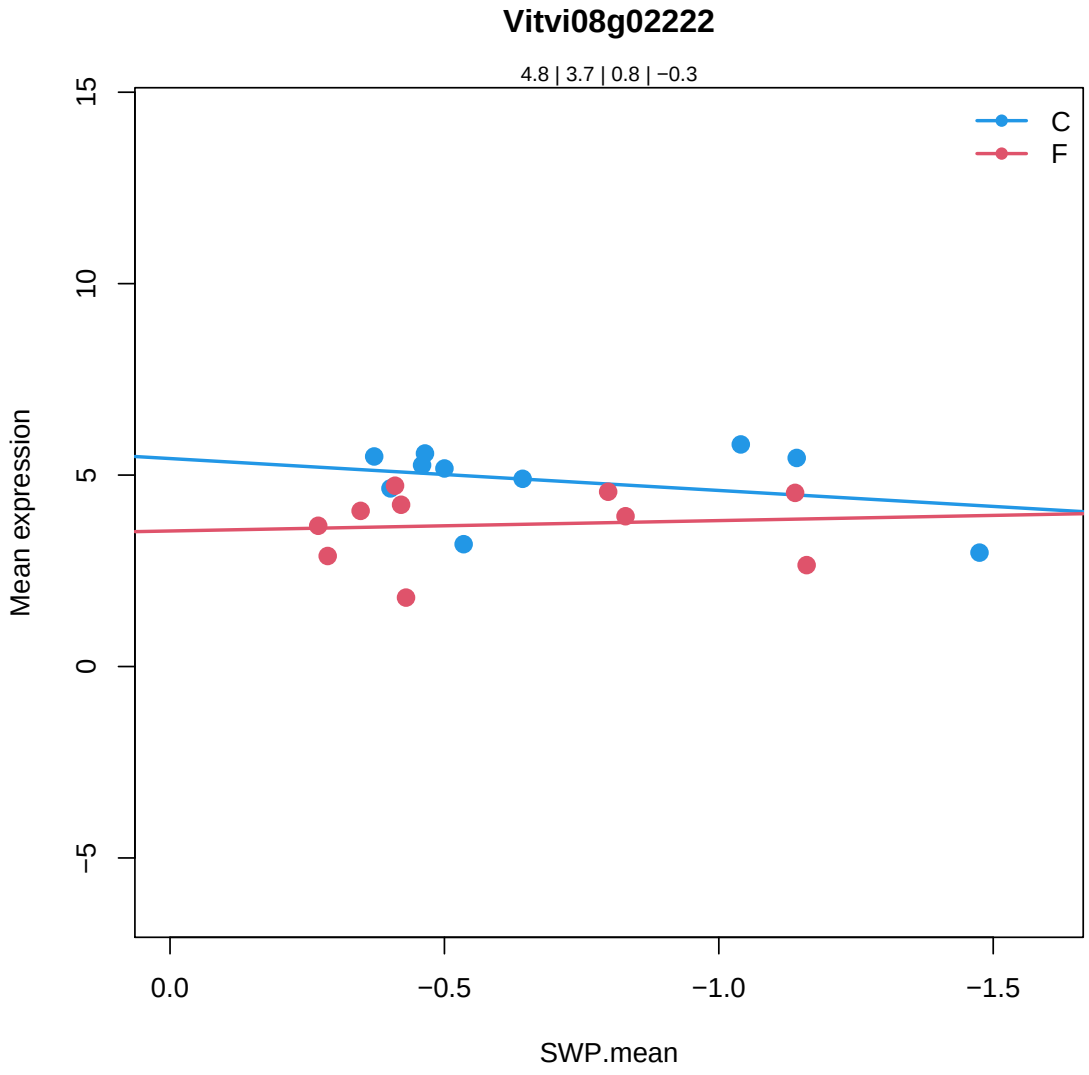
7.6.199 Vitvi08g02222: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g02222
        31.1
        cell.organisation
        Dynein light chain type 1 family protein |
        Chr1:8242614-8244136 FORWARD LENGTH=129 |
        201606
```

Coefficients for Vitvi08g02222.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.845352	6.280649e-14	***	9.796321e-14	***
SlopeC	0.8333008	0.304842		0.7891307	
MeanF-MeanC	-1.140526	0.009888343	**	0.0754345	.
SlopeF-SlopeC	-1.104608	0.3595553		0.9999488	



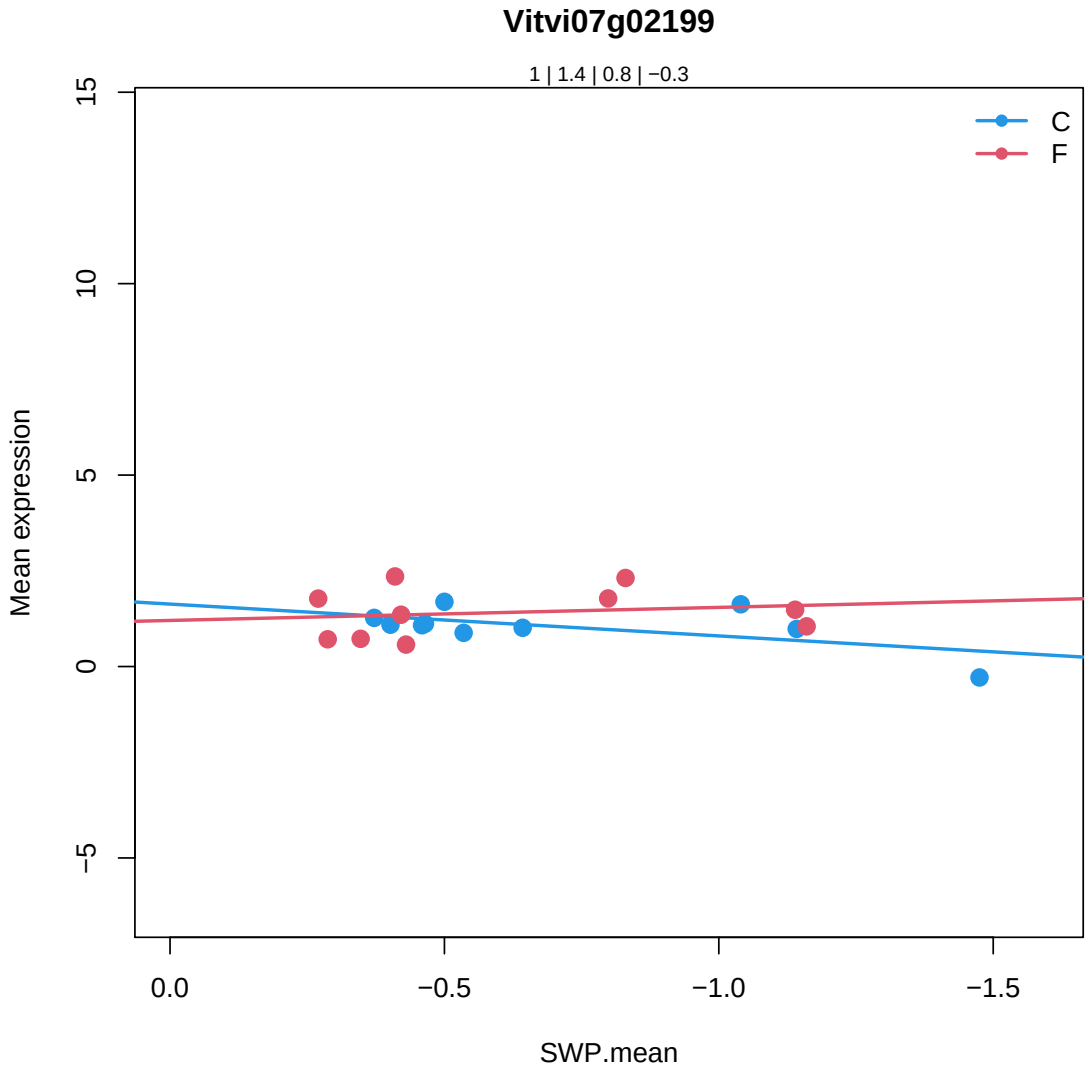
7.6.200 Vitvi07g02199: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g02199
        26.3
        misc.gluco-, galacto- and mannosidases
        beta glucosidase 2 |
        Chr4:11707370-11709932 REVERSE LENGTH=507 |
        201606
```

Coefficients for Vitvi07g02199.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.045904	6.404433e-06	***	7.259881e-06	***
SlopeC	0.831634	0.1047326		0.6180159	
MeanF-MeanC	0.3648529	0.1582177		0.4808145	
SlopeF-SlopeC	-1.172593	0.1231589		0.9999488	



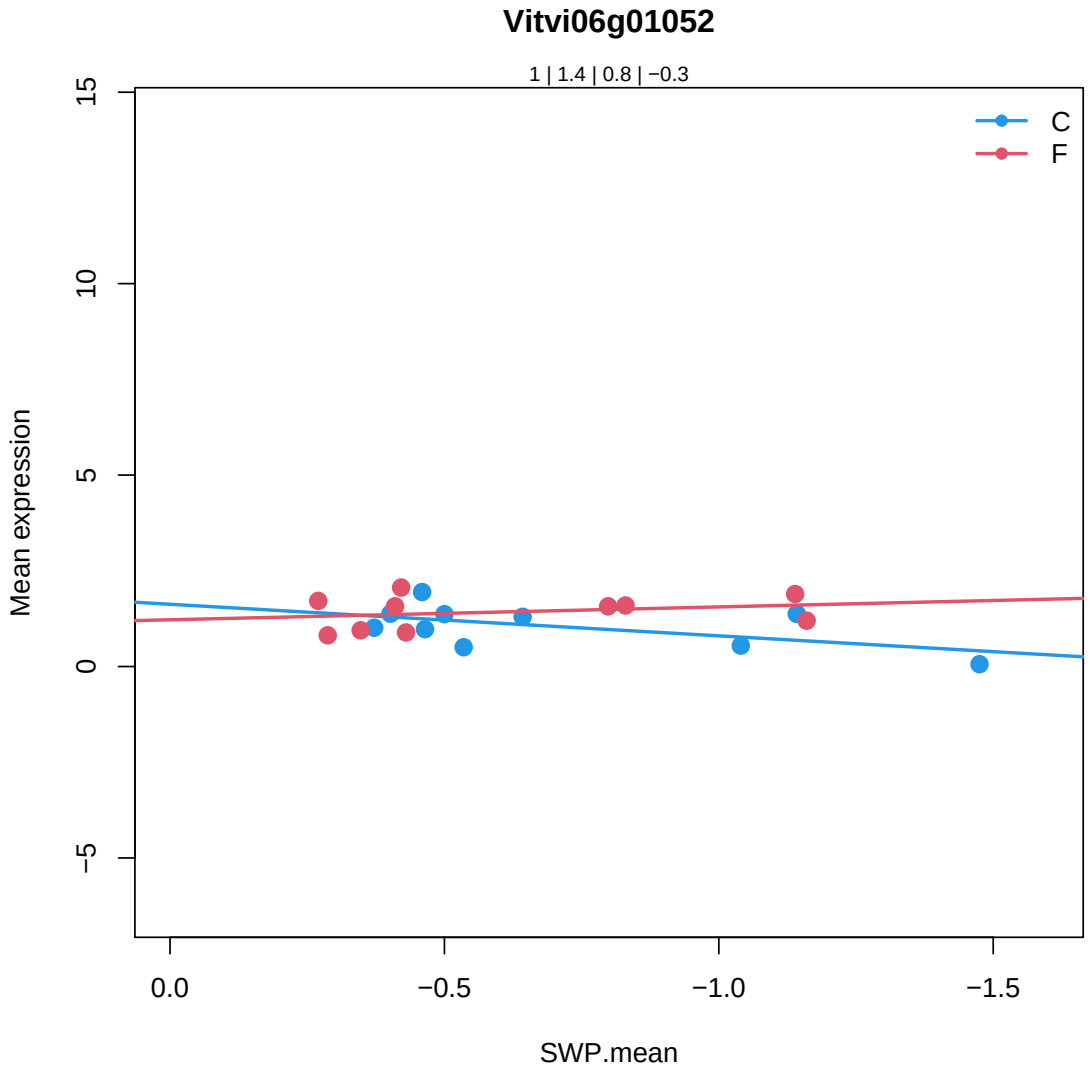
7.6.201 Vitvi06g01052: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01052
        35.2
        not assigned.unknown
        embryo defective 1379 |
        Chr5:7187416-7189521 REVERSE LENGTH=312 |
        201606
```

Coefficients for Vitvi06g01052.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.046094	5.437507e-07	***	6.32274e-07	***
SlopeC	0.8247781	0.05921083	.	0.5387954	
MeanF-MeanC	0.3791373	0.08566073	.	0.3322241	
SlopeF-SlopeC	-1.160757	0.0732041	.	0.9999488	



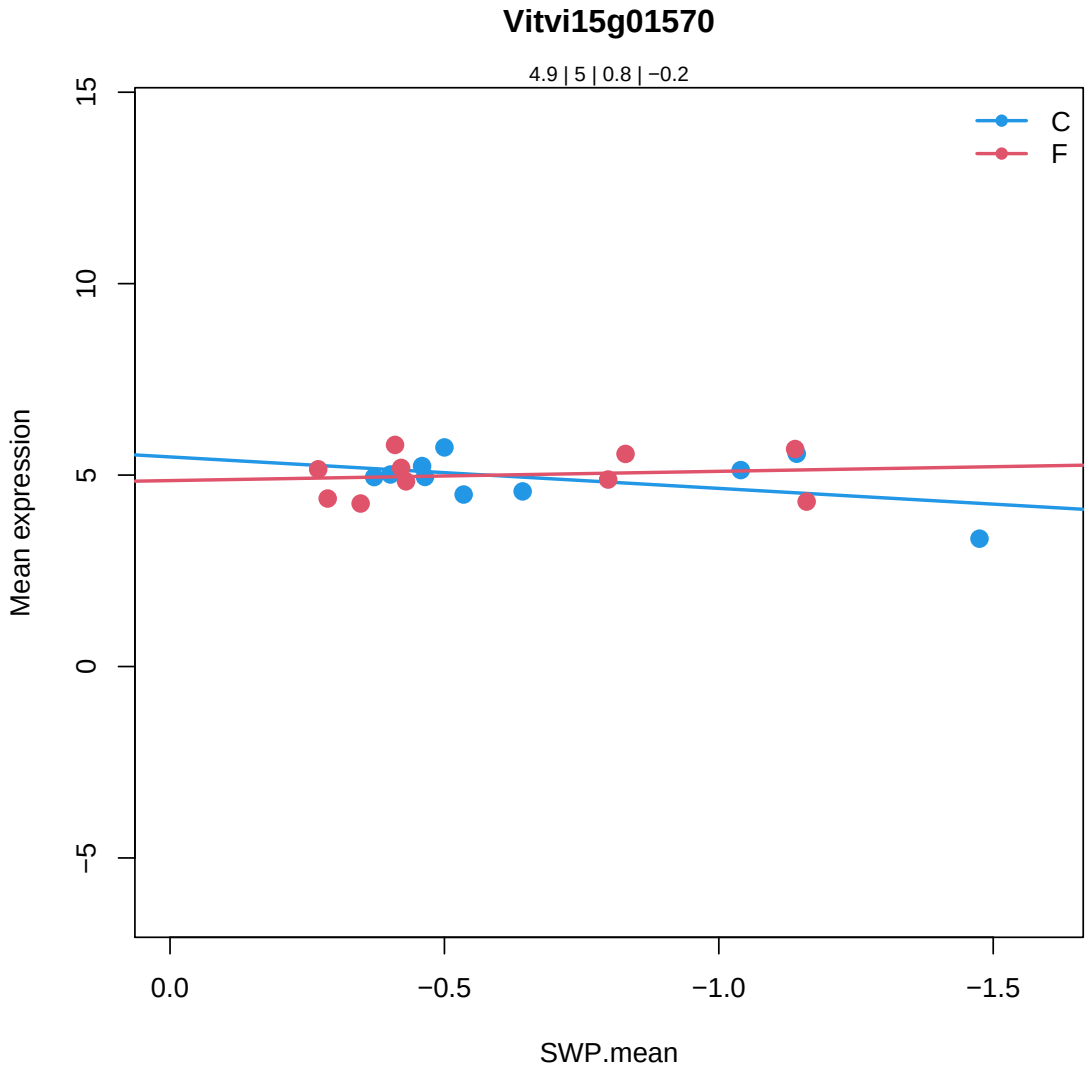
7.6.202 Vitvi15g01570: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g01570
        27.3.8
        RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family
        hypothetical protein |
        Chr5:21505319-21505993 FORWARD LENGTH=224 |
        201606
```

Coefficients for Vitvi15g01570.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.896292	6.610803e-18	***	1.817166e-17	***
SlopeC	0.8219113	0.1232143		0.644269	
MeanF-MeanC	0.1066139	0.6862621		0.8995534	
SlopeF-SlopeC	-1.063485	0.1773163		0.9999488	



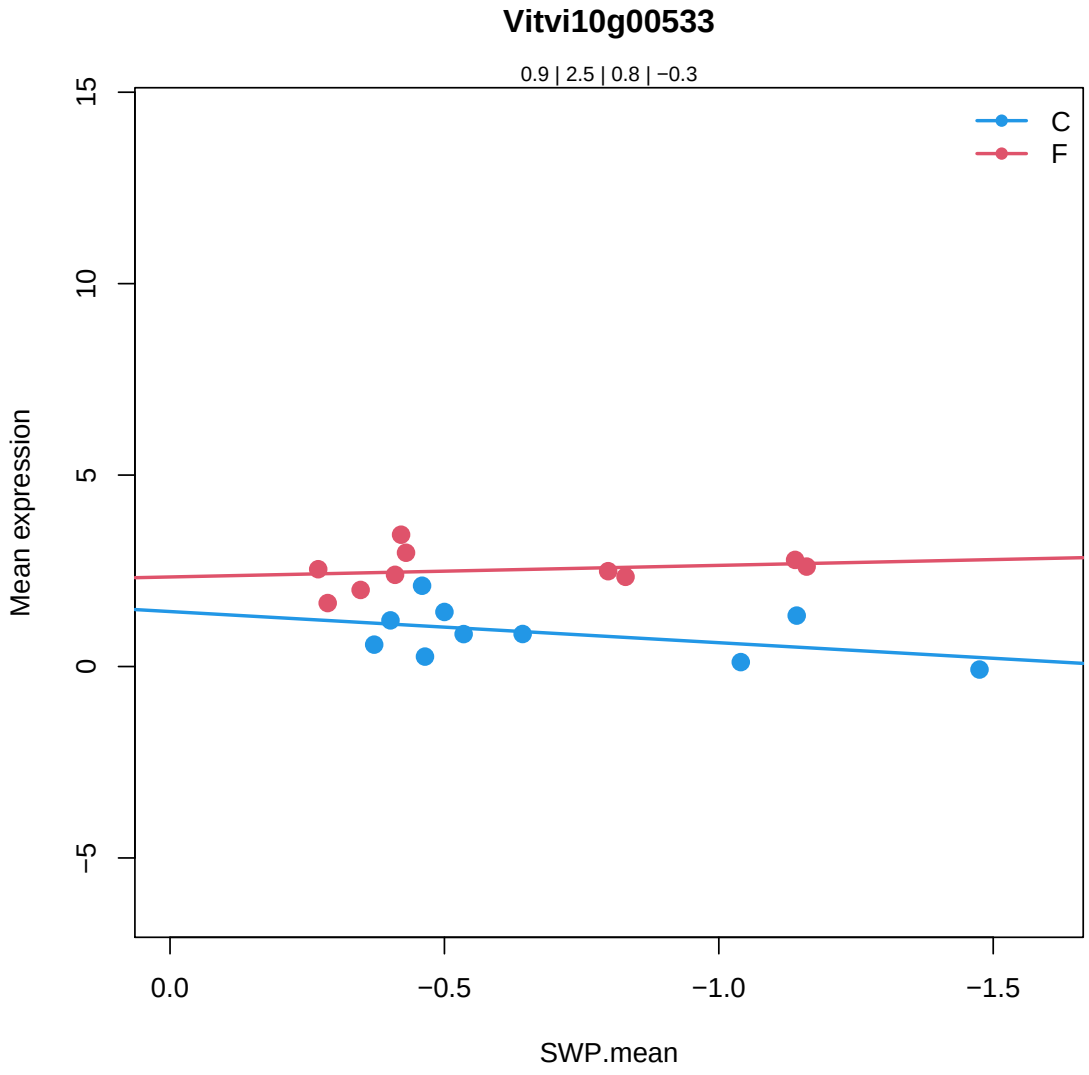
7.6.203 Vitvi10g00533: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00533
        30.1.1
        signalling.in sugar and nutrient physiology.misc
        glutamate receptor 2.7 |
        Chr2:12511479-12515893 REVERSE LENGTH=952 |
        201606
```

Coefficients for Vitvi10g00533.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8632213	7.18601e-05	***	7.956499e-05	***
SlopeC	0.8136253	0.1114676		0.6258604	
MeanF-MeanC	1.660201	1.214132e-06	***	3.871508e-05	***
SlopeF-SlopeC	-1.116493	0.140516		0.9999488	



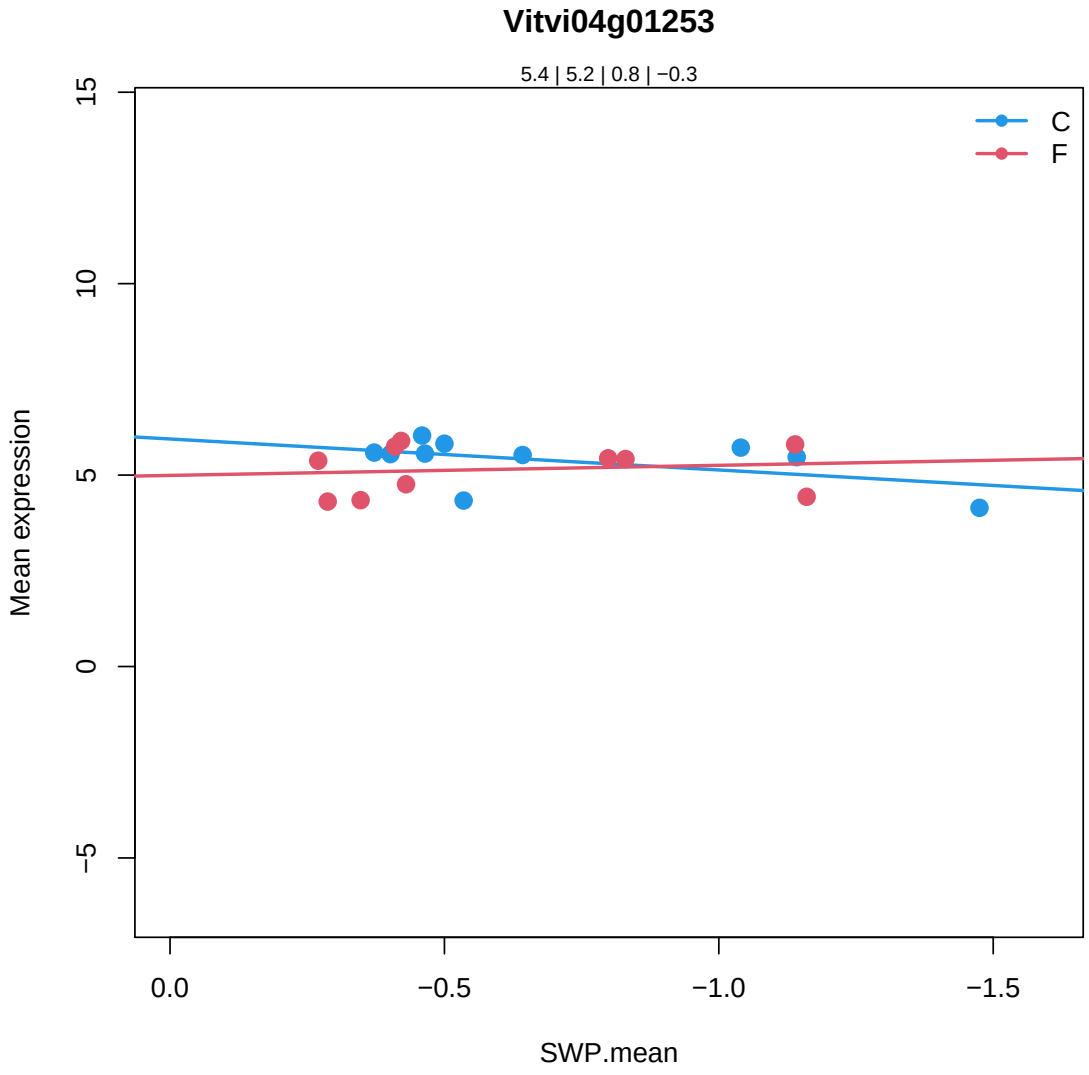
7.6.204 Vitvi04g01253: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01253
        35.2
        not assigned.unknown
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi04g01253.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.373856	1.18901e-18	***	4.014424e-18	***
SlopeC	0.8091859	0.1327897		0.654787	
MeanF-MeanC	-0.2220592	0.4082164		0.7494209	
SlopeF-SlopeC	-1.073145	0.1780958		0.9999488	



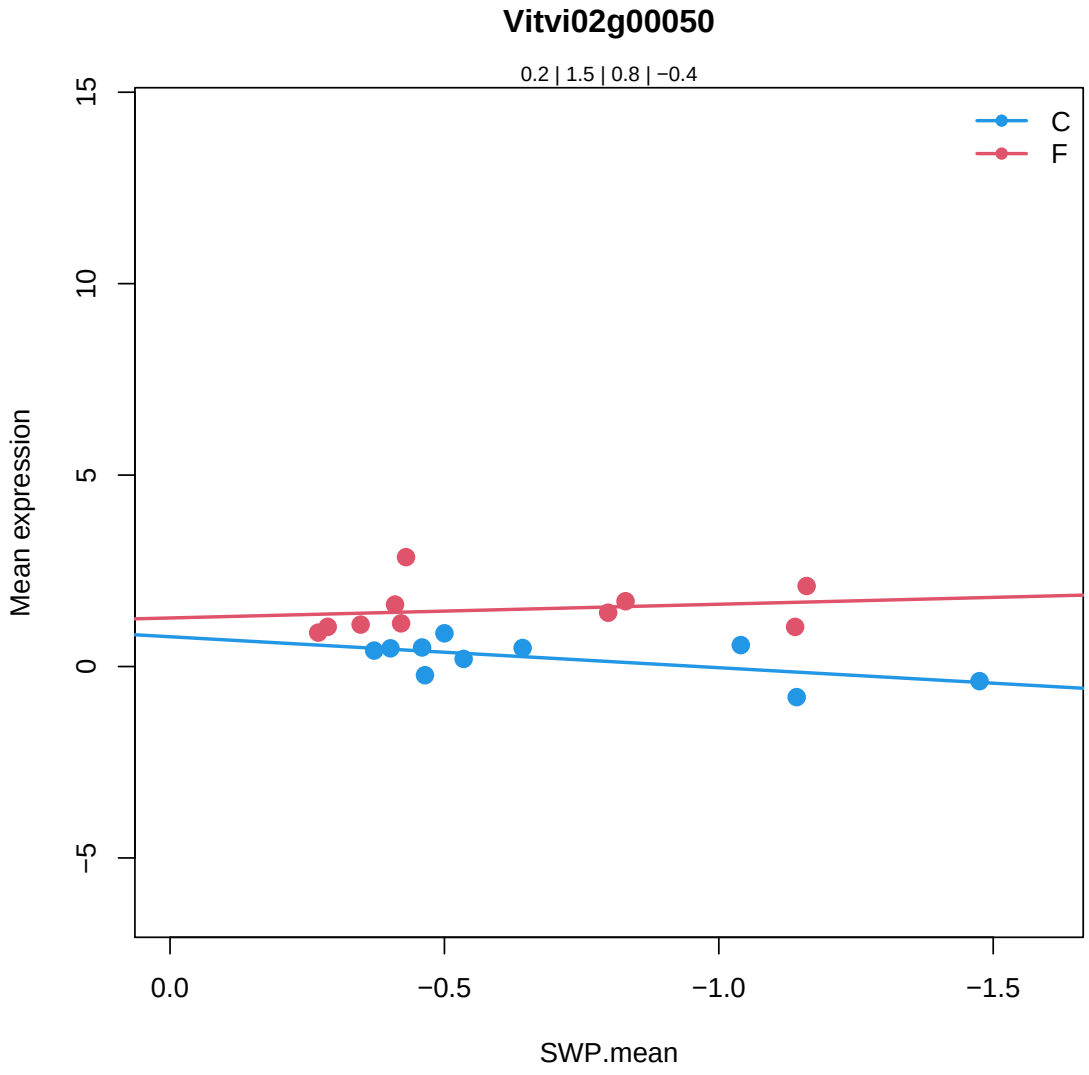
7.6.205 Vitvi02g00050: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00050
        35.2
        not assigned.unknown
        Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein fam
        Chr2:18961424-18962089 FORWARD LENGTH=221 |
        201606
```

Coefficients for Vitvi02g00050.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.2088857	0.2286666		0.2339623	
SlopeC	0.808762	0.09899795	.	0.6110181	
MeanF-MeanC	1.277586	2.409793e-05	***	0.0005354236	***
SlopeF-SlopeC	-1.166939	0.1090914		0.9999488	



7.6.206 Vitvi08g00744: type5

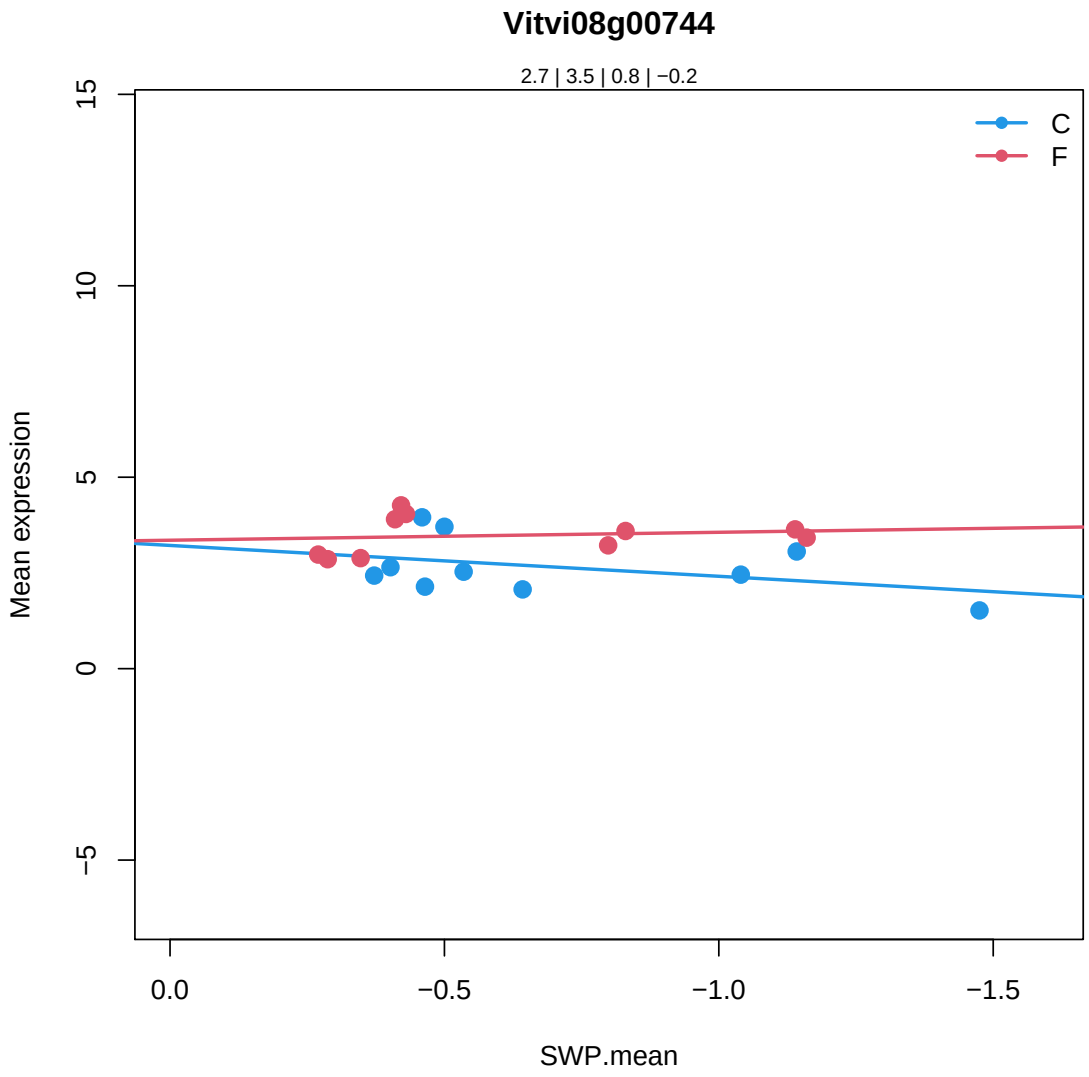
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g00744
        30.2.19
        signalling.receptor kinases.legume-lectin
        lectin receptor kinase a4.1 |
        Chr5:214517-216637 REVERSE LENGTH=706 |
        201606

Vitvi08g00744
        29.4
        protein.postranslational modification
        lectin receptor kinase a4.1 |
        Chr5:214517-216637 REVERSE LENGTH=706 |
        201606
```

Coefficients for Vitvi08g00744.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.651548	2.533499e-12	***	3.555436e-12	***
SlopeC	0.8054592	0.1382282		0.6650191	
MeanF-MeanC	0.8290338	0.005115395	**	0.04654856	*
SlopeF-SlopeC	-1.012865	0.2070723		0.9999488	


Vitvi08g00744
2.7 | 3.5 | 0.8 | −0.2
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

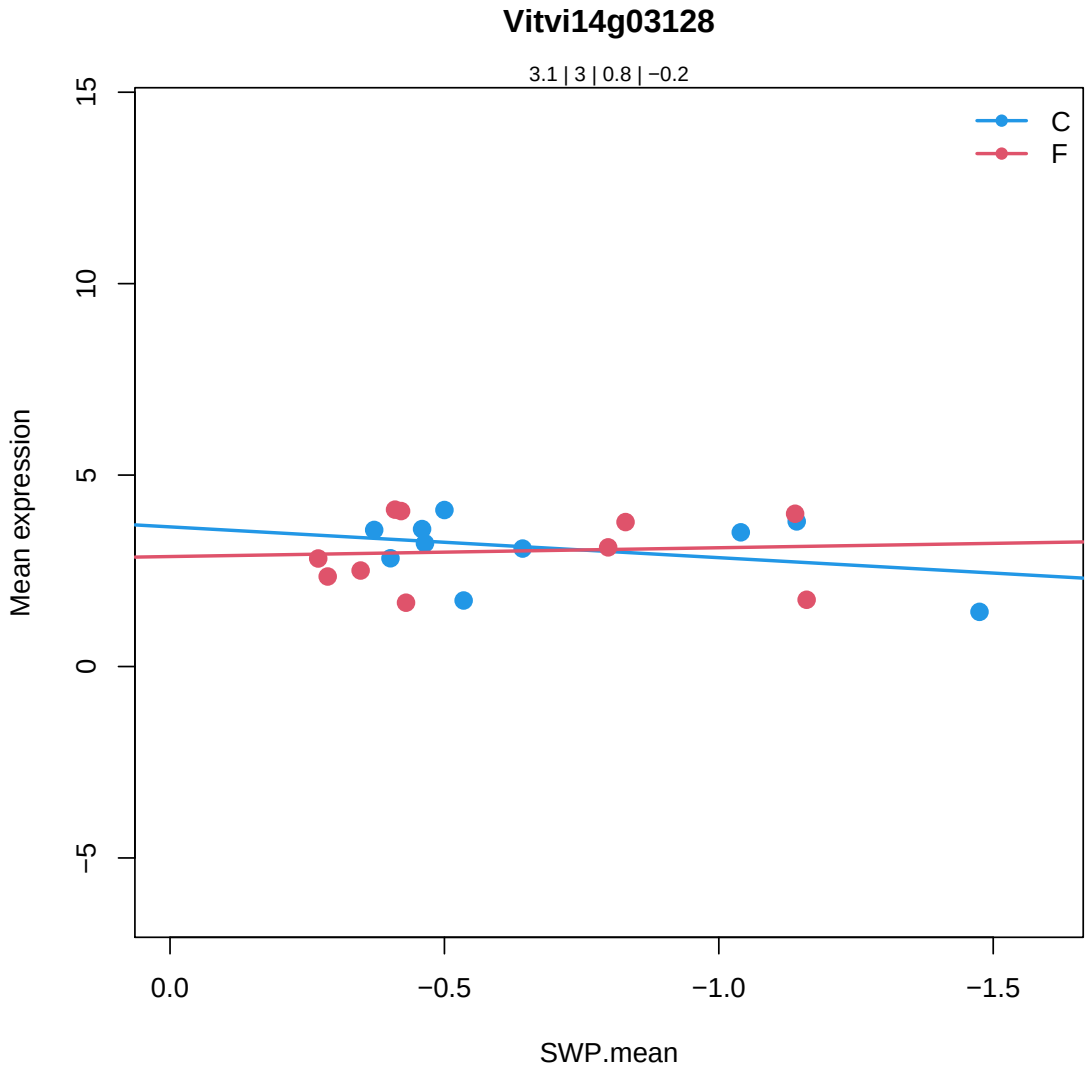
7.6.207 Vitvi14g03128: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g03128
        35.2
        not assigned.unknown
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606
```

Coefficients for Vitvi14g03128.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.081572	1.114686e-10	***	1.4555e-10	***
SlopeC	0.8045629	0.2899744		0.7812116	
MeanF-MeanC	-0.0694296	0.8555928		0.9617841	
SlopeF-SlopeC	-1.033964	0.3592802		0.9999488	



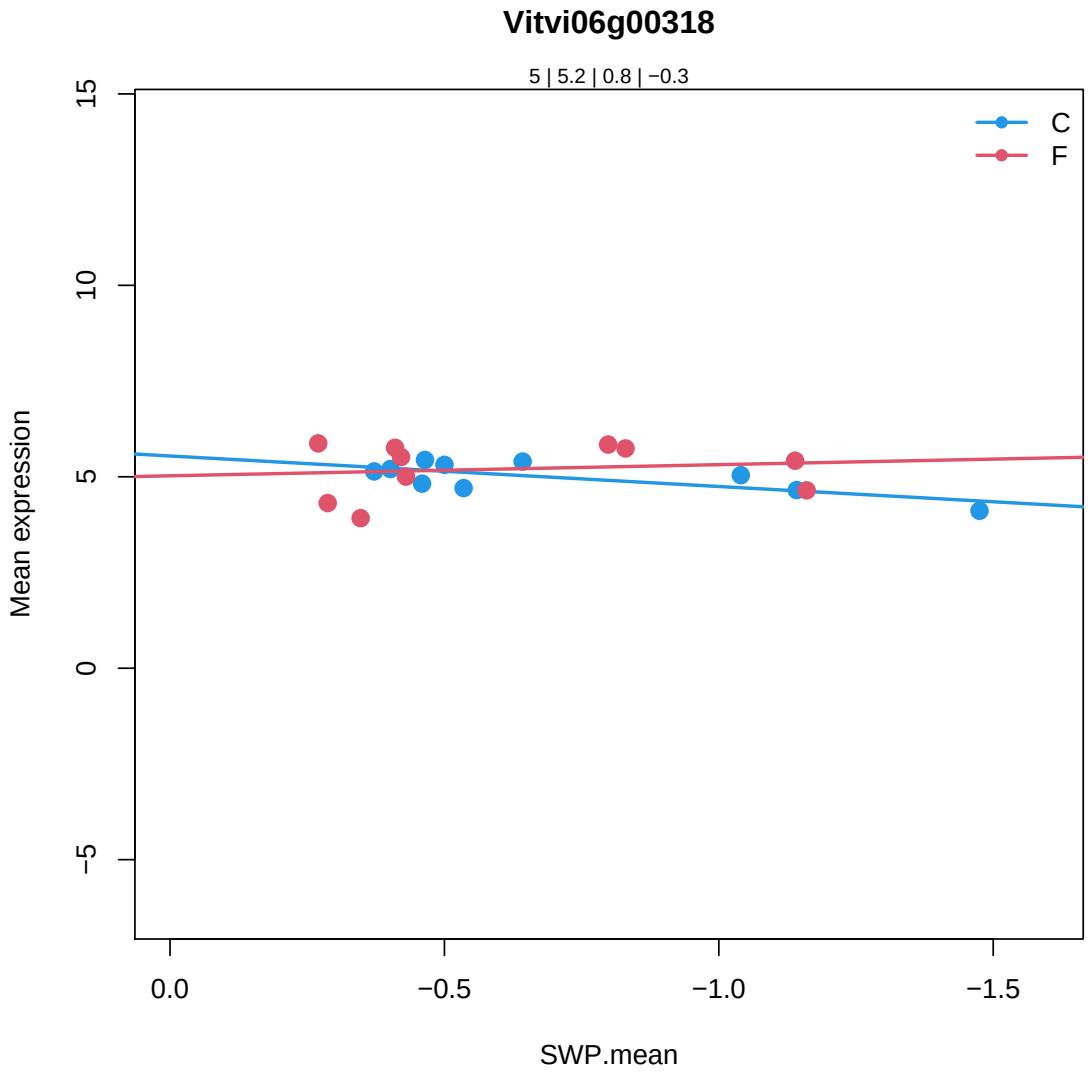
7.6.208 Vitvi06g00318: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00318
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi06g00318.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.982566	1.063937e-18	***	3.641707e-18	***
SlopeC	0.7970486	0.1096832		0.623774	
MeanF-MeanC	0.2204045	0.3740444		0.7274703	
SlopeF-SlopeC	-1.087865	0.140545		0.9999488	



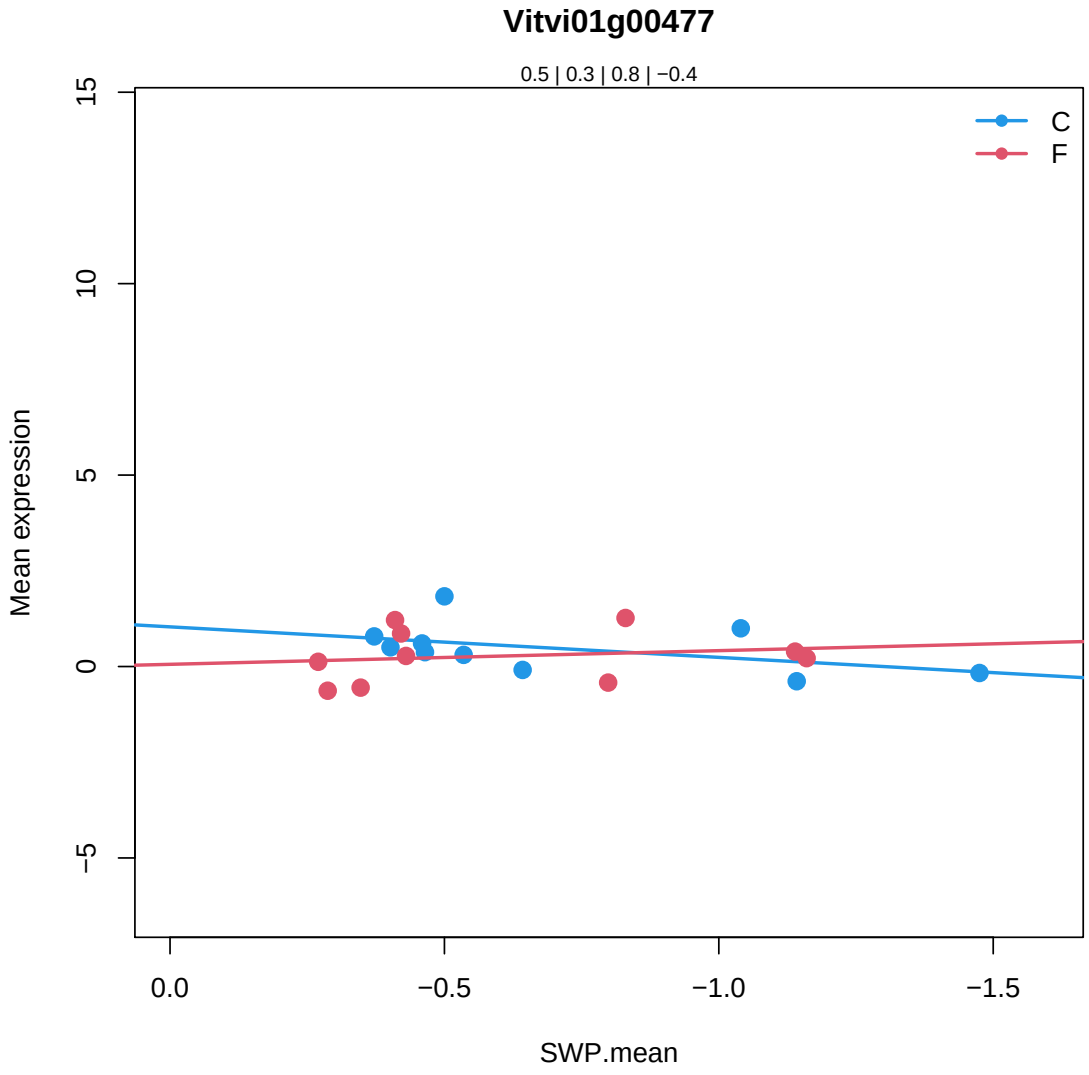
7.6.209 Vitvi01g00477: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00477
        30.2.17
        signalling.receptor kinases.DUF 26
        plasmodesmata-located protein 6 |
        Chr2:291717-292496 REVERSE LENGTH=259 |
        201606
```

Coefficients for Vitvi01g00477.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4754996	0.02487788	*	0.02609874	*
SlopeC	0.7969663	0.1606271		0.6892674	
MeanF-MeanC	-0.2008524	0.4789853		0.7941132	
SlopeF-SlopeC	-1.154042	0.1717479		0.9999488	



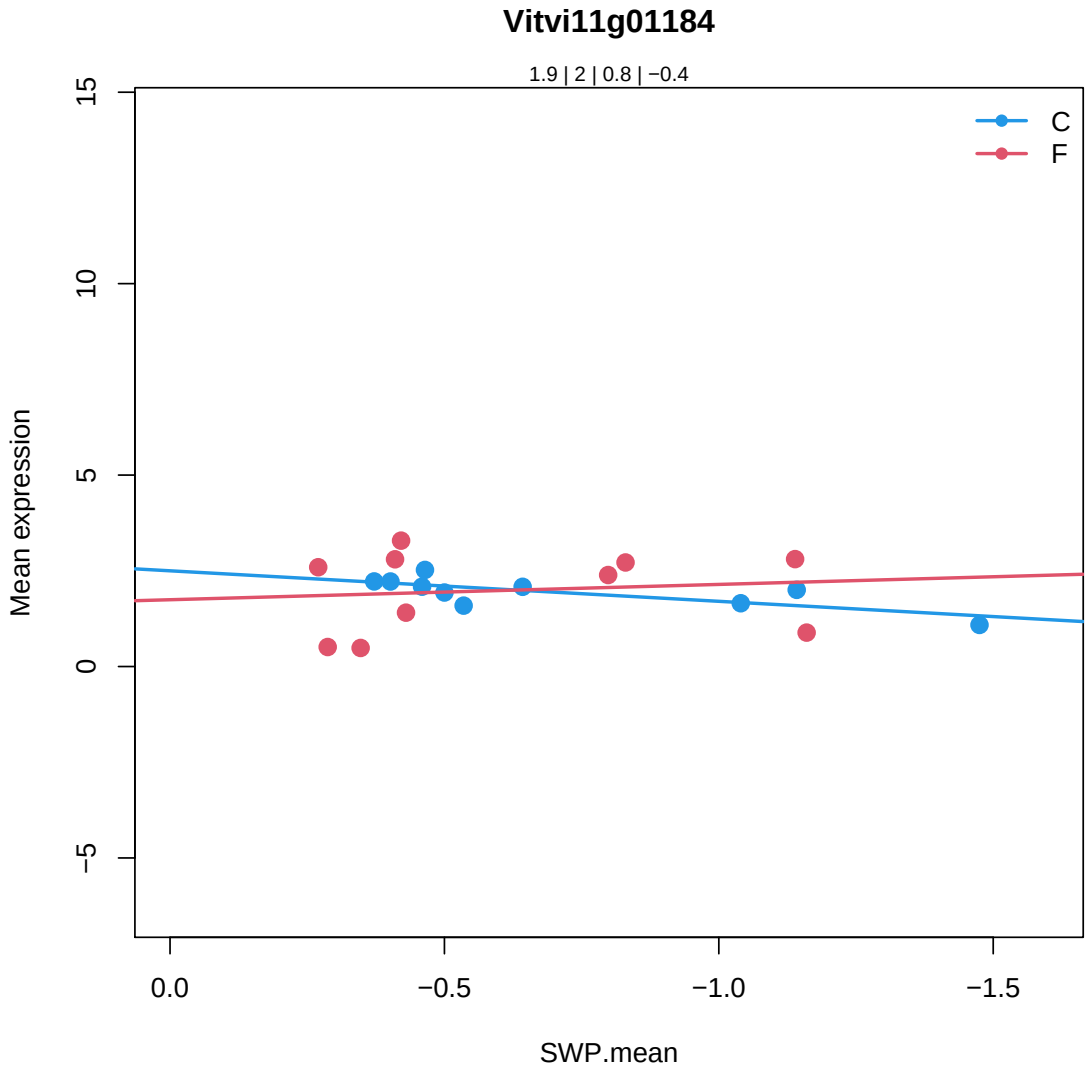
7.6.210 Vitvi11g01184: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g01184
        26.11.1
        misc.alcohol dehydrogenases.cinnamyl alcohol dehydrogenase
        Zinc-binding dehydrogenase family protein |
        Chr5:5579202-5580383 REVERSE LENGTH=239 |
        201606
```

Coefficients for Vitvi11g01184.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.939584	4.336111e-08	***	5.193383e-08	***
SlopeC	0.7966994	0.2367792		0.7522636	
MeanF-MeanC	0.04820783	0.8861545		0.9704088	
SlopeF-SlopeC	-1.196431	0.2327341		0.9999488	



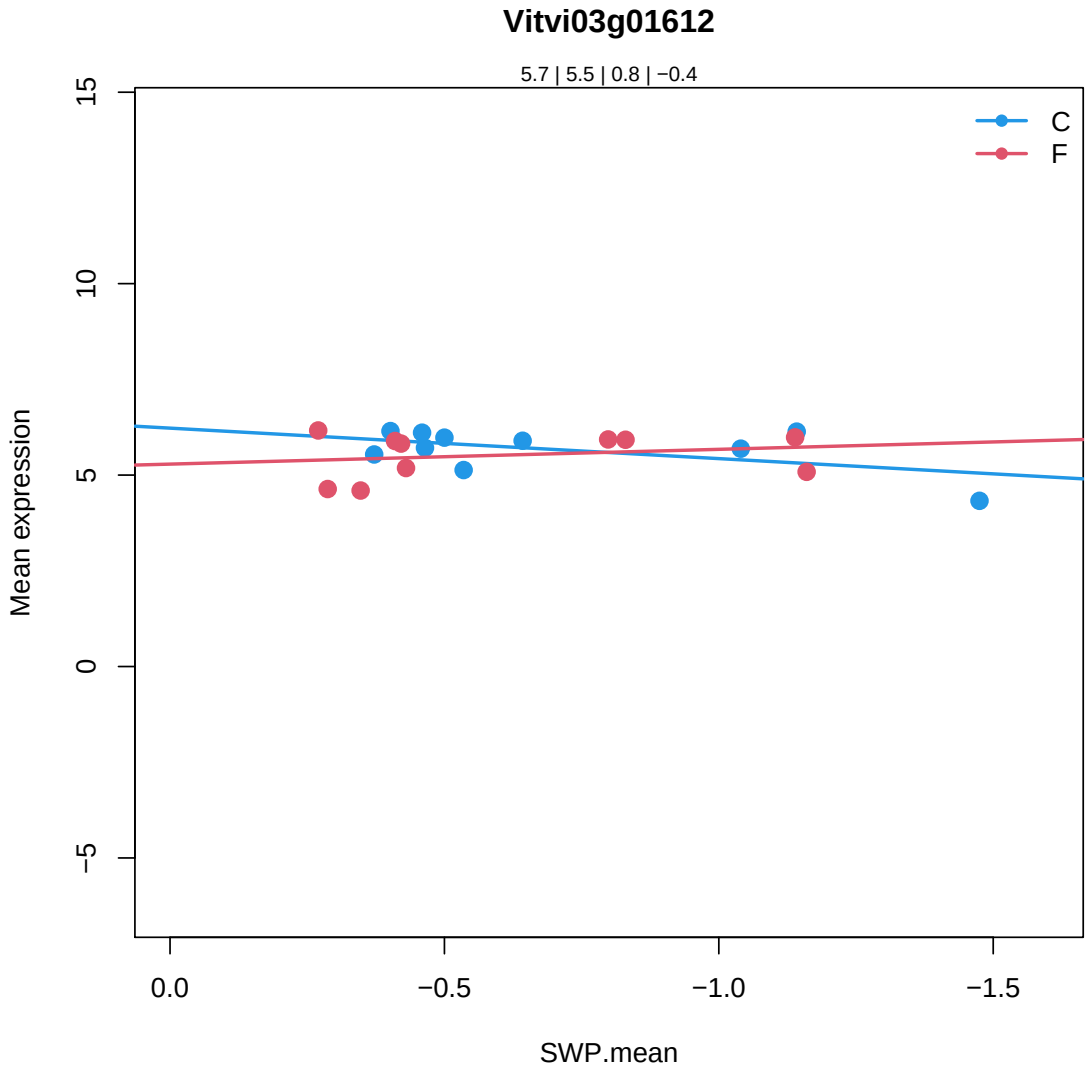
7.6.211 Vitvi03g01612: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g01612
        35.2
        not assigned.unknown
        photosystem I reaction center subunit N |
        Chr1:18504845-18505431 FORWARD LENGTH=129 |
        201606
```

Coefficients for Vitvi03g01612.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.666395	7.578552e-20	***	3.766296e-19	***
SlopeC	0.7958812	0.1110976		0.6258604	
MeanF-MeanC	-0.1447686	0.5582867		0.8379714	
SlopeF-SlopeC	-1.181929	0.1118498		0.9999488	



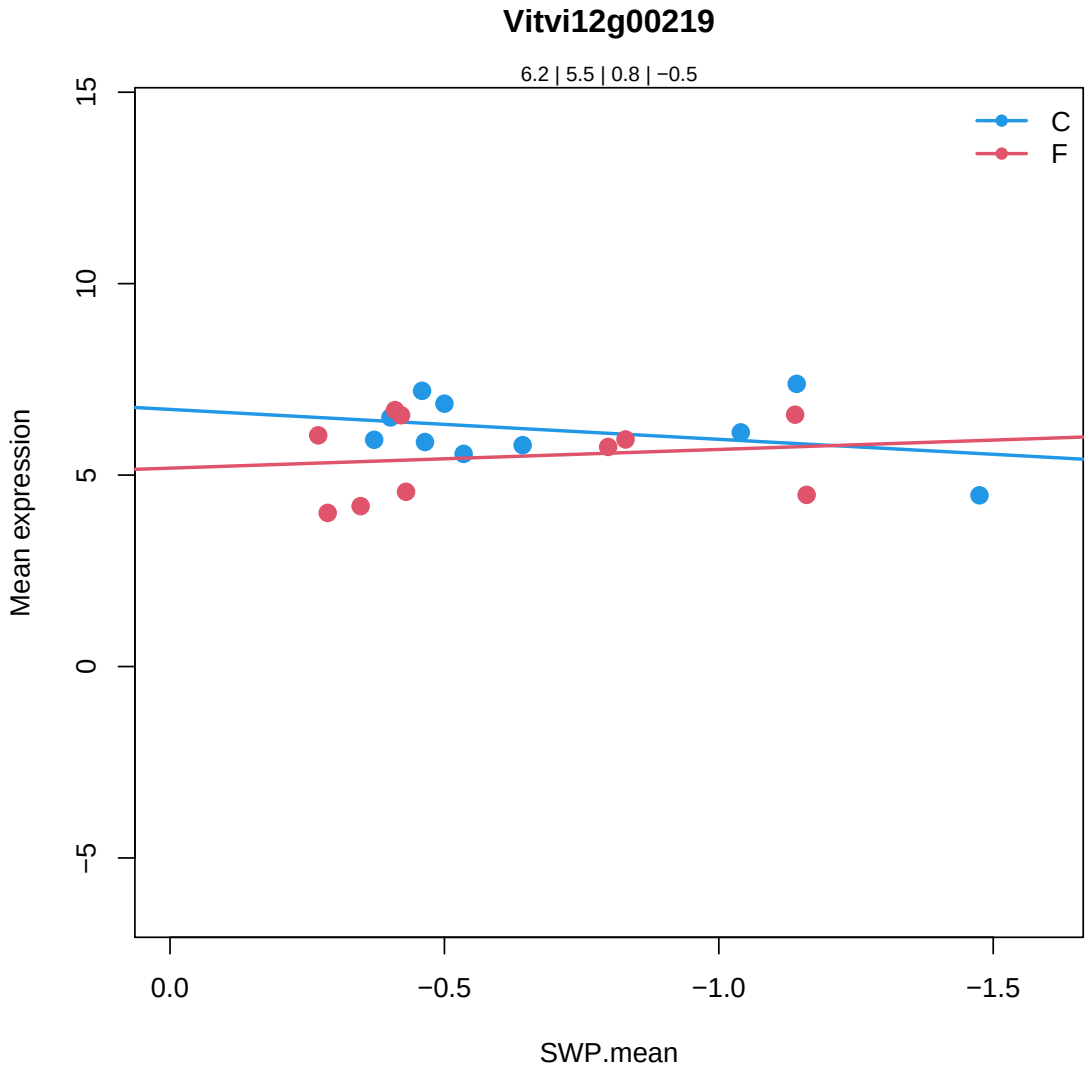
7.6.212 Vitvi12g00219: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00219
        27.3.29
        RNA.regulation of transcription.TCP transcription factor family
        TCP family transcription factor 4 |
        Chr3:5062308-5063570 FORWARD LENGTH=420 |
        201606
```

Coefficients for Vitvi12g00219.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.165733	3.838559e-16	***	7.607245e-16	***
SlopeC	0.7810084	0.3307557		0.8008627	
MeanF-MeanC	-0.6869776	0.09945791	.	0.3629515	
SlopeF-SlopeC	-1.26933	0.2892447		0.9999488	



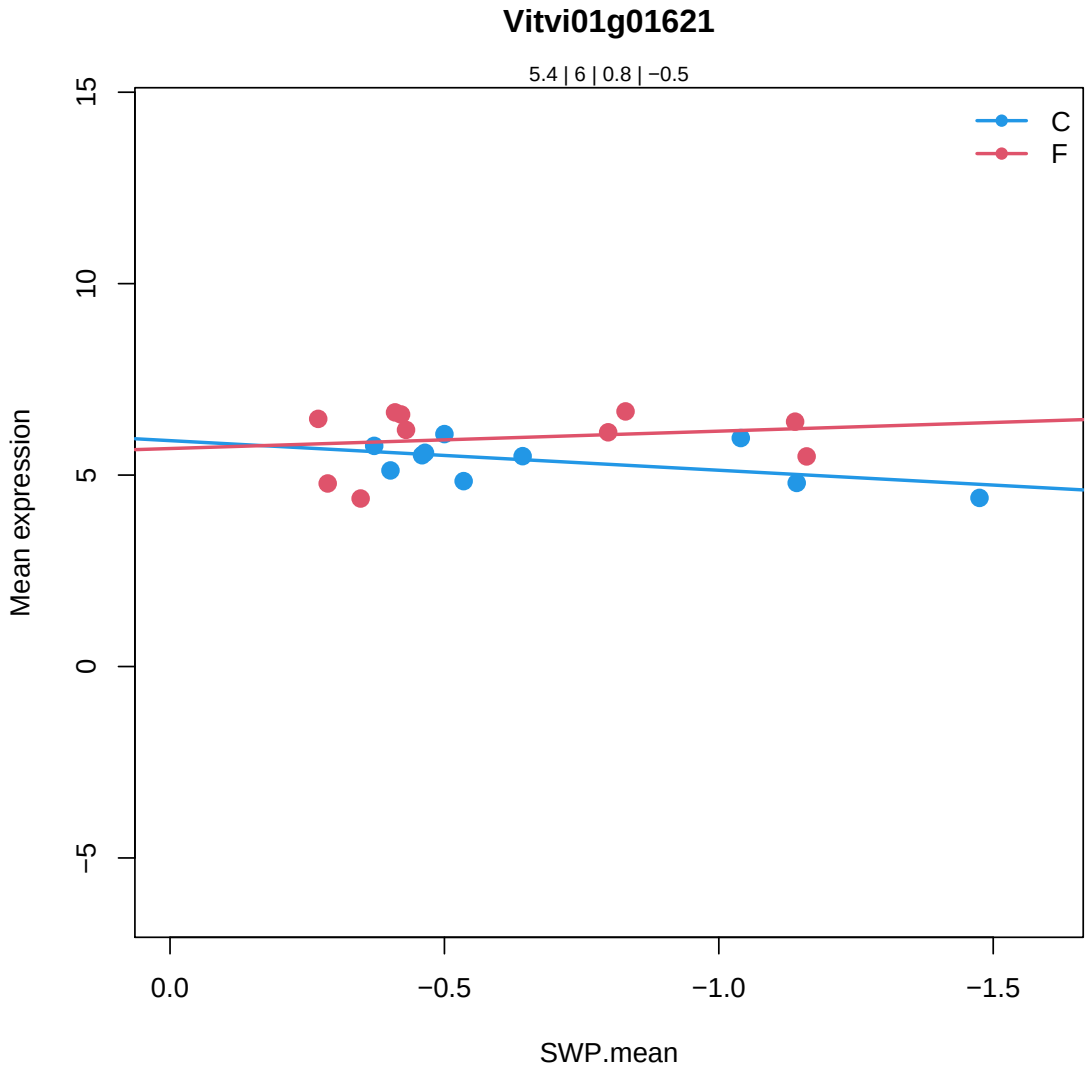
7.6.213 Vitvi01g01621: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01621
        35.2
        not assigned.unknown
        Galactose oxidase/kelch repeat superfamily protein |
        Chr1:25277294-25278529 FORWARD LENGTH=376 |
        201606
```

Coefficients for Vitvi01g01621.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.355554	8.902756e-18	***	2.375211e-17	***
SlopeC	0.7732901	0.1877659		0.7194453	
MeanF-MeanC	0.6142739	0.04524891	*	0.2244334	
SlopeF-SlopeC	-1.227167	0.1613287		0.9999488	



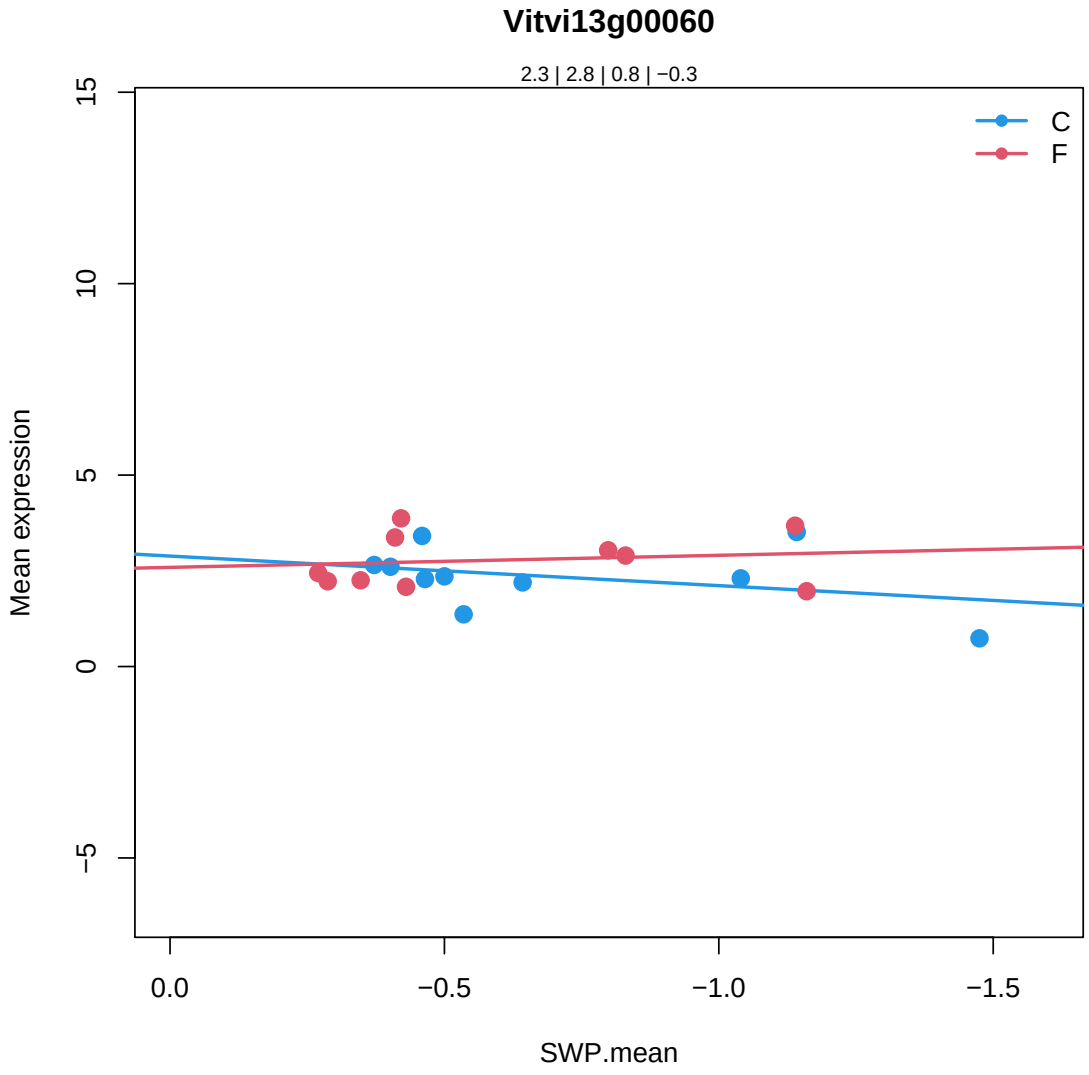
7.6.214 Vitvi13g00060: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00060
        11.2.3
        lipid metabolism.FA desaturation.omega 3 desaturase
        fatty acid desaturase 7 |
        Chr3:3499959-3502126 FORWARD LENGTH=446 |
        201606
```

Coefficients for Vitvi13g00060.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.341765	8.243813e-10	***	1.042497e-09	***
SlopeC	0.7719551	0.2326955		0.751359	
MeanF-MeanC	0.4400237	0.1826516		0.5185279	
SlopeF-SlopeC	-1.087362	0.257878		0.9999488	



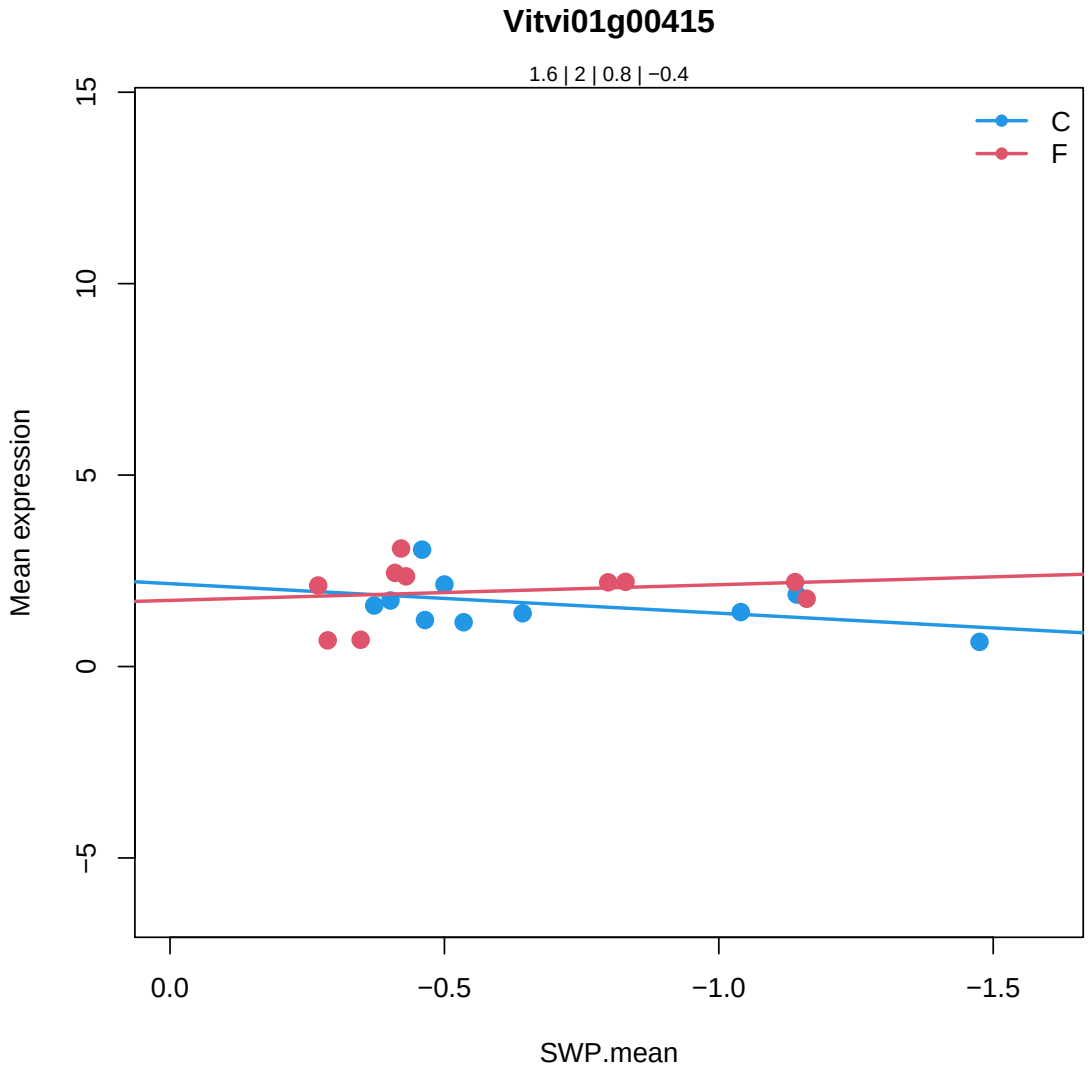
7.6.215 Vitvi01g00415: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00415
        29.5.5
        protein.degradation.serine protease
        serine carboxypeptidase-like 50 |
        Chr1:5168613-5169947 FORWARD LENGTH=444 |
        201606
```

Coefficients for Vitvi01g00415.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.621738	1.09947e-07	***	1.303019e-07	***
SlopeC	0.7706875	0.1974909		0.7250708	
MeanF-MeanC	0.354856	0.2414358		0.5990501	
SlopeF-SlopeC	-1.180675	0.1851796		0.9999488	



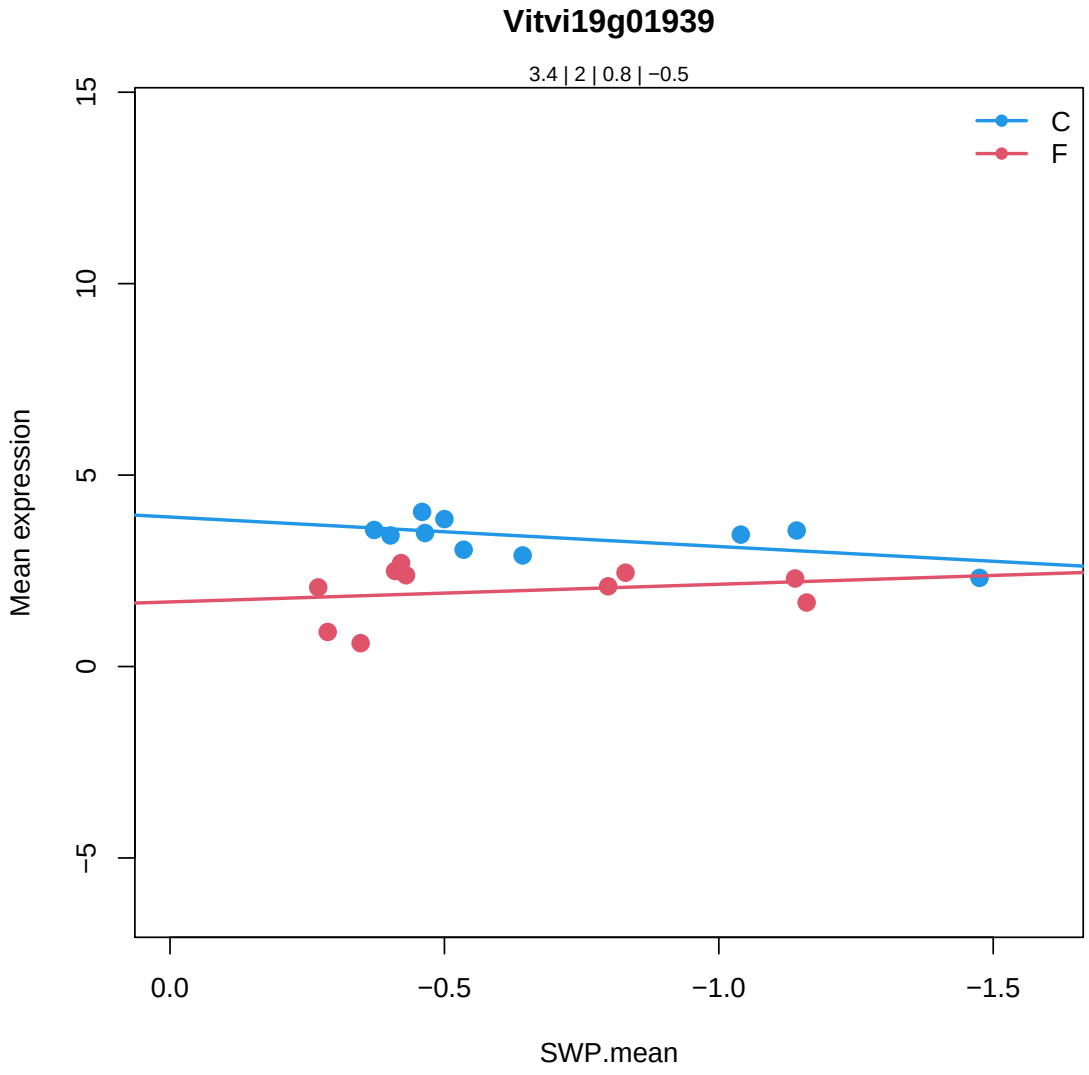
7.6.216 Vitvi19g01939: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g01939
        35.2
        not assigned.unknown
        lectin protein kinase family protein |
        Chr1:25302812-25305333 REVERSE LENGTH=581 |
        201606
```

Coefficients for Vitvi19g01939.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.362719	9.426597e-15	***	1.581162e-14	***
SlopeC	0.7703519	0.1385312		0.6650191	
MeanF-MeanC	-1.395007	1.808527e-05	***	0.0004240857	***
SlopeF-SlopeC	-1.231986	0.112856		0.9999488	



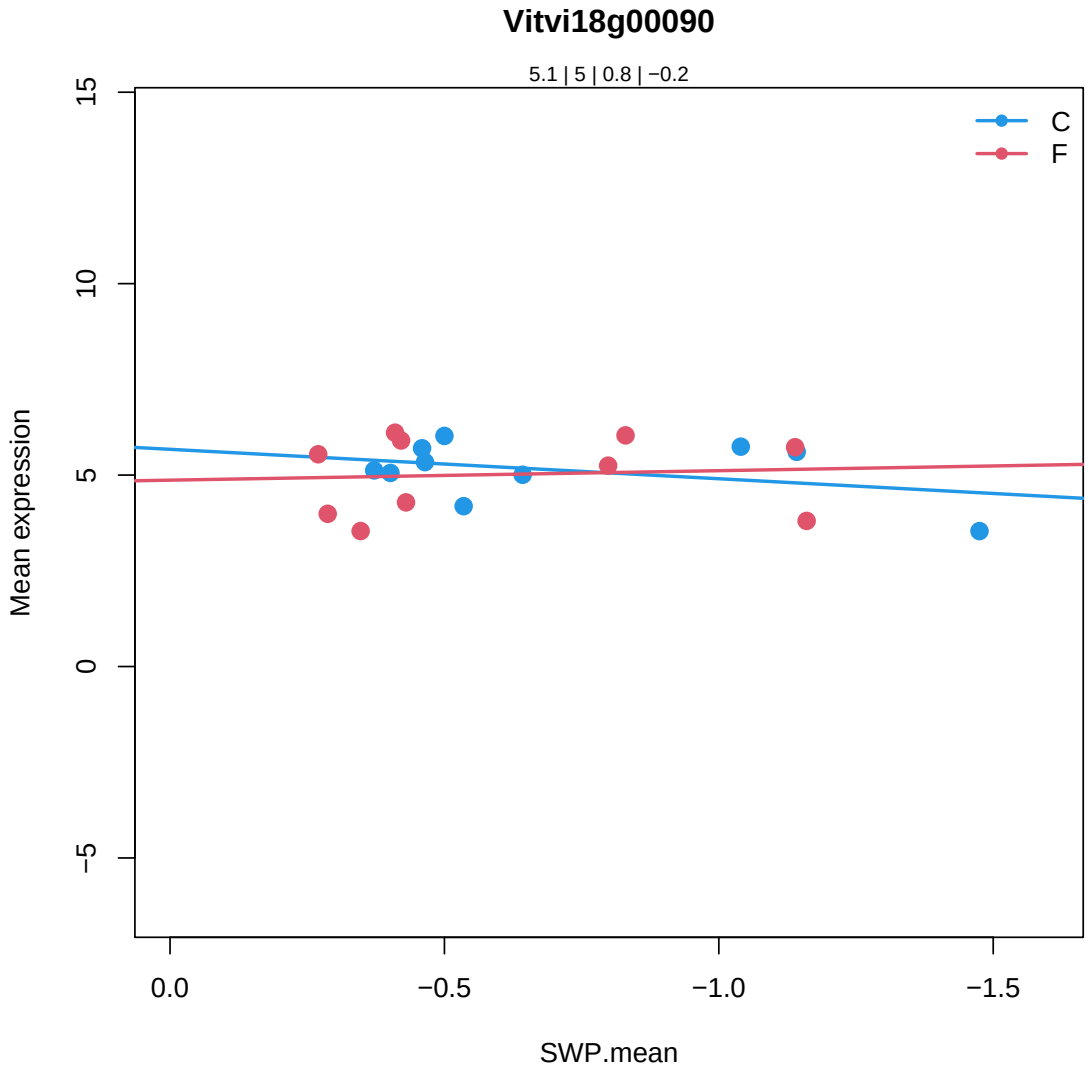
7.6.217 Vitvi18g00090: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00090
        29.4.1.57
        protein.postranslational modification.kinase.receptor like cytoplasmat
        Protein kinase superfamily protein |
        Chr1:7158422-7160022 REVERSE LENGTH=381 |
        201606
```

Coefficients for Vitvi18g00090.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.132268	3.804643e-15	***	6.683229e-15	***
SlopeC	0.7687355	0.3045275		0.7887711	
MeanF-MeanC	-0.1141578	0.7615639		0.930546	
SlopeF-SlopeC	-1.016239	0.3605294		0.9999488	



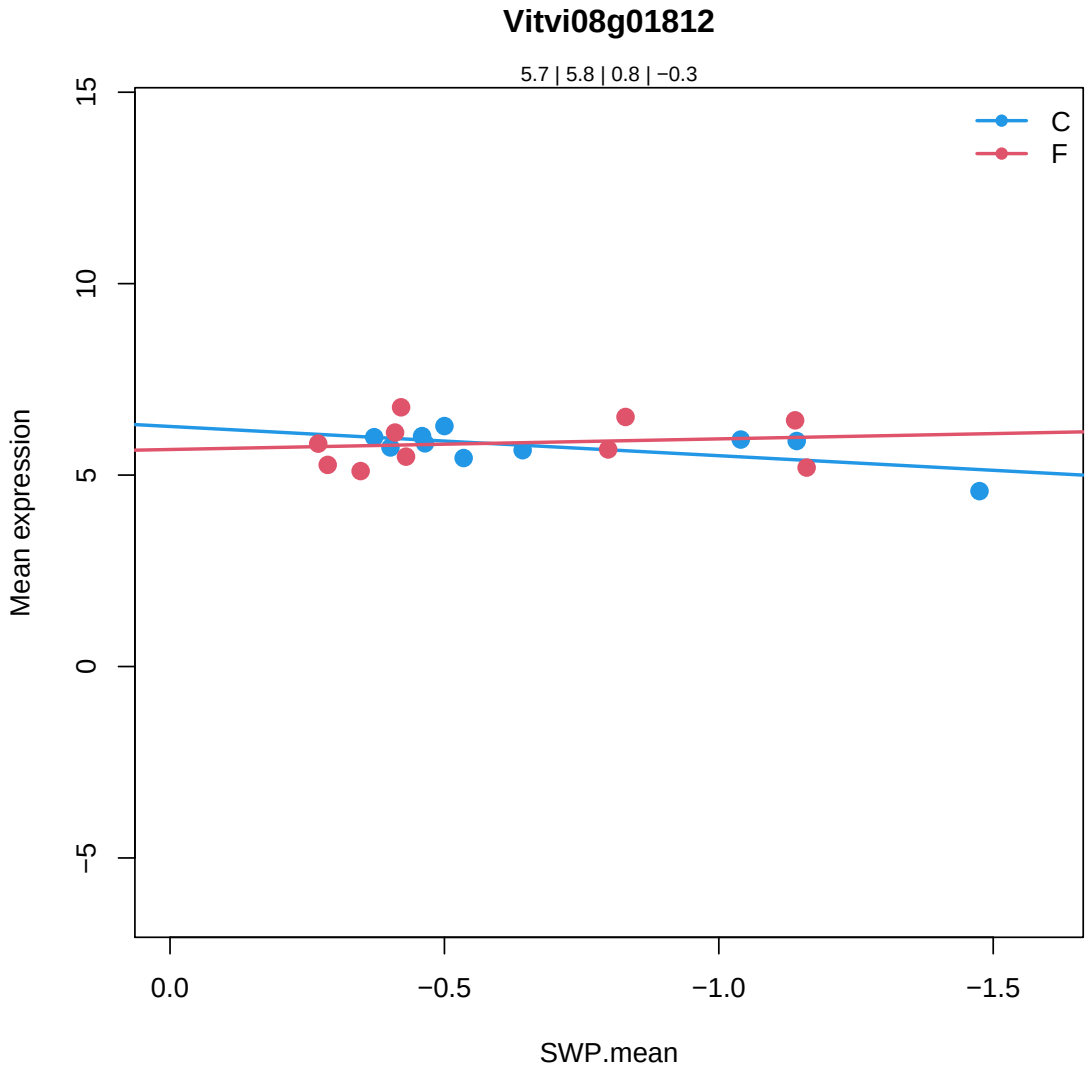
7.6.218 Vitvi08g01812: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01812
        12.3.1
        N-metabolism.N-degradation.glutamate dehydrogenase
        glutamate dehydrogenase 1 |
        Chr5:6006172-6008248 FORWARD LENGTH=411 |
        201606
```

Coefficients for Vitvi08g01812.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.733033	1.554448e-20	***	1.014251e-19	***
SlopeC	0.7635271	0.1038256		0.6154205	
MeanF-MeanC	0.1035963	0.6547875		0.8844988	
SlopeF-SlopeC	-1.040395	0.1345248		0.9999488	



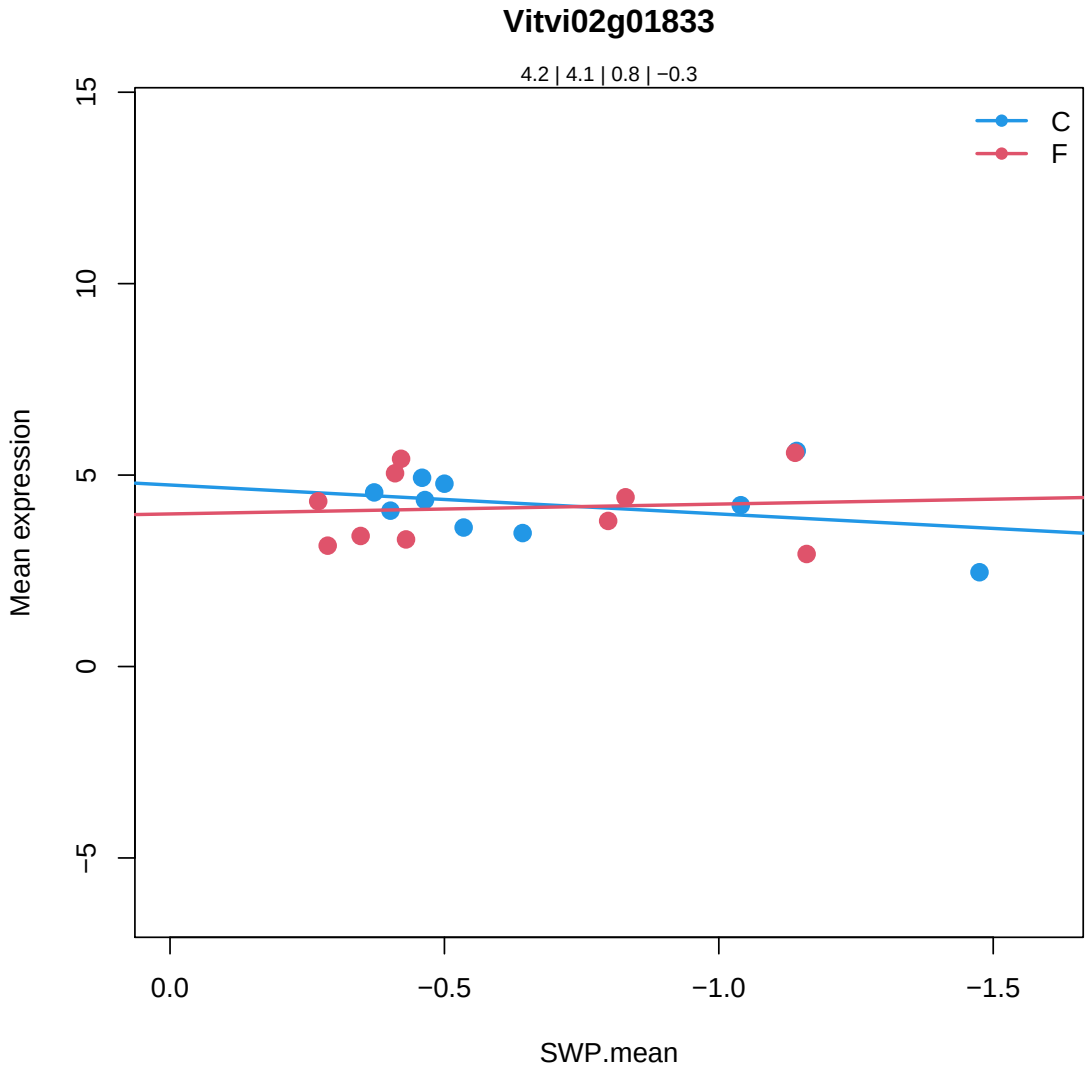
7.6.219 Vitvi02g01833: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g01833
        35.2
        not assigned.unknown
        Copper amine oxidase family protein |
        Chr1:23258253-23261772 REVERSE LENGTH=712 |
        201606
```

Coefficients for Vitvi02g01833.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.209131	3.989059e-13	***	5.873948e-13	***
SlopeC	0.7558551	0.3283242		0.8006793	
MeanF-MeanC	-0.0674087	0.8623366		0.9641172	
SlopeF-SlopeC	-1.013123	0.3776903		0.9999488	



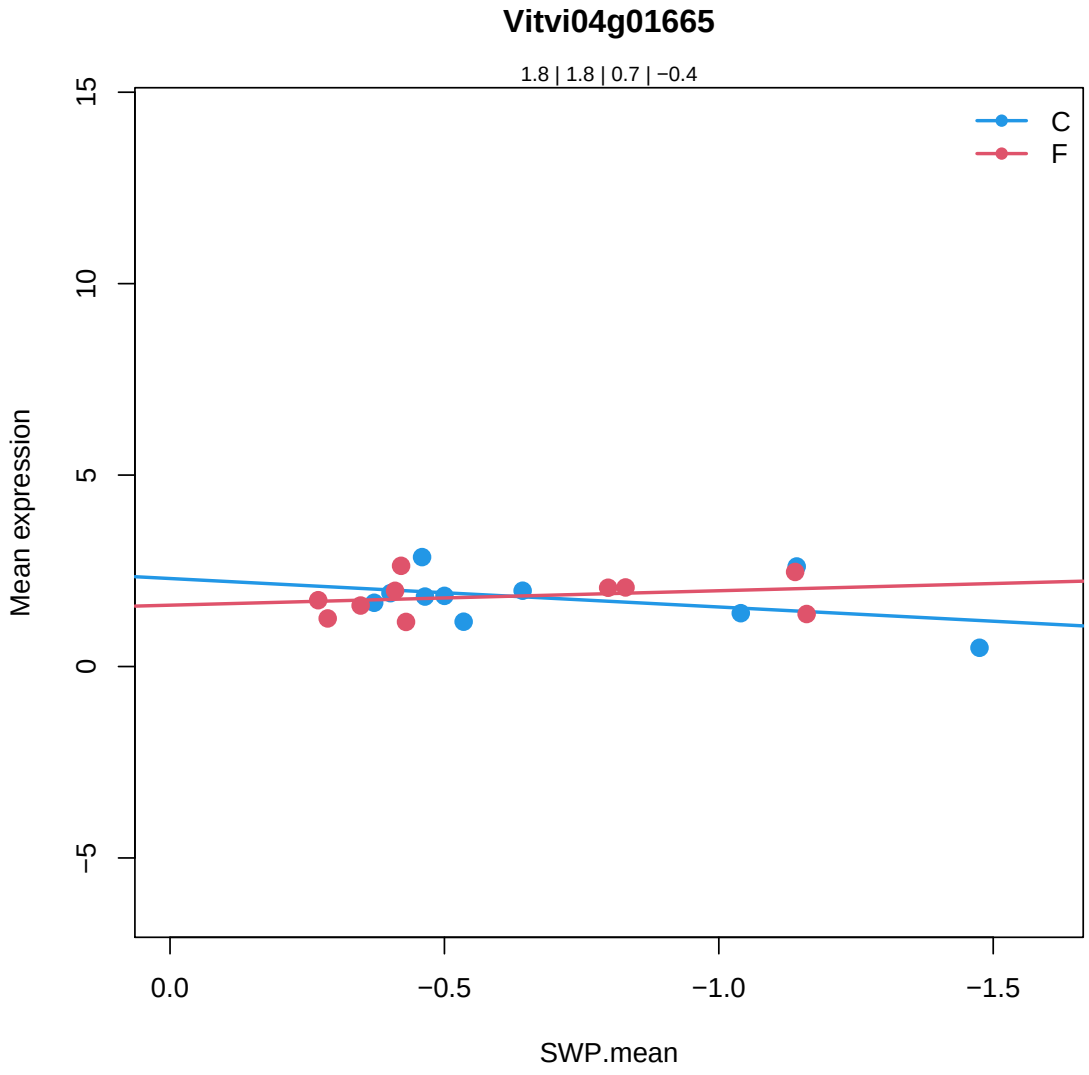
7.6.220 Vitvi04g01665: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01665
        27.3.62
        RNA.regulation of transcription.nucleosome/chromatin assembly factor g
        Transducin/WD40 repeat-like superfamily protein |
        Chr5:25833724-25836158 FORWARD LENGTH=428 |
        201606
```

Coefficients for Vitvi04g01665.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.775377	1.630884e-09	***	2.042558e-09	***
SlopeC	0.7436708	0.1476021		0.6736918	
MeanF-MeanC	0.05618618	0.8254226		0.9509522	
SlopeF-SlopeC	-1.120514	0.1429102		0.9999488	



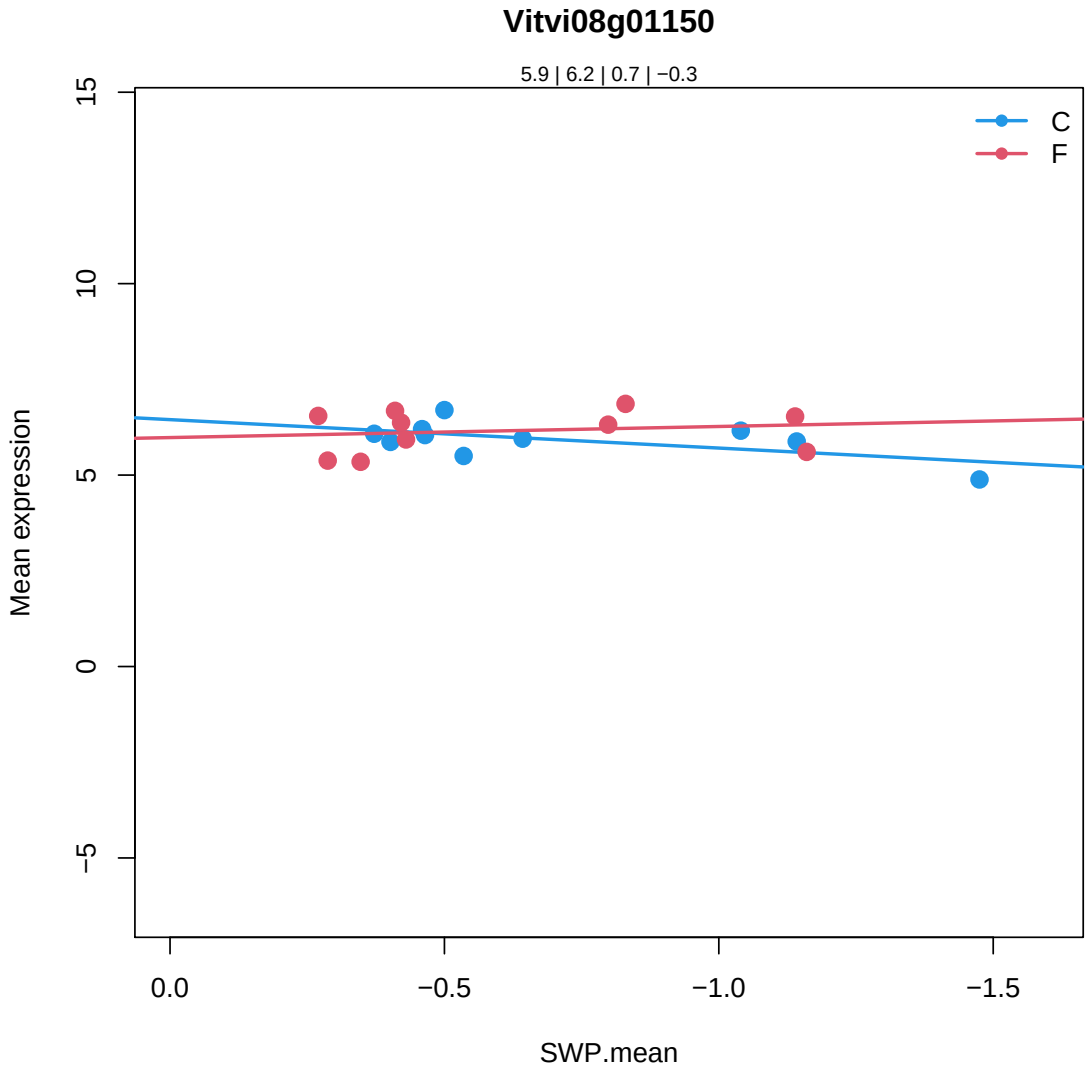
7.6.221 Vitvi08g01150: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01150
        29.2.2
        protein.synthesis.ribosome biogenesis
        2%2C3-bisphosphoglycerate-independent phosphoglycerate mutase |
        Chr3:19822813-19823298 FORWARD LENGTH=136 |
        201606
```

Coefficients for Vitvi08g01150.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.925943	4.214099e-21	***	3.550678e-20	***
SlopeC	0.7427216	0.1034738		0.6148725	
MeanF-MeanC	0.2299903	0.3117512		0.6758693	
SlopeF-SlopeC	-1.032303	0.126902		0.9999488	



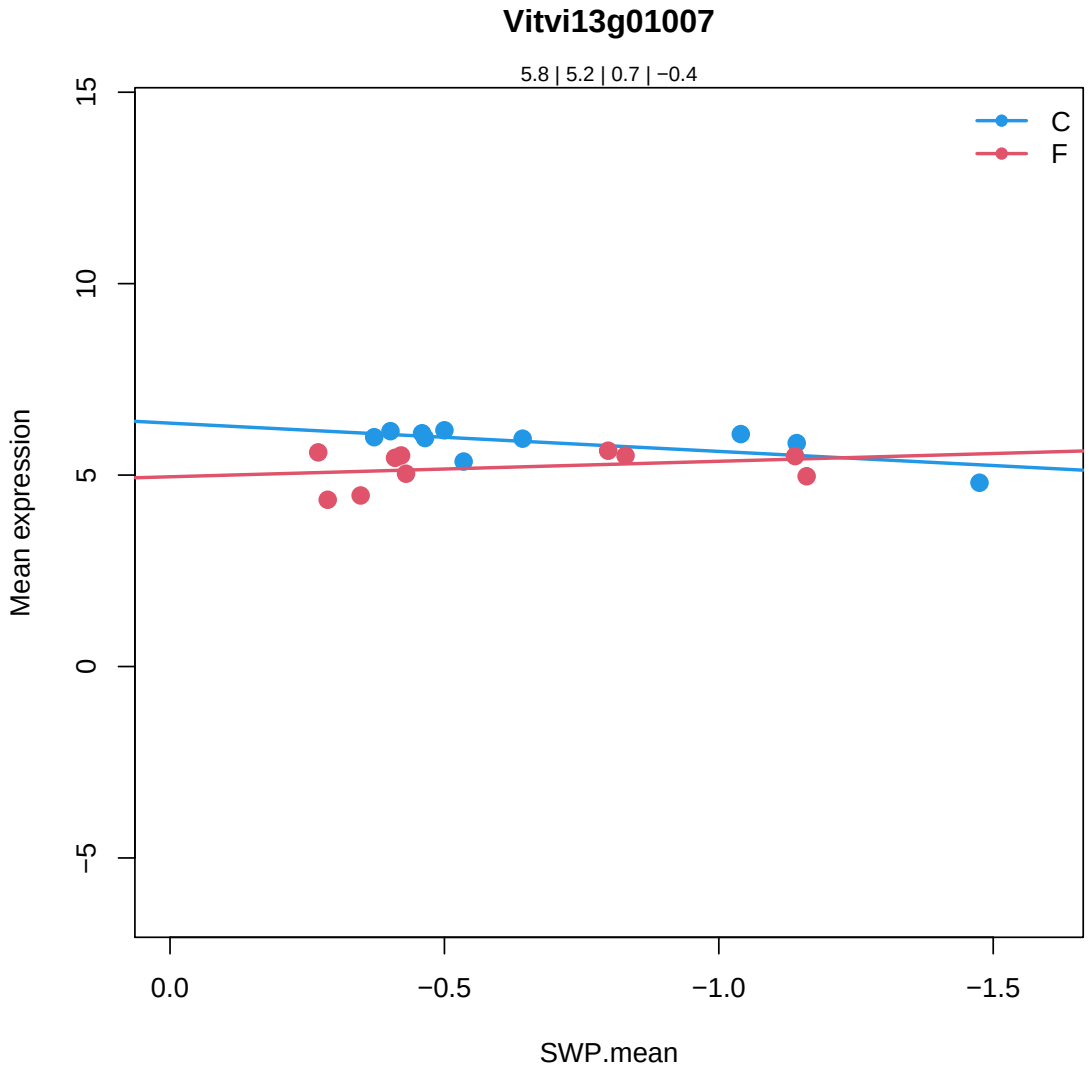
7.6.222 Vitvi13g01007: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g01007
        35.2
        not assigned.unknown
        Nuclear transport factor 2 (NTF2) family protein |
        Chr5:1402294-1403671 REVERSE LENGTH=178 |
        201606
```

Coefficients for Vitvi13g01007.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.837339	4.343214e-22	***	5.921222e-21	***
SlopeC	0.7378079	0.0696863	.	0.5587992	
MeanF-MeanC	-0.6352278	0.003902363	**	0.03762164	*
SlopeF-SlopeC	-1.143091	0.05978356	.	0.9999488	



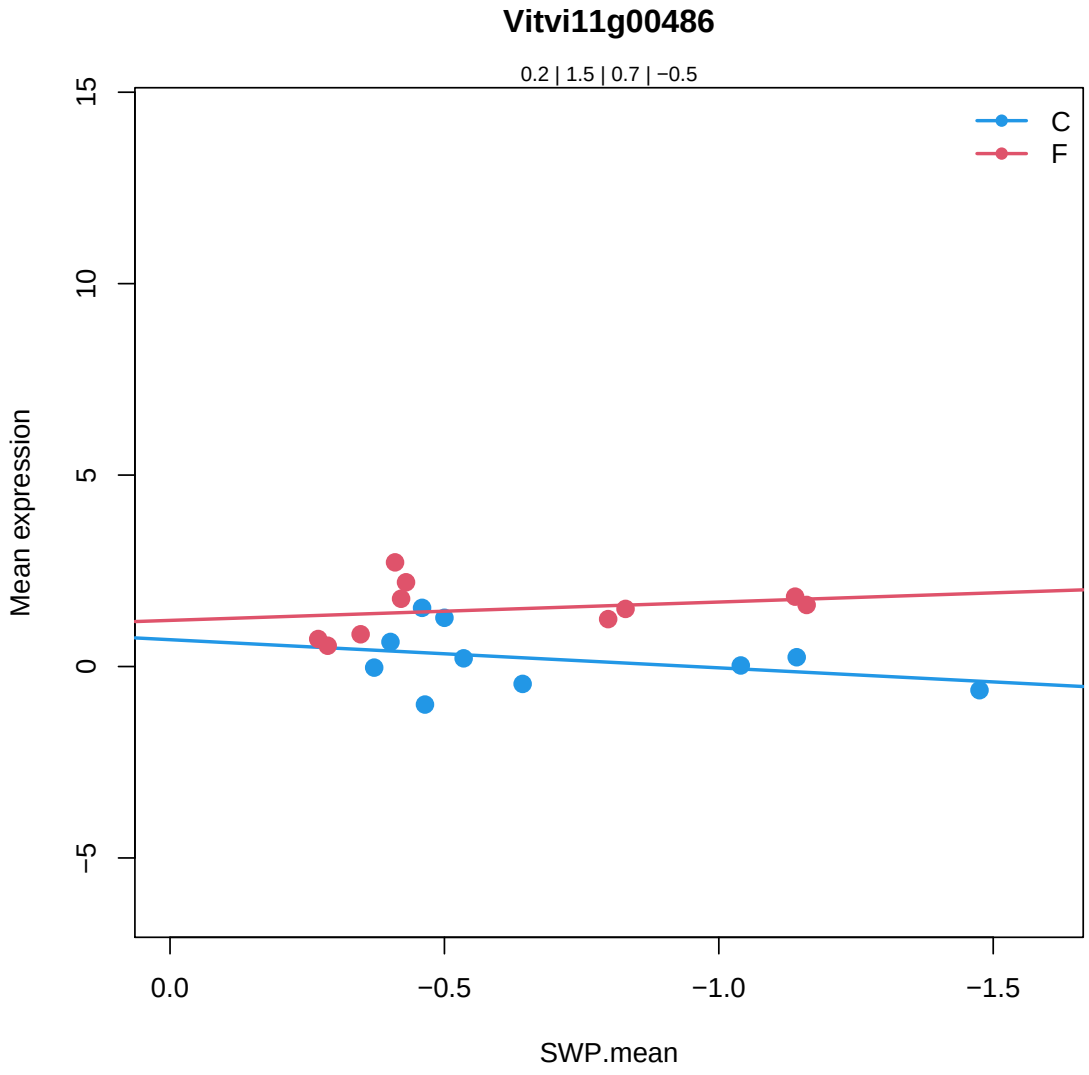
7.6.223 Vitvi11g00486: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00486
        26.19
        misc.plastocyanin-like
        early nodulin-like protein 14 |
        Chr2:10662308-10662930 FORWARD LENGTH=182 |
        201606
```

Coefficients for Vitvi11g00486.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1834837	0.4114503		0.4175316	
SlopeC	0.7350556	0.2408769		0.7548203	
MeanF-MeanC	1.313314	0.0003523208	***	0.005275121	**
SlopeF-SlopeC	-1.214325	0.1946476		0.9999488	



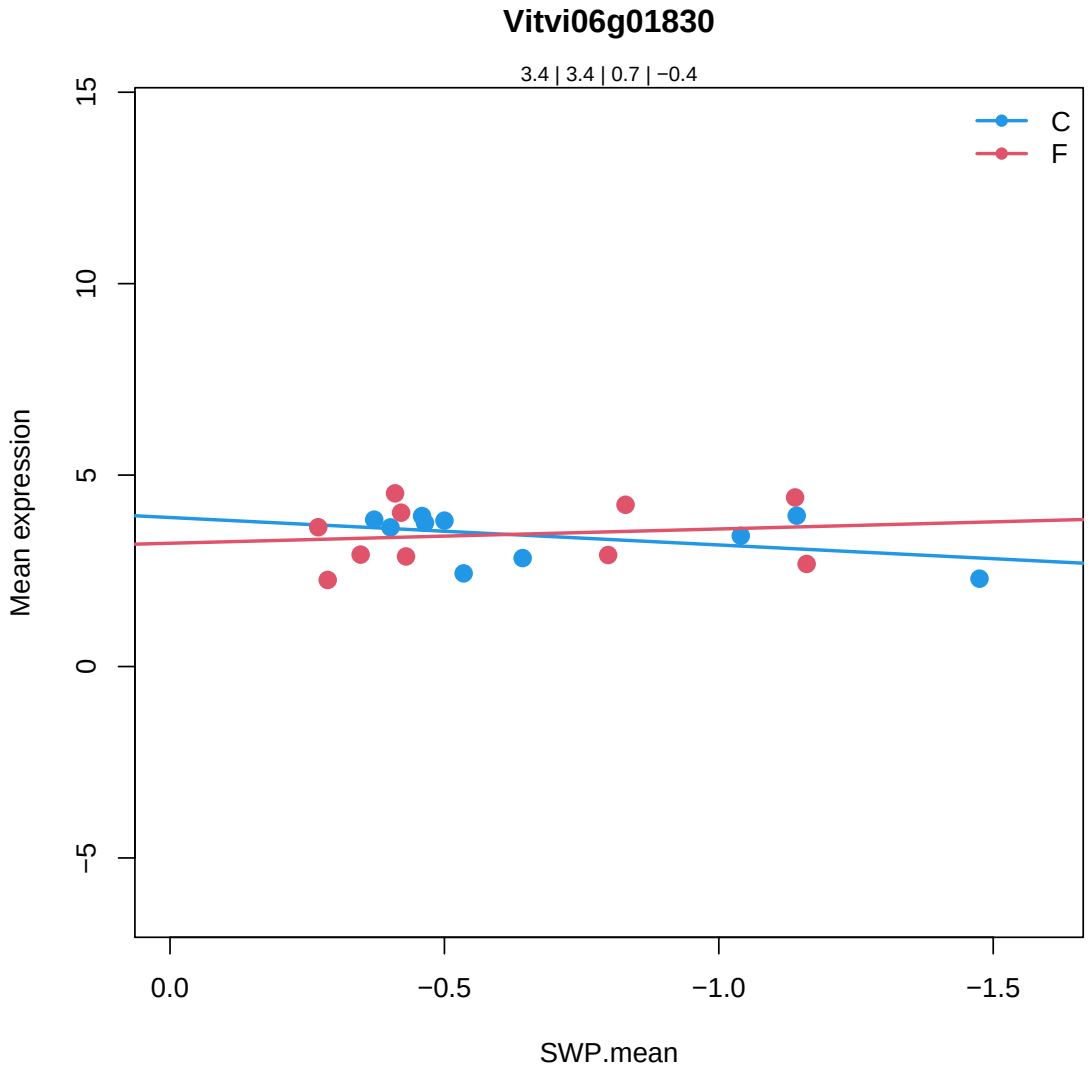
7.6.224 Vitvi06g01830: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01830
        35.2
        not assigned.unknown
        Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin
        Chr3:15615549-15617099 REVERSE LENGTH=193 |
        201606
```

Coefficients for Vitvi06g01830.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.387448	3.252919e-13	***	4.82587e-13	***
SlopeC	0.7167976	0.2466994		0.7592014	
MeanF-MeanC	0.05913579	0.8485537		0.959326	
SlopeF-SlopeC	-1.089074	0.237307		0.9999488	



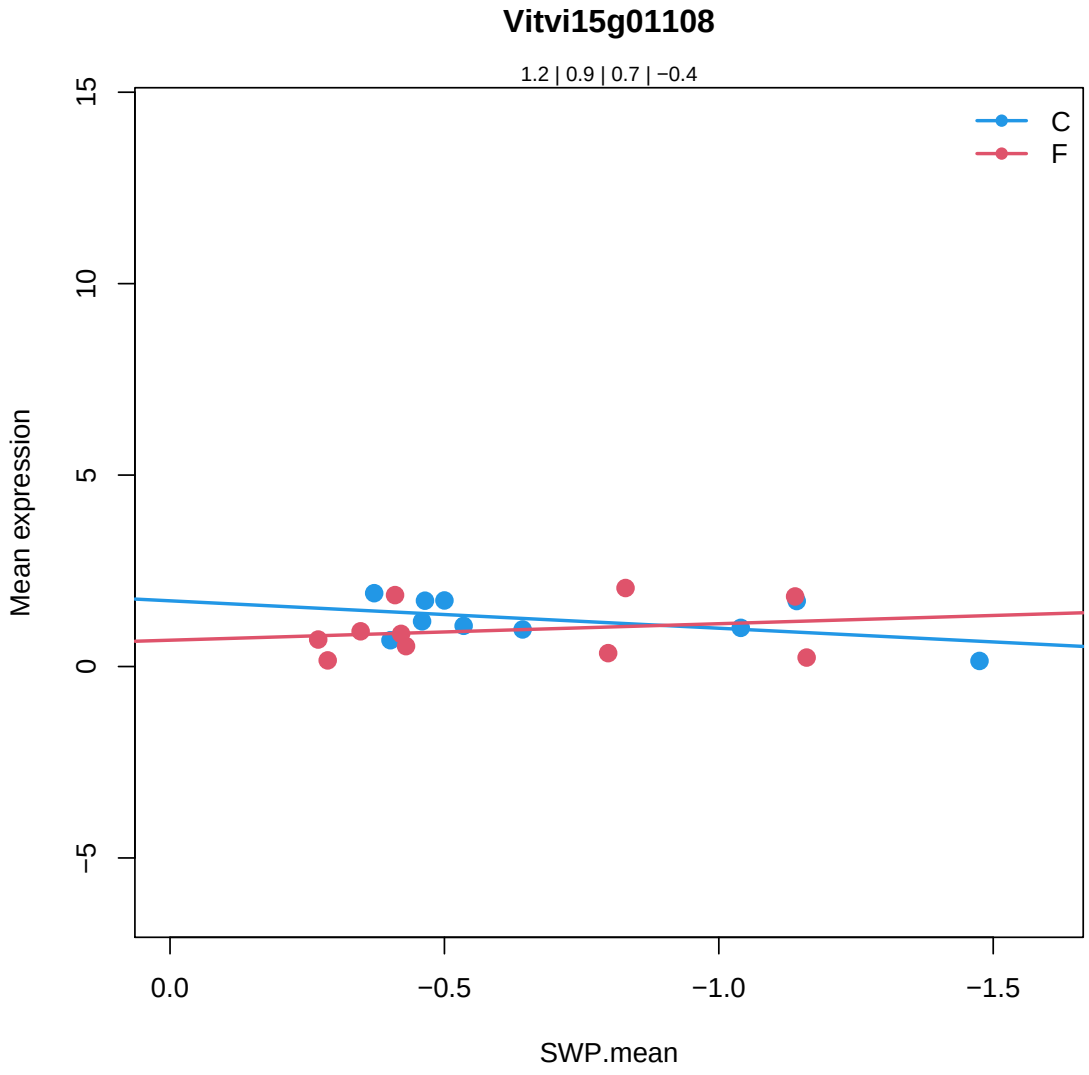
7.6.225 Vitvi15g01108: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g01108
        35.2
        not assigned.unknown
        glycerol-3-phosphate acyltransferase 4 |
        Chr1:221950-224255 REVERSE LENGTH=503 |
        201606
```

Coefficients for Vitvi15g01108.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.212277	2.442023e-06	***	2.793973e-06	***
SlopeC	0.7158632	0.1917473		0.7217253	
MeanF-MeanC	-0.2626379	0.3414597		0.7007579	
SlopeF-SlopeC	-1.146437	0.1614274		0.9999488	



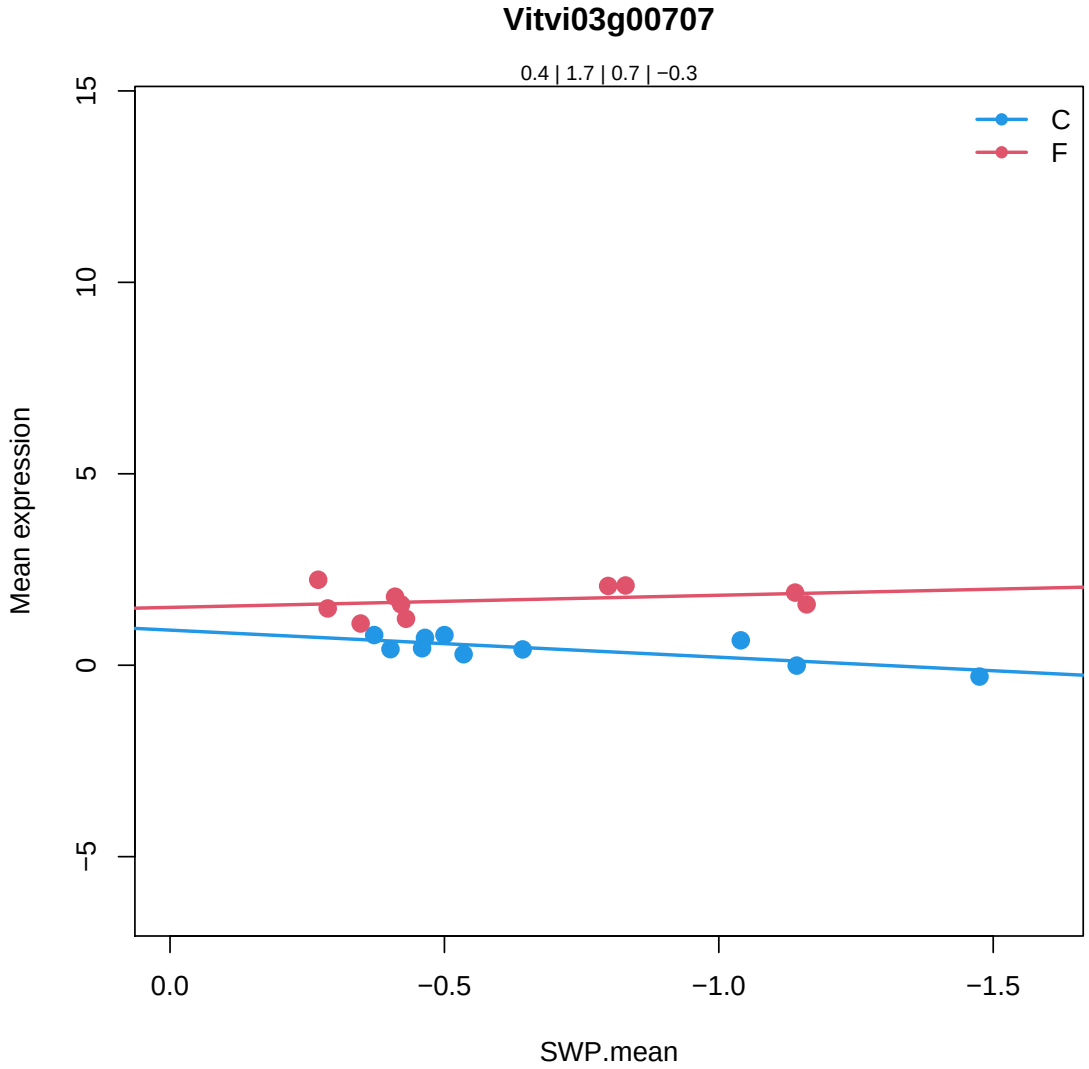
7.6.226 Vitvi03g00707: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00707
        35.2
        not assigned.unknown
        Eugenol synthase 1 OS=Ocimum basilicum (Sweet basil)
```

Coefficients for Vitvi03g00707.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4194349	0.001806005	**	0.00194428	**
SlopeC	0.7070842	0.0424875	*	0.48214	
MeanF-MeanC	1.284266	1.29424e-07	***	5.097366e-06	***
SlopeF-SlopeC	-1.024362	0.04776654	*	0.9999488	



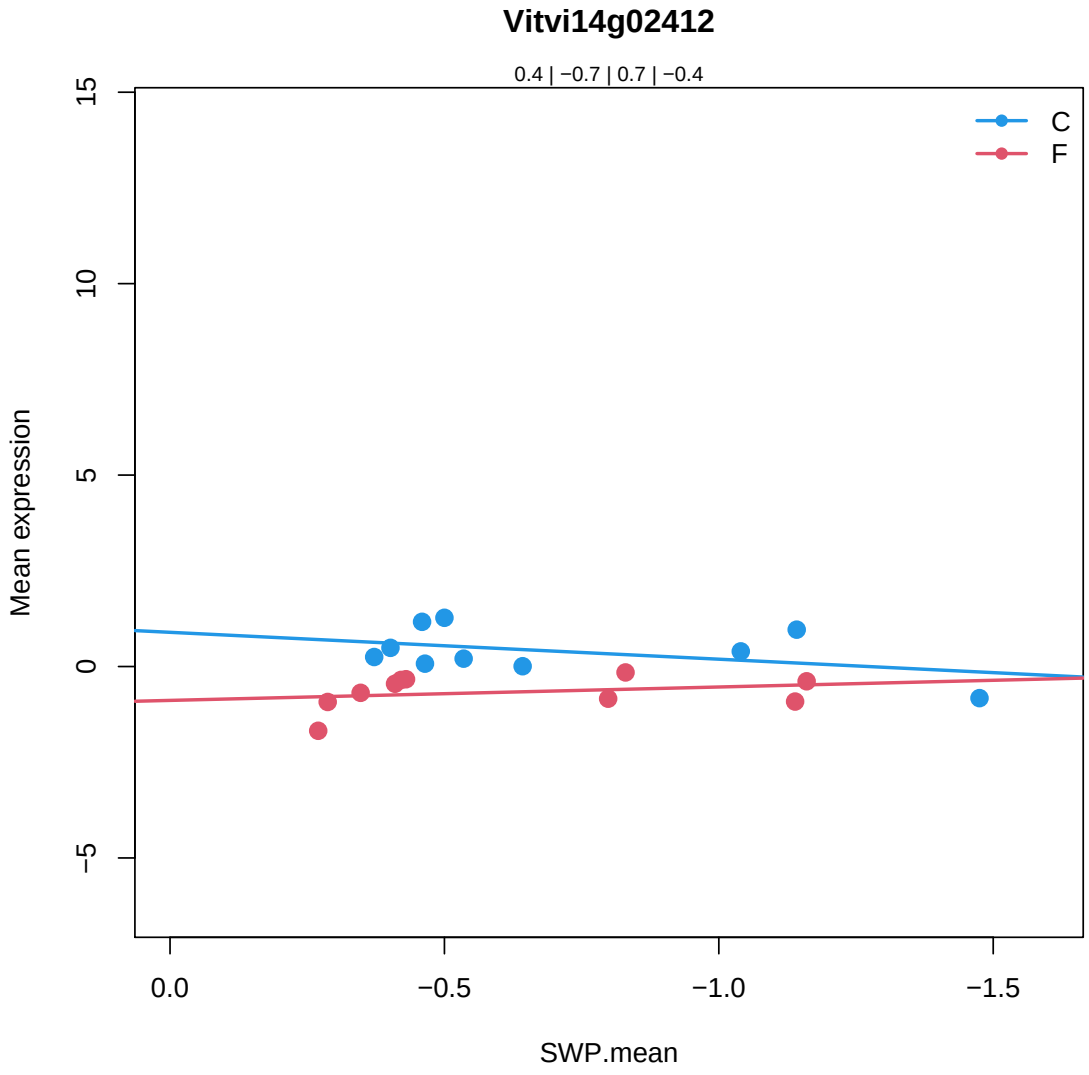
7.6.227 Vitvi14g02412: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g02412
        35.2
        not assigned.unknown
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606
```

Coefficients for Vitvi14g02412.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3995441	0.02419564	*	0.02539525	*
SlopeC	0.7021852	0.1401322		0.6667347	
MeanF-MeanC	-1.071545	0.0001479327	***	0.002494237	**
SlopeF-SlopeC	-1.052359	0.1375415		0.9999488	



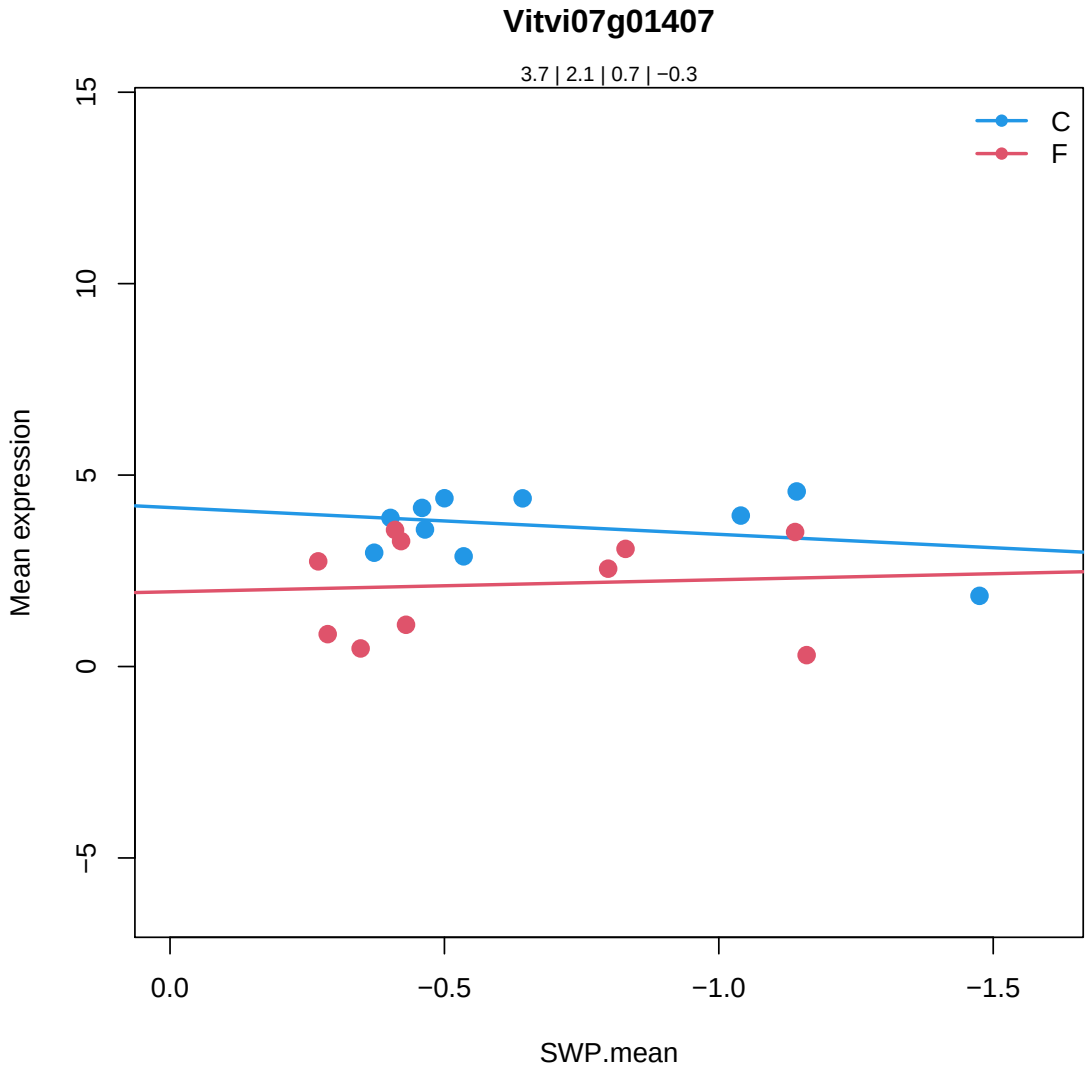
7.6.228 Vitvi07g01407: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01407
        34.12
        transport.metal
        NRAMP metal ion transporter 6 |
        Chr1:5482202-5485066 REVERSE LENGTH=527 |
        201606
```

Coefficients for Vitvi07g01407.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.660013	1.930651e-10	***	2.499744e-10	***
SlopeC	0.6997804	0.4489253		0.8555685	
MeanF-MeanC	-1.516629	0.003432362	**	0.03405993	*
SlopeF-SlopeC	-1.01482	0.4604913		0.9999488	



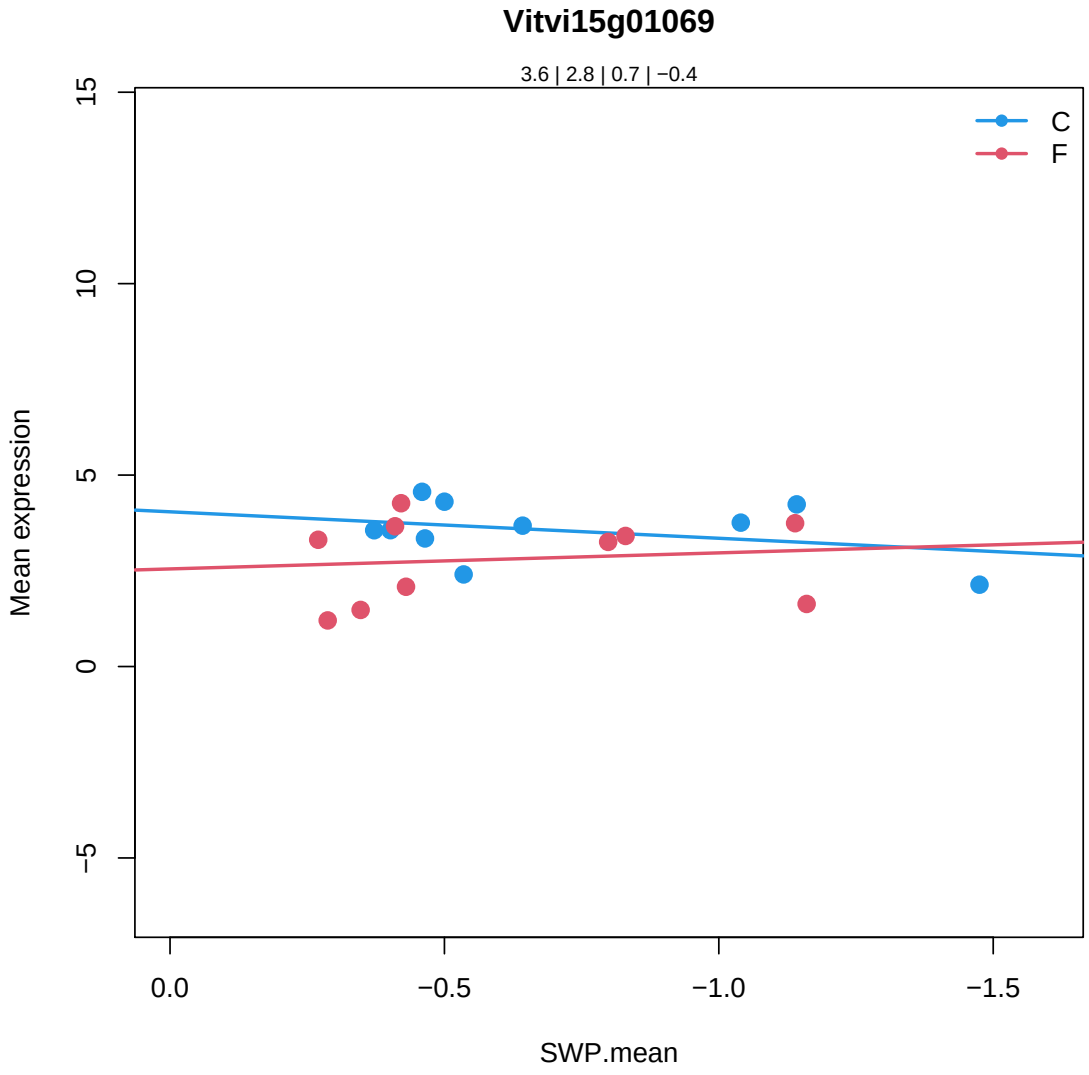
7.6.229 Vitvi15g01069: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g01069
        15.1
        metal handling.acquisition
        ferric reduction oxidase 2 |
        Chr1:209161-212810 FORWARD LENGTH=803 |
        201606
```

Coefficients for Vitvi15g01069.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.554504	1.869145e-11	***	2.521196e-11	***
SlopeC	0.6910952	0.3842001		0.8285198	
MeanF-MeanC	-0.7501806	0.07136882	.	0.3001111	
SlopeF-SlopeC	-1.110296	0.3482879		0.9999488	



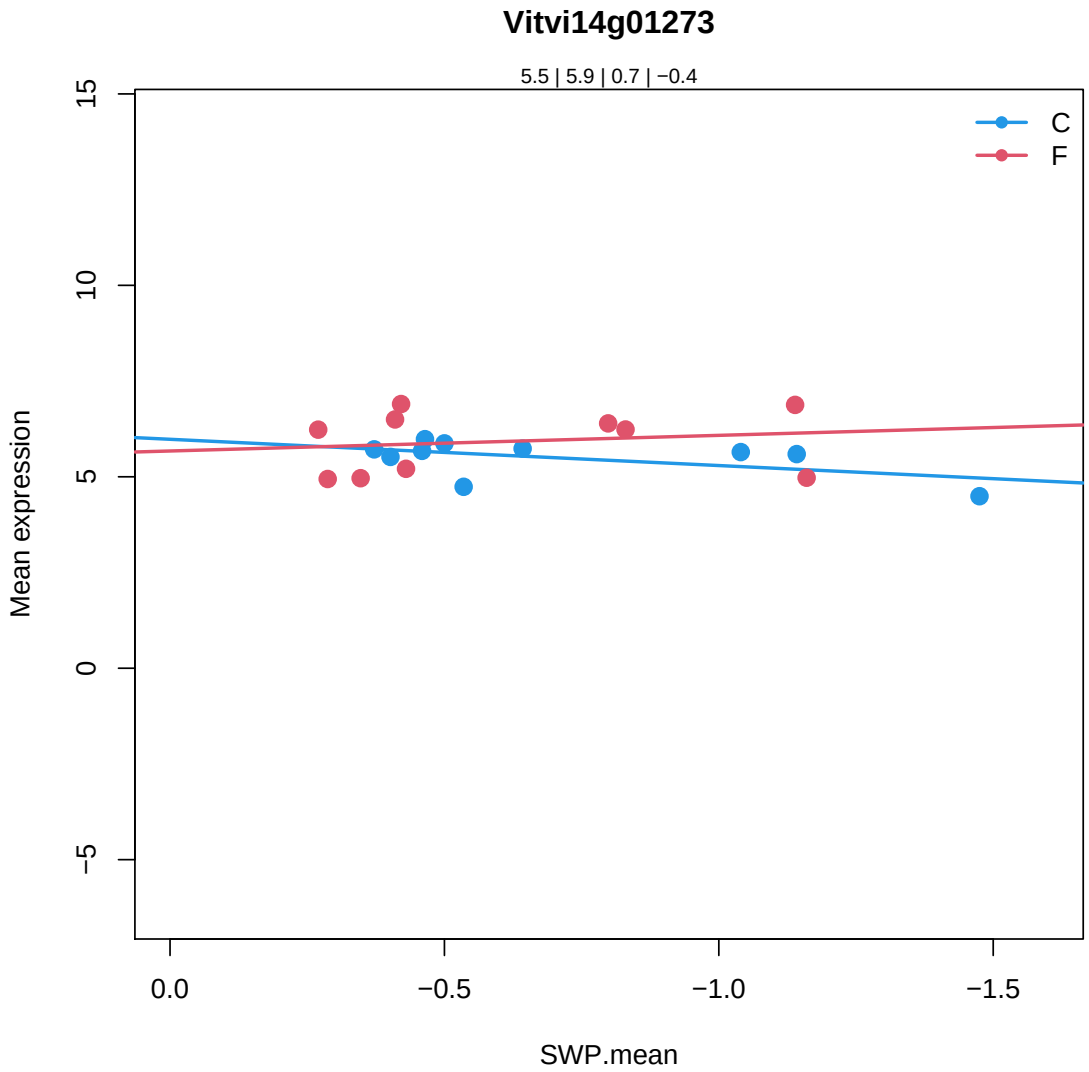
7.6.230 Vitvi14g01273: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01273
        35.2
        not assigned.unknown
        Unknown Protein
```

Coefficients for Vitvi14g01273.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.497127	3.232434e-18	***	9.647301e-18	***
SlopeC	0.6858987	0.2304428		0.7486396	
MeanF-MeanC	0.4253412	0.1467099		0.4609285	
SlopeF-SlopeC	-1.094474	0.1996726		0.9999488	



7.6.231 Vitvi04g02157: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

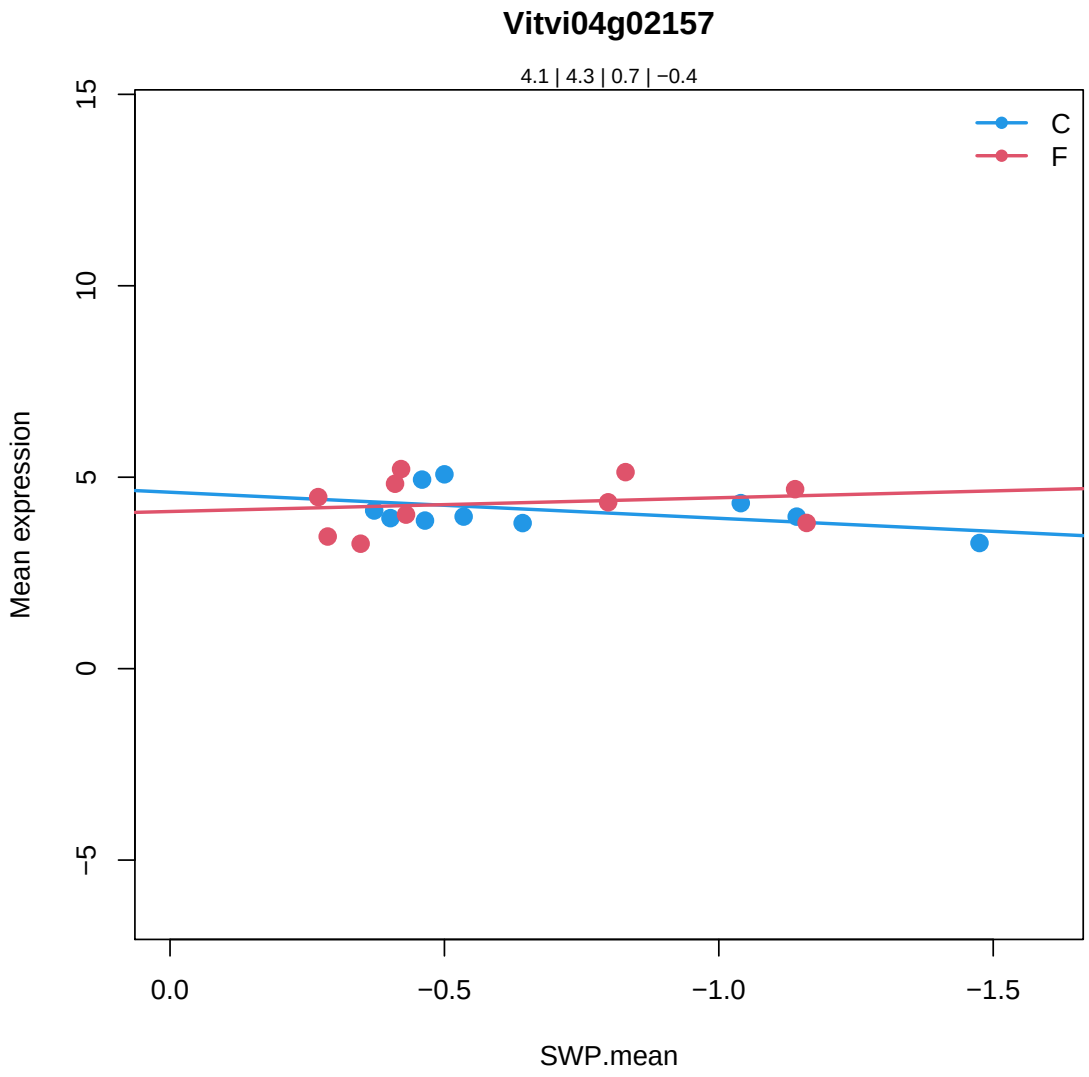
```
Vitvi04g02157
        35.2
        not assigned.unknown
        oligopeptide transporter 7 |
        Chr4:6628646-6631591 REVERSE LENGTH=552 |
        201606

Vitvi04g02157
        34.13
        transport.peptides and oligopeptides
        oligopeptide transporter 7 |
        Chr4:6628646-6631591 REVERSE LENGTH=552 |
        201606

Vitvi04g02157
        29.2.2.3.3
        protein.synthesis.ribosome biogenesis.pre-rRNA processing and modifica
        oligopeptide transporter 7 |
        Chr4:6628646-6631591 REVERSE LENGTH=552 |
        201606
```

Coefficients for Vitvi04g02157.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.128728	2.188362e-16	***	4.495285e-16	***
SlopeC	0.6813205	0.1967362		0.7250708	
MeanF-MeanC	0.1942539	0.4629983		0.785863	
SlopeF-SlopeC	-1.040139	0.1859096		0.9999488	


Vitvi04g02157
4.1 | 4.3 | 0.7 | −0.4
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

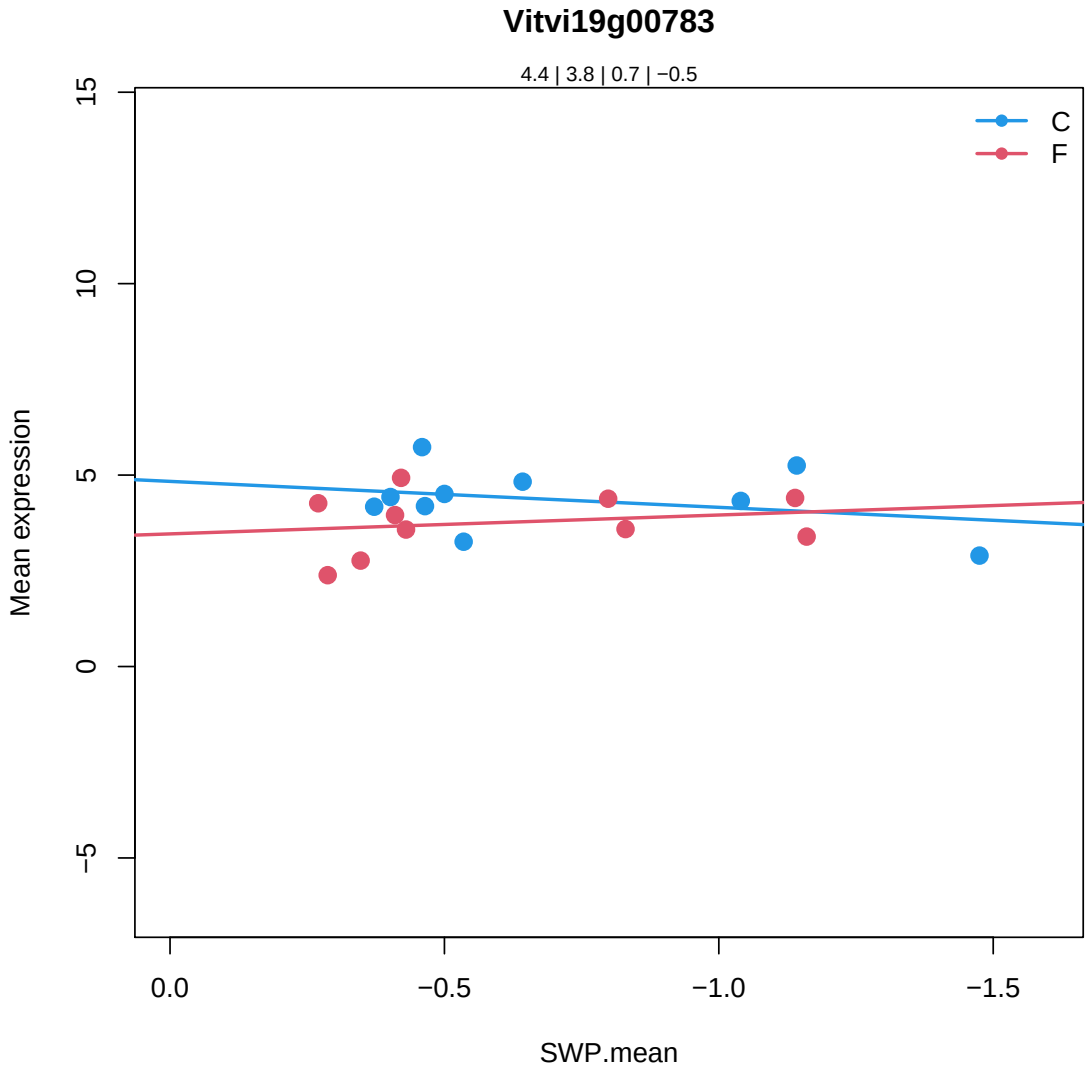
7.6.232 Vitvi19g00783: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g00783
        17.5.2
        hormone metabolism.ethylene.signal transduction
        transmembrane protein%2C putative (DUF247) |
        Chr3:18585157-18587246 REVERSE LENGTH=531 |
        201606
```

Coefficients for Vitvi19g00783.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.358524	1.62782e-14	***	2.667588e-14	***
SlopeC	0.6776998	0.3207417		0.7969607	
MeanF-MeanC	-0.5942085	0.09383684	.	0.3515019	
SlopeF-SlopeC	-1.171093	0.2508717		0.9999488	



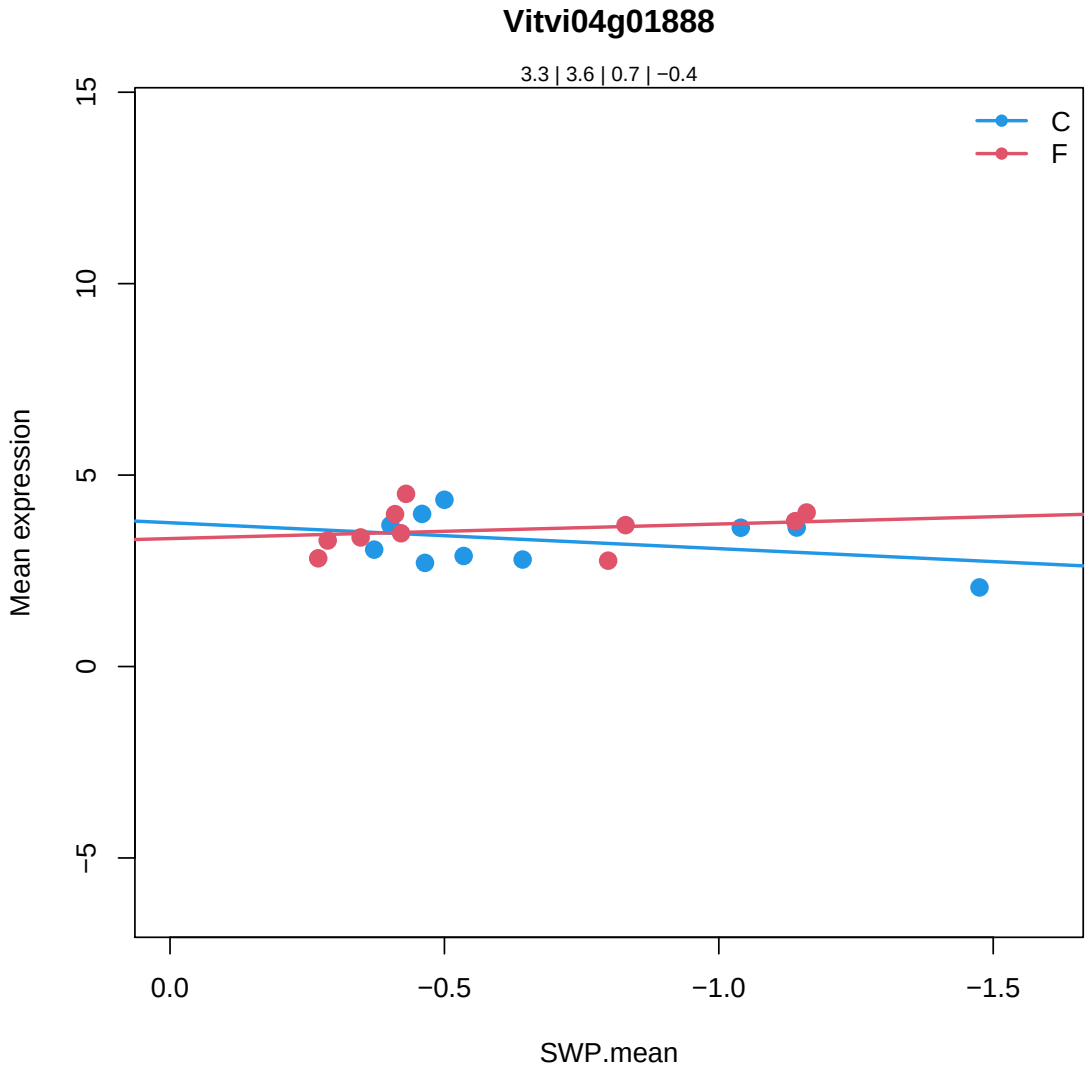
7.6.233 Vitvi04g01888: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01888
        35.2
        not assigned.unknown
        ATP synthase subunit beta |
        ChrC:52660-54156 REVERSE LENGTH=498 |
        201606
```

Coefficients for Vitvi04g01888.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.279177	3.500009e-14	***	5.578494e-14	***
SlopeC	0.6764767	0.2079709		0.7310638	
MeanF-MeanC	0.293965	0.2793333		0.6434478	
SlopeF-SlopeC	-1.056841	0.1870953		0.9999488	



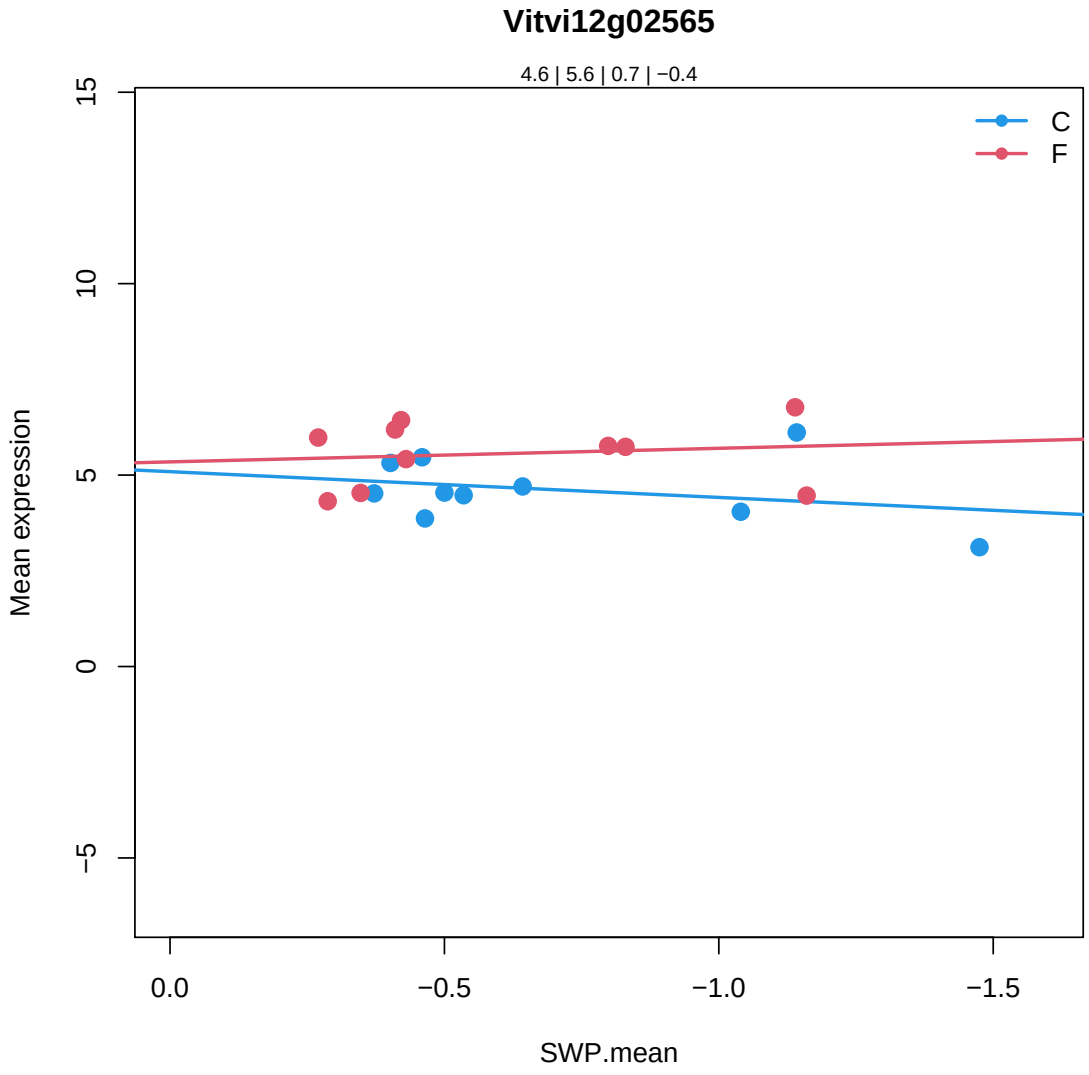
7.6.234 Vitvi12g02565: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02565
        35.2
        not assigned.unknown
        Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin
        Chr2:18626377-18626781 FORWARD LENGTH=134 |
        201606
```

Coefficients for Vitvi12g02565.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.616022	1.75637e-14	***	2.868073e-14	***
SlopeC	0.6726658	0.3531688		0.8145387	
MeanF-MeanC	0.9445848	0.01577215	*	0.1054434	
SlopeF-SlopeC	-1.027108	0.3410958		0.9999488	



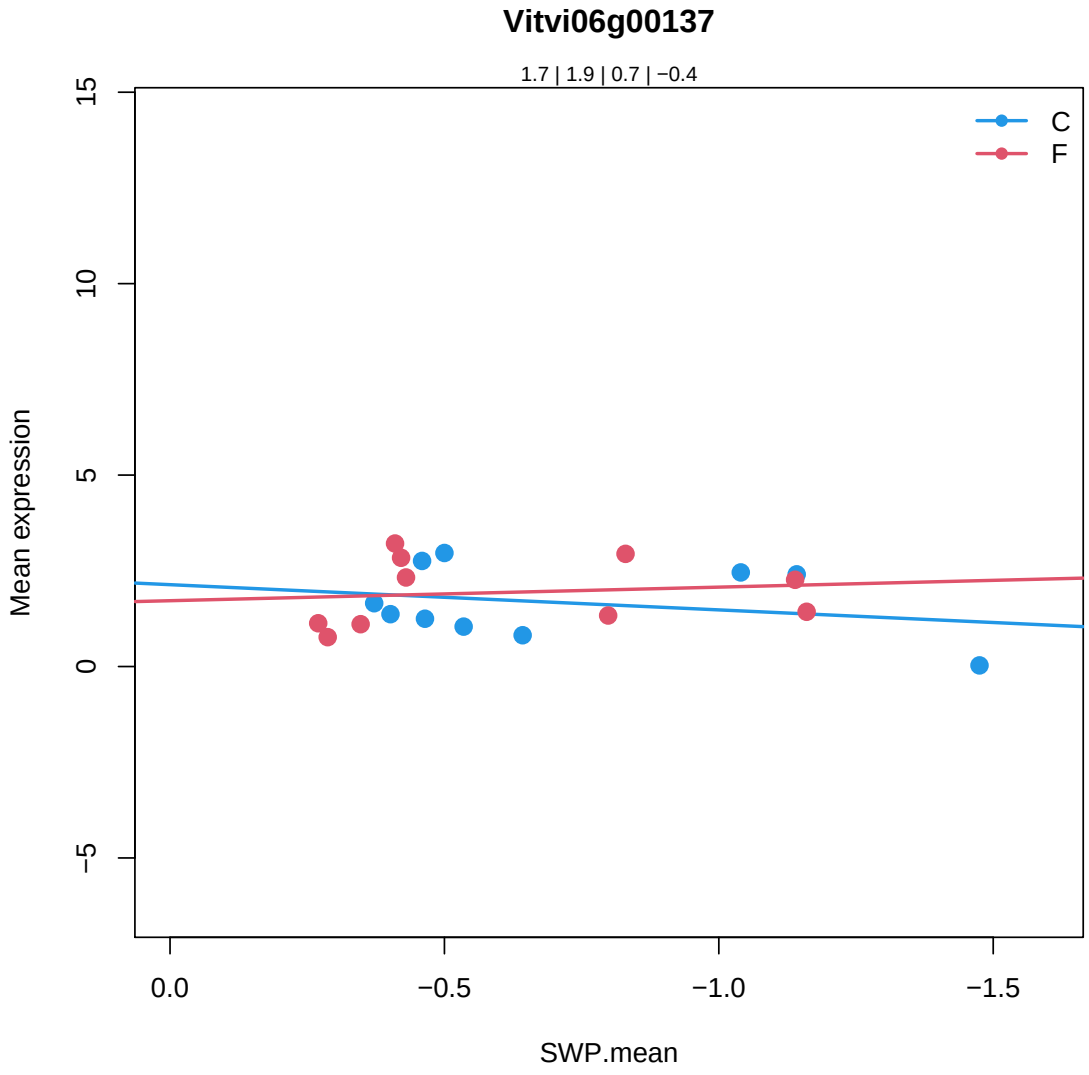
7.6.235 Vitvi06g00137: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00137
        29.4
        protein.postranslational modification
        receptor-like protein kinase 1 |
        Chr5:24498467-24501494 REVERSE LENGTH=832 |
        201606
```

Coefficients for Vitvi06g00137.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.674317	3.645014e-06	***	4.155371e-06	***
SlopeC	0.6586676	0.3923534		0.8309601	
MeanF-MeanC	0.2605074	0.504262		0.8082564	
SlopeF-SlopeC	-1.01316	0.3769807		0.9999488	



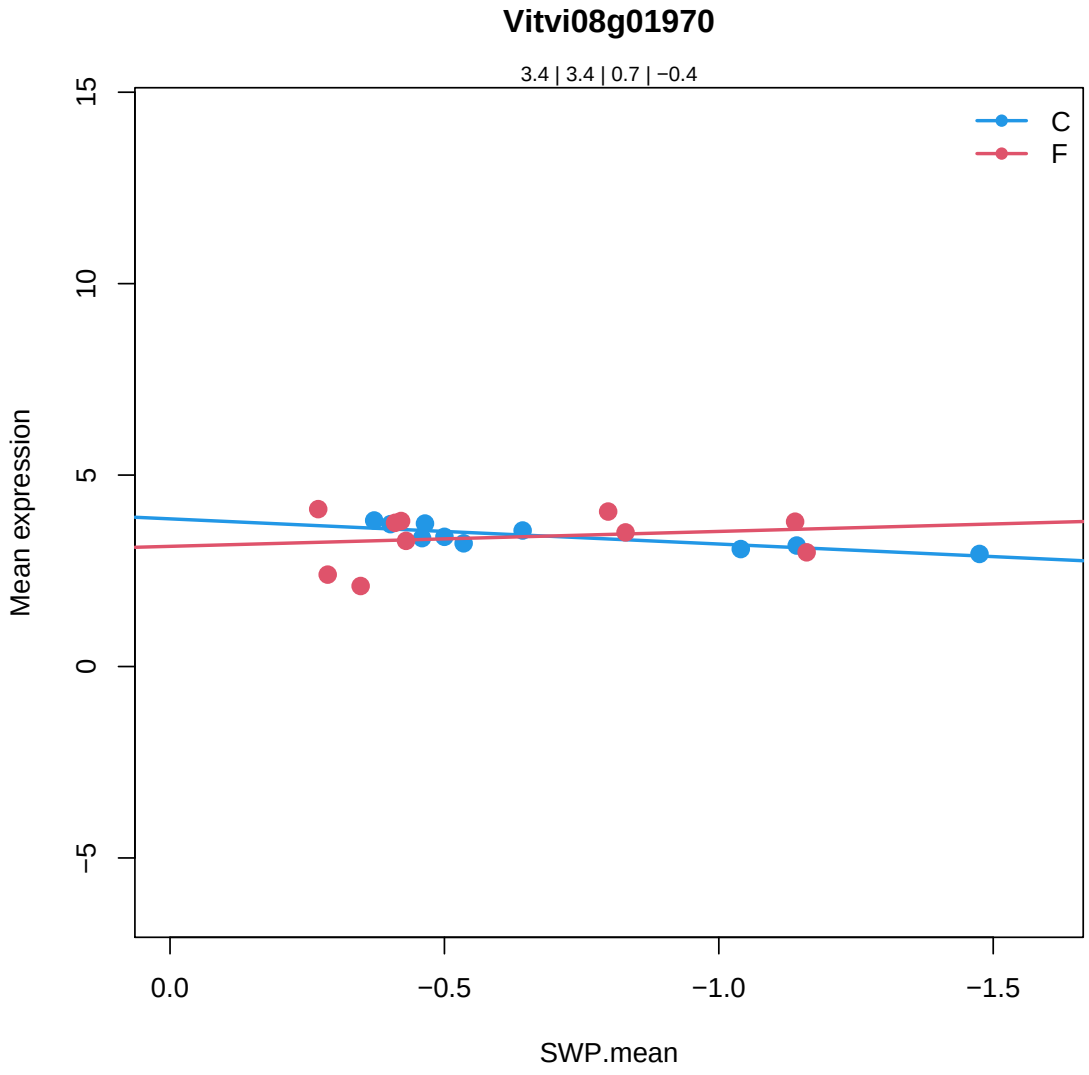
7.6.236 Vitvi08g01970: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01970
        35.2
        not assigned.unknown
        transmembrane protein |
        Chr5:5335-5769 REVERSE LENGTH=104 |
        201606
```

Coefficients for Vitvi08g01970.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.394391	9.372427e-16	***	1.759943e-15	***
SlopeC	0.657578	0.1595525		0.6889929	
MeanF-MeanC	-0.01817323	0.9375879		0.9829394	
SlopeF-SlopeC	-1.047066	0.1336462		0.9999488	



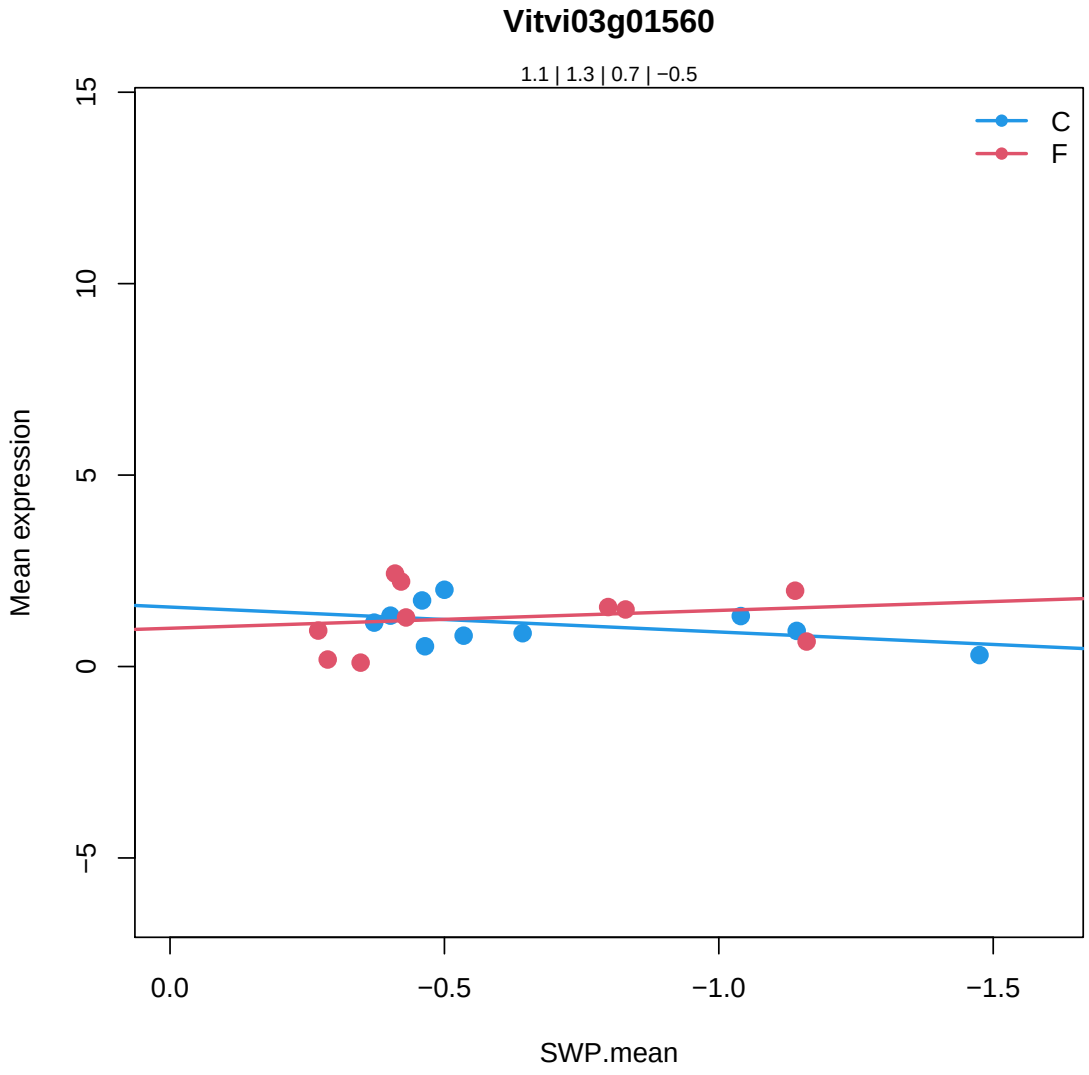
7.6.237 Vitvi03g01560: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g01560
        35.1
        not assigned.no ontology
        alpha/beta-Hydrolases superfamily protein |
        Chr1:17417623-17419296 FORWARD LENGTH=314 |
        201606
```

Coefficients for Vitvi03g01560.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.095375	2.300278e-05	***	2.576298e-05	***
SlopeC	0.6508429	0.2633015		0.7701943	
MeanF-MeanC	0.1873071	0.5223458		0.8193469	
SlopeF-SlopeC	-1.11673	0.1993374		0.9999488	



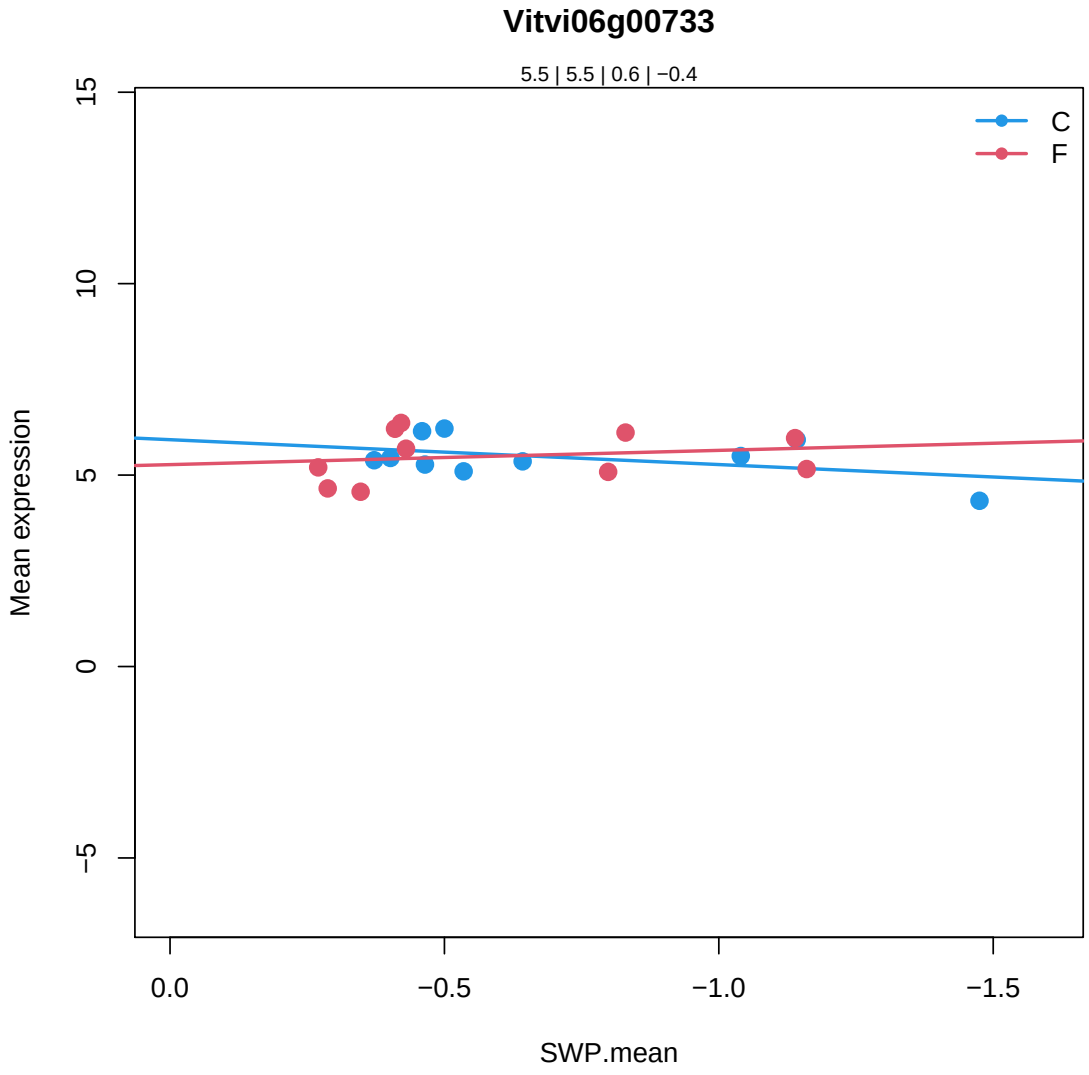
7.6.238 Vitvi06g00733: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00733
        31.4
        cell.vesicle transport
        exocyst subunit exo70 family protein B1 |
        Chr5:23621460-23623334 REVERSE LENGTH=624 |
        201606
```

Coefficients for Vitvi06g00733.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.467404	5.772865e-19	***	2.140355e-18	***
SlopeC	0.6493344	0.2157069		0.7385982	
MeanF-MeanC	0.03203928	0.9026029		0.9742947	
SlopeF-SlopeC	-1.021526	0.1916007		0.9999488	



7.6.239 Vitvi12g00220: type5

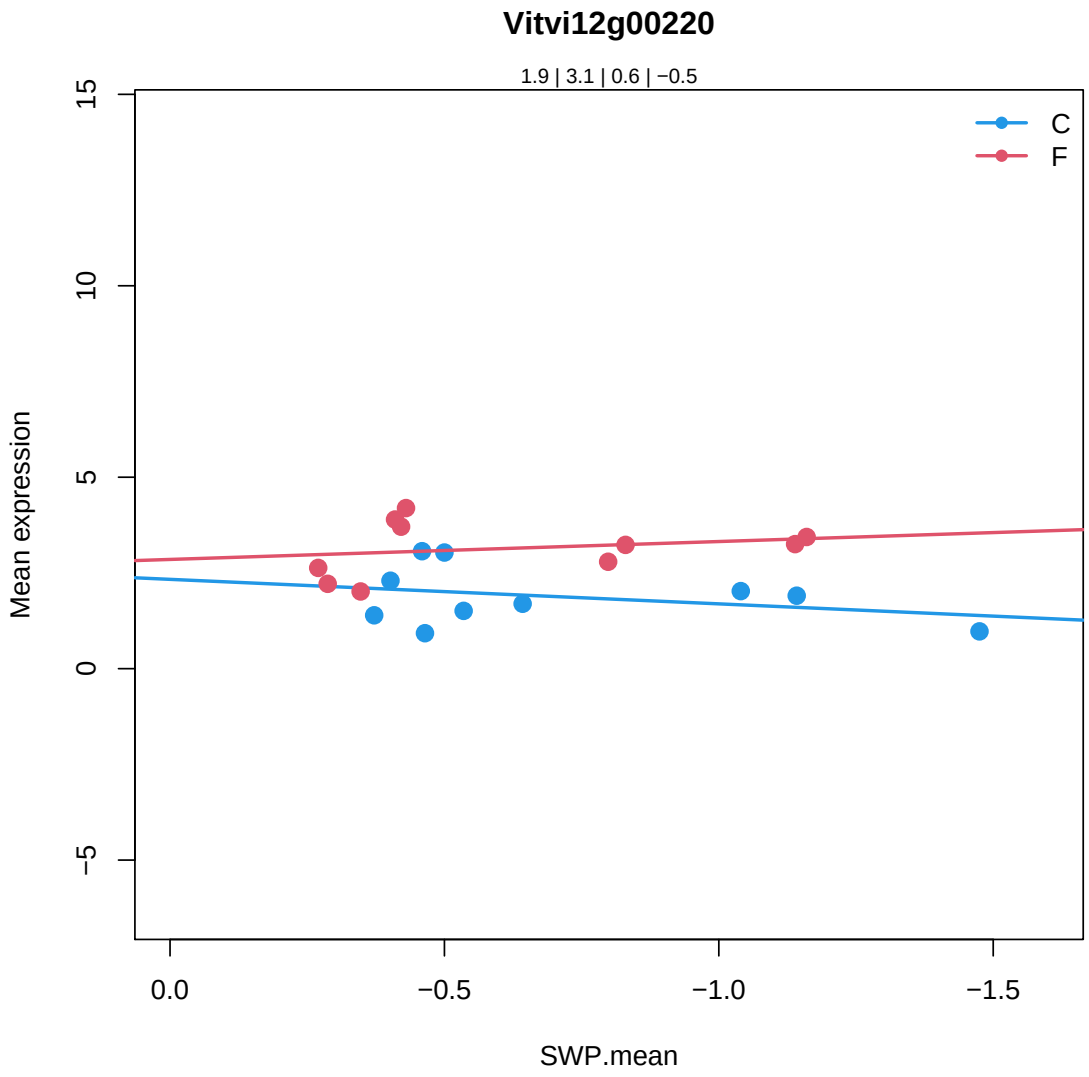
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00220
        29.5.11.4.2
        protein.degradation.ubiquitin.E3.RING
        RING/U-box superfamily protein |
        Chr2:17640907-17641617 FORWARD LENGTH=236 |
        201606

Vitvi12g00220
        27.3.11
        RNA.regulation of transcription.C2H2 zinc finger family
        RING/U-box superfamily protein |
        Chr2:17640907-17641617 FORWARD LENGTH=236 |
        201606
```

Coefficients for Vitvi12g00220.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.882167	2.077614e-08	***	2.511659e-08	***
SlopeC	0.6399723	0.3040759		0.7883526	
MeanF-MeanC	1.255296	0.0005395256	***	0.007471454	**
SlopeF-SlopeC	-1.107612	0.234076		0.9999488	


Vitvi12g00220
1.9 | 3.1 | 0.6 | −0.5
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

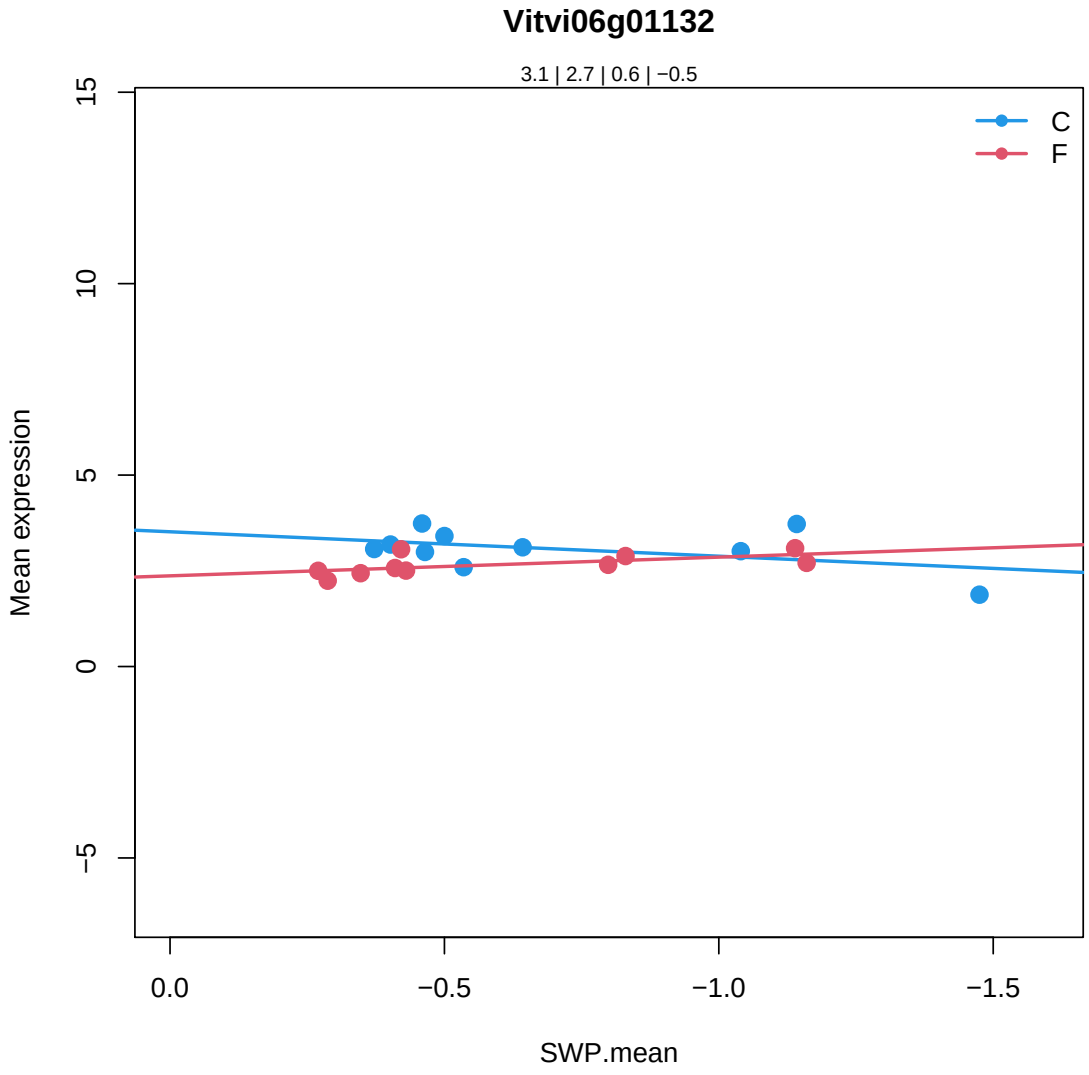
7.6.240 Vitvi06g01132: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01132
        35.1
        not assigned.no ontology
        RNA-directed DNA polymerase (reverse transcriptase)-related family pro
        Chr3:8789309-8790907 FORWARD LENGTH=532 |
        201606
```

Coefficients for Vitvi06g01132.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.07089	1.51839e-16	***	3.195265e-16	***
SlopeC	0.6377889	0.1022956		0.6140958	
MeanF-MeanC	-0.4052164	0.04460015	*	0.222228	
SlopeF-SlopeC	-1.12657	0.05542678	.	0.9999488	



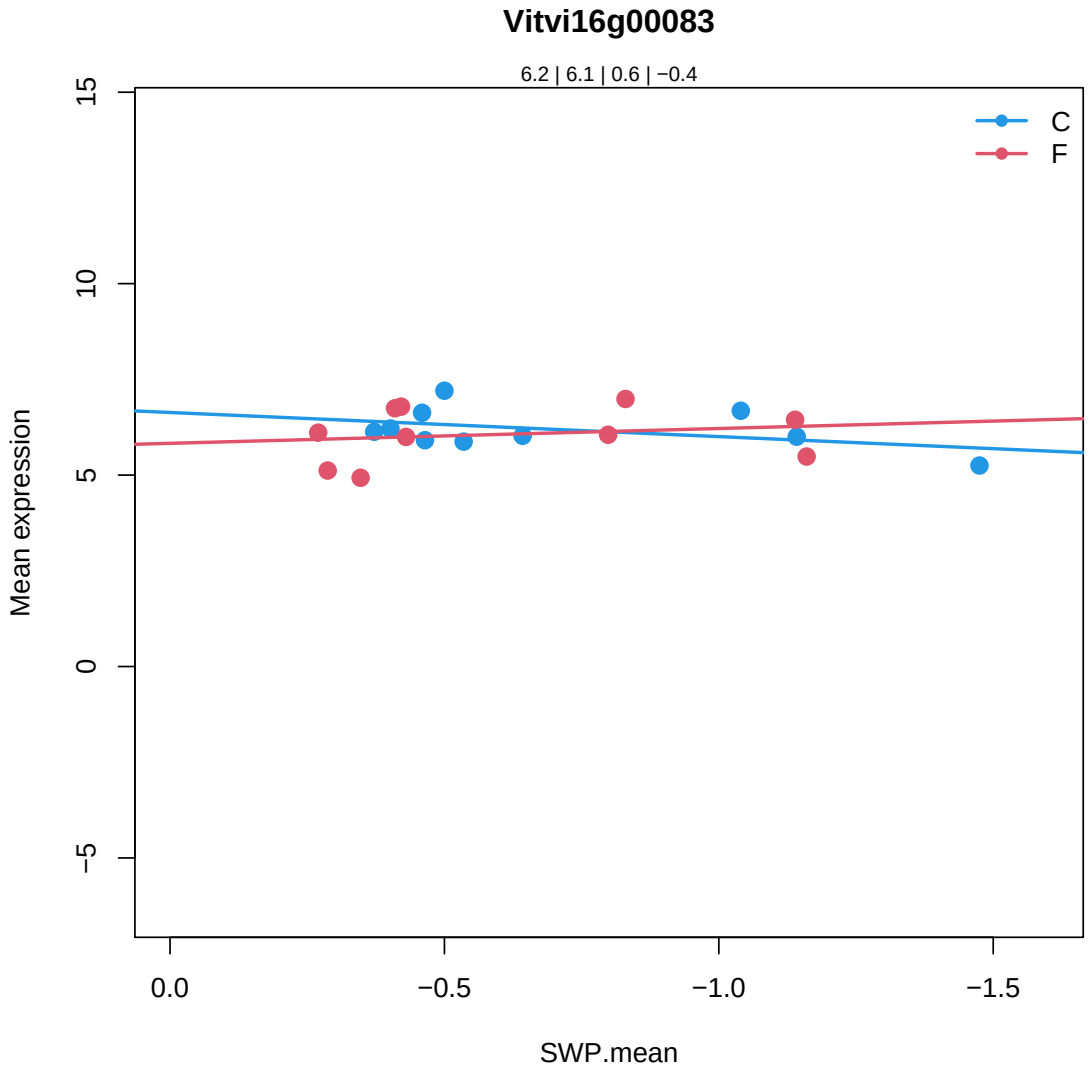
7.6.241 Vitvi16g00083: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g00083
        27.3.99
        RNA.regulation of transcription.unclassified
        PLATZ transcription factor family protein |
        Chr1:11827986-11829444 FORWARD LENGTH=174 |
        201606
```

Coefficients for Vitvi16g00083.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.191827	9.262211e-20	***	4.473214e-19	***
SlopeC	0.6301325	0.2460318		0.7588751	
MeanF-MeanC	-0.1265517	0.6422474		0.8784583	
SlopeF-SlopeC	-1.017259	0.2095596		0.9999488	



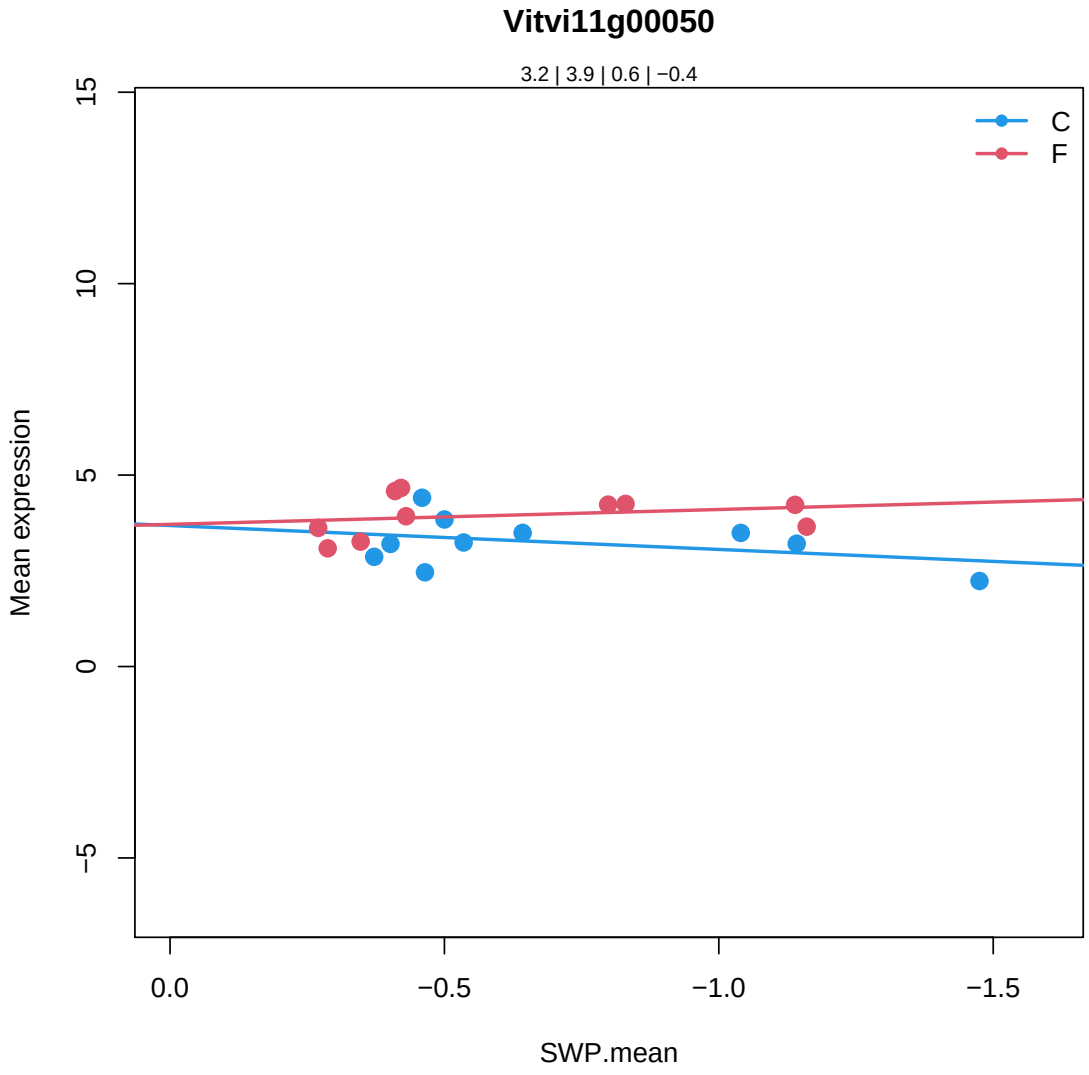
7.6.242 Vitvi11g00050: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00050
        17.7.2
        hormone metabolism.jasmonate.signal transduction
        jasmonate-zim-domain protein 1 |
        Chr1:6622312-6623271 FORWARD LENGTH=253 |
        201606
```

Coefficients for Vitvi11g00050.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.243389	1.637861e-14	***	2.683754e-14	***
SlopeC	0.6243896	0.2218807		0.741182	
MeanF-MeanC	0.7058968	0.01064075	*	0.07946417	.
SlopeF-SlopeC	-1.01224	0.1847526		0.9999488	



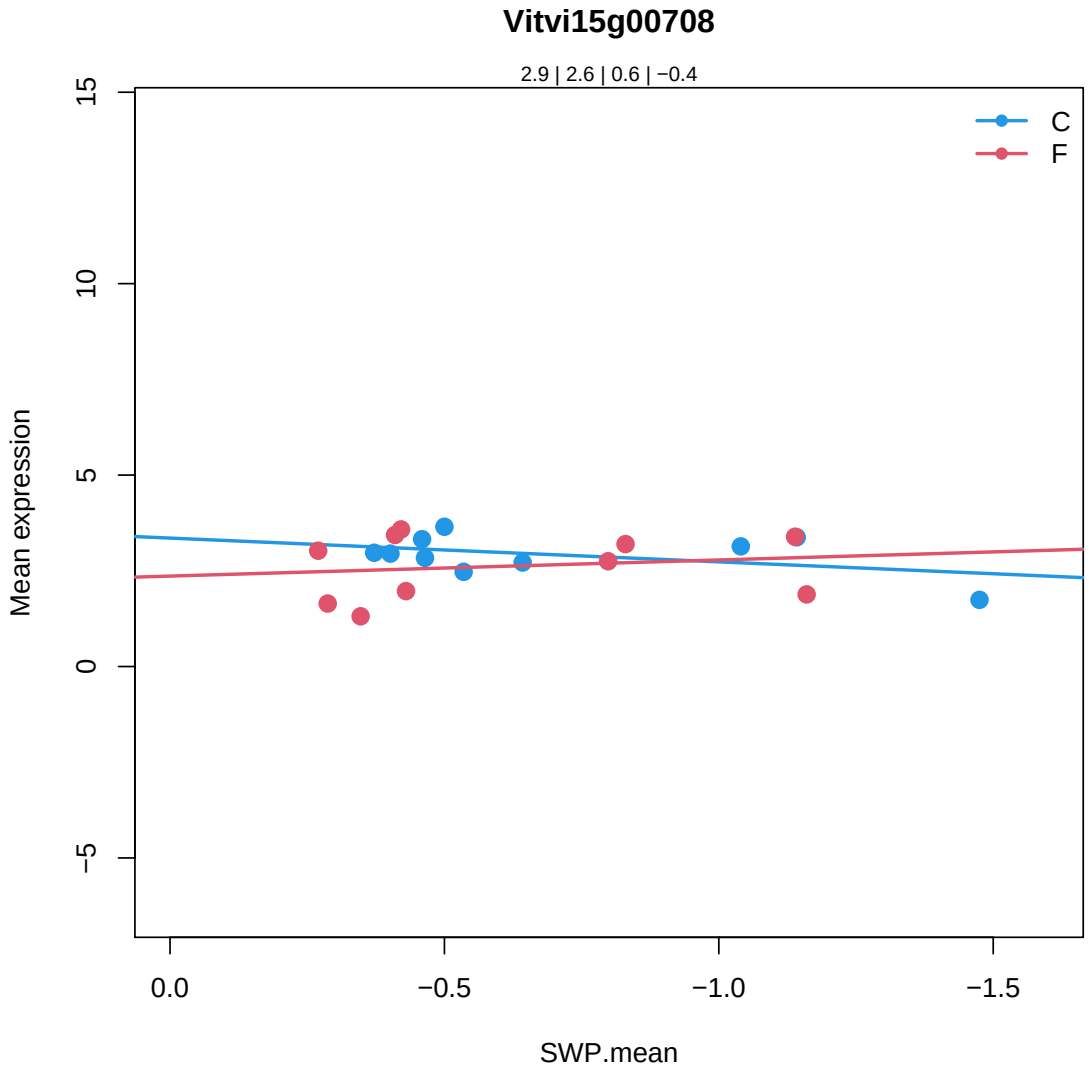
7.6.243 Vitvi15g00708: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g00708
        27.3.10
        RNA.regulation of transcription.C2C2(Zn) YABBY family
        Plant-specific transcription factor YABBY family protein |
        Chr2:18628450-18630552 REVERSE LENGTH=229 |
        201606
```

Coefficients for Vitvi15g00708.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.917418	3.680529e-12	***	5.120823e-12	***
SlopeC	0.620752	0.3018204		0.7870566	
MeanF-MeanC	-0.2989822	0.3272822		0.6873017	
SlopeF-SlopeC	-1.041661	0.2459565		0.9999488	



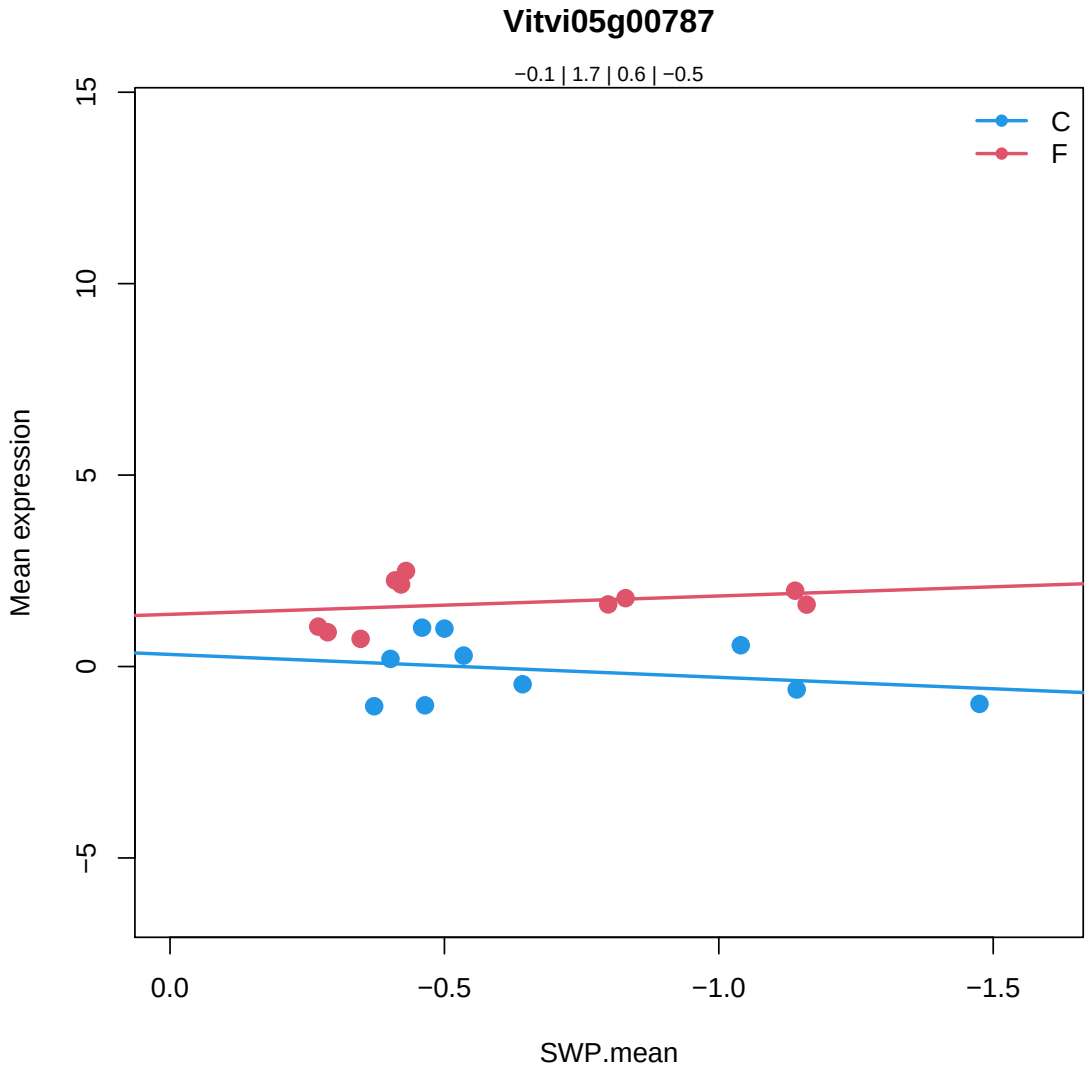
7.6.244 Vitvi05g00787: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00787
        29.3.5
        protein.targeting.peroxisomes
        Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein |
        Chr4:8235335-8236605 REVERSE LENGTH=185 |
        201606
```

Coefficients for Vitvi05g00787.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.104636	0.629645		0.6347674	
SlopeC	0.5979573	0.3261482		0.8000183	
MeanF-MeanC	1.759718	8.247862e-06	***	0.0002102239	***
SlopeF-SlopeC	-1.077391	0.2370117		0.9999488	



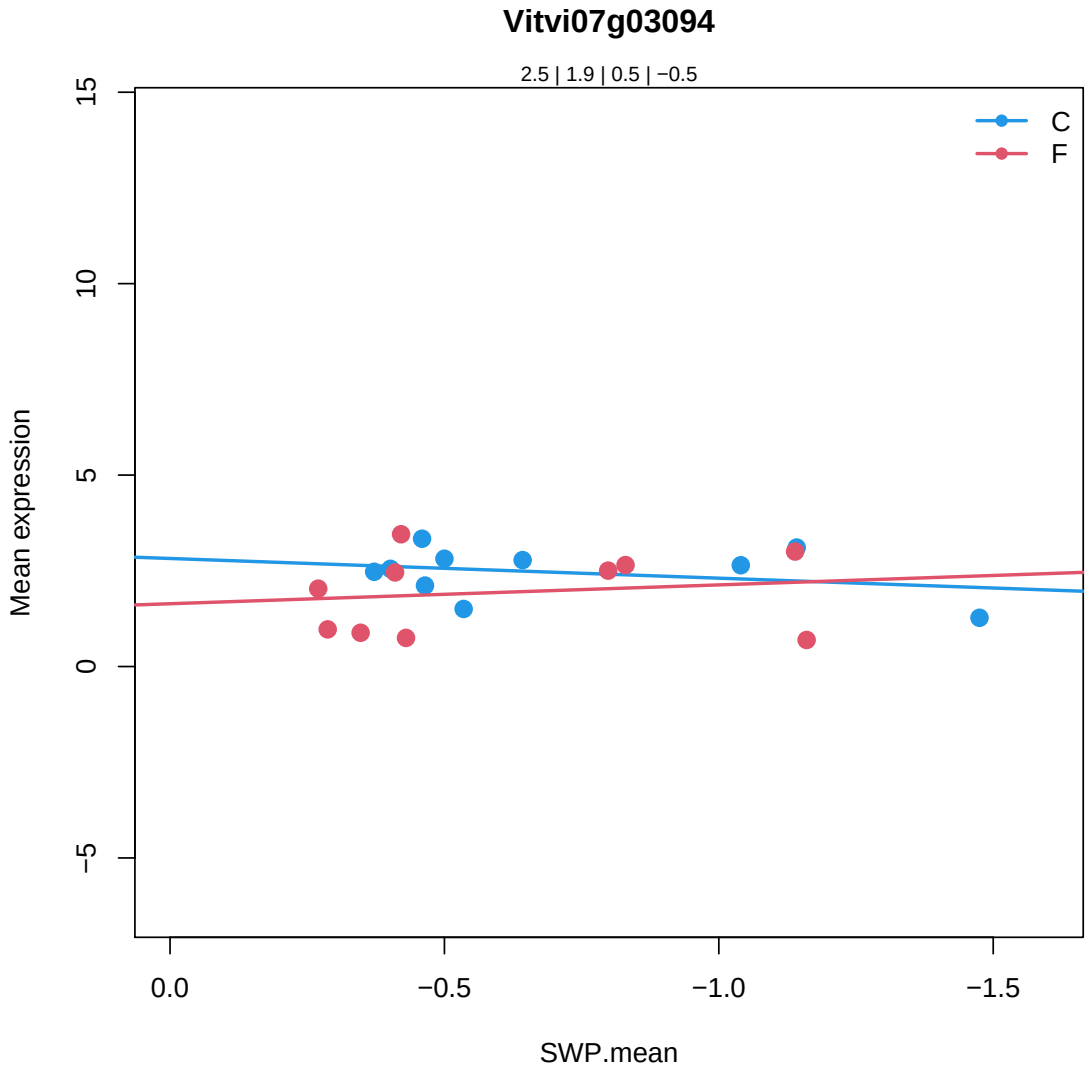
7.6.245 Vitvi07g03094: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g03094
        35.1
        not assigned.no ontology
        CBS domain protein (DUF21) |
        Chr4:16176547-16178433 REVERSE LENGTH=341 |
        201606
```

Coefficients for Vitvi07g03094.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.460036	3.427958e-09	***	4.246845e-09	***
SlopeC	0.5141899	0.4800349		0.8637342	
MeanF-MeanC	-0.5205791	0.166672		0.4954895	
SlopeF-SlopeC	-1.006261	0.3551421		0.9999488	



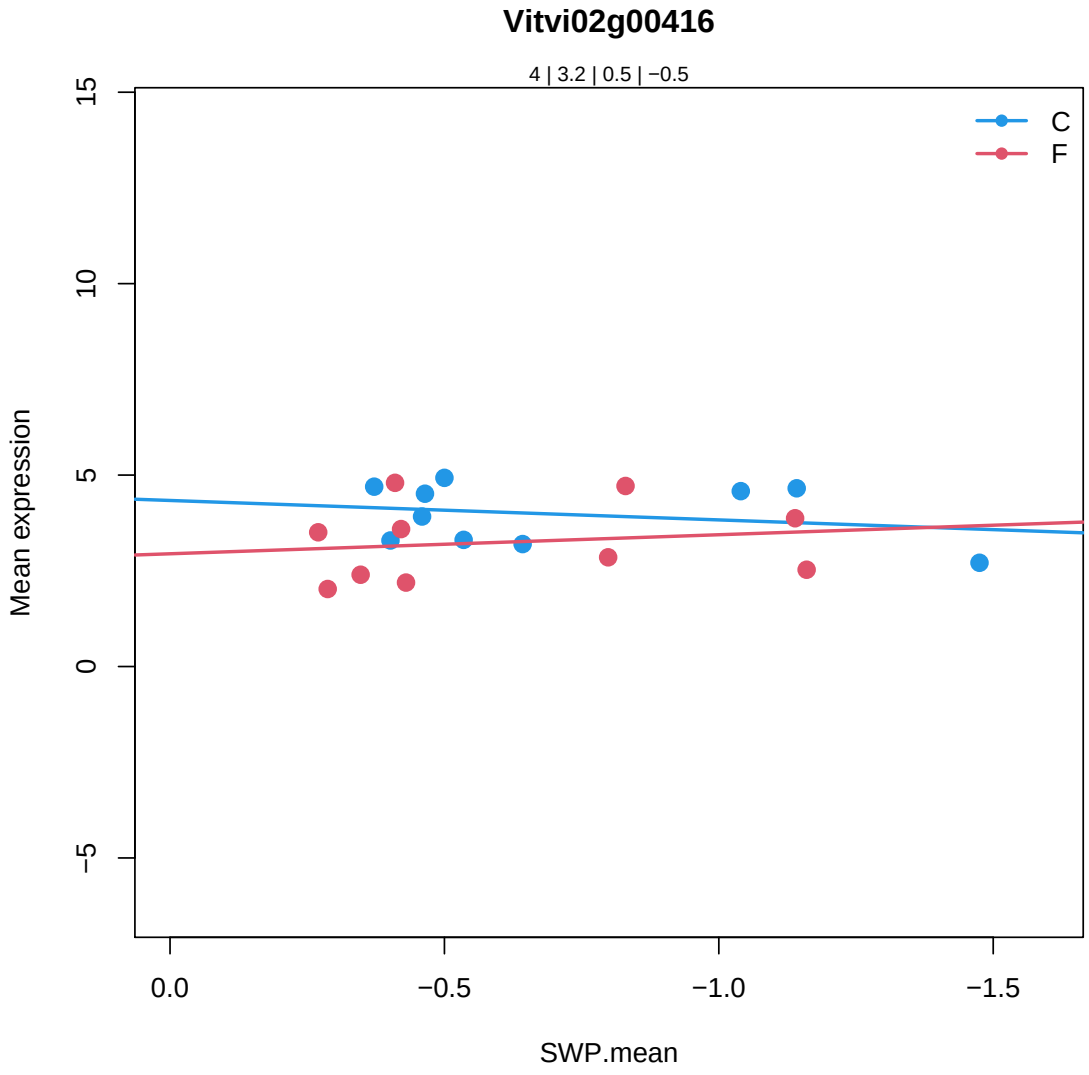
7.6.246 Vitvi02g00416: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00416
        26.8
        misc.nitrilases, nitrile lyases, berberine bridge enzymes, reticuline
        Glucose-methanol-choline (GMC) oxidoreductase family protein |
        Chr1:27452872-27455706 FORWARD LENGTH=594 |
        201606
```

Coefficients for Vitvi02g00416.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.979781	9.933756e-13	***	1.425978e-12	***
SlopeC	0.5080276	0.504488		0.8706312	
MeanF-MeanC	-0.7322868	0.0675936	.	0.2893993	
SlopeF-SlopeC	-1.00531	0.3767816		0.9999488	



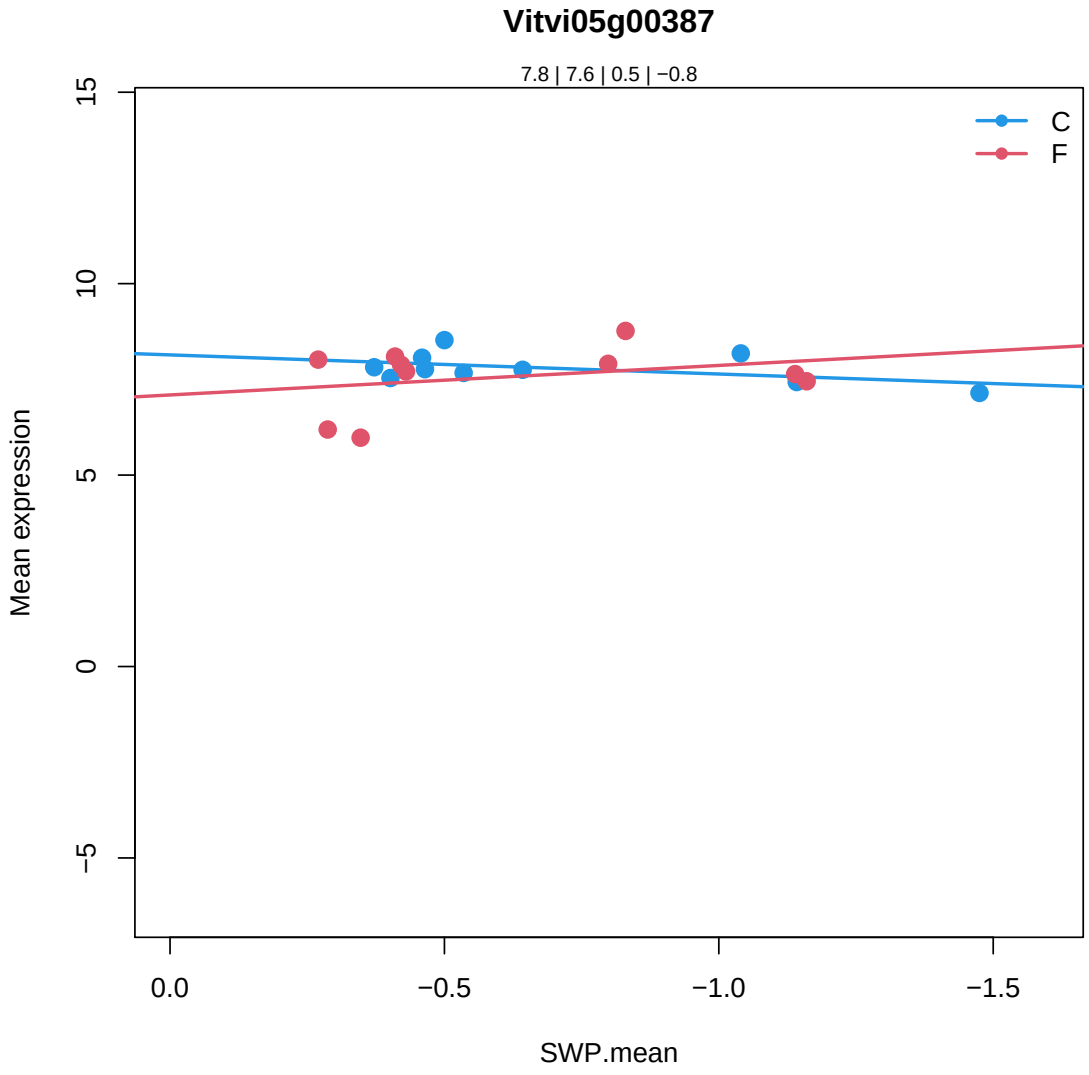
7.6.247 Vitvi05g00387: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00387
        6.5
        gluconeogenesis / glyoxylate cycle.pyruvate dikinase
        pyruvate orthophosphate dikinase |
        Chr4:8864828-8869183 REVERSE LENGTH=875 |
        201606
```

Coefficients for Vitvi05g00387.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.787698	1.626088e-21	***	1.669013e-20	***
SlopeC	0.4989933	0.3732237		0.8234798	
MeanF-MeanC	-0.2255292	0.4276107		0.7632011	
SlopeF-SlopeC	-1.270203	0.1344862		0.9999488	



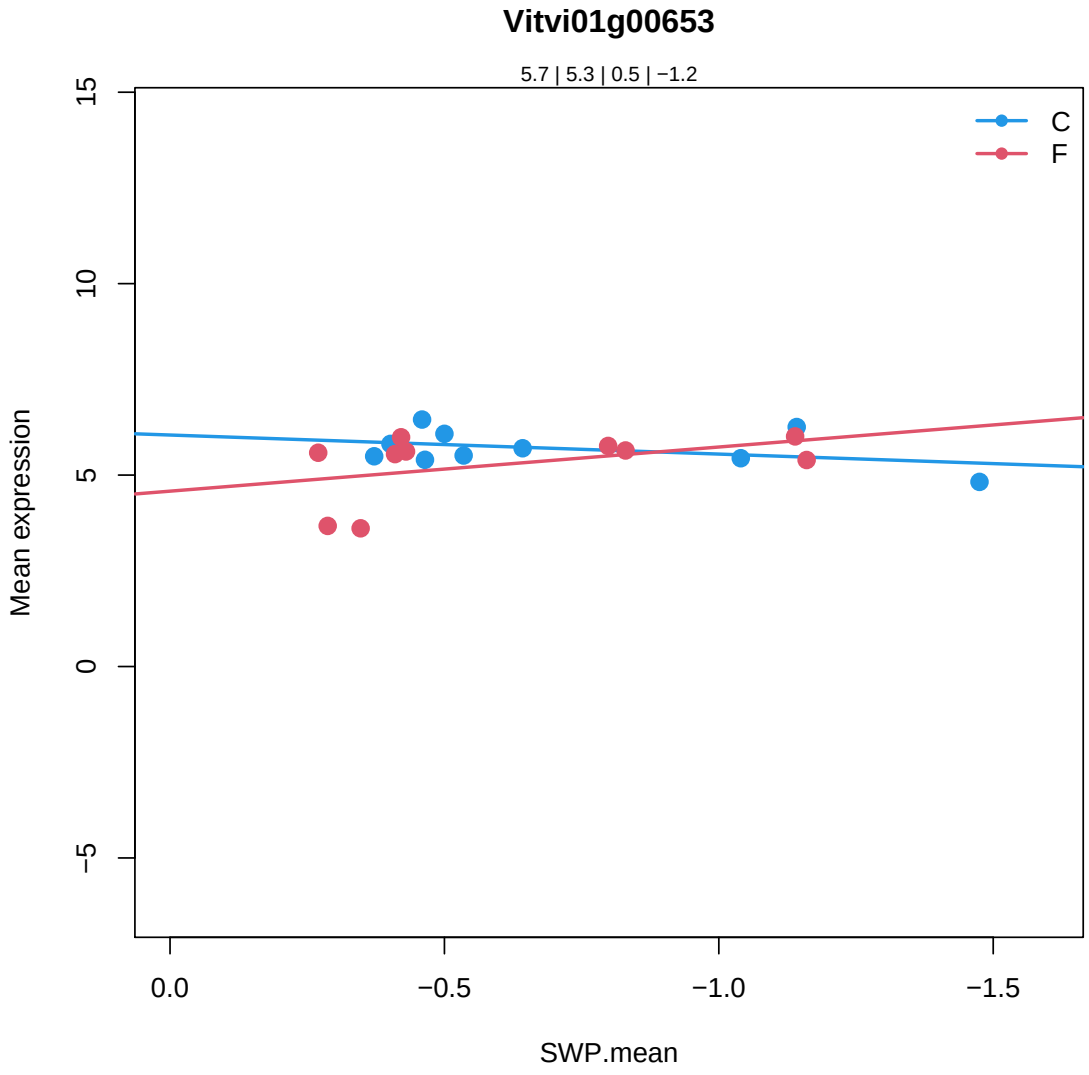
7.6.248 Vitvi01g00653: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00653
        34.99
        transport.misc
        MATE efflux family protein |
        Chr3:9761927-9765259 REVERSE LENGTH=500 |
        201606
```

Coefficients for Vitvi01g00653.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.696086	1.771334e-18	***	5.674375e-18	***
SlopeC	0.4977192	0.3835334		0.82771	
MeanF-MeanC	-0.413744	0.1601902		0.4837762	
SlopeF-SlopeC	-1.650855	0.06037514	.	0.9999488	



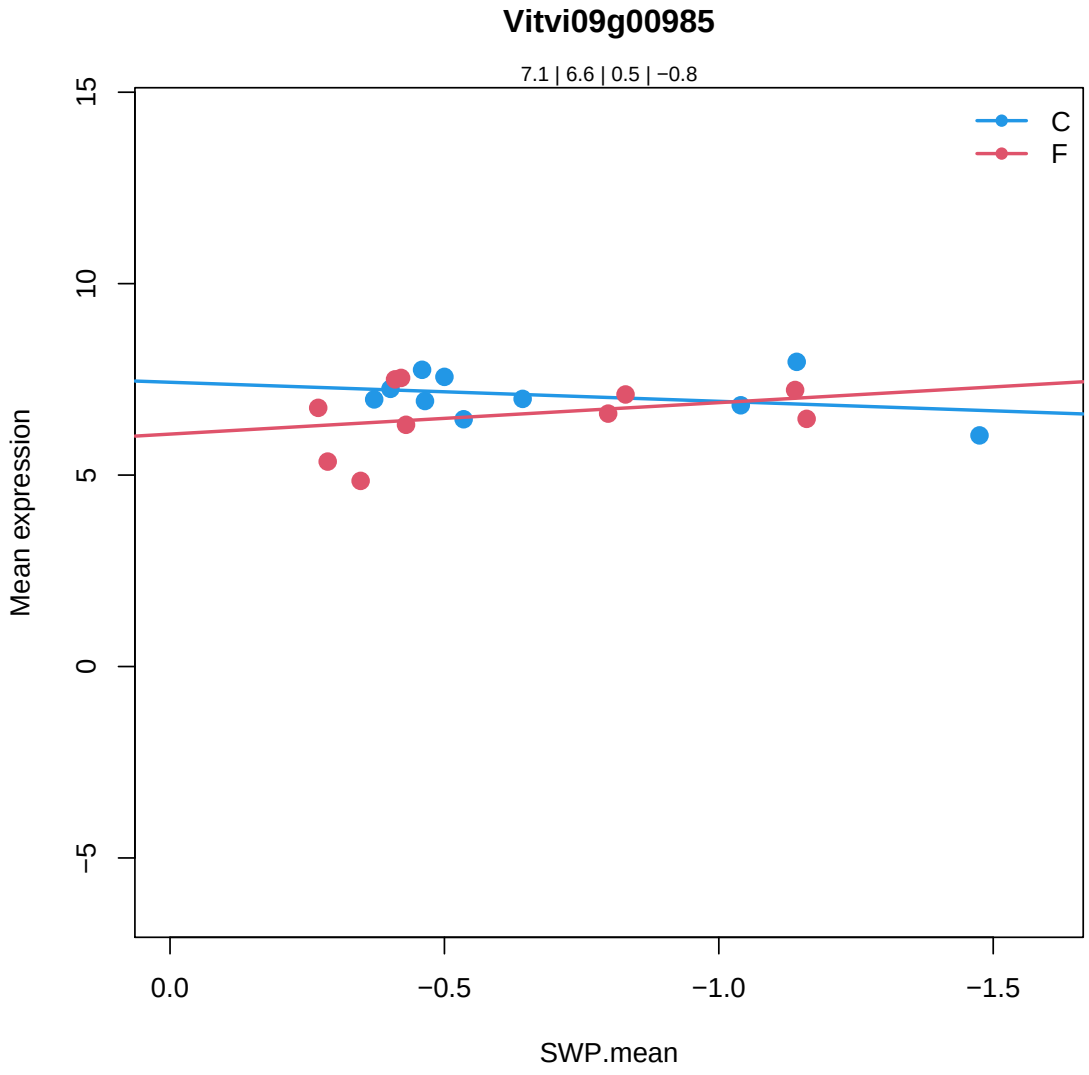
7.6.249 Vitvi09g00985: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00985
        29.4
        protein.postranslational modification
        SOS3-interacting protein 3 |
        Chr4:15067400-15068725 FORWARD LENGTH=441 |
        201606
```

Coefficients for Vitvi09g00985.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.074192	1.280776e-19	***	5.885313e-19	***
SlopeC	0.4971995	0.4262287		0.846901	
MeanF-MeanC	-0.5033526	0.1208513		0.4094278	
SlopeF-SlopeC	-1.318601	0.1628505		0.9999488	



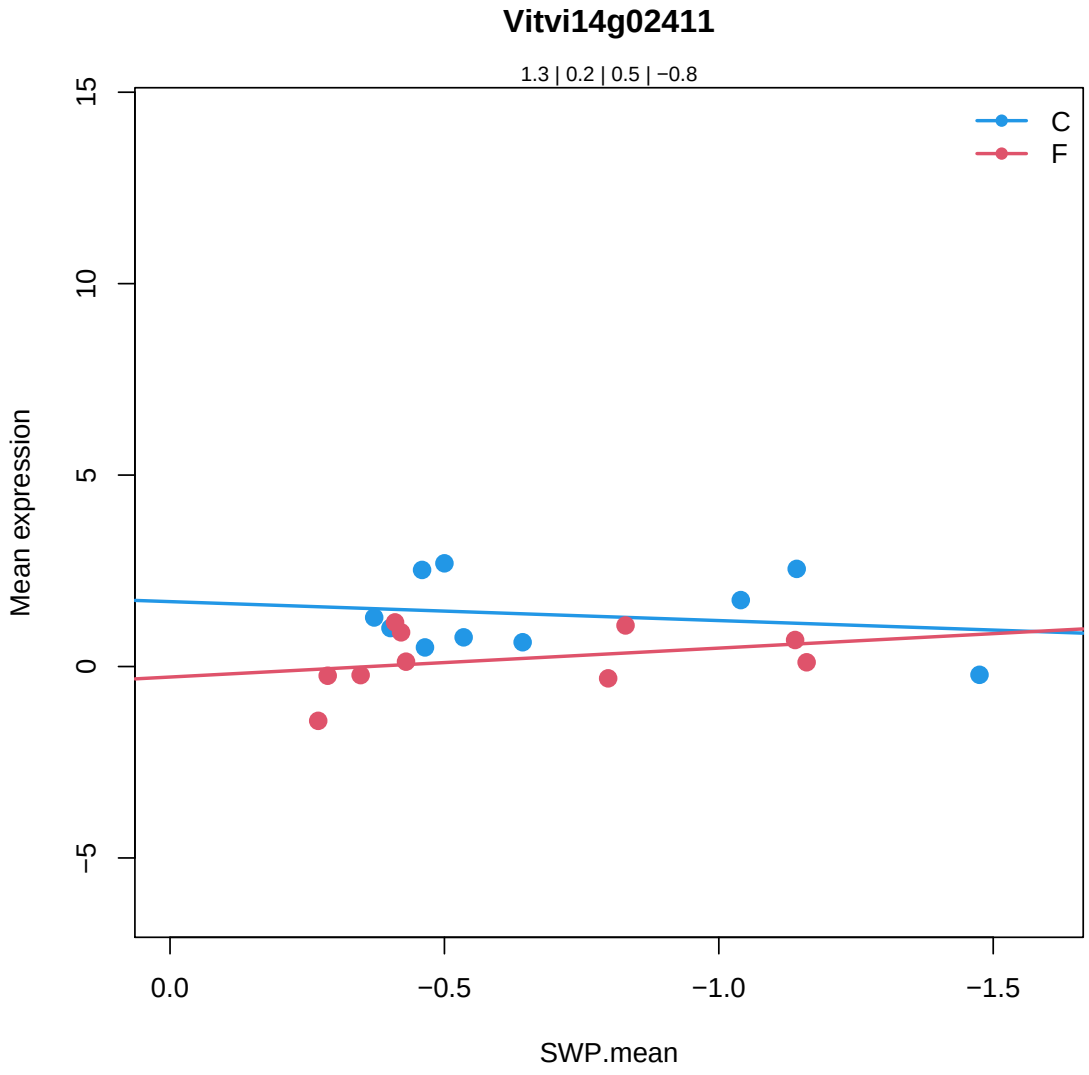
7.6.250 Vitvi14g02411: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g02411
        35.2
        not assigned.unknown
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606
```

Coefficients for Vitvi14g02411.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.34647	4.509369e-05	***	5.013626e-05	***
SlopeC	0.494922	0.5080474		0.8711742	
MeanF-MeanC	-1.161215	0.005246476	**	0.04745803	*
SlopeF-SlopeC	-1.250607	0.2657123		0.9999488	



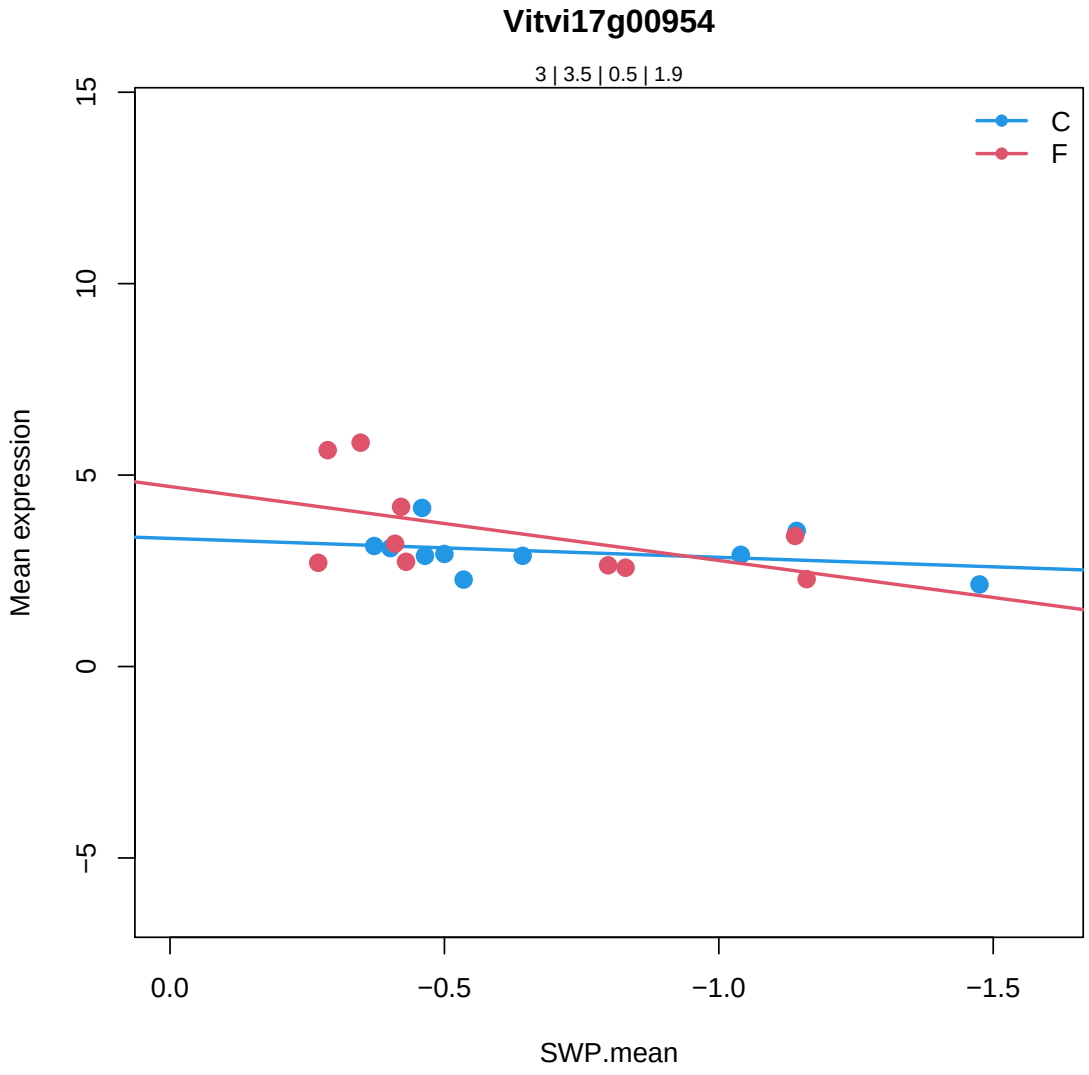
7.6.251 Vitvi17g00954: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00954
        29.5.11.4.2
        protein.degradation.ubiquitin.E3.RING
        RING domain ligase2 |
        Chr5:4648355-4650563 REVERSE LENGTH=468 |
        201606
```

Coefficients for Vitvi17g00954.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.997756	1.514848e-10	***	1.96991e-10	***
SlopeC	0.4942665	0.5075452		0.8711742	
MeanF-MeanC	0.5257968	0.1727608		0.5032391	
SlopeF-SlopeC	1.436677	0.2020142		0.9999488	



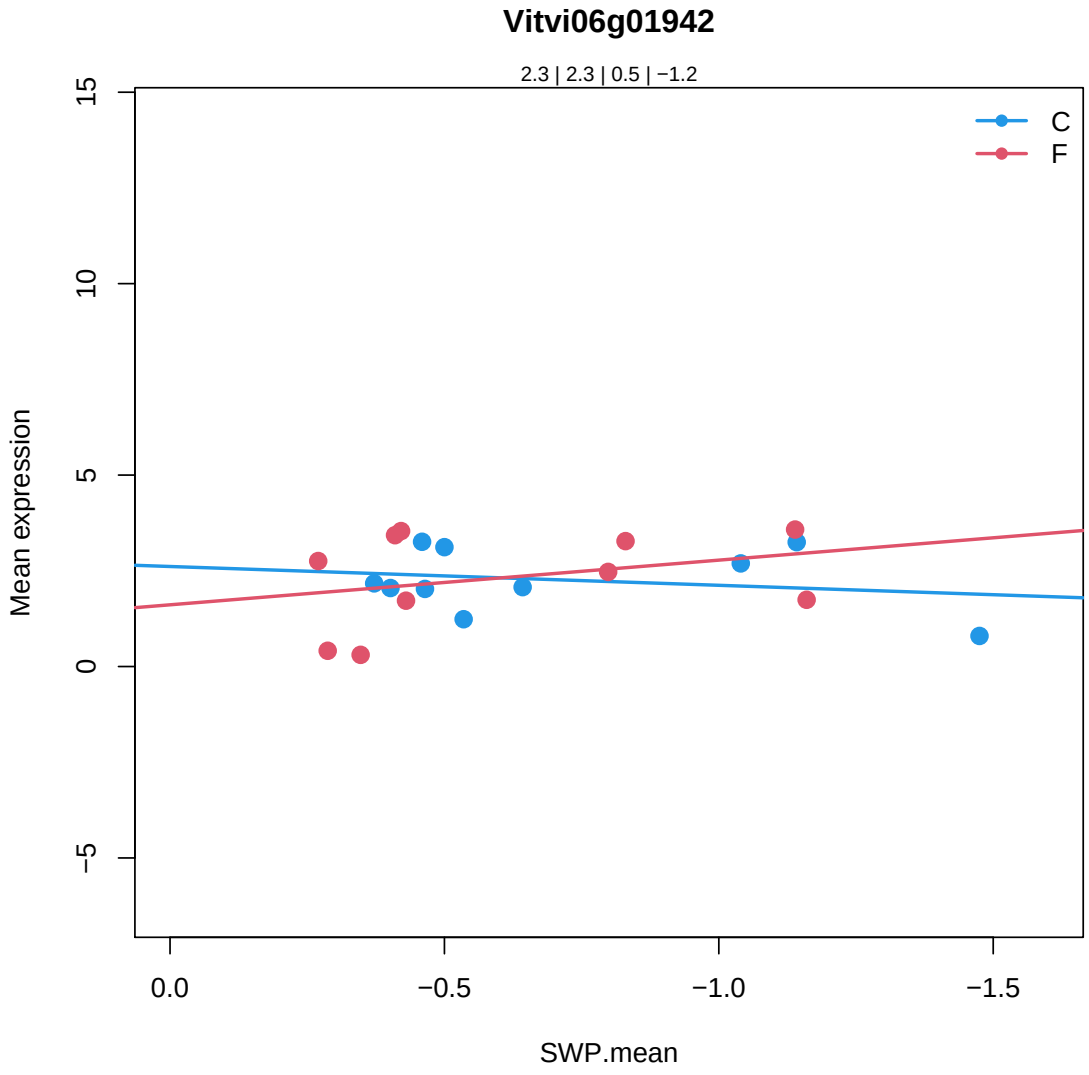
7.6.252 Vitvi06g01942: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01942
        30.11
        signalling.light
        Phototropic-responsive NPH3 family protein |
        Chr3:16361864-16364411 REVERSE LENGTH=651 |
        201606
```

Coefficients for Vitvi06g01942.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.26702	1.992691e-07	***	2.344288e-07	***
SlopeC	0.4912215	0.5651841		0.8905966	
MeanF-MeanC	0.05542072	0.8980415		0.973376	
SlopeF-SlopeC	-1.657755	0.1992438		0.9999488	



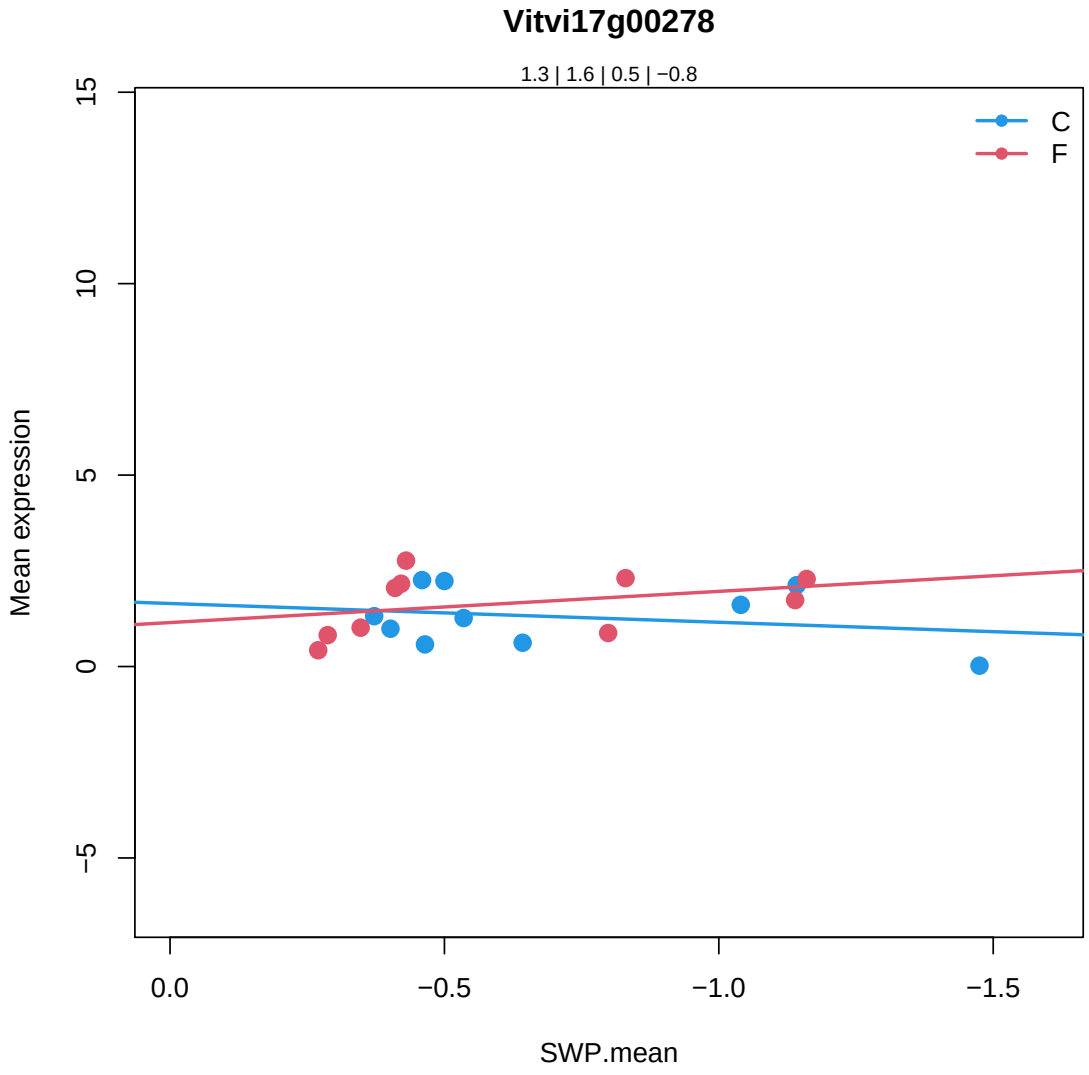
7.6.253 Vitvi17g00278: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00278
        26.3.3
        misc.gluco-, galacto- and mannosidases.alpha-mannosidase
        Glycosyl hydrolase family 38 protein |
        Chr3:9816707-9823056 FORWARD LENGTH=1019 |
        201606
```

Coefficients for Vitvi17g00278.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.301255	1.151644e-05	***	1.298613e-05	***
SlopeC	0.4906187	0.4503084		0.8555685	
MeanF-MeanC	0.3431339	0.3018331		0.6670188	
SlopeF-SlopeC	-1.305573	0.1833856		0.9999488	



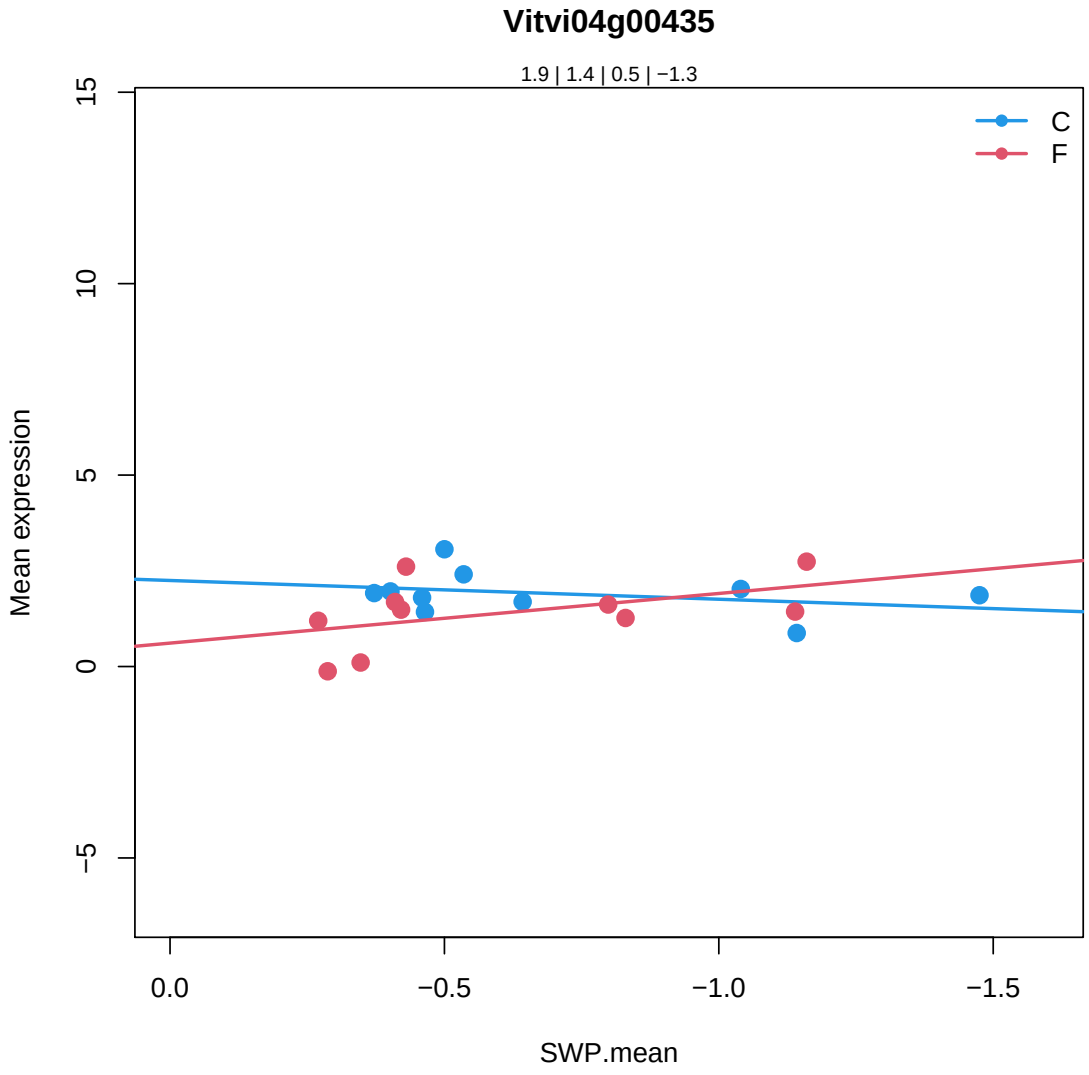
7.6.254 Vitvi04g00435: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00435
        17.6.1.12
        hormone metabolism.gibberelin.synthesis-degradation.GA3 oxidase
        gibberellin 3-oxidase 1 |
        Chr1:5344569-5346078 REVERSE LENGTH=358 |
        201606
```

Coefficients for Vitvi04g00435.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.902578	1.025284e-08	***	1.251392e-08	***
SlopeC	0.4899964	0.4148964		0.8407141	
MeanF-MeanC	-0.5012751	0.1087995		0.3845937	
SlopeF-SlopeC	-1.786553	0.054211	.	0.9999488	



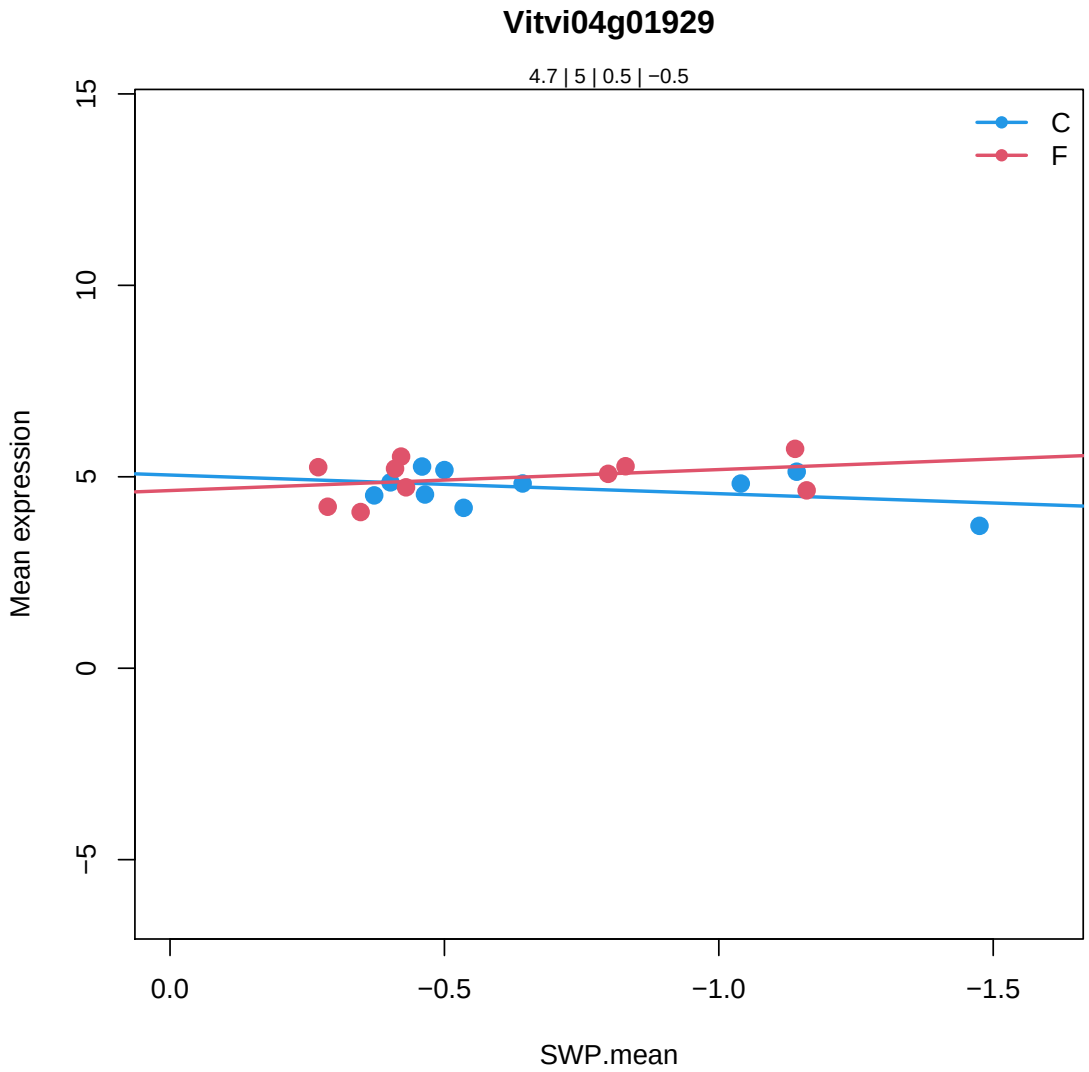
7.6.255 Vitvi04g01929: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01929
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi04g01929.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.703547	7.023631e-19	***	2.526651e-18	***
SlopeC	0.4869123	0.2828474		0.7773135	
MeanF-MeanC	0.2702737	0.2421181		0.6005475	
SlopeF-SlopeC	-1.034866	0.1303449		0.9999488	



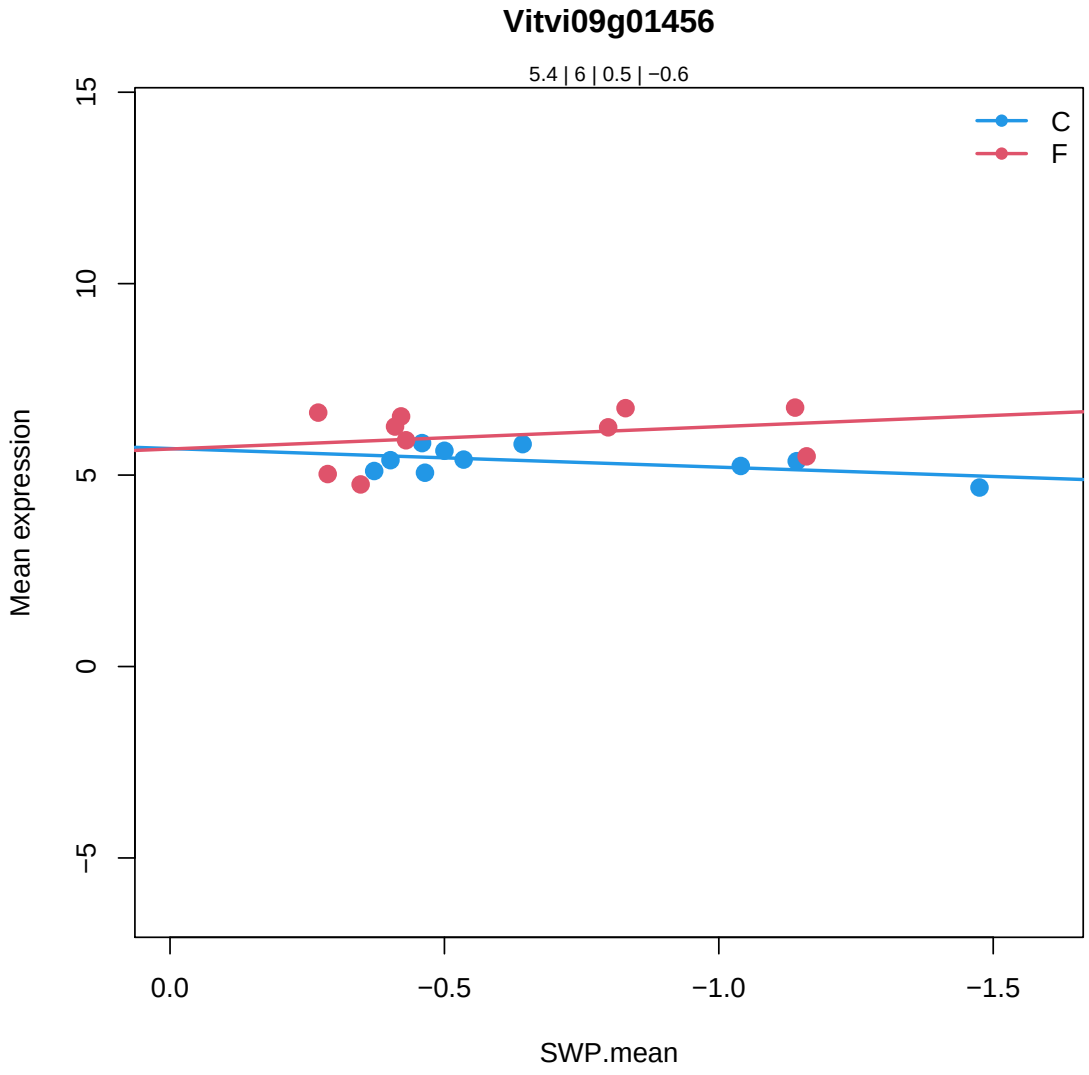
7.6.256 Vitvi09g01456: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g01456
        30.9
        signalling.lipids
        Polyketide cyclase/dehydrase and lipid transport superfamily protein |
        Chr3:4184777-4186795 FORWARD LENGTH=411 |
        201606
```

Coefficients for Vitvi09g01456.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.35137	3.136888e-19	***	1.265743e-18	***
SlopeC	0.4866378	0.3258129		0.8000183	
MeanF-MeanC	0.6855431	0.01091259	*	0.08093901	.
SlopeF-SlopeC	-1.071715	0.1513179		0.9999488	



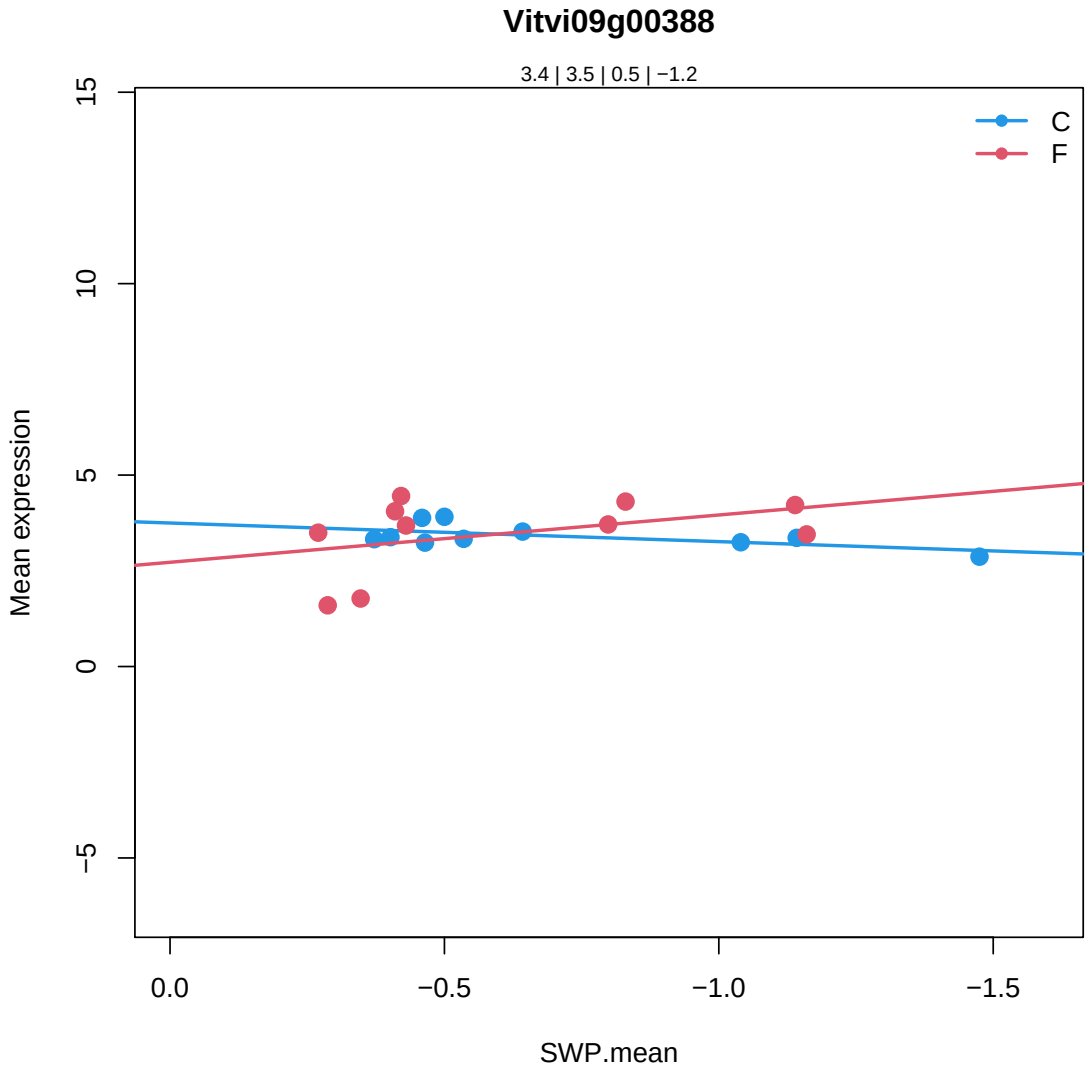
7.6.257 Vitvi09g00388: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00388
        35.2
        not assigned.unknown
        Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein fam
        Chr4:7731280-7732902 FORWARD LENGTH=215 |
        201606
```

Coefficients for Vitvi09g00388.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.406414	1.334247e-13	***	2.027982e-13	***
SlopeC	0.48595	0.4103183		0.8391347	
MeanF-MeanC	0.06822739	0.8187836		0.9499835	
SlopeF-SlopeC	-1.721251	0.05850873	.	0.9999488	



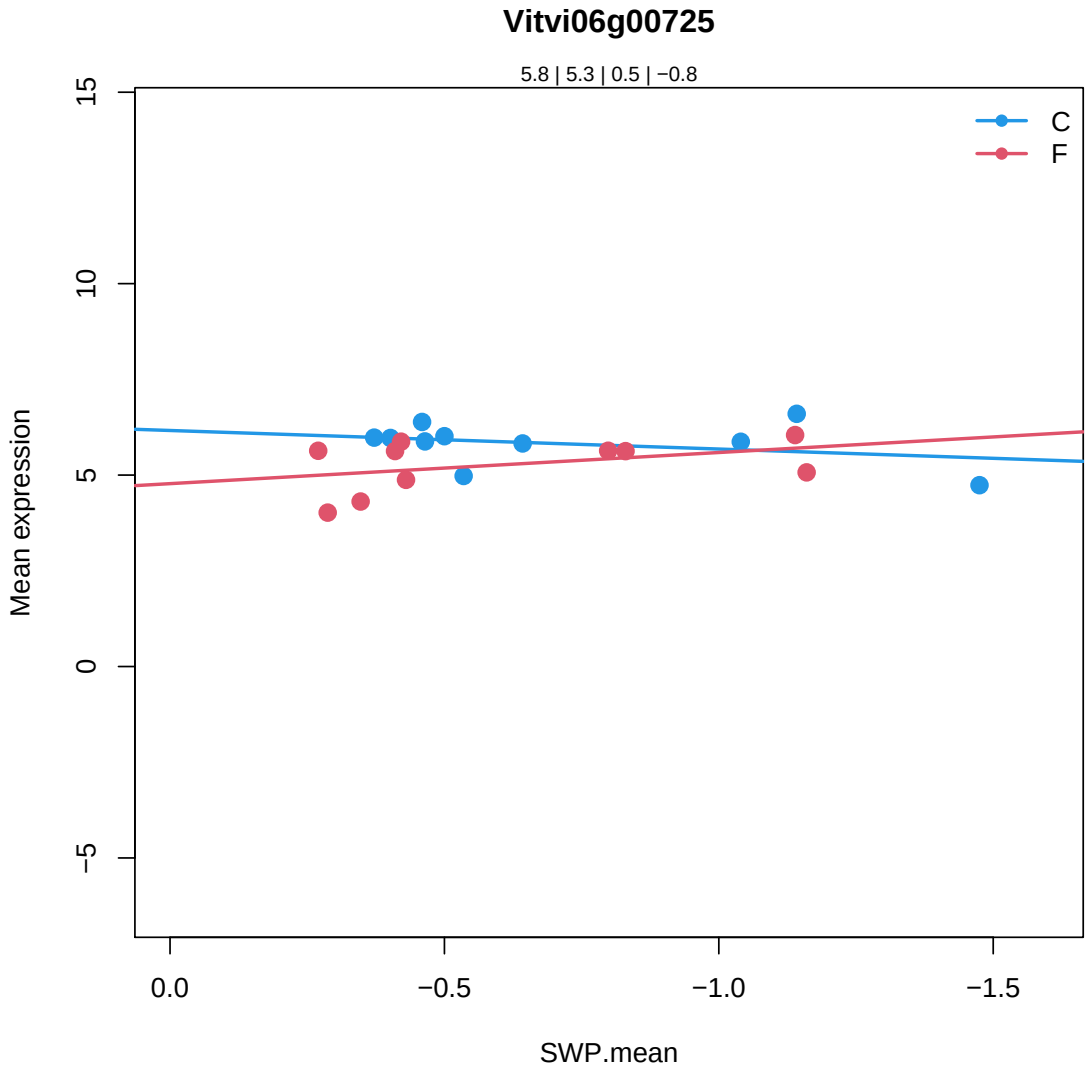
7.6.258 Vitvi06g00725: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00725
        26.27
        misc.calcineurin-like phosphoesterase family protein
        Calcineurin-like metallo-phosphoesterase superfamily protein |
        Chr1:2152949-2154968 FORWARD LENGTH=389 |
        201606
```

Coefficients for Vitvi06g00725.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.823778	2.045487e-19	***	8.725807e-19	***
SlopeC	0.4843822	0.3583461		0.8183149	
MeanF-MeanC	-0.5523368	0.04717977	*	0.2304853	
SlopeF-SlopeC	-1.29782	0.1055554		0.9999488	



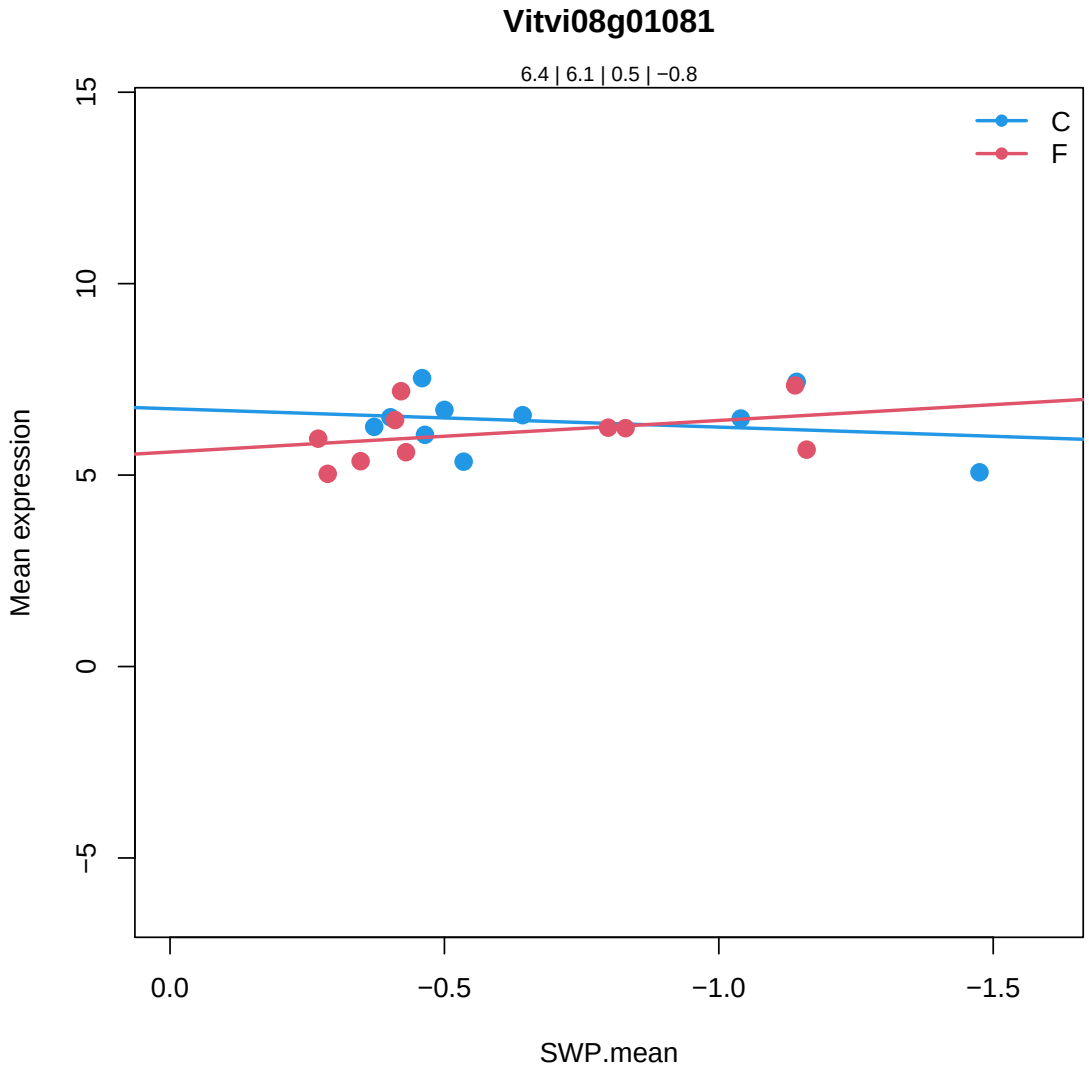
7.6.259 Vitvi08g01081: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01081
        23.4.99
        nucleotide metabolism.phosphotransfer and pyrophosphatases.misc
        pyrophosphorylase 4 |
        Chr3:19881491-19883308 FORWARD LENGTH=216 |
        201606
```

Coefficients for Vitvi08g01081.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.395406	1.578607e-18	***	5.128119e-18	***
SlopeC	0.4792914	0.4513072		0.8556817	
MeanF-MeanC	-0.2912757	0.3692045		0.724139	
SlopeF-SlopeC	-1.304323	0.1749843		0.9999488	



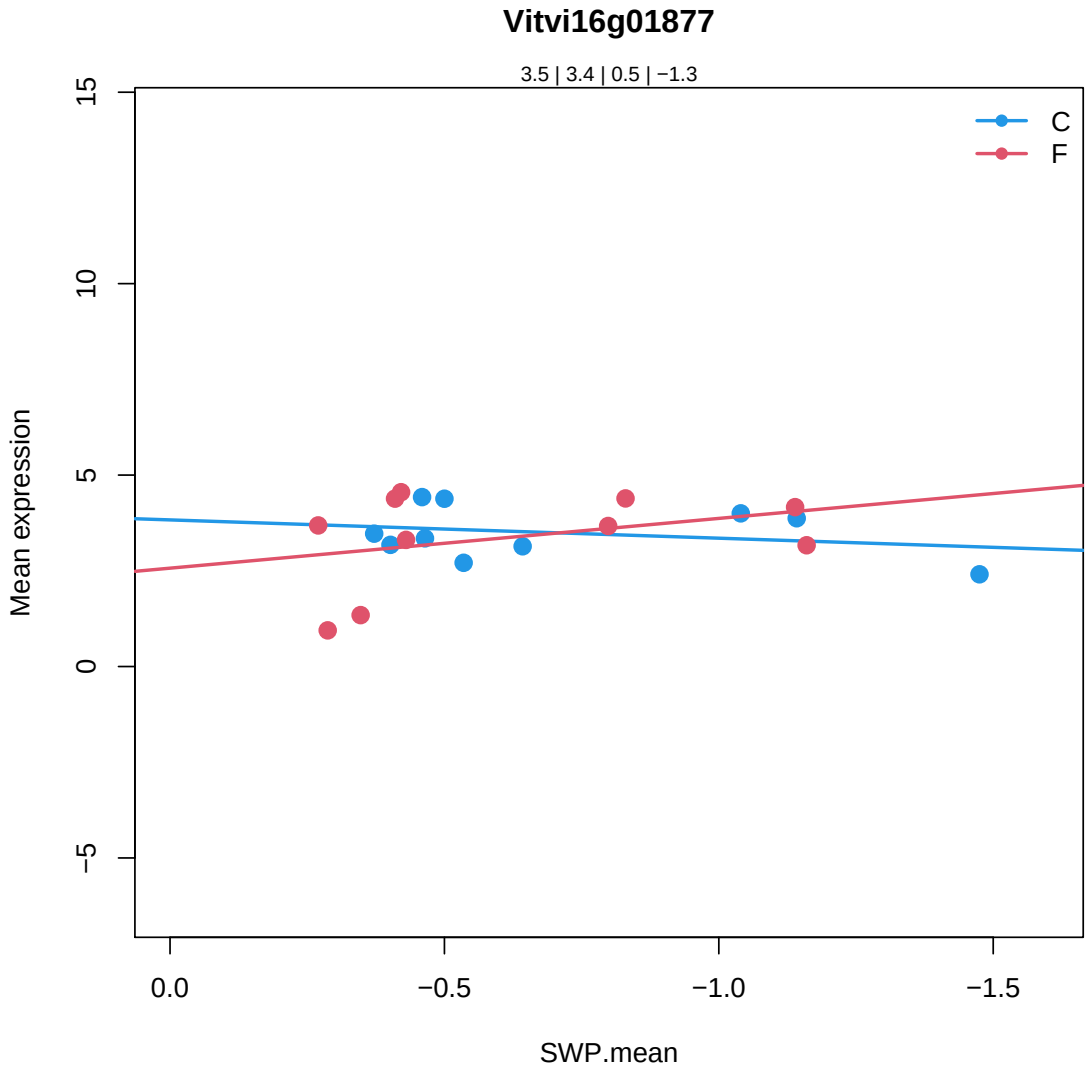
7.6.260 Vitvi16g01877: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01877
        35.2
        not assigned.unknown
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606
```

Coefficients for Vitvi16g01877.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.493249	4.208311e-11	***	5.590298e-11	***
SlopeC	0.477827	0.5555915		0.8894103	
MeanF-MeanC	-0.1326892	0.7467549		0.9258482	
SlopeF-SlopeC	-1.777585	0.1490629		0.9999488	



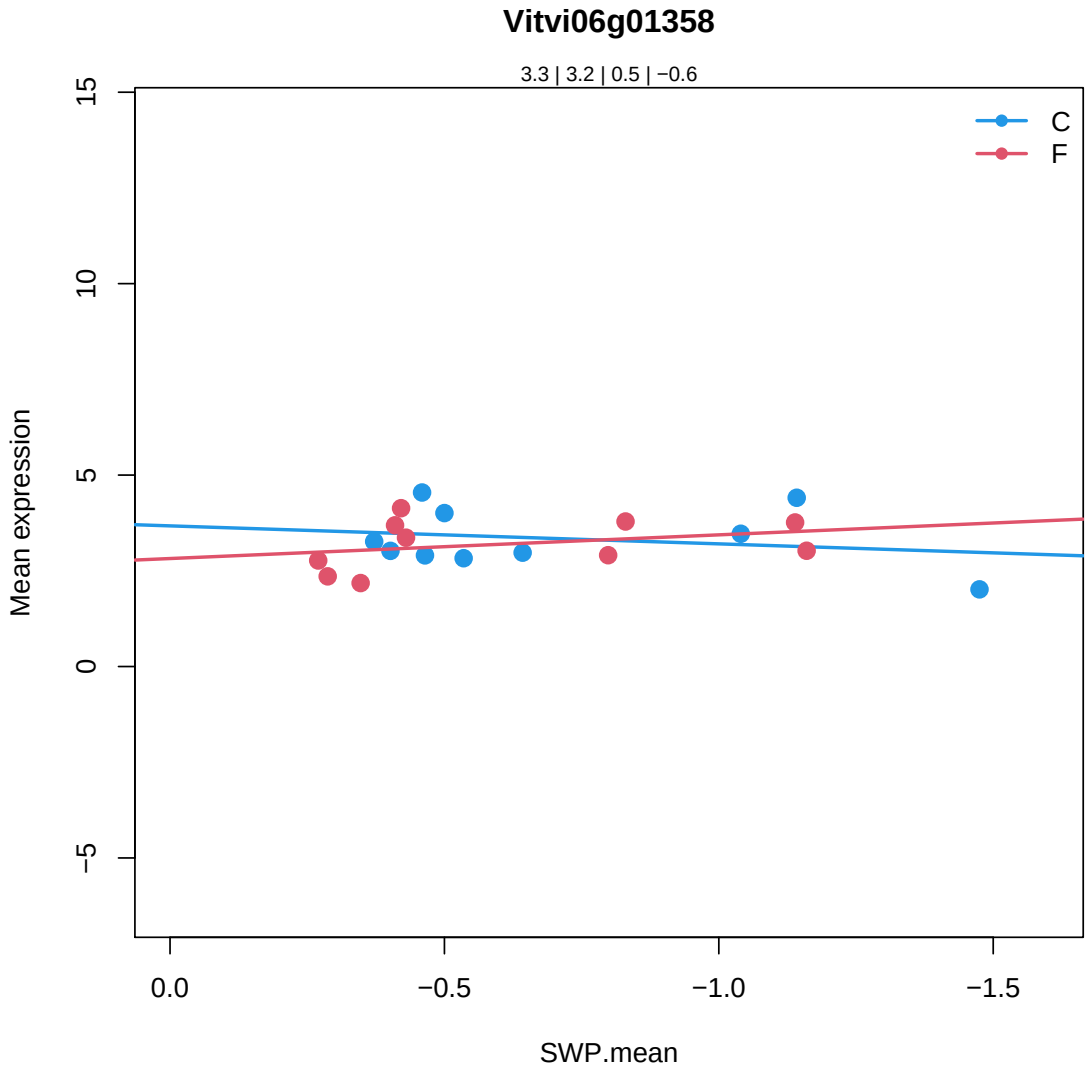
7.6.261 Vitvi06g01358: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01358
        29.5.11.4.2
        protein.degradation.ubiquitin.E3.RING
        Ring/U-Box superfamily protein |
        Chr2:11899422-11903171 REVERSE LENGTH=839 |
        201606
```

Coefficients for Vitvi06g01358.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.343189	3.984746e-13	***	5.868731e-13	***
SlopeC	0.4697774	0.4423202		0.852151	
MeanF-MeanC	-0.1460002	0.637077		0.8763266	
SlopeF-SlopeC	-1.088636	0.2361786		0.9999488	



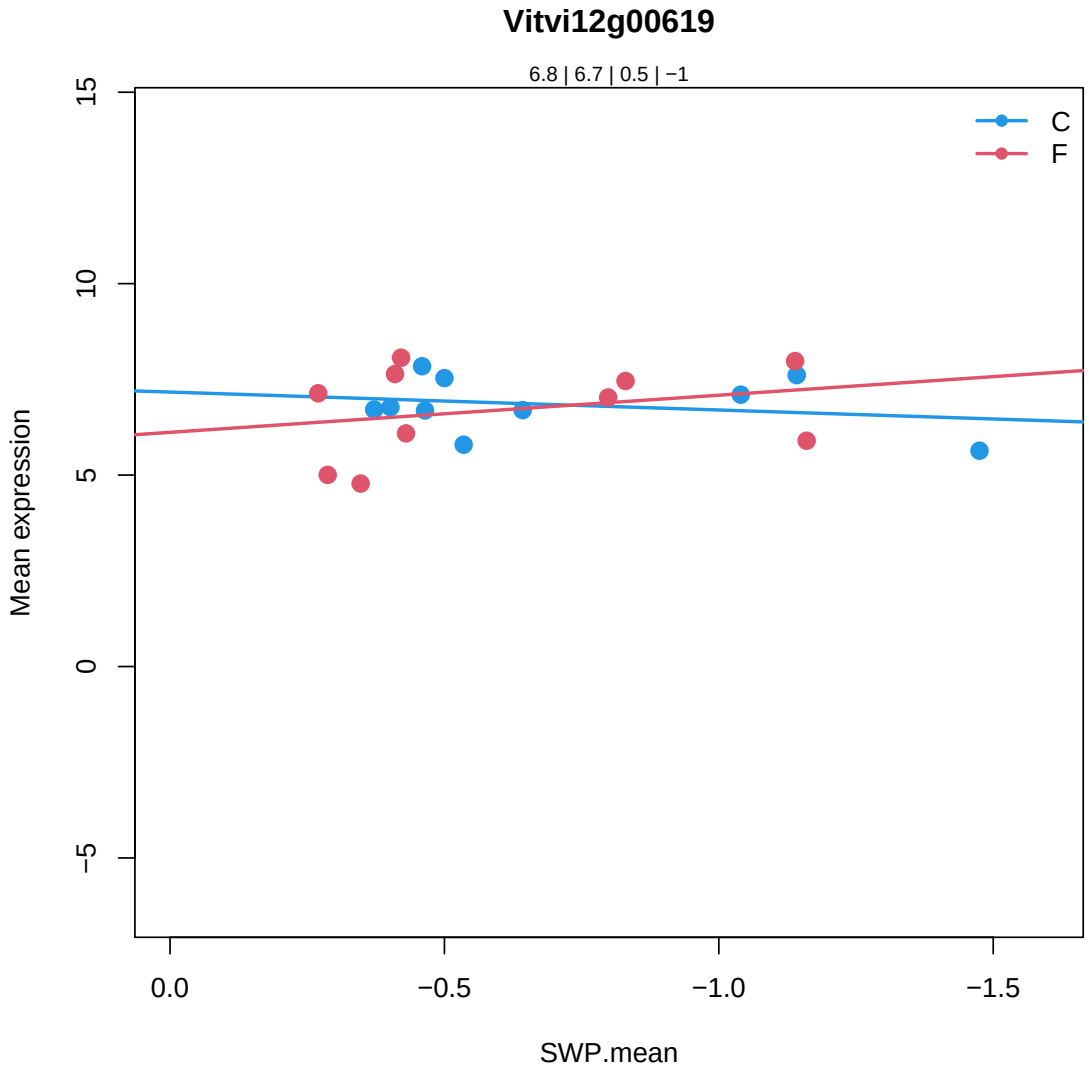
7.6.262 Vitvi12g00619: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00619
        29.4
        protein.postranslational modification
        Outer arm dynein light chain 1 protein |
        Chr4:1429092-1431431 FORWARD LENGTH=677 |
        201606
```

Coefficients for Vitvi12g00619.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.83841	6.295504e-17	***	1.418629e-16	***
SlopeC	0.4681846	0.5632414		0.8905966	
MeanF-MeanC	-0.1313442	0.7490474		0.9264858	
SlopeF-SlopeC	-1.4379	0.2388677		0.9999488	



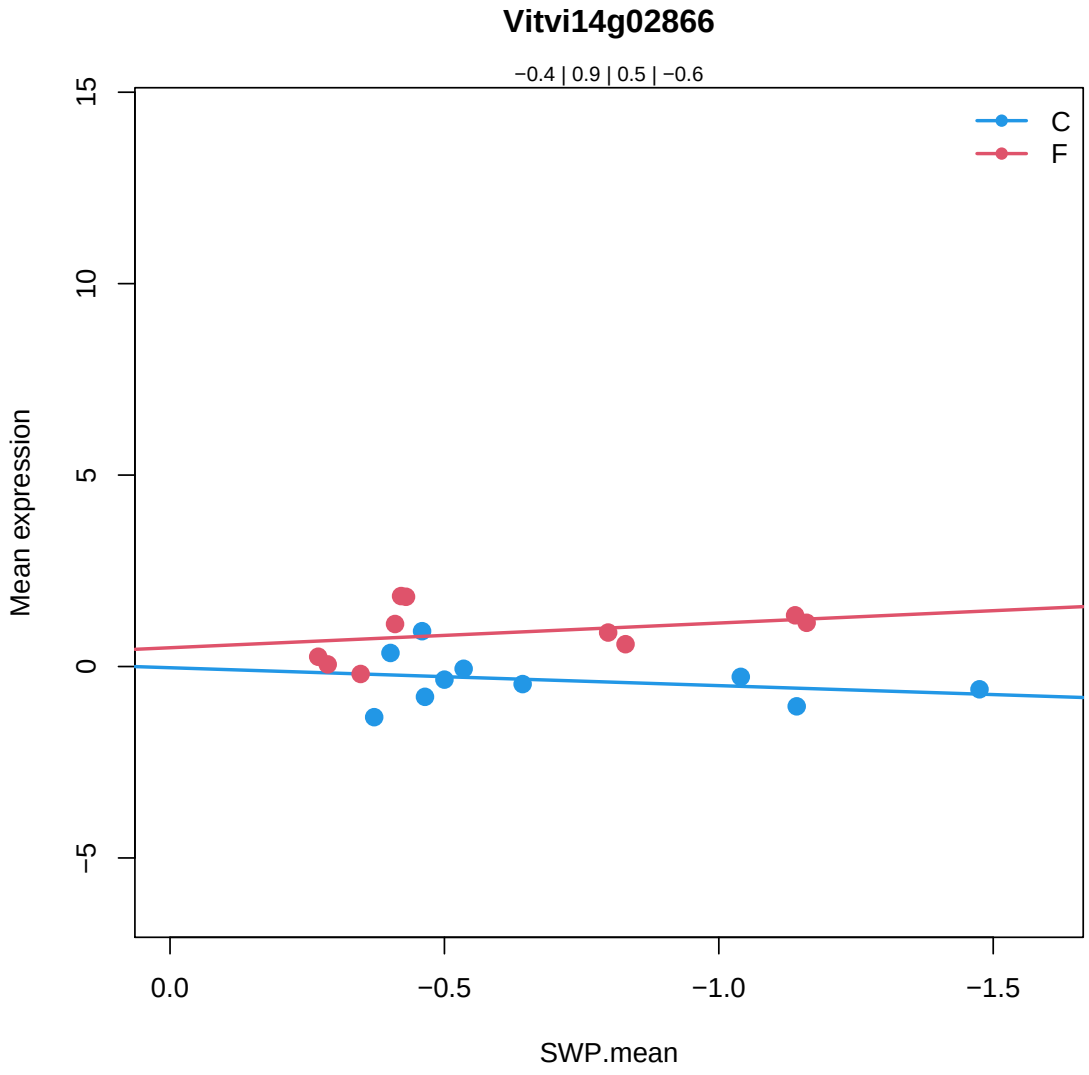
7.6.263 Vitvi14g02866: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g02866
        35.2
        not assigned.unknown
        hypothetical protein |
        Chr2:19486004-19486429 FORWARD LENGTH=141 |
        201606
```

Coefficients for Vitvi14g02866.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.360383	0.0916553	.	0.09488553	.
SlopeC	0.4673642	0.4194927		0.8427244	
MeanF-MeanC	1.243949	0.0002972839	***	0.004572353	**
SlopeF-SlopeC	-1.112702	0.2018448		0.9999488	



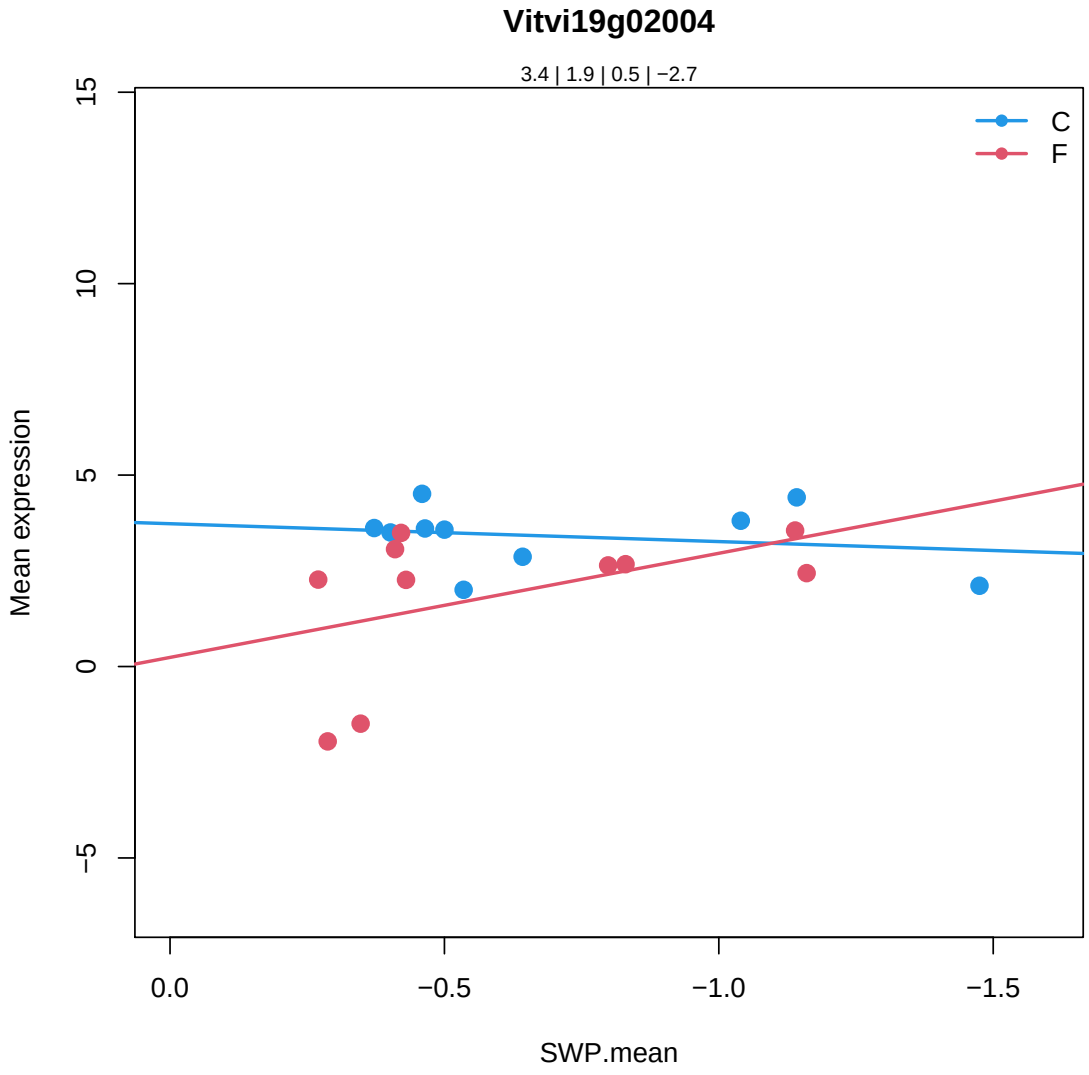
7.6.264 Vitvi19g02004: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g02004
        35.2
        not assigned.unknown
        fatty acid desaturase A |
        Chr4:13571951-13572922 FORWARD LENGTH=323 |
        201606
```

Coefficients for Vitvi19g02004.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.401391	2.600455e-08	***	3.135026e-08	***
SlopeC	0.4667448	0.6791641		0.9268622	
MeanF-MeanC	-1.506922	0.01439005	*	0.09906648	.
SlopeF-SlopeC	-3.186127	0.06784855	.	0.9999488	



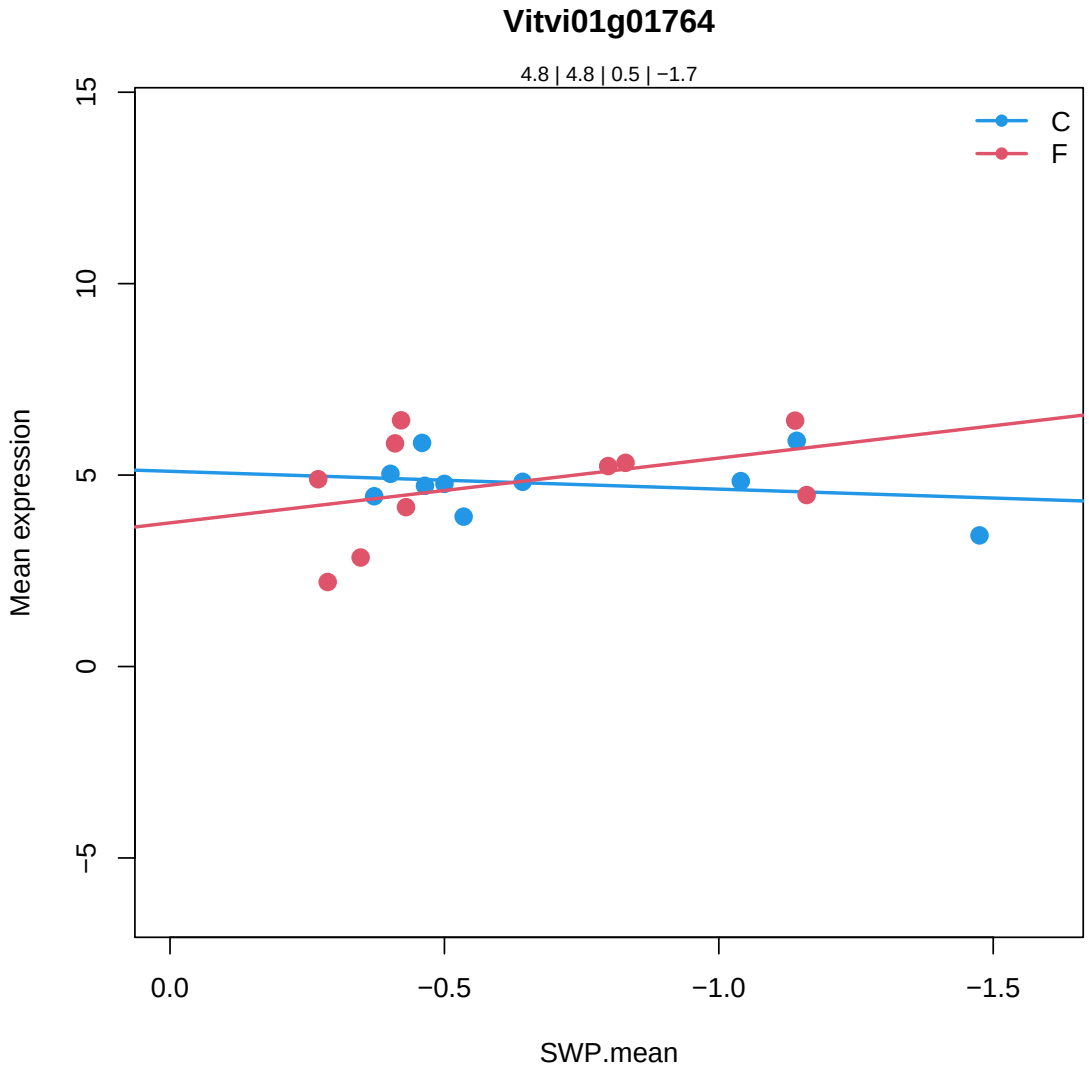
7.6.265 Vitvi01g01764: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01764
        19.99
        tetrapyrrole synthesis.unspecified
        SOUL heme-binding family protein |
        Chr1:5844766-5845539 FORWARD LENGTH=232 |
        201606
```

Coefficients for Vitvi01g01764.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.771117	5.468395e-13	***	7.984412e-13	***
SlopeC	0.4655929	0.5981785		0.9034321	
MeanF-MeanC	0.01100363	0.9803868		0.9949434	
SlopeF-SlopeC	-2.156261	0.1105399		0.9999488	



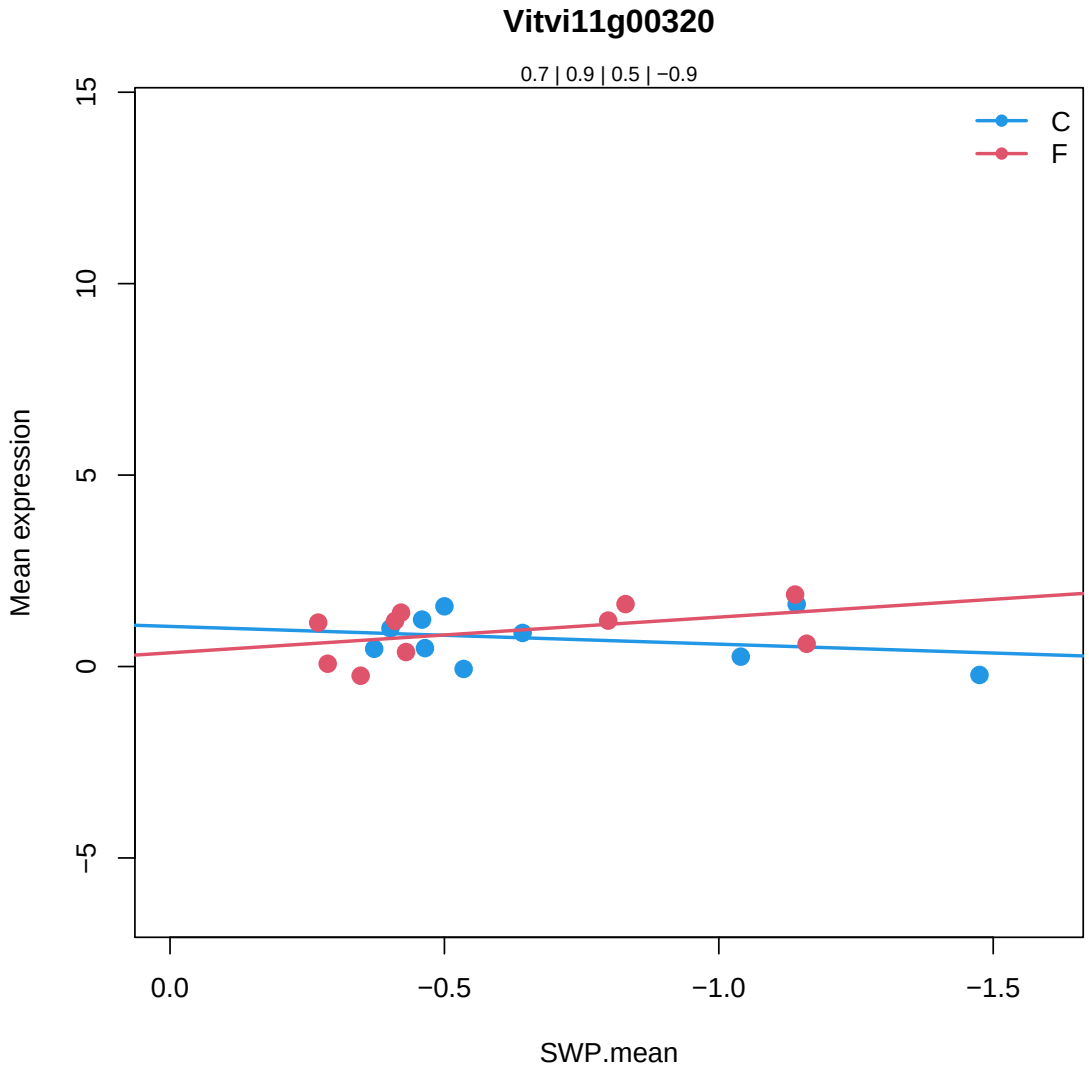
7.6.266 Vitvi11g00320: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00320
        27.3.25
        RNA.regulation of transcription.MYB domain transcription factor family
        Homeodomain-like protein |
        Chr4:15791039-15794252 FORWARD LENGTH=776 |
        201606
```

Coefficients for Vitvi11g00320.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.7215686	0.001310334	**	0.001415759	**
SlopeC	0.4635733	0.4030474		0.8360908	
MeanF-MeanC	0.2042575	0.4676524		0.7876703	
SlopeF-SlopeC	-1.395276	0.09889408	.	0.9999488	



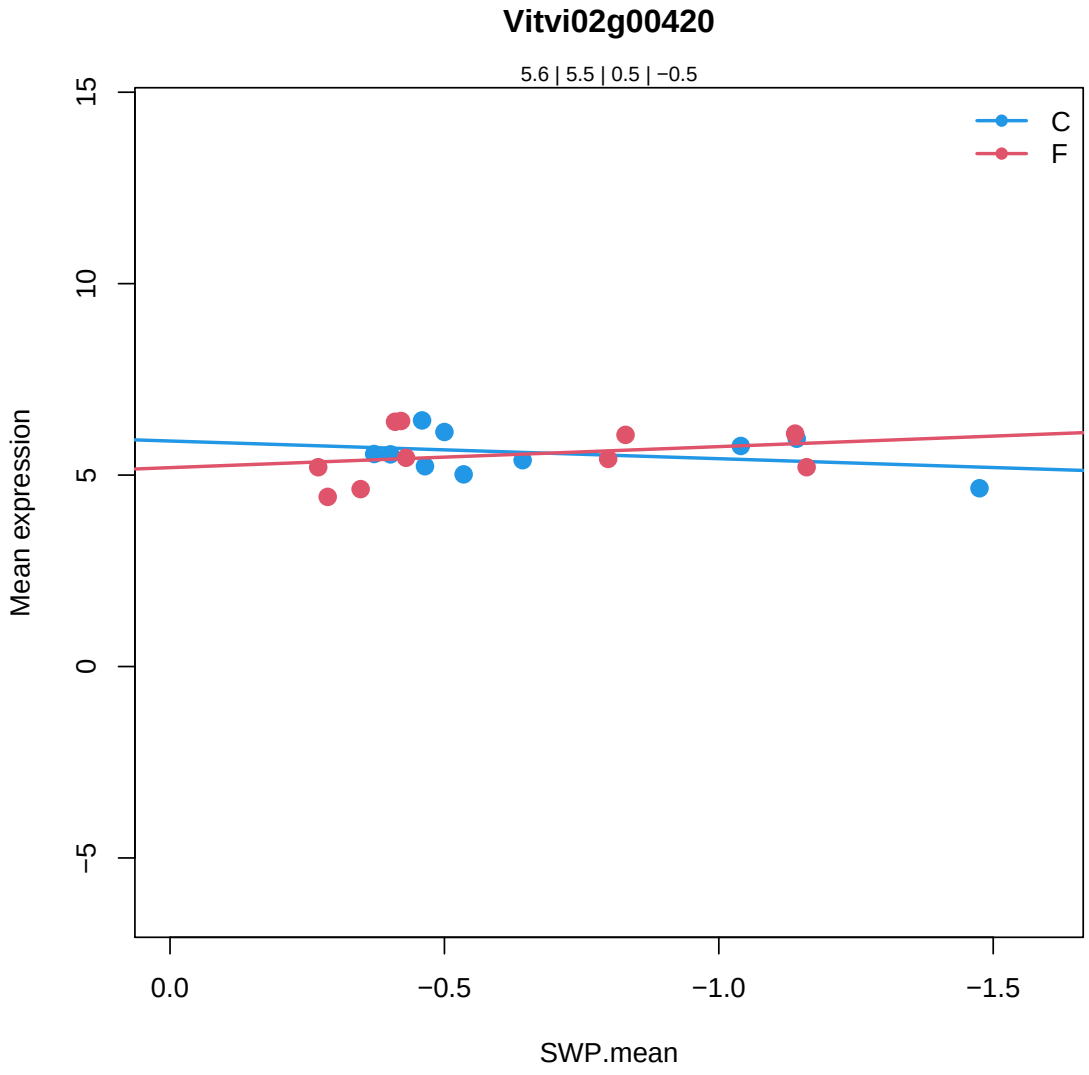
7.6.267 Vitvi02g00420: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00420
        16.1.2.2
        secondary metabolism.isoprenoids.mevalonate pathway.HMG-CoA synthase
        hydroxymethylglutaryl-CoA synthase / HMG-CoA synthase / 3-hydroxy-3-me
        Chr4:7109124-7111213 REVERSE LENGTH=406 |
        201606
```

Coefficients for Vitvi02g00420.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.564749	6.900979e-19	***	2.487224e-18	***
SlopeC	0.4619262	0.386459		0.8286997	
MeanF-MeanC	-0.03609103	0.8931775		0.9718495	
SlopeF-SlopeC	-1.011003	0.2073868		0.9999488	



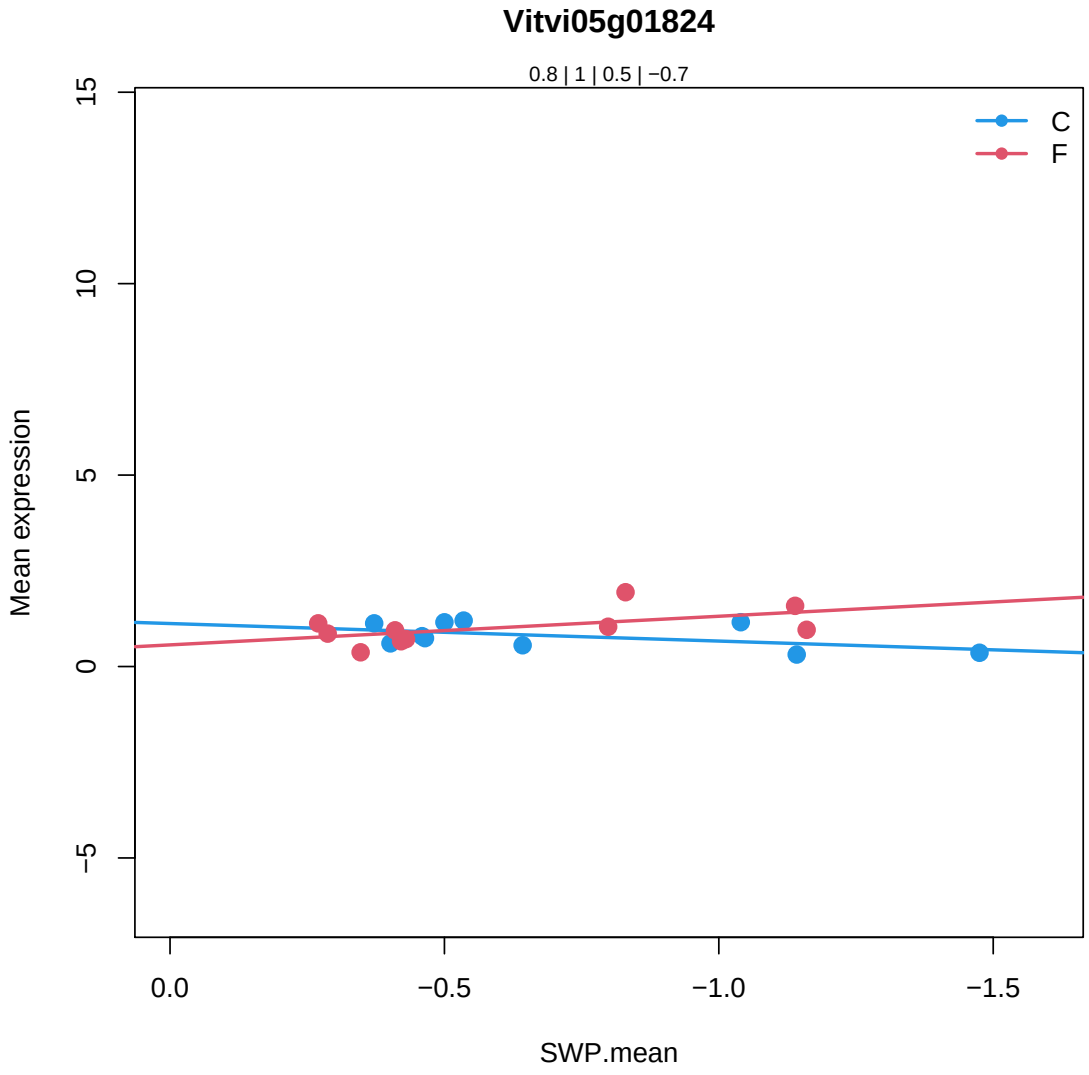
7.6.268 Vitvi05g01824: + type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01824
        33.99
        development.unspecified
        zinc knuckle (CCHC-type) family protein |
        Chr5:20308260-20312736 REVERSE LENGTH=1080 |
        201606
```

Coefficients for Vitvi05g01824.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8003549	2.182049e-06	***	2.499346e-06	***
SlopeC	0.4577899	0.2020922		0.7286987	
MeanF-MeanC	0.2198264	0.227248		0.5799497	
SlopeF-SlopeC	-1.205453	0.02976004	*	0.9999488	



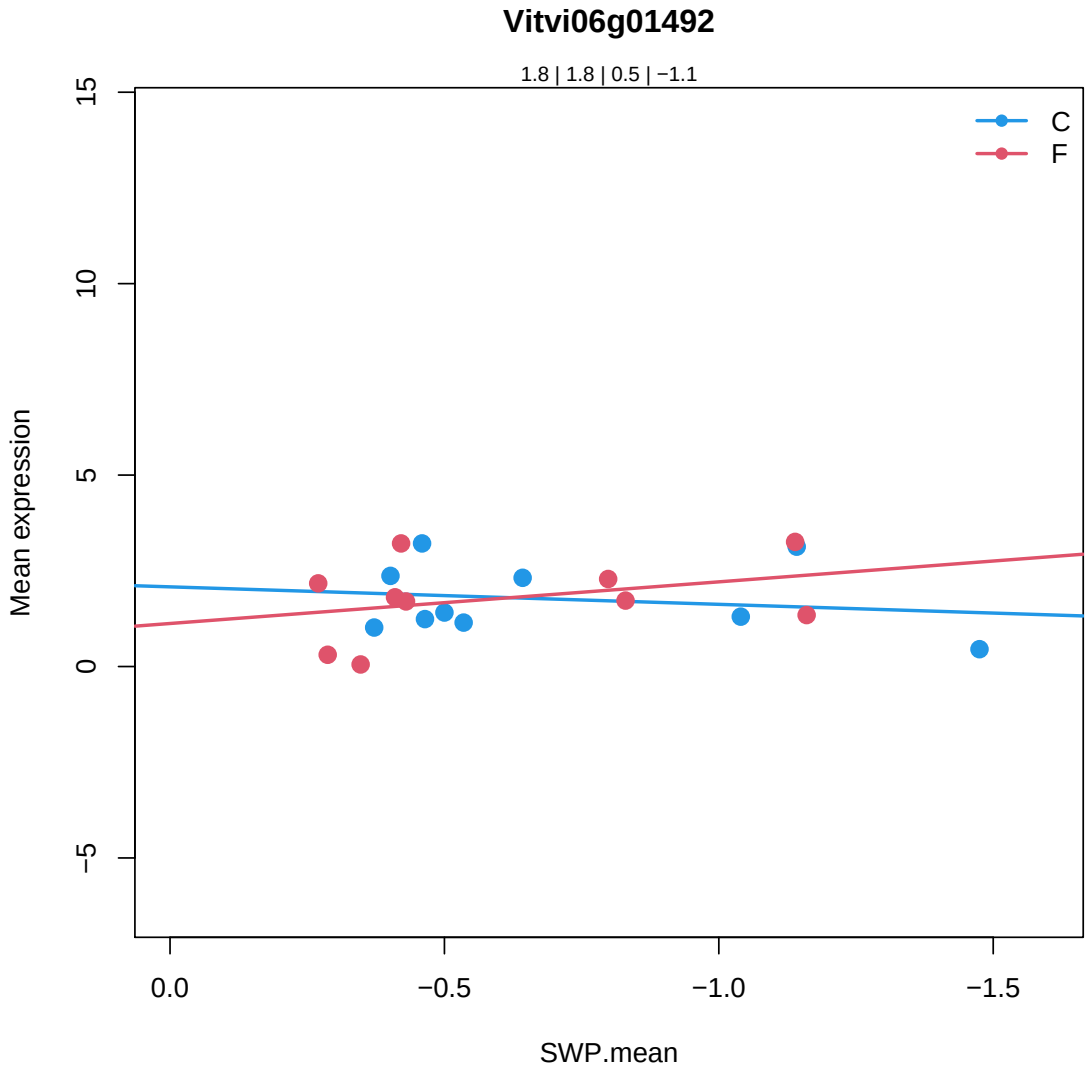
7.6.269 Vitvi06g01492: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01492
        27.3.15
        RNA.regulation of transcription.CCAAT box binding factor family, HAP3
        nuclear factor Y%2C subunit B11 |
        Chr2:11745196-11746375 REVERSE LENGTH=275 |
        201606
```

Coefficients for Vitvi06g01492.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.759774	4.054948e-06	***	4.616487e-06	***
SlopeC	0.4565532	0.5737074		0.8925427	
MeanF-MeanC	0.02627155	0.9490298		0.9872408	
SlopeF-SlopeC	-1.544391	0.2078989		0.9999488	



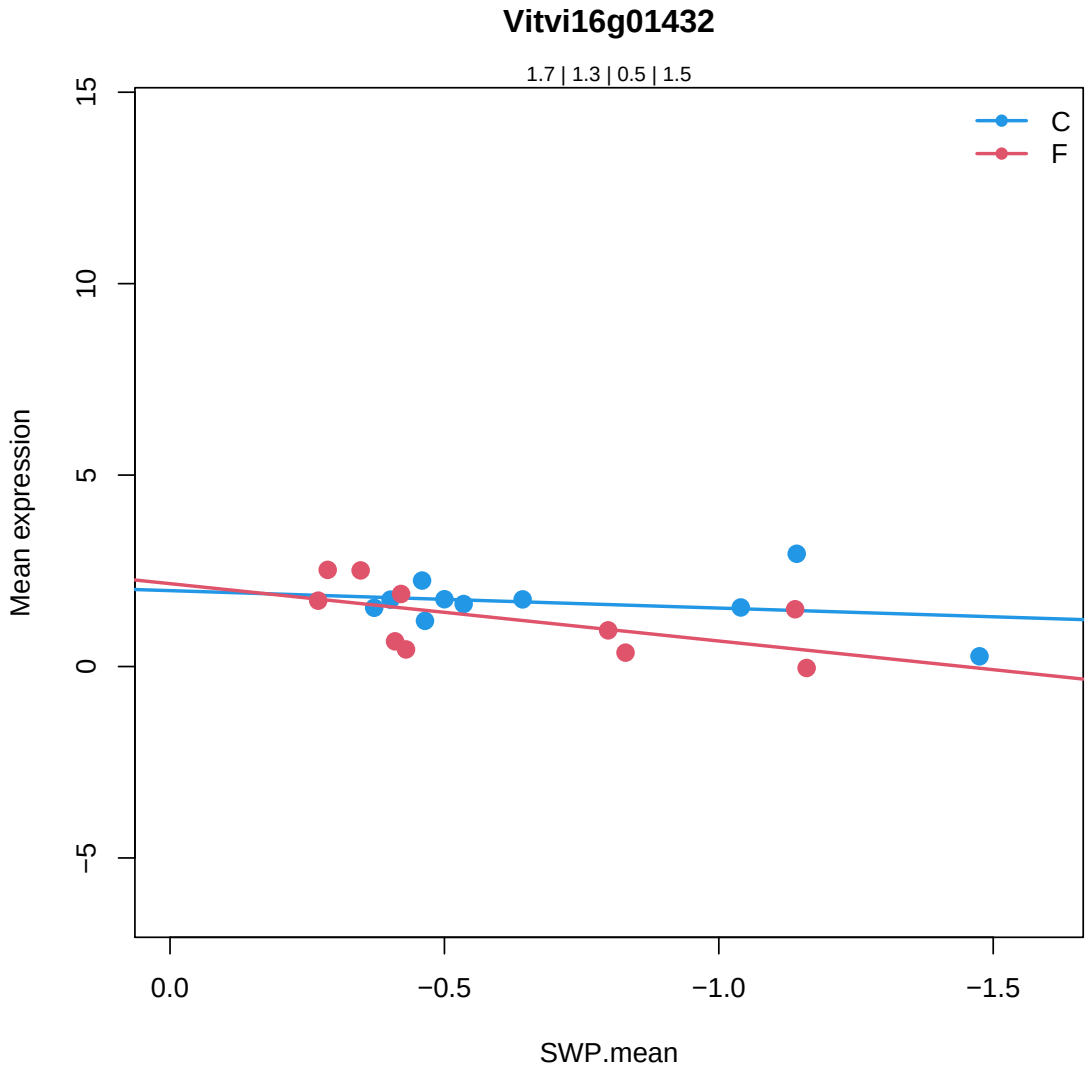
7.6.270 Vitvi16g01432: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01432
        17.5.2
        hormone metabolism.ethylene.signal transduction
        Integrase-type DNA-binding superfamily protein |
        Chr5:20800708-20801373 REVERSE LENGTH=221 |
        201606
```

Coefficients for Vitvi16g01432.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.661702	1.695298e-07	***	1.998587e-07	***
SlopeC	0.4552065	0.463674		0.8605531	
MeanF-MeanC	-0.4101639	0.1998877		0.5425982	
SlopeF-SlopeC	1.042521	0.2635582		0.9999488	



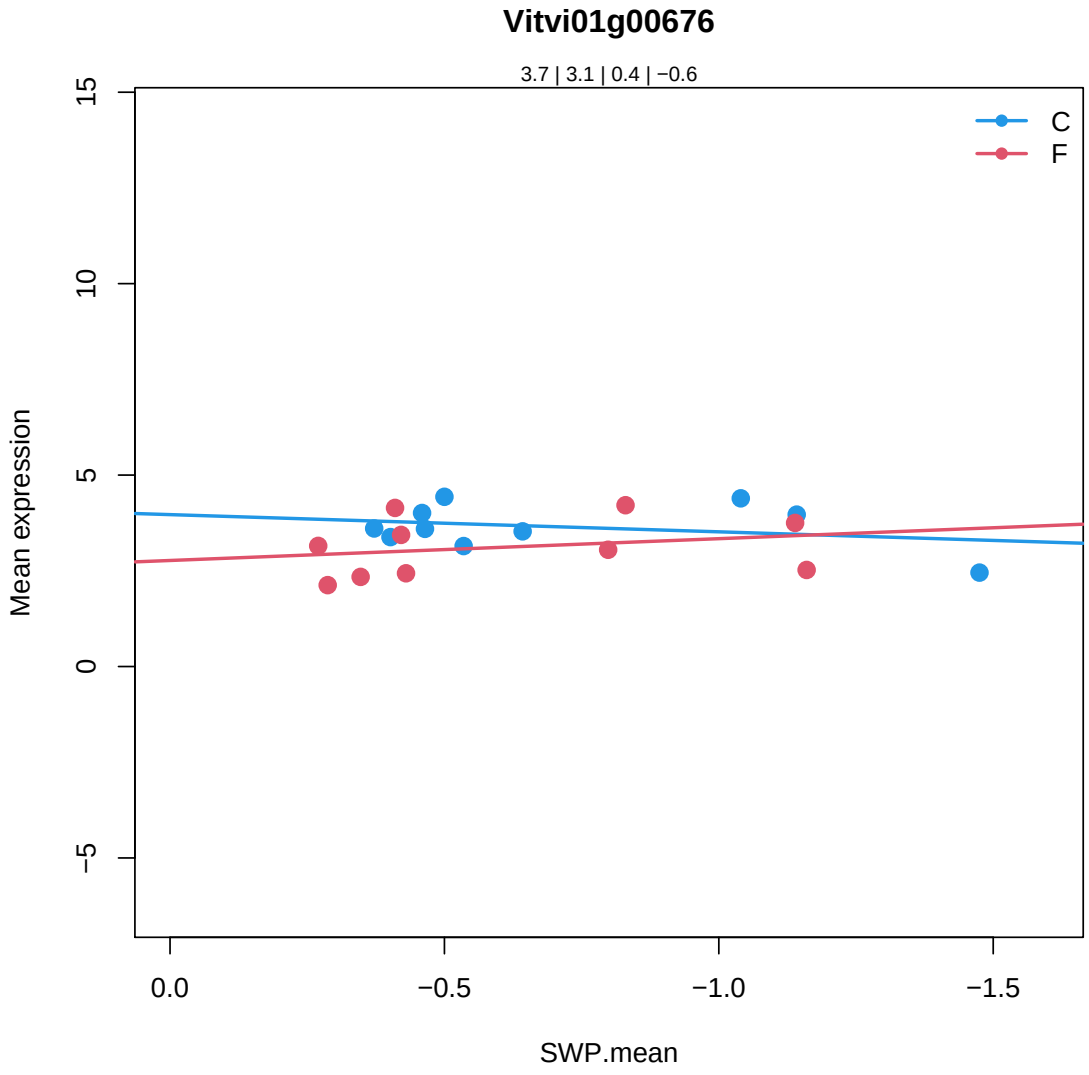
7.6.271 Vitvi01g00676: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00676
        29.5
        protein.degradation
        NEP-interacting protein%2C putative (DUF239) |
        Chr1:26597510-26599888 FORWARD LENGTH=465 |
        201606
```

Coefficients for Vitvi01g00676.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.651174	2.56943e-14	***	4.14163e-14	***
SlopeC	0.4492645	0.440249		0.8508883	
MeanF-MeanC	-0.5346467	0.07949683	.	0.3187821	
SlopeF-SlopeC	-1.018838	0.2439213		0.9999488	



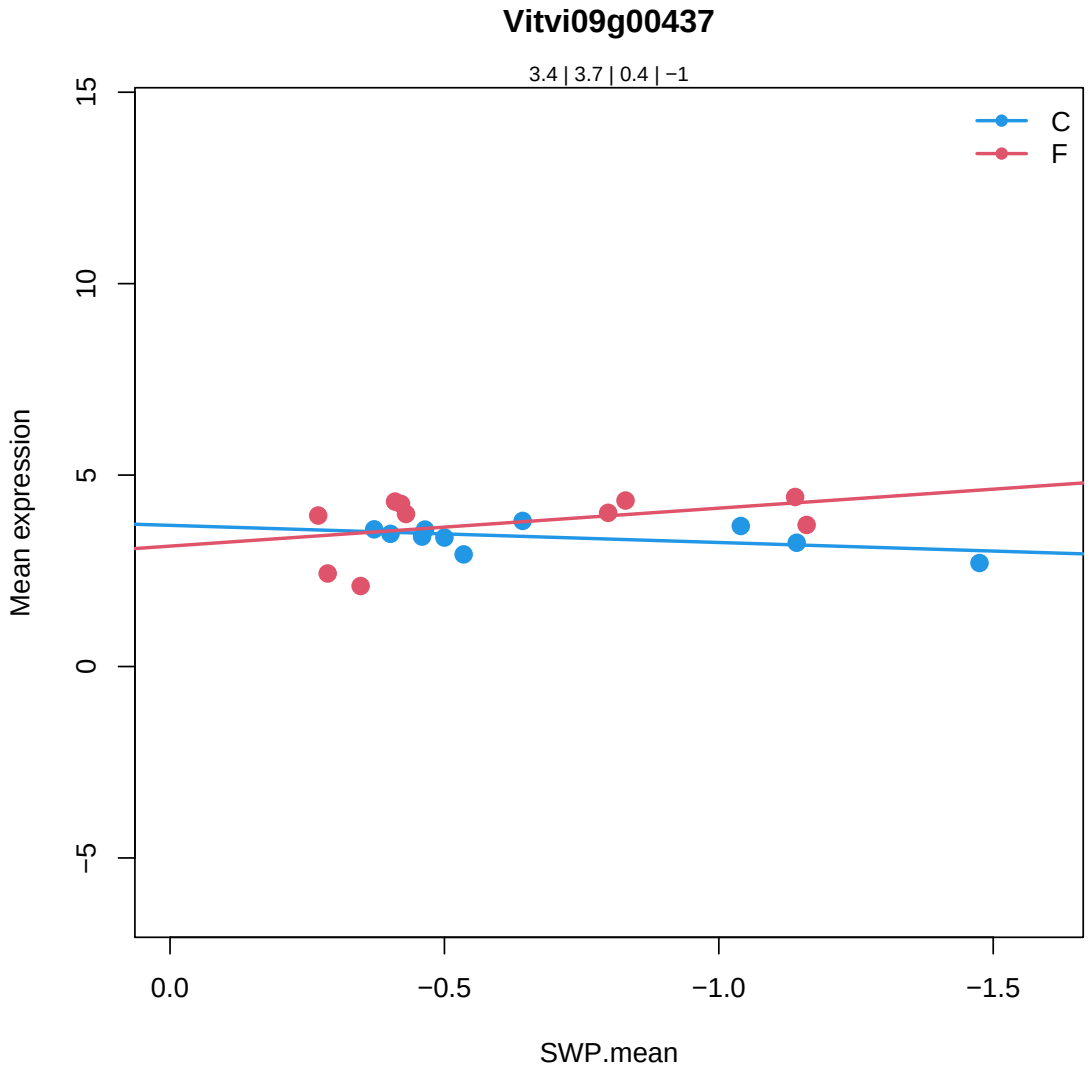
7.6.272 Vitvi09g00437: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00437
        27.3.40
        RNA.regulation of transcription.AUX/IAA family
        indole-3-acetic acid inducible 14 |
        Chr4:8348579-8349923 REVERSE LENGTH=234 |
        201606
```

Coefficients for Vitvi09g00437.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.372121	9.85359e-15	***	1.648973e-14	***
SlopeC	0.4481212	0.3830445		0.8276673	
MeanF-MeanC	0.3765413	0.1555113		0.4756778	
SlopeF-SlopeC	-1.439875	0.06791716	.	0.9999488	



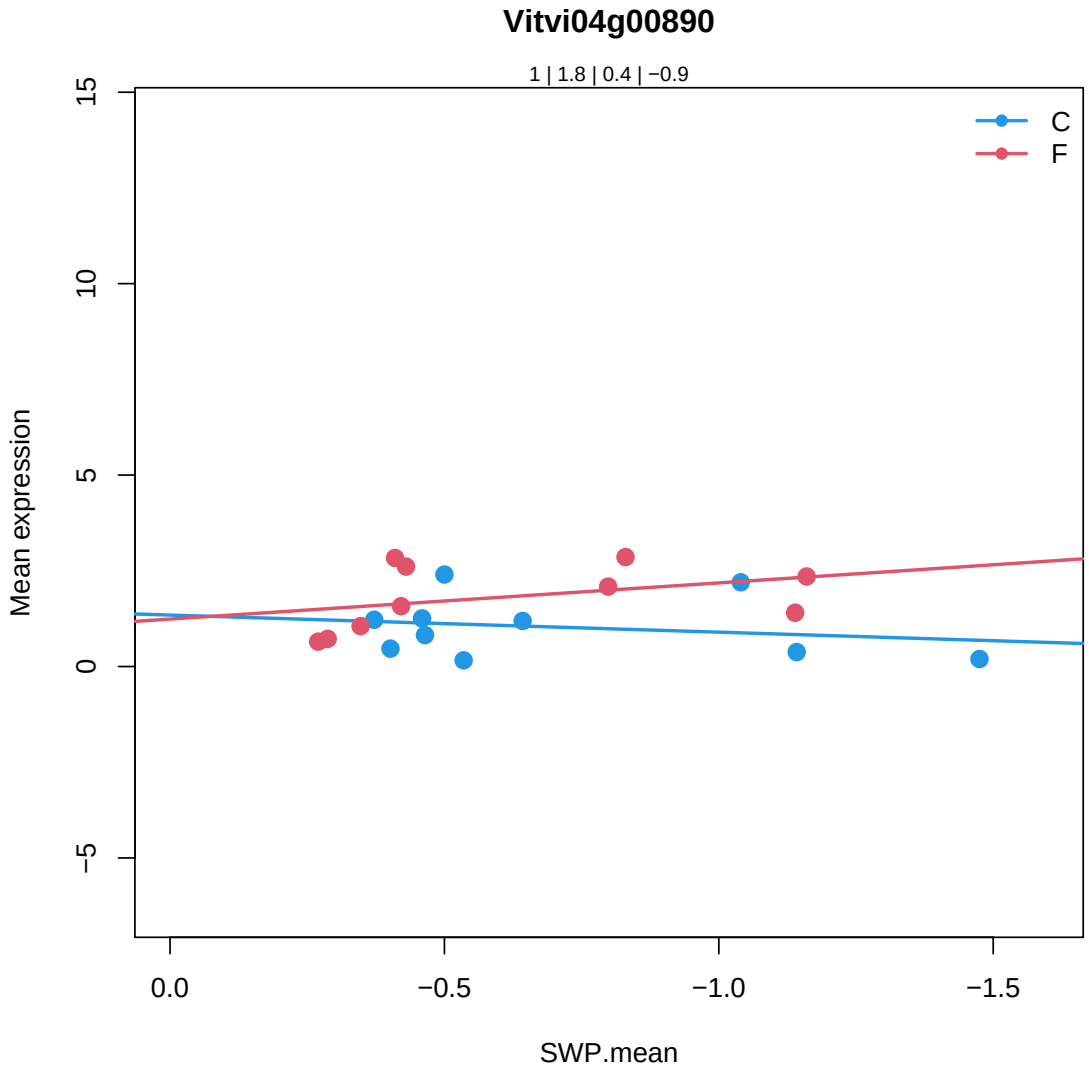
7.6.273 Vitvi04g00890: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00890
        11.1.8
        lipid metabolism.FA synthesis and FA elongation.acyl CoA ligase
        acyl activating enzyme 12 |
        Chr1:24512598-24514611 REVERSE LENGTH=578 |
        201606
```

Coefficients for Vitvi04g00890.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.029383	0.000290939	***	0.0003182498	***
SlopeC	0.4465251	0.507889		0.8711742	
MeanF-MeanC	0.7853314	0.02964733	*	0.1676363	
SlopeF-SlopeC	-1.392083	0.1727304		0.9999488	



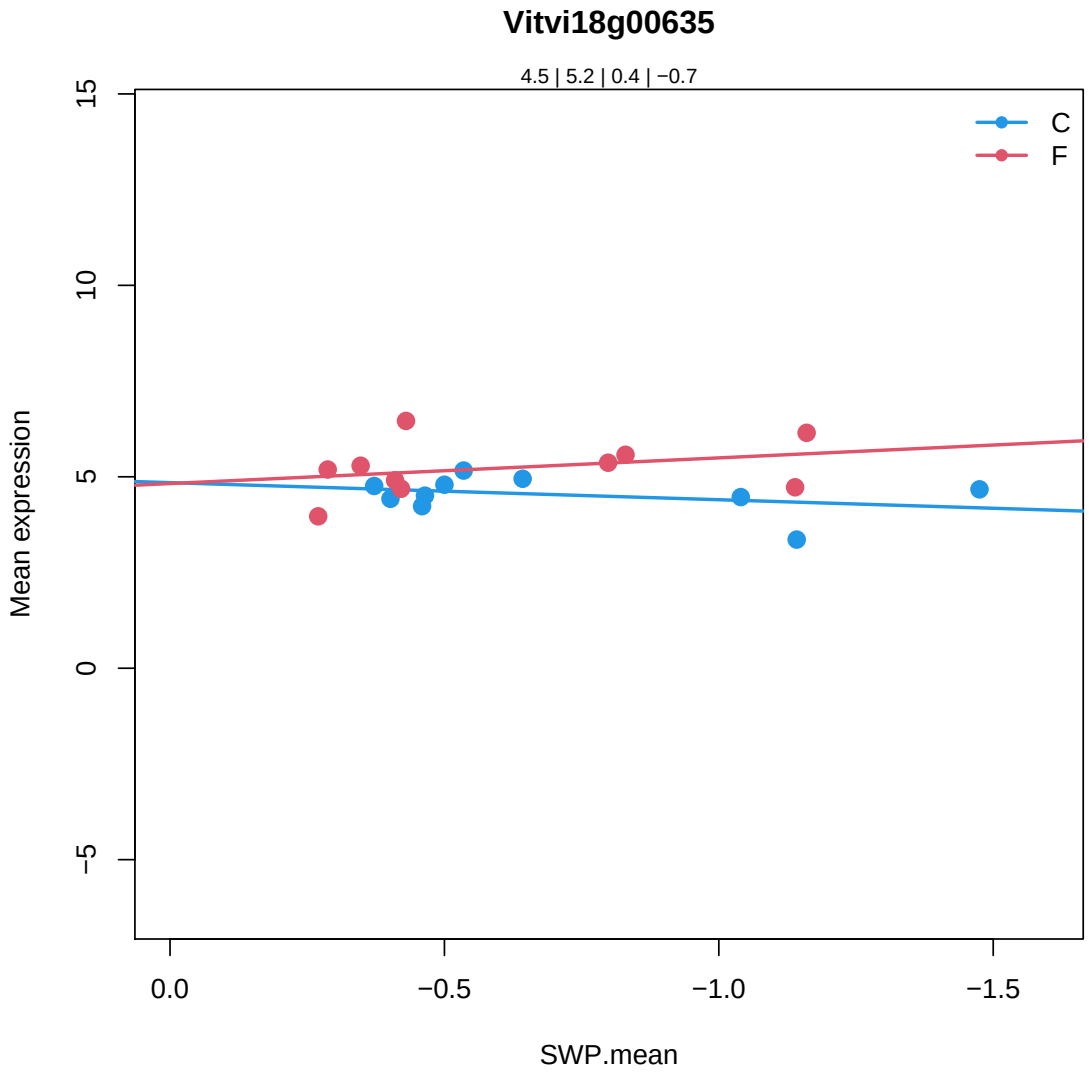
7.6.274 Vitvi18g00635: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00635
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi18g00635.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.533082	4.597538e-17	***	1.062236e-16	***
SlopeC	0.4456114	0.4015042		0.8352435	
MeanF-MeanC	0.6984197	0.01517912	*	0.102781	
SlopeF-SlopeC	-1.116103	0.1642088		0.9999488	



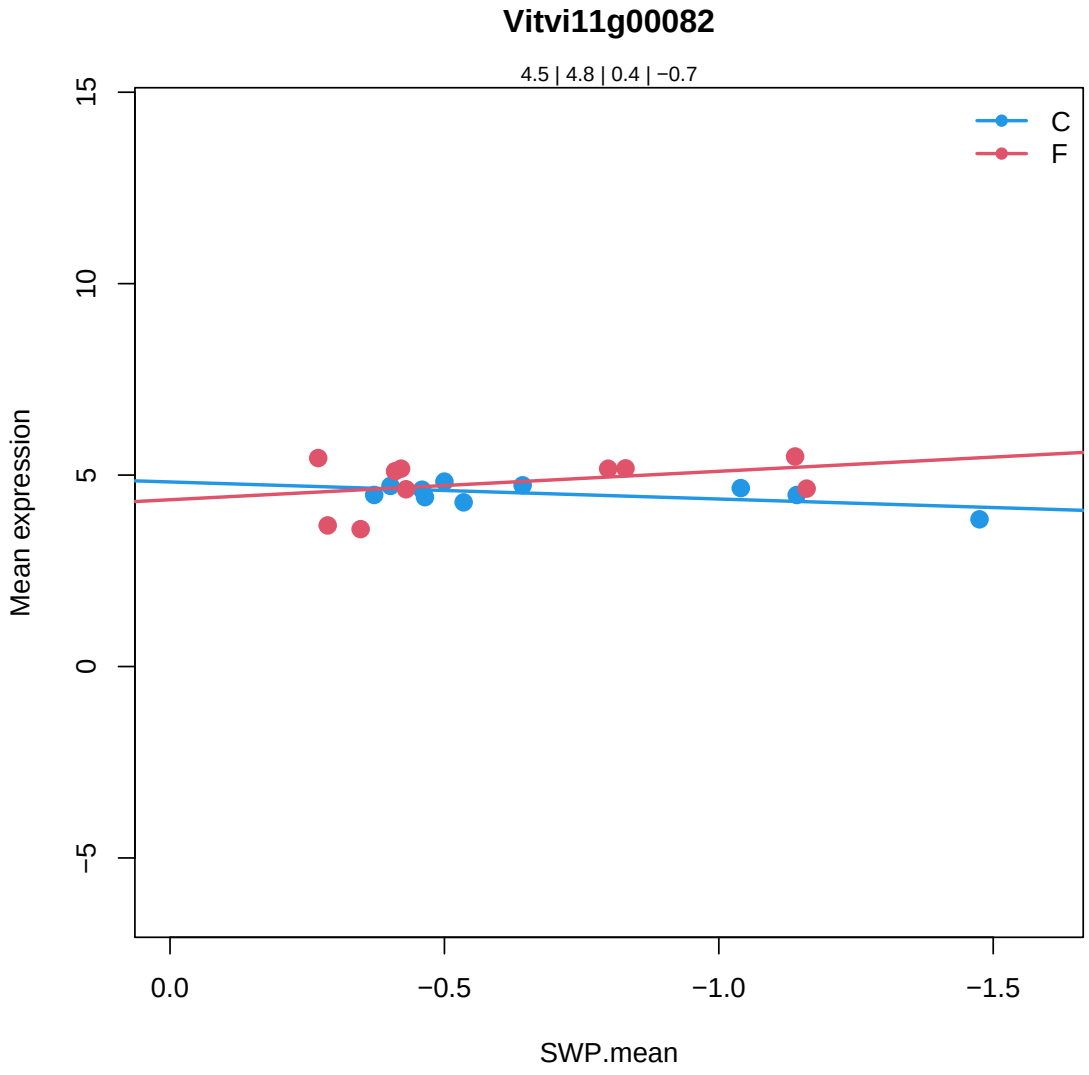
7.6.275 Vitvi11g00082: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00082
        35.2
        not assigned.unknown
        OBP3-responsive protein 4 (ORG4) |
        Chr2:2336841-2338391 FORWARD LENGTH=188 |
        201606
```

Coefficients for Vitvi11g00082.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.507237	1.497418e-18	***	4.897777e-18	***
SlopeC	0.445524	0.3216528		0.797271	
MeanF-MeanC	0.3013102	0.191168		0.5310094	
SlopeF-SlopeC	-1.188102	0.08310928	.	0.9999488	



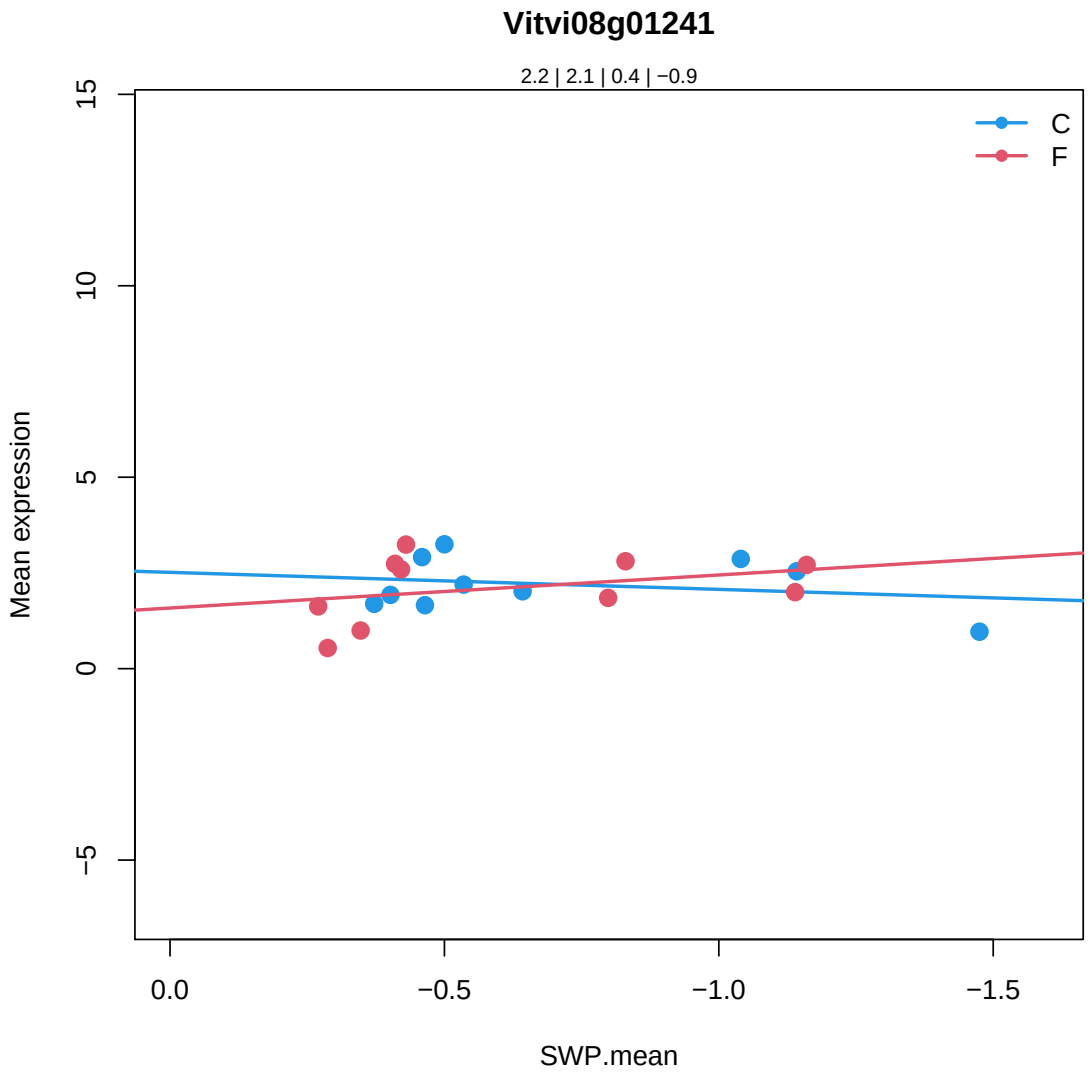
7.6.276 Vitvi08g01241: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
Vitvi08g01241
        29.4
        protein.postranslational modification
        Concanavalin A-like lectin protein kinase family protein |
        Chr3:19933153-19935186 REVERSE LENGTH=677 |
        201606

Vitvi08g01241
        30.2.19
        signalling.receptor kinases.legume-lectin
        Concanavalin A-like lectin protein kinase family protein |
        Chr3:19933153-19935186 REVERSE LENGTH=677 |
        201606
```

Coefficients for Vitvi08g01241.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.20235	3.468586e-09	***	4.296132e-09	***
SlopeC	0.4442442	0.495624		0.868806	
MeanF-MeanC	-0.09310979	0.7777574		0.9365285	
SlopeF-SlopeC	-1.307164	0.1847318		0.9999488	


Vitvi08g01241
2.2 | 2.1 | 0.4 | −0.9
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

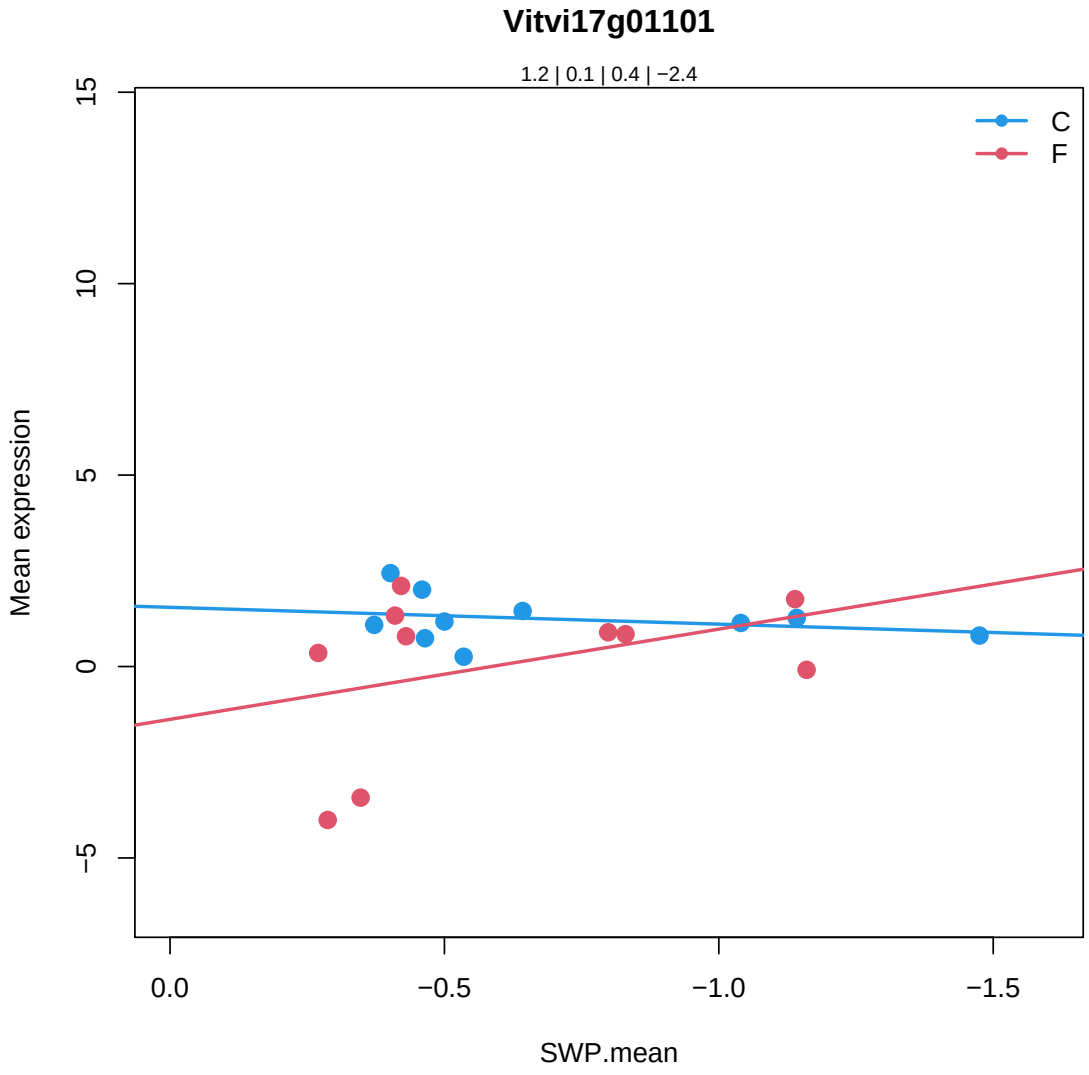
7.6.277 Vitvi17g01101: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g01101
        34.14
        transport.unspecified cations
        organic cation/carnitine transporter1 |
        Chr1:27538387-27540109 FORWARD LENGTH=539 |
        201606
```

Coefficients for Vitvi17g01101.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.237068	0.0077324	**	0.008213048	**
SlopeC	0.4385322	0.7117525		0.9350571	
MeanF-MeanC	-1.181232	0.06018117	.	0.2686036	
SlopeF-SlopeC	-2.79515	0.1234474		0.9999488	



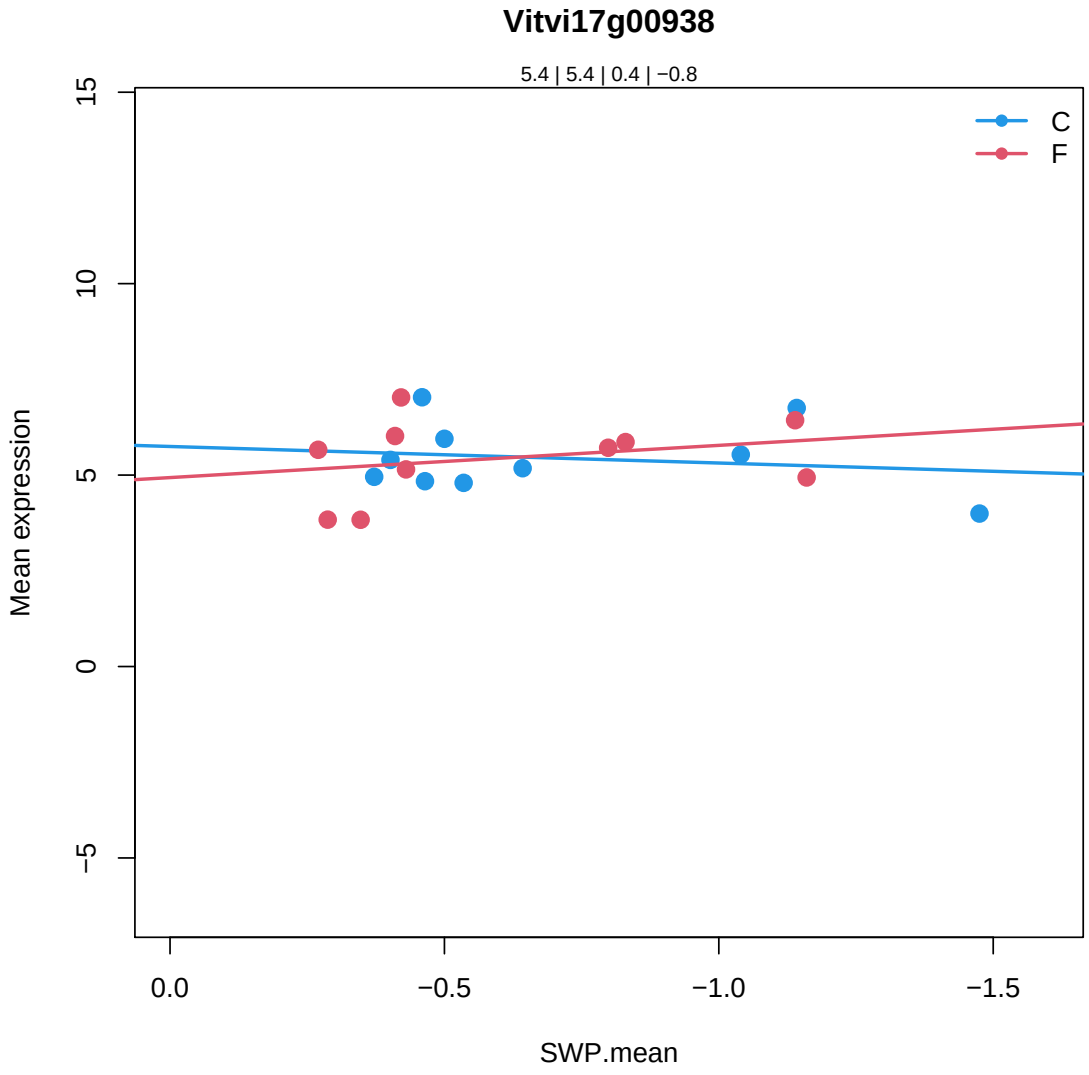
7.6.278 Vitvi17g00938: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00938
        18.7
        Co-factor and vitamine metabolism.iron-sulphur clusters
        quinolinate synthase |
        Chr5:20442803-20445706 FORWARD LENGTH=718 |
        201606
```

Coefficients for Vitvi17g00938.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.442937	6.909193e-15	***	1.173631e-14	***
SlopeC	0.4321111	0.5937919		0.9009134	
MeanF-MeanC	0.004098563	0.9920327		0.9976618	
SlopeF-SlopeC	-1.273635	0.2955444		0.9999488	



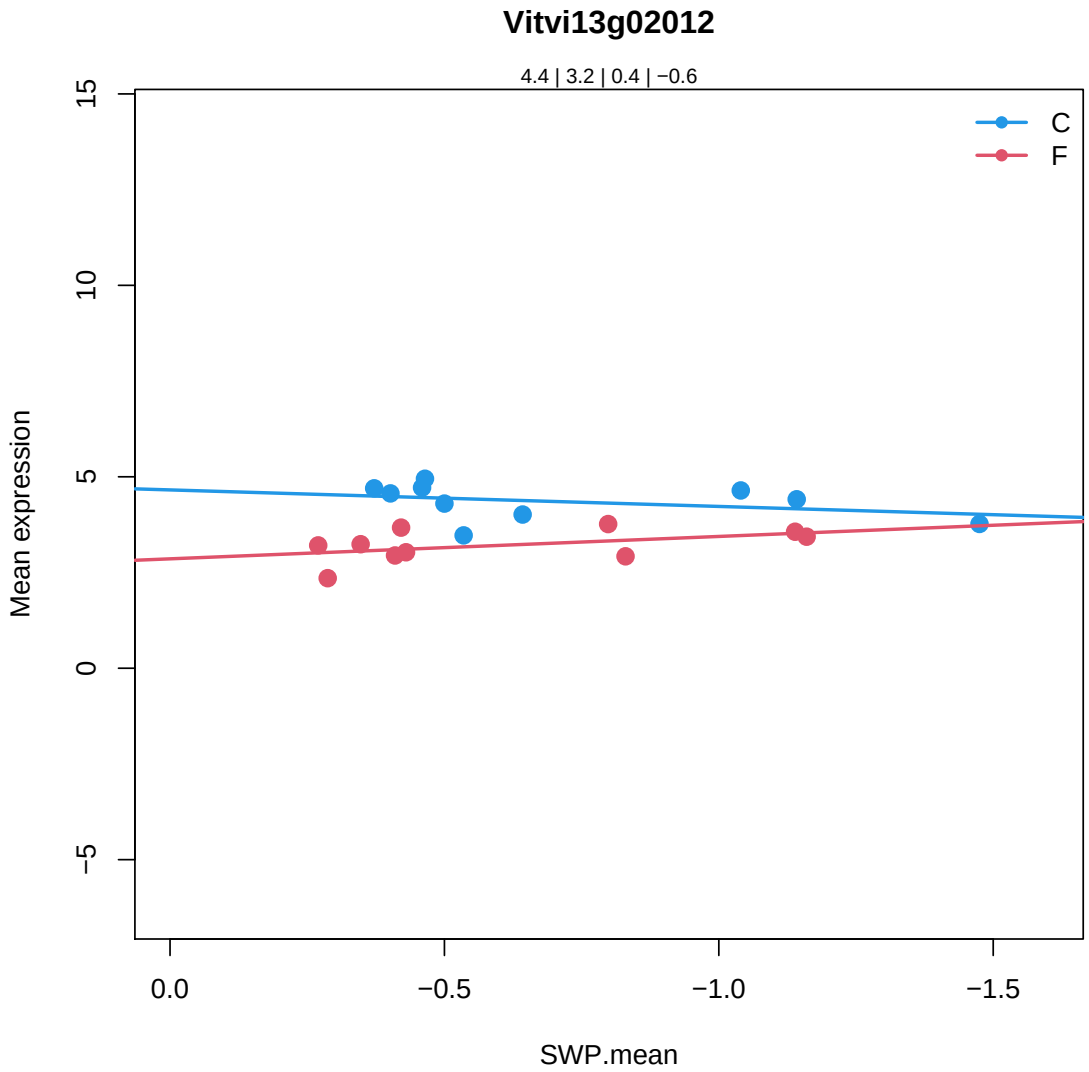
7.6.279 Vitvi13g02012: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g02012
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi13g02012.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.353644	3.231668e-19	***	1.297947e-18	***
SlopeC	0.4313421	0.2860624		0.7782707	
MeanF-MeanC	-1.140456	1.107955e-05	***	0.000277754	***
SlopeF-SlopeC	-1.015824	0.09779422	.	0.9999488	



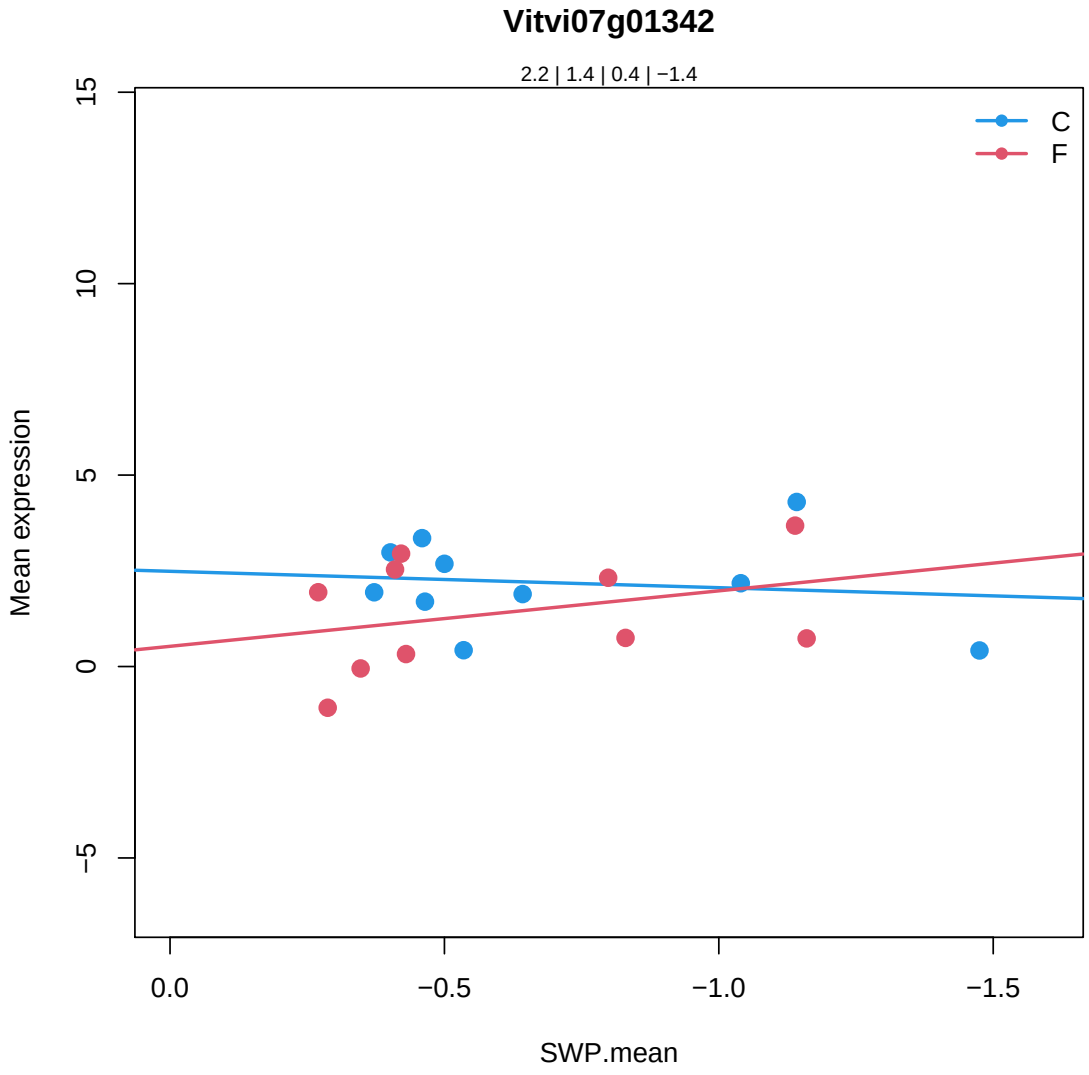
7.6.280 Vitvi07g01342: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01342
        26.22
        misc.short chain dehydrogenase/reductase (SDR)
        NAD(P)-binding Rossmann-fold superfamily protein |
        Chr3:18761247-18763835 REVERSE LENGTH=272 |
        201606
```

Coefficients for Vitvi07g01342.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.185804	1.304017e-05	***	1.468259e-05	***
SlopeC	0.4279785	0.6963245		0.9317974	
MeanF-MeanC	-0.7757887	0.172694		0.5032391	
SlopeF-SlopeC	-1.876783	0.2566185		0.9999488	

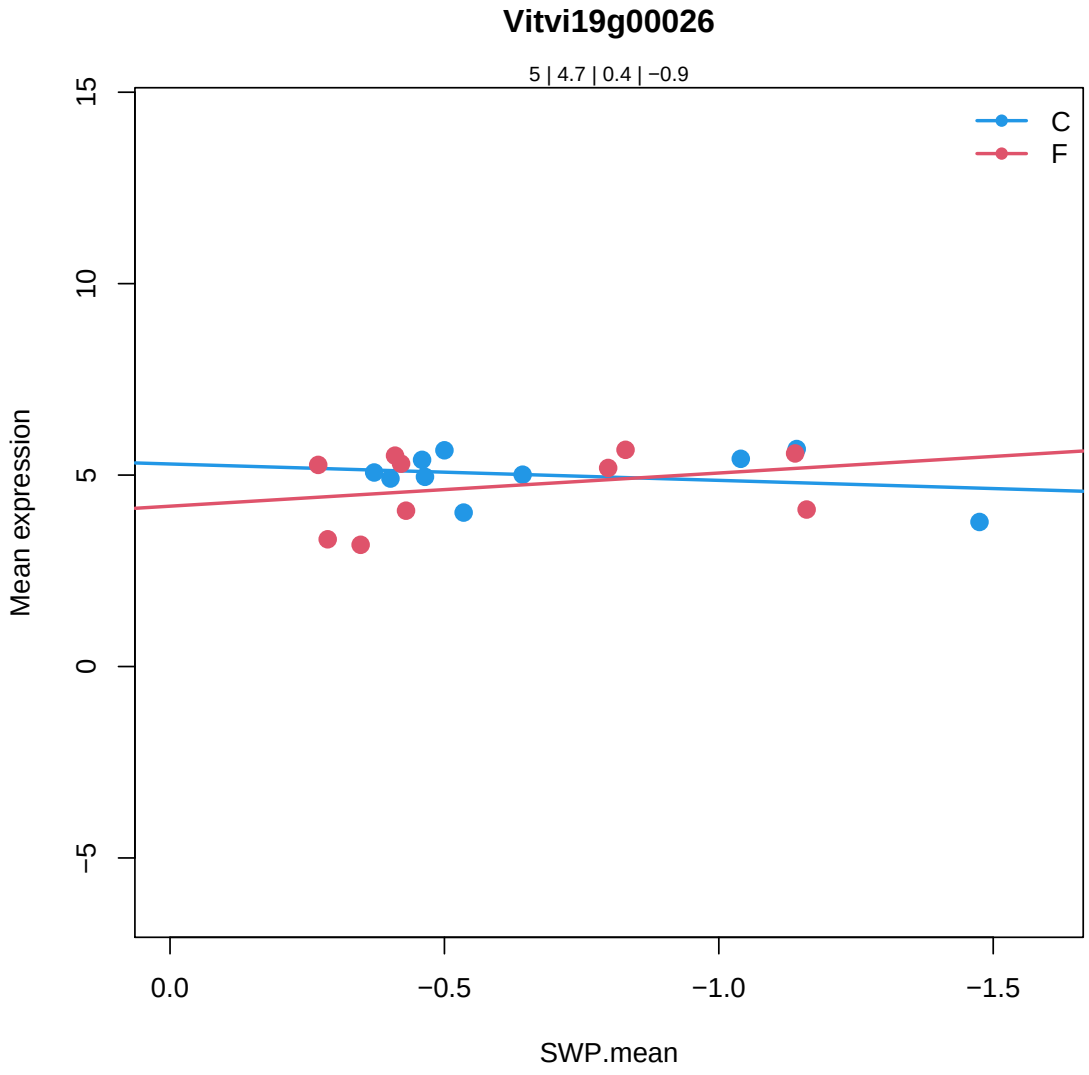


7.6.281 Vitvi19g00026: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
Vitvi19g00026
        3.2.1
        minor CHO metabolism.trehalose.TPS
        trehalose-6-phosphate synthase |
        Chr1:29552495-29557482 REVERSE LENGTH=942 |
        201606
```

Coefficients for Vitvi19g00026.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.988741	9.230898e-16	***	1.734862e-15	***
SlopeC	0.4276487	0.525588		0.8760949	
MeanF-MeanC	-0.2734493	0.4258747		0.7622145	
SlopeF-SlopeC	-1.293869	0.203485		0.9999488	



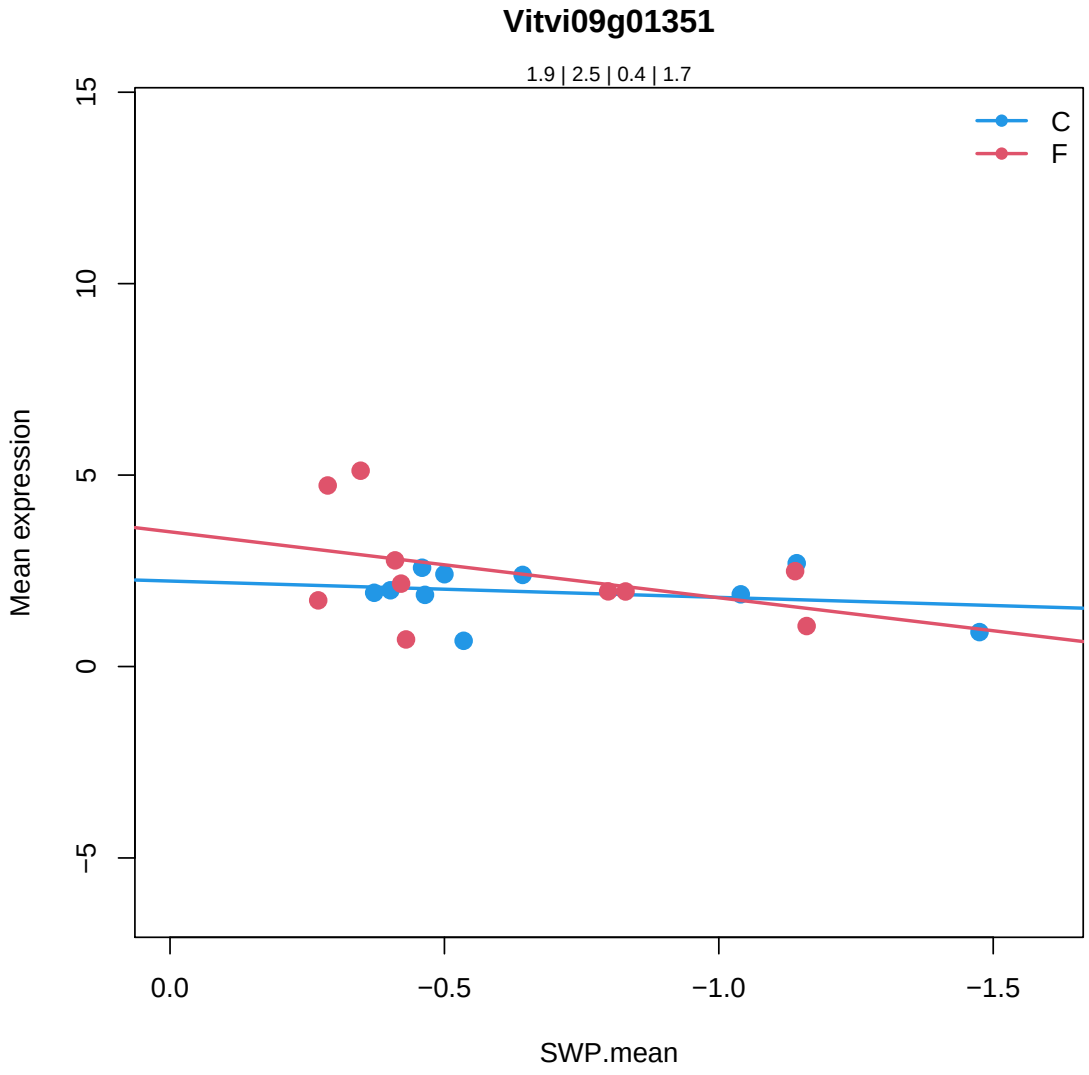
7.6.282 Vitvi09g01351: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g01351
        35.2
        not assigned.unknown
        maternal effect embryo arrest protein |
        Chr3:2393895-2394464 REVERSE LENGTH=189 |
        201606
```

Coefficients for Vitvi09g01351.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.932365	3.049495e-06	***	3.481417e-06	***
SlopeC	0.4256136	0.6256467		0.9101598	
MeanF-MeanC	0.5360561	0.2333305		0.5882274	
SlopeF-SlopeC	1.296594	0.3222939		0.9999488	



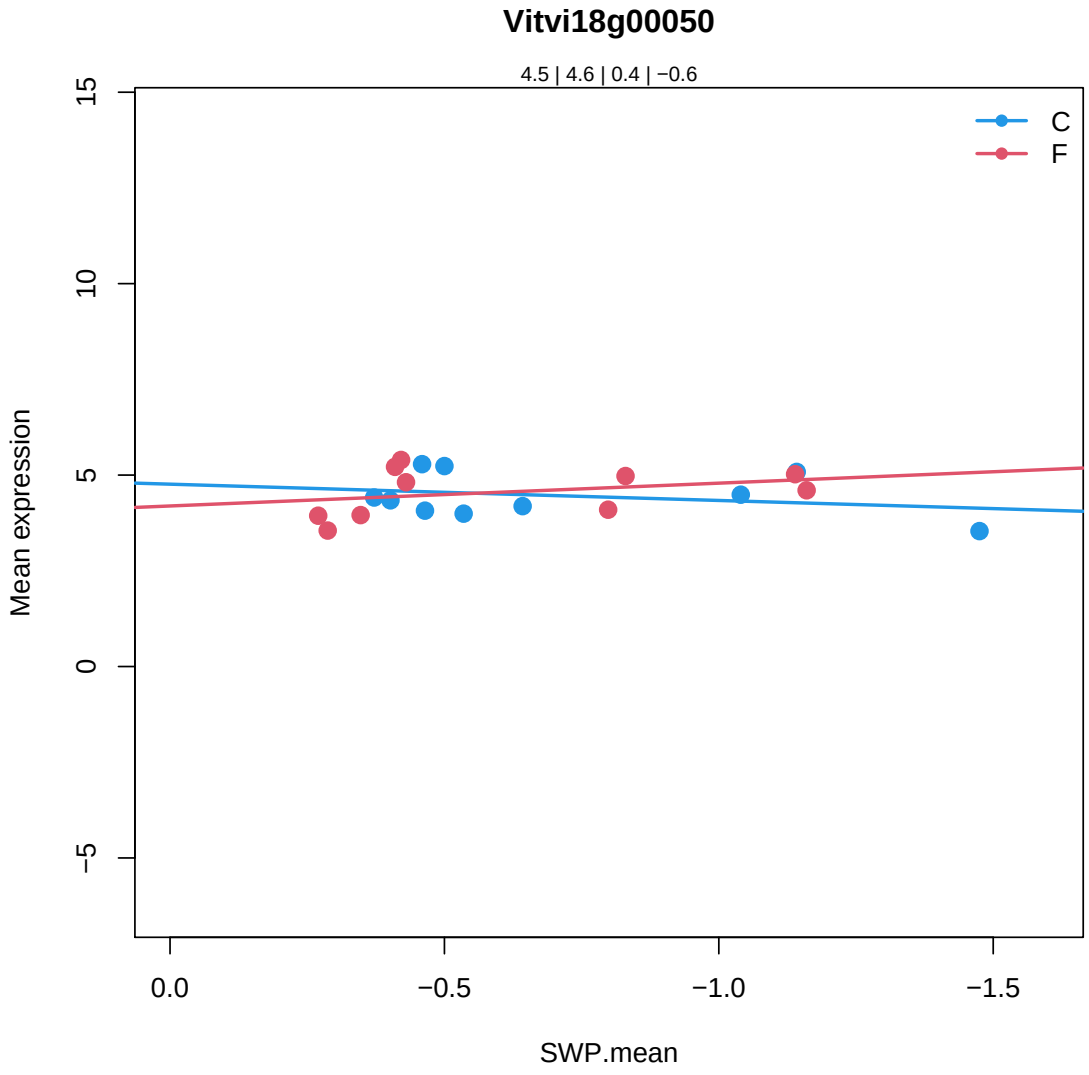
7.6.283 Vitvi18g00050: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00050
        34.7
        transport.phosphate
        phosphate transporter 1%3B9 |
        Chr1:28679115-28681874 REVERSE LENGTH=532 |
        201606
```

Coefficients for Vitvi18g00050.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.46321	4.365363e-17	***	1.011967e-16	***
SlopeC	0.4254062	0.4145884		0.8406955	
MeanF-MeanC	0.09295969	0.7240956		0.9158298	
SlopeF-SlopeC	-1.021252	0.1936553		0.9999488	



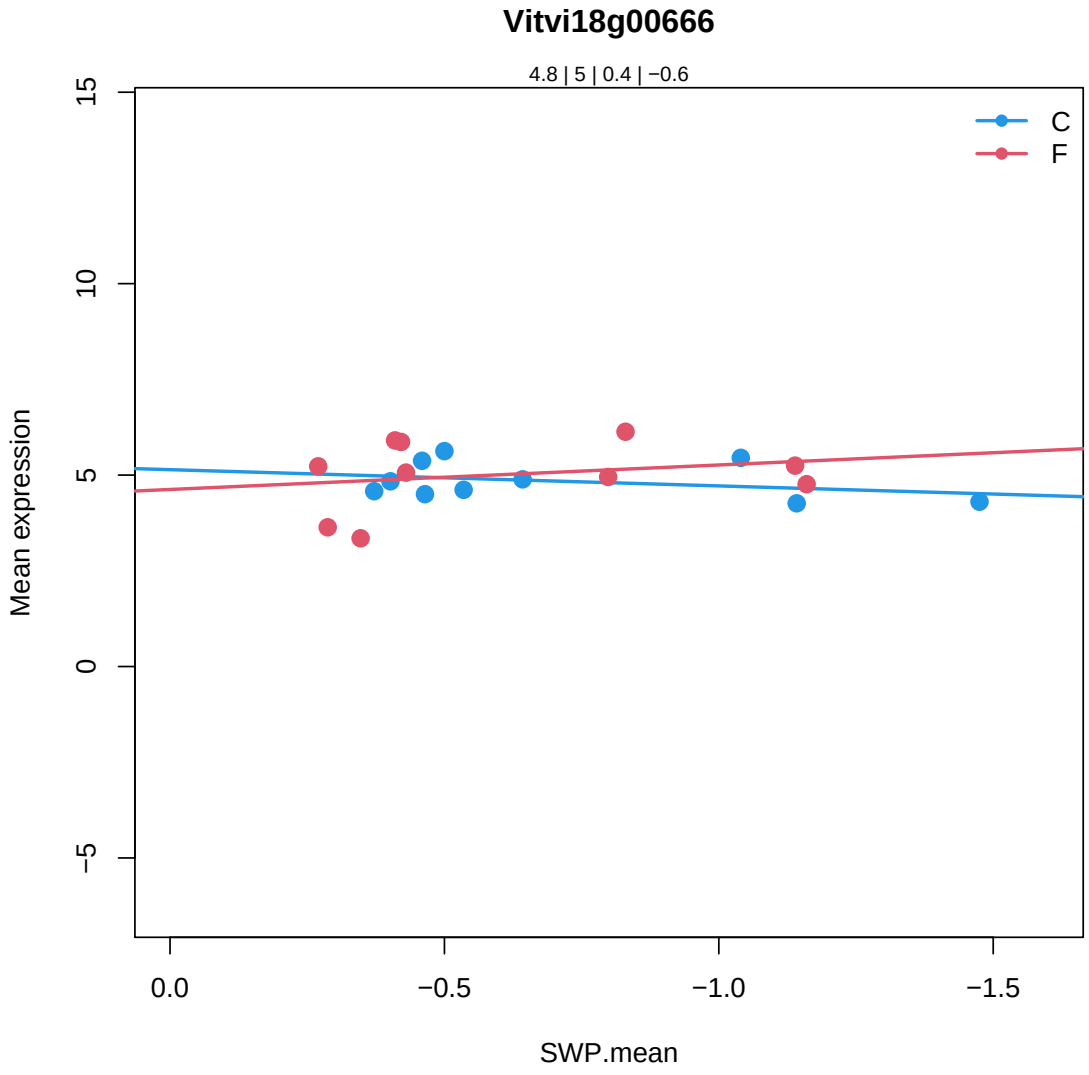
7.6.284 Vitvi18g00666: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00666
        35.1.3
        not assigned.no ontology.armadillo/beta-catenin repeat family protein
        ARM repeat superfamily protein |
        Chr3:151920-152987 FORWARD LENGTH=355 |
        201606
```

Coefficients for Vitvi18g00666.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.843262	3.313188e-16	***	6.630726e-16	***
SlopeC	0.4241513	0.4957668		0.868806	
MeanF-MeanC	0.1707556	0.5887979		0.856315	
SlopeF-SlopeC	-1.063931	0.2556815		0.9999488	



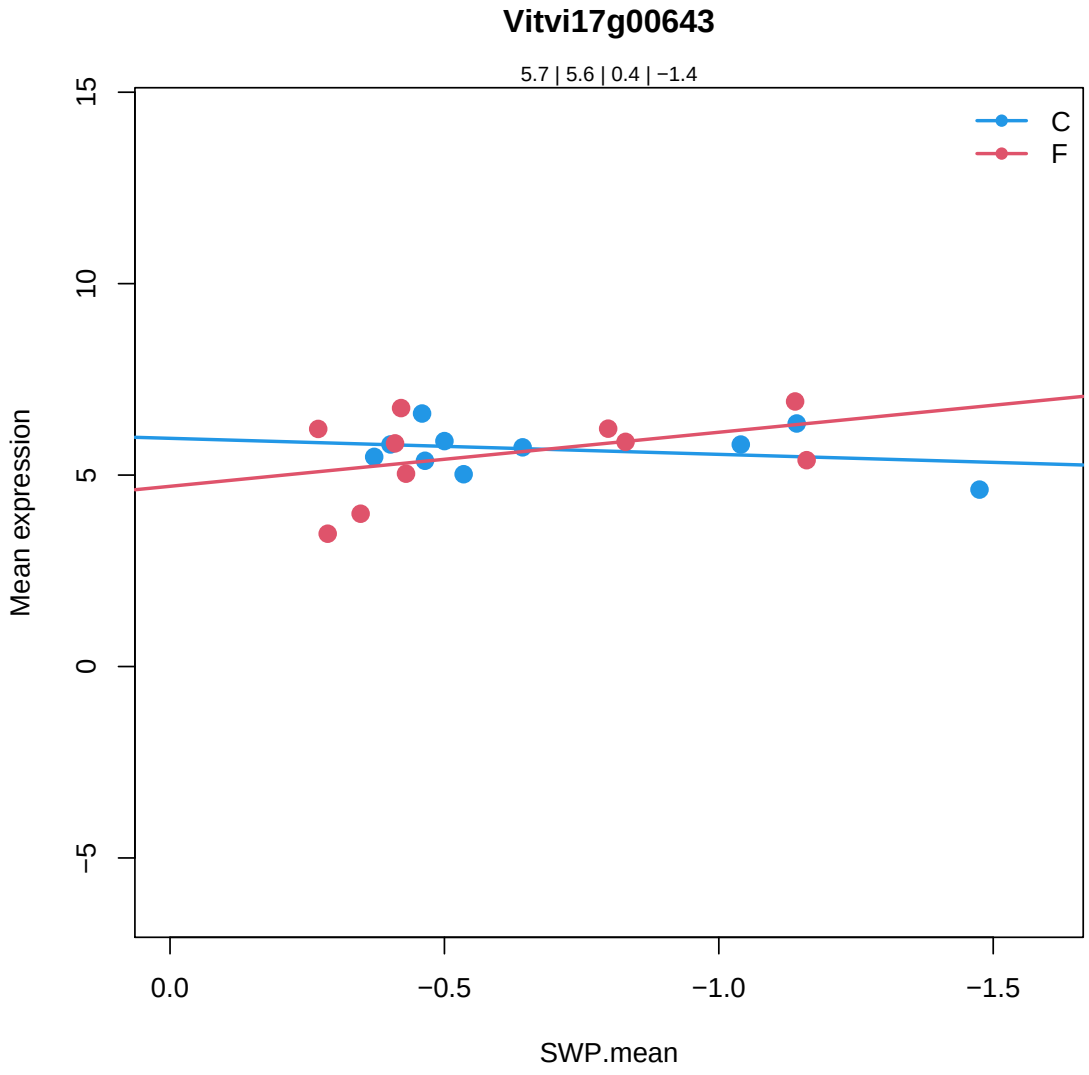
7.6.285 Vitvi17g00643: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00643
        29.5.11.4.2
        protein.degradation.ubiquitin.E3.RING
        zinc finger (C3HC4-type RING finger) family protein |
        Chr1:6421433-6425565 FORWARD LENGTH=486 |
        201606
```

Coefficients for Vitvi17g00643.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.665609	1.894979e-16	***	3.929697e-16	***
SlopeC	0.4184753	0.5544468		0.8883505	
MeanF-MeanC	-0.0987083	0.7831716		0.9384607	
SlopeF-SlopeC	-1.830247	0.09186041	.	0.9999488	



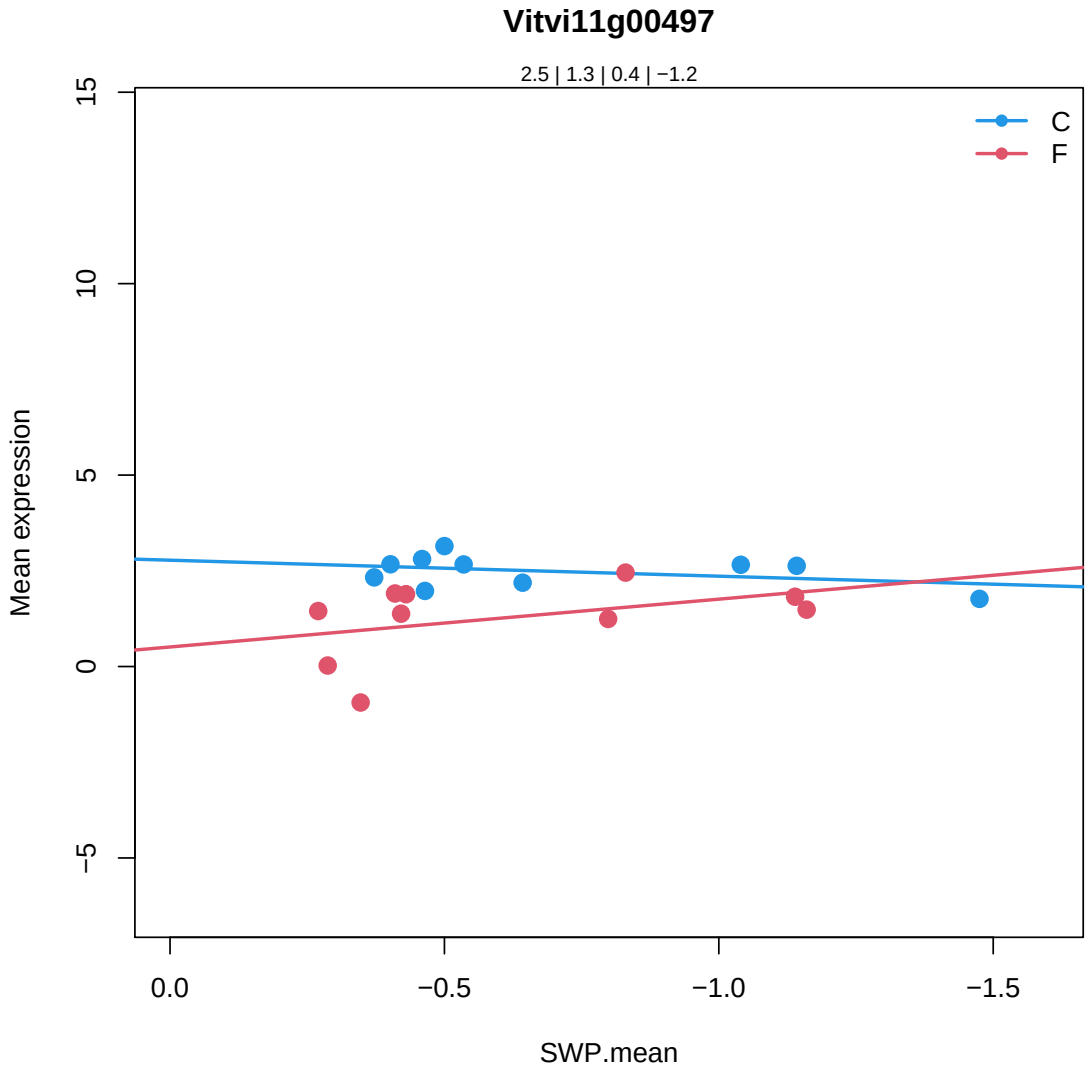
7.6.286 Vitvi11g00497: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00497
        27.3.40
        RNA.regulation of transcription.AUX/IAA family
        indole-3-acetic acid inducible 18 |
        Chr1:19305670-19307130 FORWARD LENGTH=267 |
        201606
```

Coefficients for Vitvi11g00497.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.483251	1.219422e-10	***	1.590262e-10	***
SlopeC	0.4174158	0.4944164		0.8687743	
MeanF-MeanC	-1.211958	0.0006742355	***	0.009046389	**
SlopeF-SlopeC	-1.666229	0.07601204	.	0.9999488	



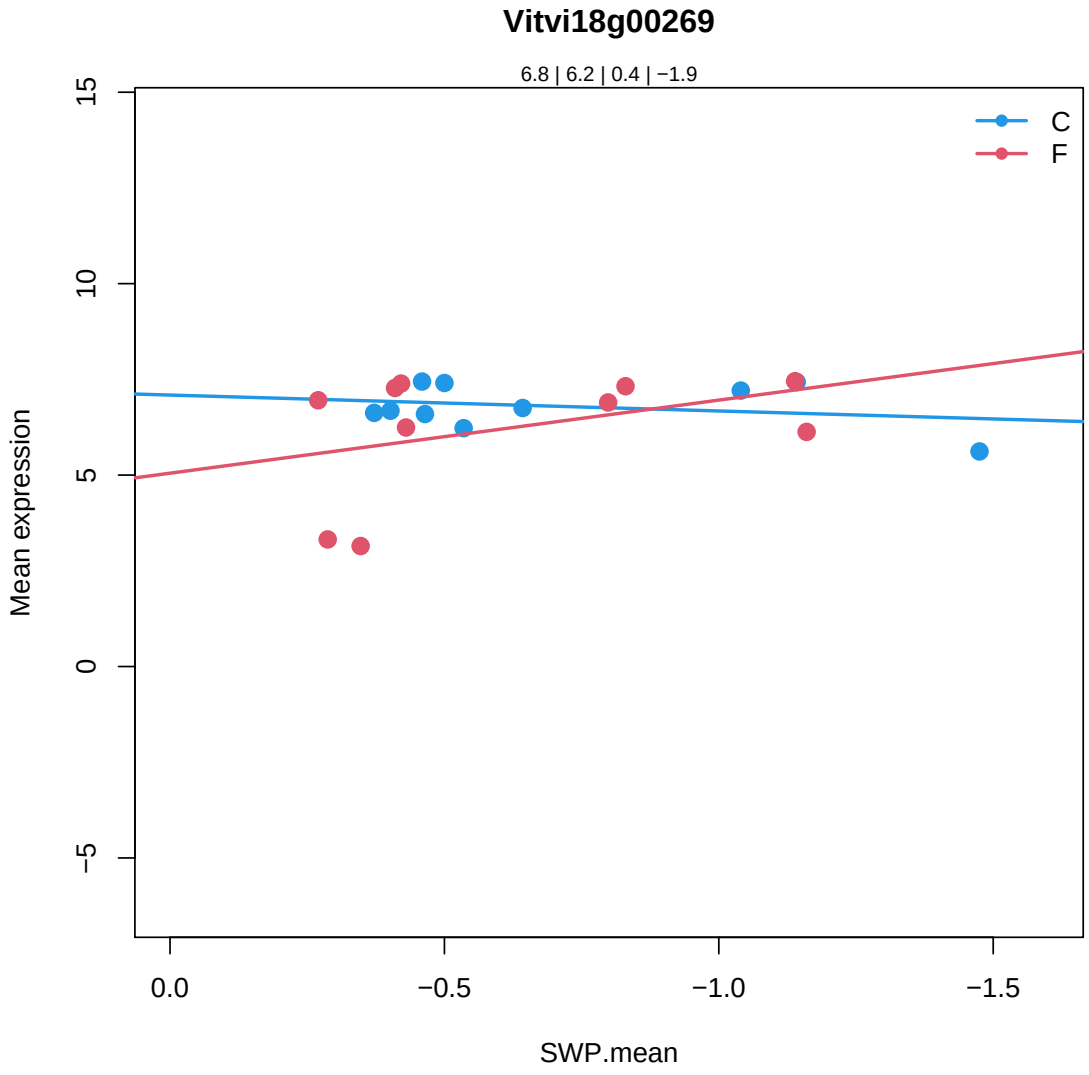
7.6.287 Vitvi18g00269: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00269
        19.16
        tetrapyrrole synthesis.chlorophyll b synthase
        Pheophorbide a oxygenase family protein with Rieske 2Fe-2S domain-cont
        Chr1:16848664-16850718 REVERSE LENGTH=434 |
        201606
```

Coefficients for Vitvi18g00269.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.797749	2.06861e-15	***	3.739741e-15	***
SlopeC	0.4156576	0.6625771		0.9225525	
MeanF-MeanC	-0.5854615	0.2334692		0.5882853	
SlopeF-SlopeC	-2.324171	0.1110042		0.9999488	



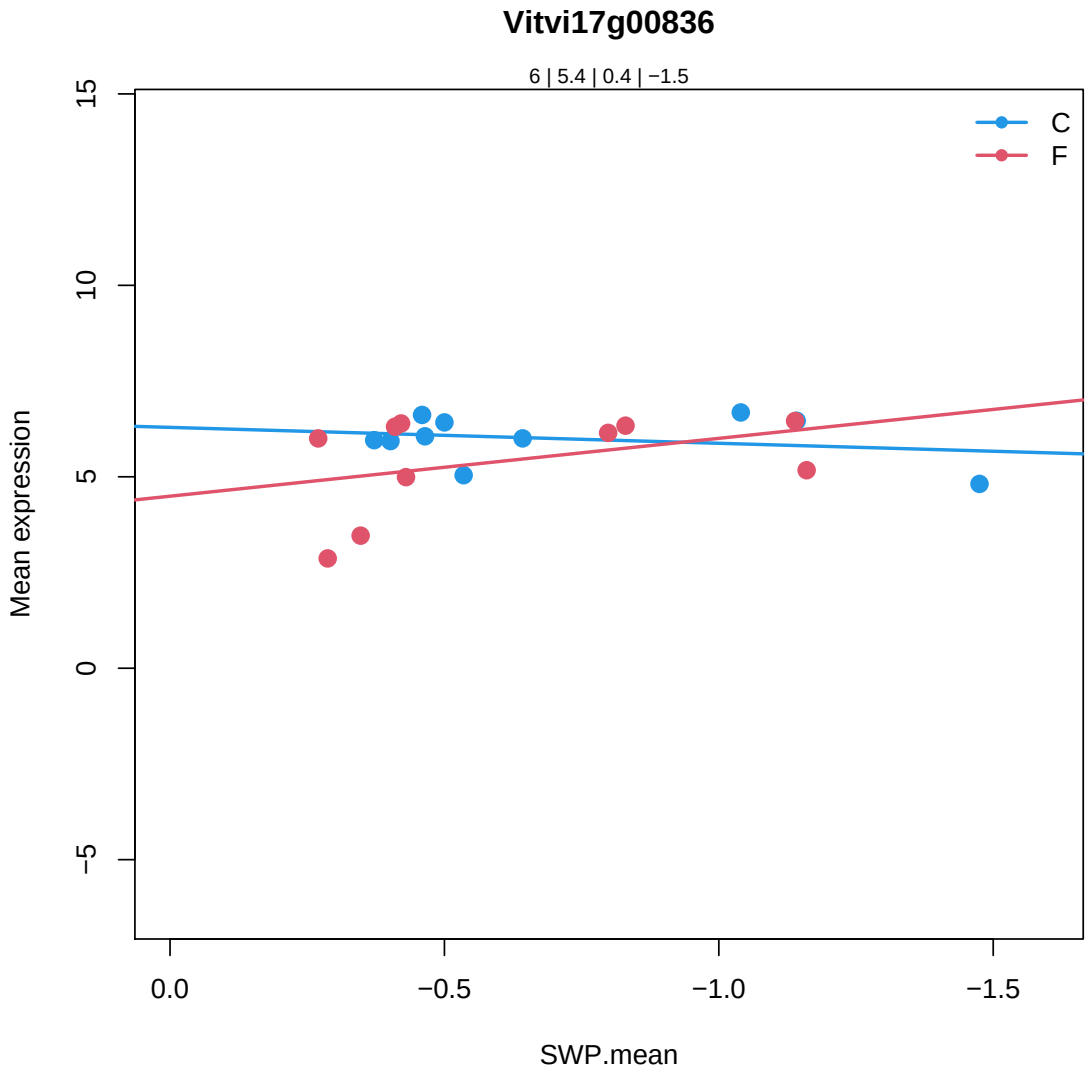
7.6.288 Vitvi17g00836: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00836
        35.2
        not assigned.unknown
        ApaG IPR007474 ApaG
```

Coefficients for Vitvi17g00836.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.998108	7.925633e-16	***	1.504577e-15	***
SlopeC	0.4152753	0.6049295		0.9047128	
MeanF-MeanC	-0.5846631	0.1603581		0.4840916	
SlopeF-SlopeC	-1.92596	0.1164161		0.9999488	



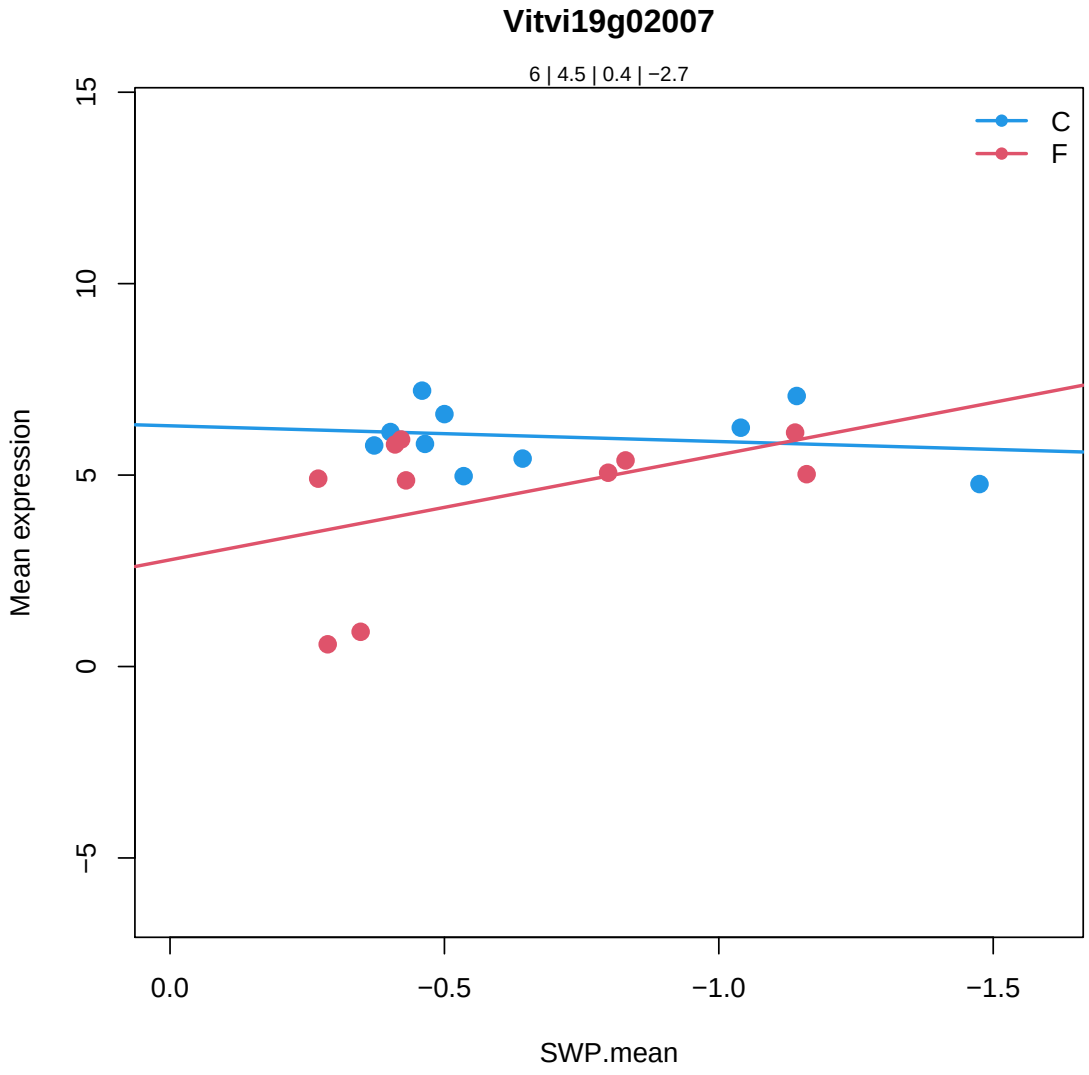
7.6.289 Vitvi19g02007: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g02007
        35.2
        not assigned.unknown
        fatty acid desaturase A |
        Chr4:13571951-13572922 FORWARD LENGTH=323 |
        201606
```

Coefficients for Vitvi19g02007.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.99801	1.023182e-12	***	1.466555e-12	***
SlopeC	0.4107341	0.7197001		0.9380929	
MeanF-MeanC	-1.541676	0.01370917	*	0.09580703	.
SlopeF-SlopeC	-3.15221	0.07448352	.	0.9999488	



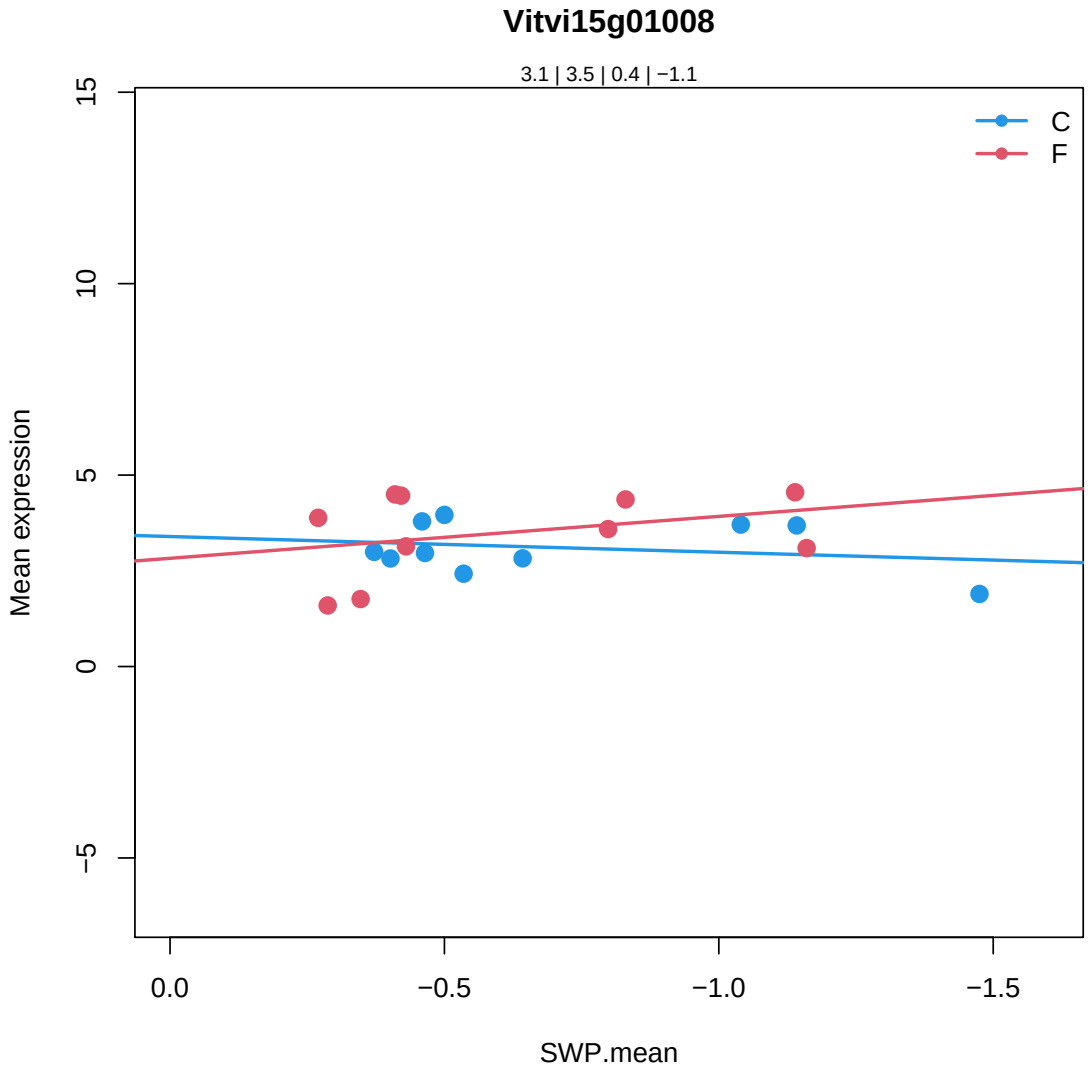
7.6.290 Vitvi15g01008: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g01008
        26.2
        misc.UDP glucosyl and glucoronyl transferases
        UDP-Glycosyltransferase superfamily protein |
        Chr4:461858-463300 REVERSE LENGTH=480 |
        201606
```

Coefficients for Vitvi15g01008.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.106689	6.867656e-11	***	9.041791e-11	***
SlopeC	0.410224	0.579169		0.8944184	
MeanF-MeanC	0.38656	0.3081256		0.6716891	
SlopeF-SlopeC	-1.505033	0.1793399		0.9999488	



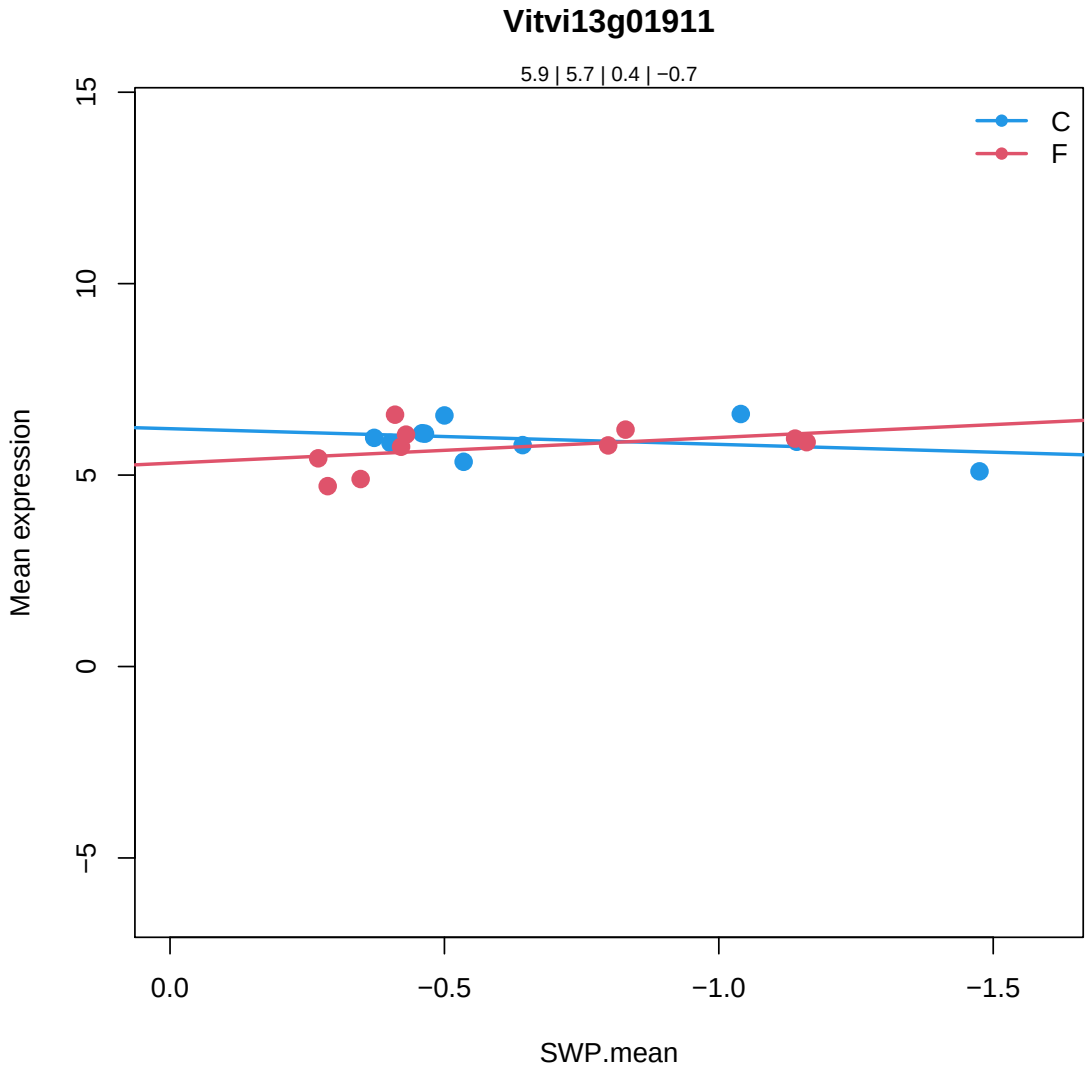
7.6.291 Vitvi13g01911: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g01911
        16.8.2
        secondary metabolism.flavonoids.chalcones
        Chalcone-flavanone isomerase family protein |
        Chr5:1563543-1564827 FORWARD LENGTH=209 |
        201606
```

Coefficients for Vitvi13g01911.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.923587	6.290315e-21	***	4.899182e-20	***
SlopeC	0.409147	0.3680091		0.8212976	
MeanF-MeanC	-0.2042277	0.3765459		0.7286165	
SlopeF-SlopeC	-1.081356	0.1170742		0.9999488	



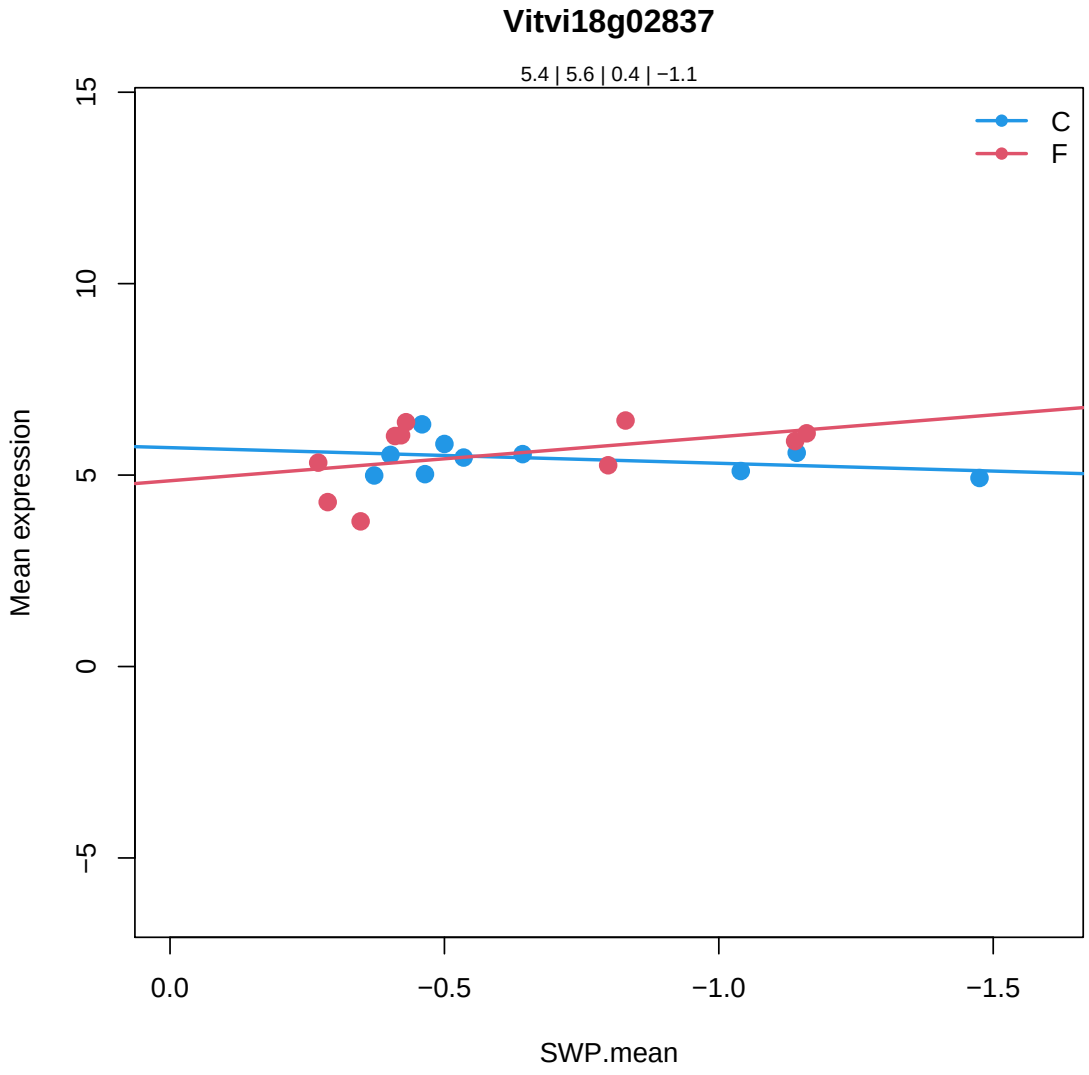
7.6.292 Vitvi18g02837: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02837
        20.1.7
        stress.biotic.PR-proteins
        pathogenesis-related family protein |
        Chr1:29621447-29622153 REVERSE LENGTH=176 |
        201606
```

Coefficients for Vitvi18g02837.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.429476	4.087801e-18	***	1.185206e-17	***
SlopeC	0.408078	0.4701871		0.8618199	
MeanF-MeanC	0.1215186	0.6709926		0.8930553	
SlopeF-SlopeC	-1.556341	0.07321479	.	0.9999488	



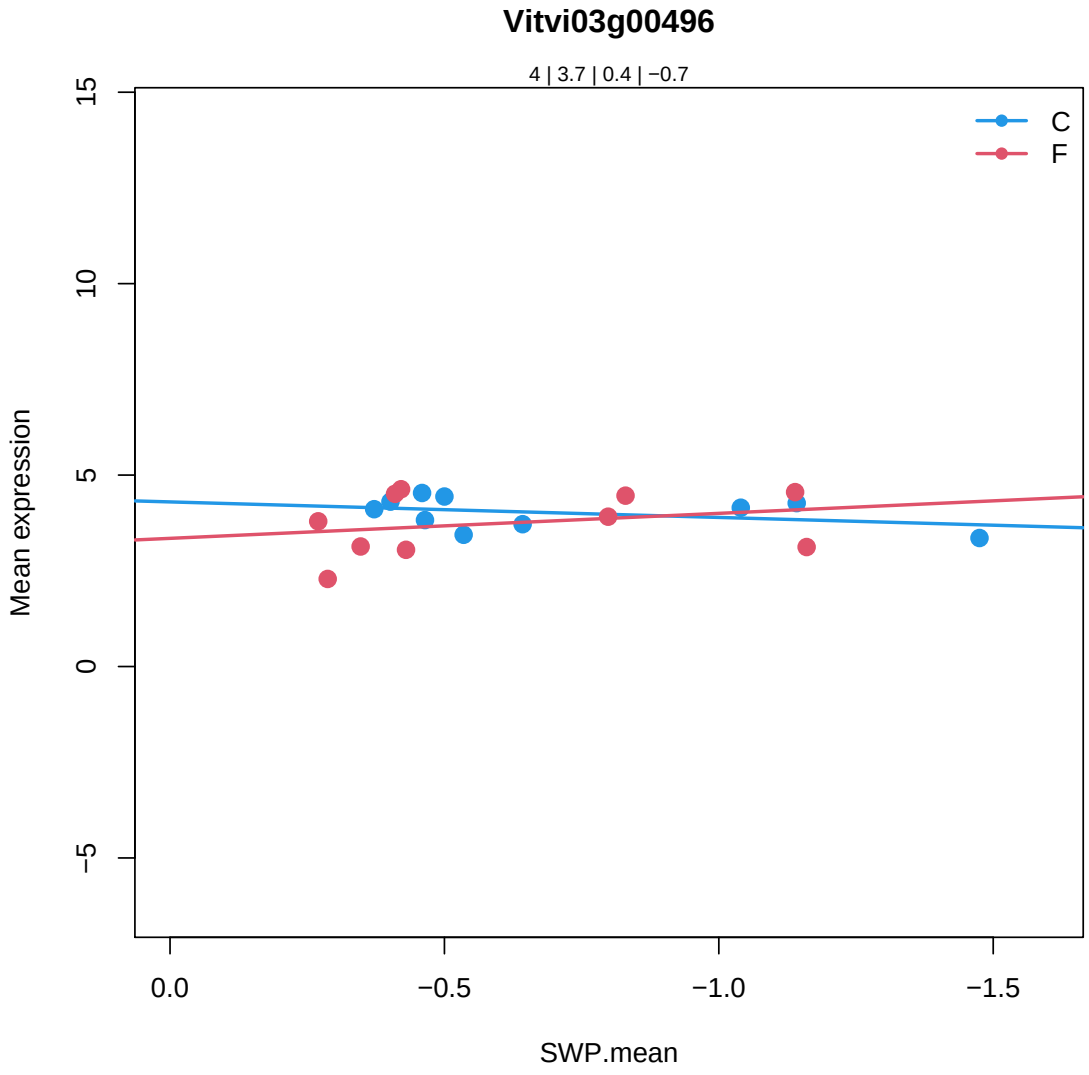
7.6.293 Vitvi03g00496: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00496
        30.3
        signalling.calcium
        Calcium-binding EF-hand family protein |
        Chr2:6831024-6831587 FORWARD LENGTH=187 |
        201606
```

Coefficients for Vitvi03g00496.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.014061	1.221587e-15	***	2.262936e-15	***
SlopeC	0.4057402	0.4610852		0.8603302	
MeanF-MeanC	-0.2686899	0.3390861		0.699087	
SlopeF-SlopeC	-1.058684	0.2021445		0.9999488	



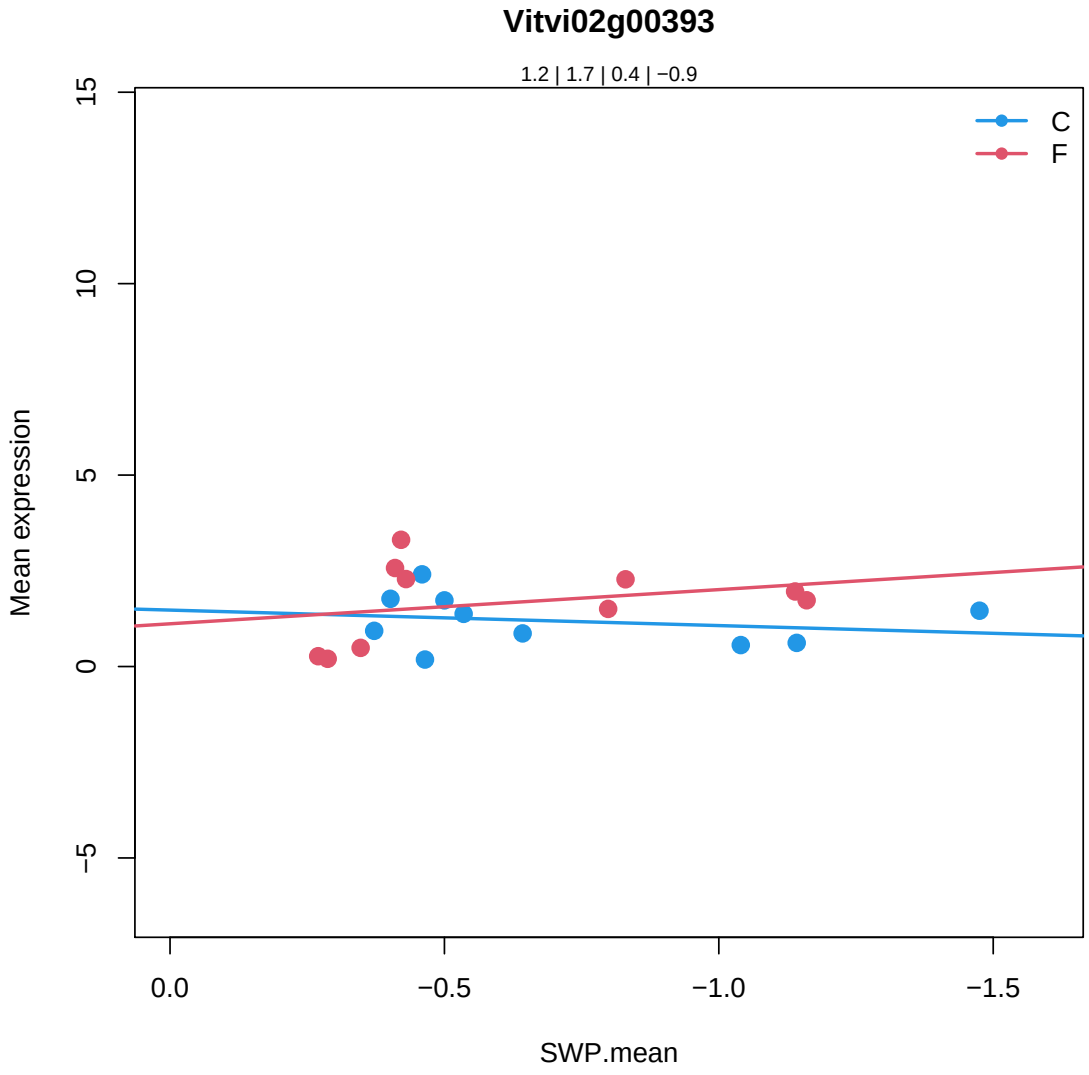
7.6.294 Vitvi02g00393: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00393
        20.1.7.5
        stress.biotic.PR-proteins.PR5 (thaumatin-like proteins)
        osmotin 34 |
        Chr4:7025127-7026113 REVERSE LENGTH=244 |
        201606
```

Coefficients for Vitvi02g00393.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.189261	0.0001434003	***	0.0001578698	***
SlopeC	0.404707	0.5785024		0.8944184	
MeanF-MeanC	0.4703394	0.2108487		0.5559169	
SlopeF-SlopeC	-1.297471	0.2375059		0.9999488	



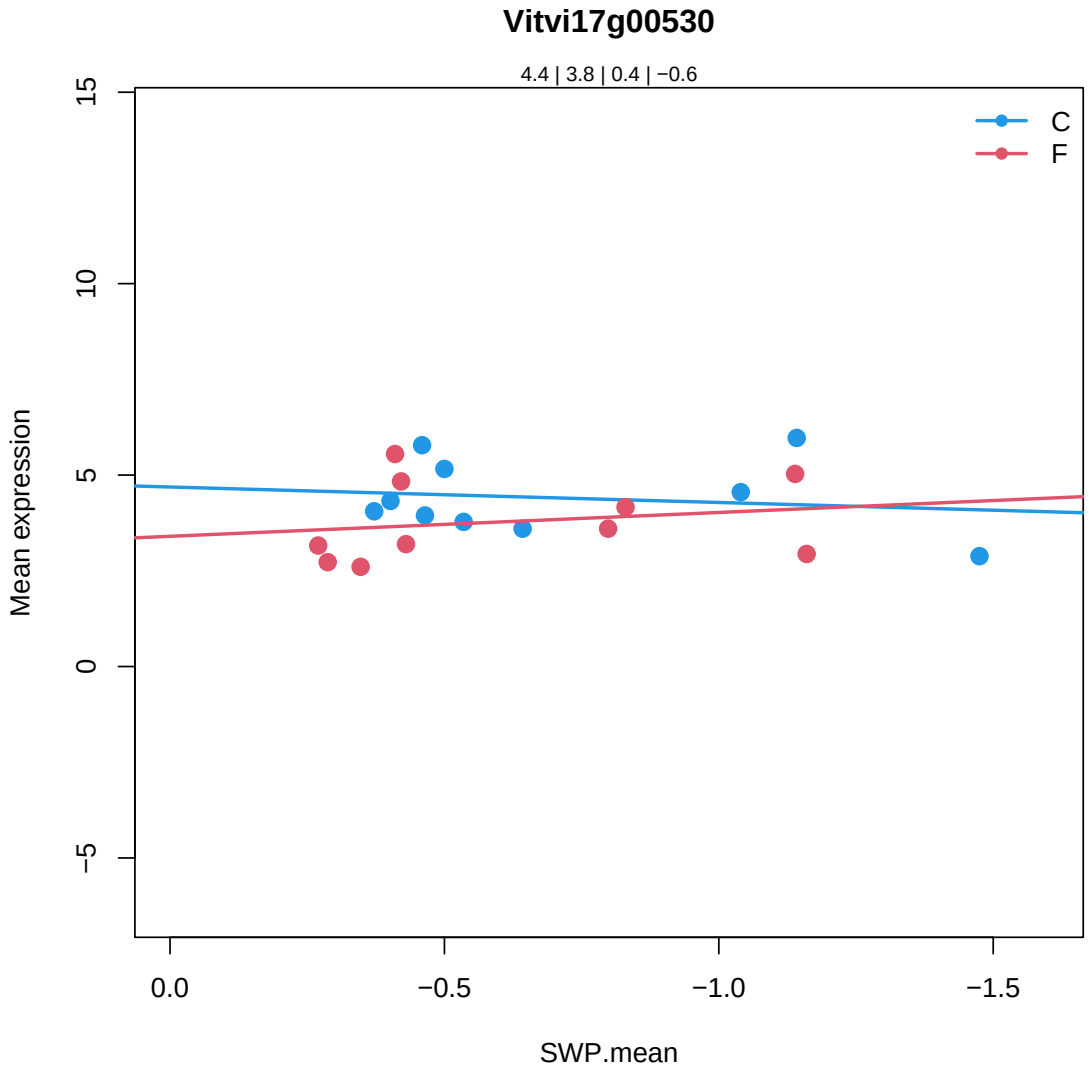
7.6.295 Vitvi17g00530: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00530
        35.2
        not assigned.unknown
        Major facilitator superfamily protein |
        Chr3:17698126-17700771 REVERSE LENGTH=636 |
        201606
```

Coefficients for Vitvi17g00530.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.404597	1.119744e-12	***	1.601495e-12	***
SlopeC	0.4041833	0.6325712		0.912027	
MeanF-MeanC	-0.6243522	0.1550232		0.475043	
SlopeF-SlopeC	-1.026356	0.417057		0.9999488	



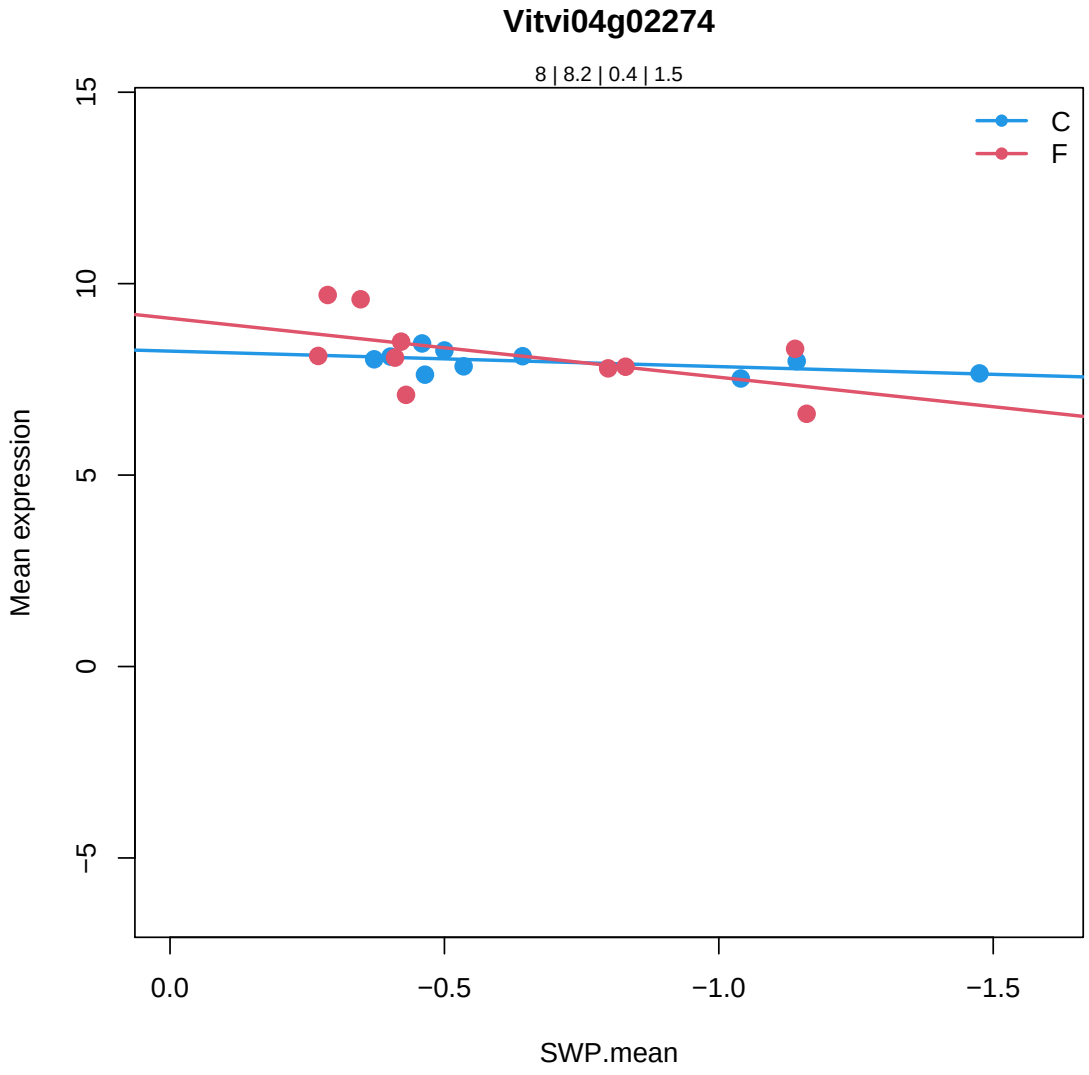
7.6.296 Vitvi04g02274: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g02274
        21.6
        redox.dismutases and catalases
        catalase 2 |
        Chr4:16700937-16702955 REVERSE LENGTH=492 |
        201606
```

Coefficients for Vitvi04g02274.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.953247	4.651584e-22	***	6.252156e-21	***
SlopeC	0.4038817	0.4528109		0.8563681	
MeanF-MeanC	0.2036409	0.4564254		0.7821943	
SlopeF-SlopeC	1.135792	0.162979		0.9999488	



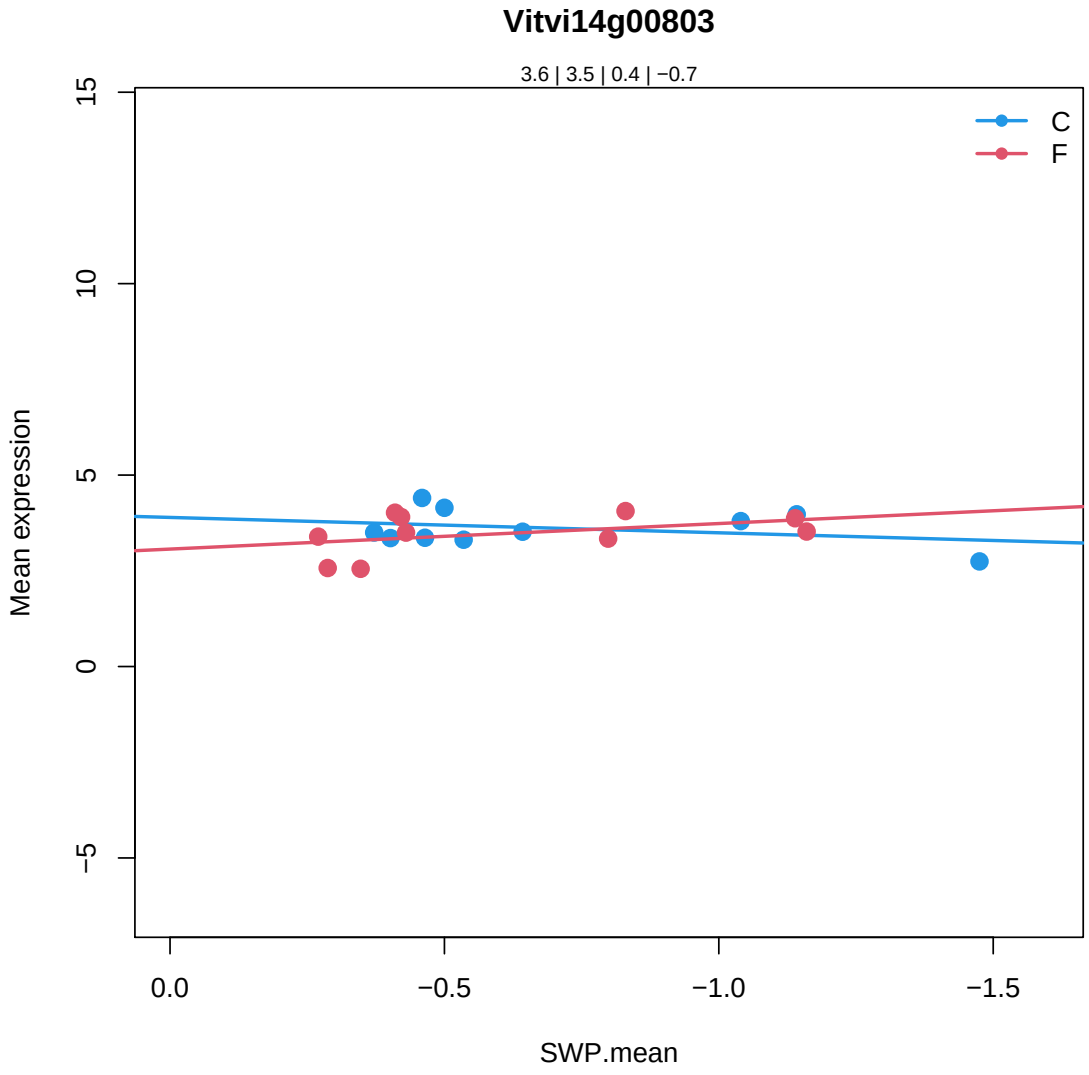
7.6.297 Vitvi14g00803: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g00803
        35.2
        not assigned.unknown
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi14g00803.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.611454	1.563434e-16	***	3.282802e-16	***
SlopeC	0.401324	0.3719293		0.8229039	
MeanF-MeanC	-0.1378773	0.5441441		0.8299692	
SlopeF-SlopeC	-1.068454	0.1174363		0.9999488	



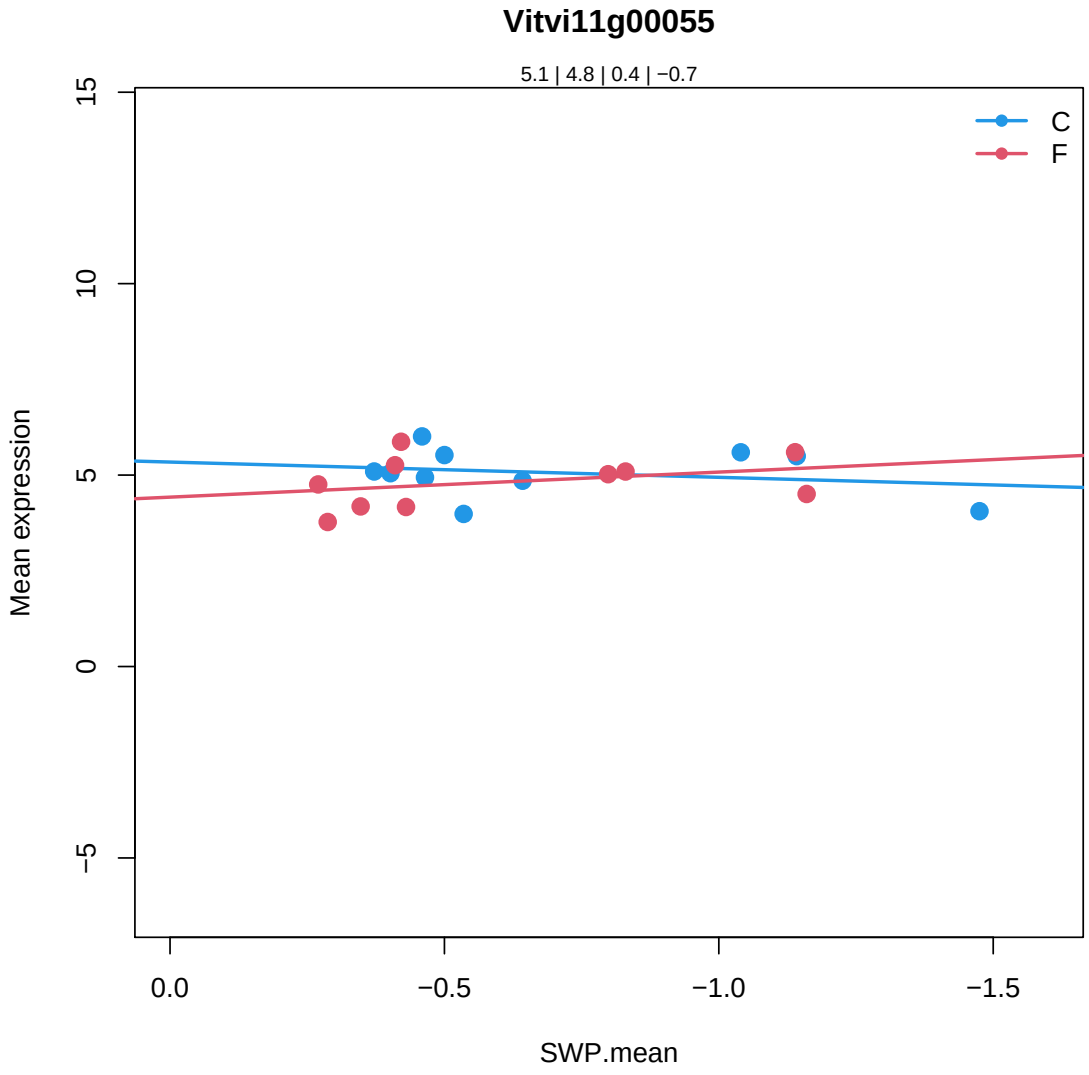
7.6.298 Vitvi11g00055: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00055
        35.2
        not assigned.unknown
        ubiquinone biosynthesis COQ9-like protein |
        Chr1:6611026-6612414 REVERSE LENGTH=311 |
        201606
```

Coefficients for Vitvi11g00055.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.059885	1.71289e-17	***	4.301132e-17	***
SlopeC	0.3985748	0.4797277		0.8634627	
MeanF-MeanC	-0.2375477	0.4083414		0.7494209	
SlopeF-SlopeC	-1.05299	0.215343		0.9999488	



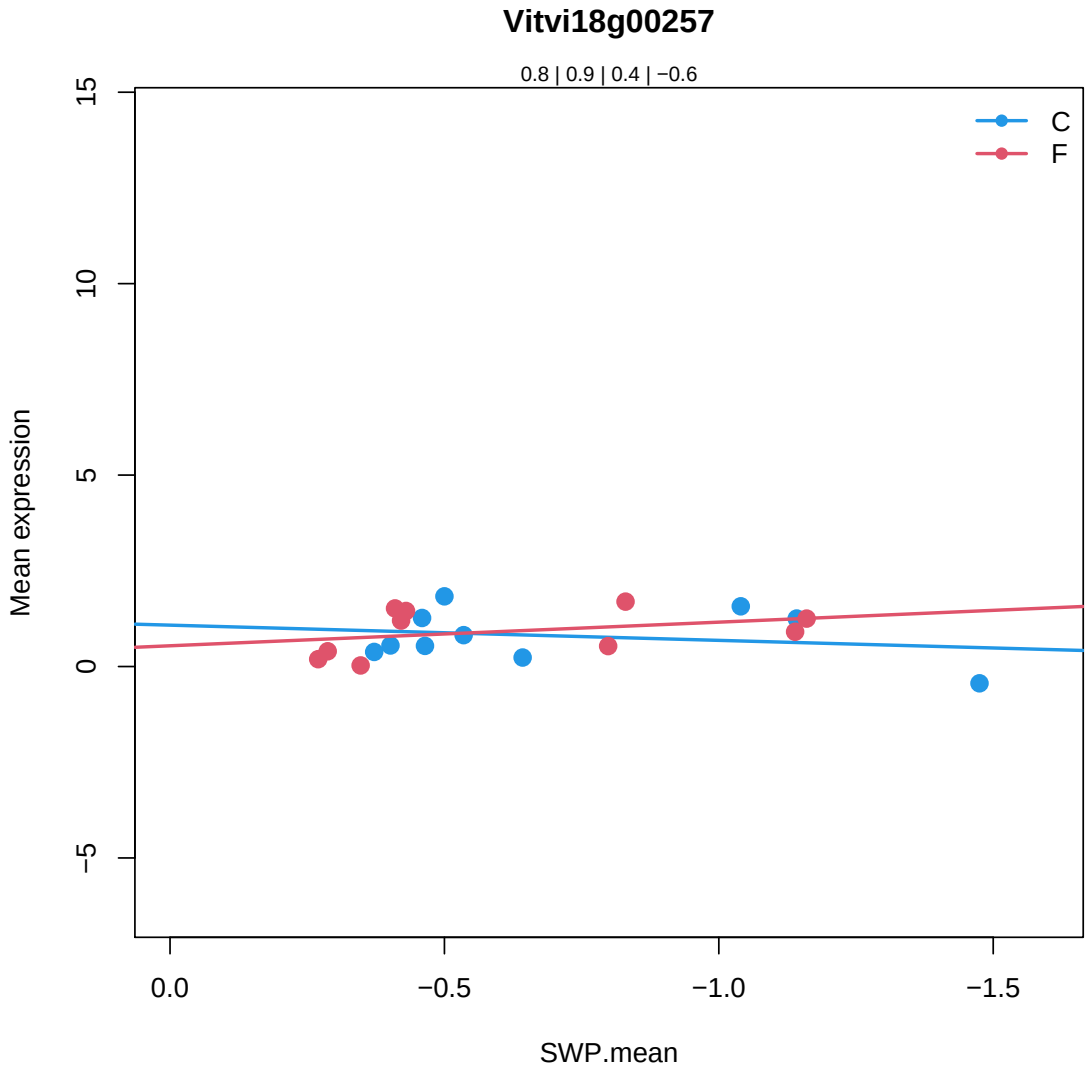
7.6.299 Vitvi18g00257: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00257
        27.3.35
        RNA.regulation of transcription.bZIP transcription factor family
        DUF630 family protein%2C putative (DUF630 and DUF632) |
        Chr1:7641580-7645078 FORWARD LENGTH=953 |
        201606
```

Coefficients for Vitvi18g00257.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8008874	0.0004759919	***	0.0005185526	***
SlopeC	0.3974594	0.4708728		0.8618199	
MeanF-MeanC	0.1163765	0.6766353		0.8951087	
SlopeF-SlopeC	-1.014506	0.2216198		0.9999488	



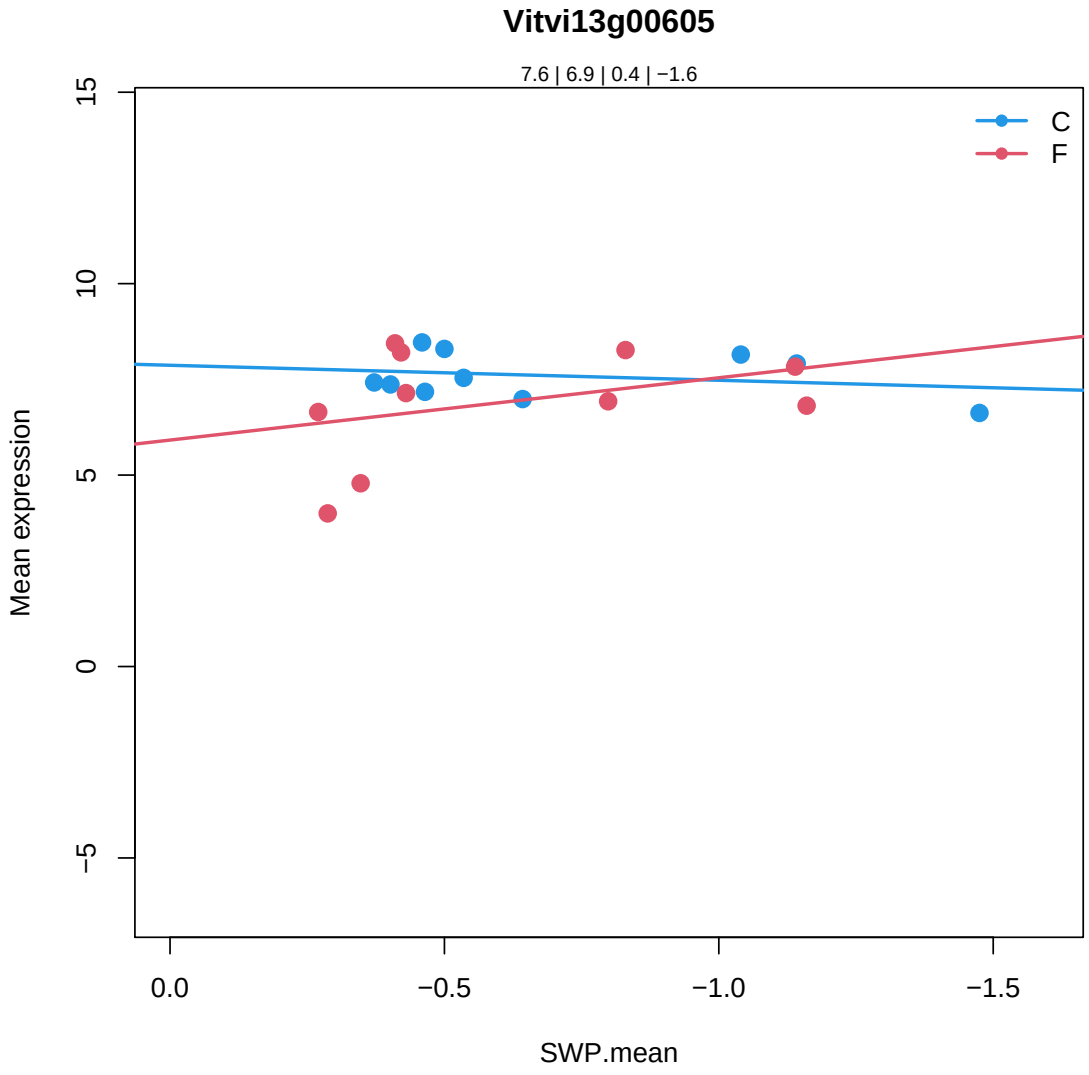
7.6.300 Vitvi13g00605: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00605
        34.19.1
        transport.major intrinsic proteins.PIP
        plasma membrane intrinsic protein 2 |
        Chr2:15613624-15614791 REVERSE LENGTH=285 |
        201606
```

Coefficients for Vitvi13g00605.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.592703	5.28452e-17	***	1.207234e-16	***
SlopeC	0.3913983	0.6601853		0.9218432	
MeanF-MeanC	-0.6872399	0.1381836		0.4448345	
SlopeF-SlopeC	-2.019107	0.1369143		0.9999488	



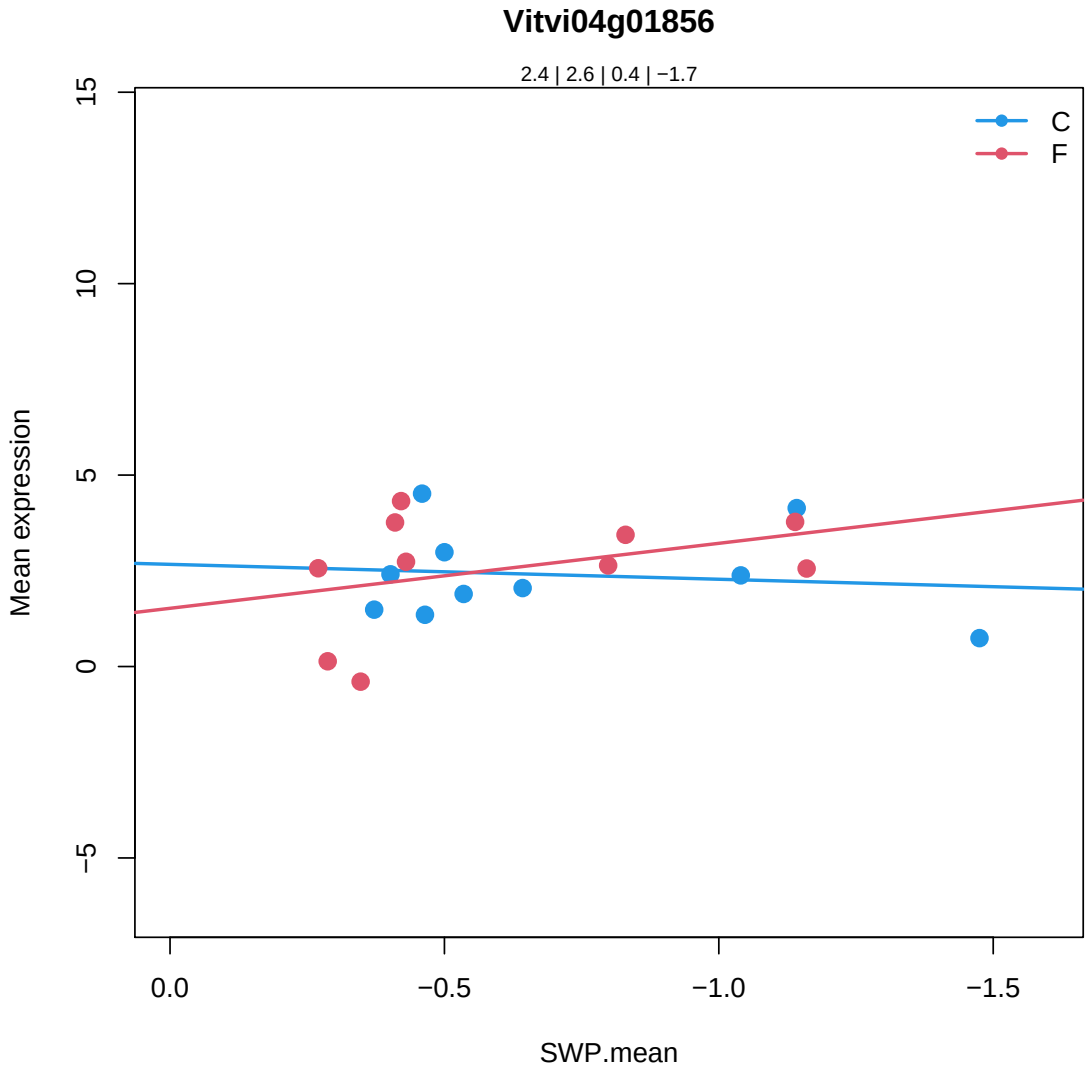
7.6.301 Vitvi04g01856: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01856
        31.1
        cell.organisation
        Ankyrin repeat family protein |
        Chr1:3390475-3392481 REVERSE LENGTH=578 |
        201606
```

Coefficients for Vitvi04g01856.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.394766	3.749757e-06	***	4.272862e-06	***
SlopeC	0.3888641	0.7226597		0.9392454	
MeanF-MeanC	0.1594426	0.7745531		0.9355874	
SlopeF-SlopeC	-2.085775	0.2087743		0.9999488	



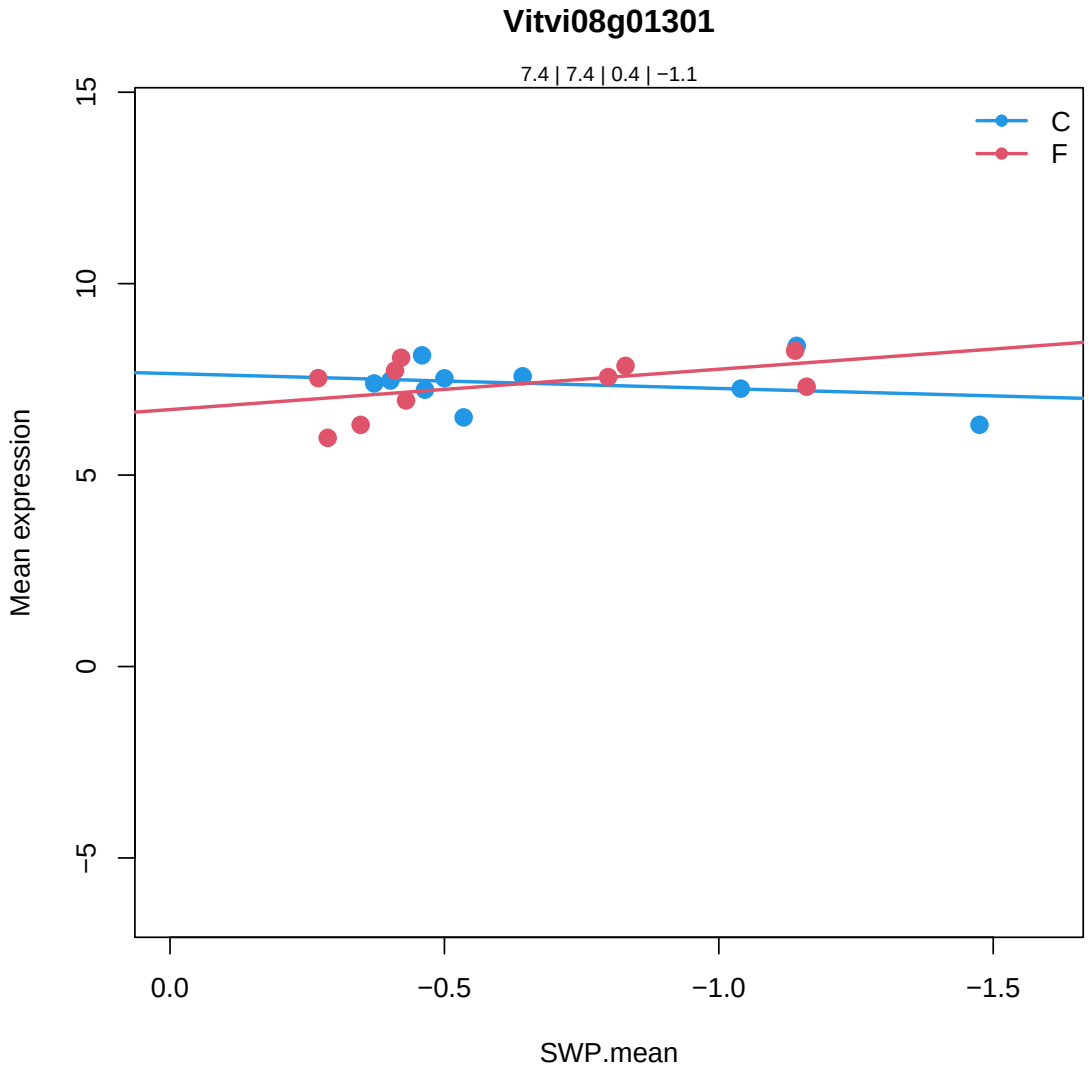
7.6.302 Vitvi08g01301: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01301
        1.3.7
        PS.calvin cycle.FBPase
        high cyclic electron flow 1 |
        Chr3:20016951-2018527 FORWARD LENGTH=417 |
        201606
```

Coefficients for Vitvi08g01301.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.377901	5.713254e-21	***	4.531308e-20	***
SlopeC	0.3885454	0.4887894		0.8662421	
MeanF-MeanC	-0.02489478	0.9300794		0.9815506	
SlopeF-SlopeC	-1.443109	0.09307152	.	0.9999488	



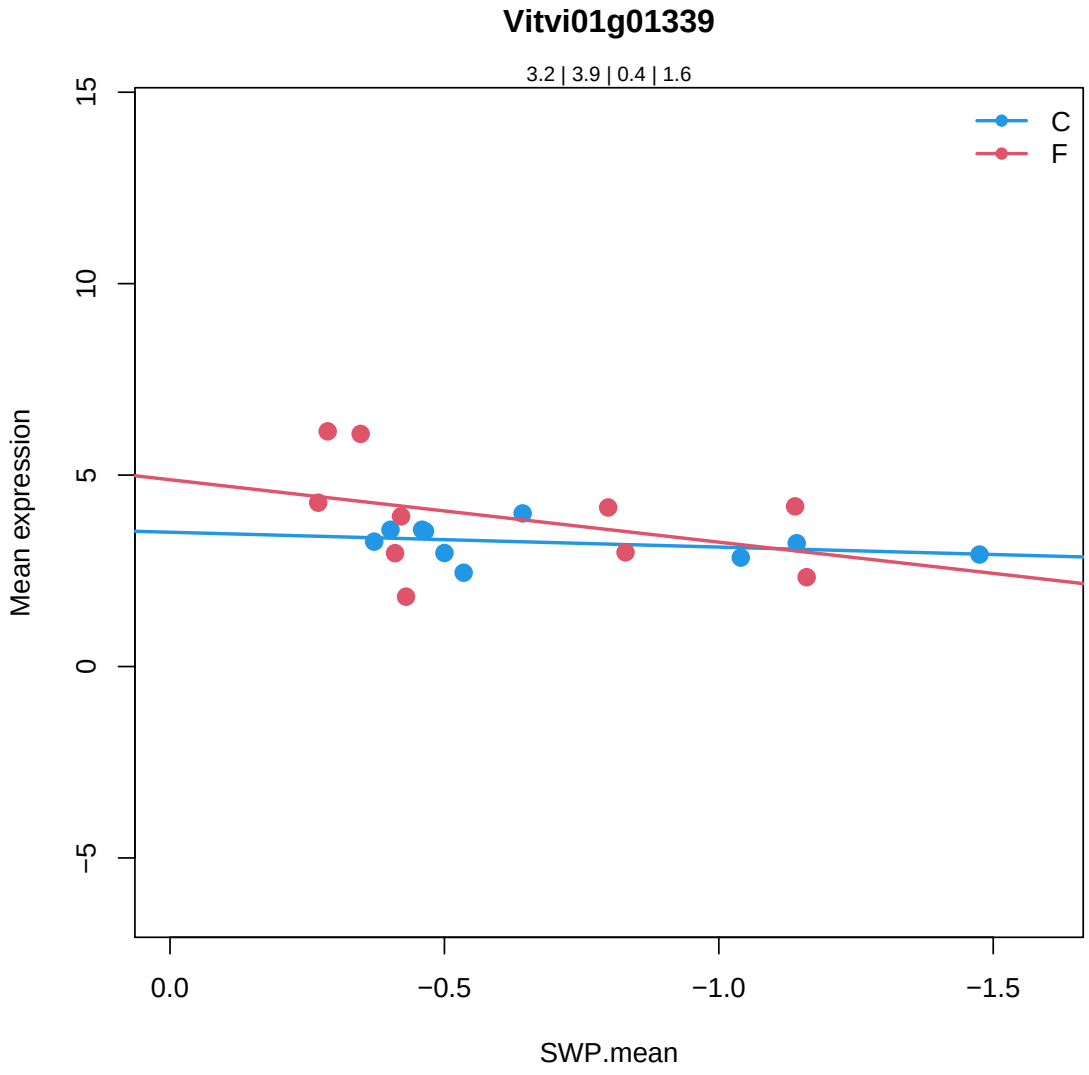
7.6.303 Vitvi01g01339: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01339
        29.6
        protein.folding
        chaperonin 60 beta |
        Chr1:20715717-20718673 REVERSE LENGTH=600 |
        201606
```

Coefficients for Vitvi01g01339.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.234282	2.977569e-10	***	3.82504e-10	***
SlopeC	0.3876818	0.641473		0.9153273	
MeanF-MeanC	0.6510742	0.1332919		0.4363021	
SlopeF-SlopeC	1.242767	0.3203684		0.9999488	



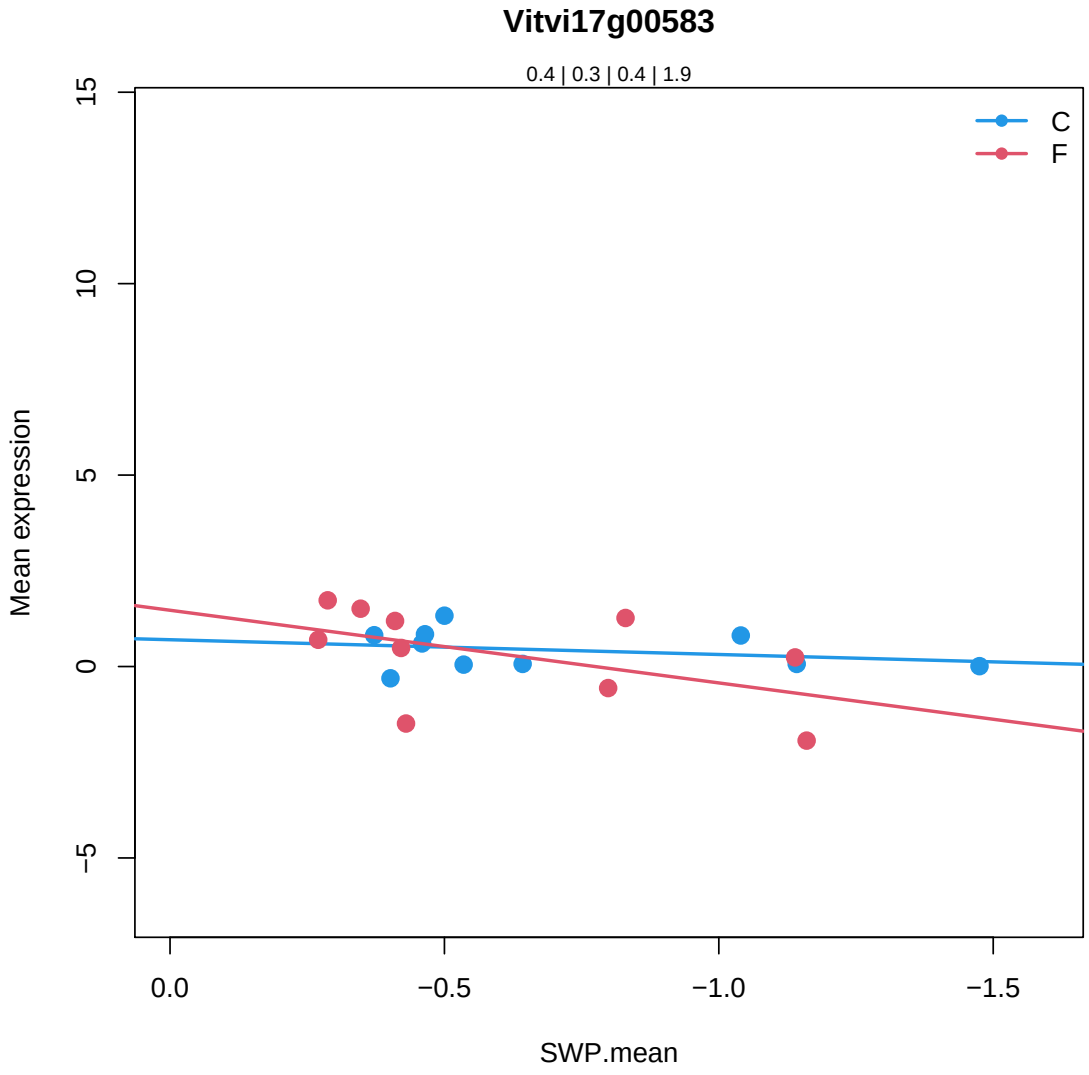
7.6.304 Vitvi17g00583: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00583
        30.11
        signalling.light
        phytochrome kinase substrate-like protein |
        Chr1:6485709-6486872 REVERSE LENGTH=387 |
        201606
```

Coefficients for Vitvi17g00583.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4285892	0.1090245		0.1126458	
SlopeC	0.3857174	0.5941439		0.901232	
MeanF-MeanC	-0.1155941	0.7528874		0.9276221	
SlopeF-SlopeC	1.512074	0.1686419		0.9999488	



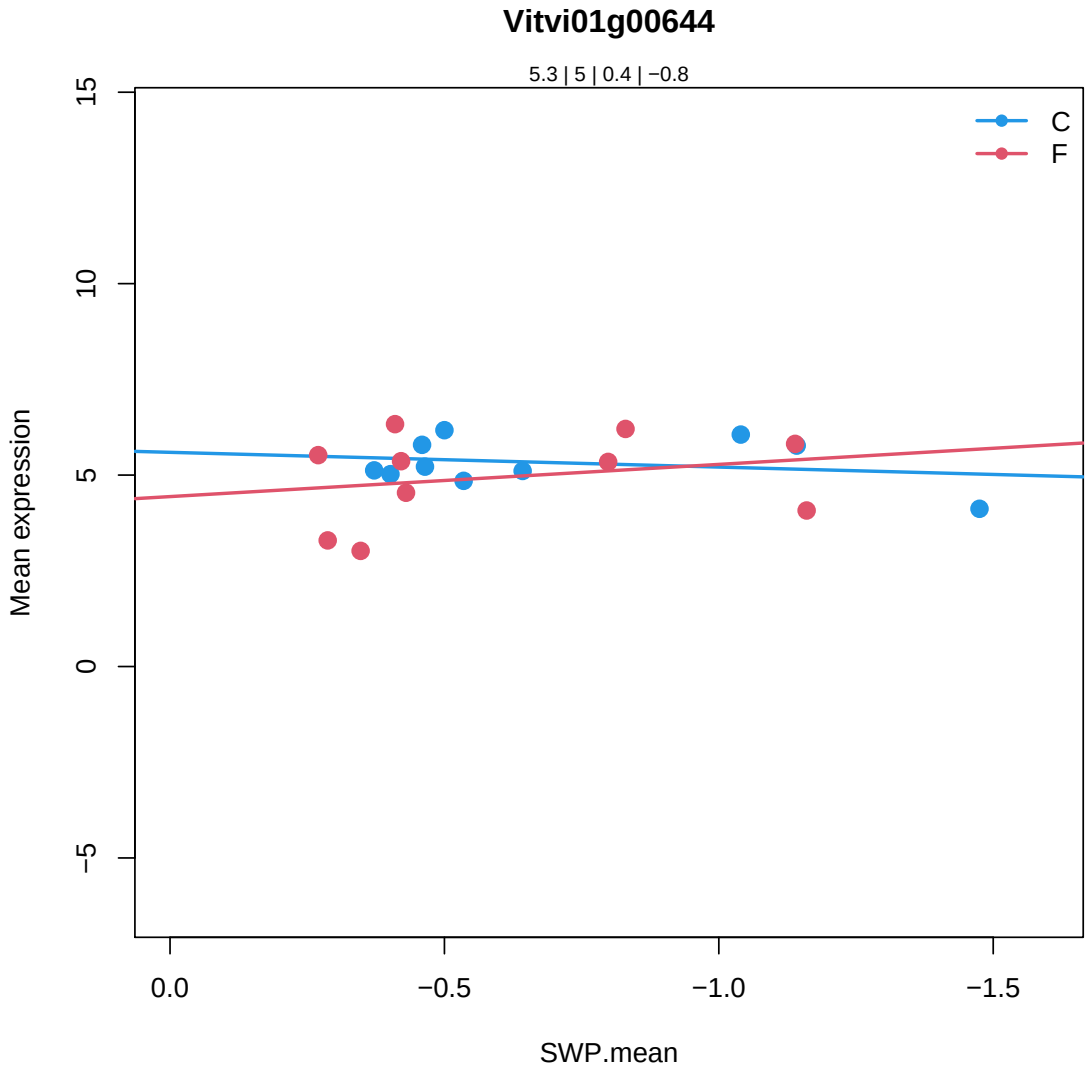
7.6.305 Vitvi01g00644: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00644
        30.11
        signalling.light
        Phototropic-responsive NPH3 family protein |
        Chr1:25467737-25469888 FORWARD LENGTH=631 |
        201606
```

Coefficients for Vitvi01g00644.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.323332	4.511379e-15	***	7.854076e-15	***
SlopeC	0.3853237	0.6193148		0.9085813	
MeanF-MeanC	-0.3730271	0.3477084		0.7072964	
SlopeF-SlopeC	-1.226483	0.2929662		0.9999488	



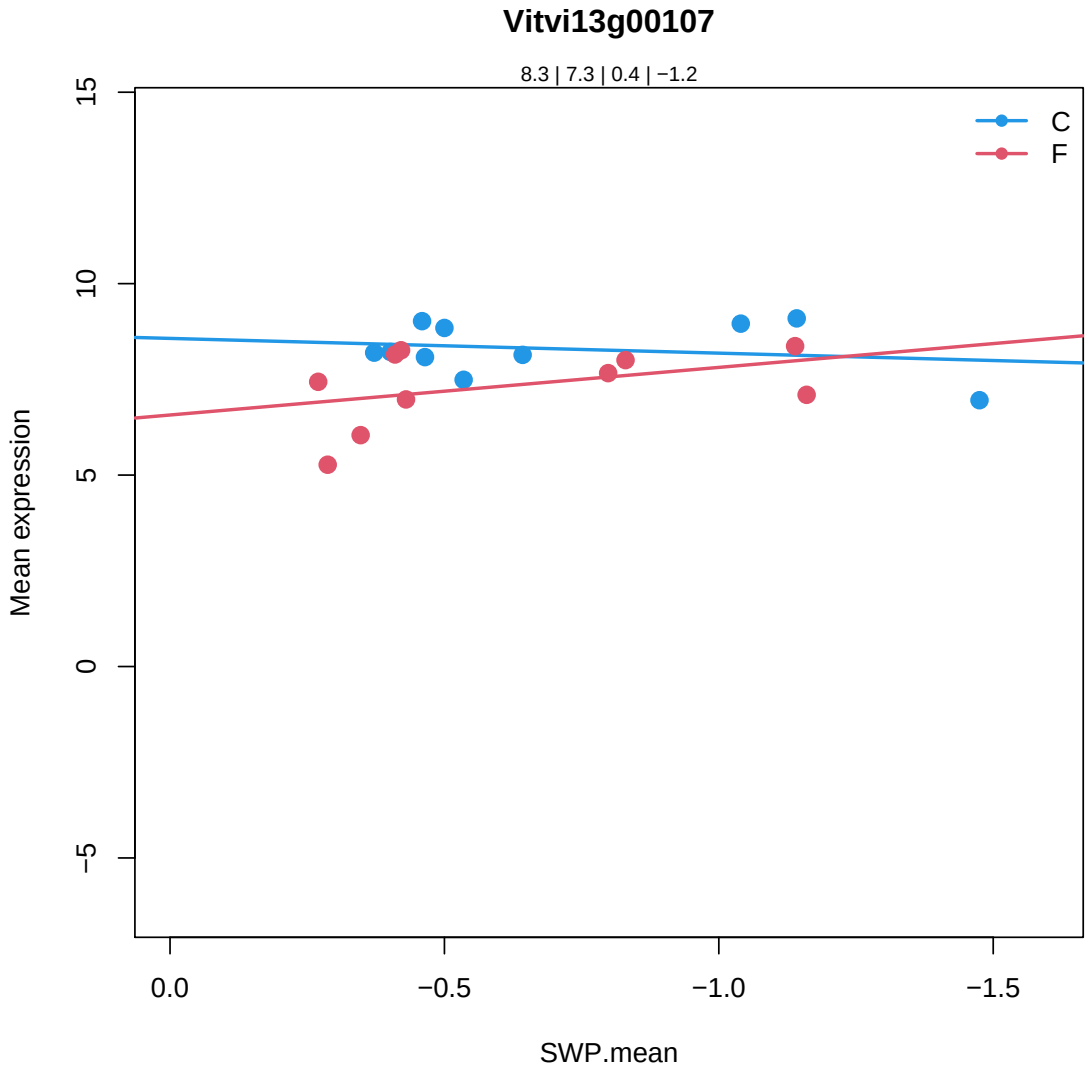
7.6.306 Vitvi13g00107: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00107
        15.2
        metal handling.binding, chelation and storage
        ferritin 4 |
        Chr2:16831501-16833214 REVERSE LENGTH=259 |
        201606
```

Coefficients for Vitvi13g00107.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	8.298815	5.271299e-20	***	2.773391e-19	***
SlopeC	0.385173	0.5821567		0.8953802	
MeanF-MeanC	-0.9724626	0.01121047	*	0.08242646	.
SlopeF-SlopeC	-1.628433	0.1271495		0.9999488	



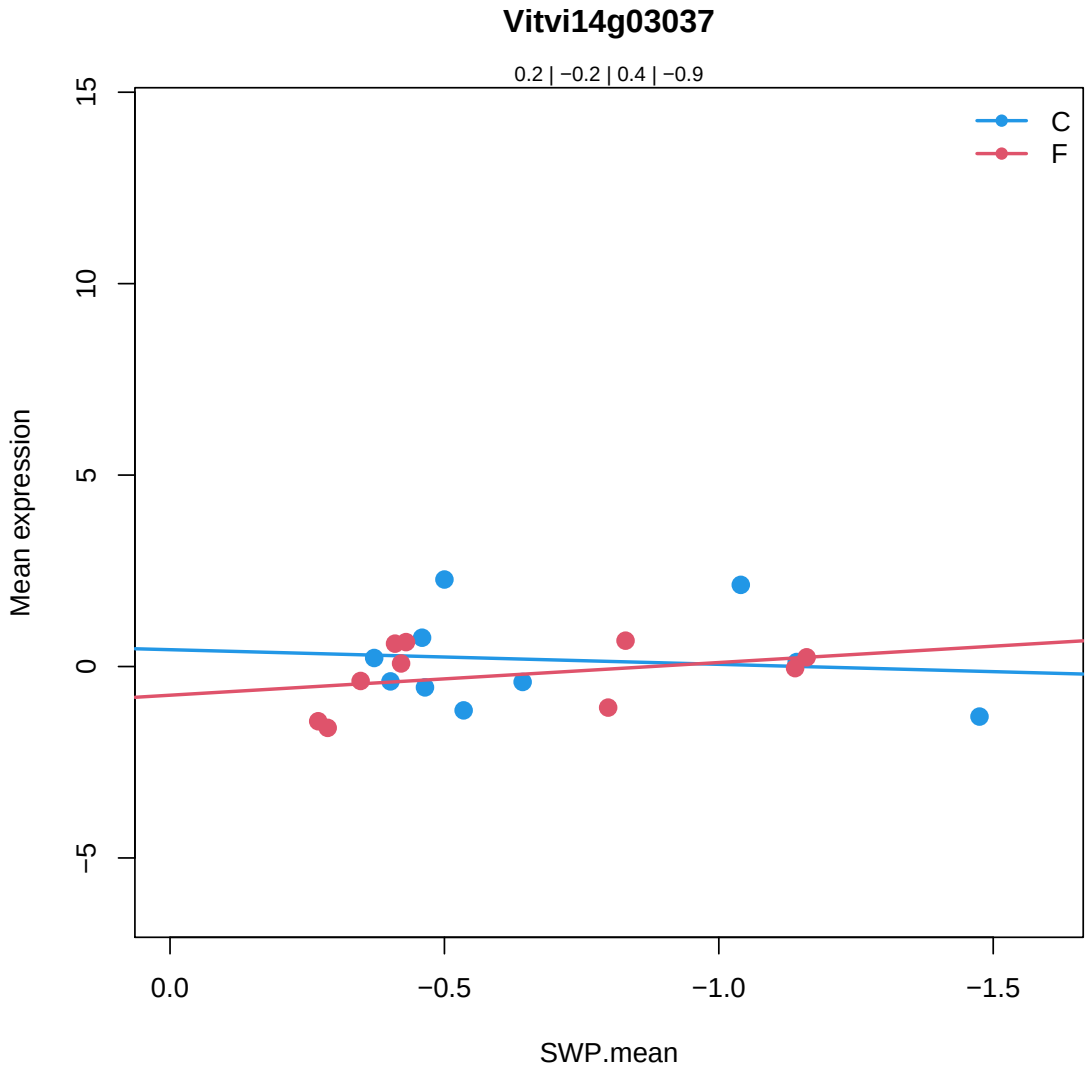
7.6.307 Vitvi14g03037: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g03037
        35.2
        not assigned.unknown
        matrix metalloproteinase |
        Chr1:26424005-26425141 FORWARD LENGTH=378 |
        201606
```

Coefficients for Vitvi14g03037.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1707031	0.5883198		0.5937344	
SlopeC	0.3821949	0.6627445		0.9225525	
MeanF-MeanC	-0.4001118	0.3725335		0.7261546	
SlopeF-SlopeC	-1.235942	0.3473352		0.9999488	



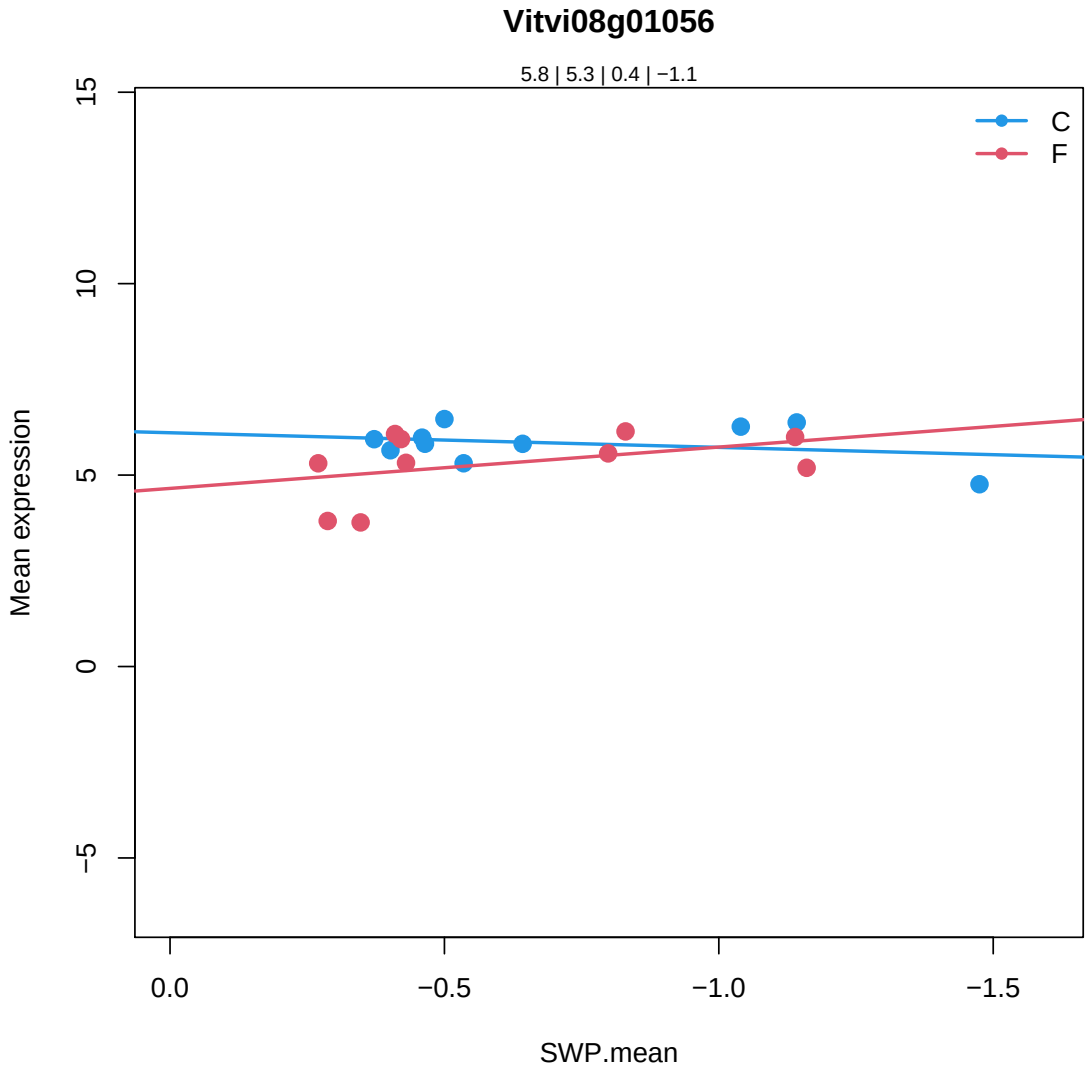
7.6.308 Vitvi08g01056: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01056
        20.1.3.1
        stress.biotic.signalling.MLO-like
        Seven transmembrane MLO family protein |
        Chr3:16617586-16621352 FORWARD LENGTH=508 |
        201606
```

Coefficients for Vitvi08g01056.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.836887	1.827358e-18	***	5.837895e-18	***
SlopeC	0.3819614	0.5129721		0.8711742	
MeanF-MeanC	-0.52726	0.08487863	.	0.3303677	
SlopeF-SlopeC	-1.461602	0.1016266		0.9999488	



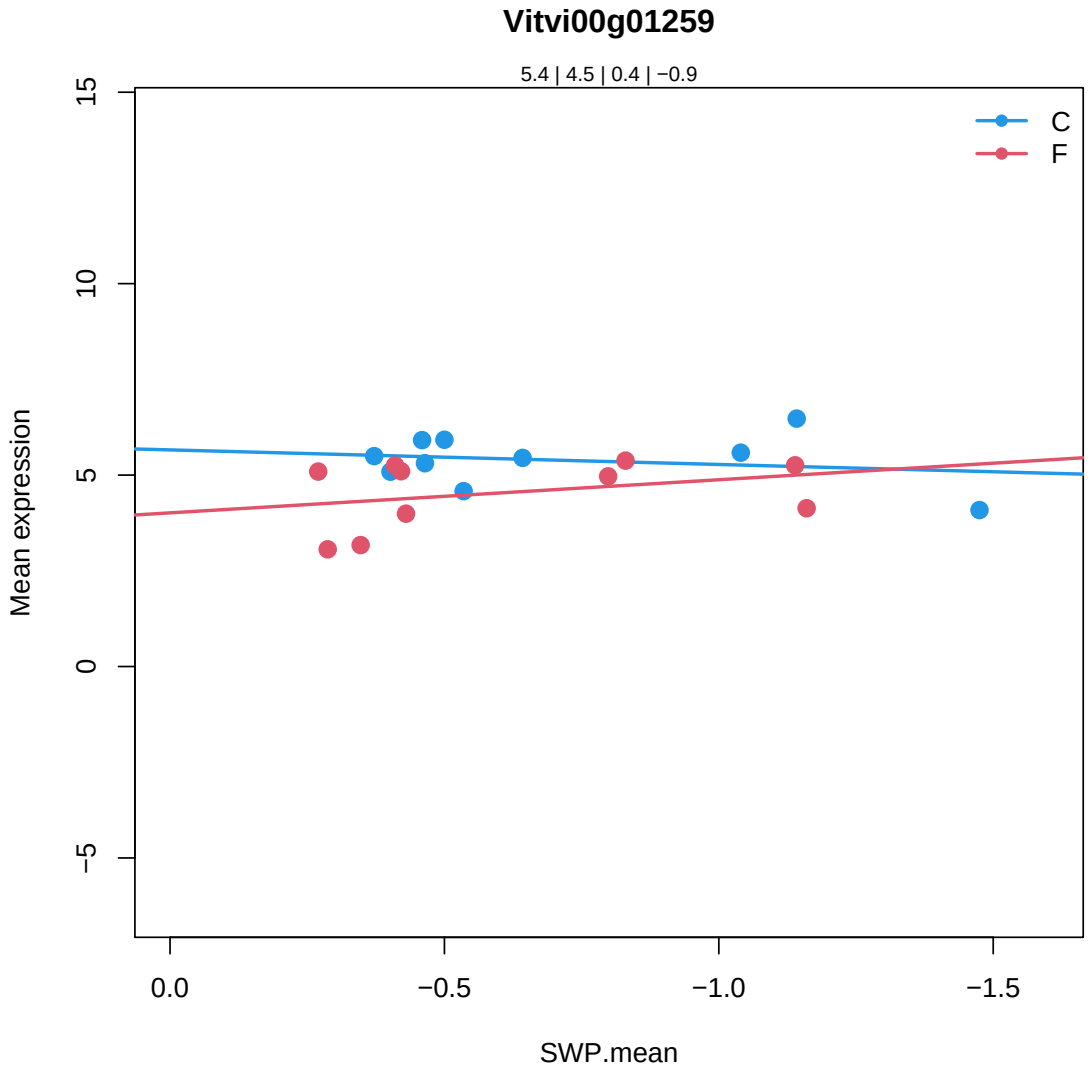
7.6.309 Vitvi00g01259: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi00g01259
        3.1.2.2
        minor CHO metabolism.raffinose family.raffinose synthases.putative
        seed imbibition 1 |
        Chr1:20835507-20838707 REVERSE LENGTH=754 |
        201606
```

Coefficients for Vitvi00g01259.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.390156	1.157491e-16	***	2.488011e-16	***
SlopeC	0.3807868	0.5625043		0.8904253	
MeanF-MeanC	-0.850278	0.01713615	*	0.1123878	
SlopeF-SlopeC	-1.24551	0.2098473		0.9999488	



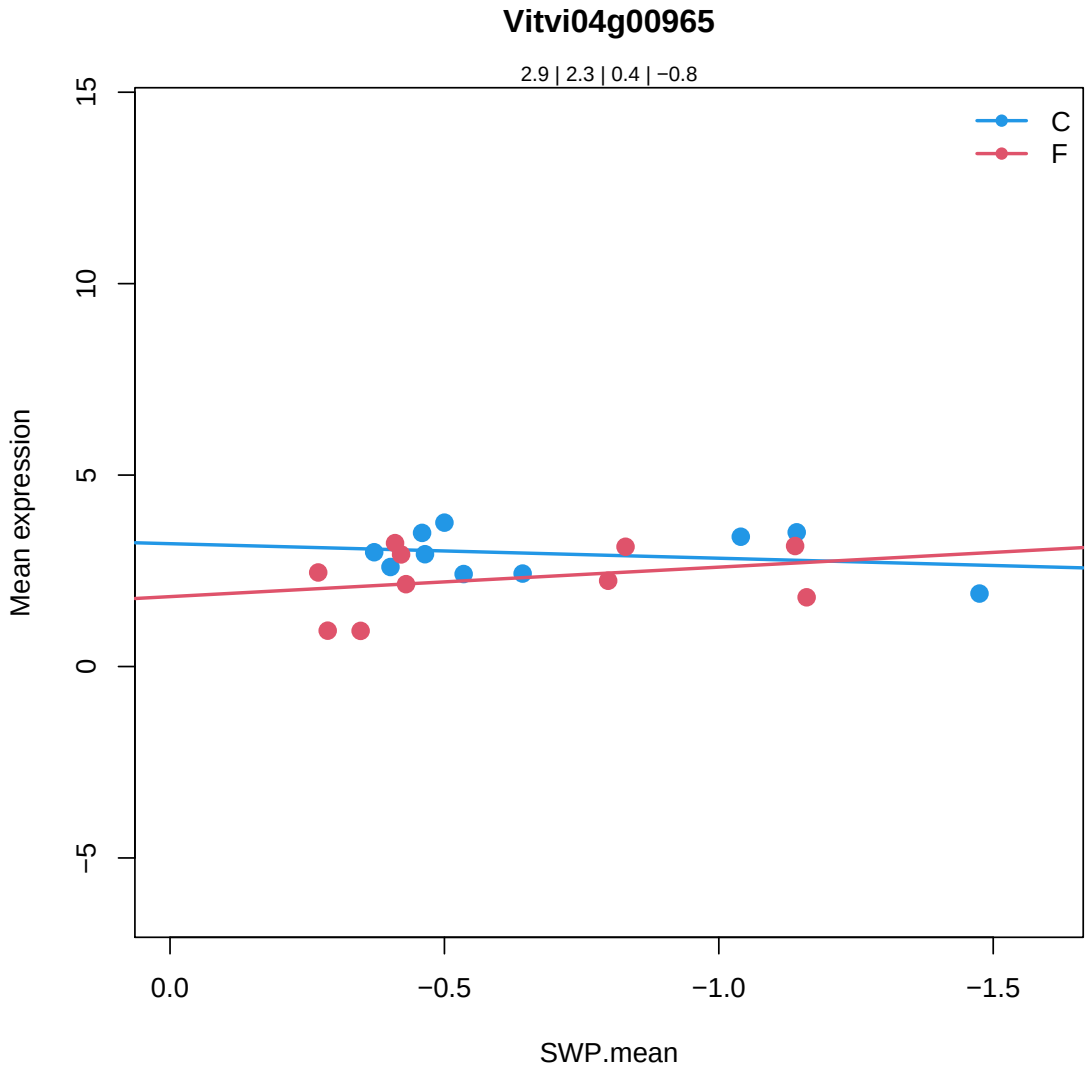
7.6.310 Vitvi04g00965: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00965
        27.3.25
        RNA.regulation of transcription.MYB domain transcription factor family
        Homeodomain-like superfamily protein |
        Chr5:5407365-5411092 REVERSE LENGTH=403 |
        201606
```

Coefficients for Vitvi04g00965.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.940733	7.197124e-12	***	9.894341e-12	***
SlopeC	0.3795029	0.5419225		0.8845521	
MeanF-MeanC	-0.6461733	0.05009234	.	0.239194	
SlopeF-SlopeC	-1.149712	0.2206558		0.9999488	



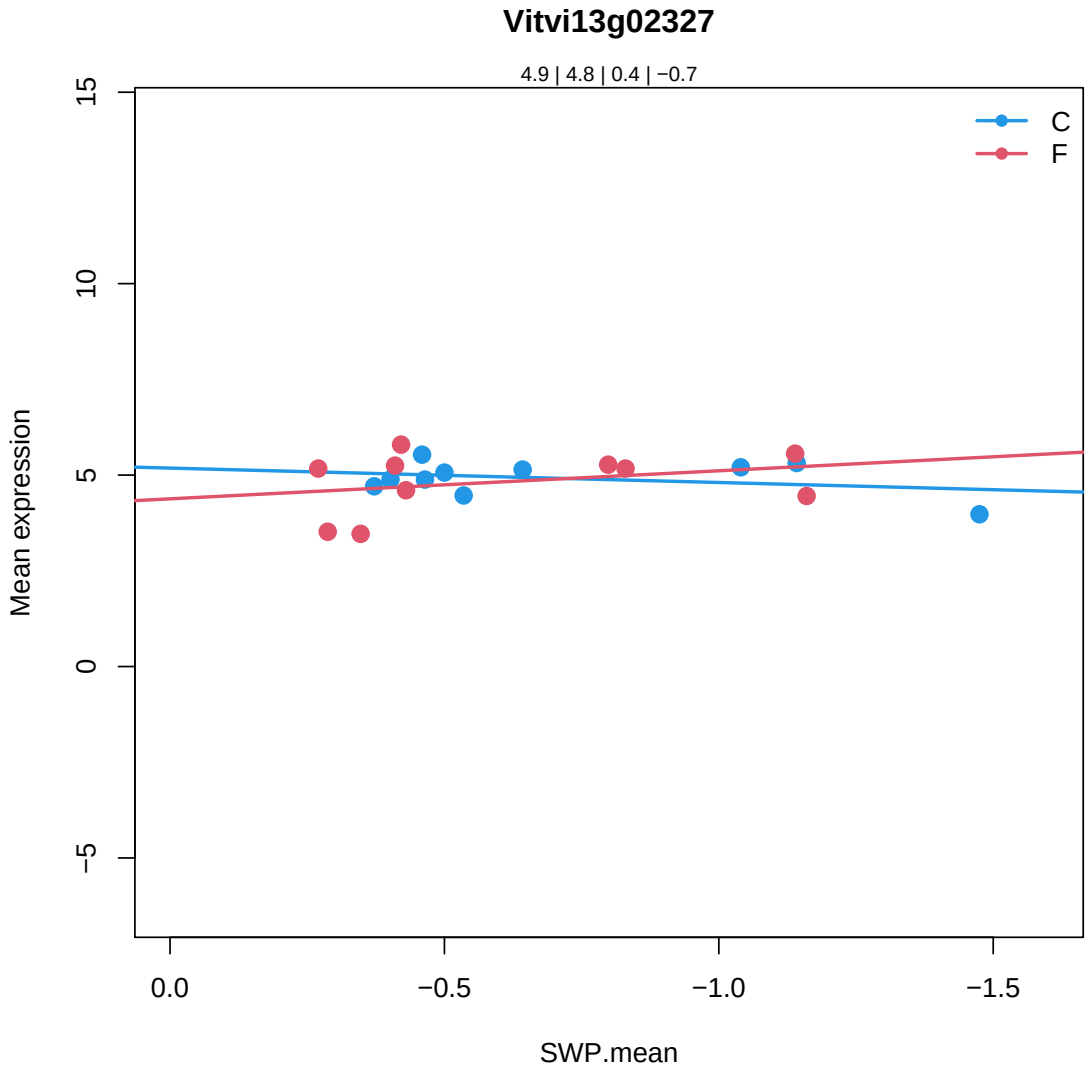
7.6.311 Vitvi13g02327: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g02327
        27.3.5
        RNA.regulation of transcription.ARR
        Major facilitator superfamily protein |
        Chr1:6199980-6201359 FORWARD LENGTH=459 |
        201606
```

Coefficients for Vitvi13g02327.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.917752	2.170993e-17	***	5.349219e-17	***
SlopeC	0.3762224	0.4971929		0.8693604	
MeanF-MeanC	-0.09209767	0.7426637		0.9240836	
SlopeF-SlopeC	-1.10806	0.1858869		0.9999488	



7.6.312 Vitvi19g01966: type5

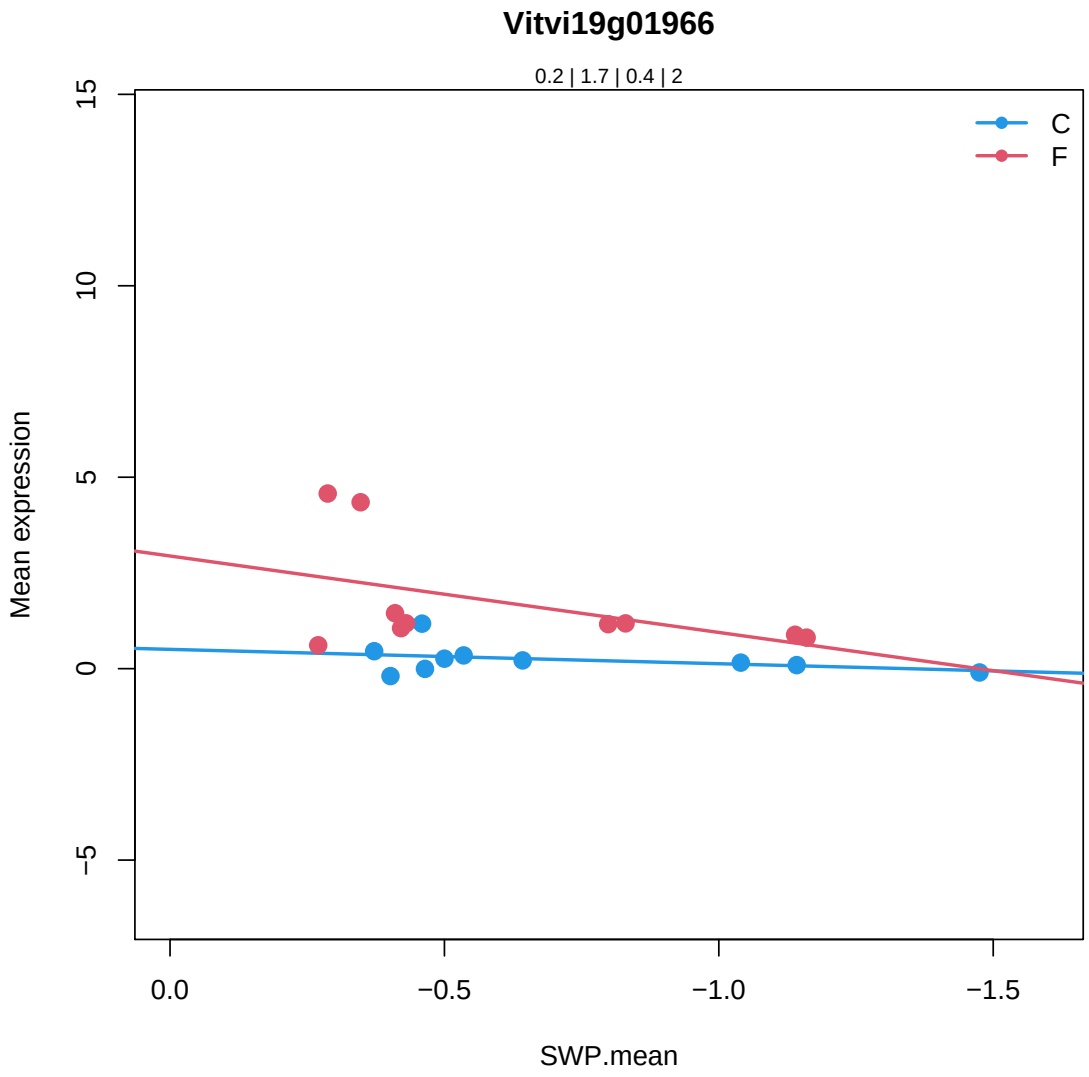
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g01966
        30.2.24
        signalling.receptor kinases.S-locus glycoprotein like
        S-locus lectin protein kinase family protein |
        Chr4:13666281-13669202 FORWARD LENGTH=783 |
        201606

Vitvi19g01966
        29.4
        protein.postranslational modification
        S-locus lectin protein kinase family protein |
        Chr4:13666281-13669202 FORWARD LENGTH=783 |
        201606
```

Coefficients for Vitvi19g01966.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.2401875	0.4085668		0.4146608	
SlopeC	0.3750725	0.6408989		0.9150039	
MeanF-MeanC	1.485613	0.001334182	**	0.01587478	*
SlopeF-SlopeC	1.621511	0.183549		0.9999488	


Vitvi19g01966
0.2 | 1.7 | 0.4 | 2
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

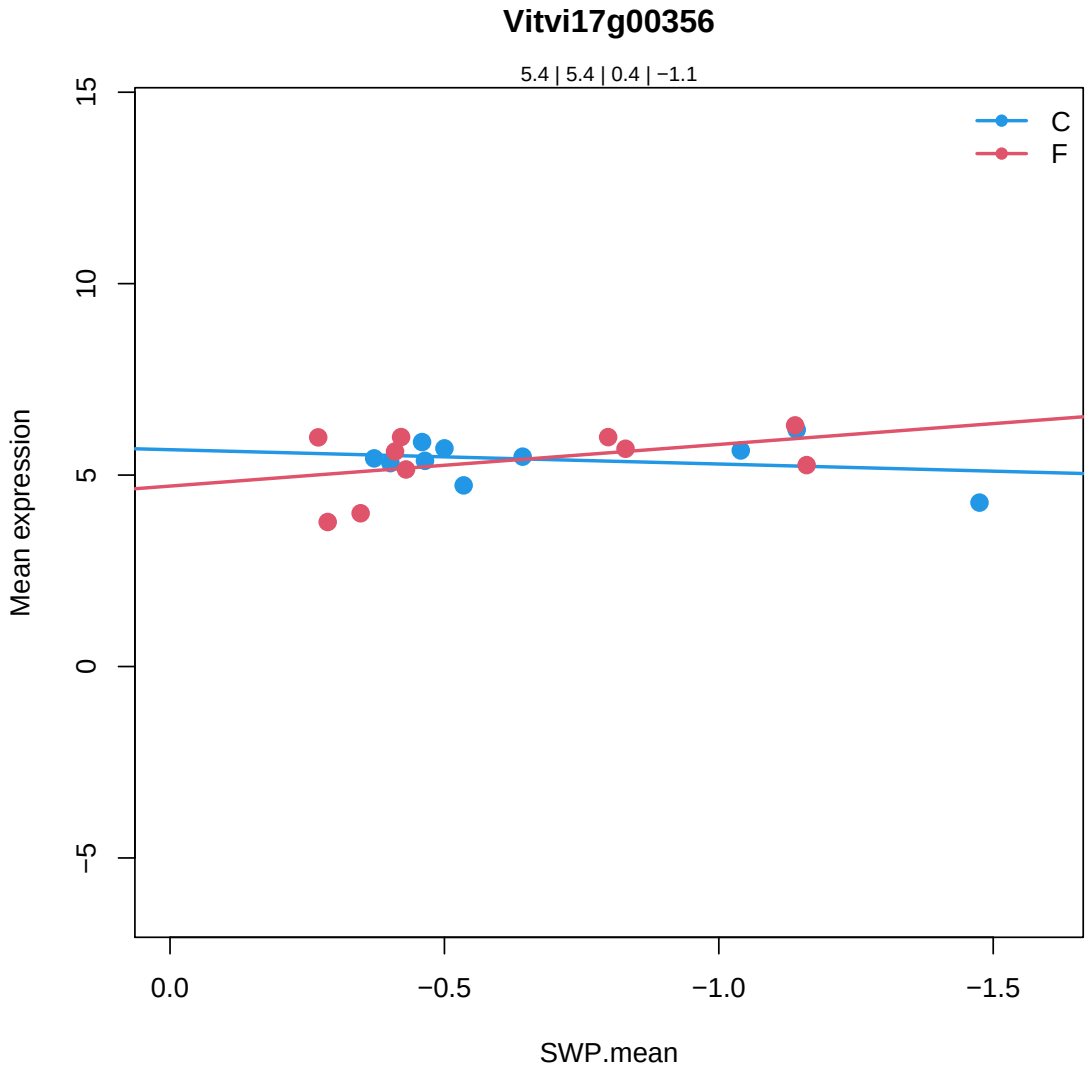
7.6.313 Vitvi17g00356: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00356
        28.1
        DNA.synthesis/chromatin structure
        DNAse I-like superfamily protein |
        Chr3:6352544-6355297 FORWARD LENGTH=445 |
        201606
```

Coefficients for Vitvi17g00356.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.399764	1.013498e-17	***	2.668465e-17	***
SlopeC	0.3739352	0.5235412		0.8753077	
MeanF-MeanC	-0.0245942	0.9339063		0.9822189	
SlopeF-SlopeC	-1.46143	0.1030434		0.9999488	



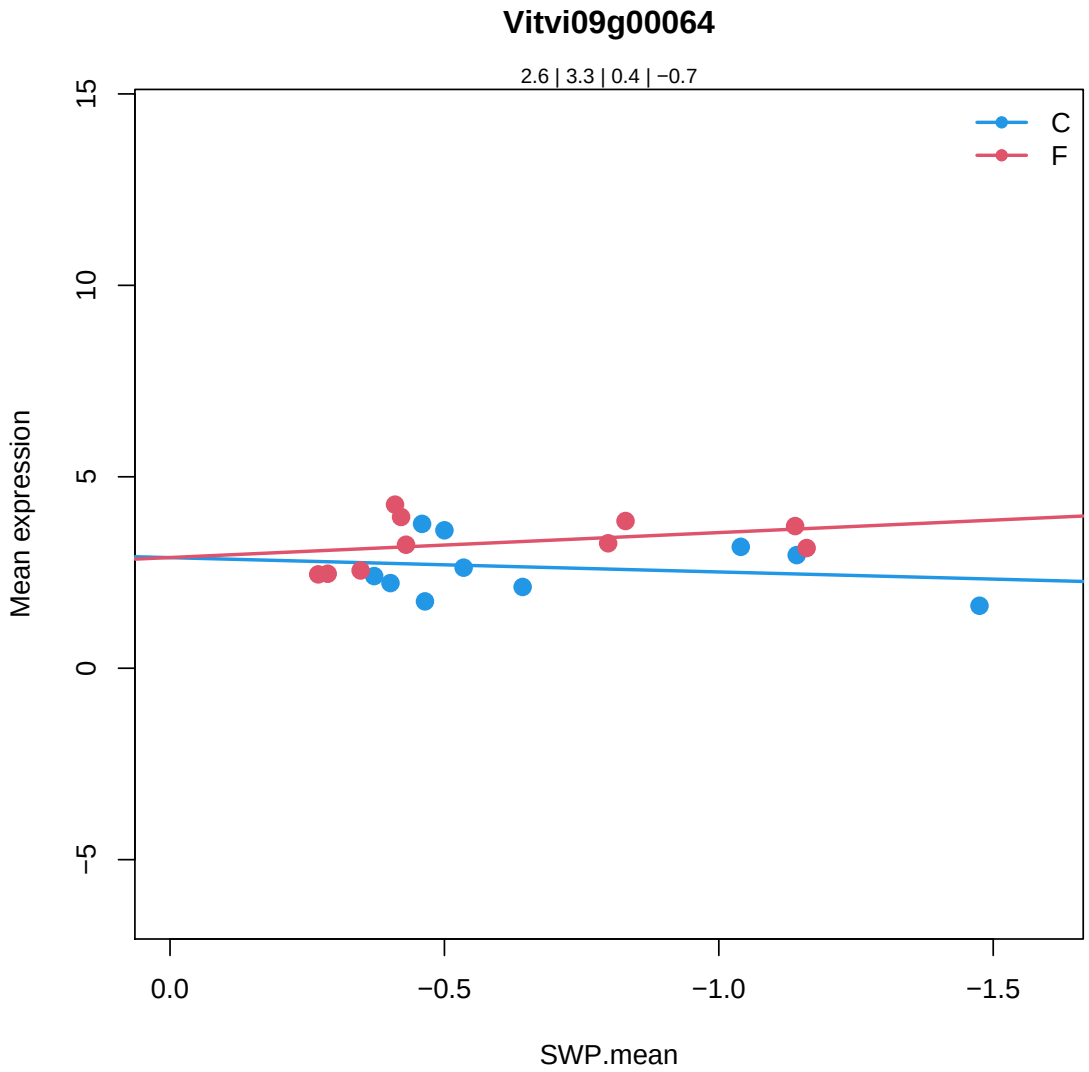
7.6.314 Vitvi09g00064: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00064
        17.7.2
        hormone metabolism.jasmonate.signal transduction
        Jasmonate ZIM domain 2 IPR010399 Tify
```

Coefficients for Vitvi09g00064.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.625212	2.453294e-11	***	3.293676e-11	***
SlopeC	0.3736454	0.5282611		0.8774693	
MeanF-MeanC	0.662728	0.03603067	*	0.1908198	
SlopeF-SlopeC	-1.024882	0.2503601		0.9999488	



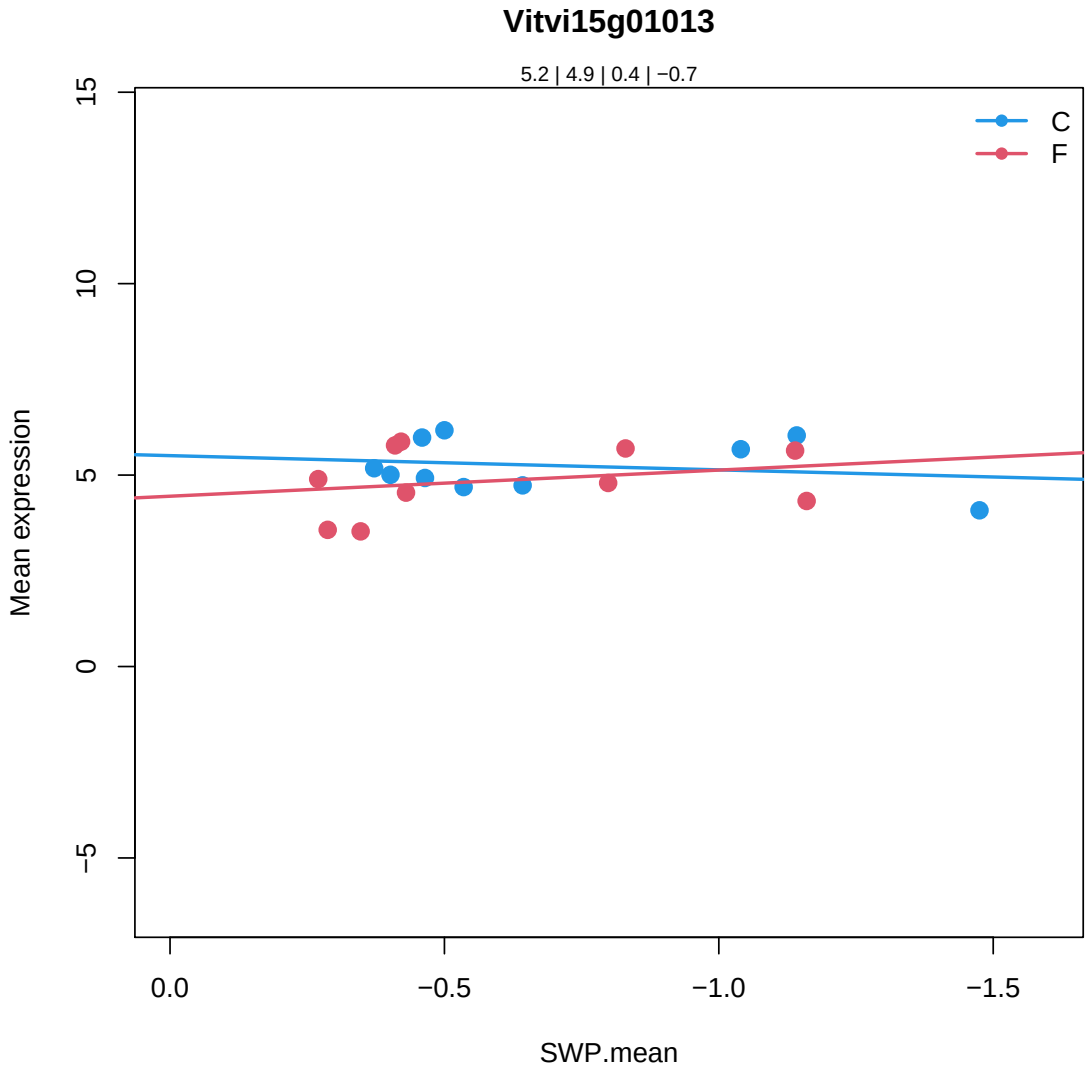
7.6.315 Vitvi15g01013: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g01013
        30.5
        signalling.G-proteins
        extra-large G-like protein%2C putative (DUF3133) |
        Chr2:19039890-19042171 FORWARD LENGTH=668 |
        201606
```

Coefficients for Vitvi15g01013.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.246671	2.690913e-16	***	5.446866e-16	***
SlopeC	0.371545	0.577242		0.8937929	
MeanF-MeanC	-0.383175	0.2634499		0.6252284	
SlopeF-SlopeC	-1.054402	0.2924574		0.9999488	



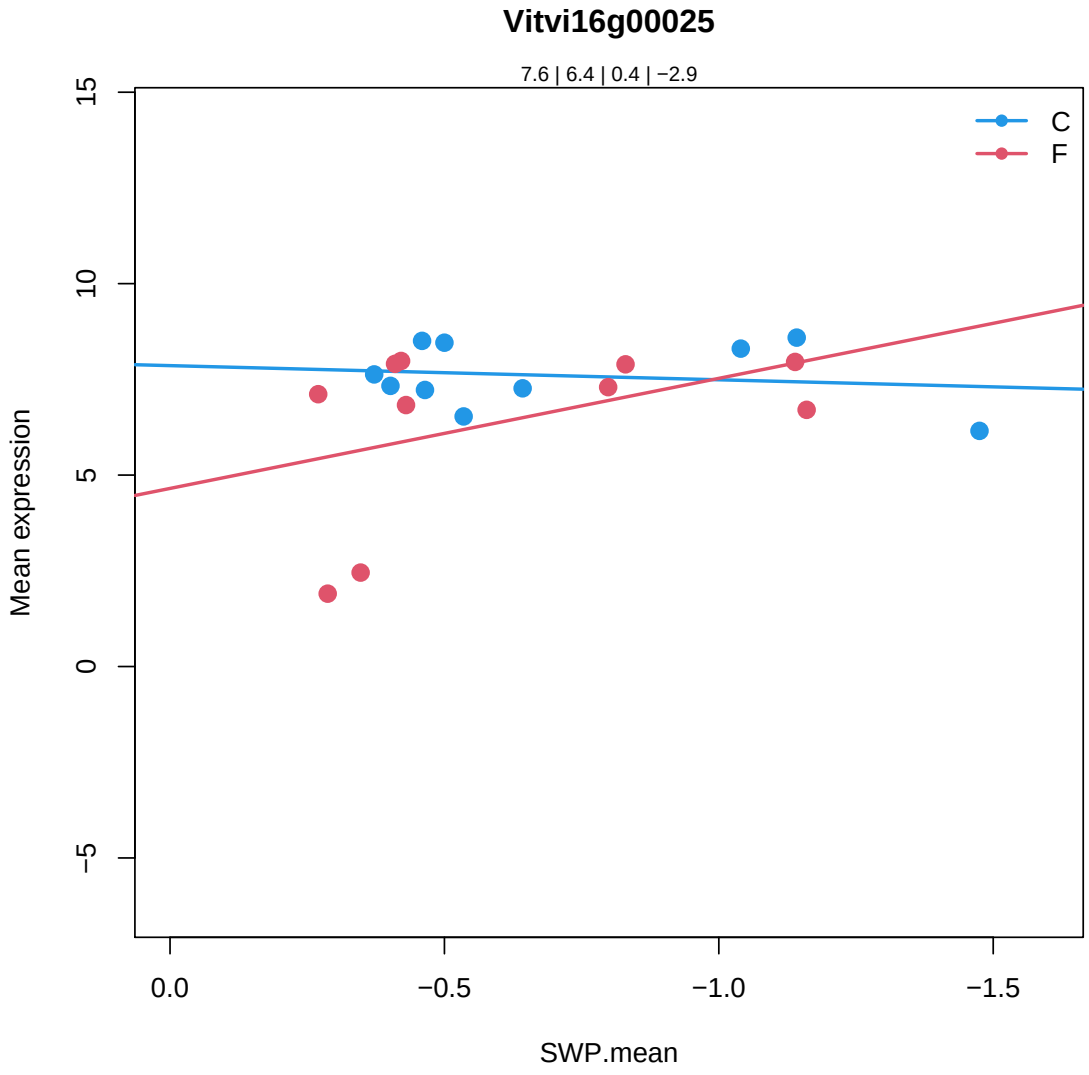
7.6.316 Vitvi16g00025: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g00025
        28.99
        DNA.unspecified
        P-loop containing nucleoside triphosphate hydrolases superfamily prote
        Chr5:14119060-14123078 REVERSE LENGTH=961 |
        201606
```

Coefficients for Vitvi16g00025.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.598812	1.213612e-13	***	1.851824e-13	***
SlopeC	0.36987	0.7761981		0.9513135	
MeanF-MeanC	-1.19583	0.0810236	.	0.3225285	
SlopeF-SlopeC	-3.244807	0.1041917		0.9999488	



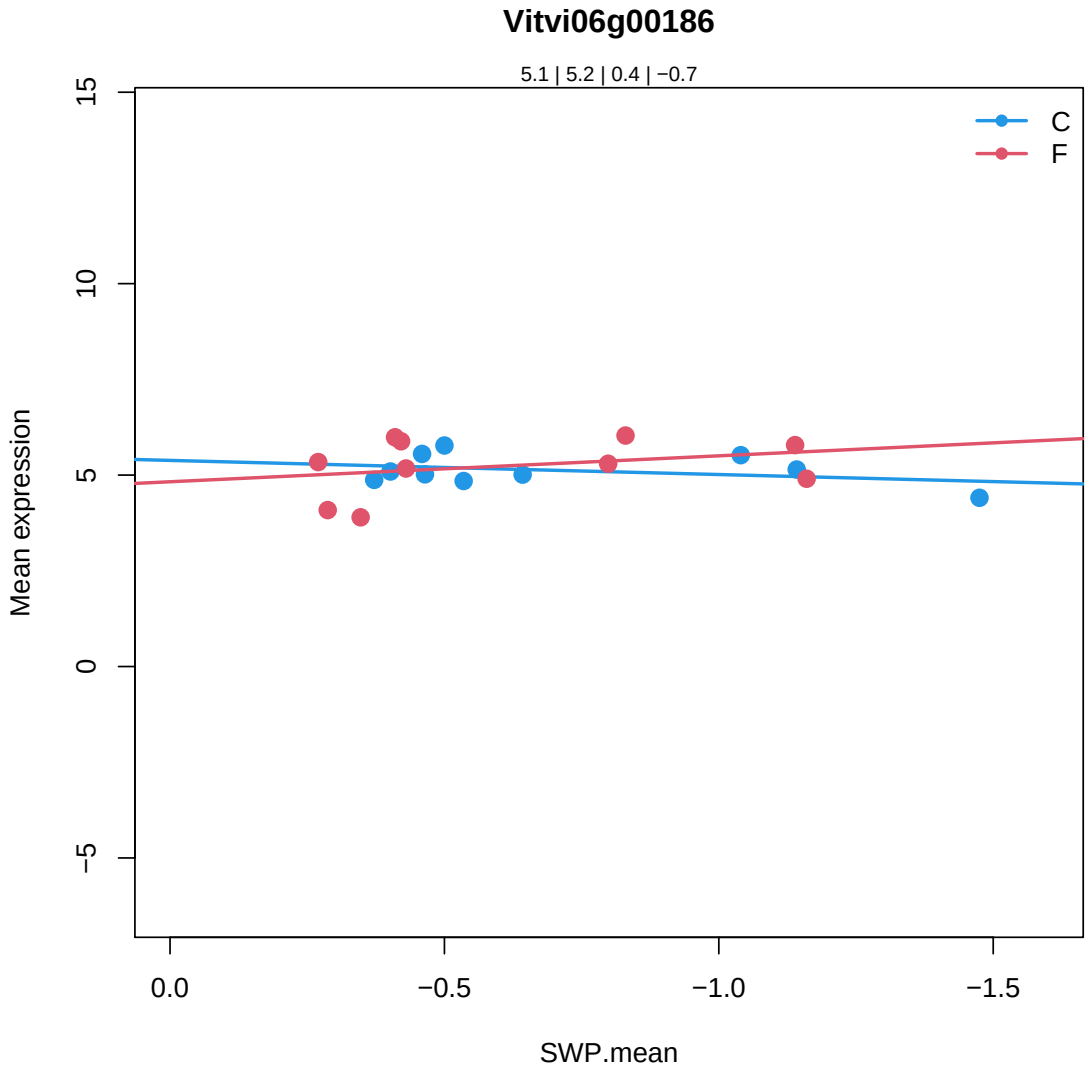
7.6.317 Vitvi06g00186: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00186
        27.3.11
        RNA.regulation of transcription.C2H2 zinc finger family
        A20/AN1-like zinc finger family protein |
        Chr3:4012707-4013189 FORWARD LENGTH=160 |
        201606
```

Coefficients for Vitvi06g00186.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.12398	2.473923e-18	***	7.616147e-18	***
SlopeC	0.3687664	0.4786257		0.8632958	
MeanF-MeanC	0.1140288	0.6652923		0.8898867	
SlopeF-SlopeC	-1.046125	0.1834999		0.9999488	



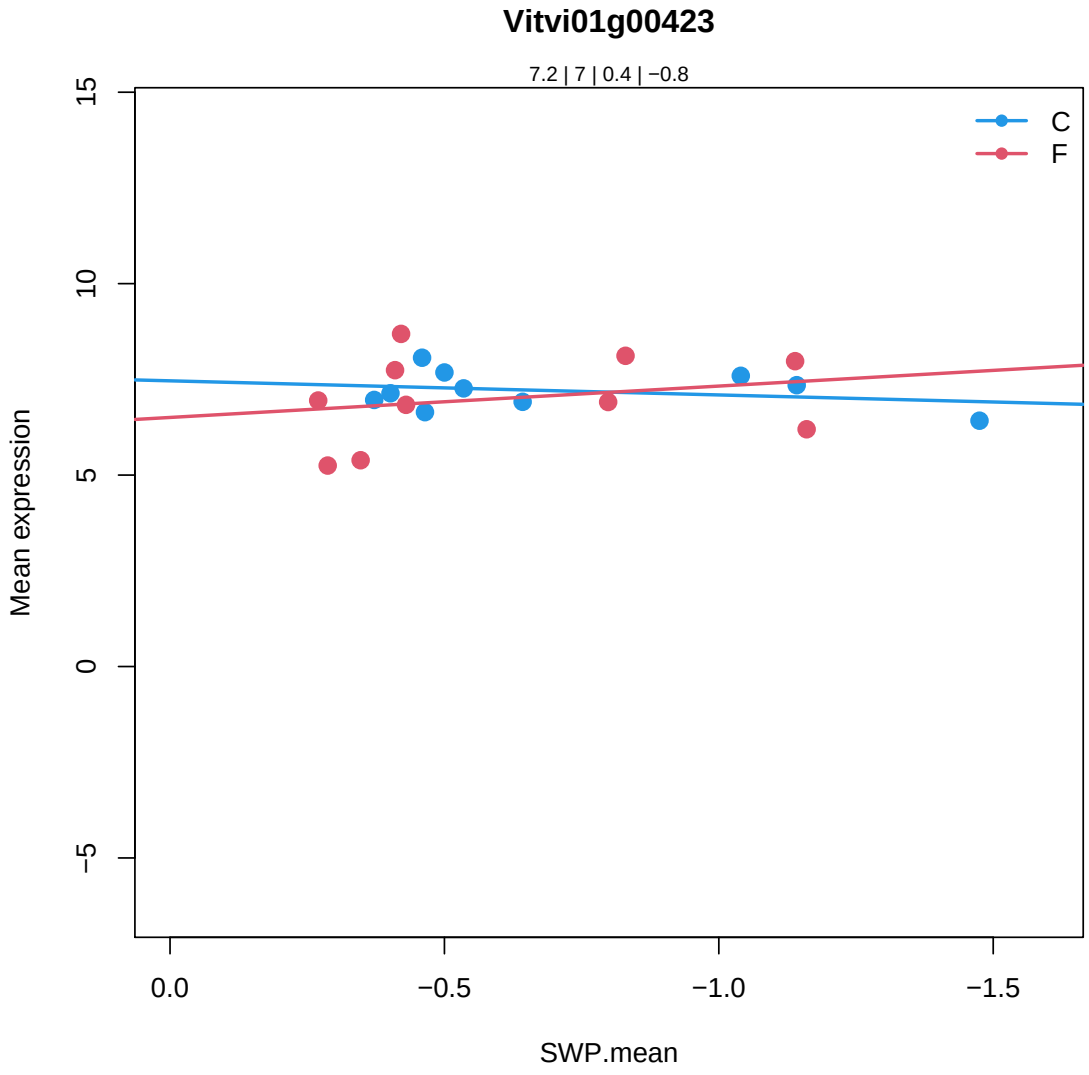
7.6.318 Vitvi01g00423: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00423
        34.6
        transport.sulphate
        sulfate transporter 91 |
        Chr1:8185238-8188954 REVERSE LENGTH=631 |
        201606
```

Coefficients for Vitvi01g00423.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.202505	2.993633e-18	***	9.006899e-18	***
SlopeC	0.3684858	0.6166625		0.9076766	
MeanF-MeanC	-0.198452	0.5959913		0.8584482	
SlopeF-SlopeC	-1.187909	0.2834285		0.9999488	



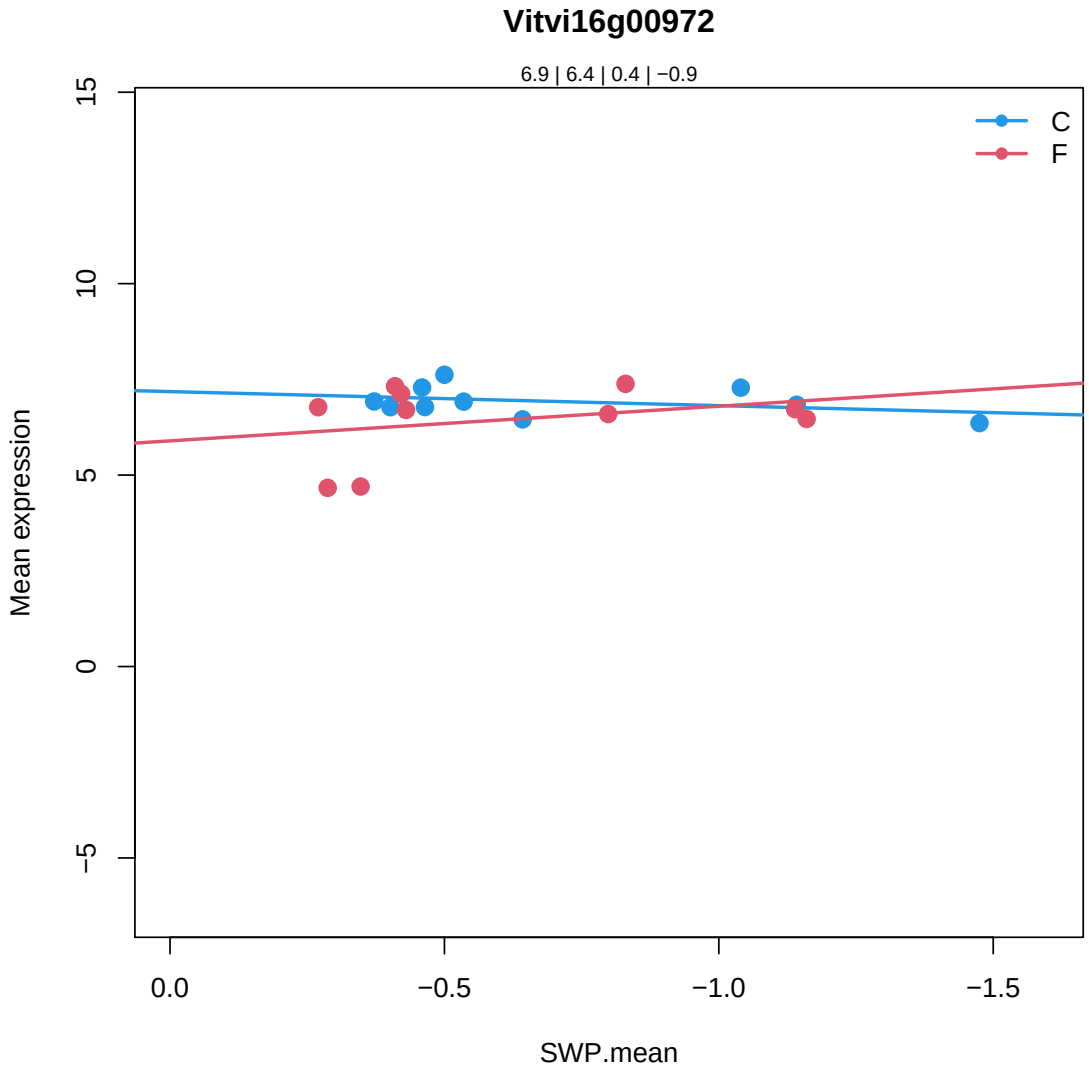
7.6.319 Vitvi16g00972: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g00972
        29.5.5
        protein.degradation.serine protease
        RHOMBOID-like protein 3 |
        Chr5:2274437-2275935 REVERSE LENGTH=346 |
        201606
```

Coefficients for Vitvi16g00972.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.922942	1.598374e-19	***	7.073872e-19	***
SlopeC	0.3663374	0.5520093		0.8875838	
MeanF-MeanC	-0.4781688	0.1353857		0.4400114	
SlopeF-SlopeC	-1.271578	0.1731112		0.9999488	



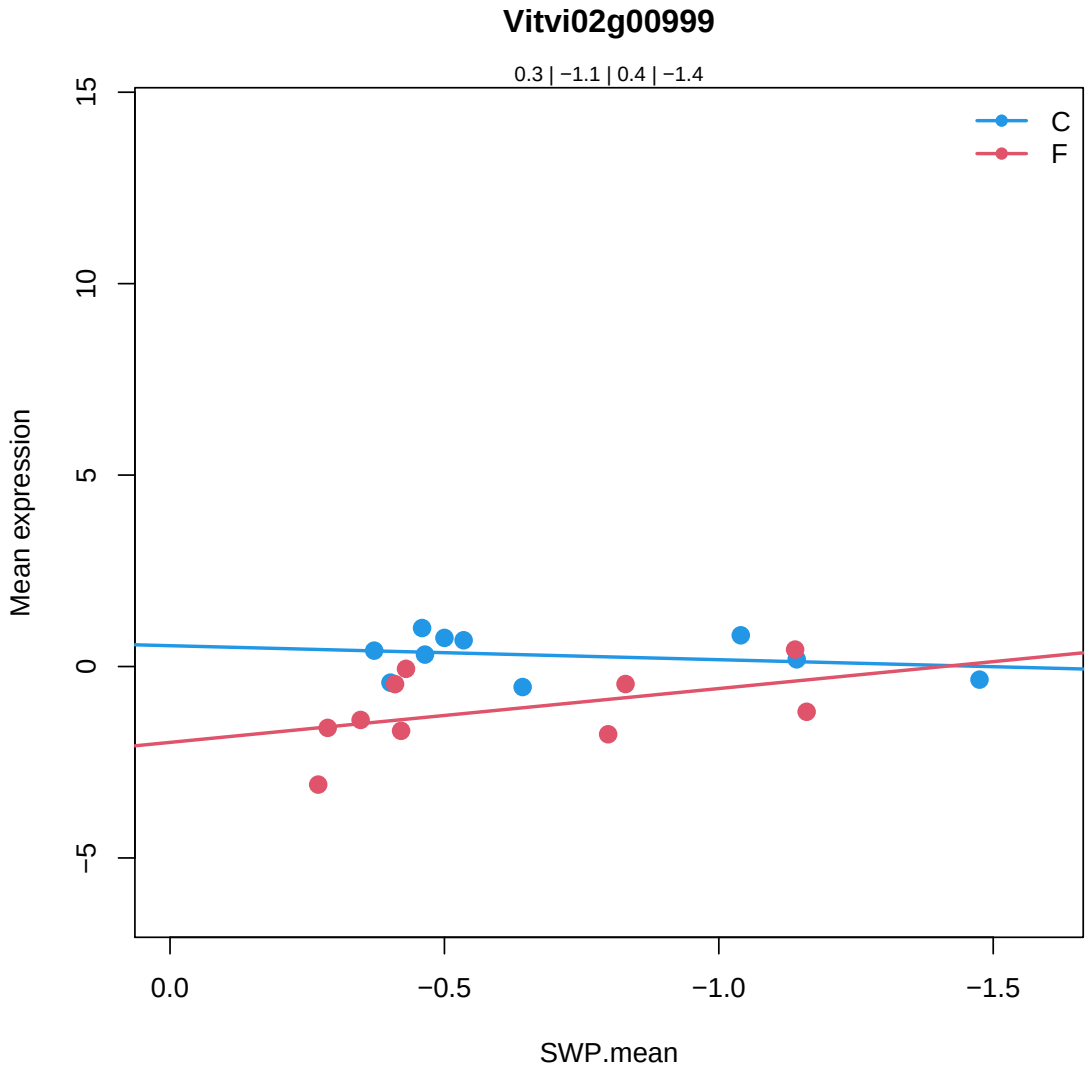
7.6.320 Vitvi02g00999: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00999
        16.8.5.1
        secondary metabolism.flavonoids.isoflavonols.isoflavone reductase
        pinoresinol reductase 1 |
        Chr1:11546472-11547953 REVERSE LENGTH=317 |
        201606
```

Coefficients for Vitvi02g00999.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.2867617	0.221979		0.2273182	
SlopeC	0.365604	0.5703373		0.8912166	
MeanF-MeanC	-1.411732	0.0002519031	***	0.003970534	**
SlopeF-SlopeC	-1.771743	0.07422436	.	0.9999488	



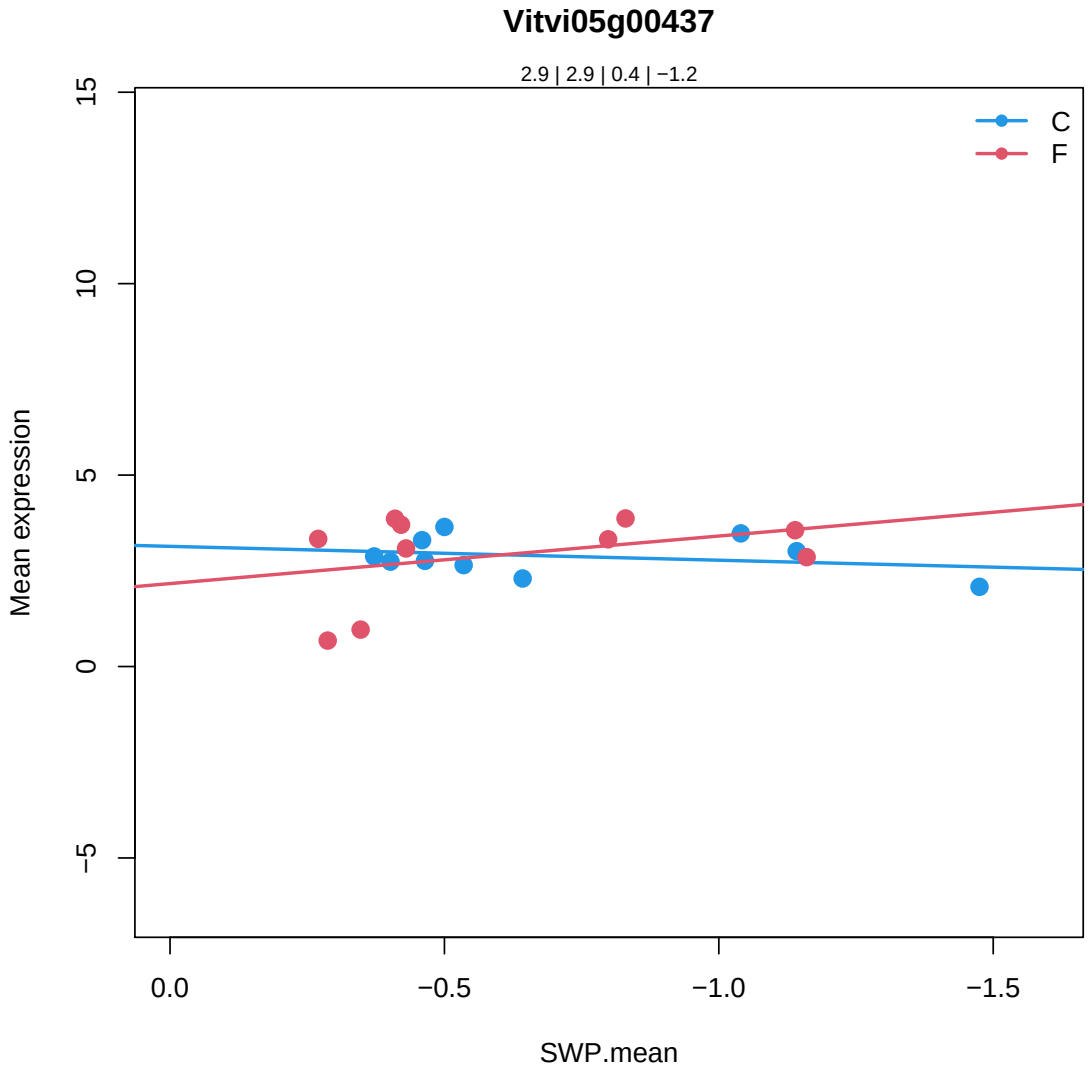
7.6.321 Vitvi05g00437: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00437
        35.2
        not assigned.unknown
        TRICHOME BIREFRINGENCE-LIKE 11 |
        Chr5:6430725-6432035 FORWARD LENGTH=350 |
        201606
```

Coefficients for Vitvi05g00437.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.883662	1.451213e-10	***	1.888125e-10	***
SlopeC	0.3619147	0.6123733		0.9067218	
MeanF-MeanC	0.03885674	0.9145252		0.9772376	
SlopeF-SlopeC	-1.603723	0.1404205		0.9999488	



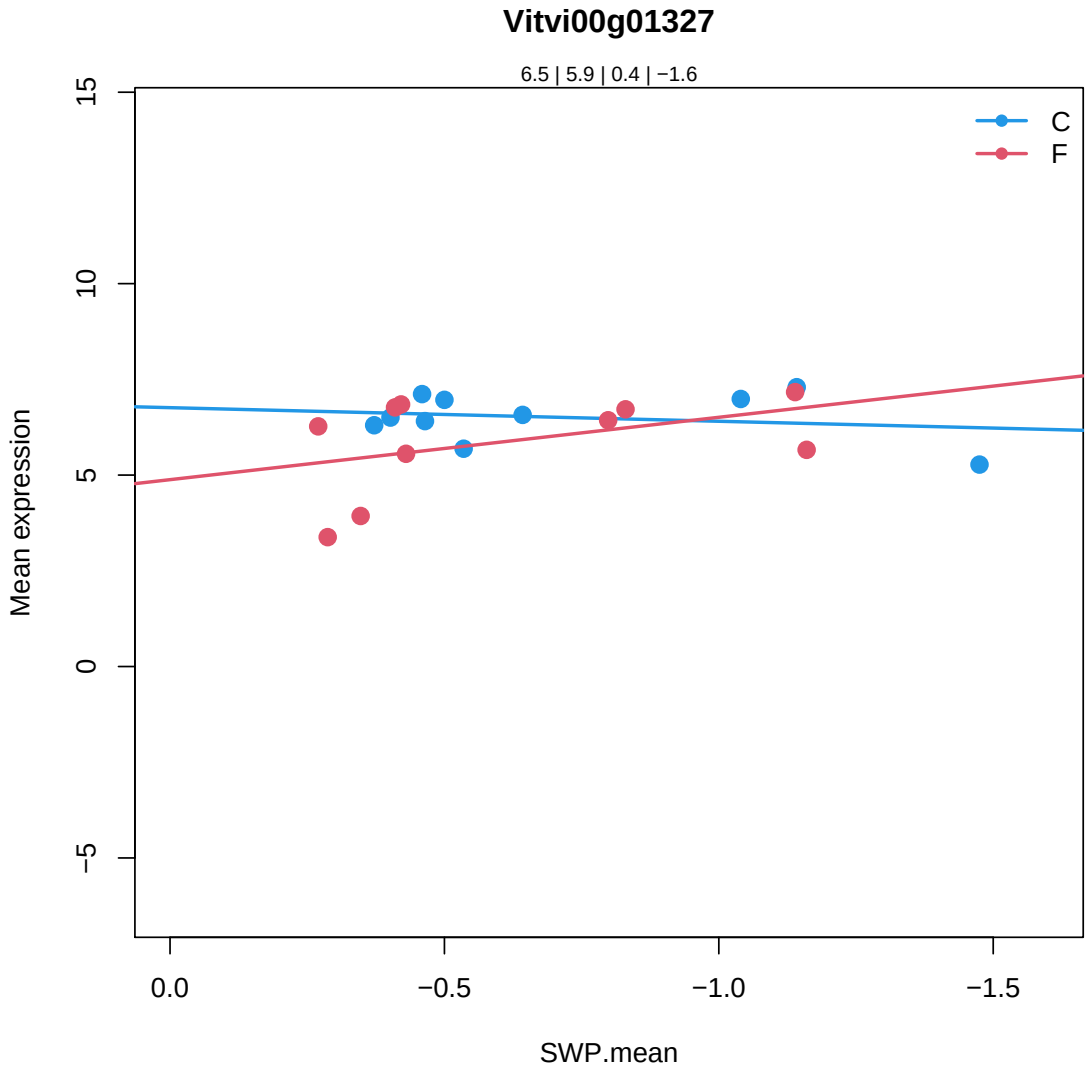
7.6.322 Vitvi00g01327: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi00g01327
        35.2
        not assigned.unknown
        DUF2996 family protein |
        Chr2:1333464-1334438 FORWARD LENGTH=199 |
        201606
```

Coefficients for Vitvi00g01327.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.511038	1.025326e-16	***	2.224312e-16	***
SlopeC	0.3553363	0.6521855		0.9194145	
MeanF-MeanC	-0.6383583	0.1208166		0.4094011	
SlopeF-SlopeC	-1.984372	0.1007387		0.9999488	



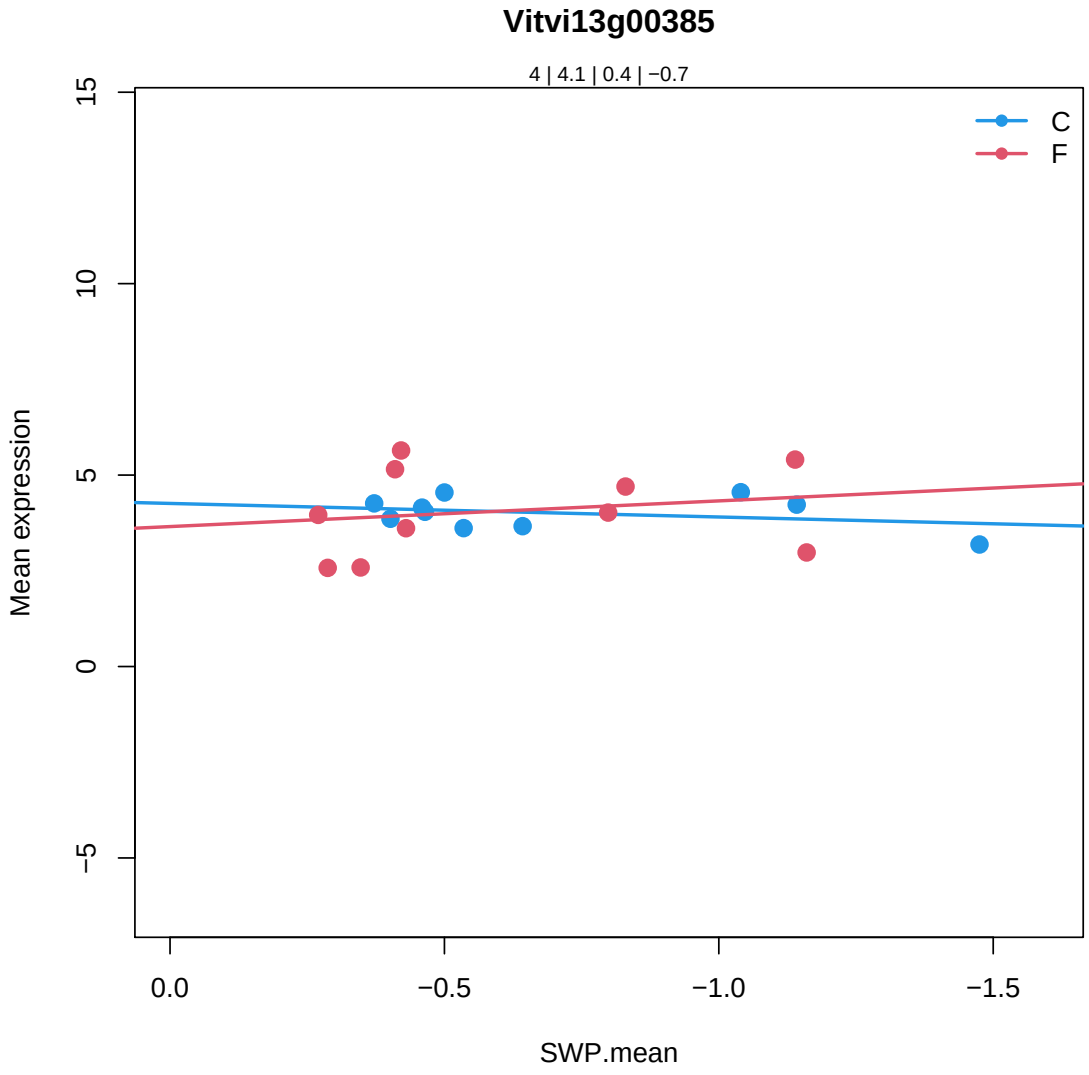
7.6.323 Vitvi13g00385: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00385
        29.5.1
        protein.degradation.subtilases
        subtilase family protein |
        Chr5:23885855-23888673 FORWARD LENGTH=693 |
        201606
```

Coefficients for Vitvi13g00385.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.010245	3.156358e-13	***	4.686267e-13	***
SlopeC	0.3542009	0.6236551		0.9099454	
MeanF-MeanC	0.05325881	0.8842971		0.9695691	
SlopeF-SlopeC	-1.024946	0.3438747		0.9999488	



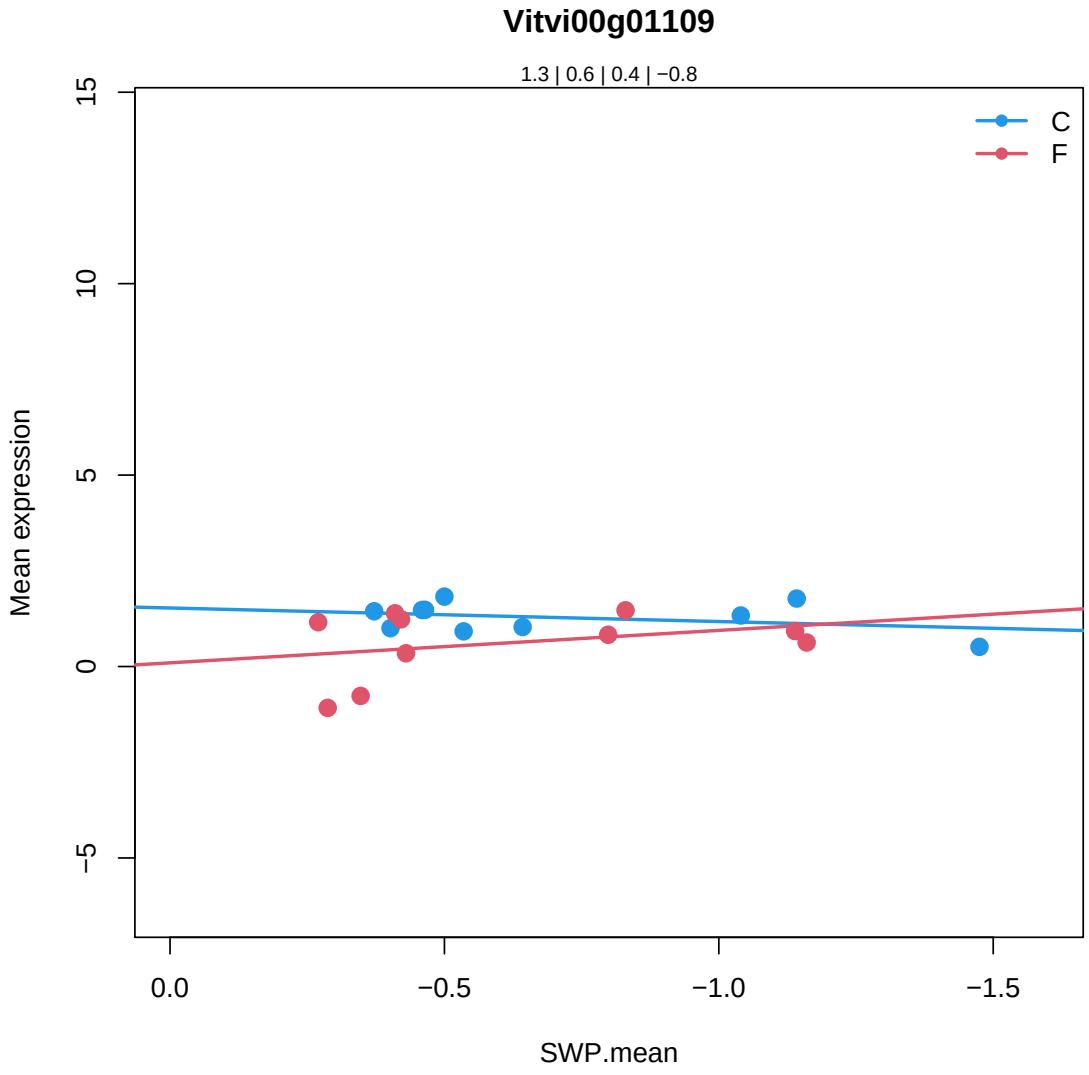
7.6.324 Vitvi00g01109: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi00g01109
        30.11
        signalling.light
        Phototropic-responsive NPH3 family protein |
        Chr5:3217028-3219368 REVERSE LENGTH=622 |
        201606
```

Coefficients for Vitvi00g01109.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.279842	2.83005e-06	***	3.23307e-06	***
SlopeC	0.3539943	0.5386496		0.8827113	
MeanF-MeanC	-0.6672536	0.03046004	*	0.170751	
SlopeF-SlopeC	-1.201884	0.1684304		0.9999488	



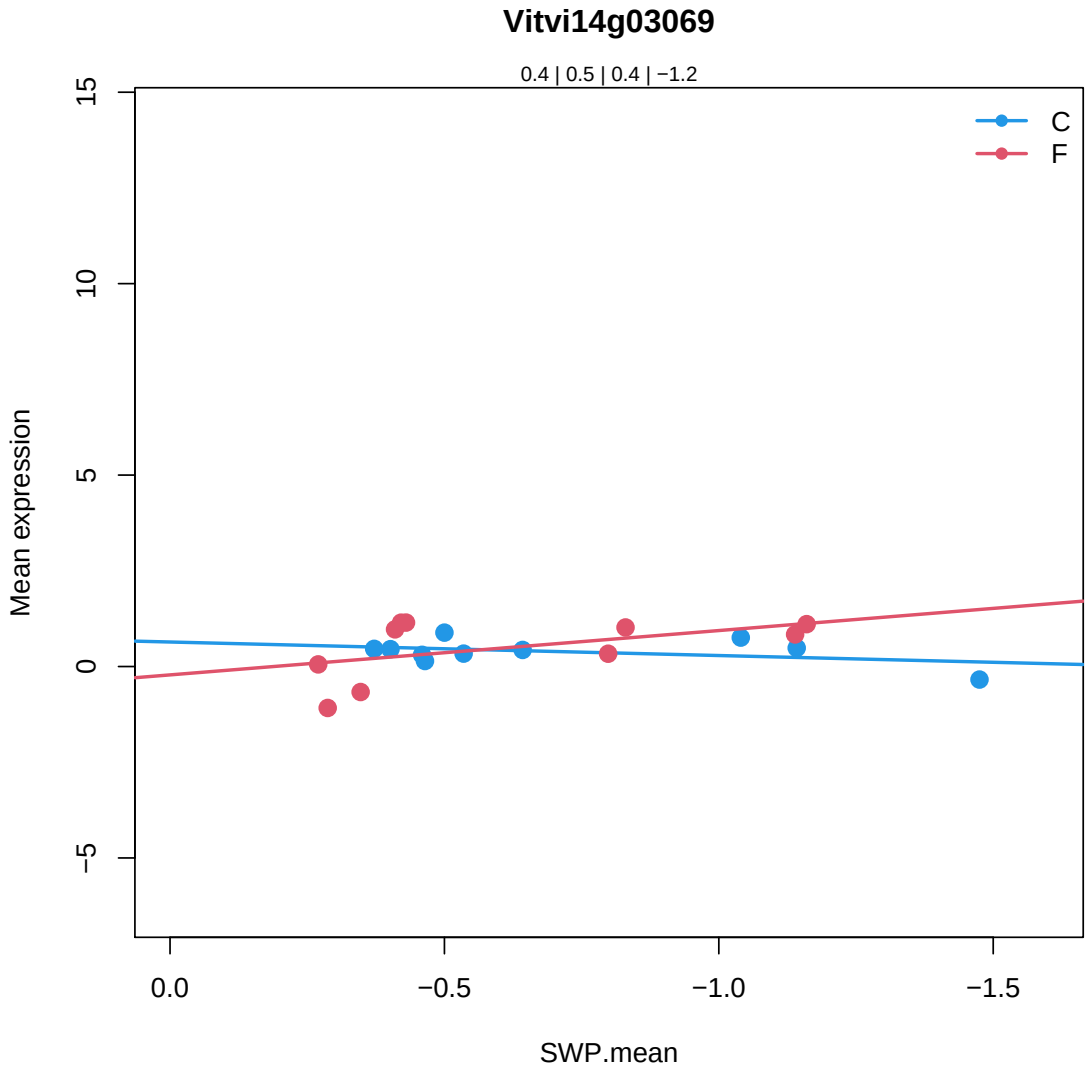
7.6.325 Vitvi14g03069: + type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g03069
        3.5
        minor CHO metabolism.others
        Leucine-rich repeat receptor-like protein kinase family protein |
        Chr4:5637467-5640496 REVERSE LENGTH=1009 |
        201606
```

Coefficients for Vitvi14g03069.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3917881	0.03656145	*	0.03819008	*
SlopeC	0.3534343	0.4774658		0.8625688	
MeanF-MeanC	0.09483512	0.7064618		0.9082497	
SlopeF-SlopeC	-1.511616	0.04992838	*	0.9999488	



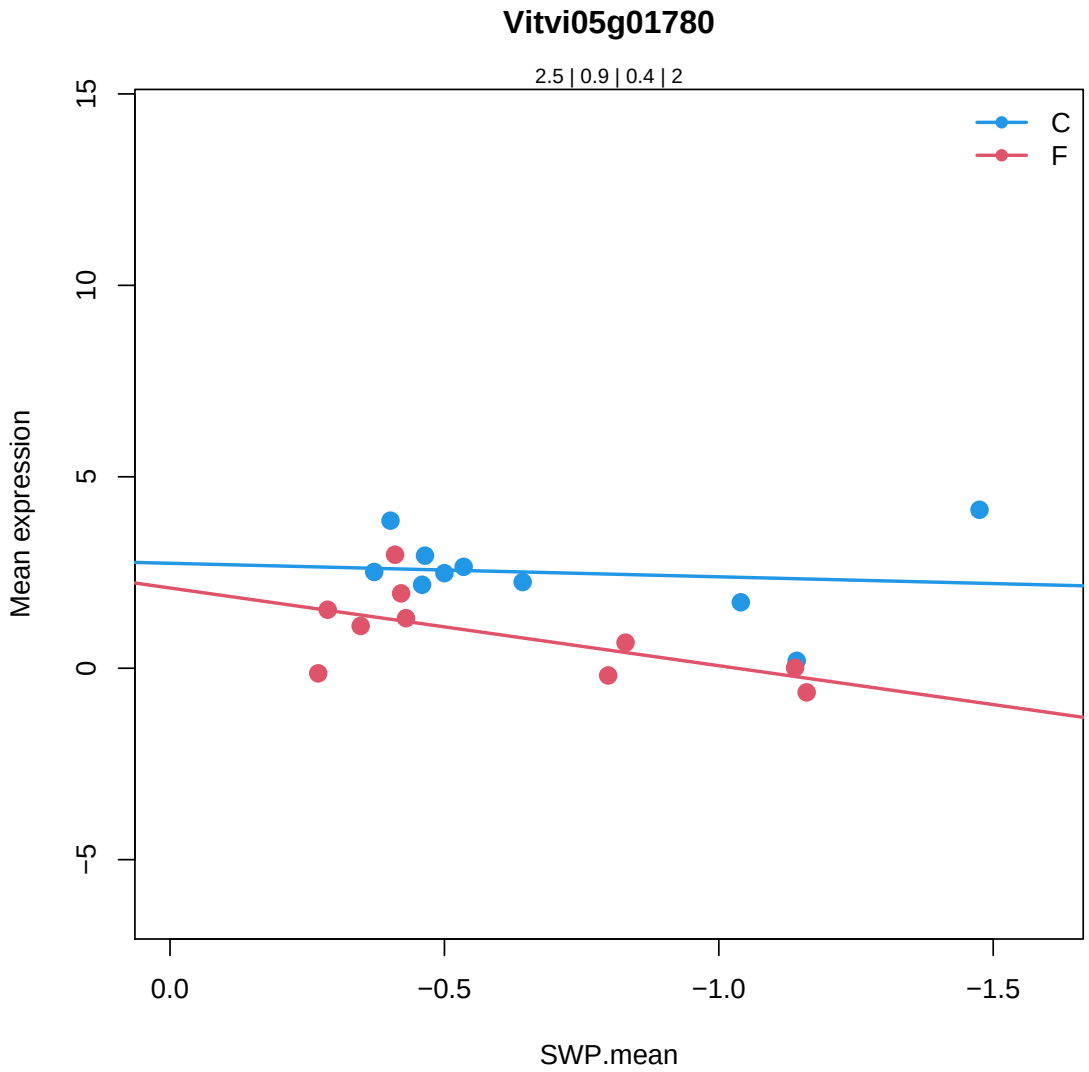
7.6.326 Vitvi05g01780: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01780
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi05g01780.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.492285	3.342069e-08	***	4.017336e-08	***
SlopeC	0.3531567	0.6739755		0.9246326	
MeanF-MeanC	-1.633824	0.0008349926	***	0.01076731	*
SlopeF-SlopeC	1.677069	0.1876866		0.9999488	



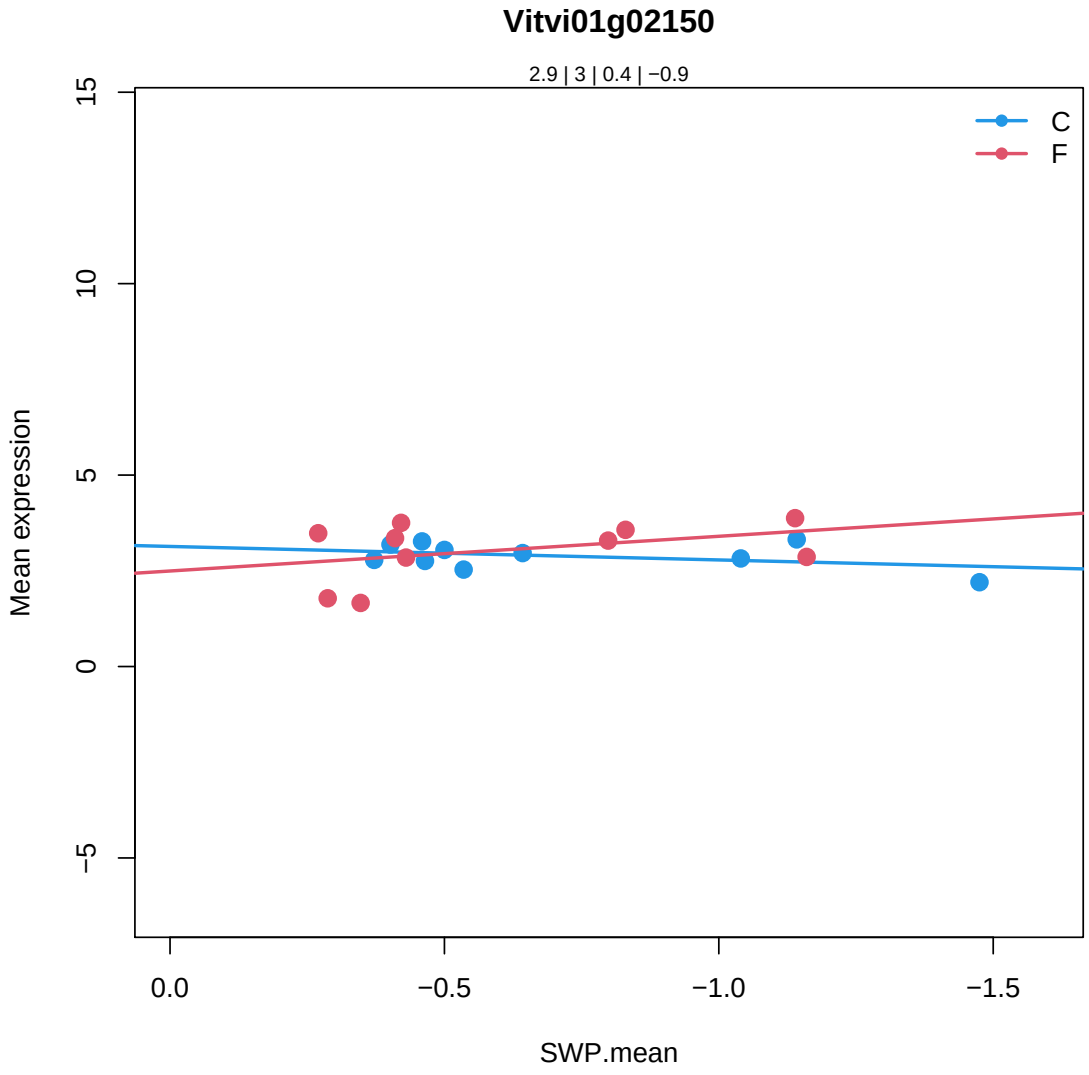
7.6.327 Vitvi01g02150: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g02150
        31.2
        cell.division
        hAT dimerization domain-containing protein |
        Chr3:5972793-5975684 REVERSE LENGTH=877 |
        201606
```

Coefficients for Vitvi01g02150.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.887924	1.499355e-13	***	2.272591e-13	***
SlopeC	0.3525228	0.4827176		0.8645993	
MeanF-MeanC	0.1591063	0.5326157		0.8257793	
SlopeF-SlopeC	-1.259108	0.1009042		0.9999488	



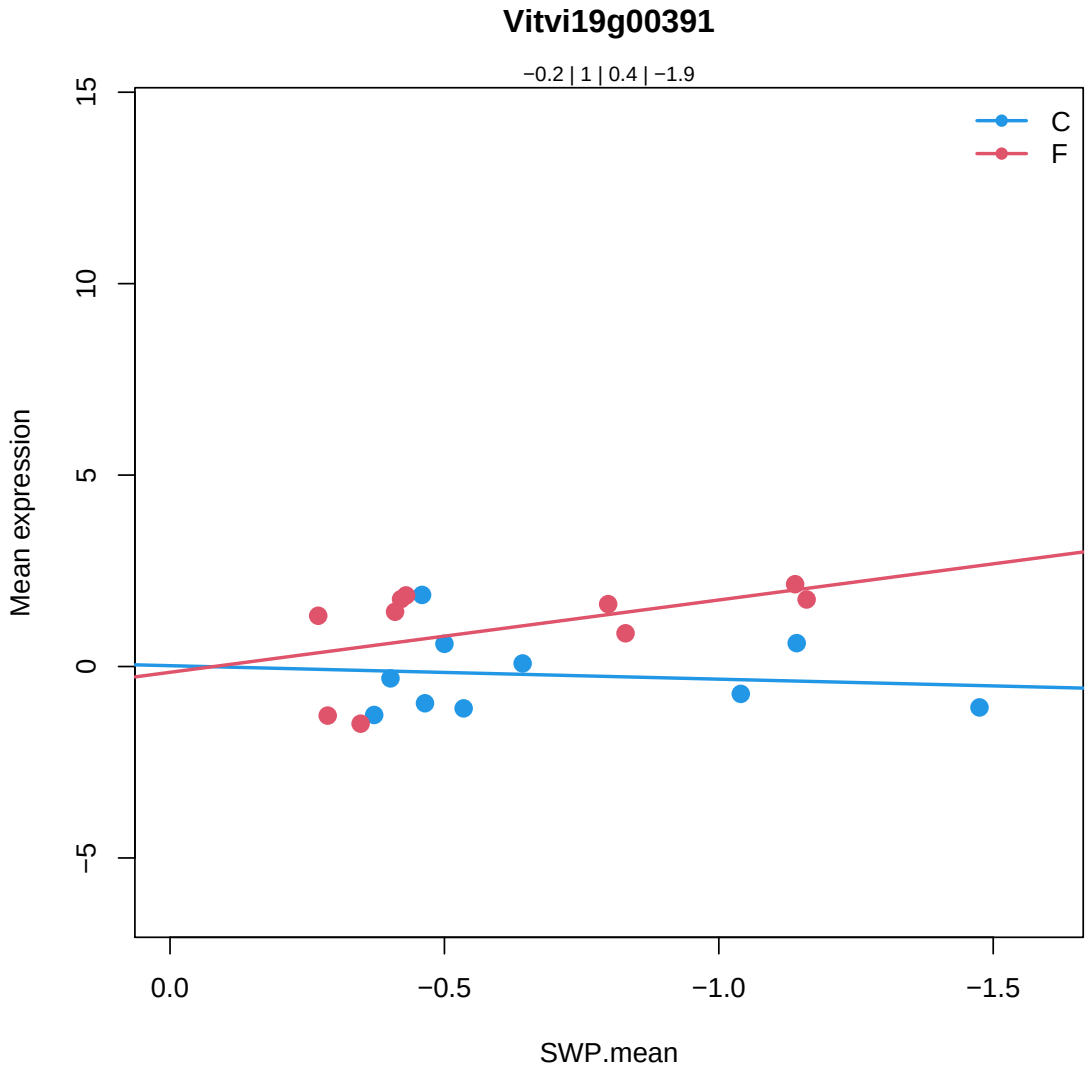
7.6.328 Vitvi19g00391: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g00391
        16.1.5
        secondary metabolism.isoprenoids.terpenoids
        terpene synthase 21 |
        Chr5:8092969-8095128 FORWARD LENGTH=545 |
        201606
```

Coefficients for Vitvi19g00391.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.2259877	0.4867558		0.4929328	
SlopeC	0.3515541	0.6962291		0.9317974	
MeanF-MeanC	1.225536	0.01285799	*	0.09162296	.
SlopeF-SlopeC	-2.240139	0.1047179		0.9999488	



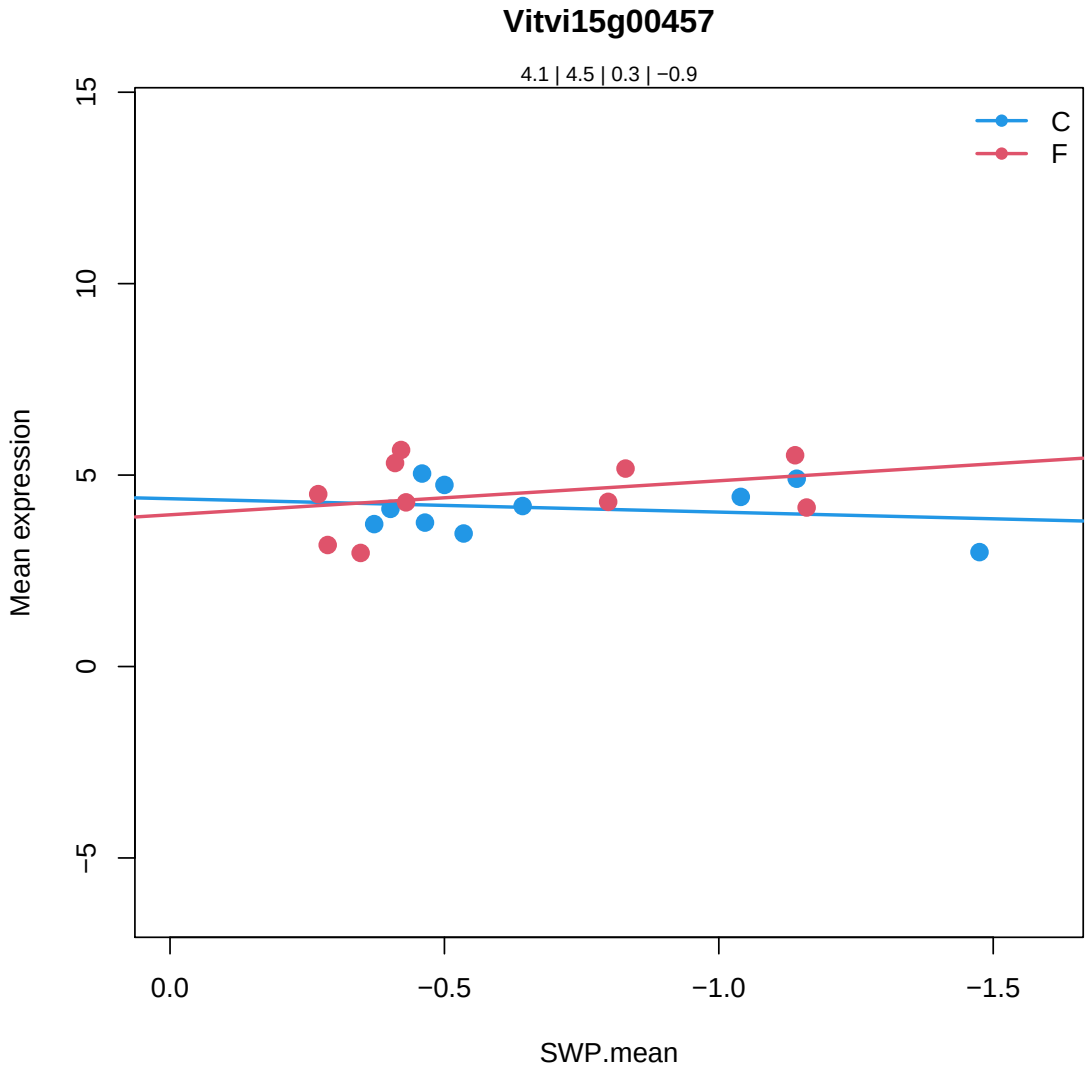
7.6.329 Vitvi15g00457: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g00457
        35.2
        not assigned.unknown
        hypothetical protein |
        Chr2:18408845-18409786 FORWARD LENGTH=313 |
        201606
```

Coefficients for Vitvi15g00457.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.136566	3.746677e-14	***	5.956075e-14	***
SlopeC	0.3498083	0.6012796		0.9040845	
MeanF-MeanC	0.36744	0.2852163		0.650399	
SlopeF-SlopeC	-1.238076	0.2207545		0.9999488	



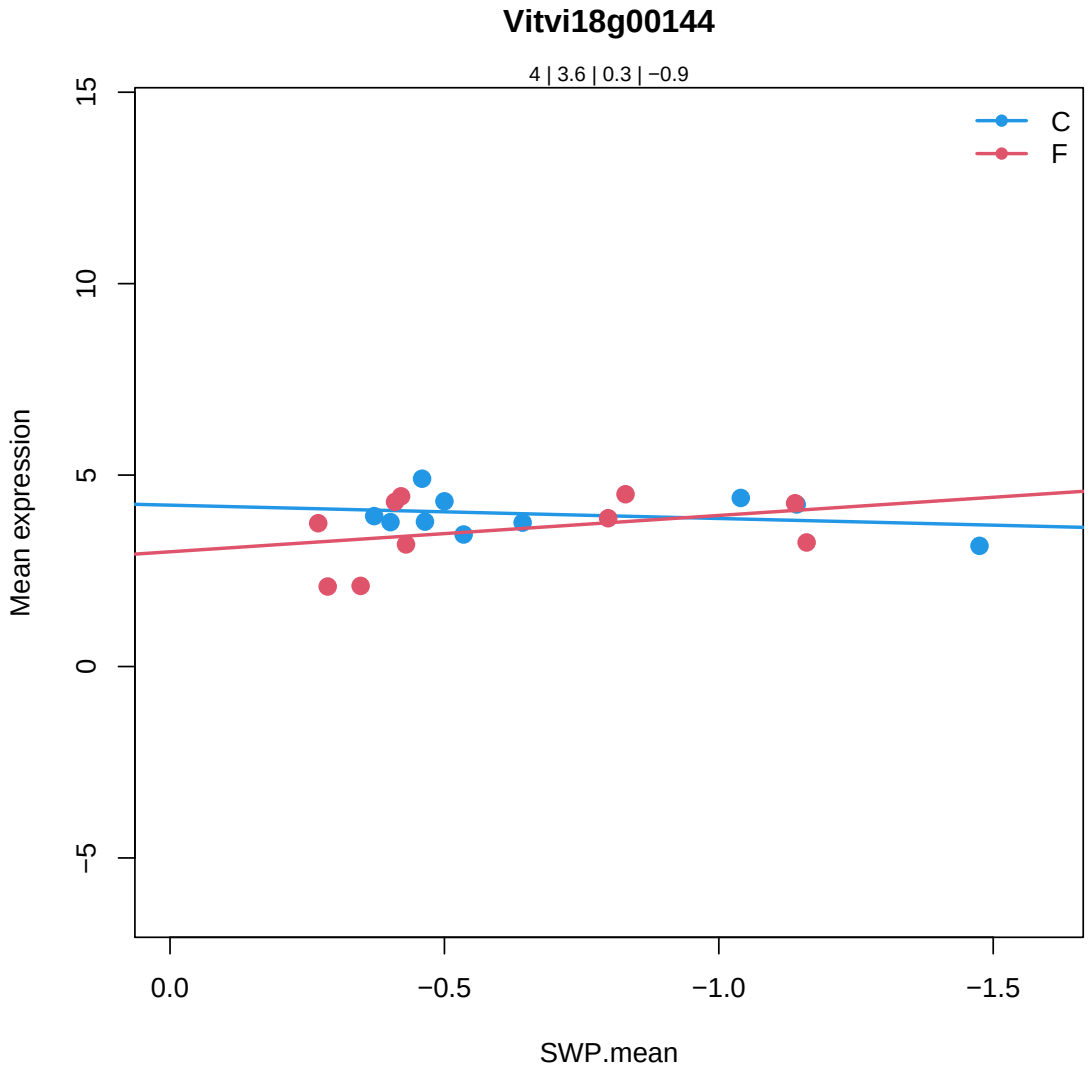
7.6.330 Vitvi18g00144: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00144
        2.2.2.1
        major CHO metabolism.degradation.starch.starch cleavage.alpha amylase
        alpha-amylase-like 2 |
        Chr1:28561647-28563914 FORWARD LENGTH=413 |
        201606
```

Coefficients for Vitvi18g00144.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.969593	1.144332e-14	***	1.901025e-14	***
SlopeC	0.3483611	0.5654591		0.8905966	
MeanF-MeanC	-0.3946886	0.2070056		0.5518943	
SlopeF-SlopeC	-1.297506	0.1585455		0.9999488	



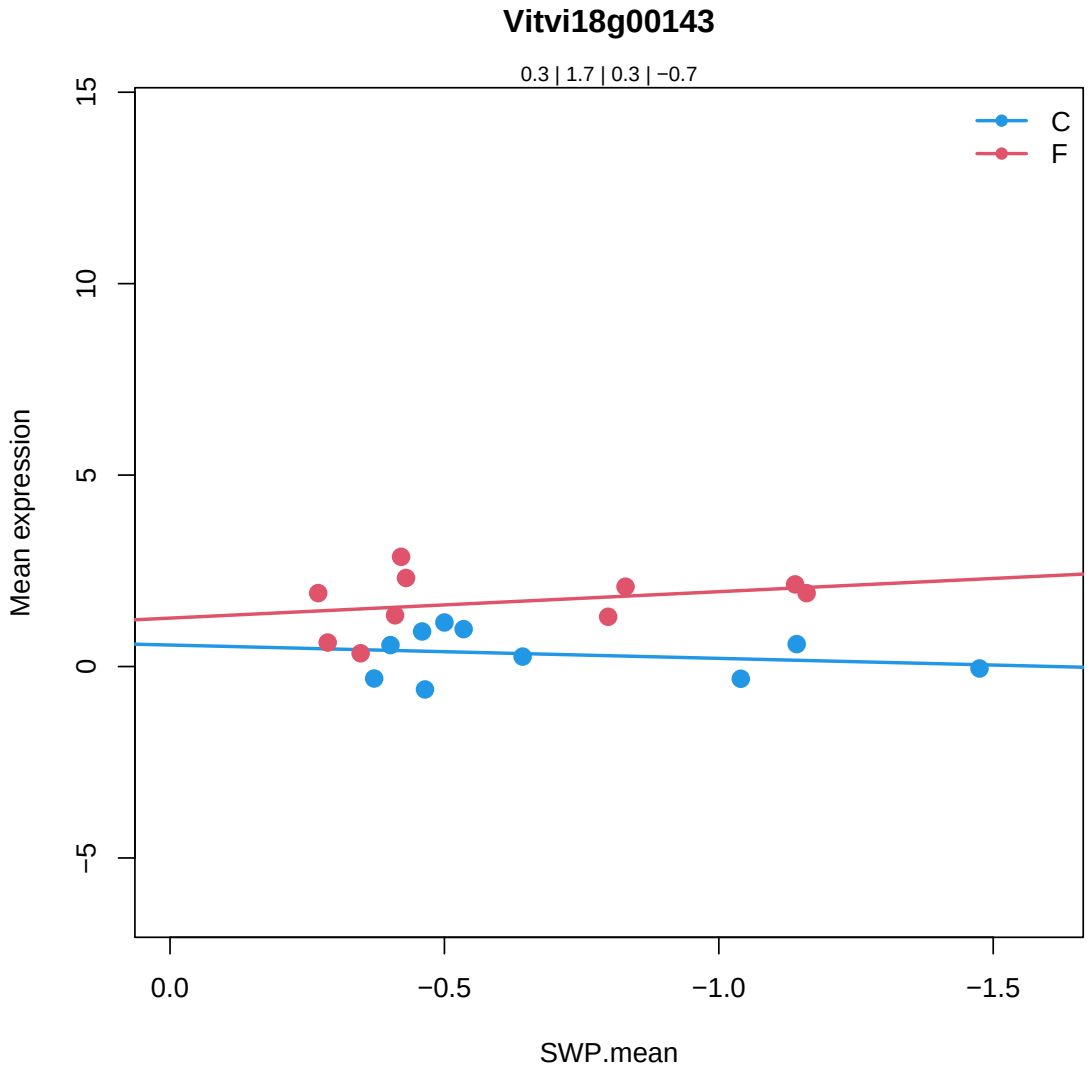
7.6.331 Vitvi18g00143: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00143
        35.2
        not assigned.unknown
        rho guanyl-nucleotide exchange factor 1 |
        Chr4:17986643-17988659 FORWARD LENGTH=548 |
        201606
```

Coefficients for Vitvi18g00143.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3160798	0.1475874		0.1519129	
SlopeC	0.3482538	0.5580887		0.8894103	
MeanF-MeanC	1.368841	0.0001474706	***	0.002494237	**
SlopeF-SlopeC	-1.038647	0.2462019		0.9999488	



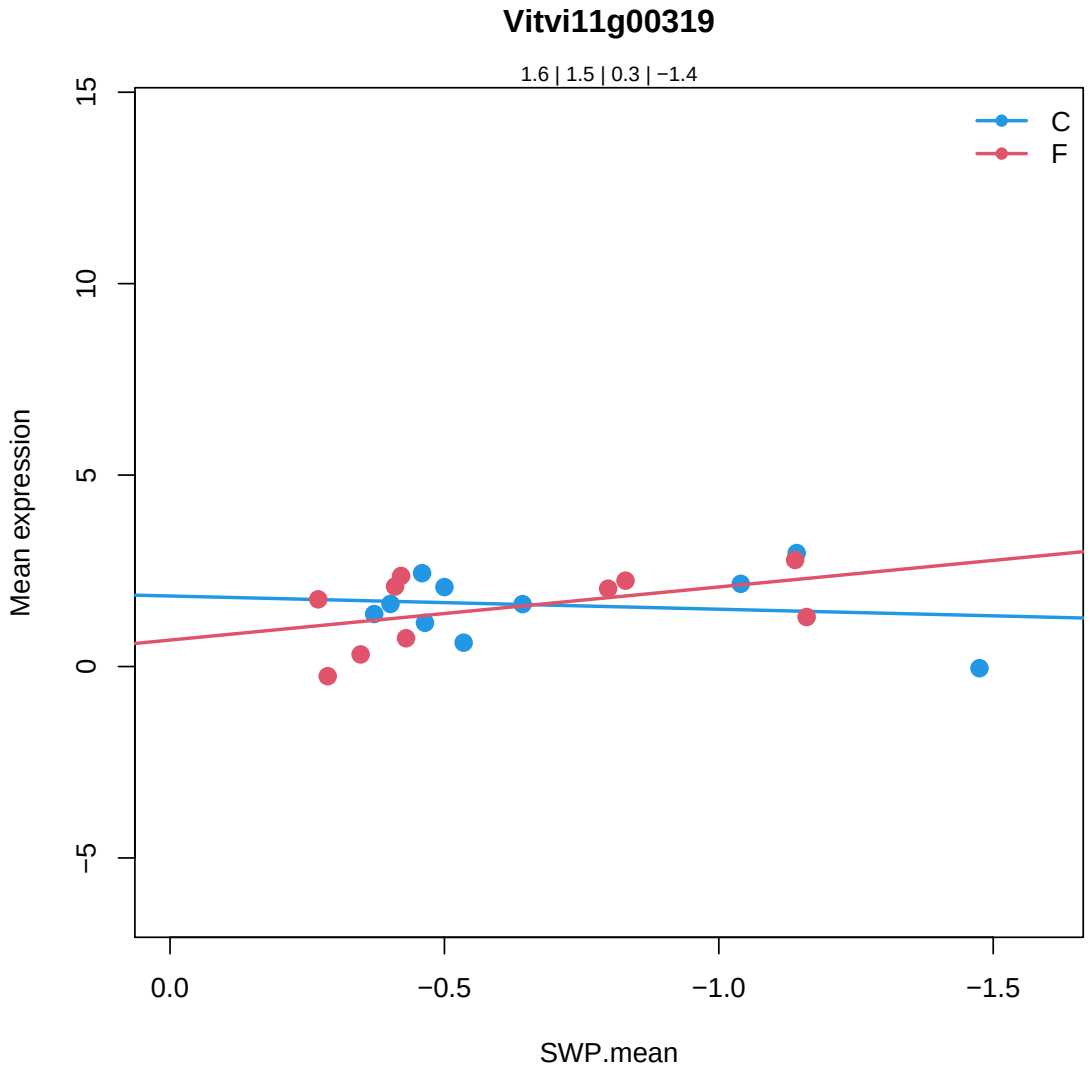
7.6.332 Vitvi11g00319: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00319
        30.5
        signalling.G-proteins
        RHO guanyl-nucleotide exchange factor 9 |
        Chr4:7680153-7682414 FORWARD LENGTH=517 |
        201606
```

Coefficients for Vitvi11g00319.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.599016	4.569264e-06	***	5.196204e-06	***
SlopeC	0.3453514	0.6419962		0.9156498	
MeanF-MeanC	-0.06301957	0.8671577		0.9650648	
SlopeF-SlopeC	-1.732601	0.126575		0.9999488	



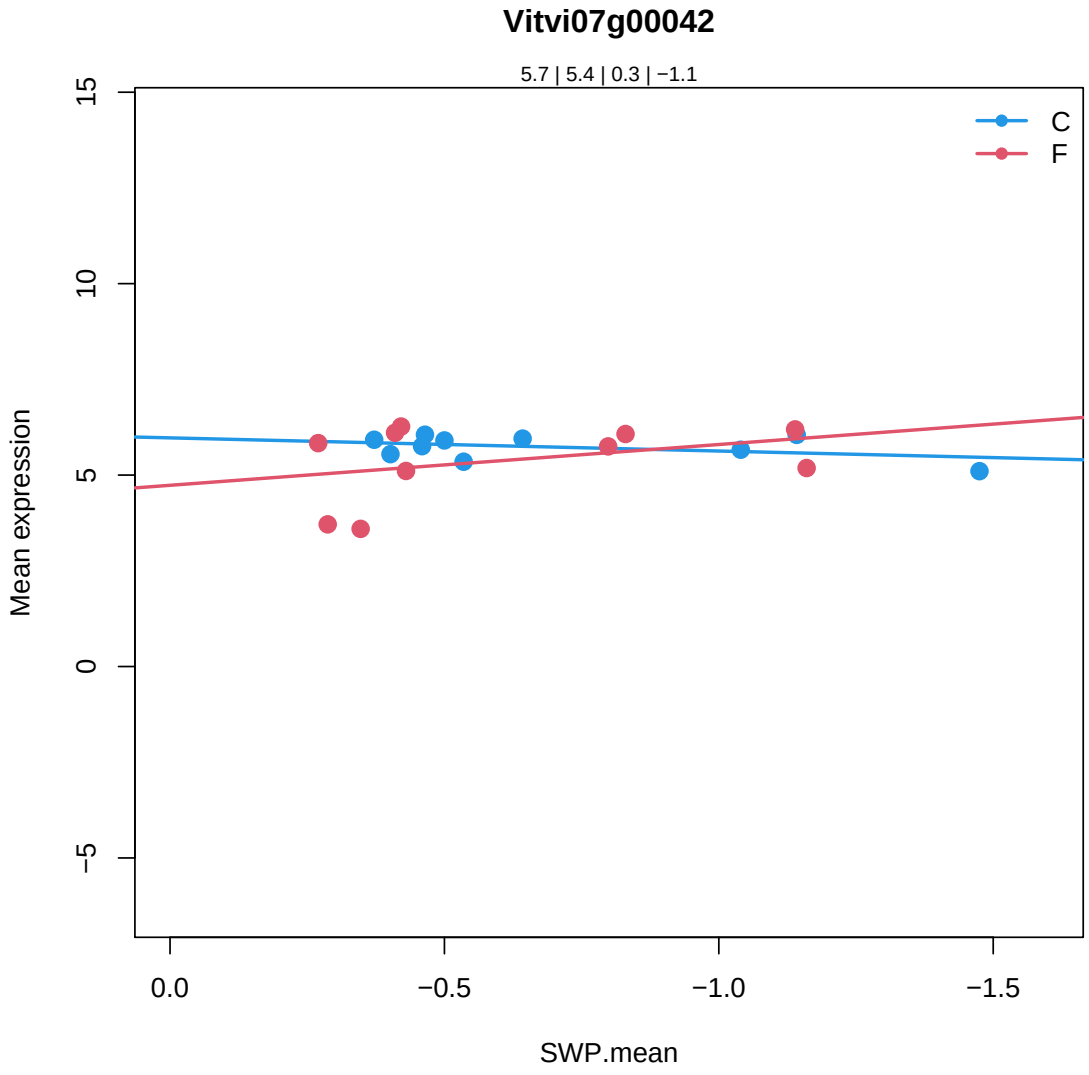
7.6.333 Vitvi07g00042: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g00042
        27.3.40
        RNA.regulation of transcription.AUX/IAA family
        indole-3-acetic acid inducible 14 |
        Chr4:8349005-8349923 REVERSE LENGTH=196 |
        201606
```

Coefficients for Vitvi07g00042.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.730013	5.182514e-18	***	1.462271e-17	***
SlopeC	0.3434569	0.5681681		0.8911394	
MeanF-MeanC	-0.3479508	0.2606733		0.6222683	
SlopeF-SlopeC	-1.408783	0.1247782		0.9999488	



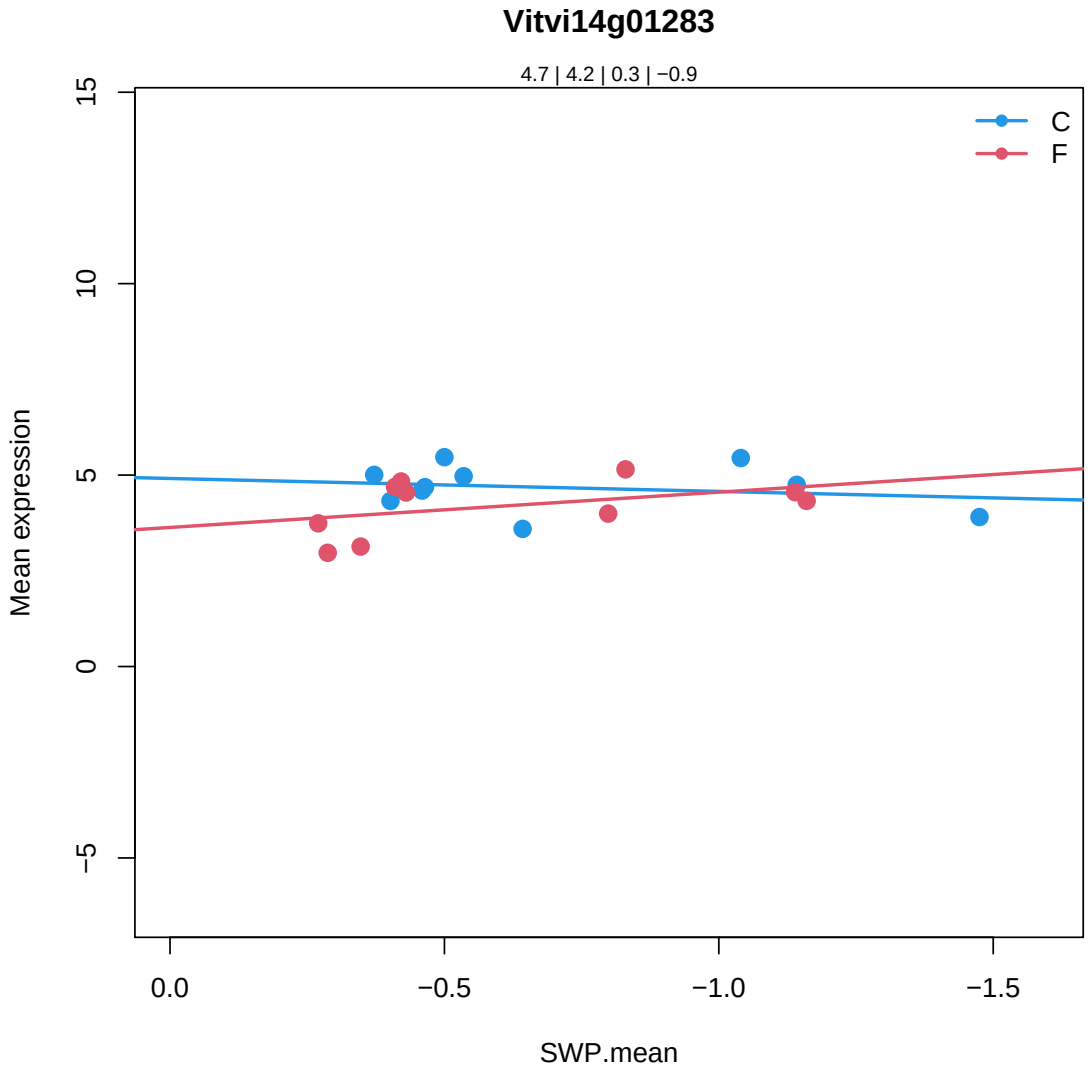
7.6.334 Vitvi14g01283: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01283
        13.2.2.2
        amino acid metabolism.degradation.glutamate family.proline
        Methylenetetrahydrofolate reductase family protein |
        Chr5:15501340-15503696 FORWARD LENGTH=466 |
        201606
```

Coefficients for Vitvi14g01283.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.673647	6.714176e-17	***	1.504299e-16	***
SlopeC	0.3380086	0.5428889		0.8847006	
MeanF-MeanC	-0.4801575	0.0983824	.	0.361249	
SlopeF-SlopeC	-1.259217	0.1363499		0.9999488	



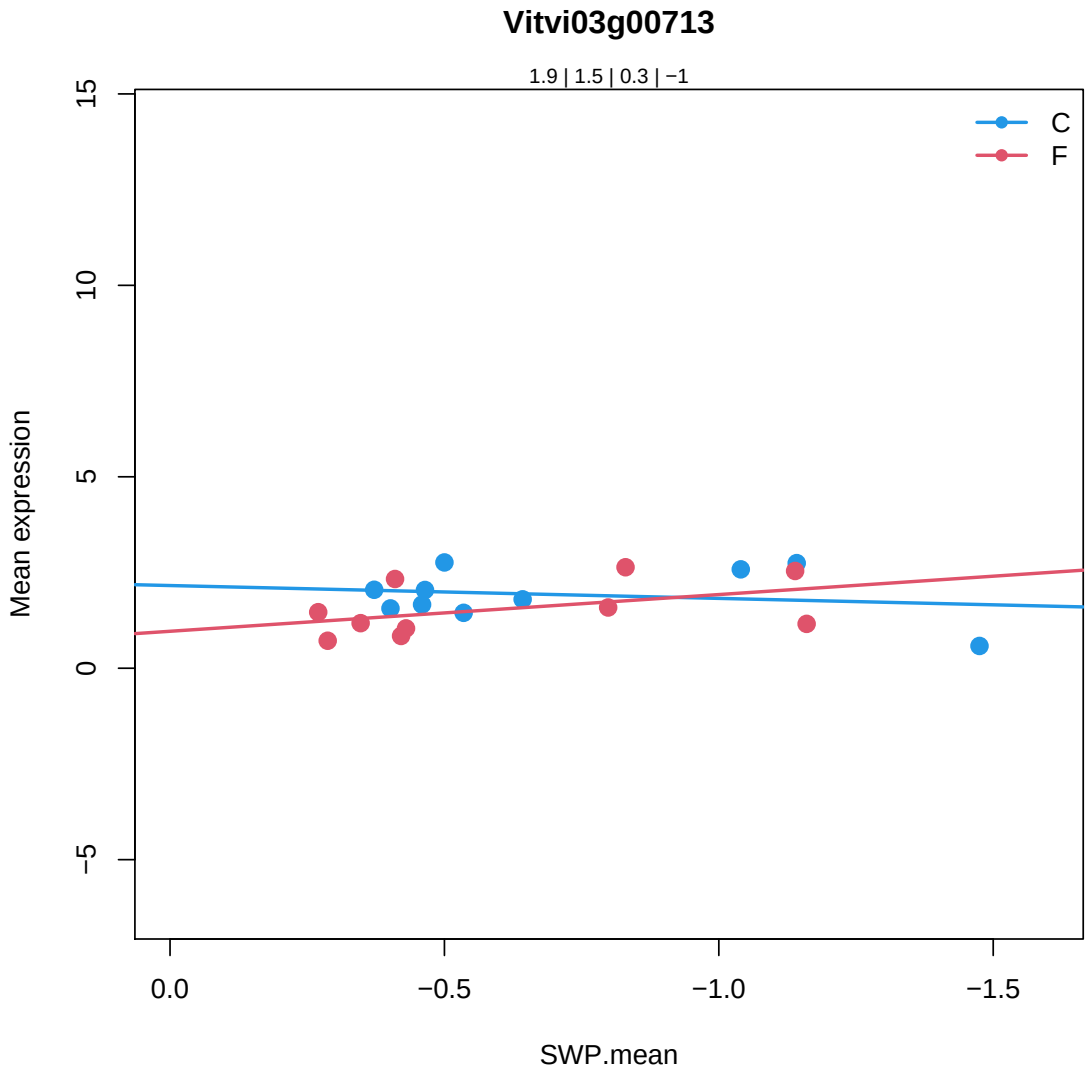
7.6.335 Vitvi03g00713: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00713
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi03g00713.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.923468	3.900247e-09	***	4.821767e-09	***
SlopeC	0.3358115	0.5574326		0.8894103	
MeanF-MeanC	-0.3742799	0.205142		0.5493677	
SlopeF-SlopeC	-1.295201	0.1371261		0.9999488	



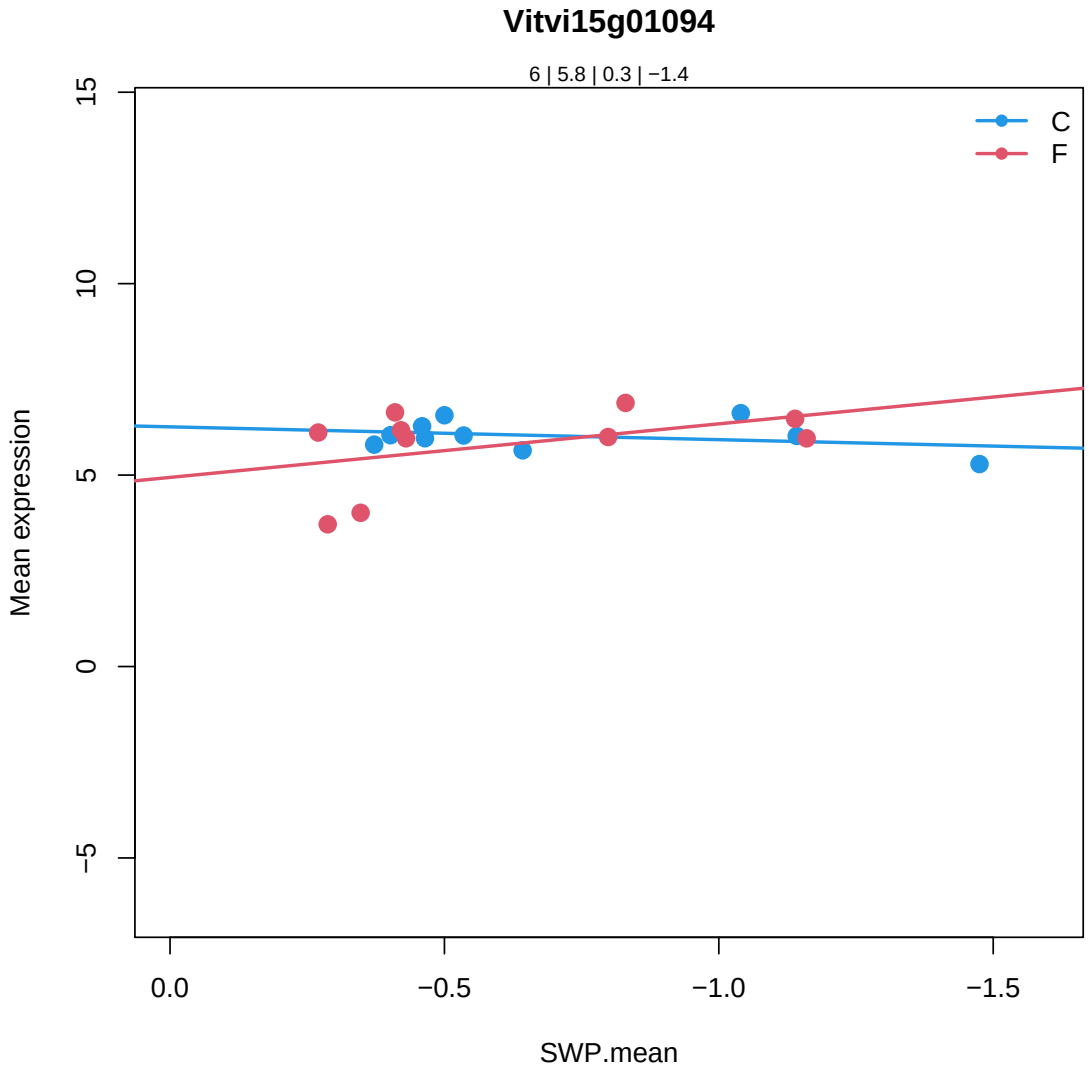
7.6.336 Vitvi15g01094: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g01094
        15.2
        metal handling.binding, chelation and storage
        Heavy metal transport/detoxification superfamily protein |
        Chr1:180401-181680 REVERSE LENGTH=204 |
        201606
```

Coefficients for Vitvi15g01094.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.024207	5.006872e-18	***	1.417962e-17	***
SlopeC	0.3351778	0.5954558		0.9017664	
MeanF-MeanC	-0.2326033	0.4698123		0.7888168	
SlopeF-SlopeC	-1.734213	0.07467536	.	0.9999488	



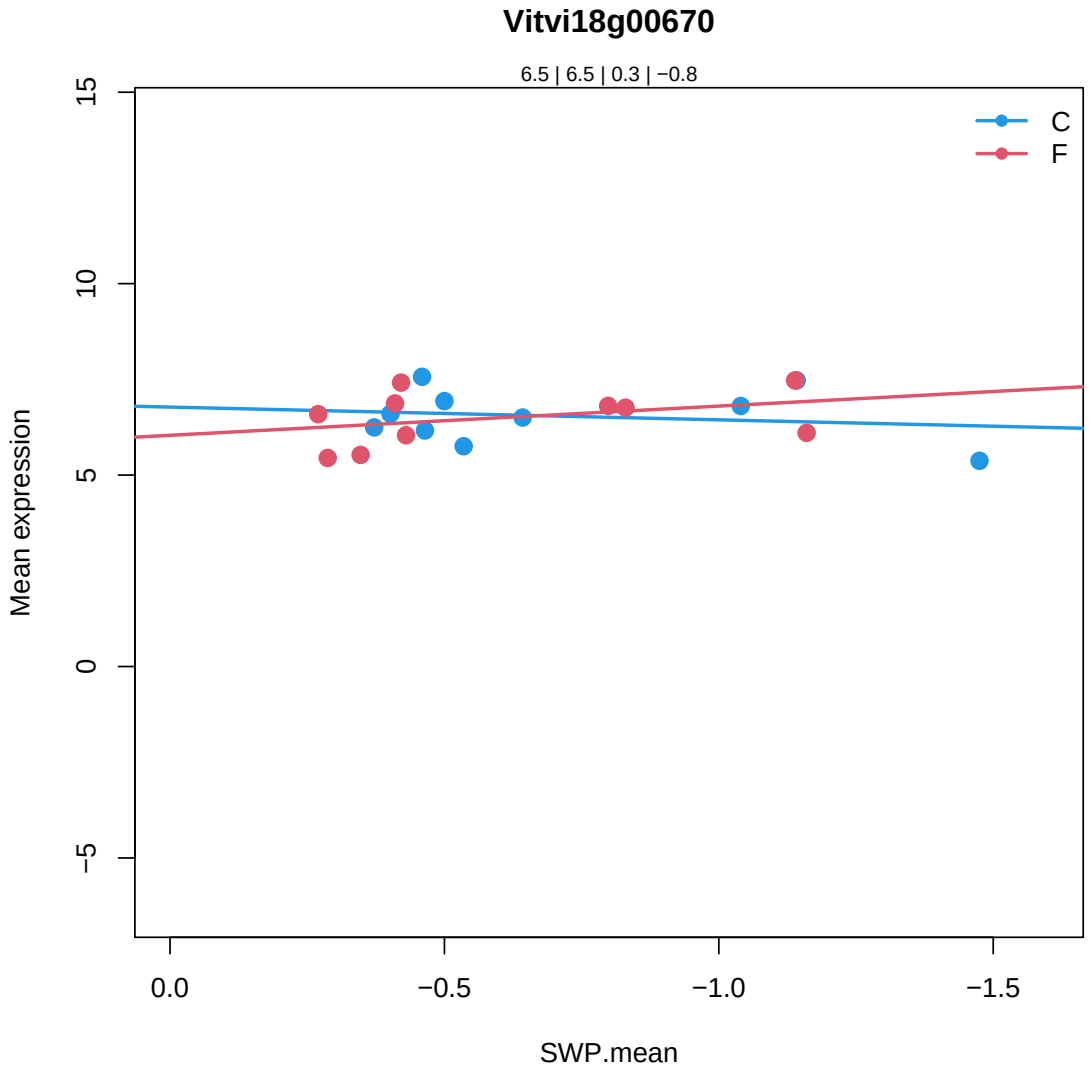
7.6.337 Vitvi18g00670: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00670
        35.1
        not assigned.no ontology
        interferon-related developmental regulator family protein / IFRD prote
        Chr1:9668895-9671322 FORWARD LENGTH=441 |
        201606
```

Coefficients for Vitvi18g00670.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.541774	2.335359e-19	***	9.811341e-19	***
SlopeC	0.3325853	0.5744889		0.8928684	
MeanF-MeanC	-0.03820572	0.8986754		0.973376	
SlopeF-SlopeC	-1.095264	0.2206591		0.9999488	



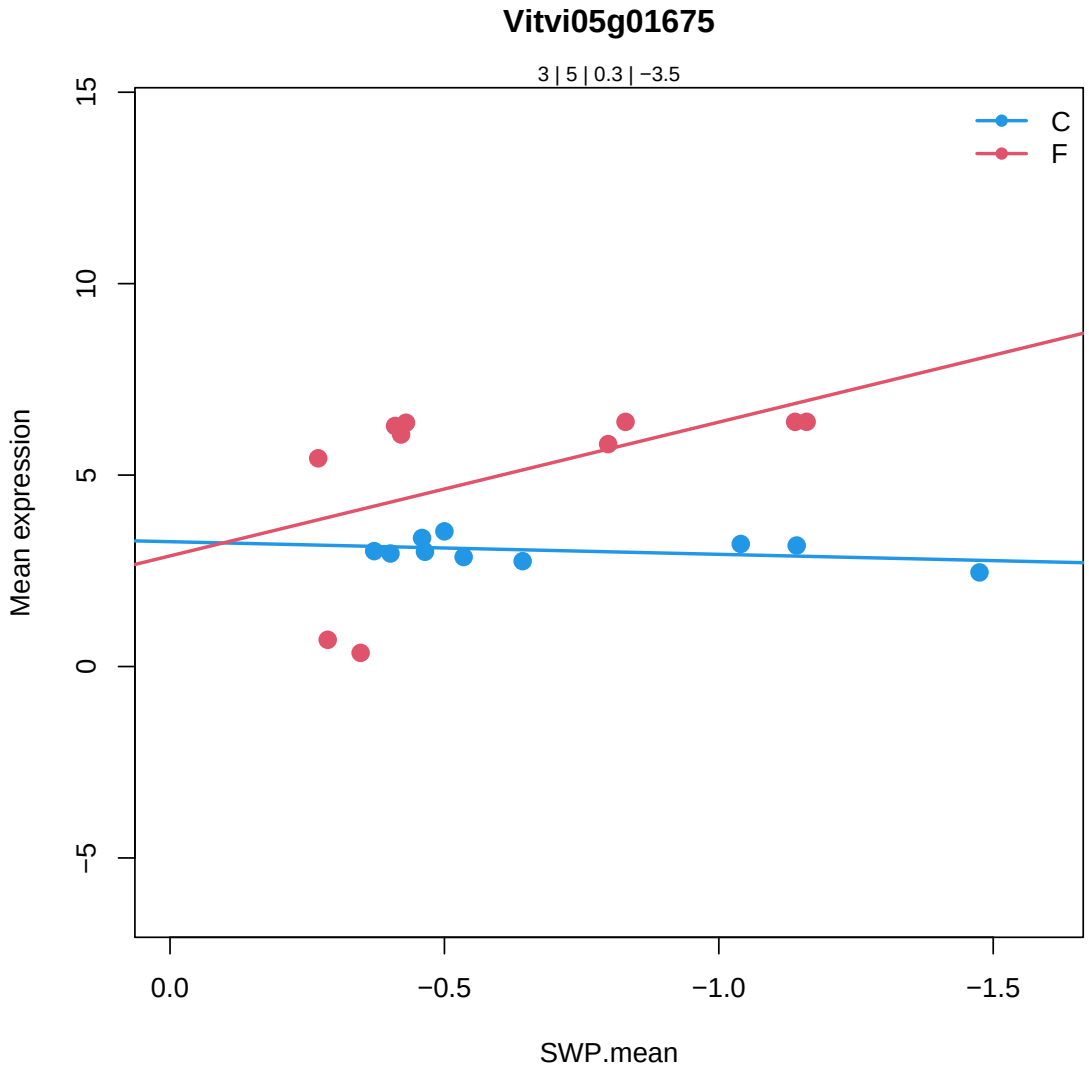
7.6.338 Vitvi05g01675: + type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01675
        26.11.1
        misc.alcohol dehydrogenases.cinnamyl alcohol dehydrogenase
        Zinc-binding dehydrogenase family protein |
        Chr5:5584983-5586991 REVERSE LENGTH=345 |
        201606
```

Coefficients for Vitvi05g01675.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.027901	6.100684e-07	***	7.084695e-07	***
SlopeC	0.3297008	0.7874006		0.9533712	
MeanF-MeanC	1.9902	0.003821472	**	0.03702916	*
SlopeF-SlopeC	-3.824121	0.04507823	*	0.9999488	



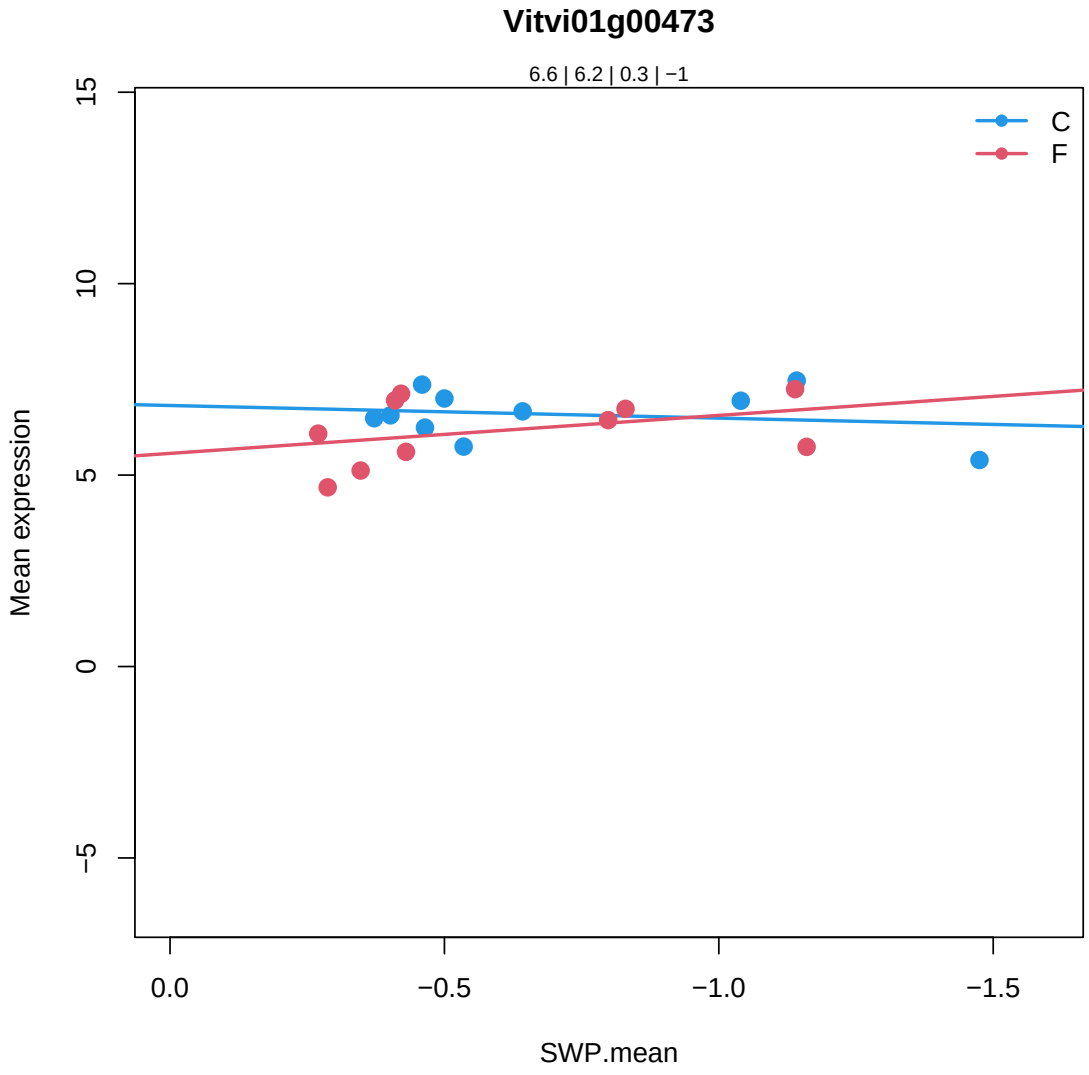
7.6.339 Vitvi01g00473: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00473
        21.1
        redox.thioredoxin
        jasmonate-zim-domain protein 3 |
        Chr3:6121143-6122691 FORWARD LENGTH=319 |
        201606
```

Coefficients for Vitvi01g00473.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.585677	9.916081e-19	***	3.421026e-18	***
SlopeC	0.3295534	0.6057835		0.9047128	
MeanF-MeanC	-0.4145979	0.208619		0.5530997	
SlopeF-SlopeC	-1.321977	0.1723698		0.9999488	



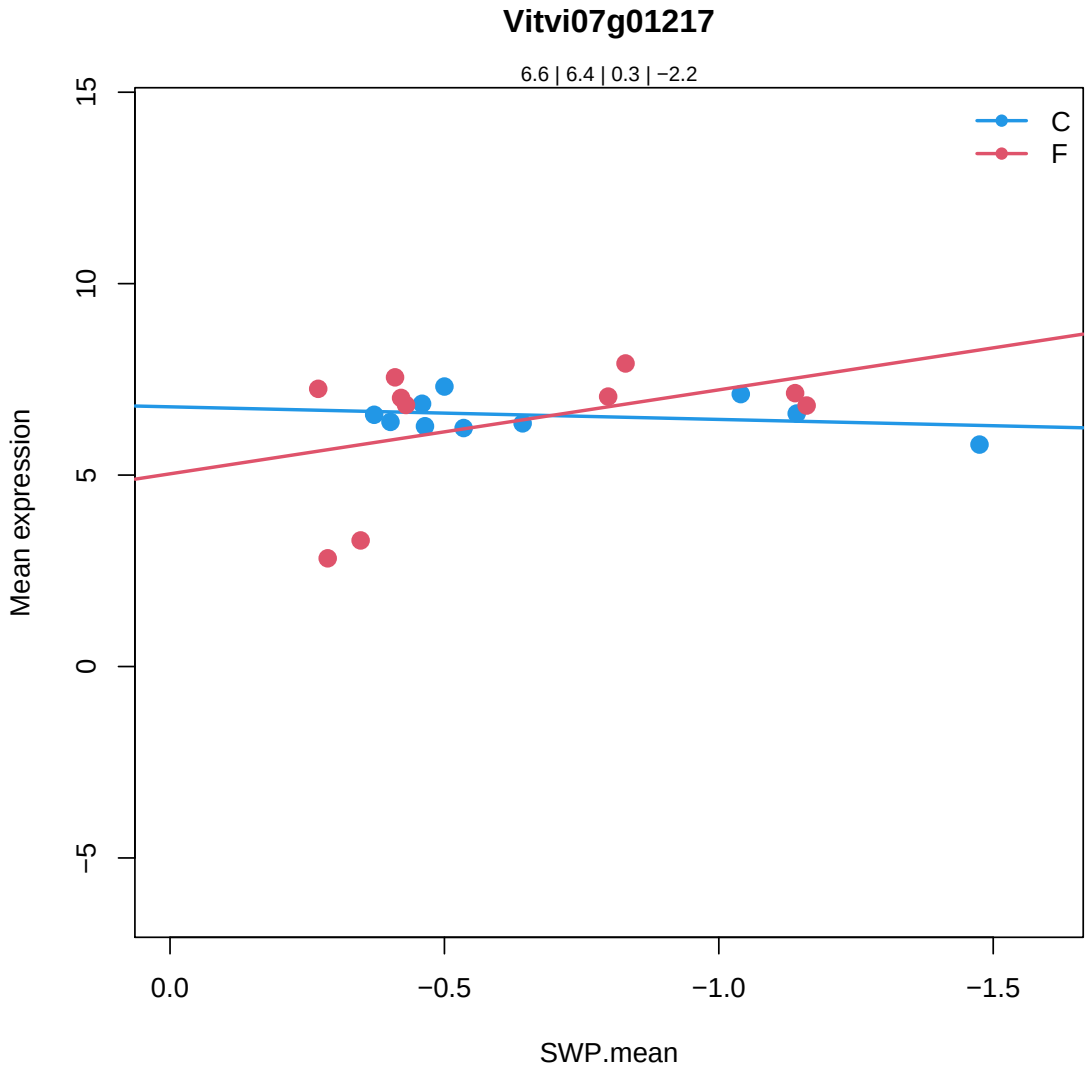
7.6.340 Vitvi07g01217: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01217
        20.1.3.1
        stress.biotic.signalling.MLO-like
        Seven transmembrane MLO family protein |
        Chr4:1144141-1147156 FORWARD LENGTH=526 |
        201606
```

Coefficients for Vitvi07g01217.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.551282	9.371349e-15	***	1.572068e-14	***
SlopeC	0.3290549	0.739068		0.9434568	
MeanF-MeanC	-0.1821918	0.7168116		0.9128164	
SlopeF-SlopeC	-2.522145	0.09660126	.	0.9999488	



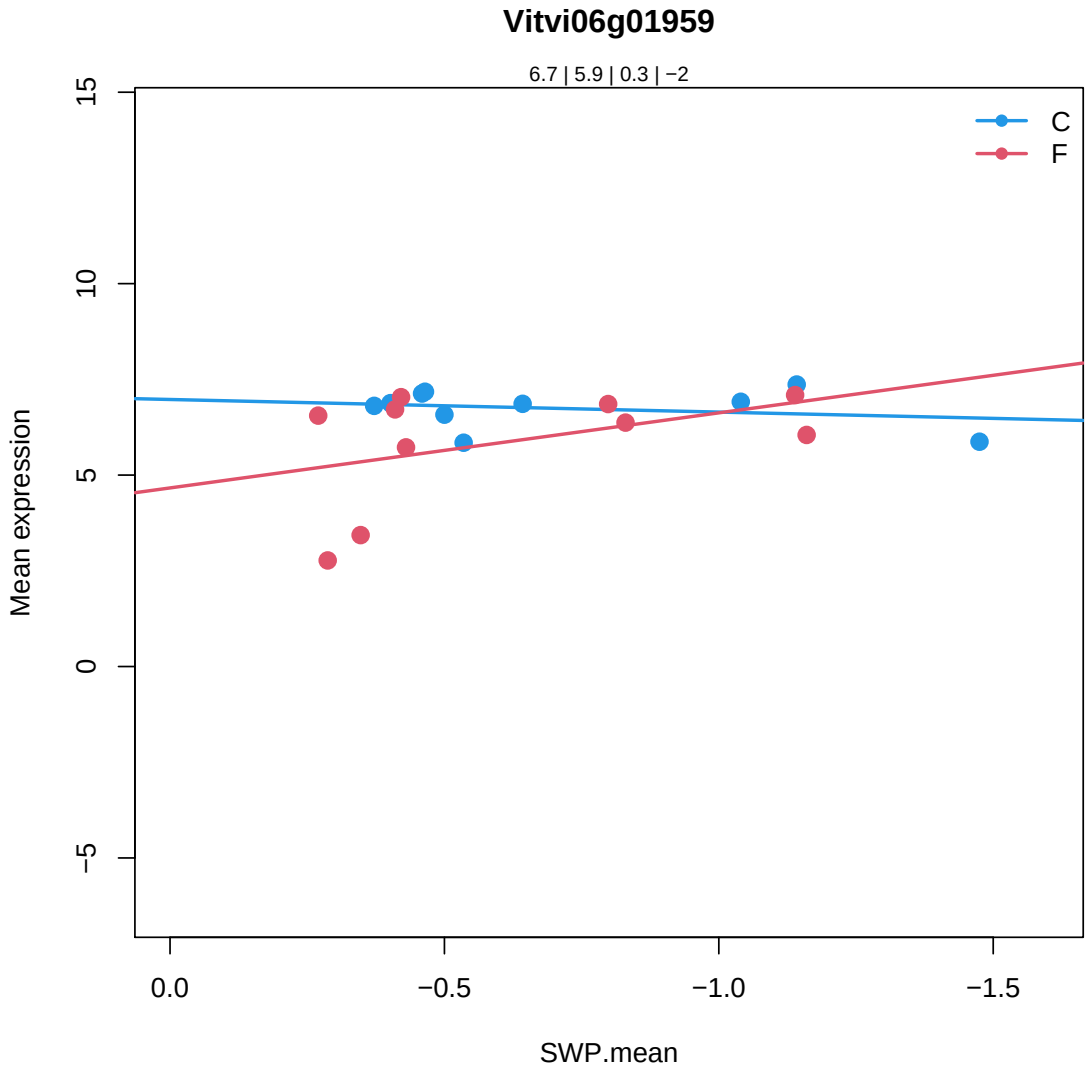
7.6.341 Vitvi06g01959: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01959
        35.2
        not assigned.unknown
        hypothetical protein |
        Chr3:19546446-19546868 REVERSE LENGTH=140 |
        201606
```

Coefficients for Vitvi06g01959.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.742876	3.661843e-16	***	7.287349e-16	***
SlopeC	0.3287882	0.7047868		0.9342808	
MeanF-MeanC	-0.8836593	0.05493261	.	0.2540454	
SlopeF-SlopeC	-2.289575	0.08652596	.	0.9999488	



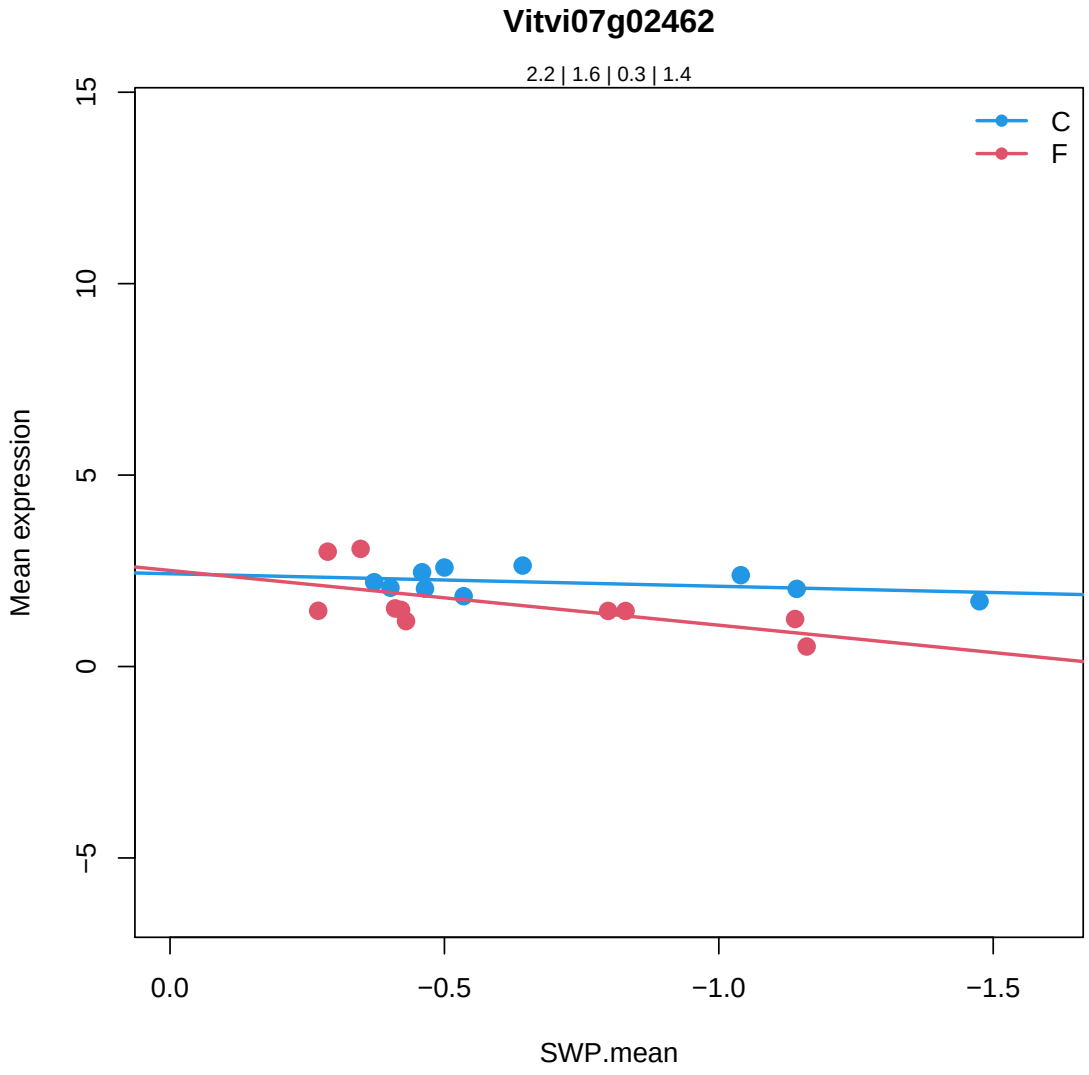
7.6.342 Vitvi07g02462: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g02462
        35.2
        not assigned.unknown
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi07g02462.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.193029	4.972348e-12	***	6.874243e-12	***
SlopeC	0.32694	0.4733698		0.8618199	
MeanF-MeanC	-0.5554196	0.0234794	*	0.1417881	
SlopeF-SlopeC	1.10247	0.1127758		0.9999488	



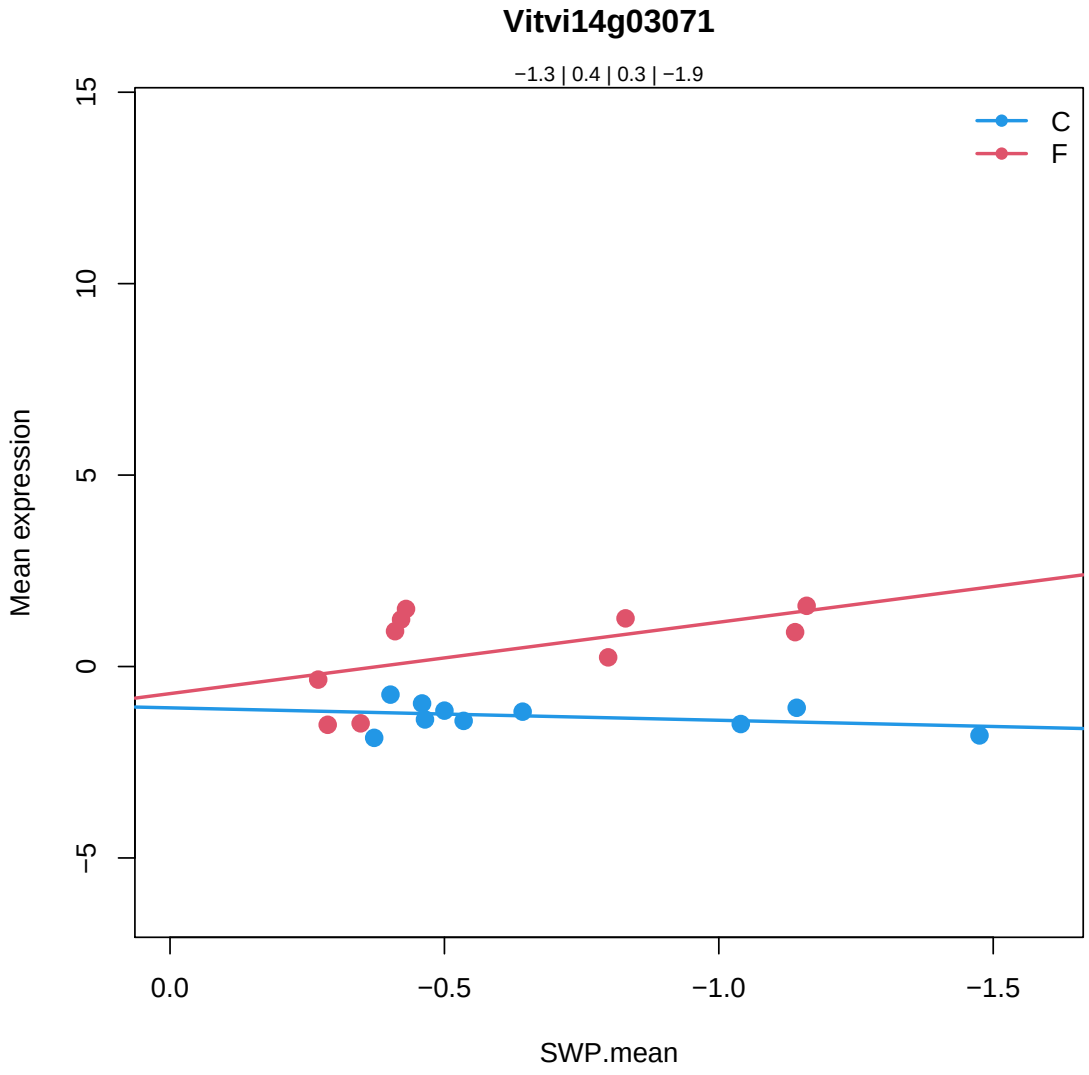
7.6.343 Vitvi14g03071: + type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g03071
        35.2
        not assigned.unknown
        kinase family with leucine-rich repeat domain-containing protein |
        Chr1:13220940-13224386 FORWARD LENGTH=1120 |
        201606
```

Coefficients for Vitvi14g03071.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.307629	9.148178e-06	***	1.034165e-05	***
SlopeC	0.3246997	0.6116398		0.9065647	
MeanF-MeanC	1.736141	2.088562e-05	***	0.0004765548	***
SlopeF-SlopeC	-2.188816	0.02941108	*	0.9999488	



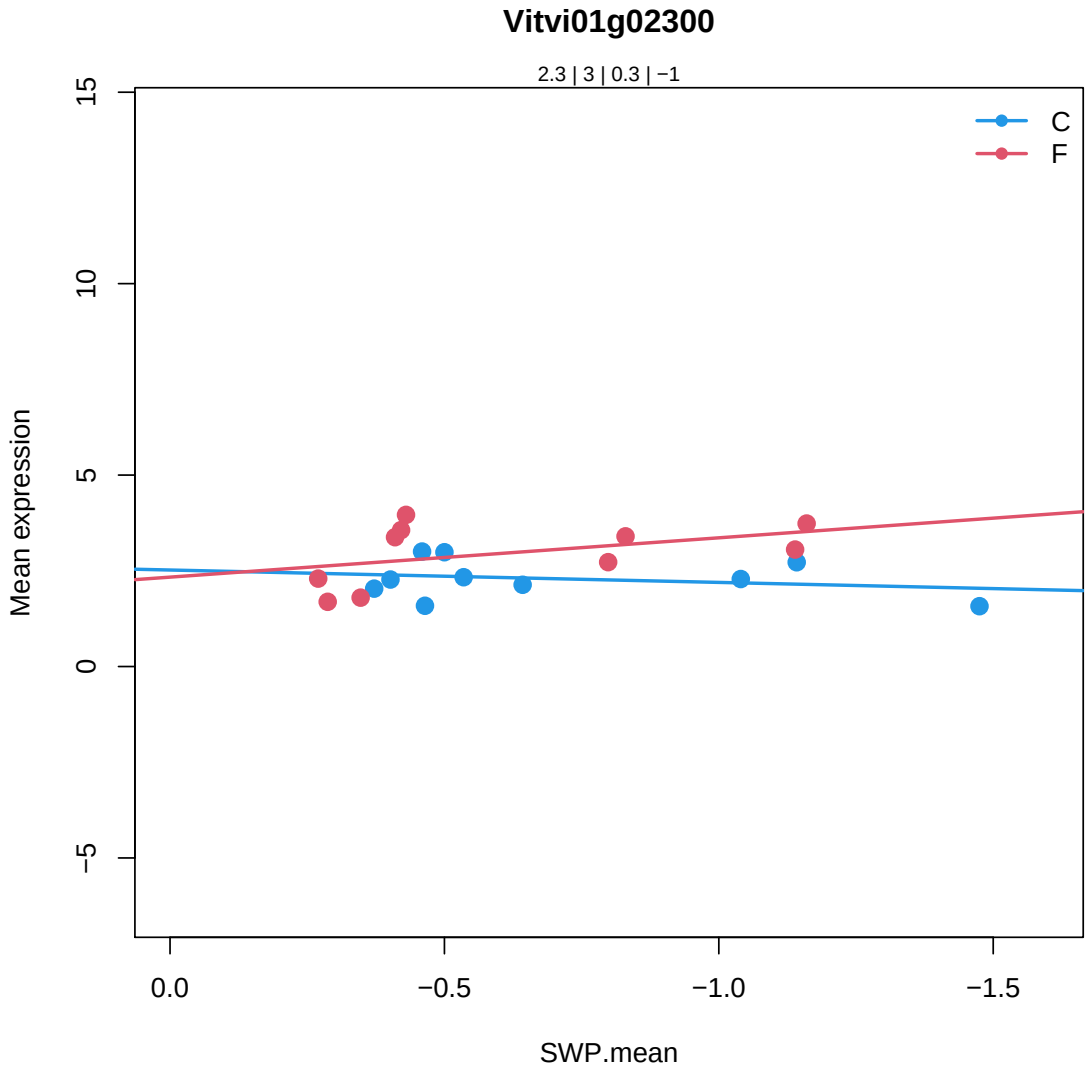
7.6.344 Vitvi01g02300: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g02300
        35.2
        not assigned.unknown
        Calcium-dependent lipid-binding (CaLB domain) family protein |
        Chr3:5617112-5618194 REVERSE LENGTH=360 |
        201606
```

Coefficients for Vitvi01g02300.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.29293	7.863323e-11	***	1.033125e-10	***
SlopeC	0.3236466	0.5563352		0.8894103	
MeanF-MeanC	0.6672004	0.02427427	*	0.1453786	
SlopeF-SlopeC	-1.350768	0.108284		0.9999488	



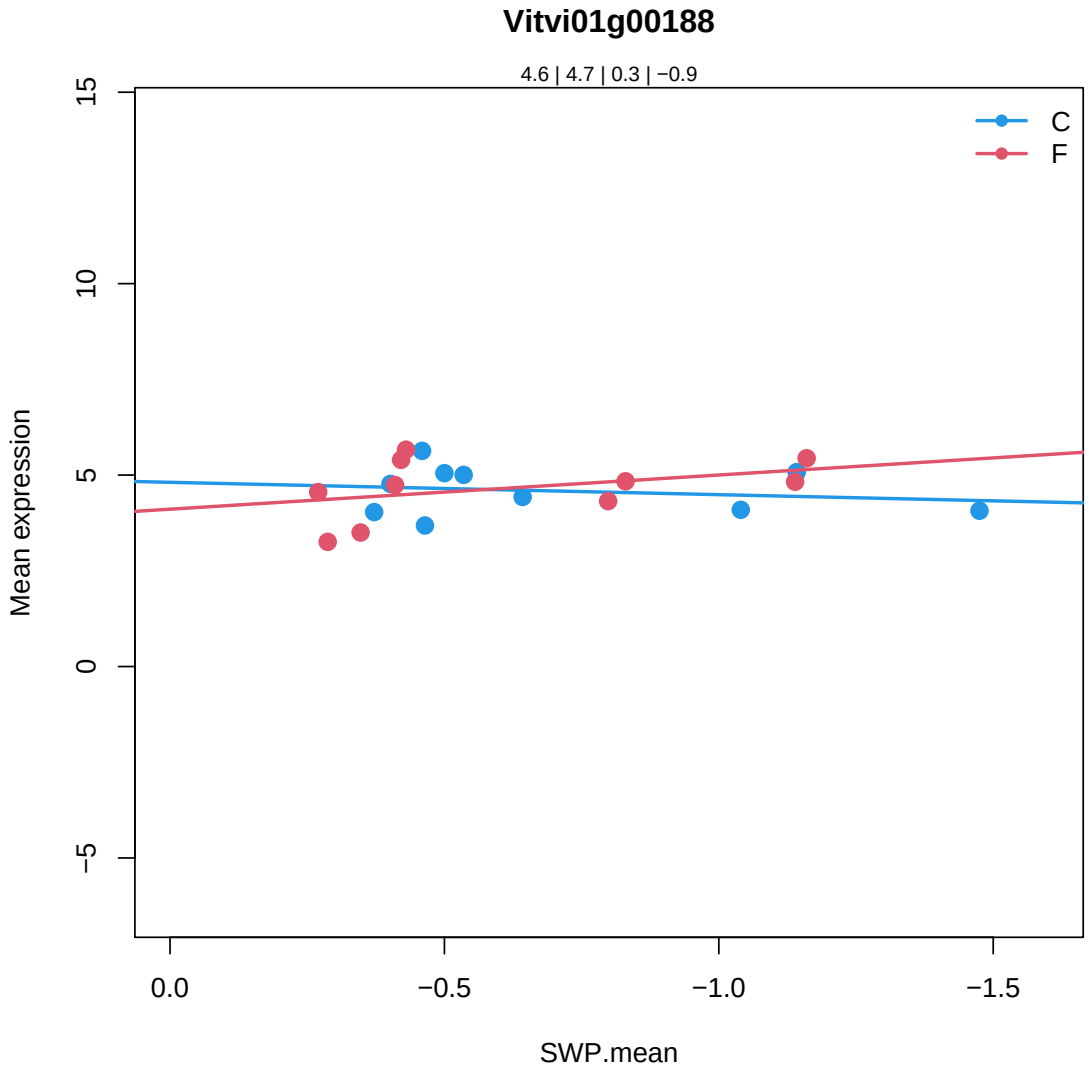
7.6.345 Vitvi01g00188: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00188
        35.2
        not assigned.unknown
        hypothetical protein (DUF1262) |
        Chr1:4633740-4635129 REVERSE LENGTH=385 |
        201606
```

Coefficients for Vitvi01g00188.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.584023	3.747525e-16	***	7.448668e-16	***
SlopeC	0.3224612	0.5857814		0.8973375	
MeanF-MeanC	0.06934197	0.8171525		0.9492107	
SlopeF-SlopeC	-1.215089	0.1755774		0.9999488	



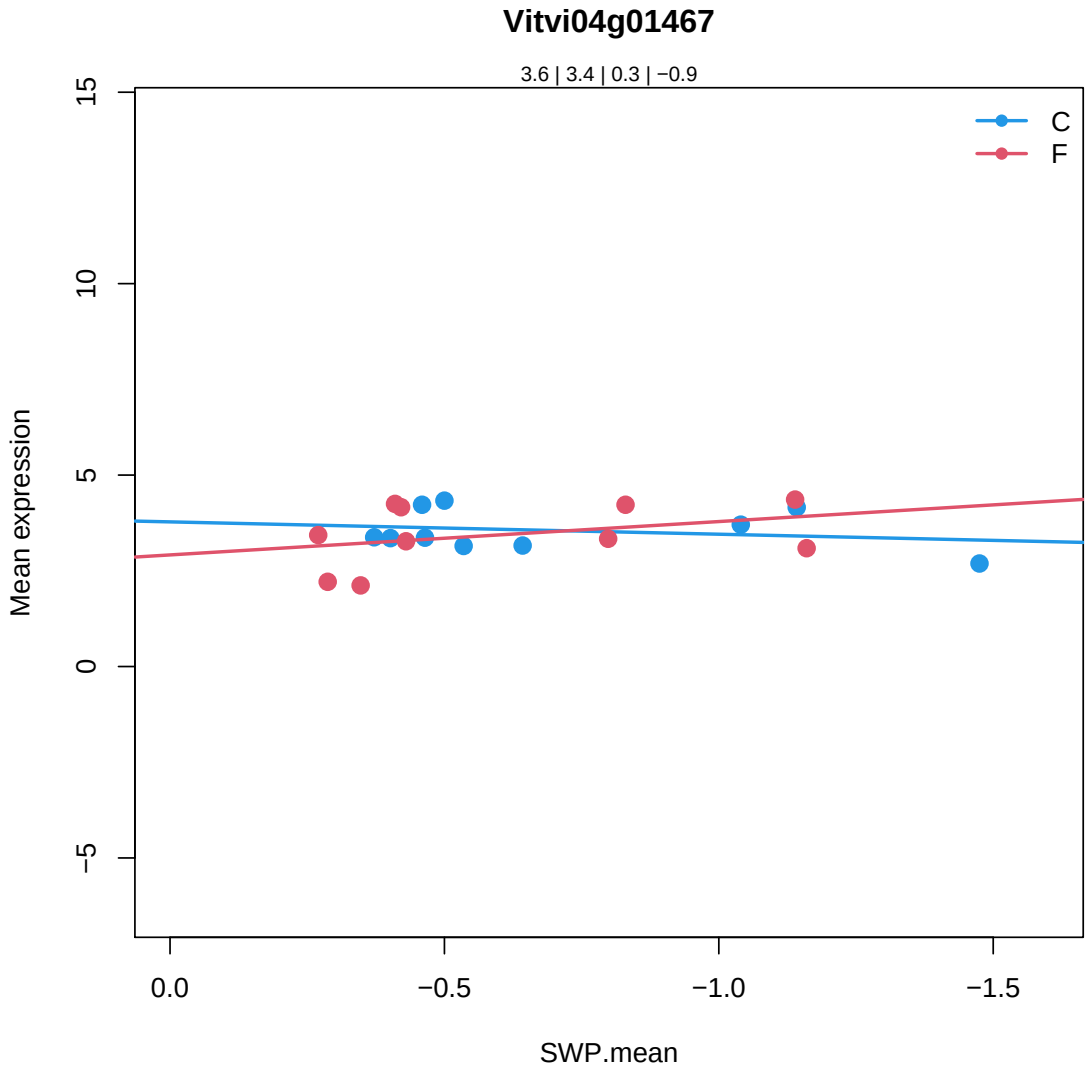
7.6.346 Vitvi04g01467: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01467
        35.1.3
        not assigned.no ontology.armadillo/beta-catenin repeat family protein
        armadillo repeat only 2 |
        Chr5:26453648-26455603 REVERSE LENGTH=651 |
        201606
```

Coefficients for Vitvi04g01467.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.551201	4.444085e-14	***	7.015903e-14	***
SlopeC	0.3219117	0.5787706		0.8944184	
MeanF-MeanC	-0.1057976	0.7190584		0.9140181	
SlopeF-SlopeC	-1.193096	0.174686		0.9999488	



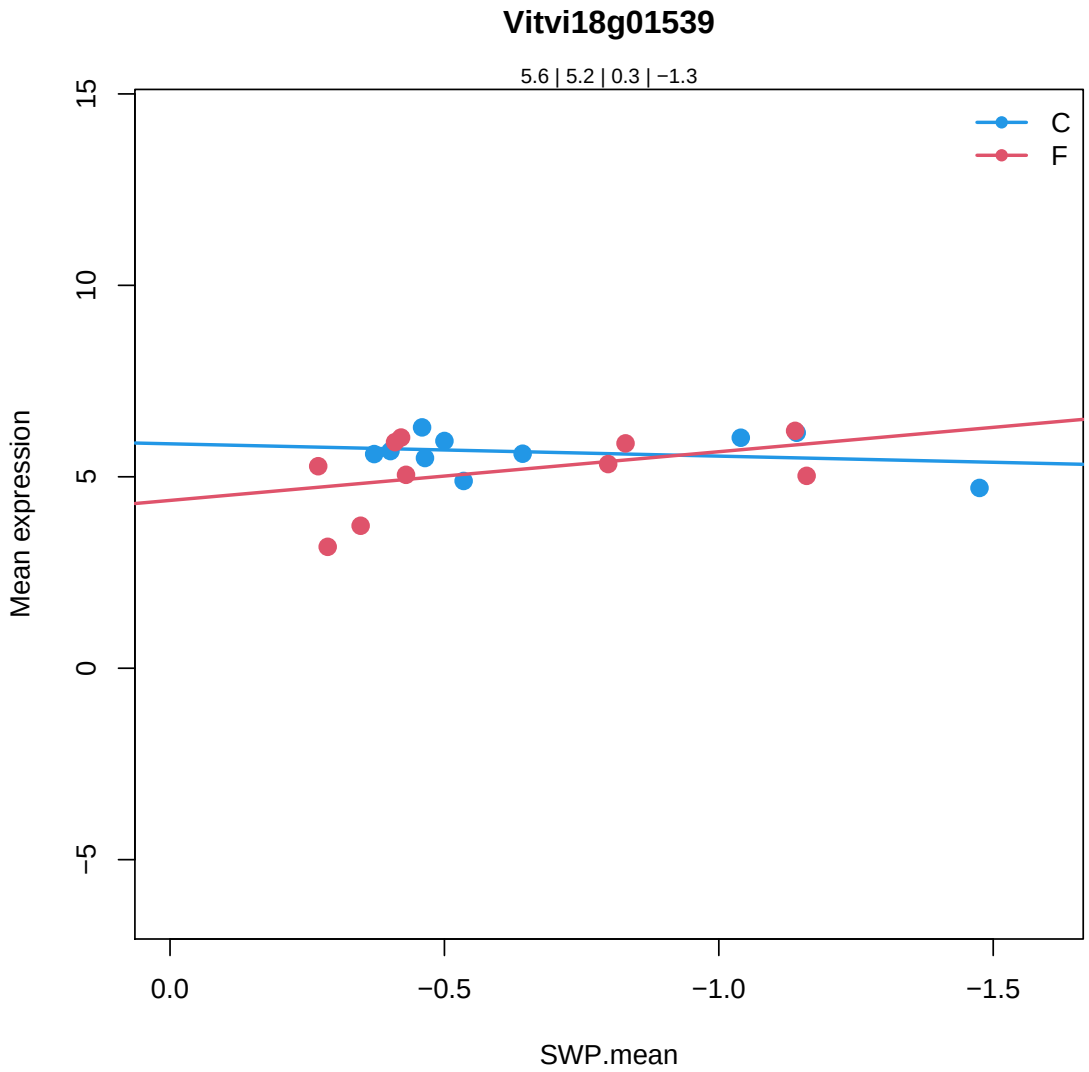
7.6.347 Vitvi18g01539: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g01539
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi18g01539.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.634959	2.222345e-17	***	5.454156e-17	***
SlopeC	0.3214707	0.6121994		0.9065647	
MeanF-MeanC	-0.4771336	0.1476508		0.4625885	
SlopeF-SlopeC	-1.593629	0.1010485		0.9999488	



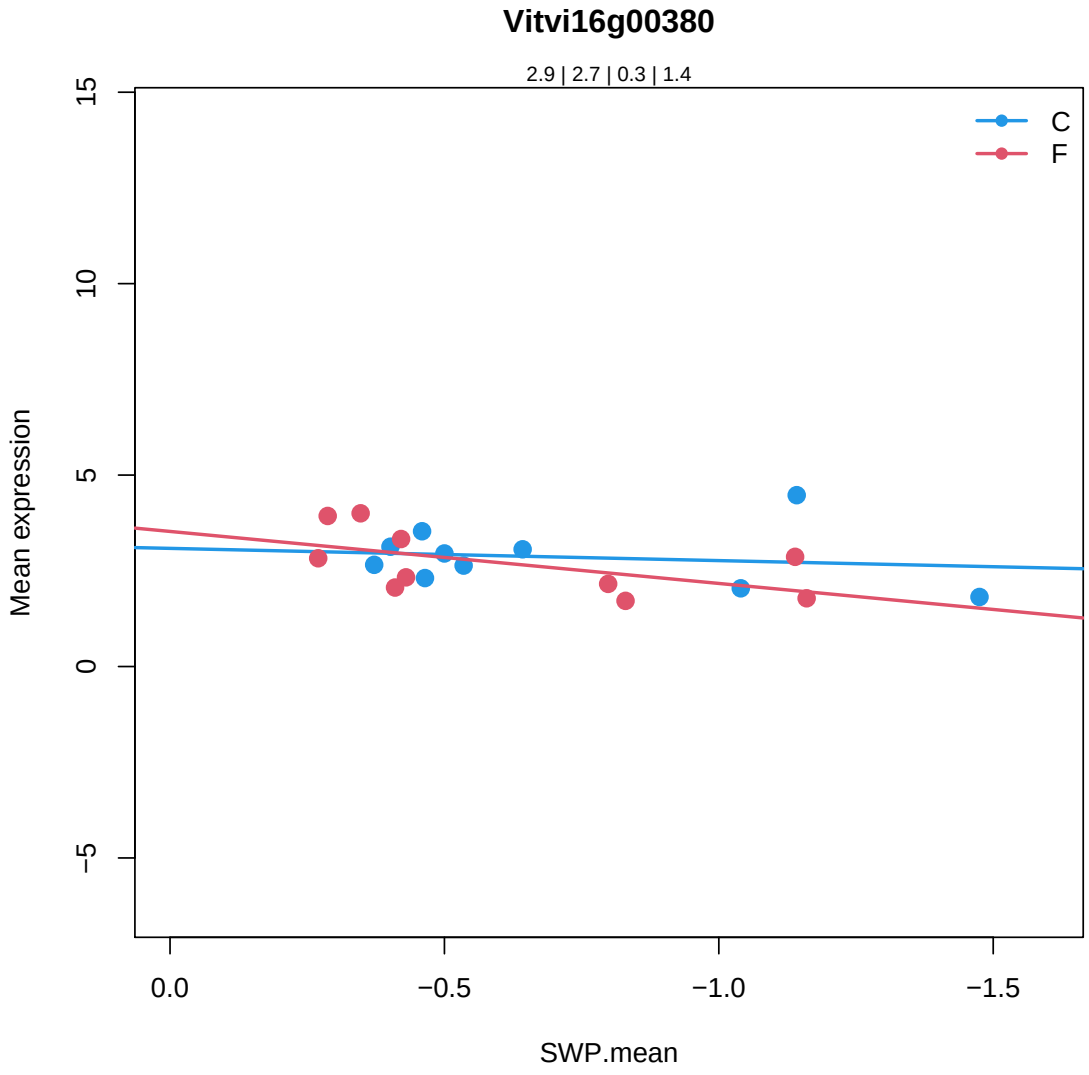
7.6.348 Vitvi16g00380: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g00380
        17.5.2
        hormone metabolism.ethylene.signal transduction
        Integrase-type DNA-binding superfamily protein |
        Chr5:20800708-20801373 REVERSE LENGTH=221 |
        201606
```

Coefficients for Vitvi16g00380.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.861106	1.85103e-11	***	2.497423e-11	***
SlopeC	0.3191185	0.6153386		0.9074064	
MeanF-MeanC	-0.1608391	0.6183199		0.8676755	
SlopeF-SlopeC	1.039128	0.2769718		0.9999488	



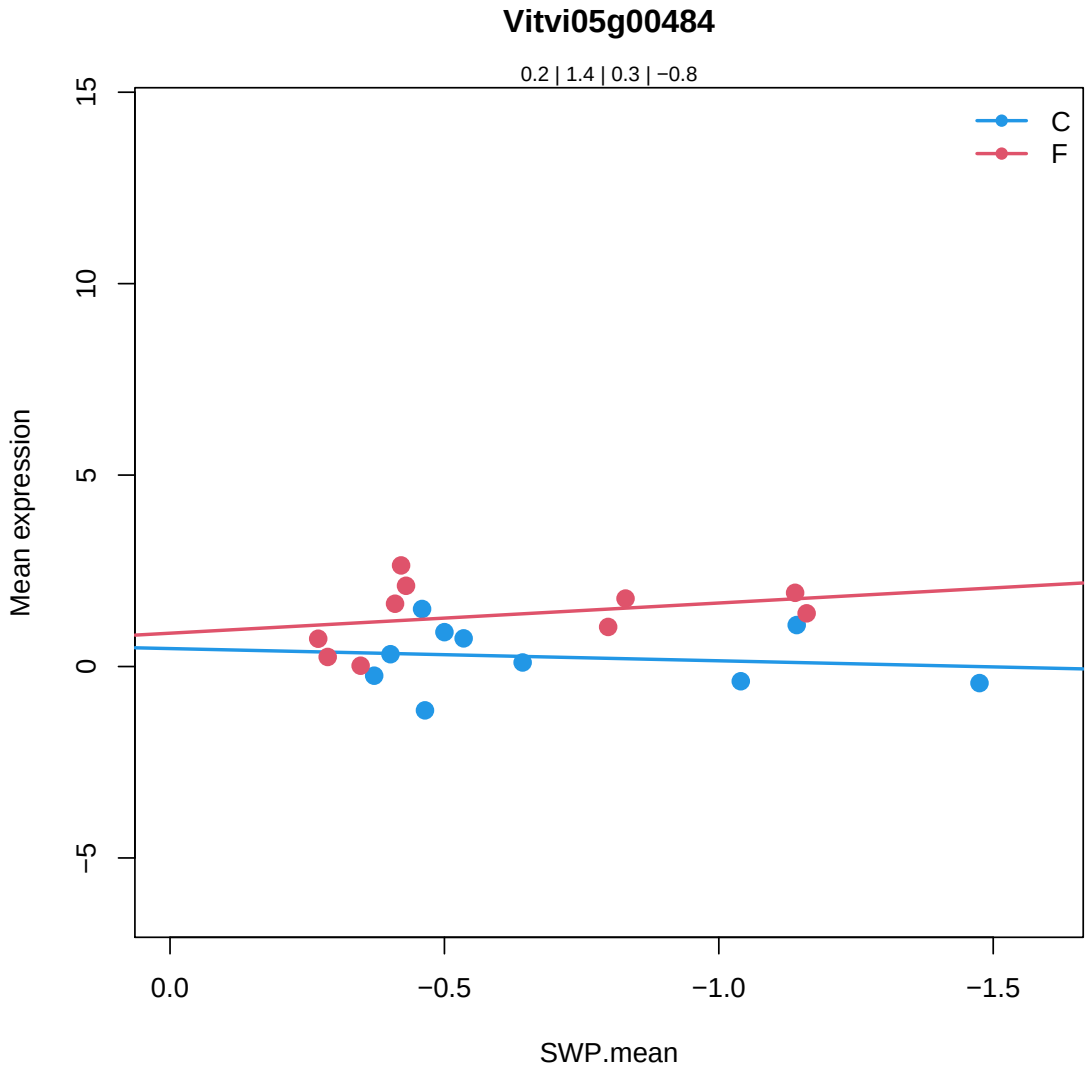
7.6.349 Vitvi05g00484: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00484
        35.2
        not assigned.unknown
        receptor-like protein kinase 1 |
        Chr5:24498467-24501494 REVERSE LENGTH=832 |
        201606
```

Coefficients for Vitvi05g00484.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.2440909	0.3292706		0.335119	
SlopeC	0.3189147	0.6439319		0.9164577	
MeanF-MeanC	1.106577	0.004223587	**	0.03986124	*
SlopeF-SlopeC	-1.107046	0.2863469		0.9999488	



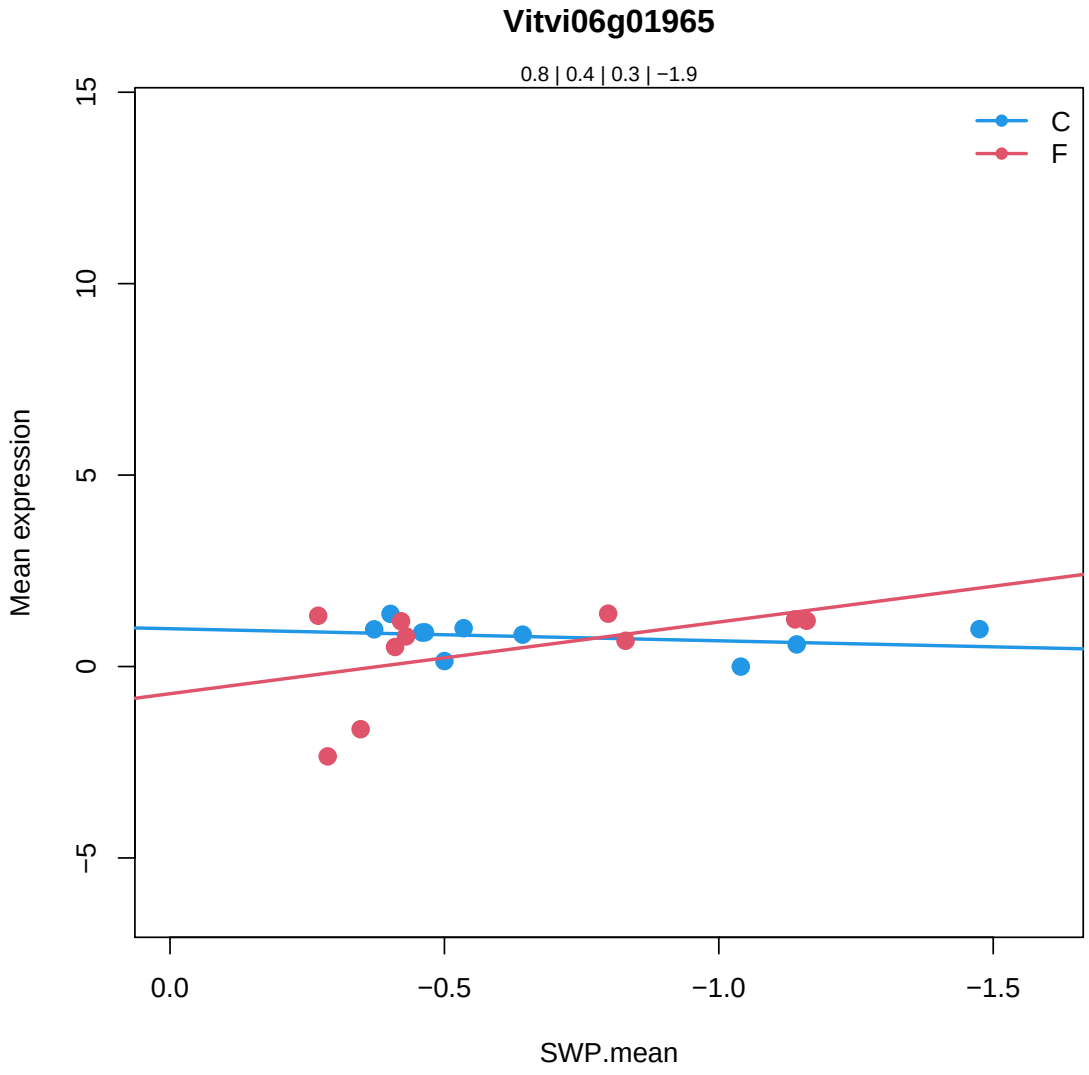
7.6.350 Vitvi06g01965: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01965
        35.2
        not assigned.unknown
        BED zinc finger and hAT dimerization domain-containing protein DAYSLEE
        Chr3:14321838-14323928 FORWARD LENGTH=696 |
        201606
```

Coefficients for Vitvi06g01965.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.7651484	0.008021156	**	0.008514413	**
SlopeC	0.3157152	0.6690095		0.9237671	
MeanF-MeanC	-0.3351699	0.3753781		0.7282614	
SlopeF-SlopeC	-2.186908	0.05635322	.	0.9999488	



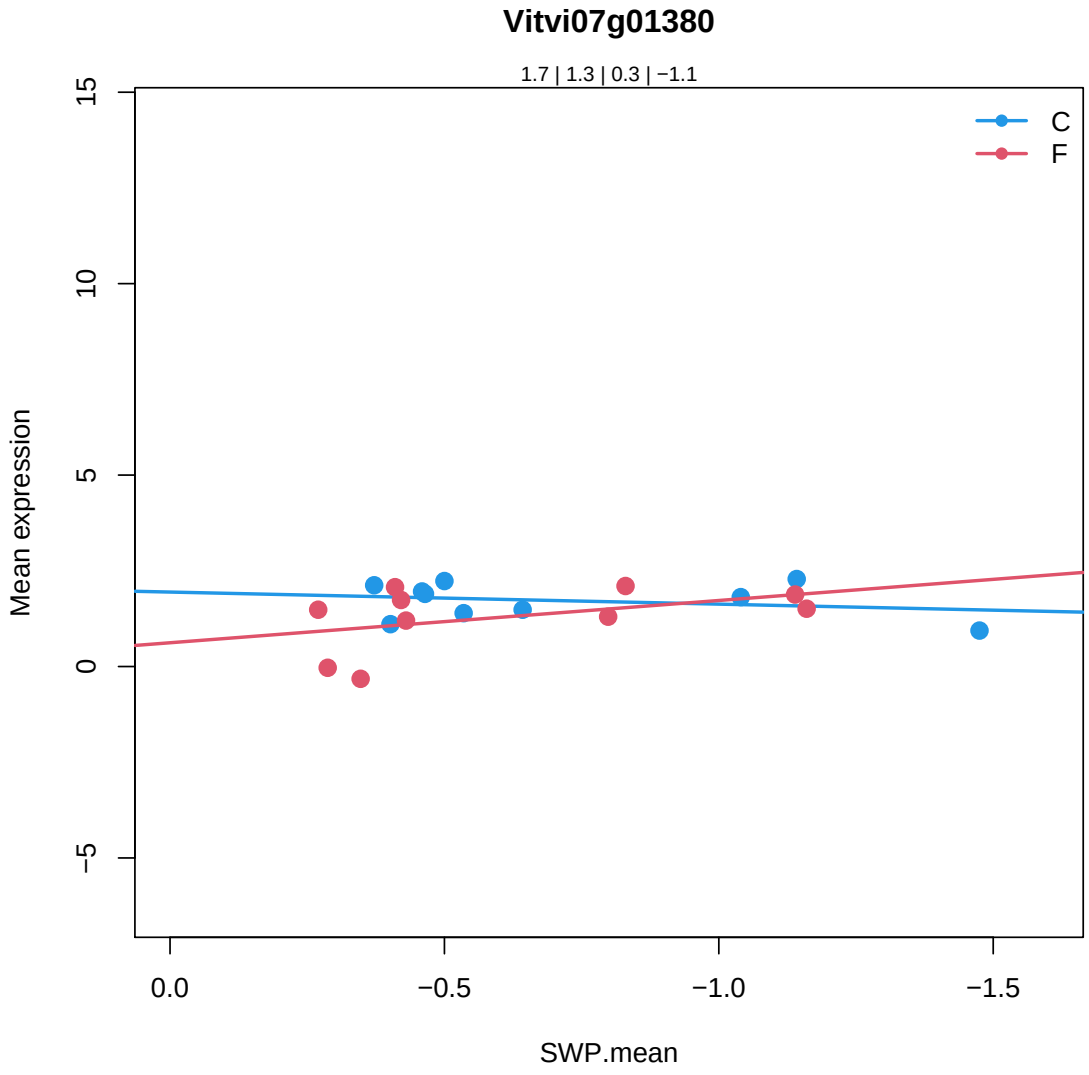
7.6.351 Vitvi07g01380: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01380
        30.11
        signalling.light
        Phototropic-responsive NPH3 family protein |
        Chr5:3217028-3219368 REVERSE LENGTH=622 |
        201606
```

Coefficients for Vitvi07g01380.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.723013	1.329231e-08	***	1.616156e-08	***
SlopeC	0.3153631	0.5666635		0.891013	
MeanF-MeanC	-0.429791	0.1333334		0.4363021	
SlopeF-SlopeC	-1.419325	0.09271126	.	0.9999488	



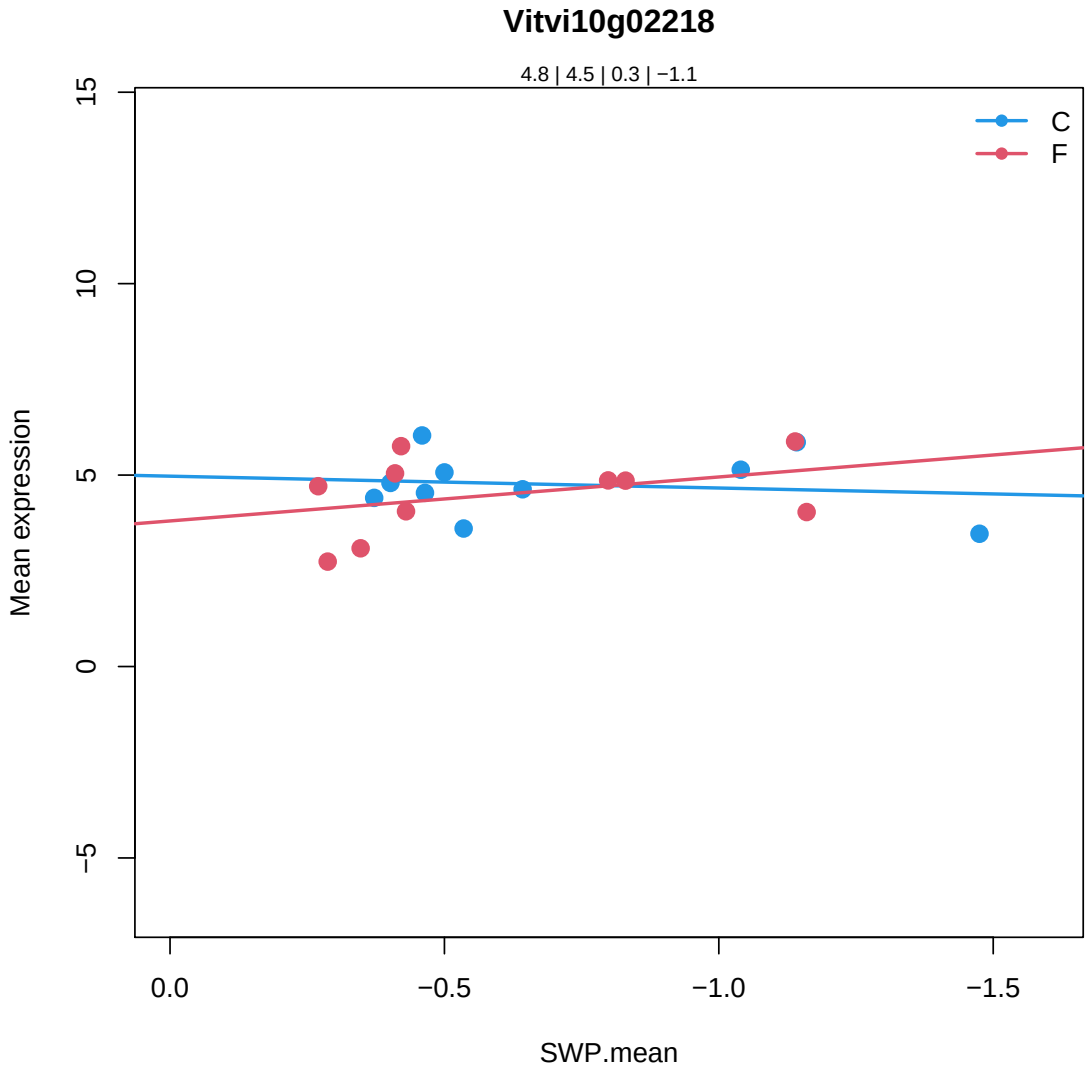
7.6.352 Vitvi10g02218: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g02218
        27.3.6
        RNA.regulation of transcription.basic helix-loop-helix family (bHLH)
        basic helix-loop-helix (bHLH) DNA-binding superfamily protein |
        Chr5:22217270-22218993 FORWARD LENGTH=234 |
        201606
```

Coefficients for Vitvi10g02218.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.753881	3.126687e-14	***	4.999681e-14	***
SlopeC	0.3089692	0.6849098		0.9291024	
MeanF-MeanC	-0.2520507	0.5161986		0.8161827	
SlopeF-SlopeC	-1.457269	0.2062306		0.9999488	



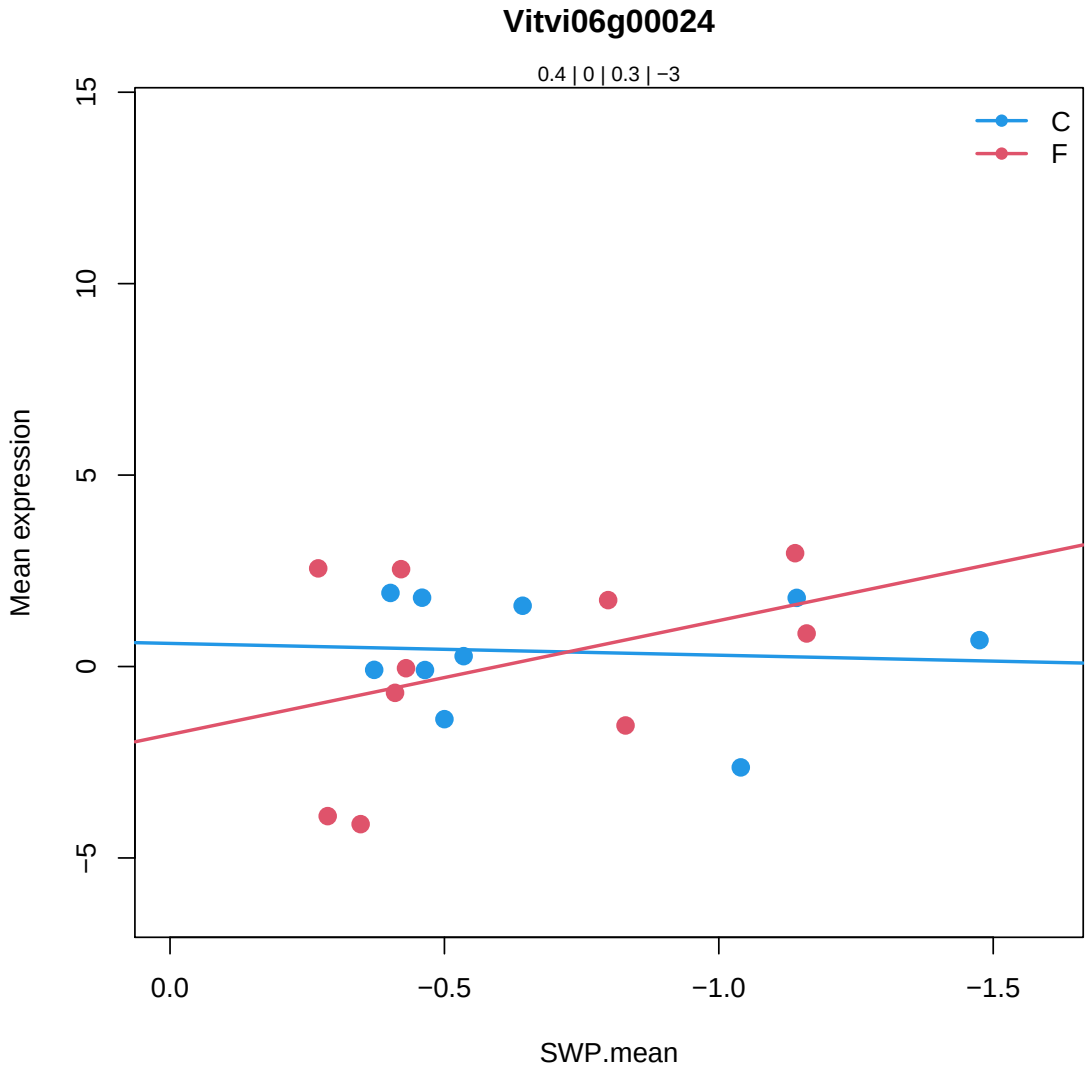
7.6.353 Vitvi06g00024: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00024
        27.3.25
        RNA.regulation of transcription.MYB domain transcription factor family
        Homeodomain-like superfamily protein |
        Chr3:1042920-1044574 REVERSE LENGTH=388 |
        201606
```

Coefficients for Vitvi06g00024.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3868611	0.5141566		0.5201975	
SlopeC	0.3085189	0.8509751		0.9721955	
MeanF-MeanC	-0.3502342	0.6753086		0.8951087	
SlopeF-SlopeC	-3.285553	0.1877762		0.9999488	



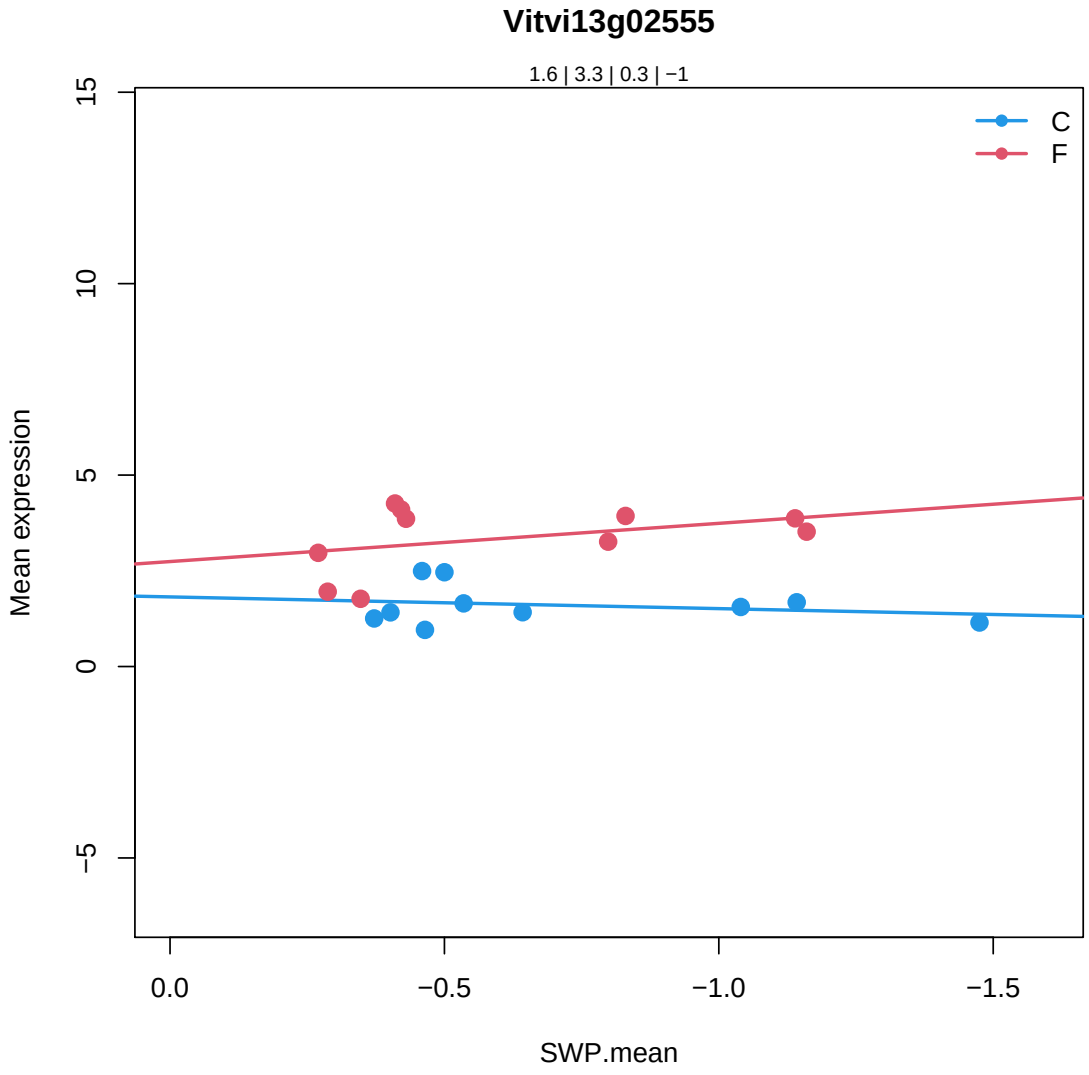
7.6.354 Vitvi13g02555: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g02555
        29.4
        protein.postranslational modification
        receptor-like protein kinase 1 |
        Chr5:24498467-24501494 REVERSE LENGTH=832 |
        201606
```

Coefficients for Vitvi13g02555.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.602909	1.402095e-07	***	1.657546e-07	***
SlopeC	0.30605	0.6040717		0.904703	
MeanF-MeanC	1.746472	6.689549e-06	***	0.0001737004	***
SlopeF-SlopeC	-1.304275	0.1464058		0.9999488	



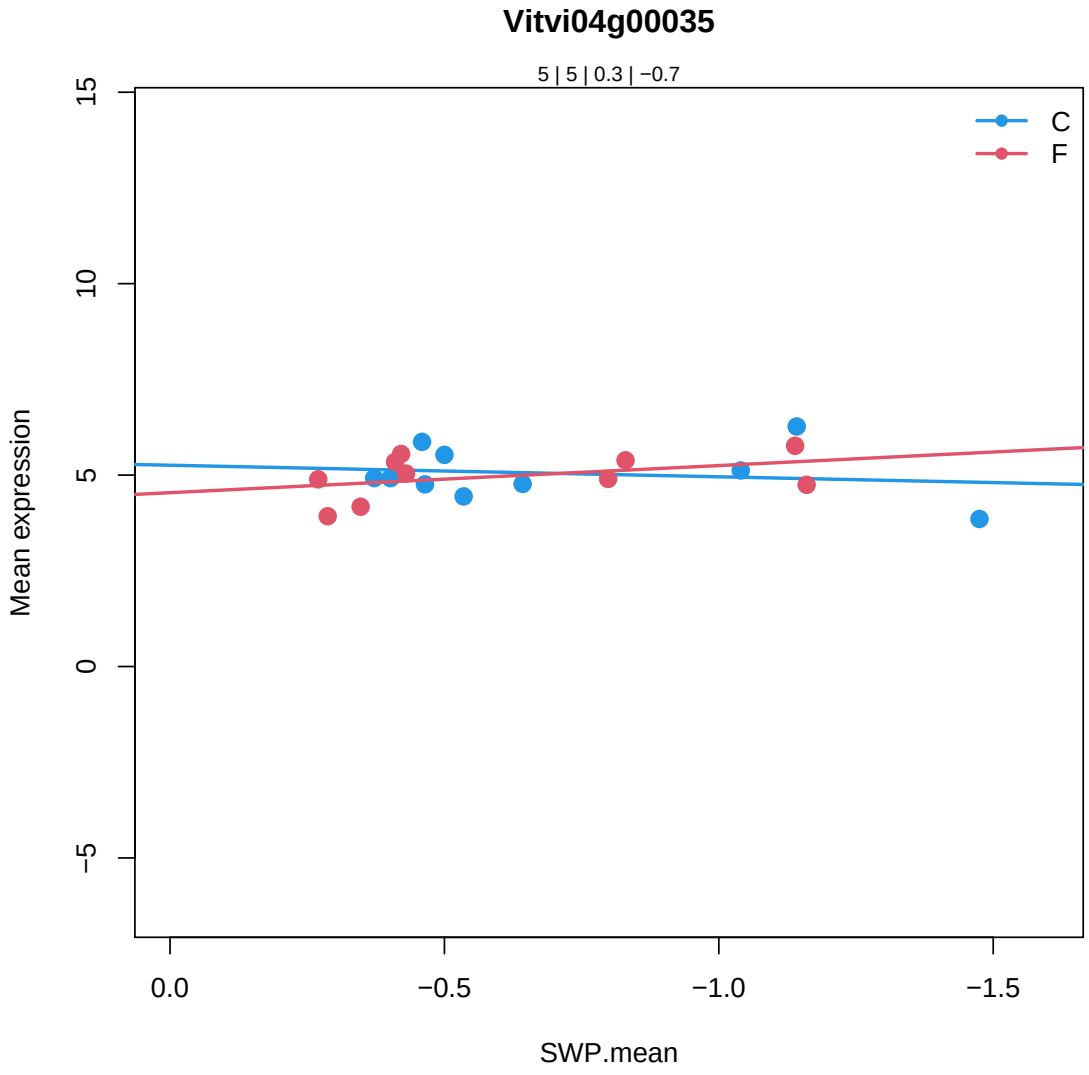
7.6.355 Vitvi04g00035: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00035
        35.1
        not assigned.no ontology
        haloacid dehalogenase-like hydrolase family protein |
        Chr2:11031159-11034302 FORWARD LENGTH=584 |
        201606
```

Coefficients for Vitvi04g00035.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.044772	1.121957e-17	***	2.922226e-17	***
SlopeC	0.3023965	0.5822161		0.8953802	
MeanF-MeanC	-0.07330934	0.7924675		0.9414352	
SlopeF-SlopeC	-1.010483	0.2232898		0.9999488	



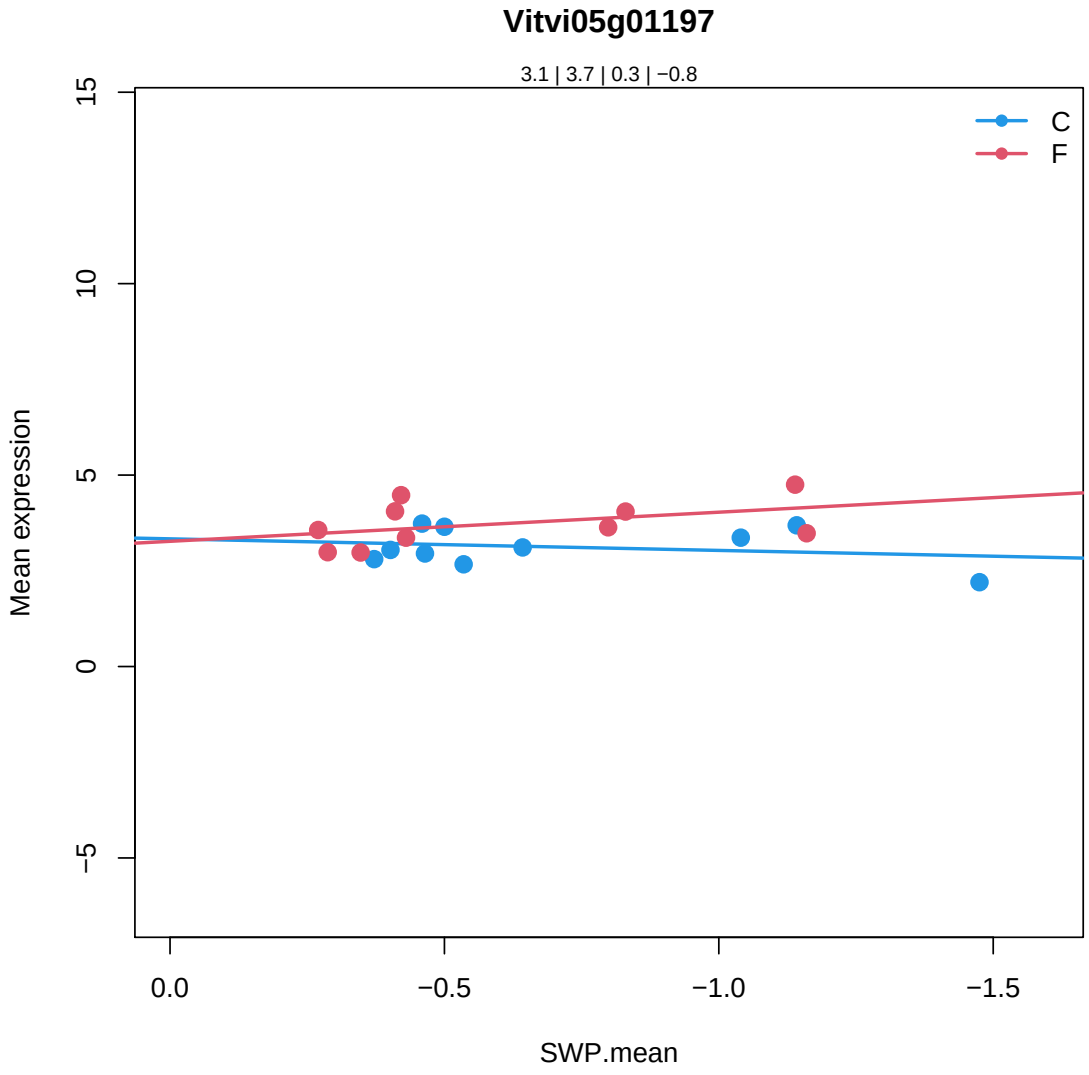
7.6.356 Vitvi05g01197: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01197
        35.2
        not assigned.unknown
        TIM-barrel signal transduction protein |
        Chr5:26521893-26524986 REVERSE LENGTH=754 |
        201606
```

Coefficients for Vitvi05g01197.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.121846	8.79067e-15	***	1.4784e-14	***
SlopeC	0.3021357	0.5211723		0.8739914	
MeanF-MeanC	0.6114854	0.0166598	*	0.1100688	
SlopeF-SlopeC	-1.062576	0.1378976		0.9999488	



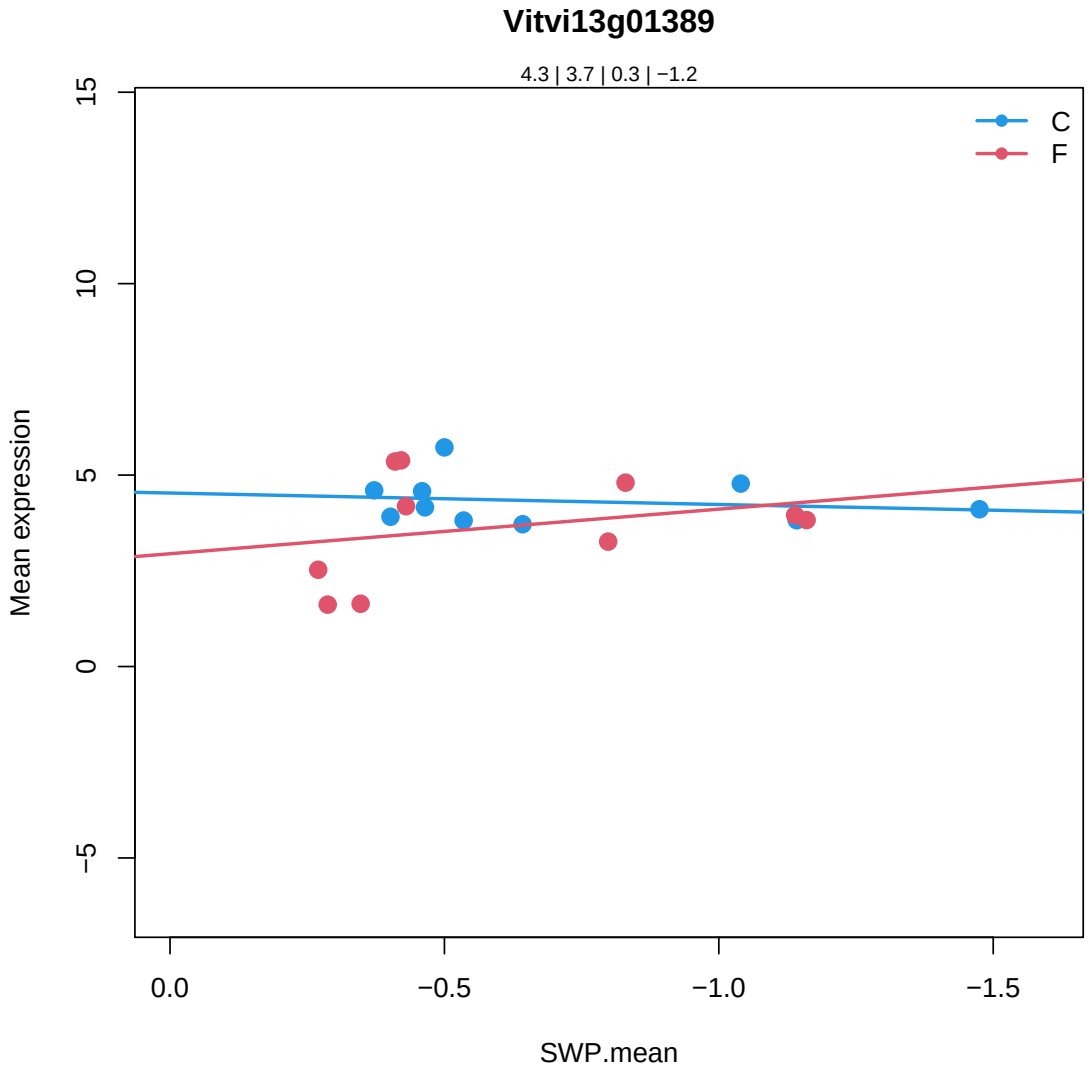
7.6.357 Vitvi13g01389: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g01389
        26.3.5
        misc.gluco-, galacto- and mannosidases.glycosyl hydrolase family 5
        alpha/beta-Hydrolases superfamily protein |
        Chr1:25766018-25767028 FORWARD LENGTH=336 |
        201606
```

Coefficients for Vitvi13g01389.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.320334	2.939879e-12	***	4.113996e-12	***
SlopeC	0.2992675	0.7308957		0.9406676	
MeanF-MeanC	-0.6654281	0.1420638		0.4524313	
SlopeF-SlopeC	-1.463353	0.2649146		0.9999488	



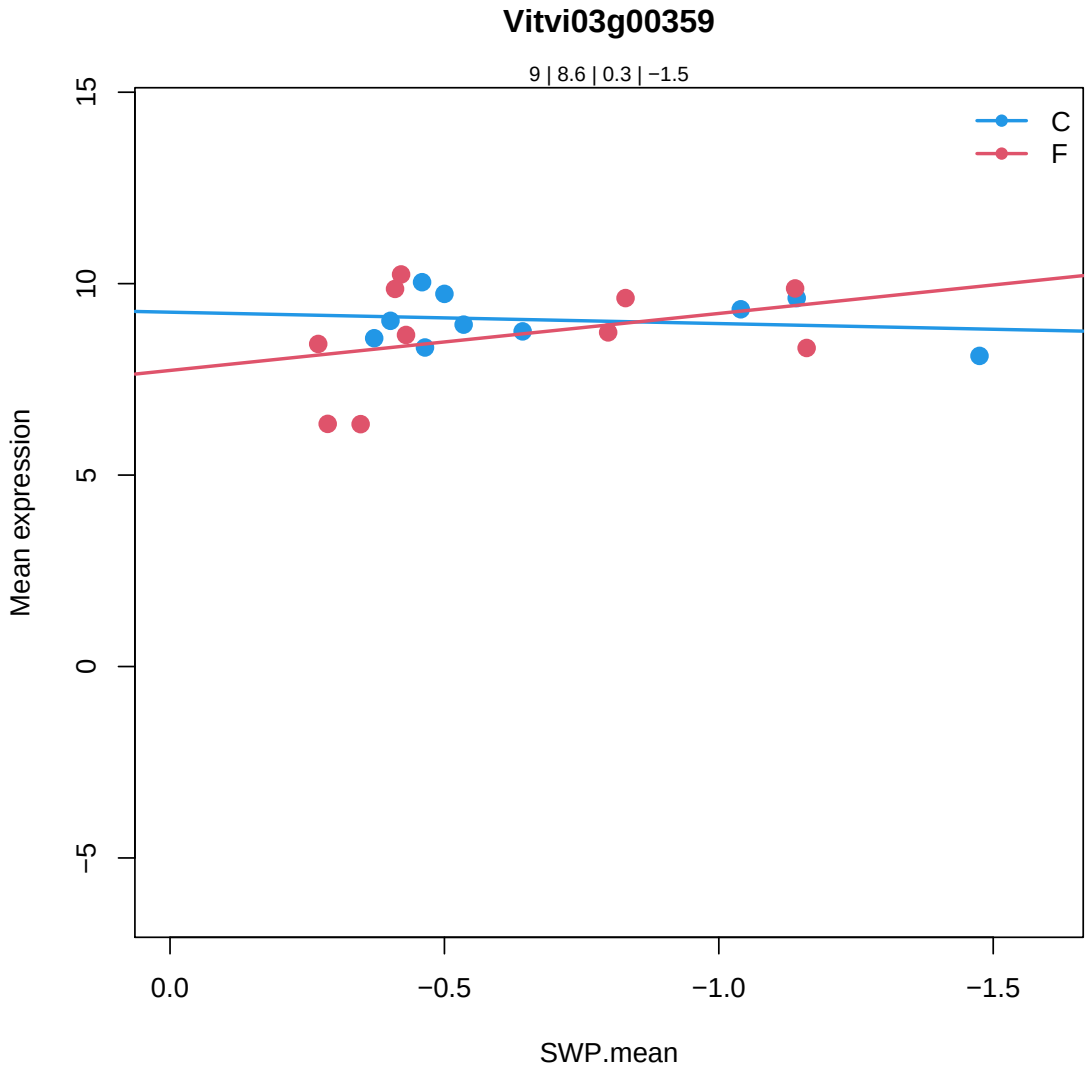
7.6.358 Vitvi03g00359: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00359
        34.2
        transport.sugars
        polyol/monosaccharide transporter 5 |
        Chr3:6489000-6491209 REVERSE LENGTH=539 |
        201606
```

Coefficients for Vitvi03g00359.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	9.045167	6.107813e-19	***	2.242719e-18	***
SlopeC	0.2970256	0.7284363		0.9399615	
MeanF-MeanC	-0.4054301	0.3553766		0.7131863	
SlopeF-SlopeC	-1.785669	0.1697227		0.9999488	



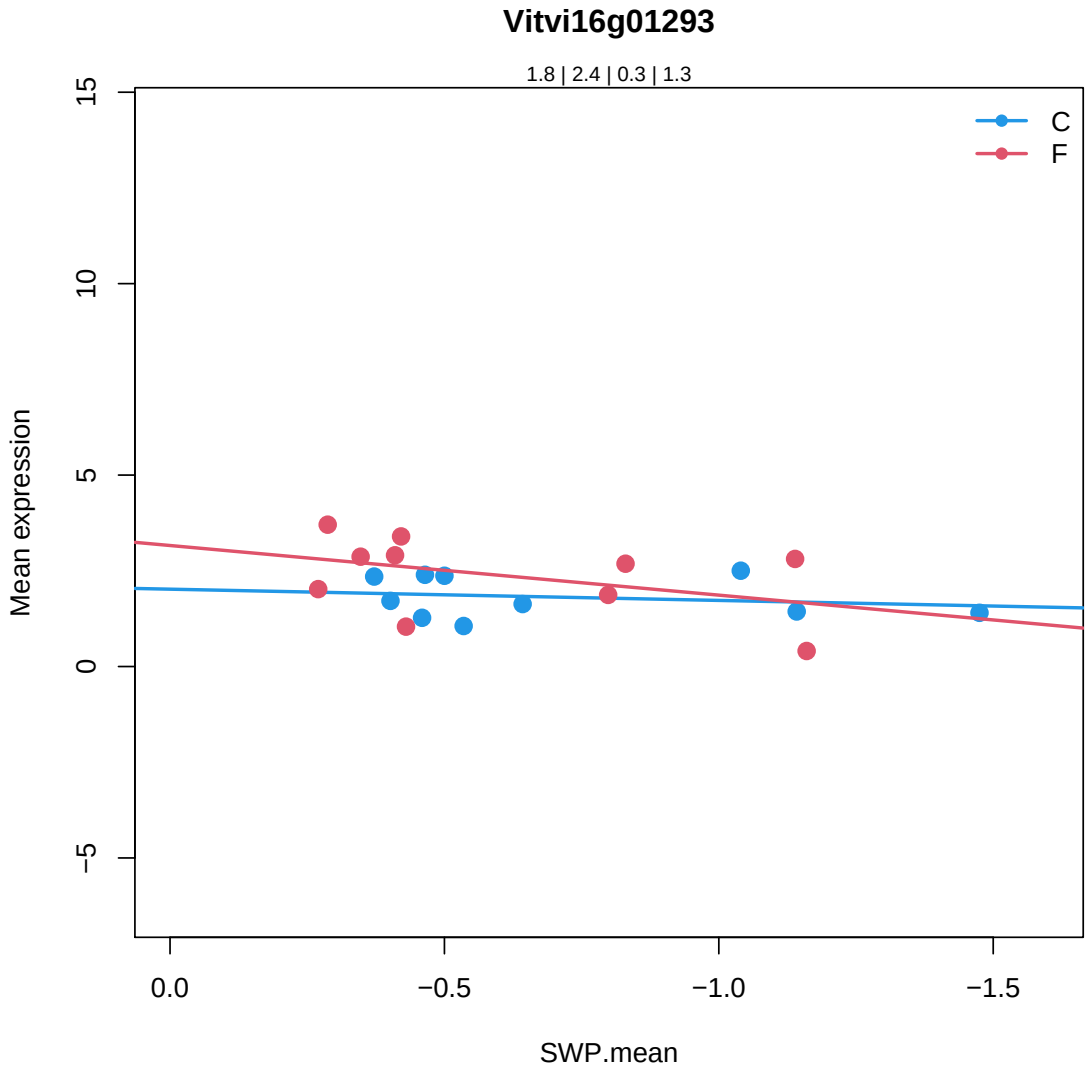
7.6.359 Vitvi16g01293: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01293
        35.2
        not assigned.unknown
        receptor Serine/Threonine kinase-like protein |
        Chr4:10087343-10090234 REVERSE LENGTH=689 |
        201606
```

Coefficients for Vitvi16g01293.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.813396	1.151912e-07	***	1.364427e-07	***
SlopeC	0.2936787	0.6558542		0.9203044	
MeanF-MeanC	0.5574085	0.1060046		0.3782122	
SlopeF-SlopeC	1.002285	0.3116115		0.9999488	



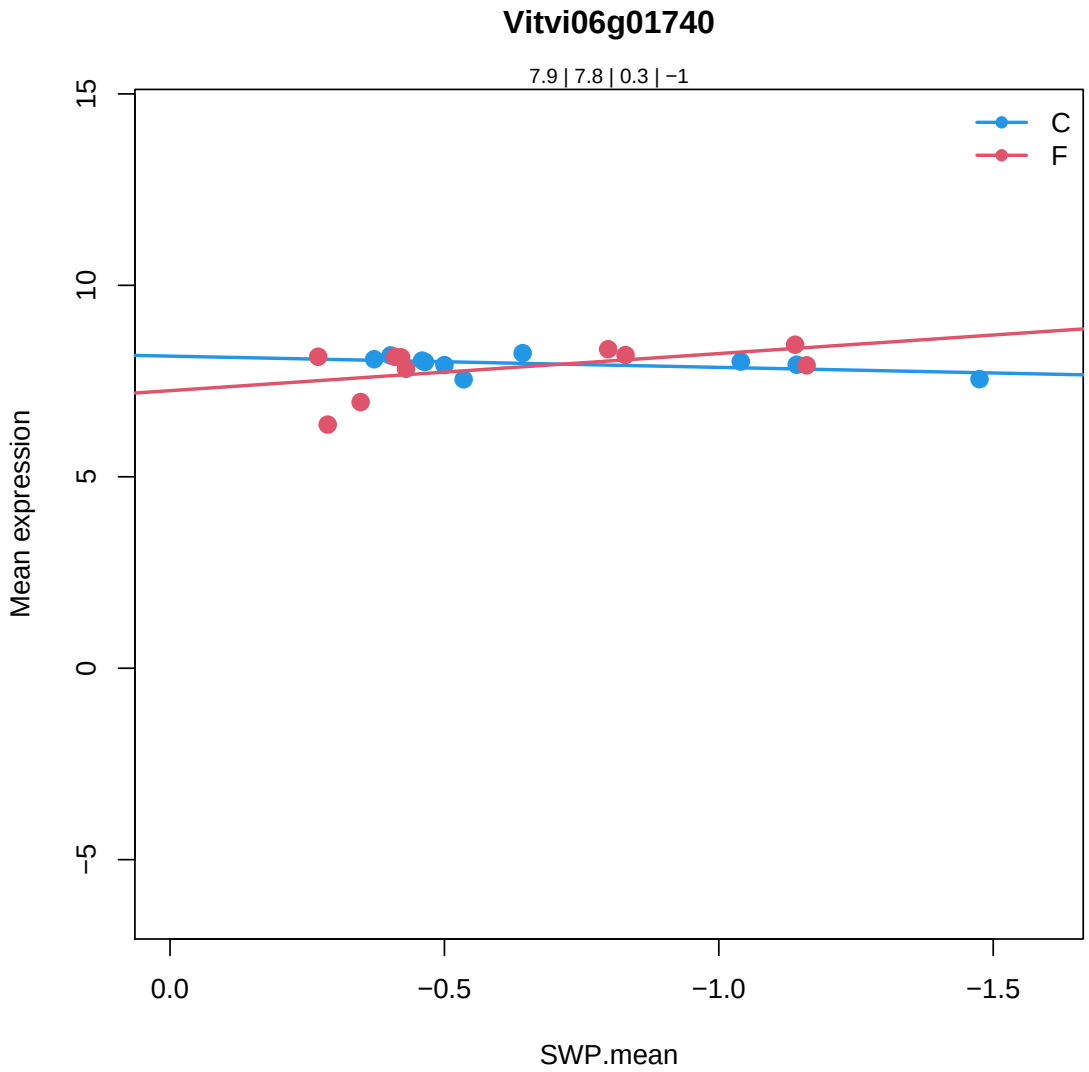
7.6.360 Vitvi06g01740: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01740
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi06g01740.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.945183	2.086903e-24	***	1.165149e-22	***
SlopeC	0.2932758	0.4811918		0.8640958	
MeanF-MeanC	-0.1056666	0.6165591		0.8673367	
SlopeF-SlopeC	-1.262628	0.05034364	.	0.9999488	



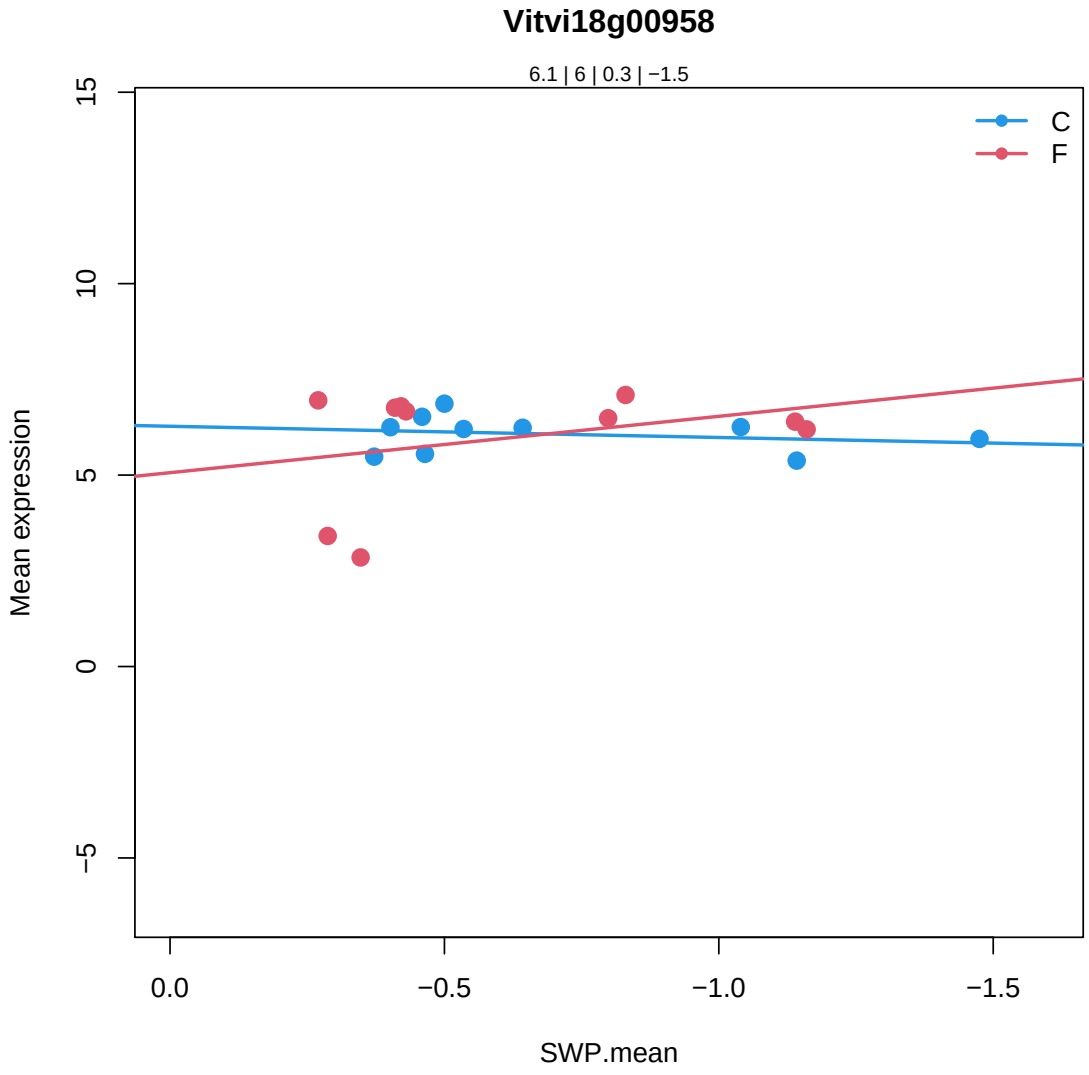
7.6.361 Vitvi18g00958: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00958
        35.2
        not assigned.unknown
        Erythronate-4-phosphate dehydrogenase family protein |
        Chr1:6712948-6713676 REVERSE LENGTH=242 |
        201606
```

Coefficients for Vitvi18g00958.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.068844	6.339308e-15	***	1.081649e-14	***
SlopeC	0.2928942	0.7441975		0.9454913	
MeanF-MeanC	-0.1092374	0.8106802		0.9474118	
SlopeF-SlopeC	-1.764915	0.194842		0.9999488	



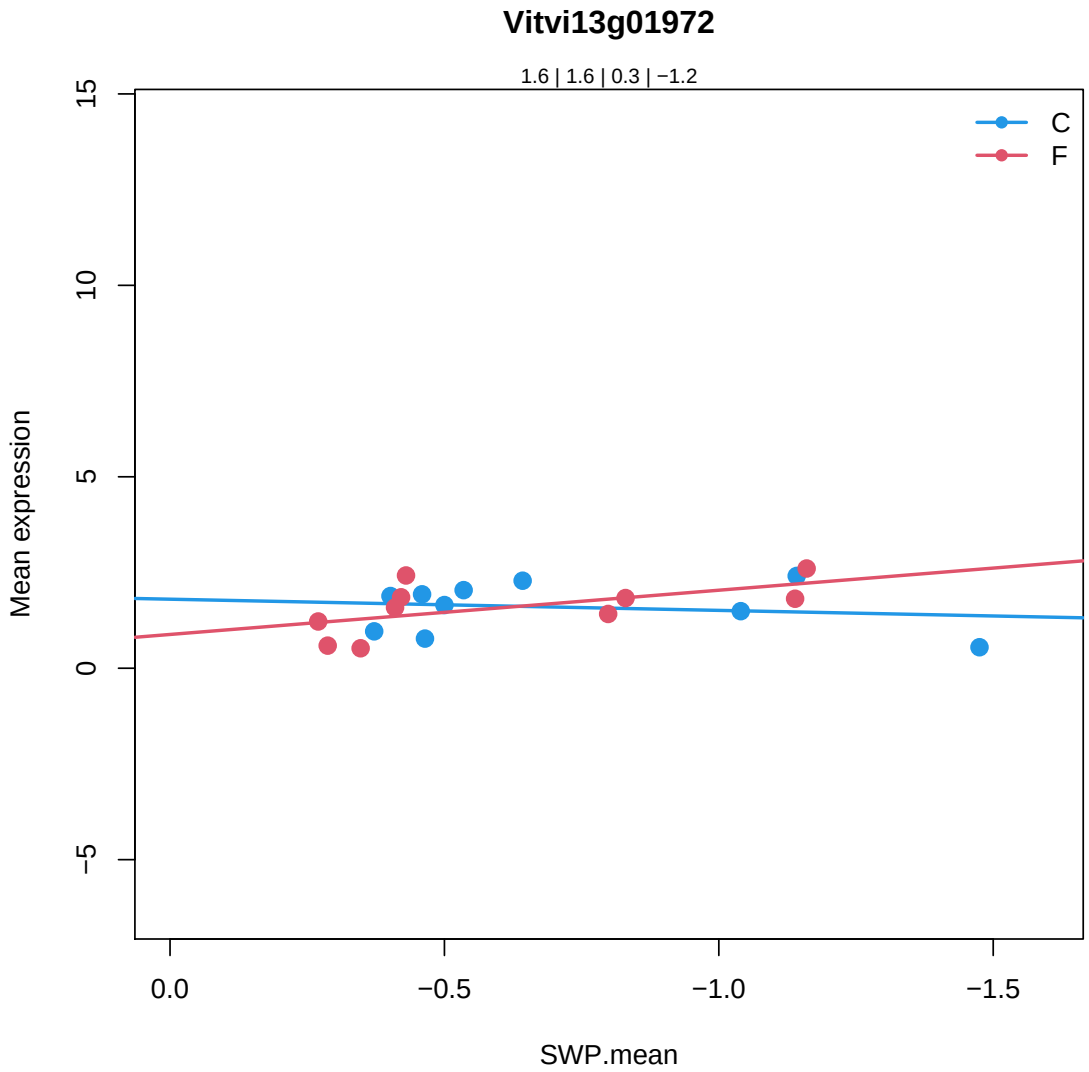
7.6.362 Vitvi13g01972: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g01972
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi13g01972.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.597442	3.015012e-08	***	3.627057e-08	***
SlopeC	0.2922733	0.5852105		0.8970963	
MeanF-MeanC	-0.01148007	0.9662414		0.9922153	
SlopeF-SlopeC	-1.447763	0.0790069	.	0.9999488	



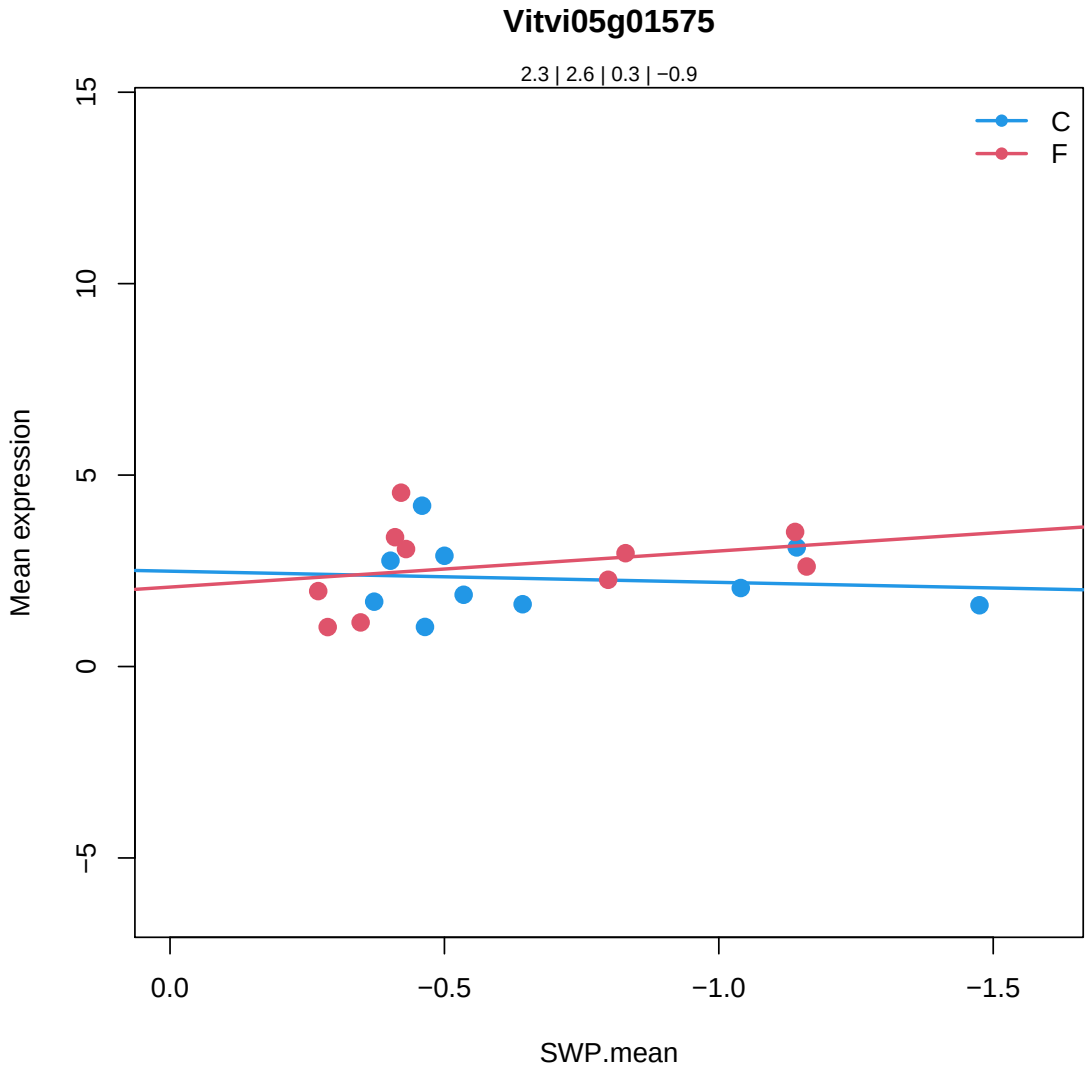
7.6.363 Vitvi05g01575: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01575
        20.1.7.3
        stress.biotic.PR-proteins.PR3/4/8/11 (chitinases and chitin binding pr
        homolog of carrot EP3-3 chitinase |
        Chr3:20145935-20147034 FORWARD LENGTH=273 |
        201606
```

Coefficients for Vitvi05g01575.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.284425	1.298036e-07	***	1.535599e-07	***
SlopeC	0.2920162	0.7267446		0.939826	
MeanF-MeanC	0.3644259	0.3943268		0.7416431	
SlopeF-SlopeC	-1.234535	0.3257699		0.9999488	



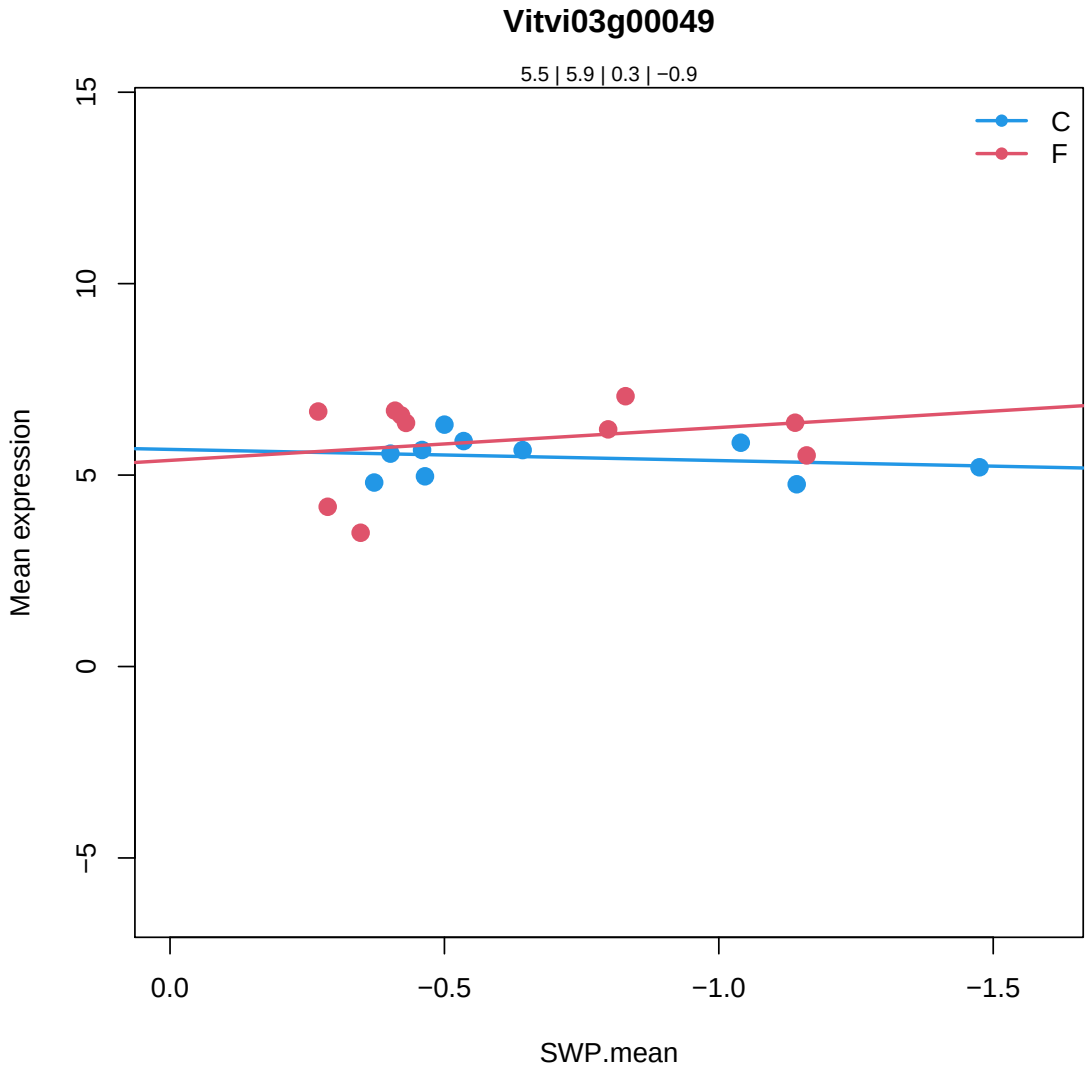
7.6.364 Vitvi03g00049: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00049
        27.3.7
        RNA.regulation of transcription.C2C2(Zn) Constans-like zinc finger fam
        B-box type zinc finger family protein |
        Chr4:18161576-18163045 FORWARD LENGTH=226 |
        201606
```

Coefficients for Vitvi03g00049.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.46554	1.397669e-15	***	2.571306e-15	***
SlopeC	0.2916635	0.6977323		0.9319854	
MeanF-MeanC	0.441084	0.2543987		0.6144105	
SlopeF-SlopeC	-1.149889	0.3086972		0.9999488	



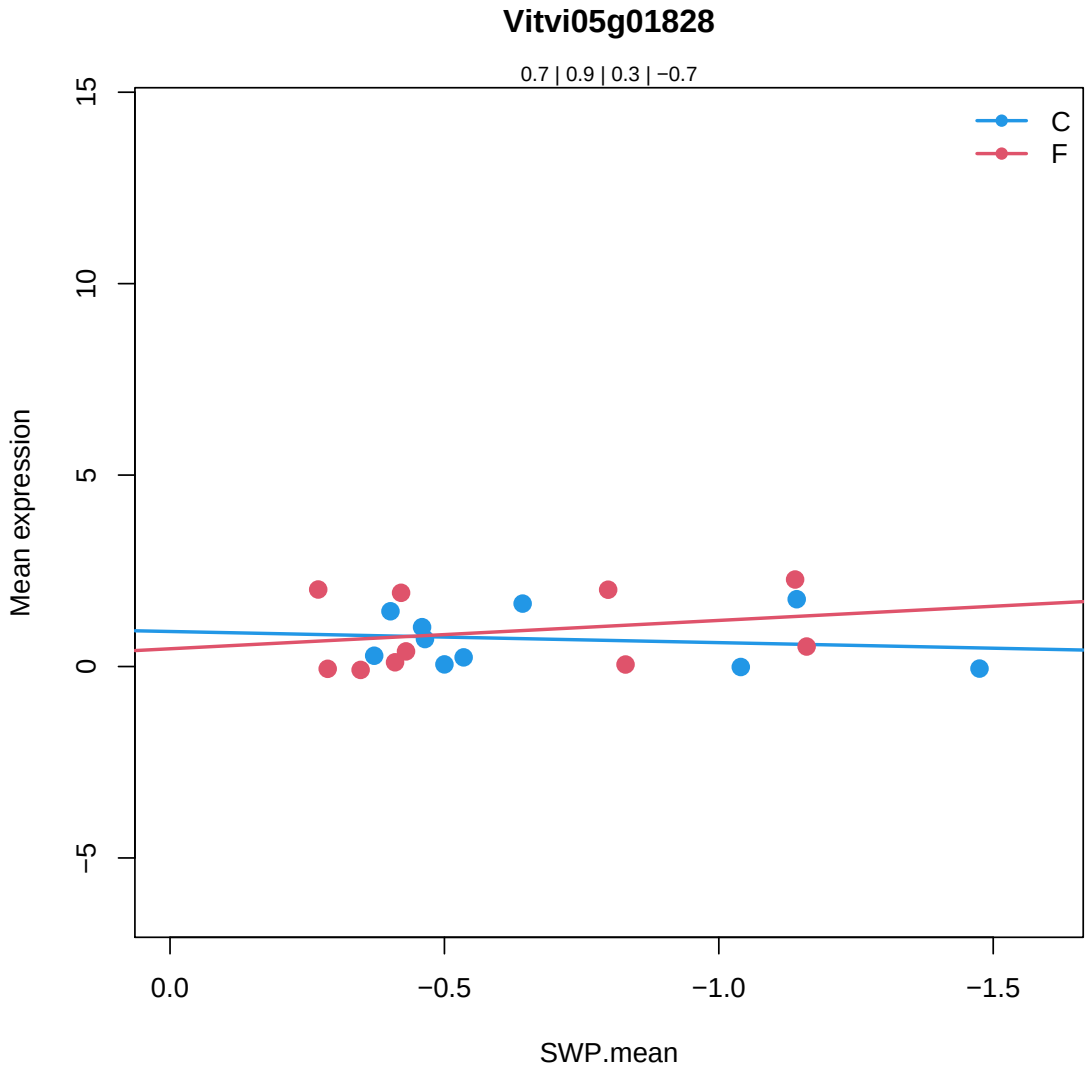
7.6.365 Vitvi05g01828: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01828
        20.1.7.1
        stress.biotic.PR-proteins.PR1 (antifungal)
        heat stable protein 1 |
        Chr3:5882318-5882896 FORWARD LENGTH=109 |
        201606
```

Coefficients for Vitvi05g01828.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.7097107	0.01162506	*	0.01229797	*
SlopeC	0.2910128	0.6883283		0.9306347	
MeanF-MeanC	0.2048571	0.579218		0.8515913	
SlopeF-SlopeC	-1.031238	0.3438027		0.9999488	



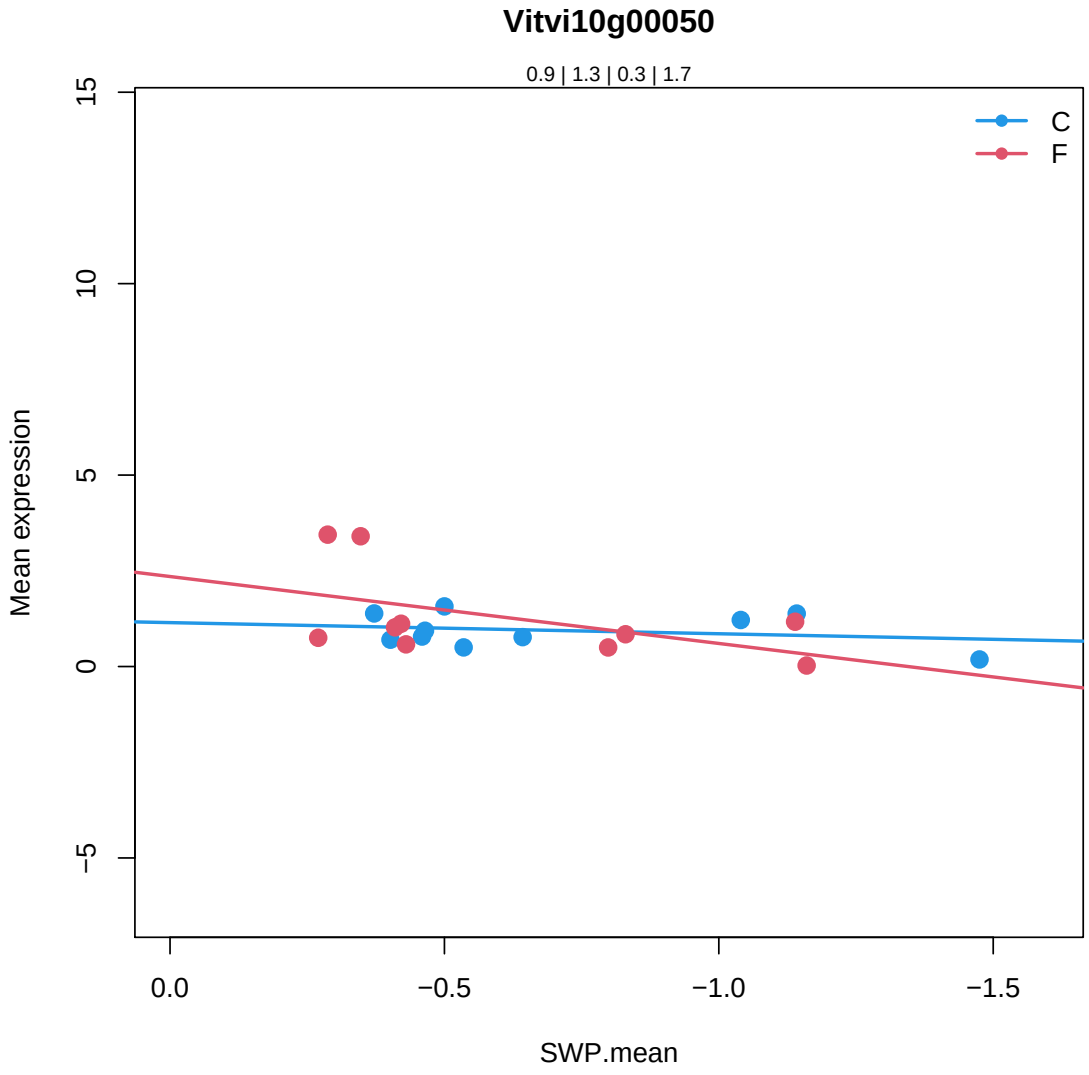
7.6.366 Vitvi10g00050: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00050
        20.1.7.3
        stress.biotic.PR-proteins.PR3/4/8/11 (chitinases and chitin binding pr
        chitin elicitor receptor kinase 1 |
        Chr3:7615543-7618530 REVERSE LENGTH=617 |
        201606
```

Coefficients for Vitvi10g00050.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.9422019	0.000689632	***	0.0007494205	***
SlopeC	0.2907029	0.6648318		0.9233473	
MeanF-MeanC	0.3429942	0.3192391		0.6801111	
SlopeF-SlopeC	1.457688	0.1534052		0.9999488	



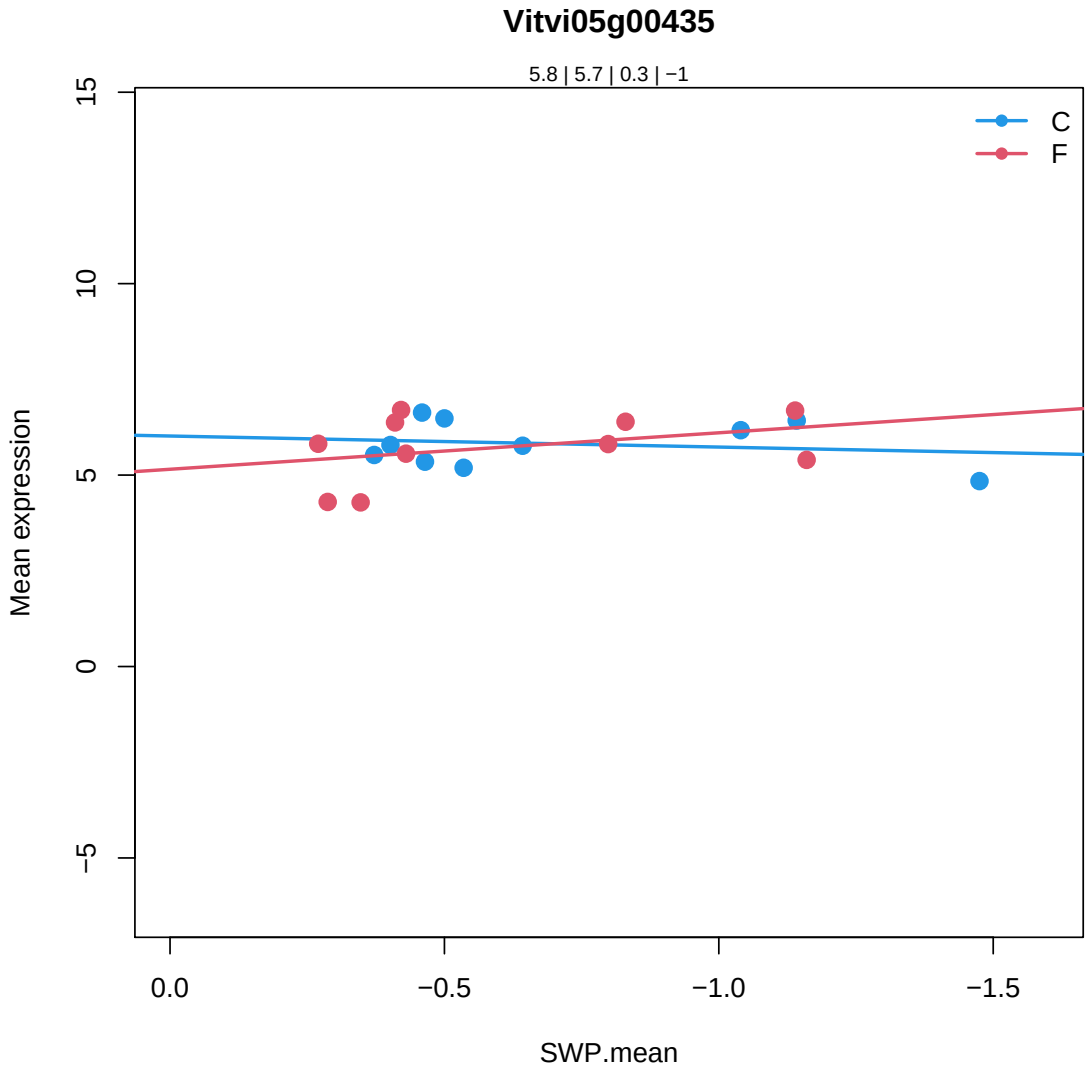
7.6.367 Vitvi05g00435: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00435
        27.3.16
        RNA.regulation of transcription.CCAAT box binding factor family, HAP5
        nuclear factor Y%2C subunit C9 |
        Chr1:2883144-2883839 FORWARD LENGTH=231 |
        201606
```

Coefficients for Vitvi05g00435.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.816973	8.239469e-18	***	2.218834e-17	***
SlopeC	0.2886762	0.6435339		0.9164577	
MeanF-MeanC	-0.08481032	0.7887656		0.9400551	
SlopeF-SlopeC	-1.241431	0.1891432		0.9999488	



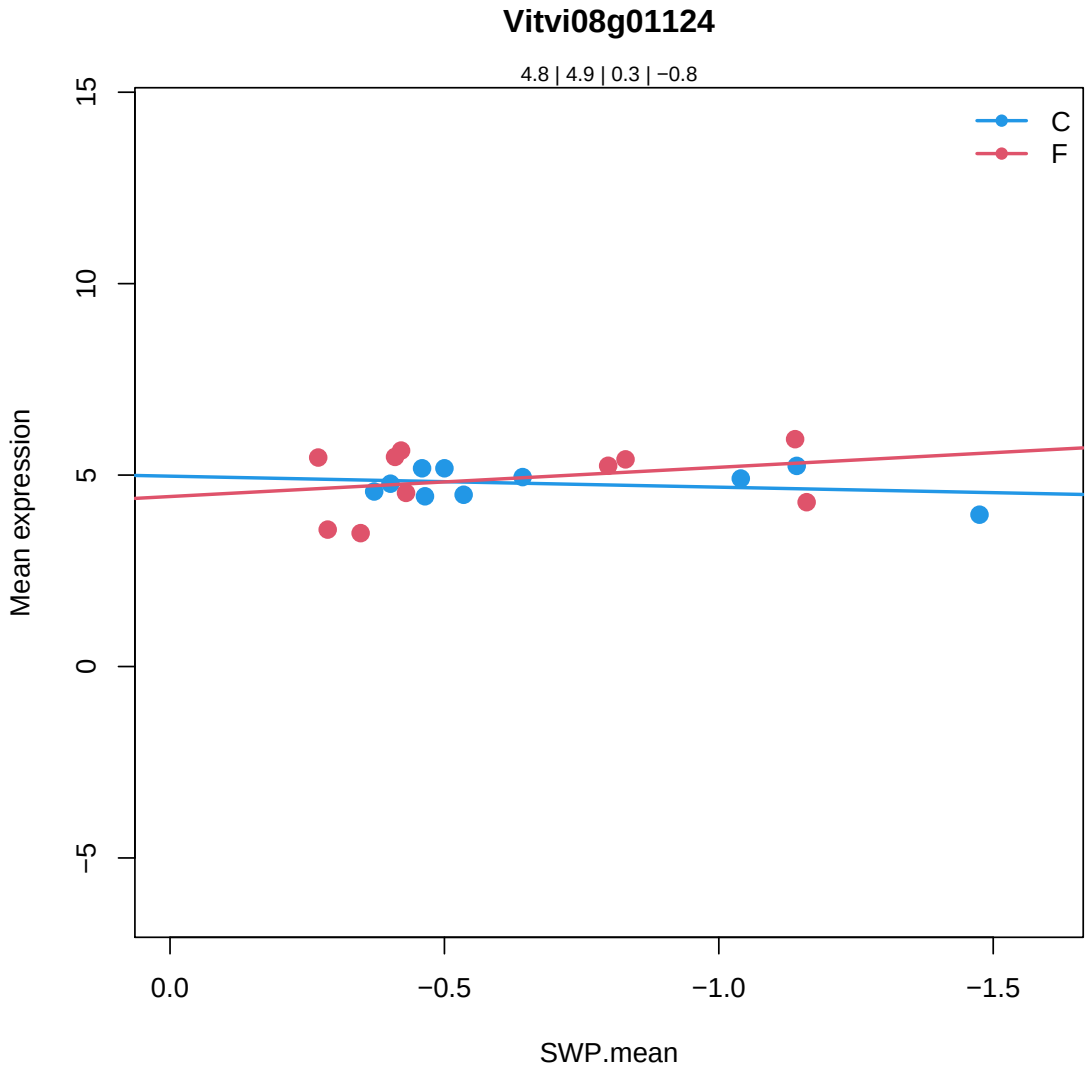
7.6.368 Vitvi08g01124: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01124
        29.4
        protein.postranslational modification
        Protein phosphatase 2C family protein |
        Chr3:19070387-19071975 FORWARD LENGTH=294 |
        201606
```

Coefficients for Vitvi08g01124.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.76949	1.004412e-16	***	2.182982e-16	***
SlopeC	0.2871181	0.6188969		0.9085813	
MeanF-MeanC	0.1354081	0.6443099		0.8791917	
SlopeF-SlopeC	-1.050747	0.2279997		0.9999488	



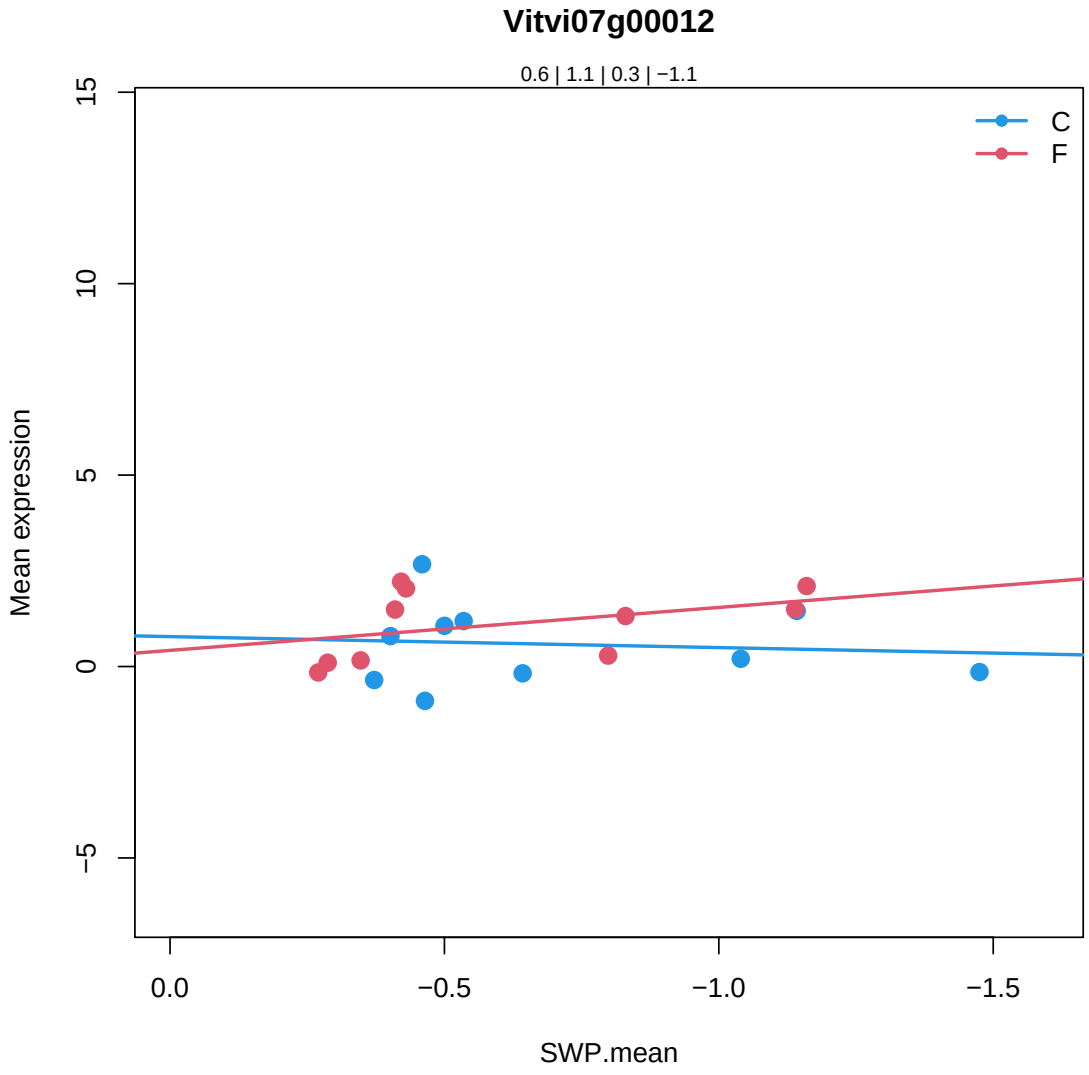
7.6.369 Vitvi07g00012: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g00012
        26.10
        misc.cytochrome P450
        cytochrome P450%2C family 94%2C subfamily B%2C polypeptide 1 |
        Chr5:25408987-25410519 REVERSE LENGTH=510 |
        201606
```

Coefficients for Vitvi07g00012.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.5795464	0.05531741	.	0.05755276	.
SlopeC	0.2868589	0.721958		0.9391174	
MeanF-MeanC	0.5250318	0.2079963		0.5525554	
SlopeF-SlopeC	-1.408865	0.2471439		0.9999488	



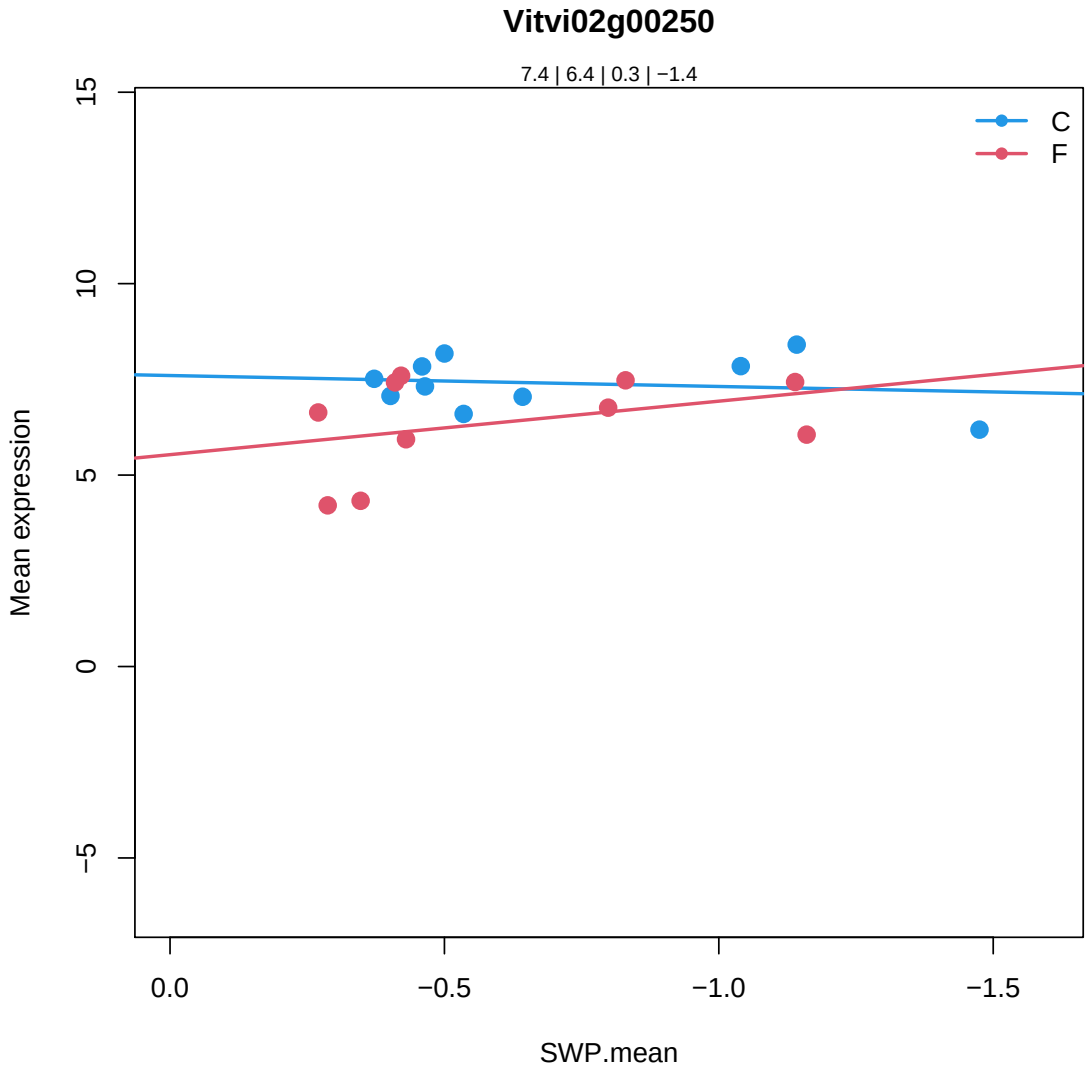
7.6.370 Vitvi02g00250: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00250
        2.1.2.2
        major CHO metabolism.synthesis.starch.starch synthase
        UDP-Glycosyltransferase superfamily protein |
        Chr1:11920582-11923506 REVERSE LENGTH=610 |
        201606
```

Coefficients for Vitvi02g00250.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.399116	1.367901e-17	***	3.503536e-17	***
SlopeC	0.2859914	0.7247393		0.9394623	
MeanF-MeanC	-1.014587	0.02104105	*	0.1306881	
SlopeF-SlopeC	-1.683128	0.1726533		0.9999488	



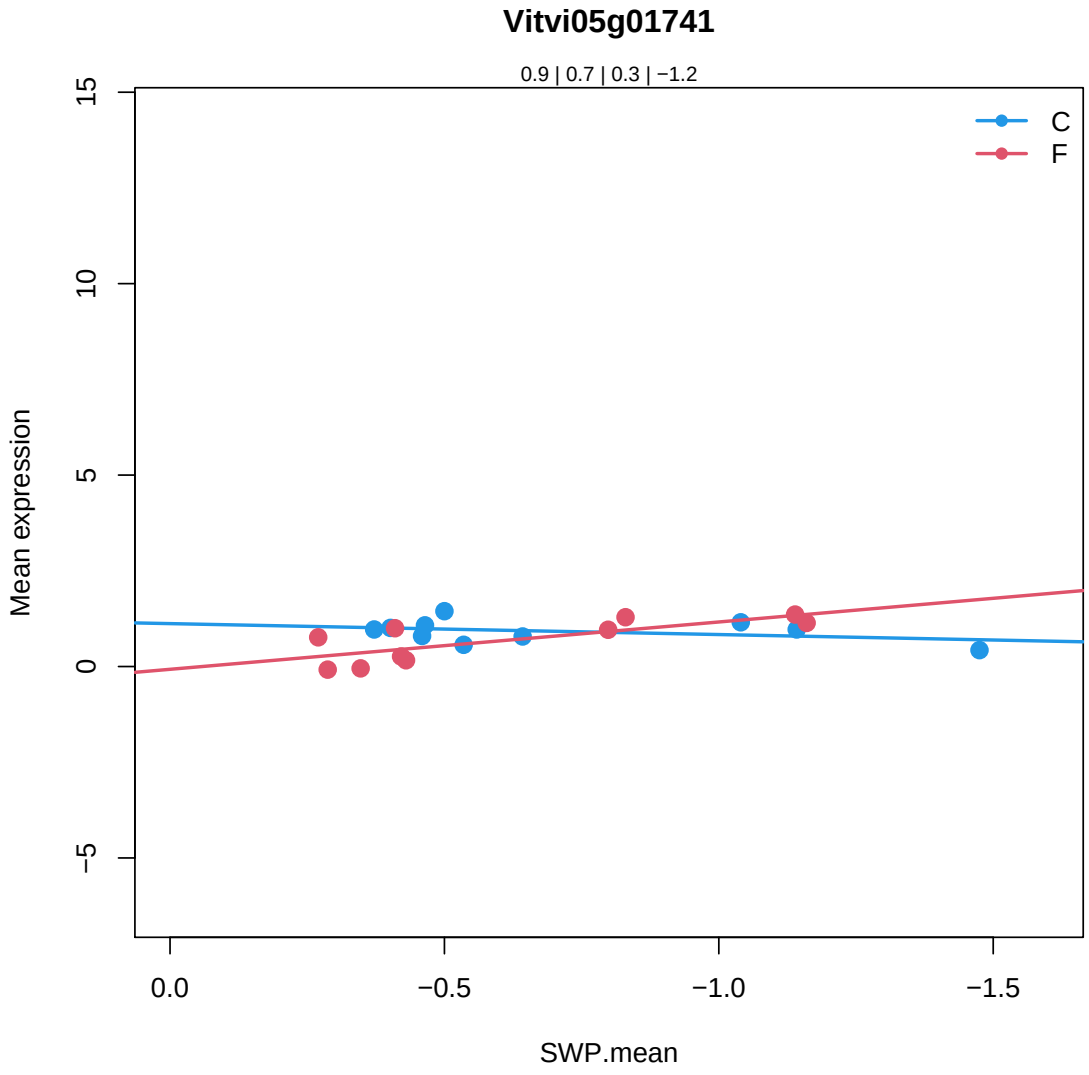
7.6.371 Vitvi05g01741: + type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01741
        16.8.2
        secondary metabolism.flavonoids.chalcones
        NAD(P)-linked oxidoreductase superfamily protein |
        Chr1:22071410-22073067 REVERSE LENGTH=326 |
        201606
```

Coefficients for Vitvi05g01741.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.9195647	1.557365e-07	***	1.838395e-07	***
SlopeC	0.2853512	0.4048484		0.836381	
MeanF-MeanC	-0.2394175	0.1750494		0.5072438	
SlopeF-SlopeC	-1.521349	0.006071775	**	0.9999488	



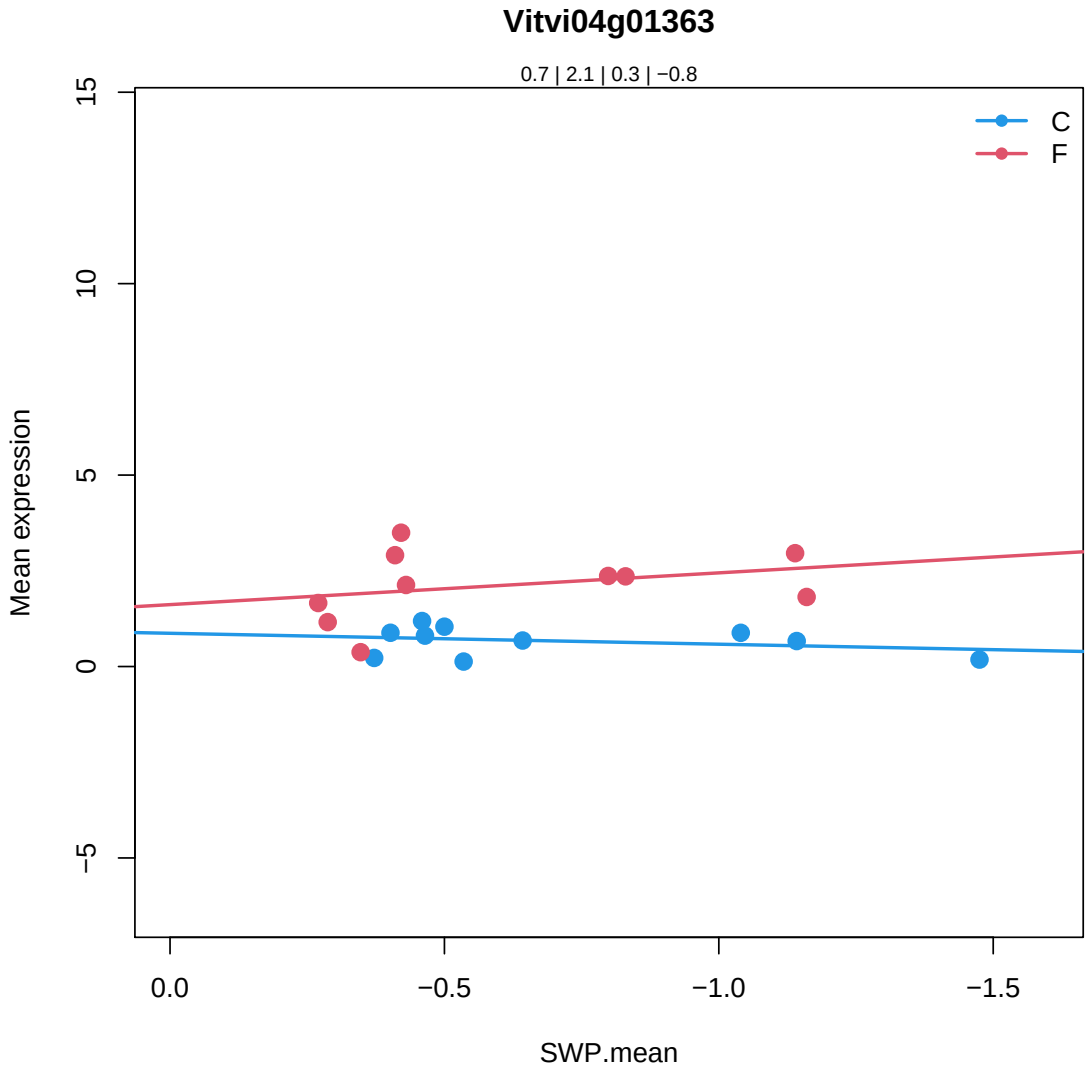
7.6.372 Vitvi04g01363: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01363
        35.2
        not assigned.unknown
        basic leucine-zipper 44 |
        Chr1:28292224-28292745 FORWARD LENGTH=173 |
        201606
```

Coefficients for Vitvi04g01363.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6674426	0.004211469	**	0.004500225	**
SlopeC	0.2851592	0.6279781		0.9108941	
MeanF-MeanC	1.454605	6.630421e-05	***	0.001264842	**
SlopeF-SlopeC	-1.114719	0.2103732		0.9999488	



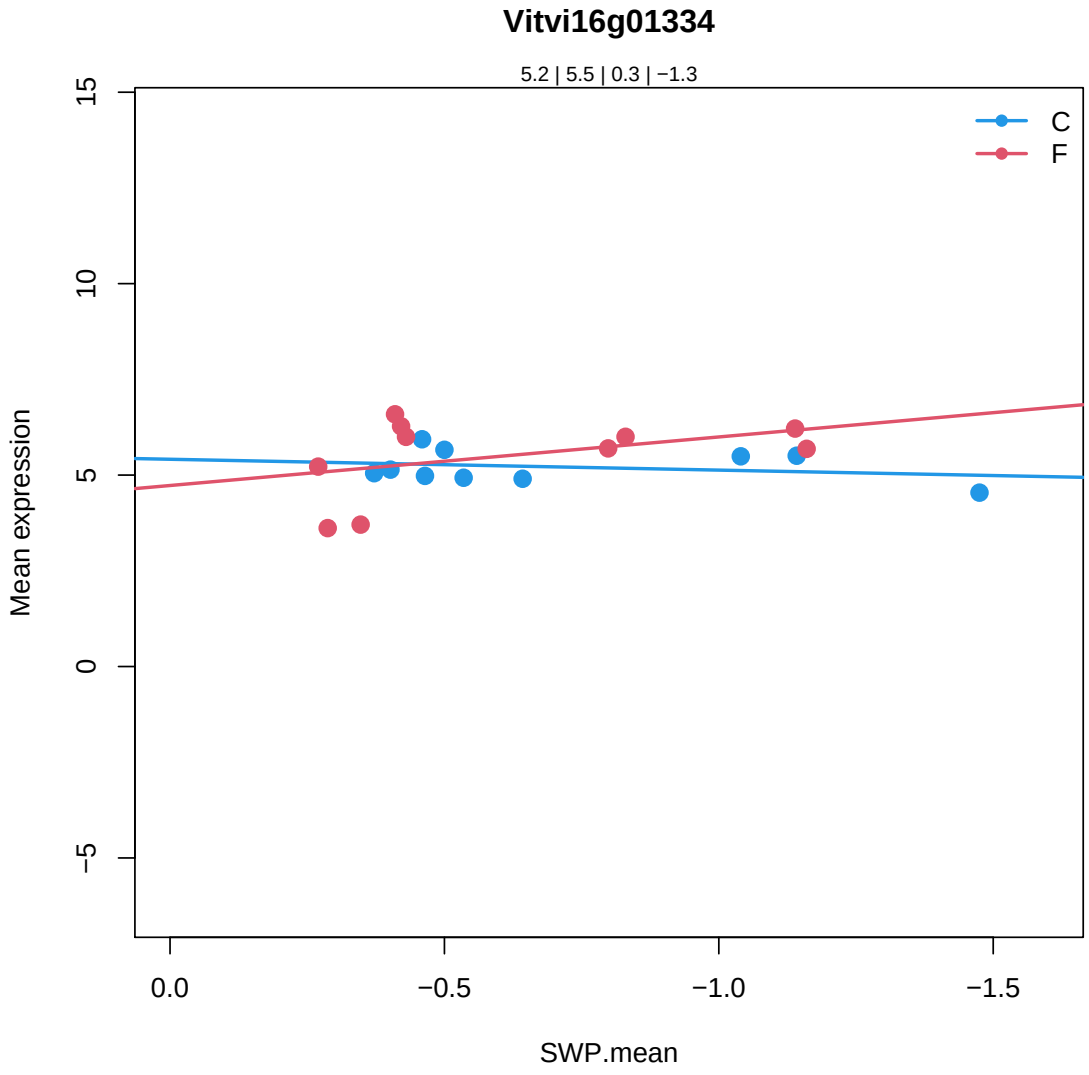
7.6.373 Vitvi16g01334: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01334
        26.6
        misc.O-methyl transferases
        O-methyltransferase 1 |
        Chr5:21982075-21984167 FORWARD LENGTH=363 |
        201606
```

Coefficients for Vitvi16g01334.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.213474	1.10026e-16	***	2.373696e-16	***
SlopeC	0.2833813	0.6545818		0.9201505	
MeanF-MeanC	0.28657	0.3767397		0.7286943	
SlopeF-SlopeC	-1.551482	0.1096508		0.9999488	



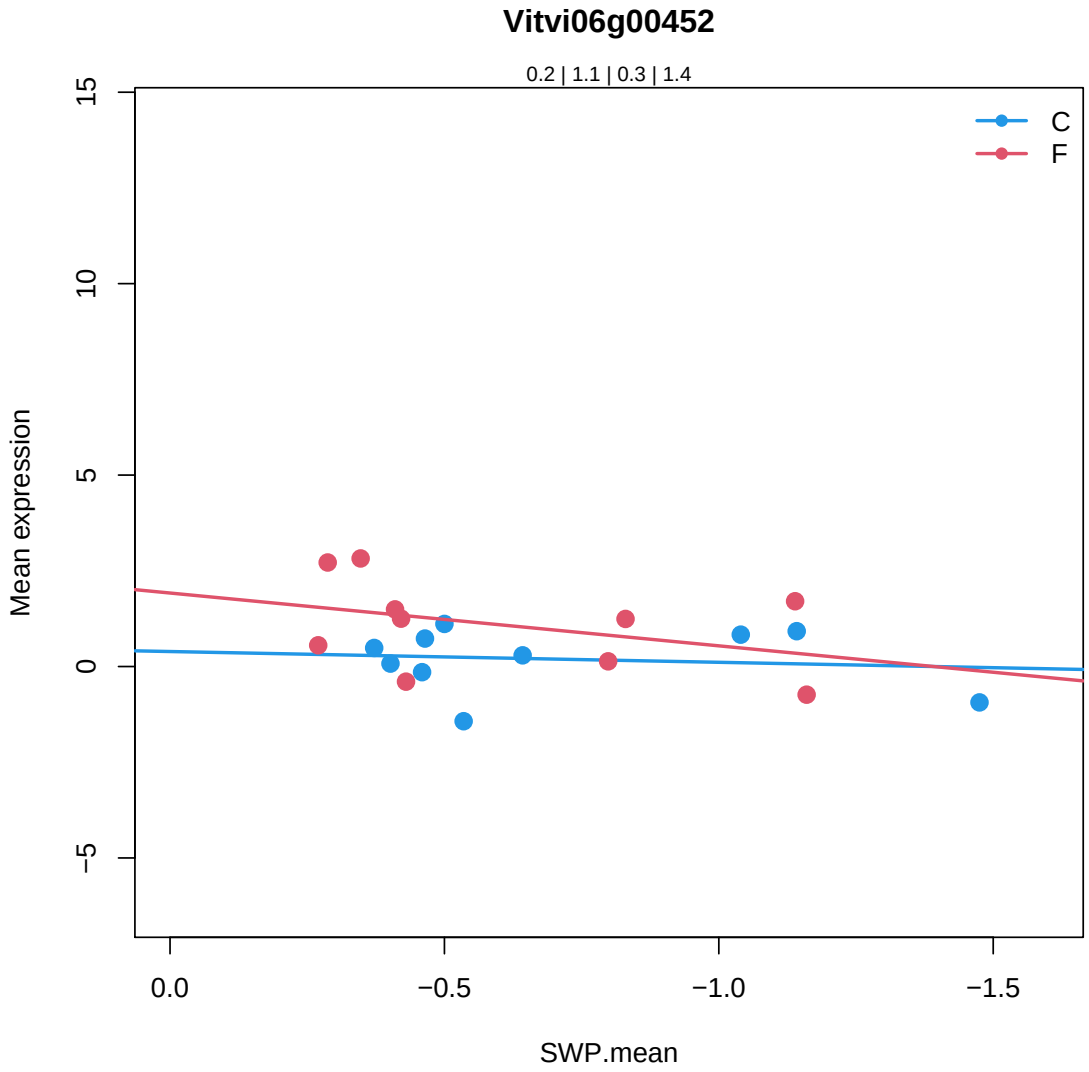
7.6.374 Vitvi06g00452: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00452
        35.2
        not assigned.unknown
        60S ribosomal protein L36 |
        Chr5:531066-532725 FORWARD LENGTH=176 |
        201606
```

Coefficients for Vitvi06g00452.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1936983	0.5151088		0.5211263	
SlopeC	0.2815984	0.7328211		0.9409827	
MeanF-MeanC	0.8850439	0.04414187	*	0.2206659	
SlopeF-SlopeC	1.097773	0.375072		0.9999488	



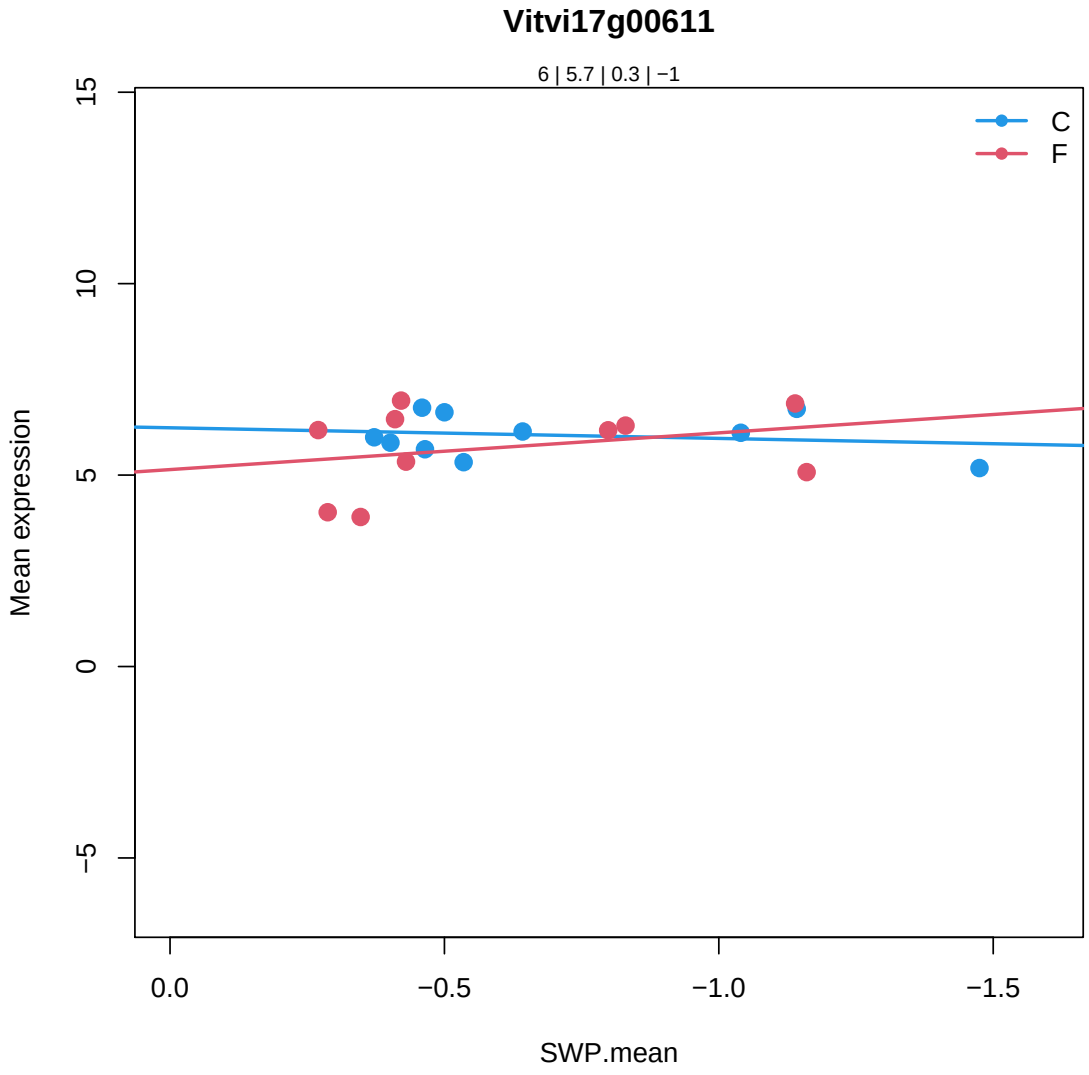
7.6.375 Vitvi17g00611: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00611
        27.3.8
        RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family
        cycling DOF factor 3 |
        Chr3:17504276-17505964 REVERSE LENGTH=448 |
        201606
```

Coefficients for Vitvi17g00611.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.039997	6.629536e-17	***	1.486428e-16	***
SlopeC	0.2773927	0.6982911		0.9319854	
MeanF-MeanC	-0.3125348	0.3935073		0.7408135	
SlopeF-SlopeC	-1.236635	0.2521899		0.9999488	



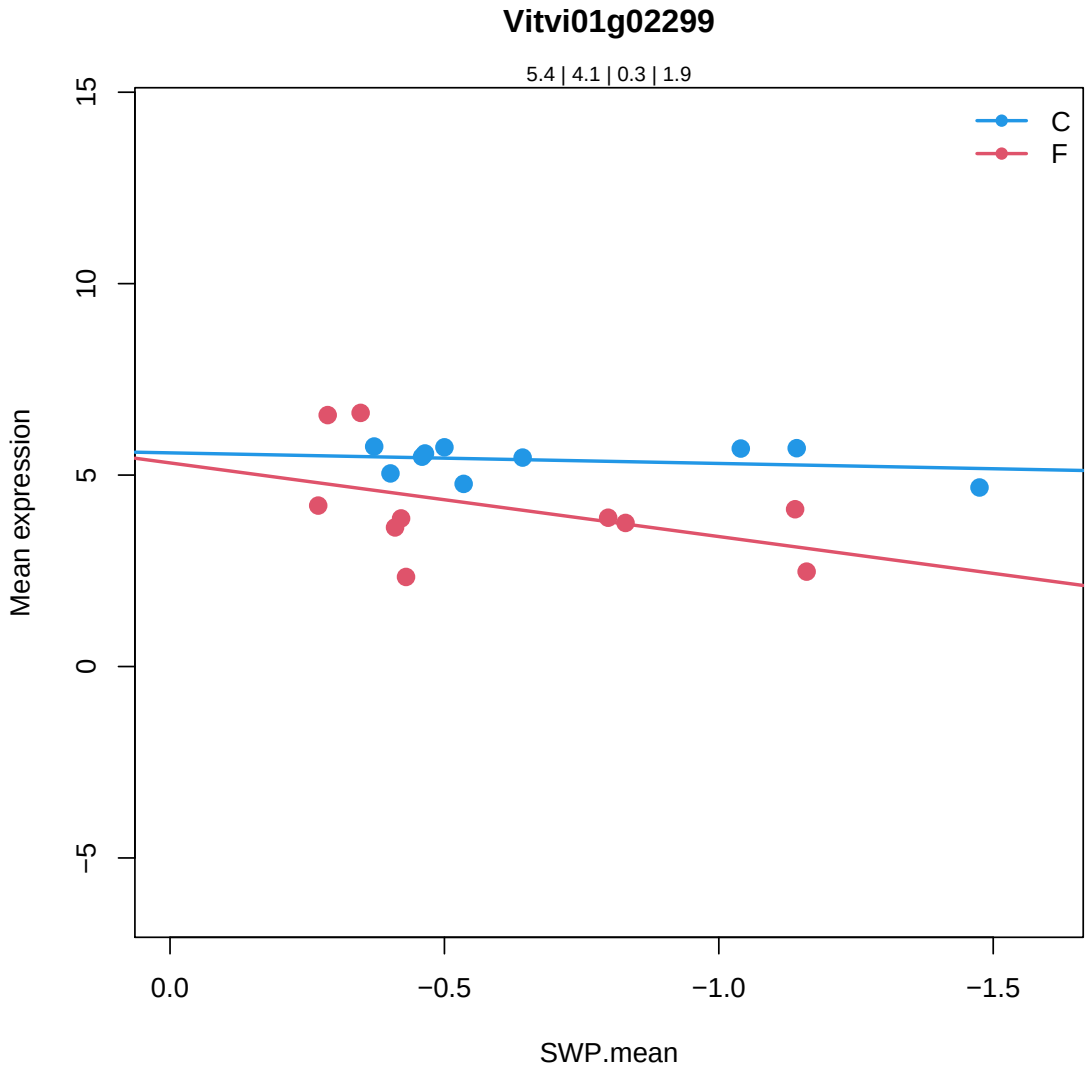
7.6.376 Vitvi01g02299: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g02299
        35.2
        not assigned.unknown
        Major facilitator superfamily protein |
        Chr5:4296854-4299079 REVERSE LENGTH=624 |
        201606
```

Coefficients for Vitvi01g02299.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.38558	7.345511e-15	***	1.245248e-14	***
SlopeC	0.2763339	0.7305845		0.9406676	
MeanF-MeanC	-1.240036	0.005587167	**	0.04964575	*
SlopeF-SlopeC	1.64721	0.1766302		0.9999488	



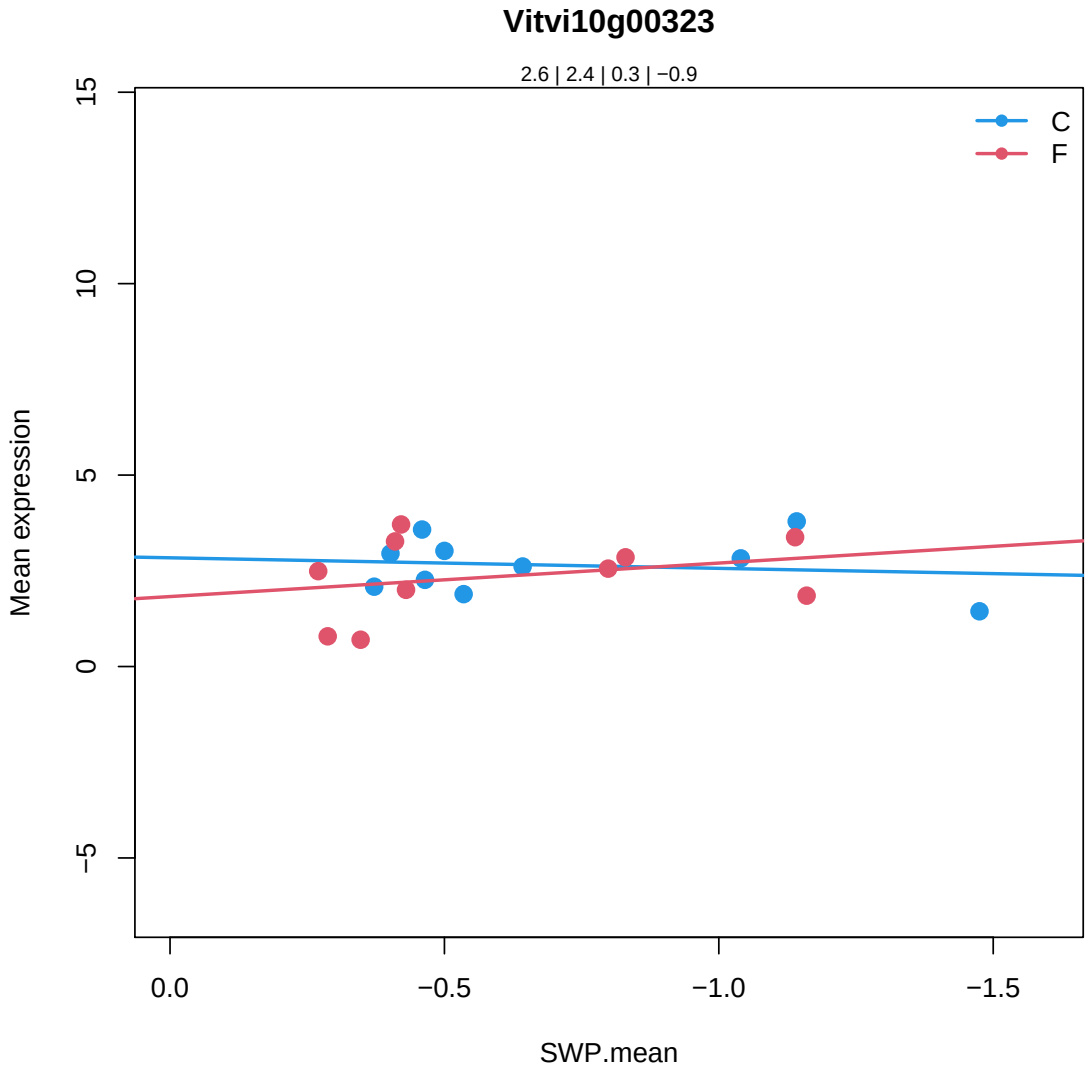
7.6.377 Vitvi10g00323: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00323
        27.3.6
        RNA.regulation of transcription.basic helix-loop-helix family (bHLH)
        basic helix-loop-helix (bHLH) DNA-binding superfamily protein |
        Chr3:7210654-7213199 REVERSE LENGTH=454 |
        201606
```

Coefficients for Vitvi10g00323.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.645695	1.480358e-09	***	1.856629e-09	***
SlopeC	0.2755805	0.7108964		0.9350571	
MeanF-MeanC	-0.2859738	0.4515646		0.77888	
SlopeF-SlopeC	-1.15004	0.3039958		0.9999488	



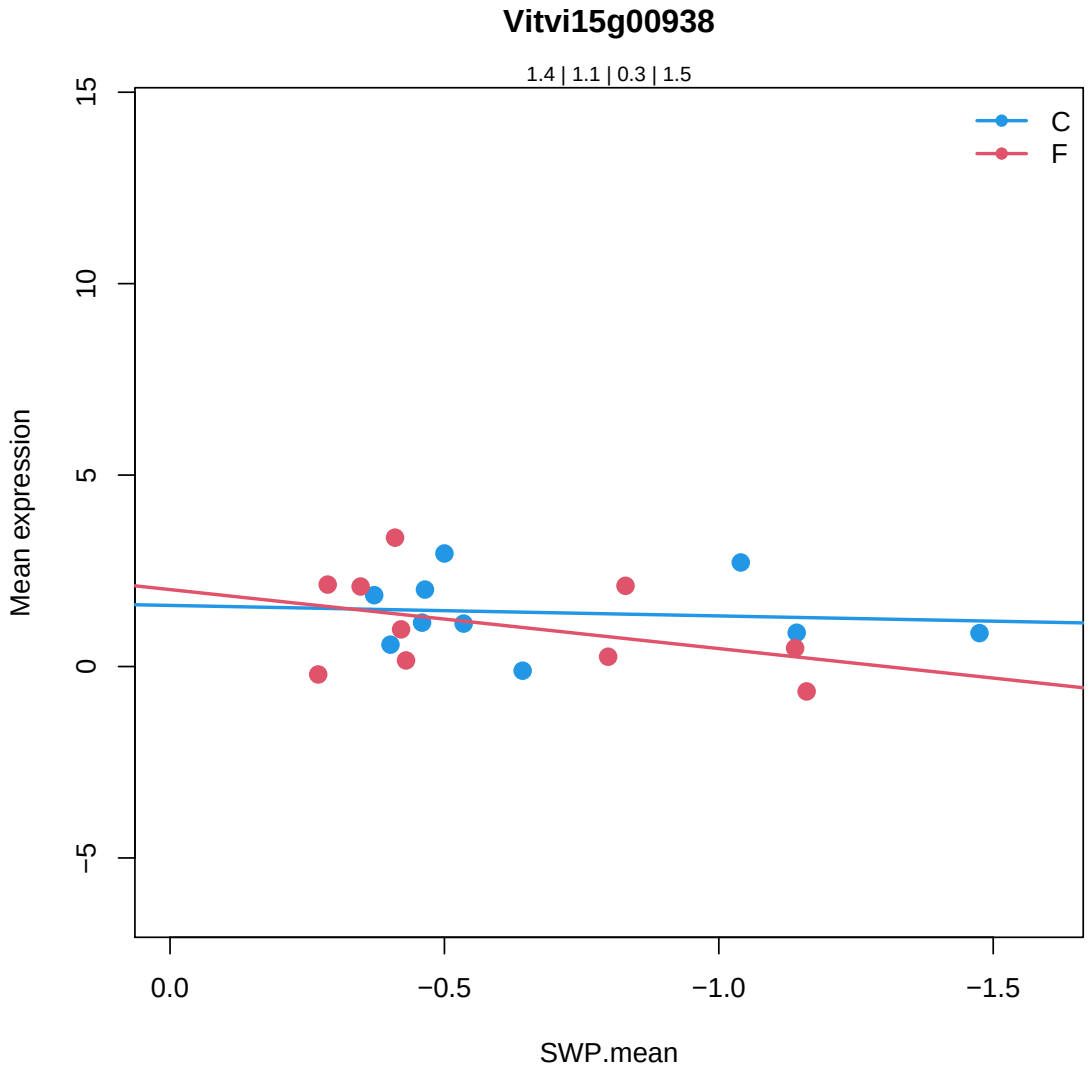
7.6.378 Vitvi15g00938: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g00938
        27.3.25
        RNA.regulation of transcription.MYB domain transcription factor family
        myb domain protein 3 |
        Chr1:8006289-8007219 FORWARD LENGTH=257 |
        201606
```

Coefficients for Vitvi15g00938.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.402506	0.0002545208	***	0.0002788131	***
SlopeC	0.2742268	0.7614849		0.9480154	
MeanF-MeanC	-0.3317438	0.47231		0.7900515	
SlopeF-SlopeC	1.266753	0.3506474		0.9999488	



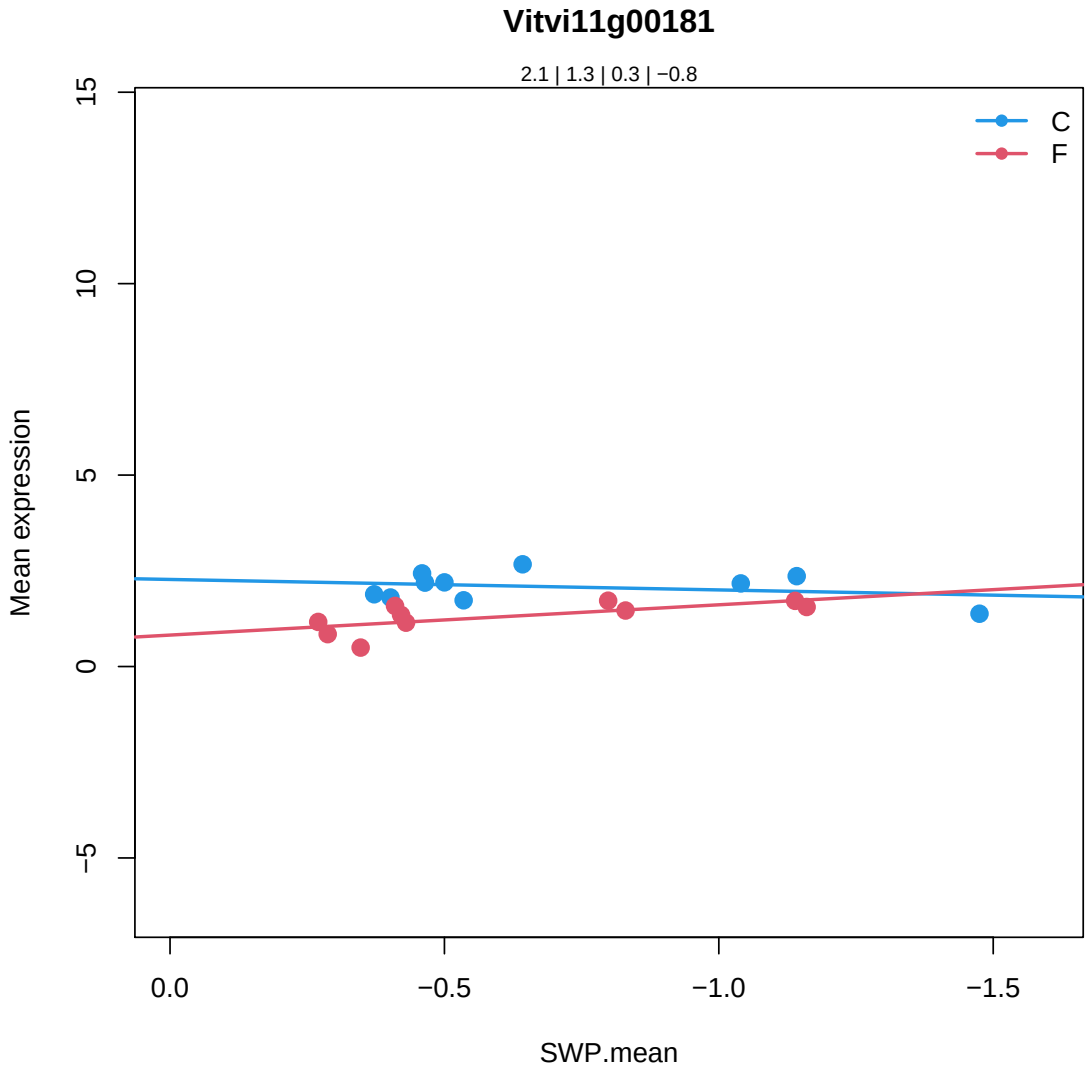
7.6.379 Vitvi11g00181: + type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00181
        33.99
        development.unspecified
        transducin family protein / WD-40 repeat family protein |
        Chr1:27022424-27024380 FORWARD LENGTH=407 |
        201606
```

Coefficients for Vitvi11g00181.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.081777	7.680607e-14	***	1.190076e-13	***
SlopeC	0.273475	0.4353422		0.8492896	
MeanF-MeanC	-0.7787816	0.0002102071	***	0.003401249	**
SlopeF-SlopeC	-1.064466	0.04979981	*	0.9999488	



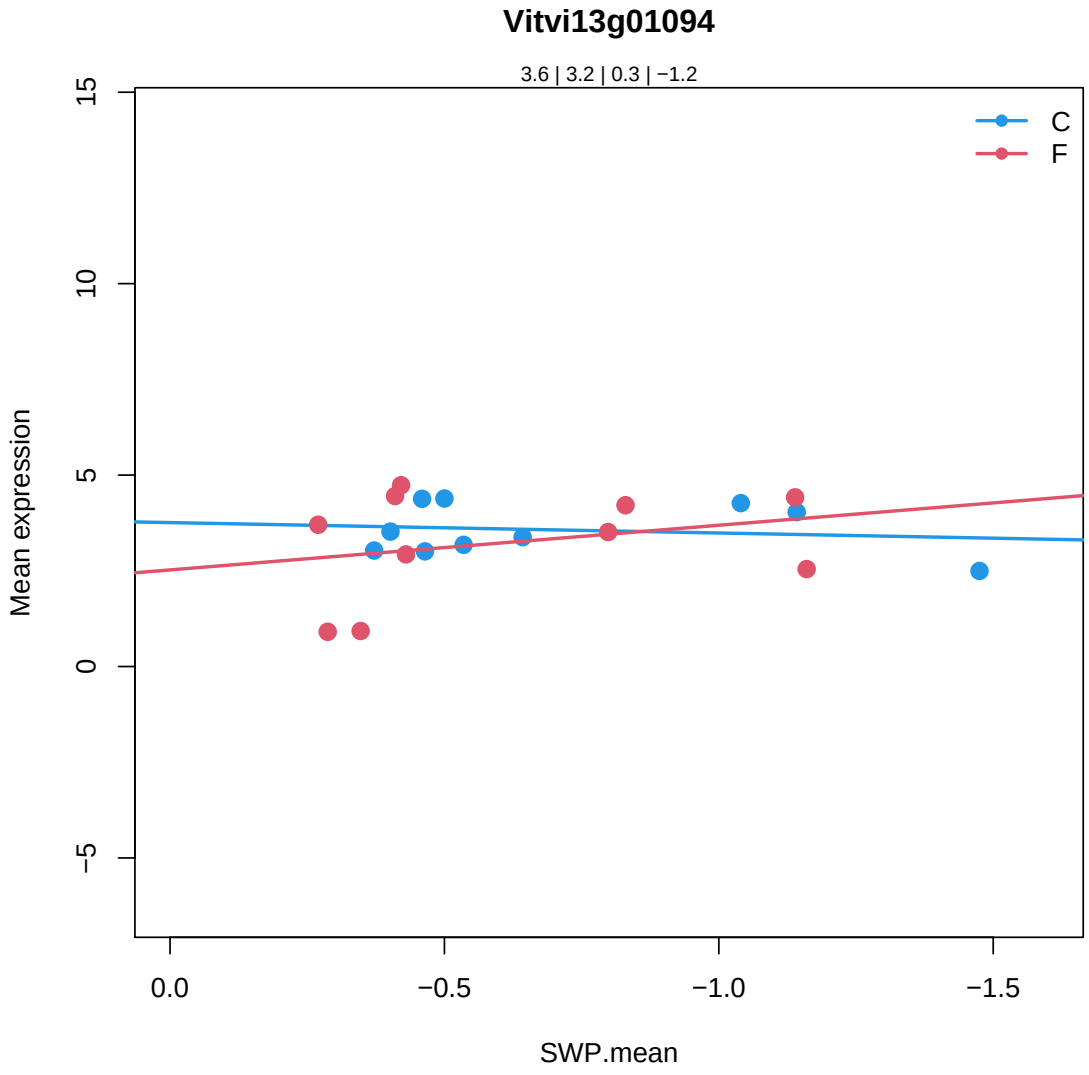
7.6.380 Vitvi13g01094: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g01094
        34.16
        transport.ABC transporters and multidrug resistance systems
        zinc induced facilitator 1 |
        Chr5:4432689-4436190 FORWARD LENGTH=442 |
        201606
```

Coefficients for Vitvi13g01094.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.568097	1.751731e-10	***	2.272137e-10	***
SlopeC	0.2711201	0.7609343		0.9479775	
MeanF-MeanC	-0.3341301	0.4631033		0.785863	
SlopeF-SlopeC	-1.437505	0.2844796		0.9999488	



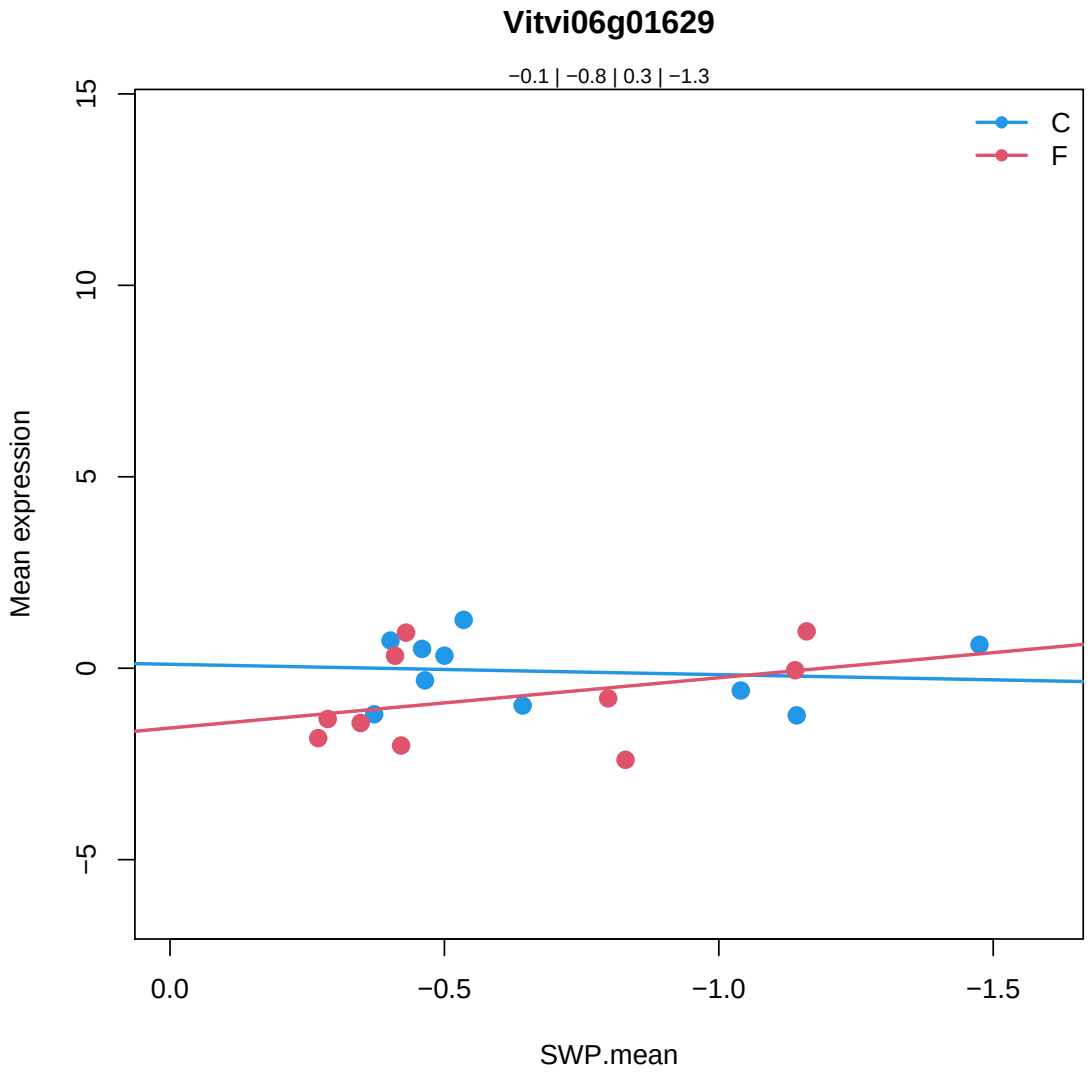
7.6.381 Vitvi06g01629: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01629
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi06g01629.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	−0.08797268	0.7770378		0.7812408	
SlopeC	0.2705435	0.7543135		0.9474313	
MeanF−MeanC	−0.6739894	0.1349236		0.4391427	
SlopeF−SlopeC	−1.583621	0.2259633		0.9999488	



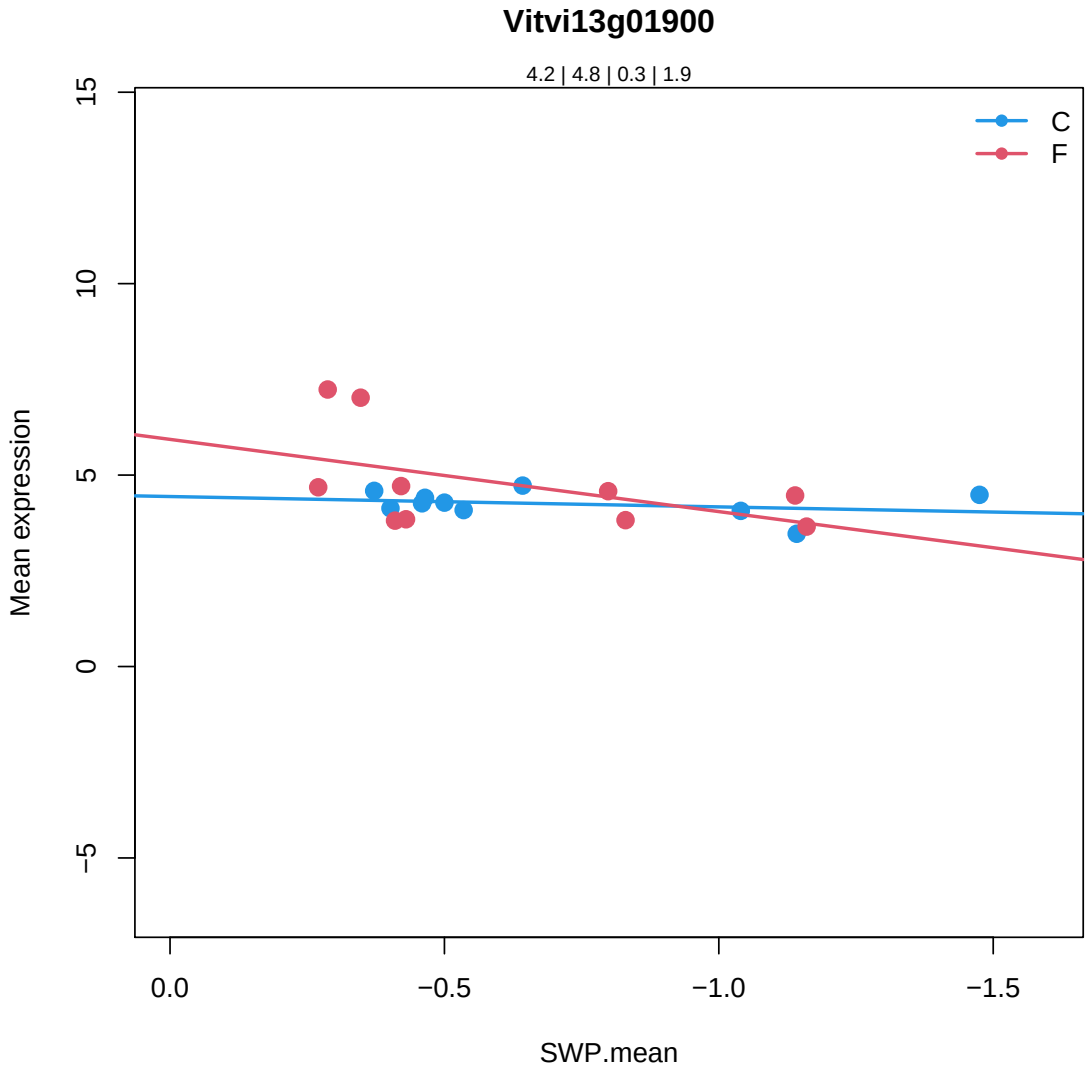
7.6.382 Vitvi13g01900: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g01900
        20.2.3
        stress.abiotic.drought/salt
        polyadenylate-binding protein interacting protein |
        Chr4:8218517-8219037 FORWARD LENGTH=143 |
        201606
```

Coefficients for Vitvi13g01900.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.24977	8.117726e-14	***	1.255381e-13	***
SlopeC	0.2703391	0.7048389		0.9342808	
MeanF-MeanC	0.5331216	0.1509645		0.4679686	
SlopeF-SlopeC	1.61592	0.1377695		0.9999488	



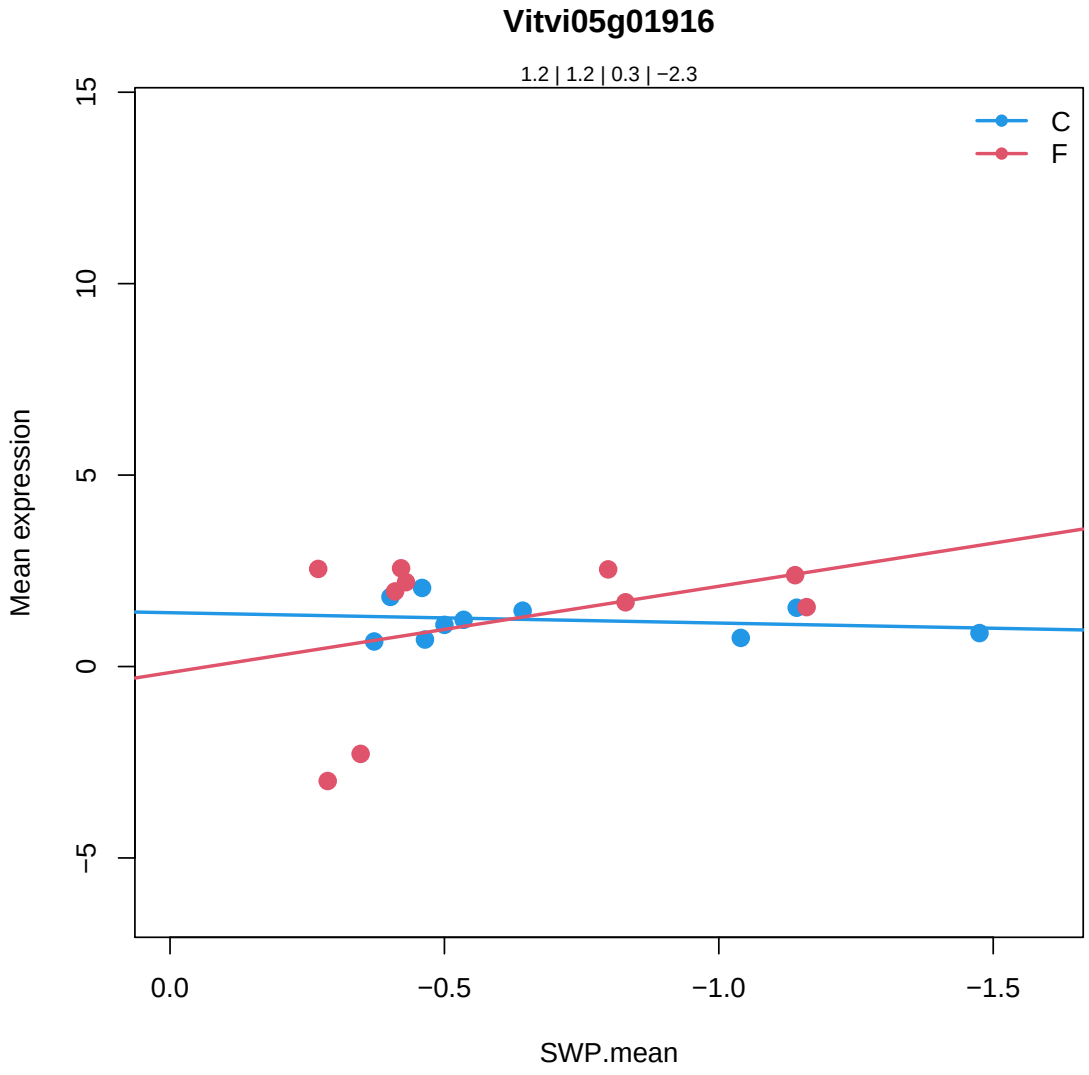
7.6.383 Vitvi05g01916: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01916
        35.2
        not assigned.unknown
        AT-hook motif nuclear-localized protein 20 |
        Chr4:8320972-8321817 FORWARD LENGTH=281 |
        201606
```

Coefficients for Vitvi05g01916.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.214898	0.007602167	**	0.008075846	**
SlopeC	0.2702258	0.8160264		0.9600088	
MeanF-MeanC	0.0005460515	0.9992616		0.9999176	
SlopeF-SlopeC	-2.523015	0.1540676		0.9999488	



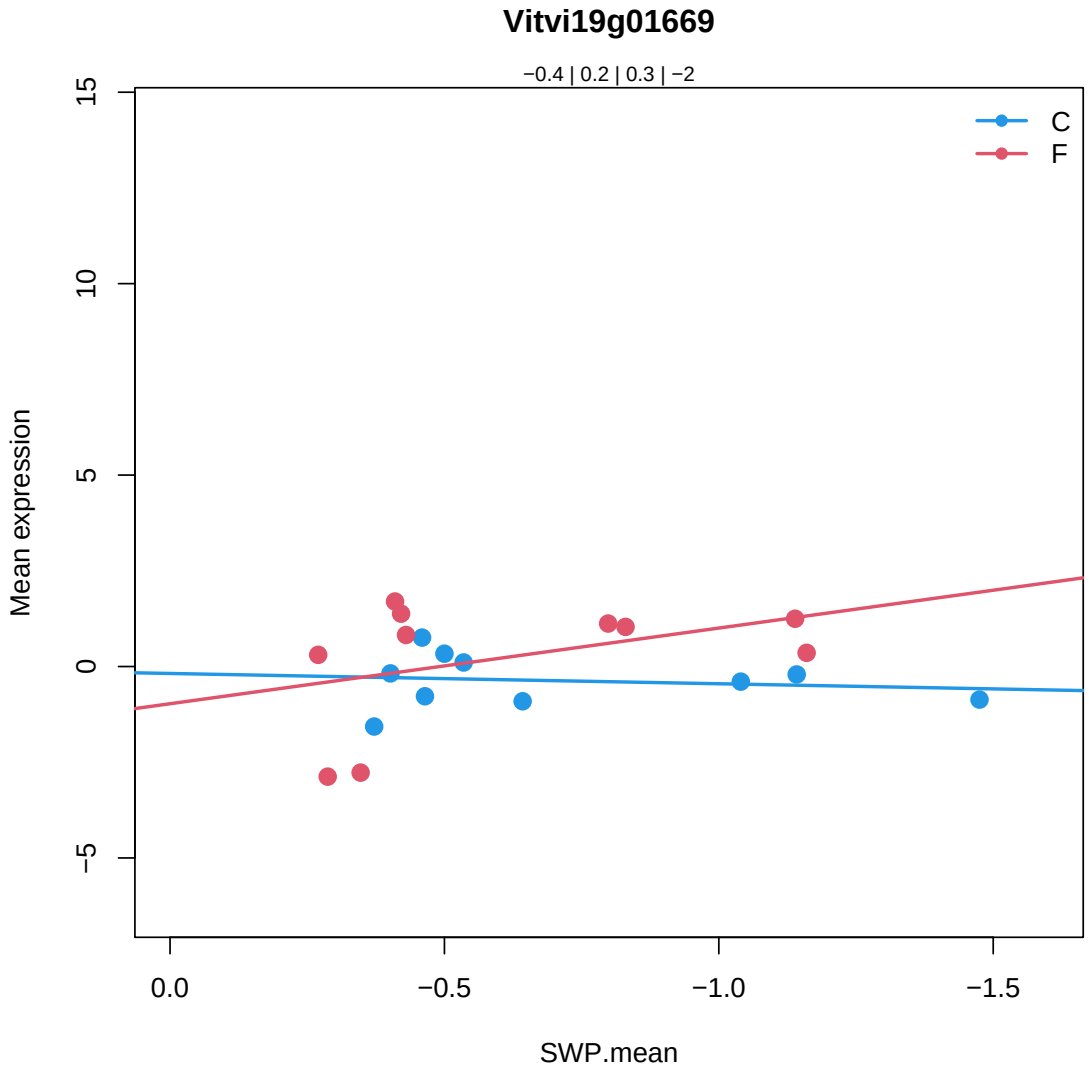
7.6.384 Vitvi19g01669: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g01669
        27.3.25
        RNA.regulation of transcription.MYB domain transcription factor family
        myb domain protein 58 |
        Chr1:5629859-5630844 REVERSE LENGTH=274 |
        201606
```

Coefficients for Vitvi19g01669.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.3703981	0.3013836		0.3071264	
SlopeC	0.2686673	0.7851157		0.9533712	
MeanF-MeanC	0.6025199	0.2364189		0.592388	
SlopeF-SlopeC	-2.245104	0.1357397		0.9999488	



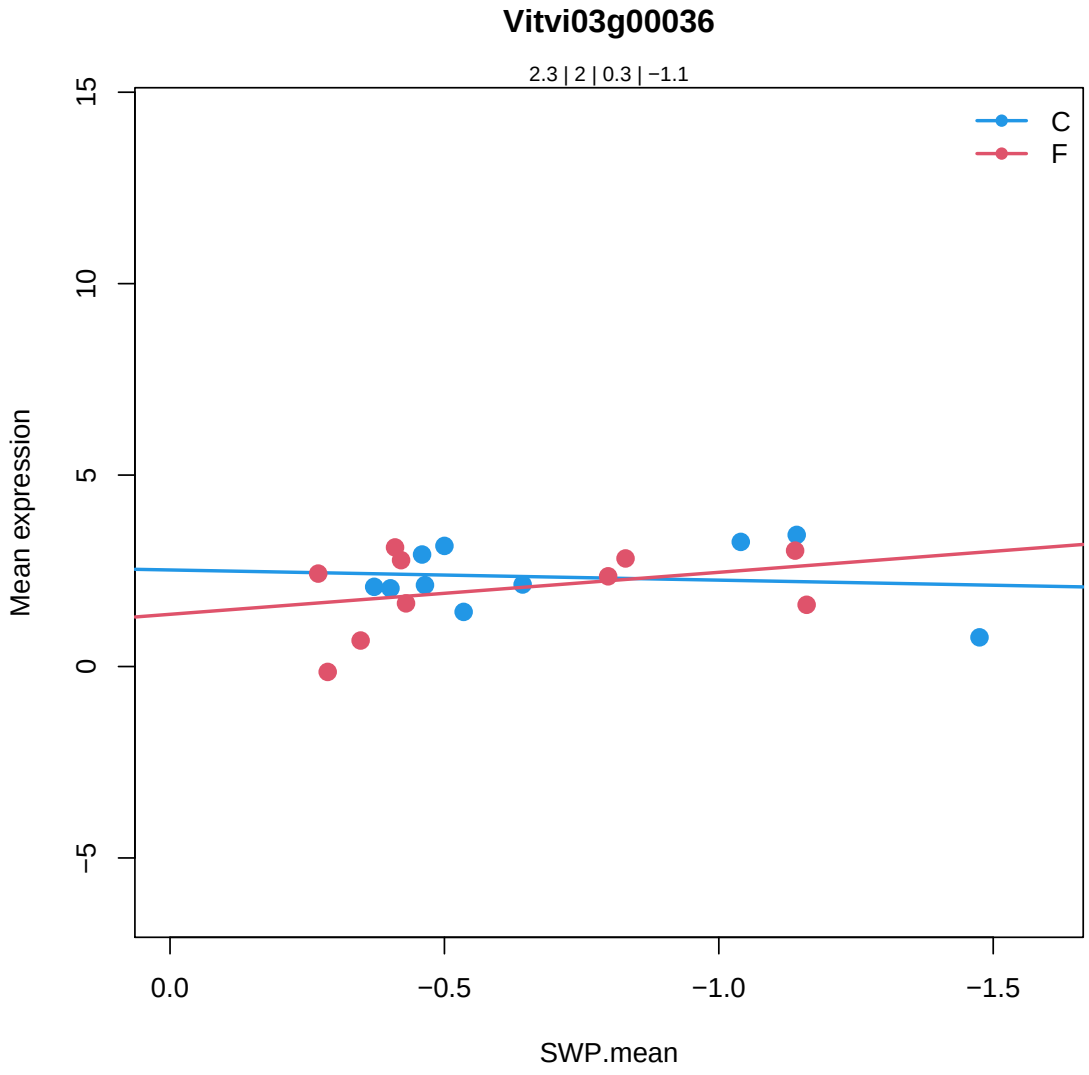
7.6.385 Vitvi03g00036: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00036
        29.5.1
        protein.degradation.subtilases
        Subtilase family protein |
        Chr4:6495900-6499010 FORWARD LENGTH=777 |
        201606
```

Coefficients for Vitvi03g00036.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.3346	3.974137e-08	***	4.765463e-08	***
SlopeC	0.2658038	0.7377958		0.9430175	
MeanF-MeanC	-0.3026157	0.4557645		0.7814132	
SlopeF-SlopeC	-1.36242	0.2556446		0.9999488	



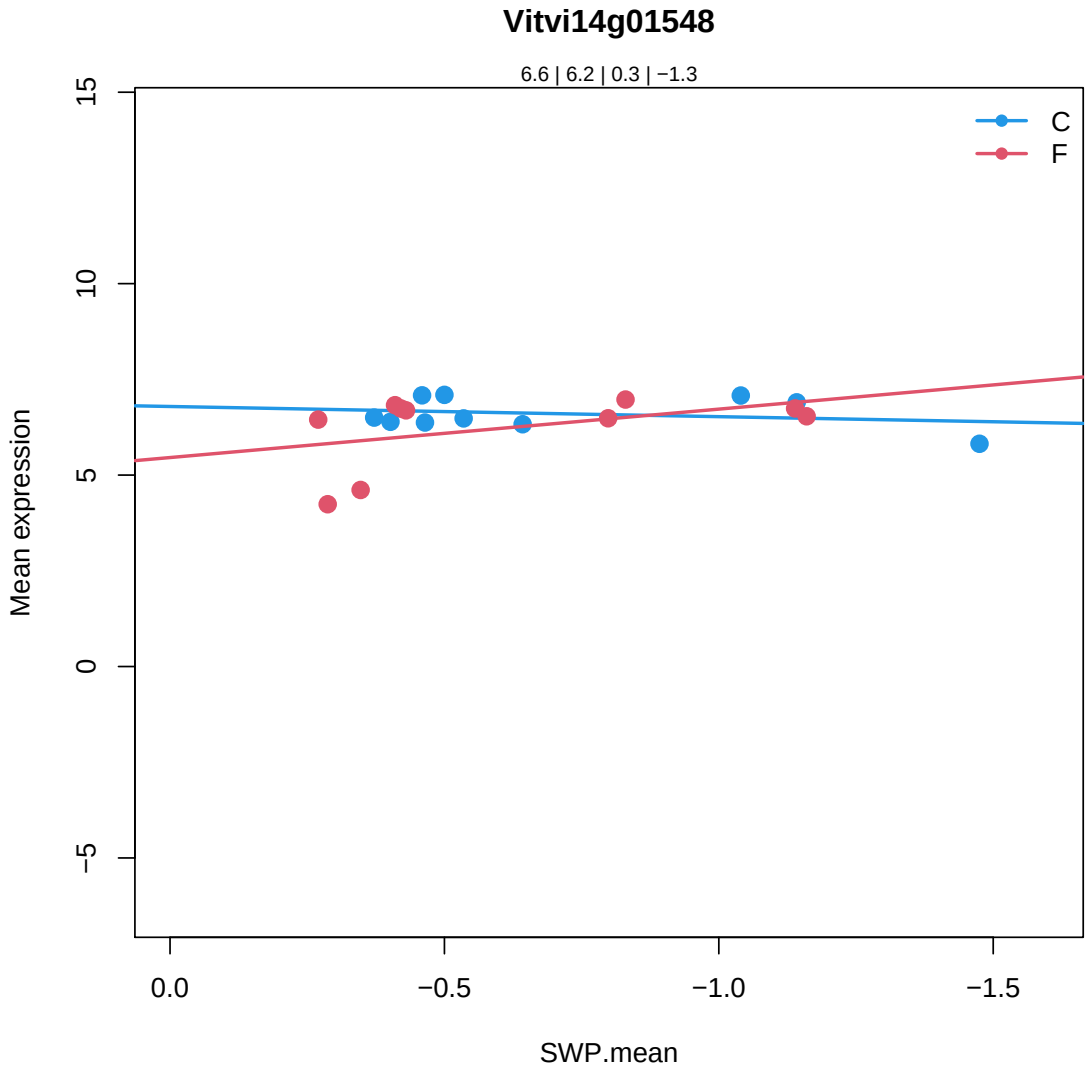
7.6.386 Vitvi14g01548: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01548
        29.5
        protein.degradation
        Peptidase family M48 family protein |
        Chr3:9998006-9999892 FORWARD LENGTH=344 |
        201606
```

Coefficients for Vitvi14g01548.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.604516	2.179852e-19	***	9.216451e-19	***
SlopeC	0.2657315	0.6553022		0.9203044	
MeanF-MeanC	-0.3761658	0.2209518		0.5717737	
SlopeF-SlopeC	-1.530592	0.09406915	.	0.9999488	



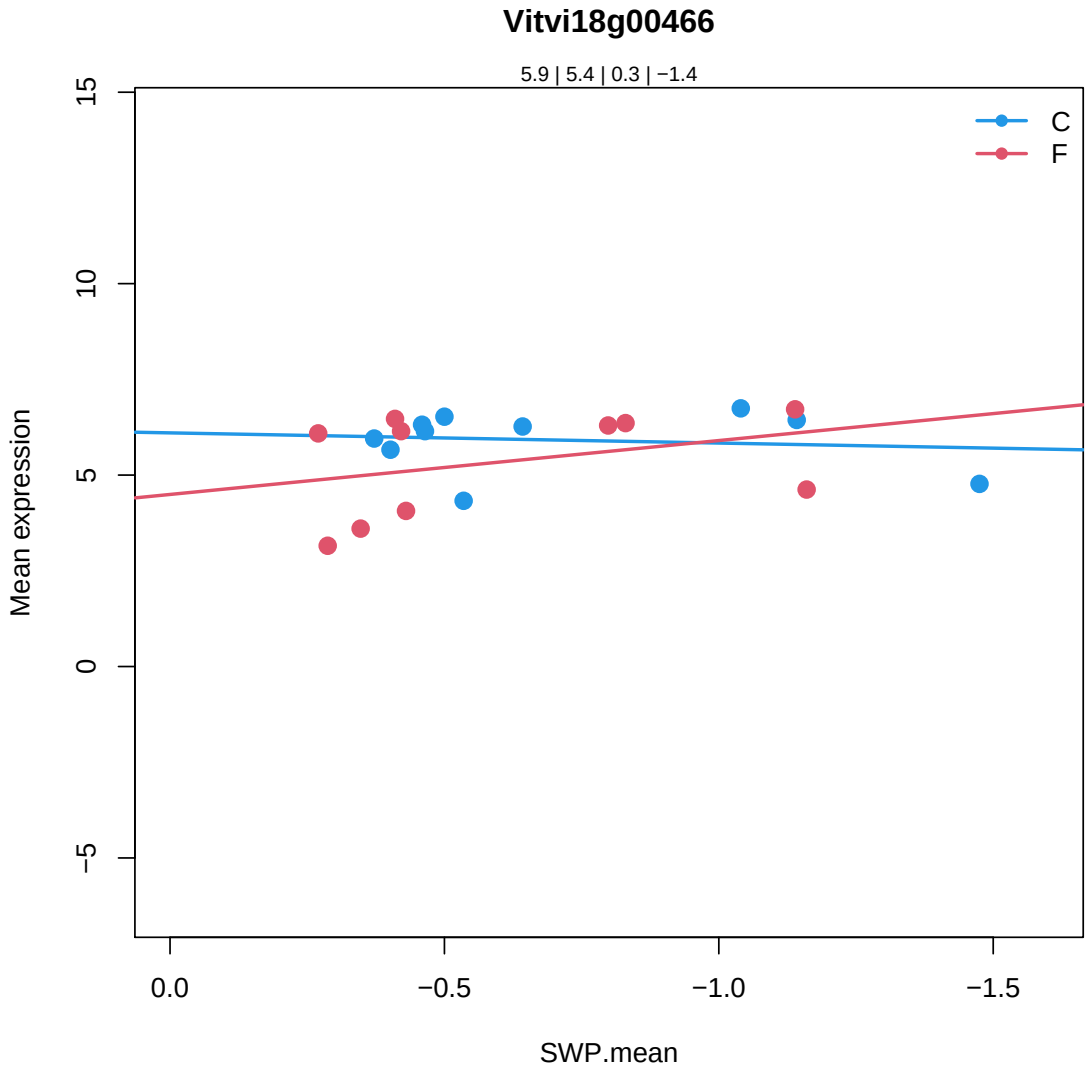
7.6.387 Vitvi18g00466: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00466
        26.7
        misc.oxidases - copper, flavone etc
        2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protei
        Chr2:15379930-15381987 FORWARD LENGTH=366 |
        201606
```

Coefficients for Vitvi18g00466.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.915228	7.288376e-15	***	1.2357e-14	***
SlopeC	0.2655572	0.7630303		0.94868	
MeanF-MeanC	-0.563652	0.2159218		0.5637342	
SlopeF-SlopeC	-1.673501	0.2097884		0.9999488	



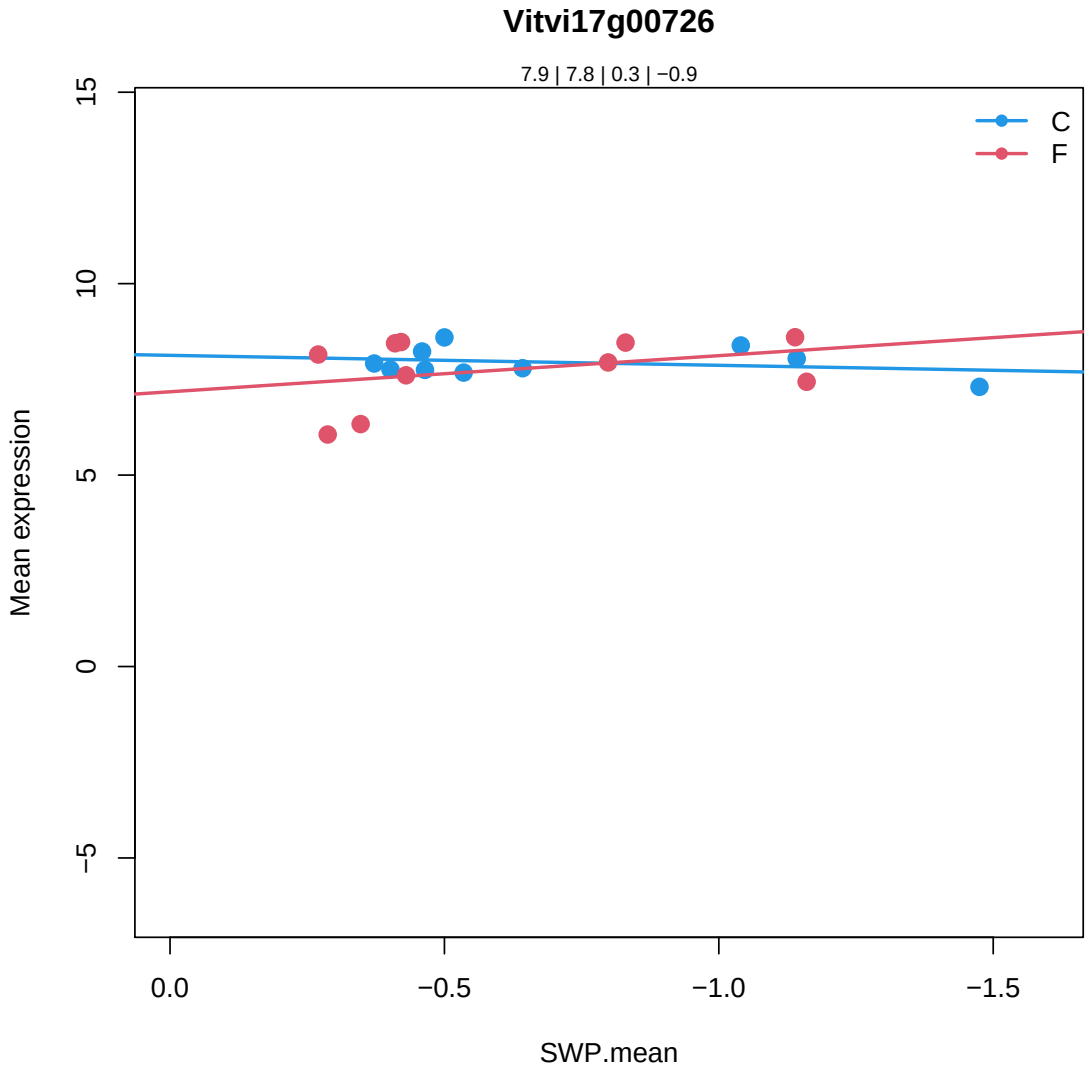
7.6.388 Vitvi17g00726: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00726
        27.3.26
        RNA.regulation of transcription.MYB-related transcription factor famil
        Homeodomain-like superfamily protein |
        Chr1:28116201-28117317 REVERSE LENGTH=239 |
        201606
```

Coefficients for Vitvi17g00726.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.944034	2.327555e-21	***	2.207902e-20	***
SlopeC	0.2603501	0.6520204		0.9194145	
MeanF-MeanC	-0.19385	0.5100638		0.8127001	
SlopeF-SlopeC	-1.203519	0.169851		0.9999488	



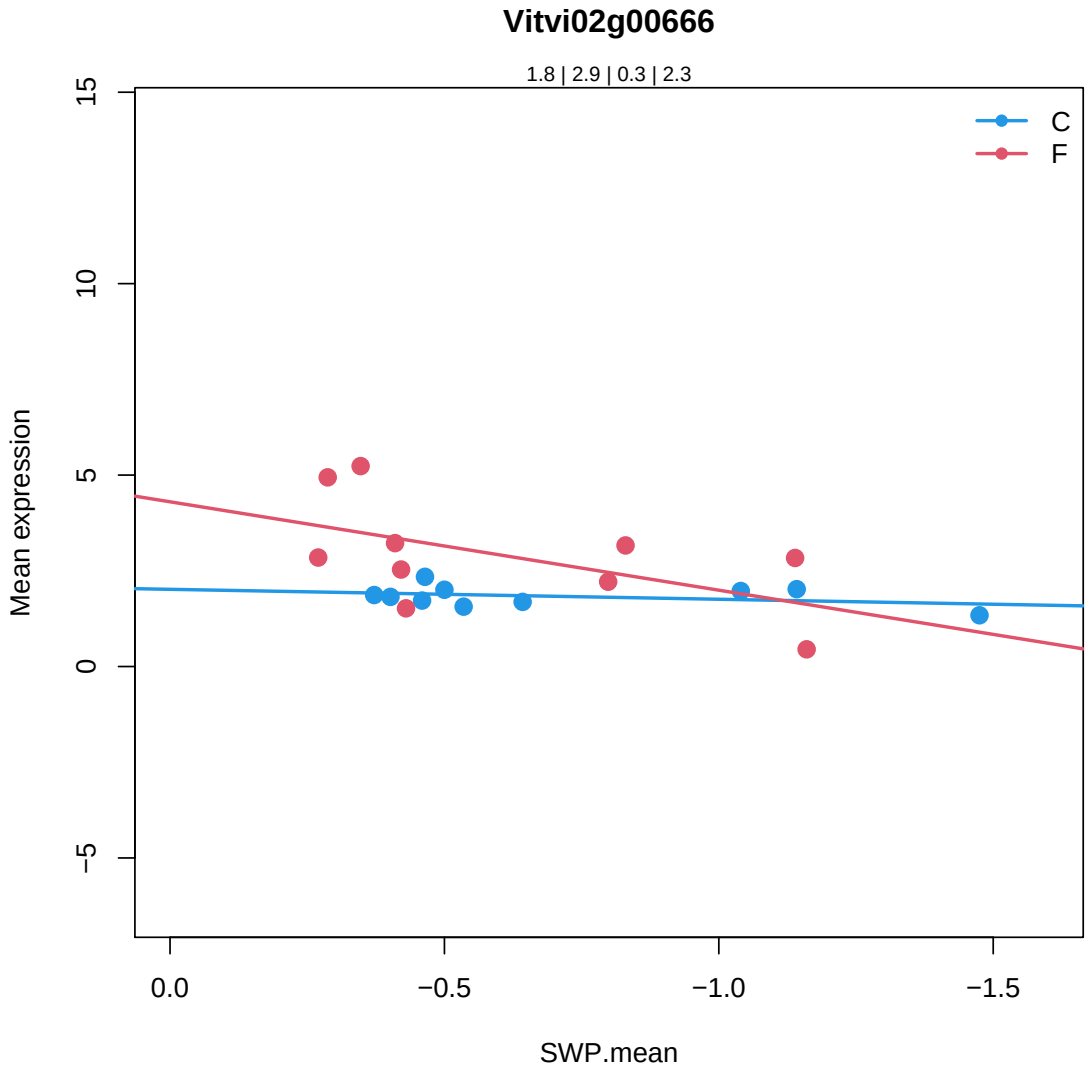
7.6.389 Vitvi02g00666: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00666
        27.3.99
        RNA.regulation of transcription.unclassified
        lsd one like 1 |
        Chr1:11768253-11769591 FORWARD LENGTH=187 |
        201606
```

Coefficients for Vitvi02g00666.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.833759	5.370324e-07	***	6.245573e-07	***
SlopeC	0.2596456	0.7237702		0.9393482	
MeanF-MeanC	1.061972	0.008812576	**	0.06916647	.
SlopeF-SlopeC	2.048877	0.07116225	.	0.9999488	



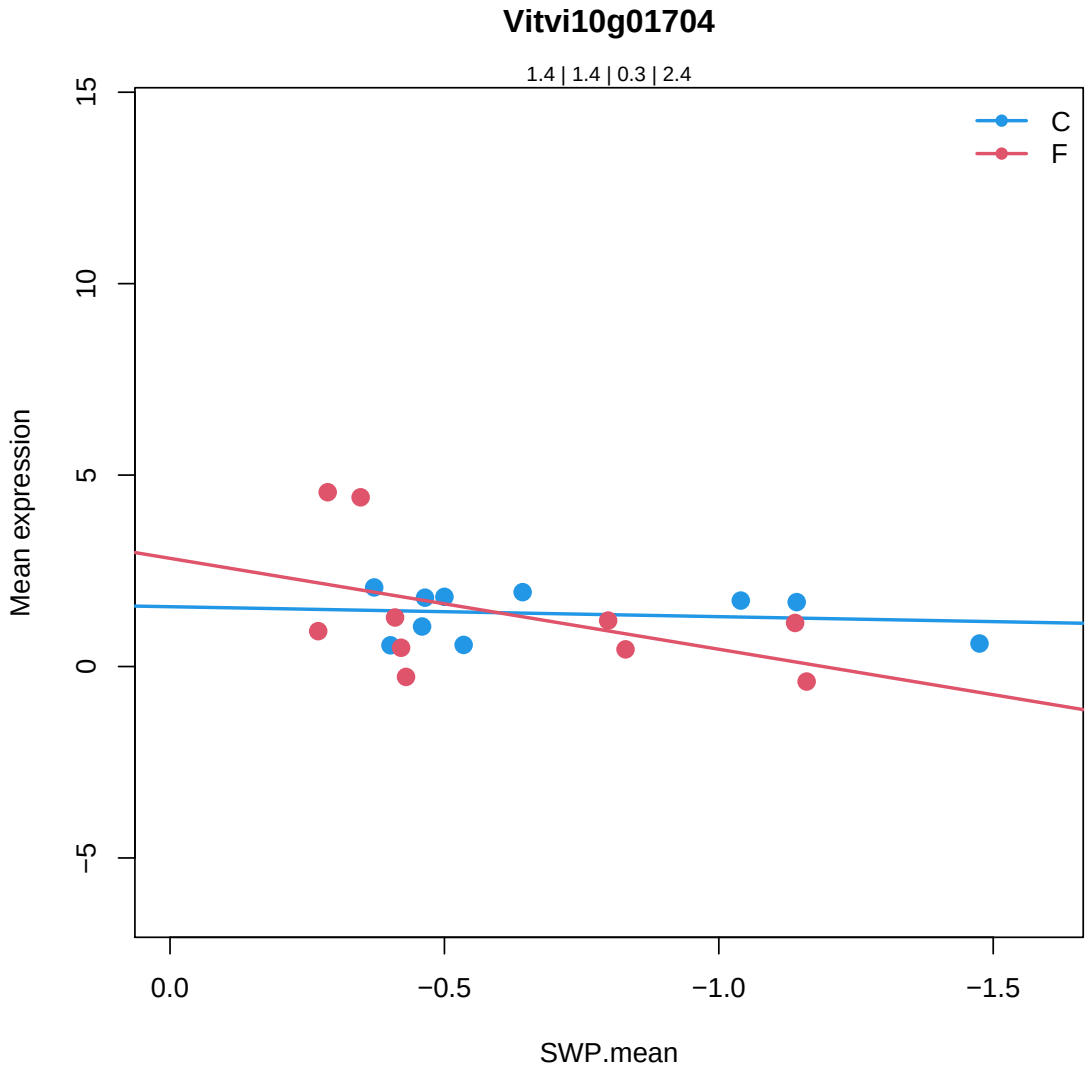
7.6.390 Vitvi10g01704: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g01704
        35.2
        not assigned.unknown
        Heavy metal transport/detoxification superfamily protein |
        Chr4:9255062-9255955 FORWARD LENGTH=261 |
        201606
```

Coefficients for Vitvi10g01704.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.379404	0.0006645531	***	0.0007224248	***
SlopeC	0.2596266	0.7904758		0.9536839	
MeanF-MeanC	-0.0007762402	0.9987521		0.9998558	
SlopeF-SlopeC	2.11457	0.1554937		0.9999488	



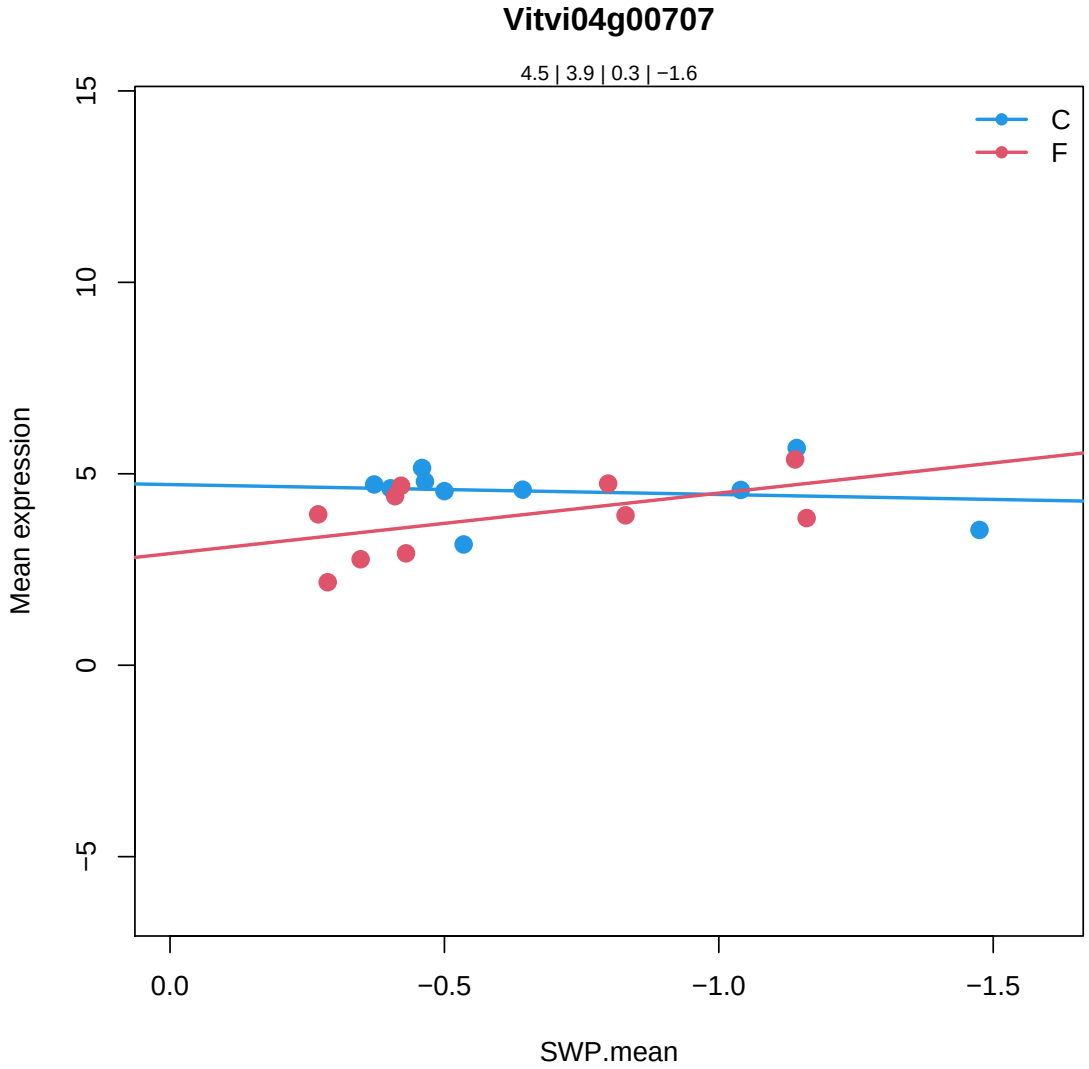
7.6.391 Vitvi04g00707: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00707
        35.2
        not assigned.unknown
        Glutamate-gated kainate-type ion channel receptor subunit GluR5 IPR017
```

Coefficients for Vitvi04g00707.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.536236	7.089449e-15	***	1.202508e-14	***
SlopeC	0.2587816	0.7014267		0.9324215	
MeanF-MeanC	-0.6585409	0.06497138	.	0.2822958	
SlopeF-SlopeC	-1.836791	0.07769185	.	0.9999488	



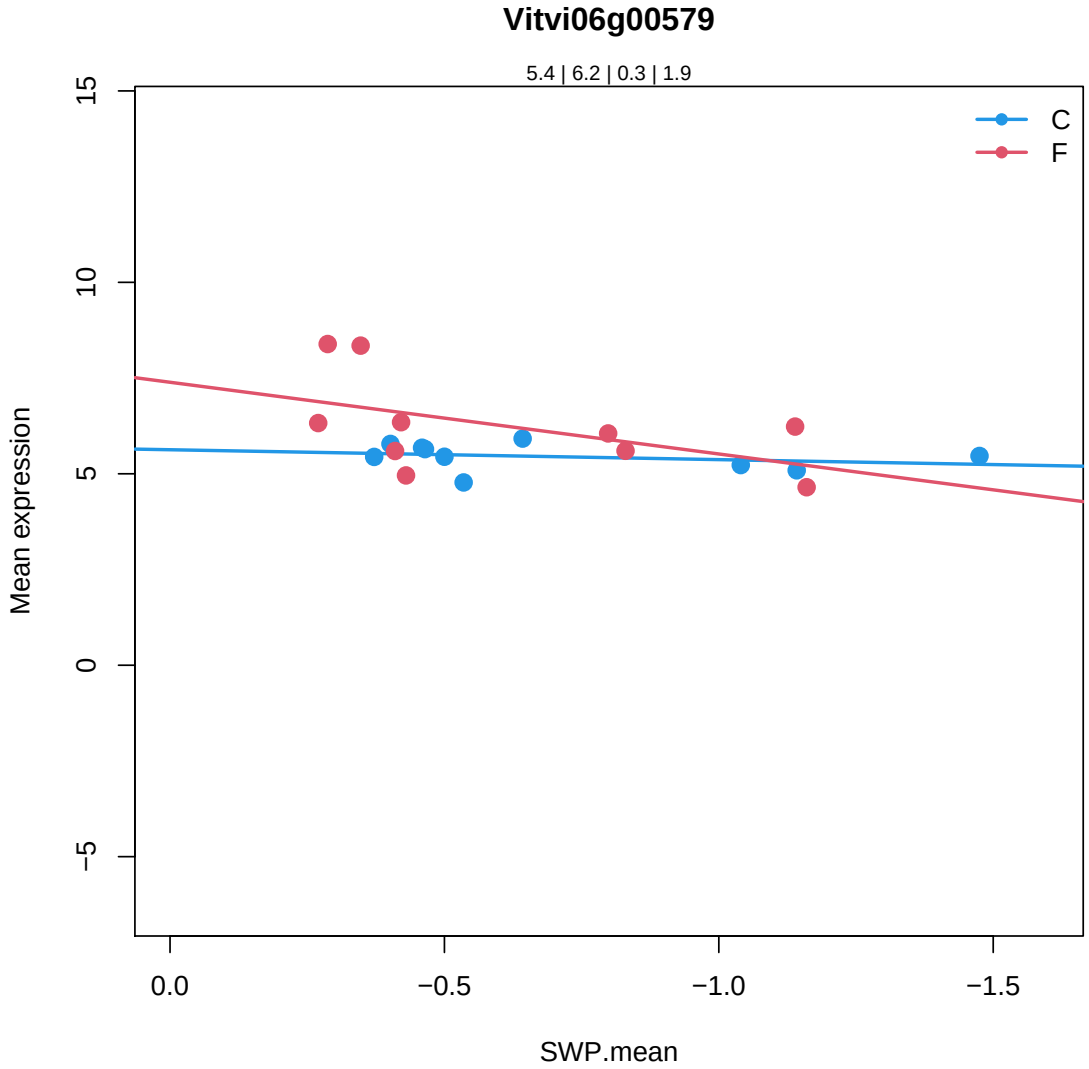
7.6.392 Vitvi06g00579: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00579
        35.2
        not assigned.unknown
        Unknown Protein
```

Coefficients for Vitvi06g00579.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.446356	2.288483e-16	***	4.689758e-16	***
SlopeC	0.2580735	0.7064069		0.9344006	
MeanF-MeanC	0.8030069	0.02922185	*	0.1661318	
SlopeF-SlopeC	1.61491	0.1231289		0.9999488	



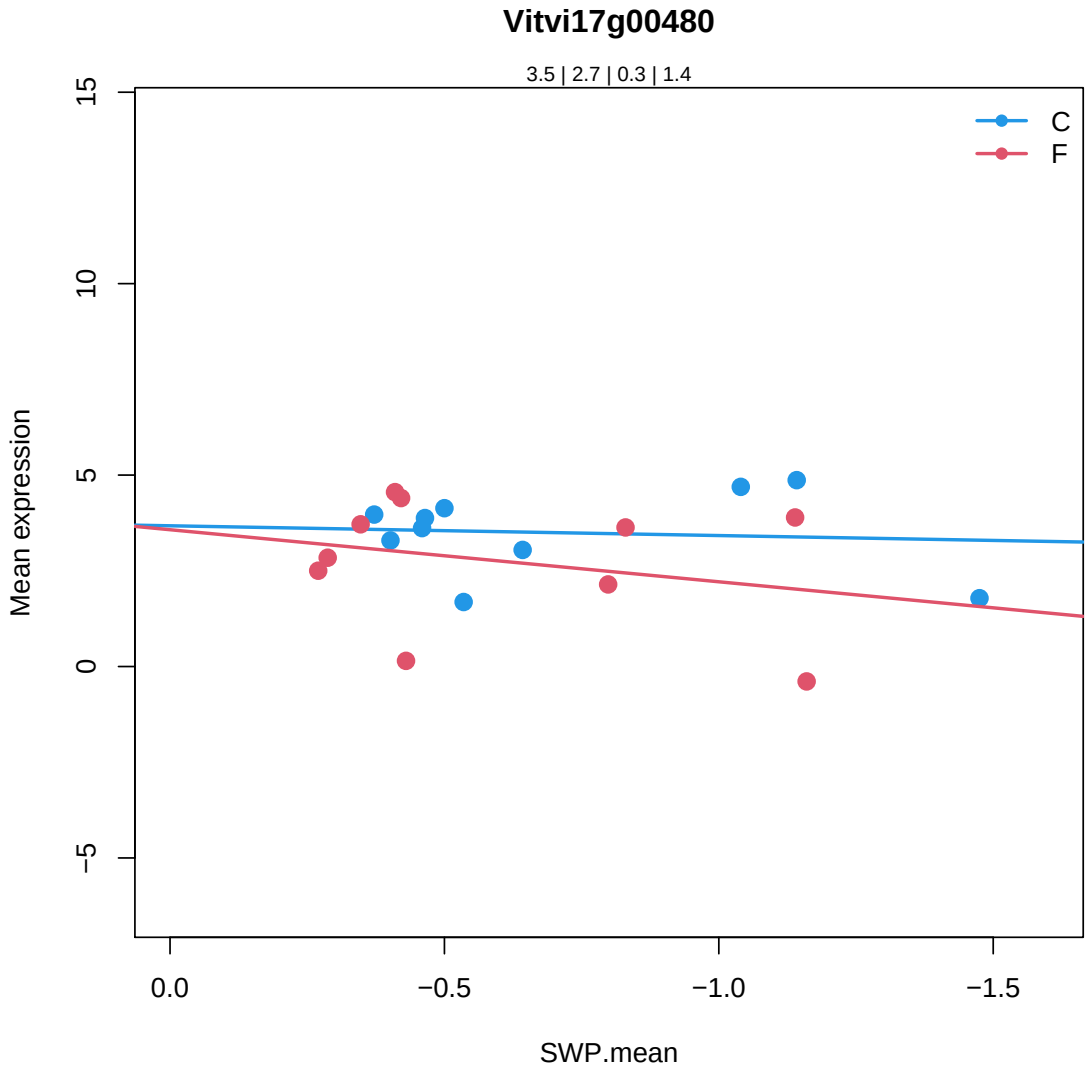
7.6.393 Vitvi17g00480: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00480
        10.2.2
        cell wall.cellulose synthesis.COBRA
        COBRA-like extracellular glycosyl-phosphatidyl inositol-anchored prote
        Chr5:24511466-24513146 REVERSE LENGTH=409 |
        201606
```

Coefficients for Vitvi17g00480.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.49628	2.373689e-08	***	2.86527e-08	***
SlopeC	0.254934	0.82486		0.9648163	
MeanF-MeanC	-0.7522289	0.2072669		0.5522621	
SlopeF-SlopeC	1.104875	0.5211217		0.9999488	



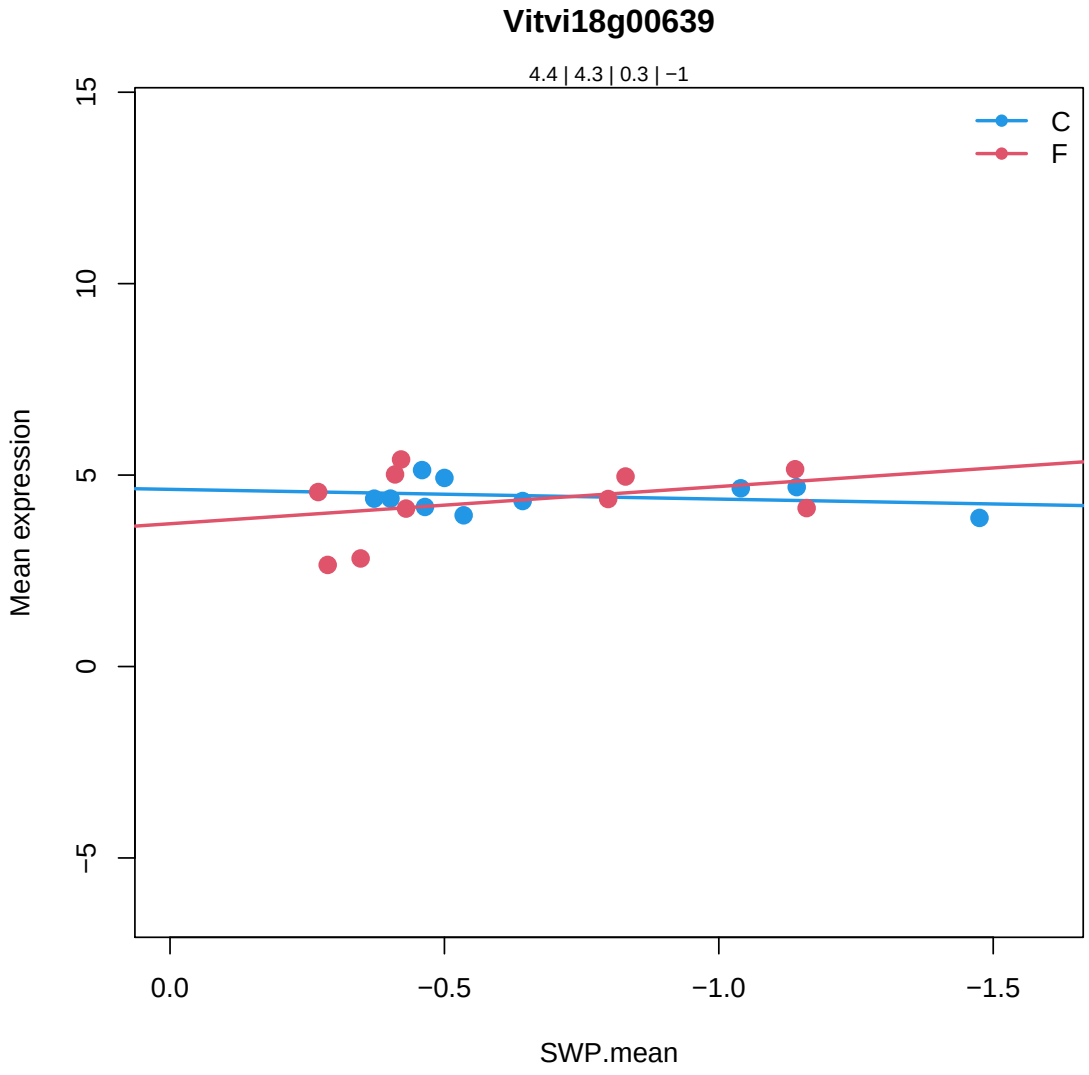
7.6.394 Vitvi18g00639: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00639
        11.8.10
        lipid metabolism.exotics (steroids, squalene etc).phosphatidylcholine-
        alpha/beta-Hydrolases superfamily protein |
        Chr1:9544607-9546168 FORWARD LENGTH=432 |
        201606
```

Coefficients for Vitvi18g00639.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.448486	8.628597e-16	***	1.628694e-15	***
SlopeC	0.254359	0.6701708		0.9240767	
MeanF-MeanC	-0.1275256	0.6744073		0.894818	
SlopeF-SlopeC	-1.225487	0.1764441		0.9999488	



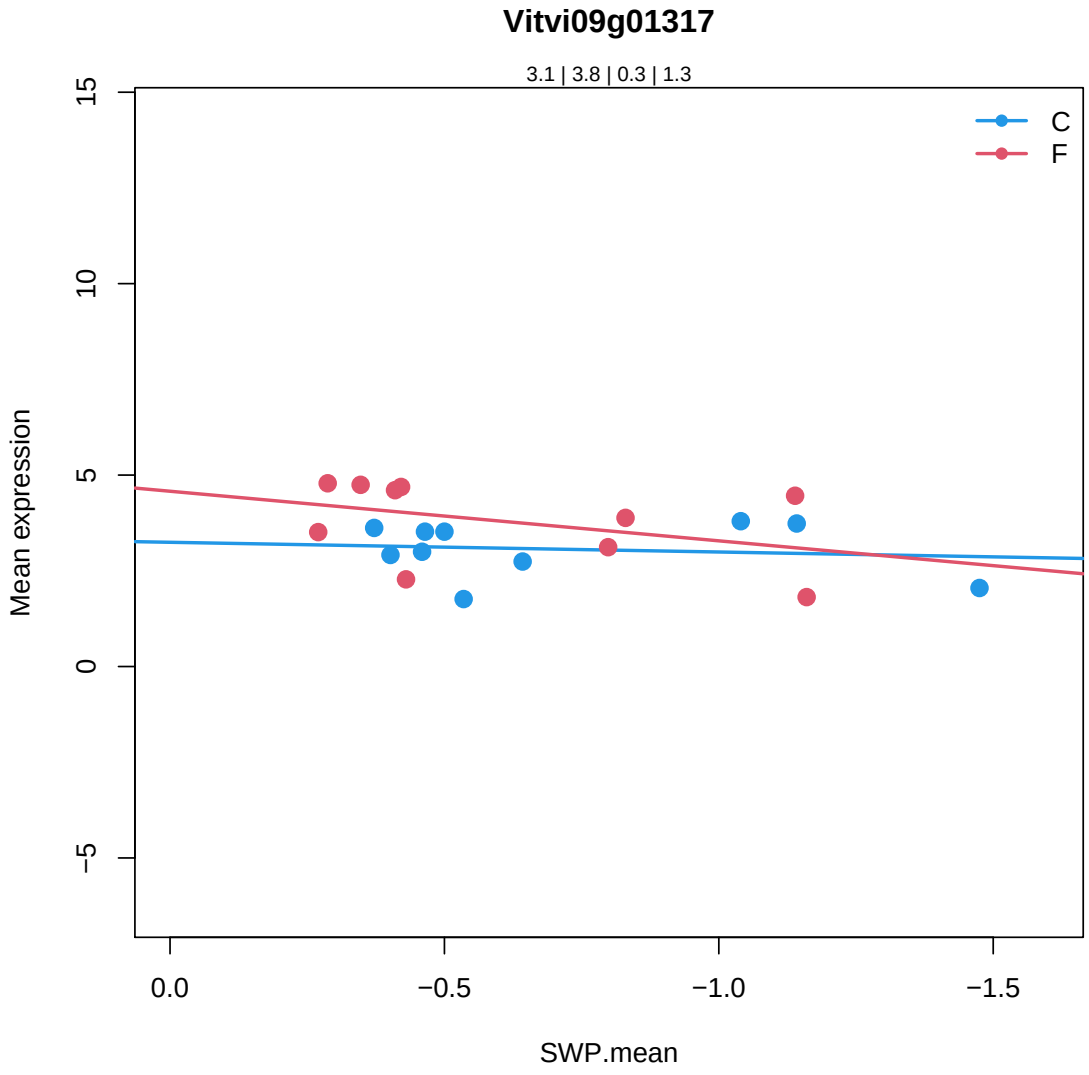
7.6.395 Vitvi09g01317: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g01317
        35.2
        not assigned.unknown
        O-fucosyltransferase family protein |
        Chr3:7432579-7434543 REVERSE LENGTH=422 |
        201606
```

Coefficients for Vitvi09g01317.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.06602	8.107109e-11	***	1.064512e-10	***
SlopeC	0.2536925	0.7299202		0.9406676	
MeanF-MeanC	0.7224628	0.06317451	.	0.2780554	
SlopeF-SlopeC	1.041766	0.3452909		0.9999488	



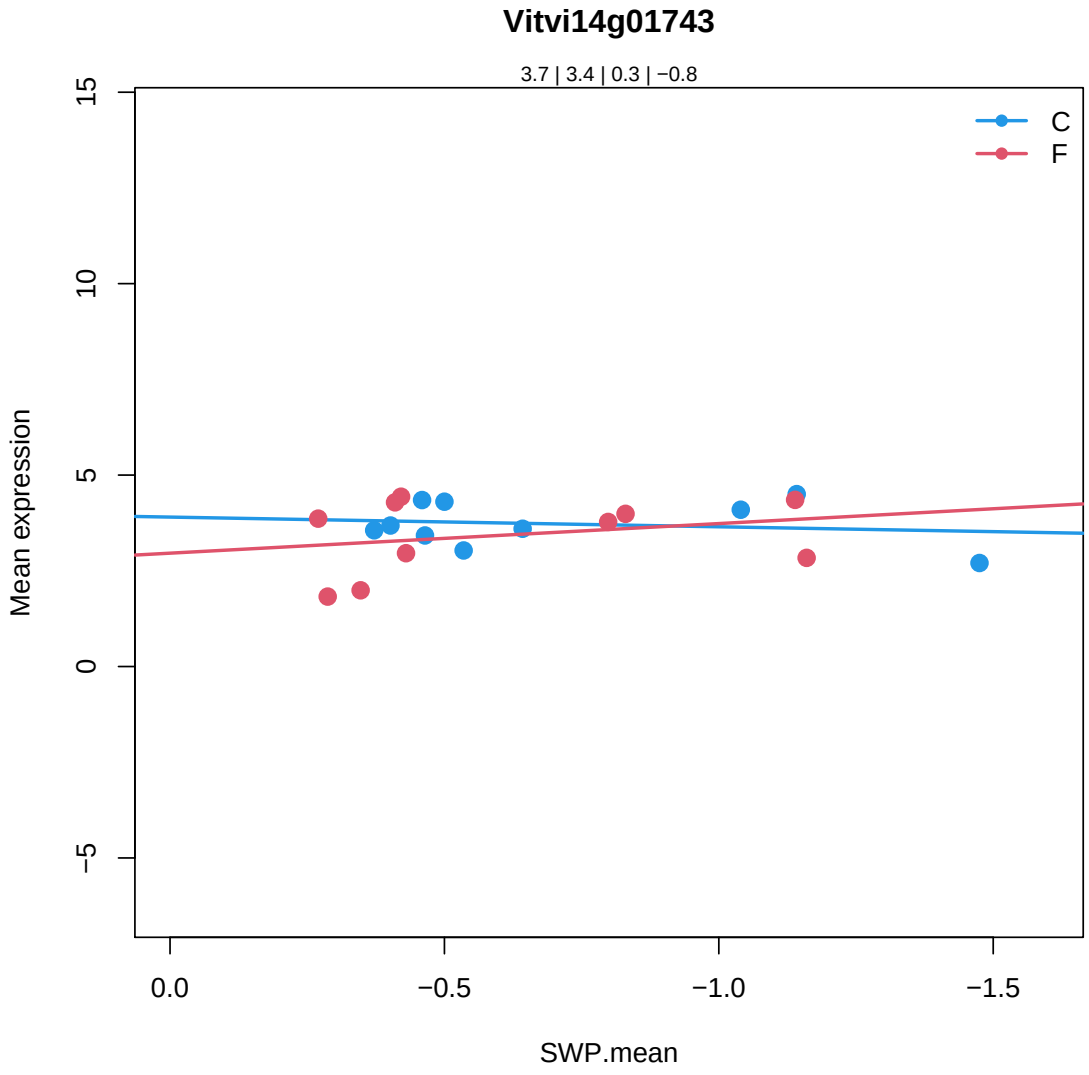
7.6.396 Vitvi14g01743: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01743
        29.2.2.3.3
        protein.synthesis.ribosome biogenesis.pre-rRNA processing and modifica
        domains rearranged methyltransferase 2 |
        Chr5:4715429-4718578 REVERSE LENGTH=626 |
        201606
```

Coefficients for Vitvi14g01743.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.724591	3.293465e-13	***	4.884121e-13	***
SlopeC	0.2534111	0.7057237		0.9344006	
MeanF-MeanC	-0.2932392	0.3933188		0.7408135	
SlopeF-SlopeC	-1.026779	0.3091186		0.9999488	



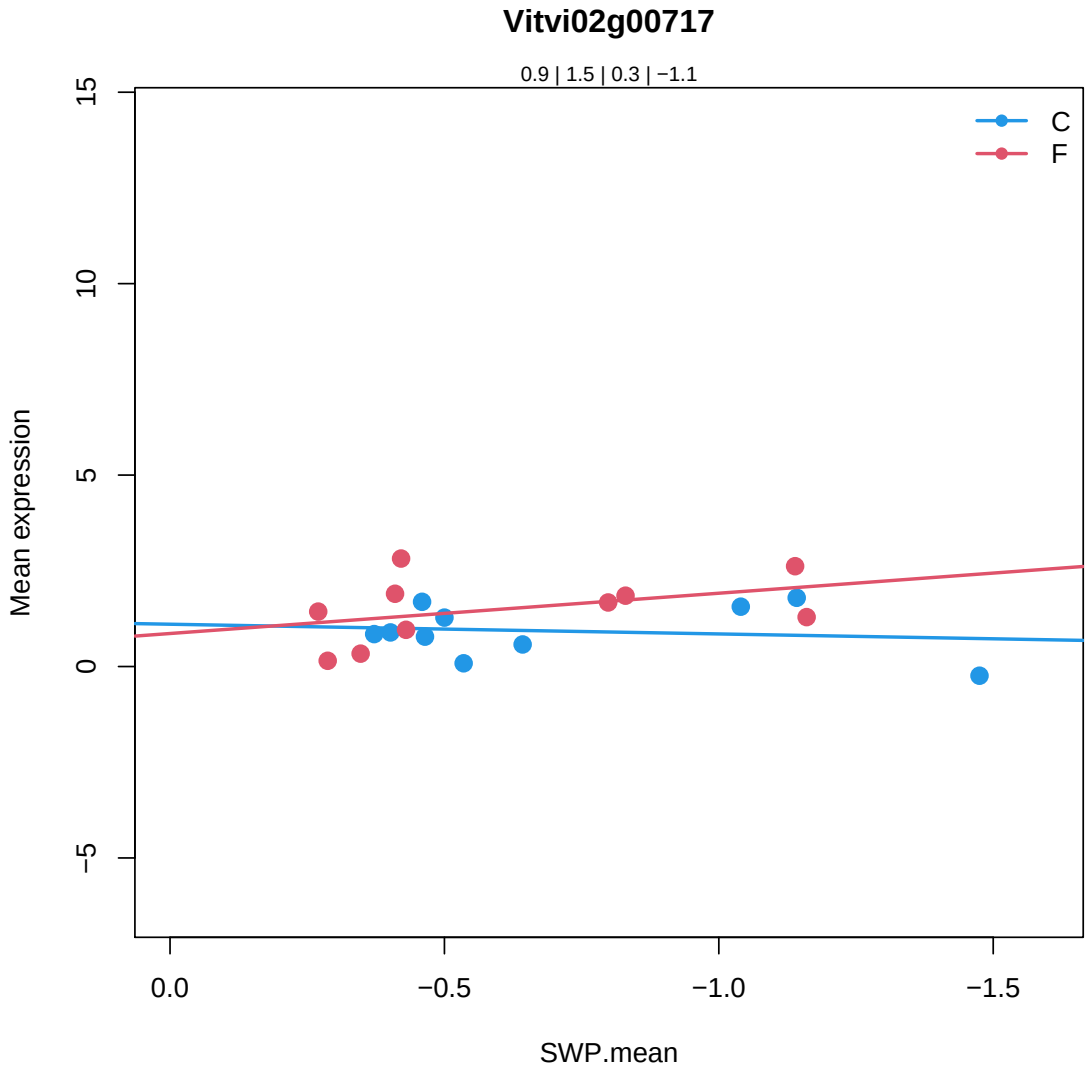
7.6.397 Vitvi02g00717: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00717
        16.2.1.7
        secondary metabolism.phenylpropanoids.lignin biosynthesis.CCR1
        NAD(P)-binding Rossmann-fold superfamily protein |
        Chr2:10178162-10179789 FORWARD LENGTH=270 |
        201606
```

Coefficients for Vitvi02g00717.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.9261384	0.0004988909	***	0.000543266	***
SlopeC	0.2533628	0.6911377		0.9312515	
MeanF-MeanC	0.5770241	0.08524198	.	0.3316126	
SlopeF-SlopeC	-1.305388	0.1775679		0.9999488	



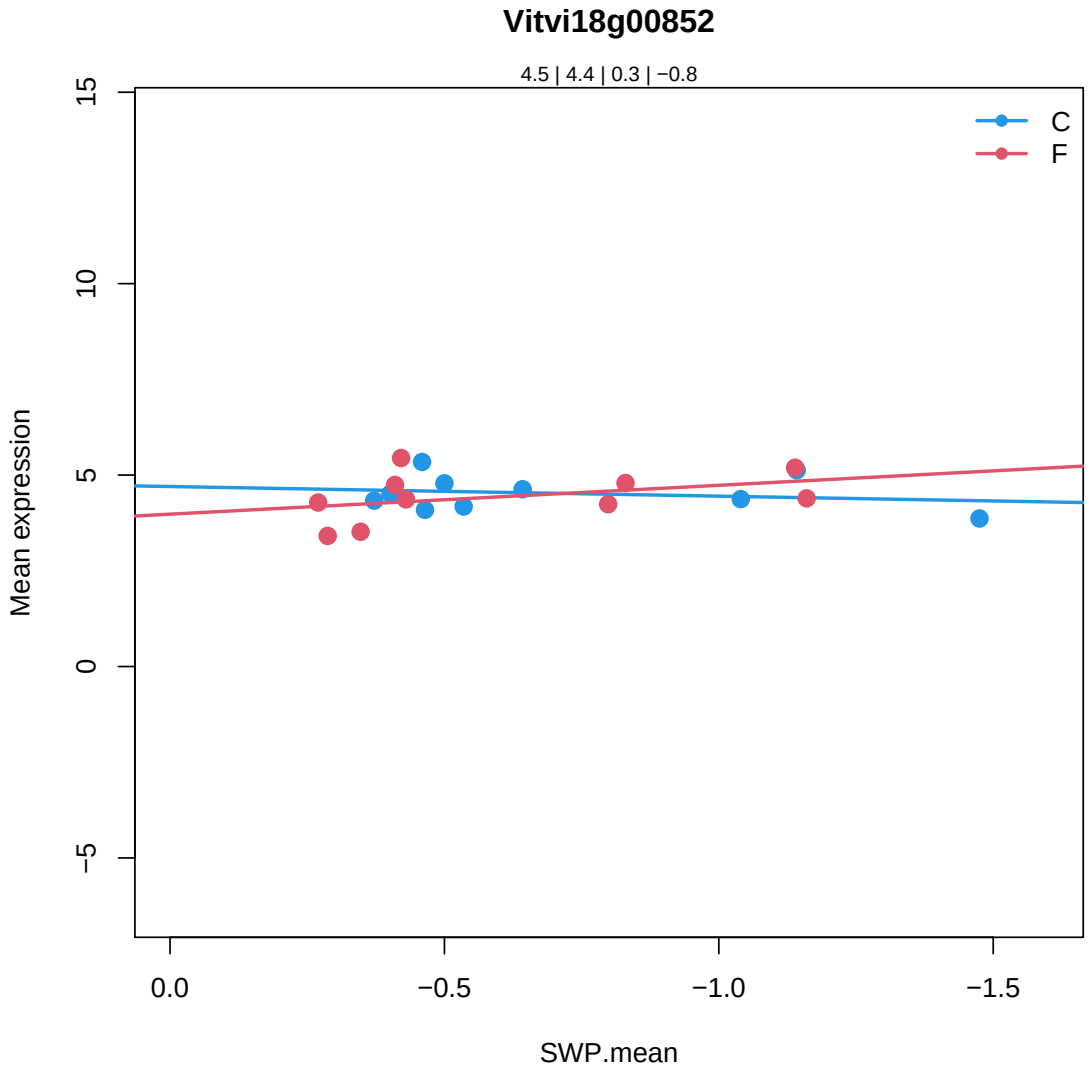
7.6.398 Vitvi18g00852: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00852
        20.1.7.6
        stress.biotic.PR-proteins.PR6 (proteinase inhibitors)
        Serine protease inhibitor (SERPIN) family protein |
        Chr1:17558271-17560061 FORWARD LENGTH=391 |
        201606
```

Coefficients for Vitvi18g00852.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.524045	7.764094e-18	***	2.100094e-17	***
SlopeC	0.2512124	0.6038059		0.9046943	
MeanF-MeanC	-0.08569543	0.7271917		0.9172341	
SlopeF-SlopeC	-1.005124	0.171167		0.9999488	



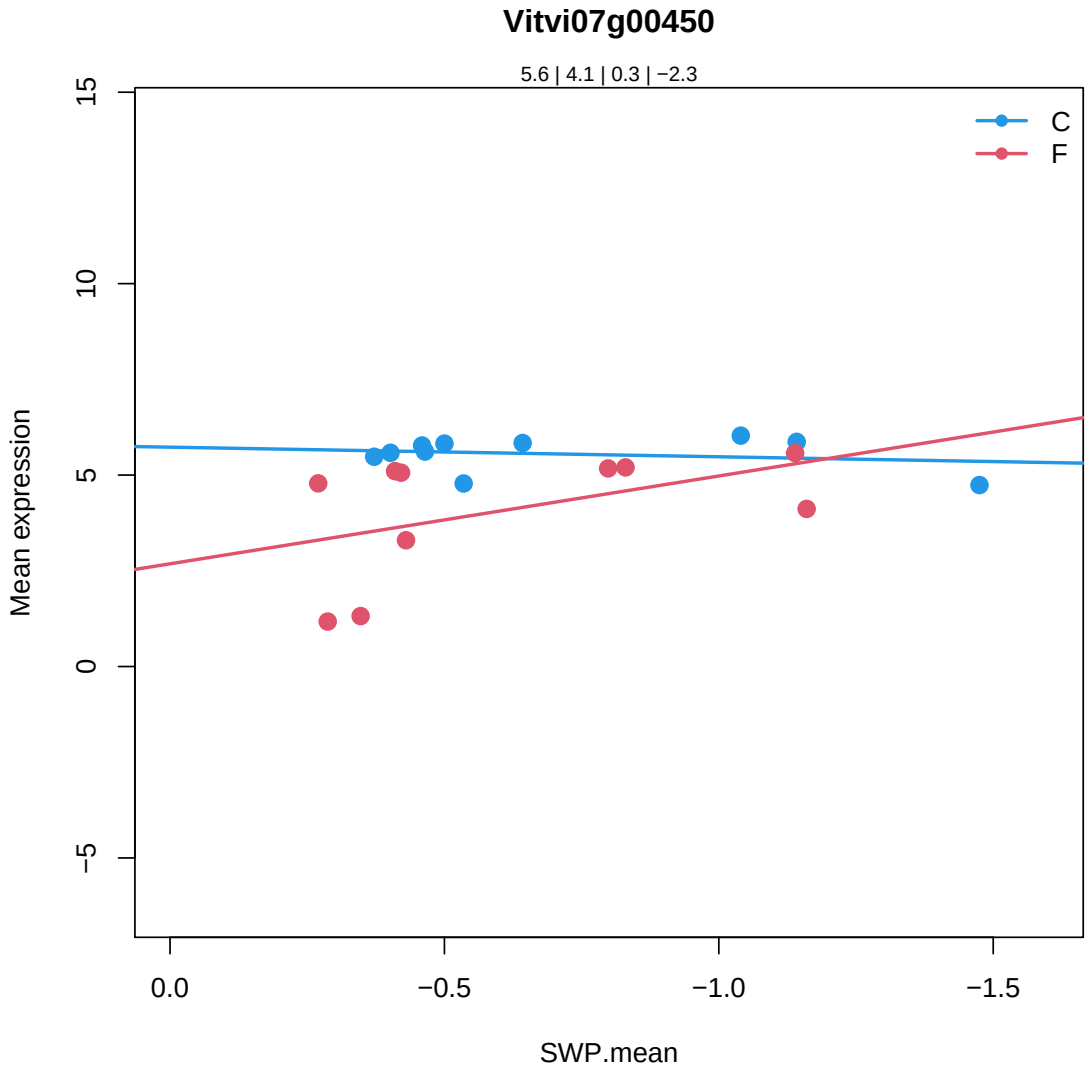
7.6.399 Vitvi07g00450: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g00450
        35.2
        not assigned.unknown
        insulin-induced protein |
        Chr4:841102-842228 FORWARD LENGTH=256 |
        201606
```

Coefficients for Vitvi07g00450.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.552274	3.119128e-14	***	4.988641e-14	***
SlopeC	0.2505644	0.7778902		0.9513135	
MeanF-MeanC	-1.47195	0.003333318	**	0.03333755	*
SlopeF-SlopeC	-2.544415	0.06451323	.	0.9999488	



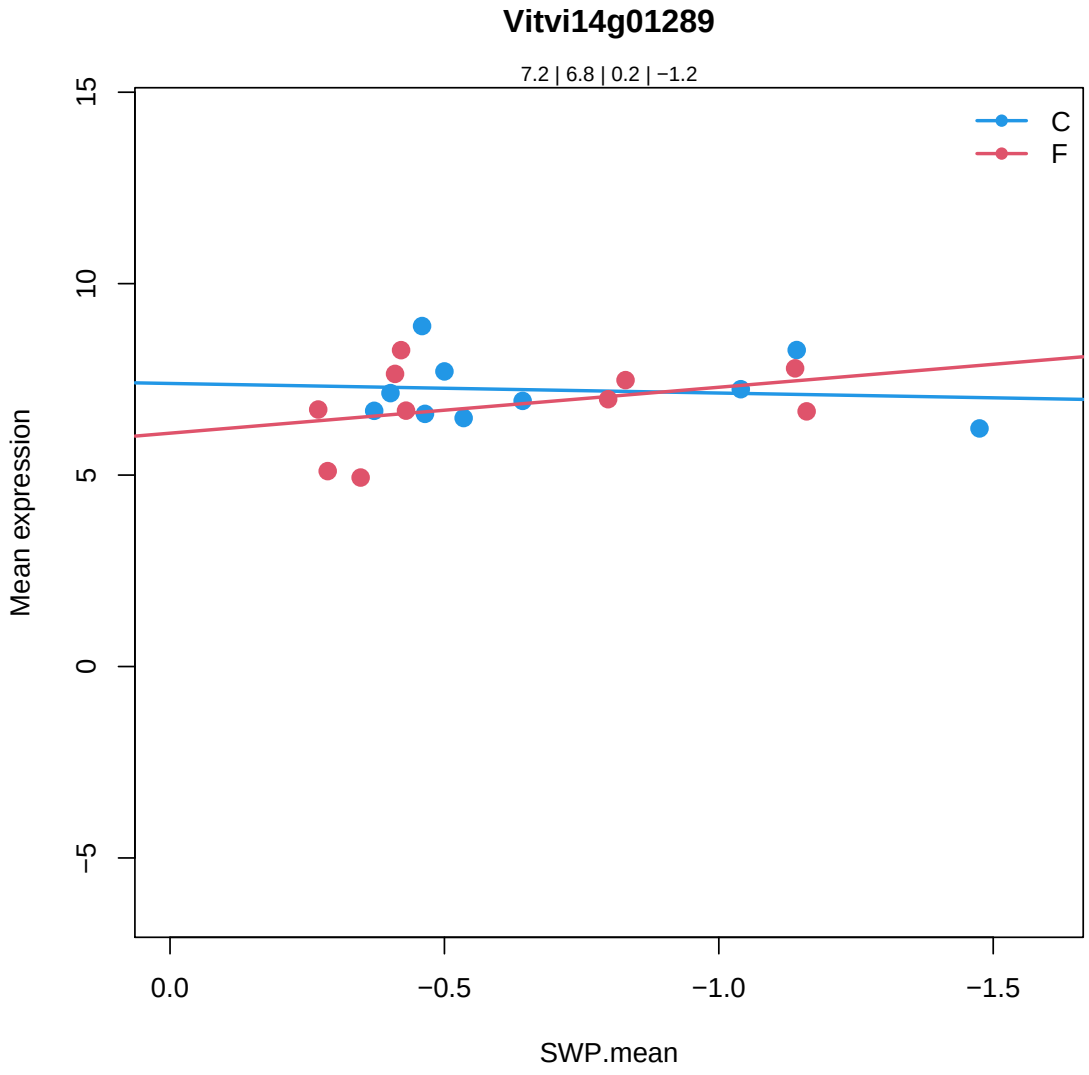
7.6.400 Vitvi14g01289: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01289
        22.1.2
        polyamine metabolism.synthesis.SAM decarboxylase
        S-adenosylmethionine decarboxylase |
        Chr3:510223-511323 FORWARD LENGTH=366 |
        201606
```

Coefficients for Vitvi14g01289.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.217124	1.286942e-17	***	3.315121e-17	***
SlopeC	0.2498223	0.7517209		0.9472461	
MeanF-MeanC	-0.3919184	0.3336859		0.6929017	
SlopeF-SlopeC	-1.44903	0.2251839		0.9999488	



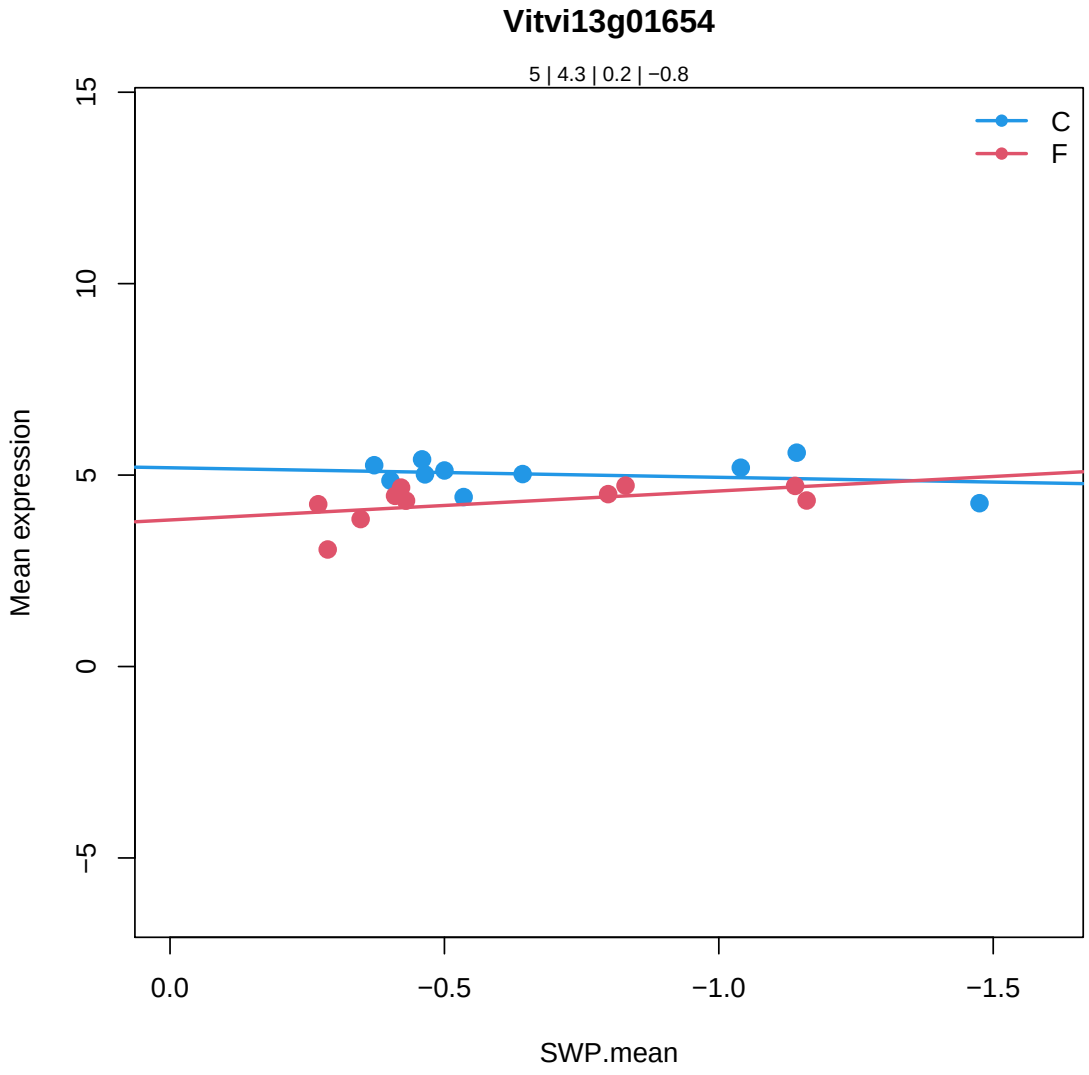
7.6.401 Vitvi13g01654: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g01654
        29.2.1.99.99
        protein.synthesis.ribosomal protein.unknown.unknown
        Uncharacterized protein family (UPF0114) |
        Chr5:4427960-4429029 FORWARD LENGTH=262 |
        201606
```

Coefficients for Vitvi13g01654.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.015749	2.303801e-20	***	1.398986e-19	***
SlopeC	0.2486945	0.5412978		0.8843962	
MeanF-MeanC	-0.726959	0.001764367	**	0.01993512	*
SlopeF-SlopeC	-1.005539	0.1062261		0.9999488	



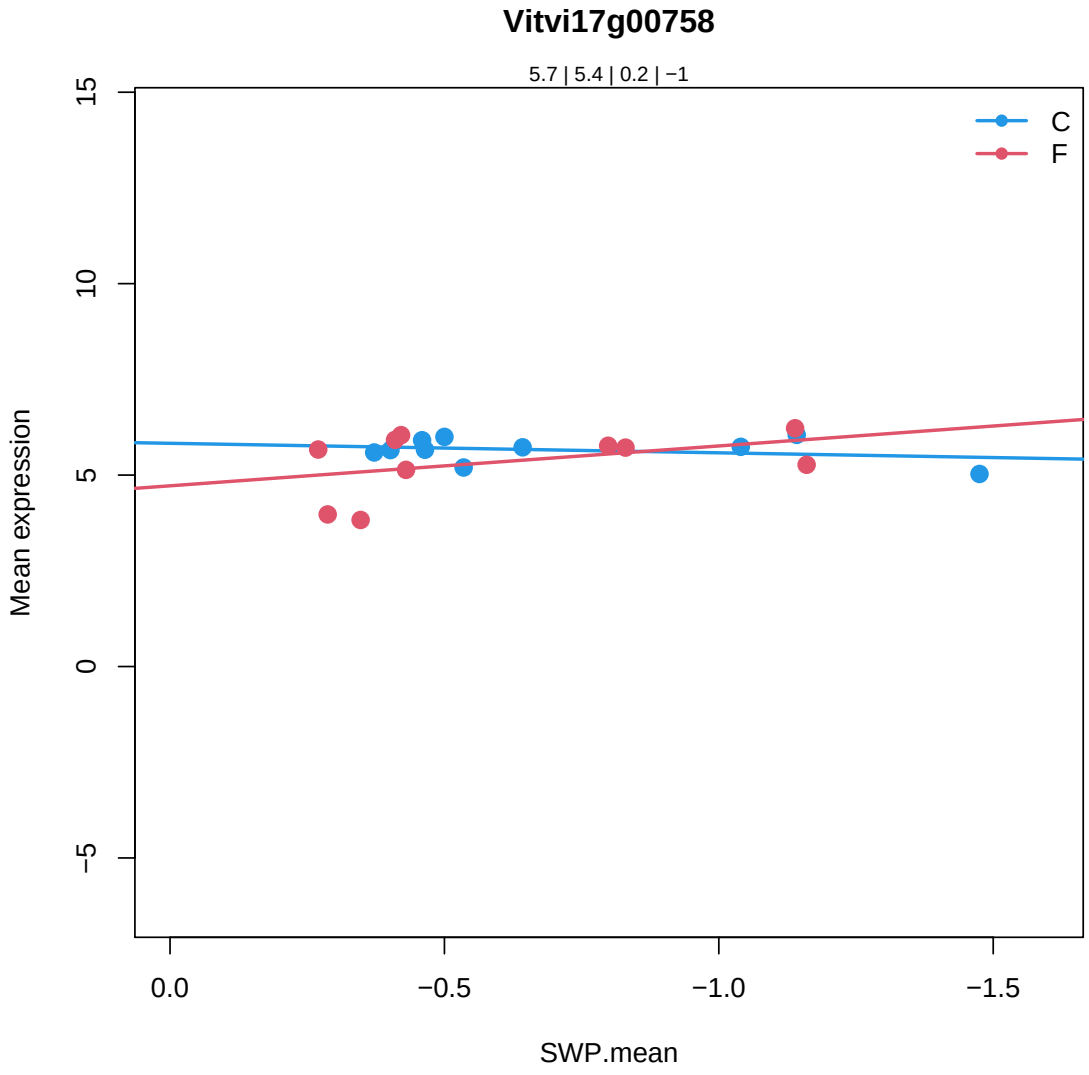
7.6.402 Vitvi17g00758: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00758
        27.3.35
        RNA.regulation of transcription.bZIP transcription factor family
        D-ribose-binding periplasmic protein |
        Chr5:20369961-20370878 FORWARD LENGTH=153 |
        201606
```

Coefficients for Vitvi17g00758.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.655145	3.272469e-19	***	1.310535e-18	***
SlopeC	0.2482399	0.6329814		0.912027	
MeanF-MeanC	-0.3011506	0.2603336		0.6218704	
SlopeF-SlopeC	-1.289348	0.105407		0.9999488	



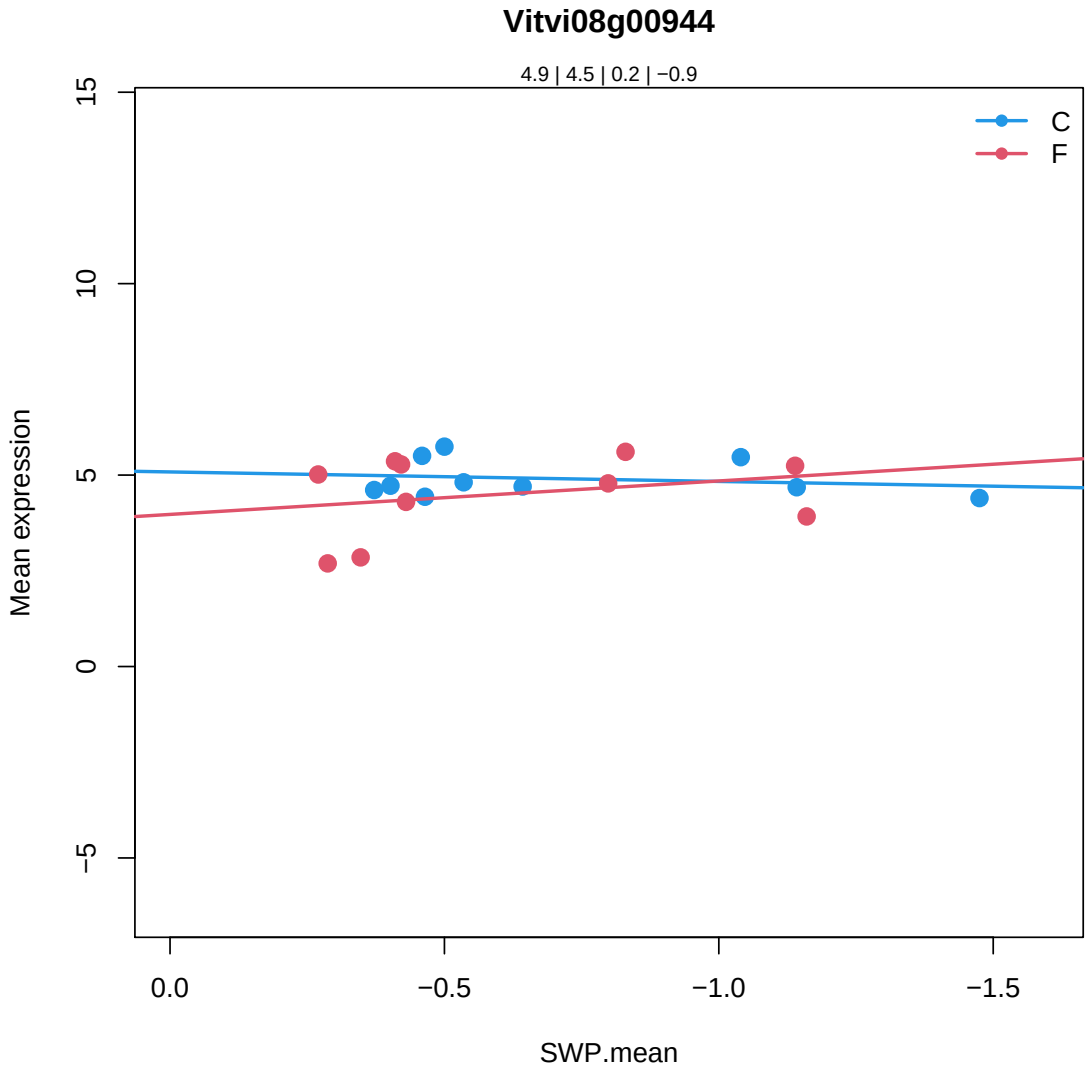
7.6.403 Vitvi08g00944: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g00944
        26.10
        misc.cytochrome P450
        cytochrome P450%2C family 94%2C subfamily D%2C polypeptide 2 |
        Chr3:20978953-20980512 FORWARD LENGTH=499 |
        201606
```

Coefficients for Vitvi08g00944.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.907362	1.466575e-15	***	2.691575e-15	***
SlopeC	0.2481131	0.713488		0.9353048	
MeanF-MeanC	-0.4024553	0.2480941		0.6081148	
SlopeF-SlopeC	-1.12172	0.2708771		0.9999488	



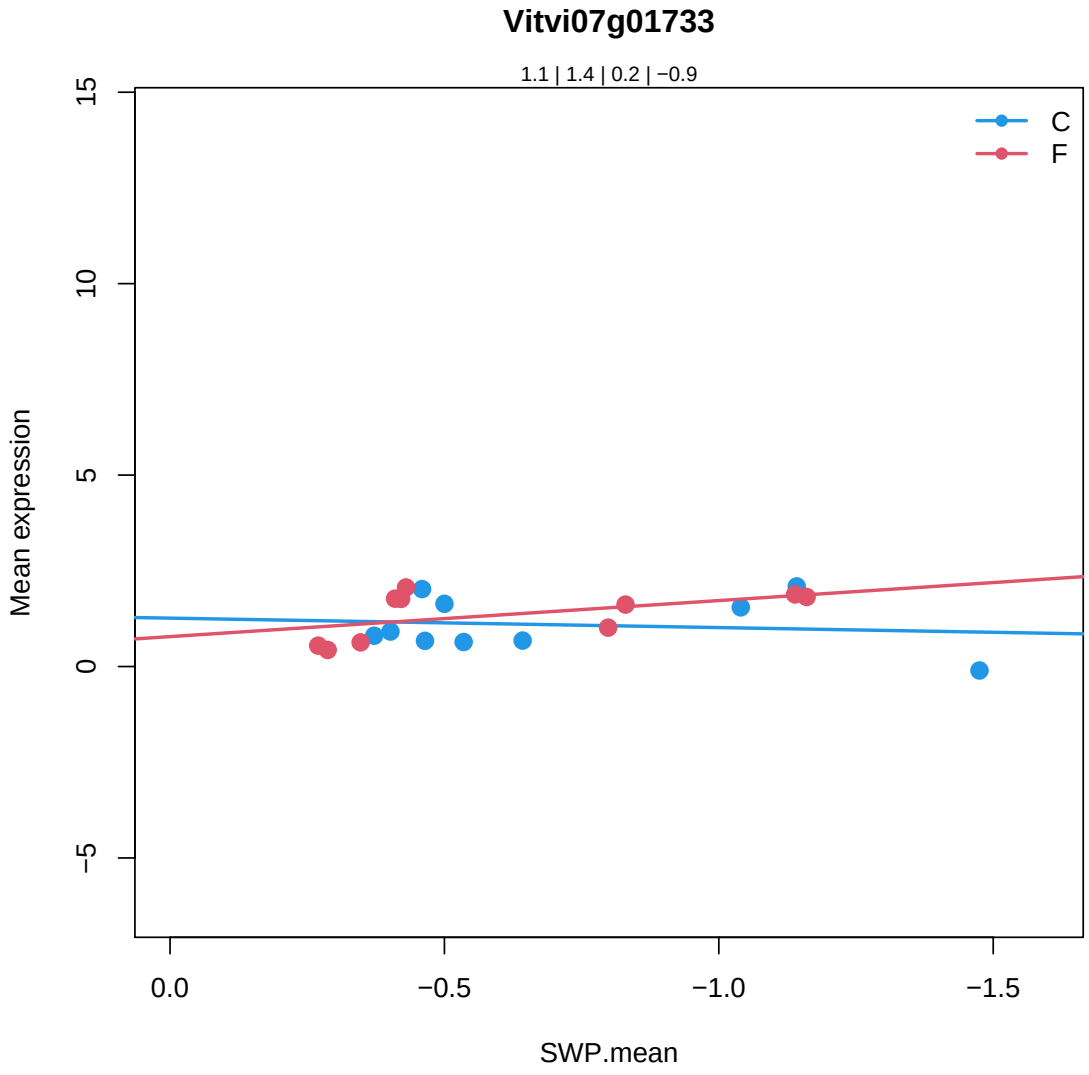
7.6.404 Vitvi07g01733: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01733
        11.9.3.5
        lipid metabolism.lipid degradation.lysophospholipases.phosphoinositide
        PLC-like phosphodiesterases superfamily protein |
        Chr4:17420098-17422047 REVERSE LENGTH=408 |
        201606
```

Coefficients for Vitvi07g01733.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.090001	1.581868e-05	***	1.778085e-05	***
SlopeC	0.2465141	0.6570821		0.9204483	
MeanF-MeanC	0.2642321	0.3530322		0.7112911	
SlopeF-SlopeC	-1.18791	0.1594415		0.9999488	



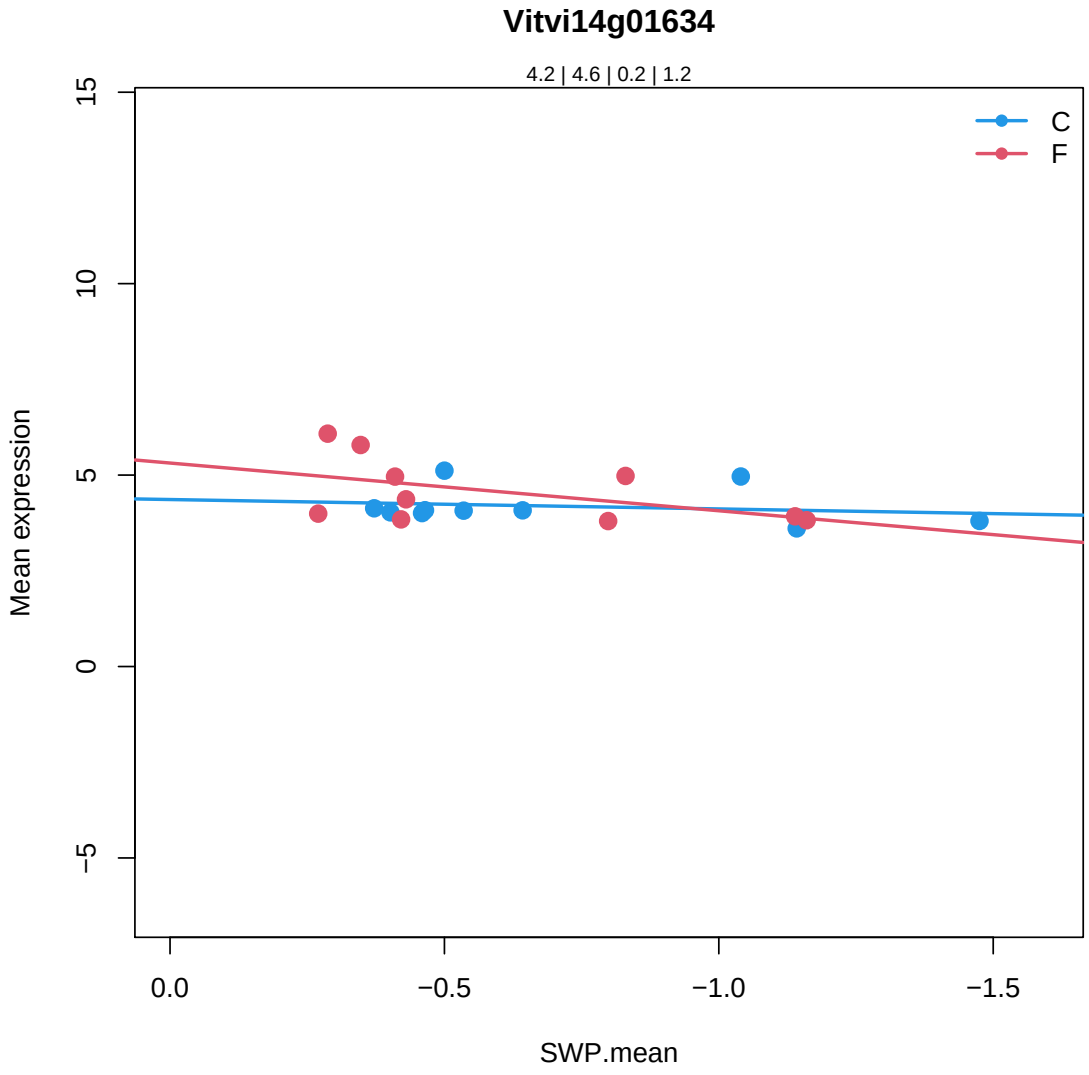
7.6.405 Vitvi14g01634: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01634
        27.3.7
        RNA.regulation of transcription.C2C2(Zn) Constans-like zinc finger fam
        CCT motif family protein |
        Chr1:2164446-2165133 REVERSE LENGTH=198 |
        201606
```

Coefficients for Vitvi14g01634.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.188562	5.653647e-16	***	1.092594e-15	***
SlopeC	0.2453016	0.6561513		0.9203044	
MeanF-MeanC	0.3663683	0.1985839		0.5407926	
SlopeF-SlopeC	1.001025	0.2291162		0.9999488	



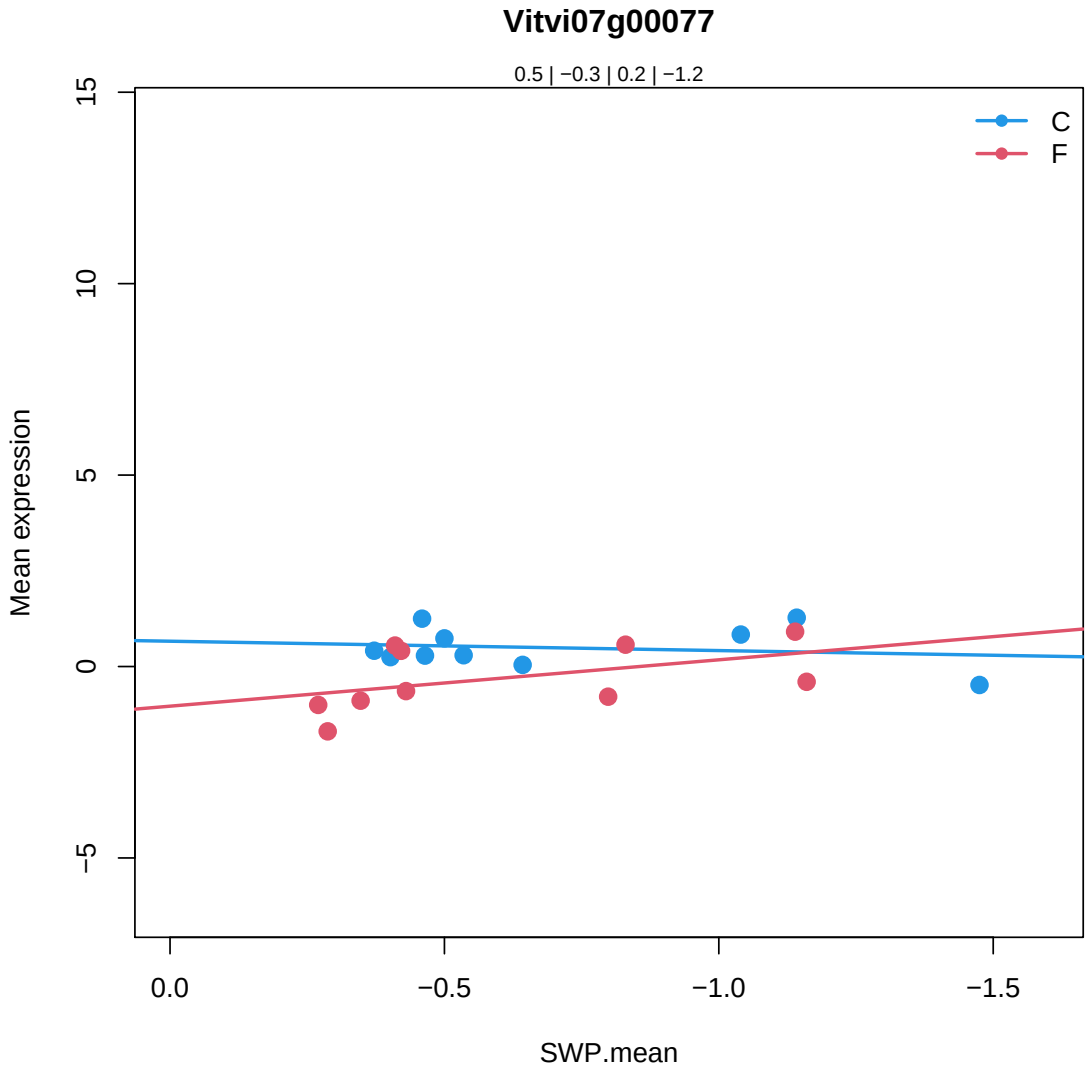
7.6.406 Vitvi07g00077: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g00077
        27.3.11
        RNA.regulation of transcription.C2H2 zinc finger family
        indeterminate(ID)-domain 12 |
        Chr4:1176190-1178495 REVERSE LENGTH=404 |
        201606
```

Coefficients for Vitvi07g00077.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4891182	0.02572984	*	0.02698137	*
SlopeC	0.244518	0.6710291		0.9241164	
MeanF-MeanC	-0.7871672	0.01247523	*	0.08943908	.
SlopeF-SlopeC	-1.455568	0.09940039	.	0.9999488	



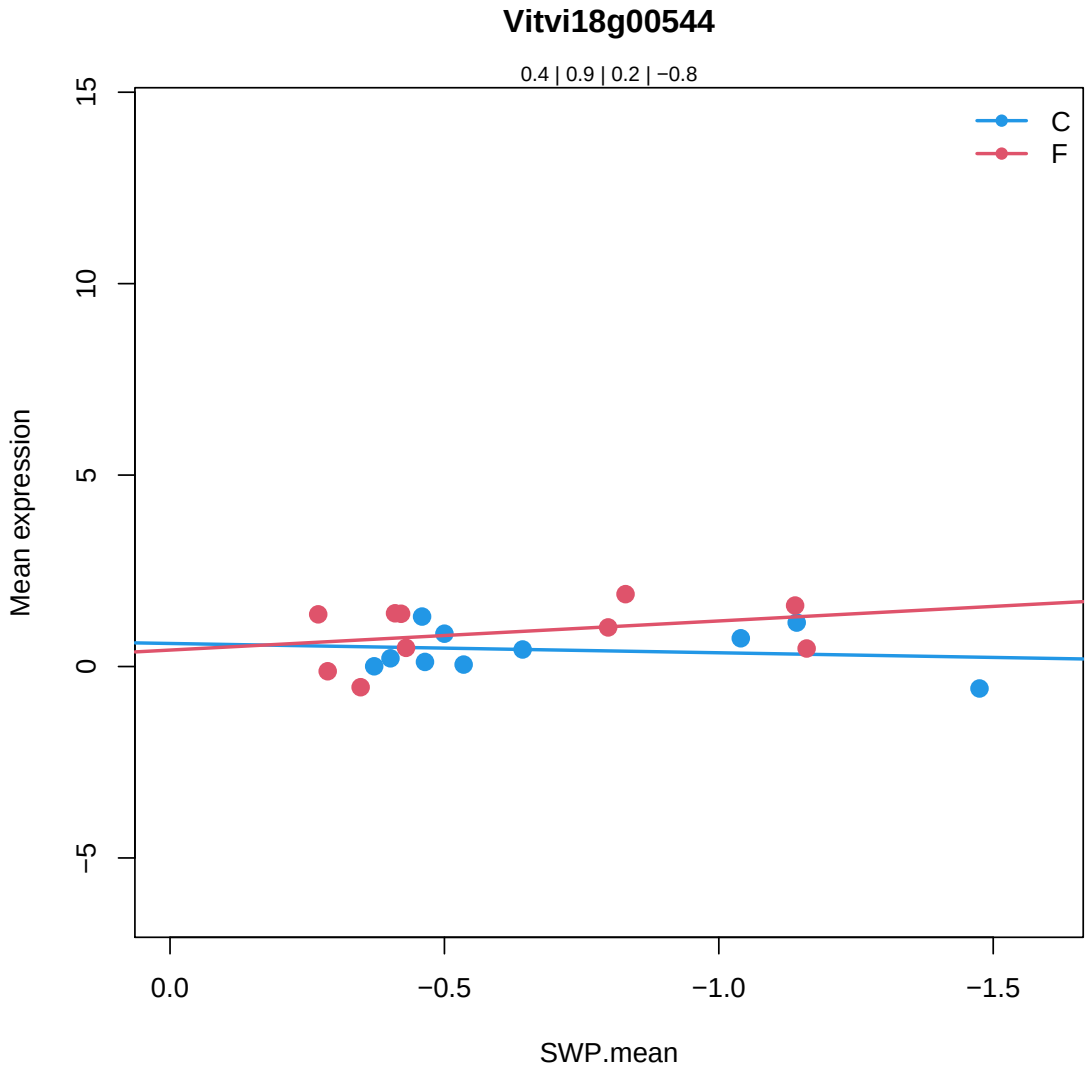
7.6.407 Vitvi18g00544: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00544
        31.1
        cell.organisation
        Di-glucose binding protein with Kinesin motor domain-containing protei
        Chr2:9599550-9604626 FORWARD LENGTH=1084 |
        201606
```

Coefficients for Vitvi18g00544.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4309422	0.05058504	.	0.05266511	.
SlopeC	0.2431034	0.6786824		0.9267397	
MeanF-MeanC	0.461869	0.1311277		0.4313009	
SlopeF-SlopeC	-1.003317	0.2569948		0.9999488	



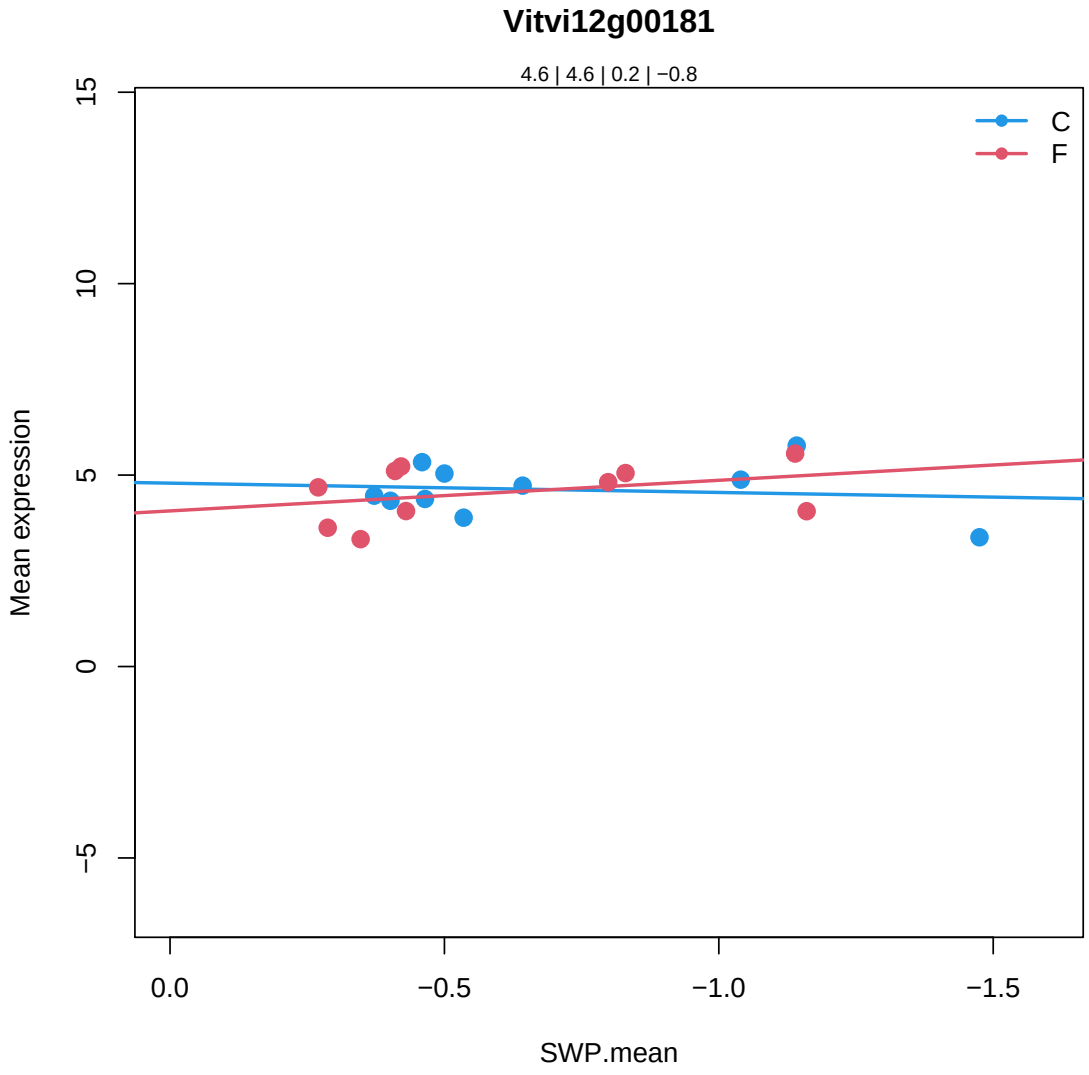
7.6.408 Vitvi12g00181: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00181
        29.4.1
        protein.postranslational modification.kinase
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi12g00181.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.618125	5.247231e-16	***	1.019221e-15	***
SlopeC	0.2427972	0.6881782		0.9306347	
MeanF-MeanC	-0.06729509	0.8265548		0.9513491	
SlopeF-SlopeC	-1.042348	0.2535003		0.9999488	



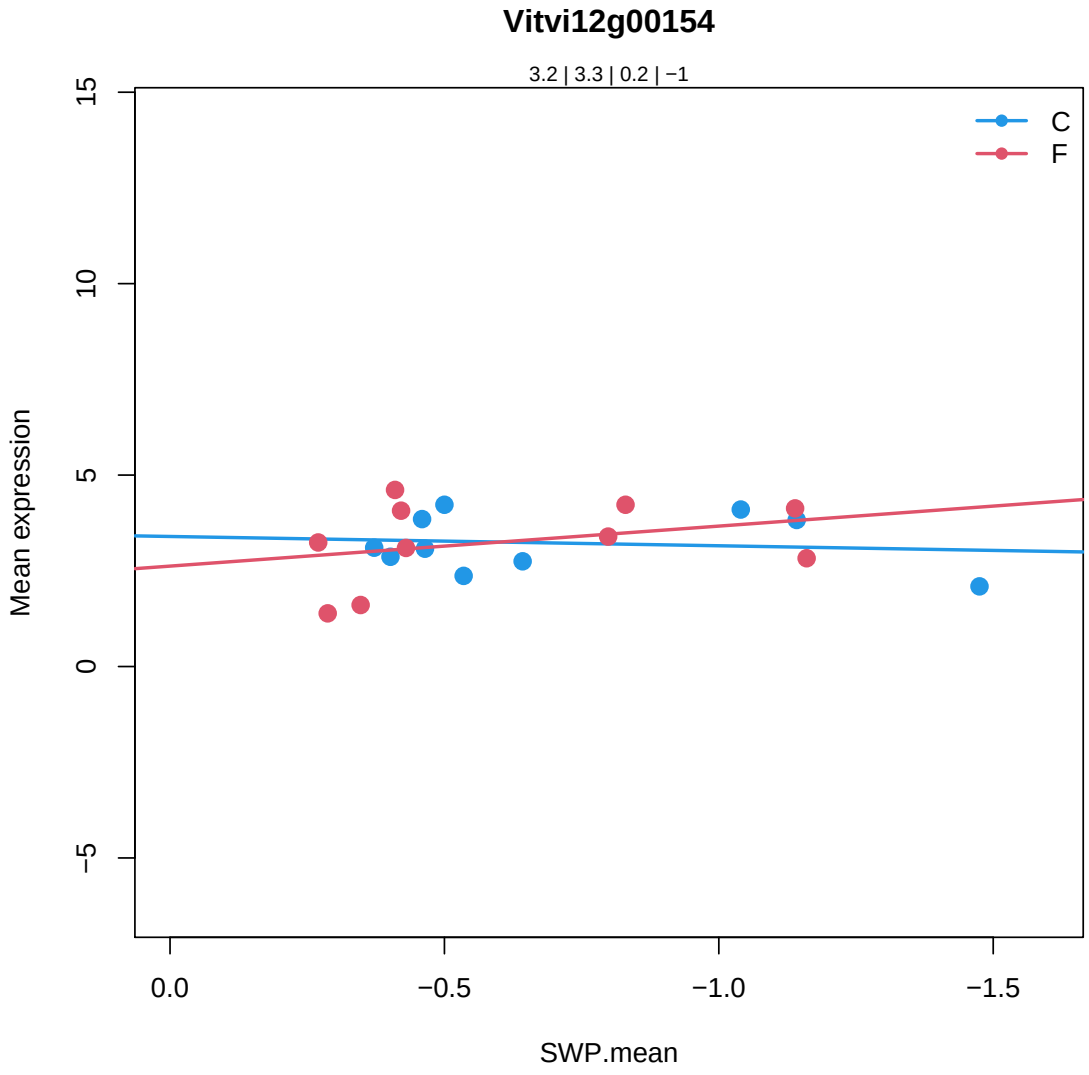
7.6.409 Vitvi12g00154: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00154
        26.8
        misc.nitrilases, nitrile lyases, berberine bridge enzymes, reticuline
        FAD-binding Berberine family protein |
        Chr5:17886365-17888071 REVERSE LENGTH=537 |
        201606
```

Coefficients for Vitvi12g00154.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.225738	6.077168e-11	***	8.016286e-11	***
SlopeC	0.242439	0.750095		0.9472203	
MeanF-MeanC	0.0333018	0.9313335		0.9817681	
SlopeF-SlopeC	-1.287286	0.2624071		0.9999488	



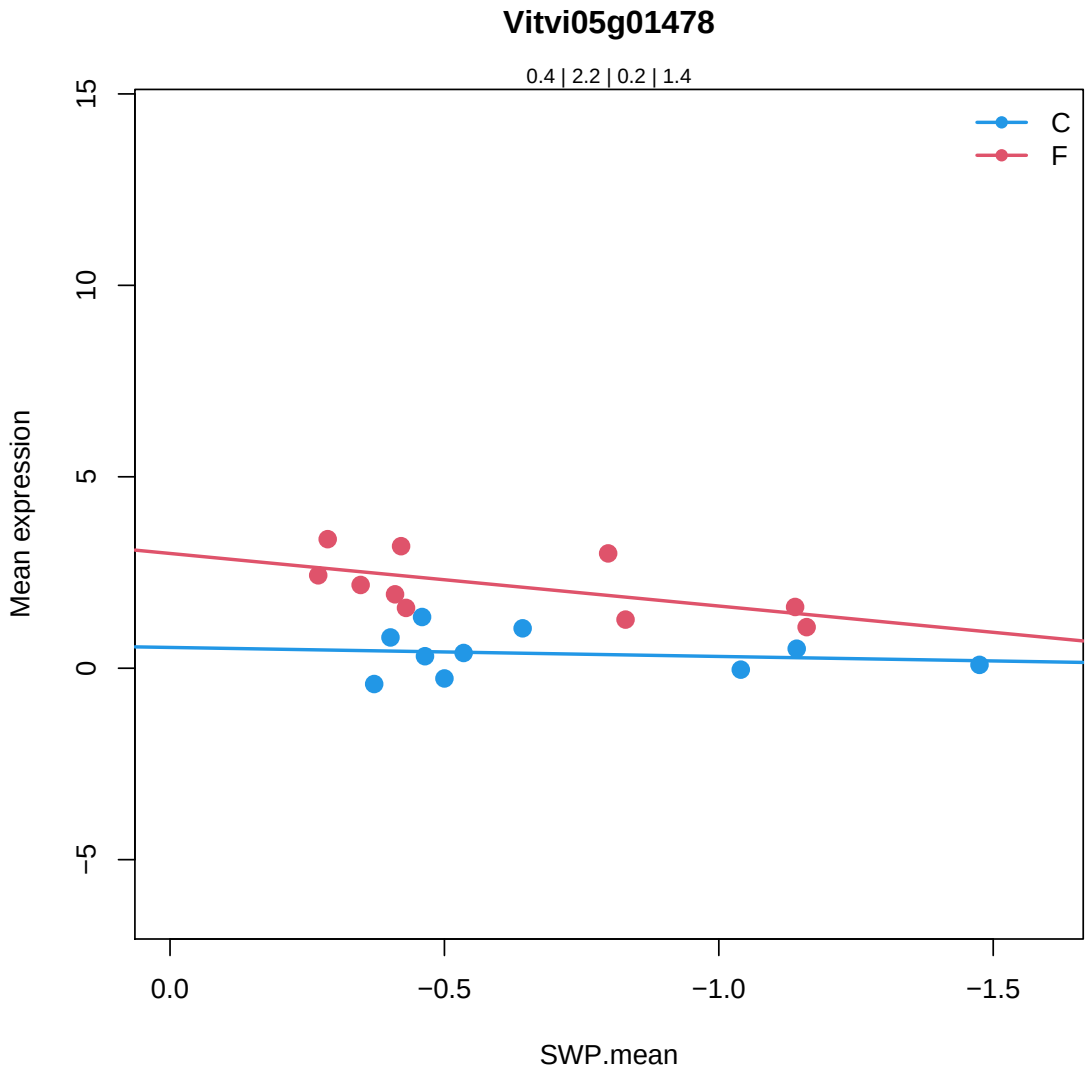
7.6.410 Vitvi05g01478: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01478
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi05g01478.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3774205	0.06500877	.	0.06751133	.
SlopeC	0.2348941	0.6678421		0.9237671	
MeanF-MeanC	1.7831	1.756493e-06	***	5.375998e-05	***
SlopeF-SlopeC	1.138472	0.1708954		0.9999488	



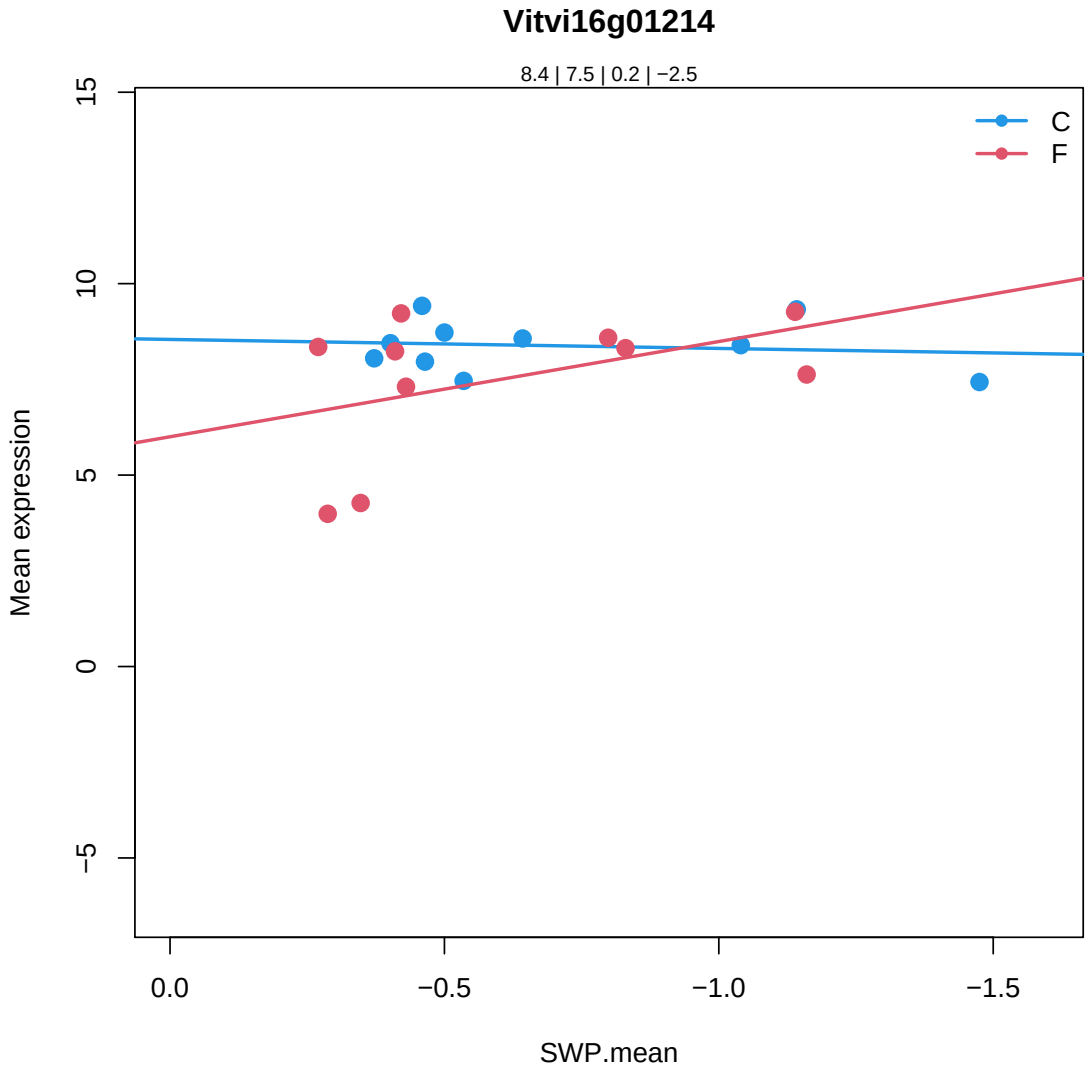
7.6.411 Vitvi16g01214: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01214
        27.3.85
        RNA.regulation of transcription.sigma like plant
        sigma factor E |
        Chr5:8157794-8159746 REVERSE LENGTH=517 |
        201606
```

Coefficients for Vitvi16g01214.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	8.377712	3.064361e-16	***	6.160247e-16	***
SlopeC	0.2347942	0.8259473		0.9653997	
MeanF-MeanC	-0.8615797	0.1226846		0.4136162	
SlopeF-SlopeC	-2.721939	0.09729539	.	0.9999488	



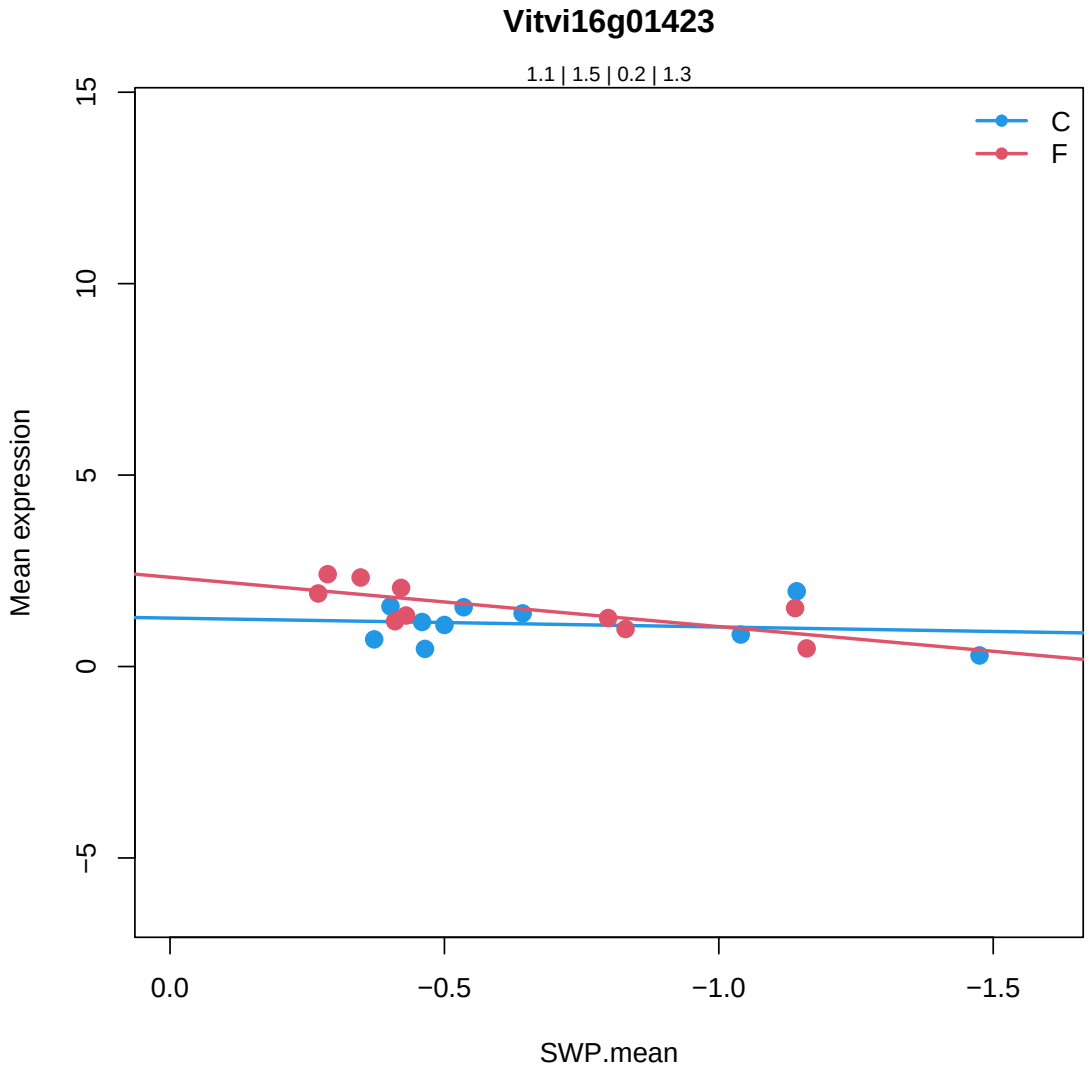
7.6.412 Vitvi16g01423: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01423
        35.2
        not assigned.unknown
        Integrase-type DNA-binding superfamily protein |
        Chr5:20800708-20801373 REVERSE LENGTH=221 |
        201606
```

Coefficients for Vitvi16g01423.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.101193	7.525024e-07	***	8.710899e-07	***
SlopeC	0.2325903	0.6067409		0.9047128	
MeanF-MeanC	0.4441991	0.06278213	.	0.2766479	
SlopeF-SlopeC	1.05609	0.1256368		0.9999488	



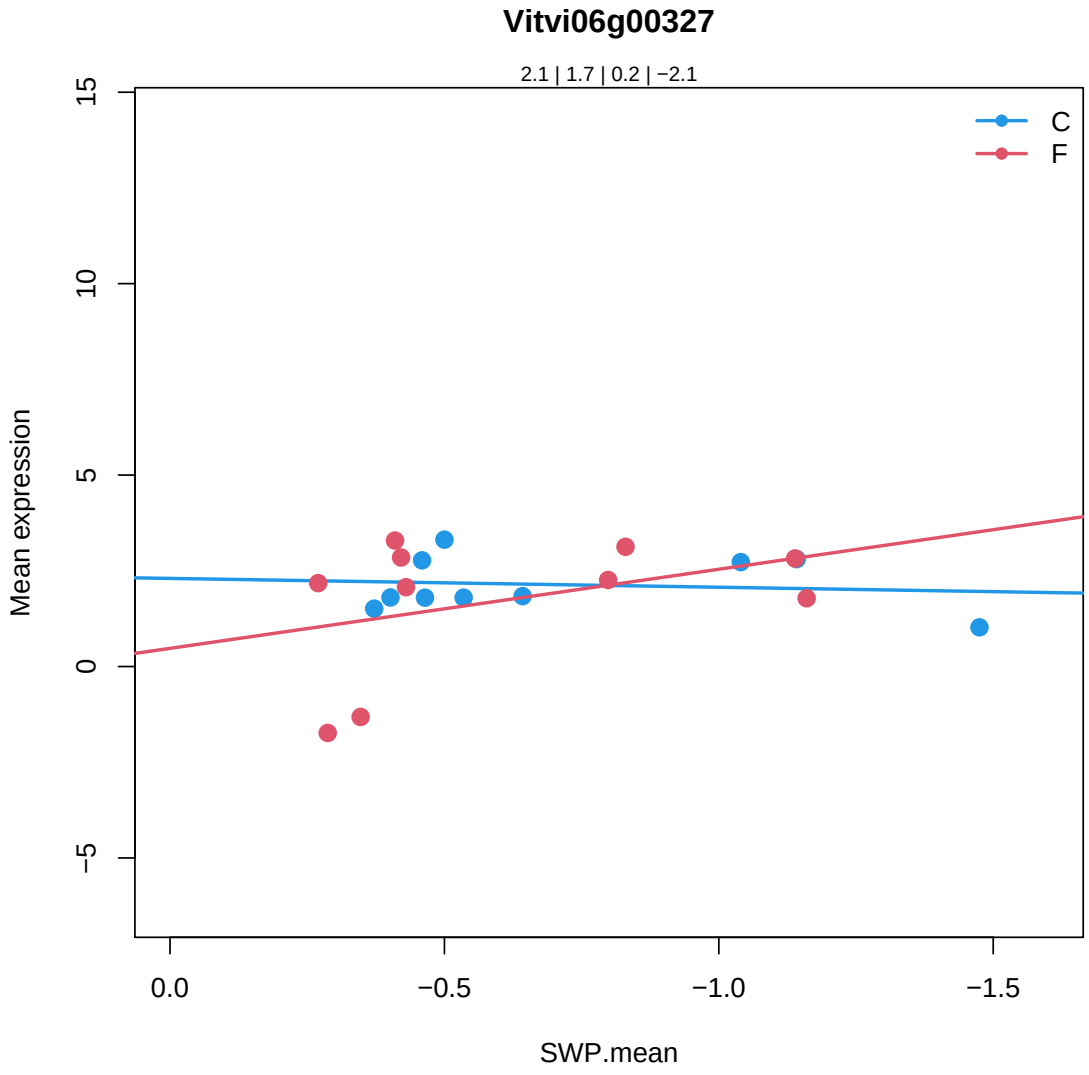
7.6.413 Vitvi06g00327: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00327
        35.2
        not assigned.unknown
        lectin protein kinase family protein |
        Chr1:12503450-12505939 FORWARD LENGTH=829 |
        201606
```

Coefficients for Vitvi06g00327.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.138951	1.054237e-05	***	1.190008e-05	***
SlopeC	0.230431	0.8270416		0.9656897	
MeanF-MeanC	-0.4060912	0.4515428		0.77888	
SlopeF-SlopeC	-2.296154	0.1532		0.9999488	



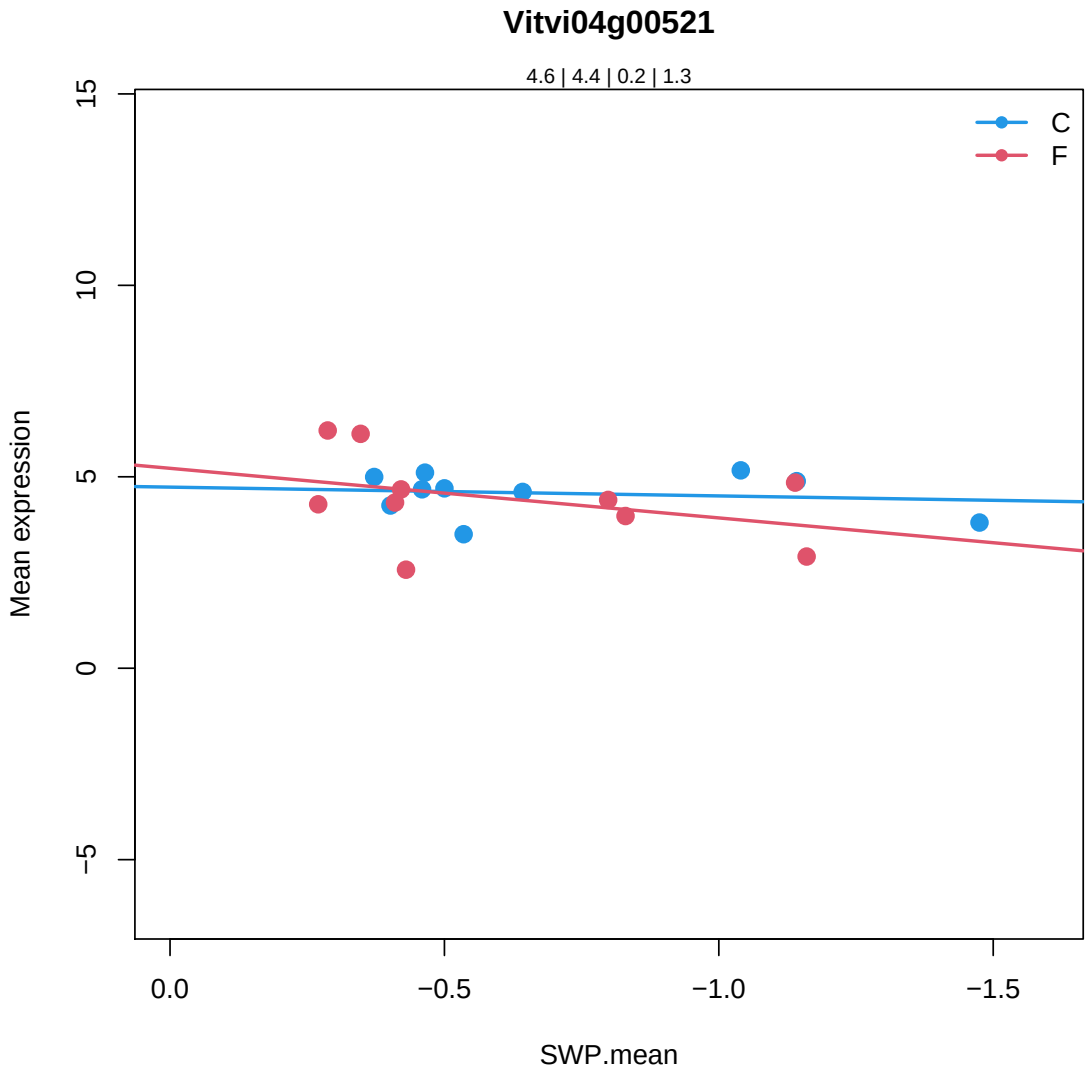
7.6.414 Vitvi04g00521: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00521
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi04g00521.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.568362	3.230713e-14	***	5.158987e-14	***
SlopeC	0.2296504	0.7538346		0.9472461	
MeanF-MeanC	-0.1365728	0.7138298		0.9117897	
SlopeF-SlopeC	1.065572	0.3331104		0.9999488	



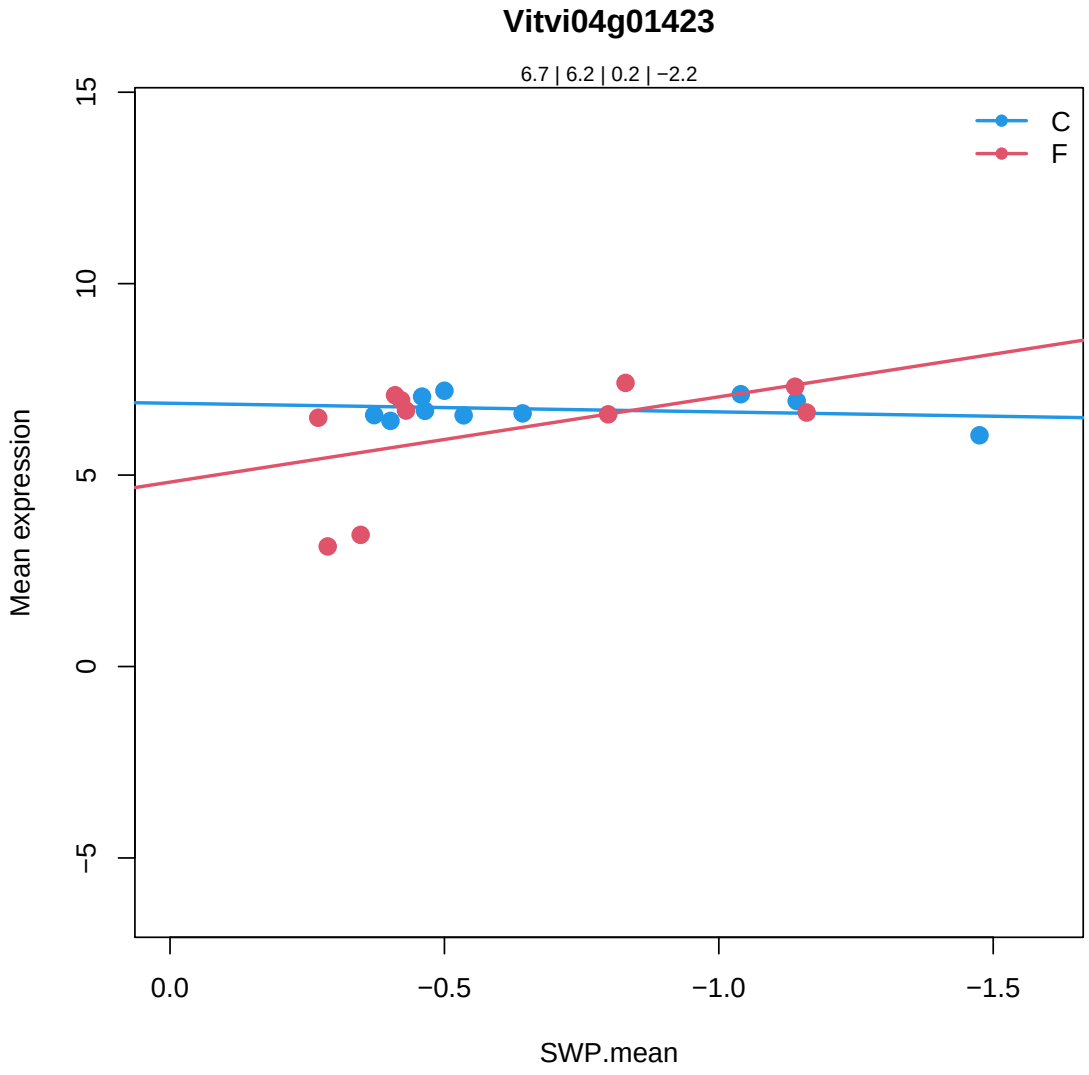
7.6.415 Vitvi04g01423: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01423
        27.3.7
        RNA.regulation of transcription.C2C2(Zn) Constans-like zinc finger fam
        B-box type zinc finger family protein |
        Chr4:18161576-18163045 FORWARD LENGTH=183 |
        201606
```

Coefficients for Vitvi04g01423.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.716982	1.815366e-16	***	3.776932e-16	***
SlopeC	0.2254381	0.7871277		0.9533712	
MeanF-MeanC	-0.5438791	0.2081442		0.5525589	
SlopeF-SlopeC	-2.453074	0.05842625	.	0.9999488	



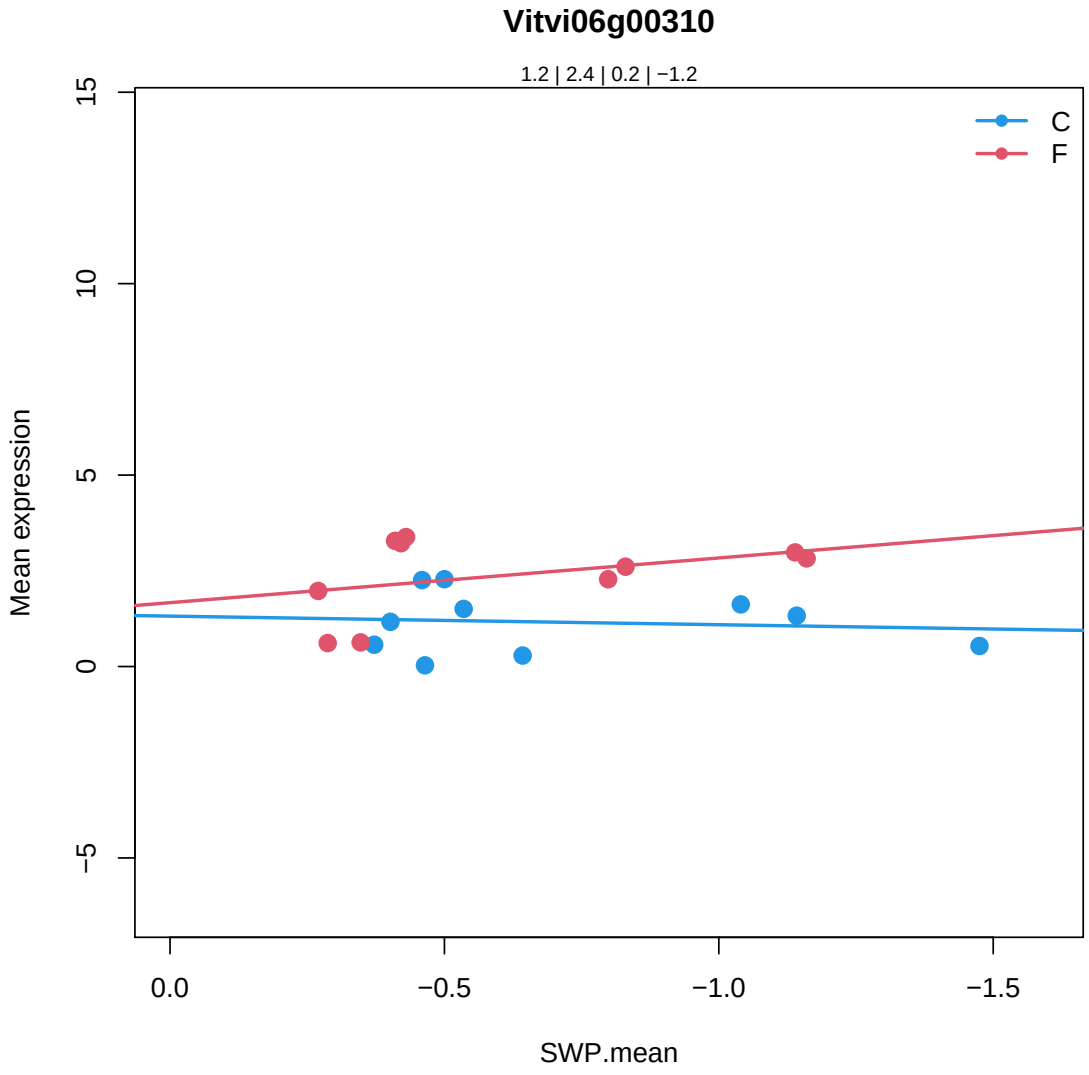
7.6.416 Vitvi06g00310: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00310
        20.1.3.1
        stress.biotic.signalling.MLO-like
        Seven transmembrane MLO family protein |
        Chr3:16617586-16621352 FORWARD LENGTH=508 |
        201606
```

Coefficients for Vitvi06g00310.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.158236	0.0002412359	***	0.0002644313	***
SlopeC	0.2240848	0.7627521		0.94868	
MeanF-MeanC	1.220791	0.00353012	**	0.03482595	*
SlopeF-SlopeC	-1.392183	0.215532		0.9999488	



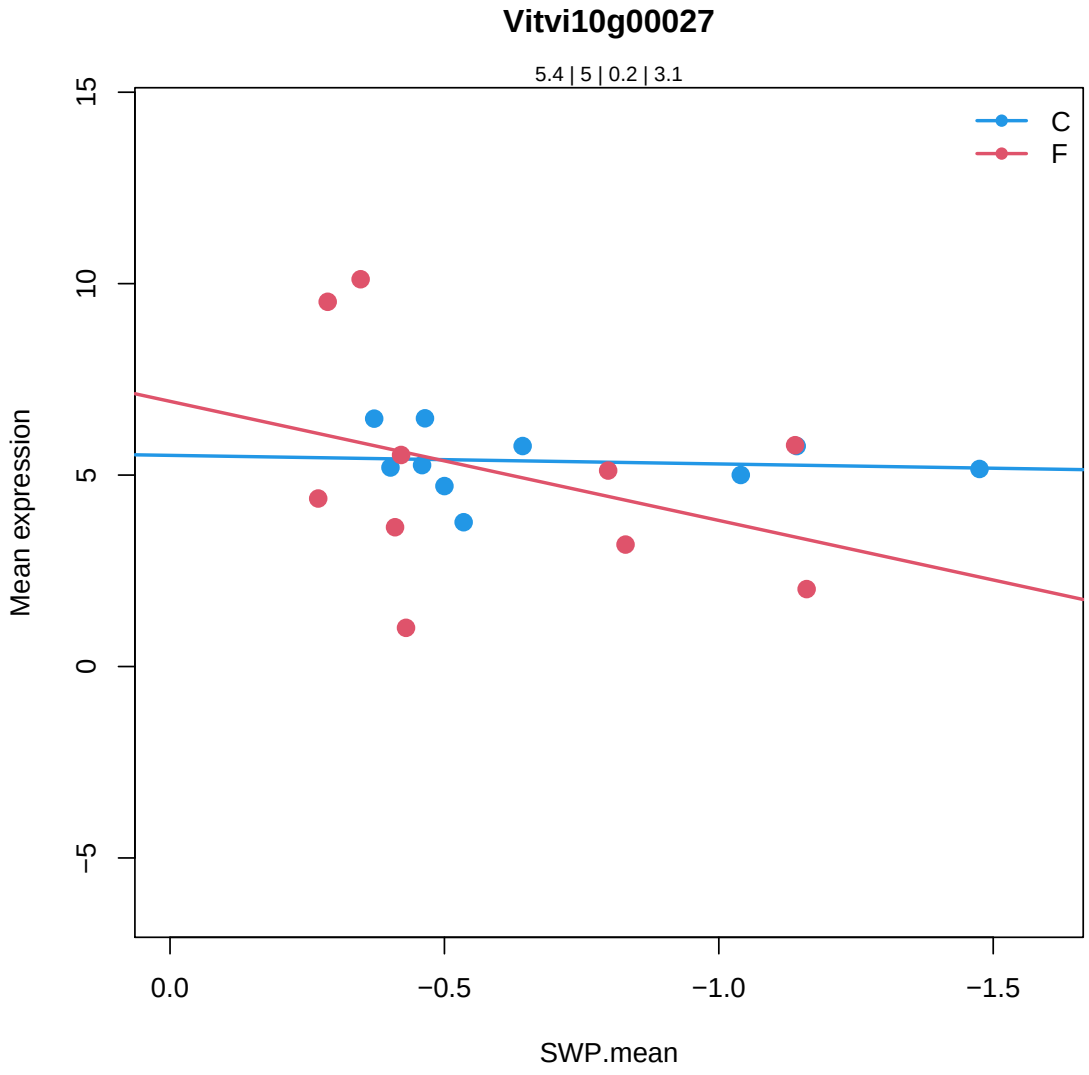
7.6.417 Vitvi10g00027: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00027
        18.2
        Co-factor and vitamine metabolism.thiamine
        thiazole biosynthetic enzyme%2C chloroplast (ARA6) (THI1) (THI4) |
        Chr5:22246634-22247891 FORWARD LENGTH=349 |
        201606
```

Coefficients for Vitvi10g00027.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.357273	8.634117e-09	***	1.055766e-08	***
SlopeC	0.2236902	0.8929712		0.9805249	
MeanF-MeanC	-0.3265925	0.6996094		0.9062933	
SlopeF-SlopeC	2.886813	0.2507124		0.9999488	



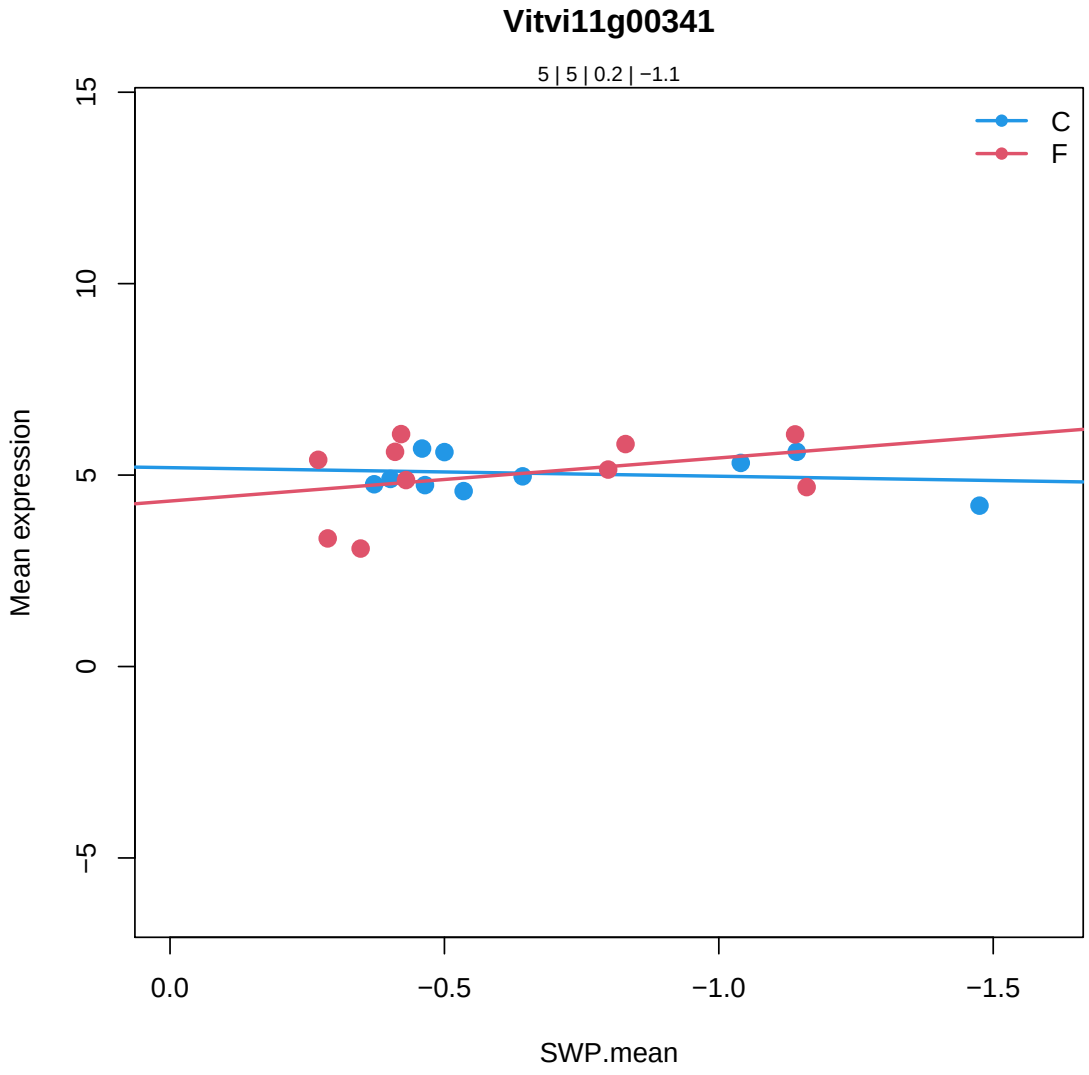
7.6.418 Vitvi11g00341: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00341
        31.1
        cell.organisation
        ATP binding microtubule motor family protein |
        Chr3:5447503-5451196 FORWARD LENGTH=684 |
        201606
```

Coefficients for Vitvi11g00341.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.036387	7.519611e-16	***	1.431958e-15	***
SlopeC	0.2235837	0.7389943		0.9434568	
MeanF-MeanC	-0.02890336	0.9323897		0.981995	
SlopeF-SlopeC	-1.349341	0.1852799		0.9999488	

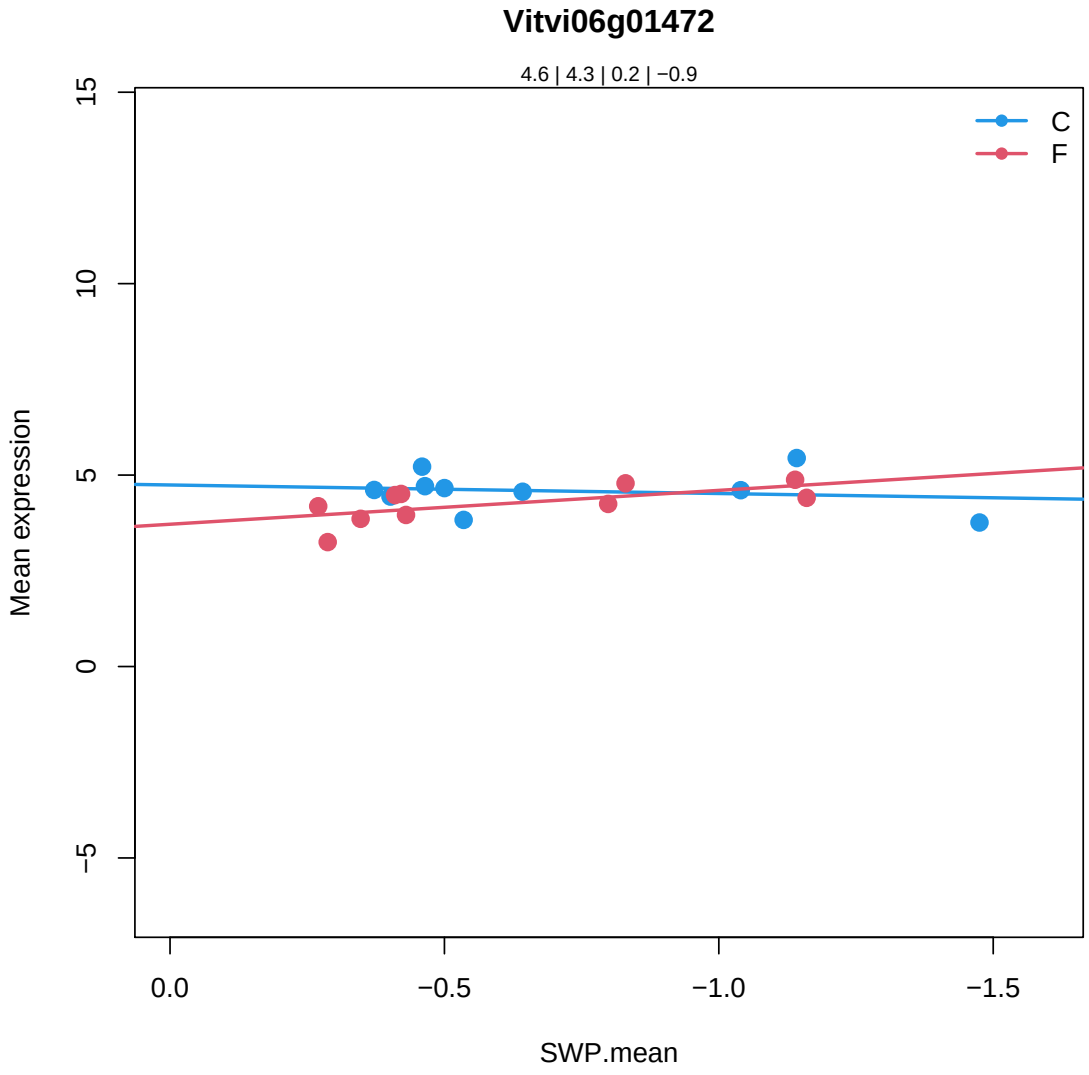


7.6.419 Vitvi06g01472: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
Vitvi06g01472
        35.2
        not assigned.unknown
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi06g01472.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.584486	4.368472e-19	***	1.686531e-18	***
SlopeC	0.2229099	0.6020563		0.904666	
MeanF-MeanC	-0.3294696	0.138444		0.4452831	
SlopeF-SlopeC	-1.107646	0.09146103	.	0.9999488	



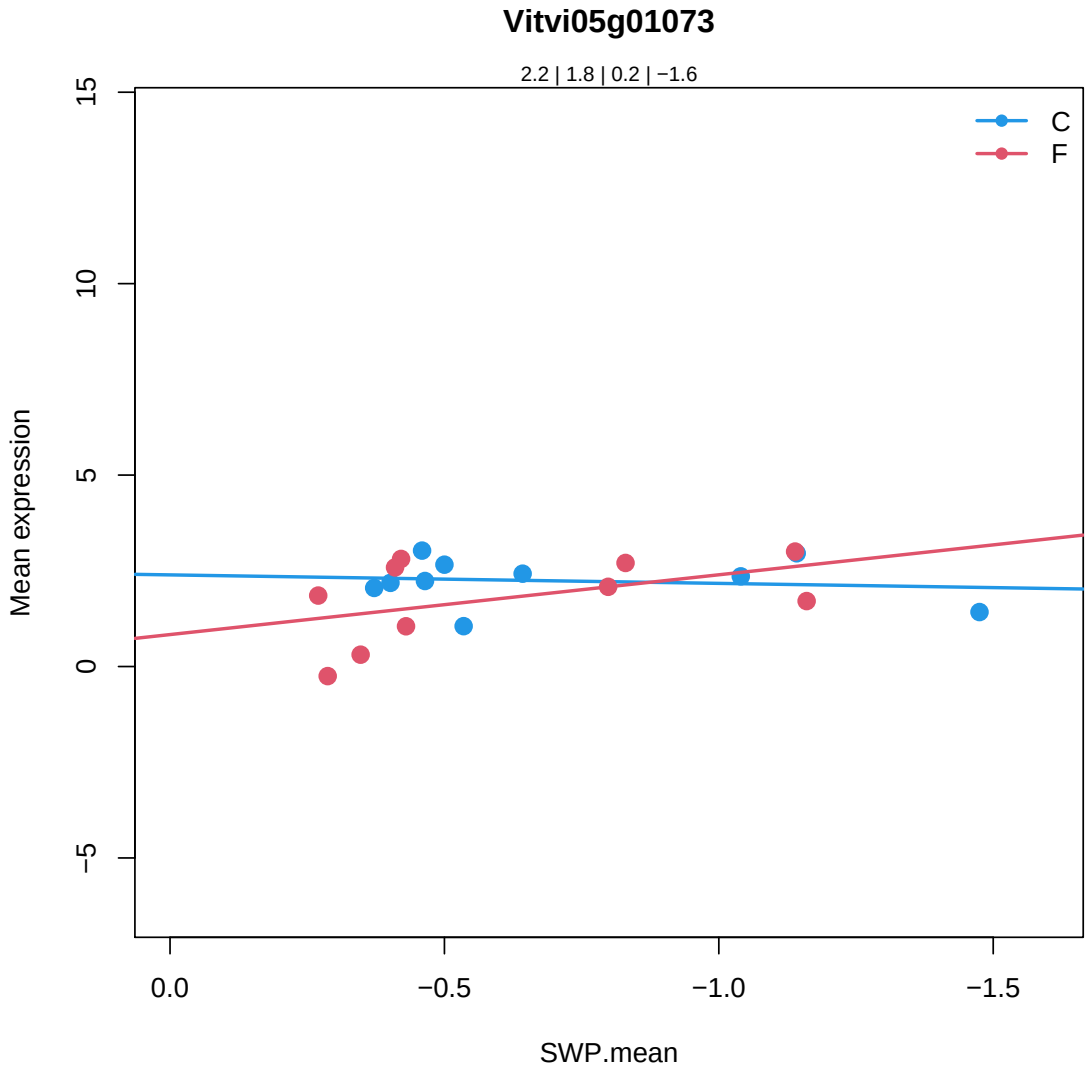
7.6.420 Vitvi05g01073: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01073
        27.3.3
        RNA.regulation of transcription.AP2/EREBP, APETALA2/ethylene-responsiv
        Integrase-type DNA-binding superfamily protein |
        Chr4:7932138-7933304 FORWARD LENGTH=388 |
        201606
```

Coefficients for Vitvi05g01073.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.237204	9.021019e-09	***	1.102368e-08	***
SlopeC	0.22165	0.7503935		0.9472461	
MeanF-MeanC	-0.4513887	0.2104542		0.5554103	
SlopeF-SlopeC	-1.783229	0.0958686	.	0.9999488	



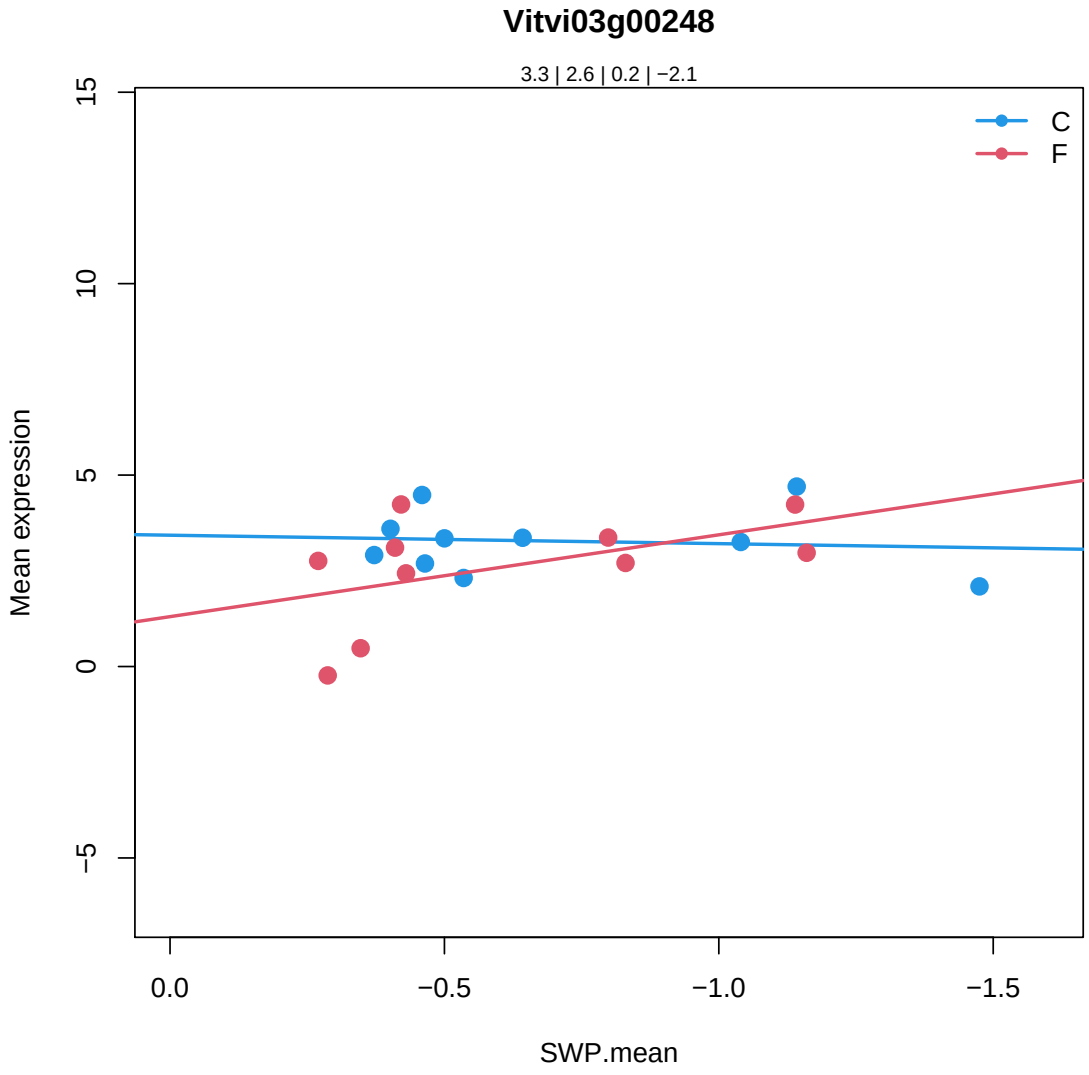
7.6.421 Vitvi03g00248: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00248
        34.9
        transport.metabolite transporters at the mitochondrial membrane
        phosphate transporter 3%3B3 |
        Chr2:7510456-7512118 FORWARD LENGTH=309 |
        201606
```

Coefficients for Vitvi03g00248.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.274755	9.271225e-10	***	1.170092e-09	***
SlopeC	0.2201906	0.8058195		0.9575465	
MeanF-MeanC	-0.6699213	0.1508798		0.4679293	
SlopeF-SlopeC	-2.357623	0.08751471	.	0.9999488	



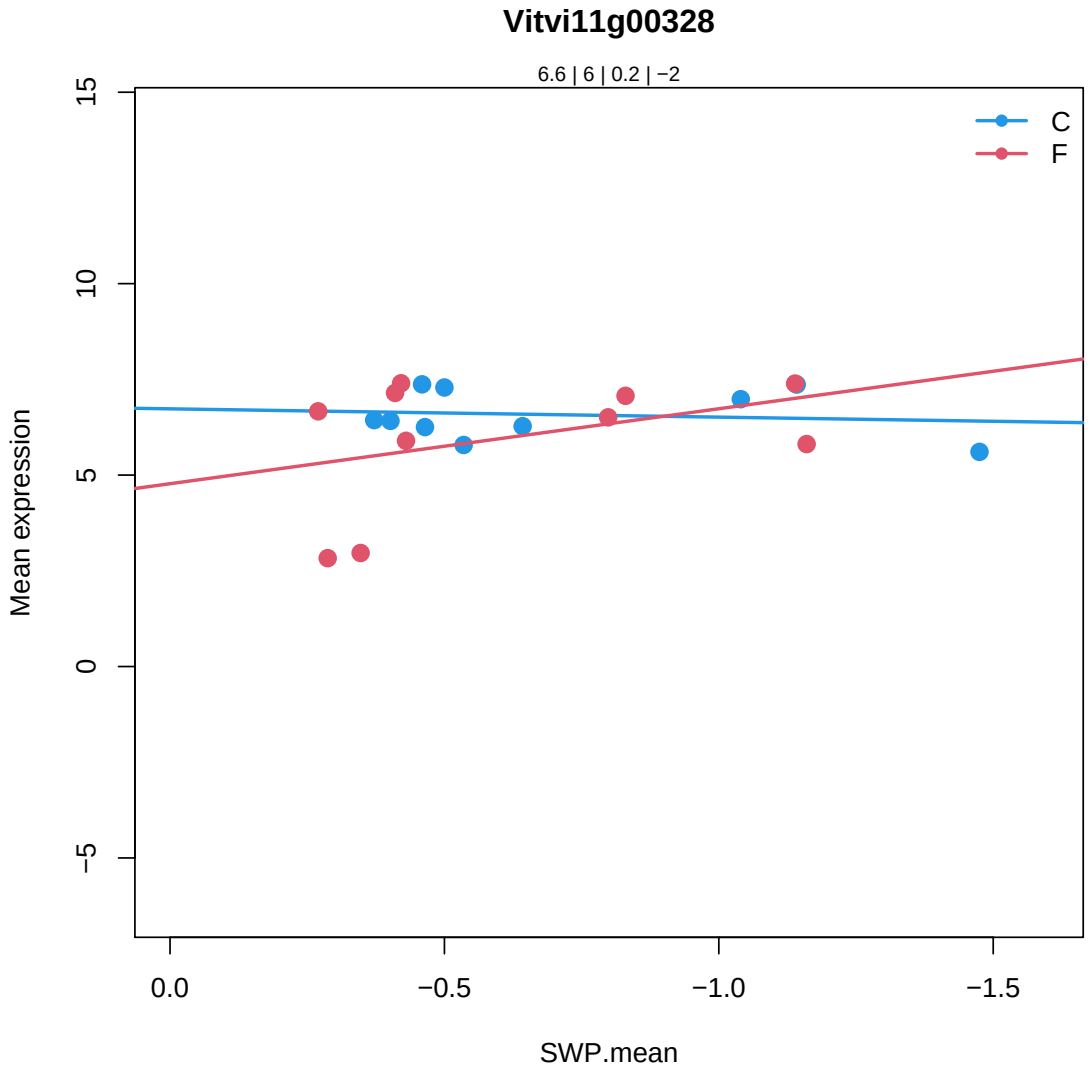
7.6.422 Vitvi11g00328: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00328
        29.4
        protein.postranslational modification
        protein kinase family protein |
        Chr5:7209422-7213700 FORWARD LENGTH=831 |
        201606
```

Coefficients for Vitvi11g00328.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.577758	1.211049e-14	***	2.007265e-14	***
SlopeC	0.2169187	0.8289055		0.9662319	
MeanF-MeanC	-0.6102972	0.2391458		0.5962654	
SlopeF-SlopeC	-2.174644	0.1551483		0.9999488	



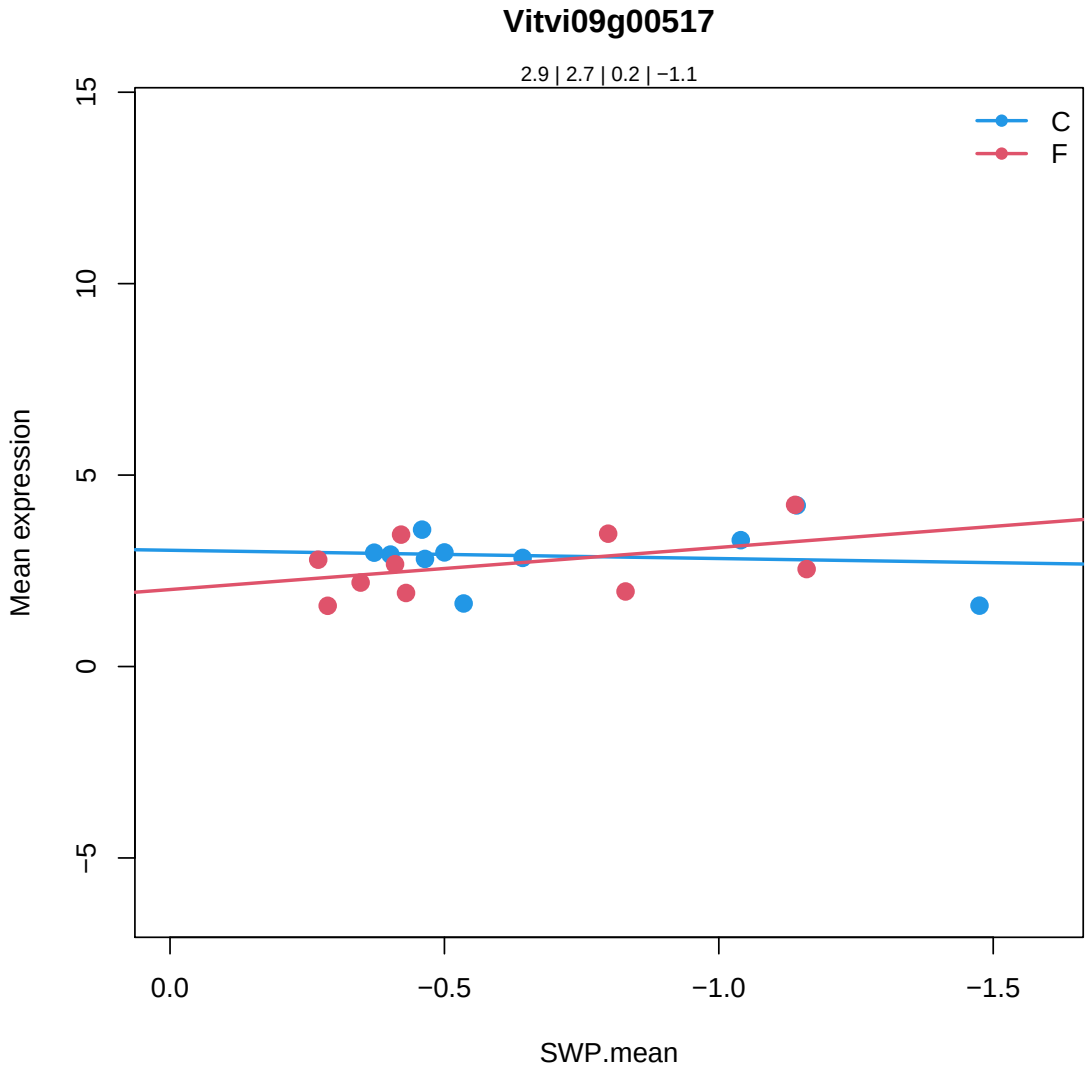
7.6.423 Vitvi09g00517: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00517
        20.2.5
        stress.abiotic.light
        DNA photolyase family protein |
        Chr3:5293475-5296548 REVERSE LENGTH=556 |
        201606
```

Coefficients for Vitvi09g00517.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.884203	3.367766e-11	***	4.491336e-11	***
SlopeC	0.2162438	0.7430362		0.9454913	
MeanF-MeanC	-0.2039242	0.5443057		0.8300457	
SlopeF-SlopeC	-1.316047	0.1885942		0.9999488	



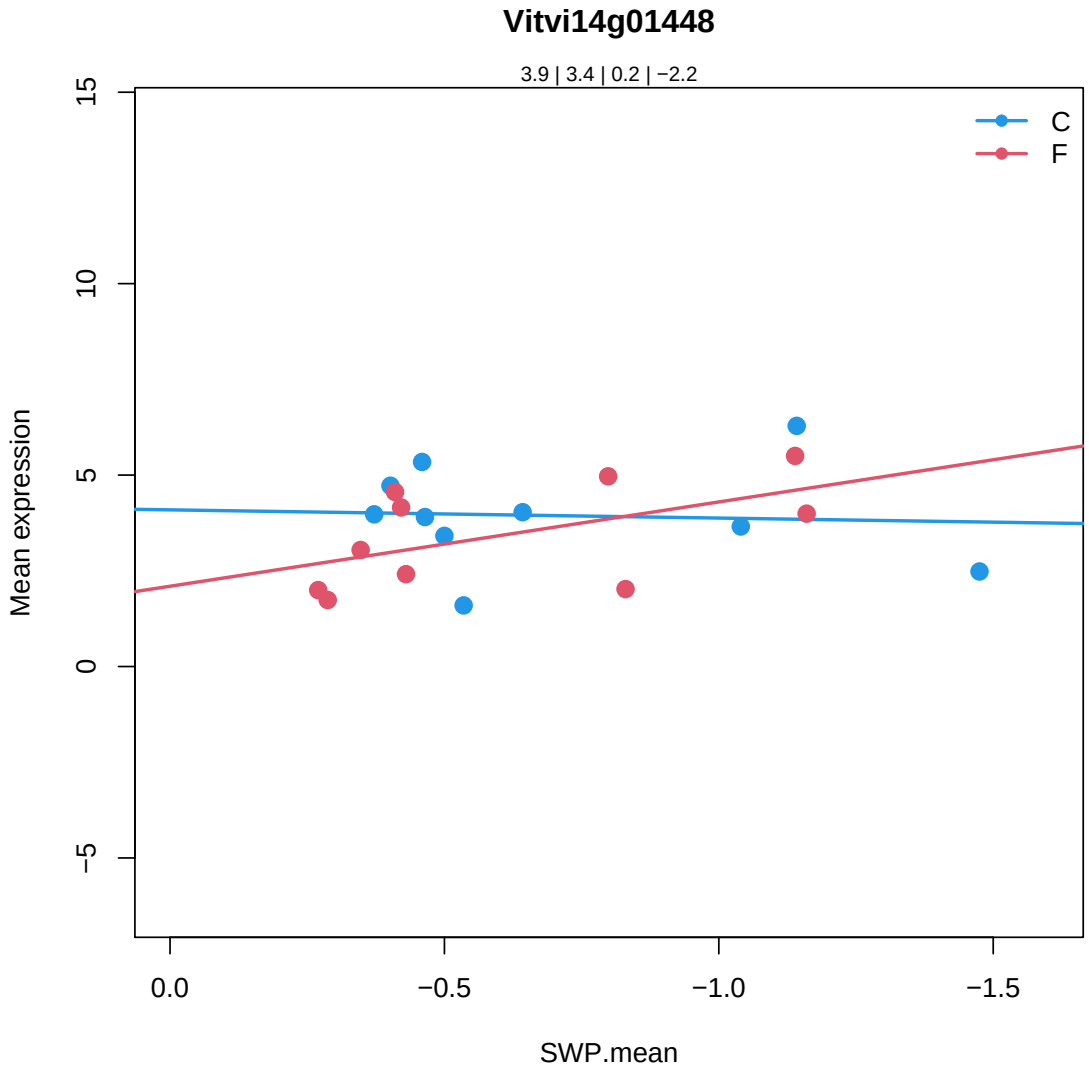
7.6.424 Vitvi14g01448: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01448
        16.8.2.1
        secondary metabolism.flavonoids.chalcones.naringenin-chalcone synthase
        Chalcone and stilbene synthase family protein |
        Chr5:4488762-4490035 FORWARD LENGTH=395 |
        201606
```

Coefficients for Vitvi14g01448.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.940695	4.532478e-10	***	5.785932e-10	***
SlopeC	0.214132	0.8362316		0.9691182	
MeanF-MeanC	-0.5024314	0.344882		0.7045706	
SlopeF-SlopeC	-2.415744	0.1273688		0.9999488	



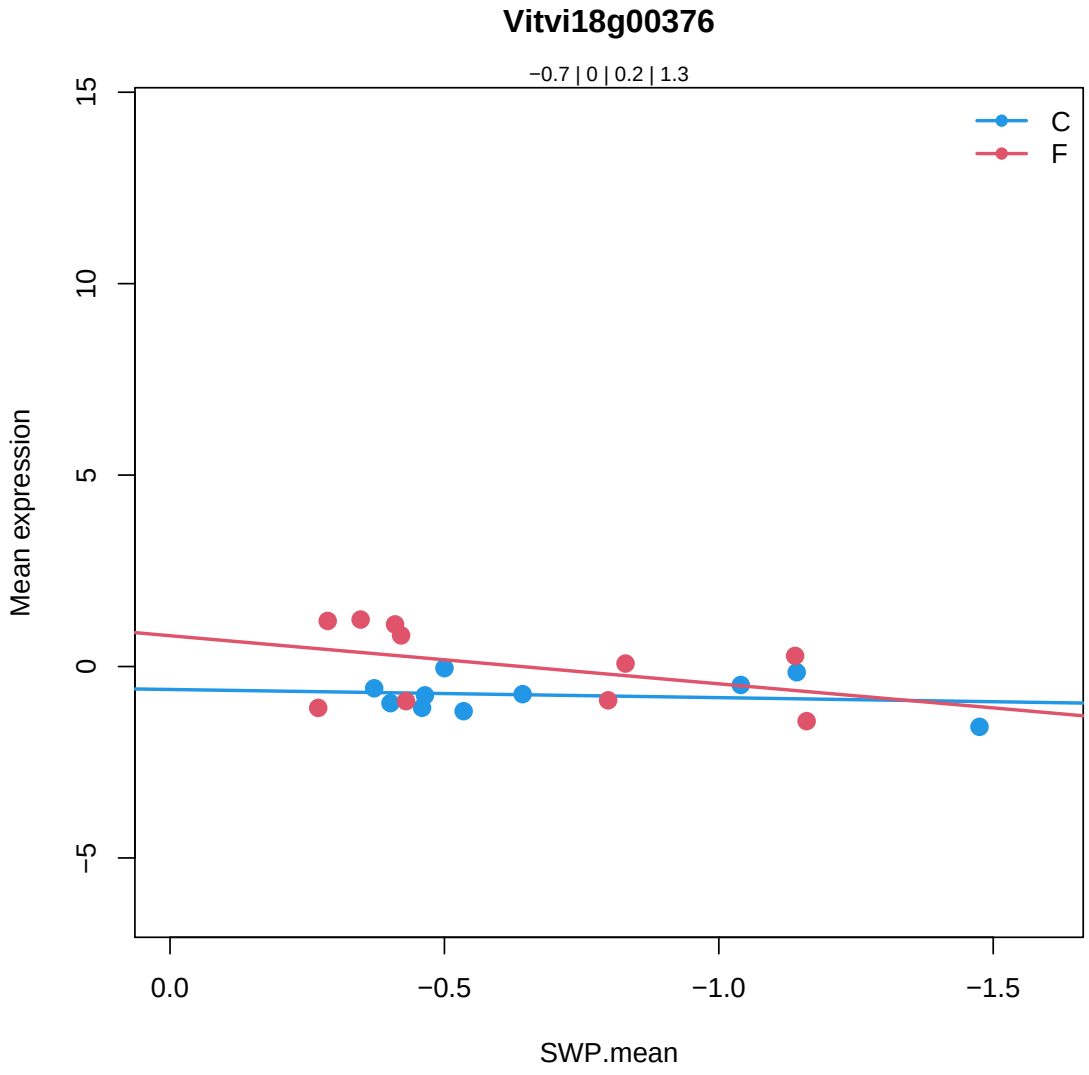
7.6.425 Vitvi18g00376: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00376
        10.6.2
        cell wall.degradation.mannan-xylose-arabinose-fucose
        Glycosyl hydrolase family protein |
        Chr1:29349796-29352868 REVERSE LENGTH=767 |
        201606
```

Coefficients for Vitvi18g00376.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.7496787	0.003505101	**	0.003750685	**
SlopeC	0.2135144	0.7403217		0.9443454	
MeanF-MeanC	0.788539	0.02347487	*	0.1417881	
SlopeF-SlopeC	1.043382	0.2825272		0.9999488	



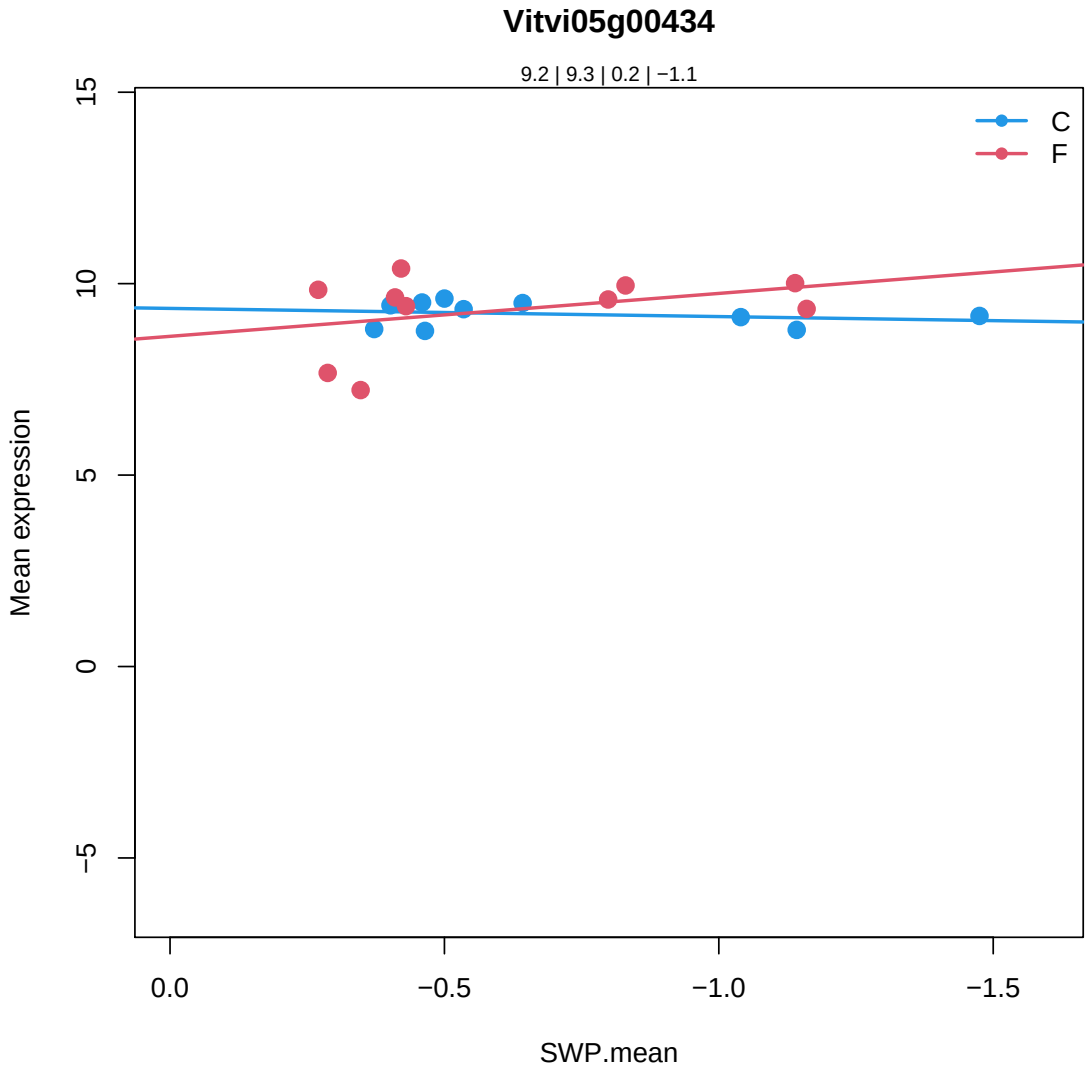
7.6.426 Vitvi05g00434: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00434
        15
        metal handling
        aluminum induced protein with YGL and LRDR motifs |
        Chr5:6424779-6425785 FORWARD LENGTH=198 |
        201606
```

Coefficients for Vitvi05g00434.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	9.203123	5.266445e-22	***	6.924394e-21	***
SlopeC	0.2130634	0.7322957		0.9408145	
MeanF-MeanC	0.1033985	0.7439563		0.9245875	
SlopeF-SlopeC	-1.333682	0.159462		0.9999488	



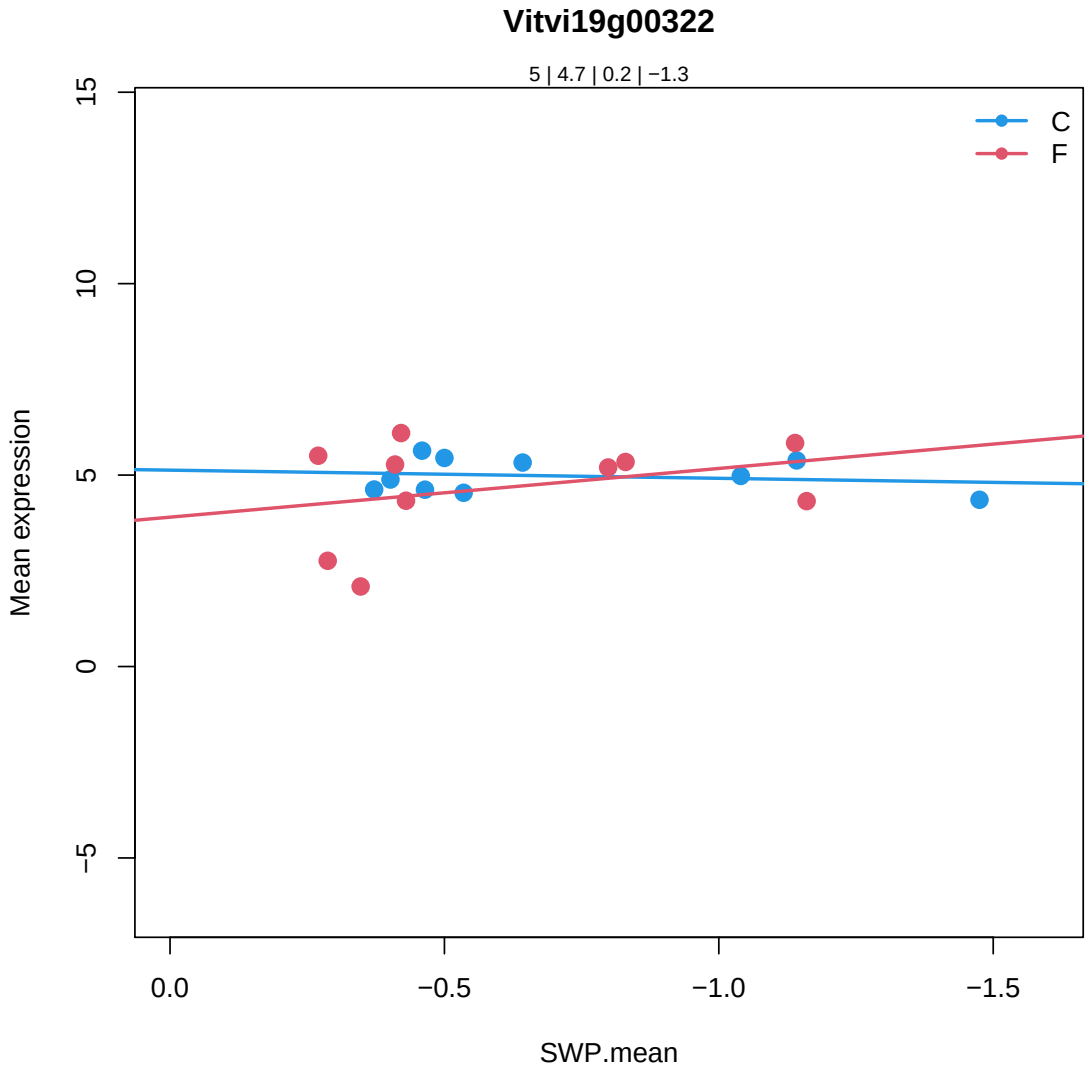
7.6.427 Vitvi19g00322: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g00322
        27.3.7
        RNA.regulation of transcription.C2C2(Zn) Constans-like zinc finger fam
        B-box type zinc finger family protein |
        Chr5:22114584-22115315 REVERSE LENGTH=215 |
        201606
```

Coefficients for Vitvi19g00322.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.978998	2.950507e-14	***	4.727386e-14	***
SlopeC	0.2128946	0.7886826		0.9533712	
MeanF-MeanC	-0.3032734	0.455201		0.7812233	
SlopeF-SlopeC	-1.485246	0.2169582		0.9999488	



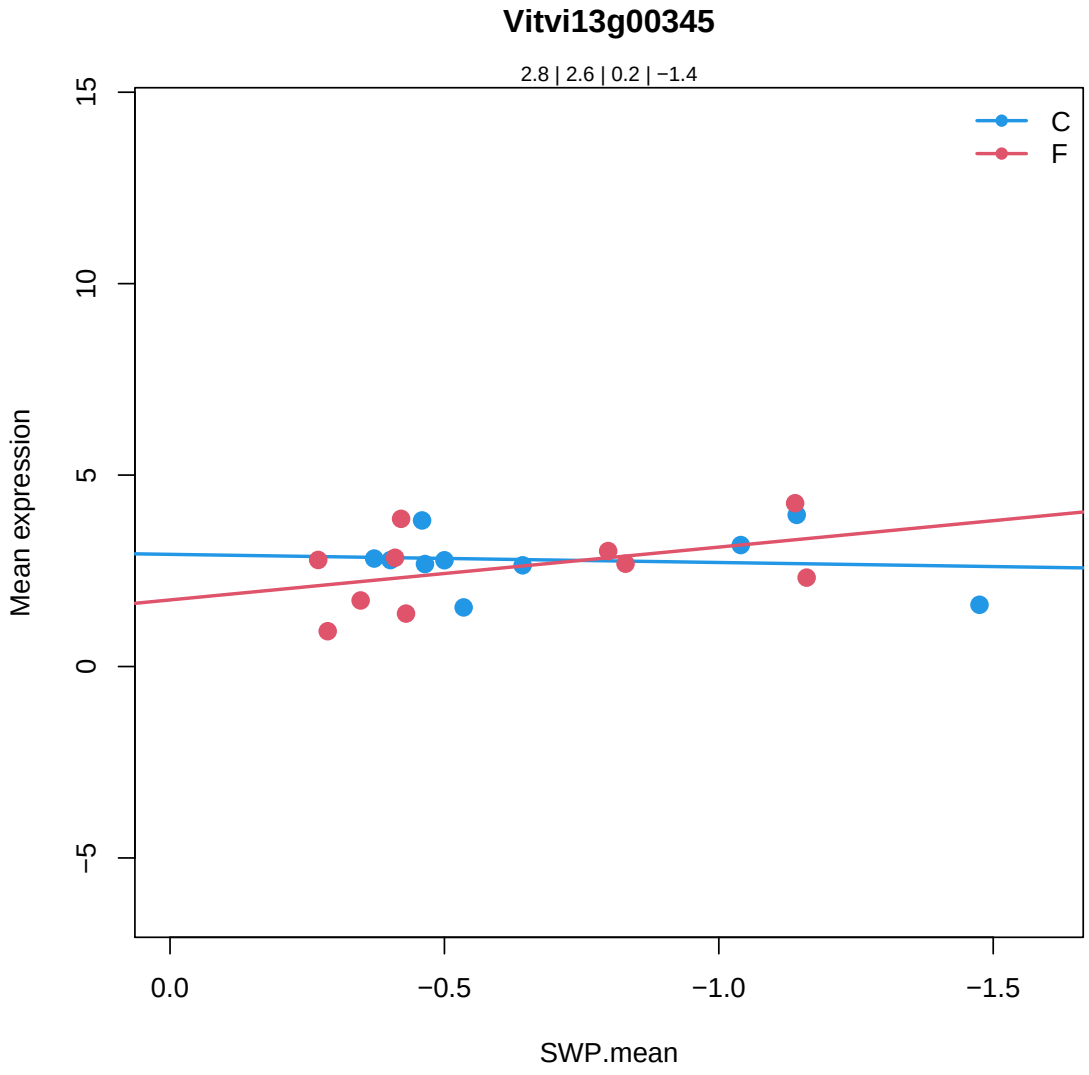
7.6.428 Vitvi13g00345: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00345
        11.8.2
        lipid metabolism.exotics (steroids, squalene etc).methylsterol monooxy
        sterol 4-alpha-methyl-oxidase 2-2 |
        Chr2:12610758-12612799 REVERSE LENGTH=272 |
        201606
```

Coefficients for Vitvi13g00345.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.779794	4.796224e-10	***	6.11647e-10	***
SlopeC	0.2126402	0.7718484		0.9510377	
MeanF-MeanC	-0.200043	0.5924155		0.8573174	
SlopeF-SlopeC	-1.592893	0.1539604		0.9999488	



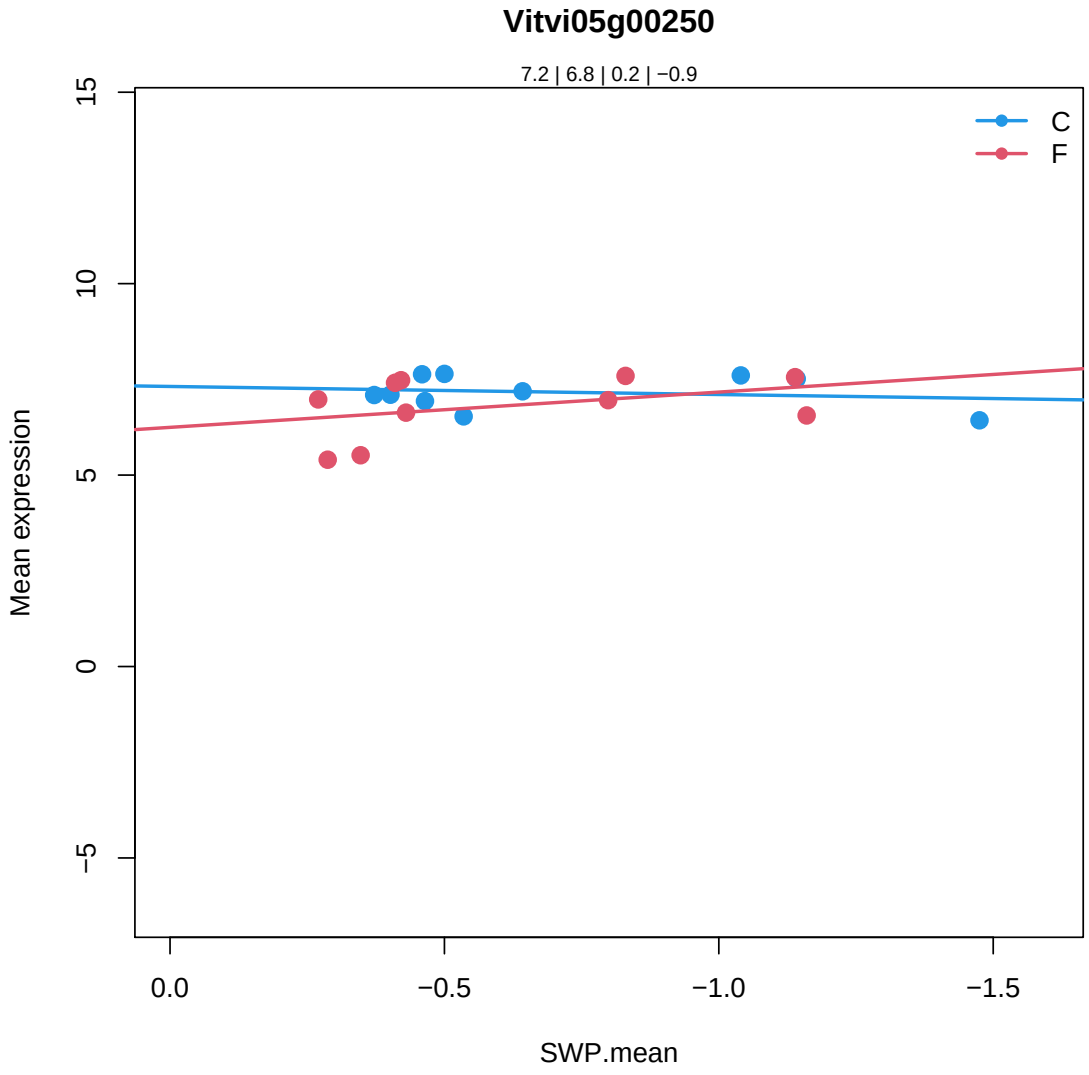
7.6.429 Vitvi05g00250: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00250
        30.1.2
        signalling.in sugar and nutrient physiology.pyruvate dehydrogenase kin
        pyruvate dehydrogenase kinase |
        Chr3:1990727-1992581 REVERSE LENGTH=366 |
        201606
```

Coefficients for Vitvi05g00250.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.166632	5.197932e-21	***	4.194117e-20	***
SlopeC	0.2107265	0.6967219		0.9319513	
MeanF-MeanC	-0.3592232	0.1991942		0.5415395	
SlopeF-SlopeC	-1.131911	0.1683656		0.9999488	



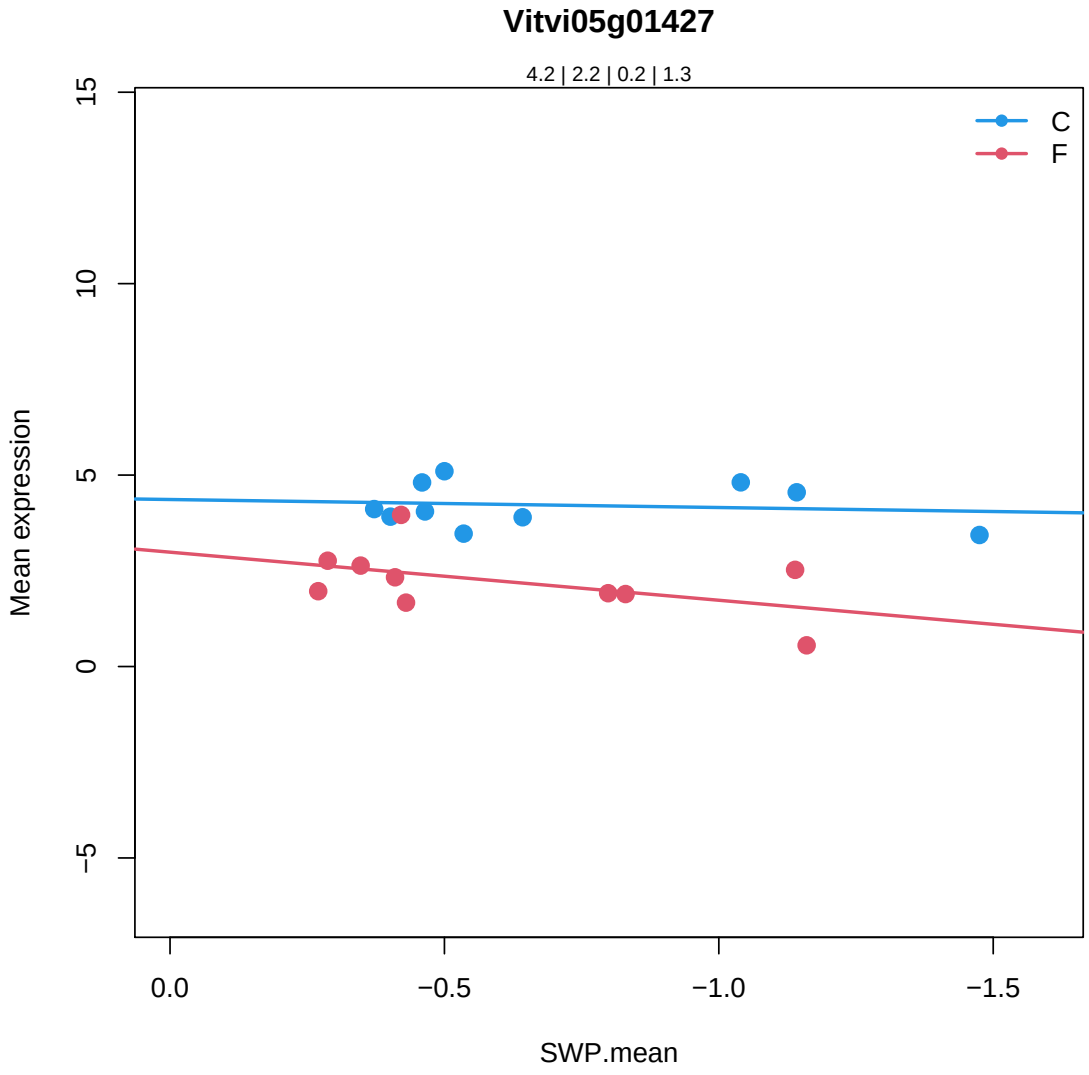
7.6.430 Vitvi05g01427: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01427
        31.1
        cell.organisation
        Ankyrin repeat family protein |
        Chr4:1554420-1556571 FORWARD LENGTH=629 |
        201606
```

Coefficients for Vitvi05g01427.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.214637	2.345638e-15	***	4.217555e-15	***
SlopeC	0.2091331	0.7246801		0.9394623	
MeanF-MeanC	-1.993649	1.138787e-06	***	3.638867e-05	***
SlopeF-SlopeC	1.046585	0.2432688		0.9999488	



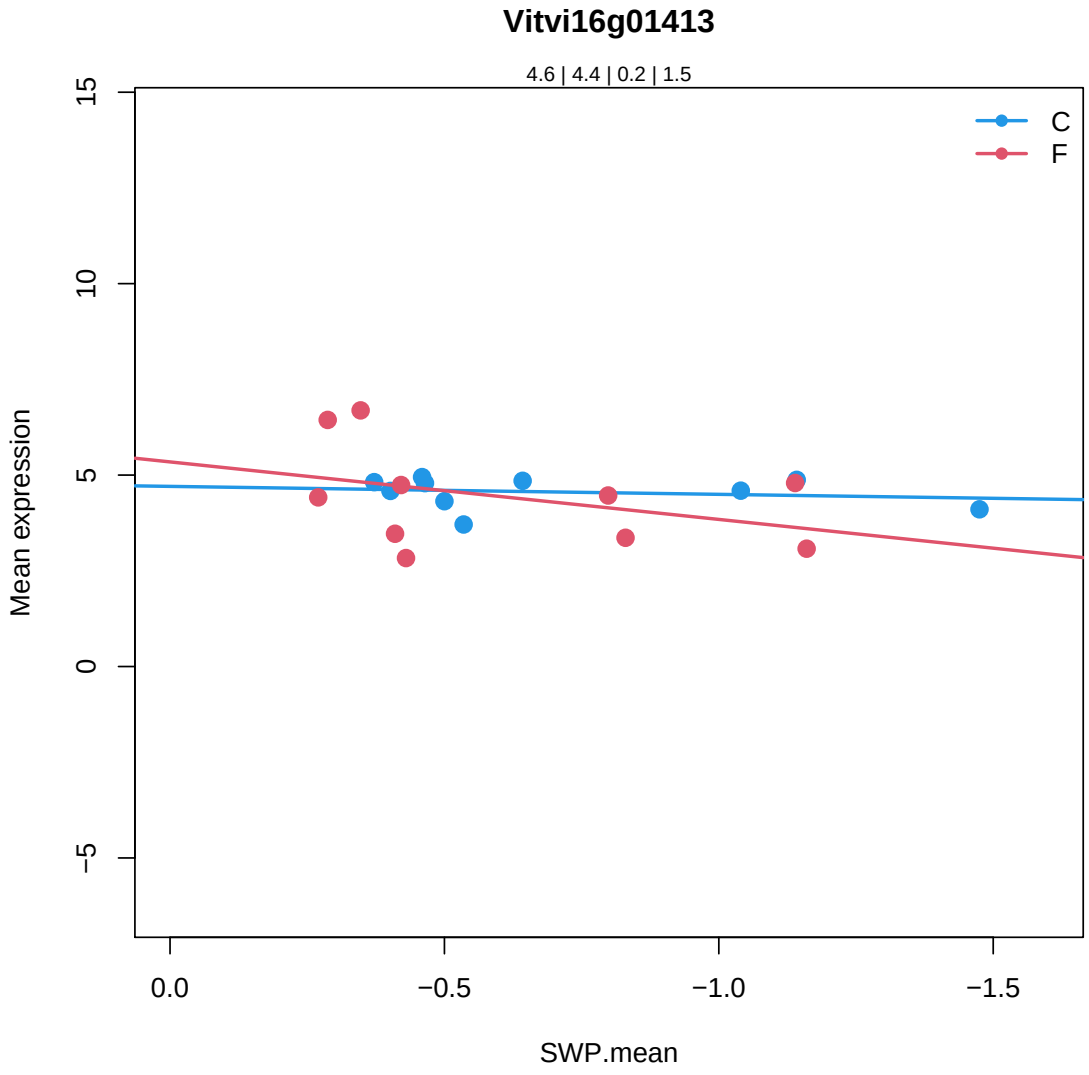
7.6.431 Vitvi16g01413: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01413
        29.5.5
        protein.degradation.serine protease
        CLP protease regulatory subunit X |
        Chr5:21644060-21647503 FORWARD LENGTH=579 |
        201606
```

Coefficients for Vitvi16g01413.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.558877	9.846034e-14	***	1.513293e-13	***
SlopeC	0.2078065	0.7878901		0.9533712	
MeanF-MeanC	-0.1302263	0.7402321		0.9225362	
SlopeF-SlopeC	1.294454	0.2667738		0.9999488	



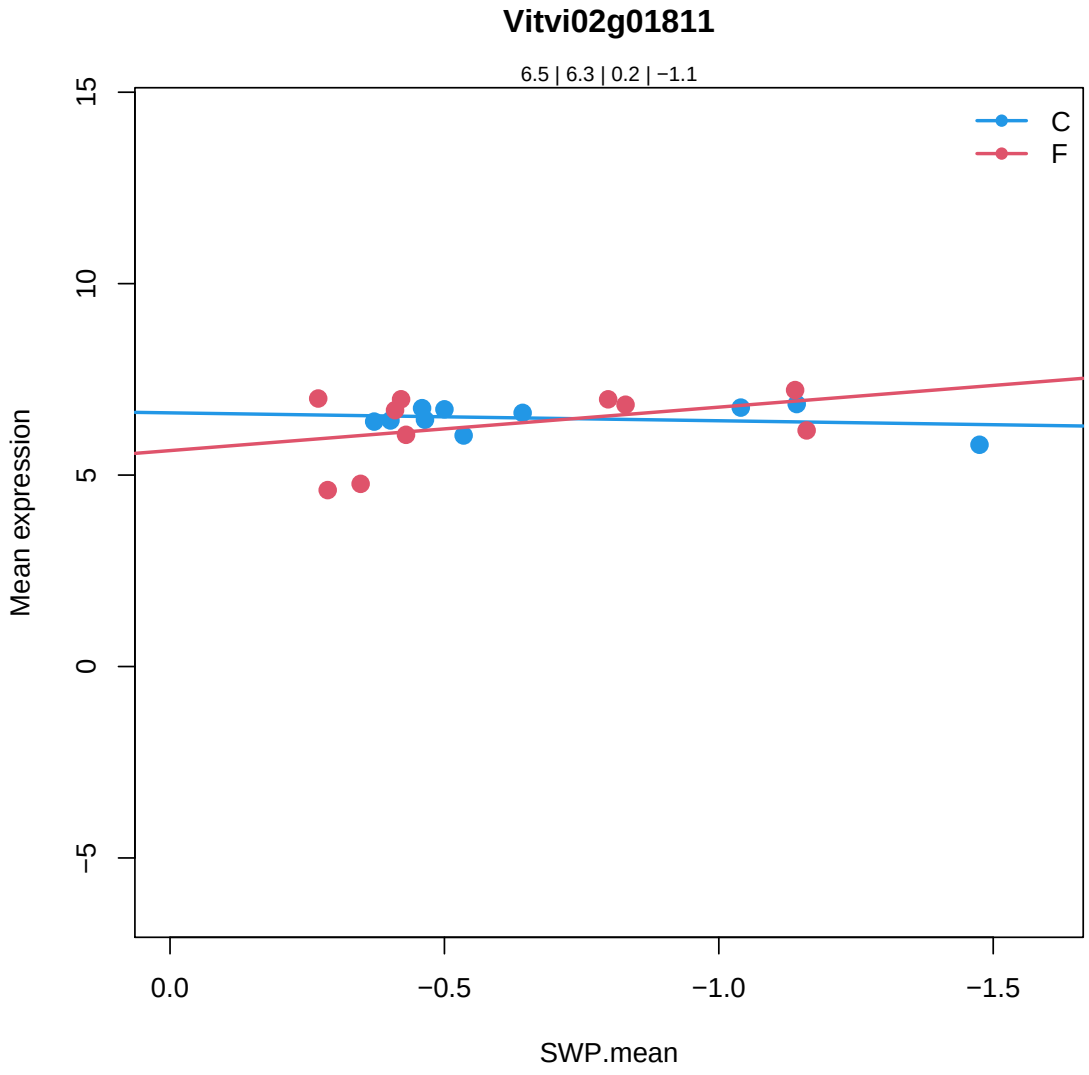
7.6.432 Vitvi02g01811: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g01811
        26.7
        misc.oxidases - copper, flavone etc
        FAD/NAD(P)-binding oxidoreductase family protein |
        Chr2:14989011-14990320 FORWARD LENGTH=325 |
        201606
```

Coefficients for Vitvi02g01811.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.4801	1.582521e-19	***	7.00982e-19	***
SlopeC	0.2063531	0.7195648		0.9380929	
MeanF-MeanC	-0.1493671	0.609723		0.8636987	
SlopeF-SlopeC	-1.341347	0.1267266		0.9999488	



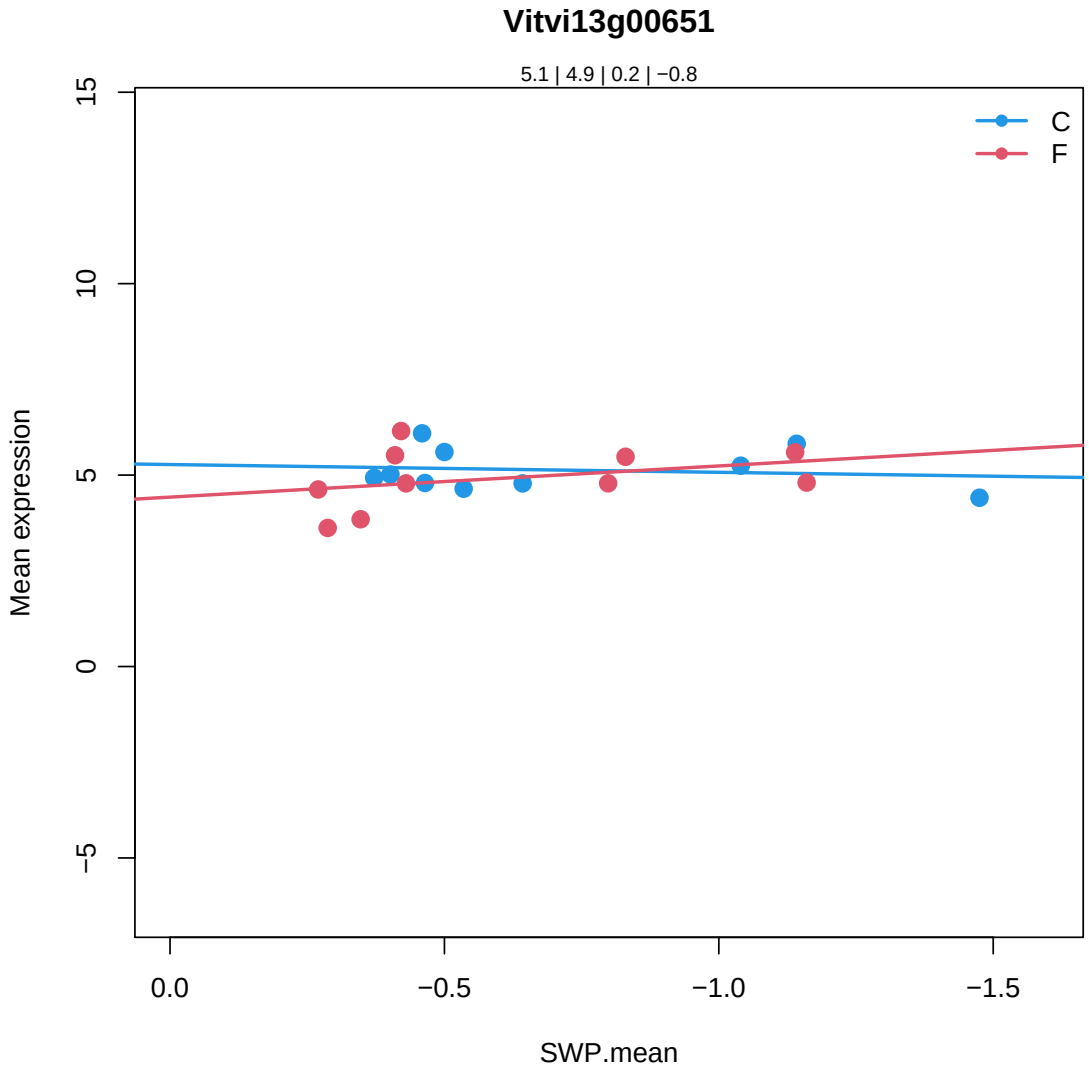
7.6.433 Vitvi13g00651: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00651
        29.5.11.4.2
        protein.degradation.ubiquitin.E3.RING
        plant U-box 14 |
        Chr3:20321524-20323848 FORWARD LENGTH=632 |
        201606
```

Coefficients for Vitvi13g00651.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.132679	1.910476e-17	***	4.755754e-17	***
SlopeC	0.2033123	0.7225084		0.9392454	
MeanF-MeanC	-0.2125058	0.4674147		0.7876703	
SlopeF-SlopeC	-1.017606	0.239458		0.9999488	



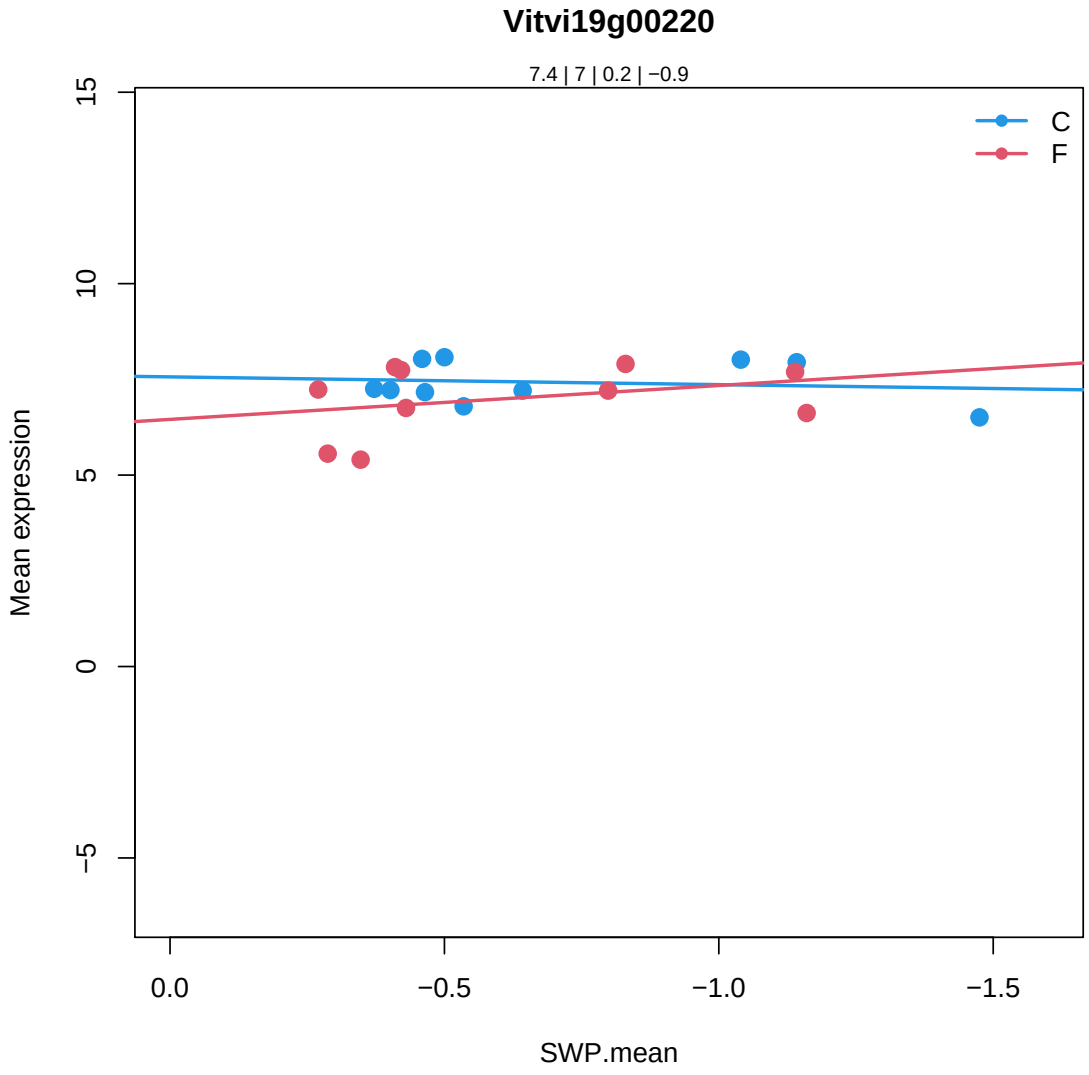
7.6.434 Vitvi19g00220: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g00220
        30.11
        signalling.light
        SPA1-related 3 |
        Chr3:5170175-5172480 REVERSE LENGTH=662 |
        201606
```

Coefficients for Vitvi19g00220.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.422236	6.31311e-20	***	3.221595e-19	***
SlopeC	0.2026926	0.7476394		0.9465952	
MeanF-MeanC	-0.4285295	0.1893402		0.5276876	
SlopeF-SlopeC	-1.08828	0.2525901		0.9999488	



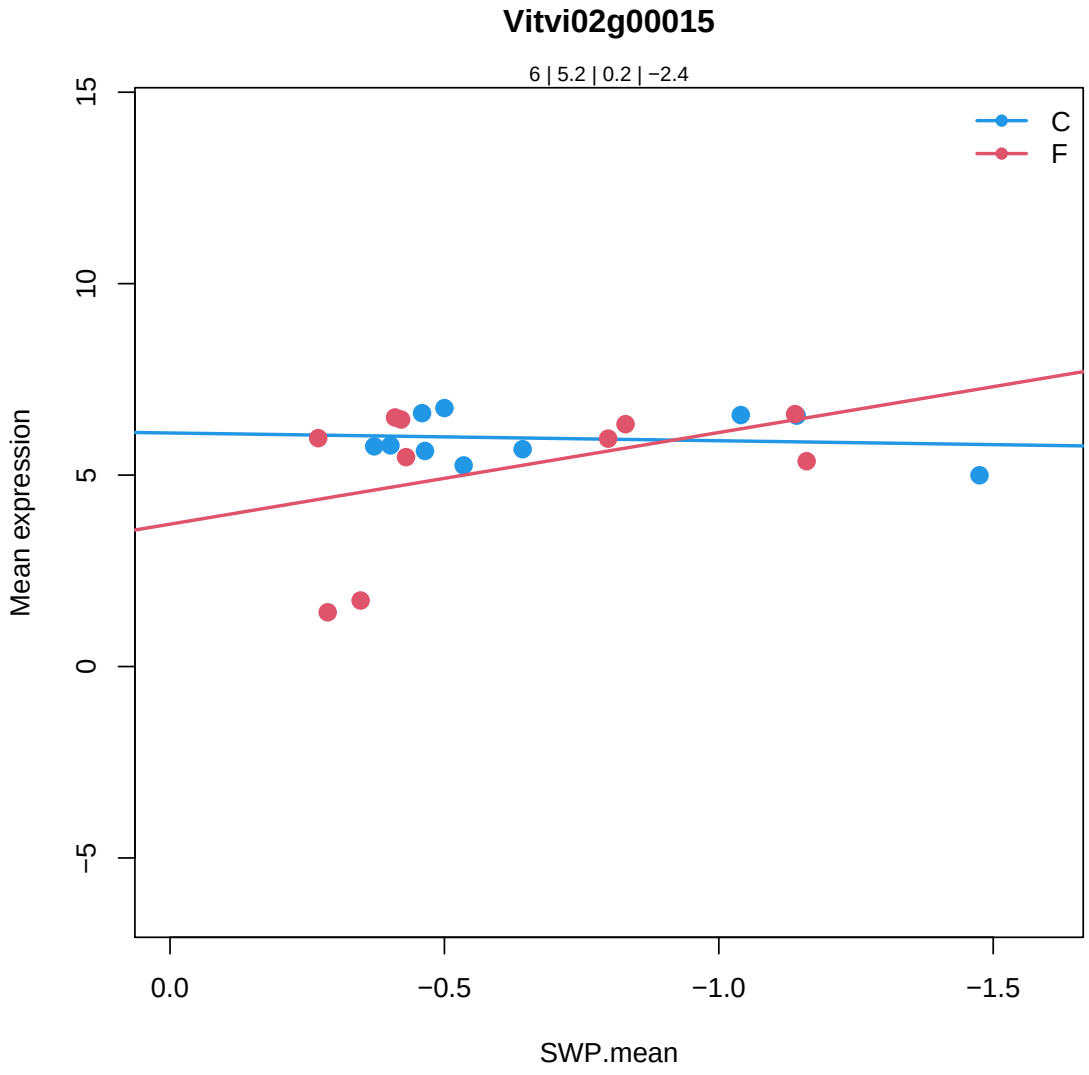
7.6.435 Vitvi02g00015: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00015
        4.1.12
        glycolysis.cytosolic branch.phosphoglycerate mutase
        Phosphoglycerate mutase family protein |
        Chr3:1466738-1468219 FORWARD LENGTH=316 |
        201606
```

Coefficients for Vitvi02g00015.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.956586	5.565937e-13	***	8.124499e-13	***
SlopeC	0.2023908	0.8541168		0.972509	
MeanF-MeanC	-0.7801629	0.1725201		0.5031349	
SlopeF-SlopeC	-2.596304	0.1233502		0.9999488	



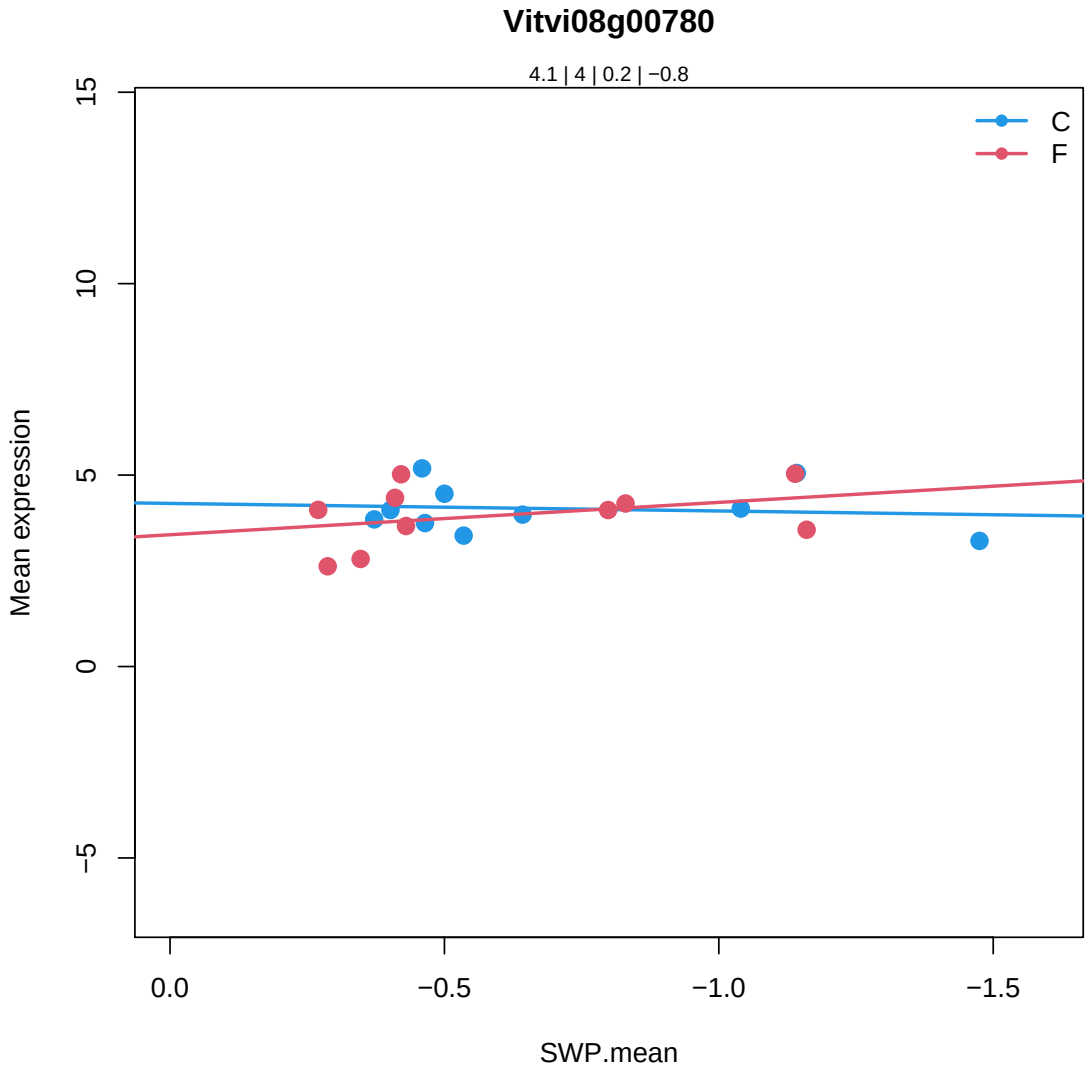
7.6.436 Vitvi08g00780: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g00780
        17.3.2.1
        hormone metabolism.brassinosteroid.signal transduction.BRI
        BRISC complex subunit Abro1-like protein |
        Chr3:2666514-2667452 REVERSE LENGTH=312 |
        201606
```

Coefficients for Vitvi08g00780.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.121006	6.397383e-15	***	1.090948e-14	***
SlopeC	0.1974651	0.7460694		0.9464048	
MeanF-MeanC	-0.1646992	0.595952		0.8584482	
SlopeF-SlopeC	-1.042518	0.2573788		0.9999488	



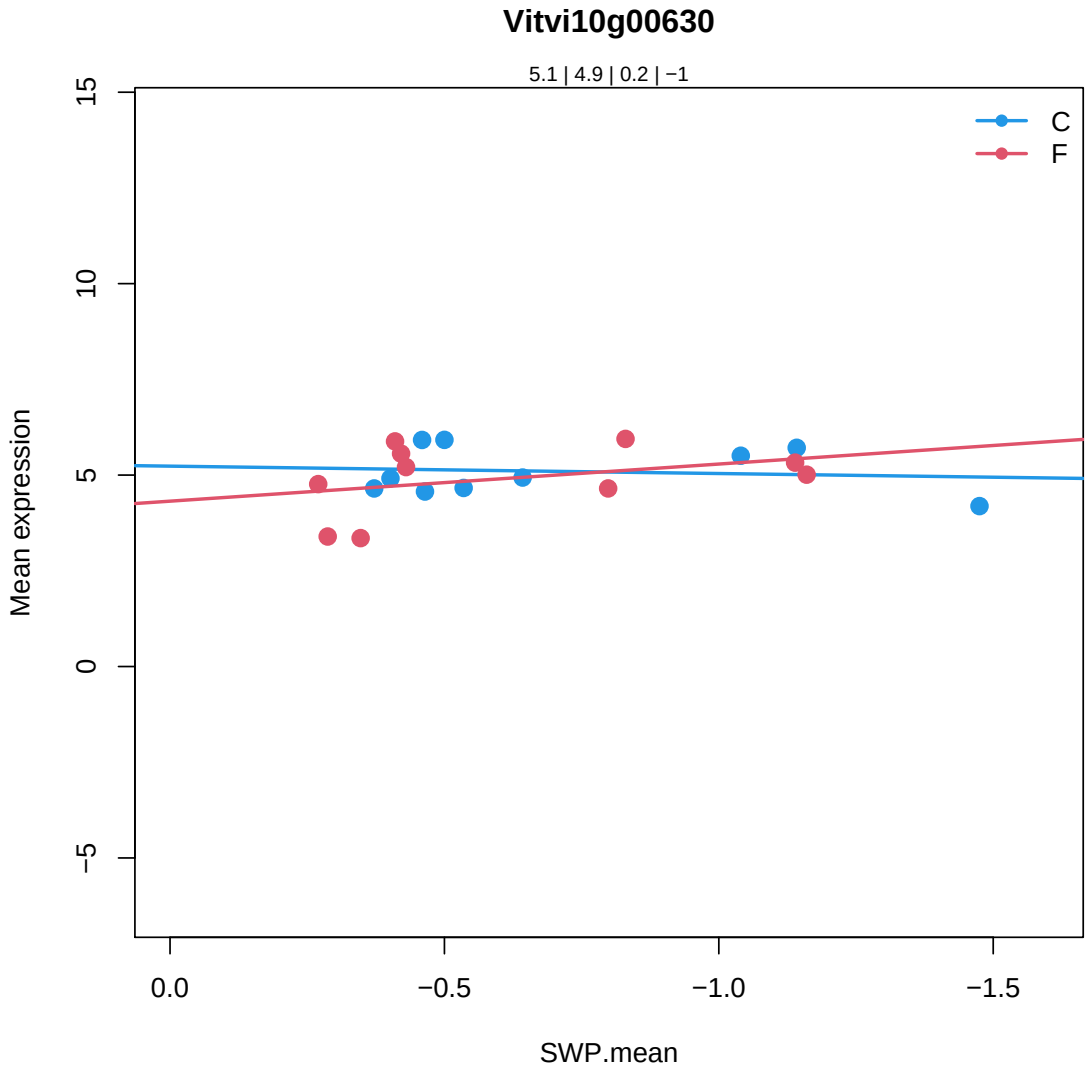
7.6.437 Vitvi10g00630: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00630
        29.5.11.4.2
        protein.degradation.ubiquitin.E3.RING
        plant U-box 17 |
        Chr1:10264412-10266601 FORWARD LENGTH=729 |
        201606
```

Coefficients for Vitvi10g00630.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.097859	2.559925e-16	***	5.201757e-16	***
SlopeC	0.1925307	0.7651019		0.9493393	
MeanF-MeanC	-0.1885716	0.5659251		0.8428601	
SlopeF-SlopeC	-1.161878	0.2331358		0.9999488	



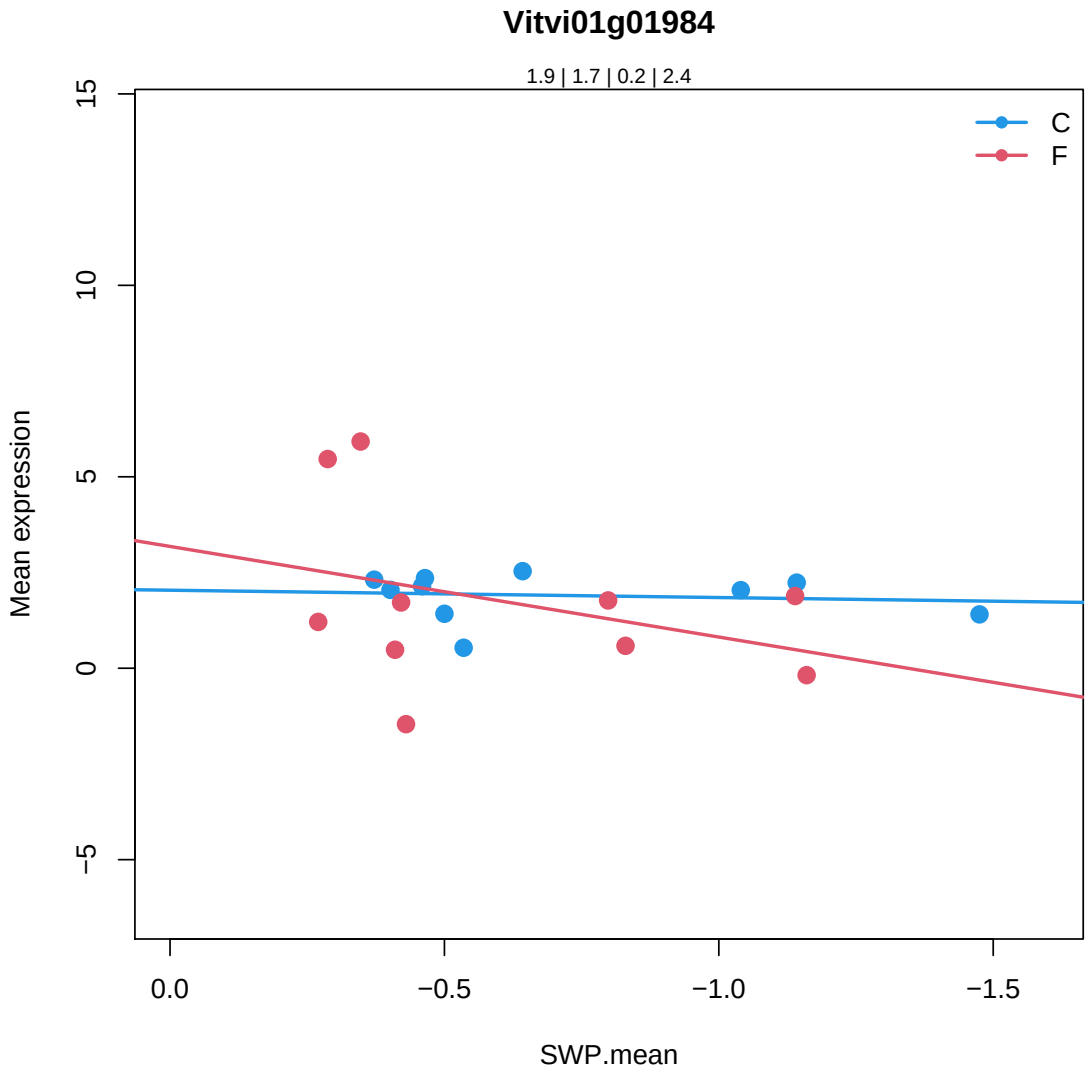
7.6.438 Vitvi01g01984: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01984
        1.1.6
        PS.lightreaction.NADH DH
        Unknown Protein
```

Coefficients for Vitvi01g01984.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.902803	0.0005459532	***	0.0005940052	***
SlopeC	0.1912234	0.8848239		0.9789842	
MeanF-MeanC	-0.1637473	0.8072977		0.9465338	
SlopeF-SlopeC	2.175521	0.2748866		0.9999488	



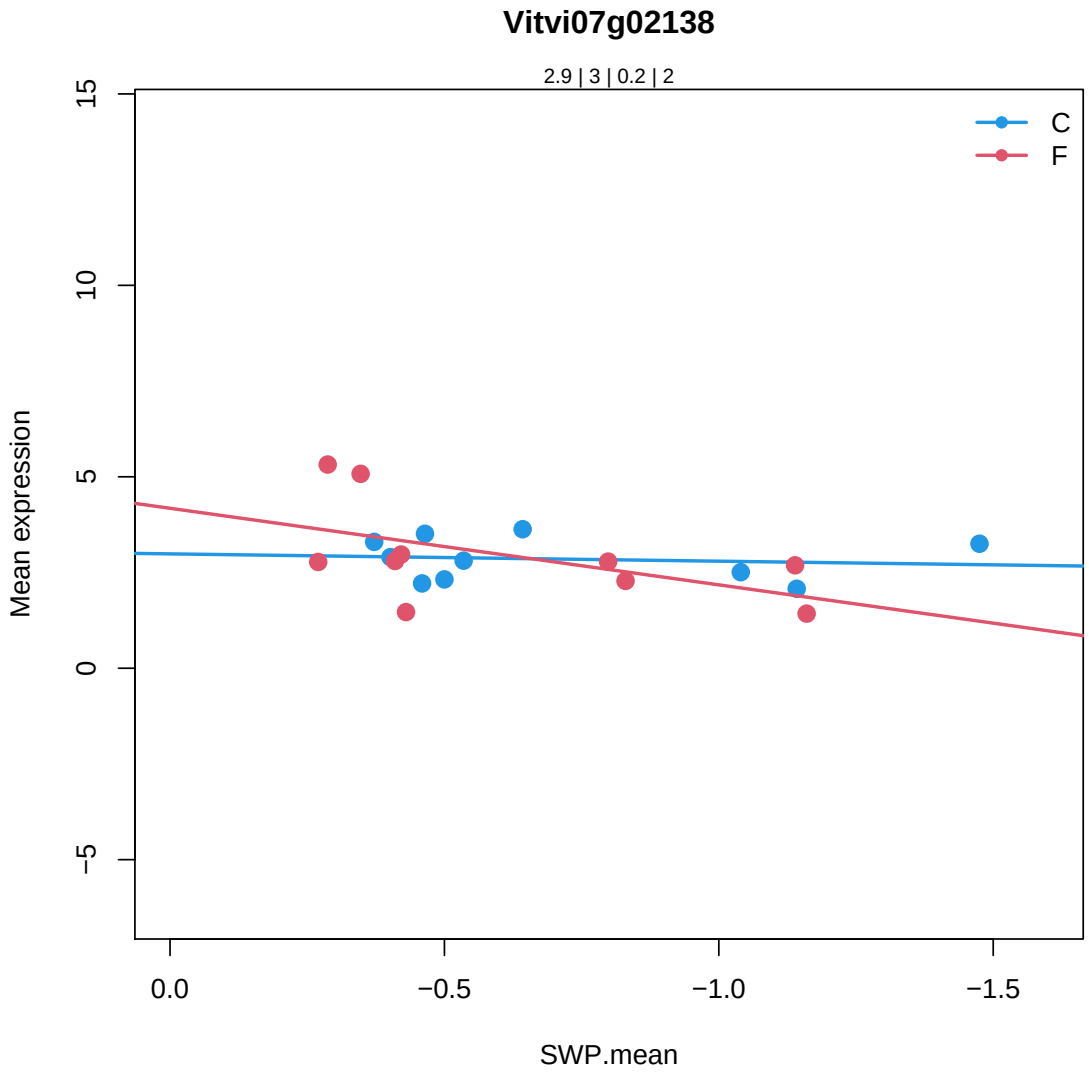
7.6.439 Vitvi07g02138: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g02138
        35.2
        not assigned.unknown
        Unknown Protein
```

Coefficients for Vitvi07g02138.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.852164	4.232212e-10	***	5.407157e-10	***
SlopeC	0.1904864	0.7987532		0.9563705	
MeanF-MeanC	0.1064843	0.7792151		0.9372393	
SlopeF-SlopeC	1.809398	0.1140301		0.9999488	



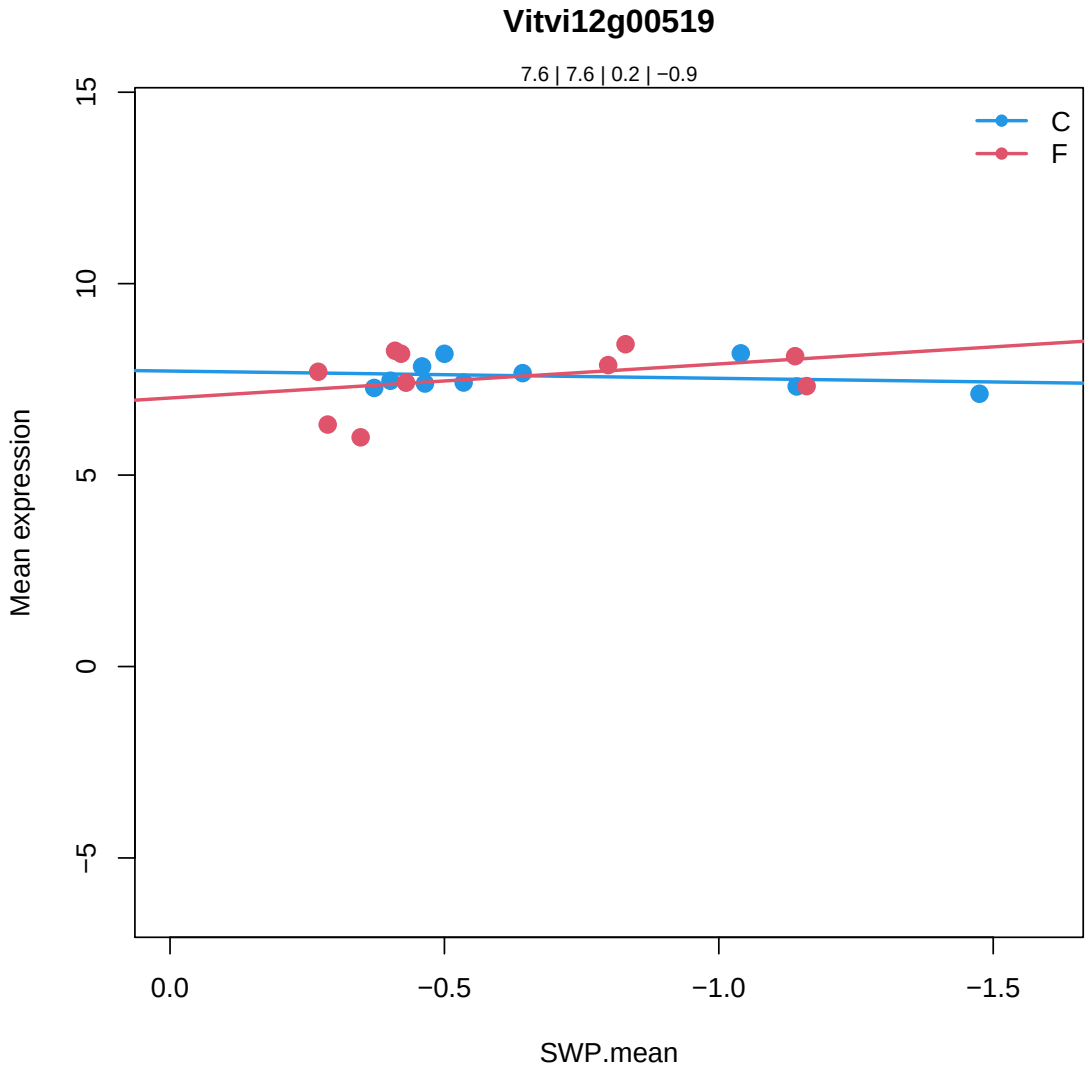
7.6.440 Vitvi12g00519: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00519
        30.1.1
        signalling.in sugar and nutrient physiology.misc
        Ras-related small GTP-binding family protein |
        Chr3:7644581-7645954 FORWARD LENGTH=248 |
        201606
```

Coefficients for Vitvi12g00519.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.583391	1.280217e-21	***	1.392796e-20	***
SlopeC	0.1898123	0.7228832		0.9392454	
MeanF-MeanC	-0.02825135	0.9171909		0.977952	
SlopeF-SlopeC	-1.079914	0.1838042		0.9999488	



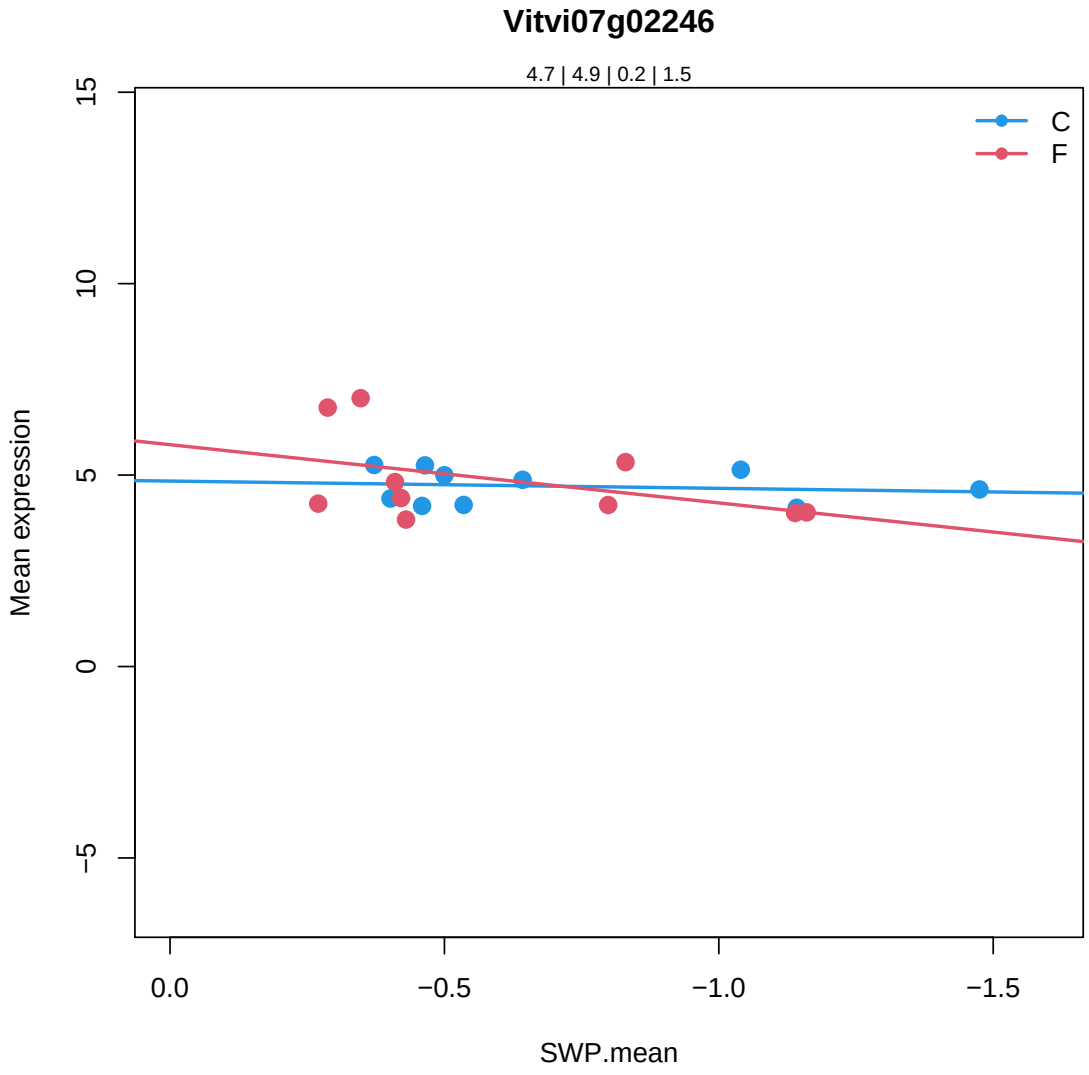
7.6.441 Vitvi07g02246: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g02246
        1.1.1.1
        PS.lightreaction.photosystem II.LHC-II
        chlorophyll A/B binding protein 1 |
        Chr1:10478071-10478874 FORWARD LENGTH=267 |
        201606
```

Coefficients for Vitvi07g02246.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.710196	4.096825e-15	***	7.170856e-15	***
SlopeC	0.1894556	0.7810532		0.9528424	
MeanF-MeanC	0.1569964	0.6509616		0.8828934	
SlopeF-SlopeC	1.331508	0.1977959		0.9999488	



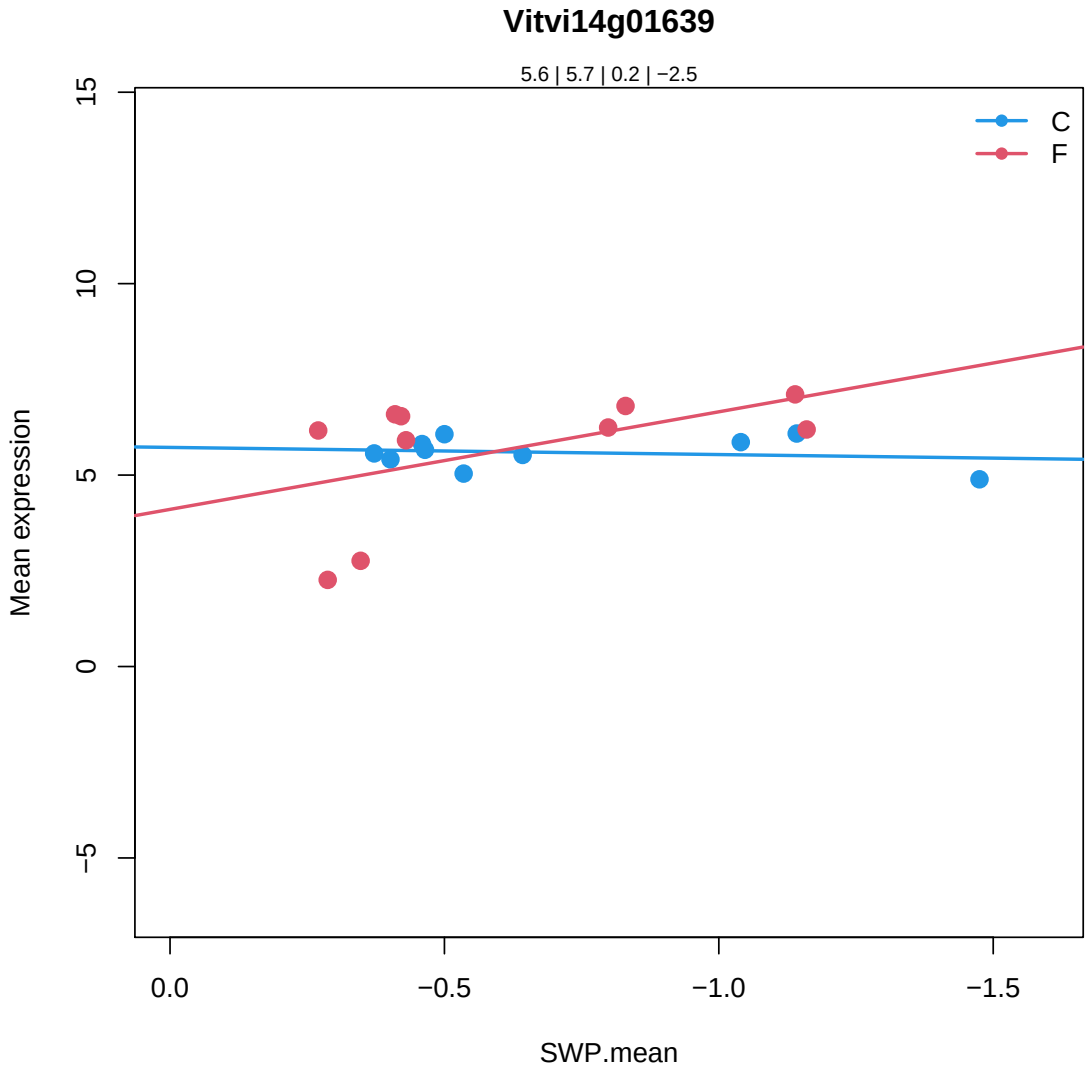
7.6.442 Vitvi14g01639: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01639
        11.5.2
        lipid metabolism.glycerol metabolism.glycerol-3-phosphate dehydrogenas
        NAD-dependent glycerol-3-phosphate dehydrogenase family protein |
        Chr5:16265071-16267258 REVERSE LENGTH=400 |
        201606
```

Coefficients for Vitvi14g01639.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.591318	3.253981e-14	***	5.195597e-14	***
SlopeC	0.1867008	0.8349487		0.9683677	
MeanF-MeanC	0.06538842	0.8858182		0.9703262	
SlopeF-SlopeC	-2.735318	0.05009161	.	0.9999488	



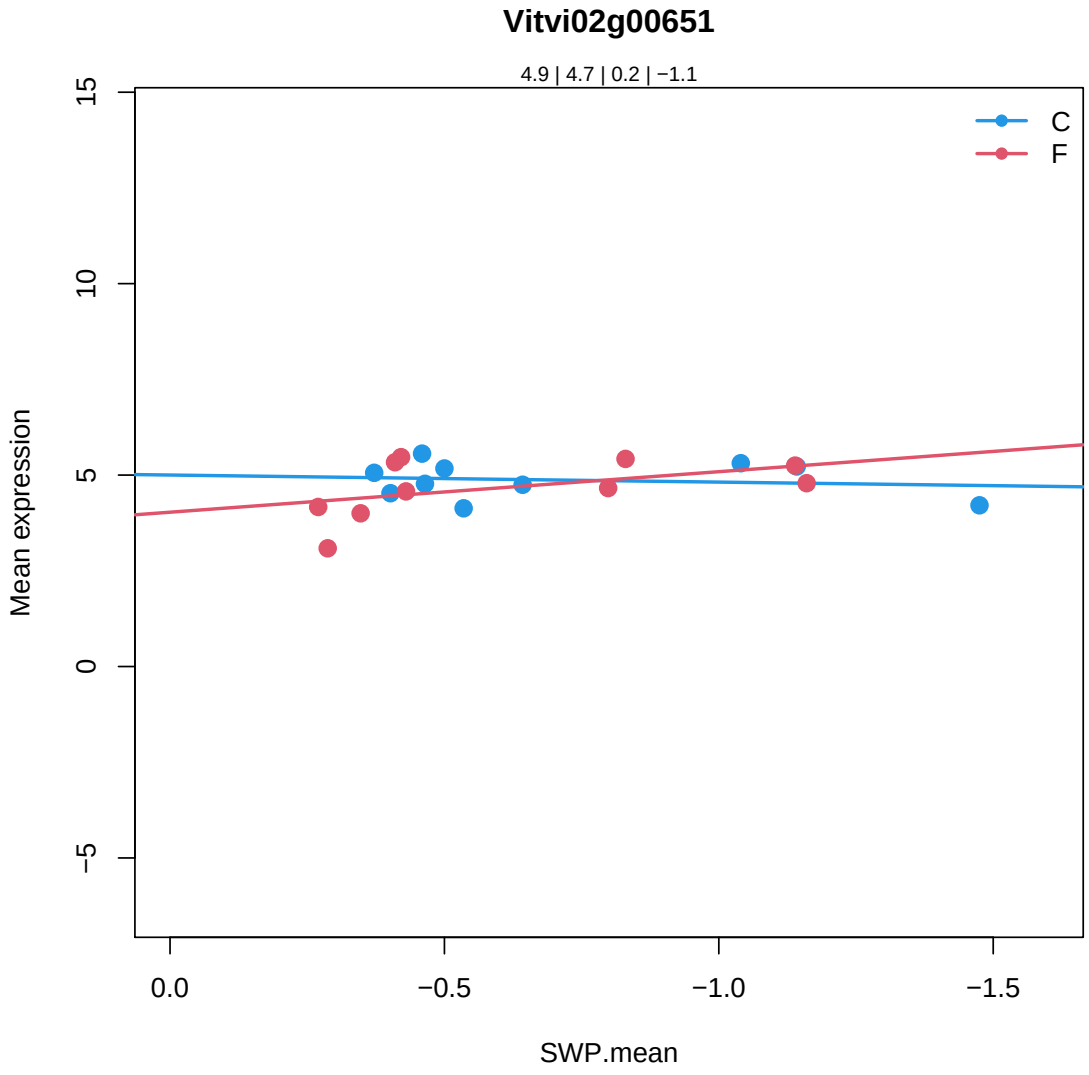
7.6.443 Vitvi02g00651: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00651
        35.1
        not assigned.no ontology
        Haloacid dehalogenase-like hydrolase (HAD) superfamily protein |
        Chr2:16194639-16195995 REVERSE LENGTH=244 |
        201606
```

Coefficients for Vitvi02g00651.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.871407	7.946544e-18	***	2.146017e-17	***
SlopeC	0.1849142	0.7226244		0.9392454	
MeanF-MeanC	-0.1963069	0.4607423		0.7843312	
SlopeF-SlopeC	-1.243492	0.1187791		0.9999488	



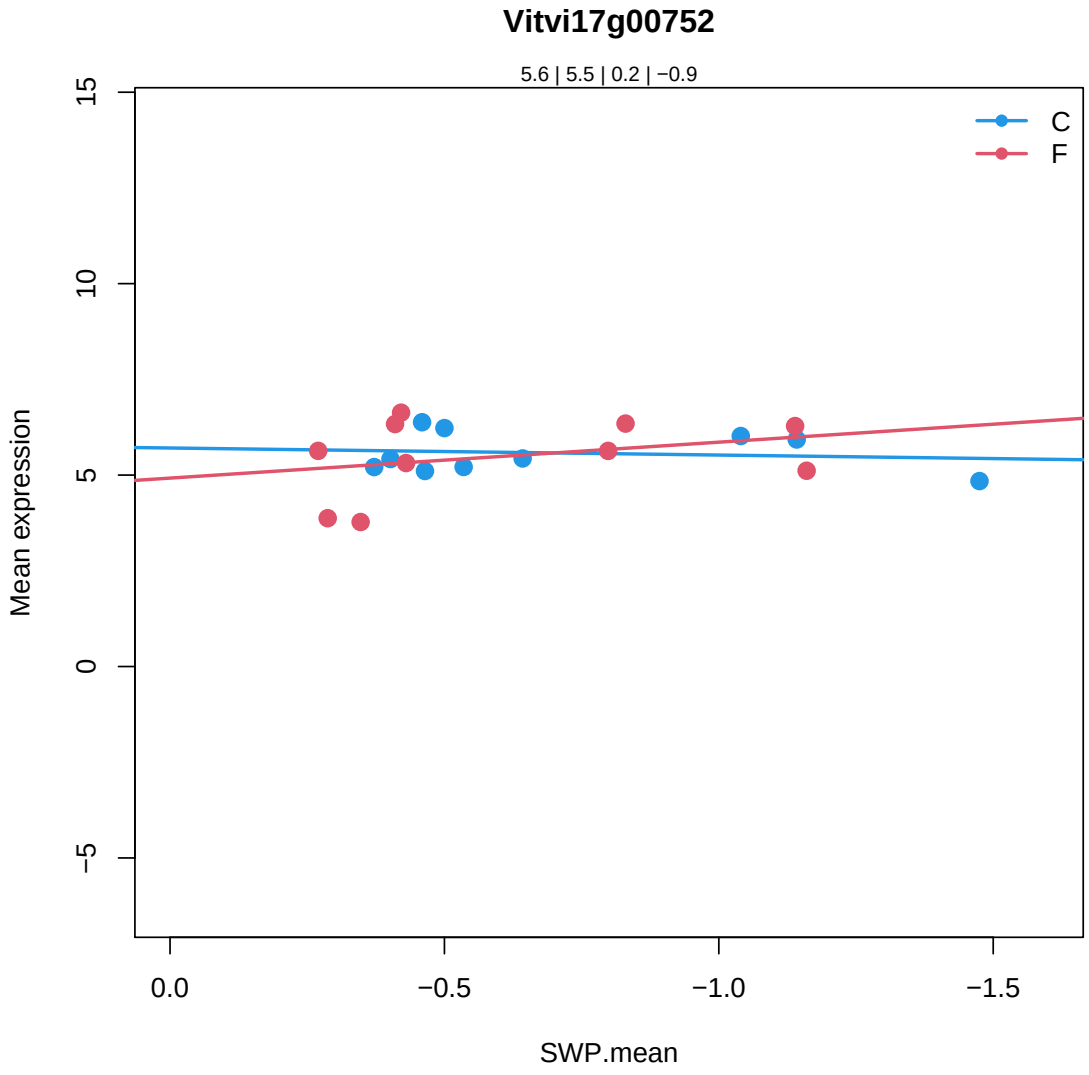
7.6.444 Vitvi17g00752: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00752
        30.3
        signalling.calcium
        Calmodulin binding protein-like protein |
        Chr5:25114362-25116092 FORWARD LENGTH=299 |
        201606
```

Coefficients for Vitvi17g00752.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.577974	7.551295e-17	***	1.675842e-16	***
SlopeC	0.1842636	0.7815416		0.9530067	
MeanF-MeanC	-0.08537474	0.8004186		0.9440396	
SlopeF-SlopeC	-1.122555	0.2630399		0.9999488	



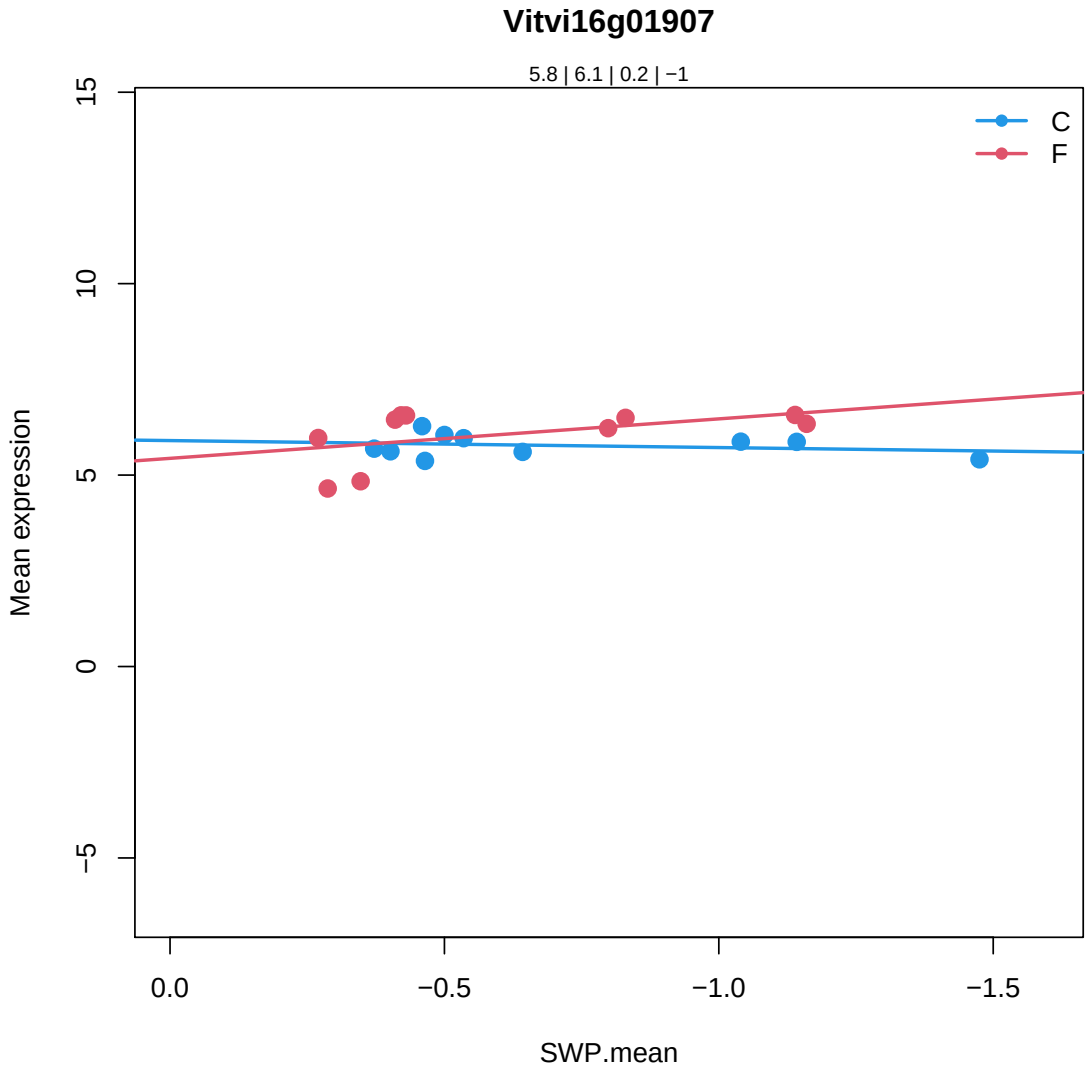
7.6.445 Vitvi16g01907: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01907
        26.22
        misc.short chain dehydrogenase/reductase (SDR)
        NAD(P)-binding Rossmann-fold superfamily protein |
        Chr4:12226288-12228107 FORWARD LENGTH=261 |
        201606
```

Coefficients for Vitvi16g01907.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.772642	1.263523e-20	***	8.604889e-20	***
SlopeC	0.1821582	0.6884205		0.9306347	
MeanF-MeanC	0.2923869	0.2130029		0.5592347	
SlopeF-SlopeC	-1.213028	0.0829634	.	0.9999488	



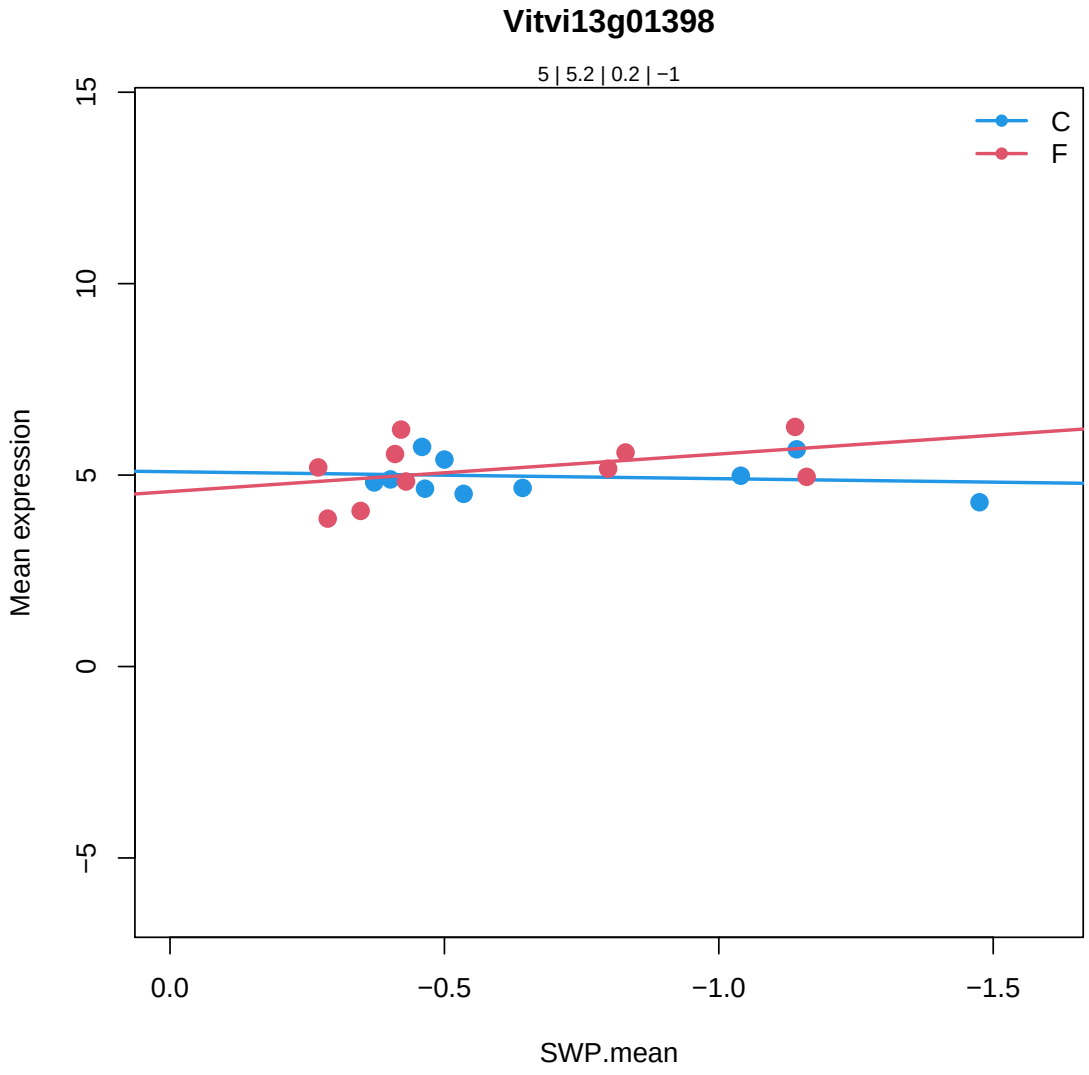
7.6.446 Vitvi13g01398: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g01398
        26.10
        misc.cytochrome P450
        RNA-directed DNA polymerase (reverse transcriptase)-related family pro
        Chr3:8789309-8790907 FORWARD LENGTH=532 |
        201606
```

Coefficients for Vitvi13g01398.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.959756	1.4602e-17	***	3.718069e-17	***
SlopeC	0.1815375	0.7395392		0.9438024	
MeanF-MeanC	0.2067974	0.4585937		0.7829195	
SlopeF-SlopeC	-1.162957	0.1616271		0.9999488	



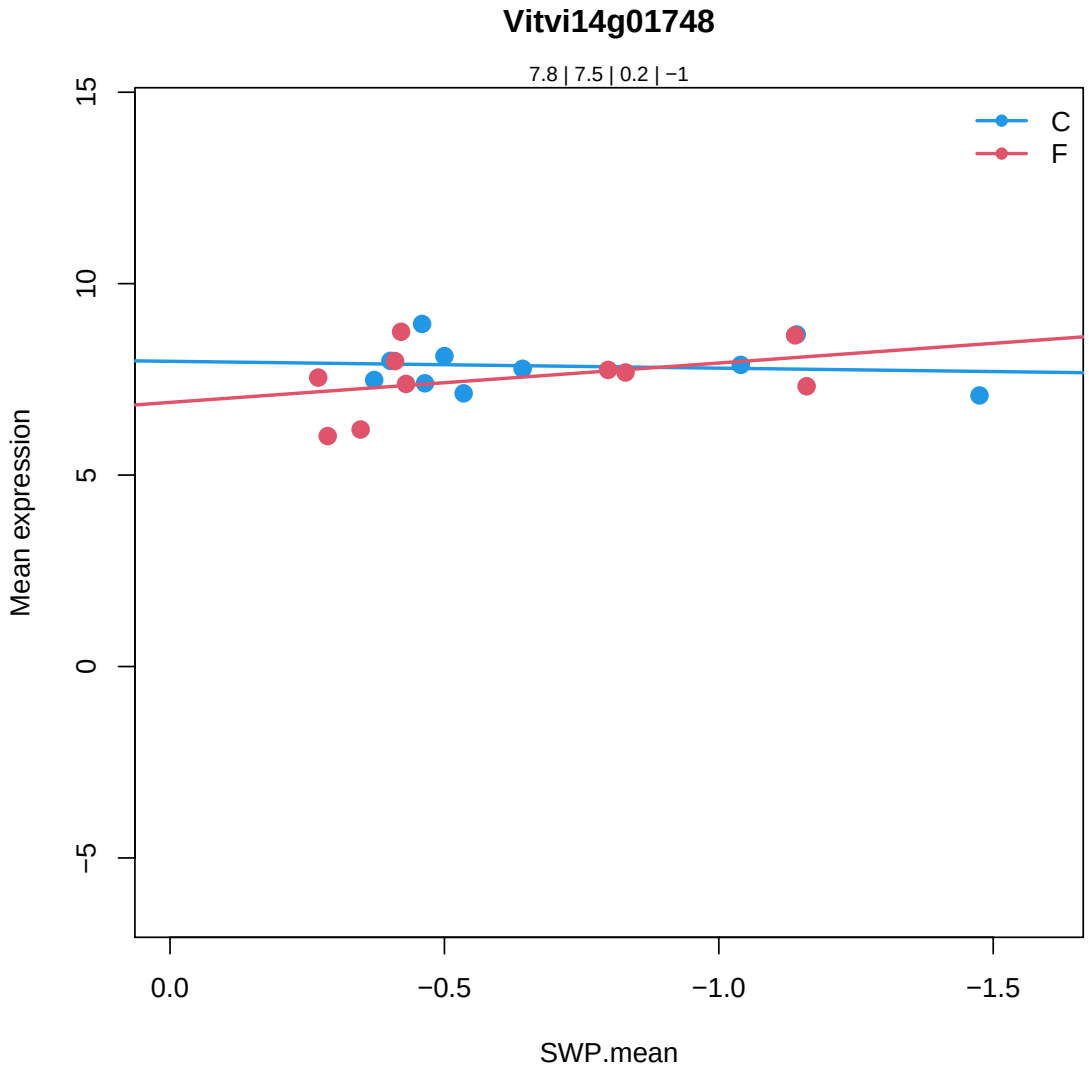
7.6.447 Vitvi14g01748: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01748
        29.4
        protein.postranslational modification
        ADP-ribosylation factor A1B |
        Chr5:4729319-4730672 FORWARD LENGTH=181 |
        201606
```

Coefficients for Vitvi14g01748.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.845961	1.933474e-20	***	1.209274e-19	***
SlopeC	0.1784711	0.7767451		0.9513135	
MeanF-MeanC	-0.3208511	0.3211406		0.6820155	
SlopeF-SlopeC	-1.207125	0.2057362		0.9999488	



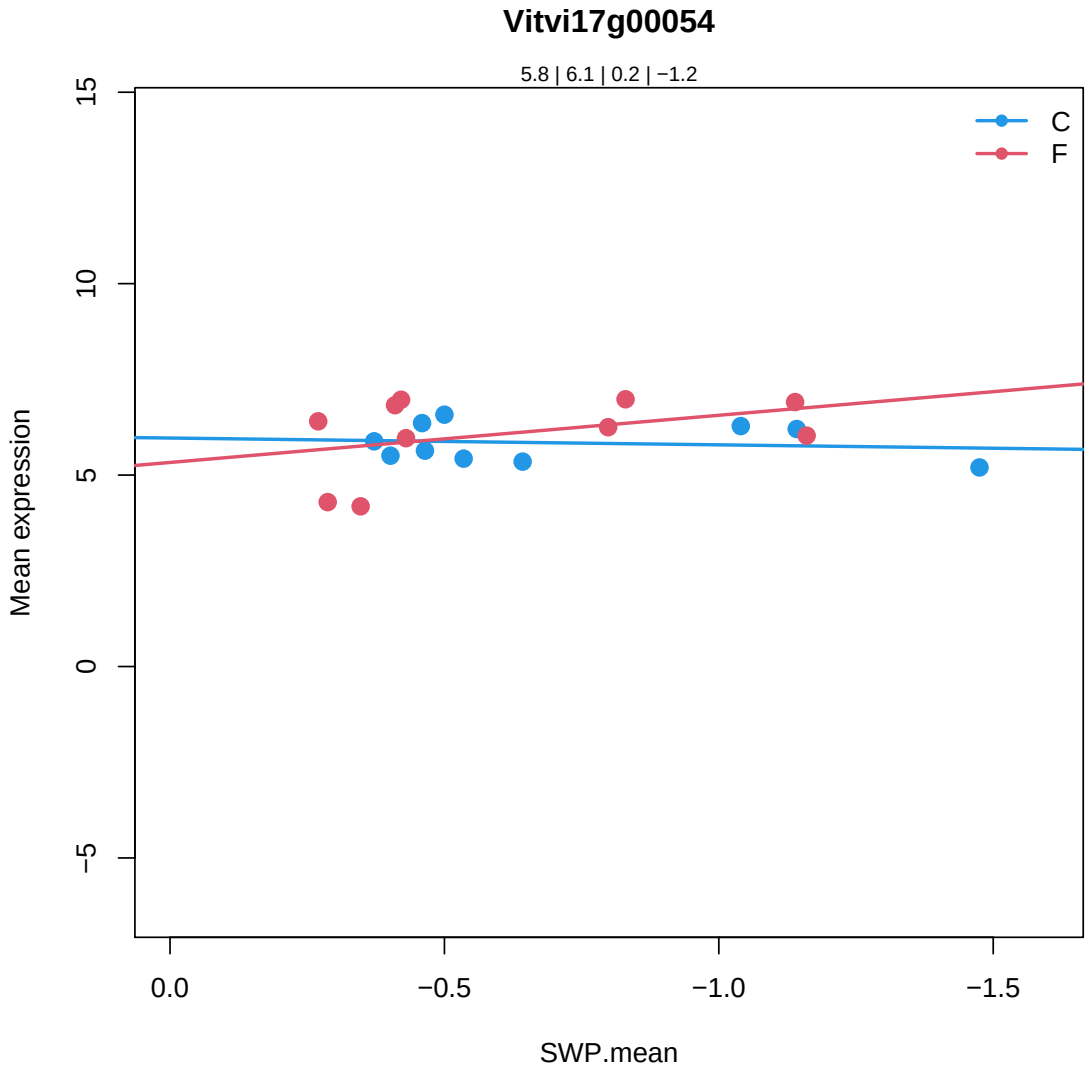
7.6.448 Vitvi17g00054: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00054
        35.2
        not assigned.unknown
        meiosis chromosome segregation family protein |
        Chr3:9907456-9910463 REVERSE LENGTH=649 |
        201606
```

Coefficients for Vitvi17g00054.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.842383	2.049163e-17	***	5.072818e-17	***
SlopeC	0.1776478	0.785744		0.9533712	
MeanF-MeanC	0.23817	0.475677		0.7917733	
SlopeF-SlopeC	-1.40969	0.1567263		0.9999488	



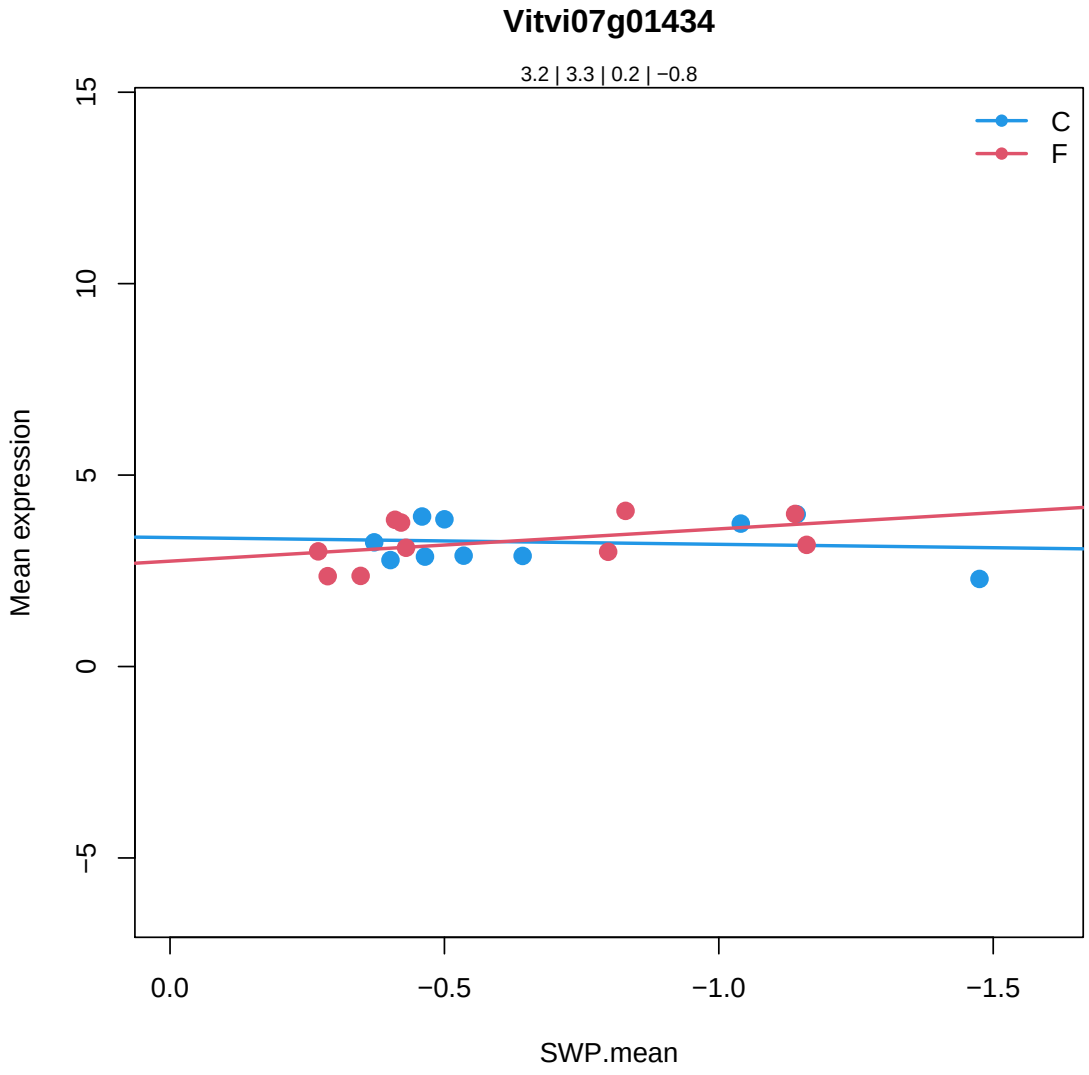
7.6.449 Vitvi07g01434: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01434
        31.2.5
        cell.division.plastid
        MSCS-like 2 |
        Chr5:3300376-3303836 REVERSE LENGTH=645 |
        201606
```

Coefficients for Vitvi07g01434.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.243679	2.602304e-14	***	4.193289e-14	***
SlopeC	0.1770325	0.7308027		0.9406676	
MeanF-MeanC	0.02159191	0.9341199		0.9822189	
SlopeF-SlopeC	-1.020376	0.1911291		0.9999488	



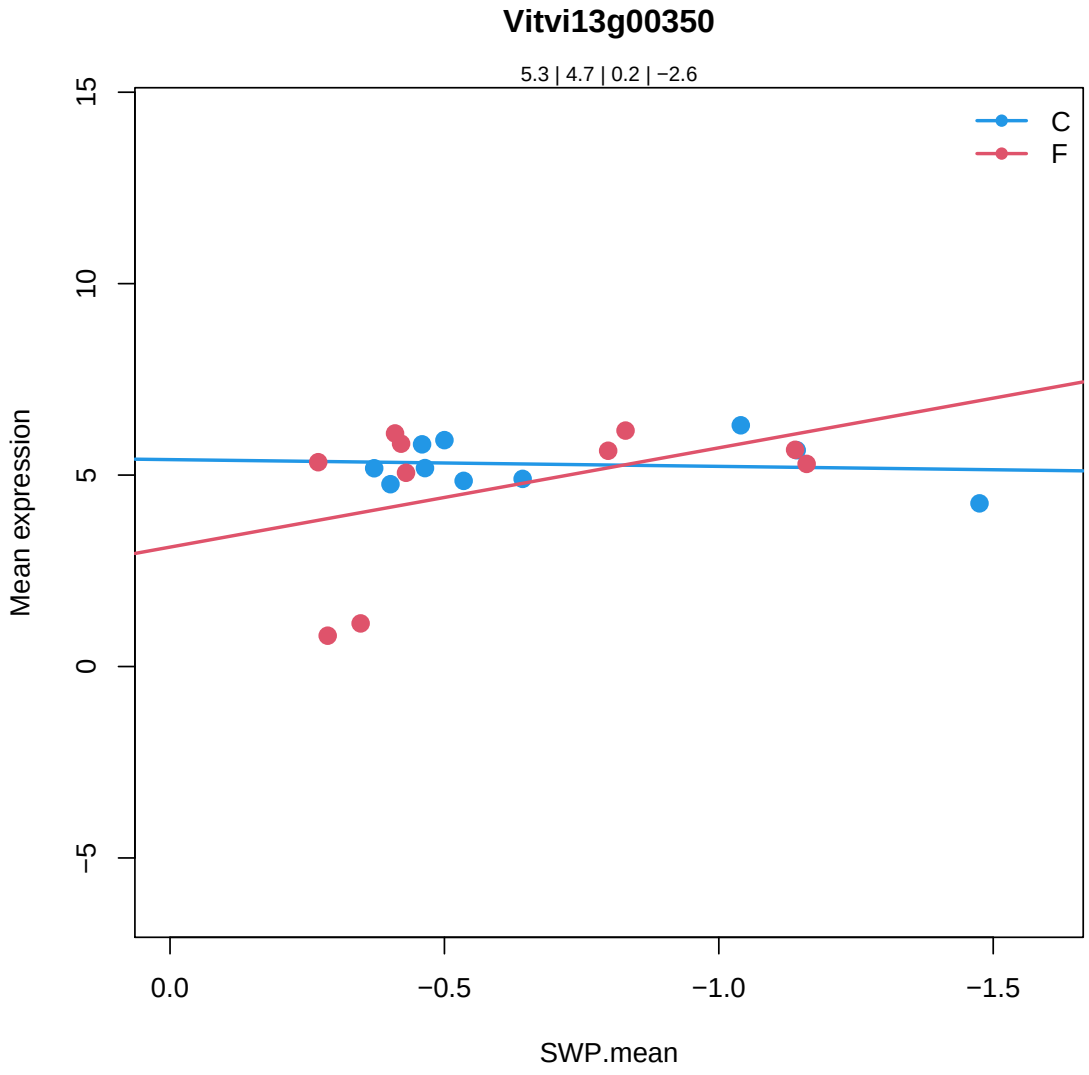
7.6.450 Vitvi13g00350: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00350
        31.2
        cell.division
        Regulator of chromosome condensation (RCC1) family protein |
        Chr3:20612766-20615730 FORWARD LENGTH=488 |
        201606
```

Coefficients for Vitvi13g00350.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.279791	7.387094e-12	***	1.015276e-11	***
SlopeC	0.1761415	0.8743711		0.9763383	
MeanF-MeanC	-0.5812761	0.3104724		0.6744662	
SlopeF-SlopeC	-2.769591	0.1054393		0.9999488	



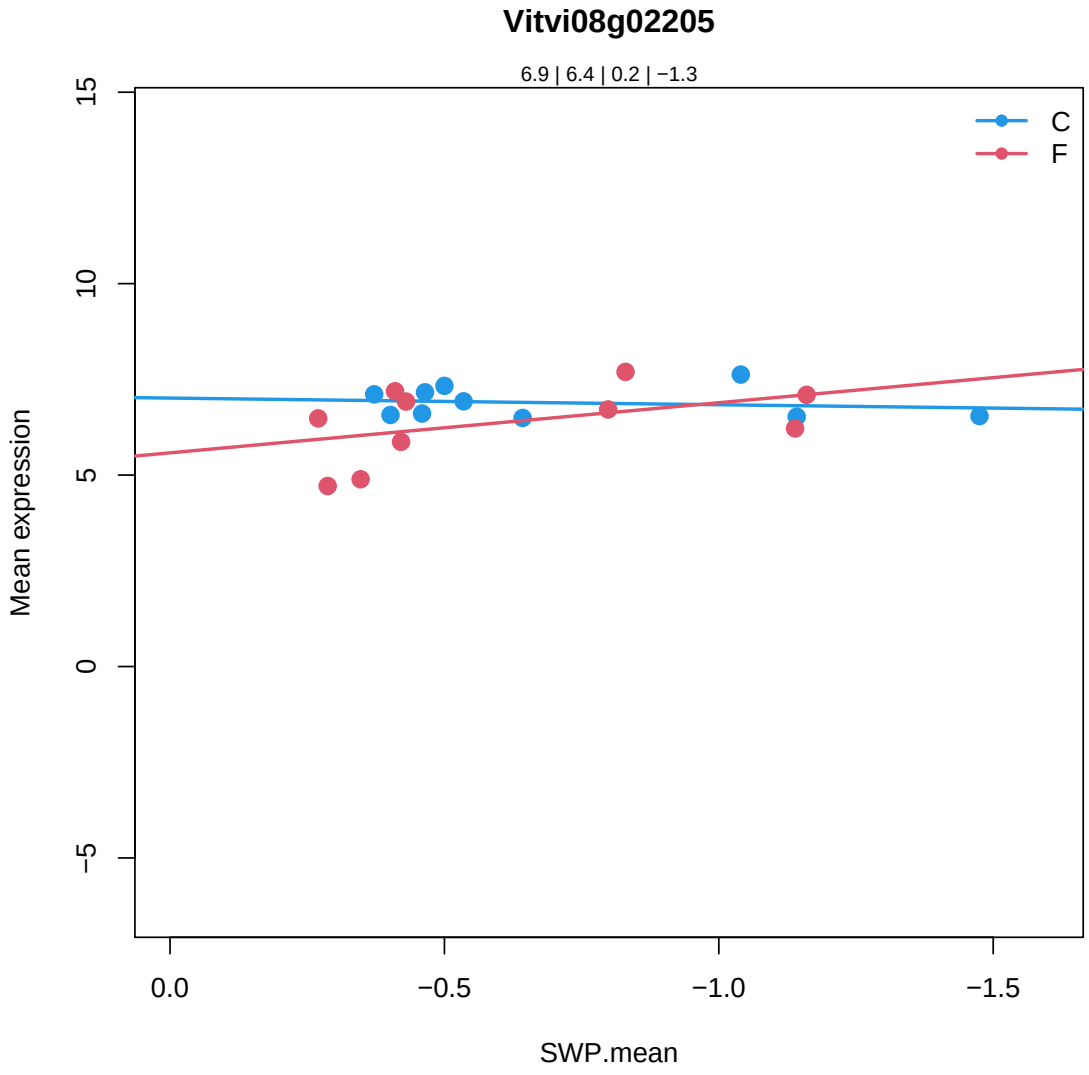
7.6.451 Vitvi08g02205: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g02205
        31.2
        cell.division
        Regulator of chromosome condensation (RCC1) family protein |
        Chr3:19940814-19943039 FORWARD LENGTH=424 |
        201606
```

Coefficients for Vitvi08g02205.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.888649	8.460876e-20	***	4.143444e-19	***
SlopeC	0.1741686	0.7688848		0.9500761	
MeanF-MeanC	-0.5101627	0.1008023		0.3659036	
SlopeF-SlopeC	-1.483383	0.1030468		0.9999488	



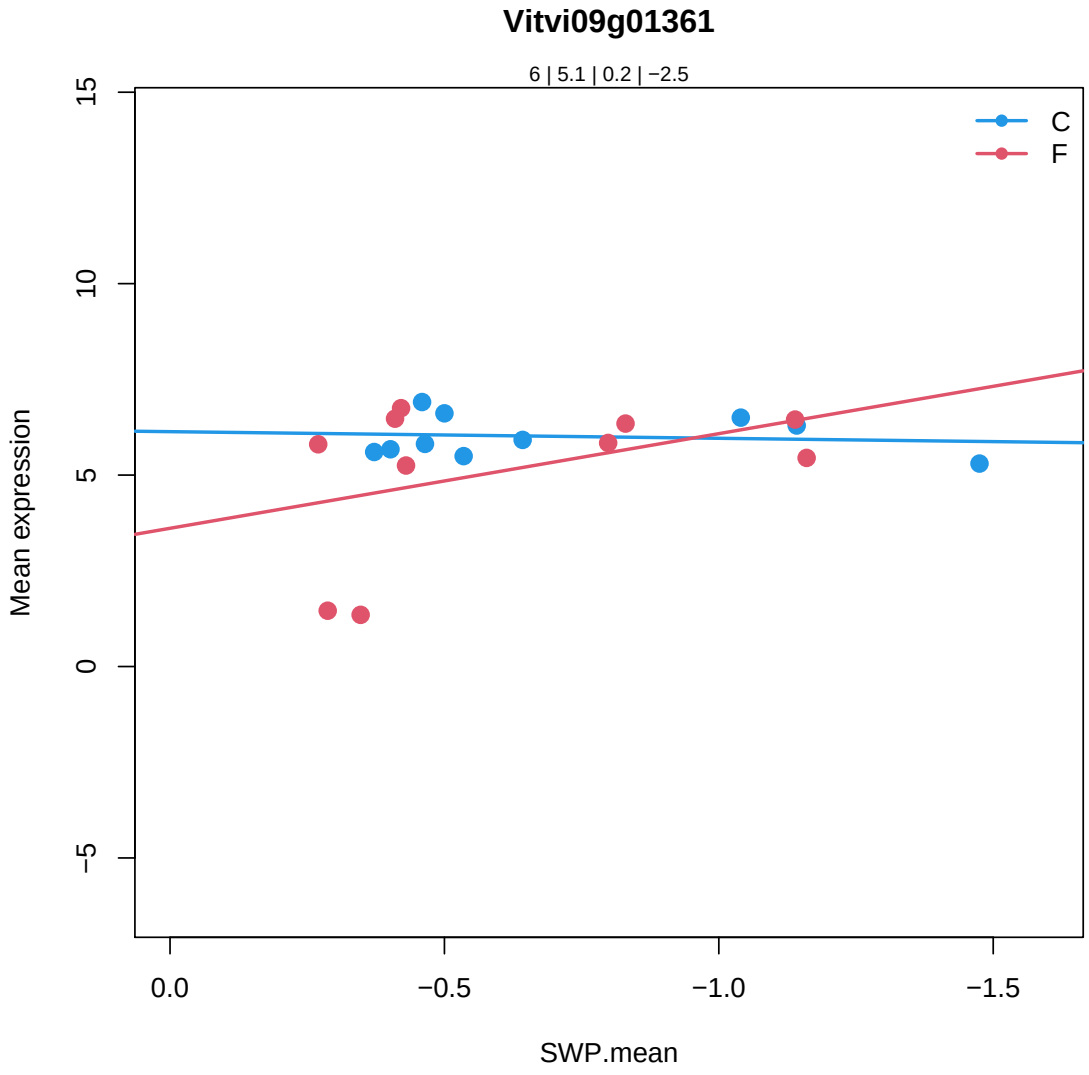
7.6.452 Vitvi09g01361: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g01361
        35.2
        not assigned.unknown
        B-box 32 |
        Chr3:7412713-7413390 REVERSE LENGTH=225 |
        201606
```

Coefficients for Vitvi09g01361.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.011911	6.380595e-13	***	9.285966e-13	***
SlopeC	0.172968	0.8771097		0.9764303	
MeanF-MeanC	-0.8955918	0.1255631		0.4194242	
SlopeF-SlopeC	-2.644642	0.1225477		0.9999488	



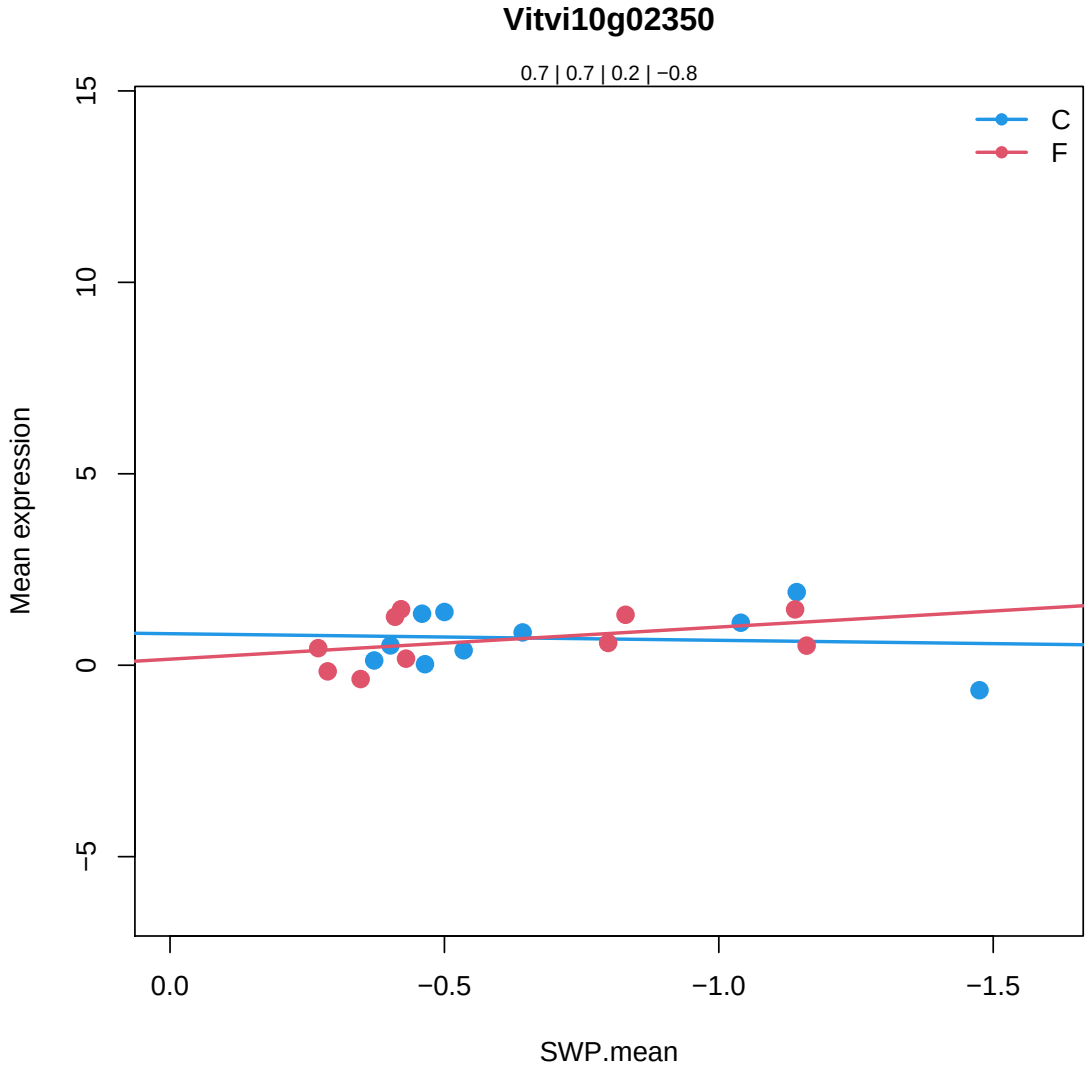
7.6.453 Vitvi10g02350: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g02350
        35.2
        not assigned.unknown
        Methionine aminopeptidase, related
```

Coefficients for Vitvi10g02350.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.7015689	0.003660853	**	0.003915974	**
SlopeC	0.172856	0.7754965		0.9513135	
MeanF-MeanC	-0.03254904	0.9157929		0.9772612	
SlopeF-SlopeC	-1.011409	0.2687389		0.9999488	



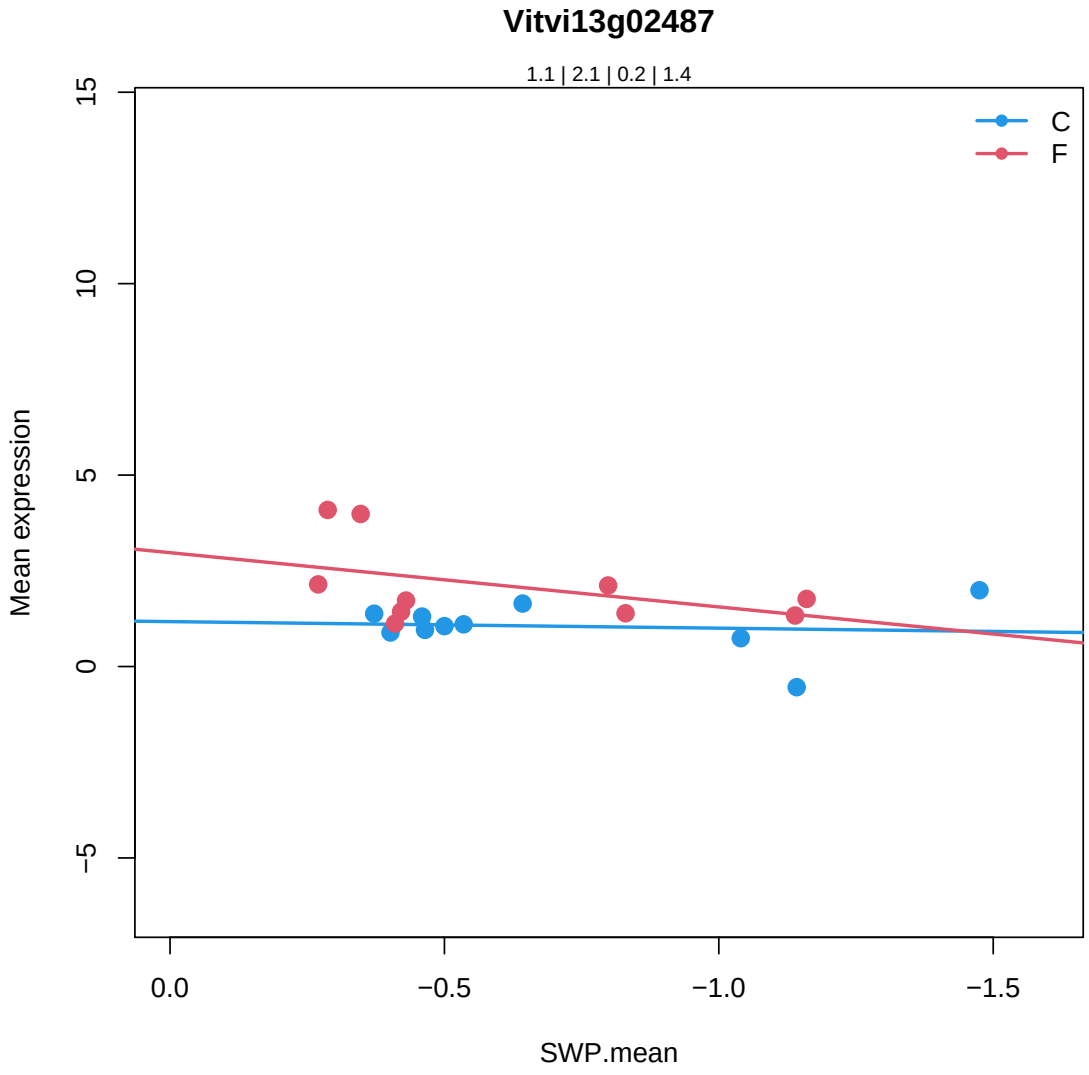
7.6.454 Vitvi13g02487: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g02487
        35.2
        not assigned.unknown
        RNA/RNP complex-1-interacting phosphatase |
        Chr3:19312753-19313097 FORWARD LENGTH=114 |
        201606
```

Coefficients for Vitvi13g02487.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.052323	0.0003893279	***	0.0004248683	***
SlopeC	0.1709966	0.8086258		0.9584039	
MeanF-MeanC	1.057754	0.006970044	**	0.05824419	.
SlopeF-SlopeC	1.245331	0.2432921		0.9999488	



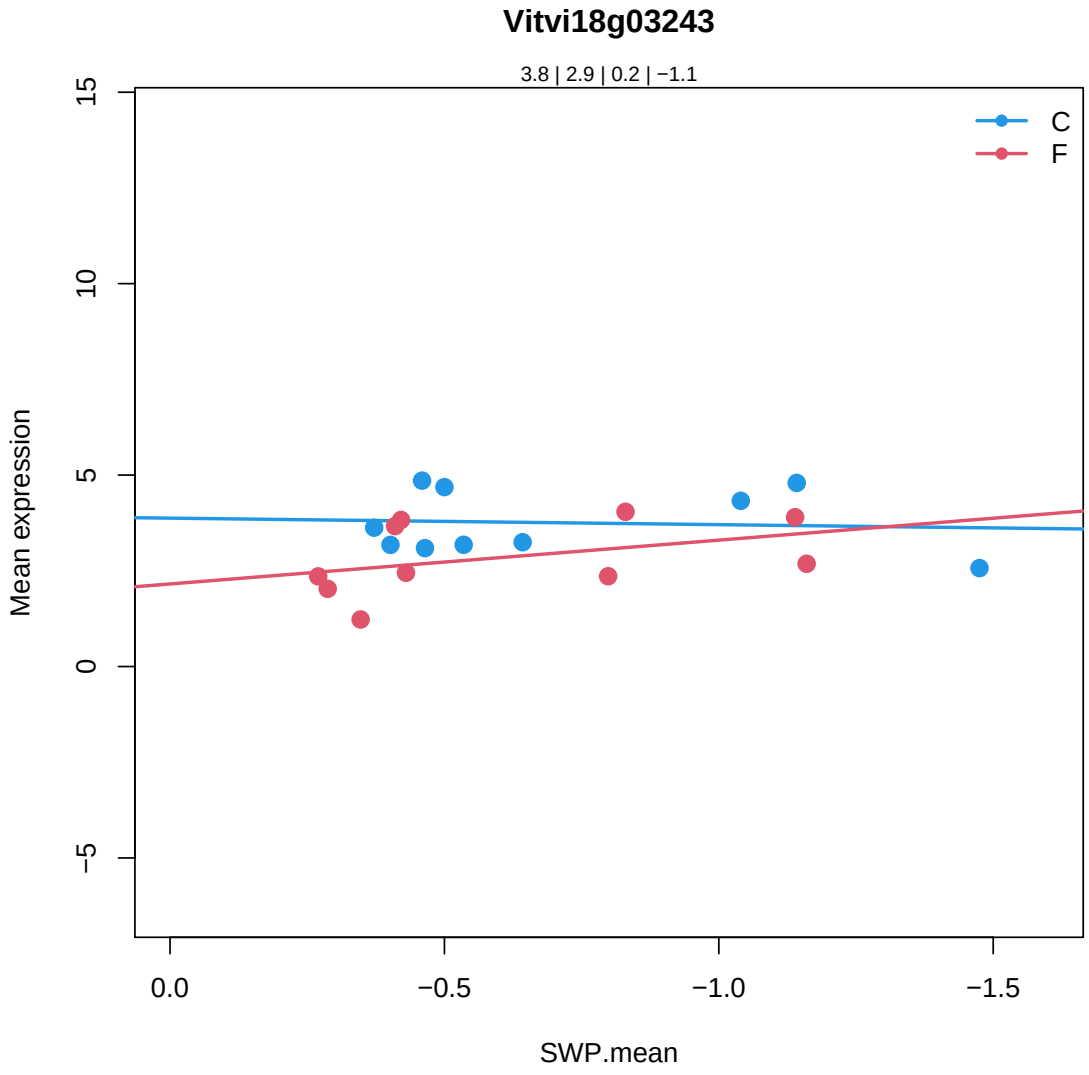
7.6.455 Vitvi18g03243: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g03243
        20.1.2.2
        stress.biotic.receptors.TIR-NBS-LRR
        disease resistance protein (TIR-NBS-LRR class) |
        Chr5:5822999-5827153 FORWARD LENGTH=1295 |
        201606
```

Coefficients for Vitvi18g03243.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.755551	1.360804e-12	***	1.936999e-12	***
SlopeC	0.1698712	0.8151274		0.9599292	
MeanF-MeanC	-0.9019443	0.02185402	*	0.1343683	
SlopeF-SlopeC	-1.314398	0.2318047		0.9999488	



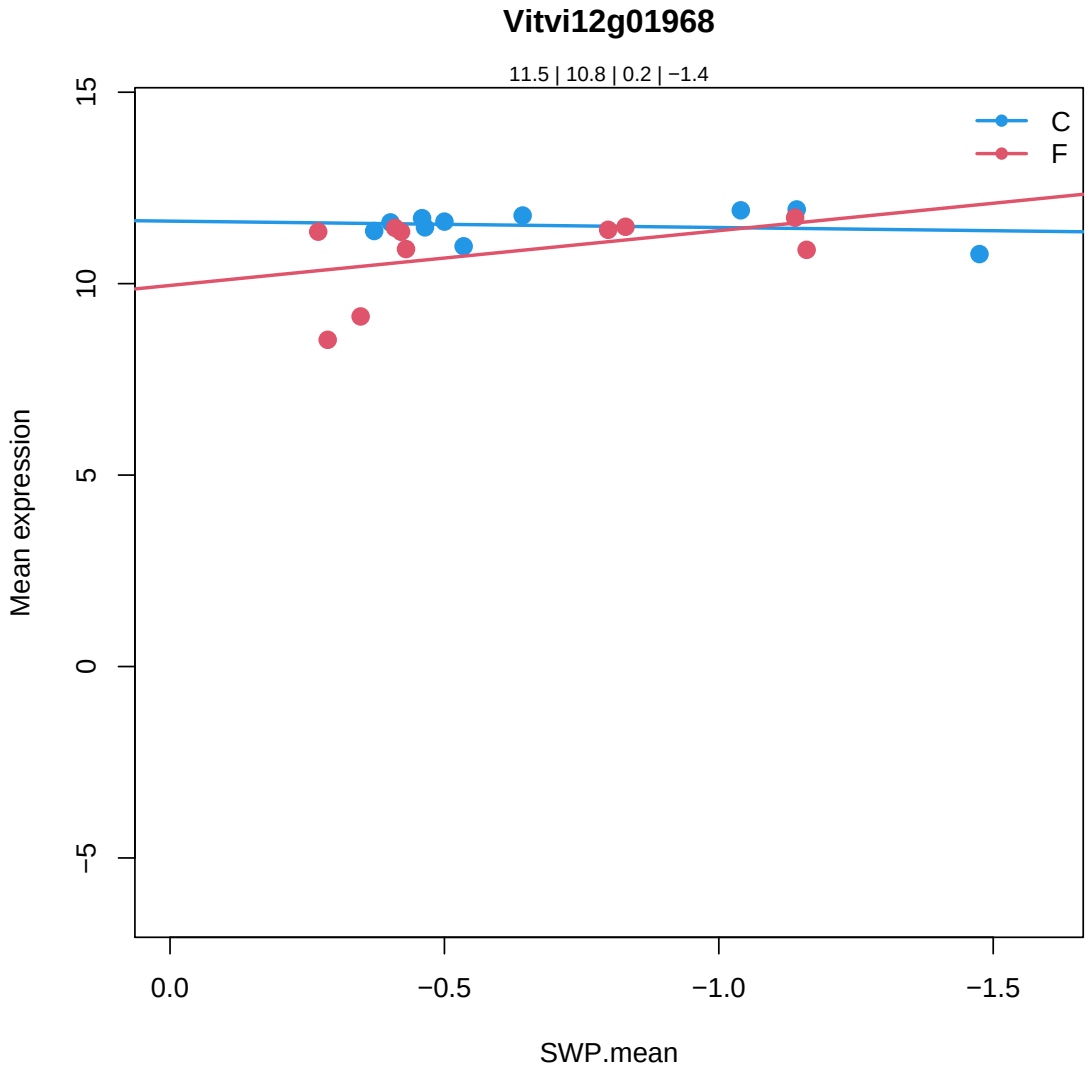
7.6.456 Vitvi12g01968: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g01968
        35.1
        not assigned.no ontology
        2Fe-2S ferredoxin-like superfamily protein |
        Chr1:22444565-22445011 FORWARD LENGTH=148 |
        201606
```

Coefficients for Vitvi12g01968.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	11.51524	8.077984e-24	***	2.874932e-22	***
SlopeC	0.1671682	0.7938726		0.9552081	
MeanF-MeanC	-0.690771	0.04305103	*	0.2168486	
SlopeF-SlopeC	-1.598362	0.1036753		0.9999488	



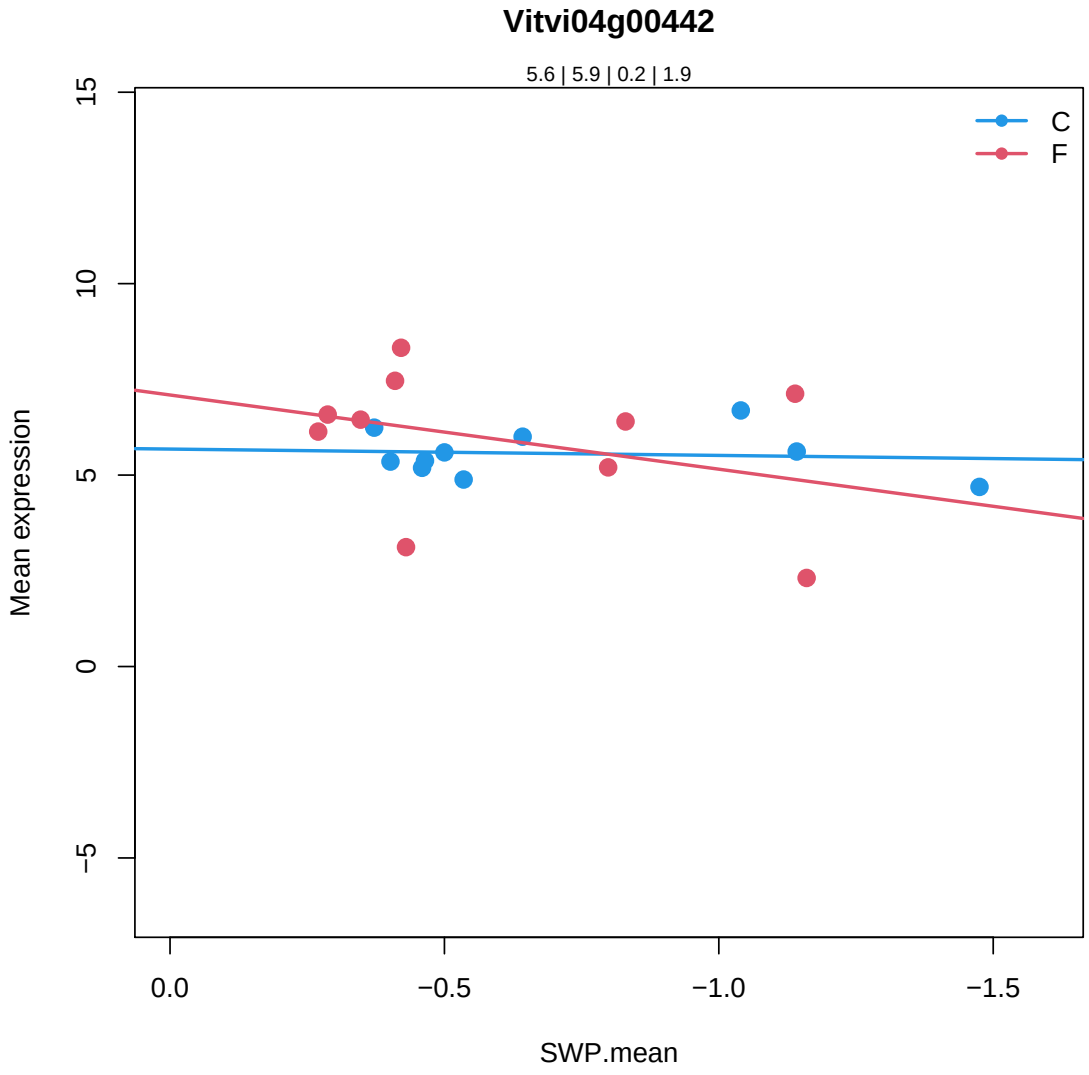
7.6.457 Vitvi04g00442: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00442
        35.2
        not assigned.unknown
        choice-of-anchor C domain protein%2C putative (Protein of unknown func
        Chr4:15663036-15664124 REVERSE LENGTH=325 |
        201606
```

Coefficients for Vitvi04g00442.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.562781	2.040064e-12	***	2.874876e-12	***
SlopeC	0.1655964	0.8801491		0.9769322	
MeanF-MeanC	0.3480957	0.534705		0.8264856	
SlopeF-SlopeC	1.772206	0.2847354		0.9999488	



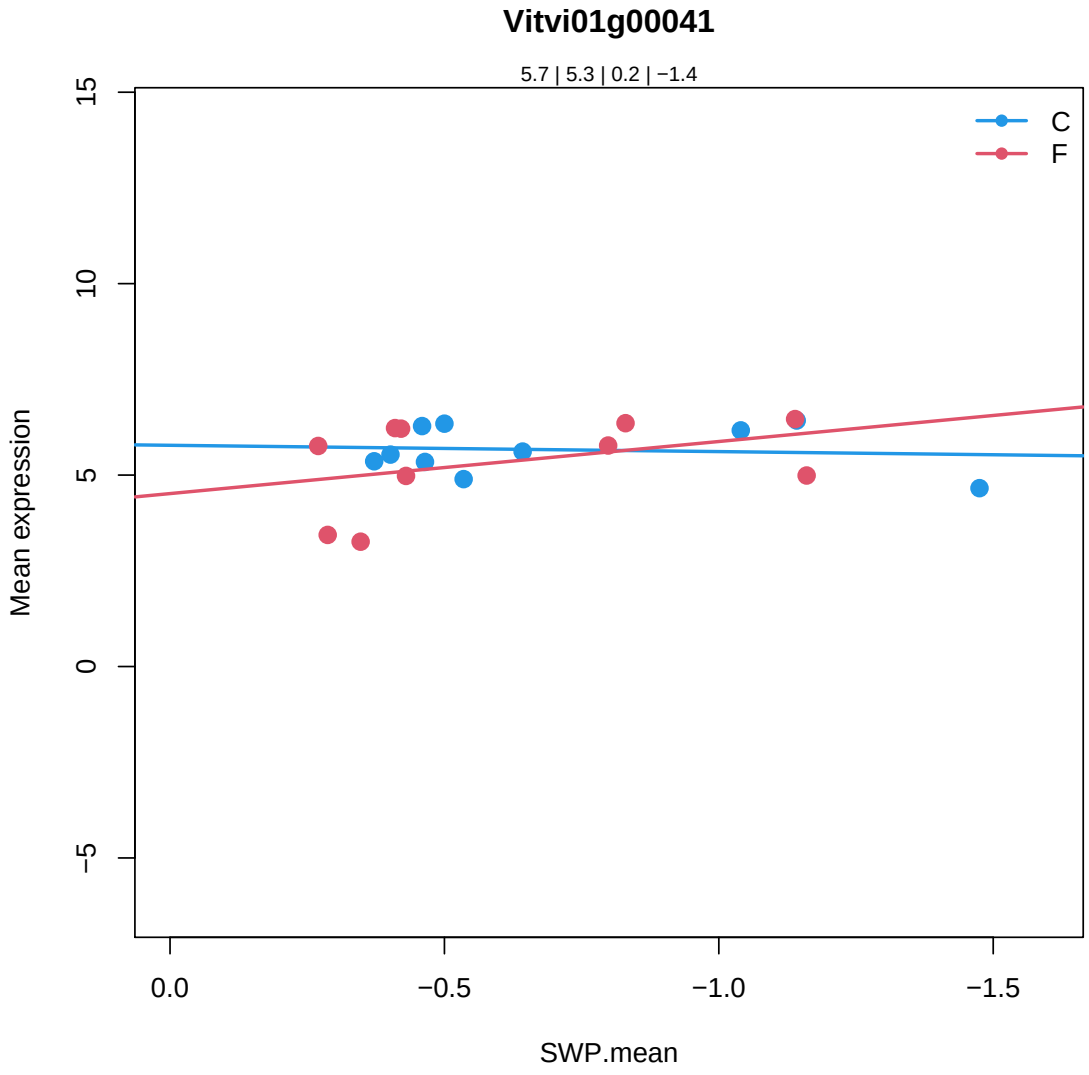
7.6.458 Vitvi01g00041: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00041
        35.2
        not assigned.unknown
        hypothetical protein |
        Chr5:24562431-24564395 REVERSE LENGTH=590 |
        201606
```

Coefficients for Vitvi01g00041.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.662073	6.75655e-16	***	1.293111e-15	***
SlopeC	0.1646082	0.8262617		0.9654923	
MeanF-MeanC	-0.3168227	0.4094446		0.7501809	
SlopeF-SlopeC	-1.52445	0.1810239		0.9999488	



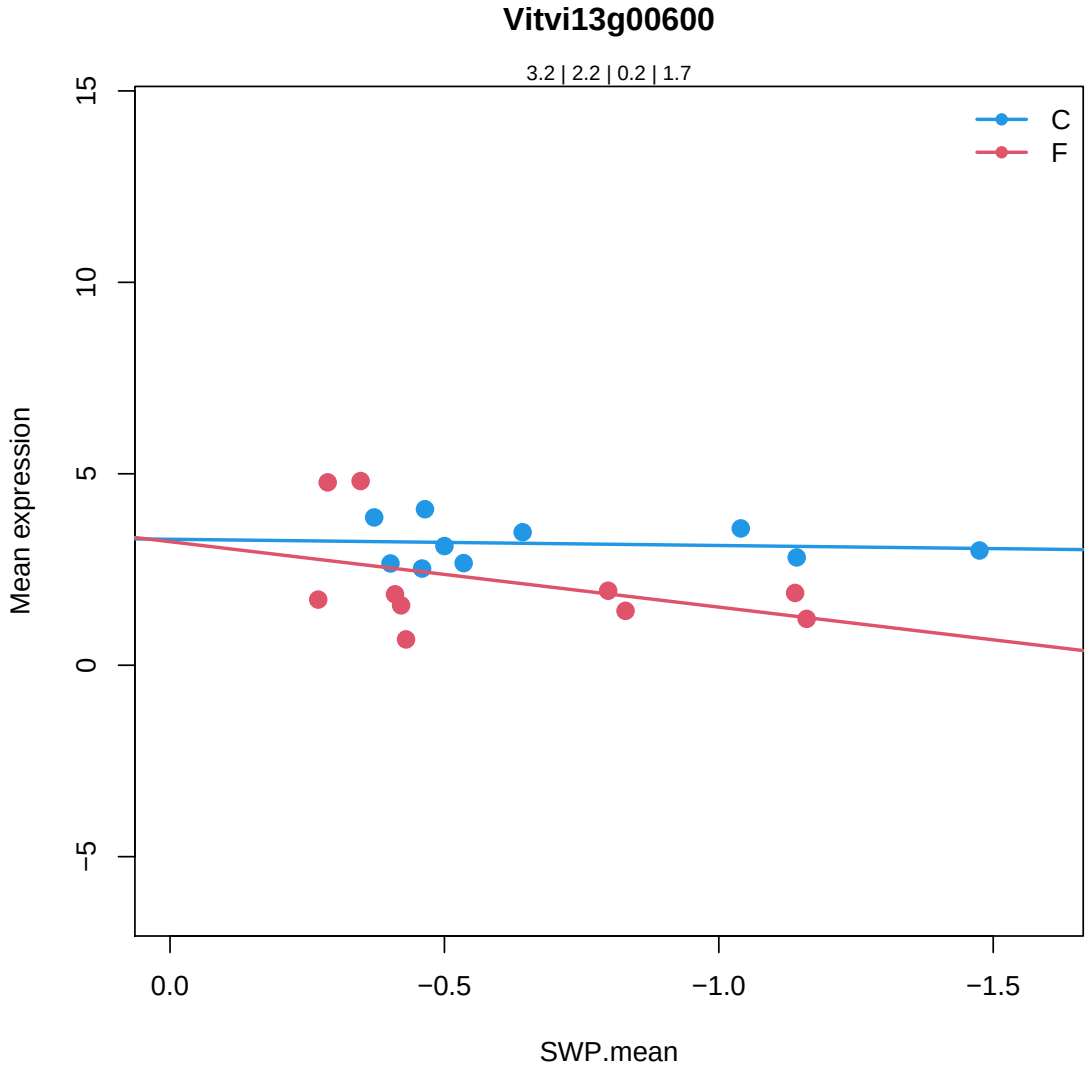
7.6.459 Vitvi13g00600: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00600
        34.3
        transport.amino acids
        Tyrosine-specific transport protein IPR018227 Tryptophan_tyrosine perm
```

Coefficients for Vitvi13g00600.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.175325	5.143251e-10	***	6.550253e-10	***
SlopeC	0.1619251	0.8472215		0.9711946	
MeanF-MeanC	-0.990095	0.02867047	*	0.1640545	
SlopeF-SlopeC	1.546758	0.2242124		0.9999488	



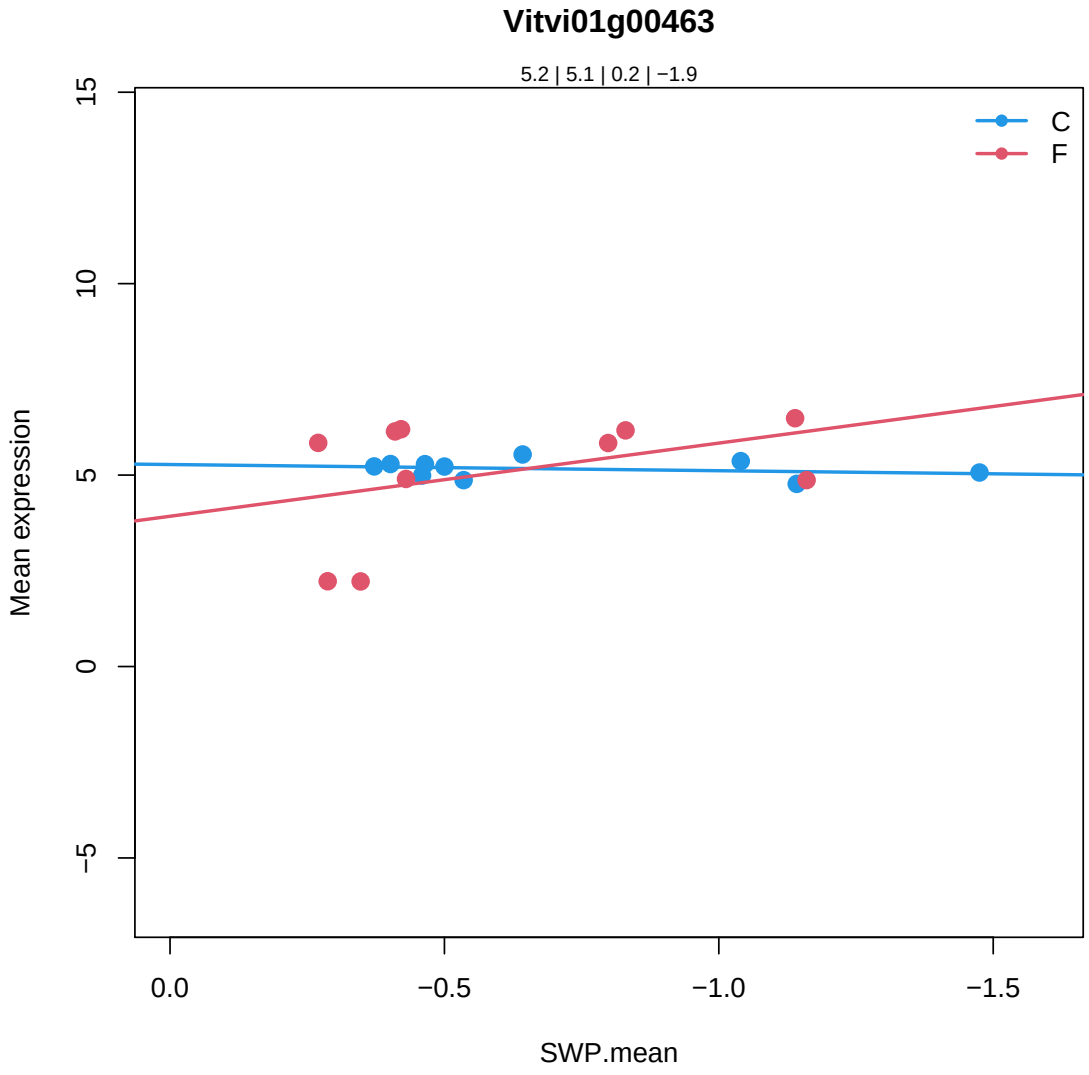
7.6.460 Vitvi01g00463: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00463
        35.1
        not assigned.no ontology
        PLANT CADMIUM RESISTANCE 2 |
        Chr1:5128591-5129458 REVERSE LENGTH=152 |
        201606
```

Coefficients for Vitvi01g00463.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.161753	1.136374e-13	***	1.737796e-13	***
SlopeC	0.1617388	0.8542417		0.972509	
MeanF-MeanC	-0.07328533	0.8699129		0.9657814	
SlopeF-SlopeC	-2.072604	0.1240367		0.9999488	



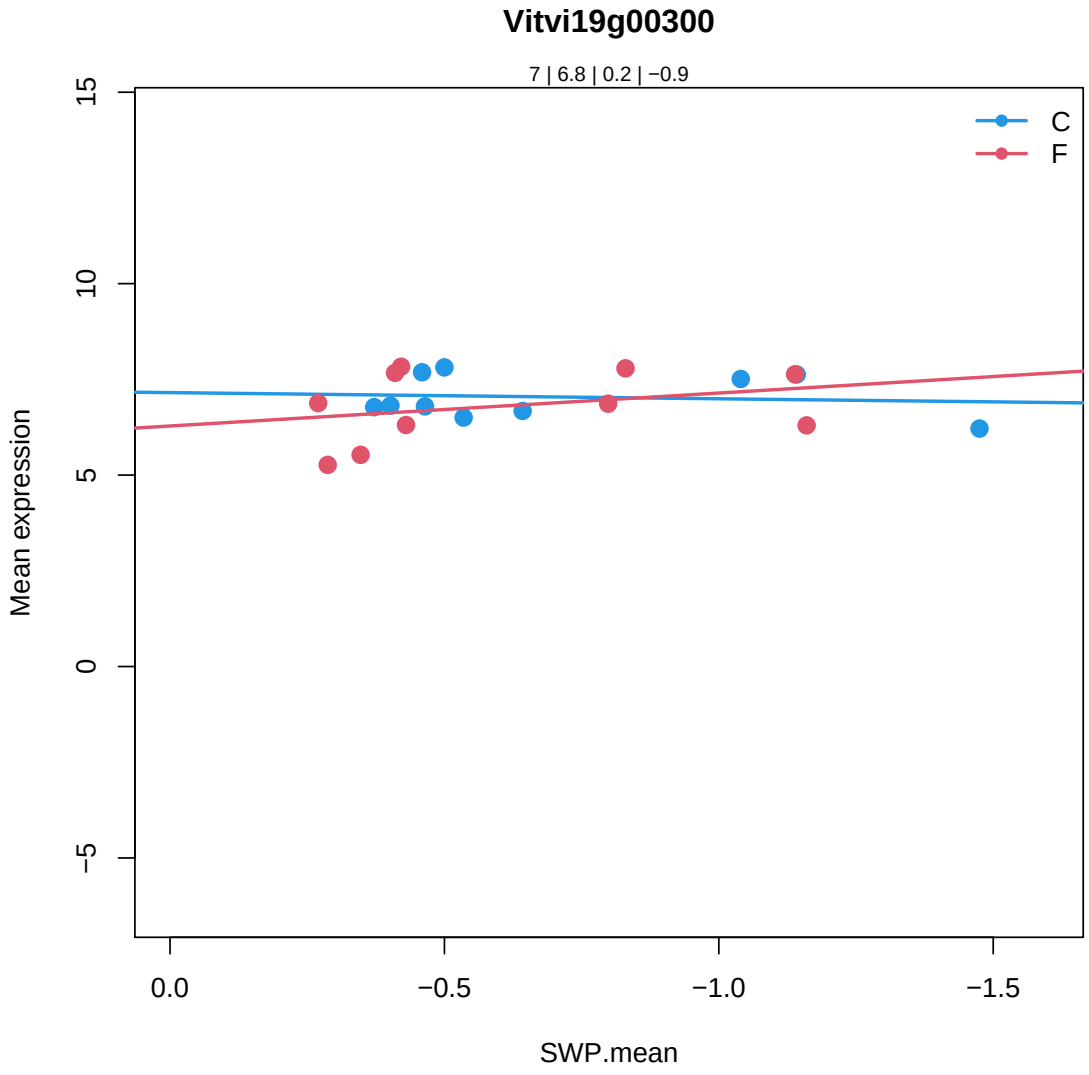
7.6.461 Vitvi19g00300: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g00300
        34.22
        transport.cyclic nucleotide or calcium regulated channels
        cyclic nucleotide-gated cation channel 4 |
        Chr5:22025684-22029971 REVERSE LENGTH=694 |
        201606
```

Coefficients for Vitvi19g00300.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.040695	3.383422e-19	***	1.349148e-18	***
SlopeC	0.1606139	0.8039297		0.9573096	
MeanF-MeanC	-0.2342	0.4786716		0.7941132	
SlopeF-SlopeC	-1.021481	0.2947332		0.9999488	



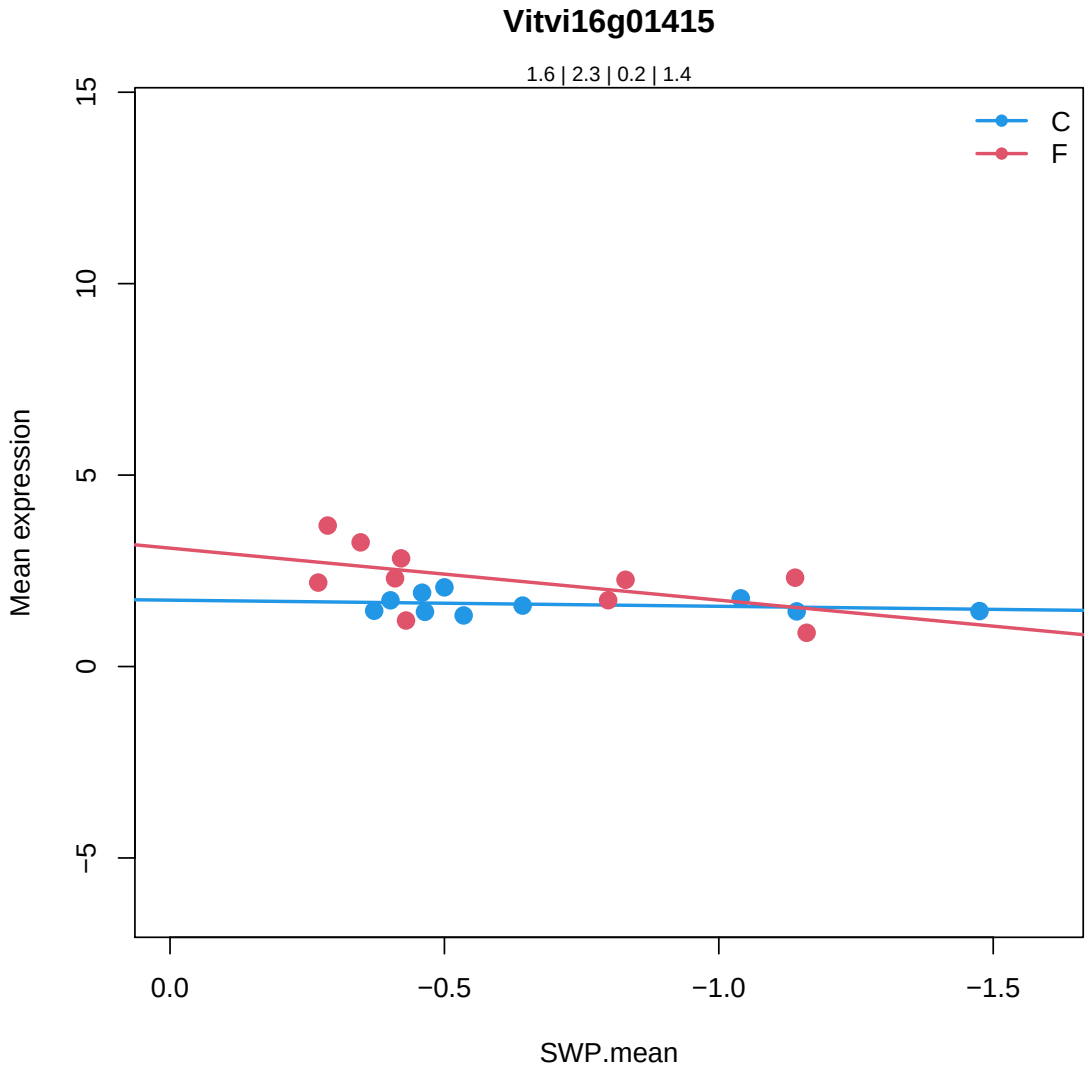
7.6.462 Vitvi16g01415: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01415
        30.3
        signalling.calcium
        Calcium-binding EF-hand family protein |
        Chr5:8238781-8239986 REVERSE LENGTH=197 |
        201606
```

Coefficients for Vitvi16g01415.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.620175	5.364283e-09	***	6.602794e-09	***
SlopeC	0.1599036	0.7440011		0.9454913	
MeanF-MeanC	0.6441642	0.0157761	*	0.1054434	
SlopeF-SlopeC	1.198378	0.1103162		0.9999488	



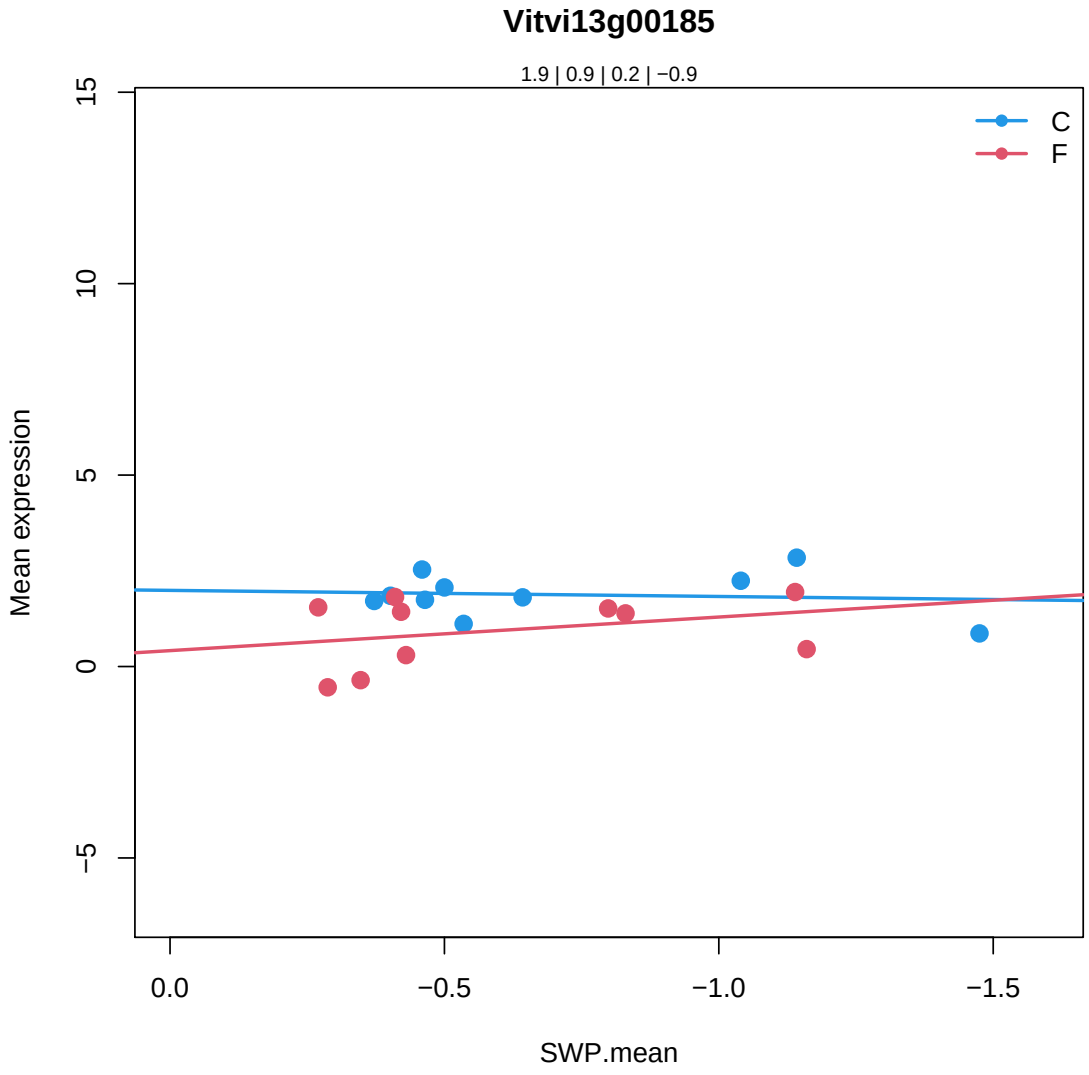
7.6.463 Vitvi13g00185: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00185
        11.5.2
        lipid metabolism.glycerol metabolism.glycerol-3-phosphate dehydrogenas
        NAD-dependent glycerol-3-phosphate dehydrogenase family protein |
        Chr2:16974484-16976241 FORWARD LENGTH=319 |
        201606
```

Coefficients for Vitvi13g00185.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.876765	4.249198e-08	***	5.090887e-08	***
SlopeC	0.1590033	0.8039353		0.9573096	
MeanF-MeanC	-0.9275143	0.008751498	**	0.06878879	.
SlopeF-SlopeC	-1.036502	0.2831611		0.9999488	



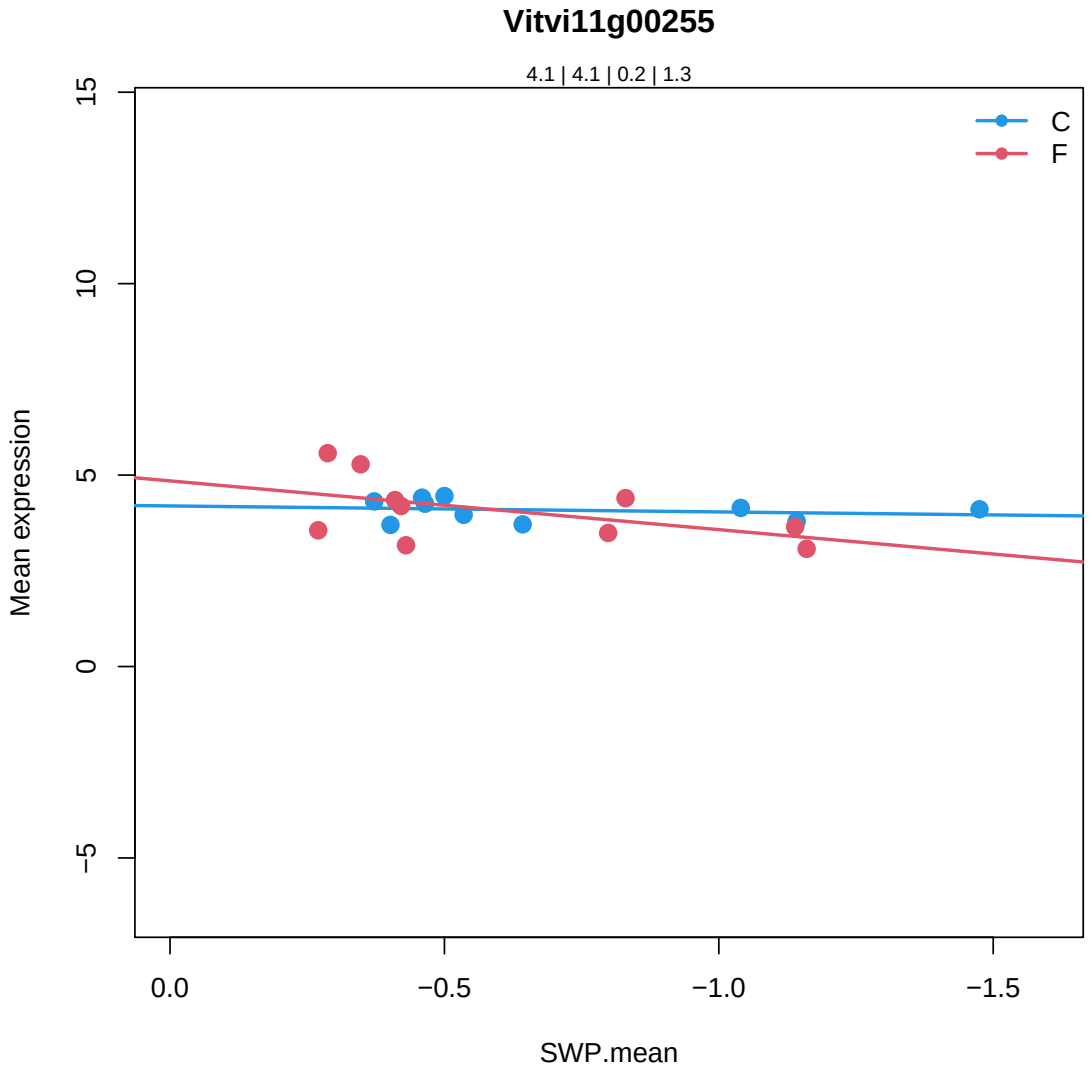
7.6.464 Vitvi11g00255: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00255
        29.5
        protein.degradation
        Peptidase M28 family protein |
        Chr5:6673986-6676767 FORWARD LENGTH=681 |
        201606
```

Coefficients for Vitvi11g00255.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.084049	1.373569e-16	***	2.913435e-16	***
SlopeC	0.1560559	0.75539		0.9474313	
MeanF-MeanC	-0.01159977	0.9636231		0.9916973	
SlopeF-SlopeC	1.11711	0.1437015		0.9999488	



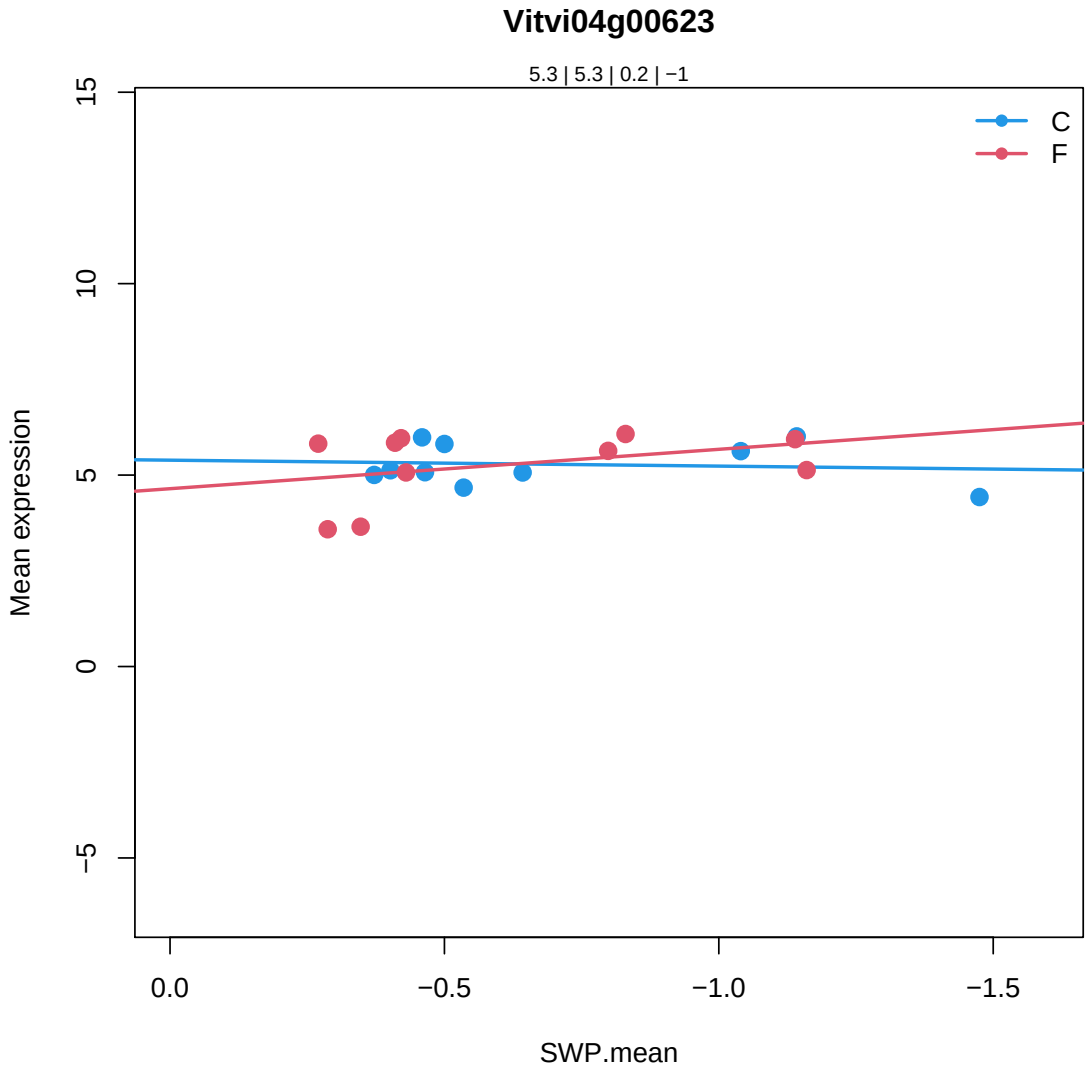
7.6.465 Vitvi04g00623: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00623
        11.10.1
        lipid metabolism.glycolipid synthesis.MGDG synthase
        monogalactosyl diacylglycerol synthase 1 |
        Chr4:15374222-15376961 FORWARD LENGTH=559 |
        201606
```

Coefficients for Vitvi04g00623.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.280205	7.806206e-17	***	1.727384e-16	***
SlopeC	0.1547955	0.8058732		0.9575465	
MeanF-MeanC	-0.009508719	0.9762912		0.9943622	
SlopeF-SlopeC	-1.18341	0.2149052		0.9999488	



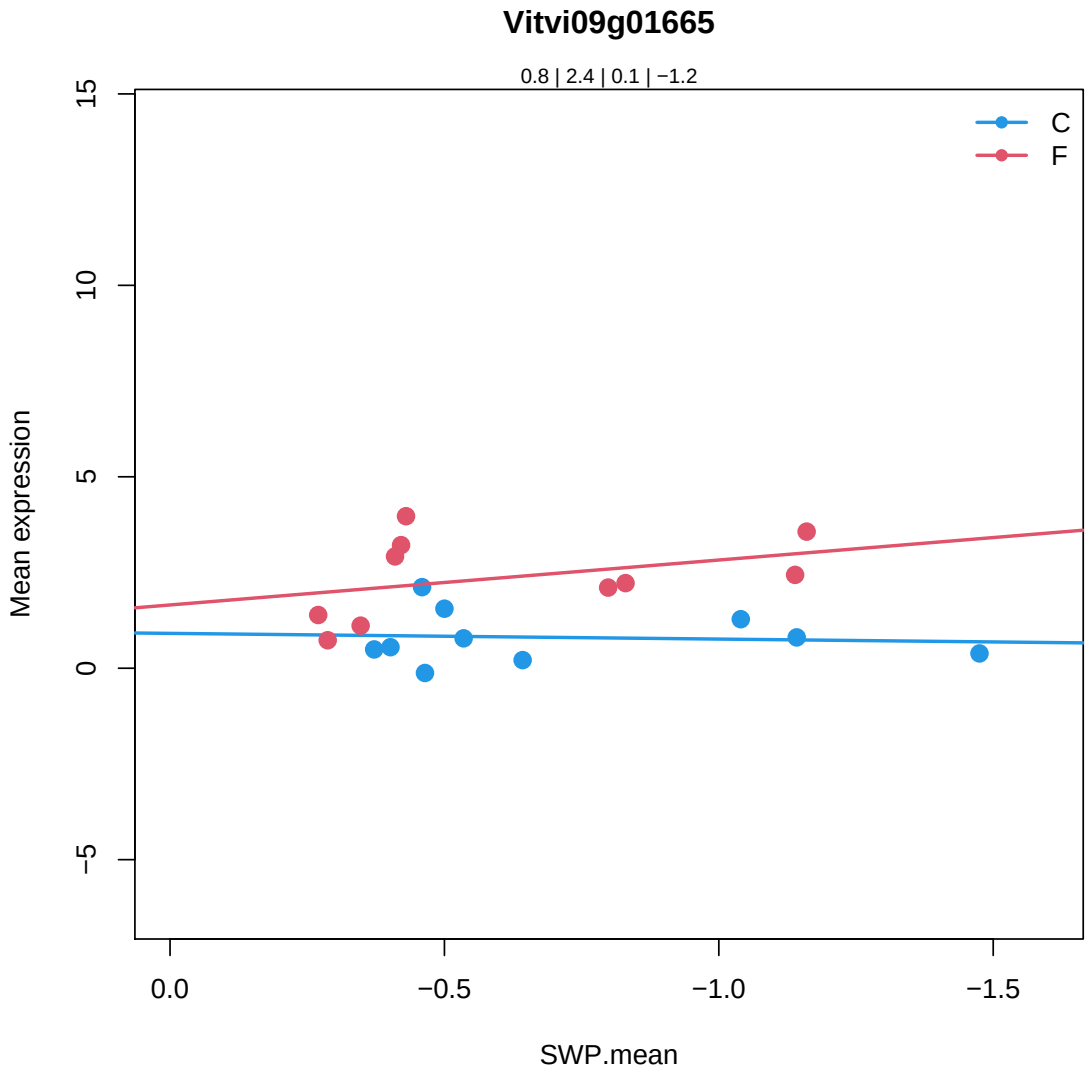
7.6.466 Vitvi09g01665: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g01665
        35.2
        not assigned.unknown
        Blue copper protein IPR003245 Plastocyanin-like
```

Coefficients for Vitvi09g01665.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8050814	0.005020212	**	0.005354284	**
SlopeC	0.1490119	0.8372173		0.9692779	
MeanF-MeanC	1.562052	0.0003129503	***	0.00477646	**
SlopeF-SlopeC	-1.322599	0.228304		0.9999488	



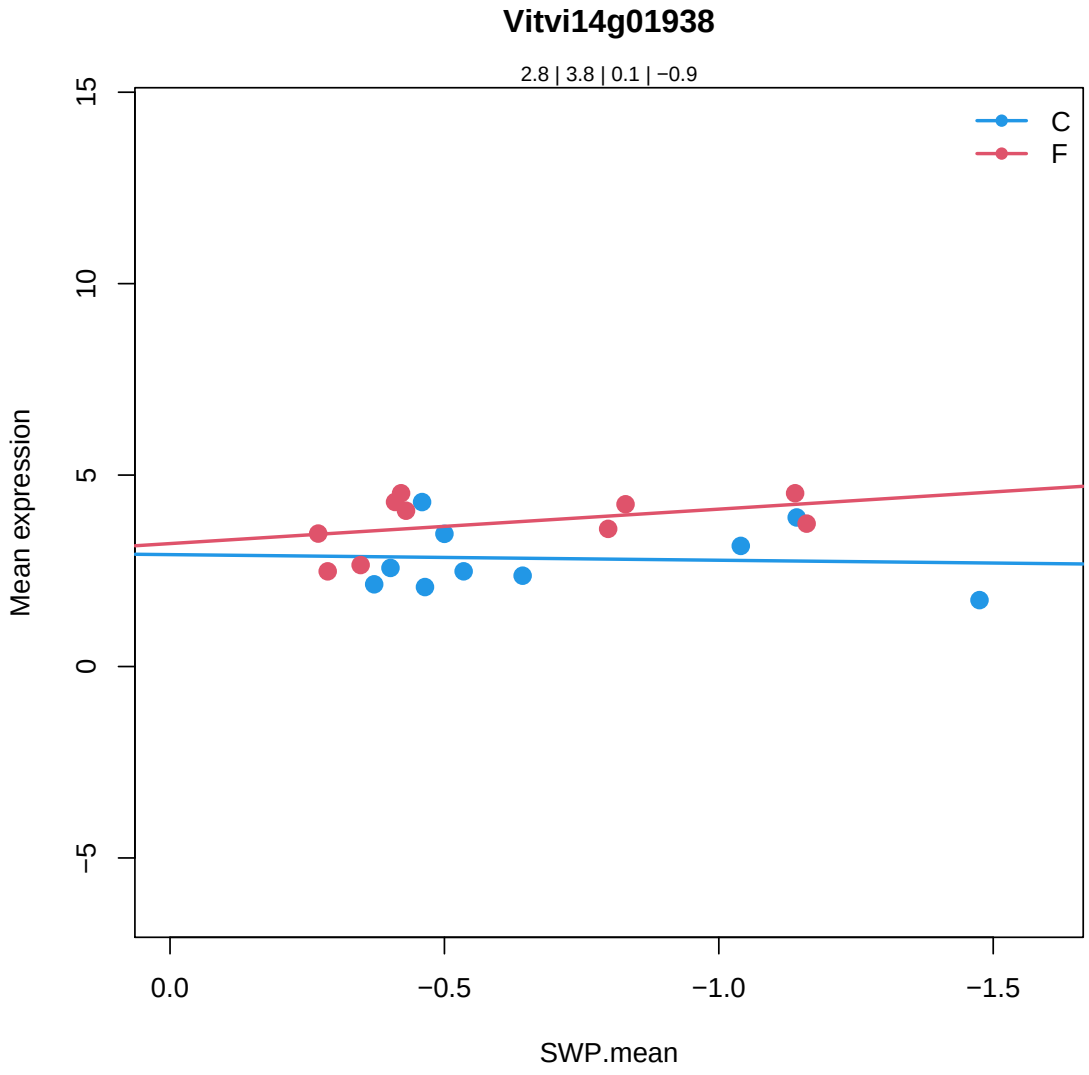
7.6.467 Vitvi14g01938: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01938
        4.2.4
        glycolysis.plastid branch.phosphofructokinase (PFK)
        phosphofructokinase 5 |
        Chr2:9545670-9548414 FORWARD LENGTH=537 |
        201606
```

Coefficients for Vitvi14g01938.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.819198	4.523318e-11	***	6.002474e-11	***
SlopeC	0.1463675	0.8230319		0.9643522	
MeanF-MeanC	0.9398054	0.009254623	**	0.07182089	.
SlopeF-SlopeC	-1.04567	0.2892231		0.9999488	



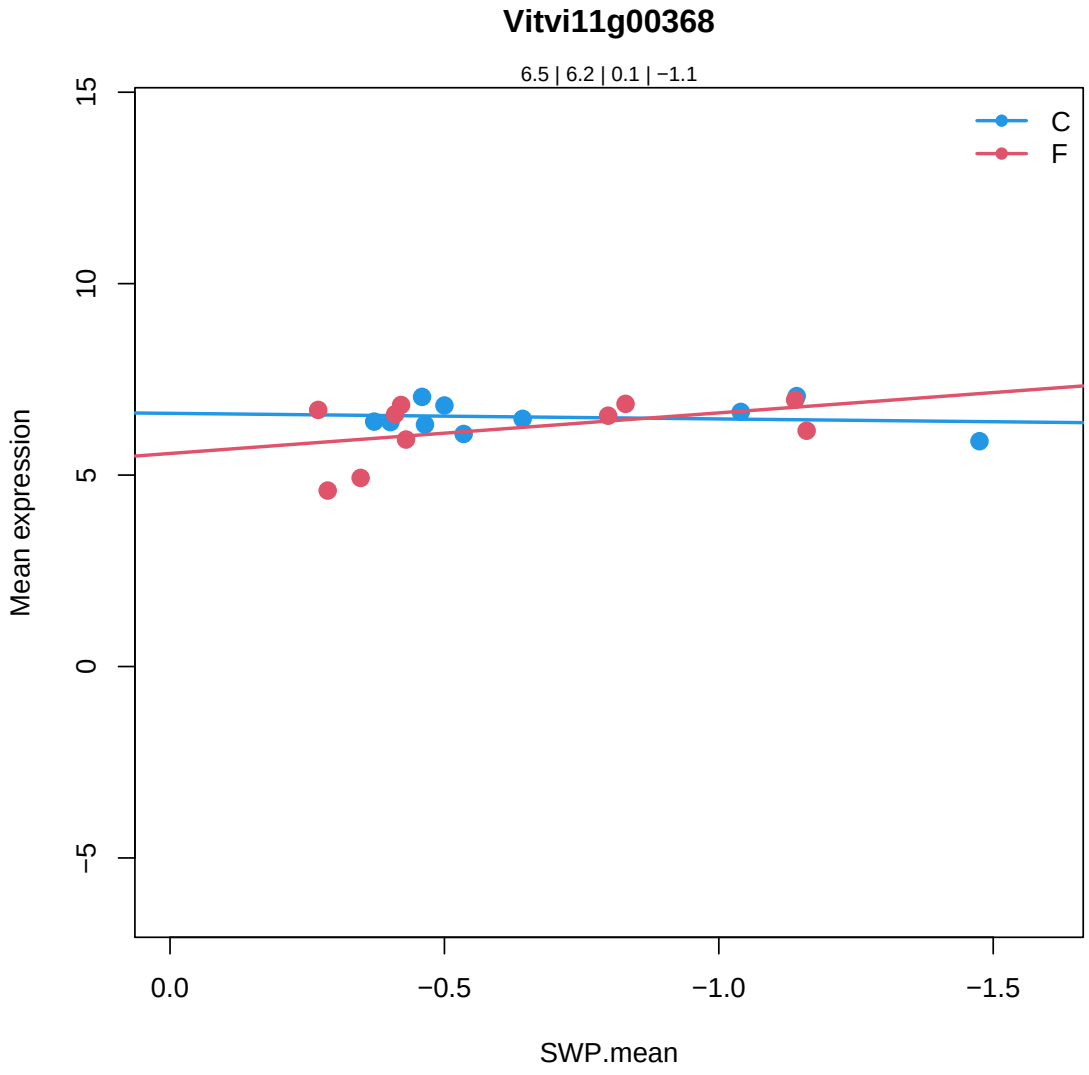
7.6.468 Vitvi11g00368: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00368
        29.8
        protein.assembly and cofactor ligation
        ATP binding protein |
        Chr3:8868731-8872154 REVERSE LENGTH=532 |
        201606
```

Coefficients for Vitvi11g00368.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.509763	2.885526e-20	***	1.678031e-19	***
SlopeC	0.145961	0.7838765		0.9533027	
MeanF-MeanC	-0.2993896	0.2748078		0.6389961	
SlopeF-SlopeC	-1.206368	0.1376379		0.9999488	



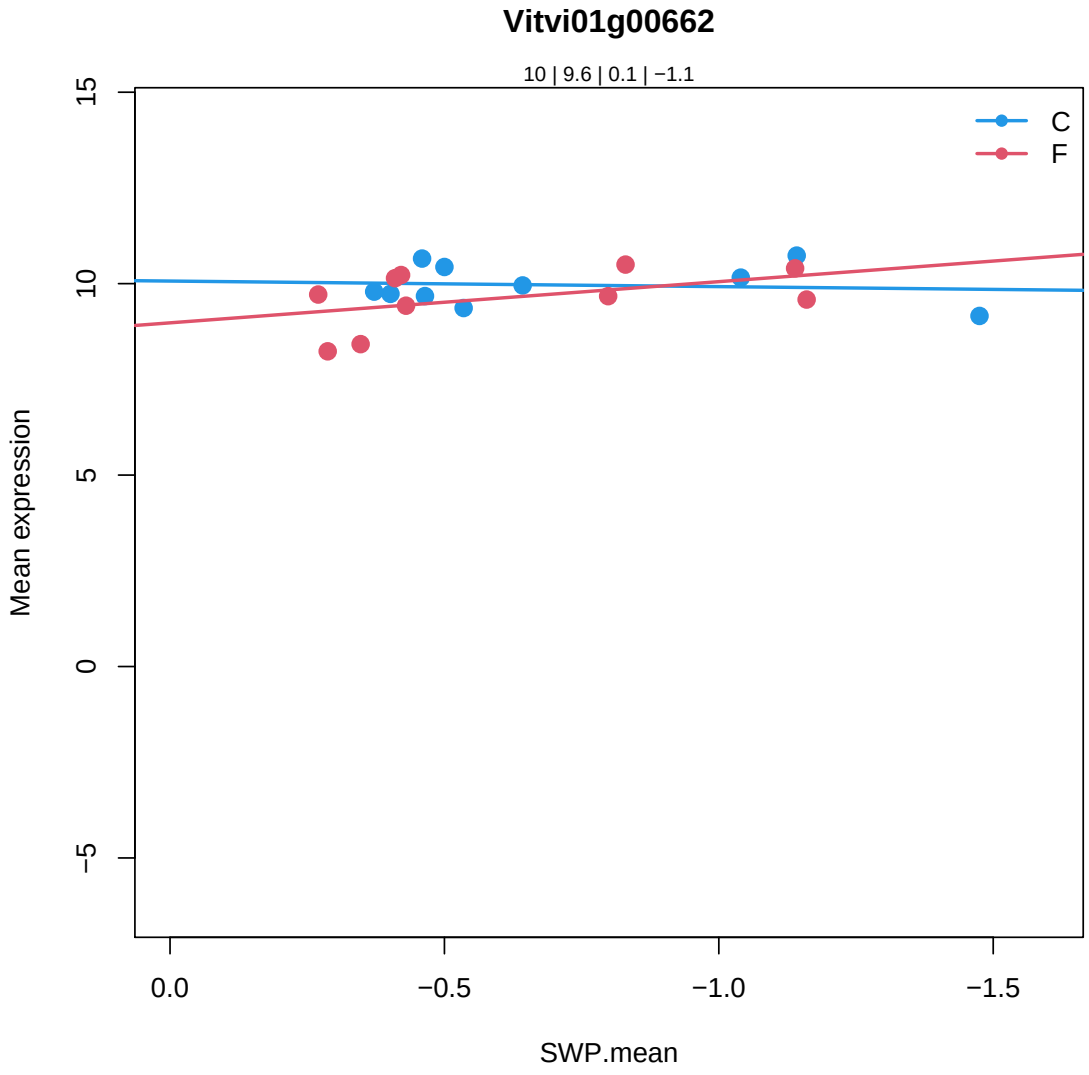
7.6.469 Vitvi01g00662: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00662
        13.1.1.3.1
        amino acid metabolism.synthesis.central amino acid metabolism.alanine.
        glutamate:glyoxylate aminotransferase |
        Chr1:8268720-8271329 REVERSE LENGTH=481 |
        201606
```

Coefficients for Vitvi01g00662.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	9.96519	5.514942e-24	***	2.265734e-22	***
SlopeC	0.1452501	0.7894081		0.9533712	
MeanF-MeanC	-0.3338378	0.234679		0.5899994	
SlopeF-SlopeC	-1.220842	0.1413242		0.9999488	



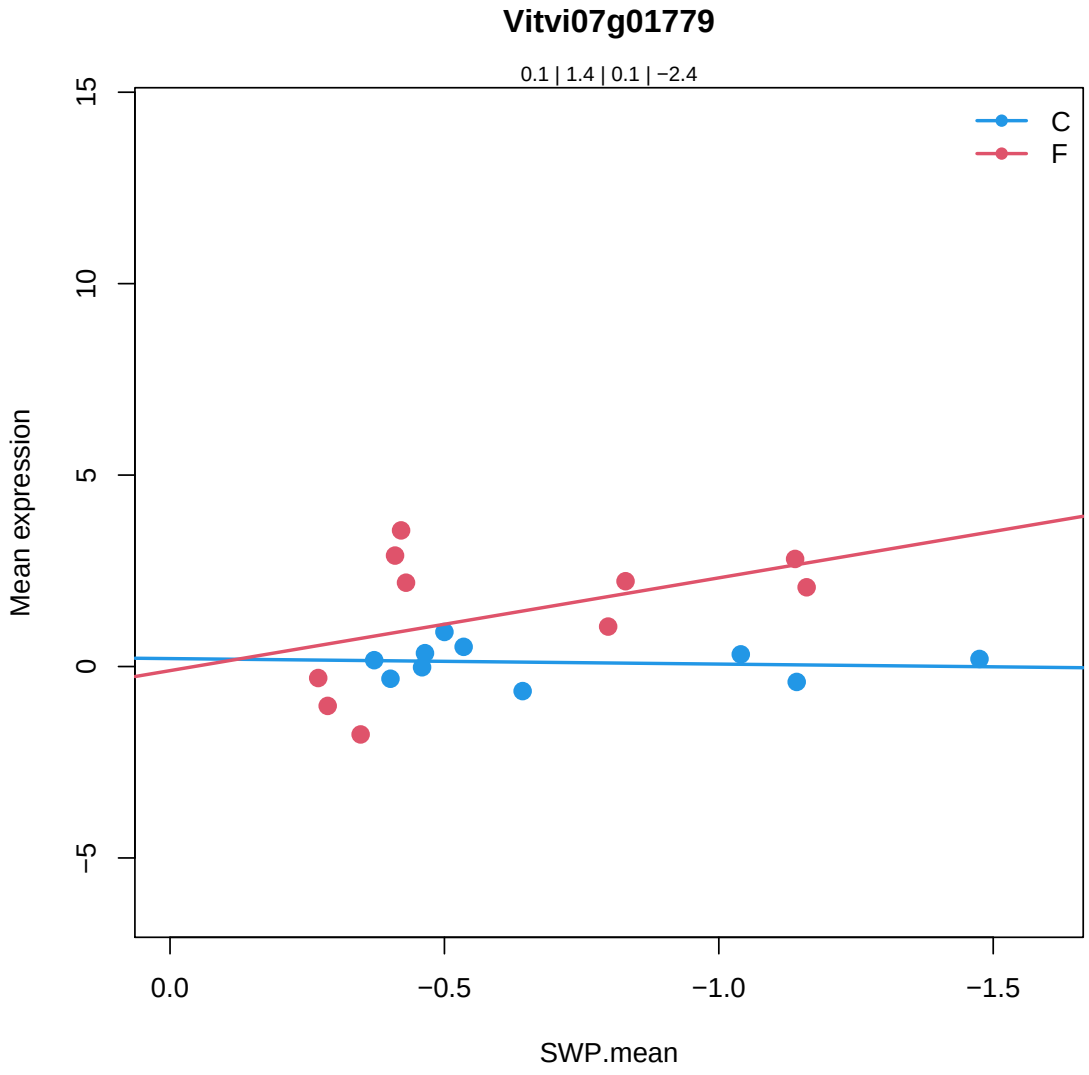
7.6.470 Vitvi07g01779: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01779
        34.6
        transport.sulphate
        STAS domain / Sulfate transporter family |
        Chr1:29317965-29323249 REVERSE LENGTH=677 |
        201606
```

Coefficients for Vitvi07g01779.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1061768	0.7659189		0.7703158	
SlopeC	0.1430805	0.8852476		0.9789972	
MeanF-MeanC	1.262582	0.01906637	*	0.1219474	
SlopeF-SlopeC	-2.565898	0.09271658	.	0.9999488	



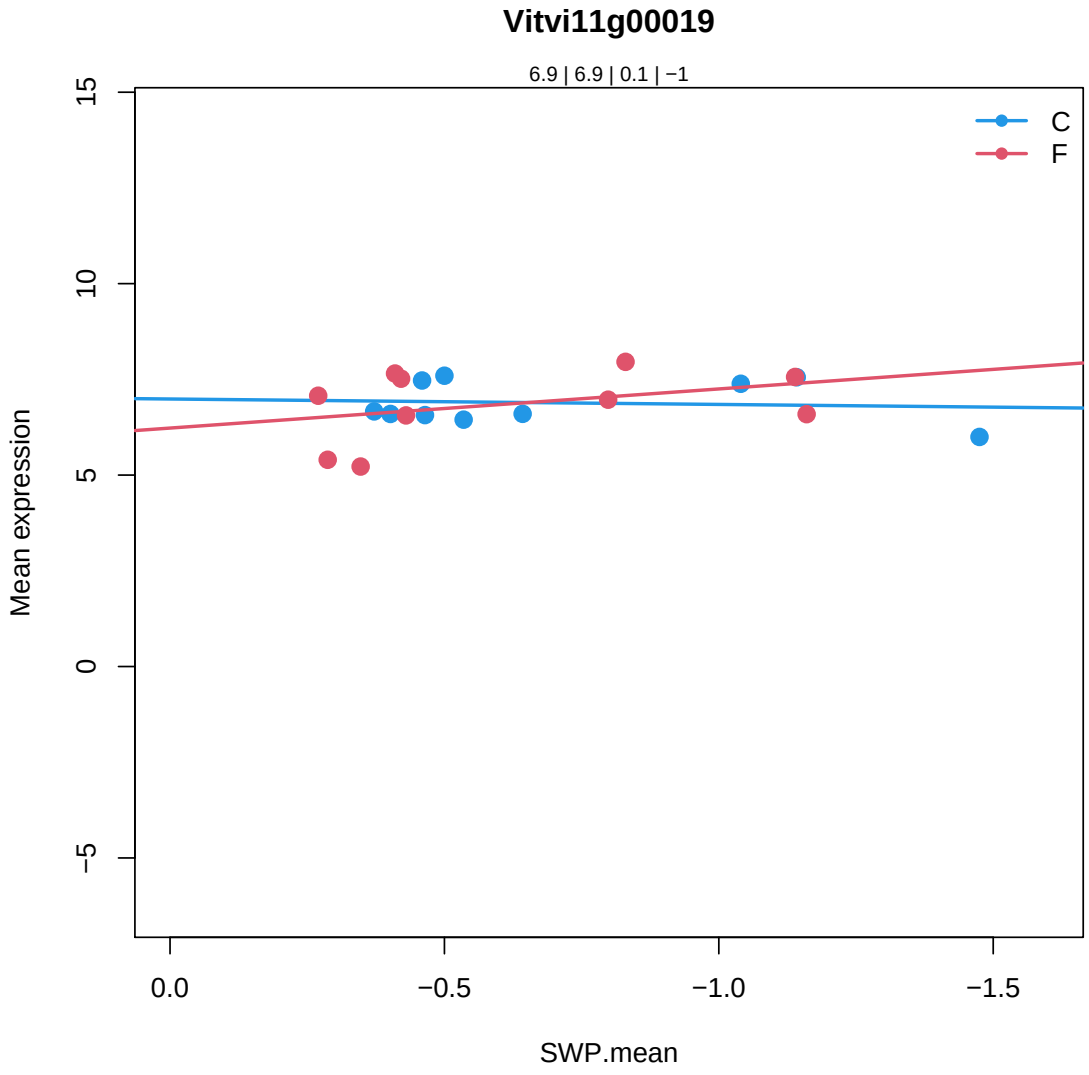
7.6.471 Vitvi11g00019: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00019
        30.4.1
        signalling.phosphinositides.phosphatidylinositol-4-phosphate 5-kinase
        phosphatidylinositol-4-phosphate 5-kinase family protein |
        Chr3:4754624-4761185 FORWARD LENGTH=1791 |
        201606
```

Coefficients for Vitvi11g00019.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.887385	3.321195e-19	***	1.326911e-18	***
SlopeC	0.1418423	0.822479		0.9640425	
MeanF-MeanC	-0.03705868	0.9081547		0.9759422	
SlopeF-SlopeC	-1.163655	0.2240916		0.9999488	



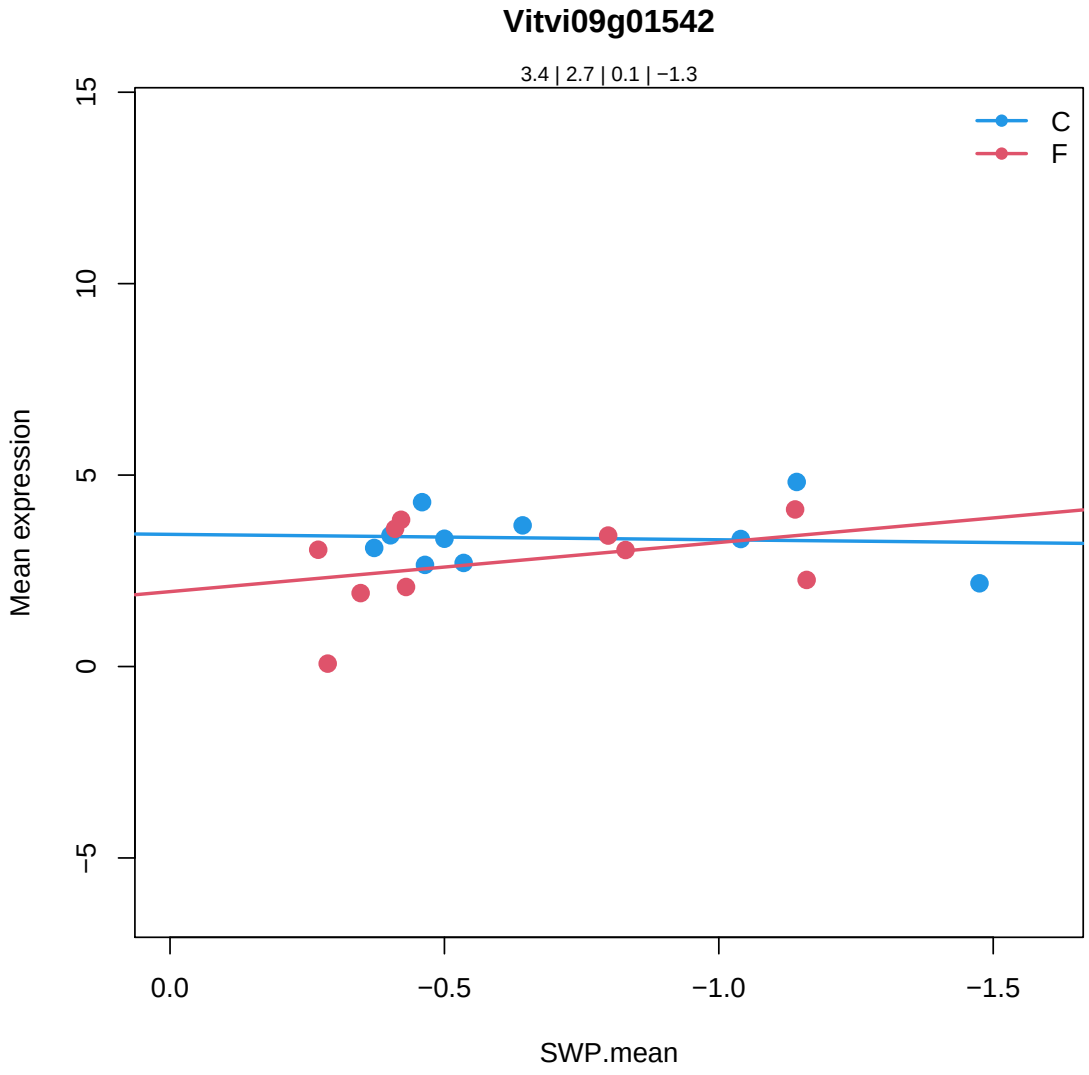
7.6.472 Vitvi09g01542: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g01542
        26.13
        misc.acid and other phosphatases
        Pyridoxal phosphate phosphatase-related protein |
        Chr1:6090763-6091975 REVERSE LENGTH=279 |
        201606
```

Coefficients for Vitvi09g01542.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.352298	1.059001e-10	***	1.384212e-10	***
SlopeC	0.1415909	0.861941		0.9742151	
MeanF-MeanC	-0.614644	0.1474081		0.4620685	
SlopeF-SlopeC	-1.424813	0.2470659		0.9999488	



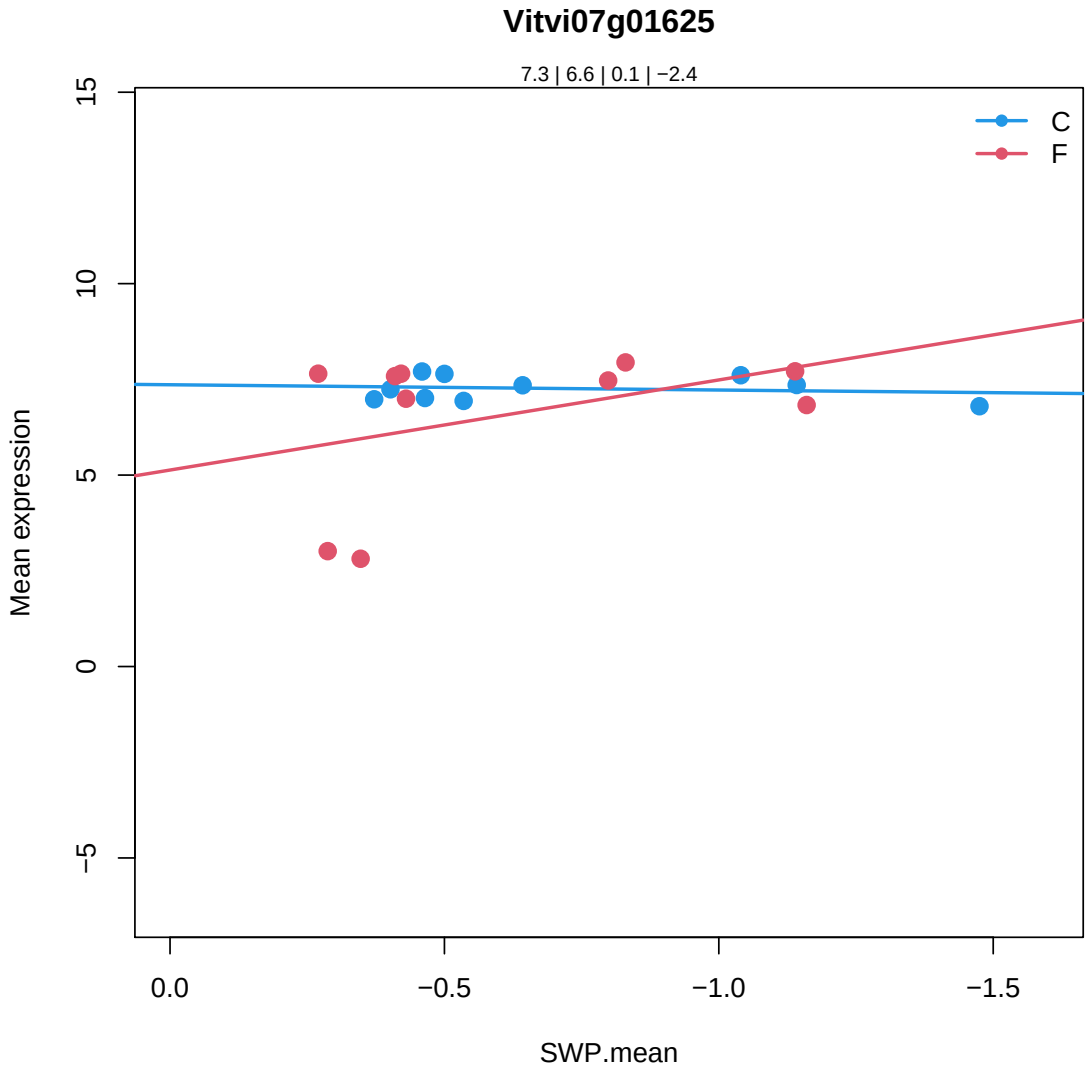
7.6.473 Vitvi07g01625: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01625
        35.2
        not assigned.unknown
        DUF1230 family protein (DUF1230) |
        Chr5:26877667-26879465 REVERSE LENGTH=327 |
        201606
```

Coefficients for Vitvi07g01625.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.262097	5.444524e-15	***	9.375825e-15	***
SlopeC	0.1377329	0.8970951		0.9815383	
MeanF-MeanC	-0.6966094	0.2066727		0.5512875	
SlopeF-SlopeC	-2.491219	0.1263736		0.9999488	



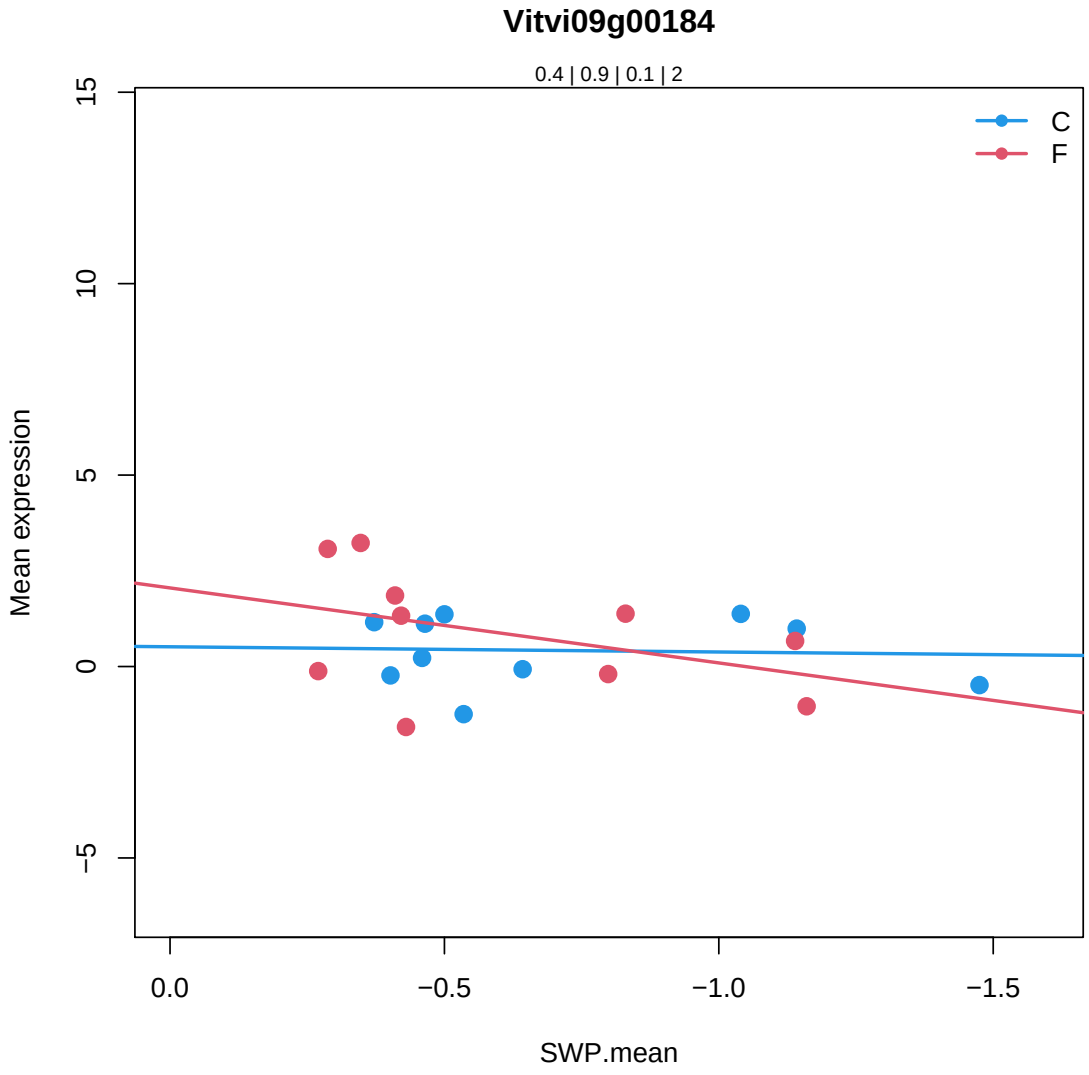
7.6.474 Vitvi09g00184: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00184
        30.2.18
        signalling.receptor kinases.extensin
        Protein kinase superfamily protein |
        Chr5:23010801-23015559 REVERSE LENGTH=1113 |
        201606
```

Coefficients for Vitvi09g00184.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4195451	0.2609339		0.2663154	
SlopeC	0.1359552	0.8942681		0.980859	
MeanF-MeanC	0.4398767	0.4014414		0.7457367	
SlopeF-SlopeC	1.822721	0.2389029		0.9999488	



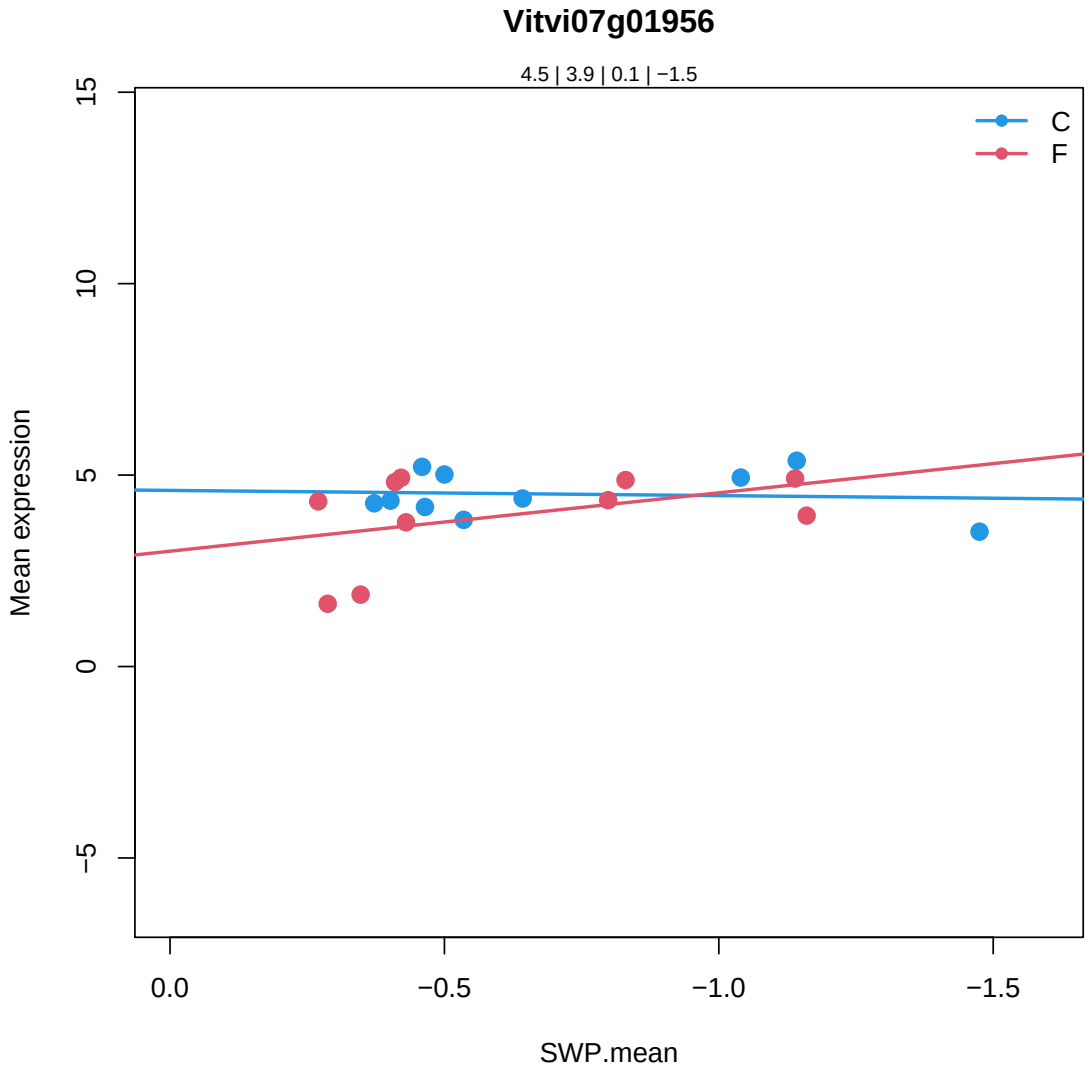
7.6.475 Vitvi07g01956: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01956
        35.2
        not assigned.unknown
        polyketide cyclase/dehydrase/lipid transporter |
        Chr5:2841536-2845335 REVERSE LENGTH=719 |
        201606
```

Coefficients for Vitvi07g01956.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.50395	9.037011e-14	***	1.391897e-13	***
SlopeC	0.135755	0.8581263		0.9733541	
MeanF-MeanC	-0.5632006	0.1543163		0.4738292	
SlopeF-SlopeC	-1.660808	0.1515396		0.9999488	



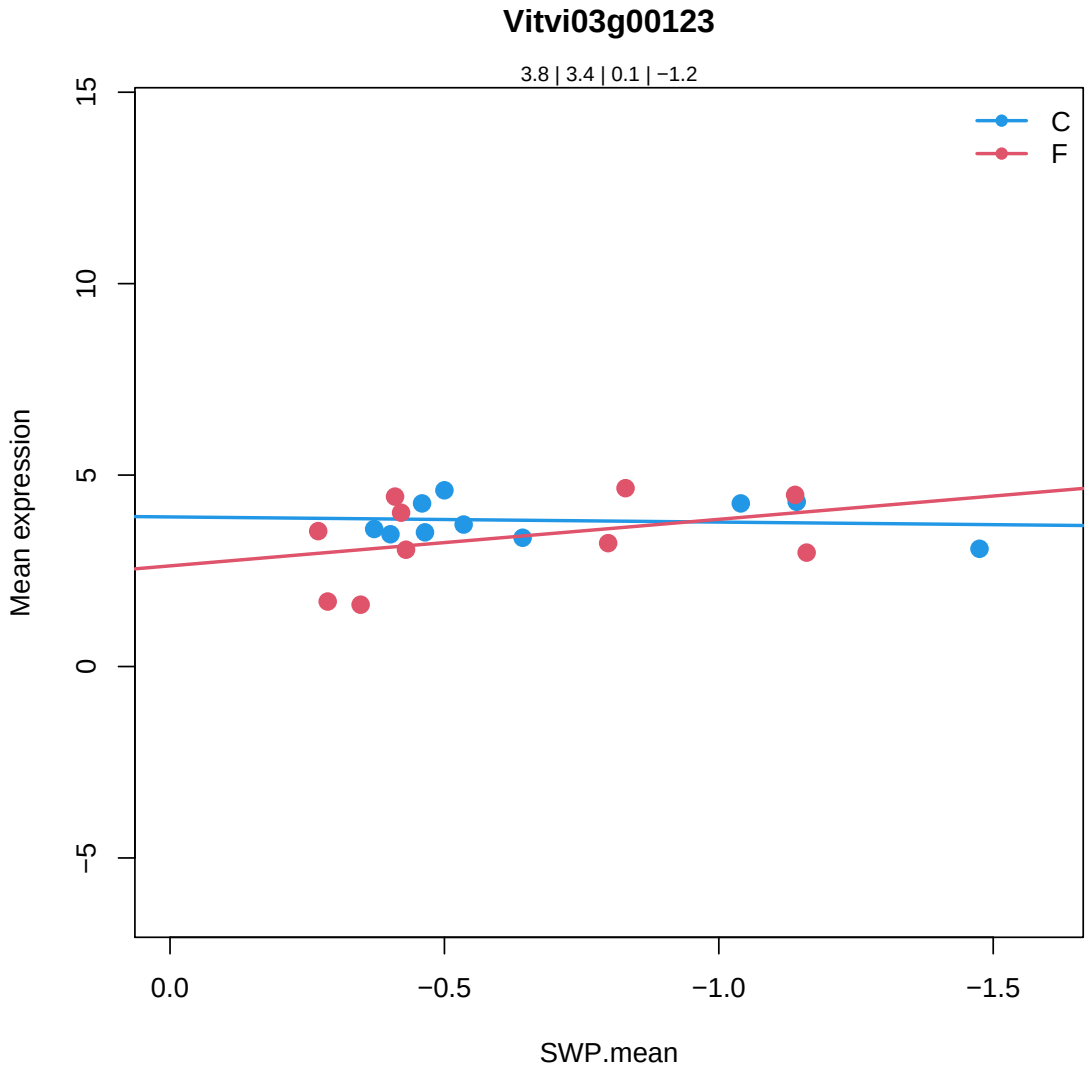
7.6.476 Vitvi03g00123: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00123
        20.1.7.5
        stress.biotic.PR-proteins.PR5 (thaumatin-like proteins)
        Pathogenesis-related thaumatin superfamily protein |
        Chr4:18069856-18071227 REVERSE LENGTH=281 |
        201606
```

Coefficients for Vitvi03g00123.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.812063	3.098021e-13	***	4.600997e-13	***
SlopeC	0.1343119	0.8443029		0.970108	
MeanF-MeanC	-0.4430073	0.2108352		0.5559169	
SlopeF-SlopeC	-1.350289	0.1934045		0.9999488	



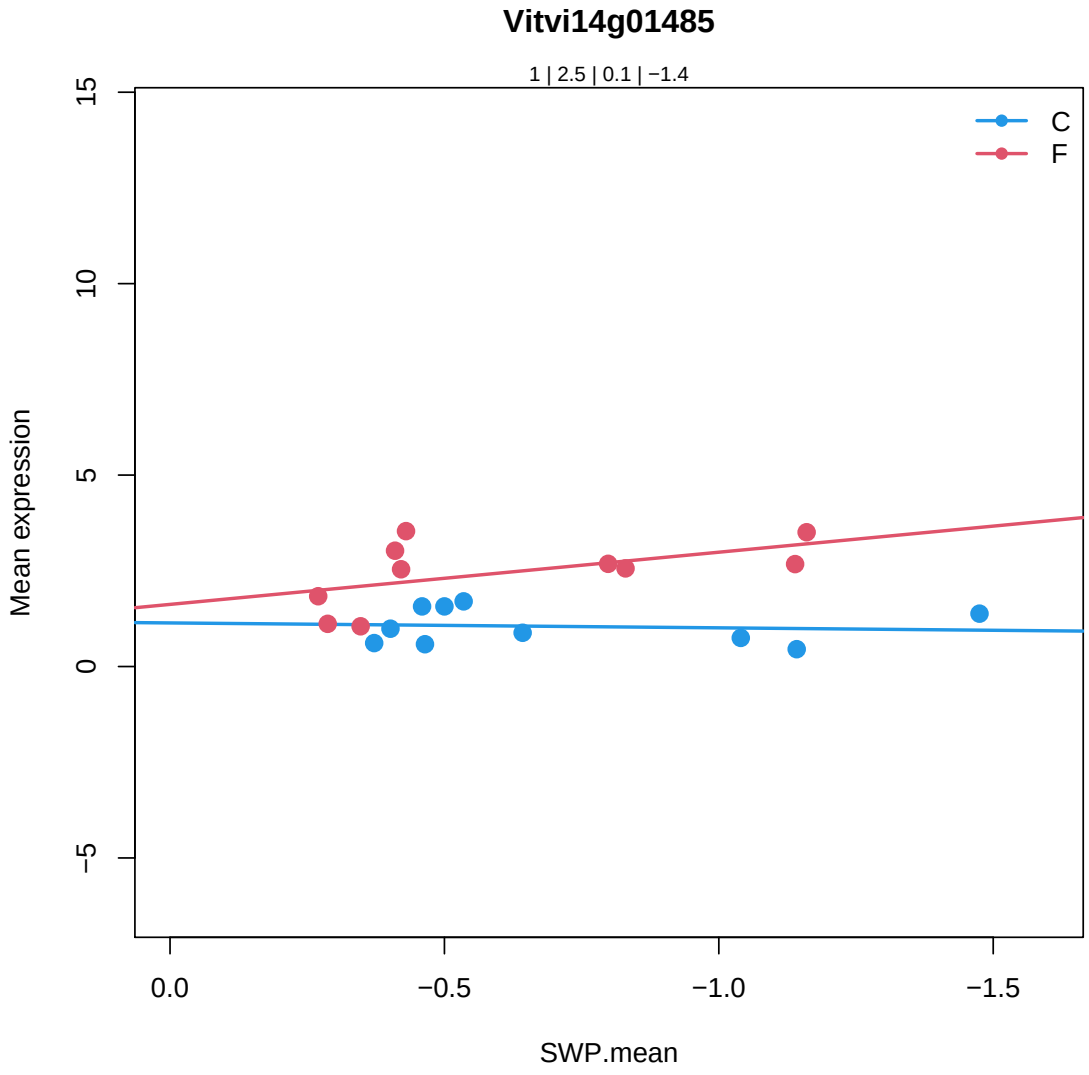
7.6.477 Vitvi14g01485: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01485
        17.1.3
        hormone metabolism.abscisic acid.induced-regulated-responsive-activate
        GRAM domain family protein |
        Chr5:4207081-4208079 FORWARD LENGTH=272 |
        201606
```

Coefficients for Vitvi14g01485.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.048431	2.305848e-05	***	2.582346e-05	***
SlopeC	0.1278416	0.8158969		0.9600047	
MeanF-MeanC	1.404394	4.521096e-05	***	0.0009067177	***
SlopeF-SlopeC	-1.490661	0.07865823	.	0.9999488	



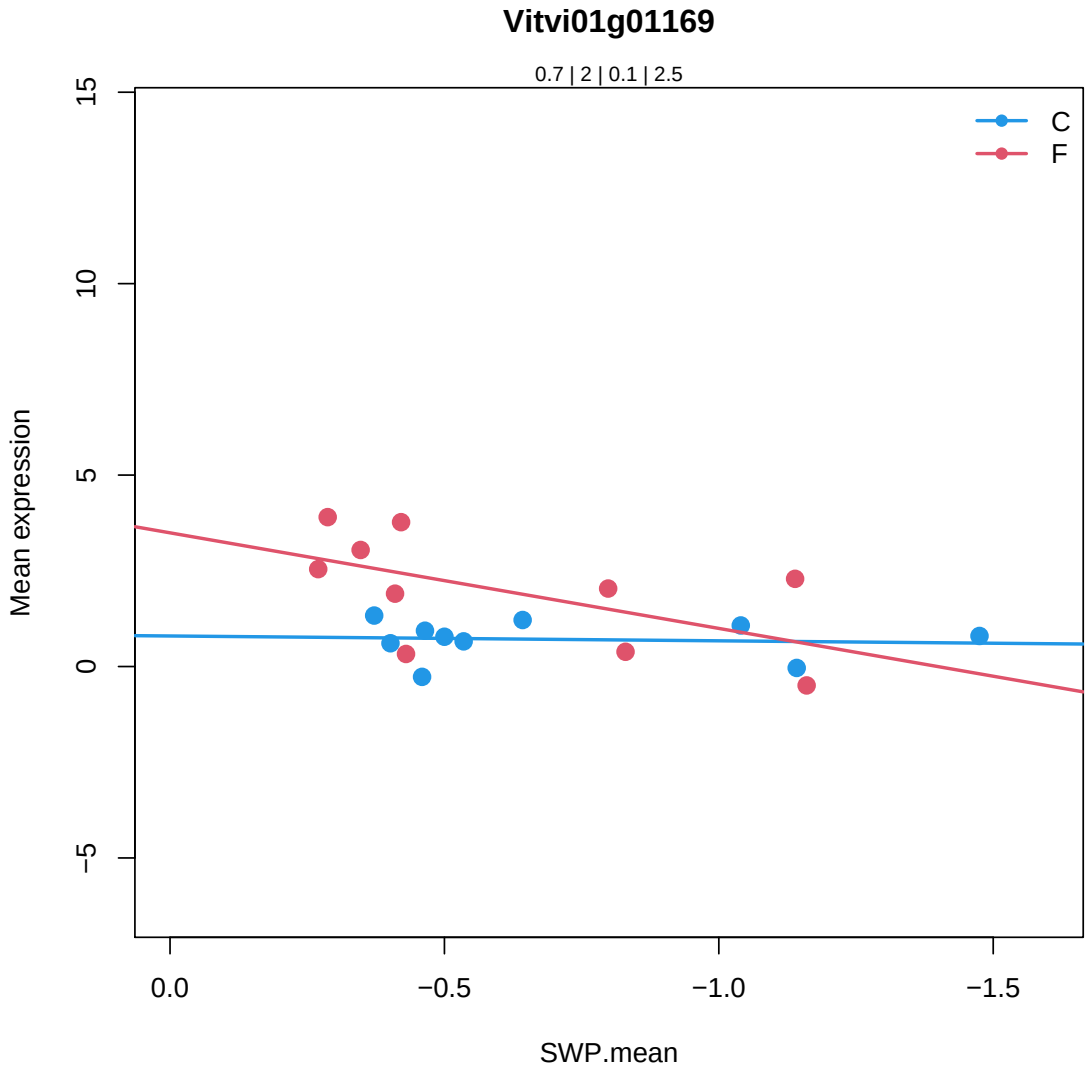
7.6.478 Vitvi01g01169: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01169
        28.2
        DNA.repair
        DNA glycosylase superfamily protein |
        Chr5:18024461-18025893 REVERSE LENGTH=353 |
        201606
```

Coefficients for Vitvi01g01169.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.7085306	0.01947902	*	0.02048428	*
SlopeC	0.1261609	0.8731049		0.9762394	
MeanF-MeanC	1.262078	0.004416771	**	0.04135161	*
SlopeF-SlopeC	2.370177	0.05383022	.	0.9999488	



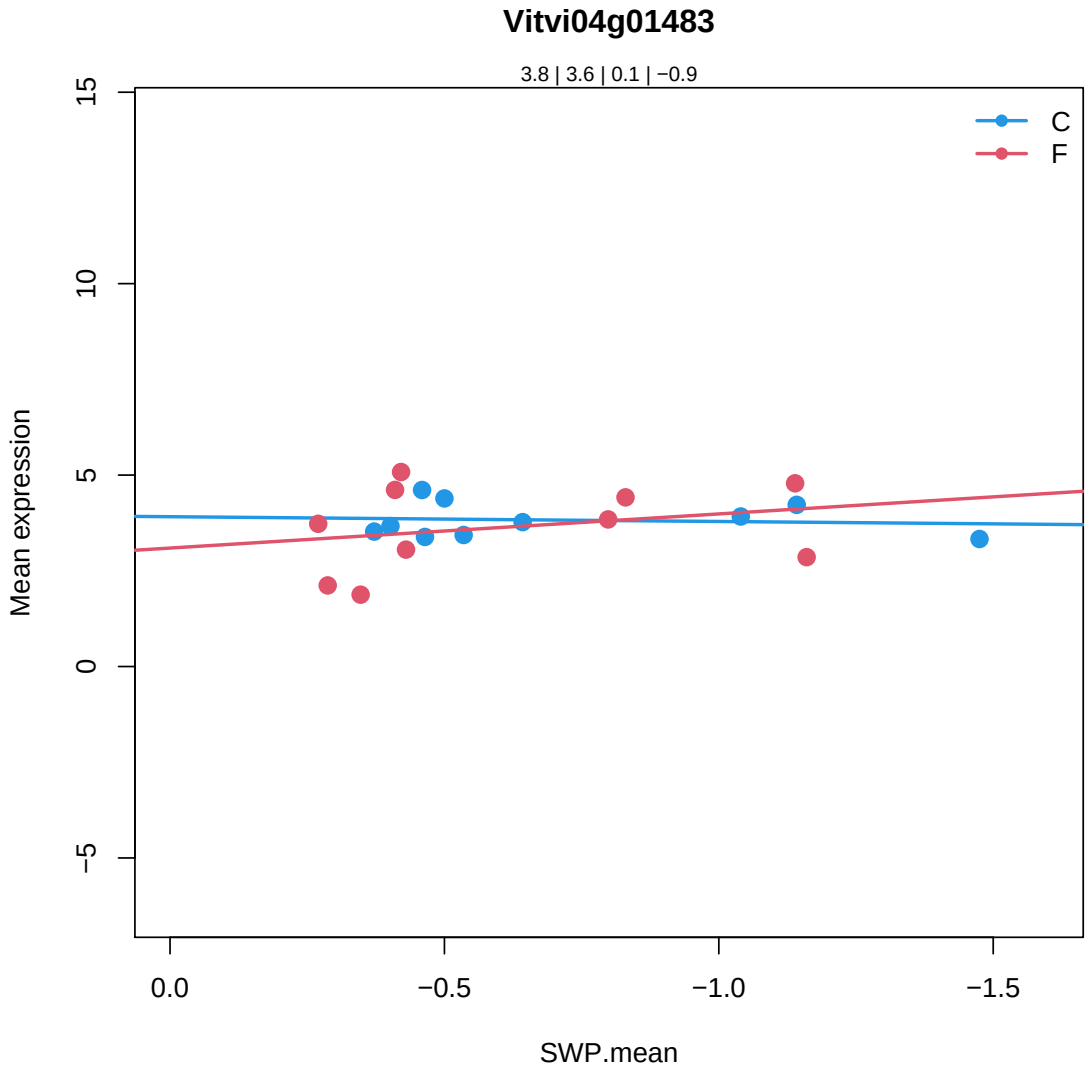
7.6.479 Vitvi04g01483: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01483
        17.4.2
        hormone metabolism.cytokinin.signal transduction
        histidine kinase 1 |
        Chr2:7743133-7748013 REVERSE LENGTH=1207 |
        201606
```

Coefficients for Vitvi04g01483.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.825269	6.027353e-13	***	8.782878e-13	***
SlopeC	0.1245939	0.8606452		0.9738952	
MeanF-MeanC	-0.1884892	0.602384		0.8612137	
SlopeF-SlopeC	-1.016114	0.3411309		0.9999488	



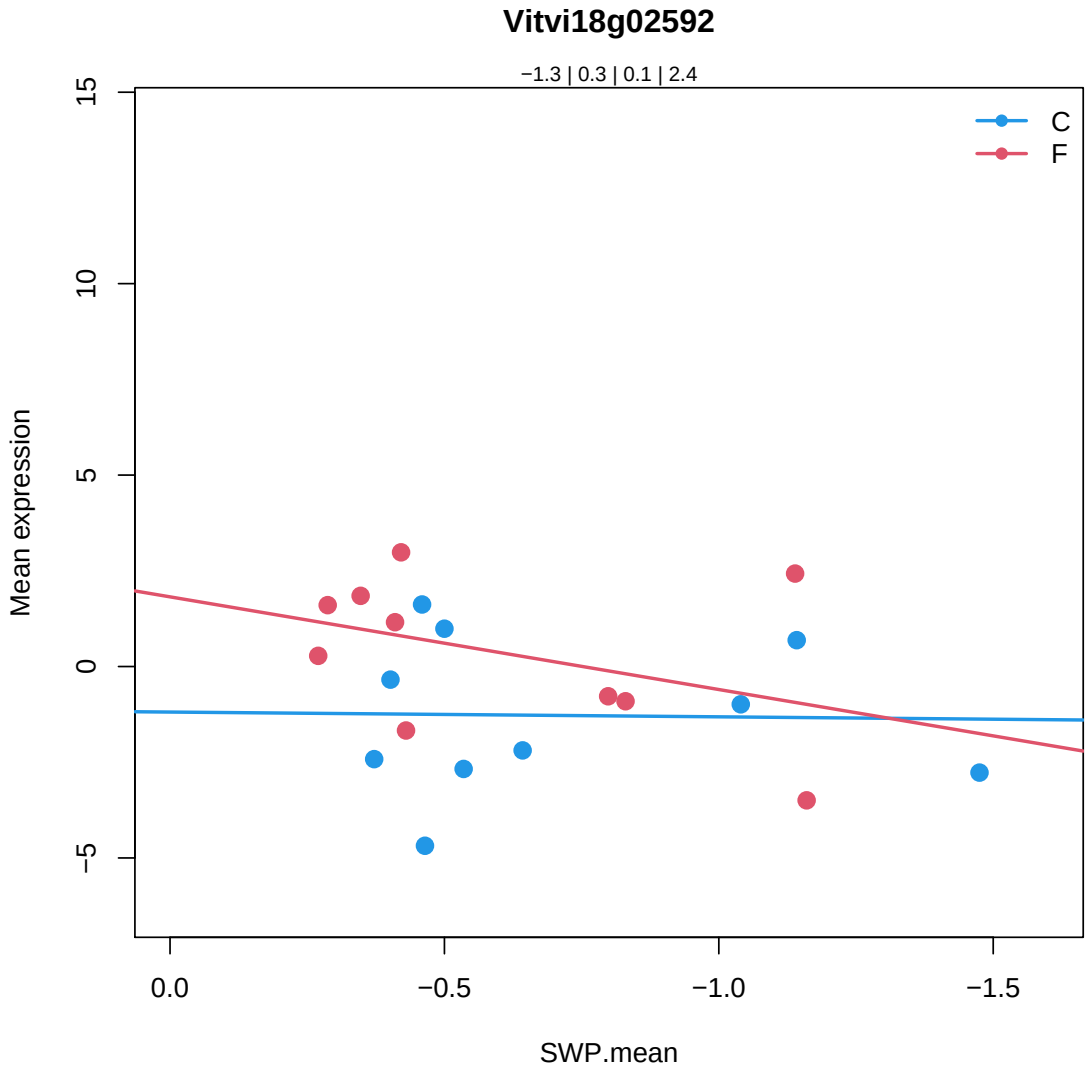
7.6.480 Vitvi18g02592: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02592
        26.12
        misc.peroxidases
        Peroxidase superfamily protein |
        Chr5:1579142-1580819 REVERSE LENGTH=324 |
        201606
```

Coefficients for Vitvi18g02592.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.277313	0.03463876	*	0.03620407	*
SlopeC	0.1244362	0.9377718		0.9891708	
MeanF-MeanC	1.621751	0.05546714	.	0.256018	
SlopeF-SlopeC	2.296027	0.3383703		0.9999488	



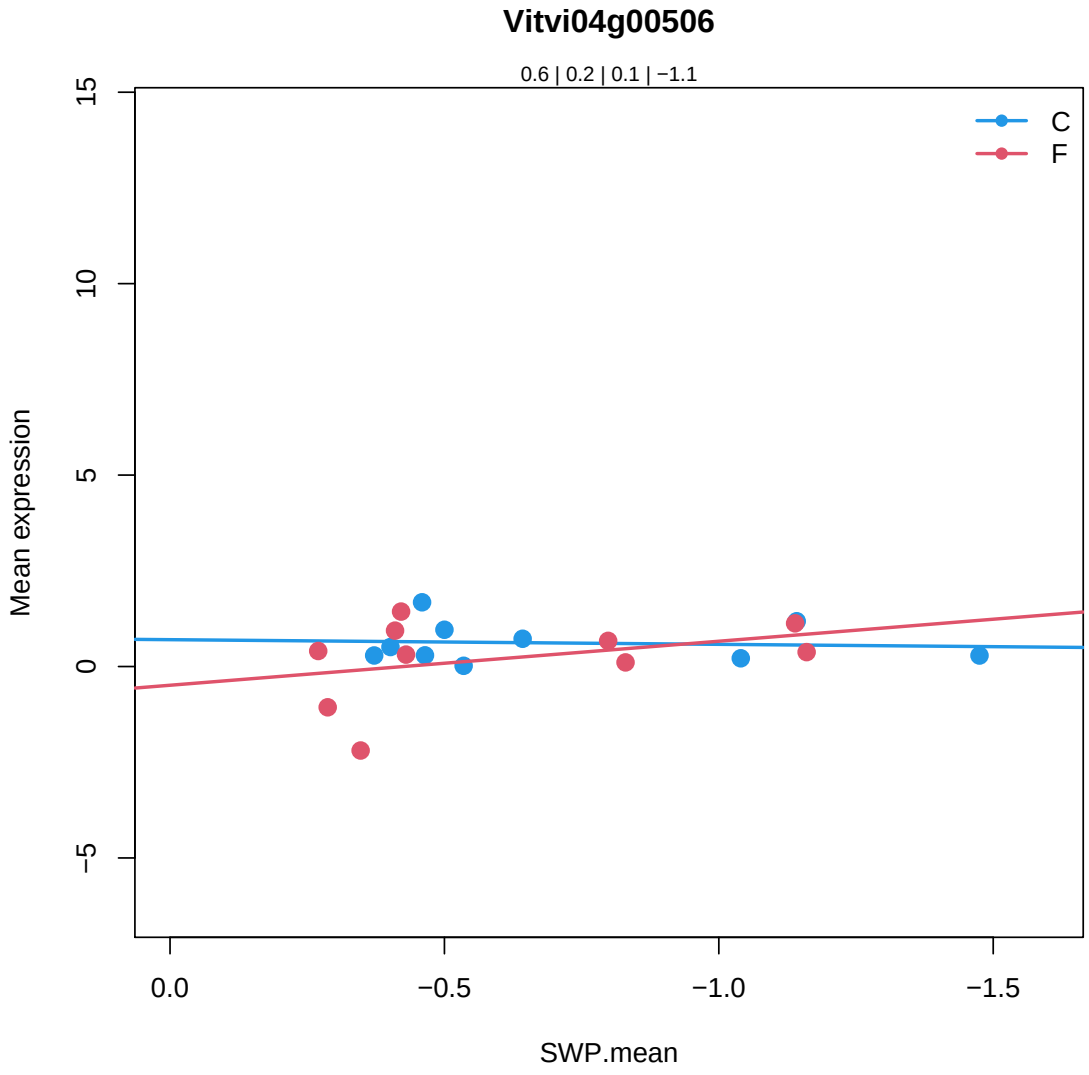
7.6.481 Vitvi04g00506: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00506
        13
        amino acid metabolism
        ACT-like superfamily protein |
        Chr5:8787865-8789530 REVERSE LENGTH=377 |
        201606
```

Coefficients for Vitvi04g00506.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6154715	0.0201124	*	0.02114597	*
SlopeC	0.1217058	0.8600363		0.9737594	
MeanF-MeanC	-0.4044597	0.2561323		0.6167348	
SlopeF-SlopeC	-1.271442	0.2238367		0.9999488	



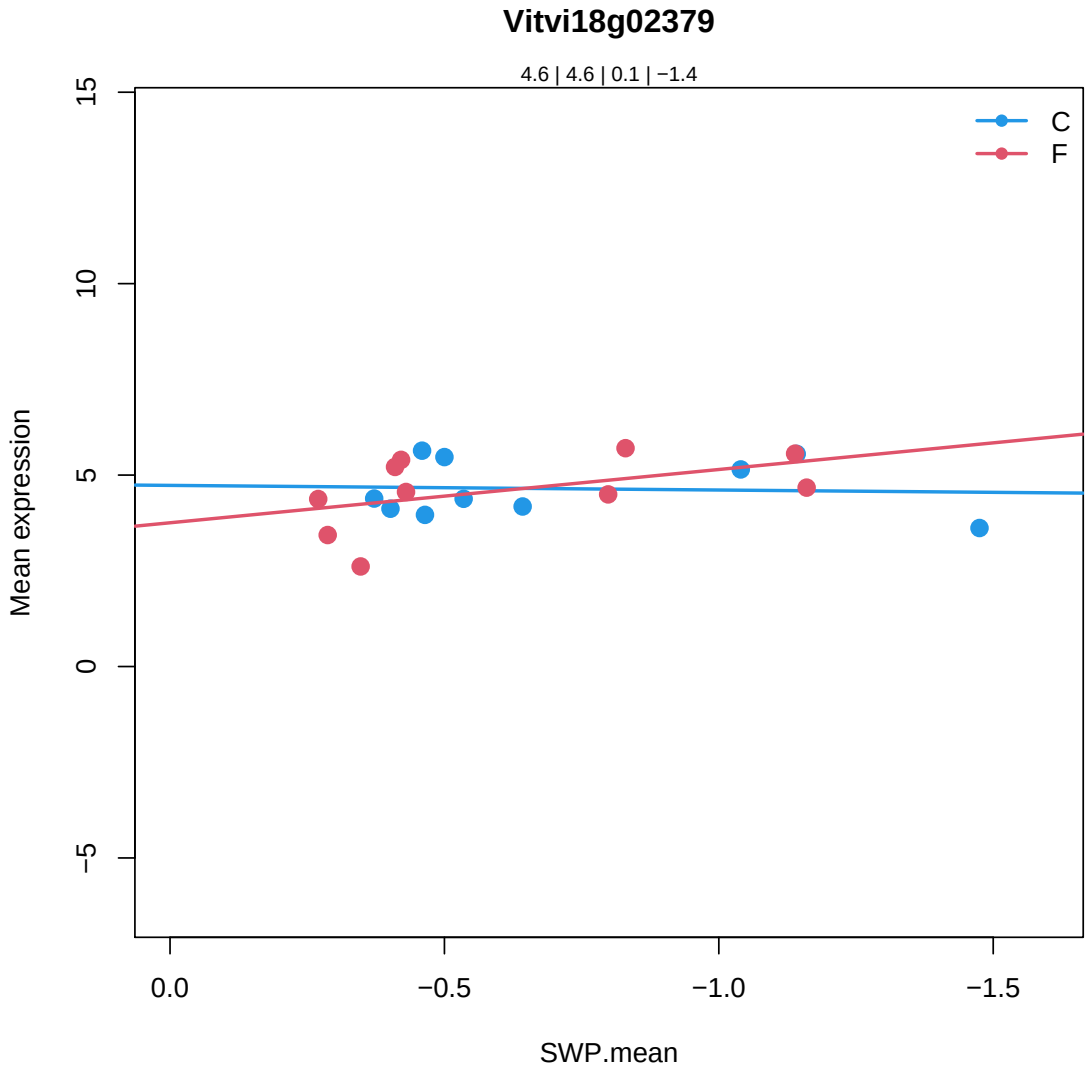
7.6.482 Vitvi18g02379: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02379
        35.2
        not assigned.unknown
        disease resistance protein (TIR-NBS-LRR class) |
        Chr1:26148836-26153374 REVERSE LENGTH=1400 |
        201606
```

Coefficients for Vitvi18g02379.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.645467	5.859704e-15	***	1.004088e-14	***
SlopeC	0.1208399	0.8597351		0.9737381	
MeanF-MeanC	-0.0434184	0.9005779		0.9740454	
SlopeF-SlopeC	-1.512344	0.1471974		0.9999488	



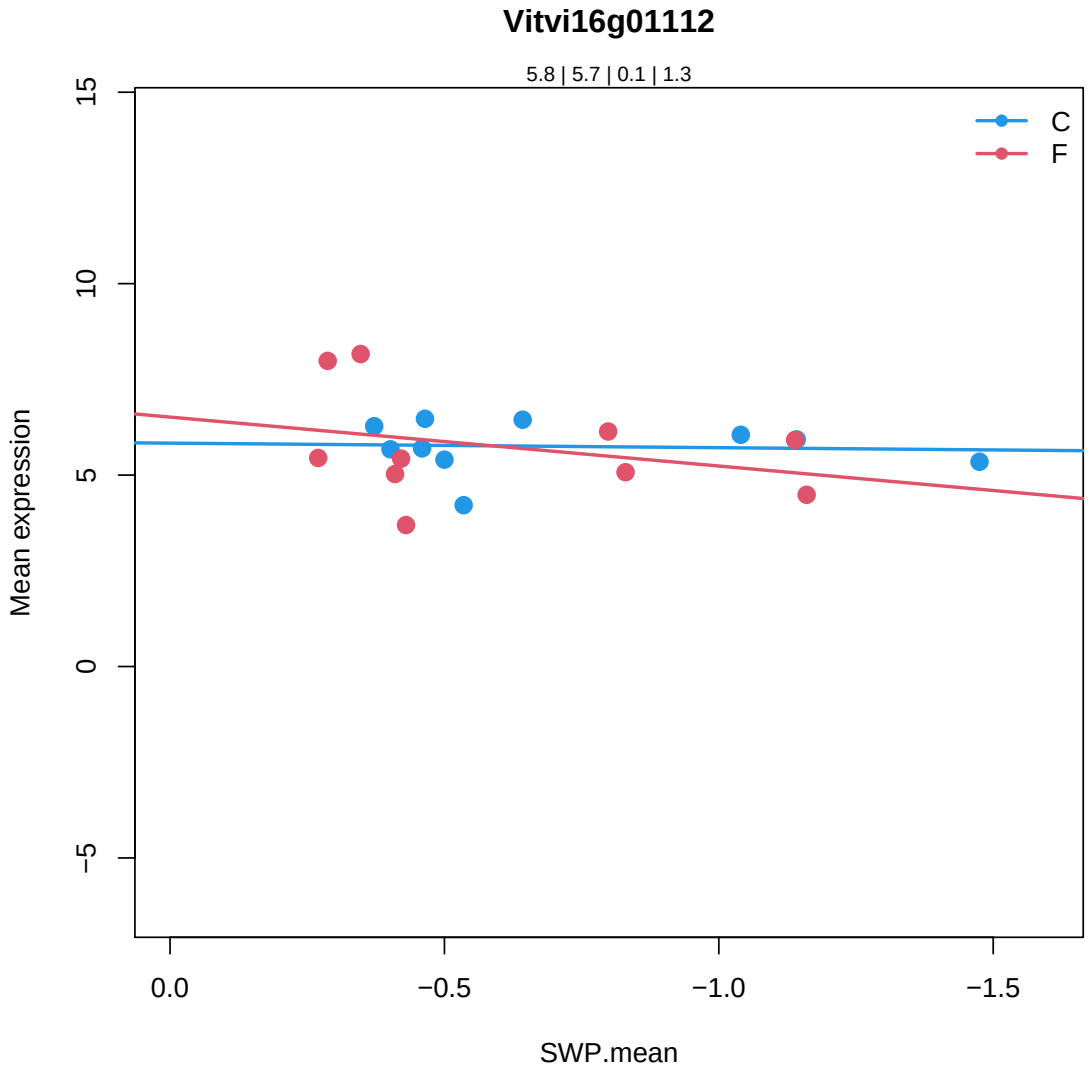
7.6.483 Vitvi16g01112: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01112
        35.2
        not assigned.unknown
        transmembrane protein%2C putative (DUF3464) |
        Chr5:21390943-21391449 REVERSE LENGTH=168 |
        201606
```

Coefficients for Vitvi16g01112.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.750989	1.733671e-14	***	2.832524e-14	***
SlopeC	0.1181199	0.8947694		0.9809086	
MeanF-MeanC	-0.01502747	0.9735858		0.9939369	
SlopeF-SlopeC	1.159989	0.3869464		0.9999488	



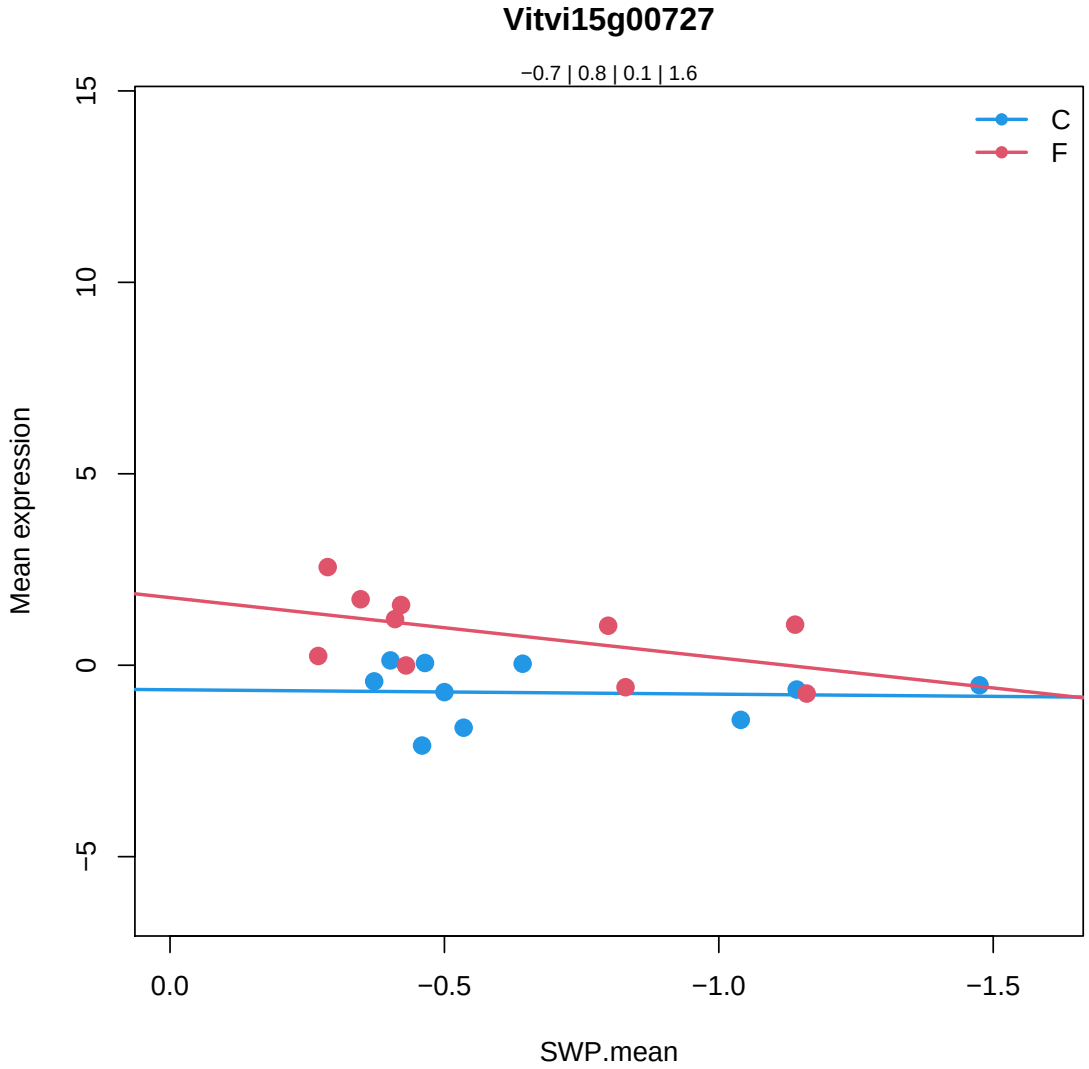
7.6.484 Vitvi15g00727: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g00727
        35.2
        not assigned.unknown
        Unknown Protein
```

Coefficients for Vitvi15g00727.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	−0.7217807	0.009994891	**	0.01058593	*
SlopeC	0.1155023	0.8724035		0.9762394	
MeanF−MeanC	1.529218	0.0003576357	***	0.005333741	**
SlopeF−SlopeC	1.457204	0.1824867		0.9999488	



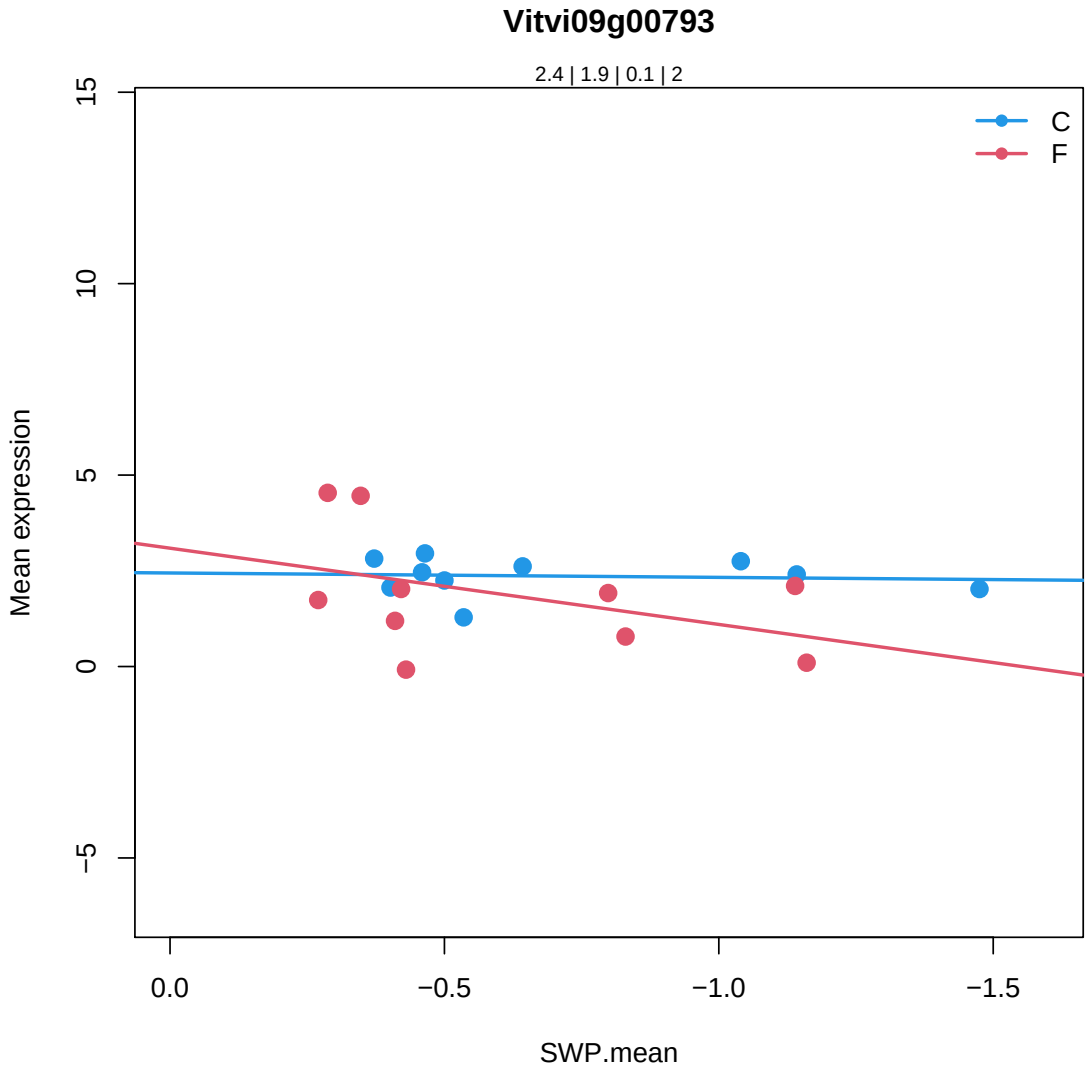
7.6.485 Vitvi09g00793: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00793
        29.5.11.4.3.2
        protein.degradation.ubiquitin.E3.SCF.FBOX
        RNI-like superfamily protein |
        Chr1:30290828-30292231 FORWARD LENGTH=467 |
        201606
```

Coefficients for Vitvi09g00793.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.36215	2.35959e-07	***	2.769298e-07	***
SlopeC	0.114891	0.8979874		0.9819807	
MeanF-MeanC	-0.4849755	0.2933083		0.6599654	
SlopeF-SlopeC	1.876377	0.1689679		0.9999488	



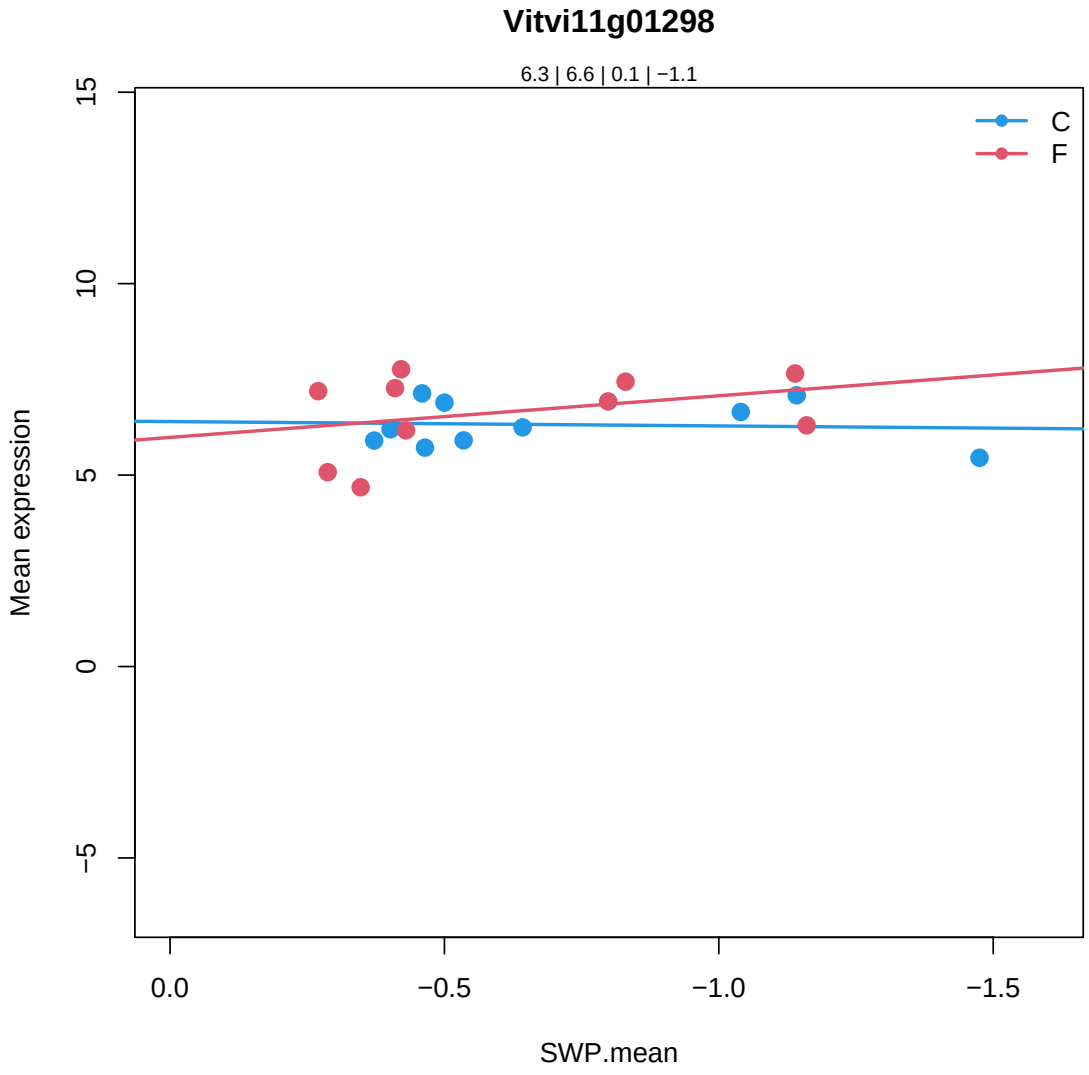
7.6.486 Vitvi11g01298: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g01298
        29.4.1
        protein.postranslational modification.kinase
        CBL-interacting protein kinase 23 |
        Chr1:10655270-10658524 FORWARD LENGTH=482 |
        201606
```

Coefficients for Vitvi11g01298.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.317446	2.110077e-17	***	5.213453e-17	***
SlopeC	0.113399	0.8726109		0.9762394	
MeanF-MeanC	0.3286273	0.365195		0.7220524	
SlopeF-SlopeC	-1.200993	0.2609265		0.9999488	



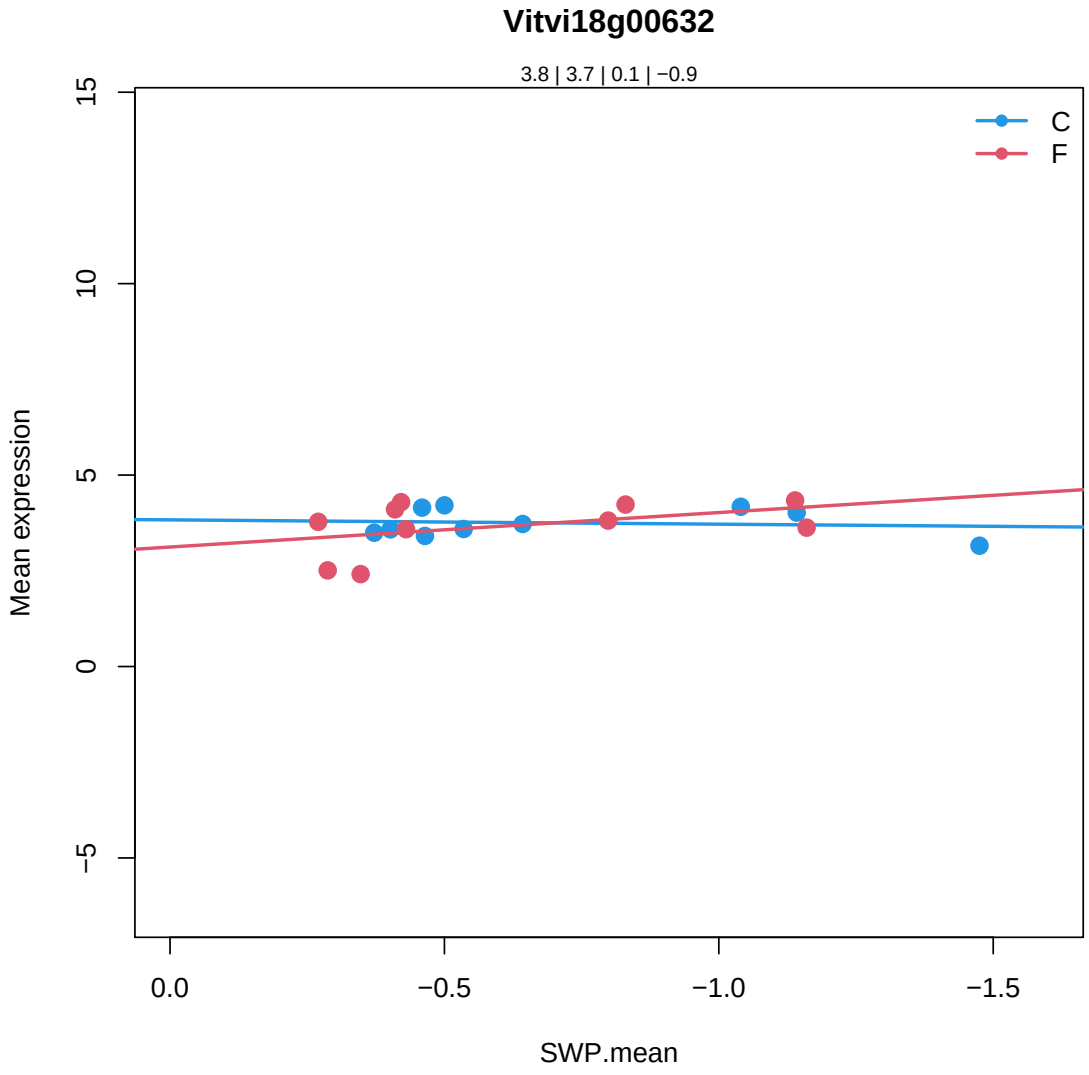
7.6.487 Vitvi18g00632: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00632
        35.2
        not assigned.unknown
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi18g00632.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.75097	2.048209e-16	***	4.226754e-16	***
SlopeC	0.1121977	0.8108666		0.9590407	
MeanF-MeanC	-0.08164954	0.7320815		0.918522	
SlopeF-SlopeC	-1.012375	0.1564081		0.9999488	



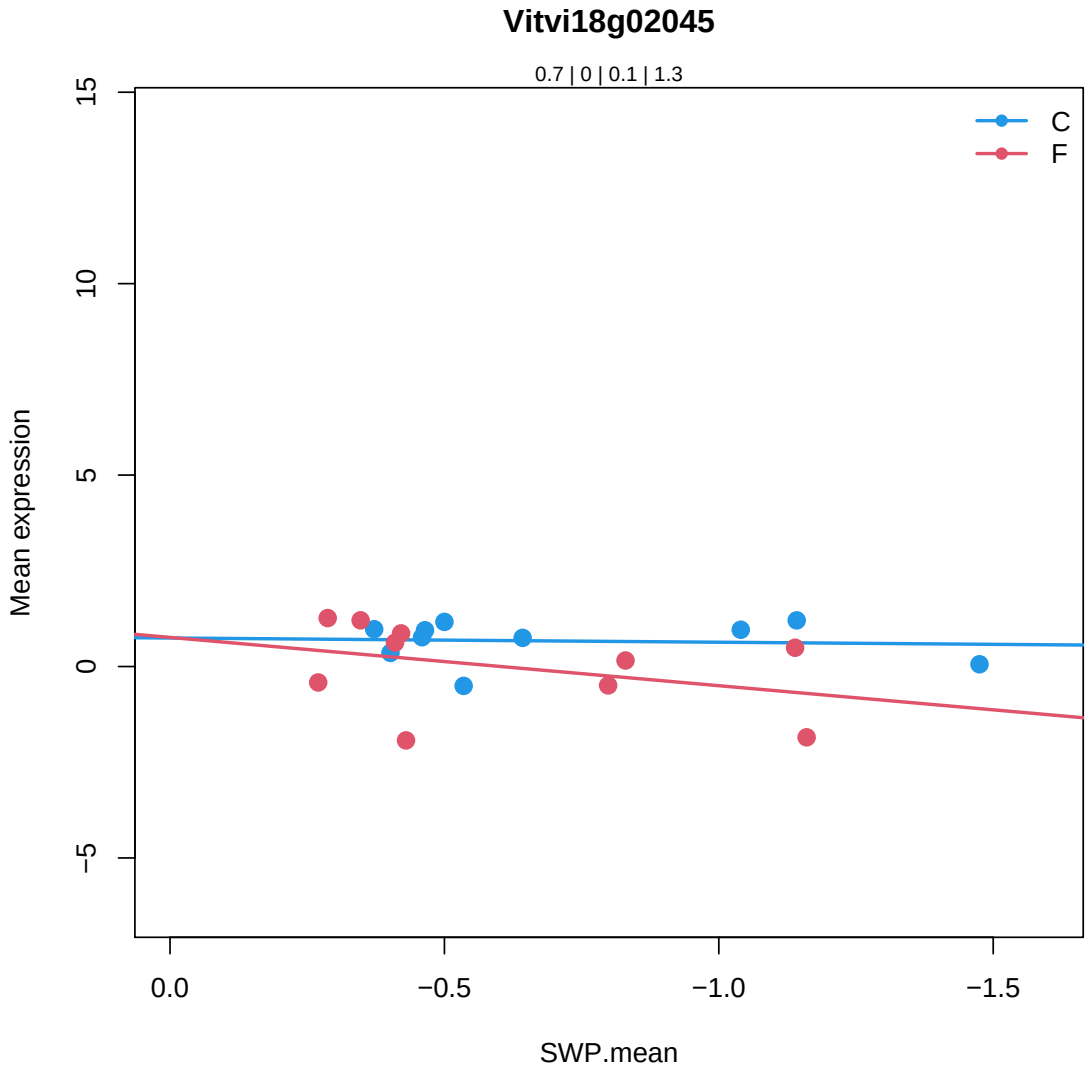
7.6.488 Vitvi18g02045: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02045
        35.2
        not assigned.unknown
        UDP-glucosyl transferase 88A1 |
        Chr3:5619355-5620833 REVERSE LENGTH=462 |
        201606
```

Coefficients for Vitvi18g02045.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6672339	0.01706075	*	0.01797097	*
SlopeC	0.1102208	0.8793991		0.97674	
MeanF-MeanC	-0.6755775	0.07791605	.	0.314902	
SlopeF-SlopeC	1.15047	0.293515		0.9999488	



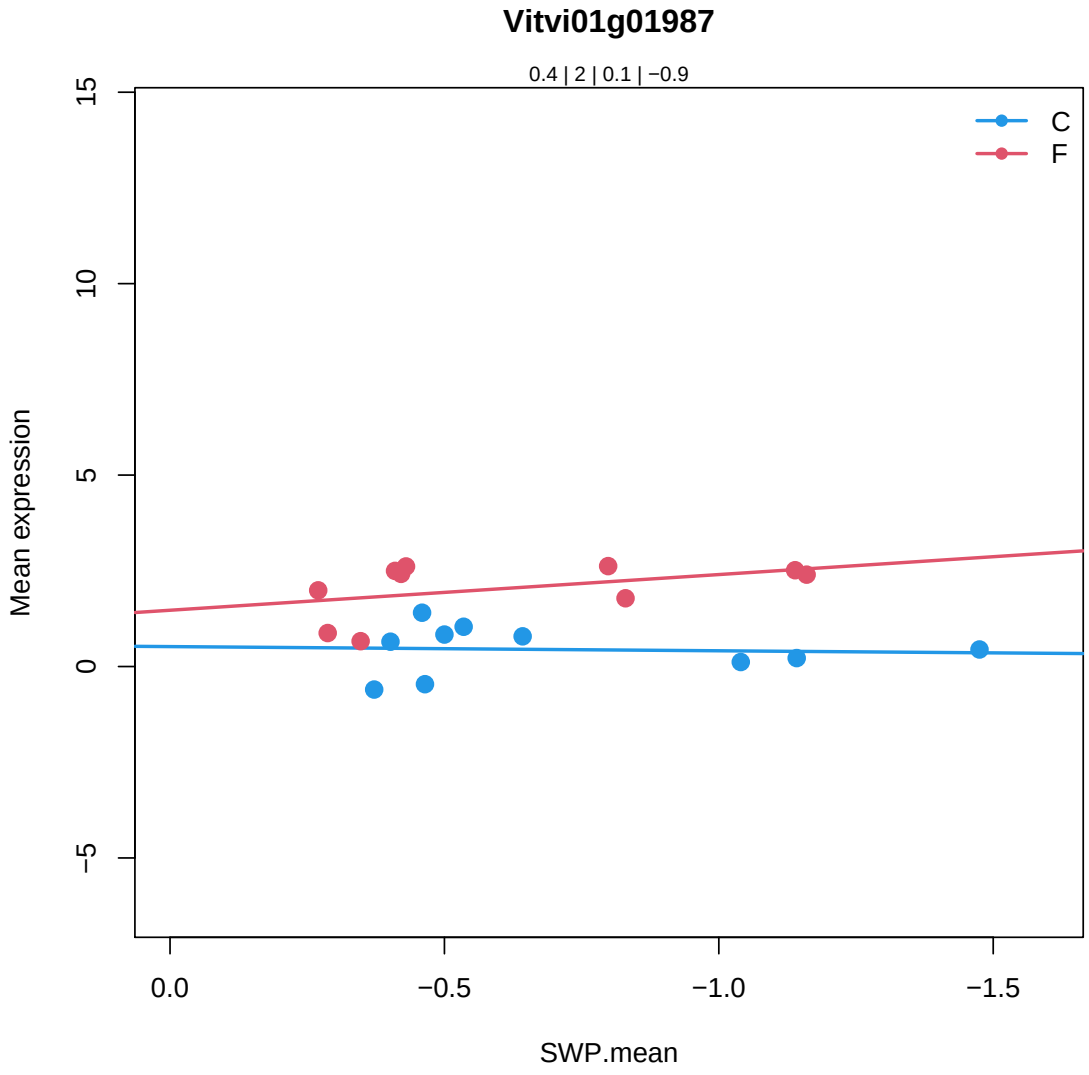
7.6.489 Vitvi01g01987: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01987
        35.1
        not assigned.no ontology
        PLAC8 family protein |
        Chr5:13707084-13707818 FORWARD LENGTH=152 |
        201606
```

Coefficients for Vitvi01g01987.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4432564	0.03919311	*	0.04091653	*
SlopeC	0.1092832	0.8475115		0.9712609	
MeanF-MeanC	1.594287	1.414786e-05	***	0.0003440135	***
SlopeF-SlopeC	-1.041545	0.2260889		0.9999488	



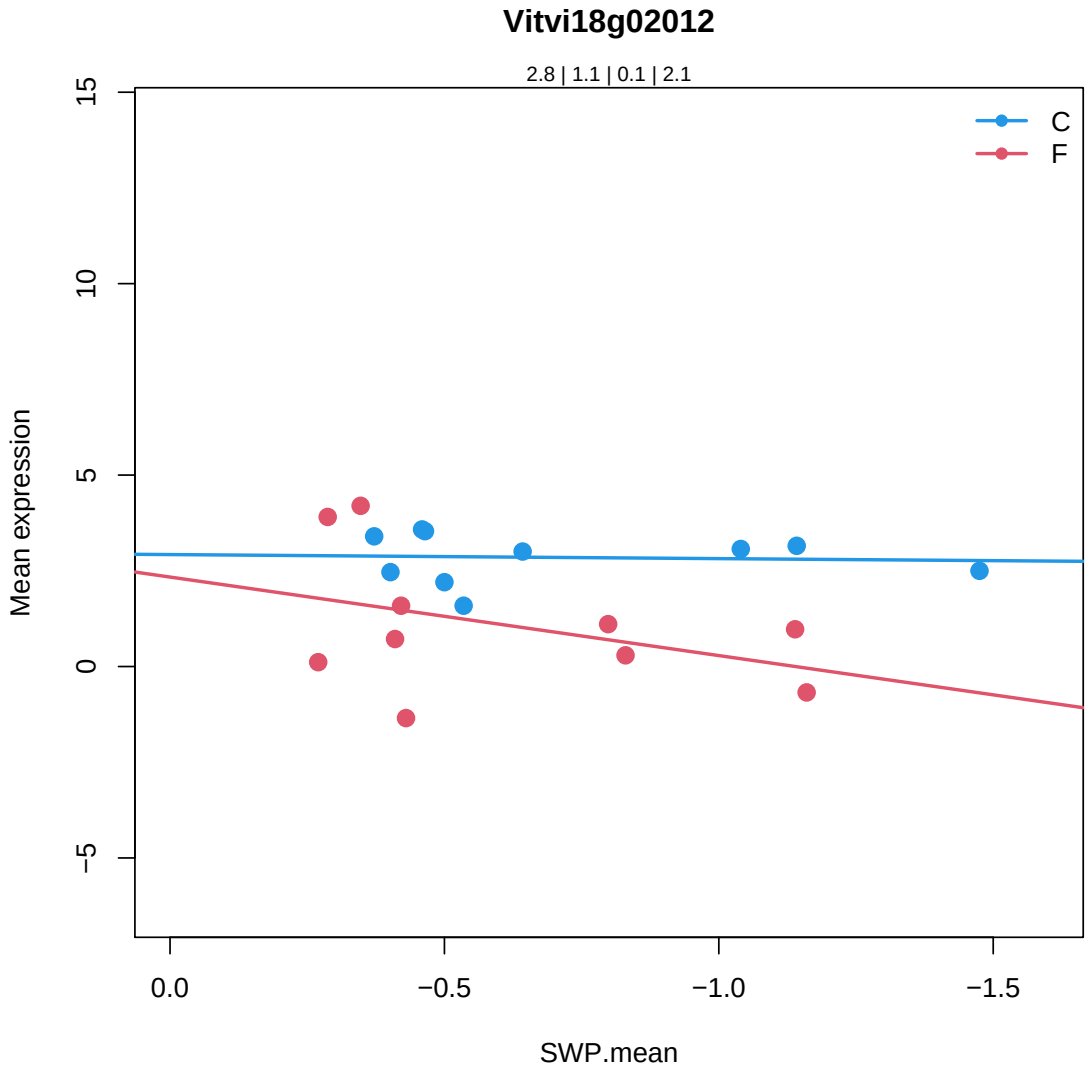
7.6.490 Vitvi18g02012: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02012
        26.2
        misc.UDP glucosyl and glucoronyl transferases
        UDP-glucosyl transferase 88A1 |
        Chr3:5618847-5620833 REVERSE LENGTH=446 |
        201606
```

Coefficients for Vitvi18g02012.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.849471	1.2602e-07	***	1.491301e-07	***
SlopeC	0.1057251	0.9189502		0.9851716	
MeanF-MeanC	-1.76252	0.002789493	**	0.02898258	*
SlopeF-SlopeC	1.945201	0.2167274		0.9999488	



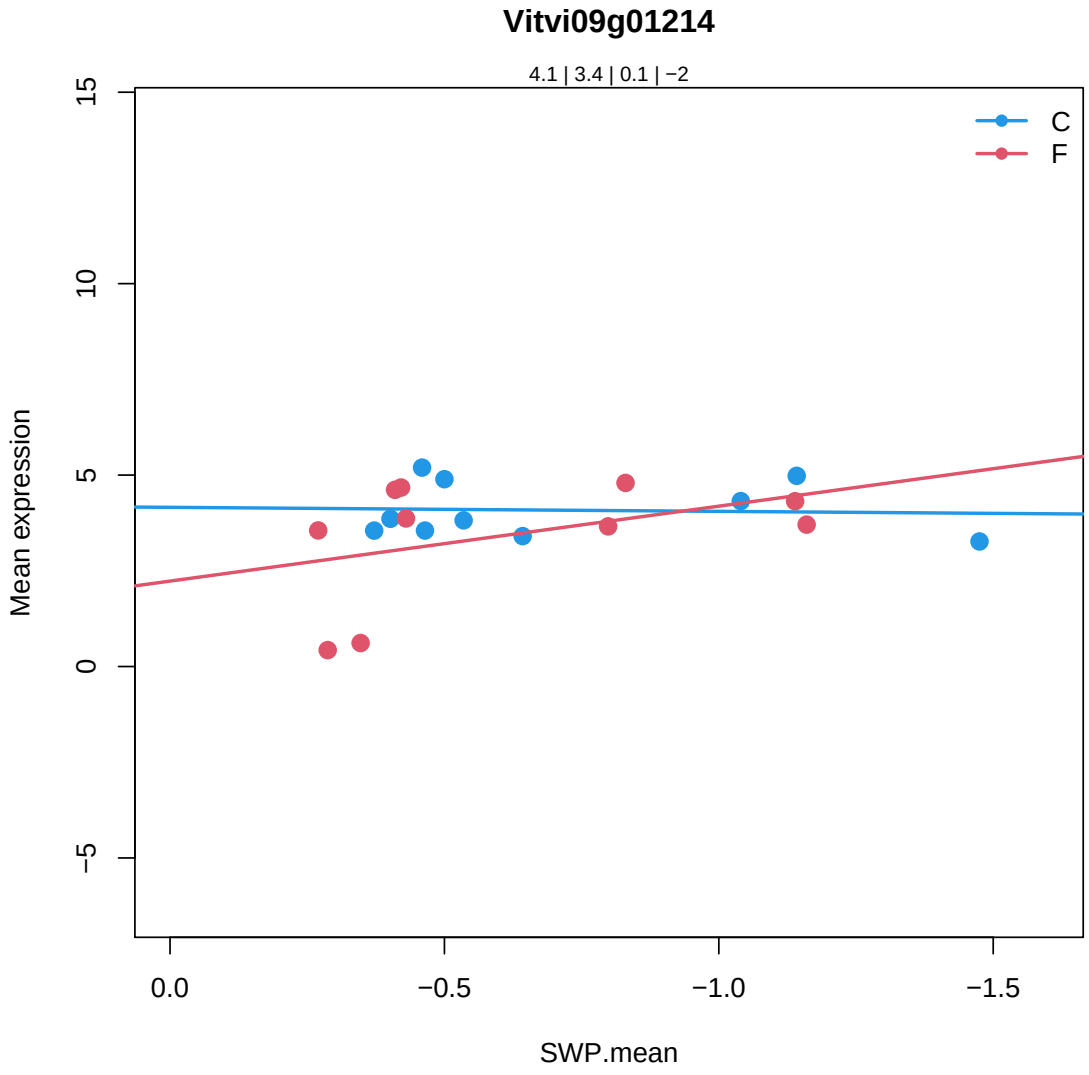
7.6.491 Vitvi09g01214: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g01214
        30.2.12
        signalling.receptor kinases.leucine rich repeat XII
        Leucine-rich repeat protein kinase family protein |
        Chr3:17527611-17530748 FORWARD LENGTH=1010 |
        201606
```

Coefficients for Vitvi09g01214.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.083621	5.230828e-11	***	6.919056e-11	***
SlopeC	0.105182	0.9122911		0.9839968	
MeanF-MeanC	-0.6604063	0.1828124		0.5186478	
SlopeF-SlopeC	-2.062439	0.156524		0.9999488	



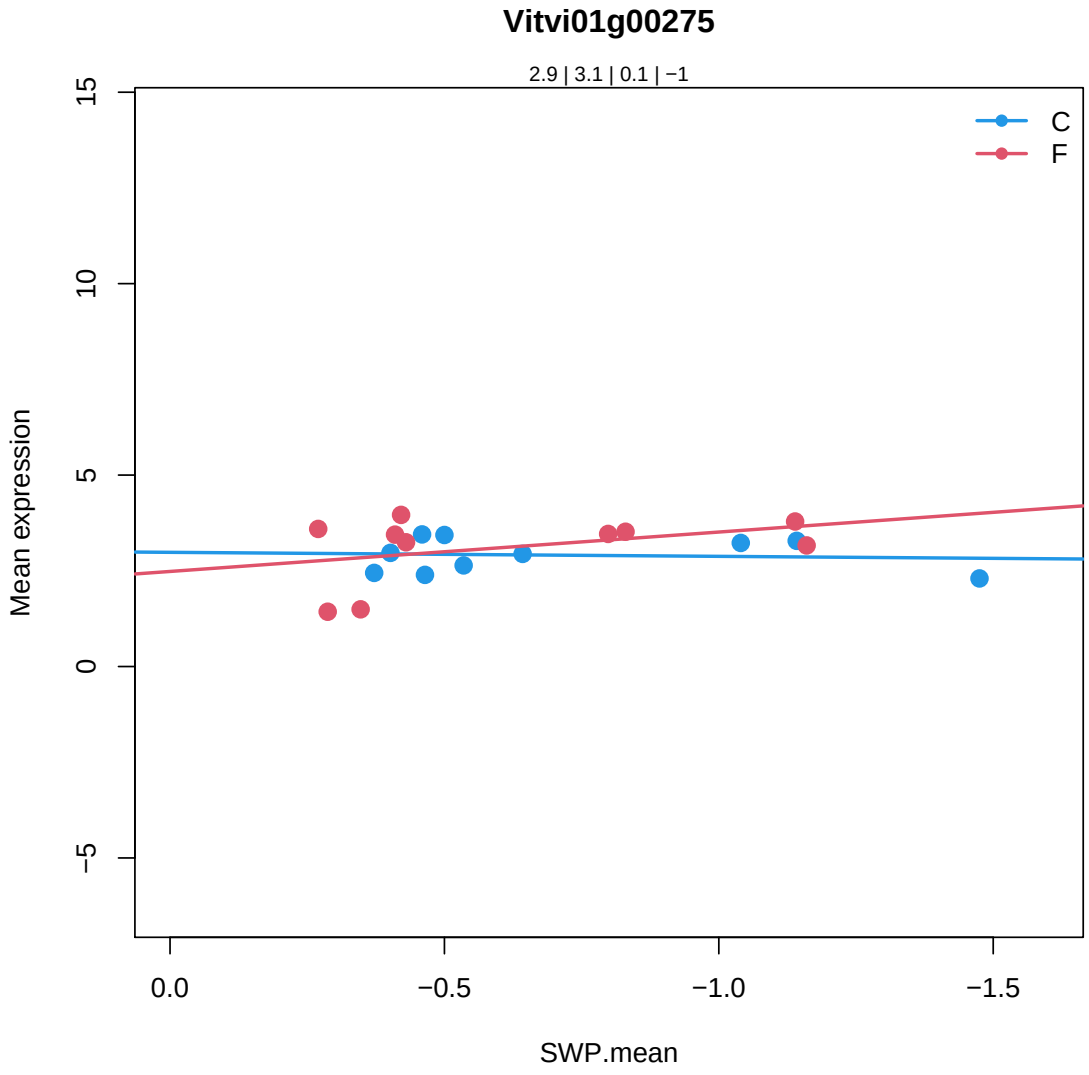
7.6.492 Vitvi01g00275: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00275
        34.13
        transport.peptides and oligopeptides
        Glycolipid transfer protein (GLTP) family protein |
        Chr4:18410172-18410861 FORWARD LENGTH=229 |
        201606
```

Coefficients for Vitvi01g00275.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.908405	2.6981e-12	***	3.78267e-12	***
SlopeC	0.104755	0.857301		0.973332	
MeanF-MeanC	0.201541	0.4983321		0.8050427	
SlopeF-SlopeC	-1.133877	0.1996083		0.9999488	



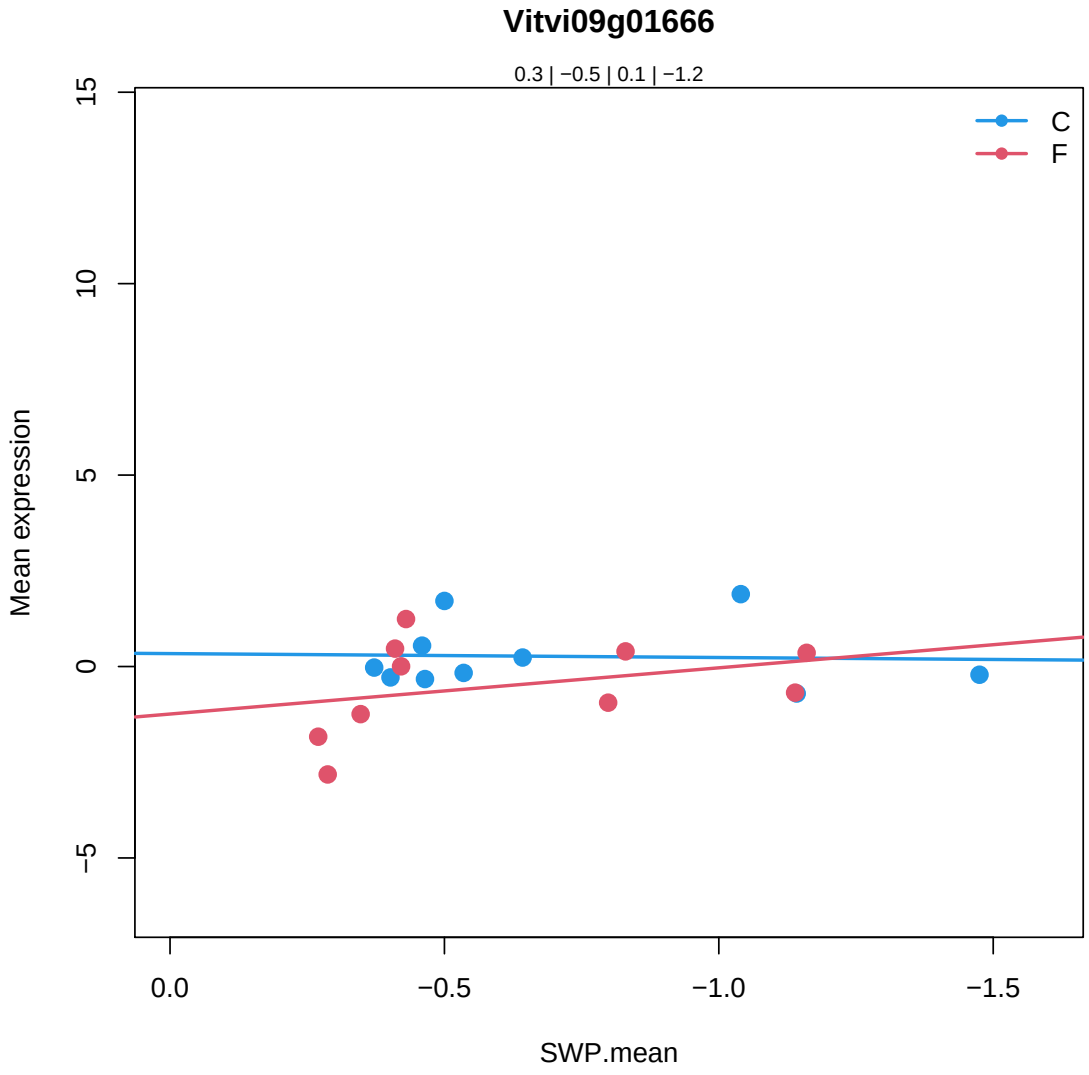
7.6.493 Vitvi09g01666: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g01666
        26.19
        misc.plastocyanin-like
        blue-copper-binding protein |
        Chr5:6826626-6827408 FORWARD LENGTH=196 |
        201606
```

Coefficients for Vitvi09g01666.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.2654889	0.3983376		0.4044944	
SlopeC	0.1020938	0.9062908		0.9834679	
MeanF-MeanC	-0.7713295	0.09087187	.	0.3453176	
SlopeF-SlopeC	-1.309283	0.3161619		0.9999488	



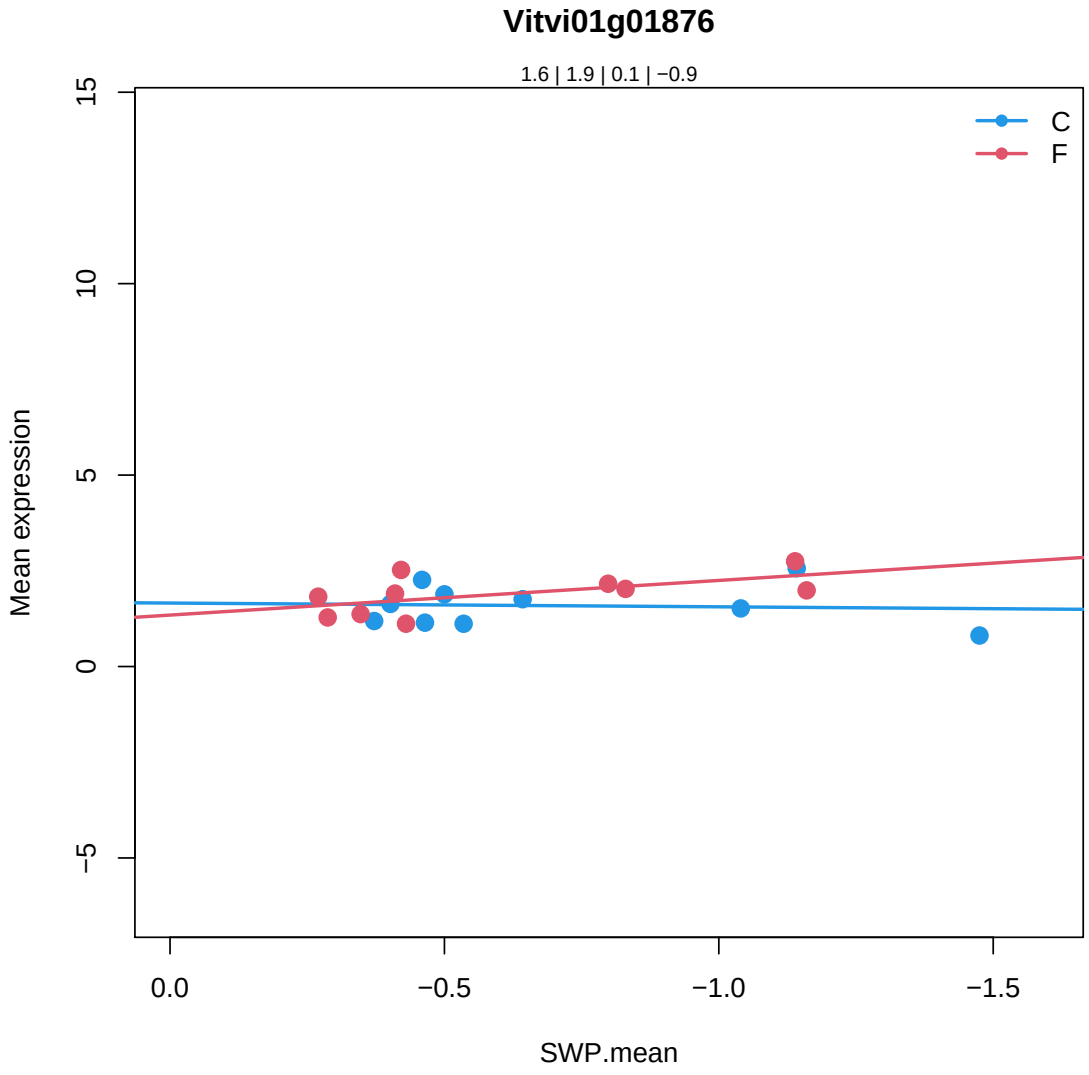
7.6.494 Vitvi01g01876: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01876
        35.2
        not assigned.unknown
        ribonuclease H2 subunit C-like protein |
        Chr2:16468220-16469113 REVERSE LENGTH=162 |
        201606
```

Coefficients for Vitvi01g01876.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.588574	2.22008e-09	***	2.767293e-09	***
SlopeC	0.09819362	0.8295898		0.966584	
MeanF-MeanC	0.3059667	0.1957087		0.5367814	
SlopeF-SlopeC	-1.002598	0.1495859		0.9999488	



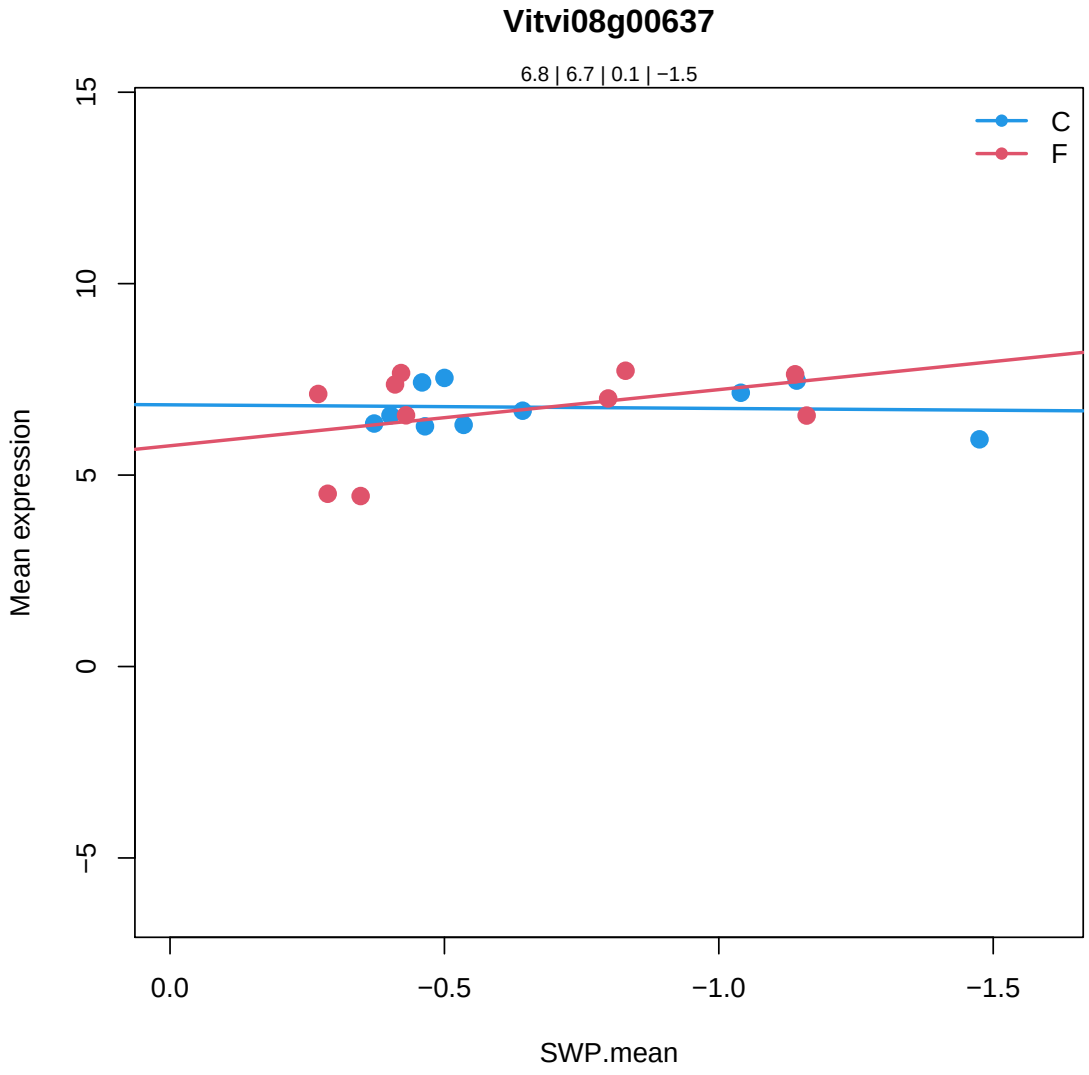
7.6.495 Vitvi08g00637: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g00637
        11.10.2
        lipid metabolism.glycolipid synthesis.DGDG synthase
        UDP-Glycosyltransferase superfamily protein |
        Chr3:3681679-3684495 REVERSE LENGTH=639 |
        201606
```

Coefficients for Vitvi08g00637.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.768097	2.027213e-17	***	5.023374e-17	***
SlopeC	0.09426377	0.9007874		0.9825248	
MeanF-MeanC	-0.1092558	0.7763811		0.9363692	
SlopeF-SlopeC	-1.560492	0.1748942		0.9999488	



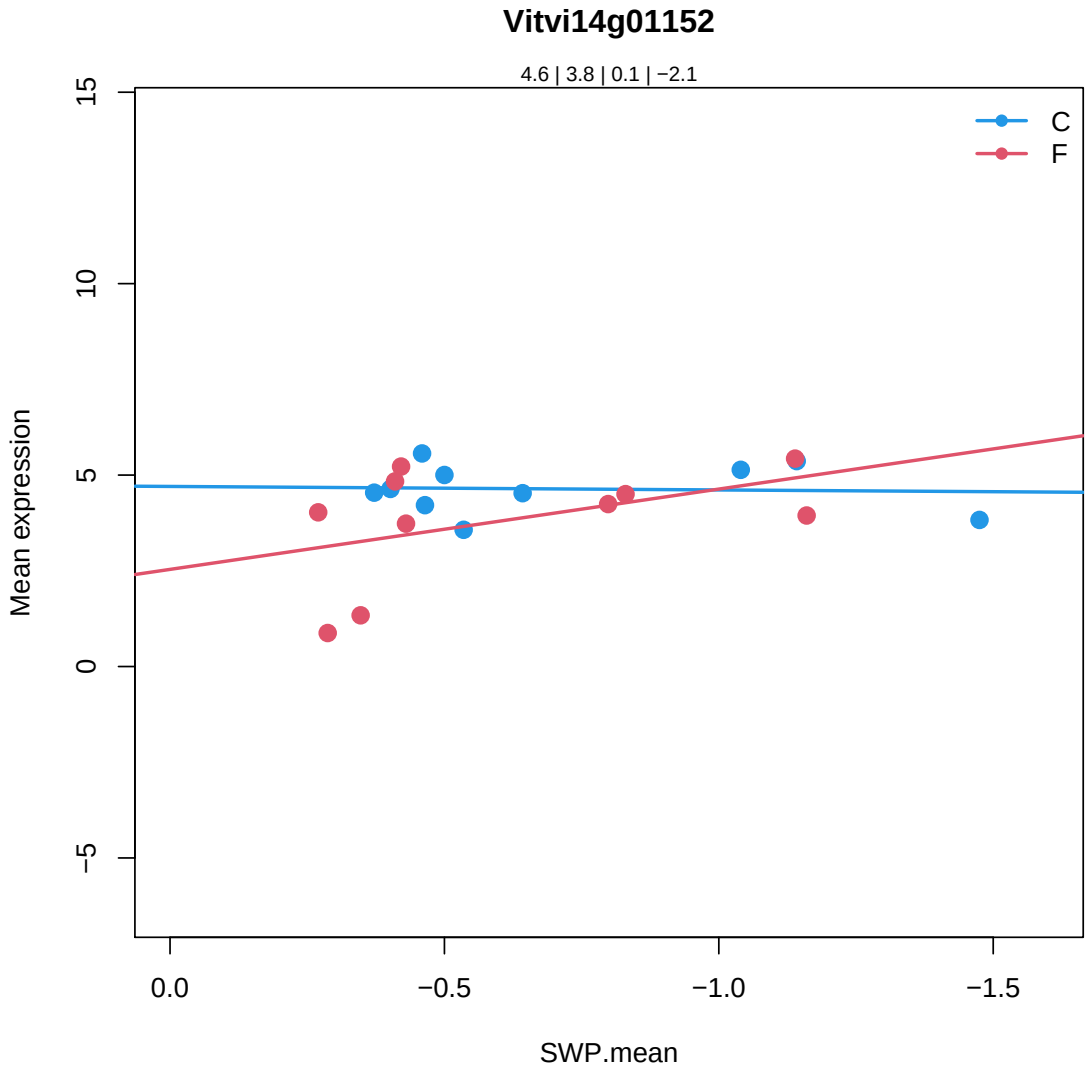
7.6.496 Vitvi14g01152: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01152
        17.3.1.2.6
        hormone metabolism.brassinosteroid.synthesis-degradation.sterols.DWF7
        sterol 1 |
        Chr3:547048-548615 FORWARD LENGTH=281 |
        201606
```

Coefficients for Vitvi14g01152.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.638805	1.22124e-12	***	1.742408e-12	***
SlopeC	0.09131105	0.9184623		0.9851716	
MeanF-MeanC	-0.8241429	0.07977182	.	0.3193704	
SlopeF-SlopeC	-2.189018	0.1097702		0.9999488	



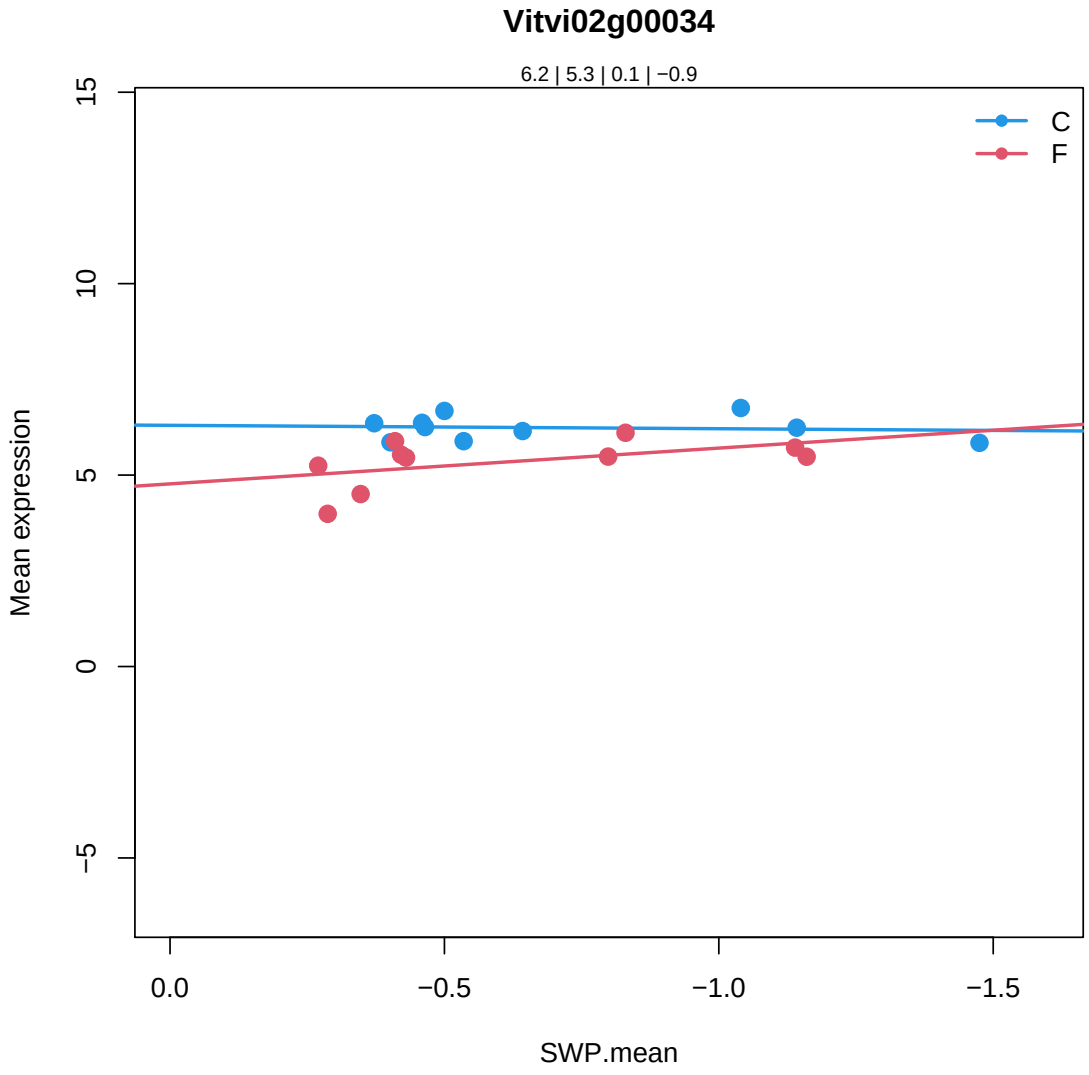
7.6.497 Vitvi02g00034: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00034
        16.1.1.5
        secondary metabolism.isoprenoids.non-mevalonate pathway.MCS
        isoprenoid F |
        Chr1:23738923-23740336 REVERSE LENGTH=231 |
        201606
```

Coefficients for Vitvi02g00034.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.237147	7.011764e-22	***	8.591102e-21	***
SlopeC	0.0887453	0.8355441		0.9686896	
MeanF-MeanC	-0.8976534	0.000405494	***	0.005897268	**
SlopeF-SlopeC	-1.022835	0.1182923		0.9999488	



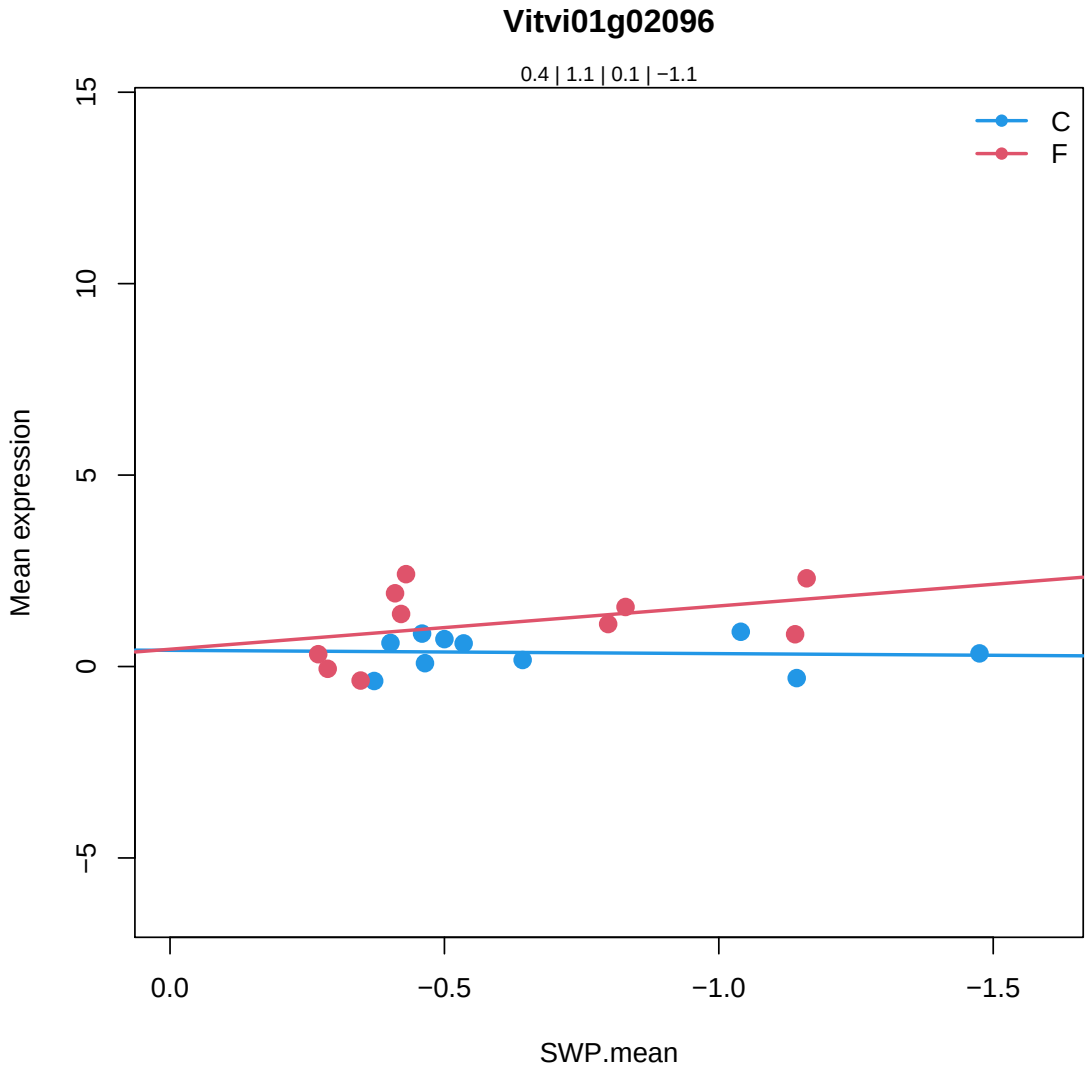
7.6.498 Vitvi01g02096: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g02096
        35.2
        not assigned.unknown
        CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase |
        Chr3:17790571-17790804 REVERSE LENGTH=77 |
        201606
```

Coefficients for Vitvi01g02096.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3621782	0.1096398		0.1132663	
SlopeC	0.086035	0.8880065		0.97938	
MeanF-MeanC	0.7780523	0.01906427	*	0.1219474	
SlopeF-SlopeC	-1.21662	0.1898365		0.9999488	



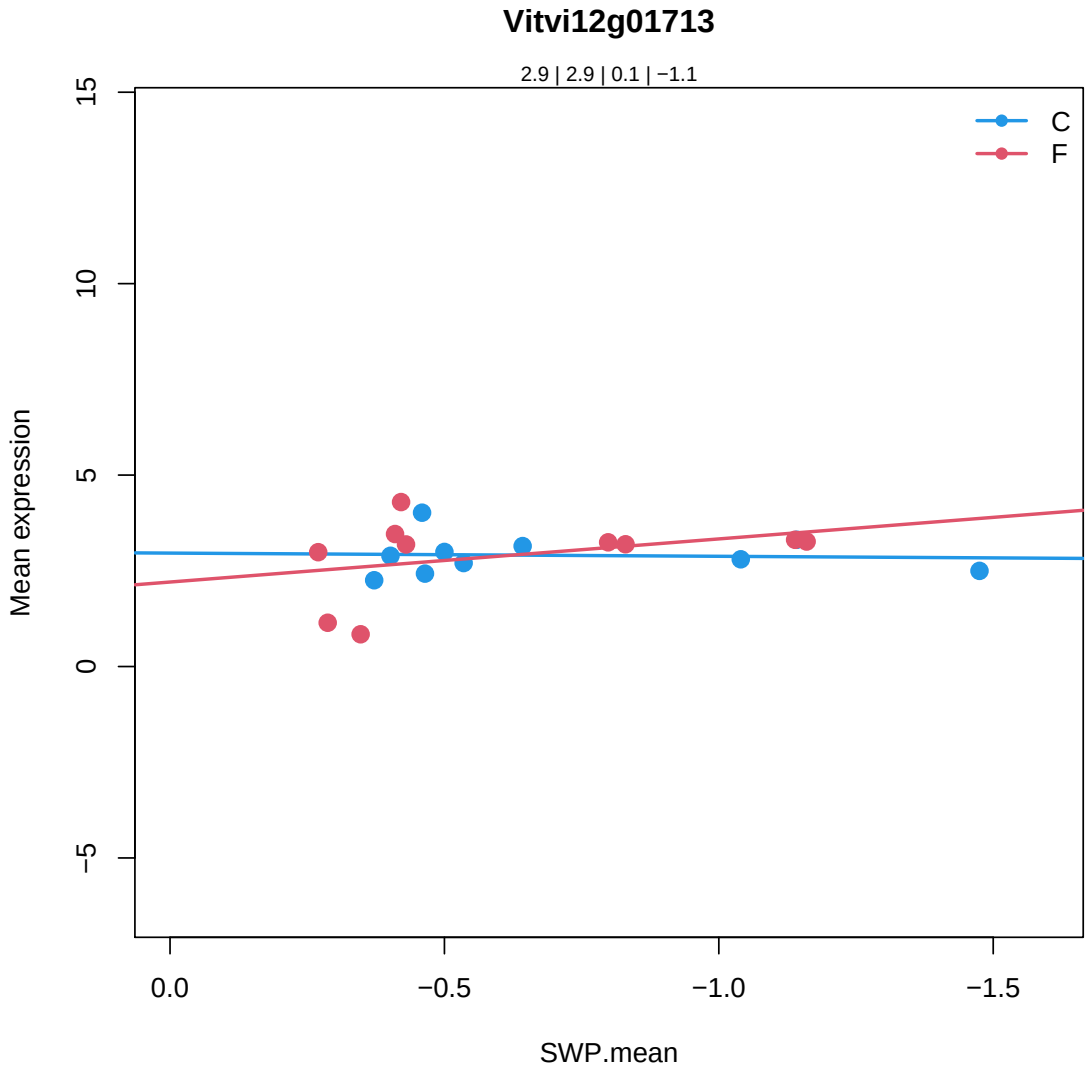
7.6.499 Vitvi12g01713: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g01713
        26.2
        misc.UDP glucosyl and glucoronyl transferases
        UDP-Glycosyltransferase superfamily protein |
        Chr3:7667099-7668556 FORWARD LENGTH=485 |
        201606
```

Coefficients for Vitvi12g01713.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.903701	5.195839e-11	***	6.87516e-11	***
SlopeC	0.08323551	0.9024034		0.9825783	
MeanF-MeanC	-0.01121432	0.9740675		0.9940651	
SlopeF-SlopeC	-1.209589	0.2388711		0.9999488	



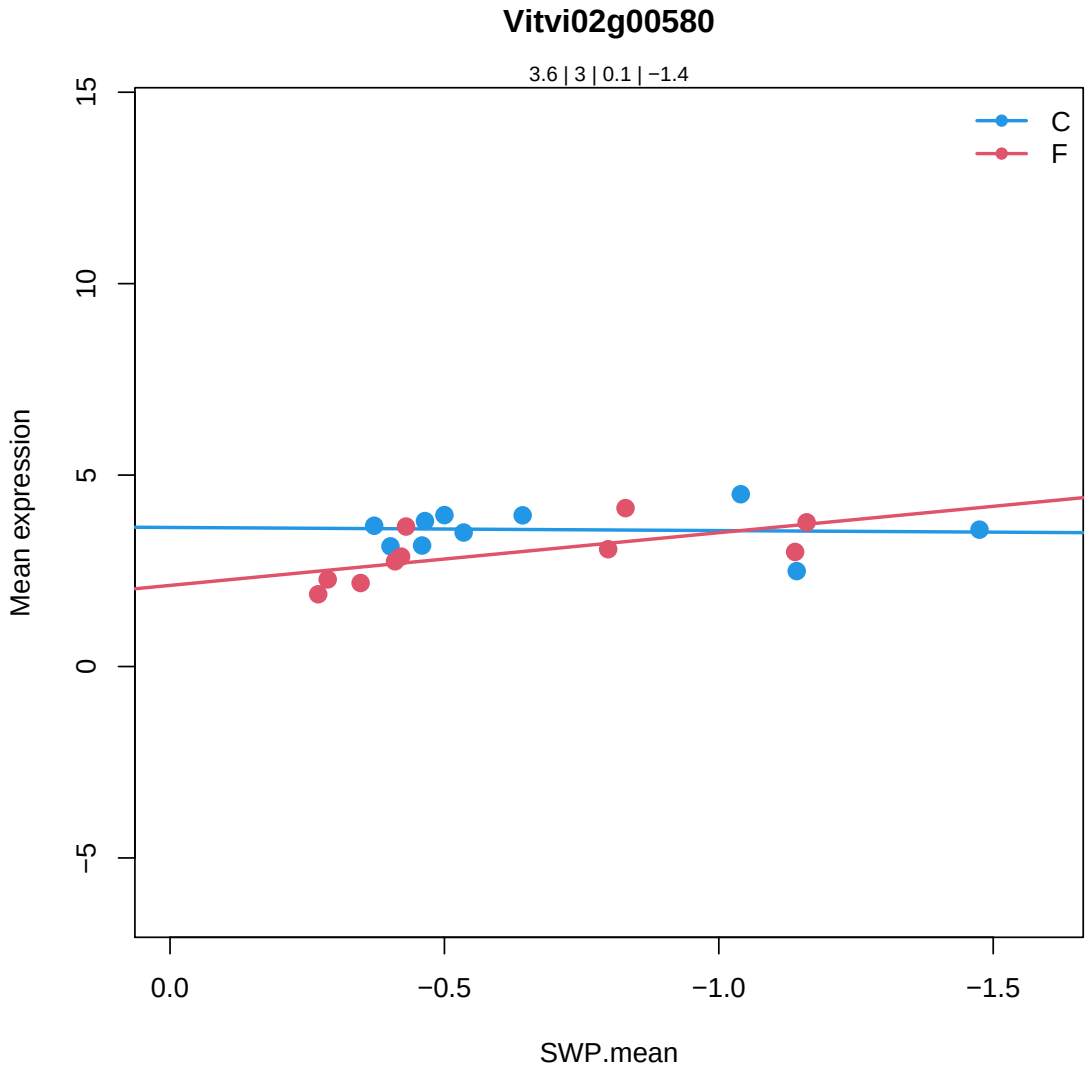
7.6.500 Vitvi02g00580: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00580
        29.4.1
        protein.postranslational modification.kinase
        SNF1-related protein kinase 2.5 |
        Chr5:25481631-25483495 REVERSE LENGTH=360 |
        201606
```

Coefficients for Vitvi02g00580.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.574387	2.319701e-15	***	4.173873e-15	***
SlopeC	0.08140146	0.8713652		0.9760939	
MeanF-MeanC	-0.6169264	0.02327754	*	0.140904	
SlopeF-SlopeC	-1.458455	0.06156251	.	0.9999488	



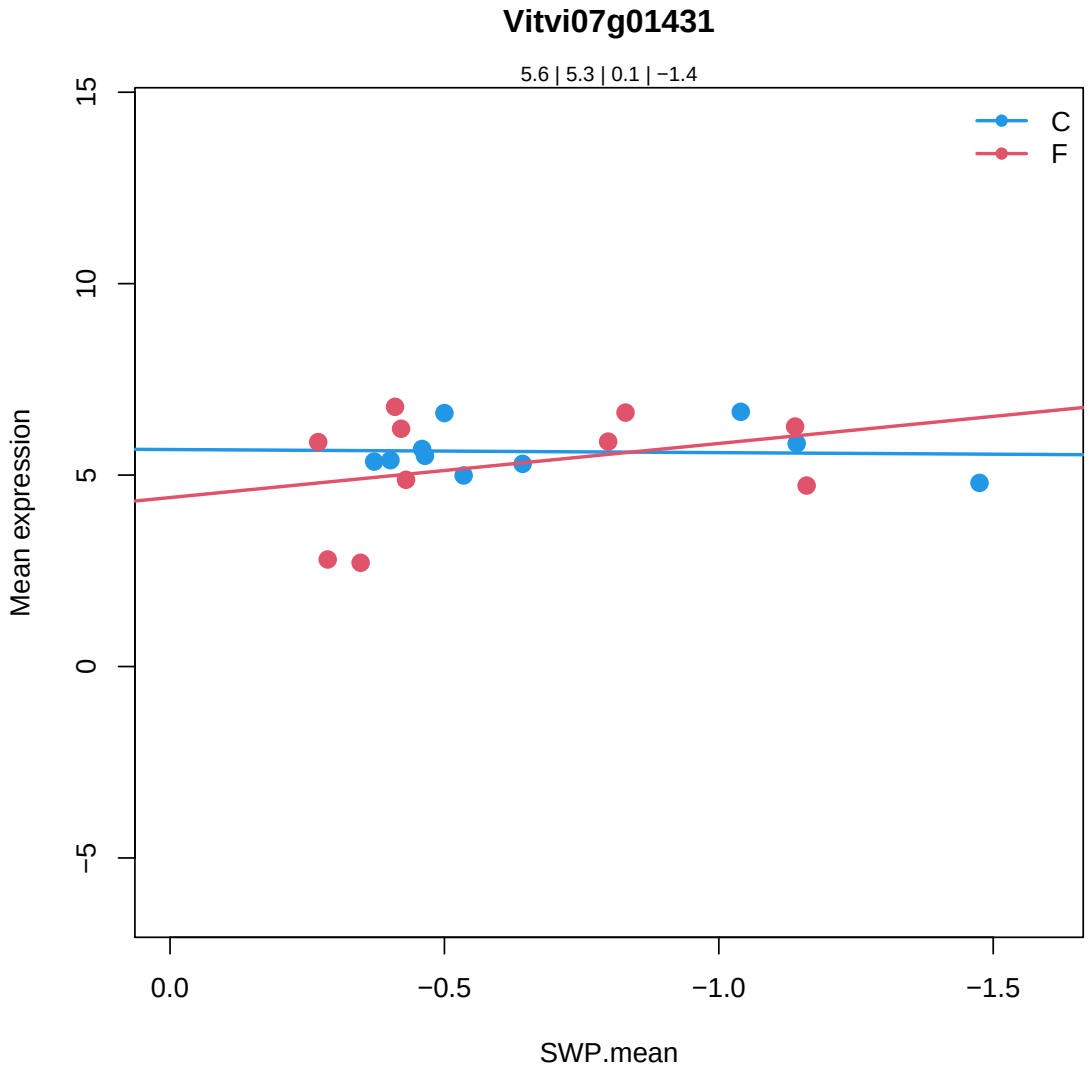
7.6.501 Vitvi07g01431: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01431
        29.4.1
        protein.postranslational modification.kinase
        hypothetical protein |
        Chr4:17874002-17874379 REVERSE LENGTH=125 |
        201606
```

Coefficients for Vitvi07g01431.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.610058	4.316321e-14	***	6.8225e-14	***
SlopeC	0.08118977	0.9290167		0.987284	
MeanF-MeanC	-0.3363068	0.4706025		0.7894788	
SlopeF-SlopeC	-1.4944	0.2773297		0.9999488	



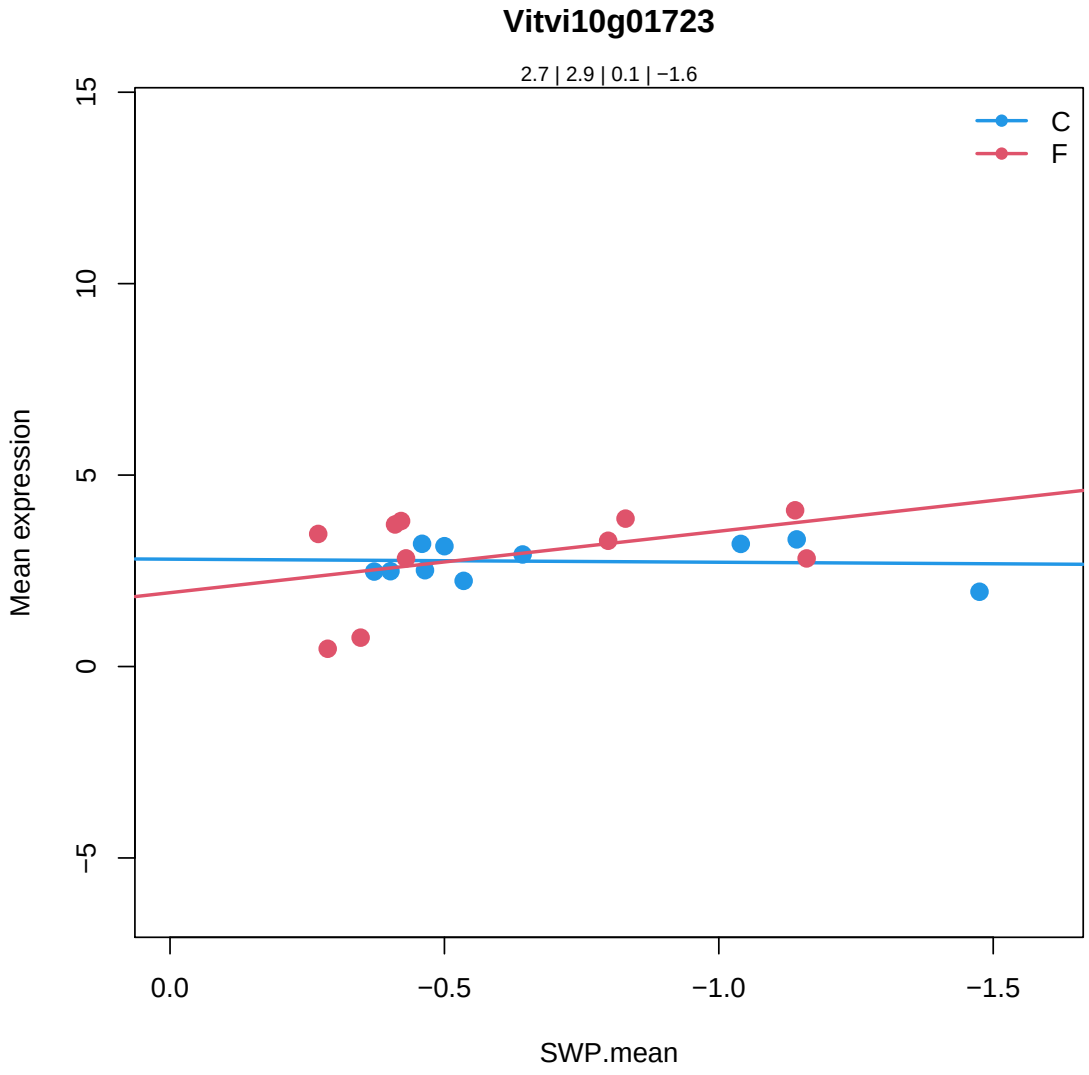
7.6.502 Vitvi10g01723: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g01723
        29.5.11.4.2
        protein.degradation.ubiquitin.E3.RING
        Zinc finger (C3HC4-type RING finger) family protein |
        Chr2:16274135-16276651 FORWARD LENGTH=692 |
        201606
```

Coefficients for Vitvi10g01723.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.746999	9.944396e-10	***	1.253701e-09	***
SlopeC	0.08026882	0.9152049		0.9842726	
MeanF-MeanC	0.1594749	0.6778774		0.8956583	
SlopeF-SlopeC	-1.685384	0.1431492		0.9999488	



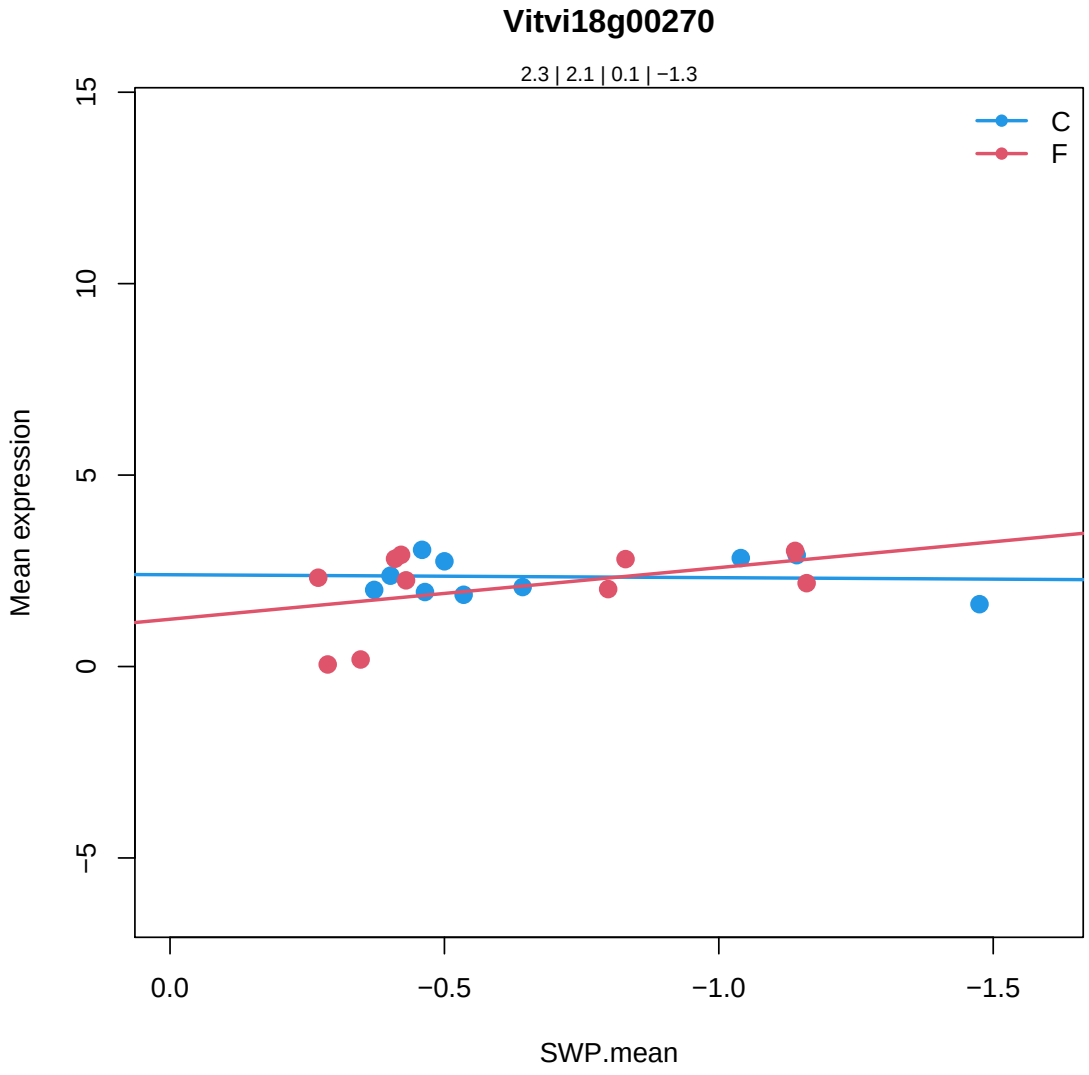
7.6.503 Vitvi18g00270: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00270
        35.2
        not assigned.unknown
        TRAM%2C LAG1 and CLN8 (TLC) lipid-sensing domain containing protein |
        Chr1:7654357-7655691 FORWARD LENGTH=288 |
        201606
```

Coefficients for Vitvi18g00270.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.343011	2.021217e-09	***	2.522714e-09	***
SlopeC	0.07669202	0.9087443		0.9837899	
MeanF-MeanC	-0.2866762	0.4031356		0.7473786	
SlopeF-SlopeC	-1.425264	0.162023		0.9999488	



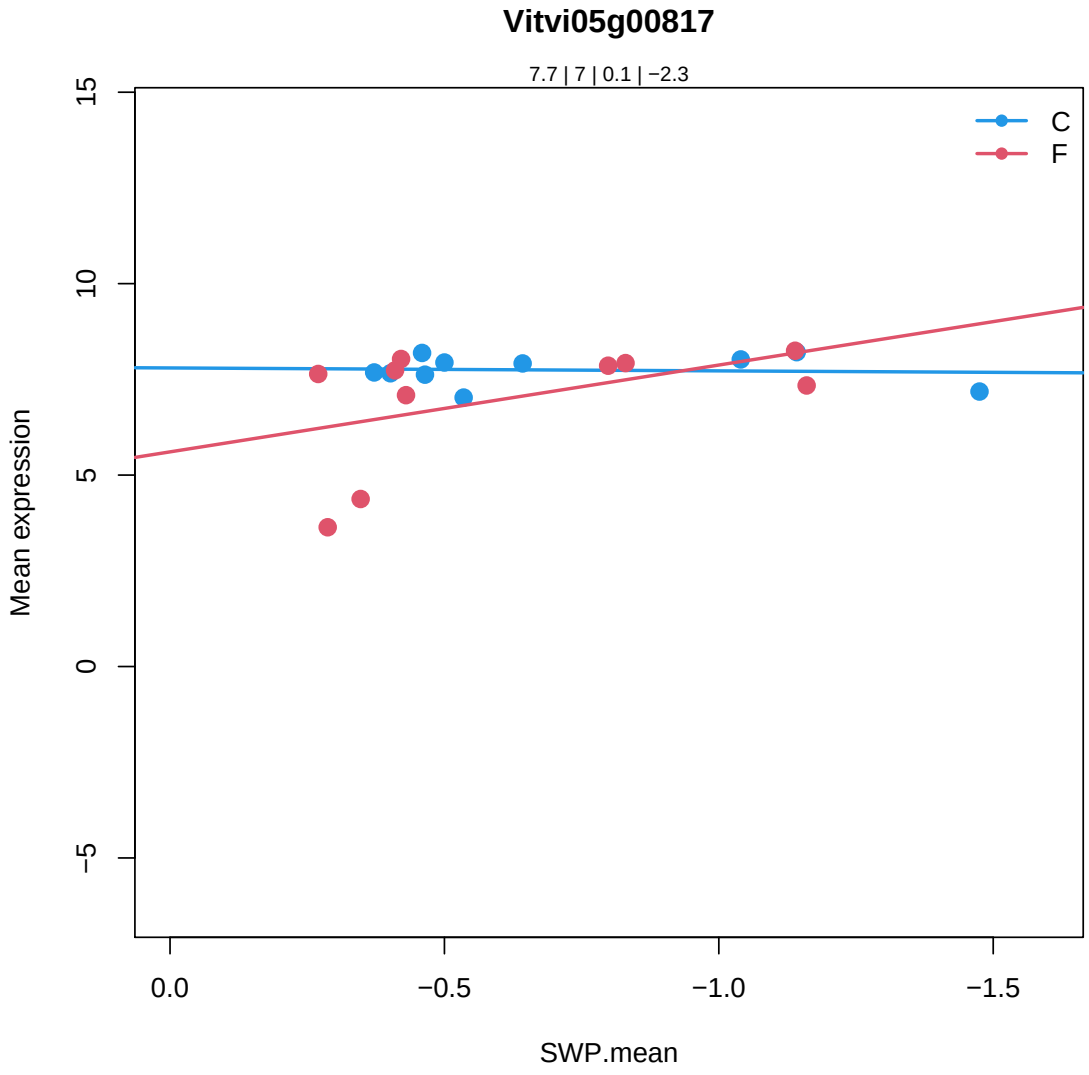
7.6.504 Vitvi05g00817: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00817
        1.1.40
        PS.lightreaction.cyclic electron flow-chlororespiration
        proton gradient regulation 5 |
        Chr2:2081204-2081687 REVERSE LENGTH=133 |
        201606
```

Coefficients for Vitvi05g00817.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.744301	2.589511e-17	***	6.274933e-17	***
SlopeC	0.07654634	0.9303178		0.987284	
MeanF-MeanC	-0.7566705	0.09972295	.	0.3635439	
SlopeF-SlopeC	-2.344279	0.08265792	.	0.9999488	



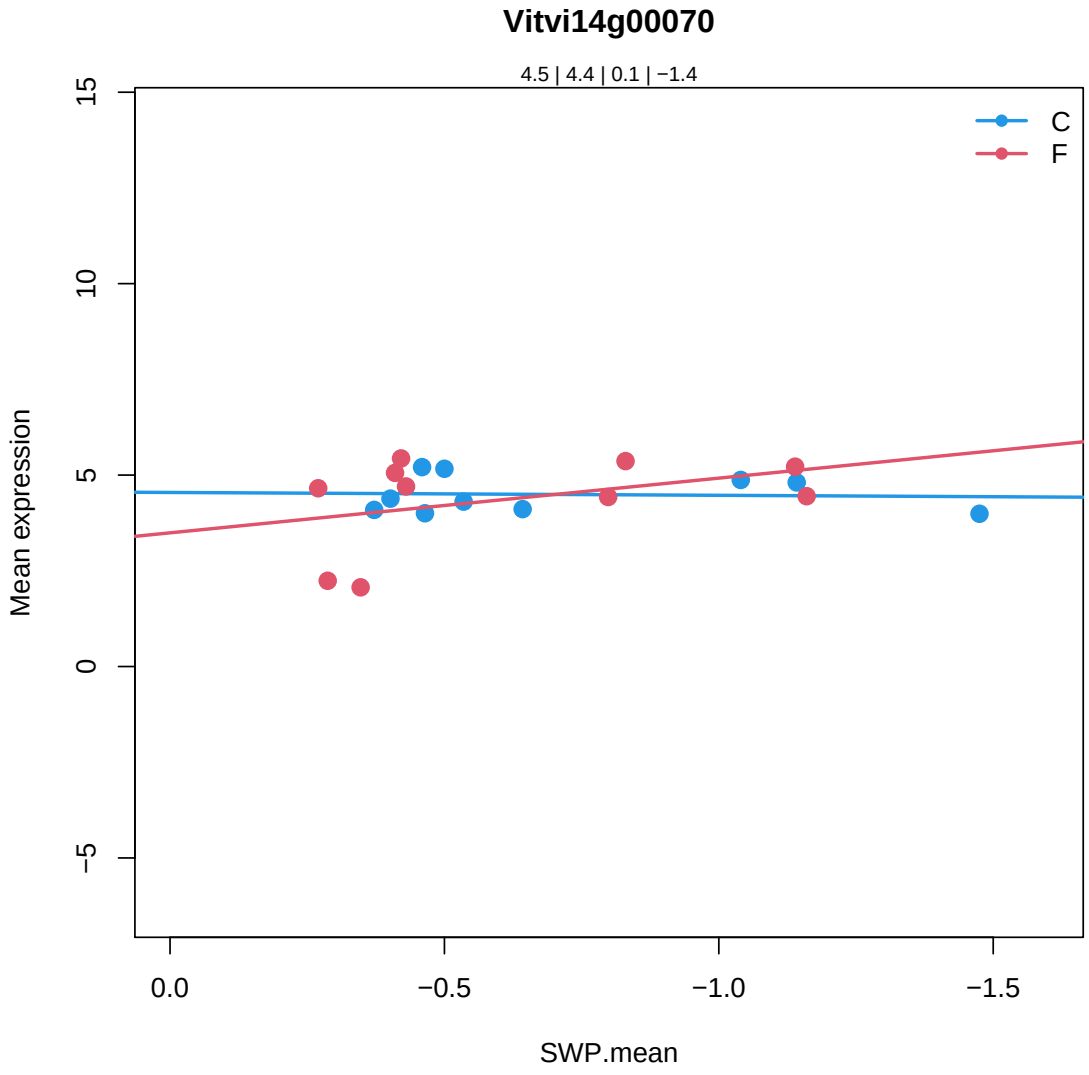
7.6.505 Vitvi14g00070: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g00070
        2.2.1.3.1
        major CHO metabolism.degradation.sucrose.invertases.neutral
        Plant neutral invertase family protein |
        Chr1:21192593-21194948 FORWARD LENGTH=616 |
        201606
```

Coefficients for Vitvi14g00070.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.493671	4.695305e-14	***	7.400045e-14	***
SlopeC	0.0742324	0.9193482		0.9851716	
MeanF-MeanC	-0.131885	0.7237756		0.915577	
SlopeF-SlopeC	-1.503295	0.1775912		0.9999488	



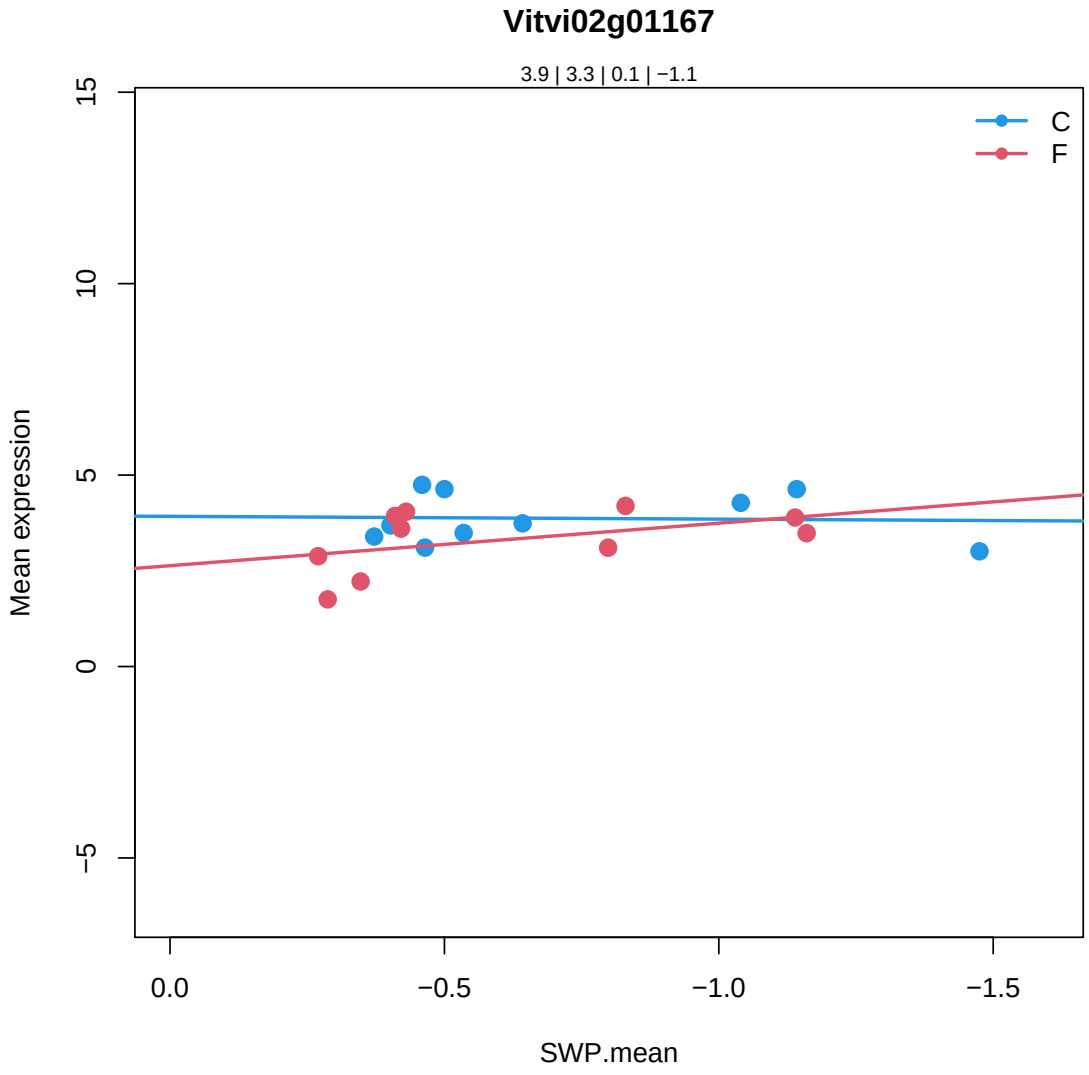
7.6.506 Vitvi02g01167: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g01167
        34.3
        transport.amino acids
        Amino acid permease family protein |
        Chr1:11418875-11420362 REVERSE LENGTH=495 |
        201606
```

Coefficients for Vitvi02g01167.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.870546	1.83887e-14	***	2.999899e-14	***
SlopeC	0.07287202	0.9037711		0.983176	
MeanF-MeanC	-0.5602546	0.07809603	.	0.3151735	
SlopeF-SlopeC	-1.183359	0.1959556		0.9999488	



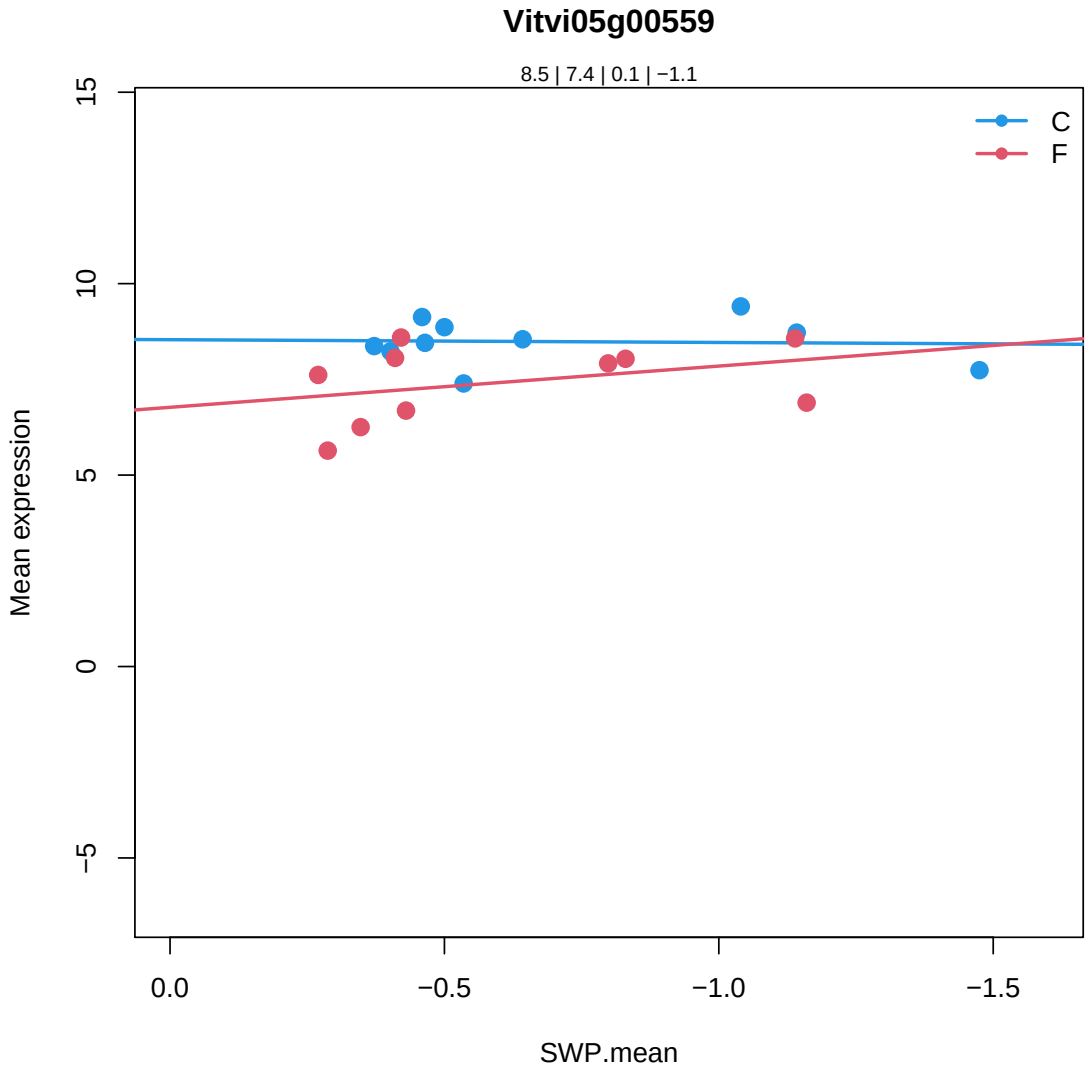
7.6.507 Vitvi05g00559: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00559
        15.3
        metal handling.regulation
        RmlC-like cupins superfamily protein |
        Chr5:17627364-17629122 REVERSE LENGTH=187 |
        201606
```

Coefficients for Vitvi05g00559.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	8.484797	1.883571e-20	***	1.181943e-19	***
SlopeC	0.07225561	0.9152821		0.9842726	
MeanF-MeanC	-1.058923	0.005291634	**	0.0477249	*
SlopeF-SlopeC	-1.149313	0.2626696		0.9999488	



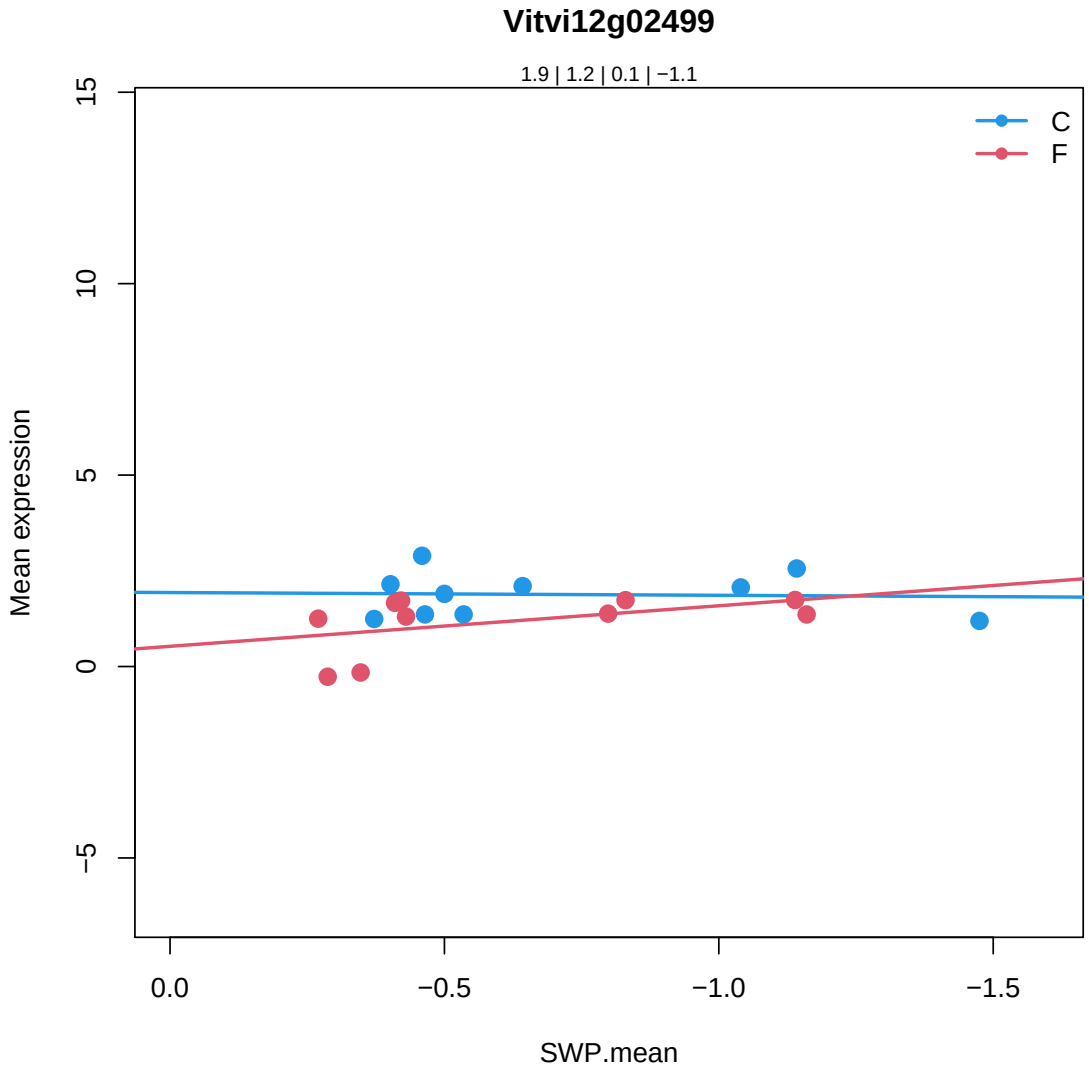
7.6.508 Vitvi12g02499: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02499
        23.3.3
        nucleotide metabolism.salvage.NUDIX hydrolases
        nudix hydrolase homolog 2 |
        Chr5:19310391-19312084 REVERSE LENGTH=278 |
        201606
```

Coefficients for Vitvi12g02499.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.881537	3.40859e-09	***	4.224224e-09	***
SlopeC	0.07198233	0.8965246		0.9814571	
MeanF-MeanC	-0.7088173	0.01848972	*	0.1191453	
SlopeF-SlopeC	-1.130806	0.1790753		0.9999488	



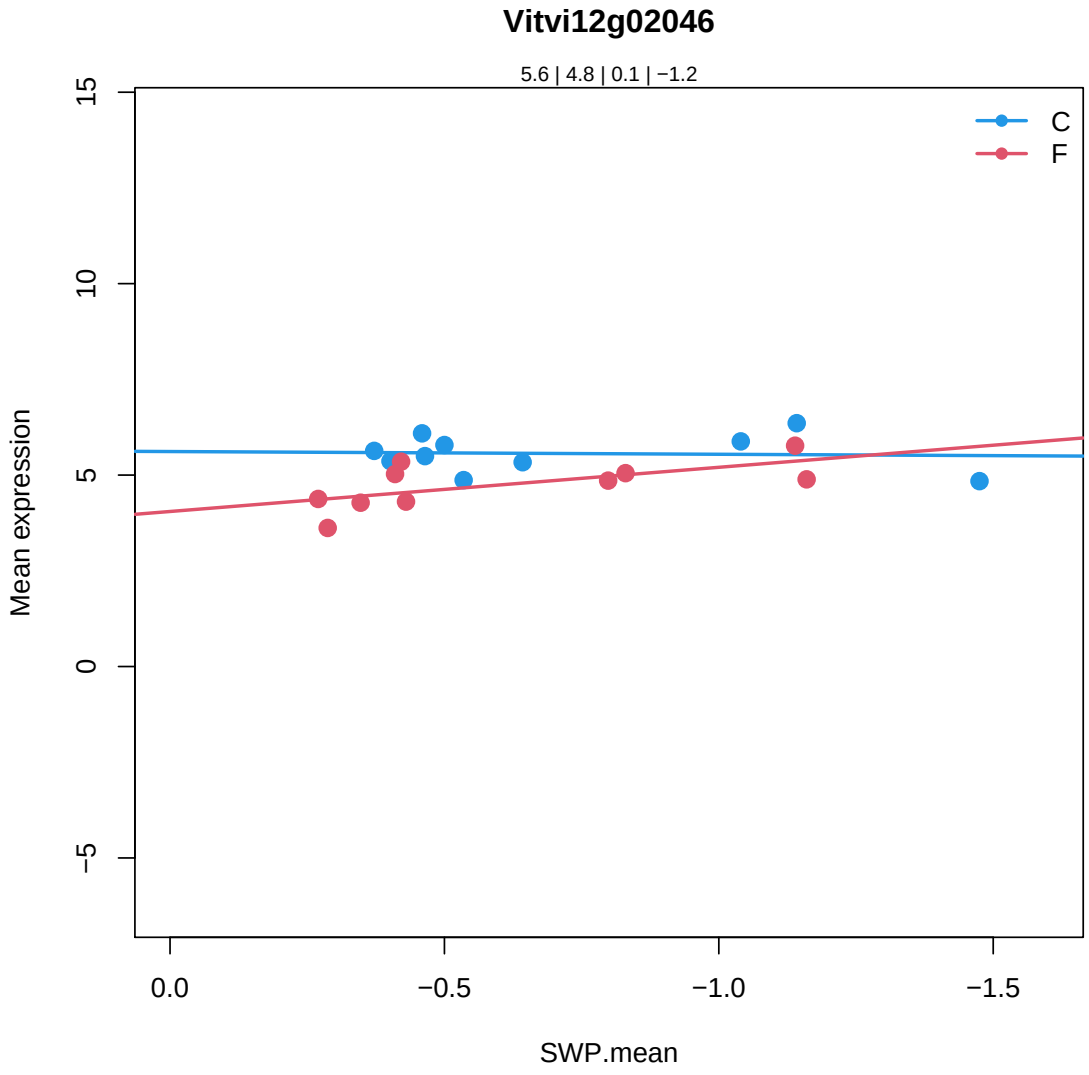
7.6.509 Vitvi12g02046: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02046
        16.1.4
        secondary metabolism.isoprenoids.carotenoids
        FAD/NAD(P)-binding oxidoreductase family protein |
        Chr1:21395254-21398135 FORWARD LENGTH=574 |
        201606
```

Coefficients for Vitvi12g02046.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.564789	2.297503e-20	***	1.395717e-19	***
SlopeC	0.07135099	0.8739526		0.9762394	
MeanF-MeanC	-0.8129226	0.001647466	**	0.01889442	*
SlopeF-SlopeC	-1.225509	0.07773851	.	0.9999488	



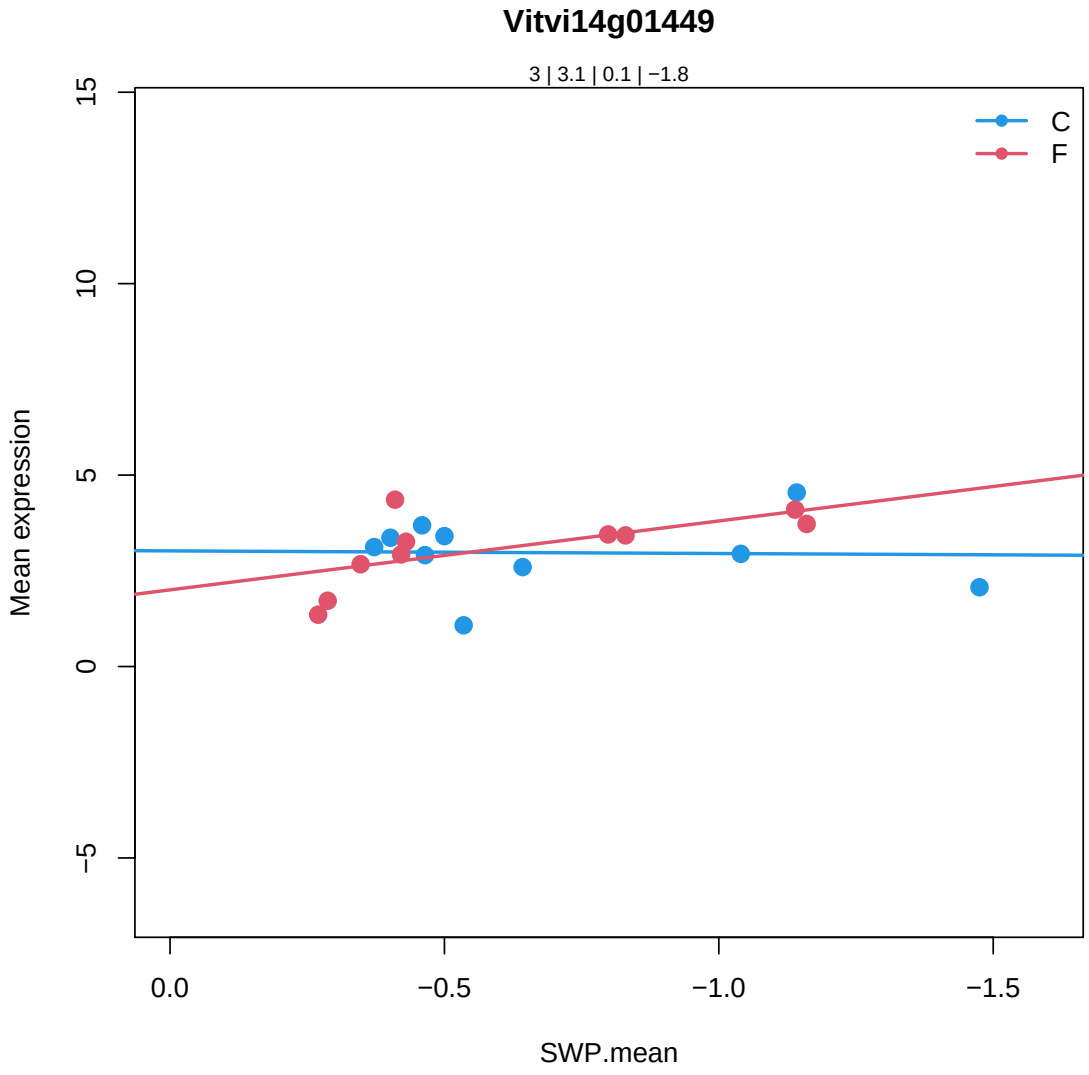
7.6.510 Vitvi14g01449: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01449
        35.2
        not assigned.unknown
        Chalcone and stilbene synthase family protein |
        Chr5:4488762-4490035 FORWARD LENGTH=395 |
        201606
```

Coefficients for Vitvi14g01449.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.971534	1.104454e-10	***	1.44251e-10	***
SlopeC	0.06838841	0.9246574		0.9862379	
MeanF-MeanC	0.1265672	0.7309499		0.918522	
SlopeF-SlopeC	-1.868025	0.09335079	.	0.9999488	



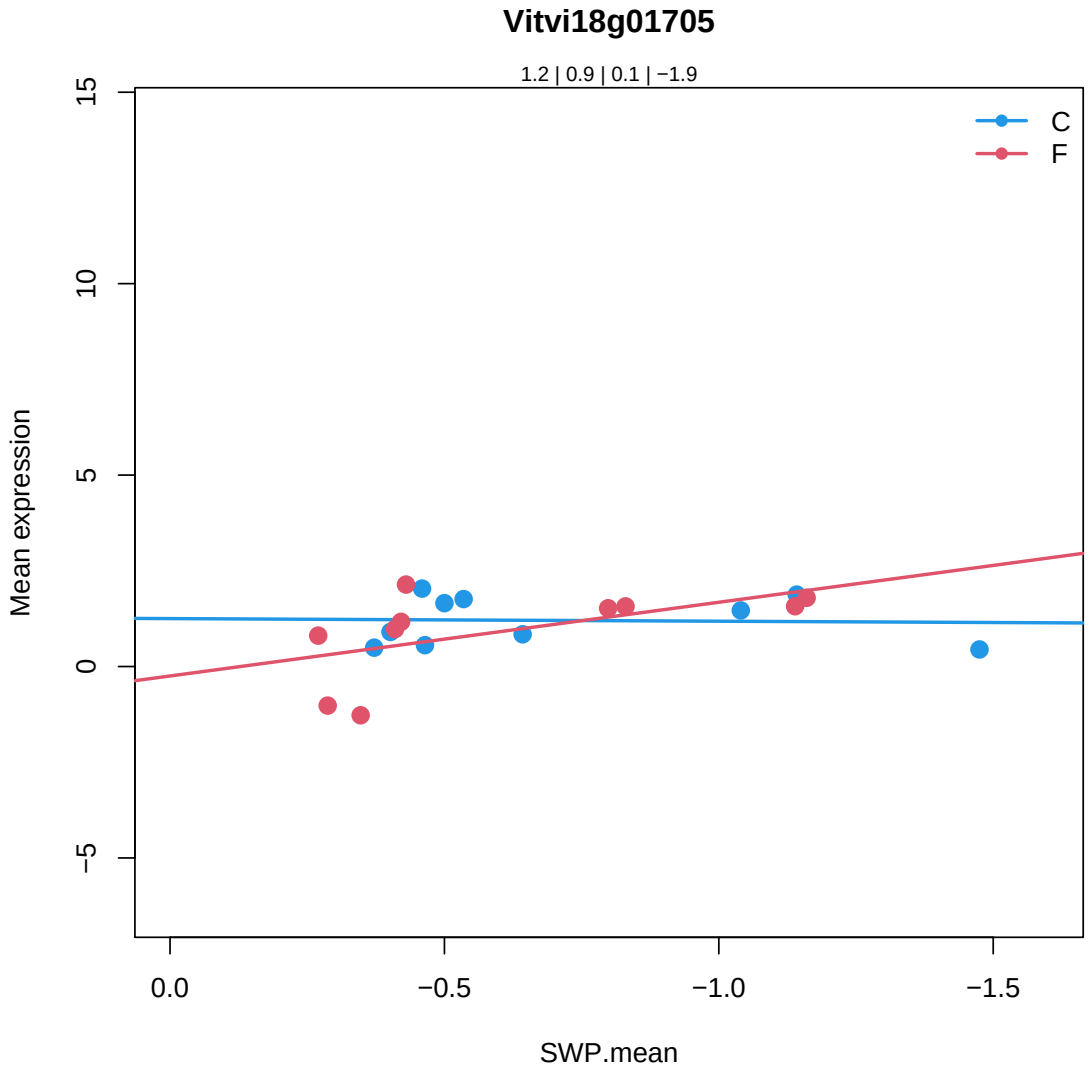
7.6.511 Vitvi18g01705: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g01705
        20.1.2.2
        stress.biotic.receptors.TIR-NBS-LRR
        Disease resistance protein (TIR-NBS-LRR class) family |
        Chr5:14567771-14571916 REVERSE LENGTH=1191 |
        201606
```

Coefficients for Vitvi18g01705.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.20347	7.166322e-05	***	7.935277e-05	***
SlopeC	0.06796223	0.9216802		0.9855654	
MeanF-MeanC	-0.2776611	0.4327328		0.766636	
SlopeF-SlopeC	-1.993147	0.06309416	.	0.9999488	



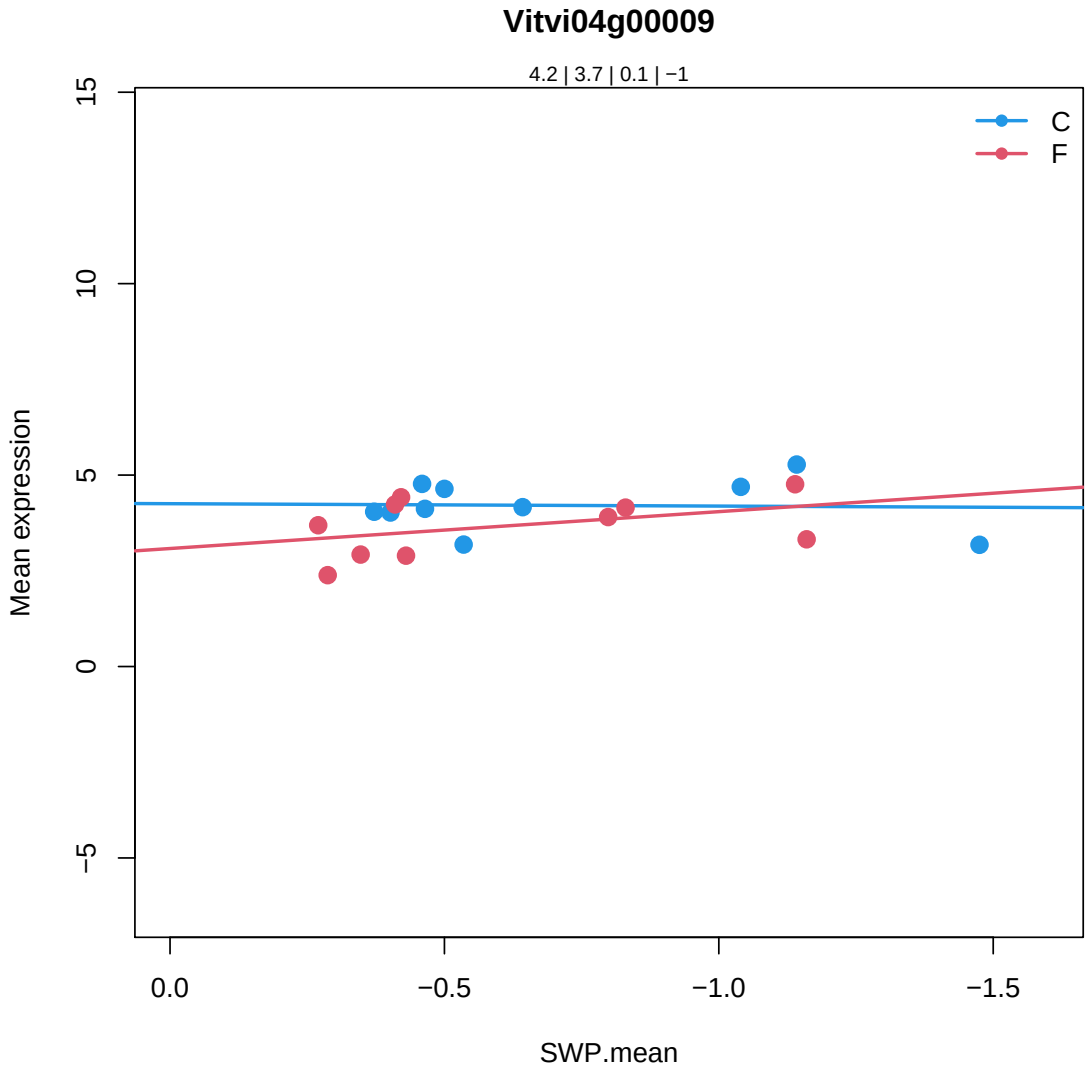
7.6.512 Vitvi04g00009: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00009
        8.2.10
        TCA / organic transformation.other organic acid transformations.malic
        NADP-malic enzyme 3 |
        Chr5:9024549-9027498 FORWARD LENGTH=530 |
        201606
```

Coefficients for Vitvi04g00009.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.208661	2.788749e-15	***	4.967988e-15	***
SlopeC	0.06233068	0.9168716		0.9845986	
MeanF-MeanC	-0.5403923	0.08573724	.	0.3324363	
SlopeF-SlopeC	-1.025475	0.2558604		0.9999488	



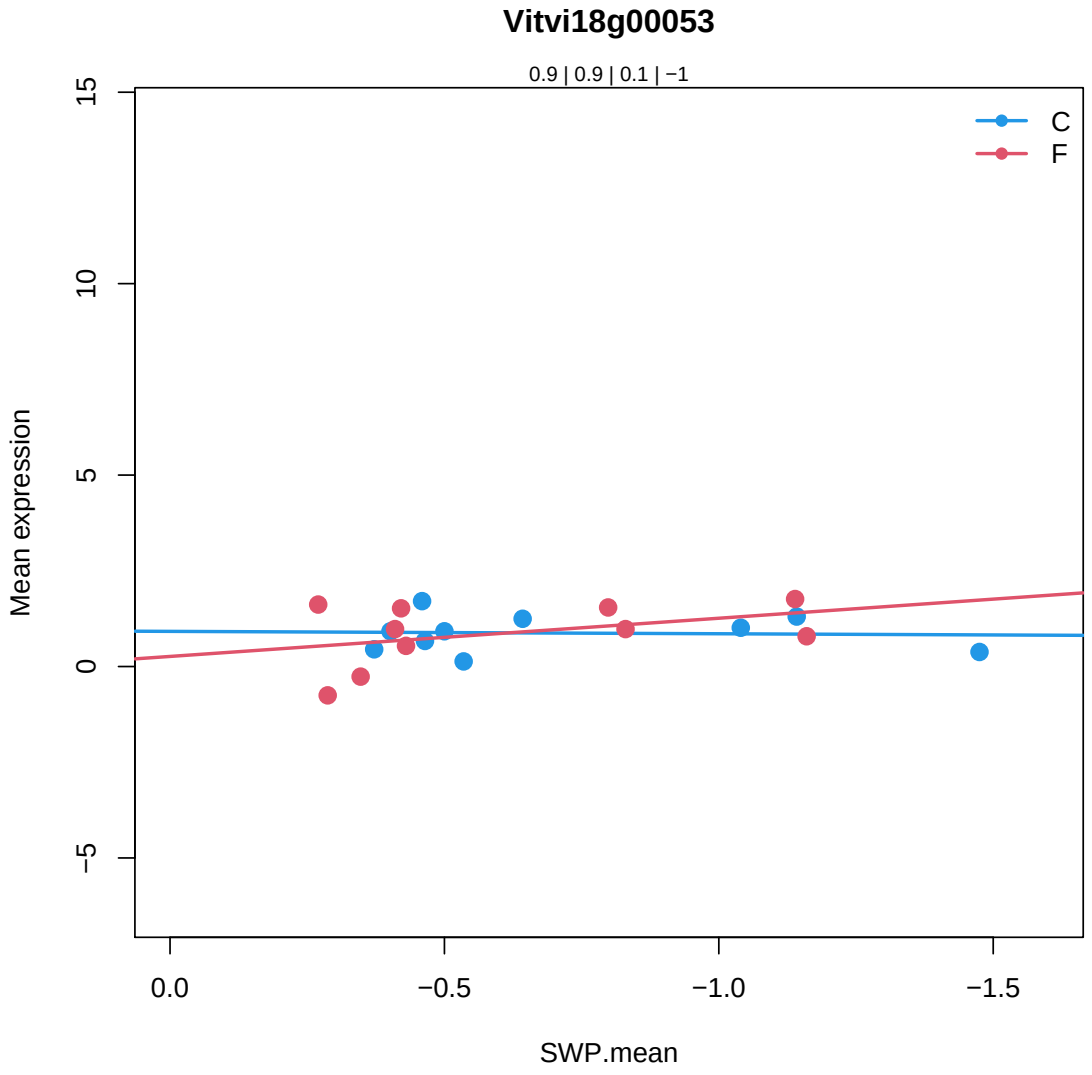
7.6.513 Vitvi18g00053: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00053
        35.2
        not assigned.unknown
        Late embryogenesis abundant protein%2C group 6 |
        Chr2:14252187-14252414 FORWARD LENGTH=75 |
        201606
```

Coefficients for Vitvi18g00053.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.874121	0.000259623	***	0.0002843818	***
SlopeC	0.06201541	0.9123832		0.9839968	
MeanF-MeanC	-0.003102512	0.9913584		0.9974135	
SlopeF-SlopeC	-1.060048	0.2146776		0.9999488	



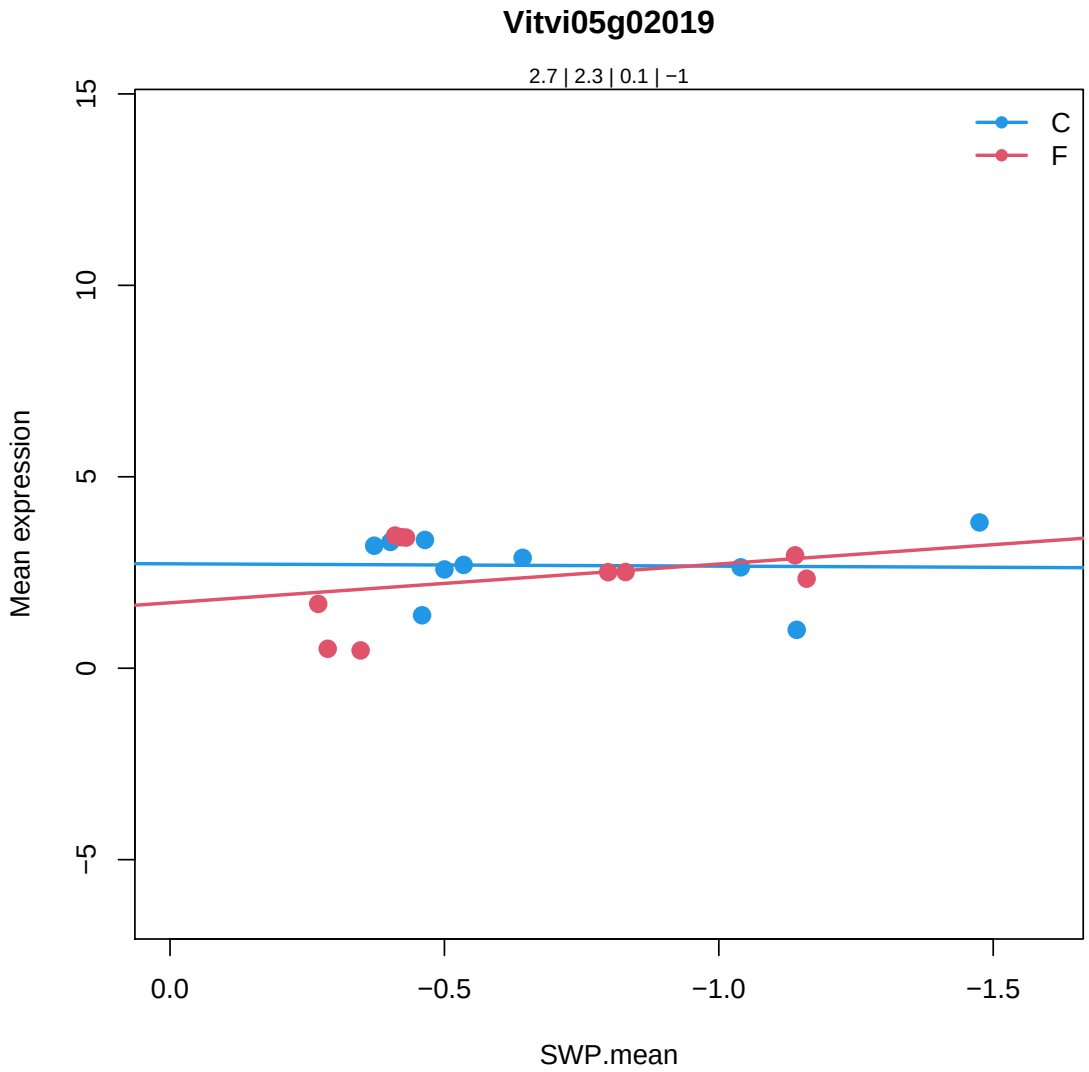
7.6.514 Vitvi05g02019: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g02019
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi05g02019.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.683862	7.490197e-09	***	9.17656e-09	***
SlopeC	0.06064106	0.9414708		0.9899572	
MeanF-MeanC	-0.3578289	0.3980377		0.7437542	
SlopeF-SlopeC	-1.072548	0.3871485		0.9999488	



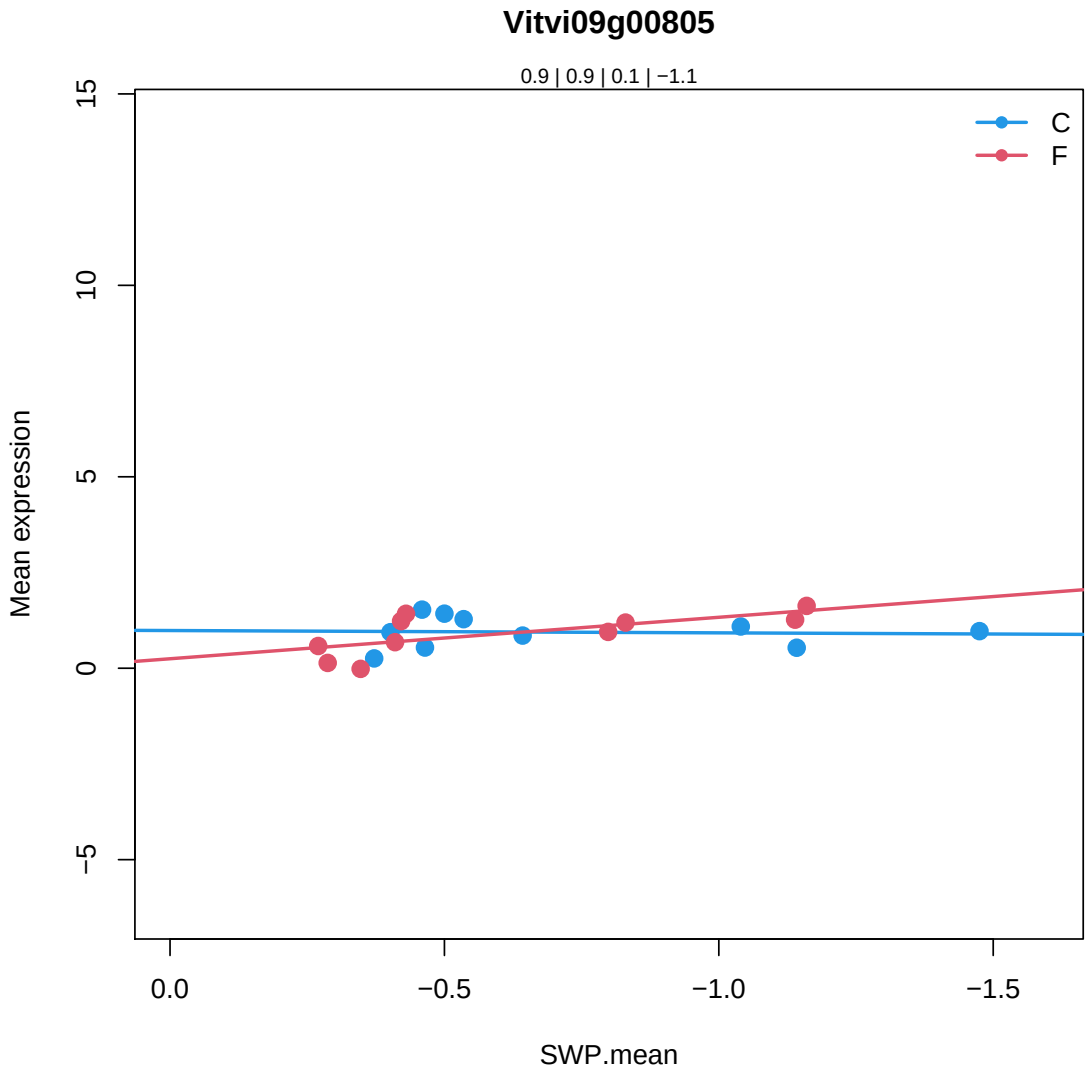
7.6.515 Vitvi09g00805: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00805
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi09g00805.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.9419277	1.214425e-06	***	1.399113e-06	***
SlopeC	0.0605072	0.8791621		0.97674	
MeanF-MeanC	-0.03488535	0.863104		0.964228	
SlopeF-SlopeC	-1.143637	0.06389146	.	0.9999488	



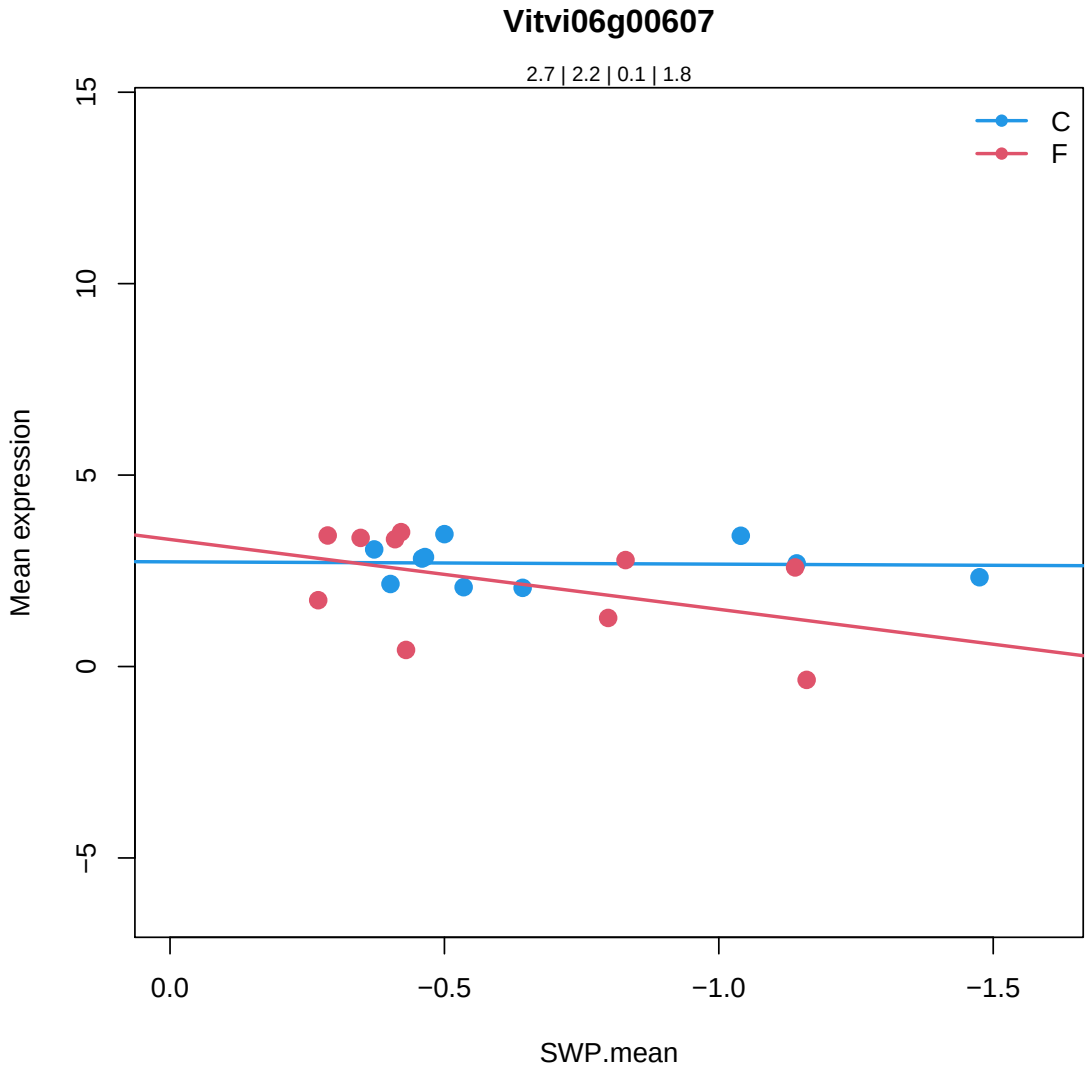
7.6.516 Vitvi06g00607: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00607
        27.3.11
        RNA.regulation of transcription.C2H2 zinc finger family
        zinc finger (C2H2 type) family protein |
        Chr2:12679346-12680467 FORWARD LENGTH=373 |
        201606
```

Coefficients for Vitvi06g00607.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.691509	4.004299e-09	***	4.949199e-09	***
SlopeC	0.05993864	0.940198		0.9898527	
MeanF-MeanC	-0.484718	0.2403579		0.5976459	
SlopeF-SlopeC	1.76397	0.1479695		0.9999488	



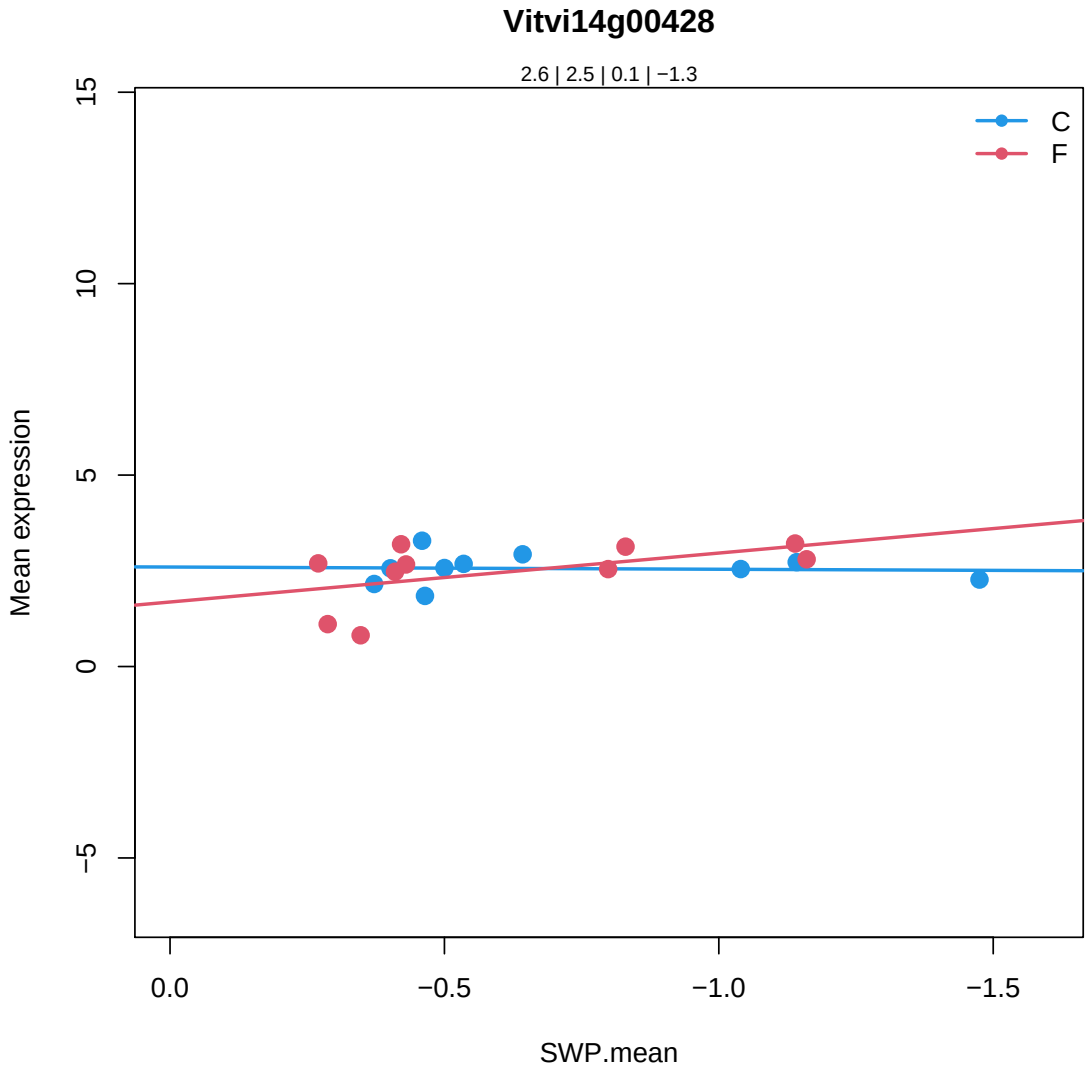
7.6.517 Vitvi14g00428: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g00428
        27.3.17
        RNA.regulation of transcription.CPP(Zn) CPP1-related transcription fac
        TESMIN/TSO1-like CXC 2 |
        Chr4:8481522-8484825 REVERSE LENGTH=674 |
        201606
```

Coefficients for Vitvi14g00428.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.557436	3.719132e-12	***	5.173589e-12	***
SlopeC	0.05781101	0.9115964		0.9837899	
MeanF-MeanC	-0.09375209	0.7235414		0.9155087	
SlopeF-SlopeC	-1.336342	0.09534056	.	0.9999488	



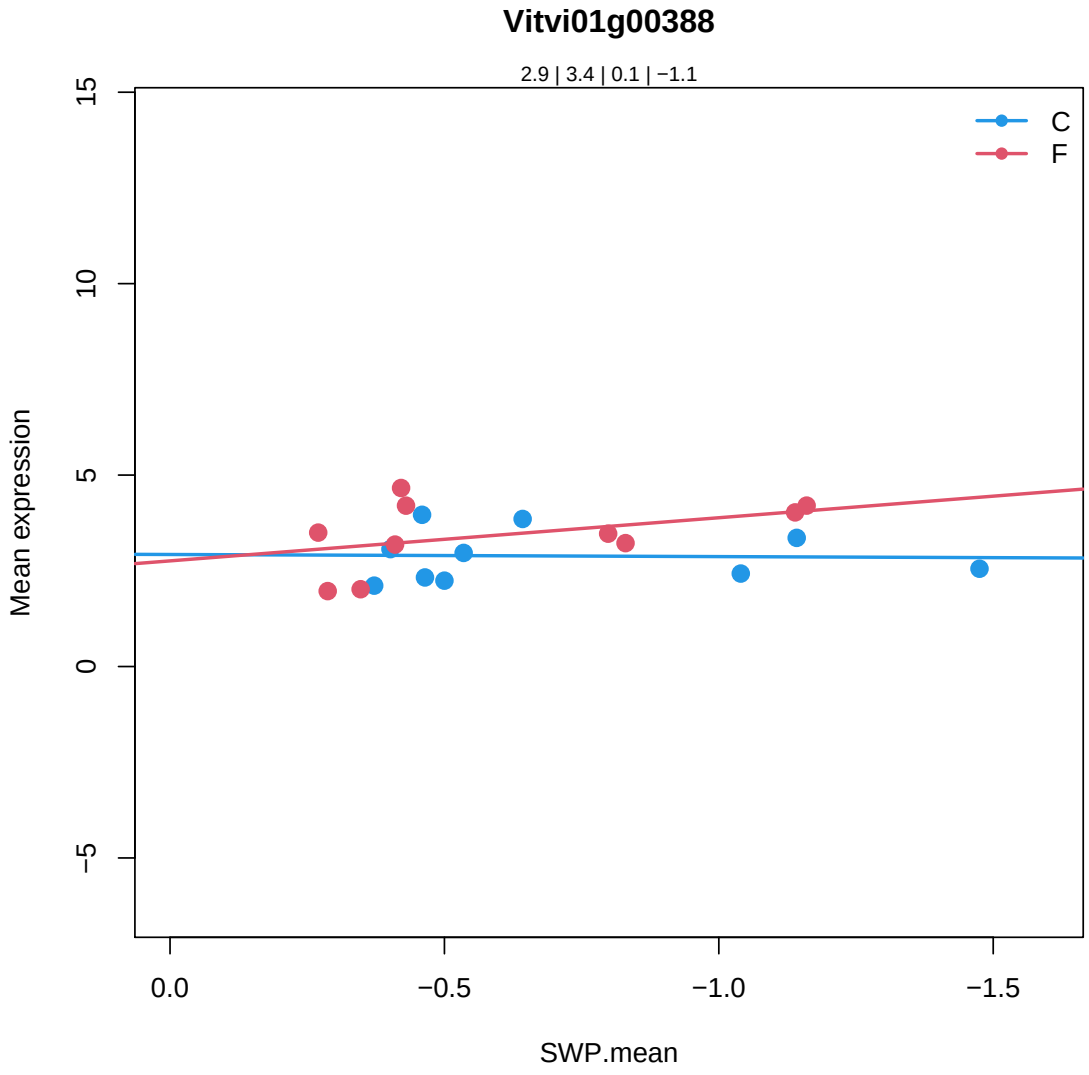
7.6.518 Vitvi01g00388: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00388
        35.2
        not assigned.unknown
        mediator of RNA polymerase II transcription subunit |
        Chr2:151221-151691 REVERSE LENGTH=156 |
        201606
```

Coefficients for Vitvi01g00388.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.887161	2.209735e-11	***	2.972708e-11	***
SlopeC	0.05495732	0.9320981		0.9880952	
MeanF-MeanC	0.5581999	0.0993487	.	0.362787	
SlopeF-SlopeC	-1.181837	0.2263433		0.9999488	



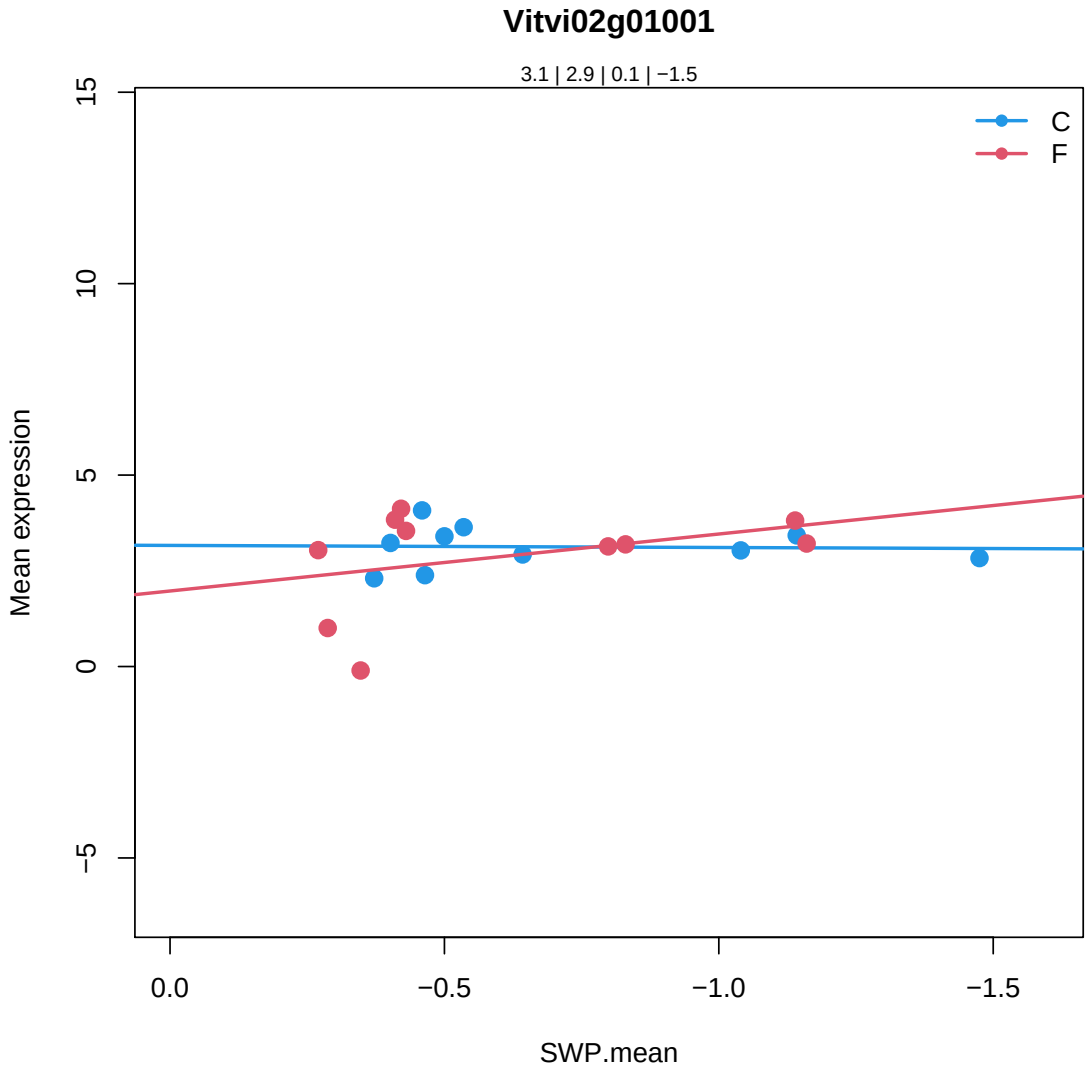
7.6.519 Vitvi02g01001: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g01001
        16.8.5.1
        secondary metabolism.flavonoids.isoflavonols.isoflavone reductase
        pinoresinol reductase 1 |
        Chr1:11546472-11547953 REVERSE LENGTH=317 |
        201606
```

Coefficients for Vitvi02g01001.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.124928	4.265008e-10	***	5.448601e-10	***
SlopeC	0.05442906	0.9469697		0.9907125	
MeanF-MeanC	-0.2460184	0.5558453		0.8369815	
SlopeF-SlopeC	-1.542841	0.2136545		0.9999488	



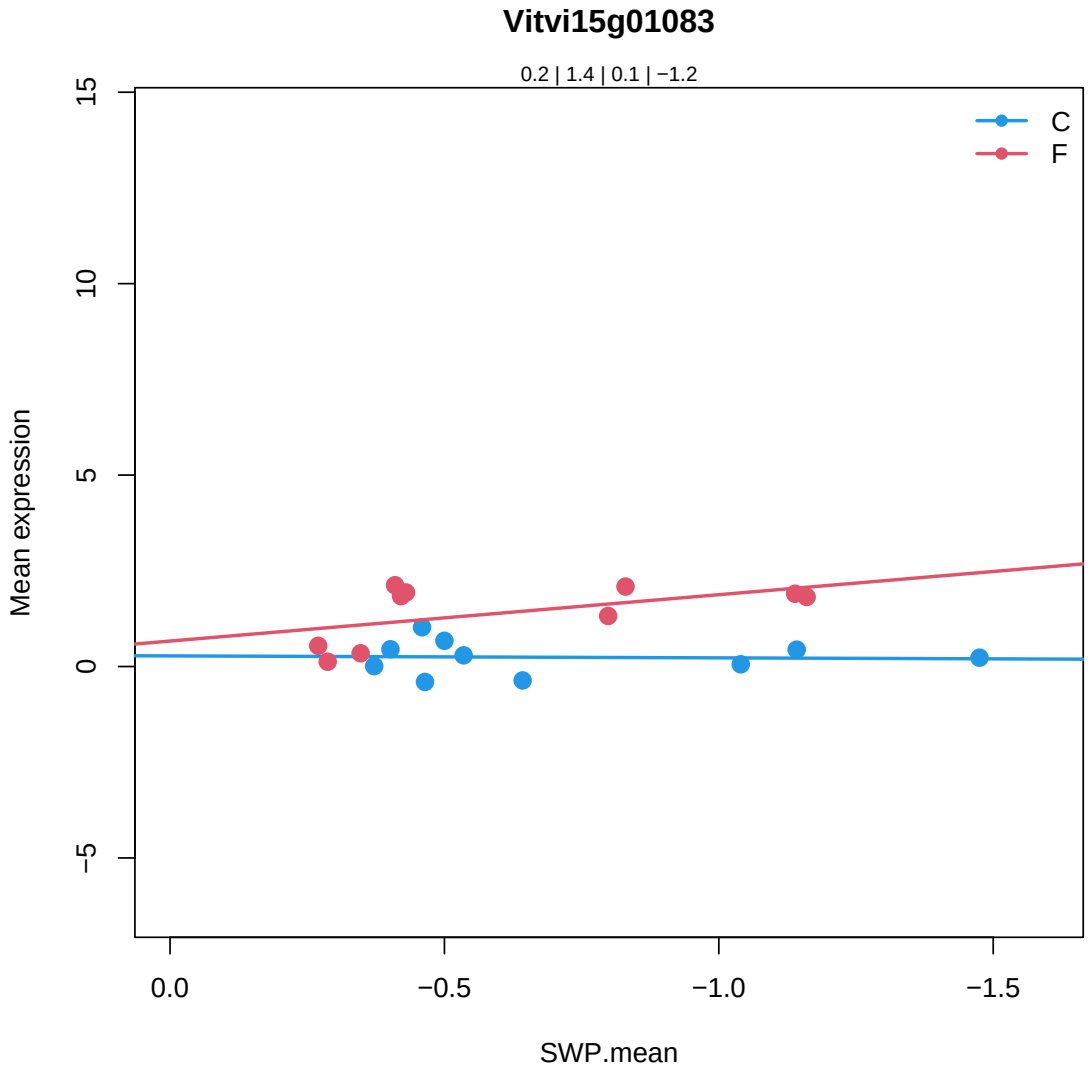
7.6.520 Vitvi15g01083: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g01083
        33.2
        development.late embryogenesis abundant
        Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein fam
        Chr2:18961424-18962089 FORWARD LENGTH=221 |
        201606
```

Coefficients for Vitvi15g01083.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.2411005	0.1922246		0.1971793	
SlopeC	0.05116495	0.9191535		0.9851716	
MeanF-MeanC	1.161826	0.000152068	***	0.002547056	**
SlopeF-SlopeC	-1.261935	0.1032309		0.9999488	



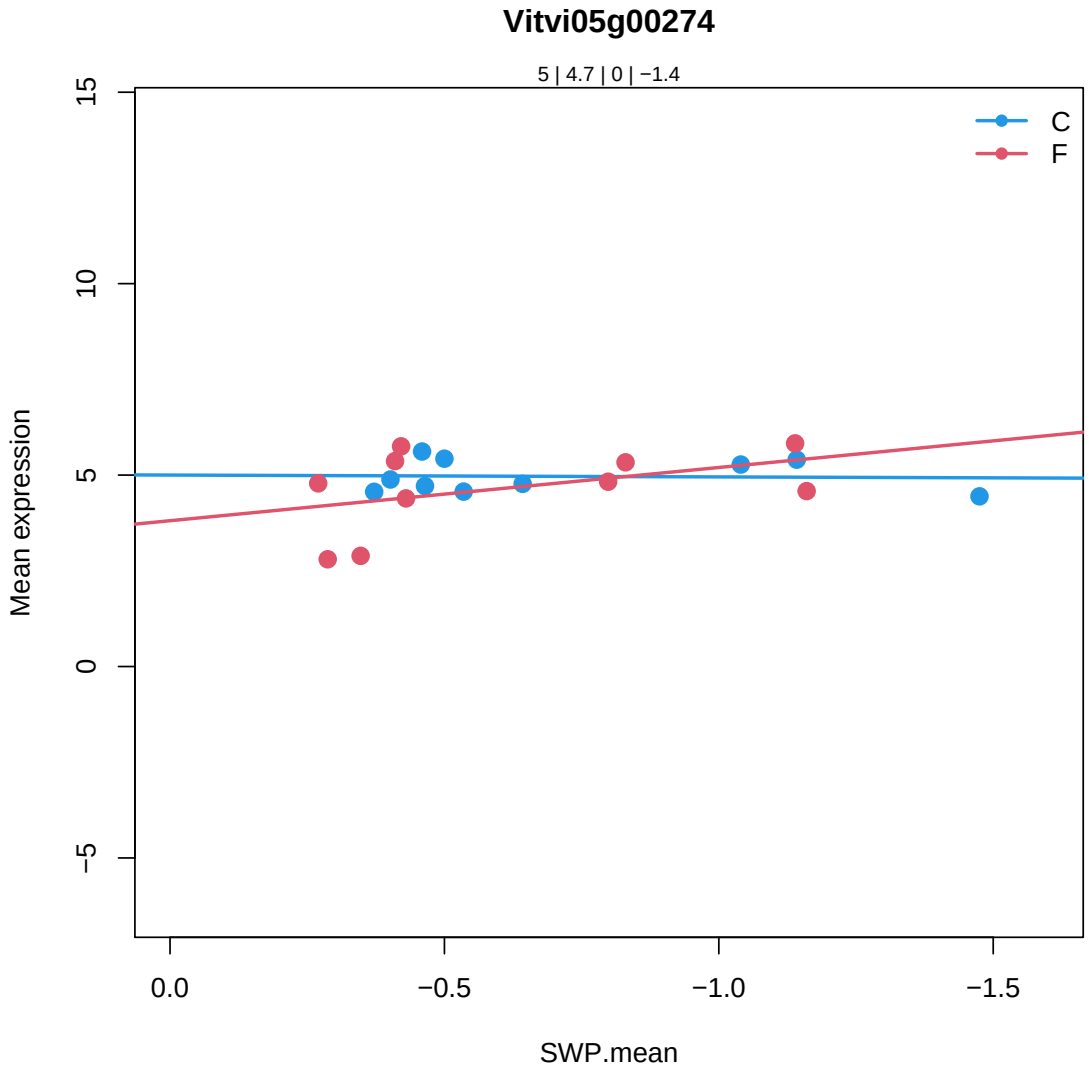
7.6.521 Vitvi05g00274: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00274
        27.3.35
        RNA.regulation of transcription.bZIP transcription factor family
        HY5-homolog |
        Chr3:6024131-6024585 FORWARD LENGTH=120 |
        201606
```

Coefficients for Vitvi05g00274.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.966484	3.869387e-16	***	7.663356e-16	***
SlopeC	0.04825214	0.9398883		0.9898527	
MeanF-MeanC	-0.3115639	0.34325		0.7032012	
SlopeF-SlopeC	-1.438367	0.1410966		0.9999488	



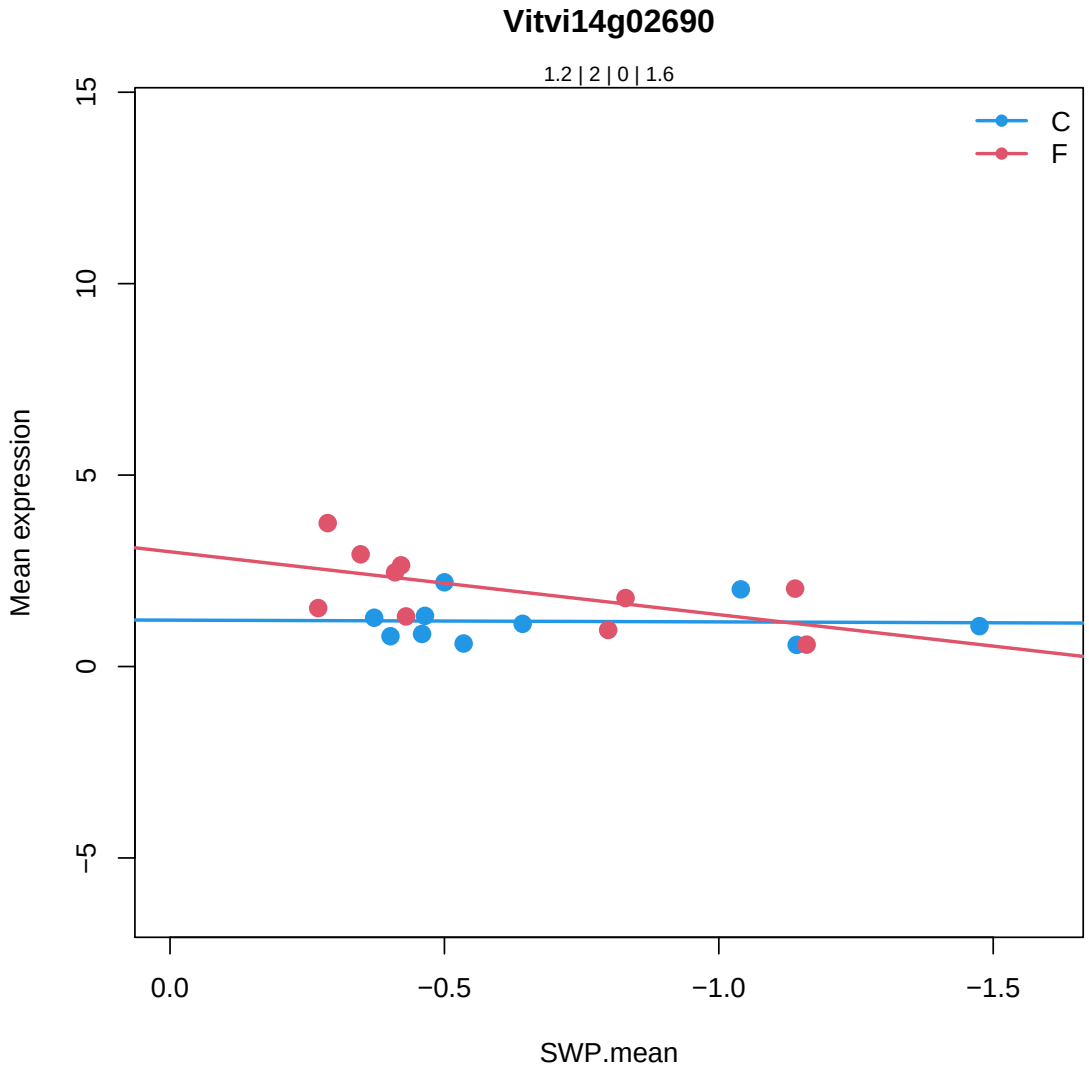
7.6.522 Vitvi14g02690: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g02690
        31.1
        cell.organisation
        Ankyrin repeat family protein |
        Chr4:1553453-1556571 FORWARD LENGTH=652 |
        201606
```

Coefficients for Vitvi14g02690.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.178886	1.483769e-05	***	1.669171e-05	***
SlopeC	0.04572887	0.9388672		0.9897783	
MeanF-MeanC	0.8171705	0.01245685	*	0.08938559	.
SlopeF-SlopeC	1.596933	0.08264025	.	0.9999488	



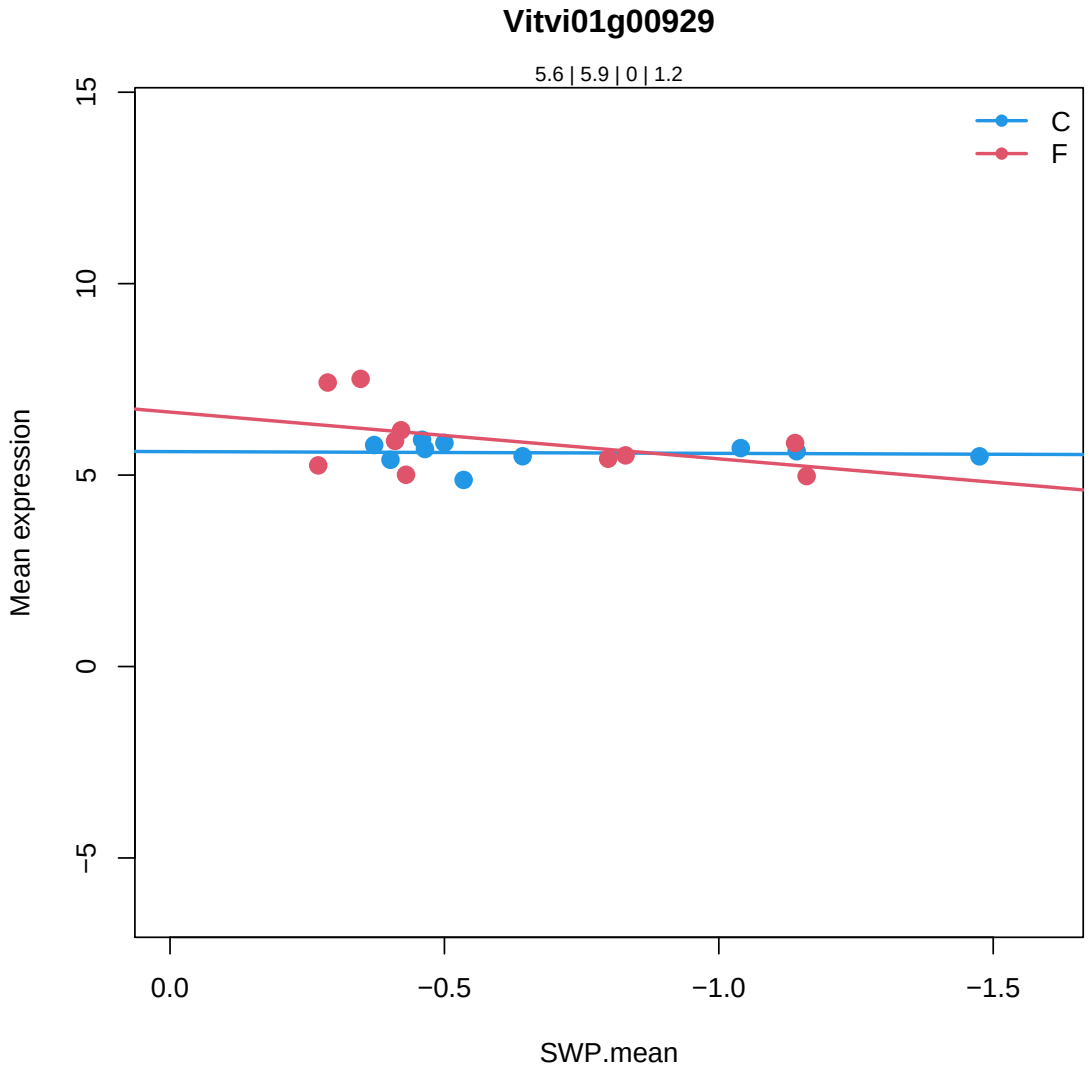
7.6.523 Vitvi01g00929: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00929
        35.1
        not assigned.no ontology
        SPFH/Band 7/PHB domain-containing membrane-associated protein family |
        Chr5:25201320-25202535 FORWARD LENGTH=286 |
        201606
```

Coefficients for Vitvi01g00929.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.580757	1.087627e-18	***	3.711128e-18	***
SlopeC	0.04564884	0.9328578		0.988165	
MeanF-MeanC	0.319993	0.2526636		0.6126469	
SlopeF-SlopeC	1.176161	0.1545647		0.9999488	



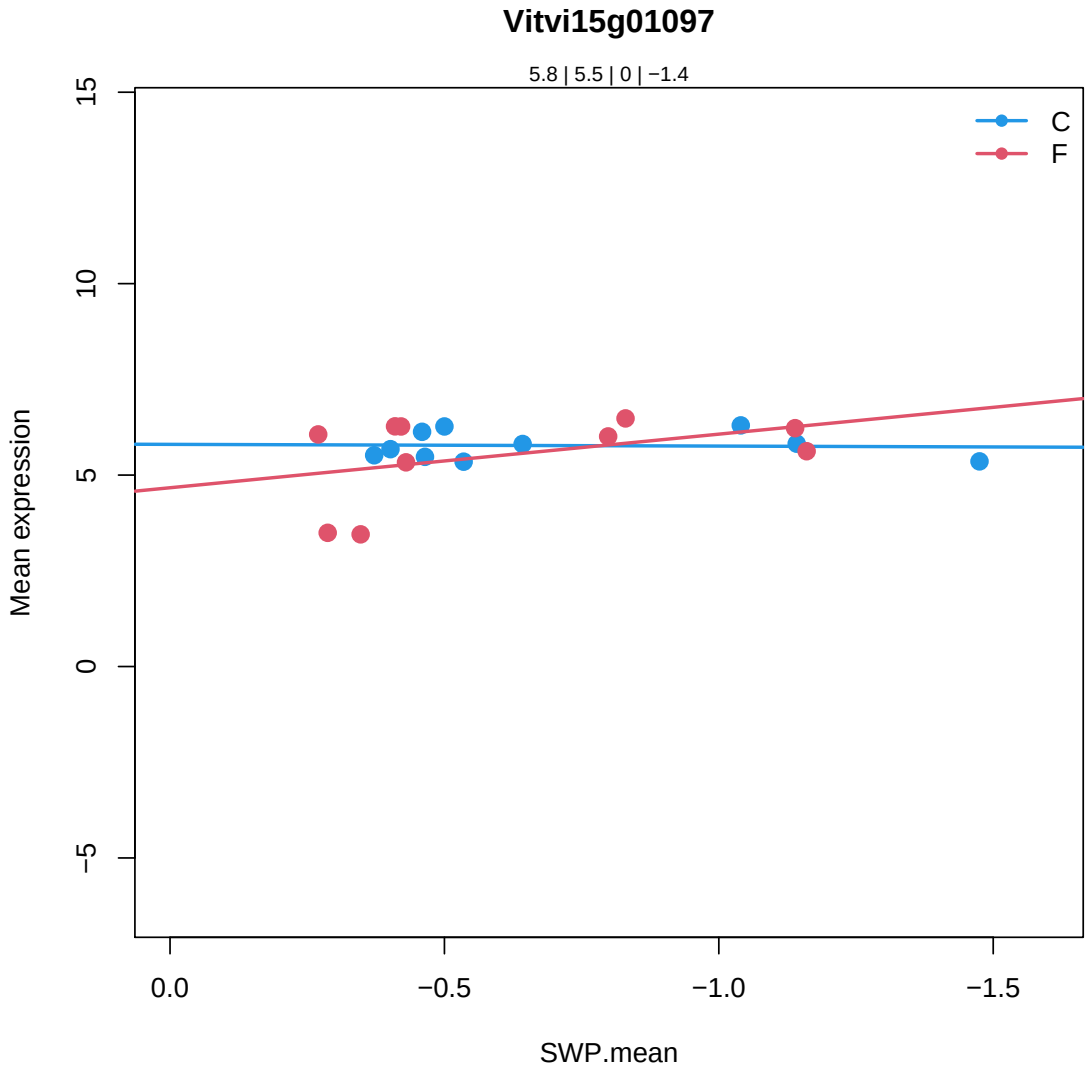
7.6.524 Vitvi15g01097: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g01097
        27.3.25
        RNA.regulation of transcription.MYB domain transcription factor family
        Homeodomain-like superfamily protein |
        Chr4:535288-536854 FORWARD LENGTH=303 |
        201606
```

Coefficients for Vitvi15g01097.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.770636	3.665724e-17	***	8.638367e-17	***
SlopeC	0.04487441	0.9460593		0.9905351	
MeanF-MeanC	-0.2487521	0.4634785		0.7859992	
SlopeF-SlopeC	-1.444661	0.153249		0.9999488	



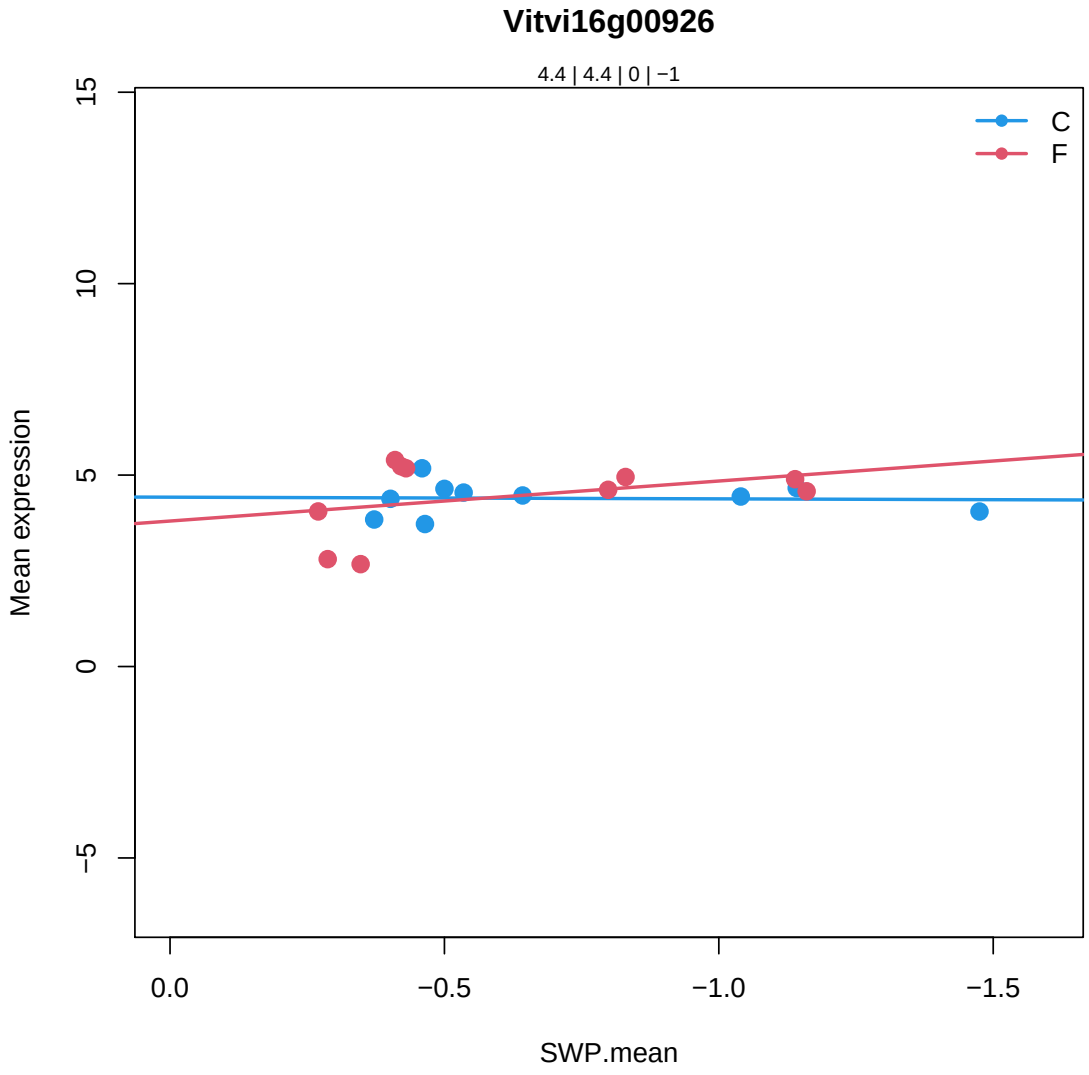
7.6.525 Vitvi16g00926: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g00926
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        peptidoglycan-binding LysM domain-containing protein |
        Chr5:24958325-24958633 FORWARD LENGTH=102 |
        201606
```

Coefficients for Vitvi16g00926.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.391962	2.353484e-15	***	4.230665e-15	***
SlopeC	0.04324878	0.9442063		0.9903035	
MeanF-MeanC	0.04441358	0.8875855		0.9704865	
SlopeF-SlopeC	-1.088611	0.2441846		0.9999488	



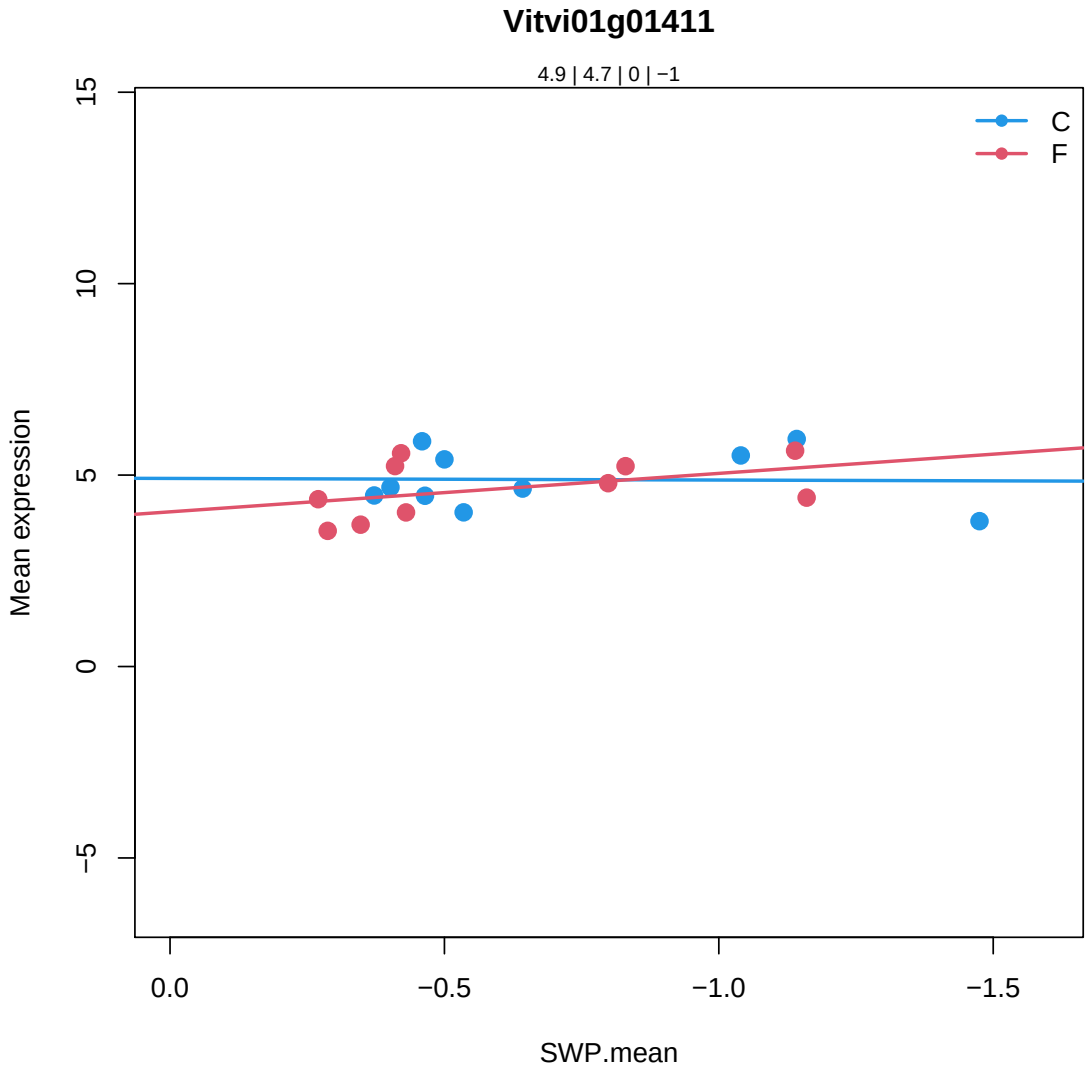
7.6.526 Vitvi01g01411: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01411
        35.1.19
        not assigned.no ontology.C2 domain-containing protein
        N-terminal-transmembrane-C2 domain type 5.1 |
        Chr1:18618255-18621643 REVERSE LENGTH=634 |
        201606
```

Coefficients for Vitvi01g01411.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.88264	3.34763e-16	***	6.696138e-16	***
SlopeC	0.04224127	0.9460838		0.9905351	
MeanF-MeanC	-0.23104	0.4695747		0.7886784	
SlopeF-SlopeC	-1.046221	0.2674338		0.9999488	

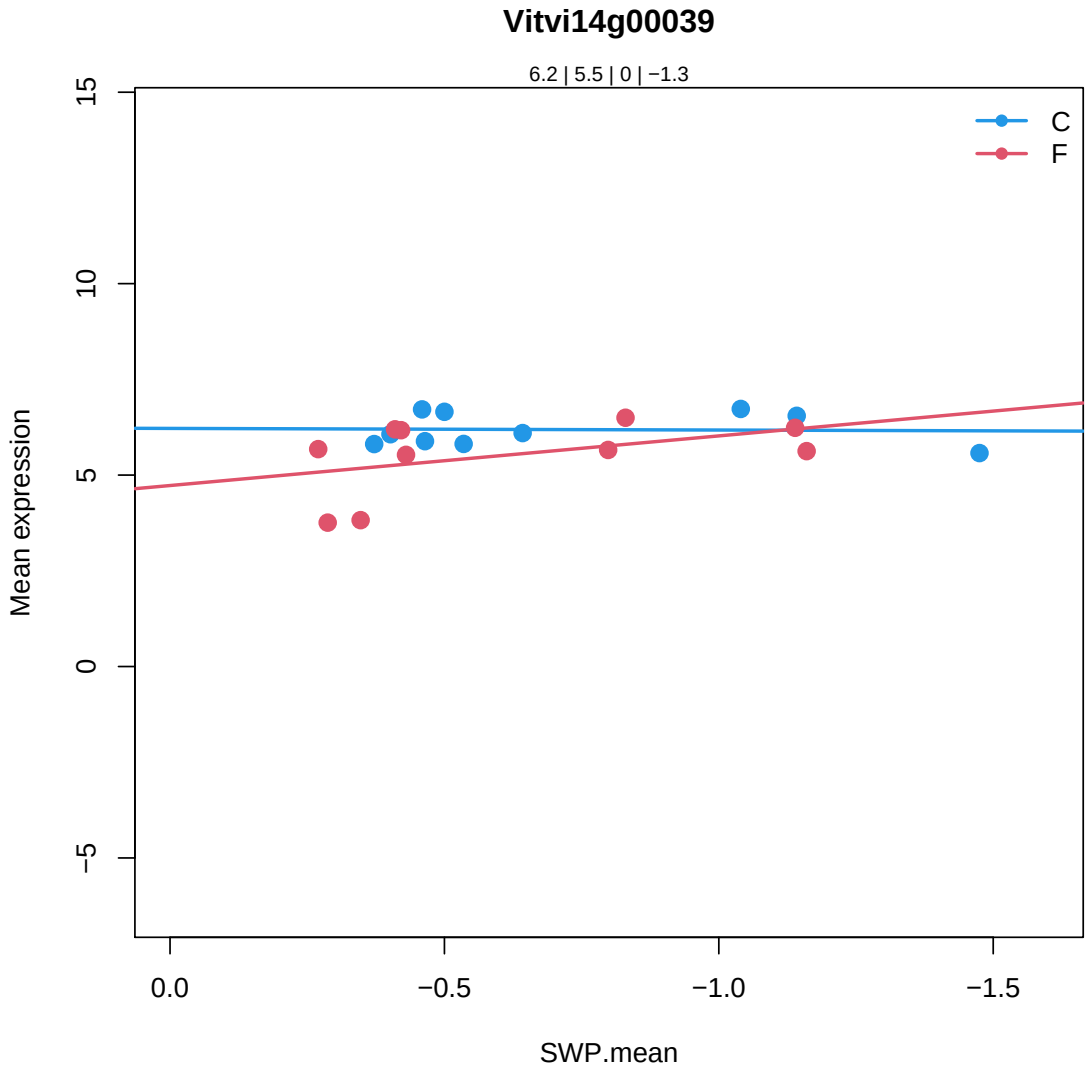


7.6.527 Vitvi14g00039: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
Vitvi14g00039
        35.2
        not assigned.unknown
        myosin heavy chain%2C cardiac protein |
        Chr5:9407981-9409735 REVERSE LENGTH=358 |
        201606
```

Coefficients for Vitvi14g00039.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.18892	9.010951e-19	***	3.146504e-18	***
SlopeC	0.04192199	0.9438752		0.9902806	
MeanF-MeanC	-0.6721593	0.0353026	*	0.188458	
SlopeF-SlopeC	-1.337999	0.141271		0.9999488	



7.6.528 Vitvi13g00149: type5

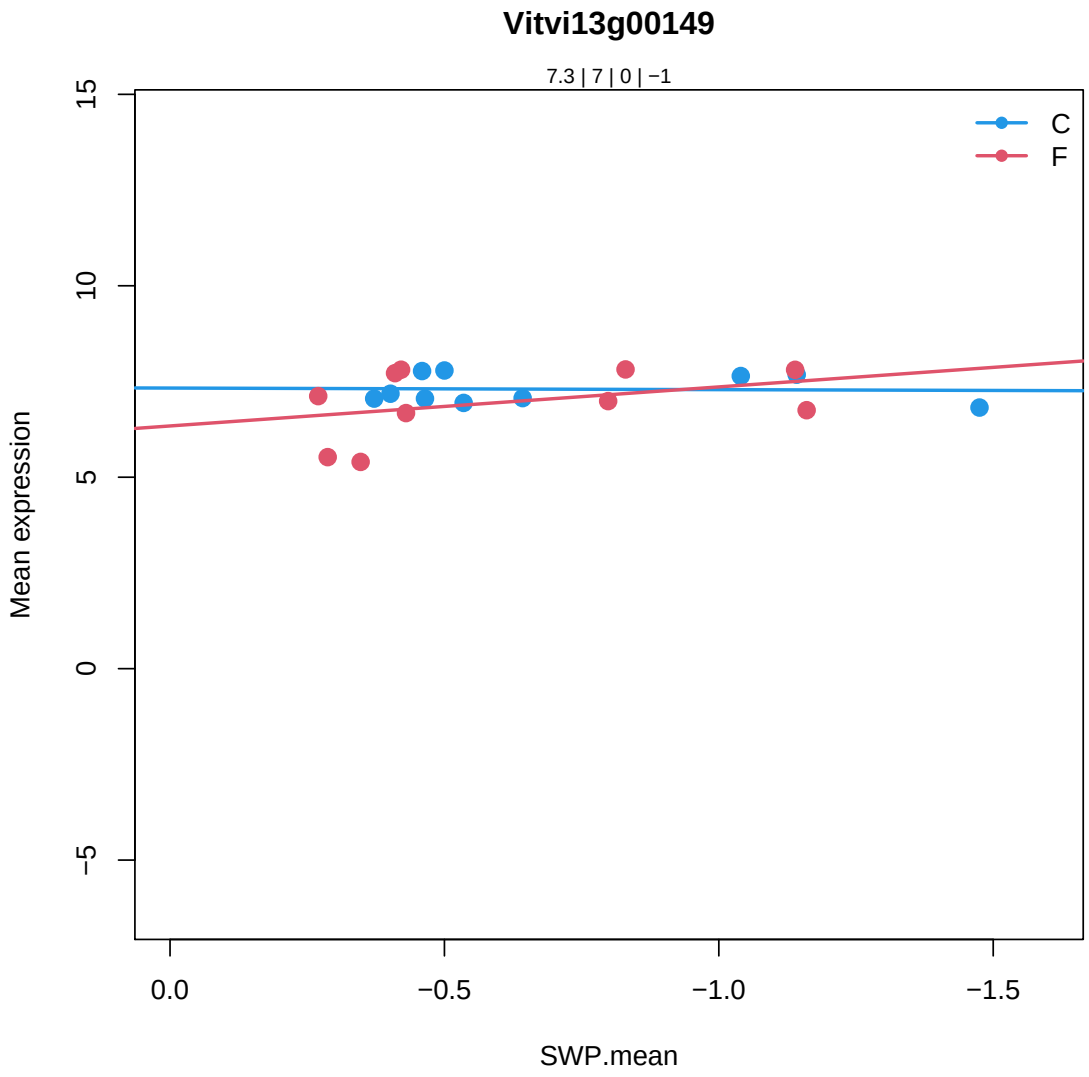
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00149
        35.2
        not assigned.unknown
        SOS3-interacting protein 1 |
        Chr5:23597092-23598531 REVERSE LENGTH=479 |
        201606

Vitvi13g00149
        29.4
        protein.postranslational modification
        SOS3-interacting protein 1 |
        Chr5:23597092-23598531 REVERSE LENGTH=479 |
        201606
```

Coefficients for Vitvi13g00149.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.299357	1.204028e-20	***	8.247997e-20	***
SlopeC	0.04140766	0.9422938		0.9899572	
MeanF-MeanC	-0.3394496	0.2504759		0.6100597	
SlopeF-SlopeC	-1.061324	0.220764		0.9999488	


Vitvi13g00149
7.3 | 7 | 0 | −1
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

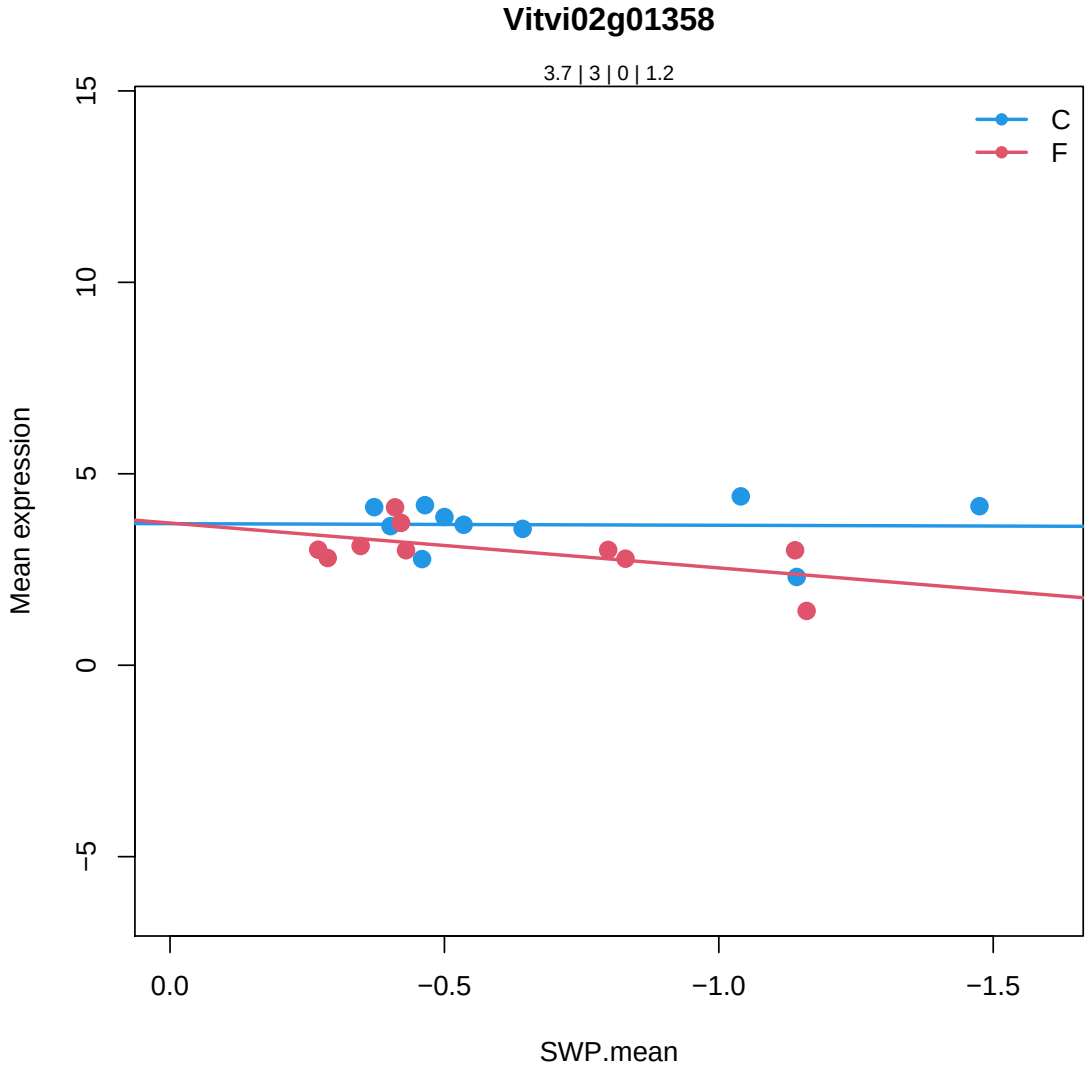
7.6.529 Vitvi02g01358: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g01358
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi02g01358.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.668085	8.659653e-15	***	1.457492e-14	***
SlopeC	0.04138081	0.9400563		0.9898527	
MeanF-MeanC	-0.6692103	0.02443828	*	0.1460126	
SlopeF-SlopeC	1.130798	0.1767225		0.9999488	



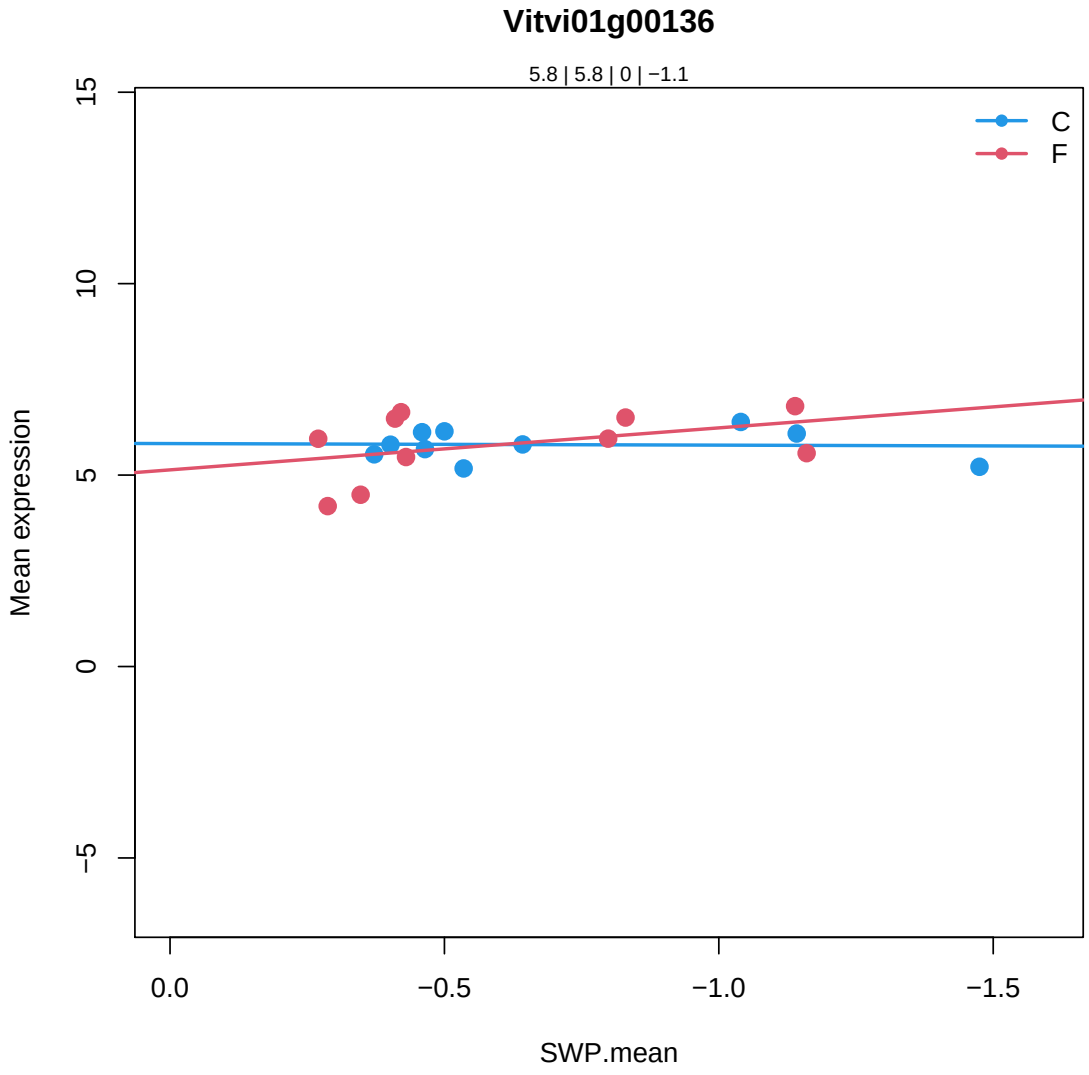
7.6.530 Vitvi01g00136: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00136
        31.4
        cell.vesicle transport
        synaptobrevin-related protein 1 |
        Chr2:14043785-14045337 REVERSE LENGTH=221 |
        201606
```

Coefficients for Vitvi01g00136.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.793844	1.23958e-18	***	4.161602e-18	***
SlopeC	0.04074705	0.9426118		0.9899572	
MeanF-MeanC	0.01011884	0.971944		0.9934113	
SlopeF-SlopeC	-1.137732	0.1859727		0.9999488	



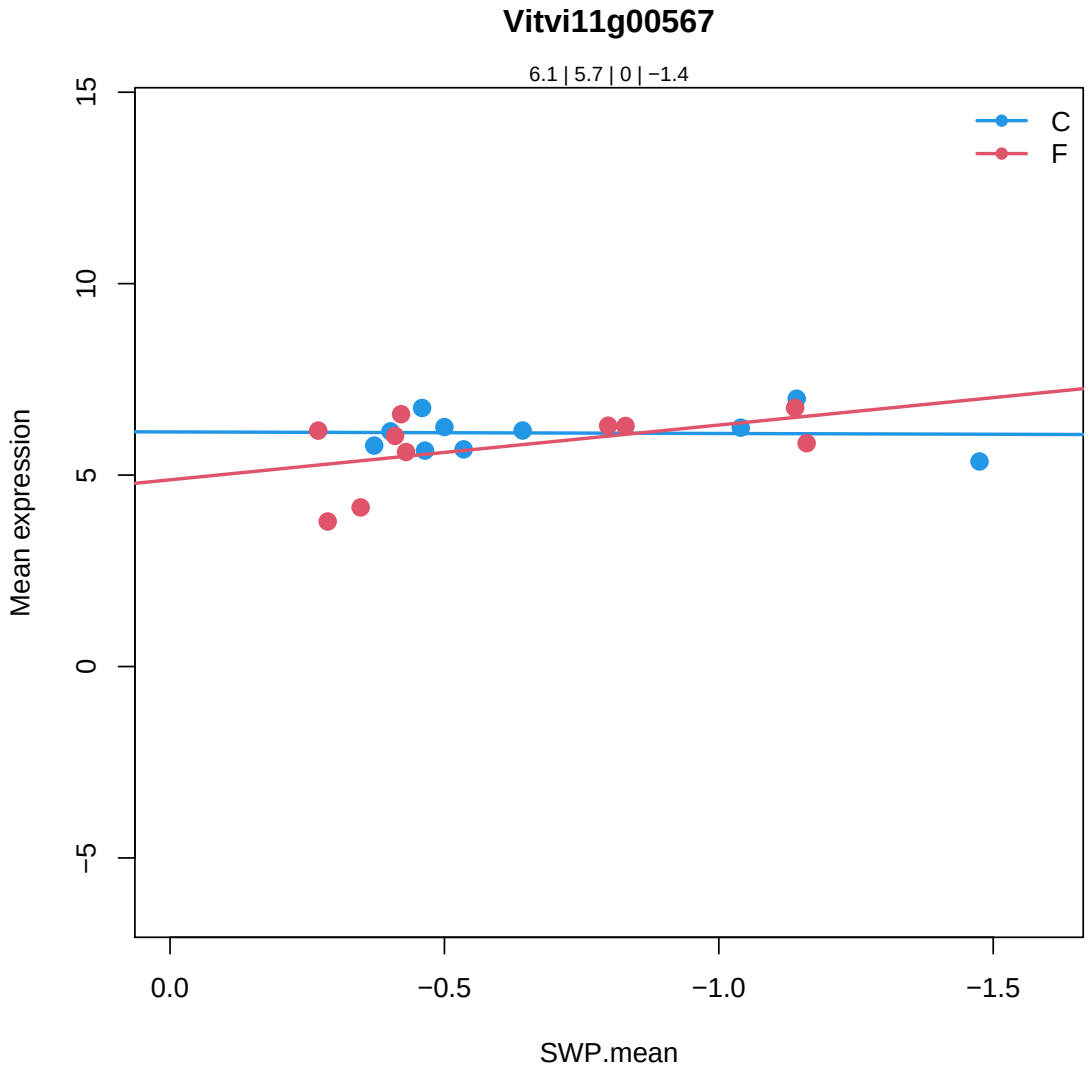
7.6.531 Vitvi11g00567: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00567
        34.7
        transport.phosphate
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi11g00567.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.098335	2.891171e-18	***	8.717554e-18	***
SlopeC	0.04037232	0.9481146		0.9911528	
MeanF-MeanC	-0.3505821	0.2731202		0.6367235	
SlopeF-SlopeC	-1.471452	0.1215198		0.9999488	



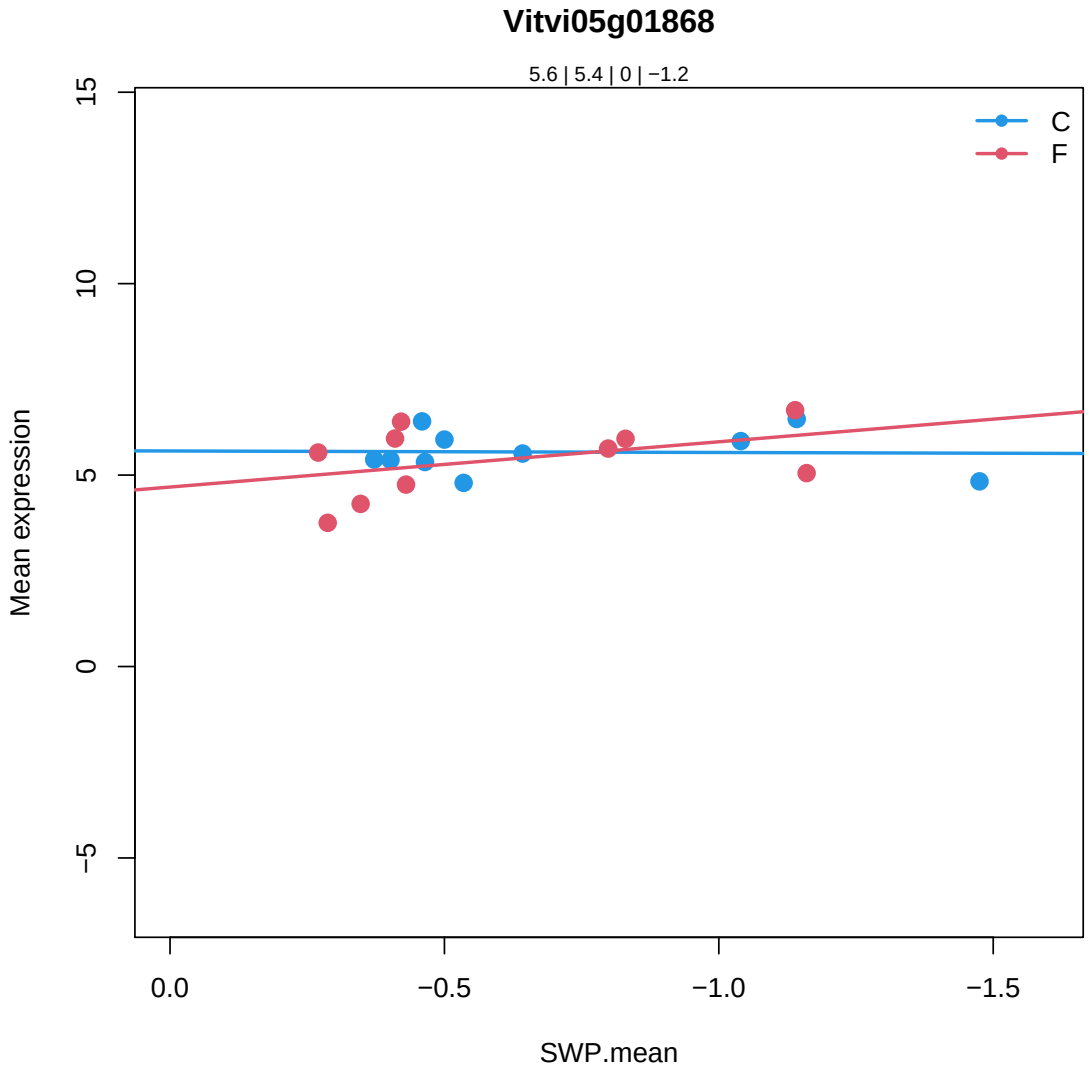
7.6.532 Vitvi05g01868: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01868
        35.2
        not assigned.unknown
        PH-response transcription factor |
        Chr4:8875932-8877567 FORWARD LENGTH=337 |
        201606
```

Coefficients for Vitvi05g01868.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.601797	2.37684e-17	***	5.796447e-17	***
SlopeC	0.03898937	0.9506954		0.9922795	
MeanF-MeanC	-0.1941575	0.5464009		0.8313658	
SlopeF-SlopeC	-1.221139	0.2019139		0.9999488	



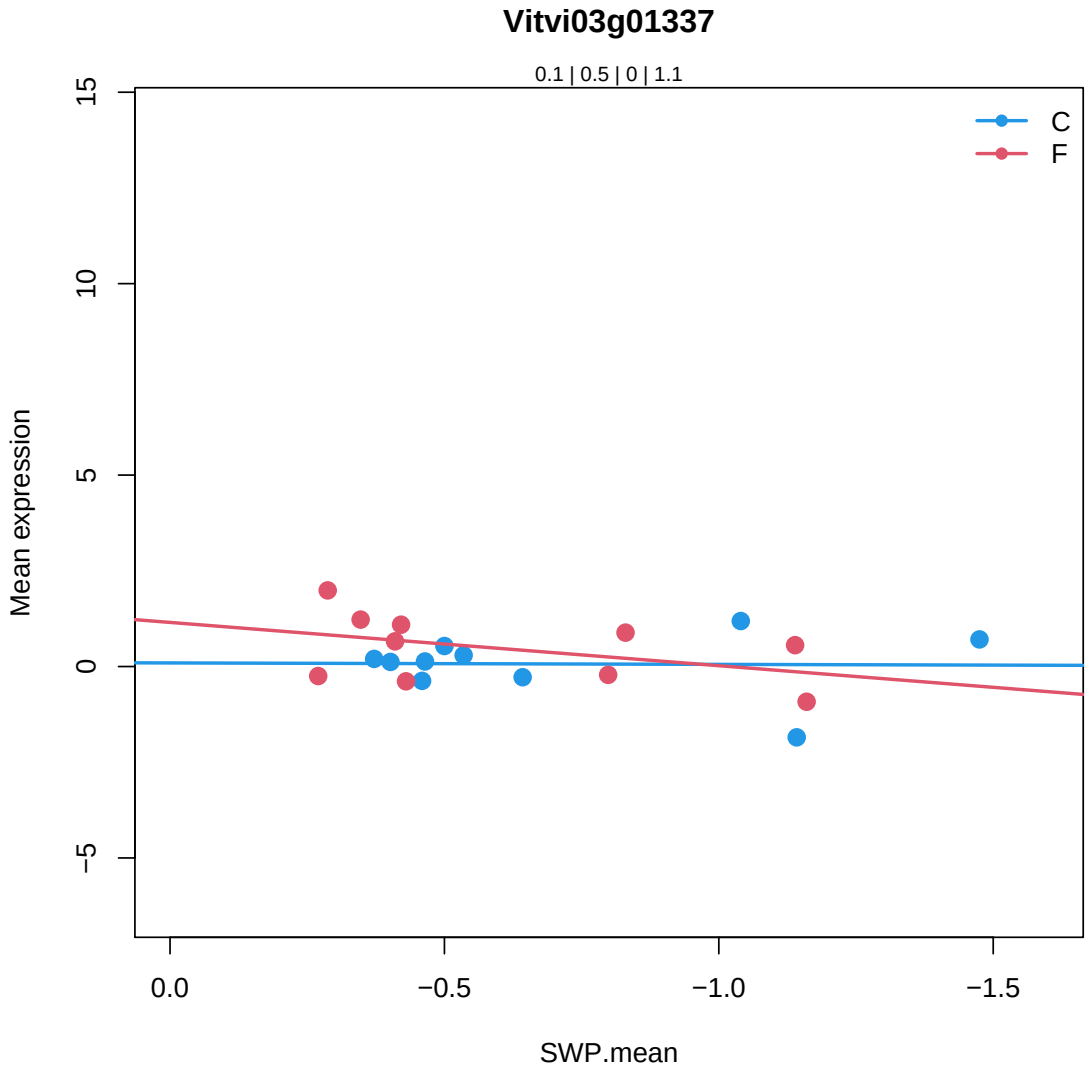
7.6.533 Vitvi03g01337: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g01337
        35.2
        not assigned.unknown
        SAUR-like auxin-responsive protein family |
        Chr1:28383250-28383714 REVERSE LENGTH=154 |
        201606
```

Coefficients for Vitvi03g01337.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.06699014	0.7884233		0.7925833	
SlopeC	0.03750429	0.9568984		0.9928124	
MeanF-MeanC	0.3962323	0.268286		0.6306625	
SlopeF-SlopeC	1.092515	0.2964171		0.9999488	



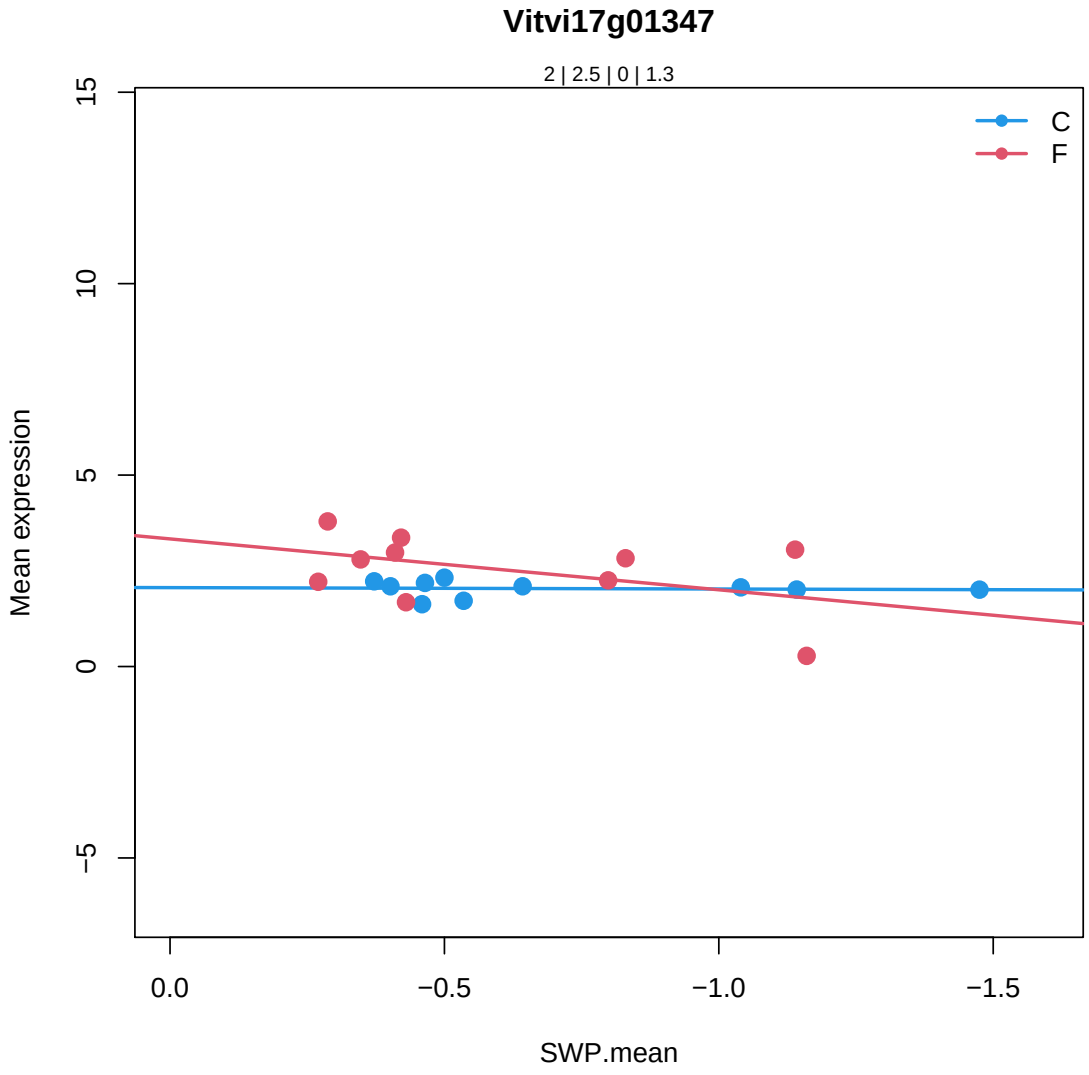
7.6.534 Vitvi17g01347: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g01347
        27.3.99
        RNA.regulation of transcription.unclassified
        SHOOT GRAVITROPISM-like protein |
        Chr3:17994048-17994595 FORWARD LENGTH=158 |
        201606
```

Coefficients for Vitvi17g01347.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.034935	1.356567e-09	***	1.703897e-09	***
SlopeC	0.03606528	0.9493873		0.9918417	
MeanF-MeanC	0.4881348	0.1016914		0.3679914	
SlopeF-SlopeC	1.292789	0.1365571		0.9999488	



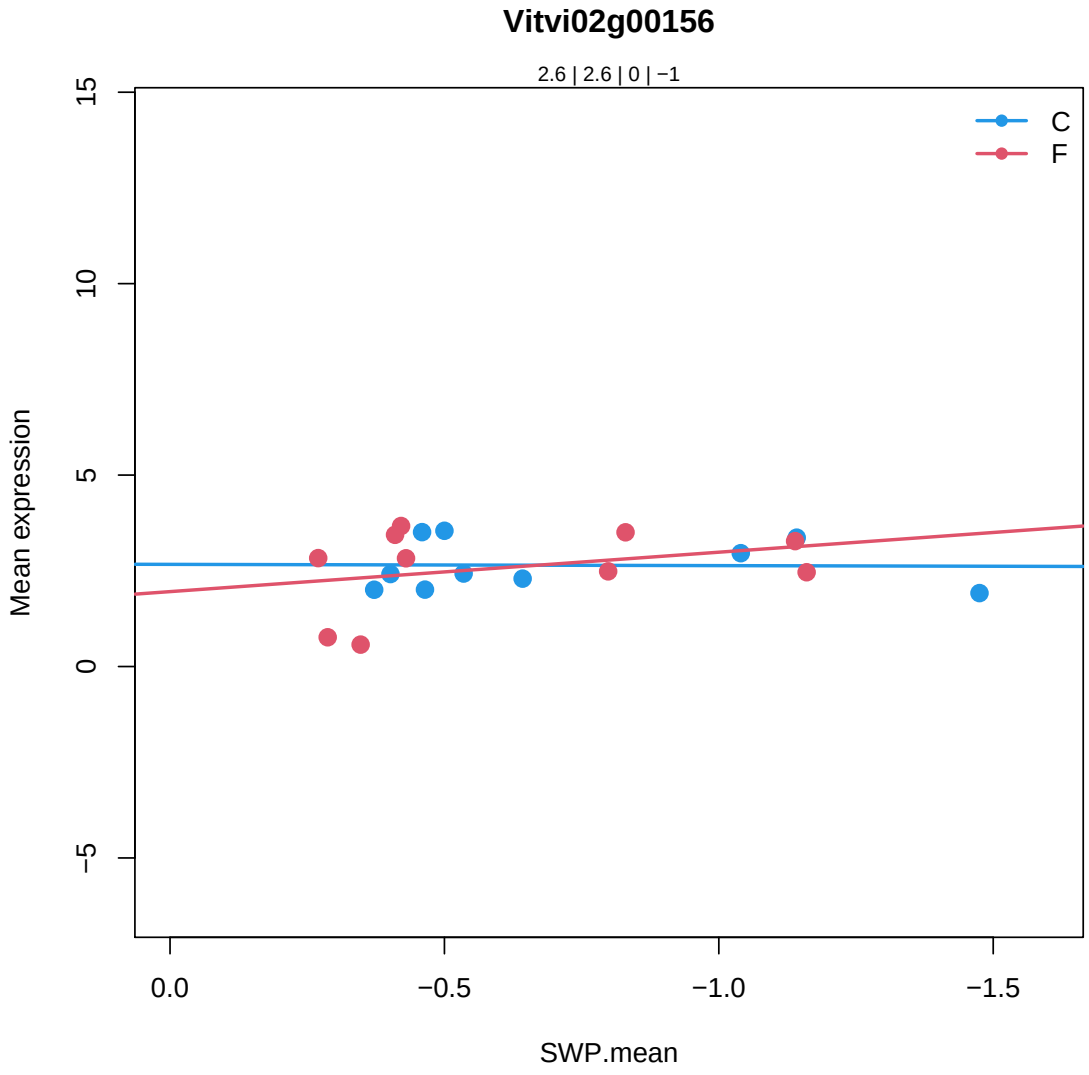
7.6.535 Vitvi02g00156: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00156
        35.2
        not assigned.unknown
        Galactose-binding protein |
        Chr1:8099150-8101220 FORWARD LENGTH=660 |
        201606
```

Coefficients for Vitvi02g00156.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.64497	1.281317e-09	***	1.61084e-09	***
SlopeC	0.03271315	0.9645539		0.9943952	
MeanF-MeanC	-0.0618388	0.8687772		0.965202	
SlopeF-SlopeC	-1.062509	0.3374547		0.9999488	



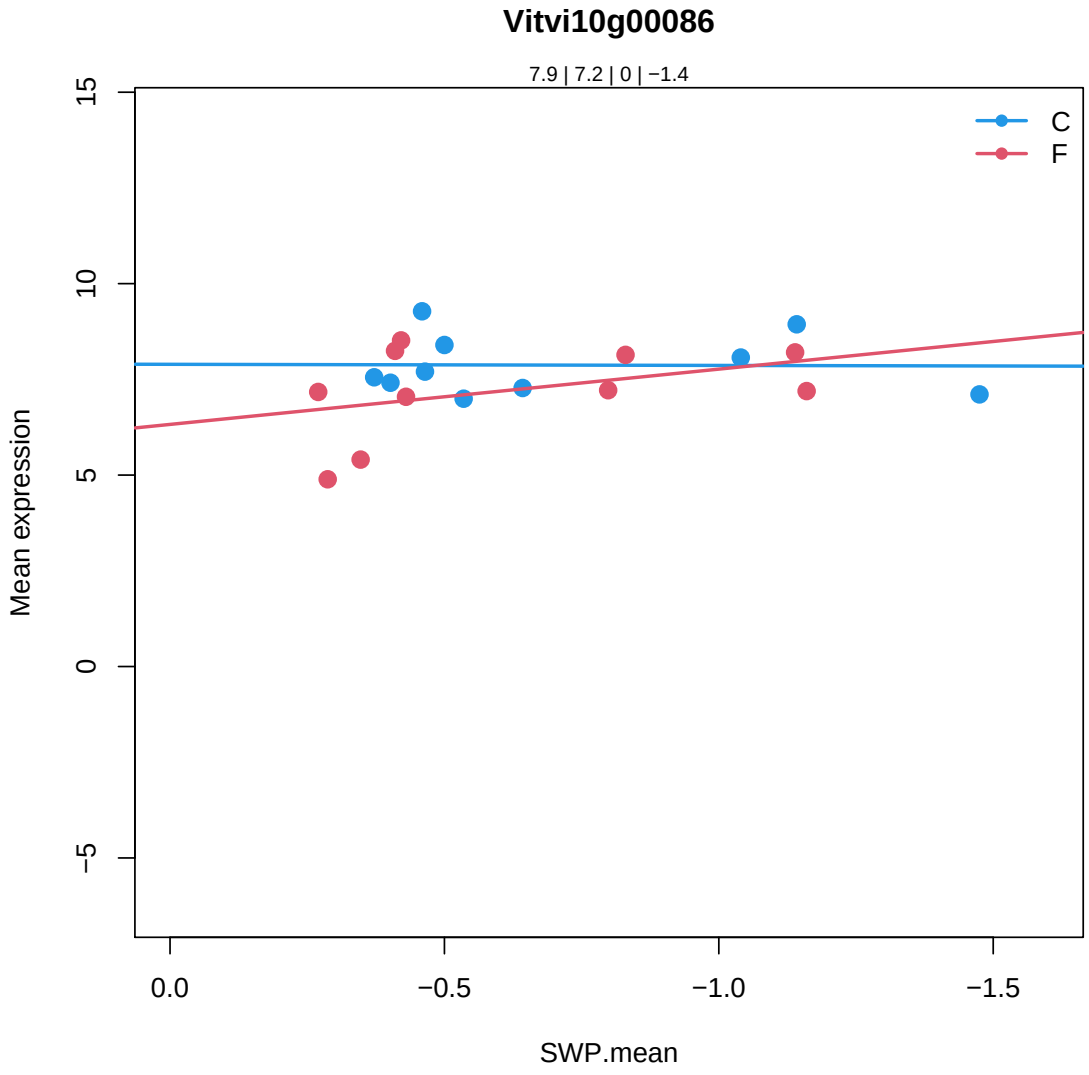
7.6.536 Vitvi10g00086: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00086
        14.2
        S-assimilation.APR
        APS reductase 3 |
        Chr4:11657284-11658973 REVERSE LENGTH=458 |
        201606
```

Coefficients for Vitvi10g00086.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.872661	3.924538e-18	***	1.143963e-17	***
SlopeC	0.02889794	0.9716345		0.9961209	
MeanF-MeanC	-0.6697836	0.1155182		0.397725	
SlopeF-SlopeC	-1.472878	0.2313023		0.9999488	



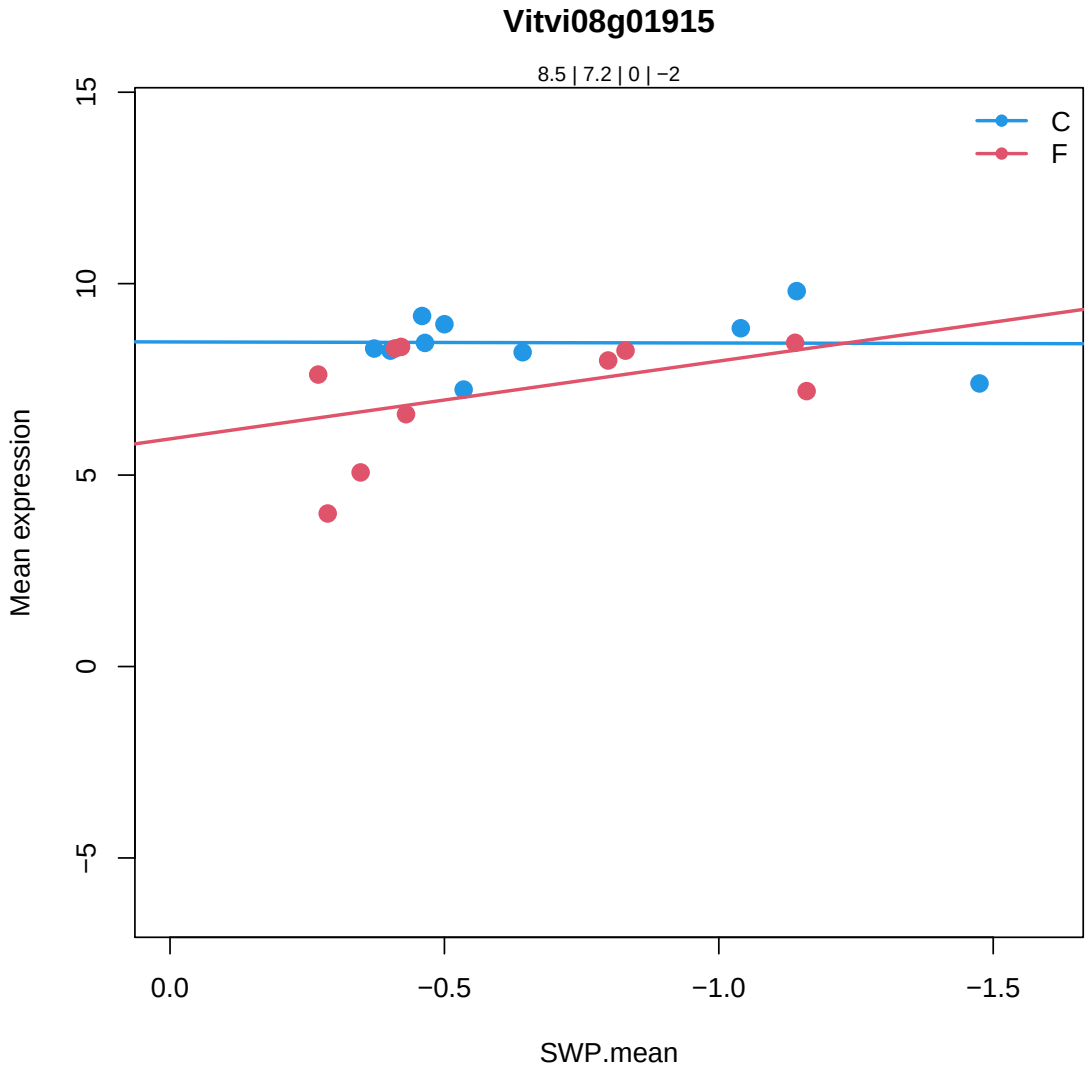
7.6.537 Vitvi08g01915: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01915
        19.10
        tetrapyrrole synthesis.magnesium chelatase
        magnesium-chelatase subunit chlH%2C chloroplast%2C putative / Mg-proto
        Chr5:4387567-4392082 REVERSE LENGTH=1381 |
        201606
```

Coefficients for Vitvi08g01915.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	8.457666	1.560842e-17	***	3.949917e-17	***
SlopeC	0.02775976	0.9762615		0.9963787	
MeanF-MeanC	-1.274937	0.01267845	*	0.09068273	.
SlopeF-SlopeC	-2.060202	0.1478986		0.9999488	



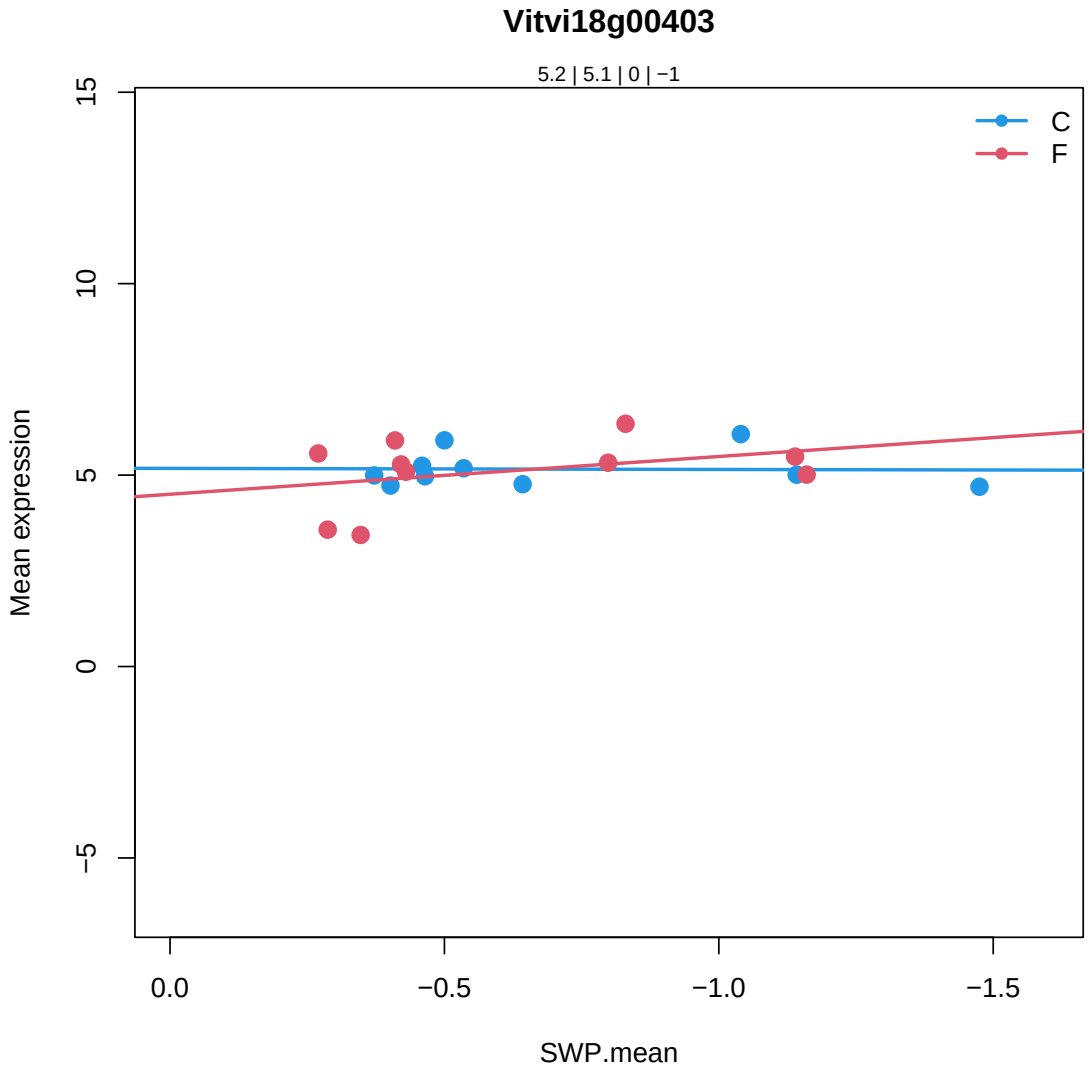
7.6.538 Vitvi18g00403: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00403
        35.2
        not assigned.unknown
        transmembrane protein |
        Chr1:12685317-12687435 FORWARD LENGTH=481 |
        201606
```

Coefficients for Vitvi18g00403.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.154956	6.564638e-17	***	1.472961e-16	***
SlopeC	0.02768045	0.96377		0.9940305	
MeanF-MeanC	-0.05484497	0.859515		0.9632816	
SlopeF-SlopeC	-1.01372	0.2706328		0.9999488	



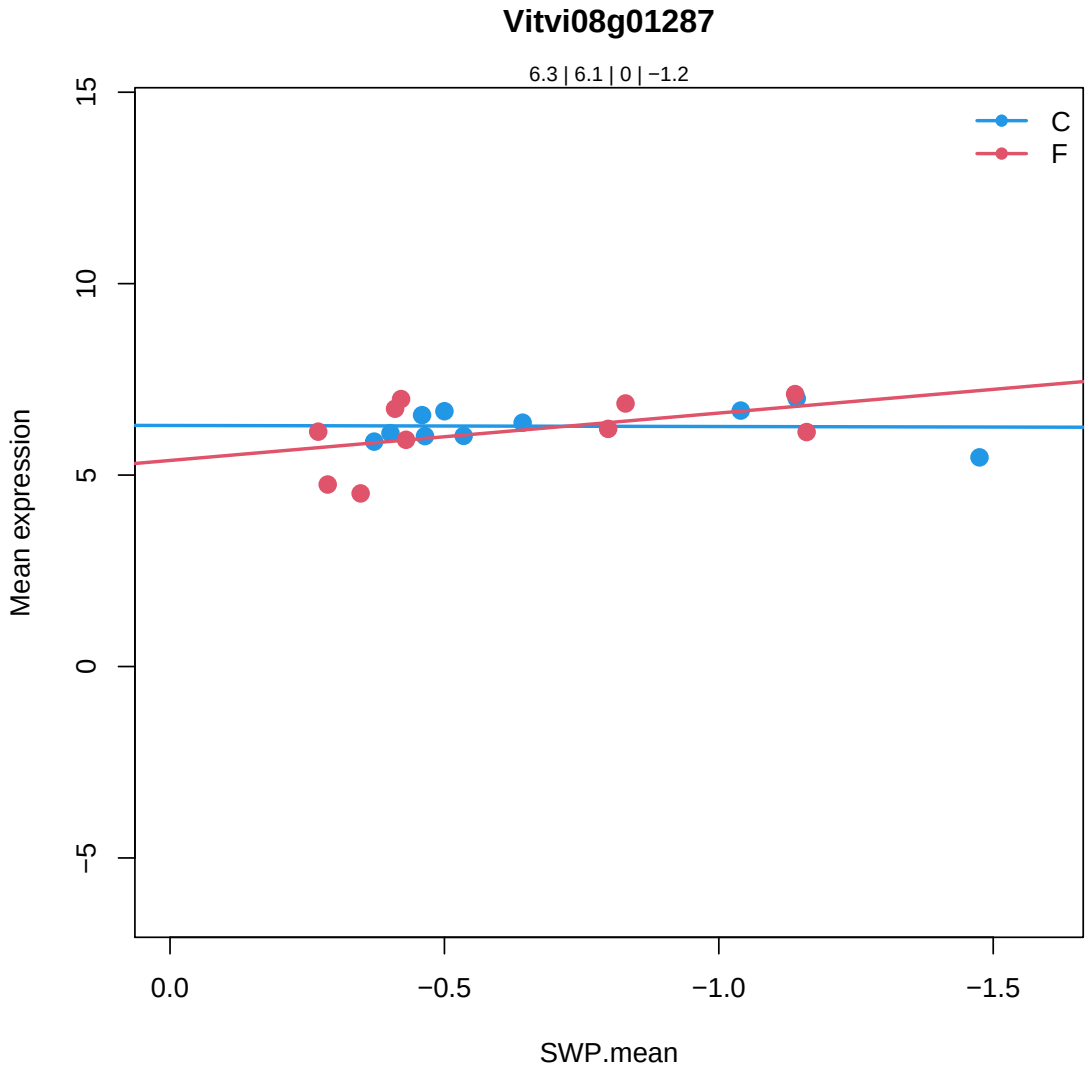
7.6.539 Vitvi08g01287: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01287
        35.2
        not assigned.unknown
        TIP41-like protein |
        Chr3:19996757-19997858 FORWARD LENGTH=301 |
        201606
```

Coefficients for Vitvi08g01287.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.276216	2.548475e-19	***	1.056113e-18	***
SlopeC	0.0272595	0.9617606		0.9939741	
MeanF-MeanC	-0.1400268	0.6289761		0.8733583	
SlopeF-SlopeC	-1.264905	0.1450568		0.9999488	



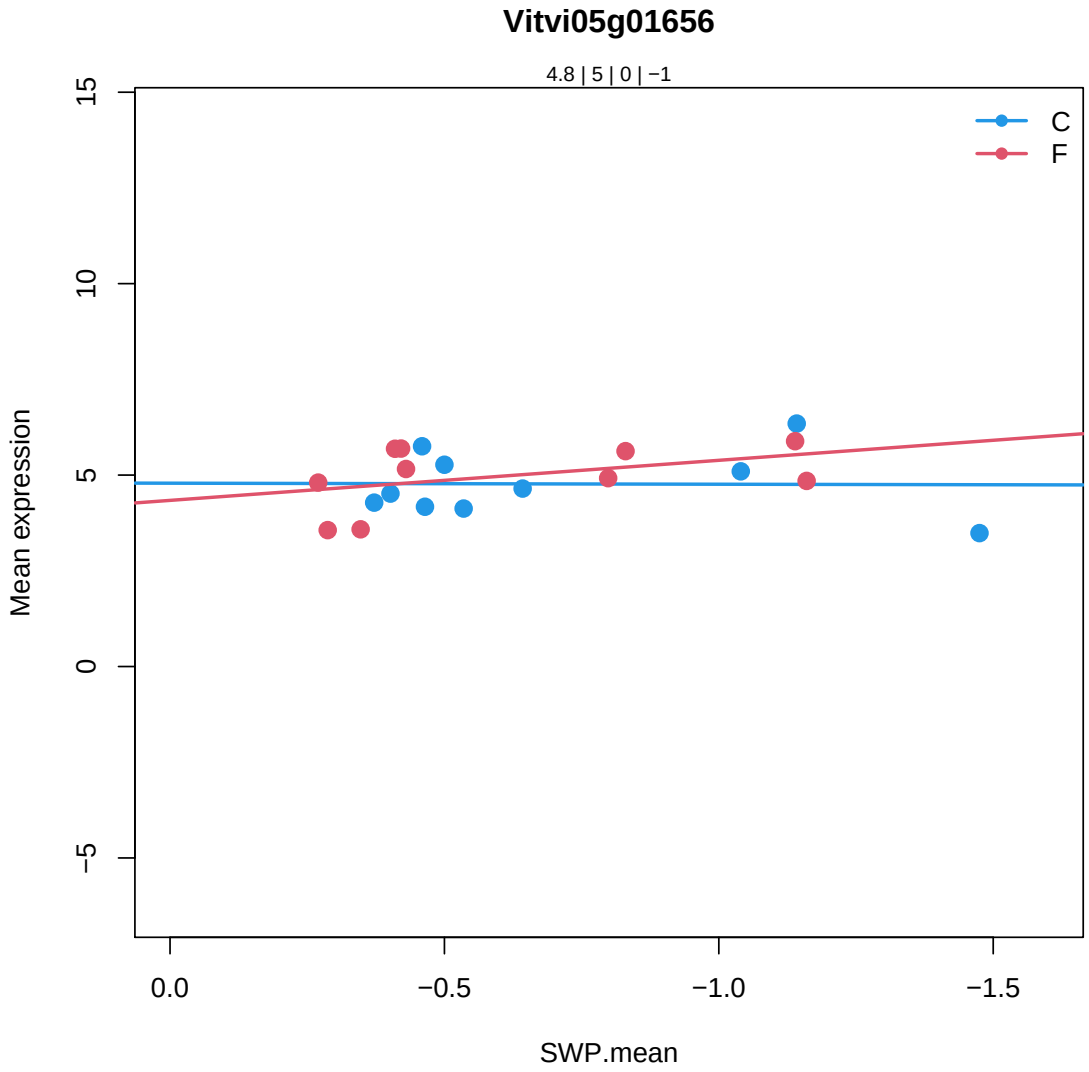
7.6.540 Vitvi05g01656: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01656
        29.4
        protein.postranslational modification
        Integrin-linked protein kinase family |
        Chr3:22103006-22105323 REVERSE LENGTH=477 |
        201606
```

Coefficients for Vitvi05g01656.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.769116	4.470931e-15	***	7.784548e-15	***
SlopeC	0.02710239	0.9687811		0.9954269	
MeanF-MeanC	0.2074113	0.5573259		0.8379714	
SlopeF-SlopeC	-1.073673	0.3036488		0.9999488	



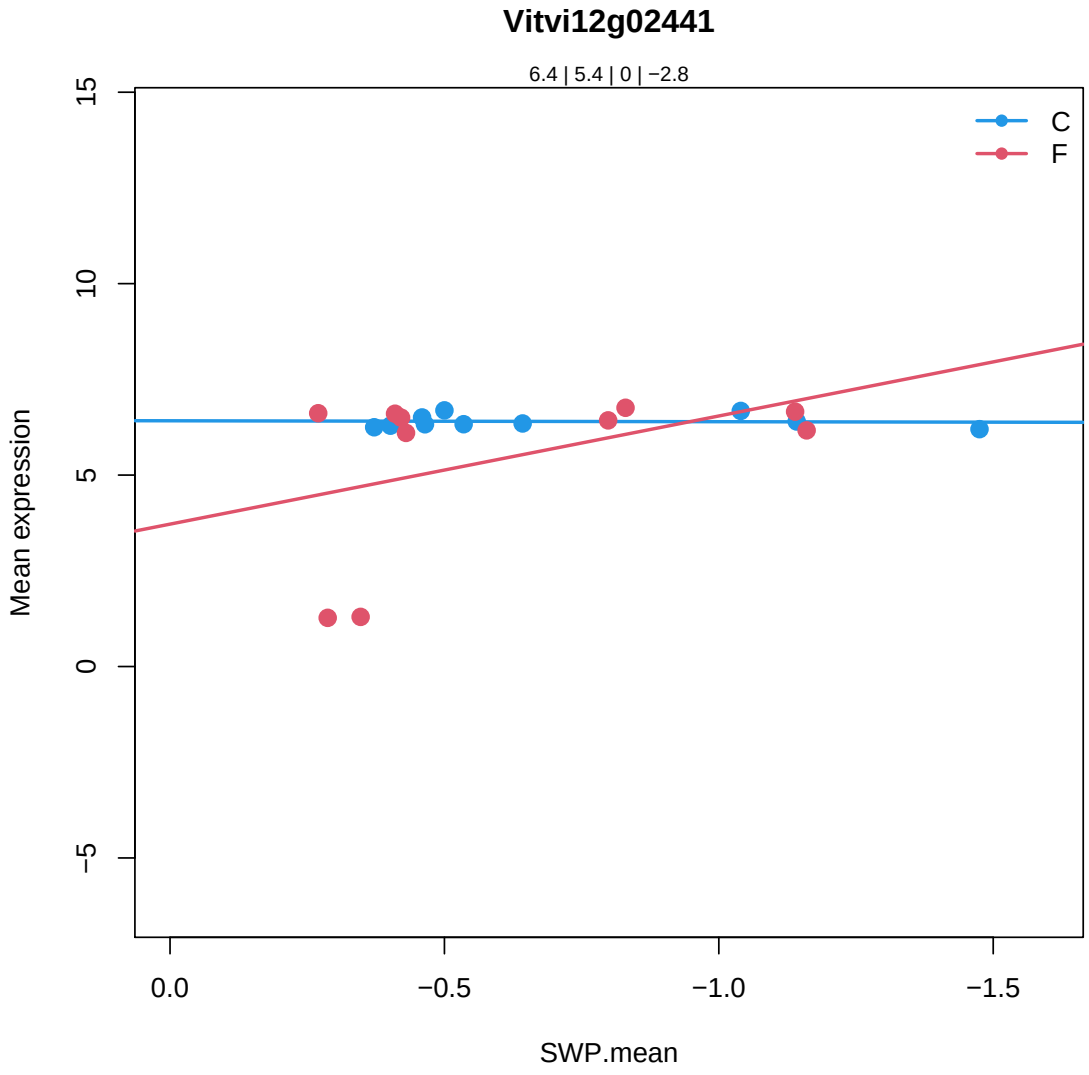
7.6.541 Vitvi12g02441: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02441
        27.3.7
        RNA.regulation of transcription.C2C2(Zn) Constans-like zinc finger fam
        B-box type zinc finger family protein |
        Chr4:13675853-13676616 FORWARD LENGTH=223 |
        201606
```

Coefficients for Vitvi12g02441.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.401049	4.065163e-13	***	5.983122e-13	***
SlopeC	0.02401503	0.9835357		0.9979351	
MeanF-MeanC	-0.9613183	0.114726		0.396071	
SlopeF-SlopeC	-2.848841	0.1106466		0.9999488	



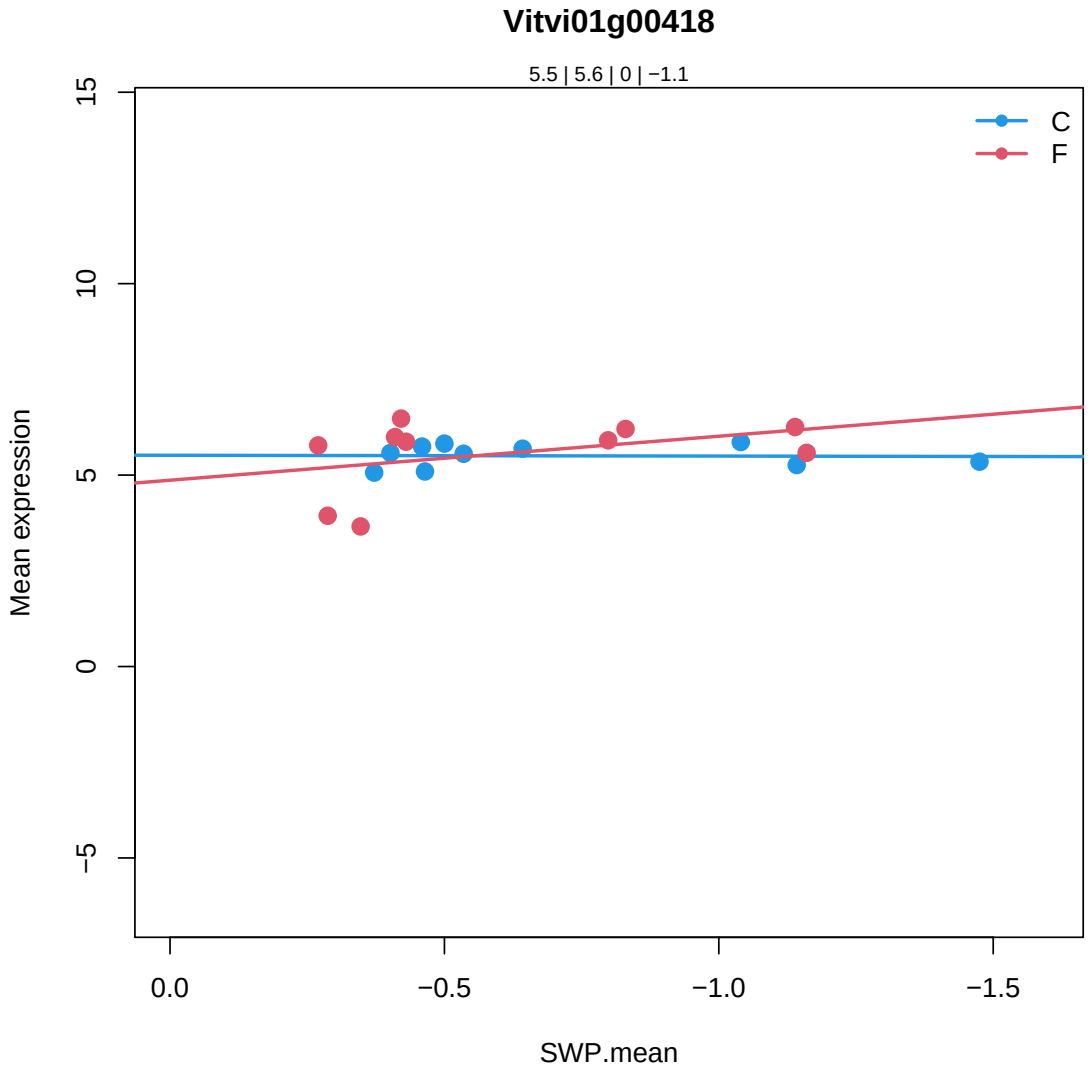
7.6.542 Vitvi01g00418: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00418
        30.4.3
        signalling.phosphinositides.bis(5'-nucleosyl)-tetraphosphatase (assyme
        nudix hydrolase homolog 25 |
        Chr1:10582700-10583821 FORWARD LENGTH=175 |
        201606
```

Coefficients for Vitvi01g00418.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.502468	6.125399e-18	***	1.695973e-17	***
SlopeC	0.02101547	0.9711097		0.9959396	
MeanF-MeanC	0.06348959	0.829666		0.9526278	
SlopeF-SlopeC	-1.16993	0.1847043		0.9999488	



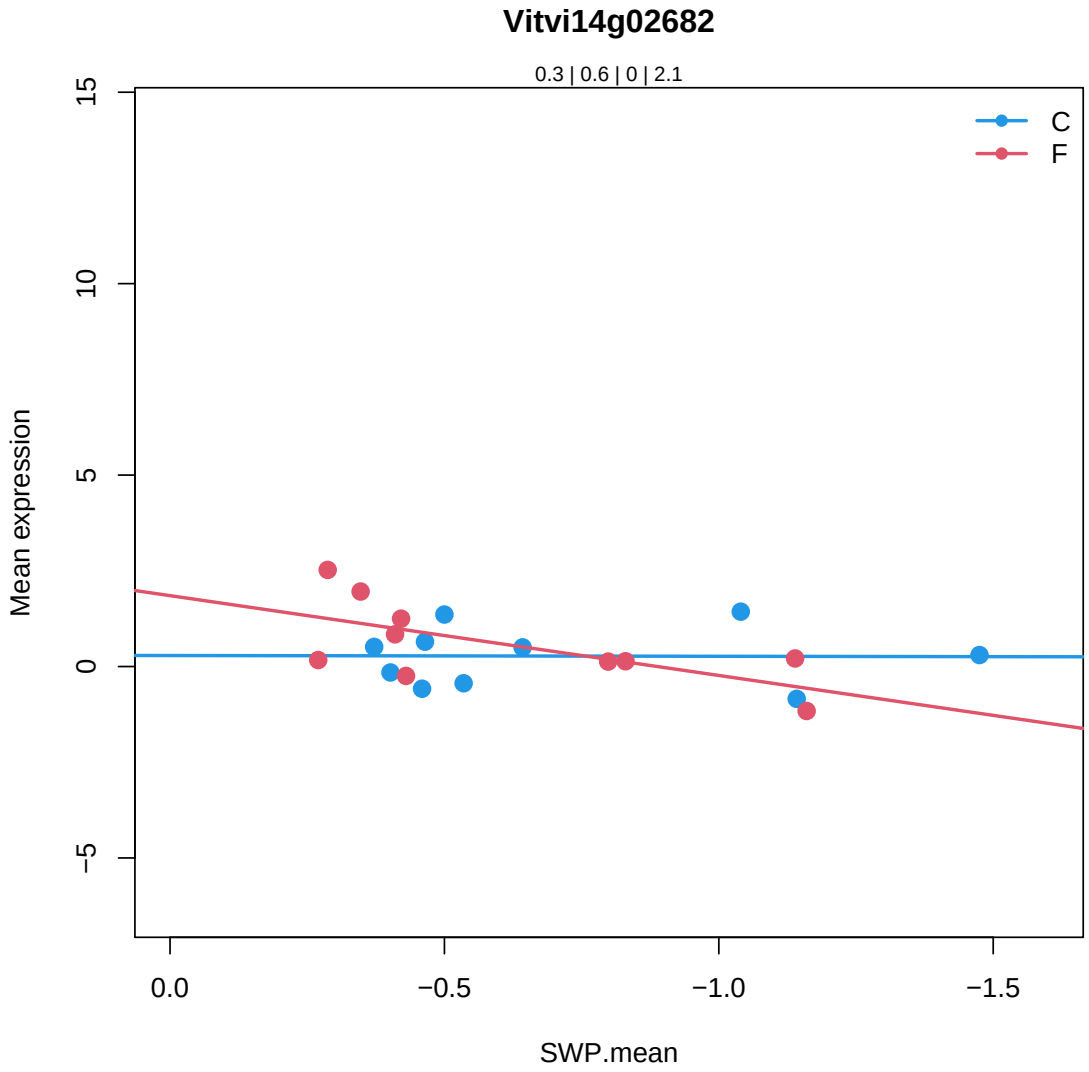
7.6.543 Vitvi14g02682: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g02682
        31.1
        cell.organisation
        Ankyrin repeat family protein |
        Chr4:1554420-1556571 FORWARD LENGTH=629 |
        201606
```

Coefficients for Vitvi14g02682.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.2730829	0.2749453		0.280428	
SlopeC	0.01968125	0.9771146		0.9966352	
MeanF-MeanC	0.3078497	0.3817249		0.7331307	
SlopeF-SlopeC	2.064588	0.05326133	.	0.9999488	



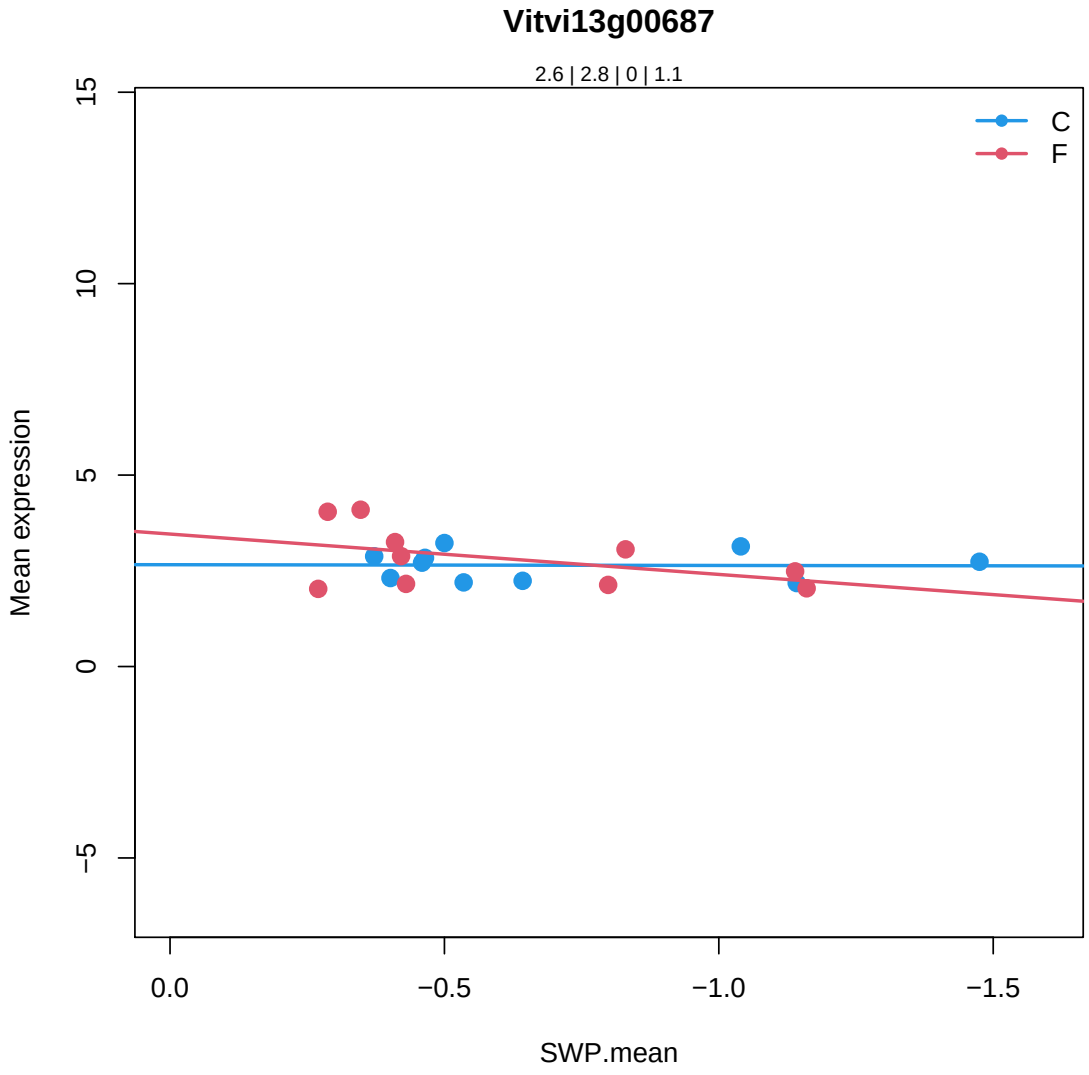
7.6.544 Vitvi13g00687: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00687
        35.1
        not assigned.no ontology
        ACT-like superfamily protein |
        Chr2:15451834-15453550 REVERSE LENGTH=410 |
        201606
```

Coefficients for Vitvi13g00687.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.645428	1.452835e-12	***	2.064718e-12	***
SlopeC	0.01911107	0.9702916		0.9957745	
MeanF-MeanC	0.1719108	0.5120177		0.8136412	
SlopeF-SlopeC	1.03501	0.1845373		0.9999488	



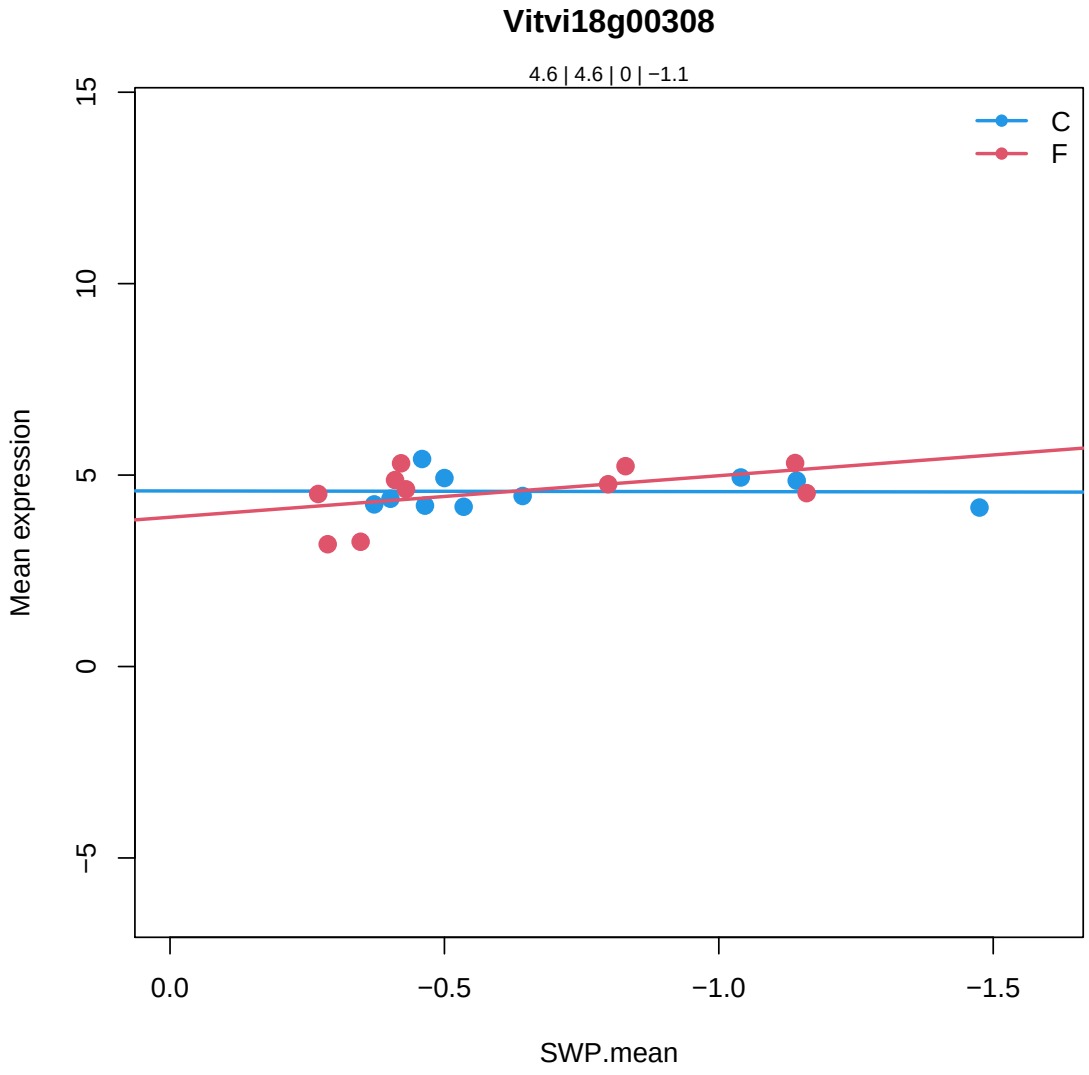
7.6.545 Vitvi18g00308: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00308
        35.1
        not assigned.no ontology
        camphor resistance CrcB family protein |
        Chr2:17398083-17399910 FORWARD LENGTH=461 |
        201606
```

Coefficients for Vitvi18g00308.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.57304	1.953194e-17	***	4.855747e-17	***
SlopeC	0.01786723	0.9720471		0.9961209	
MeanF-MeanC	-0.01307485	0.9597684		0.9914232	
SlopeF-SlopeC	-1.10283	0.1560234		0.9999488	



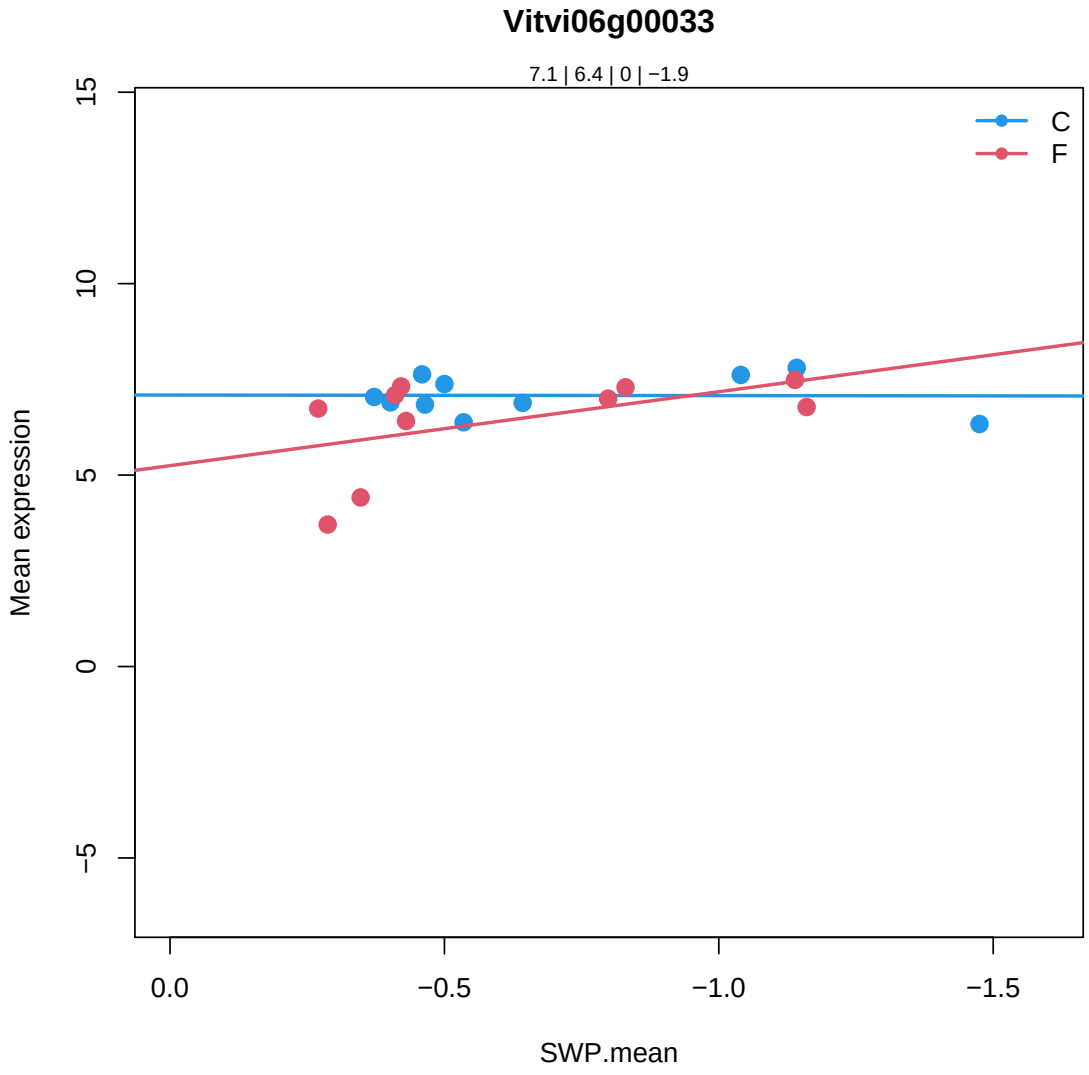
7.6.546 Vitvi06g00033: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00033
        35.2
        not assigned.unknown
        protein containing PDZ domain%2C a K-box domain%2C and a TPR region |
        Chr1:20713822-20715351 FORWARD LENGTH=335 |
        201606
```

Coefficients for Vitvi06g00033.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.07999	5.017052e-18	***	1.420582e-17	***
SlopeC	0.01420072	0.9846793		0.9979351	
MeanF-MeanC	-0.6572797	0.09111471	.	0.3456204	
SlopeF-SlopeC	-1.945244	0.08790897	.	0.9999488	



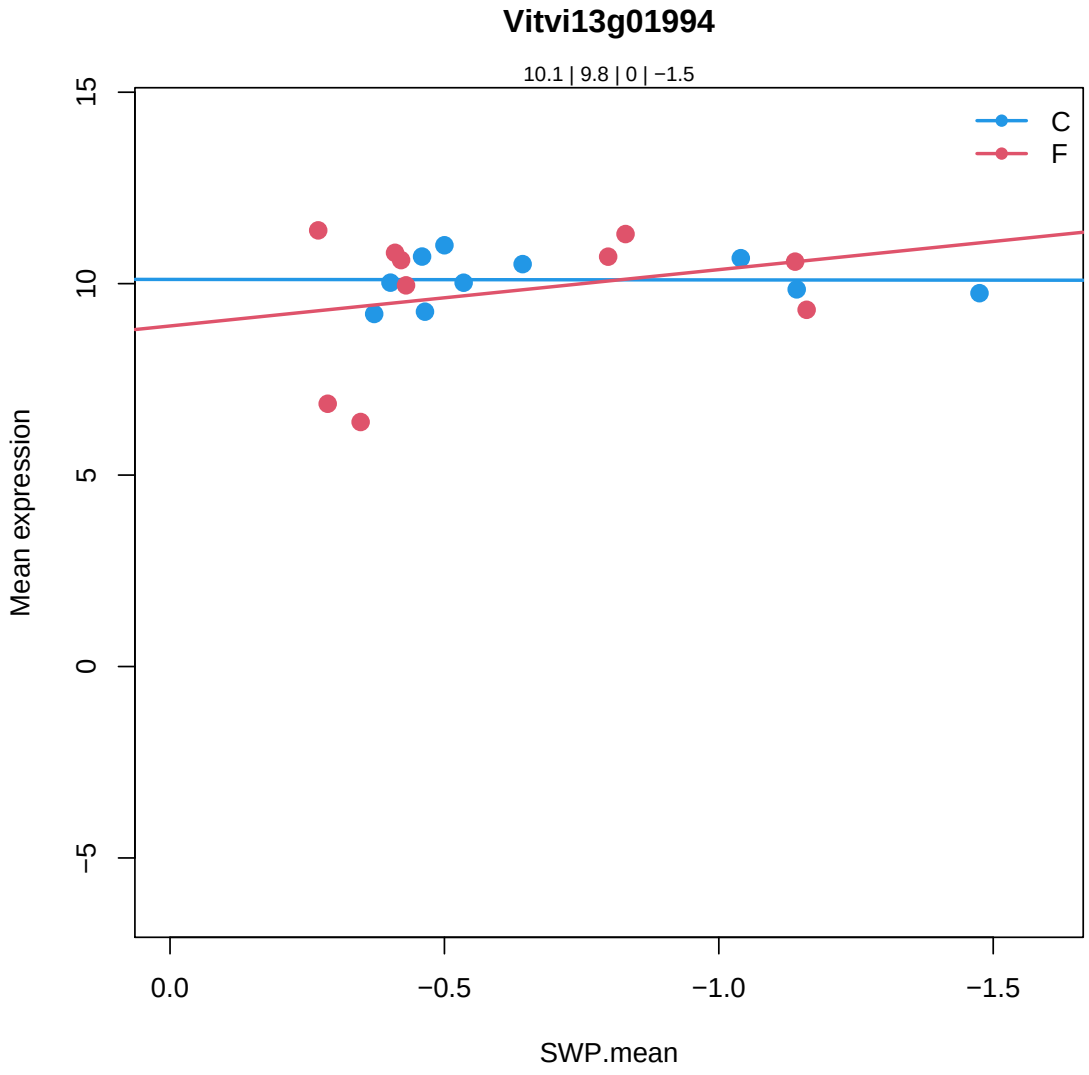
7.6.547 Vitvi13g01994: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g01994
        1.3.13
        PS.calvin cycle.rubisco interacting
        rubisco activase |
        Chr2:16571046-16573345 REVERSE LENGTH=446 |
        201606
```

Coefficients for Vitvi13g01994.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	10.10108	6.233033e-18	***	1.722021e-17	***
SlopeC	0.01249475	0.990649		0.9983274	
MeanF-MeanC	-0.3104117	0.568282		0.8447911	
SlopeF-SlopeC	-1.48391	0.3546151		0.9999488	



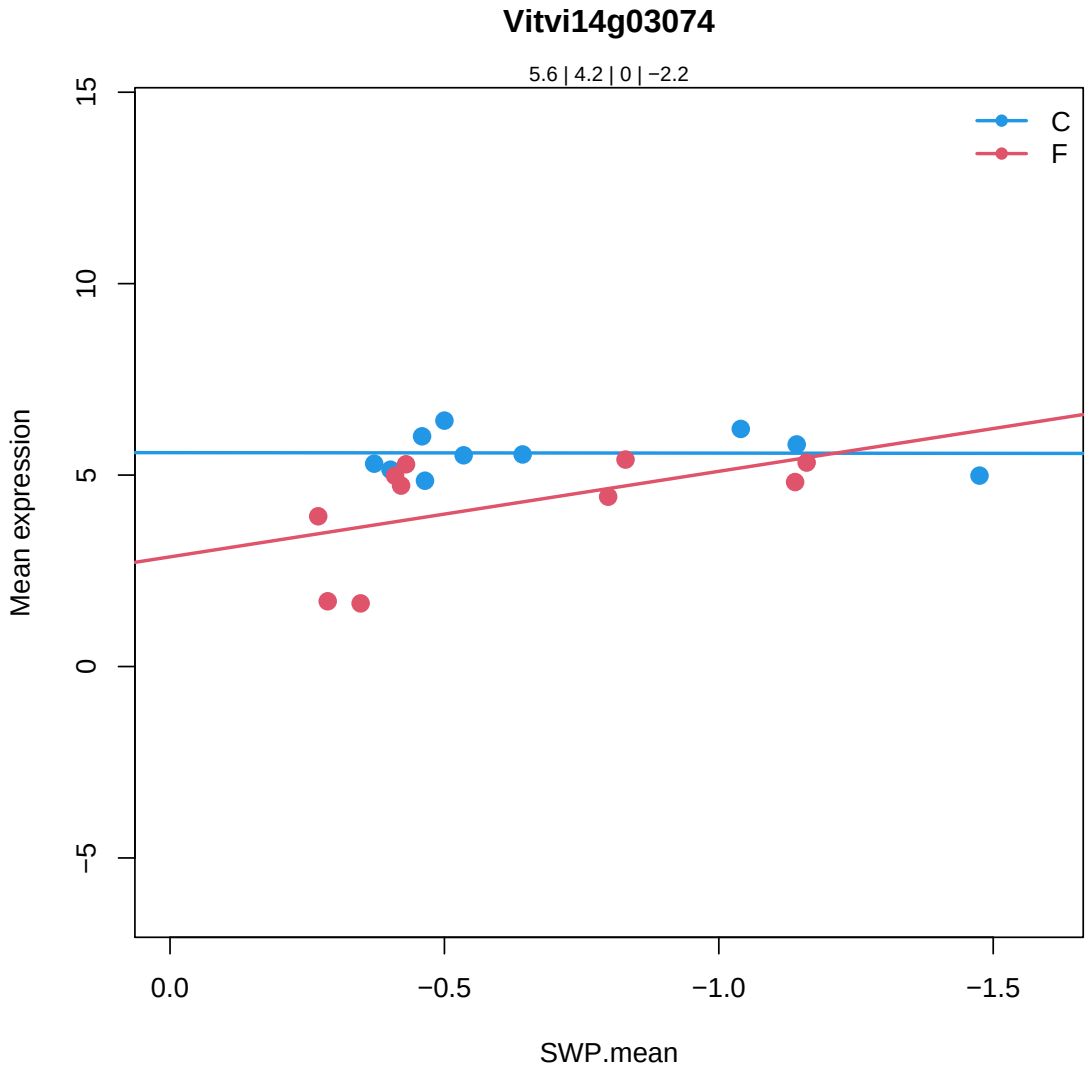
7.6.548 Vitvi14g03074: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g03074
        35.2
        not assigned.unknown
        Leucine-rich repeat receptor-like protein kinase family protein |
        Chr4:5637467-5640496 REVERSE LENGTH=1009 |
        201606
```

Coefficients for Vitvi14g03074.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.577211	2.156211e-15	***	3.89257e-15	***
SlopeC	0.01214811	0.9875953		0.9983274	
MeanF-MeanC	-1.352187	0.002376485	**	0.02527731	*
SlopeF-SlopeC	-2.246425	0.06382701	.	0.9999488	



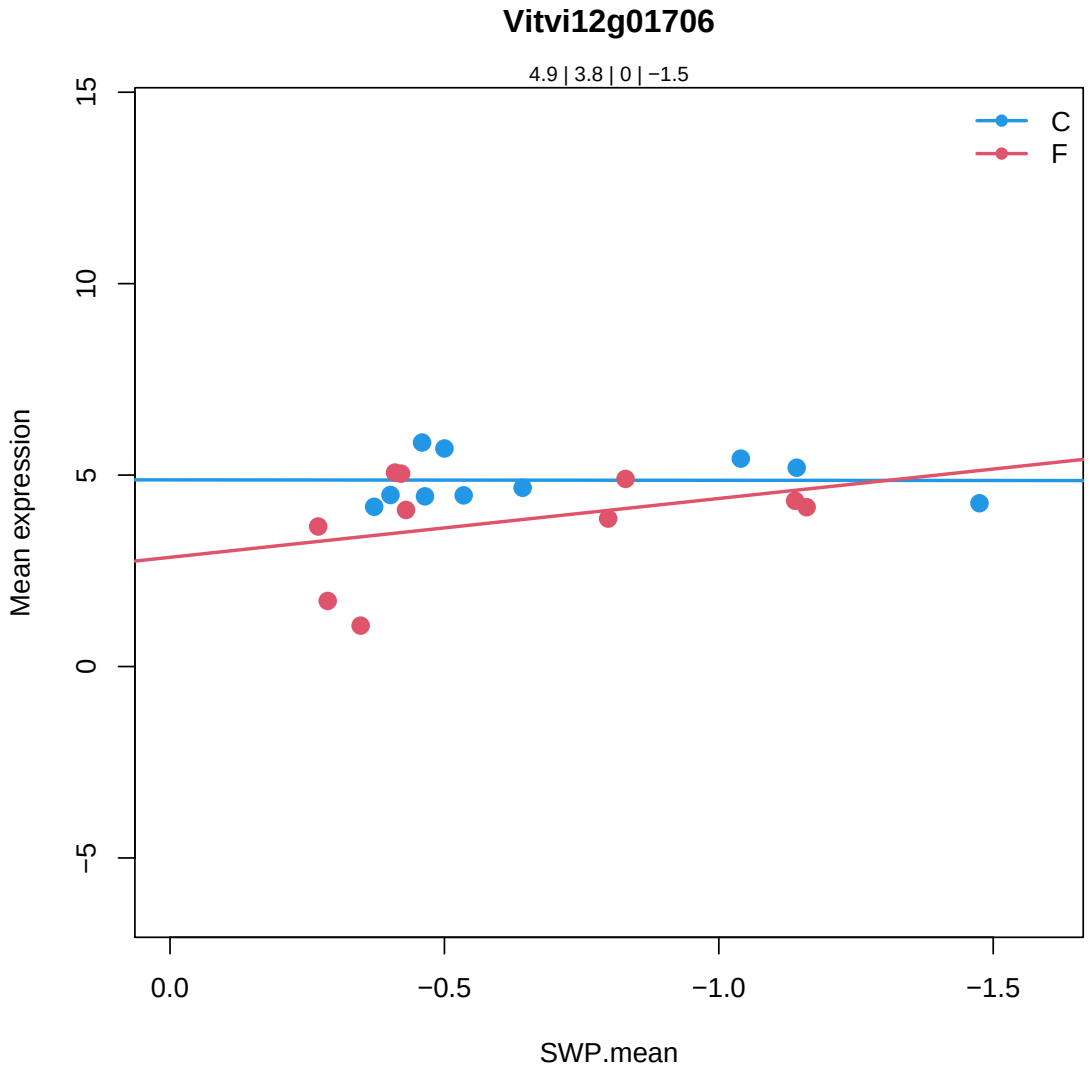
7.6.549 Vitvi12g01706: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g01706
        35.2
        not assigned.unknown
        UDP-Glycosyltransferase superfamily protein |
        Chr3:7667099-7668556 FORWARD LENGTH=485 |
        201606
```

Coefficients for Vitvi12g01706.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.866765	1.322232e-13	***	2.010721e-13	***
SlopeC	0.01082603	0.989669		0.9983274	
MeanF-MeanC	-1.078341	0.01779101	*	0.11549	
SlopeF-SlopeC	-1.547571	0.2218507		0.9999488	



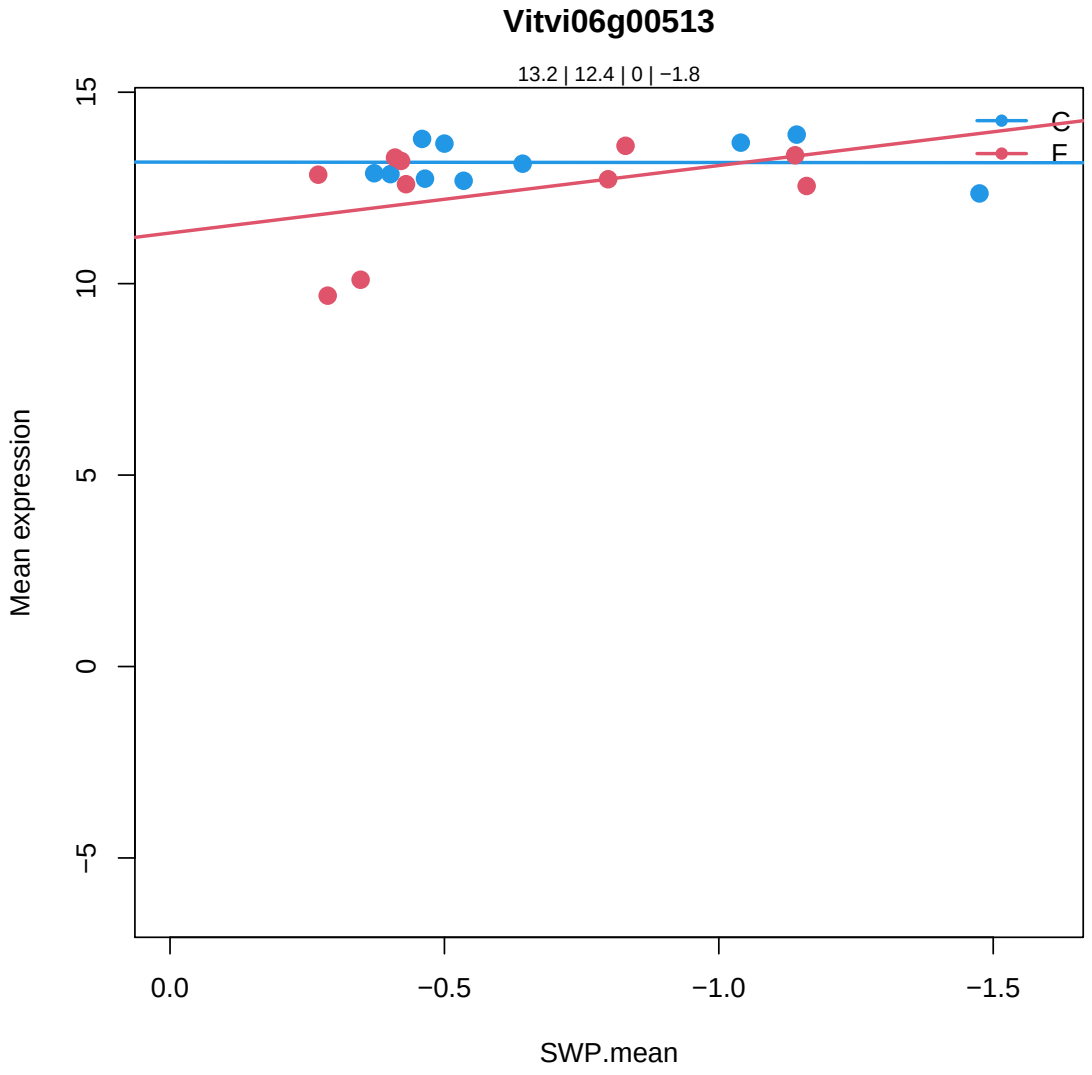
7.6.550 Vitvi06g00513: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00513
        1.3.13
        PS.calvin cycle.rubisco interacting
        rubisco activase |
        Chr2:16570951-16573345 REVERSE LENGTH=474 |
        201606
```

Coefficients for Vitvi06g00513.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	13.16716	5.996242e-23	***	1.265855e-21	***
SlopeC	0.009496457	0.9905675		0.9983274	
MeanF-MeanC	-0.7714218	0.06941063	.	0.2946955	
SlopeF-SlopeC	-1.772379	0.1482385		0.9999488	



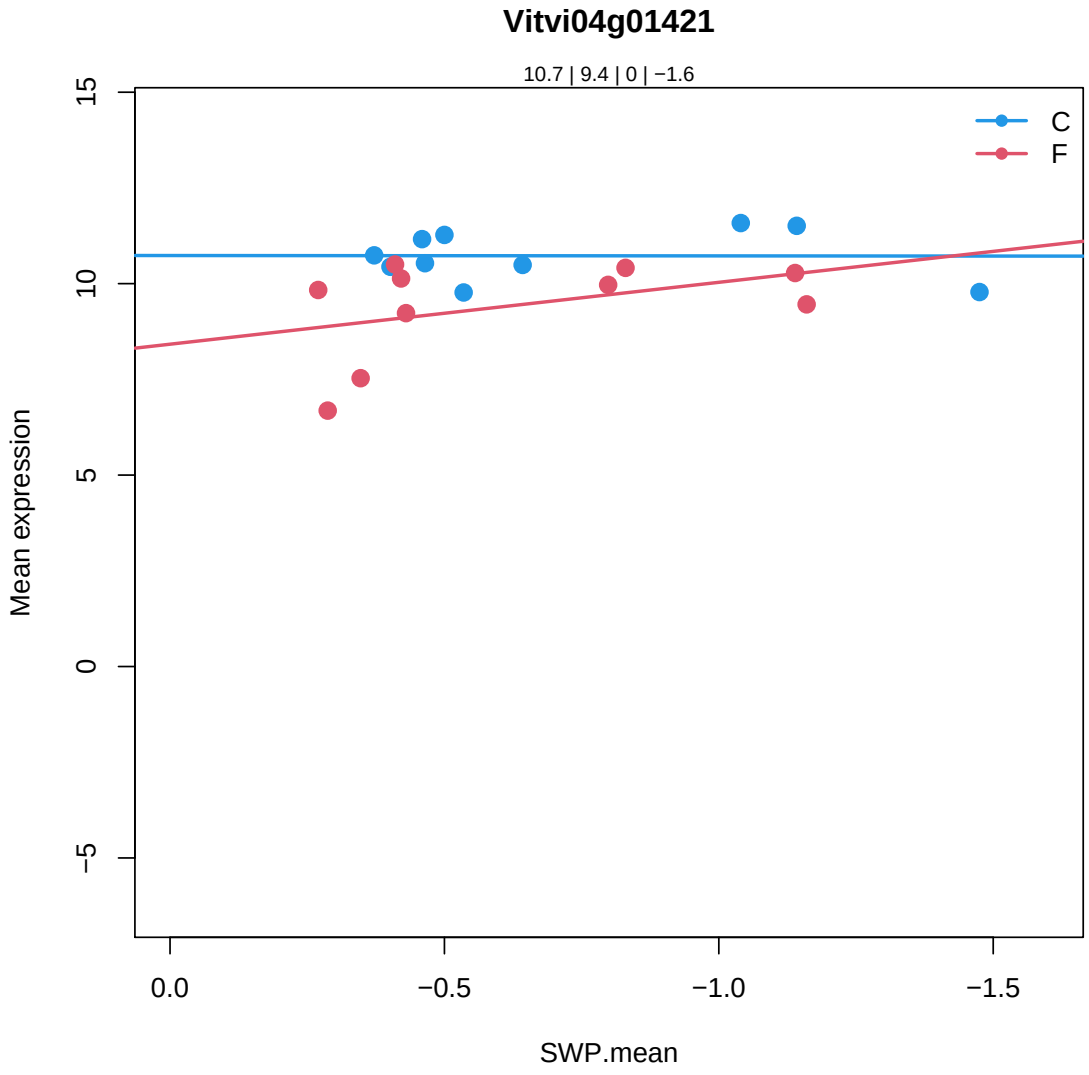
7.6.551 Vitvi04g01421: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01421
        1.3.6
        PS.calvin cycle.aldolase
        fructose-bisphosphate aldolase 1 |
        Chr2:9128416-9130152 REVERSE LENGTH=399 |
        201606
```

Coefficients for Vitvi04g01421.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	10.72777	4.215446e-21	***	3.550678e-20	***
SlopeC	0.009195738	0.9908277		0.9983274	
MeanF-MeanC	-1.324901	0.003368974	**	0.03362796	*
SlopeF-SlopeC	-1.625479	0.1814085		0.9999488	



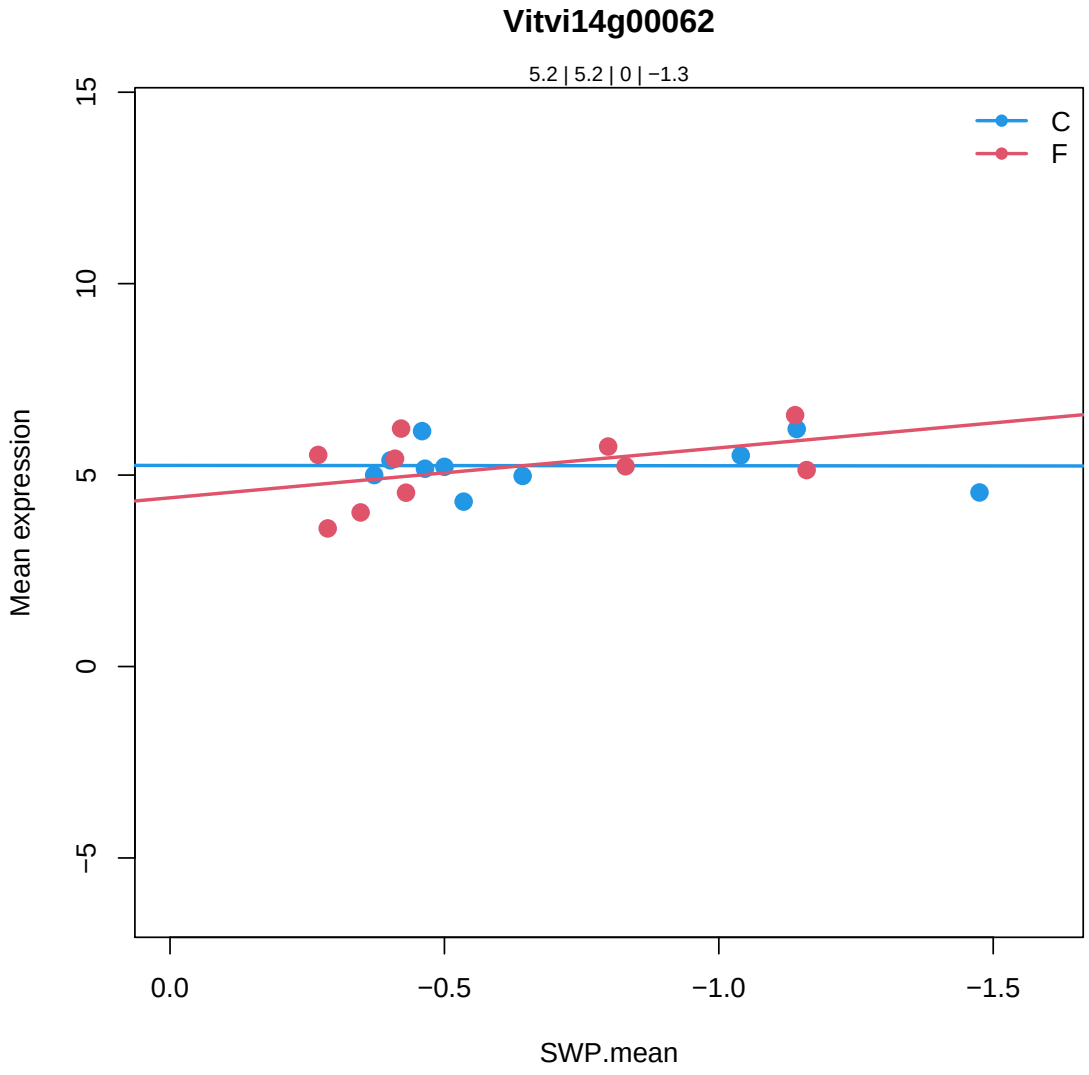
7.6.552 Vitvi14g00062: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g00062
        34.16
        transport.ABC transporters and multidrug resistance systems
        non-intrinsic ABC protein 9 |
        Chr5:467269-469041 REVERSE LENGTH=328 |
        201606
```

Coefficients for Vitvi14g00062.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.245747	7.48926e-17	***	1.663642e-16	***
SlopeC	0.008536745	0.989086		0.9983274	
MeanF-MeanC	-0.04474354	0.8878602		0.9704865	
SlopeF-SlopeC	-1.31302	0.1670797		0.9999488	



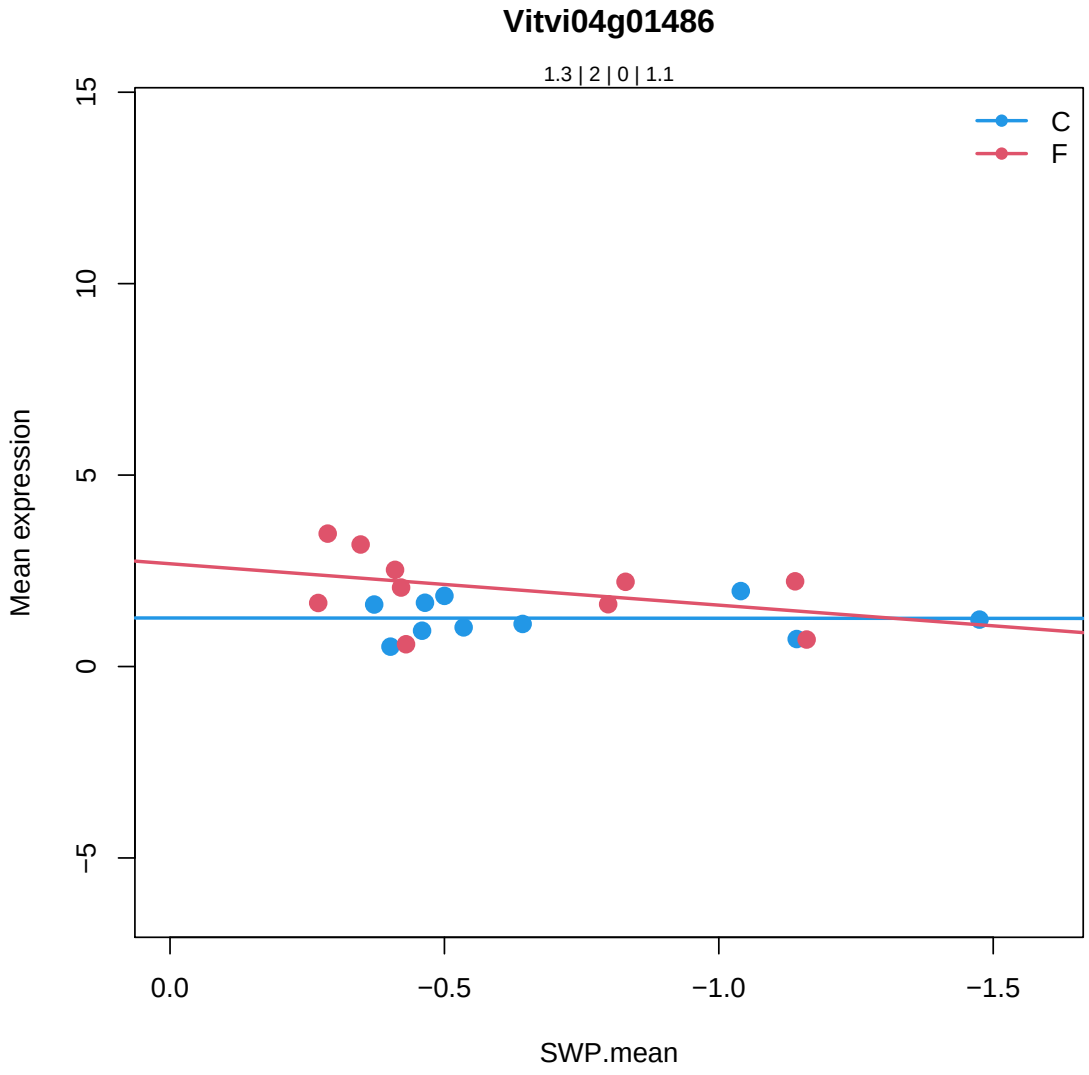
7.6.553 Vitvi04g01486: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01486
        27.3.25
        RNA.regulation of transcription.MYB domain transcription factor family
        myb domain protein 4 |
        Chr4:18053866-18054876 FORWARD LENGTH=282 |
        201606
```

Coefficients for Vitvi04g01486.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.262867	8.344434e-06	***	9.440055e-06	***
SlopeC	0.006480899	0.9915442		0.9986379	
MeanF-MeanC	0.7625605	0.02141466	*	0.1321467	
SlopeF-SlopeC	1.074327	0.2454463		0.9999488	



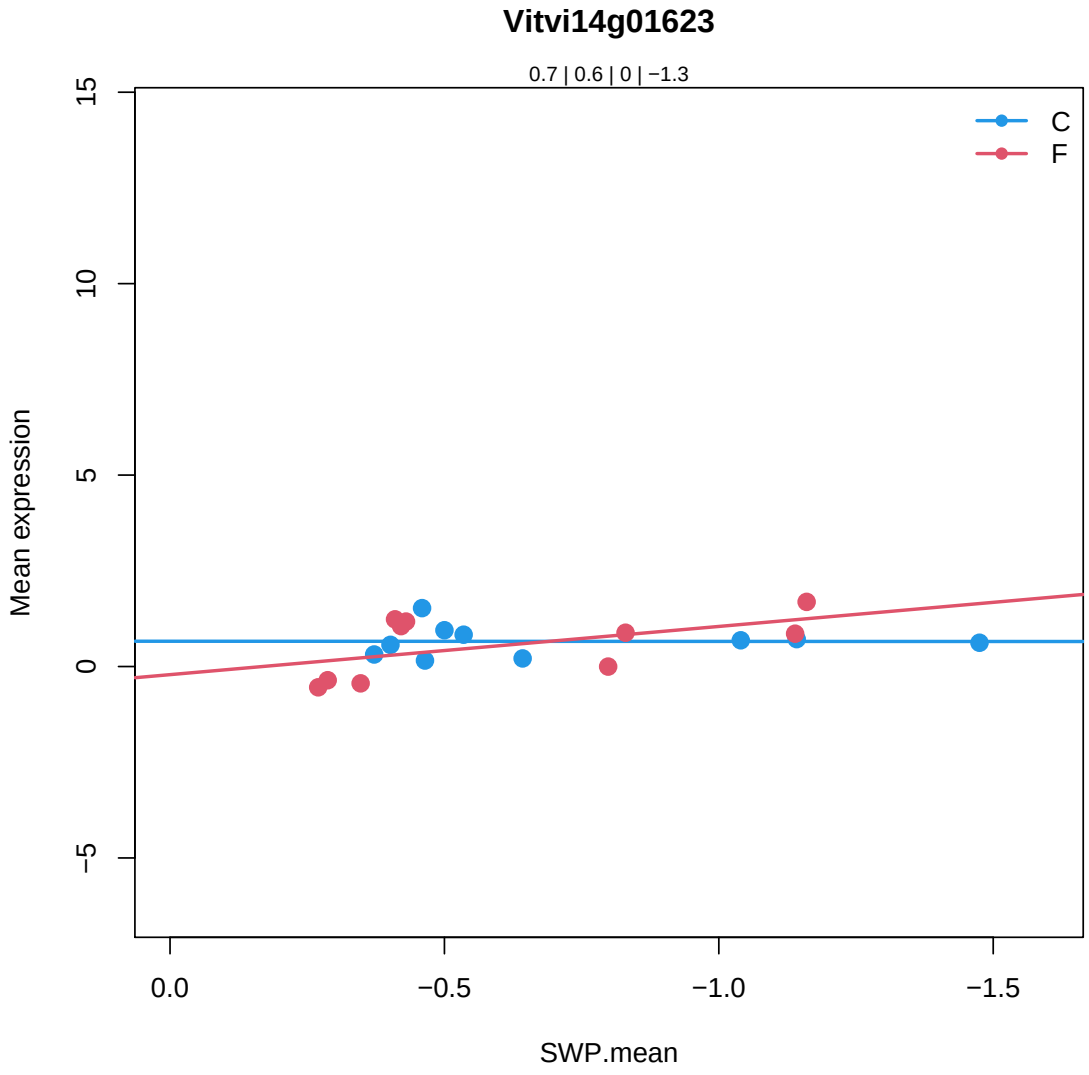
7.6.554 Vitvi14g01623: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01623
        35.2
        not assigned.unknown
        histone-lysine N-methyltransferase trithorax-like protein |
        Chr5:16290770-16291402 FORWARD LENGTH=210 |
        201606
```

Coefficients for Vitvi14g01623.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6572031	0.001488471	**	0.00160652	**
SlopeC	0.004425275	0.9930506		0.9989481	
MeanF-MeanC	-0.1025295	0.6919161		0.901923	
SlopeF-SlopeC	-1.263449	0.1054439		0.9999488	



7.6.555 Vitvi14g02869: type5

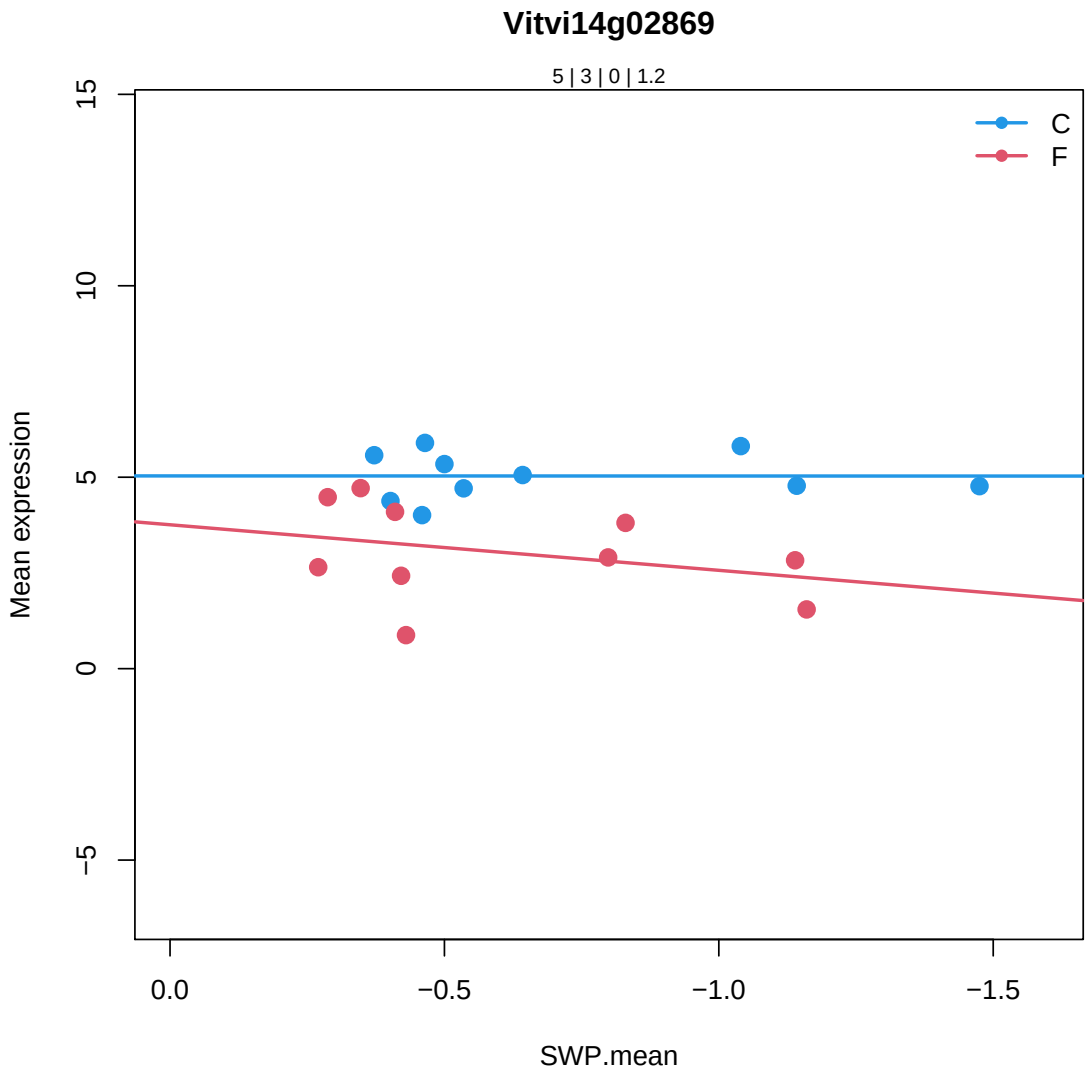
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g02869
        26.21
        misc.protease inhibitor/seed storage/lipid transfer protein (LTP) fami
        Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin
        Chr3:6267102-6267392 FORWARD LENGTH=96 |
        201606

Vitvi14g02869
        11.6
        lipid metabolism.lipid transfer proteins etc
        Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin
        Chr3:6267102-6267392 FORWARD LENGTH=96 |
        201606
```

Coefficients for Vitvi14g02869.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.032301	2.830101e-14	***	4.543065e-14	***
SlopeC	0.002512245	0.9974959		0.9997917	
MeanF-MeanC	-1.999555	6.051136e-05	***	0.001167486	**
SlopeF-SlopeC	1.187555	0.324484		0.9999488	


Vitvi14g02869
5 | 3 | 0 | 1.2
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

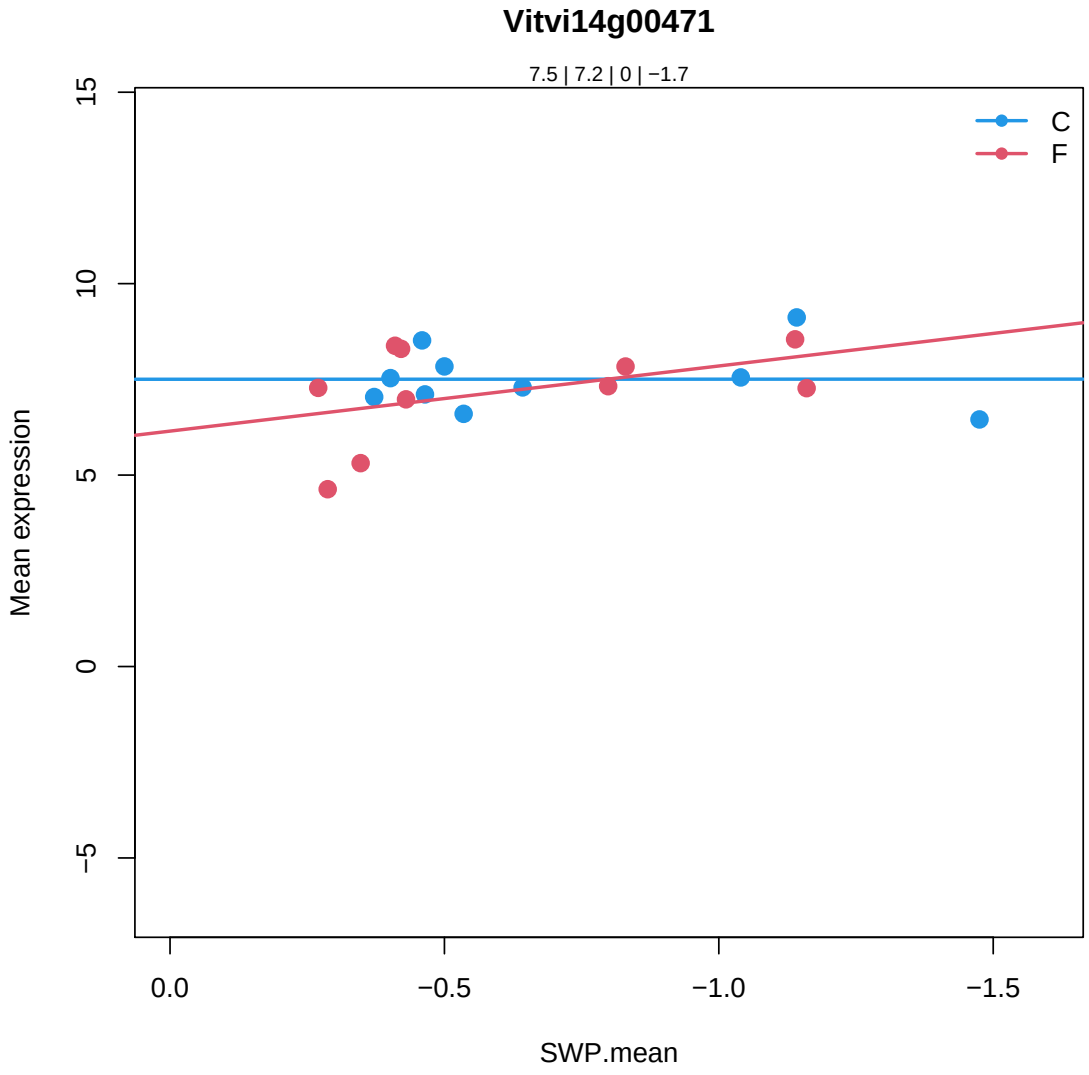
7.6.556 Vitvi14g00471: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g00471
        21.2.1.1
        redox.ascorbate and glutathione.ascorbate.GME
        GDP-D-mannose 3'%2C5'-epimerase |
        Chr5:10862472-10864024 REVERSE LENGTH=377 |
        201606
```

Coefficients for Vitvi14g00471.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.504239	2.445374e-17	***	5.952154e-17	***
SlopeC	-0.002162994	0.9979596		0.9998348	
MeanF-MeanC	-0.3197105	0.4600356		0.7837111	
SlopeF-SlopeC	-1.699055	0.1862614		0.9999488	



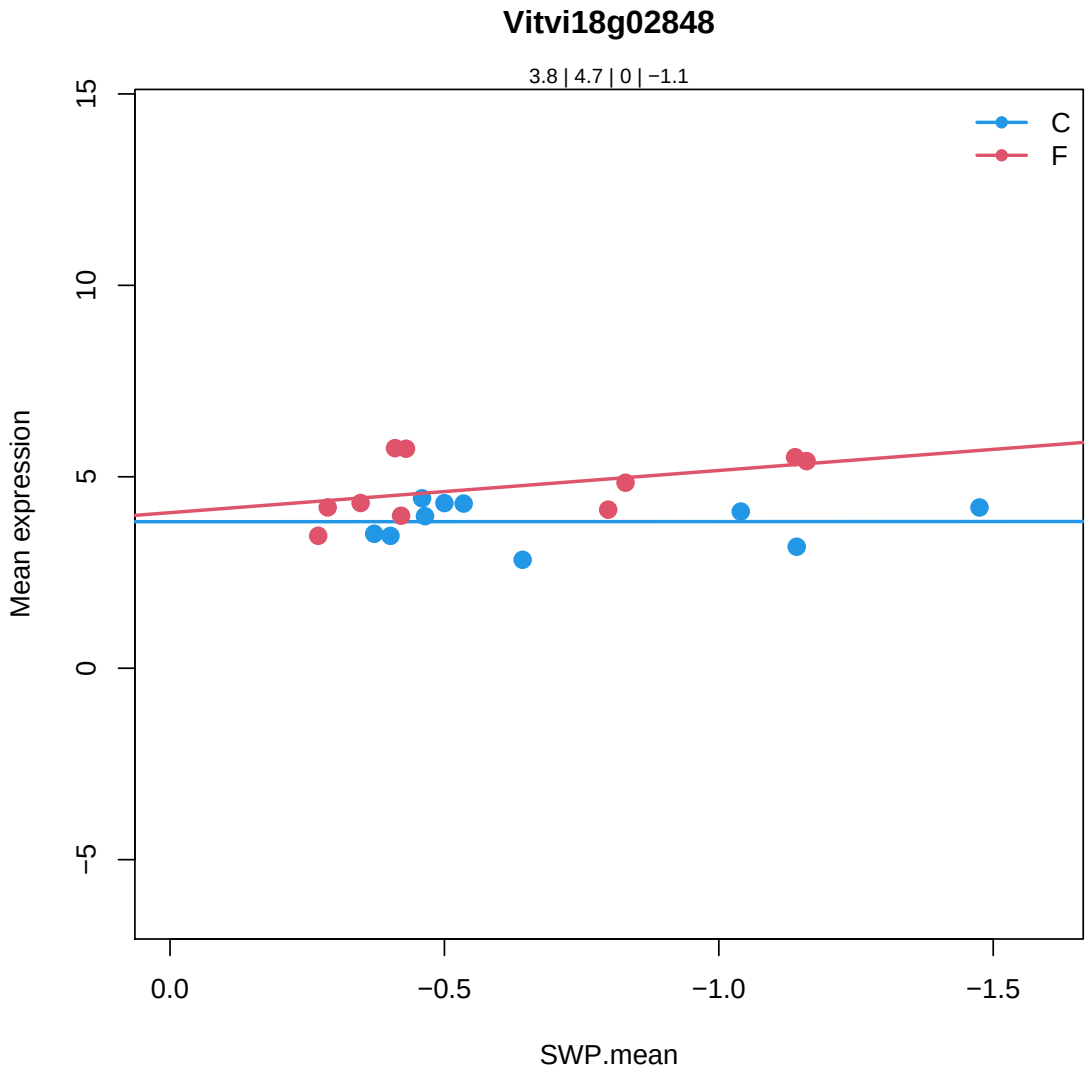
7.6.557 Vitvi18g02848: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02848
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi18g02848.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.828542	7.801896e-15	***	1.318803e-14	***
SlopeC	-0.003095835	0.9956769		0.9992827	
MeanF-MeanC	0.9058067	0.004689342	**	0.04344727	*
SlopeF-SlopeC	-1.09896	0.2049158		0.9999488	



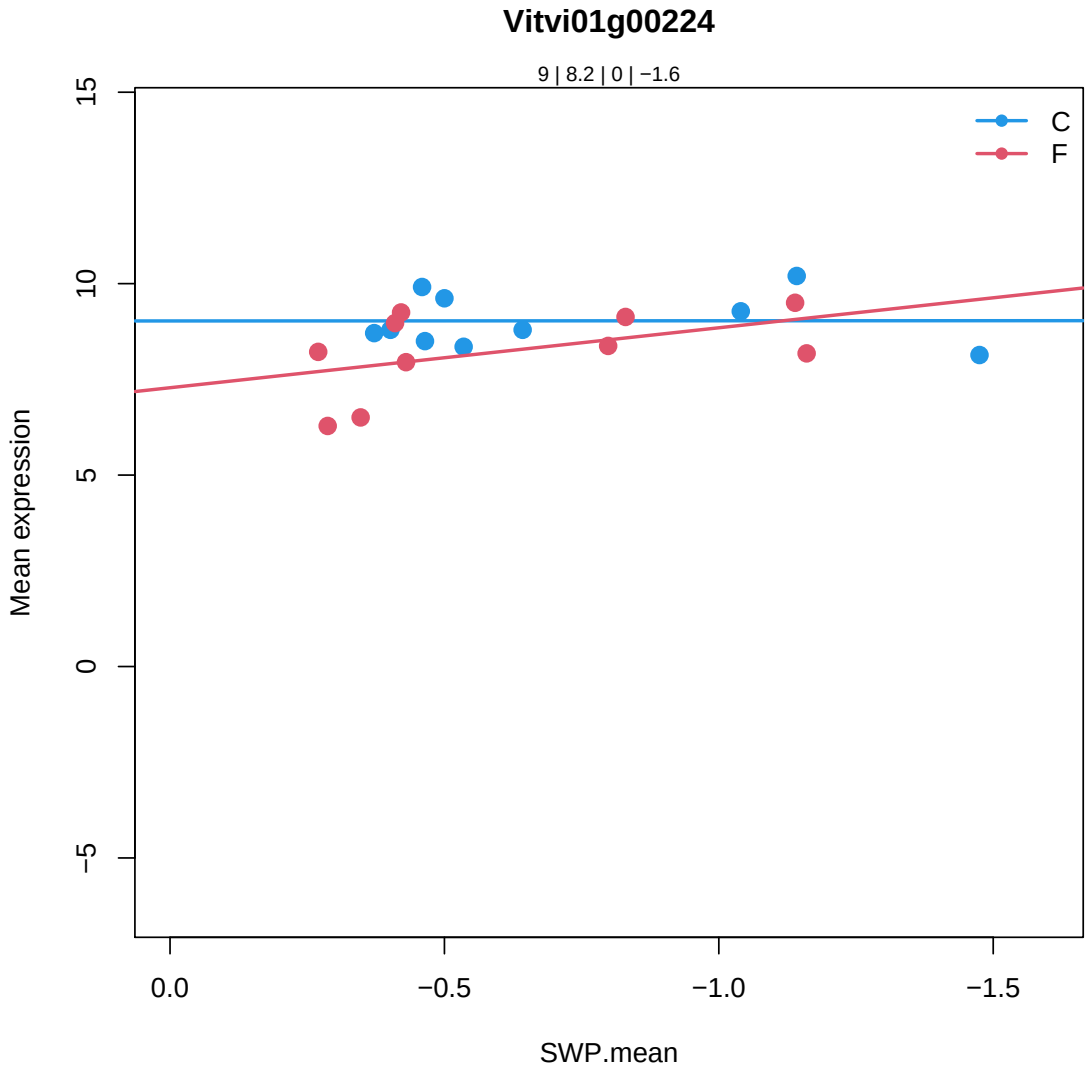
7.6.558 Vitvi01g00224: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00224
        35.1.41
        not assigned.no ontology.hydroxyproline rich proteins
        Hydroxyproline-rich glycoprotein family protein |
        Chr3:9354061-9357757 FORWARD LENGTH=863 |
        201606
```

Coefficients for Vitvi01g00224.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	9.028752	1.56474e-20	***	1.018786e-19	***
SlopeC	-0.003988821	0.9955572		0.9992827	
MeanF-MeanC	-0.7933484	0.03855783	*	0.2013356	
SlopeF-SlopeC	-1.561581	0.1529442		0.9999488	



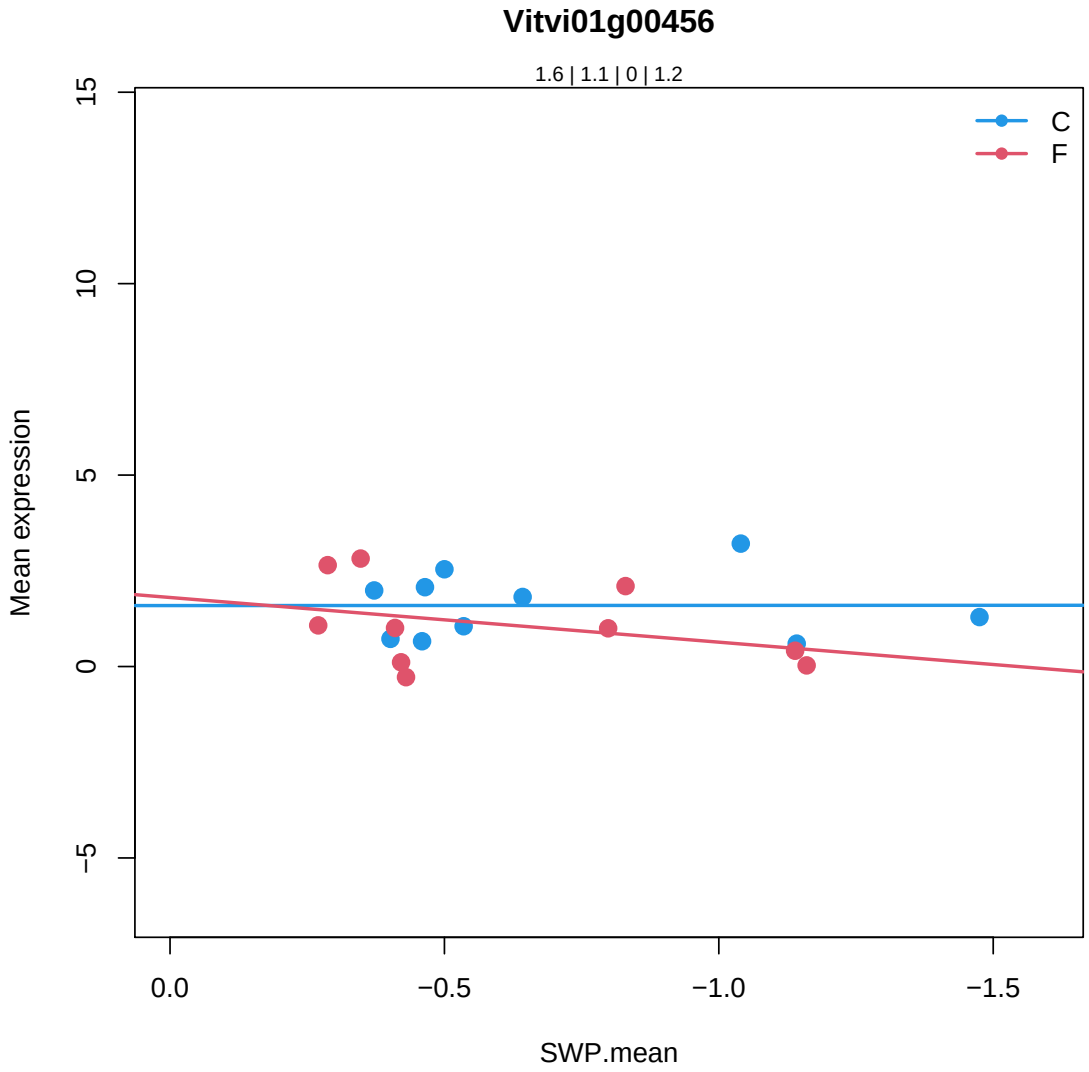
7.6.559 Vitvi01g00456: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00456
        10.8.1
        cell wall.pectinesterases.PME
        Plant invertase/pectin methylesterase inhibitor superfamily |
        Chr3:22444955-22447226 FORWARD LENGTH=519 |
        201606
```

Coefficients for Vitvi01g00456.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.594834	1.523107e-05	***	1.712793e-05	***
SlopeC	-0.004531663	0.9955262		0.9992827	
MeanF-MeanC	-0.5028807	0.2289433		0.5817863	
SlopeF-SlopeC	1.171399	0.3354988		0.9999488	



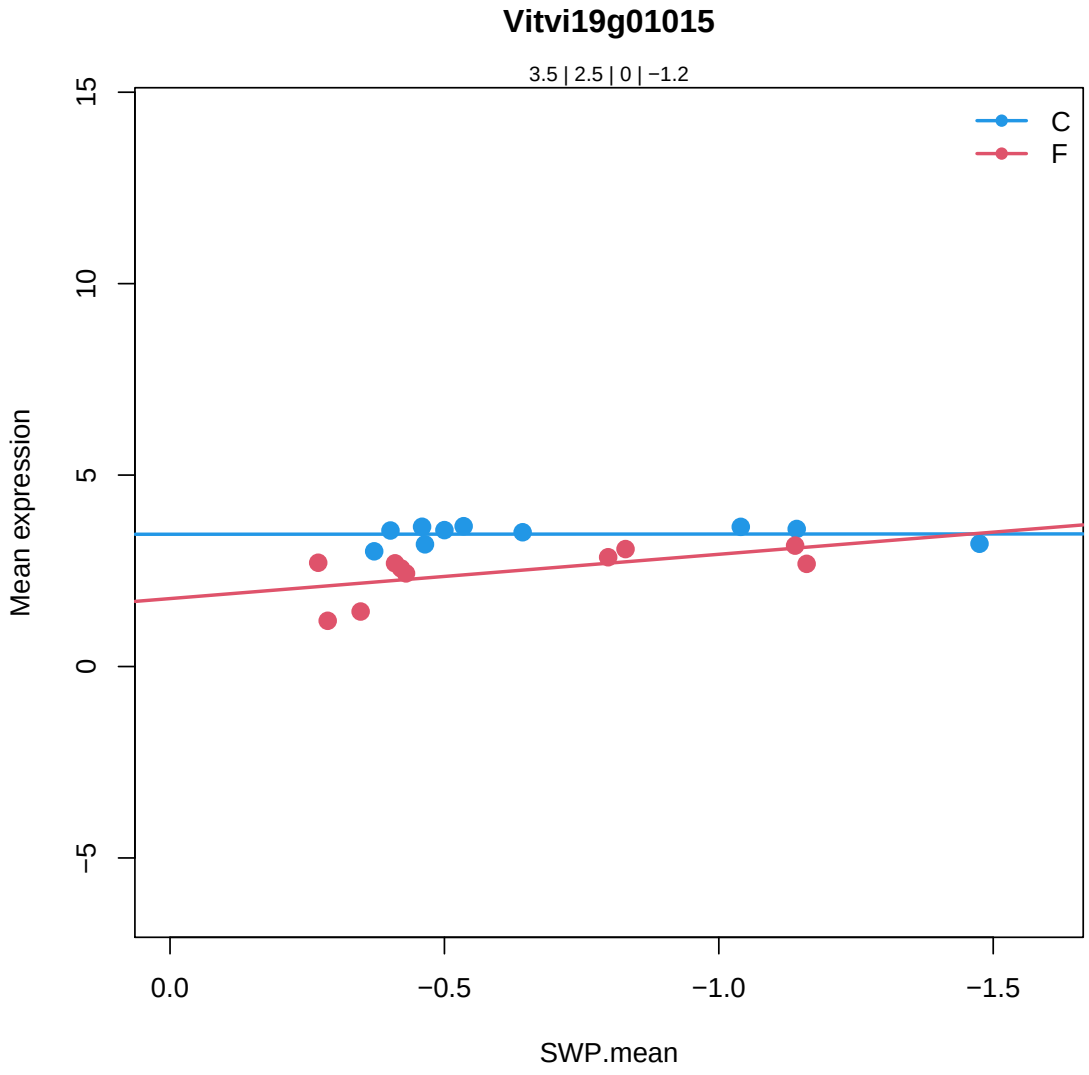
7.6.560 Vitvi19g01015: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g01015
        26.10
        misc.cytochrome P450
        cytochrome P450%2C family 72%2C subfamily A%2C polypeptide 15 |
        Chr3:4937410-4939310 FORWARD LENGTH=512 |
        201606
```

Coefficients for Vitvi19g01015.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.458204	3.151105e-17	***	7.508072e-17	***
SlopeC	-0.005369354	0.9891427		0.9983274	
MeanF-MeanC	-0.9790934	6.546952e-05	***	0.001250484	**
SlopeF-SlopeC	-1.151342	0.06026527	.	0.9999488	



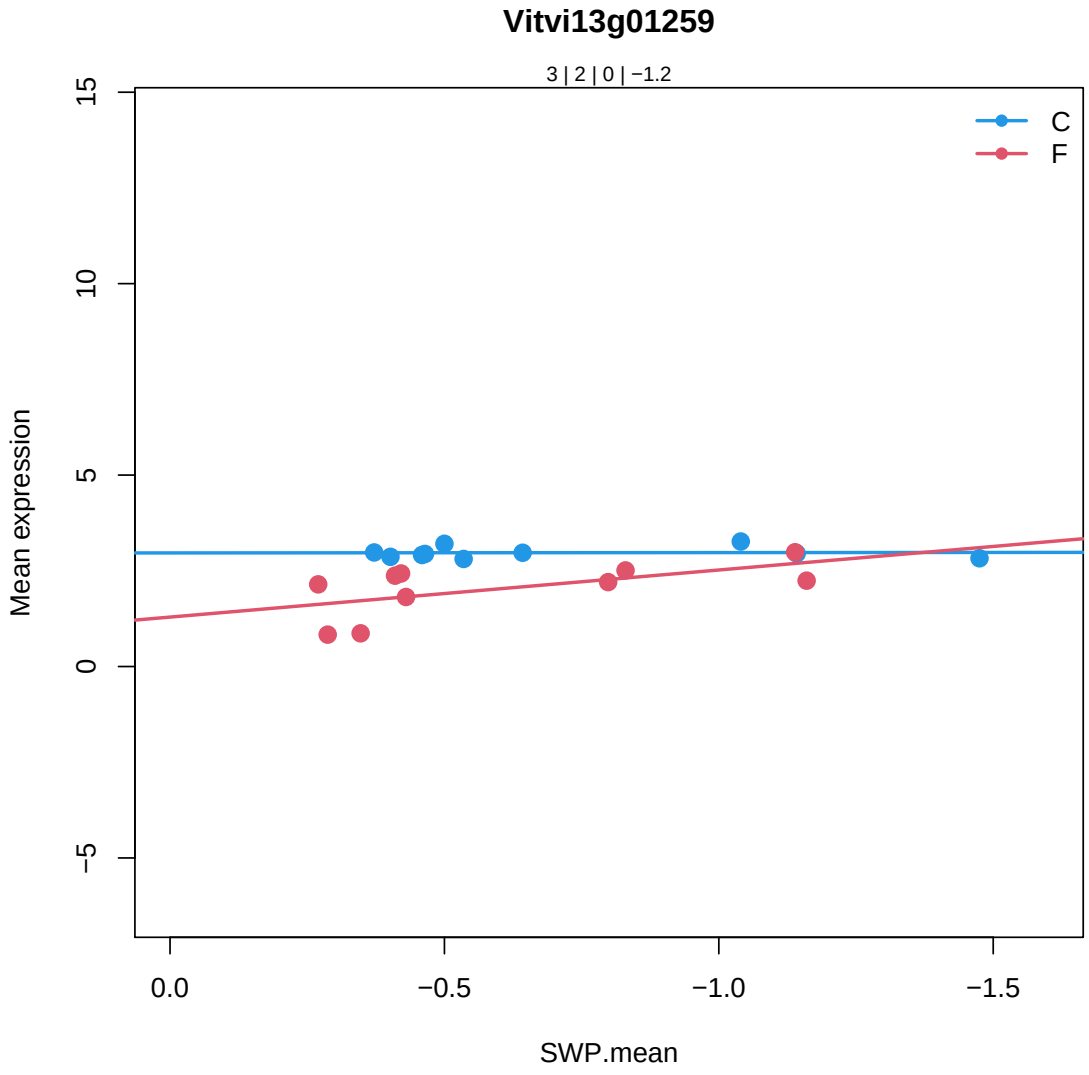
7.6.561 Vitvi13g01259: + type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g01259
        17.3.1.1.1
        hormone metabolism.brassinosteroid.synthesis-degradation.BRs.DET2
        3-oxo-5-alpha-steroid 4-dehydrogenase family protein |
        Chr5:5227982-5229012 FORWARD LENGTH=268 |
        201606
```

Coefficients for Vitvi13g01259.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.972622	7.670963e-16	***	1.459139e-15	***
SlopeC	-0.008212234	0.983452		0.9979351	
MeanF-MeanC	-0.9320424	0.0001202803	***	0.002114546	**
SlopeF-SlopeC	-1.221738	0.04797052	*	0.9999488	



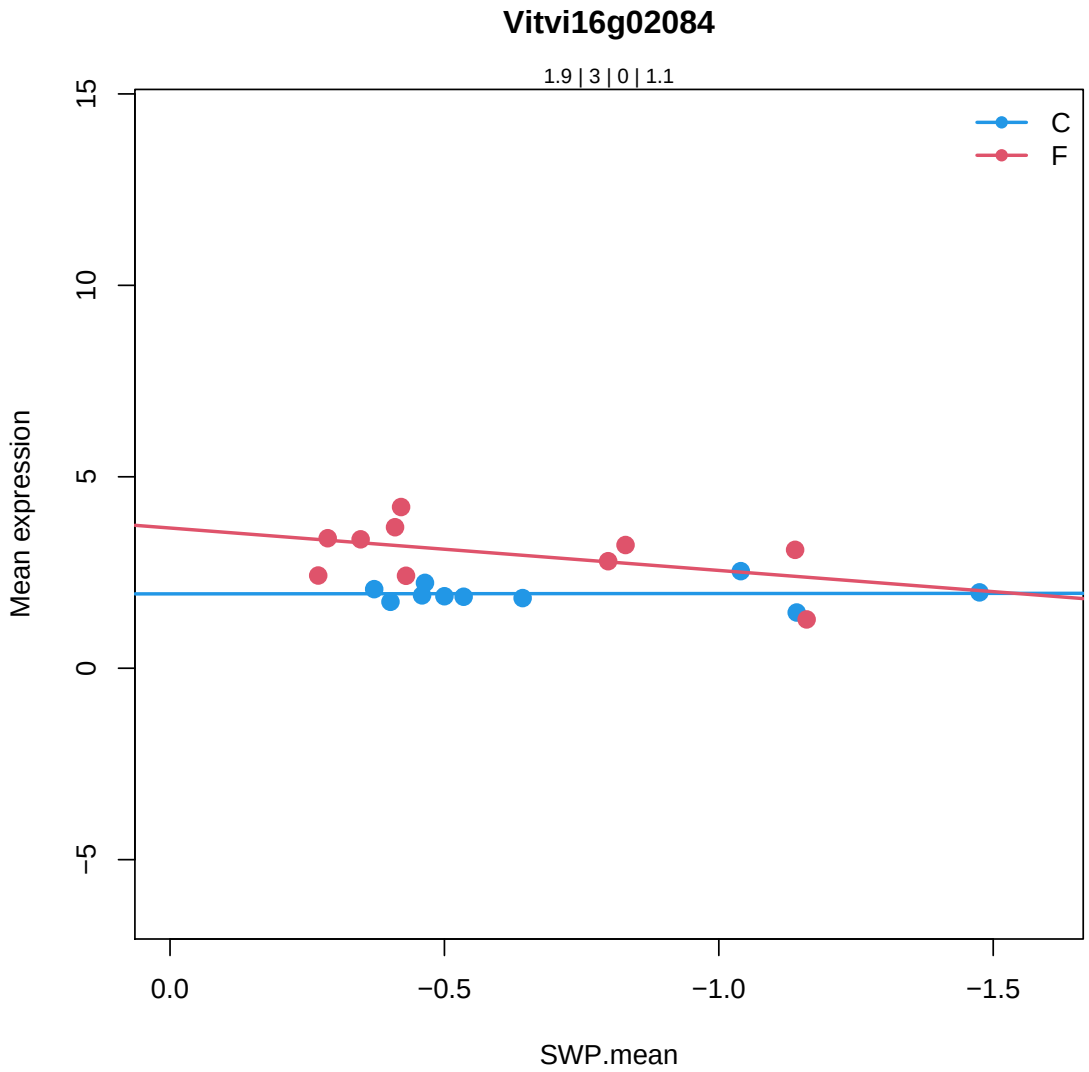
7.6.562 Vitvi16g02084: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g02084
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi16g02084.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.948149	2.811032e-10	***	3.613845e-10	***
SlopeC	-0.008413336	0.9865383		0.9983274	
MeanF-MeanC	1.03871	0.0004417303	***	0.006357746	**
SlopeF-SlopeC	1.116152	0.1427326		0.9999488	



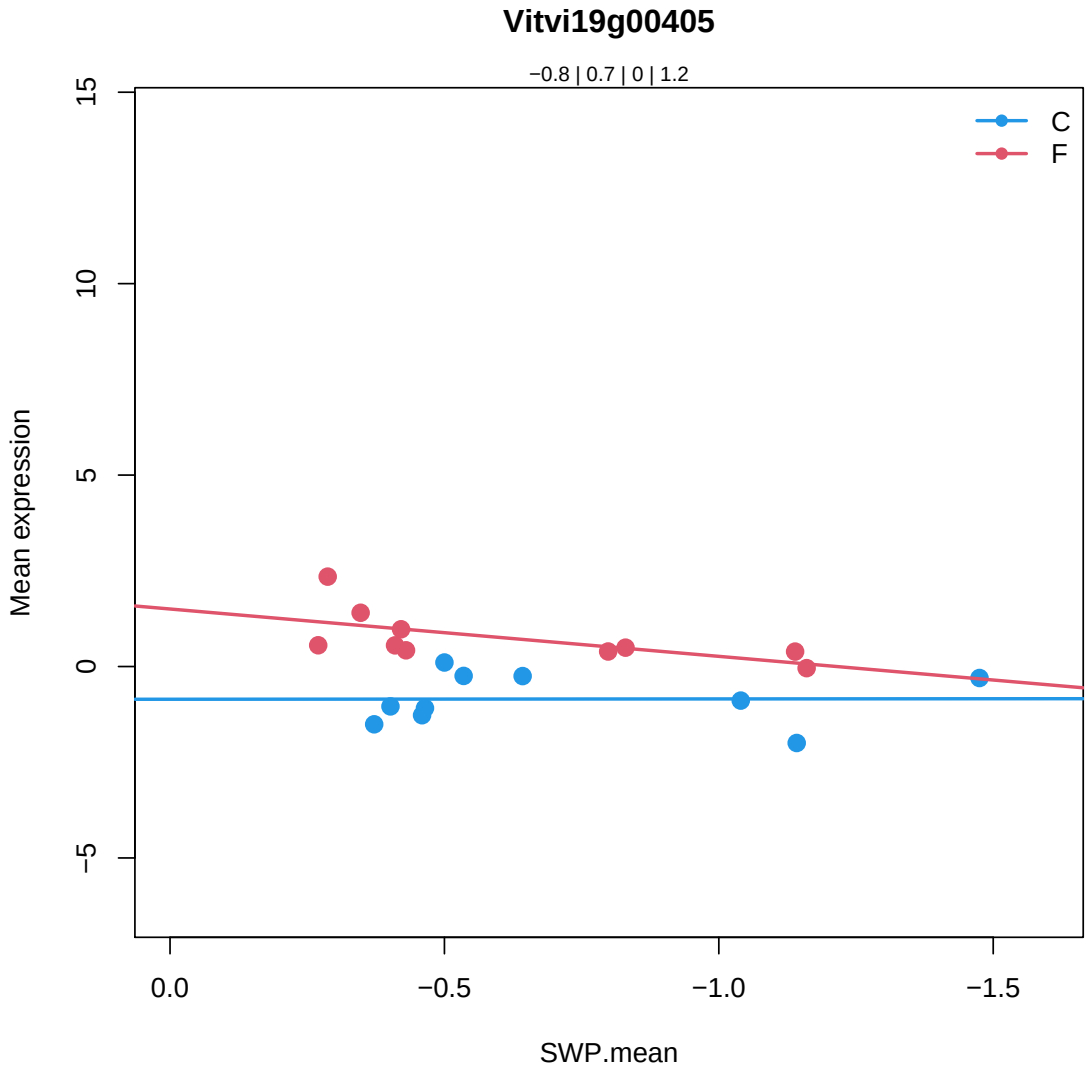
7.6.563 Vitvi19g00405: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g00405
        21.1
        redox.thioredoxin
        C-terminal cysteine residue is changed to a serine 1 |
        Chr1:3874518-3875311 FORWARD LENGTH=118 |
        201606
```

Coefficients for Vitvi19g00405.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.8489142	0.0002129772	***	0.000233674	***
SlopeC	-0.008554299	0.9872947		0.9983274	
MeanF-MeanC	1.597579	6.526056e-06	***	0.0001700344	***
SlopeF-SlopeC	1.245449	0.129667		0.9999488	



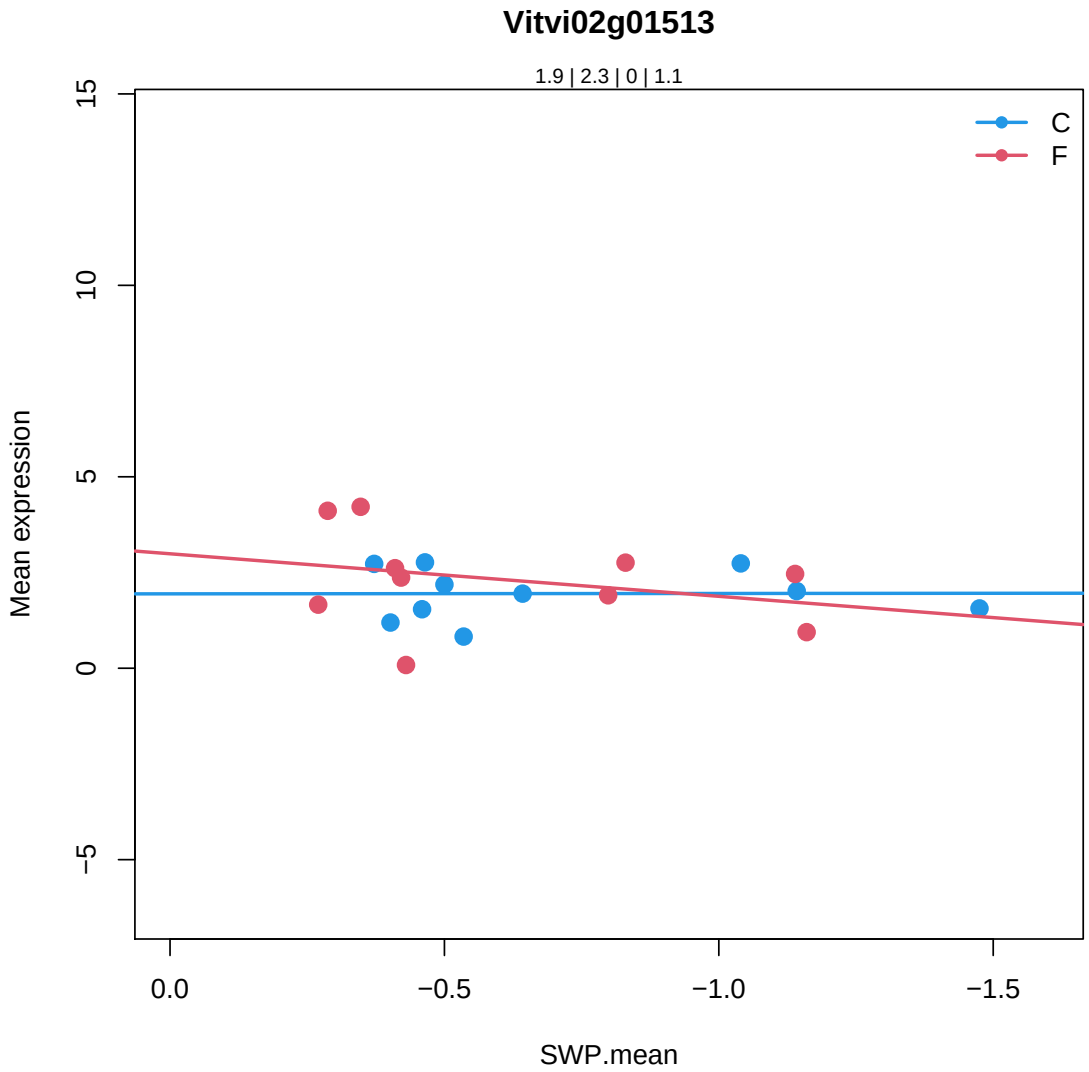
7.6.564 Vitvi02g01513: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g01513
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi02g01513.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.949564	1.394435e-06	***	1.604316e-06	***
SlopeC	-0.009667805	0.990721		0.9983274	
MeanF-MeanC	0.3622814	0.3953321		0.7421262	
SlopeF-SlopeC	1.121037	0.3695109		0.9999488	



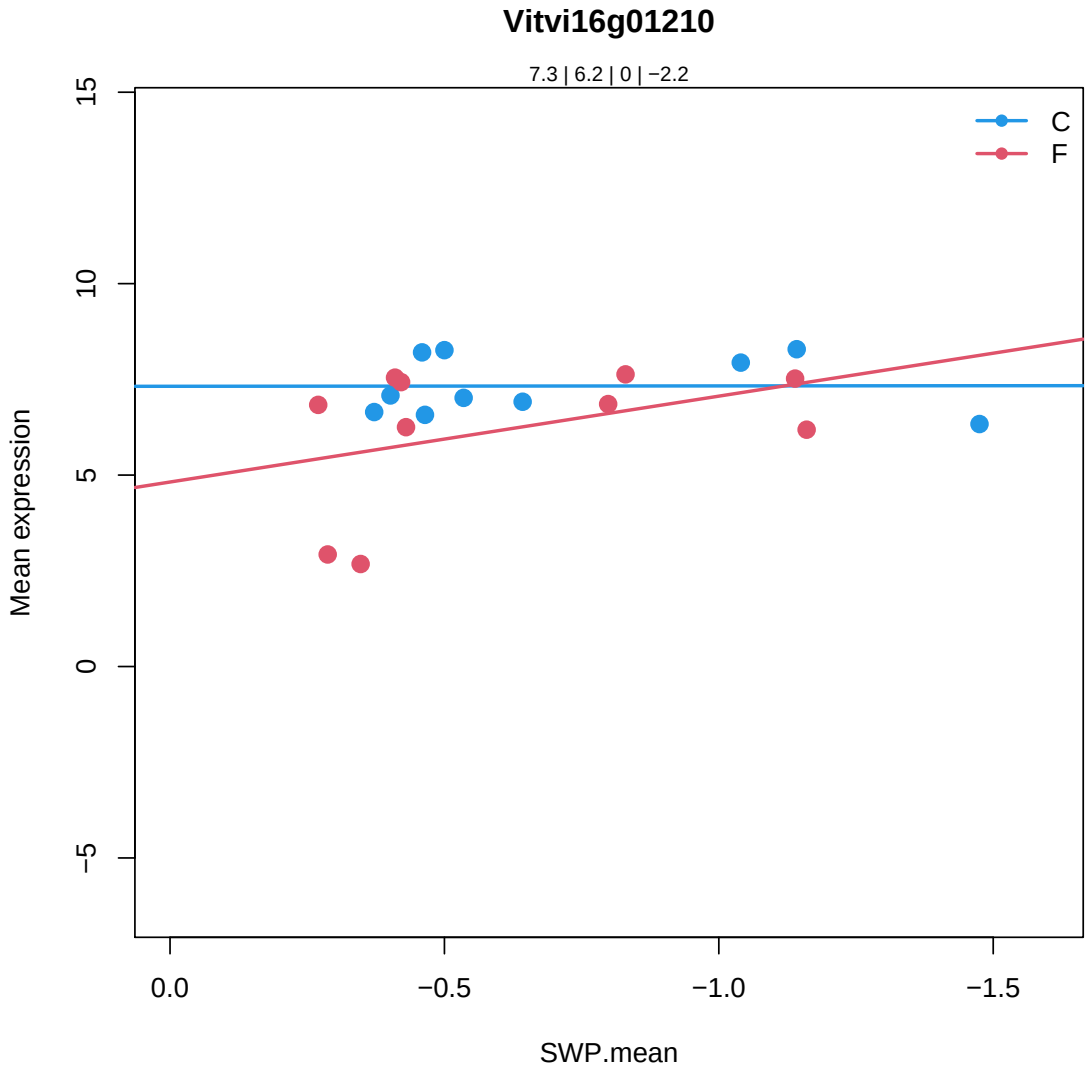
7.6.565 Vitvi16g01210: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01210
        34.16
        transport.ABC transporters and multidrug resistance systems
        multidrug resistance-associated protein 14 |
        Chr3:21863519-21868701 REVERSE LENGTH=1453 |
        201606
```

Coefficients for Vitvi16g01210.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.325649	7.702025e-15	***	1.302644e-14	***
SlopeC	-0.009695296	0.9929198		0.9989481	
MeanF-MeanC	-1.140561	0.04992636	*	0.2387006	
SlopeF-SlopeC	-2.233358	0.1789447		0.9999488	



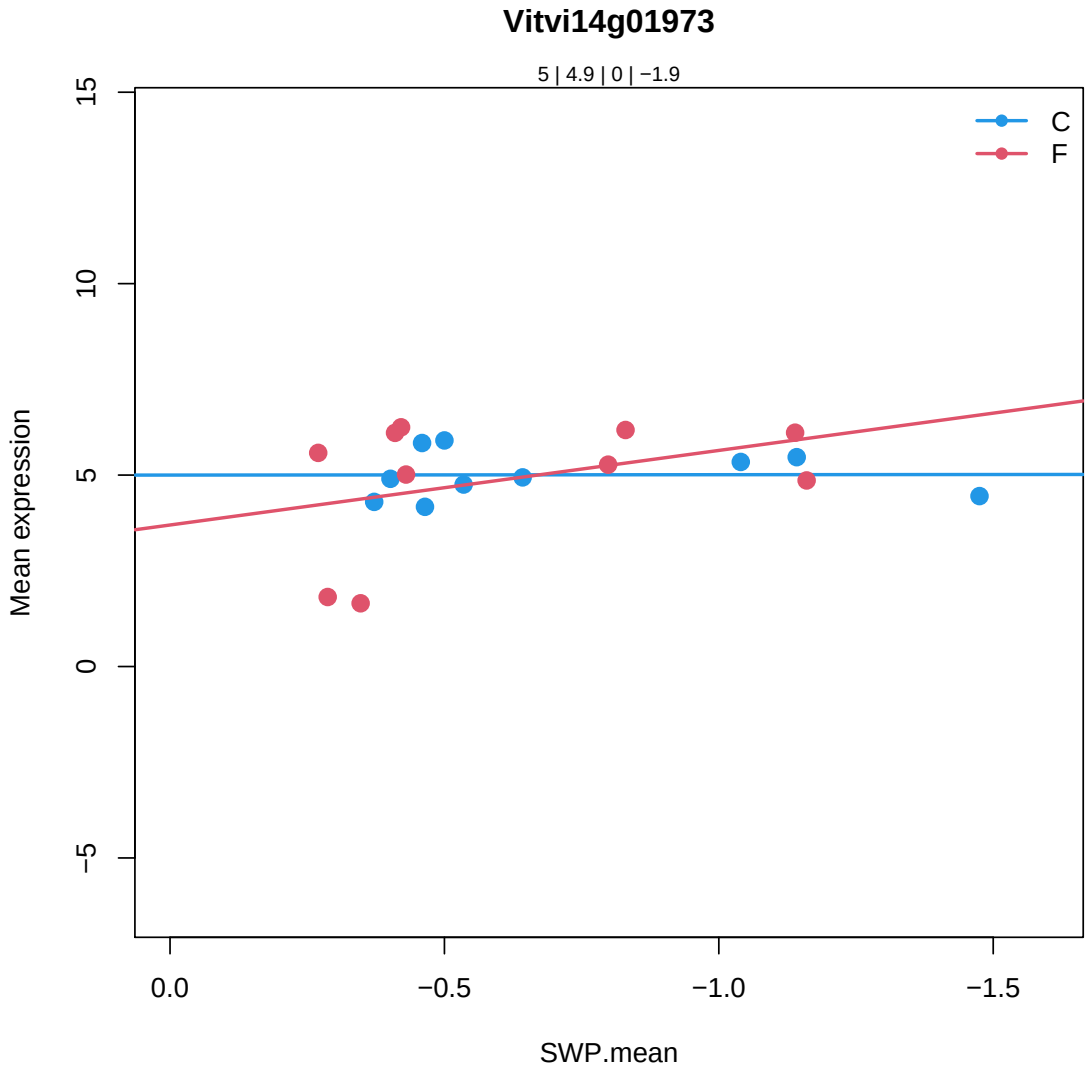
7.6.566 Vitvi14g01973: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01973
        27.3.8
        RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family
        cycling DOF factor 2 |
        Chr5:15878920-15880712 FORWARD LENGTH=457 |
        201606
```

Coefficients for Vitvi14g01973.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.006928	3.240597e-12	***	4.522357e-12	***
SlopeC	-0.00983594	0.9922457		0.9989481	
MeanF-MeanC	-0.1242458	0.8092882		0.9471564	
SlopeF-SlopeC	-1.937491	0.2069598		0.9999488	



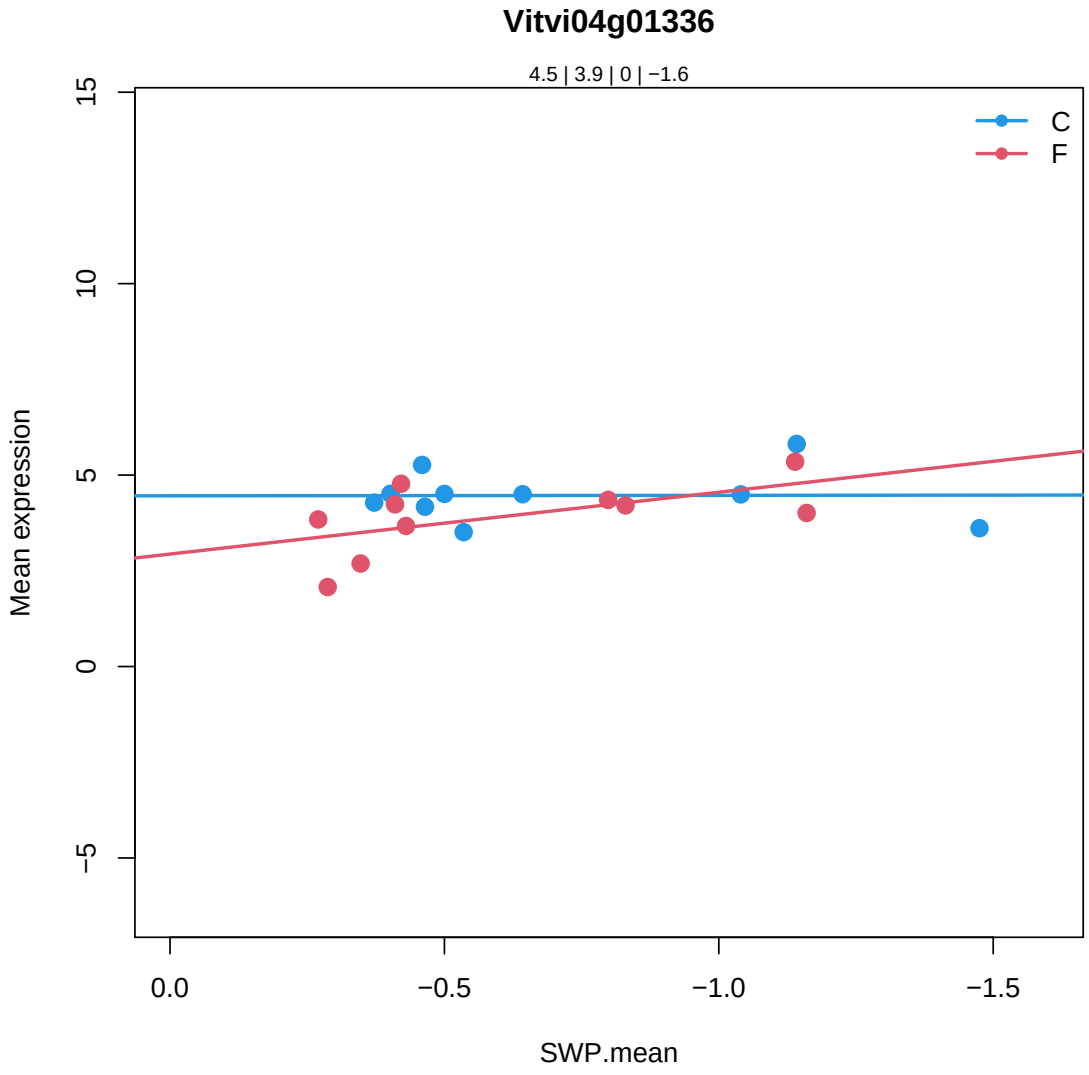
7.6.567 Vitvi04g01336: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01336
        26.13
        misc.acid and other phosphatases
        Phosphatidic acid phosphatase (PAP2) family protein |
        Chr5:26534978-26535951 FORWARD LENGTH=227 |
        201606
```

Coefficients for Vitvi04g01336.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.466751	2.823013e-15	***	5.026677e-15	***
SlopeC	-0.01152755	0.9854958		0.9983274	
MeanF-MeanC	-0.5462224	0.1008565		0.3659259	
SlopeF-SlopeC	-1.602838	0.1001617		0.9999488	



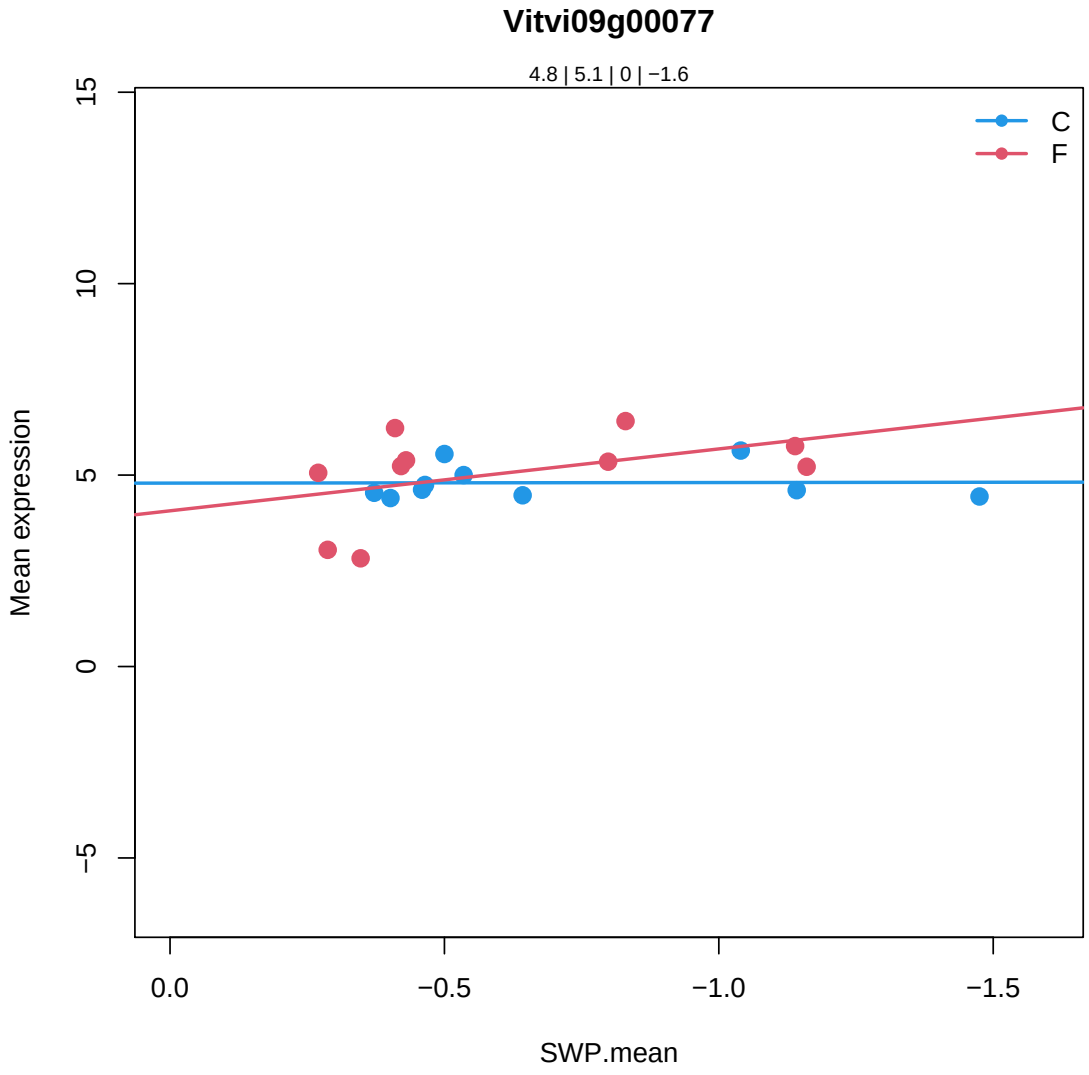
7.6.568 Vitvi09g00077: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00077
        35.2
        not assigned.unknown
        DUF1677 family protein (DUF1677) |
        Chr1:27303906-27304403 FORWARD LENGTH=165 |
        201606
```

Coefficients for Vitvi09g00077.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.800401	5.152576e-15	***	8.9083e-15	***
SlopeC	-0.01505888	0.9828835		0.9979351	
MeanF-MeanC	0.251053	0.4842131		0.7975755	
SlopeF-SlopeC	-1.601271	0.1356058		0.9999488	



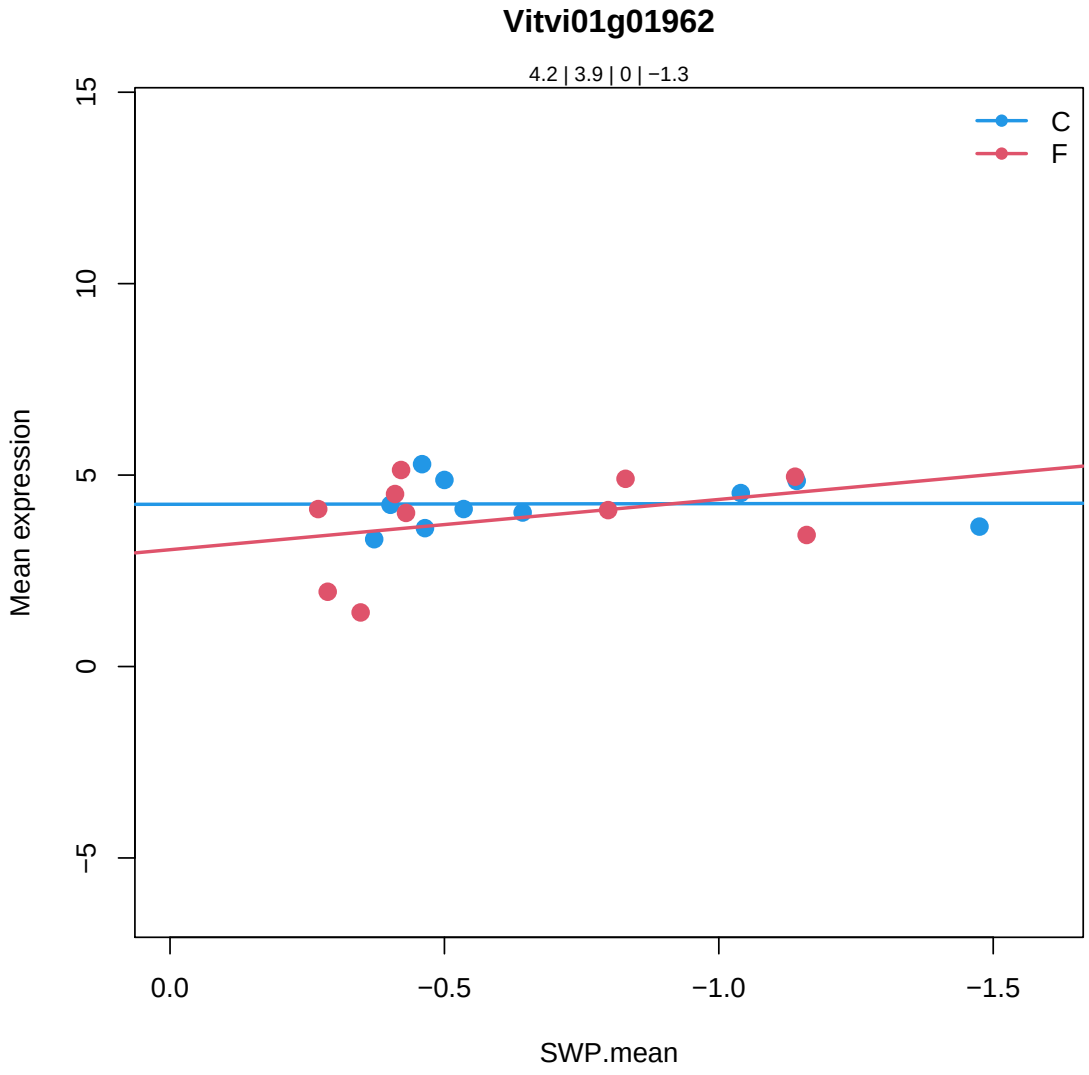
7.6.569 Vitvi01g01962: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01962
        34.99
        transport.misc
        MATE efflux family protein |
        Chr1:26824762-26826748 FORWARD LENGTH=485 |
        201606
```

Coefficients for Vitvi01g01962.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.24871	8.162743e-13	***	1.178187e-12	***
SlopeC	-0.01622724	0.9838217		0.9979351	
MeanF-MeanC	-0.3981466	0.3330941		0.6922185	
SlopeF-SlopeC	-1.29599	0.2831651		0.9999488	



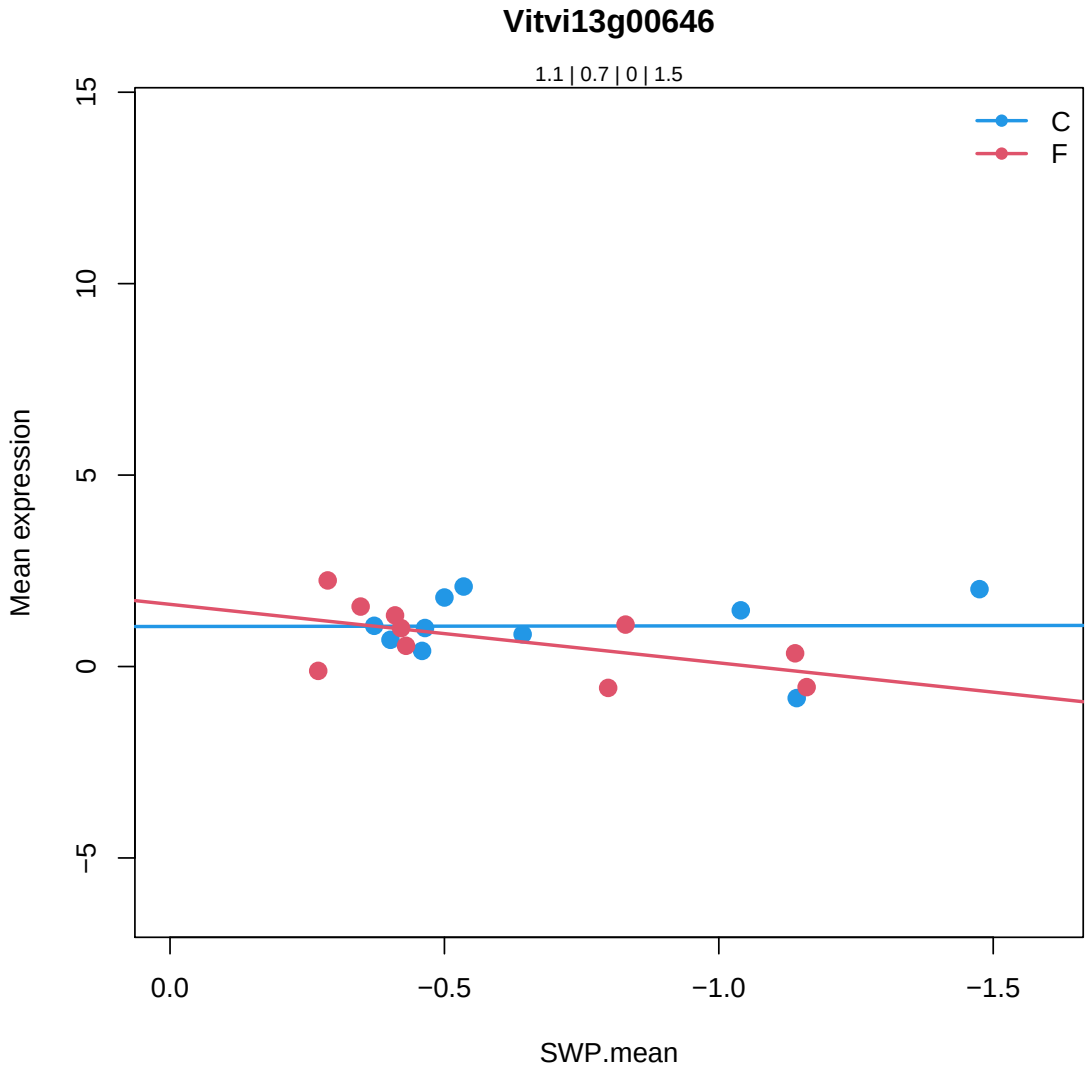
7.6.570 Vitvi13g00646: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00646
        34.3
        transport.amino acids
        Transmembrane amino acid transporter family protein |
        Chr2:16323589-16326744 REVERSE LENGTH=496 |
        201606
```

Coefficients for Vitvi13g00646.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.056996	0.0003636383	***	0.0003969757	***
SlopeC	-0.01637442	0.9814415		0.9979351	
MeanF-MeanC	-0.3647955	0.3138199		0.6760825	
SlopeF-SlopeC	1.545191	0.1502295		0.9999488	



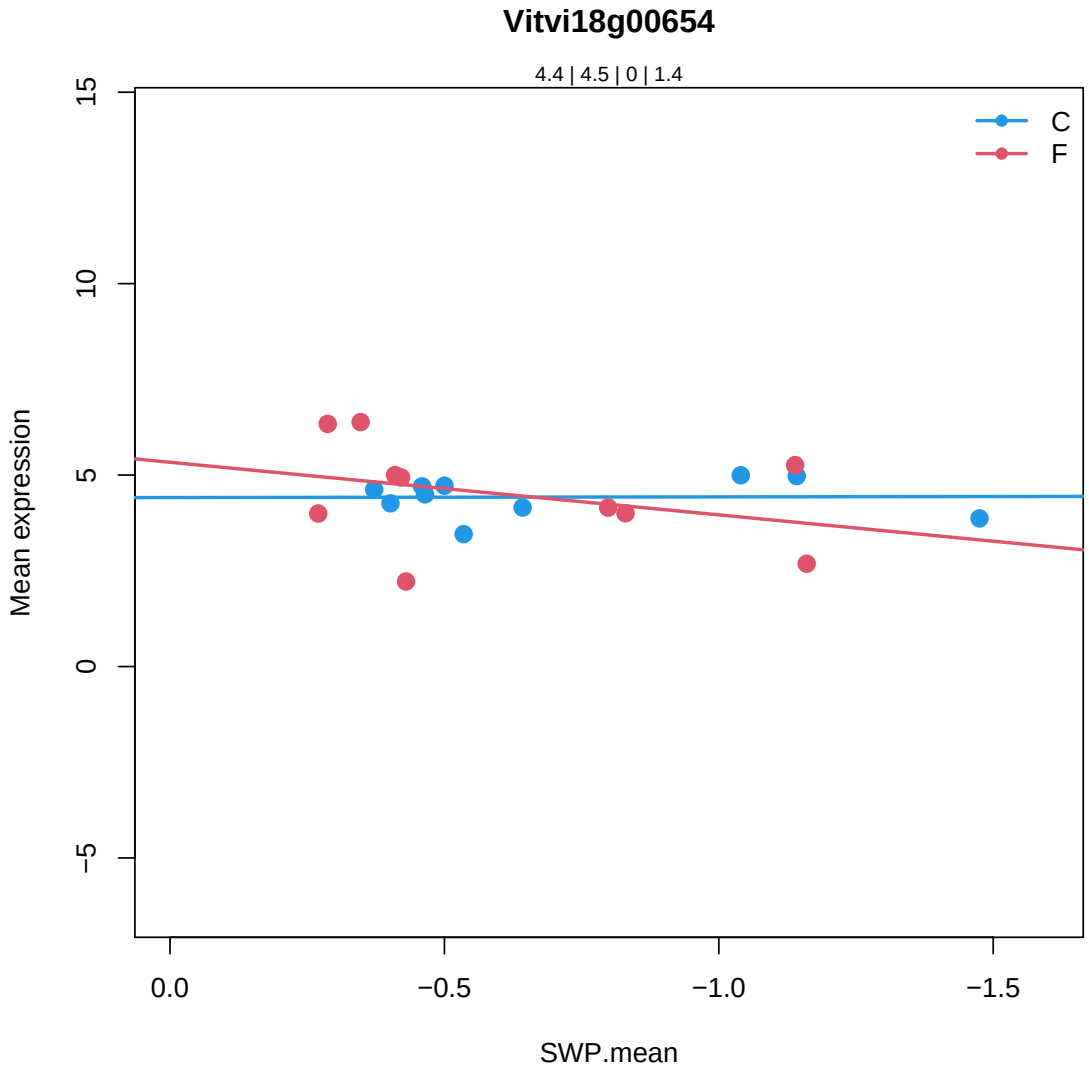
7.6.571 Vitvi18g00654: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00654
        27.3.50
        RNA.regulation of transcription.general transcription
        GATA type zinc finger transcription factor family protein |
        Chr1:3346677-3347446 REVERSE LENGTH=148 |
        201606
```

Coefficients for Vitvi18g00654.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.425505	7.123648e-13	***	1.033e-12	***
SlopeC	-0.01705013	0.983567		0.9979351	
MeanF-MeanC	0.07174377	0.8646619		0.964386	
SlopeF-SlopeC	1.390759	0.2660285		0.9999488	



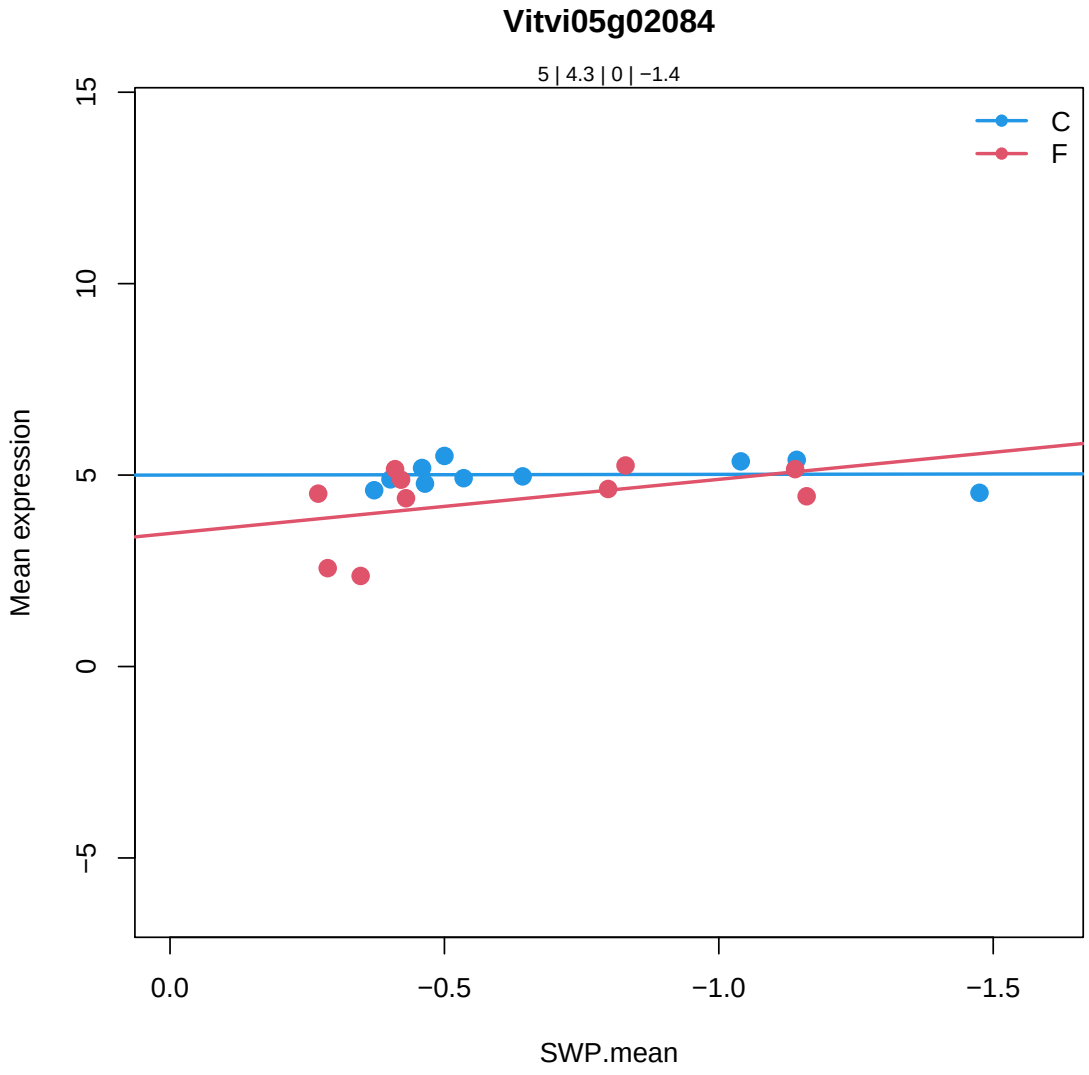
7.6.572 Vitvi05g02084: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g02084
        31.1
        cell.organisation
        ankyrin repeat family protein |
        Chr1:914222-916222 REVERSE LENGTH=616 |
        201606
```

Coefficients for Vitvi05g02084.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.012959	9.16102e-17	***	2.005058e-16	***
SlopeC	-0.01881114	0.9750812		0.9962426	
MeanF-MeanC	-0.6762669	0.03617111	*	0.1913566	
SlopeF-SlopeC	-1.393457	0.1303907		0.9999488	



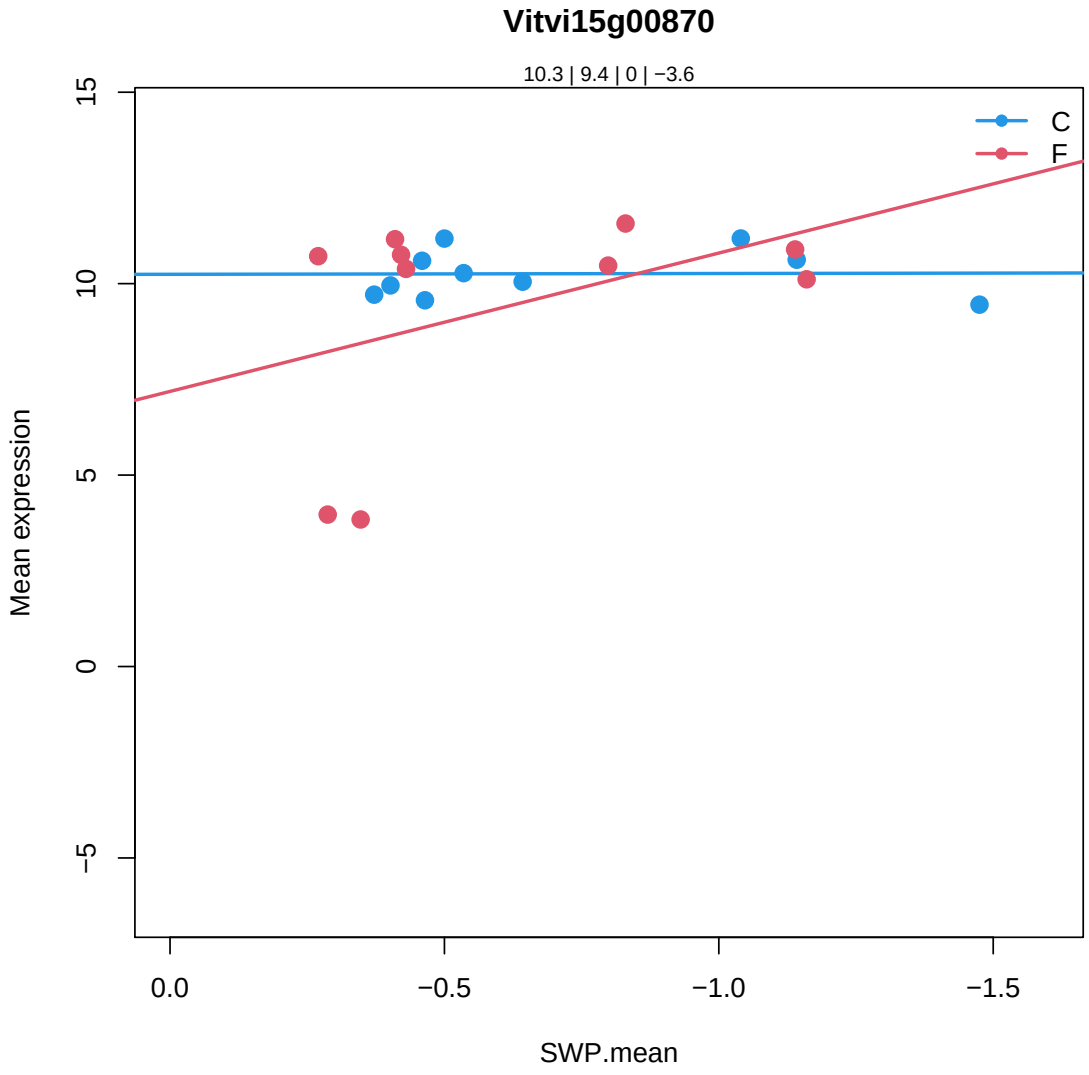
7.6.573 Vitvi15g00870: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g00870
        35.2
        not assigned.unknown
        Homeodomain-like superfamily protein |
        Chr1:33992-37061 REVERSE LENGTH=645 |
        201606
```

Coefficients for Vitvi15g00870.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	10.25864	1.478874e-14	***	2.431869e-14	***
SlopeC	-0.02089706	0.9894484		0.9983274	
MeanF-MeanC	-0.8716246	0.2844279		0.6495729	
SlopeF-SlopeC	-3.592952	0.1368253		0.9999488	



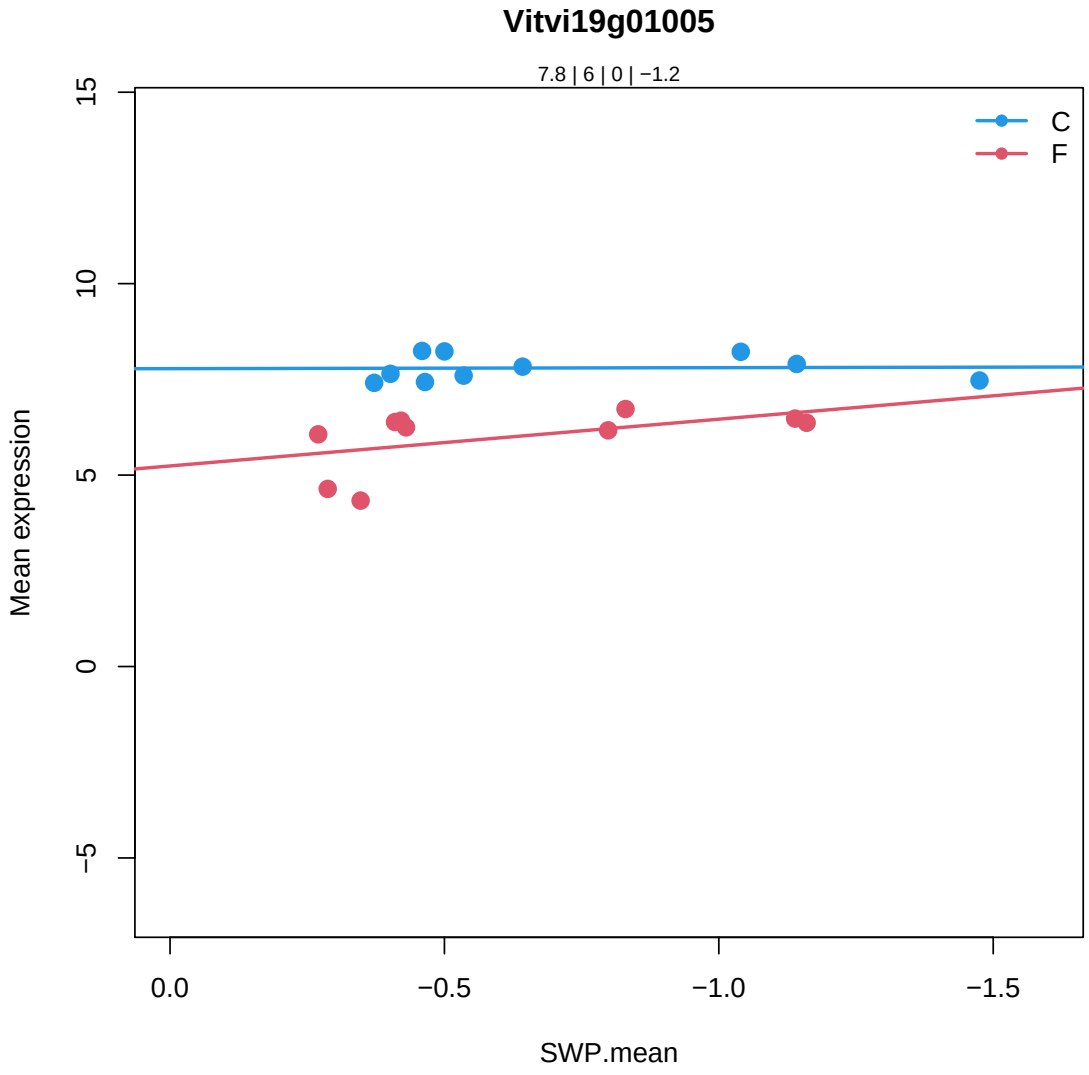
7.6.574 Vitvi19g01005: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g01005
        26.10
        misc.cytochrome P450
        cytochrome P450%2C family 72%2C subfamily A%2C polypeptide 7 |
        Chr3:4912565-4914503 FORWARD LENGTH=512 |
        201606
```

Coefficients for Vitvi19g01005.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.797772	1.514227e-22	***	2.59033e-21	***
SlopeC	-0.02577132	0.9586405		0.9932673	
MeanF-MeanC	-1.815469	3.239862e-07	***	1.18422e-05	***
SlopeF-SlopeC	-1.195553	0.1165604		0.9999488	



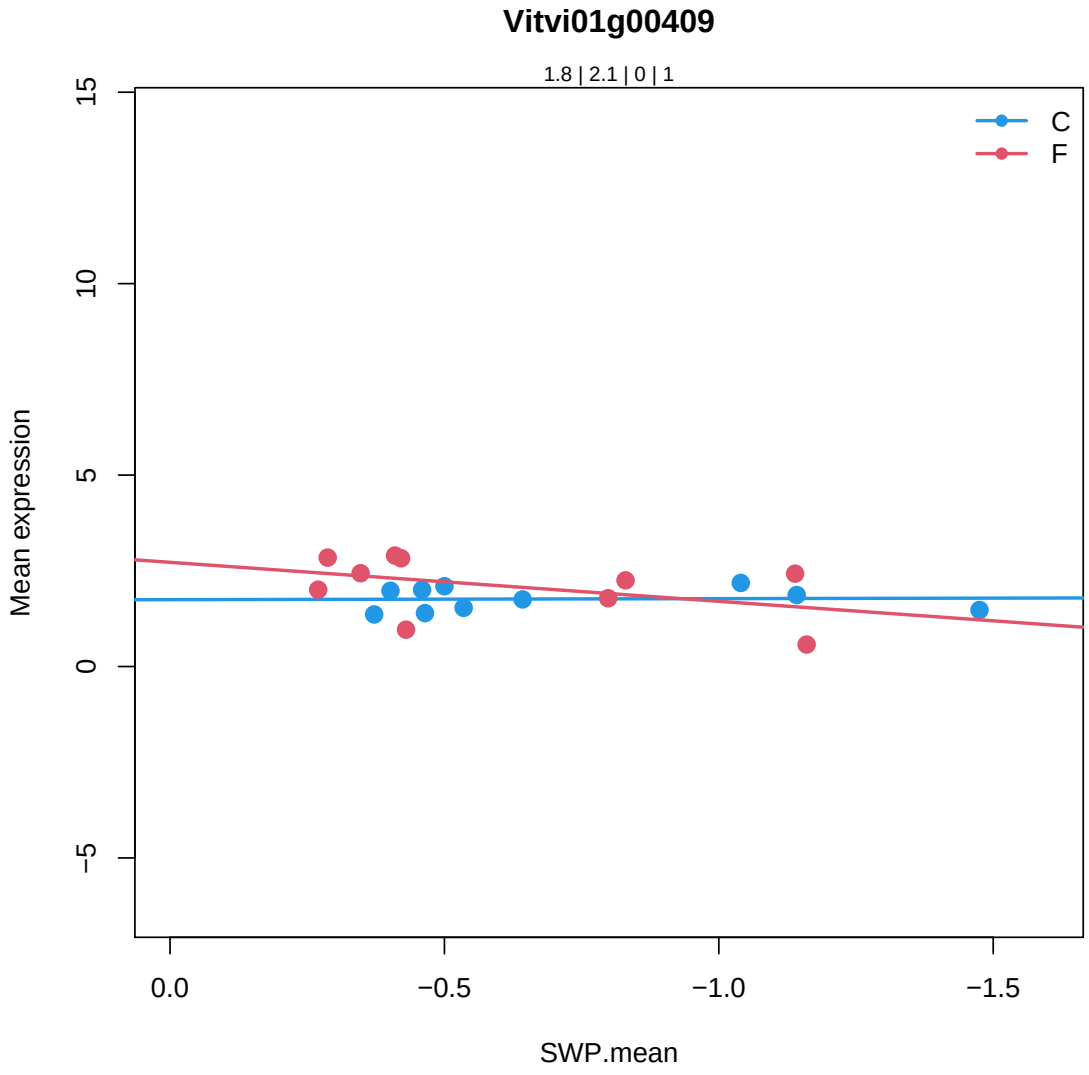
7.6.575 Vitvi01g00409: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00409
        35.2
        not assigned.unknown
        TPX2 (targeting protein for Xklp2) protein family |
        Chr1:26752779-26755242 FORWARD LENGTH=478 |
        201606
```

Coefficients for Vitvi01g00409.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.764749	1.682325e-09	***	2.1056e-09	***
SlopeC	-0.02660027	0.9574625		0.993035	
MeanF-MeanC	0.3359647	0.1939973		0.5350755	
SlopeF-SlopeC	1.045285	0.1686108		0.9999488	



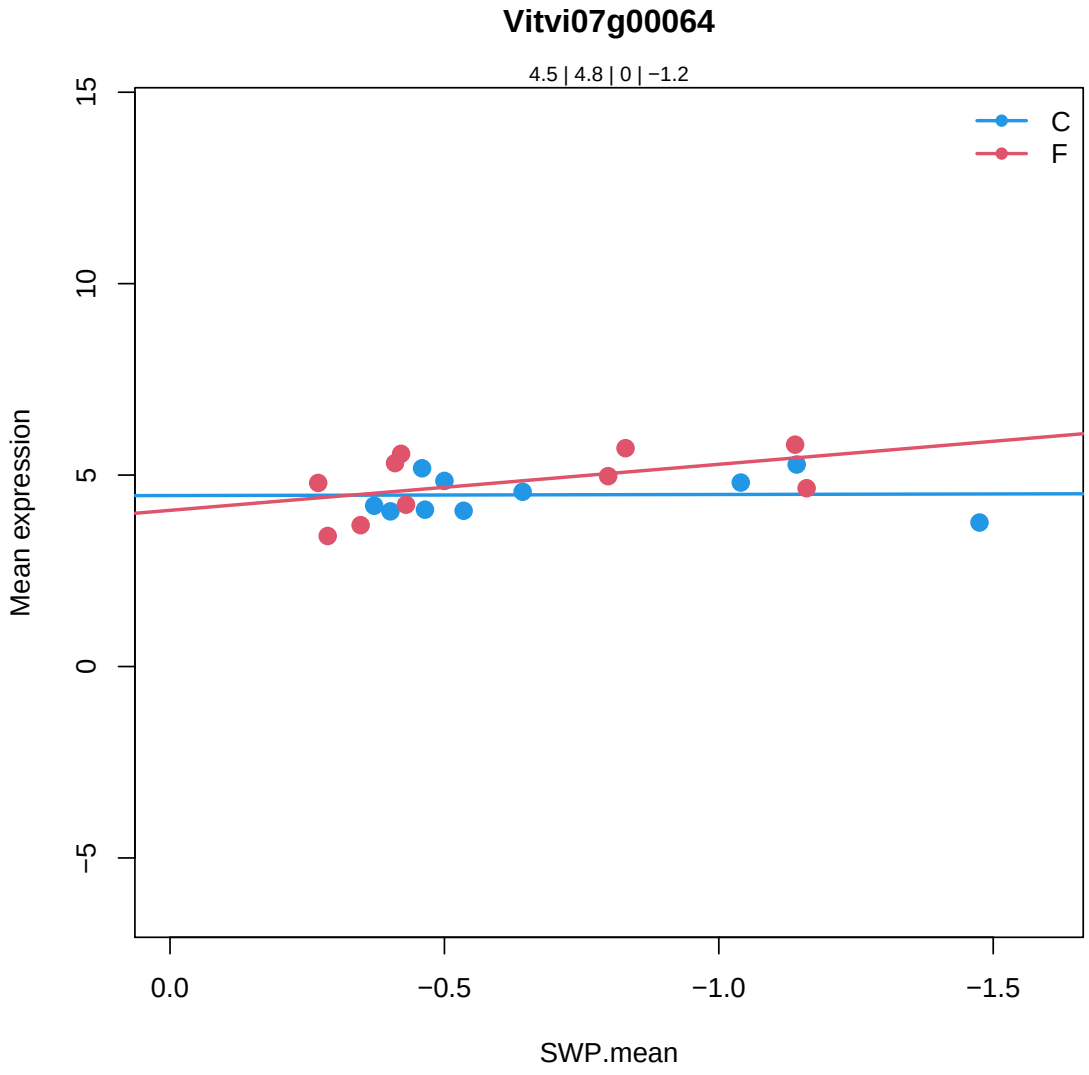
7.6.576 Vitvi07g00064: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g00064
        35.2
        not assigned.unknown
        zinc finger CCCH domain protein |
        Chr3:23420605-23422201 FORWARD LENGTH=508 |
        201606
```

Coefficients for Vitvi07g00064.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.484717	1.853743e-16	***	3.848866e-16	***
SlopeC	-0.02753854	0.9606023		0.9938569	
MeanF-MeanC	0.3267202	0.2562278		0.6167758	
SlopeF-SlopeC	-1.175195	0.1662846		0.9999488	



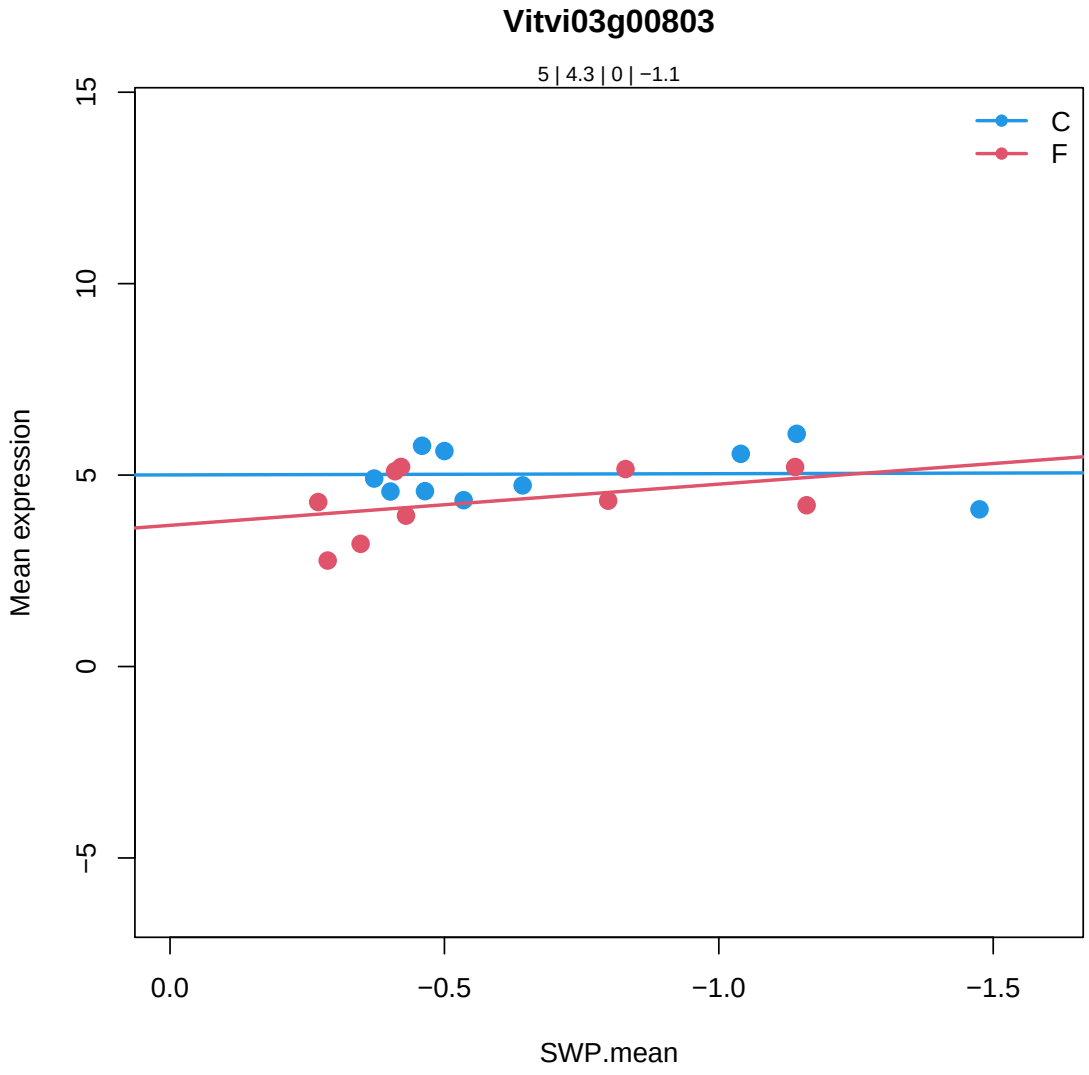
7.6.577 Vitvi03g00803: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00803
        34.15
        transport.potassium
        K+ efflux antiporter 3 |
        Chr4:2453174-2457490 FORWARD LENGTH=776 |
        201606
```

Coefficients for Vitvi03g00803.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.026575	2.535705e-16	***	5.160109e-16	***
SlopeC	-0.03185989	0.9599476		0.9937458	
MeanF-MeanC	-0.6835444	0.04359474	*	0.2186479	
SlopeF-SlopeC	-1.044236	0.2755644		0.9999488	



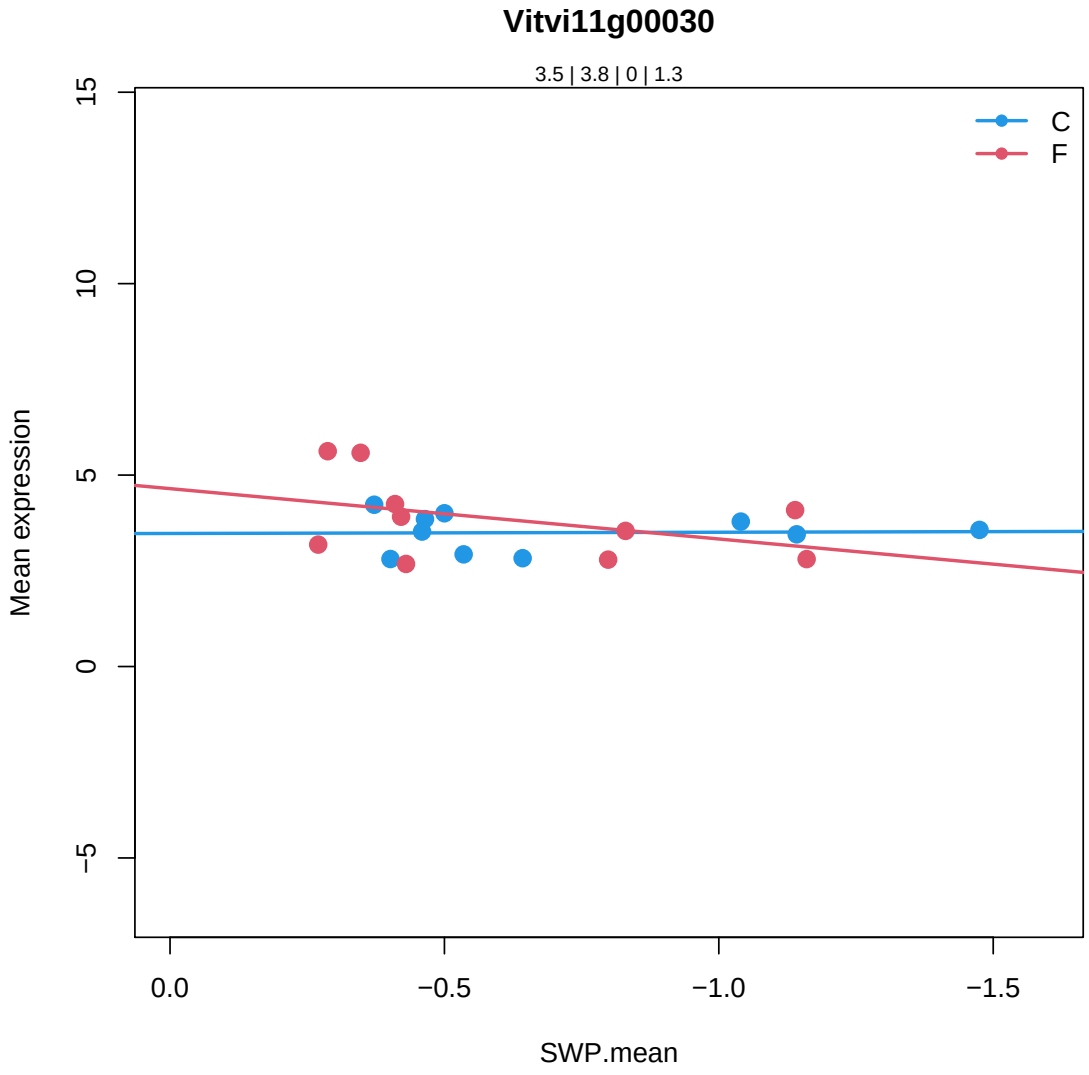
7.6.578 Vitvi11g00030: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00030
        2.2.1.5
        major CHO metabolism.degradation.sucrose.Susy
        sucrose synthase 4 |
        Chr3:15179204-15182577 REVERSE LENGTH=808 |
        201606
```

Coefficients for Vitvi11g00030.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.497426	1.177706e-12	***	1.682185e-12	***
SlopeC	-0.03211816	0.9618334		0.9939741	
MeanF-MeanC	0.3473629	0.3144448		0.6764669	
SlopeF-SlopeC	1.346928	0.1866672		0.9999488	



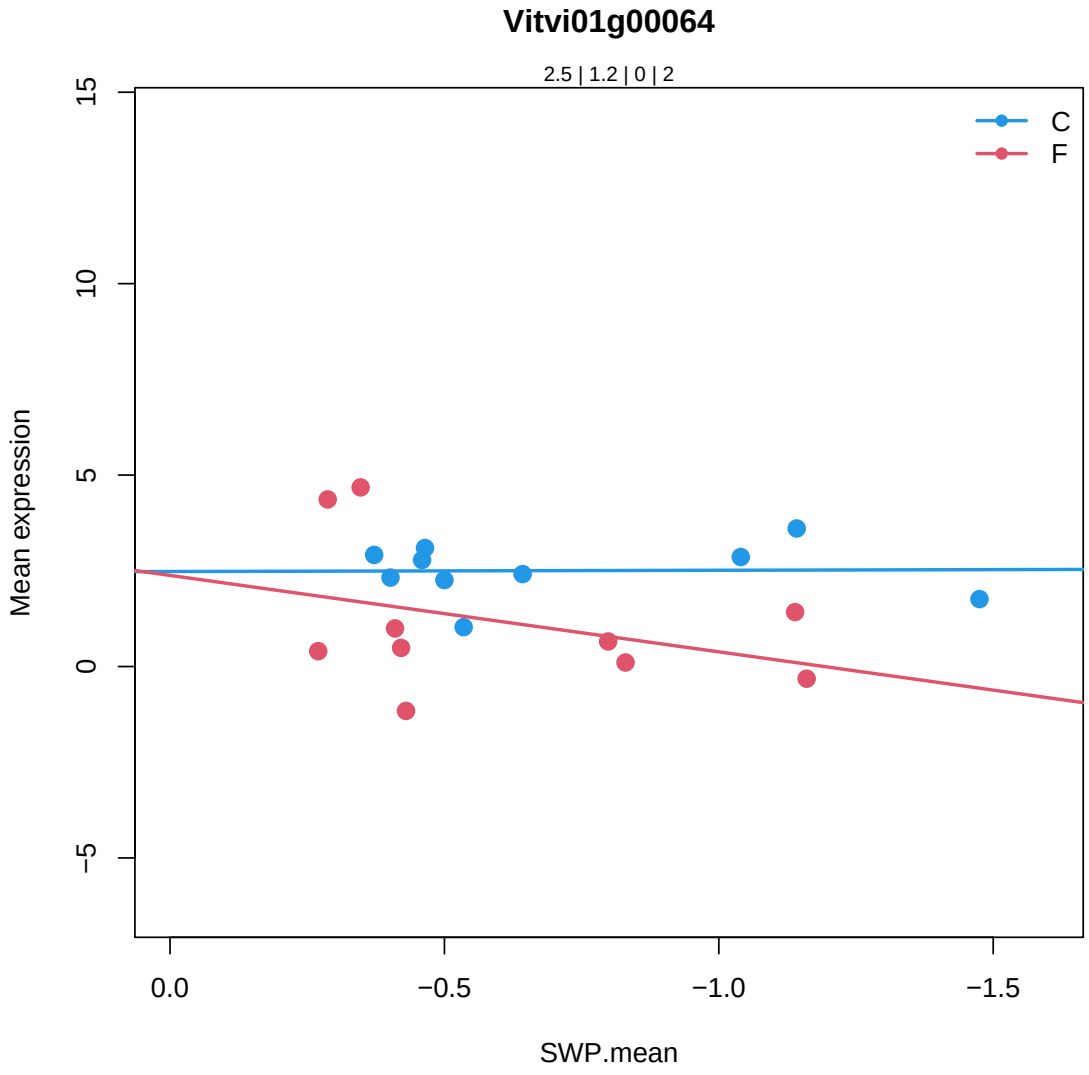
7.6.579 Vitvi01g00064: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00064
        2.2.2.2
        major CHO metabolism.degradation.starch.starch phosphorylase
        Glycosyl transferase%2C family 35 |
        Chr3:11252871-11257587 FORWARD LENGTH=962 |
        201606
```

Coefficients for Vitvi01g00064.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.50421	3.137274e-06	***	3.580556e-06	***
SlopeC	-0.03291293	0.9767566		0.9965809	
MeanF-MeanC	-1.341287	0.02762602	*	0.1599574	
SlopeF-SlopeC	2.030061	0.2351312		0.9999488	



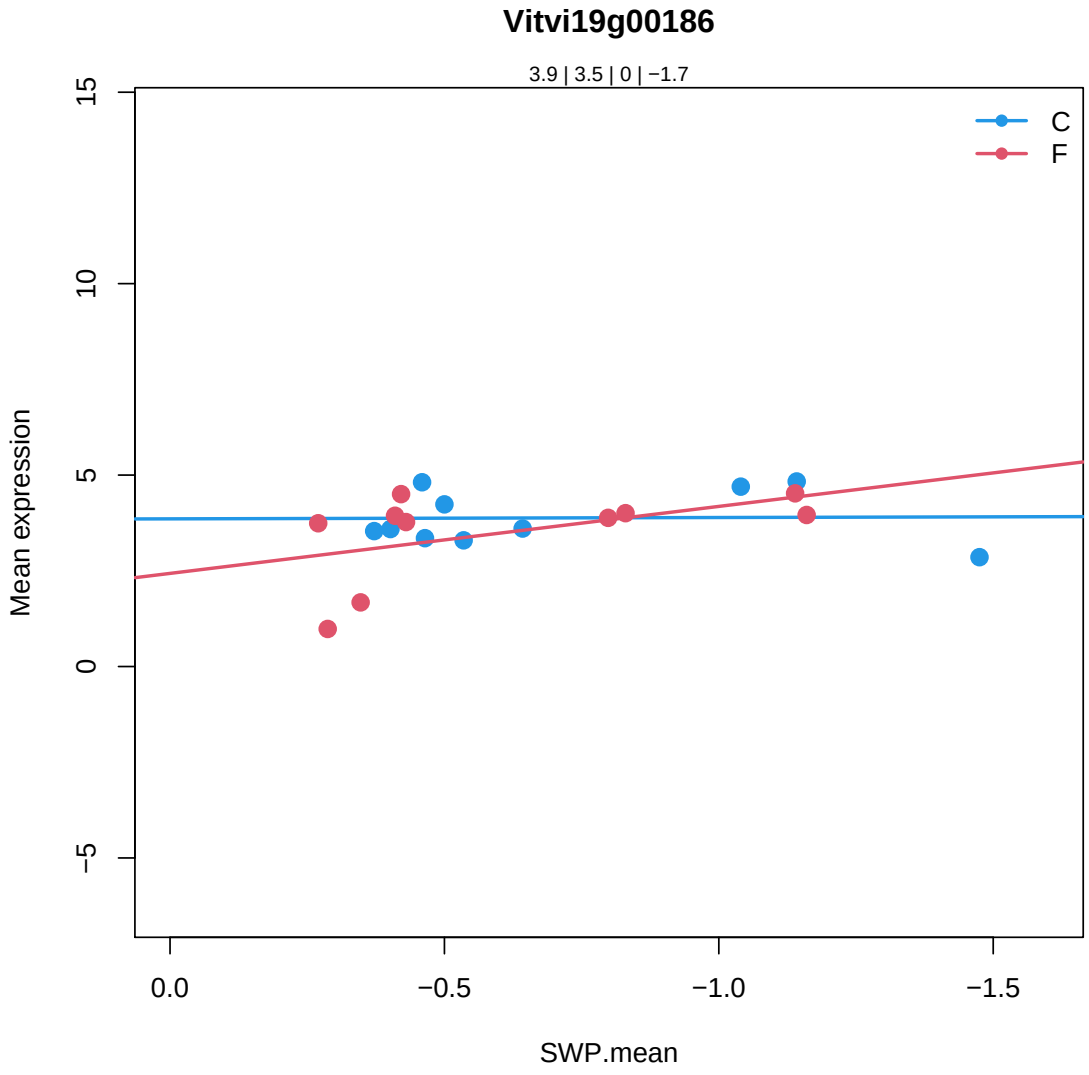
7.6.580 Vitvi19g00186: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g00186
        13.1.6.4.3
        amino acid metabolism.synthesis.aromatic aa.tyrosine.tyrosine transami
        Tyrosine transaminase family protein |
        Chr5:21910676-21912594 FORWARD LENGTH=414 |
        201606
```

Coefficients for Vitvi19g00186.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.881047	1.356374e-12	***	1.931053e-12	***
SlopeC	-0.03502947	0.9627574		0.9939741	
MeanF-MeanC	-0.3831151	0.3207448		0.6816197	
SlopeF-SlopeC	-1.714626	0.1349038		0.9999488	



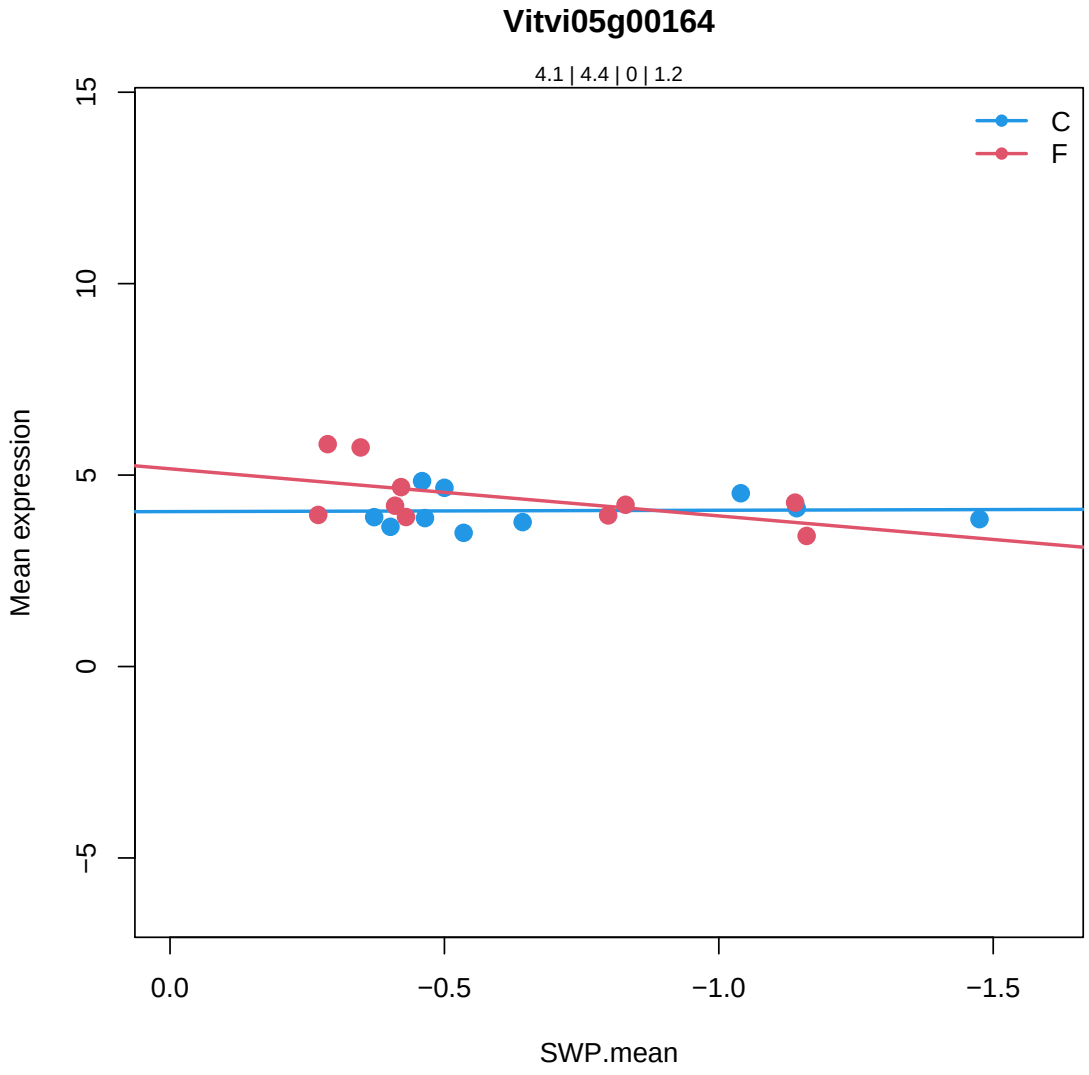
7.6.581 Vitvi05g00164: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00164
        2.2.1.3.1
        major CHO metabolism.degradation.sucrose.invertases.neutral
        Plant neutral invertase family protein |
        Chr3:2012952-2015471 FORWARD LENGTH=465 |
        201606
```

Coefficients for Vitvi05g00164.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.070877	2.361348e-16	***	4.831096e-16	***
SlopeC	-0.03541628	0.944856		0.9903035	
MeanF-MeanC	0.3431073	0.1962747		0.5377709	
SlopeF-SlopeC	1.265454	0.1074602		0.9999488	



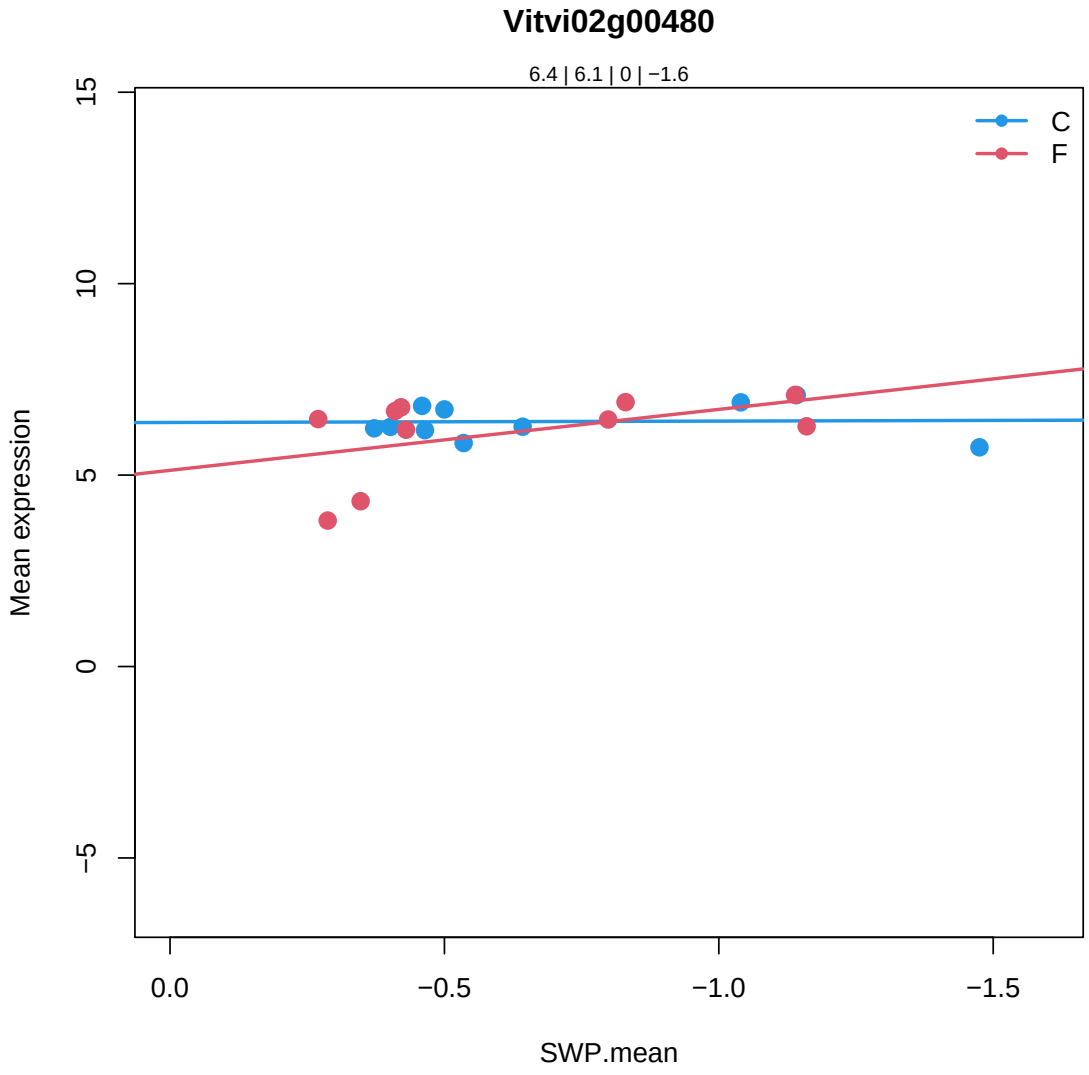
7.6.582 Vitvi02g00480: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00480
        29.2.5
        protein.synthesis.release
        Class I peptide chain release factor |
        Chr1:23272789-23274211 REVERSE LENGTH=206 |
        201606
```

Coefficients for Vitvi02g00480.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.39893	3.29411e-18	***	9.803677e-18	***
SlopeC	-0.03559795	0.9566613		0.9927945	
MeanF-MeanC	-0.3051053	0.3642071		0.7210582	
SlopeF-SlopeC	-1.555837	0.1210273		0.9999488	



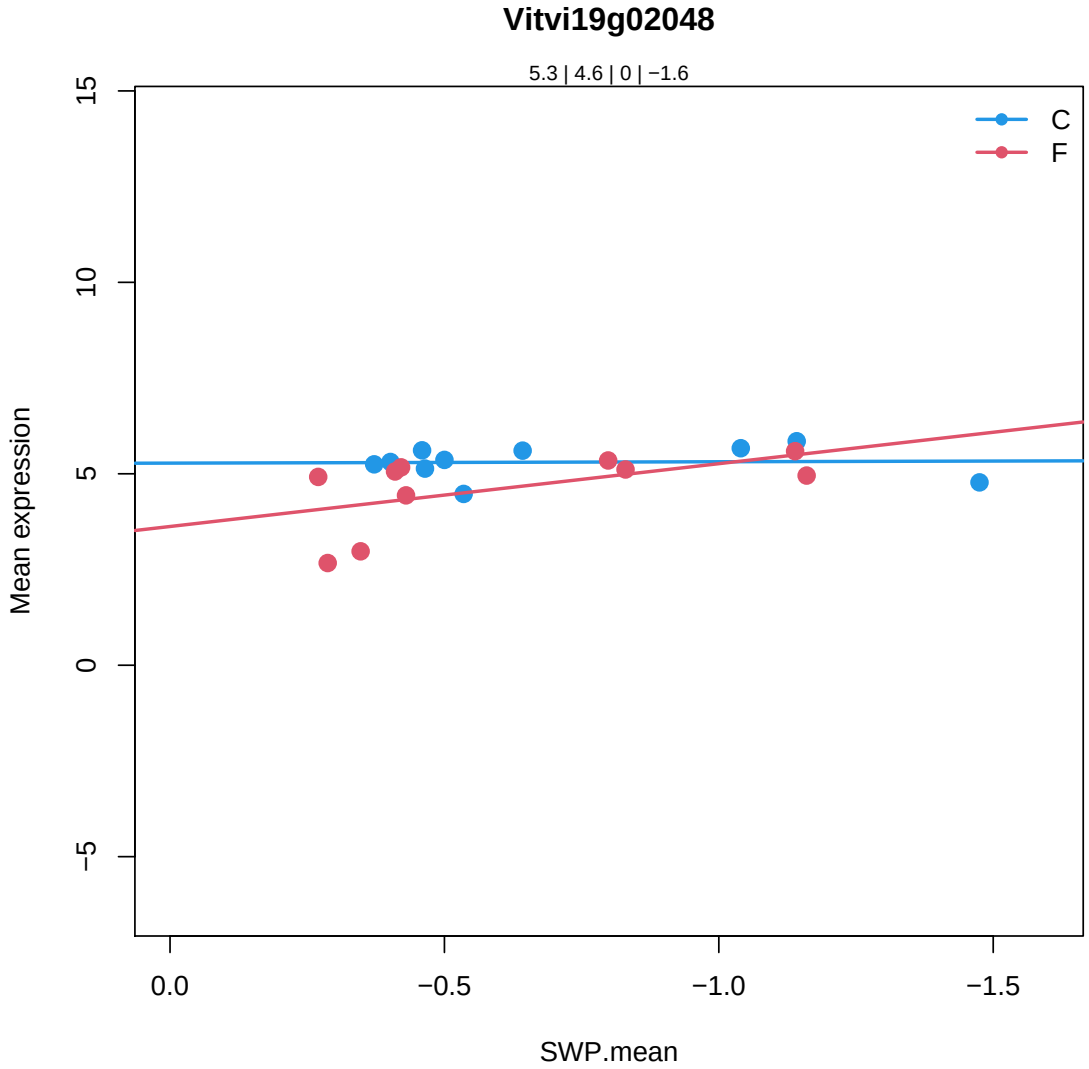
7.6.583 Vitvi19g02048: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g02048
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi19g02048.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.303617	1.181788e-17	***	3.063403e-17	***
SlopeC	-0.03577059	0.9505891		0.9922795	
MeanF-MeanC	-0.6806445	0.02859903	*	0.1638757	
SlopeF-SlopeC	-1.604744	0.07238462	.	0.9999488	



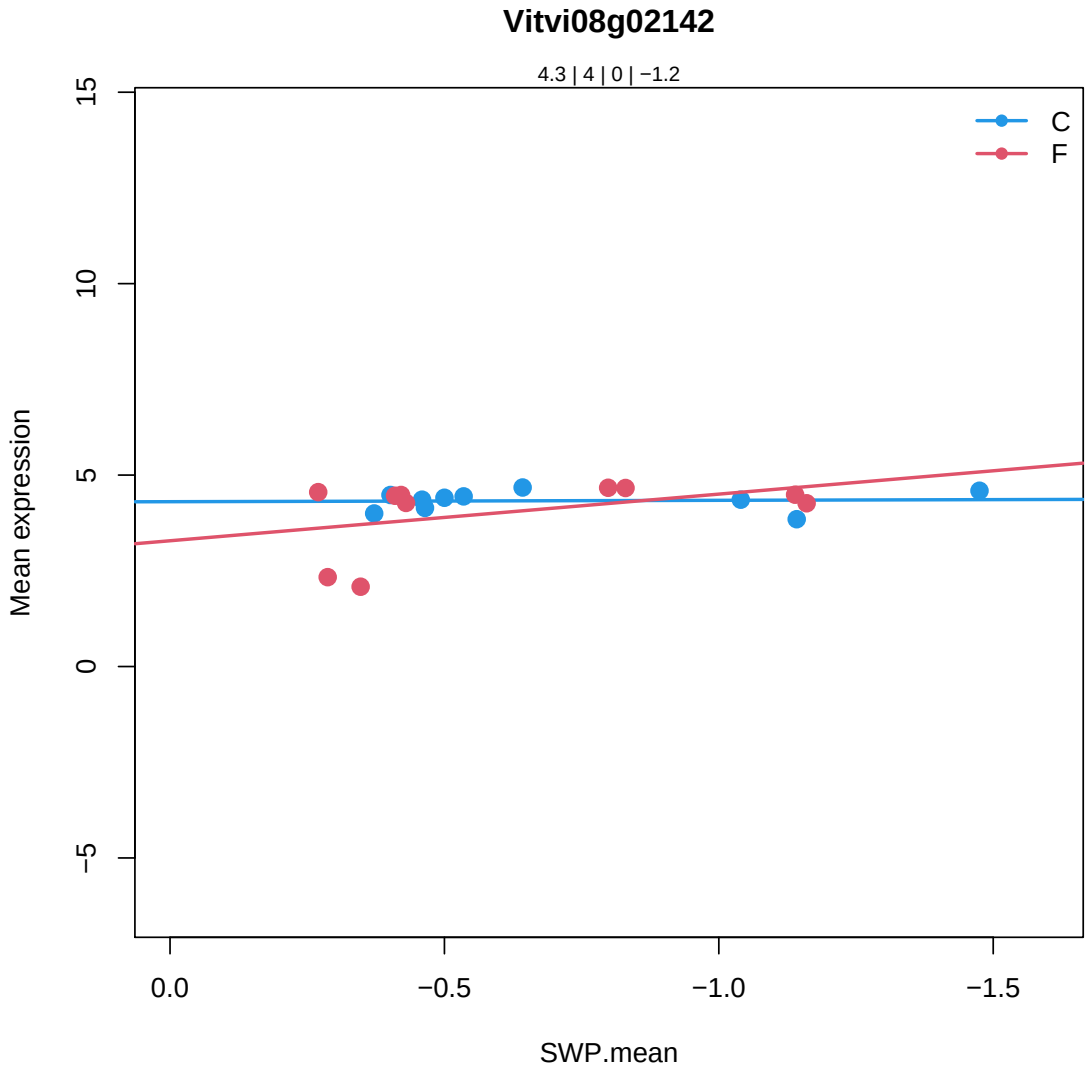
7.6.584 Vitvi08g02142: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g02142
        35.2
        not assigned.unknown
        DNA/RNA polymerases superfamily protein |
        ChrM:227709-228431 REVERSE LENGTH=240 |
        201606
```

Coefficients for Vitvi08g02142.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.32991	6.029301e-16	***	1.160336e-15	***
SlopeC	-0.03584517	0.9498582		0.9918977	
MeanF-MeanC	-0.3031886	0.3015172		0.6668204	
SlopeF-SlopeC	-1.182619	0.1727756		0.9999488	



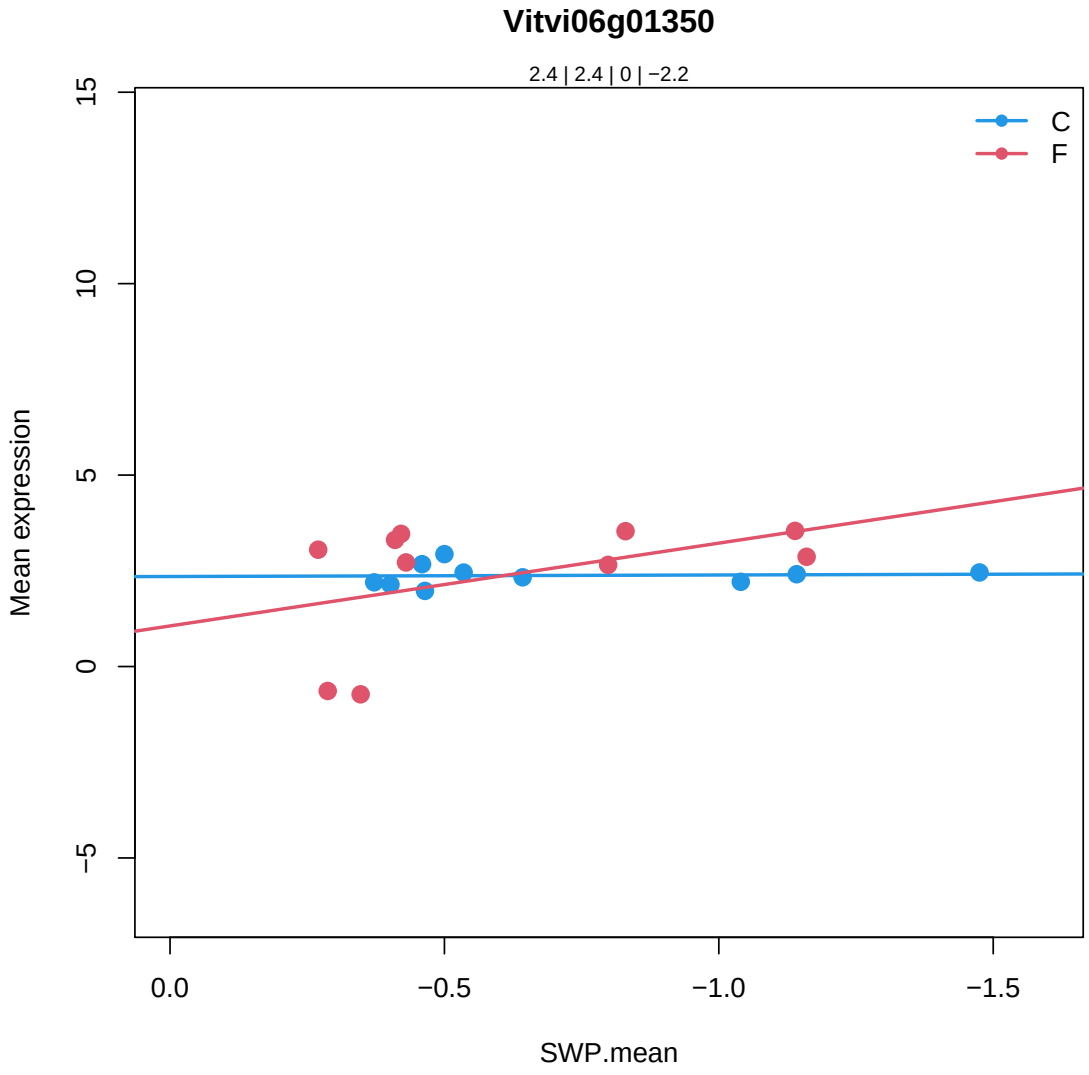
7.6.585 Vitvi06g01350: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01350
        27.3.11
        RNA.regulation of transcription.C2H2 zinc finger family
        C2H2-type zinc finger family protein |
        Chr2:12024321-12025181 FORWARD LENGTH=286 |
        201606
```

Coefficients for Vitvi06g01350.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.378478	1.871945e-07	***	2.204279e-07	***
SlopeC	-0.03982735	0.9642676		0.9943773	
MeanF-MeanC	-0.001000824	0.9982329		0.9998558	
SlopeF-SlopeC	-2.122684	0.1191913		0.9999488	



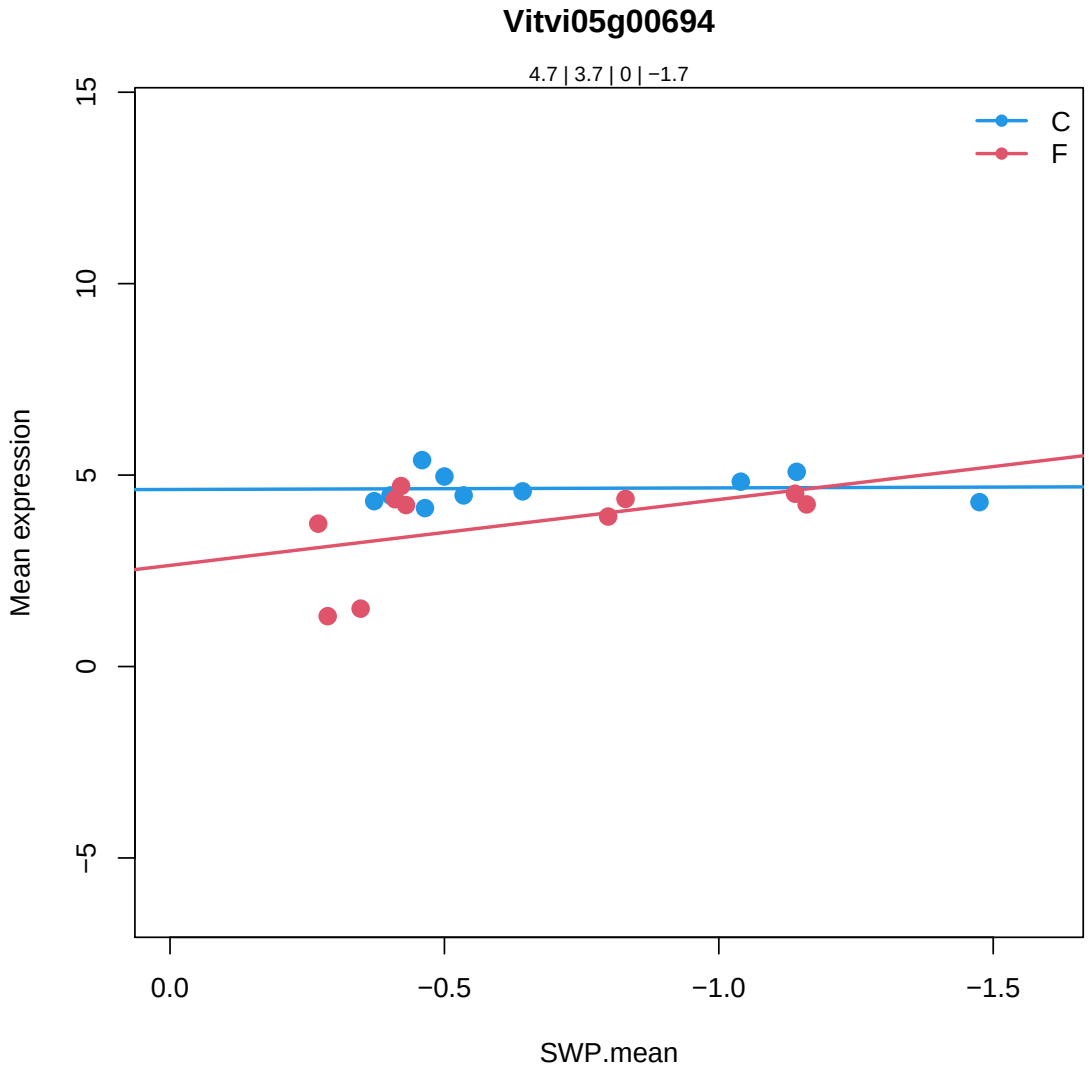
7.6.586 Vitvi05g00694: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00694
        17.5.1
        hormone metabolism.ethylene.synthesis-degradation
        2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protei
        Chr1:2025618-2026764 FORWARD LENGTH=284 |
        201606
```

Coefficients for Vitvi05g00694.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.652677	9.229542e-15	***	1.549815e-14	***
SlopeC	-0.04107271	0.9532222		0.9925445	
MeanF-MeanC	-0.9631057	0.01218355	*	0.08784371	.
SlopeF-SlopeC	-1.679419	0.1175975		0.9999488	



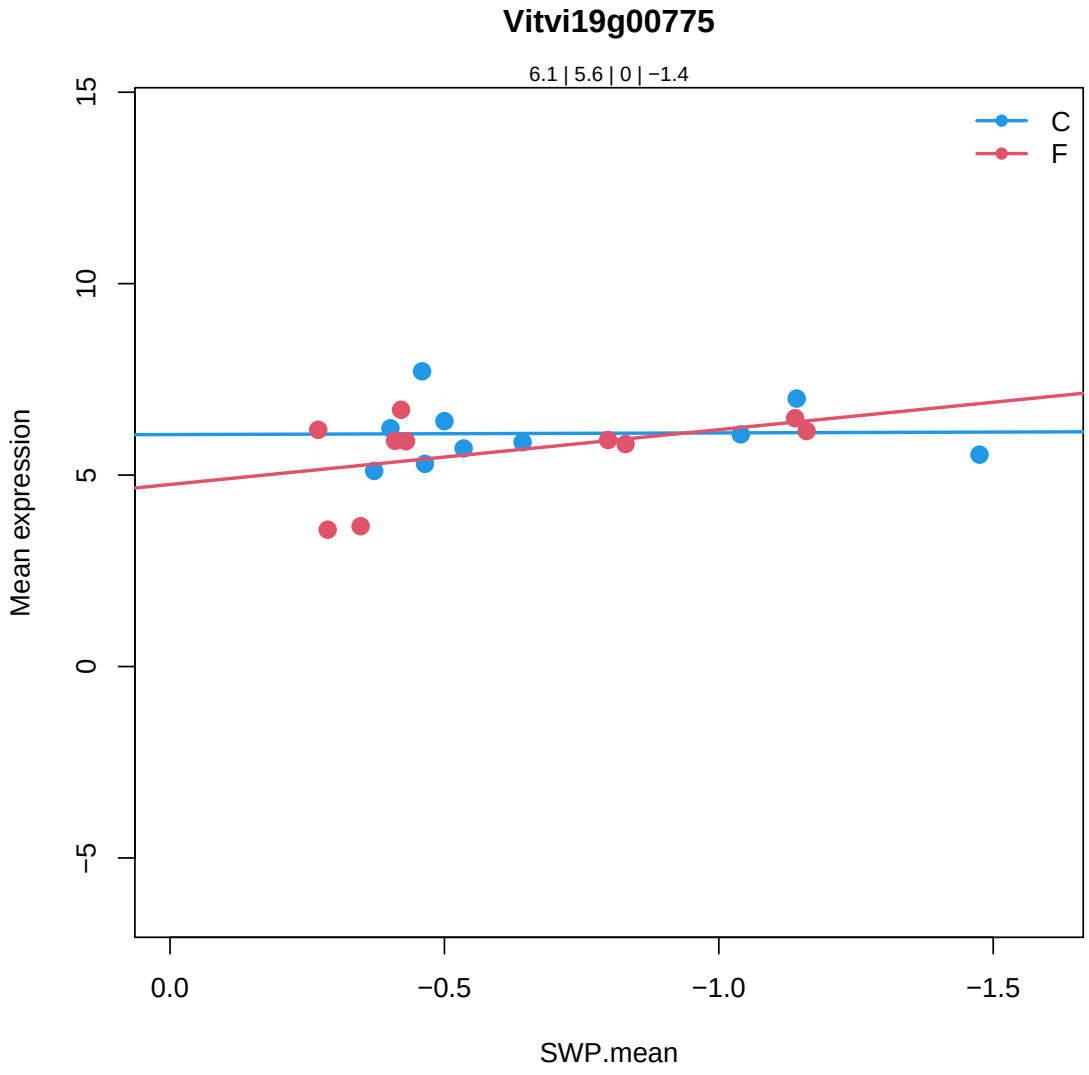
7.6.587 Vitvi19g00775: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g00775
        20.2.1
        stress.abiotic.heat
        Chaperone DnaJ-domain superfamily protein |
        Chr3:4310827-4311300 REVERSE LENGTH=157 |
        201606
```

Coefficients for Vitvi19g00775.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.088611	1.997841e-16	***	4.128256e-16	***
SlopeC	-0.04318962	0.9546593		0.9925951	
MeanF-MeanC	-0.4620605	0.2391805		0.5962654	
SlopeF-SlopeC	-1.388812	0.2273496		0.9999488	



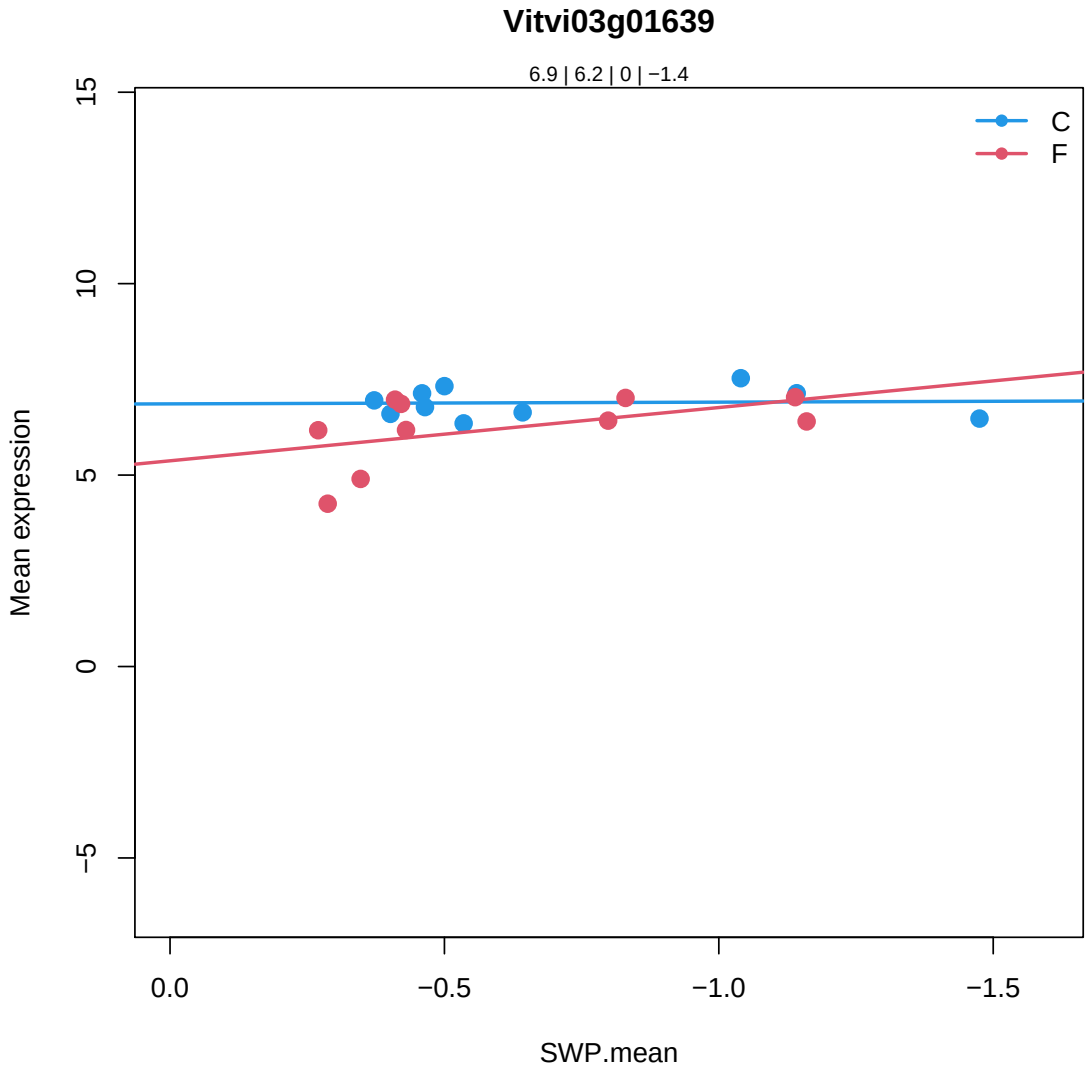
7.6.588 Vitvi03g01639: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g01639
        35.2
        not assigned.unknown
        tubulin alpha-6 chain |
        Chr1:18520144-18521600 REVERSE LENGTH=209 |
        201606
```

Coefficients for Vitvi03g01639.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.891312	2.824309e-20	***	1.651885e-19	***
SlopeC	-0.04487145	0.9364006		0.9890256	
MeanF-MeanC	-0.6710029	0.02693591	*	0.157121	
SlopeF-SlopeC	-1.346037	0.1182998		0.9999488	



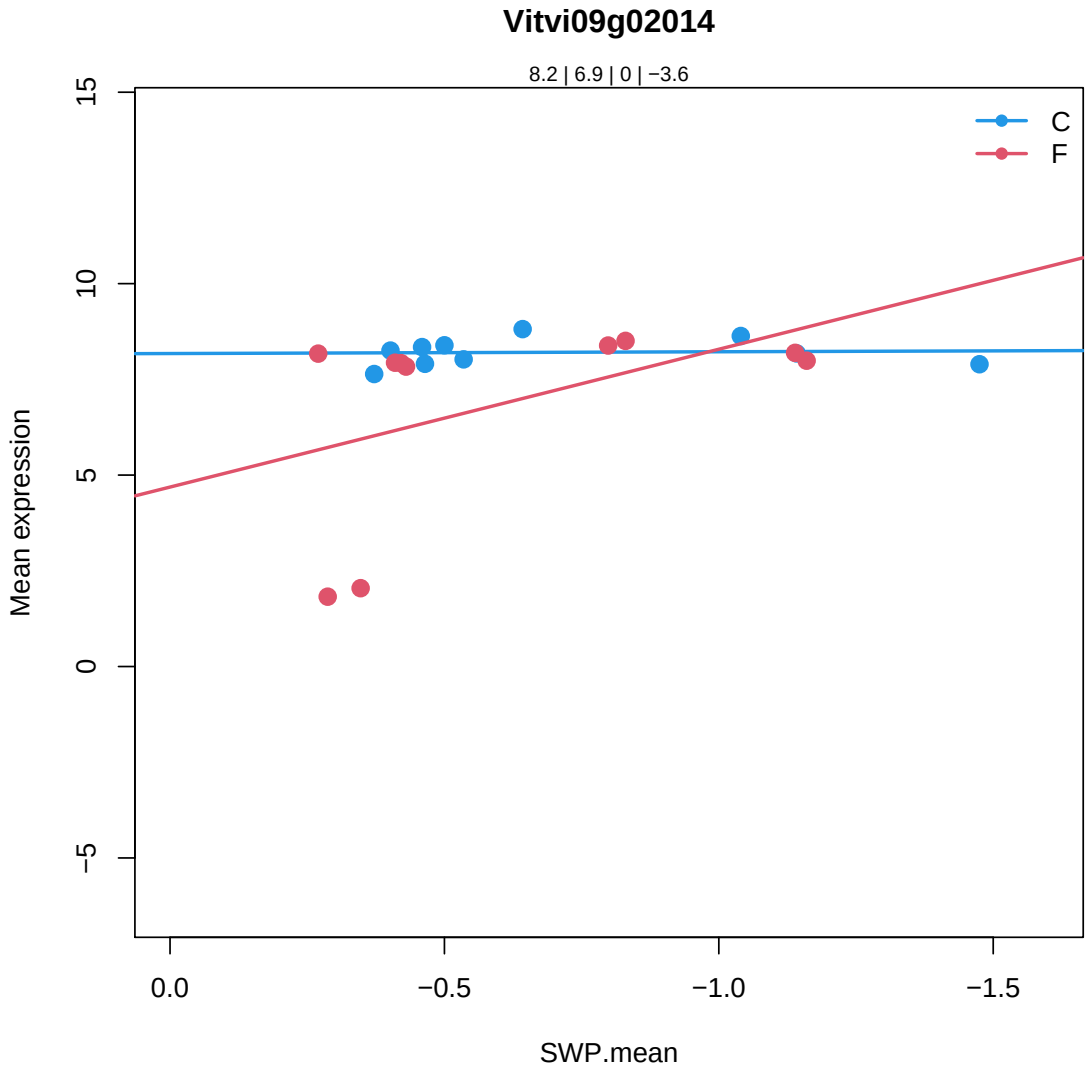
7.6.589 Vitvi09g02014: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g02014
        35.2
        not assigned.unknown
        hypothetical protein |
        Chr1:5726617-5727312 REVERSE LENGTH=202 |
        201606
```

Coefficients for Vitvi09g02014.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	8.206843	6.668827e-14	***	1.037524e-13	***
SlopeC	-0.04628244	0.9729004		0.9962426	
MeanF-MeanC	-1.326783	0.06586435	.	0.2847474	
SlopeF-SlopeC	-3.553714	0.09042245	.	0.9999488	



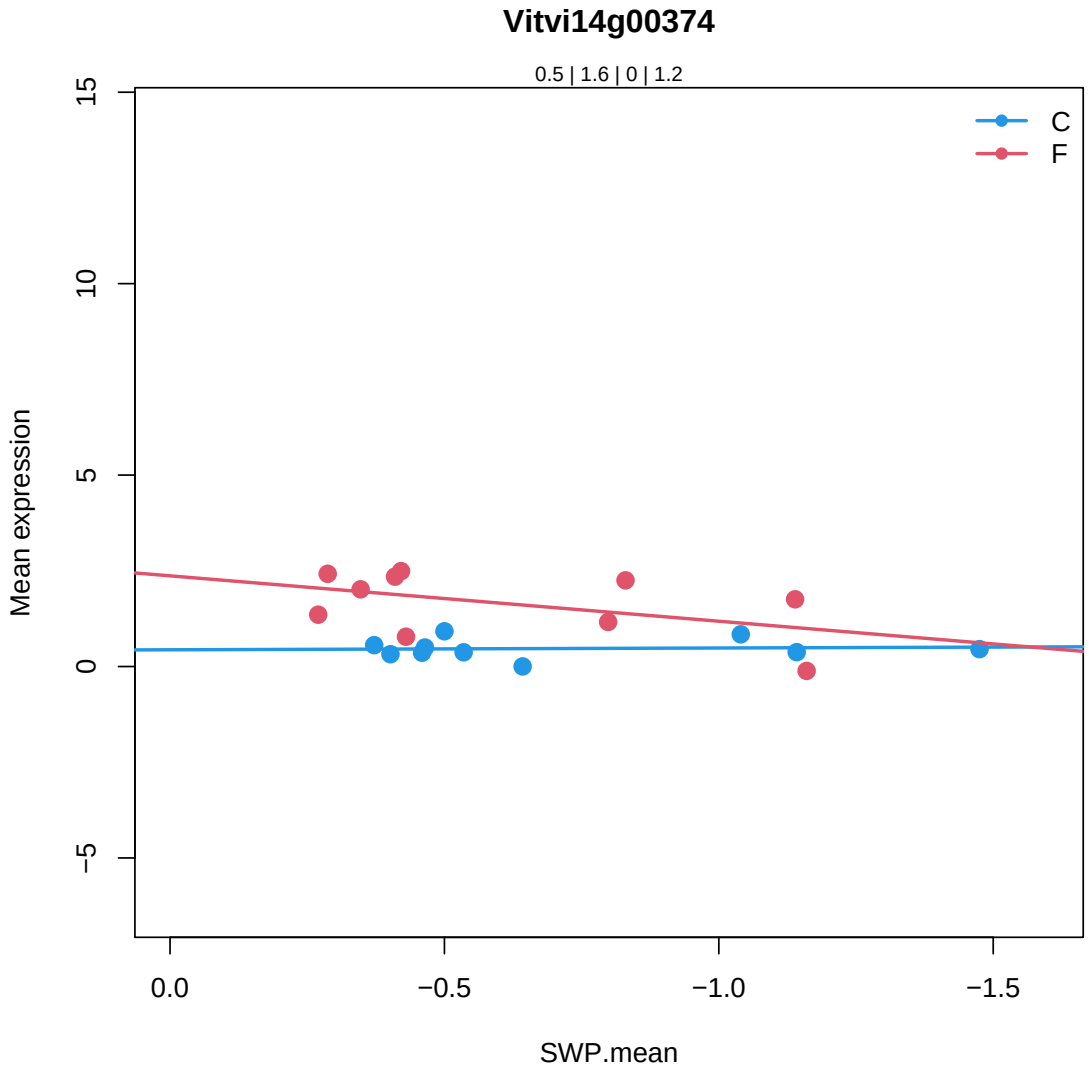
7.6.590 Vitvi14g00374: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g00374
        20.1.2.1
        stress.biotic.receptors.CC-NBS-LRR
        NB-ARC domain-containing disease resistance protein |
        Chr4:13620977-13623934 REVERSE LENGTH=985 |
        201606
```

Coefficients for Vitvi14g00374.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4696243	0.01604316	*	0.01691311	*
SlopeC	-0.0468298	0.9262229		0.9864486	
MeanF-MeanC	1.176391	0.0001373333	***	0.002357246	**
SlopeF-SlopeC	1.232238	0.112201		0.9999488	



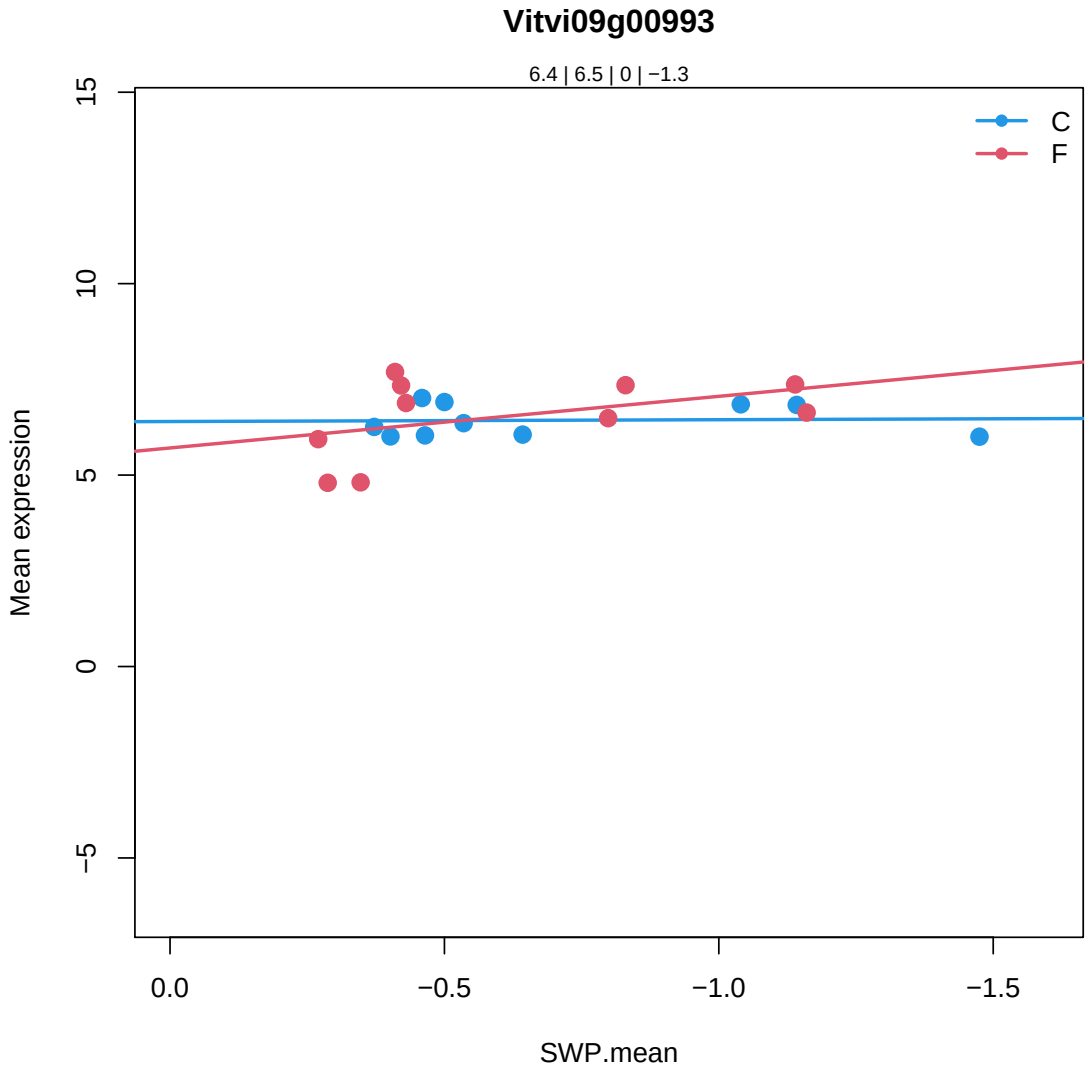
7.6.591 Vitvi09g00993: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00993
        16.8.3.1
        secondary metabolism.flavonoids.dihydroflavonols.dihydroflavonol 4-red
        cinnamoyl coa reductase 1 |
        Chr1:5479798-5481915 FORWARD LENGTH=246 |
        201606
```

Coefficients for Vitvi09g00993.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.431895	1.364295e-18	***	4.520563e-18	***
SlopeC	-0.0473167	0.940249		0.9898527	
MeanF-MeanC	0.09766993	0.7610752		0.9304918	
SlopeF-SlopeC	-1.301486	0.1753527		0.9999488	



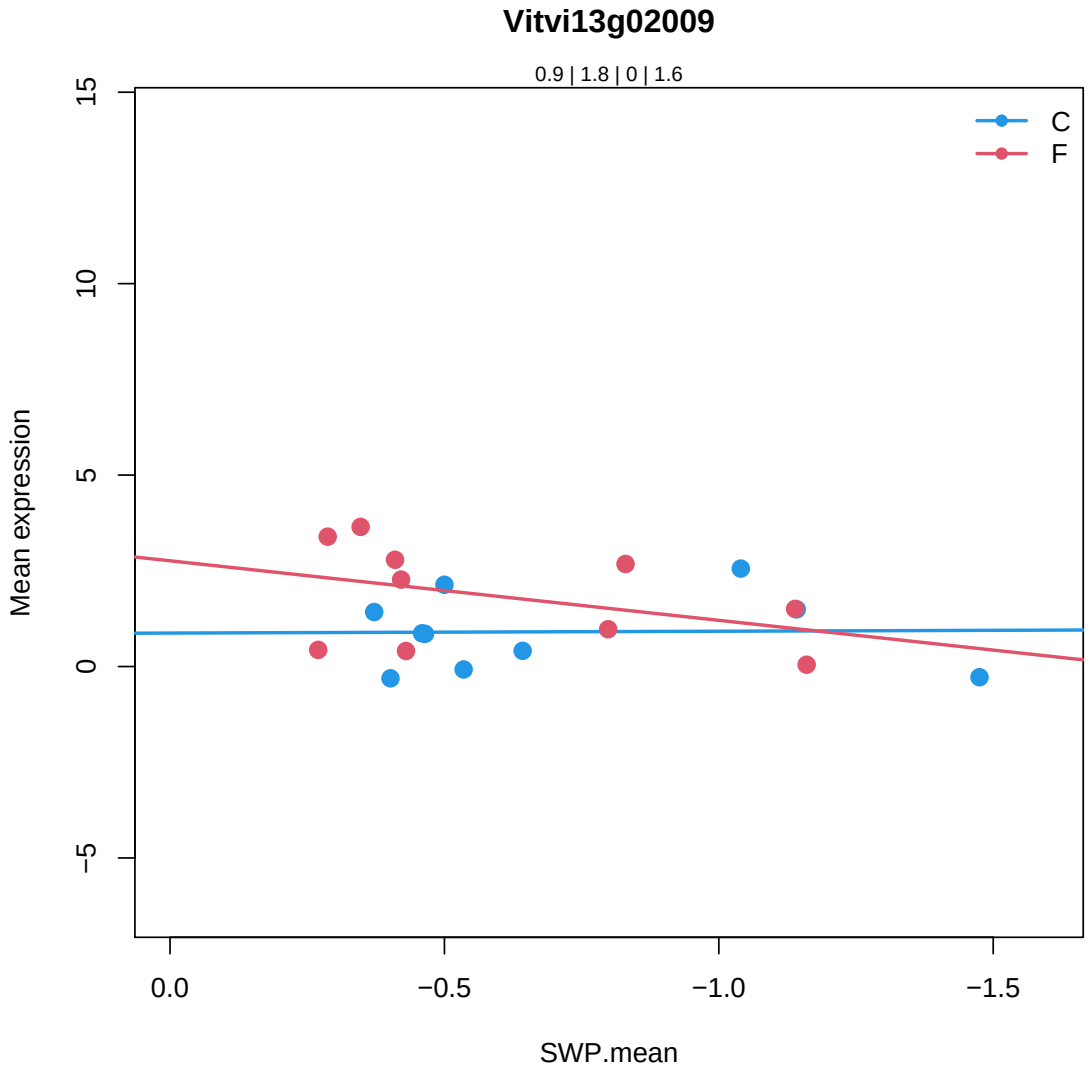
7.6.592 Vitvi13g02009: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g02009
        29.5.1
        protein.degradation.subtilases
        subtilase 4.13 |
        Chr5:23864897-23868020 REVERSE LENGTH=732 |
        201606
```

Coefficients for Vitvi13g02009.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.9070904	0.01172714	*	0.01240424	*
SlopeC	-0.04757836	0.9590588		0.9933601	
MeanF-MeanC	0.9067801	0.06470823	.	0.2816632	
SlopeF-SlopeC	1.602349	0.2527889		0.9999488	



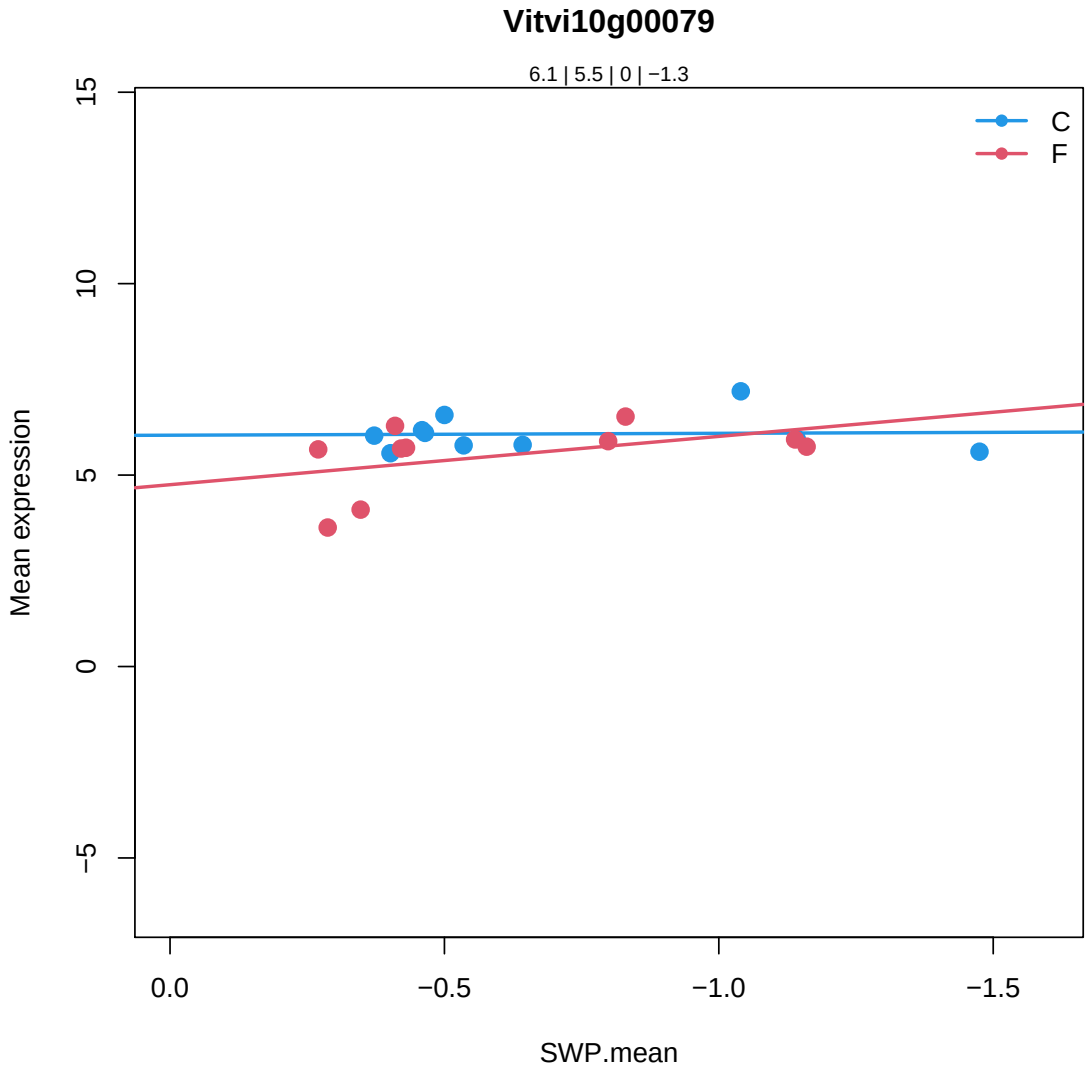
7.6.593 Vitvi10g00079: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00079
        35.2
        not assigned.unknown
        orotidine 5'-phosphate decarboxylase |
        Chr1:22995615-22997003 REVERSE LENGTH=267 |
        201606
```

Coefficients for Vitvi10g00079.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.075713	1.070264e-18	***	3.660078e-18	***
SlopeC	-0.0493672	0.9332517		0.988165	
MeanF-MeanC	-0.5582257	0.07303803	.	0.3035849	
SlopeF-SlopeC	-1.212224	0.1763791		0.9999488	



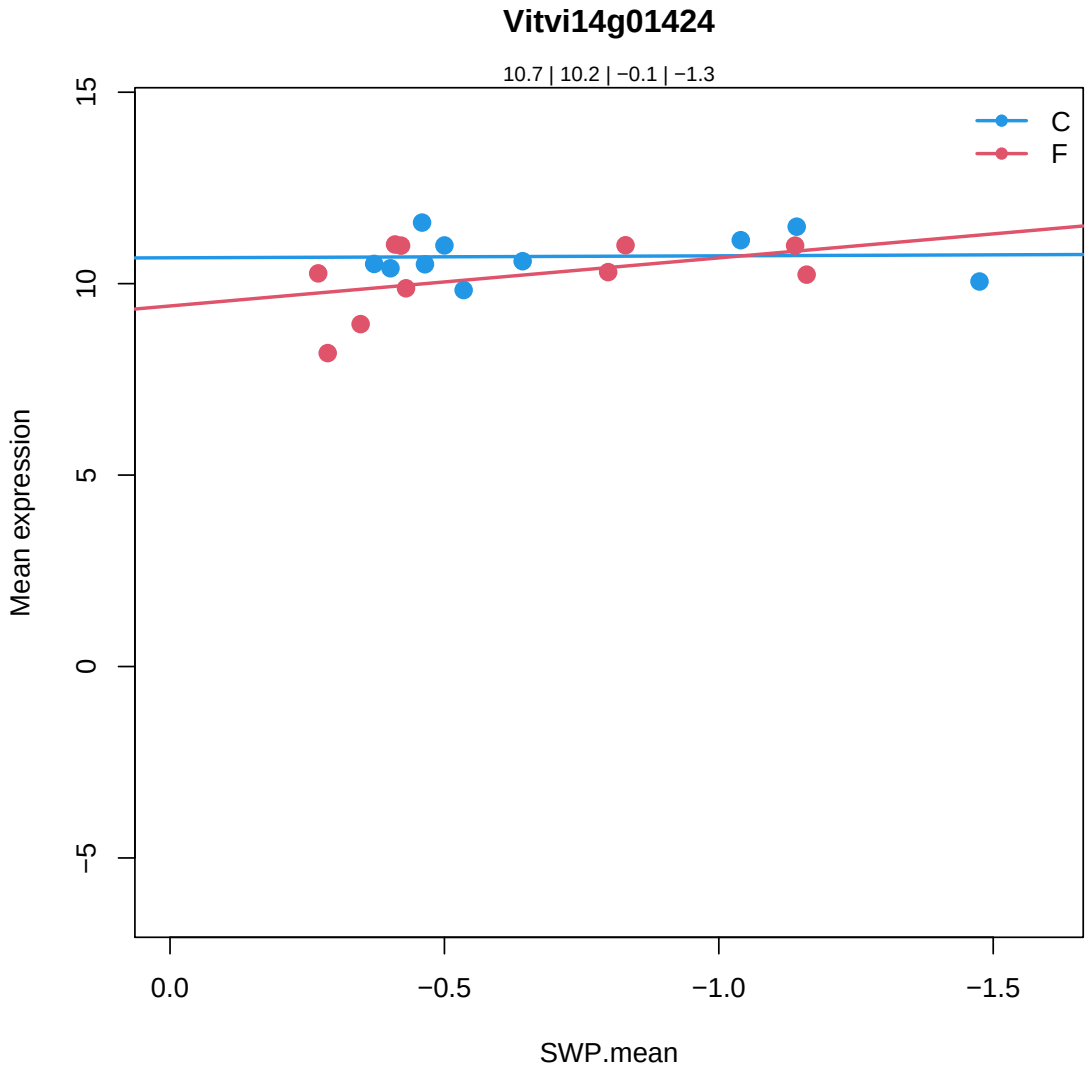
7.6.594 Vitvi14g01424: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01424
        1.3.4
        PS.calvin cycle.GAP
        glyceraldehyde 3-phosphate dehydrogenase A subunit 2 |
        Chr1:4392634-4394409 REVERSE LENGTH=441 |
        201606
```

Coefficients for Vitvi14g01424.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	10.71095	3.55729e-23	***	8.445517e-22	***
SlopeC	-0.05166203	0.9354229		0.9889957	
MeanF-MeanC	-0.5290021	0.1132239		0.3935947	
SlopeF-SlopeC	-1.203753	0.2130489		0.9999488	



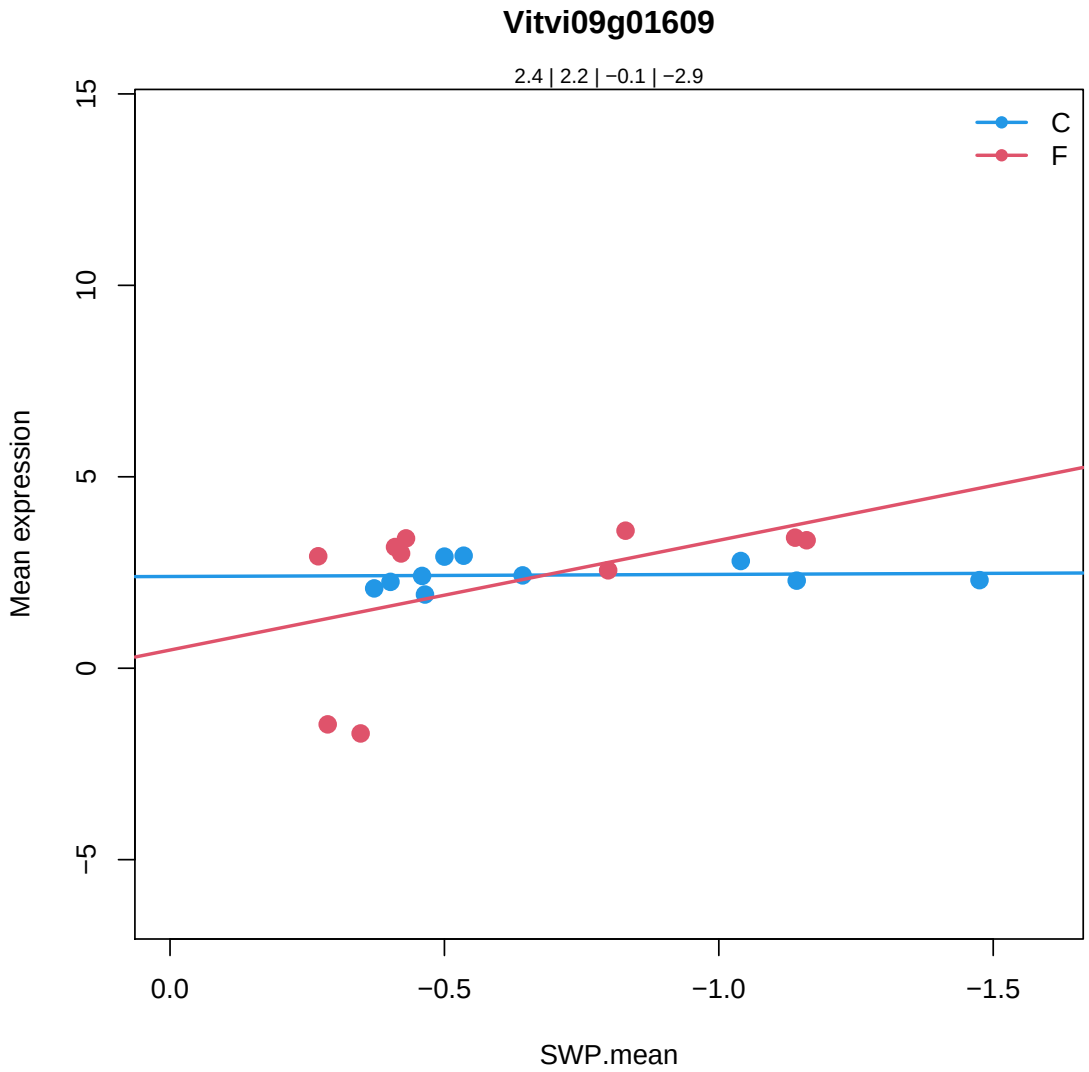
7.6.595 Vitvi09g01609: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g01609
        35.2
        not assigned.unknown
        Unknown Protein
```

Coefficients for Vitvi09g01609.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.434131	2.014194e-06	***	2.309338e-06	***
SlopeC	-0.05467525	0.9590377		0.9933601	
MeanF-MeanC	-0.2132905	0.6939848		0.903615	
SlopeF-SlopeC	-2.811312	0.08672848	.	0.9999488	



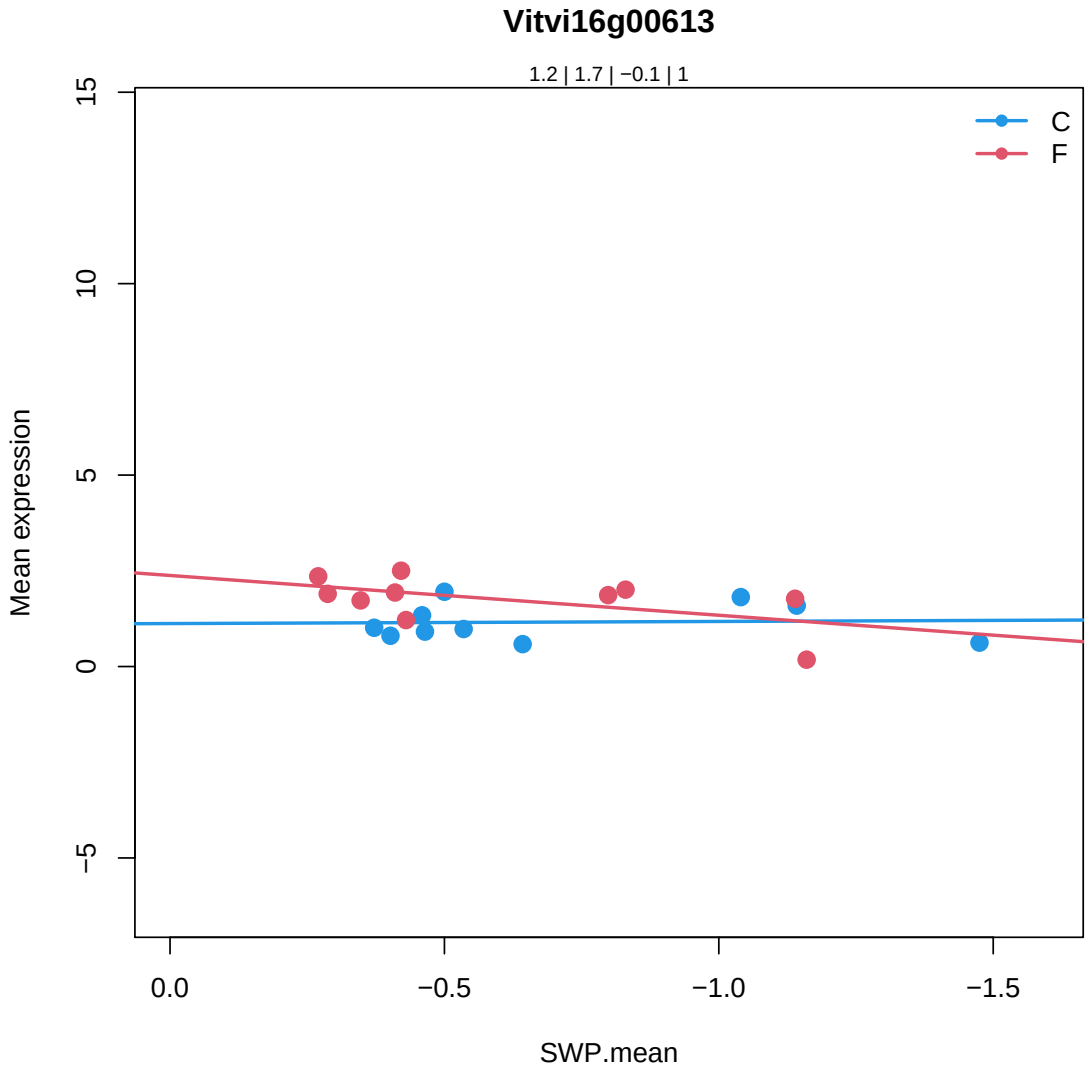
7.6.596 Vitvi16g00613: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g00613
        27.3.67
        RNA.regulation of transcription.putative transcription regulator
        transcription regulator |
        Chr1:373694-386682 FORWARD LENGTH=2378 |
        201606
```

Coefficients for Vitvi16g00613.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.160529	7.659453e-07	***	8.865841e-07	***
SlopeC	-0.05501755	0.9078581		0.9837899	
MeanF-MeanC	0.5842883	0.02309998	*	0.140219	
SlopeF-SlopeC	1.094212	0.1322304		0.9999488	



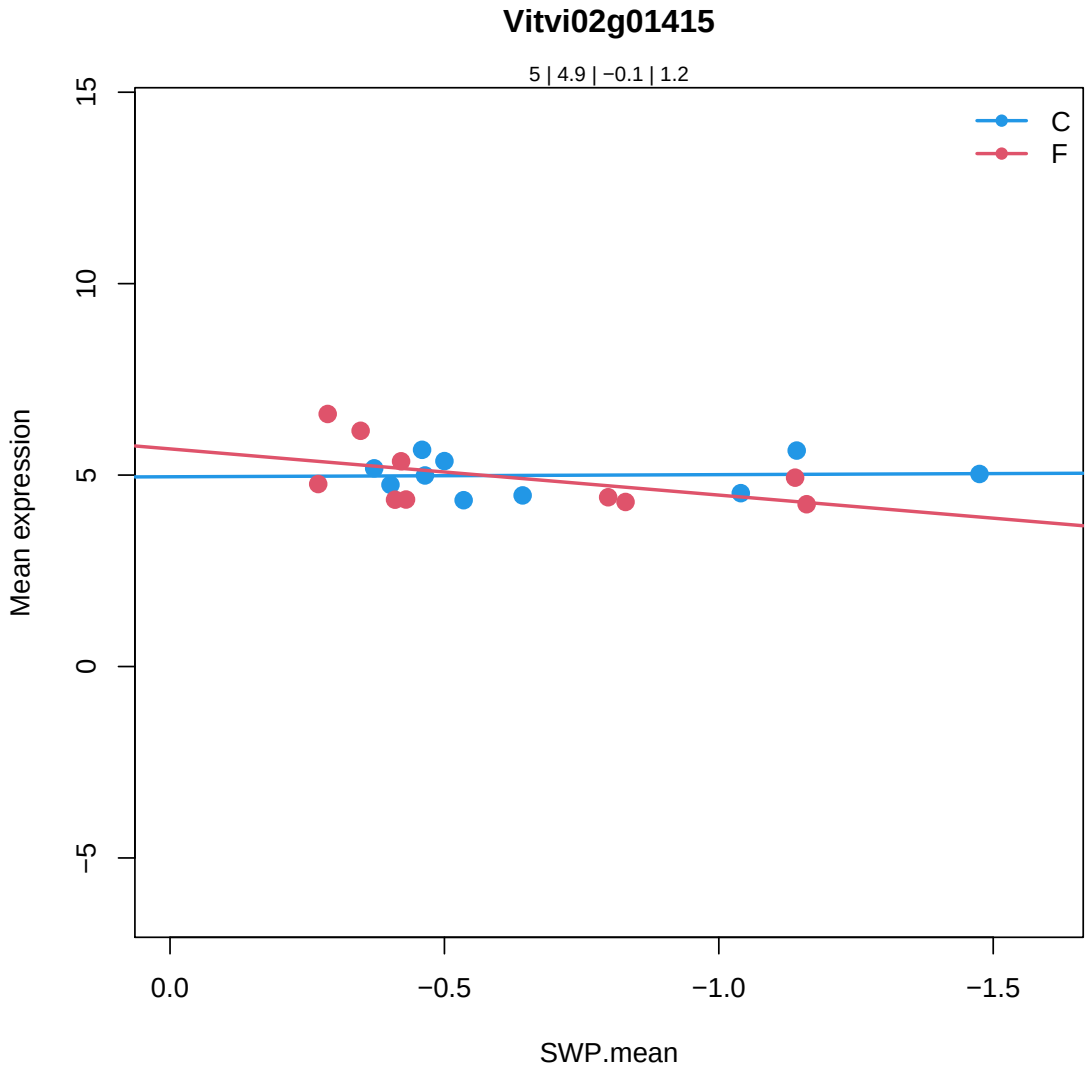
7.6.597 Vitvi02g01415: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g01415
        26.10
        misc.cytochrome P450
        cytochrome P450%2C family 76%2C subfamily C%2C polypeptide 4 |
        Chr2:18773541-18775654 REVERSE LENGTH=511 |
        201606
```

Coefficients for Vitvi02g01415.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.994569	1.255518e-17	***	3.238003e-17	***
SlopeC	-0.05549042	0.9189375		0.9851716	
MeanF-MeanC	-0.04593949	0.8683782		0.965202	
SlopeF-SlopeC	1.261775	0.1303025		0.9999488	



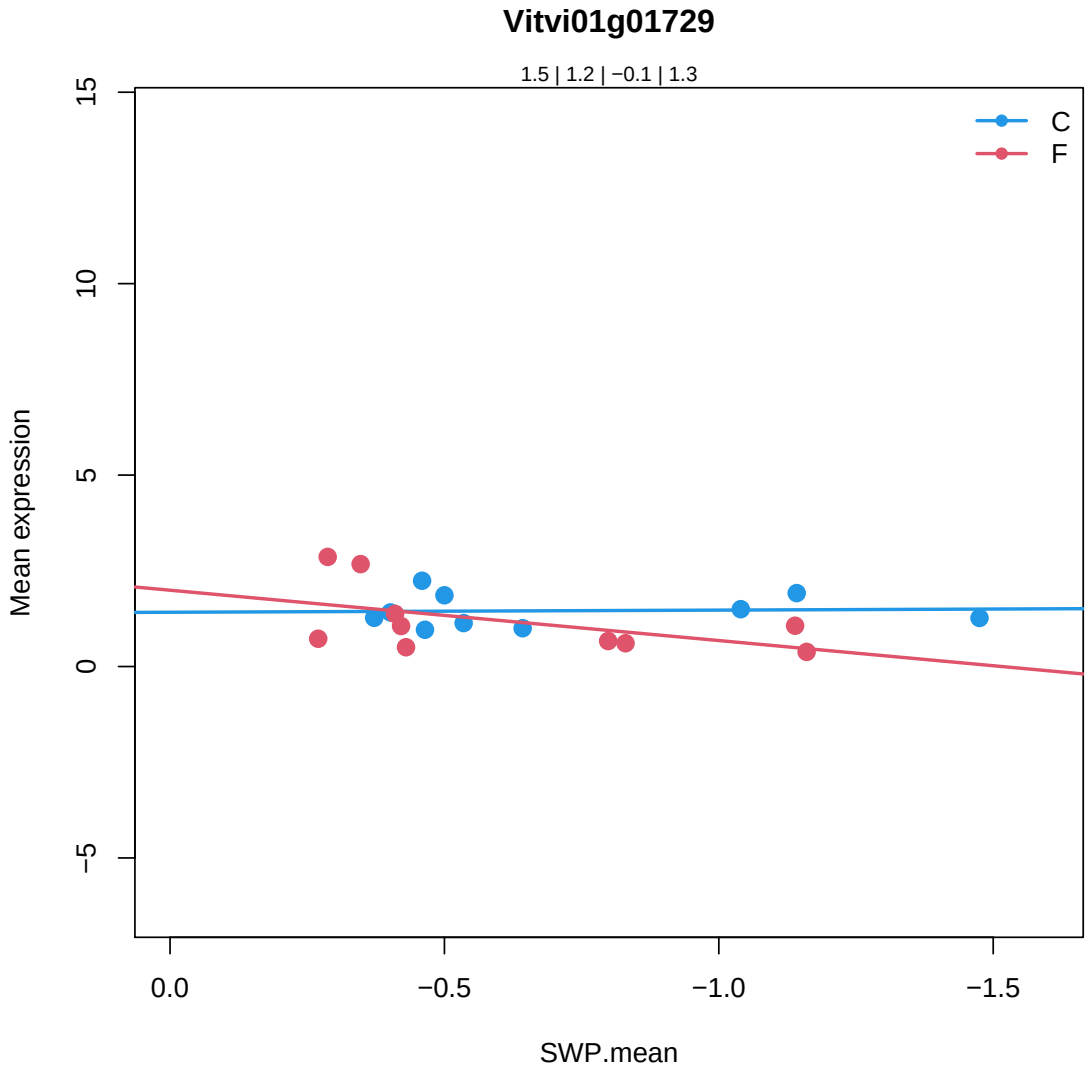
7.6.598 Vitvi01g01729: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01729
        27.3.7
        RNA.regulation of transcription.C2C2(Zn) Constans-like zinc finger fam
        B-box type zinc finger protein with CCT domain-containing protein |
        Chr1:9775768-9777657 REVERSE LENGTH=433 |
        201606
```

Coefficients for Vitvi01g01729.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.456284	2.051731e-07	***	2.412814e-07	***
SlopeC	-0.05589291	0.9186956		0.9851716	
MeanF-MeanC	-0.2643659	0.3472304		0.7068069	
SlopeF-SlopeC	1.370607	0.1032652		0.9999488	



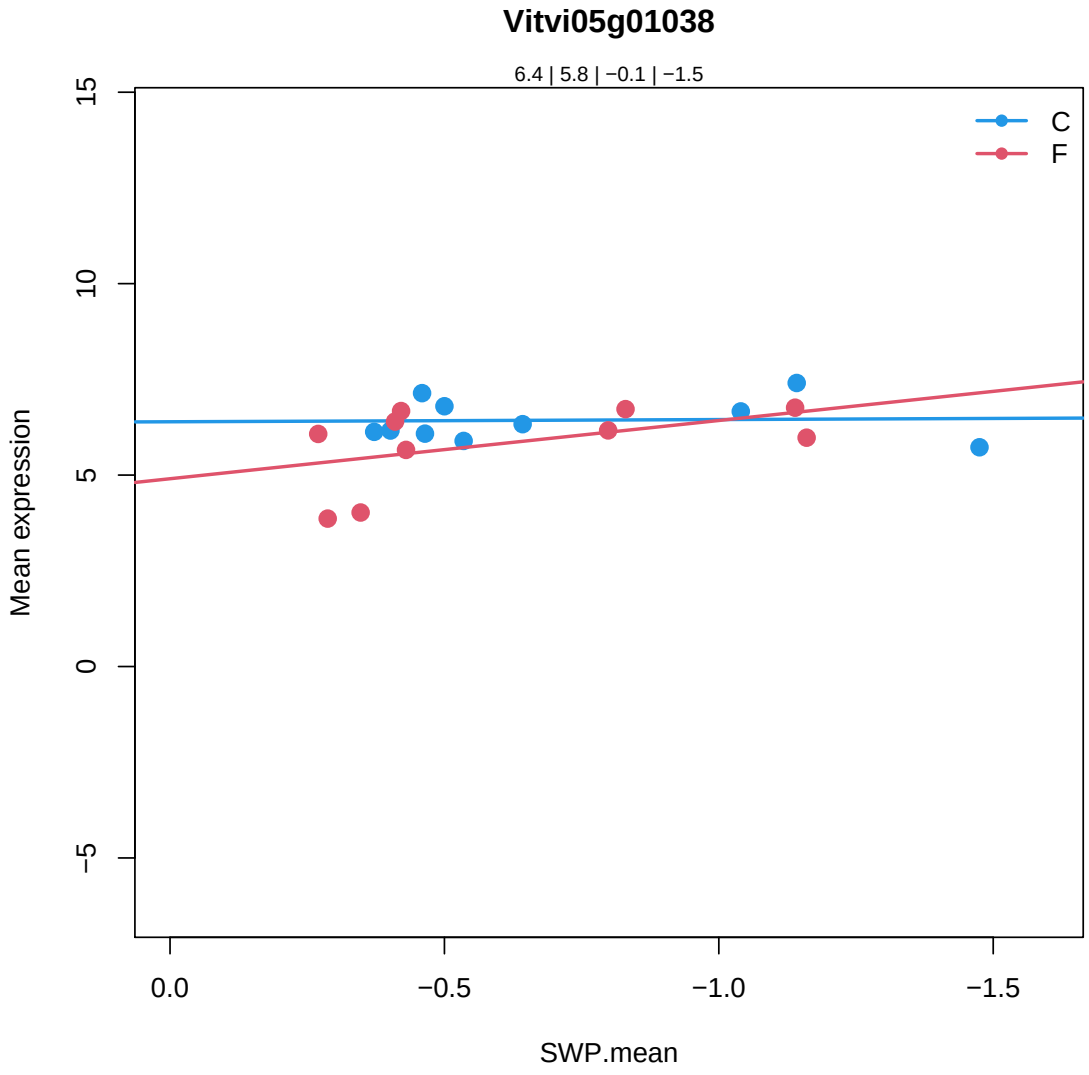
7.6.599 Vitvi05g01038: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01038
        29.4.1
        protein.postranslational modification.kinase
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi05g01038.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.432747	2.962564e-18	***	8.920467e-18	***
SlopeC	-0.057884	0.9296036		0.987284	
MeanF-MeanC	-0.6013758	0.08166096	.	0.3238814	
SlopeF-SlopeC	-1.463245	0.143576		0.9999488	



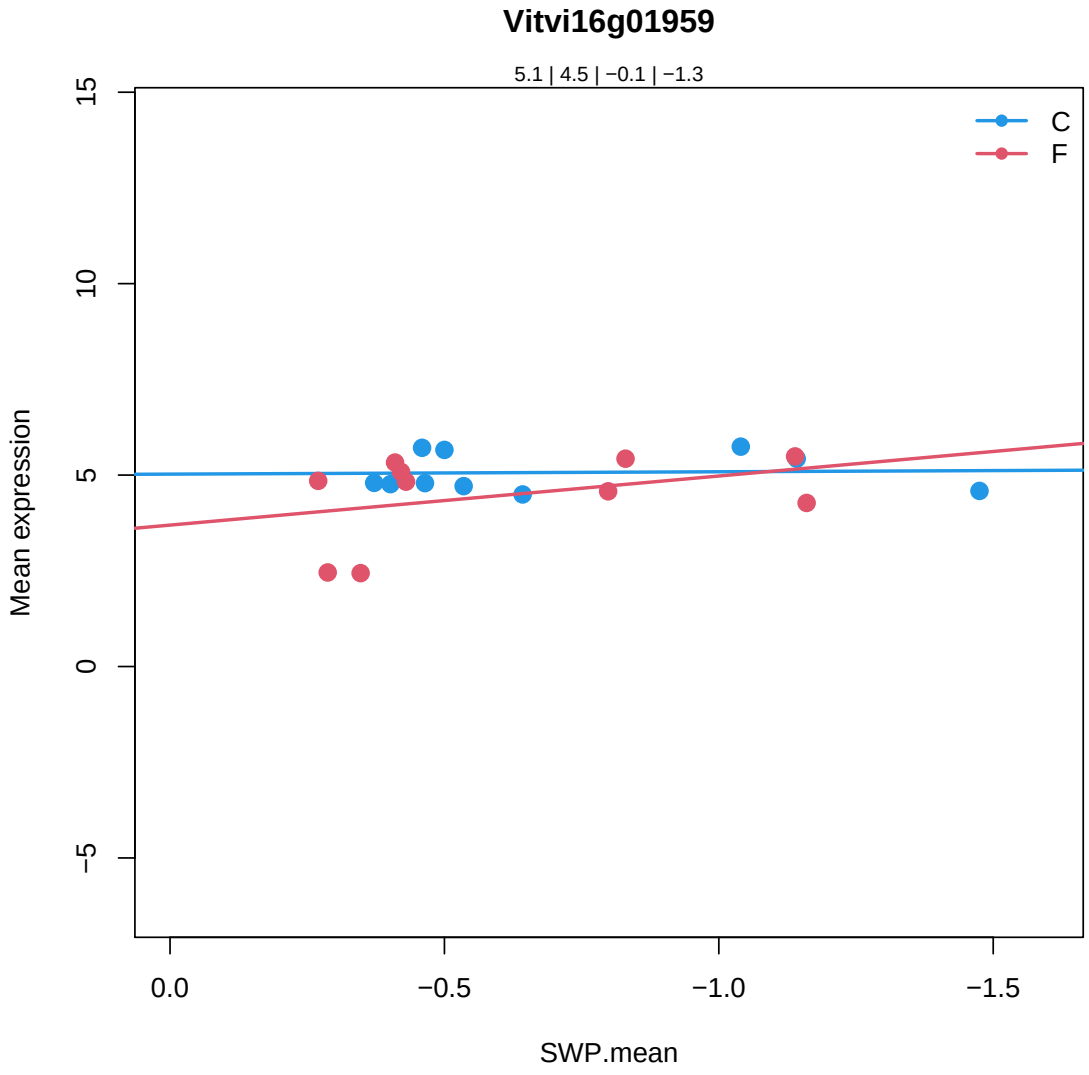
7.6.600 Vitvi16g01959: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01959
        35.2
        not assigned.unknown
        membrane-associated kinase regulator |
        Chr5:21452893-21453692 REVERSE LENGTH=235 |
        201606
```

Coefficients for Vitvi16g01959.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.068011	1.793953e-15	***	3.261382e-15	***
SlopeC	-0.06128556	0.9306001		0.9873456	
MeanF-MeanC	-0.5934963	0.1077126		0.382337	
SlopeF-SlopeC	-1.220571	0.2512656		0.9999488	



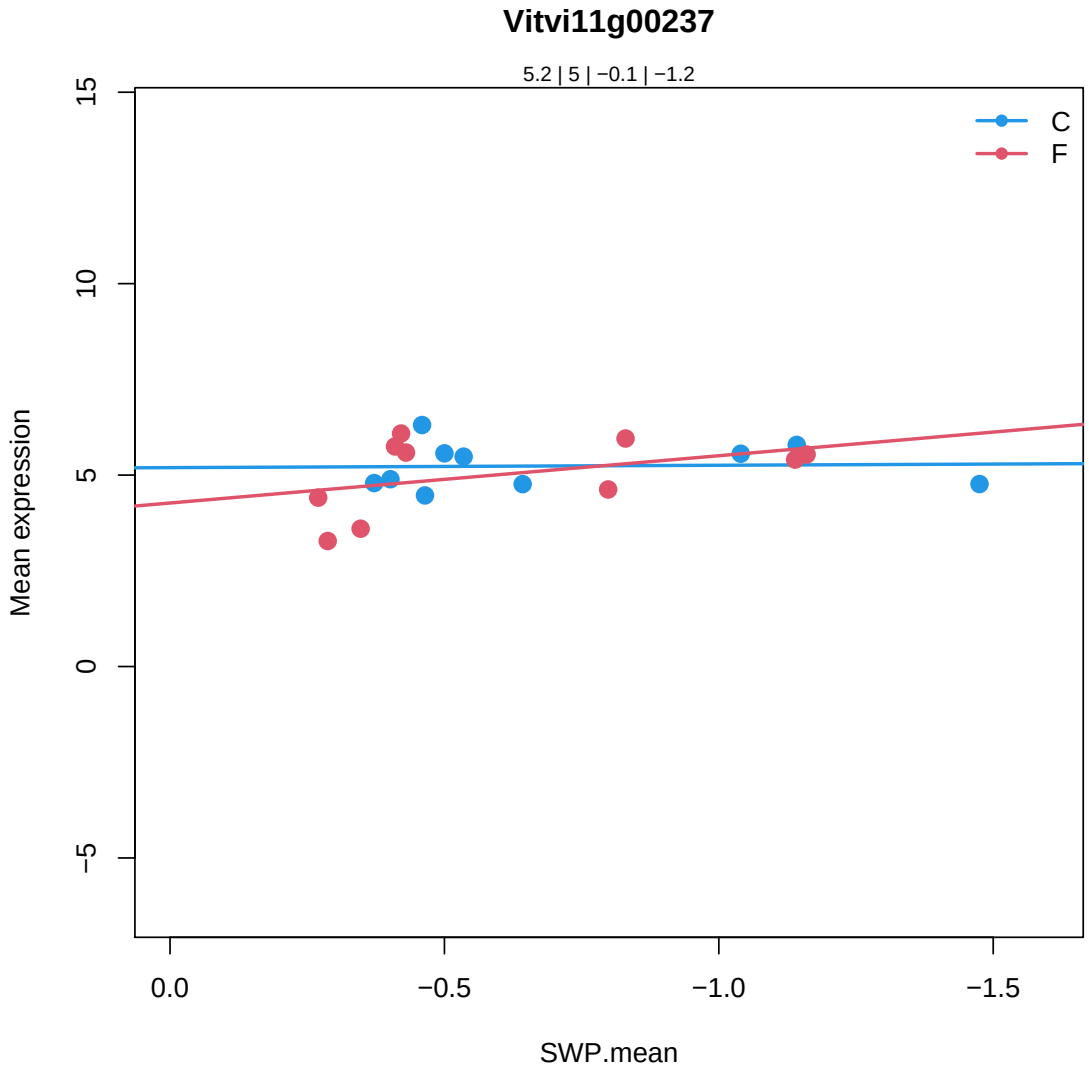
7.6.601 Vitvi11g00237: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00237
        4.3.4
        glycolysis.unclear/dually targeted.phosphofructokinase (PFK)
        phosphofructokinase 1 |
        Chr4:14403621-14406071 REVERSE LENGTH=473 |
        201606
```

Coefficients for Vitvi11g00237.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.238036	2.106144e-16	***	4.338088e-16	***
SlopeC	-0.06197922	0.9246385		0.9862379	
MeanF-MeanC	-0.215169	0.5202712		0.8185611	
SlopeF-SlopeC	-1.17271	0.2369278		0.9999488	



7.6.602 Vitvi18g00743: type5

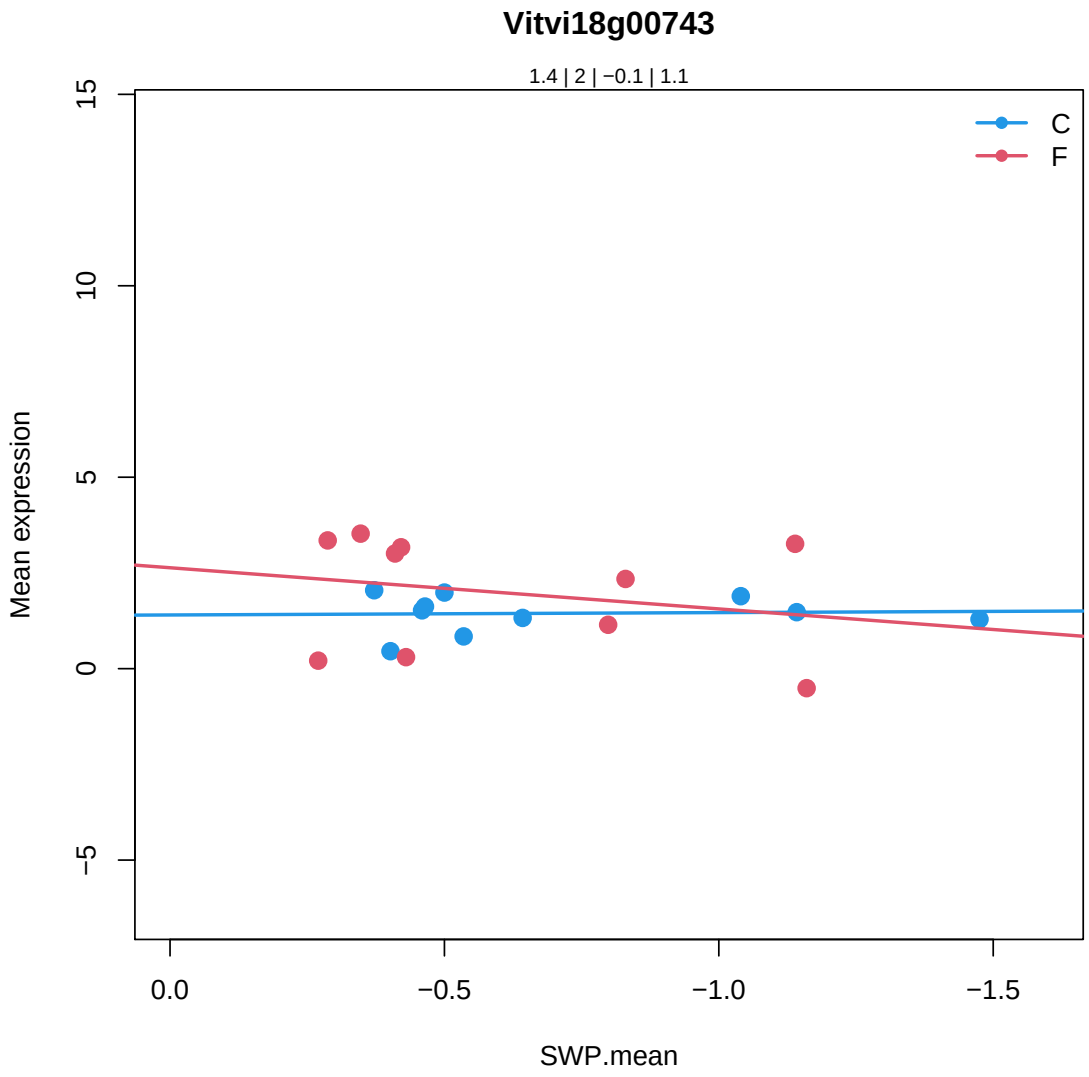
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00743
        10.5.3
        cell wall.cell wall proteins.LRR
        Leucine-rich repeat (LRR) family protein |
        Chr3:6696395-6698073 REVERSE LENGTH=493 |
        201606

Vitvi18g00743
        20.1.2
        stress.biotic.receptors
        Leucine-rich repeat (LRR) family protein |
        Chr3:6696395-6698073 REVERSE LENGTH=493 |
        201606
```

Coefficients for Vitvi18g00743.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.445913	0.0002711241	***	0.0002968731	***
SlopeC	-0.0621841	0.9470333		0.9907125	
MeanF-MeanC	0.5340397	0.2686602		0.6310555	
SlopeF-SlopeC	1.137471	0.417863		0.9999488	


Vitvi18g00743
1.4 | 2 | −0.1 | 1.1
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

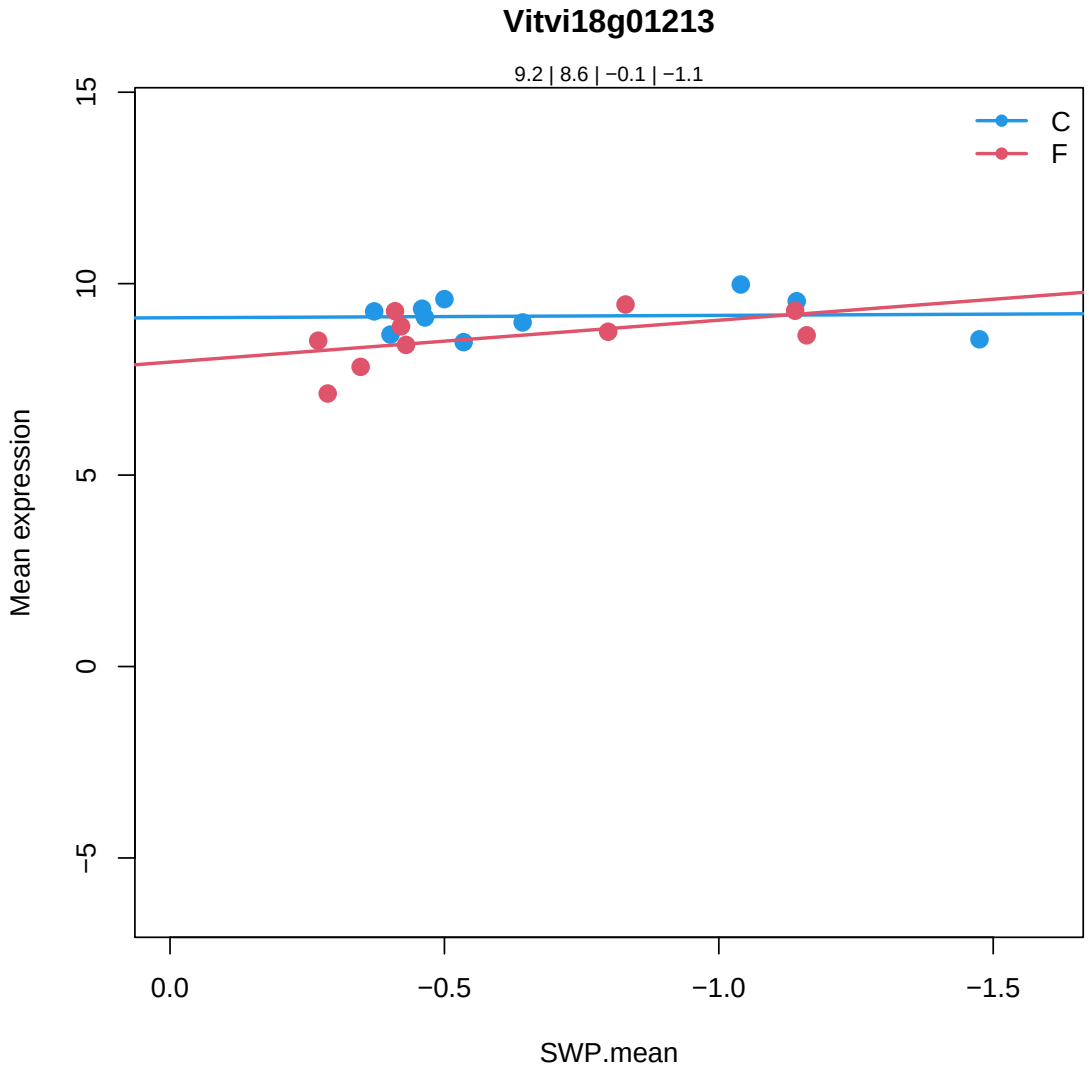
7.6.603 Vitvi18g01213: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g01213
        21.1
        redox.thioredoxin
        thioredoxin M-type 4 |
        Chr3:5188448-5189457 FORWARD LENGTH=193 |
        201606
```

Coefficients for Vitvi18g01213.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	9.152344	5.895213e-24	***	2.323477e-22	***
SlopeC	-0.06290591	0.9000246		0.9825248	
MeanF-MeanC	-0.5351746	0.04512017	*	0.2240136	
SlopeF-SlopeC	-1.031415	0.1756837		0.9999488	



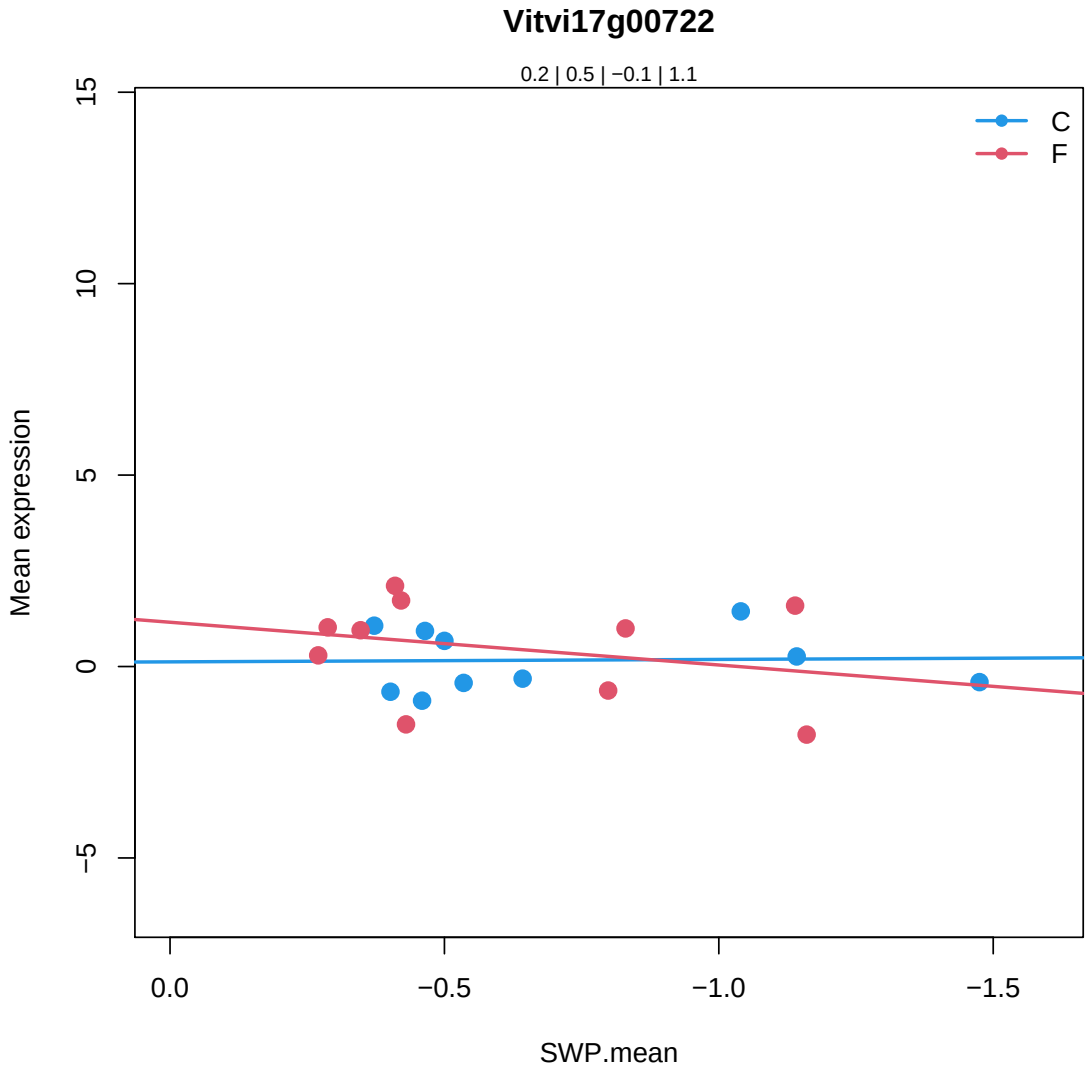
7.6.604 Vitvi17g00722: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00722
        35.2
        not assigned.unknown
        ARM repeat superfamily protein |
        Chr1:9455669-9457917 REVERSE LENGTH=625 |
        201606
```

Coefficients for Vitvi17g00722.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1663645	0.6128781		0.6182322	
SlopeC	−0.0637138	0.9443066		0.9903035	
MeanF−MeanC	0.3099614	0.5059821		0.8095076	
SlopeF−SlopeC	1.180085	0.3888426		0.9999488	



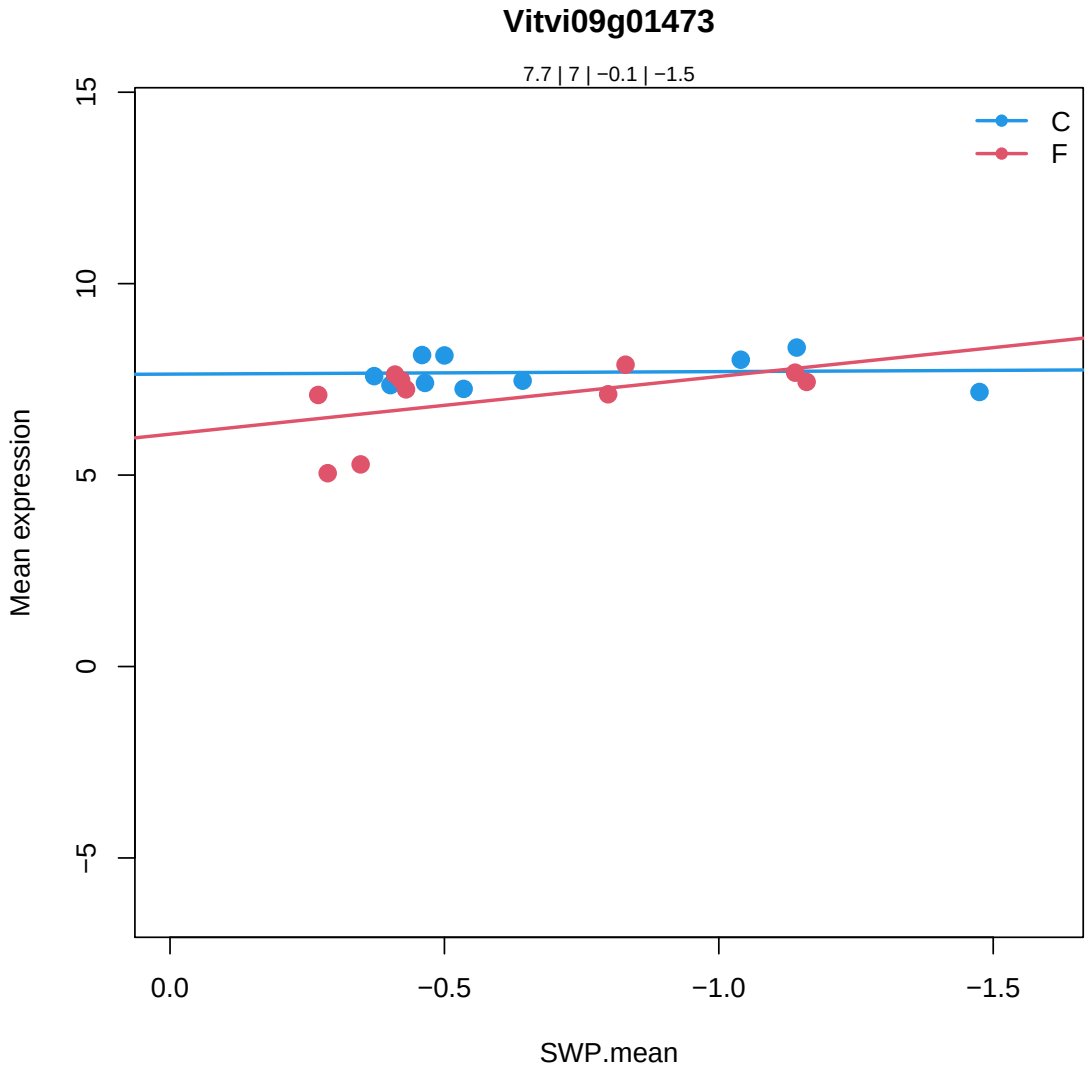
7.6.605 Vitvi09g01473: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g01473
        35.2
        not assigned.unknown
        high chlorophyll fluorescence phenotype 173 |
        Chr1:5723161-5726248 FORWARD LENGTH=631 |
        201606
```

Coefficients for Vitvi09g01473.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.682879	7.639427e-21	***	5.716257e-20	***
SlopeC	-0.06514188	0.9119803		0.9838904	
MeanF-MeanC	-0.6963722	0.02827491	*	0.1625674	
SlopeF-SlopeC	-1.441812	0.1107905		0.9999488	



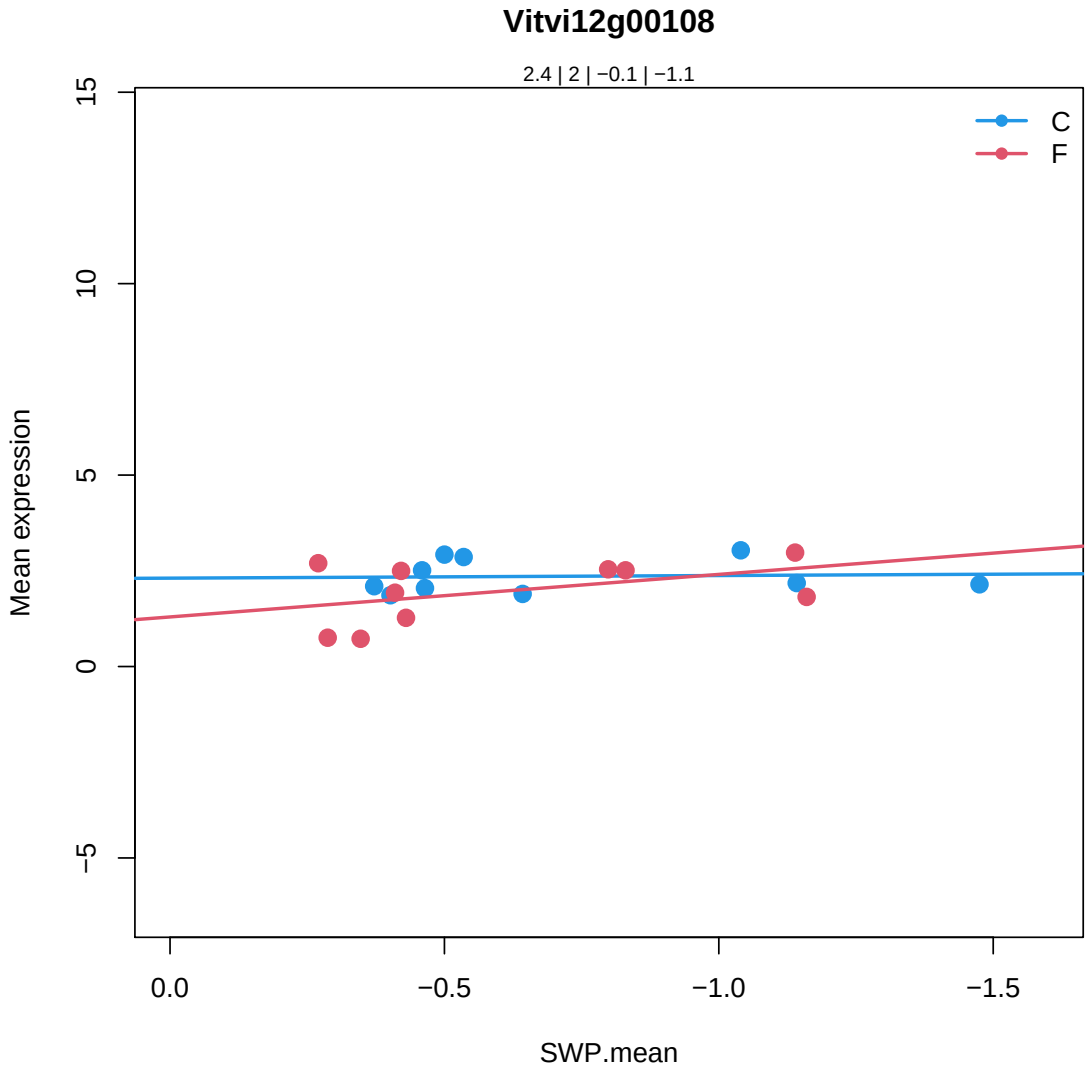
7.6.606 Vitvi12g00108: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00108
        35.2
        not assigned.unknown
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi12g00108.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.355764	2.938049e-11	***	3.931327e-11	***
SlopeC	-0.06842547	0.8980981		0.9819807	
MeanF-MeanC	-0.3841294	0.1667903		0.4954895	
SlopeF-SlopeC	-1.042973	0.1984209		0.9999488	



7.6.607 Vitvi04g00112: type5

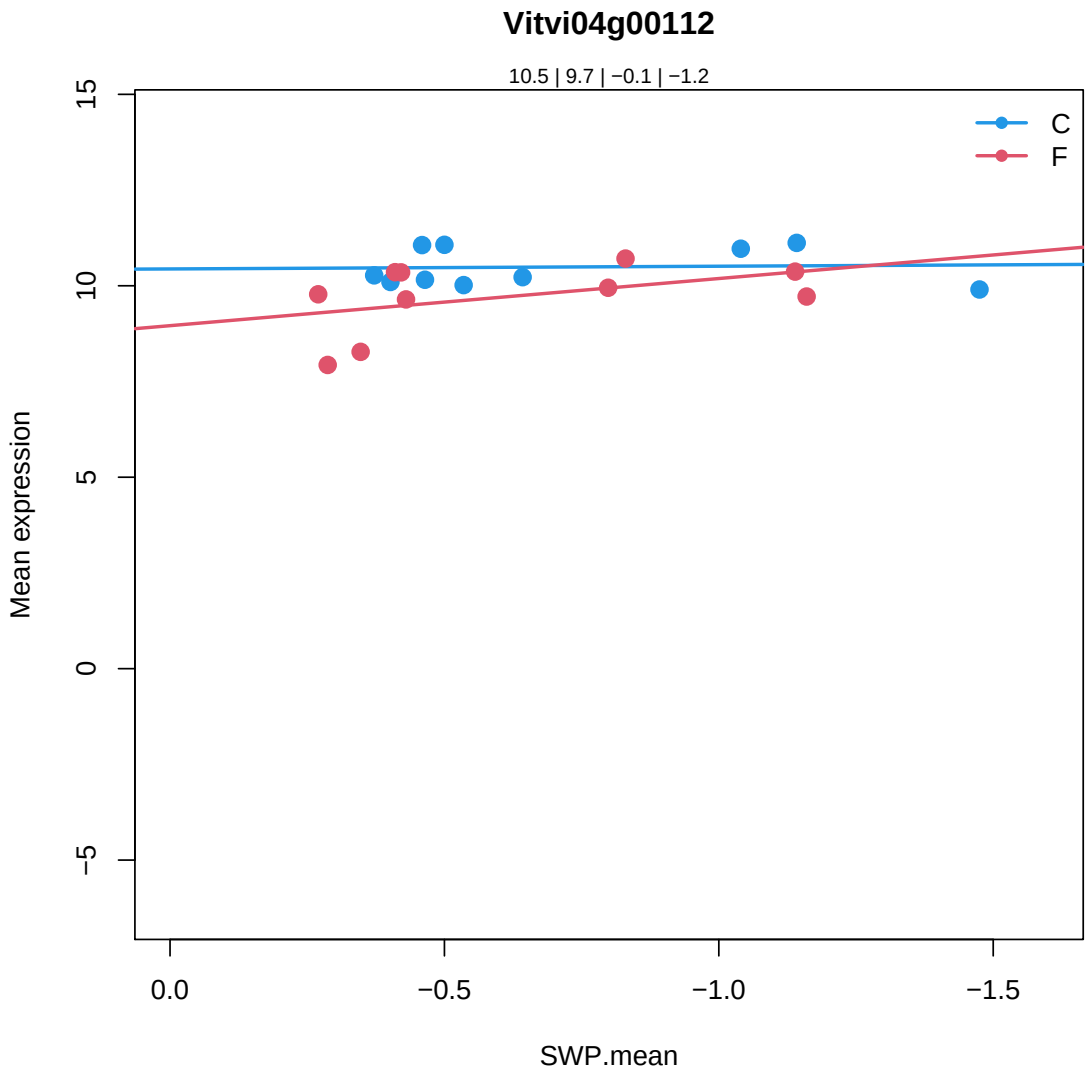
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00112
        35.2
        not assigned.unknown
        glycine decarboxylase P-protein 1 |
        Chr4:15927133-15931150 REVERSE LENGTH=976 |
        201606

Vitvi04g00112
        1.2.4.1
        PS.photorespiration.glycine cleavage.P subunit
        glycine decarboxylase P-protein 1 |
        Chr4:15927133-15931150 REVERSE LENGTH=976 |
        201606
```

Coefficients for Vitvi04g00112.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	10.48939	1.138871e-23	***	3.815092e-22	***
SlopeC	-0.07061662	0.9050342		0.983424	
MeanF-MeanC	-0.7814351	0.01555352	*	0.1044347	
SlopeF-SlopeC	-1.160762	0.1964383		0.9999488	


Vitvi04g00112
10.5 | 9.7 | −0.1 | −1.2
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

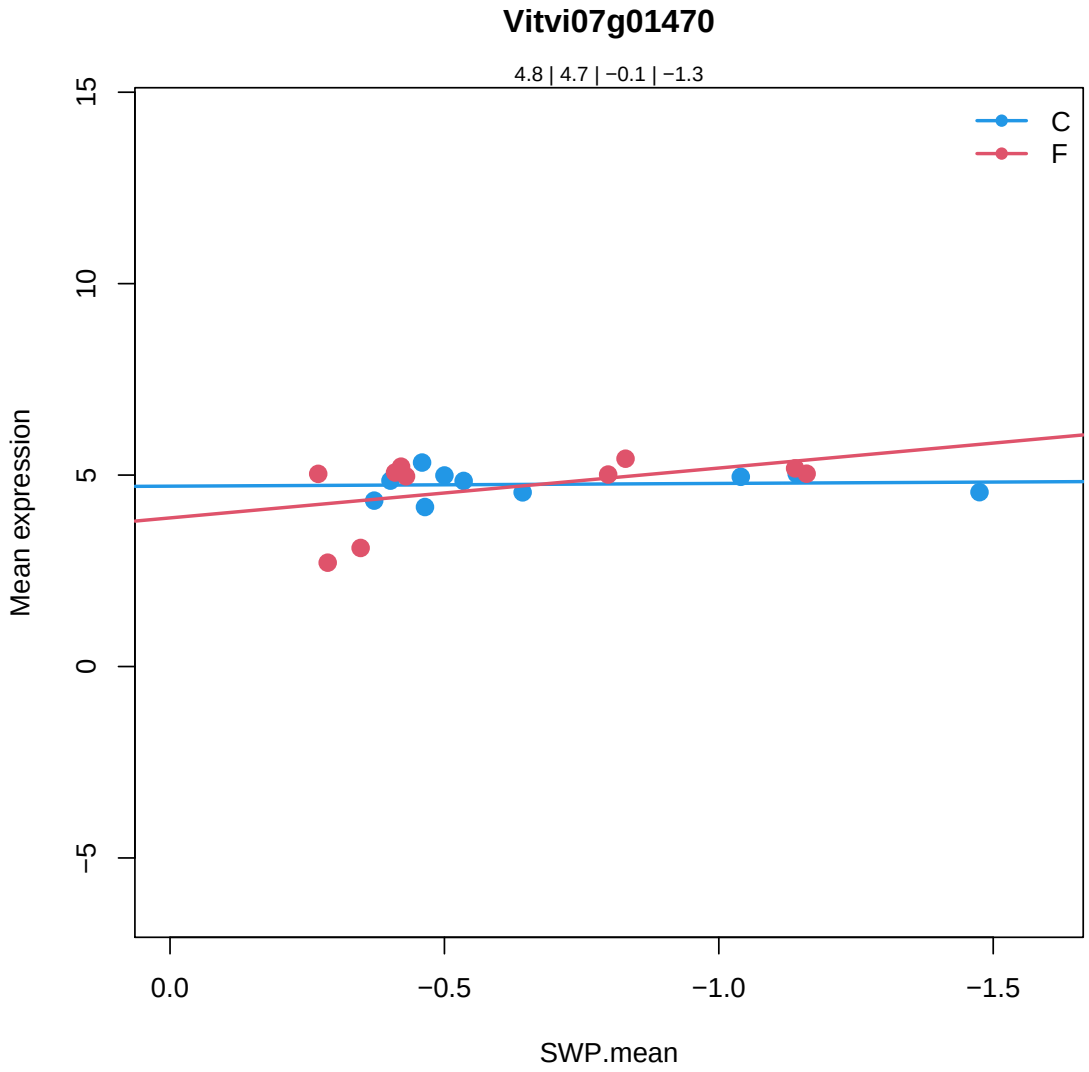
7.6.608 Vitvi07g01470: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01470
        35.2
        not assigned.unknown
        MATE efflux family protein |
        Chr5:26123241-26126352 REVERSE LENGTH=486 |
        201606
```

Coefficients for Vitvi07g01470.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.760475	7.607079e-17	***	1.686187e-16	***
SlopeC	-0.07129487	0.8999151		0.9825248	
MeanF-MeanC	-0.08561069	0.7665839		0.9321541	
SlopeF-SlopeC	-1.231236	0.154298		0.9999488	



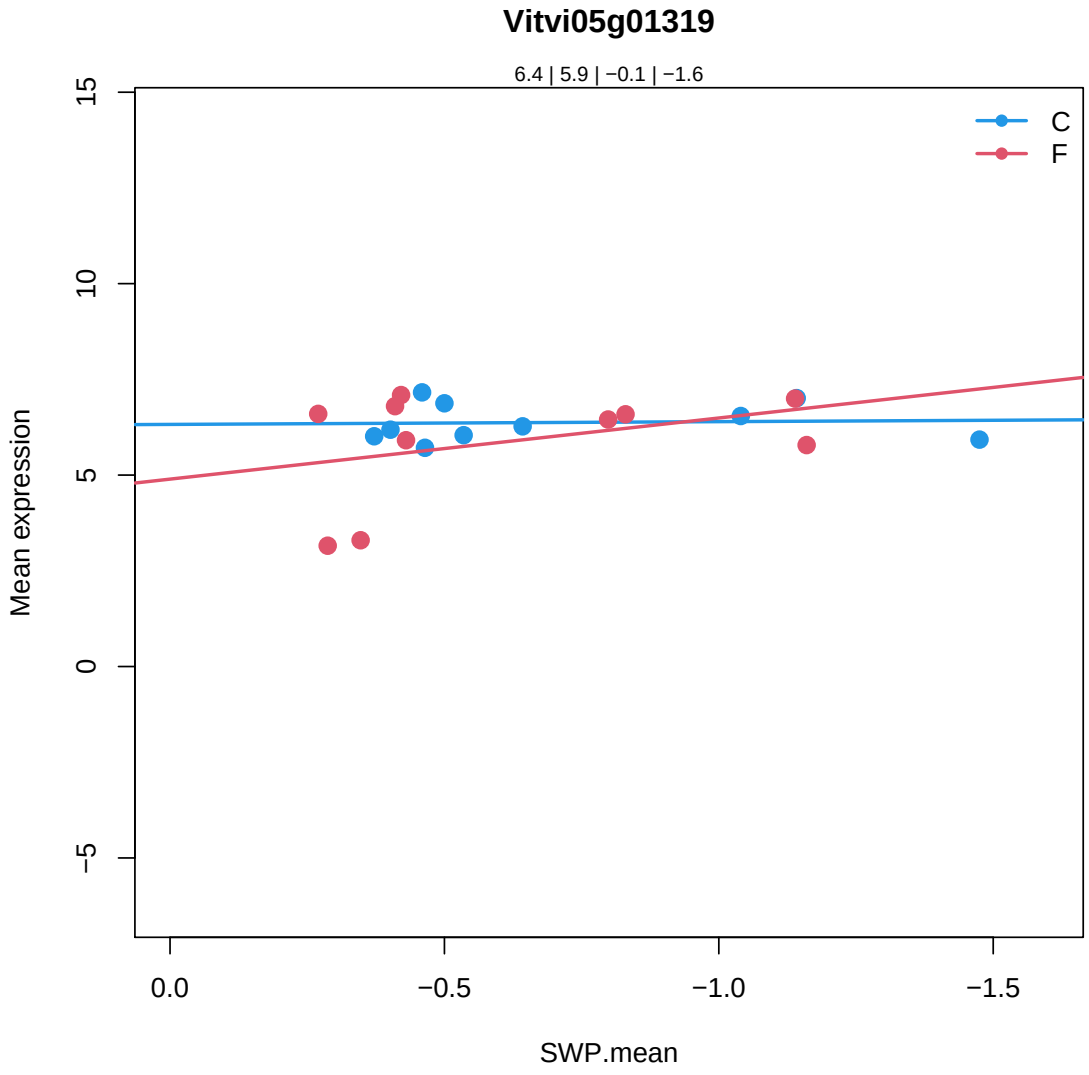
7.6.609 Vitvi05g01319: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01319
        17.2.3
        hormone metabolism.auxin.induced-regulated-responsive-activated
        Auxin-responsive family protein |
        Chr4:7589670-7591074 REVERSE LENGTH=394 |
        201606
```

Coefficients for Vitvi05g01319.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.374021	9.04446e-16	***	1.702342e-15	***
SlopeC	-0.07173805	0.9332029		0.988165	
MeanF-MeanC	-0.5069057	0.2513683		0.61038	
SlopeF-SlopeC	-1.524558	0.2391141		0.9999488	



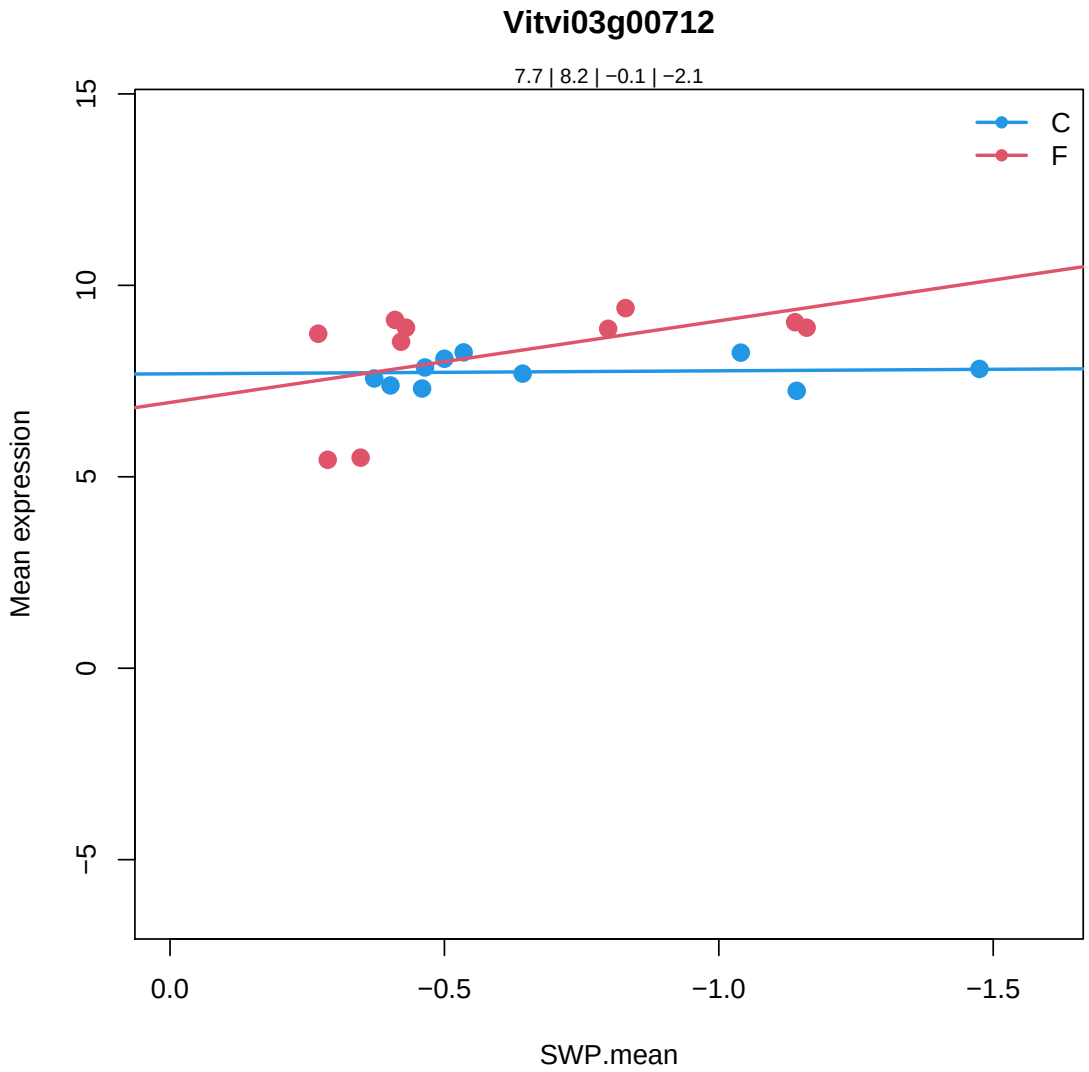
7.6.610 Vitvi03g00712: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00712
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi03g00712.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.744266	4.044006e-18	***	1.173624e-17	***
SlopeC	-0.07900518	0.9213969		0.985539	
MeanF-MeanC	0.4957387	0.2311173		0.584776	
SlopeF-SlopeC	-2.052156	0.09575741	.	0.9999488	



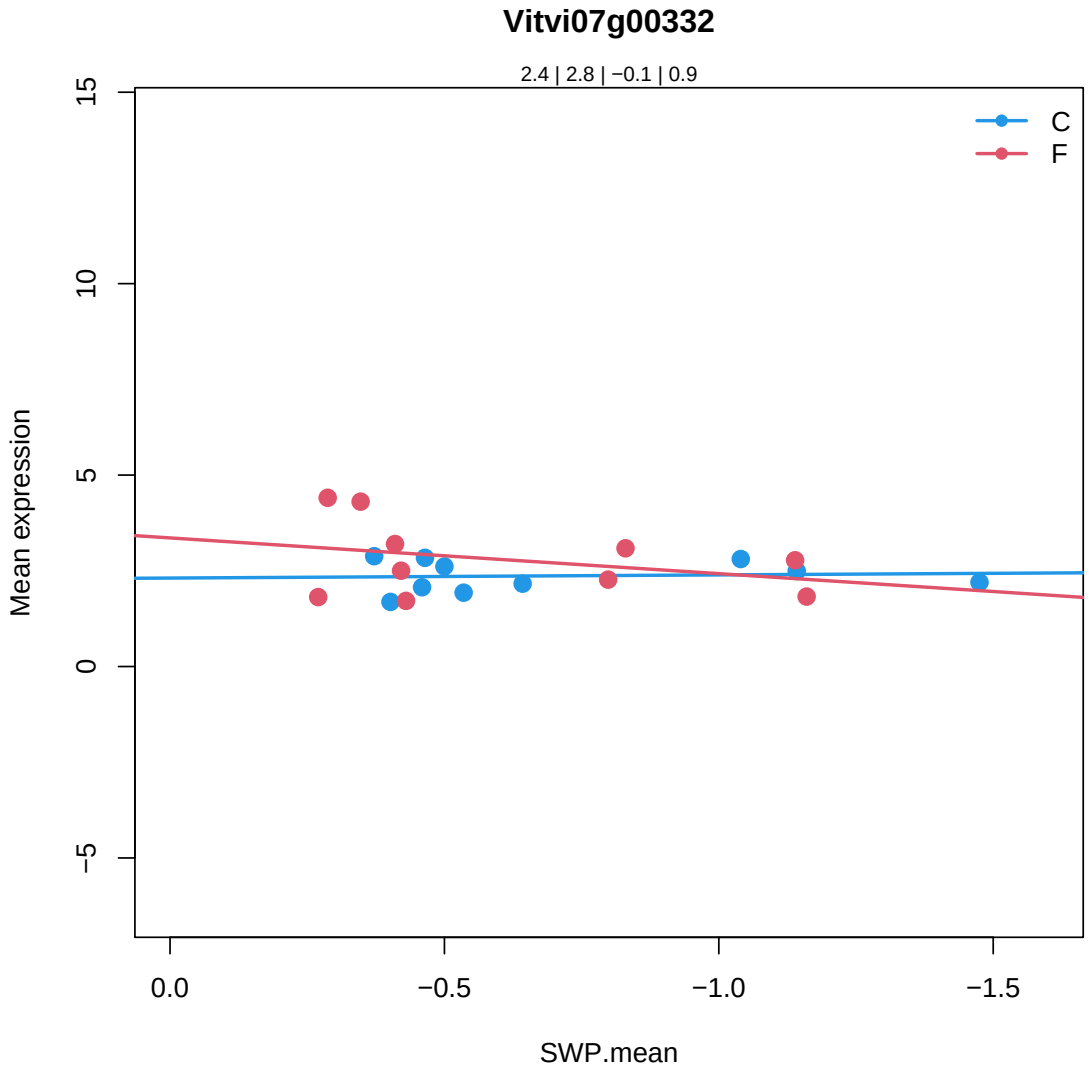
7.6.611 Vitvi07g00332: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g00332
        35.2
        not assigned.unknown
        magnesium/proton exchanger |
        Chr2:19524518-19526828 REVERSE LENGTH=539 |
        201606
```

Coefficients for Vitvi07g00332.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.36824	4.64226e-10	***	5.924089e-10	***
SlopeC	-0.08202566	0.8952782		0.9810792	
MeanF-MeanC	0.4218925	0.1918009		0.5315116	
SlopeF-SlopeC	1.015418	0.2801965		0.9999488	



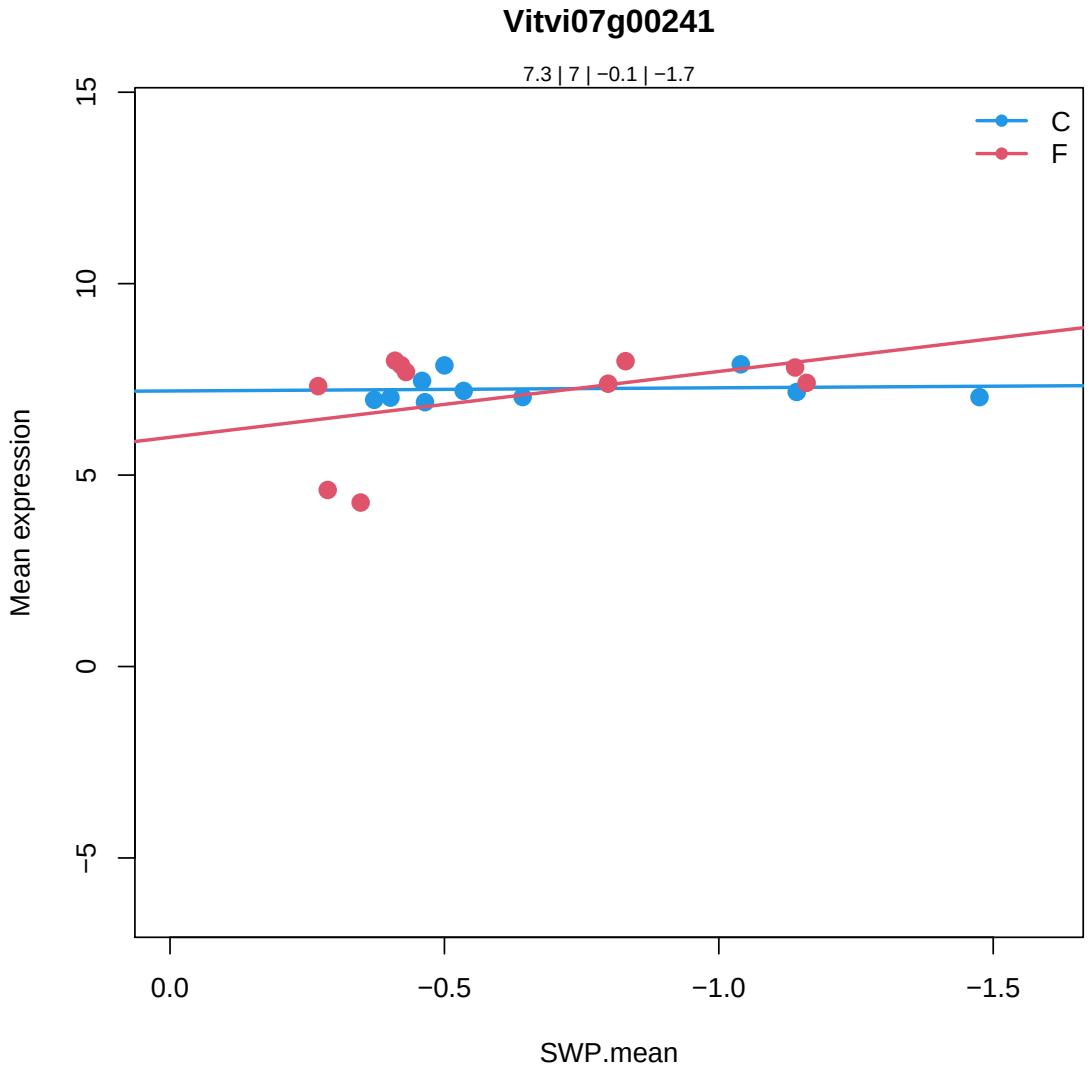
7.6.612 Vitvi07g00241: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g00241
        26.7
        misc.oxidases - copper, flavone etc
        Flavin-containing monooxygenase family protein |
        Chr1:18091681-18093774 FORWARD LENGTH=383 |
        201606
```

Coefficients for Vitvi07g00241.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.255119	1.032843e-17	***	2.71424e-17	***
SlopeC	-0.08287329	0.9158831		0.9842726	
MeanF-MeanC	-0.2205328	0.5816263		0.8525001	
SlopeF-SlopeC	-1.637385	0.1703559		0.9999488	



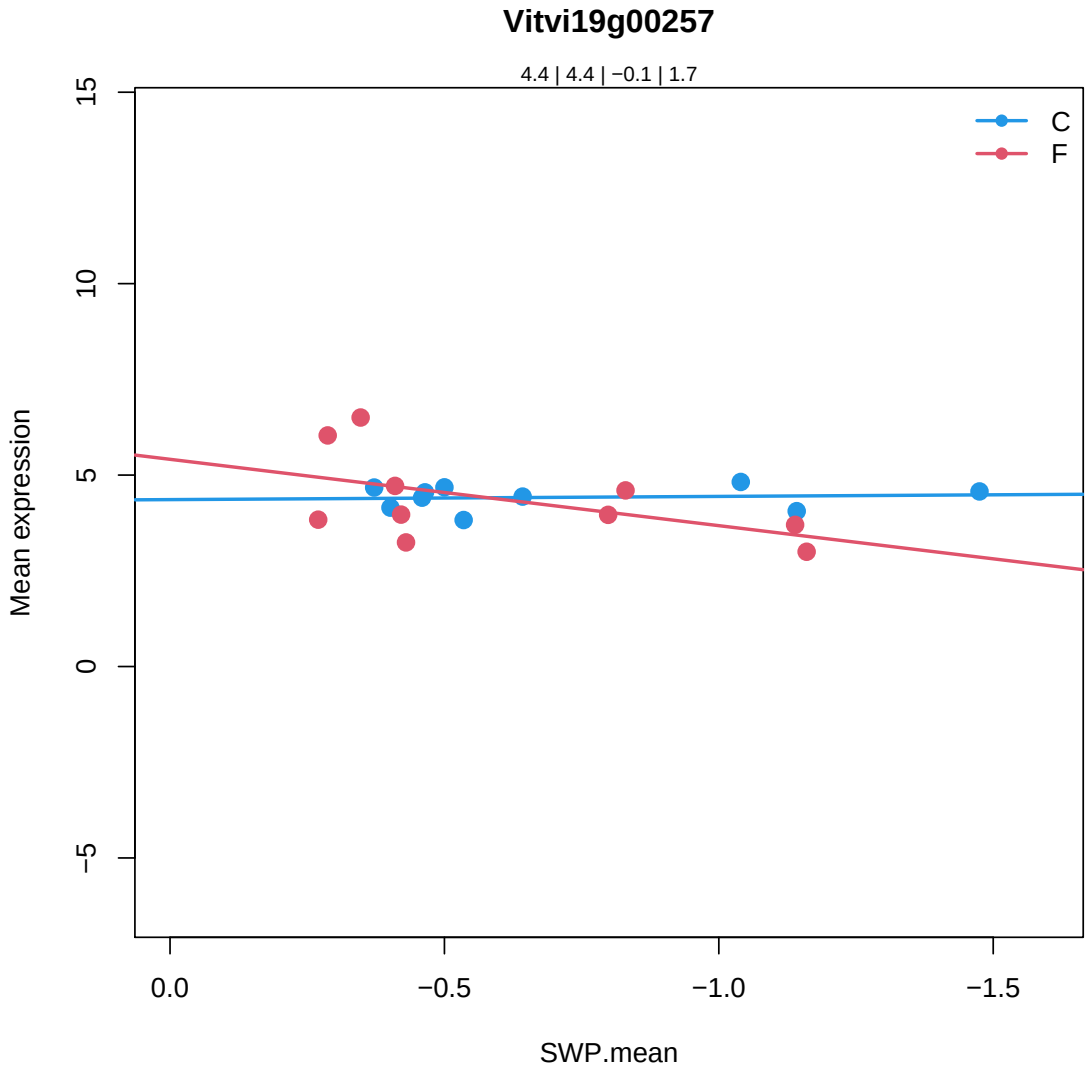
7.6.613 Vitvi19g00257: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g00257
        19.14
        tetrapyrrole synthesis.protochlorophyllide reductase
        protochlorophyllide oxidoreductase B |
        Chr4:13725648-13727107 FORWARD LENGTH=401 |
        201606
```

Coefficients for Vitvi19g00257.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.417754	3.021412e-15	***	5.359289e-15	***
SlopeC	-0.08373763	0.8941537		0.9808342	
MeanF-MeanC	-0.06188627	0.8466479		0.959326	
SlopeF-SlopeC	1.816305	0.06285784	.	0.9999488	



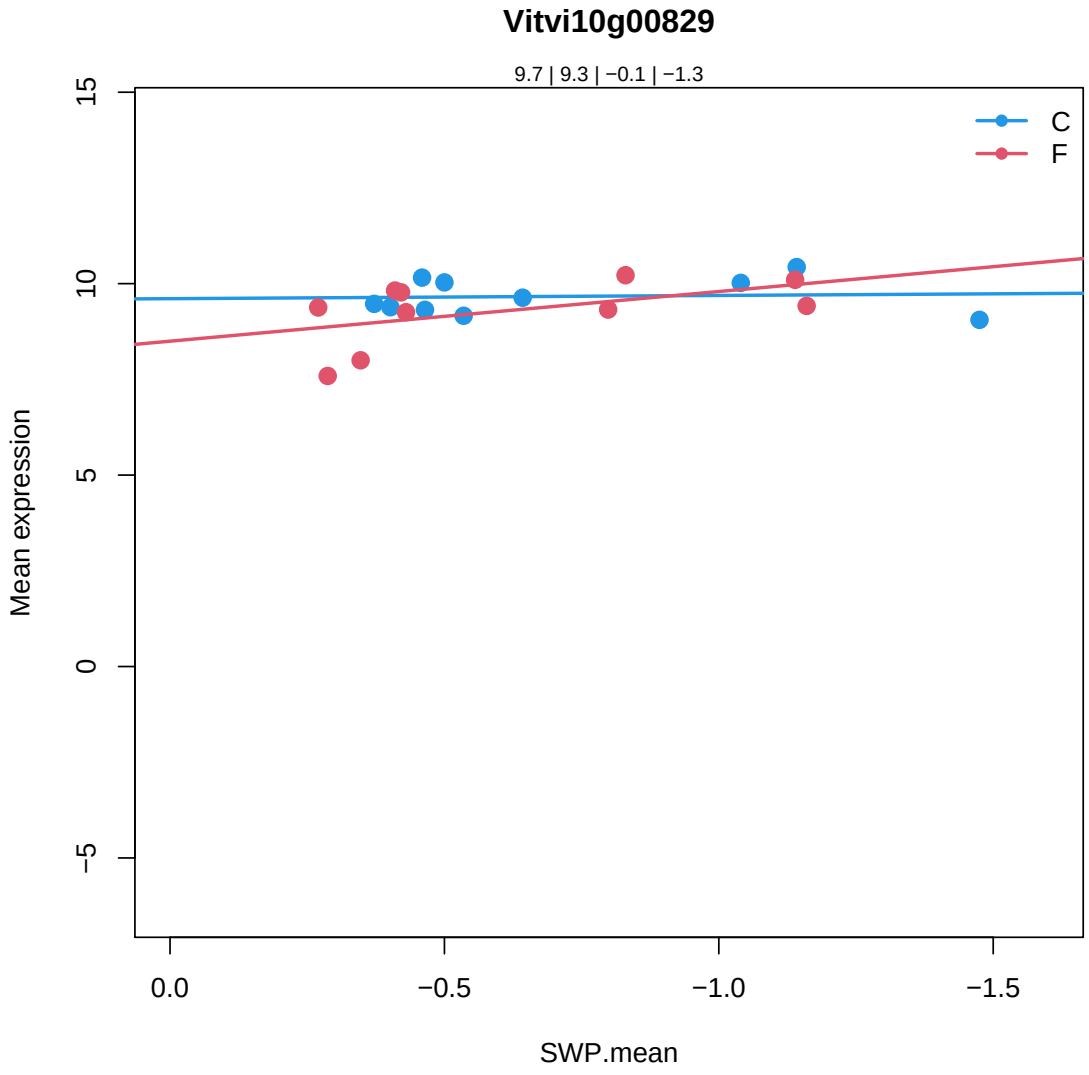
7.6.614 Vitvi10g00829: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00829
        1.2.2
        PS.photorespiration.glycolate oxydase
        Aldolase-type TIM barrel family protein |
        Chr3:4818667-4820748 FORWARD LENGTH=373 |
        201606
```

Coefficients for Vitvi10g00829.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	9.666329	1.206625e-23	***	3.921319e-22	***
SlopeC	-0.0845114	0.8772169		0.9764303	
MeanF-MeanC	-0.3789952	0.1819898		0.5174946	
SlopeF-SlopeC	-1.212587	0.1463314		0.9999488	



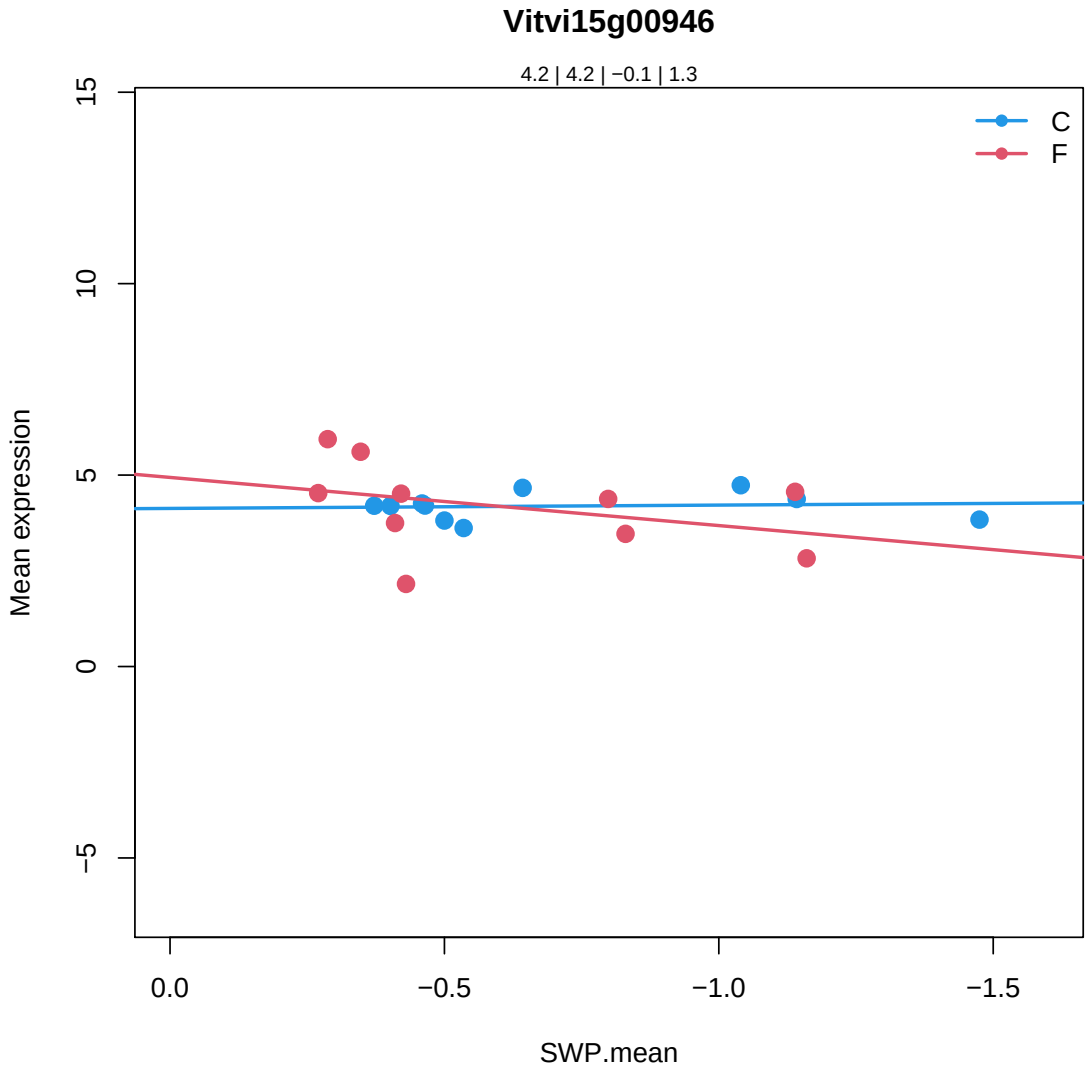
7.6.615 Vitvi15g00946: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g00946
        27.3.4
        RNA.regulation of transcription.auxin response transcription factor fa
        auxin response factor 18 |
        Chr3:22888595-22891179 FORWARD LENGTH=551 |
        201606
```

Coefficients for Vitvi15g00946.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.189849	5.978856e-14	***	9.338018e-14	***
SlopeC	-0.08696398	0.8999774		0.9825248	
MeanF-MeanC	-0.01717103	0.9610545		0.9914232	
SlopeF-SlopeC	1.344497	0.2003774		0.9999488	



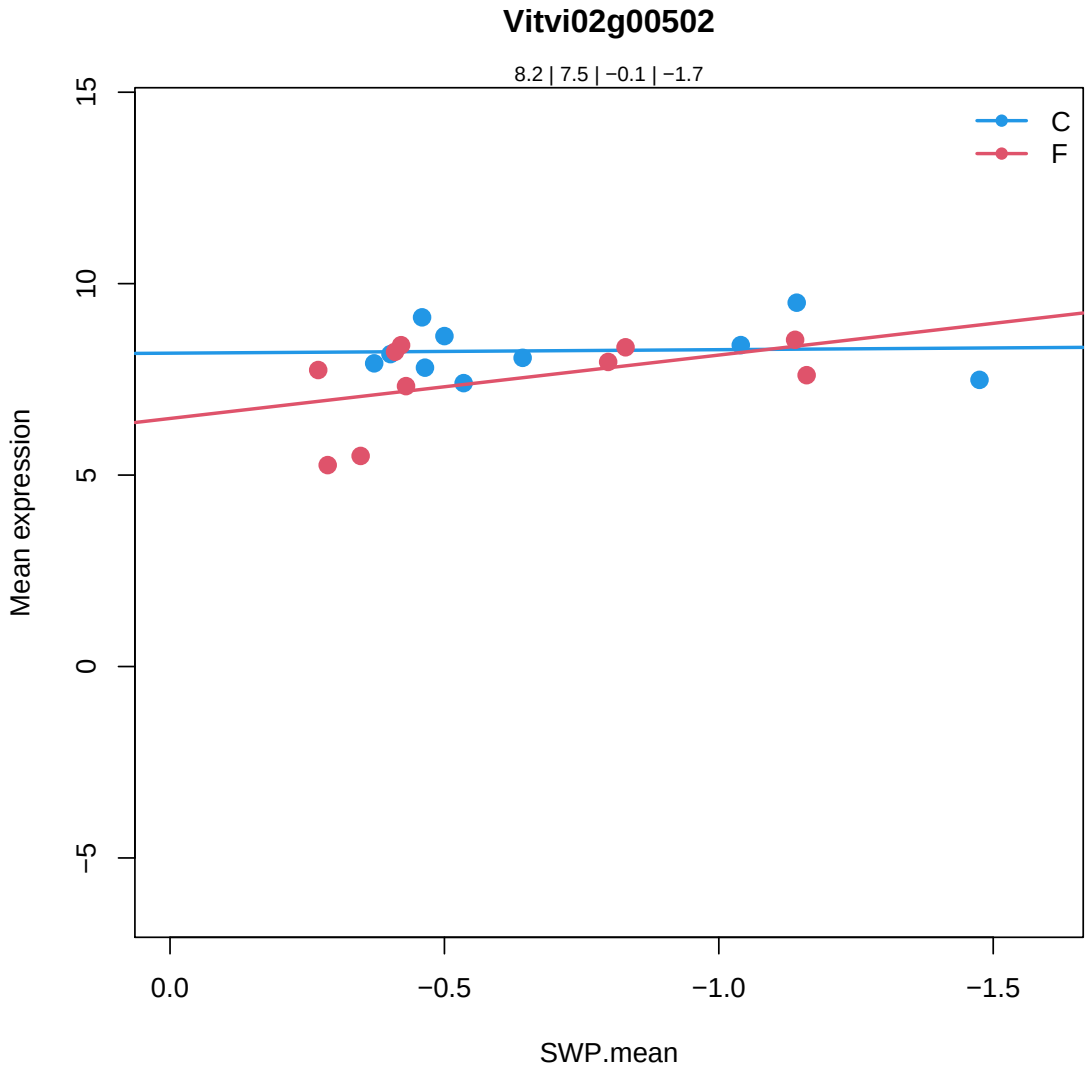
7.6.616 Vitvi02g00502: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00502
        29.2.4
        protein.synthesis.elongation
        Translation elongation factor EFG/EF2 protein |
        Chr1:23233622-23236321 REVERSE LENGTH=783 |
        201606
```

Coefficients for Vitvi02g00502.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	8.248068	2.254587e-19	***	9.500805e-19	***
SlopeC	-0.09112577	0.9023828		0.9825783	
MeanF-MeanC	-0.7607844	0.05402702	.	0.2518287	
SlopeF-SlopeC	-1.565007	0.1665296		0.9999488	



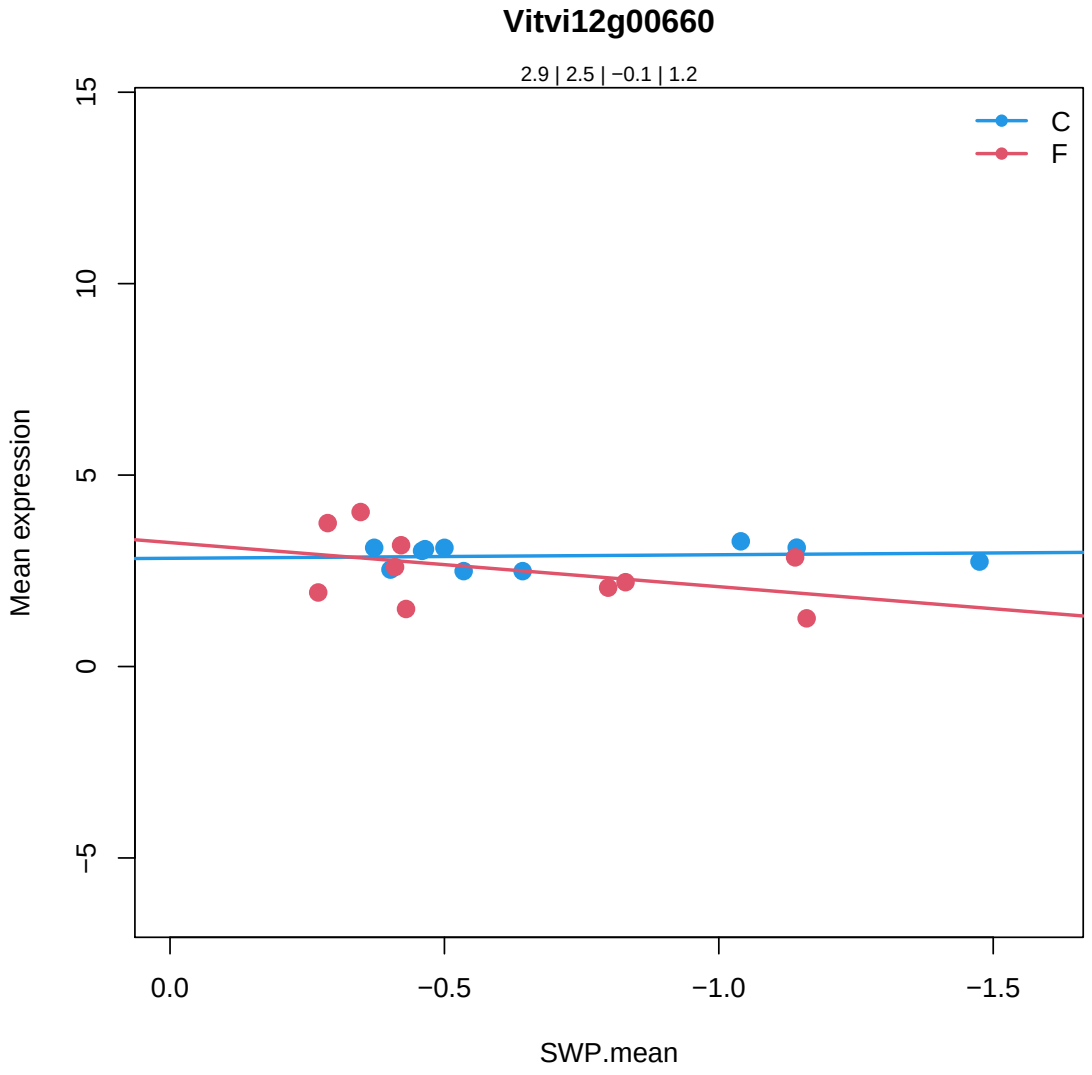
7.6.617 Vitvi12g00660: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00660
        29.4.1
        protein.postranslational modification.kinase
        Protein kinase superfamily protein |
        Chr5:22506477-22507757 REVERSE LENGTH=314 |
        201606
```

Coefficients for Vitvi12g00660.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.891564	1.124337e-12	***	1.607613e-12	***
SlopeC	-0.09287596	0.8668074		0.9755597	
MeanF-MeanC	-0.356477	0.2136511		0.5600633	
SlopeF-SlopeC	1.245155	0.1409015		0.9999488	



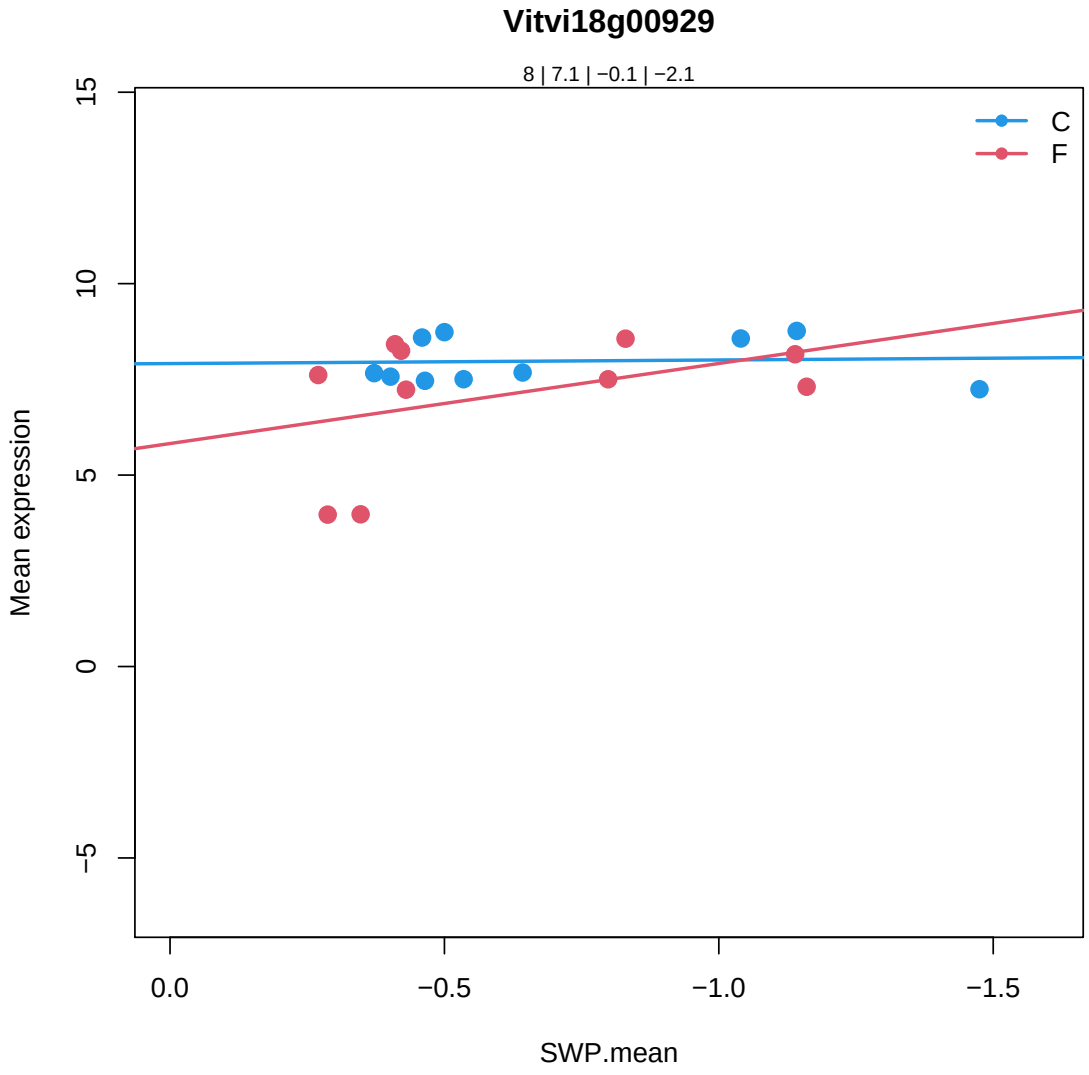
7.6.618 Vitvi18g00929: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00929
        35.1
        not assigned.no ontology
        J-domain protein required for chloroplast accumulation response 1 |
        Chr1:28191108-28193769 REVERSE LENGTH=651 |
        201606
```

Coefficients for Vitvi18g00929.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.9778	1.649448e-16	***	3.451996e-16	***
SlopeC	-0.09365678	0.9243392		0.9862379	
MeanF-MeanC	-0.8799929	0.08989202	.	0.3425335	
SlopeF-SlopeC	-1.997575	0.1827106		0.9999488	



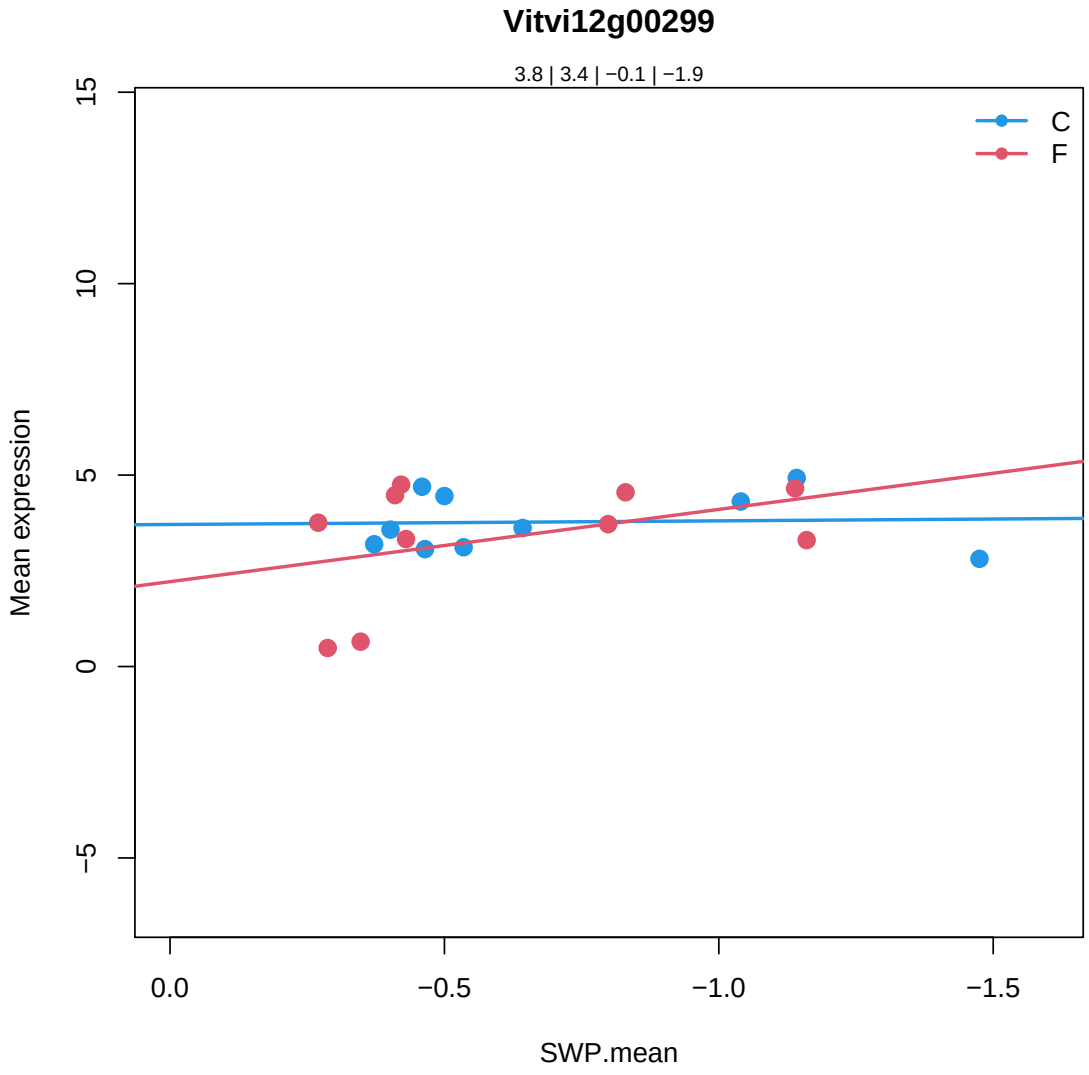
7.6.619 Vitvi12g00299: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00299
        30.11
        signalling.light
        SPA1-related 3 |
        Chr3:5169327-5171601 REVERSE LENGTH=595 |
        201606
```

Coefficients for Vitvi12g00299.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.77602	2.419932e-10	***	3.119207e-10	***
SlopeC	-0.09499337	0.9210747		0.985539	
MeanF-MeanC	-0.4096339	0.404456		0.7479549	
SlopeF-SlopeC	-1.792227	0.2174056		0.9999488	



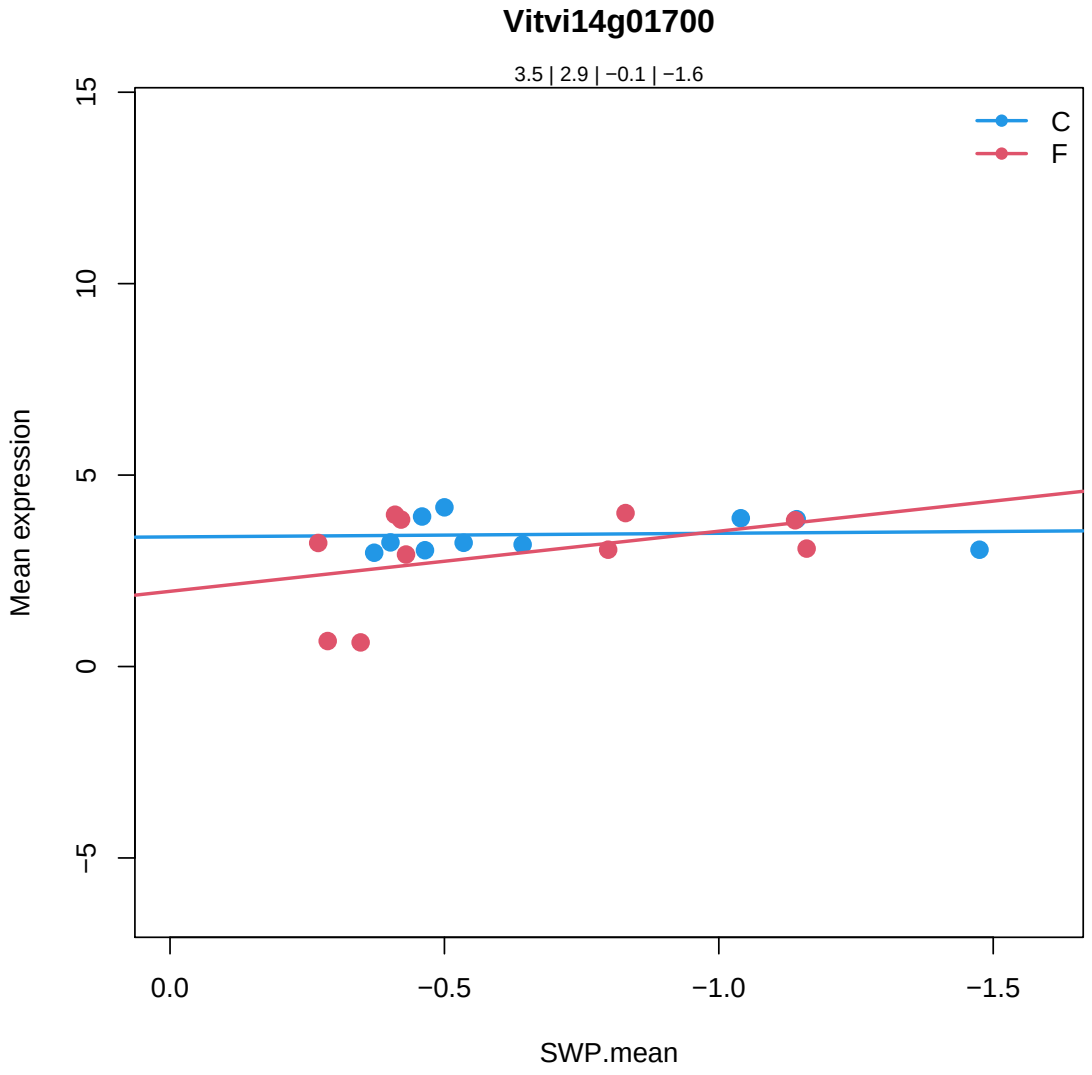
7.6.620 Vitvi14g01700: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01700
        35.2
        not assigned.unknown
        RNI-like superfamily protein |
        Chr5:16208255-16209745 REVERSE LENGTH=496 |
        201606
```

Coefficients for Vitvi14g01700.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.451249	1.024575e-11	***	1.397331e-11	***
SlopeC	-0.09519906	0.8977278		0.9819807	
MeanF-MeanC	-0.5304587	0.1683395		0.497254	
SlopeF-SlopeC	-1.475435	0.1897227		0.9999488	



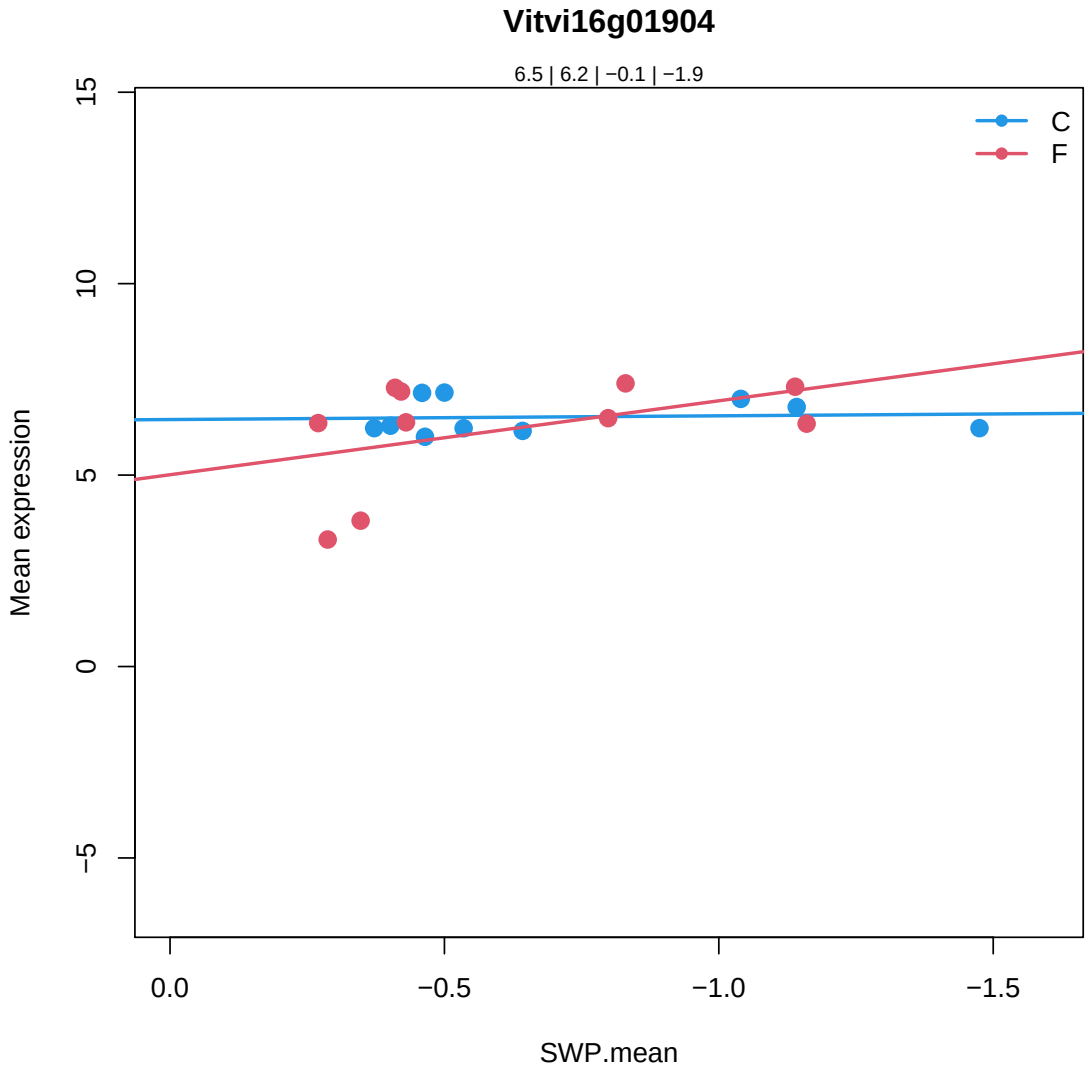
7.6.621 Vitvi16g01904: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01904
        27.3.67
        RNA.regulation of transcription.putative transcription regulator
        transmembrane protein |
        Chr5:21281817-21282545 FORWARD LENGTH=242 |
        201606
```

Coefficients for Vitvi16g01904.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.518743	2.257109e-16	***	4.627772e-16	***
SlopeC	-0.09709368	0.9055412		0.983424	
MeanF-MeanC	-0.333319	0.4263121		0.7622334	
SlopeF-SlopeC	-1.833724	0.1422092		0.9999488	



7.6.622 Vitvi17g00277: type5

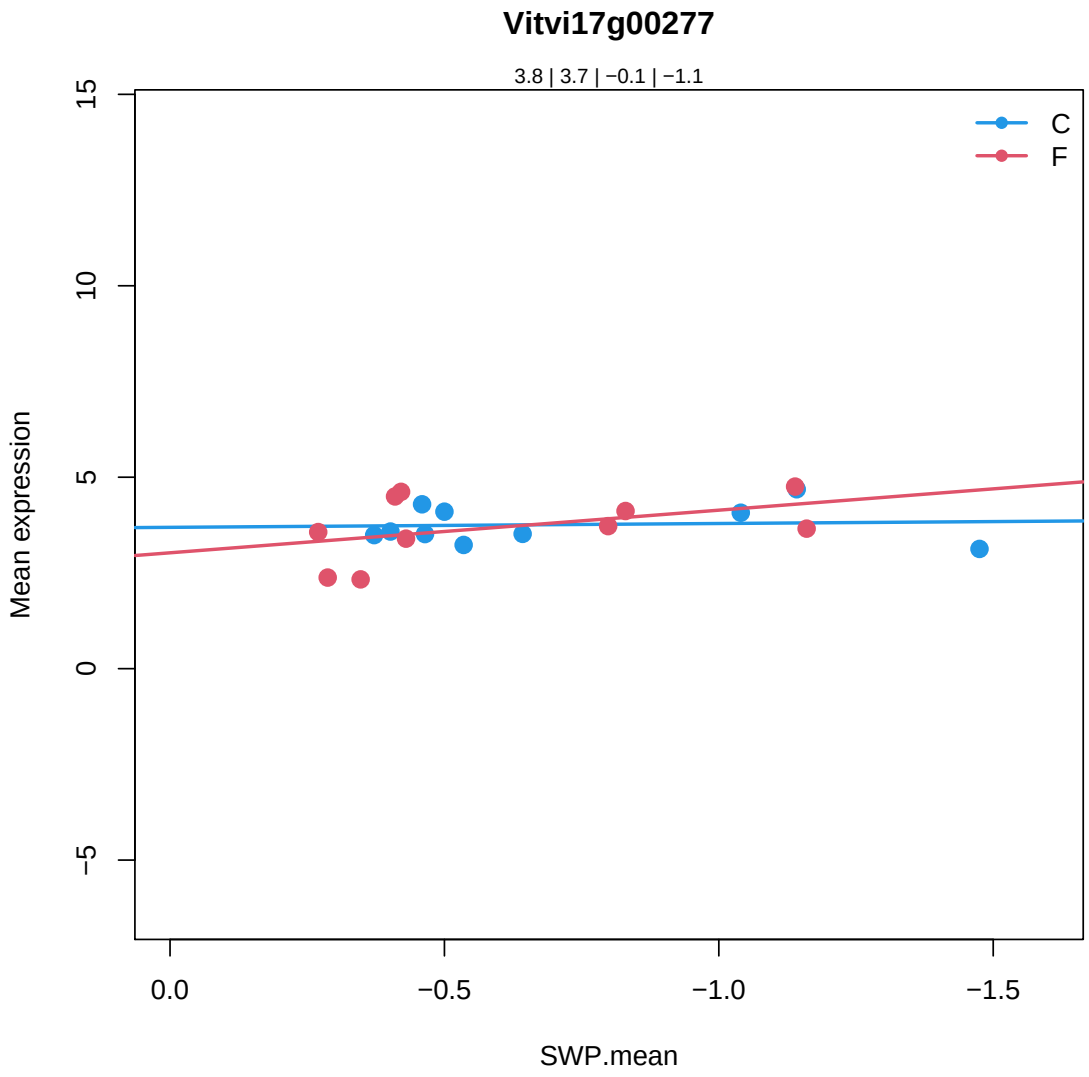
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00277
        29.5.11.4.2
        protein.degradation.ubiquitin.E3.RING
        RING/U-box superfamily protein |
        Chr1:27739366-27741161 REVERSE LENGTH=367 |
        201606

Vitvi17g00277
        27.3.11
        RNA.regulation of transcription.C2H2 zinc finger family
        RING/U-box superfamily protein |
        Chr1:27739366-27741161 REVERSE LENGTH=367 |
        201606
```

Coefficients for Vitvi17g00277.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.761062	9.915876e-15	***	1.658122e-14	***
SlopeC	-0.1004001	0.8597427		0.9737381	
MeanF-MeanC	-0.05716873	0.8431086		0.9585164	
SlopeF-SlopeC	-1.012737	0.2386871		0.9999488	


Vitvi17g00277
3.8 | 3.7 | −0.1 | −1.1
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

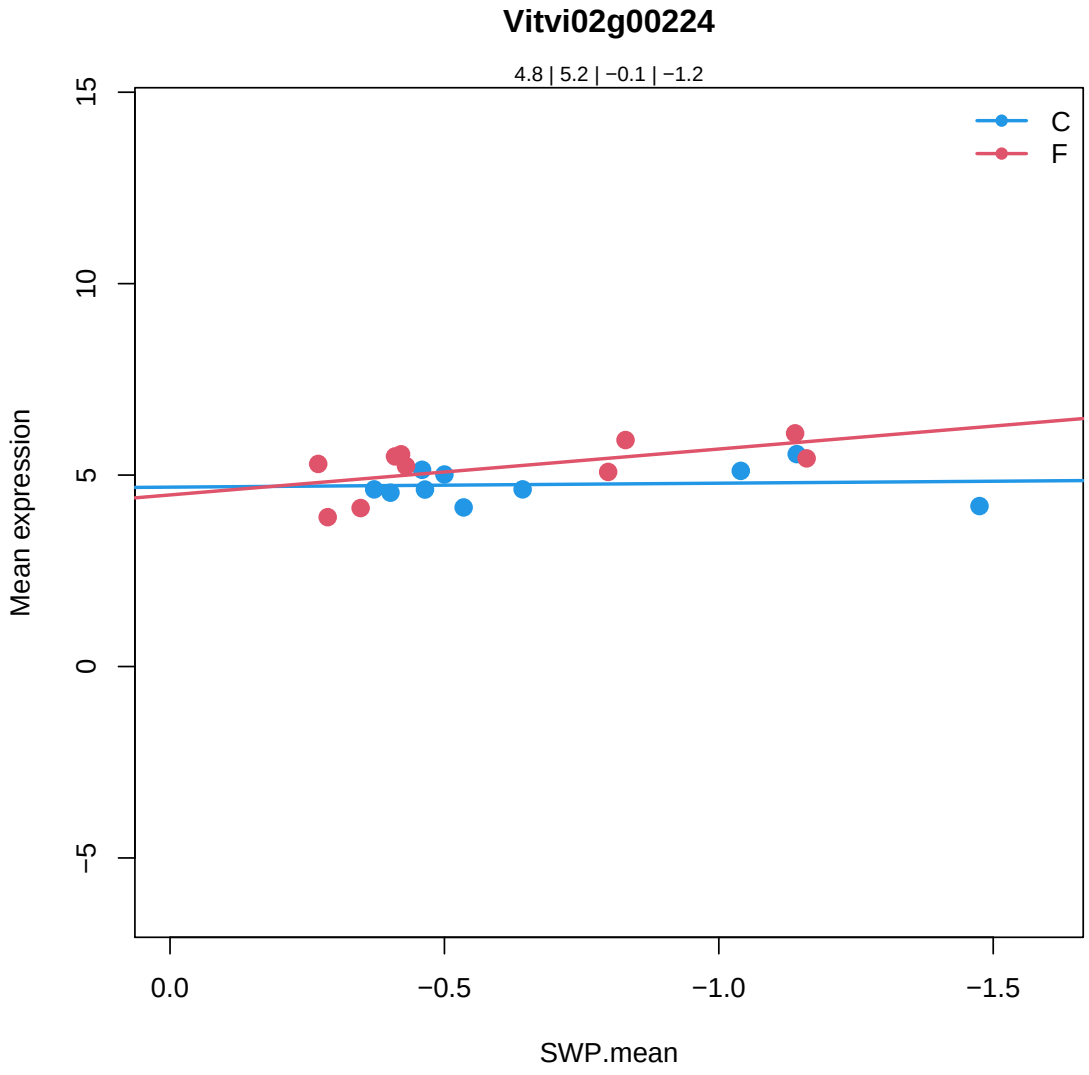
7.6.623 Vitvi02g00224: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00224
        33.2
        development.late embryogenesis abundant
        esterase/lipase/thioesterase family protein |
        Chr3:18880074-18881940 REVERSE LENGTH=408 |
        201606
```

Coefficients for Vitvi02g00224.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.757151	1.376246e-18	***	4.555208e-18	***
SlopeC	-0.1030837	0.8254156		0.9650214	
MeanF-MeanC	0.4546243	0.06598298	.	0.2849851	
SlopeF-SlopeC	-1.095784	0.1253873		0.9999488	



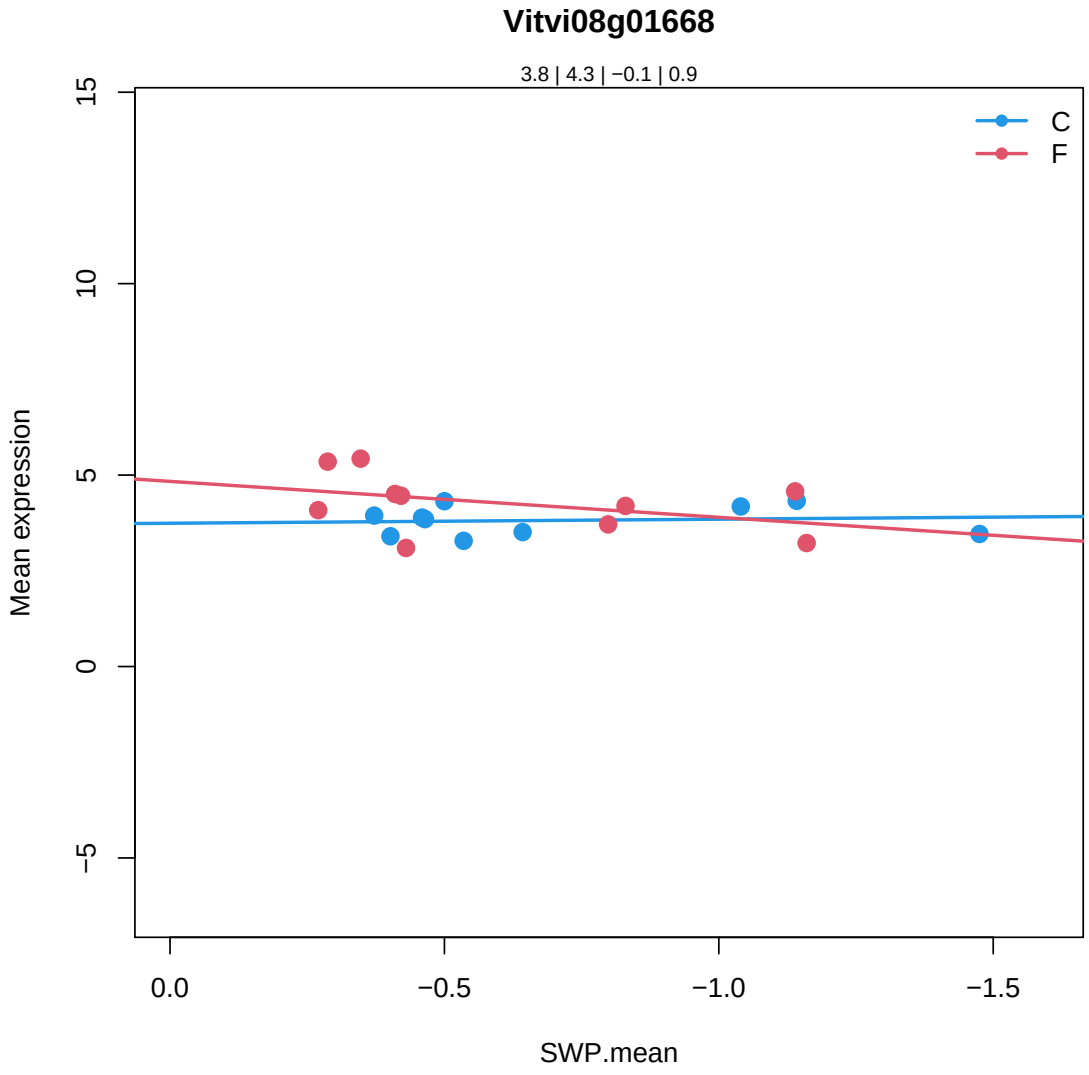
7.6.624 Vitvi08g01668: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01668
        27.2
        RNA.transcription
        Glutaredoxin family protein |
        Chr3:21124174-21125427 FORWARD LENGTH=417 |
        201606
```

Coefficients for Vitvi08g01668.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.816399	1.062107e-15	***	1.982201e-15	***
SlopeC	-0.1057921	0.8377757		0.9692779	
MeanF-MeanC	0.4471354	0.09924999	.	0.3626024	
SlopeF-SlopeC	1.044275	0.1834977		0.9999488	



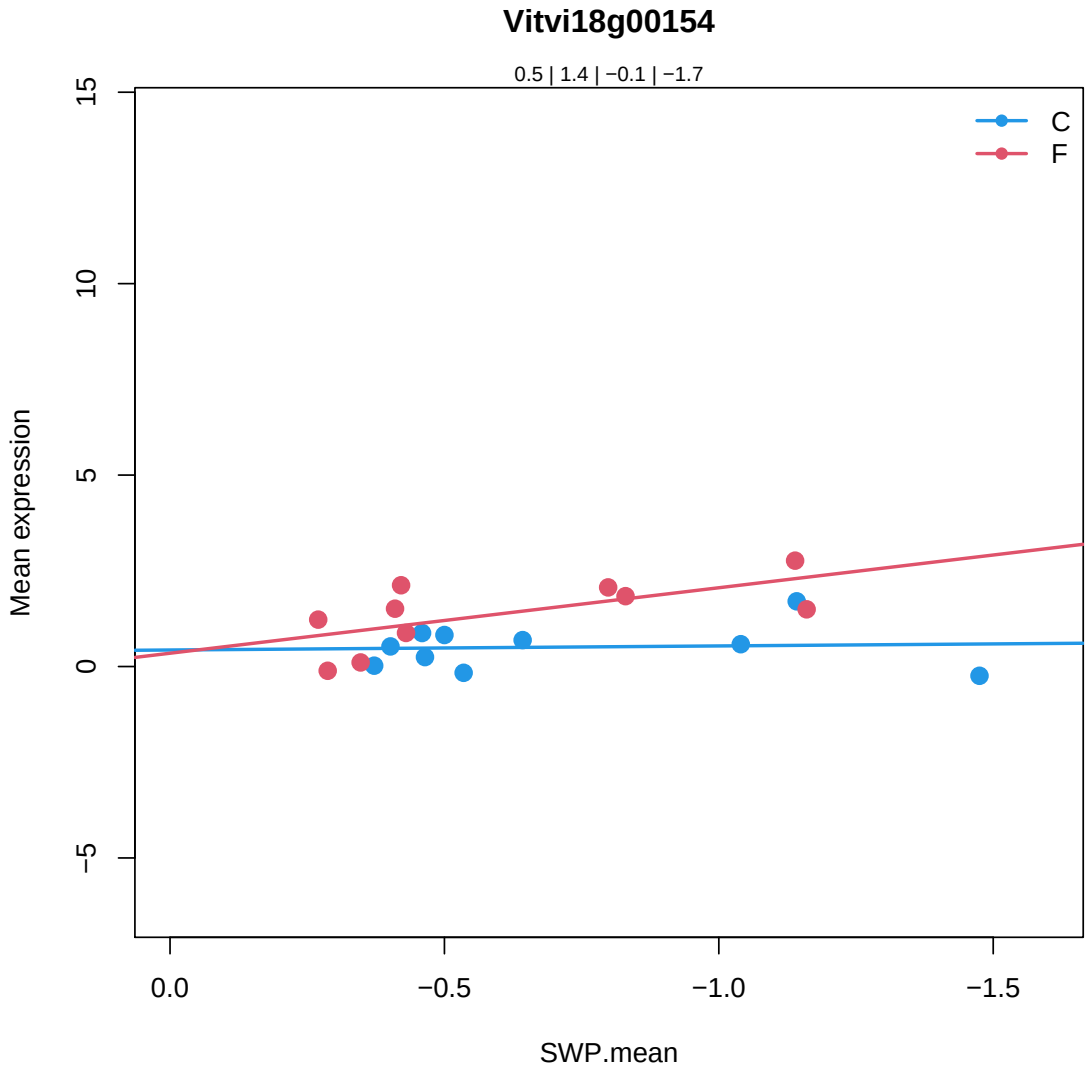
7.6.625 Vitvi18g00154: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00154
        29.4
        protein.postranslational modification
        ACT-like protein tyrosine kinase family protein |
        Chr4:17999432-18003193 FORWARD LENGTH=508 |
        201606
```

Coefficients for Vitvi18g00154.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.5058717	0.01887407	*	0.01985496	*
SlopeC	-0.1060377	0.8500358		0.9719233	
MeanF-MeanC	0.8832002	0.004908278	**	0.04506746	*
SlopeF-SlopeC	-1.604135	0.06499196	.	0.9999488	



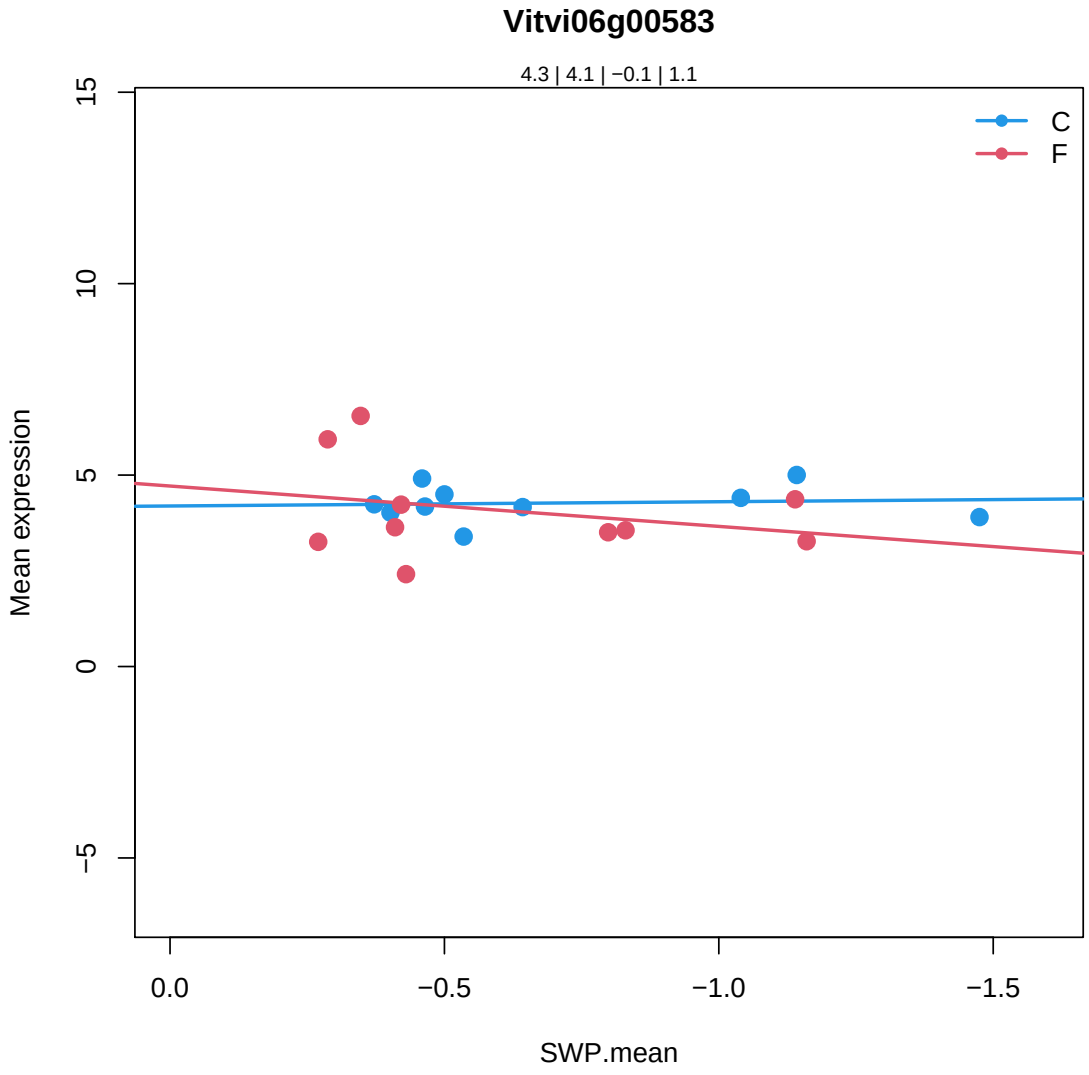
7.6.626 Vitvi06g00583: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00583
        2.2.2.2
        major CHO metabolism.degradation.starch.starch phosphorylase
        alpha-glucan phosphorylase 2 |
        Chr3:17301625-17306111 REVERSE LENGTH=841 |
        201606
```

Coefficients for Vitvi06g00583.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.270697	4.942037e-13	***	7.239279e-13	***
SlopeC	-0.1115512	0.8869018		0.9791994	
MeanF-MeanC	-0.1991403	0.6183883		0.8676755	
SlopeF-SlopeC	1.165916	0.3234269		0.9999488	



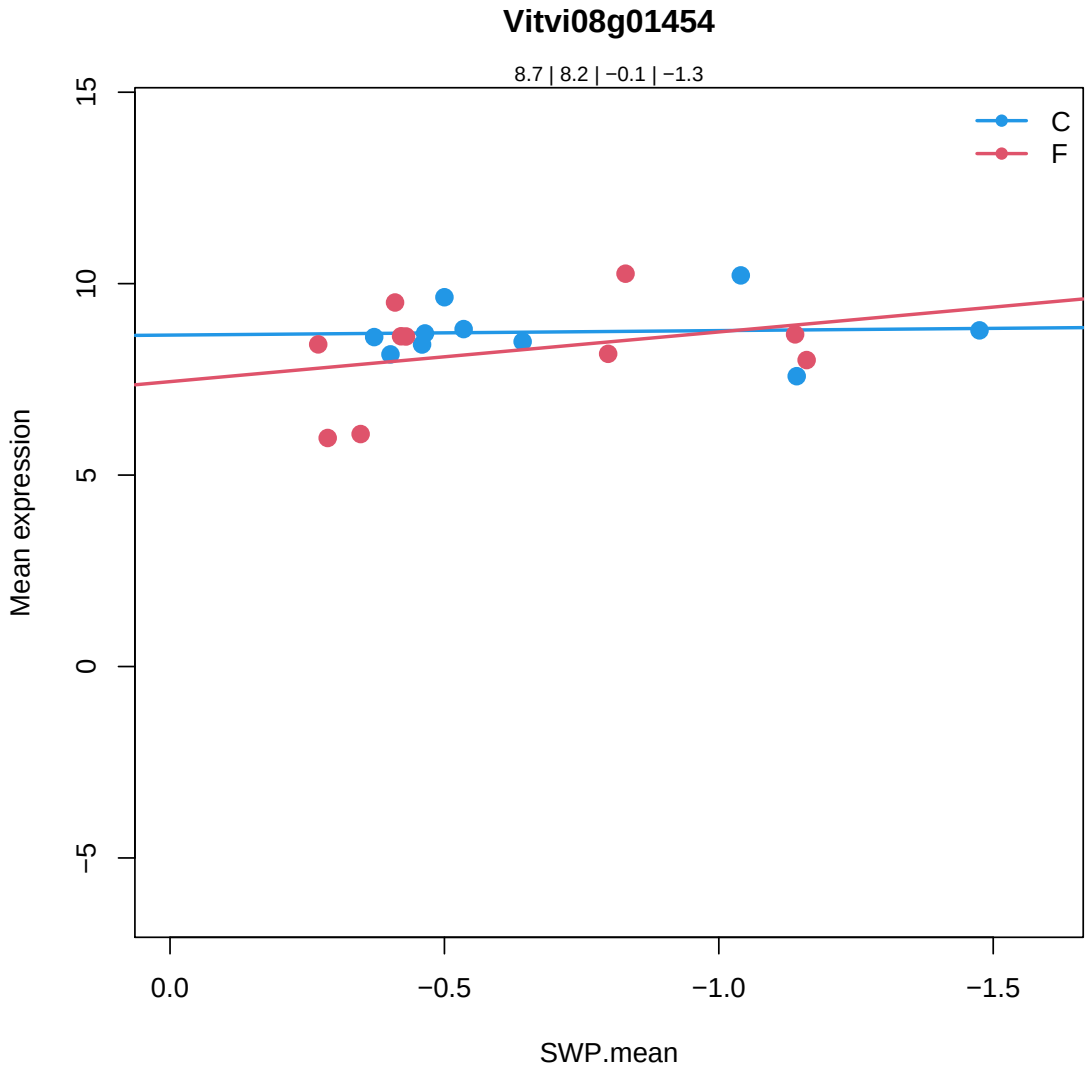
7.6.627 Vitvi08g01454: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01454
        8.3
        TCA / organic transformation.carbonic anhydrases
        alpha carbonic anhydrase 1 |
        Chr3:19538804-19541116 REVERSE LENGTH=284 |
        201606
```

Coefficients for Vitvi08g01454.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	8.738559	1.858401e-18	***	5.92713e-18	***
SlopeC	-0.1170435	0.8930468		0.9805373	
MeanF-MeanC	-0.5074139	0.2586582		0.6203357	
SlopeF-SlopeC	-1.181075	0.3665674		0.9999488	



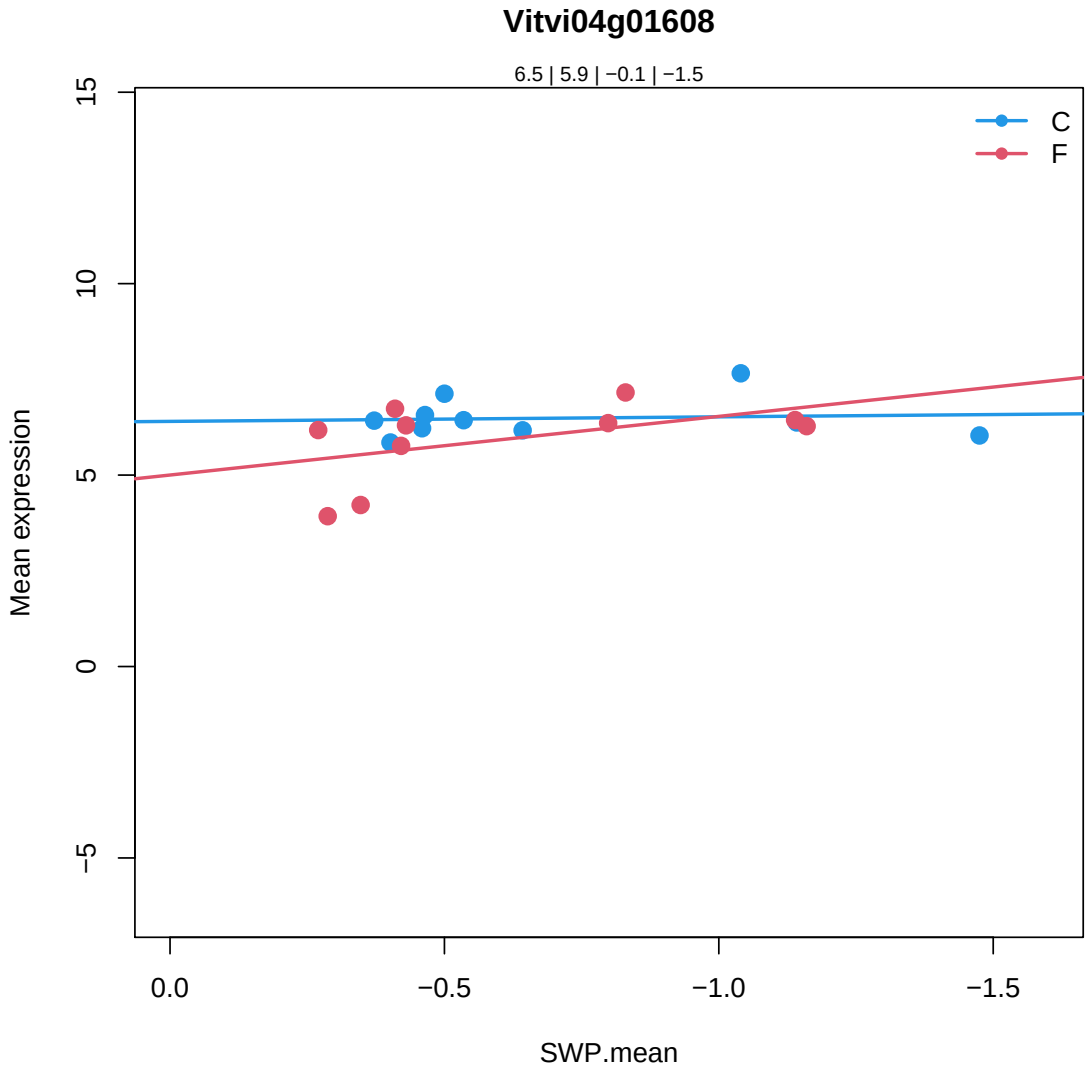
7.6.628 Vitvi04g01608: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01608
        31.1
        cell.organisation
        Plastid-lipid associated protein PAP / fibrillin family protein |
        Chr5:3056464-3057380 REVERSE LENGTH=236 |
        201606
```

Coefficients for Vitvi04g01608.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.485647	1.805821e-18	***	5.776353e-18	***
SlopeC	-0.1187025	0.854061		0.972509	
MeanF-MeanC	-0.5512493	0.1034334		0.3725265	
SlopeF-SlopeC	-1.412665	0.1511534		0.9999488	



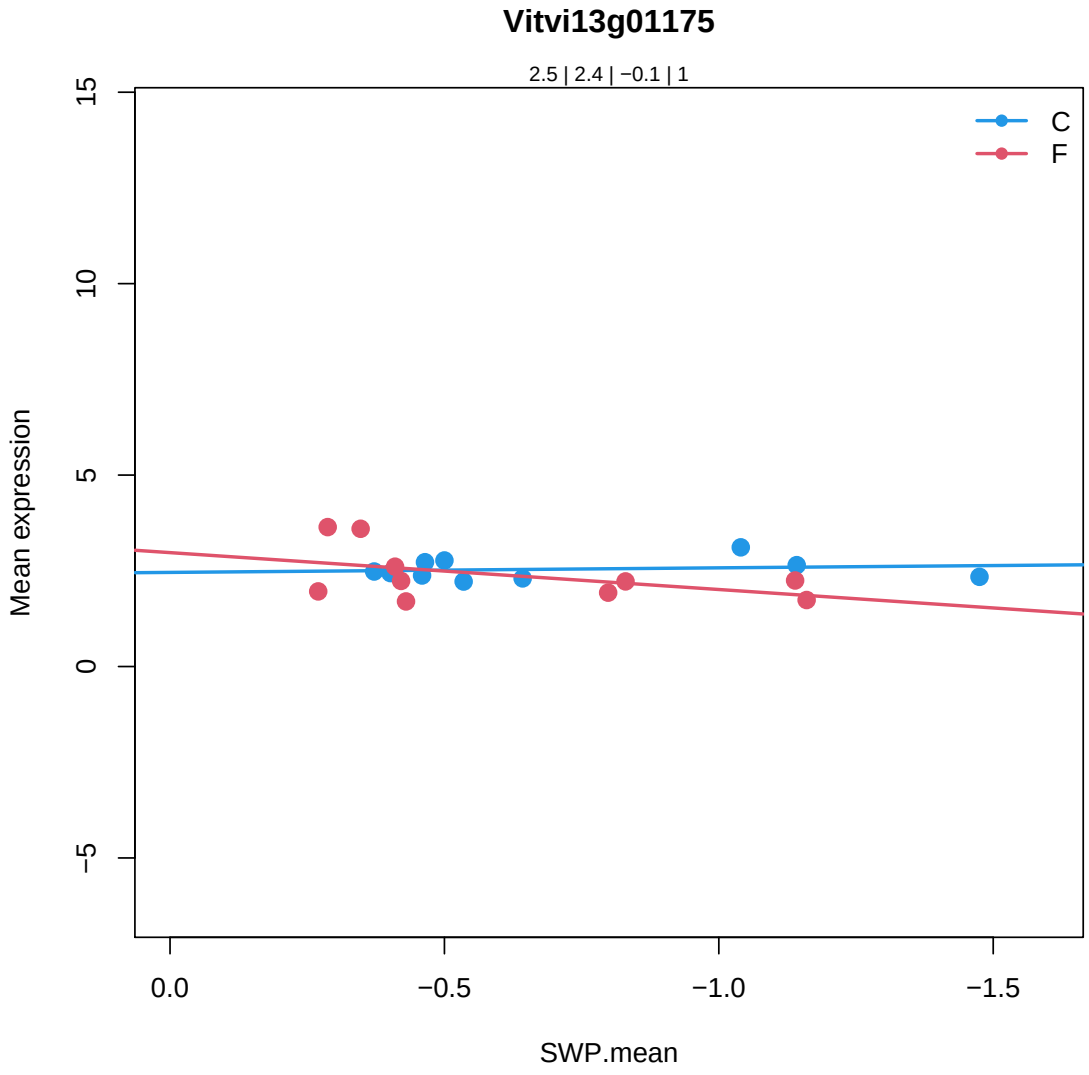
7.6.629 Vitvi13g01175: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g01175
        16.8.3.1
        secondary metabolism.flavonoids.dihydroflavonols.dihydroflavonol 4-red
        NAD(P)-binding Rossmann-fold superfamily protein |
        Chr5:6556493-6558123 FORWARD LENGTH=326 |
        201606
```

Coefficients for Vitvi13g01175.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.541731	2.118776e-13	***	3.181086e-13	***
SlopeC	-0.1195086	0.7894304		0.9533712	
MeanF-MeanC	-0.153986	0.5004116		0.8062657	
SlopeF-SlopeC	1.08266	0.1143643		0.9999488	



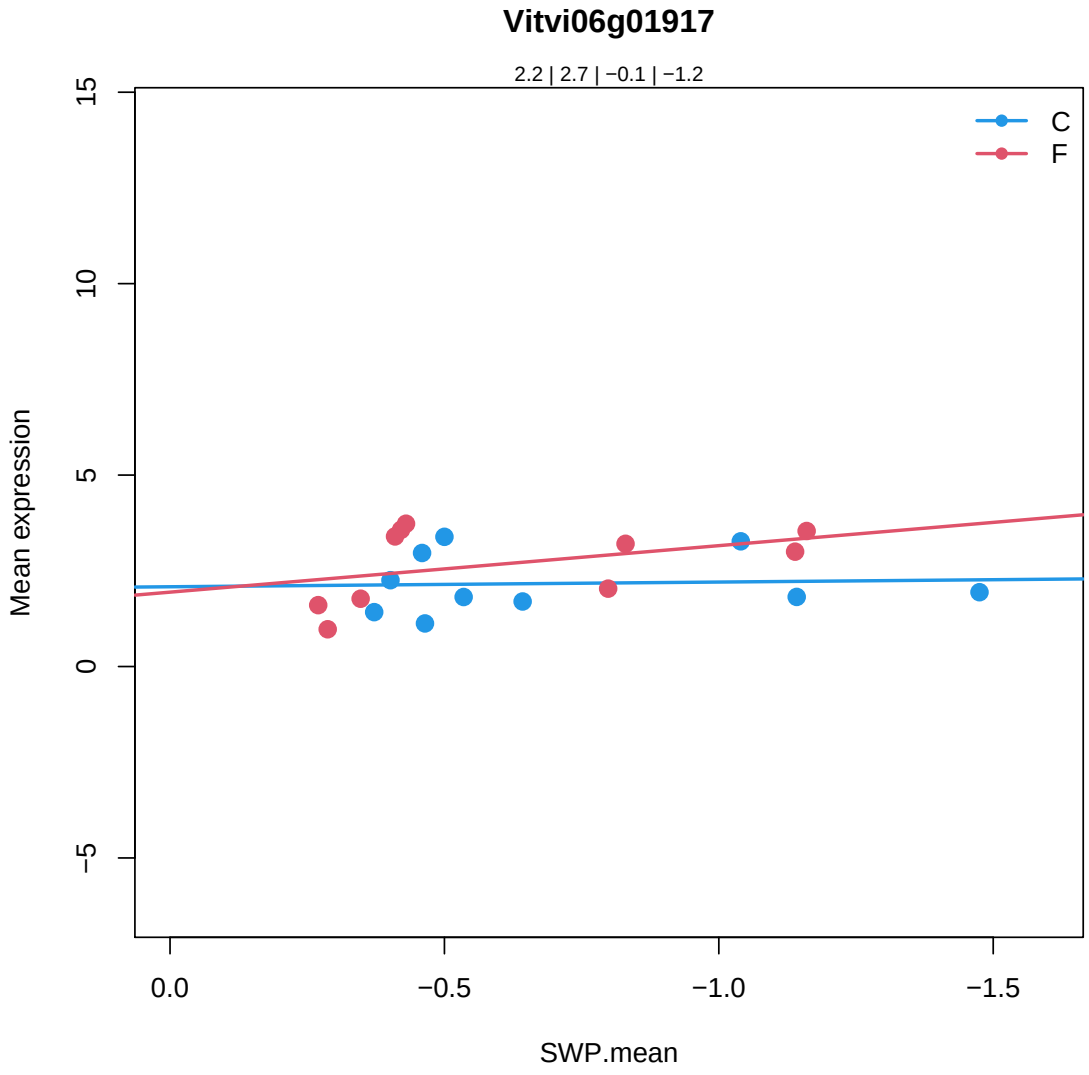
7.6.630 Vitvi06g01917: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01917
        26.4.1
        misc.beta 1,3 glucan hydrolases.glucan endo-1,3-beta-glucosidase
        beta-1%2C3-glucanase 3 |
        Chr3:21181916-21183045 REVERSE LENGTH=341 |
        201606
```

Coefficients for Vitvi06g01917.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.169409	2.778364e-08	***	3.346067e-08	***
SlopeC	-0.122553	0.8650988		0.9750528	
MeanF-MeanC	0.5127058	0.171407		0.5011673	
SlopeF-SlopeC	-1.091814	0.314873		0.9999488	



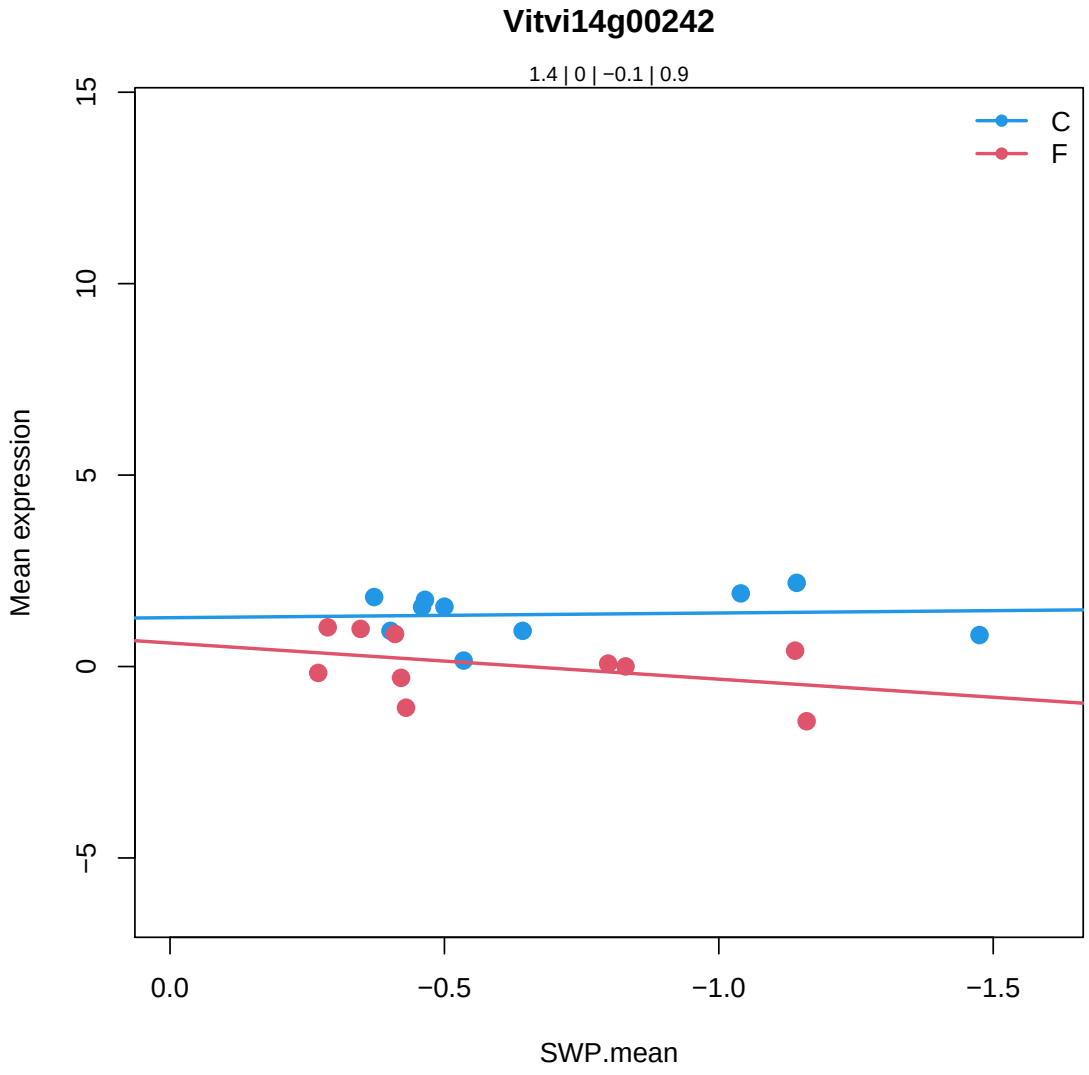
7.6.631 Vitvi14g00242: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g00242
        30.2.12
        signalling.receptor kinases.leucine rich repeat XII
        Leucine-rich repeat protein kinase family protein |
        Chr3:17527611-17530748 FORWARD LENGTH=1010 |
        201606
```

Coefficients for Vitvi14g00242.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.361181	2.878775e-06	***	3.288487e-06	***
SlopeC	-0.1229587	0.8404072		0.9695893	
MeanF-MeanC	-1.323076	0.0002938871	***	0.004533833	**
SlopeF-SlopeC	1.067241	0.2475666		0.9999488	



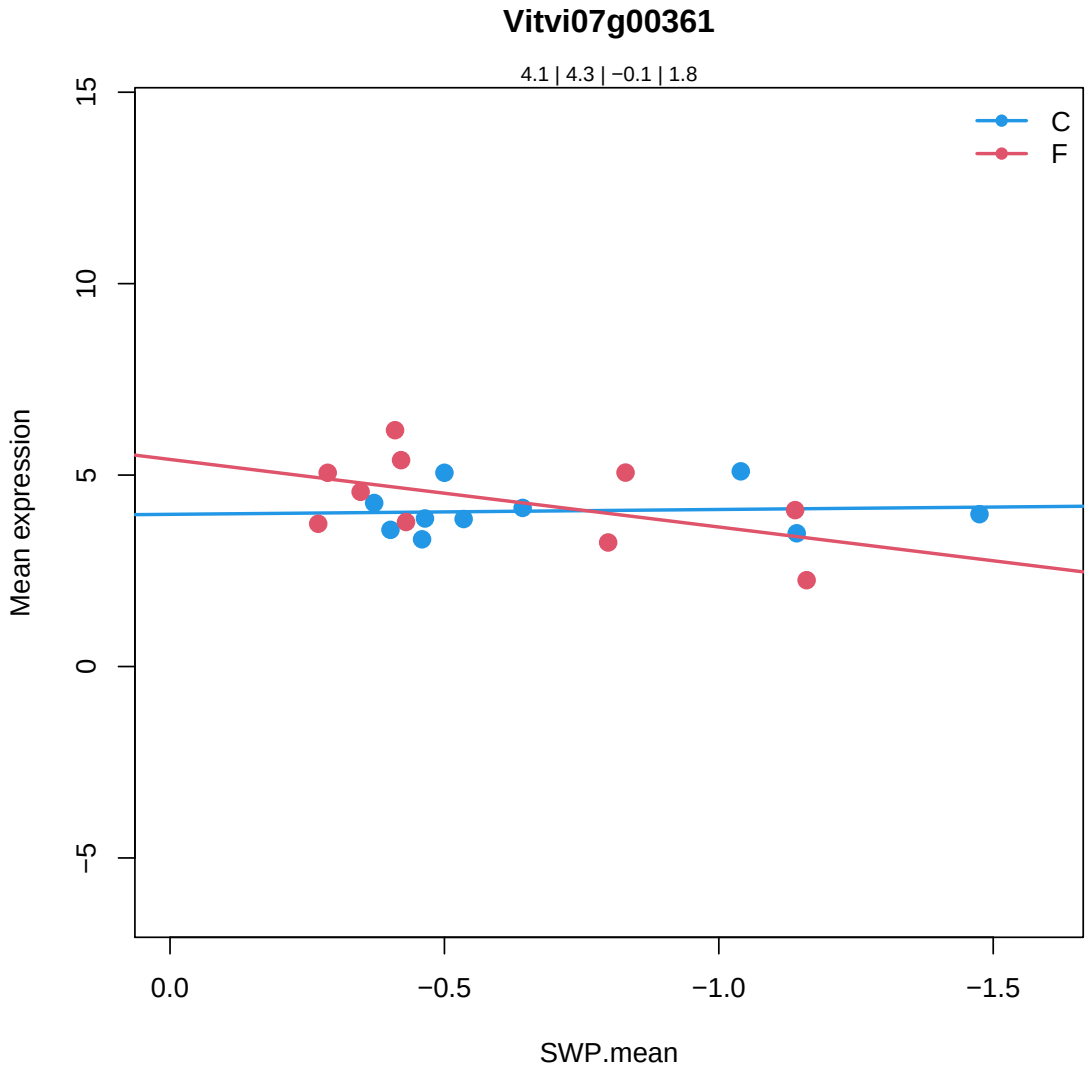
7.6.632 Vitvi07g00361: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g00361
        30.1.1
        signalling.in sugar and nutrient physiology.misc
        EXORDIUM like 2 |
        Chr5:25703980-25704897 FORWARD LENGTH=305 |
        201606
```

Coefficients for Vitvi07g00361.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.064003	1.316041e-13	***	2.002505e-13	***
SlopeC	-0.1264505	0.8562993		0.9730549	
MeanF-MeanC	0.2690784	0.4512967		0.778837	
SlopeF-SlopeC	1.890751	0.07945877	.	0.9999488	



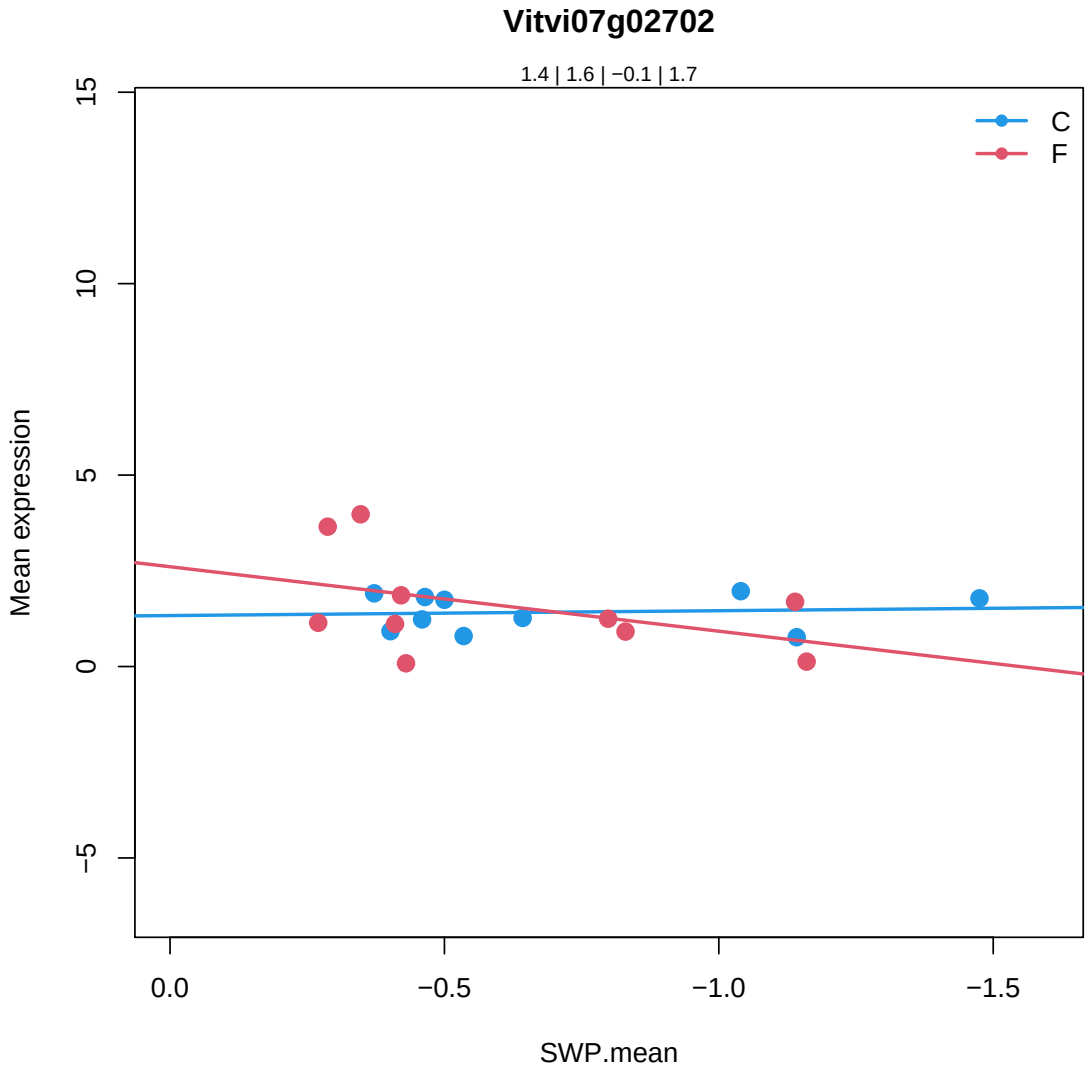
7.6.633 Vitvi07g02702: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g02702
        29.5.11.4.2
        protein.degradation.ubiquitin.E3.RING
        RING/U-box superfamily protein |
        Chr1:28668915-28669472 FORWARD LENGTH=185 |
        201606
```

Coefficients for Vitvi07g02702.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.419693	3.236396e-05	***	3.610418e-05	***
SlopeC	-0.1264966	0.8684339		0.9759642	
MeanF-MeanC	0.1606243	0.6795427		0.8961403	
SlopeF-SlopeC	1.809485	0.1217563		0.9999488	



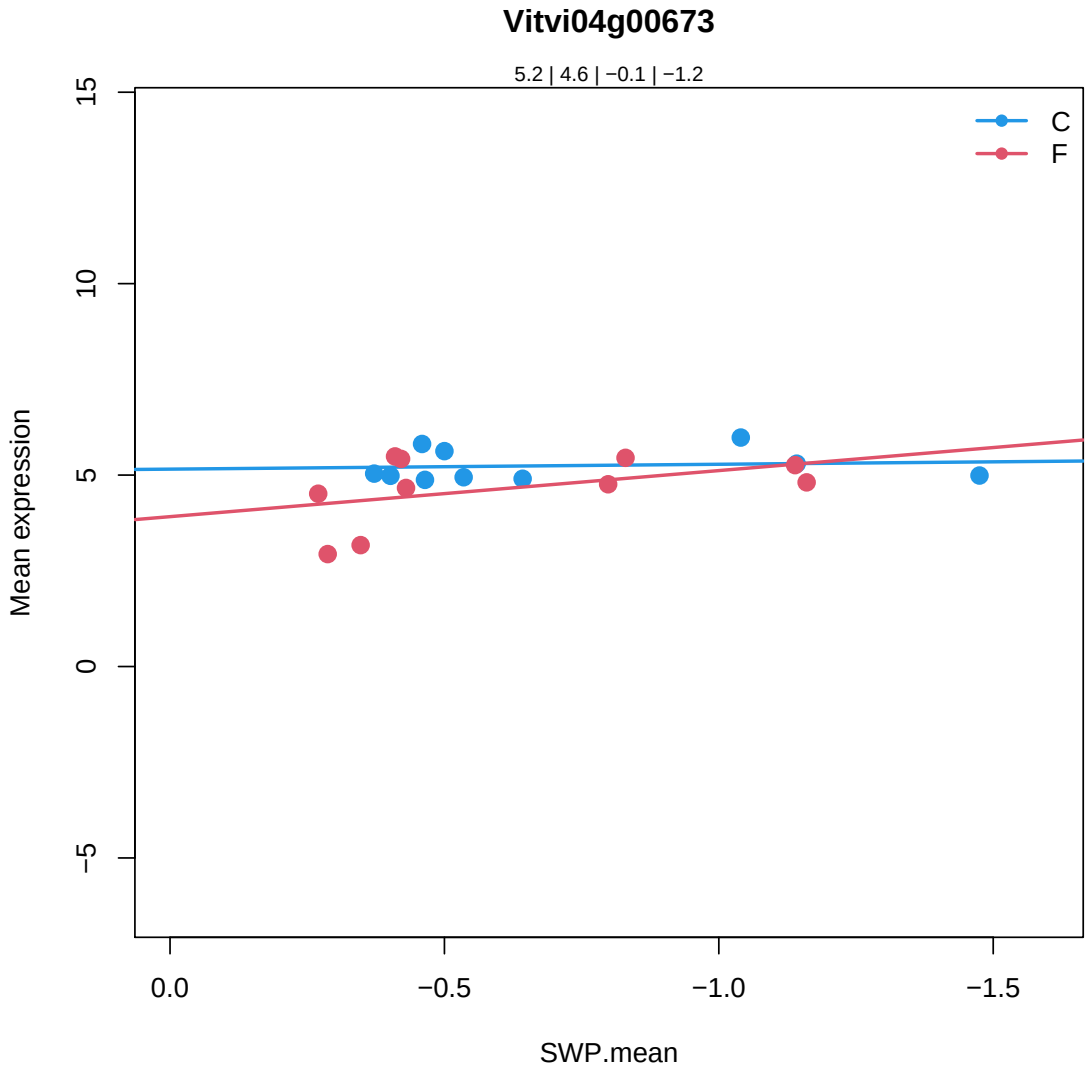
7.6.634 Vitvi04g00673: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00673
        35.1
        not assigned.no ontology
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi04g00673.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.244404	1.119957e-17	***	2.917517e-17	***
SlopeC	-0.1274177	0.8230079		0.9643522	
MeanF-MeanC	-0.5971108	0.04894964	*	0.2356571	
SlopeF-SlopeC	-1.075838	0.2126572		0.9999488	



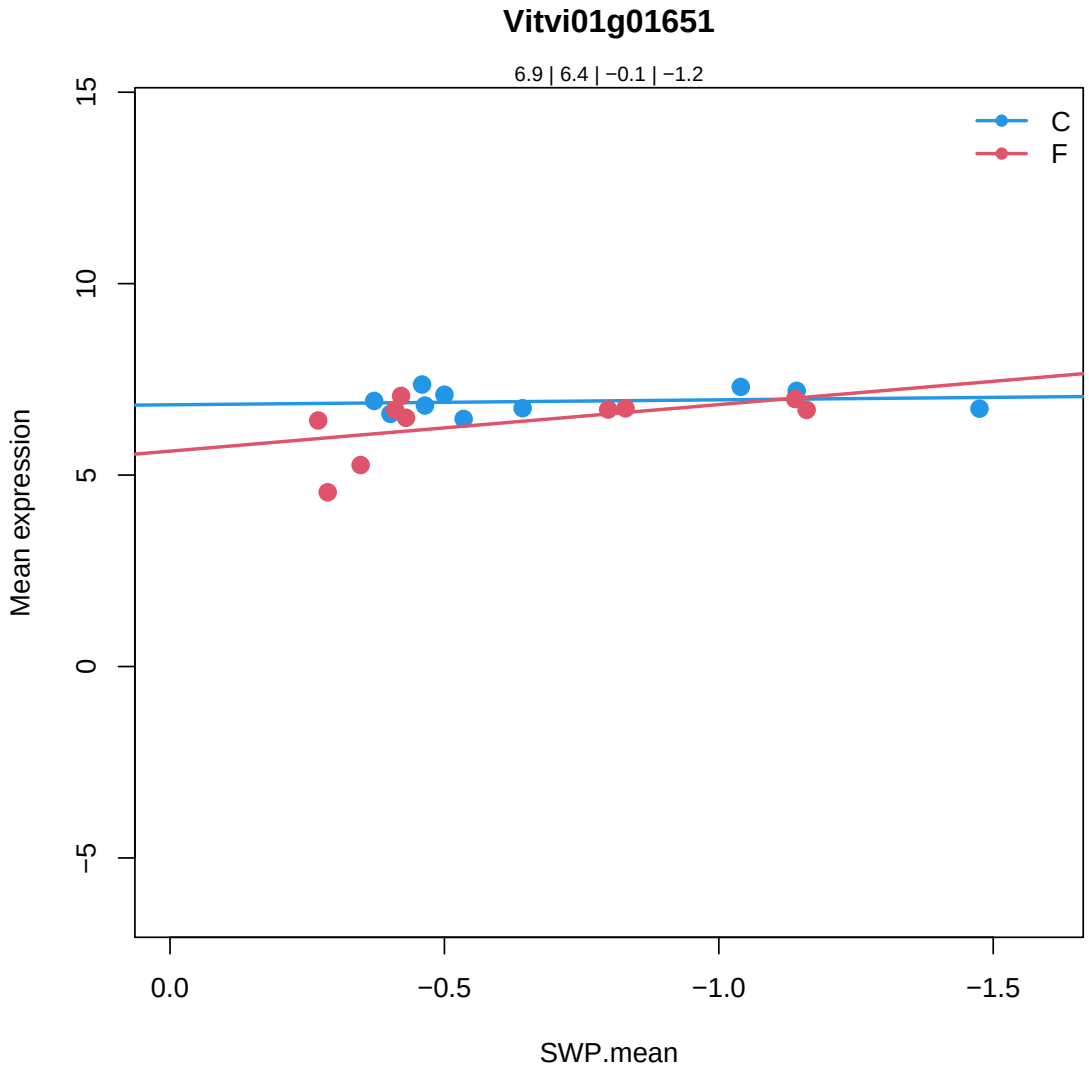
7.6.635 Vitvi01g01651: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01651
        27.3.99
        RNA.regulation of transcription.unclassified
        chaperone protein dnaJ-like protein |
        Chr5:17357693-17357986 REVERSE LENGTH=97 |
        201606
```

Coefficients for Vitvi01g01651.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.926757	1.289916e-21	***	1.400673e-20	***
SlopeC	-0.1291143	0.791657		0.9539439	
MeanF-MeanC	-0.5612236	0.03243569	*	0.1784782	
SlopeF-SlopeC	-1.086747	0.144976		0.9999488	



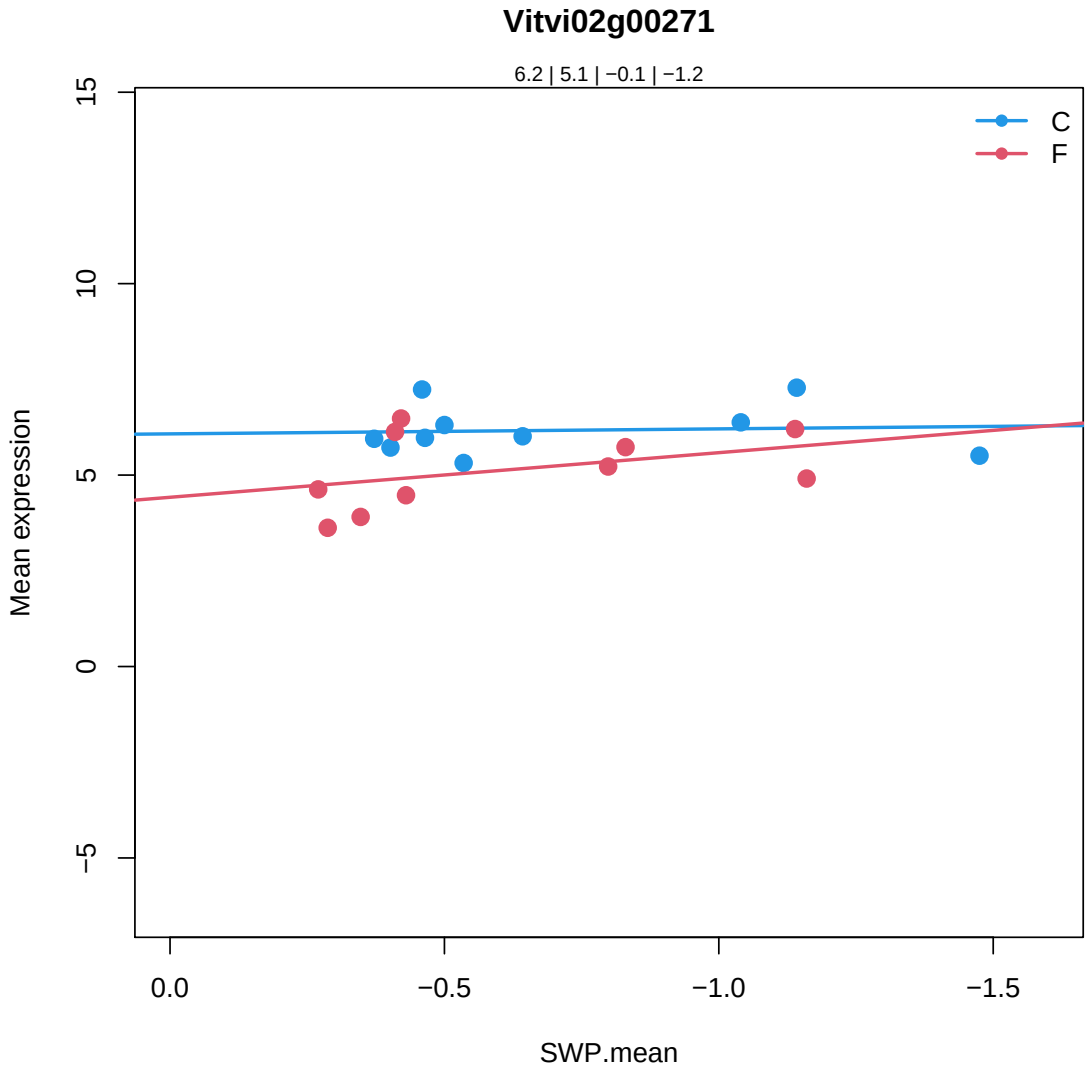
7.6.636 Vitvi02g00271: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00271
        16.8.3
        secondary metabolism.flavonoids.dihydroflavonols
        2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protei
        Chr4:6483900-6485179 FORWARD LENGTH=348 |
        201606
```

Coefficients for Vitvi02g00271.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.167721	1.648024e-17	***	4.154679e-17	***
SlopeC	-0.1302093	0.8486712		0.9719233	
MeanF-MeanC	-1.037678	0.006300036	**	0.05397703	.
SlopeF-SlopeC	-1.034954	0.3138476		0.9999488	



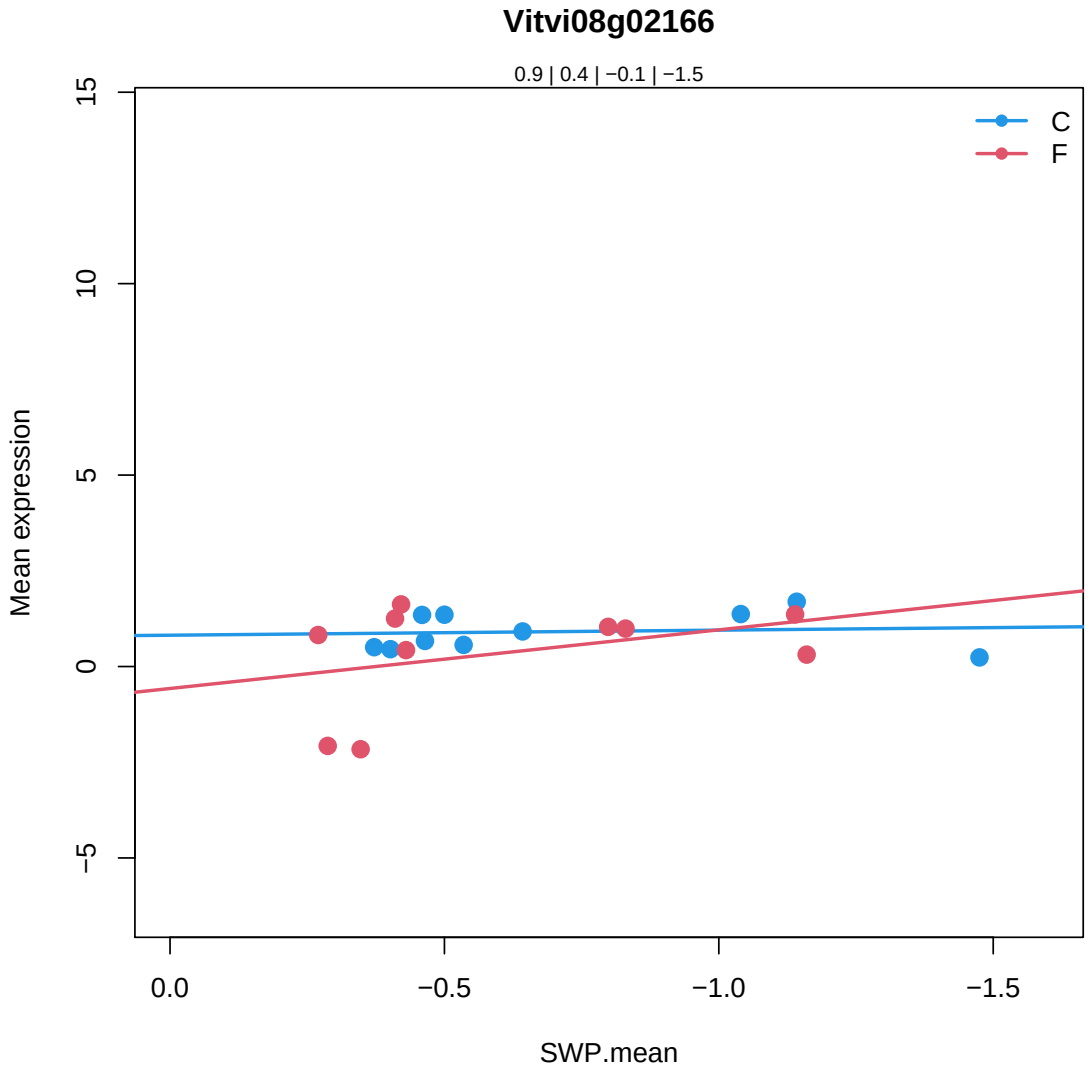
7.6.637 Vitvi08g02166: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g02166
        35.2
        not assigned.unknown
        F-box family protein |
        Chr2:16487151-16488464 REVERSE LENGTH=387 |
        201606
```

Coefficients for Vitvi08g02166.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.9105064	0.00458475	**	0.004893953	**
SlopeC	−0.1323582	0.8701996		0.9760939	
MeanF−MeanC	−0.5515313	0.1893189		0.5276876	
SlopeF−SlopeC	−1.399463	0.2529575		0.9999488	



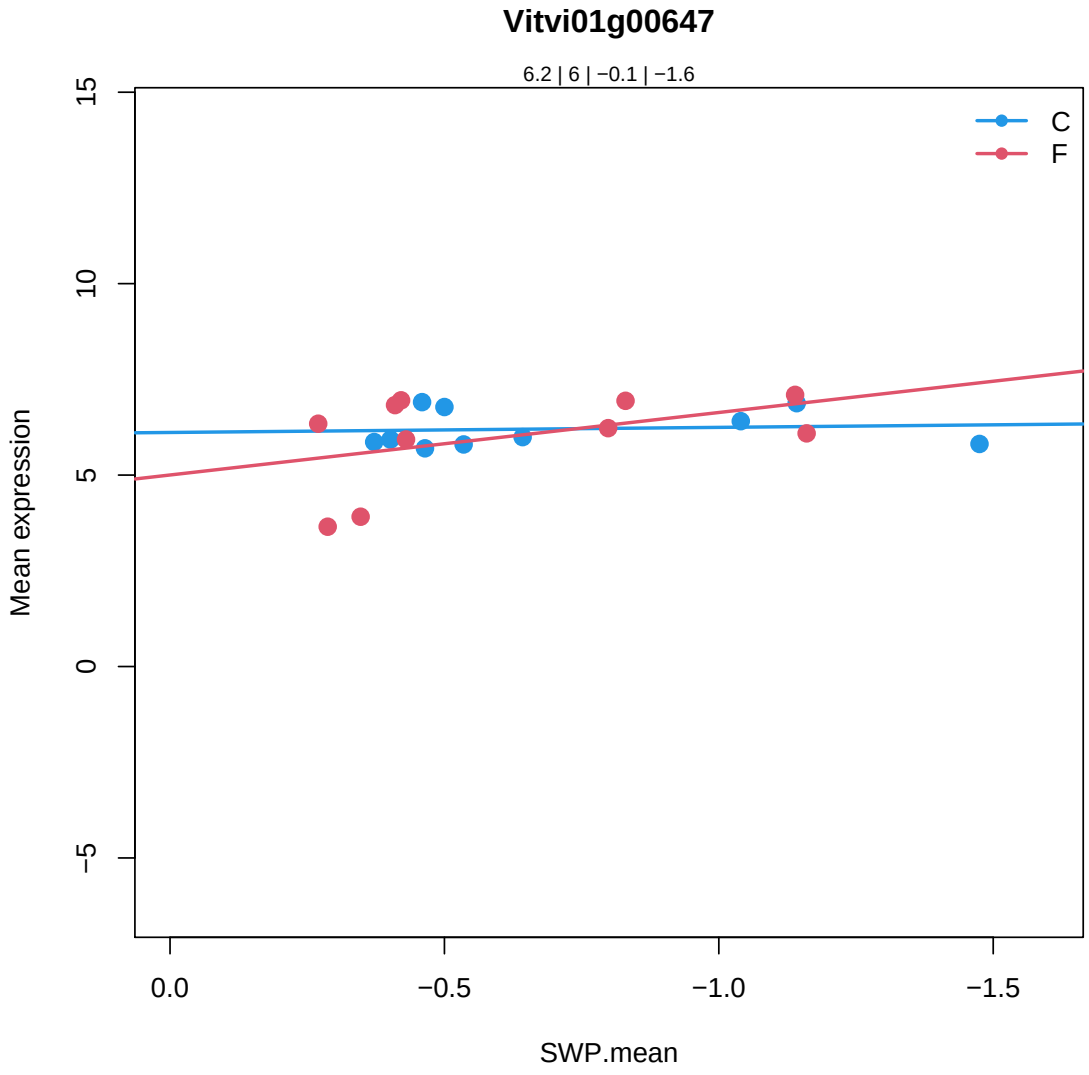
7.6.638 Vitvi01g00647: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00647
        34.7
        transport.phosphate
        phosphate transporter 2%3B1 |
        Chr3:9756416-9758413 FORWARD LENGTH=587 |
        201606
```

Coefficients for Vitvi01g00647.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.206136	5.446406e-17	***	1.240869e-16	***
SlopeC	-0.1331211	0.8547784		0.9727141	
MeanF-MeanC	-0.2096118	0.5720594		0.8473237	
SlopeF-SlopeC	-1.498995	0.1753803		0.9999488	



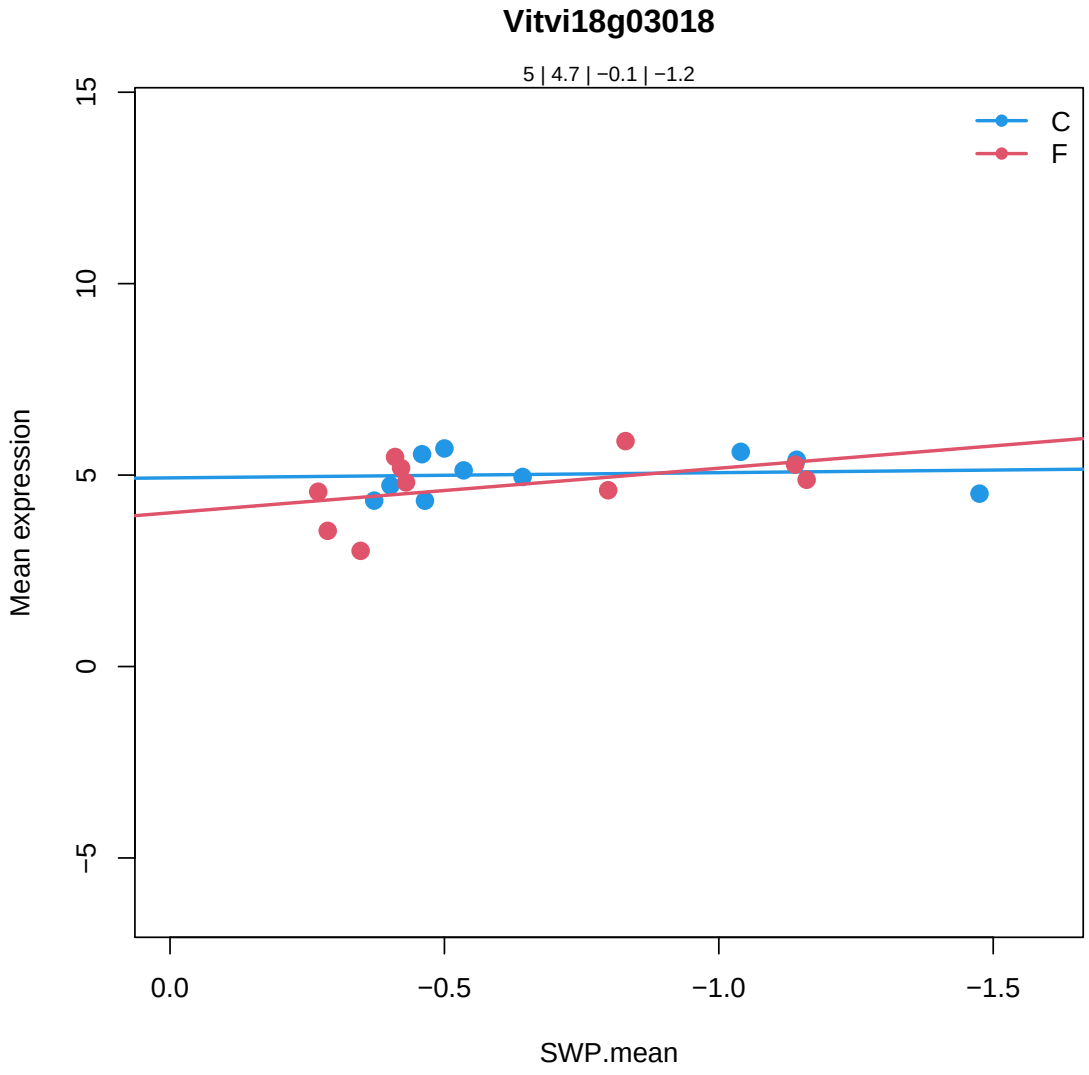
7.6.639 Vitvi18g03018: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g03018
        20.1.2.2
        stress.biotic.receptors.TIR-NBS-LRR
        Disease resistance protein (TIR-NBS-LRR class) family |
        Chr5:6074069-6078569 REVERSE LENGTH=1245 |
        201606
```

Coefficients for Vitvi18g03018.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.022701	4.274814e-17	***	9.932425e-17	***
SlopeC	-0.1362358	0.8149051		0.9599292	
MeanF-MeanC	-0.2989872	0.3176029		0.6790186	
SlopeF-SlopeC	-1.029199	0.242111		0.9999488	



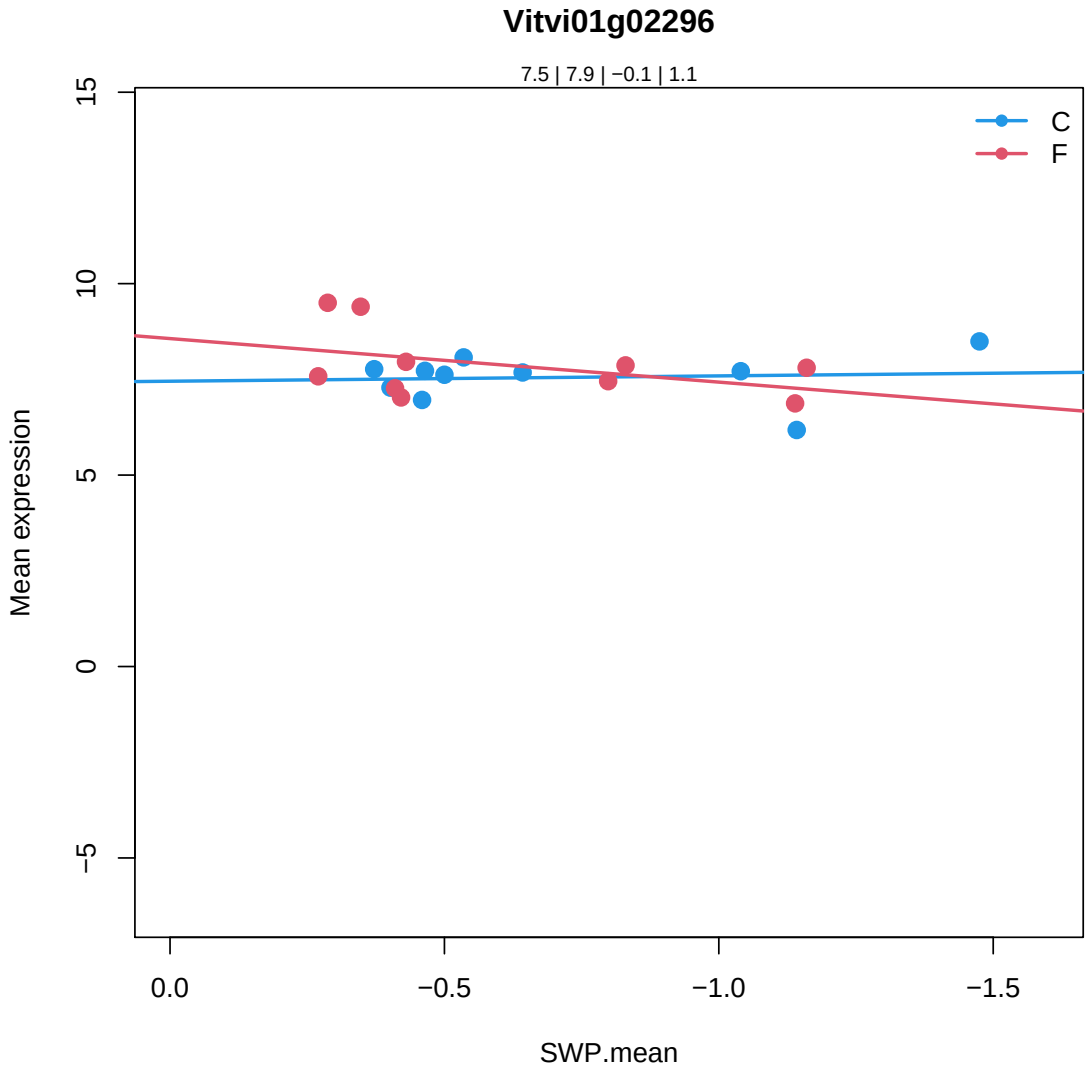
7.6.640 Vitvi01g02296: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g02296
        30.11
        signalling.light
        CCR-like protein |
        Chr3:9827868-9828461 FORWARD LENGTH=141 |
        201606
```

Coefficients for Vitvi01g02296.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.549058	4.895082e-20	***	2.607859e-19	***
SlopeC	-0.1392845	0.8257373		0.9652495	
MeanF-MeanC	0.3231307	0.3203931		0.6811354	
SlopeF-SlopeC	1.276258	0.1842064		0.9999488	



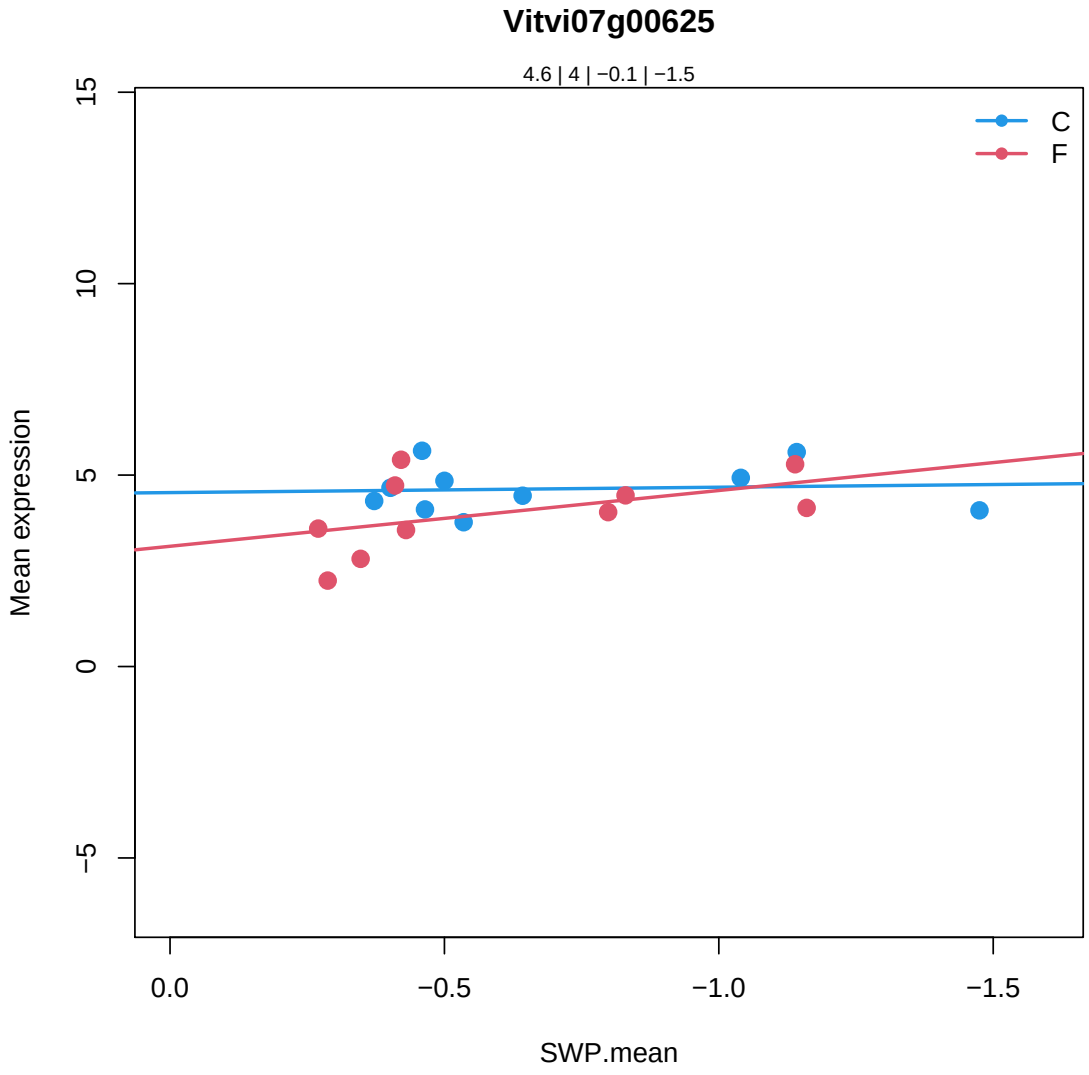
7.6.641 Vitvi07g00625: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g00625
        34.16
        transport.ABC transporters and multidrug resistance systems
        P-loop containing nucleoside triphosphate hydrolases superfamily prote
        Chr1:994084-995594 FORWARD LENGTH=226 |
        201606
```

Coefficients for Vitvi07g00625.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.641389	2.880111e-15	***	5.122363e-15	***
SlopeC	-0.1402892	0.8316435		0.9669817	
MeanF-MeanC	-0.6136326	0.07787526	.	0.3148906	
SlopeF-SlopeC	-1.316528	0.1889343		0.9999488	



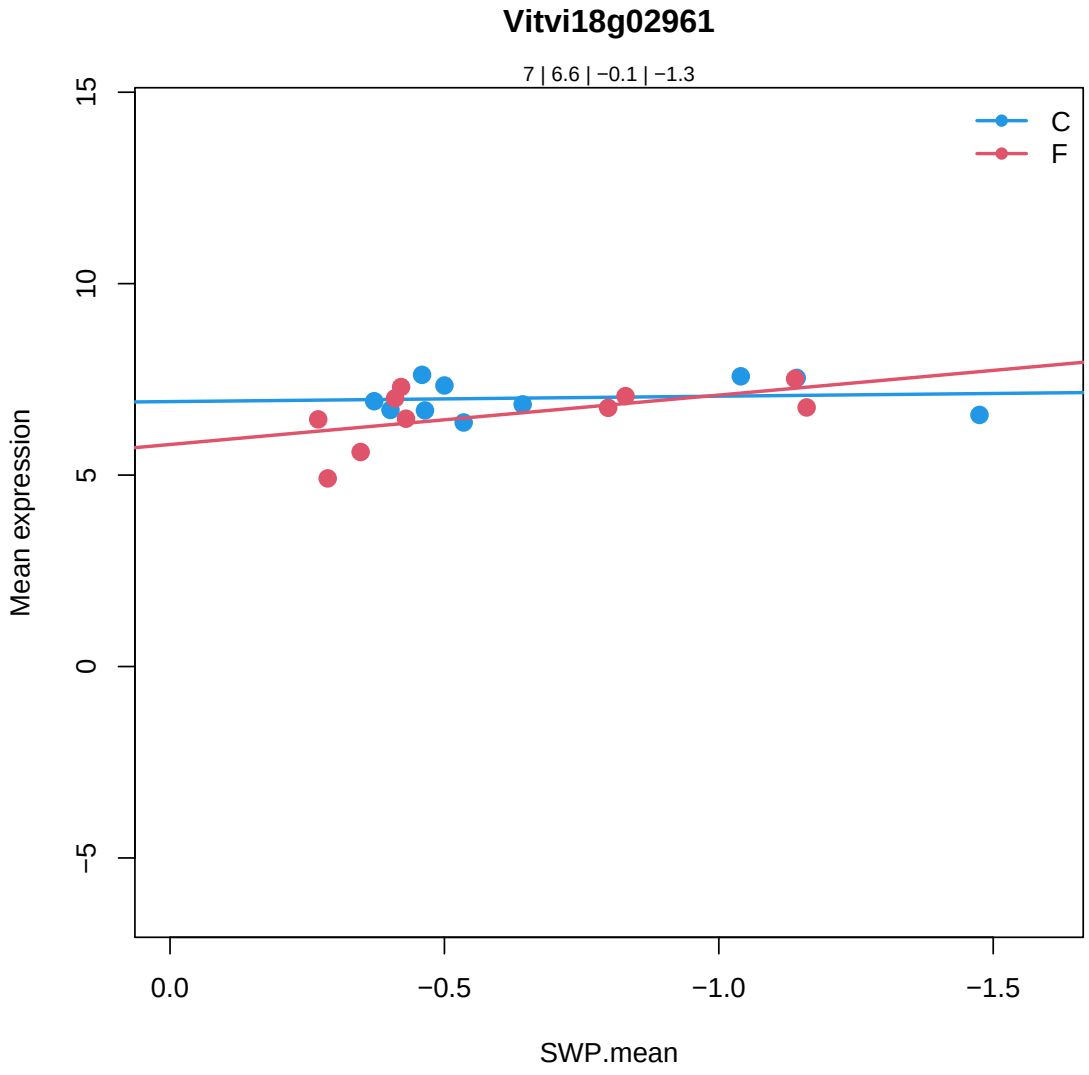
7.6.642 Vitvi18g02961: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02961
        1.1.2.1
        PS.lightreaction.photosystem I.LHC-I
        one-helix protein 2 |
        Chr1:12358151-12358902 REVERSE LENGTH=172 |
        201606
```

Coefficients for Vitvi18g02961.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.018345	2.499342e-21	***	2.335682e-20	***
SlopeC	-0.1415248	0.7818147		0.9530067	
MeanF-MeanC	-0.4335404	0.1054861		0.3771414	
SlopeF-SlopeC	-1.148905	0.1407109		0.9999488	



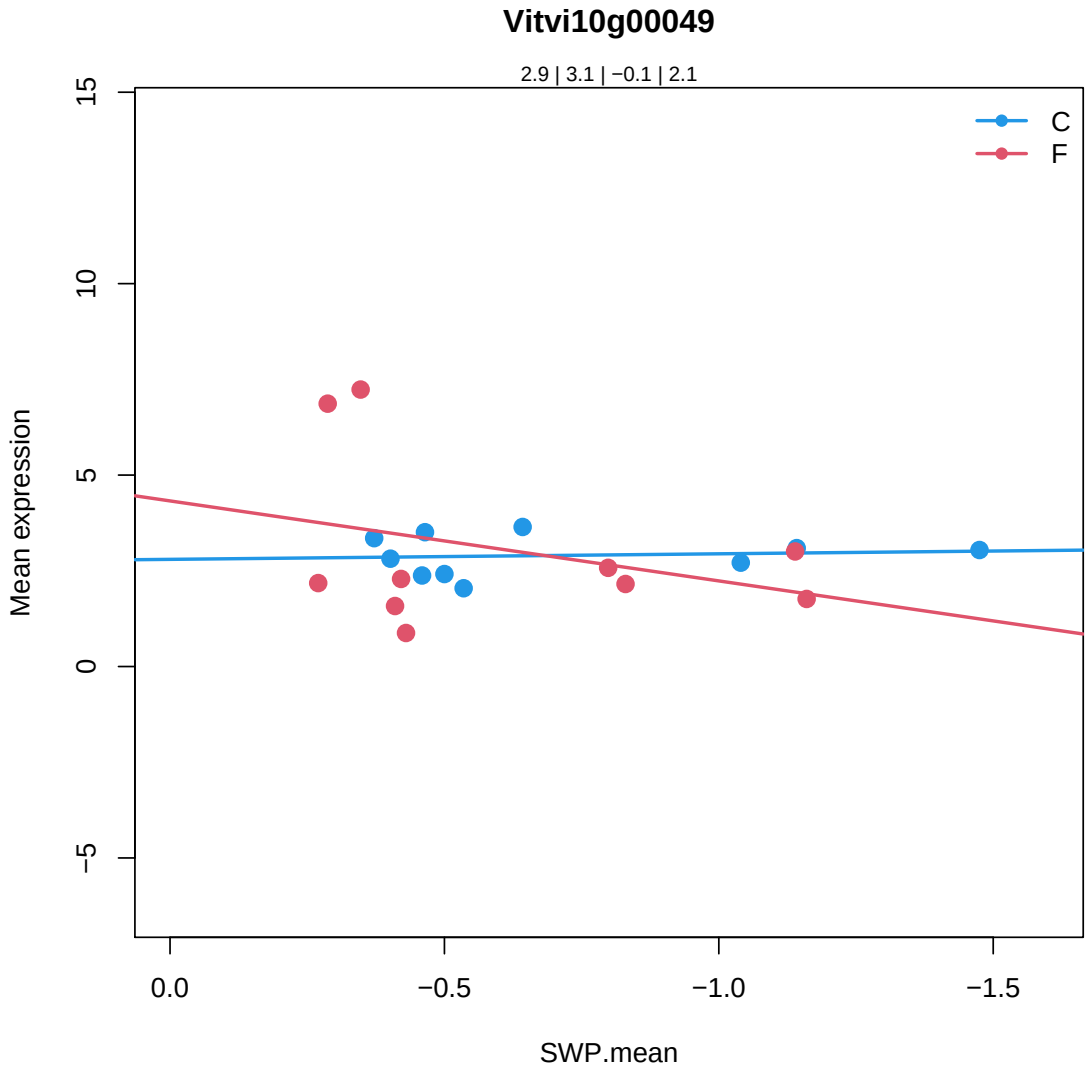
7.6.643 Vitvi10g00049: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00049
        35.2
        not assigned.unknown
        Chaperonin-like RbcX protein |
        Chr4:2116700-2118563 REVERSE LENGTH=174 |
        201606
```

Coefficients for Vitvi10g00049.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.900545	1.569081e-06	***	1.803207e-06	***
SlopeC	-0.1446943	0.9076268		0.9837899	
MeanF-MeanC	0.1517371	0.8109098		0.9474118	
SlopeF-SlopeC	2.234213	0.2364319		0.9999488	



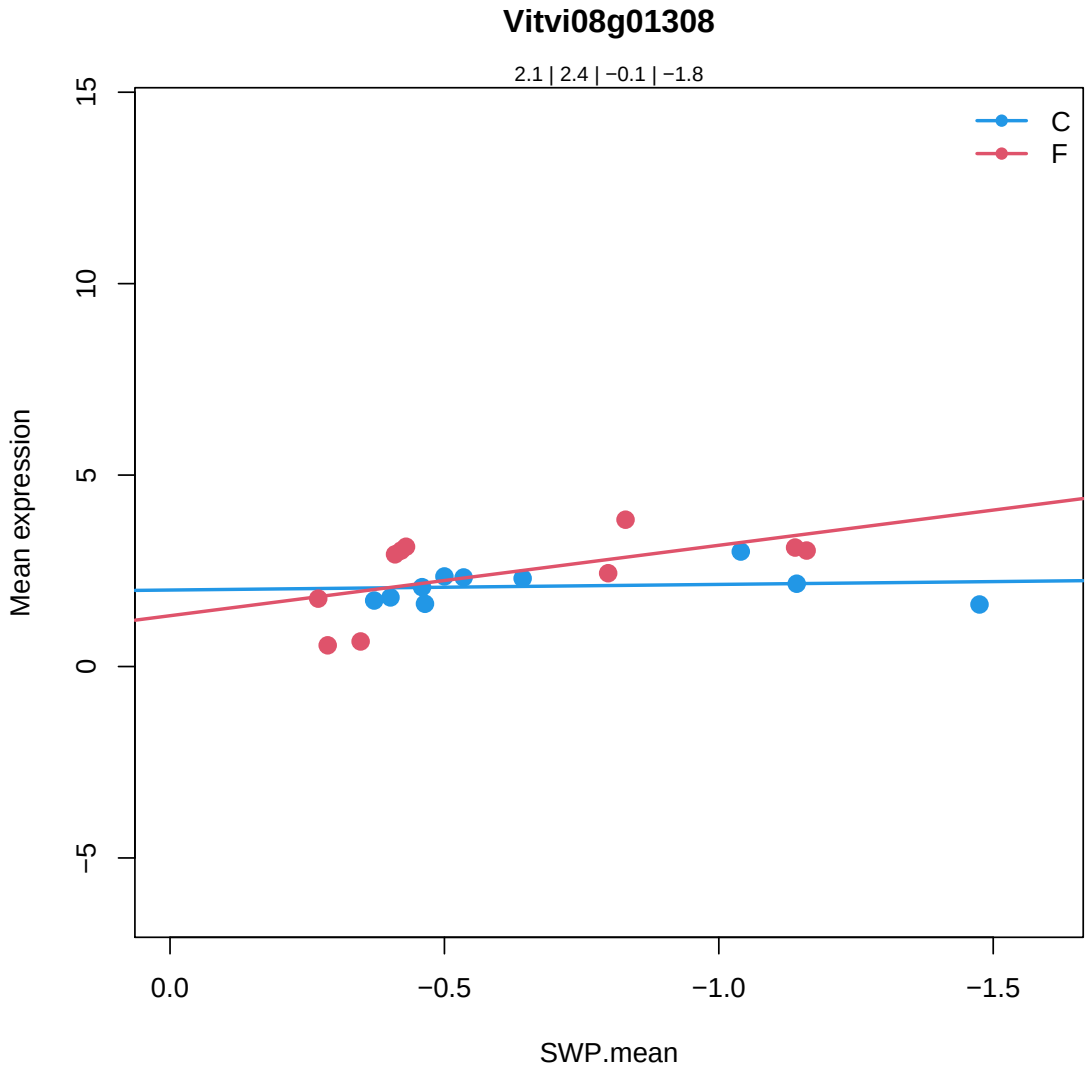
7.6.644 Vitvi08g01308: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01308
        17.2
        hormone metabolism.auxin
        O-fucosyltransferase family protein |
        Chr2:15894162-15897452 REVERSE LENGTH=638 |
        201606
```

Coefficients for Vitvi08g01308.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.100496	3.383772e-09	***	4.194149e-09	***
SlopeC	-0.146926	0.8120581		0.9594257	
MeanF-MeanC	0.3469194	0.2758675		0.639993	
SlopeF-SlopeC	-1.692049	0.0762798	.	0.9999488	



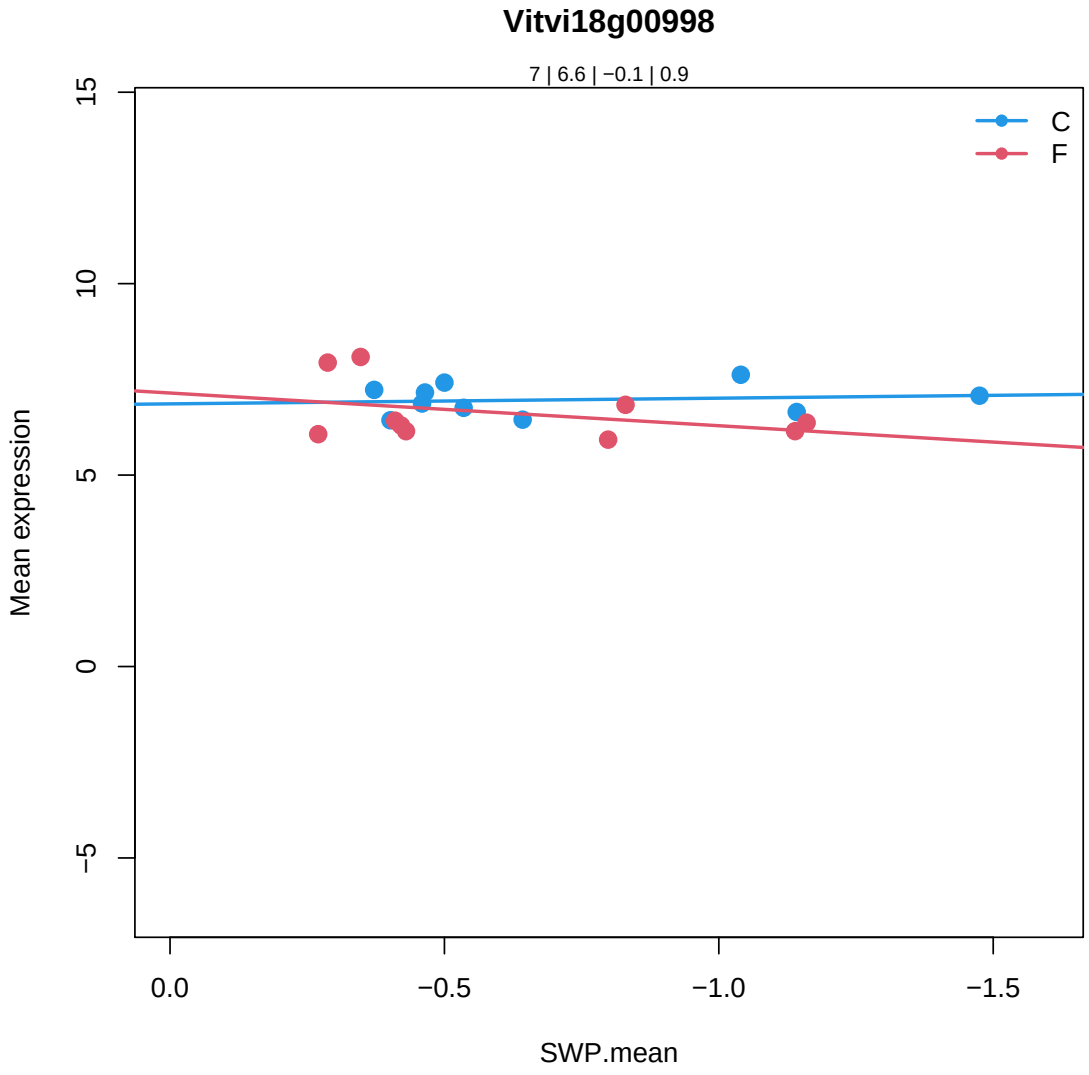
7.6.645 Vitvi18g00998: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00998
        20.2.4
        stress.abiotic.touch/wounding
        bifunctional nuclease in basal defense response 1 |
        Chr1:28281789-28283631 REVERSE LENGTH=325 |
        201606
```

Coefficients for Vitvi18g00998.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.964359	4.407025e-21	***	3.686711e-20	***
SlopeC	-0.1484221	0.7756888		0.9513135	
MeanF-MeanC	-0.3416549	0.2051434		0.5493677	
SlopeF-SlopeC	1.002236	0.2043329		0.9999488	



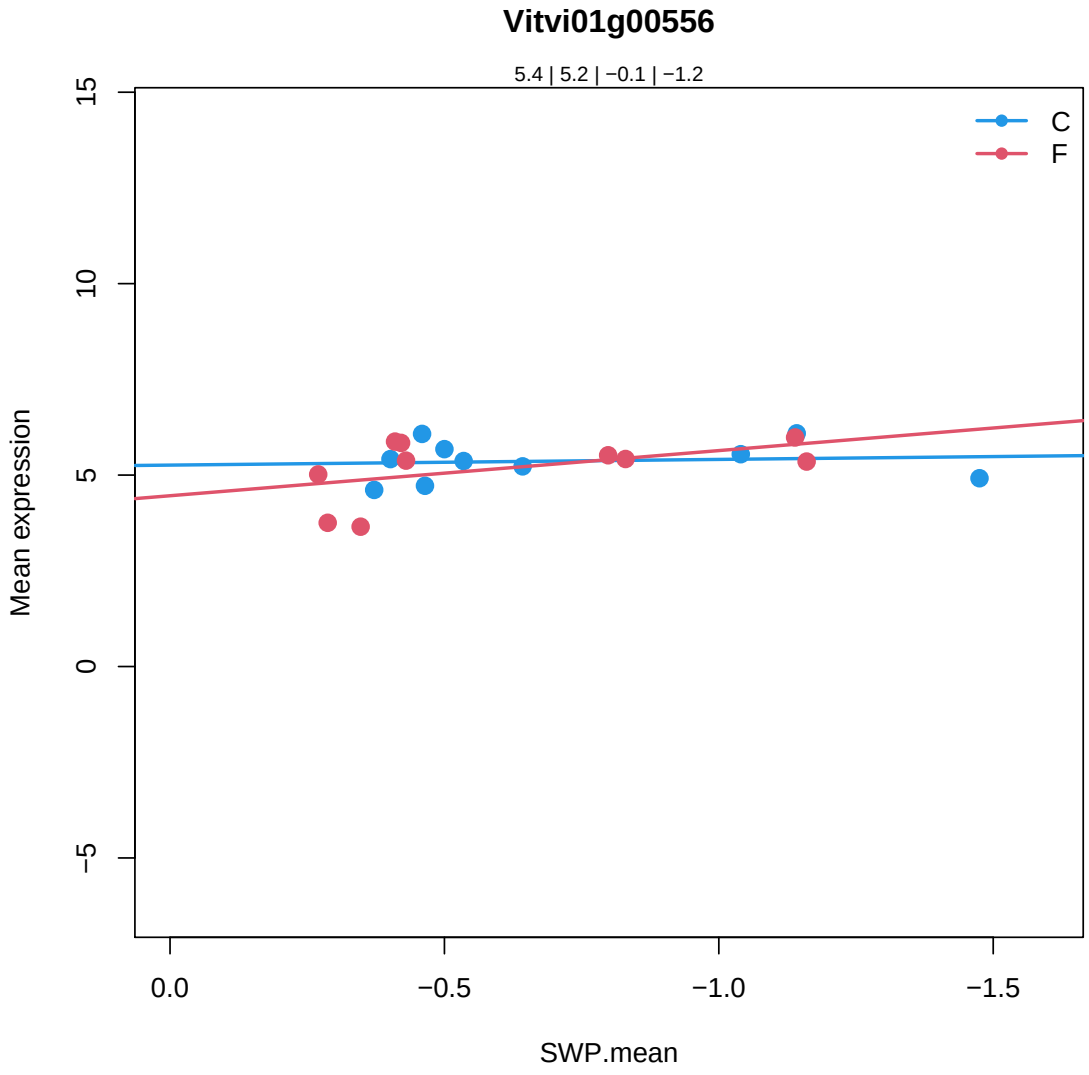
7.6.646 Vitvi01g00556: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00556
        16.8.2
        secondary metabolism.flavonoids.chalcones
        NAD(P)-linked oxidoreductase superfamily protein |
        Chr1:22071410-22073067 REVERSE LENGTH=326 |
        201606
```

Coefficients for Vitvi01g00556.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.364988	4.239001e-18	***	1.22369e-17	***
SlopeC	-0.1486872	0.7892685		0.9533712	
MeanF-MeanC	-0.1862615	0.511933		0.8136412	
SlopeF-SlopeC	-1.030551	0.22113		0.9999488	



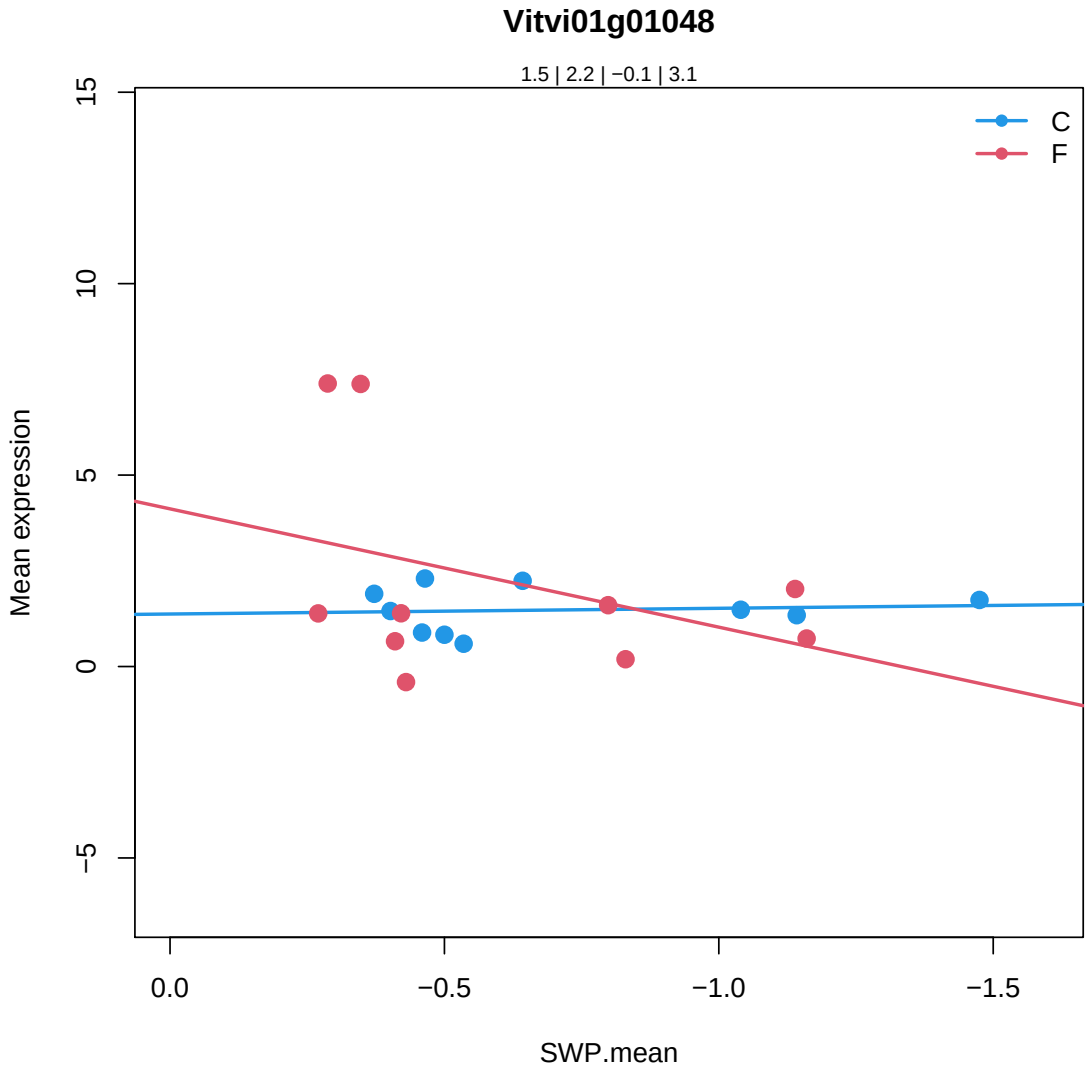
7.6.647 Vitvi01g01048: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01048
        35.2
        not assigned.unknown
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi01g01048.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.475931	0.0138706	*	0.01464402	*
SlopeC	-0.1494626	0.9232035		0.9858811	
MeanF-MeanC	0.7591408	0.3406161		0.7000202	
SlopeF-SlopeC	3.239226	0.1698987		0.9999488	



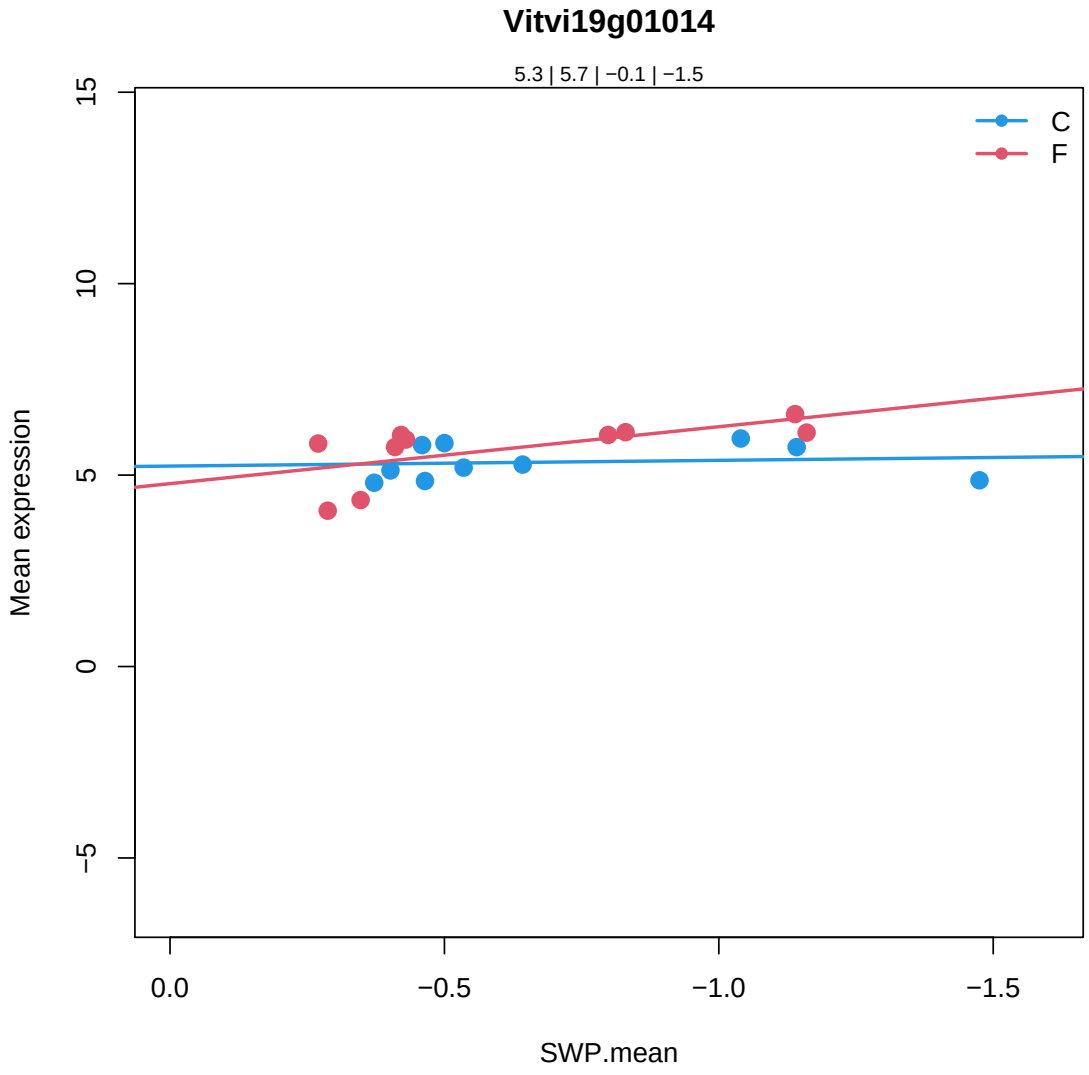
7.6.648 Vitvi19g01014: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g01014
        26.10
        misc.cytochrome P450
        cytochrome P450%2C family 72%2C subfamily A%2C polypeptide 15 |
        Chr3:4937410-4939310 FORWARD LENGTH=512 |
        201606
```

Coefficients for Vitvi19g01014.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.340224	4.367712e-19	***	1.686531e-18	***
SlopeC	-0.1498355	0.7629922		0.94868	
MeanF-MeanC	0.3418221	0.1846456		0.5211243	
SlopeF-SlopeC	-1.337111	0.08100206	.	0.9999488	



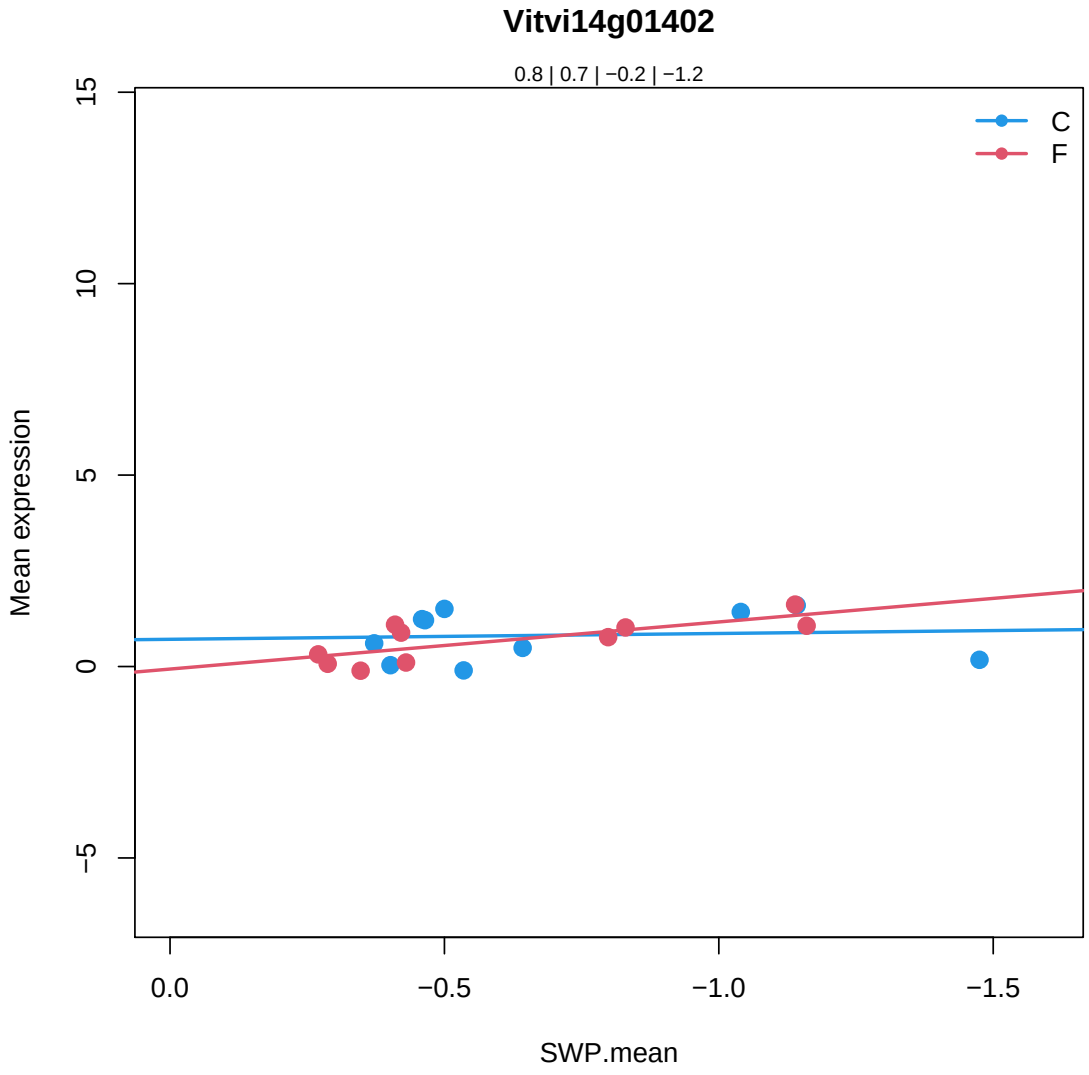
7.6.649 Vitvi14g01402: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01402
        35.1
        not assigned.no ontology
        Haloacid dehalogenase-like hydrolase (HAD) superfamily protein |
        Chr3:11589775-11591833 REVERSE LENGTH=559 |
        201606
```

Coefficients for Vitvi14g01402.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8175647	9.744588e-05	***	0.0001075893	***
SlopeC	-0.1521013	0.7526906		0.9472461	
MeanF-MeanC	-0.1346156	0.5841692		0.8536005	
SlopeF-SlopeC	-1.07843	0.1430178		0.9999488	



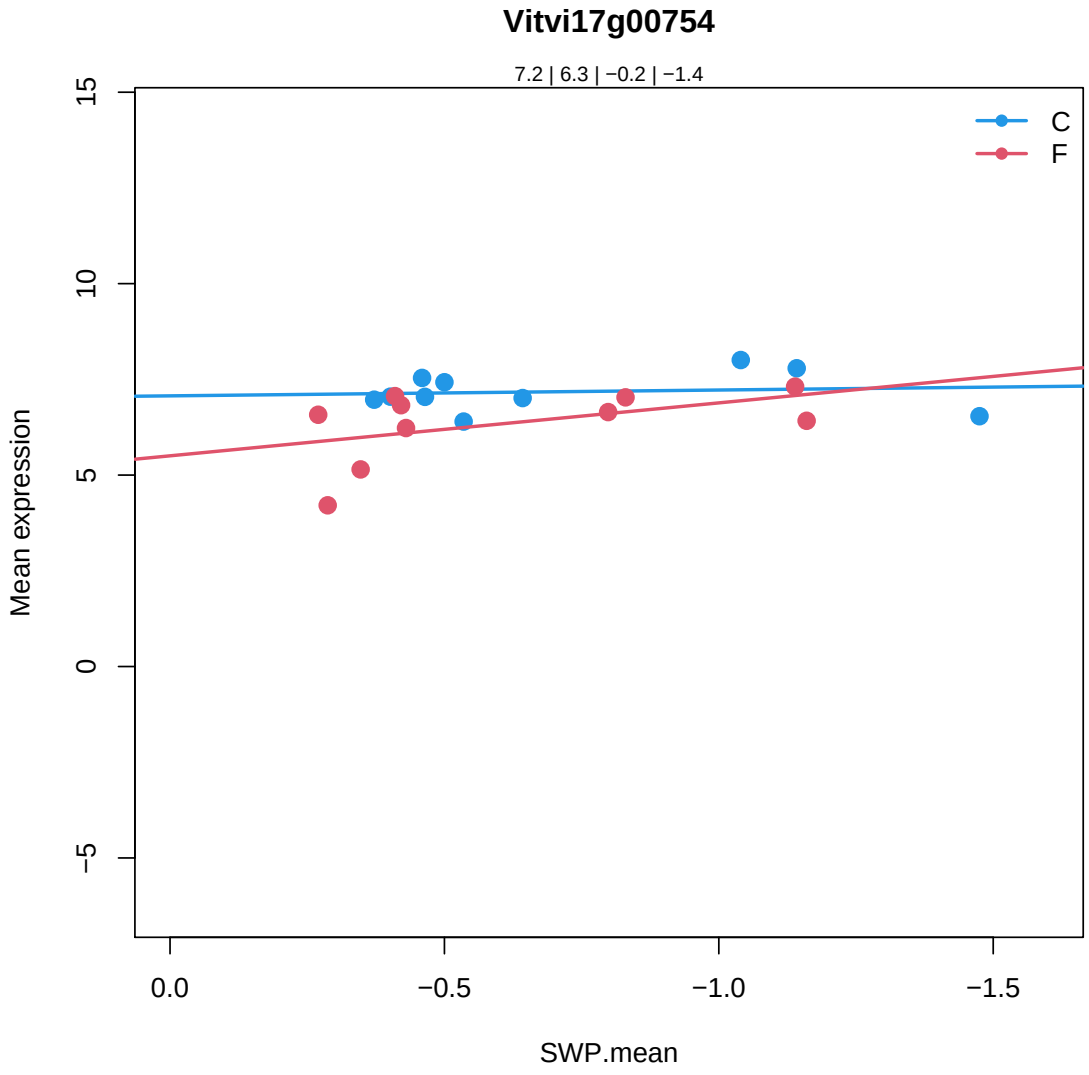
7.6.650 Vitvi17g00754: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00754
        35.2
        not assigned.unknown
        Putative thiol-disulfide oxidoreductase DCC |
        Chr5:20371916-20373172 FORWARD LENGTH=214 |
        201606
```

Coefficients for Vitvi17g00754.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.176409	5.702259e-20	***	2.955248e-19	***
SlopeC	-0.1523422	0.8014711		0.9568295	
MeanF-MeanC	-0.8311372	0.01233354	*	0.08871533	.
SlopeF-SlopeC	-1.230024	0.1814881		0.9999488	



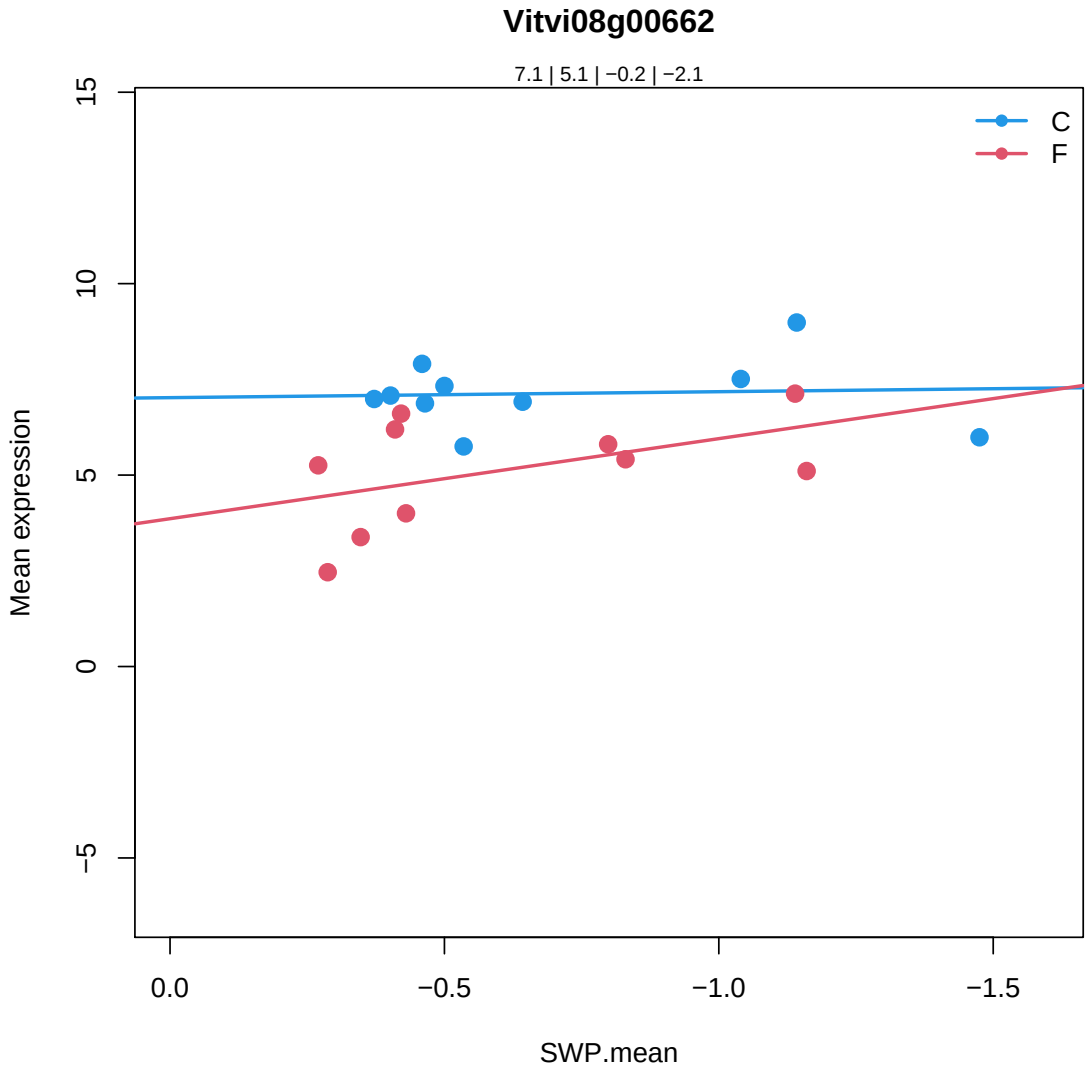
7.6.651 Vitvi08g00662: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g00662
        11.2.3
        lipid metabolism.FA desaturation.omega 3 desaturase
        fatty acid desaturase 7 |
        Chr3:3499959-3502126 FORWARD LENGTH=446 |
        201606
```

Coefficients for Vitvi08g00662.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.131549	5.18266e-16	***	1.007321e-15	***
SlopeC	-0.1554342	0.867576		0.975839	
MeanF-MeanC	-1.997009	0.0003312959	***	0.005009536	**
SlopeF-SlopeC	-1.935515	0.1723518		0.9999488	



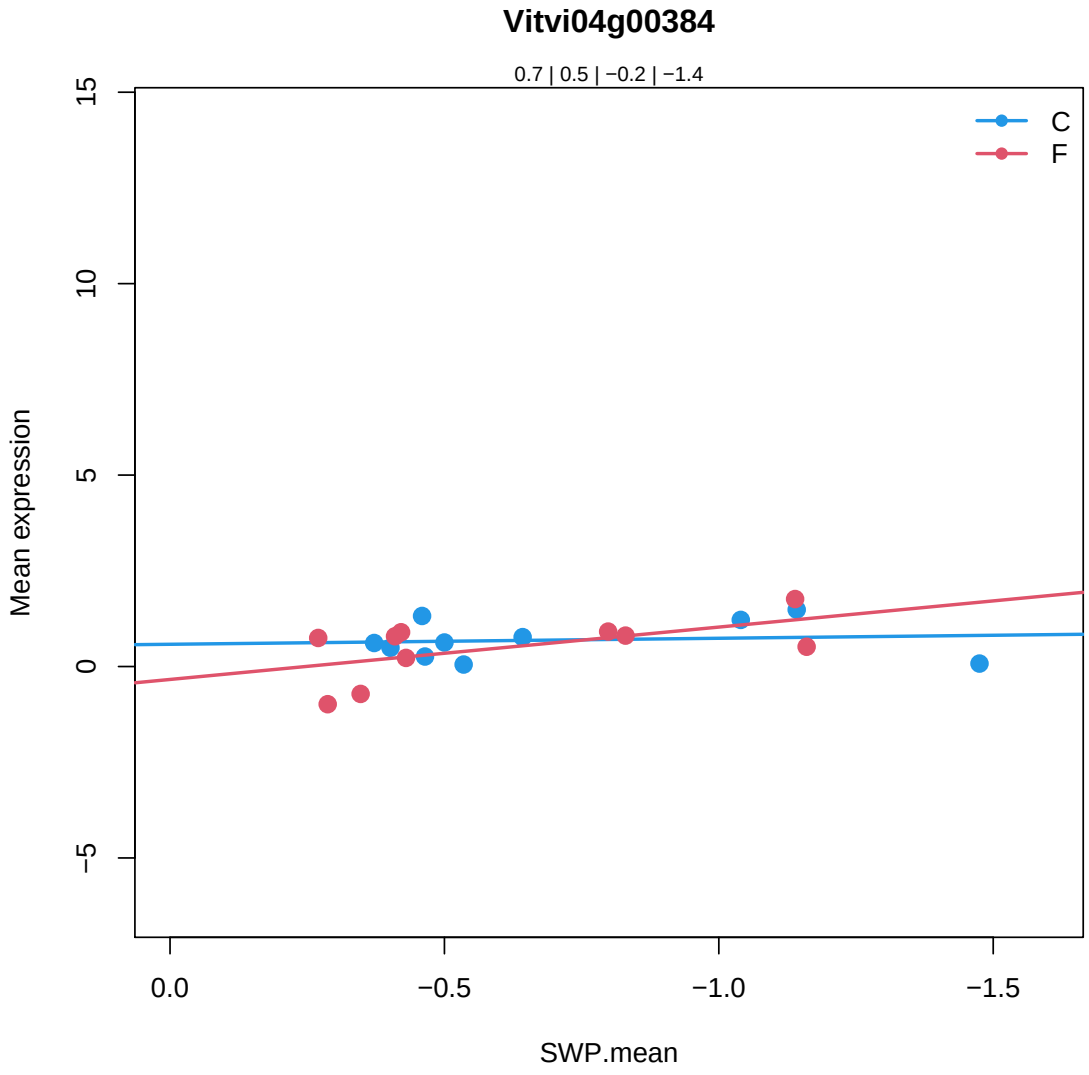
7.6.652 Vitvi04g00384: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00384
        35.2
        not assigned.unknown
        DNAse I-like superfamily protein |
        Chr1:16528880-16531065 REVERSE LENGTH=626 |
        201606
```

Coefficients for Vitvi04g00384.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6911406	0.001332214	**	0.001439093	**
SlopeC	−0.1569714	0.7663036		0.9497688	
MeanF−MeanC	−0.1957254	0.4682935		0.7879158	
SlopeF−SlopeC	−1.210766	0.1334078		0.9999488	



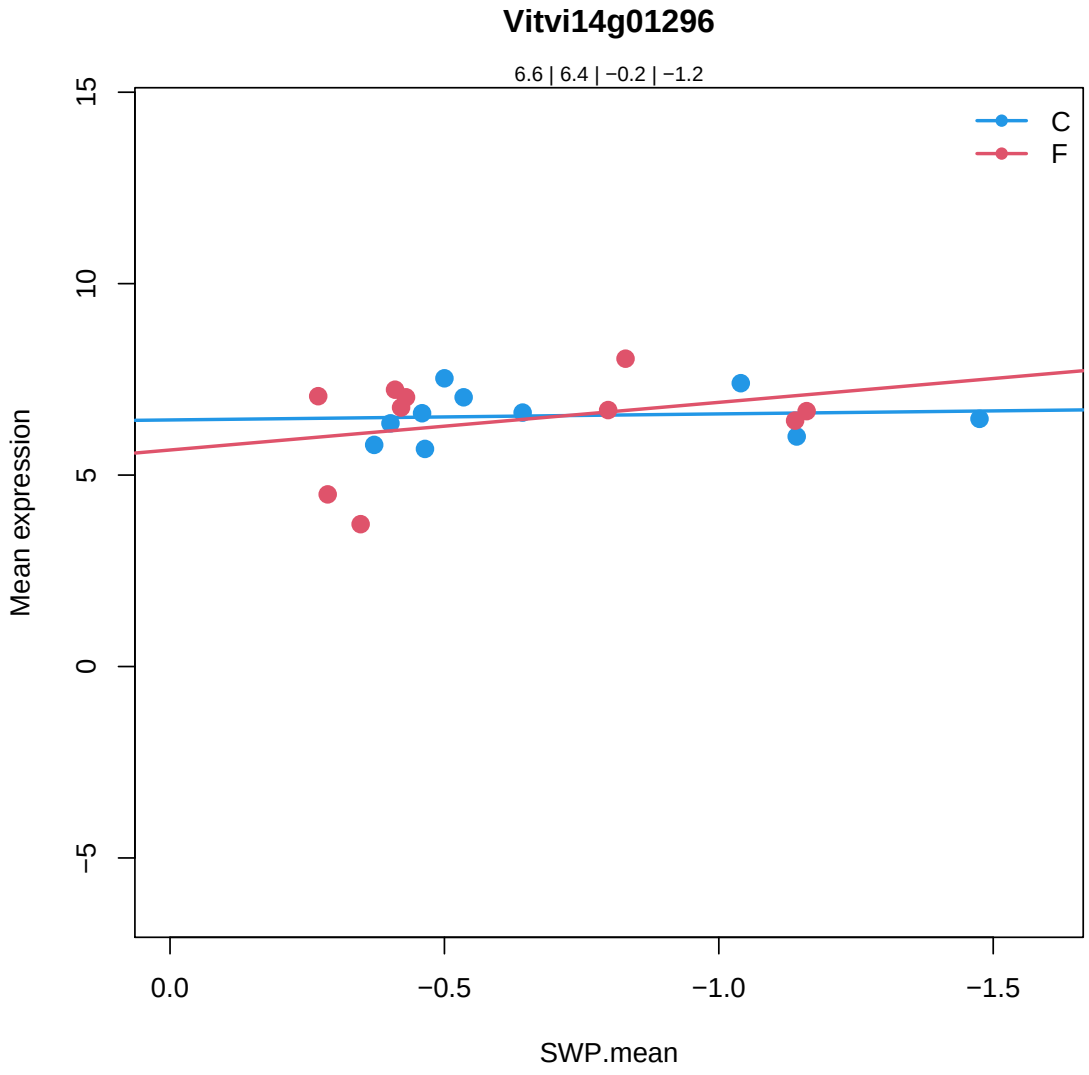
7.6.653 Vitvi14g01296: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01296
        27.3.7
        RNA.regulation of transcription.C2C2(Zn) Constans-like zinc finger fam
        B-box type zinc finger protein with CCT domain-containing protein |
        Chr5:5171873-5172697 REVERSE LENGTH=274 |
        201606
```

Coefficients for Vitvi14g01296.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.550534	2.604404e-16	***	5.283685e-16	***
SlopeC	-0.1576493	0.8490267		0.9719233	
MeanF-MeanC	-0.1374908	0.7441739		0.9245875	
SlopeF-SlopeC	-1.0871	0.3819434		0.9999488	



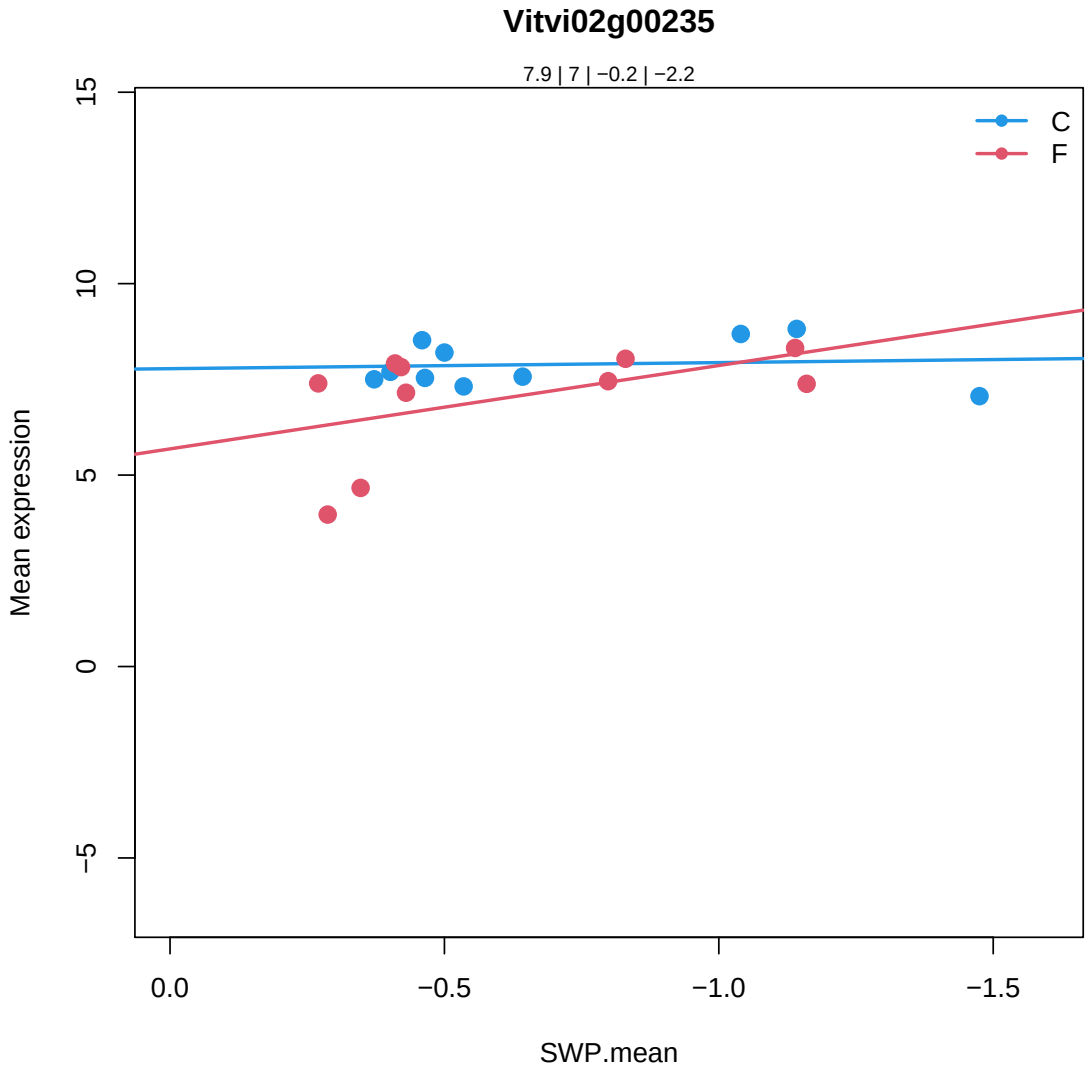
7.6.654 Vitvi02g00235: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00235
        35.2
        not assigned.unknown
        beta-carotene isomerase D27 |
        Chr1:24036071-24036768 FORWARD LENGTH=204 |
        201606
```

Coefficients for Vitvi02g00235.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.890663	7.696105e-18	***	2.084293e-17	***
SlopeC	-0.1585789	0.8505488		0.9719233	
MeanF-MeanC	-0.8800076	0.04950307	*	0.237403	
SlopeF-SlopeC	-2.019059	0.1174086		0.9999488	



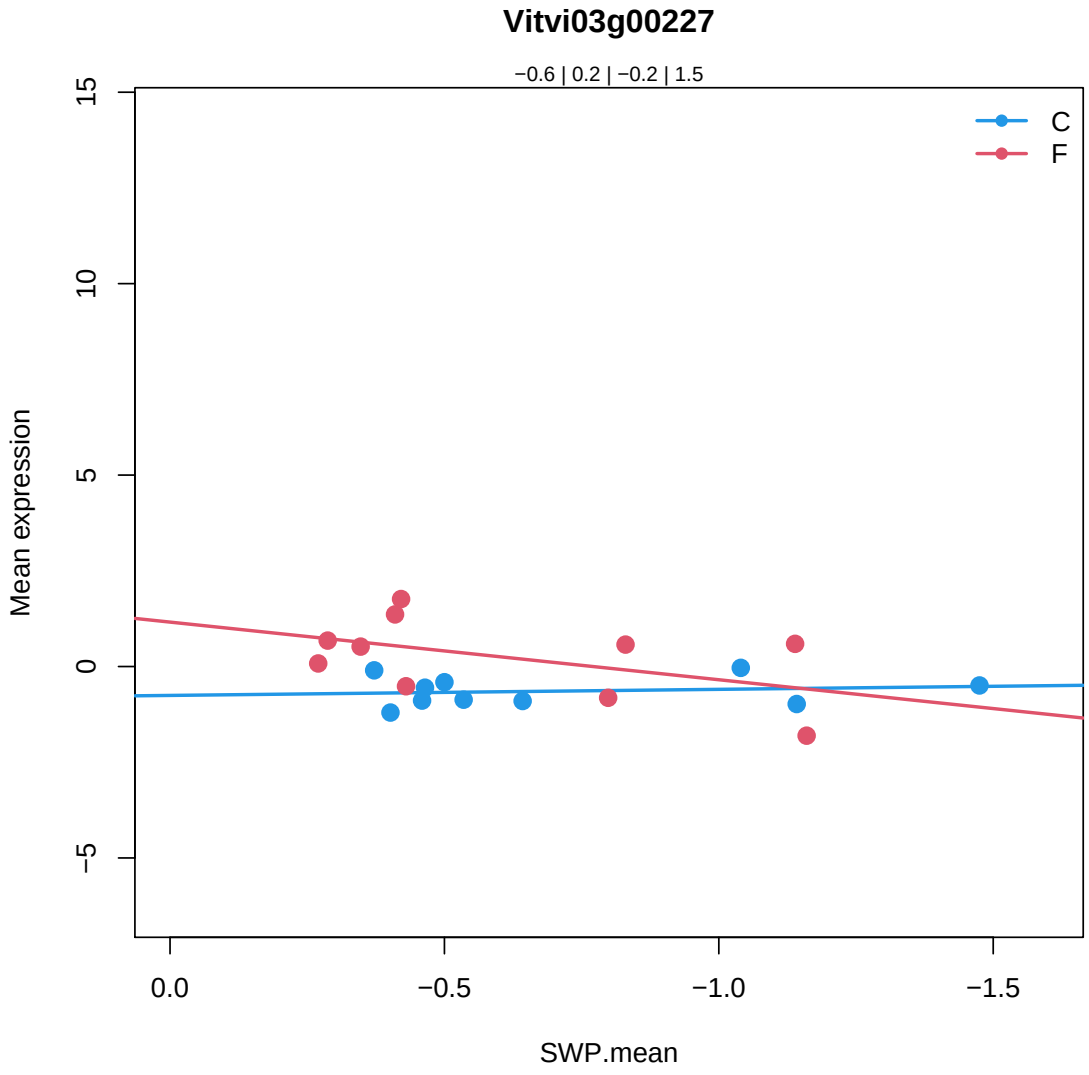
7.6.655 Vitvi03g00227: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00227
        29.5.11.4.2
        protein.degradation.ubiquitin.E3.RING
        Plant U-Box 15 |
        Chr5:16928086-16930367 REVERSE LENGTH=660 |
        201606
```

Coefficients for Vitvi03g00227.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	−0.643352	0.00752582	**	0.007995856	**
SlopeC	−0.158787	0.7960109		0.9558518	
MeanF−MeanC	0.885949	0.00898043	**	0.07019472	.
SlopeF−SlopeC	1.664433	0.07913165	.	0.9999488	



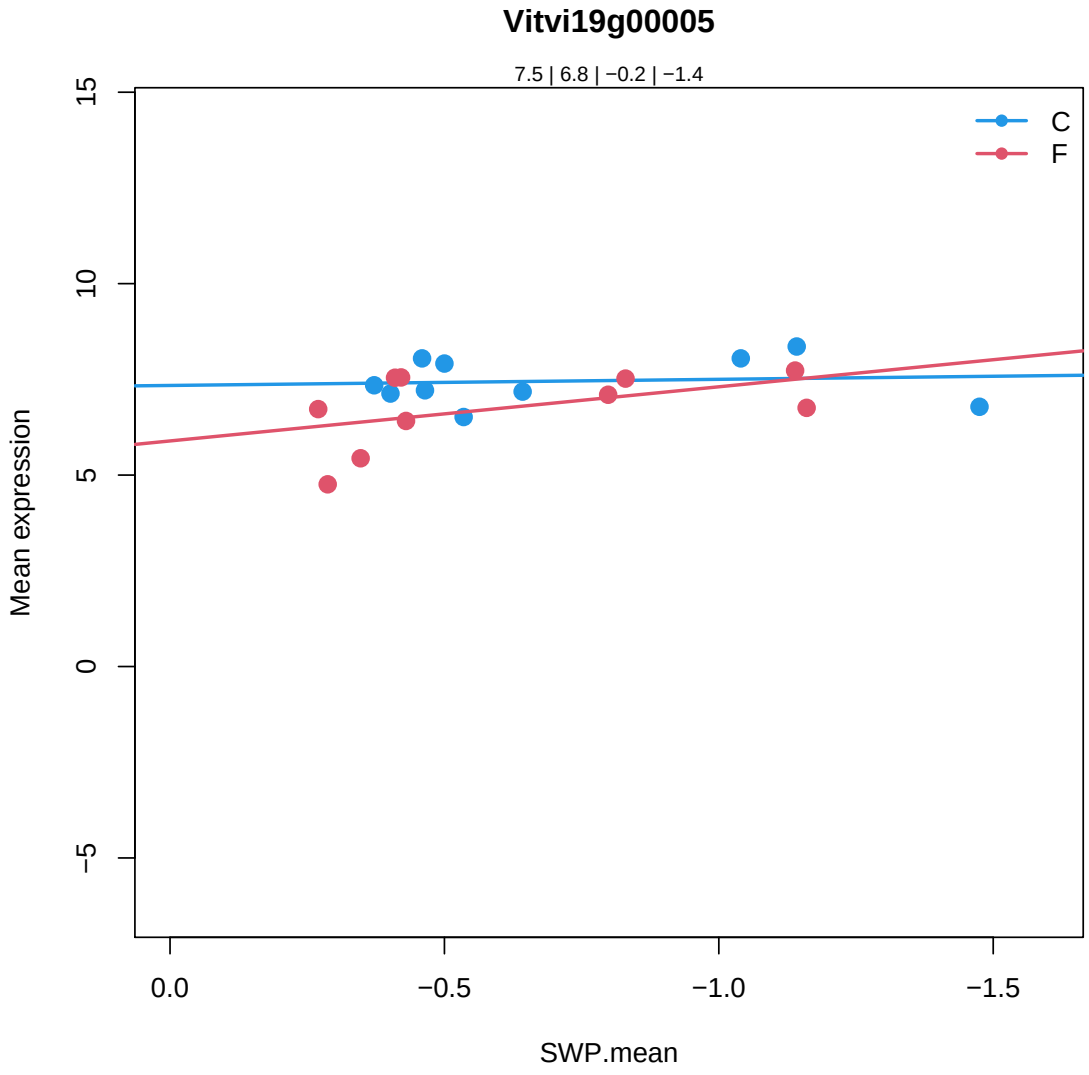
7.6.656 Vitvi19g00005: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g00005
        16.1.2.8
        secondary metabolism.isoprenoids.mevalonate pathway.geranyl diphosphat
        RNA polymerase subunit beta |
        ChrC:23111-26329 REVERSE LENGTH=1072 |
        201606
```

Coefficients for Vitvi19g00005.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.453364	9.194207e-20	***	4.450242e-19	***
SlopeC	-0.1598476	0.803878		0.9573096	
MeanF-MeanC	-0.7002716	0.04164351	*	0.2119905	
SlopeF-SlopeC	-1.25468	0.1988096		0.9999488	



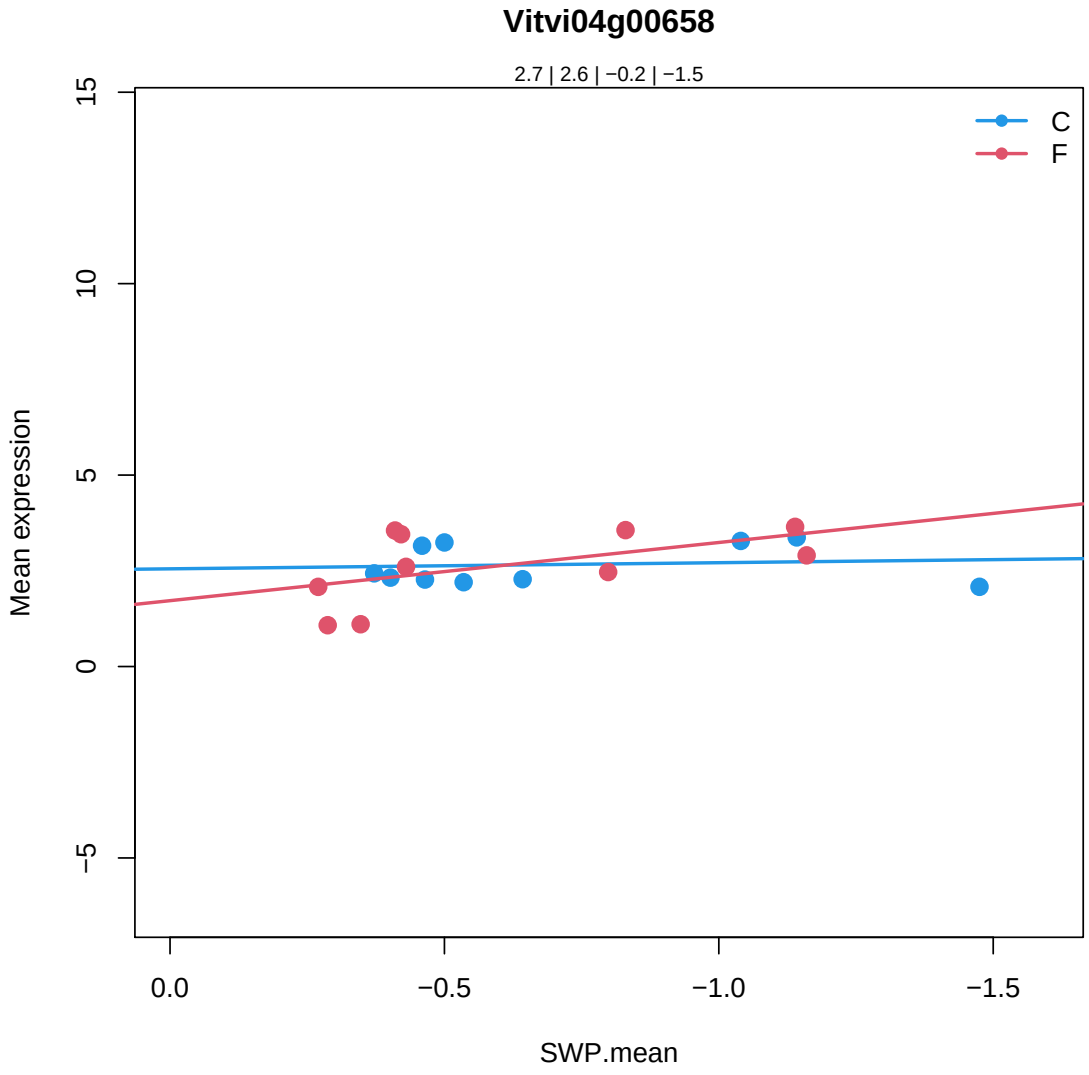
7.6.657 Vitvi04g00658: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00658
        20.1.2
        stress.biotic.receptors
        enhanced disease resistance-like protein (DUF1336) |
        Chr5:3399072-3399980 FORWARD LENGTH=302 |
        201606
```

Coefficients for Vitvi04g00658.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.663627	2.930268e-11	***	3.92126e-11	***
SlopeC	-0.159951	0.7912942		0.9539329	
MeanF-MeanC	-0.01819404	0.9527421		0.9884756	
SlopeF-SlopeC	-1.359767	0.1405179		0.9999488	



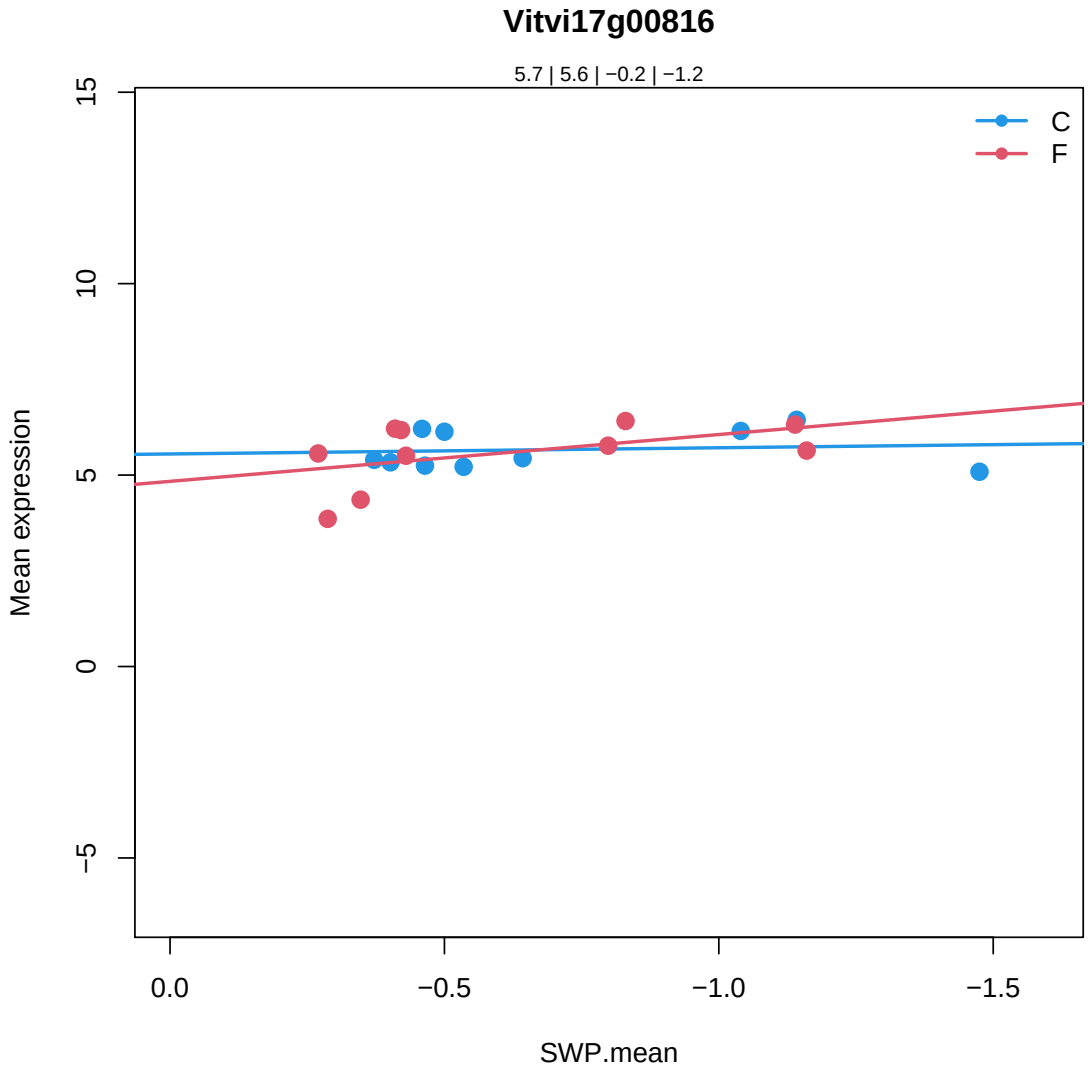
7.6.658 Vitvi17g00816: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00816
        16.1.1.2
        secondary metabolism.isoprenoids.non-mevalonate pathway.DXR
        1-deoxy-D-xylulose 5-phosphate reductoisomerase |
        Chr5:25214358-25217289 REVERSE LENGTH=497 |
        201606
```

Coefficients for Vitvi17g00816.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.665702	1.578266e-18	***	5.128104e-18	***
SlopeC	-0.1621067	0.7723992		0.9511155	
MeanF-MeanC	-0.08470659	0.7662296		0.9321541	
SlopeF-SlopeC	-1.060929	0.2114662		0.9999488	



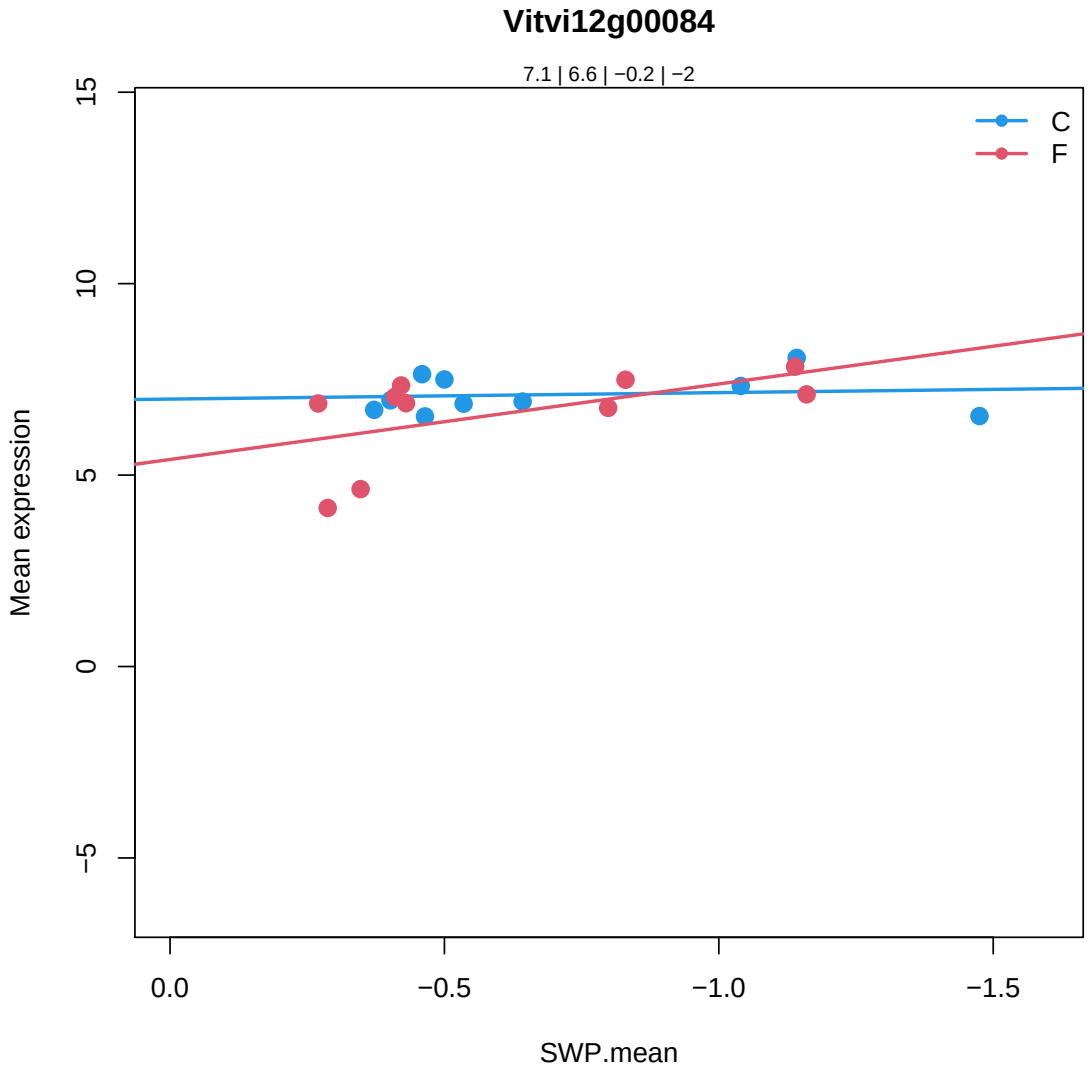
7.6.659 Vitvi12g00084: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00084
        16.1.4.1
        secondary metabolism.isoprenoids.carotenoids.phytoene synthase
        PHYTOENE SYNTHASE |
        Chr5:5659839-5662087 REVERSE LENGTH=422 |
        201606
```

Coefficients for Vitvi12g00084.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.103286	1.077671e-18	***	3.682101e-18	***
SlopeC	-0.1684573	0.80706		0.9576577	
MeanF-MeanC	-0.4942634	0.1679252		0.496438	
SlopeF-SlopeC	-1.803282	0.0895334	.	0.9999488	



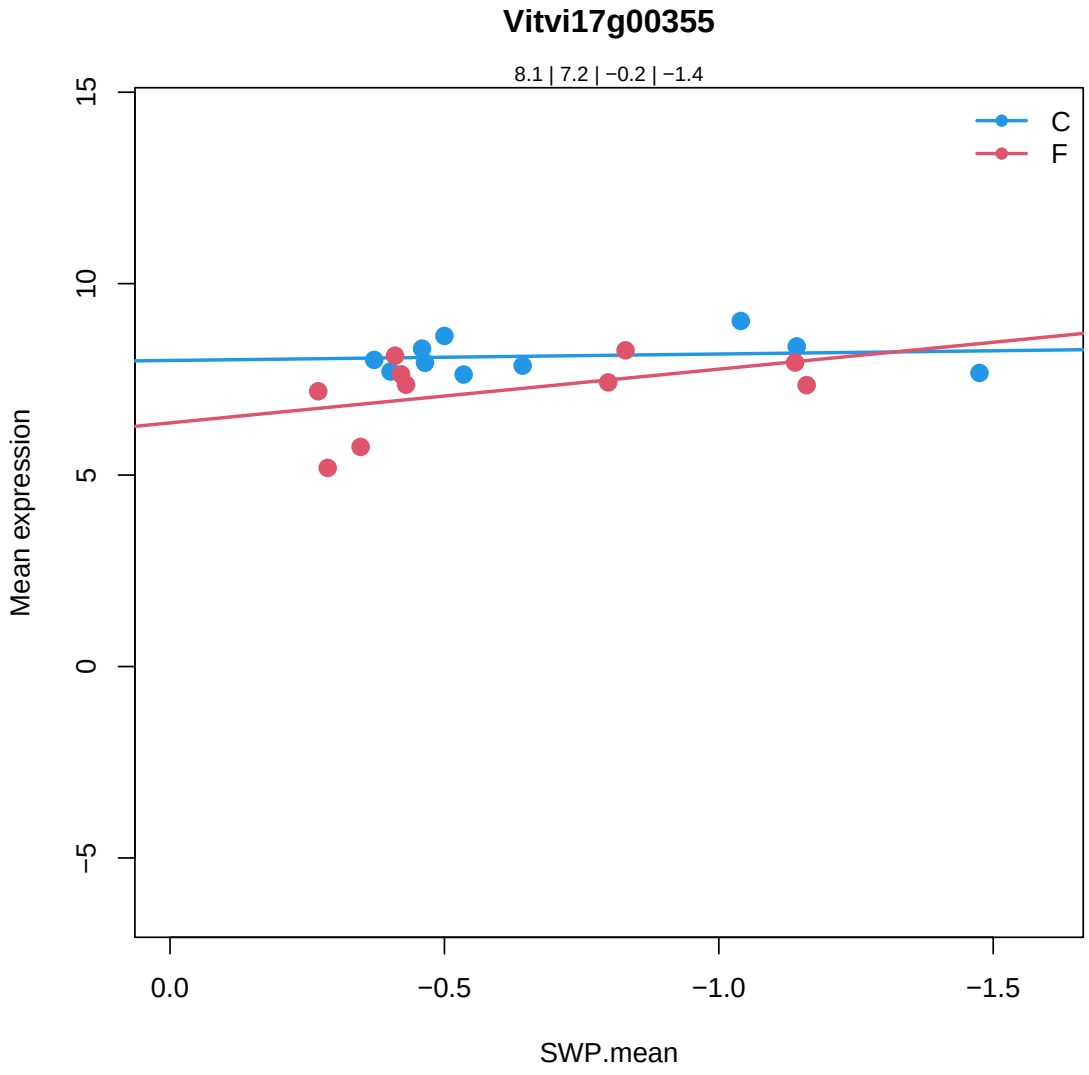
7.6.660 Vitvi17g00355: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00355
        29.2.1.1.3.2.1712
        protein.synthesis.ribosomal protein.prokaryotic.unknown organellar.50S
        Ribosomal protein L12/ ATP-dependent Clp protease adaptor protein ClpS
        Chr1:25778058-25779083 REVERSE LENGTH=159 |
        201606
```

Coefficients for Vitvi17g00355.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	8.111922	5.045689e-21	***	4.097304e-20	***
SlopeC	-0.1685632	0.7824927		0.9530067	
MeanF-MeanC	-0.8934033	0.008164247	**	0.06542558	.
SlopeF-SlopeC	-1.235	0.1829749		0.9999488	



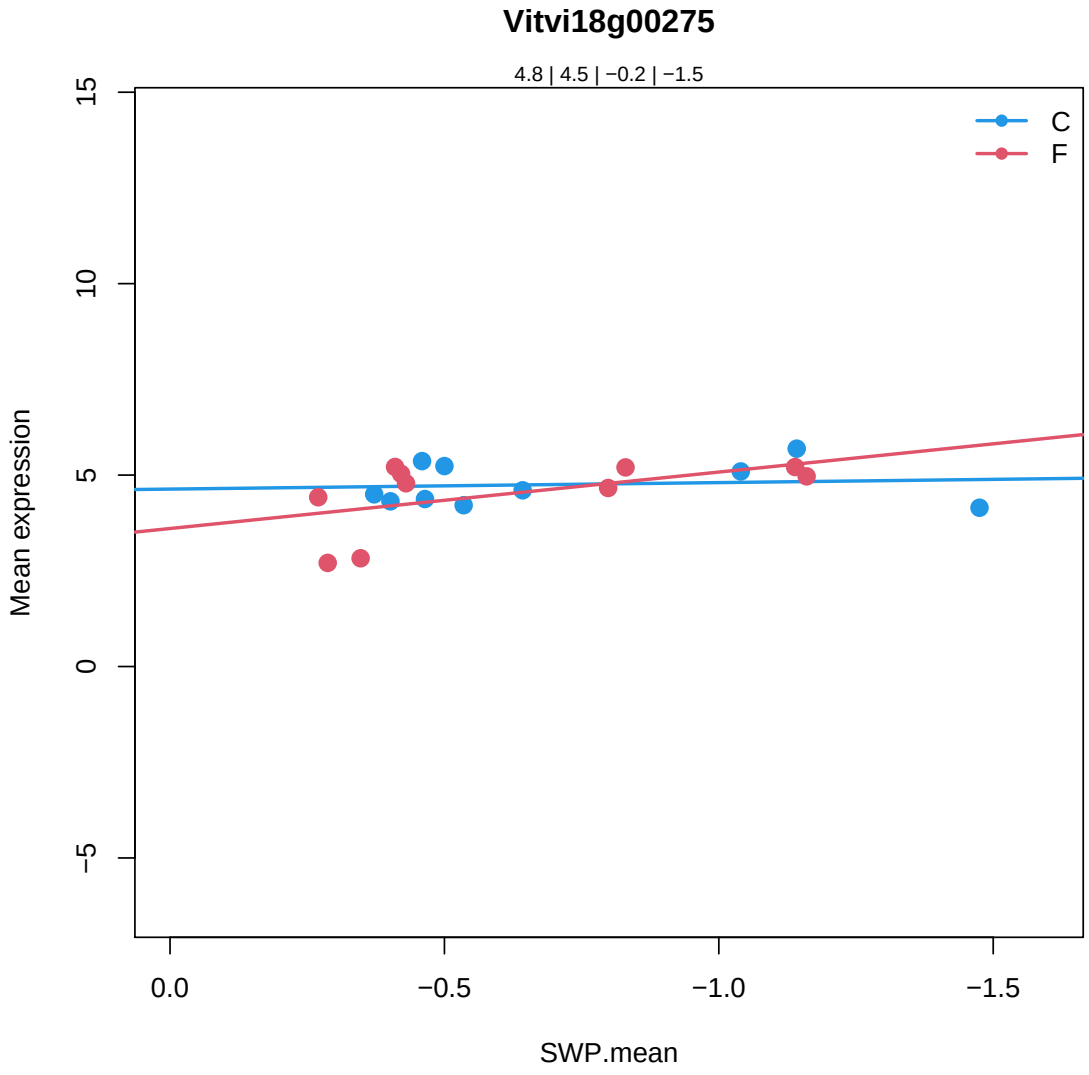
7.6.661 Vitvi18g00275: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00275
        11.1.9
        lipid metabolism.FA synthesis and FA elongation.long chain fatty acid
        long chain acyl-CoA synthetase 9 |
        Chr1:29148501-29151776 REVERSE LENGTH=691 |
        201606
```

Coefficients for Vitvi18g00275.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.753207	2.6426e-16	***	5.356185e-16	***
SlopeC	-0.1693399	0.7783635		0.9513135	
MeanF-MeanC	-0.2507727	0.4154929		0.7539575	
SlopeF-SlopeC	-1.304979	0.1545502		0.9999488	



7.6.662 Vitvi13g00019: type5

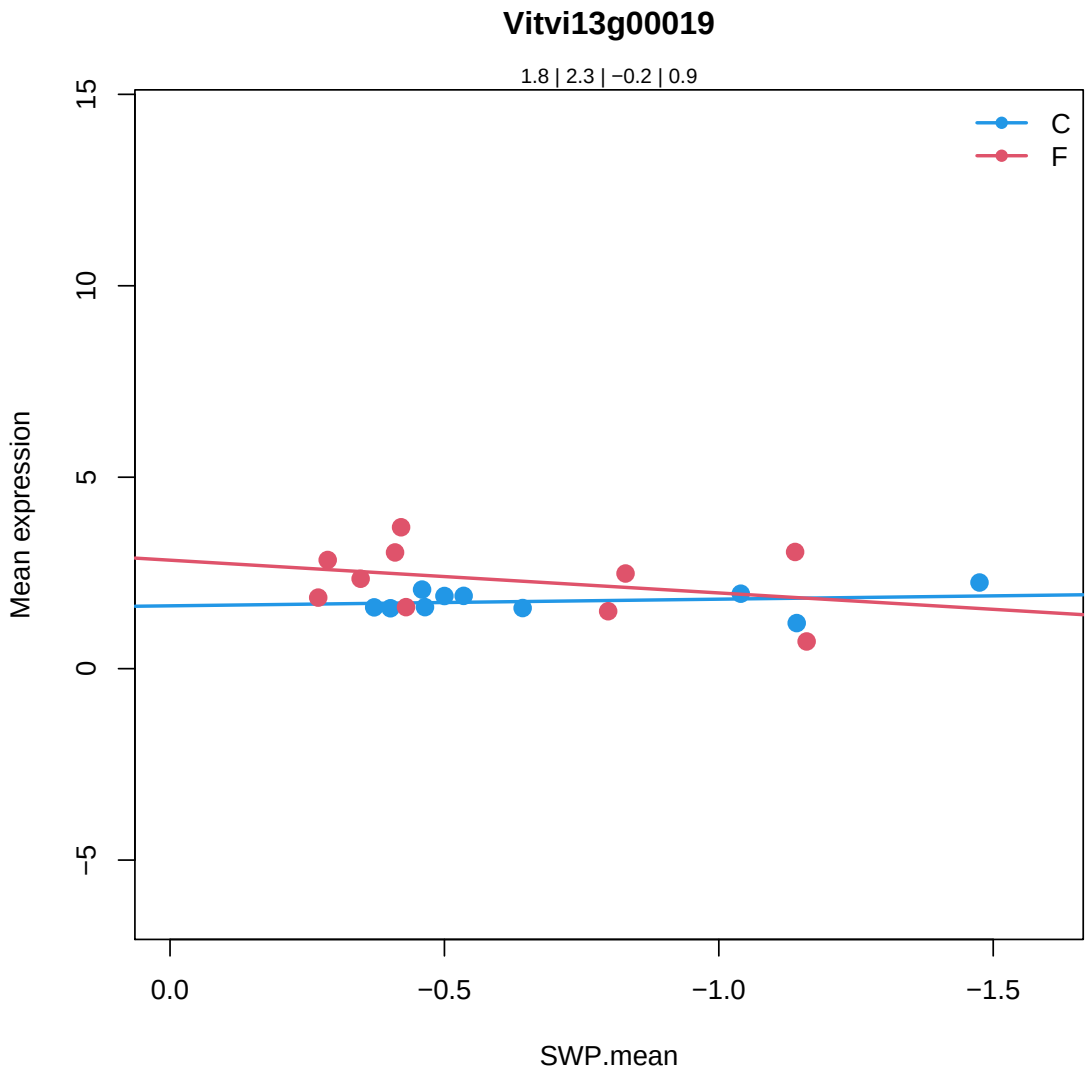
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00019
        34.3
        transport.amino acids
        Transmembrane amino acid transporter family protein |
        Chr2:15973493-15975972 FORWARD LENGTH=409 |
        201606

Vitvi13g00019
        17.2.2
        hormone metabolism.auxin.signal transduction
        Transmembrane amino acid transporter family protein |
        Chr2:15973493-15975972 FORWARD LENGTH=409 |
        201606
```

Coefficients for Vitvi13g00019.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.762644	1.379053e-08	***	1.675797e-08	***
SlopeC	-0.1734013	0.757966		0.9477286	
MeanF-MeanC	0.5490904	0.06508961	.	0.2826484	
SlopeF-SlopeC	1.028874	0.2268286		0.9999488	


Vitvi13g00019
1.8 | 2.3 | −0.2 | 0.9
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

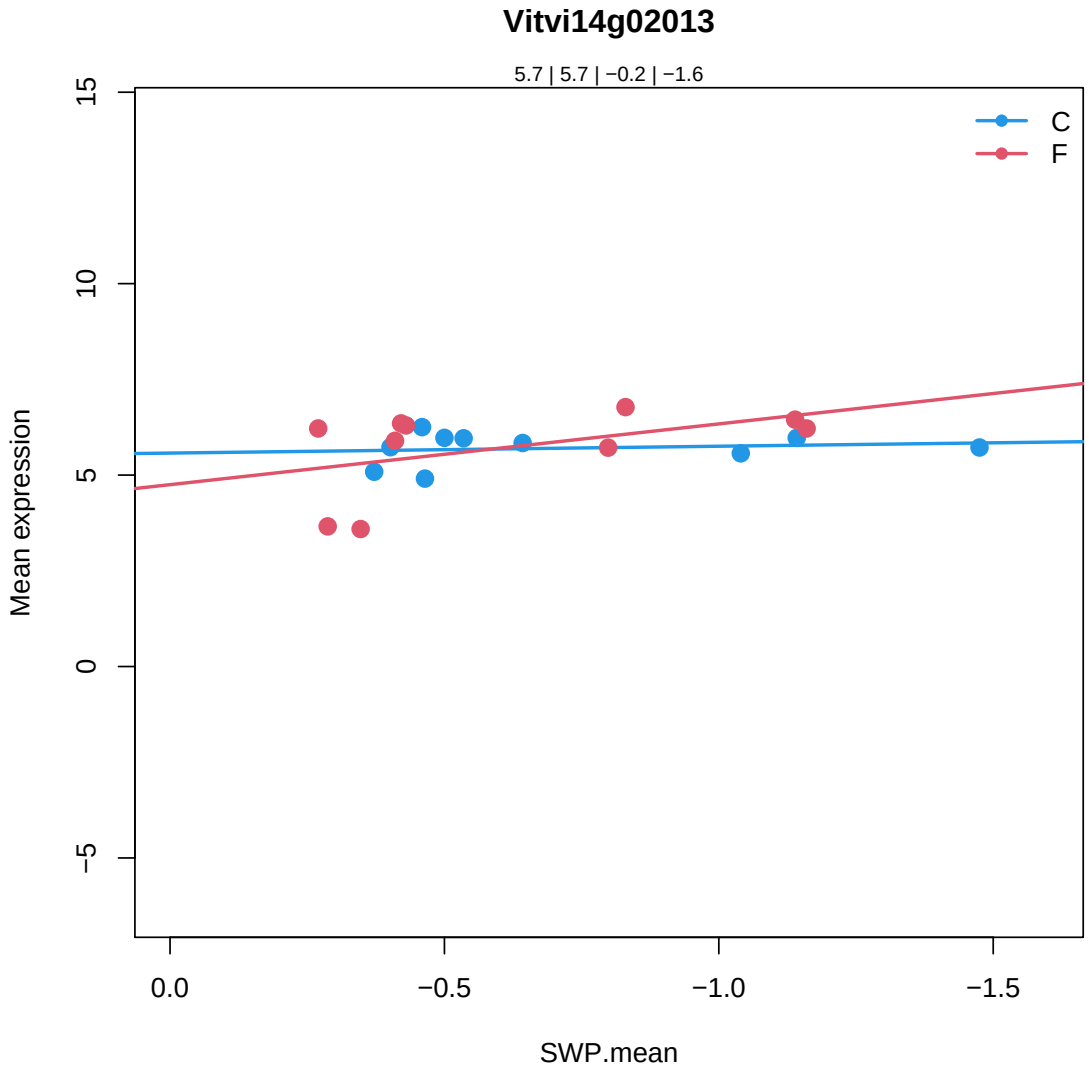
7.6.663 Vitvi14g02013: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g02013
        35.1
        not assigned.no ontology
        PPR containing protein (DUF179) |
        Chr3:11191780-11192868 FORWARD LENGTH=317 |
        201606
```

Coefficients for Vitvi14g02013.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.700437	4.399489e-17	***	1.018794e-16	***
SlopeC	-0.1786642	0.7871018		0.9533712	
MeanF-MeanC	0.01608431	0.9618185		0.9914232	
SlopeF-SlopeC	-1.408062	0.1620564		0.9999488	



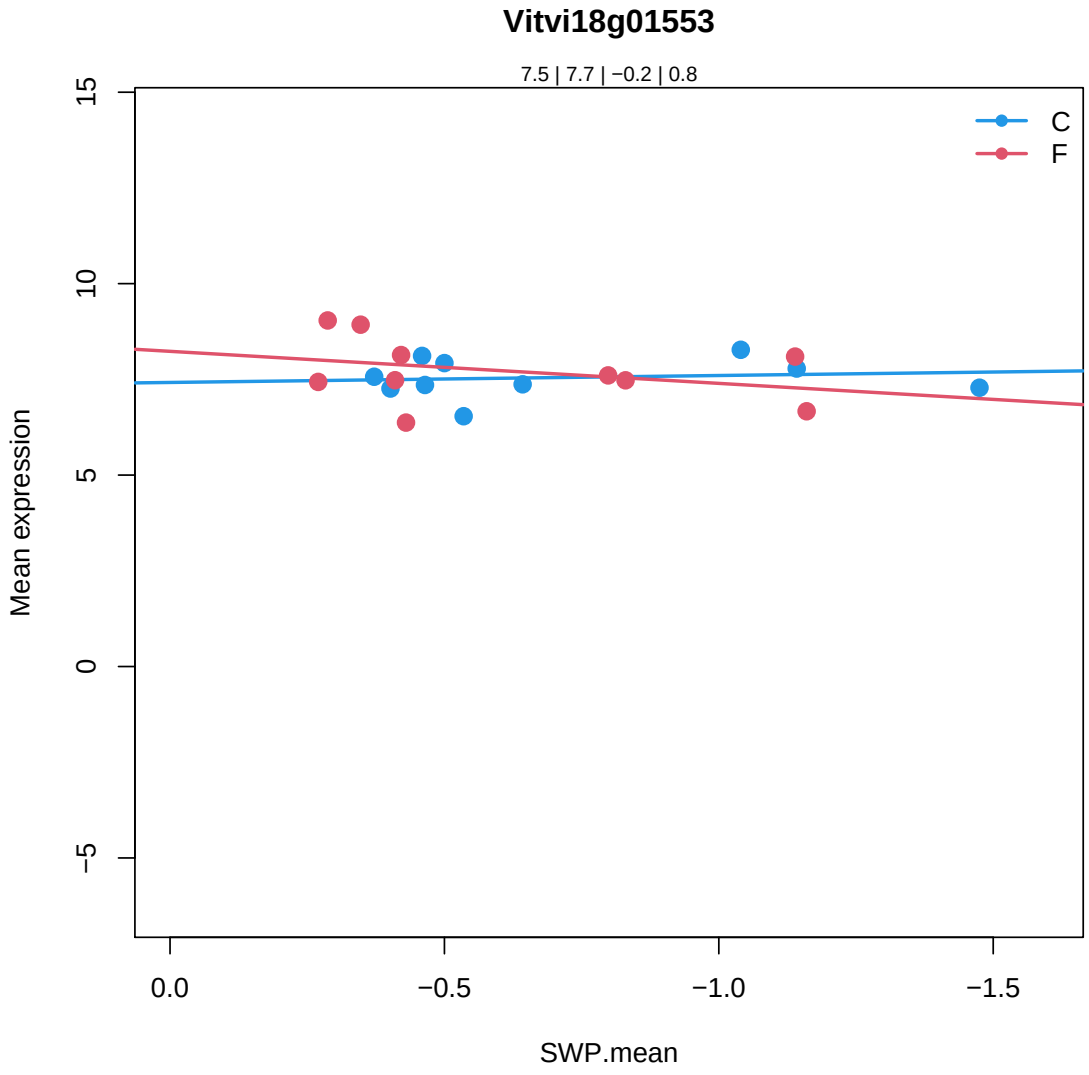
7.6.664 Vitvi18g01553: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g01553
        33.99
        development.unspecified
        gigantea protein (GI) |
        Chr1:8062398-8067447 FORWARD LENGTH=1173 |
        201606
```

Coefficients for Vitvi18g01553.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.546439	1.203216e-20	***	8.246139e-20	***
SlopeC	-0.1814408	0.7592326		0.9479775	
MeanF-MeanC	0.175831	0.5601647		0.8391185	
SlopeF-SlopeC	1.018233	0.2546555		0.9999488	



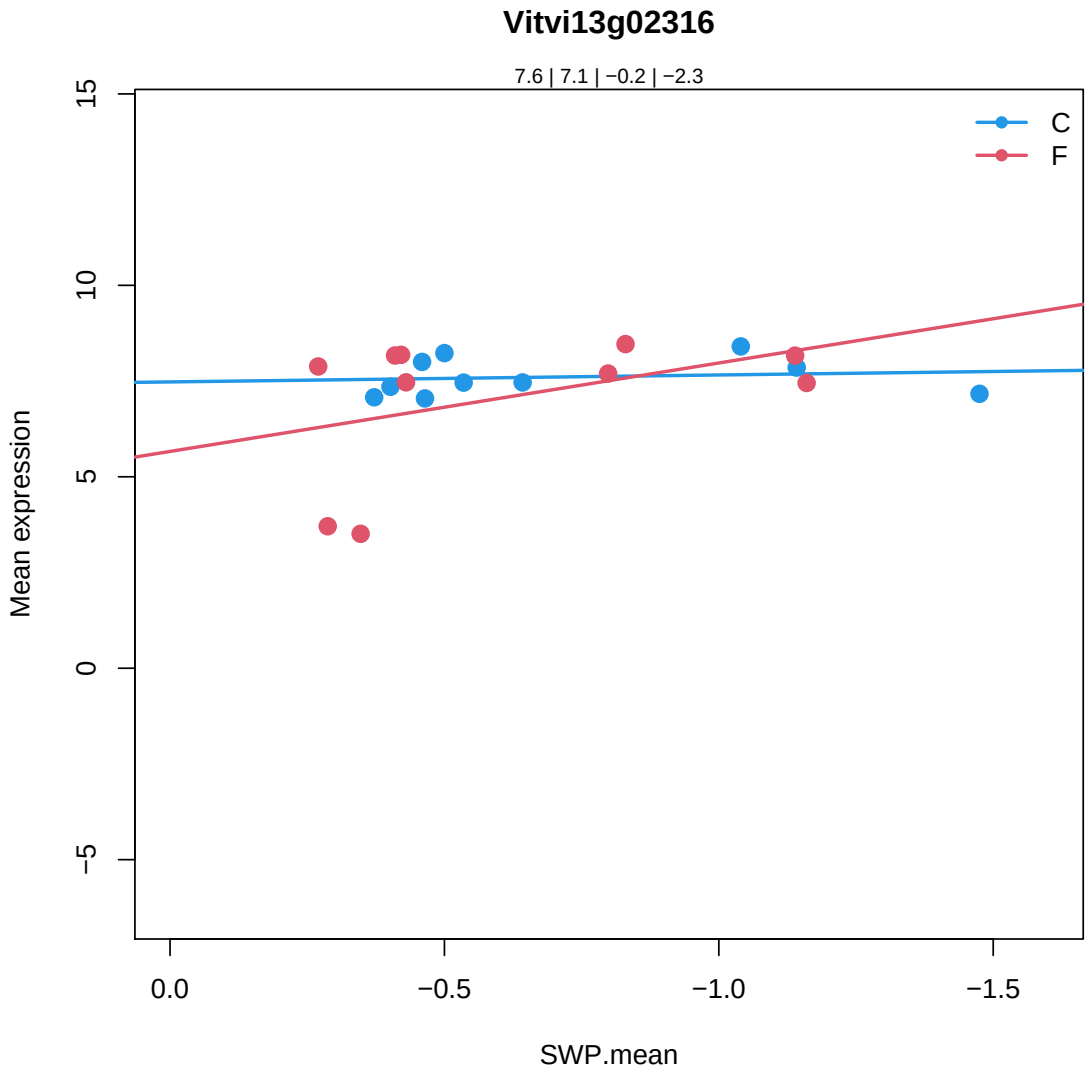
7.6.665 Vitvi13g02316: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g02316
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi13g02316.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.605129	1.054538e-15	***	1.968557e-15	***
SlopeC	-0.1815475	0.8599814		0.9737594	
MeanF-MeanC	-0.5356114	0.3116603		0.6758182	
SlopeF-SlopeC	-2.128751	0.1739056		0.9999488	



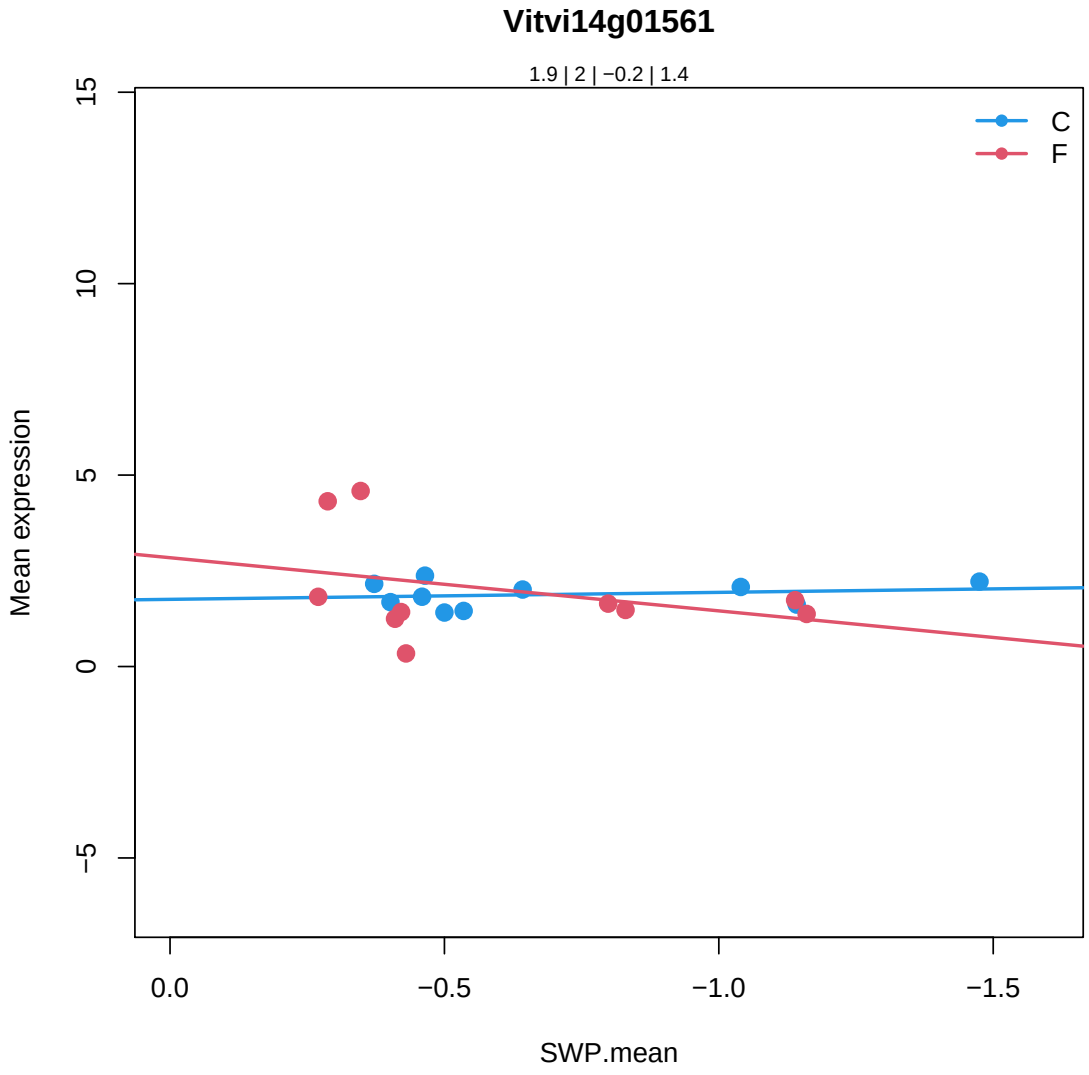
7.6.666 Vitvi14g01561: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01561
        29.2.2.3.3
        protein.synthesis.ribosome biogenesis.pre-rRNA processing and modifica
        S-adenosyl-L-methionine-dependent methyltransferases superfamily prote
        Chr3:10027163-10030062 REVERSE LENGTH=518 |
        201606
```

Coefficients for Vitvi14g01561.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.882139	1.067042e-06	***	1.231364e-06	***
SlopeC	-0.1820961	0.8173871		0.9609421	
MeanF-MeanC	0.1135771	0.7769946		0.9364656	
SlopeF-SlopeC	1.570496	0.1896602		0.9999488	



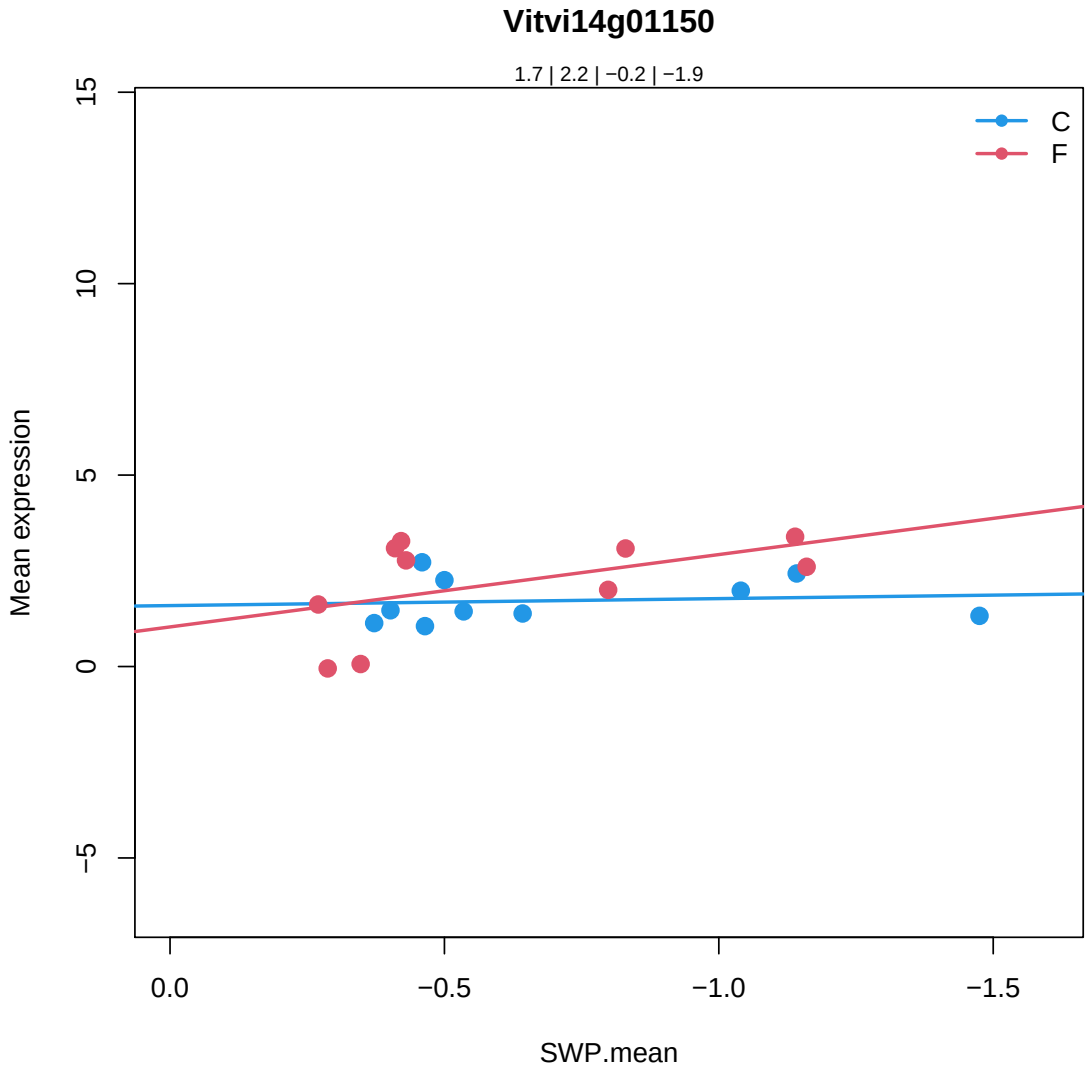
7.6.667 Vitvi14g01150: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01150
        35.2
        not assigned.unknown
        receptor serine/threonine kinase |
        Chr1:26452975-26456088 FORWARD LENGTH=799 |
        201606
```

Coefficients for Vitvi14g01150.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.719196	1.882832e-06	***	2.16019e-06	***
SlopeC	-0.1824438	0.8075193		0.9578053	
MeanF-MeanC	0.4660863	0.2285061		0.5813536	
SlopeF-SlopeC	-1.707377	0.1355617		0.9999488	



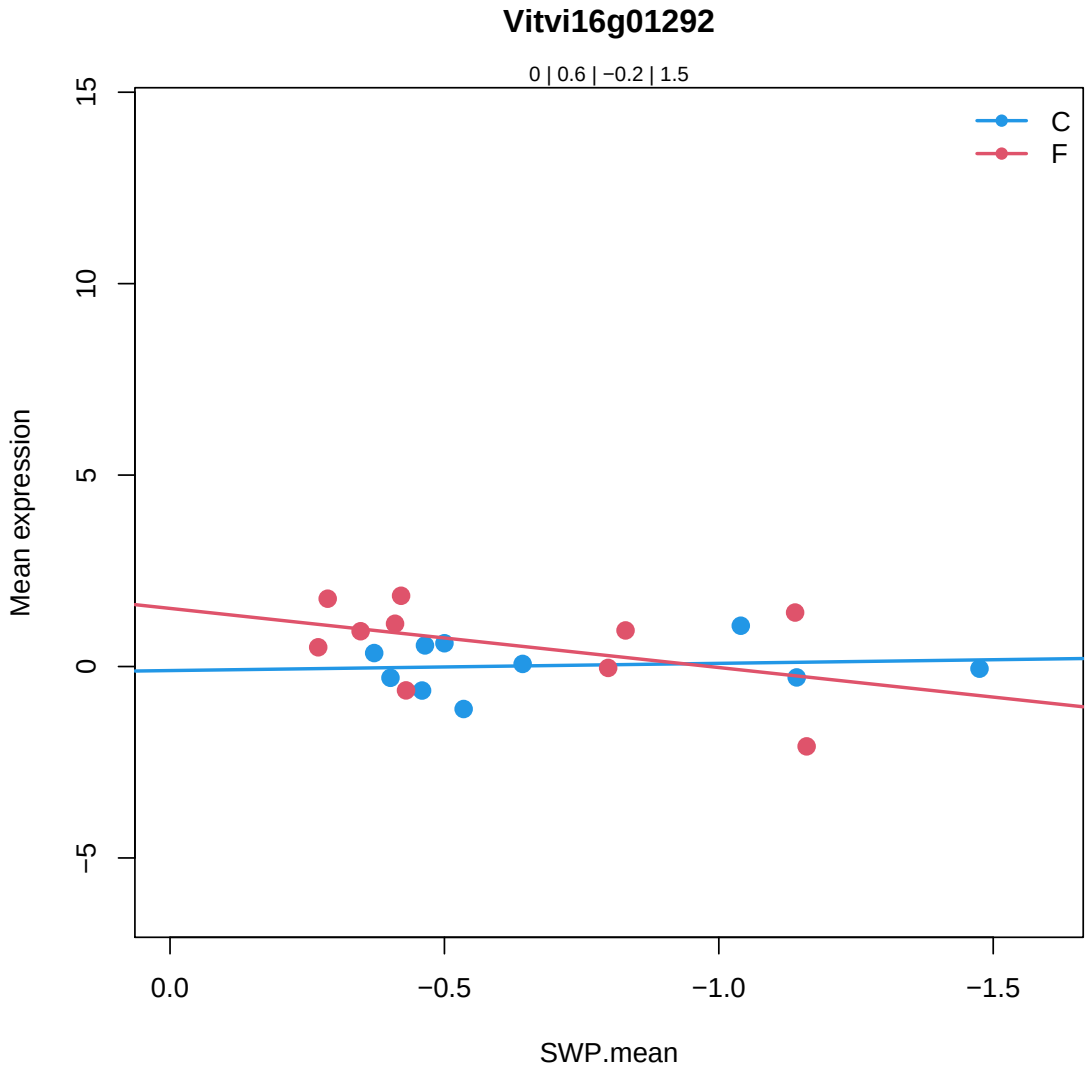
7.6.668 Vitvi16g01292: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01292
        30.2
        signalling.receptor kinases
        Protein kinase superfamily protein |
        Chr1:24961634-24963941 REVERSE LENGTH=666 |
        201606
```

Coefficients for Vitvi16g01292.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.0268689	0.9216906		0.9232049	
SlopeC	−0.1885938	0.8042434		0.9573096	
MeanF−MeanC	0.549684	0.1646155		0.4920915	
SlopeF−SlopeC	1.732947	0.135949		0.9999488	



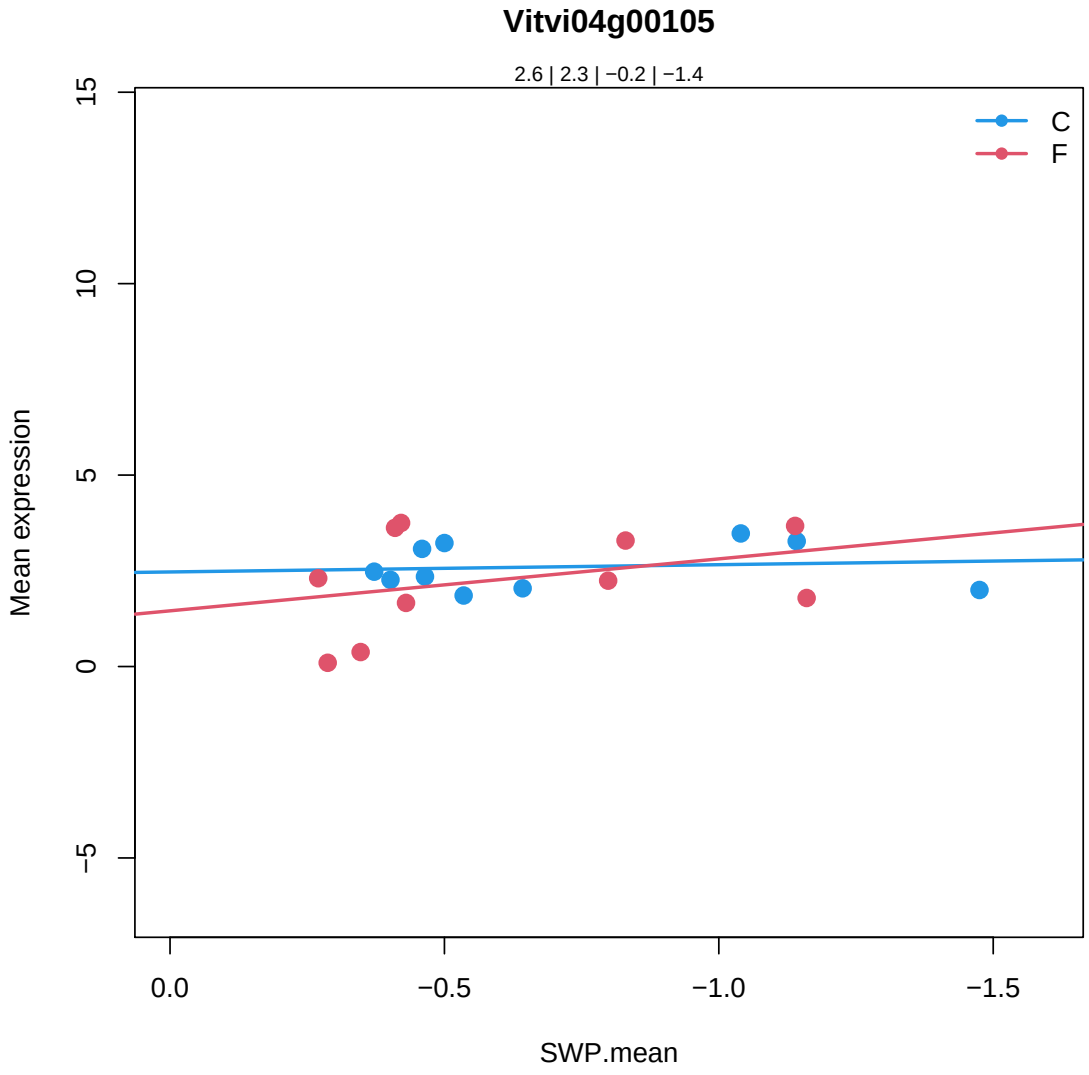
7.6.669 Vitvi04g00105: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00105
        35.2
        not assigned.unknown
        harpin-induced protein |
        Chr5:3831770-3832633 FORWARD LENGTH=287 |
        201606
```

Coefficients for Vitvi04g00105.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.603059	1.279398e-08	***	1.556311e-08	***
SlopeC	-0.1894362	0.8188054		0.9617935	
MeanF-MeanC	-0.3220639	0.4464276		0.7764977	
SlopeF-SlopeC	-1.167541	0.3475943		0.9999488	



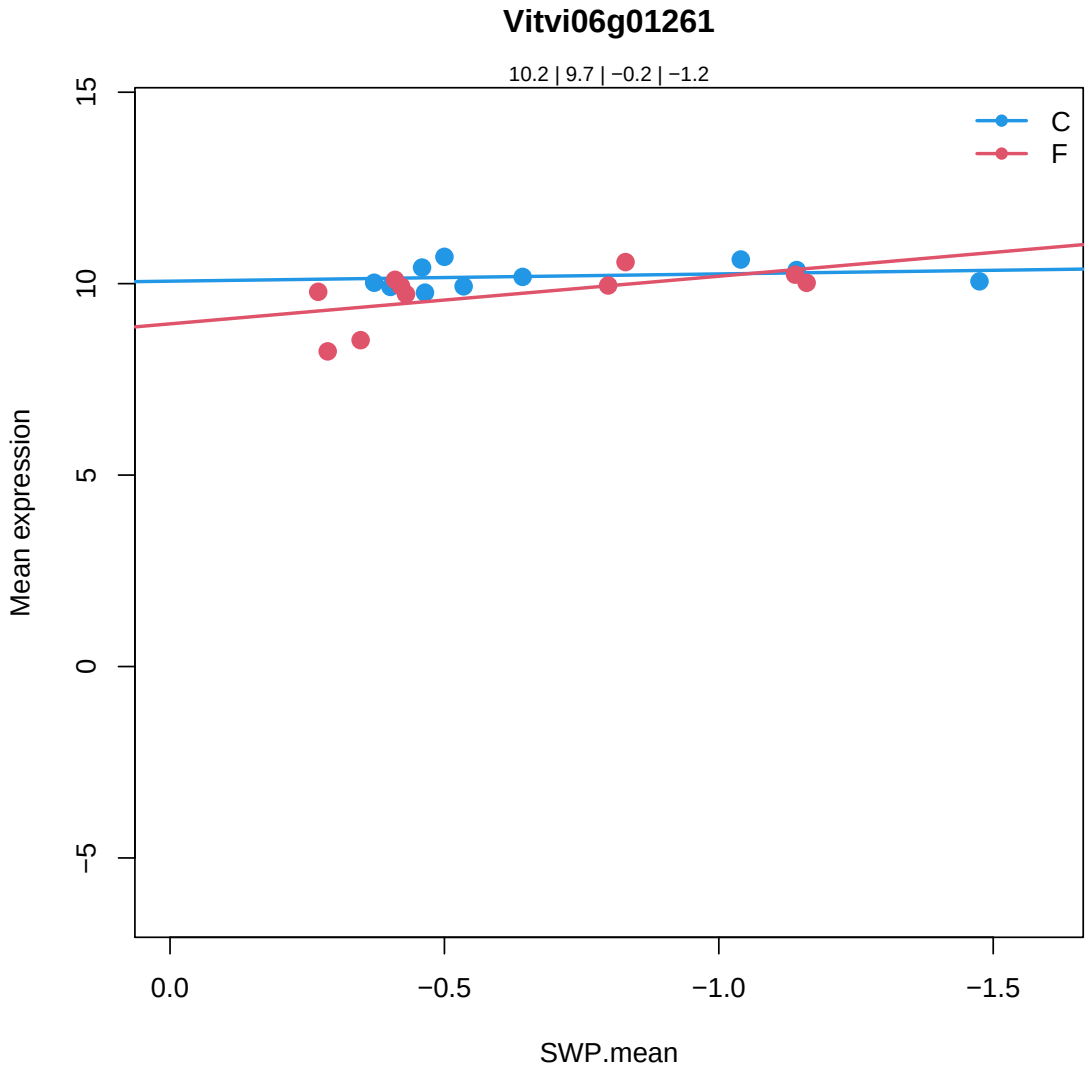
7.6.670 Vitvi06g01261: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01261
        13.1.1.3.11
        amino acid metabolism.synthesis.central amino acid metabolism.alanine.
        alanine:glyoxylate aminotransferase |
        Chr2:5539417-5540902 REVERSE LENGTH=401 |
        201606
```

Coefficients for Vitvi06g01261.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	10.19736	6.061597e-26	***	1.015284e-23	***
SlopeC	-0.1895267	0.6742512		0.9246326	
MeanF-MeanC	-0.4901788	0.04152961	*	0.2117038	
SlopeF-SlopeC	-1.054035	0.125951		0.9999488	



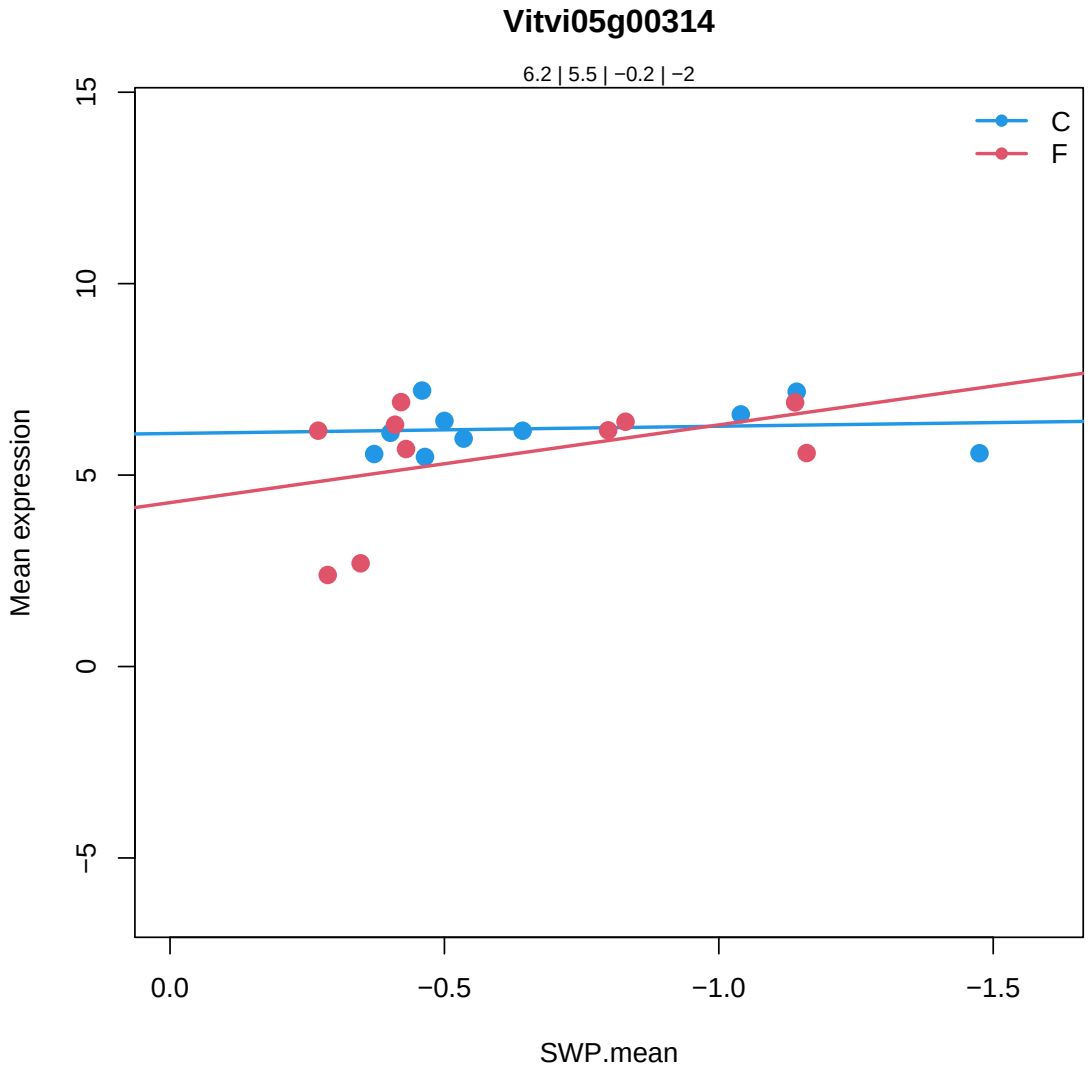
7.6.671 Vitvi05g00314: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00314
        29.4
        protein.postranslational modification
        Protein phosphatase 2C family protein |
        Chr3:5636248-5637702 REVERSE LENGTH=457 |
        201606
```

Coefficients for Vitvi05g00314.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.219378	1.186884e-14	***	1.968926e-14	***
SlopeC	-0.1895893	0.8414983		0.9696754	
MeanF-MeanC	-0.7014961	0.1551703		0.4752071	
SlopeF-SlopeC	-1.840642	0.2006361		0.9999488	



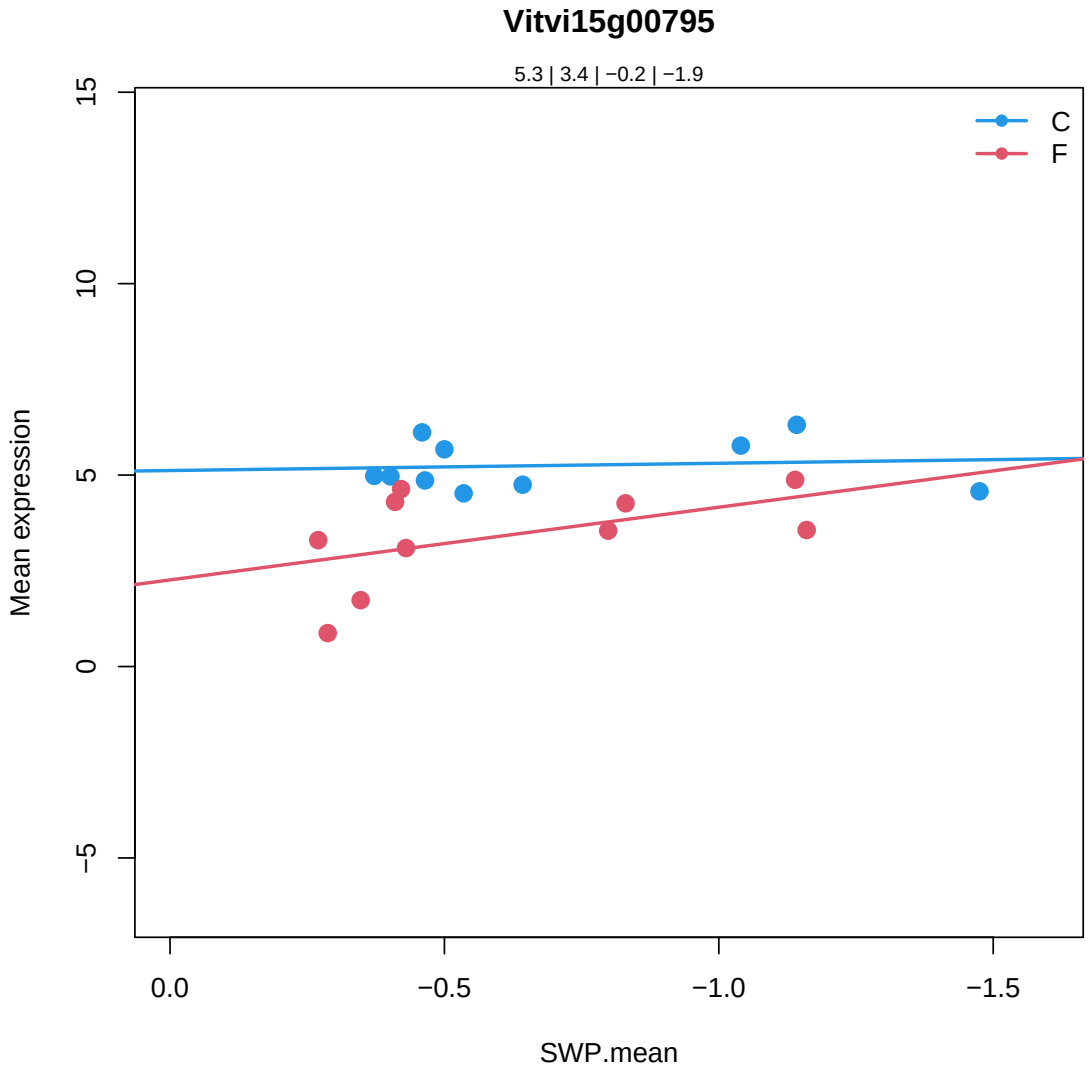
7.6.672 Vitvi15g00795: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g00795
        26.10
        misc.cytochrome P450
        cytochrome P450%2C family 76%2C subfamily C%2C polypeptide 6 |
        Chr1:12220957-12222171 REVERSE LENGTH=404 |
        201606
```

Coefficients for Vitvi15g00795.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.252041	4.859016e-15	***	8.432326e-15	***
SlopeC	-0.1898245	0.8043535		0.9573096	
MeanF-MeanC	-1.833566	9.910431e-05	***	0.001796133	**
SlopeF-SlopeC	-1.708449	0.1439725		0.9999488	



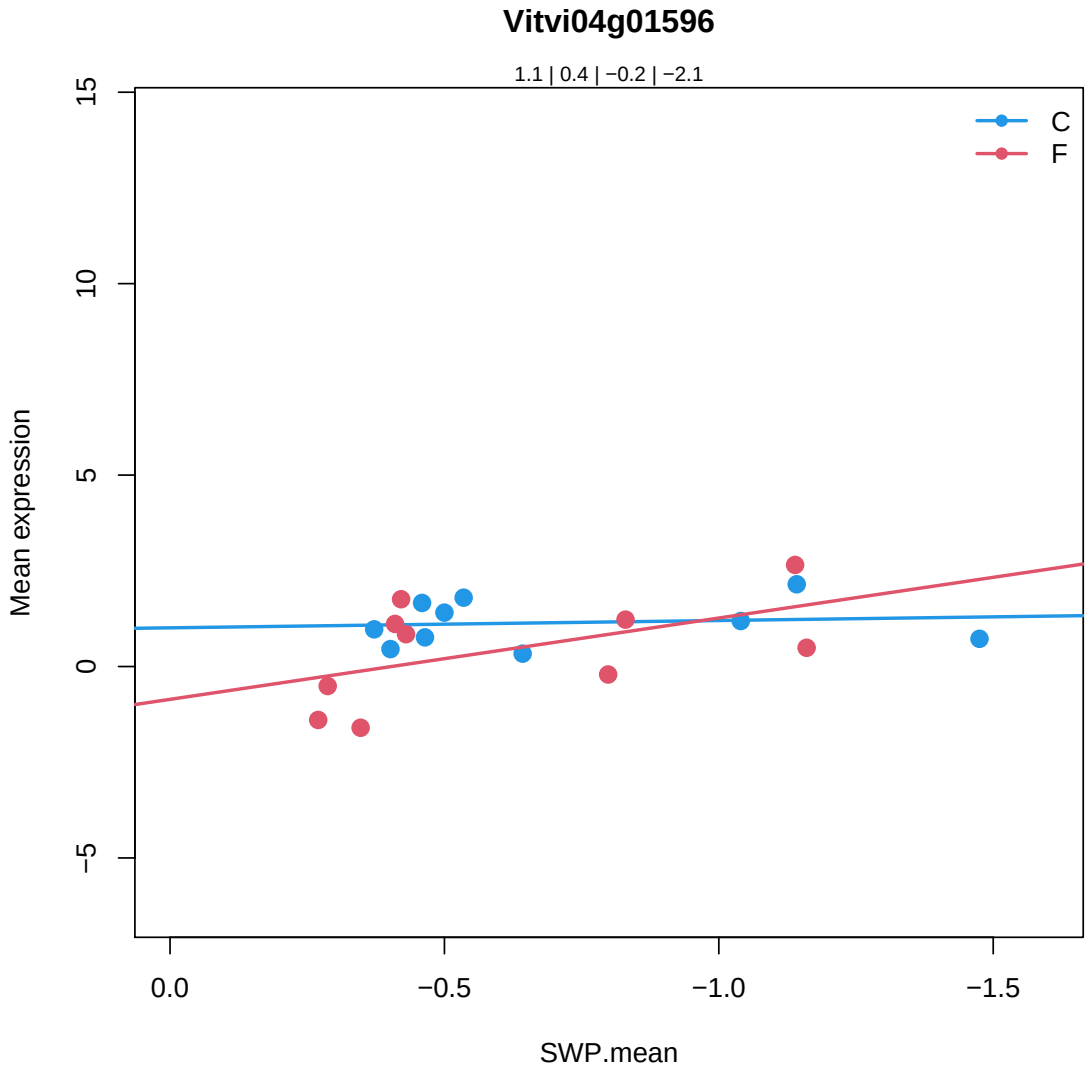
7.6.673 Vitvi04g01596: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01596
        33.99
        development.unspecified
        nodulin MtN21 /EamA-like transporter family protein |
        Chr5:25865190-25866845 REVERSE LENGTH=359 |
        201606
```

Coefficients for Vitvi04g01596.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.144737	0.0004533685	***	0.0004942242	***
SlopeC	−0.1906355	0.806855		0.9575689	
MeanF−MeanC	−0.7078581	0.08463556	.	0.3297585	
SlopeF−SlopeC	−1.933551	0.1061387		0.9999488	



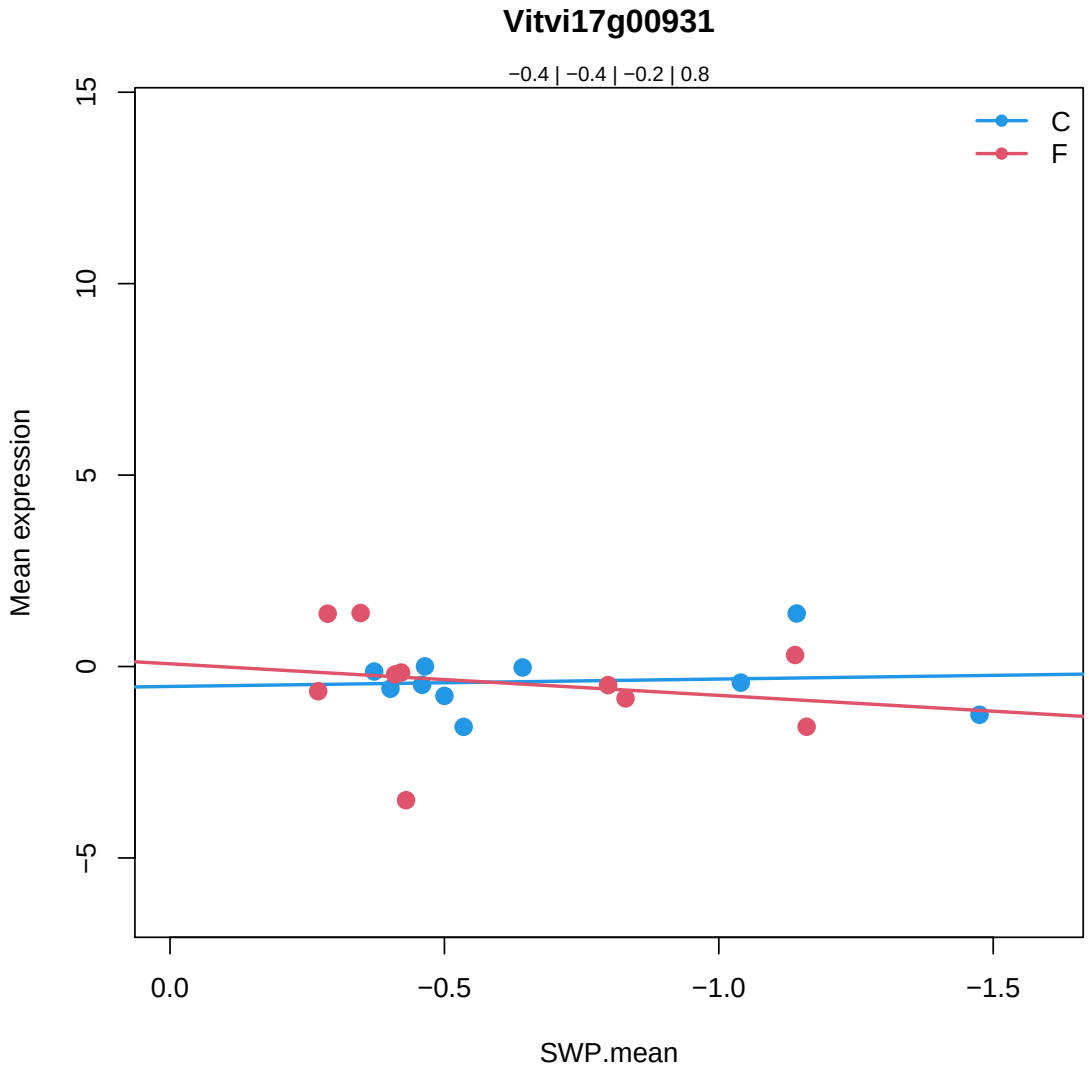
7.6.674 Vitvi17g00931: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00931
        35.2
        not assigned.unknown
        DUF868 family protein (DUF868) |
        Chr4:7480896-7481753 FORWARD LENGTH=285 |
        201606
```

Coefficients for Vitvi17g00931.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.3848154	0.2680225		0.2734403	
SlopeC	-0.1932421	0.83931		0.9694237	
MeanF-MeanC	-0.04678593	0.9230299		0.9797555	
SlopeF-SlopeC	1.018573	0.4751547		0.9999488	



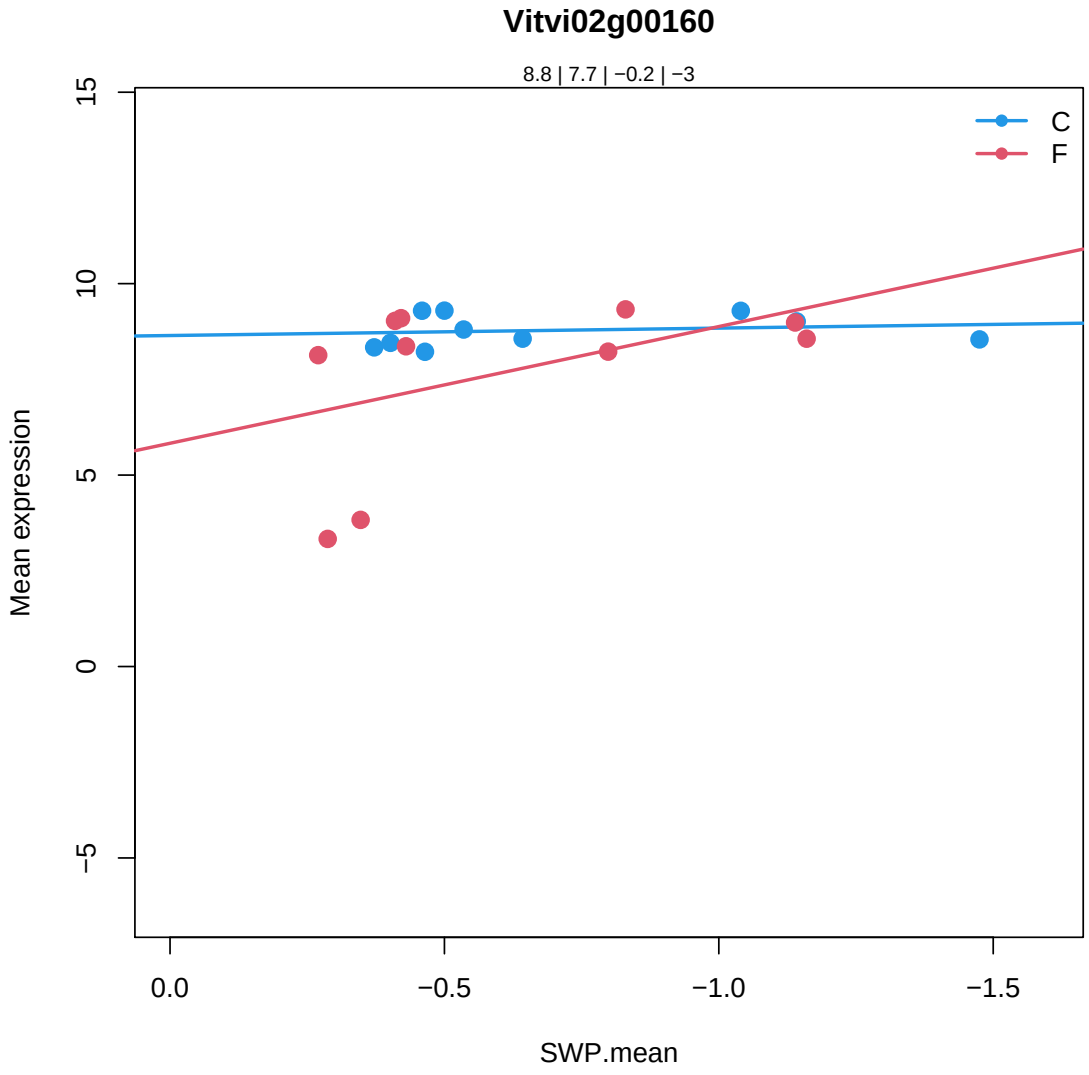
7.6.675 Vitvi02g00160: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00160
        21.4
        redox.glutaredoxins
        Glutaredoxin family protein |
        Chr1:23953270-23954376 FORWARD LENGTH=368 |
        201606
```

Coefficients for Vitvi02g00160.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	8.780784	6.921898e-16	***	1.323759e-15	***
SlopeC	-0.1937055	0.8678407		0.9758833	
MeanF-MeanC	-1.092576	0.07539069	.	0.3088952	
SlopeF-SlopeC	-2.854744	0.1099476		0.9999488	



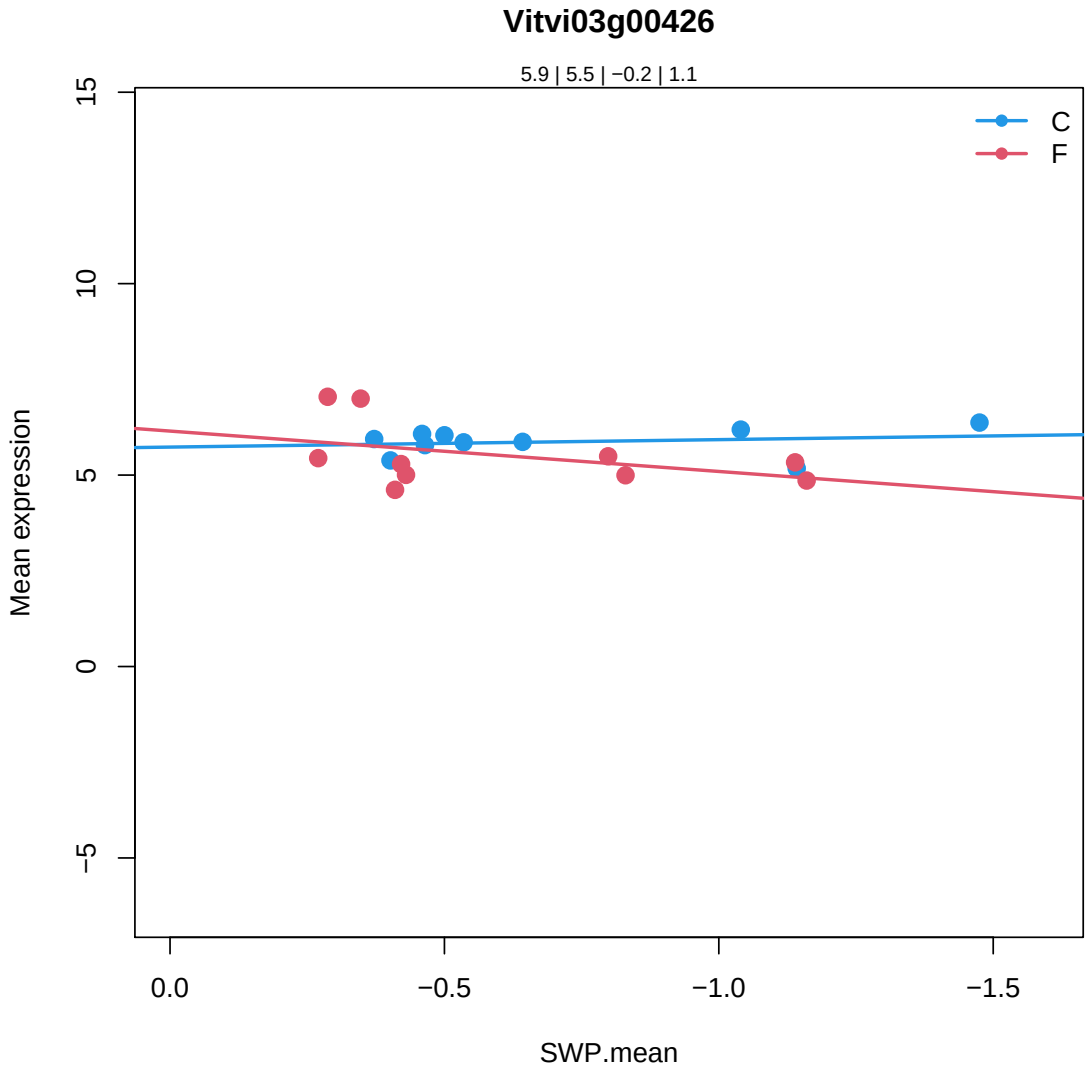
7.6.676 Vitvi03g00426: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00426
        35.2
        not assigned.unknown
        maternal effect embryo arrest 14 |
        Chr2:6921196-6921978 REVERSE LENGTH=203 |
        201606
```

Coefficients for Vitvi03g00426.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.867768	2.501932e-19	***	1.039936e-18	***
SlopeC	-0.1945327	0.7145801		0.9358678	
MeanF-MeanC	-0.3609827	0.1901991		0.5291138	
SlopeF-SlopeC	1.249095	0.1245074		0.9999488	



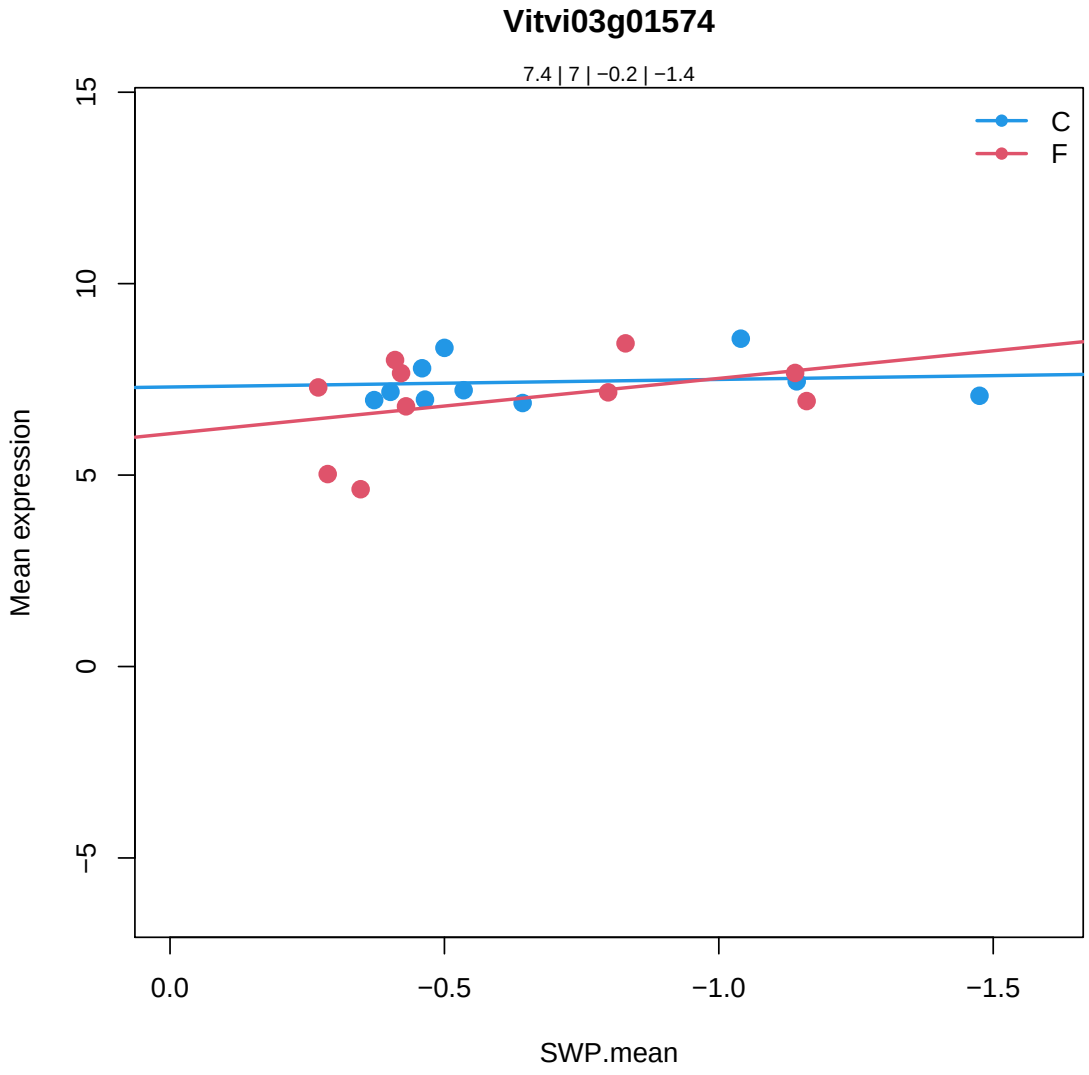
7.6.677 Vitvi03g01574: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g01574
        35.2
        not assigned.unknown
        abscisic acid responsive elements-binding factor 2 |
        Chr1:17166189-17167415 REVERSE LENGTH=408 |
        201606
```

Coefficients for Vitvi03g01574.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.439492	3.634782e-18	***	1.067706e-17	***
SlopeC	-0.1974947	0.7964765		0.9558518	
MeanF-MeanC	-0.4786147	0.22657		0.5795233	
SlopeF-SlopeC	-1.246055	0.2805636		0.9999488	



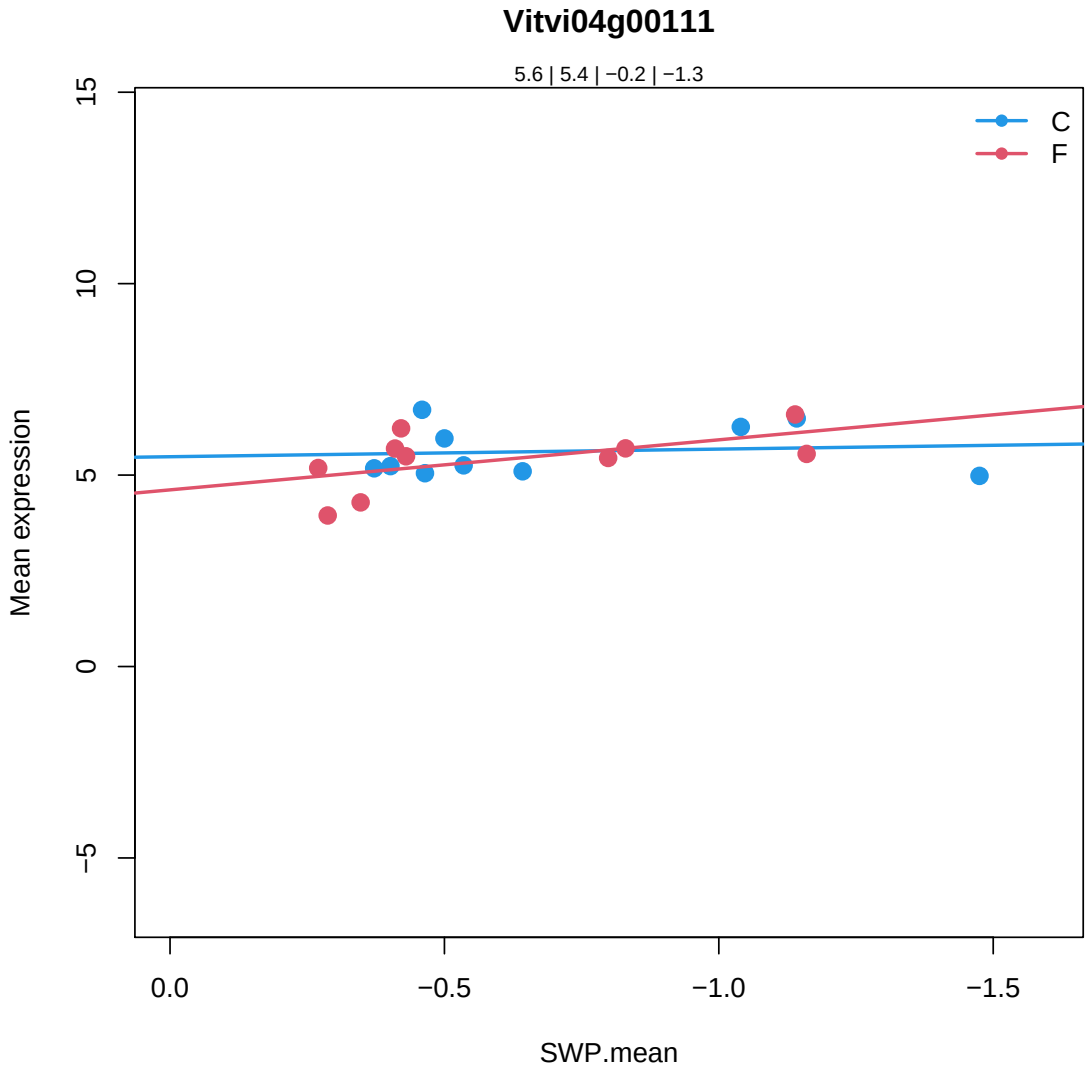
7.6.678 Vitvi04g00111: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00111
        27.3.9
        RNA.regulation of transcription.C2C2(Zn) GATA transcription factor fam
        cytokinin-responsive gata factor 1 |
        Chr4:13253210-13254659 FORWARD LENGTH=352 |
        201606
```

Coefficients for Vitvi04g00111.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.619093	3.662915e-18	***	1.07469e-17	***
SlopeC	-0.1988899	0.7311932		0.9406676	
MeanF-MeanC	-0.2091289	0.479322		0.7942106	
SlopeF-SlopeC	-1.108615	0.2062351		0.9999488	



7.6.679 Vitvi10g00605: type5

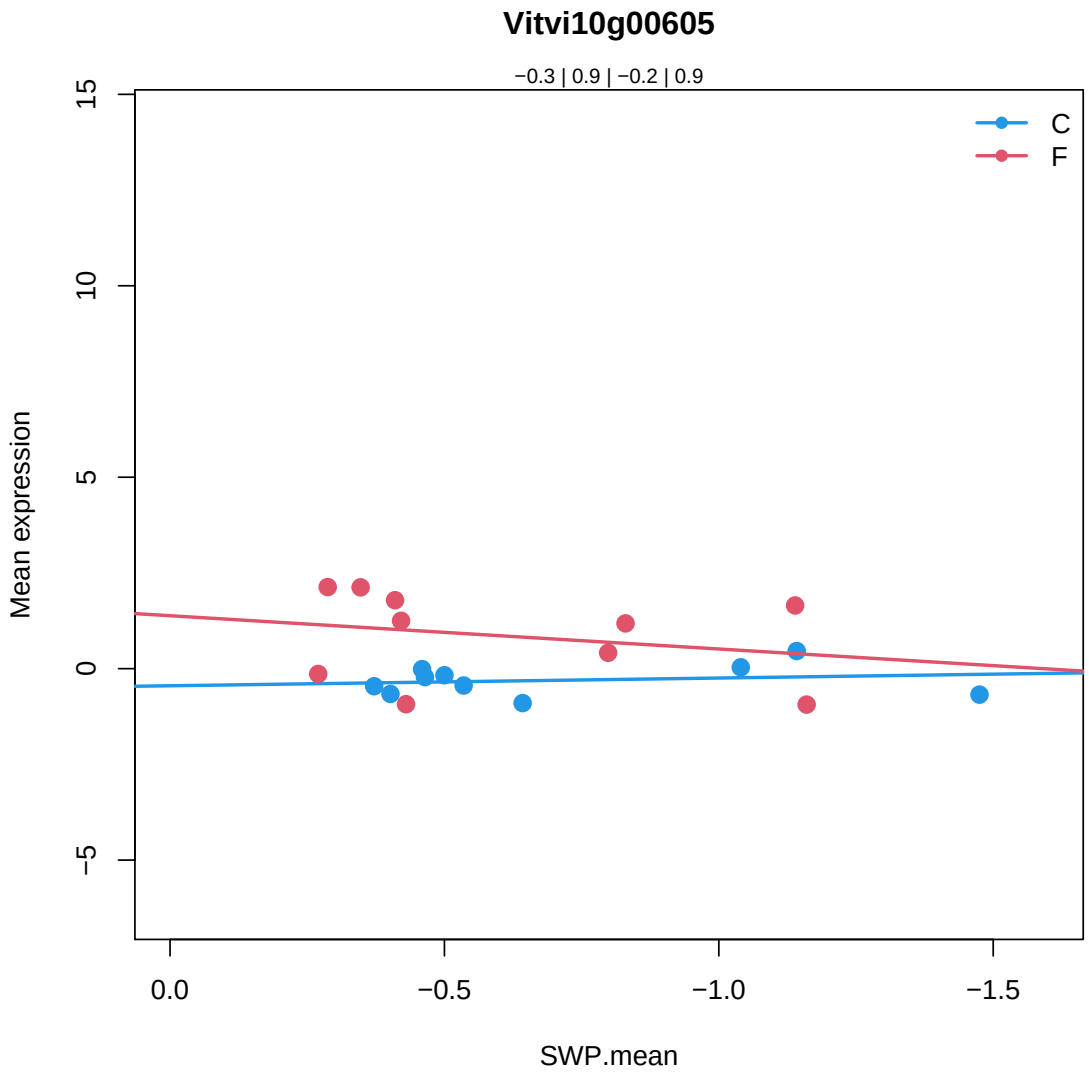
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00605
        30.2.2
        signalling.receptor kinases.leucine rich repeat II
        Leucine-rich repeat protein kinase family protein |
        Chr5:18566946-18569419 REVERSE LENGTH=571 |
        201606

Vitvi10g00605
        20.1.2
        stress.biotic.receptors
        Leucine-rich repeat protein kinase family protein |
        Chr5:18566946-18569419 REVERSE LENGTH=571 |
        201606
```

Coefficients for Vitvi10g00605.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.3050466	0.2537278		0.2591169	
SlopeC	-0.2019426	0.7828616		0.9531413	
MeanF-MeanC	1.15817	0.004762555	**	0.04396782	*
SlopeF-SlopeC	1.070843	0.3311783		0.9999488	


Vitvi10g00605
−0.3 | 0.9 | −0.2 | 0.9
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

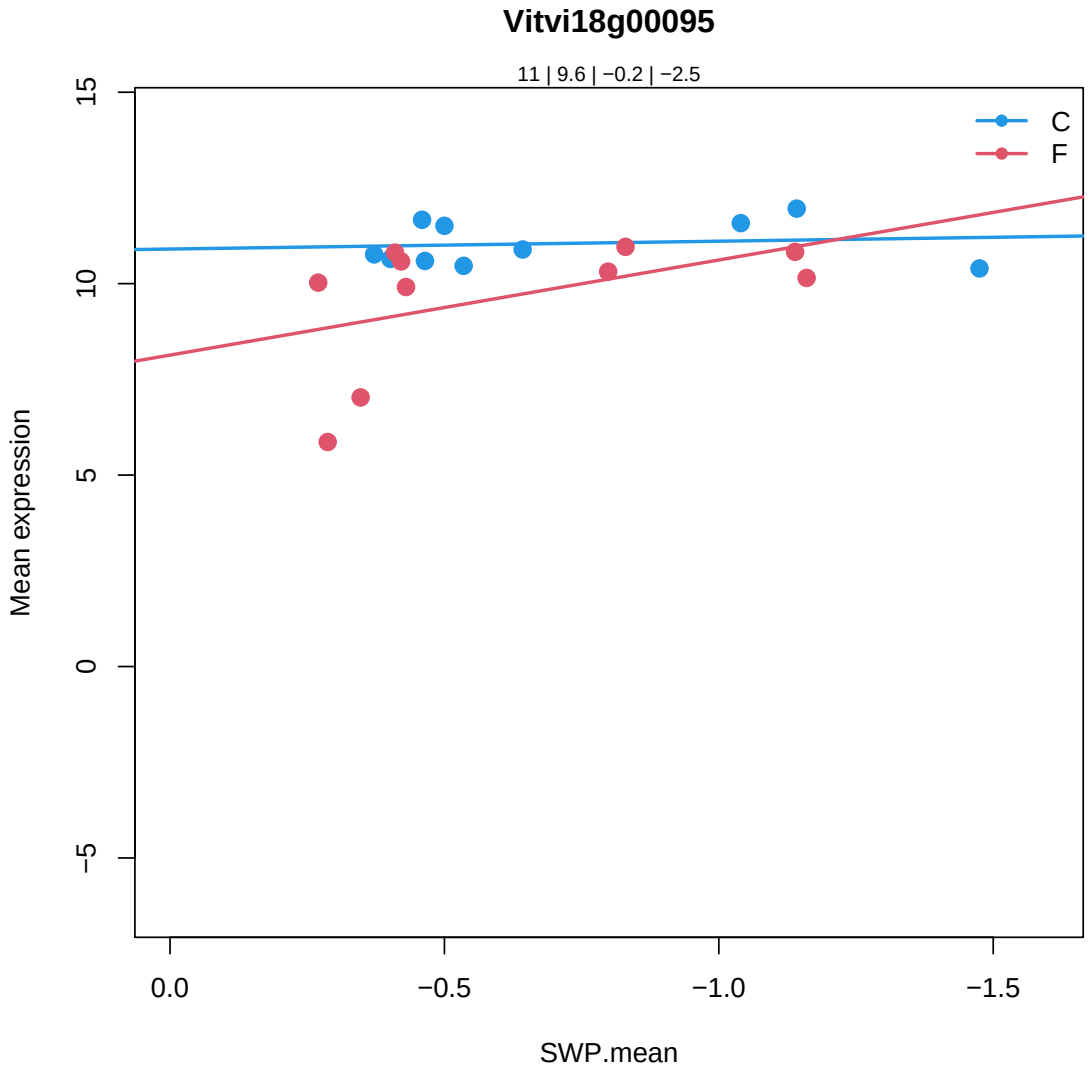
7.6.680 Vitvi18g00095: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00095
        21.6
        redox.dismutases and catalases
        catalase 2 |
        Chr4:16700937-16702955 REVERSE LENGTH=492 |
        201606
```

Coefficients for Vitvi18g00095.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	11.04727	1.126924e-19	***	5.270503e-19	***
SlopeC	-0.2041556	0.8321327		0.9669878	
MeanF-MeanC	-1.399968	0.008552013	**	0.06760881	.
SlopeF-SlopeC	-2.279565	0.1220916		0.9999488	



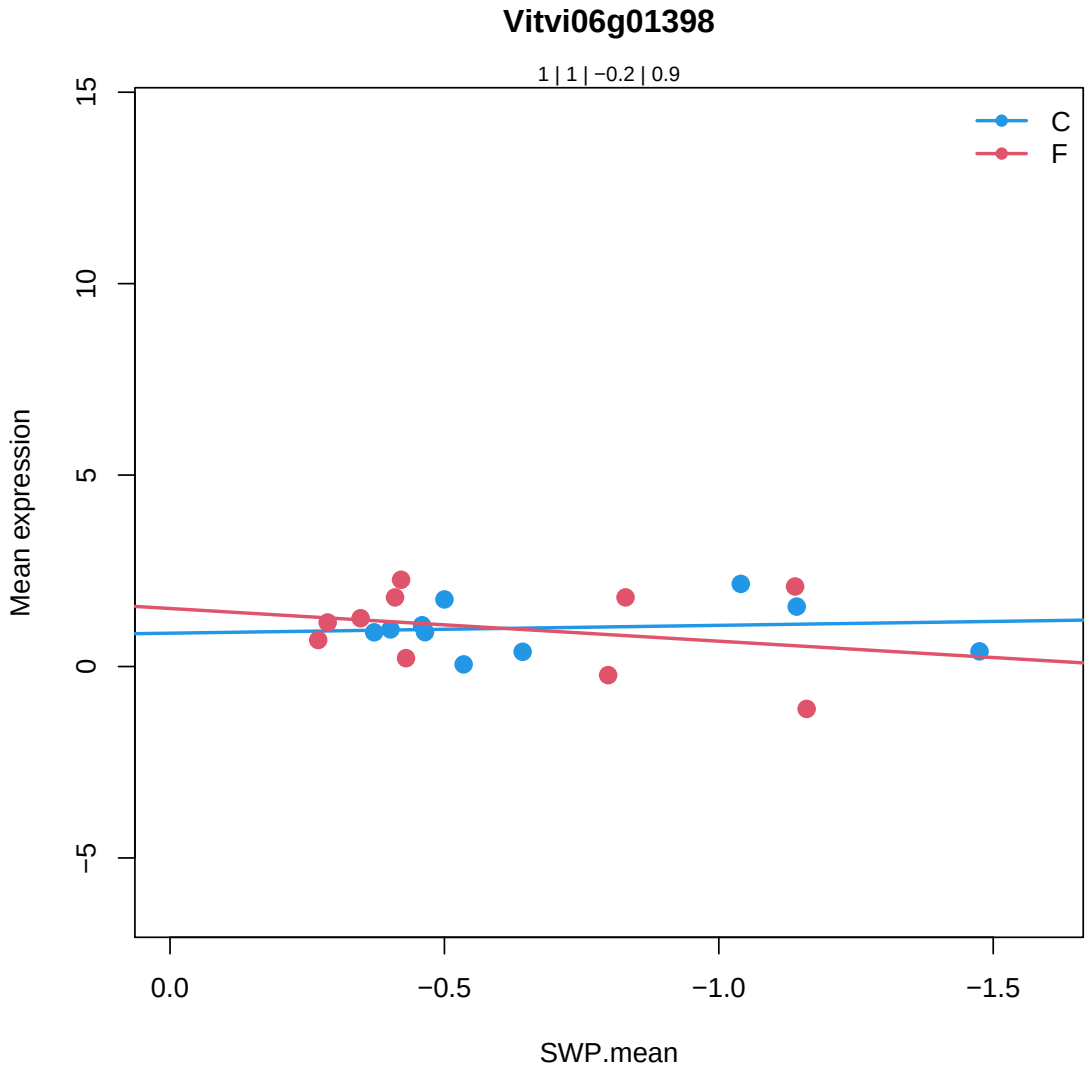
7.6.681 Vitvi06g01398: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01398
        10.2.1
        cell wall.cellulose synthesis.cellulose synthase
        cellulose synthase-like A02 |
        Chr5:7555379-7559866 REVERSE LENGTH=534 |
        201606
```

Coefficients for Vitvi06g01398.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.014673	0.0009869258	***	0.001068899	**
SlopeC	-0.2048102	0.7847392		0.9533712	
MeanF-MeanC	-0.01924872	0.9596876		0.9914232	
SlopeF-SlopeC	1.058515	0.3475303		0.9999488	



7.6.682 Vitvi00g01320: type5

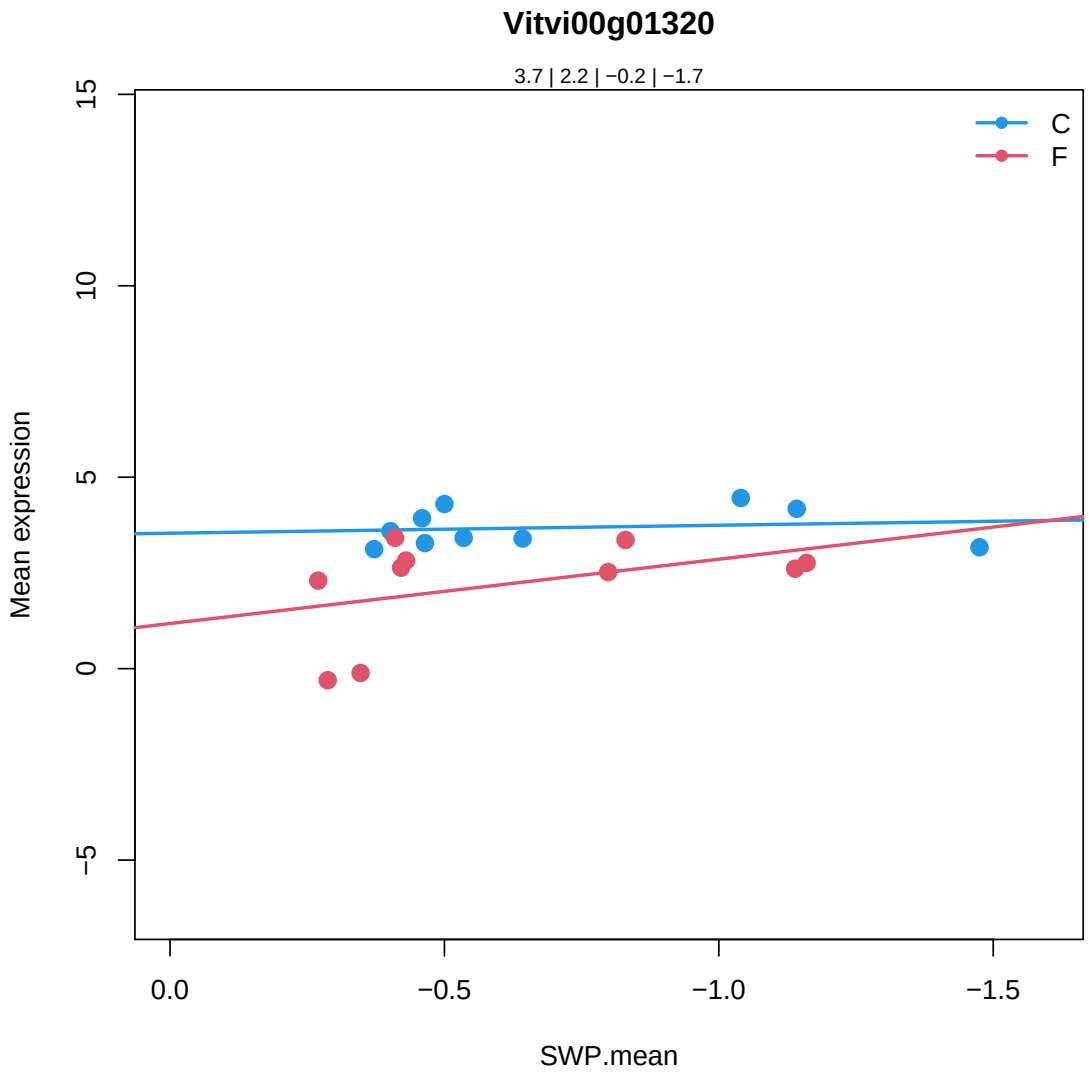
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi00g01320
        29.5.11.4.2
        protein.degradation.ubiquitin.E3.RING
        plant U-box 8 |
        Chr4:11356143-11357267 REVERSE LENGTH=374 |
        201606

Vitvi00g01320
        35.2
        not assigned.unknown
        plant U-box 8 |
        Chr4:11356143-11357267 REVERSE LENGTH=374 |
        201606
```

Coefficients for Vitvi00g01320.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.683425	6.235563e-12	***	8.592574e-12	***
SlopeC	-0.2077702	0.7875161		0.9533712	
MeanF-MeanC	-1.481705	0.0009480829	***	0.01196248	*
SlopeF-SlopeC	-1.472132	0.2076405		0.9999488	


Vitvi00g01320
3.7 | 2.2 | −0.2 | −1.7
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

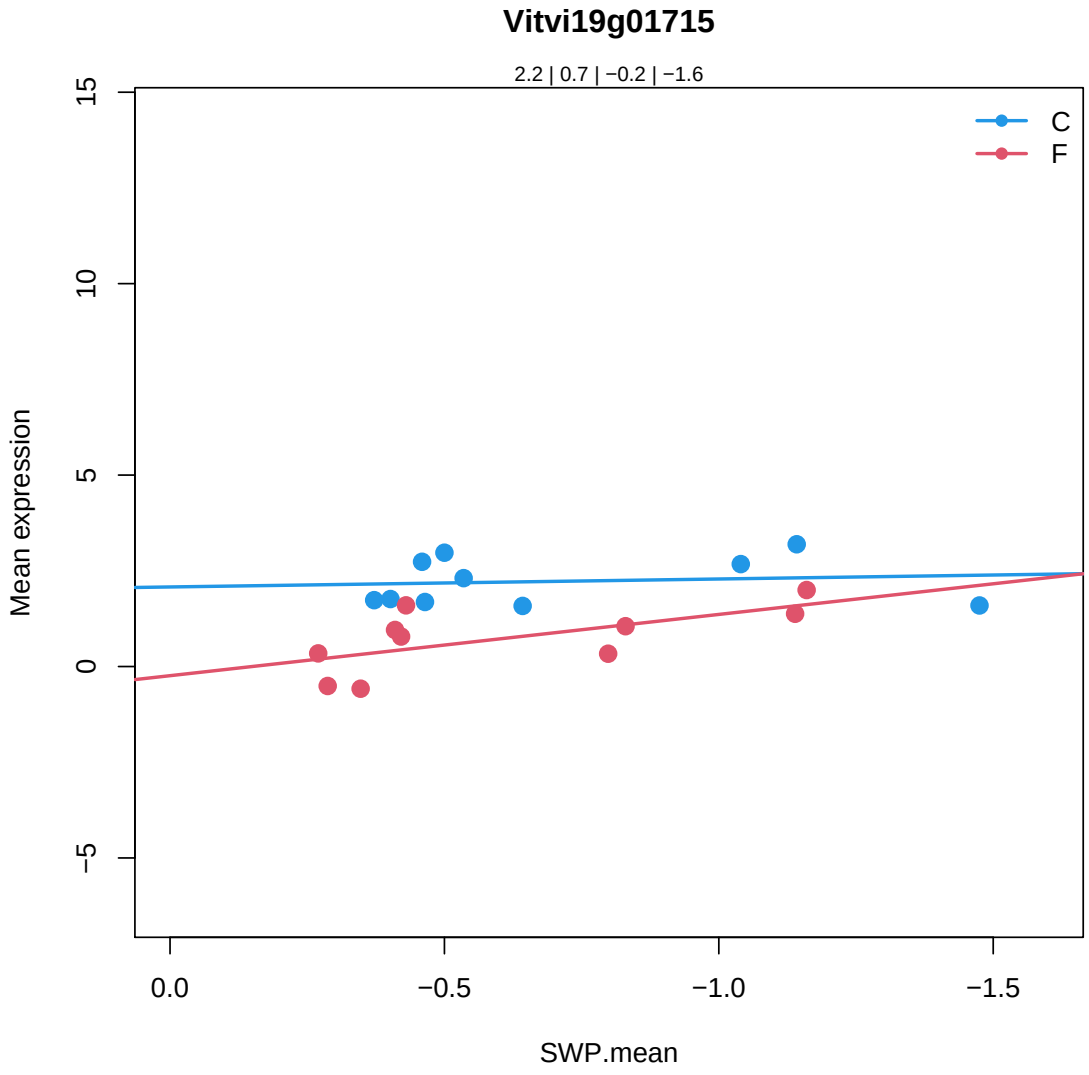
7.6.683 Vitvi19g01715: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g01715
        34.12
        transport.metal
        Cation efflux family protein |
        Chr1:5579300-5580585 FORWARD LENGTH=315 |
        201606
```

Coefficients for Vitvi19g01715.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.224069	2.212116e-10	***	2.855685e-10	***
SlopeC	-0.2082918	0.7113119		0.9350571	
MeanF-MeanC	-1.488937	2.947183e-05	***	0.0006389896	***
SlopeF-SlopeC	-1.391626	0.1067773		0.9999488	



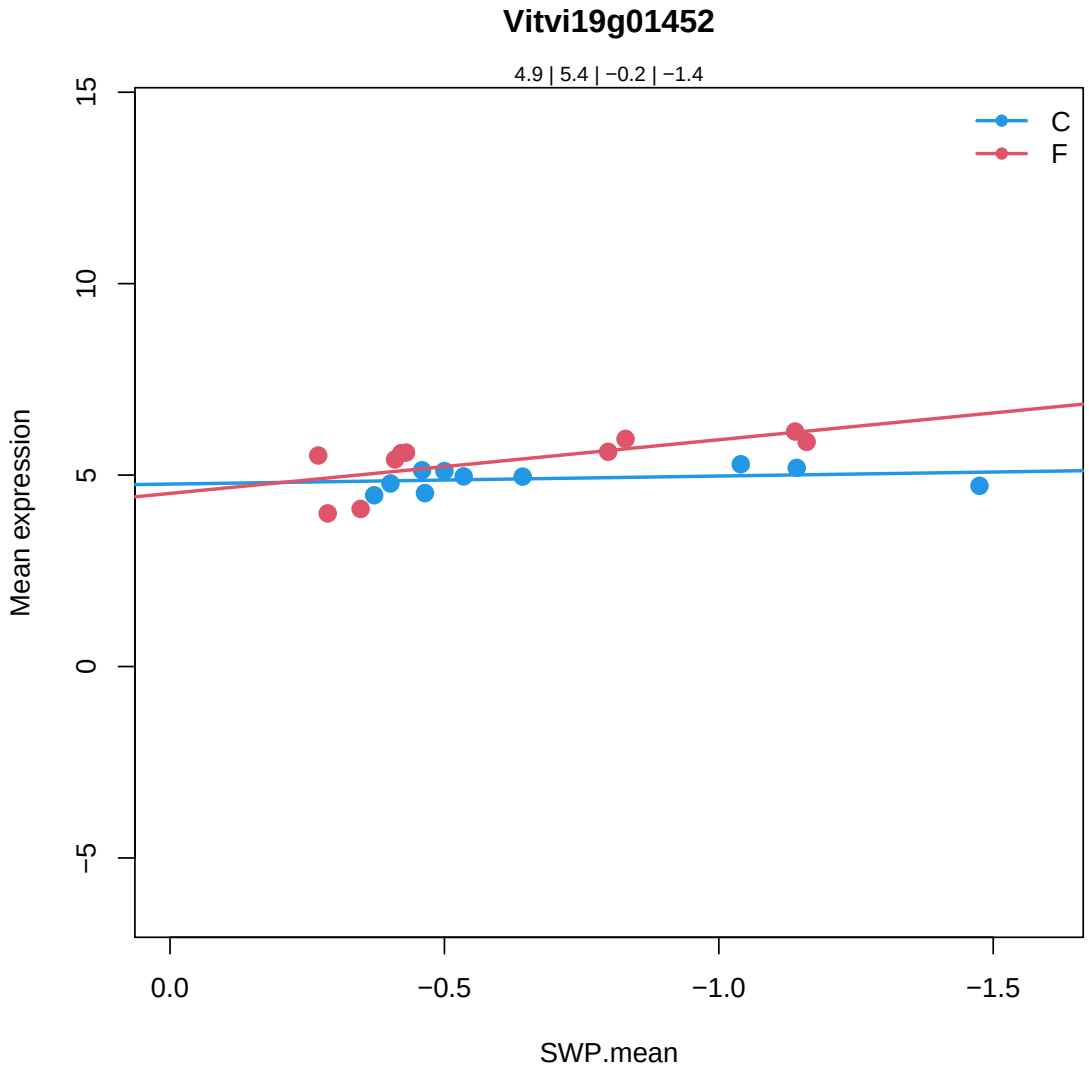
7.6.684 Vitvi19g01452: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g01452
        26.10
        misc.cytochrome P450
        cytochrome P450%2C family 72%2C subfamily A%2C polypeptide 15 |
        Chr3:4937410-4939310 FORWARD LENGTH=512 |
        201606
```

Coefficients for Vitvi19g01452.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.912685	5.623185e-20	***	2.918236e-19	***
SlopeC	-0.2093746	0.614258		0.9074064	
MeanF-MeanC	0.4623986	0.03715814	*	0.1955506	
SlopeF-SlopeC	-1.192366	0.06349788	.	0.9999488	



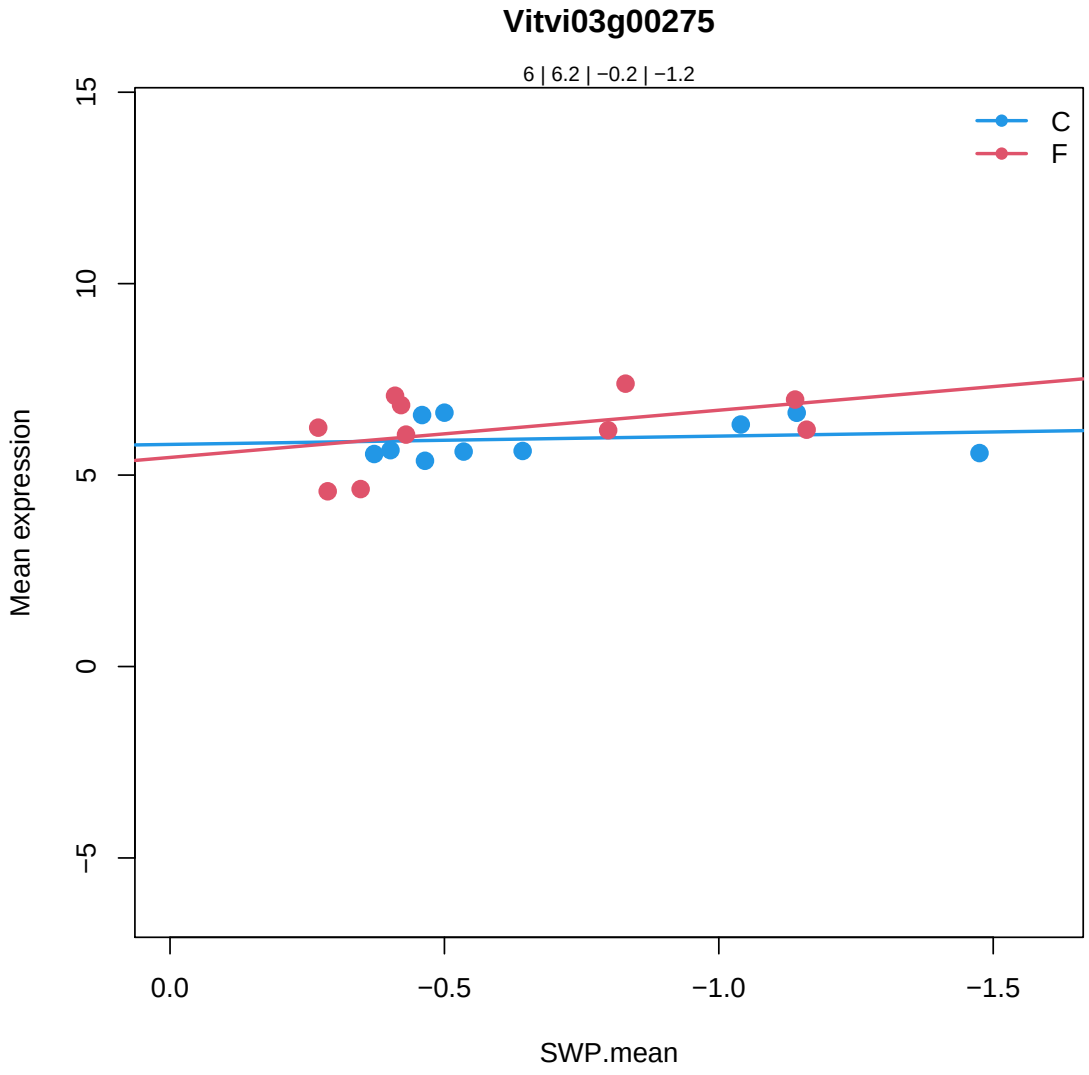
7.6.685 Vitvi03g00275: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00275
        34.18
        transport.unspecified anions
        chloride channel E |
        Chr4:16836384-16839345 REVERSE LENGTH=710 |
        201606
```

Coefficients for Vitvi03g00275.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.953661	4.155626e-18	***	1.202811e-17	***
SlopeC	-0.2166769	0.7255295		0.9394623	
MeanF-MeanC	0.2586266	0.4127774		0.7524882	
SlopeF-SlopeC	-1.016727	0.2744965		0.9999488	



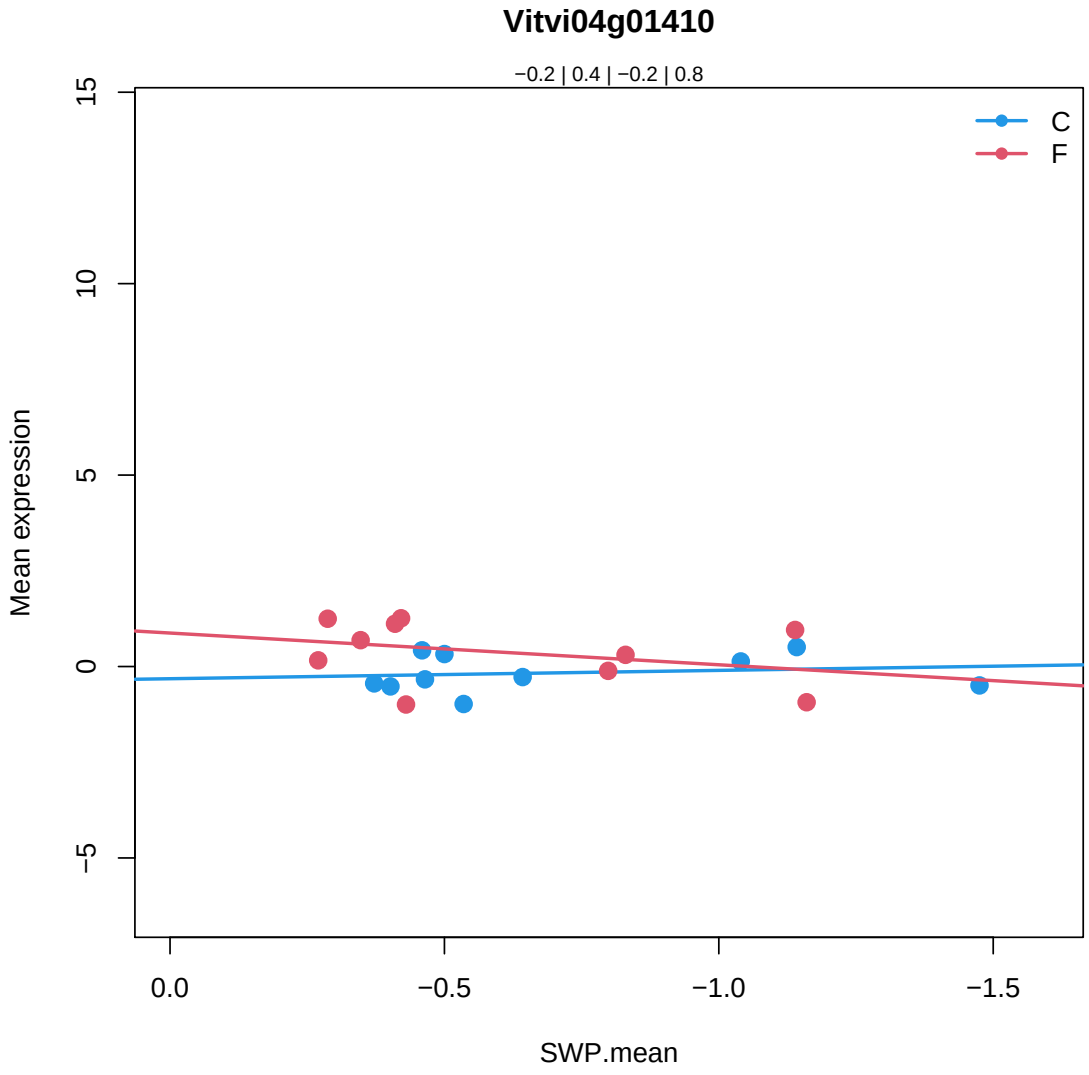
7.6.686 Vitvi04g01410: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01410
        27.3.9
        RNA.regulation of transcription.C2C2(Zn) GATA transcription factor fam
        GATA transcription factor 5 |
        Chr5:26496208-26497309 REVERSE LENGTH=339 |
        201606
```

Coefficients for Vitvi04g01410.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.1658532	0.4285882		0.4346335	
SlopeC	-0.21749	0.7074466		0.9346979	
MeanF-MeanC	0.5354664	0.07933692	.	0.3185599	
SlopeF-SlopeC	1.046057	0.2323834		0.9999488	



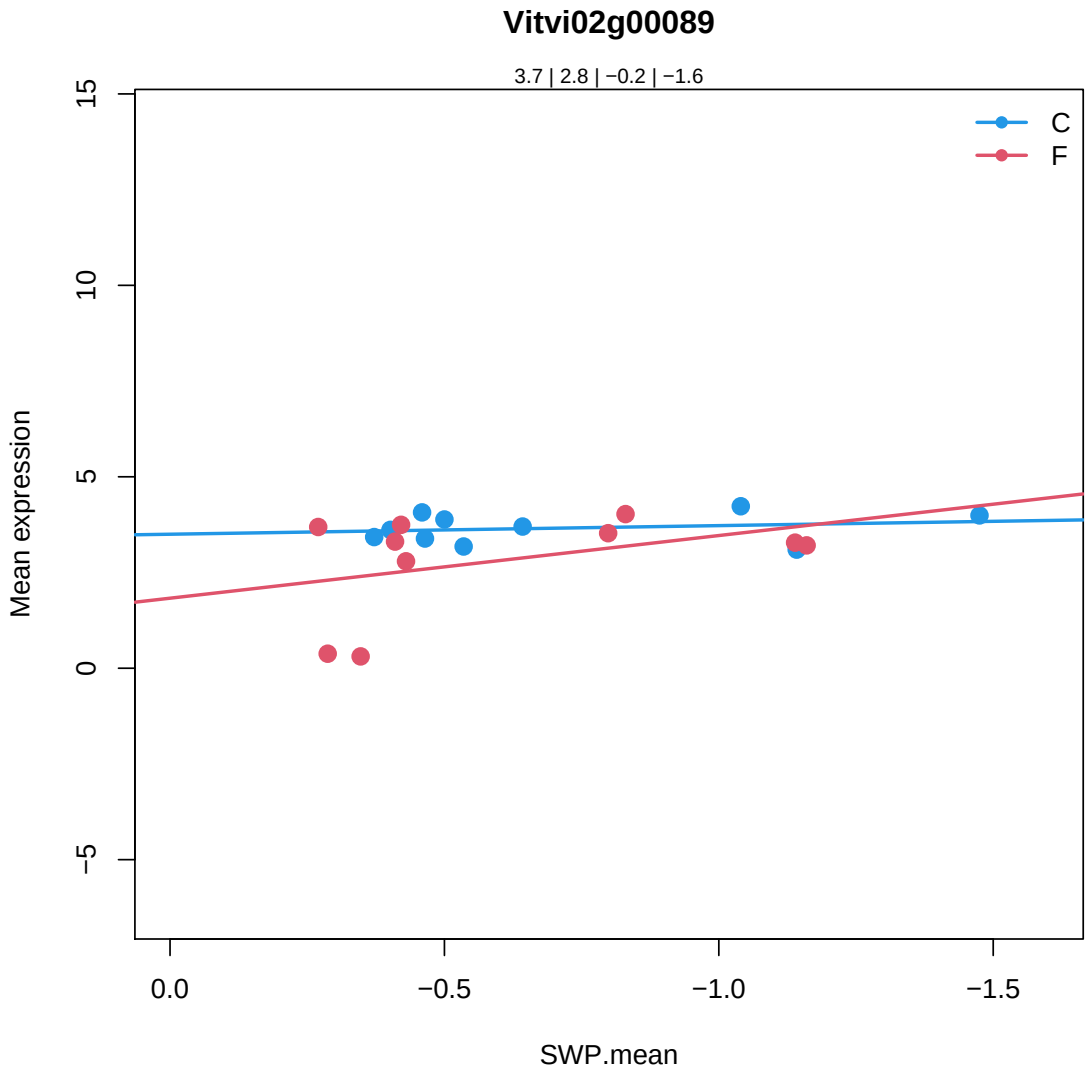
7.6.687 Vitvi02g00089: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00089
        27.3.35
        RNA.regulation of transcription.bZIP transcription factor family
        NA
```

Coefficients for Vitvi02g00089.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.657914	7.574557e-12	***	1.040374e-11	***
SlopeC	-0.2247162	0.7713862		0.9510377	
MeanF-MeanC	-0.8318589	0.04373411	*	0.2191306	
SlopeF-SlopeC	-1.411951	0.2275588		0.9999488	



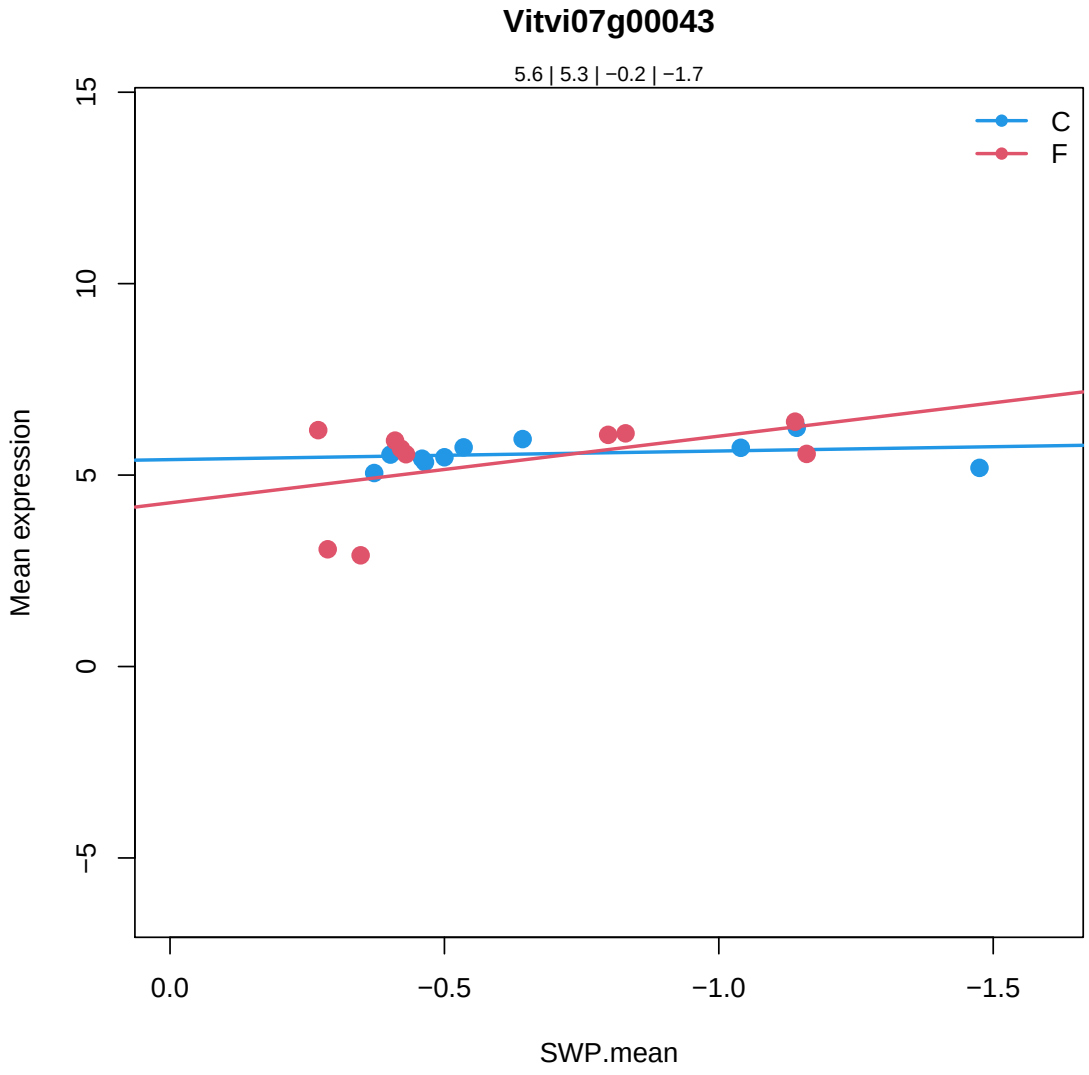
7.6.688 Vitvi07g00043: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g00043
        27.3.40
        RNA.regulation of transcription.AUX/IAA family
        AUX/IAA transcriptional regulator family protein |
        Chr5:17550465-17551206 FORWARD LENGTH=186 |
        201606
```

Coefficients for Vitvi07g00043.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.561628	3.249313e-16	***	6.50631e-16	***
SlopeC	-0.2247581	0.7520075		0.9472461	
MeanF-MeanC	-0.2255398	0.5341529		0.8262547	
SlopeF-SlopeC	-1.5164	0.1612769		0.9999488	



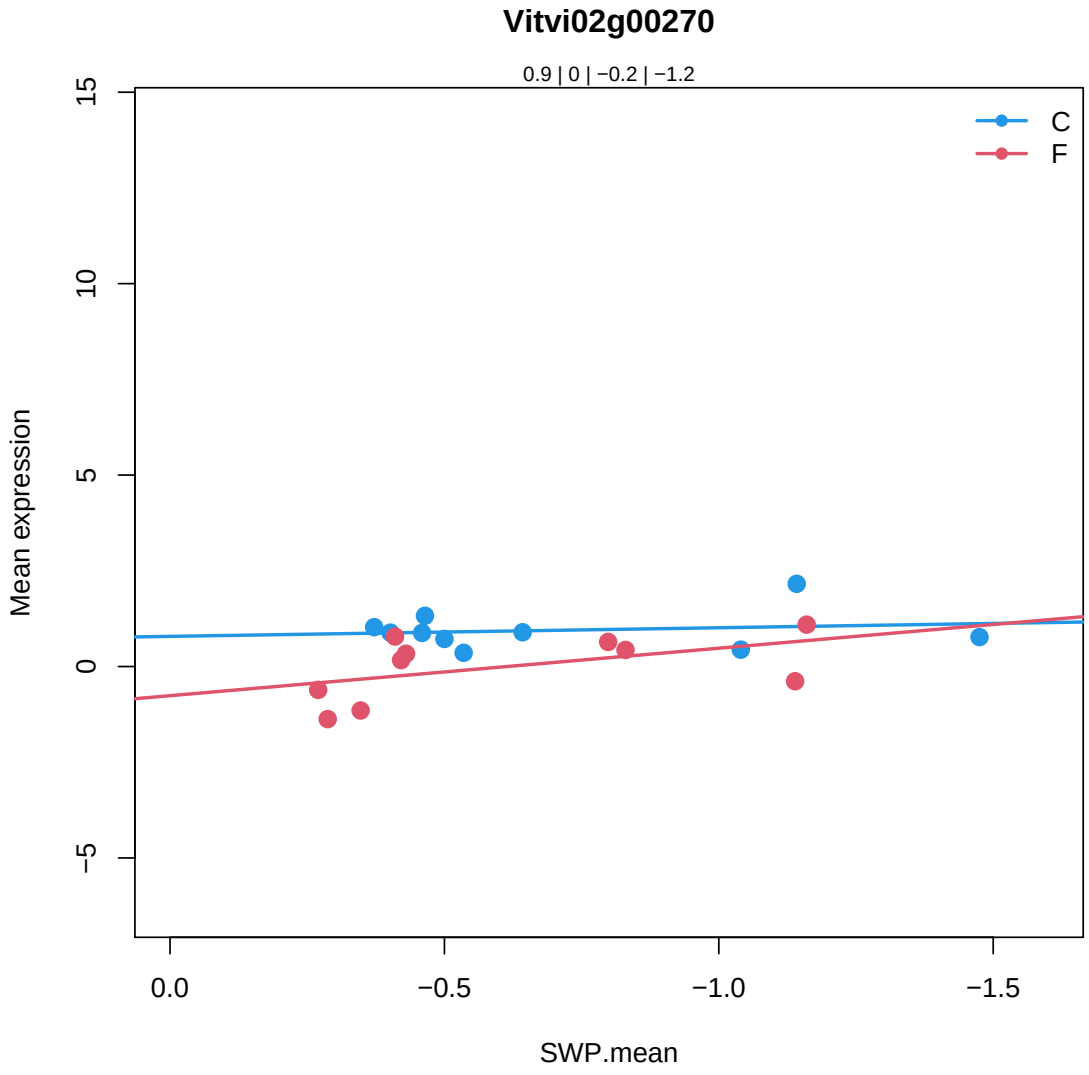
7.6.689 Vitvi02g00270: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00270
        16.8.3
        secondary metabolism.flavonoids.dihydroflavonols
        2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protei
        Chr4:6491089-6492342 FORWARD LENGTH=349 |
        201606
```

Coefficients for Vitvi02g00270.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.9455081	8.406928e-05	***	9.296844e-05	***
SlopeC	-0.2251233	0.6831781		0.9282223	
MeanF-MeanC	-0.9519251	0.002392235	**	0.025374	*
SlopeF-SlopeC	-1.014751	0.2237016		0.9999488	



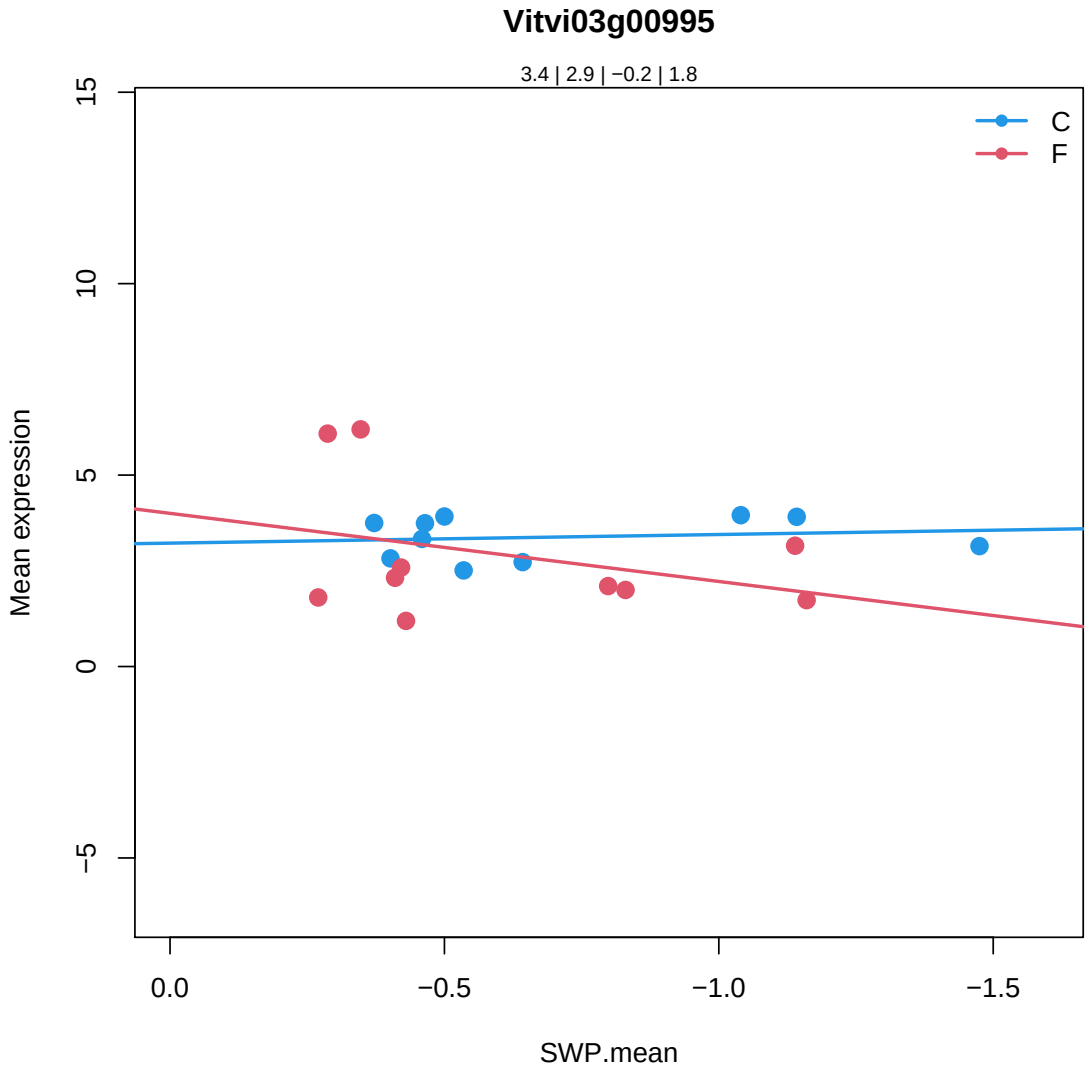
7.6.690 Vitvi03g00995: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00995
        35.2
        not assigned.unknown
        nicotinamidase 1 |
        Chr2:9589604-9590846 REVERSE LENGTH=244 |
        201606
```

Coefficients for Vitvi03g00995.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.380909	6.864526e-09	***	8.423566e-09	***
SlopeC	−0.2252086	0.8278634		0.9659517	
MeanF−MeanC	−0.4645233	0.3816796		0.7331307	
SlopeF−SlopeC	2.00419	0.2020341		0.9999488	



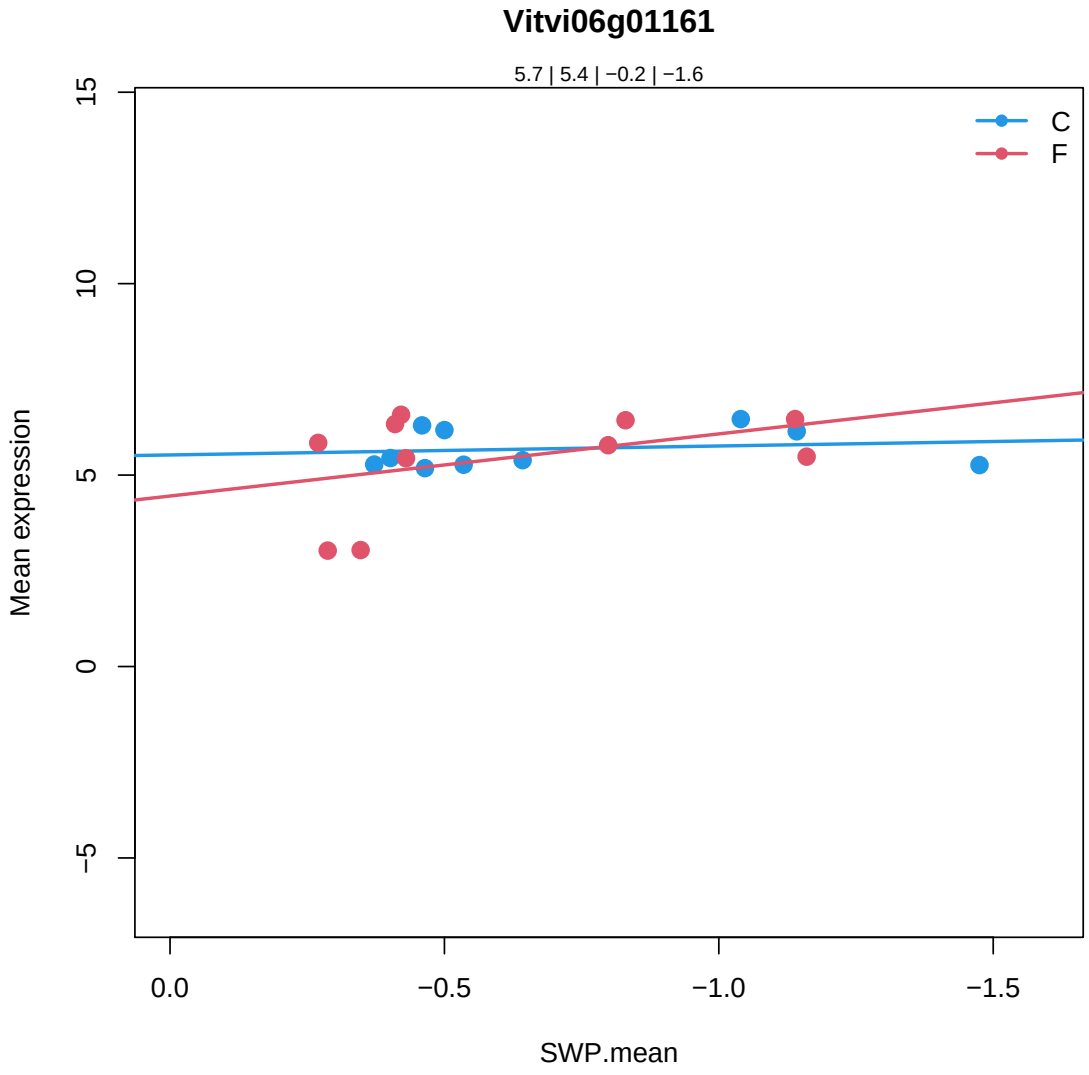
7.6.691 Vitvi06g01161: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01161
        13.2.4.4
        amino acid metabolism.degradation.branched chain group.leucine
        Aldolase superfamily protein |
        Chr2:11429192-11431960 REVERSE LENGTH=388 |
        201606
```

Coefficients for Vitvi06g01161.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.689954	1.64644e-15	***	3.005753e-15	***
SlopeC	-0.2340014	0.7663581		0.9497688	
MeanF-MeanC	-0.2485892	0.5360328		0.8271956	
SlopeF-SlopeC	-1.38864	0.243273		0.9999488	



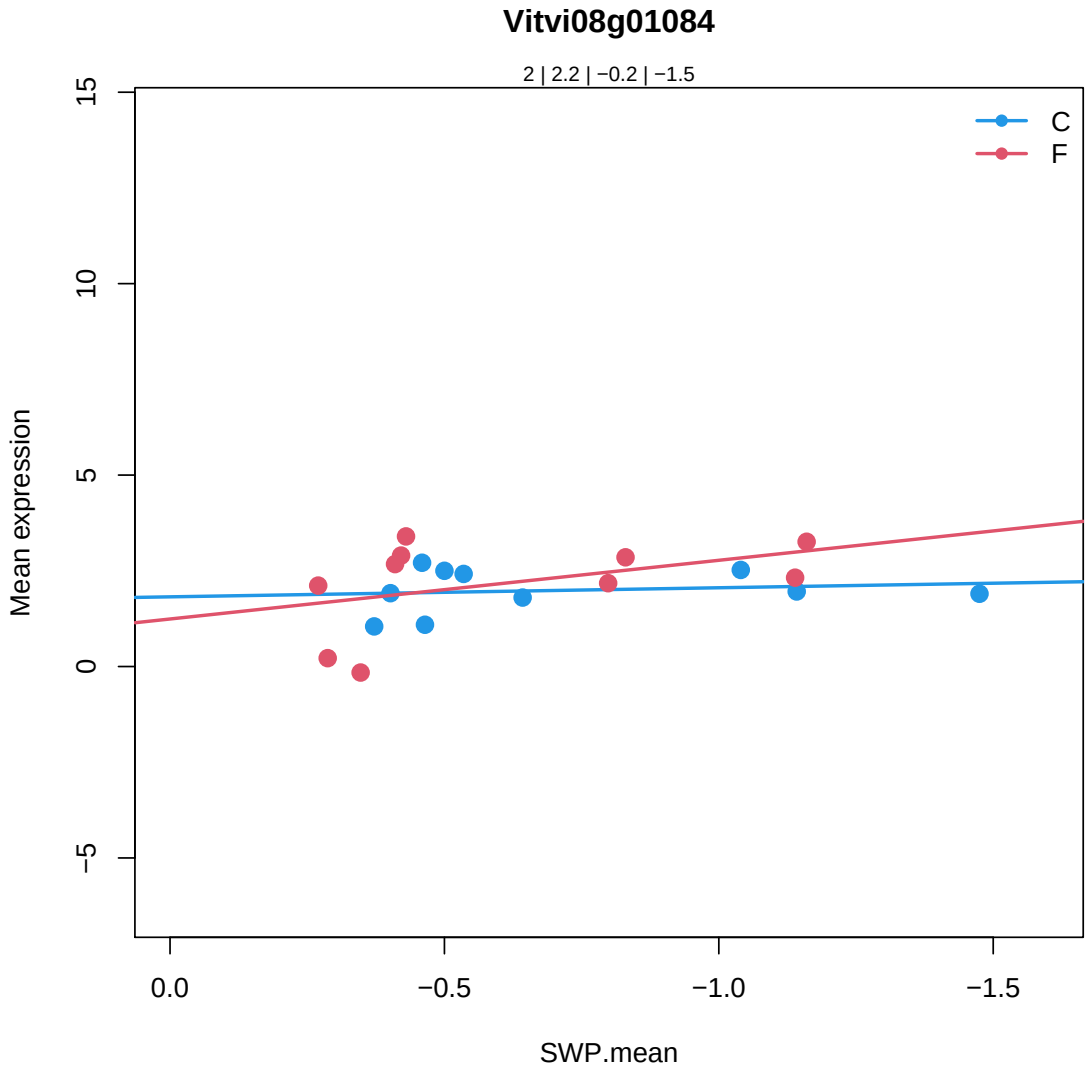
7.6.692 Vitvi08g01084: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01084
        35.2
        not assigned.unknown
        DNAse I-like superfamily protein |
        Chr2:15719230-15721885 FORWARD LENGTH=479 |
        201606
```

Coefficients for Vitvi08g01084.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.986564	1.871747e-07	***	2.204216e-07	***
SlopeC	-0.2372294	0.7496445		0.9471084	
MeanF-MeanC	0.1886141	0.6183061		0.8676755	
SlopeF-SlopeC	-1.296106	0.2483867		0.9999488	



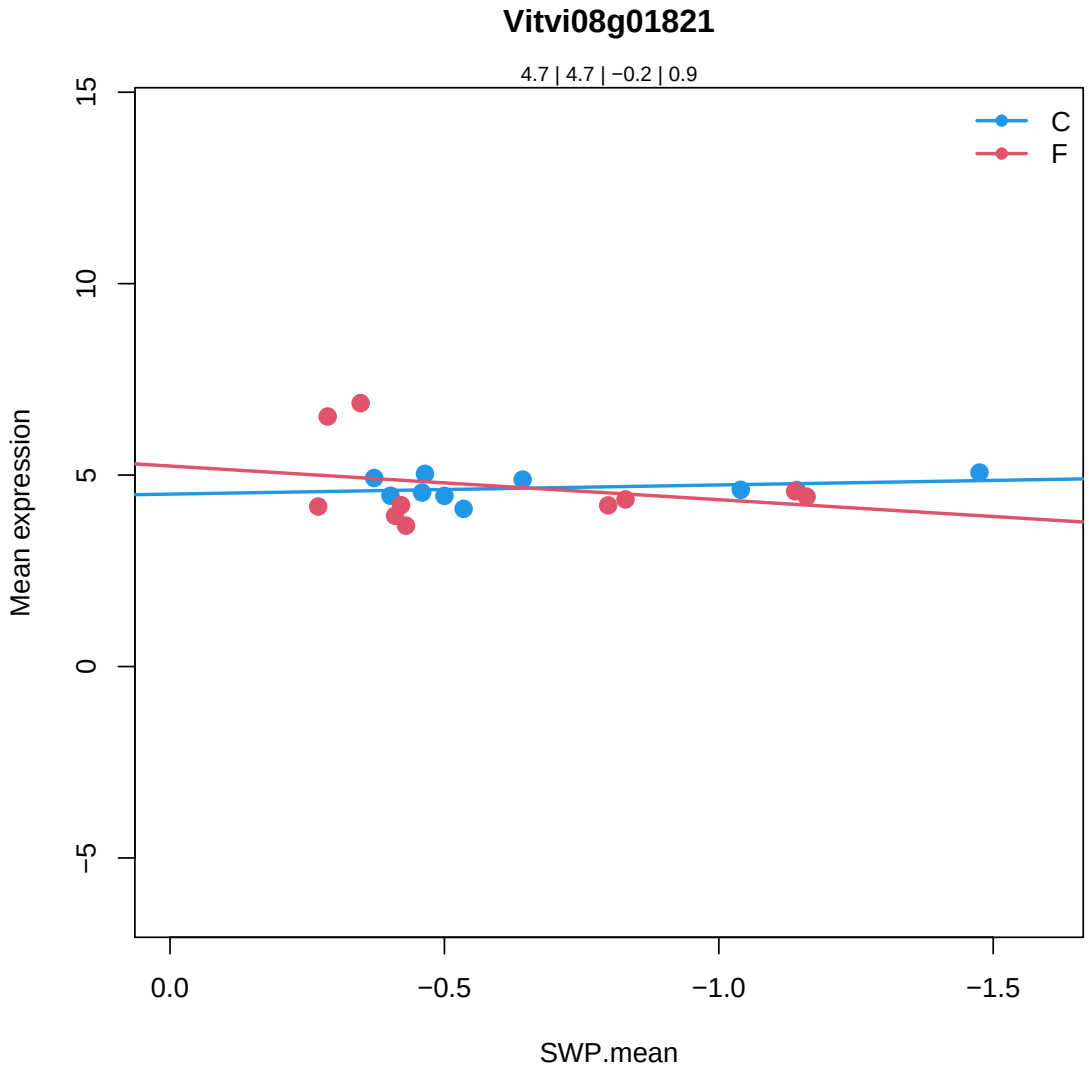
7.6.693 Vitvi08g01821: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01821
        1.1.40
        PS.lightreaction.cyclic electron flow-chlororespiration
        NDH-dependent cyclic electron flow 5 |
        Chr1:20674852-20675857 FORWARD LENGTH=308 |
        201606
```

Coefficients for Vitvi08g01821.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.670842	2.829091e-15	***	5.035735e-15	***
SlopeC	-0.23892	0.719048		0.9377709	
MeanF-MeanC	0.02949112	0.93029		0.9815506	
SlopeF-SlopeC	1.117387	0.2646776		0.9999488	



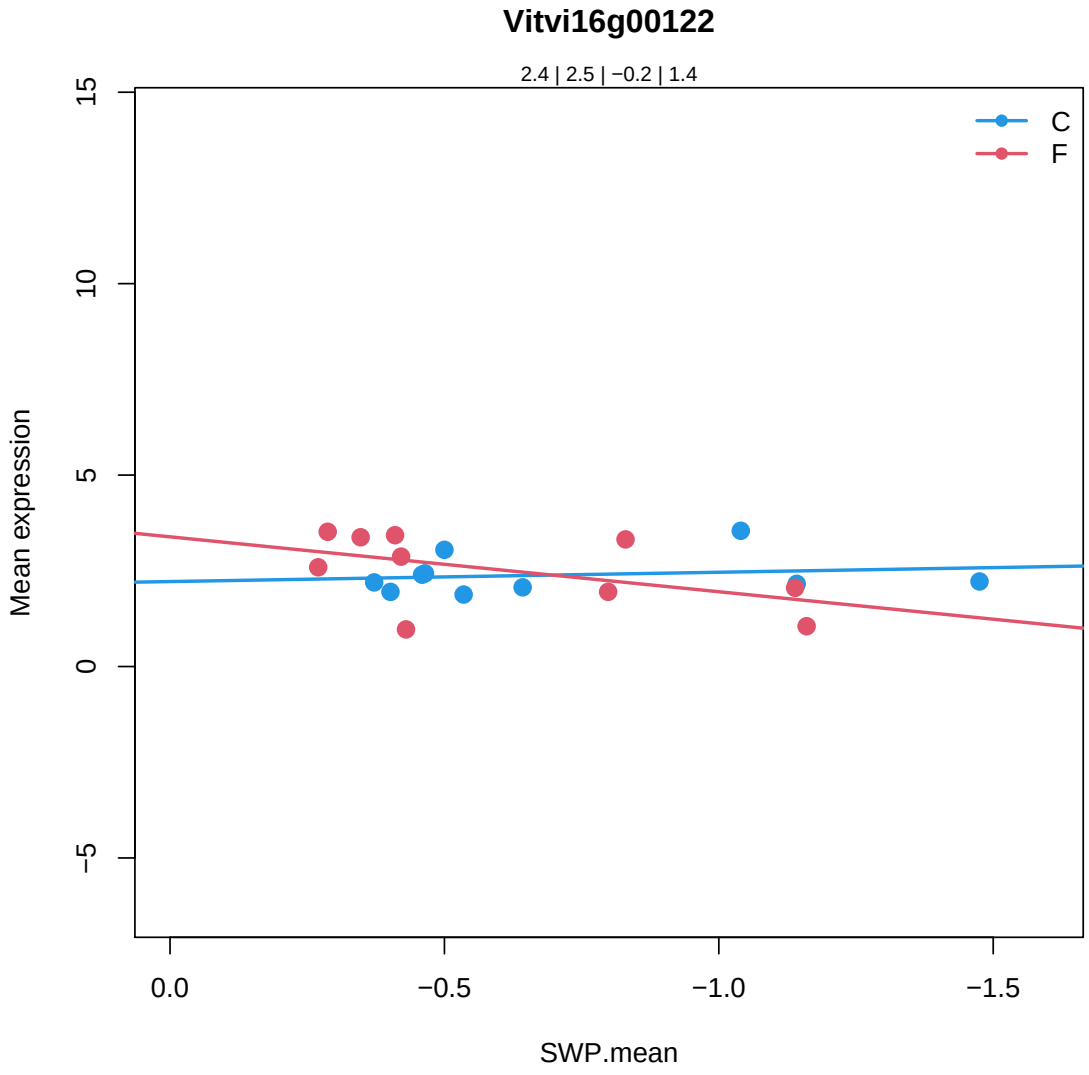
7.6.694 Vitvi16g00122: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g00122
        35.1
        not assigned.no ontology
        Phosphorylase superfamily protein |
        Chr4:12610060-12611126 FORWARD LENGTH=199 |
        201606
```

Coefficients for Vitvi16g00122.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.38968	2.314777e-10	***	2.985937e-10	***
SlopeC	-0.2432765	0.6882766		0.9306347	
MeanF-MeanC	0.1236257	0.6883638		0.9005271	
SlopeF-SlopeC	1.677468	0.07319082	.	0.9999488	



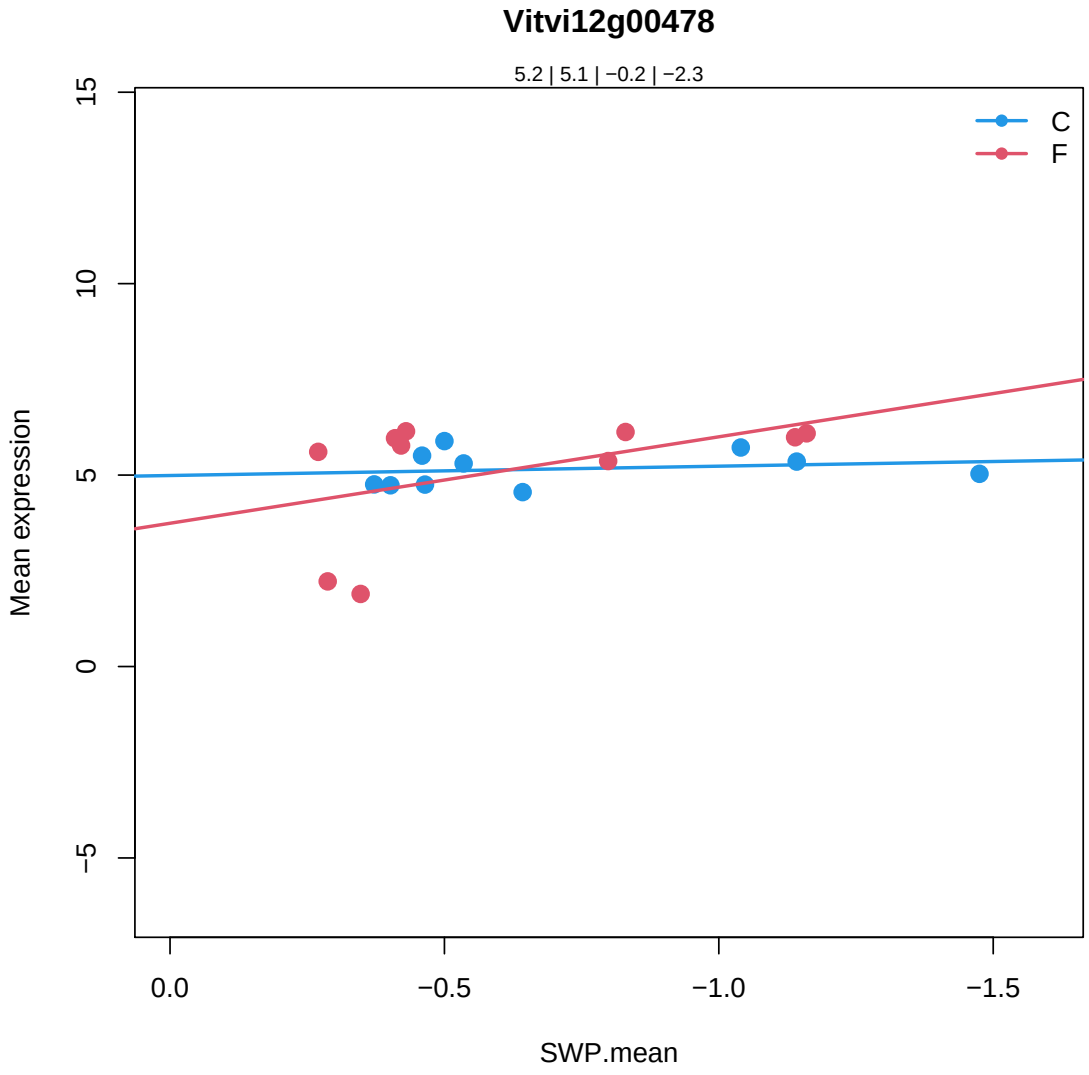
7.6.695 Vitvi12g00478: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00478
        35.1
        not assigned.no ontology
        Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein |
        Chr4:1501907-1503503 FORWARD LENGTH=361 |
        201606
```

Coefficients for Vitvi12g00478.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.160011	1.616356e-13	***	2.443855e-13	***
SlopeC	-0.2434733	0.7858833		0.9533712	
MeanF-MeanC	-0.04277148	0.9251437		0.9803281	
SlopeF-SlopeC	-2.014384	0.140849		0.9999488	



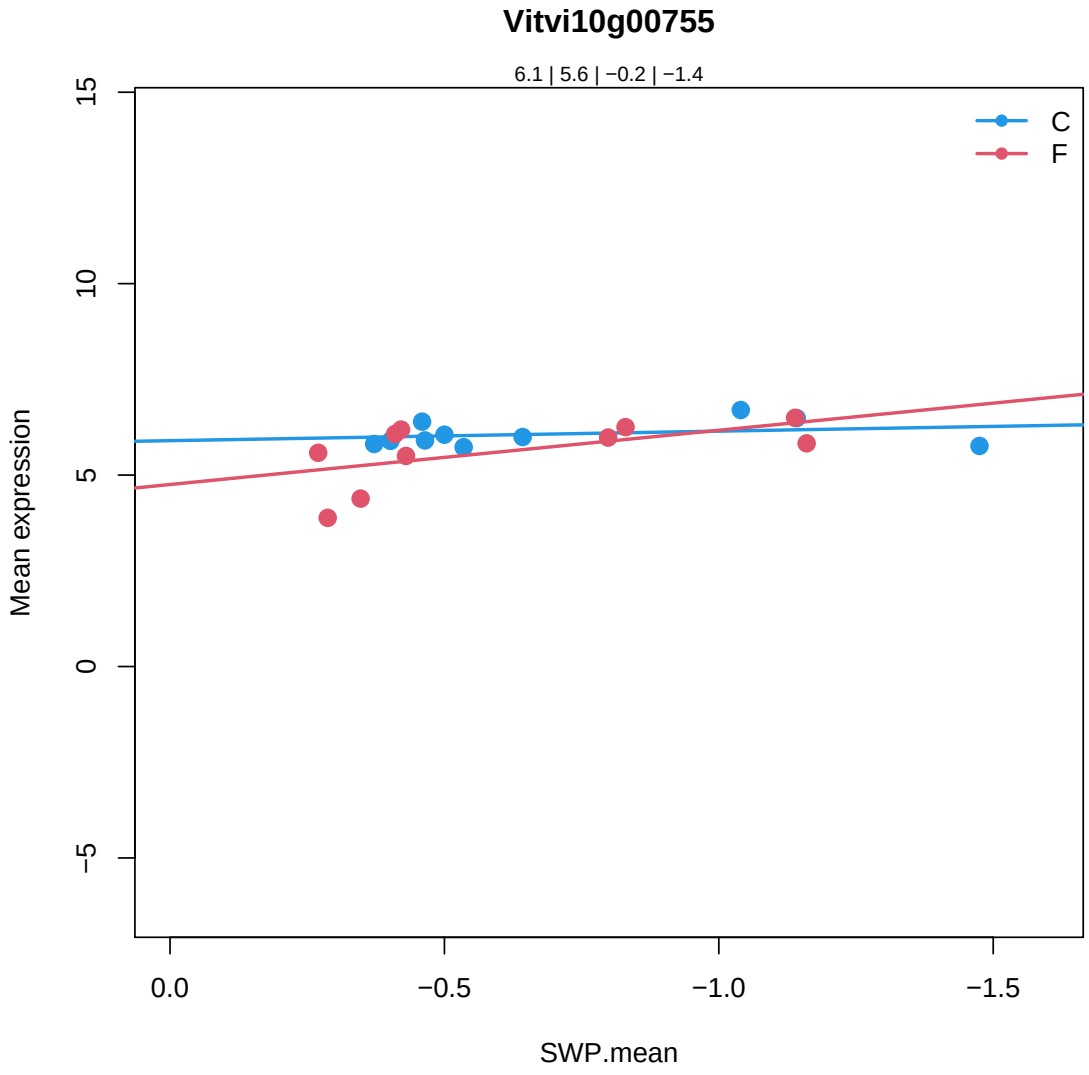
7.6.696 Vitvi10g00755: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00755
        35.1
        not assigned.no ontology
        NAD(P)-binding Rossmann-fold superfamily protein |
        Chr2:14529635-14530732 FORWARD LENGTH=280 |
        201606
```

Coefficients for Vitvi10g00755.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.073076	2.367918e-20	***	1.429945e-19	***
SlopeC	-0.2484981	0.6141477		0.9074064	
MeanF-MeanC	-0.4563731	0.07837799	.	0.31602	
SlopeF-SlopeC	-1.167899	0.1208155		0.9999488	



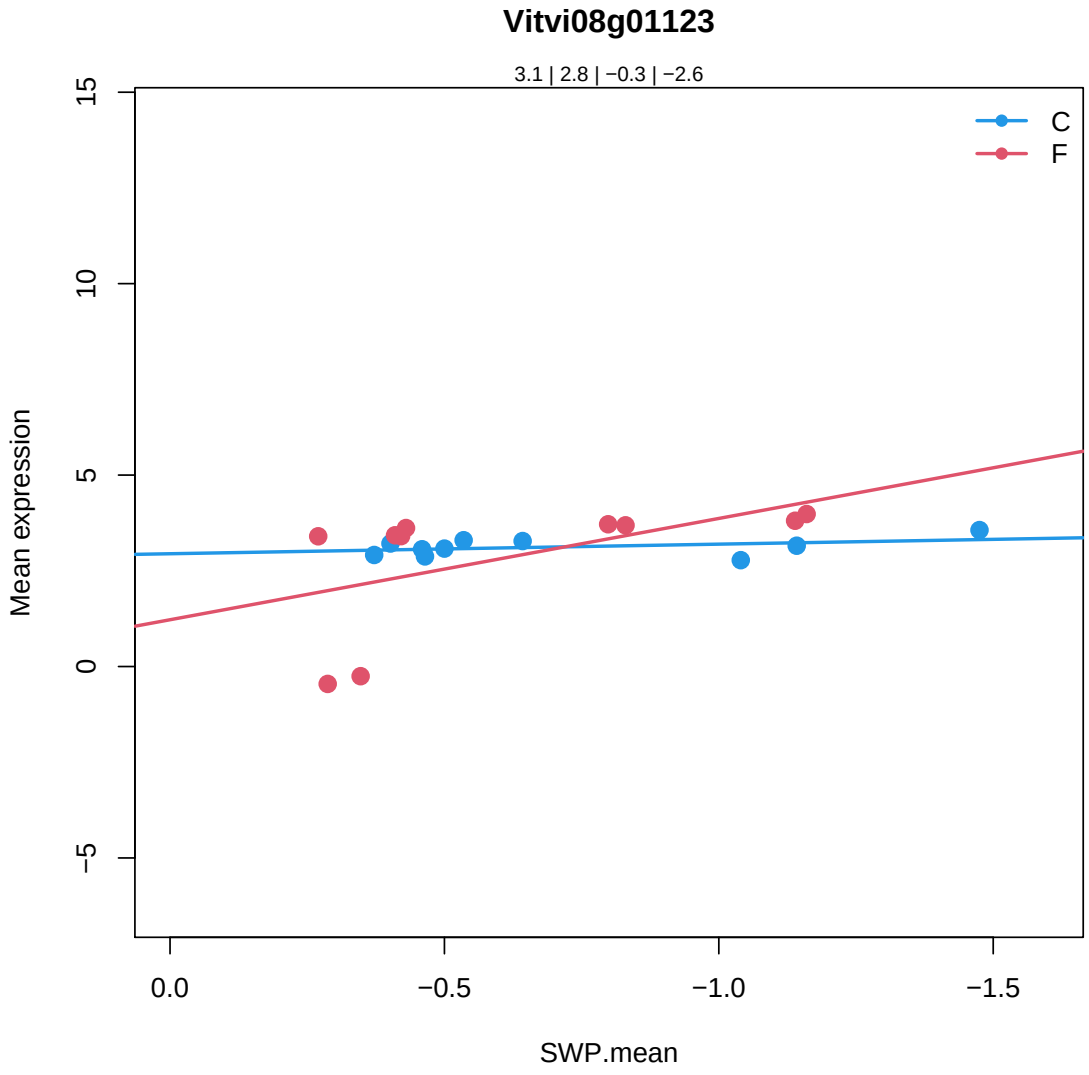
7.6.697 Vitvi08g01123: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01123
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        RING/U-box superfamily protein |
        Chr5:620101-620952 FORWARD LENGTH=283 |
        201606
```

Coefficients for Vitvi08g01123.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.121527	1.06218e-09	***	1.338438e-09	***
SlopeC	-0.2506405	0.7708566		0.9509831	
MeanF-MeanC	-0.2879987	0.512032		0.8136412	
SlopeF-SlopeC	-2.395258	0.07180596	.	0.9999488	



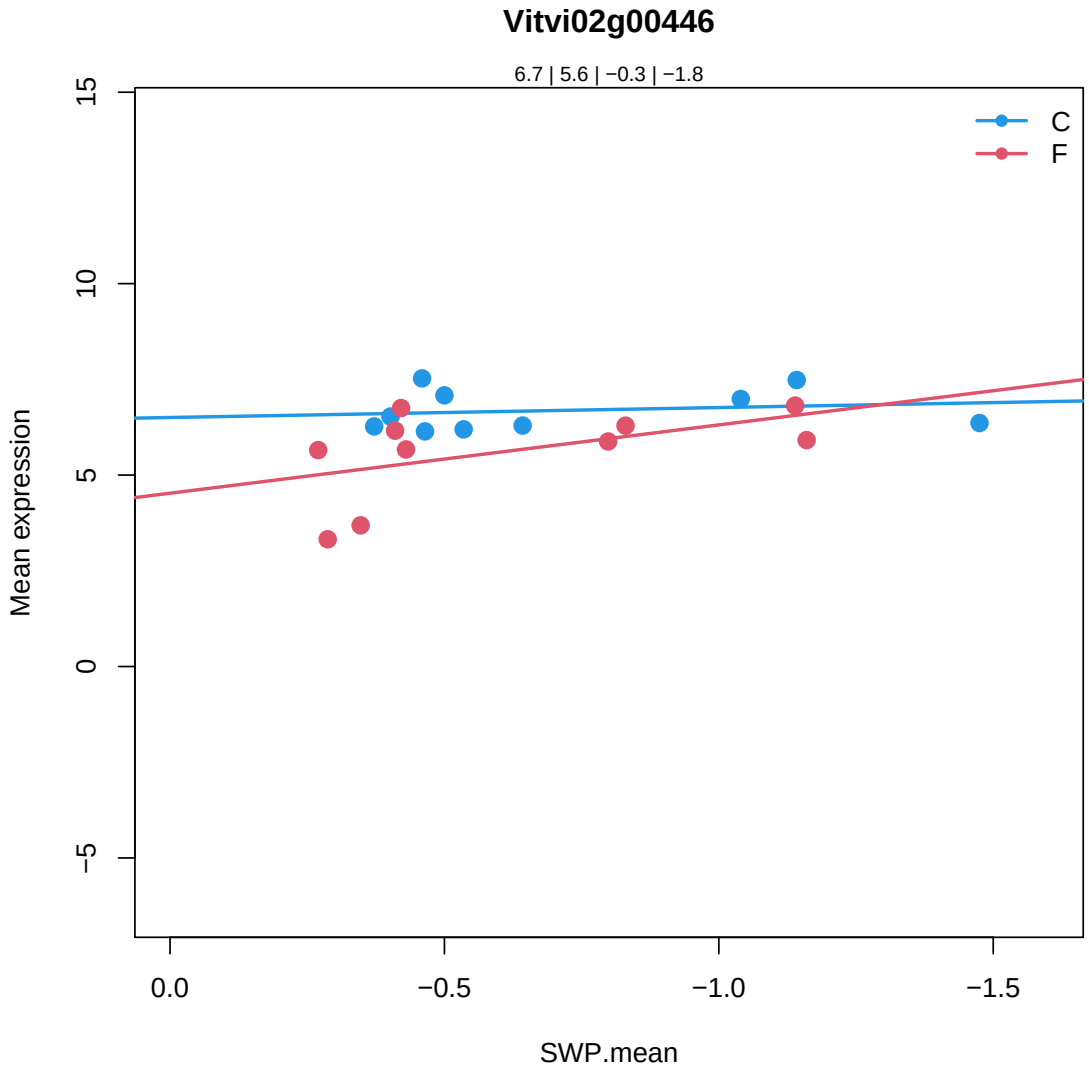
7.6.698 Vitvi02g00446: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00446
        35.2
        not assigned.unknown
        cytochrome P450%2C family 76%2C subfamily C%2C polypeptide 2 |
        Chr2:18779935-18781922 REVERSE LENGTH=512 |
        201606
```

Coefficients for Vitvi02g00446.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.686432	4.391443e-18	***	1.263867e-17	***
SlopeC	-0.2596034	0.7087968		0.9346979	
MeanF-MeanC	-1.072912	0.005621902	**	0.04984818	*
SlopeF-SlopeC	-1.524501	0.1499294		0.9999488	



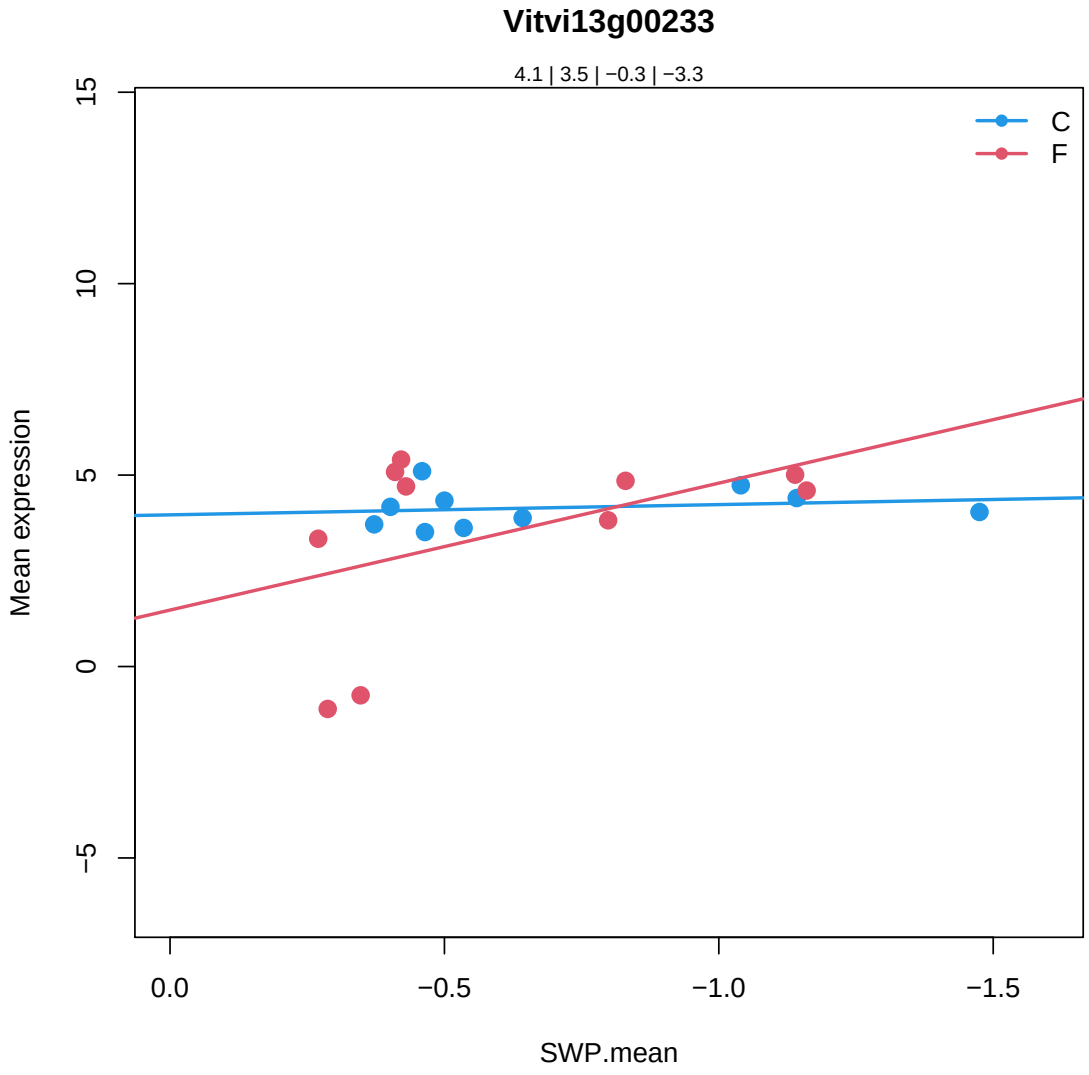
7.6.699 Vitvi13g00233: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00233
        35.2
        not assigned.unknown
        exocyst subunit exo70 family protein H2 |
        Chr2:16447096-16449009 REVERSE LENGTH=637 |
        201606
```

Coefficients for Vitvi13g00233.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.149428	7.549148e-09	***	9.24804e-09	***
SlopeC	-0.2676308	0.8341394		0.967871	
MeanF-MeanC	-0.6551813	0.3187257		0.6800137	
SlopeF-SlopeC	-3.048163	0.1194204		0.9999488	



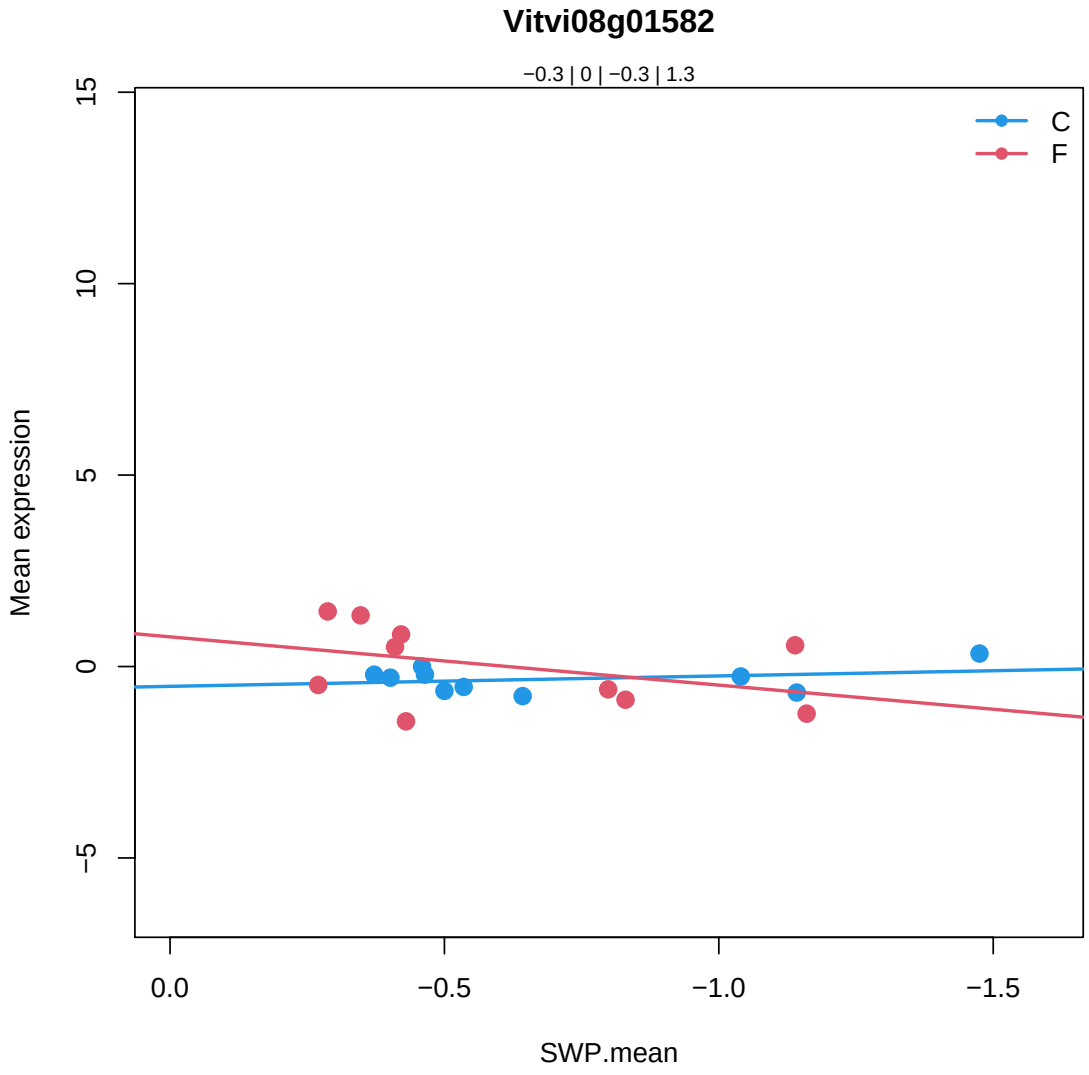
7.6.700 Vitvi08g01582: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01582
        26.2
        misc.UDP glucosyl and glucoronyl transferases
        UDP-Glycosyltransferase superfamily protein |
        Chr2:15417618-15419108 REVERSE LENGTH=496 |
        201606
```

Coefficients for Vitvi08g01582.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.3266665	0.1562115		0.160703	
SlopeC	-0.2721566	0.6642967		0.9233473	
MeanF-MeanC	0.3334847	0.3005846		0.6662078	
SlopeF-SlopeC	1.532648	0.1104504		0.9999488	



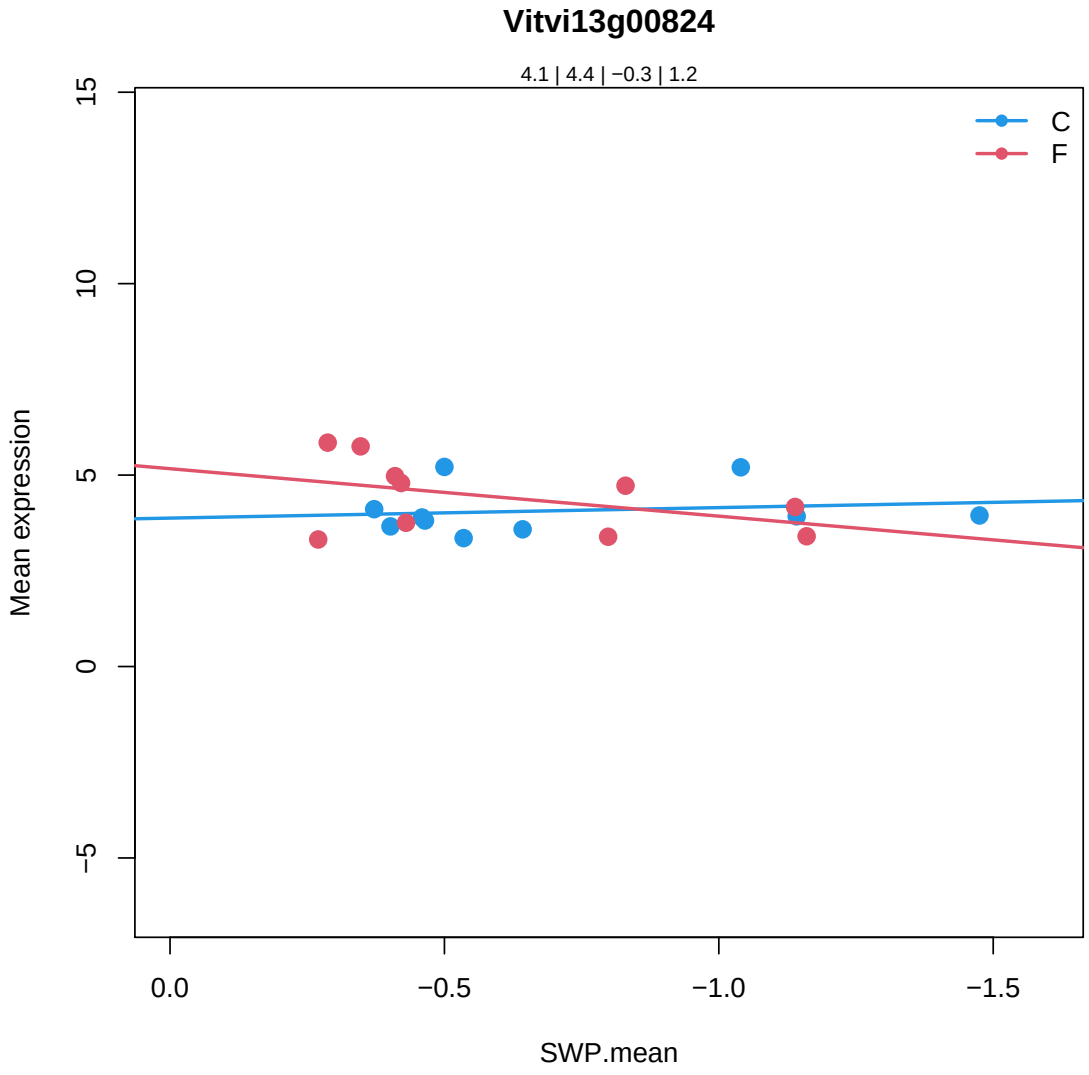
7.6.701 Vitvi13g00824: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00824
        31.1
        cell.organisation
        RNA-directed DNA polymerase (reverse transcriptase)-related family pro
        Chr3:8789309-8790907 FORWARD LENGTH=532 |
        201606
```

Coefficients for Vitvi13g00824.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.06913	2.949111e-14	***	4.725647e-14	***
SlopeC	-0.2740854	0.6732507		0.9246326	
MeanF-MeanC	0.342419	0.3050614		0.6685796	
SlopeF-SlopeC	1.513357	0.1273654		0.9999488	



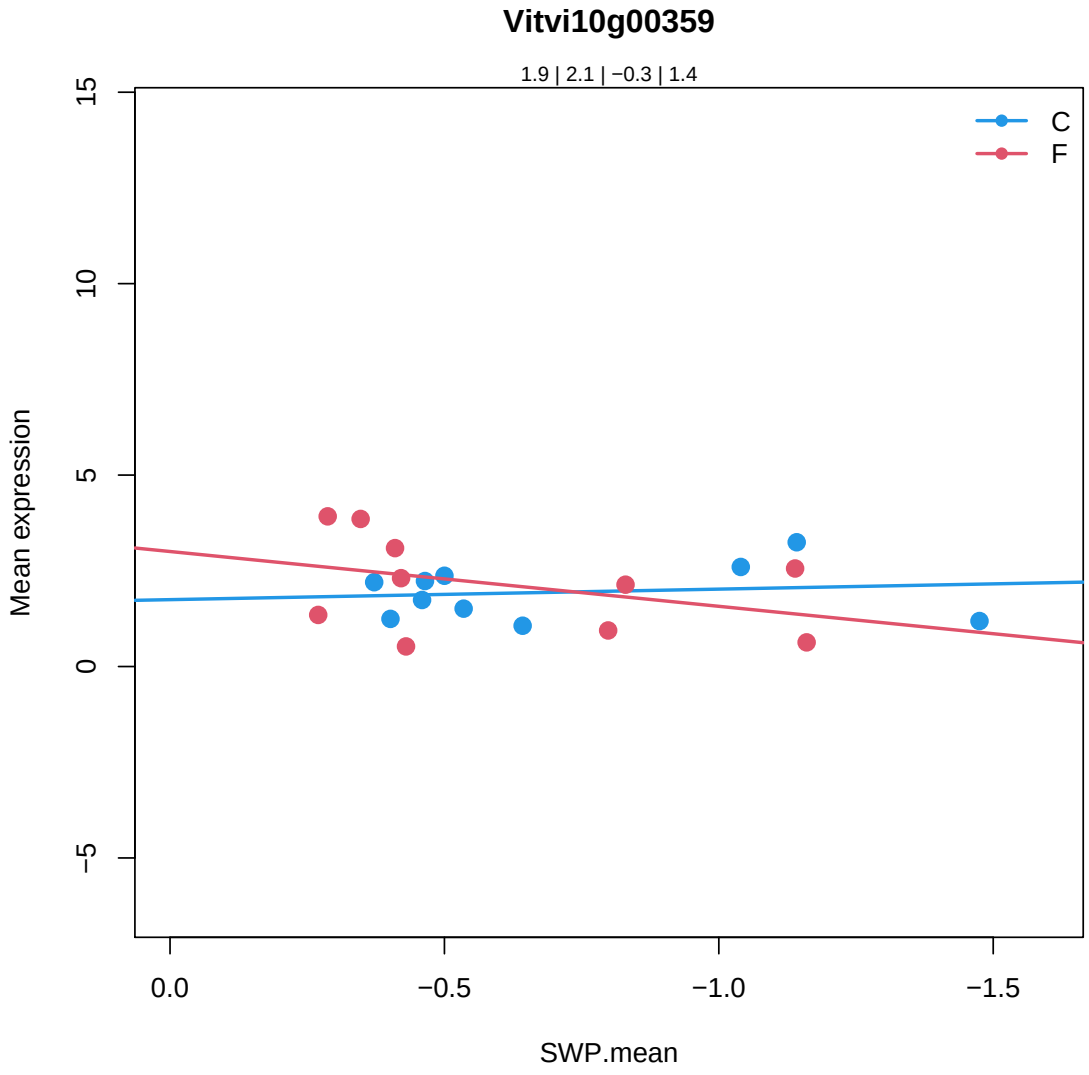
7.6.702 Vitvi10g00359: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00359
        35.1.3
        not assigned.no ontology.armadillo/beta-catenin repeat family protein
        ARM repeat superfamily protein |
        Chr1:22634099-22635820 FORWARD LENGTH=573 |
        201606
```

Coefficients for Vitvi10g00359.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.939563	1.012599e-06	***	1.169245e-06	***
SlopeC	-0.2746717	0.7346611		0.941727	
MeanF-MeanC	0.1922304	0.6411631		0.8777751	
SlopeF-SlopeC	1.705824	0.1663439		0.9999488	



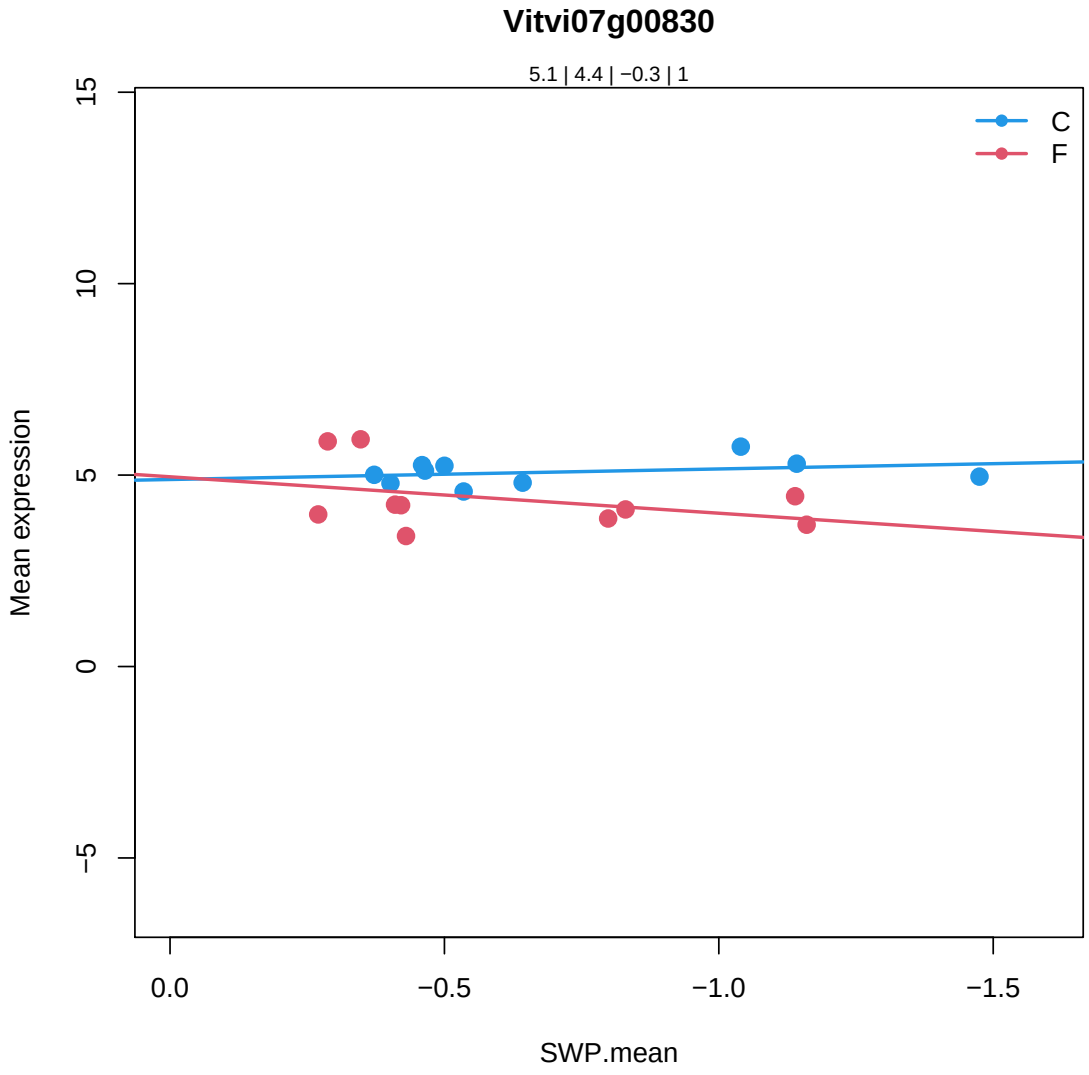
7.6.703 Vitvi07g00830: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g00830
        35.2
        not assigned.unknown
        hypothetical protein |
        Chr4:7668292-7669166 REVERSE LENGTH=185 |
        201606
```

Coefficients for Vitvi07g00830.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.078297	7.080454e-18	***	1.932324e-17	***
SlopeC	-0.2753415	0.6107447		0.9065647	
MeanF-MeanC	-0.7029073	0.01675715	*	0.110616	
SlopeF-SlopeC	1.226528	0.1367272		0.9999488	



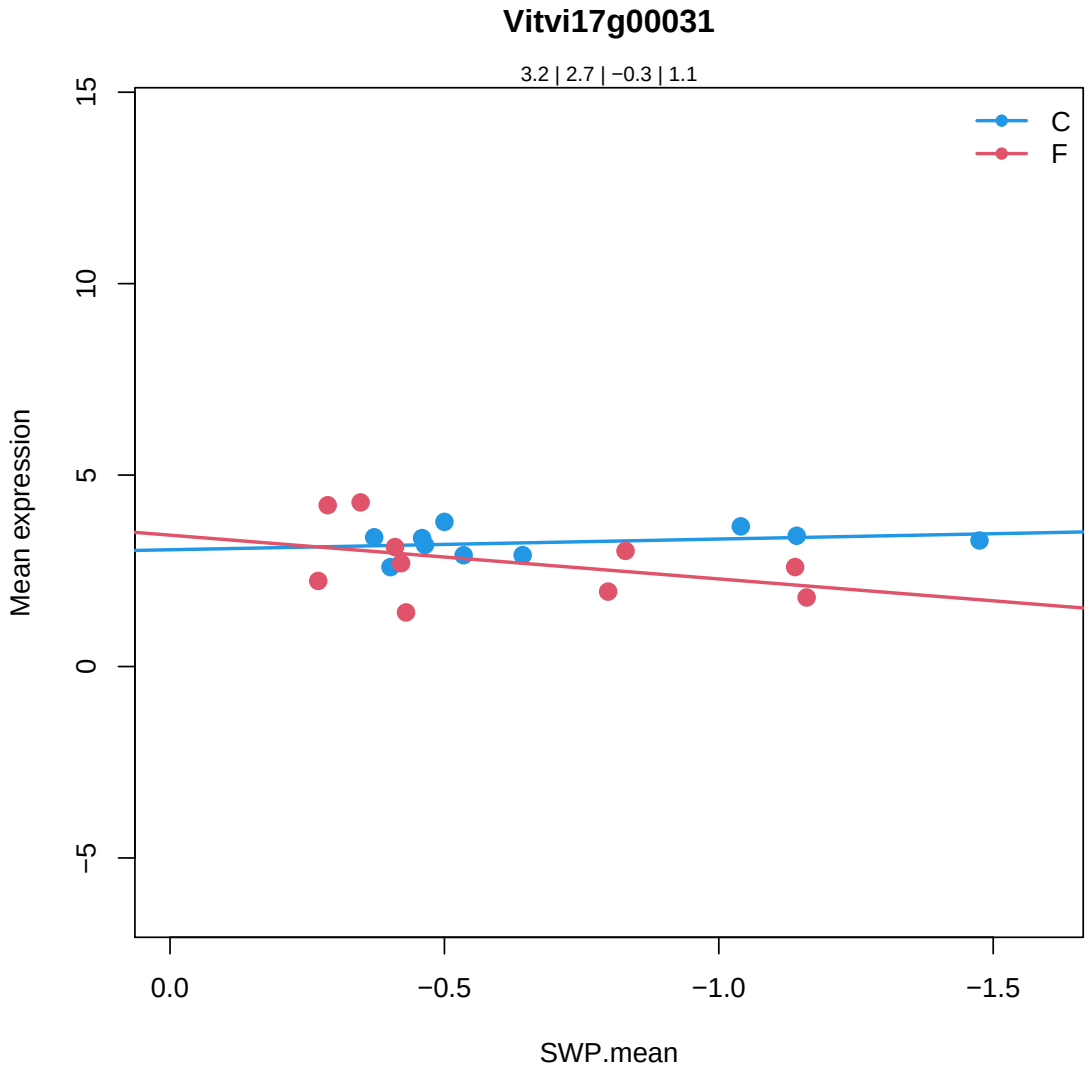
7.6.704 Vitvi17g00031: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00031
        26.3.3
        misc.gluco-, galacto- and mannosidases.alpha-mannosidase
        Glycosyl hydrolase family 38 protein |
        Chr3:9816707-9823056 FORWARD LENGTH=1019 |
        201606
```

Coefficients for Vitvi17g00031.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.245982	3.55717e-13	***	5.256267e-13	***
SlopeC	-0.2798199	0.6340032		0.9122741	
MeanF-MeanC	-0.5119315	0.09649755	.	0.3576855	
SlopeF-SlopeC	1.423119	0.1134402		0.9999488	



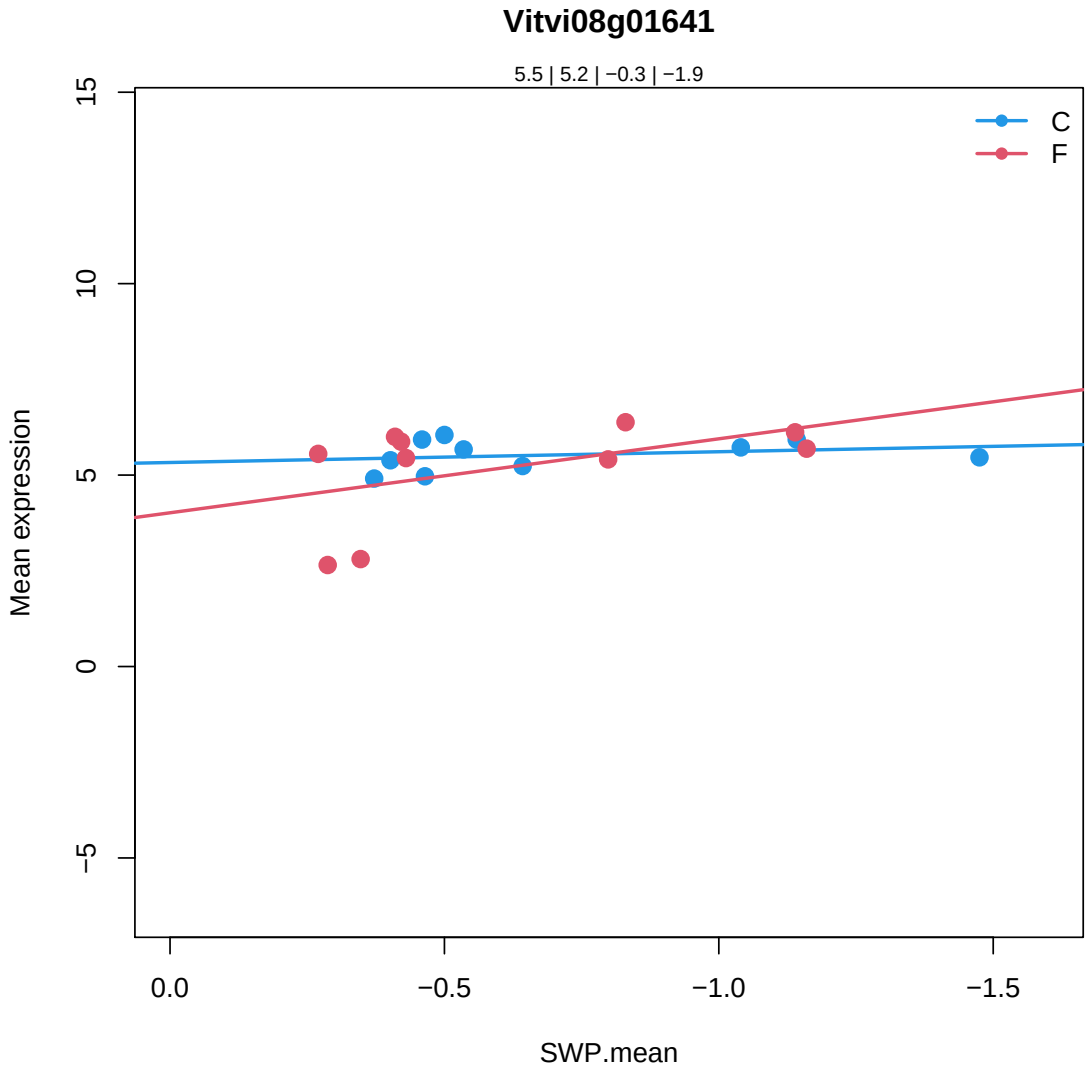
7.6.705 Vitvi08g01641: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01641
        34.3
        transport.amino acids
        Transmembrane amino acid transporter family protein |
        Chr2:17167561-17170145 REVERSE LENGTH=536 |
        201606
```

Coefficients for Vitvi08g01641.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.525886	7.951446e-16	***	1.509289e-15	***
SlopeC	−0.280978	0.7036238		0.9337836	
MeanF−MeanC	−0.333471	0.3780163		0.729517	
SlopeF−SlopeC	−1.65118	0.1425484		0.9999488	



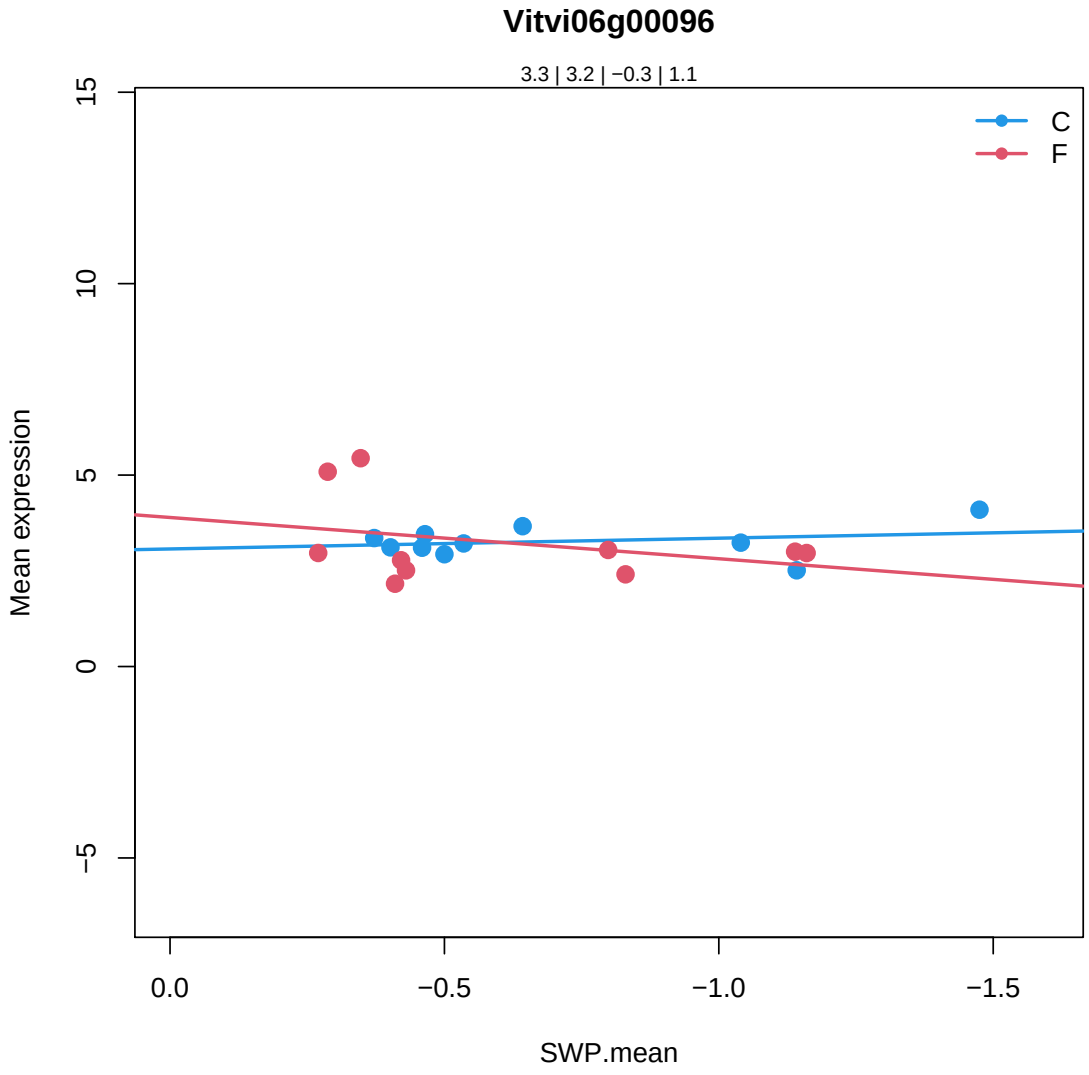
7.6.706 Vitvi06g00096: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00096
        35.2
        not assigned.unknown
        6%2C7-dimethyl-8-ribityllumazine synthase |
        Chr3:13489595-13490704 FORWARD LENGTH=249 |
        201606
```

Coefficients for Vitvi06g00096.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.267949	6.547688e-12	***	9.016973e-12	***
SlopeC	-0.2810505	0.6822067		0.9280144	
MeanF-MeanC	-0.0321023	0.9265542		0.9806927	
SlopeF-SlopeC	1.358443	0.1917401		0.9999488	



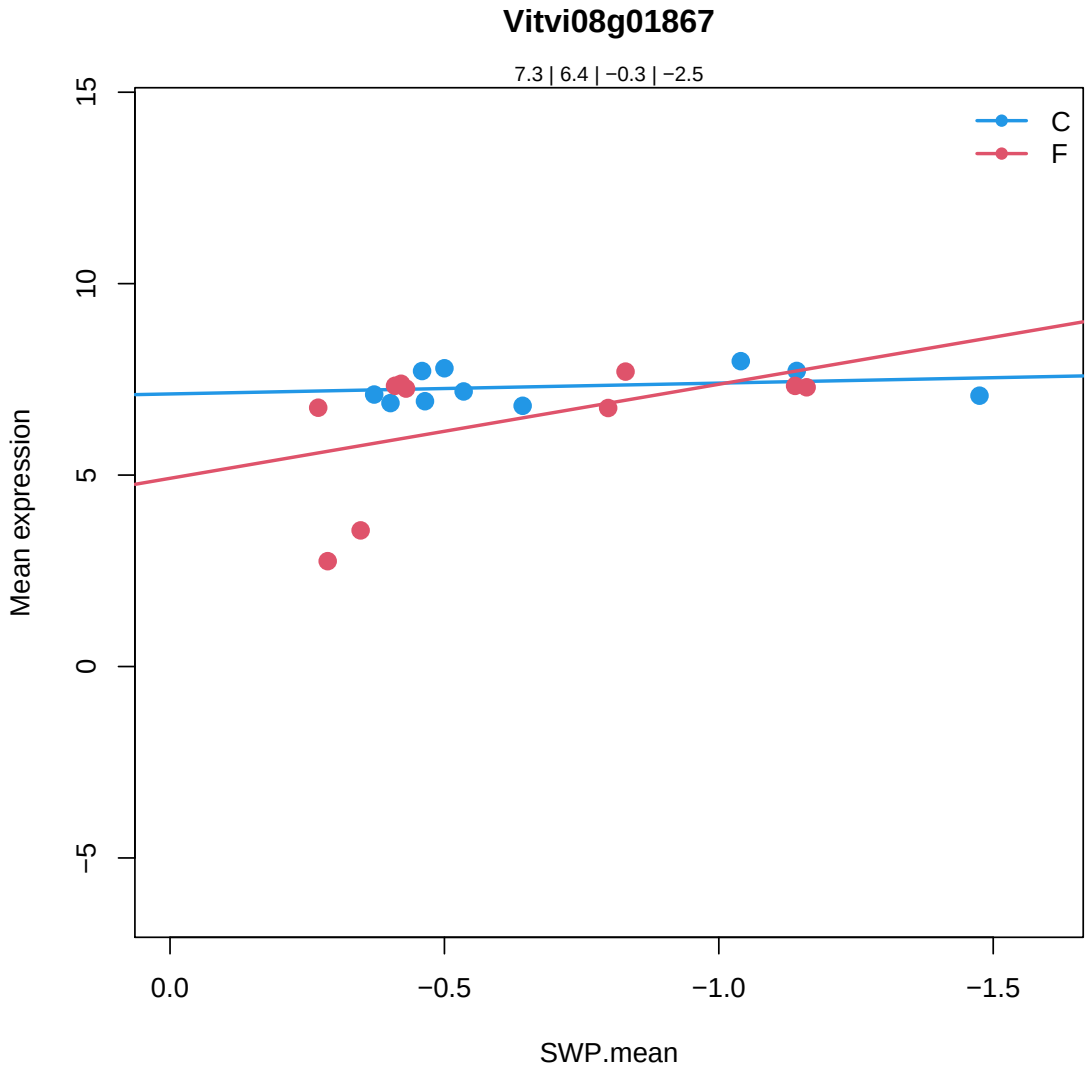
7.6.707 Vitvi08g01867: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01867
        29.5
        protein.degradation
        Peptidase S41 family protein |
        Chr3:21381664-21383629 FORWARD LENGTH=370 |
        201606
```

Coefficients for Vitvi08g01867.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.318216	3.920092e-16	***	7.753703e-16	***
SlopeC	-0.2826572	0.7647097		0.9491522	
MeanF-MeanC	-0.9062074	0.06934472	.	0.2946414	
SlopeF-SlopeC	-2.173633	0.1319412		0.9999488	



7.6.708 Vitvi06g00215: type5

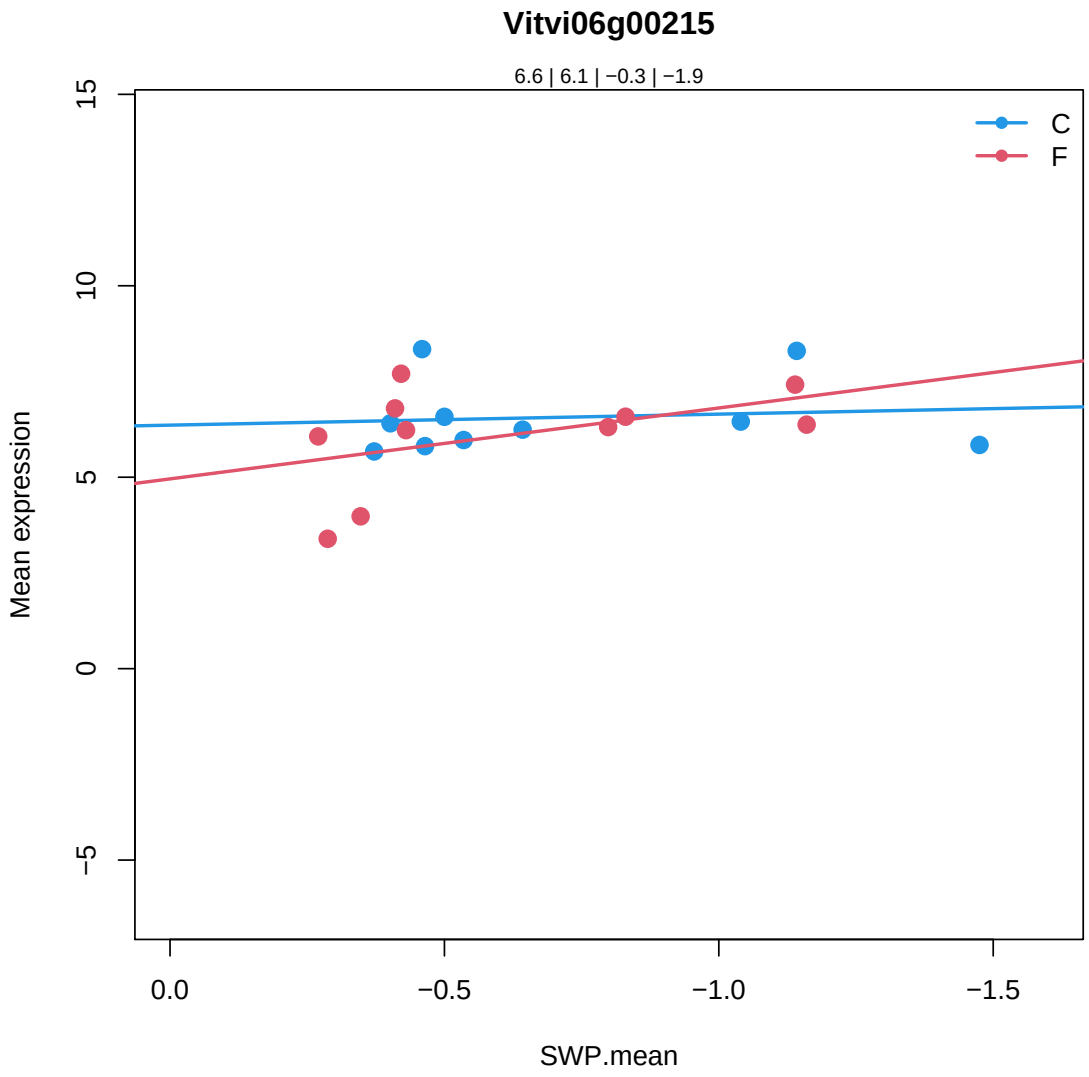
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00215
        34.9
        transport.metabolite transporters at the mitochondrial membrane
        dicarboxylate transporter 1 |
        Chr5:4059927-4061919 REVERSE LENGTH=557 |
        201606

Vitvi06g00215
        34.8
        transport.metabolite transporters at the envelope membrane
        dicarboxylate transporter 1 |
        Chr5:4059927-4061919 REVERSE LENGTH=557 |
        201606
```

Coefficients for Vitvi06g00215.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.562228	2.384807e-15	***	4.28394e-15	***
SlopeC	-0.2875795	0.7558685		0.9474841	
MeanF-MeanC	-0.4776809	0.3149218		0.6769067	
SlopeF-SlopeC	-1.564903	0.2622583		0.9999488	


Vitvi06g00215
6.6 | 6.1 | −0.3 | −1.9
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

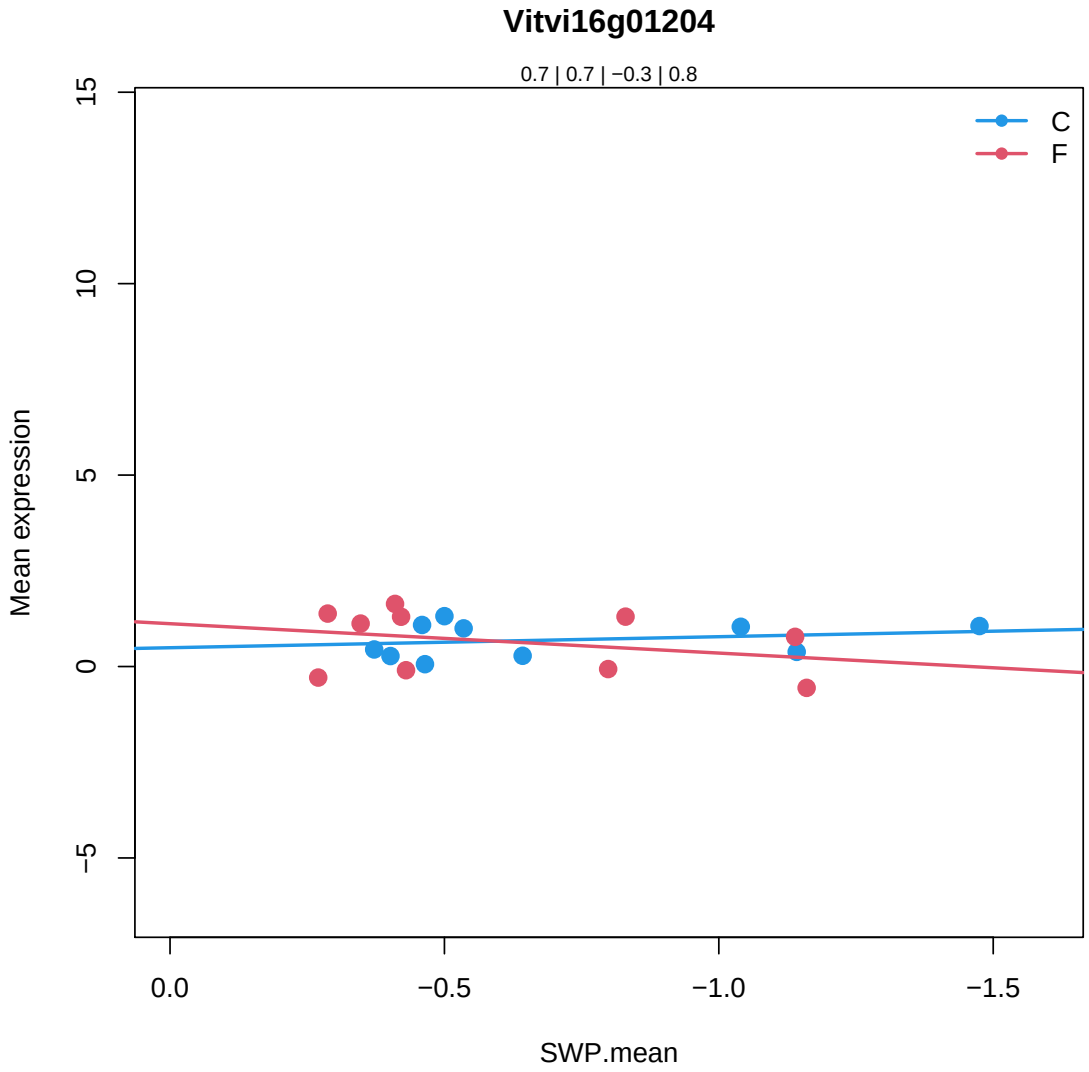
7.6.709 Vitvi16g01204: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01204
        30.2.3
        signalling.receptor kinases.leucine rich repeat III
        Leucine-rich repeat protein kinase family protein |
        Chr4:12367063-12369159 FORWARD LENGTH=638 |
        201606
```

Coefficients for Vitvi16g01204.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6931869	0.002035803	**	0.002188891	**
SlopeC	-0.287955	0.6056337		0.9047128	
MeanF-MeanC	-0.04257597	0.8802765		0.968959	
SlopeF-SlopeC	1.055305	0.2106824		0.9999488	



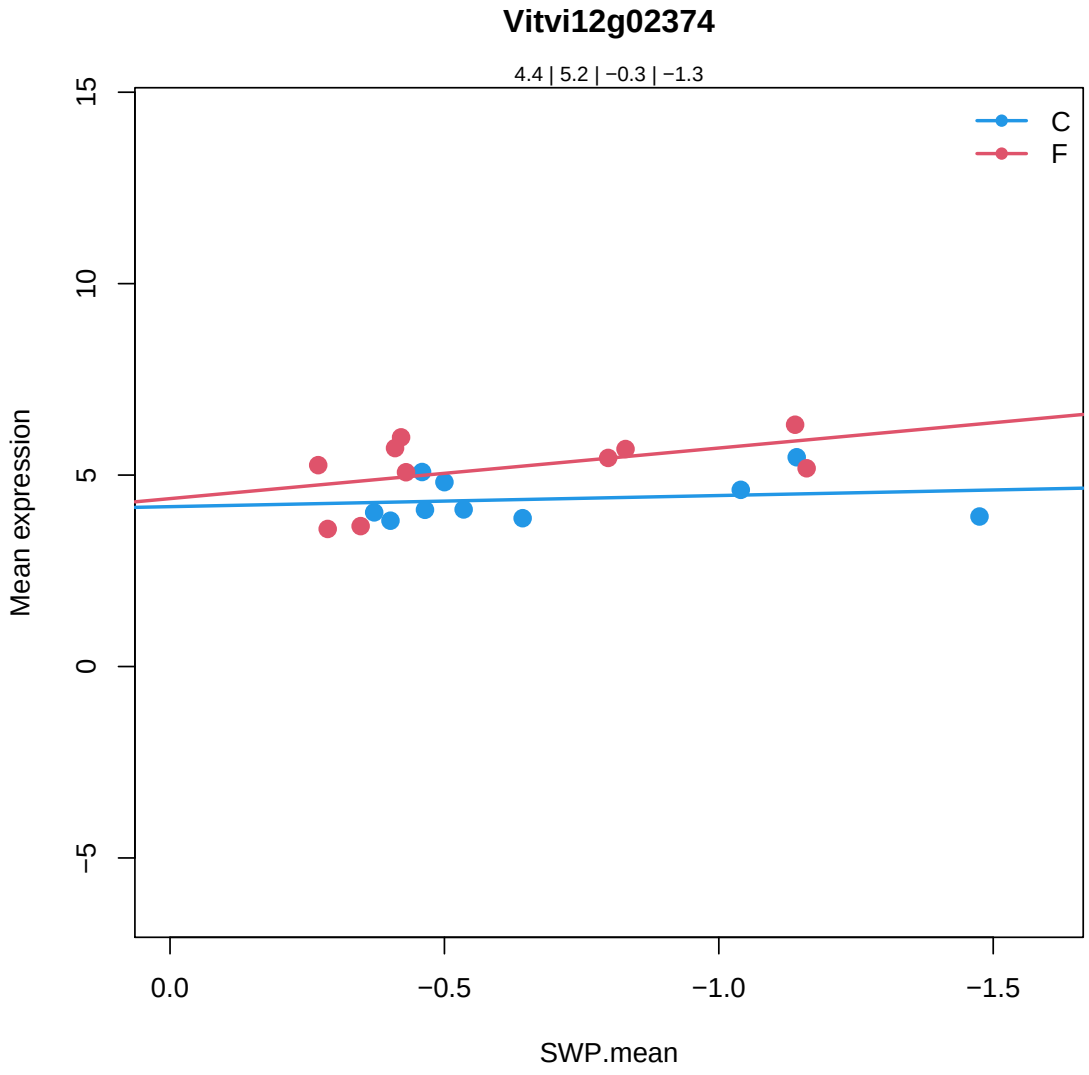
7.6.710 Vitvi12g02374: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02374
        10.2.1
        cell wall.cellulose synthesis.cellulose synthase
        MuDR family transposase |
        Chr1:23844954-23847206 FORWARD LENGTH=750 |
        201606
```

Coefficients for Vitvi12g02374.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.379603	1.300151e-15	***	2.400594e-15	***
SlopeC	-0.2902832	0.6286547		0.9108941	
MeanF-MeanC	0.8106928	0.0133866	*	0.09428772	.
SlopeF-SlopeC	-1.030796	0.2545994		0.9999488	



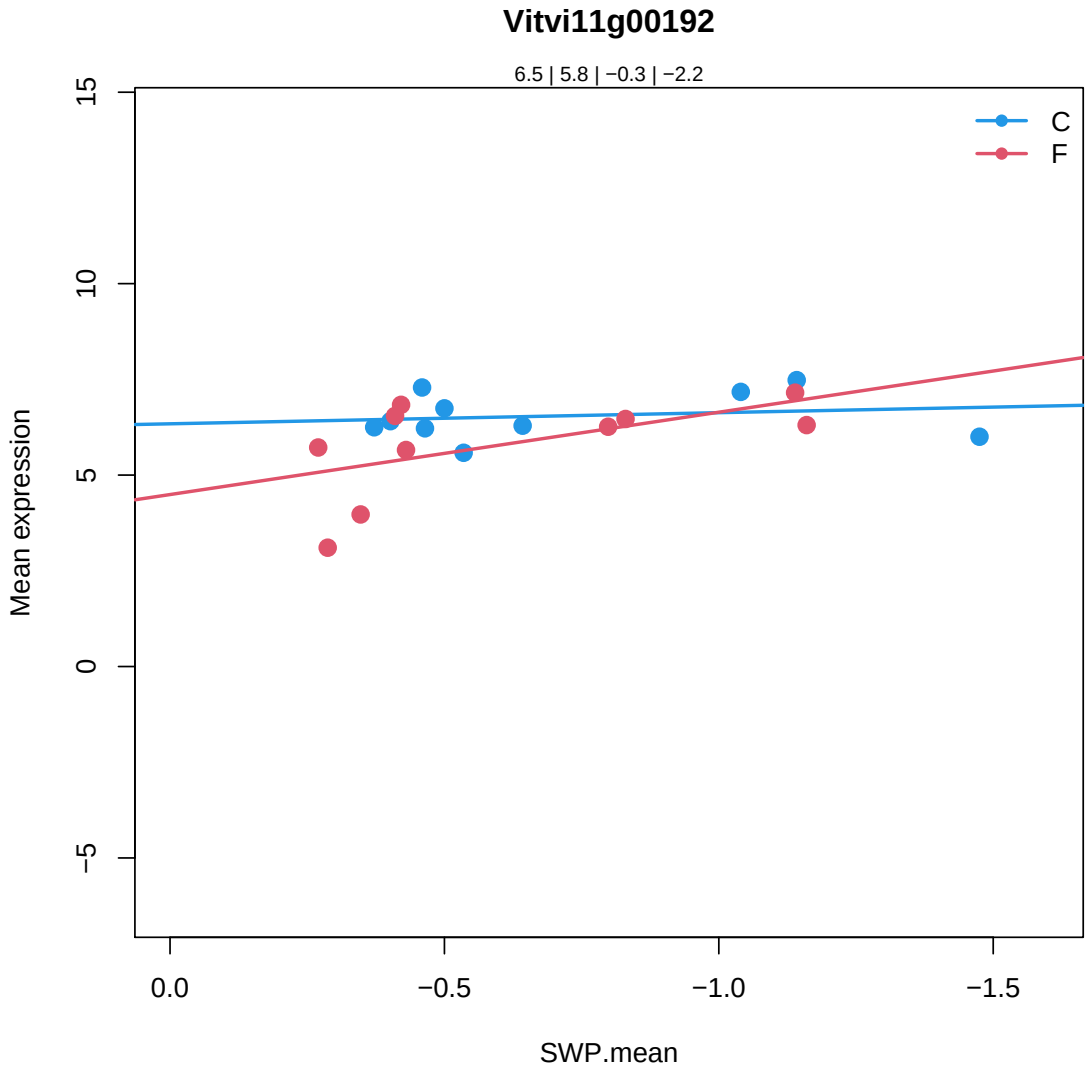
7.6.711 Vitvi11g00192: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00192
        29.2.2.3.3
        protein.synthesis.ribosome biogenesis.pre-rRNA processing and modifica
        S-adenosyl-L-methionine-dependent methyltransferases superfamily prote
        Chr4:14512736-14514404 REVERSE LENGTH=317 |
        201606
```

Coefficients for Vitvi11g00192.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.543284	2.32731e-17	***	5.6884e-17	***
SlopeC	-0.2906447	0.693358		0.9312515	
MeanF-MeanC	-0.7417095	0.05758378	.	0.2614498	
SlopeF-SlopeC	-1.859992	0.1001266		0.9999488	



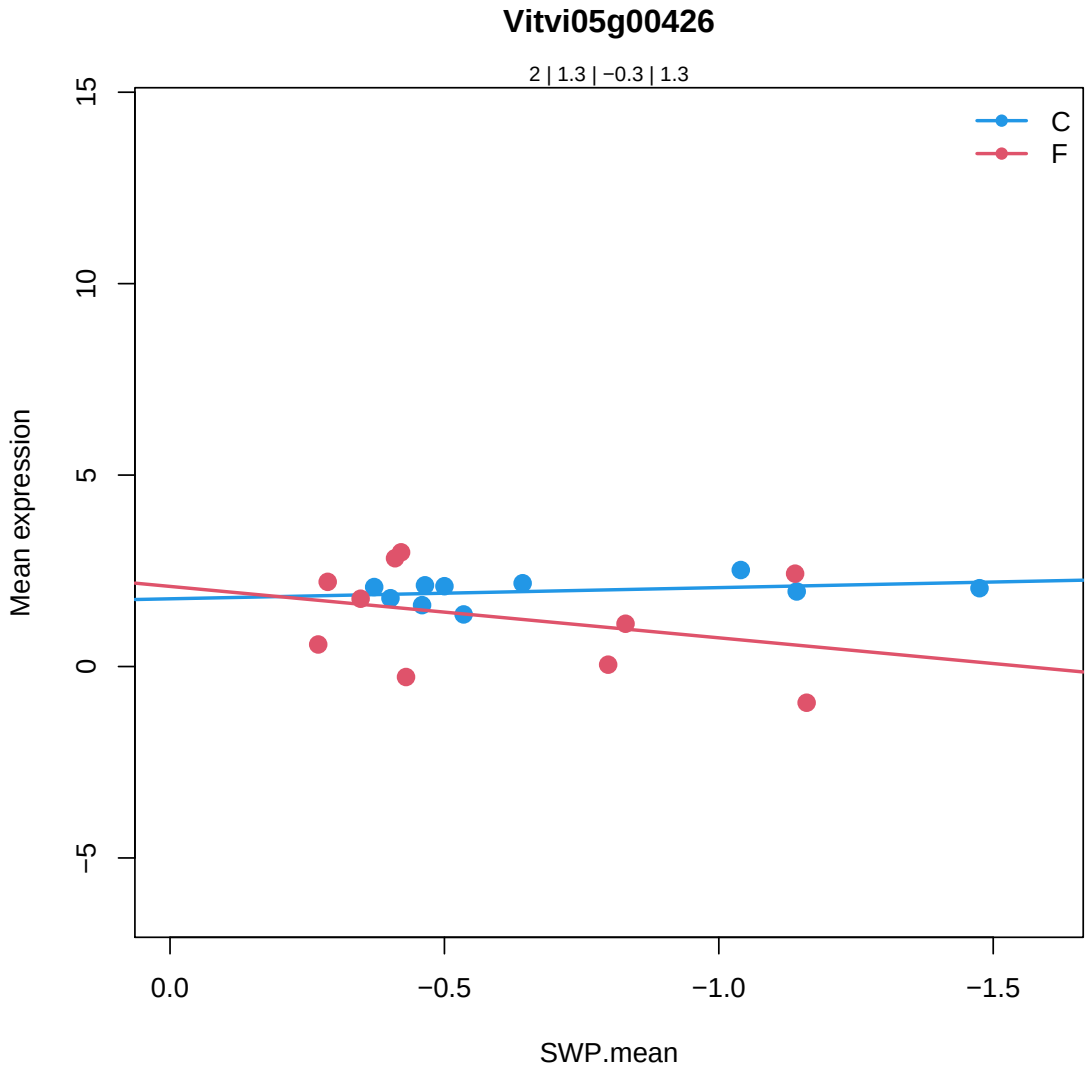
7.6.712 Vitvi05g00426: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00426
        15.2
        metal handling.binding, chelation and storage
        Heavy metal transport/detoxification superfamily protein |
        Chr5:6387910-6389855 FORWARD LENGTH=465 |
        201606
```

Coefficients for Vitvi05g00426.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.97414	6.600325e-07	***	7.653264e-07	***
SlopeC	-0.292347	0.7153996		0.9362587	
MeanF-MeanC	-0.7004089	0.09594443	.	0.3565923	
SlopeF-SlopeC	1.635113	0.1792677		0.9999488	



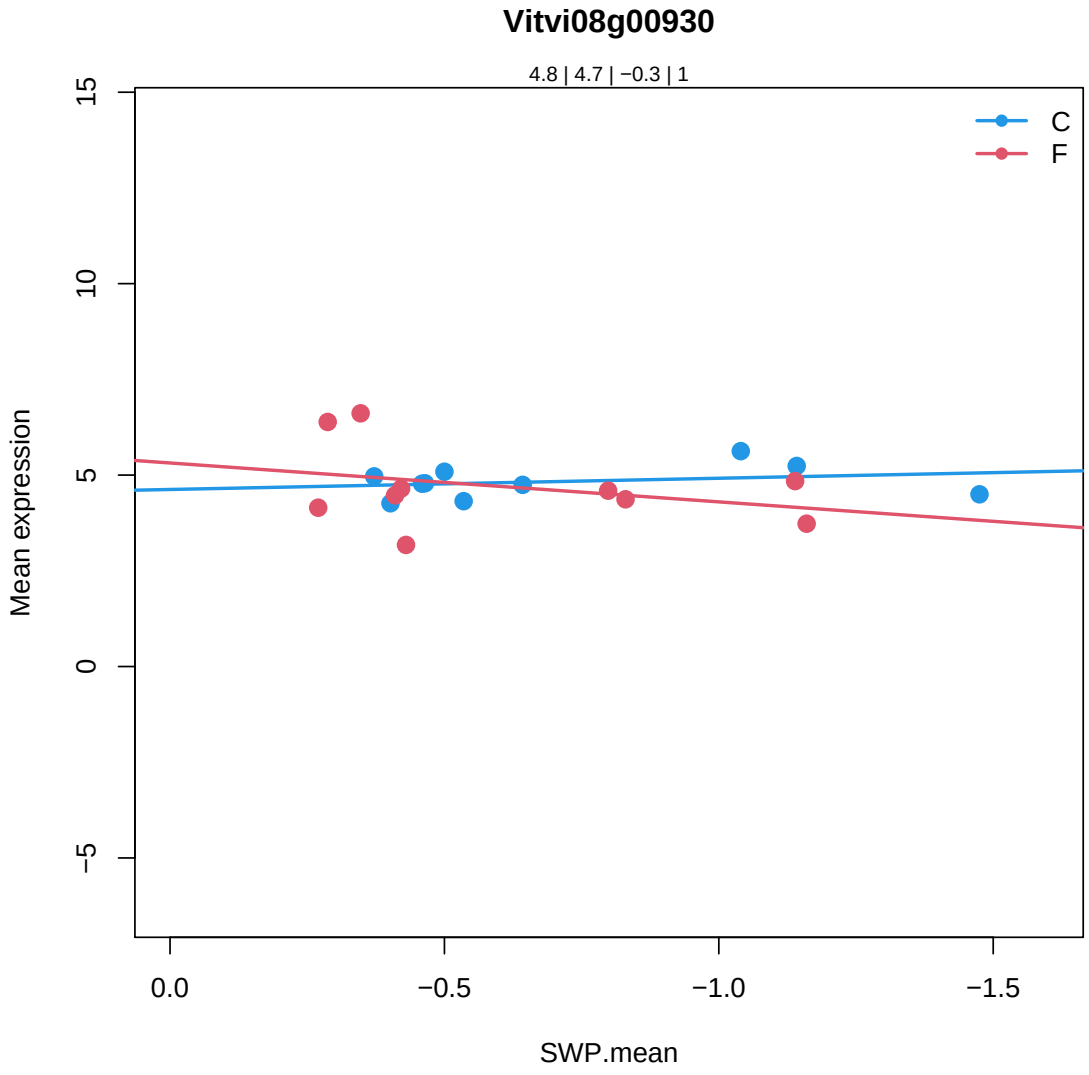
7.6.713 Vitvi08g00930: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g00930
        2.2.2.4
        major CHO metabolism.degradation.starch.D enzyme
        disproportionating enzyme 2 |
        Chr2:17045368-17050779 FORWARD LENGTH=955 |
        201606
```

Coefficients for Vitvi08g00930.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.830005	1.50177e-15	***	2.752192e-15	***
SlopeC	-0.2931755	0.6599429		0.9218432	
MeanF-MeanC	-0.1328711	0.6947054		0.9038582	
SlopeF-SlopeC	1.309049	0.1947499		0.9999488	



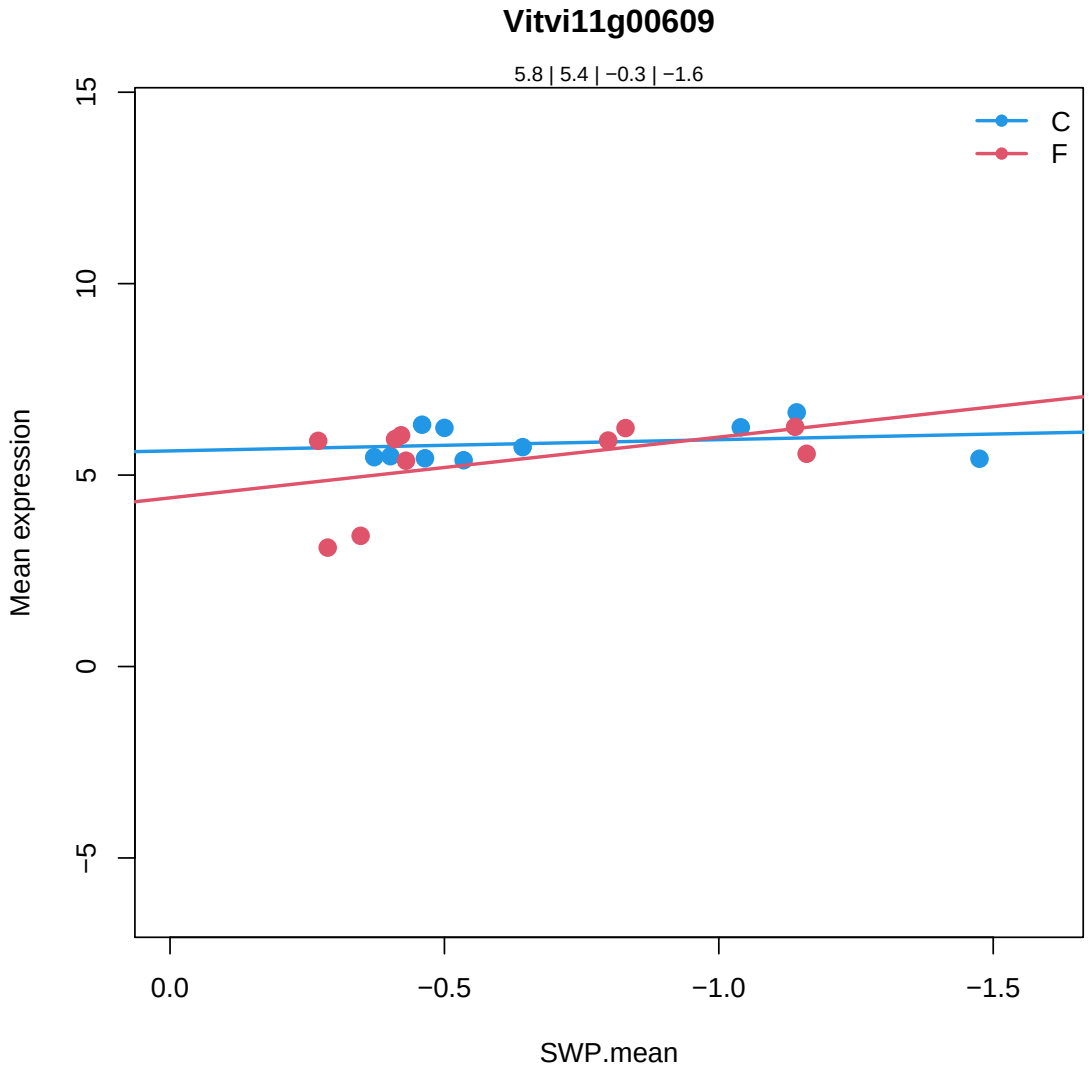
7.6.714 Vitvi11g00609: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00609
        23.4.1
        nucleotide metabolism.phosphotransfer and pyrophosphatases.adenylate k
        RNA-directed DNA polymerase (reverse transcriptase)-related family pro
        Chr3:8789309-8790907 FORWARD LENGTH=532 |
        201606
```

Coefficients for Vitvi11g00609.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.837416	4.262795e-17	***	9.909032e-17	***
SlopeC	-0.2938104	0.6644485		0.9233473	
MeanF-MeanC	-0.4661308	0.184004		0.5202294	
SlopeF-SlopeC	-1.293353	0.2071031		0.9999488	



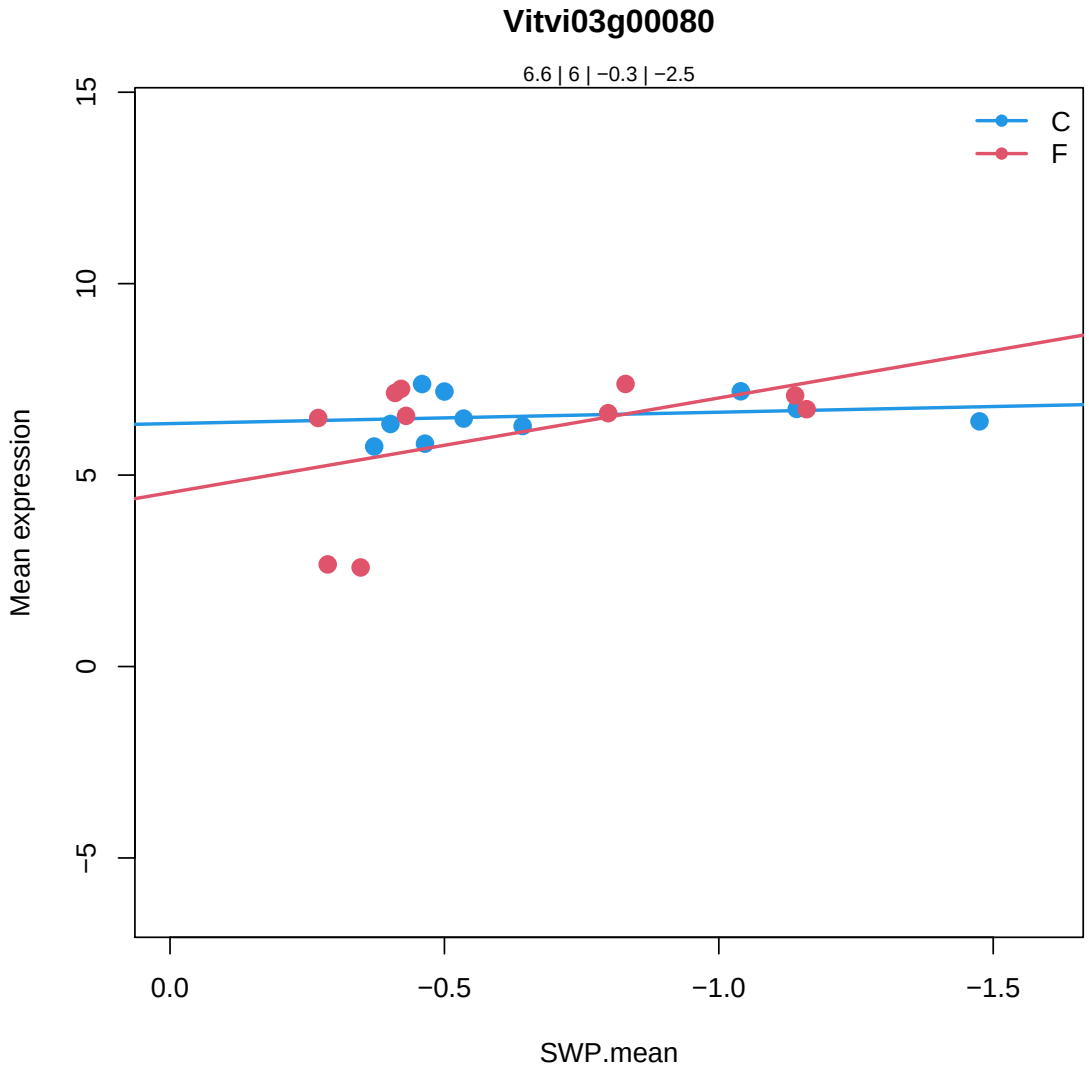
7.6.715 Vitvi03g00080: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00080
        30.3
        signalling.calcium
        Calcium-binding EF-hand family protein |
        Chr4:18115607-18118860 REVERSE LENGTH=375 |
        201606
```

Coefficients for Vitvi03g00080.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.5536	1.528656e-14	***	2.51021e-14	***
SlopeC	-0.2966889	0.7694223		0.9502904	
MeanF-MeanC	-0.505334	0.3309596		0.6907427	
SlopeF-SlopeC	-2.1751	0.1581657		0.9999488	



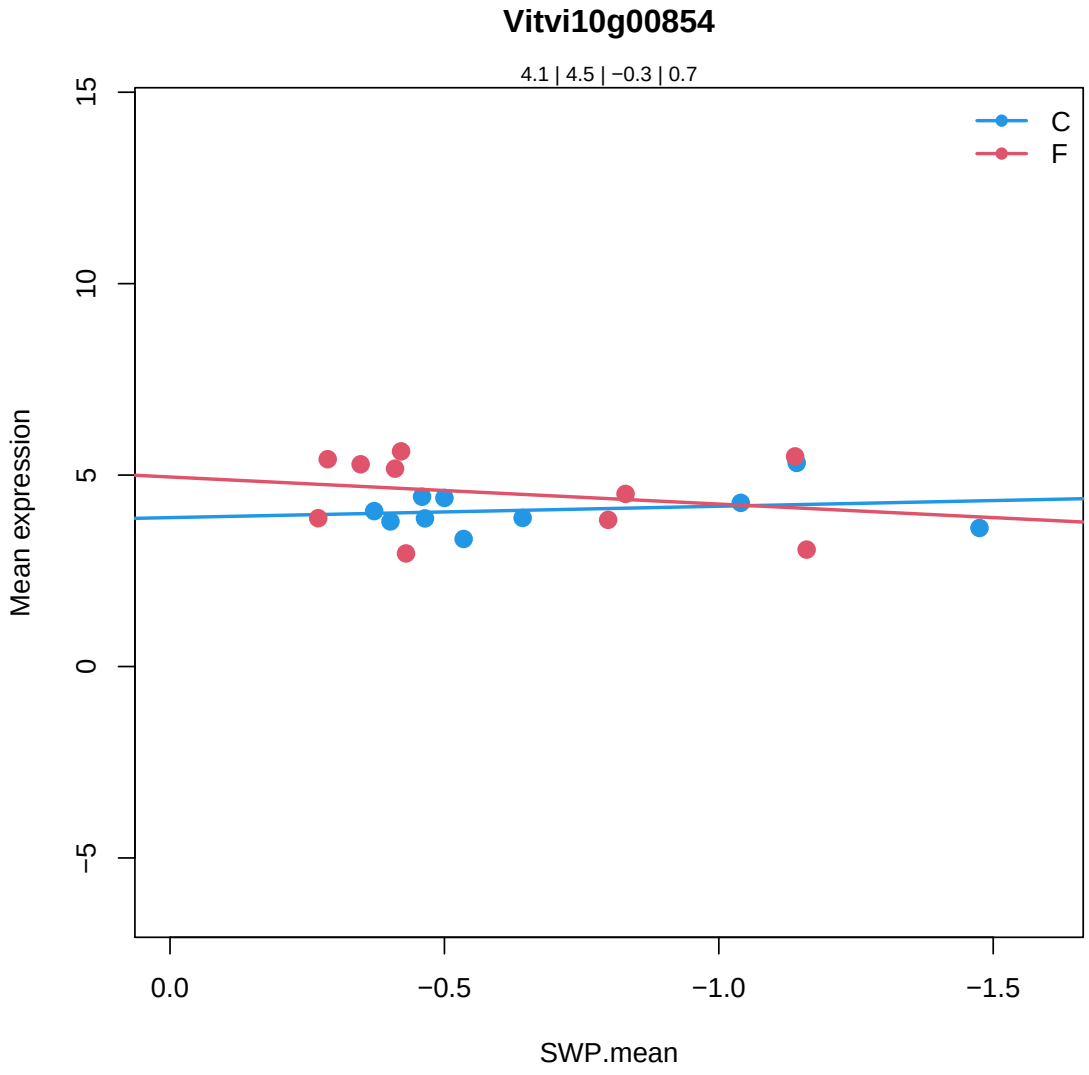
7.6.716 Vitvi10g00854: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00854
        27.3.4
        RNA.regulation of transcription.auxin response transcription factor fa
        auxin response factor 6 |
        Chr1:10686125-10690036 REVERSE LENGTH=935 |
        201606
```

Coefficients for Vitvi10g00854.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.097505	8.619894e-14	***	1.329533e-13	***
SlopeC	-0.2969884	0.6671269		0.9237671	
MeanF-MeanC	0.4214518	0.2366609		0.5928969	
SlopeF-SlopeC	1.004197	0.332874		0.9999488	



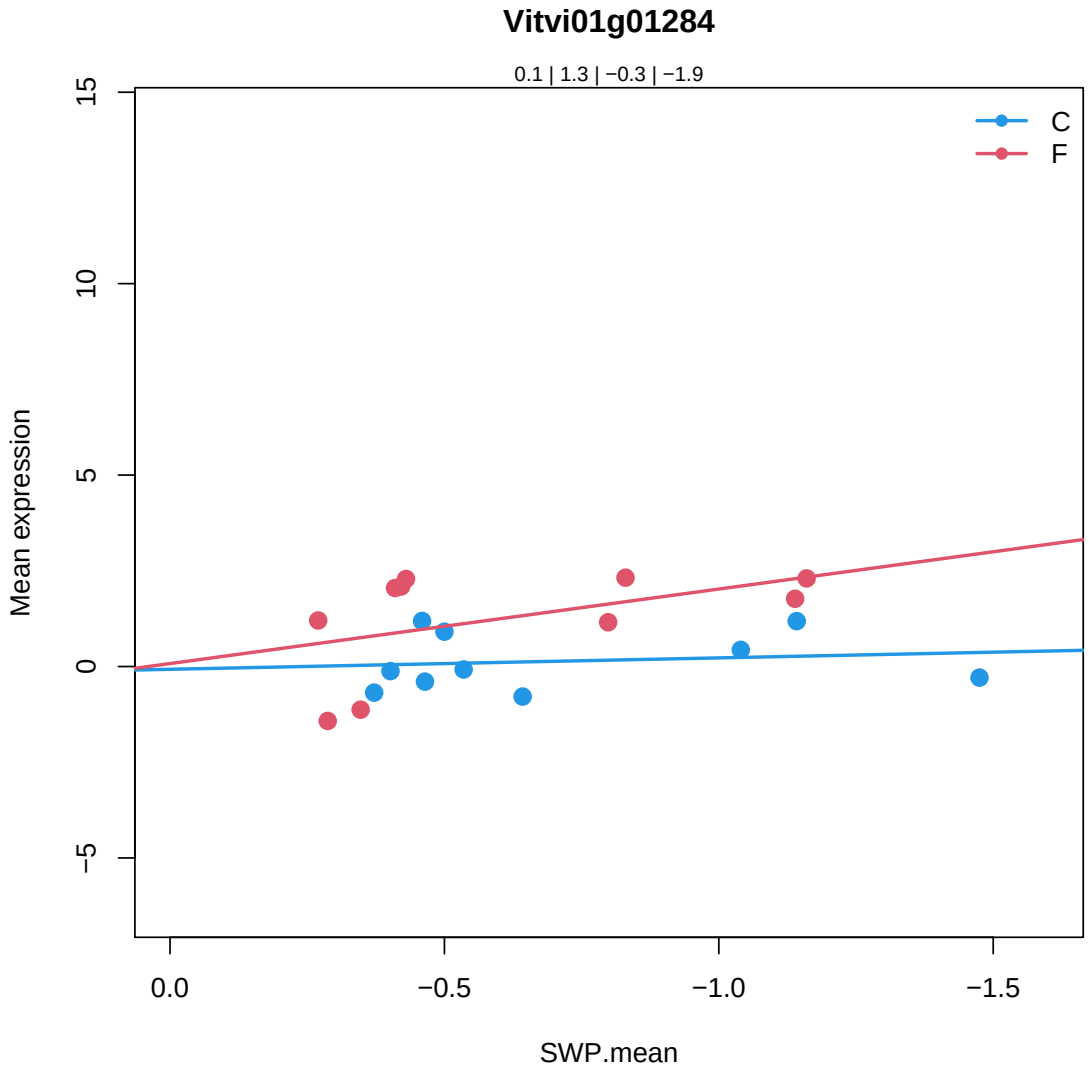
7.6.717 Vitvi01g01284: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01284
        26.2
        misc.UDP glucosyl and glucoronyl transferases
        UDP-Glycosyltransferase superfamily protein |
        Chr3:7867806-7870053 FORWARD LENGTH=461 |
        201606
```

Coefficients for Vitvi01g01284.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1370866	0.6571859		0.6620507	
SlopeC	−0.297883	0.7286342		0.9401373	
MeanF−MeanC	1.125667	0.01607415	*	0.1069411	
SlopeF−SlopeC	−1.648302	0.2051119		0.9999488	



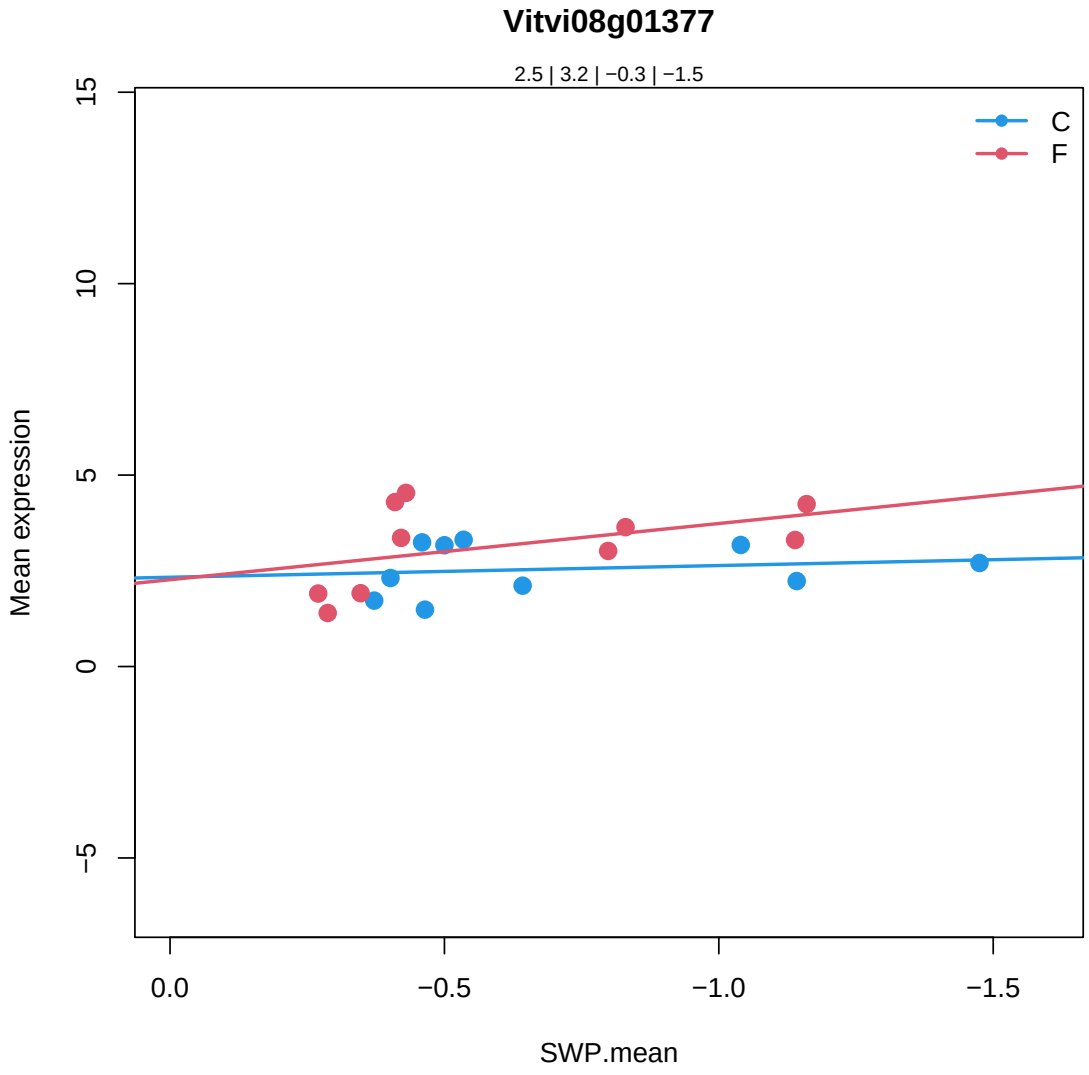
7.6.718 Vitvi08g01377: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01377
        35.2
        not assigned.unknown
        NDR1/HIN1-like 3 |
        Chr5:1931016-1931711 REVERSE LENGTH=231 |
        201606
```

Coefficients for Vitvi08g01377.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.546234	1.480026e-09	***	1.856366e-09	***
SlopeC	-0.3056505	0.669429		0.9237671	
MeanF-MeanC	0.6151542	0.10097		0.366226	
SlopeF-SlopeC	-1.162307	0.2809919		0.9999488	



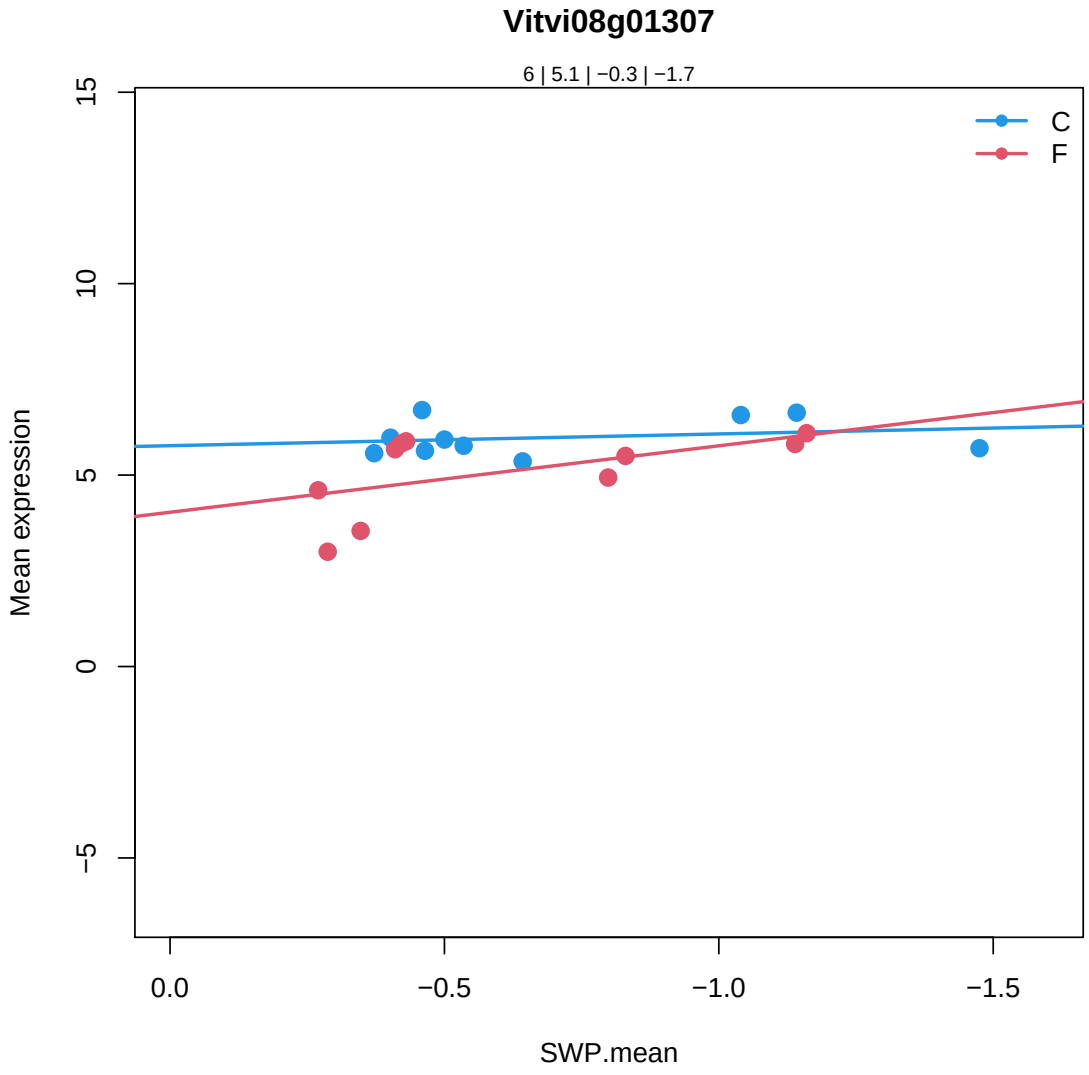
7.6.719 Vitvi08g01307: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01307
        2.2.1.1
        major CHO metabolism.degradation.sucrose.fructokinase
        SOUL heme-binding family protein |
        Chr2:15890964-15891704 FORWARD LENGTH=246 |
        201606
```

Coefficients for Vitvi08g01307.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.983136	3.838417e-18	***	1.121863e-17	***
SlopeC	-0.3068699	0.6199446		0.9089858	
MeanF-MeanC	-0.8969256	0.008573436	**	0.06774303	.
SlopeF-SlopeC	-1.428891	0.1300606		0.9999488	



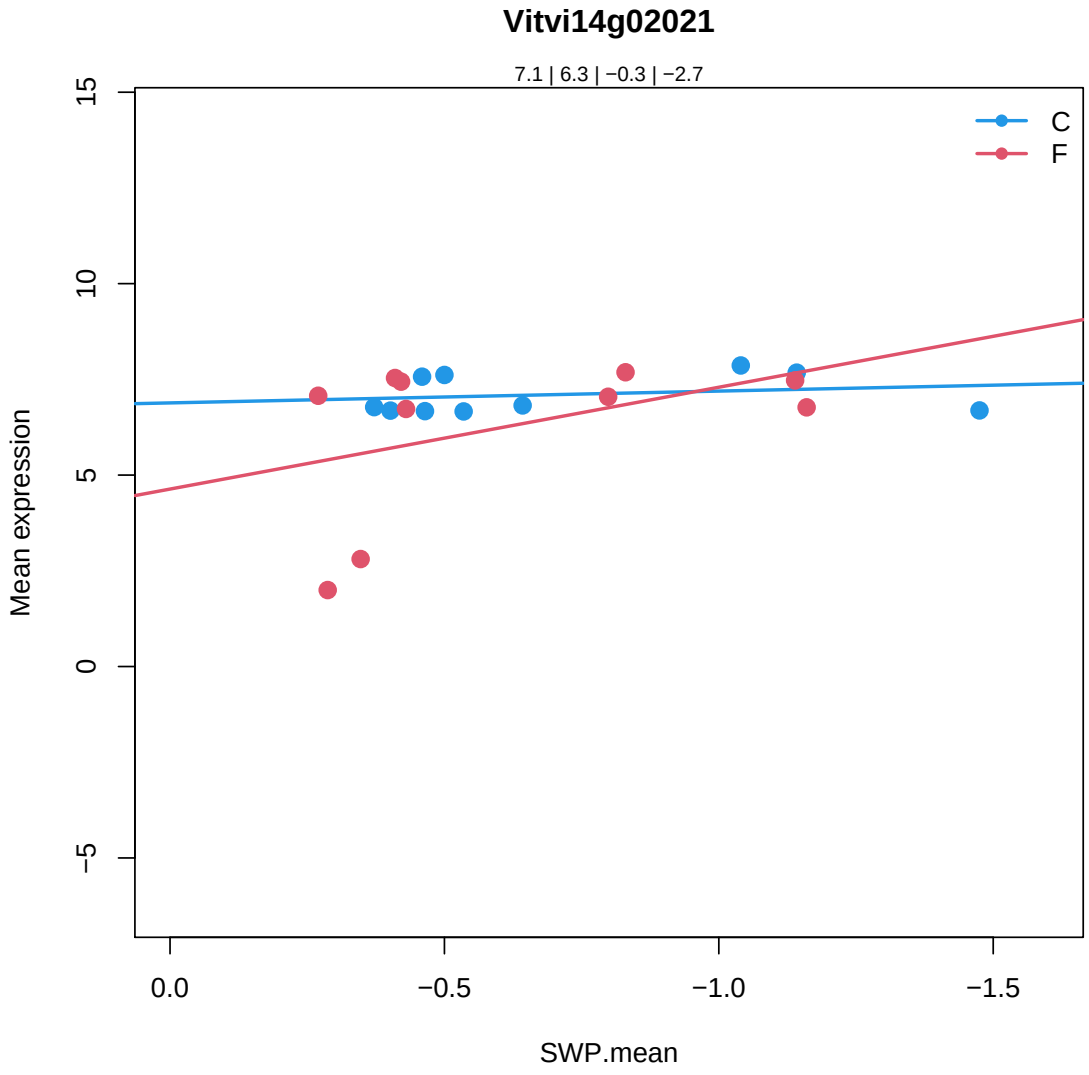
7.6.720 Vitvi14g02021: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g02021
        35.2
        not assigned.unknown
        lysine-tRNA ligase |
        Chr3:17055-18782 REVERSE LENGTH=372 |
        201606
```

Coefficients for Vitvi14g02021.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.102064	2.663483e-14	***	4.285528e-14	***
SlopeC	-0.3086503	0.7842441		0.9533027	
MeanF-MeanC	-0.8470095	0.1490293		0.4650909	
SlopeF-SlopeC	-2.350934	0.17032		0.9999488	



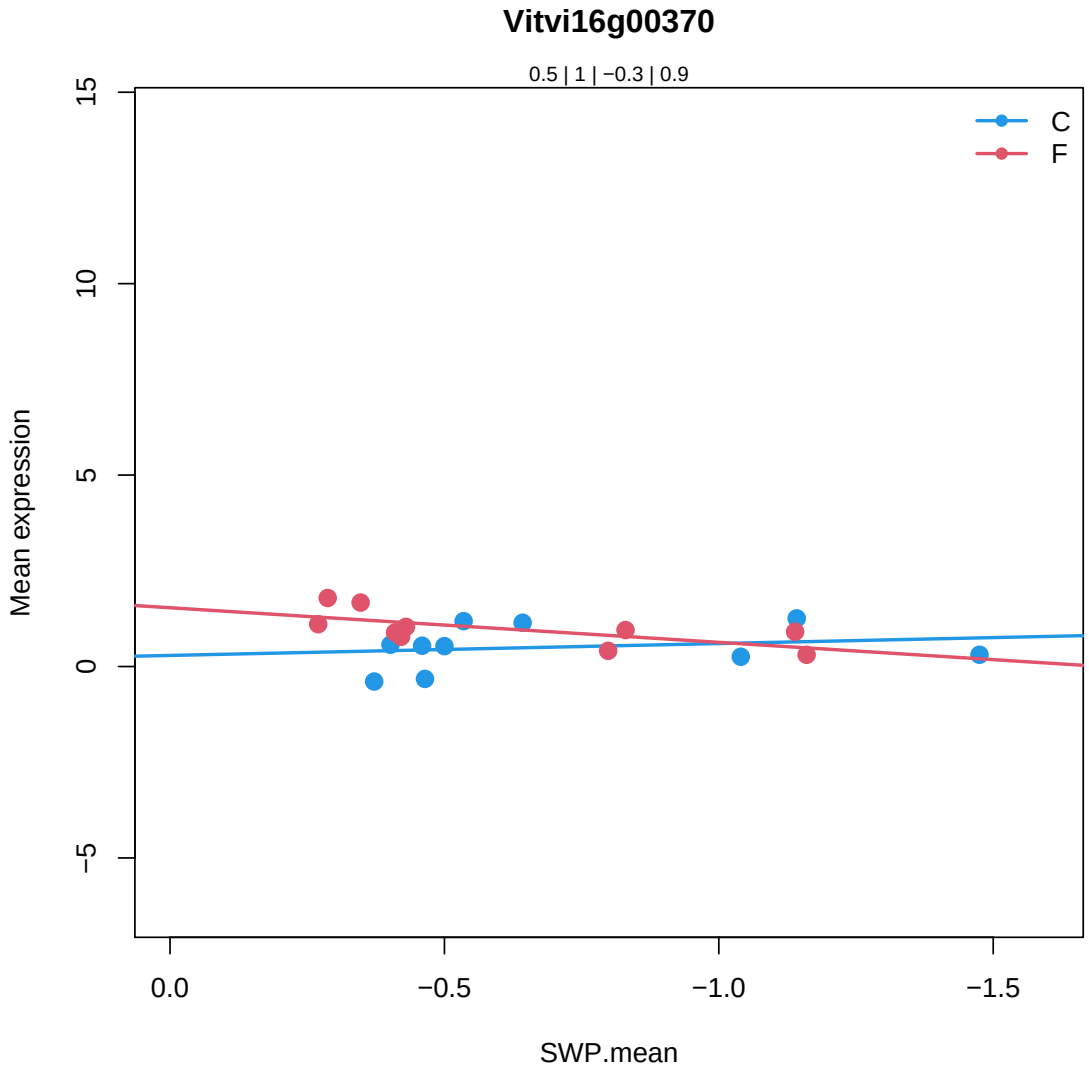
7.6.721 Vitvi16g00370: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g00370
        17.5.2
        hormone metabolism.ethylene.signal transduction
        Integrase-type DNA-binding superfamily protein |
        Chr5:20800708-20801373 REVERSE LENGTH=221 |
        201606
```

Coefficients for Vitvi16g00370.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.5075733	0.00405384	**	0.004333307	**
SlopeC	−0.310389	0.4870225		0.8654145	
MeanF−MeanC	0.4766569	0.04429863	*	0.2211625	
SlopeF−SlopeC	1.213985	0.07687415	.	0.9999488	



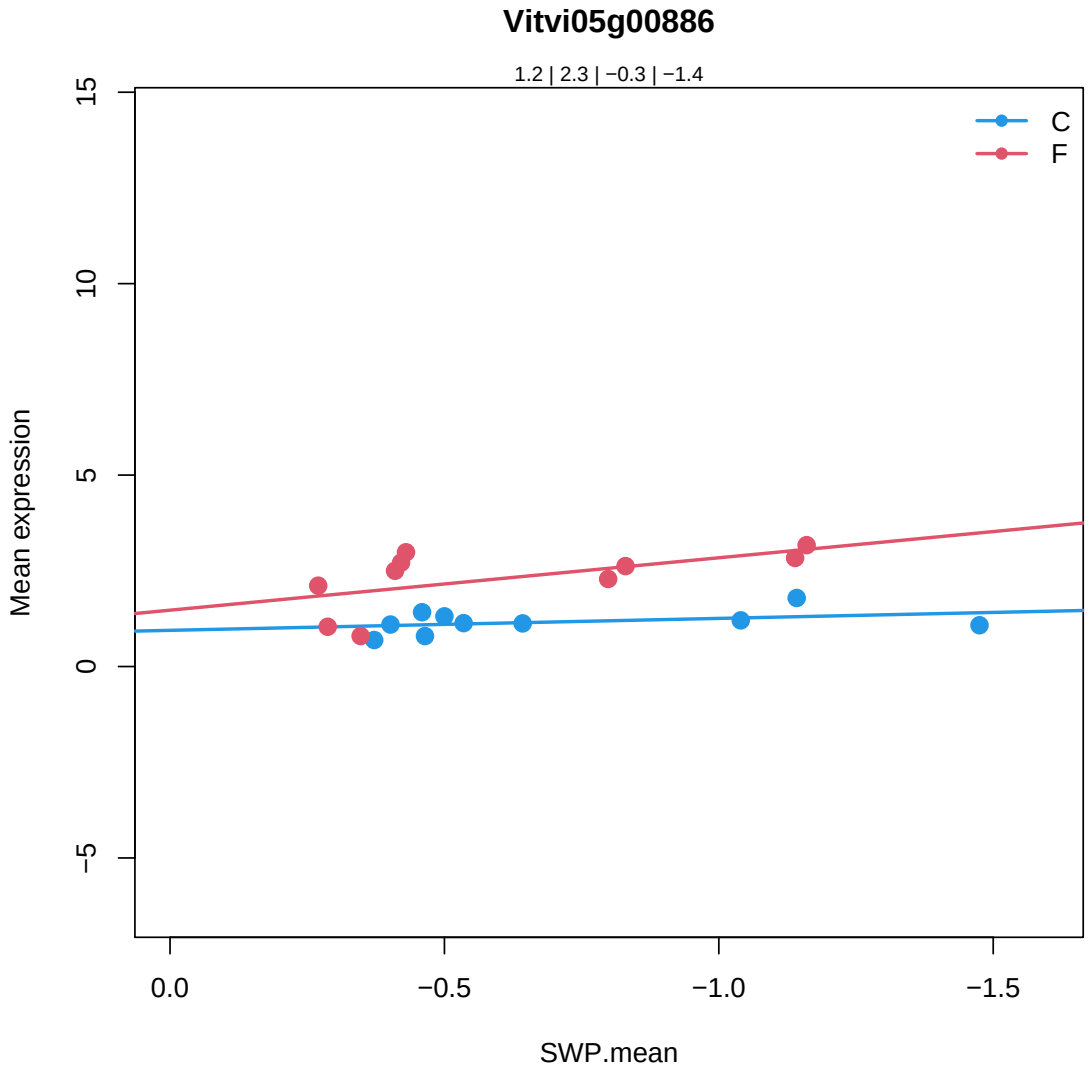
7.6.722 Vitvi05g00886: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00886
        35.2
        not assigned.unknown
        beta-amylase 1 |
        Chr3:8641722-8644199 FORWARD LENGTH=575 |
        201606
```

Coefficients for Vitvi05g00886.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.164233	4.625346e-07	***	5.384932e-07	***
SlopeC	-0.3117496	0.5013782		0.8699607	
MeanF-MeanC	1.141102	6.775583e-05	***	0.0012829	**
SlopeF-SlopeC	-1.056868	0.1339456		0.9999488	



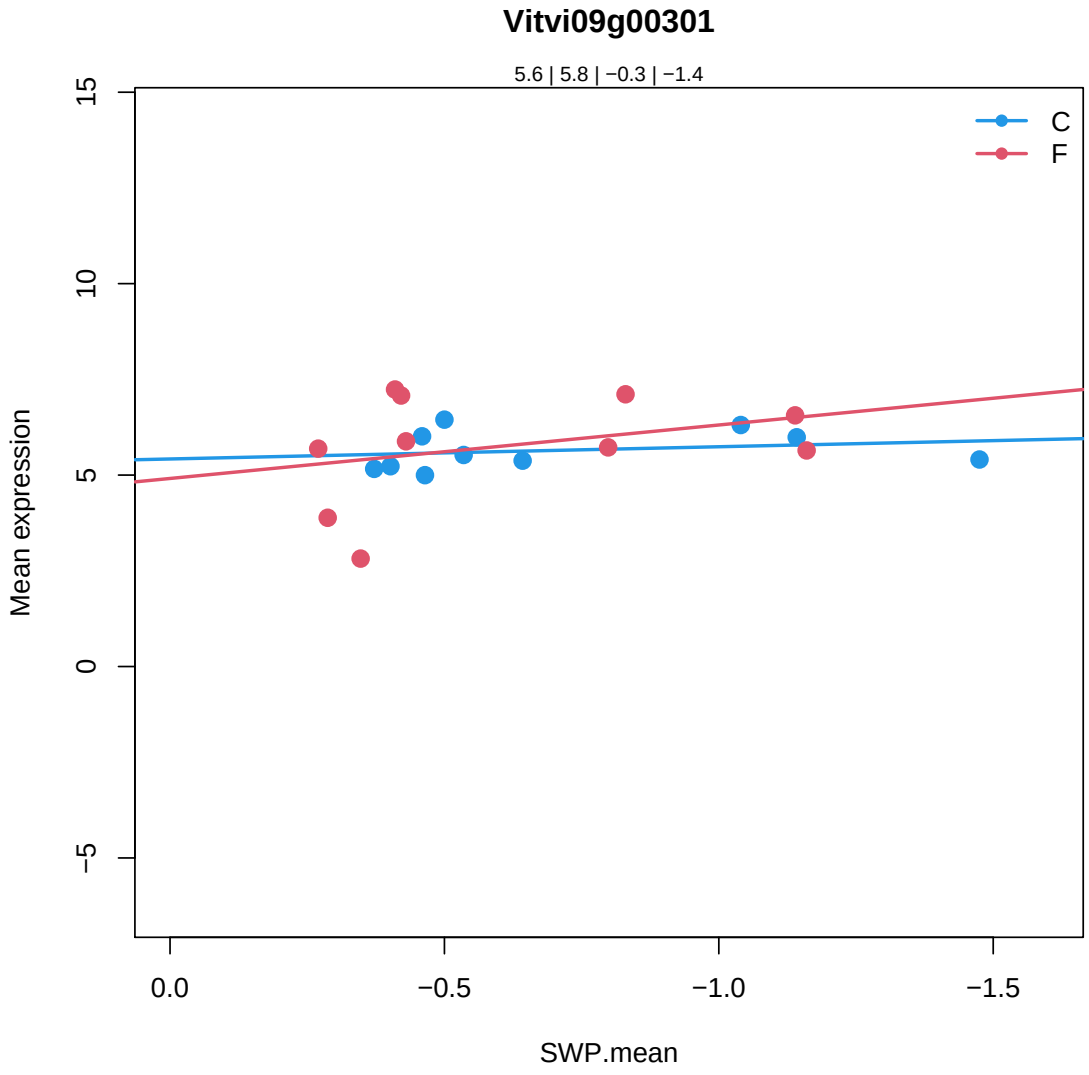
7.6.723 Vitvi09g00301: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00301
        8.2.10
        TCA / organic transformation.other organic acid transformations.malic
        NADP-malic enzyme 3 |
        Chr5:9024549-9027498 FORWARD LENGTH=530 |
        201606
```

Coefficients for Vitvi09g00301.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.645311	1.161925e-14	***	1.929411e-14	***
SlopeC	-0.3194354	0.7105188		0.935038	
MeanF-MeanC	0.117128	0.7887434		0.9400551	
SlopeF-SlopeC	-1.077441	0.4034254		0.9999488	



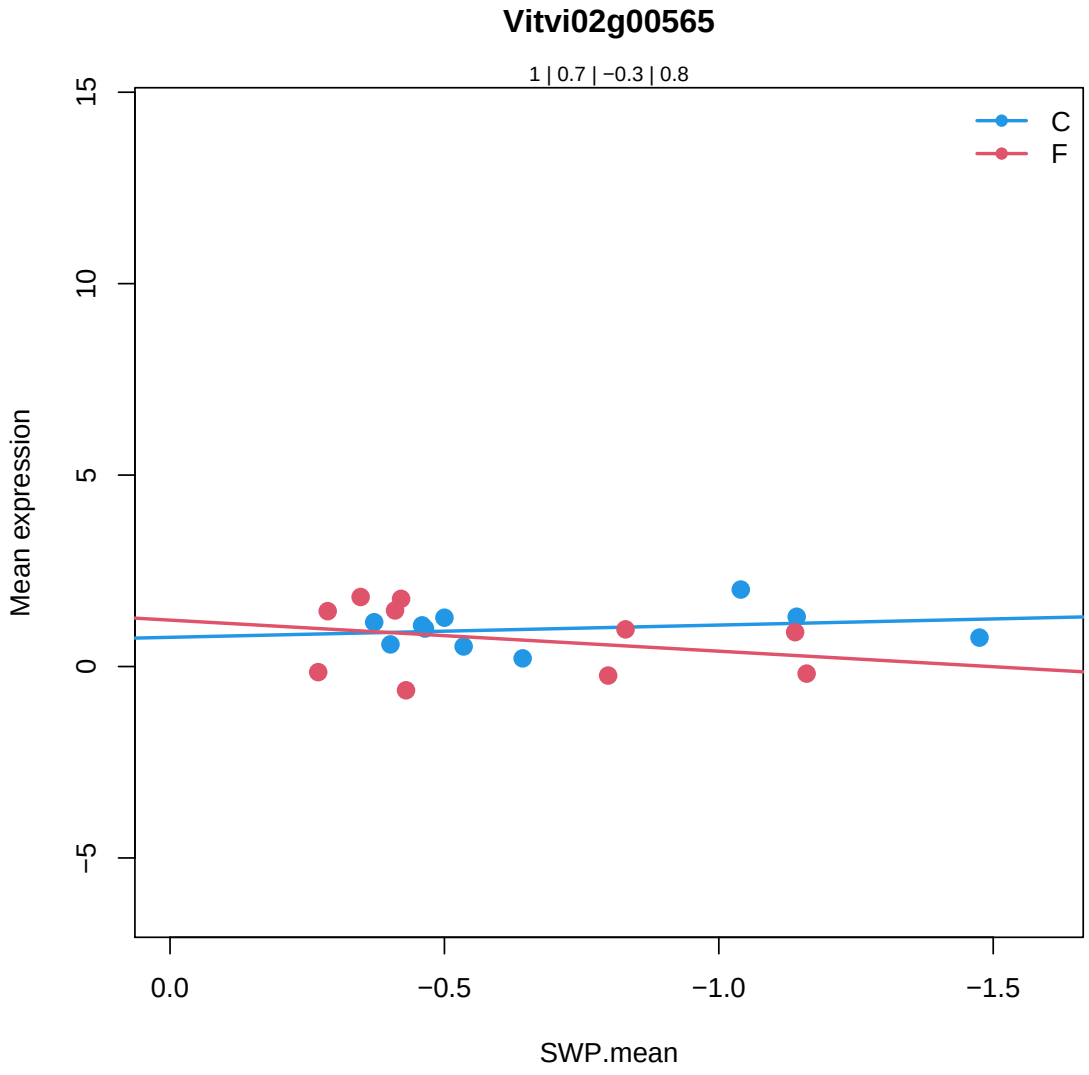
7.6.724 Vitvi02g00565: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00565
        17.2.3
        hormone metabolism.auxin.induced-regulated-responsive-activated
        O-fucosyltransferase family protein |
        Chr4:9372727-9375910 FORWARD LENGTH=549 |
        201606
```

Coefficients for Vitvi02g00565.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.9877923	0.0002082013	***	0.0002285326	***
SlopeC	−0.3202202	0.6088		0.9055186	
MeanF−MeanC	−0.2705399	0.397539		0.7433799	
SlopeF−SlopeC	1.131369	0.2309386		0.9999488	



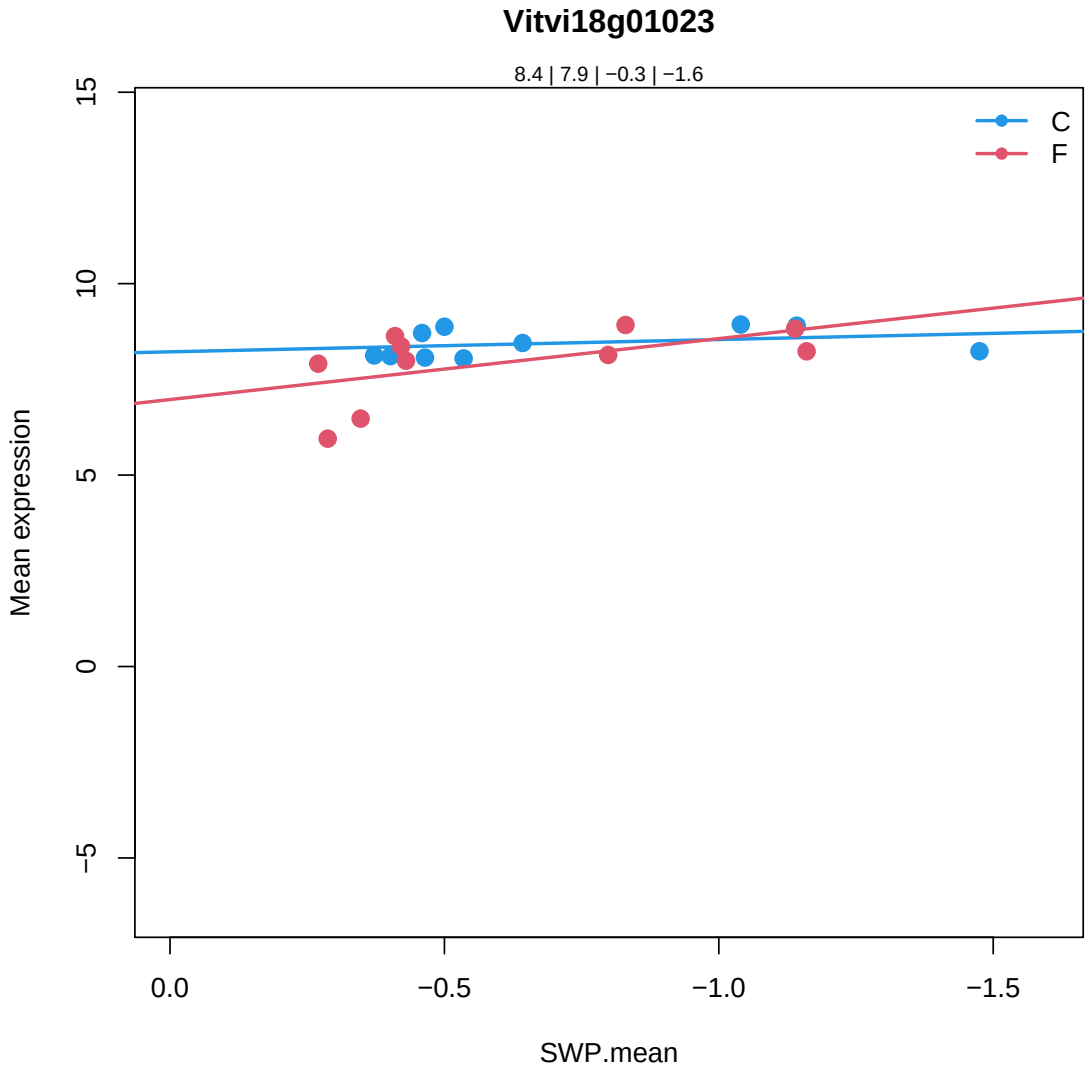
7.6.725 Vitvi18g01023: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g01023
        35.2
        not assigned.unknown
        ATP-dependent protease La (LON) domain protein |
        Chr1:28327986-28328822 FORWARD LENGTH=278 |
        201606
```

Coefficients for Vitvi18g01023.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	8.444799	3.0502e-22	***	4.526889e-21	***
SlopeC	-0.3215564	0.5647311		0.8905966	
MeanF-MeanC	-0.5022459	0.0864078	.	0.333932	
SlopeF-SlopeC	-1.269695	0.1353771		0.9999488	



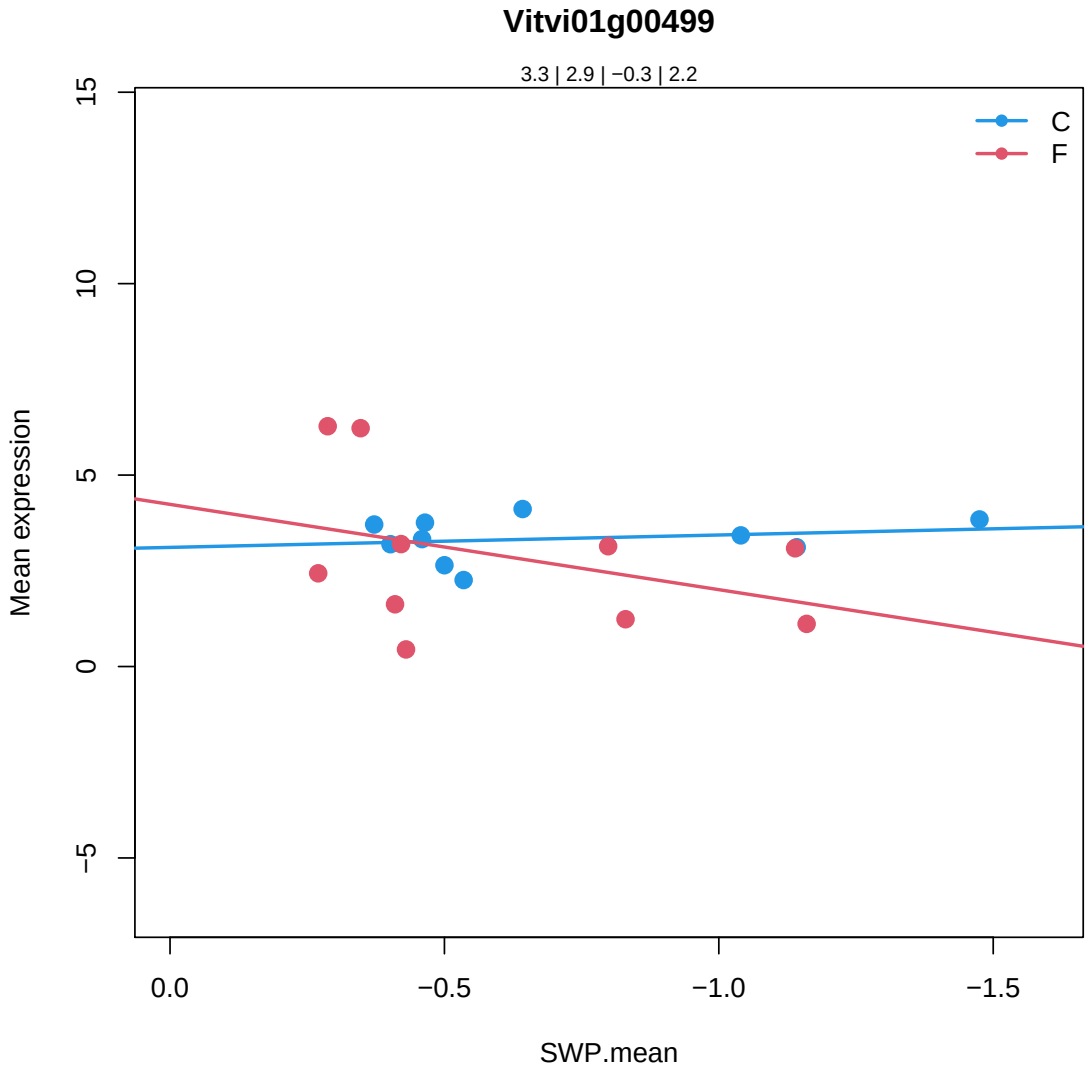
7.6.726 Vitvi01g00499: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00499
        29.5.11.4.3.2
        protein.degradation.ubiquitin.E3.SCF.FBOX
        flavin-binding%2C kelch repeat%2C f box 1 |
        Chr1:25508737-25510697 FORWARD LENGTH=619 |
        201606
```

Coefficients for Vitvi01g00499.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.338622	4.411033e-08	***	5.282703e-08	***
SlopeC	-0.323465	0.7770267		0.9513135	
MeanF-MeanC	-0.4605614	0.4306082		0.7652319	
SlopeF-SlopeC	2.551102	0.1432014		0.9999488	



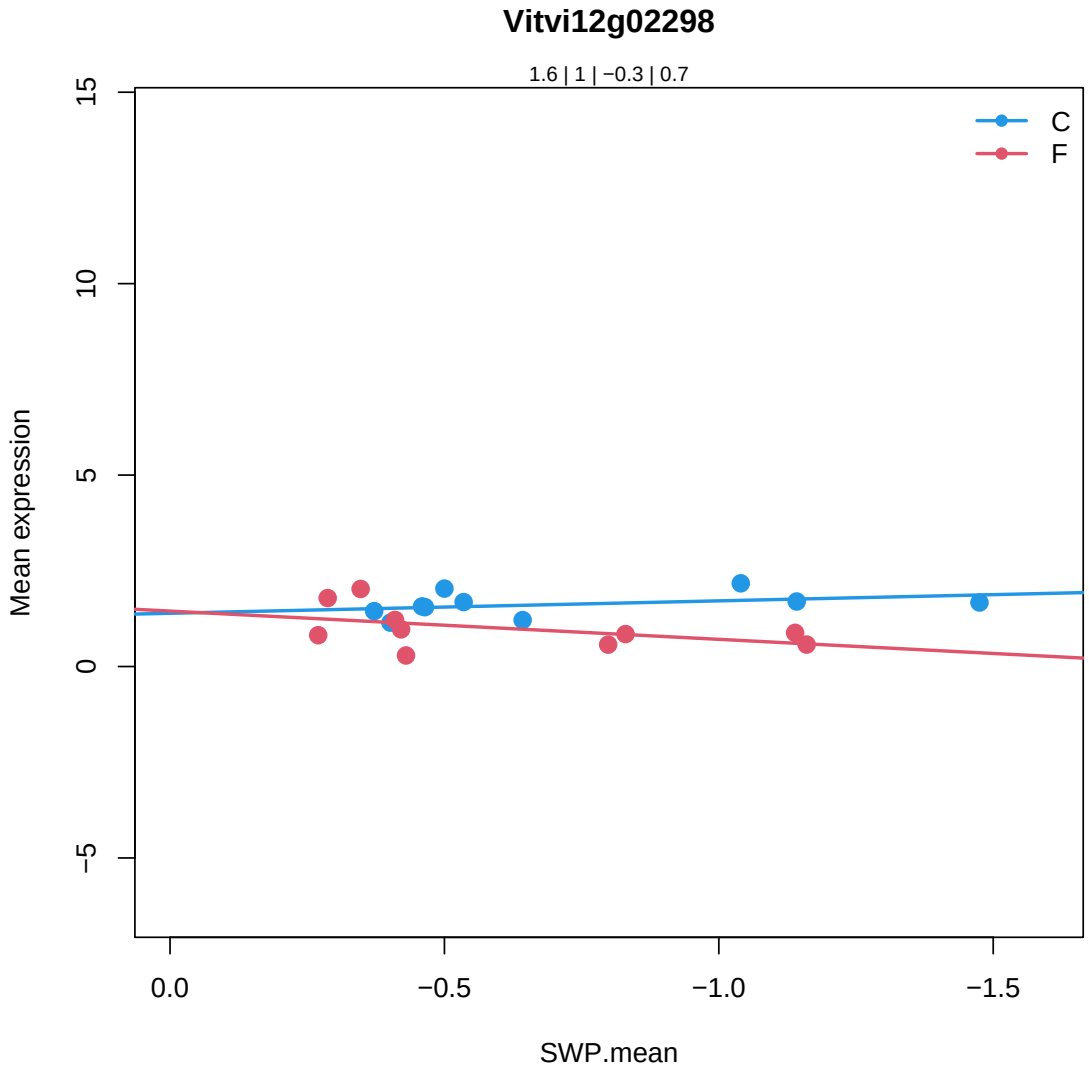
7.6.727 Vitvi12g02298: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02298
        13.1.6.4.3
        amino acid metabolism.synthesis.aromatic aa.tyrosine.tyrosine transami
        Tyrosine transaminase family protein |
        Chr5:21910676-21912594 FORWARD LENGTH=414 |
        201606
```

Coefficients for Vitvi12g02298.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.618633	1.049627e-10	***	1.372195e-10	***
SlopeC	-0.3242258	0.4128673		0.8397754	
MeanF-MeanC	-0.6207367	0.004799954	**	0.04425947	*
SlopeF-SlopeC	1.061781	0.08004186	.	0.9999488	



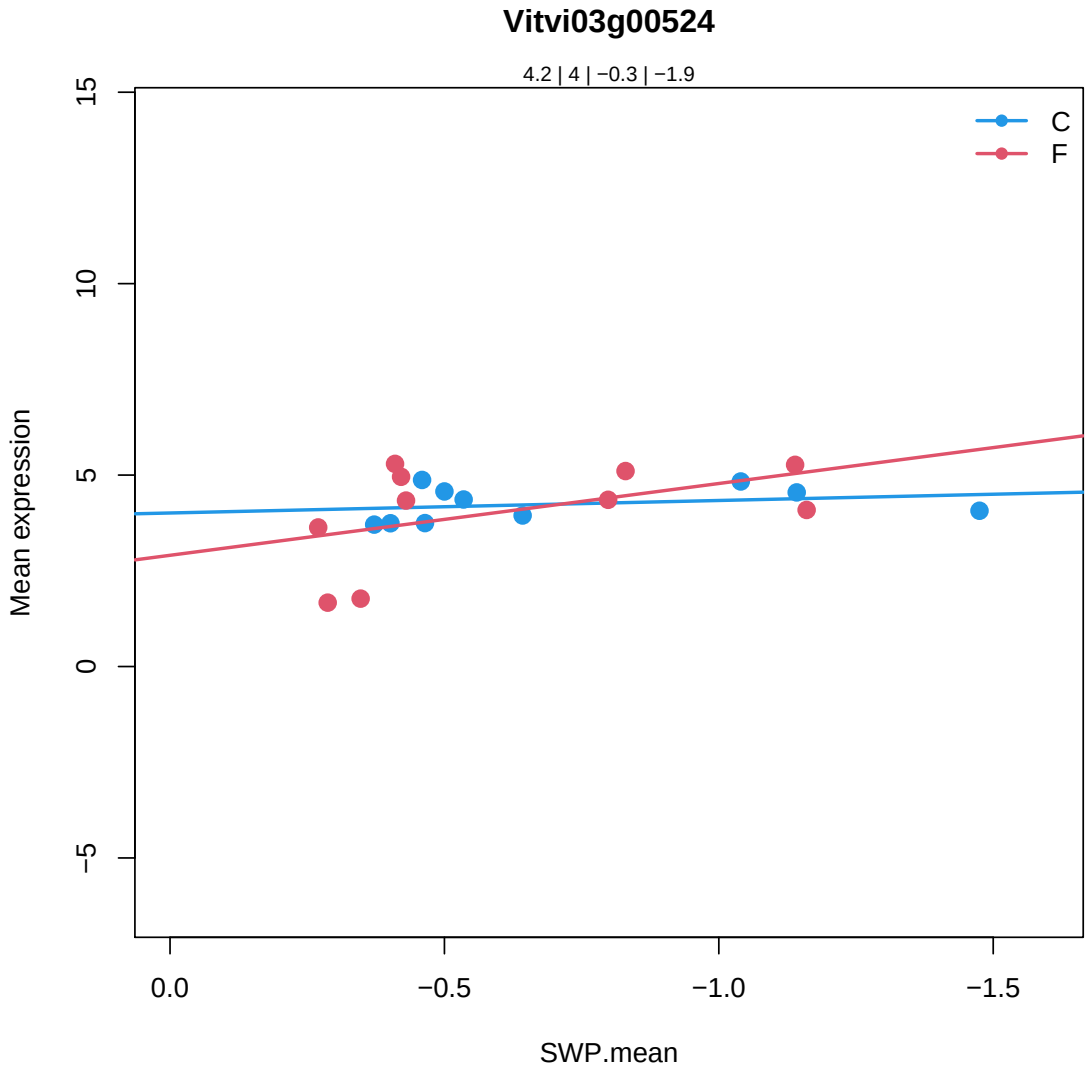
7.6.728 Vitvi03g00524: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00524
        29.2.2.3.3
        protein.synthesis.ribosome biogenesis.pre-rRNA processing and modifica
        S-adenosyl-L-methionine-dependent methyltransferases superfamily prote
        Chr4:16310763-16311973 FORWARD LENGTH=286 |
        201606
```

Coefficients for Vitvi03g00524.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.239322	2.7688e-13	***	4.126532e-13	***
SlopeC	-0.3269155	0.6660834		0.9237354	
MeanF-MeanC	-0.1922087	0.6179519		0.8676253	
SlopeF-SlopeC	-1.547959	0.178187		0.9999488	



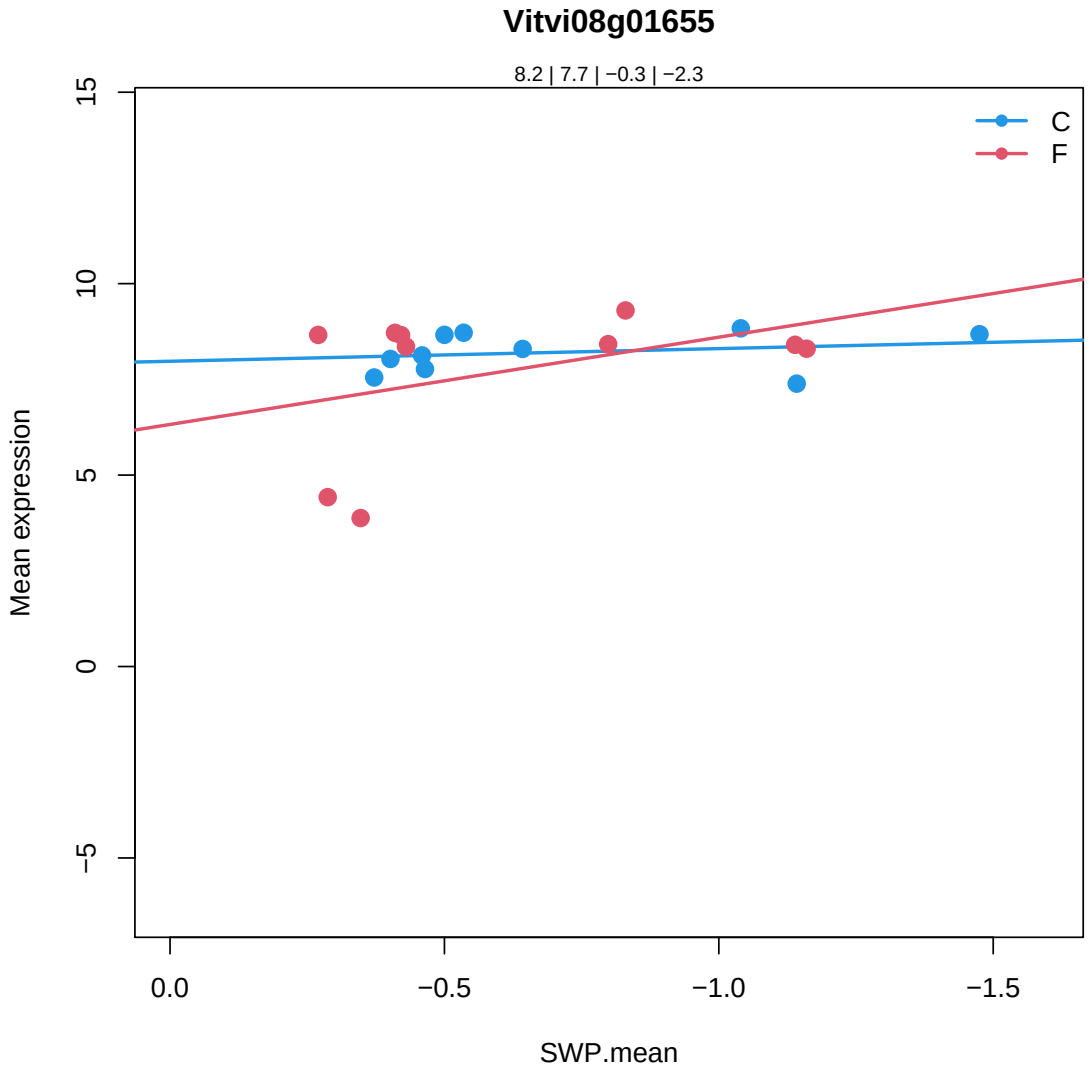
7.6.729 Vitvi08g01655: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01655
        35.1
        not assigned.no ontology
        Haloacid dehalogenase-like hydrolase (HAD) superfamily protein |
        Chr2:17200862-17202551 REVERSE LENGTH=290 |
        201606
```

Coefficients for Vitvi08g01655.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	8.205085	4.421212e-16	***	8.67956e-16	***
SlopeC	−0.3306441	0.7562384		0.9476846	
MeanF−MeanC	−0.4940443	0.3656485		0.7224758	
SlopeF−SlopeC	−1.948725	0.2265431		0.9999488	



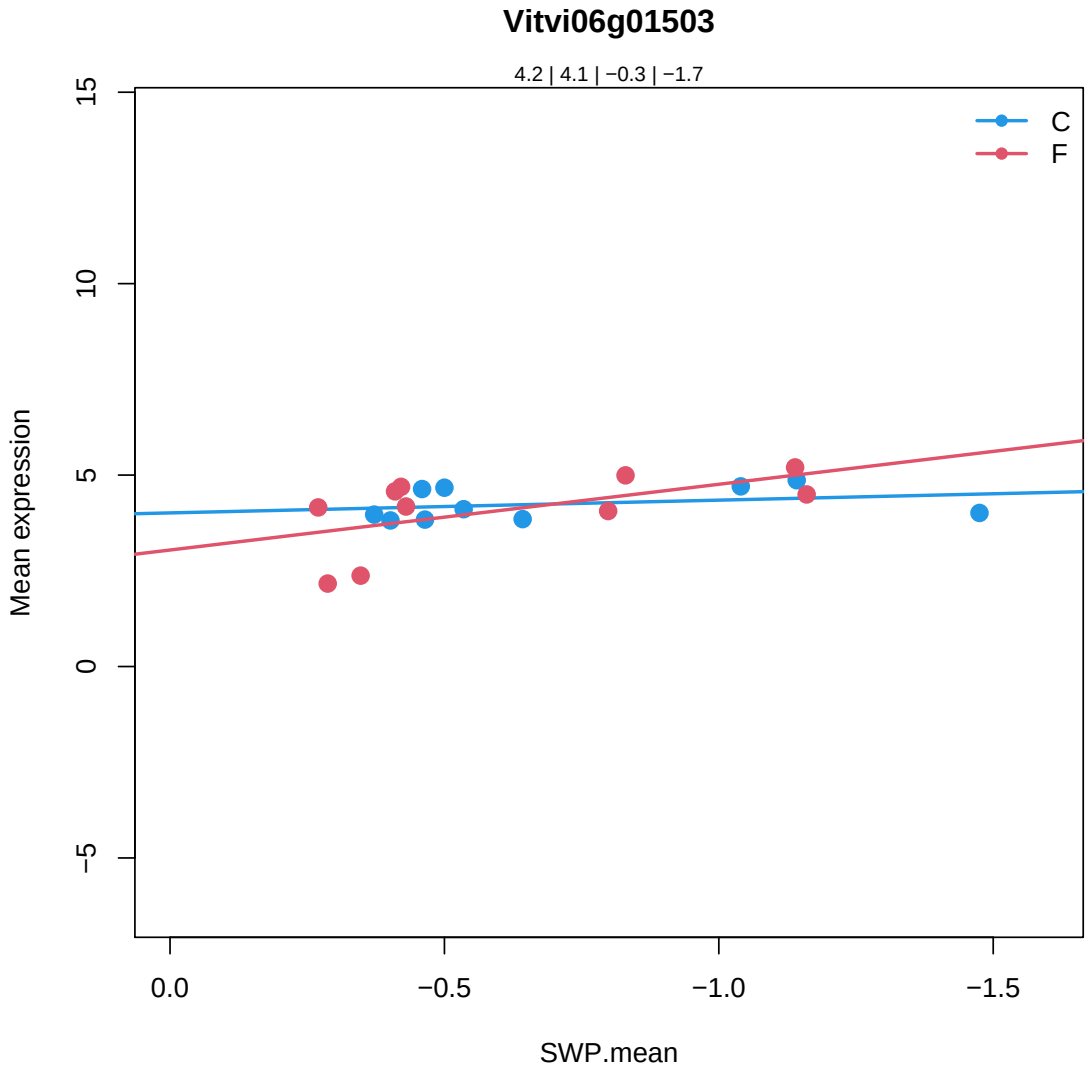
7.6.730 Vitvi06g01503: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01503
        29.2.1.99.99
        protein.synthesis.ribosomal protein.unknown.unknown
        FANTASTIC four-like protein (DUF3049) |
        Chr5:7418383-7418991 REVERSE LENGTH=202 |
        201606
```

Coefficients for Vitvi06g01503.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.246463	1.253966e-15	***	2.320377e-15	***
SlopeC	-0.3331244	0.5668024		0.891013	
MeanF-MeanC	-0.157635	0.5937066		0.8577063	
SlopeF-SlopeC	-1.38381	0.1190609		0.9999488	



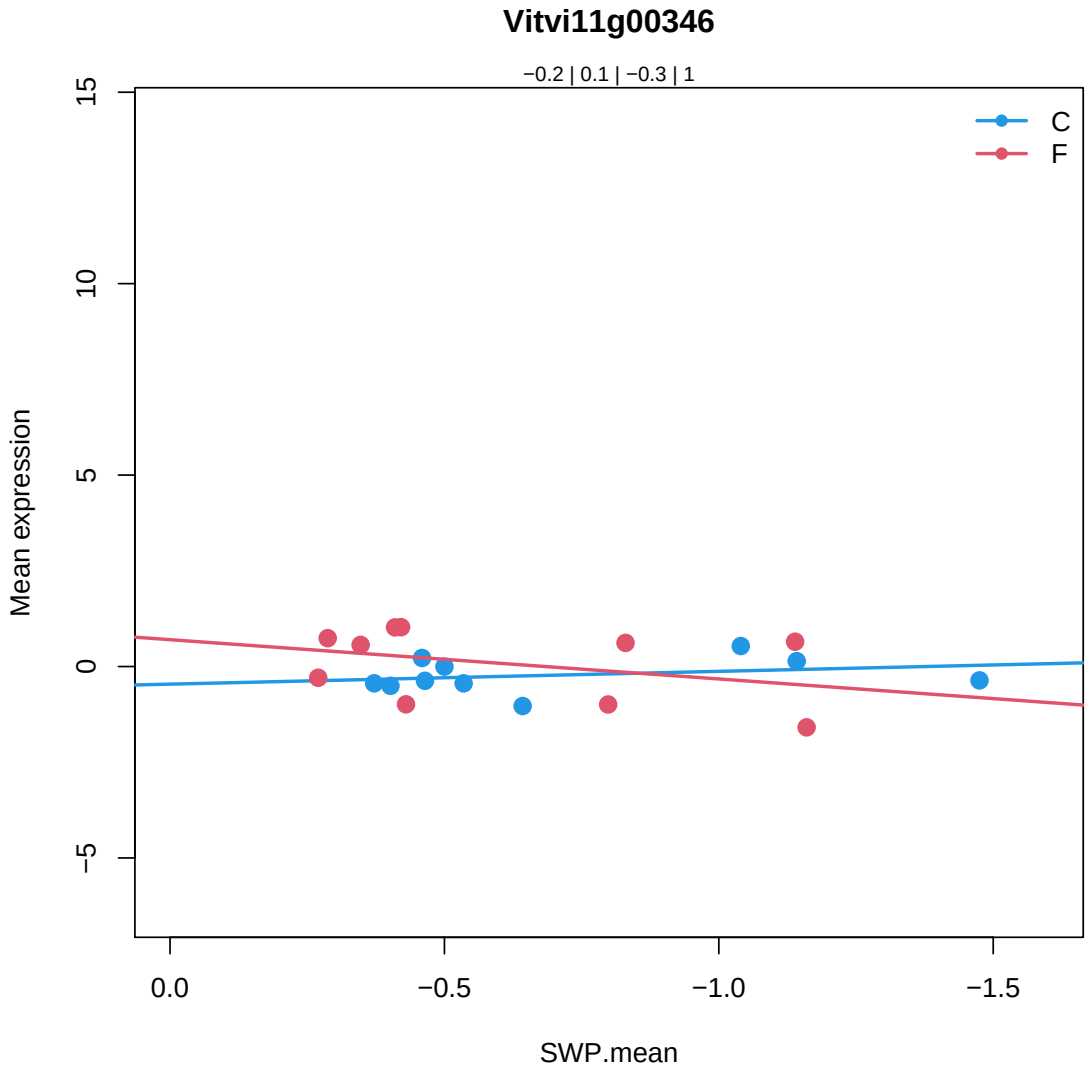
7.6.731 Vitvi11g00346: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00346
        35.2
        not assigned.unknown
        Regulator of Vps4 activity in the MVB pathway protein |
        Chr4:15617634-15620642 FORWARD LENGTH=732 |
        201606
```

Coefficients for Vitvi11g00346.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.2256634	0.3112147		0.3169752	
SlopeC	-0.3339113	0.5869122		0.898013	
MeanF-MeanC	0.3014733	0.3381297		0.697961	
SlopeF-SlopeC	1.359662	0.1458599		0.9999488	



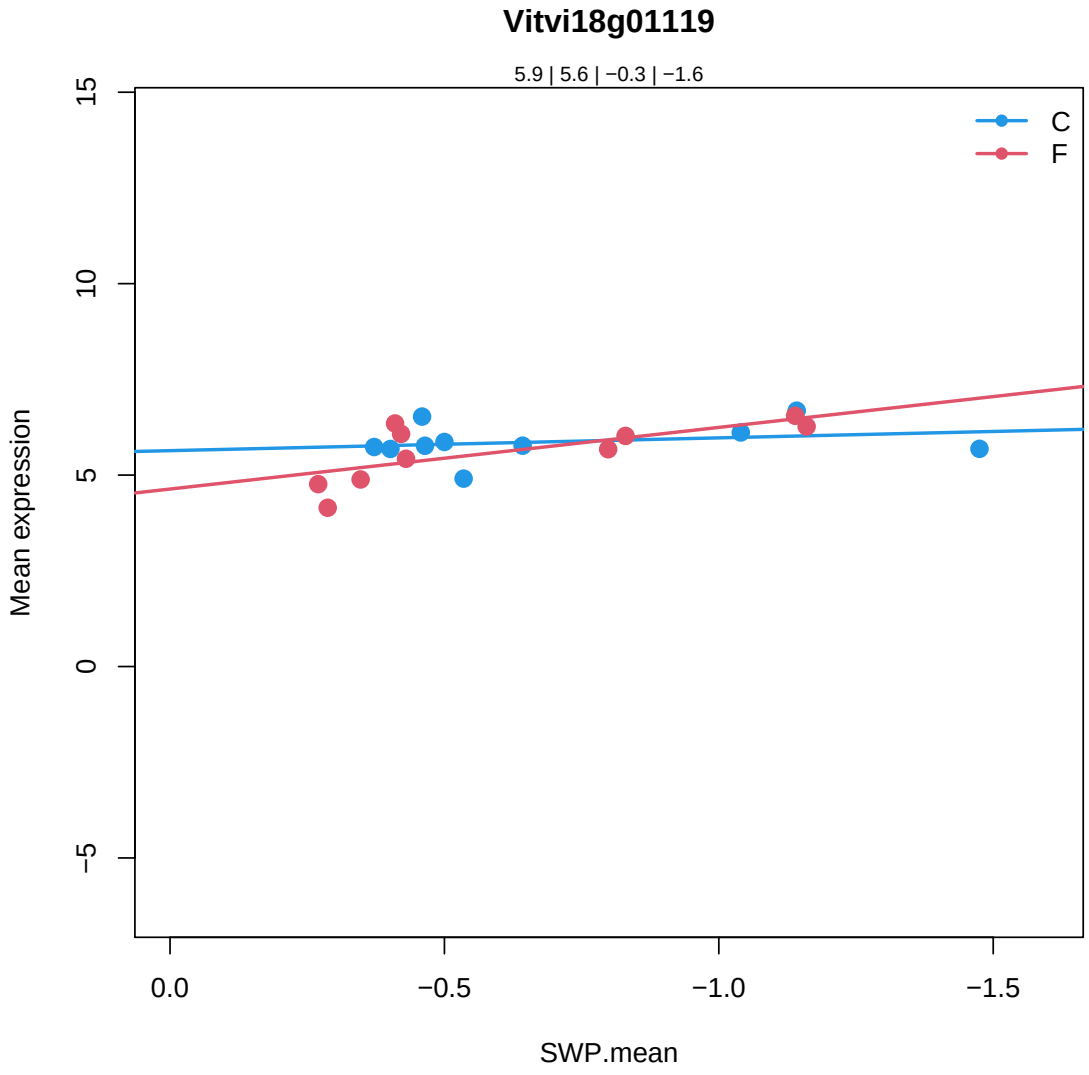
7.6.732 Vitvi18g01119: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g01119
        16.8.3.2
        secondary metabolism.flavonoids.dihydroflavonols.flavanone 3-hydroxyla
        flavanone 3-hydroxylase |
        Chr3:19025661-19026658 FORWARD LENGTH=274 |
        201606
```

Coefficients for Vitvi18g01119.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.872852	3.083095e-20	***	1.769857e-19	***
SlopeC	-0.3339927	0.4900872		0.8665066	
MeanF-MeanC	-0.2569098	0.2997655		0.6662078	
SlopeF-SlopeC	-1.275567	0.08563605	.	0.9999488	



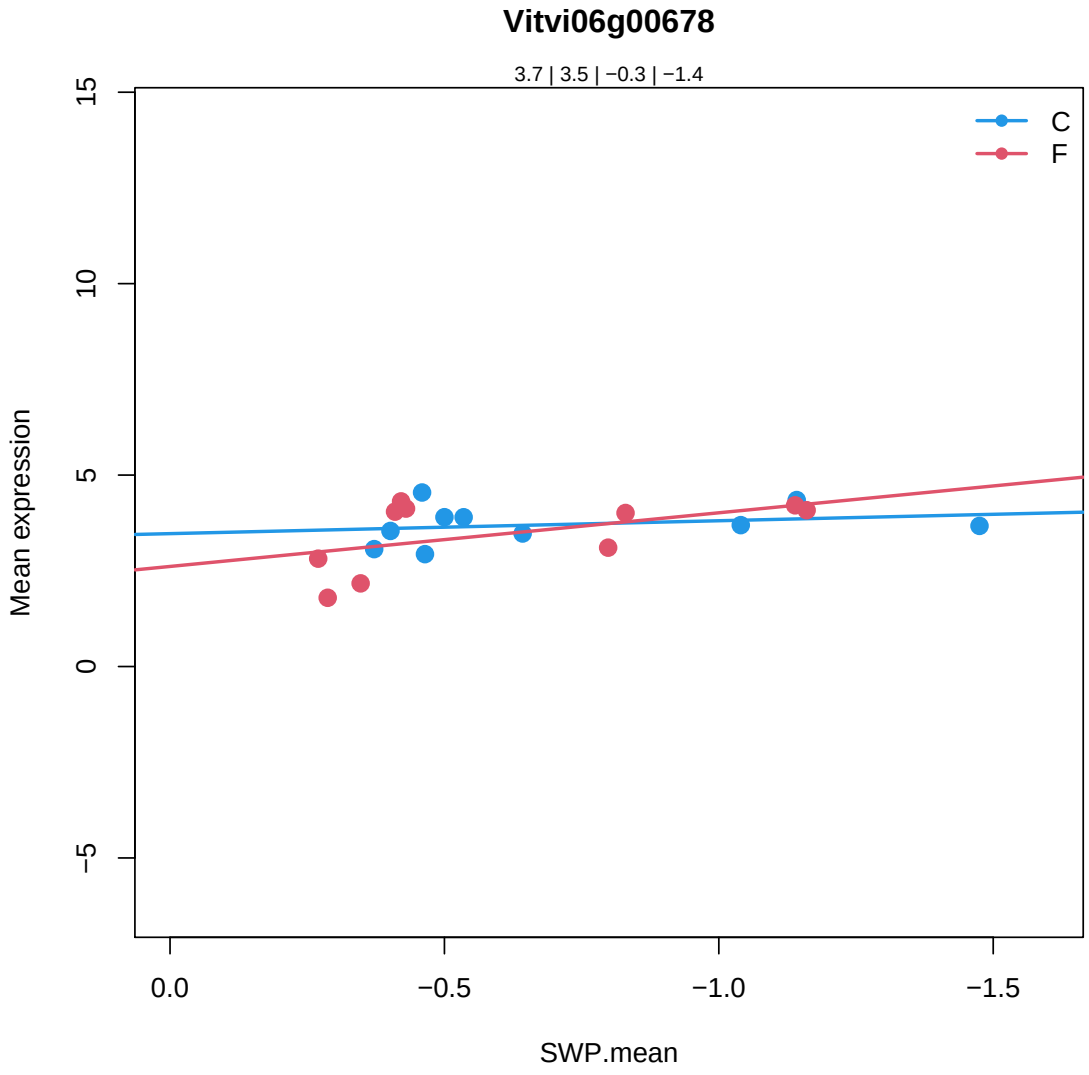
7.6.733 Vitvi06g00678: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00678
        34.12
        transport.metal
        ZIP metal ion transporter family |
        Chr2:12838730-12840112 REVERSE LENGTH=341 |
        201606
```

Coefficients for Vitvi06g00678.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.707226	1.983749e-14	***	3.22727e-14	***
SlopeC	-0.3365154	0.5629273		0.8904253	
MeanF-MeanC	-0.2399574	0.4188436		0.7569053	
SlopeF-SlopeC	-1.065085	0.2249241		0.9999488	



7.6.734 Vitvi16g01371: type5

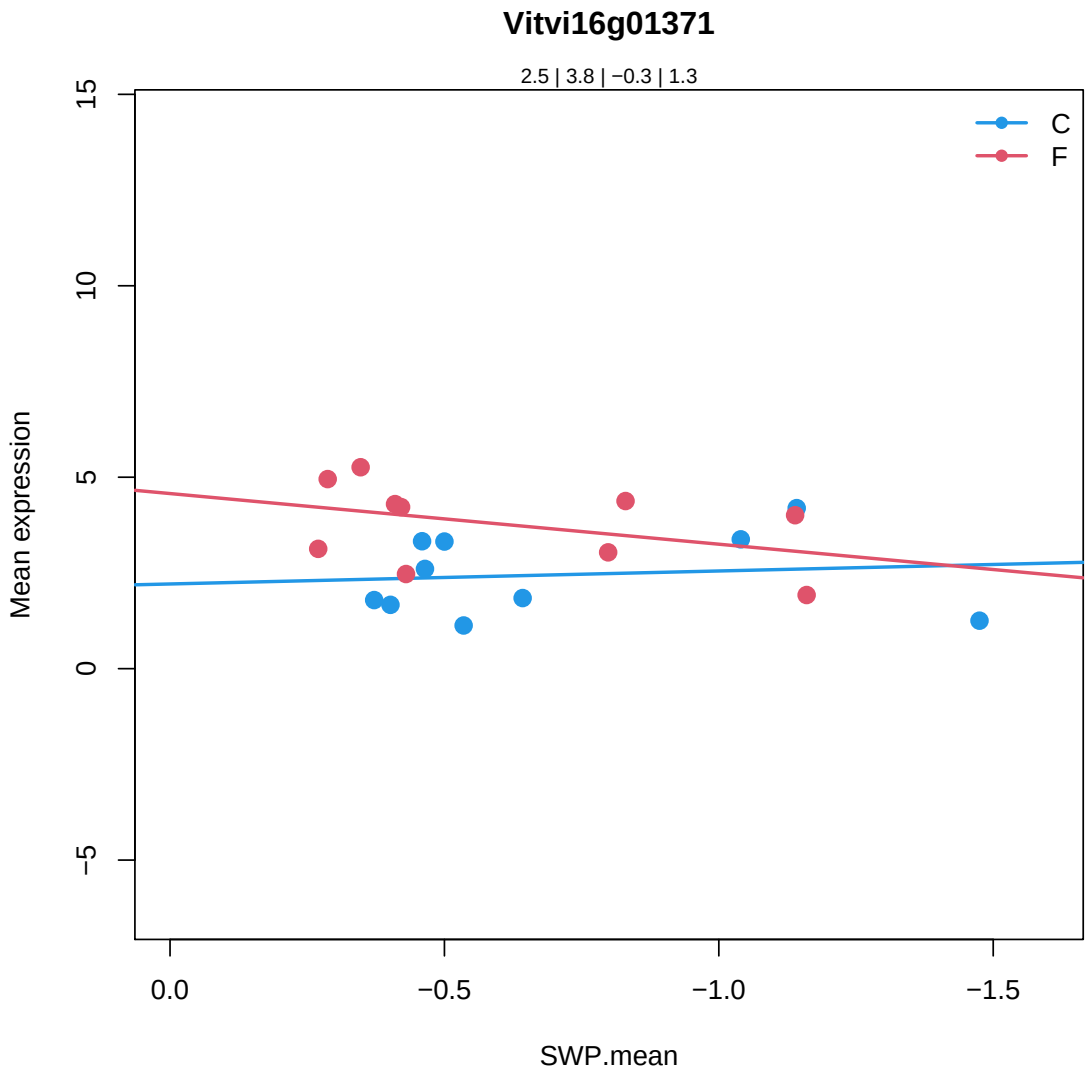
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01371
        34.13
        transport.peptides and oligopeptides
        YELLOW STRIPE like 3 |
        Chr5:21756662-21758776 FORWARD LENGTH=513 |
        201606

Vitvi16g01371
        34.12
        transport.metal
        YELLOW STRIPE like 3 |
        Chr5:21756662-21758776 FORWARD LENGTH=513 |
        201606
```

Coefficients for Vitvi16g01371.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.450378	6.531257e-08	***	7.78338e-08	***
SlopeC	-0.339585	0.6927294		0.9312515	
MeanF-MeanC	1.316998	0.005906463	**	0.05176901	.
SlopeF-SlopeC	1.66238	0.2016225		0.9999488	


Vitvi16g01371
2.5 | 3.8 | −0.3 | 1.3
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

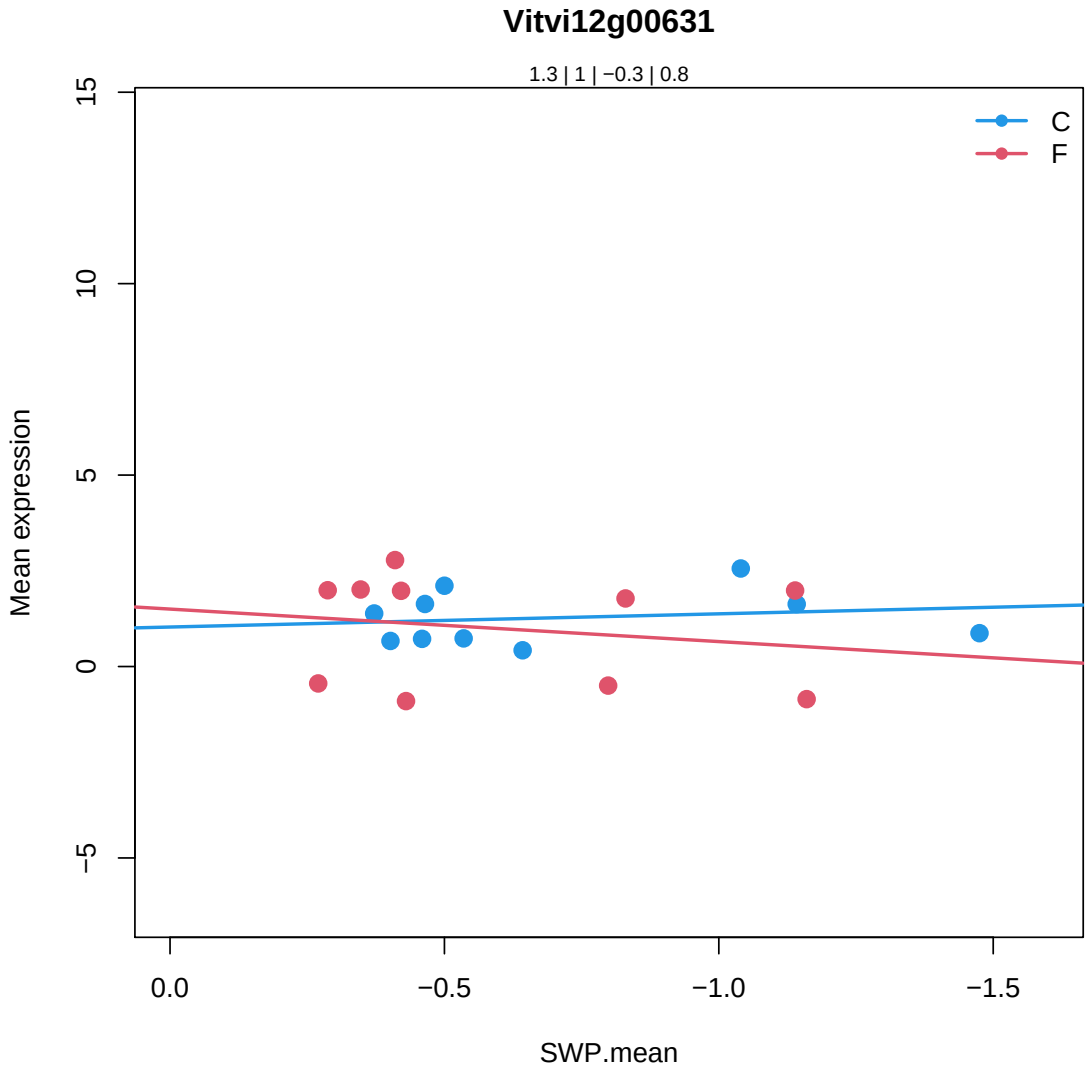
7.6.735 Vitvi12g00631: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00631
        35.2
        not assigned.unknown
        transmembrane protein |
        Chr4:13965300-13966697 REVERSE LENGTH=304 |
        201606
```

Coefficients for Vitvi12g00631.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.273722	0.0009869892	***	0.001068899	**
SlopeC	−0.3446551	0.7144324		0.9357548	
MeanF−MeanC	−0.2909446	0.5445307		0.8301397	
SlopeF−SlopeC	1.193524	0.3978471		0.9999488	



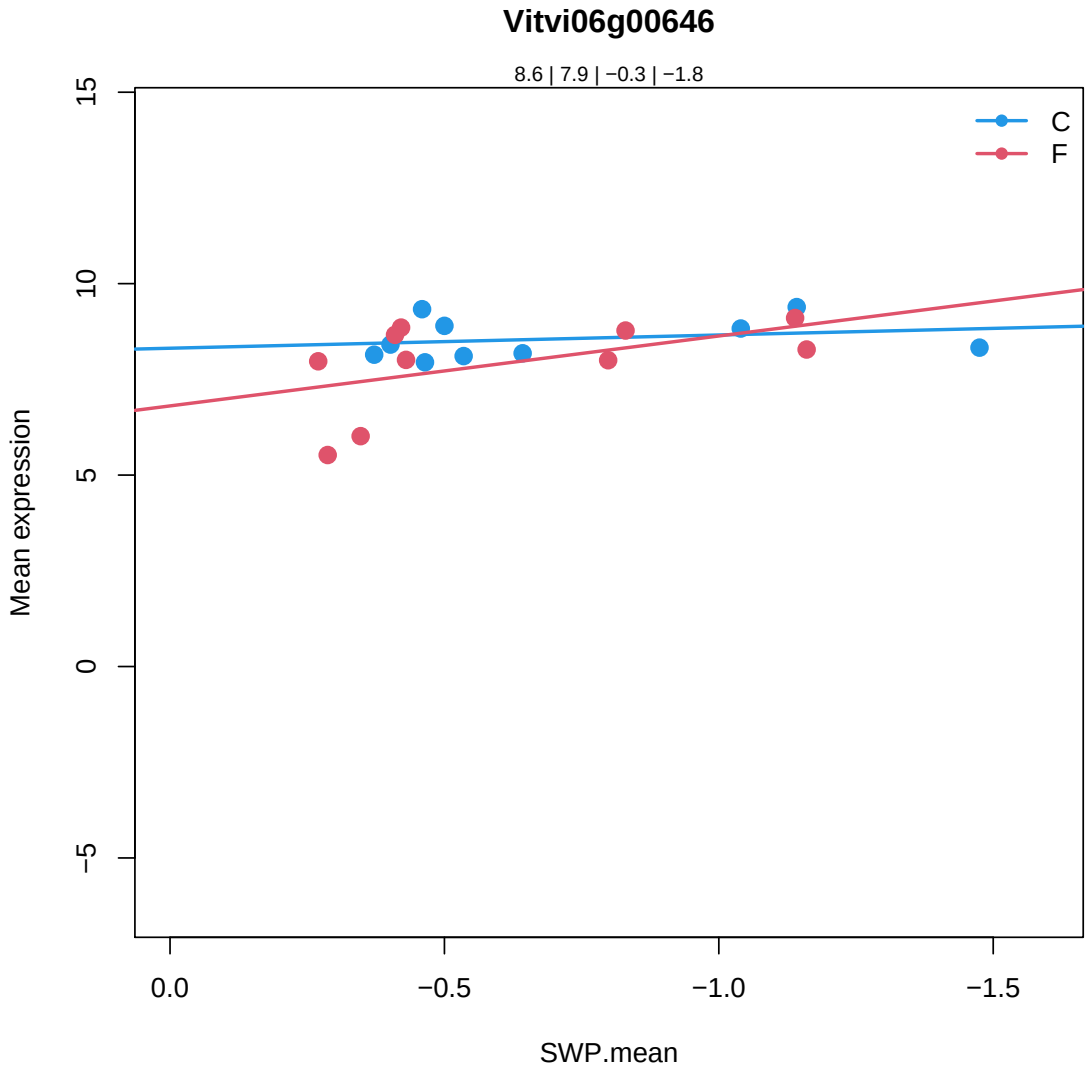
7.6.736 Vitvi06g00646: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00646
        18
        Co-factor and vitamine metabolism
        Aldolase-type TIM barrel family protein |
        Chr5:172576-173505 REVERSE LENGTH=309 |
        201606
```

Coefficients for Vitvi06g00646.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	8.555959	2.651399e-20	***	1.564561e-19	***
SlopeC	-0.3455025	0.6206393		0.9091736	
MeanF-MeanC	-0.6366878	0.0826493	.	0.3258501	
SlopeF-SlopeC	-1.480577	0.1626518		0.9999488	



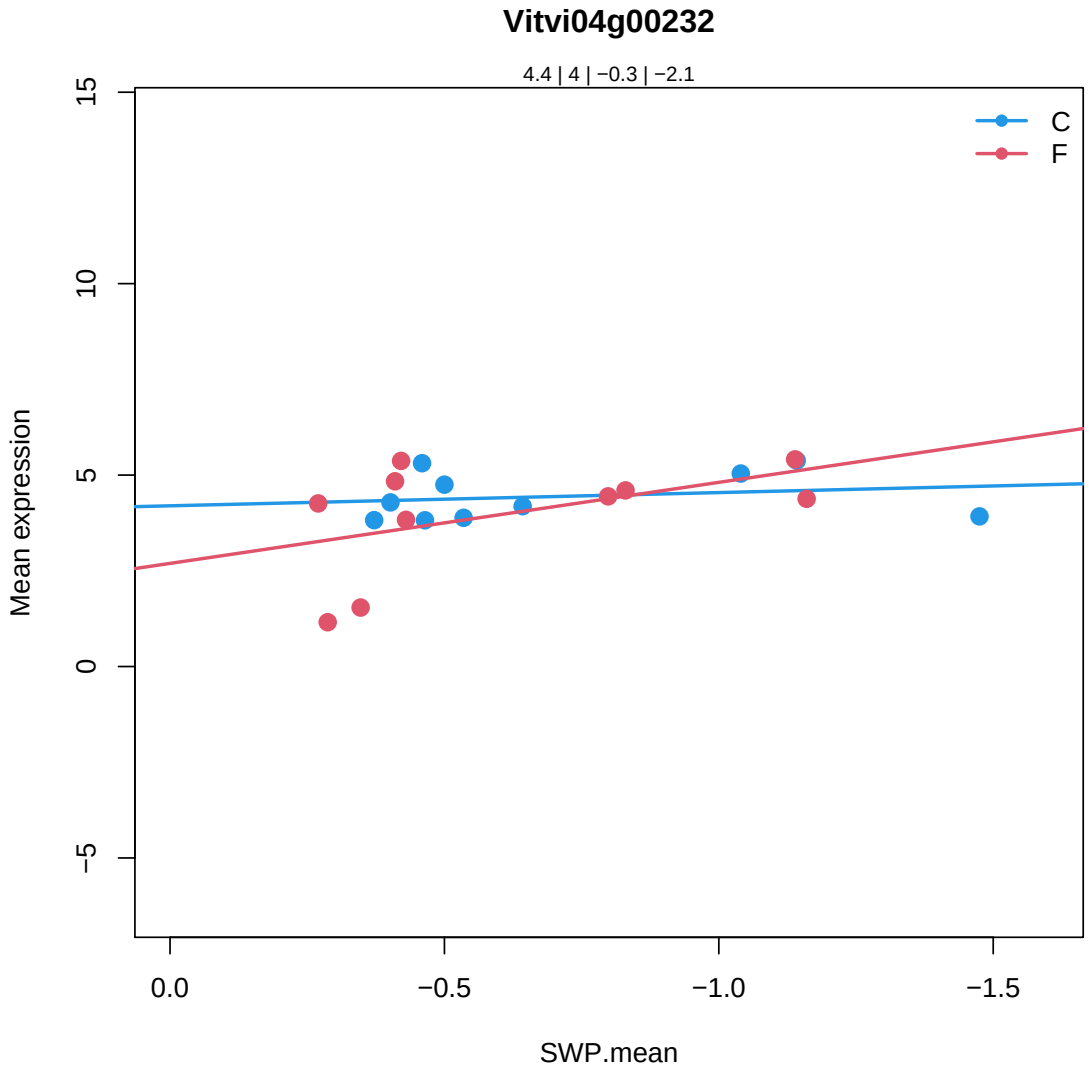
7.6.737 Vitvi04g00232: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00232
        28.2
        DNA.repair
        cryptochrome 3 |
        Chr5:8535399-8538145 REVERSE LENGTH=569 |
        201606
```

Coefficients for Vitvi04g00232.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.44014	1.046319e-12	***	1.498589e-12	***
SlopeC	-0.3455255	0.6838886		0.9283744	
MeanF-MeanC	-0.4572432	0.2945316		0.661003	
SlopeF-SlopeC	-1.771156	0.1695503		0.9999488	



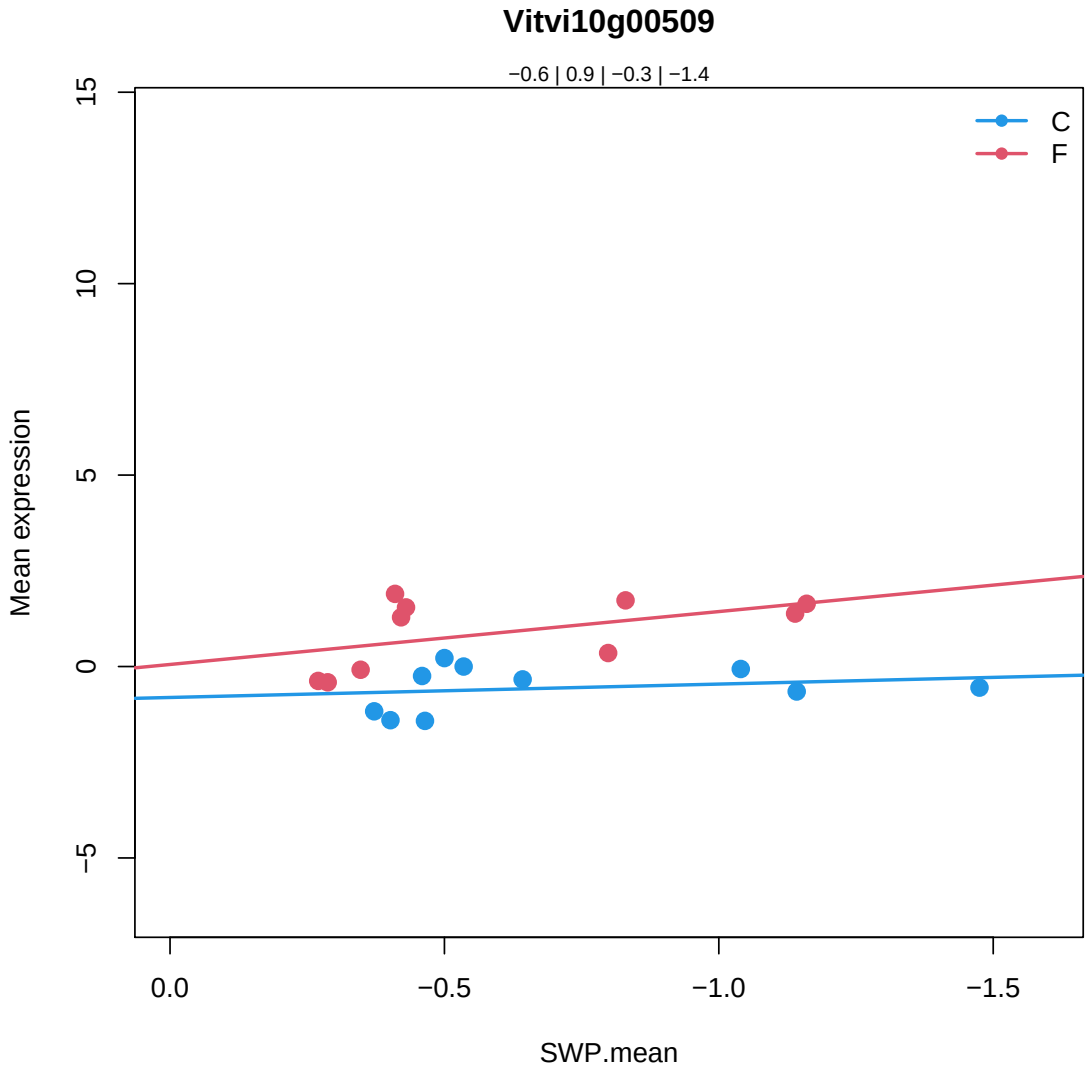
7.6.738 Vitvi10g00509: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00509
        20.1.3.1
        stress.biotic.signalling.MLO-like
        Seven transmembrane MLO family protein |
        Chr1:3801546-3803870 REVERSE LENGTH=418 |
        201606
```

Coefficients for Vitvi10g00509.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.5625775	0.01593093	*	0.01679829	*
SlopeC	-0.3496925	0.5648206		0.8905966	
MeanF-MeanC	1.457905	9.219838e-05	***	0.001682979	**
SlopeF-SlopeC	-1.031658	0.2591776		0.9999488	



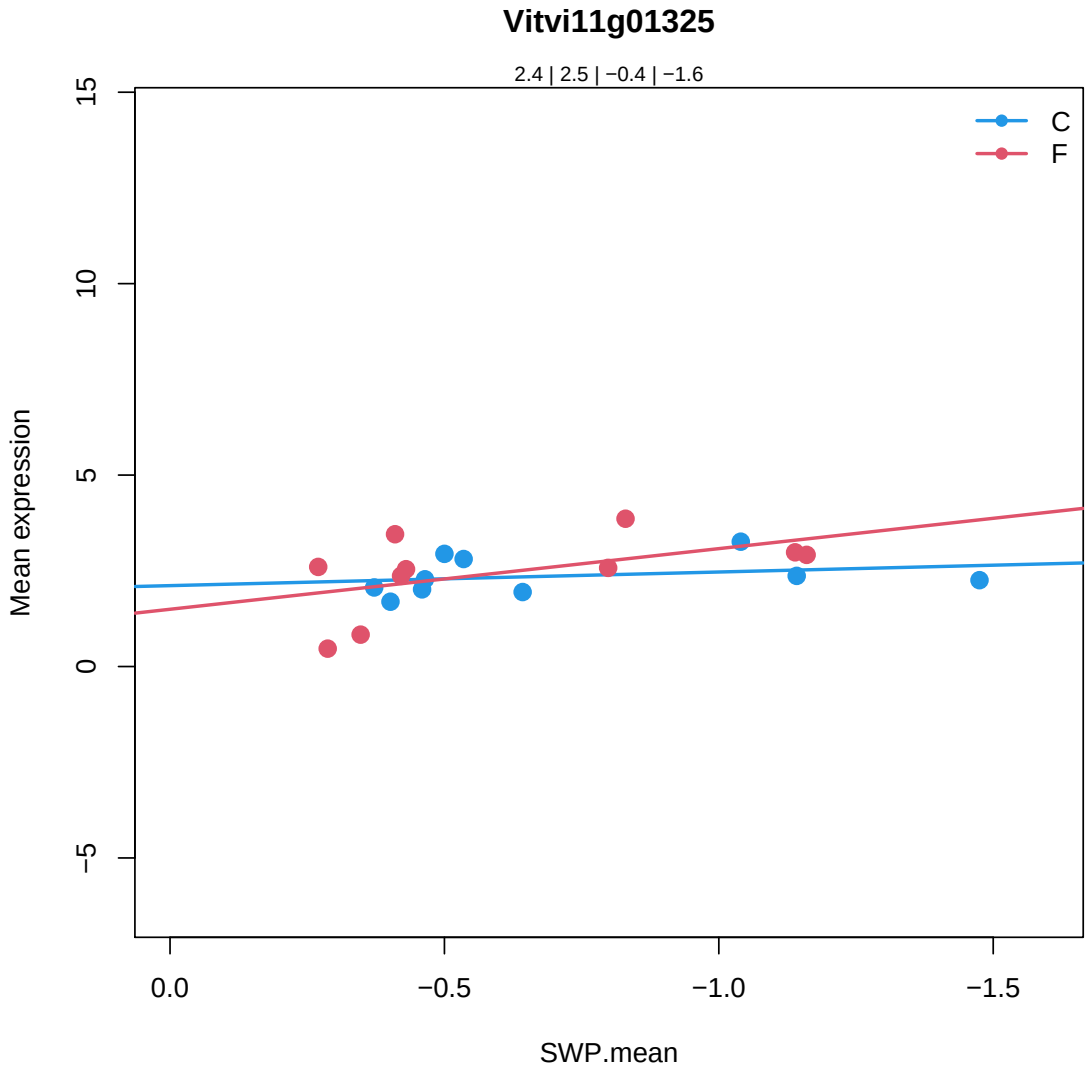
7.6.739 Vitvi11g01325: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g01325
        35.2
        not assigned.unknown
        transmembrane protein |
        Chr5:7040046-7040627 REVERSE LENGTH=193 |
        201606
```

Coefficients for Vitvi11g01325.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.362785	6.07443e-10	***	7.721973e-10	***
SlopeC	-0.3558692	0.5741312		0.8926765	
MeanF-MeanC	0.09714109	0.7622027		0.9306652	
SlopeF-SlopeC	-1.227871	0.199768		0.9999488	



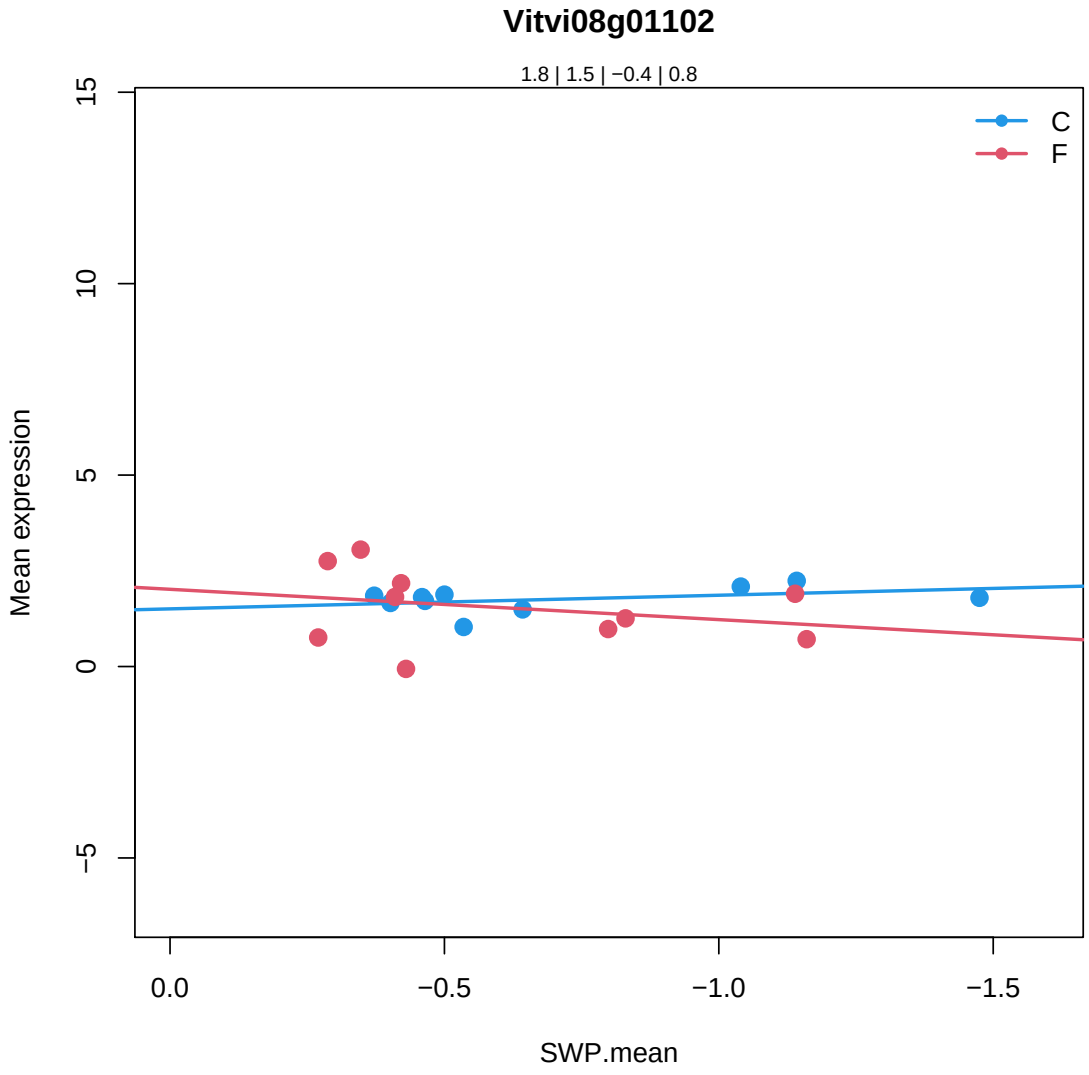
7.6.740 Vitvi08g01102: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01102
        10.6.3
        cell wall.degradation.pectate lyases and polygalacturonases
        Pectin lyase-like superfamily protein |
        Chr3:20439060-20440225 FORWARD LENGTH=307 |
        201606
```

Coefficients for Vitvi08g01102.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.755807	5.793269e-08	***	6.914722e-08	***
SlopeC	-0.3561141	0.5610319		0.8900454	
MeanF-MeanC	-0.2214473	0.4778722		0.793865	
SlopeF-SlopeC	1.148158	0.2145196		0.9999488	



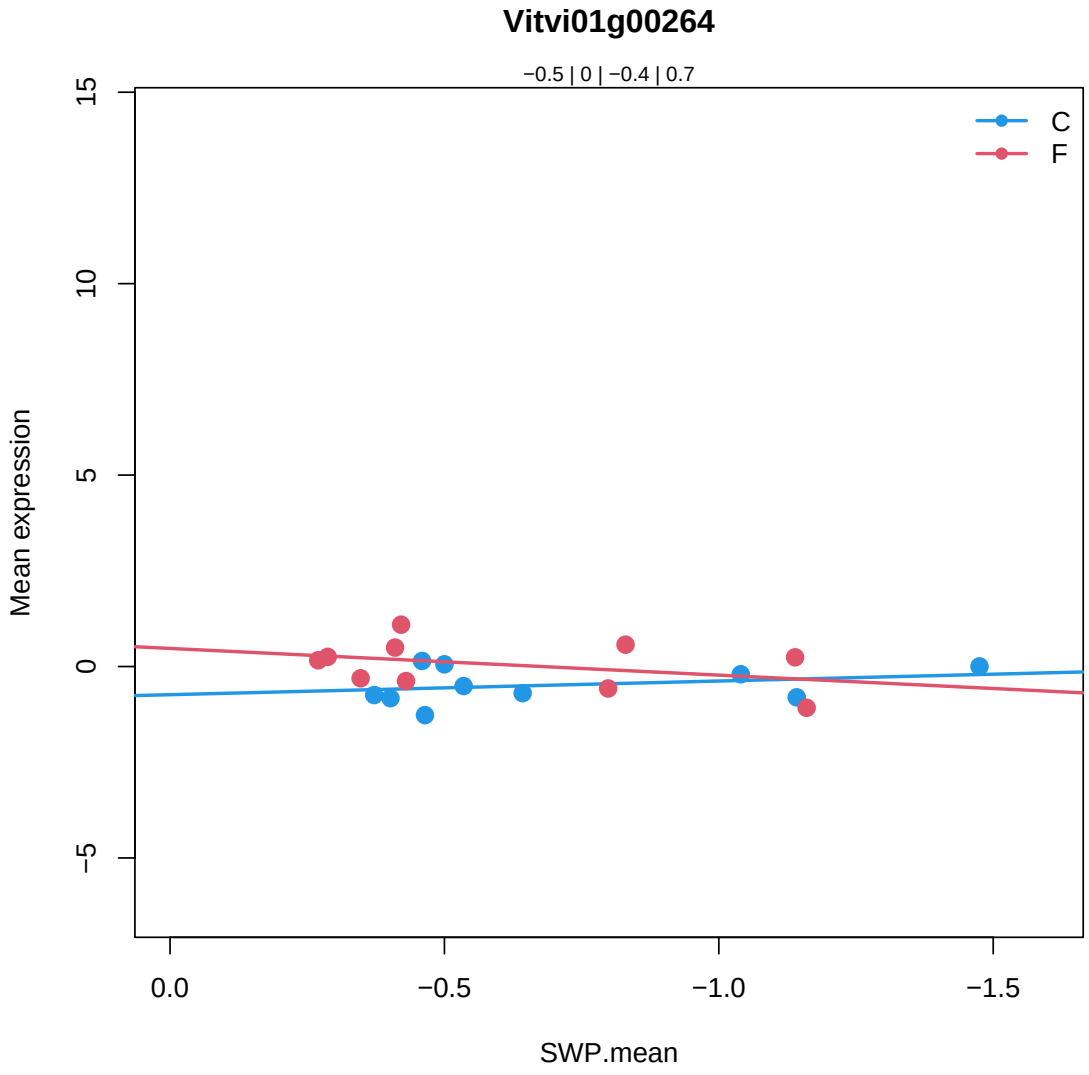
7.6.741 Vitvi01g00264: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00264
        35.1
        not assigned.no ontology
        alpha/beta-Hydrolases superfamily protein |
        Chr1:25766018-25767028 FORWARD LENGTH=336 |
        201606
```

Coefficients for Vitvi01g00264.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	−0.4849619	0.009431699	**	0.009996312	**
SlopeC	−0.3570588	0.4586912		0.8587853	
MeanF−MeanC	0.5322664	0.03786849	*	0.198484	
SlopeF−SlopeC	1.054566	0.14886		0.9999488	



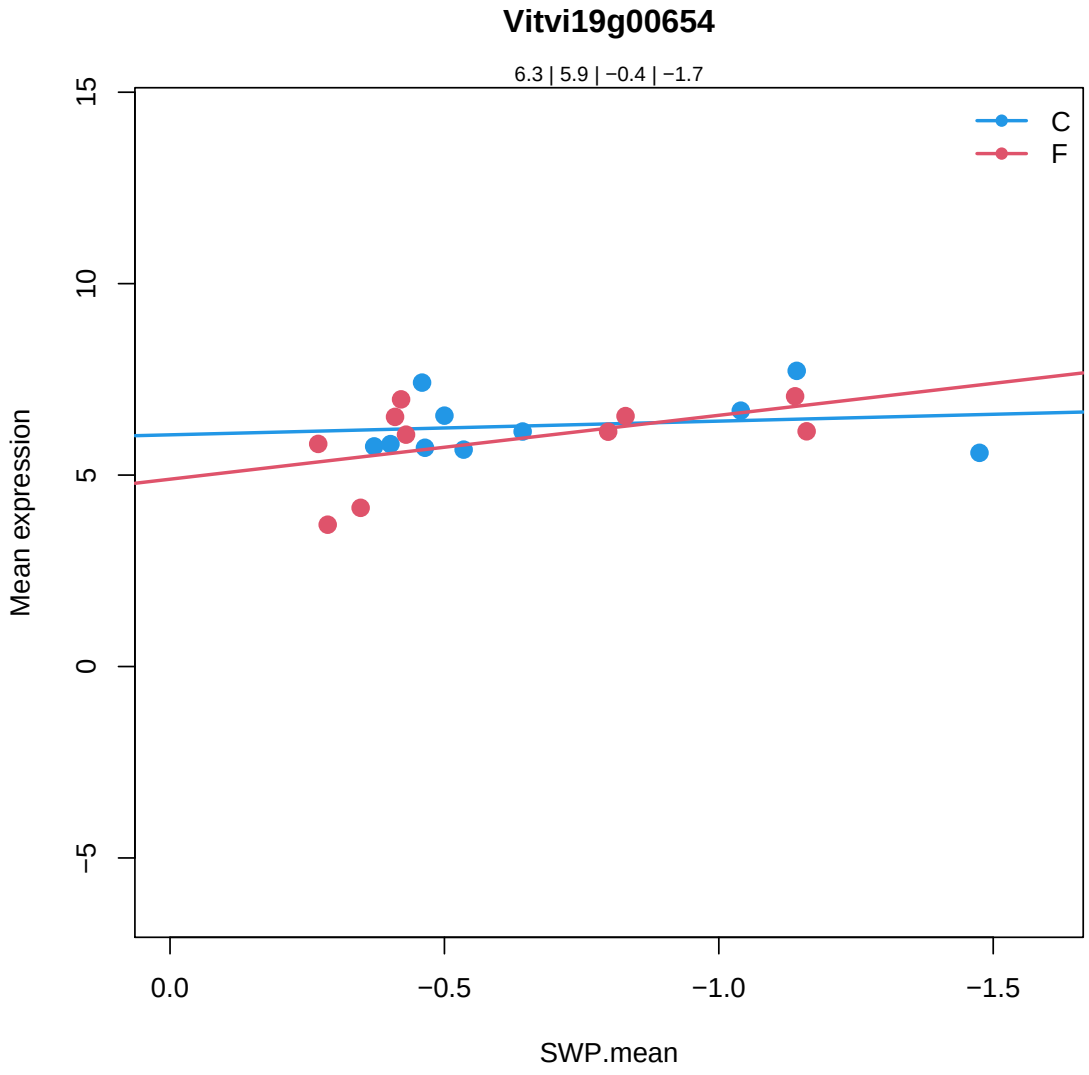
7.6.742 Vitvi19g00654: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g00654
        13.1.5.3.2
        amino acid metabolism.synthesis.serine-glycine-cysteine group.cysteine
        serine acetyltransferase 2%3B1 |
        Chr1:20912378-20913322 FORWARD LENGTH=314 |
        201606
```

Coefficients for Vitvi19g00654.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.302687	5.769362e-17	***	1.309555e-16	***
SlopeC	-0.3577424	0.6299262		0.9111539	
MeanF-MeanC	-0.3936917	0.3017008		0.666964	
SlopeF-SlopeC	-1.311121	0.2418288		0.9999488	



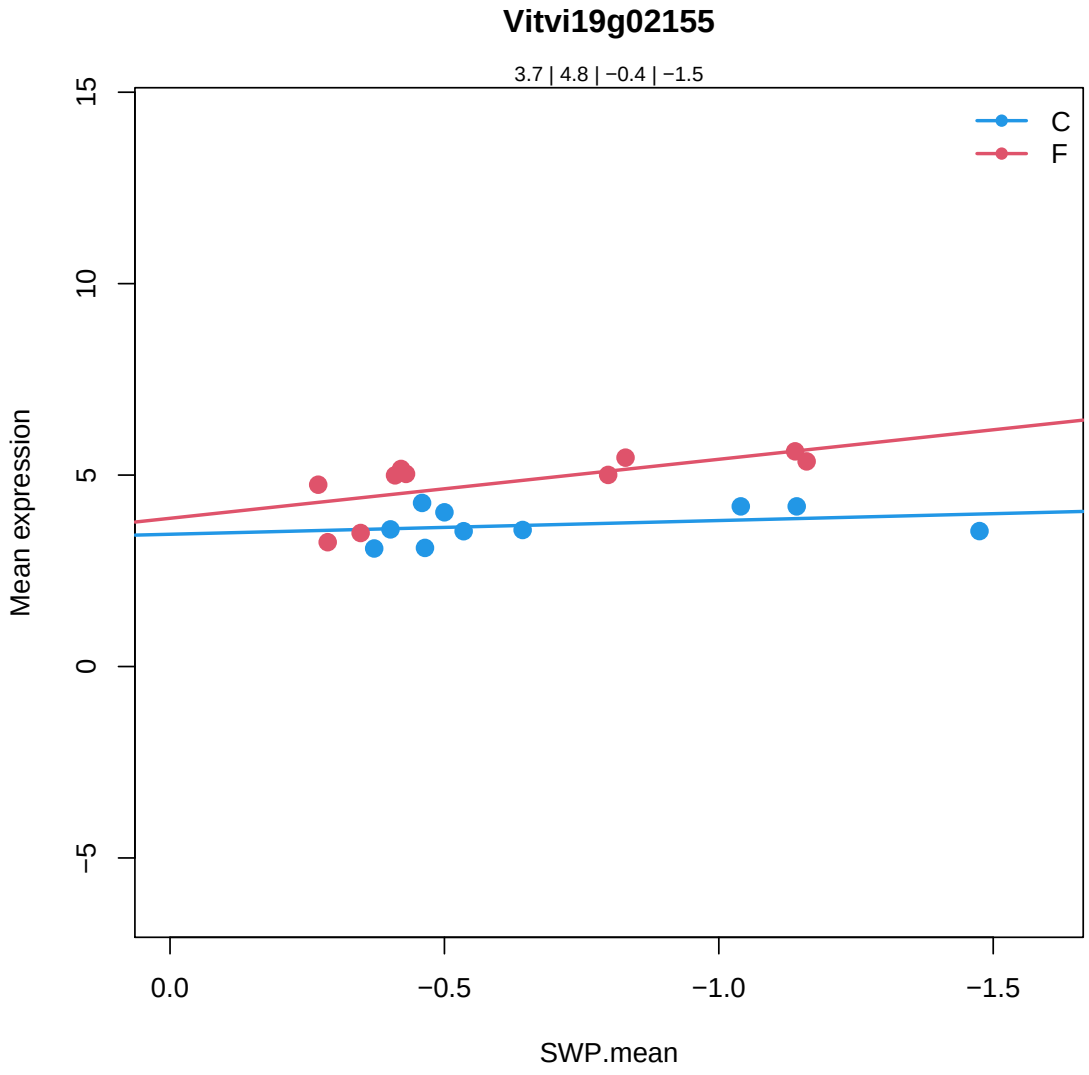
7.6.743 Vitvi19g02155: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g02155
        26.10
        misc.cytochrome P450
        cytochrome P450%2C family 72%2C subfamily A%2C polypeptide 15 |
        Chr3:4937410-4939310 FORWARD LENGTH=512 |
        201606
```

Coefficients for Vitvi19g02155.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.70633	3.792541e-16	***	7.527791e-16	***
SlopeC	-0.3578616	0.4561085		0.8579805	
MeanF-MeanC	1.103896	0.0001455722	***	0.002468088	**
SlopeF-SlopeC	-1.183277	0.1062559		0.9999488	



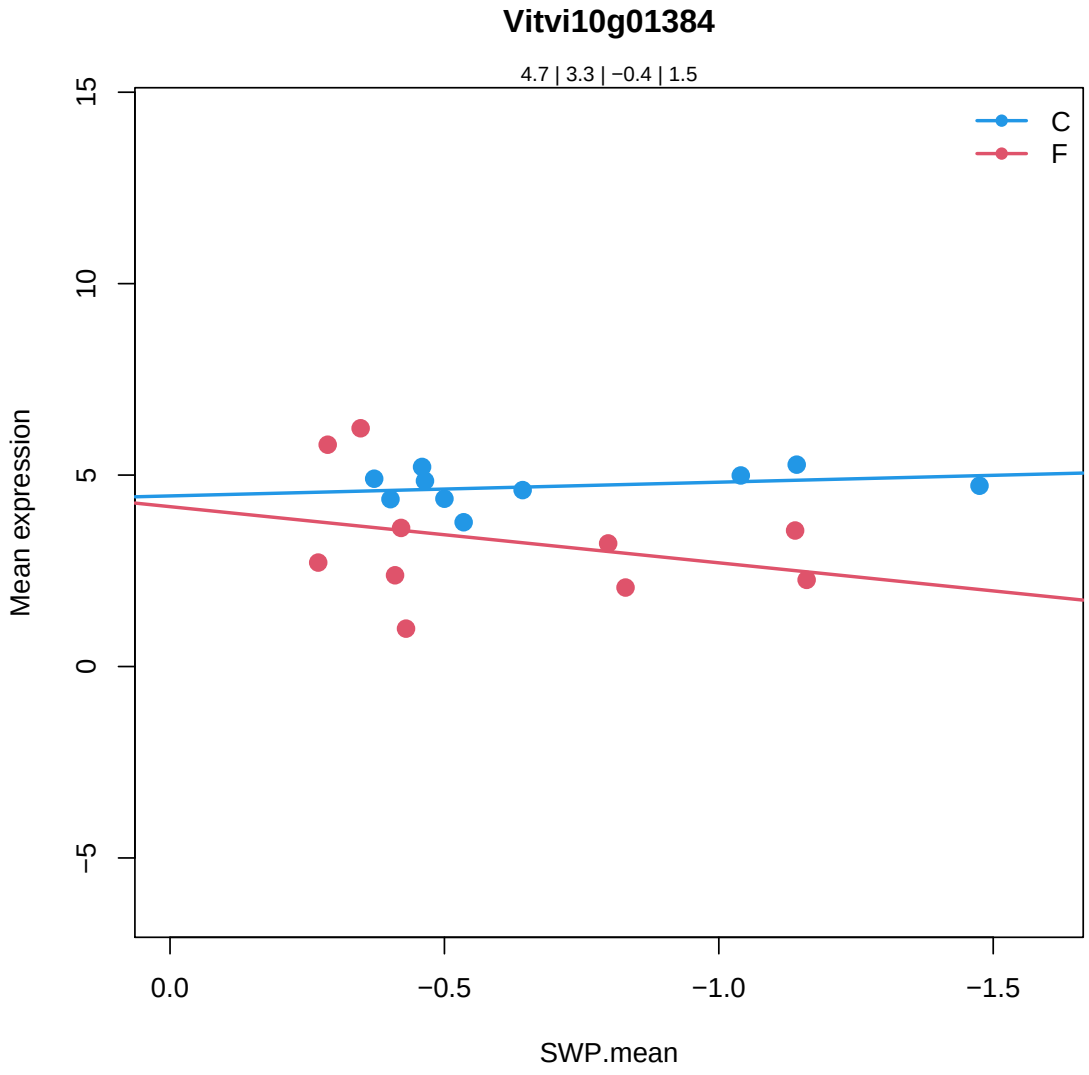
7.6.744 Vitvi10g01384: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g01384
        20.2.1
        stress.abiotic.heat
        DNAJ heat shock N-terminal domain-containing protein |
        Chr5:7826857-7828534 REVERSE LENGTH=465 |
        201606
```

Coefficients for Vitvi10g01384.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.707878	3.540685e-12	***	4.931206e-12	***
SlopeC	-0.3586635	0.7079896		0.9346979	
MeanF-MeanC	-1.426409	0.007201088	**	0.05968406	.
SlopeF-SlopeC	1.825551	0.2080516		0.9999488	



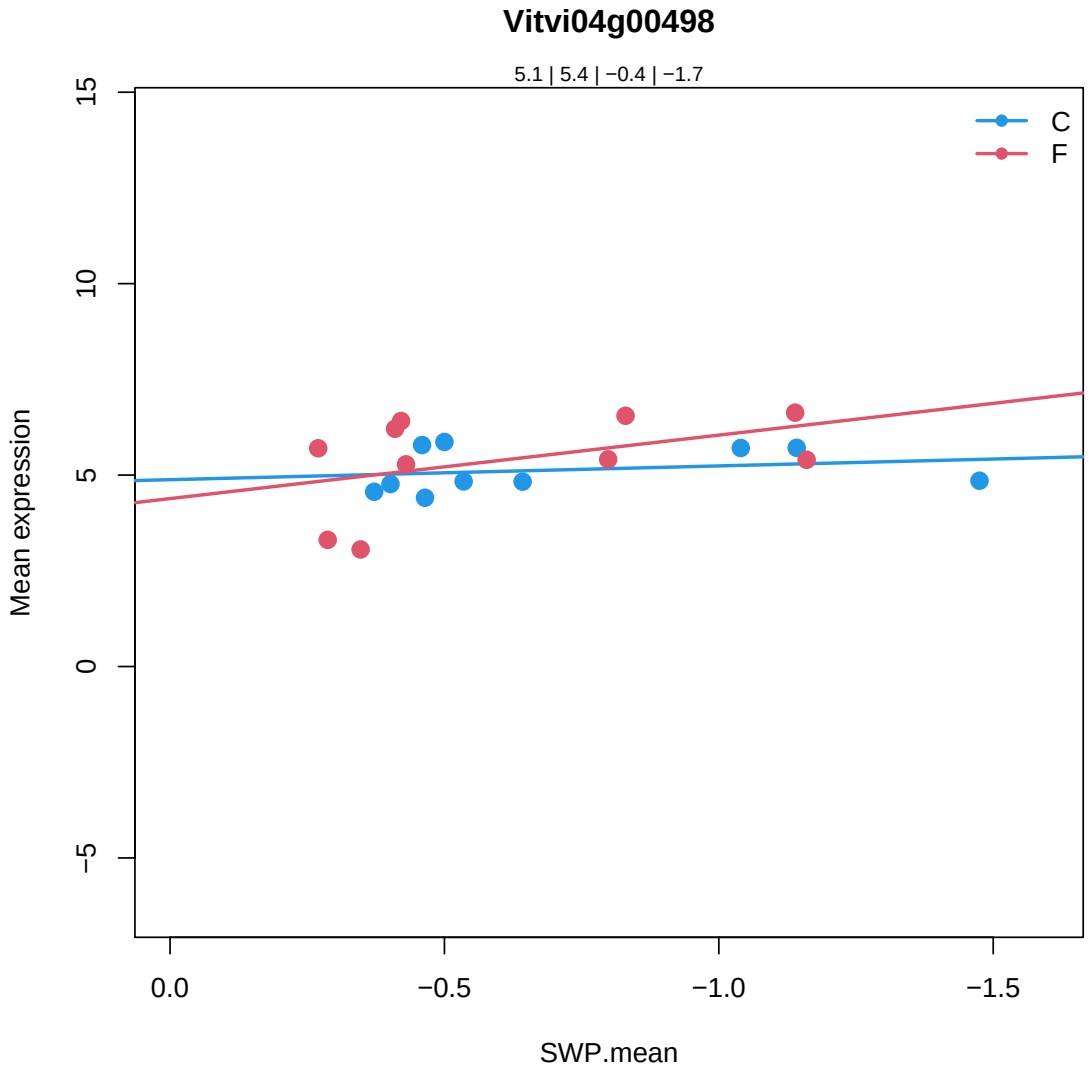
7.6.745 Vitvi04g00498: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00498
        35.1
        not assigned.no ontology
        Myosin heavy chain-related protein |
        Chr4:15545052-15547689 FORWARD LENGTH=783 |
        201606
```

Coefficients for Vitvi04g00498.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.132339	6.42457e-15	***	1.095216e-14	***
SlopeC	-0.359382	0.6365995		0.9127878	
MeanF-MeanC	0.2635831	0.4966606		0.8043031	
SlopeF-SlopeC	-1.29841	0.257458		0.9999488	



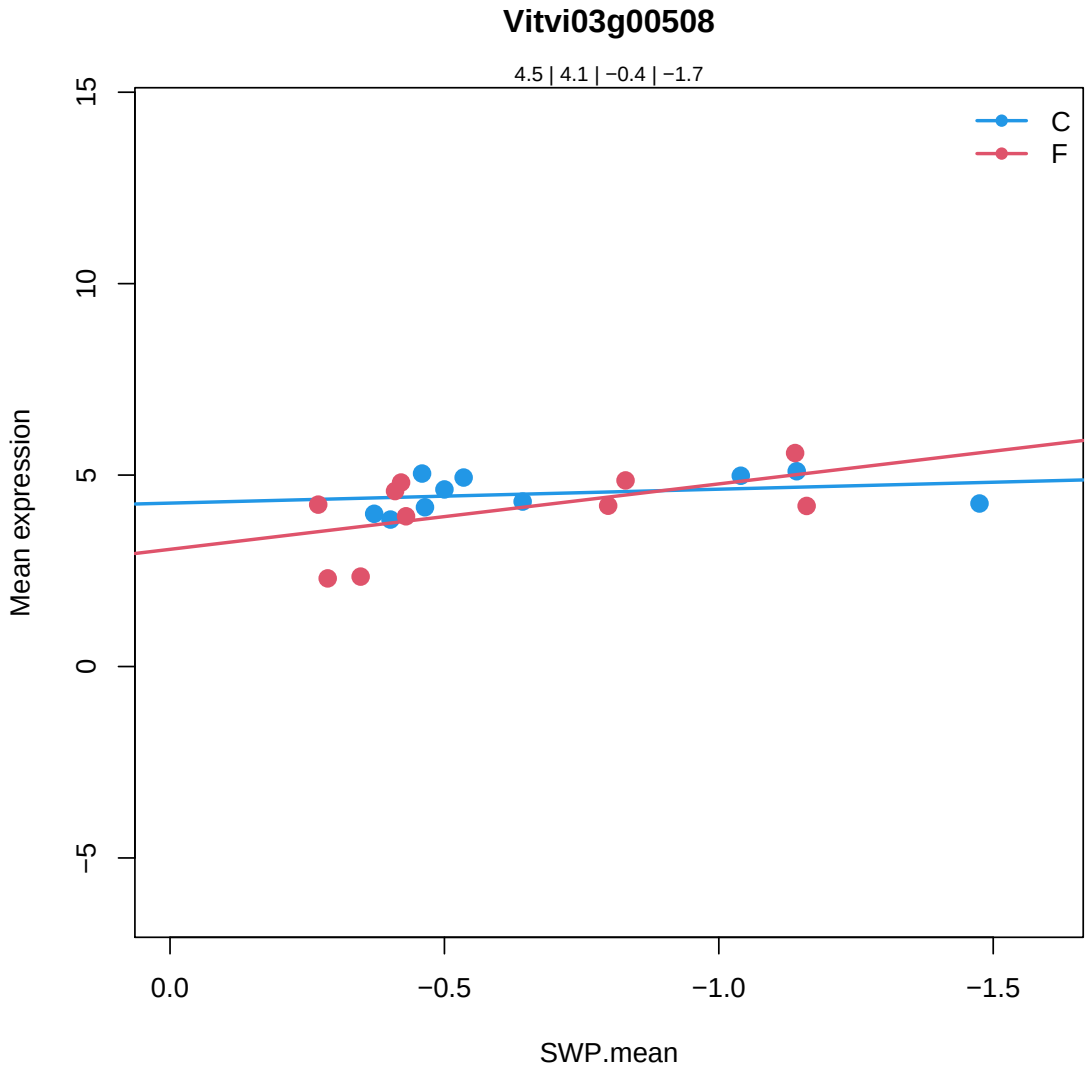
7.6.746 Vitvi03g00508: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00508
        26.10
        misc.cytochrome P450
        cytochrome P450%2C family 707%2C subfamily A%2C polypeptide 4 |
        Chr3:6673885-6676400 REVERSE LENGTH=468 |
        201606
```

Coefficients for Vitvi03g00508.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.523486	8.113208e-16	***	1.538079e-15	***
SlopeC	-0.3636981	0.5488856		0.8871816	
MeanF-MeanC	-0.4217311	0.1789828		0.5136018	
SlopeF-SlopeC	-1.345338	0.1447064		0.9999488	



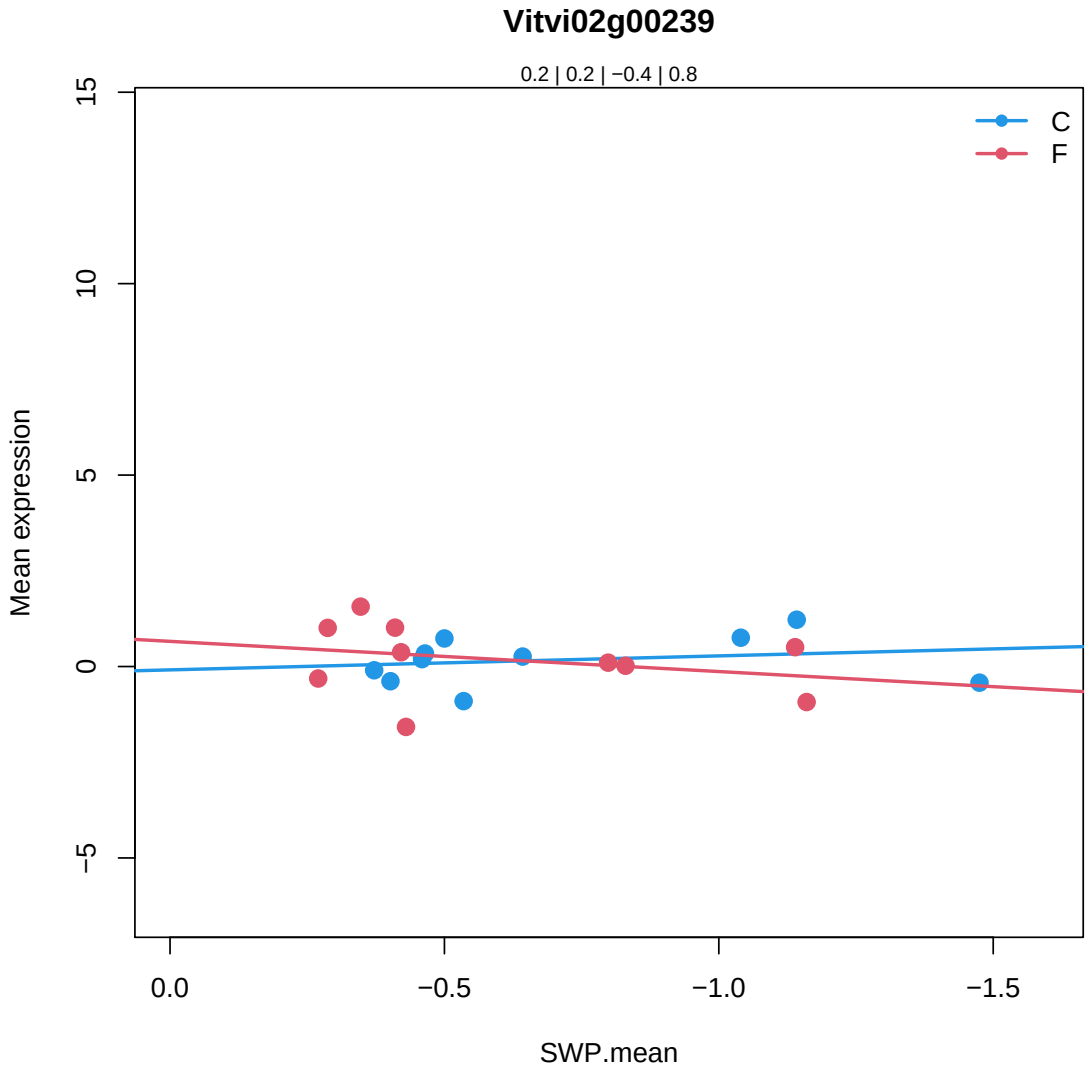
7.6.747 Vitvi02g00239: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00239
        27.3.50
        RNA.regulation of transcription.general transcription
        growth-regulating factor 8 |
        Chr4:12535972-12539387 FORWARD LENGTH=493 |
        201606
```

Coefficients for Vitvi02g00239.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1691063	0.4858805		0.4921118	
SlopeC	−0.3654503	0.5874424		0.8981764	
MeanF−MeanC	0.007641297	0.9821326		0.9955756	
SlopeF−SlopeC	1.153934	0.2553994		0.9999488	



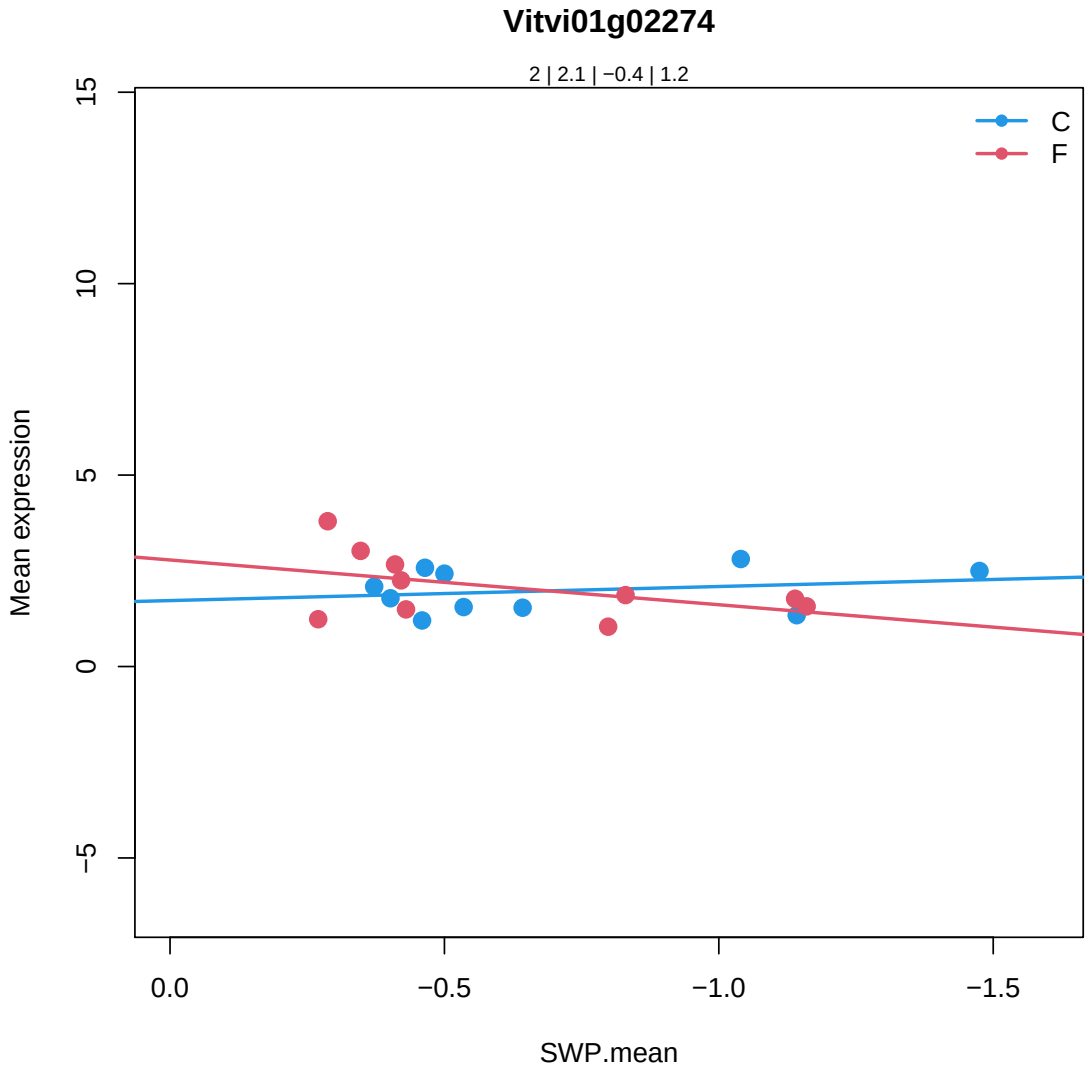
7.6.748 Vitvi01g02274: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g02274
        35.2
        not assigned.unknown
        transmembrane protein%2C putative (DUF 3339) |
        Chr5:25423460-25423669 FORWARD LENGTH=69 |
        201606
```

Coefficients for Vitvi01g02274.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.980737	4.052169e-09	***	5.007554e-09	***
SlopeC	-0.3677717	0.5337865		0.8804214	
MeanF-MeanC	0.08954222	0.7648684		0.931681	
SlopeF-SlopeC	1.537238	0.08990911	.	0.9999488	



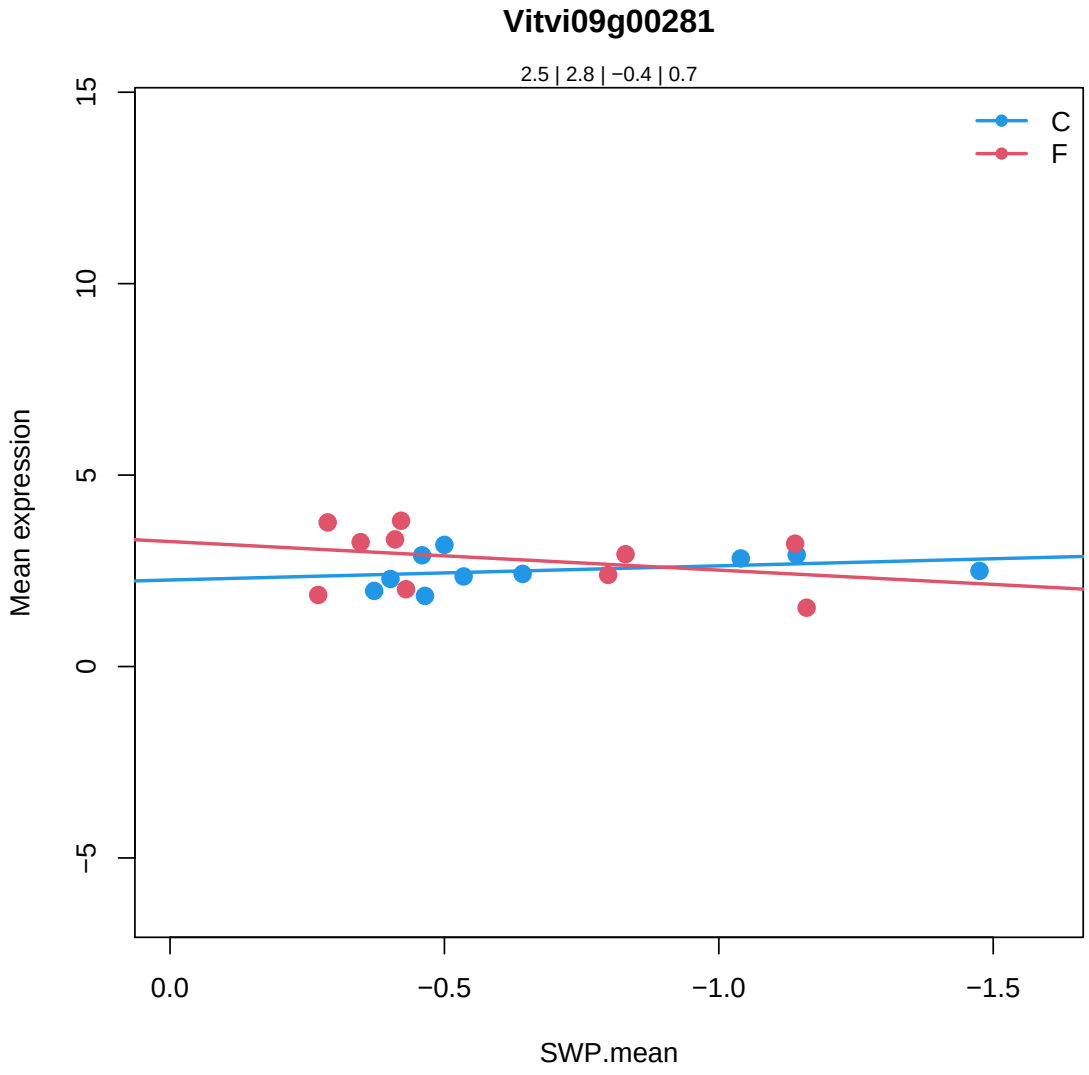
7.6.749 Vitvi09g00281: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00281
        27.3.40
        RNA.regulation of transcription.AUX/IAA family
        phytochrome-associated protein 1 |
        Chr3:5612801-5614208 REVERSE LENGTH=269 |
        201606
```

Coefficients for Vitvi09g00281.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.519719	1.218326e-11	***	1.656237e-11	***
SlopeC	-0.3699855	0.4999831		0.8698903	
MeanF-MeanC	0.2895756	0.3025228		0.667635	
SlopeF-SlopeC	1.116232	0.1785524		0.9999488	



7.6.750 Vitvi06g01739: type5

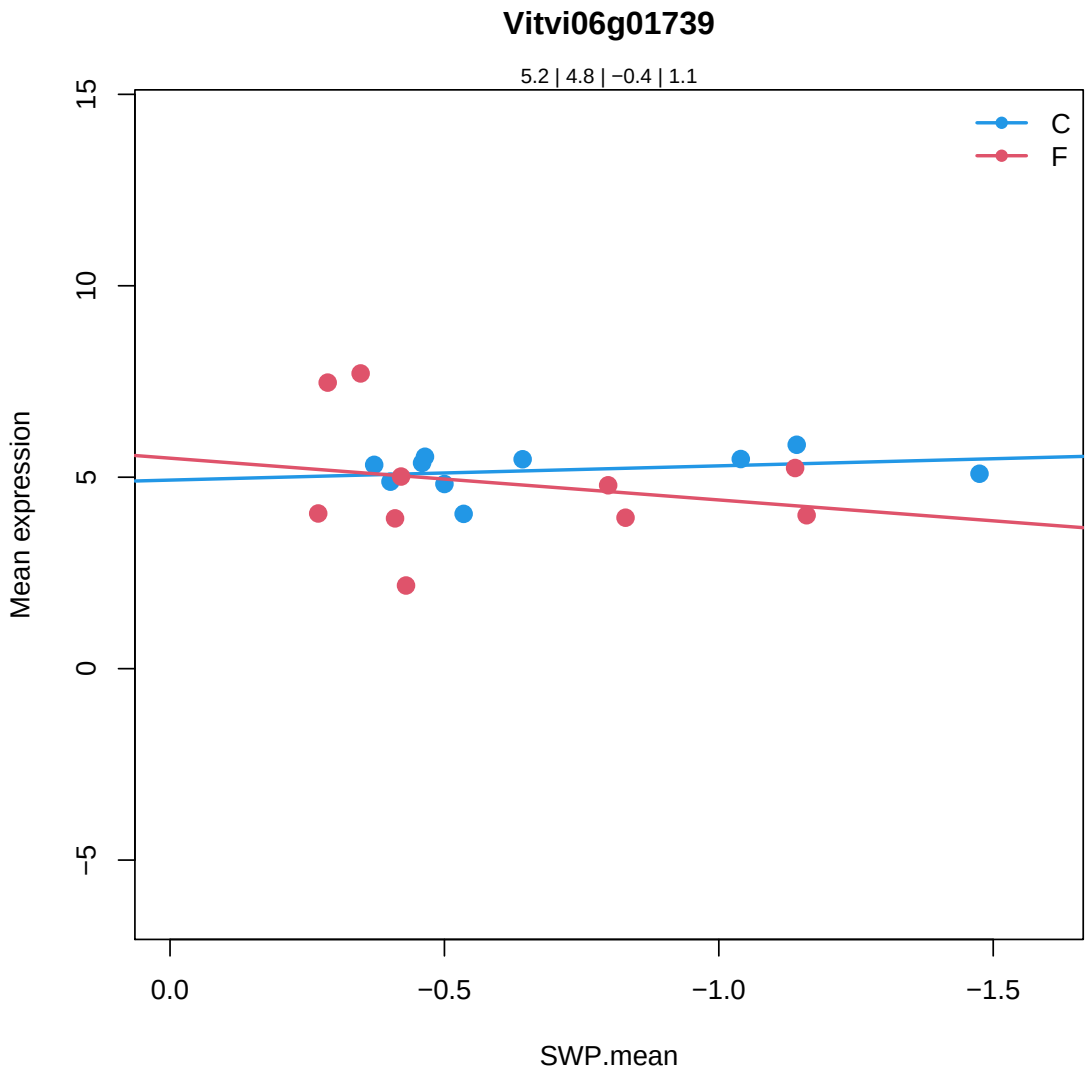
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01739
        35.2
        not assigned.unknown
        thiaminC |
        Chr2:12667395-12669569 FORWARD LENGTH=644 |
        201606

Vitvi06g01739
        18.2
        Co-factor and vitamine metabolism.thiamine
        thiaminC |
        Chr2:12667395-12669569 FORWARD LENGTH=644 |
        201606
```

Coefficients for Vitvi06g01739.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.186057	1.574047e-12	***	2.232194e-12	***
SlopeC	-0.3717055	0.7133195		0.9353048	
MeanF-MeanC	-0.3535274	0.4935332		0.8027207	
SlopeF-SlopeC	1.462645	0.335945		0.9999488	


Vitvi06g01739
5.2 | 4.8 | −0.4 | 1.1
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

7.6.751 Vitvi11g00480: type5

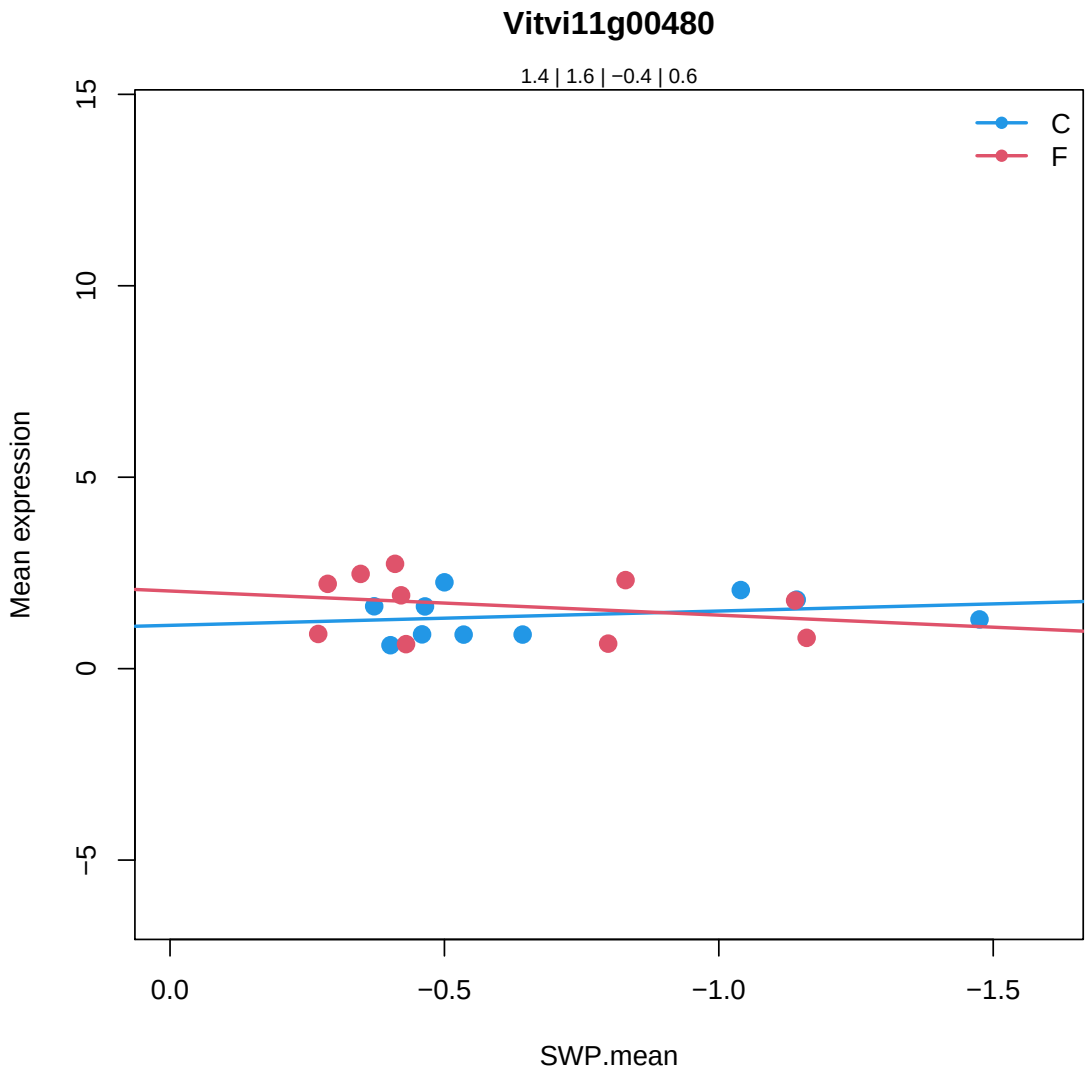
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00480
        33.99
        development.unspecified
        TPX2 (targeting protein for Xklp2) protein family |
        Chr4:15609801-15611867 FORWARD LENGTH=437 |
        201606

Vitvi11g00480
        31.1
        cell.organisation
        TPX2 (targeting protein for Xklp2) protein family |
        Chr4:15609801-15611867 FORWARD LENGTH=437 |
        201606
```

Coefficients for Vitvi11g00480.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.393524	1.363599e-06	***	1.569313e-06	***
SlopeC	-0.373643	0.5307666		0.8782917	
MeanF-MeanC	0.2502048	0.4105277		0.7510872	
SlopeF-SlopeC	1.003878	0.2627436		0.9999488	


Vitvi11g00480
1.4 | 1.6 | −0.4 | 0.6
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

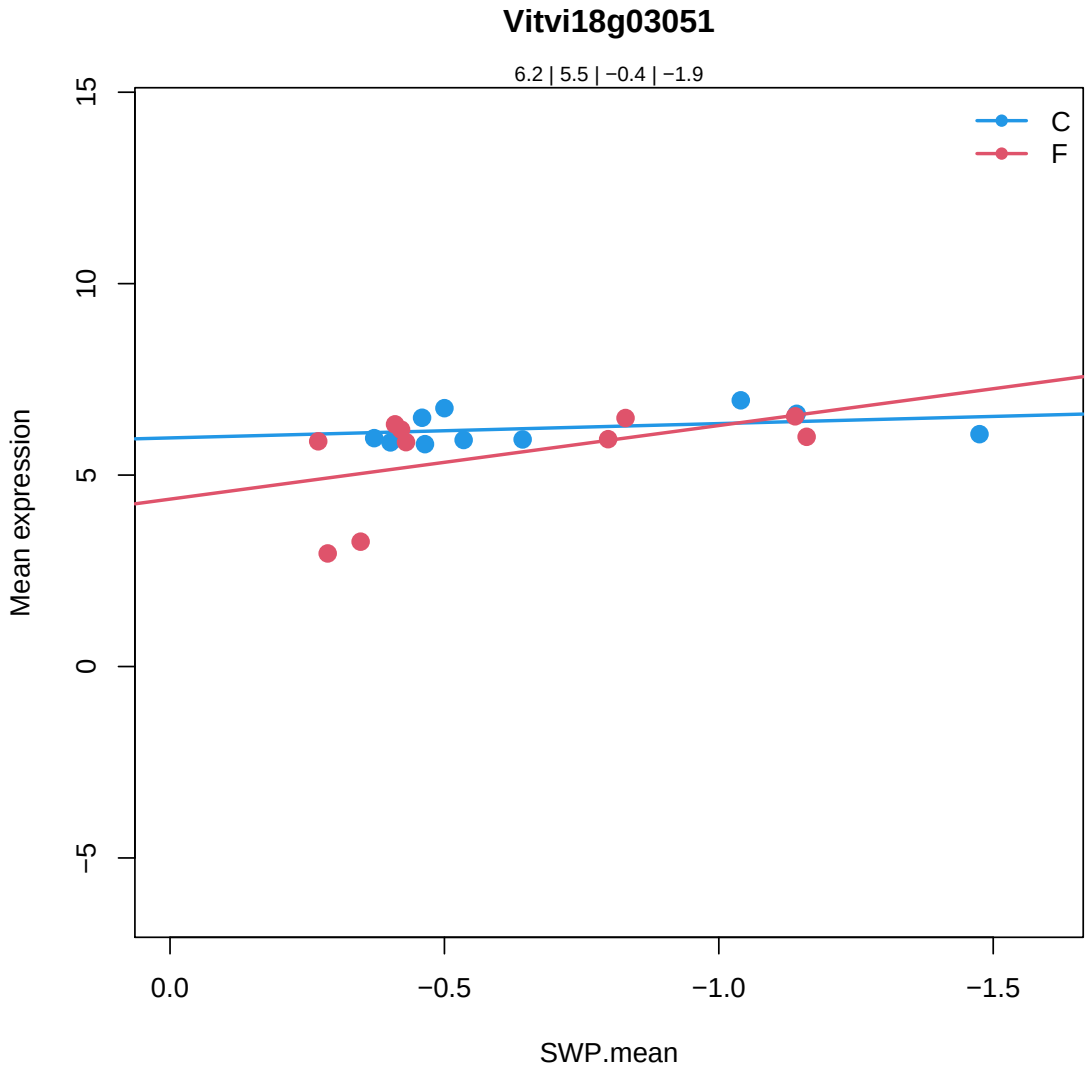
7.6.752 Vitvi18g03051: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g03051
        20.2.1
        stress.abiotic.heat
        Chaperone DnaJ-domain superfamily protein |
        Chr4:5931317-5932152 REVERSE LENGTH=249 |
        201606
```

Coefficients for Vitvi18g03051.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.233839	4.614745e-17	***	1.065242e-16	***
SlopeC	-0.3745514	0.6062977		0.9047128	
MeanF-MeanC	-0.6908052	0.07126465	.	0.2998939	
SlopeF-SlopeC	-1.547711	0.1609326		0.9999488	



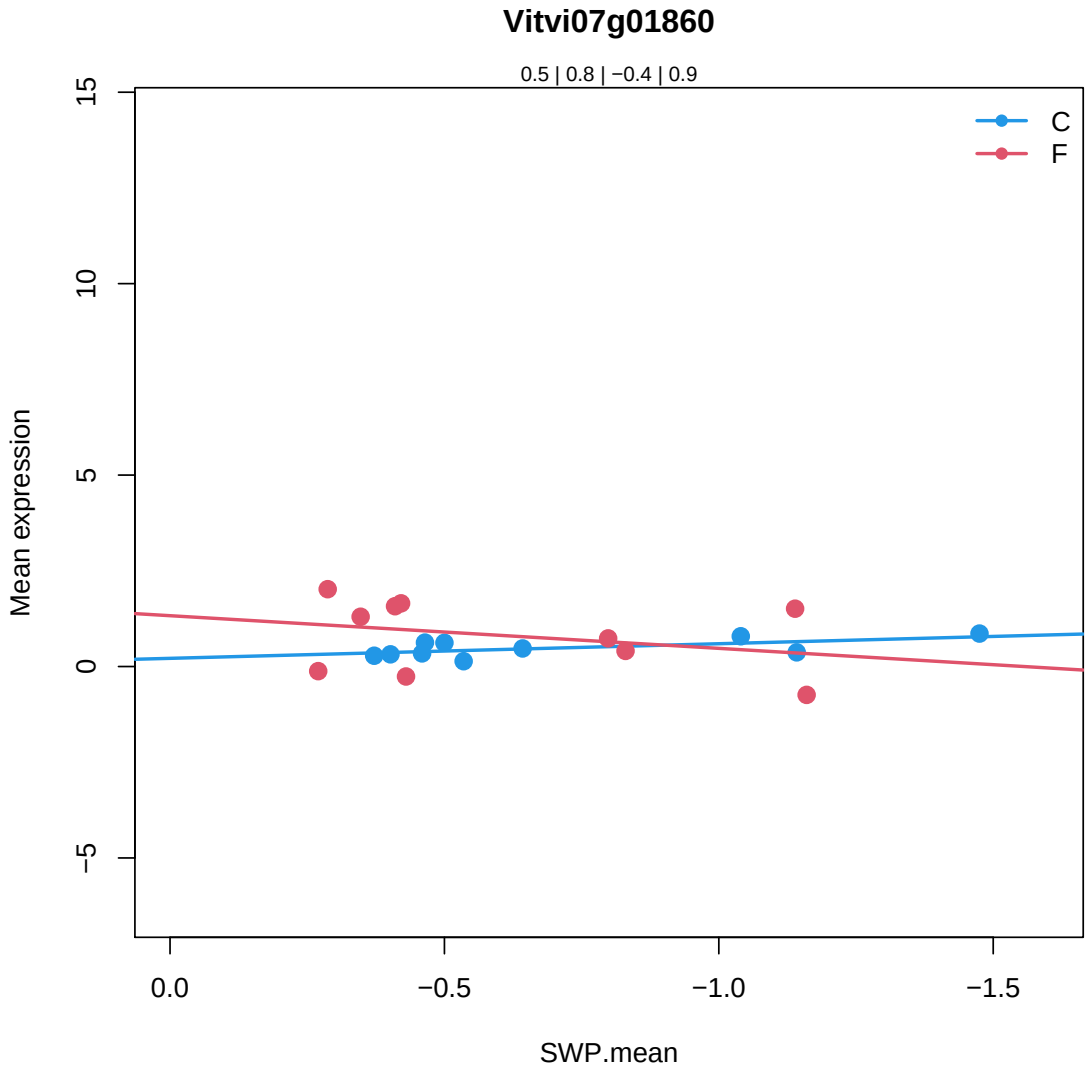
7.6.753 Vitvi07g01860: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01860
        27.3.32
        RNA.regulation of transcription.WRKY domain transcription factor famil
        WRKY DNA-binding protein 13 |
        Chr4:18332937-18334789 REVERSE LENGTH=304 |
        201606
```

Coefficients for Vitvi07g01860.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4817975	0.02760389	*	0.02893464	*
SlopeC	−0.3813722	0.5084585		0.8711742	
MeanF−MeanC	0.3256248	0.2711362		0.6342186	
SlopeF−SlopeC	1.234506	0.1580914		0.9999488	



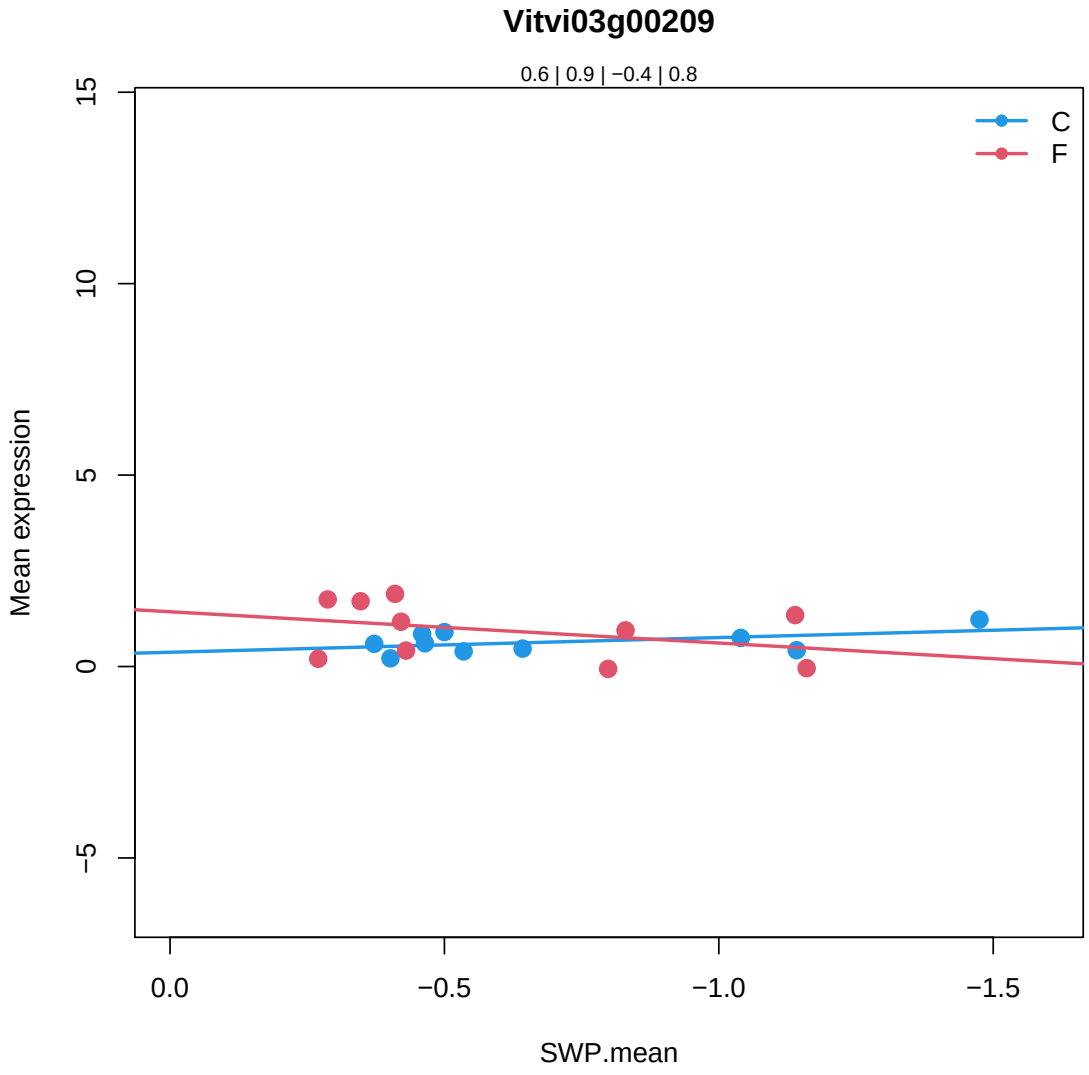
7.6.754 Vitvi03g00209: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00209
        10.7
        cell wall.modification
        expansin-like A3 |
        Chr3:16893058-16893789 FORWARD LENGTH=215 |
        201606
```

Coefficients for Vitvi03g00209.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6420043	0.001209416	**	0.001307927	**
SlopeC	−0.383232	0.4325951		0.8481624	
MeanF−MeanC	0.2905928	0.2458719		0.6059142	
SlopeF−SlopeC	1.200218	0.1068908		0.9999488	



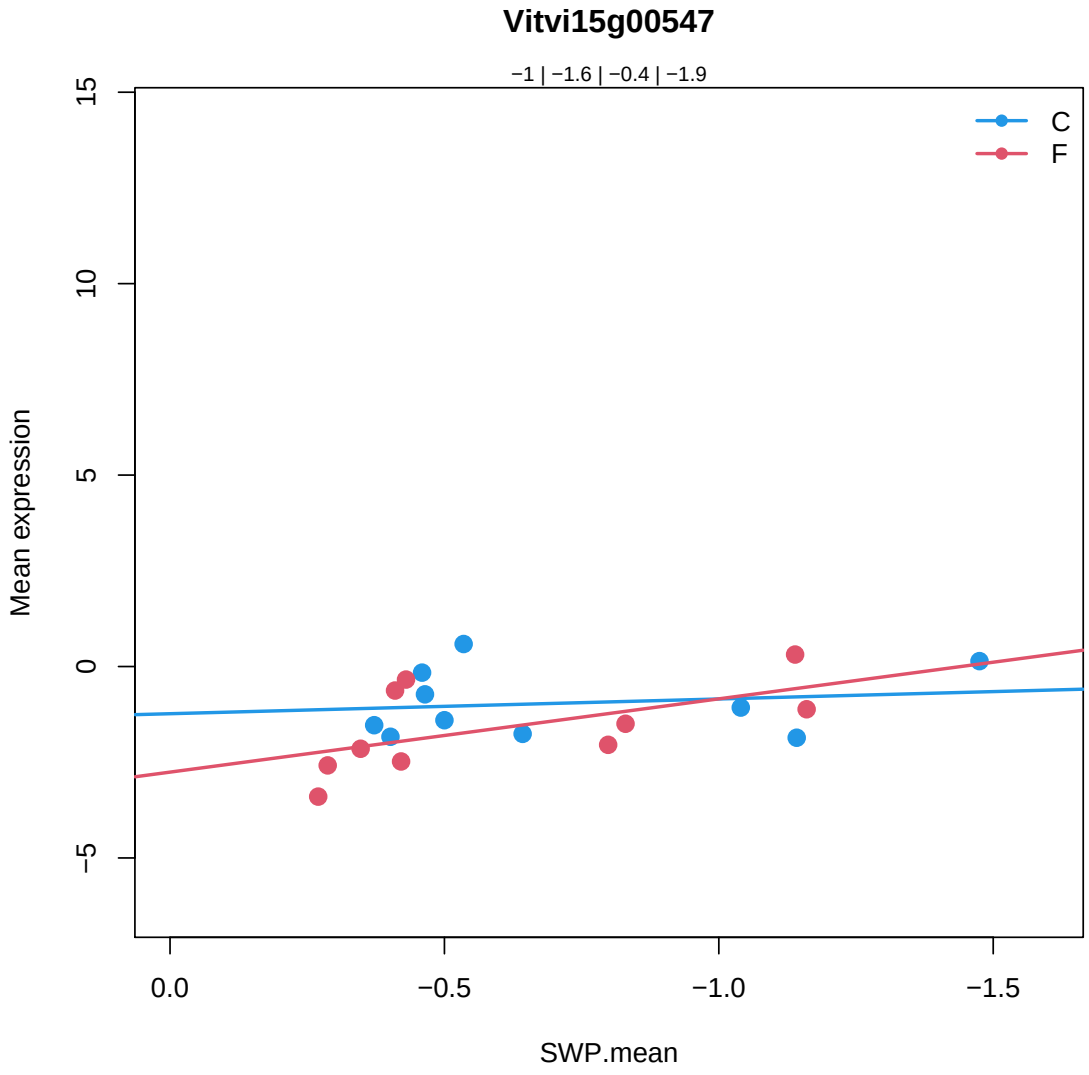
7.6.755 Vitvi15g00547: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g00547
        26.7
        misc.oxidases - copper, flavone etc
        Cupredoxin superfamily protein |
        Chr3:22278029-22278762 REVERSE LENGTH=187 |
        201606
```

Coefficients for Vitvi15g00547.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	−0.9620584	0.002070391	**	0.002225608	**
SlopeC	−0.3852937	0.6192702		0.9085813	
MeanF−MeanC	−0.630081	0.1194085		0.406346	
SlopeF−SlopeC	−1.528322	0.1930914		0.9999488	



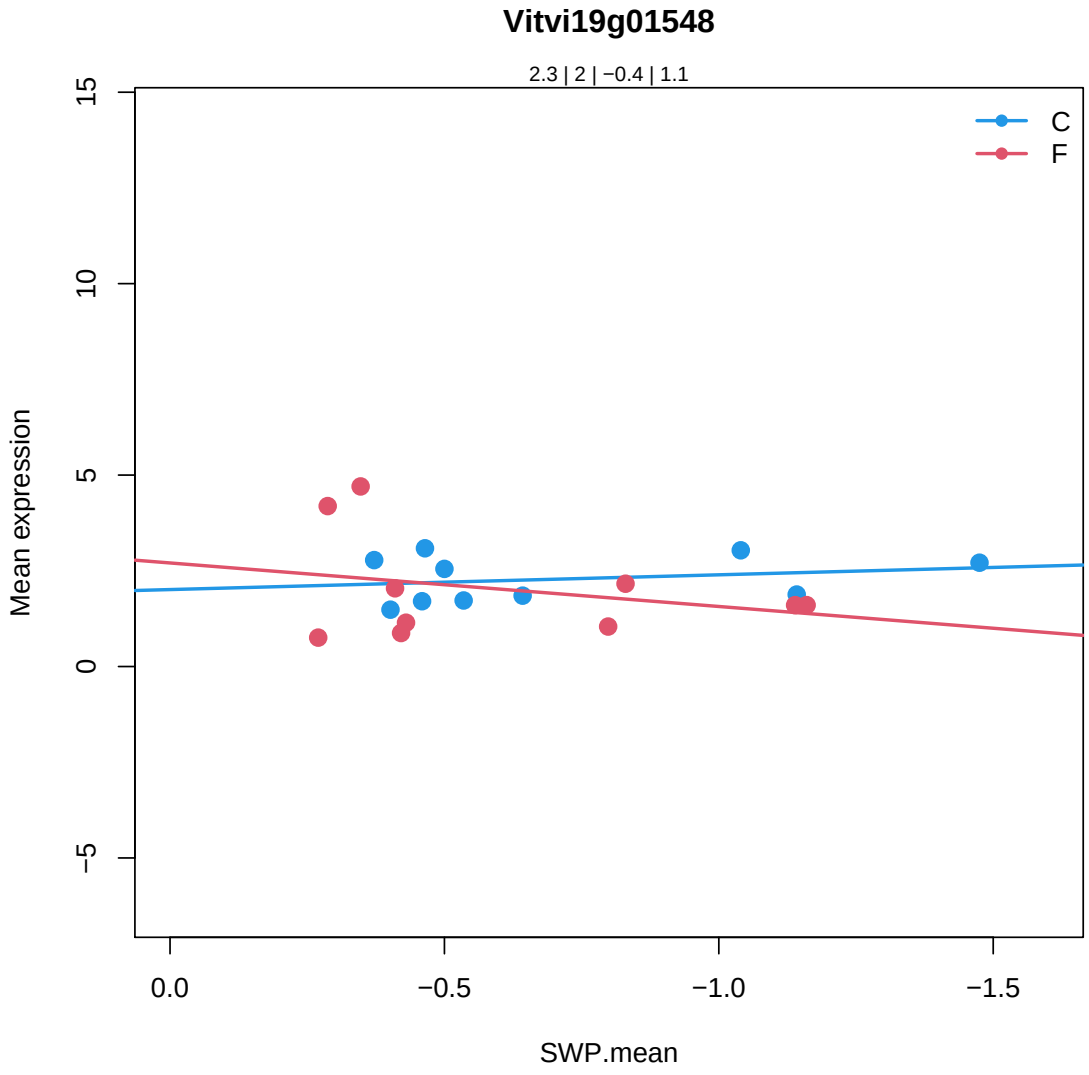
7.6.756 Vitvi19g01548: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g01548
        35.2
        not assigned.unknown
        Lojap-related protein |
        Chr3:4128465-4129616 FORWARD LENGTH=238 |
        201606
```

Coefficients for Vitvi19g01548.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.280774	2.137362e-07	***	2.512546e-07	***
SlopeC	-0.3854838	0.6546329		0.9201505	
MeanF-MeanC	-0.2686136	0.5405711		0.8286051	
SlopeF-SlopeC	1.521969	0.2419335		0.9999488	



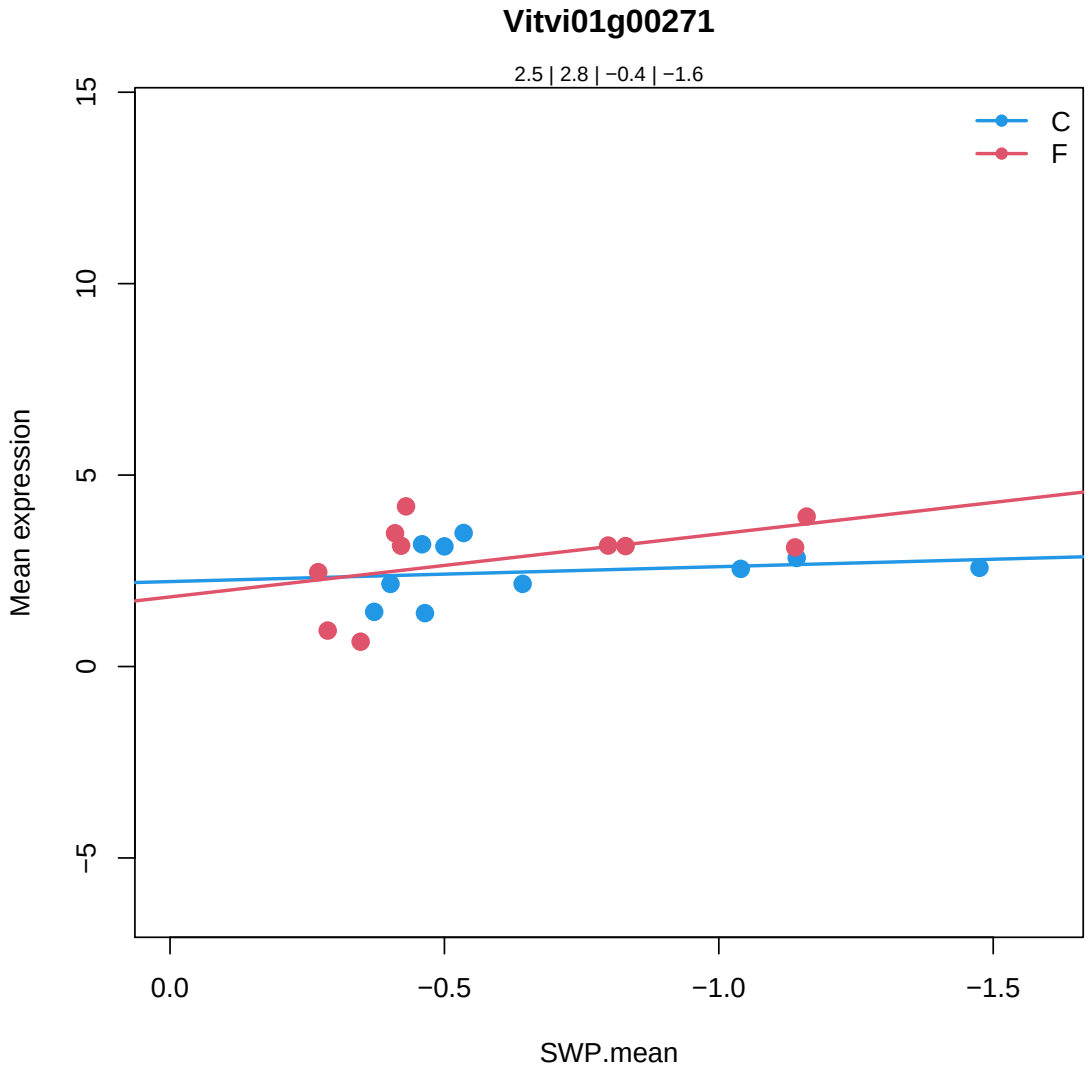
7.6.757 Vitvi01g00271: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00271
        35.2
        not assigned.unknown
        Regulator of Vps4 activity in the MVB pathway protein |
        Chr1:4569622-4571043 REVERSE LENGTH=409 |
        201606
```

Coefficients for Vitvi01g00271.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.491931	4.778988e-09	***	5.895696e-09	***
SlopeC	-0.3889571	0.6038381		0.9046943	
MeanF-MeanC	0.3279942	0.3919699		0.7402965	
SlopeF-SlopeC	-1.256234	0.2657067		0.9999488	



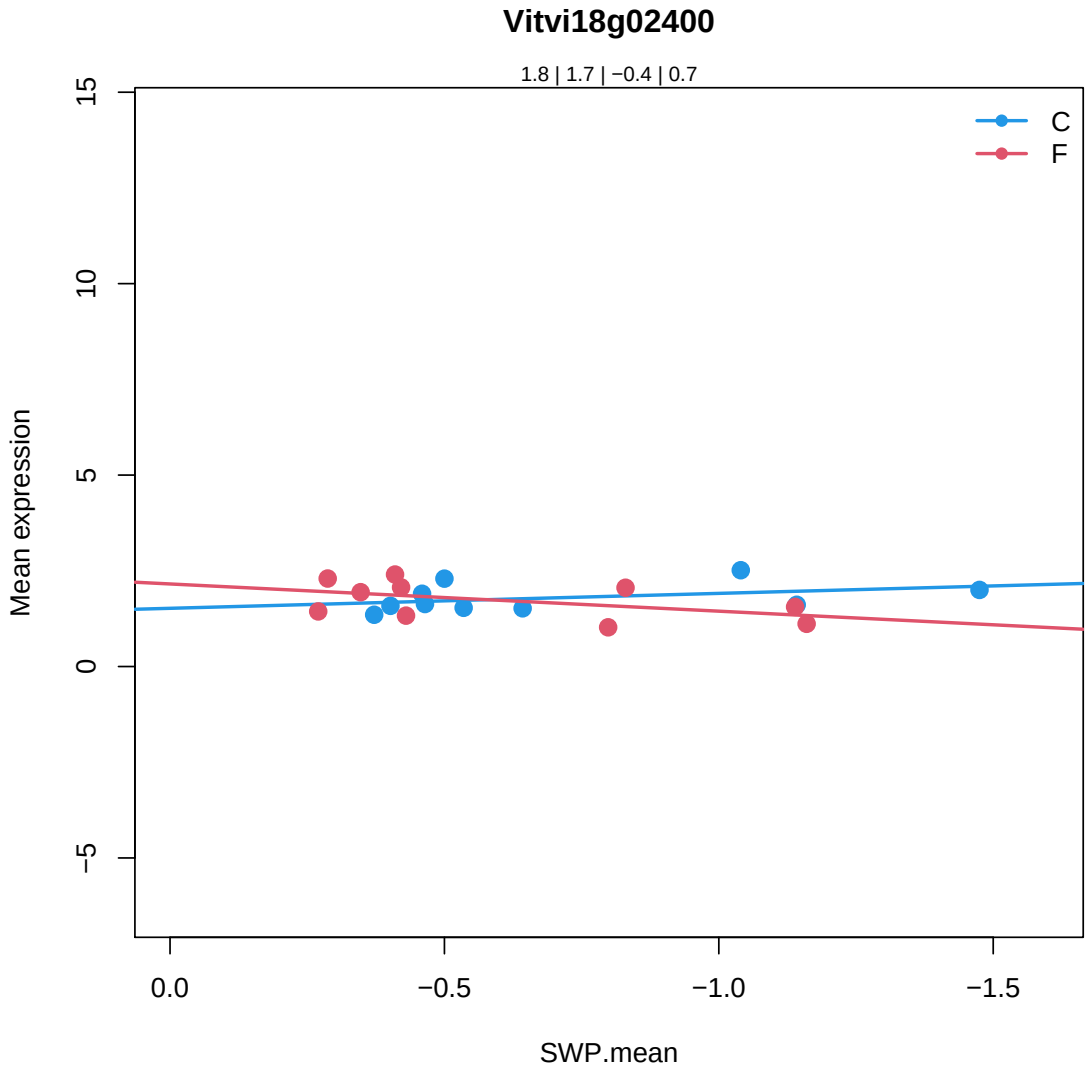
7.6.758 Vitvi18g02400: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02400
        27.3.63
        RNA.regulation of transcription.PHD finger transcription factor
        RING/FYVE/PHD zinc finger superfamily protein |
        Chr1:12121063-12122928 REVERSE LENGTH=592 |
        201606
```

Coefficients for Vitvi18g02400.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.794474	1.073575e-11	***	1.462196e-11	***
SlopeC	-0.3896152	0.3185091		0.7966107	
MeanF-MeanC	-0.07136267	0.7164854		0.9126186	
SlopeF-SlopeC	1.10078	0.06582129	.	0.9999488	



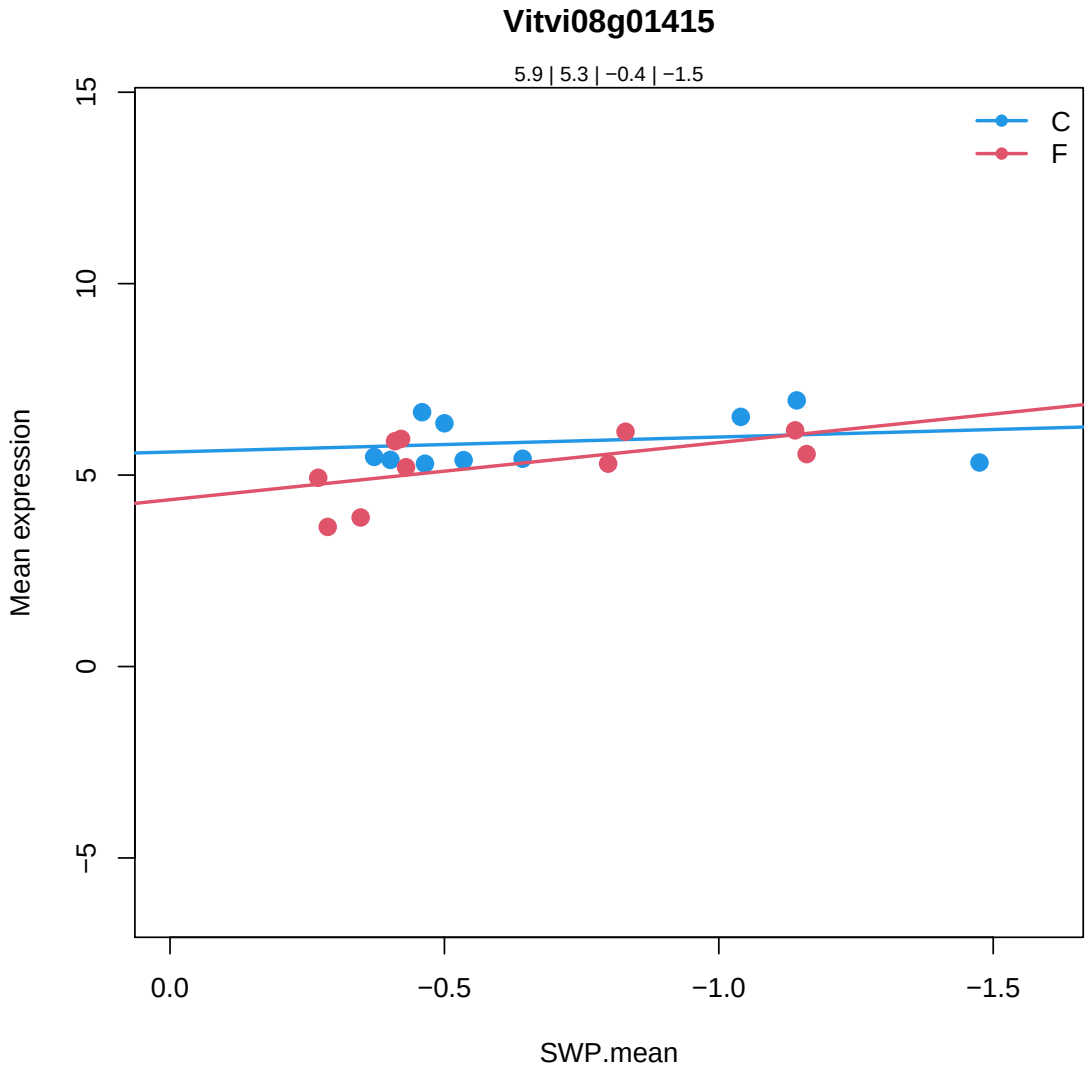
7.6.759 Vitvi08g01415: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01415
        35.2
        not assigned.unknown
        LETM1-like protein |
        Chr3:3639553-3645506 FORWARD LENGTH=872 |
        201606
```

Coefficients for Vitvi08g01415.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.87772	2.994549e-18	***	9.007878e-18	***
SlopeC	-0.3920705	0.5148425		0.8719143	
MeanF-MeanC	-0.612829	0.05423618	.	0.2524177	
SlopeF-SlopeC	-1.099874	0.2253859		0.9999488	



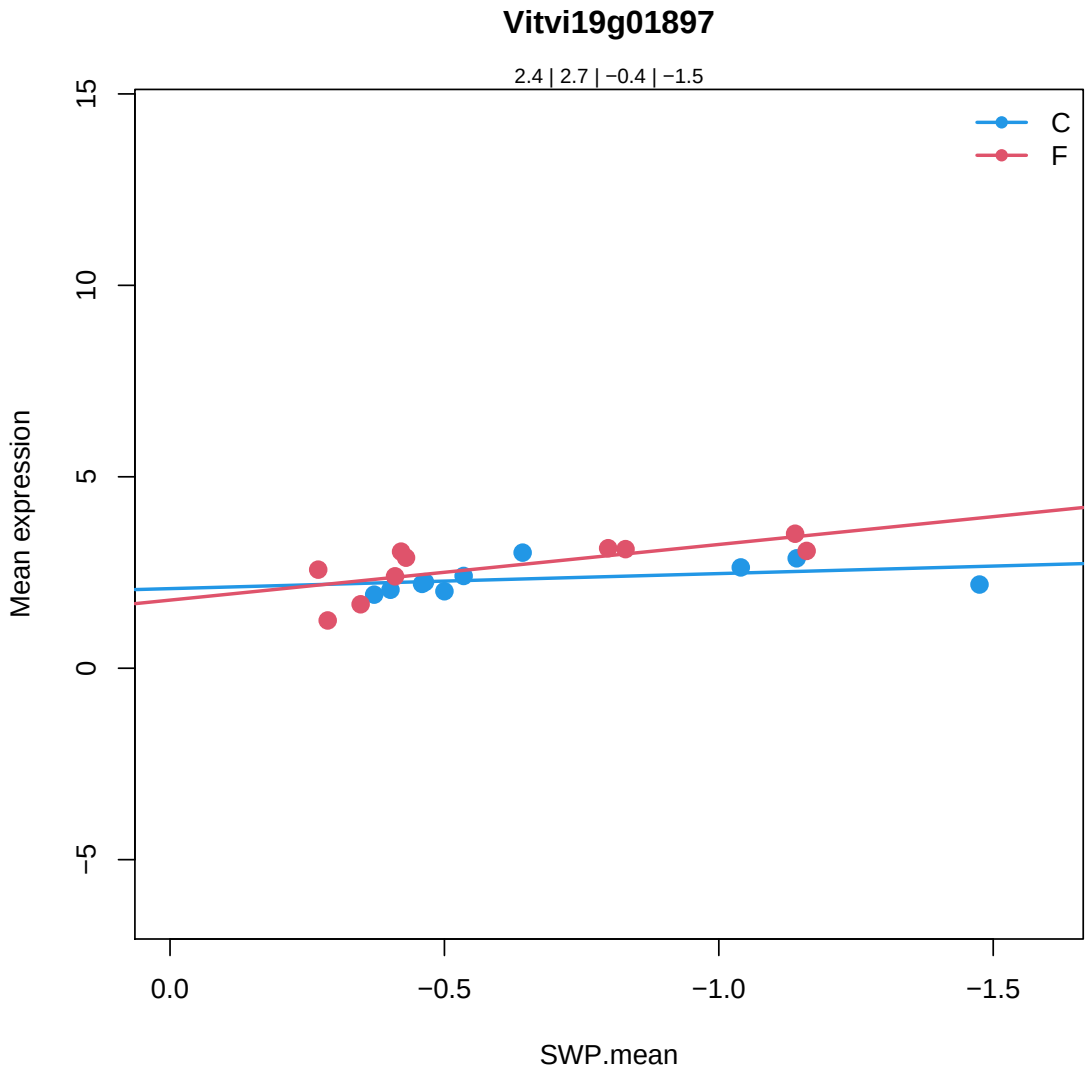
7.6.760 Vitvi19g01897: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g01897
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi19g01897.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.354961	2.282341e-13	***	3.421267e-13	***
SlopeC	-0.3926741	0.3500345		0.8124192	
MeanF-MeanC	0.3093912	0.1531899		0.4717012	
SlopeF-SlopeC	-1.060563	0.09733345	.	0.9999488	



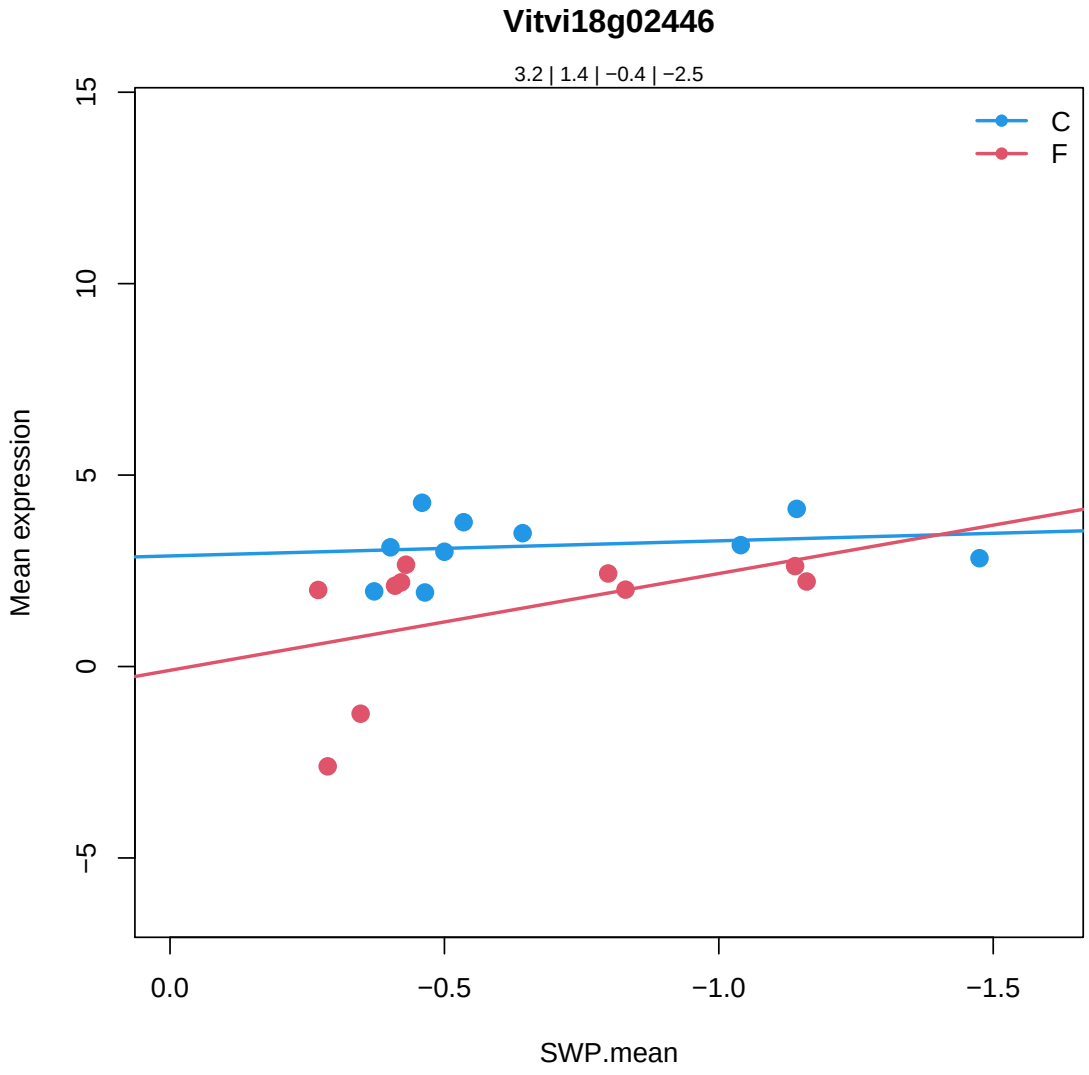
7.6.761 Vitvi18g02446: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02446
        16.1.5
        secondary metabolism.isoprenoids.terpenoids
        terpene synthase 21 |
        Chr5:8092969-8095128 FORWARD LENGTH=547 |
        201606
```

Coefficients for Vitvi18g02446.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.165086	2.576314e-08	***	3.106413e-08	***
SlopeC	-0.3940815	0.7071927		0.9346979	
MeanF-MeanC	-1.724404	0.003528654	**	0.03482595	*
SlopeF-SlopeC	-2.13365	0.1803668		0.9999488	



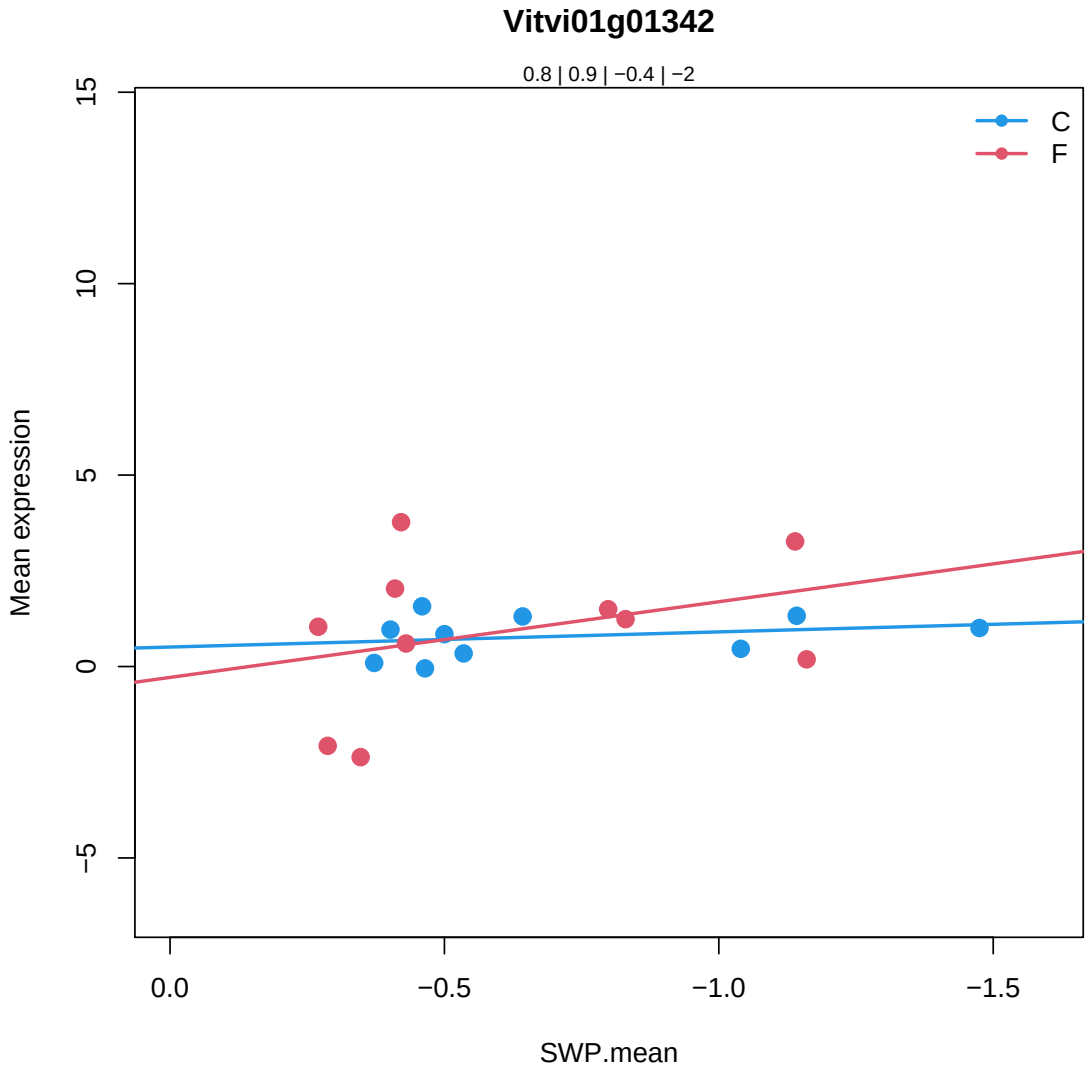
7.6.762 Vitvi01g01342: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01342
        27.3.35
        RNA.regulation of transcription.bZIP transcription factor family
        basic leucine-zipper 42 |
        Chr3:12139512-12140033 FORWARD LENGTH=173 |
        201606
```

Coefficients for Vitvi01g01342.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.7869473	0.06611055	.	0.06863681	.
SlopeC	−0.3958923	0.7296468		0.9406676	
MeanF−MeanC	0.1324959	0.8198622		0.9500031	
SlopeF−SlopeC	−1.580688	0.3580392		0.9999488	



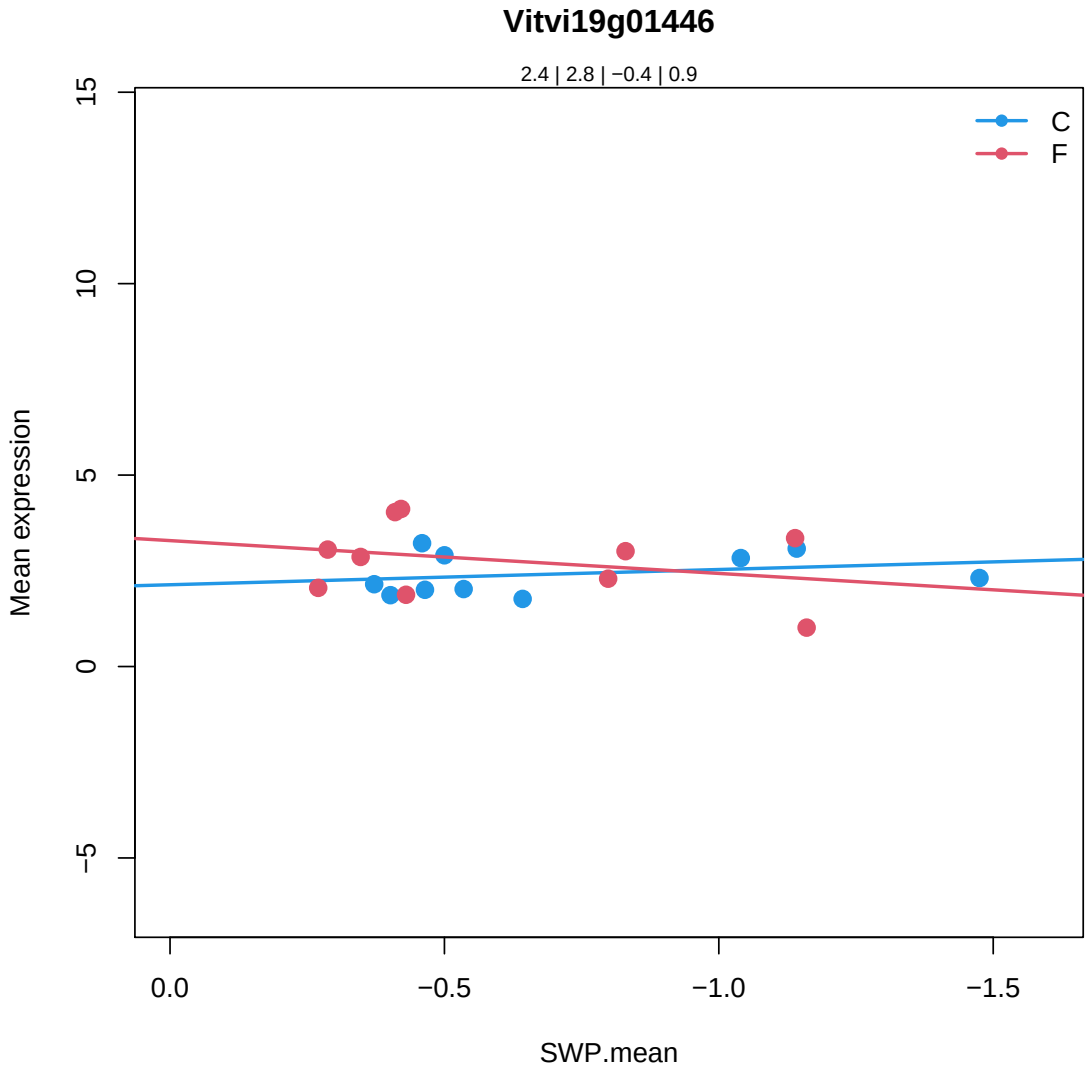
7.6.763 Vitvi19g01446: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g01446
        30.2.11
        signalling.receptor kinases.leucine rich repeat XI
        Leucine-rich receptor-like protein kinase family protein |
        Chr1:5891375-5894855 FORWARD LENGTH=1133 |
        201606
```

Coefficients for Vitvi19g01446.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.415384	7.18783e-10	***	9.106975e-10	***
SlopeC	-0.3980262	0.5426751		0.8847006	
MeanF-MeanC	0.3511641	0.2948802		0.6610628	
SlopeF-SlopeC	1.254886	0.203915		0.9999488	



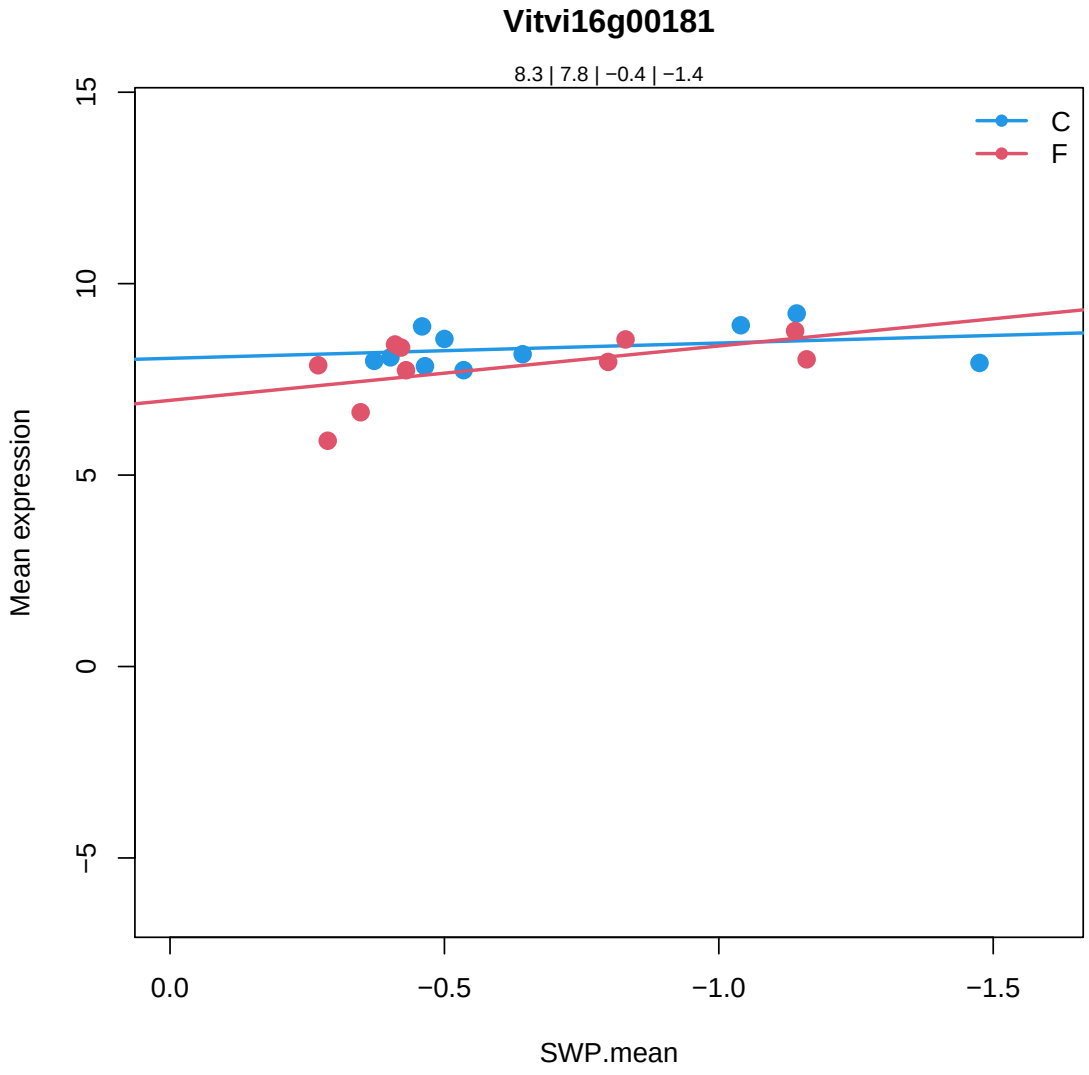
7.6.764 Vitvi16g00181: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g00181
        29.8
        protein.assembly and cofactor ligation
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi16g00181.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	8.329548	5.343418e-22	***	6.99694e-21	***
SlopeC	-0.398273	0.4821549		0.8645993	
MeanF-MeanC	-0.5125688	0.08418229	.	0.3286646	
SlopeF-SlopeC	-1.022629	0.2305747		0.9999488	



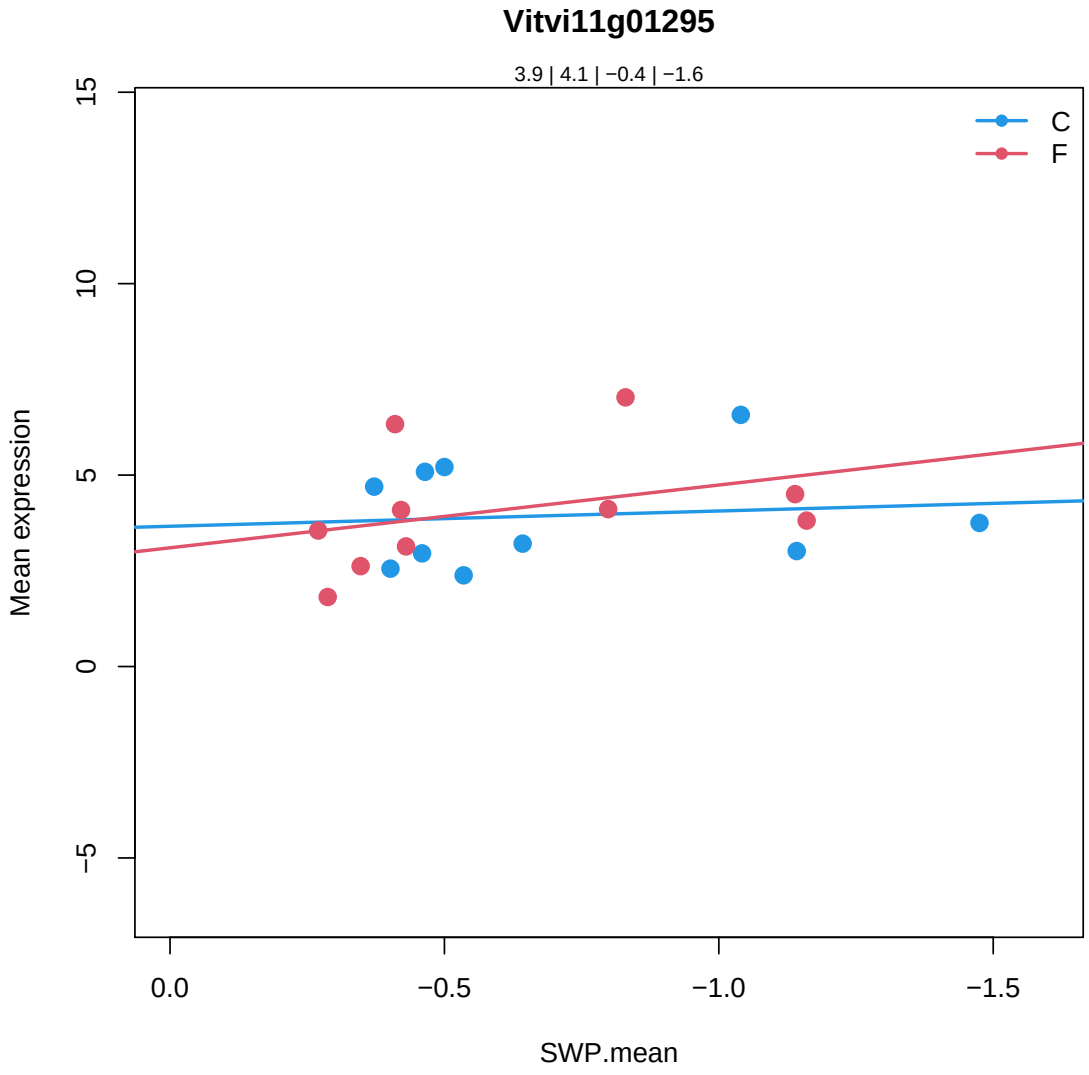
7.6.765 Vitvi11g01295: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g01295
        35.2
        not assigned.unknown
        CAP (Cysteine-rich secretory proteins%2C Antigen 5%2C and Pathogenesis
        Chr4:13121107-13121679 FORWARD LENGTH=190 |
        201606
```

Coefficients for Vitvi11g01295.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.94327	4.79709e-09	***	5.917549e-09	***
SlopeC	-0.3986597	0.7363878		0.9430092	
MeanF-MeanC	0.1563818	0.7949209		0.9422338	
SlopeF-SlopeC	-1.240831	0.4834123		0.9999488	



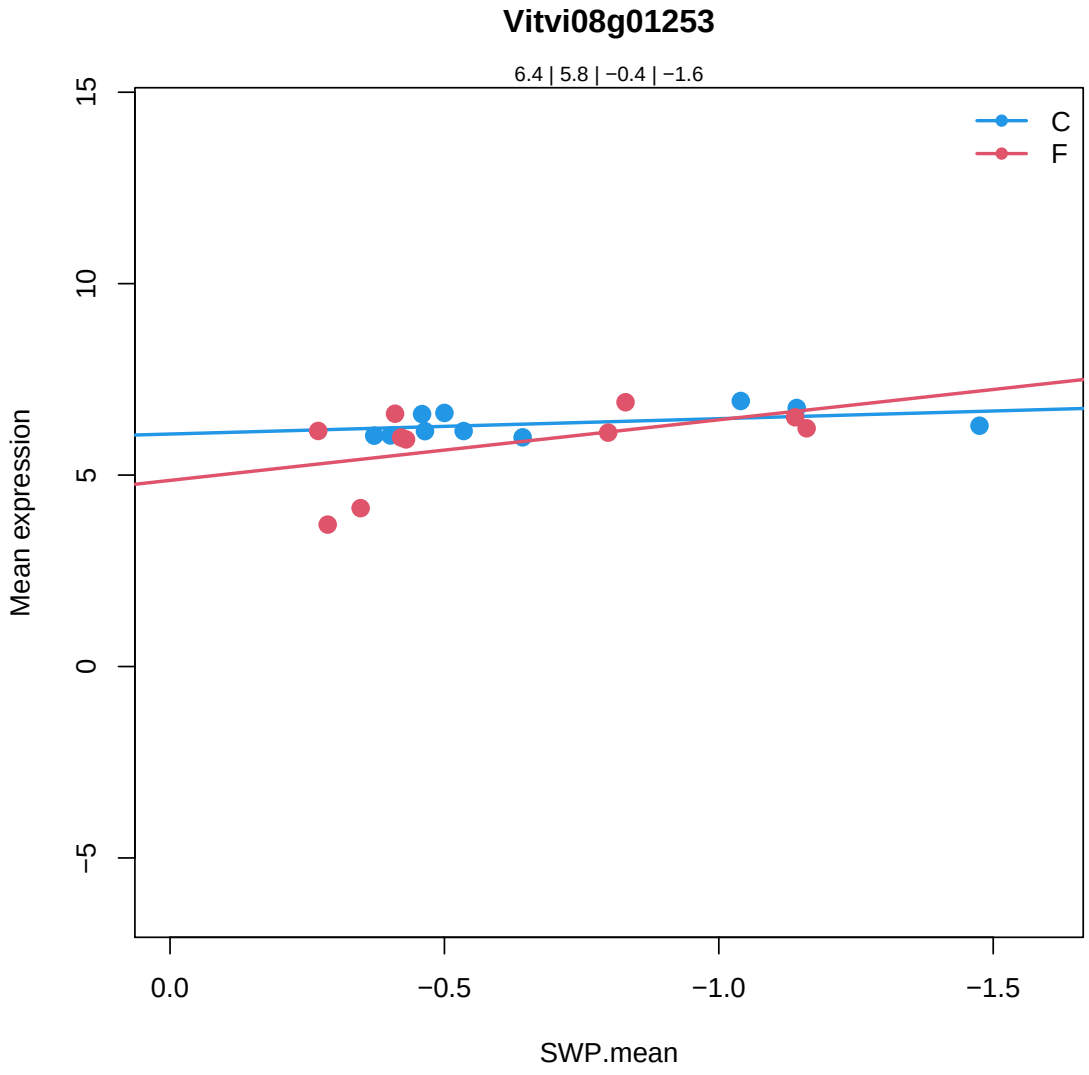
7.6.766 Vitvi08g01253: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01253
        26.8
        misc.nitrilases, nitrile lyases, berberine bridge enzymes, reticuline
        NAD(P)-binding Rossmann-fold superfamily protein |
        Chr5:1824066-1825833 REVERSE LENGTH=264 |
        201606
```

Coefficients for Vitvi08g01253.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.353777	4.425932e-19	***	1.70569e-18	***
SlopeC	-0.4008308	0.4998964		0.8698903	
MeanF-MeanC	-0.5284544	0.08926361	.	0.3414416	
SlopeF-SlopeC	-1.181912	0.1880869		0.9999488	



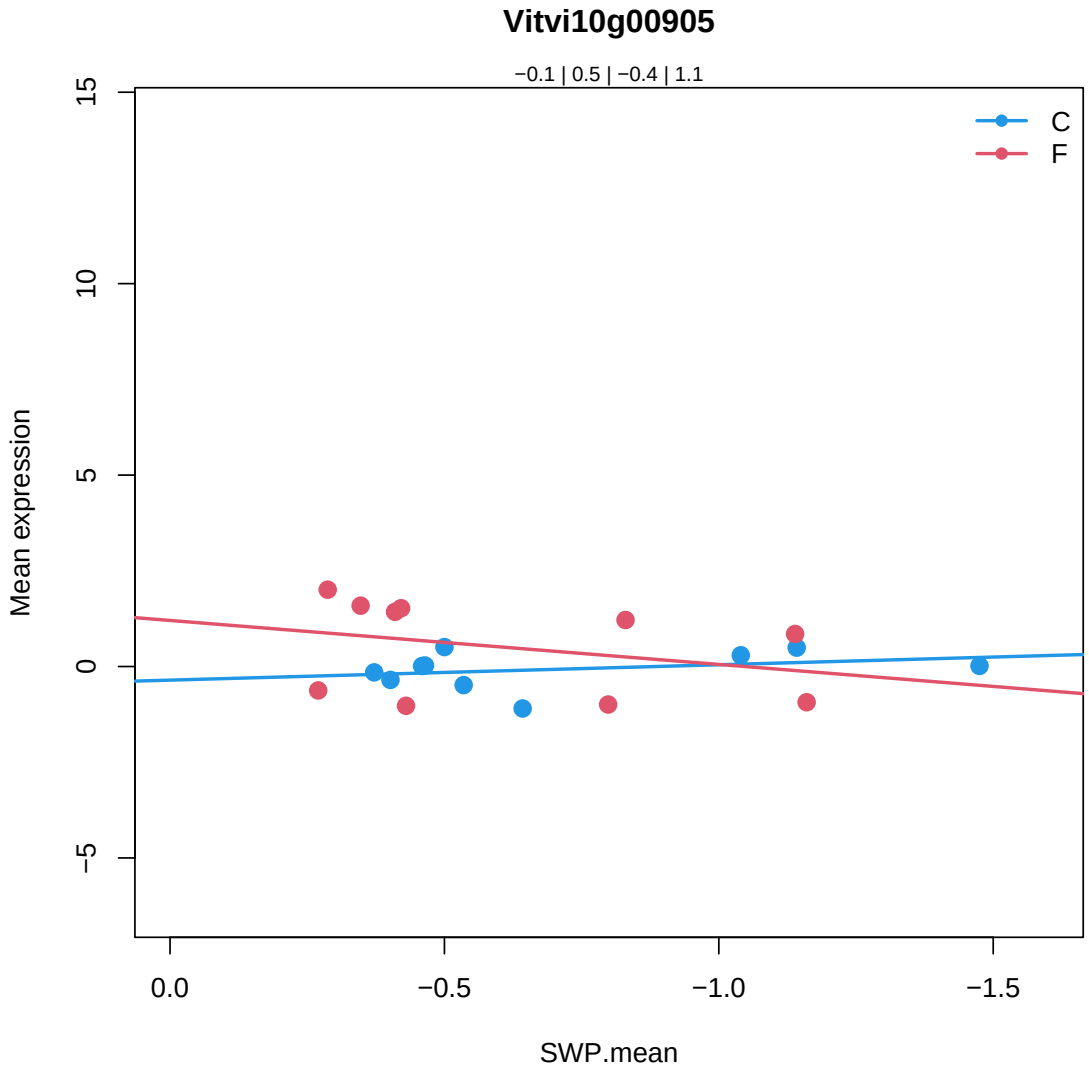
7.6.767 Vitvi10g00905: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00905
        17.2.3
        hormone metabolism.auxin.induced-regulated-responsive-activated
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi10g00905.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.0734336	0.7886056		0.7927142	
SlopeC	-0.4015895	0.5990574		0.903916	
MeanF-MeanC	0.5767829	0.1461779		0.4604349	
SlopeF-SlopeC	1.549894	0.180648		0.9999488	



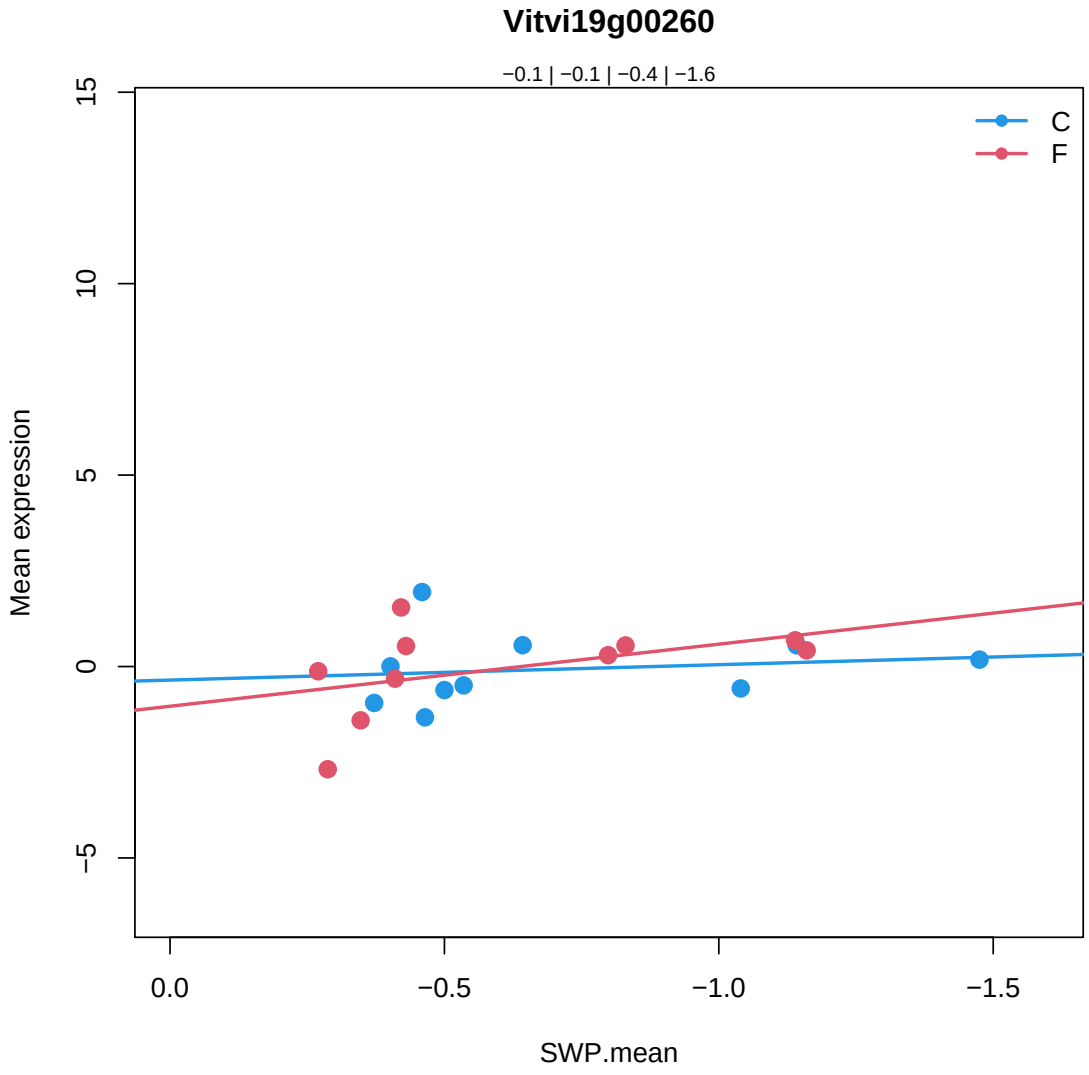
7.6.768 Vitvi19g00260: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g00260
        35.2
        not assigned.unknown
        Integrase-type DNA-binding superfamily protein |
        Chr4:13974905-13975783 REVERSE LENGTH=292 |
        201606
```

Coefficients for Vitvi19g00260.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.0718246	0.8129218		0.8166186	
SlopeC	-0.4020035	0.6346857		0.9123743	
MeanF-MeanC	0.02176697	0.9595274		0.9914232	
SlopeF-SlopeC	-1.21944	0.3368782		0.9999488	



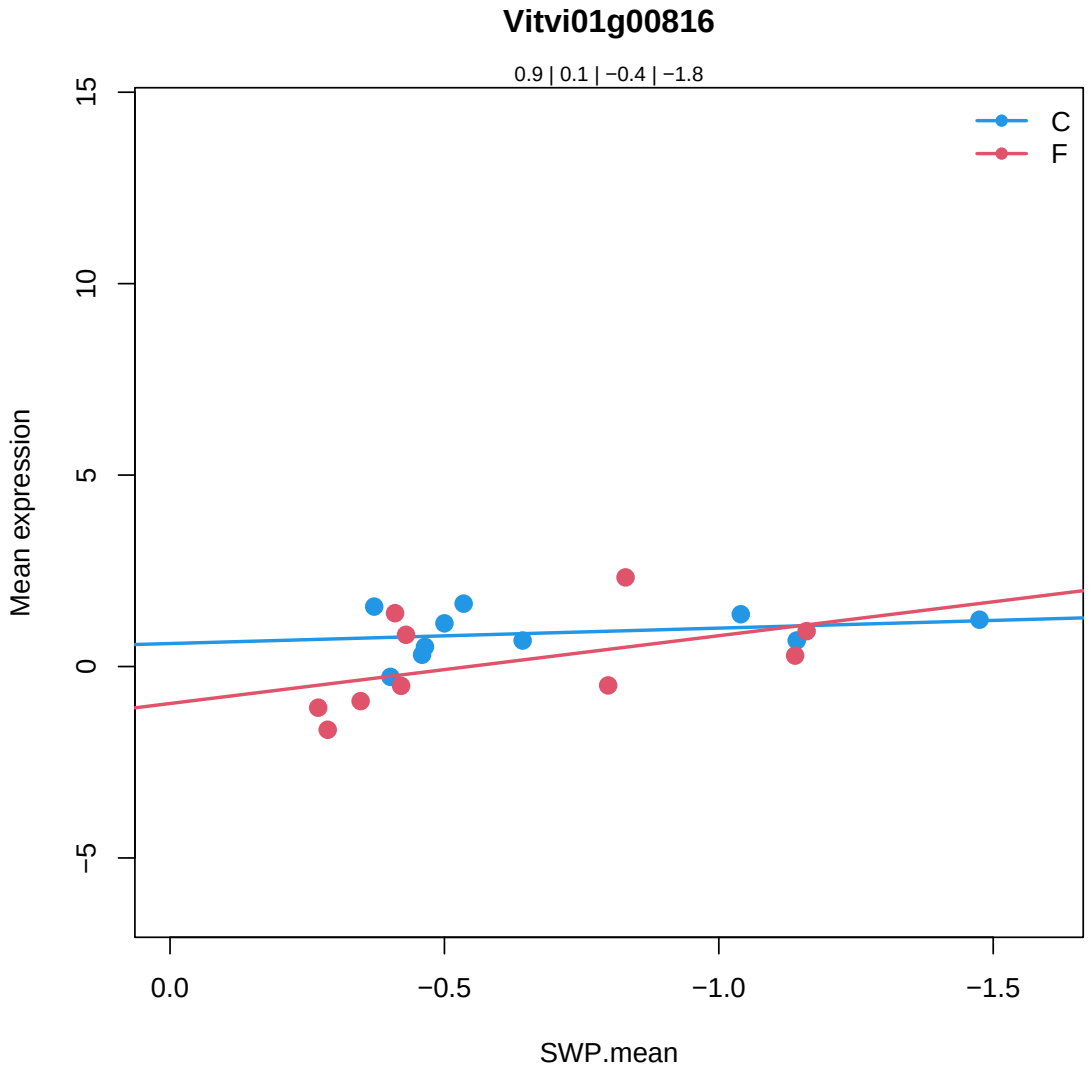
7.6.769 Vitvi01g00816: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00816
        20.1
        stress.biotic
        MLP-like protein 423 |
        Chr1:8500653-8501458 REVERSE LENGTH=155 |
        201606
```

Coefficients for Vitvi01g00816.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8832799	0.003160742	**	0.003385288	**
SlopeC	-0.402681	0.591619		0.9005224	
MeanF-MeanC	-0.7706377	0.05273513	.	0.2477483	
SlopeF-SlopeC	-1.368099	0.2272006		0.9999488	



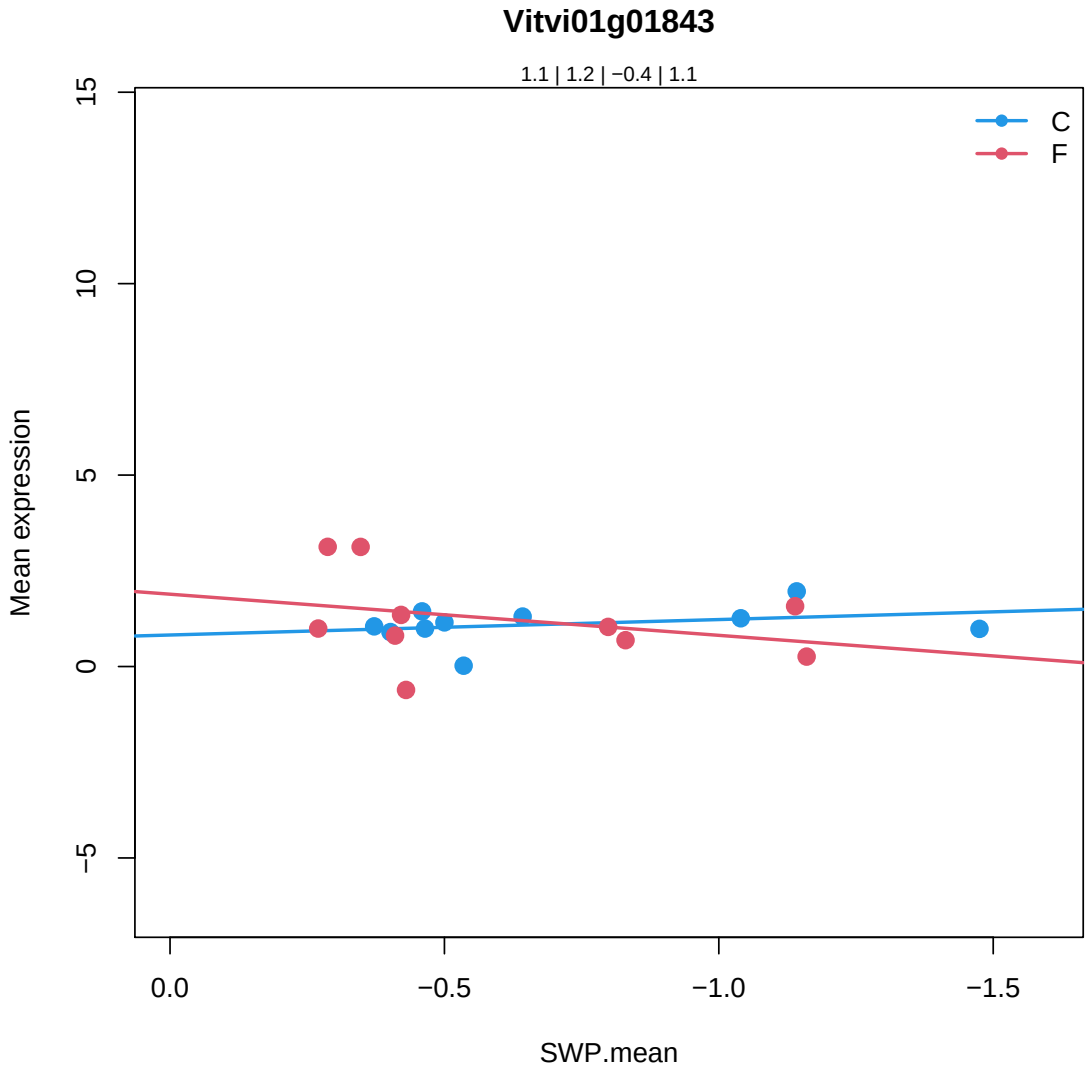
7.6.770 Vitvi01g01843: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01843
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr1:2514374-2516599 REVERSE LENGTH=741 |
        201606
```

Coefficients for Vitvi01g01843.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.106384	0.0003104367	***	0.0003393342	***
SlopeC	−0.403246	0.5797533		0.8944184	
MeanF−MeanC	0.1276476	0.7296378		0.9183434	
SlopeF−SlopeC	1.47762	0.180499		0.9999488	



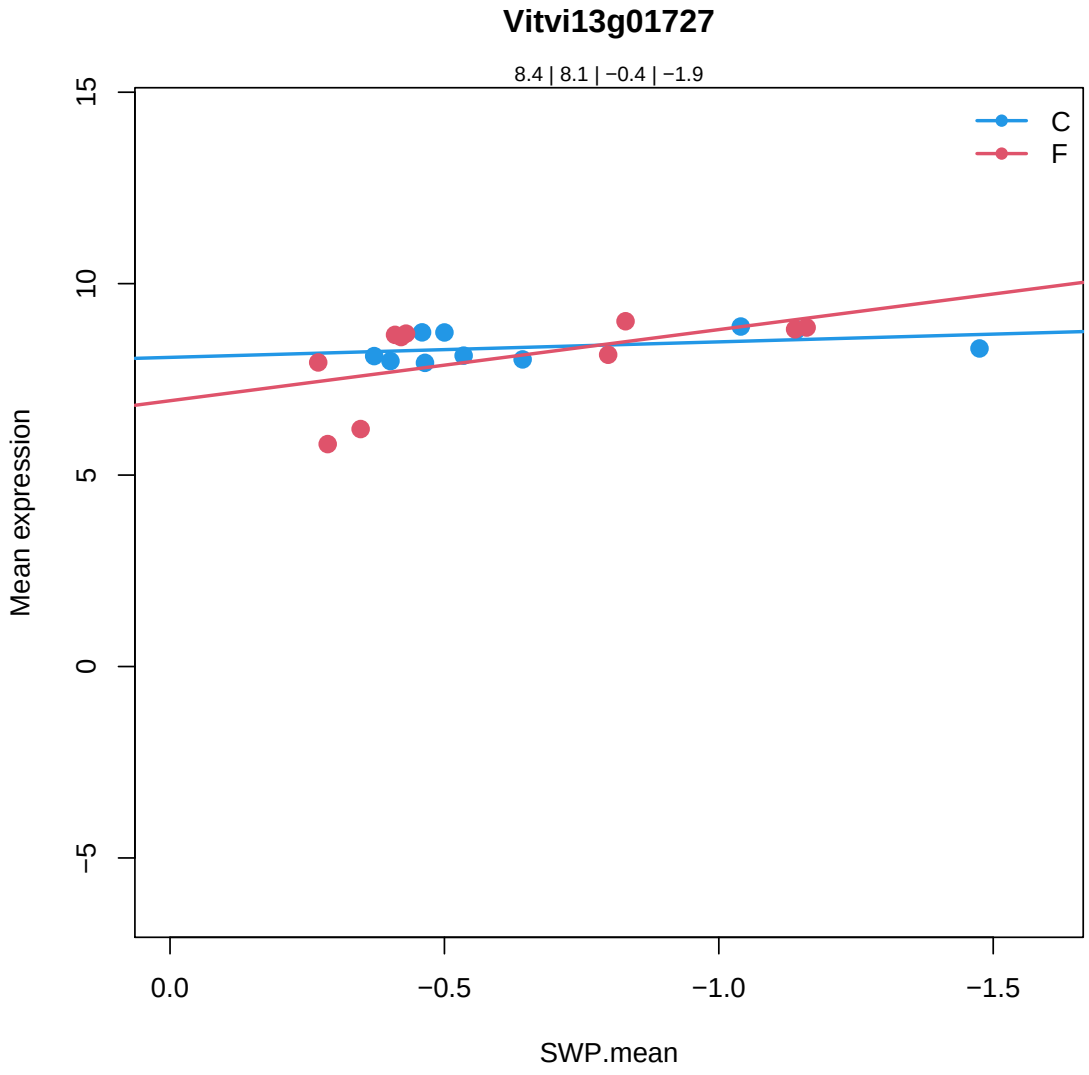
7.6.771 Vitvi13g01727: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g01727
        17.1.1.1.10
        hormone metabolism.abscisic acid.synthesis-degradation.synthesis.9-cis
        carotenoid cleavage dioxygenase 1 |
        Chr3:23452940-23455896 FORWARD LENGTH=538 |
        201606
```

Coefficients for Vitvi13g01727.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	8.358828	3.856292e-21	***	3.307687e-20	***
SlopeC	-0.4044752	0.5166974		0.8725275	
MeanF-MeanC	-0.2850994	0.3707404		0.7250225	
SlopeF-SlopeC	-1.453568	0.1260231		0.9999488	



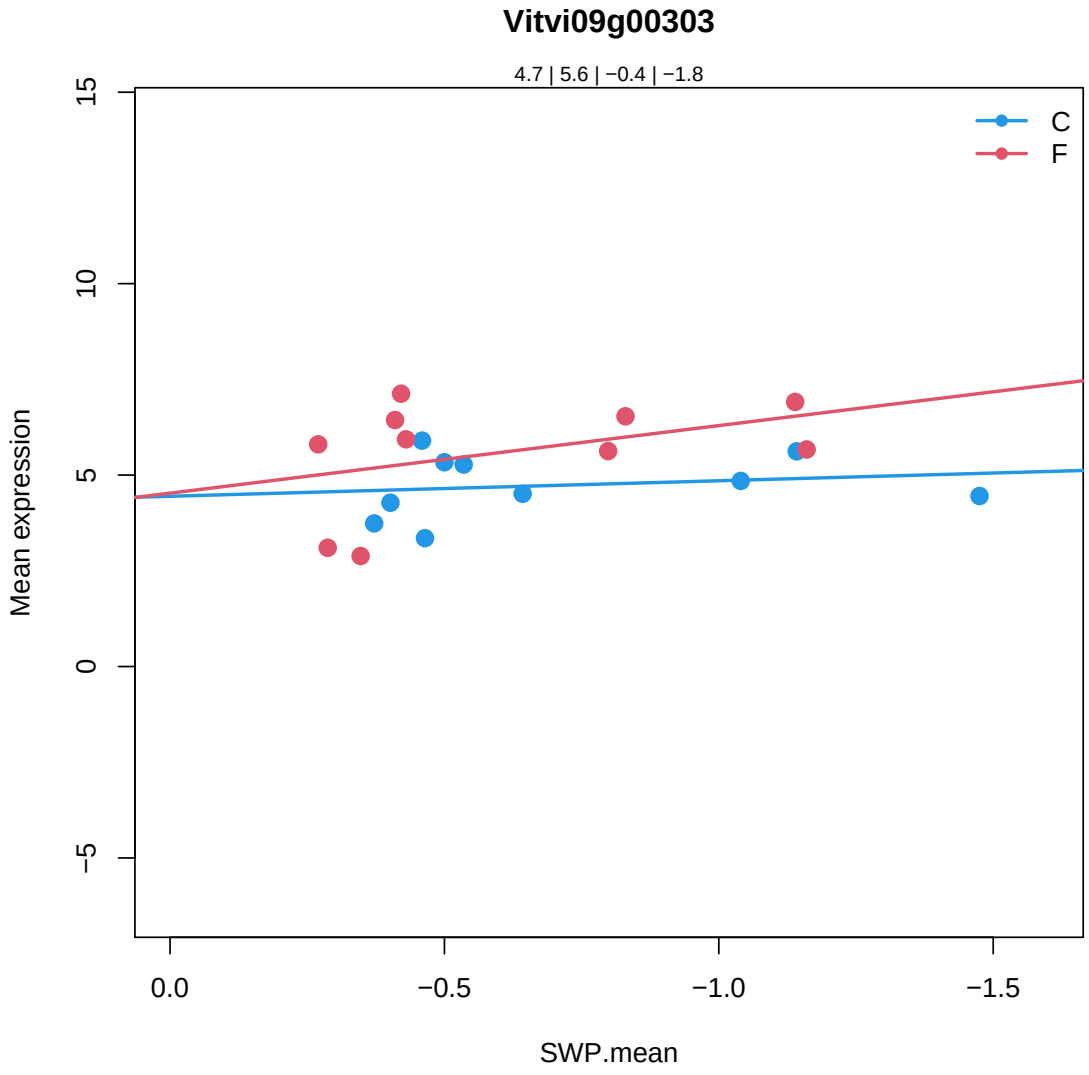
7.6.772 Vitvi09g00303: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00303
        34.16
        transport.ABC transporters and multidrug resistance systems
        pleiotropic drug resistance 1 |
        Chr3:5539897-5546263 FORWARD LENGTH=1411 |
        201606
```

Coefficients for Vitvi09g00303.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.73112	1.740727e-12	***	2.463068e-12	***
SlopeC	-0.4047651	0.6628311		0.9225525	
MeanF-MeanC	0.8715695	0.07479004	.	0.3078422	
SlopeF-SlopeC	-1.360039	0.3293618		0.9999488	



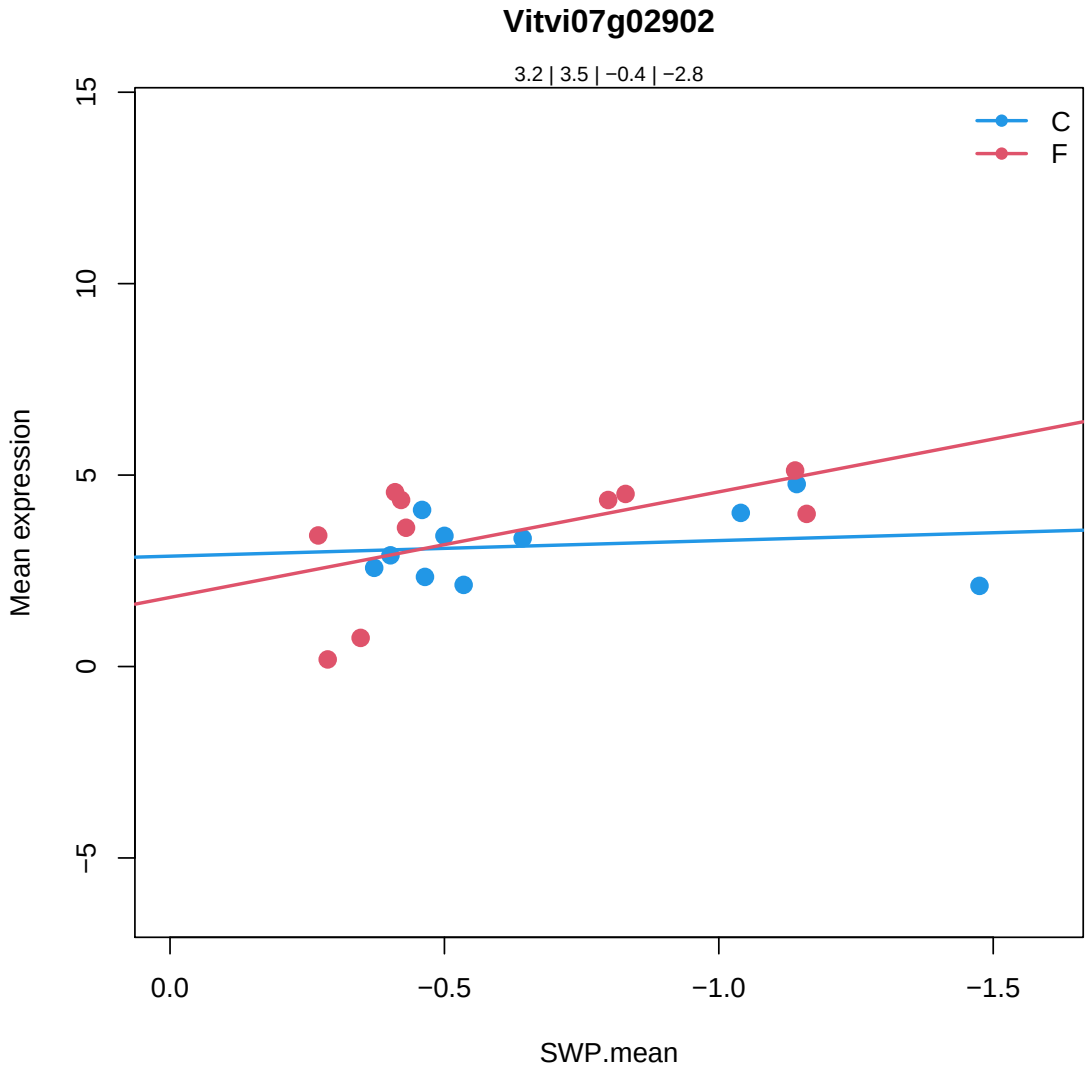
7.6.773 Vitvi07g02902: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g02902
        35.2
        not assigned.unknown
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi07g02902.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.168757	6.998453e-09	***	8.586527e-09	***
SlopeC	-0.4080718	0.6750206		0.9250732	
MeanF-MeanC	0.3157186	0.5245143		0.8203845	
SlopeF-SlopeC	-2.349575	0.1146809		0.9999488	



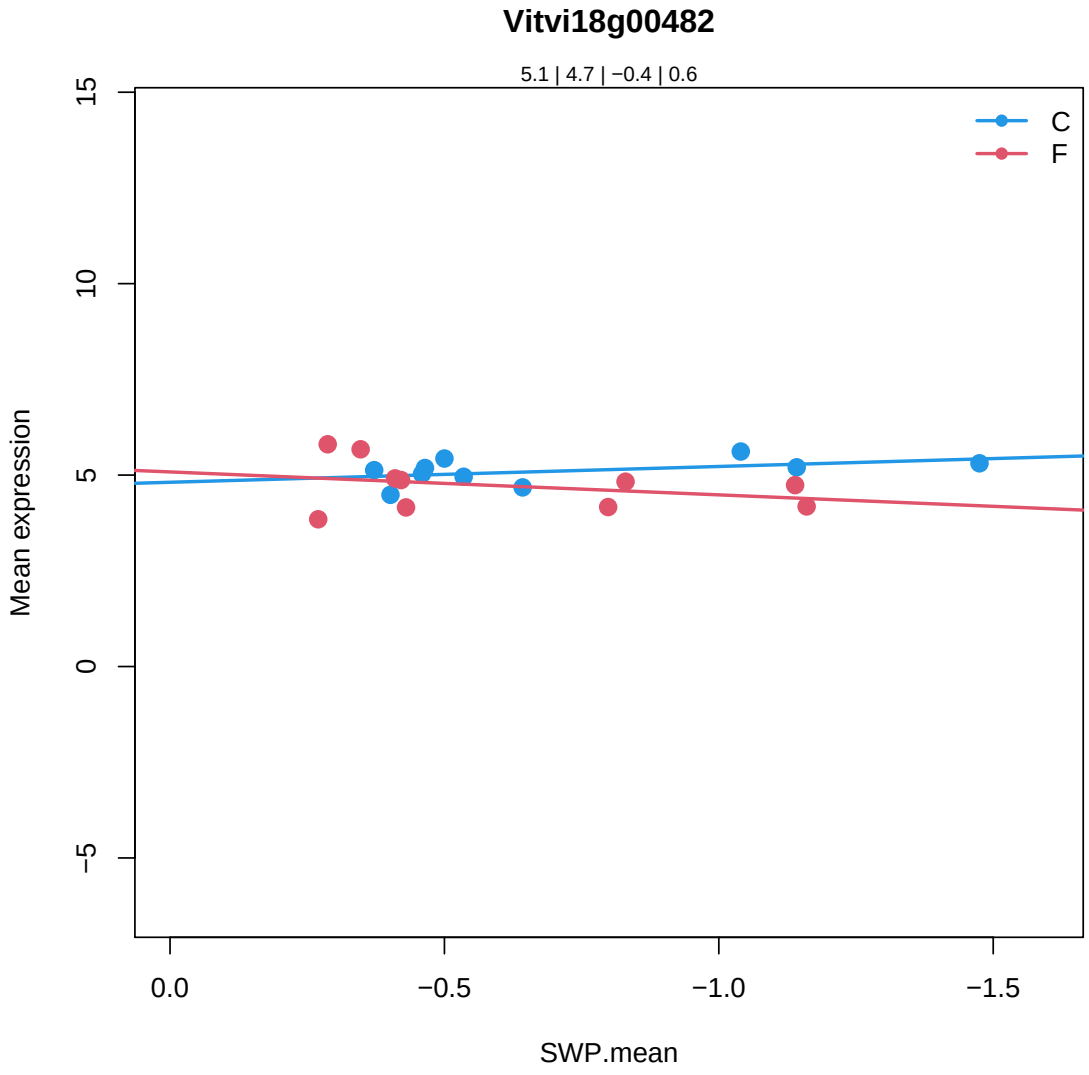
7.6.774 Vitvi18g00482: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00482
        35.2
        not assigned.unknown
        purine permease 3 |
        Chr1:9860303-9861434 REVERSE LENGTH=351 |
        201606
```

Coefficients for Vitvi18g00482.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.102113	1.710749e-19	***	7.501505e-19	***
SlopeC	-0.4126646	0.3674931		0.8212976	
MeanF-MeanC	-0.3848627	0.105695		0.3776377	
SlopeF-SlopeC	1.011391	0.1441334		0.9999488	



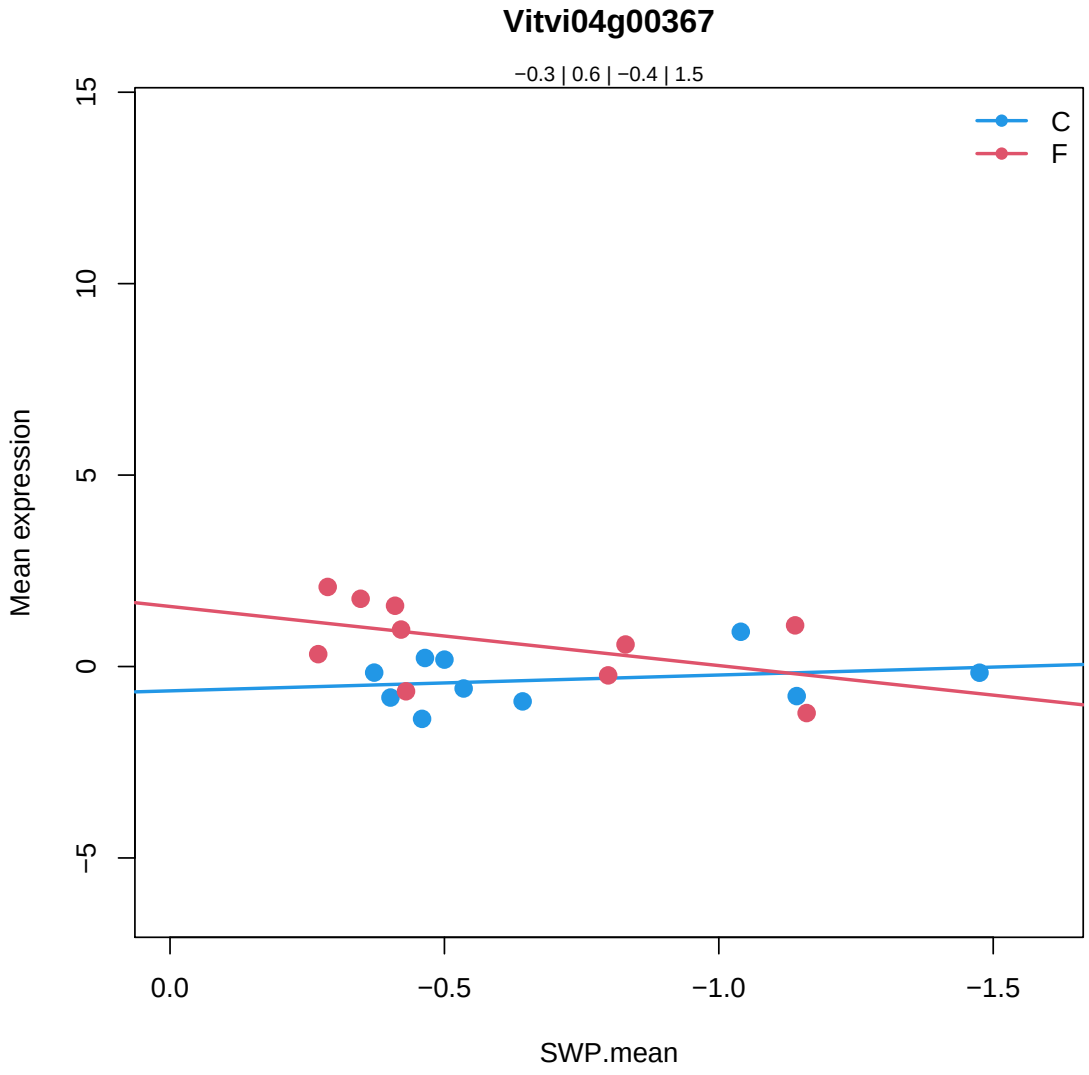
7.6.775 Vitvi04g00367: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00367
        13.1.6.2
        amino acid metabolism.synthesis.aromatic aa.phenylalanine and tyrosine
        Pyridoxal phosphate (PLP)-dependent transferases superfamily protein |
        Chr1:30208736-30210643 REVERSE LENGTH=394 |
        201606
```

Coefficients for Vitvi04g00367.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.3447749	0.1773875		0.1821559	
SlopeC	-0.4139839	0.5535275		0.8877183	
MeanF-MeanC	0.9726928	0.01102633	*	0.08160258	.
SlopeF-SlopeC	1.957949	0.06922995	.	0.9999488	



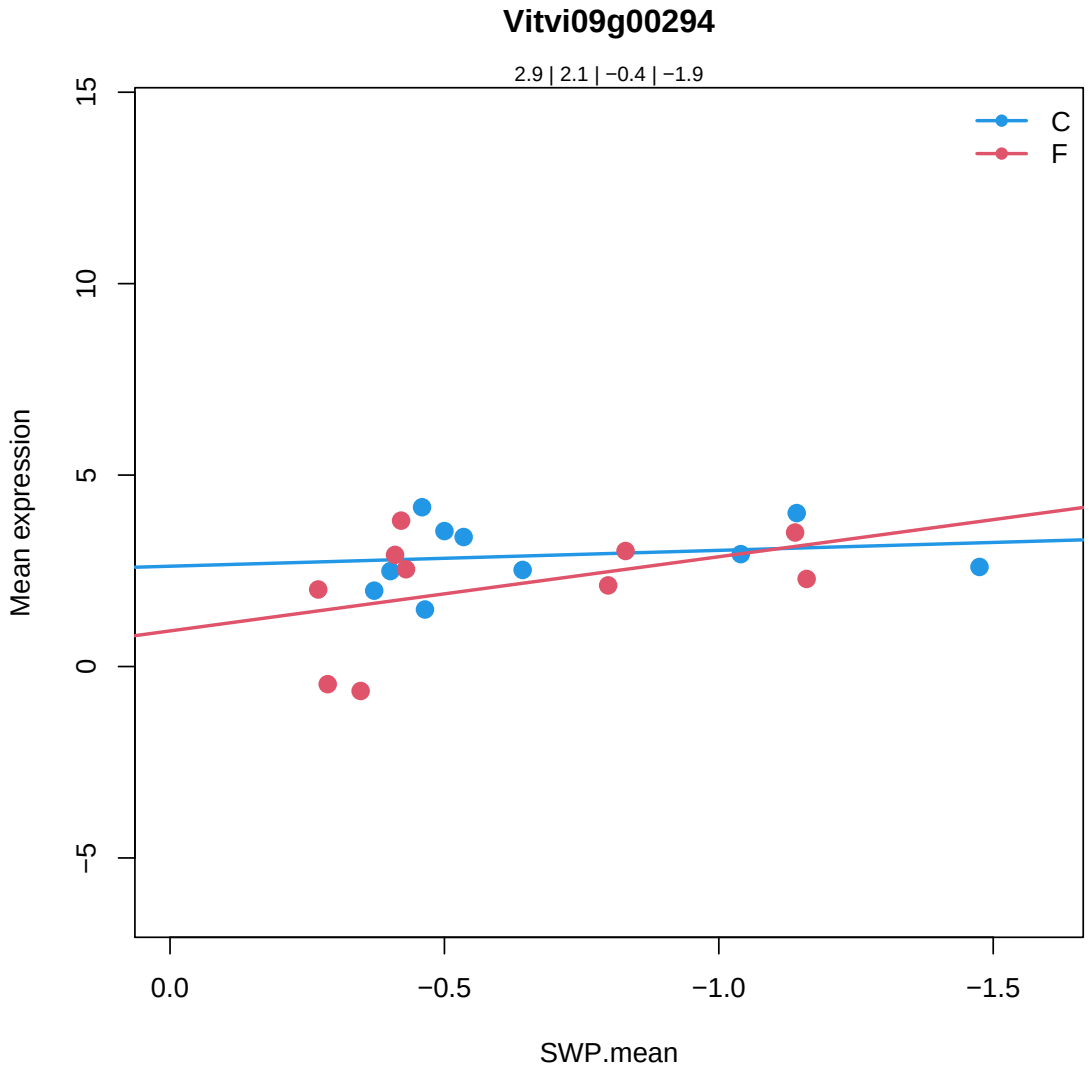
7.6.776 Vitvi09g00294: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00294
        34.16
        transport.ABC transporters and multidrug resistance systems
        pleiotropic drug resistance 1 |
        Chr3:5539897-5546263 FORWARD LENGTH=1411 |
        201606
```

Coefficients for Vitvi09g00294.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.91062	2.07796e-08	***	2.511878e-08	***
SlopeC	-0.4141778	0.6638648		0.9233166	
MeanF-MeanC	-0.8006285	0.1083032		0.3833652	
SlopeF-SlopeC	-1.523474	0.288222		0.9999488	



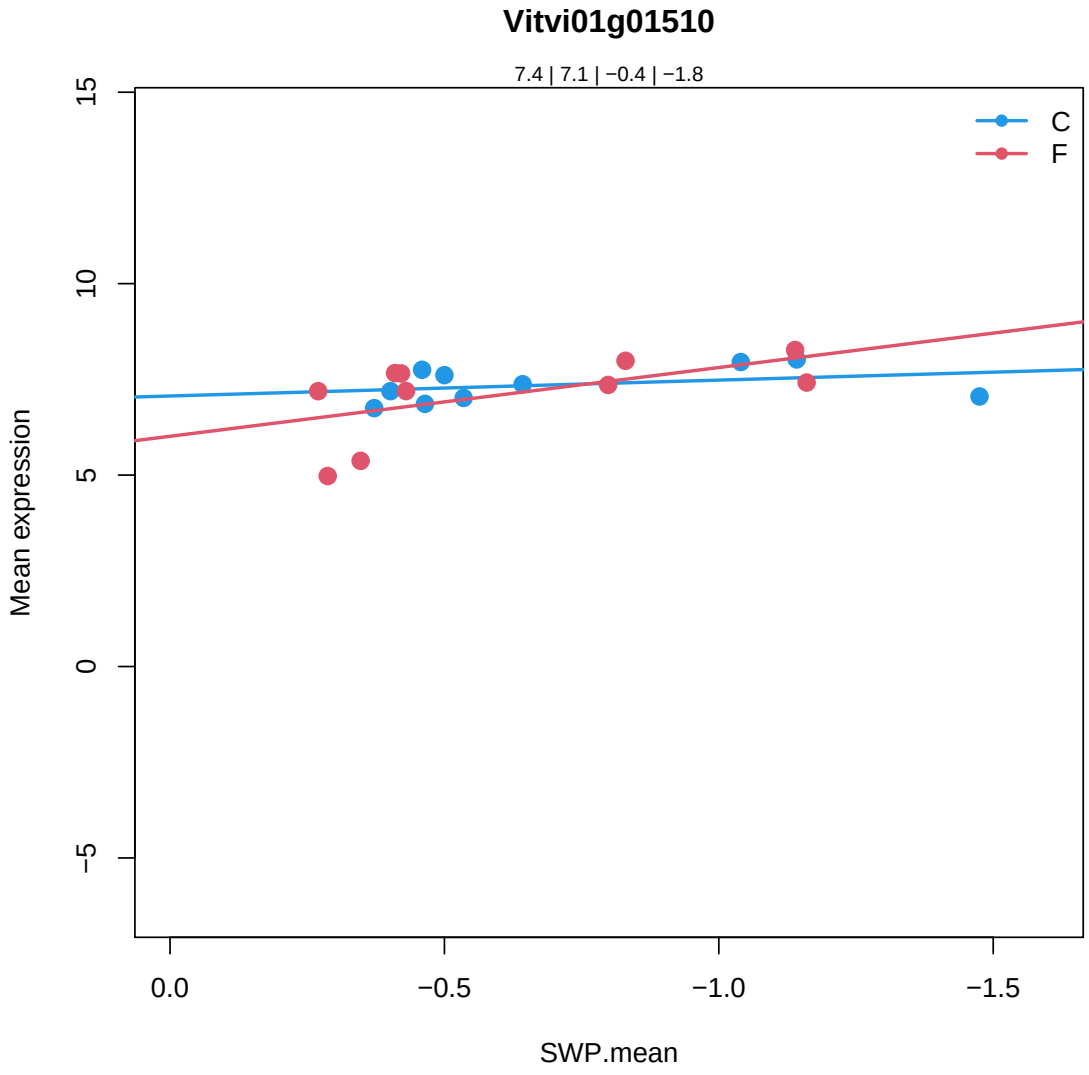
7.6.777 Vitvi01g01510: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01510
        29.5
        protein.degradation
        multidrug resistance protein |
        Chr1:25374295-25375810 FORWARD LENGTH=231 |
        201606
```

Coefficients for Vitvi01g01510.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.357213	3.602601e-20	***	2.01171e-19	***
SlopeC	-0.4149721	0.4967713		0.8692215	
MeanF-MeanC	-0.2498636	0.421846		0.7592482	
SlopeF-SlopeC	-1.380808	0.1368378		0.9999488	



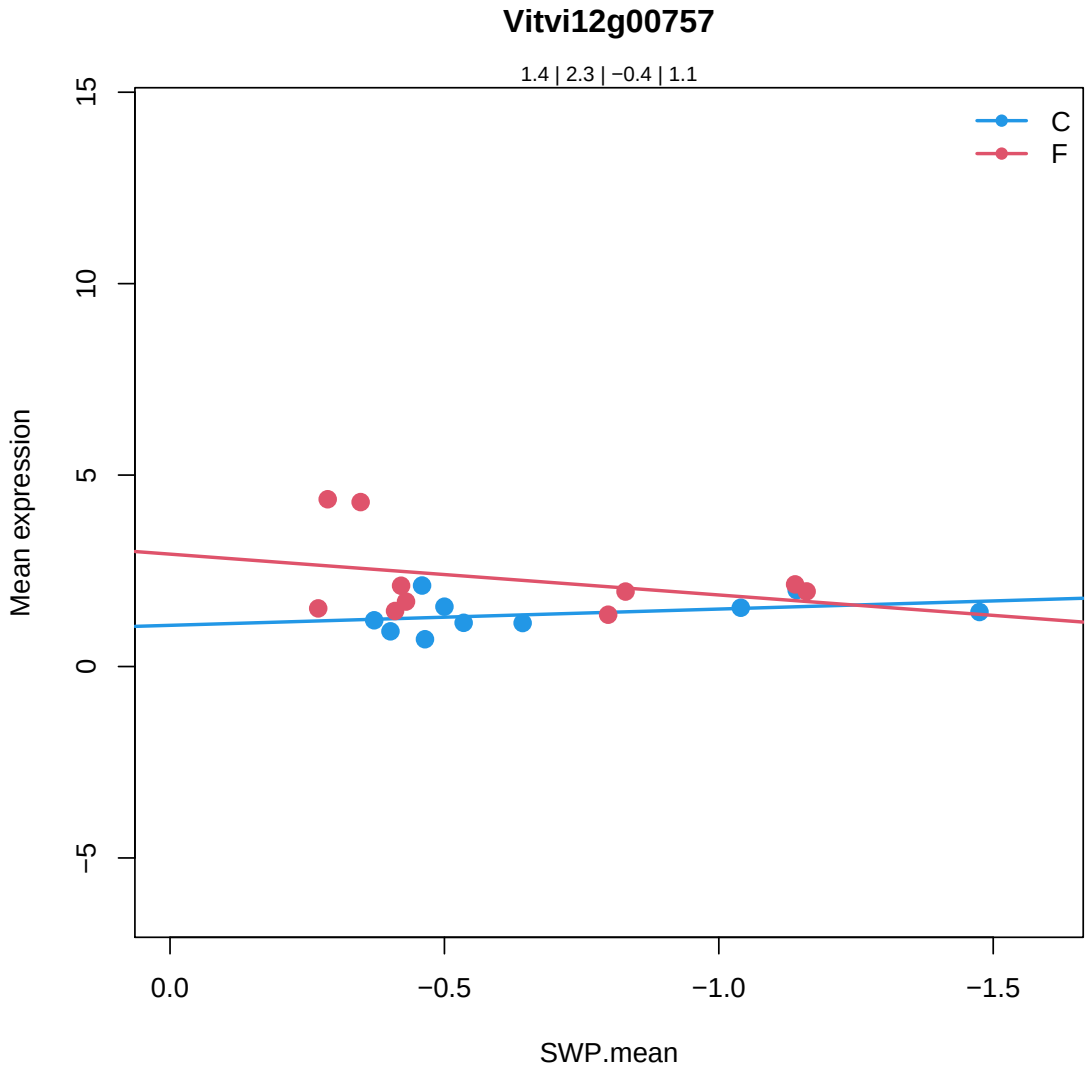
7.6.778 Vitvi12g00757: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00757
        27.3.7
        RNA.regulation of transcription.C2C2(Zn) Constans-like zinc finger fam
        CONSTANS-like 9 |
        Chr3:2442494-2443901 FORWARD LENGTH=372 |
        201606
```

Coefficients for Vitvi12g00757.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.374449	1.281335e-05	***	1.44304e-05	***
SlopeC	-0.4248558	0.5383483		0.882594	
MeanF-MeanC	0.910983	0.01522229	*	0.1029208	
SlopeF-SlopeC	1.490932	0.1549024		0.9999488	



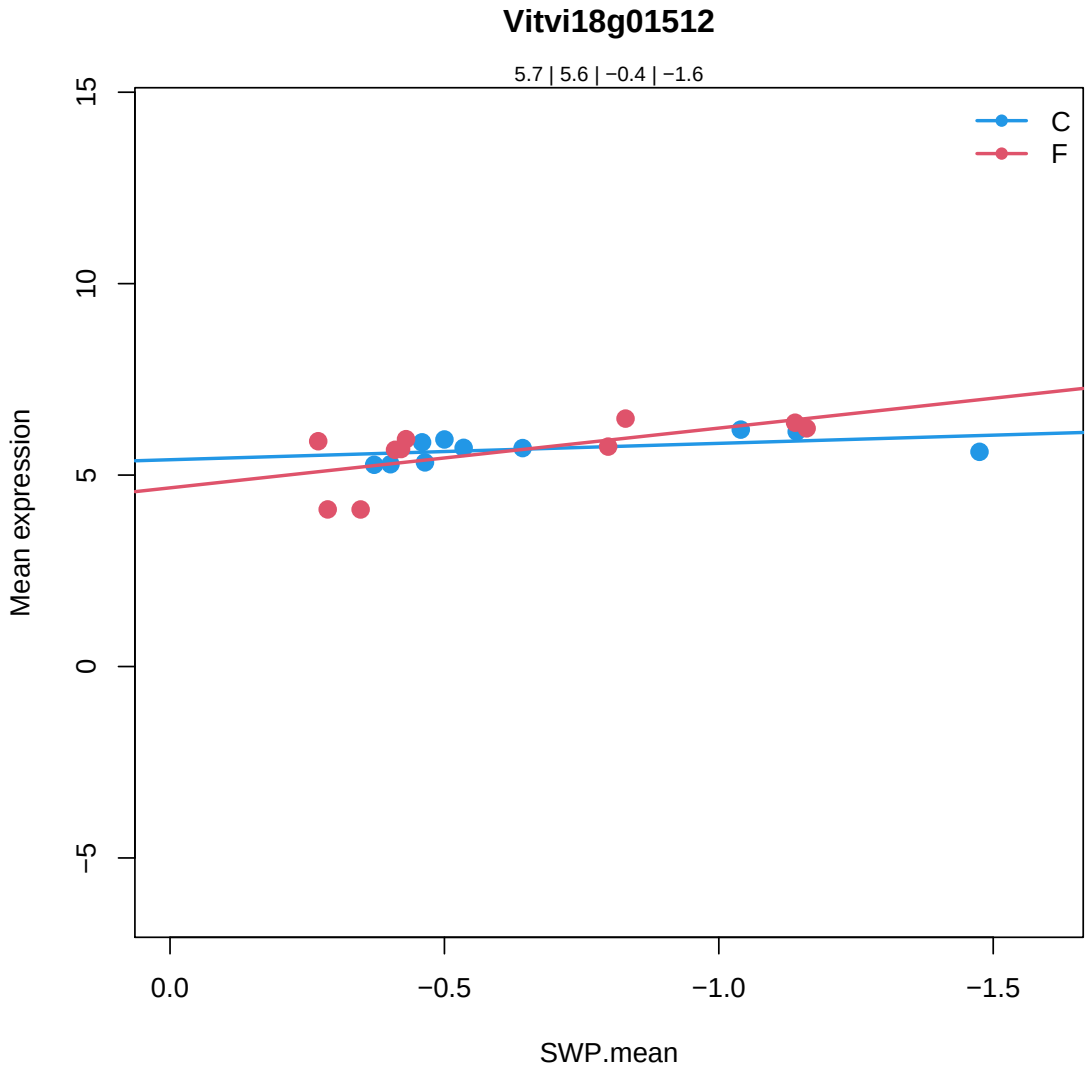
7.6.779 Vitvi18g01512: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g01512
        35.2
        not assigned.unknown
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi18g01512.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.701484	3.255015e-20	***	1.851229e-19	***
SlopeC	-0.4282137	0.3652531		0.8198525	
MeanF-MeanC	-0.08411948	0.7242301		0.9159239	
SlopeF-SlopeC	-1.132673	0.1147767		0.9999488	



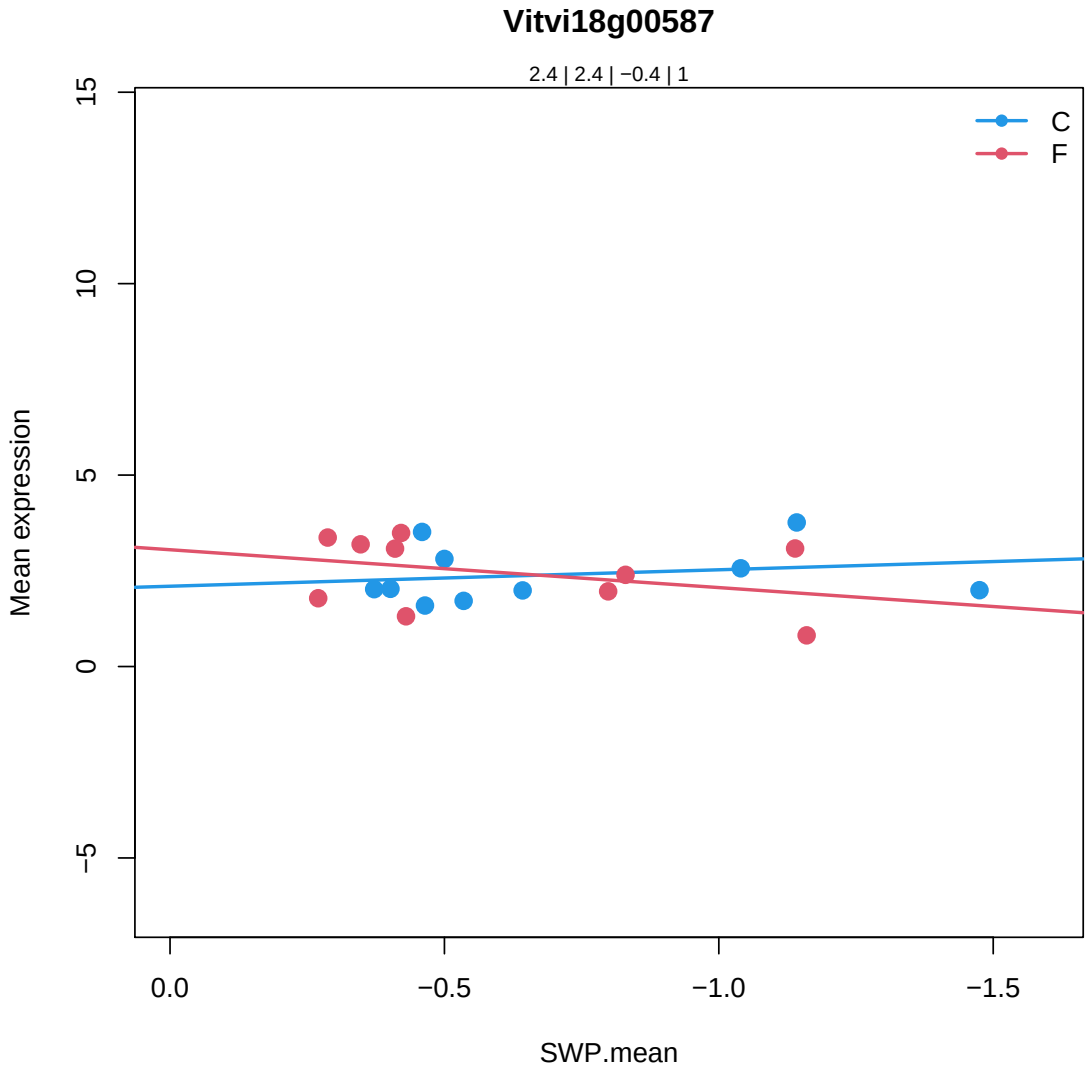
7.6.780 Vitvi18g00587: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00587
        35.2
        not assigned.unknown
        Leucine-rich receptor-like protein kinase family protein |
        Chr1:3252408-3255428 FORWARD LENGTH=977 |
        201606
```

Coefficients for Vitvi18g00587.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.399042	2.469059e-09	***	3.074121e-09	***
SlopeC	-0.4295363	0.5370874		0.8821075	
MeanF-MeanC	0.04855713	0.8903532		0.9712828	
SlopeF-SlopeC	1.418035	0.1783762		0.9999488	



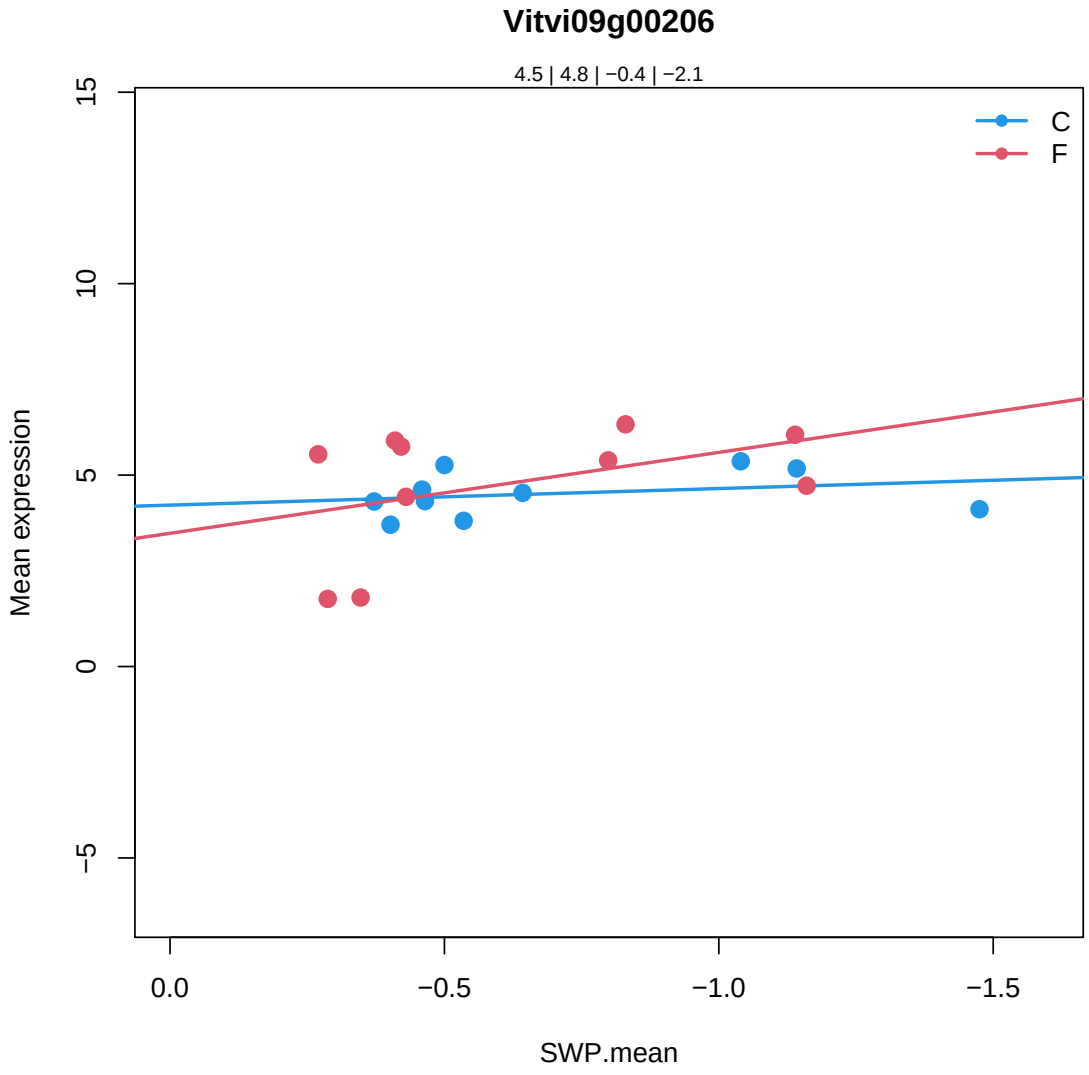
7.6.781 Vitvi09g00206: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00206
        34.16
        transport.ABC transporters and multidrug resistance systems
        multidrug resistance-associated protein 6 |
        Chr3:7457668-7463389 REVERSE LENGTH=1459 |
        201606
```

Coefficients for Vitvi09g00206.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.519678	7.539569e-12	***	1.035765e-11	***
SlopeC	-0.4326739	0.6510914		0.9192081	
MeanF-MeanC	0.2473882	0.6111958		0.8643119	
SlopeF-SlopeC	-1.680872	0.2443088		0.9999488	



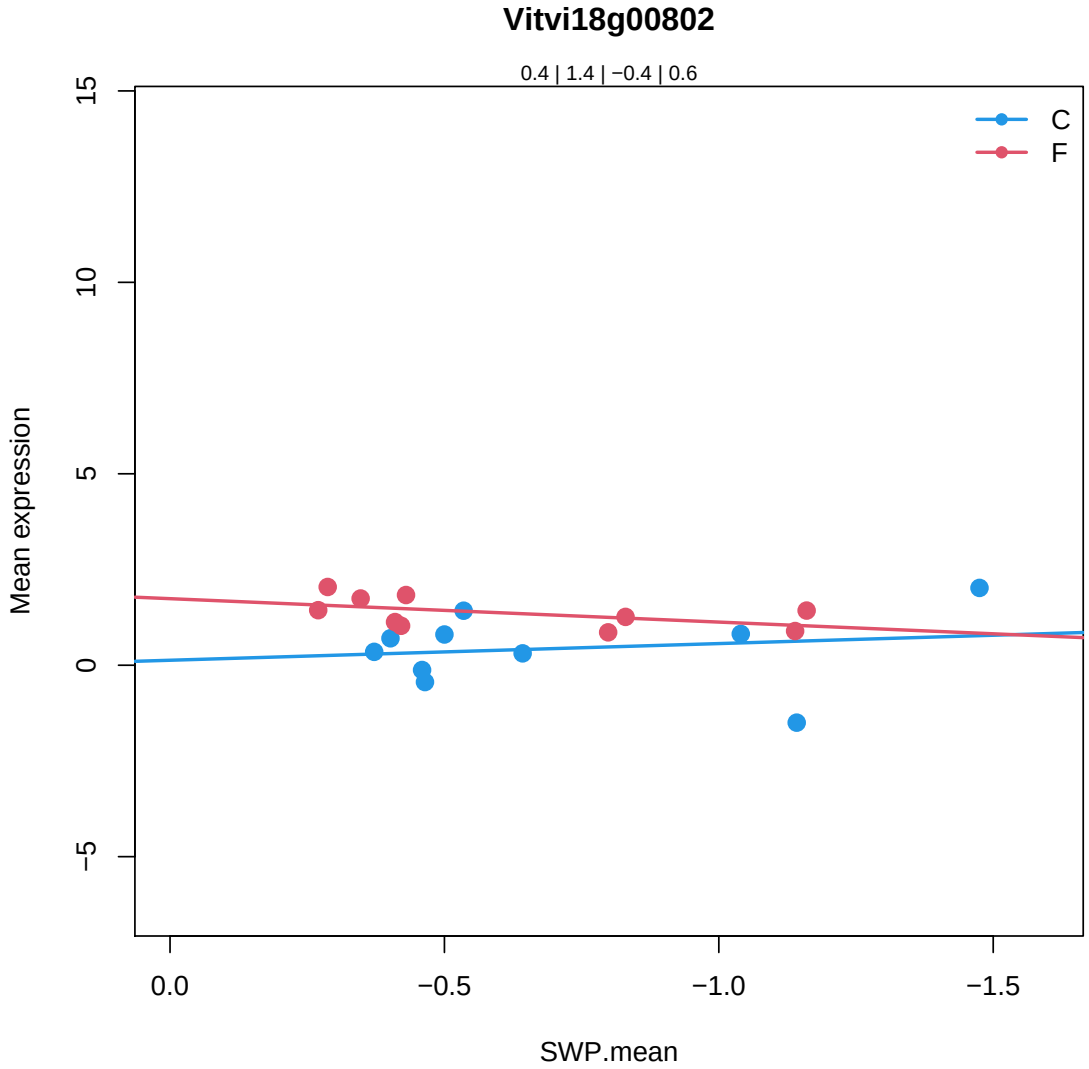
7.6.782 Vitvi18g00802: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00802
        35.2
        not assigned.unknown
        Os07g0619200 protein (Fragment) IPR018248 EF hand
```

Coefficients for Vitvi18g00802.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4360284	0.06578239	.	0.06830076	.
SlopeC	−0.4351891	0.4941609		0.8687743	
MeanF−MeanC	0.9294735	0.008022088	**	0.06457655	.
SlopeF−SlopeC	1.046354	0.2735783		0.9999488	



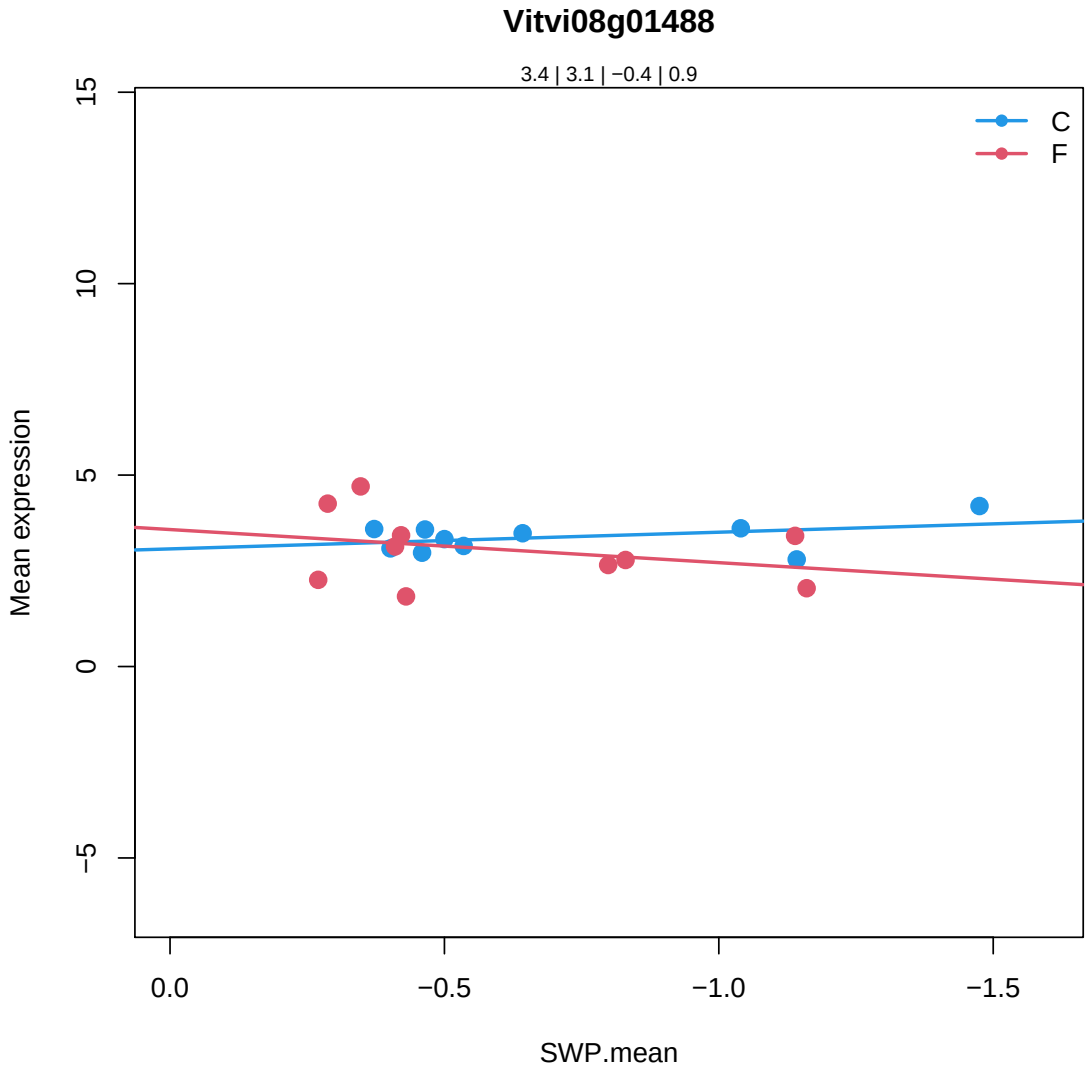
7.6.783 Vitvi08g01488: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01488
        26.28
        misc.GDSL-motif lipase
        GDSL-like Lipase/Acylhydrolase superfamily protein |
        Chr5:915650-918326 FORWARD LENGTH=359 |
        201606
```

Coefficients for Vitvi08g01488.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.378333	2.059845e-13	***	3.09587e-13	***
SlopeC	-0.4355855	0.4657956		0.8617488	
MeanF-MeanC	-0.3277071	0.2839346		0.6491854	
SlopeF-SlopeC	1.300763	0.1508167		0.9999488	



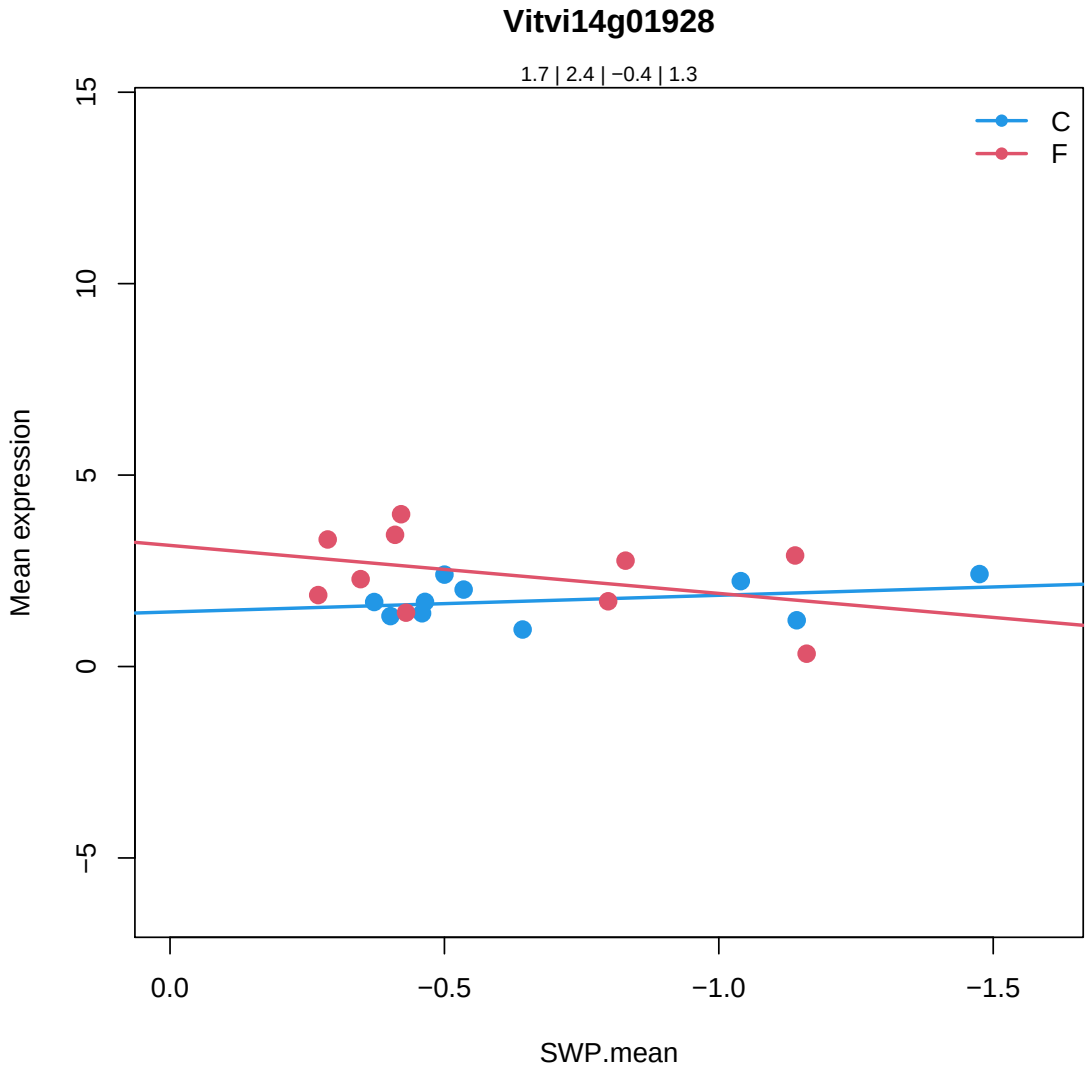
7.6.784 Vitvi14g01928: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01928
        34.16
        transport.ABC transporters and multidrug resistance systems
        ATP binding cassette subfamily B19 |
        Chr3:10870287-10877286 REVERSE LENGTH=1252 |
        201606
```

Coefficients for Vitvi14g01928.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.730746	4.33446e-07	***	5.050519e-07	***
SlopeC	-0.435762	0.5252897		0.8758851	
MeanF-MeanC	0.6685591	0.06449325	.	0.2811802	
SlopeF-SlopeC	1.689809	0.1069876		0.9999488	



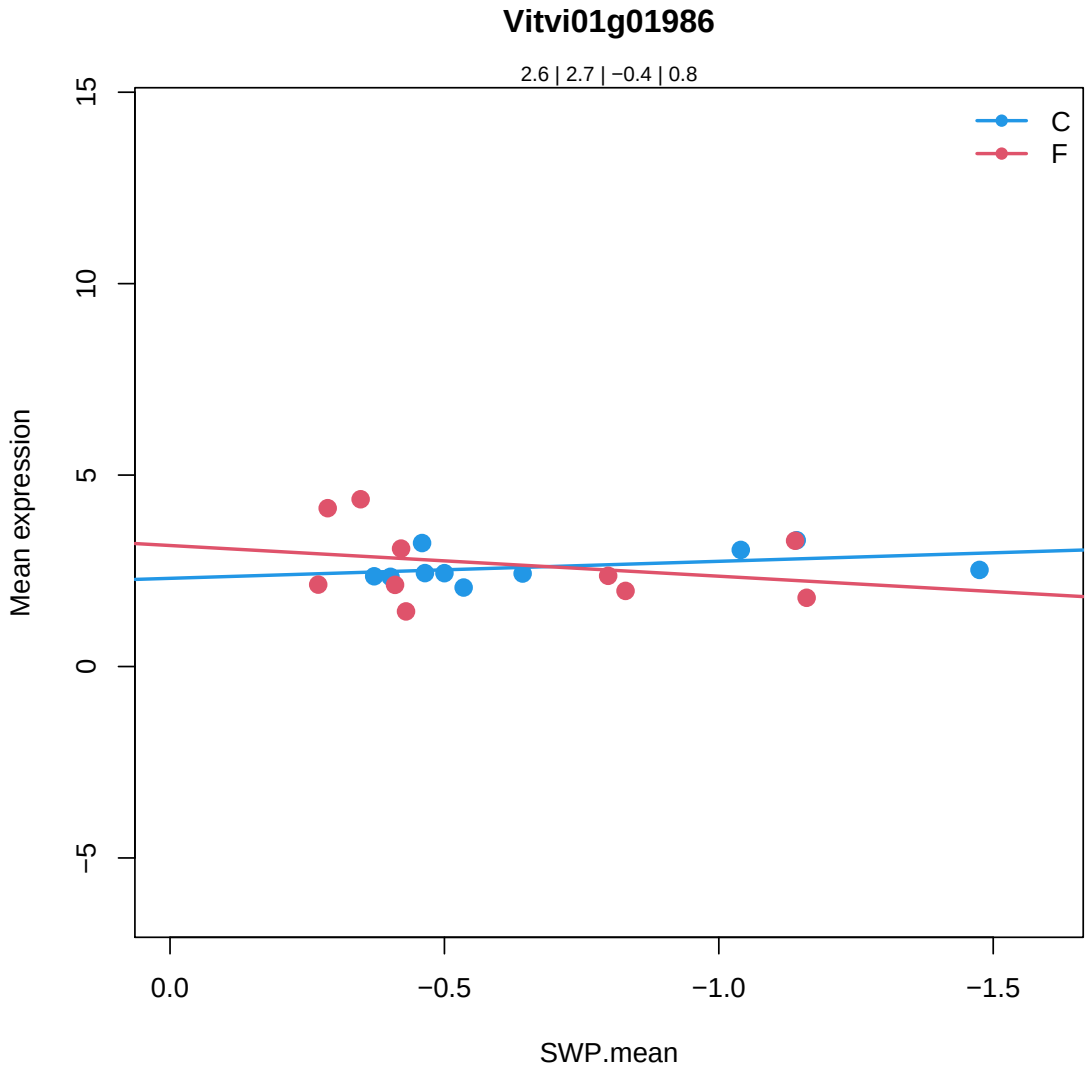
7.6.785 Vitvi01g01986: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01986
        31.1
        cell.organisation
        Arp2/3 complex%2C 34 kD subunit p34-Arc |
        Chr1:10961106-10962999 FORWARD LENGTH=318 |
        201606
```

Coefficients for Vitvi01g01986.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.615769	1.089043e-10	***	1.422748e-10	***
SlopeC	-0.4446713	0.4869793		0.8654145	
MeanF-MeanC	0.05612657	0.862228		0.9641172	
SlopeF-SlopeC	1.246408	0.1968202		0.9999488	



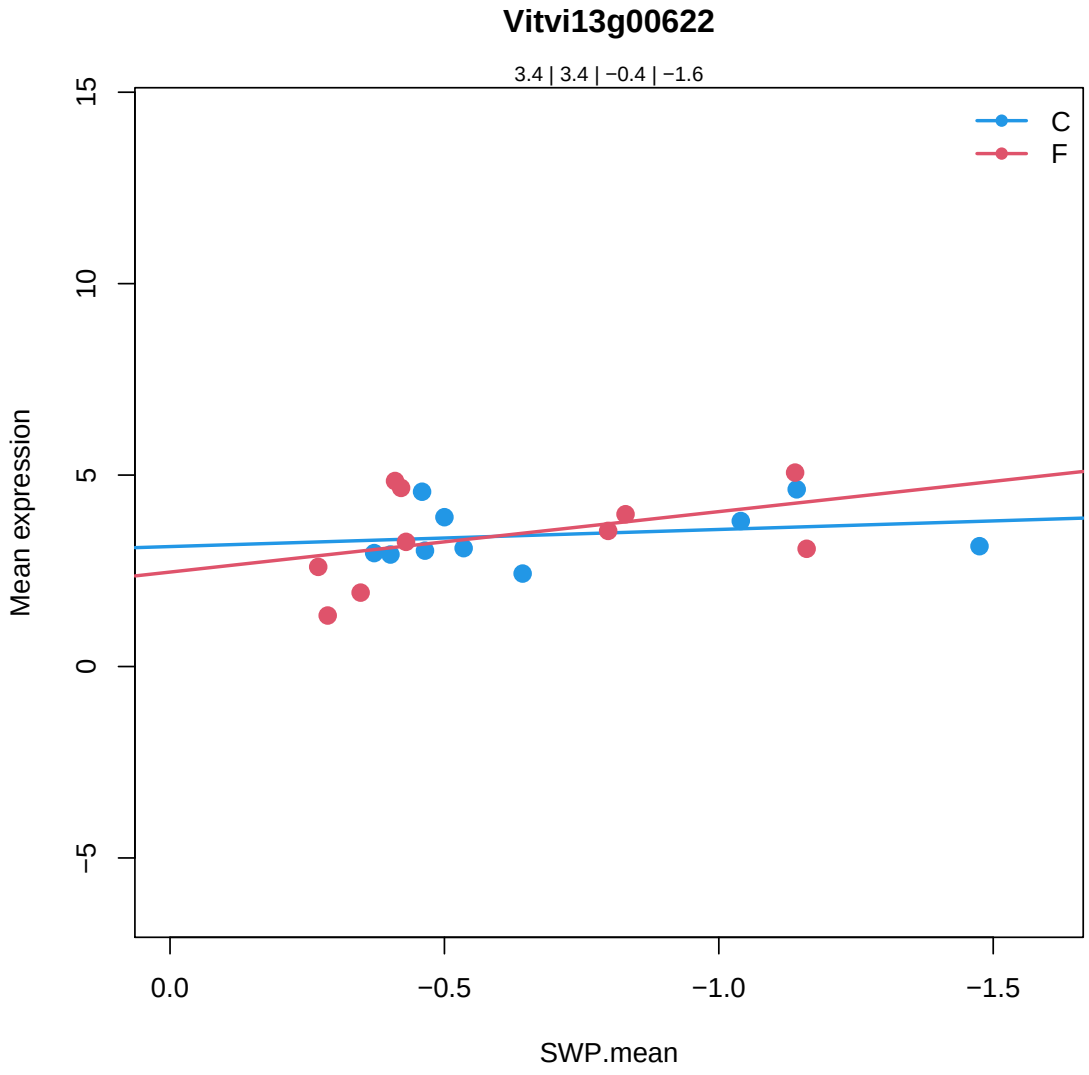
7.6.786 Vitvi13g00622: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00622
        16.2.1.1
        secondary metabolism.phenylpropanoids.lignin biosynthesis.PAL
        phenylalanine ammonia-lyase 2 |
        Chr3:19744256-19746619 REVERSE LENGTH=717 |
        201606
```

Coefficients for Vitvi13g00622.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.446684	4.563151e-11	***	6.054278e-11	***
SlopeC	-0.4467062	0.5779952		0.8942787	
MeanF-MeanC	-0.01772356	0.965238		0.9919971	
SlopeF-SlopeC	-1.132527	0.3466409		0.9999488	



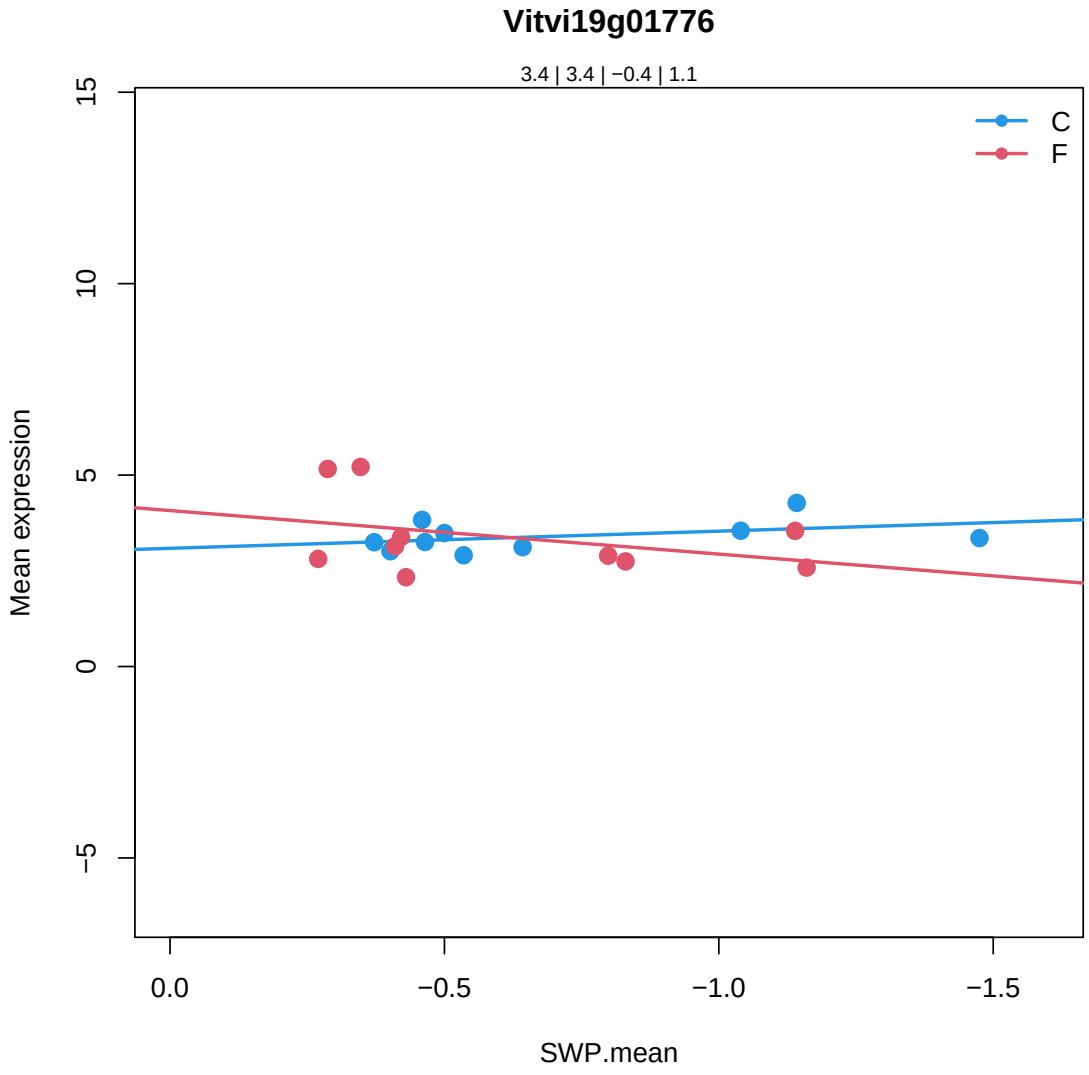
7.6.787 Vitvi19g01776: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g01776
        23.1.1.10
        nucleotide metabolism.synthesis.pyrimidine.CTP synthetase
        CTP synthase family protein |
        Chr3:4020351-4024086 REVERSE LENGTH=591 |
        201606
```

Coefficients for Vitvi19g01776.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.402161	4.557519e-13	***	6.690976e-13	***
SlopeC	-0.4485013	0.4736556		0.861922	
MeanF-MeanC	-0.02214074	0.9441851		0.9855729	
SlopeF-SlopeC	1.585558	0.09755089	.	0.9999488	



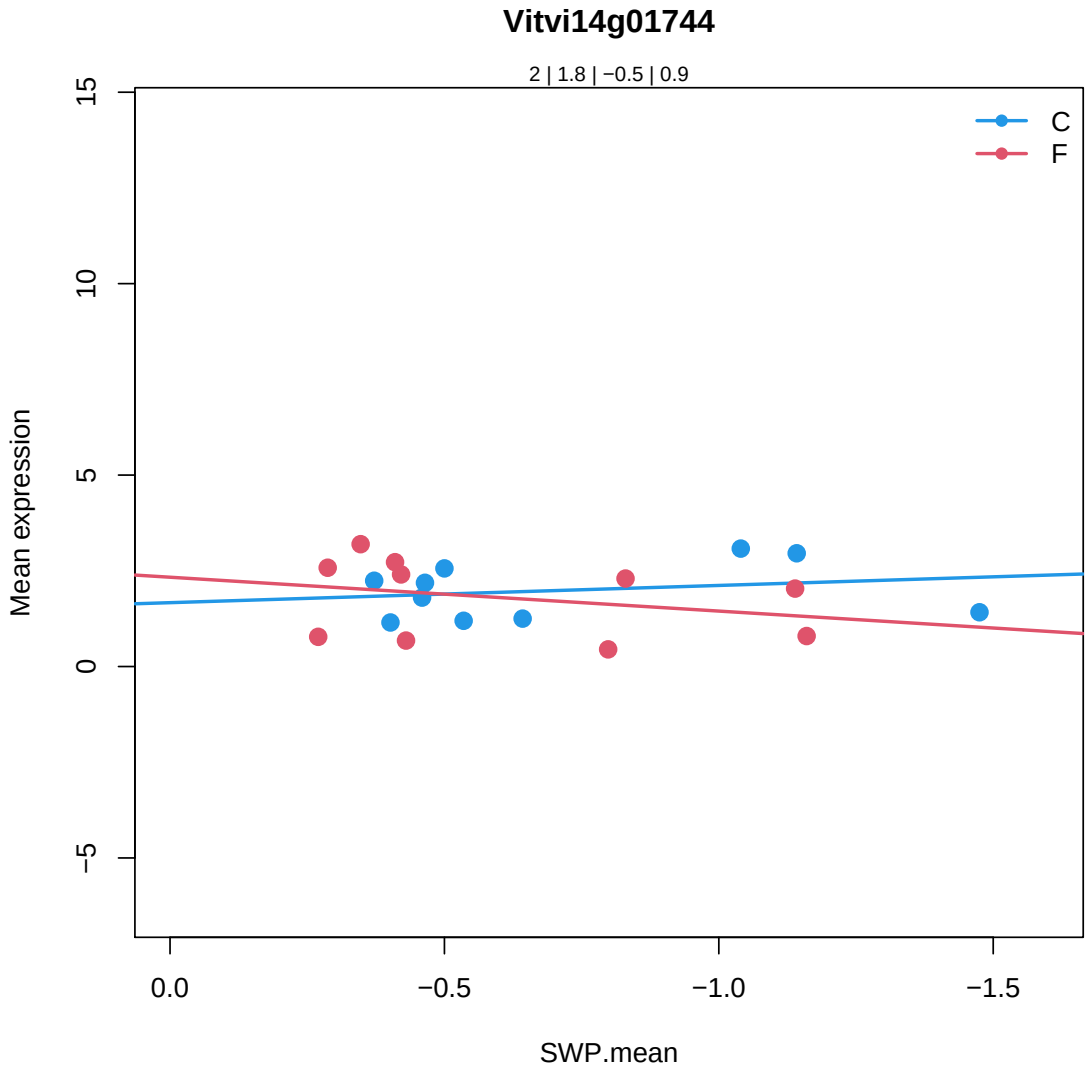
7.6.788 Vitvi14g01744: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01744
        29.4.1
        protein.postranslational modification.kinase
        shaggy-like kinase 13 |
        Chr5:4719350-4721772 REVERSE LENGTH=410 |
        201606
```

Coefficients for Vitvi14g01744.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.983891	1.319633e-07	***	1.560942e-07	***
SlopeC	-0.4502155	0.5366791		0.8821075	
MeanF-MeanC	-0.1904681	0.6066039		0.8620618	
SlopeF-SlopeC	1.334838	0.2244624		0.9999488	



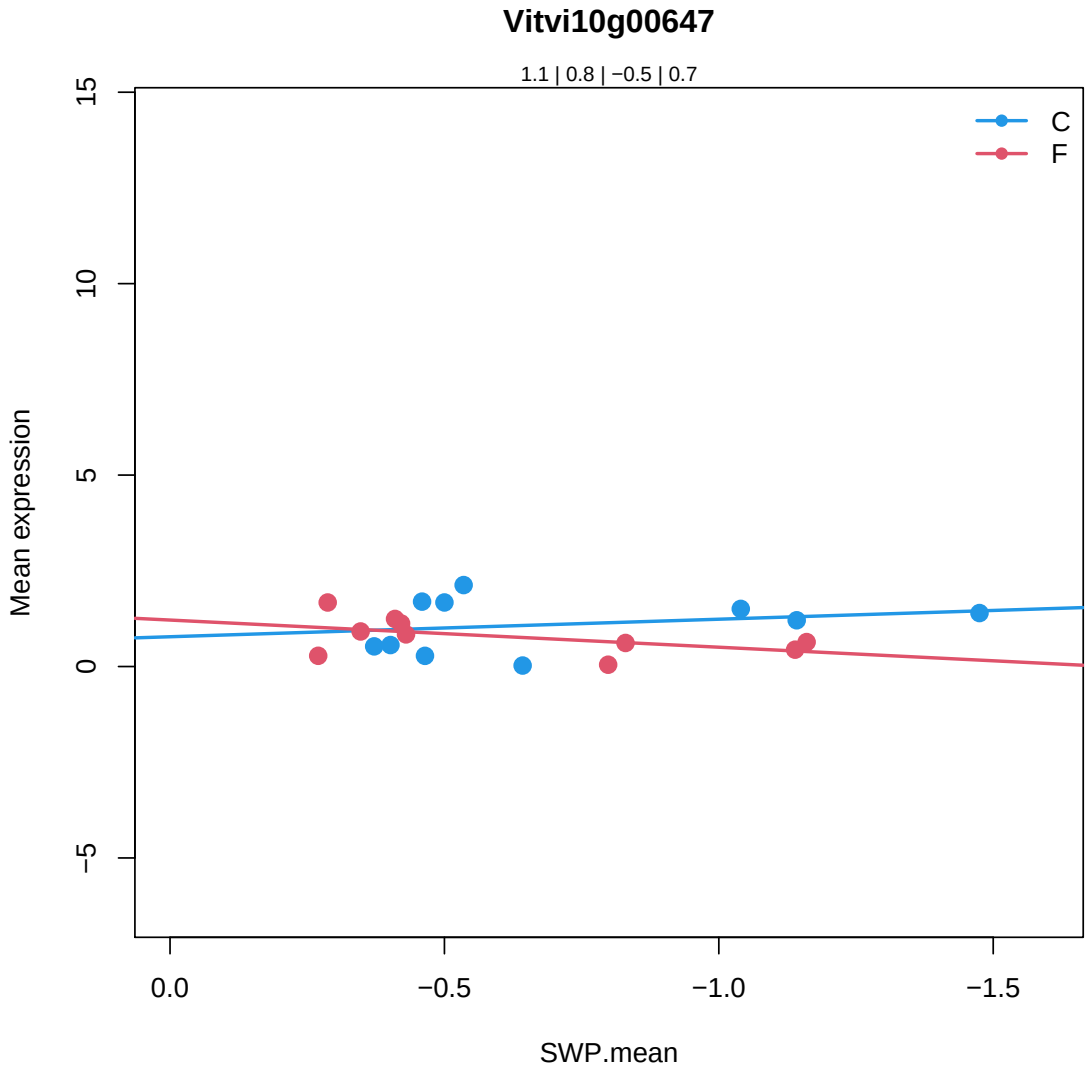
7.6.789 Vitvi10g00647: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00647
        30.2.8.2
        signalling.receptor kinases.leucine rich repeat VIII.type 2
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi10g00647.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.099437	4.696994e-06	***	5.340264e-06	***
SlopeC	-0.4577989	0.3743008		0.8243434	
MeanF-MeanC	-0.318114	0.2282406		0.5812567	
SlopeF-SlopeC	1.167017	0.1348043		0.9999488	



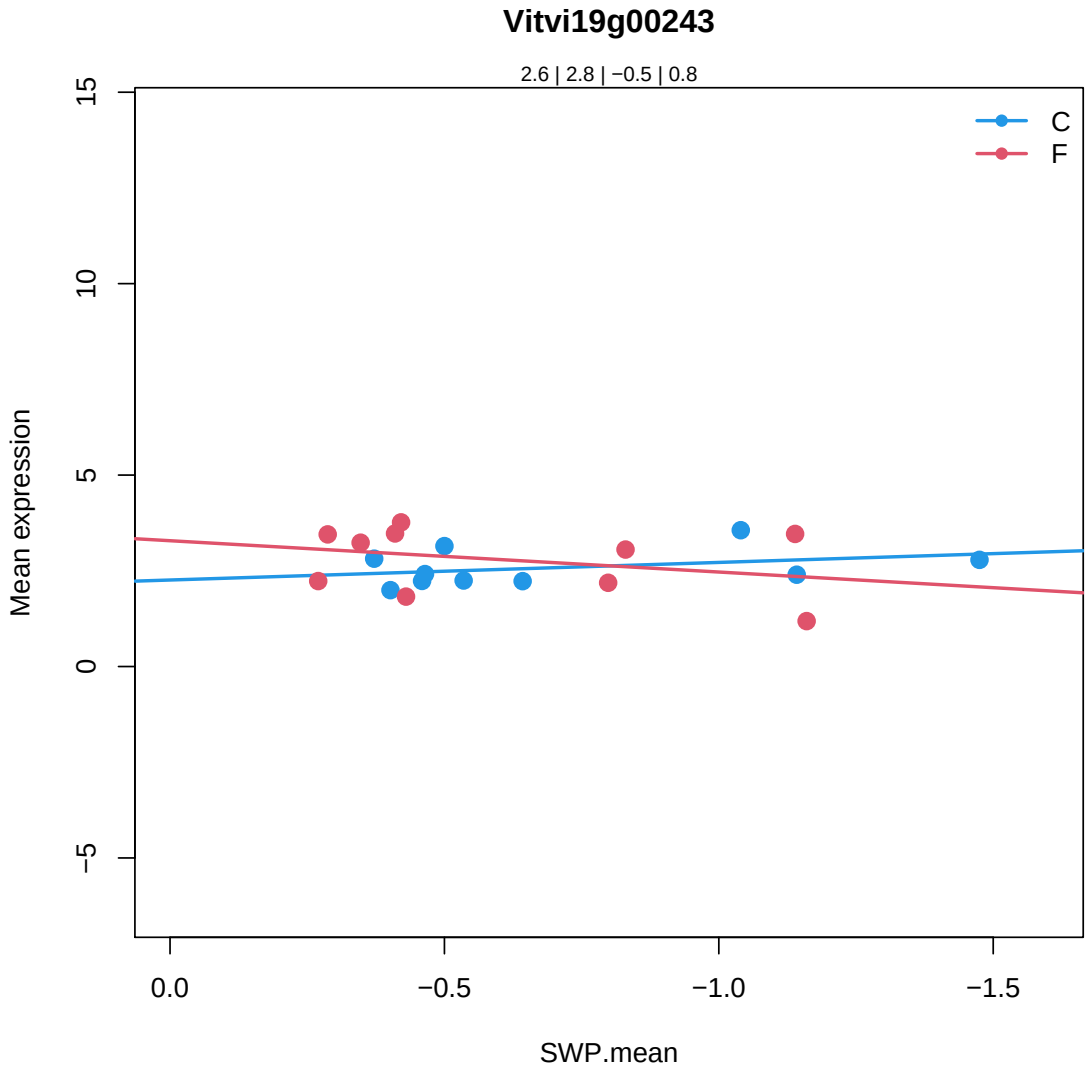
7.6.790 Vitvi19g00243: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g00243
        20.1.3.1
        stress.biotic.signalling.MLO-like
        Seven transmembrane MLO family protein |
        Chr5:21823055-21826289 FORWARD LENGTH=573 |
        201606
```

Coefficients for Vitvi19g00243.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.582426	2.741308e-11	***	3.671941e-11	***
SlopeC	-0.4593127	0.434501		0.8492896	
MeanF-MeanC	0.2047678	0.4923638		0.8018602	
SlopeF-SlopeC	1.27704	0.1513652		0.9999488	



7.6.791 Vitvi06g00213: type5

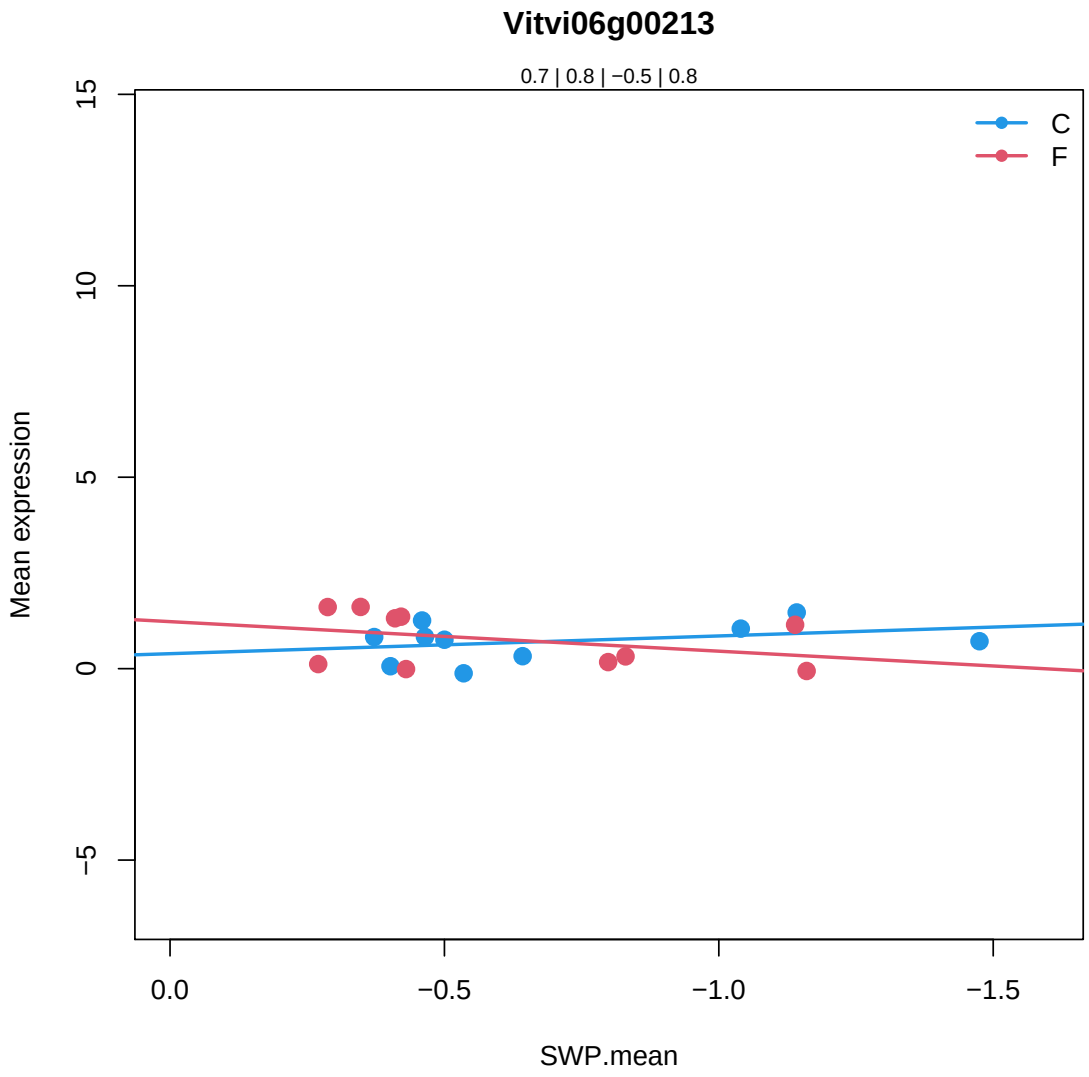
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00213
        17.3.1.2.5
        hormone metabolism.brassinosteroid.synthesis-degradation.sterols.HYD1
        C-8%2C7 sterol isomerase |
        Chr1:6949160-6950135 FORWARD LENGTH=223 |
        201606

Vitvi06g00213
        35.2
        not assigned.unknown
        C-8%2C7 sterol isomerase |
        Chr1:6949160-6950135 FORWARD LENGTH=223 |
        201606
```

Coefficients for Vitvi06g00213.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.7163675	0.0007561913	***	0.0008209892	***
SlopeC	-0.4630258	0.3722038		0.8230278	
MeanF-MeanC	0.04119098	0.8747618		0.967316	
SlopeF-SlopeC	1.234941	0.117017		0.9999488	


Vitvi06g00213
0.7 | 0.8 | −0.5 | 0.8
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

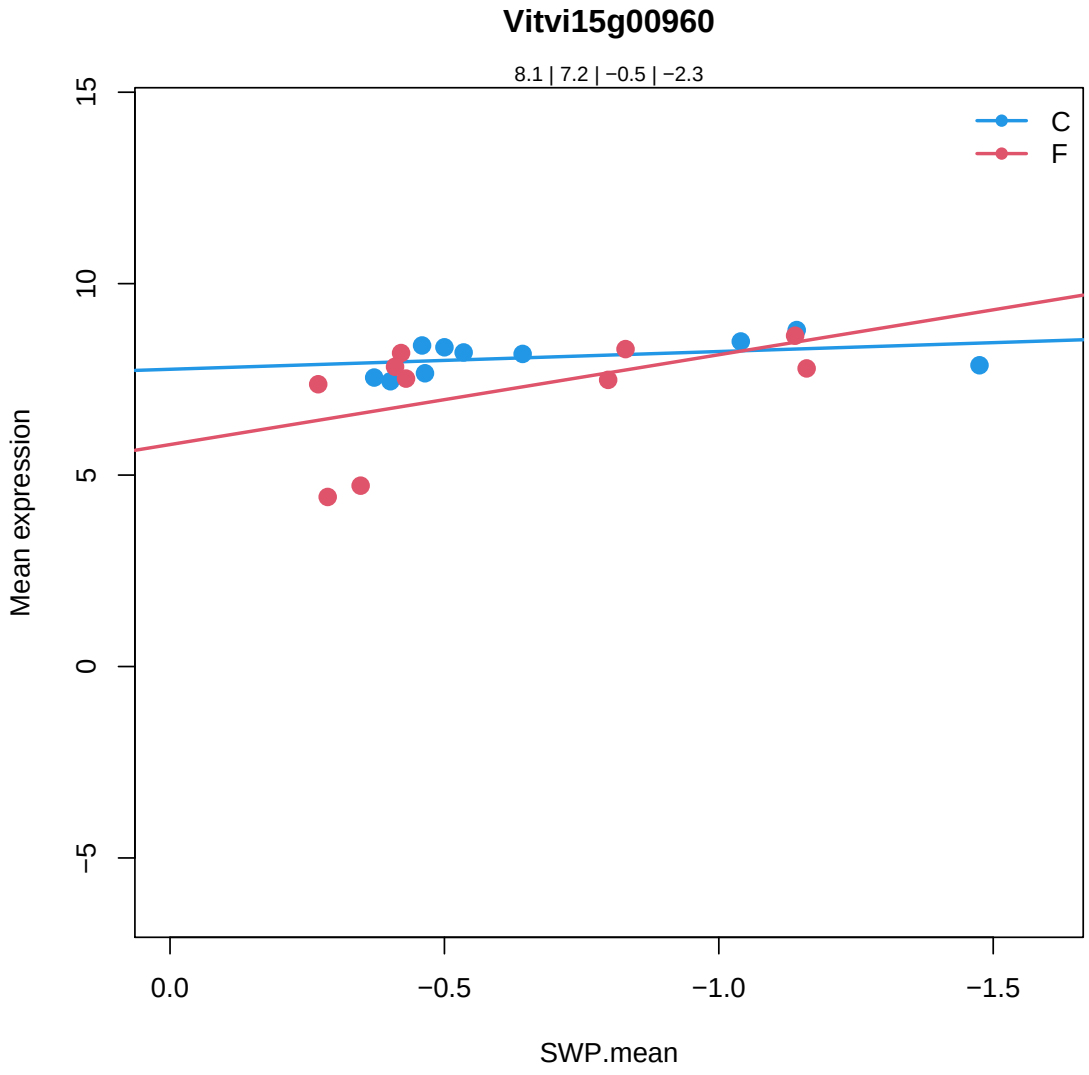
7.6.792 Vitvi15g00960: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g00960
        9.9
        mitochondrial electron transport / ATP synthesis.F1-ATPase
        O-acyltransferase (WSD1-like) family protein |
        Chr5:21656951-21659207 REVERSE LENGTH=486 |
        201606
```

Coefficients for Vitvi15g00960.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	8.089268	6.660504e-19	***	2.413107e-18	***
SlopeC	-0.4636752	0.5472908		0.886252	
MeanF-MeanC	-0.8628785	0.03589615	*	0.1904382	
SlopeF-SlopeC	-1.882293	0.1098787		0.9999488	



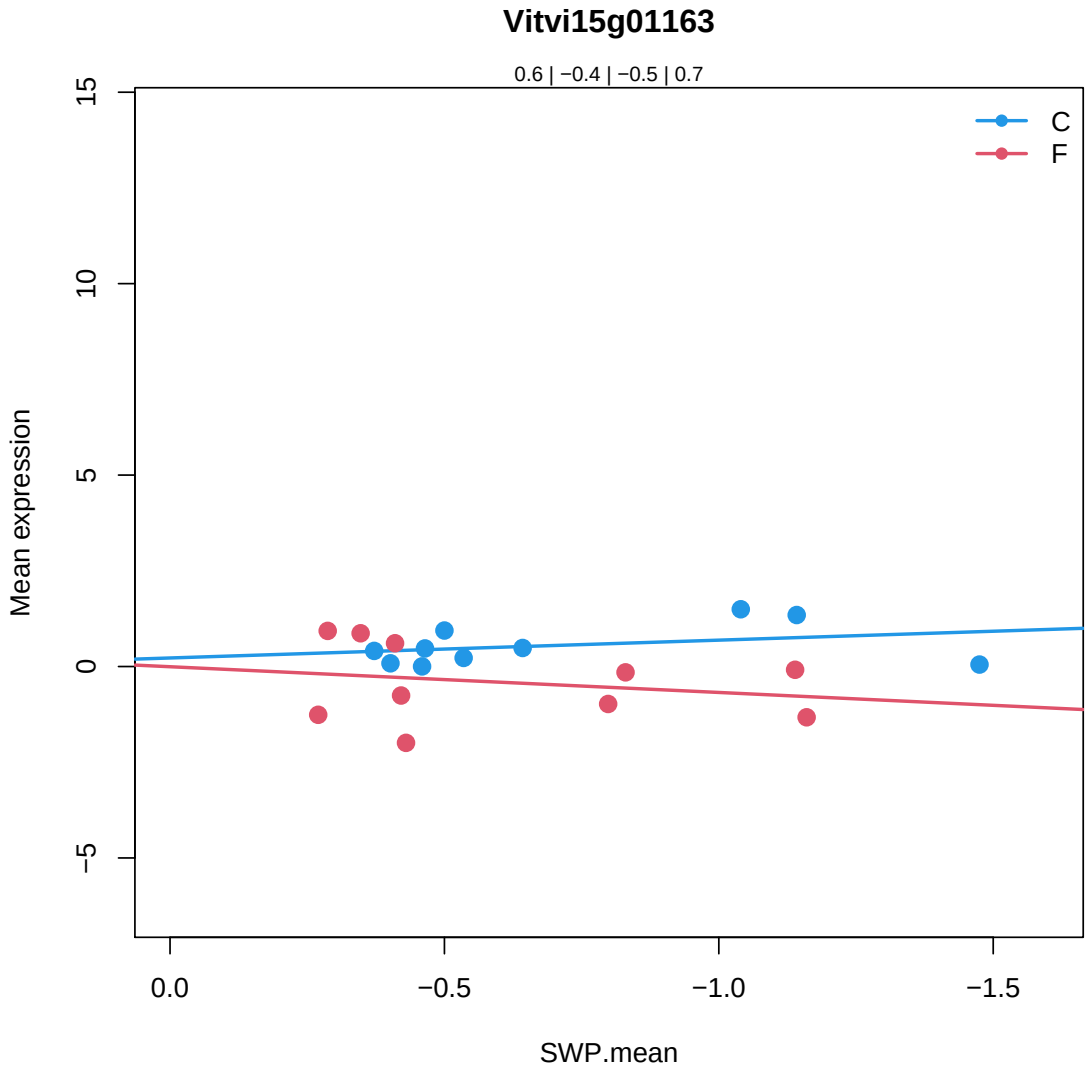
7.6.793 Vitvi15g01163: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g01163
        35.2
        not assigned.unknown
        Disease resistance protein (CC-NBS-LRR class) family |
        Chr1:21690962-21693891 REVERSE LENGTH=907 |
        201606
```

Coefficients for Vitvi15g01163.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.5504811	0.03157202	*	0.03302366	*
SlopeC	−0.4655608	0.4919429		0.8670232	
MeanF−MeanC	−0.9653788	0.009415294	**	0.07266224	.
SlopeF−SlopeC	1.137423	0.2637302		0.9999488	



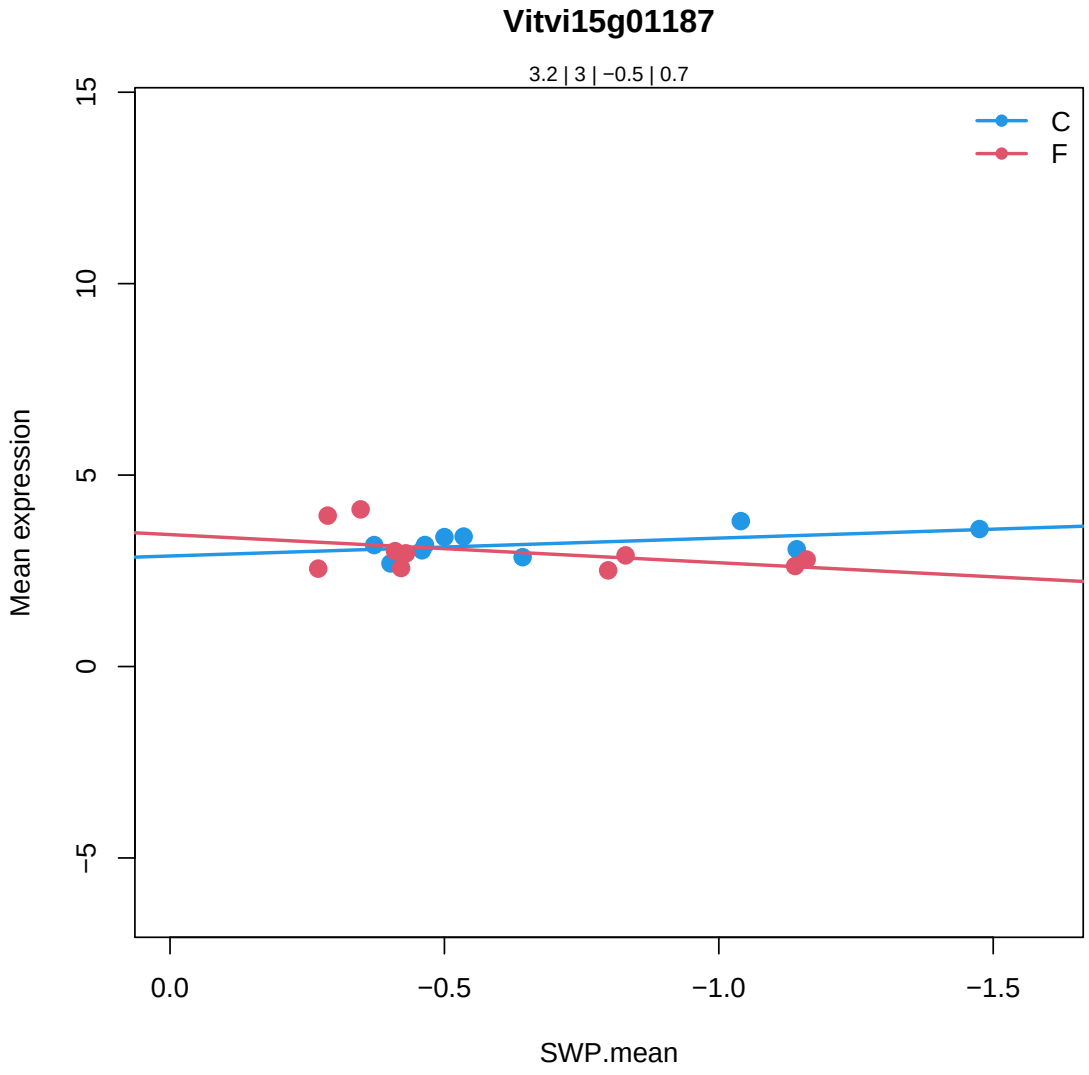
7.6.794 Vitvi15g01187: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g01187
        26.22
        misc.short chain dehydrogenase/reductase (SDR)
        NAD(P)-binding Rossmann-fold superfamily protein |
        Chr1:293595-294888 FORWARD LENGTH=260 |
        201606
```

Coefficients for Vitvi15g01187.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.215352	2.069679e-16	***	4.266439e-16	***
SlopeC	-0.4669091	0.2526443		0.7631876	
MeanF-MeanC	-0.217761	0.2927409		0.6593523	
SlopeF-SlopeC	1.20221	0.05453693	.	0.9999488	



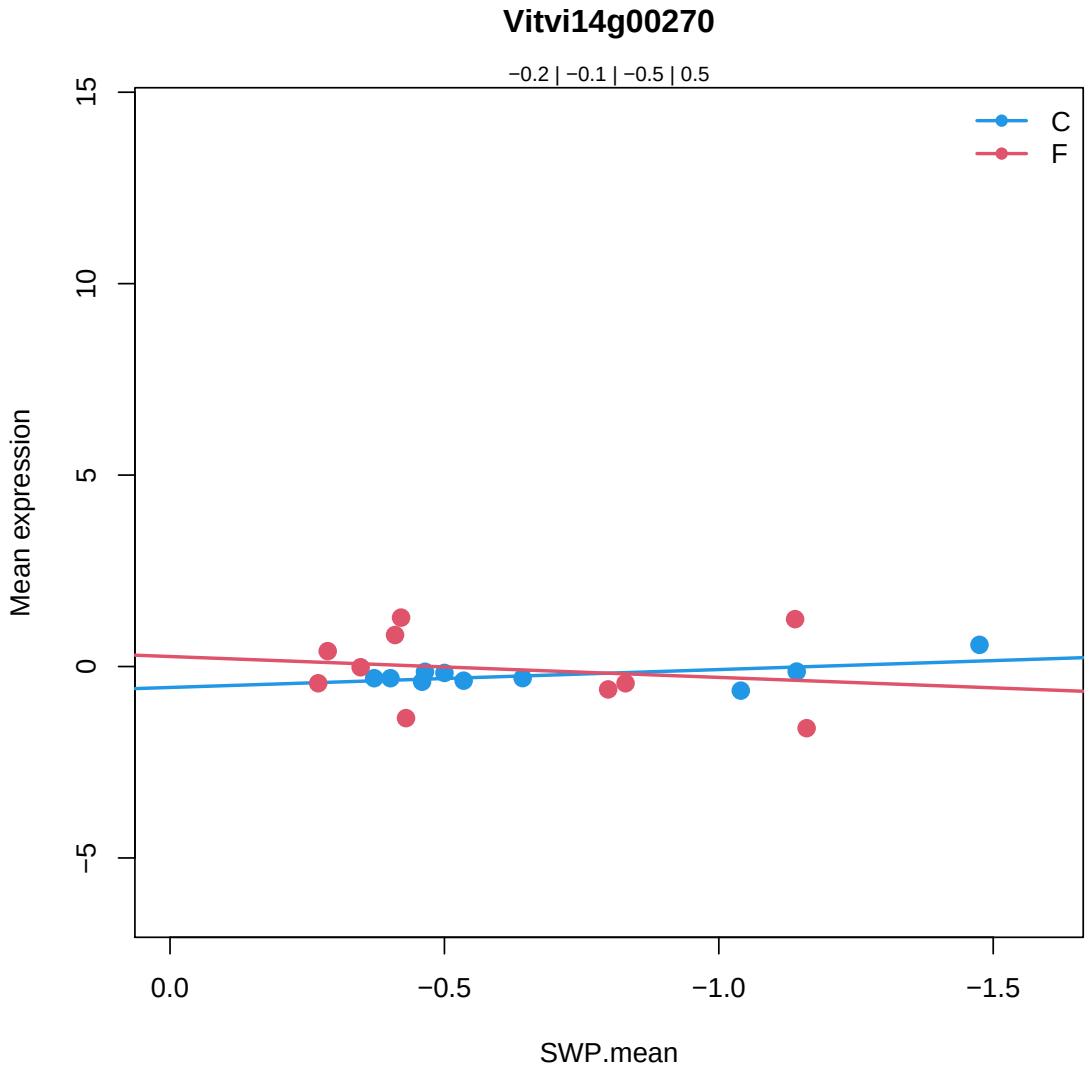
7.6.795 Vitvi14g00270: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g00270
        15.2
        metal handling.binding, chelation and storage
        Heavy metal transport/detoxification superfamily protein |
        Chr3:1853193-1854673 REVERSE LENGTH=349 |
        201606
```

Coefficients for Vitvi14g00270.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.218363	0.3390296		0.3449362	
SlopeC	-0.4676344	0.4597929		0.8600587	
MeanF-MeanC	0.1470655	0.6461227		0.8800896	
SlopeF-SlopeC	1.013111	0.2853754		0.9999488	



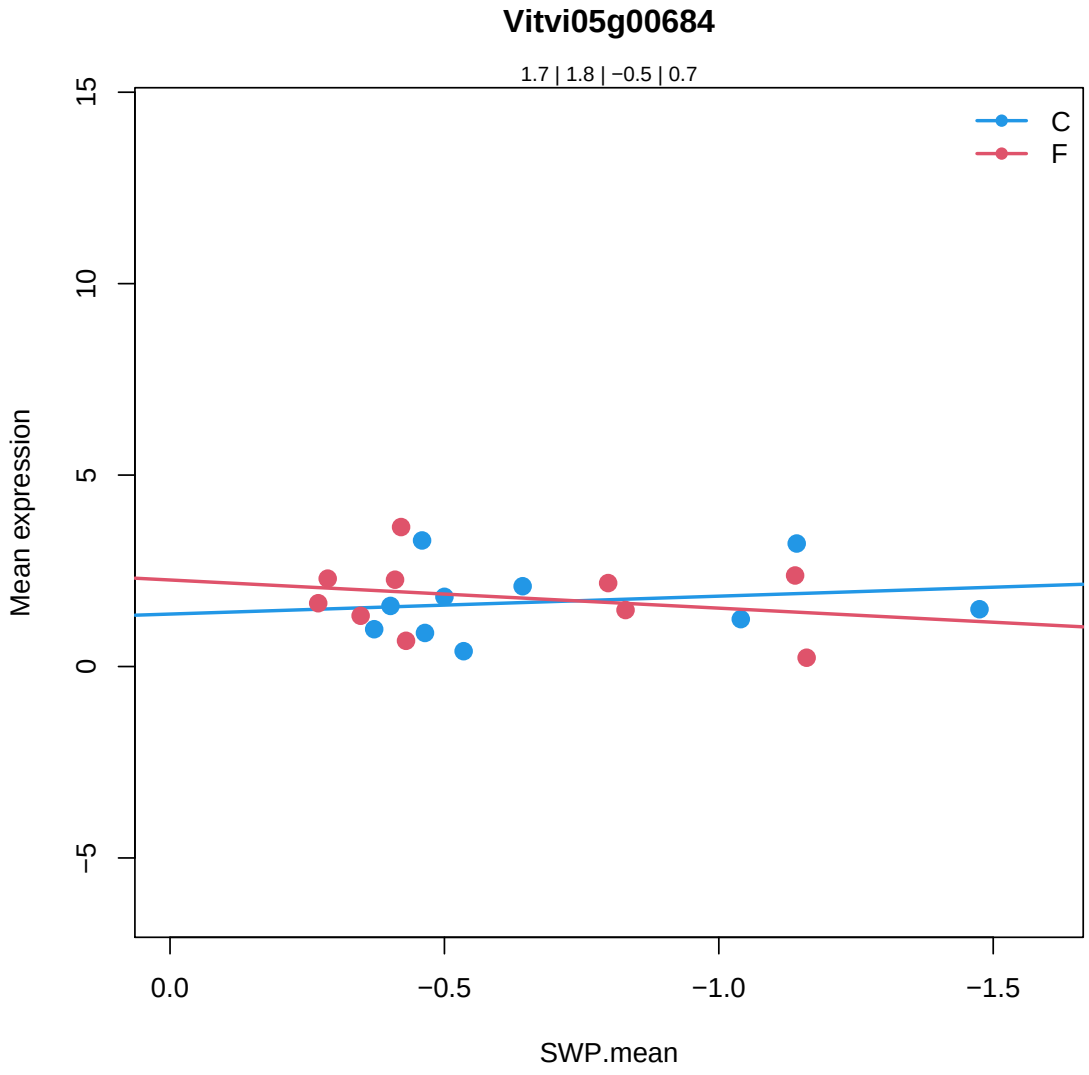
7.6.796 Vitvi05g00684: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00684
        17.5.2
        hormone metabolism.ethylene.signal transduction
        Signal transduction histidine kinase%2C hybrid-type%2C ethylene sensor
        Chr3:8255156-8256970 FORWARD LENGTH=604 |
        201606
```

Coefficients for Vitvi05g00684.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.698736	5.098952e-06	***	5.79511e-06	***
SlopeC	-0.4677685	0.5570933		0.8894103	
MeanF-MeanC	0.1130156	0.7795026		0.9372393	
SlopeF-SlopeC	1.203304	0.3140555		0.9999488	



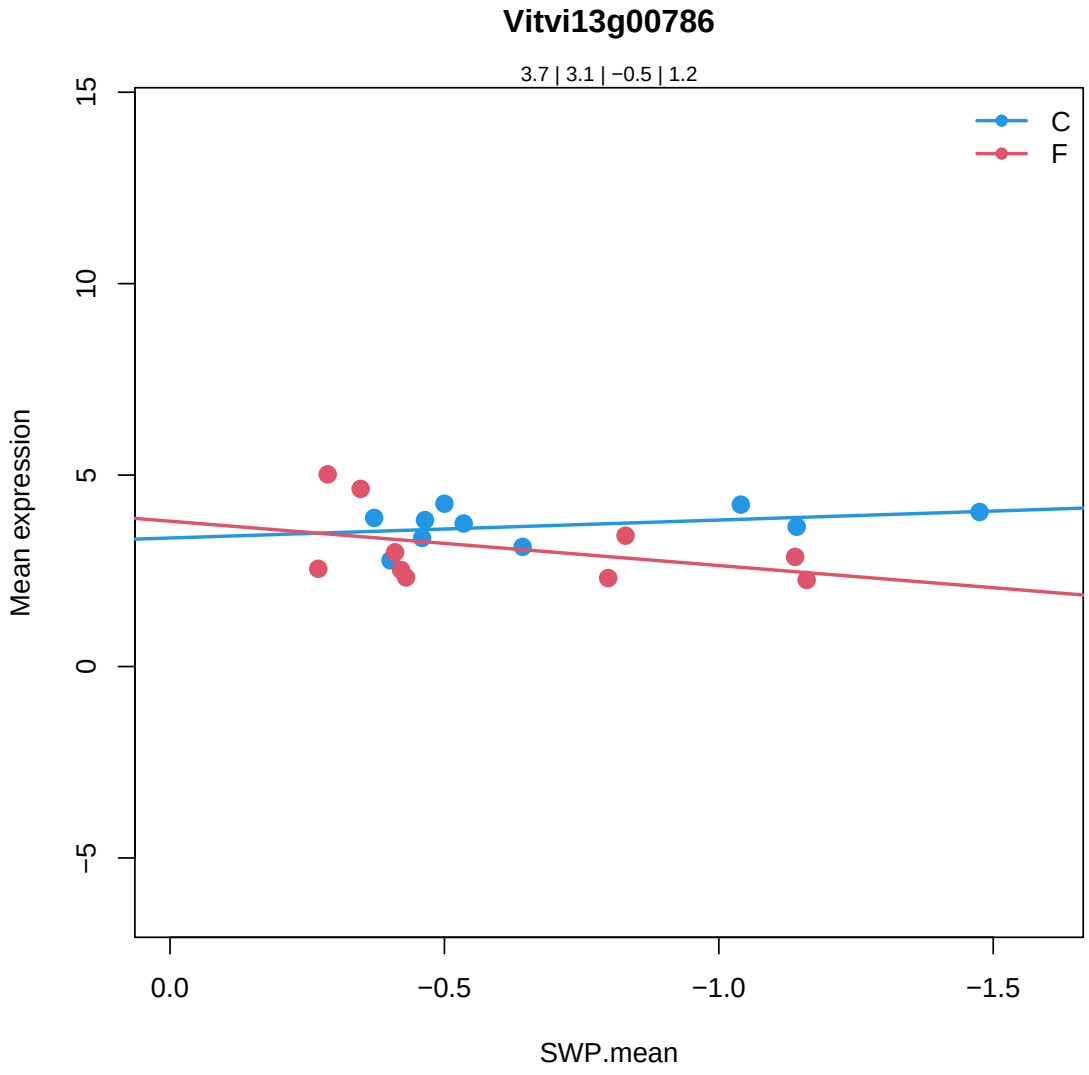
7.6.797 Vitvi13g00786: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00786
        34.16
        transport.ABC transporters and multidrug resistance systems
        pleiotropic drug resistance 11 |
        Chr1:24978239-24984461 FORWARD LENGTH=1454 |
        201606
```

Coefficients for Vitvi13g00786.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.686237	8.886889e-14	***	1.369467e-13	***
SlopeC	-0.468976	0.4530161		0.8563681	
MeanF-MeanC	-0.5965845	0.0692346	.	0.2943731	
SlopeF-SlopeC	1.62695	0.08900758	.	0.9999488	



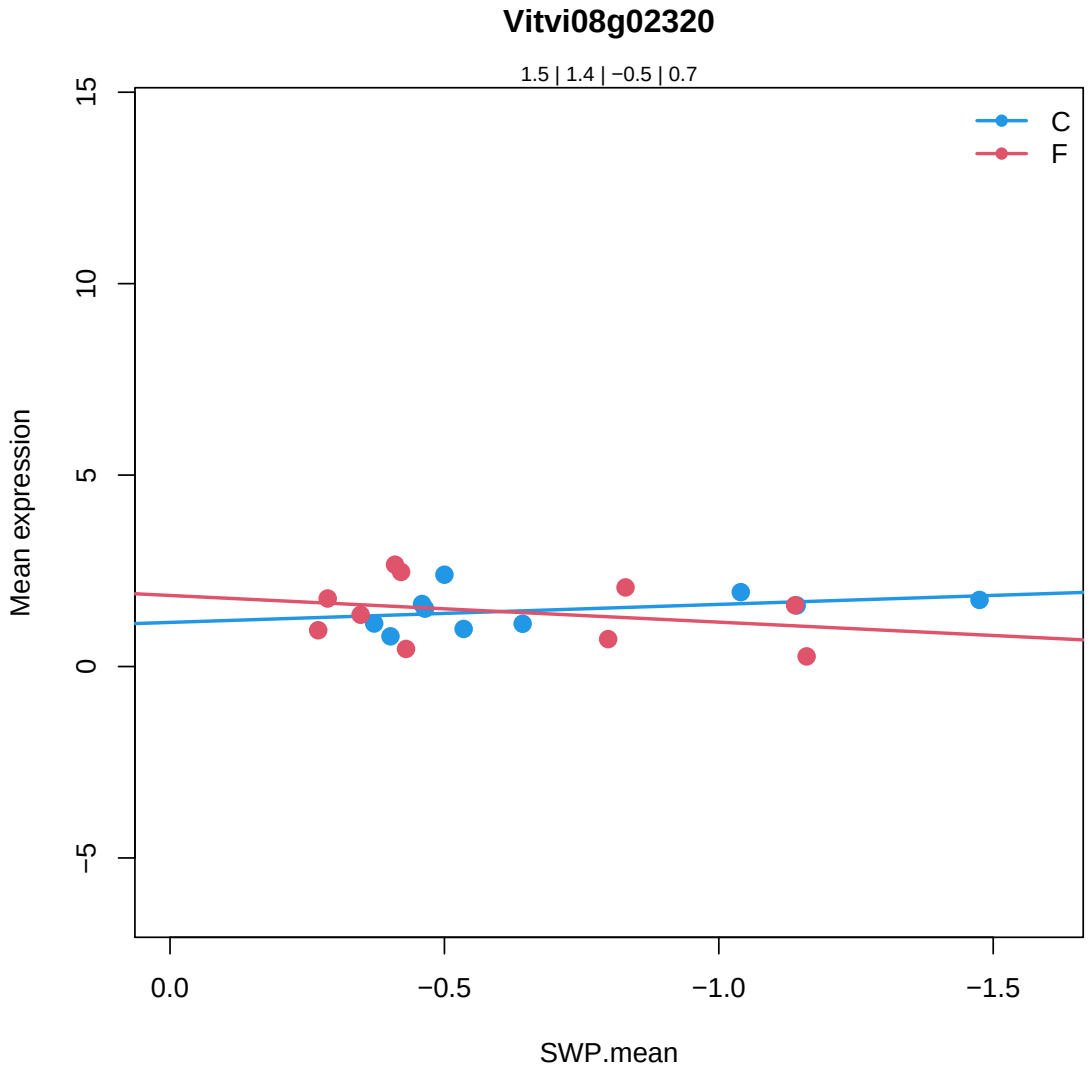
7.6.798 Vitvi08g02320: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g02320
        35.2
        not assigned.unknown
        transmembrane protein%2C putative (DUF247) |
        Chr3:18601857-18603738 REVERSE LENGTH=541 |
        201606
```

Coefficients for Vitvi08g02320.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.482734	3.059811e-07	***	3.578976e-07	***
SlopeC	-0.4705653	0.4142883		0.8406955	
MeanF-MeanC	-0.05186314	0.8584478		0.9628006	
SlopeF-SlopeC	1.167301	0.1795264		0.9999488	



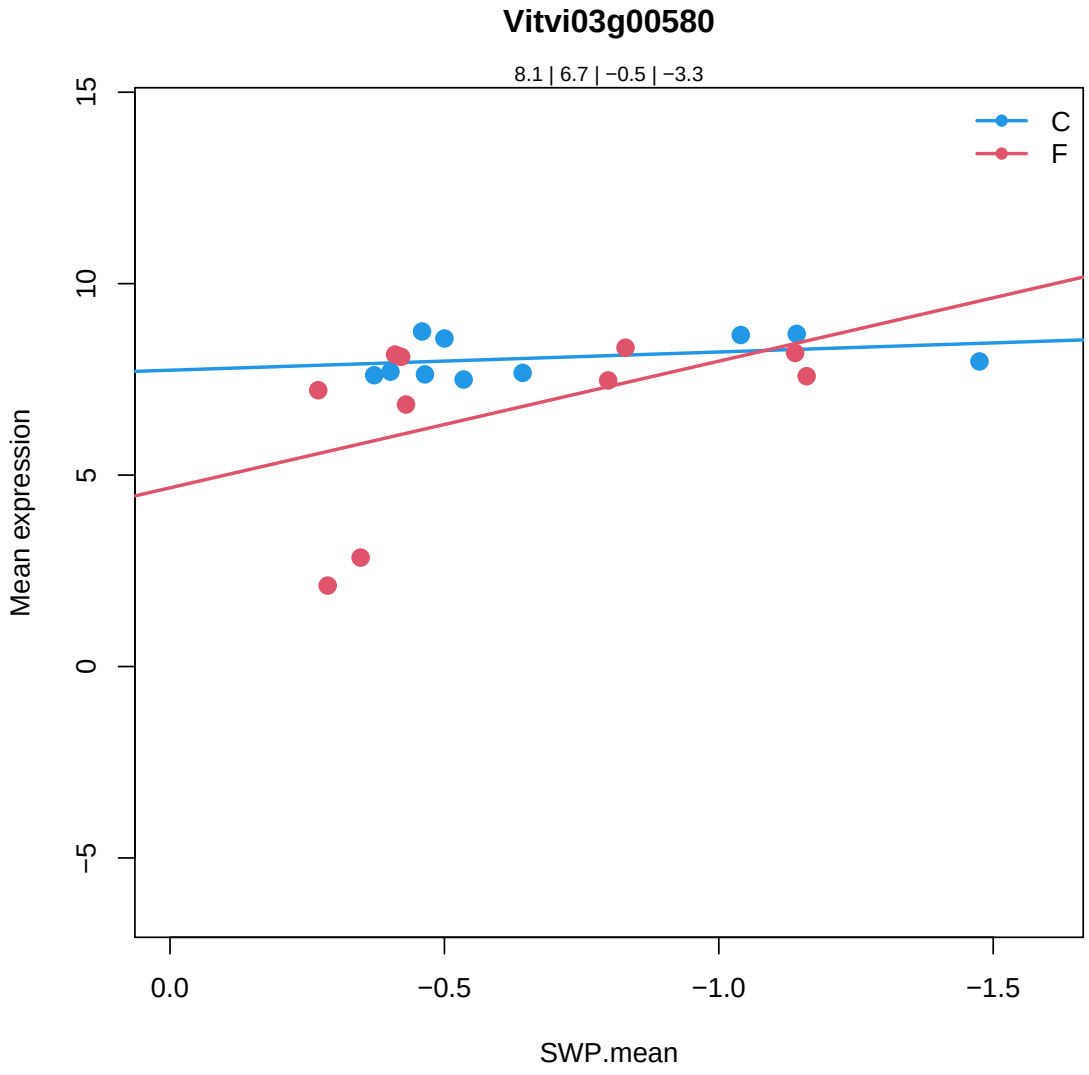
7.6.799 Vitvi03g00580: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00580
        35.2
        not assigned.unknown
        hypothetical protein |
        Chr2:6491706-6493286 REVERSE LENGTH=526 |
        201606
```

Coefficients for Vitvi03g00580.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	8.073395	6.043421e-15	***	1.033477e-14	***
SlopeC	-0.475253	0.6901238		0.9312028	
MeanF-MeanC	-1.390809	0.02985651	*	0.1685188	
SlopeF-SlopeC	-2.832606	0.1202108		0.9999488	



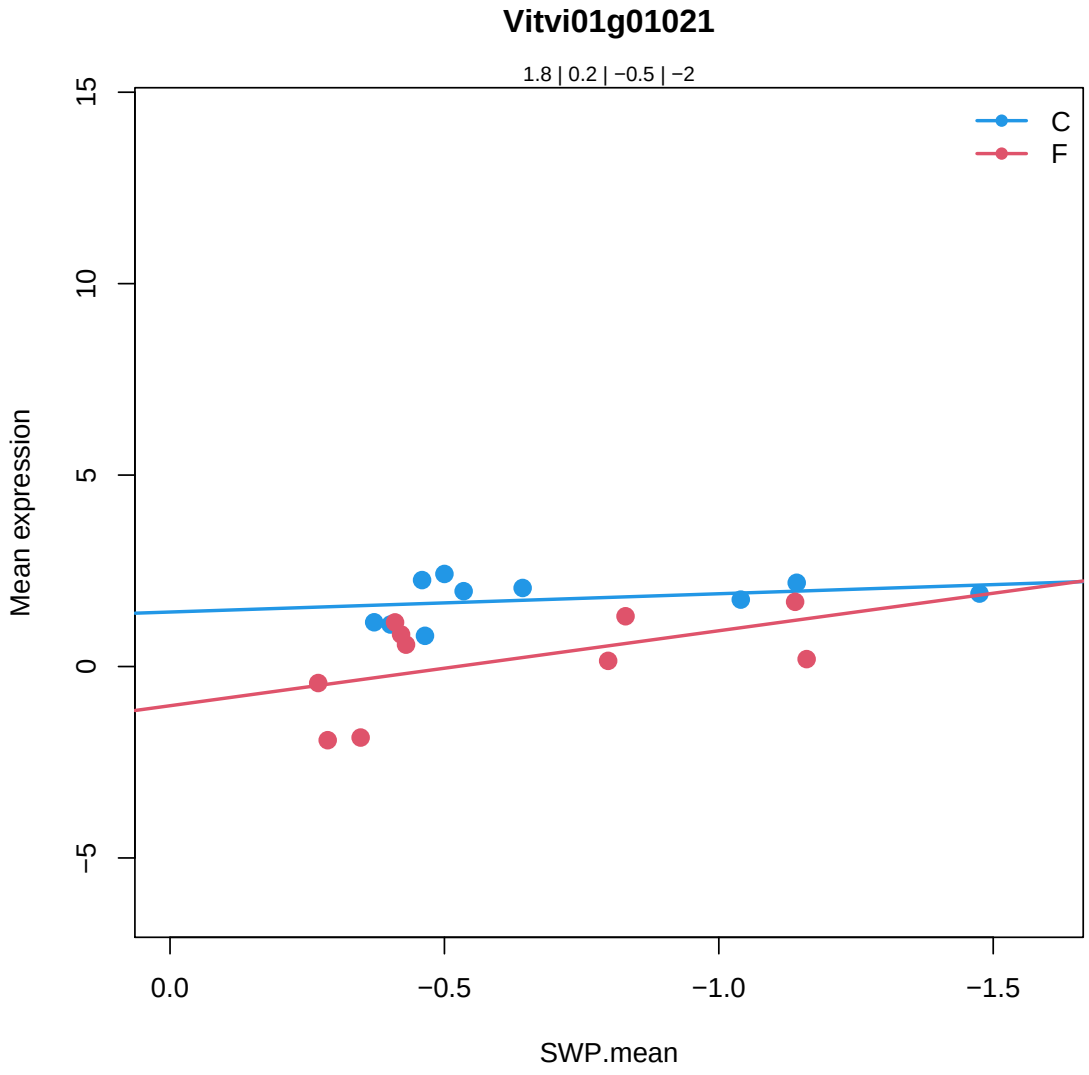
7.6.800 Vitvi01g01021: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01021
        27.1.19
        RNA.processing.ribonucleases
        ribonuclease 1 |
        Chr2:873714-874667 FORWARD LENGTH=230 |
        201606
```

Coefficients for Vitvi01g01021.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.758743	6.402902e-07	***	7.427737e-07	***
SlopeC	-0.477187	0.5048389		0.8706312	
MeanF-MeanC	-1.589466	0.0002147614	***	0.003456592	**
SlopeF-SlopeC	-1.48126	0.1715283		0.9999488	



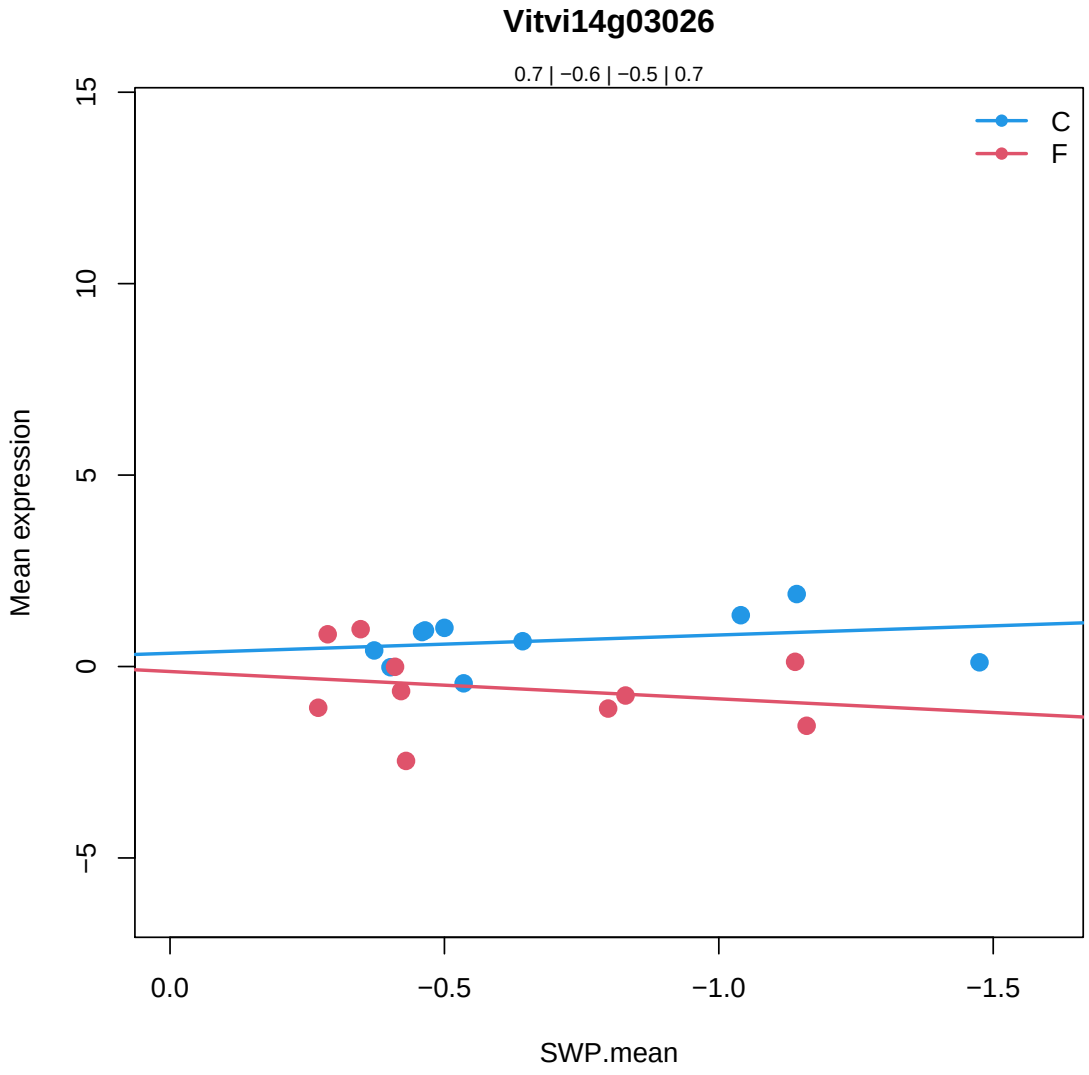
7.6.801 Vitvi14g03026: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g03026
        35.2
        not assigned.unknown
        UDP-Glycosyltransferase superfamily protein |
        Chr2:7316938-7317876 FORWARD LENGTH=312 |
        201606
```

Coefficients for Vitvi14g03026.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6816671	0.01752647	*	0.01845261	*
SlopeC	-0.4775566	0.5237861		0.8753077	
MeanF-MeanC	-1.247321	0.003112844	**	0.03158853	*
SlopeF-SlopeC	1.191214	0.2894511		0.9999488	



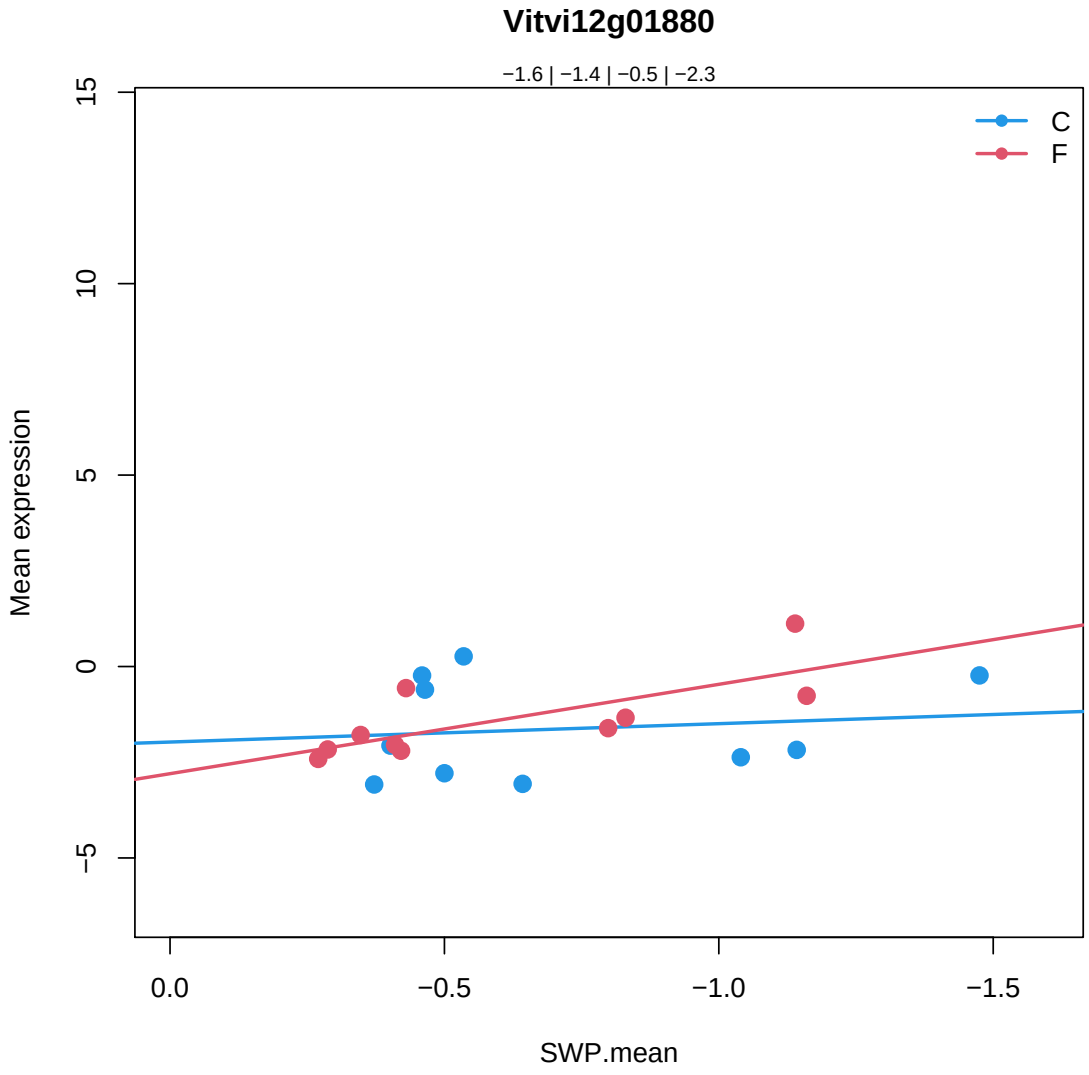
7.6.802 Vitvi12g01880: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g01880
        33.1
        development.storage proteins
        RmlC-like cupins superfamily protein |
        Chr1:2404300-2405863 REVERSE LENGTH=356 |
        201606
```

Coefficients for Vitvi12g01880.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.635458	2.953379e-05	***	3.29759e-05	***
SlopeC	-0.4795472	0.5841254		0.8963999	
MeanF-MeanC	0.2583273	0.5620367		0.840611	
SlopeF-SlopeC	-1.854219	0.1632476		0.9999488	



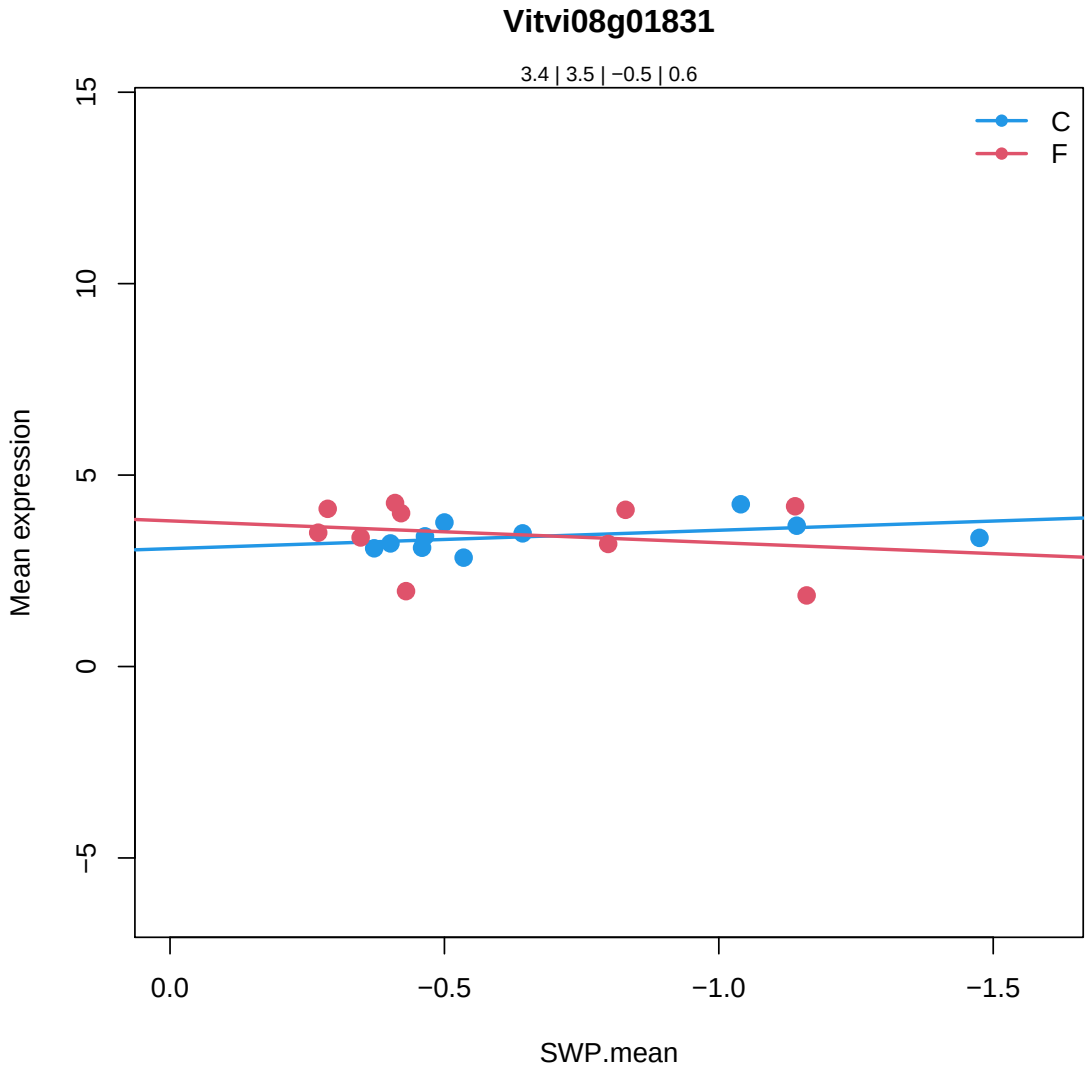
7.6.803 Vitvi08g01831: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01831
        27.3.9
        RNA.regulation of transcription.C2C2(Zn) GATA transcription factor fam
        GATA transcription factor 9 |
        Chr4:15875598-15876615 FORWARD LENGTH=308 |
        201606
```

Coefficients for Vitvi08g01831.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.416169	1.285935e-13	***	1.958846e-13	***
SlopeC	-0.4802276	0.4162281		0.8411037	
MeanF-MeanC	0.04021677	0.8926372		0.9718495	
SlopeF-SlopeC	1.050163	0.2364427		0.9999488	



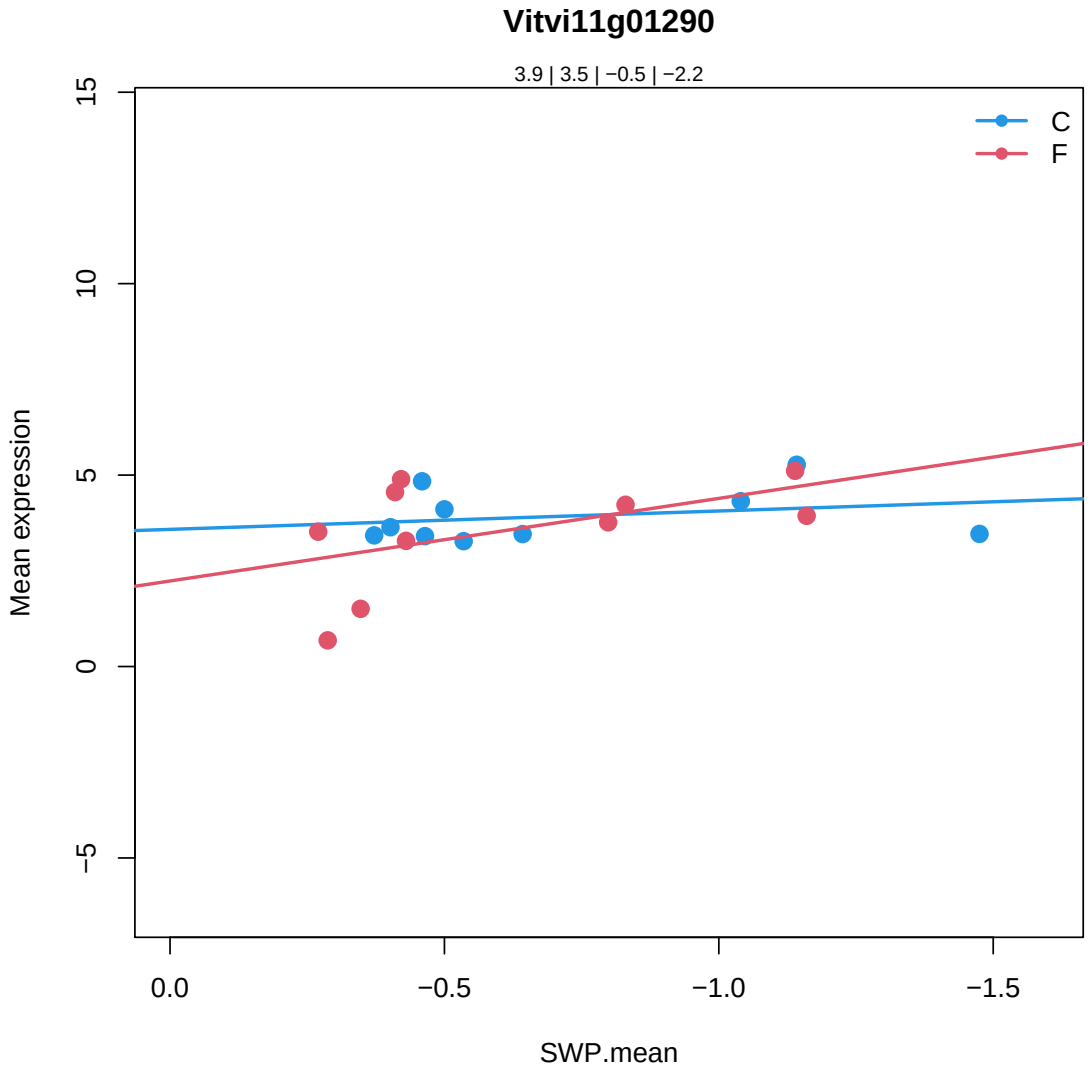
7.6.804 Vitvi11g01290: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g01290
        26.2
        misc.UDP glucosyl and glucoronyl transferases
        UDP-glucosyl transferase 78D2 |
        Chr5:5607828-5609392 REVERSE LENGTH=460 |
        201606
```

Coefficients for Vitvi11g01290.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.919397	8.267876e-12	***	1.134182e-11	***
SlopeC	-0.4805001	0.5649423		0.8905966	
MeanF-MeanC	-0.3712263	0.3841505		0.7345655	
SlopeF-SlopeC	-1.676868	0.1846648		0.9999488	



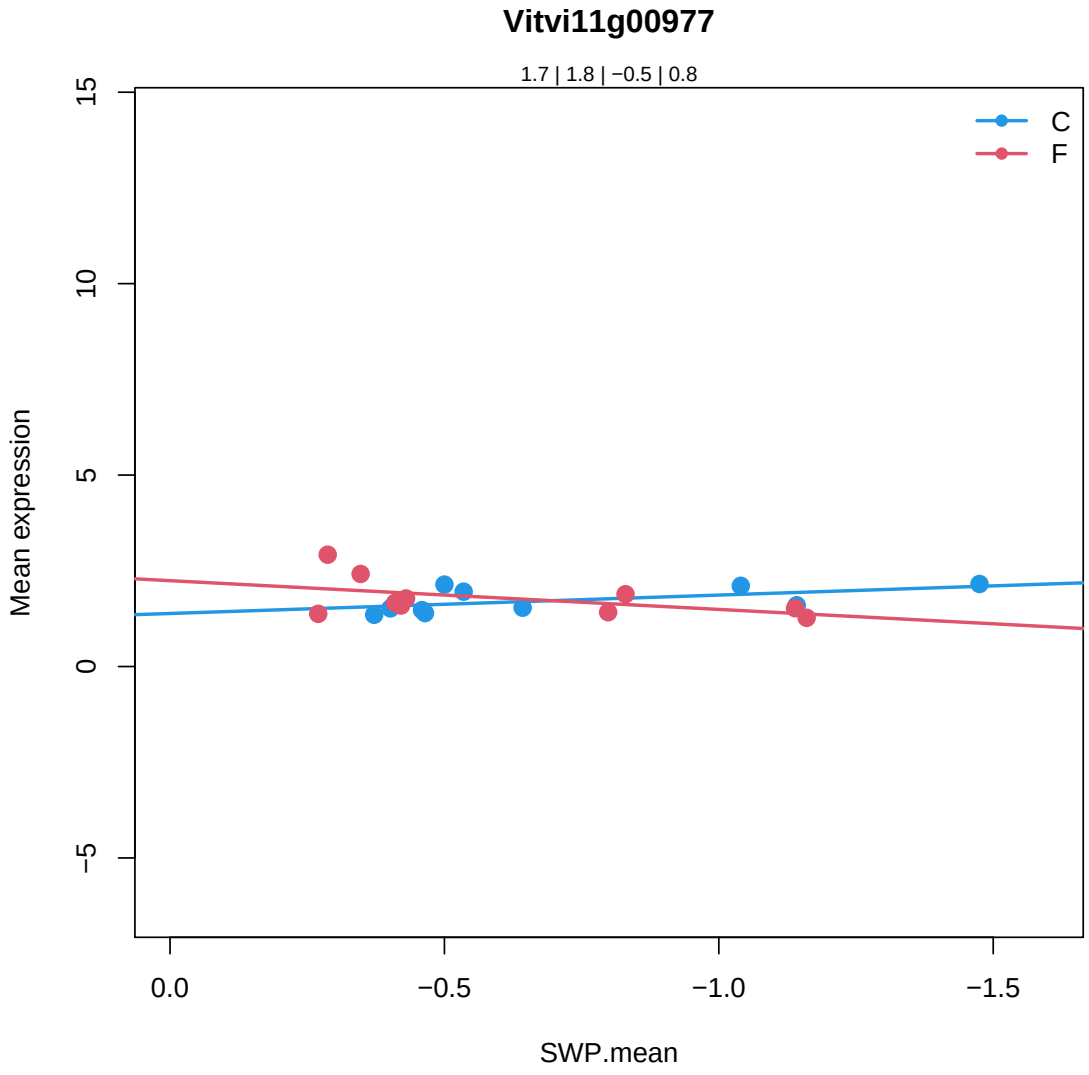
7.6.805 Vitvi11g00977: + type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00977
        35.2
        not assigned.unknown
        transmembrane protein |
        Chr4:9480699-9481640 FORWARD LENGTH=313 |
        201606
```

Coefficients for Vitvi11g00977.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.723104	1.190331e-11	***	1.619045e-11	***
SlopeC	-0.4807601	0.2056155		0.7302381	
MeanF-MeanC	0.06149194	0.7457561		0.9251843	
SlopeF-SlopeC	1.23153	0.03531398	*	0.9999488	



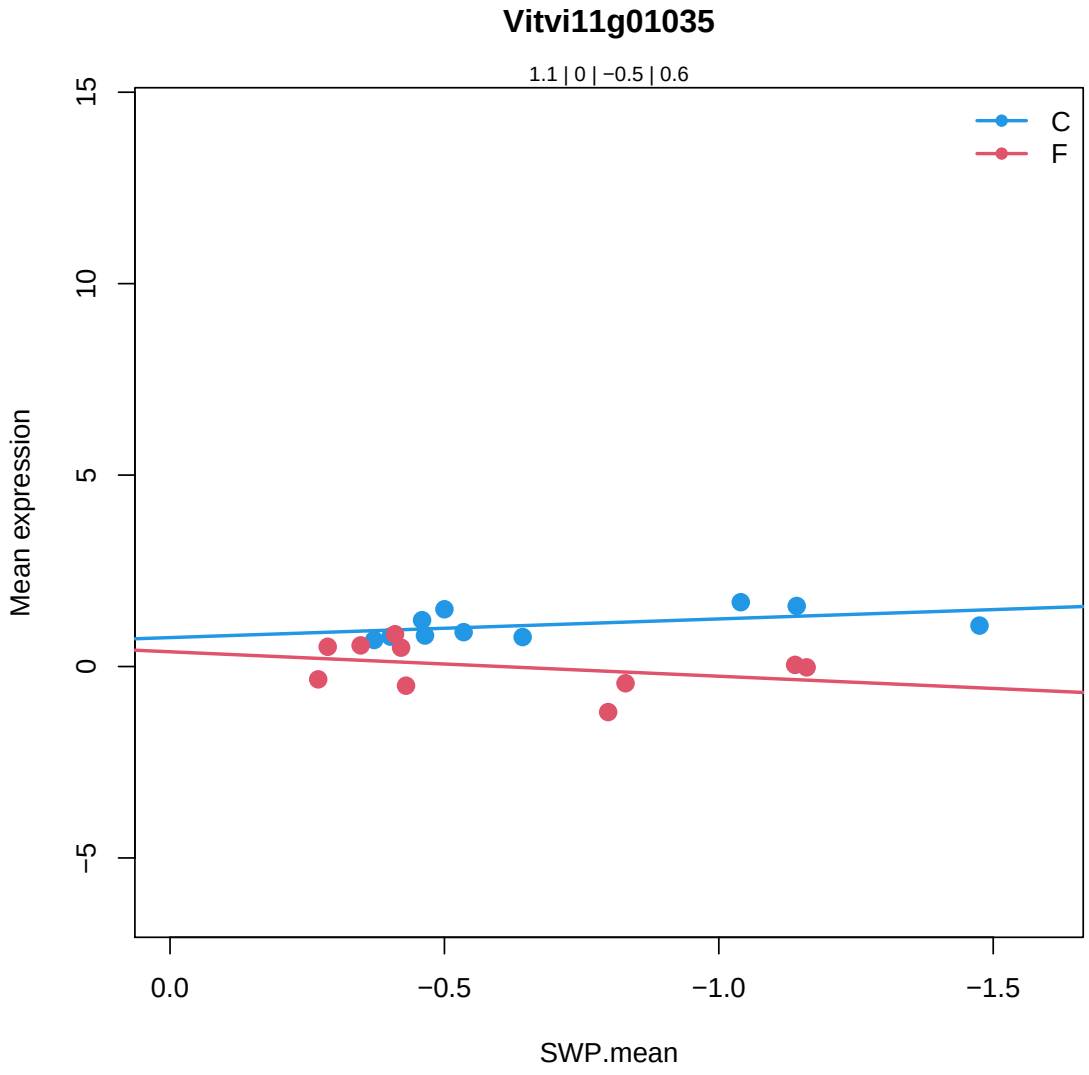
7.6.806 Vitvi11g01035: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g01035
        27.3.67
        RNA.regulation of transcription.putative transcription regulator
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr5:2941864-2943324 FORWARD LENGTH=409 |
        201606
```

Coefficients for Vitvi11g01035.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.098306	5.987994e-07	***	6.954888e-07	***
SlopeC	-0.4873226	0.2775446		0.7756987	
MeanF-MeanC	-1.102454	6.245191e-05	***	0.001200368	**
SlopeF-SlopeC	1.125635	0.09816708	.	0.9999488	



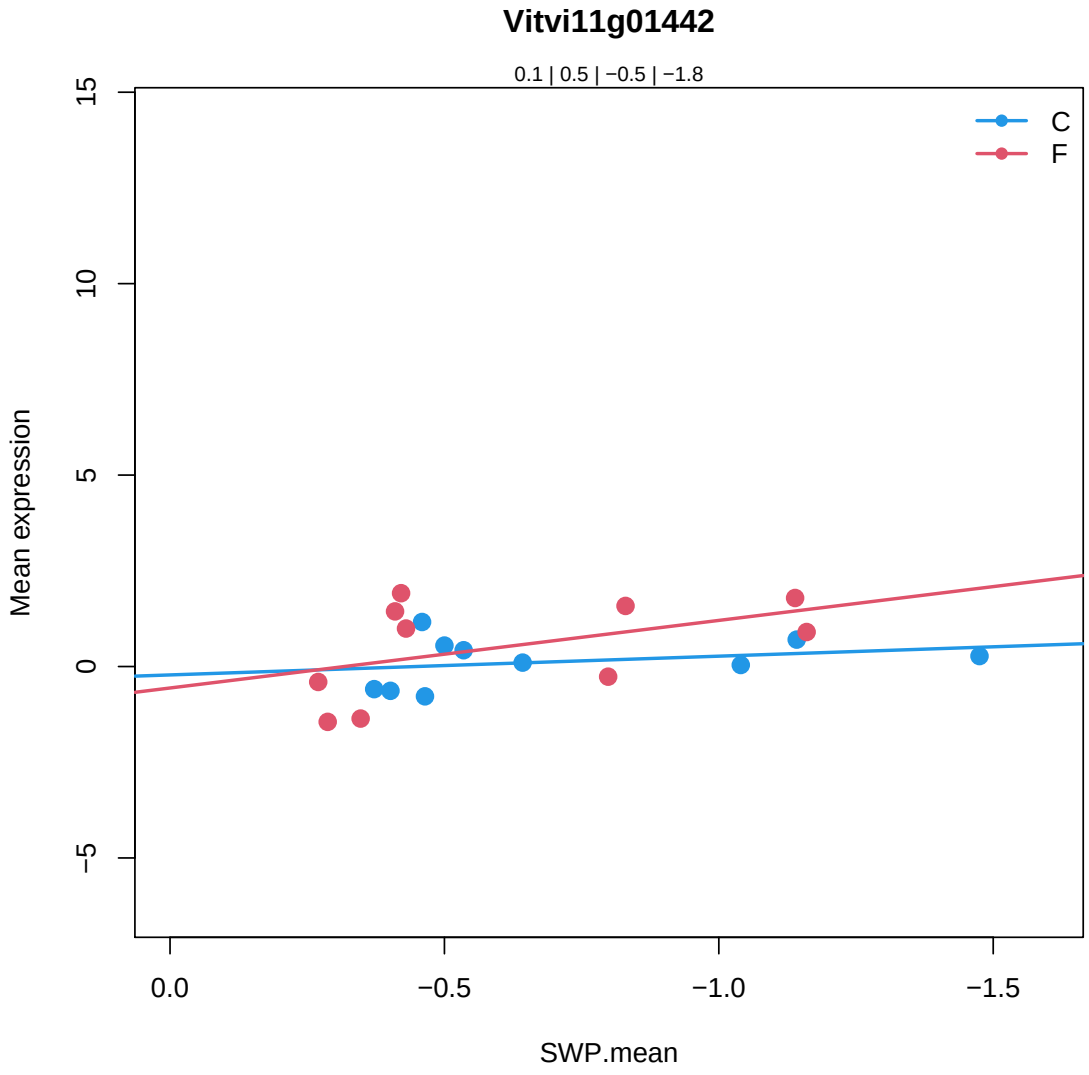
7.6.807 Vitvi11g01442: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g01442
        26.12
        misc.peroxidases
        peroxidase superfamily protein |
        Chr2:17296986-17298690 REVERSE LENGTH=328 |
        201606
```

Coefficients for Vitvi11g01442.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1247095	0.6532776		0.658157	
SlopeC	−0.4898251	0.5269377		0.8766422	
MeanF−MeanC	0.3898907	0.3251033		0.6853699	
SlopeF−SlopeC	−1.275414	0.2729539		0.9999488	



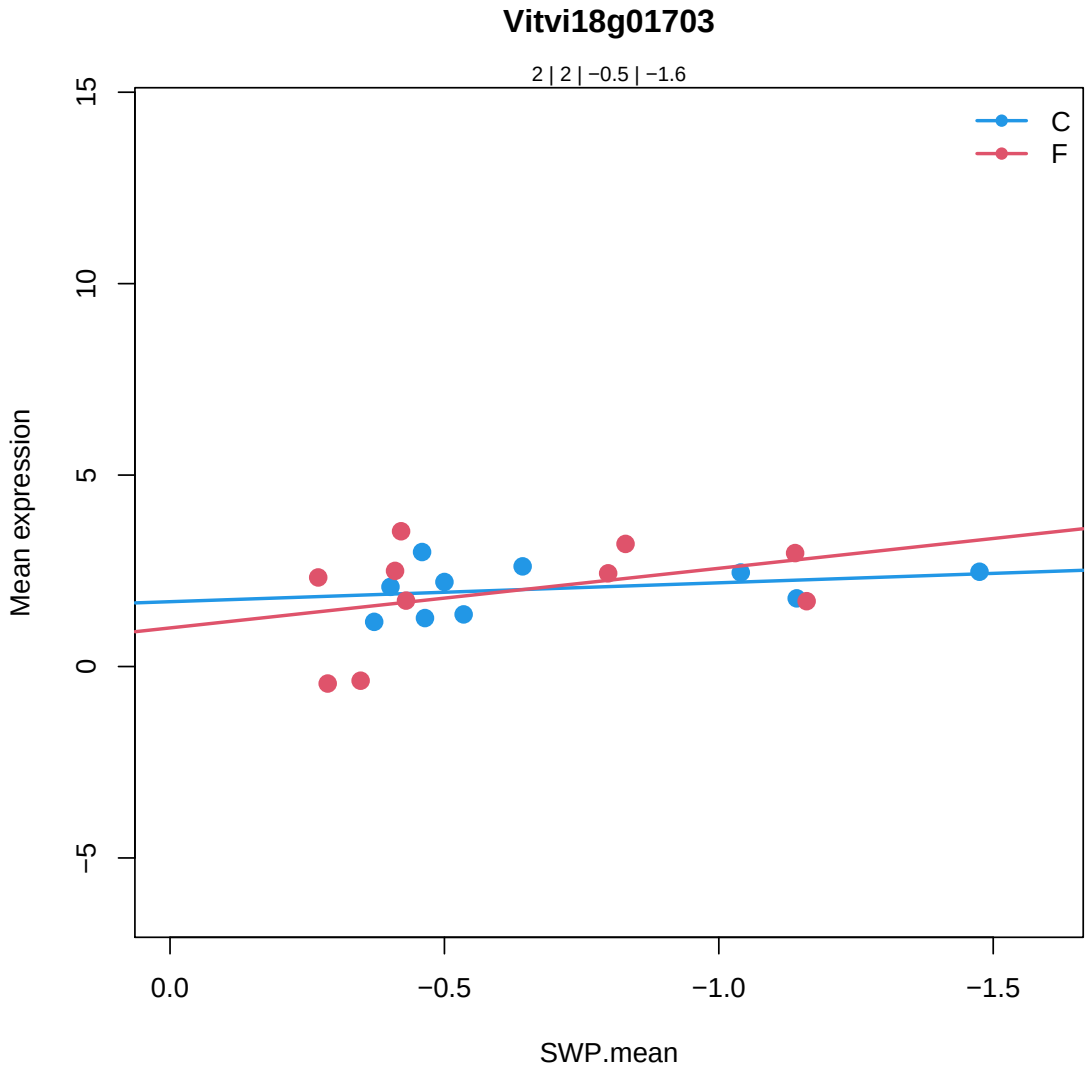
7.6.808 Vitvi18g01703: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g01703
        34.16
        transport.ABC transporters and multidrug resistance systems
        ATP-binding casette family G25 |
        Chr1:27082587-27088163 REVERSE LENGTH=662 |
        201606
```

Coefficients for Vitvi18g01703.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.03966	7.819745e-07	***	9.04863e-07	***
SlopeC	-0.4932996	0.5569834		0.8894103	
MeanF-MeanC	-0.08289888	0.8454864		0.959326	
SlopeF-SlopeC	-1.06371	0.3969233		0.9999488	



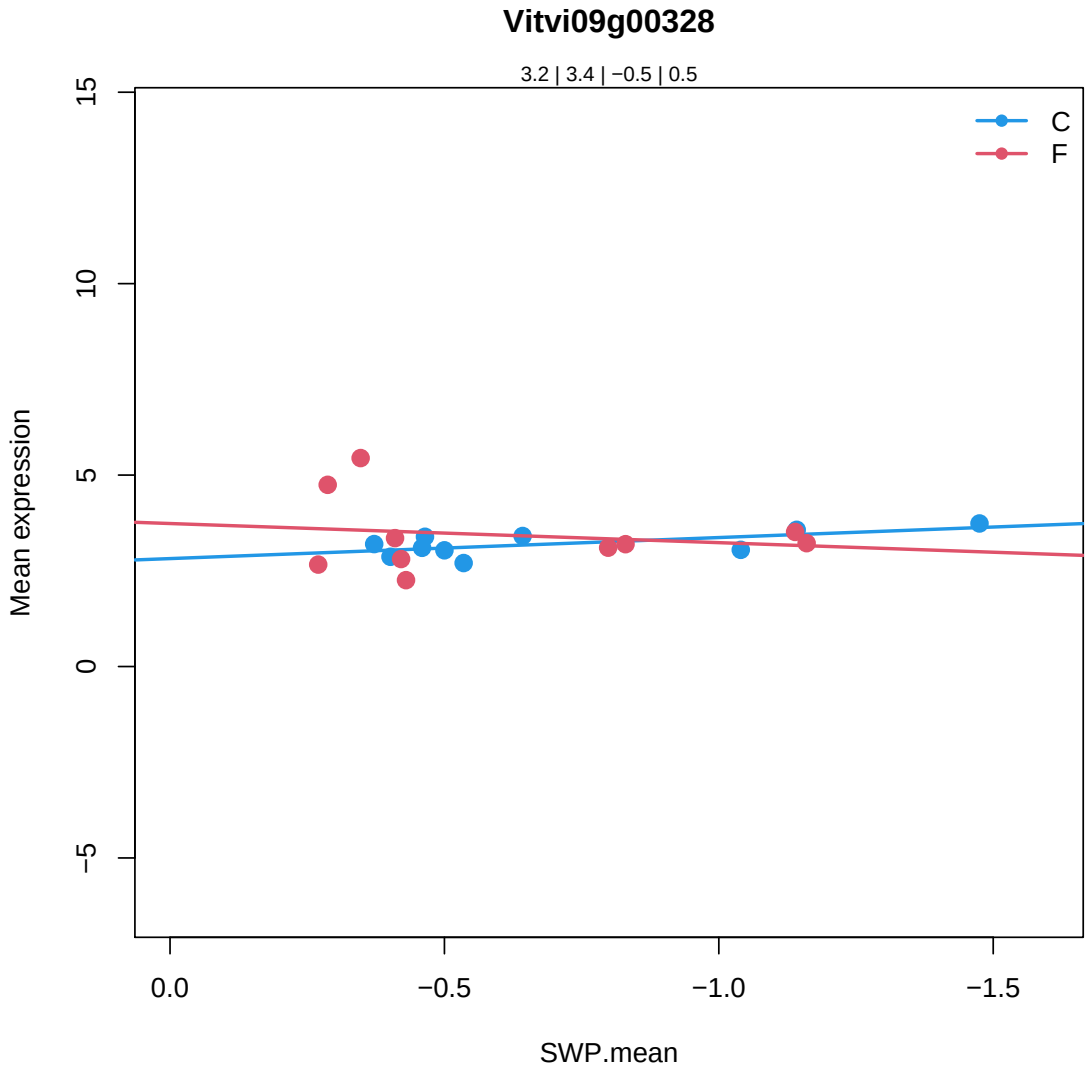
7.6.809 Vitvi09g00328: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00328
        1.1.5.2
        PS.lightreaction.other electron carrier (ox/red).ferredoxin
        NDH-dependent cyclic electron flow 1 |
        Chr3:5507091-5508320 REVERSE LENGTH=204 |
        201606
```

Coefficients for Vitvi09g00328.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.205232	8.766123e-13	***	1.262646e-12	***
SlopeC	-0.5494276	0.3691235		0.822541	
MeanF-MeanC	0.2249951	0.4678671		0.7877201	
SlopeF-SlopeC	1.049092	0.2521111		0.9999488	



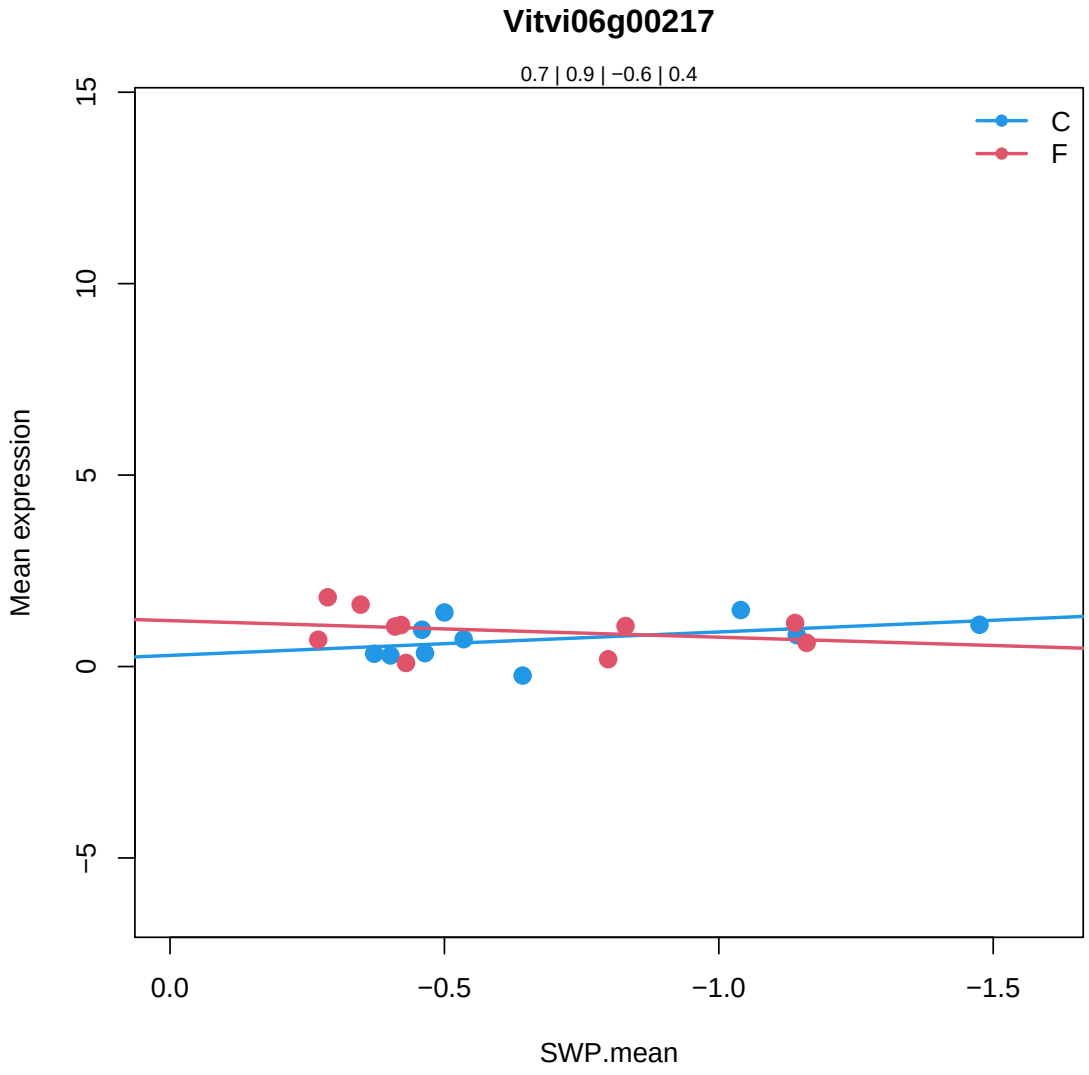
7.6.810 Vitvi06g00217: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00217
        35.2
        not assigned.unknown
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr2:16987269-16989851 FORWARD LENGTH=860 |
        201606
```

Coefficients for Vitvi06g00217.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.7205738	0.0002992223	***	0.0003271933	***
SlopeC	−0.6118045	0.2025609		0.7293041	
MeanF−MeanC	0.2141403	0.3754516		0.7282614	
SlopeF−SlopeC	1.044694	0.1461229		0.9999488	



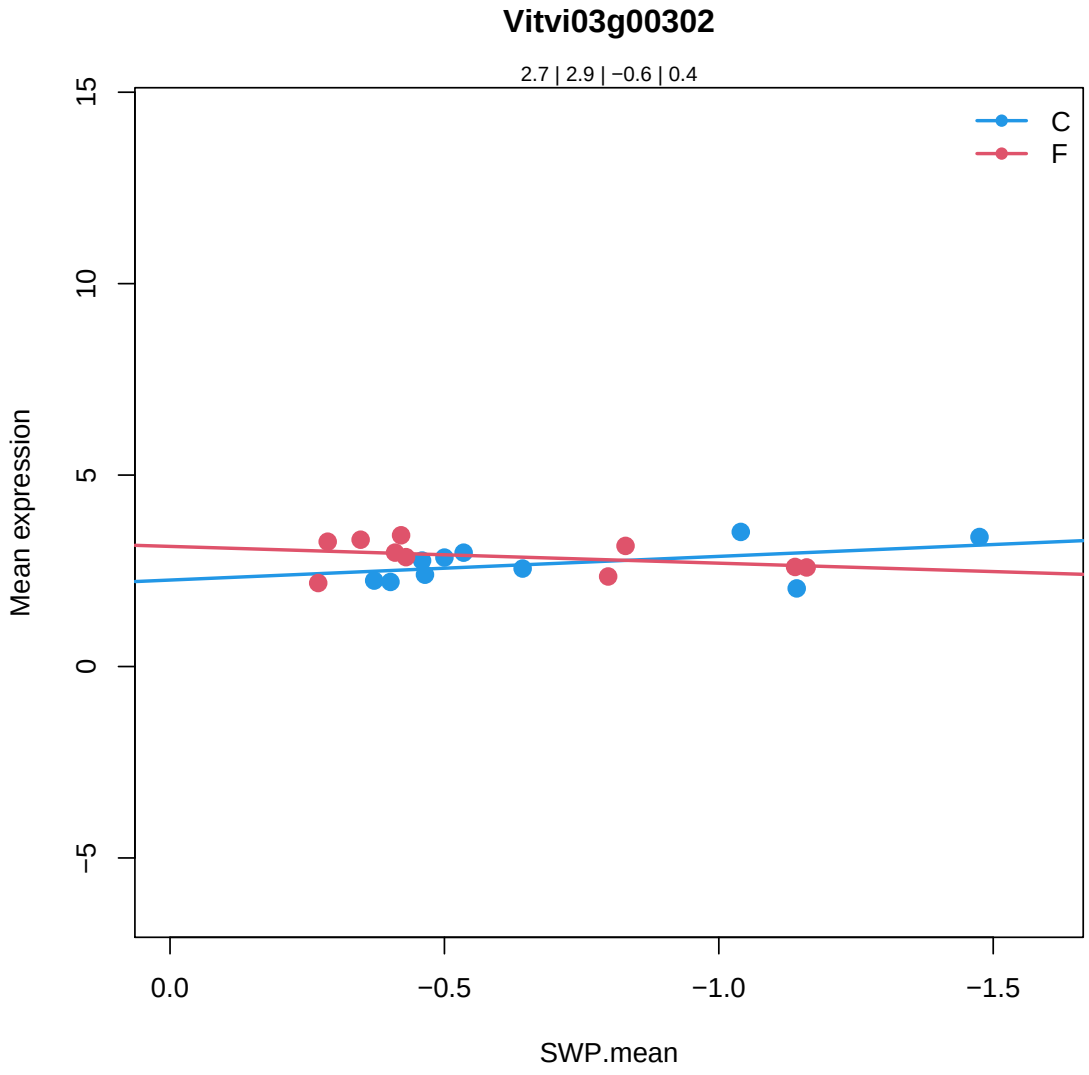
7.6.811 Vitvi03g00302: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00302
        29.2.1.2.1.25
        protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S25
        tRNA-methyltransferase non-catalytic subunit trm6MTase subunit |
        Chr5:26530274-26531032 REVERSE LENGTH=252 |
        201606
```

Coefficients for Vitvi03g00302.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.693274	9.972177e-15	***	1.666988e-14	***
SlopeC	-0.6187677	0.1384951		0.6650191	
MeanF-MeanC	0.1767917	0.3966704		0.7426604	
SlopeF-SlopeC	1.056953	0.09163842	.	0.9999488	



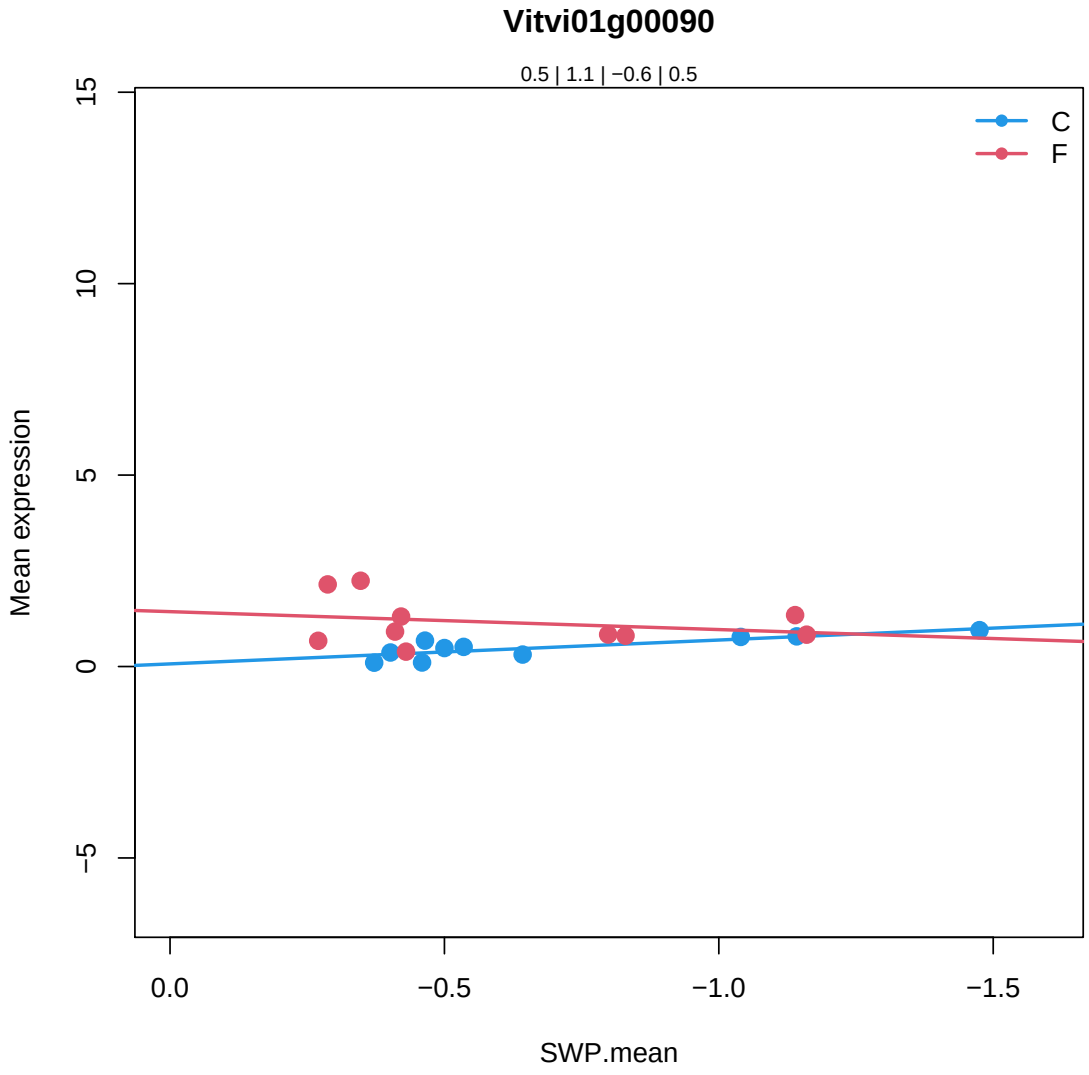
7.6.812 Vitvi01g00090: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00090
        35.2
        not assigned.unknown
        translocator assembly/maintenance protein |
        Chr3:17563254-17565162 REVERSE LENGTH=332 |
        201606
```

Coefficients for Vitvi01g00090.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.5064992	0.002629639	**	0.002819823	**
SlopeC	−0.6231258	0.1471112		0.6736918	
MeanF−MeanC	0.6412401	0.006053254	**	0.05242256	.
SlopeF−SlopeC	1.091169	0.09098574	.	0.9999488	



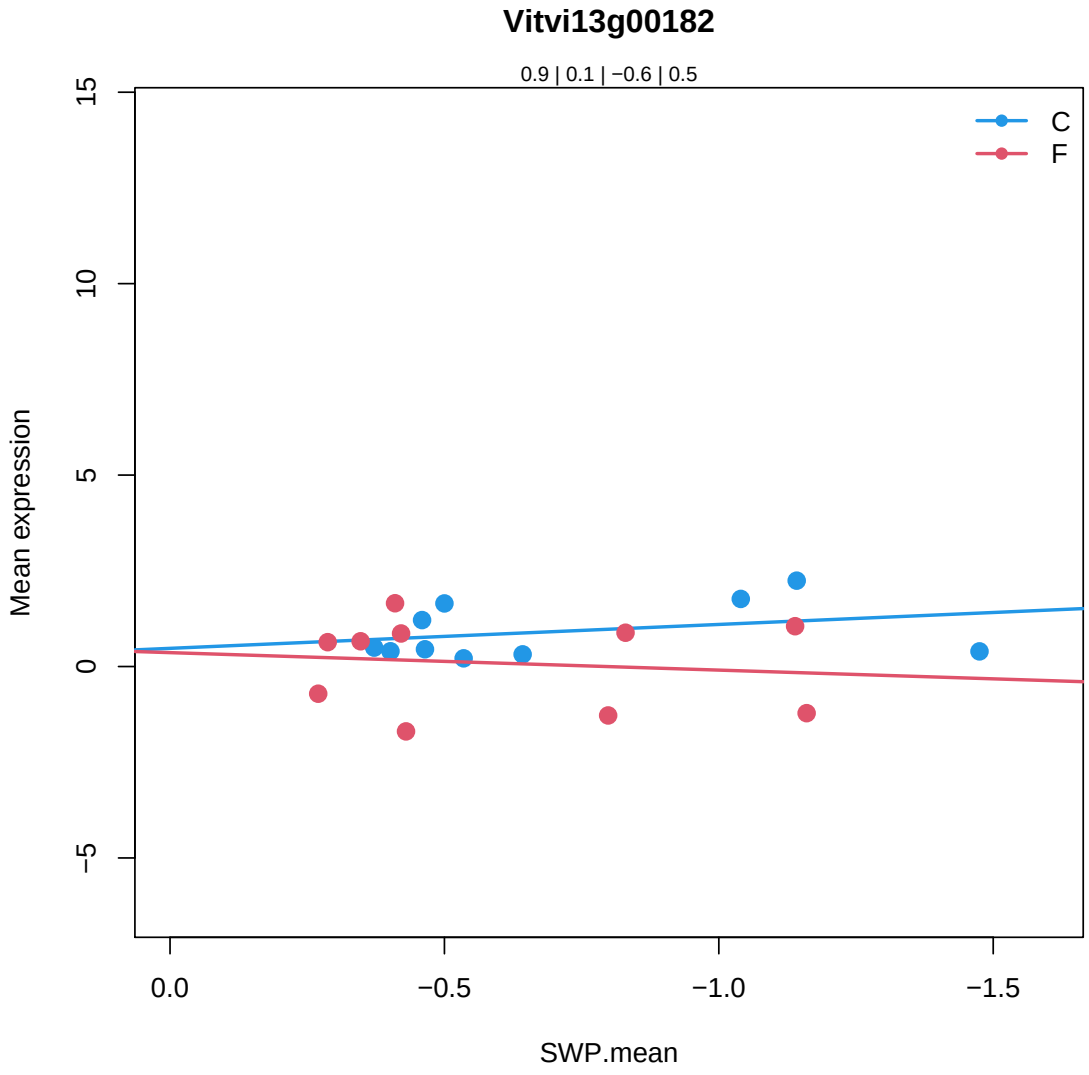
7.6.813 Vitvi13g00182: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00182
        30.2.7
        signalling.receptor kinases.leucine rich repeat VII
        Leucine-rich repeat protein kinase family protein |
        Chr3:20899403-20902390 REVERSE LENGTH=964 |
        201606
```

Coefficients for Vitvi13g00182.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.9135345	0.004809755	**	0.005131977	**
SlopeC	−0.6243269	0.4482982		0.8555685	
MeanF−MeanC	−0.8292117	0.05625157	.	0.2580935	
SlopeF−SlopeC	1.080246	0.3791869		0.9999488	



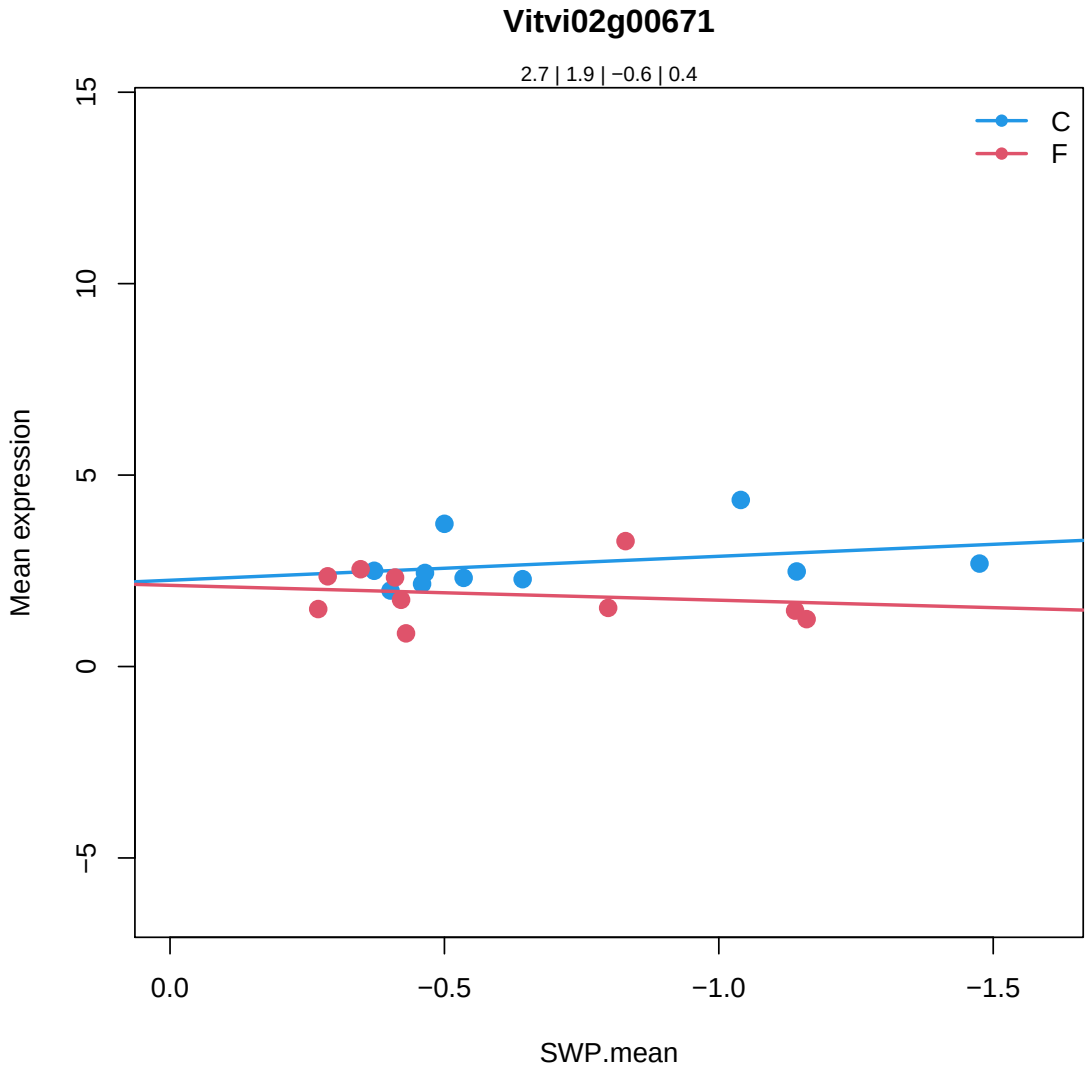
7.6.814 Vitvi02g00671: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00671
        35.2
        not assigned.unknown
        aluminum-activated%2C malate transporter 12 |
        Chr4:9975482-9977722 FORWARD LENGTH=560 |
        201606
```

Coefficients for Vitvi02g00671.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.69311	3.938247e-11	***	5.238851e-11	***
SlopeC	-0.6255577	0.3189161		0.7966107	
MeanF-MeanC	-0.809675	0.01661267	*	0.109805	
SlopeF-SlopeC	1.01416	0.2786758		0.9999488	



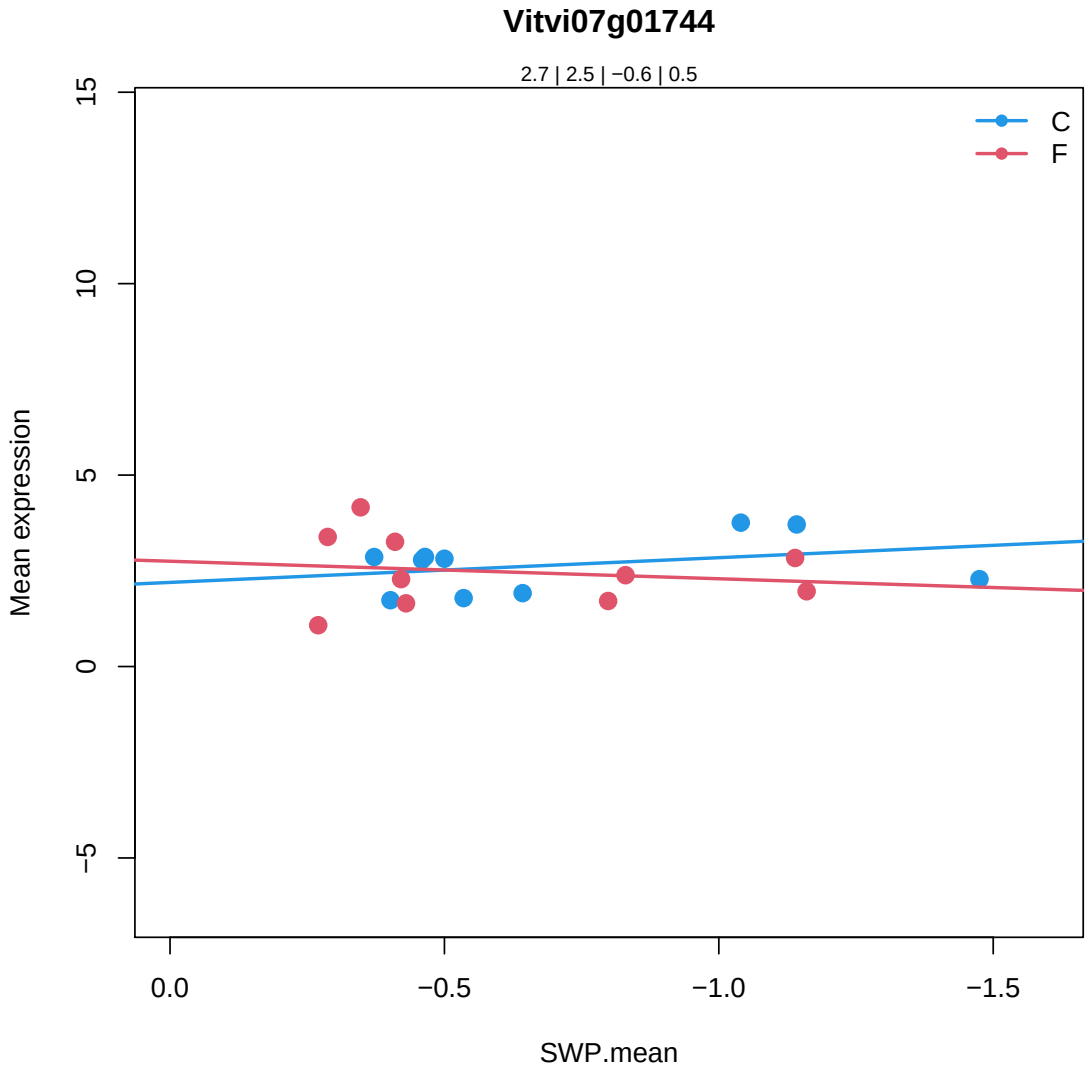
7.6.815 Vitvi07g01744: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01744
        27.3.99
        RNA.regulation of transcription.unclassified
        Remorin family protein |
        Chr1:17130703-17133548 REVERSE LENGTH=555 |
        201606
```

Coefficients for Vitvi07g01744.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.650544	4.819122e-10	***	6.144129e-10	***
SlopeC	-0.6457322	0.3602099		0.8183149	
MeanF-MeanC	-0.1798307	0.6137169		0.8664039	
SlopeF-SlopeC	1.103491	0.2949754		0.9999488	



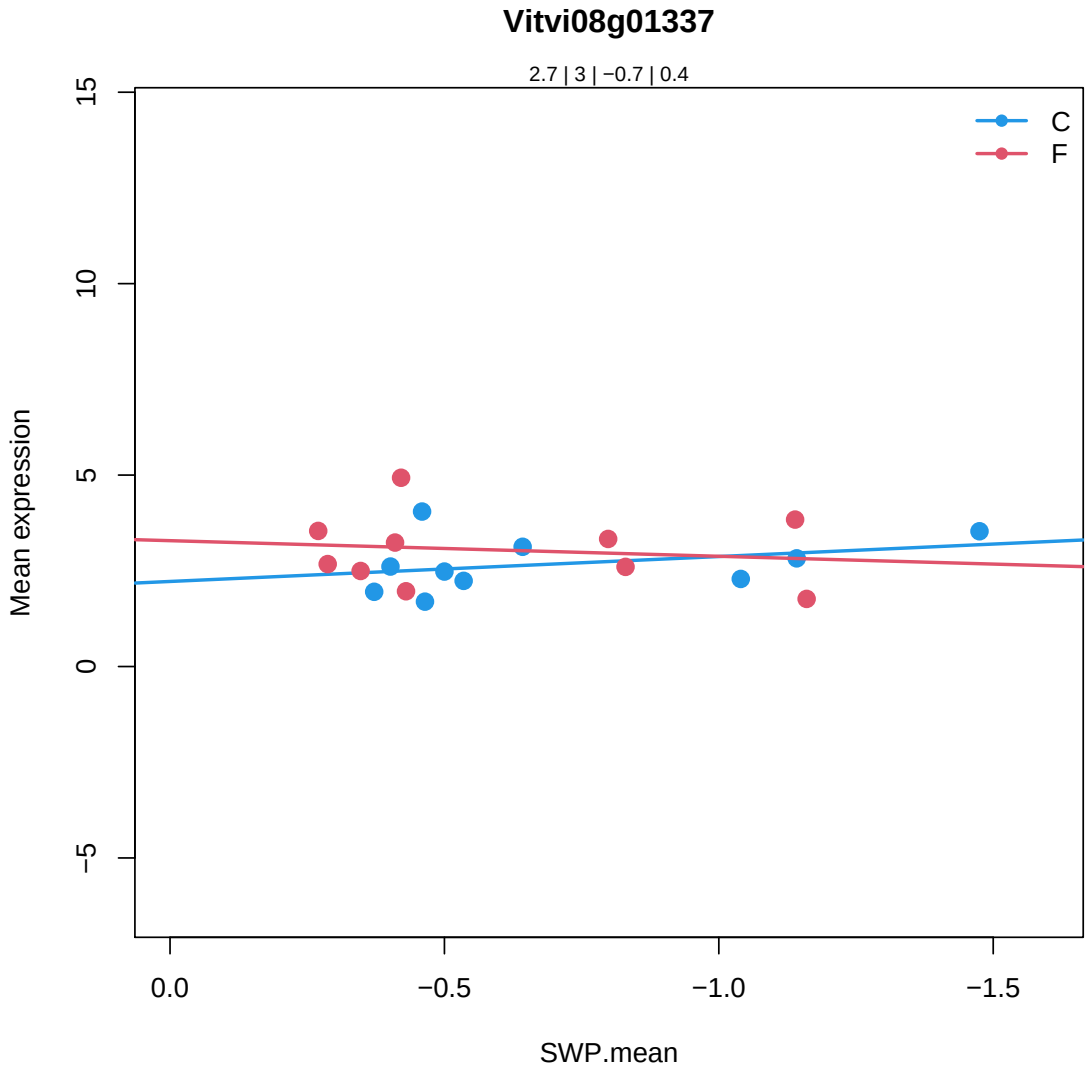
7.6.816 Vitvi08g01337: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01337
        16
        secondary metabolism
        HXXXD-type acyl-transferase family protein |
        Chr5:84554-85981 FORWARD LENGTH=475 |
        201606
```

Coefficients for Vitvi08g01337.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.679353	4.144586e-10	***	5.298313e-10	***
SlopeC	-0.651164	0.3574564		0.8183149	
MeanF-MeanC	0.3589656	0.3191372		0.6800376	
SlopeF-SlopeC	1.058533	0.3157887		0.9999488	



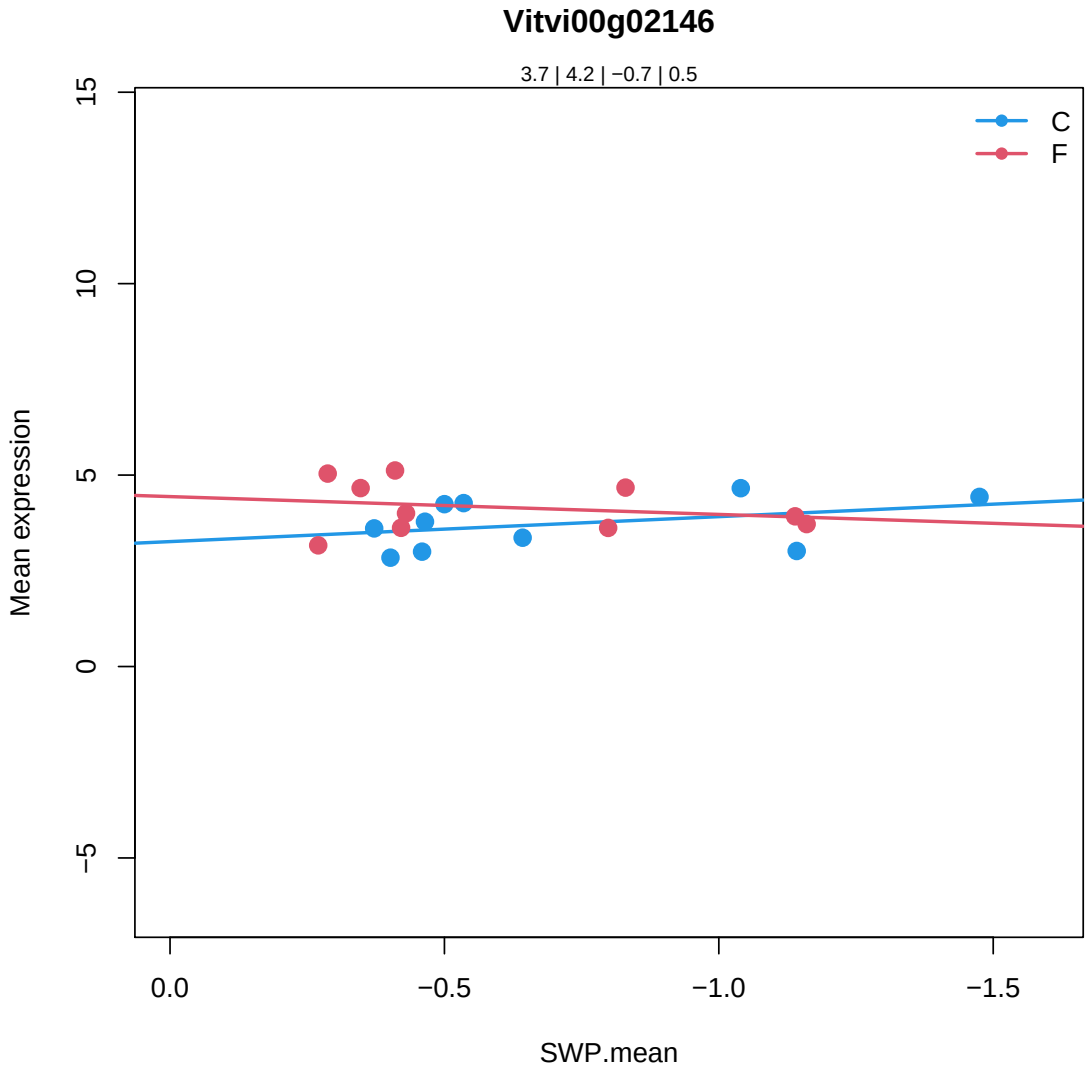
7.6.817 Vitvi00g02146: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi00g02146
        33.99
        development.unspecified
        phytosulfokine 4 precursor |
        Chr3:18465750-18466254 FORWARD LENGTH=79 |
        201606
```

Coefficients for Vitvi00g02146.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.720953	8.948435e-15	***	1.503937e-14	***
SlopeC	-0.6518096	0.2511105		0.7618555	
MeanF-MeanC	0.4334658	0.1374281		0.4436001	
SlopeF-SlopeC	1.117515	0.1883597		0.9999488	



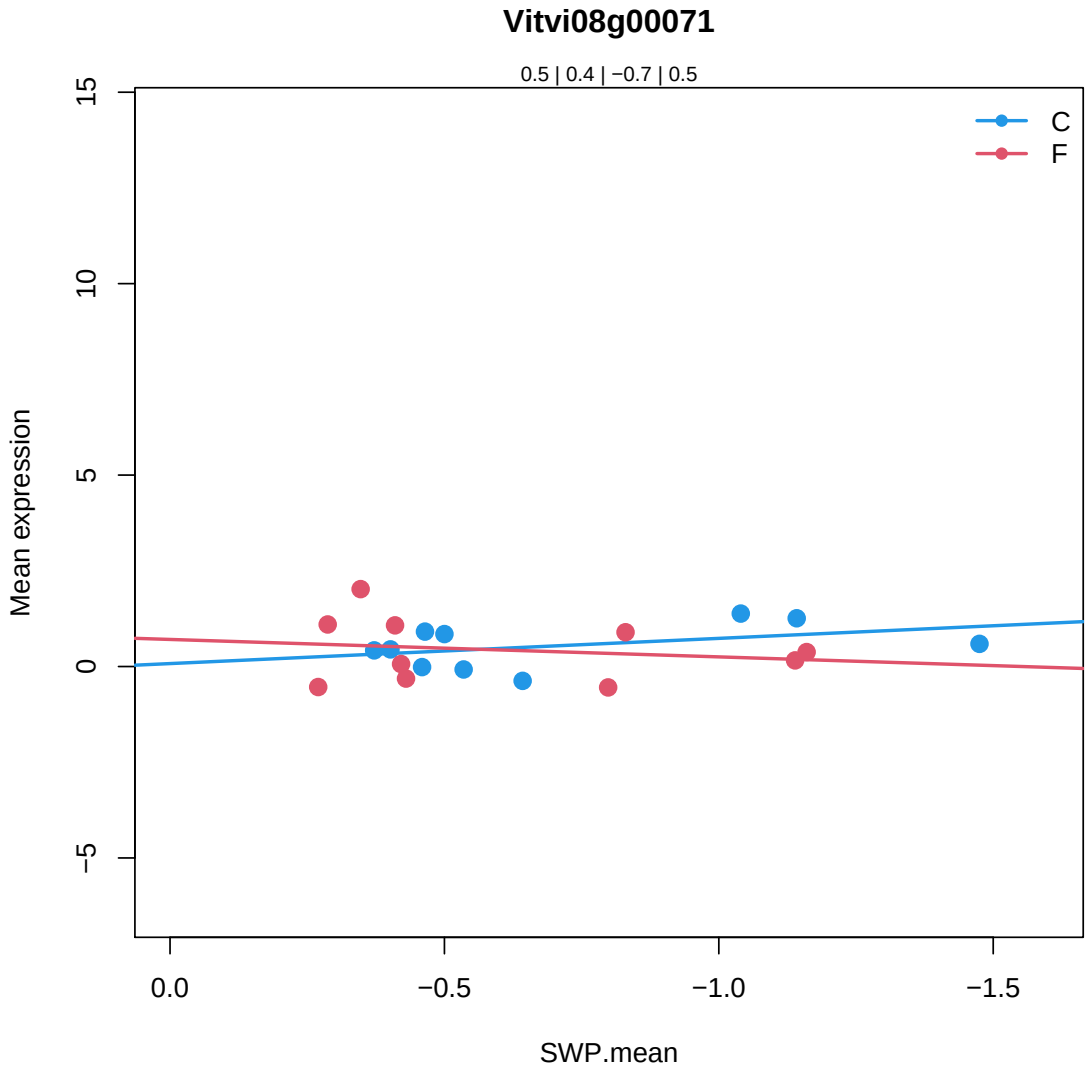
7.6.818 Vitvi08g00071: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g00071
        13.1.5.3.1
        amino acid metabolism.synthesis.serine-glycine-cysteine group.cysteine
        cysteine synthase 26 |
        Chr3:878388-880400 REVERSE LENGTH=404 |
        201606
```

Coefficients for Vitvi08g00071.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.5395038	0.01956772	*	0.02057614	*
SlopeC	−0.6581636	0.2807653		0.7773135	
MeanF−MeanC	−0.1100505	0.7194378		0.9141106	
SlopeF−SlopeC	1.113877	0.2218508		0.9999488	



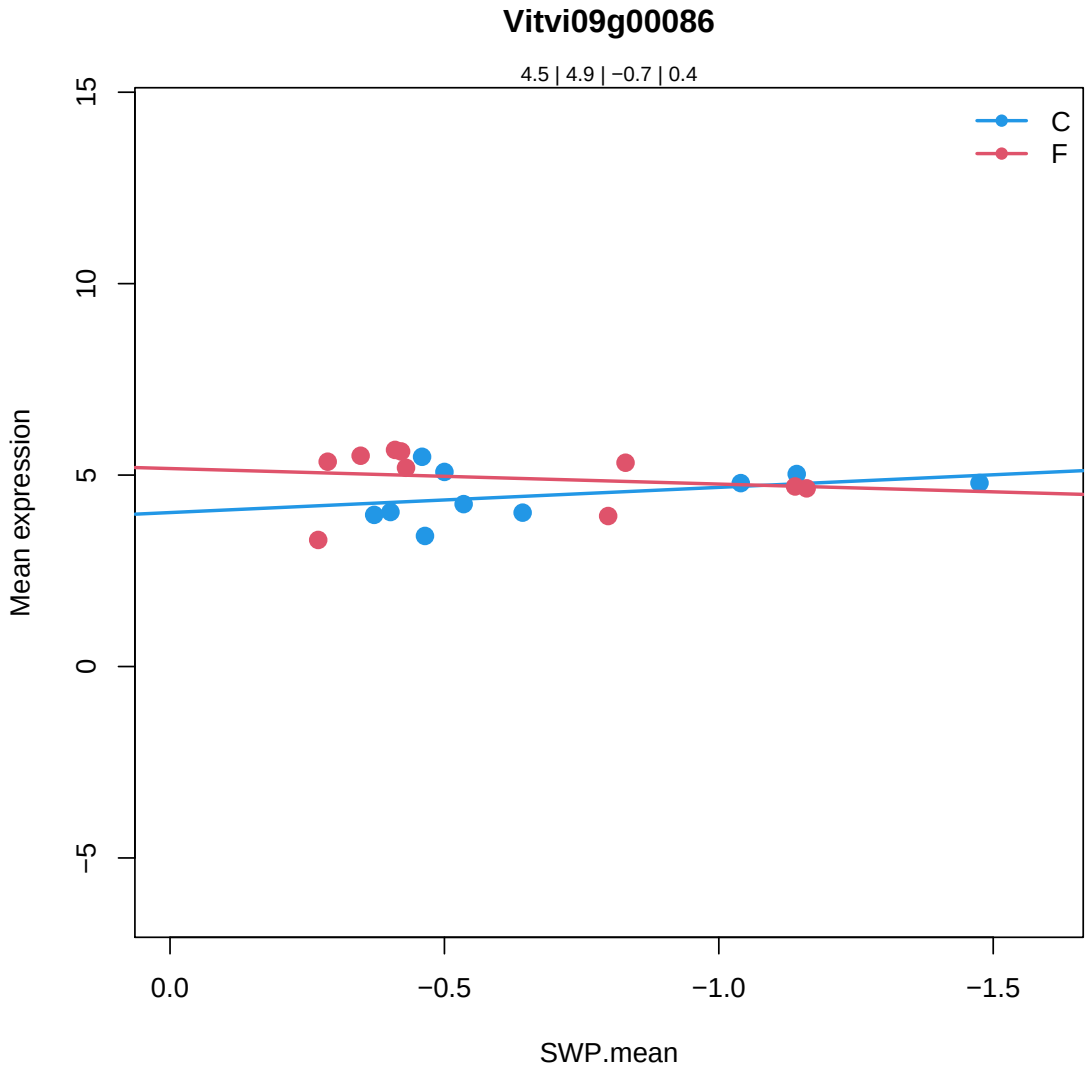
7.6.819 Vitvi09g00086: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00086
        26.10
        misc.cytochrome P450
        cytochrome P450%2C family 76%2C subfamily C%2C polypeptide 4 |
        Chr2:18773541-18775654 REVERSE LENGTH=511 |
        201606
```

Coefficients for Vitvi09g00086.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.483676	8.993579e-16	***	1.693602e-15	***
SlopeC	-0.6581727	0.2808115		0.7773135	
MeanF-MeanC	0.4396261	0.1604694		0.4841107	
SlopeF-SlopeC	1.063618	0.2427415		0.9999488	



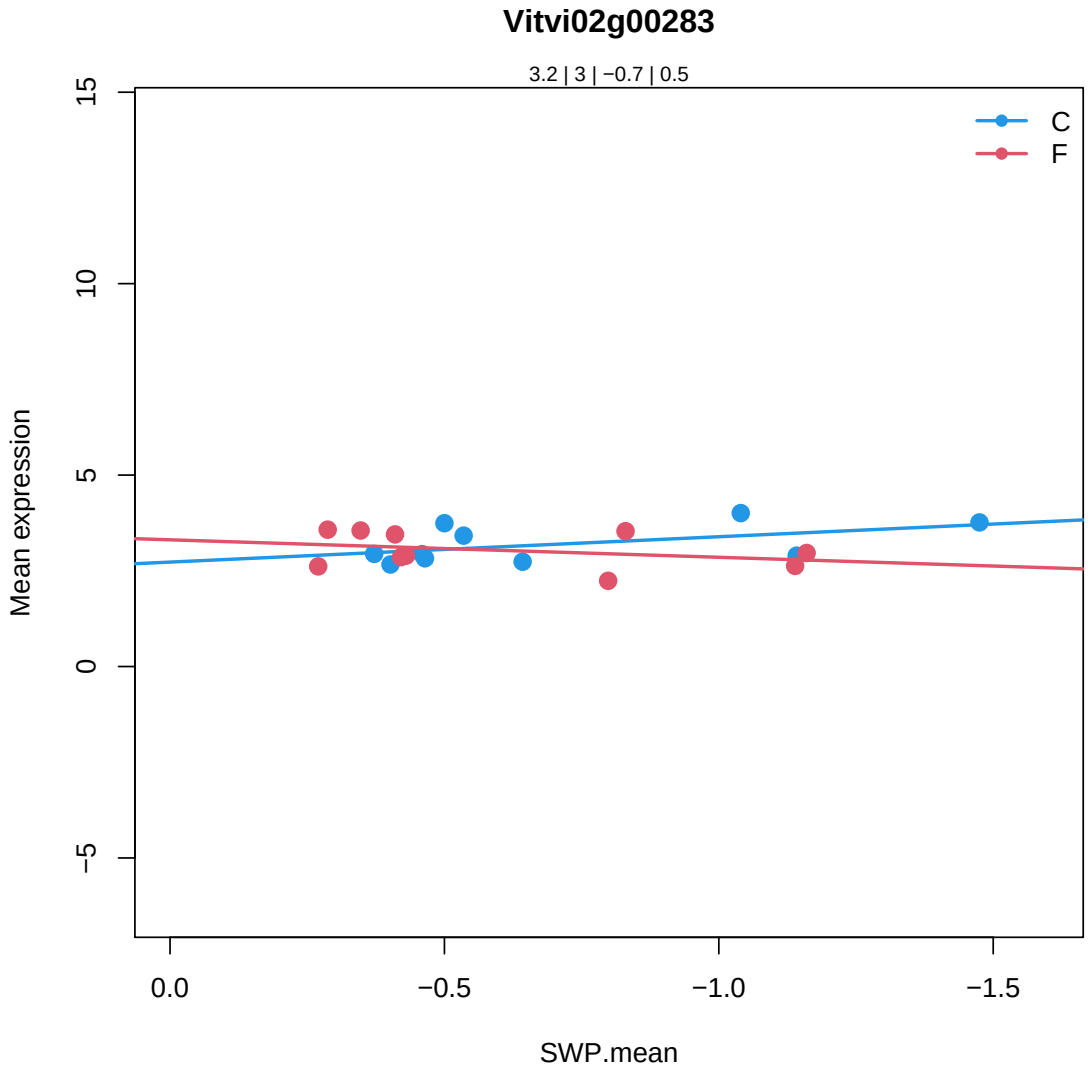
7.6.820 Vitvi02g00283: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00283
        16.2.1.10
        secondary metabolism.phenylpropanoids.lignin biosynthesis.CAD
        cinnamyl-alcohol dehydrogenase |
        Chr1:27359346-27360876 REVERSE LENGTH=355 |
        201606
```

Coefficients for Vitvi02g00283.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.193054	5.209794e-16	***	1.012078e-15	***
SlopeC	-0.6621416	0.1230922		0.644269	
MeanF-MeanC	-0.1618892	0.4485148		0.7774043	
SlopeF-SlopeC	1.118383	0.08250609	.	0.9999488	



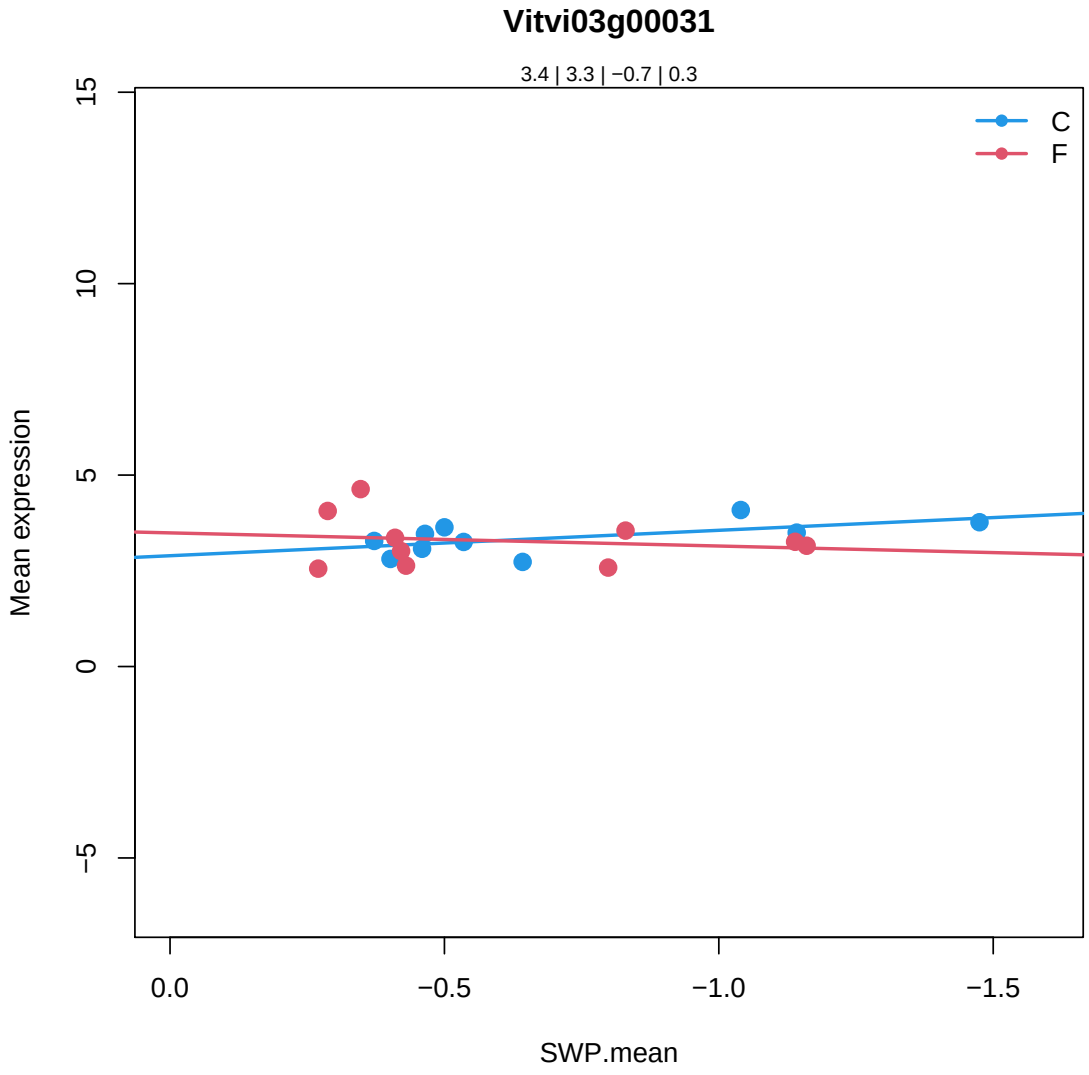
7.6.821 Vitvi03g00031: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00031
        35.2
        not assigned.unknown
        RNA-binding CRS1 / YhbY (CRM) domain protein |
        Chr2:9136451-9137267 REVERSE LENGTH=222 |
        201606
```

Coefficients for Vitvi03g00031.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.36035	3.257116e-15	***	5.763288e-15	***
SlopeC	-0.6639908	0.1762957		0.7089139	
MeanF-MeanC	-0.07934242	0.7455531		0.9251584	
SlopeF-SlopeC	1.007253	0.1684808		0.9999488	



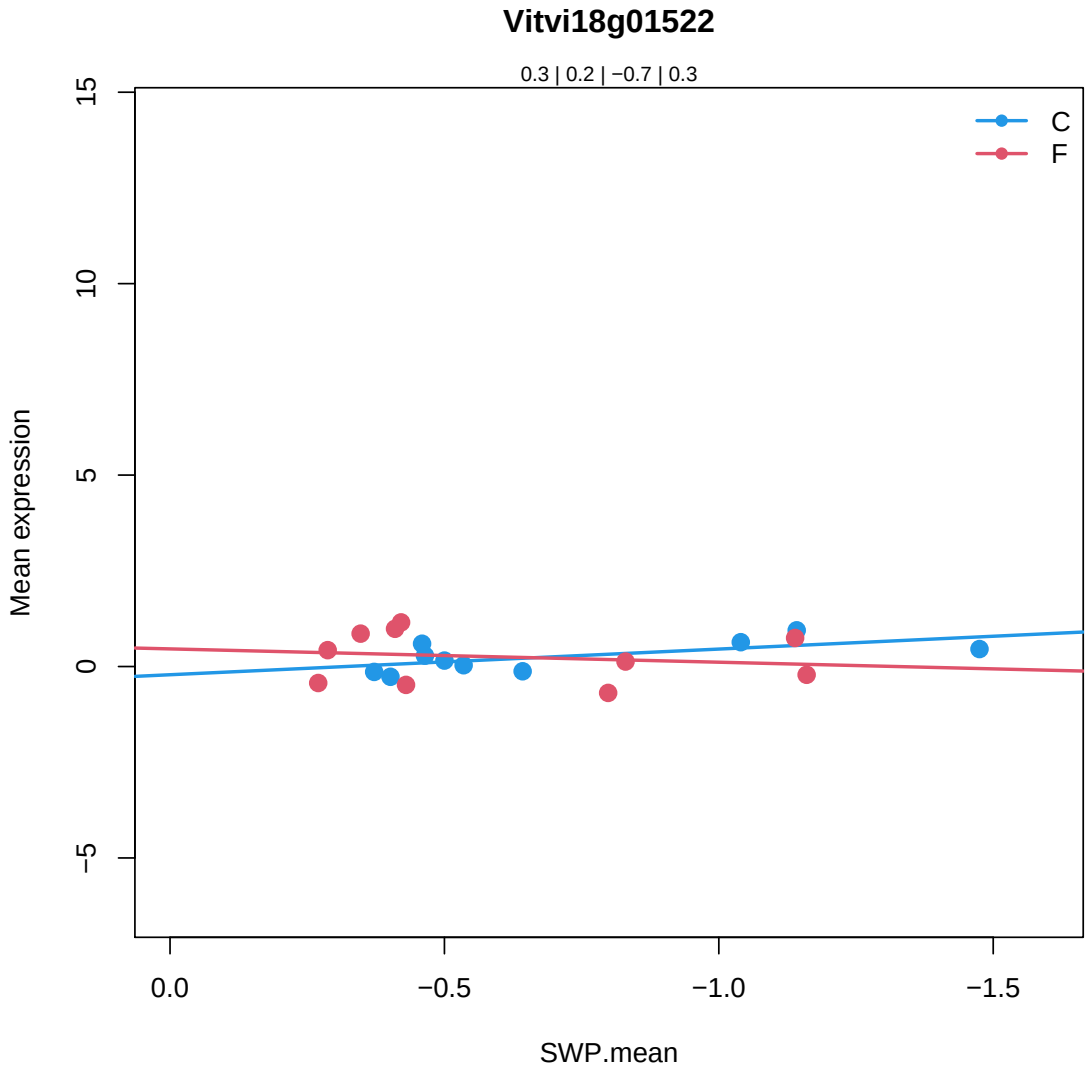
7.6.822 Vitvi18g01522: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g01522
        11.8.1
        lipid metabolism.exotics (steroids, squalene etc).sphingolipids
        sphingoid base hydroxylase 1 |
        Chr1:26193933-26195466 REVERSE LENGTH=260 |
        201606
```

Coefficients for Vitvi18g01522.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.256735	0.1432675		0.1475461	
SlopeC	-0.6701831	0.1683718		0.6981292	
MeanF-MeanC	-0.008505994	0.9719338		0.9934113	
SlopeF-SlopeC	1.017842	0.1602289		0.9999488	



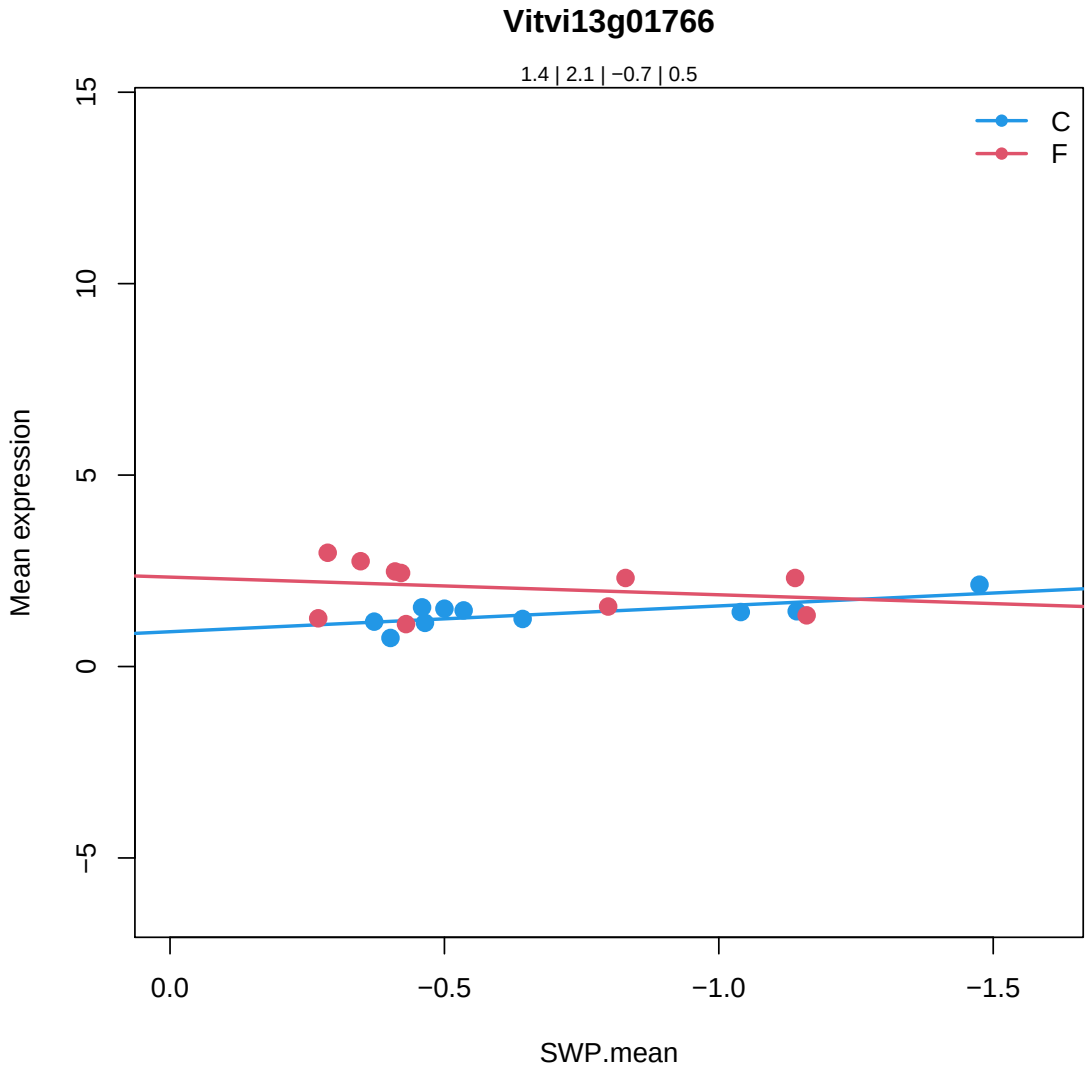
7.6.823 Vitvi13g01766: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g01766
        26.10
        misc.cytochrome P450
        cytochrome P450%2C family 705%2C subfamily A%2C polypeptide 21 |
        Chr3:7024576-7025789 FORWARD LENGTH=378 |
        201606
```

Coefficients for Vitvi13g01766.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.382262	2.809743e-08	***	3.383055e-08	***
SlopeC	-0.6742275	0.1524695		0.6839811	
MeanF-MeanC	0.6718169	0.008290653	**	0.06627451	.
SlopeF-SlopeC	1.135361	0.1077601		0.9999488	



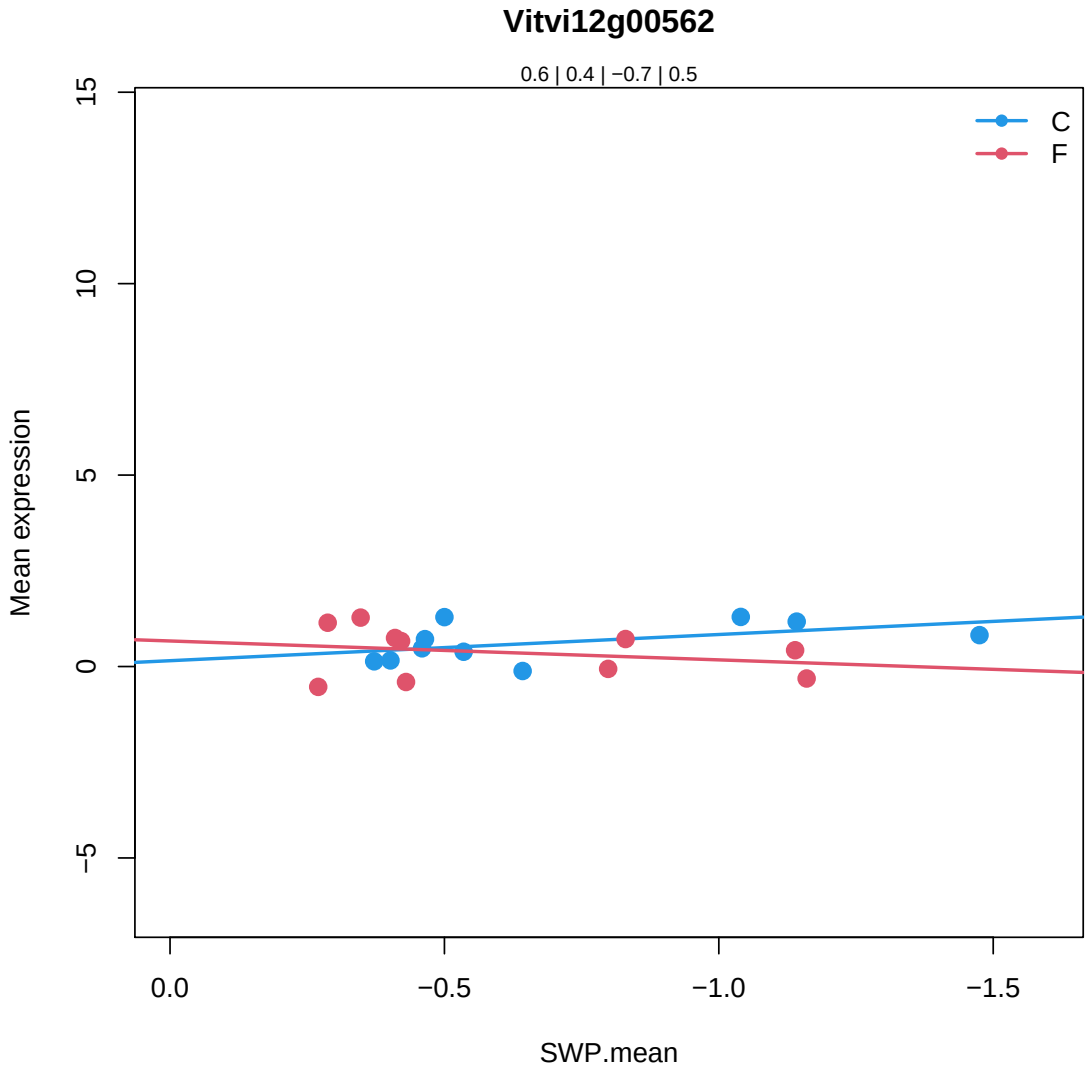
7.6.824 Vitvi12g00562: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00562
        35.1.27
        not assigned.no ontology.tetratricopeptide repeat (TPR)
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr4:17572040-17573938 REVERSE LENGTH=632 |
        201606
```

Coefficients for Vitvi12g00562.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6329572	0.001618867	**	0.001745486	**
SlopeC	-0.6843264	0.1754512		0.7085966	
MeanF-MeanC	-0.2667986	0.2944463		0.661003	
SlopeF-SlopeC	1.1776	0.1198321		0.9999488	



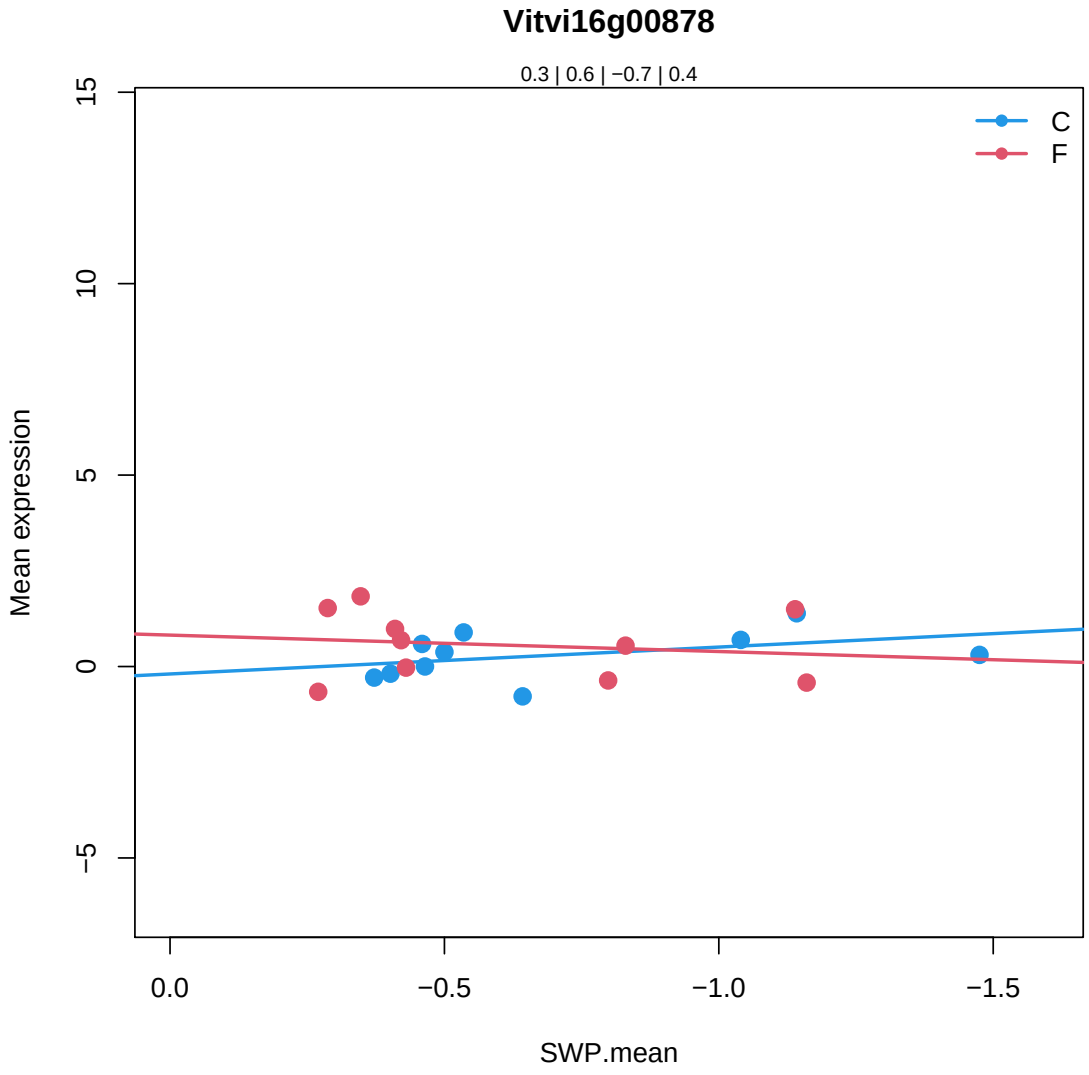
7.6.825 Vitvi16g00878: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g00878
        29.5.1
        protein.degradation.subtilases
        subtilase 1.3 |
        Chr5:21020266-21022608 FORWARD LENGTH=780 |
        201606
```

Coefficients for Vitvi16g00878.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.2991344	0.2077812		0.2128933	
SlopeC	−0.7020389	0.2853722		0.7782707	
MeanF−MeanC	0.2604023	0.4327553		0.766636	
SlopeF−SlopeC	1.130575	0.2487823		0.9999488	



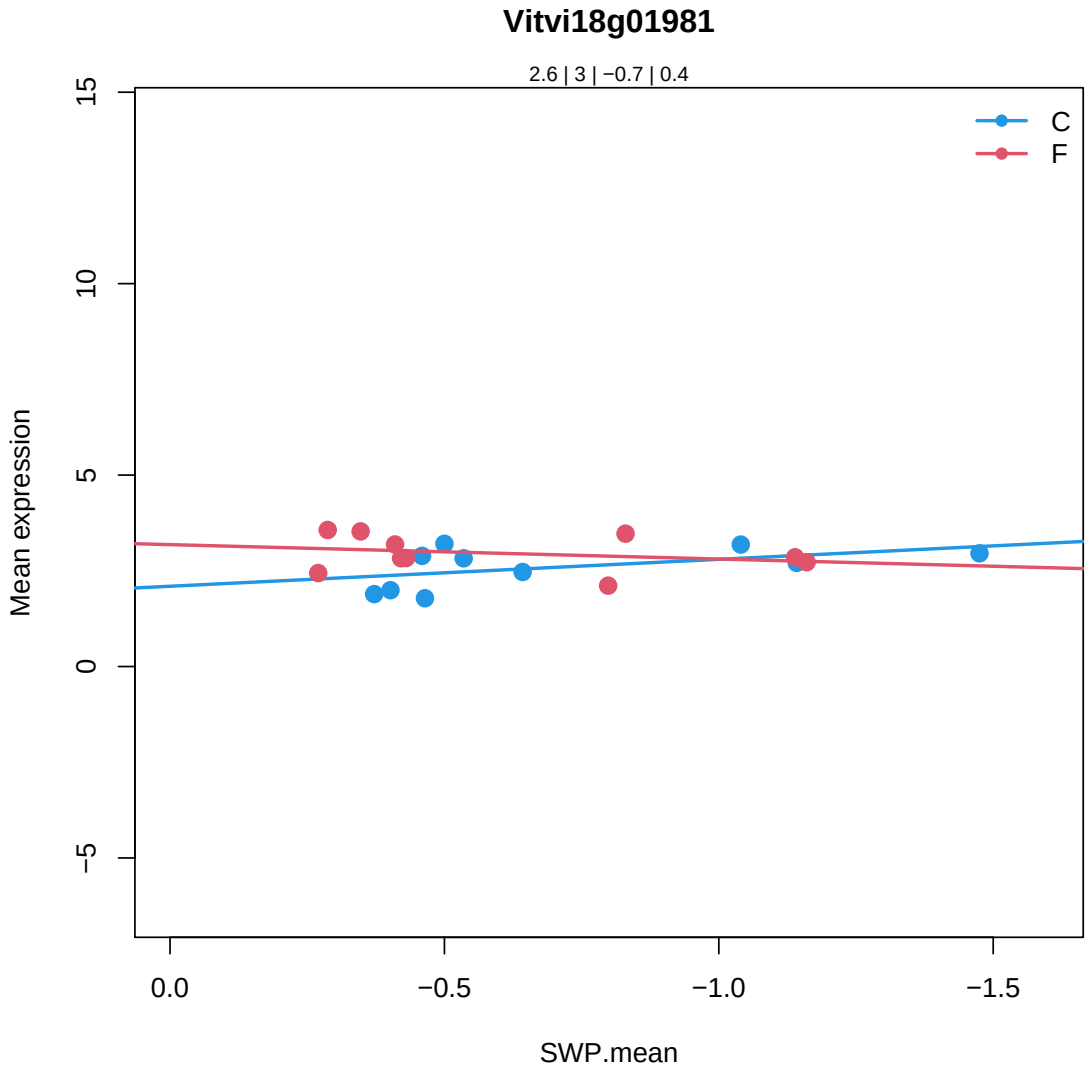
7.6.826 Vitvi18g01981: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g01981
        34.13
        transport.peptides and oligopeptides
        Major facilitator superfamily protein |
        Chr1:27134168-27136257 FORWARD LENGTH=561 |
        201606
```

Coefficients for Vitvi18g01981.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.590461	8.872203e-14	***	1.367342e-13	***
SlopeC	-0.7030808	0.1175654		0.6341652	
MeanF-MeanC	0.3637257	0.1115585		0.3895474	
SlopeF-SlopeC	1.079582	0.1070202		0.9999488	



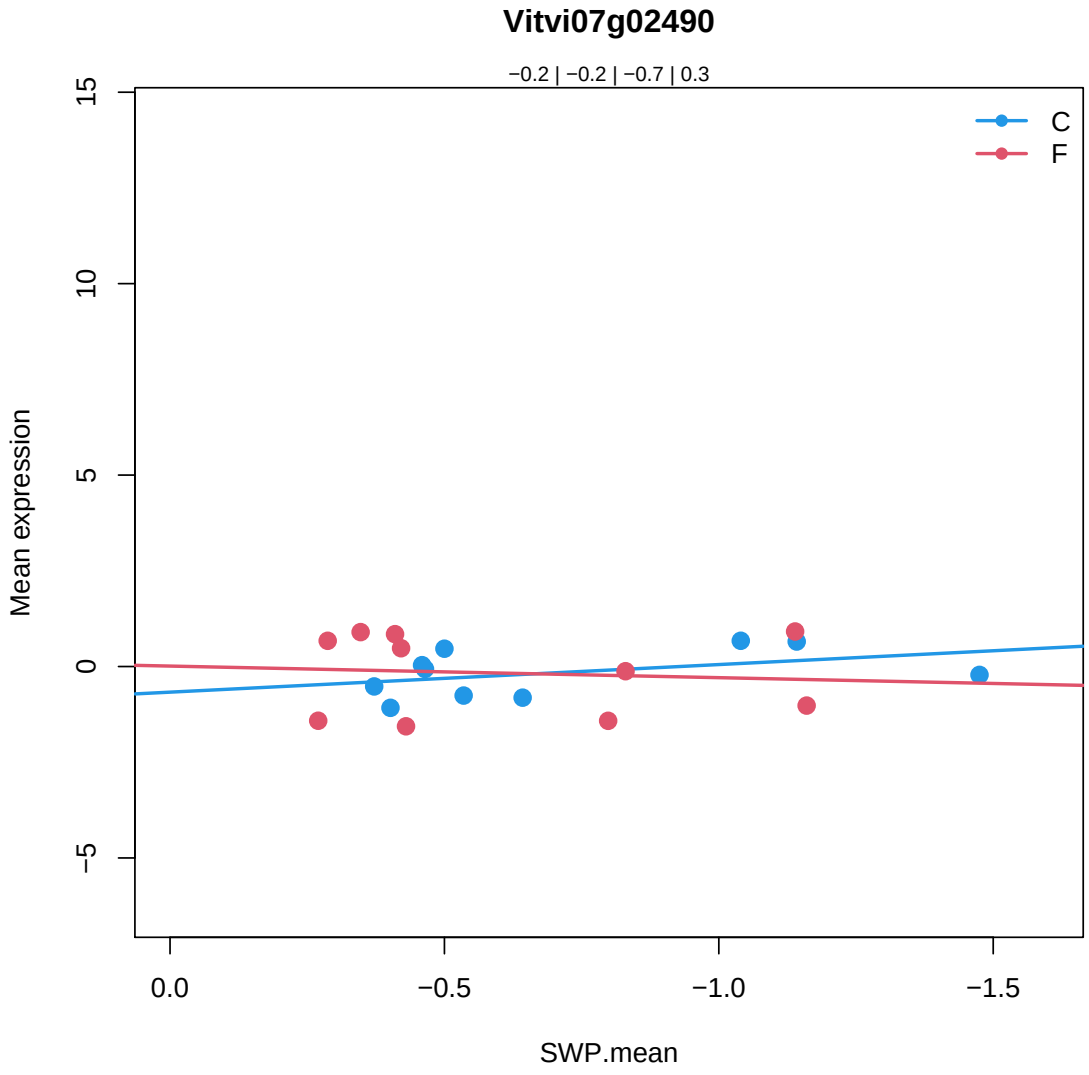
7.6.827 Vitvi07g02490: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g02490
        35.2
        not assigned.unknown
        formin homology 1 |
        Chr3:9251320-9254826 REVERSE LENGTH=1051 |
        201606
```

Coefficients for Vitvi07g02490.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.1629507	0.5353245		0.5412189	
SlopeC	-0.7206479	0.3277459		0.8001767	
MeanF-MeanC	-0.01023589	0.977933		0.9944396	
SlopeF-SlopeC	1.023365	0.3499494		0.9999488	



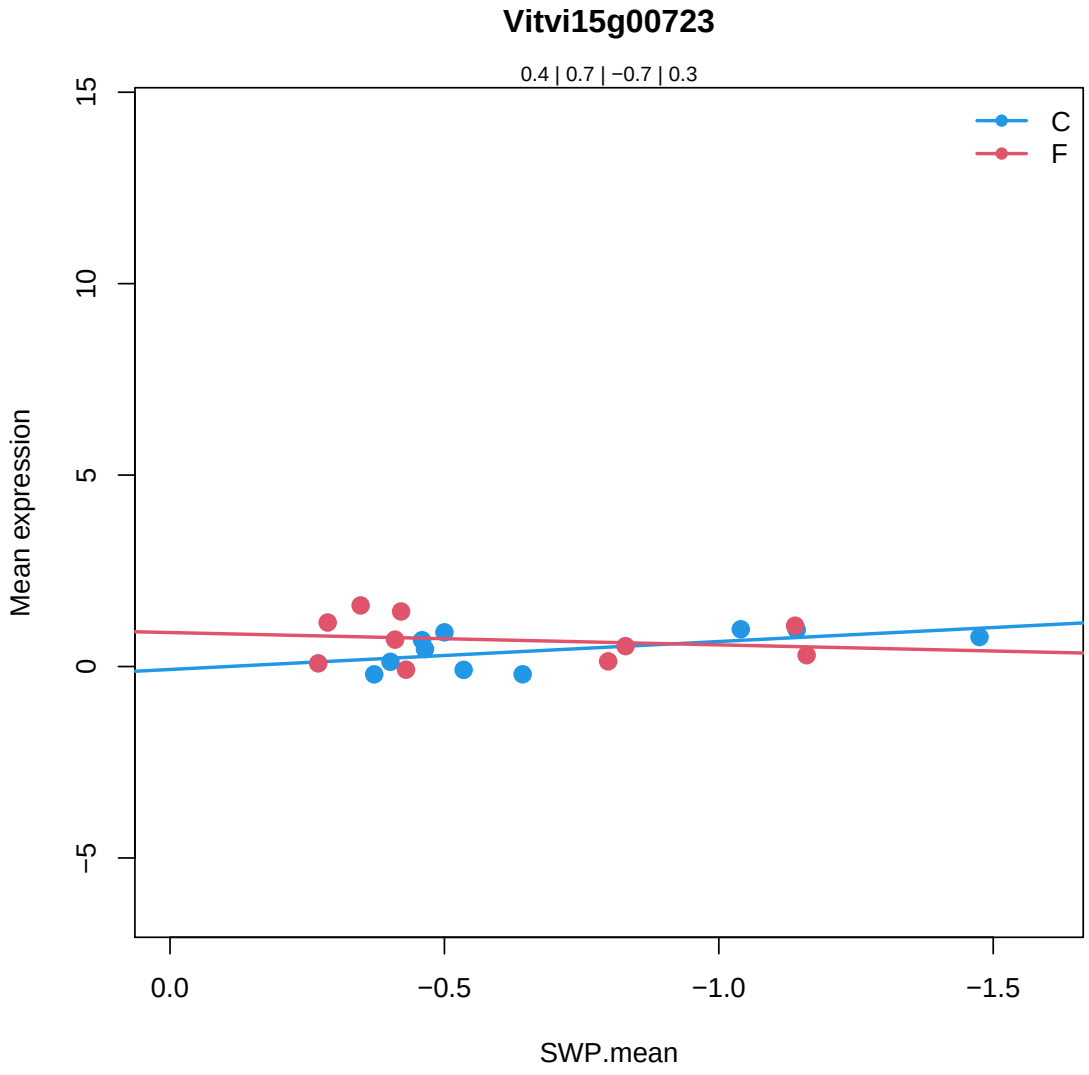
7.6.828 Vitvi15g00723: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g00723
        35.1.27
        not assigned.no ontology.tetratricopeptide repeat (TPR)
        Pentatricopeptide repeat (PPR) superfamily protein |
        Chr2:18694816-18696657 REVERSE LENGTH=613 |
        201606
```

Coefficients for Vitvi15g00723.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4364537	0.01492206	*	0.01574211	*
SlopeC	−0.7300903	0.1261503		0.6471837	
MeanF−MeanC	0.2547419	0.2867893		0.6520349	
SlopeF−SlopeC	1.051593	0.1381678		0.9999488	



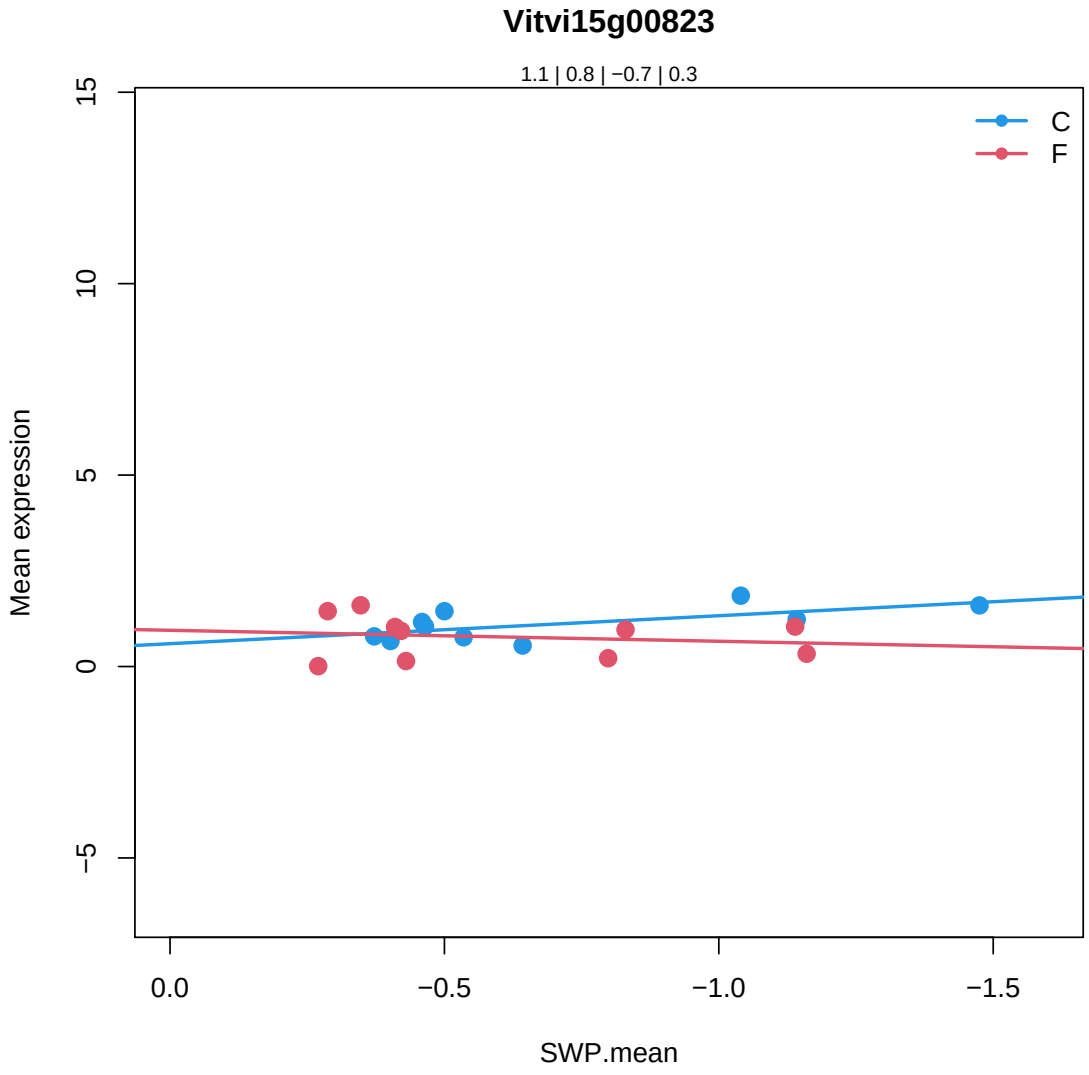
7.6.829 Vitvi15g00823: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g00823
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr2:12712884-12715100 FORWARD LENGTH=738 |
        201606
```

Coefficients for Vitvi15g00823.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.109774	3.265513e-07	***	3.816944e-07	***
SlopeC	-0.7304559	0.09994279	.	0.6121177	
MeanF-MeanC	-0.3381551	0.1320103		0.4332689	
SlopeF-SlopeC	1.017021	0.1223646		0.9999488	



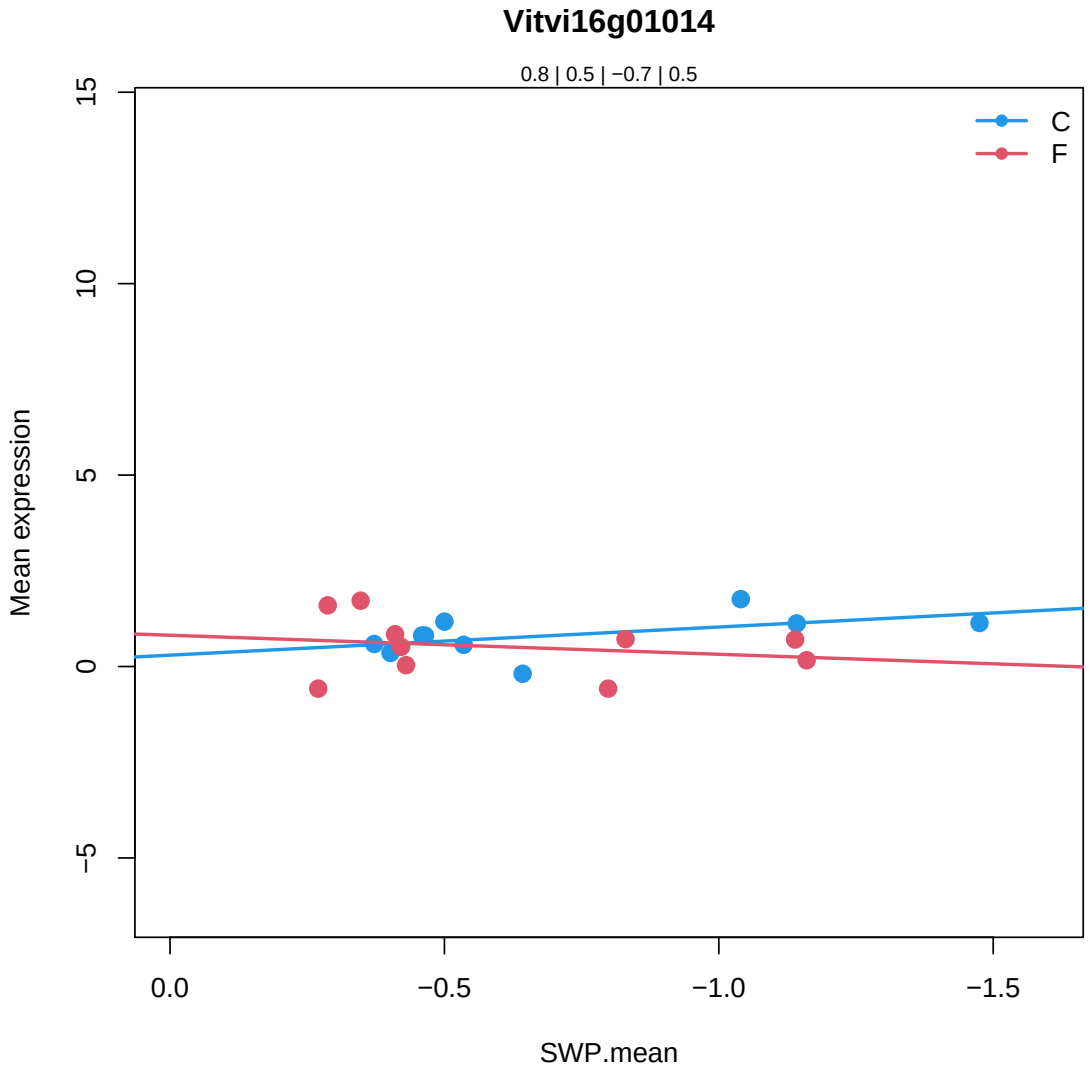
7.6.830 Vitvi16g01014: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01014
        35.2
        not assigned.unknown
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr3:11188803-11190605 FORWARD LENGTH=600 |
        201606
```

Coefficients for Vitvi16g01014.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8134541	0.0004965221	***	0.0005407252	***
SlopeC	-0.735166	0.1971447		0.7250708	
MeanF-MeanC	-0.2997555	0.2975317		0.6640861	
SlopeF-SlopeC	1.231943	0.1485471		0.9999488	



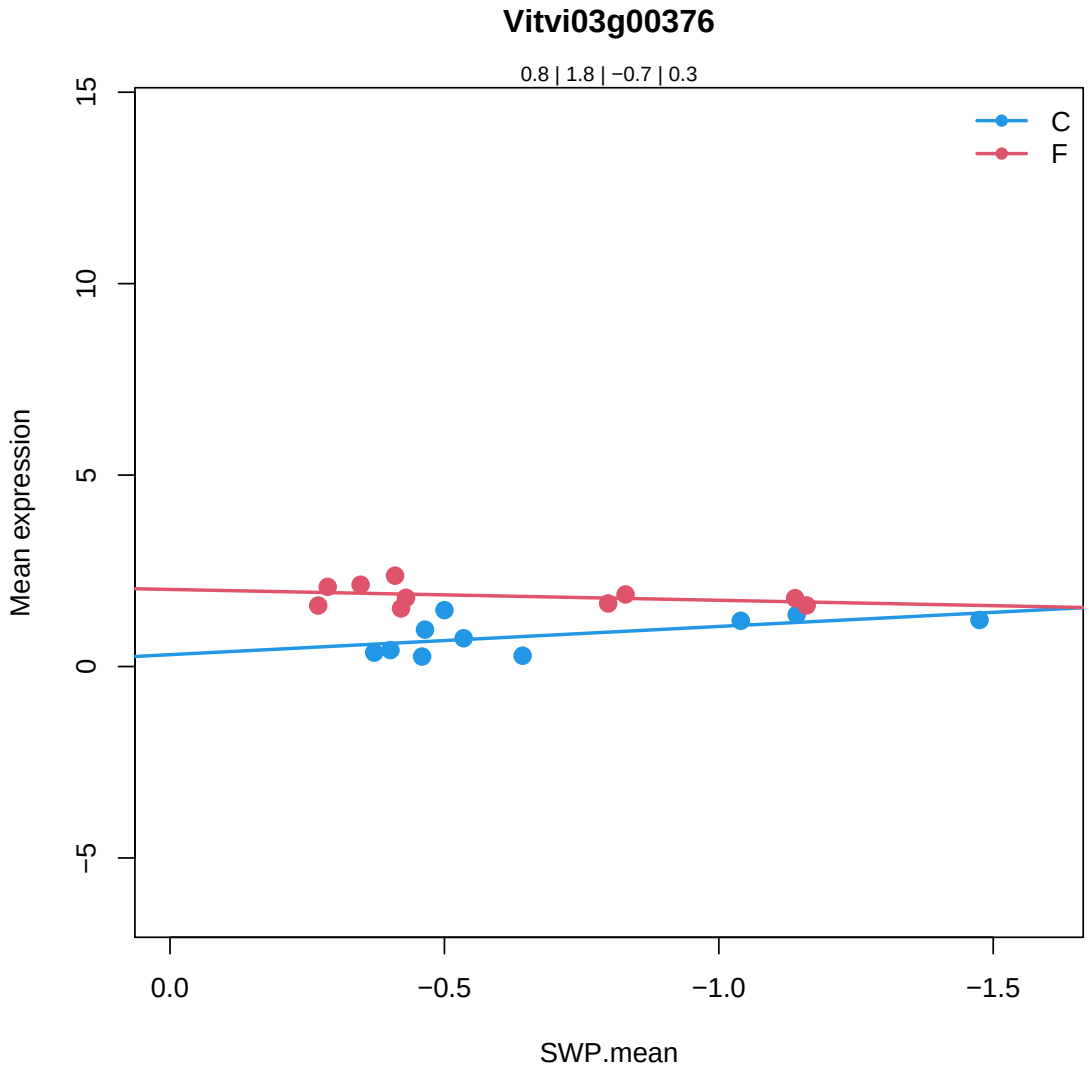
7.6.831 Vitvi03g00376: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00376
        29.2.2.3.3
        protein.synthesis.ribosome biogenesis.pre-rRNA processing and modifica
        S-adenosyl-L-methionine-dependent methyltransferases superfamily prote
        Chr4:16432011-16433752 FORWARD LENGTH=248 |
        201606
```

Coefficients for Vitvi03g00376.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8273535	1.000357e-06	***	1.15546e-06	***
SlopeC	-0.736501	0.04221765	*	0.4812642	
MeanF-MeanC	1.012874	7.756271e-06	***	0.0001986909	***
SlopeF-SlopeC	1.018753	0.05745149	.	0.9999488	



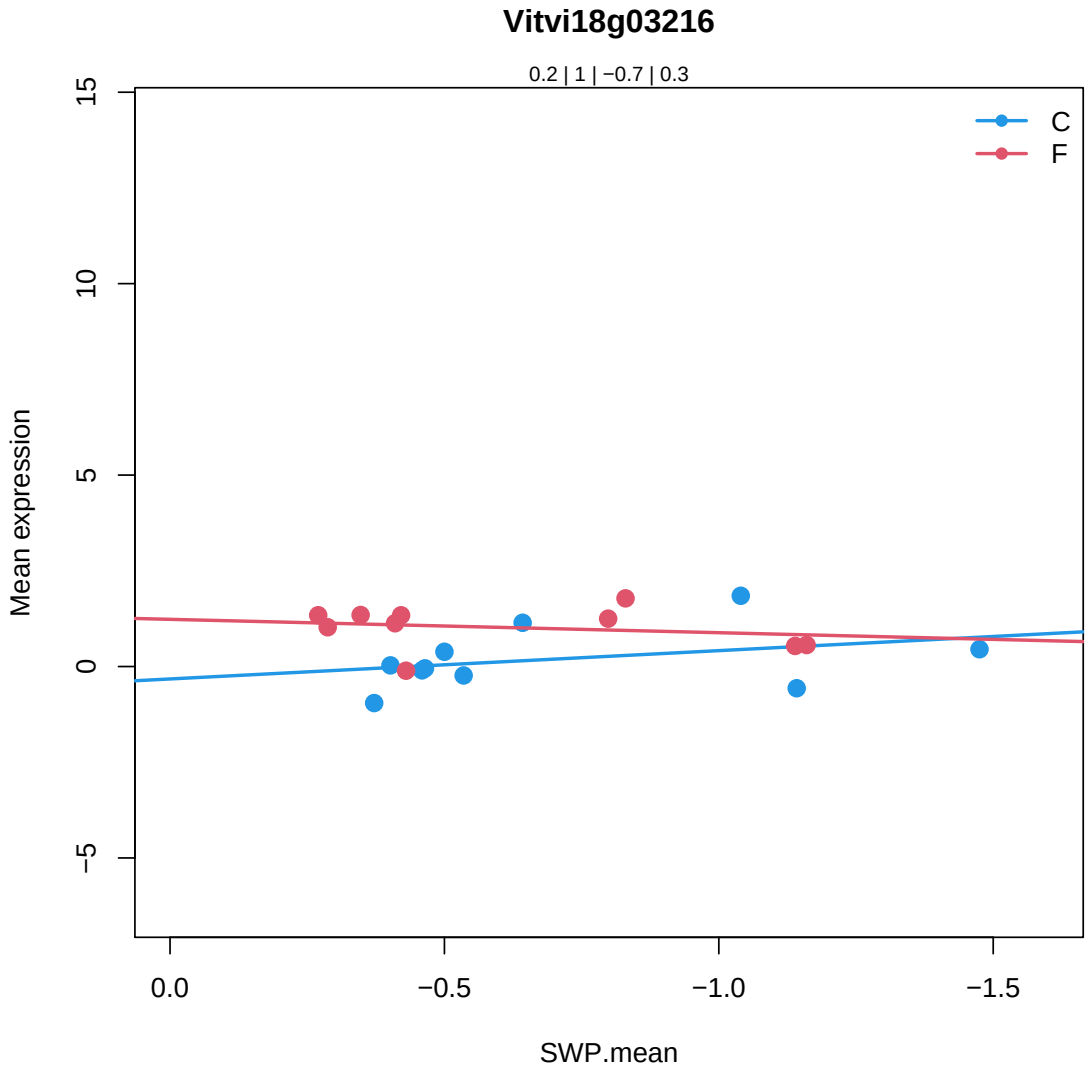
7.6.832 Vitvi18g03216: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g03216
        35.2
        not assigned.unknown
        ankyrin repeat/KH domain protein (DUF1442) |
        Chr2:18698619-18699360 FORWARD LENGTH=215 |
        201606
```

Coefficients for Vitvi18g03216.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1950856	0.3549756		0.3610395	
SlopeC	−0.7398573	0.2112142		0.7355098	
MeanF−MeanC	0.8244658	0.01000827	*	0.07604488	.
SlopeF−SlopeC	1.089169	0.2160577		0.9999488	



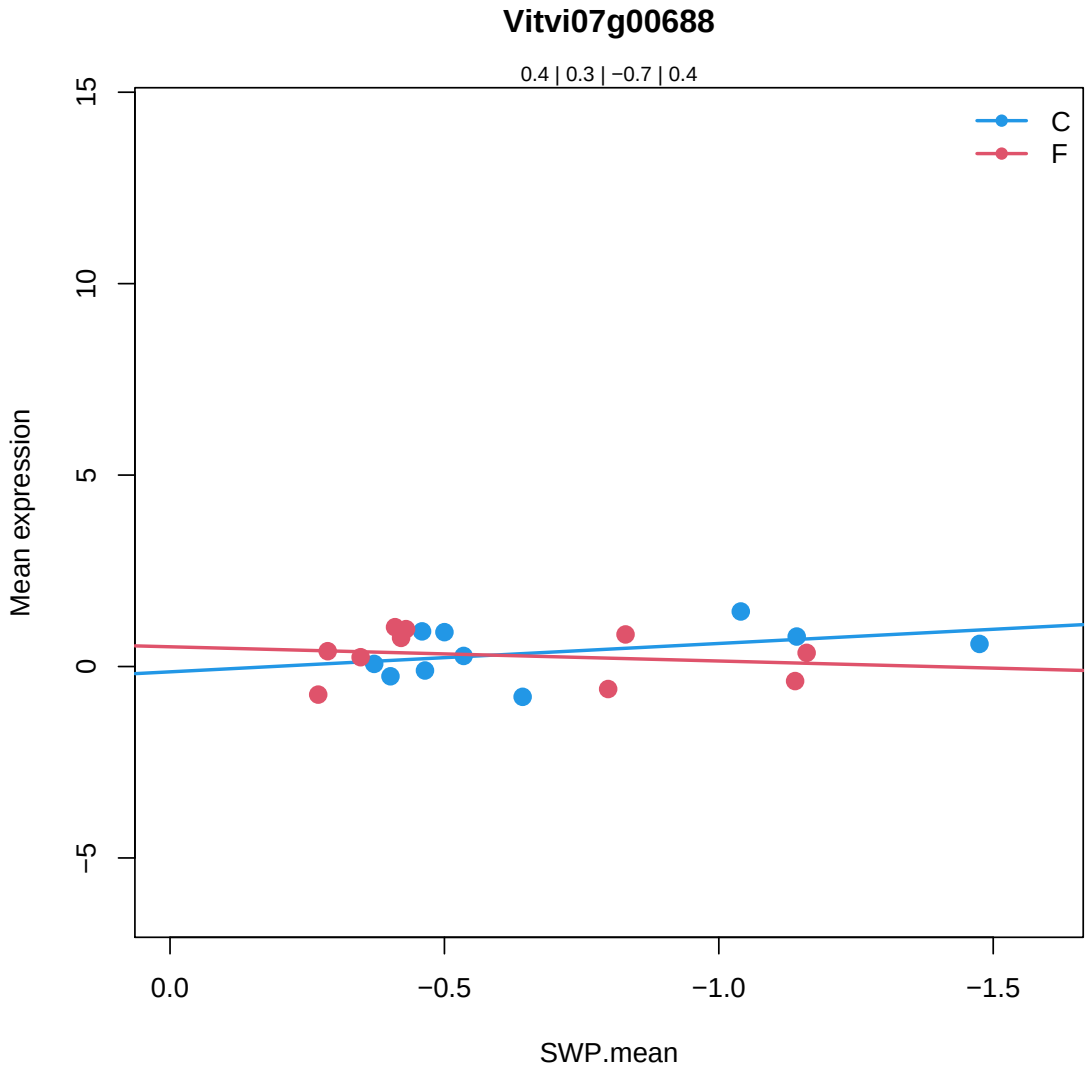
7.6.833 Vitvi07g00688: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g00688
        30.2.11
        signalling.receptor kinases.leucine rich repeat XI
        Leucine-rich repeat transmembrane protein kinase family protein |
        Chr4:14144155-14147276 REVERSE LENGTH=1013 |
        201606
```

Coefficients for Vitvi07g00688.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.381778	0.06501446	.	0.06751263	.
SlopeC	-0.7409735	0.1889557		0.7197362	
MeanF-MeanC	-0.09305067	0.740735		0.9229759	
SlopeF-SlopeC	1.112574	0.1852394		0.9999488	



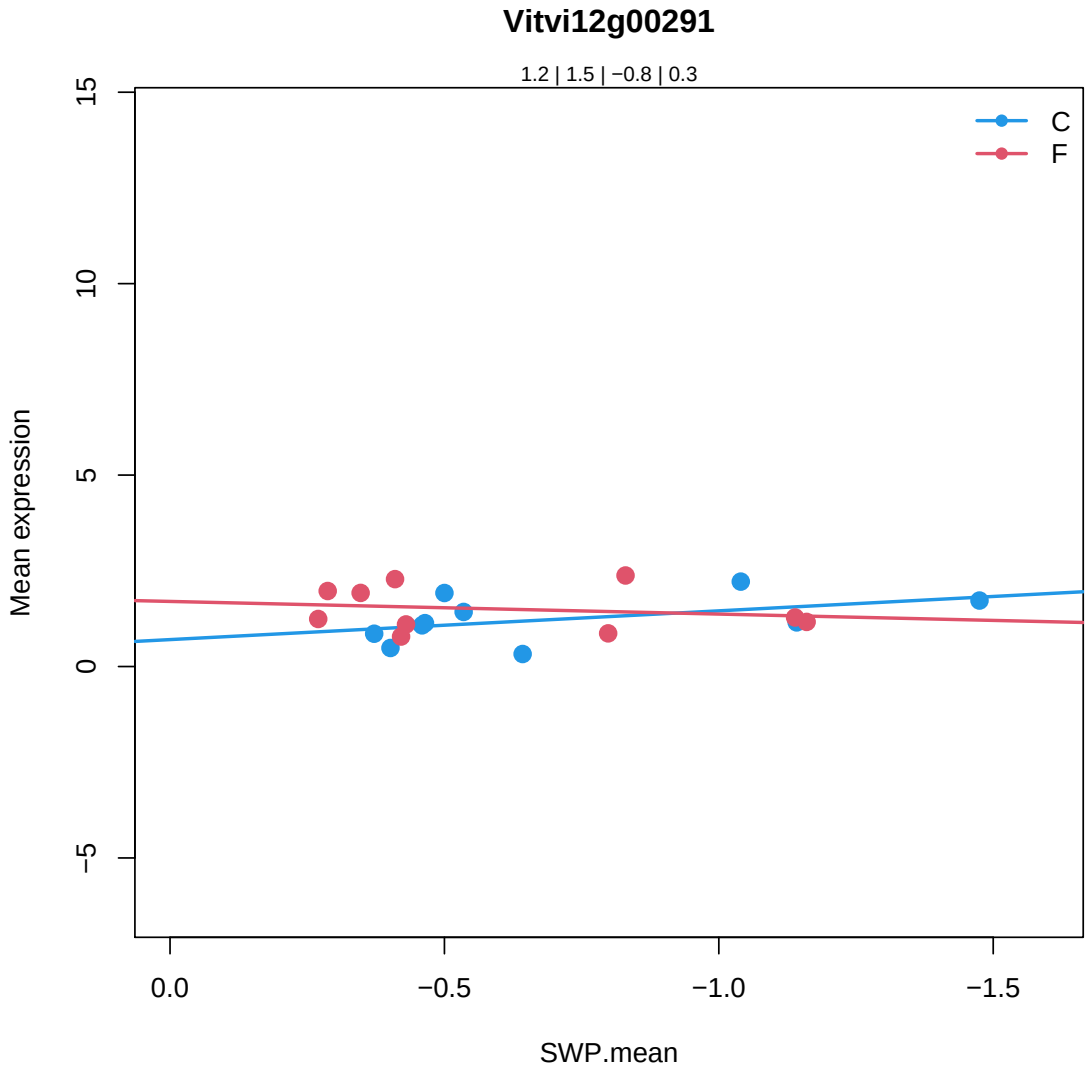
7.6.834 Vitvi12g00291: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00291
        3.5
        minor CHO metabolism.others
        haloacid dehalogenase-like hydrolase family protein |
        Chr5:21861155-21864817 REVERSE LENGTH=507 |
        201606
```

Coefficients for Vitvi12g00291.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.231244	7.284149e-07	***	8.43655e-07	***
SlopeC	-0.7511886	0.1450666		0.6700964	
MeanF-MeanC	0.267593	0.3010371		0.6665323	
SlopeF-SlopeC	1.081628	0.1579726		0.9999488	



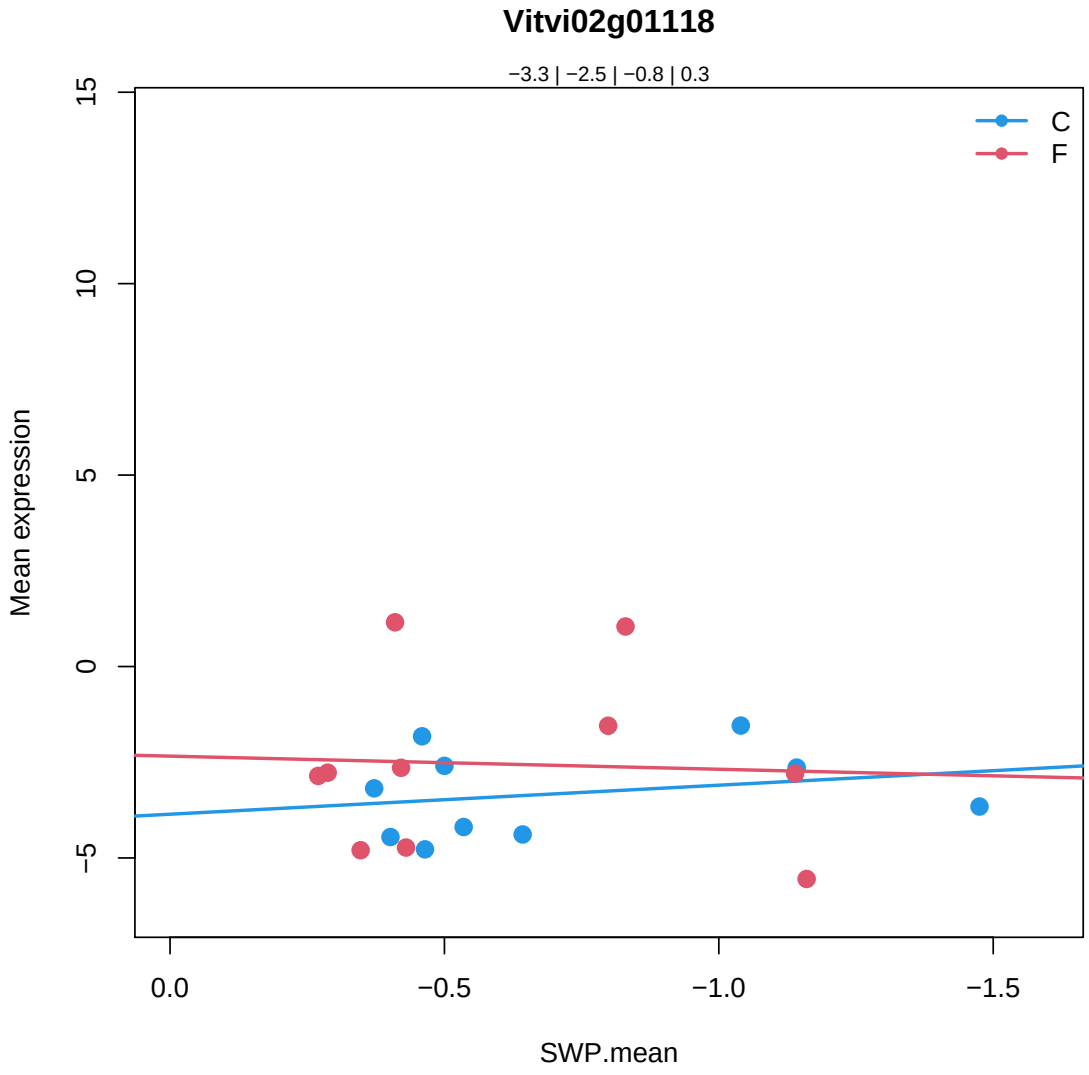
7.6.835 Vitvi02g01118: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g01118
        20.1
        stress.biotic
        HXXXD-type acyl-transferase family protein |
        Chr5:5782061-5783682 REVERSE LENGTH=461 |
        201606
```

Coefficients for Vitvi02g01118.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-3.32473	2.488925e-06	***	2.846995e-06	***
SlopeC	-0.7579984	0.6085774		0.9054994	
MeanF-MeanC	0.7752426	0.3073441		0.6707486	
SlopeF-SlopeC	1.100654	0.6172983		0.9999488	



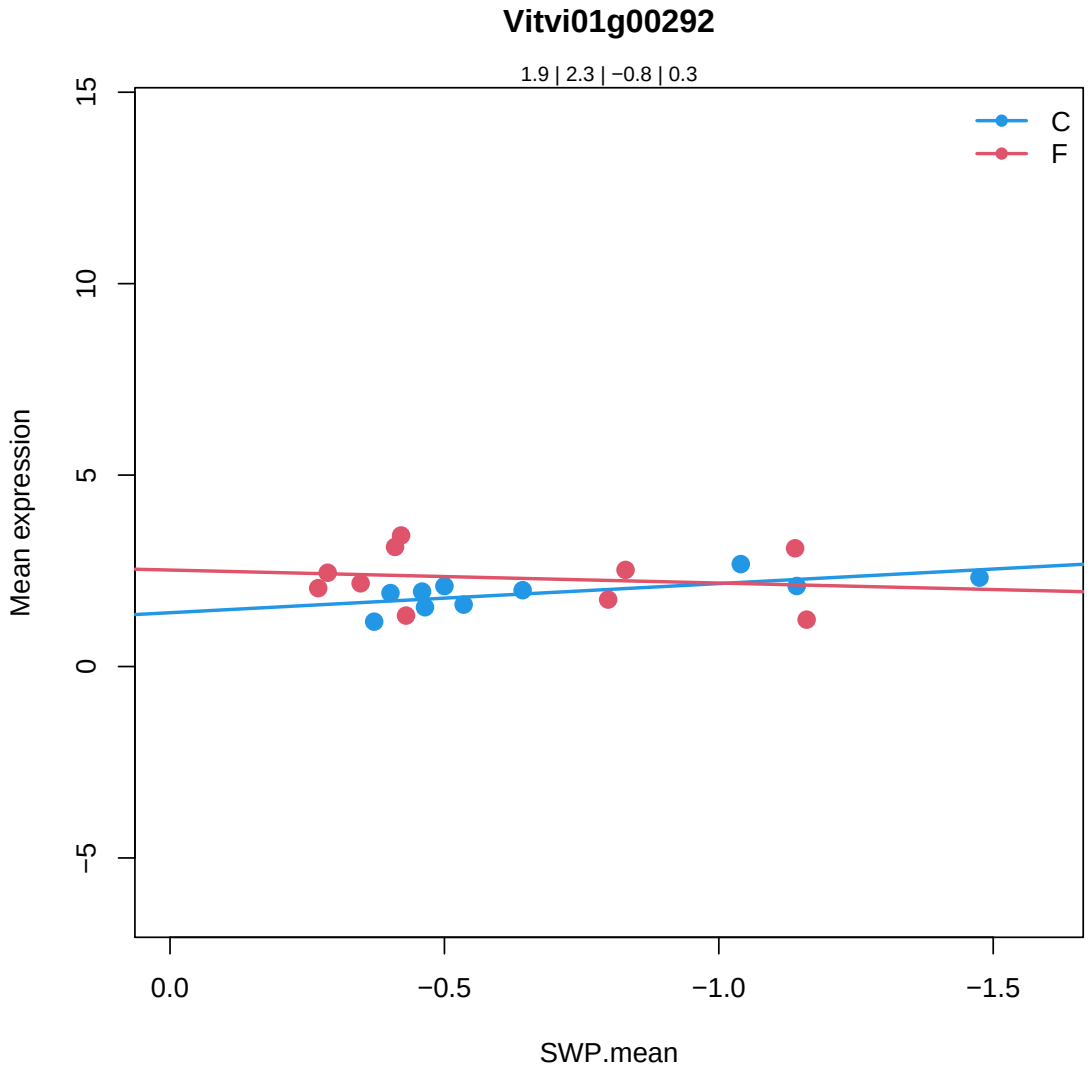
7.6.836 Vitvi01g00292: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00292
        35.2
        not assigned.unknown
        sodium/hydrogen exchanger (DUF1218) |
        Chr1:4589218-4590362 REVERSE LENGTH=188 |
        201606
```

Coefficients for Vitvi01g00292.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.940335	5.194075e-10	***	6.613875e-10	***
SlopeC	-0.7603596	0.1487779		0.6741002	
MeanF-MeanC	0.3721951	0.1636704		0.4902338	
SlopeF-SlopeC	1.099494	0.1601209		0.9999488	



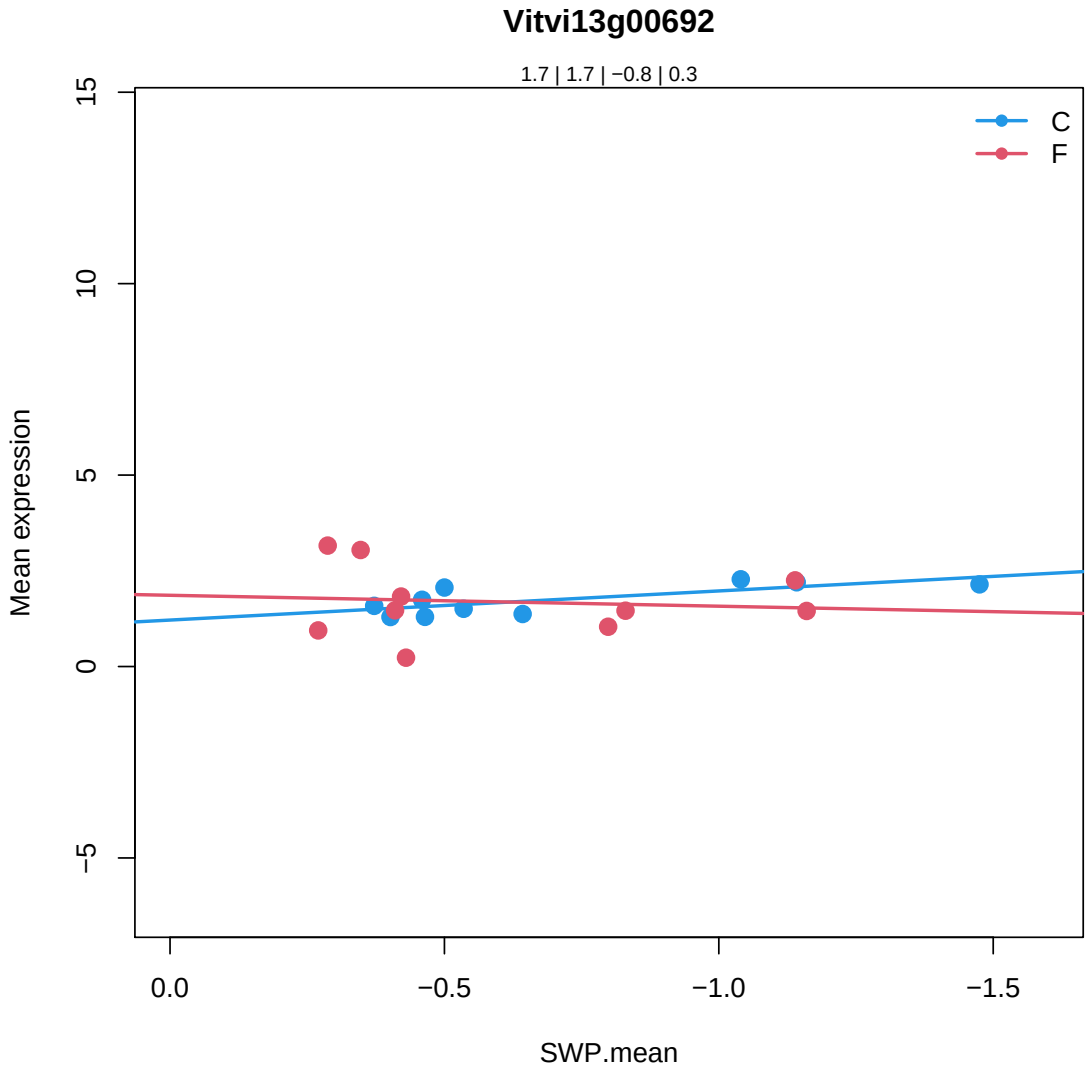
7.6.837 Vitvi13g00692: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00692
        2.2.2.9
        major CHO metabolism.degradation.starch.limit dextrinase/pullulanase
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi13g00692.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.748096	3.650016e-08	***	4.382665e-08	***
SlopeC	-0.7609122	0.2062966		0.7302381	
MeanF-MeanC	-0.06135393	0.838168		0.9564181	
SlopeF-SlopeC	1.0459	0.2418612		0.9999488	



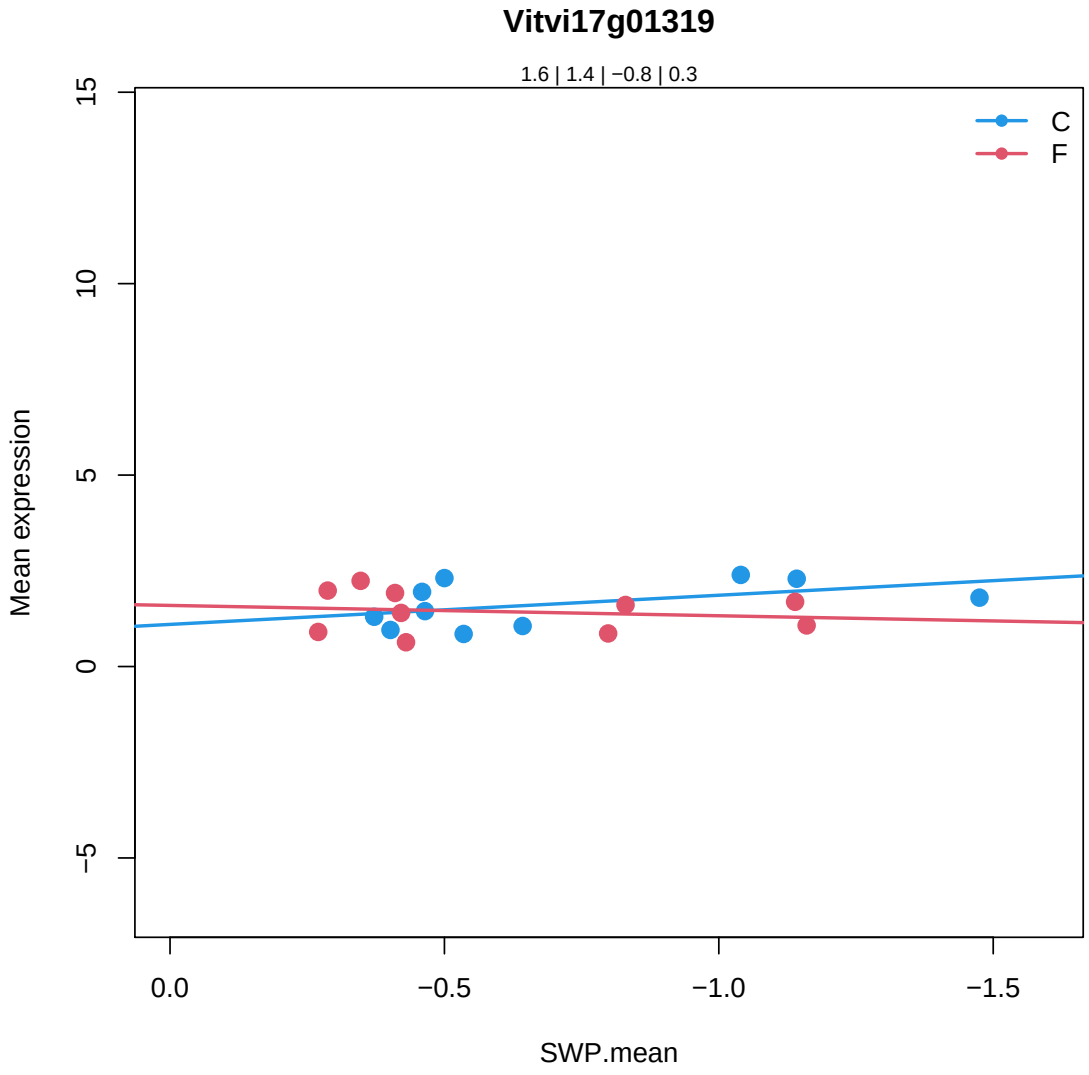
7.6.838 Vitvi17g01319: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g01319
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr1:2514374-2516599 REVERSE LENGTH=741 |
        201606
```

Coefficients for Vitvi17g01319.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.635296	3.538185e-09	***	4.380911e-09	***
SlopeC	-0.7619051	0.1243808		0.6458457	
MeanF-MeanC	-0.2042436	0.4083013		0.7494209	
SlopeF-SlopeC	1.031774	0.1601119		0.9999488	



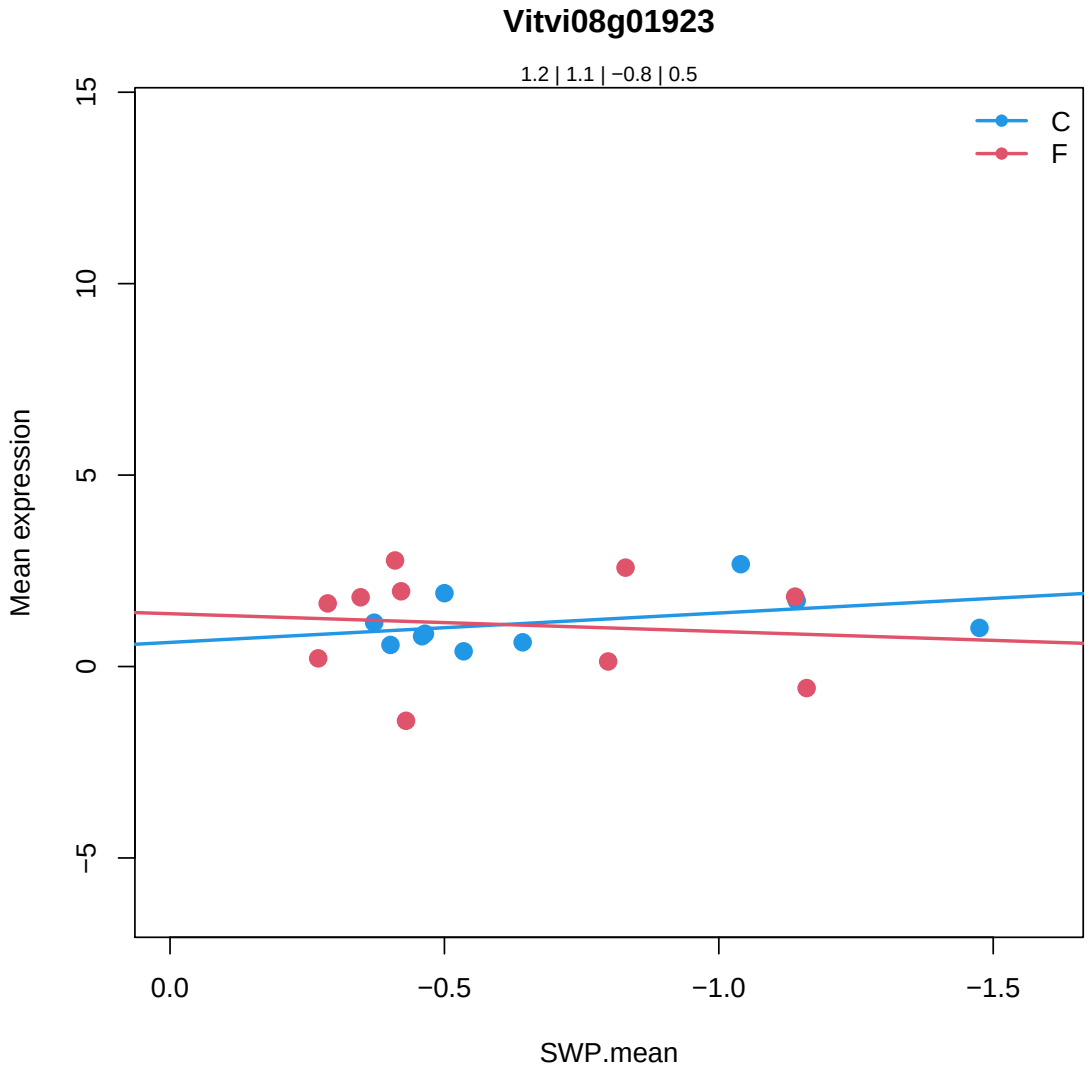
7.6.839 Vitvi08g01923: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01923
        35.2
        not assigned.unknown
        transmembrane protein |
        Chr3:21238547-21239971 FORWARD LENGTH=474 |
        201606
```

Coefficients for Vitvi08g01923.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.169703	0.001707347	**	0.001839238	**
SlopeC	−0.7671885	0.4075492		0.8377166	
MeanF−MeanC	−0.0734672	0.8750395		0.967316	
SlopeF−SlopeC	1.231188	0.3724813		0.9999488	



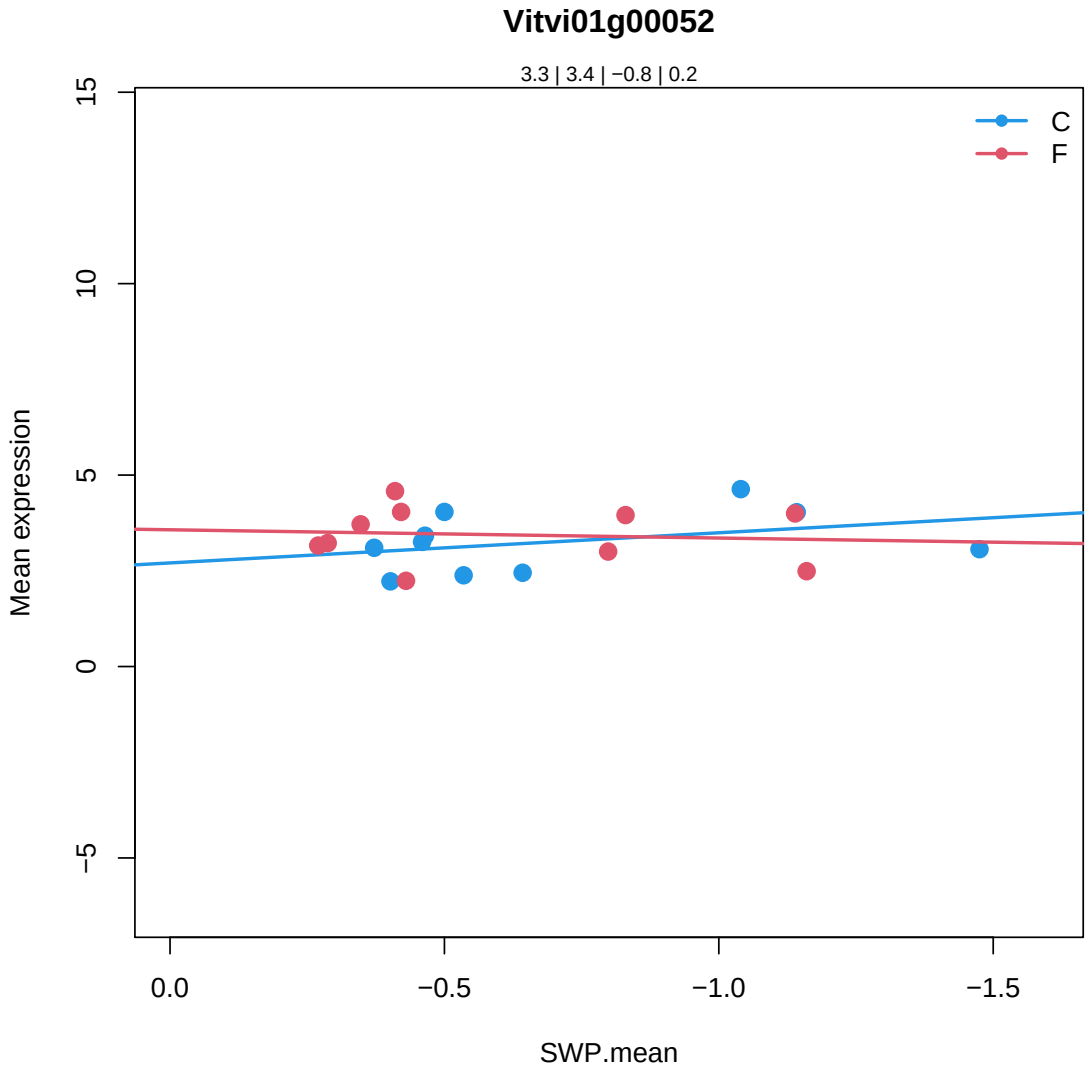
7.6.840 Vitvi01g00052: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00052
        2.2.2.6
        major CHO metabolism.degradation.starch.transporter
        Glucose-6-phosphate/phosphate translocator-like protein |
        Chr5:18698019-18700212 FORWARD LENGTH=297 |
        201606
```

Coefficients for Vitvi01g00052.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.259138	1.868977e-12	***	2.640125e-12	***
SlopeC	-0.787113	0.2271033		0.7466585	
MeanF-MeanC	0.1807789	0.5800413		0.8515913	
SlopeF-SlopeC	1.002586	0.2990763		0.9999488	



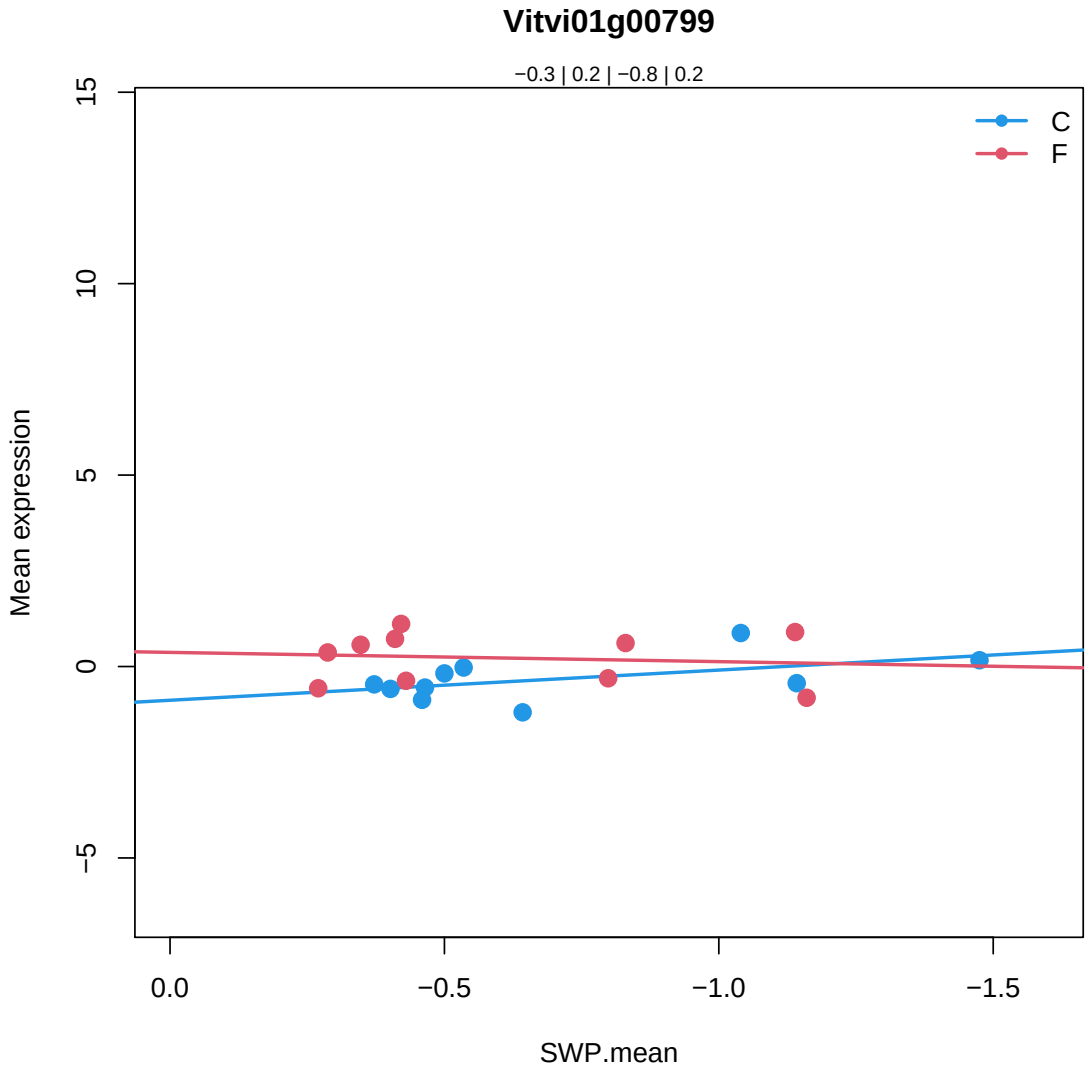
7.6.841 Vitvi01g00799: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00799
        35.1
        not assigned.no ontology
        NHL domain-containing protein |
        Chr1:26466086-26468471 REVERSE LENGTH=509 |
        201606
```

Coefficients for Vitvi01g00799.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.3270336	0.09616368	.	0.09946572	.
SlopeC	-0.7881297	0.146309		0.6722139	
MeanF-MeanC	0.5487453	0.05125536	.	0.2430722	
SlopeF-SlopeC	1.029777	0.1996793		0.9999488	



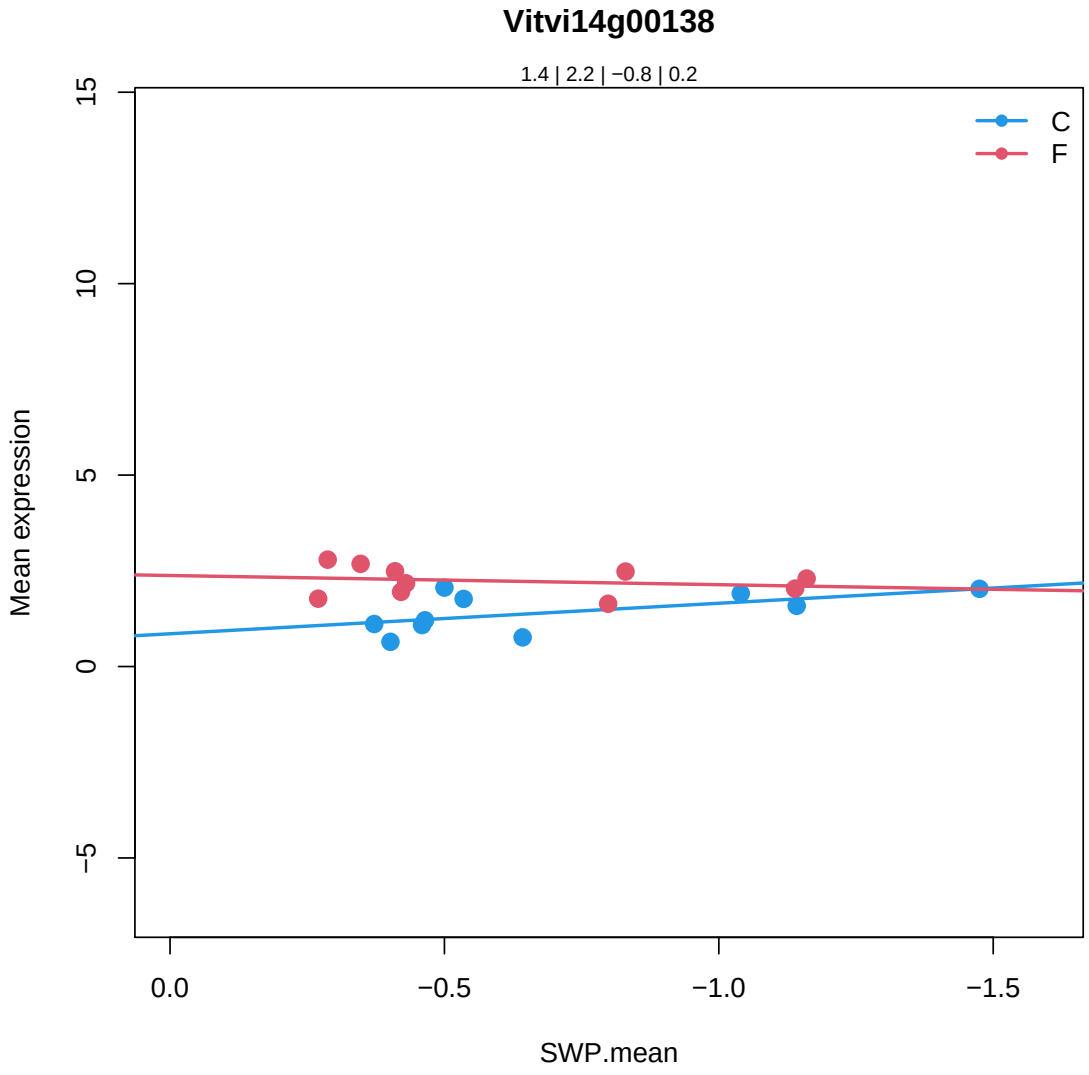
7.6.842 Vitvi14g00138: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g00138
        8.1.8
        TCA / organic transformation.TCA.fumarase
        FUMARASE 2 |
        Chr5:20729687-20733476 FORWARD LENGTH=510 |
        201606
```

Coefficients for Vitvi14g00138.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.41547	1.330321e-09	***	1.671069e-09	***
SlopeC	-0.7964358	0.05373213	.	0.519002	
MeanF-MeanC	0.8152853	0.0004812198	***	0.00681871	**
SlopeF-SlopeC	1.036274	0.08851763	.	0.9999488	



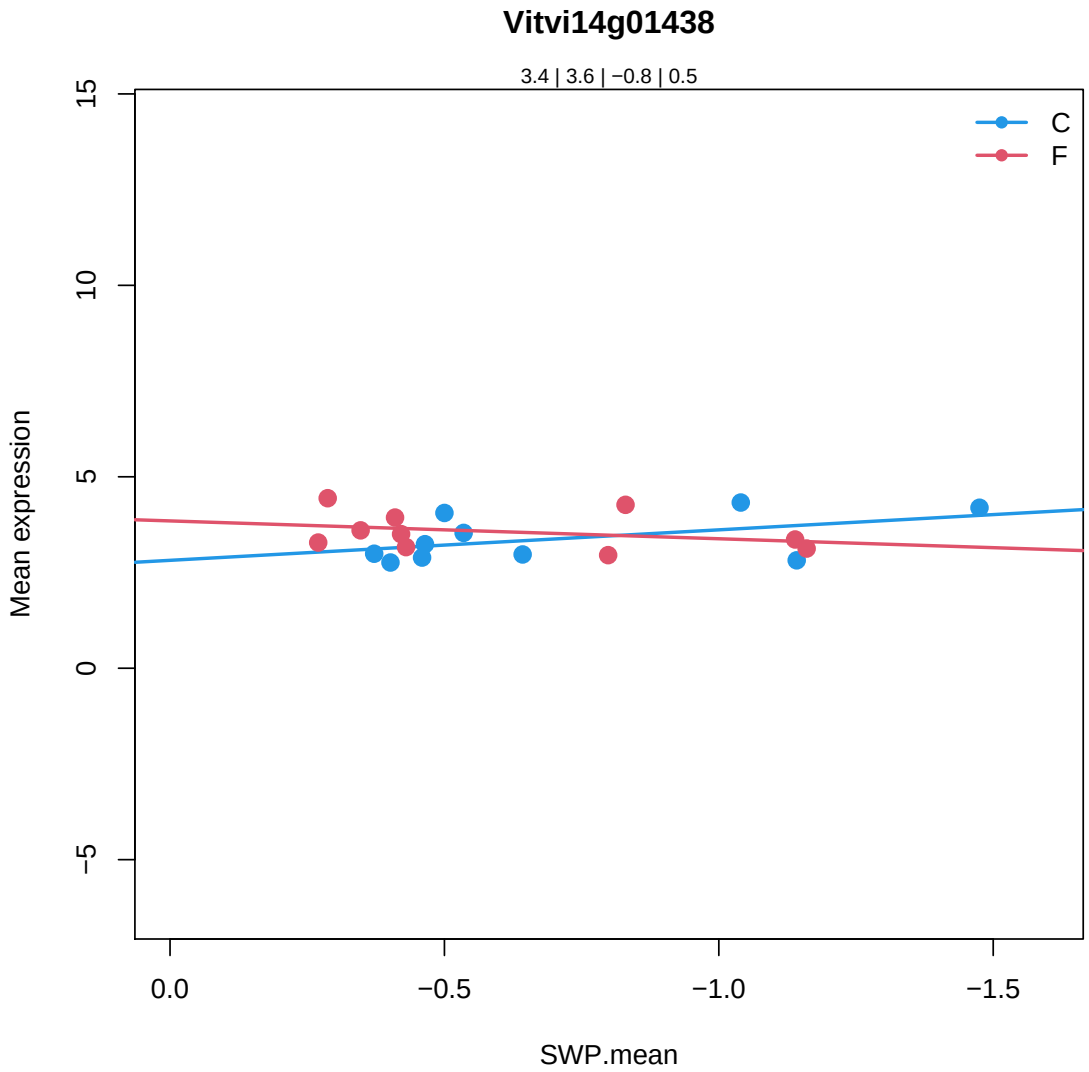
7.6.843 Vitvi14g01438: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01438
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi14g01438.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.37773	1.435823e-15	***	2.63736e-15	***
SlopeC	-0.7965291	0.09669175	.	0.6081385	
MeanF-MeanC	0.1854431	0.4349486		0.7674876	
SlopeF-SlopeC	1.262477	0.07814693	.	0.9999488	



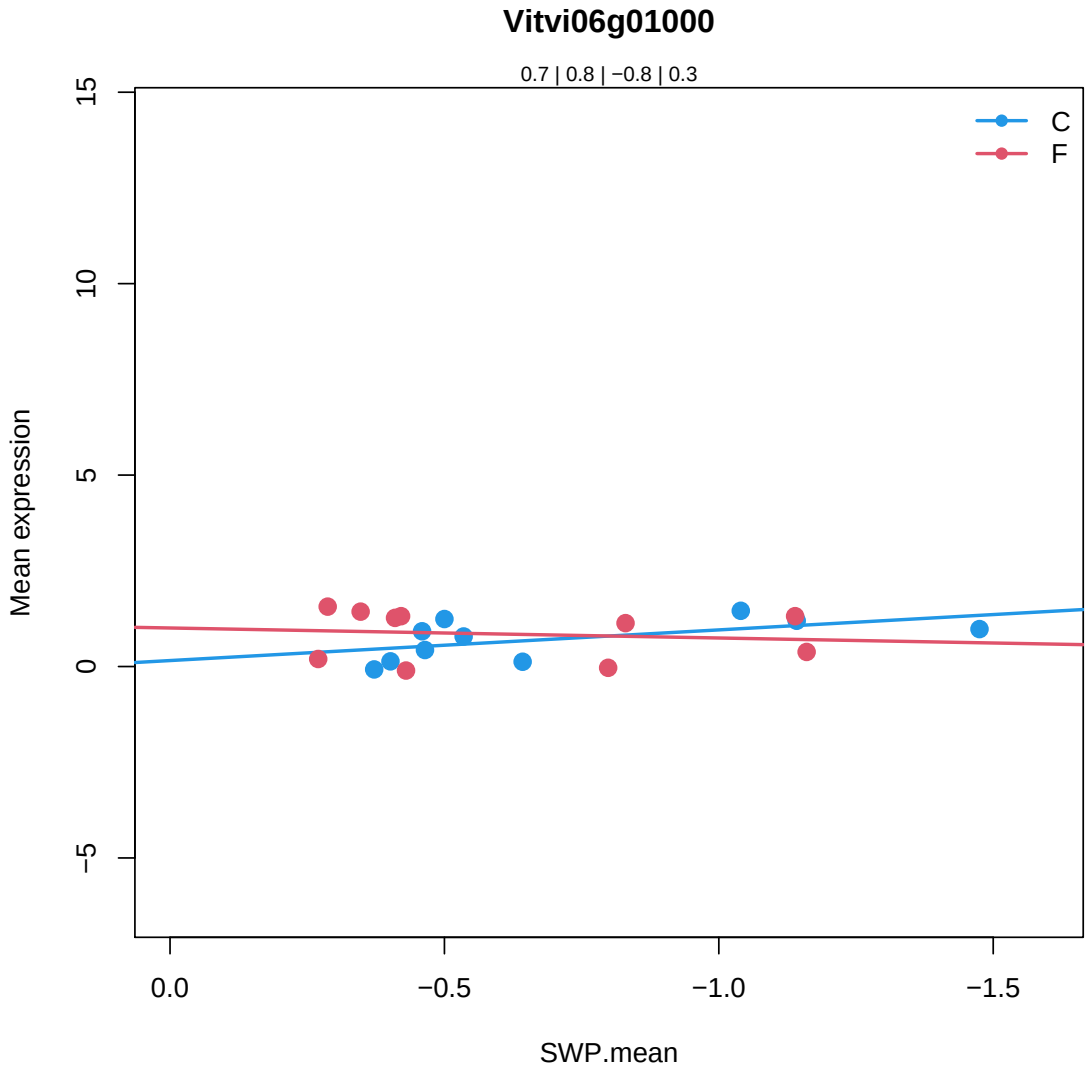
7.6.844 Vitvi06g01000: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01000
        35.1.27
        not assigned.no ontology.tetratricopeptide repeat (TPR)
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr1:20001263-20003416 FORWARD LENGTH=717 |
        201606
```

Coefficients for Vitvi06g01000.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.718633	0.0005959904	***	0.0006480763	***
SlopeC	−0.8008626	0.1217963		0.64341	
MeanF−MeanC	0.1282031	0.617088		0.8674289	
SlopeF−SlopeC	1.061934	0.165639		0.9999488	



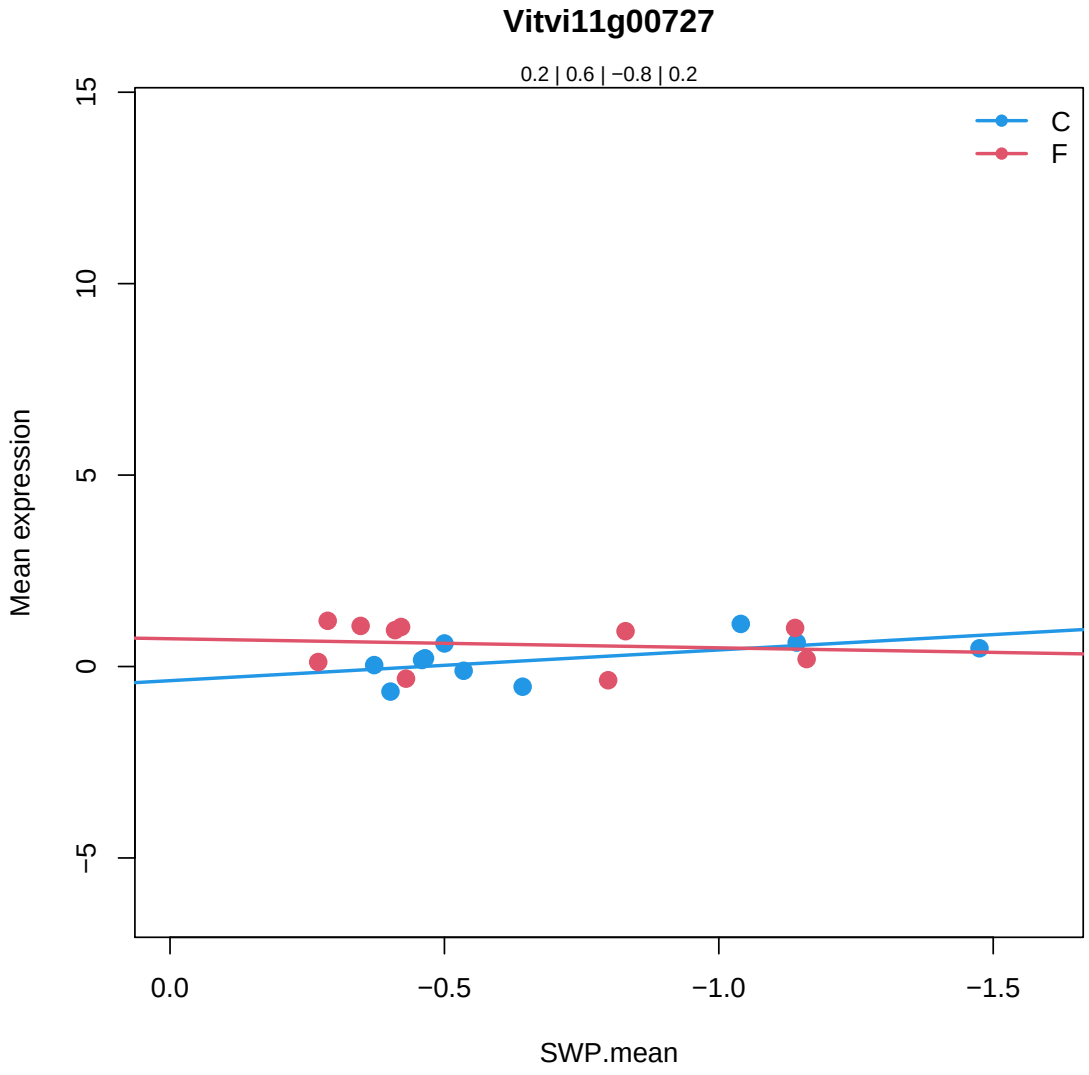
7.6.845 Vitvi11g00727: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00727
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        Pentatricopeptide repeat (PPR) superfamily protein |
        Chr4:14962617-14964995 REVERSE LENGTH=792 |
        201606
```

Coefficients for Vitvi11g00727.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1943637	0.2711063		0.2765495	
SlopeC	−0.8027951	0.1080473		0.6223948	
MeanF−MeanC	0.3858955	0.1273966		0.4235991	
SlopeF−SlopeC	1.040225	0.1587782		0.9999488	



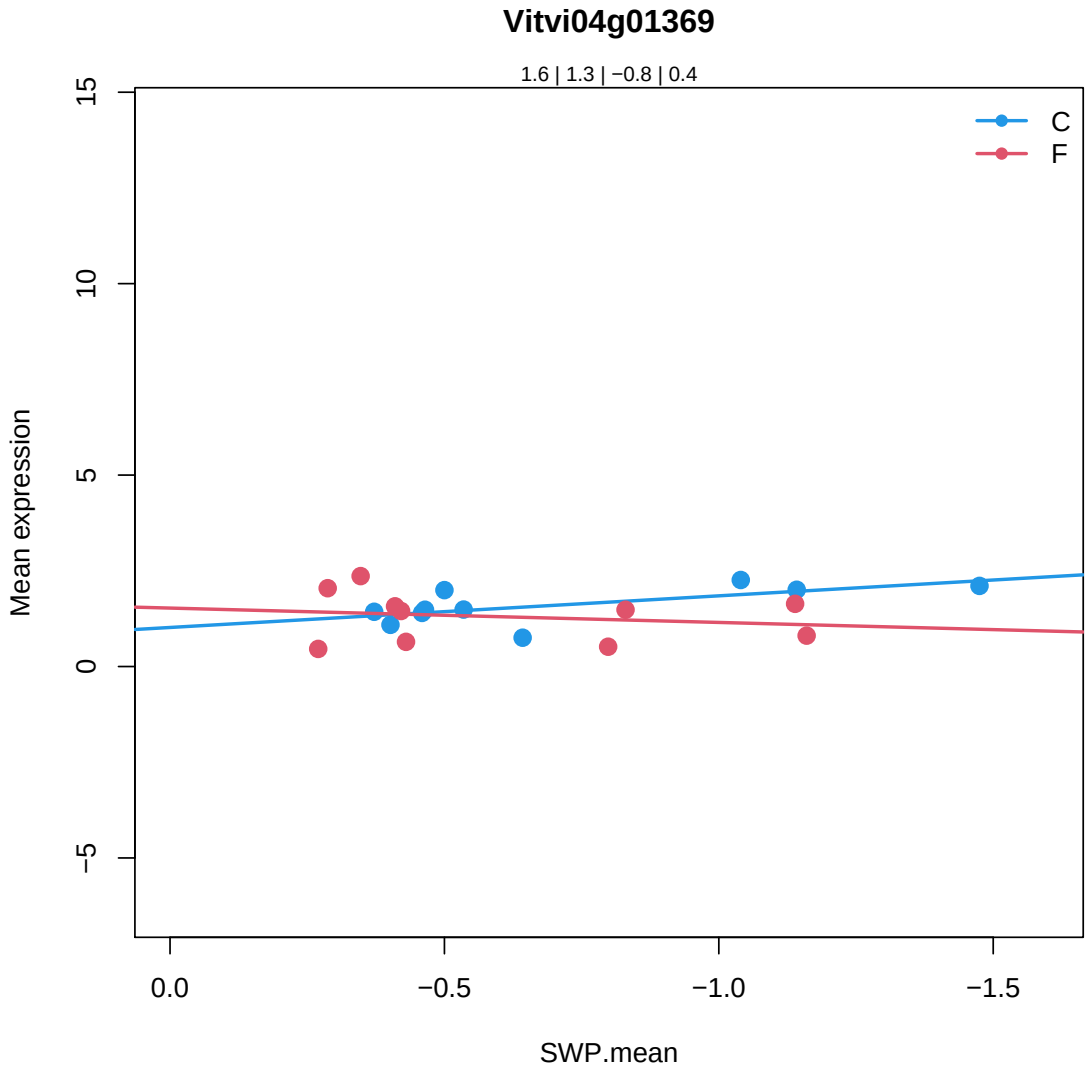
7.6.846 Vitvi04g01369: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01369
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        Pentatricopeptide repeat (PPR) superfamily protein |
        Chr5:17814336-17816309 FORWARD LENGTH=657 |
        201606
```

Coefficients for Vitvi04g01369.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.600727	5.092567e-09	***	6.274932e-09	***
SlopeC	-0.826434	0.09697244	.	0.6084506	
MeanF-MeanC	-0.3029978	0.2240994		0.5757177	
SlopeF-SlopeC	1.201411	0.1044988		0.9999488	



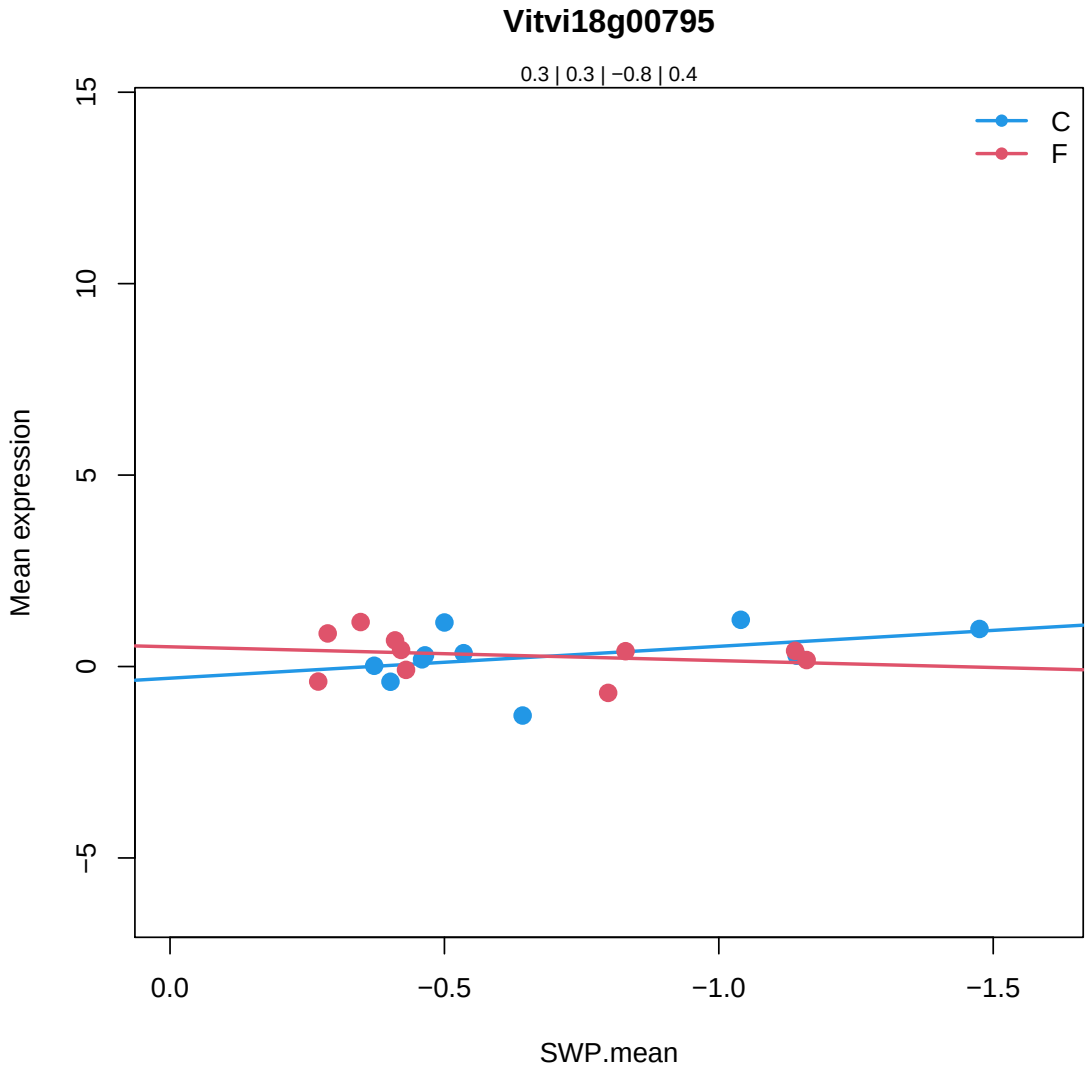
7.6.847 Vitvi18g00795: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00795
        35.1.27
        not assigned.no ontology.tetratricopeptide repeat (TPR)
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr2:1706787-1708865 REVERSE LENGTH=692 |
        201606
```

Coefficients for Vitvi18g00795.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.2801062	0.1677261		0.1723742	
SlopeC	−0.8325669	0.1417481		0.6676582	
MeanF−MeanC	0.01497616	0.9574484		0.9902577	
SlopeF−SlopeC	1.192805	0.156506		0.9999488	



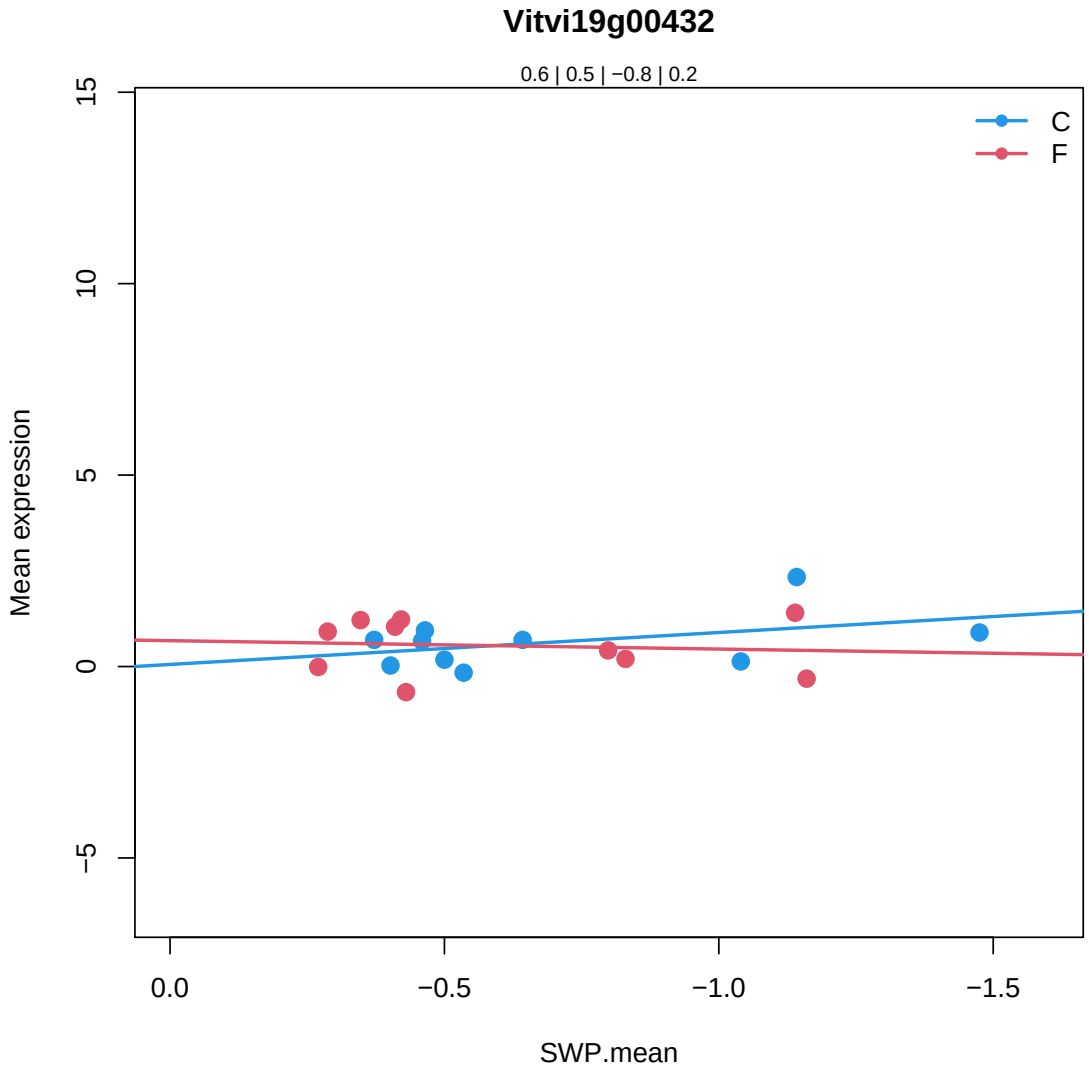
7.6.848 Vitvi19g00432: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g00432
        17.6.1.13
        hormone metabolism.gibberelin.synthesis-degradation.GA2 oxidase
        gibberellin 2-oxidase 8 |
        Chr4:11302751-11306601 FORWARD LENGTH=338 |
        201606
```

Coefficients for Vitvi19g00432.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6402129	0.006281264	**	0.006682419	**
SlopeC	-0.8343219	0.1702931		0.7007579	
MeanF-MeanC	-0.09864549	0.7445723		0.9246461	
SlopeF-SlopeC	1.053522	0.2417842		0.9999488	



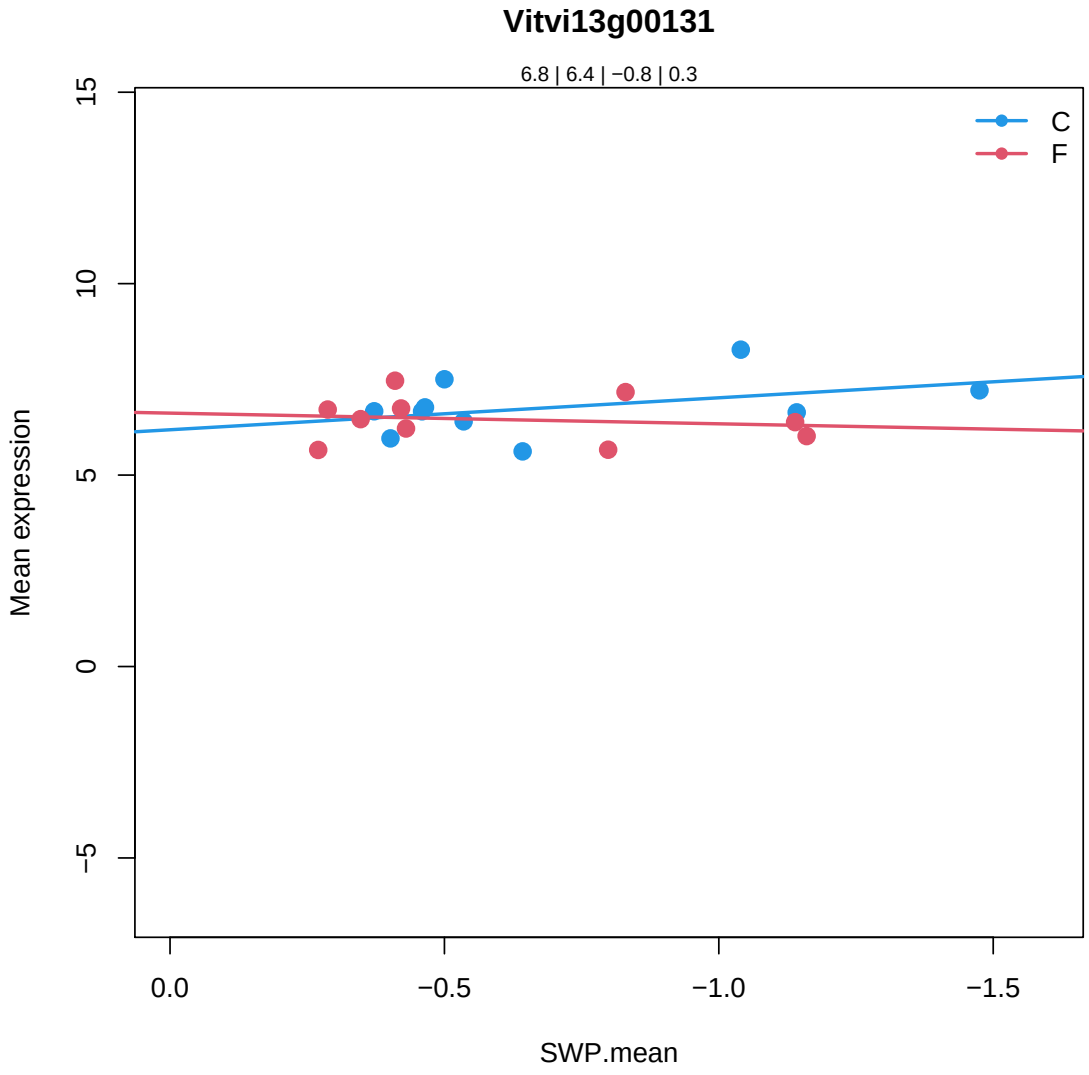
7.6.849 Vitvi13g00131: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00131
        35.2
        not assigned.unknown
        senescence associated gene 20 |
        Chr3:3442776-3443108 FORWARD LENGTH=110 |
        201606
```

Coefficients for Vitvi13g00131.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.770622	4.730446e-20	***	2.531653e-19	***
SlopeC	-0.8347559	0.150328		0.6773924	
MeanF-MeanC	-0.3225305	0.2693558		0.6319653	
SlopeF-SlopeC	1.113787	0.195137		0.9999488	



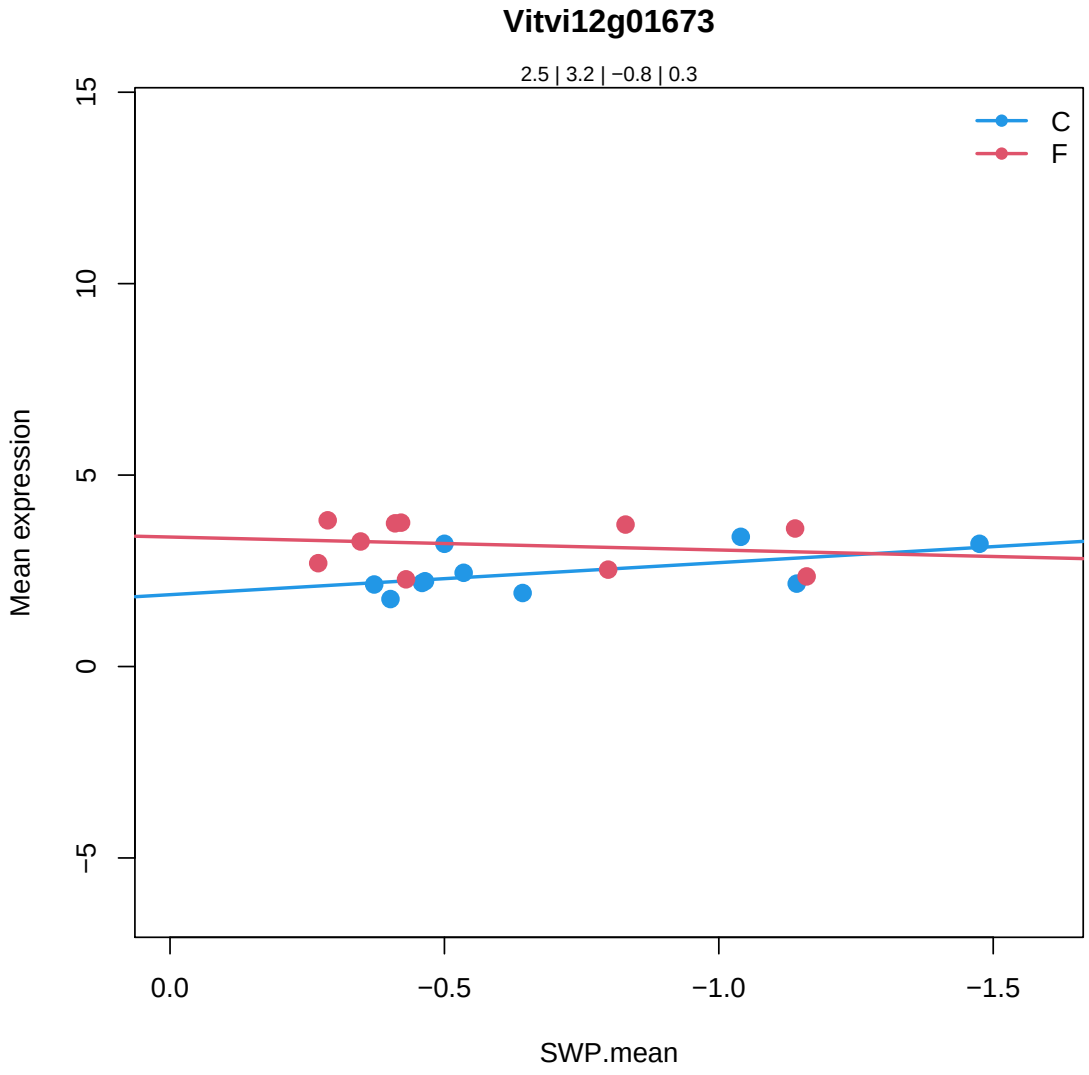
7.6.850 Vitvi12g01673: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g01673
        33.2
        development.late embryogenesis abundant
        Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein fam
        Chr2:78038-79176 FORWARD LENGTH=231 |
        201606
```

Coefficients for Vitvi12g01673.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.464366	5.007571e-12	***	6.922311e-12	***
SlopeC	-0.8367173	0.1111383		0.6258604	
MeanF-MeanC	0.7110324	0.01113776	*	0.08230338	.
SlopeF-SlopeC	1.17523	0.1315032		0.9999488	



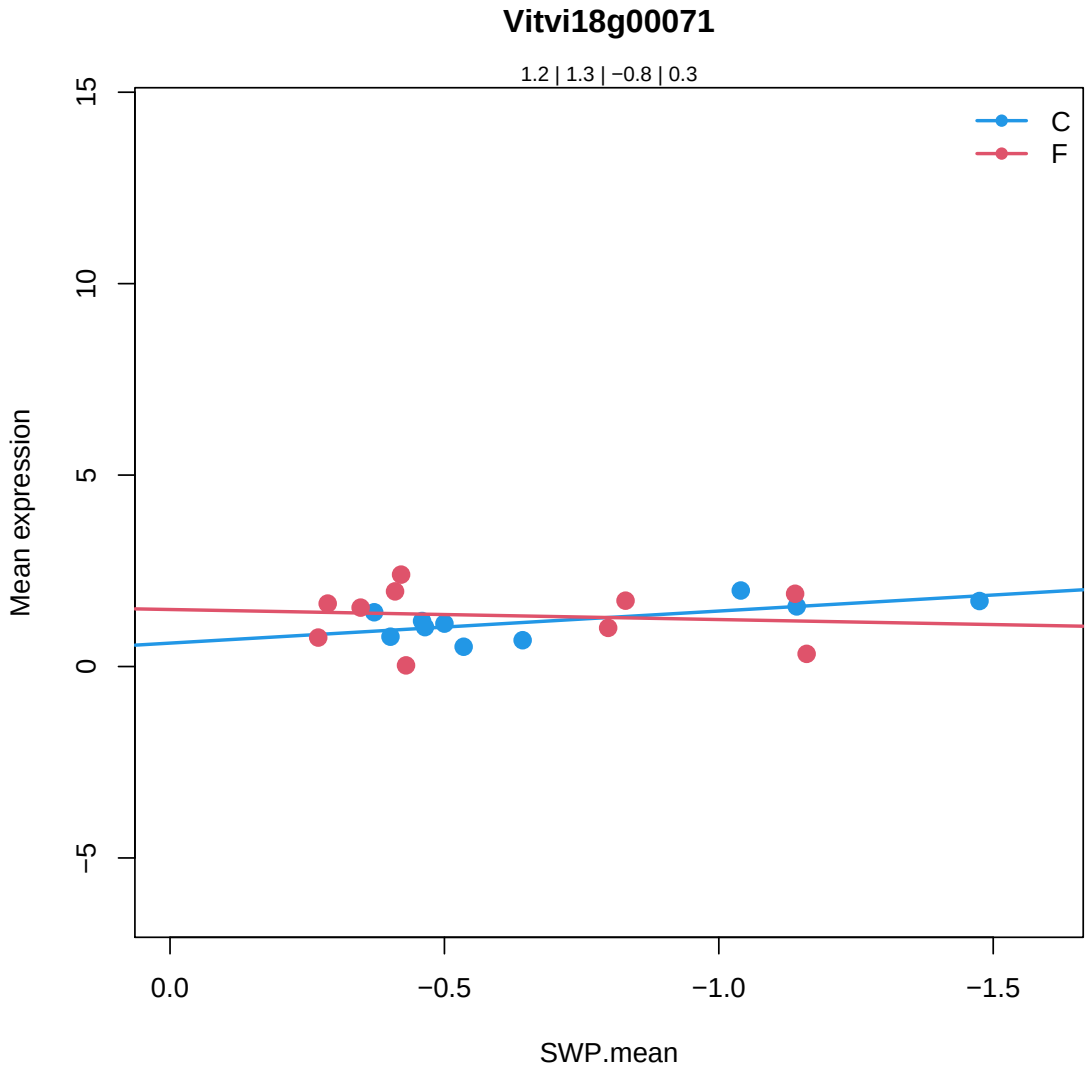
7.6.851 Vitvi18g00071: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00071
        30.1.1
        signalling.in sugar and nutrient physiology.misc
        glutamate receptor 3.3 |
        Chr1:15973489-15976703 FORWARD LENGTH=933 |
        201606
```

Coefficients for Vitvi18g00071.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.199882	2.366544e-06	***	2.708633e-06	***
SlopeC	-0.837568	0.1249231		0.6458879	
MeanF-MeanC	0.1290381	0.6332992		0.8752605	
SlopeF-SlopeC	1.099313	0.1734055		0.9999488	



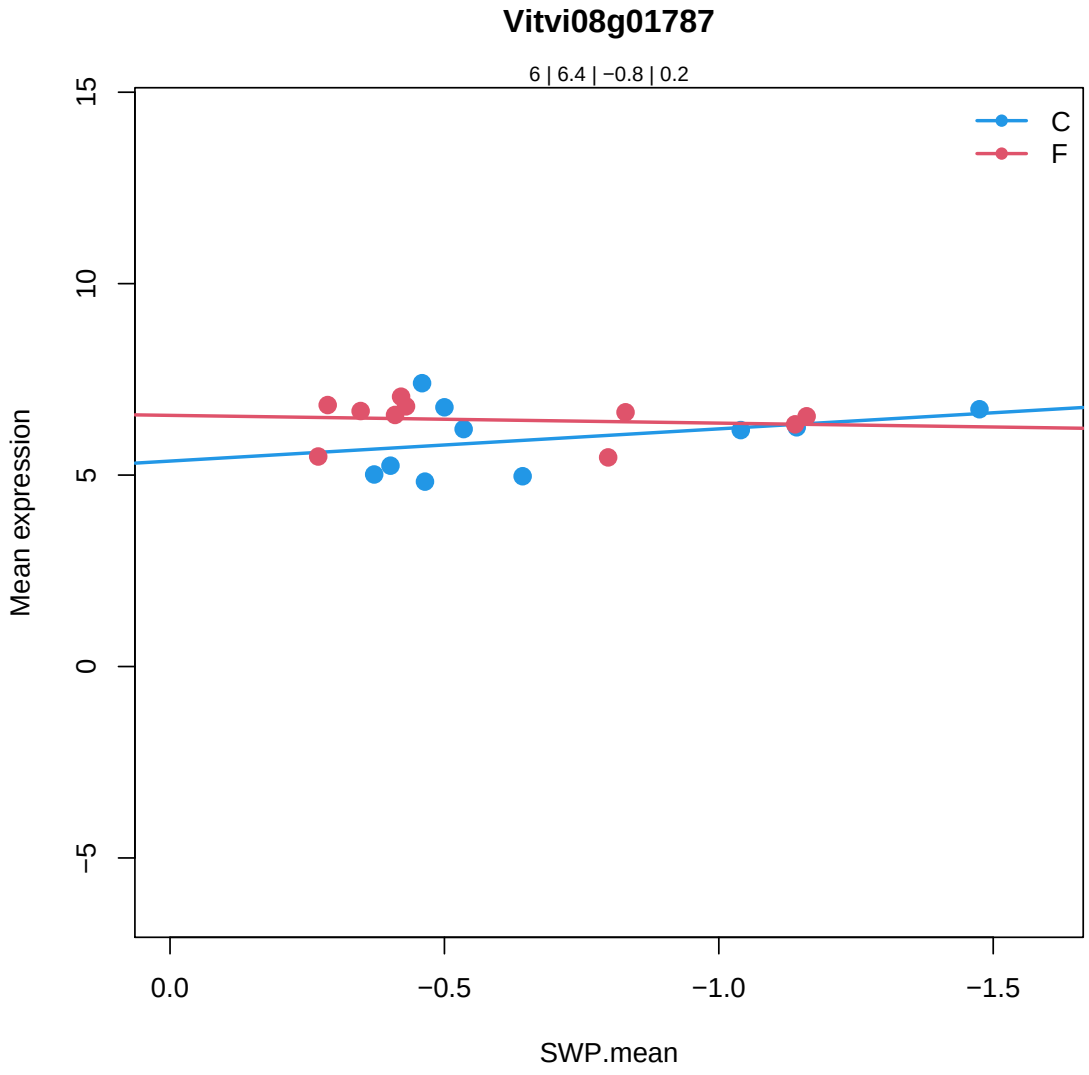
7.6.852 Vitvi08g01787: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01787
        35.2
        not assigned.unknown
        Galactose oxidase/kelch repeat superfamily protein |
        Chr2:18253731-18254960 FORWARD LENGTH=409 |
        201606
```

Coefficients for Vitvi08g01787.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.95722	3.616216e-18	***	1.064061e-17	***
SlopeC	-0.8410798	0.1790351		0.7115654	
MeanF-MeanC	0.4788959	0.13433		0.4382189	
SlopeF-SlopeC	1.043543	0.2595856		0.9999488	



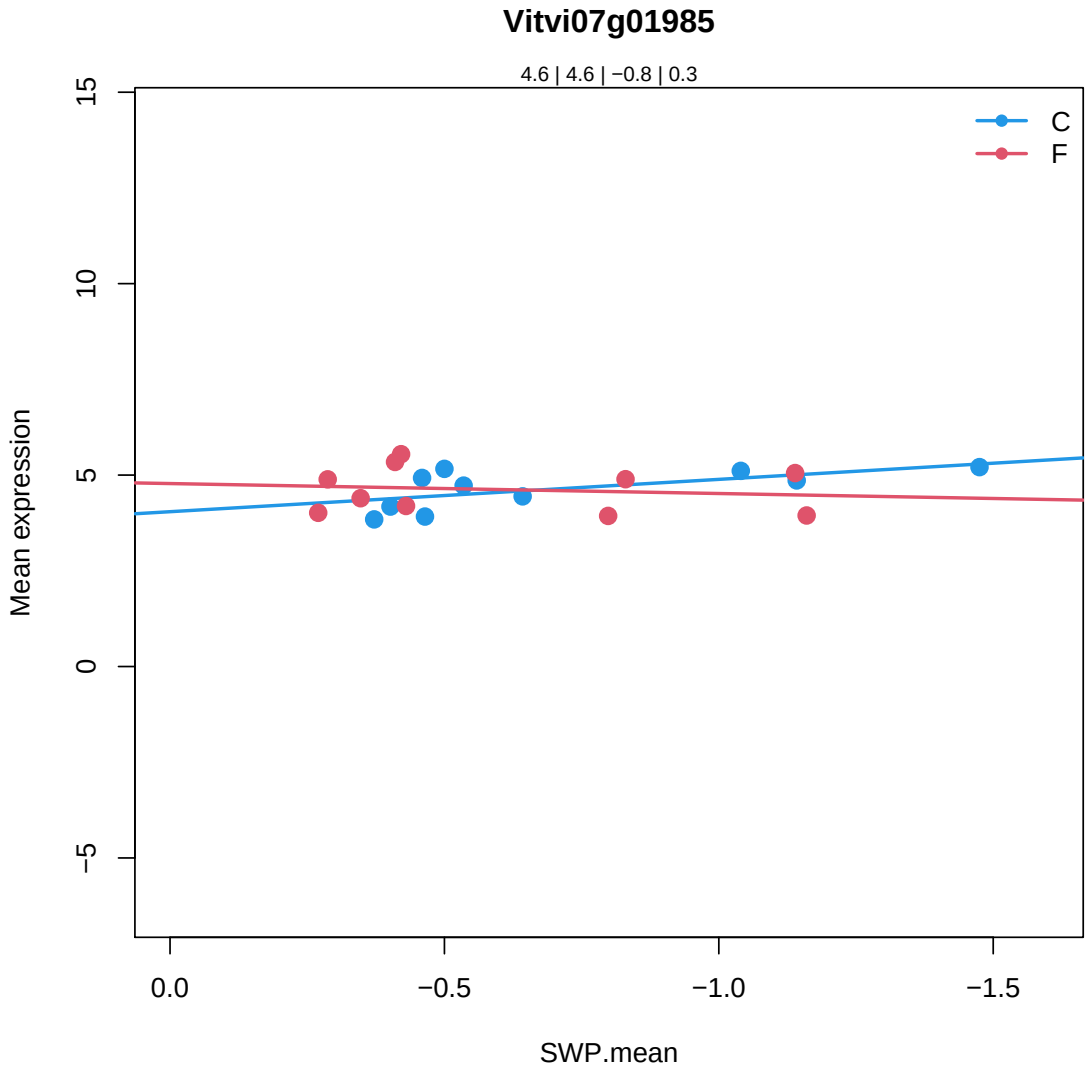
7.6.853 Vitvi07g01985: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01985
        35.2
        not assigned.unknown
        Plant calmodulin-binding protein-like protein |
        Chr2:16216999-16218837 FORWARD LENGTH=612 |
        201606
```

Coefficients for Vitvi07g01985.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.637127	2.401397e-18	***	7.427373e-18	***
SlopeC	-0.8445132	0.08158789	.	0.5779075	
MeanF-MeanC	-0.01697718	0.9430565		0.9853726	
SlopeF-SlopeC	1.104511	0.1229465		0.9999488	



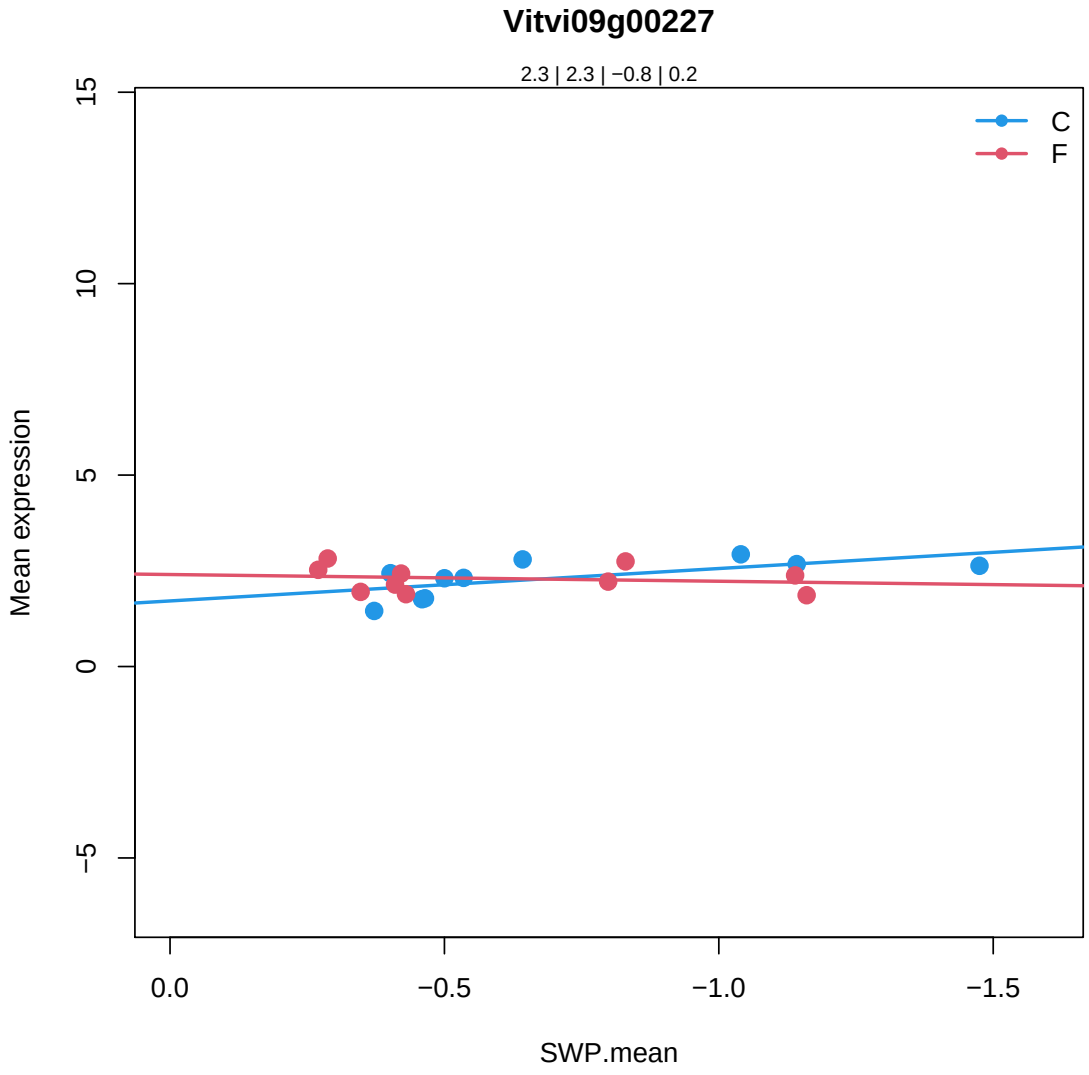
7.6.854 Vitvi09g00227: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00227
        35.2
        not assigned.unknown
        basic helix-loop-helix (bHLH) DNA-binding superfamily protein |
        Chr3:7507720-7508841 FORWARD LENGTH=373 |
        201606
```

Coefficients for Vitvi09g00227.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.308075	2.497482e-14	***	4.03248e-14	***
SlopeC	-0.8466286	0.02855972	*	0.4275443	
MeanF-MeanC	-0.01236324	0.9468559		0.986373	
SlopeF-SlopeC	1.022488	0.0702936	.	0.9999488	



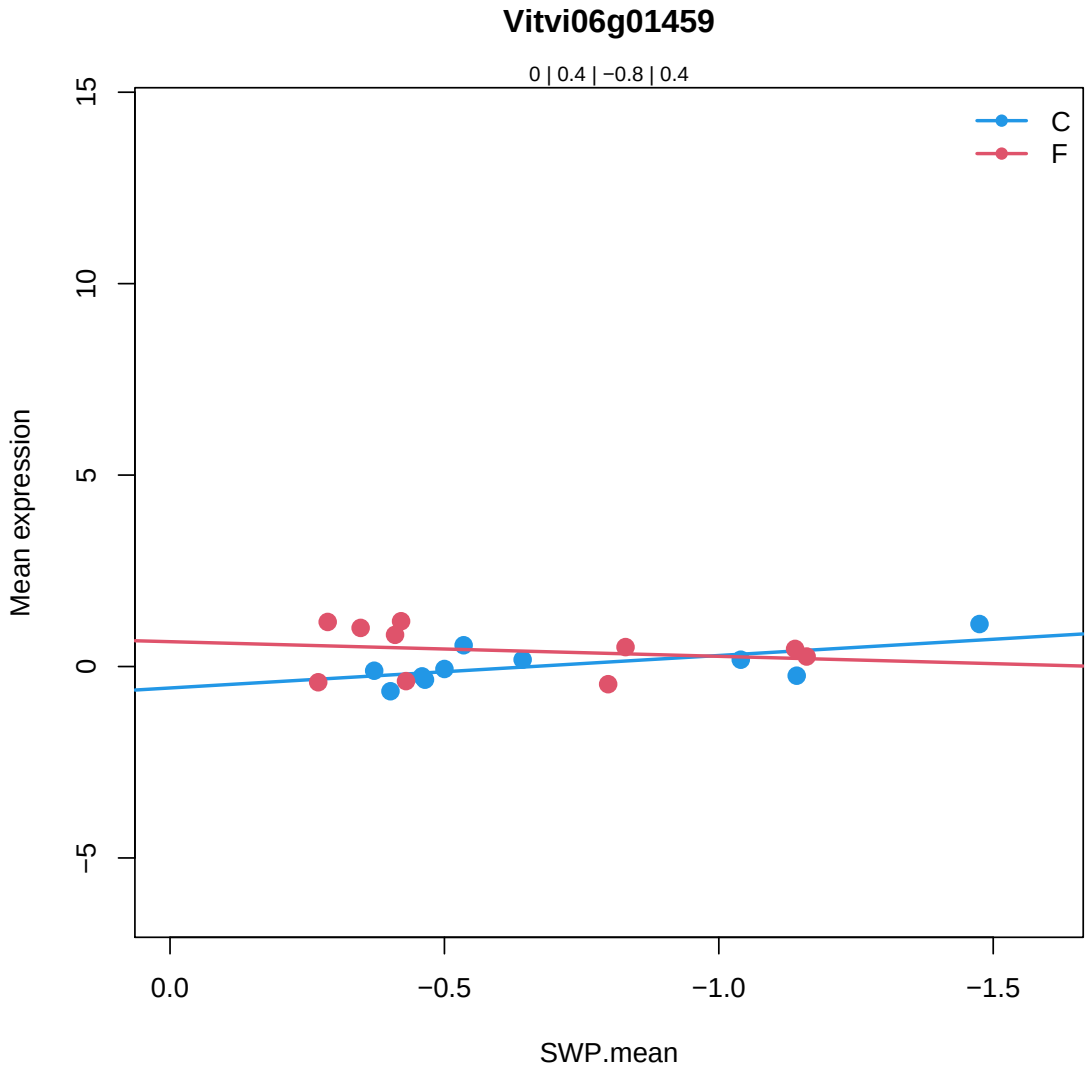
7.6.855 Vitvi06g01459: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01459
        29.5.1
        protein.degradation.subtilases
        Subtilisin-like serine endopeptidase family protein |
        Chr2:1401450-1407694 REVERSE LENGTH=772 |
        201606
```

Coefficients for Vitvi06g01459.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.0358832	0.8358979		0.8390909	
SlopeC	-0.8481194	0.08903161	.	0.5952322	
MeanF-MeanC	0.3797329	0.1312854		0.4317265	
SlopeF-SlopeC	1.230442	0.09685214	.	0.9999488	



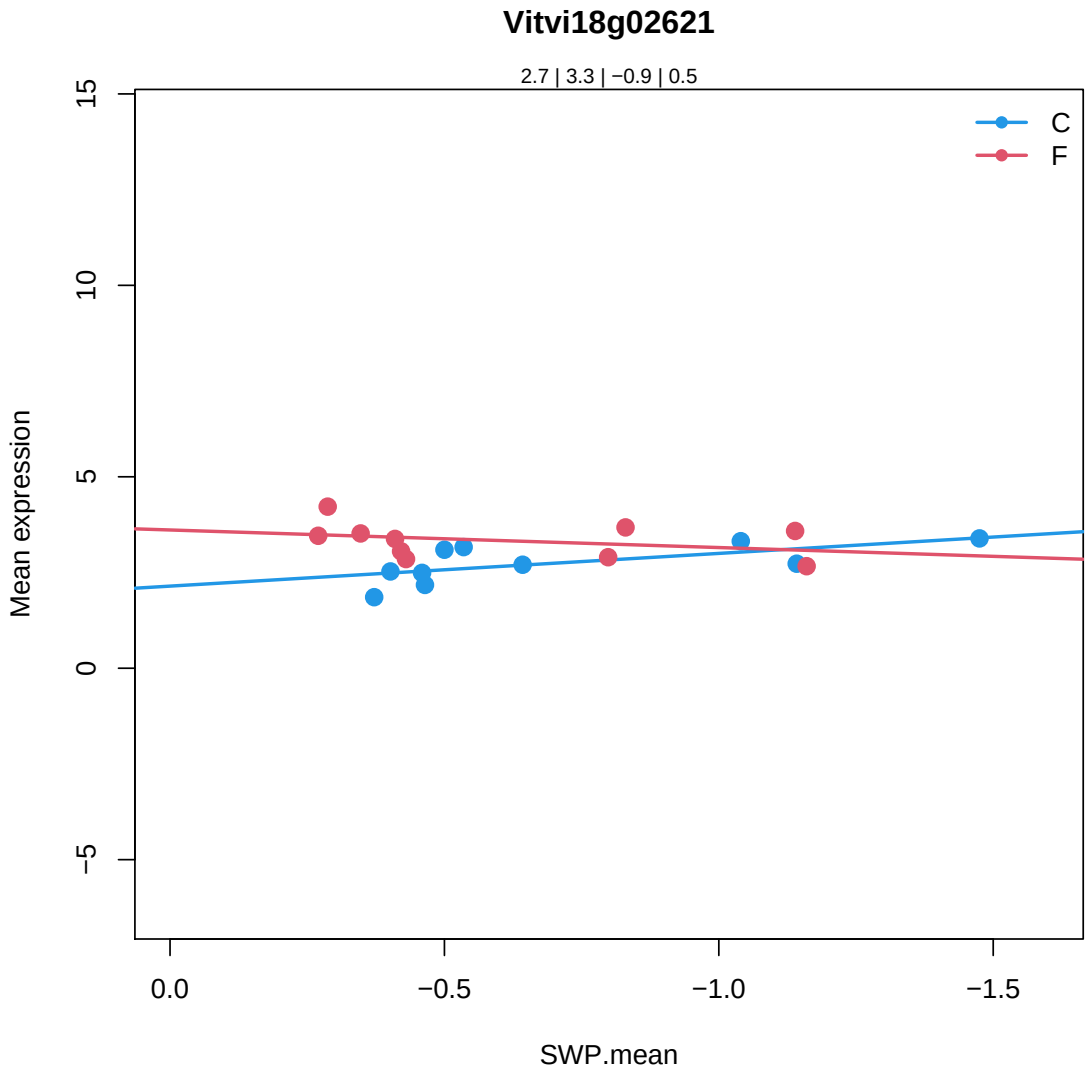
7.6.856 Vitvi18g02621: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02621
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi18g02621.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.744793	5.380202e-15	***	9.273441e-15	***
SlopeC	-0.854416	0.04317342	*	0.48214	
MeanF-MeanC	0.586176	0.008431779	**	0.06700583	.
SlopeF-SlopeC	1.313299	0.03735183	*	0.9999488	



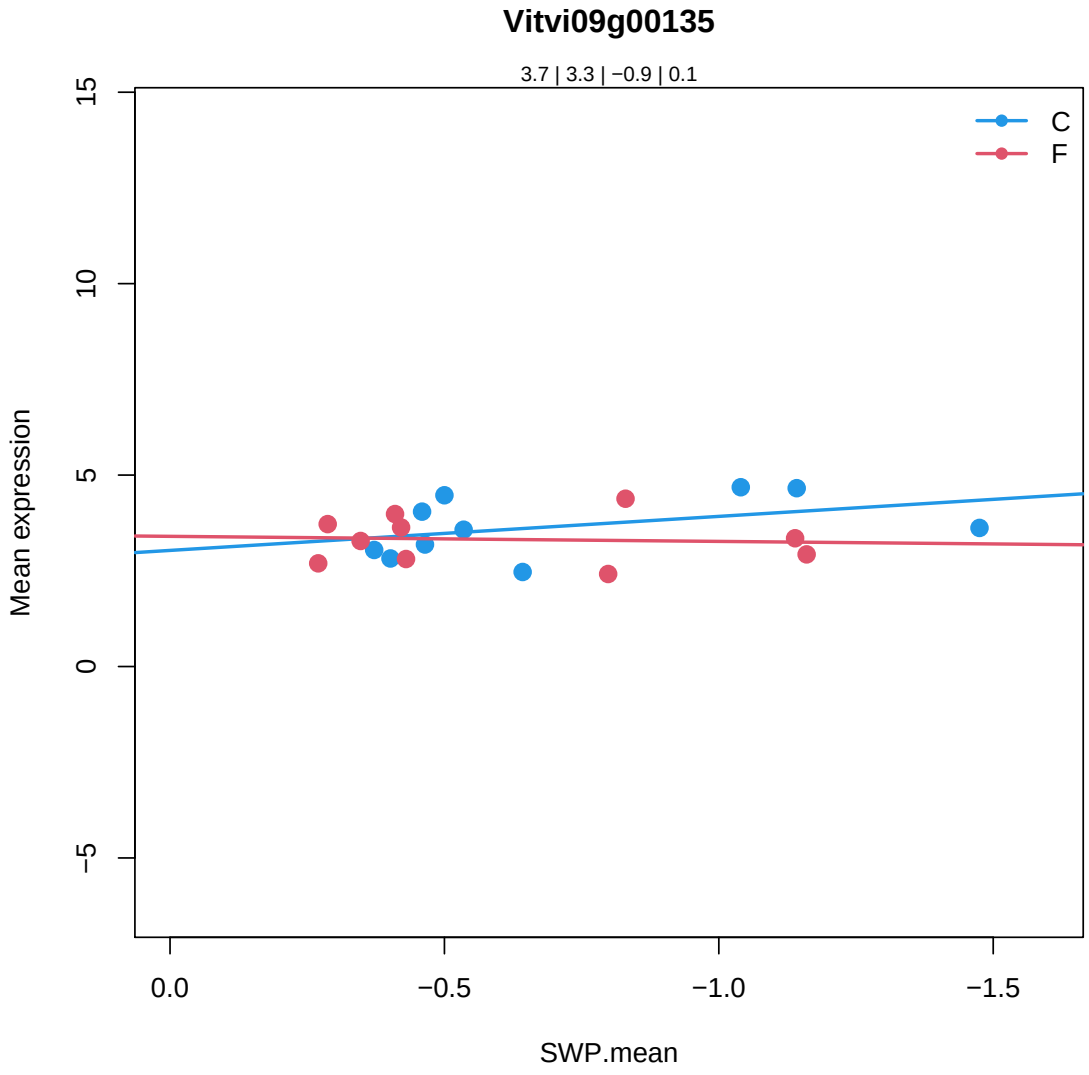
7.6.857 Vitvi09g00135: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00135
        29.2.2
        protein.synthesis.ribosome biogenesis
        midasin-like protein |
        Chr1:25069727-25095526 REVERSE LENGTH=5400 |
        201606
```

Coefficients for Vitvi09g00135.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.657098	3.307772e-14	***	5.279273e-14	***
SlopeC	-0.8889279	0.1396391		0.6655343	
MeanF-MeanC	-0.3378612	0.2640057		0.6258264	
SlopeF-SlopeC	1.020922	0.2494741		0.9999488	



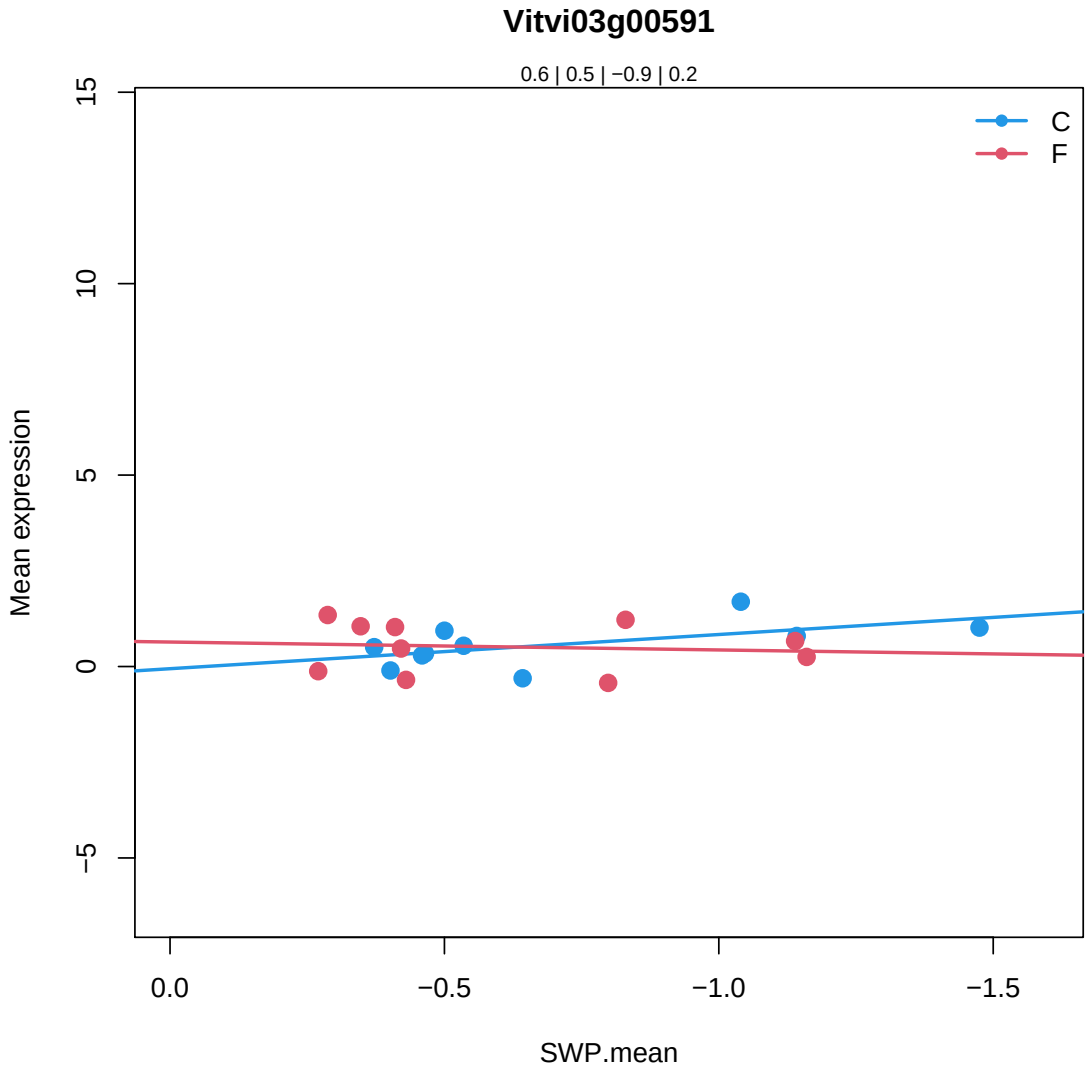
7.6.858 Vitvi03g00591: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00591
        35.2
        not assigned.unknown
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr2:12712884-12715100 FORWARD LENGTH=738 |
        201606
```

Coefficients for Vitvi03g00591.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.5708901	0.004914042	**	0.005242516	**
SlopeC	-0.8929253	0.0922191	.	0.6008919	
MeanF-MeanC	-0.05763071	0.8250341		0.9508165	
SlopeF-SlopeC	1.099508	0.1592727		0.9999488	



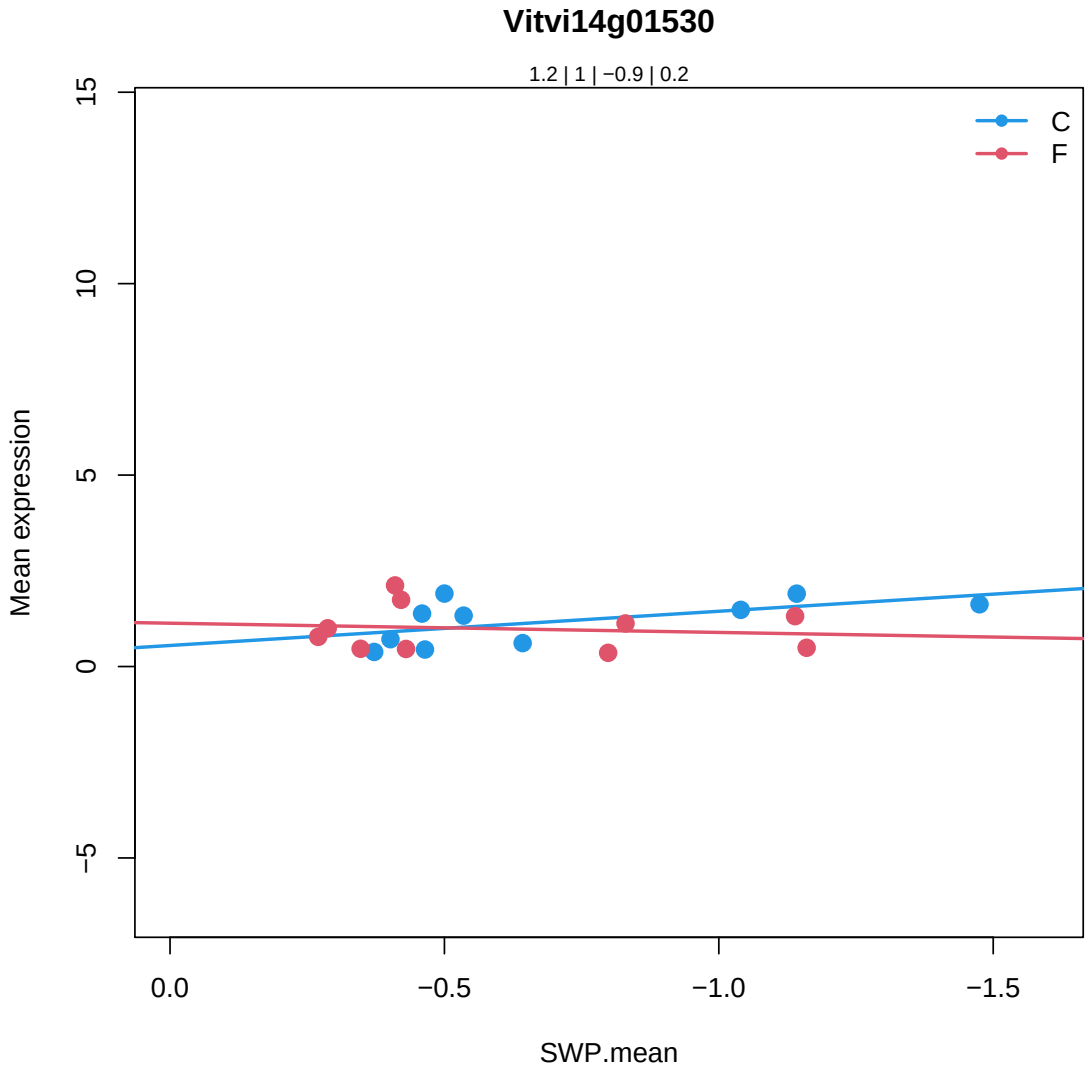
7.6.859 Vitvi14g01530: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01530
        33.99
        development.unspecified
        Major facilitator superfamily protein |
        Chr5:4556308-4558447 FORWARD LENGTH=579 |
        201606
```

Coefficients for Vitvi14g01530.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.177404	1.034865e-06	***	1.194593e-06	***
SlopeC	-0.8939279	0.07992428	.	0.5748584	
MeanF-MeanC	-0.1931944	0.4430276		0.7735854	
SlopeF-SlopeC	1.134791	0.1315606		0.9999488	



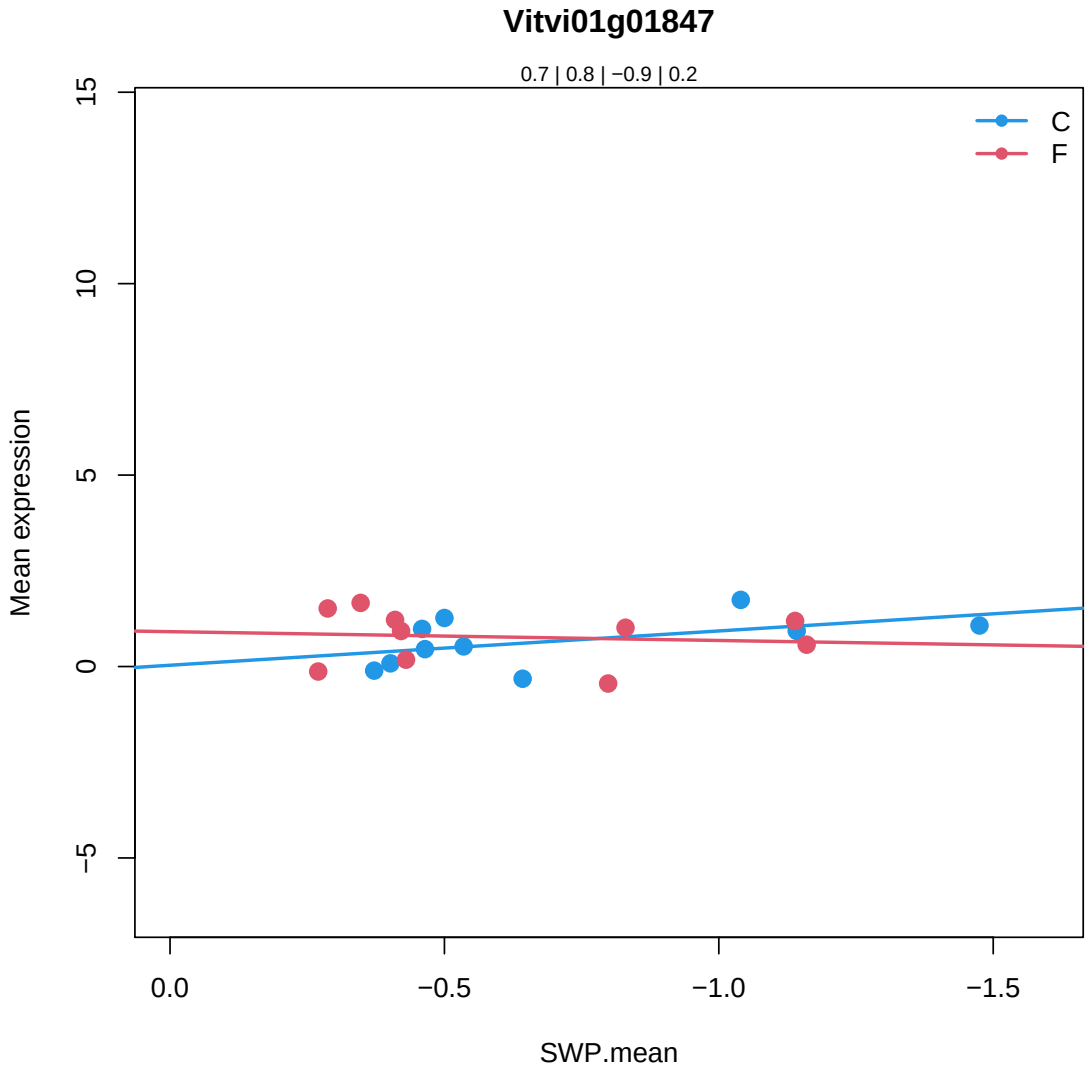
7.6.860 Vitvi01g01847: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01847
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr5:26551879-26553741 FORWARD LENGTH=620 |
        201606
```

Coefficients for Vitvi01g01847.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6626813	0.003163485	**	0.003387988	**
SlopeC	−0.8955888	0.1210663		0.6409492	
MeanF−MeanC	0.1072979	0.7073203		0.9088809	
SlopeF−SlopeC	1.125847	0.1868623		0.9999488	



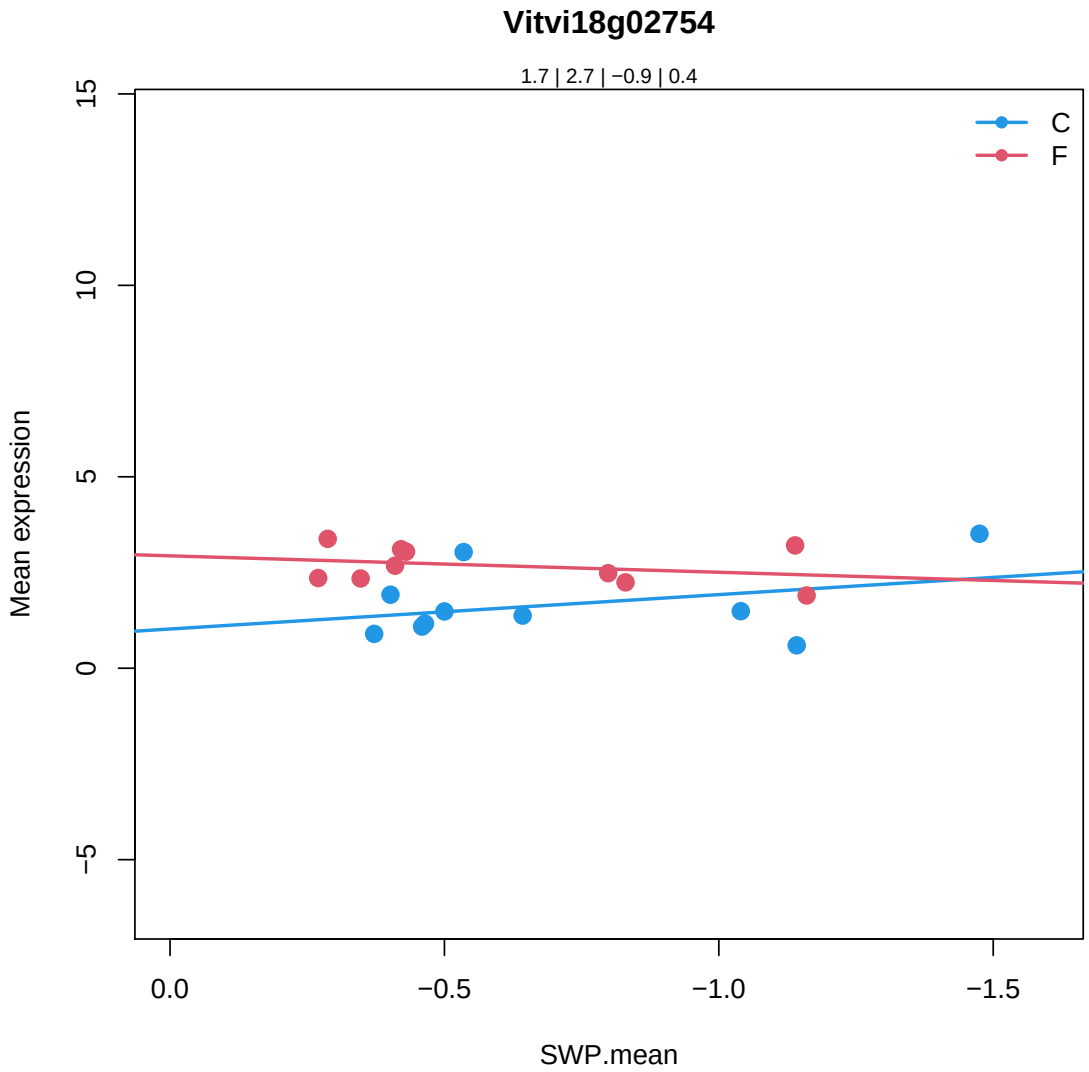
7.6.861 Vitvi18g02754: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02754
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi18g02754.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.655841	1.422989e-07	***	1.681725e-07	***
SlopeC	-0.8983868	0.1496991		0.6760634	
MeanF-MeanC	1.018028	0.003107803	**	0.03155839	*
SlopeF-SlopeC	1.327423	0.1525375		0.9999488	



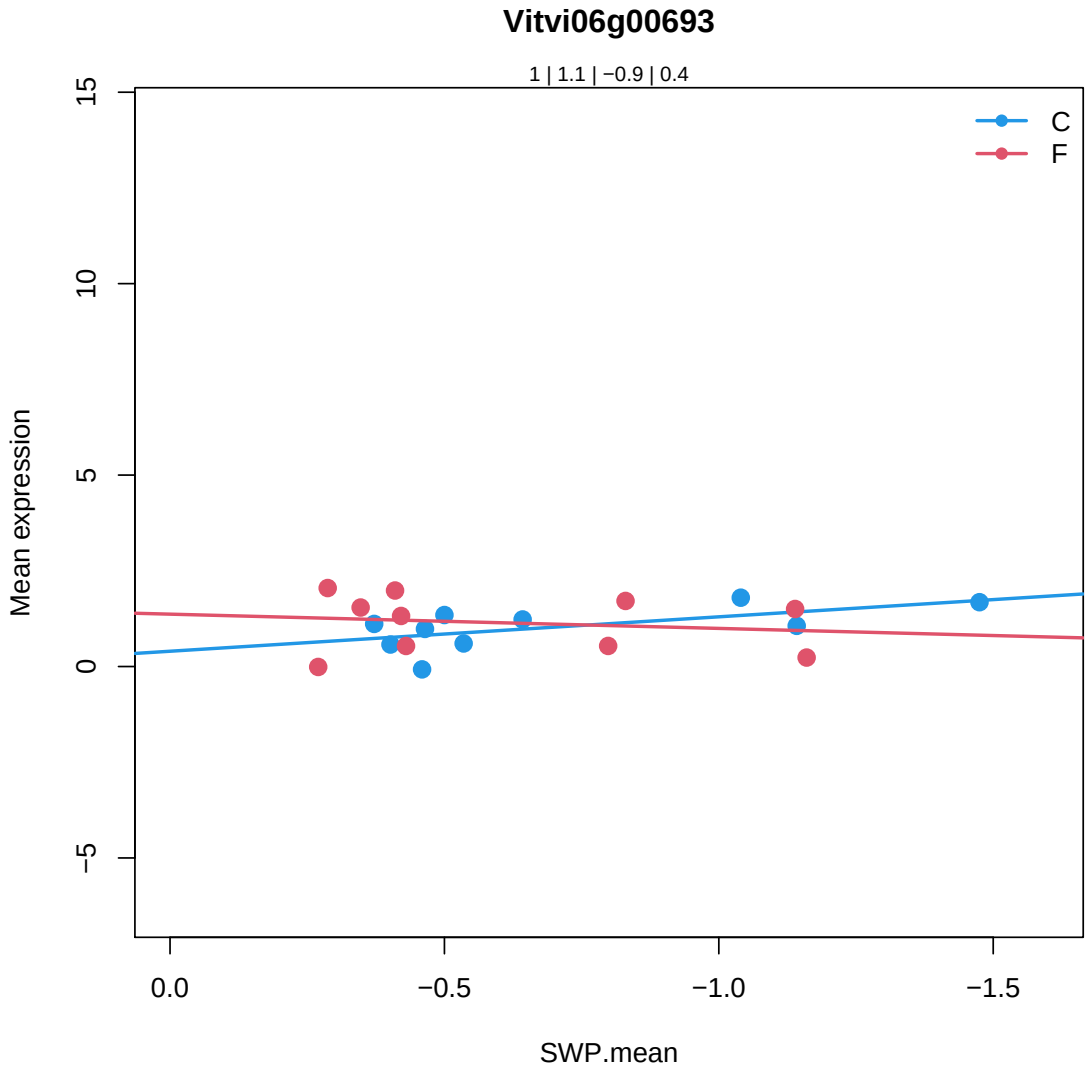
7.6.862 Vitvi06g00693: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00693
        29.4.1
        protein.postranslational modification.kinase
        Protein kinase superfamily protein |
        Chr5:23655312-23657943 FORWARD LENGTH=604 |
        201606
```

Coefficients for Vitvi06g00693.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.030935	2.448557e-05	***	2.739551e-05	***
SlopeC	-0.8990479	0.1079107		0.6223948	
MeanF-MeanC	0.1097023	0.6911251		0.9015976	
SlopeF-SlopeC	1.271384	0.1255508		0.9999488	



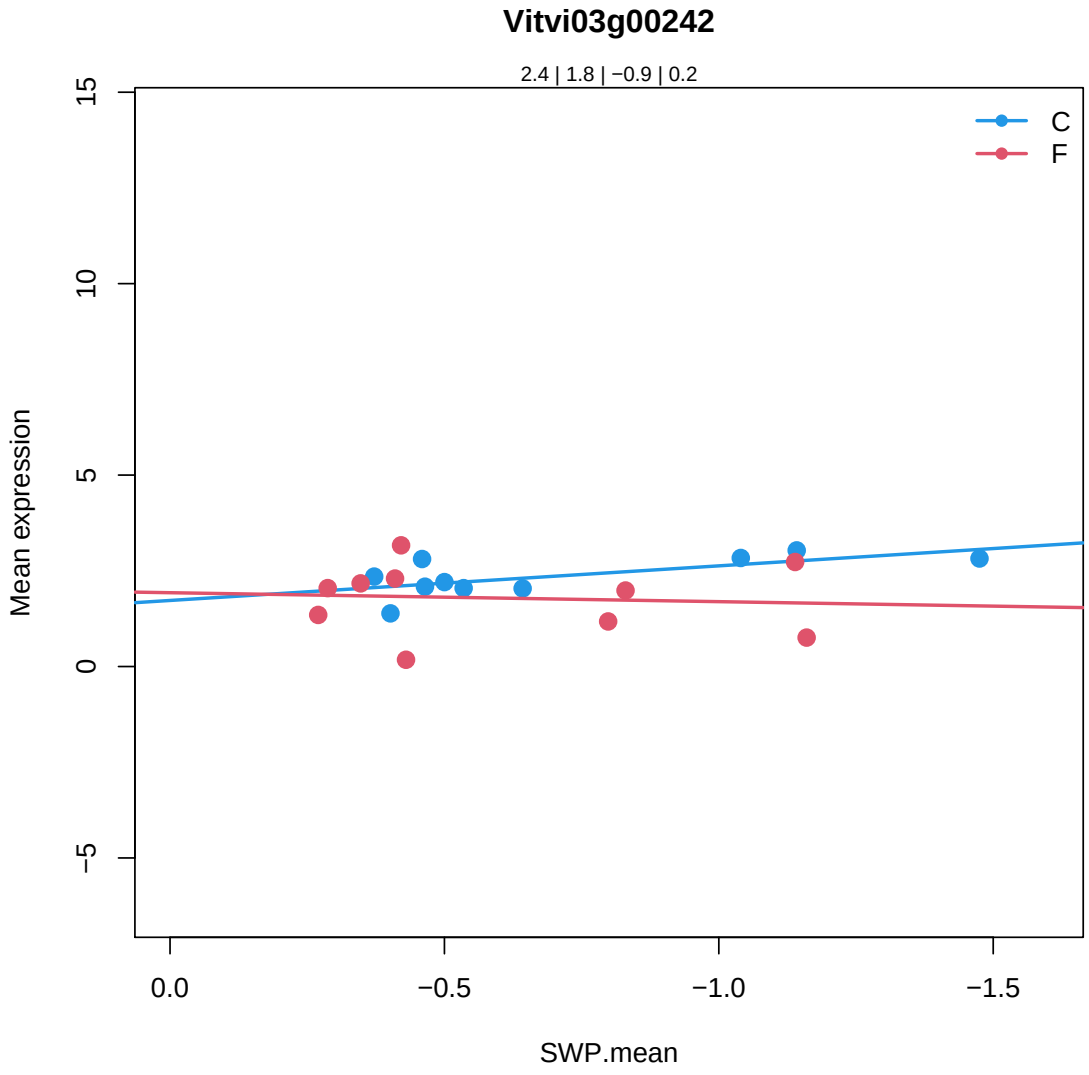
7.6.863 Vitvi03g00242: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00242
        33.99
        development.unspecified
        EXORDIUM like 5 |
        Chr2:7494892-7495983 REVERSE LENGTH=363 |
        201606
```

Coefficients for Vitvi03g00242.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.360824	3.306261e-10	***	4.240493e-10	***
SlopeC	-0.9039128	0.1481744		0.6736918	
MeanF-MeanC	-0.5755883	0.07388402	.	0.3056841	
SlopeF-SlopeC	1.137399	0.2183225		0.9999488	



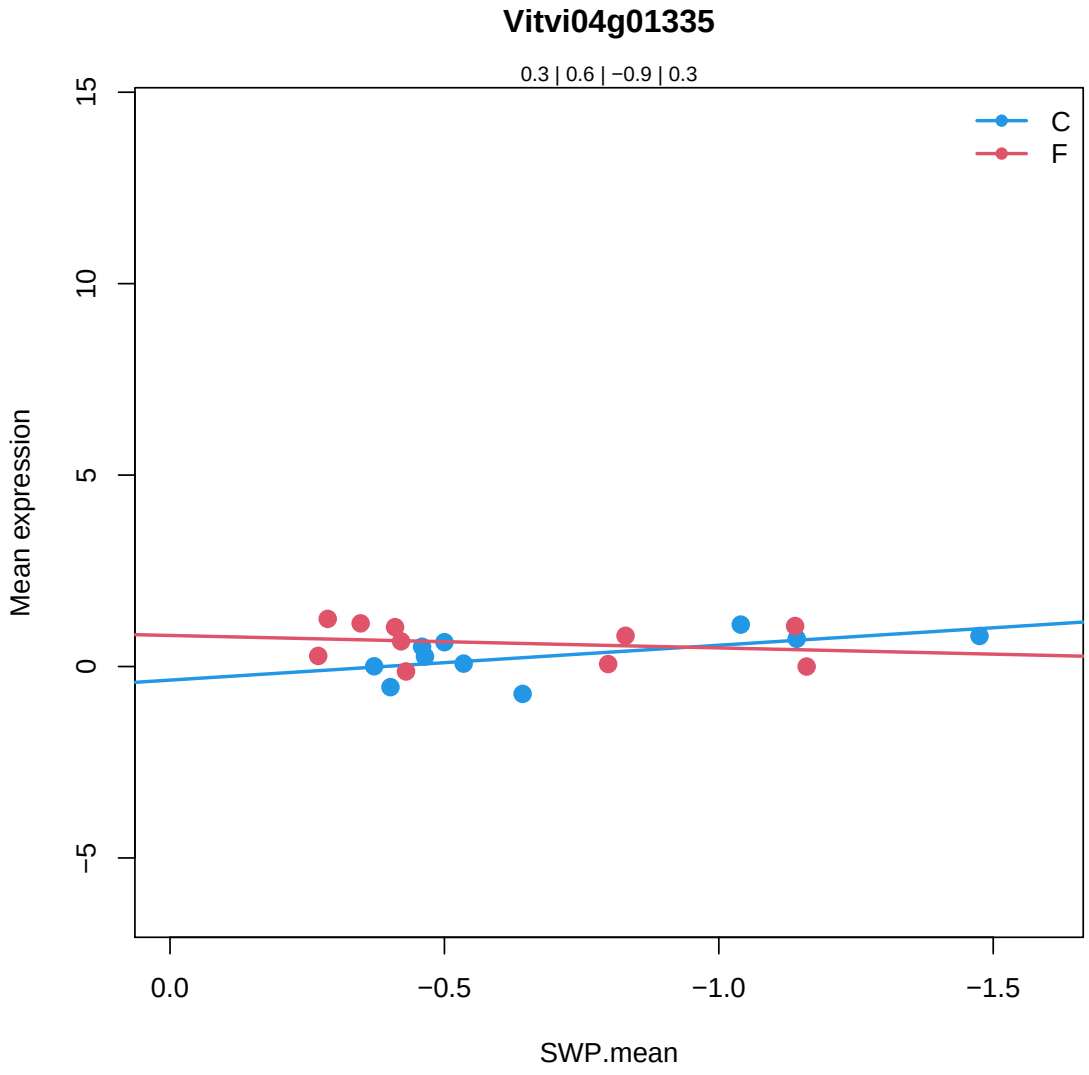
7.6.864 Vitvi04g01335: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01335
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr3:17651912-17654032 FORWARD LENGTH=706 |
        201606
```

Coefficients for Vitvi04g01335.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.28547	0.09223973	.	0.09546533	.
SlopeC	-0.9109576	0.05588047	.	0.5283686	
MeanF-MeanC	0.3272234	0.1675433		0.4962484	
SlopeF-SlopeC	1.236427	0.07912393	.	0.9999488	



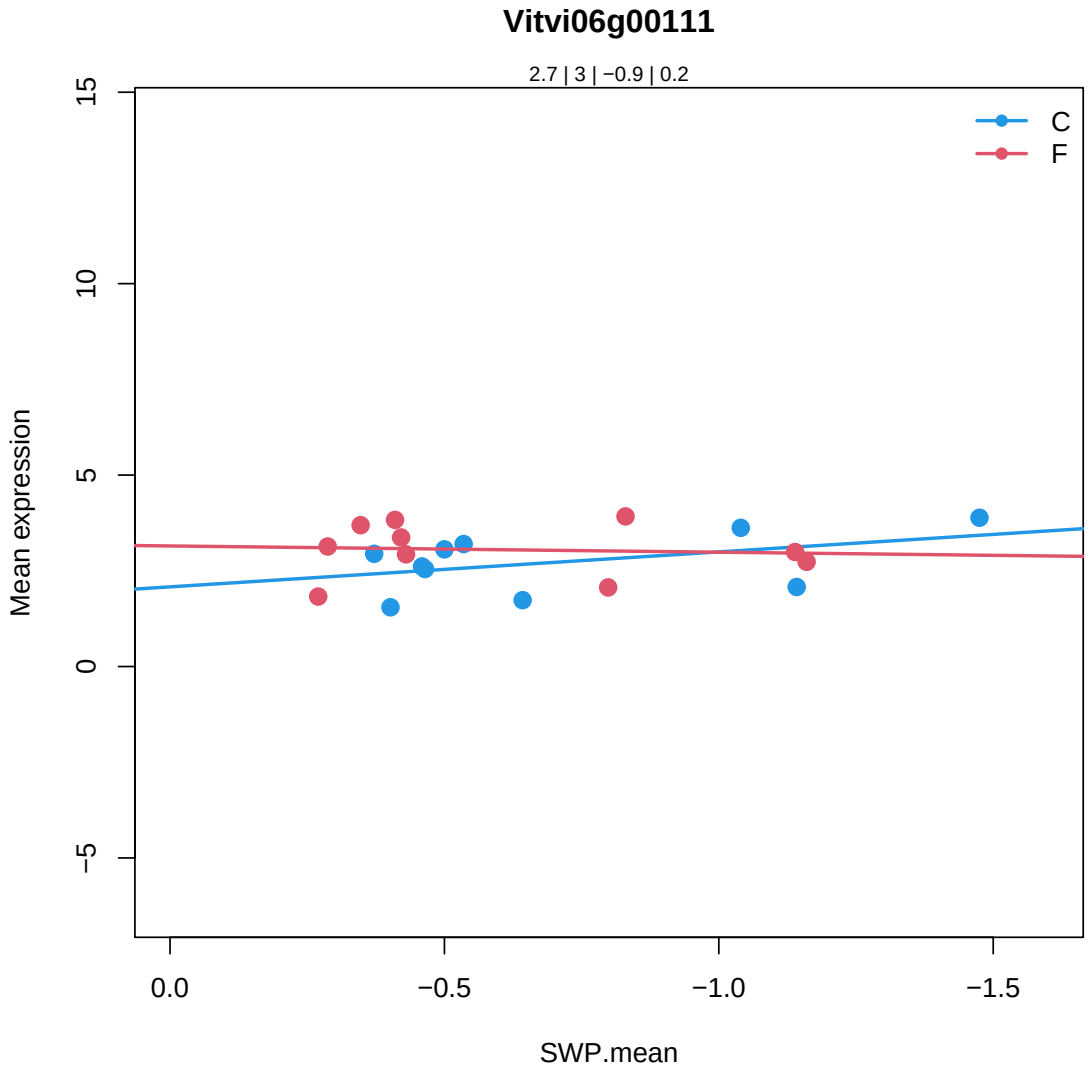
7.6.865 Vitvi06g00111: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00111
        26.12
        misc.peroxidases
        peroxidase 2 |
        Chr5:2077567-2078857 REVERSE LENGTH=335 |
        201606
```

Coefficients for Vitvi06g00111.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.722538	2.282276e-11	***	3.067318e-11	***
SlopeC	-0.9131056	0.1440177		0.6693663	
MeanF-MeanC	0.326774	0.297573		0.6640861	
SlopeF-SlopeC	1.076427	0.2428202		0.9999488	



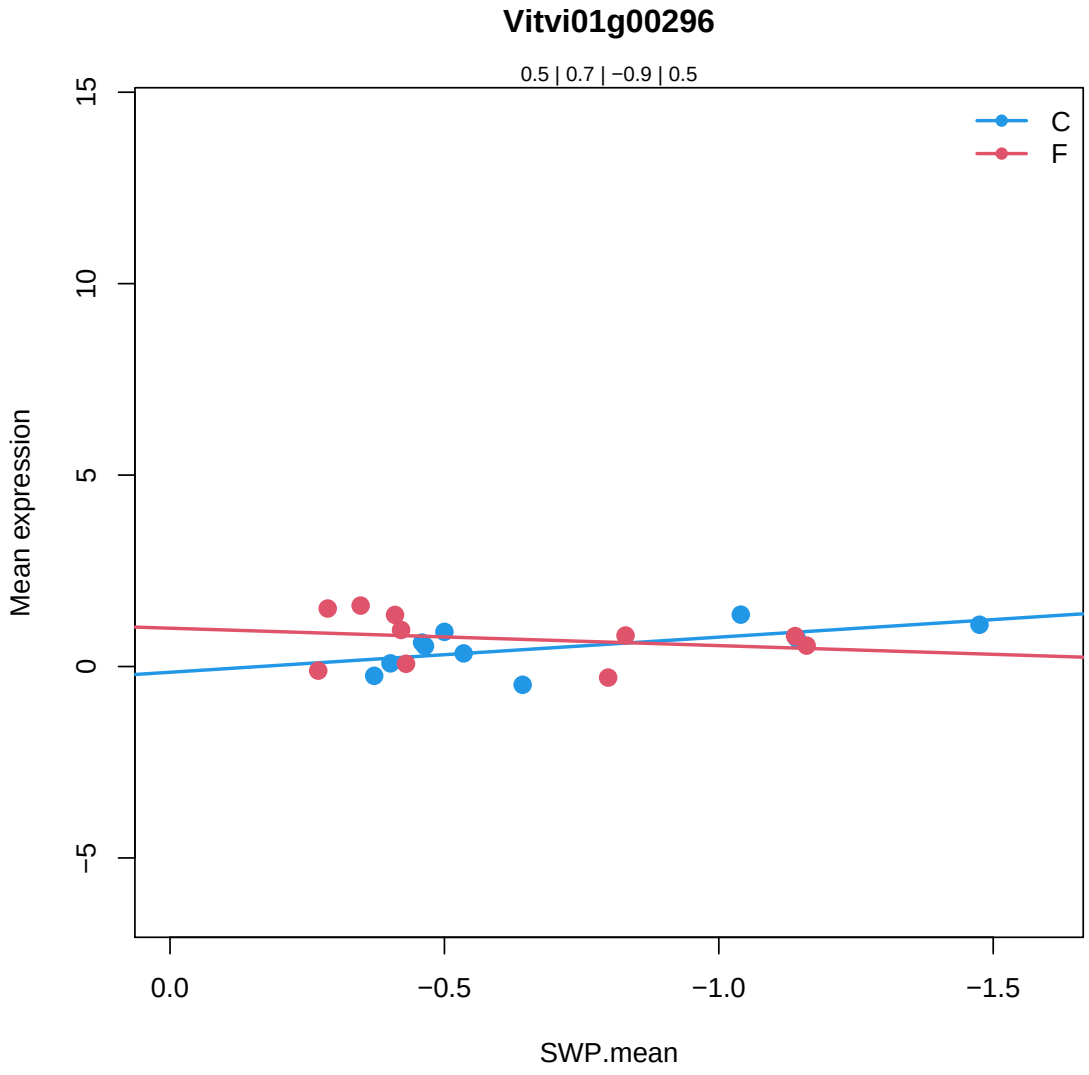
7.6.866 Vitvi01g00296: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00296
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr1:4601526-4603174 FORWARD LENGTH=474 |
        201606
```

Coefficients for Vitvi01g00296.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4951902	0.01227525	*	0.01297589	*
SlopeC	-0.9173828	0.08261048	.	0.5797186	
MeanF-MeanC	0.2282066	0.3827713		0.7336772	
SlopeF-SlopeC	1.371773	0.08128641	.	0.9999488	



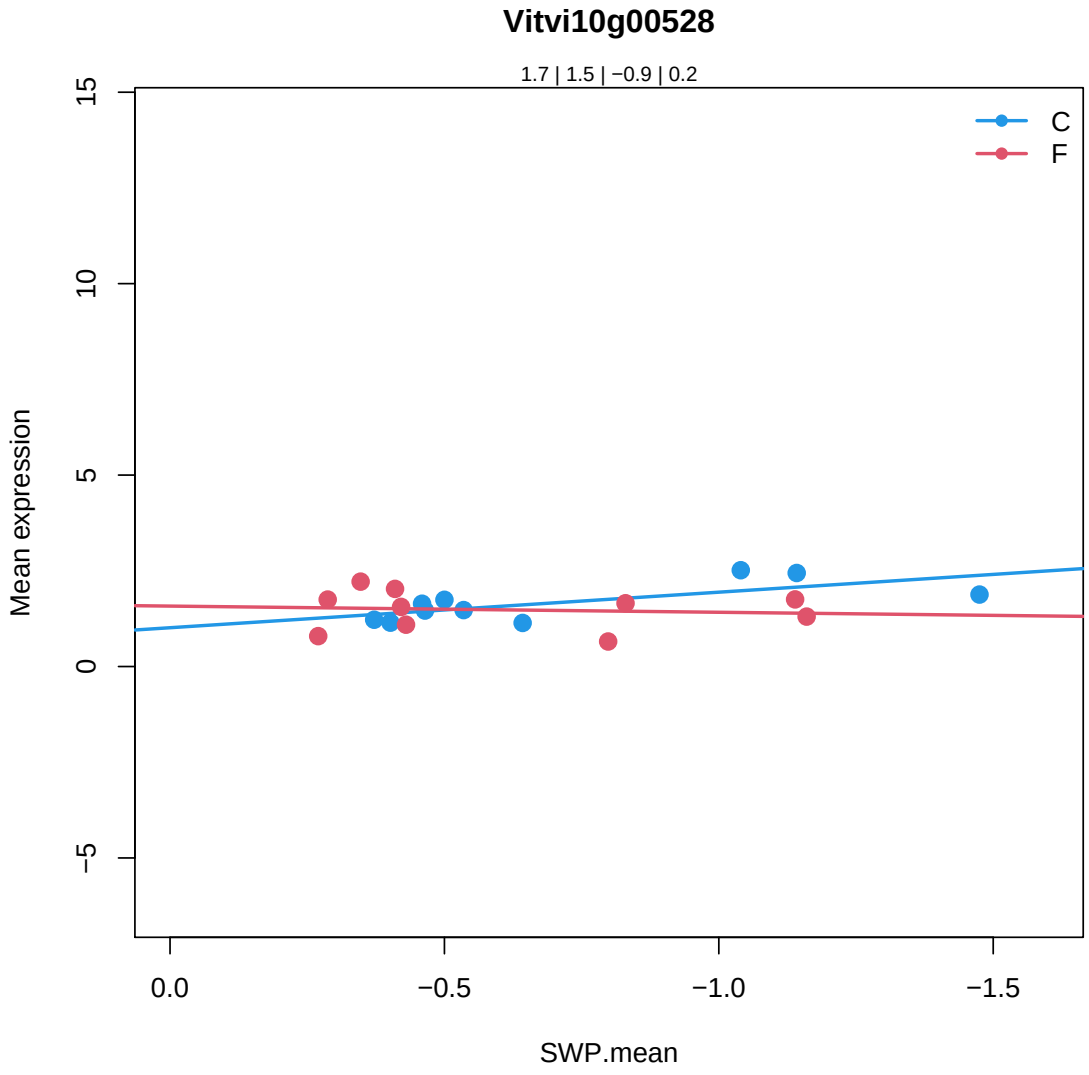
7.6.867 Vitvi10g00528: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00528
        35.2
        not assigned.unknown
        ATP synthase F1 complex assembly factor |
        Chr2:14382843-14384198 REVERSE LENGTH=248 |
        201606
```

Coefficients for Vitvi10g00528.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.665975	1.950829e-10	***	2.525011e-10	***
SlopeC	-0.9282422	0.03531822	*	0.4497245	
MeanF-MeanC	-0.1862762	0.3849762		0.7350095	
SlopeF-SlopeC	1.089708	0.09061613	.	0.9999488	



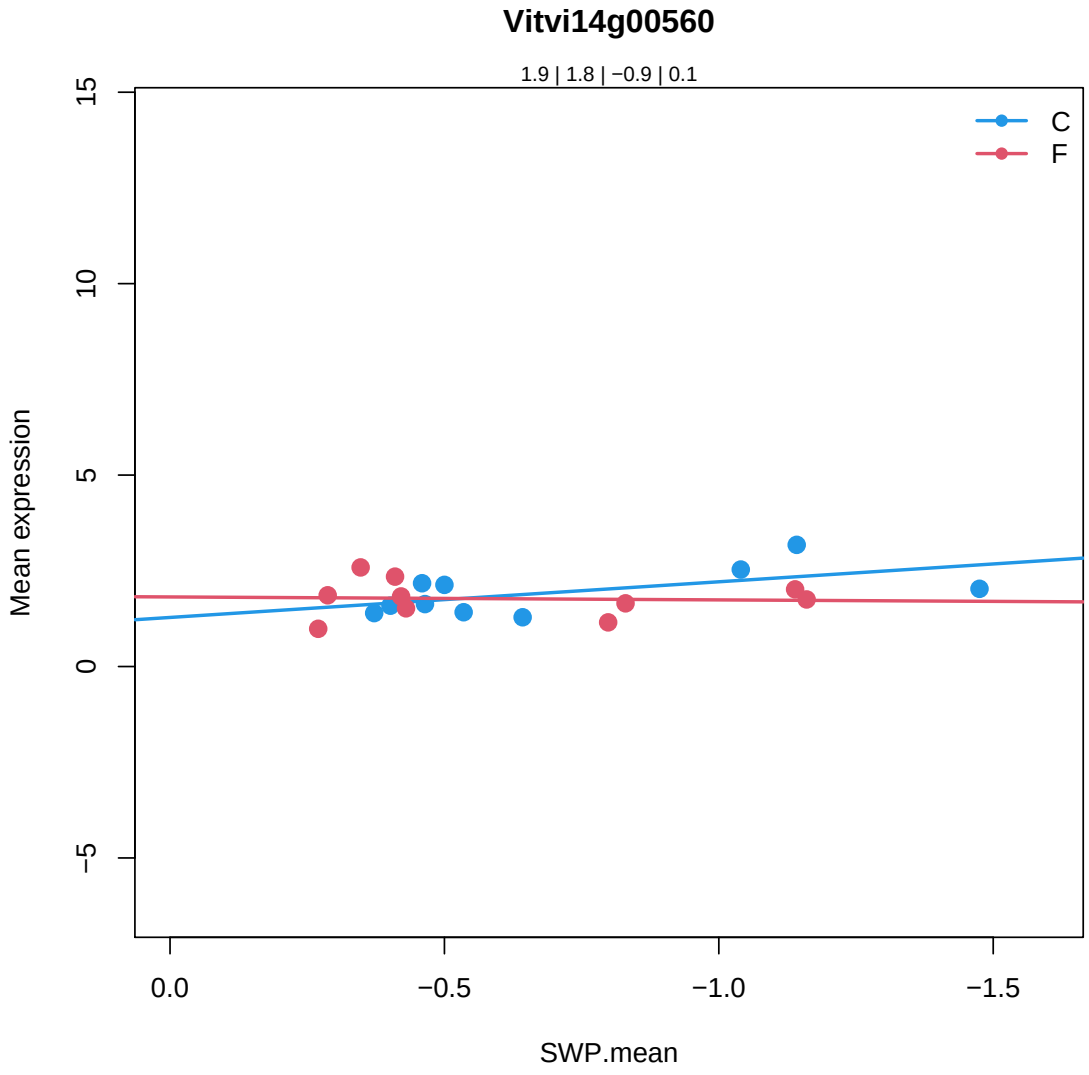
7.6.868 Vitvi14g00560: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g00560
        31.3.1
        cell.cycle.peptidylprolyl isomerase
        rotamase cyclophilin 2 |
        Chr3:20806987-20807517 REVERSE LENGTH=176 |
        201606
```

Coefficients for Vitvi14g00560.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.936489	5.061916e-11	***	6.703773e-11	***
SlopeC	-0.9313122	0.04922746	*	0.5059508	
MeanF-MeanC	-0.1664568	0.4714833		0.7896675	
SlopeF-SlopeC	1.008619	0.1438881		0.9999488	



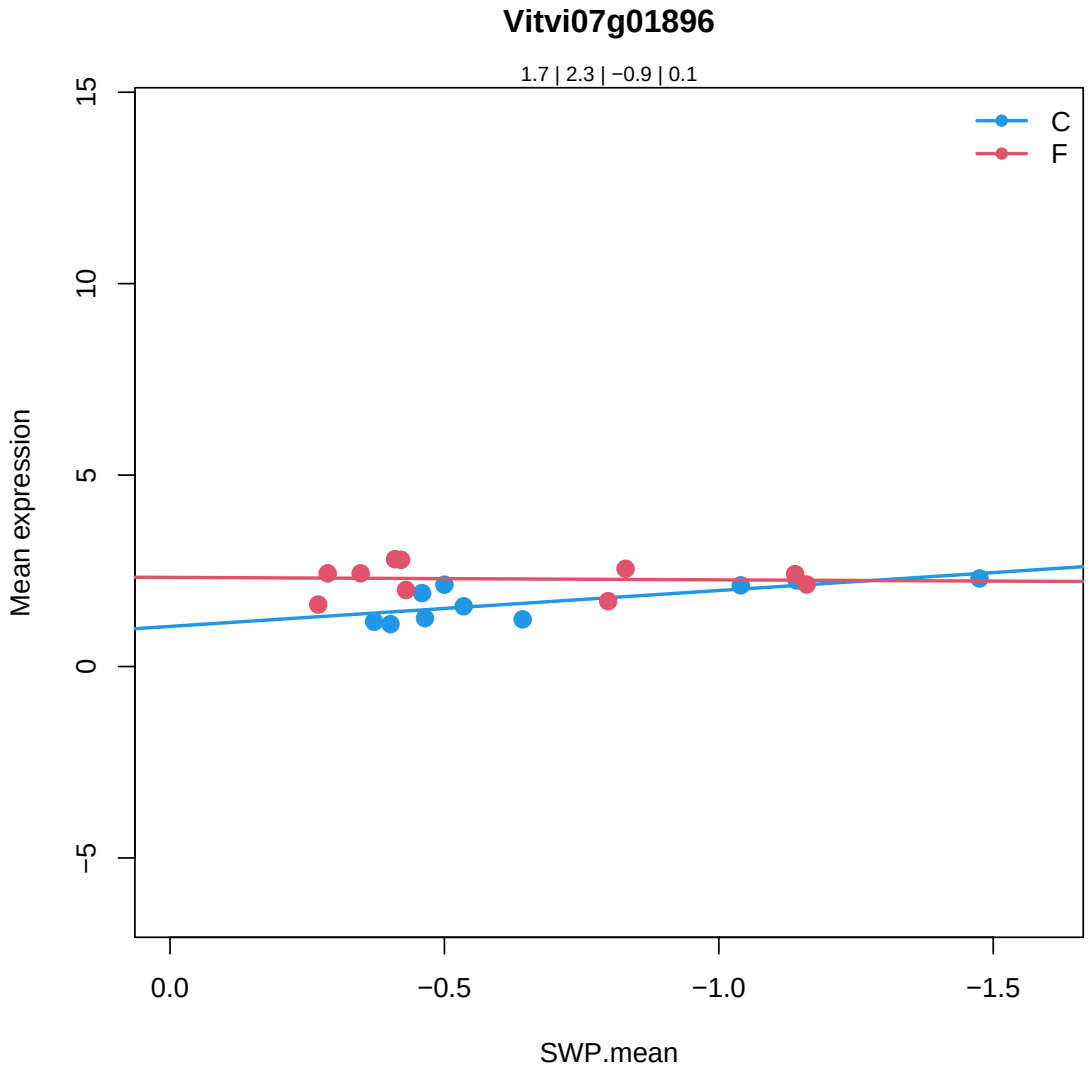
7.6.869 Vitvi07g01896: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01896
        20.1.3.1
        stress.biotic.signalling.MLO-like
        Seven transmembrane MLO family protein |
        Chr2:7568018-7570758 FORWARD LENGTH=542 |
        201606
```

Coefficients for Vitvi07g01896.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.706661	1.749224e-11	***	2.362785e-11	***
SlopeC	-0.9374562	0.01977763	*	0.374907	
MeanF-MeanC	0.5816307	0.005663348	**	0.05012855	.
SlopeF-SlopeC	1.001513	0.08469207	.	0.9999488	



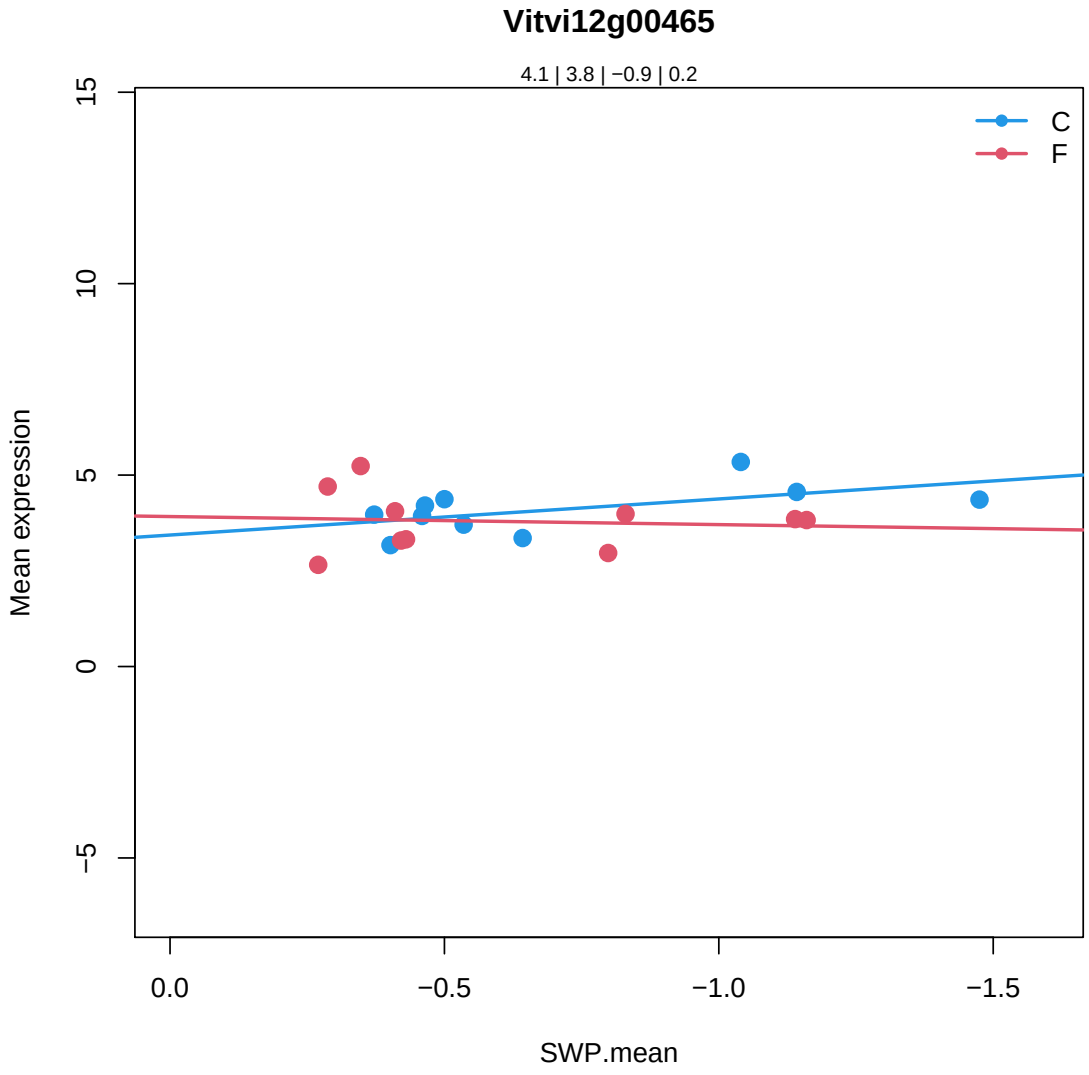
7.6.870 Vitvi12g00465: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00465
        27.1.19
        RNA.processing.ribonucleases
        Metallo-hydrolase/oxidoreductase superfamily protein |
        Chr2:1576808-1578611 FORWARD LENGTH=354 |
        201606
```

Coefficients for Vitvi12g00465.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.09662	2.686475e-15	***	4.799819e-15	***
SlopeC	-0.9422887	0.1149096		0.632338	
MeanF-MeanC	-0.3082216	0.3020818		0.6671976	
SlopeF-SlopeC	1.152761	0.1908788		0.9999488	



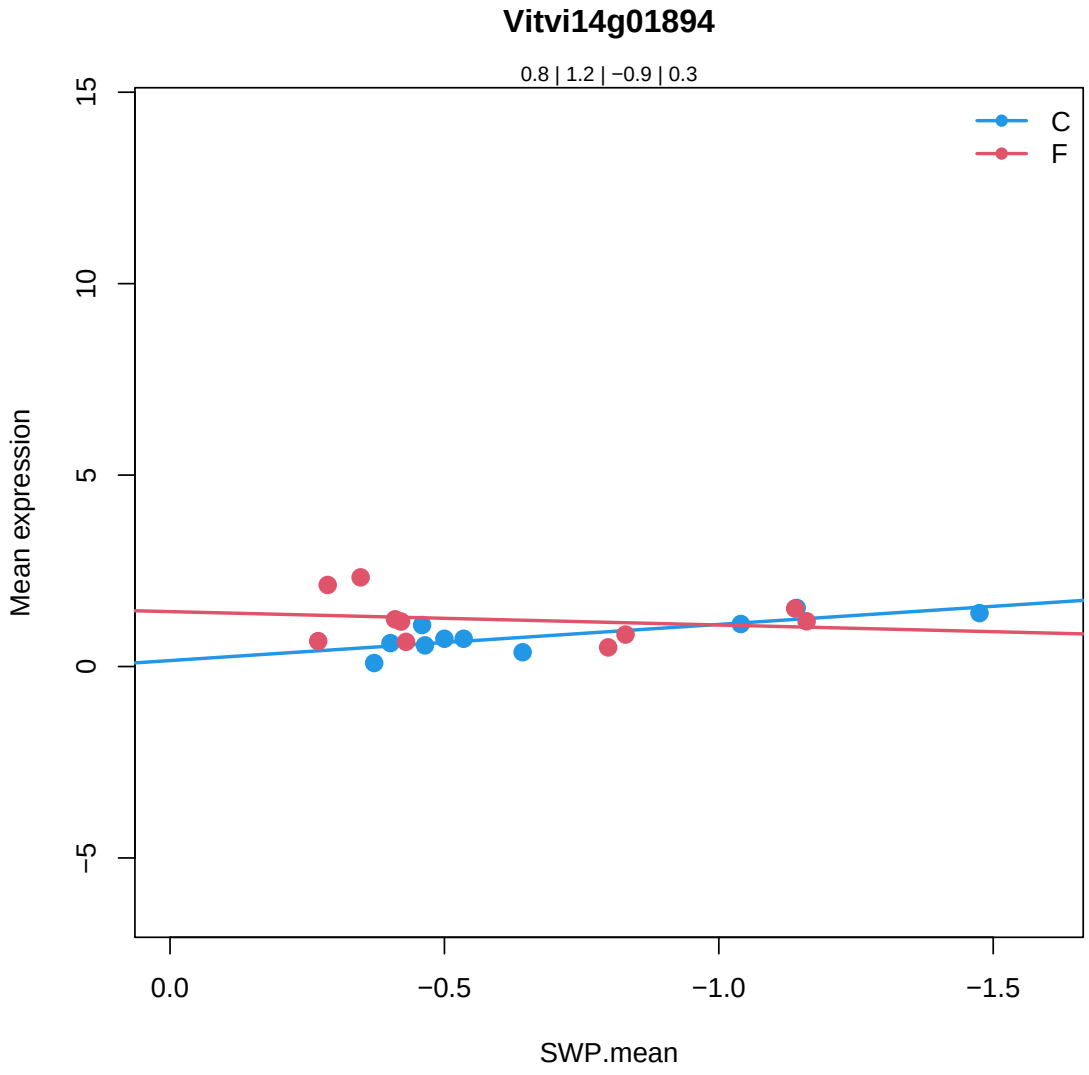
7.6.871 Vitvi14g01894: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01894
        35.2
        not assigned.unknown
        NADH dehydrogenase ubiquinone complex I%2C assembly factor-like protei
        Chr3:10760017-10761834 FORWARD LENGTH=373 |
        201606
```

Coefficients for Vitvi14g01894.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.81945	3.552917e-05	***	3.96149e-05	***
SlopeC	-0.9445819	0.04288773	*	0.48214	
MeanF-MeanC	0.4010264	0.08630498	.	0.3337038	
SlopeF-SlopeC	1.294153	0.06050847	.	0.9999488	



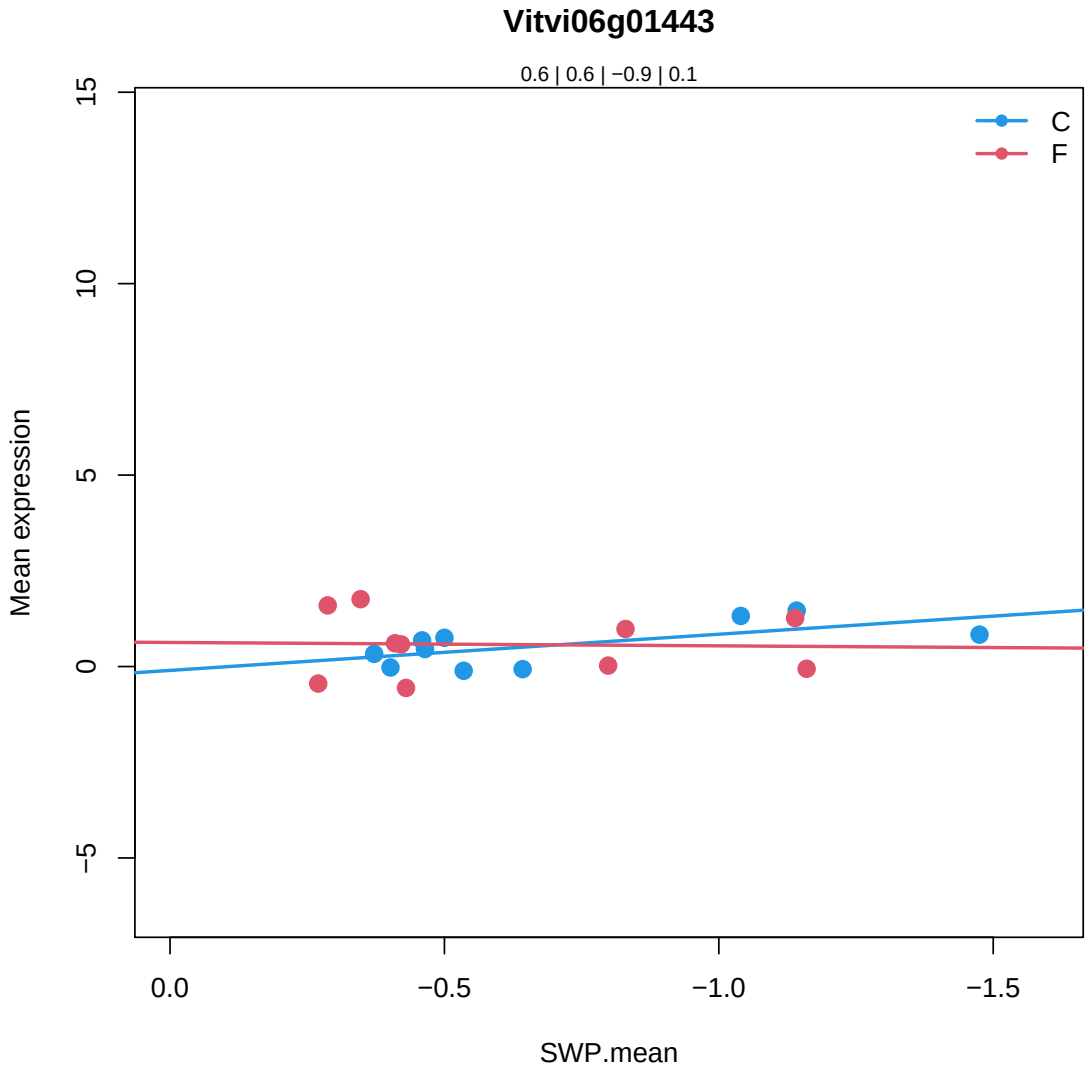
7.6.872 Vitvi06g01443: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01443
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        Pentatricopeptide repeat (PPR) superfamily protein |
        Chr4:7939611-7942898 REVERSE LENGTH=1064 |
        201606
```

Coefficients for Vitvi06g01443.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.5627085	0.01206203	*	0.01275315	*
SlopeC	−0.9452836	0.1123145		0.6275283	
MeanF−MeanC	0.01182501	0.9678725		0.9925468	
SlopeF−SlopeC	1.033982	0.2368607		0.9999488	



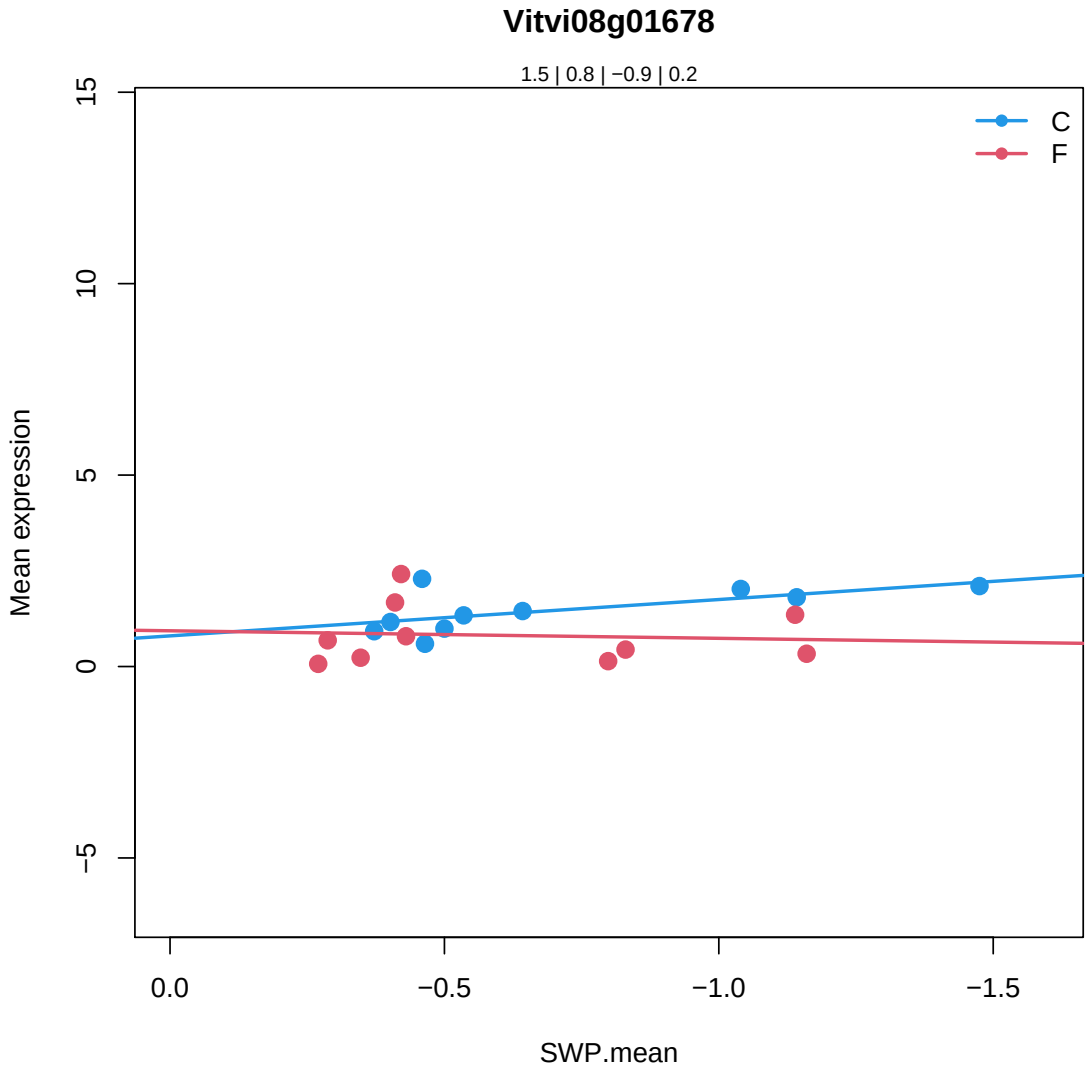
7.6.873 Vitvi08g01678: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01678
        31.1
        cell.organisation
        Ankyrin repeat family protein / BTB/POZ domain-containing protein |
        Chr2:17238019-17240203 REVERSE LENGTH=491 |
        201606
```

Coefficients for Vitvi08g01678.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.467563	2.239938e-07	***	2.631098e-07	***
SlopeC	-0.949355	0.09778574	.	0.6084506	
MeanF-MeanC	-0.6545755	0.02852149	*	0.1636764	
SlopeF-SlopeC	1.146432	0.1744642		0.9999488	



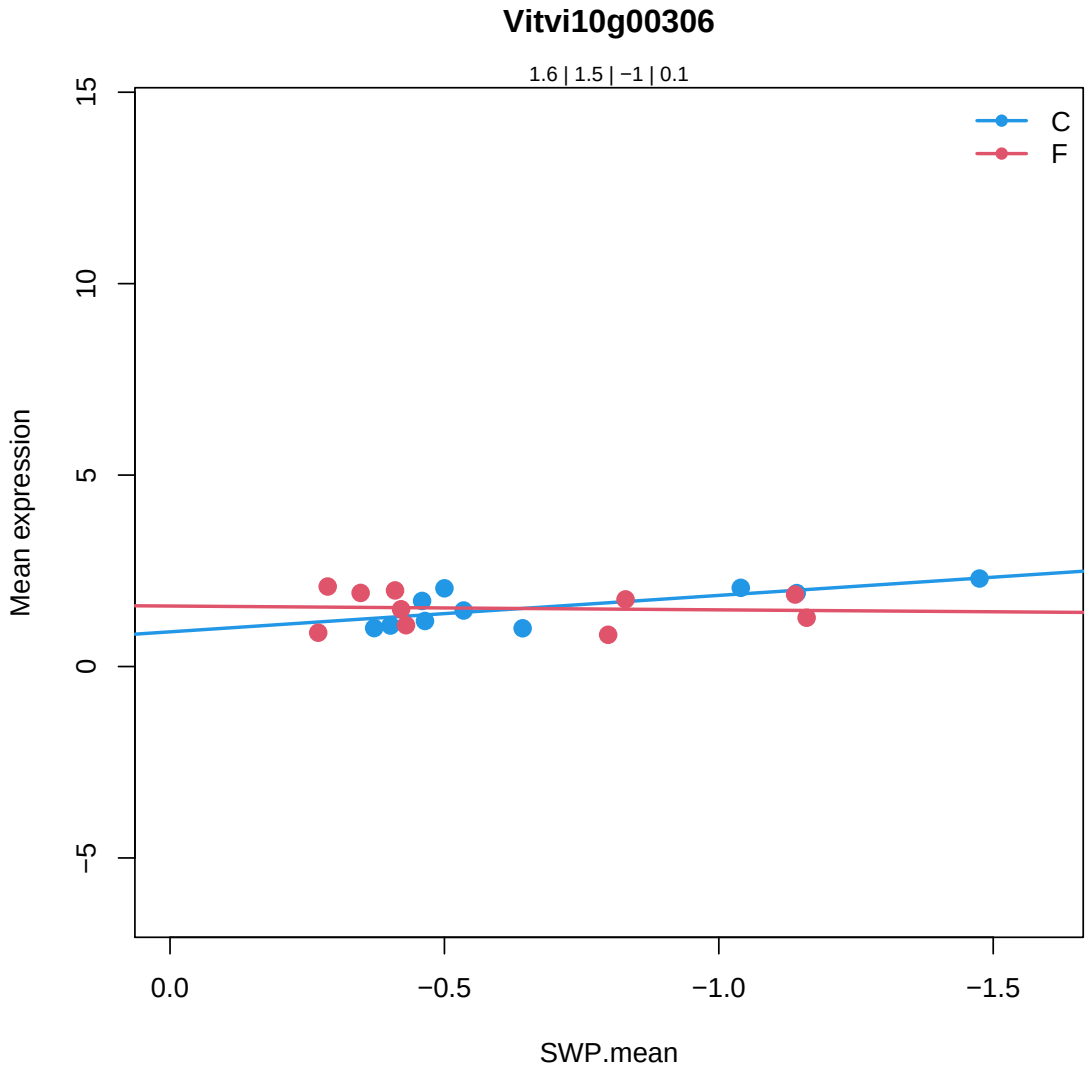
7.6.874 Vitvi10g00306: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00306
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr3:8672774-8674675 FORWARD LENGTH=633 |
        201606
```

Coefficients for Vitvi10g00306.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.574821	2.48663e-10	***	3.203551e-10	***
SlopeC	-0.9512945	0.02534127	*	0.4079655	
MeanF-MeanC	-0.05579162	0.7841823		0.9384607	
SlopeF-SlopeC	1.051281	0.0884615	.	0.9999488	



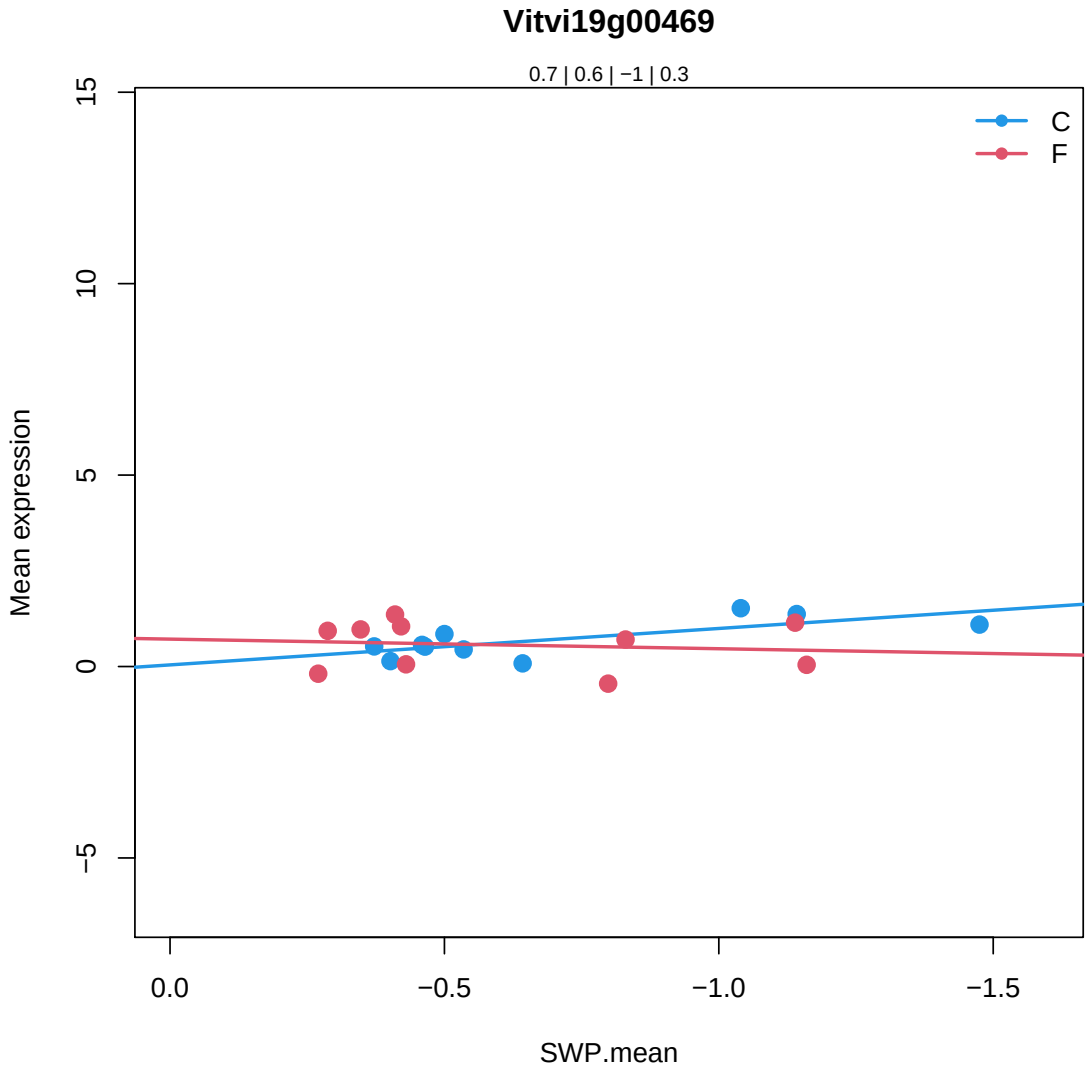
7.6.875 Vitvi19g00469: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g00469
        35.2
        not assigned.unknown
        ARM repeat superfamily protein |
        Chr4:13581581-13585070 REVERSE LENGTH=864 |
        201606
```

Coefficients for Vitvi19g00469.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.7113119	0.0003003171	***	0.0003283668	***
SlopeC	−0.9513856	0.05070835	.	0.5104439	
MeanF−MeanC	−0.1488699	0.5307279		0.8249652	
SlopeF−SlopeC	1.20206	0.09314673	.	0.9999488	



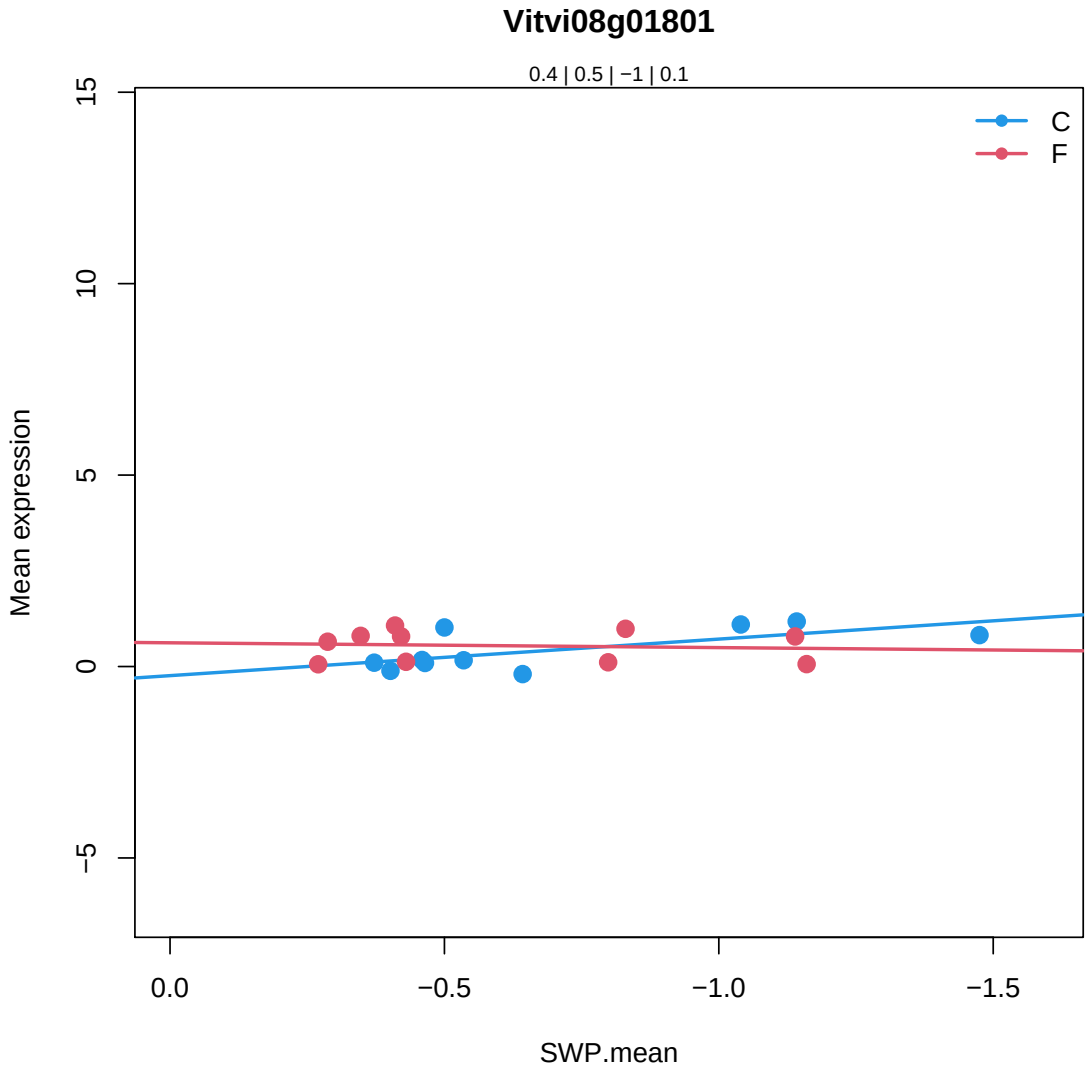
7.6.876 Vitvi08g01801: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01801
        34.9
        transport.metabolite transporters at the mitochondrial membrane
        Mitochondrial substrate carrier family protein |
        Chr5:6679591-6681845 REVERSE LENGTH=298 |
        201606
```

Coefficients for Vitvi08g01801.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.432837	0.005256826	**	0.005602723	**
SlopeC	-0.9541921	0.0223919	*	0.3929231	
MeanF-MeanC	0.1101358	0.582036		0.8528545	
SlopeF-SlopeC	1.079596	0.07505468	.	0.9999488	



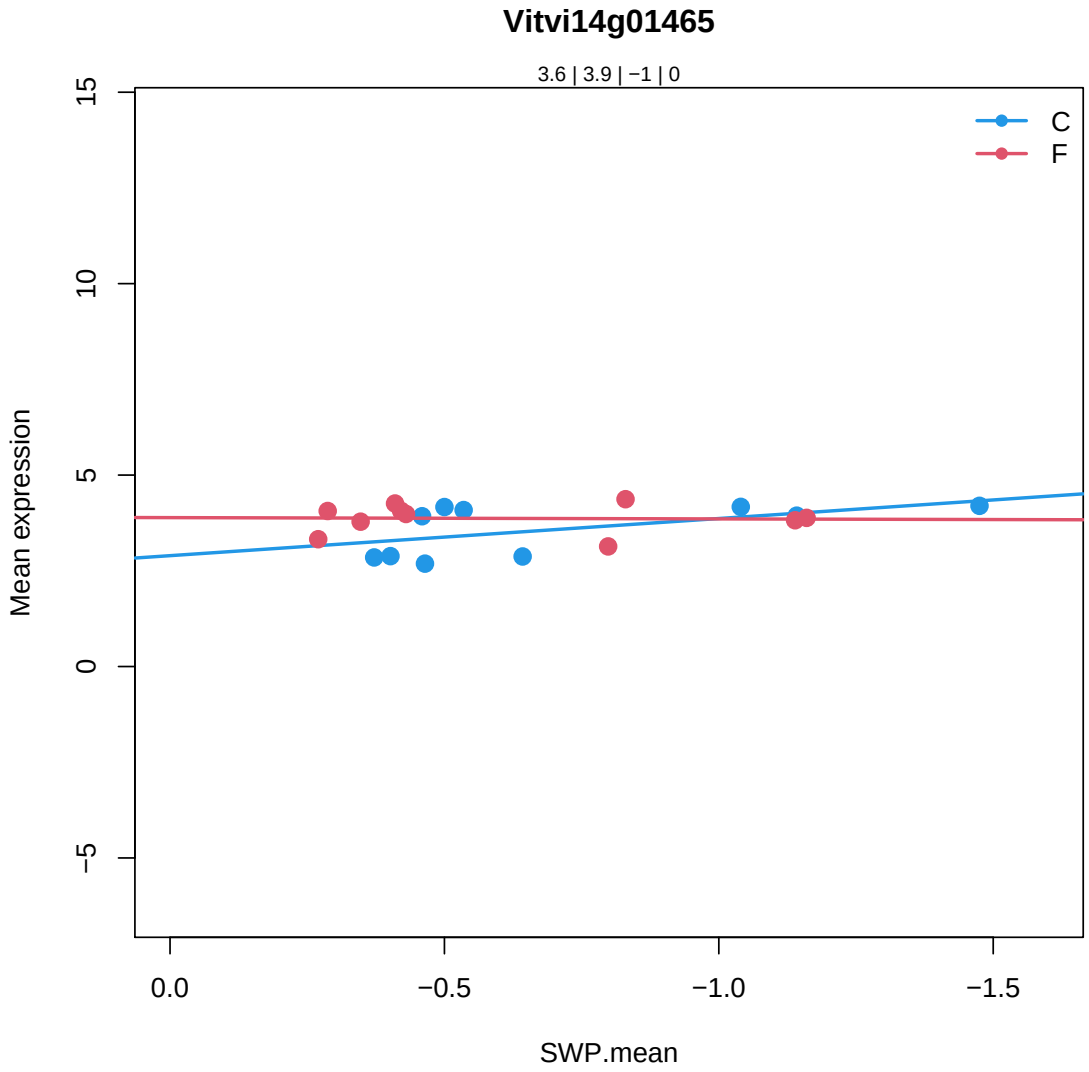
7.6.877 Vitvi14g01465: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01465
        26.3.3
        misc.gluco-, galacto- and mannosidases.alpha-mannosidase
        Glycosyl hydrolase family 38 protein |
        Chr3:9816707-9823056 FORWARD LENGTH=1019 |
        201606
```

Coefficients for Vitvi14g01465.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.577502	1.734989e-16	***	3.621073e-16	***
SlopeC	-0.9699762	0.03779777	*	0.4649827	
MeanF-MeanC	0.290884	0.20536		0.5495404	
SlopeF-SlopeC	1.003766	0.1383695		0.9999488	



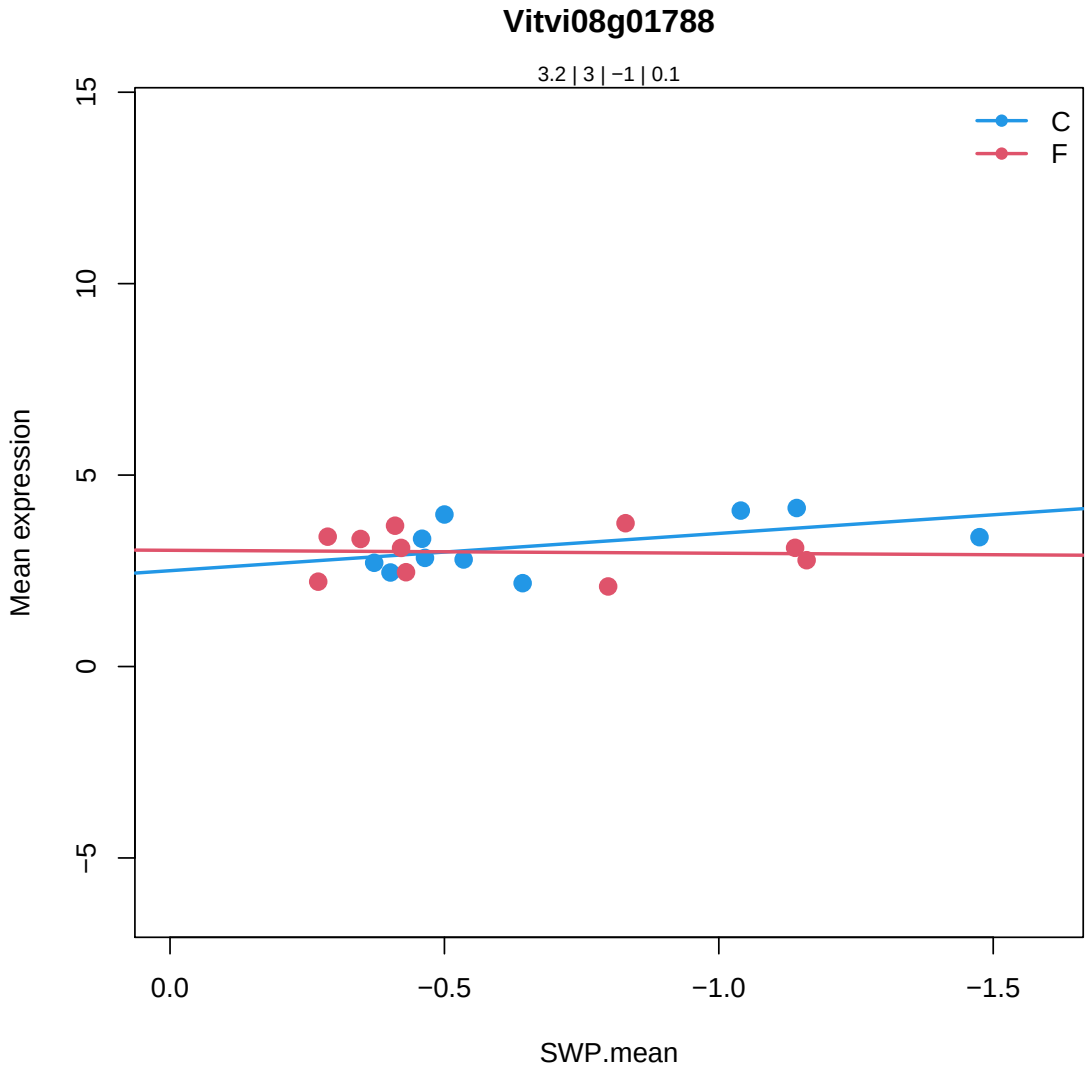
7.6.878 Vitvi08g01788: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01788
        35.1.14
        not assigned.no ontology.S RNA-binding domain-containing protein
        RIBOSOMAL RNA PROCESSING 5 |
        Chr3:3793957-3806626 REVERSE LENGTH=1920 |
        201606
```

Coefficients for Vitvi08g01788.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.187216	6.635143e-14	***	1.032705e-13	***
SlopeC	-0.9734415	0.07638912	.	0.5694531	
MeanF-MeanC	-0.1986892	0.4628221		0.785863	
SlopeF-SlopeC	1.050561	0.1910881		0.9999488	



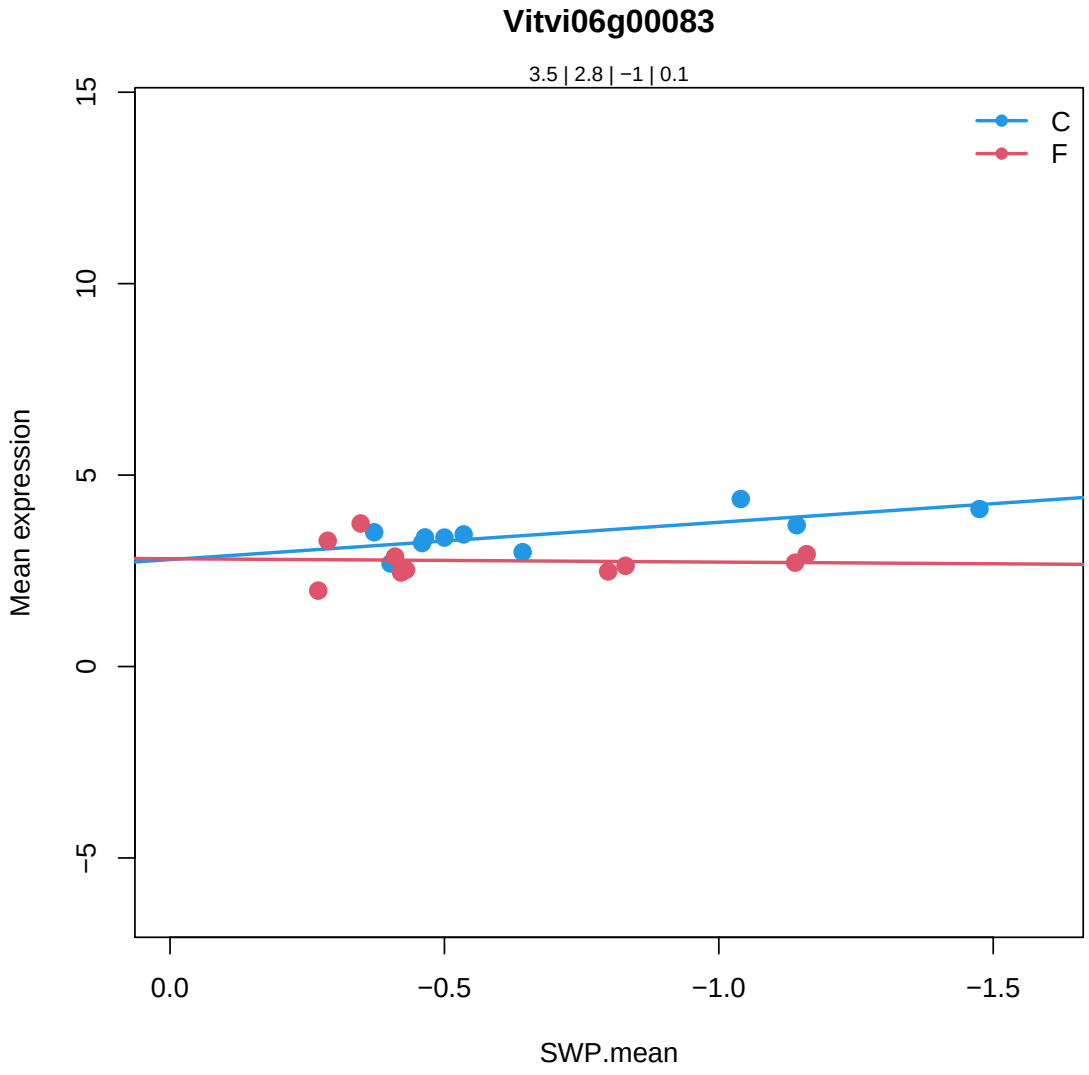
7.6.879 Vitvi06g00083: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00083
        35.2
        not assigned.unknown
        Lipase/lipooxygenase%2C PLAT/LH2 family protein |
        Chr1:20623099-20624533 REVERSE LENGTH=390 |
        201606
```

Coefficients for Vitvi06g00083.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.477654	4.353704e-17	***	1.009725e-16	***
SlopeC	-0.9737478	0.02322112	*	0.3983963	
MeanF-MeanC	-0.7161726	0.001908343	**	0.02124687	*
SlopeF-SlopeC	1.061493	0.08753282	.	0.9999488	



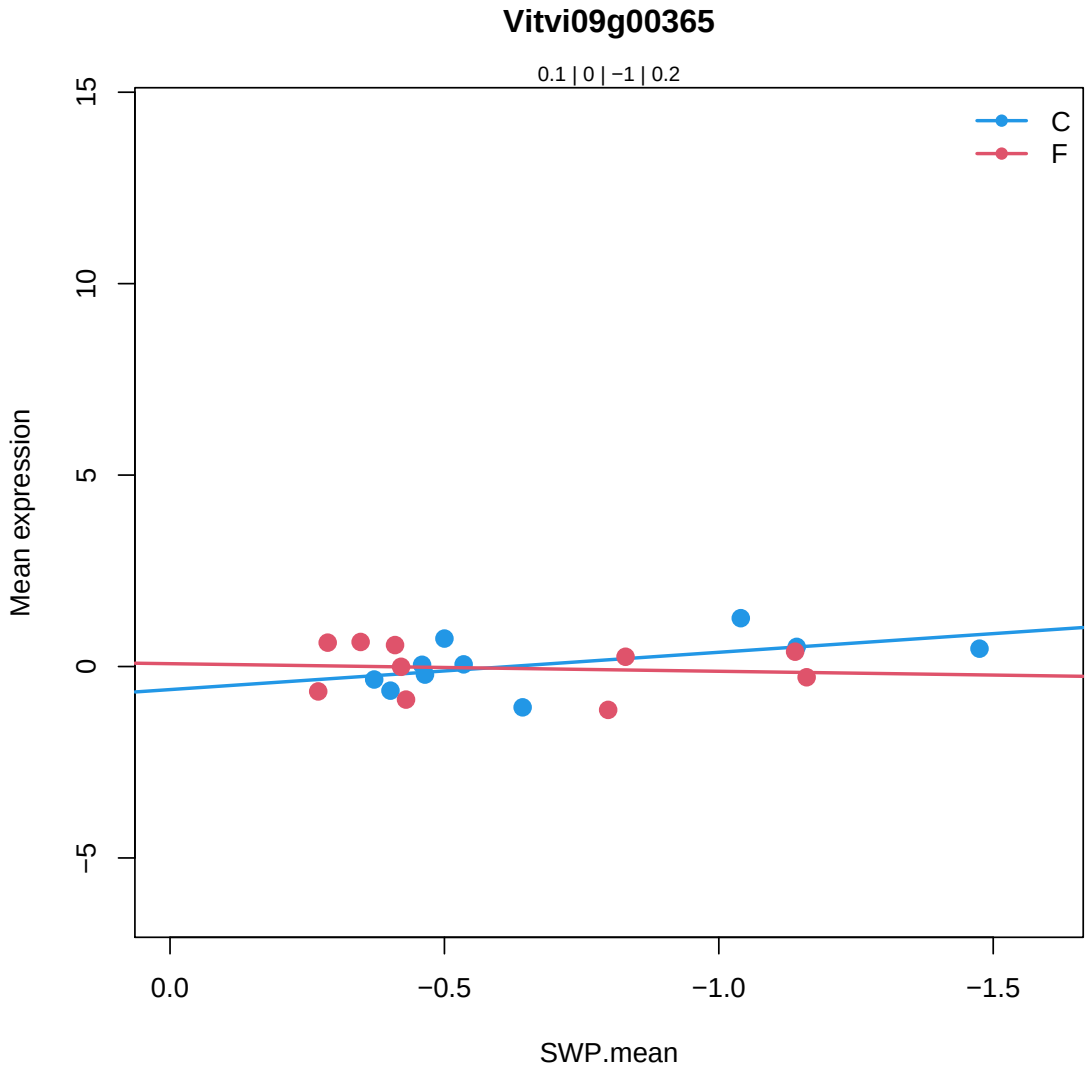
7.6.880 Vitvi09g00365: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00365
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr3:8347200-8349347 FORWARD LENGTH=715 |
        201606
```

Coefficients for Vitvi09g00365.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.08249499	0.6757658		0.6805883	
SlopeC	-0.974269	0.08594763	.	0.5889741	
MeanF-MeanC	-0.1294394	0.6427765		0.8785748	
SlopeF-SlopeC	1.172426	0.1600579		0.9999488	



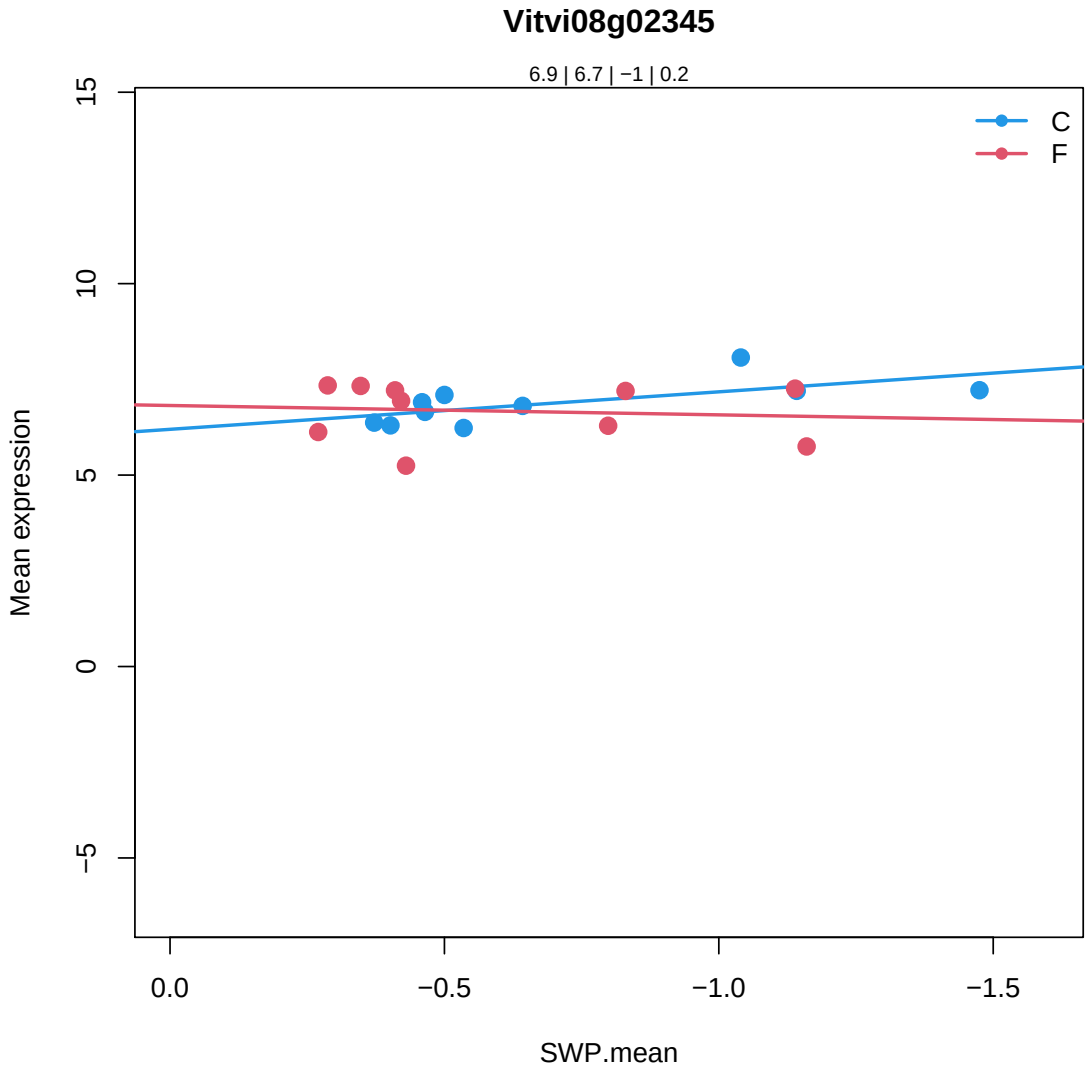
7.6.881 Vitvi08g02345: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g02345
        11.2.4
        lipid metabolism.FA desaturation.omega 6 desaturase
        fatty acid desaturase 2 |
        Chr3:3860592-3861743 REVERSE LENGTH=383 |
        201606
```

Coefficients for Vitvi08g02345.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.883684	1.348146e-20	***	9.080175e-20	***
SlopeC	-0.9792743	0.08167143	.	0.5779075	
MeanF-MeanC	-0.2152845	0.43812		0.7700124	
SlopeF-SlopeC	1.223912	0.1396363		0.9999488	



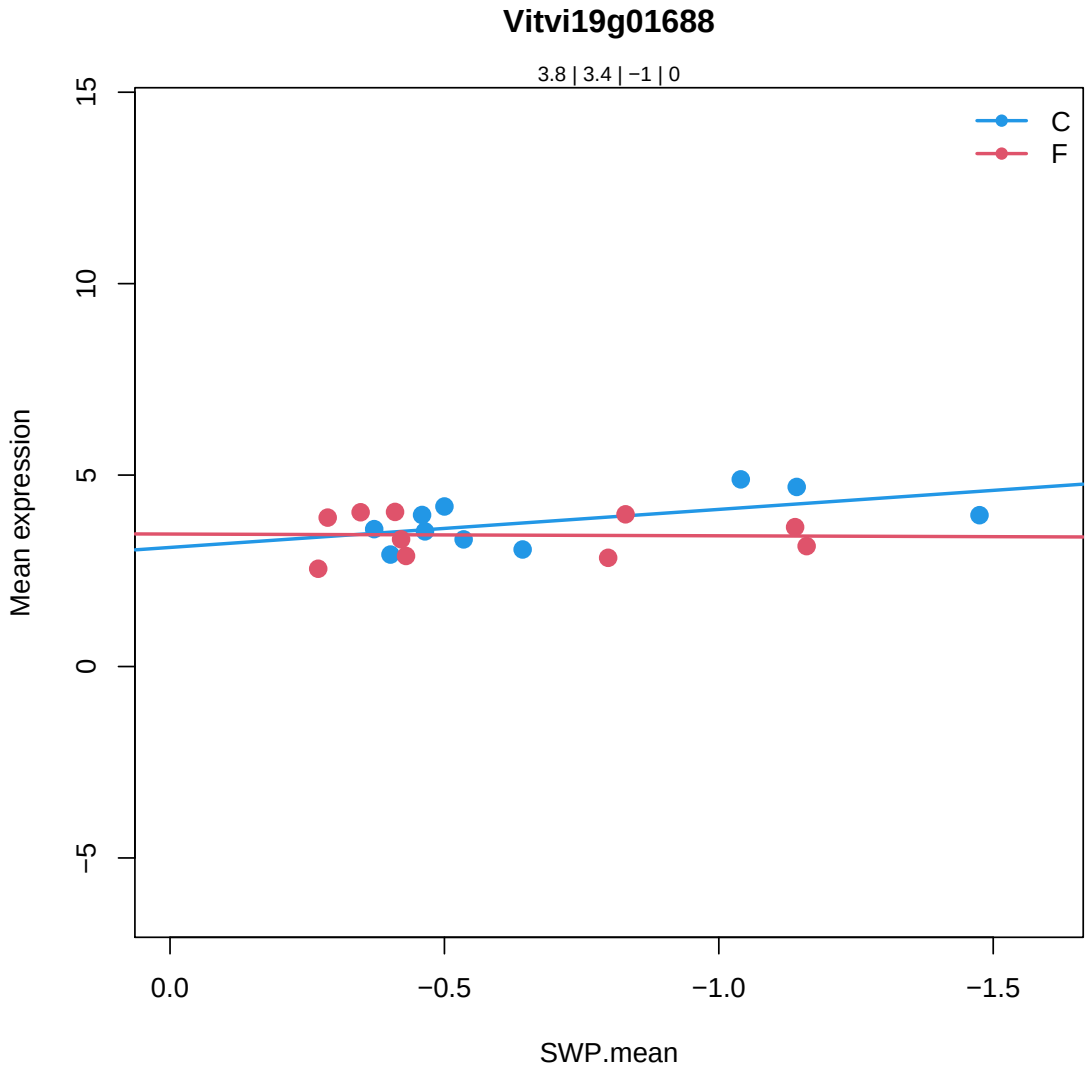
7.6.882 Vitvi19g01688: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g01688
        27.3.67
        RNA.regulation of transcription.putative transcription regulator
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi19g01688.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.80854	4.766301e-16	***	9.31623e-16	***
SlopeC	-0.9935493	0.05515929	.	0.5234981	
MeanF-MeanC	-0.3768143	0.144844		0.4581267	
SlopeF-SlopeC	1.03919	0.168497		0.9999488	



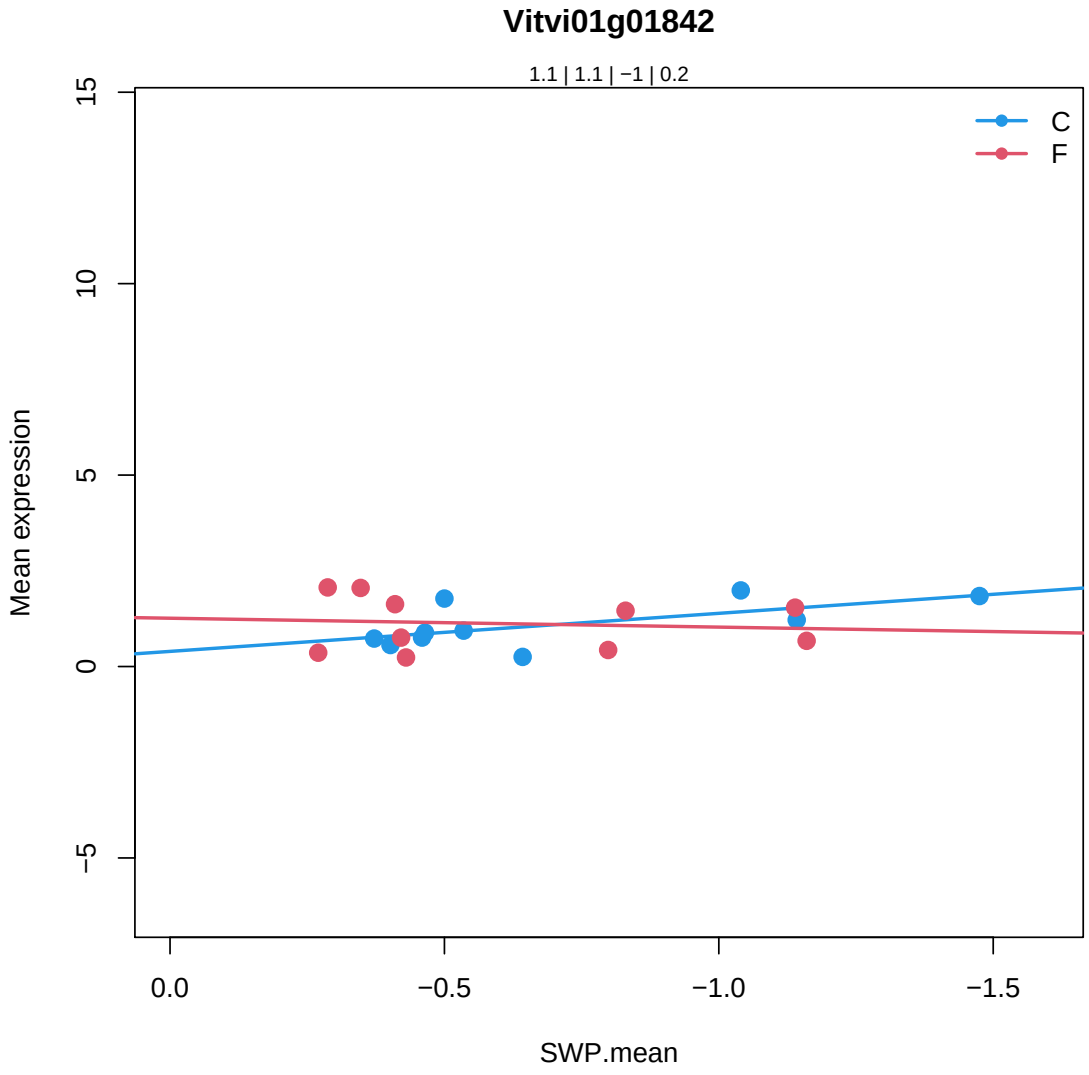
7.6.883 Vitvi01g01842: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01842
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr5:26551879-26553741 FORWARD LENGTH=620 |
        201606
```

Coefficients for Vitvi01g01842.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.093919	8.338846e-06	***	9.434433e-06	***
SlopeC	-0.9940718	0.07114062	.	0.5628482	
MeanF-MeanC	0.02553919	0.9244394		0.9799906	
SlopeF-SlopeC	1.226263	0.1302023		0.9999488	



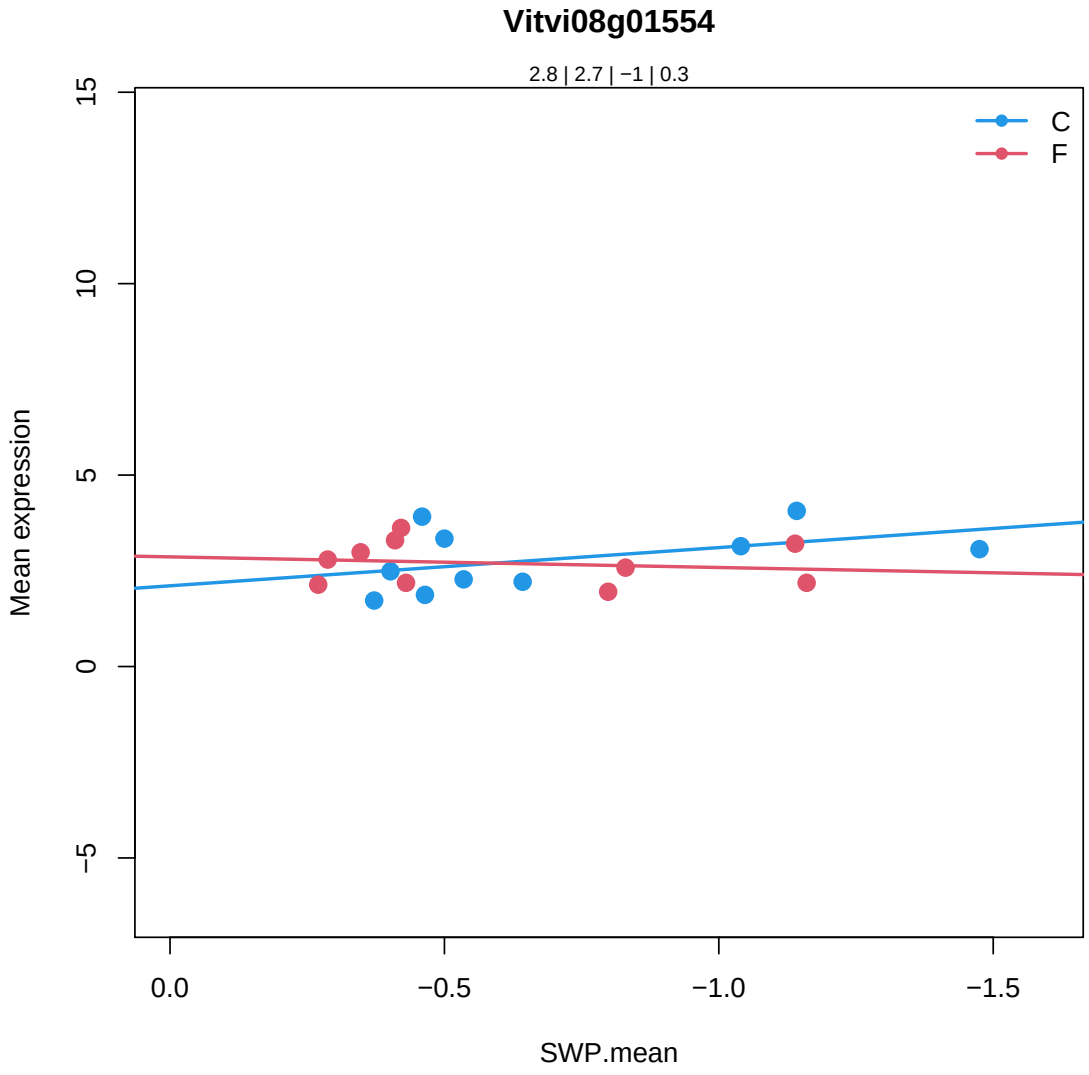
7.6.884 Vitvi08g01554: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01554
        13.1.4.5.1
        amino acid metabolism.synthesis.branched chain group.isoleucine specif
        L-O-methylthreonine resistant 1 |
        Chr3:3099164-3101741 REVERSE LENGTH=592 |
        201606
```

Coefficients for Vitvi08g01554.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.8099	4.189199e-12	***	5.80946e-12	***
SlopeC	-0.9984016	0.09353325	.	0.6025344	
MeanF-MeanC	-0.1153637	0.6938799		0.903615	
SlopeF-SlopeC	1.275664	0.1464992		0.9999488	



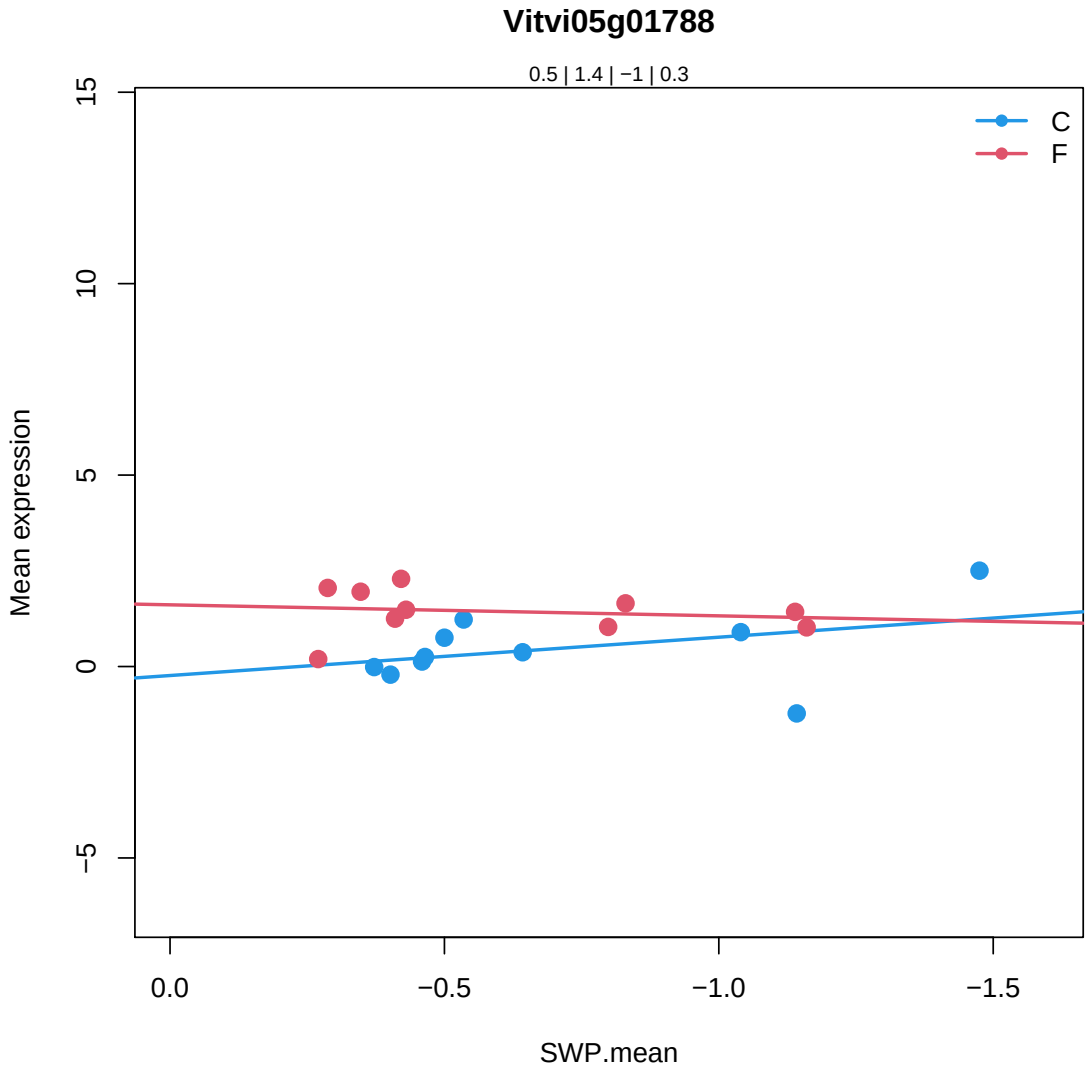
7.6.885 Vitvi05g01788: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01788
        35.2
        not assigned.unknown
        cell wall / vacuolar inhibitor of fructosidase 1 |
        Chr1:17682425-17683516 REVERSE LENGTH=166 |
        201606
```

Coefficients for Vitvi05g01788.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4680901	0.06062583	.	0.06301547	.
SlopeC	−1.000404	0.1427787		0.6681823	
MeanF−MeanC	0.9676216	0.008546151	**	0.06759753	.
SlopeF−SlopeC	1.288259	0.2019768		0.9999488	



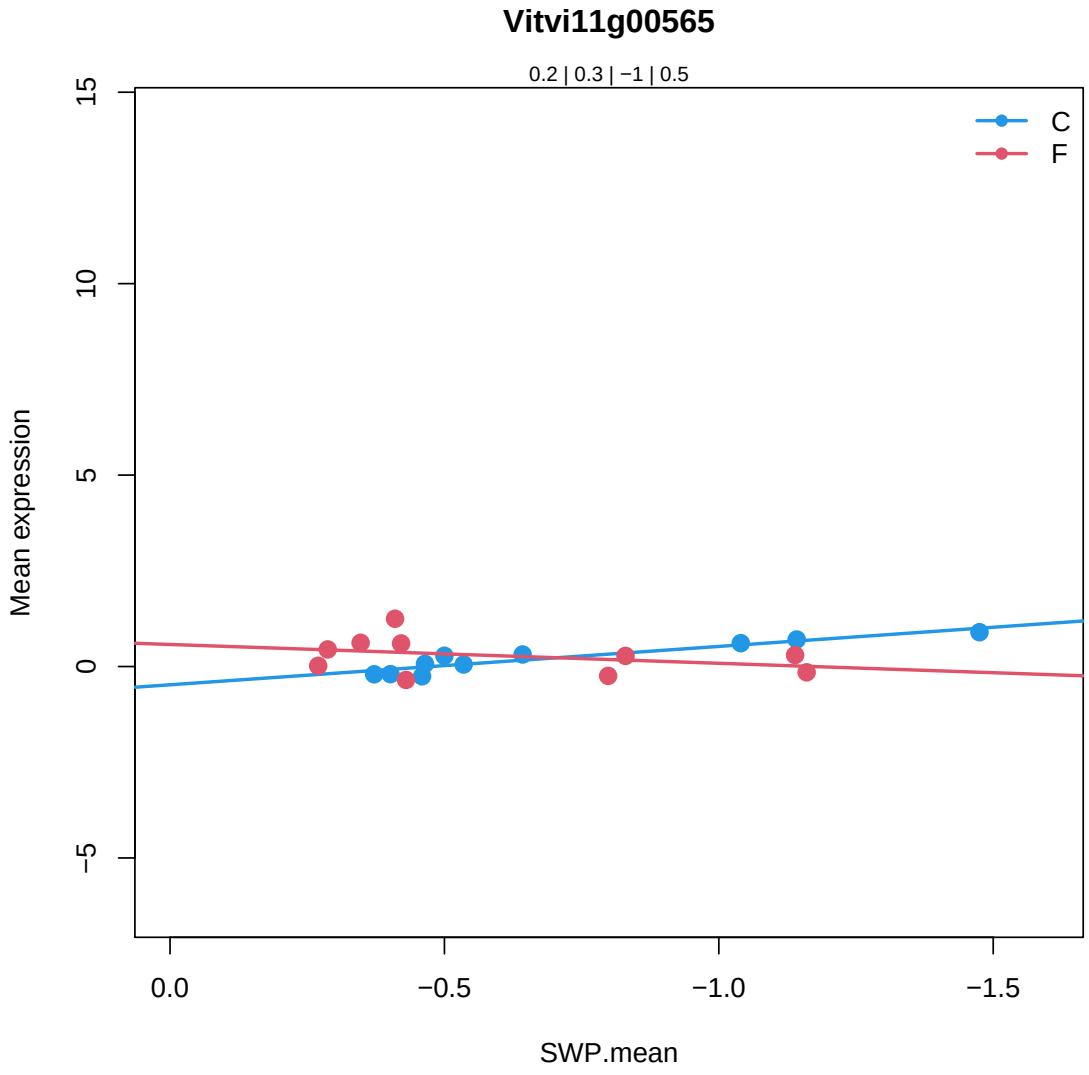
7.6.886 Vitvi11g00565: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00565
        8.1.5
        TCA / organic transformation.TCA.2-oxoglutarate dehydrogenase
        2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protei
        Chr1:18279910-18280873 FORWARD LENGTH=269 |
        201606
```

Coefficients for Vitvi11g00565.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.2270541	0.08332643	.	0.08632827	.
SlopeC	-1.001793	0.008829987	**	0.2903326	
MeanF-MeanC	0.04928551	0.7830797		0.9384607	
SlopeF-SlopeC	1.493249	0.008744783	**	0.9999488	



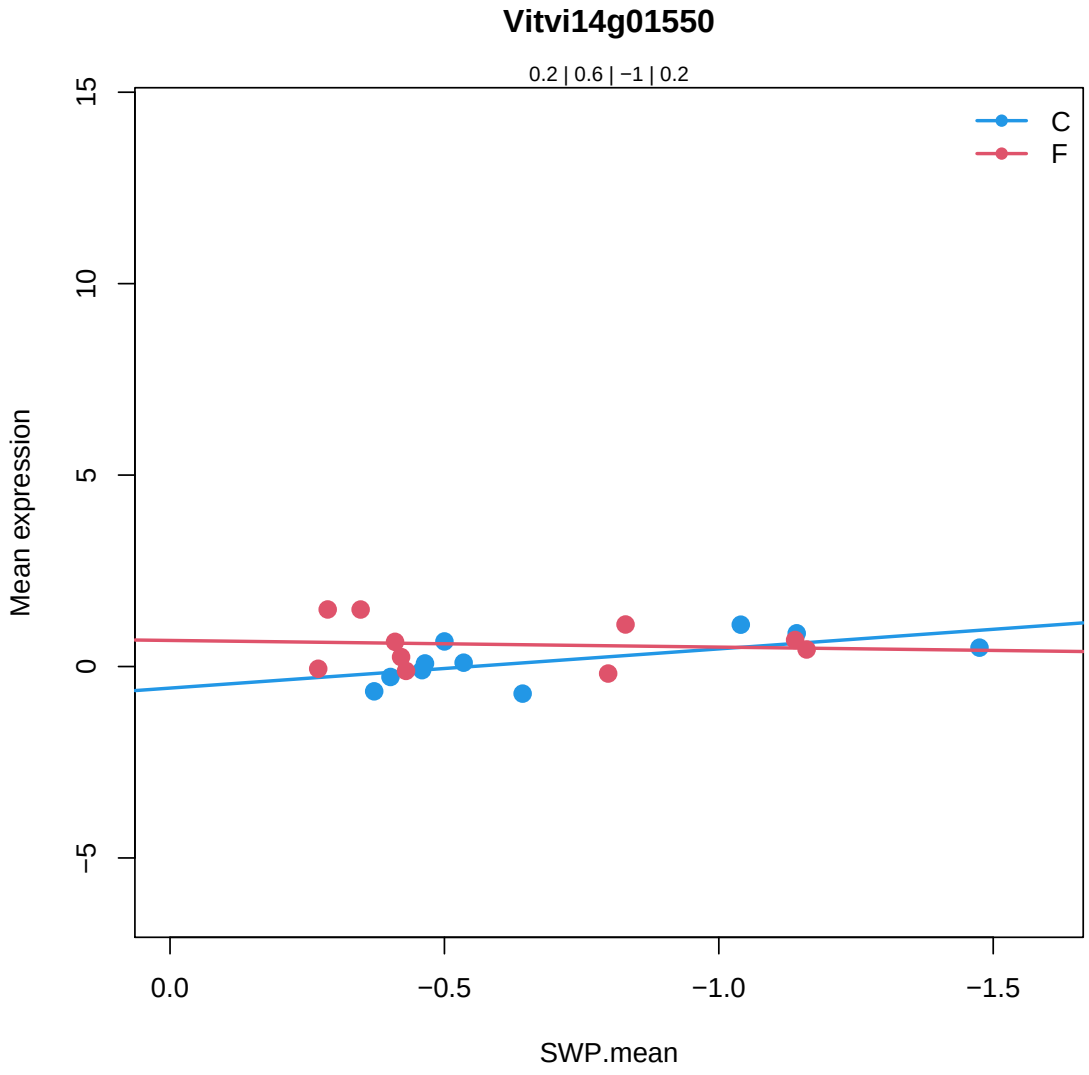
7.6.887 Vitvi14g01550: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01550
        35.2
        not assigned.unknown
        Pentatricopeptide repeat (PPR) superfamily protein |
        Chr5:1999181-2001049 REVERSE LENGTH=622 |
        201606
```

Coefficients for Vitvi14g01550.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1563232	0.391667		0.3977738	
SlopeC	−1.023882	0.05192913	.	0.5134996	
MeanF−MeanC	0.4186256	0.1123903		0.3914655	
SlopeF−SlopeC	1.19804	0.120266		0.9999488	



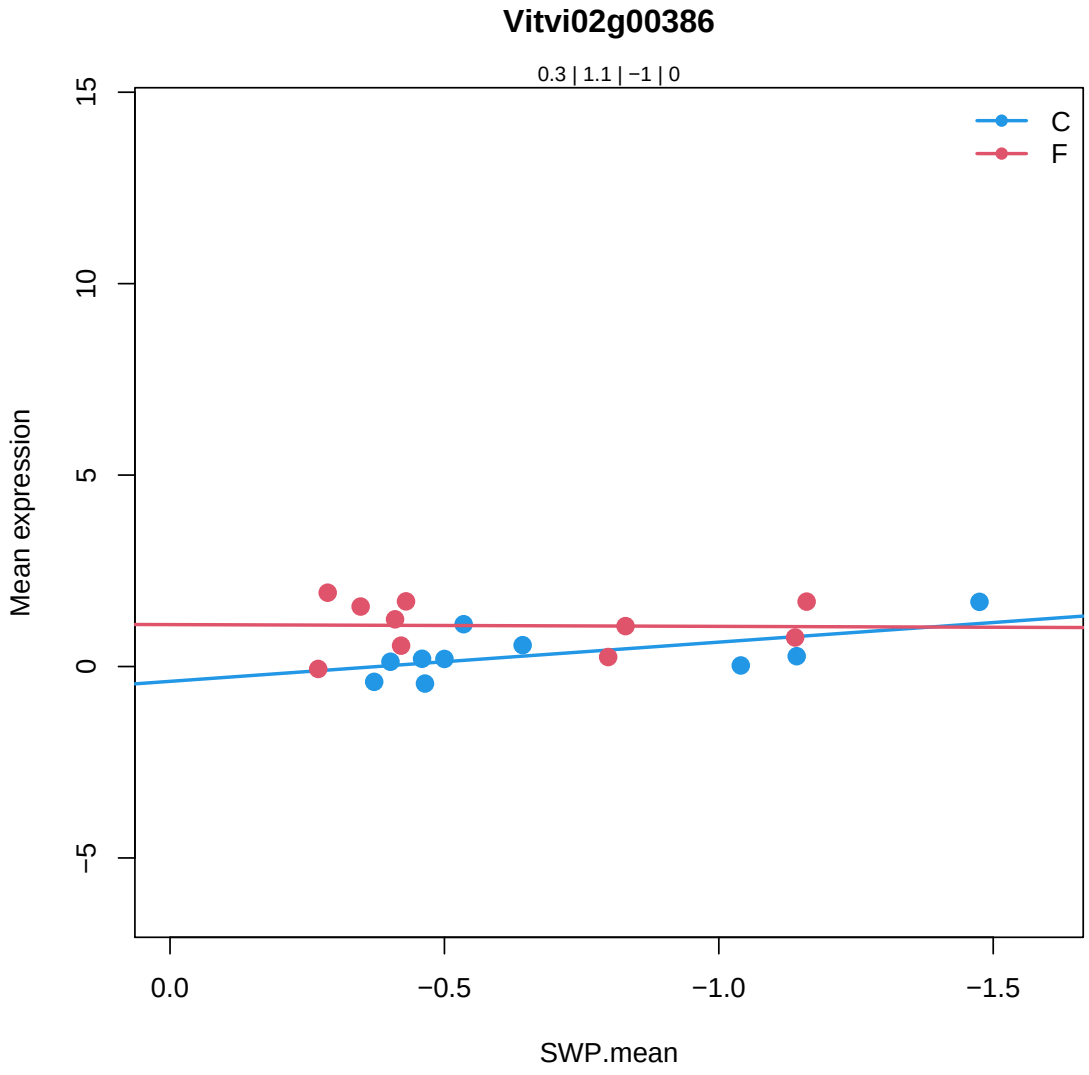
7.6.888 Vitvi02g00386: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00386
        35.2
        not assigned.unknown
        BON association protein 2 |
        Chr2:18847125-18847748 REVERSE LENGTH=207 |
        201606
```

Coefficients for Vitvi02g00386.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3327331	0.09704358	.	0.1003554	
SlopeC	−1.024065	0.06830576	.	0.5569429	
MeanF−MeanC	0.7336602	0.01309656	*	0.09271607	.
SlopeF−SlopeC	1.069985	0.1918549		0.9999488	



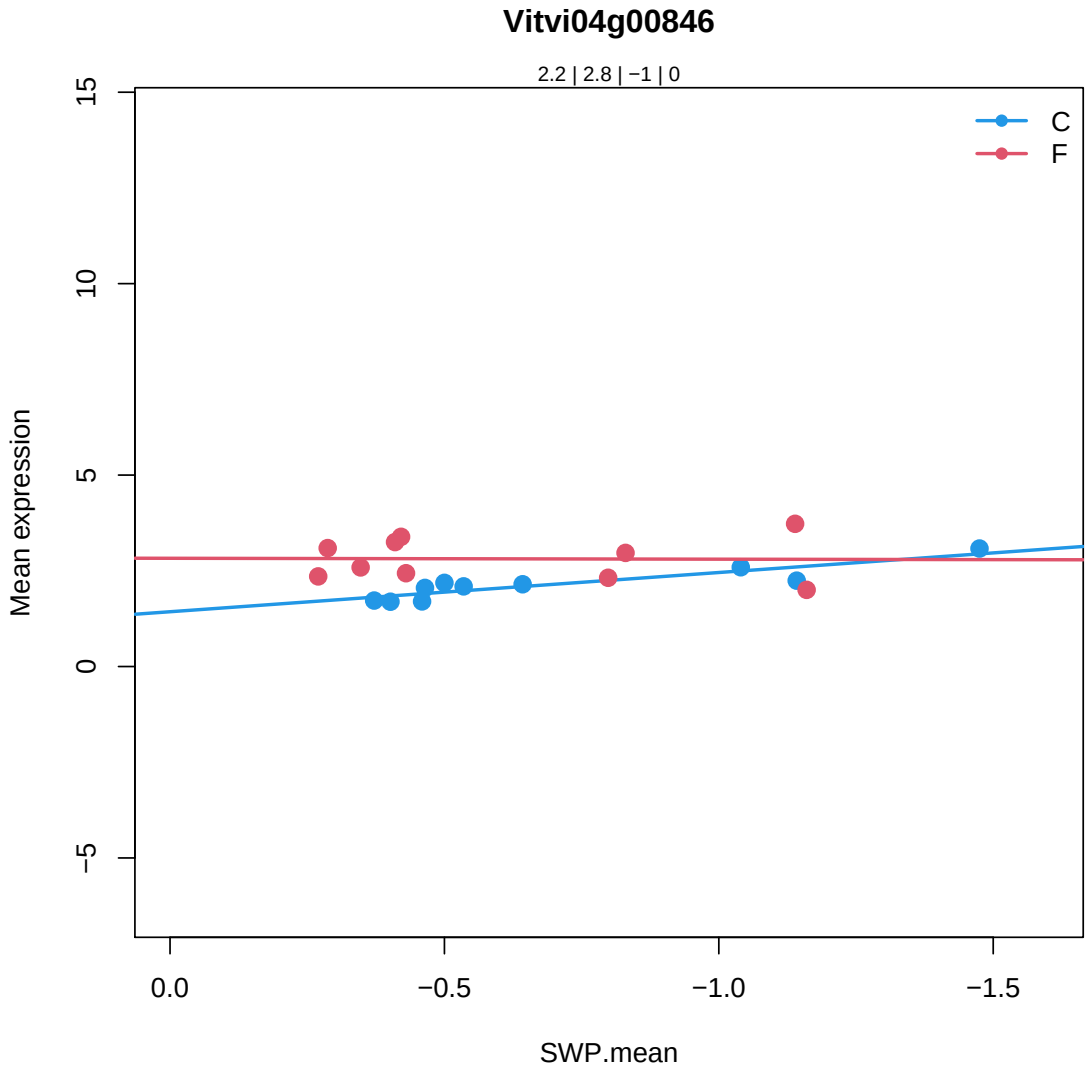
7.6.889 Vitvi04g00846: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00846
        10.7
        cell wall.modification
        expansin A13 |
        Chr3:742655-743975 REVERSE LENGTH=266 |
        201606
```

Coefficients for Vitvi04g00846.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.151144	7.375078e-13	***	1.069053e-12	***
SlopeC	-1.024244	0.01764257	*	0.3571759	
MeanF-MeanC	0.6612191	0.003629047	**	0.03561747	*
SlopeF-SlopeC	1.047604	0.09151676	.	0.9999488	



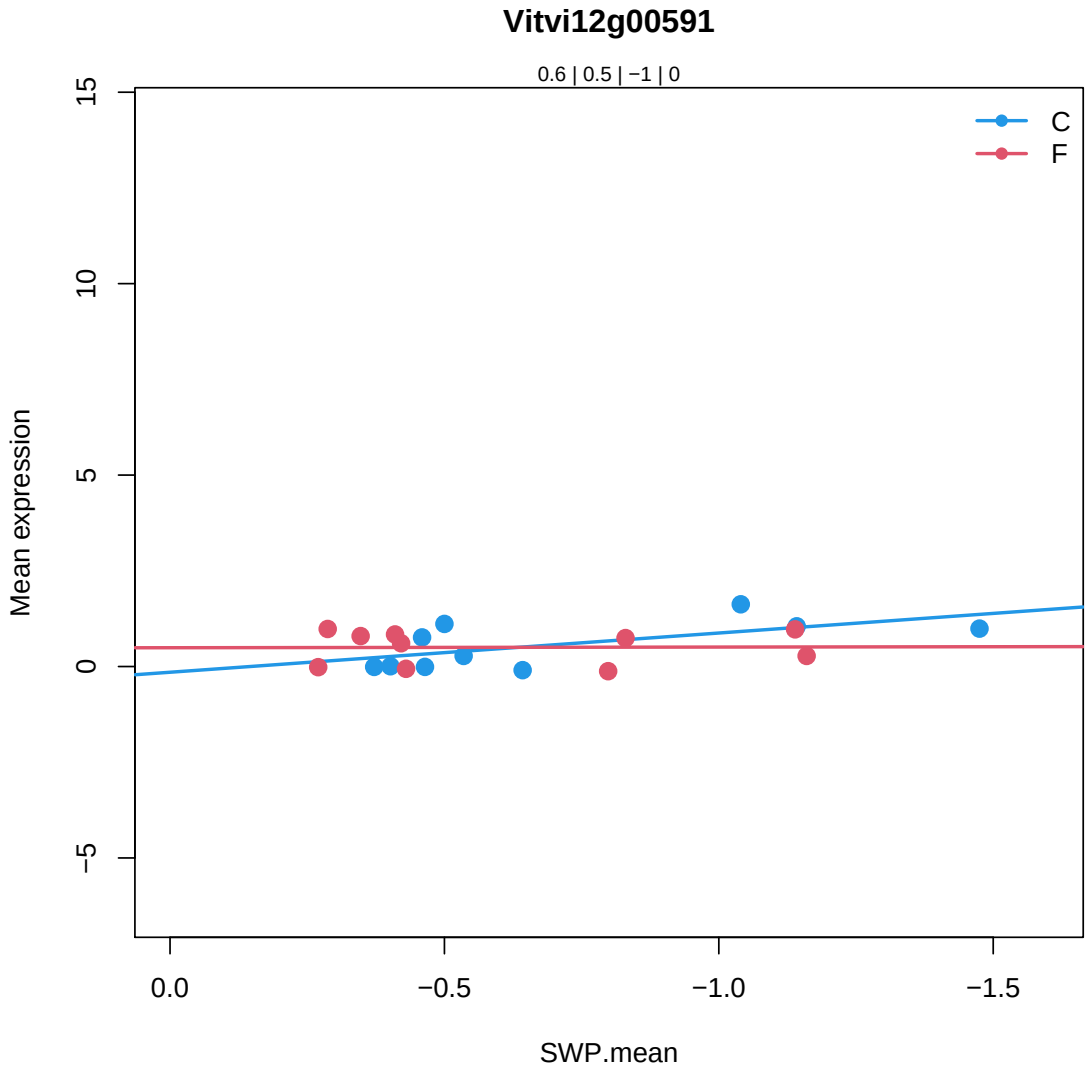
7.6.890 Vitvi12g00591: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00591
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        mitochondrial editing factor 22 |
        Chr3:4057027-4059193 REVERSE LENGTH=694 |
        201606
```

Coefficients for Vitvi12g00591.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.5705382	0.001250294	**	0.001351368	**
SlopeC	-1.024546	0.02570099	*	0.409336	
MeanF-MeanC	-0.06958884	0.7518399		0.927496	
SlopeF-SlopeC	1.007297	0.1279596		0.9999488	



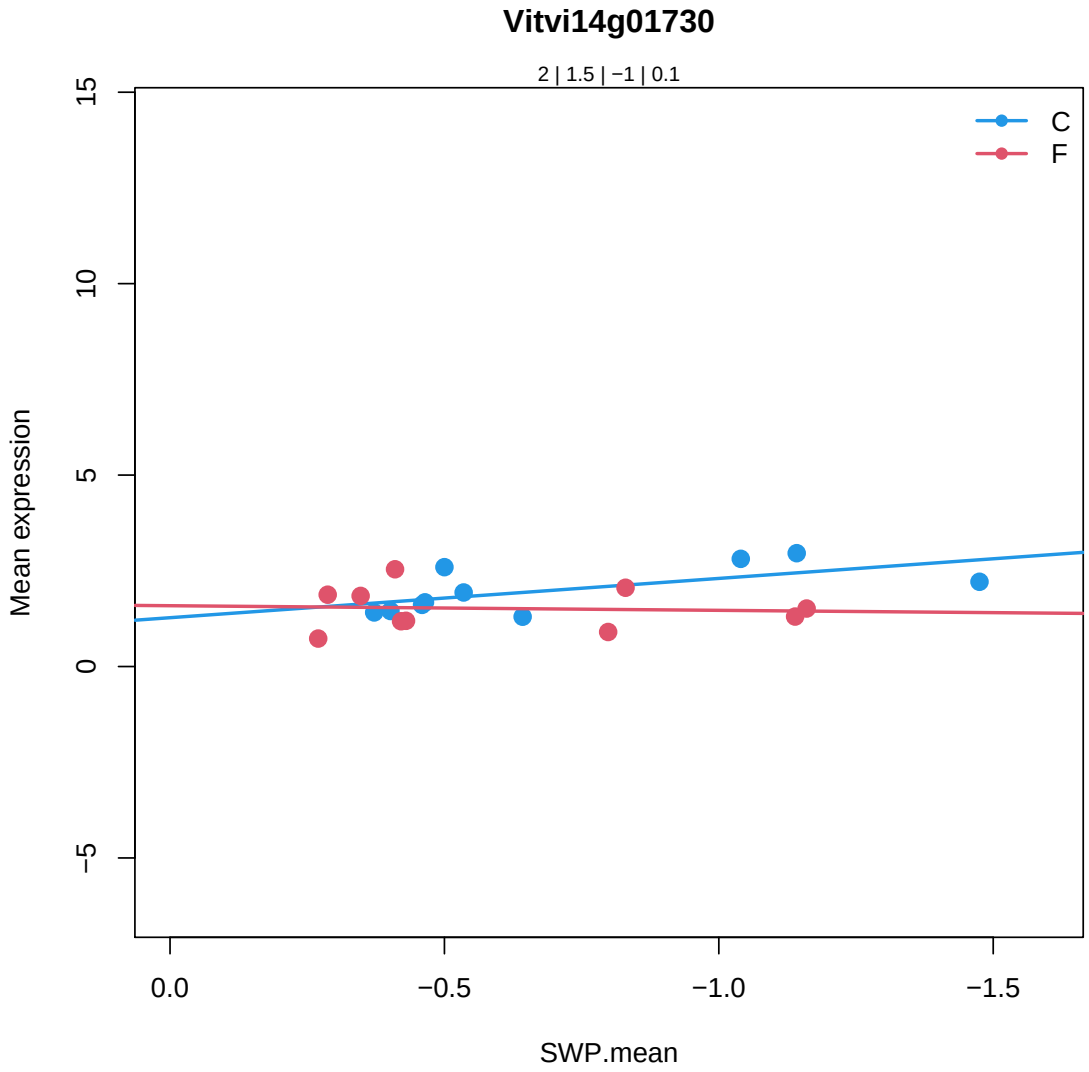
7.6.891 Vitvi14g01730: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g01730
        27.1
        RNA.processing
        polyribonucleotide nucleotidyltransferase |
        Chr5:4697612-4703013 REVERSE LENGTH=991 |
        201606
```

Coefficients for Vitvi14g01730.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.996371	7.716974e-11	***	1.014509e-10	***
SlopeC	-1.025678	0.04073917	*	0.4769174	
MeanF-MeanC	-0.4819713	0.05683871	.	0.2595373	
SlopeF-SlopeC	1.146192	0.1166557		0.9999488	



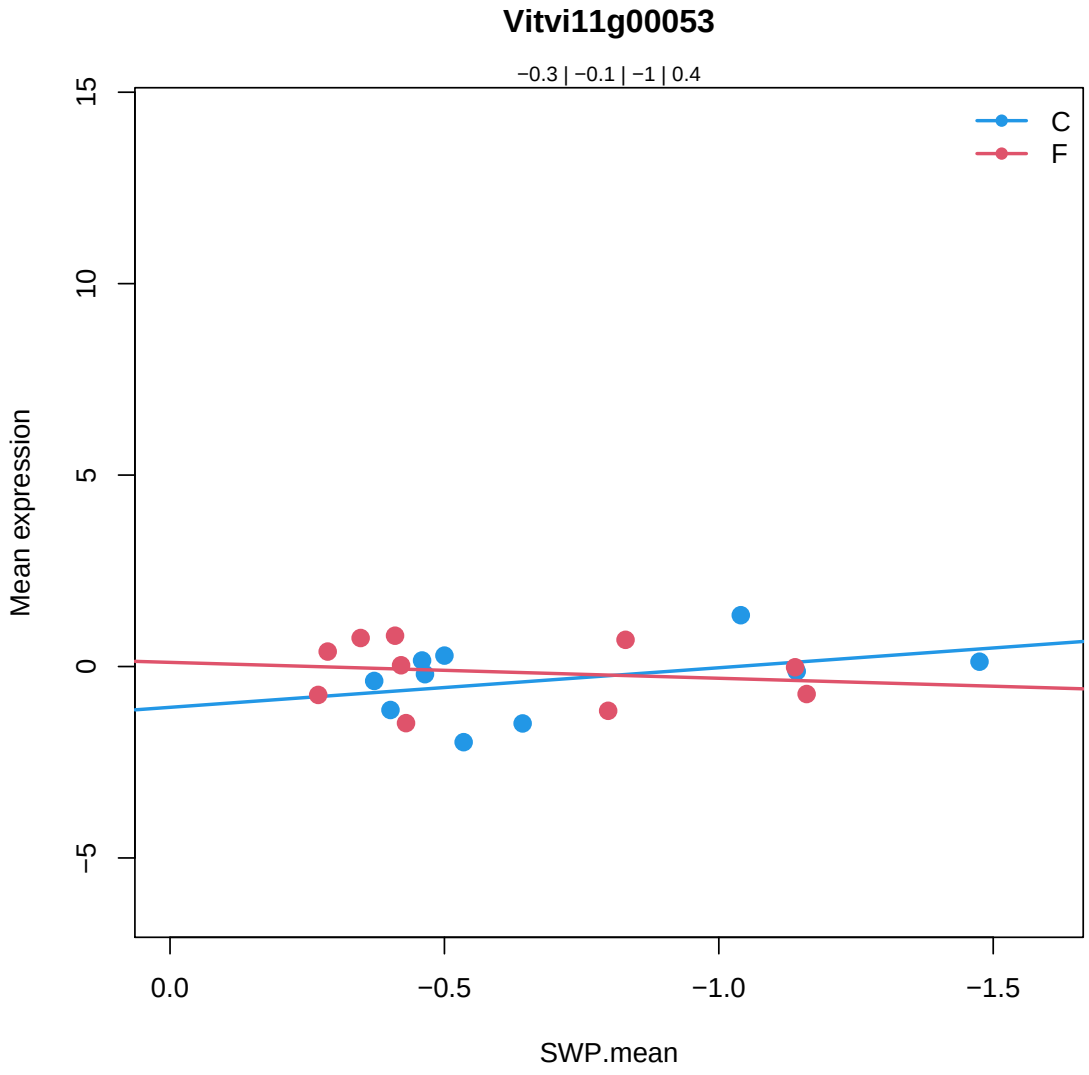
7.6.892 Vitvi11g00053: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00053
        30.2.3
        signalling.receptor kinases.leucine rich repeat III
        Leucine-rich repeat protein kinase family protein |
        Chr3:14954587-14956577 FORWARD LENGTH=633 |
        201606
```

Coefficients for Vitvi11g00053.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.3393111	0.2033324		0.2084471	
SlopeC	-1.033567	0.165243		0.6962465	
MeanF-MeanC	0.1946529	0.6000028		0.8604564	
SlopeF-SlopeC	1.448781	0.1901388		0.9999488	



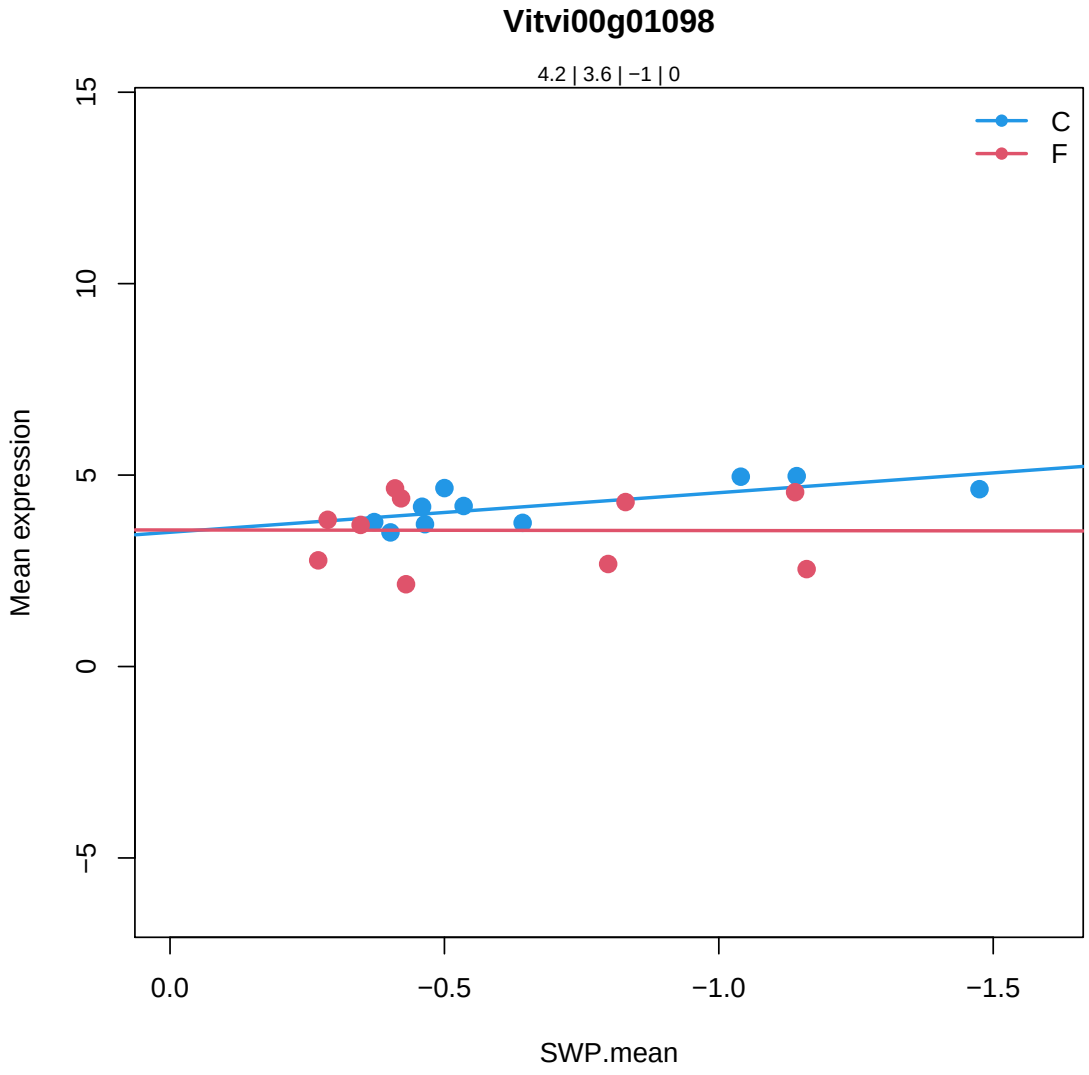
7.6.893 Vitvi00g01098: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi00g01098
        30.2.11
        signalling.receptor kinases.leucine rich repeat XI
        Leucine-rich receptor-like protein kinase family protein |
        Chr5:26281826-26284945 FORWARD LENGTH=1003 |
        201606
```

Coefficients for Vitvi00g01098.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.233102	5.937817e-15	***	1.016444e-14	***
SlopeC	-1.033906	0.1078236		0.6223948	
MeanF-MeanC	-0.6765433	0.04220562	*	0.2138932	
SlopeF-SlopeC	1.049314	0.2650937		0.9999488	



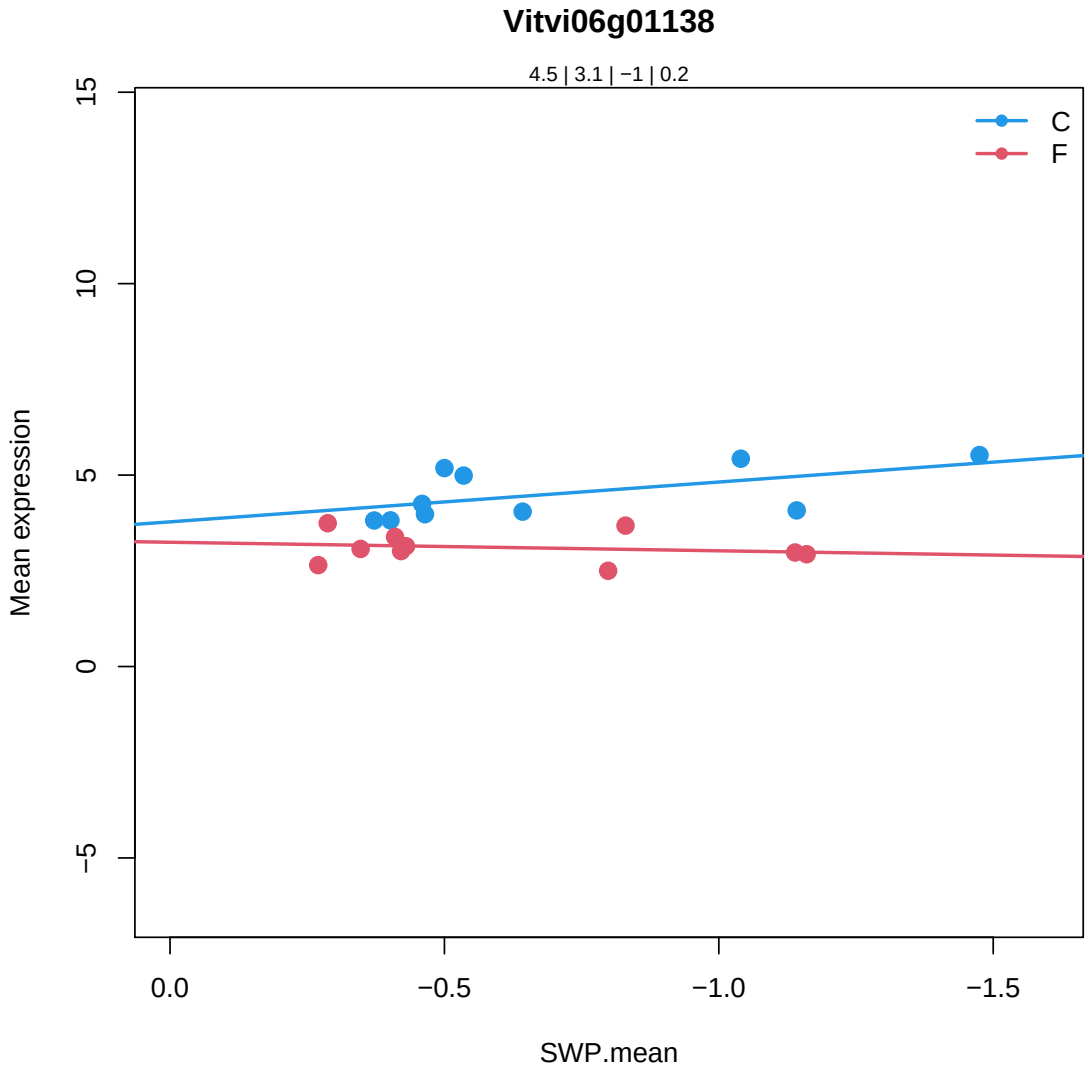
7.6.894 Vitvi06g01138: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01138
        26.2
        misc.UDP glucosyl and glucoronyl transferases
        UDP-Glycosyltransferase superfamily protein |
        Chr2:12874658-12876122 FORWARD LENGTH=456 |
        201606
```

Coefficients for Vitvi06g01138.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.509679	2.303989e-18	***	7.165353e-18	***
SlopeC	-1.0396	0.03042043	*	0.4320841	
MeanF-MeanC	-1.40016	3.926967e-06	***	0.0001085224	***
SlopeF-SlopeC	1.262554	0.07218674	.	0.9999488	



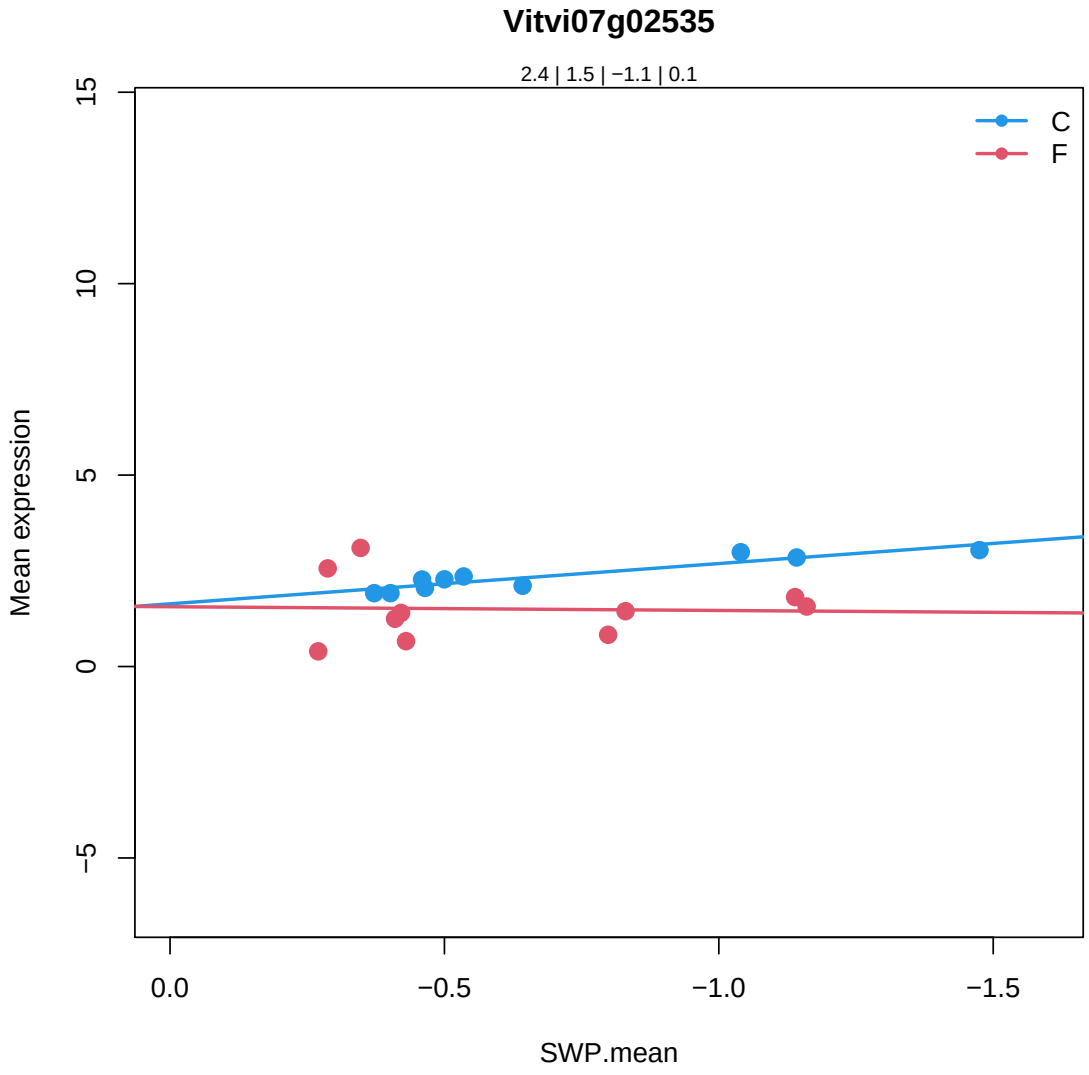
7.6.895 Vitvi07g02535: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g02535
        11.1.5
        lipid metabolism.FA synthesis and FA elongation.beta hydroxyacyl ACP d
        Thioesterase superfamily protein |
        Chr5:3185819-3187159 FORWARD LENGTH=219 |
        201606
```

Coefficients for Vitvi07g02535.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.376839	2.592e-11	***	3.476527e-11	***
SlopeC	-1.051795	0.05979592	.	0.5399345	
MeanF-MeanC	-0.8749301	0.003738041	**	0.03638264	*
SlopeF-SlopeC	1.149527	0.1589567		0.9999488	



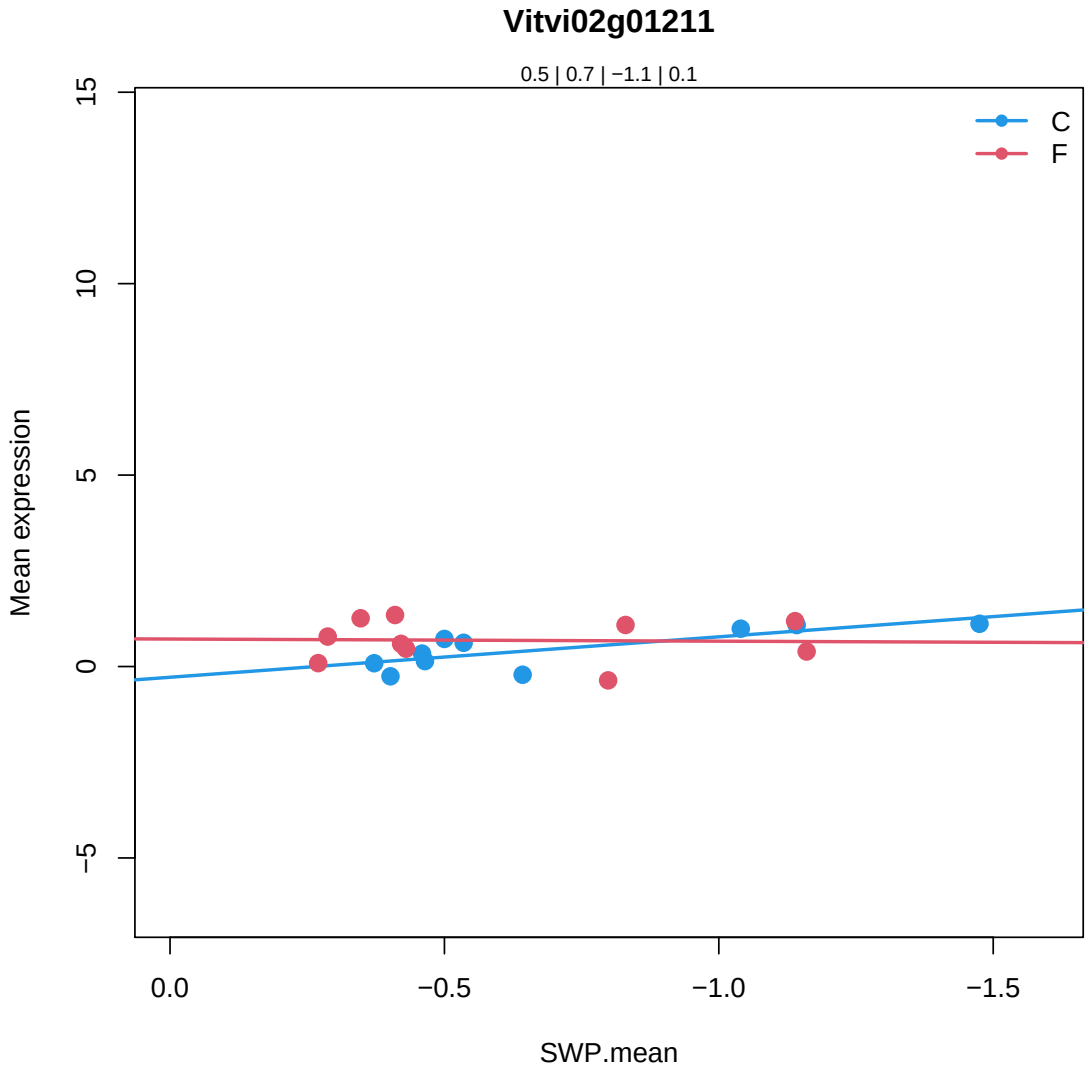
7.6.896 Vitvi02g01211: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g01211
        35.2
        not assigned.unknown
        Ubiquitin carboxyl-terminal hydrolase family protein |
        Chr1:29767314-29768555 REVERSE LENGTH=413 |
        201606
```

Coefficients for Vitvi02g01211.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4619115	0.006600427	**	0.007019027	**
SlopeC	−1.056003	0.02190249	*	0.3904795	
MeanF−MeanC	0.2214386	0.3193035		0.6801111	
SlopeF−SlopeC	1.112511	0.09452298	.	0.9999488	



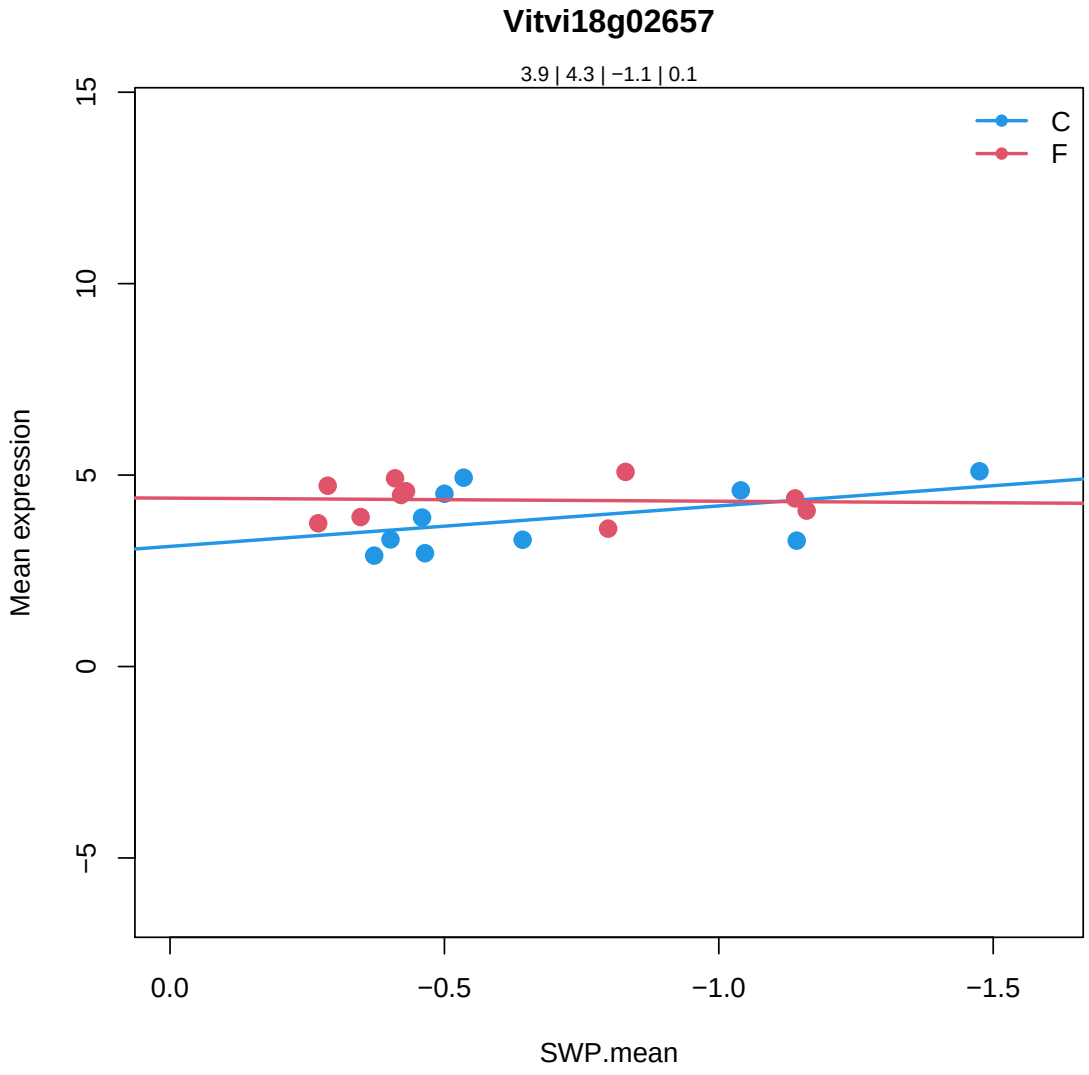
7.6.897 Vitvi18g02657: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02657
        26.10
        misc.cytochrome P450
        Cytochrome P450 superfamily protein |
        Chr1:24825446-24826502 FORWARD LENGTH=327 |
        201606
```

Coefficients for Vitvi18g02657.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.880691	3.75993e-15	***	6.609256e-15	***
SlopeC	-1.056889	0.06908287	.	0.557719	
MeanF-MeanC	0.4676813	0.1102459		0.3871816	
SlopeF-SlopeC	1.137543	0.1806		0.9999488	



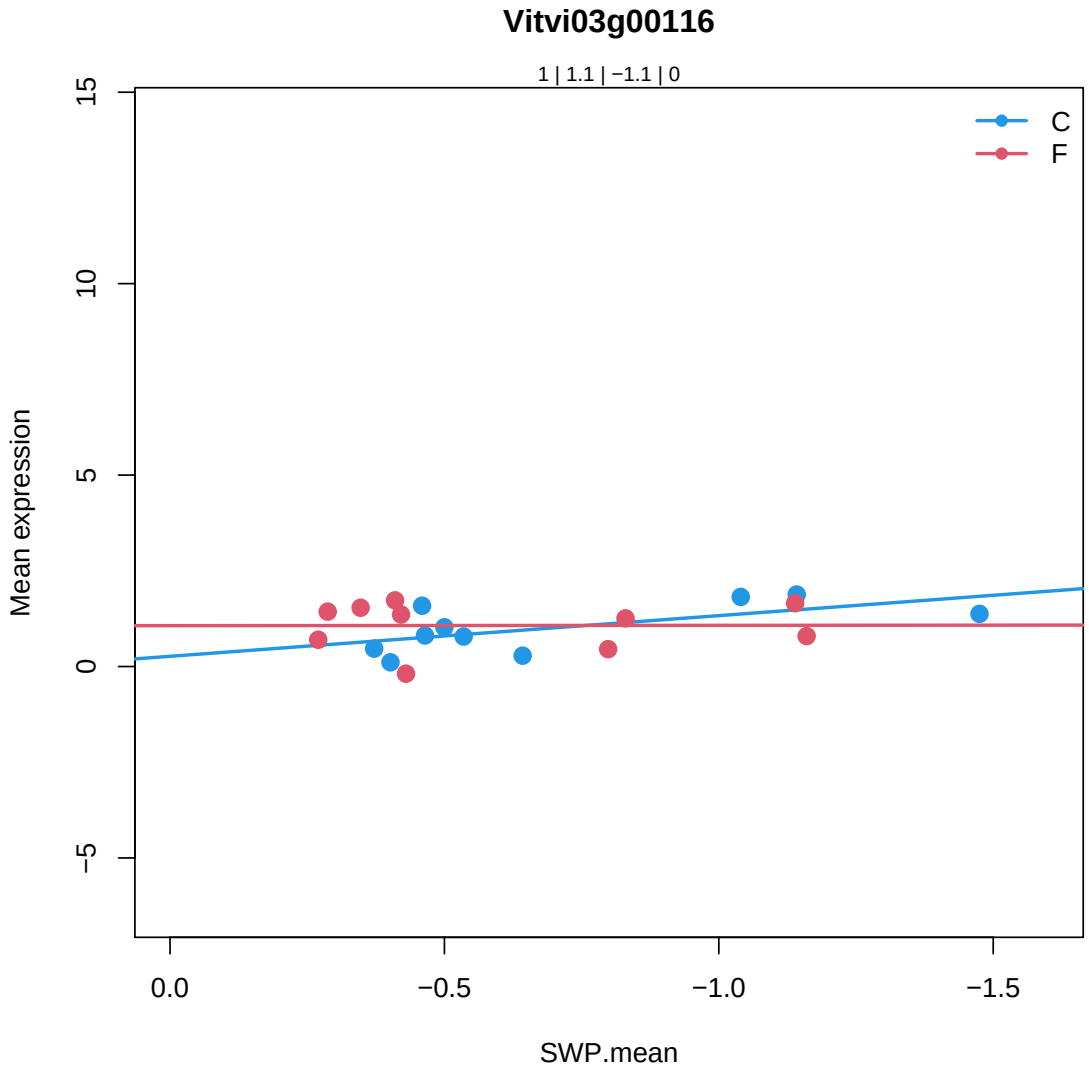
7.6.898 Vitvi03g00116: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00116
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        Pentatricopeptide repeat (PPR-like) superfamily protein |
        Chr2:9045695-9047488 REVERSE LENGTH=597 |
        201606
```

Coefficients for Vitvi03g00116.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.0138	1.171224e-05	***	1.320301e-05	***
SlopeC	-1.062595	0.04445911	*	0.4889219	
MeanF-MeanC	0.05853406	0.8192307		0.9499835	
SlopeF-SlopeC	1.054115	0.1691395		0.9999488	



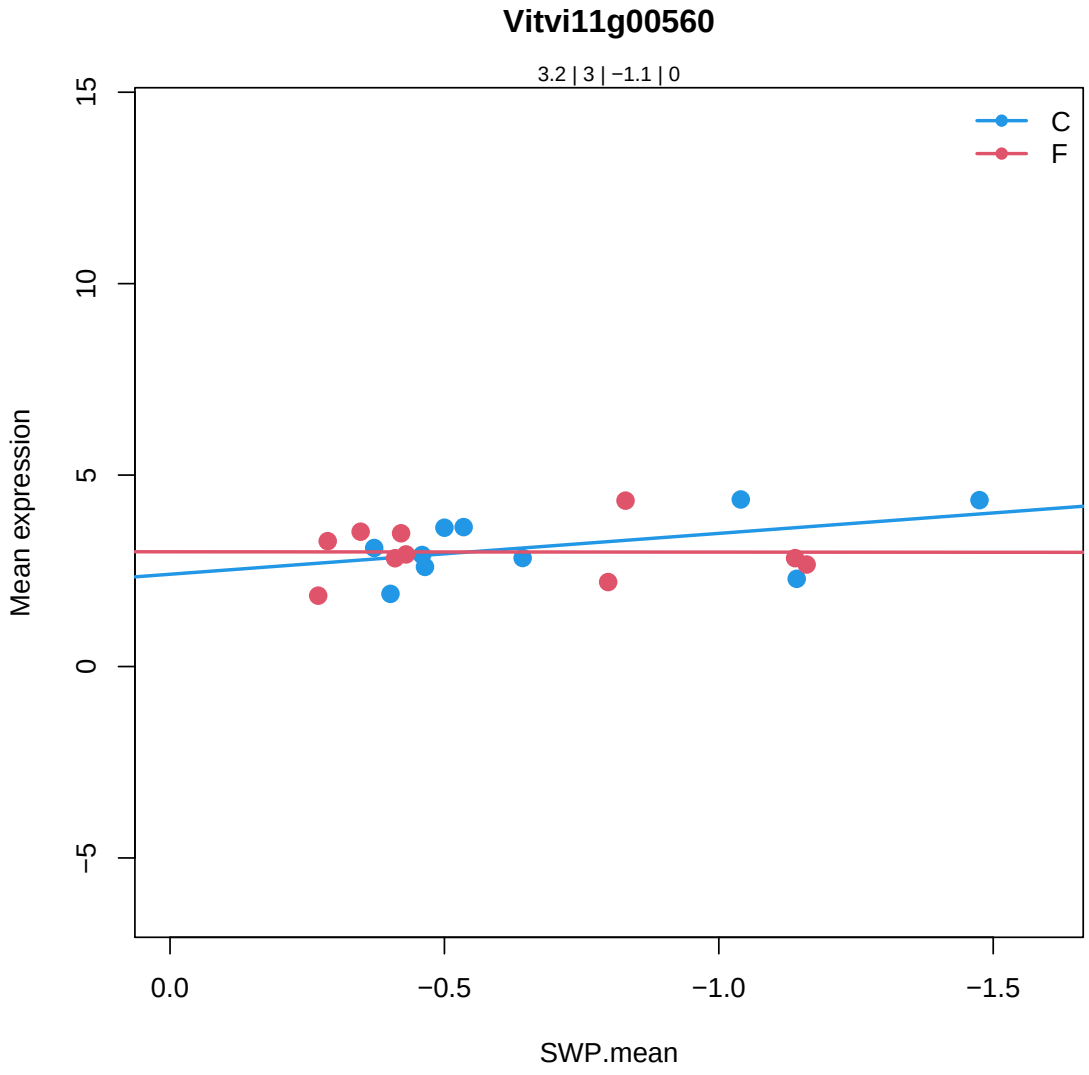
7.6.899 Vitvi11g00560: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00560
        34.30
        transport.H+ transporting pyrophosphatase
        Inorganic H pyrophosphatase family protein |
        Chr1:5399115-5402185 FORWARD LENGTH=642 |
        201606
```

Coefficients for Vitvi11g00560.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.160445	1.894319e-12	***	2.675179e-12	***
SlopeC	-1.067022	0.09670298	.	0.6081385	
MeanF-MeanC	-0.1691298	0.5936166		0.8577063	
SlopeF-SlopeC	1.075486	0.2523246		0.9999488	



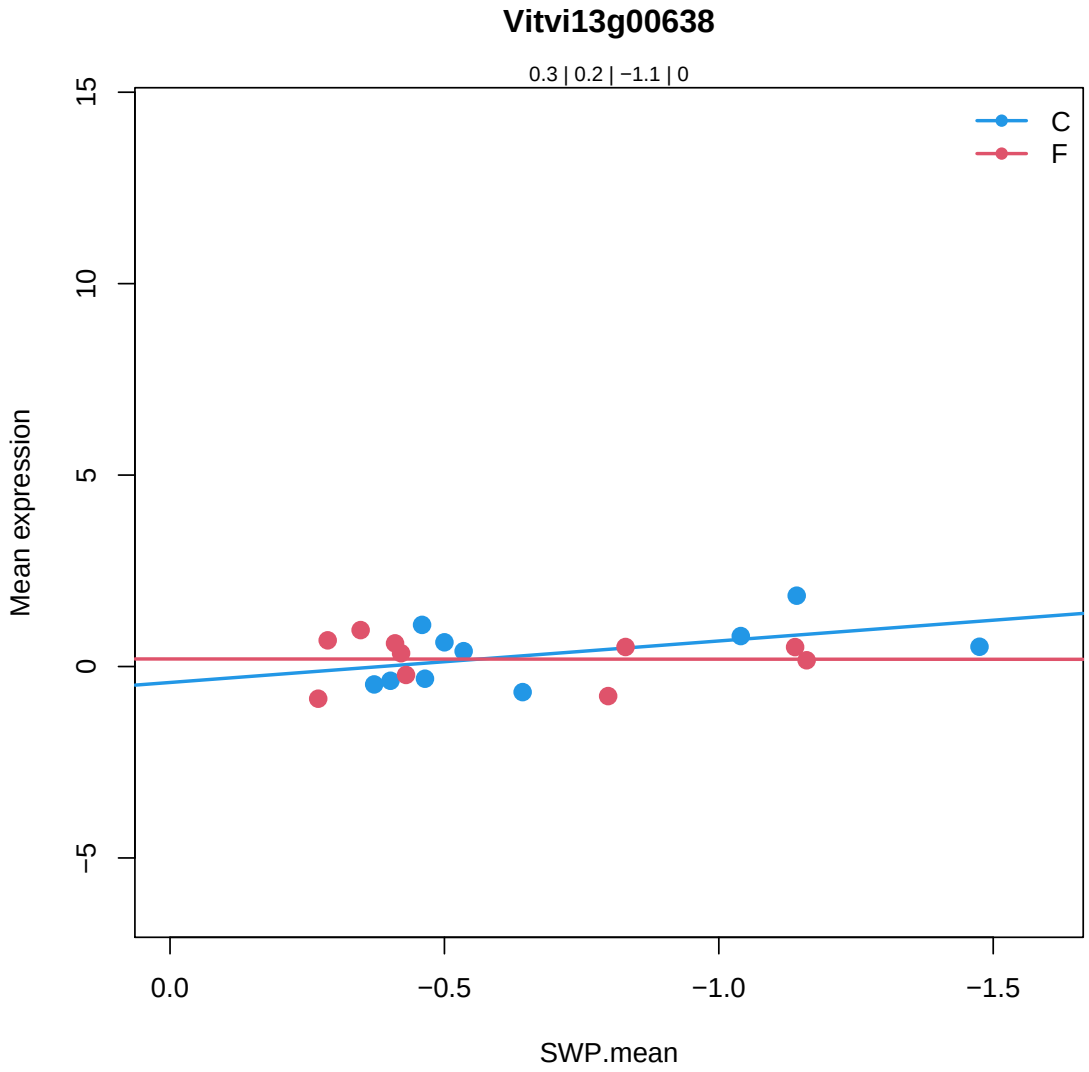
7.6.900 Vitvi13g00638: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00638
        34.16
        transport.ABC transporters and multidrug resistance systems
        ABC transporter family protein |
        Chr5:24425824-24430269 REVERSE LENGTH=1109 |
        201606
```

Coefficients for Vitvi13g00638.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.345515	0.1052049		0.1087215	
SlopeC	-1.084082	0.06990818	.	0.5594697	
MeanF-MeanC	-0.1520297	0.604071		0.8616377	
SlopeF-SlopeC	1.089562	0.211393		0.9999488	



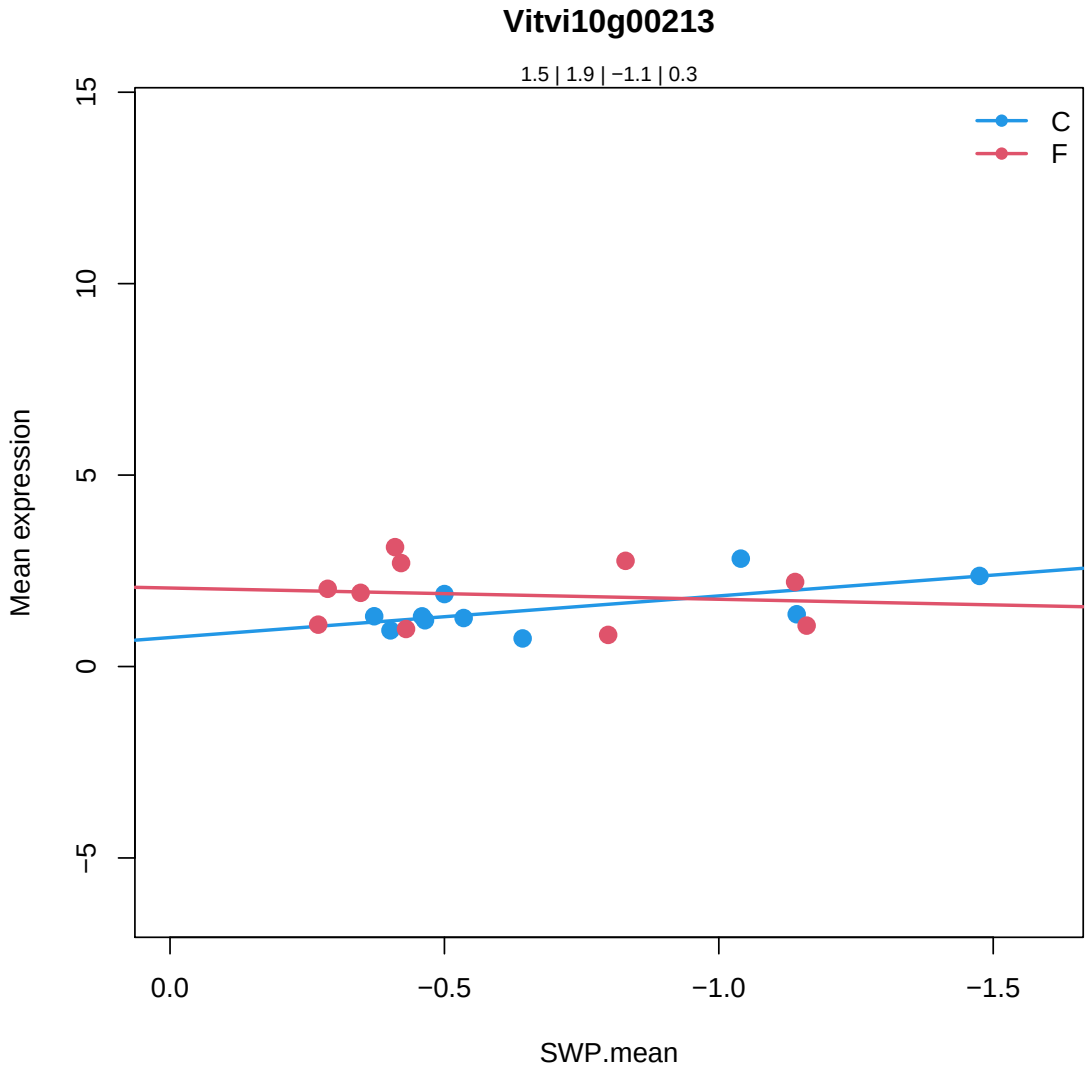
7.6.901 Vitvi10g00213: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00213
        26.4.1
        misc.beta 1,3 glucan hydrolases.glucan endo-1,3-beta-glucosidase
        O-Glycosyl hydrolases family 17 protein |
        Chr4:9646541-9648045 FORWARD LENGTH=475 |
        201606
```

Coefficients for Vitvi10g00213.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.521381	4.38752e-07	***	5.110392e-07	***
SlopeC	-1.087578	0.08087681	.	0.5764511	
MeanF-MeanC	0.3495544	0.2594535		0.6210326	
SlopeF-SlopeC	1.380921	0.1327203		0.9999488	



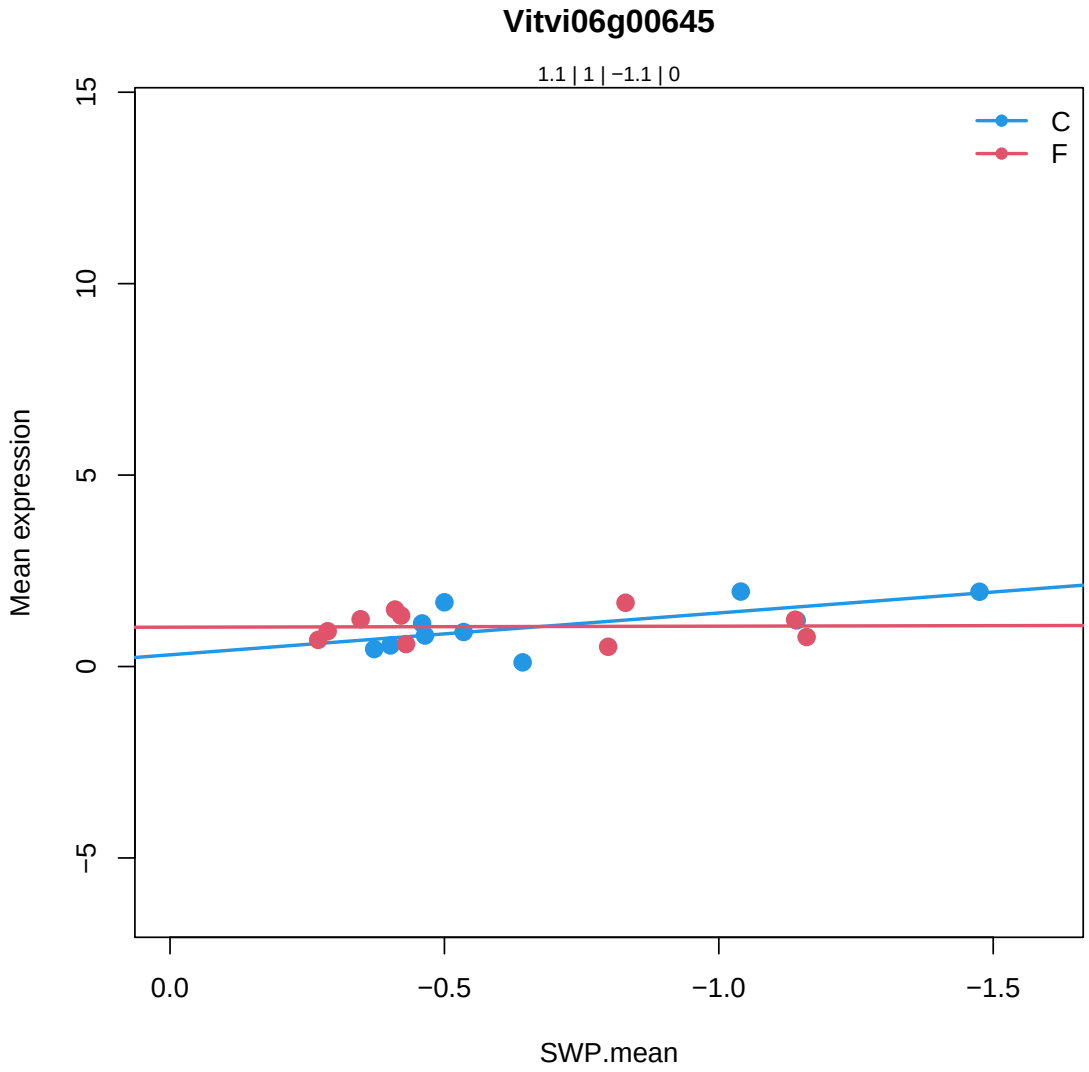
7.6.902 Vitvi06g00645: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00645
        35.2
        not assigned.unknown
        O-glucosyltransferase rumi-like protein (DUF821) |
        Chr1:2217073-2219379 REVERSE LENGTH=507 |
        201606
```

Coefficients for Vitvi06g00645.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.074367	4.068789e-07	***	4.744586e-07	***
SlopeC	-1.093261	0.01581111	*	0.3462543	
MeanF-MeanC	-0.03128984	0.8840732		0.9695691	
SlopeF-SlopeC	1.066747	0.1001968		0.9999488	



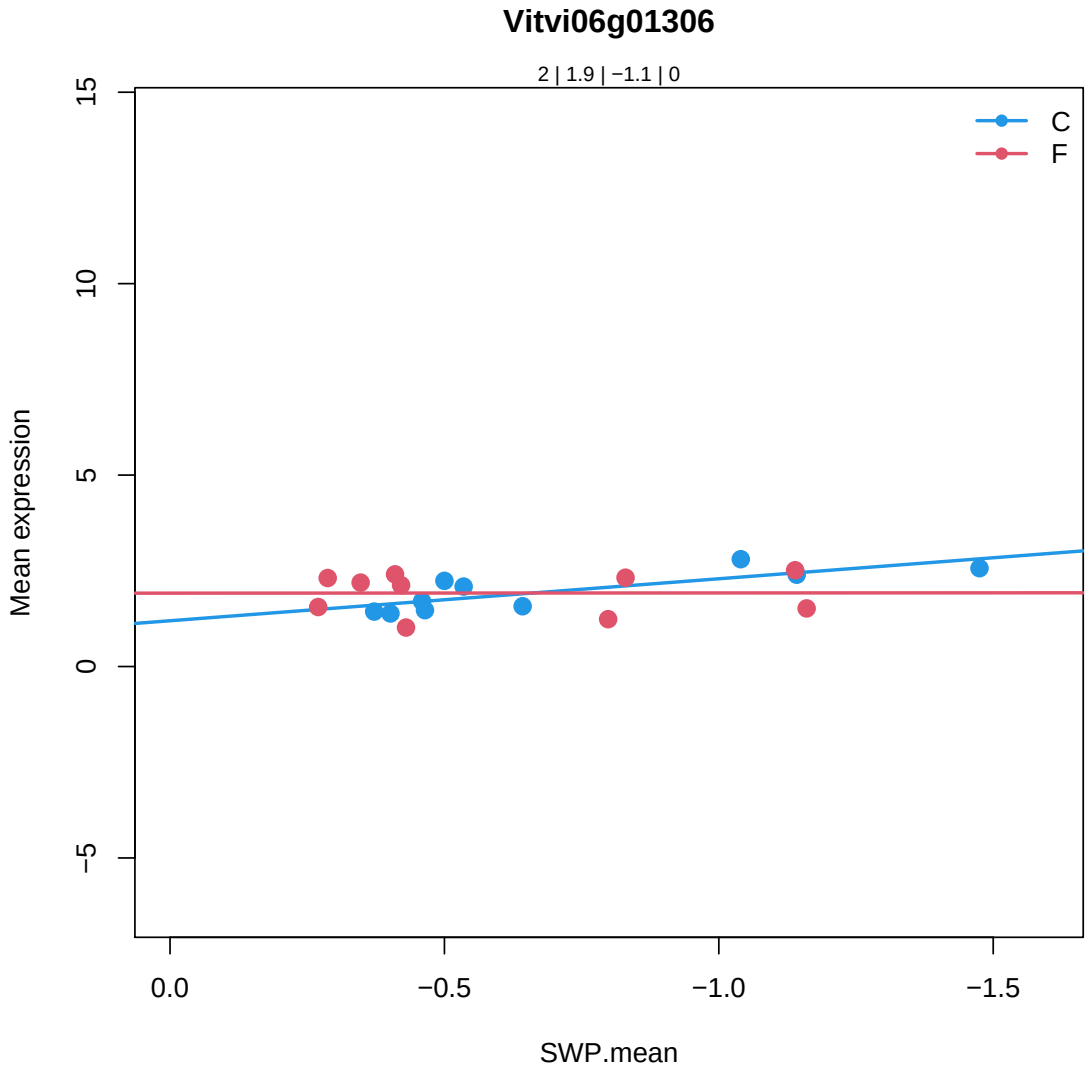
7.6.903 Vitvi06g01306: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01306
        34.16
        transport.ABC transporters and multidrug resistance systems
        ABC-2 type transporter family protein |
        Chr2:11956432-11959782 FORWARD LENGTH=730 |
        201606
```

Coefficients for Vitvi06g01306.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.966156	9.411191e-12	***	1.285929e-11	***
SlopeC	-1.096755	0.01508525	*	0.3381314	
MeanF-MeanC	-0.04658118	0.8273827		0.951843	
SlopeF-SlopeC	1.091432	0.09156015	.	0.9999488	



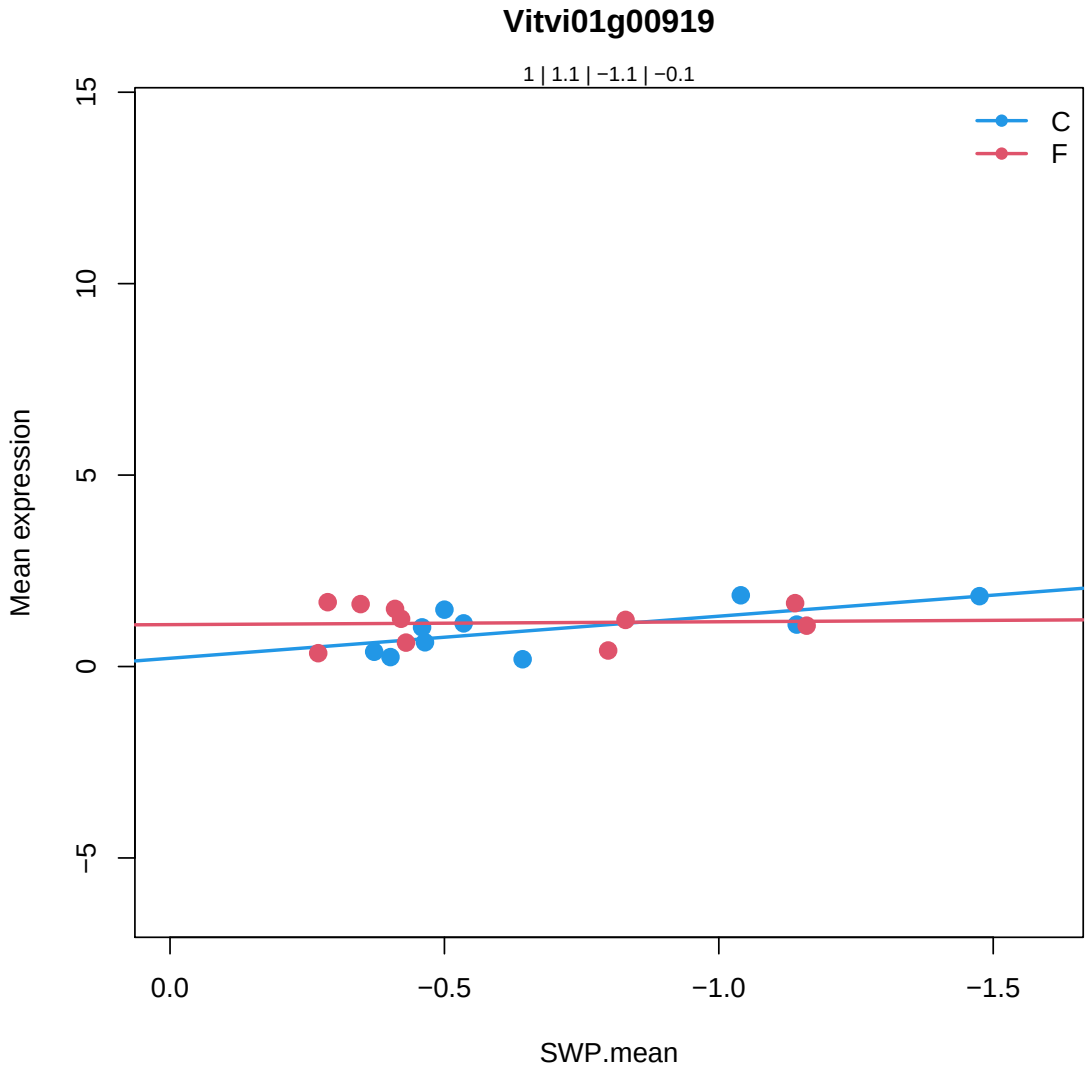
7.6.904 Vitvi01g00919: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00919
        34.4
        transport.nitrate
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr5:16169315-16171153 FORWARD LENGTH=612 |
        201606
```

Coefficients for Vitvi01g00919.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.9879988	3.912865e-06	***	4.457057e-06	***
SlopeC	-1.099294	0.02262073	*	0.3958499	
MeanF-MeanC	0.1513134	0.5130123		0.814217	
SlopeF-SlopeC	1.024777	0.1385244		0.9999488	



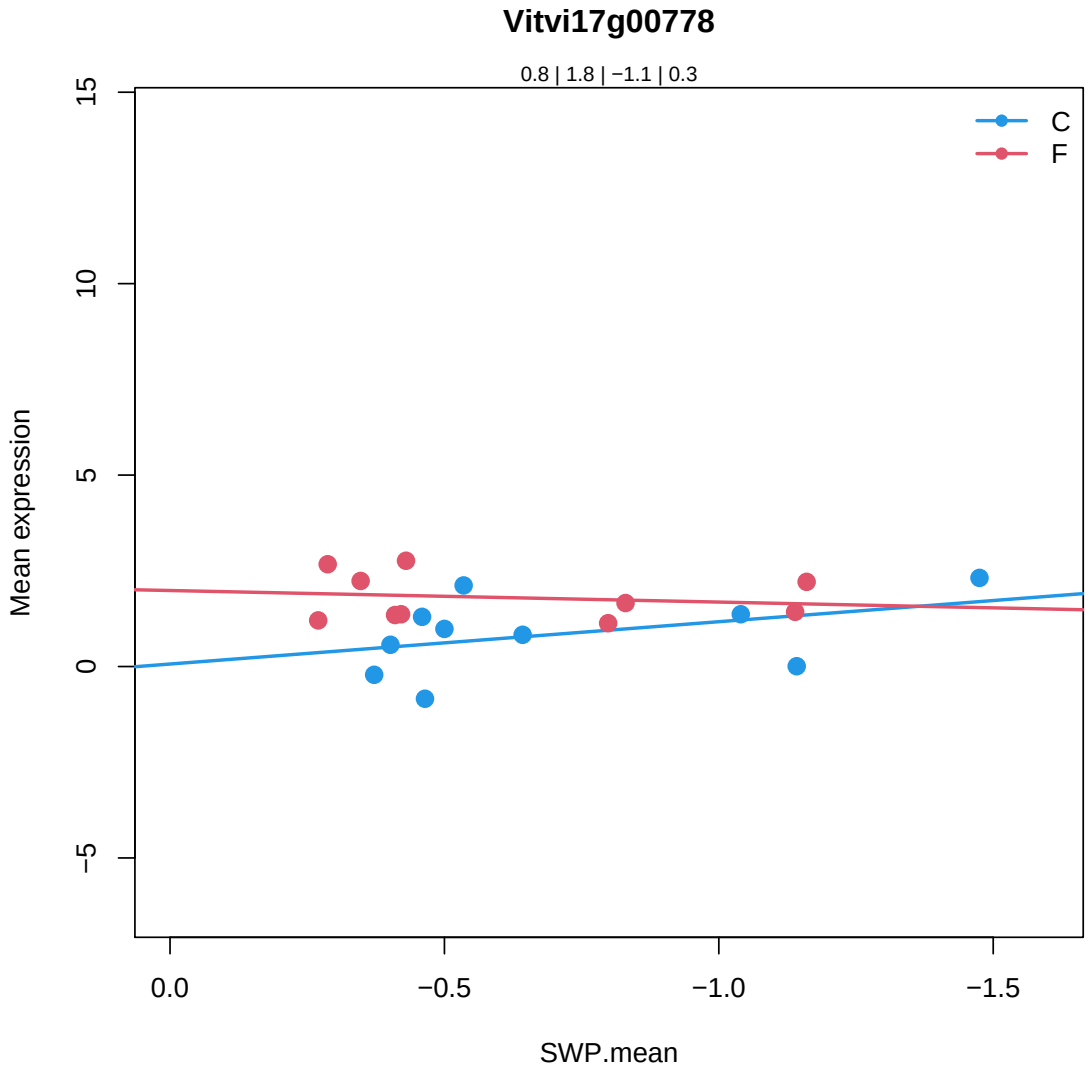
7.6.905 Vitvi17g00778: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00778
        3.2.3
        minor CHO metabolism.trehalose.potential TPS/TPP
        trehalose-phosphatase/synthase 9 |
        Chr1:8432695-8435506 FORWARD LENGTH=867 |
        201606
```

Coefficients for Vitvi17g00778.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8422634	0.00184006	**	0.001980524	**
SlopeC	−1.105516	0.1082995		0.622671	
MeanF−MeanC	0.9587796	0.009268482	**	0.07185667	.
SlopeF−SlopeC	1.407454	0.1661537		0.9999488	



7.6.906 Vitvi01g01632: * type5

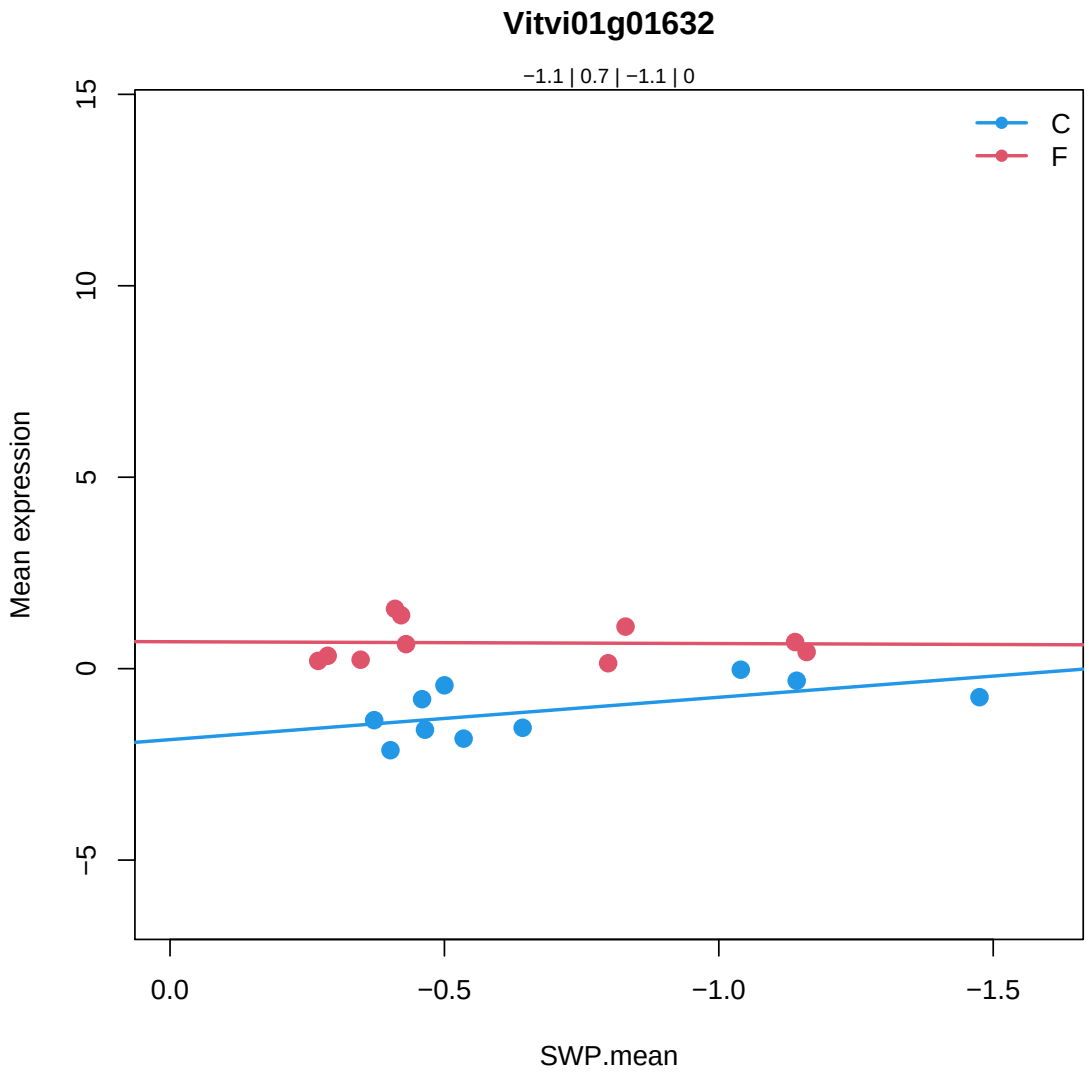
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01632
        35.2
        not assigned.unknown
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr4:679487-681904 FORWARD LENGTH=805 |
        201606

Vitvi01g01632
        35.1.27
        not assigned.no ontology.tetratricopeptide repeat (TPR)
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr4:679487-681904 FORWARD LENGTH=805 |
        201606
```

Coefficients for Vitvi01g01632.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.07624	3.979672e-06	***	4.532479e-06	***
SlopeC	-1.106815	0.03378215	*	0.4433084	
MeanF-MeanC	1.749955	5.170037e-07	***	1.811533e-05	***
SlopeF-SlopeC	1.154724	0.1265502		0.9999488	


Vitvi01g01632
−1.1 | 0.7 | −1.1 | 0
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

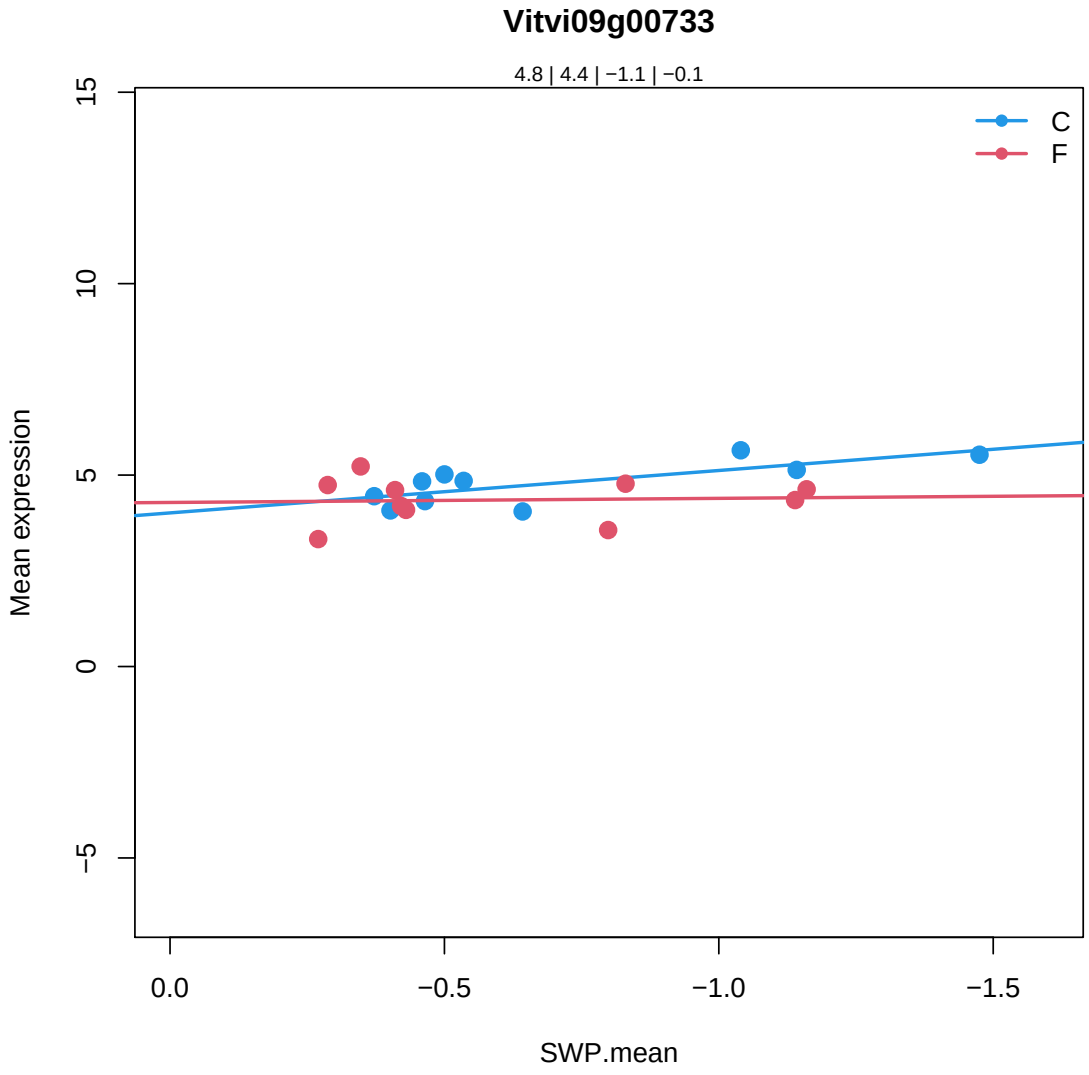
7.6.907 Vitvi09g00733: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00733
        31.1
        cell.organisation
        RNA-directed DNA polymerase (reverse transcriptase)-related family pro
        Chr3:8789309-8790907 FORWARD LENGTH=532 |
        201606
```

Coefficients for Vitvi09g00733.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.790823	6.365048e-19	***	2.322625e-18	***
SlopeC	-1.107735	0.02187455	*	0.3904795	
MeanF-MeanC	-0.4407742	0.06627446	.	0.2855966	
SlopeF-SlopeC	1.00062	0.1481108		0.9999488	



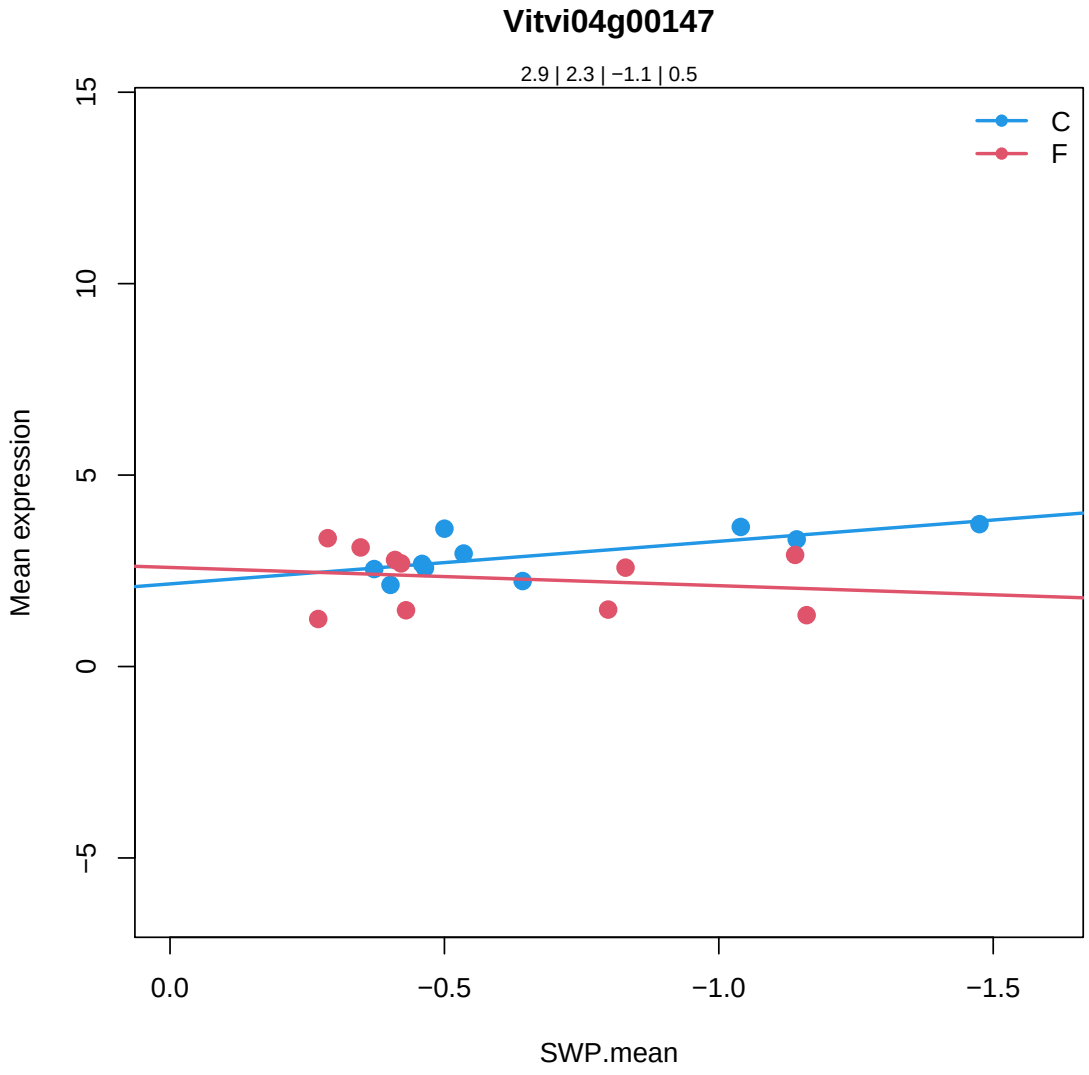
7.6.908 Vitvi04g00147: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00147
        30.99
        signalling.unspecified
        mechanosensitive channel of small conductance-like 10 |
        Chr5:3898182-3900923 REVERSE LENGTH=734 |
        201606
```

Coefficients for Vitvi04g00147.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.939881	1.241929e-12	***	1.771594e-12	***
SlopeC	-1.112465	0.05954374	.	0.5395753	
MeanF-MeanC	-0.6426727	0.03425886	*	0.1850367	
SlopeF-SlopeC	1.588519	0.0697677	.	0.9999488	



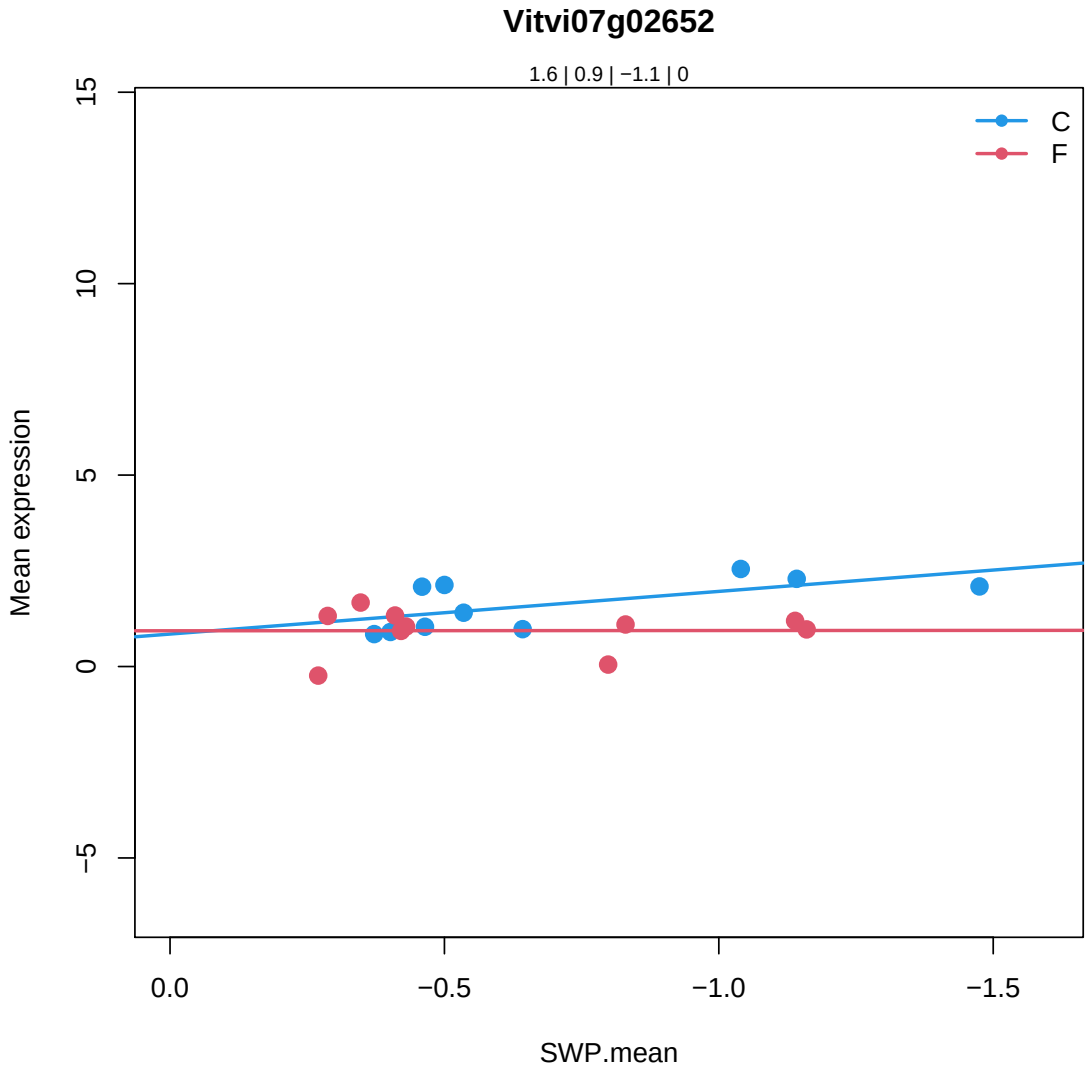
7.6.909 Vitvi07g02652: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g02652
        35.2
        not assigned.unknown
        N-acetyl-l-glutamate synthase 1 |
        Chr2:9749988-9752737 FORWARD LENGTH=609 |
        201606
```

Coefficients for Vitvi07g02652.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.631129	6.704113e-09	***	8.228707e-09	***
SlopeC	-1.114349	0.03429585	*	0.4436999	
MeanF-MeanC	-0.6941623	0.01132823	*	0.0831719	.
SlopeF-SlopeC	1.107596	0.1457311		0.9999488	



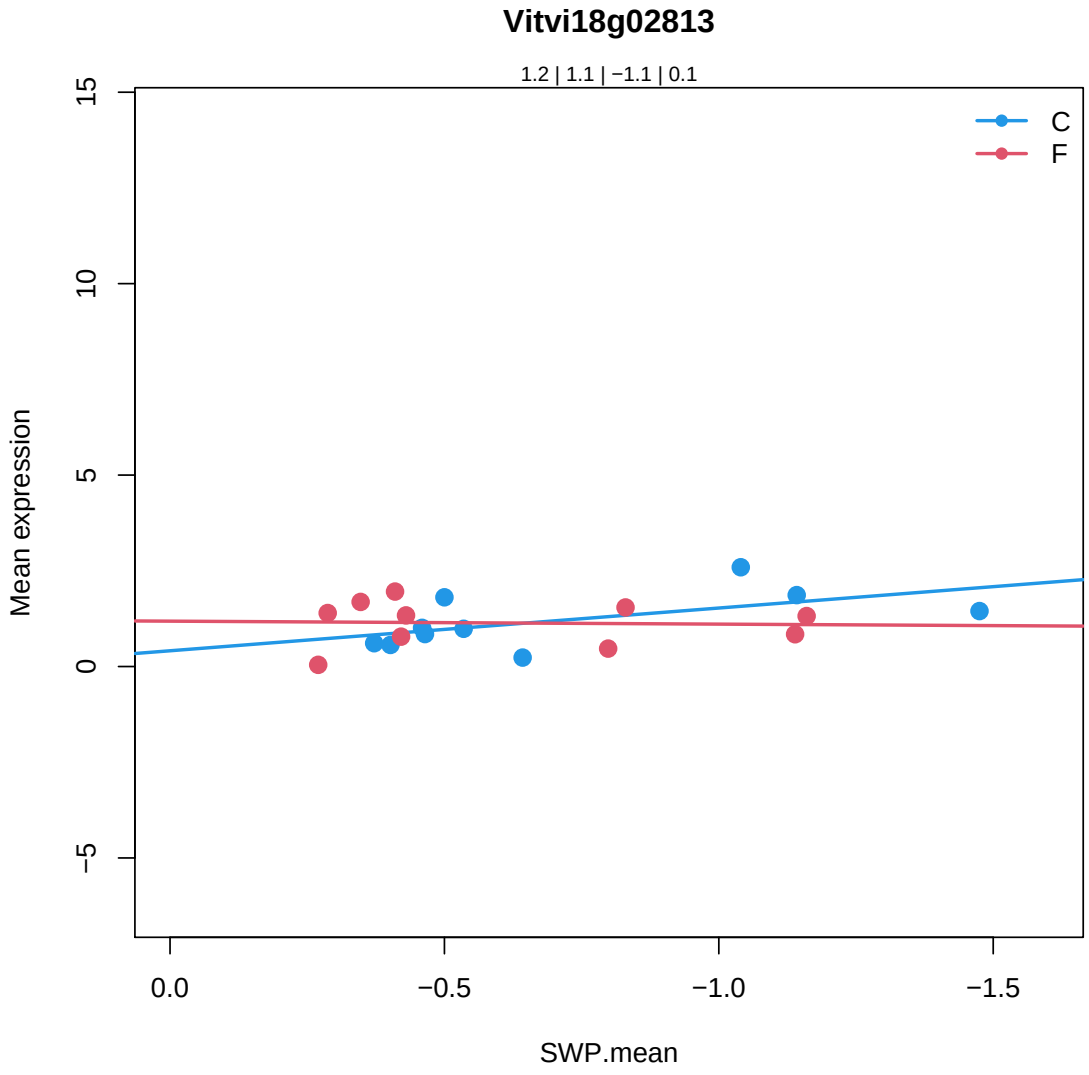
7.6.910 Vitvi18g02813: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02813
        27.3.50
        RNA.regulation of transcription.general transcription
        DNA-directed RNA polymerase I subunit RPA12-like protein |
        Chr1:6956973-6957561 FORWARD LENGTH=63 |
        201606
```

Coefficients for Vitvi18g02813.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.196039	2.287961e-06	***	2.619328e-06	***
SlopeC	-1.116426	0.04396074	*	0.486332	
MeanF-MeanC	-0.0588539	0.8264315		0.9513491	
SlopeF-SlopeC	1.193798	0.1387322		0.9999488	



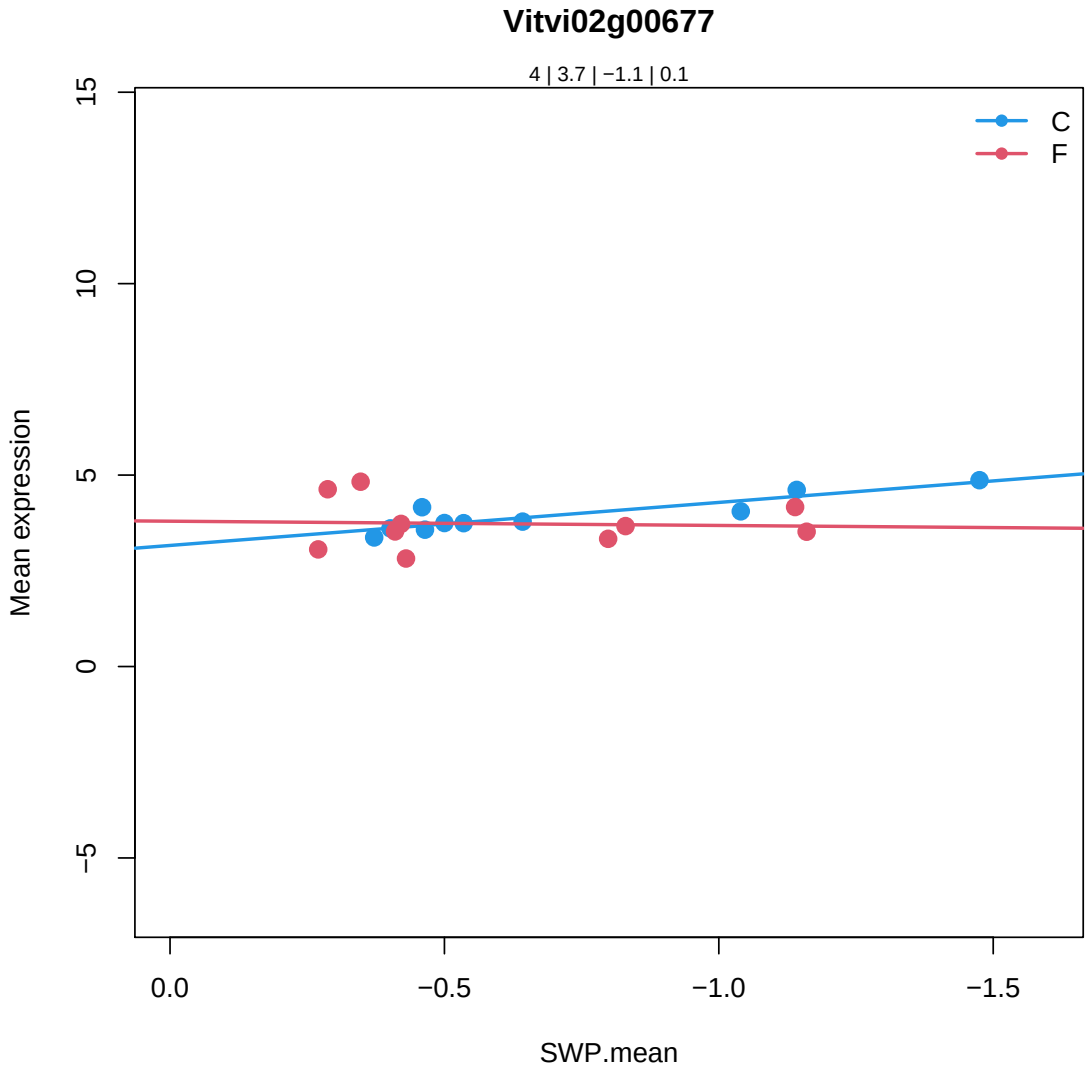
7.6.911 Vitvi02g00677: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00677
        26.13
        misc.acid and other phosphatases
        pentatricopeptide (PPR) repeat-containing protein |
        Chr5:18897510-18899645 REVERSE LENGTH=711 |
        201606
```

Coefficients for Vitvi02g00677.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.95195	2.713878e-17	***	6.545083e-17	***
SlopeC	-1.123722	0.01889173	*	0.3680156	
MeanF-MeanC	-0.2242423	0.3298983		0.6895654	
SlopeF-SlopeC	1.234825	0.07448318	.	0.9999488	



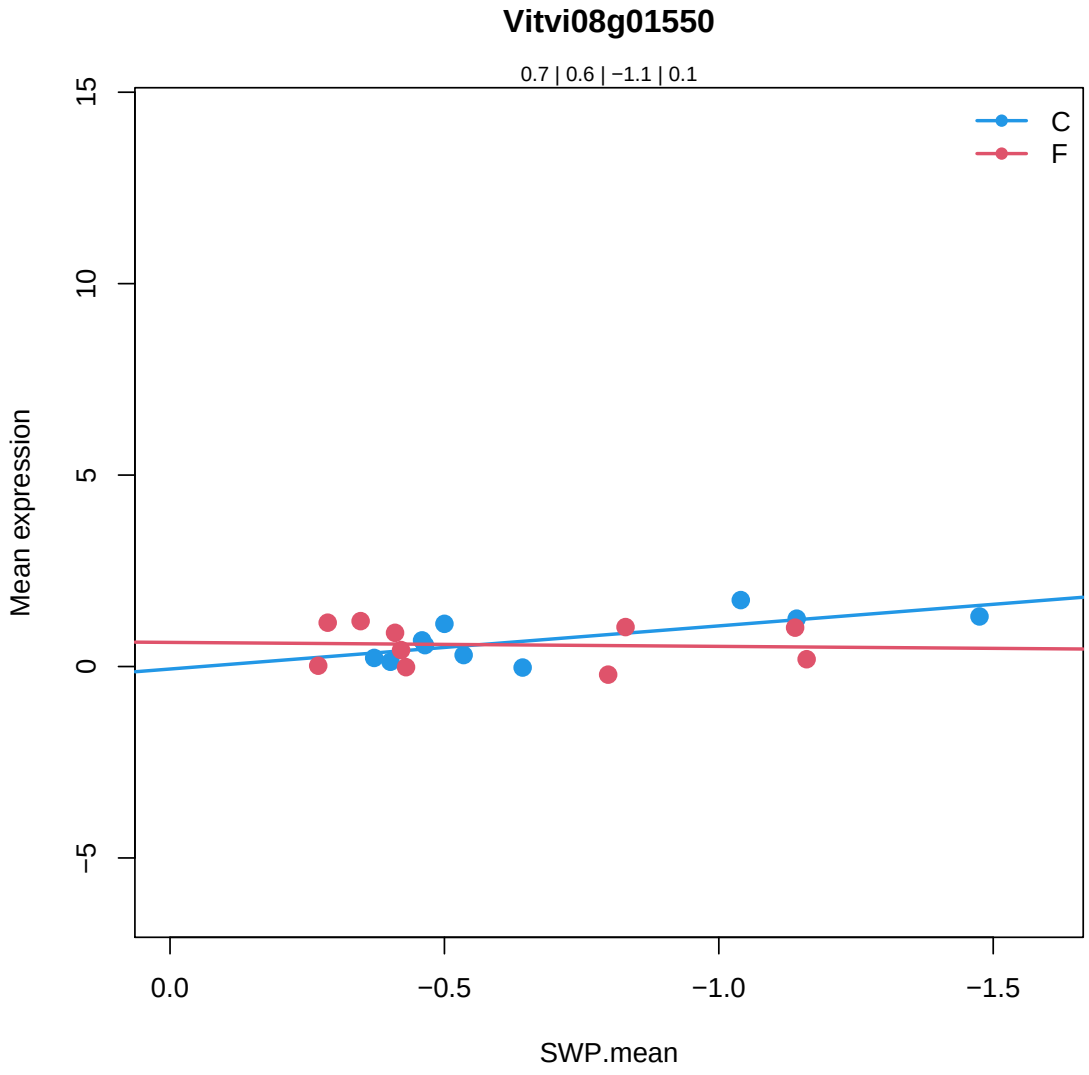
7.6.912 Vitvi08g01550: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01550
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        Pentatricopeptide repeat (PPR) superfamily protein |
        Chr5:1010894-1013584 REVERSE LENGTH=896 |
        201606
```

Coefficients for Vitvi08g01550.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.7267588	0.0001663577	***	0.0001829191	***
SlopeC	-1.126549	0.01906306	*	0.3696682	
MeanF-MeanC	-0.1600147	0.4862815		0.7979226	
SlopeF-SlopeC	1.230091	0.07665047	.	0.9999488	



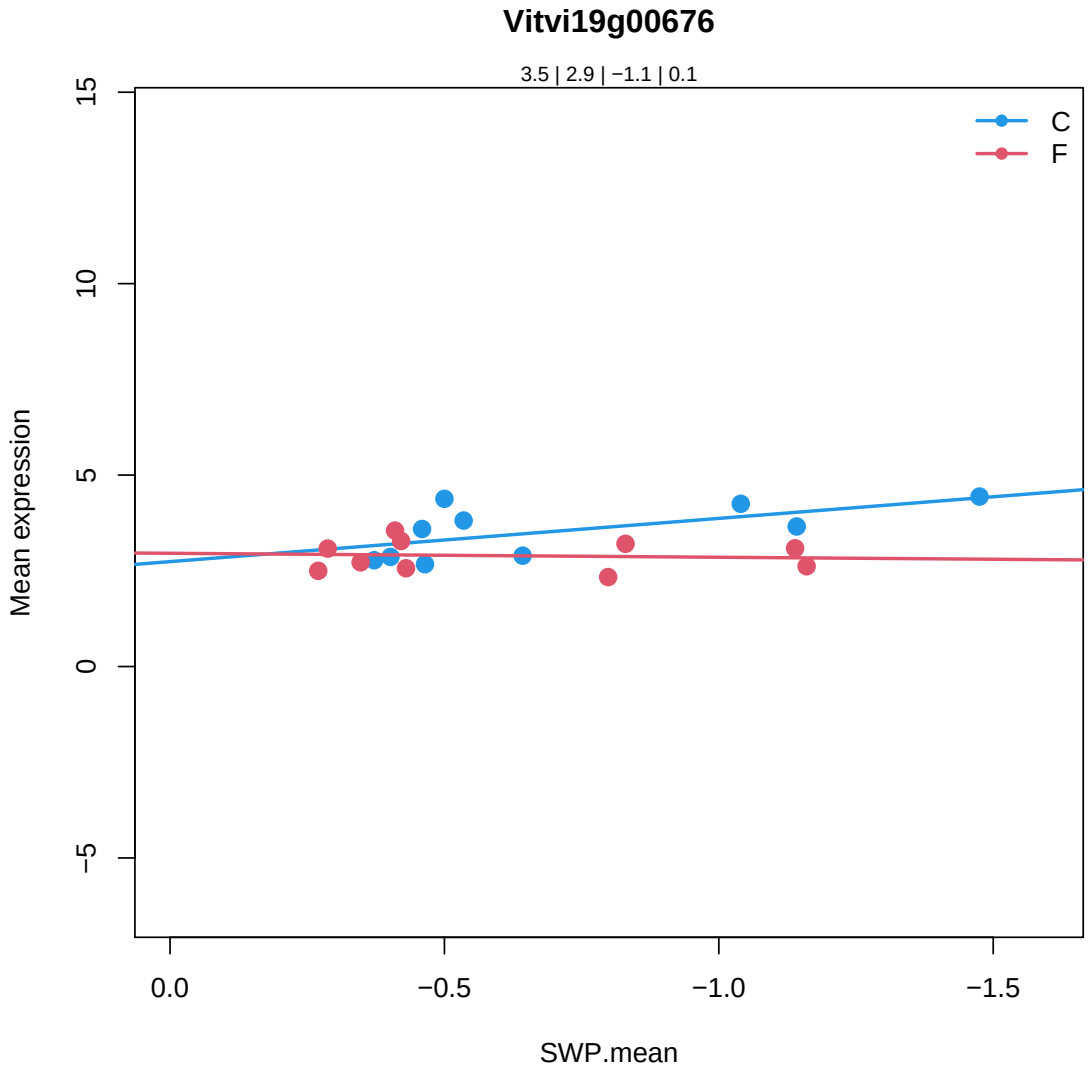
7.6.913 Vitvi19g00676: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g00676
        29.1.3
        protein.aa activation.threonine-tRNA ligase
        Threonyl-tRNA synthetase |
        Chr5:9437351-9441568 FORWARD LENGTH=709 |
        201606
```

Coefficients for Vitvi19g00676.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.533538	2.604042e-16	***	5.283653e-16	***
SlopeC	-1.129058	0.0181412	*	0.3617849	
MeanF-MeanC	-0.6394703	0.009457264	**	0.0729123	.
SlopeF-SlopeC	1.232851	0.07423087	.	0.9999488	



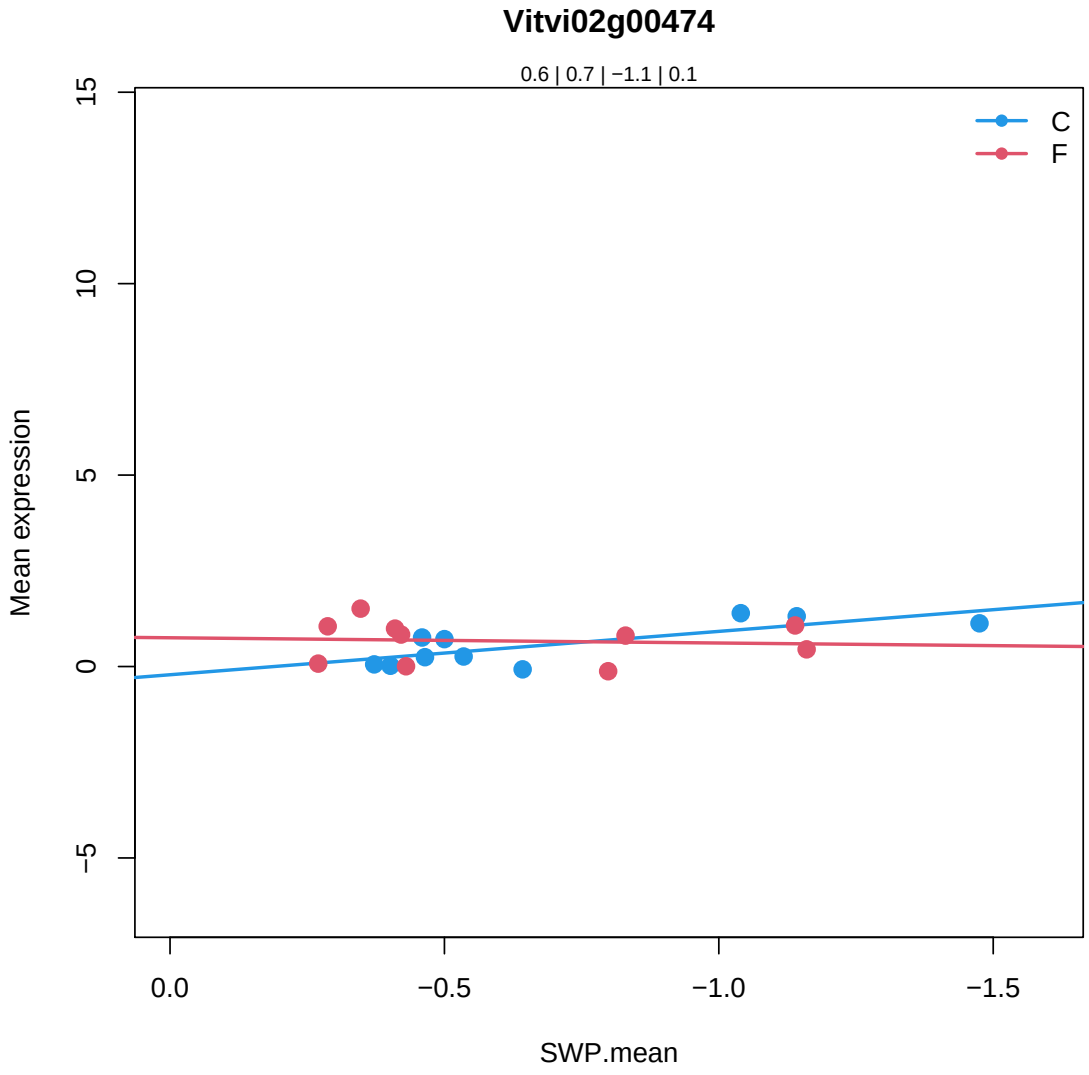
7.6.914 Vitvi02g00474: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00474
        35.1.27
        not assigned.no ontology.tetratricopeptide repeat (TPR)
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr4:11960553-11962289 FORWARD LENGTH=578 |
        201606
```

Coefficients for Vitvi02g00474.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.5812292	0.001041477	**	0.001127349	**
SlopeC	-1.132748	0.0146578	*	0.3359386	
MeanF-MeanC	0.08612878	0.6952023		0.9039646	
SlopeF-SlopeC	1.269689	0.05839566	.	0.9999488	



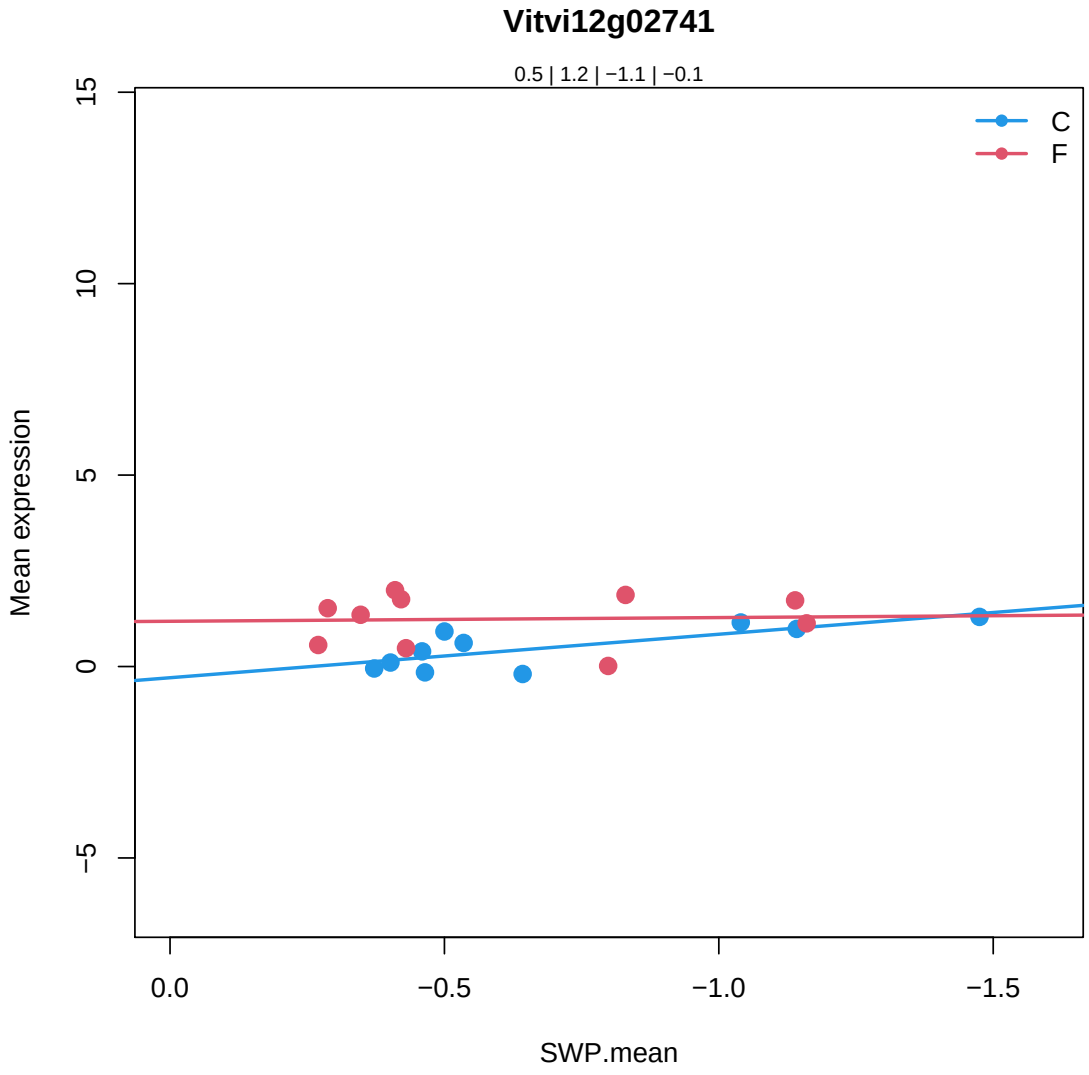
7.6.915 Vitvi12g02741: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g02741
        35.2
        not assigned.unknown
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi12g02741.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.5057246	0.008809469	**	0.009345346	**
SlopeC	−1.135635	0.02990774	*	0.4304569	
MeanF−MeanC	0.7345422	0.007373856	**	0.0607526	.
SlopeF−SlopeC	1.039054	0.1672023		0.9999488	



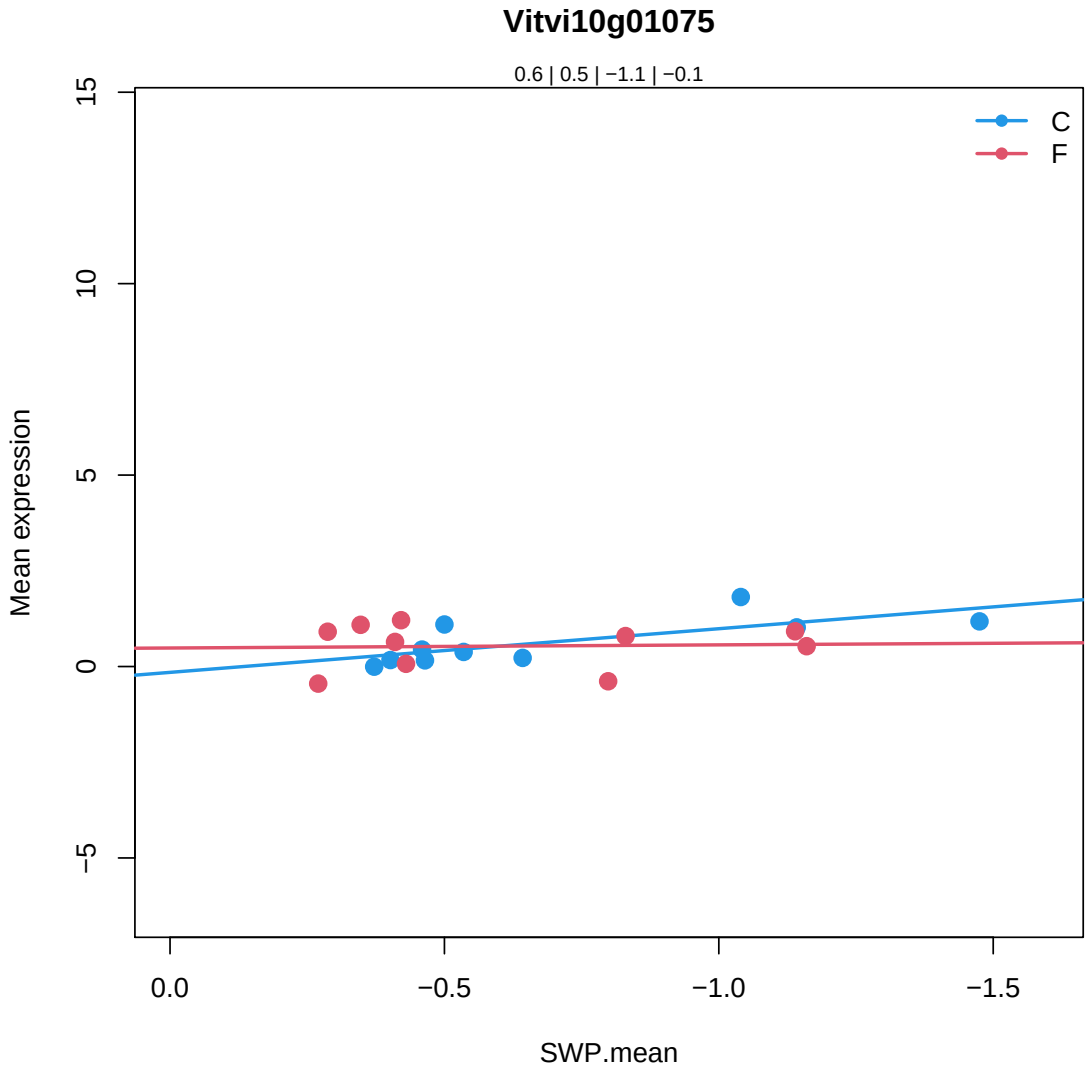
7.6.916 Vitvi10g01075: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g01075
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr4:11336479-11339052 FORWARD LENGTH=857 |
        201606
```

Coefficients for Vitvi10g01075.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6486238	0.0008102264	***	0.0008792162	***
SlopeC	-1.140381	0.02240193	*	0.3929231	
MeanF-MeanC	-0.1151481	0.6298965		0.8738061	
SlopeF-SlopeC	1.05855	0.1394387		0.9999488	



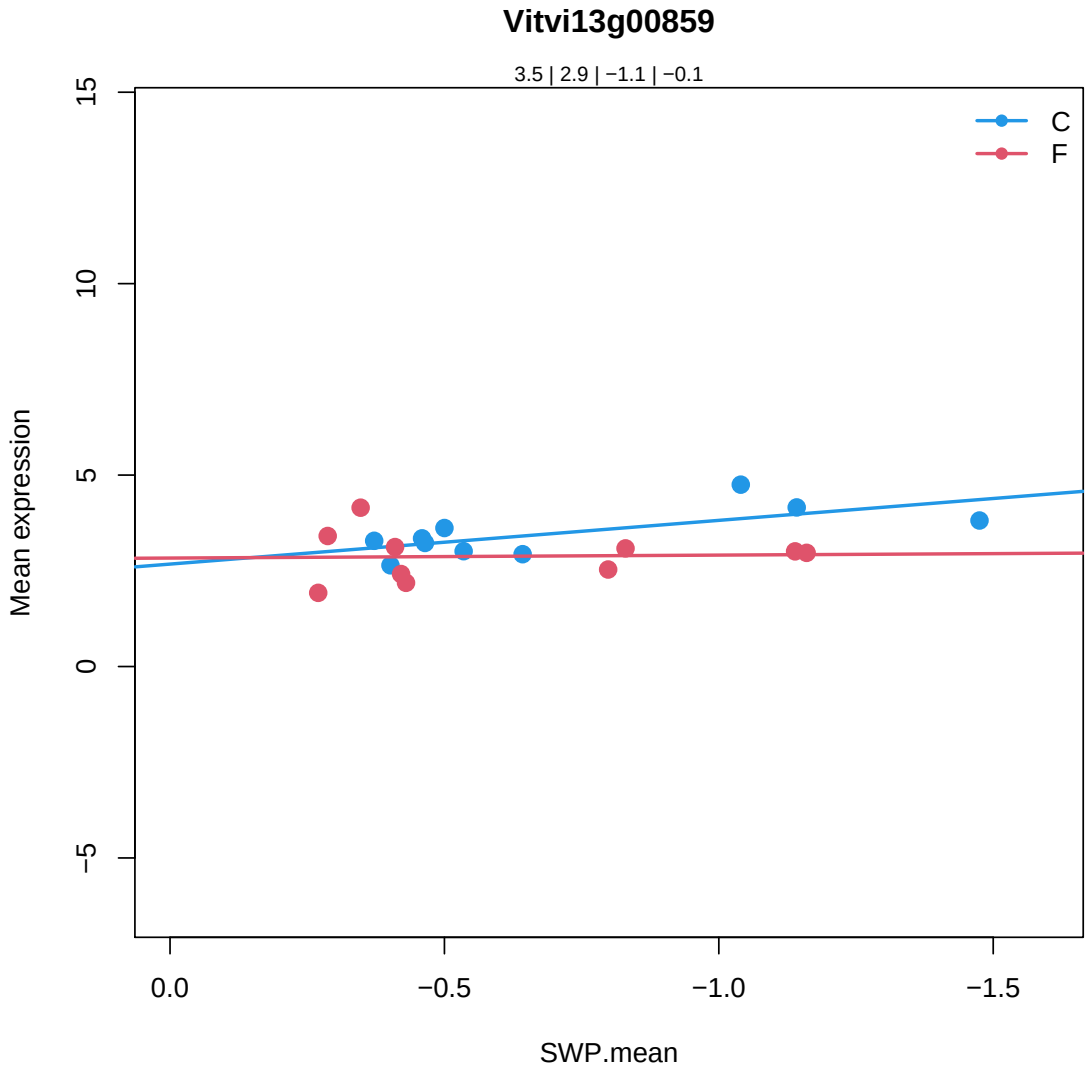
7.6.917 Vitvi13g00859: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00859
        27.4
        RNA.RNA binding
        RNA-binding (RRM/RBD/RNP motifs) family protein |
        Chr3:7331739-7333749 FORWARD LENGTH=379 |
        201606
```

Coefficients for Vitvi13g00859.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.478162	4.431501e-15	***	7.721187e-15	***
SlopeC	-1.14185	0.03235555	*	0.4375894	
MeanF-MeanC	-0.5985475	0.02782374	*	0.1606399	
SlopeF-SlopeC	1.064812	0.1660523		0.9999488	



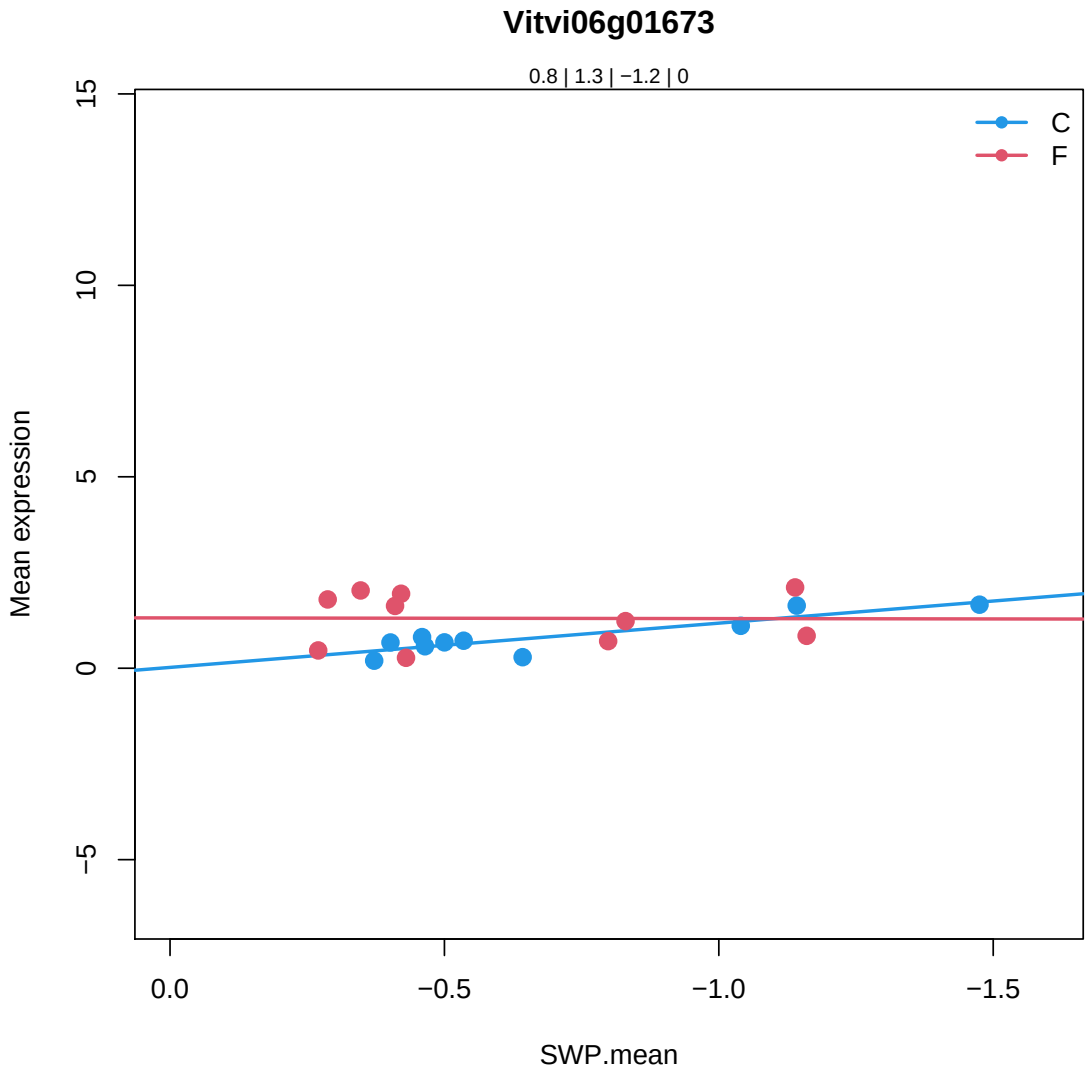
7.6.918 Vitvi06g01673: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01673
        35.2
        not assigned.unknown
        Chitinase 2 IPR001223 Glycoside hydrolase, family 18, catalytic domain
```

Coefficients for Vitvi06g01673.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8337968	6.433963e-05	***	7.132106e-05	***
SlopeC	-1.155645	0.02225867	*	0.3929231	
MeanF-MeanC	0.4692519	0.06209673	.	0.2747111	
SlopeF-SlopeC	1.173261	0.1073201		0.9999488	



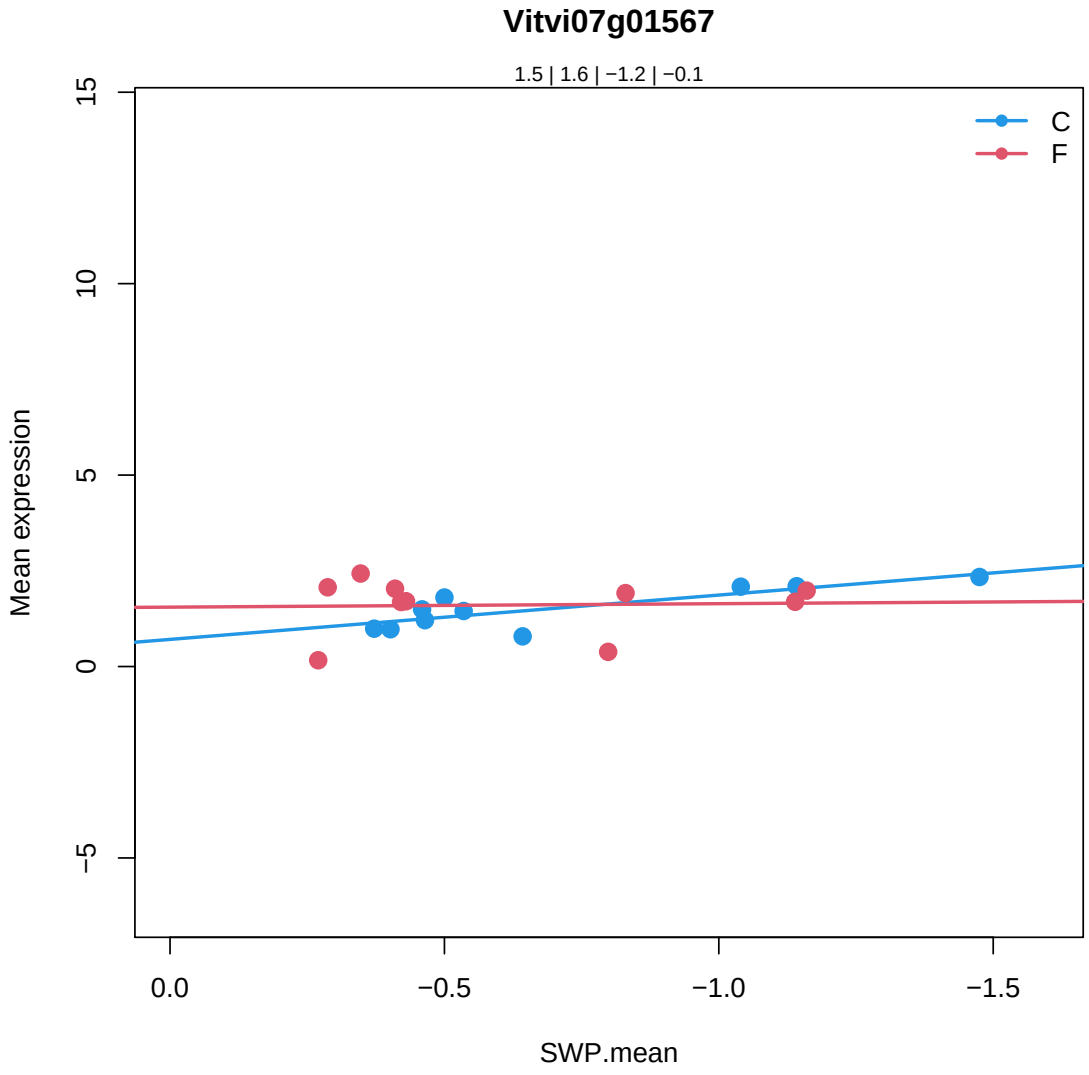
7.6.919 Vitvi07g01567: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01567
        26.24
        misc.GCN5-related N-acetyltransferase
        N-acetyl-l-glutamate synthase 1 |
        Chr2:9749988-9752737 FORWARD LENGTH=609 |
        201606
```

Coefficients for Vitvi07g01567.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.522445	3.389314e-08	***	4.073483e-08	***
SlopeC	−1.157657	0.03245873	*	0.4378194	
MeanF−MeanC	0.0831812	0.7496272		0.9264858	
SlopeF−SlopeC	1.067706	0.1708131		0.9999488	



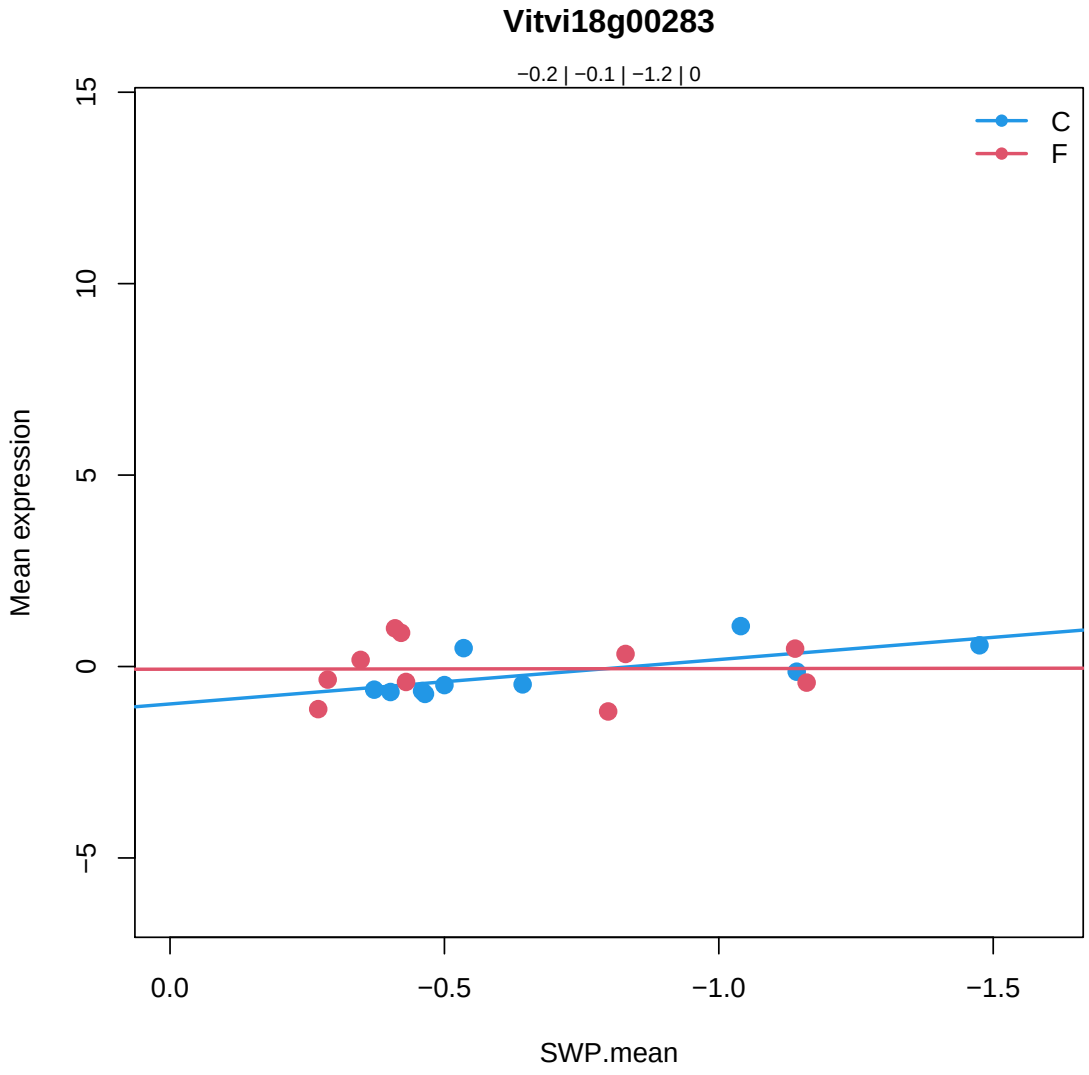
7.6.920 Vitvi18g00283: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00283
        35.1
        not assigned.no ontology
        lysm domain GPI-anchored protein 1 precursor |
        Chr1:7680689-7682048 FORWARD LENGTH=316 |
        201606
```

Coefficients for Vitvi18g00283.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	−0.1624794	0.4185417		0.4245865	
SlopeC	−1.159442	0.0462368	*	0.4942085	
MeanF−MeanC	0.1018475	0.7182435		0.9136595	
SlopeF−SlopeC	1.143733	0.1751686		0.9999488	



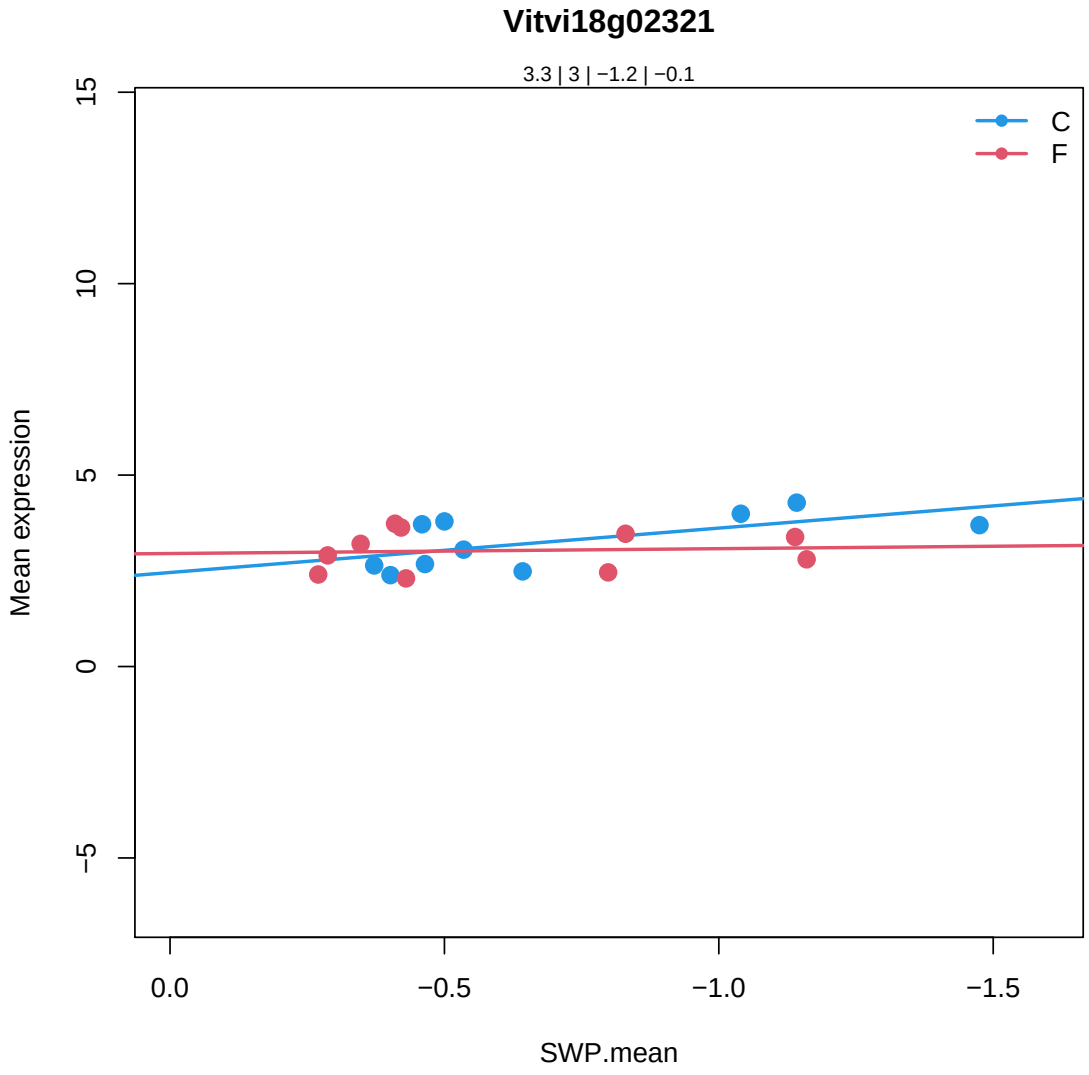
7.6.921 Vitvi18g02321: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02321
        13.1.3.6.1
        amino acid metabolism.synthesis.aspartate family.misc.homoserine
        aspartate kinase-homoserine dehydrogenase ii |
        Chr4:10725229-10729536 FORWARD LENGTH=916 |
        201606
```

Coefficients for Vitvi18g02321.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.270712	7.795213e-15	***	1.31782e-14	***
SlopeC	-1.160047	0.02529636	*	0.4079655	
MeanF-MeanC	-0.2427397	0.333298		0.6923986	
SlopeF-SlopeC	1.03348	0.1645106		0.9999488	



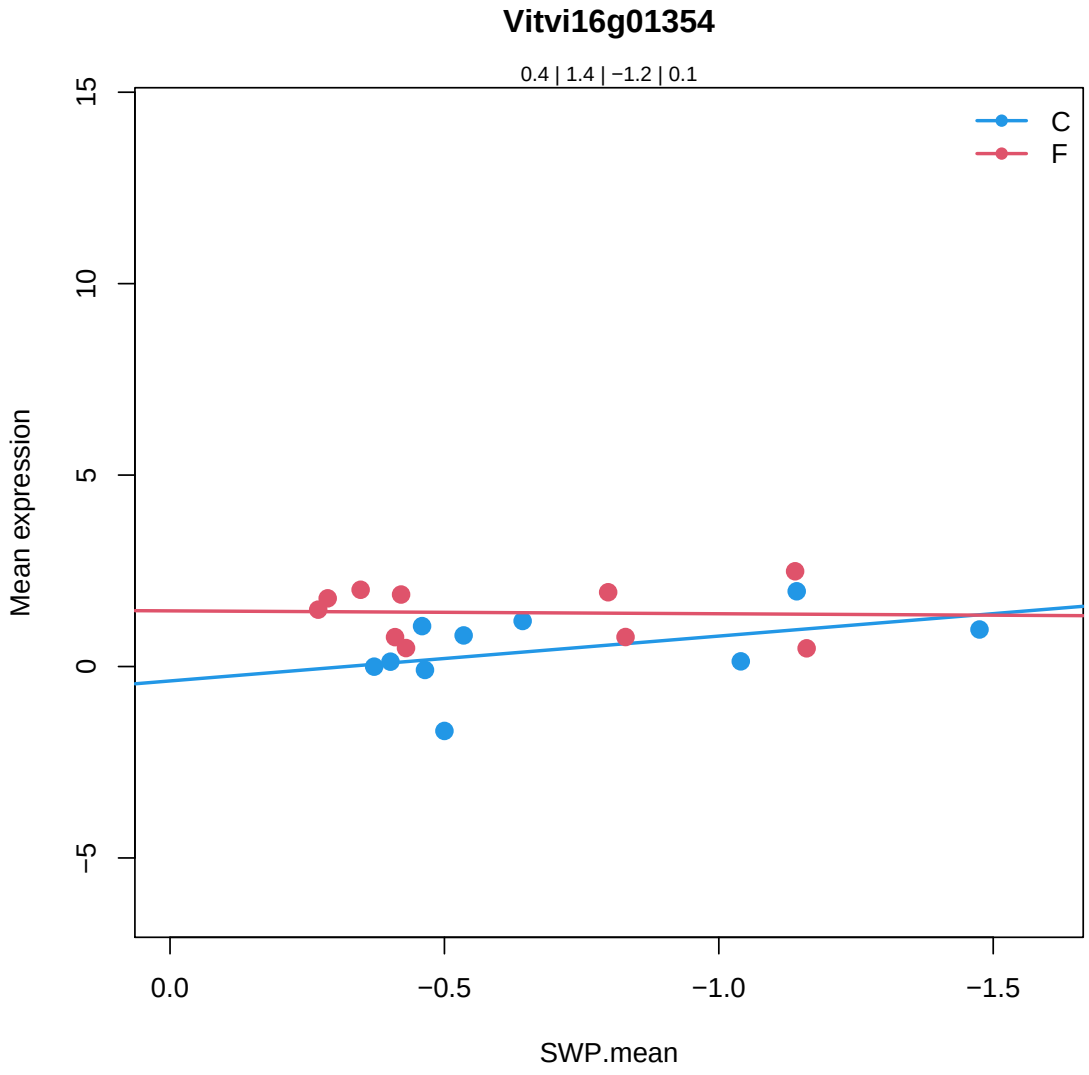
7.6.922 Vitvi16g01354: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01354
        27.3.50
        RNA.regulation of transcription.general transcription
        growth-regulating factor 8 |
        Chr4:12535972-12539387 FORWARD LENGTH=493 |
        201606
```

Coefficients for Vitvi16g01354.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4473378	0.08435288	.	0.08737387	.
SlopeC	-1.17177	0.1028232		0.6141191	
MeanF-MeanC	0.9599574	0.01195456	*	0.08685009	.
SlopeF-SlopeC	1.24711	0.2362656		0.9999488	



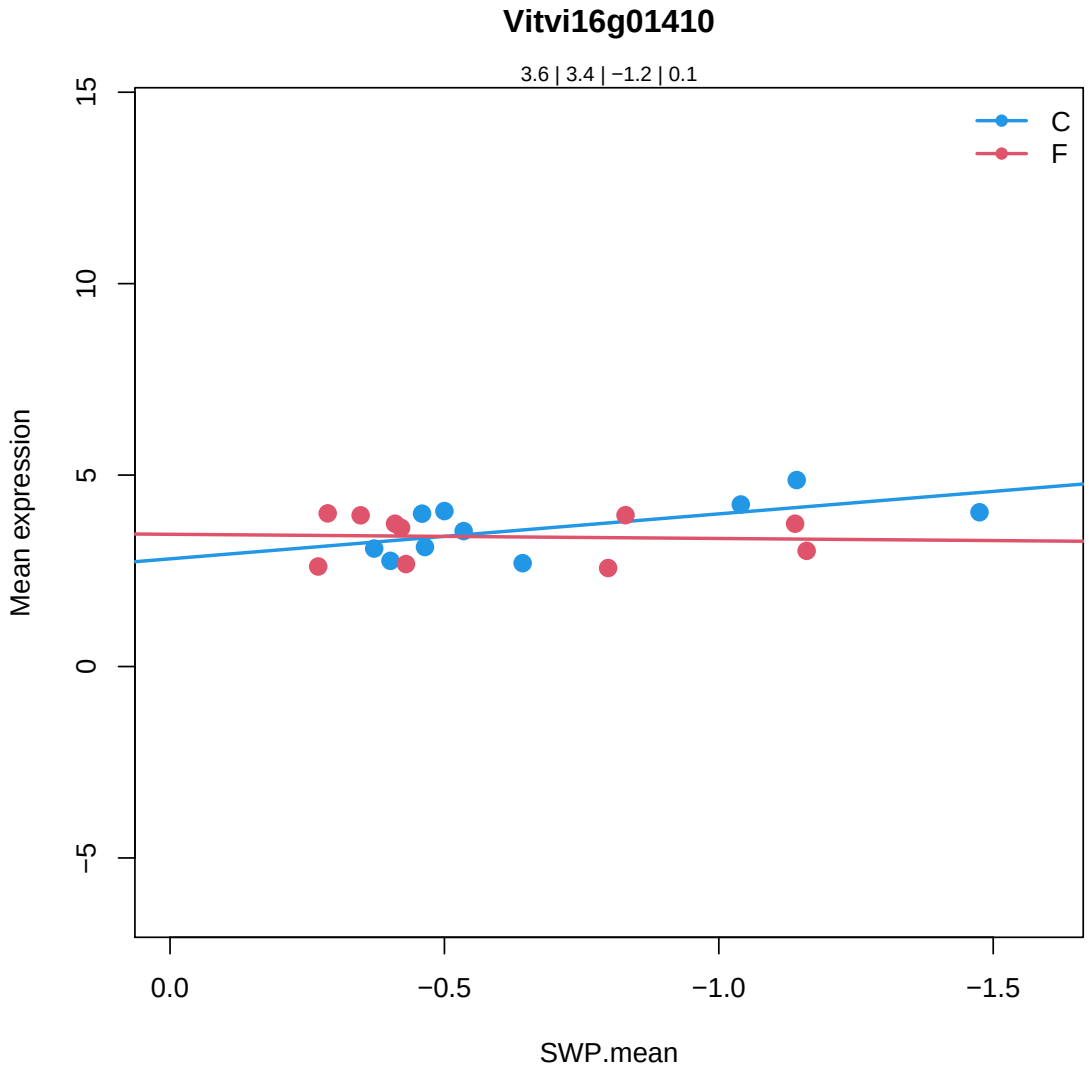
7.6.923 Vitvi16g01410: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01410
        27.3.57
        RNA.regulation of transcription.JUMONJI family
        Transcription factor jumonji (jmjC) domain-containing protein |
        Chr4:427035-431086 FORWARD LENGTH=775 |
        201606
```

Coefficients for Vitvi16g01410.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.638151	3.103687e-15	***	5.500743e-15	***
SlopeC	-1.174418	0.0322547	*	0.4372376	
MeanF-MeanC	-0.2515051	0.3454355		0.7050251	
SlopeF-SlopeC	1.283387	0.1072172		0.9999488	



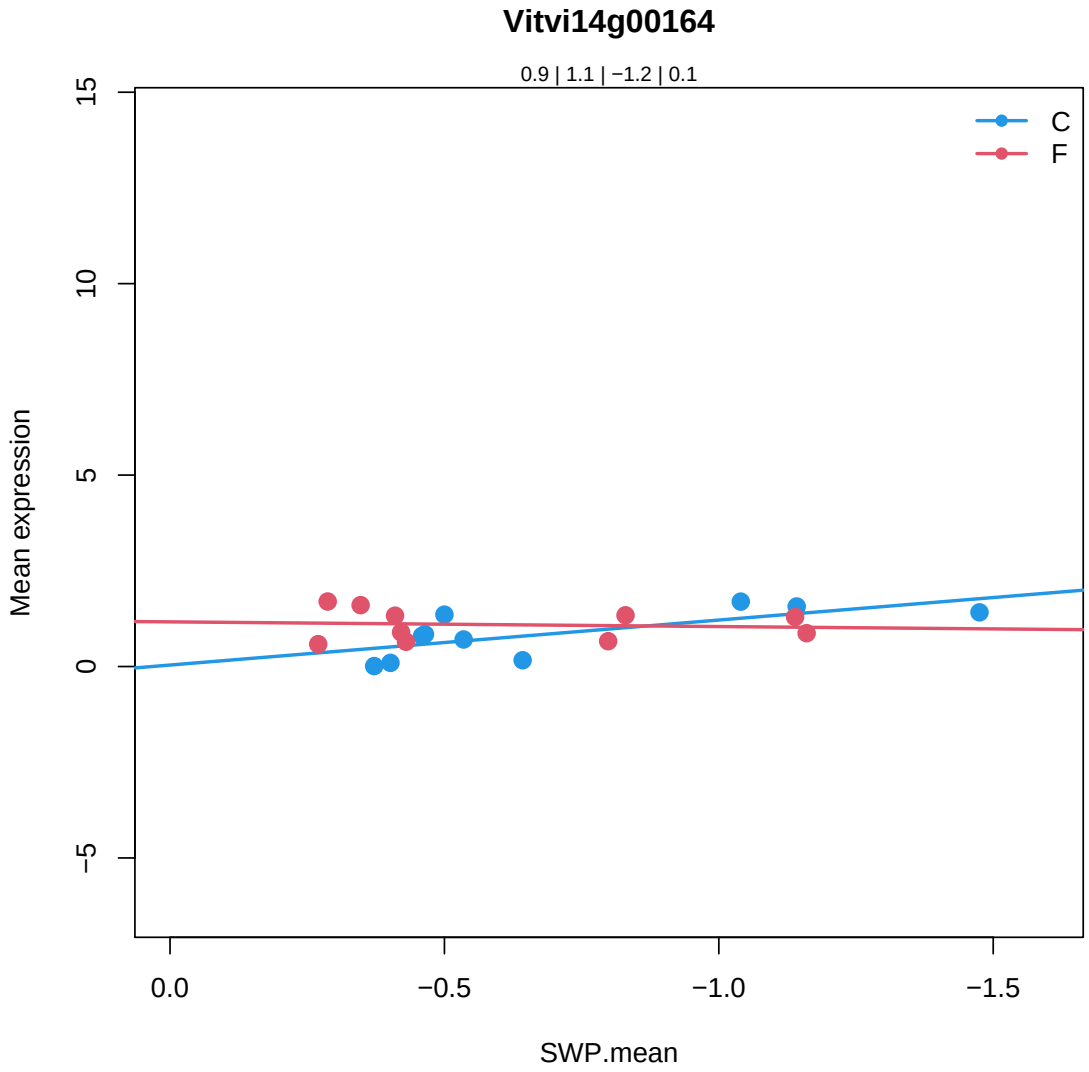
7.6.924 Vitvi14g00164: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g00164
        35.2
        not assigned.unknown
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr5:26551879-26553741 FORWARD LENGTH=620 |
        201606
```

Coefficients for Vitvi14g00164.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.864983	6.635351e-06	***	7.518848e-06	***
SlopeC	-1.175062	0.008704899	**	0.2903326	
MeanF-MeanC	0.2265453	0.2857129		0.6508498	
SlopeF-SlopeC	1.297163	0.04390236	*	0.9999488	



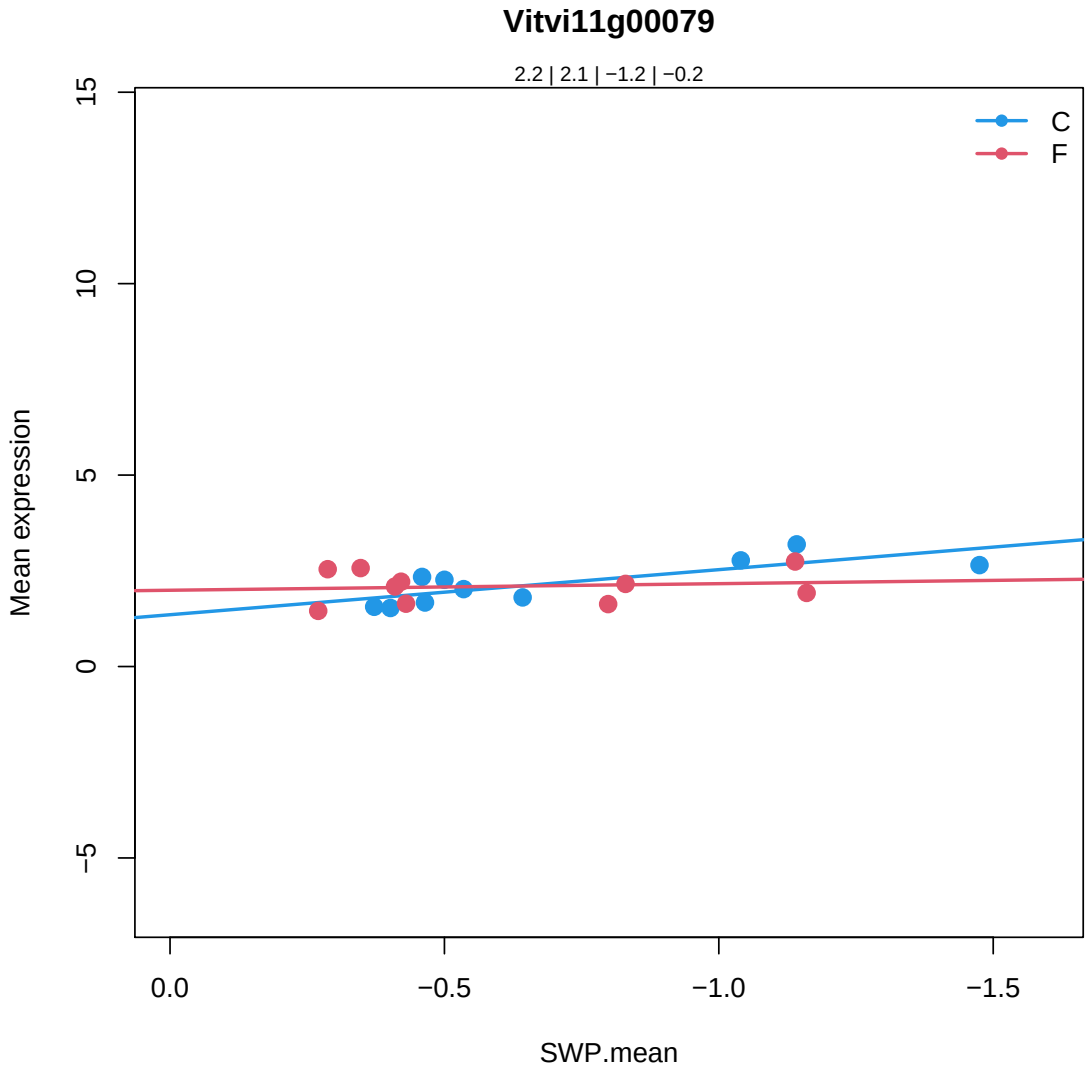
7.6.925 Vitvi11g00079: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00079
        31.1
        cell.organisation
        tubulin-tyrosine ligase |
        Chr1:29138490-29142965 REVERSE LENGTH=855 |
        201606
```

Coefficients for Vitvi11g00079.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.180234	2.634358e-13	***	3.934243e-13	***
SlopeC	-1.177145	0.005700244	**	0.2614474	
MeanF-MeanC	-0.08376485	0.6715296		0.8932689	
SlopeF-SlopeC	1.005071	0.09234856	.	0.9999488	



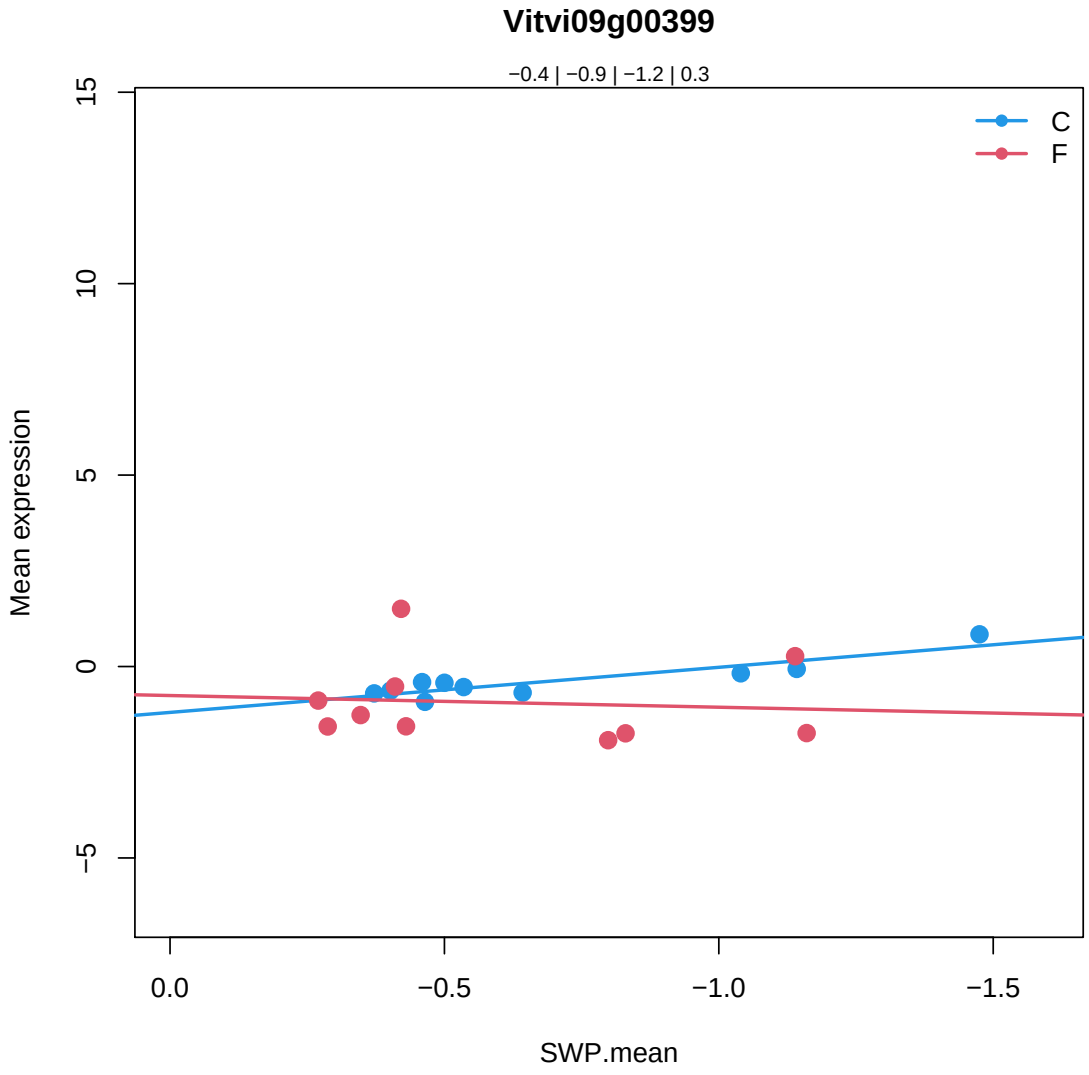
7.6.926 Vitvi09g00399: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00399
        34.6
        transport.sulphate
        sulfate transporter 3%3B4 |
        Chr3:5427081-5430679 FORWARD LENGTH=653 |
        201606
```

Coefficients for Vitvi09g00399.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.3706355	0.1378581		0.1420232	
SlopeC	-1.177968	0.09252688	.	0.6008919	
MeanF-MeanC	-0.5732956	0.1063215		0.3789878	
SlopeF-SlopeC	1.483178	0.1509		0.9999488	



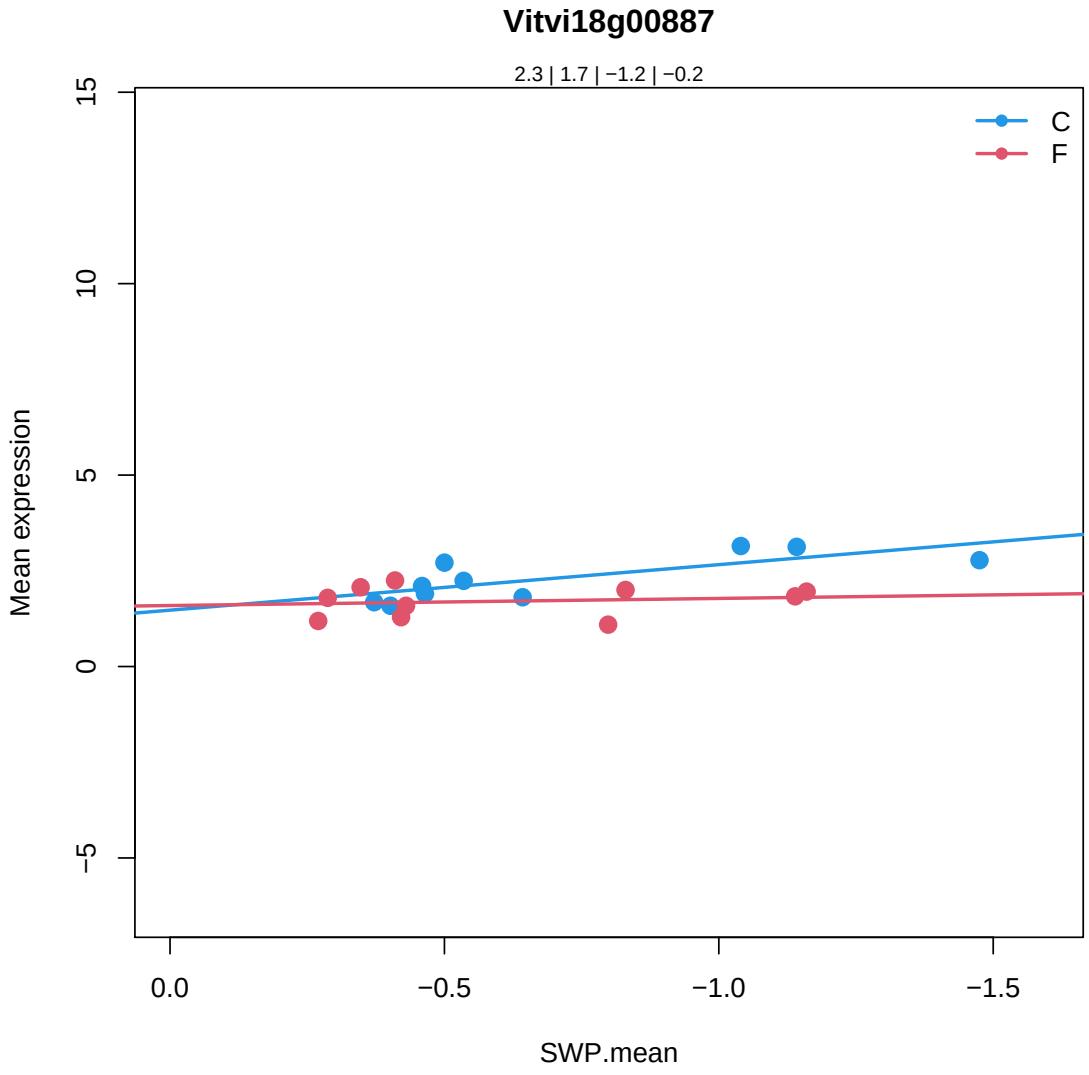
7.6.927 Vitvi18g00887: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00887
        35.2
        not assigned.unknown
        tRNA-processing ribonuclease BN |
        Chr1:17911469-17913149 FORWARD LENGTH=340 |
        201606
```

Coefficients for Vitvi18g00887.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.307888	7.272183e-14	***	1.128973e-13	***
SlopeC	-1.188875	0.005021548	**	0.2519891	
MeanF-MeanC	-0.6022097	0.005151034	**	0.0467823	*
SlopeF-SlopeC	1.00304	0.09061847	.	0.9999488	



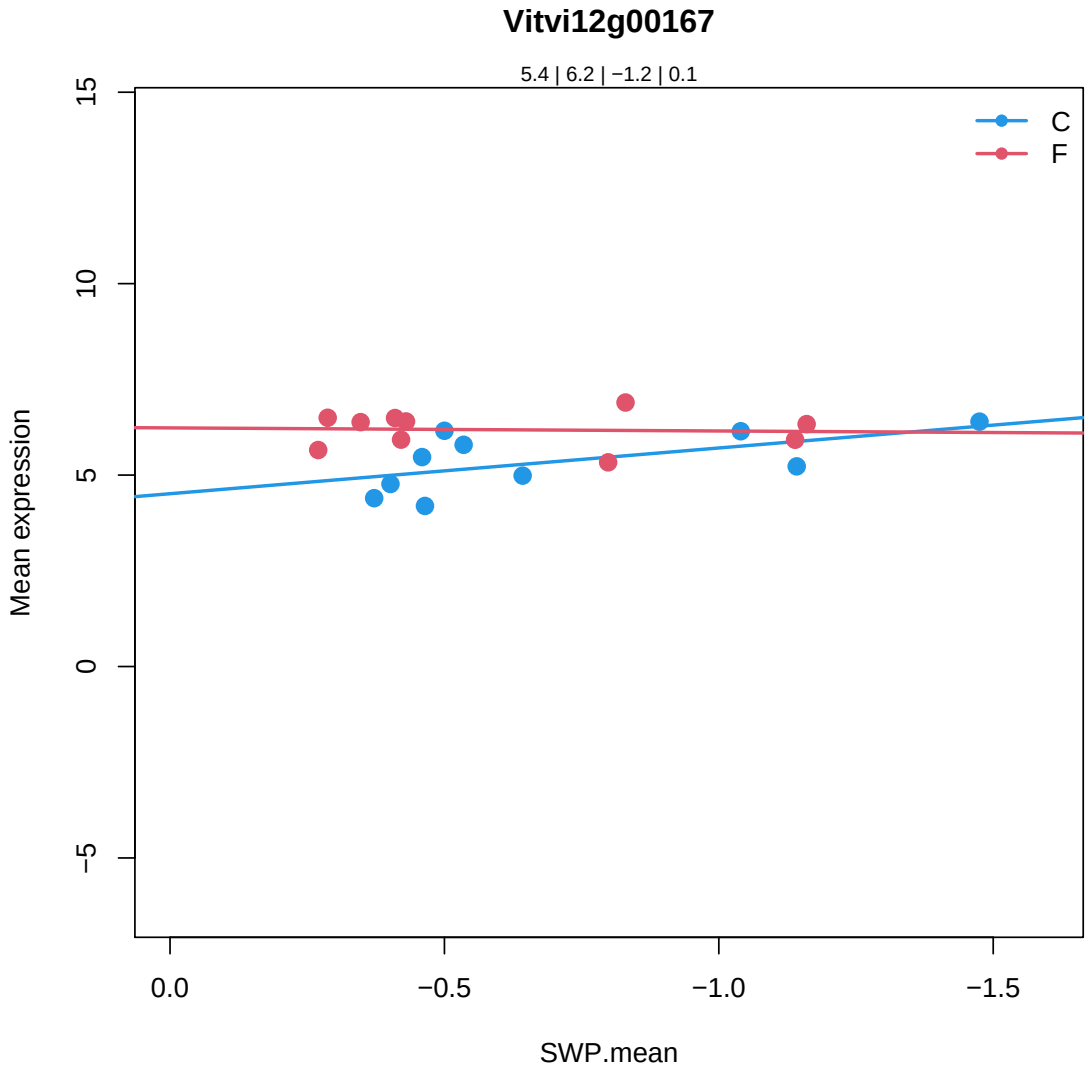
7.6.928 Vitvi12g00167: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00167
        11.9.2.1
        lipid metabolism.lipid degradation.lipases.triacylglycerol lipase
        alpha/beta-Hydrolases superfamily protein |
        Chr2:17776356-17777682 REVERSE LENGTH=412 |
        201606
```

Coefficients for Vitvi12g00167.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.353018	4.5318e-19	***	1.73994e-18	***
SlopeC	-1.194606	0.0242132	*	0.4033416	
MeanF-MeanC	0.8301038	0.003227025	**	0.03248766	*
SlopeF-SlopeC	1.275187	0.09634423	.	0.9999488	



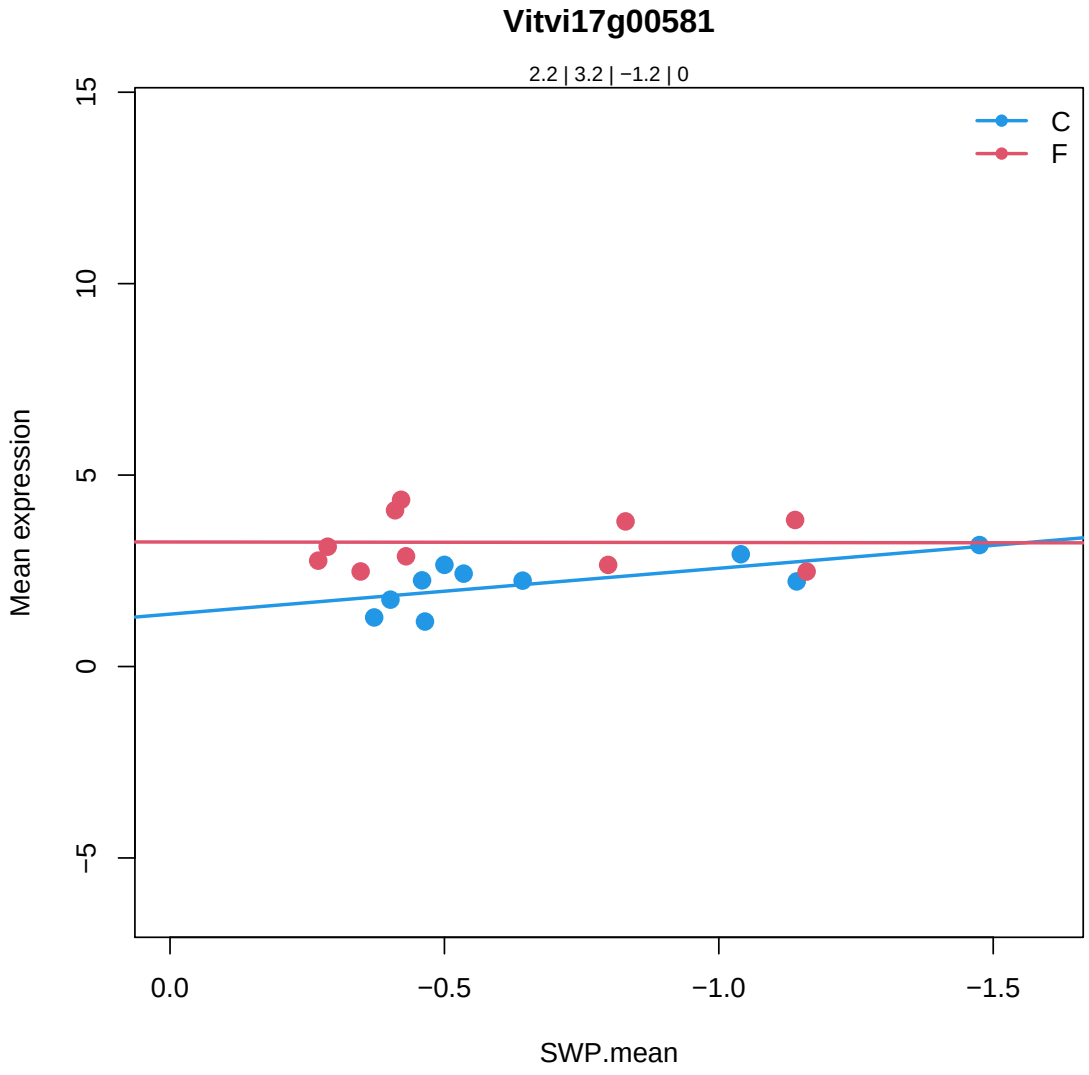
7.6.929 Vitvi17g00581: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00581
        27.3.29
        RNA.regulation of transcription.TCP transcription factor family
        TEOSINTE BRANCHED%2C cycloidea and PCF (TCP) 14 |
        Chr3:17559004-17560473 FORWARD LENGTH=489 |
        201606
```

Coefficients for Vitvi17g00581.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.210217	1.014874e-10	***	1.327331e-10	***
SlopeC	-1.197976	0.03406733	*	0.4433084	
MeanF-MeanC	1.034009	0.0009148225	***	0.01161977	*
SlopeF-SlopeC	1.211173	0.1387365		0.9999488	



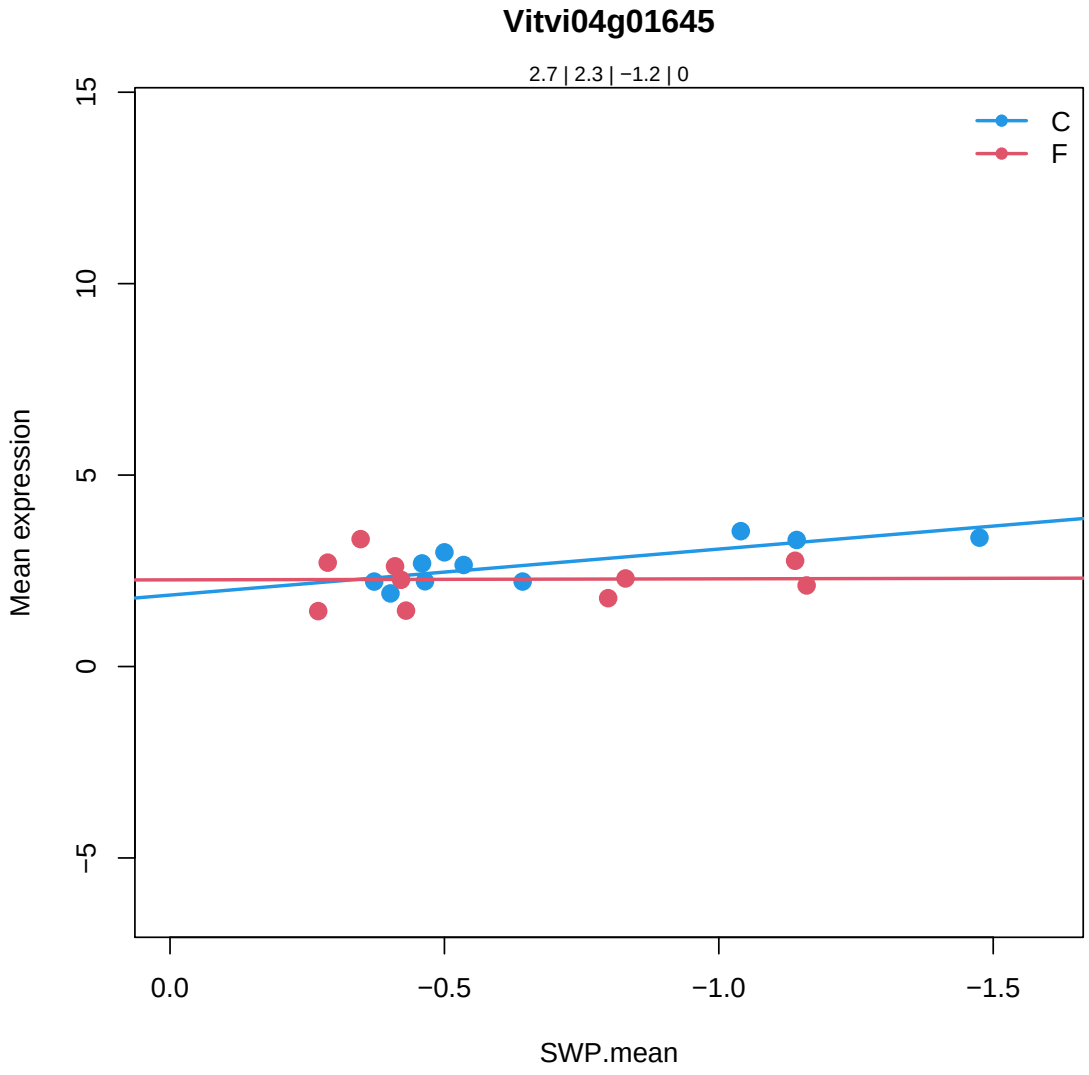
7.6.930 Vitvi04g01645: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g01645
        23.4.3
        nucleotide metabolism.phosphotransfer and pyrophosphatases.uridylate k
        Amino acid kinase family protein |
        Chr3:6427533-6429520 FORWARD LENGTH=339 |
        201606
```

Coefficients for Vitvi04g01645.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.710547	8.412228e-14	***	1.298925e-13	***
SlopeC	-1.201948	0.01413411	*	0.3359386	
MeanF-MeanC	-0.4312483	0.07298608	.	0.3035849	
SlopeF-SlopeC	1.175331	0.09353518	.	0.9999488	



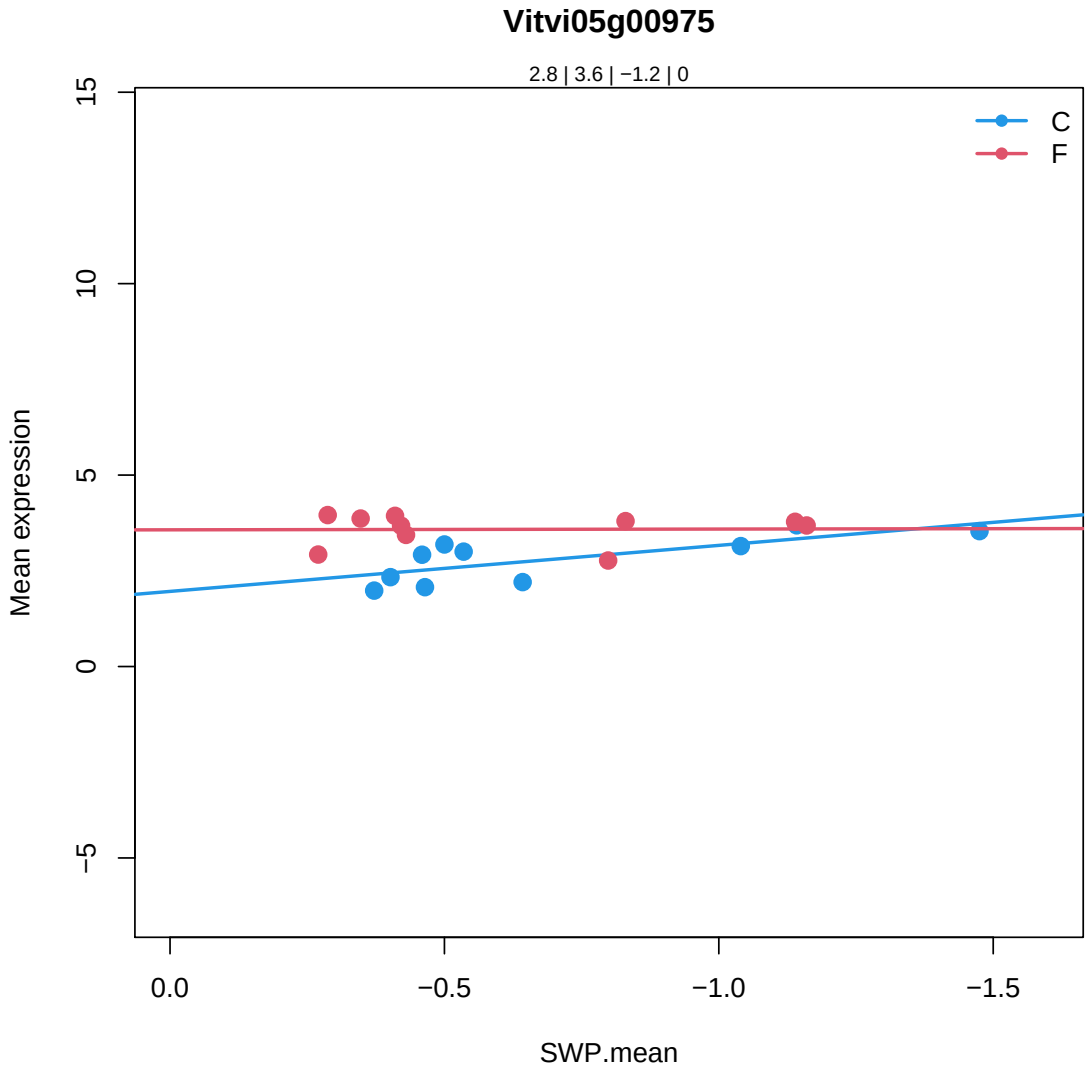
7.6.931 Vitvi05g00975: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00975
        35.1
        not assigned.no ontology
        dehydratase family |
        Chr3:8648780-8652323 FORWARD LENGTH=608 |
        201606
```

Coefficients for Vitvi05g00975.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.807025	3.816632e-15	***	6.702742e-15	***
SlopeC	-1.201992	0.006612213	**	0.2704293	
MeanF-MeanC	0.7753896	0.0009785367	***	0.01228935	*
SlopeF-SlopeC	1.182359	0.05981501	.	0.9999488	



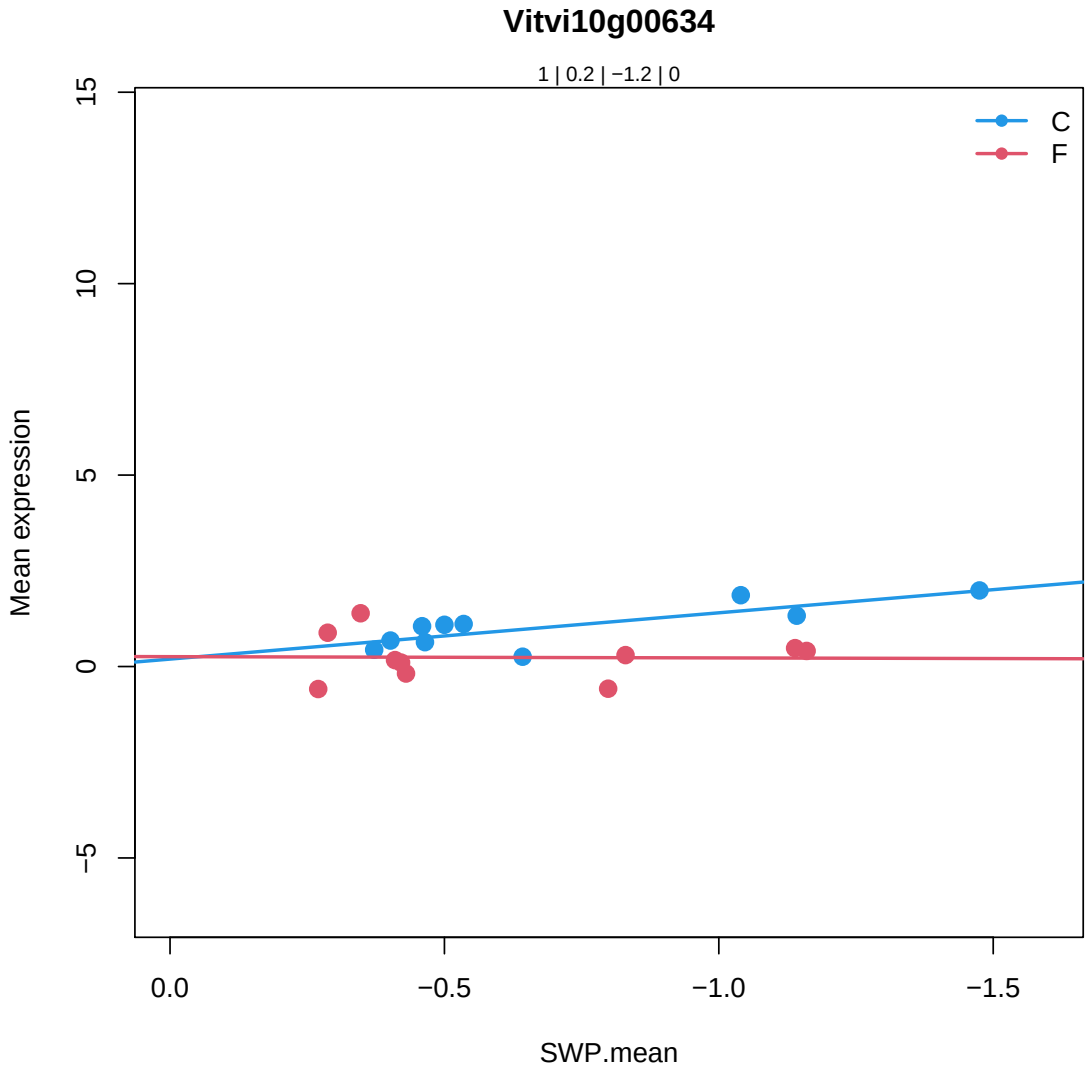
7.6.932 Vitvi10g00634: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00634
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        Pentatricopeptide repeat (PPR-like) superfamily protein |
        Chr4:10338719-10340356 REVERSE LENGTH=545 |
        201606
```

Coefficients for Vitvi10g00634.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.043788	2.288003e-06	***	2.619328e-06	***
SlopeC	-1.208691	0.01464324	*	0.3359386	
MeanF-MeanC	-0.8061123	0.002164152	**	0.02342756	*
SlopeF-SlopeC	1.241513	0.08080222	.	0.9999488	



7.6.933 Vitvi06g01693: type5

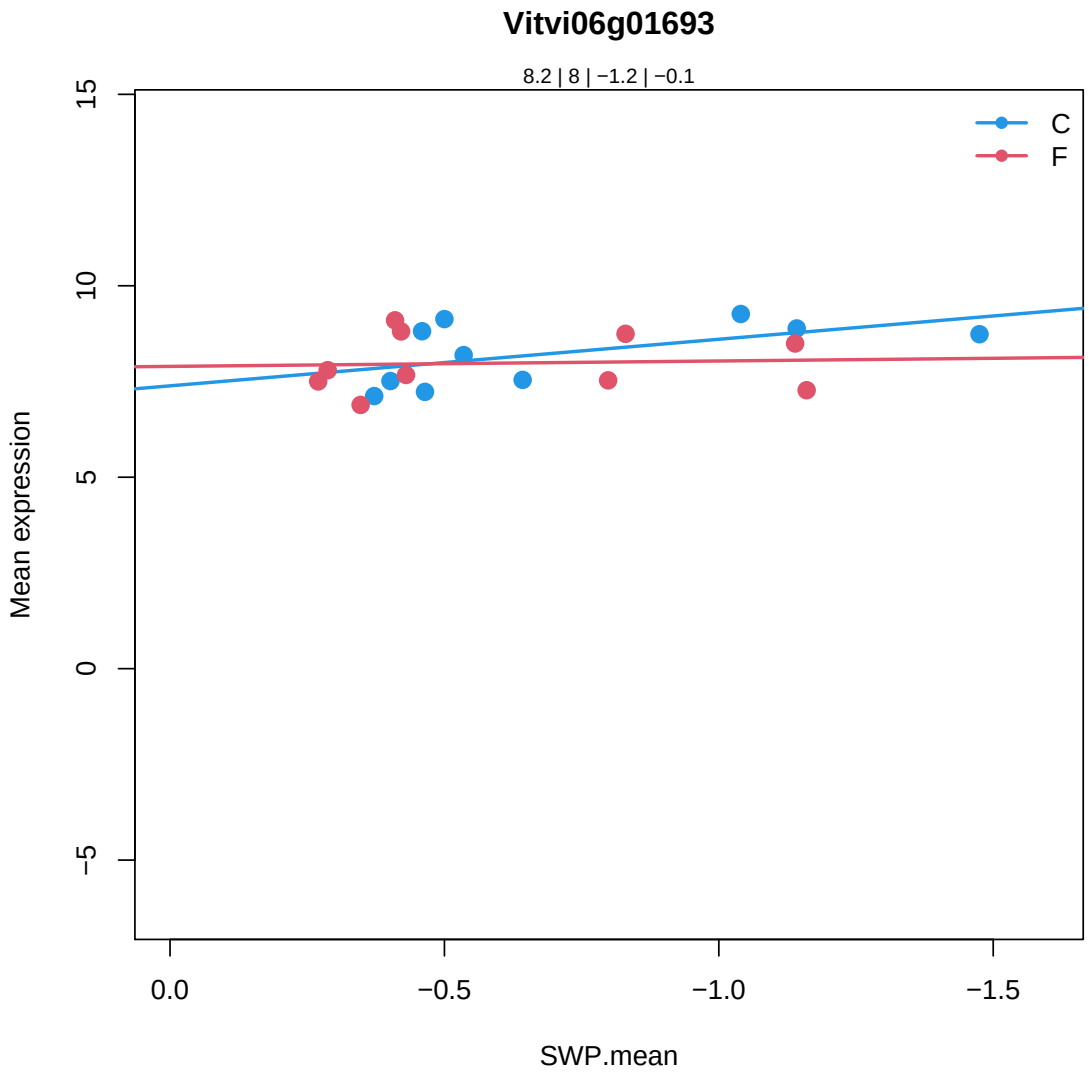
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01693
        29.6
        protein.folding
        heat shock cognate protein 70-1 |
        Chr5:554055-556334 REVERSE LENGTH=651 |
        201606

Vitvi06g01693
        20.2.1
        stress.abiotic.heat
        heat shock cognate protein 70-1 |
        Chr5:554055-556334 REVERSE LENGTH=651 |
        201606
```

Coefficients for Vitvi06g01693.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	8.241509	5.812023e-21	***	4.594754e-20	***
SlopeC	-1.21654	0.06156603	.	0.5439939	
MeanF-MeanC	-0.2614585	0.4134491		0.7529615	
SlopeF-SlopeC	1.075376	0.2542176		0.9999488	


Vitvi06g01693
8.2 | 8 | −1.2 | −0.1
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

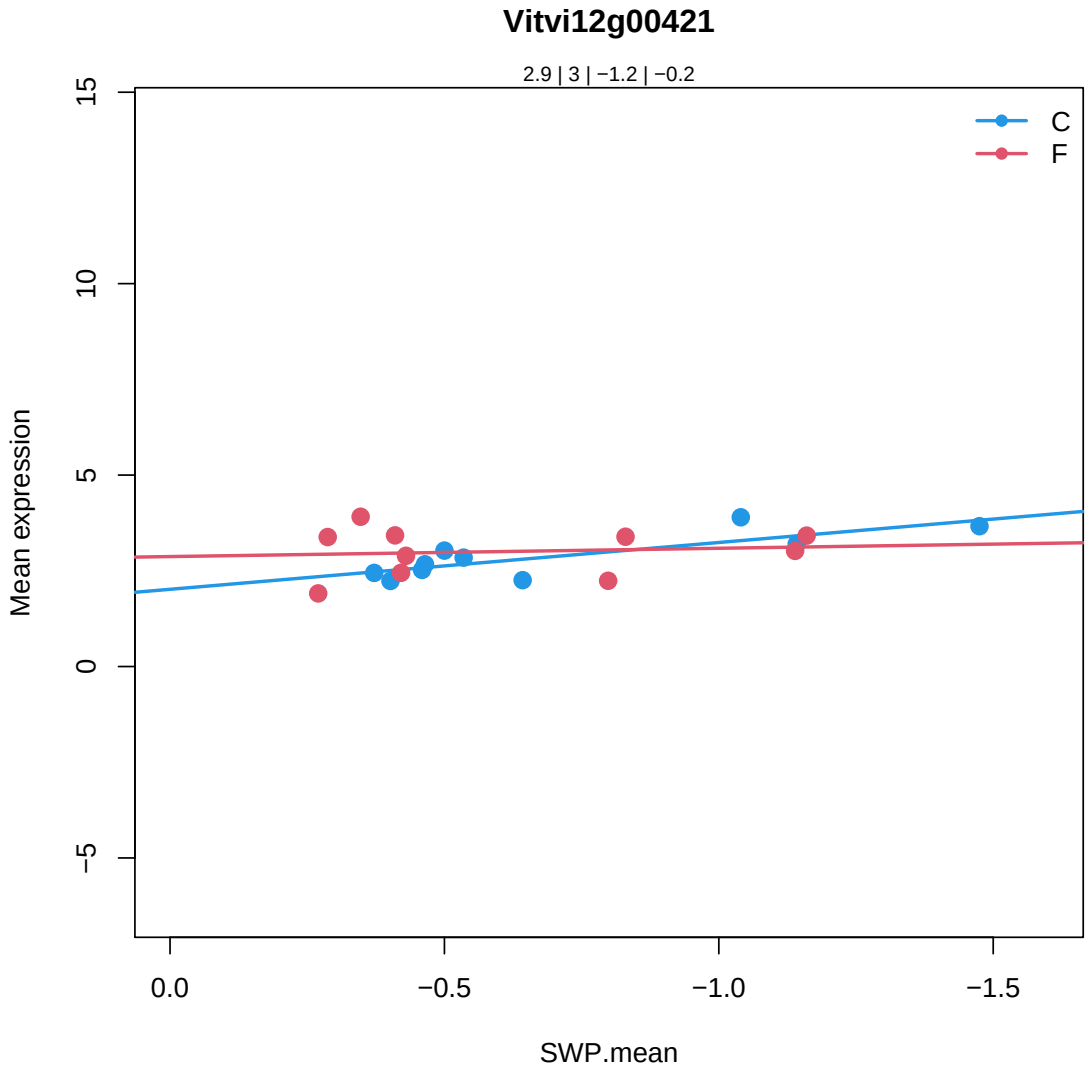
7.6.934 Vitvi12g00421: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00421
        35.2
        not assigned.unknown
        RmlC-like cupins superfamily protein |
        Chr2:13851547-13851966 FORWARD LENGTH=139 |
        201606
```

Coefficients for Vitvi12g00421.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.876046	3.8792e-14	***	6.159039e-14	***
SlopeC	-1.22249	0.01444618	*	0.3359386	
MeanF-MeanC	0.1273132	0.5911976		0.8571324	
SlopeF-SlopeC	1.005623	0.1558306		0.9999488	



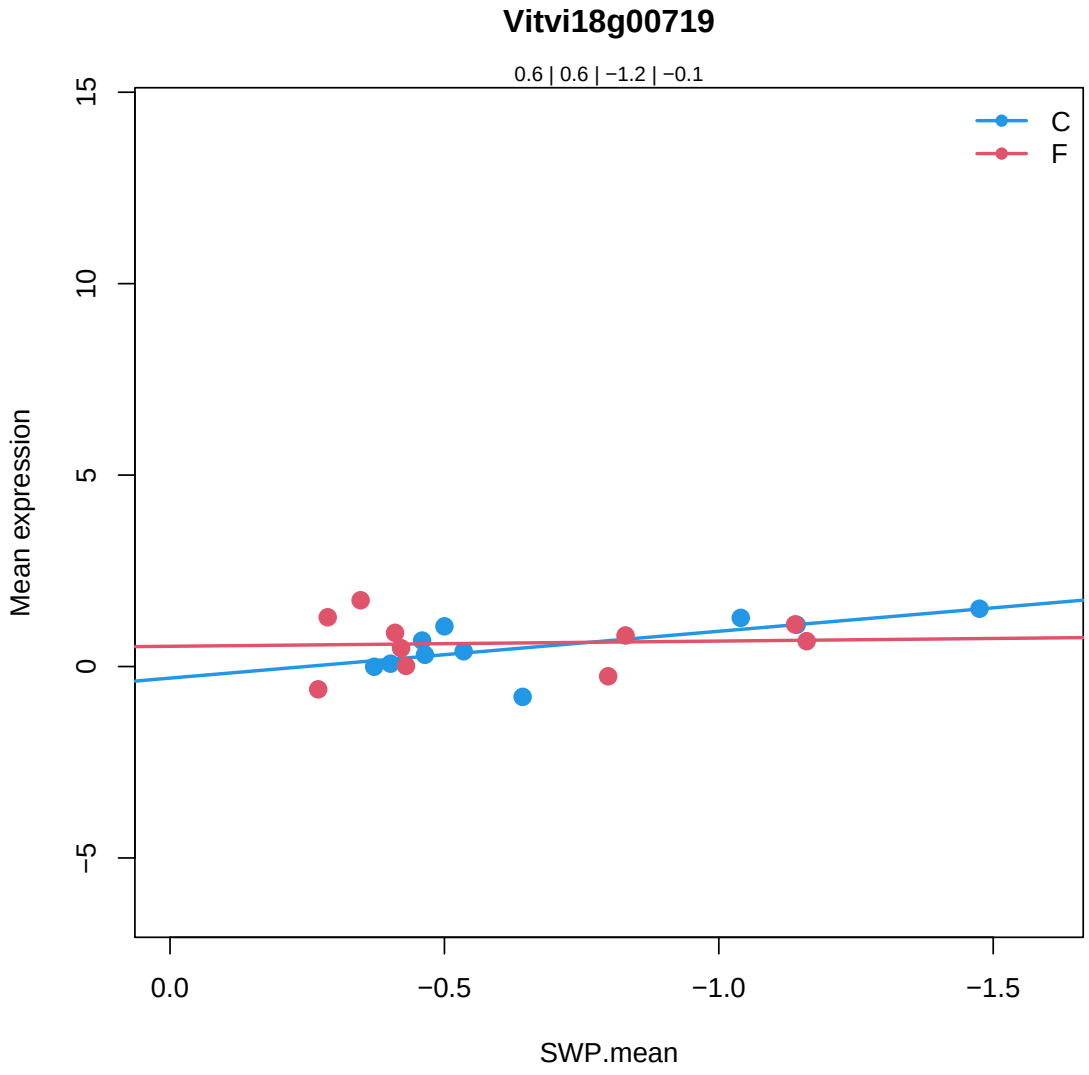
7.6.935 Vitvi18g00719: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00719
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr2:11783927-11786533 REVERSE LENGTH=868 |
        201606
```

Coefficients for Vitvi18g00719.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.5574438	0.01025824	*	0.01086335	*
SlopeC	−1.223513	0.0372992	*	0.4620709	
MeanF−MeanC	0.0537164	0.8497311		0.9599037	
SlopeF−SlopeC	1.087694	0.1987432		0.9999488	



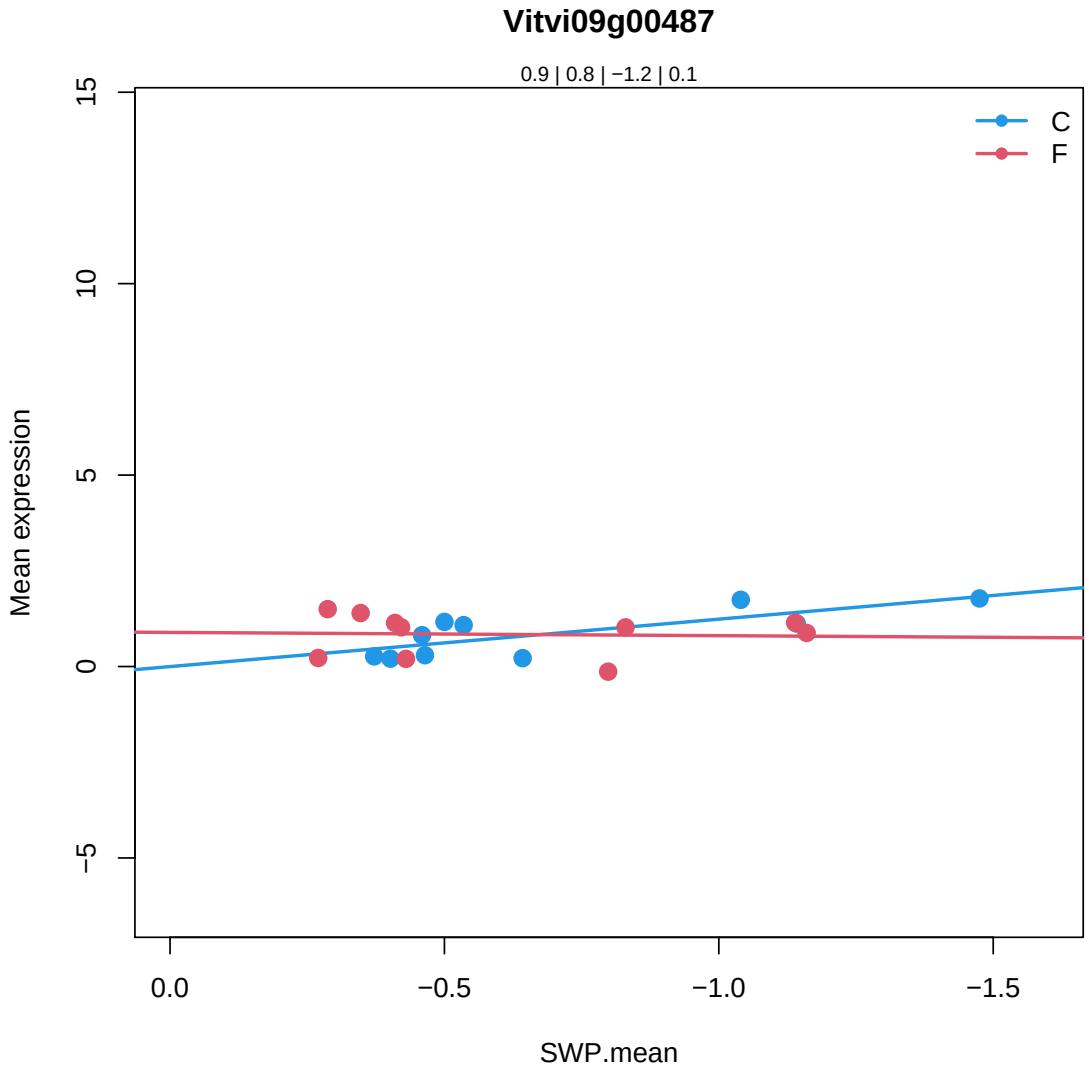
7.6.936 Vitvi09g00487: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi09g00487
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr1:5329111-5331711 FORWARD LENGTH=866 |
        201606
```

Coefficients for Vitvi09g00487.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8689511	1.826661e-05	***	2.050369e-05	***
SlopeC	-1.238775	0.01044287	*	0.3096058	
MeanF-MeanC	-0.02978717	0.8956239		0.9727746	
SlopeF-SlopeC	1.323722	0.05662693	.	0.9999488	



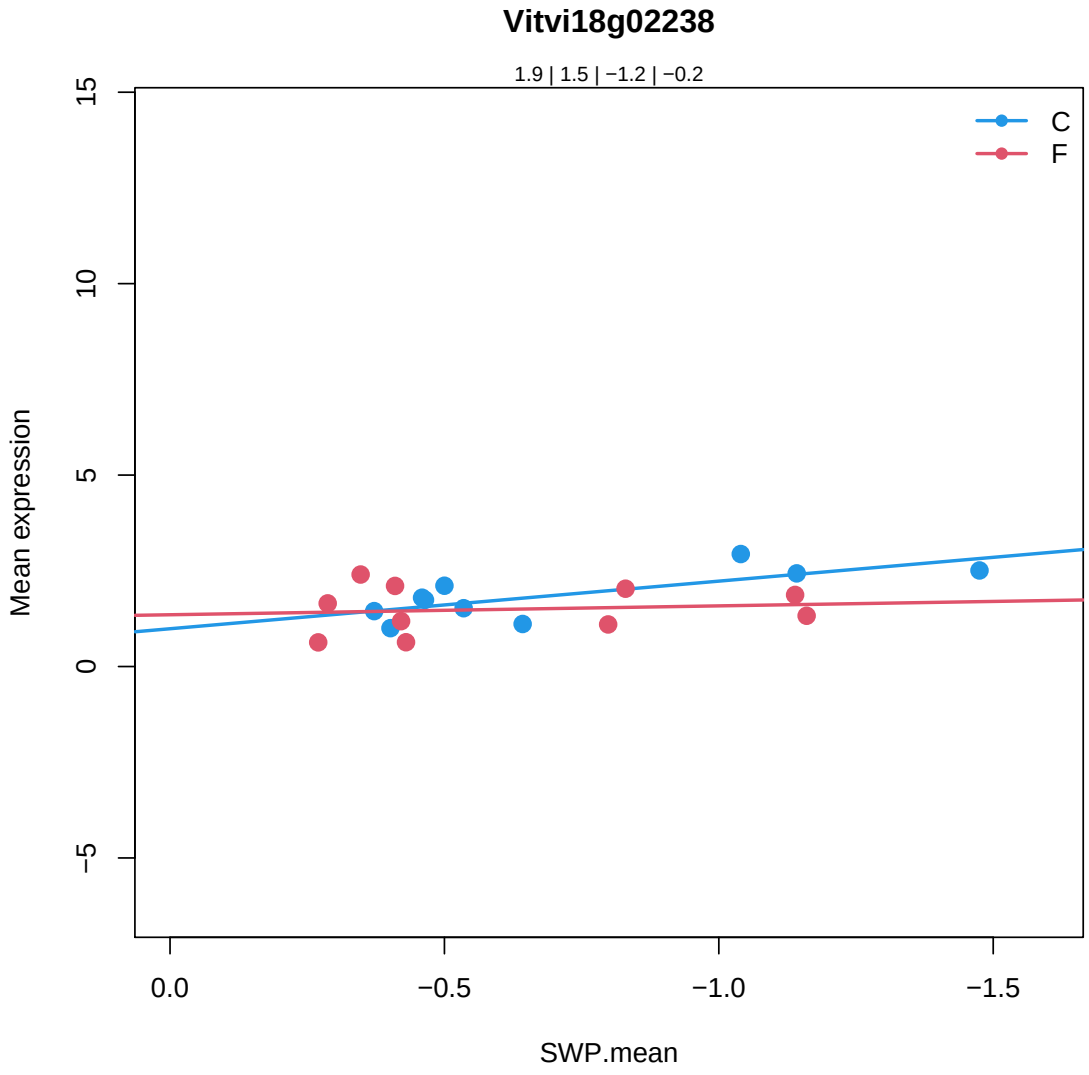
7.6.937 Vitvi18g02238: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02238
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        Pentatricopeptide repeat (PPR-like) superfamily protein |
        Chr1:26928247-26930316 REVERSE LENGTH=689 |
        201606
```

Coefficients for Vitvi18g02238.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.860798	3.294286e-10	***	4.22549e-10	***
SlopeC	-1.243054	0.01591251	*	0.3479749	
MeanF-MeanC	-0.3675654	0.1424269		0.453209	
SlopeF-SlopeC	1.011442	0.1668175		0.9999488	



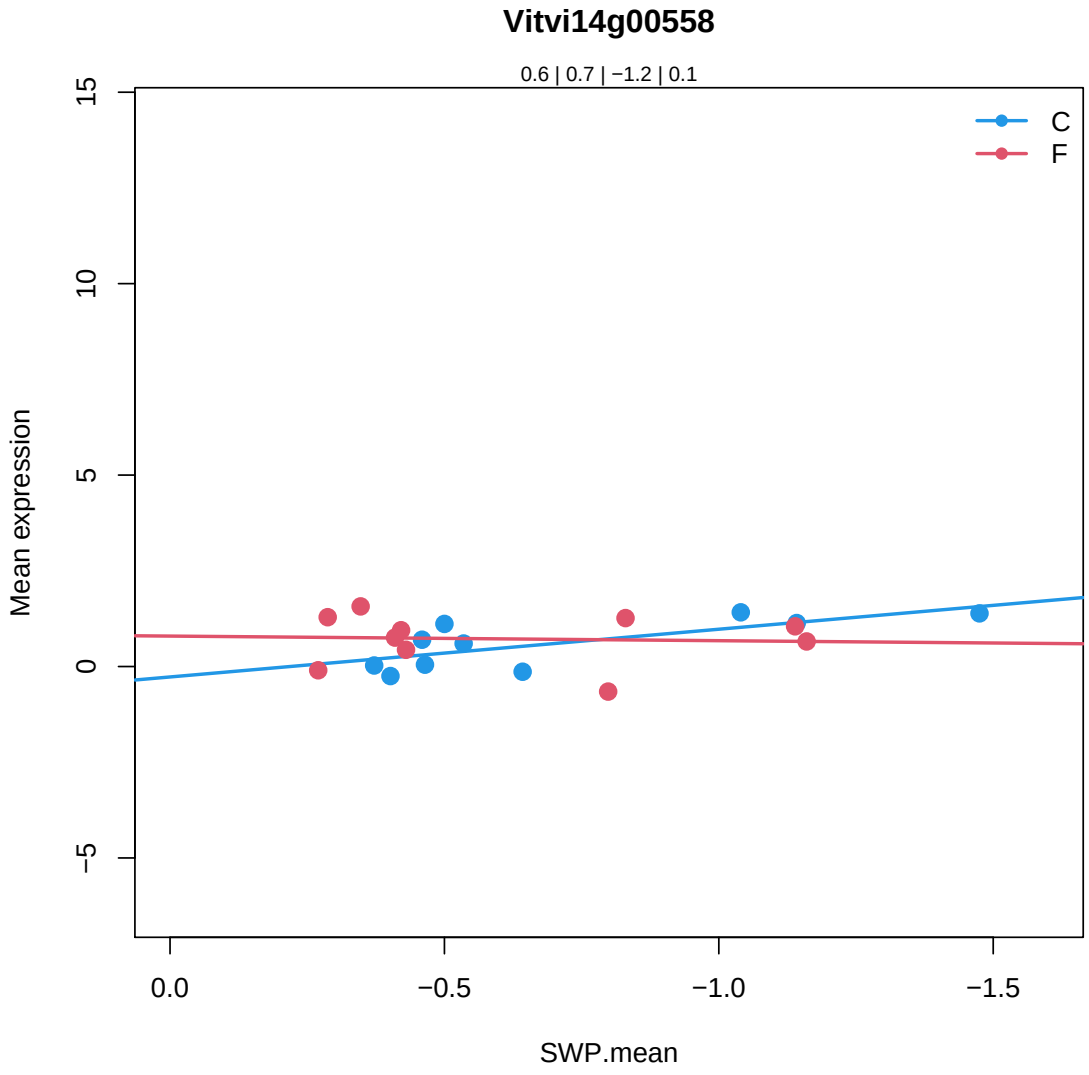
7.6.938 Vitvi14g00558: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g00558
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        Pentatricopeptide repeat (PPR) superfamily protein |
        Chr1:3791454-3793883 REVERSE LENGTH=809 |
        201606
```

Coefficients for Vitvi14g00558.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.603939	0.003324594	**	0.003559279	**
SlopeC	−1.246881	0.02291544	*	0.3972124	
MeanF−MeanC	0.1174143	0.6544137		0.8844988	
SlopeF−SlopeC	1.367196	0.08508289	.	0.9999488	



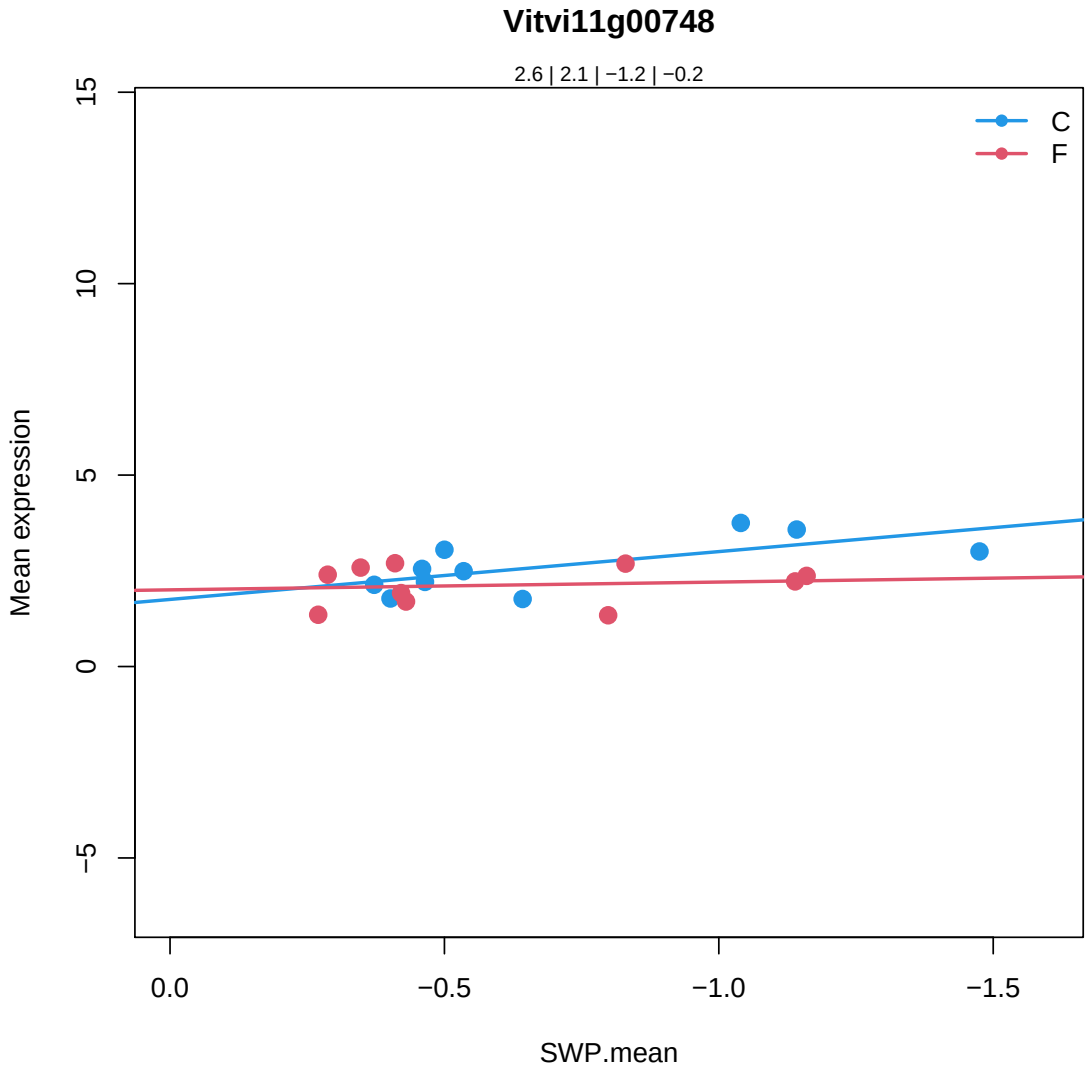
7.6.939 Vitvi11g00748: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00748
        27.2
        RNA.transcription
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi11g00748.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.630458	3.428107e-13	***	5.074904e-13	***
SlopeC	-1.249511	0.01428957	*	0.3359386	
MeanF-MeanC	-0.5042474	0.04612708	*	0.2274849	
SlopeF-SlopeC	1.045936	0.1483019		0.9999488	



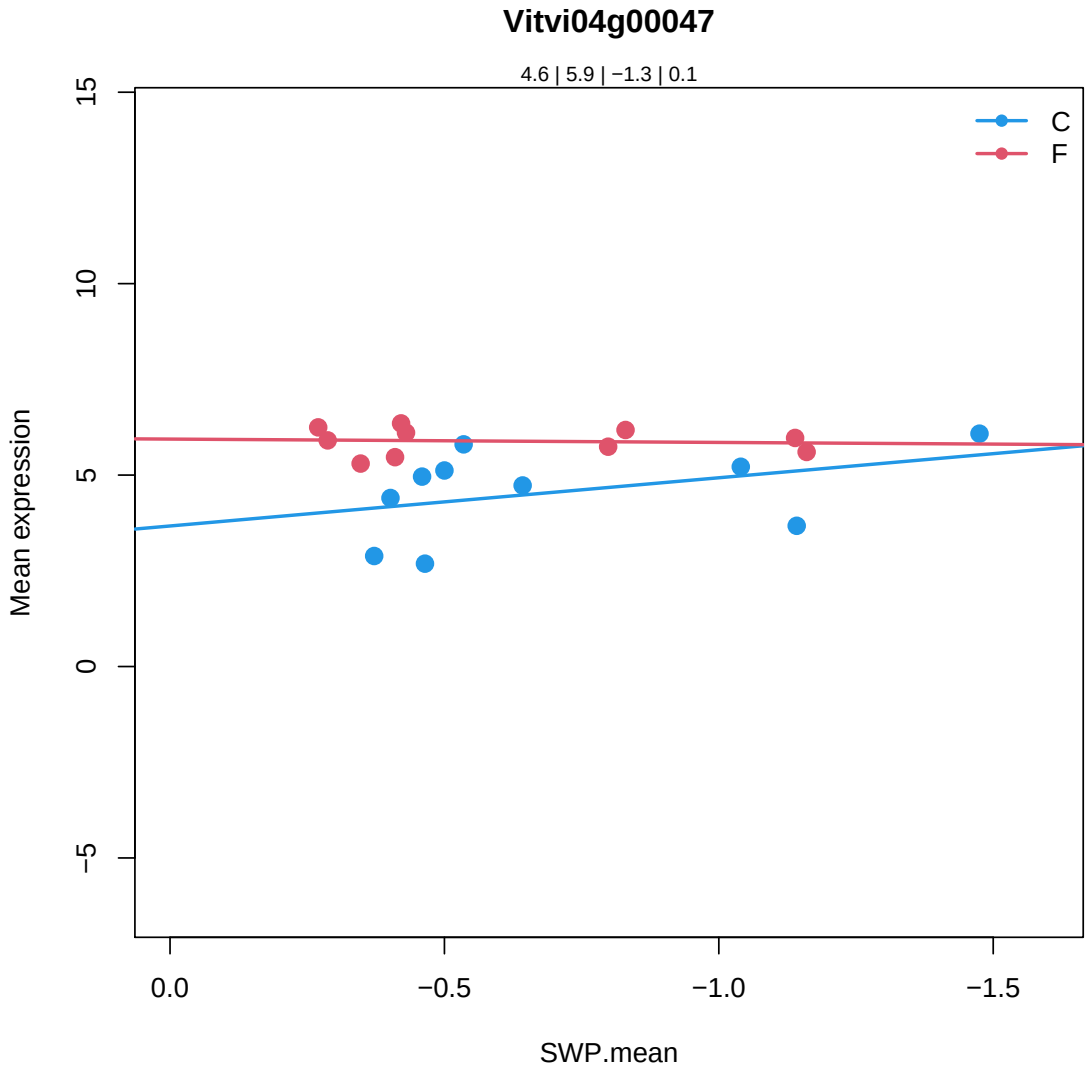
7.6.940 Vitvi04g00047: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00047
        27.3.12
        RNA.regulation of transcription.C3H zinc finger family
        CCCH-type zinc finger family protein |
        Chr2:8550419-8551498 FORWARD LENGTH=359 |
        201606
```

Coefficients for Vitvi04g00047.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.555891	6.401745e-15	***	1.091569e-14	***
SlopeC	-1.258919	0.07212352	.	0.5630621	
MeanF-MeanC	1.331065	0.0007355189	***	0.009664465	**
SlopeF-SlopeC	1.346165	0.1882636		0.9999488	



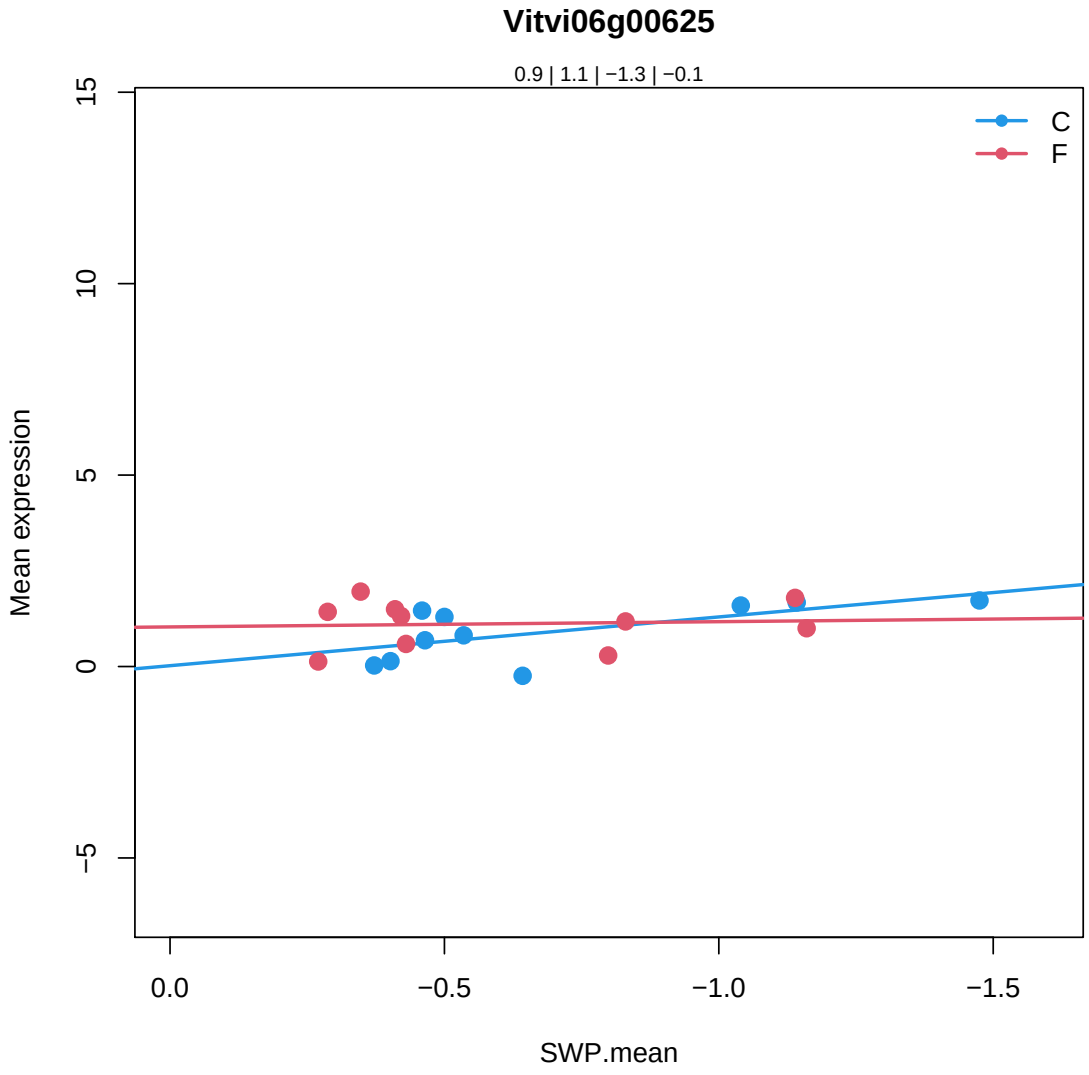
7.6.941 Vitvi06g00625: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00625
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr2:12712884-12715100 FORWARD LENGTH=738 |
        201606
```

Coefficients for Vitvi06g00625.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.9169155	7.188066e-05	***	7.958198e-05	***
SlopeC	-1.273426	0.02314572	*	0.3983963	
MeanF-MeanC	0.2006294	0.4566433		0.7823039	
SlopeF-SlopeC	1.136528	0.1569757		0.9999488	



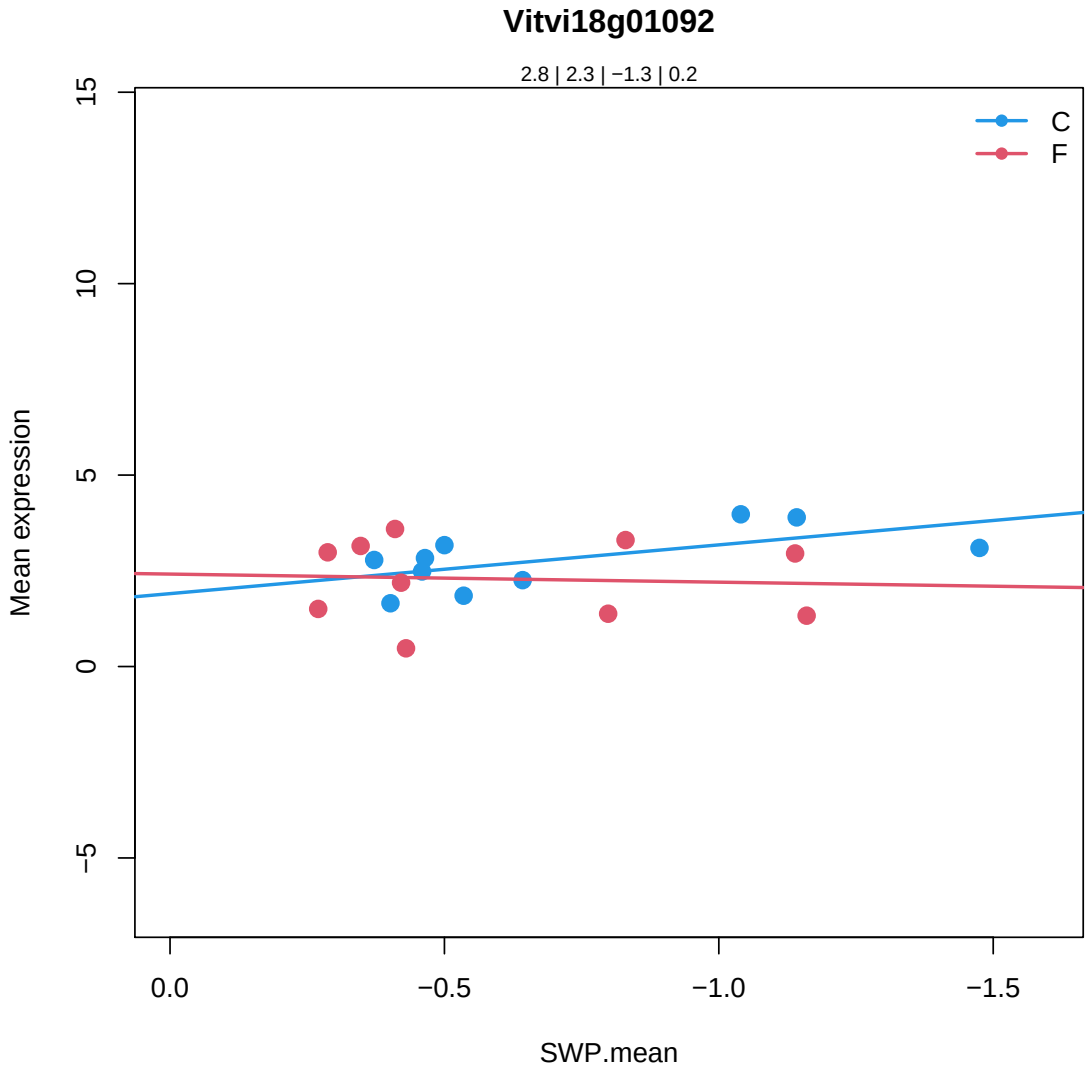
7.6.942 Vitvi18g01092: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g01092
        35.2
        not assigned.unknown
        filament-like protein (DUF869) |
        Chr1:6856212-6859513 REVERSE LENGTH=982 |
        201606
```

Coefficients for Vitvi18g01092.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.799136	4.548924e-10	***	5.80644e-10	***
SlopeC	-1.273685	0.09408957	.	0.6033077	
MeanF-MeanC	-0.5136521	0.1788355		0.5134321	
SlopeF-SlopeC	1.484889	0.184185		0.9999488	



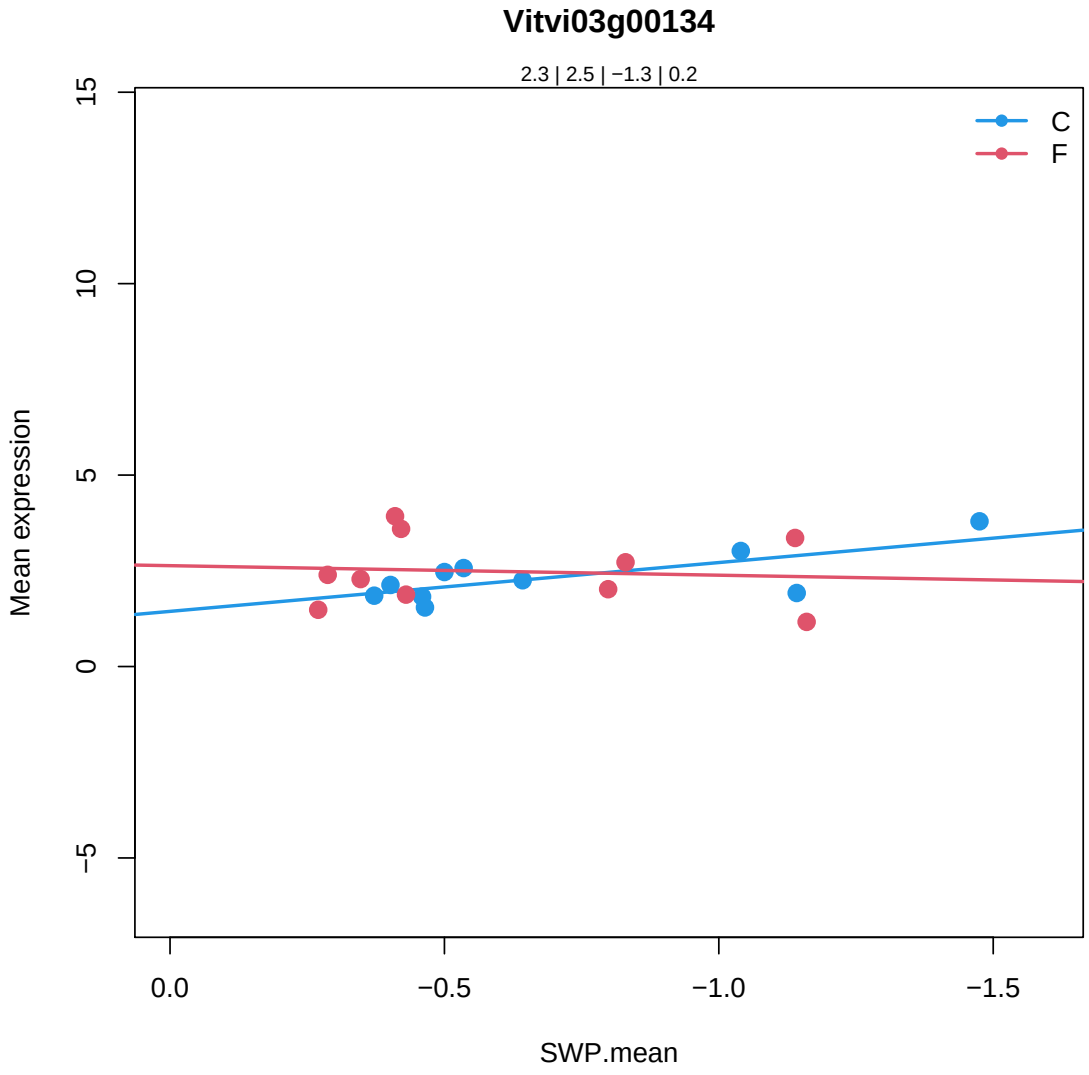
7.6.943 Vitvi03g00134: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00134
        34.3
        transport.amino acids
        amino acid permease 2 |
        Chr5:2866867-2868863 FORWARD LENGTH=493 |
        201606
```

Coefficients for Vitvi03g00134.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.336791	6.723684e-10	***	8.530248e-10	***
SlopeC	-1.274914	0.05218372	.	0.5134996	
MeanF-MeanC	0.1454279	0.6492151		0.8819203	
SlopeF-SlopeC	1.523829	0.1133353		0.9999488	



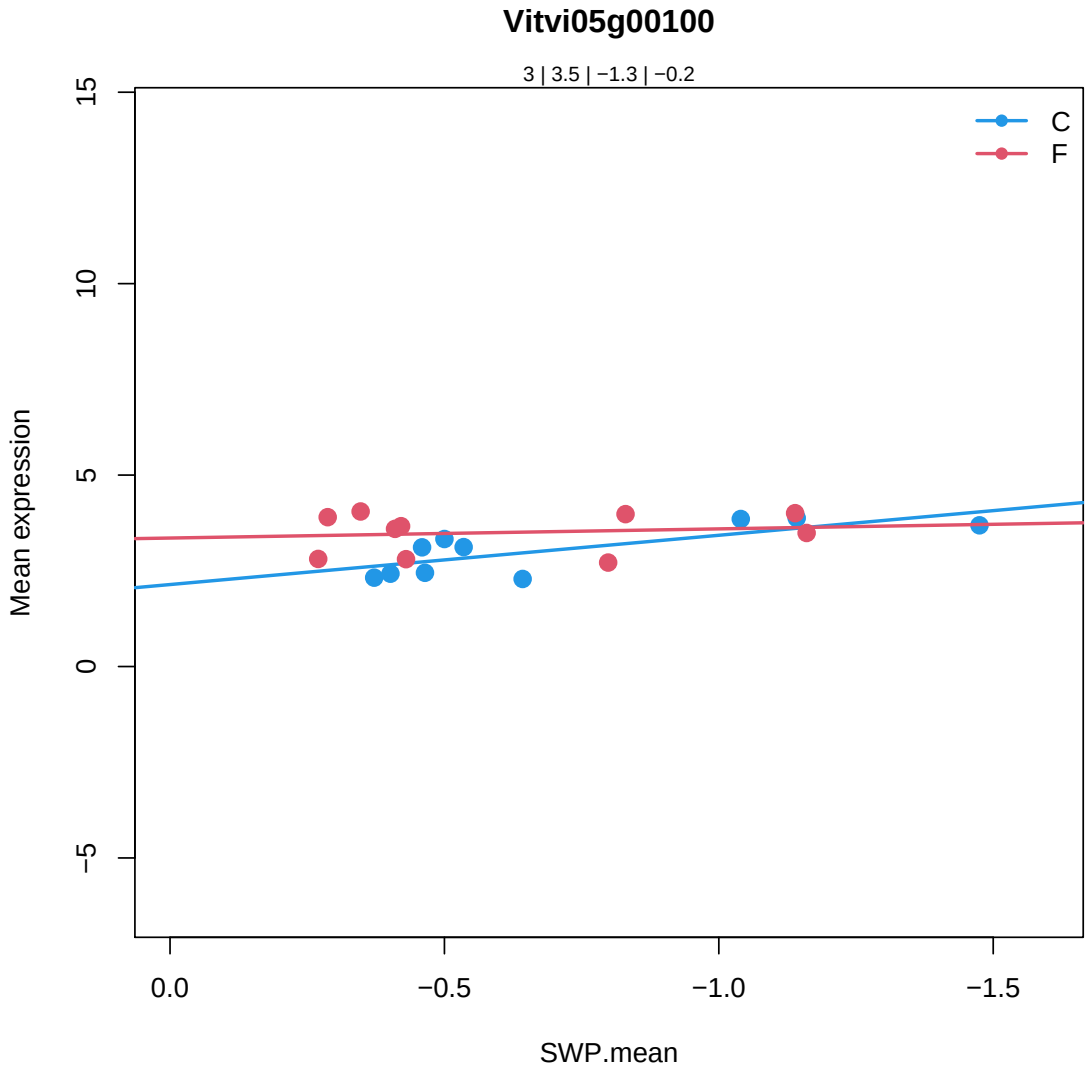
7.6.944 Vitvi05g00100: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00100
        11.1.31
        lipid metabolism.FA synthesis and FA elongation.pyruvate DH
        dihydrolipoamide dehydrogenase |
        Chr4:9153570-9157133 REVERSE LENGTH=567 |
        201606
```

Coefficients for Vitvi05g00100.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.04577	5.089591e-15	***	8.808397e-15	***
SlopeC	-1.286687	0.007982168	**	0.2832315	
MeanF-MeanC	0.4552597	0.05430791	.	0.2525382	
SlopeF-SlopeC	1.047423	0.1243026		0.9999488	



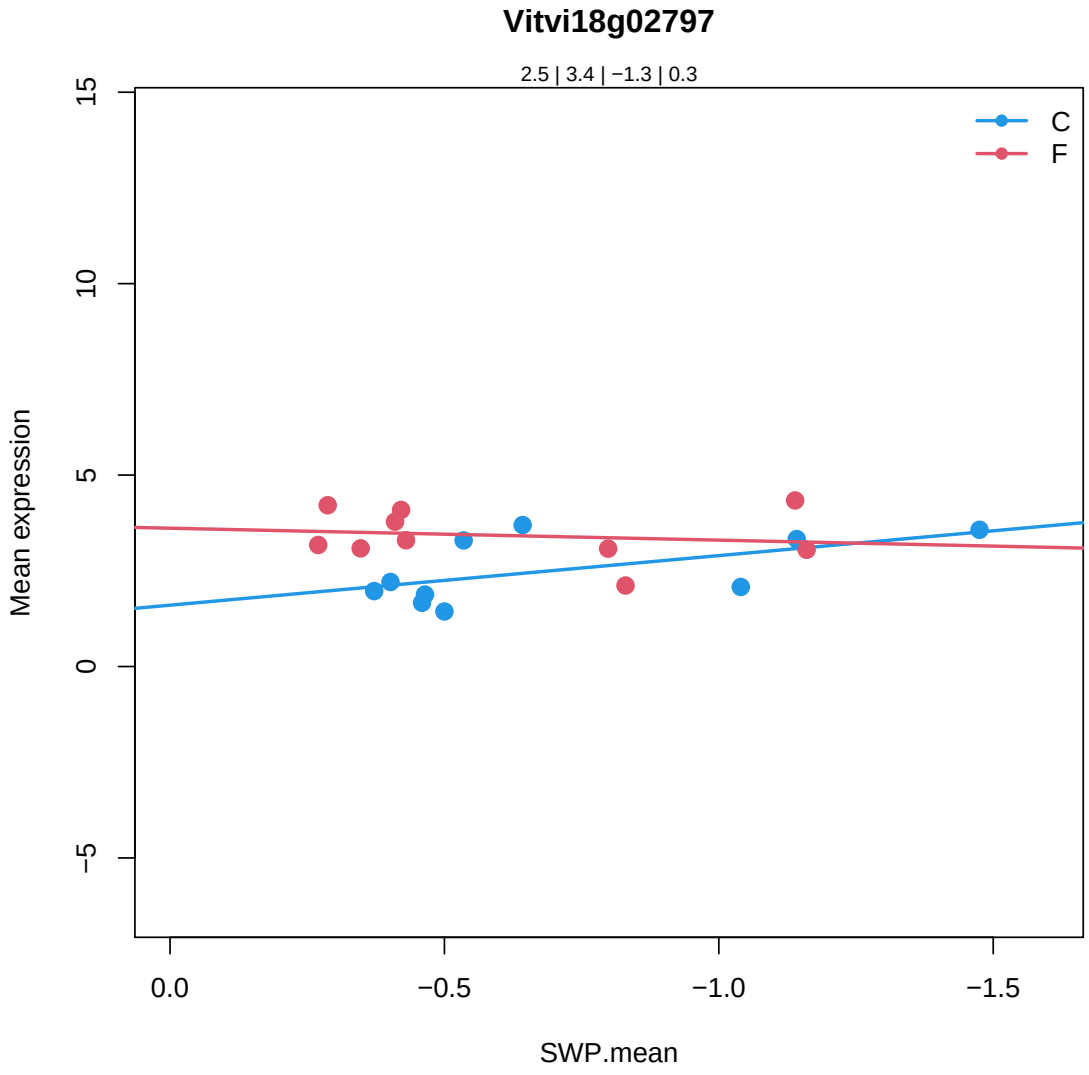
7.6.945 Vitvi18g02797: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g02797
        17.6.3
        hormone metabolism.gibberelin.induced-regulated-responsive-activated
        GAST1 protein homolog 1 |
        Chr1:28441813-28442284 REVERSE LENGTH=98 |
        201606
```

Coefficients for Vitvi18g02797.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.512377	8.809645e-11	***	1.155266e-10	***
SlopeC	-1.294656	0.04149115	*	0.4793992	
MeanF-MeanC	0.9099366	0.006740657	**	0.05686247	.
SlopeF-SlopeC	1.606374	0.08467281	.	0.9999488	



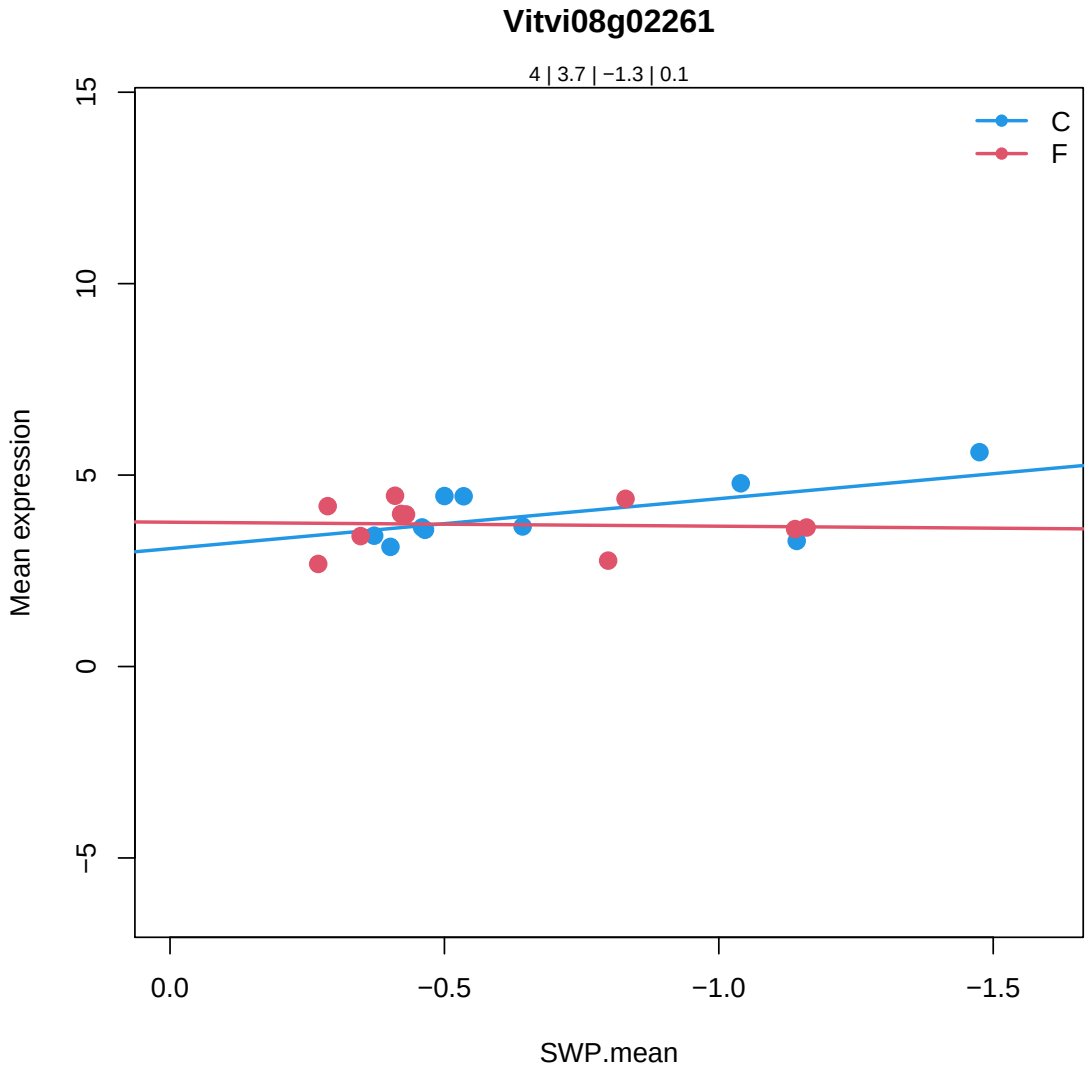
7.6.946 Vitvi08g02261: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g02261
        17.5.1
        hormone metabolism.ethylene.synthesis-degradation
        2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protei
        Chr5:23994434-23995715 REVERSE LENGTH=364 |
        201606
```

Coefficients for Vitvi08g02261.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.996522	1.49655e-15	***	2.743285e-15	***
SlopeC	-1.304465	0.02556117	*	0.4079655	
MeanF-MeanC	-0.2908902	0.3041916		0.6685796	
SlopeF-SlopeC	1.408742	0.09598748	.	0.9999488	



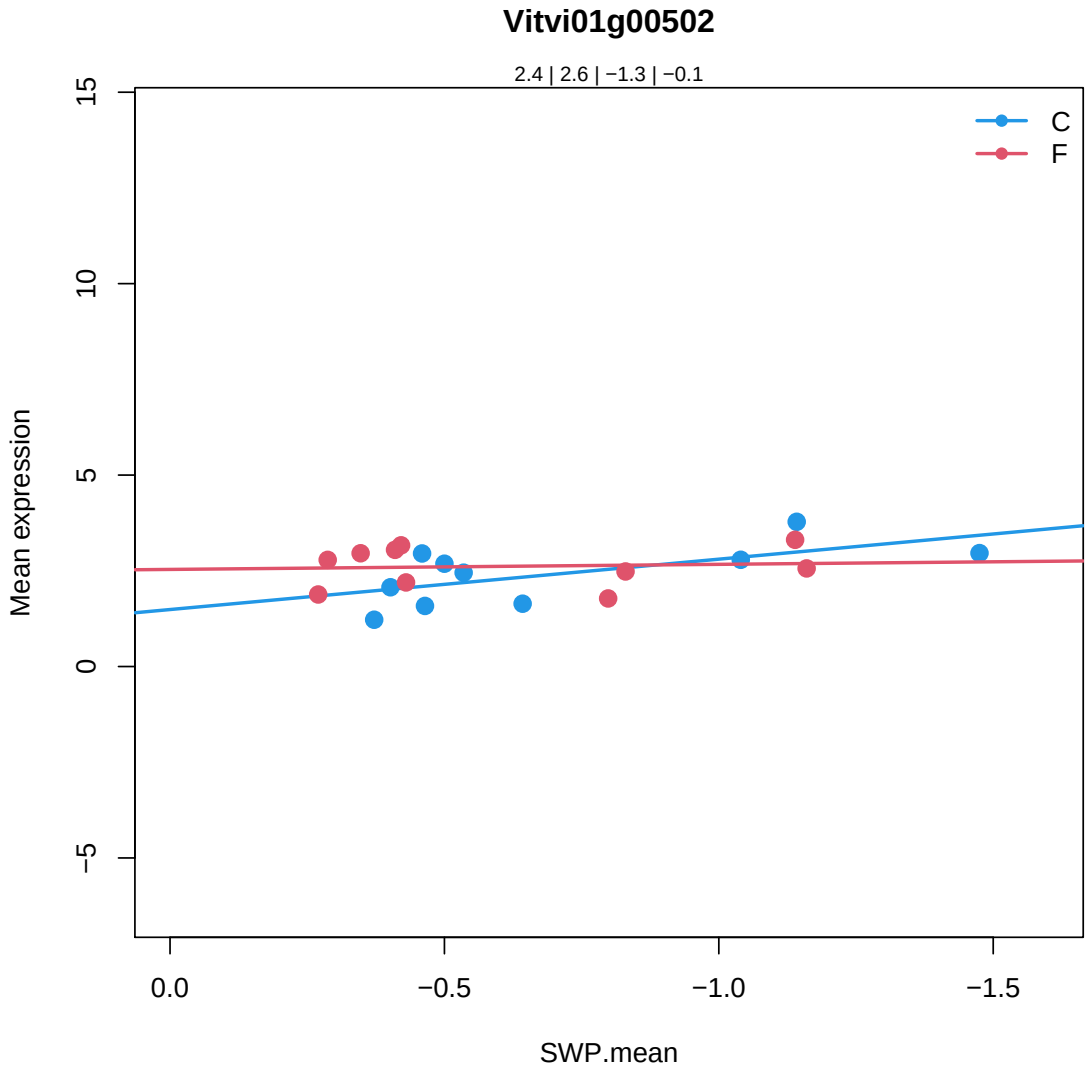
7.6.947 Vitvi01g00502: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g00502
        13.1.3.6.1.2
        amino acid metabolism.synthesis.aspartate family.misc.homoserine.aspar
        semialdehyde dehydrogenase family protein |
        Chr1:5103152-5104633 REVERSE LENGTH=306 |
        201606
```

Coefficients for Vitvi01g00502.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.413206	8.411788e-12	***	1.153405e-11	***
SlopeC	-1.315606	0.01665137	*	0.3523917	
MeanF-MeanC	0.2032294	0.4385991		0.770394	
SlopeF-SlopeC	1.182865	0.1313114		0.9999488	



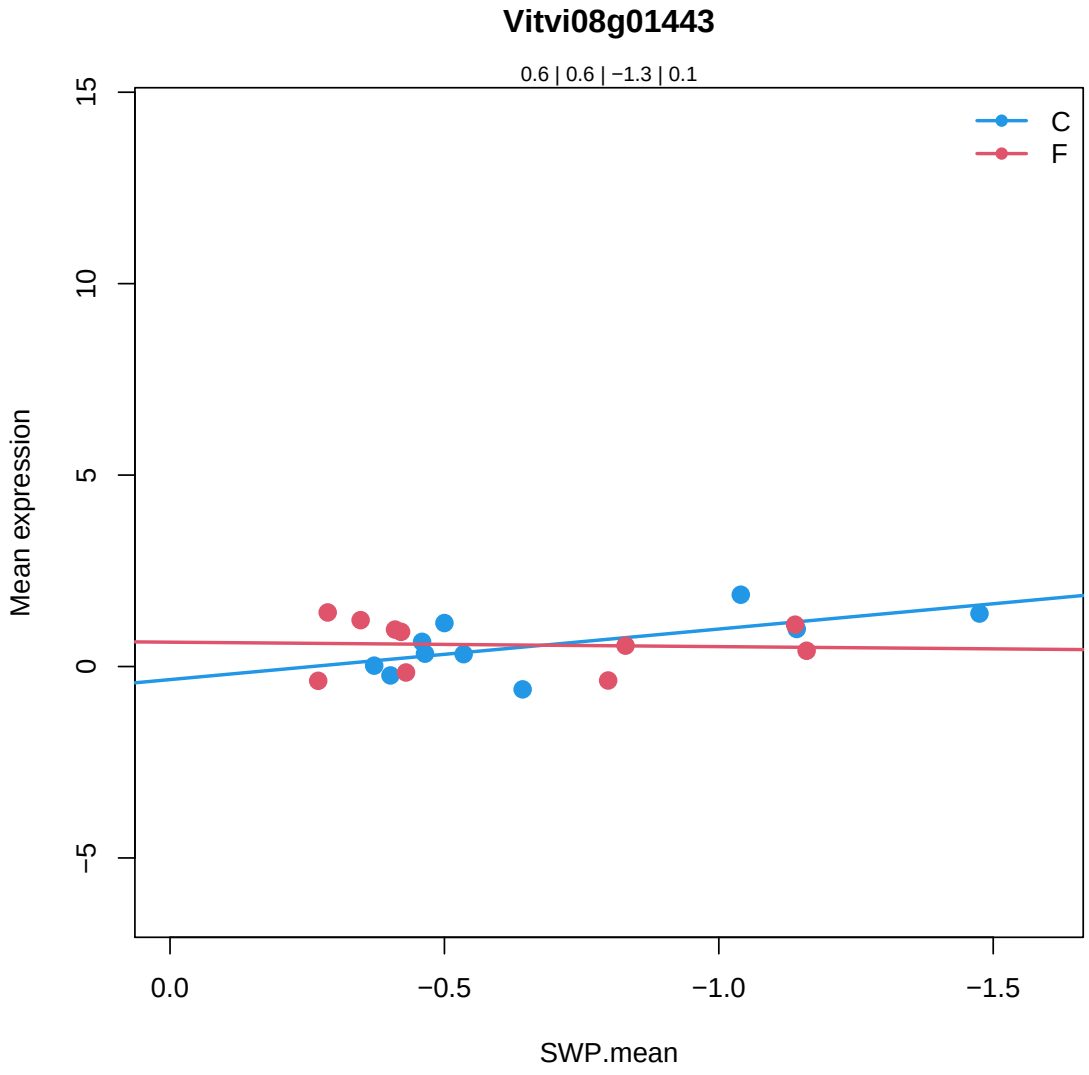
7.6.948 Vitvi08g01443: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01443
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        Pentatricopeptide repeat (PPR) superfamily protein |
        Chr3:3608250-3610121 FORWARD LENGTH=623 |
        201606
```

Coefficients for Vitvi08g01443.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.5867599	0.006986403	**	0.007426891	**
SlopeC	-1.320297	0.02486413	*	0.4073896	
MeanF-MeanC	-0.02205916	0.937531		0.9829394	
SlopeF-SlopeC	1.436502	0.09204181	.	0.9999488	



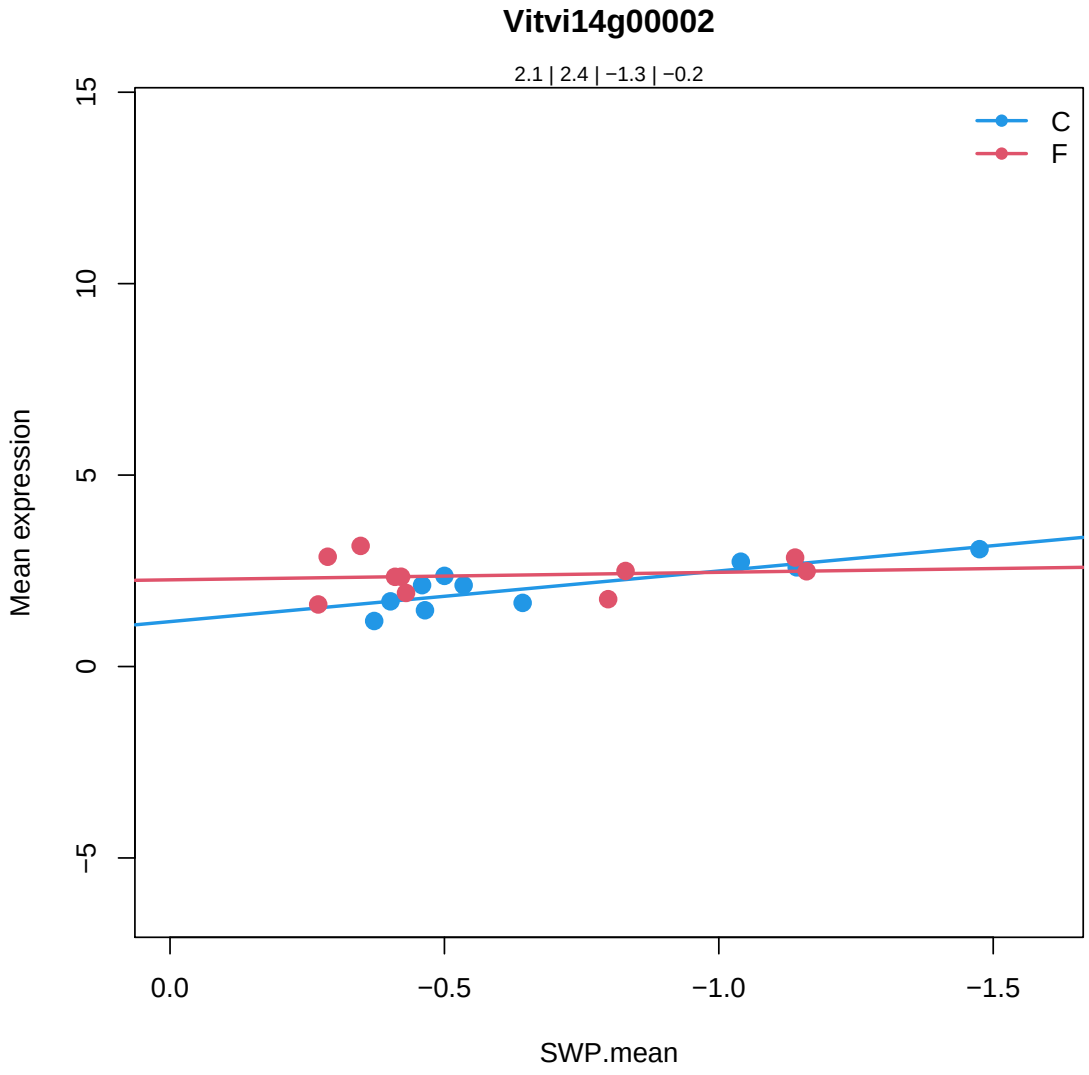
7.6.949 Vitvi14g00002: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g00002
        35.2
        not assigned.unknown
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr5:901452-902719 REVERSE LENGTH=363 |
        201606
```

Coefficients for Vitvi14g00002.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.102921	1.382061e-12	***	1.966338e-12	***
SlopeC	-1.322743	0.003428821	**	0.2223919	
MeanF-MeanC	0.2804428	0.184288		0.5204591	
SlopeF-SlopeC	1.126414	0.07349697	.	0.9999488	



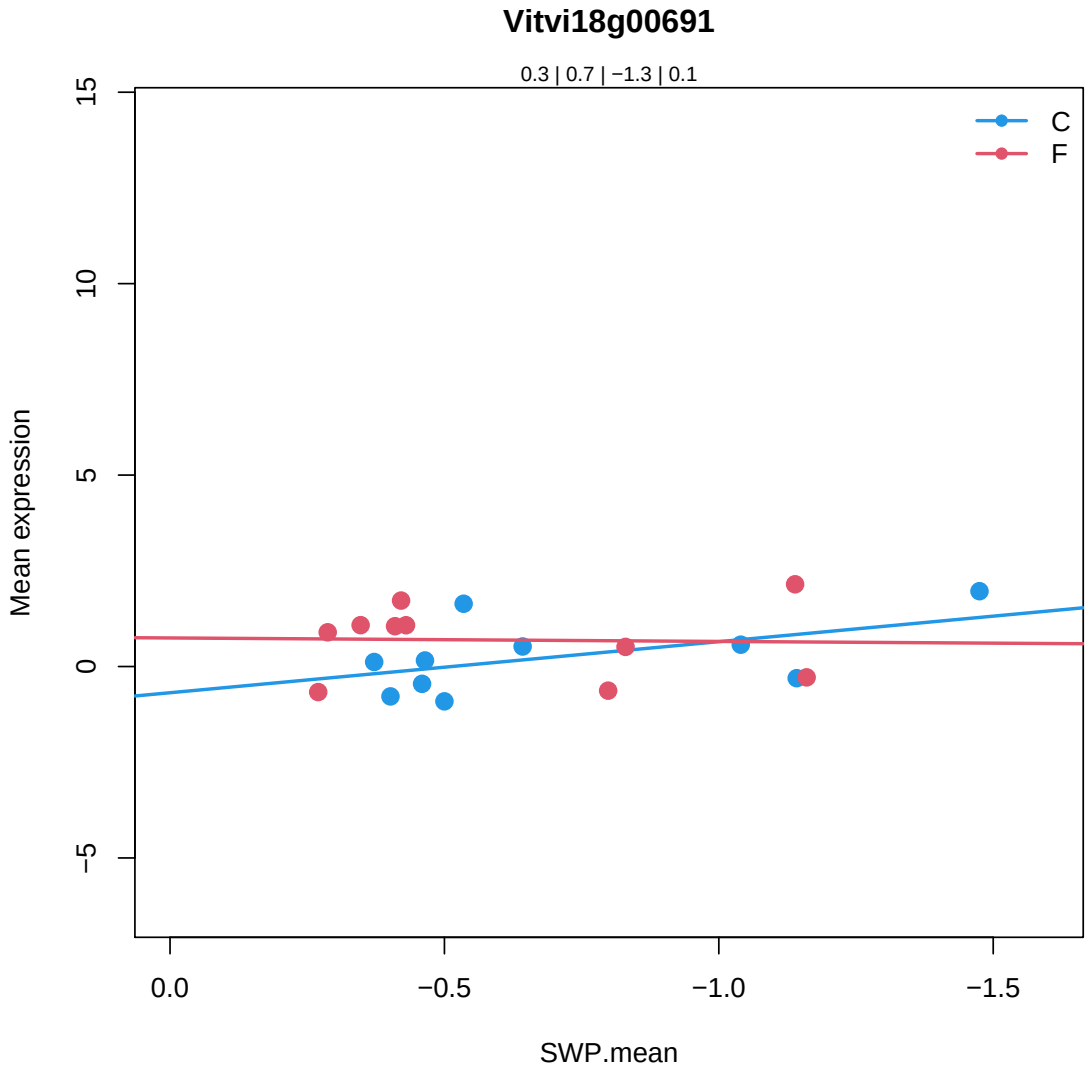
7.6.950 Vitvi18g00691: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00691
        17.6
        hormone metabolism.gibberelin
        Gibberellin-regulated family protein |
        Chr2:6404210-6405043 FORWARD LENGTH=108 |
        201606
```

Coefficients for Vitvi18g00691.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.2527062	0.3580813		0.3641253	
SlopeC	-1.33343	0.08903244	.	0.5952322	
MeanF-MeanC	0.4378028	0.2625801		0.6244727	
SlopeF-SlopeC	1.423996	0.2148744		0.9999488	



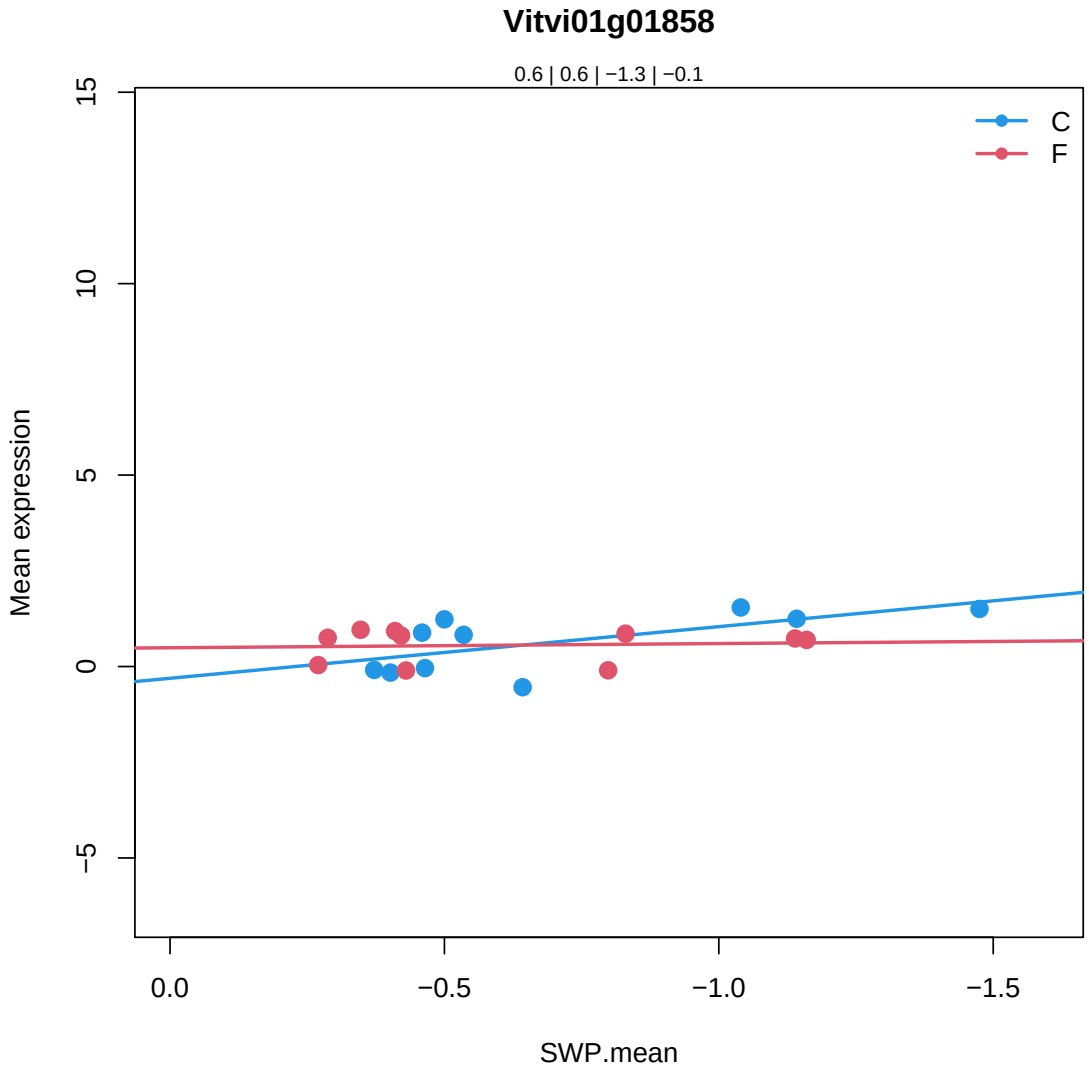
7.6.951 Vitvi01g01858: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01858
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr3:21255731-21258403 REVERSE LENGTH=890 |
        201606
```

Coefficients for Vitvi01g01858.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6407777	0.0009651205	***	0.001045439	**
SlopeC	-1.348418	0.008628417	**	0.2903326	
MeanF-MeanC	-0.08392415	0.7268459		0.9171057	
SlopeF-SlopeC	1.238854	0.08852597	.	0.9999488	



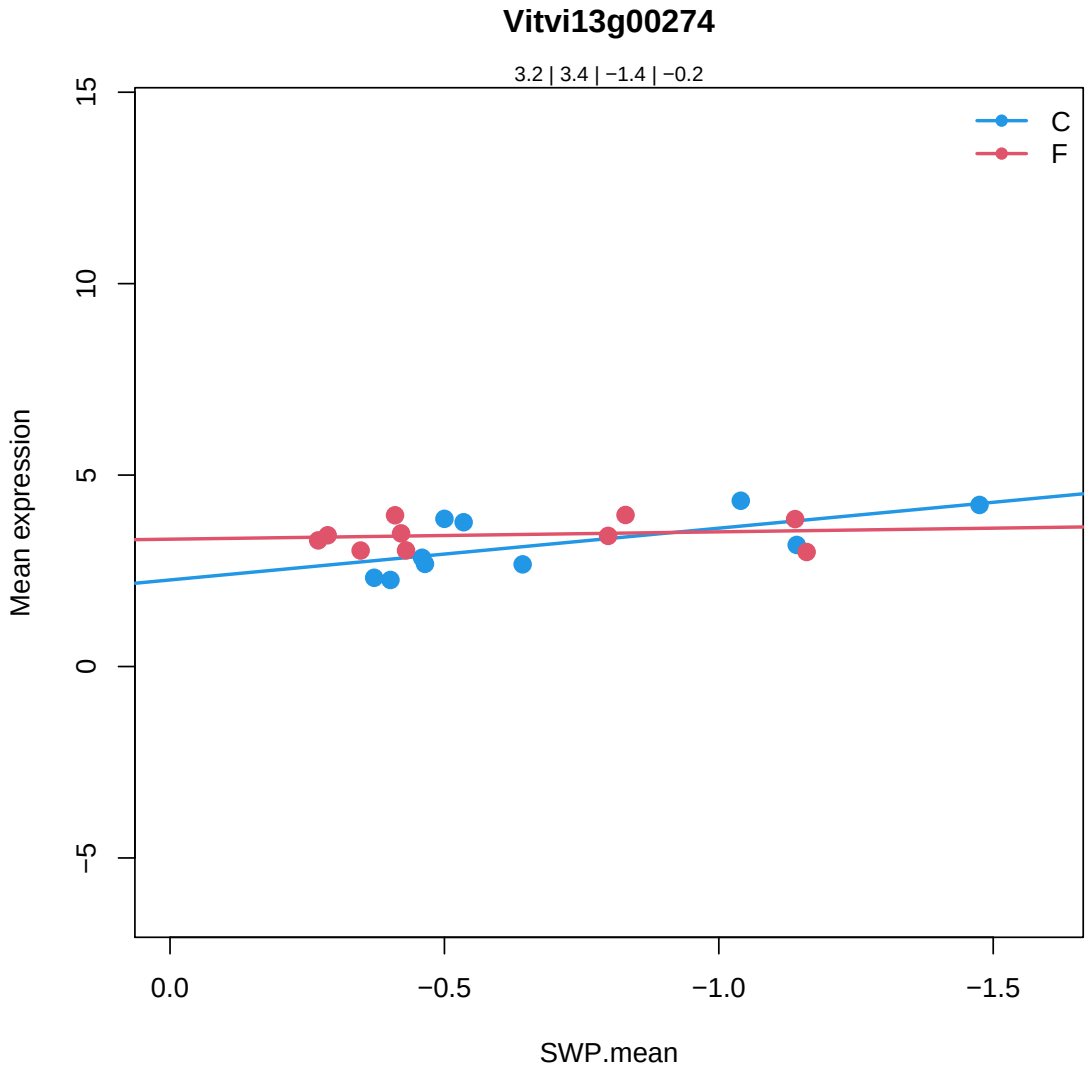
7.6.952 Vitvi13g00274: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00274
        27.3.67
        RNA.regulation of transcription.putative transcription regulator
        zinc knuckle (CCHC-type) family protein |
        Chr1:28371420-28372717 REVERSE LENGTH=257 |
        201606
```

Coefficients for Vitvi13g00274.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.211715	2.575937e-15	***	4.609348e-15	***
SlopeC	-1.352329	0.006500055	**	0.2686129	
MeanF-MeanC	0.2305079	0.323389		0.6839315	
SlopeF-SlopeC	1.160522	0.09655117	.	0.9999488	



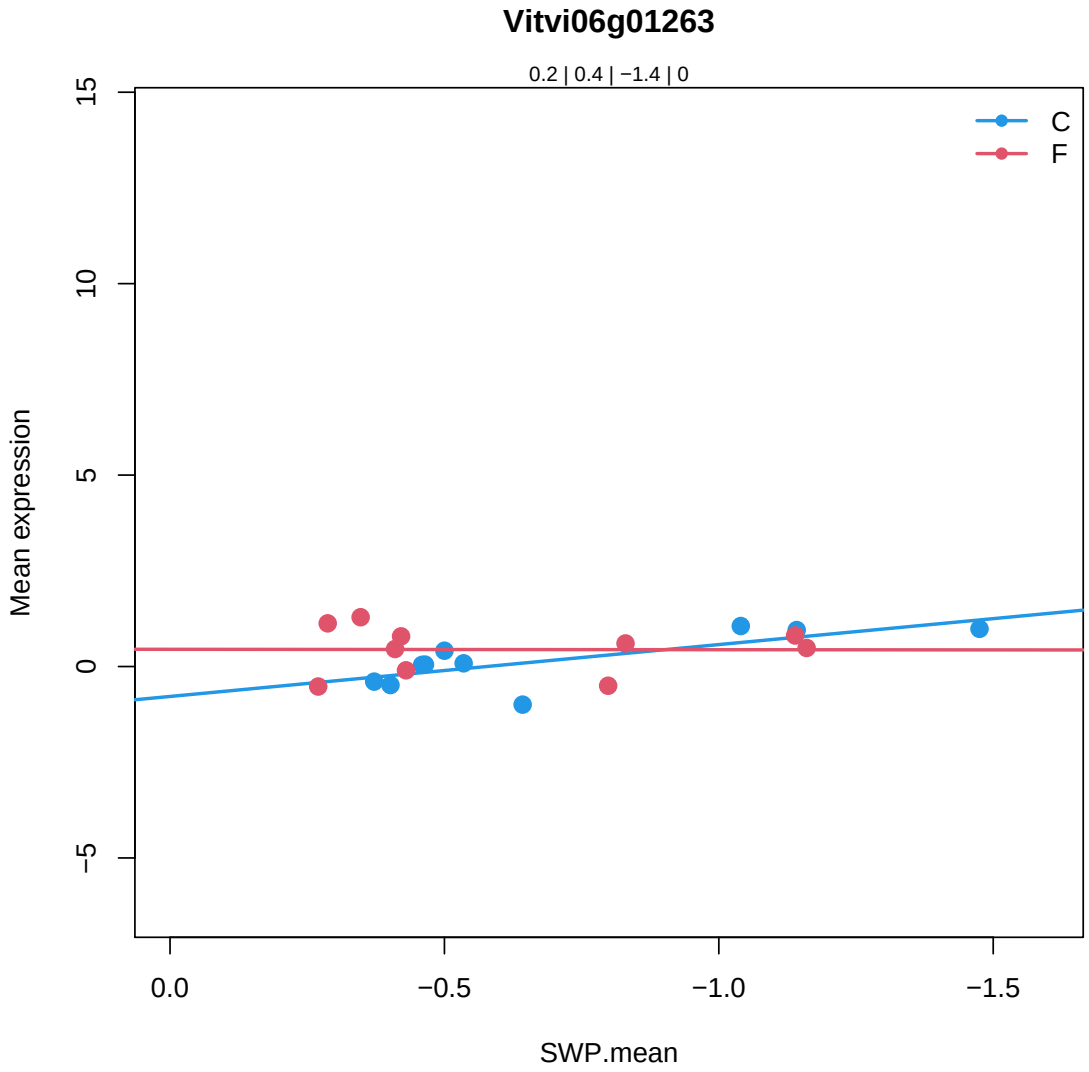
7.6.953 Vitvi06g01263: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01263
        35.2
        not assigned.unknown
        Pentatricopeptide repeat (PPR) superfamily protein |
        Chr2:5671493-5673586 FORWARD LENGTH=697 |
        201606
```

Coefficients for Vitvi06g01263.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.170939	0.3472187		0.3531973	
SlopeC	−1.354772	0.0121834	*	0.3229093	
MeanF−MeanC	0.2721938	0.2912059		0.6568833	
SlopeF−SlopeC	1.365147	0.07760779	.	0.9999488	



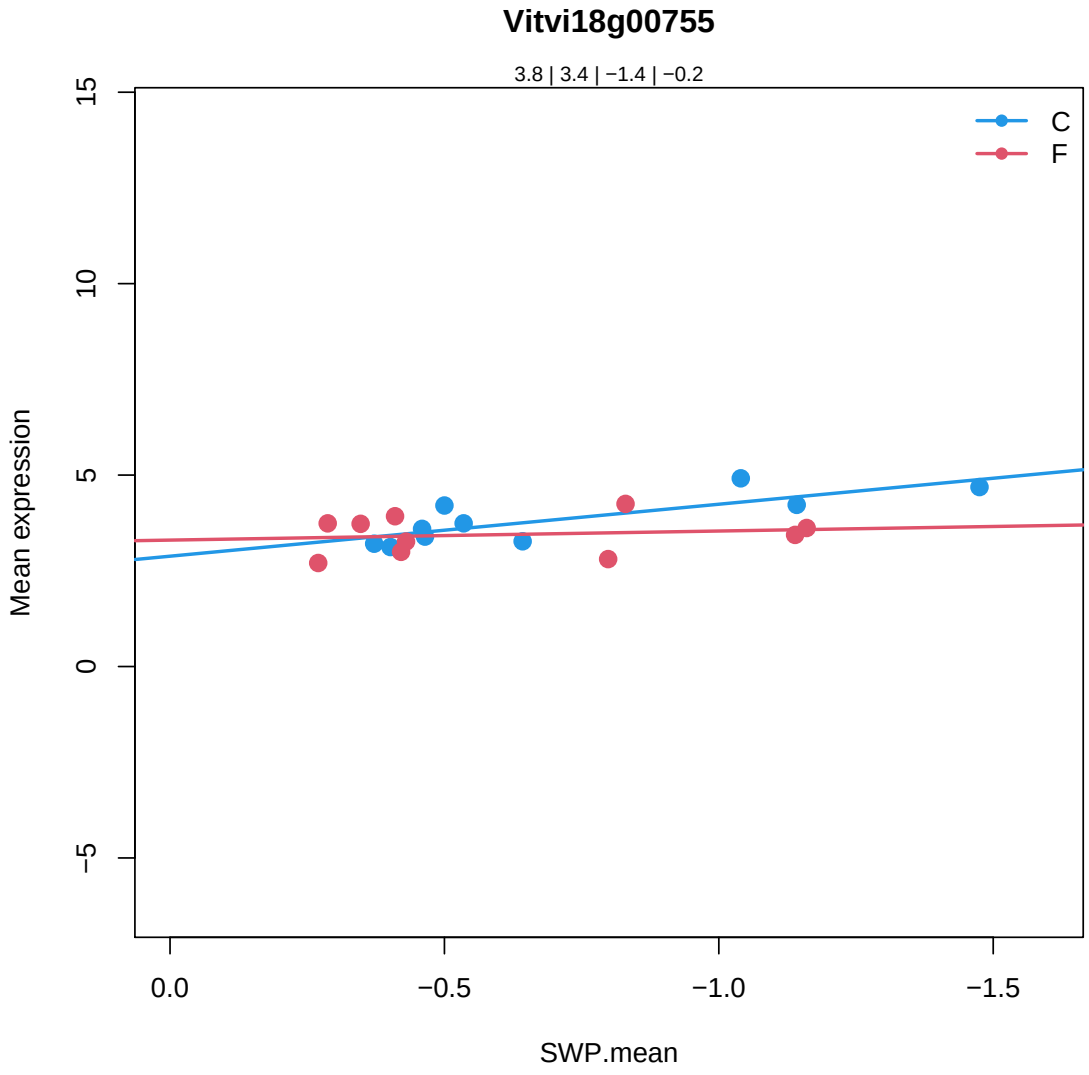
7.6.954 Vitvi18g00755: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00755
        35.2
        not assigned.unknown
        C2H2-like zinc finger protein |
        Chr5:21121626-21122816 REVERSE LENGTH=396 |
        201606
```

Coefficients for Vitvi18g00755.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.835448	1.40665e-17	***	3.593723e-17	***
SlopeC	-1.357465	0.003649272	**	0.224984	
MeanF-MeanC	-0.3893104	0.07954003	.	0.3188714	
SlopeF-SlopeC	1.120158	0.08451957	.	0.9999488	



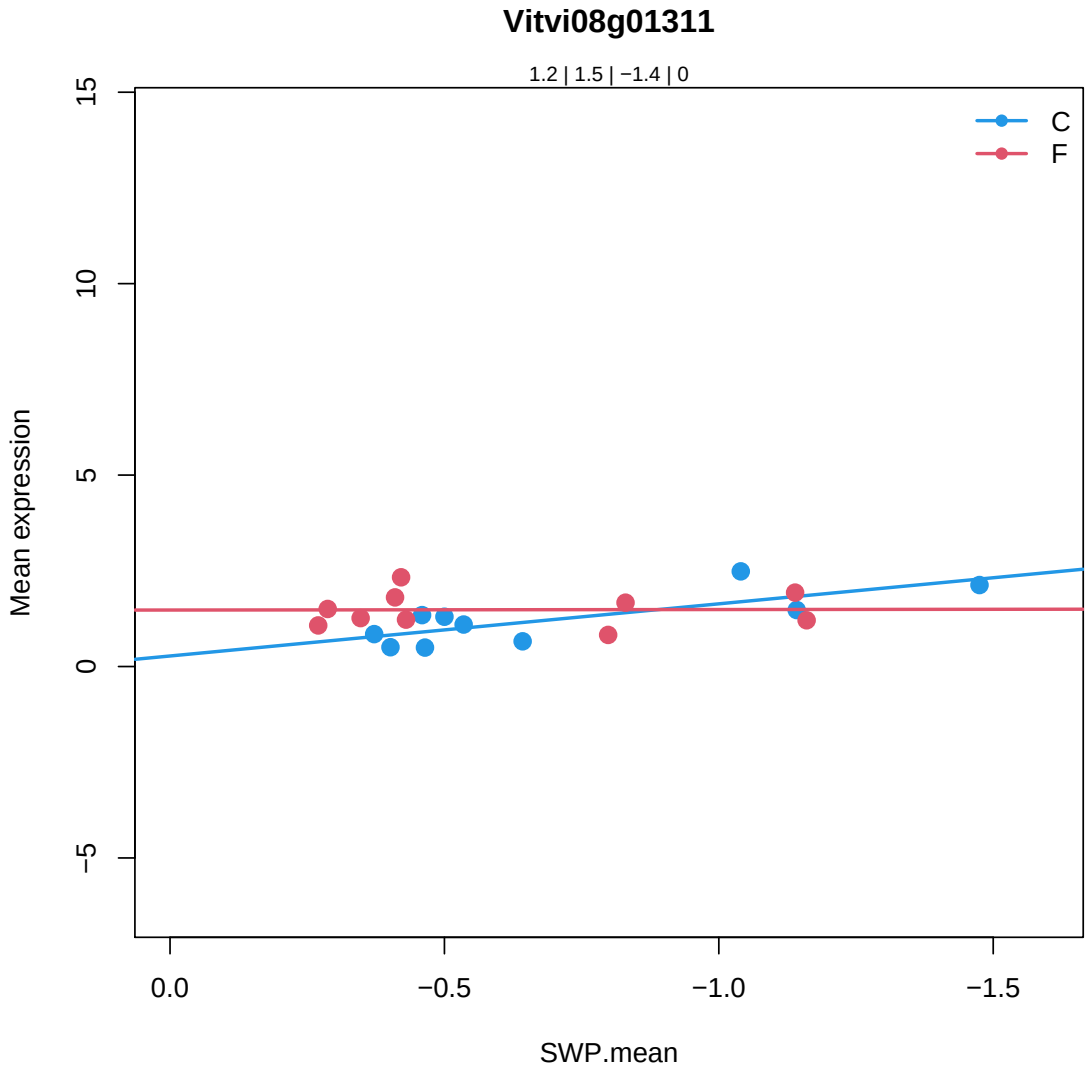
7.6.955 Vitvi08g01311: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01311
        11.8.1.1
        lipid metabolism.exotics (steroids, squalene etc).sphingolipids.cerami
        Neutral/alkaline non-lysosomal ceramidase |
        Chr1:2264829-2268306 REVERSE LENGTH=779 |
        201606
```

Coefficients for Vitvi08g01311.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.232907	4.183749e-08	***	5.013657e-08	***
SlopeC	-1.362252	0.003494074	**	0.2238297	
MeanF-MeanC	0.2501114	0.248942		0.6089022	
SlopeF-SlopeC	1.349329	0.0402378	*	0.9999488	



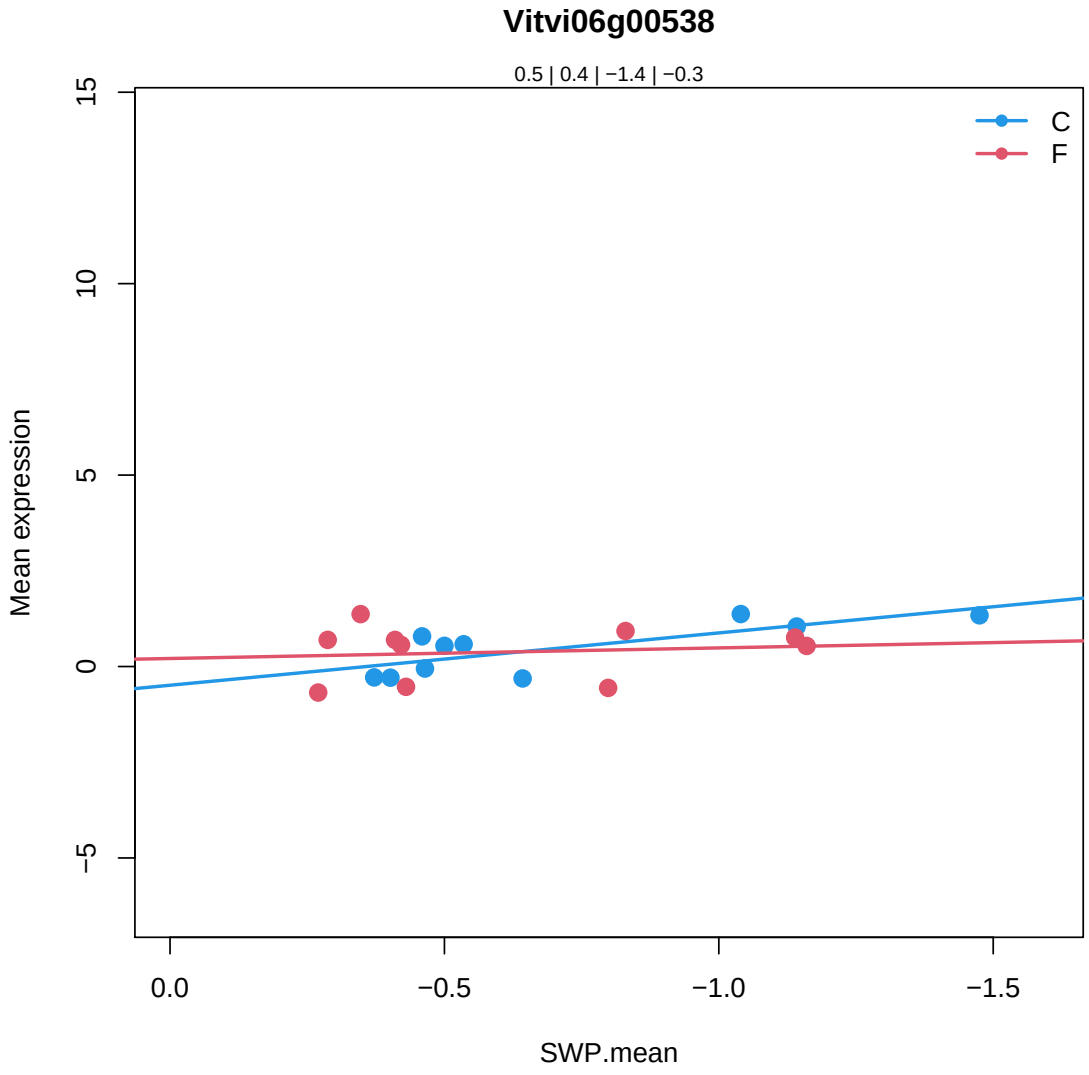
7.6.956 Vitvi06g00538: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00538
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr3:17231975-17233948 REVERSE LENGTH=657 |
        201606
```

Coefficients for Vitvi06g00538.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4718822	0.01863428	*	0.01960406	*
SlopeC	-1.36638	0.01482815	*	0.3368266	
MeanF-MeanC	-0.09409006	0.7231465		0.9153129	
SlopeF-SlopeC	1.089484	0.1701332		0.9999488	



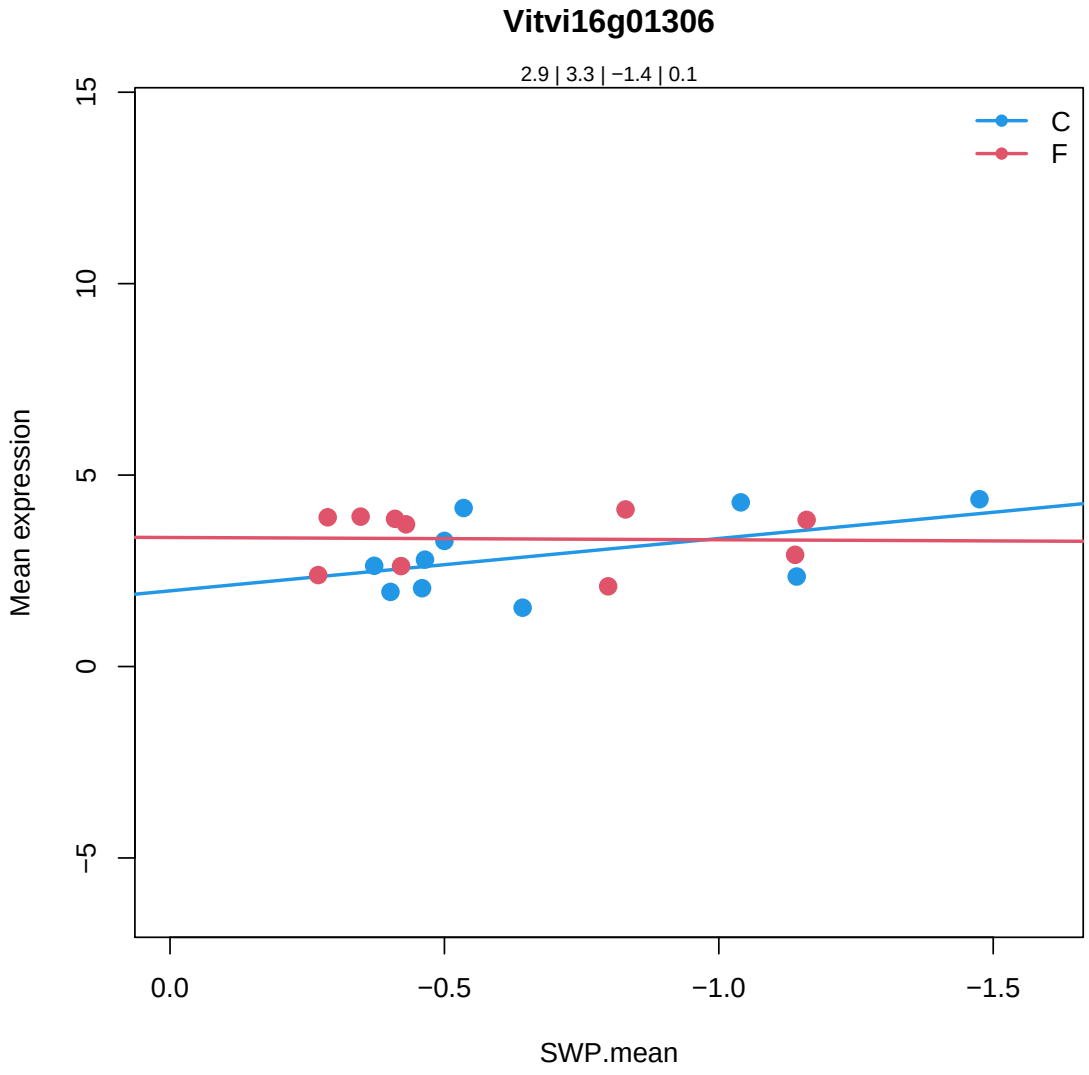
7.6.957 Vitvi16g01306: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01306
        33.99
        development.unspecified
        SPIRAL1-like1 |
        Chr1:9117950-9118611 REVERSE LENGTH=113 |
        201606
```

Coefficients for Vitvi16g01306.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.937985	9.053983e-11	***	1.186797e-10	***
SlopeC	-1.368489	0.06344435	.	0.5471512	
MeanF-MeanC	0.3958314	0.2776926		0.6414961	
SlopeF-SlopeC	1.427996	0.1841541		0.9999488	



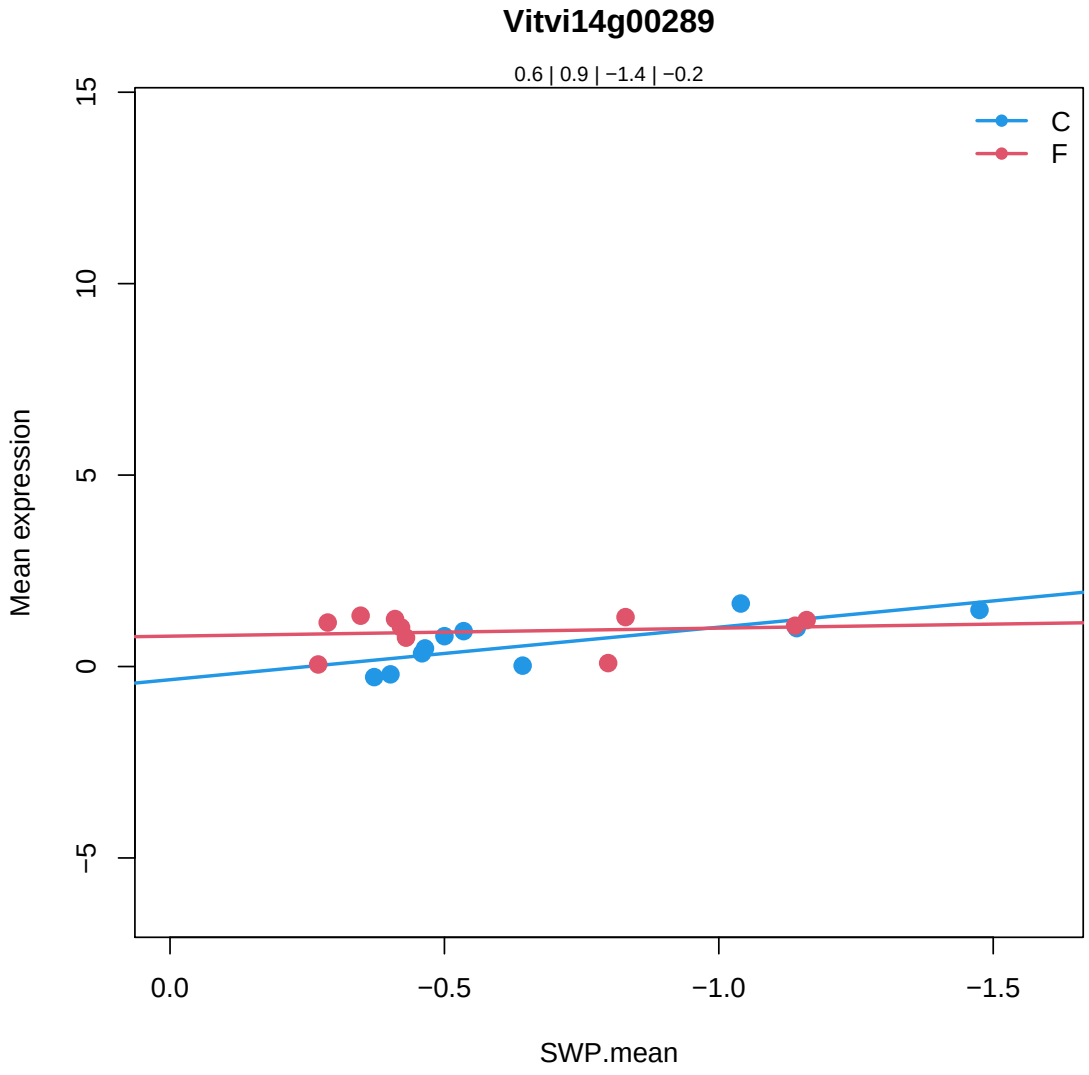
7.6.958 Vitvi14g00289: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g00289
        29.3
        protein.targeting
        DNAse I-like superfamily protein |
        Chr1:16528880-16531065 REVERSE LENGTH=626 |
        201606
```

Coefficients for Vitvi14g00289.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6200009	0.0004739409	***	0.000516355	***
SlopeC	−1.371905	0.00355021	**	0.2245324	
MeanF−MeanC	0.3002036	0.1730164		0.5034585	
SlopeF−SlopeC	1.162026	0.07616347	.	0.9999488	



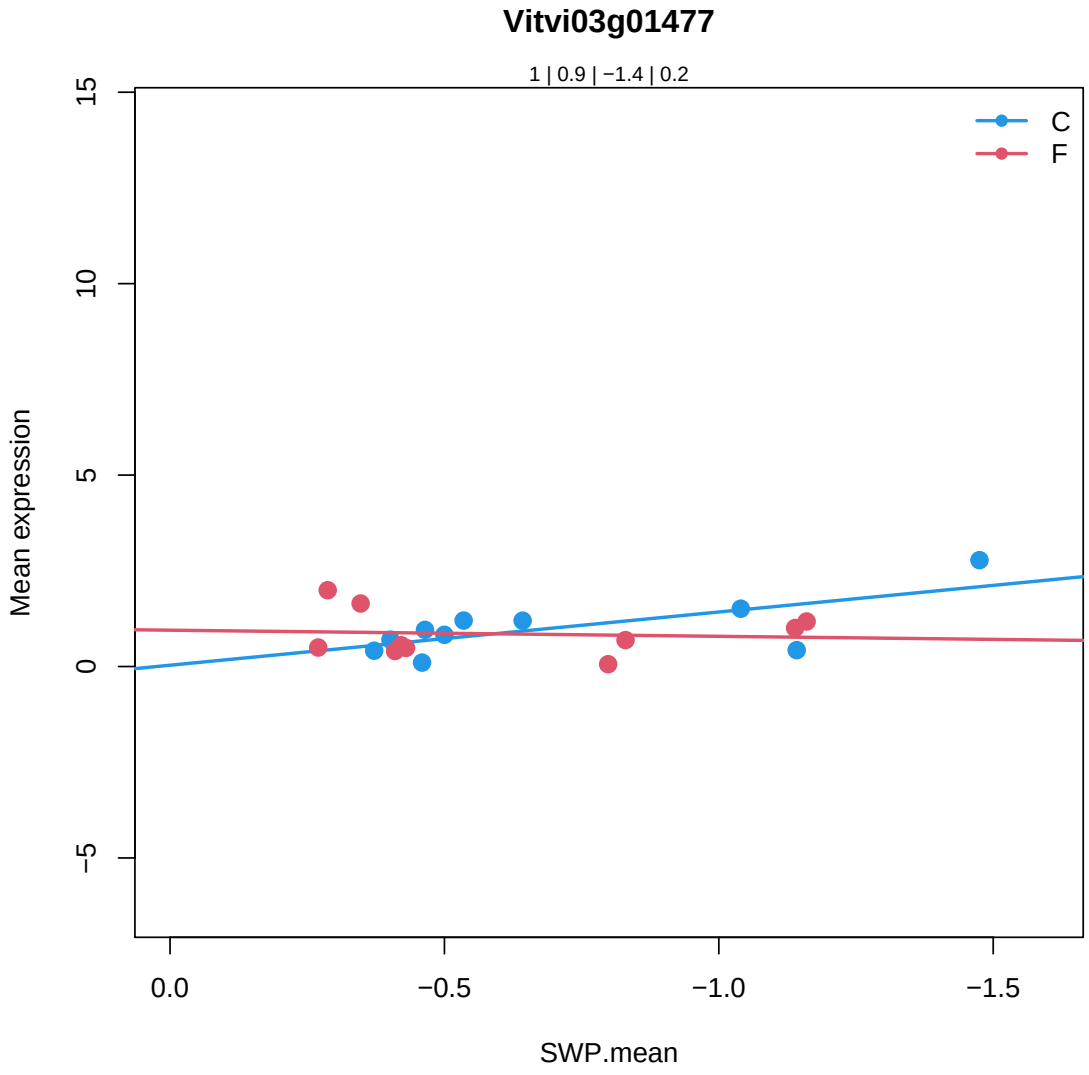
7.6.959 Vitvi03g01477: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g01477
        16.8.3.1
        secondary metabolism.flavonoids.dihydroflavonols.dihydroflavonol 4-red
        dihydroflavonol 4-reductase-like1 |
        Chr4:16834091-16835611 REVERSE LENGTH=326 |
        201606
```

Coefficients for Vitvi03g01477.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.011488	1.570897e-05	***	1.766014e-05	***
SlopeC	-1.39005	0.01220331	*	0.3229093	
MeanF-MeanC	-0.1602163	0.5413811		0.8287366	
SlopeF-SlopeC	1.549999	0.05272398	.	0.9999488	



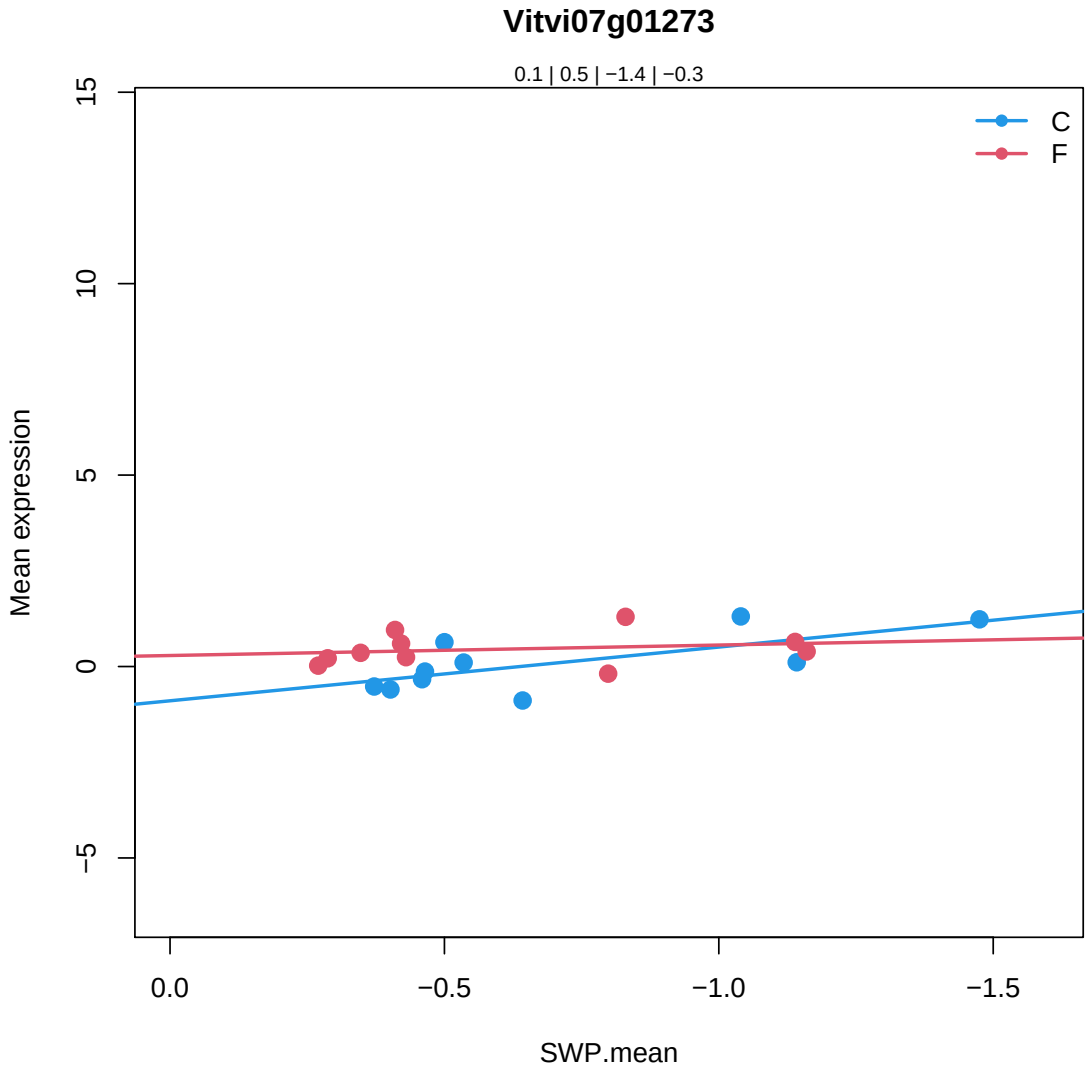
7.6.960 Vitvi07g01273: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01273
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr2:12712884-12715100 FORWARD LENGTH=738 |
        201606
```

Coefficients for Vitvi07g01273.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.0913918	0.5752921		0.5808945	
SlopeC	-1.40351	0.004852617	**	0.249877	
MeanF-MeanC	0.3625277	0.1251466		0.418859	
SlopeF-SlopeC	1.130026	0.1037963		0.9999488	



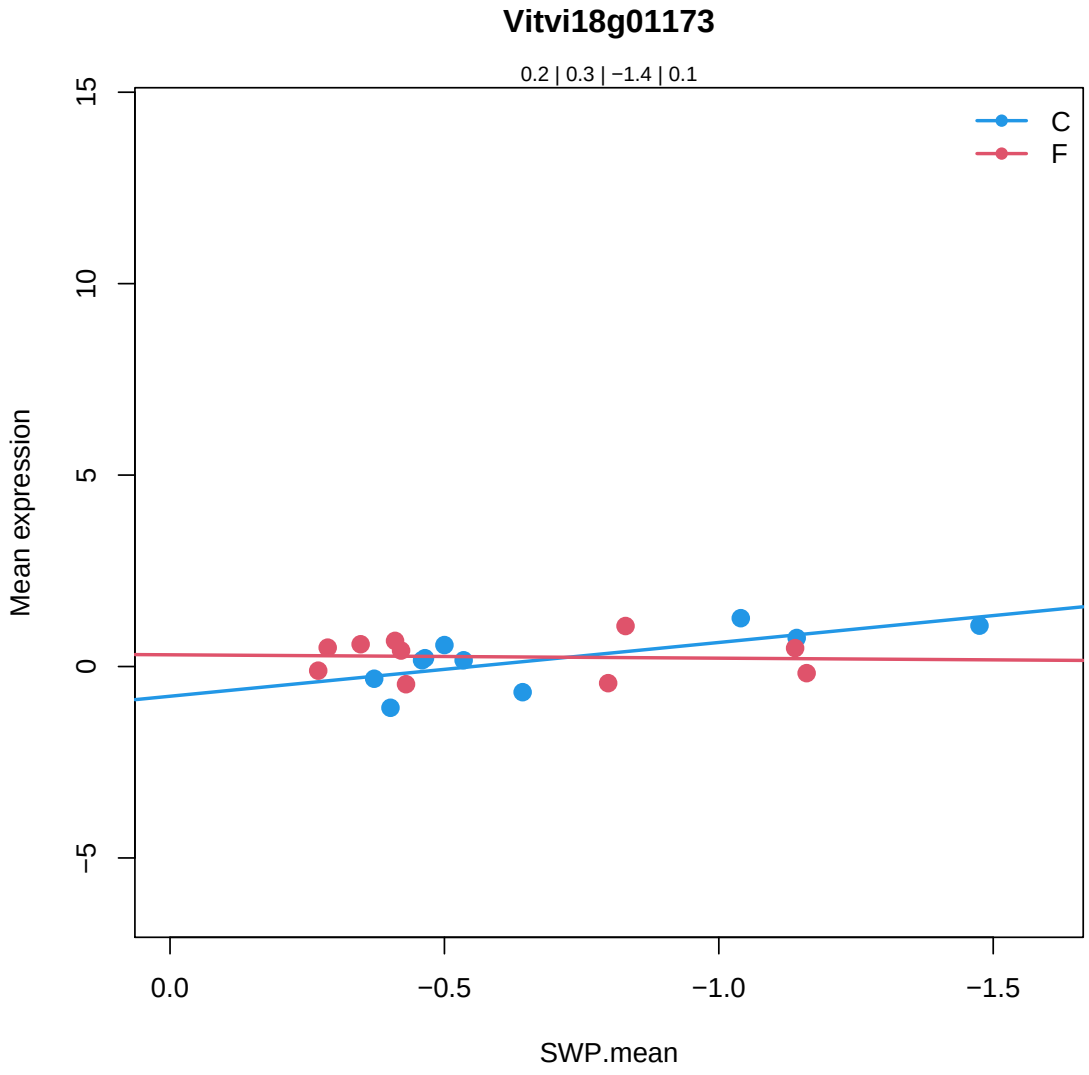
7.6.961 Vitvi18g01173: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g01173
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr1:16687637-16689538 REVERSE LENGTH=633 |
        201606
```

Coefficients for Vitvi18g01173.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.2109583	0.2238741		0.2291973	
SlopeC	-1.404465	0.006761575	**	0.2740956	
MeanF-MeanC	0.04103108	0.8648496		0.9643899	
SlopeF-SlopeC	1.492503	0.04400192	*	0.9999488	



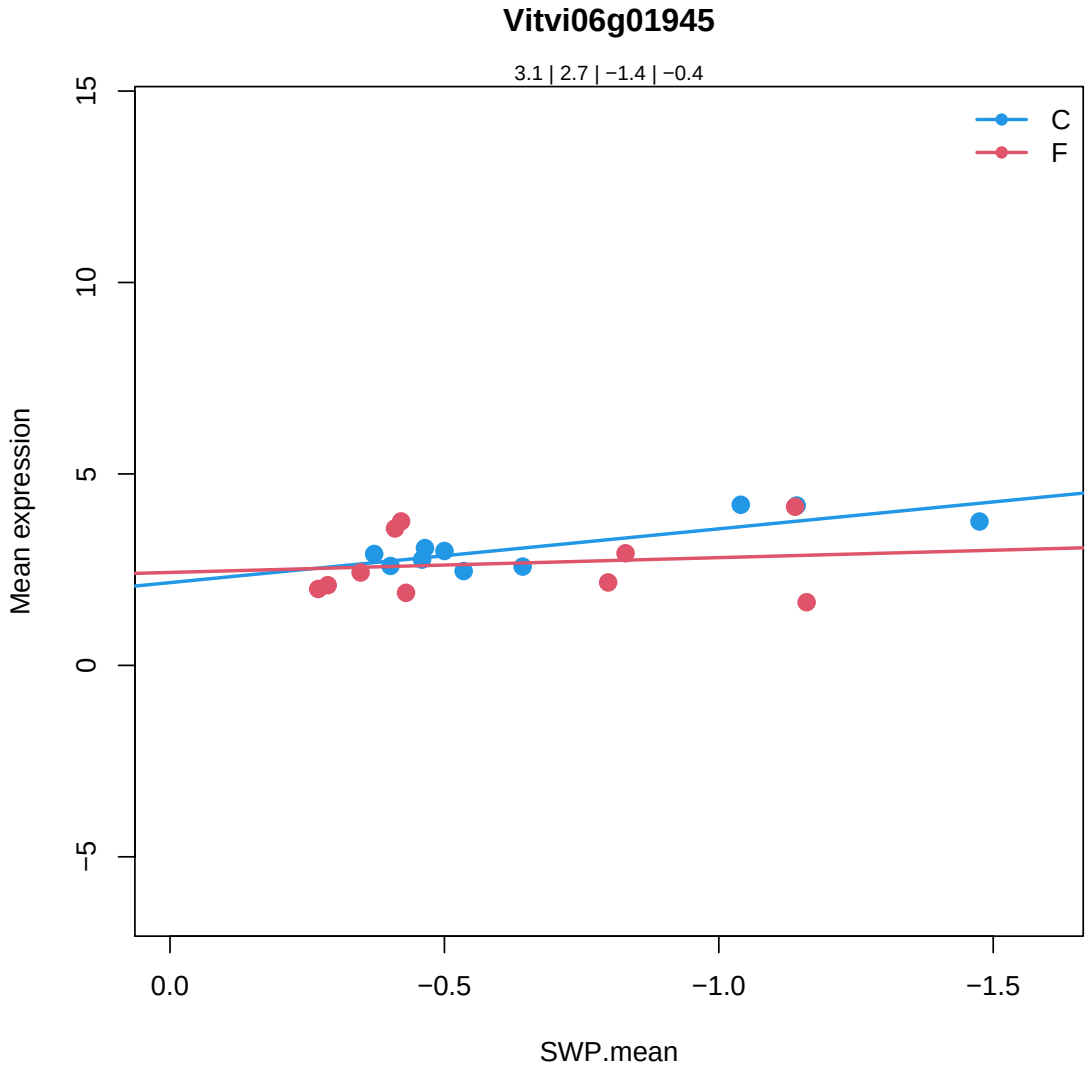
7.6.962 Vitvi06g01945: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g01945
        35.2
        not assigned.unknown
        [Sotub09g011190.1.1]: Unknown Protein [Sotub09g011190.1.1]: Unknown Pr
        [stNIB-v1_0001639]
```

Coefficients for Vitvi06g01945.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.149129	7.526933e-13	***	1.090236e-12	***
SlopeC	-1.404928	0.02519981	*	0.4079655	
MeanF-MeanC	-0.4863834	0.1158344		0.3985435	
SlopeF-SlopeC	1.01834	0.2541055		0.9999488	



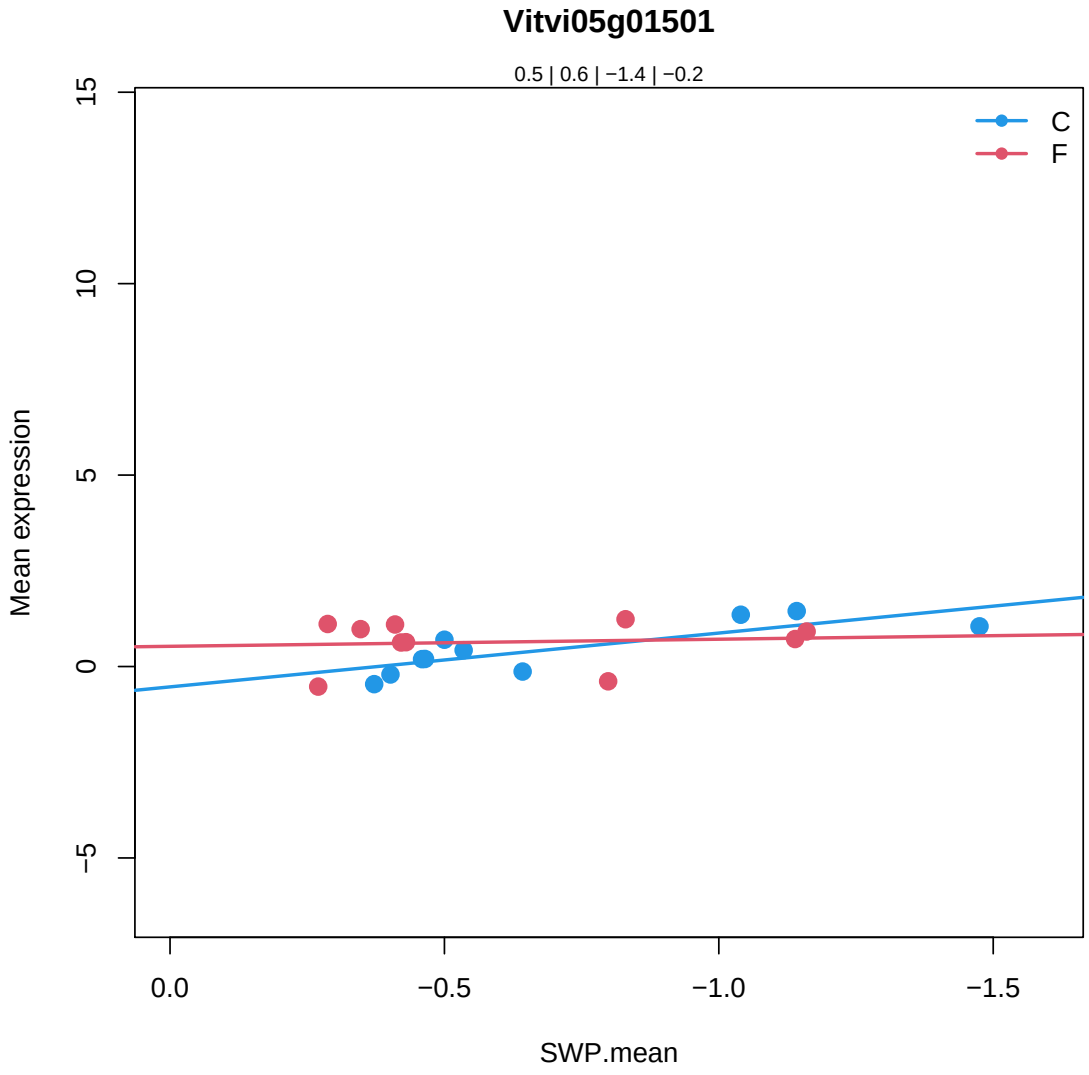
7.6.963 Vitvi05g01501: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01501
        35.2
        not assigned.unknown
        Ubiquitin carboxyl-terminal hydrolase family protein |
        Chr1:27024875-27026287 REVERSE LENGTH=470 |
        201606
```

Coefficients for Vitvi05g01501.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4564253	0.01289476	*	0.01362226	*
SlopeC	−1.405565	0.006680934	**	0.2715488	
MeanF−MeanC	0.1839346	0.4479938		0.7774043	
SlopeF−SlopeC	1.220162	0.09421236	.	0.9999488	



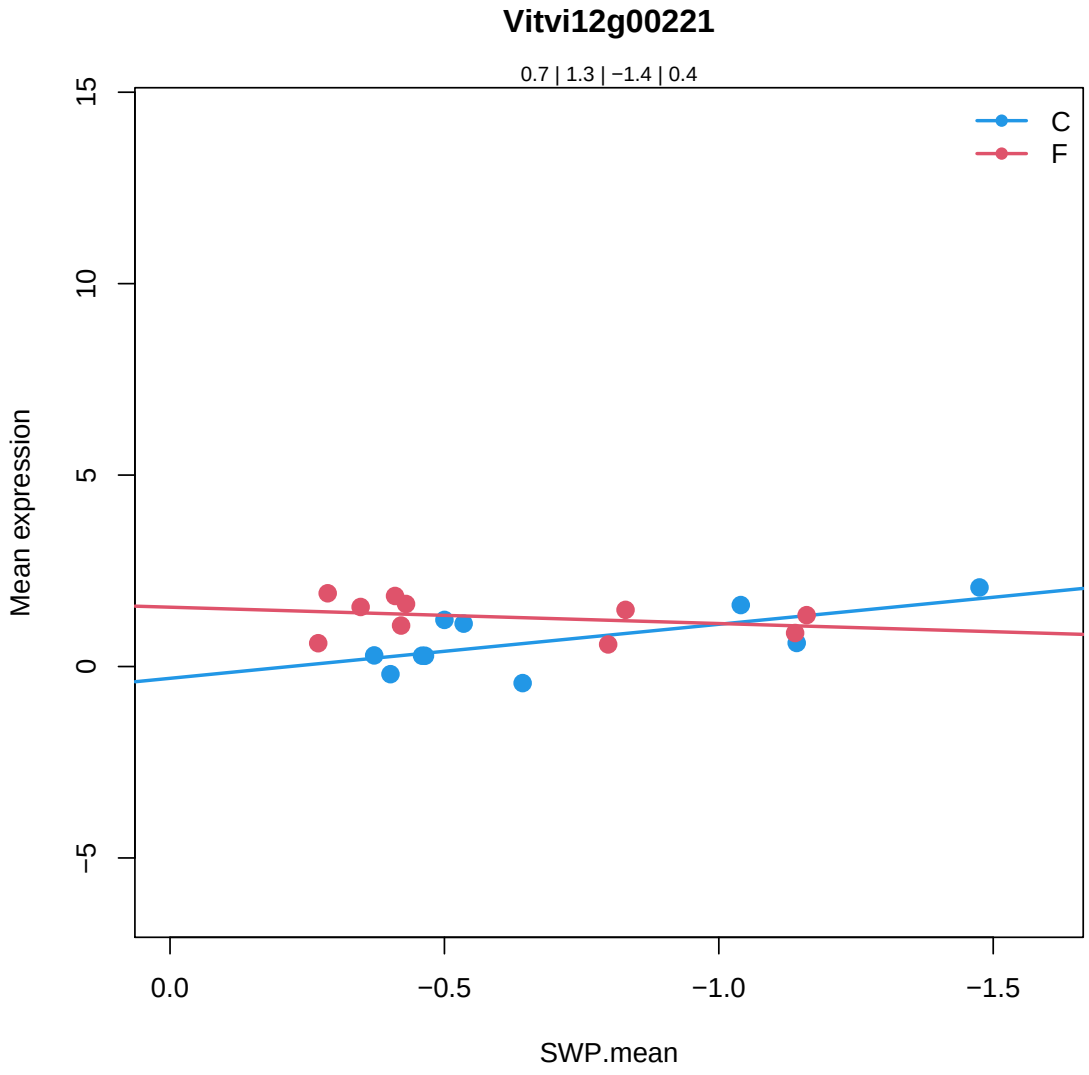
7.6.964 Vitvi12g00221: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00221
        26.4
        misc.beta 1,3 glucan hydrolases
        plasmodesmata callose-binding protein 5 |
        Chr3:21515397-21516329 REVERSE LENGTH=180 |
        201606
```

Coefficients for Vitvi12g00221.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.684193	0.0006906173	***	0.0007504377	***
SlopeC	−1.411136	0.007776019	**	0.280858	
MeanF−MeanC	0.60527	0.0216148	*	0.1332199	
SlopeF−SlopeC	1.837758	0.01770561	*	0.9999488	



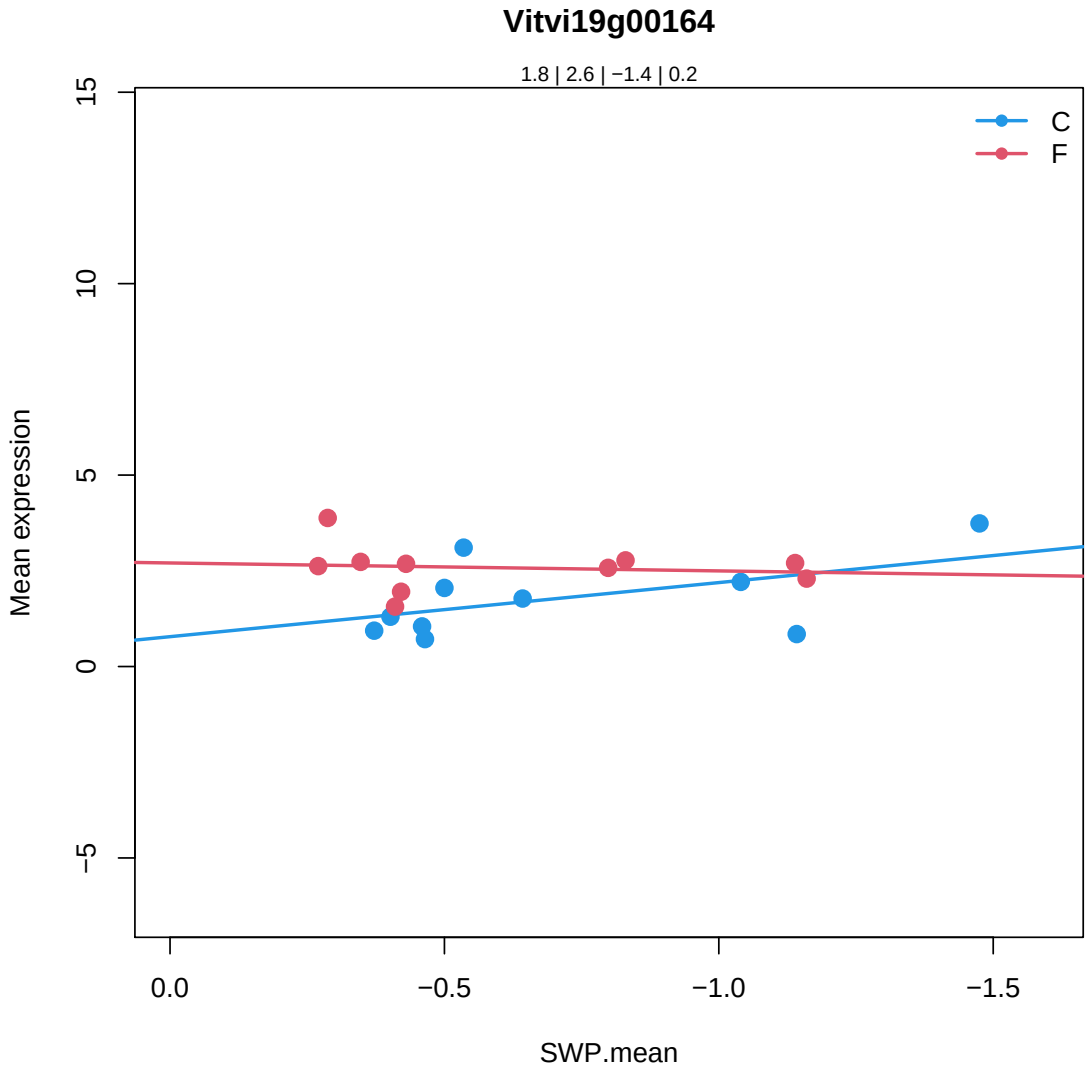
7.6.965 Vitvi19g00164: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g00164
        35.2
        not assigned.unknown
        DUF1685 family protein |
        Chr2:17796382-17797185 REVERSE LENGTH=267 |
        201606
```

Coefficients for Vitvi19g00164.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.77274	1.247367e-07	***	1.476345e-07	***
SlopeC	-1.412822	0.03786573	*	0.4650681	
MeanF-MeanC	0.8055865	0.02139297	*	0.1321374	
SlopeF-SlopeC	1.620281	0.1026062		0.9999488	



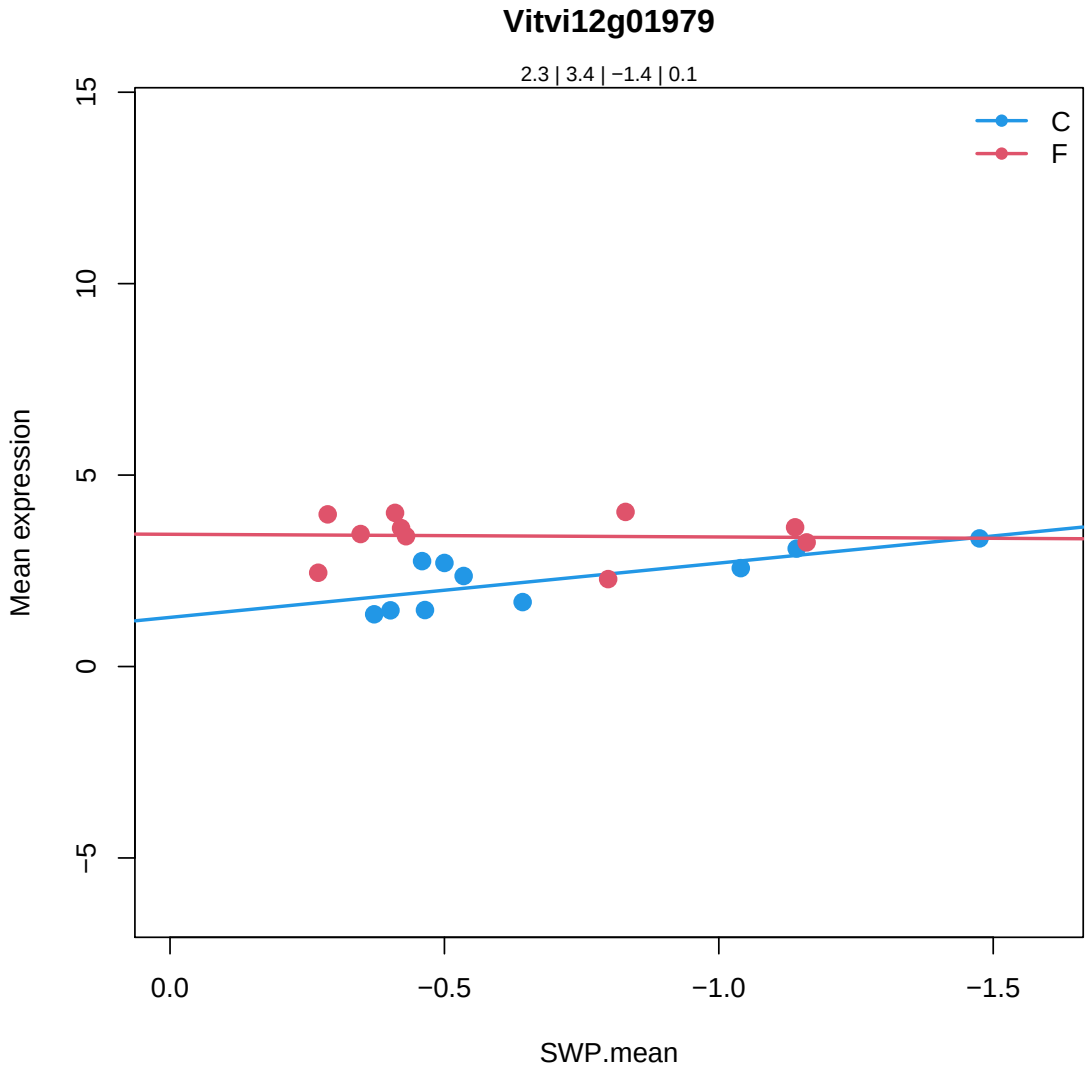
7.6.966 Vitvi12g01979: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g01979
        35.2
        not assigned.unknown
        AAA-ATPase 1 |
        Chr5:16020218-16021762 REVERSE LENGTH=514 |
        201606
```

Coefficients for Vitvi12g01979.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.28063	1.79151e-11	***	2.418618e-11	***
SlopeC	-1.418156	0.009515865	**	0.2978251	
MeanF-MeanC	1.130429	0.000204347	***	0.00332806	**
SlopeF-SlopeC	1.4879	0.05748842	.	0.9999488	



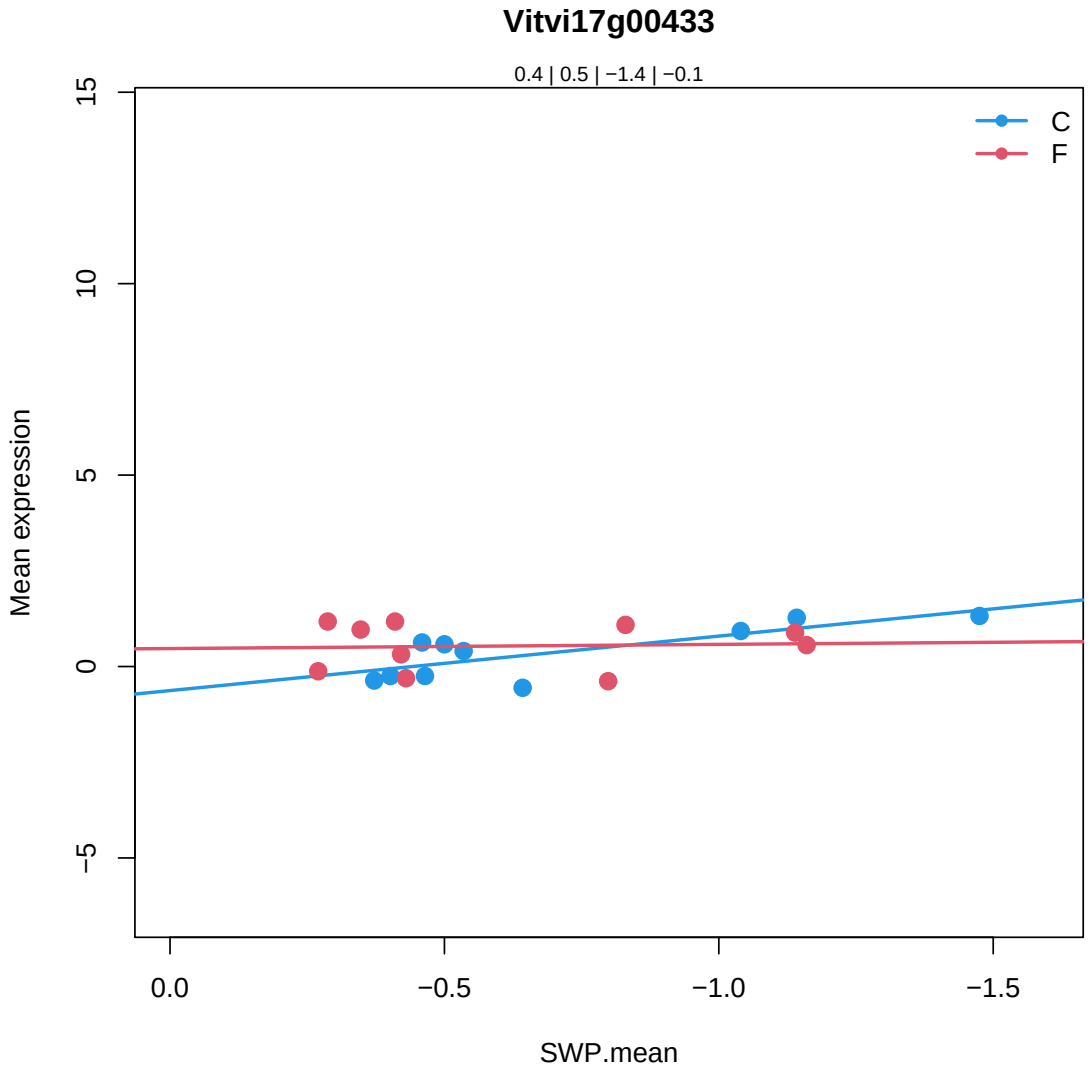
7.6.967 Vitvi17g00433: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00433
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        Pentatricopeptide repeat (PPR) superfamily protein |
        Chr1:6363172-6366084 FORWARD LENGTH=970 |
        201606
```

Coefficients for Vitvi17g00433.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3717033	0.04355893	*	0.04543388	*
SlopeC	−1.423288	0.007498882	**	0.2777732	
MeanF−MeanC	0.1634486	0.5119284		0.8136412	
SlopeF−SlopeC	1.314451	0.0809148	.	0.9999488	



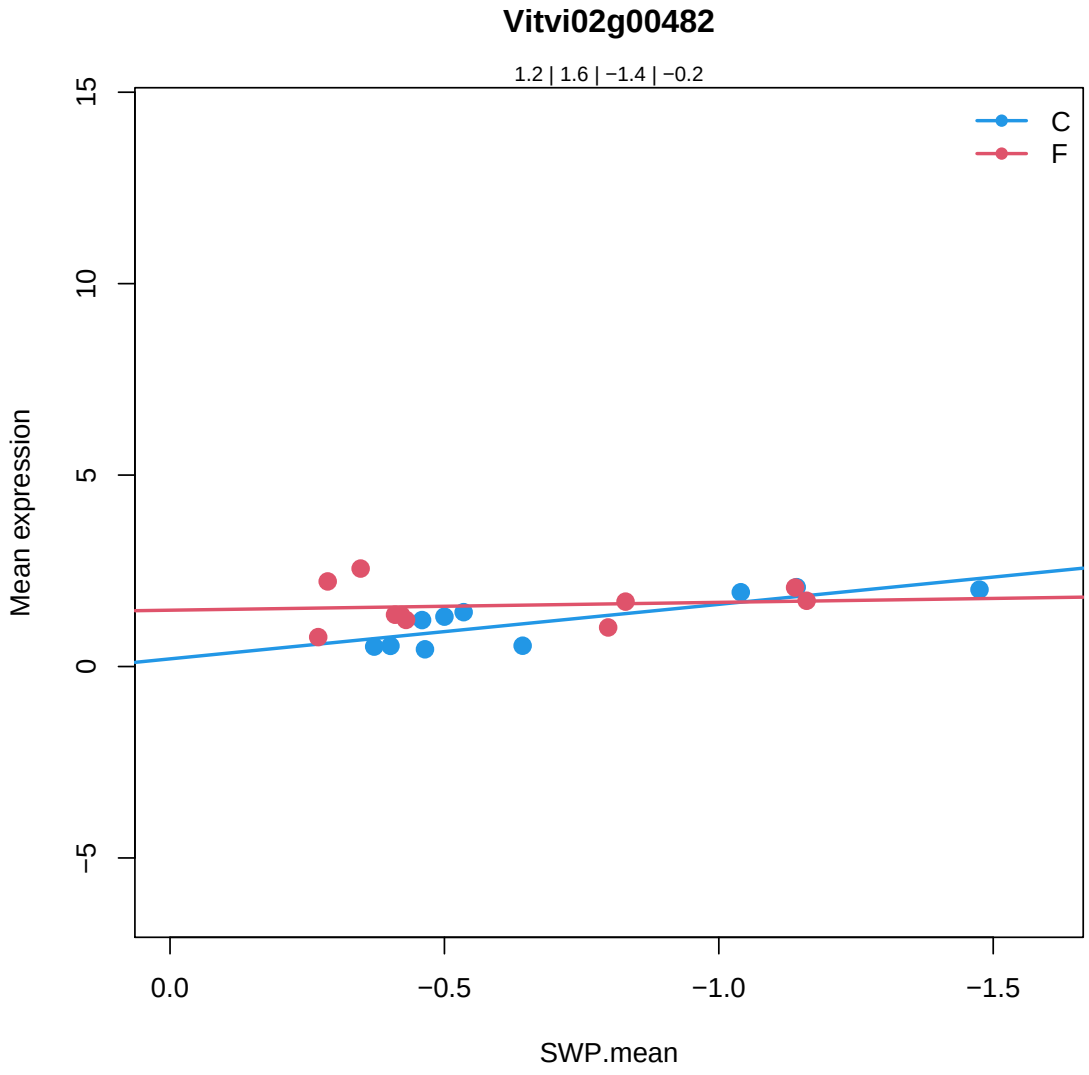
7.6.968 Vitvi02g00482: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00482
        35.1
        not assigned.no ontology
        Glycine cleavage T-protein family |
        Chr4:7263640-7265425 FORWARD LENGTH=393 |
        201606
```

Coefficients for Vitvi02g00482.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.200788	1.748664e-07	***	2.060704e-07	***
SlopeC	-1.423896	0.00399862	**	0.232622	
MeanF-MeanC	0.3950054	0.09279914	.	0.3492455	
SlopeF-SlopeC	1.219059	0.0775069	.	0.9999488	



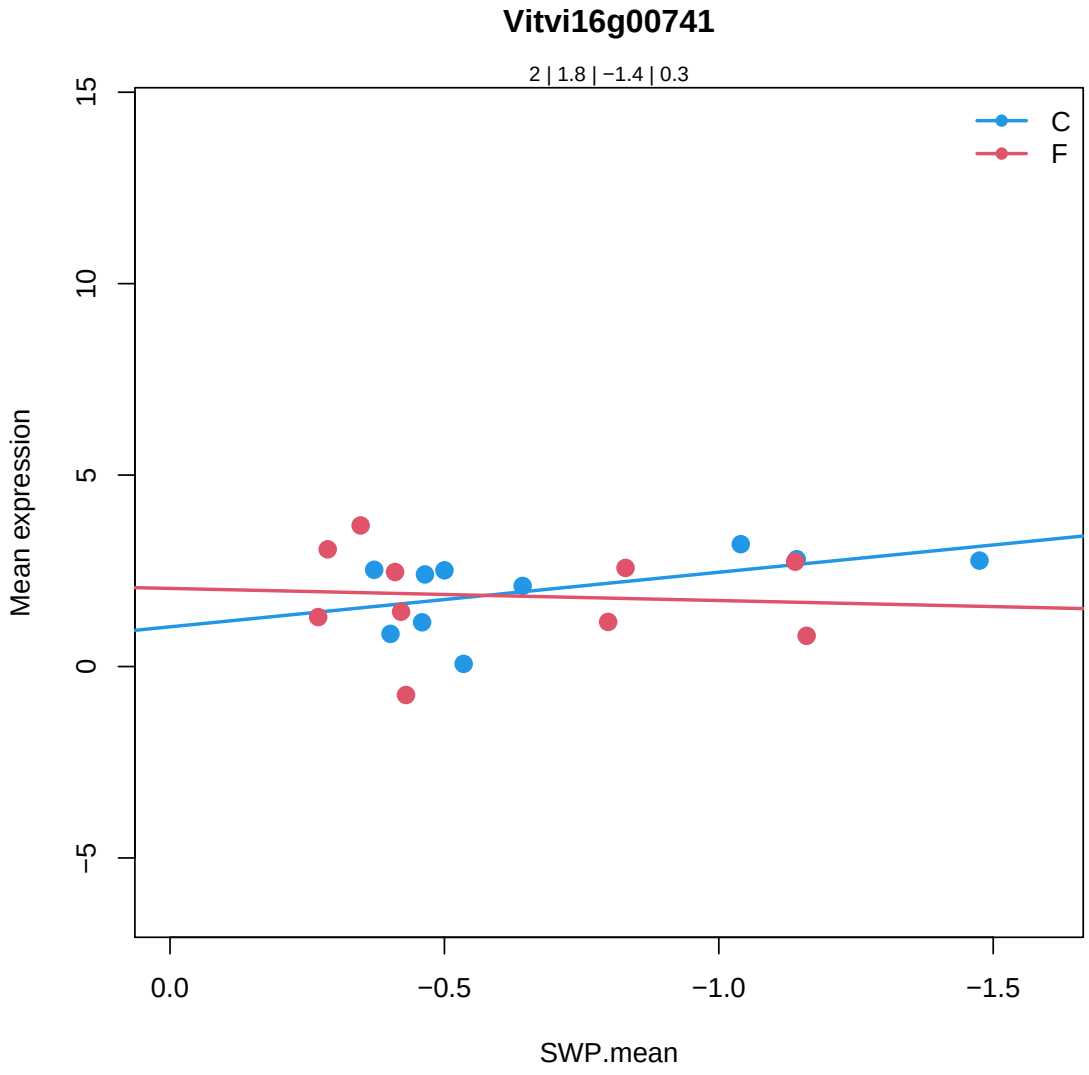
7.6.969 Vitvi16g00741: type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g00741
        35.2
        not assigned.unknown
        Plant invertase/pectin methylesterase inhibitor superfamily protein |
        Chr4:12936005-12936610 REVERSE LENGTH=201 |
        201606
```

Coefficients for Vitvi16g00741.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.038821	3.243889e-06	***	3.701405e-06	***
SlopeC	-1.425438	0.1323751		0.654787	
MeanF-MeanC	-0.1921416	0.6823876		0.8978723	
SlopeF-SlopeC	1.741549	0.2127985		0.9999488	



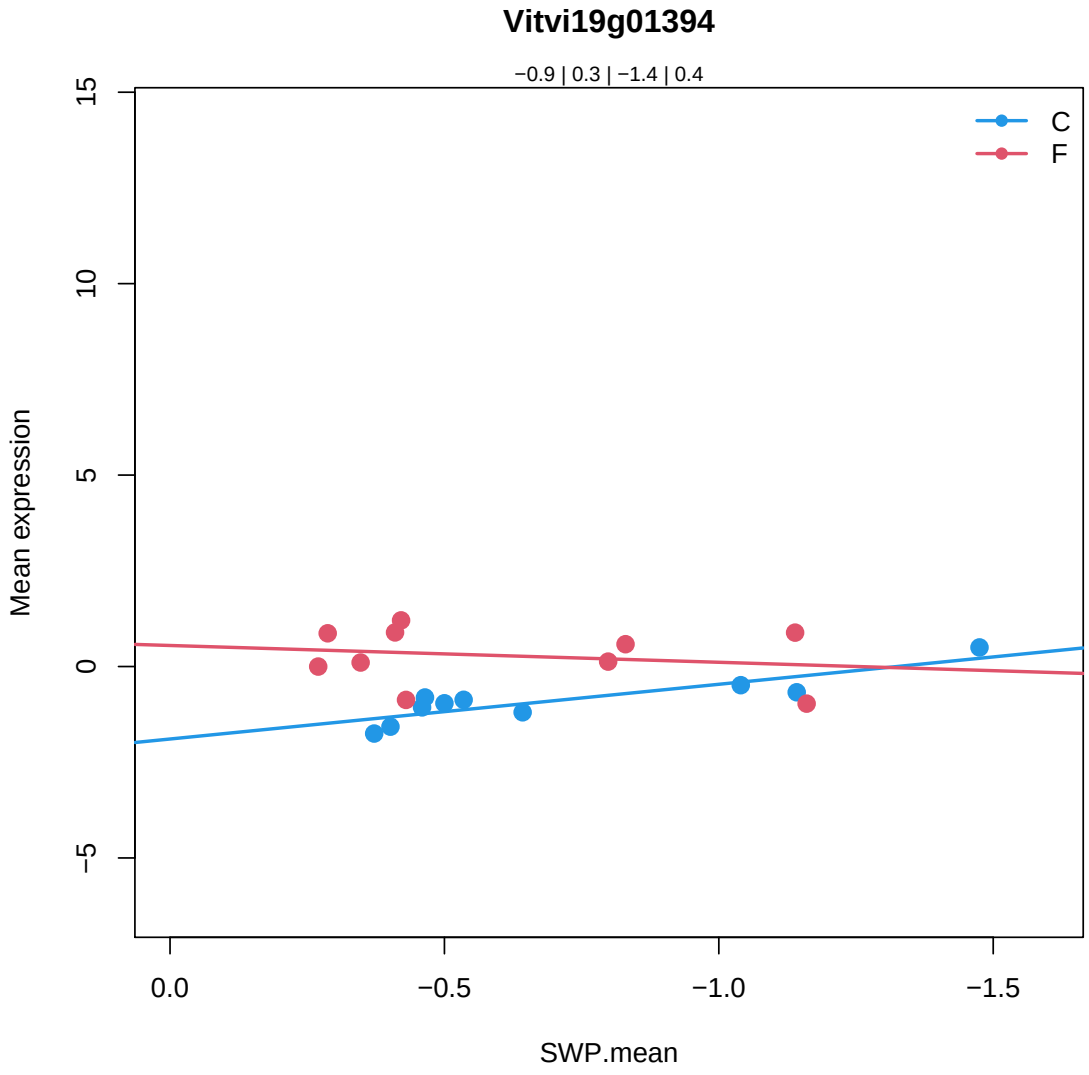
7.6.970 Vitvi19g01394: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g01394
        24.1
        biodegradation of xenobiotics.hydroxyacylglutathione hydrolase
        glyoxalase II 3 |
        Chr1:19991542-19993250 REVERSE LENGTH=294 |
        201606
```

Coefficients for Vitvi19g01394.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.8885535	6.857932e-05	***	7.596555e-05	***
SlopeC	-1.429122	0.009593869	**	0.2990384	
MeanF-MeanC	1.170469	0.0001541636	***	0.002576493	**
SlopeF-SlopeC	1.8677	0.02071857	*	0.9999488	



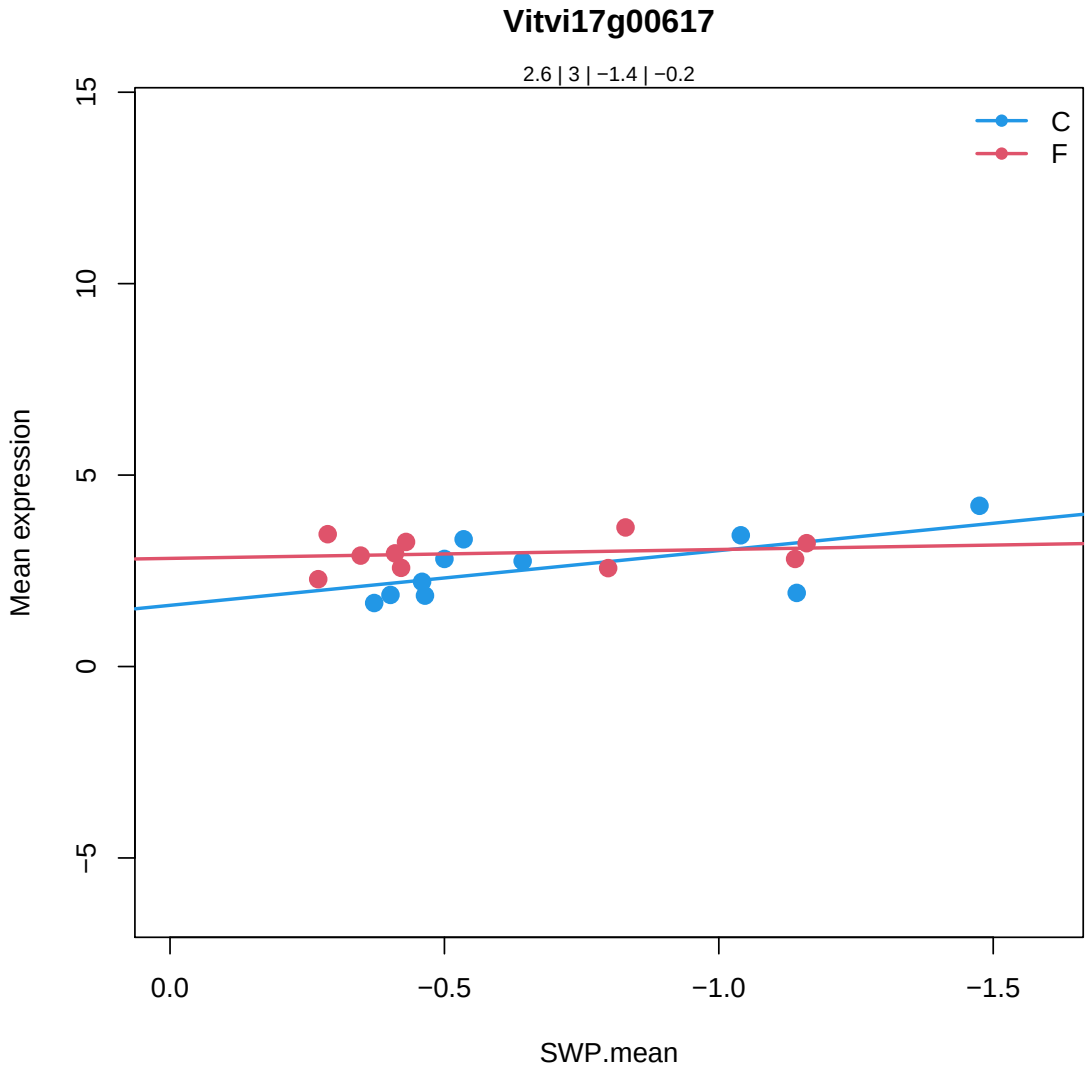
7.6.971 Vitvi17g00617: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00617
        21.1
        redox.thioredoxin
        atypical CYS HIS rich thioredoxin 5 |
        Chr5:24707658-24708684 FORWARD LENGTH=245 |
        201606
```

Coefficients for Vitvi17g00617.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.602806	1.042905e-12	***	1.493841e-12	***
SlopeC	-1.429148	0.008203731	**	0.2854824	
MeanF-MeanC	0.3624063	0.1606788		0.484391	
SlopeF-SlopeC	1.197134	0.1157372		0.9999488	



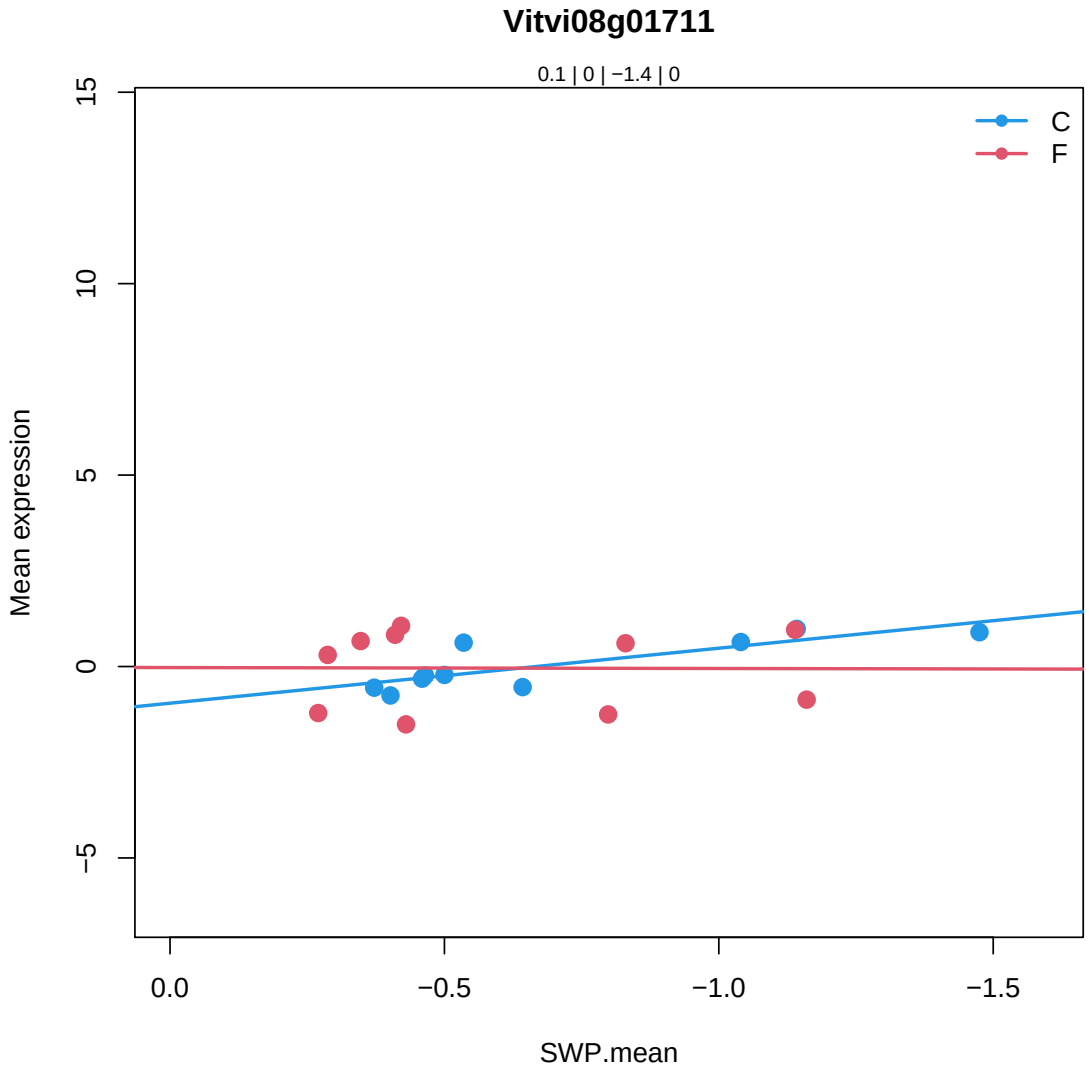
7.6.972 Vitvi08g01711: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01711
        13.1.6.5.3
        amino acid metabolism.synthesis.aromatic aa.tryptophan.phosphoribosyan
        Calcium-dependent lipid-binding (CaLB domain) plant phosphoribosyltran
        Chr3:21431198-21433519 REVERSE LENGTH=773 |
        201606
```

Coefficients for Vitvi08g01711.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.05198144	0.8298938		0.8332285	
SlopeC	-1.436395	0.04223351	*	0.4812642	
MeanF-MeanC	-0.0939751	0.783668		0.9384607	
SlopeF-SlopeC	1.460519	0.154576		0.9999488	



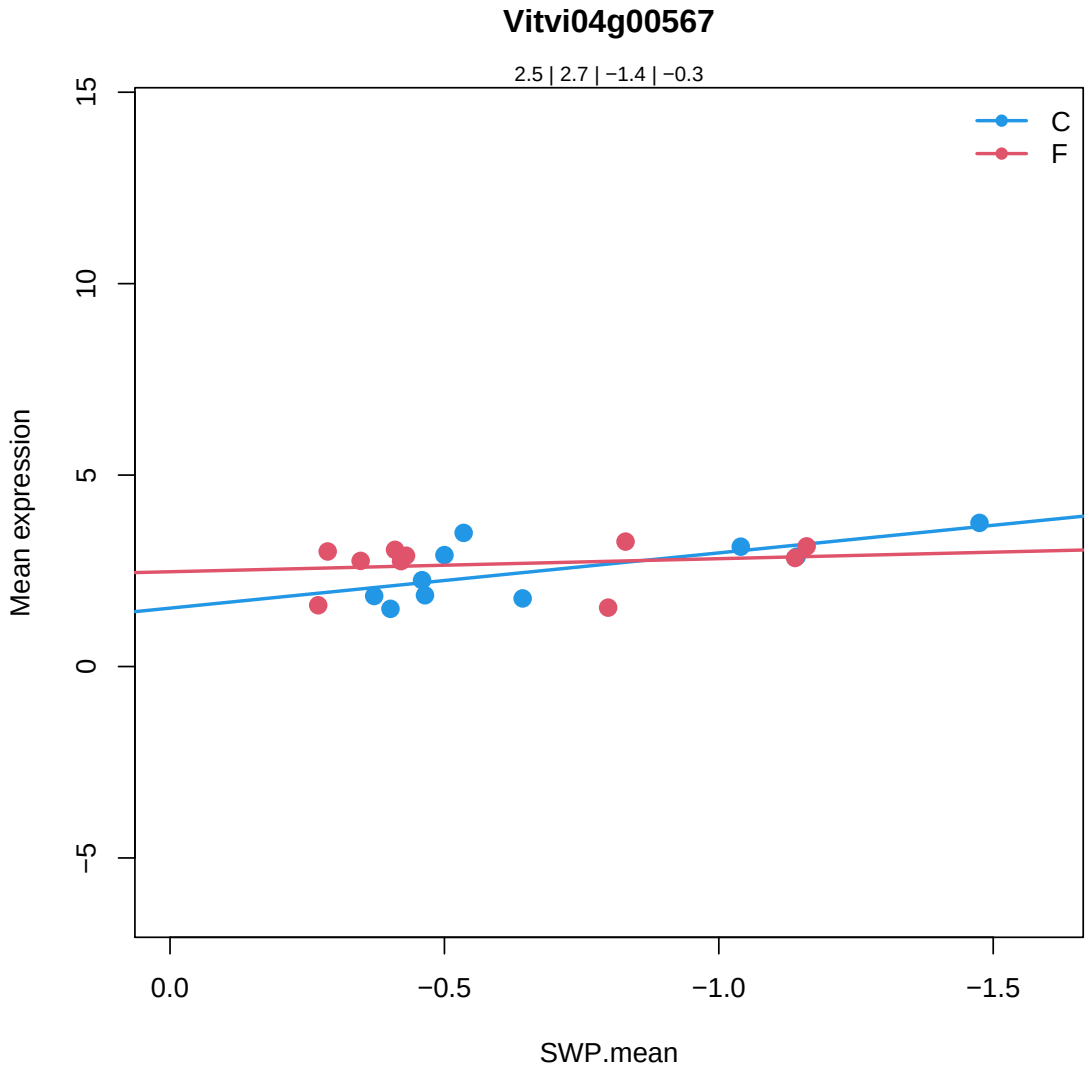
7.6.973 Vitvi04g00567: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi04g00567
        33.99
        development.unspecified
        WUS-interacting protein 2 |
        Chr3:5364792-5371869 REVERSE LENGTH=1135 |
        201606
```

Coefficients for Vitvi04g00567.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.539239	5.144394e-12	***	7.105651e-12	***
SlopeC	-1.442884	0.01115788	*	0.3143947	
MeanF-MeanC	0.143755	0.5918513		0.857223	
SlopeF-SlopeC	1.101621	0.1686848		0.9999488	



7.6.974 Vitvi02g00187: type5

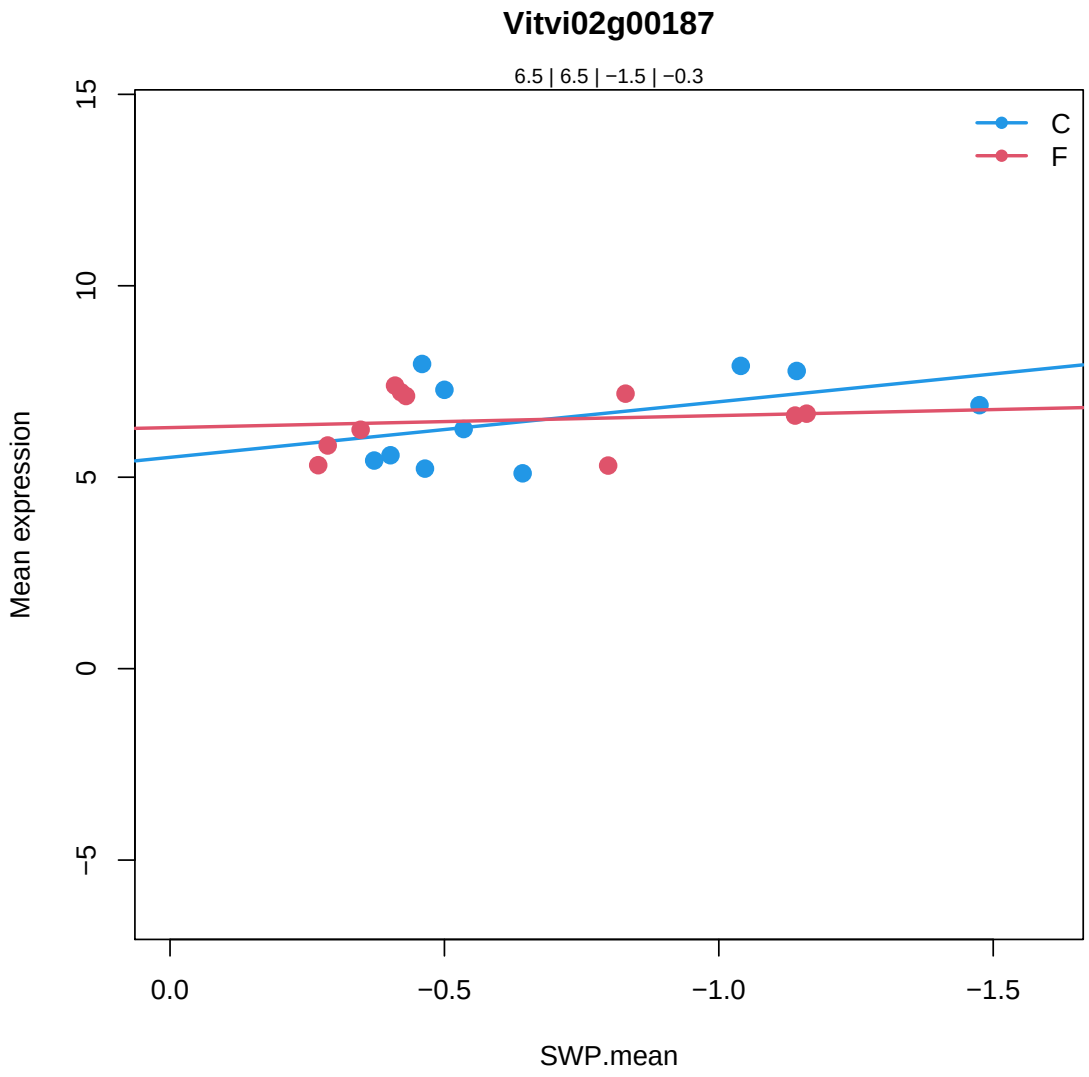
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi02g00187
        20.2.1
        stress.abiotic.heat
        Heat shock protein 70 (Hsp 70) family protein |
        Chr5:16807697-16810480 REVERSE LENGTH=668 |
        201606

Vitvi02g00187
        29.6
        protein.folding
        Heat shock protein 70 (Hsp 70) family protein |
        Chr5:16807697-16810480 REVERSE LENGTH=668 |
        201606
```

Coefficients for Vitvi02g00187.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.539731	6.428266e-17	***	1.446194e-16	***
SlopeC	-1.451927	0.07068034	.	0.5610989	
MeanF-MeanC	-0.05280152	0.8930282		0.9718495	
SlopeF-SlopeC	1.138185	0.3276102		0.9999488	


Vitvi02g00187
6.5 | 6.5 | −1.5 | −0.3
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

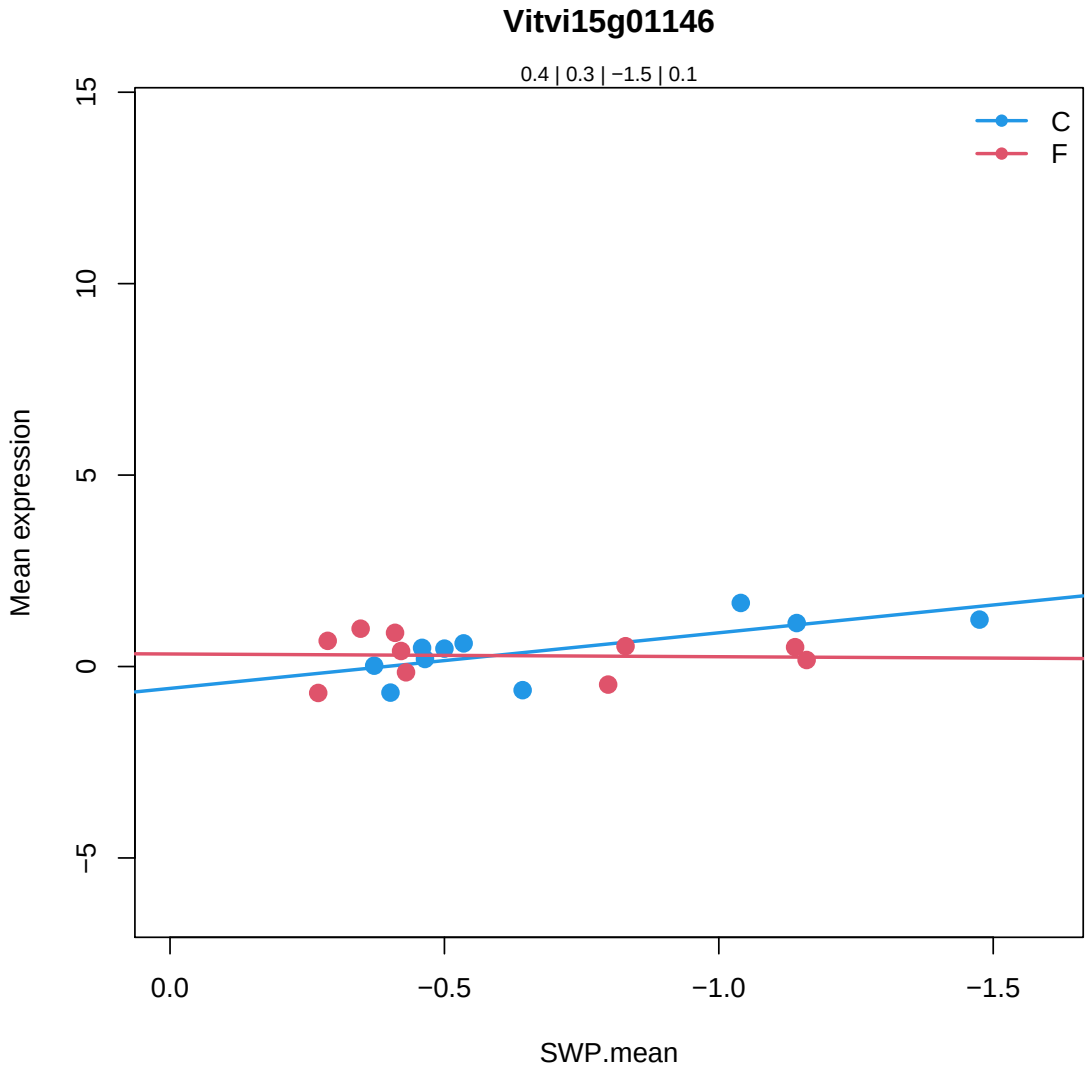
7.6.975 Vitvi15g01146: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g01146
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr5:5543834-5546386 FORWARD LENGTH=850 |
        201606
```

Coefficients for Vitvi15g01146.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4498396	0.0183206	*	0.01927938	*
SlopeC	-1.452373	0.007306367	**	0.2775469	
MeanF-MeanC	-0.1664114	0.5112706		0.8131635	
SlopeF-SlopeC	1.523929	0.0487875	*	0.9999488	



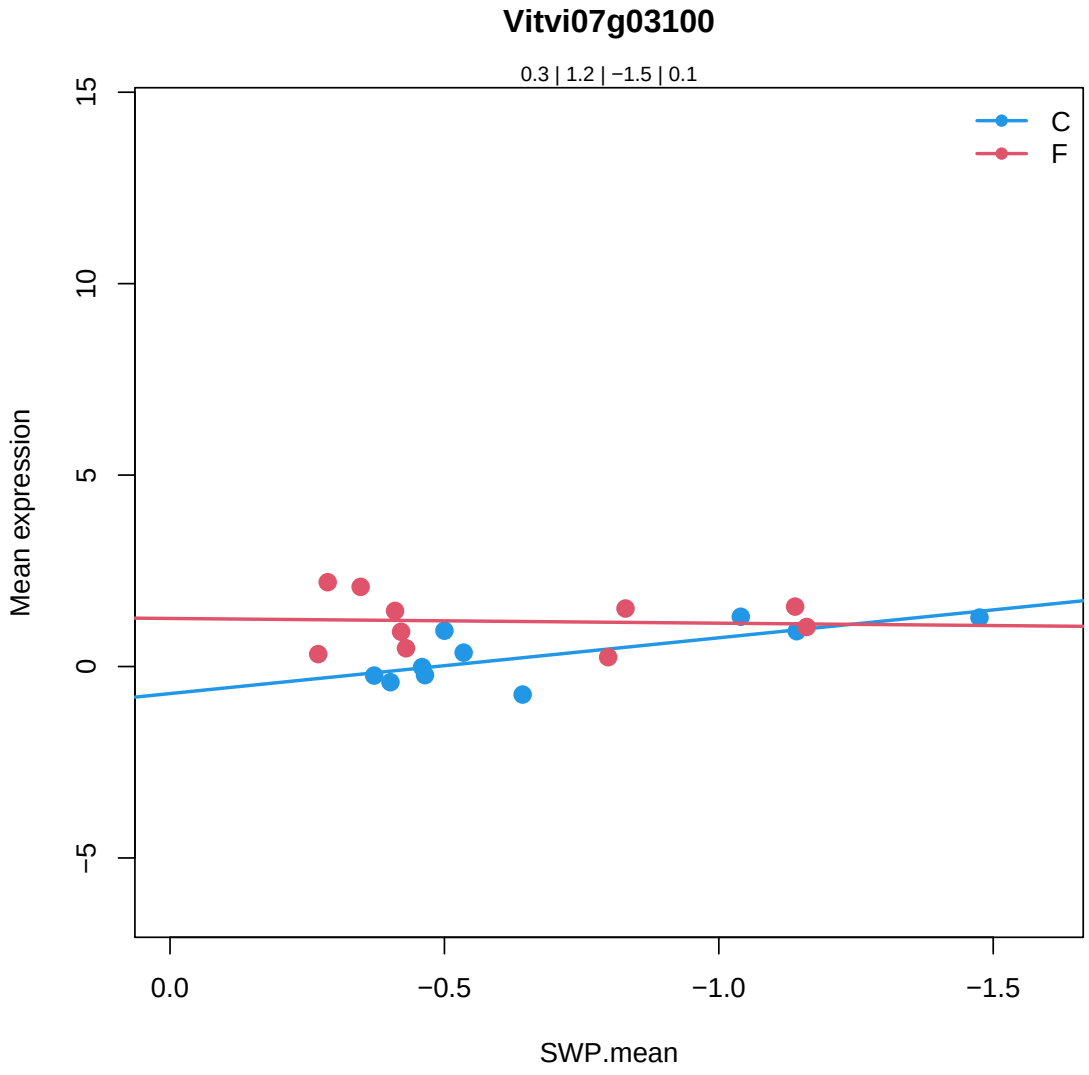
7.6.976 Vitvi07g03100: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g03100
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        Pentatricopeptide repeat (PPR) superfamily protein |
        Chr3:18437845-18440010 FORWARD LENGTH=721 |
        201606
```

Coefficients for Vitvi07g03100.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3178312	0.1127528		0.1164506	
SlopeC	−1.456836	0.01255164	*	0.3271124	
MeanF−MeanC	0.8620873	0.004513181	**	0.04204762	*
SlopeF−SlopeC	1.58038	0.05998928	.	0.9999488	



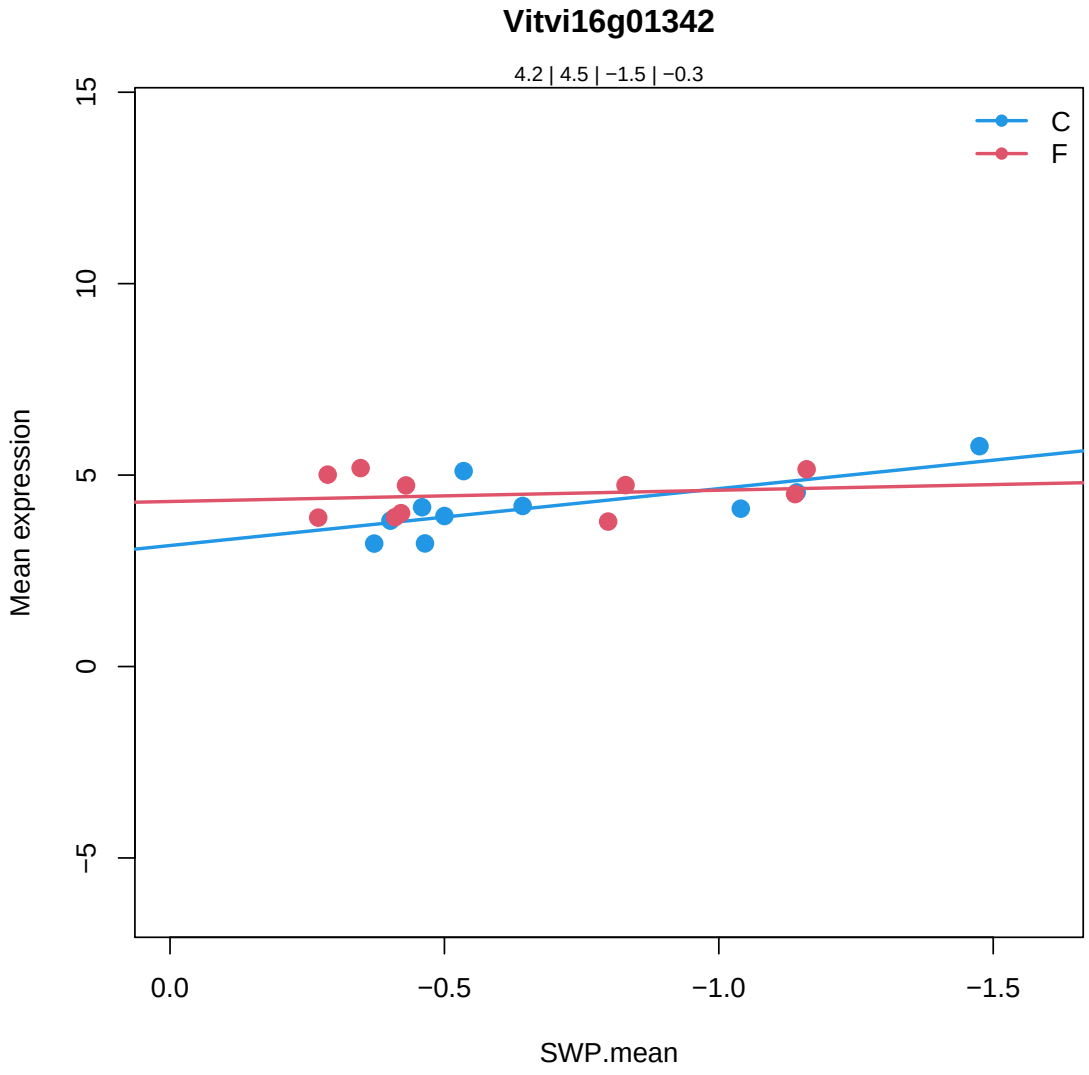
7.6.977 Vitvi16g01342: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01342
        29.2.1.1.1.1.530
        protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subuni
        30S ribosomal protein |
        Chr5:8365690-8367178 FORWARD LENGTH=308 |
        201606
```

Coefficients for Vitvi16g01342.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.204788	6.178553e-17	***	1.39537e-16	***
SlopeC	-1.485787	0.006225227	**	0.2647742	
MeanF-MeanC	0.2845484	0.2657451		0.6280799	
SlopeF-SlopeC	1.191357	0.1168513		0.9999488	



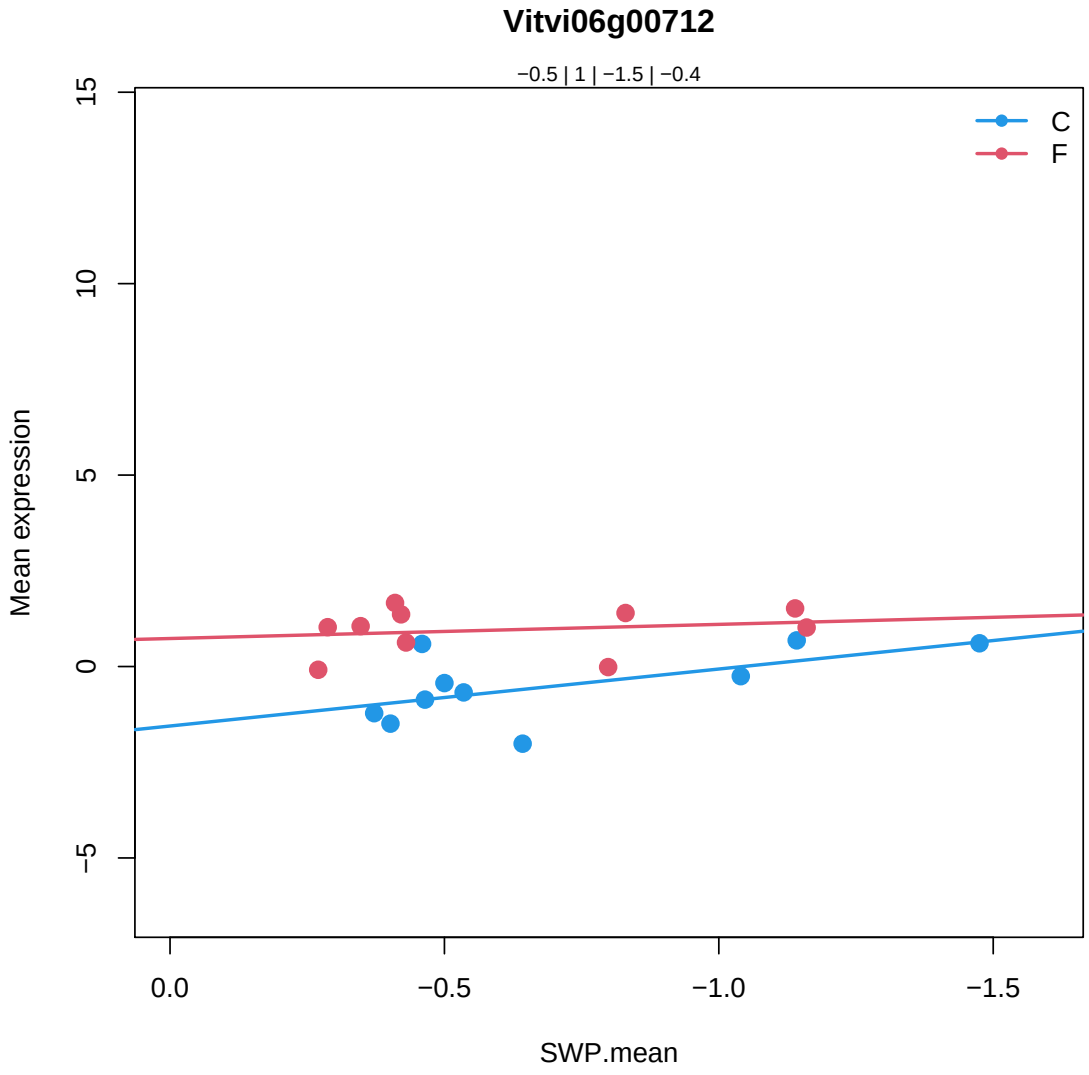
7.6.978 Vitvi06g00712: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00712
        26.2
        misc.UDP glucosyl and glucoronyl transferases
        UDP-Glycosyltransferase superfamily protein |
        Chr2:12874658-12876122 FORWARD LENGTH=456 |
        201606
```

Coefficients for Vitvi06g00712.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.5073415	0.02473766	*	0.02595343	*
SlopeC	-1.488268	0.01861511	*	0.3661052	
MeanF-MeanC	1.463744	6.73865e-05	***	0.001277494	**
SlopeF-SlopeC	1.118902	0.2120851		0.9999488	



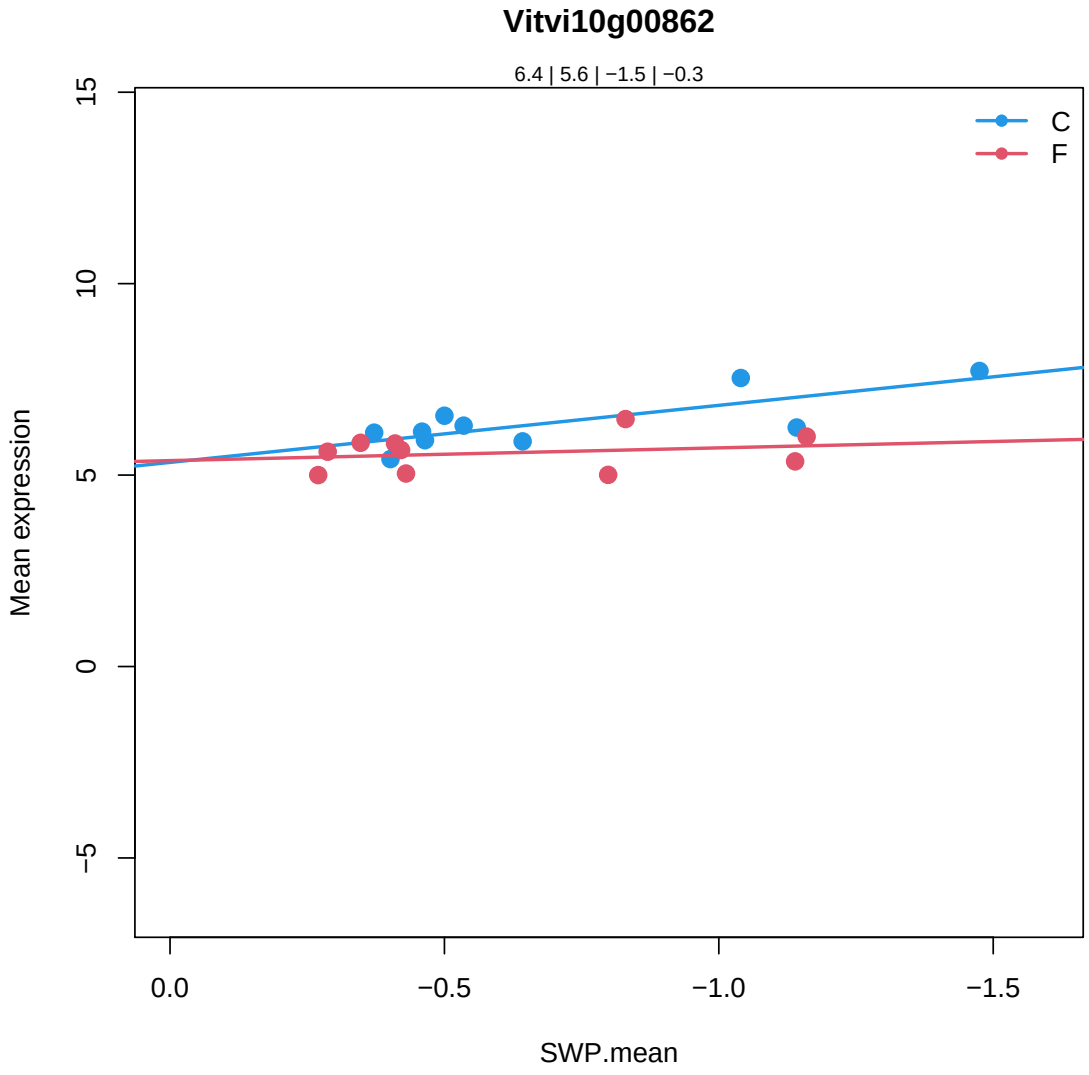
7.6.979 Vitvi10g00862: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00862
        20.2.3
        stress.abiotic.drought/salt
        Early-responsive to dehydration stress protein (ERD4) |
        Chr1:10715892-10718799 FORWARD LENGTH=724 |
        201606
```

Coefficients for Vitvi10g00862.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.378891	6.583362e-22	***	8.158016e-21	***
SlopeC	-1.490197	0.00228778	**	0.1817854	
MeanF-MeanC	-0.7986152	0.001462482	**	0.01706827	*
SlopeF-SlopeC	1.157242	0.08505315	.	0.9999488	



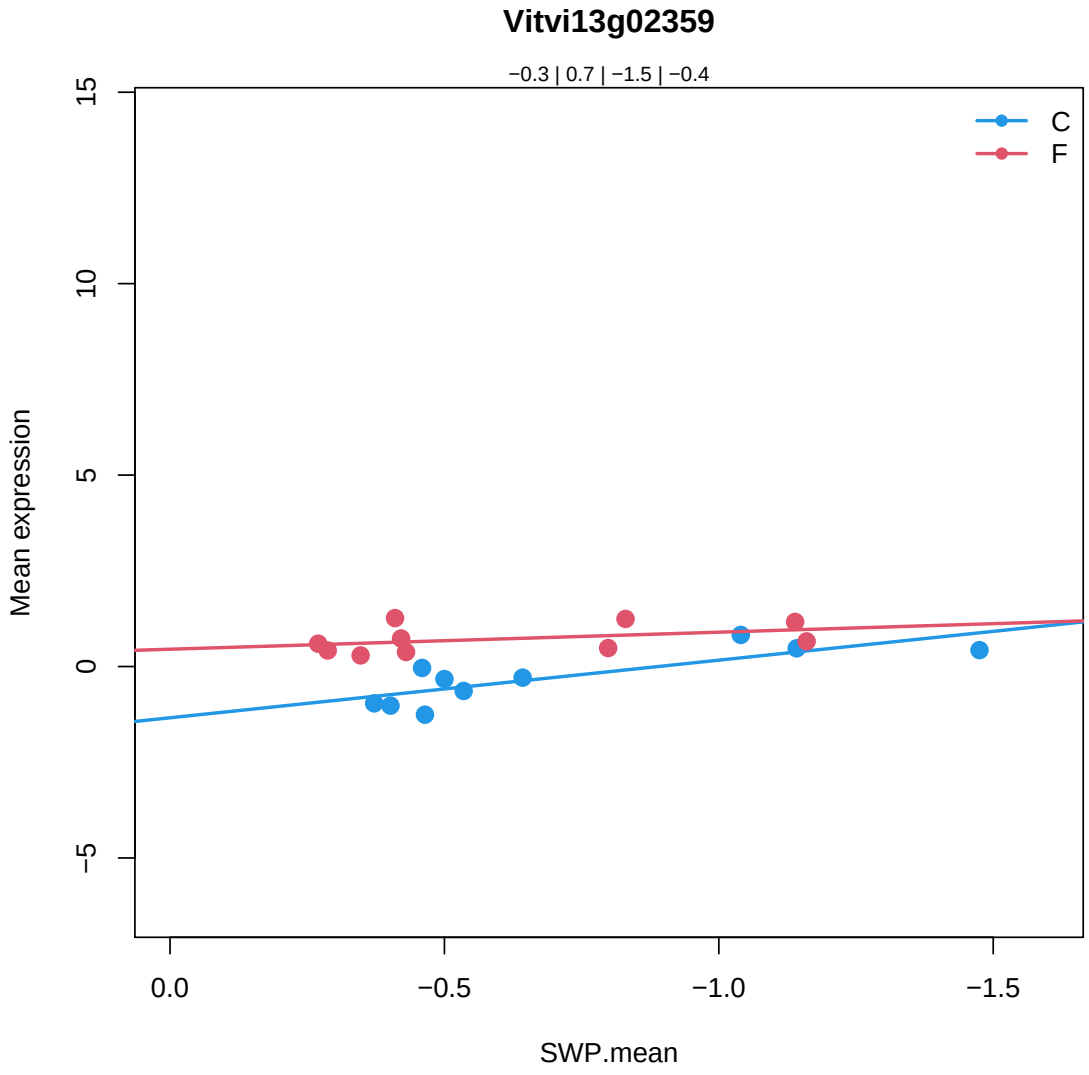
7.6.980 Vitvi13g02359: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g02359
        27.2
        RNA.transcription
        RNA polymerase II fifth largest subunit%2C E |
        Chr3:20173673-20175297 FORWARD LENGTH=233 |
        201606
```

Coefficients for Vitvi13g02359.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.28085	0.04842468	*	0.05043659	.
SlopeC	-1.504967	0.0005830364	***	0.1005065	
MeanF-MeanC	1.003501	2.853815e-05	***	0.0006213979	***
SlopeF-SlopeC	1.060049	0.06991798	.	0.9999488	



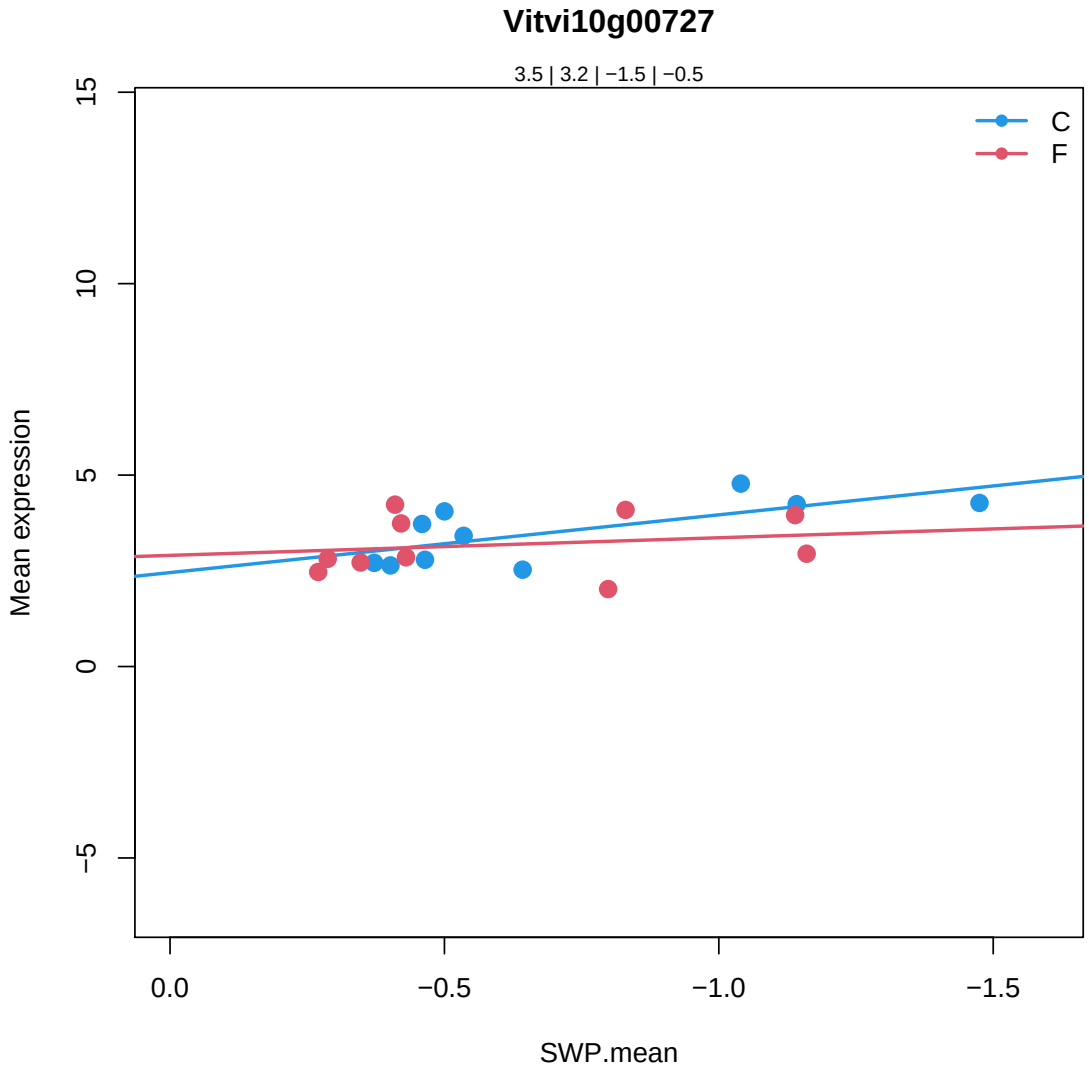
7.6.981 Vitvi10g00727: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00727
        35.2
        not assigned.unknown
        S-adenosyl-L-methionine-dependent methyltransferases superfamily prote
        Chr1:10430025-10431161 FORWARD LENGTH=378 |
        201606
```

Coefficients for Vitvi10g00727.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.514183	7.242488e-14	***	1.124478e-13	***
SlopeC	-1.50876	0.016338	*	0.3492619	
MeanF-MeanC	-0.3310847	0.2730593		0.6366788	
SlopeF-SlopeC	1.048456	0.2369698		0.9999488	



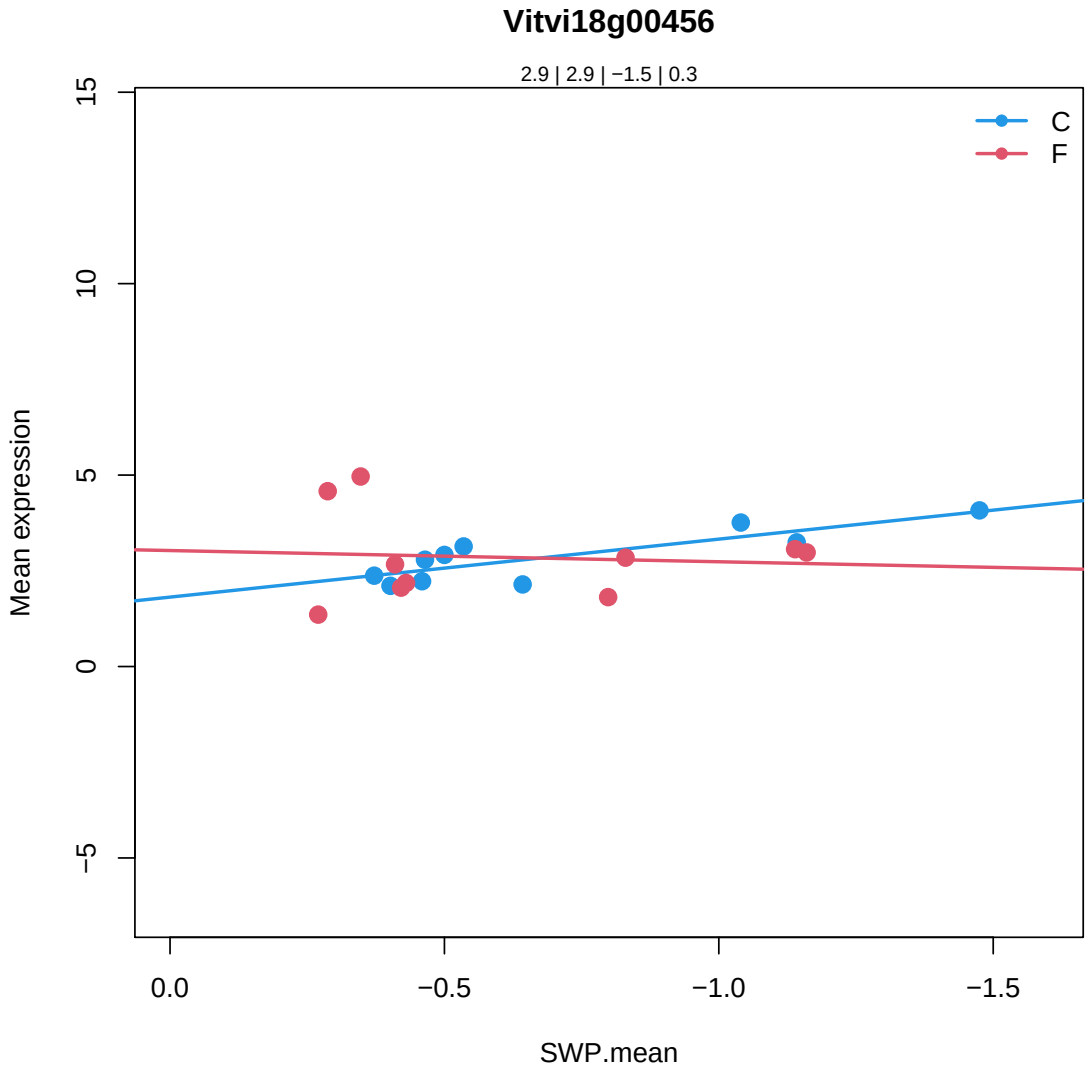
7.6.982 Vitvi18g00456: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00456
        27.4
        RNA.RNA binding
        RNA-binding (RRM/RBD/RNP motifs) family protein |
        Chr4:5795075-5797193 REVERSE LENGTH=244 |
        201606
```

Coefficients for Vitvi18g00456.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.877216	2.388256e-10	***	3.079418e-10	***
SlopeC	-1.514254	0.04784277	*	0.5004518	
MeanF-MeanC	-0.02668527	0.9426689		0.9852678	
SlopeF-SlopeC	1.807297	0.1068721		0.9999488	



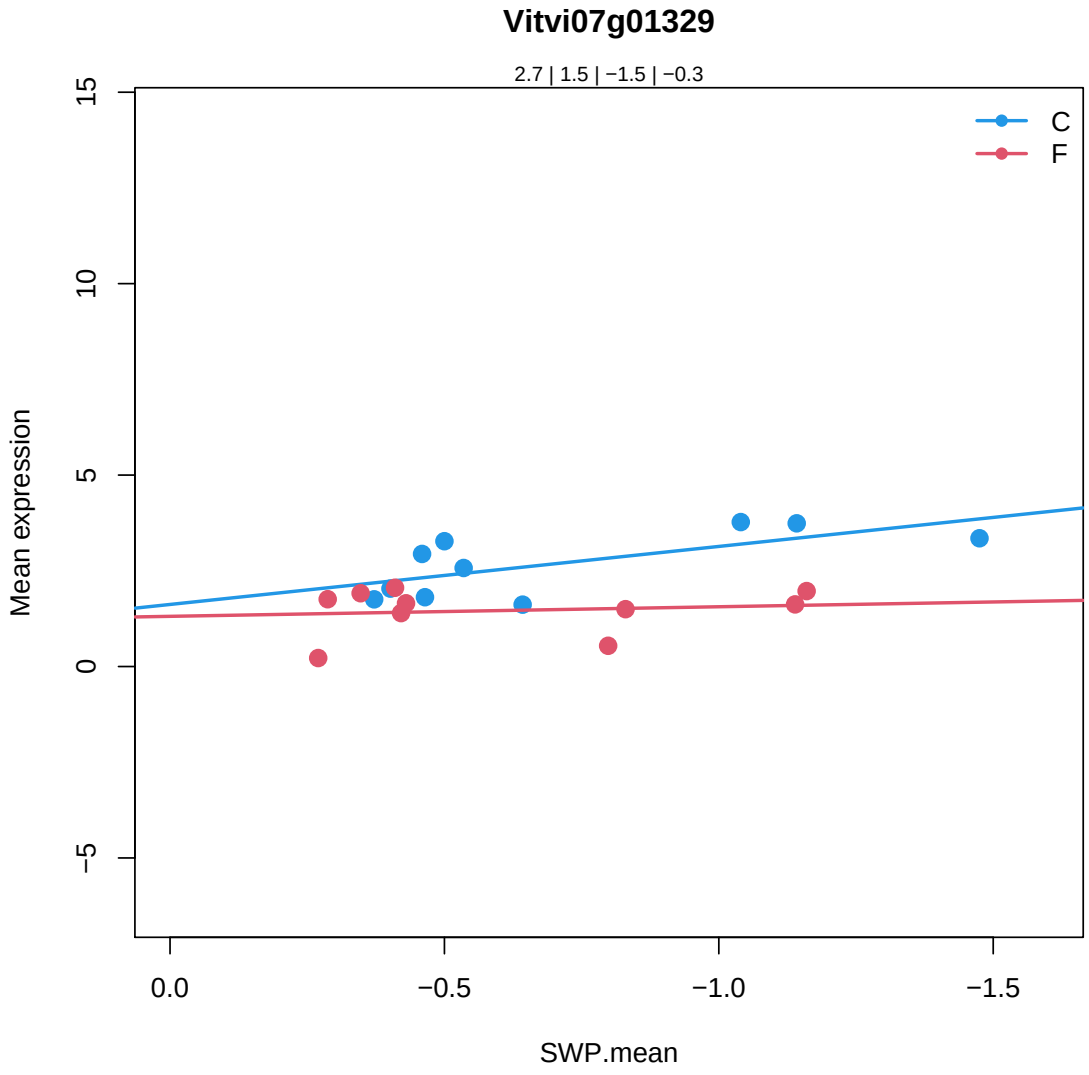
7.6.983 Vitvi07g01329: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01329
        29.2.1.1.3.2
        protein.synthesis.ribosomal protein.prokaryotic.unknown organellar.50S
        Ribosomal protein L25/Gln-tRNA synthetase%2C anti-codon-binding domain
        Chr5:26701233-26702531 REVERSE LENGTH=249 |
        201606
```

Coefficients for Vitvi07g01329.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.686338	3.285794e-12	***	4.584172e-12	***
SlopeC	-1.5151	0.01010604	*	0.3042563	
MeanF-MeanC	-1.22352	0.0001964968	***	0.00321008	**
SlopeF-SlopeC	1.26484	0.1282284		0.9999488	



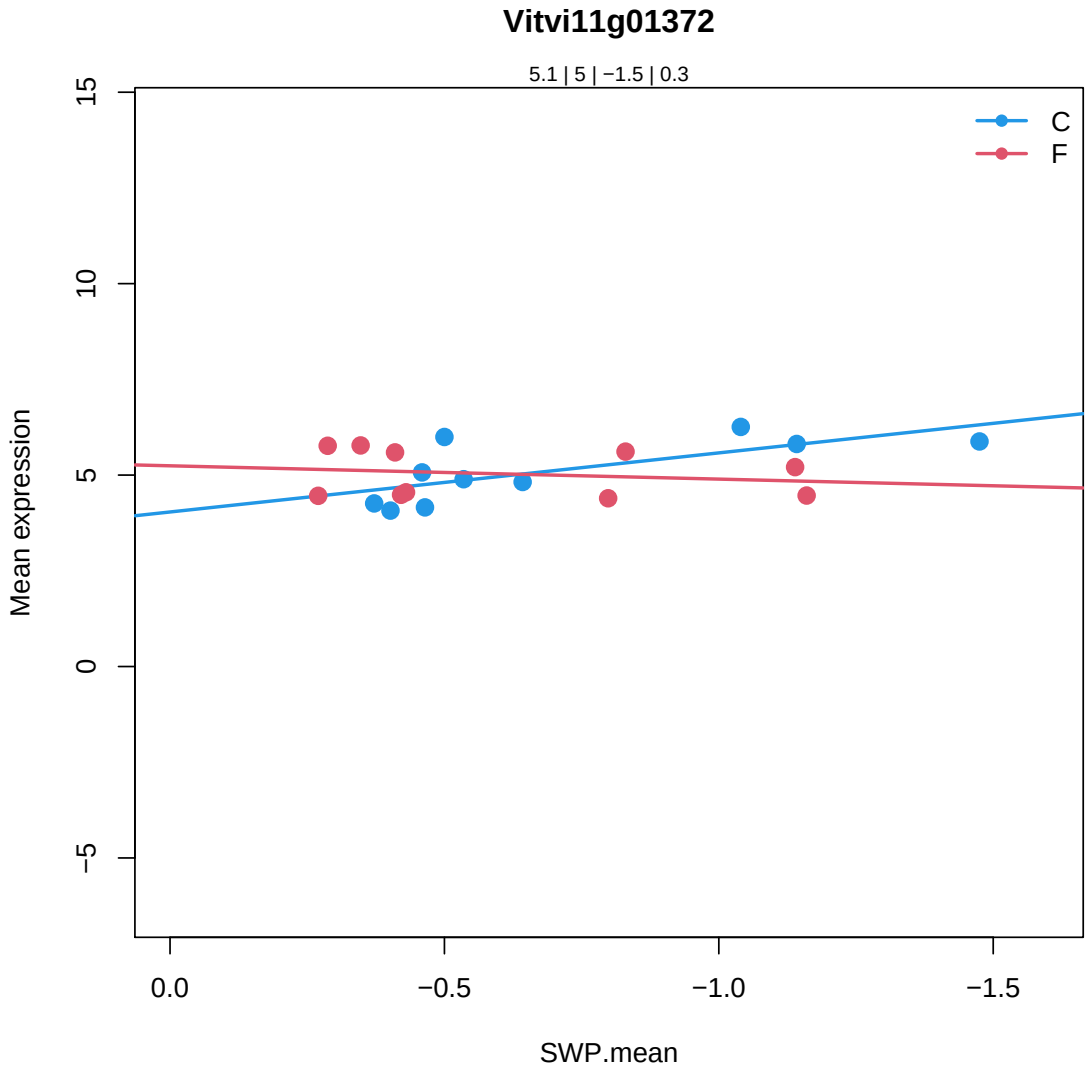
7.6.984 Vitvi11g01372: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g01372
        35.2
        not assigned.unknown
        cotton fiber protein |
        Chr4:13240403-13241263 REVERSE LENGTH=286 |
        201606
```

Coefficients for Vitvi11g01372.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.121222	3.520043e-18	***	1.039689e-17	***
SlopeC	-1.543159	0.007219073	**	0.2775469	
MeanF-MeanC	-0.09068252	0.7347937		0.920122	
SlopeF-SlopeC	1.890763	0.02324771	*	0.9999488	



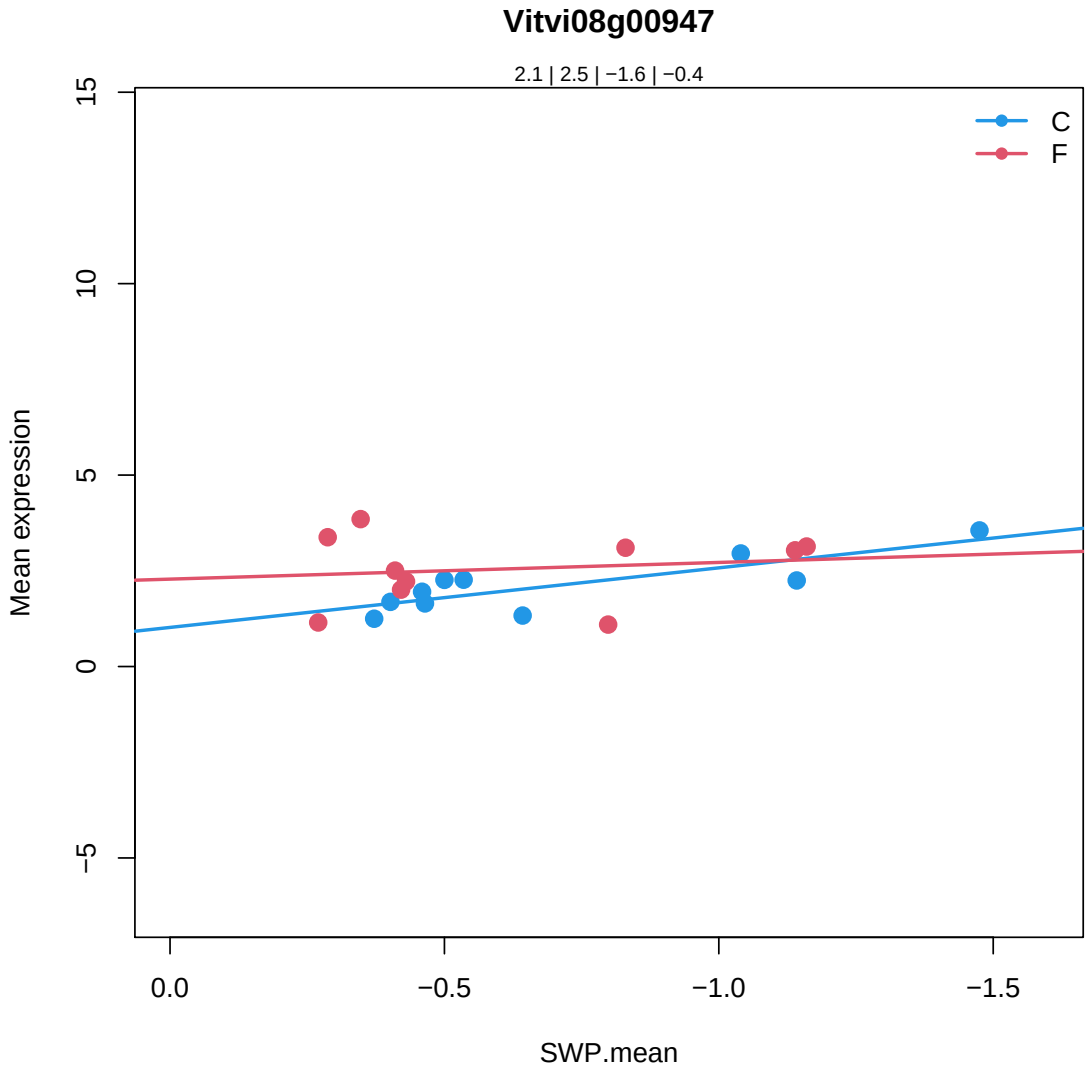
7.6.985 Vitvi08g00947: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g00947
        1.1.1.2
        PS.lightreaction.photosystem II.PSII polypeptide subunits
        thylakoid lumenal protein (Mog1/PsbP/DUF1795-like photosystem II react
        Chr3:20984807-20985913 FORWARD LENGTH=262 |
        201606
```

Coefficients for Vitvi08g00947.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.11524	3.04576e-09	***	3.781645e-09	***
SlopeC	−1.556099	0.01859056	*	0.3660946	
MeanF−MeanC	0.4325672	0.1779484		0.5121393	
SlopeF−SlopeC	1.120267	0.2313121		0.9999488	



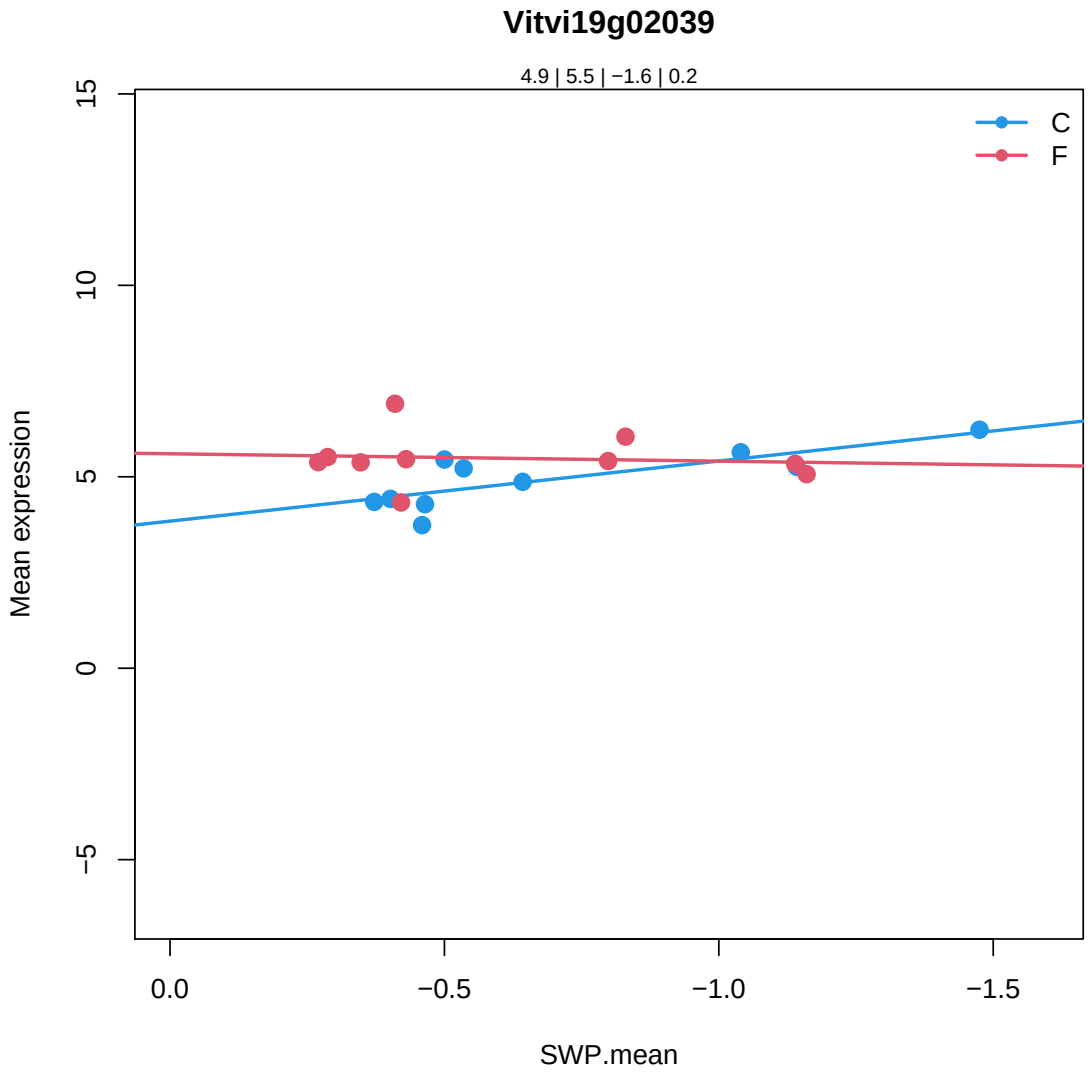
7.6.986 Vitvi19g02039: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g02039
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi19g02039.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.945639	4.074331e-18	***	1.18175e-17	***
SlopeC	-1.570053	0.005261189	**	0.2574116	
MeanF-MeanC	0.5378022	0.0484205	*	0.2344426	
SlopeF-SlopeC	1.763052	0.02882351	*	0.9999488	



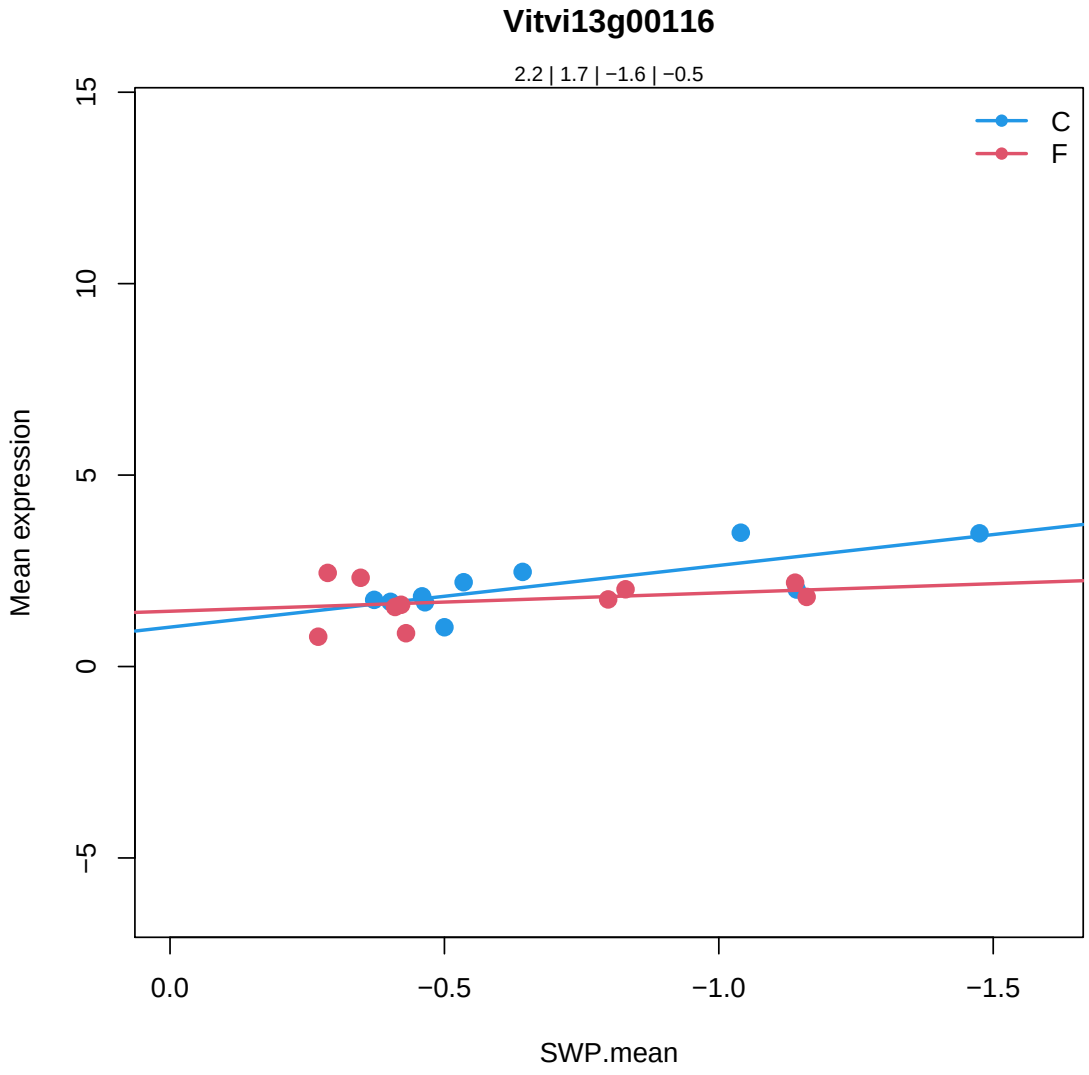
7.6.987 Vitvi13g00116: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00116
        27.3.44
        RNA.regulation of transcription.chromatin remodeling factors
        Integrase-type DNA-binding superfamily protein |
        Chr2:16848665-16849850 REVERSE LENGTH=348 |
        201606
```

Coefficients for Vitvi13g00116.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.162112	1.932432e-11	***	2.604716e-11	***
SlopeC	-1.611757	0.002639293	**	0.1962347	
MeanF-MeanC	-0.426496	0.09094627	.	0.3454281	
SlopeF-SlopeC	1.132392	0.1231173		0.9999488	



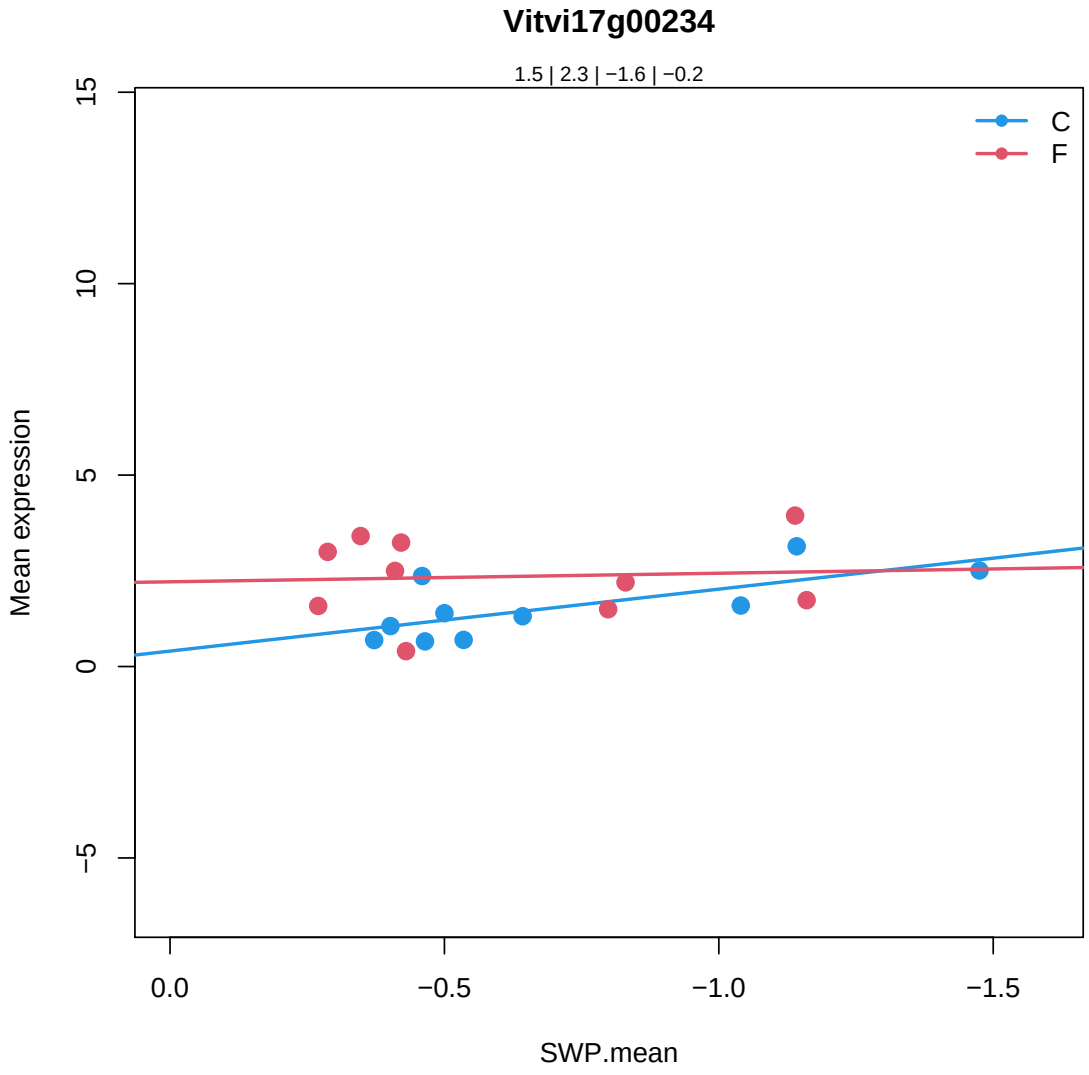
7.6.988 Vitvi17g00234: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00234
        26.3
        misc.gluco-, galacto- and mannosidases
        B-S glucosidase 44 |
        Chr3:6191586-6194124 FORWARD LENGTH=512 |
        201606
```

Coefficients for Vitvi17g00234.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.540657	8.003222e-06	***	9.060094e-06	***
SlopeC	-1.617545	0.0388646	*	0.4697654	
MeanF-MeanC	0.8082059	0.04198657	*	0.2133198	
SlopeF-SlopeC	1.394215	0.2162015		0.9999488	



7.6.989 Vitvi11g00339: * type5

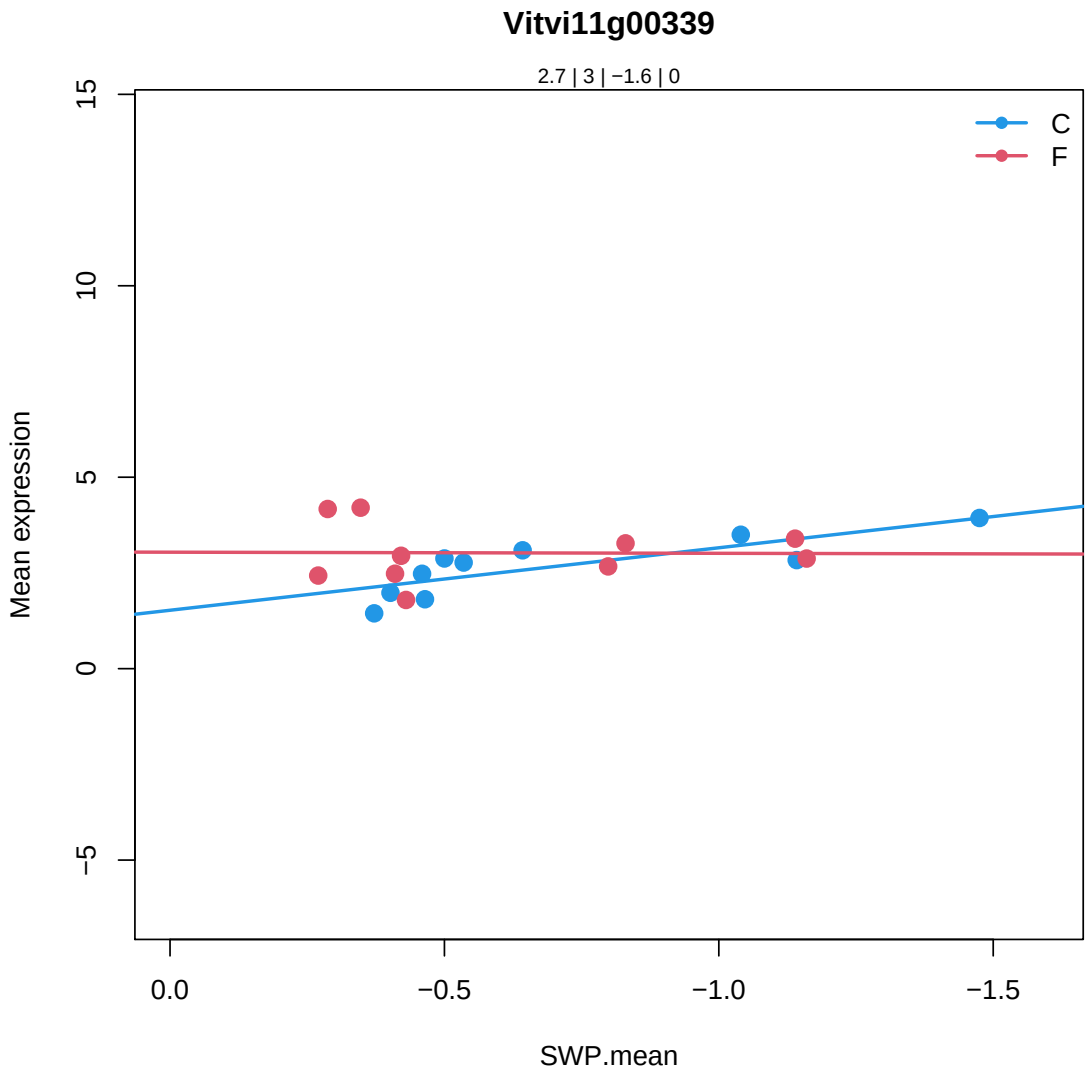
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00339
        27.3.23
        RNA.regulation of transcription.heat-shock transcription factor family
        heat shock transcription factor C1 |
        Chr3:8941455-8942531 FORWARD LENGTH=330 |
        201606

Vitvi11g00339
        20.2.1
        stress.abiotic.heat
        heat shock transcription factor C1 |
        Chr3:8941455-8942531 FORWARD LENGTH=330 |
        201606
```

Coefficients for Vitvi11g00339.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.672273	5.736418e-12	***	7.911191e-12	***
SlopeC	-1.631756	0.007240258	**	0.2775469	
MeanF-MeanC	0.3517247	0.2218079		0.5733079	
SlopeF-SlopeC	1.660741	0.05503922	.	0.9999488	


Vitvi11g00339
2.7 | 3 | −1.6 | 0
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

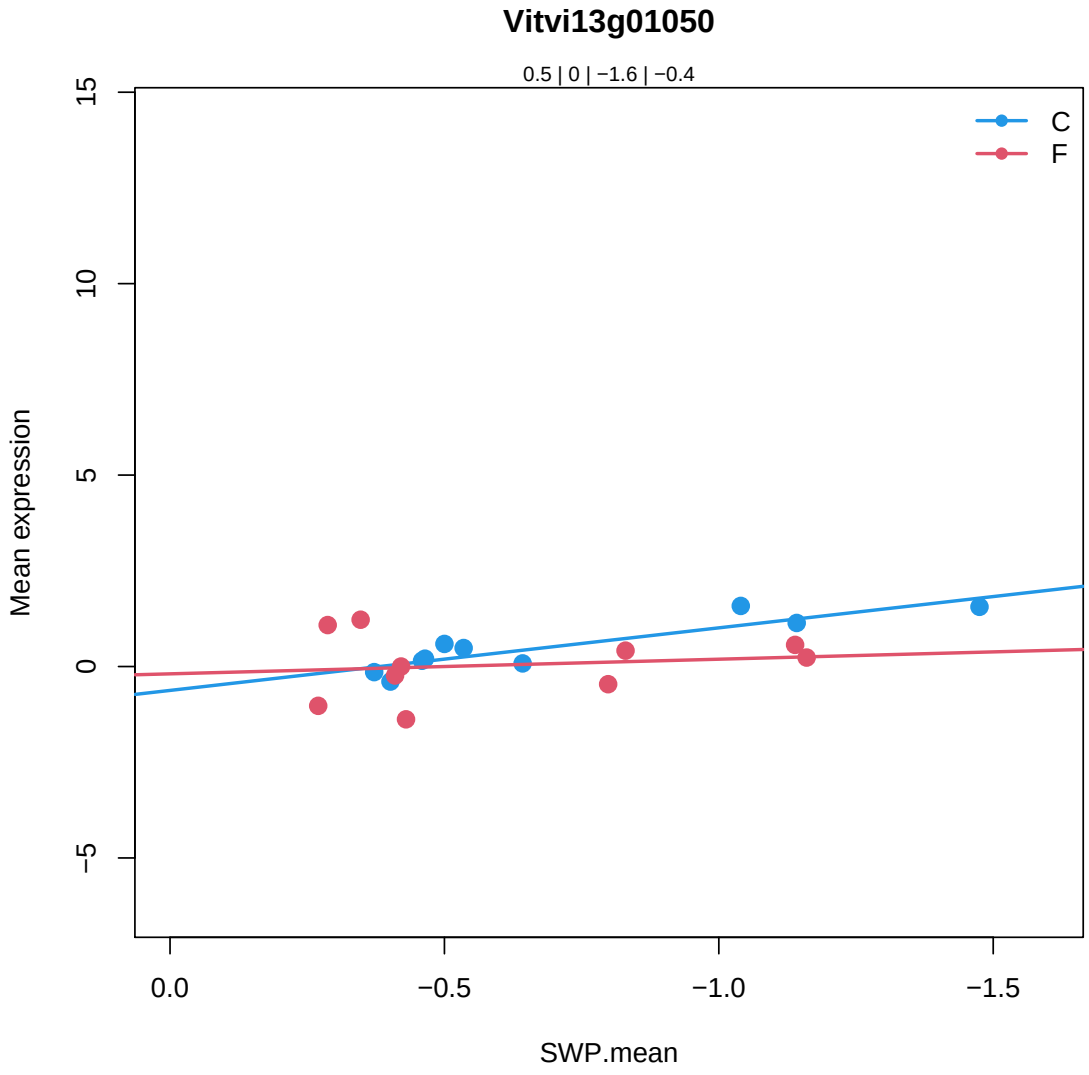
7.6.990 Vitvi13g01050: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g01050
        35.2
        not assigned.unknown
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi13g01050.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.5247521	0.01491315	*	0.0157338	*
SlopeC	-1.633953	0.007320159	**	0.2775469	
MeanF-MeanC	-0.4831327	0.09922176	.	0.3626024	
SlopeF-SlopeC	1.251894	0.1418538		0.9999488	



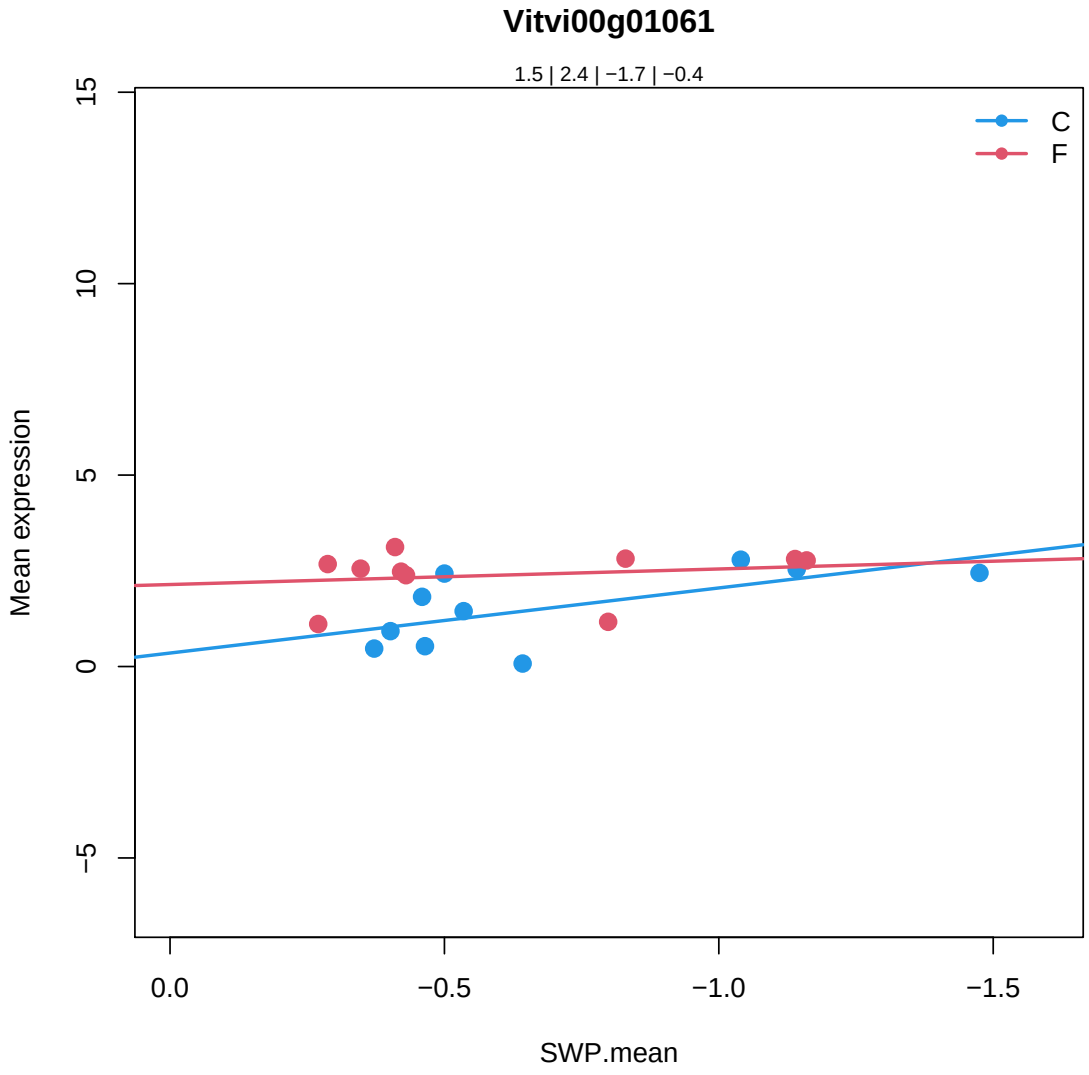
7.6.991 Vitvi00g01061: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi00g01061
        29.2.1.1.3.2
        protein.synthesis.ribosomal protein.prokaryotic.unknown organellar.50S
        Ribosomal protein L25/Gln-tRNA synthetase%2C anti-codon-binding domain
        Chr5:26701233-26702531 REVERSE LENGTH=249 |
        201606
```

Coefficients for Vitvi00g01061.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.547063	6.495818e-07	***	7.533804e-07	***
SlopeC	-1.7003	0.01199121	*	0.3229093	
MeanF-MeanC	0.8416015	0.01408382	*	0.09748667	.
SlopeF-SlopeC	1.293995	0.1747658		0.9999488	



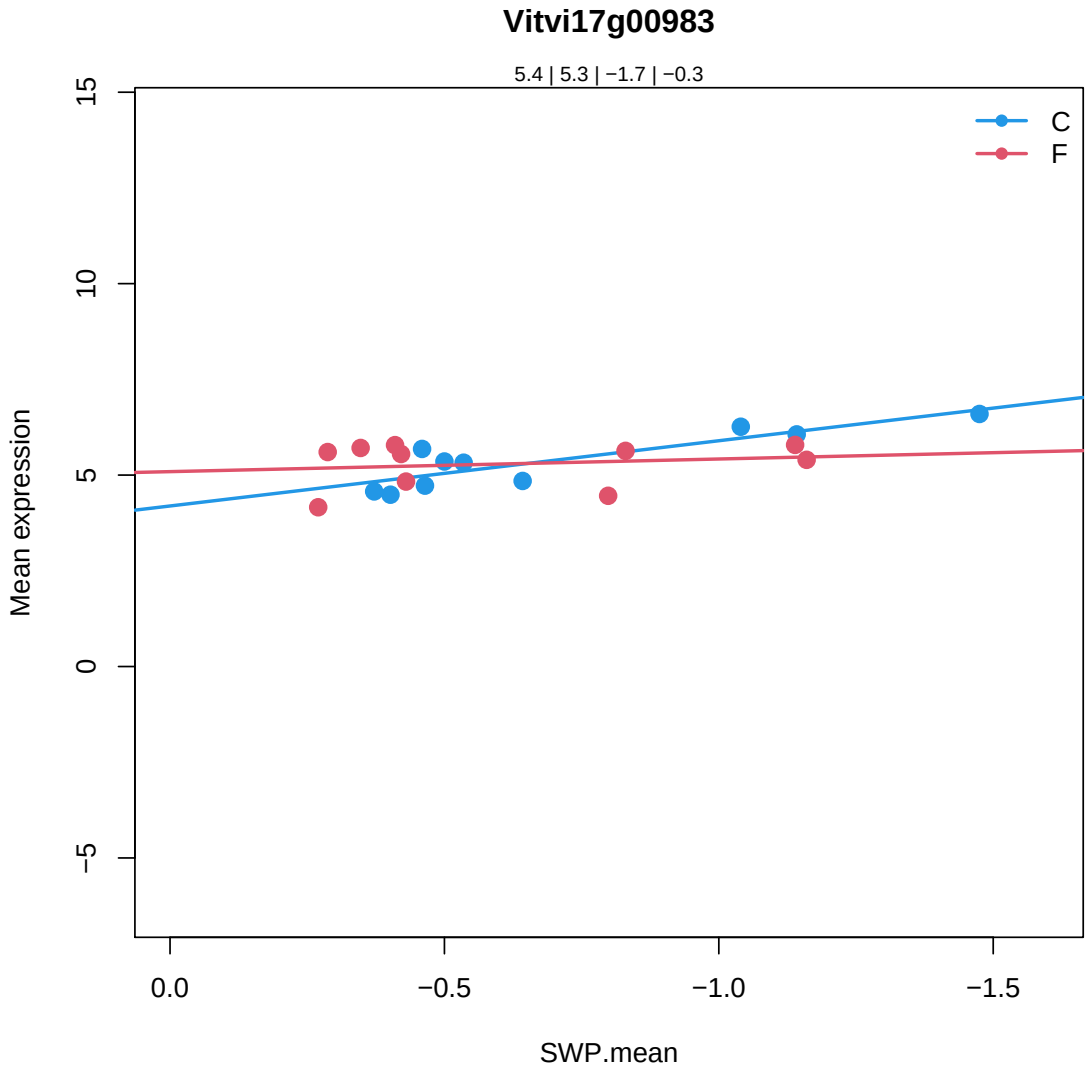
7.6.992 Vitvi17g00983: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi17g00983
        13.2.3.4
        amino acid metabolism.degradation.aspartate family.methionine
        S-adenosyl-L-homocysteine hydrolase |
        Chr4:8055176-8056676 FORWARD LENGTH=364 |
        201606
```

Coefficients for Vitvi17g00983.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.391223	5.299681e-20	***	2.7864e-19	***
SlopeC	-1.703942	0.00100803	**	0.1271346	
MeanF-MeanC	-0.1002029	0.6643193		0.8892987	
SlopeF-SlopeC	1.374057	0.05166023	.	0.9999488	



7.6.993 Vitvi06g00668: type5

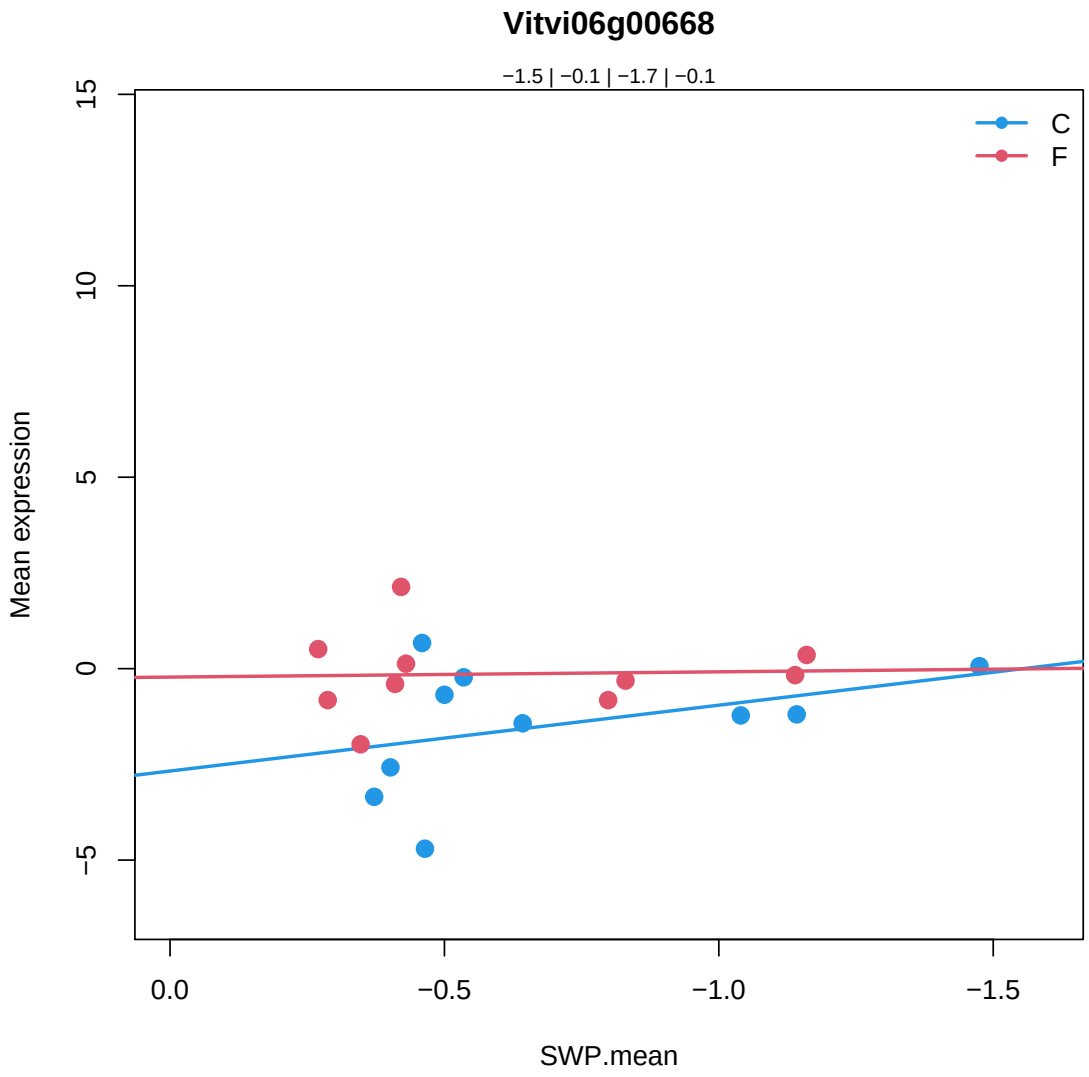
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi06g00668
        30.6
        signalling.MAP kinases
        mitogen-activated protein kinase kinase kinase 13 |
        Chr1:2194279-2195778 REVERSE LENGTH=499 |
        201606

Vitvi06g00668
        29.4
        protein.postranslational modification
        mitogen-activated protein kinase kinase kinase 13 |
        Chr1:2194279-2195778 REVERSE LENGTH=499 |
        201606
```

Coefficients for Vitvi06g00668.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.464965	0.001070088	**	0.001158071	**
SlopeC	-1.720059	0.1254121		0.6460361	
MeanF-MeanC	1.328022	0.02435779	*	0.1456157	
SlopeF-SlopeC	1.582692	0.3351886		0.9999488	


Vitvi06g00668
−1.5 | −0.1 | −1.7 | −0.1
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

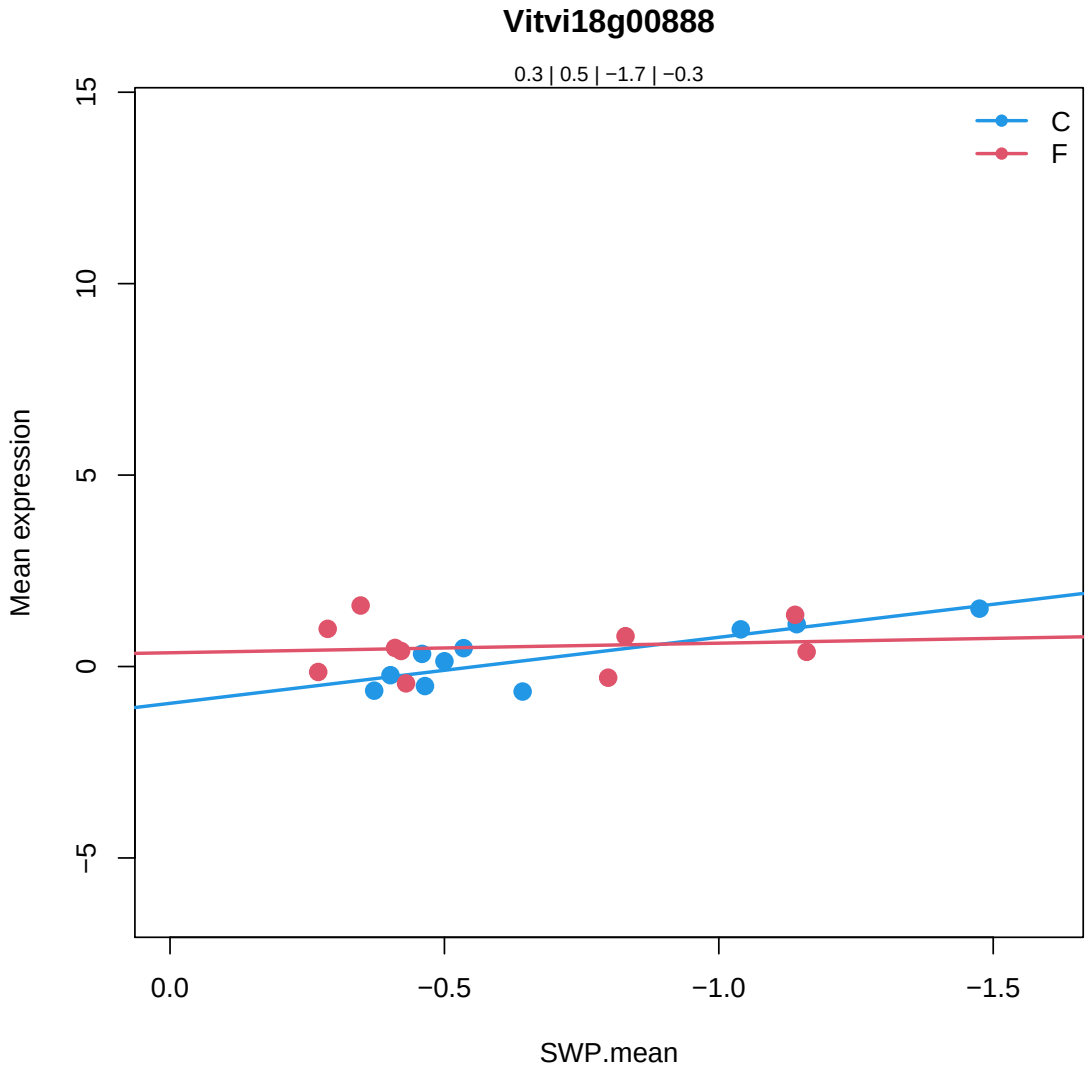
7.6.994 Vitvi18g00888: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g00888
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        Tetratricopeptide repeat (TPR)-like superfamily protein |
        Chr2:6831855-6833594 REVERSE LENGTH=579 |
        201606
```

Coefficients for Vitvi18g00888.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.2511973	0.1754668		0.1802078	
SlopeC	-1.724159	0.002307552	**	0.1817854	
MeanF-MeanC	0.2605364	0.3155807		0.6775717	
SlopeF-SlopeC	1.473723	0.06005934	.	0.9999488	



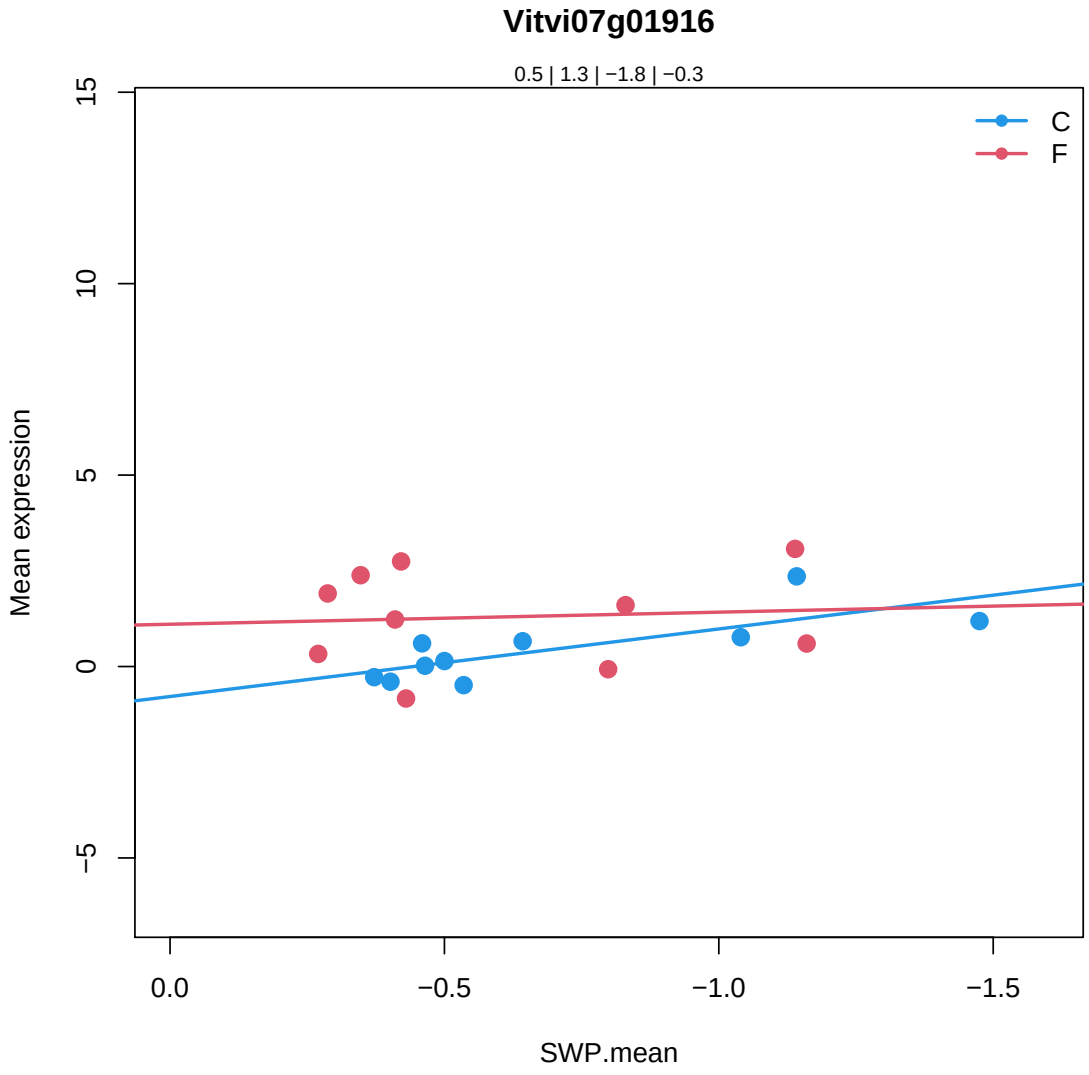
7.6.995 Vitvi07g01916: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01916
        26.3.2
        misc.gluco-, galacto- and mannosidases.beta-galactosidase
        beta-galactosidase 10 |
        Chr5:25537242-25541315 FORWARD LENGTH=741 |
        201606
```

Coefficients for Vitvi07g01916.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4571496	0.1359567		0.1401211	
SlopeC	-1.764483	0.04316903	*	0.48214	
MeanF-MeanC	0.8391124	0.05708875	.	0.2603671	
SlopeF-SlopeC	1.448762	0.2487201		0.9999488	



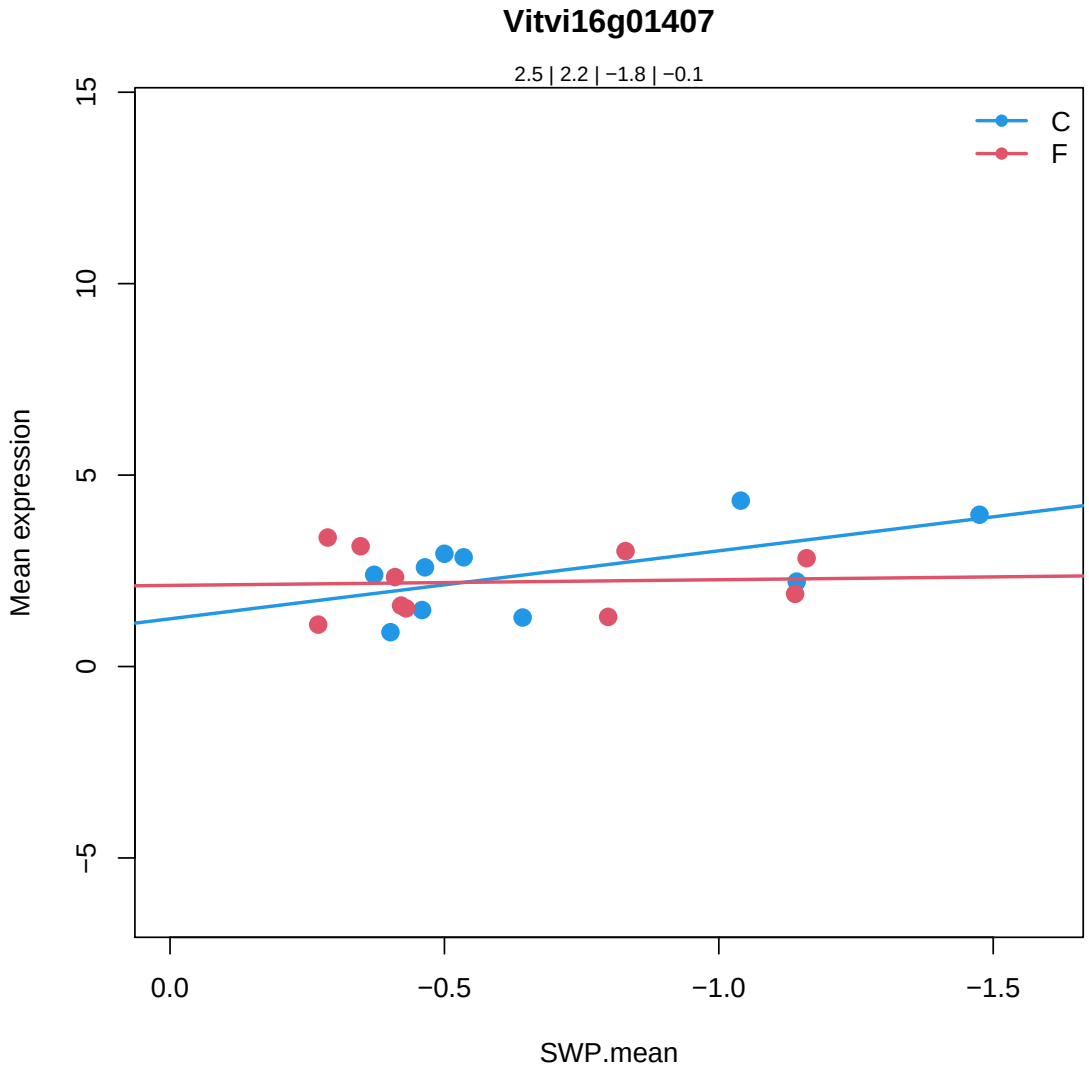
7.6.996 Vitvi16g01407: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01407
        35.2
        not assigned.unknown
        gamma-irradiation and mitomycin c induced 1 |
        Chr5:8251378-8261401 REVERSE LENGTH=1598 |
        201606
```

Coefficients for Vitvi16g01407.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.494859	3.342244e-09	***	4.145036e-09	***
SlopeC	-1.776023	0.02286552	*	0.3972124	
MeanF-MeanC	-0.2861575	0.4456018		0.7758583	
SlopeF-SlopeC	1.627958	0.1456835		0.9999488	



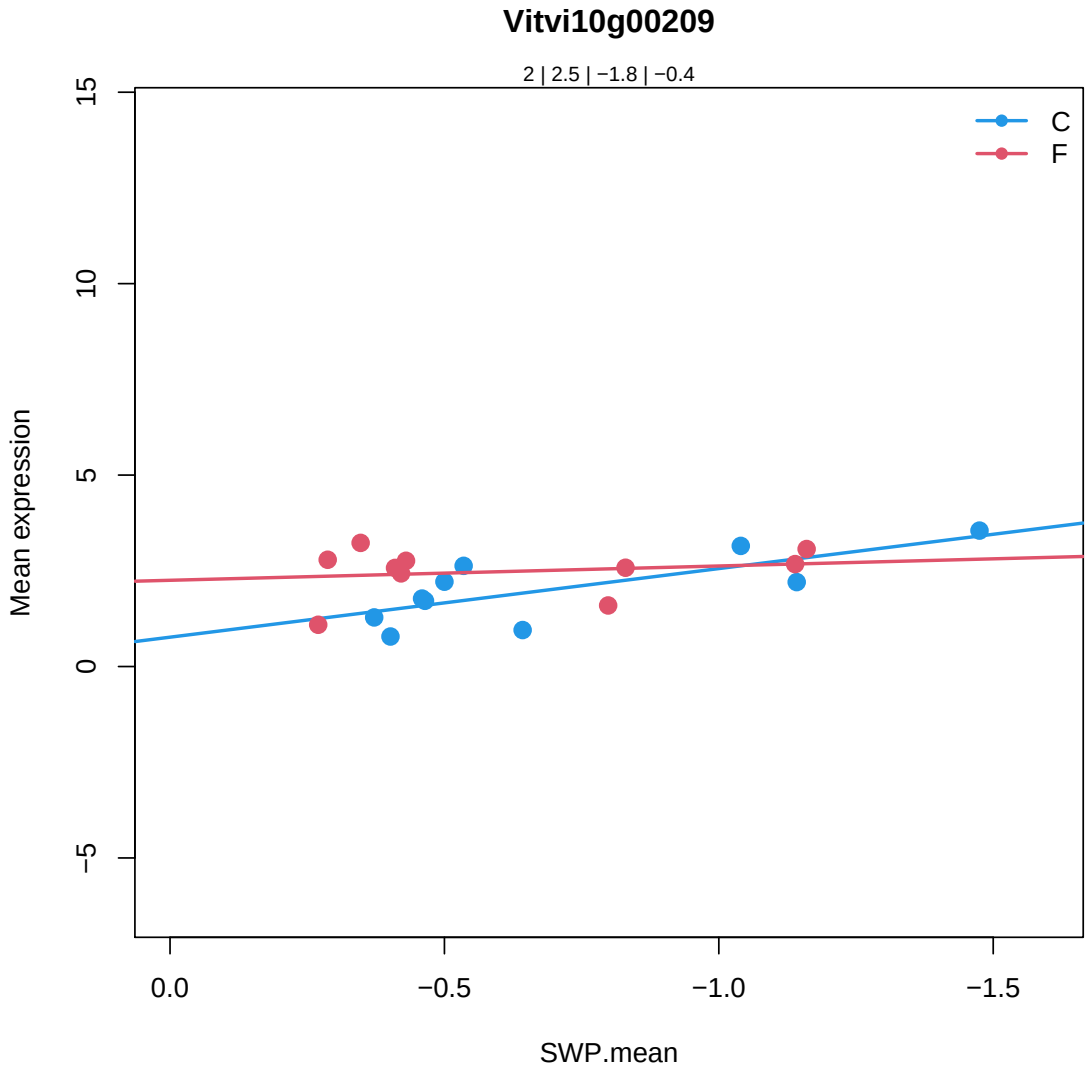
7.6.997 Vitvi10g00209: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00209
        29.5.3
        protein.degradation.cysteine protease
        Cystatin/monellin superfamily protein |
        Chr5:19286596-19286964 REVERSE LENGTH=122 |
        201606
```

Coefficients for Vitvi10g00209.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.025897	9.224933e-10	***	1.164346e-09	***
SlopeC	-1.791669	0.00354923	**	0.2245324	
MeanF-MeanC	0.453612	0.1175142		0.4025964	
SlopeF-SlopeC	1.417894	0.09600652	.	0.9999488	



7.6.998 Vitvi18g01299: * type5

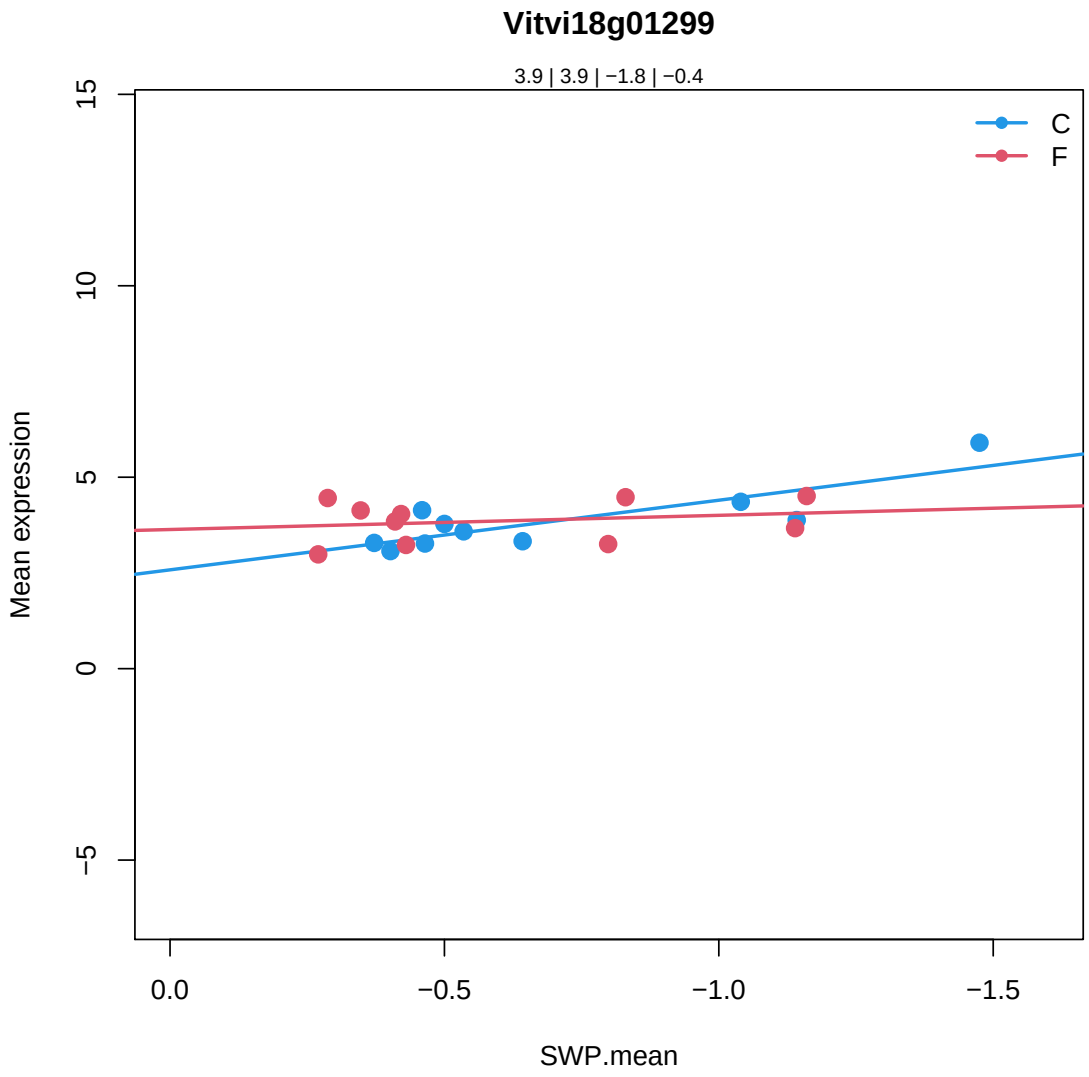
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi18g01299
        35.2
        not assigned.unknown
        Pyridoxal phosphate (PLP)-dependent transferases superfamily protein |
        Chr1:16486534-16488298 REVERSE LENGTH=482 |
        201606

Vitvi18g01299
        13.2.7
        amino acid metabolism.degradation.histidine
        Pyridoxal phosphate (PLP)-dependent transferases superfamily protein |
        Chr1:16486534-16488298 REVERSE LENGTH=482 |
        201606
```

Coefficients for Vitvi18g01299.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.859142	1.028323e-16	***	2.230496e-16	***
SlopeC	-1.818321	0.0007156598	***	0.1076608	
MeanF-MeanC	0.000469719	0.9984185		0.9998558	
SlopeF-SlopeC	1.447752	0.04668631	*	0.9999488	


Vitvi18g01299
3.9 | 3.9 | −1.8 | −0.4
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

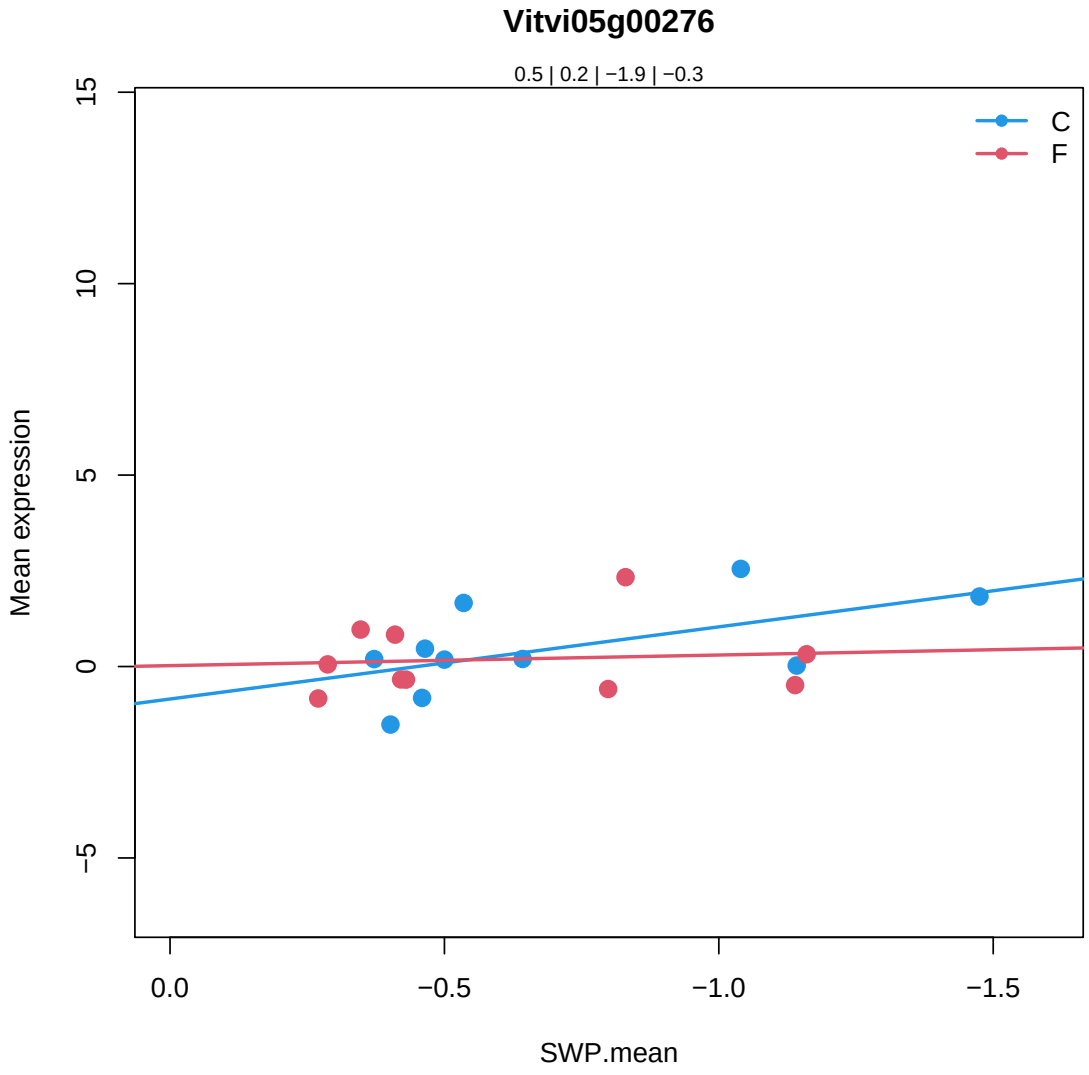
7.6.999 Vitvi05g00276: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g00276
        10.8.2
        cell wall.pectinesterases.acetyl esterase
        Pectinacetylesterase family protein |
        Chr5:9319096-9320816 FORWARD LENGTH=298 |
        201606
```

Coefficients for Vitvi05g00276.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4765793	0.120058		0.1239031	
SlopeC	−1.884728	0.03148617	*	0.4323533	
MeanF−MeanC	−0.2847568	0.5012804		0.8068978	
SlopeF−SlopeC	1.607493	0.2011498		0.9999488	



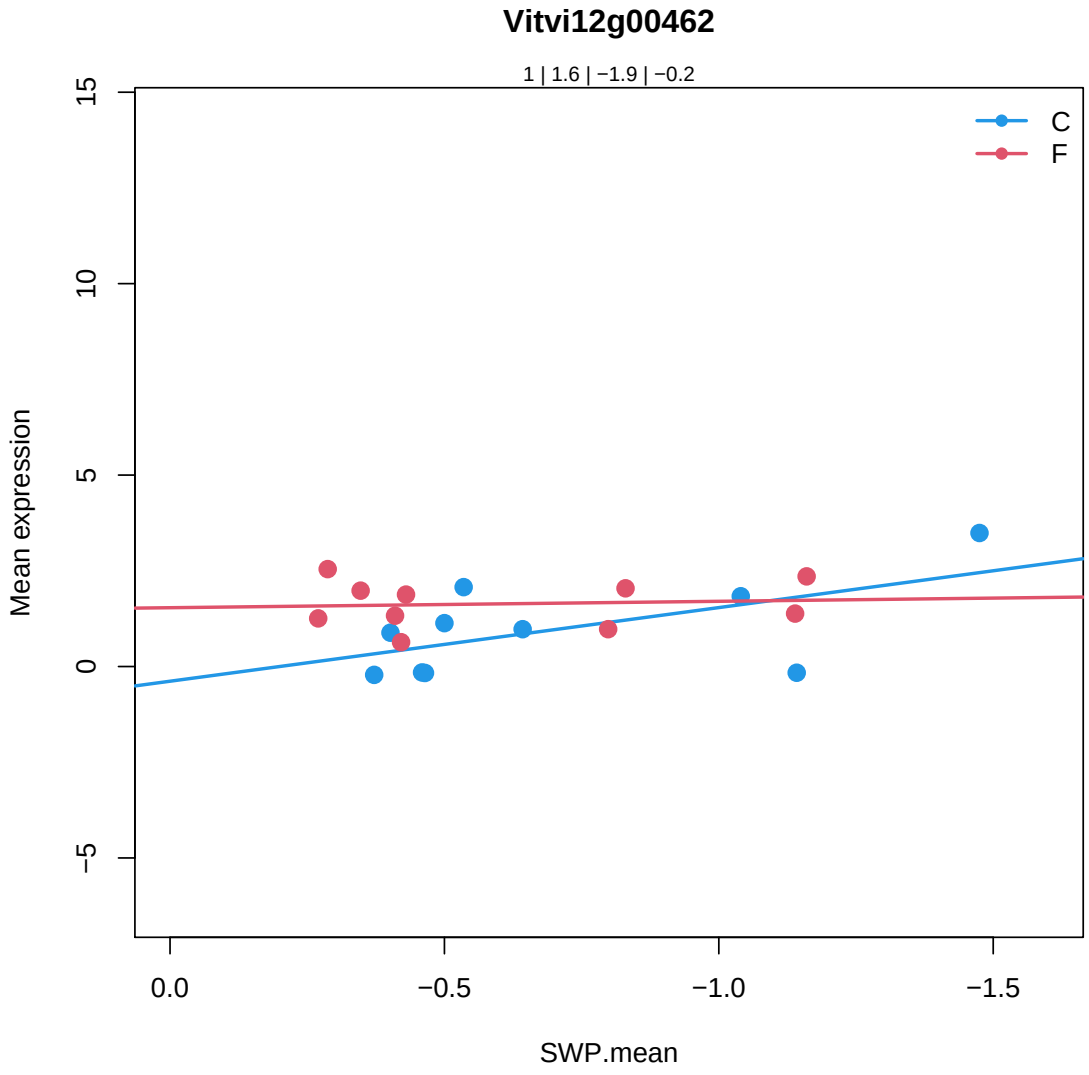
7.6.1000 Vitvi12g00462: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00462
        35.2
        not assigned.unknown
        phosphoenolpyruvate carboxylase%2C putative (DUF506) |
        Chr1:4064751-4066319 REVERSE LENGTH=295 |
        201606
```

Coefficients for Vitvi12g00462.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.9680959	0.0008894302	***	0.0009644089	***
SlopeC	−1.922833	0.01178741	*	0.3196864	
MeanF−MeanC	0.6696248	0.07294111	.	0.3035849	
SlopeF−SlopeC	1.755307	0.10585		0.9999488	



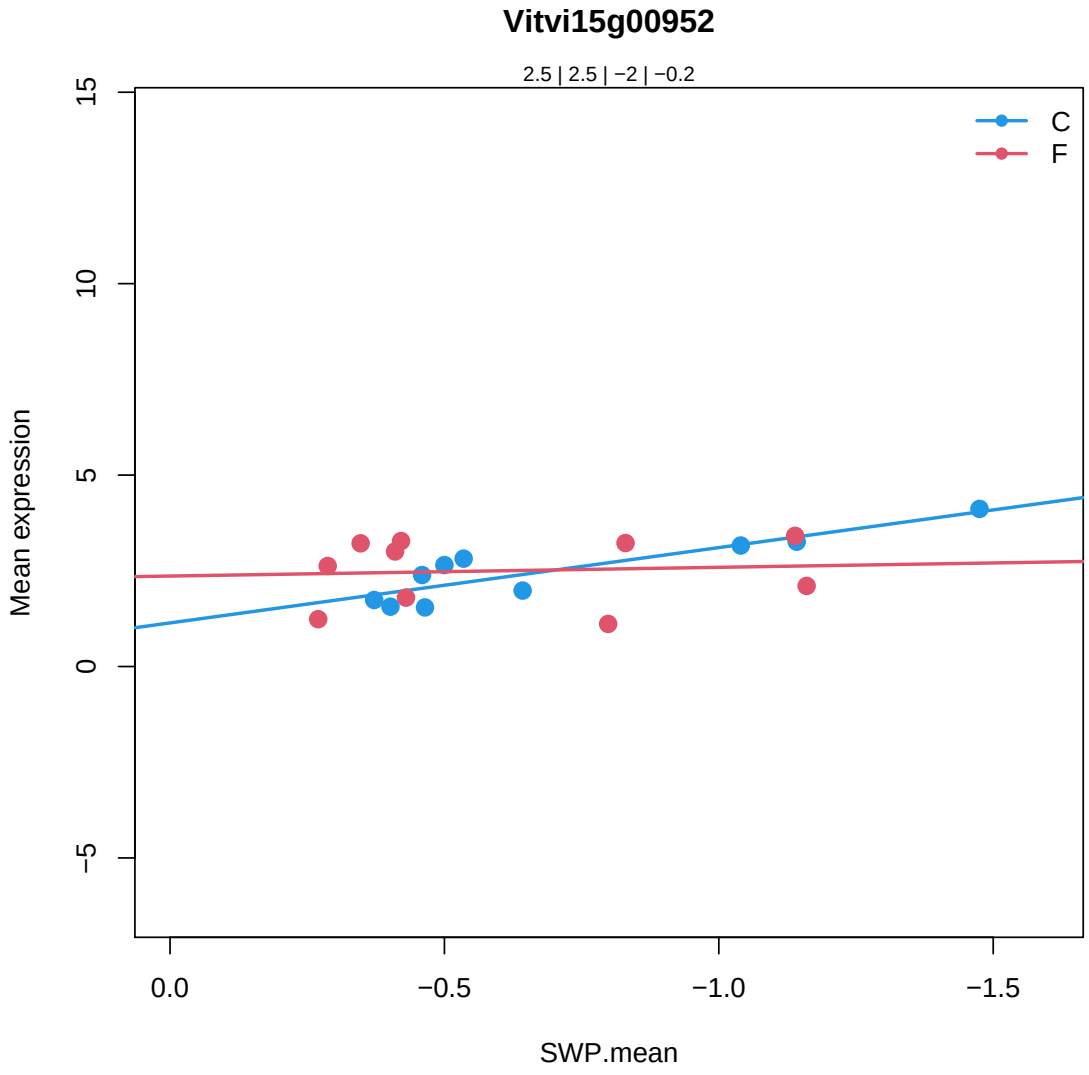
7.6.1001 Vitvi15g00952: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g00952
        29.5.4
        protein.degradation.aspartate protease
        Eukaryotic aspartyl protease family protein |
        Chr1:117065-118522 FORWARD LENGTH=485 |
        201606
```

Coefficients for Vitvi15g00952.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.522118	6.152168e-11	***	8.11241e-11	***
SlopeC	-1.967486	0.002995023	**	0.2077722	
MeanF-MeanC	-0.0206313	0.9456001		0.9858795	
SlopeF-SlopeC	1.739328	0.05975886	.	0.9999488	



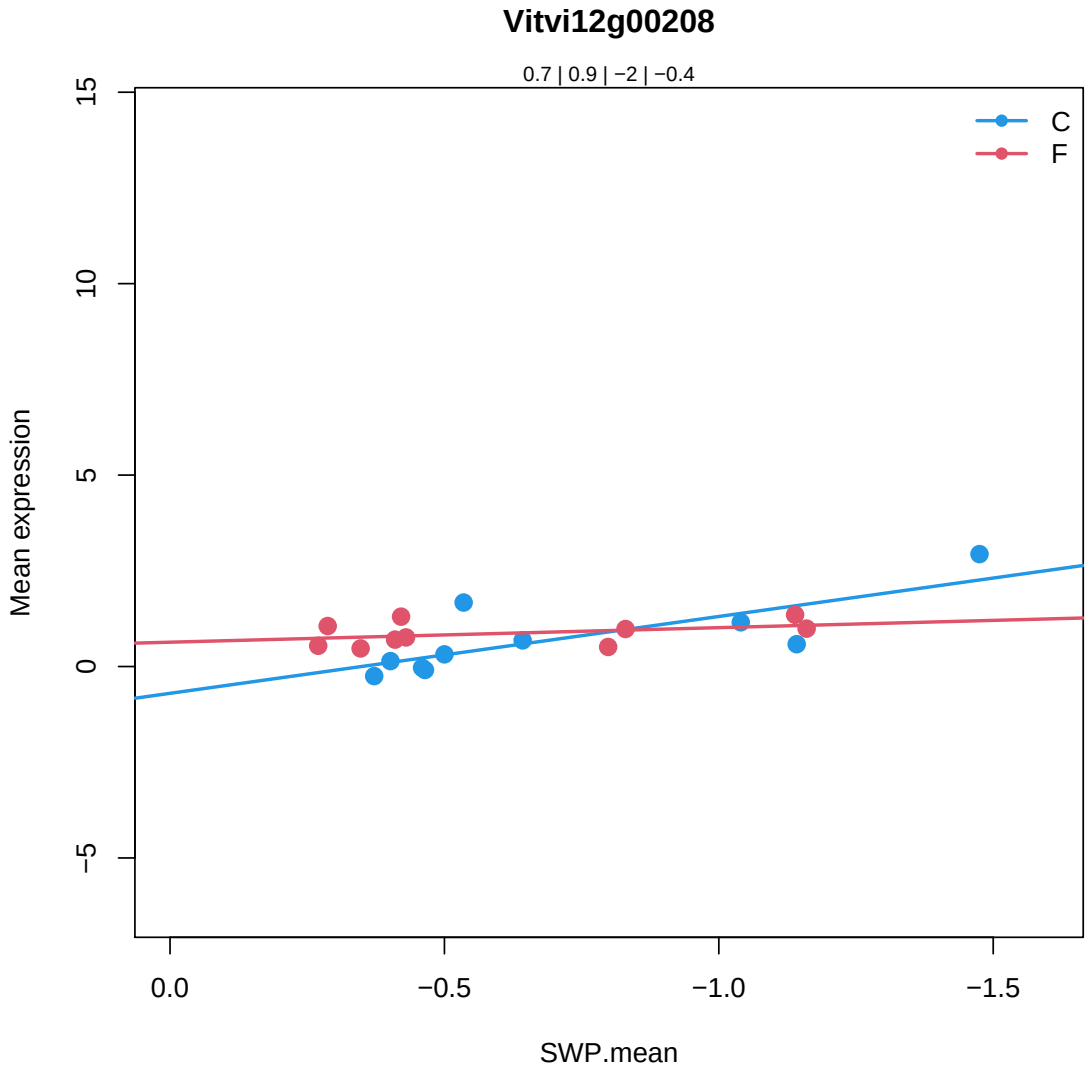
7.6.1002 Vitvi12g00208: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi12g00208
        17.5.1
        hormone metabolism.ethylene.synthesis-degradation
        2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protei
        Chr1:2025618-2027094 FORWARD LENGTH=365 |
        201606
```

Coefficients for Vitvi12g00208.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.711212	0.0002269437	***	0.0002488543	***
SlopeC	−2.007259	0.0001945396	***	0.08013978	.
MeanF−MeanC	0.1553532	0.5019296		0.807344	
SlopeF−SlopeC	1.627465	0.02326239	*	0.9999488	



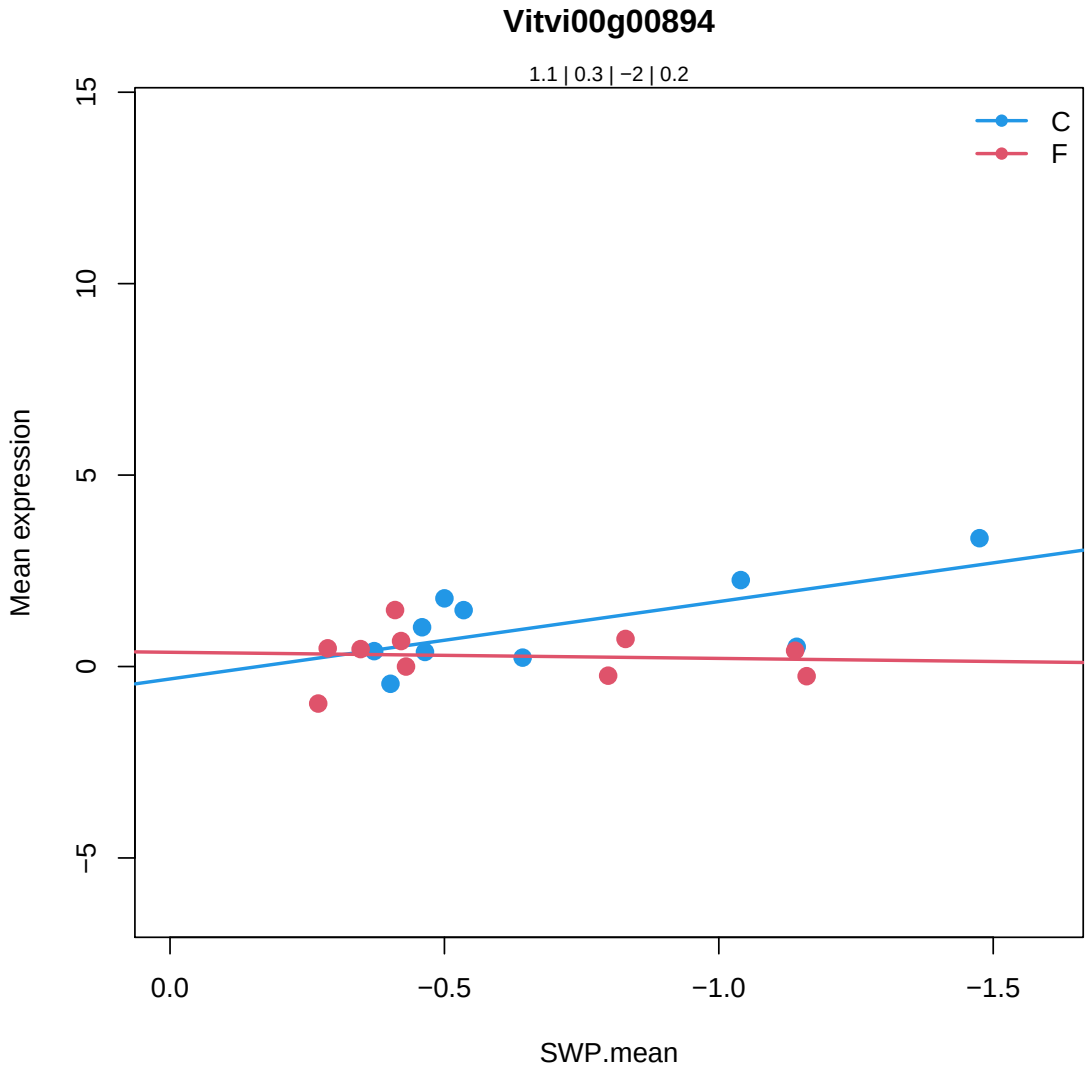
7.6.1003 Vitvi00g00894: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi00g00894
        26.10
        misc.cytochrome P450
        cytochrome P450%2C family 81%2C subfamily D%2C polypeptide 3 |
        Chr4:17564953-17566706 REVERSE LENGTH=500 |
        201606
```

Coefficients for Vitvi00g00894.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.096441	0.0001105001	***	0.0001219229	***
SlopeC	-2.021627	0.004991736	**	0.2519339	
MeanF-MeanC	-0.8222664	0.02044618	*	0.1283229	
SlopeF-SlopeC	2.181716	0.03374317	*	0.9999488	



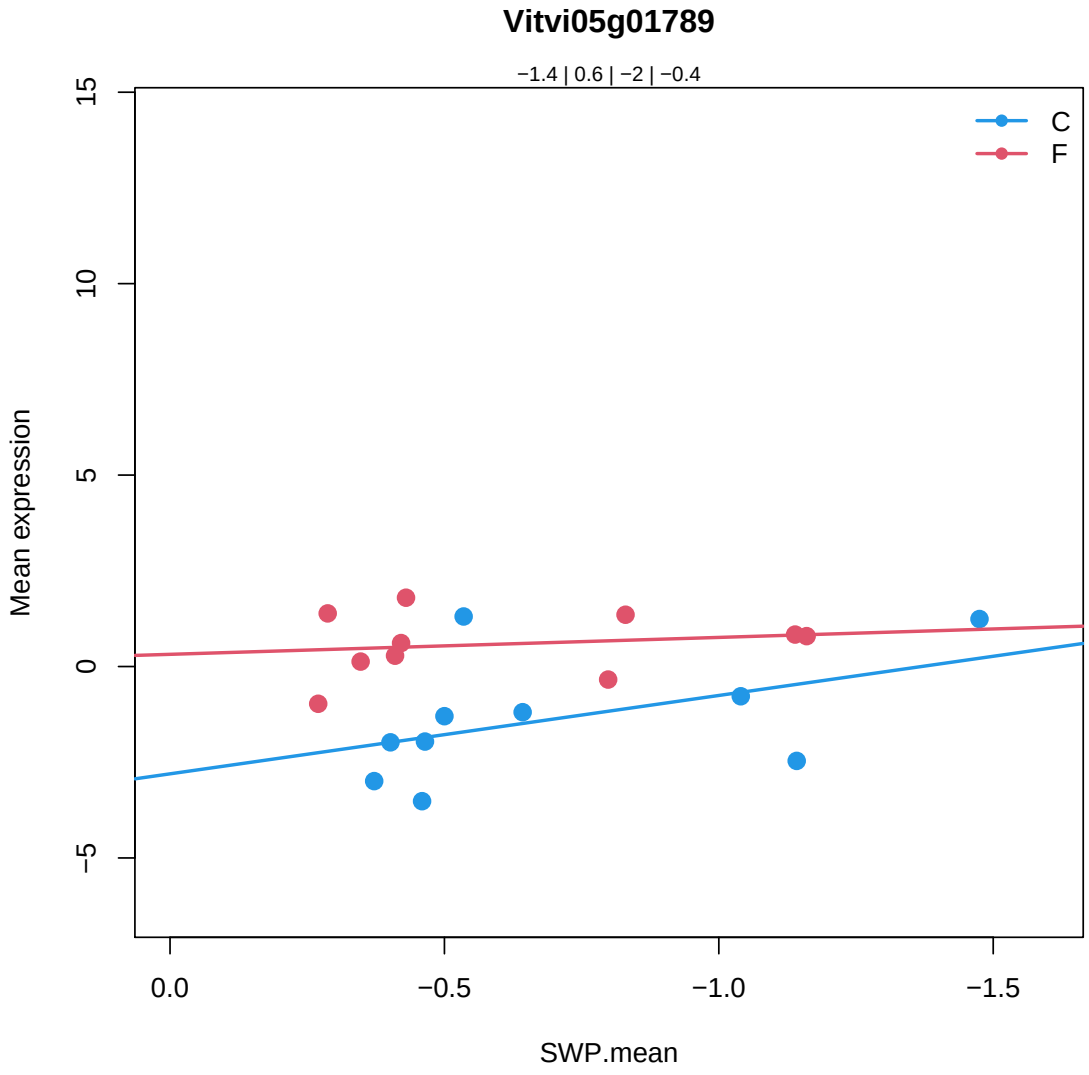
7.6.1004 Vitvi05g01789: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g01789
        35.2
        not assigned.unknown
        hAT dimerization domain-containing protein |
        Chr3:5972793-5975684 REVERSE LENGTH=877 |
        201606
```

Coefficients for Vitvi05g01789.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.363668	0.0007159484	***	0.0007777411	***
SlopeC	-2.046809	0.04501978	*	0.4904752	
MeanF-MeanC	1.951171	0.0006402893	***	0.008670318	**
SlopeF-SlopeC	1.605349	0.2743618		0.9999488	



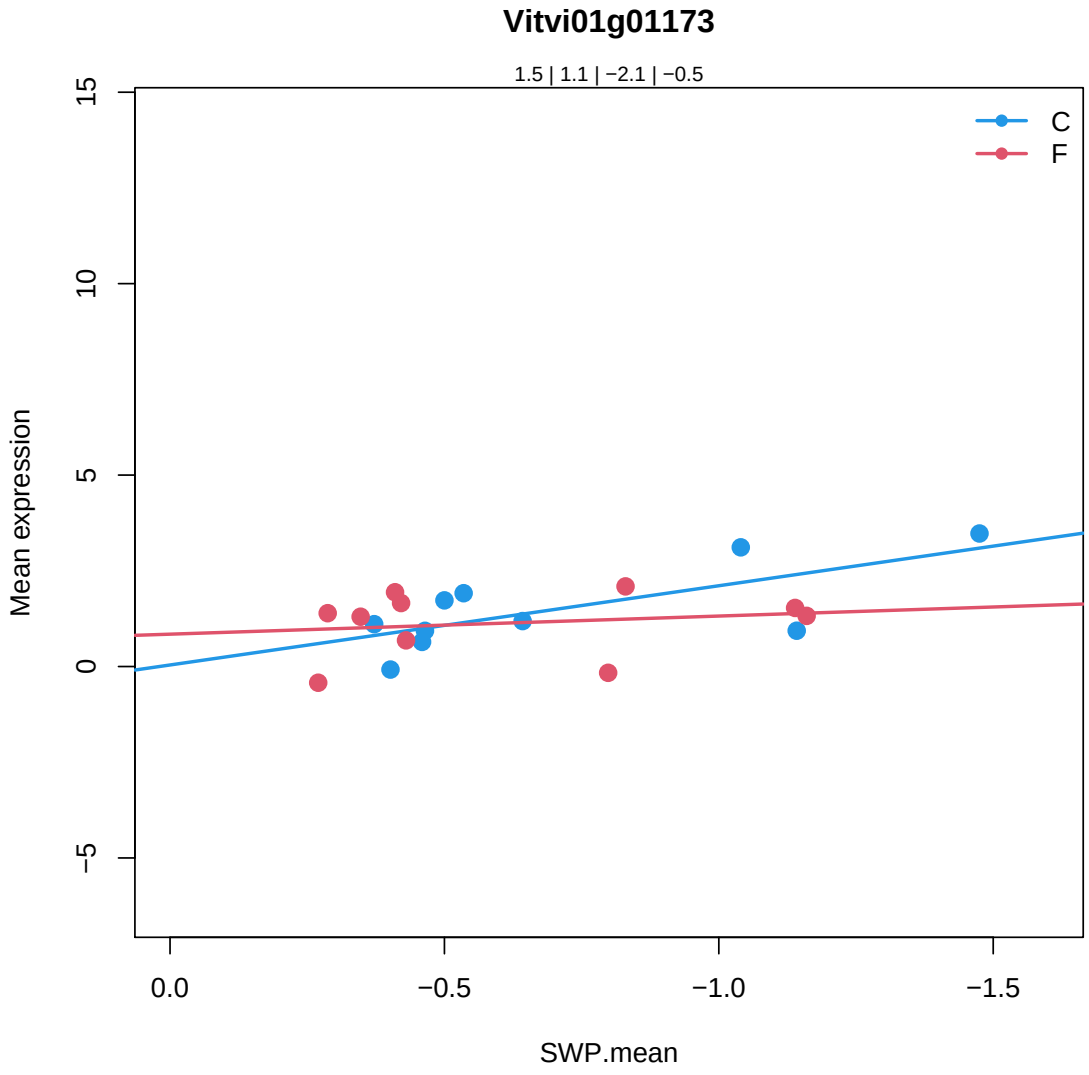
7.6.1005 Vitvi01g01173: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g01173
        35.2
        not assigned.unknown
        glycosyltransferase family protein (DUF23) |
        Chr4:10896810-10898794 FORWARD LENGTH=504 |
        201606
```

Coefficients for Vitvi01g01173.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.495083	4.190921e-06	***	4.769508e-06	***
SlopeC	-2.069299	0.006114888	**	0.2647742	
MeanF-MeanC	-0.3620394	0.3069294		0.6700737	
SlopeF-SlopeC	1.59637	0.1296355		0.9999488	



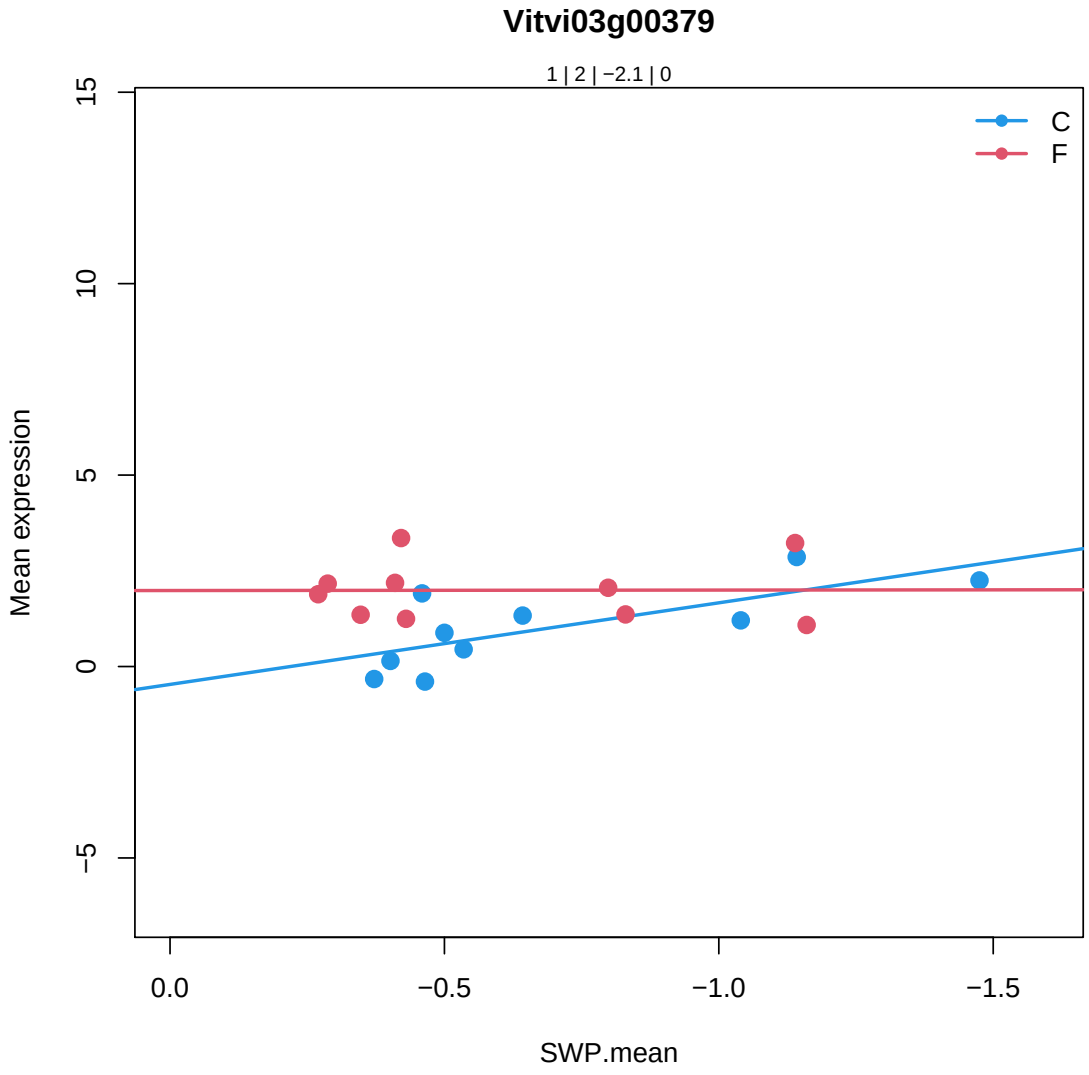
7.6.1006 Vitvi03g00379: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi03g00379
        21.3
        redox.heme
        hemoglobin 1 |
        Chr2:6982782-6983522 REVERSE LENGTH=160 |
        201606
```

Coefficients for Vitvi03g00379.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.030871	0.0002454846	***	0.0002690692	***
SlopeC	−2.130936	0.003660677	**	0.224984	
MeanF−MeanC	0.9607862	0.008587949	**	0.06775747	.
SlopeF−SlopeC	2.119206	0.04061071	*	0.9999488	



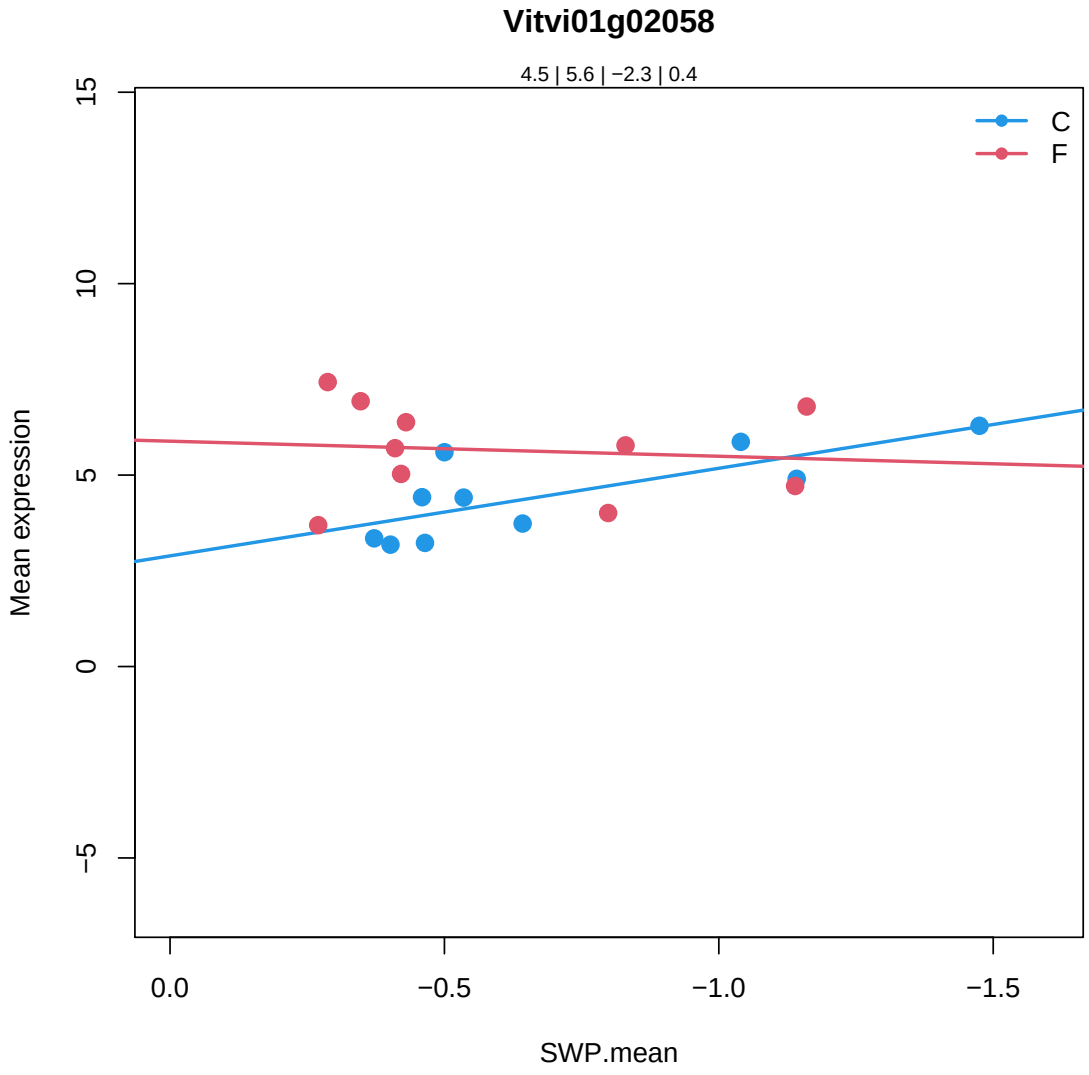
7.6.1007 Vitvi01g02058: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi01g02058
        35.1.26
        not assigned.no ontology.DC1 domain containing protein
        DC1 domain-containing protein |
        Chr1:22261978-22264243 FORWARD LENGTH=578 |
        201606
```

Coefficients for Vitvi01g02058.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.498078	1.402763e-12	***	1.995232e-12	***
SlopeC	-2.287997	0.01456258	*	0.3359386	
MeanF-MeanC	1.147159	0.01577985	*	0.1054434	
SlopeF-SlopeC	2.681258	0.04844408	*	0.9999488	



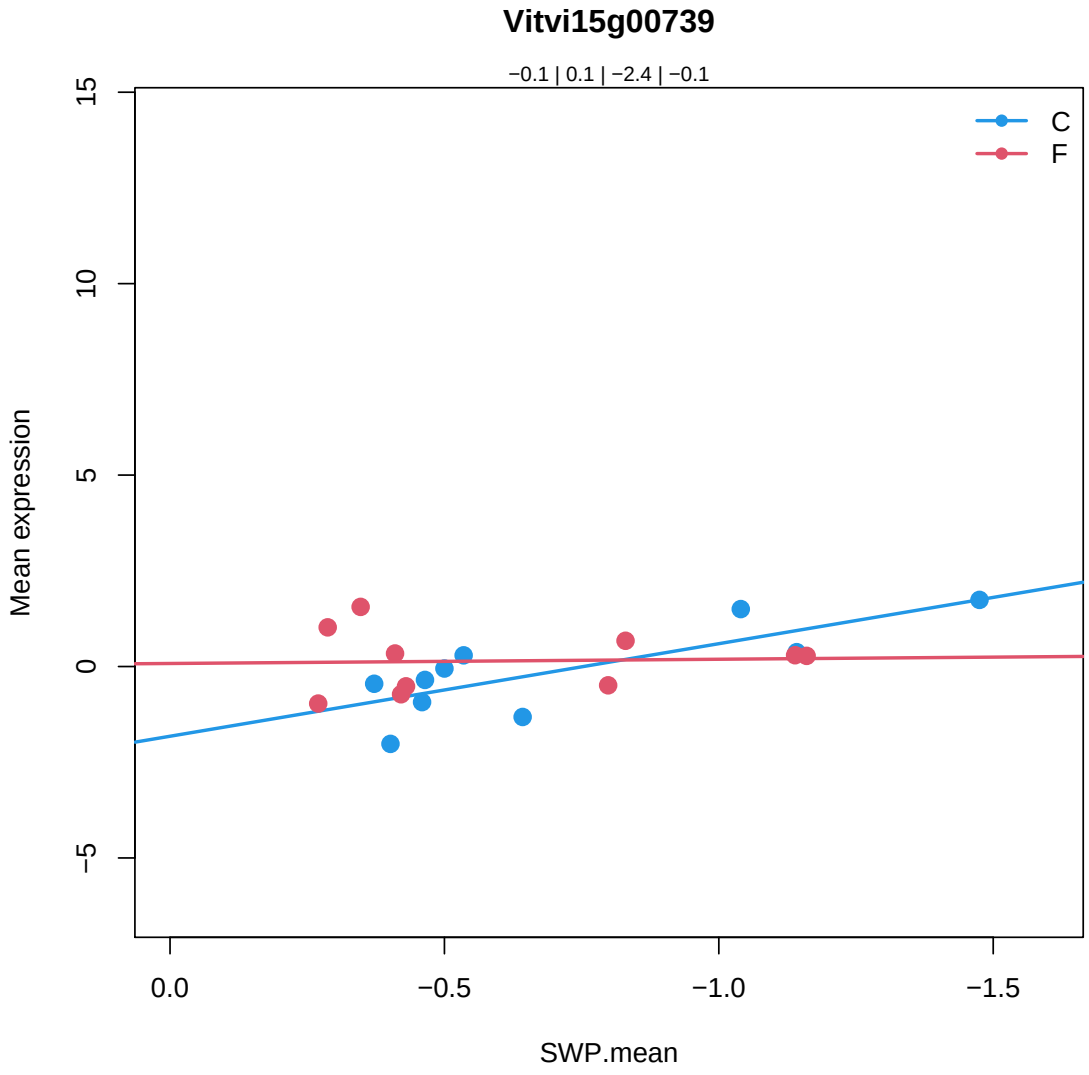
7.6.1008 Vitvi15g00739: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi15g00739
        31.1
        cell.organisation
        microtubule-associated protein 65-9 |
        Chr5:25005756-25008096 FORWARD LENGTH=549 |
        201606
```

Coefficients for Vitvi15g00739.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.121504	0.6138651		0.6191869	
SlopeC	-2.417377	0.001416796	**	0.1479249	
MeanF-MeanC	0.2679126	0.4334342		0.7672943	
SlopeF-SlopeC	2.306901	0.02855227	*	0.9999488	



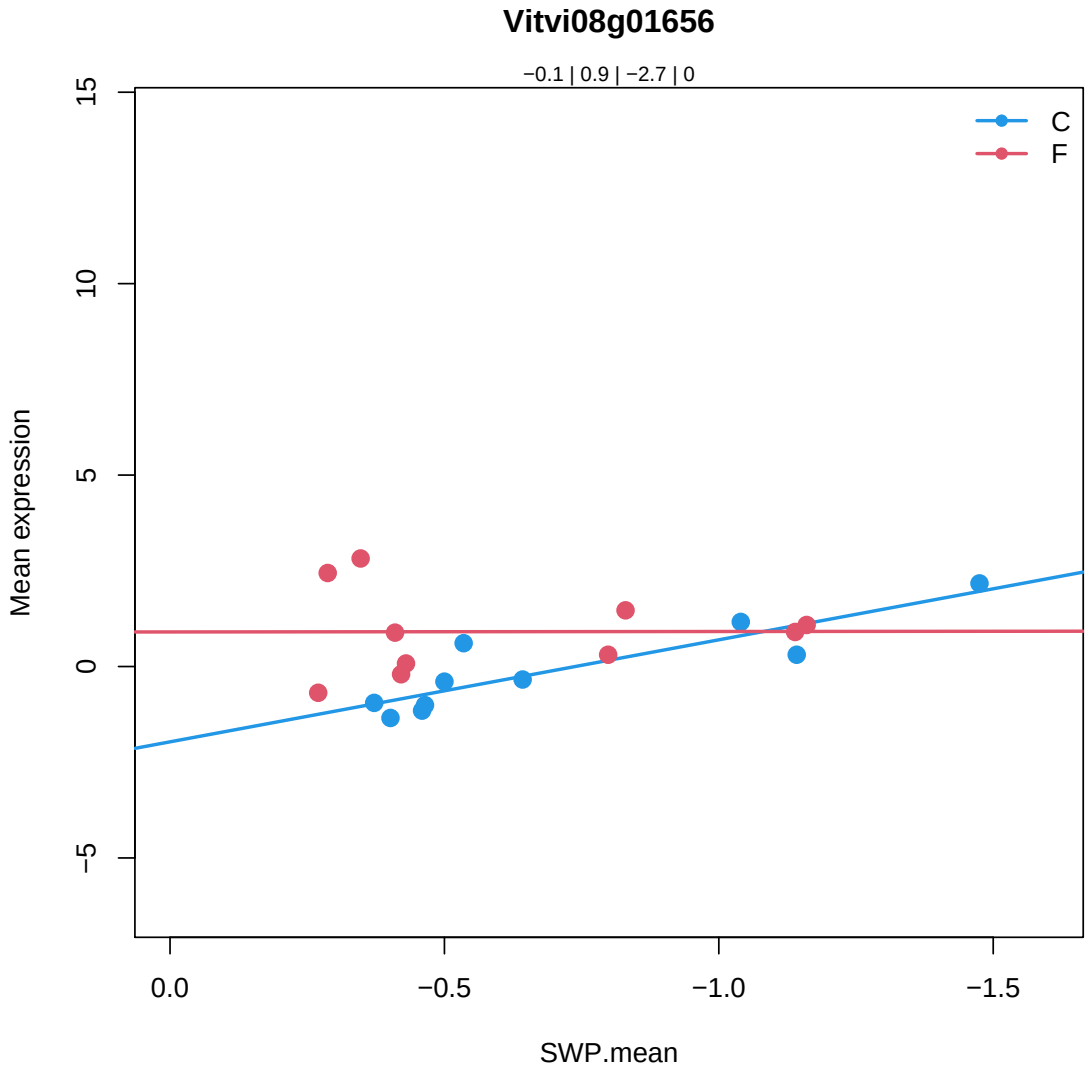
7.6.1009 Vitvi08g01656: * type5

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g01656
        16.4.1
        secondary metabolism.N misc.alkaloid-like
        strictosidine synthase-like 2 |
        Chr2:17210599-17212904 REVERSE LENGTH=376 |
        201606
```

Coefficients for Vitvi08g01656.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.09373959	0.7272465		0.7318077	
SlopeC	-2.664662	0.001599851	**	0.1556102	
MeanF-MeanC	1.003909	0.01398203	*	0.0970465	.
SlopeF-SlopeC	2.653252	0.02470524	*	0.9999488	



```
> #
> fit2 <- eBayes(fit2)
> fit2[testvar,]$coefficients
              (Intercept)        swp  varietyF swp:varietyF
Vitvi01g01391    1.595041 -0.7685916 0.2722187    0.4814101
> head(fit2[1:6,]$coefficients)
              (Intercept)          swp   varietyF swp:varietyF
Vitvi15g01736    5.550751  1.593545190 -0.2500355  -0.31758915
Vitvi07g02832   -2.634115  0.508155686  5.4166972  -0.25109586
Vitvi07g02830   -1.750650  1.548036562  4.3321685  -0.90607176
Vitvi07g02812   -1.381363 -0.009794742  2.3030352   0.40349136
Vitvi07g02811    2.236177  0.566269561  1.2588734   0.02240192
Vitvi09g02033   -2.842837  0.419564483  4.1984533  -0.76028515
```

A Metadata files

A.1 Project metadata

Table 2: Project metadata

Item	Value
project:	_p_VinskaTrta
Short Name:	VinskaTrta
Title:	Vine related research
Description:	*
pISA projects path:	D:/DEJAVNOSTI/OMIKE/pISA-projects
Local pISA-tree organisation:	NIB
pISA project creation date:	2020-11-13
pISA project creator:	AB
Project funding code:	*
Project coordinator:	Marusa Pompe Novak
Project partners:	*
Project start date:	*
Project end date:	*
Principal investigator:	*
License:	CC BY 4.0
Sharing permission:	Private
Upload to FAIRDOMHub:	Yes

A.2 Investigation metadata

Table 3: Investigation metadata

Item	Value
Investigation:	_I_EnViRoS
Short Name:	EnViRoS
Title:	Integration of data from different platforms
Description:	*
Phenodata:	./phenodata_20201113.txt
pISA Investigation creation date:	2020-11-13
pISA Investigation creator:	AB
Principal investigator:	*
License:	CC BY 4.0
Sharing permission:	Private
Upload to FAIRDOMHub:	Yes

A.3 Study metadata

Table 4: Study metadata

Item	Value
Study:	_S_01_Integ
Short Name:	01_Integ
Title:	*
Description:	*
Raw Data:	
pISA Study creation date:	2020-11-13
pISA Study creator:	AB
Principal investigator:	*
License:	CC BY 4.0
Sharing permission:	Private
Upload to FAIRDOMHub:	Yes

A.4 Assay metadata

Table 5: Assay metadata

Item	Value
Assay:	_A_01_Desc-R
Short Name:	01_Desc-R
Assay Class:	DRY
Assay Type:	R
Title:	Data overview and descriptive statistical presentation
Description:	First we will organize the data and perfom preliminary data analyses to overview what we have.
pISA Assay creation date:	2020-11-13
pISA Assay creator:	Andrej Blejec
Analyst:	Andrej Blejec
Phenodata:	Phenodata_20201109.txt
Featuredata:	Transcripts1819-02.txt
Featuredata metabolites:	Featuredata_metabolites_210127.txt
Transcript data 18:	/input/Transcripts 2018.txt
Transcript data 19:	/input/Transcripts 2019.txt
Metabolite data 18:	/input/Metabolites_2018_raw_-data.txt
Metabolite data 19:	/input/Metabolites_2019_raw_-data.txt
Water potential data:	/input/Stem water potential 2018 2019.txt
Interesting bins:	Bin_selection.txt

B SessionInfo

Windows 10 x64 (build 19041)

- R version 4.0.2 (2020-06-22), x86_64-w64-mingw32
- Locale: LC_COLLATE=Slovenian_Slovenia.1250, LC_CTYPE=Slovenian_Slovenia.1250, LC_MONETARY=Slovenian_Slovenia.1250, LC_NUMERIC=C, LC_TIME=Slovenian_Slovenia.1250
- Running under: Windows 10 x64 (build 19041)
- Matrix products: default
- Base packages: base, datasets, graphics, grDevices, grid, methods, parallel, stats, utils
- Other packages: amisc 0.1.0, Biobase 2.50.0, BiocGenerics 0.36.0, dotCall64 1.0-0, fields 11.6, Formula 1.2-4, ggplot2 3.3.3, Hmisc 4.4-1, knitr 1.30, lattice 0.20-41, limma 3.46.0, lubridate 1.7.9.2, MASS 7.3-51.6, reshape2 1.4.4, spam 2.6-0, survival 3.2-7, xtable 1.8-4
- Loaded via a namespace (and not attached): backports 1.2.0, base64enc 0.1-3, checkmate 2.0.0, cluster 2.1.0, colorspace 1.4-1, compiler 4.0.2, crayon 1.3.4, data.table 1.13.2, digest 0.6.27, dplyr 1.0.2, ellipsis 0.3.1, evaluate 0.14, foreign 0.8-80, generics 0.1.0, glue 1.4.2, gridExtra 2.3, gtable 0.3.0, highr 0.8, htmlTable 2.1.0, htmltools 0.5.0, htmlwidgets 1.5.3, jpeg 0.1-8.1, latticeExtra 0.6-29, lifecycle 0.2.0, magrittr 2.0.1, maps 3.3.0, Matrix 1.2-18, munsell 0.5.0, nnet 7.3-14, pillar 1.4.7, pkgconfig 2.0.3, plyr 1.8.6, png 0.1-7, purrr 0.3.4, R6 2.5.0, RColorBrewer 1.1-2, Rcpp 1.0.5, rlang 0.4.8, rpart 4.1-15, rstudioapi 0.13, scales 1.1.1, splines 4.0.2, stringi 1.5.3, stringr 1.4.0, tibble 3.0.4, tidyselect 1.1.0, tools 4.0.2, vctrs 0.3.4, withr 2.3.0, xfun 0.19

Analysis project path: [link]

Local	Network
D:	O:
DEJAVNOSTI	DEJAVNOSTI
OMIKE	OMIKE
pISA-projects	pISA-projects
_p_VinskaTrta	_p_VinskaTrta
_I_EnViRoS	_I_EnViRoS
_S_01_Integ	_S_01_Integ
_A_01_Desc-R	_A_01_Desc-R
other	other

Main file : ../doc/50_Expression-water-stress.Rnw
Main file : ../scripts/50_Expression-water-stress.Rnw
Project file: [link]

View as vignette

Source files can be viewed by pasting this code to R console:

```
projectName <-"other"
mainFile <-"50_Expression-water-stress"
commandArgs()
library(tkWidgets)
openPDF(file.path(dirname(getwd()),"doc",
paste(mainFile,"PDF",sep=".")))
viewVignette("viewVignette", projectName,
file.path("../doc",paste(mainFile,"Rnw",sep=".")))
```