Expression analysis - water potential

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February 3, 2021

Parameters:

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

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1 Task

Final document in folder /reports:

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

2 Information from pISA

Data directory

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

Results directory

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

```
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

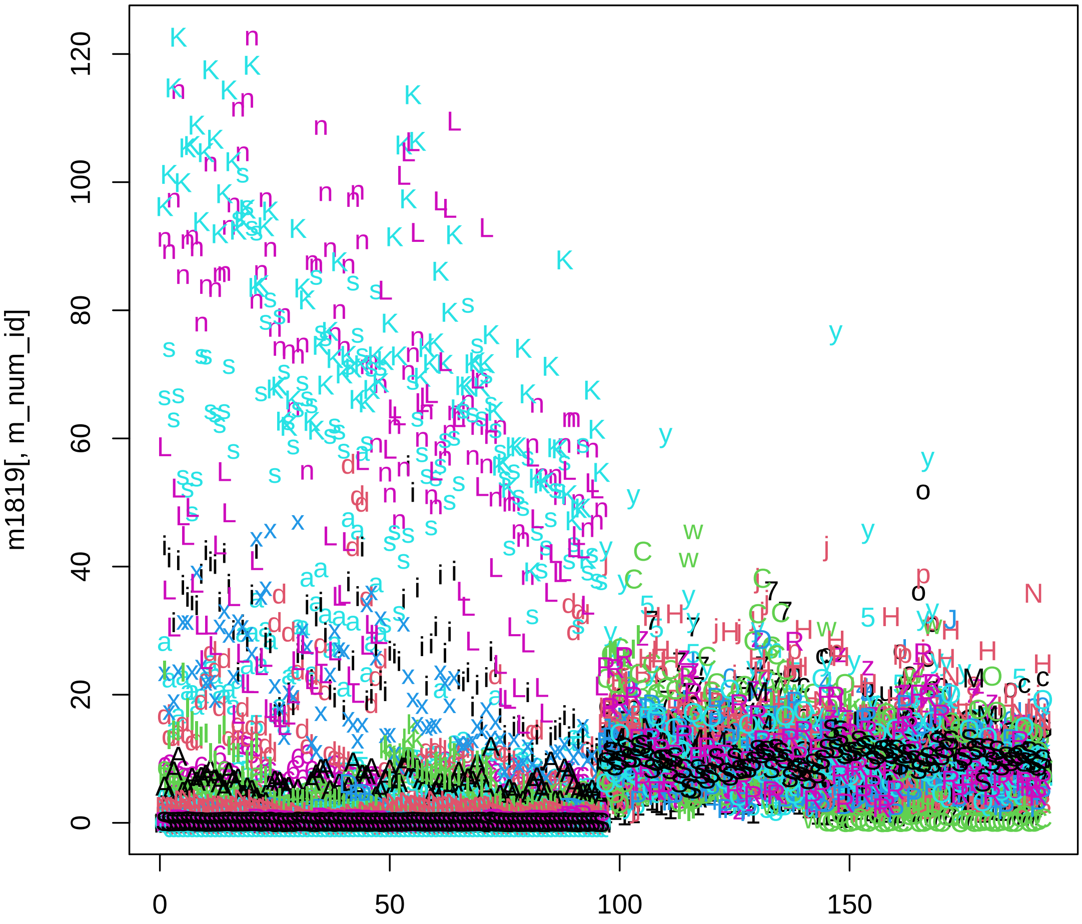
```
> dim(m1819)
[1] 192  60
> dim(t1819)
[1] 15242    80
> head(colnames(t1819))
[1] "C18_11d_WS1" "C18_11d_WS2" "C18_11d_WS3" "C18_11d_WS4"
[5] "C18_11d_WW1" "C18_11d_WW2"
> head(rownames(m1819))
[1] "C18_11d_WS1" "C18_11d_WS2" "C18_11d_WS3" "C18_11d_WS4"
[5] "C18_11d_WW1" "C18_11d_WW2"
> sum(colnames(t1819)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

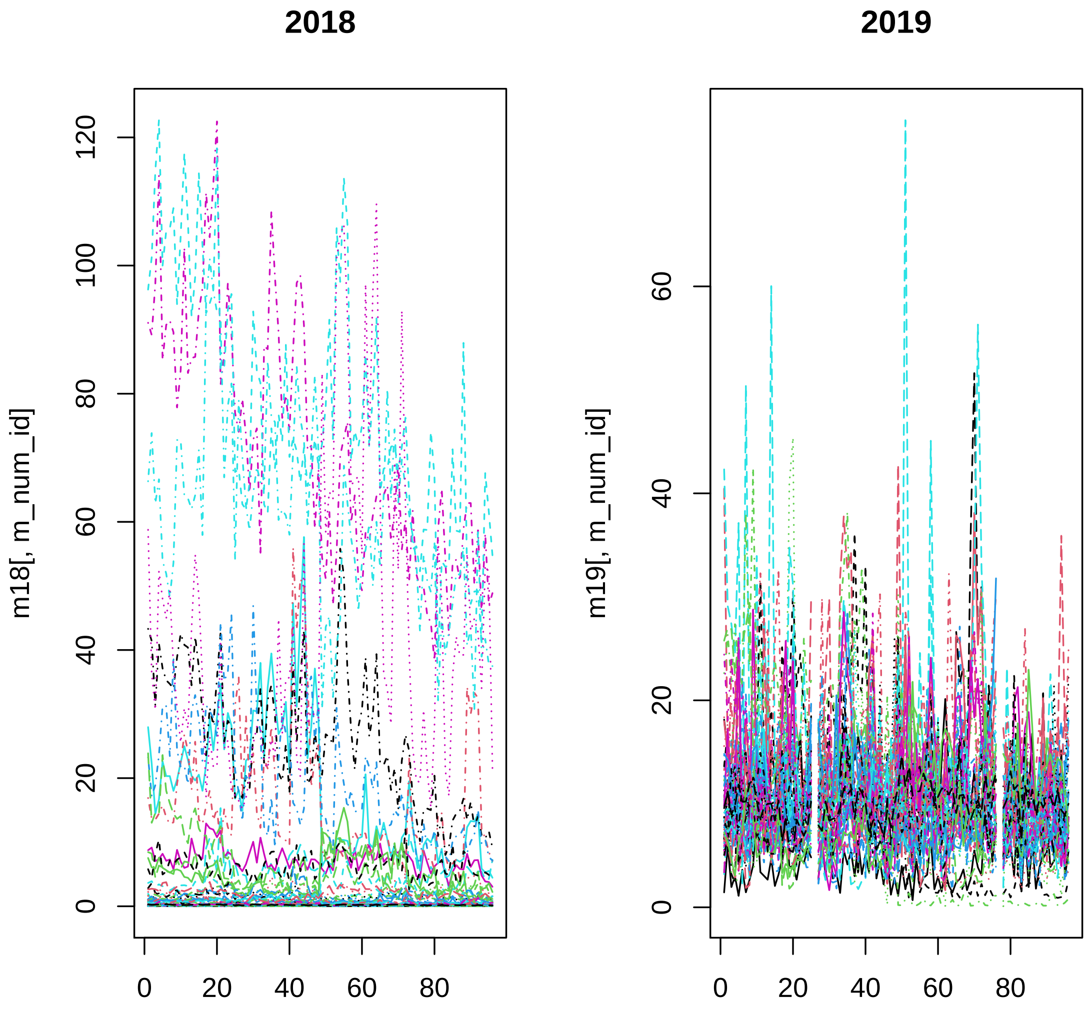
Phenodata for metabolomics data will be prepared when needed from the total phenodata. Selection of needed metabolomics data will be finalized in data analysis scripts.

3.7 Visualize metabolites

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



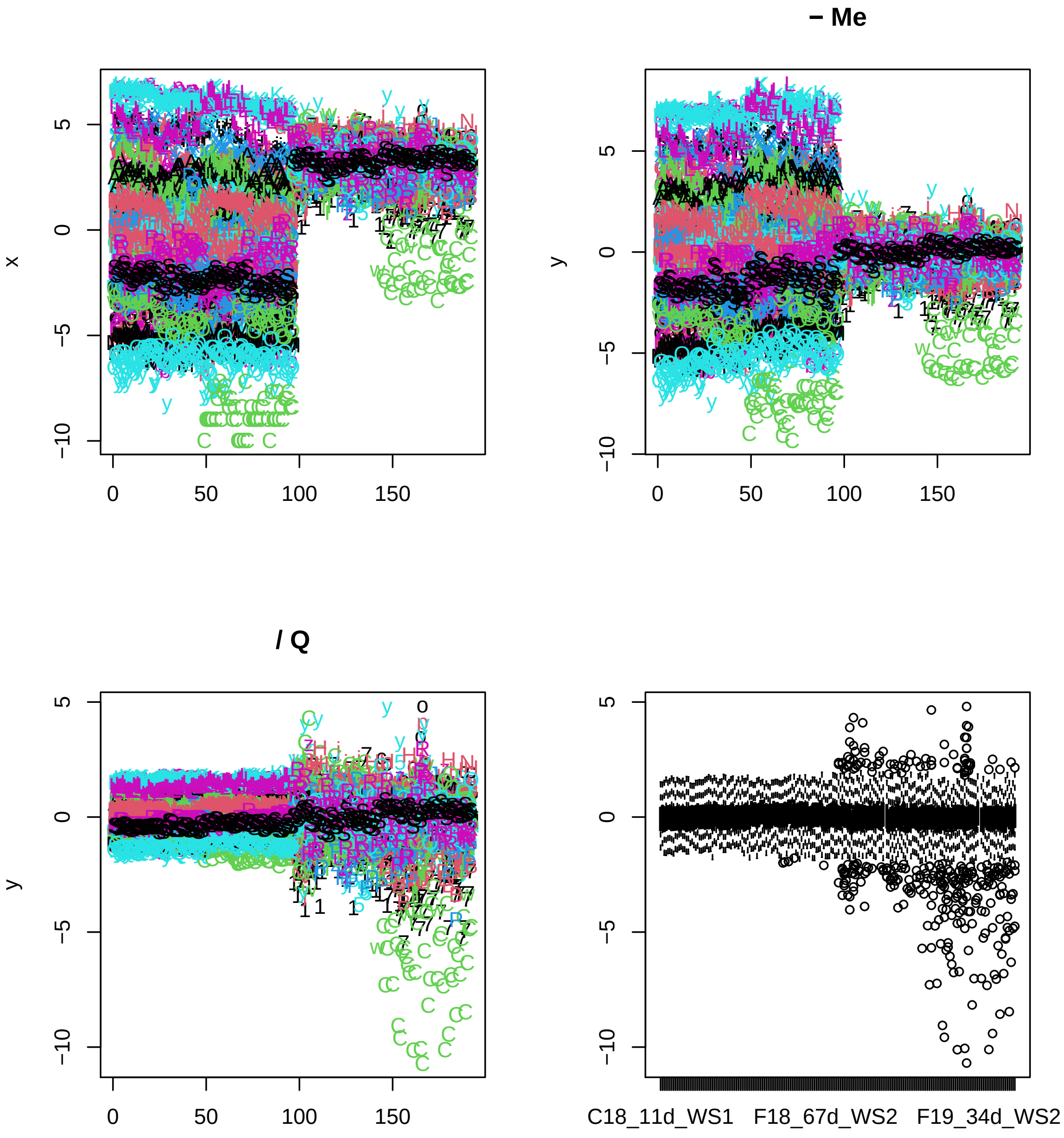
```
> par(mfrow=c(1,2))
> matplot(m18[,m_num_id], main="2018", type="l")
> matplot(m19[,m_num_id], main="2019", type="l")
```



Median standardization of samples

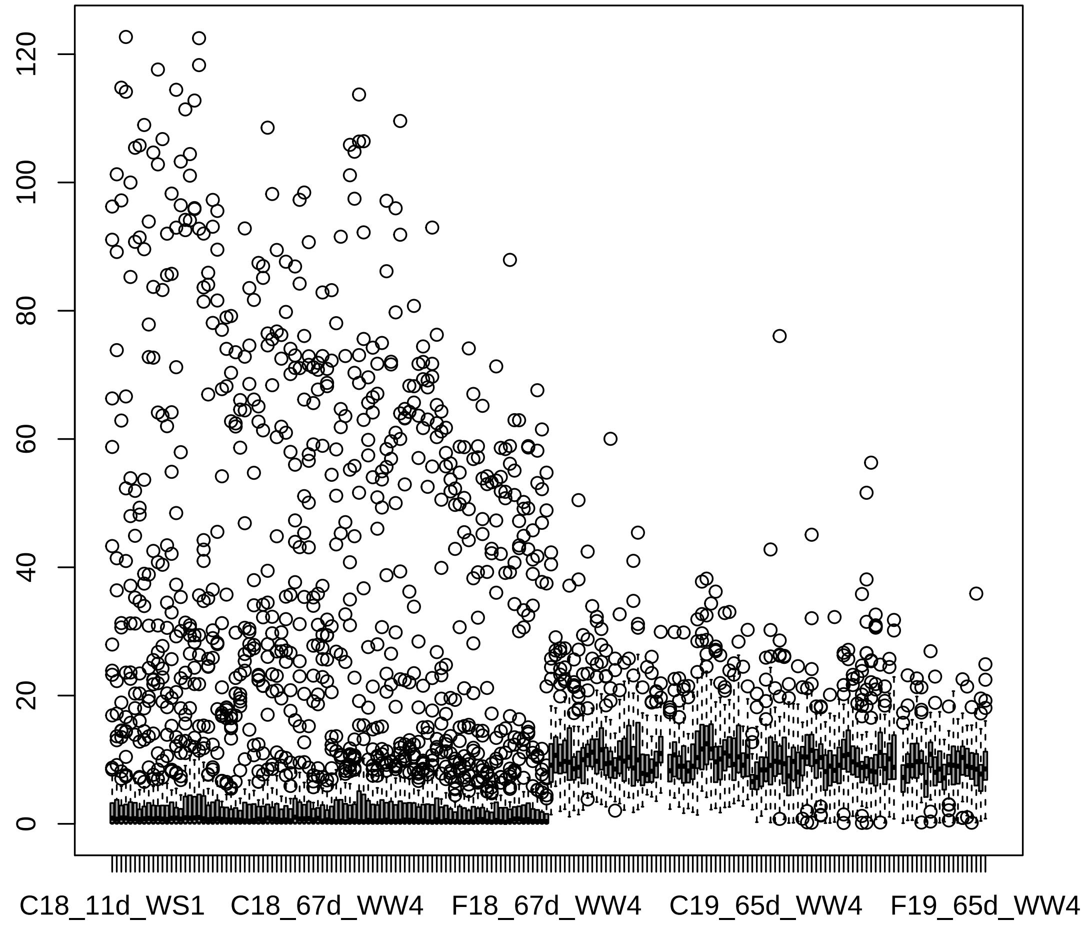
```
> my.parallel <- function(x, m=1:ncol(x), ...){
+ m <- m[m<ncol(x)]
+ par(mar=c(4,8,3,1))
+ xlim <- range(x,na.rm=TRUE)
+ n1 <- nrow(x)
+ plot(0,0,xlim=xlim,ylim=c(n1,1) , type="n", axes=FALSE, ann=FALSE)
+ title(paste(range(m),collapse=":"))
+ axis(1)
+ axis(2,at=1:n1,labels=rownames(x), las=2)
+ 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))
```

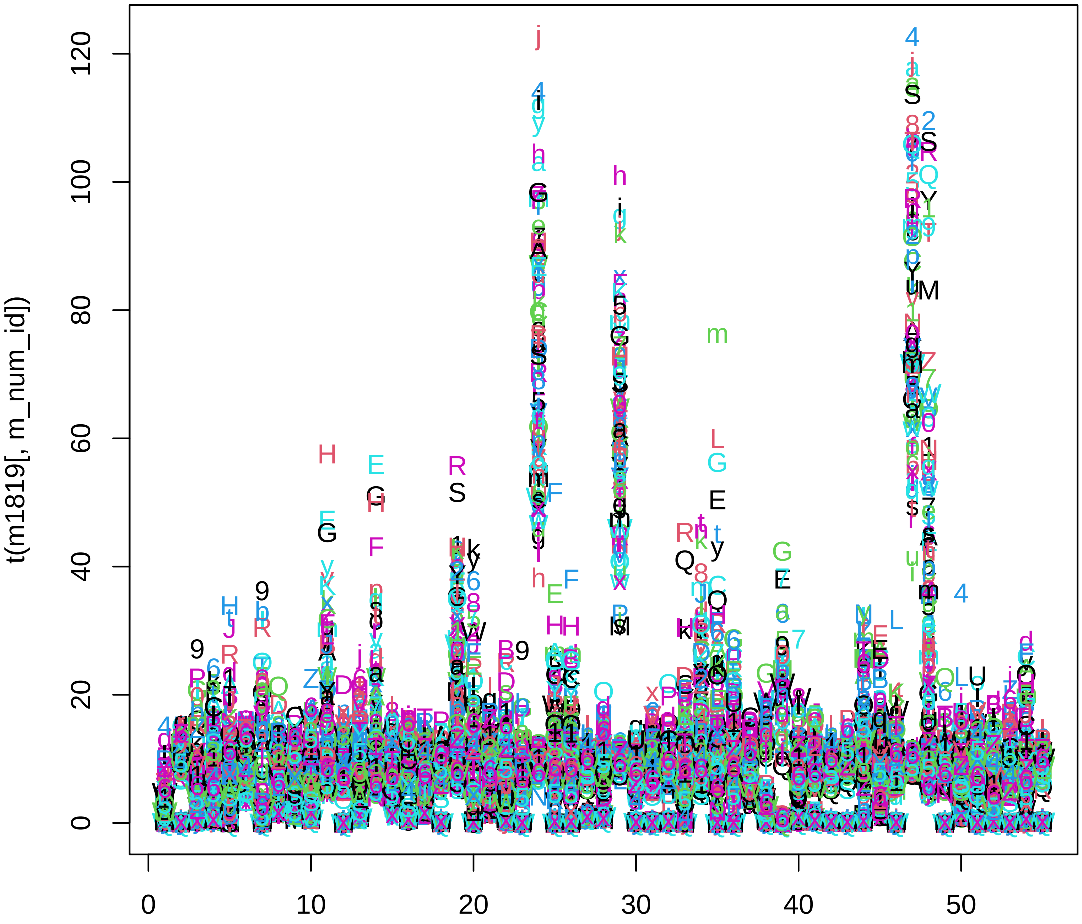


Data are highly skewed with marked differences between years

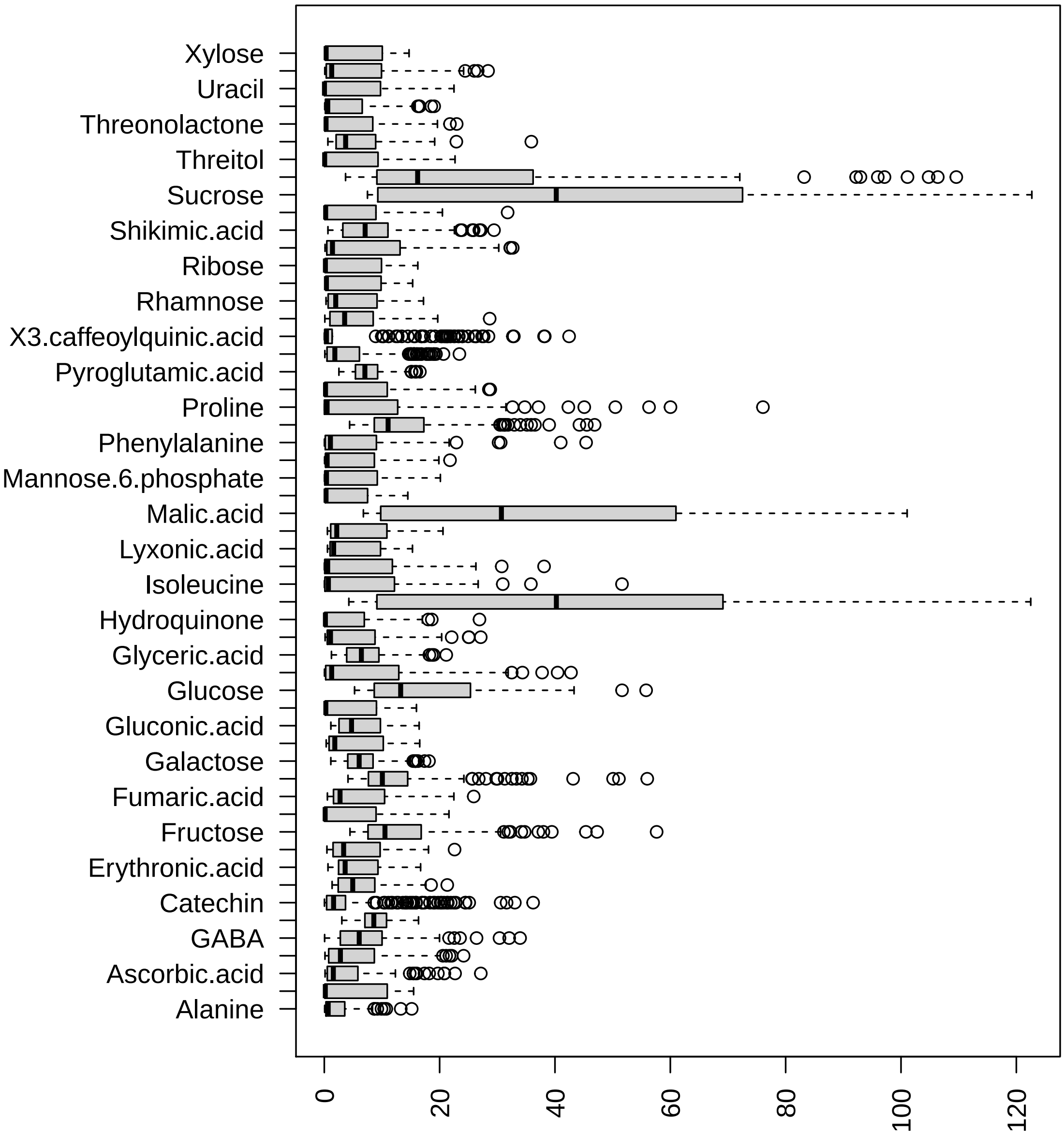
```
> boxplot(t(m1819[,m_num_id]), col=8)
```



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

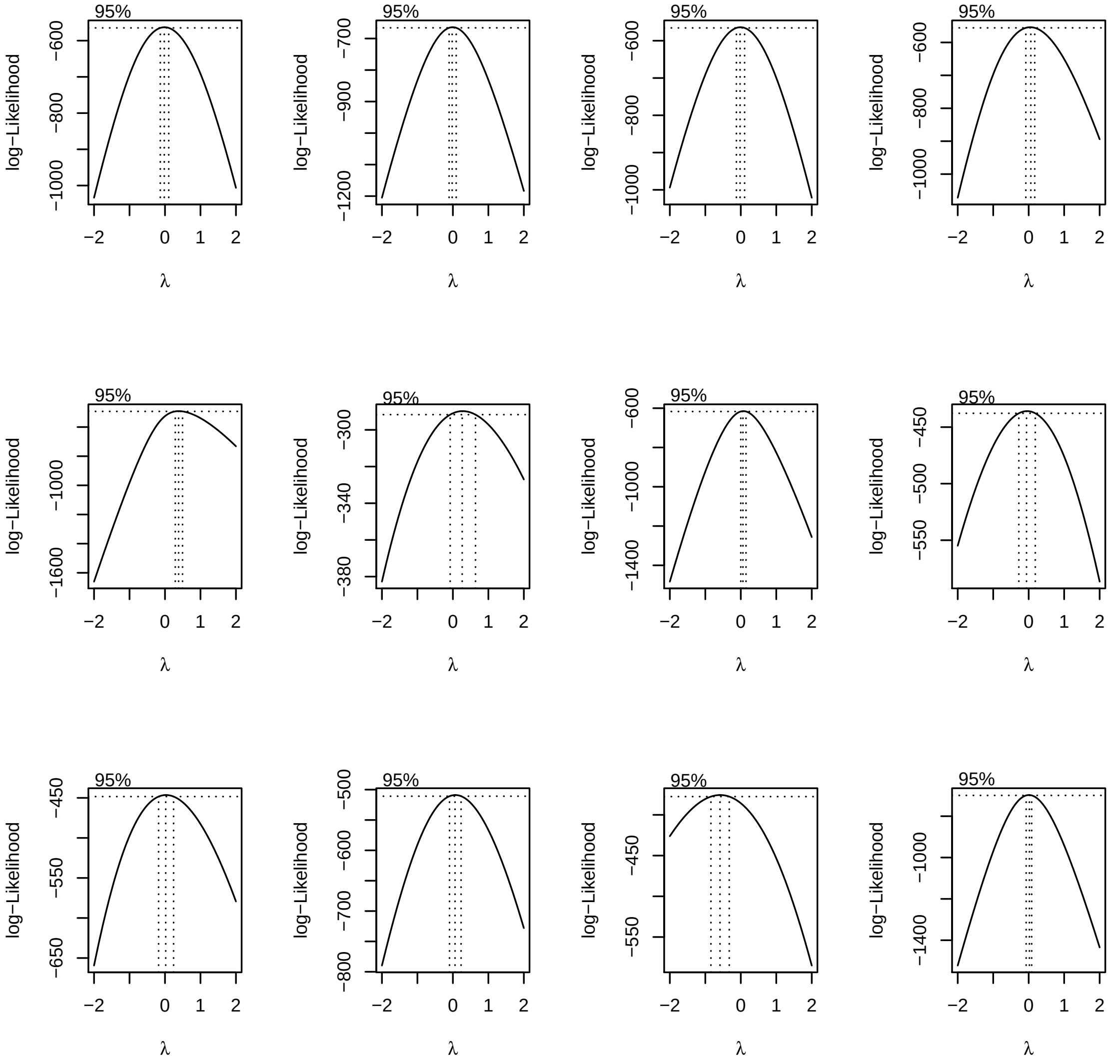


```
> par(mar=c(4,10,3,1))
> boxplot(m1819[,m_num_id], horizontal=TRUE, las=2)
```



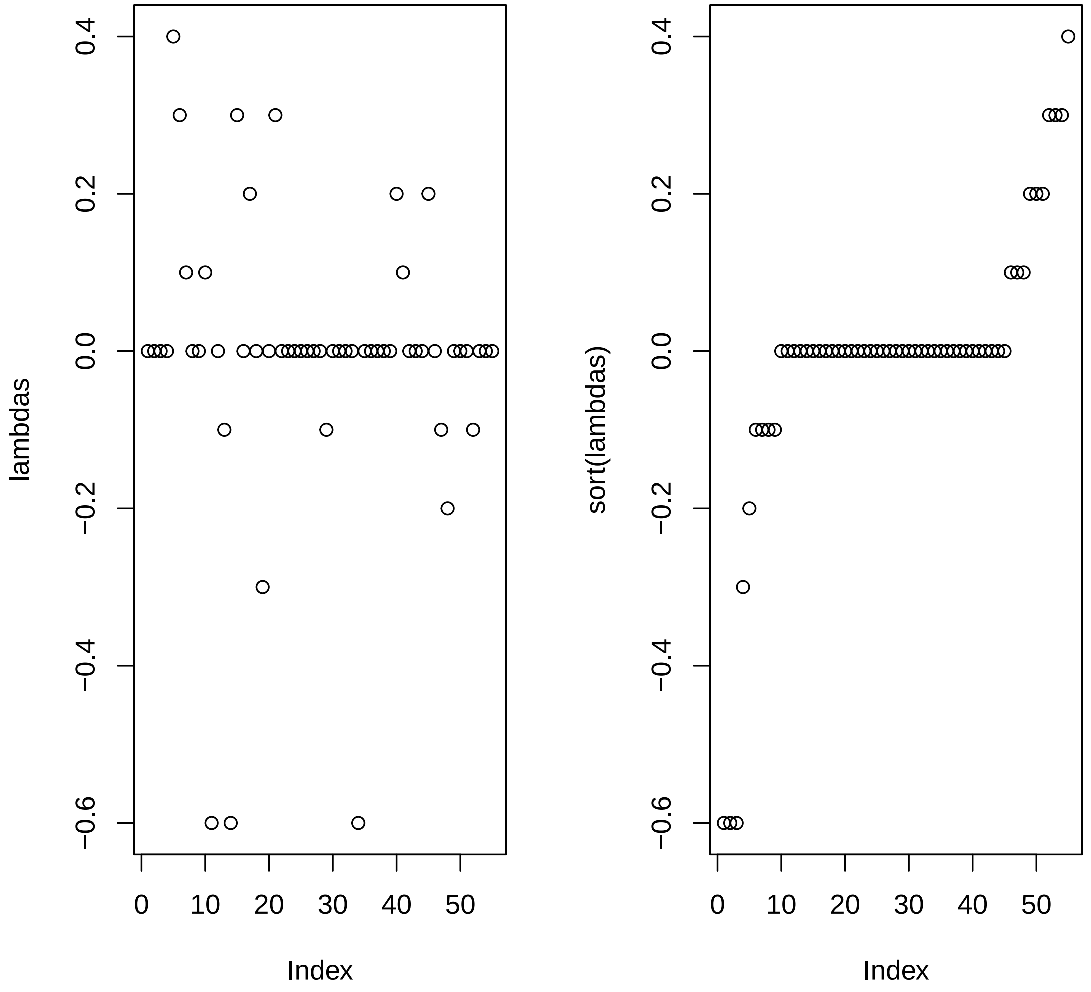
Box-Cox transformation

```
> 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)
```



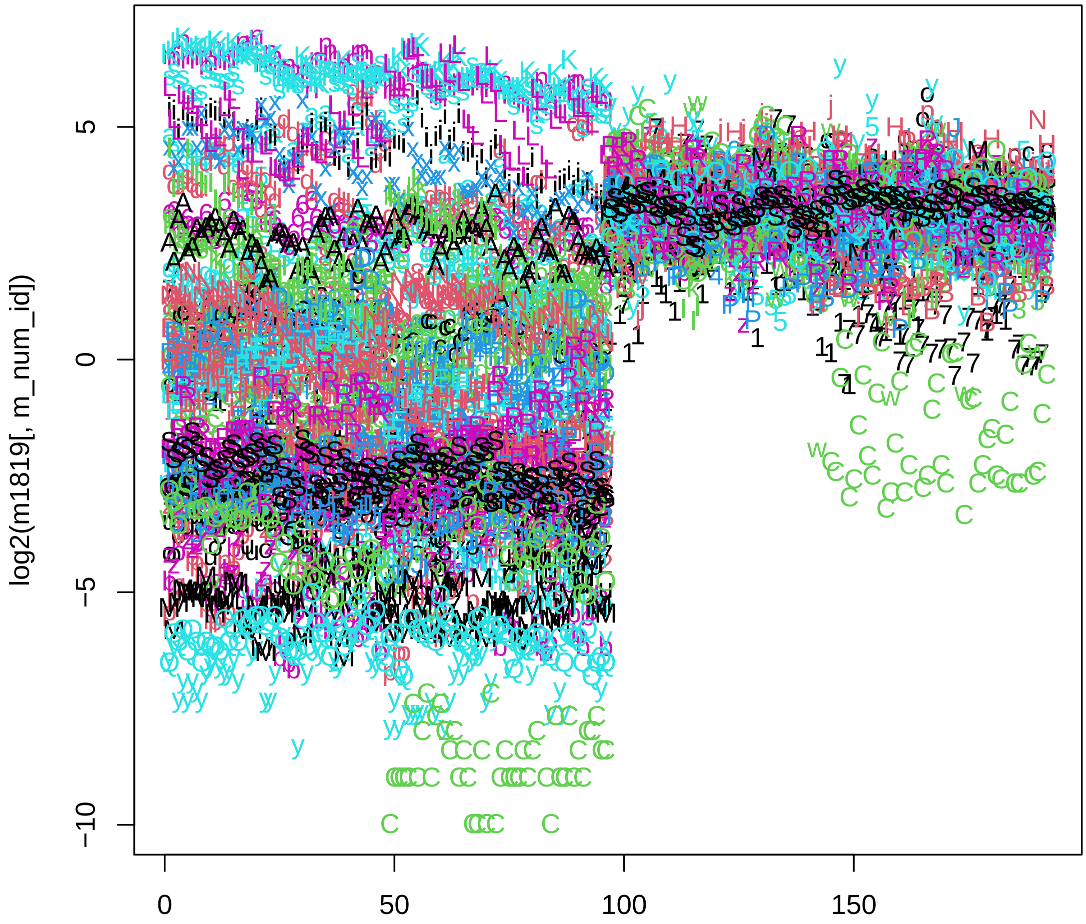
```
          Alanine           Arabinose       Ascorbic.acid
      -0.02020202         -0.02020202         -0.02020202
    Aspartic.acid                GABA   Trans.Caffeic.acid
       0.06060606          0.38383838          0.26262626
         Catechin         Citric.acid     Erythronic.acid
       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))
```



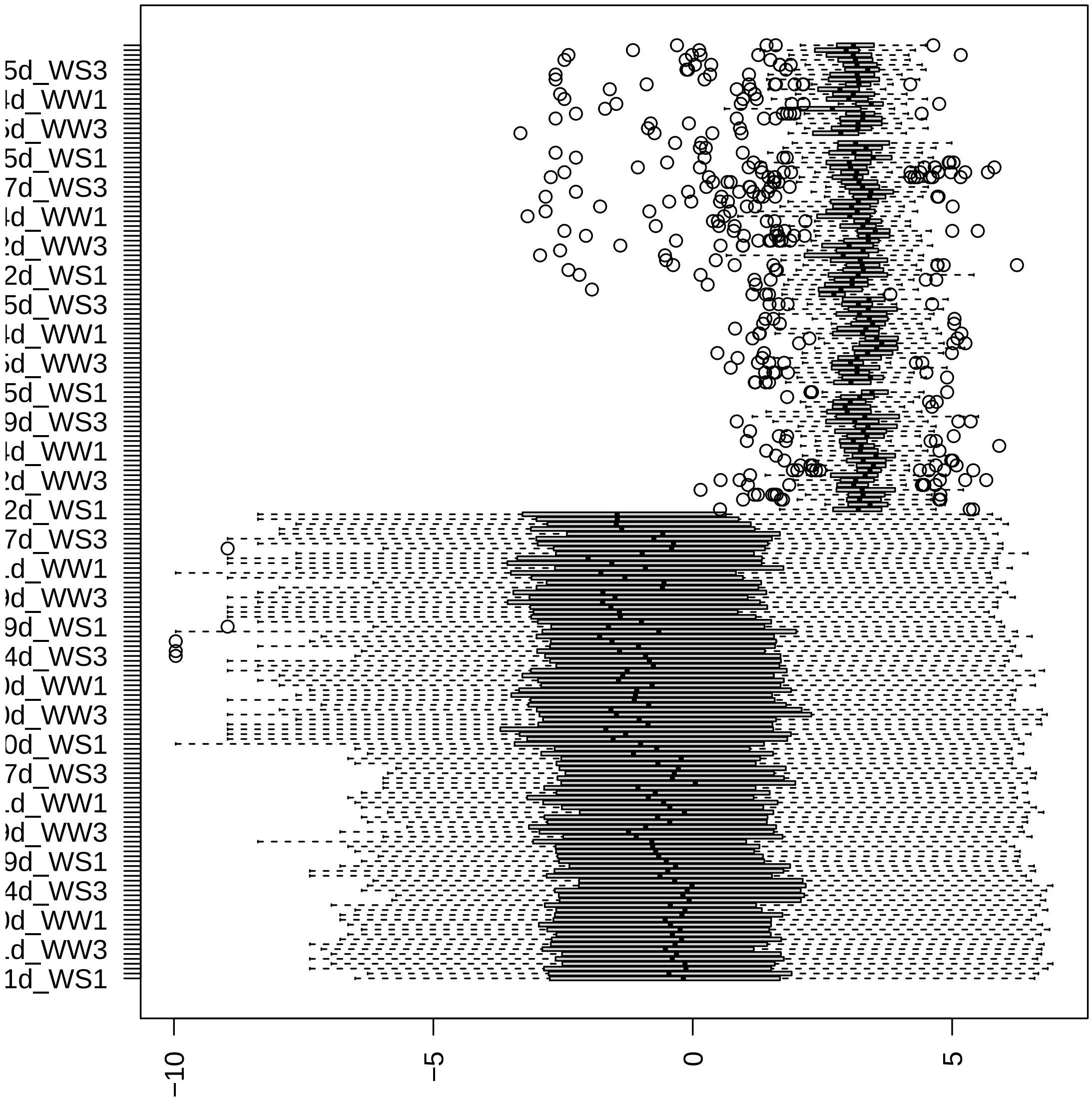
It seems that logarithm is adequate.

```
> 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

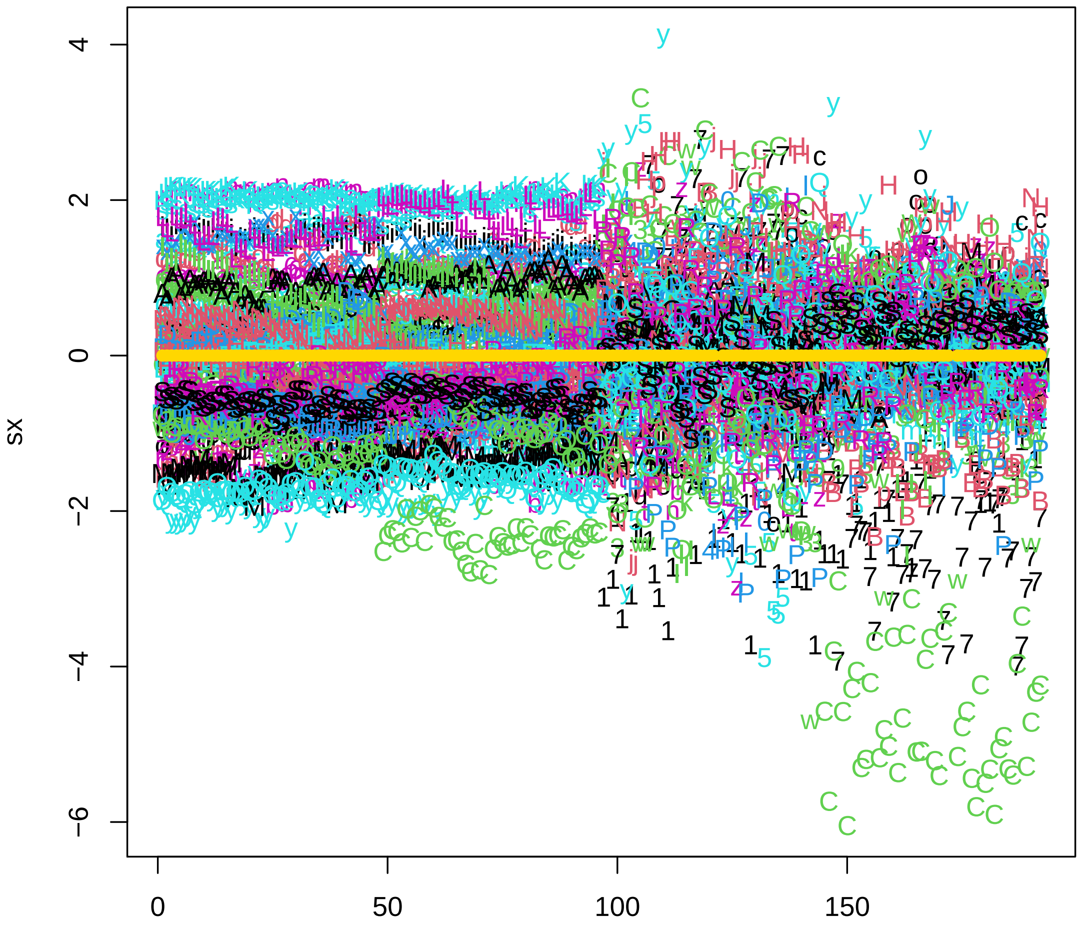
For CCA standardized values are needed

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)
```



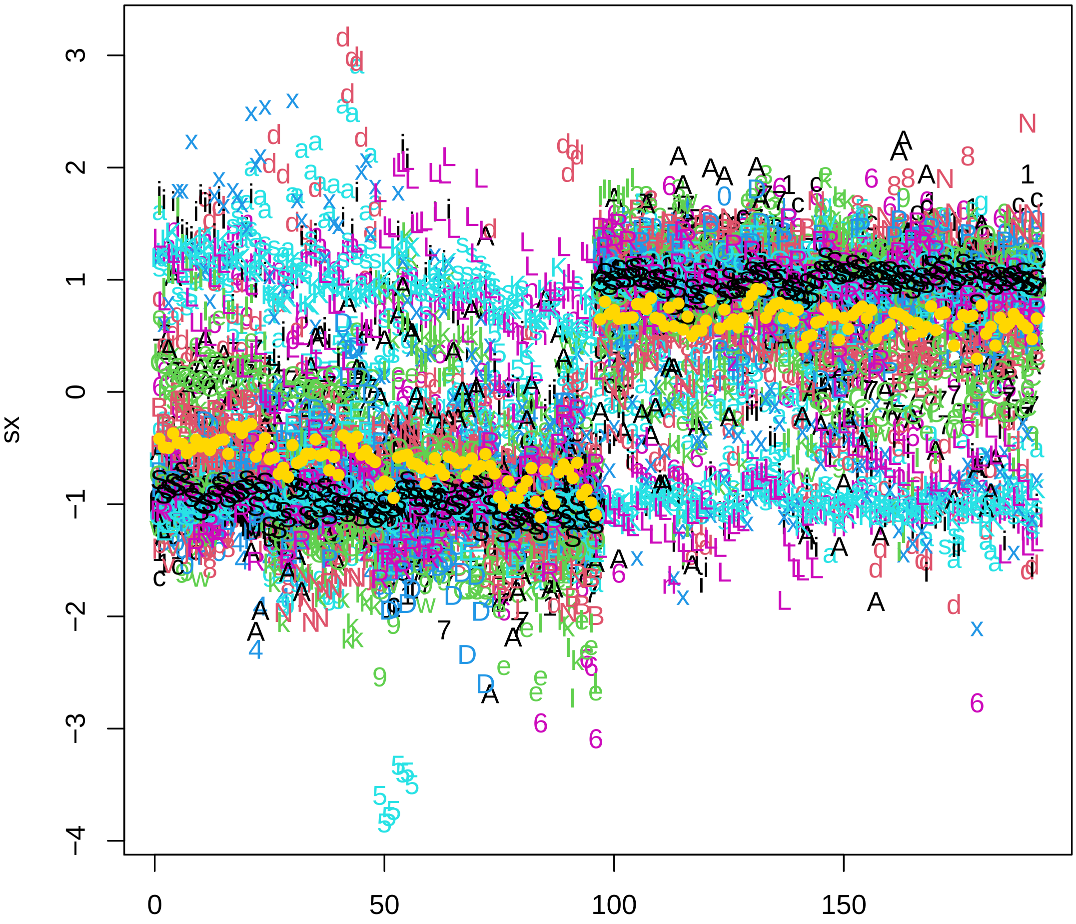
```
> head(apply(sx,1,mean, na.rm=TRUE))
  C18_11d_WS1   C18_11d_WS2   C18_11d_WS3   C18_11d_WS4   C18_11d_WW1
 3.156507e-18  2.714645e-17 -5.391442e-19  2.231091e-17  9.791331e-18
  C18_11d_WW2
-2.039877e-17
```

```
> 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

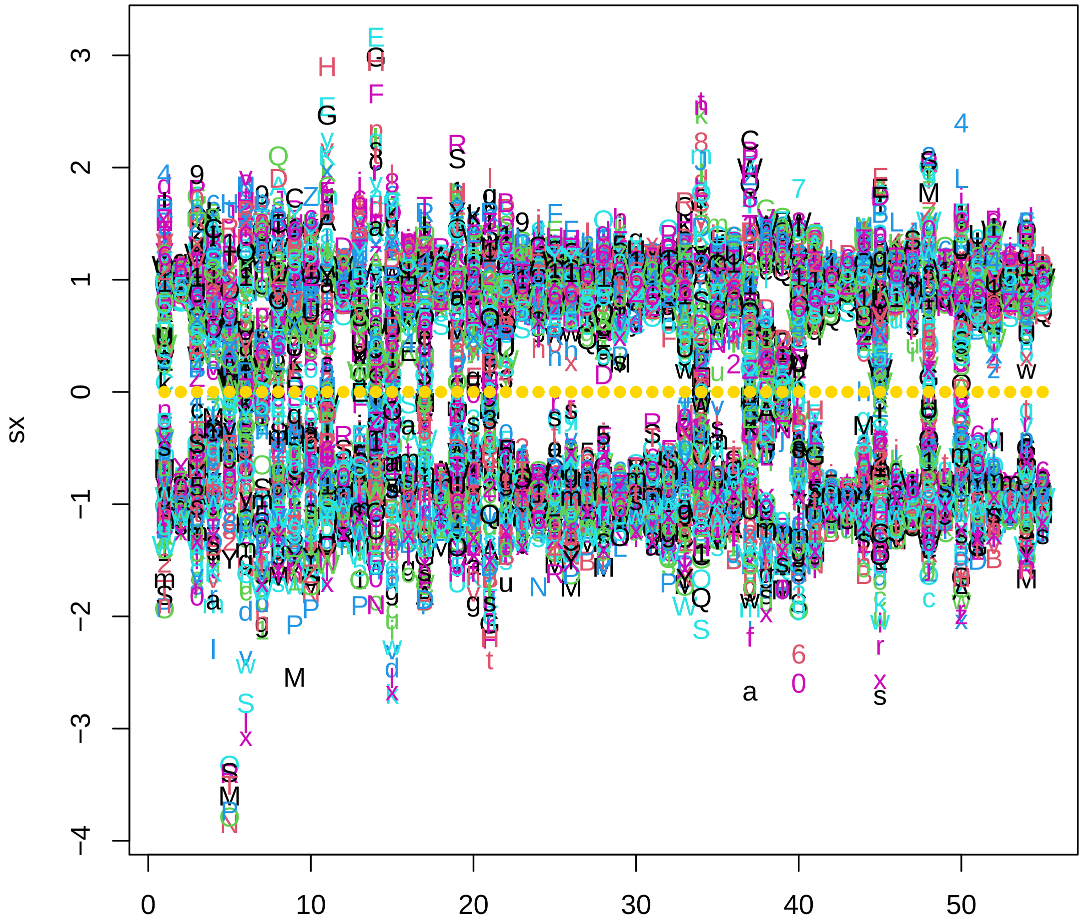
```
> x <- log2(m1819[,m_num_id])
> sx <- scale(x)
> matplot(sx)
> points(1:nrow(sx), apply(sx,1,mean, na.rm=TRUE), col="gold", pch=16)
```



```
> 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)
```

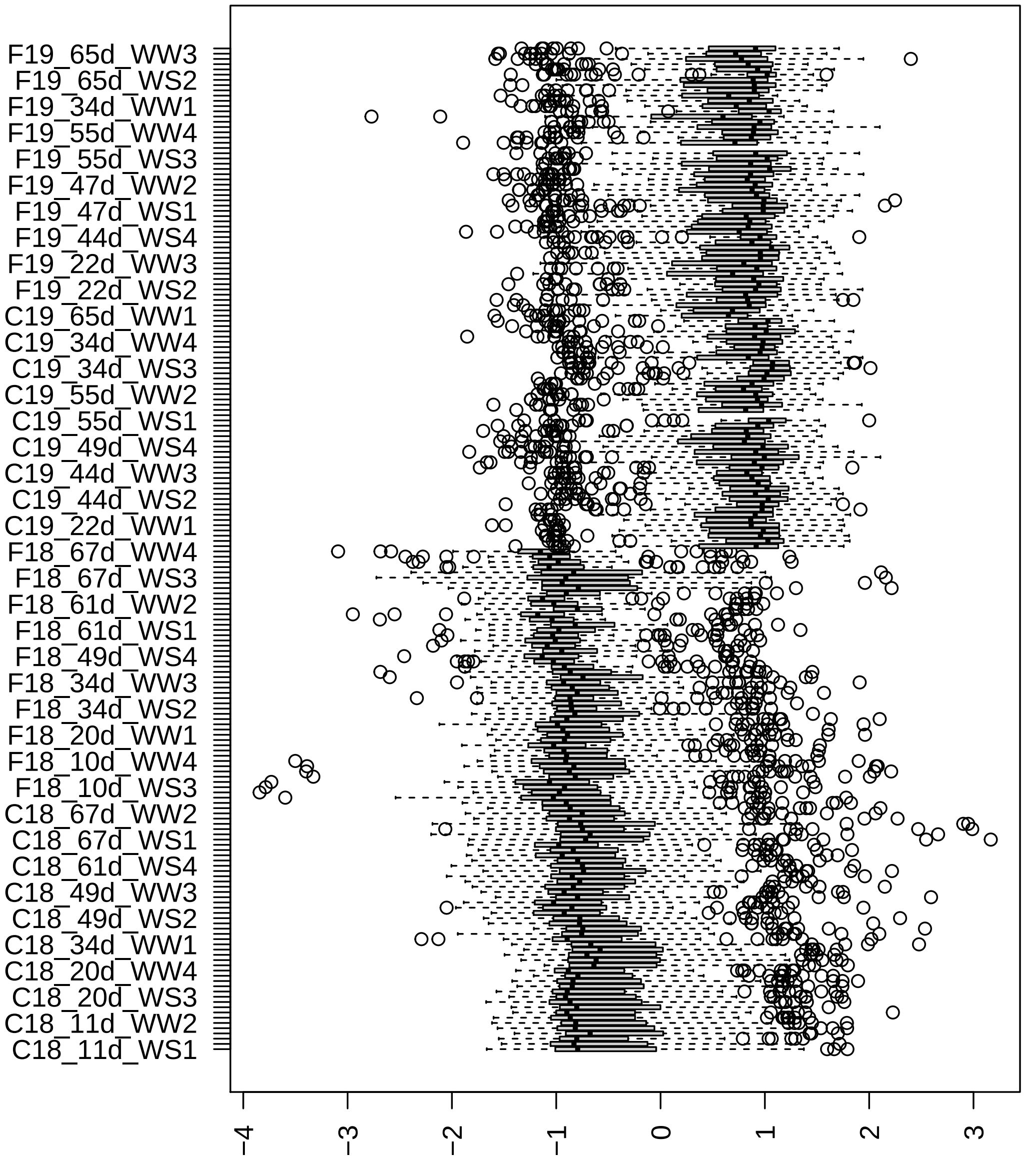


```
> head(apply(sx,2,mean, na.rm=TRUE))
C18_11d_WS1 C18_11d_WS2 C18_11d_WS3 C18_11d_WS4 C18_11d_WW1
 -0.4172622  -0.4925258  -0.4993865  -0.3693033  -0.4525290
C18_11d_WW2
 -0.4644972
```

```
> 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.txt"
> 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
```

```
              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.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
```

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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
```

```
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
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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
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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
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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
```

```
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


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

     name                   description      class nrow ncol
12 mfdata Metabolites featuredata 18/19 data.frame   55    3
```

```
                           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`
[1] "Vitvi01g00140" "Vitvi03g00287" "Vitvi07g01777" "Vitvi09g00246"
[5] "Vitvi17g00279" "Vitvi18g00994"

$`3.99`
character(0)

$`5`
[1] "Vitvi01g00787" "Vitvi04g01402" "Vitvi04g01668" "Vitvi06g00210"
```

```
[5] "Vitvi06g01689" "Vitvi06g01690"

$`6`
[1] "Vitvi07g03070" "Vitvi00g01243" "Vitvi00g01382" "Vitvi03g00785"
[5] "Vitvi05g00387" "Vitvi05g00388"

$`8.1`
[1] "Vitvi07g03070" "Vitvi01g00274" "Vitvi01g00861" "Vitvi01g01724"
[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`
[1] "Vitvi07g03049" "Vitvi00g00869" "Vitvi02g01749" "Vitvi01g00035"
[5] "Vitvi01g00502" "Vitvi01g00536"

$`16.1`
[1] "Vitvi10g02269" "Vitvi02g00020" "Vitvi02g00034" "Vitvi02g00420"
[5] "Vitvi02g00831" "Vitvi03g00262"

$`16.2`
[1] "Vitvi07g03081" "Vitvi07g03083" "Vitvi01g02214" "Vitvi01g01561"
[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)
```

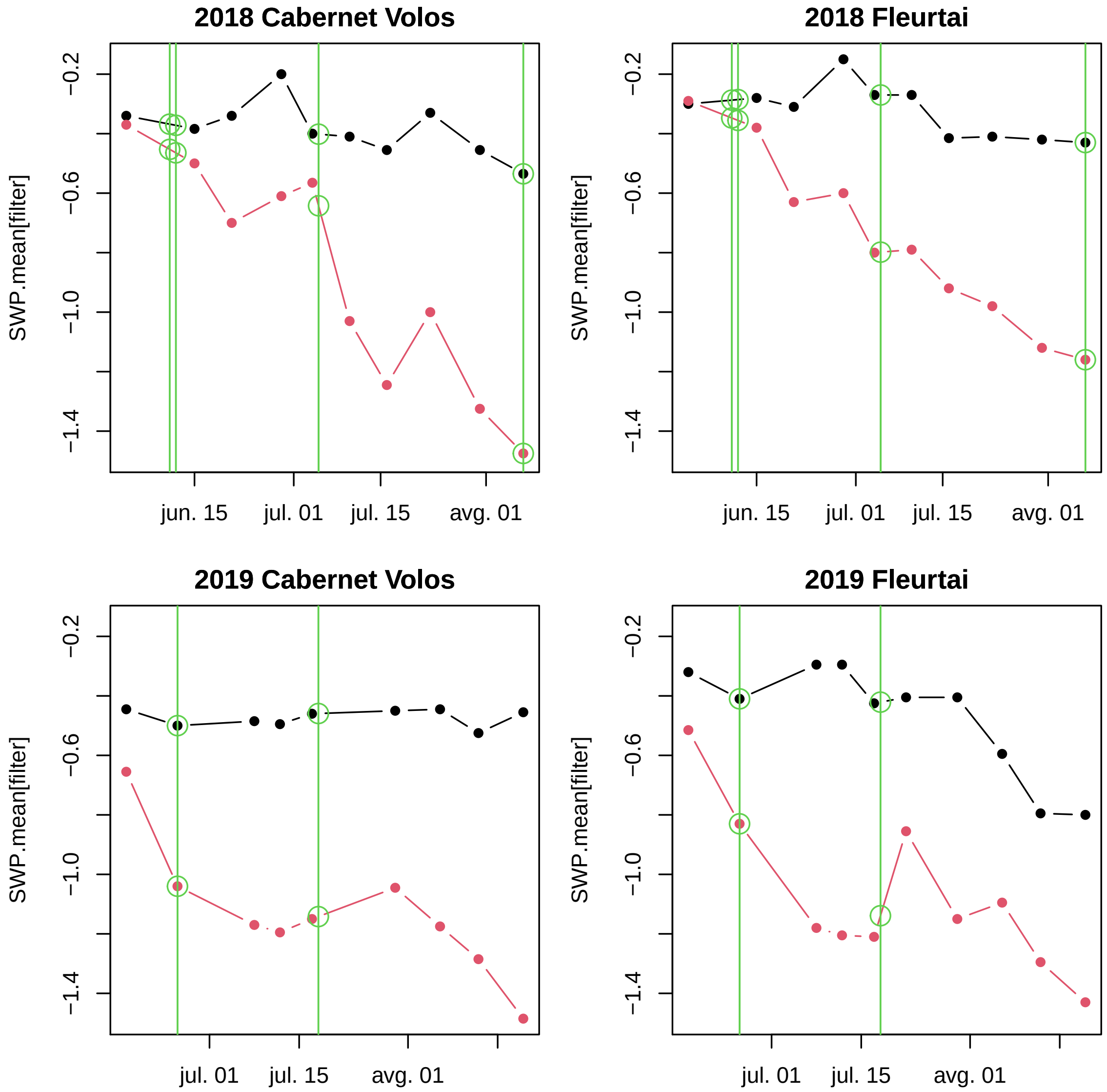
```
< table of extent 0 >
```

```
> 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 2019-06-2
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:

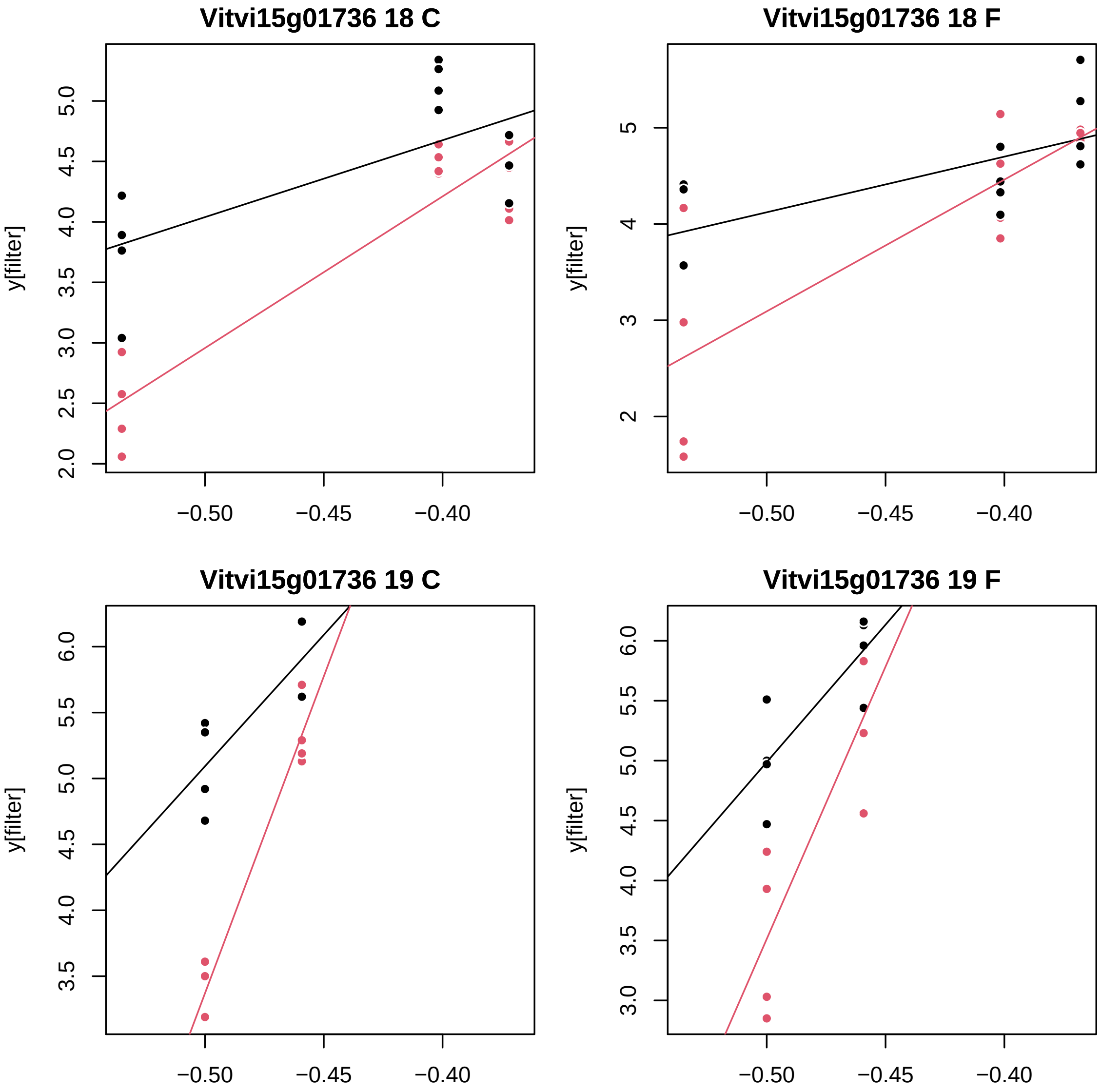
```
> t1819[1,]
              C18_11d_WS1 C18_11d_WS2 C18_11d_WS3 C18_11d_WS4
Vitvi15g01736    4.664602    4.109897     4.44822    4.013955
              C18_11d_WW1 C18_11d_WW2 C18_11d_WW3 C18_11d_WW4
Vitvi15g01736    4.717536    4.154237    4.475261    4.466465
              C18_34d_WS1 C18_34d_WS2 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:
```

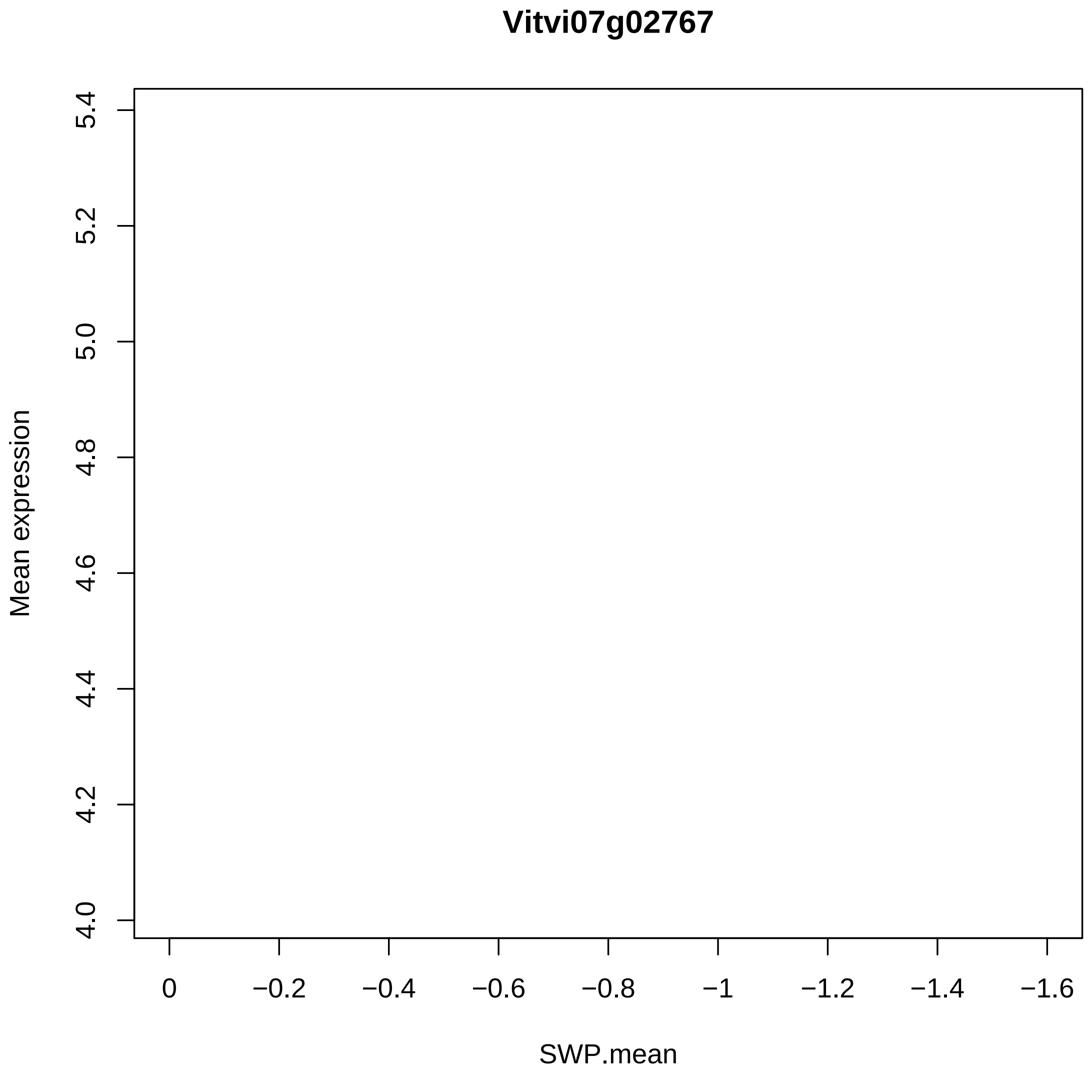
```
  (Intercept)  pd$swp[select]
        26.23           45.44
> .testing <- FALSE
```

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)
```

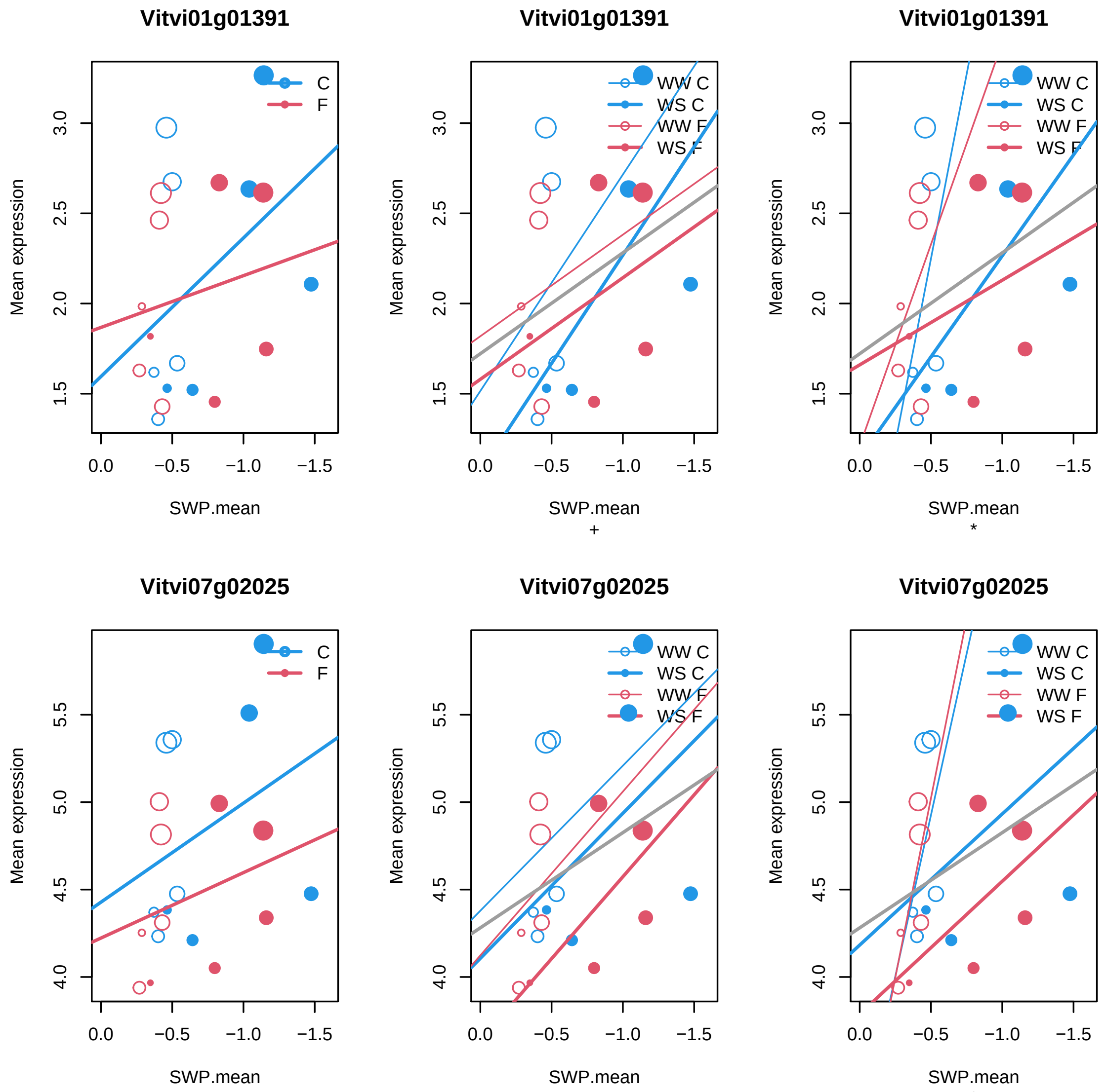


```
> legend("topright", bty="n", pch=pchs, col=cols,legend <- vlvls)
Error in as.graphicsAnnot(legend): argument "legend" is missing, with no defau
> #
> for(i in 1:length(vlvls)){
+ for( j in 1:length(tlvls)){
+ tfilter <- wpas$treat %in% tlvls[j]
+ vfilter <- wpas$variety %in% vlvls[i]
+ yy <- means[as.character(wpa$date),tlvls[j],vlvls[i]]
+ wpa <- wpas[tfilter & vfilter,]
+ all(wpa$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"
```

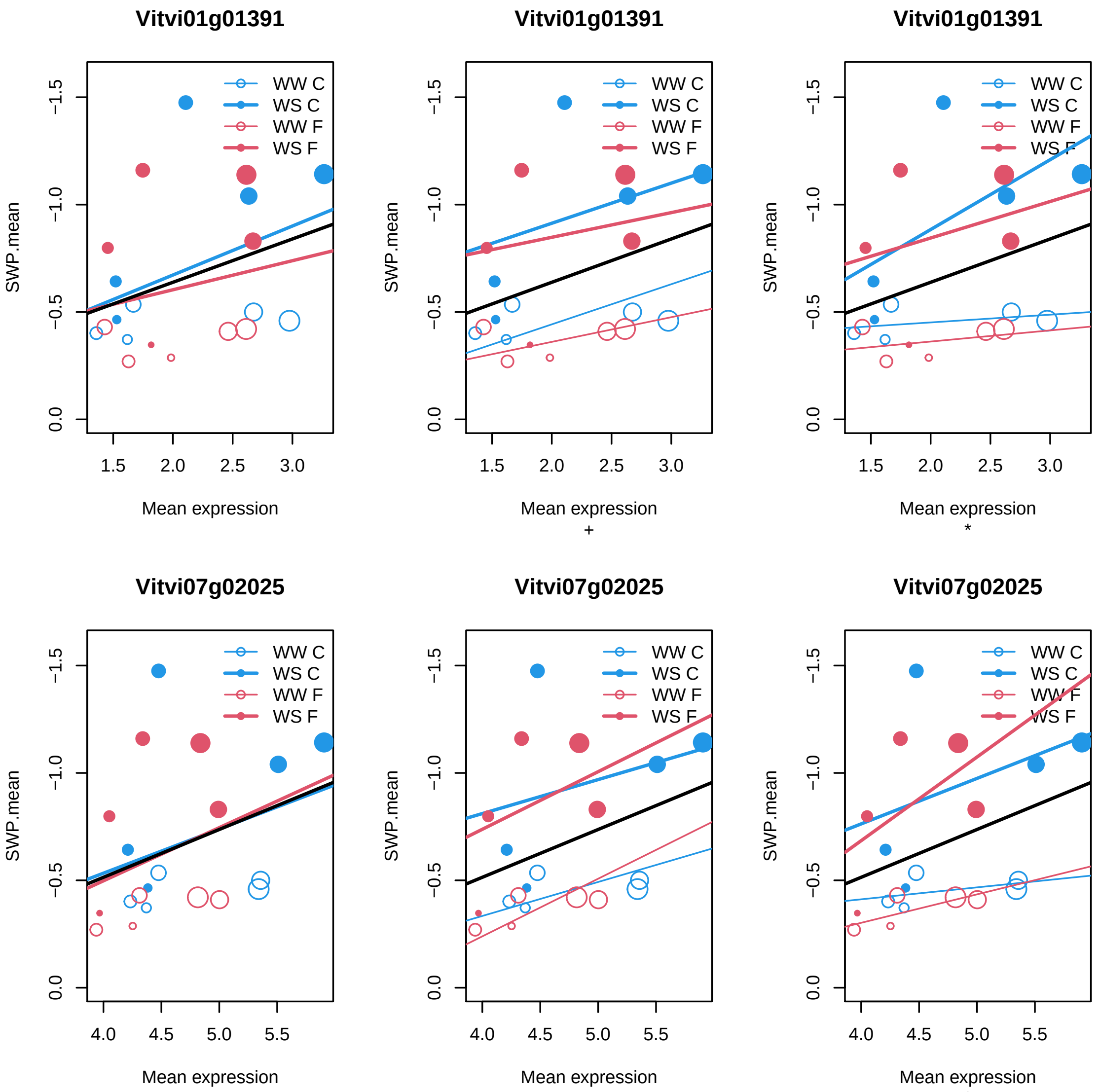
4.2 Water potential vs Expression

```
> 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
```

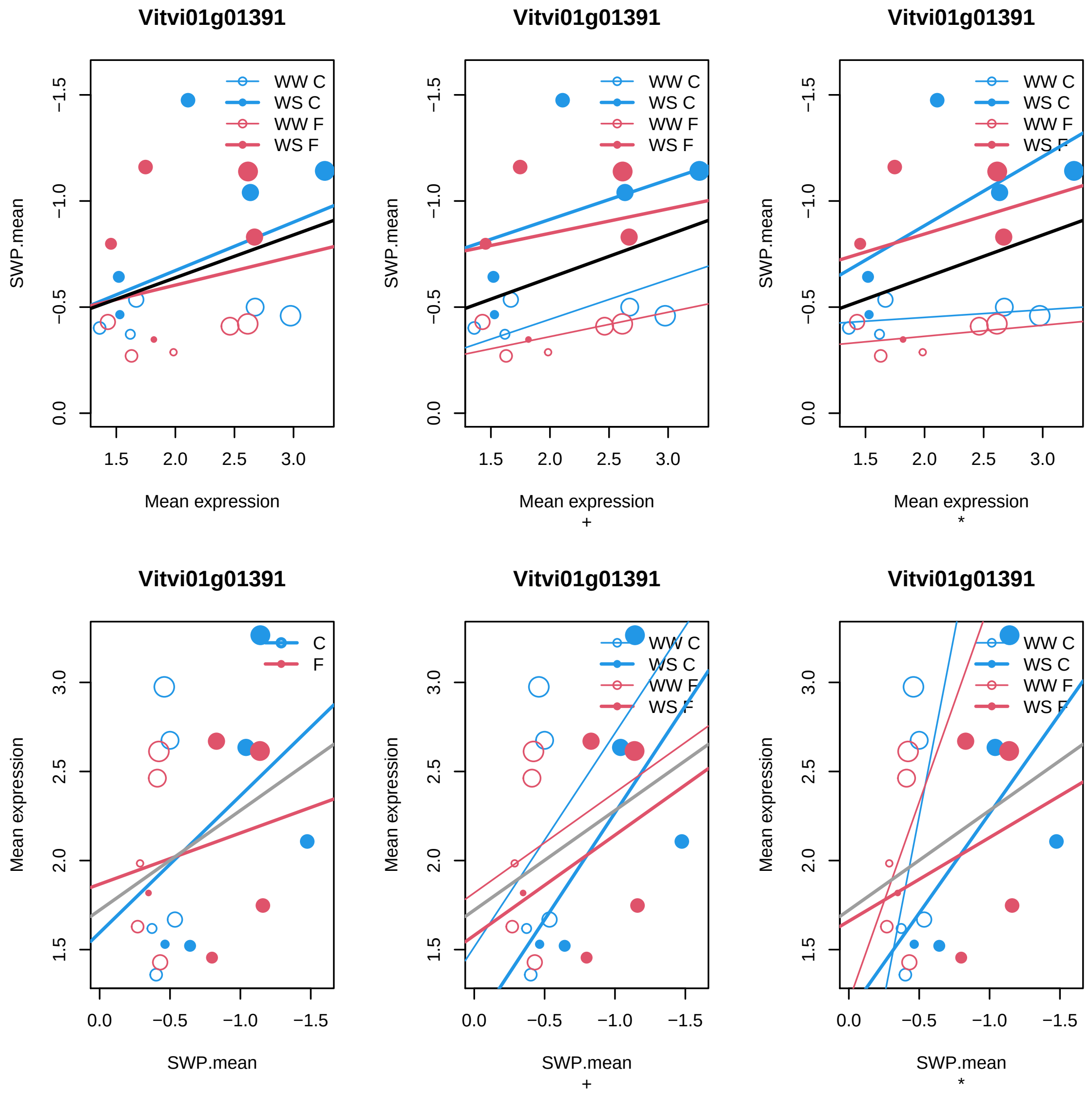
```
+ fits[["r"]] <- cor(ally,allx,use="complete")
+ if (verbose) print(summary(fit))
+ abline(fit$coefficients,lwd=2)
+ #points(-swps,means,cex=1.5)
+ invisible(fits)
+ }
```

```
> 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 
```

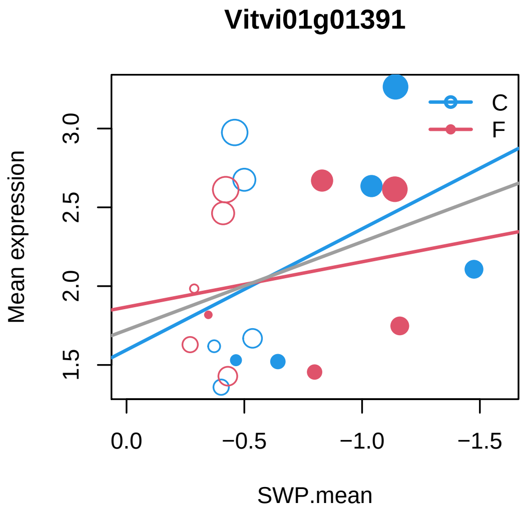
```
F18_10d_WW3 F18_10d_WW4 F18_34d_WS1 F18_34d_WS2 F18_34d_WS3
  1.9447357   1.7887485   1.5892246   1.3699329   1.4469174
F18_34d_WS4 F18_34d_WW1 F18_34d_WW2 F18_34d_WW3 F18_34d_WW4
  1.4139991   1.5153857   1.4749029   1.9144891   1.6107161
F18_67d_WS1 F18_67d_WS2 F18_67d_WS3 F18_67d_WS4 F18_67d_WW1
  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
```

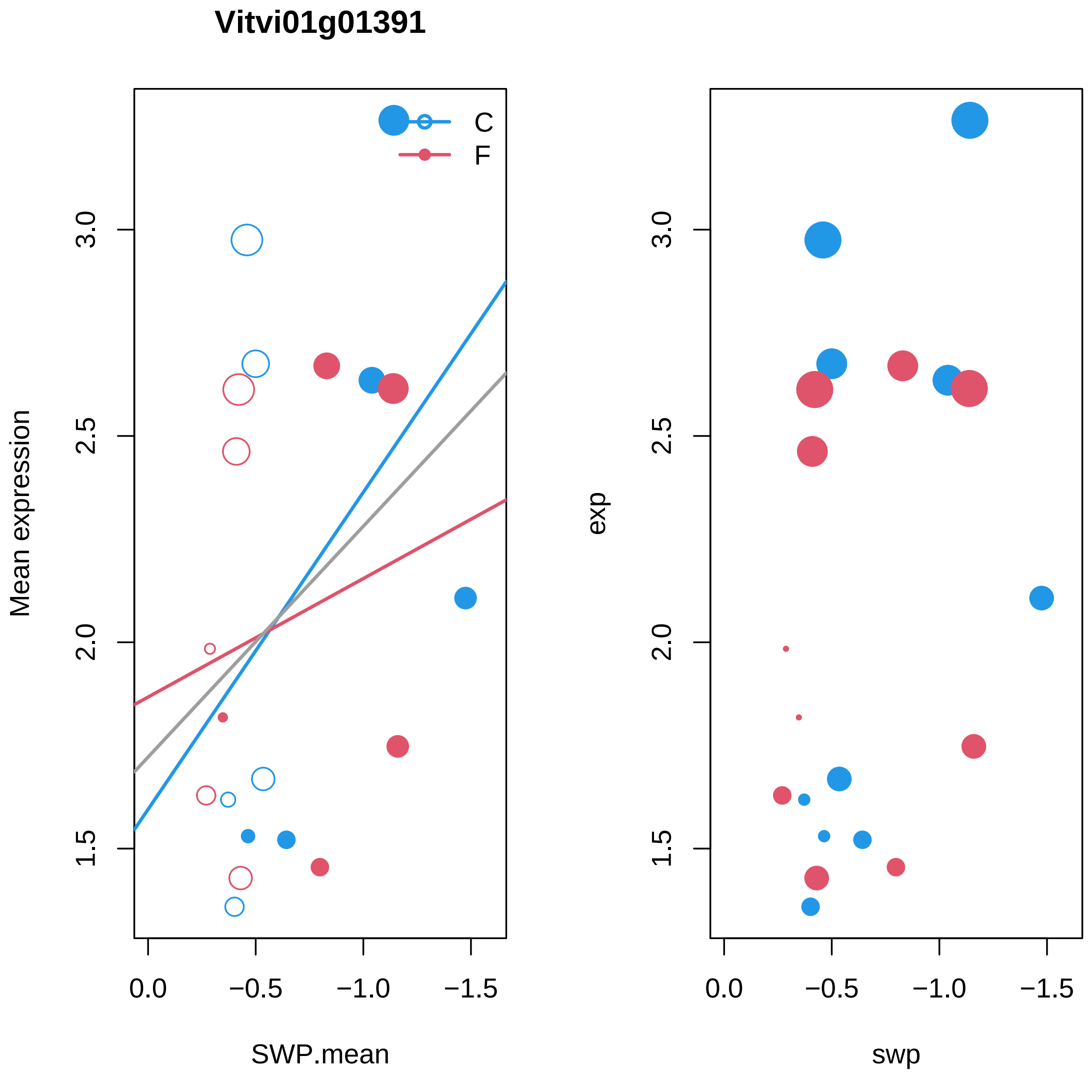
```
             swp treat variety sday       date
WW.C1 -0.3680000    WW       C    1 2018-06-11
WW.C2 -0.3720000    WW       C    2 2018-06-12
WW.C3 -0.4016667    WW       C    3 2018-07-05
WW.C4 -0.5350000    WW       C    4 2018-08-07
WW.C5 -0.5000000    WW       C    5 2019-06-26
WW.C6 -0.4592308    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-2-2-0.5-1-0.5-1/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

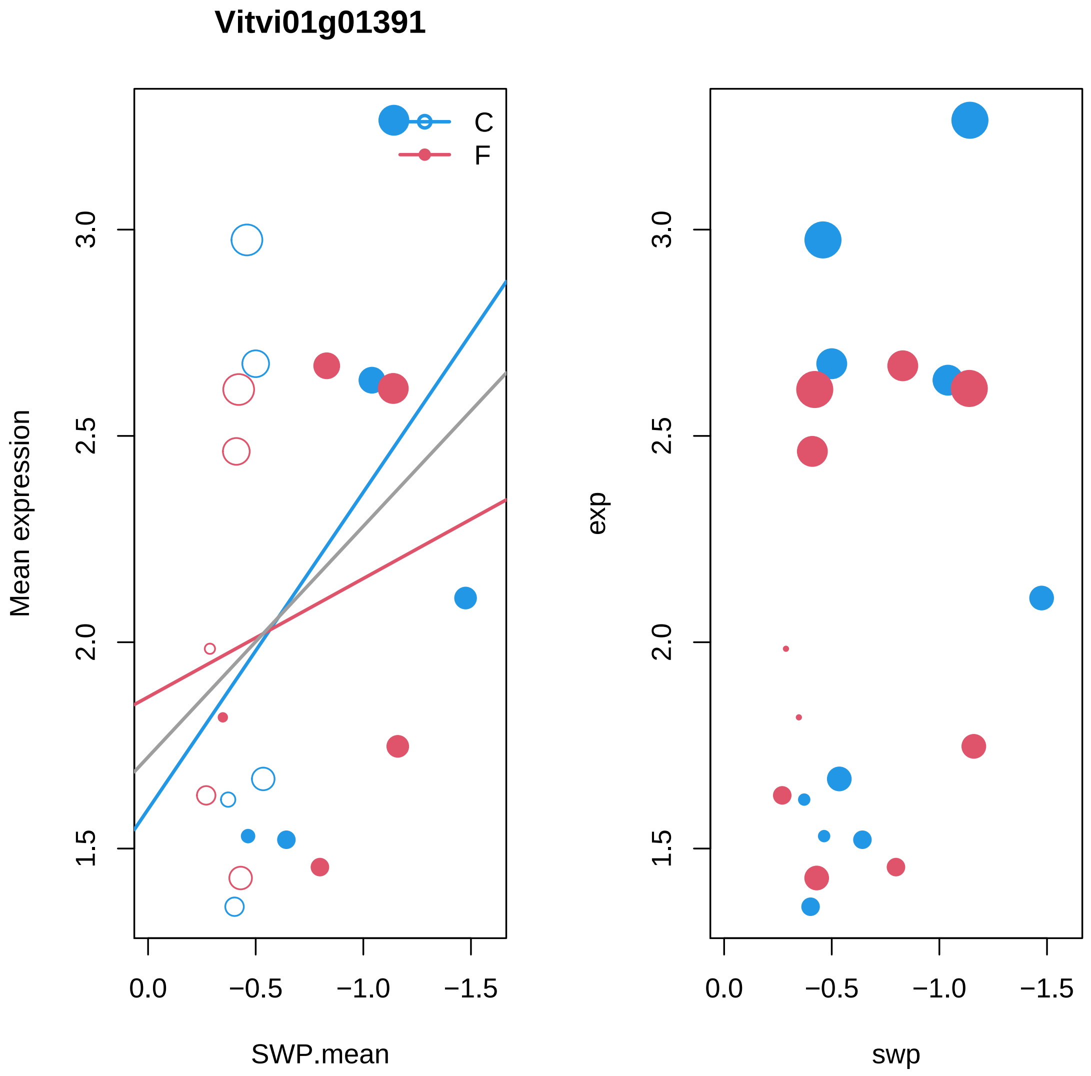
```
> FUN <- function(x) unlist(as.data.frame(tapply(unlist(x),pd[,c("date","treat
> FUN(exprs[1,])
   WW.C1    WW.C2    WW.C3    WW.C4    WW.C5    WW.C6    WS.C1 
      NA 4.453375 5.153464 3.727798 5.092500 5.905000       NA 
   WS.C2    WS.C3    WS.C4    WS.C5    WS.C6    WW.F1    WW.F2 
4.309168 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)
```

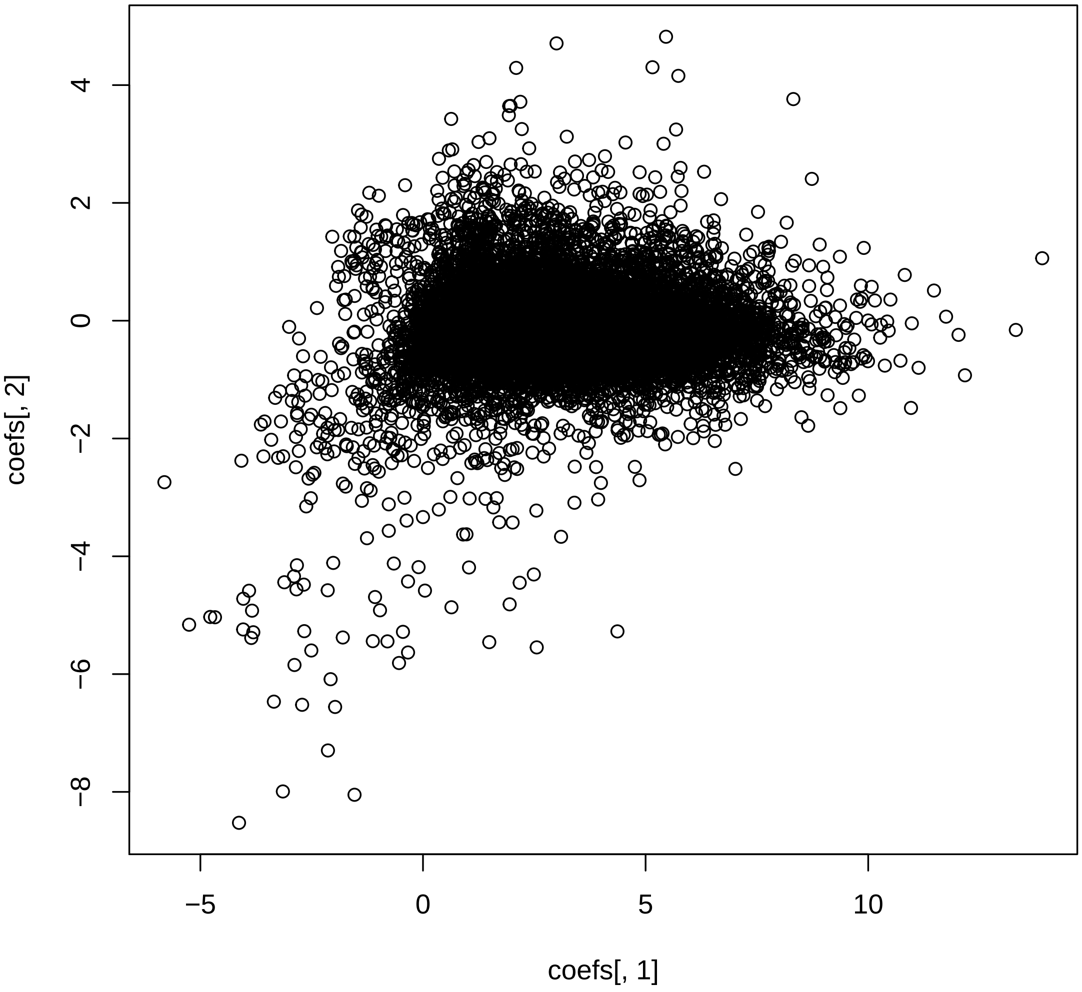
```
              (Intercept)       swp
Vitvi15g01736  5.42287213 1.4417521
Vitvi07g02832  0.79297631 1.4868377
Vitvi07g02830  1.05522190 2.1023461
Vitvi07g02812  0.02875199 0.5715781
Vitvi07g02811  3.02521622 0.8198777
Vitvi09g02033 -0.13442101 0.9949253
```

```
> 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
```

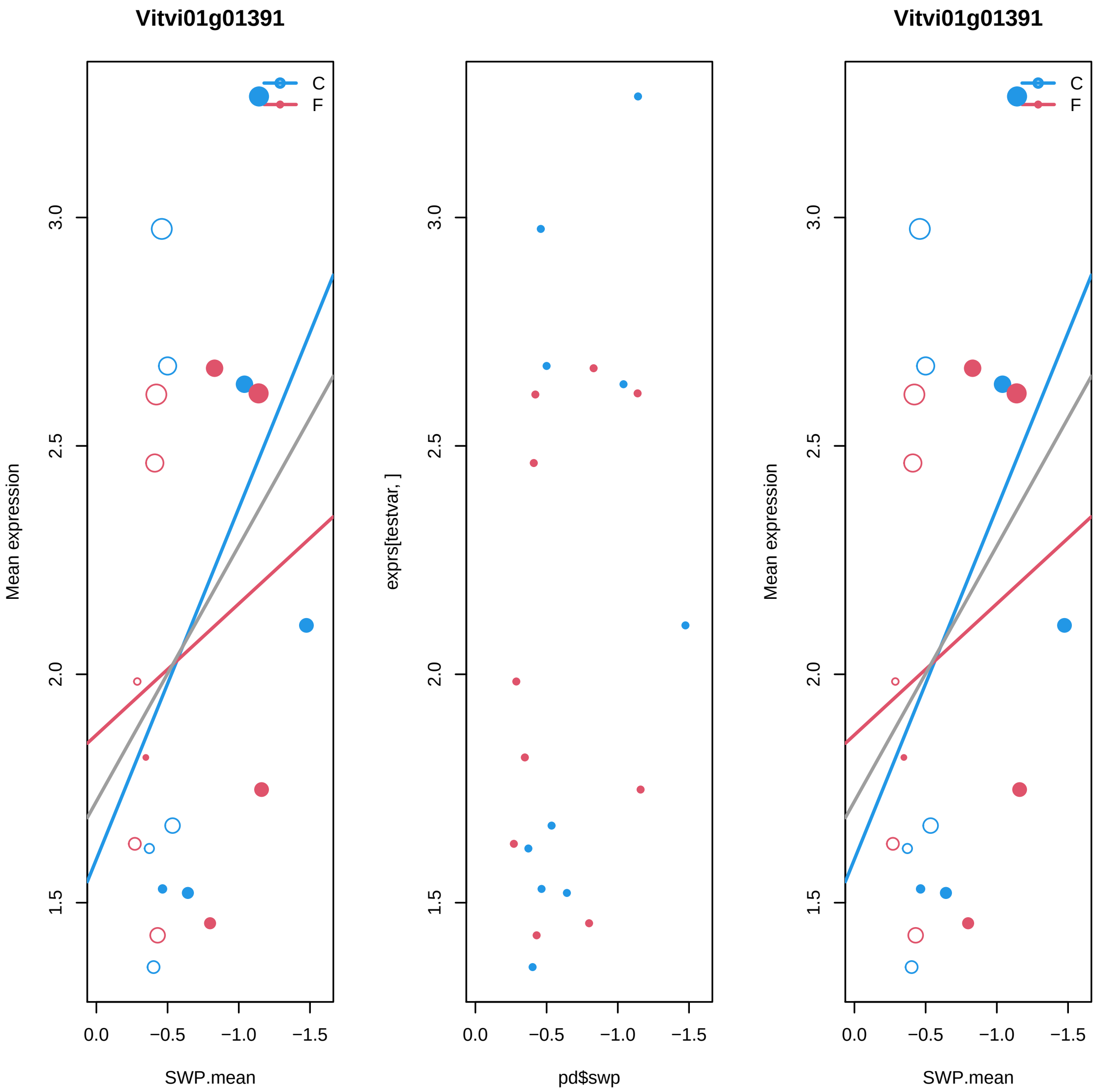
```
> tail(design2)
   (Intercept)        swp varietyF swp:varietyF
15           1 -0.4210000        1   -0.4210000
16           1 -0.3472727        1   -0.3472727
17           1 -0.7983333        1   -0.7983333
18           1 -1.1600000        1   -1.1600000
19           1 -0.8300000        1   -0.8300000
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]
```

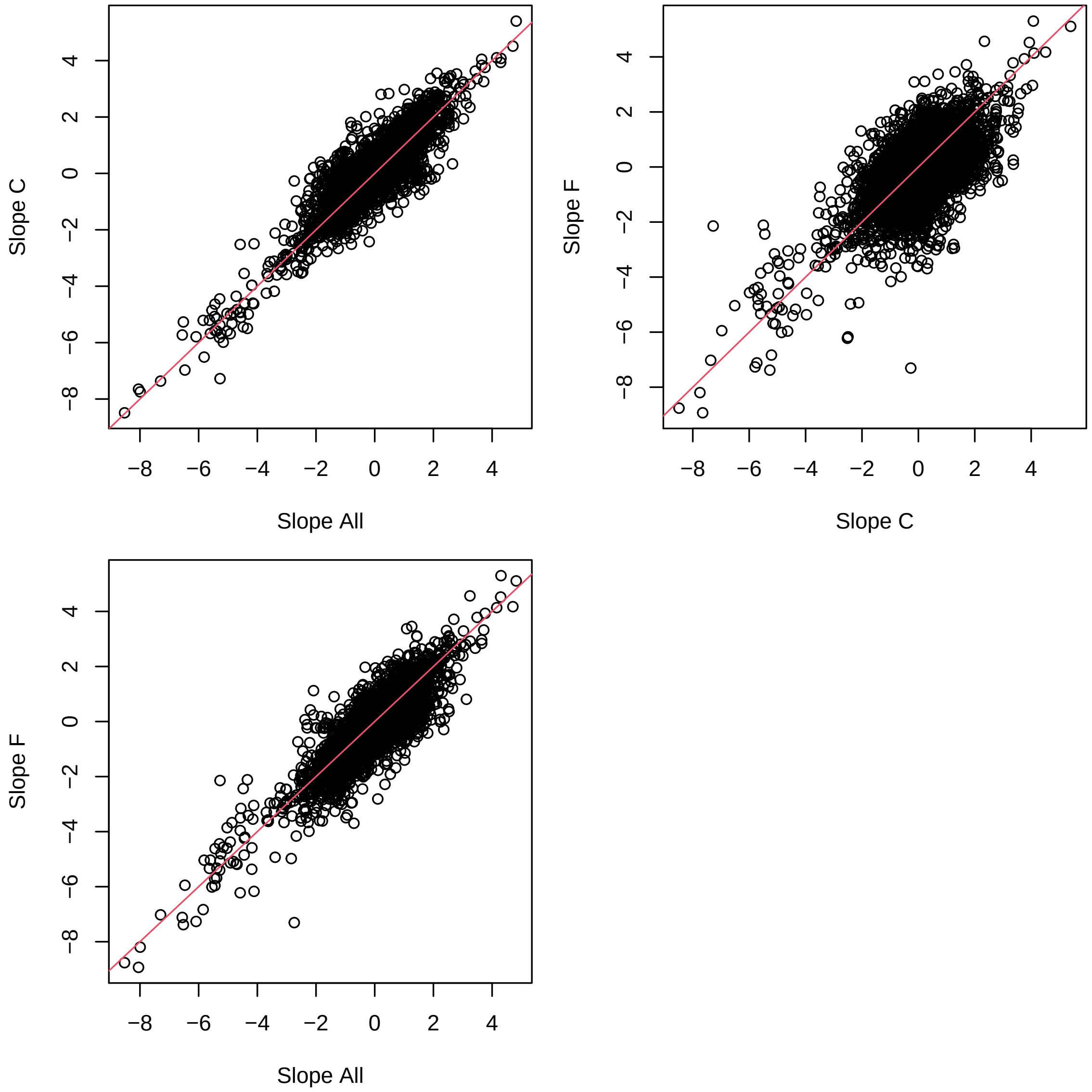
```
   pd1$swp
-0.2871816
```

```
> 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

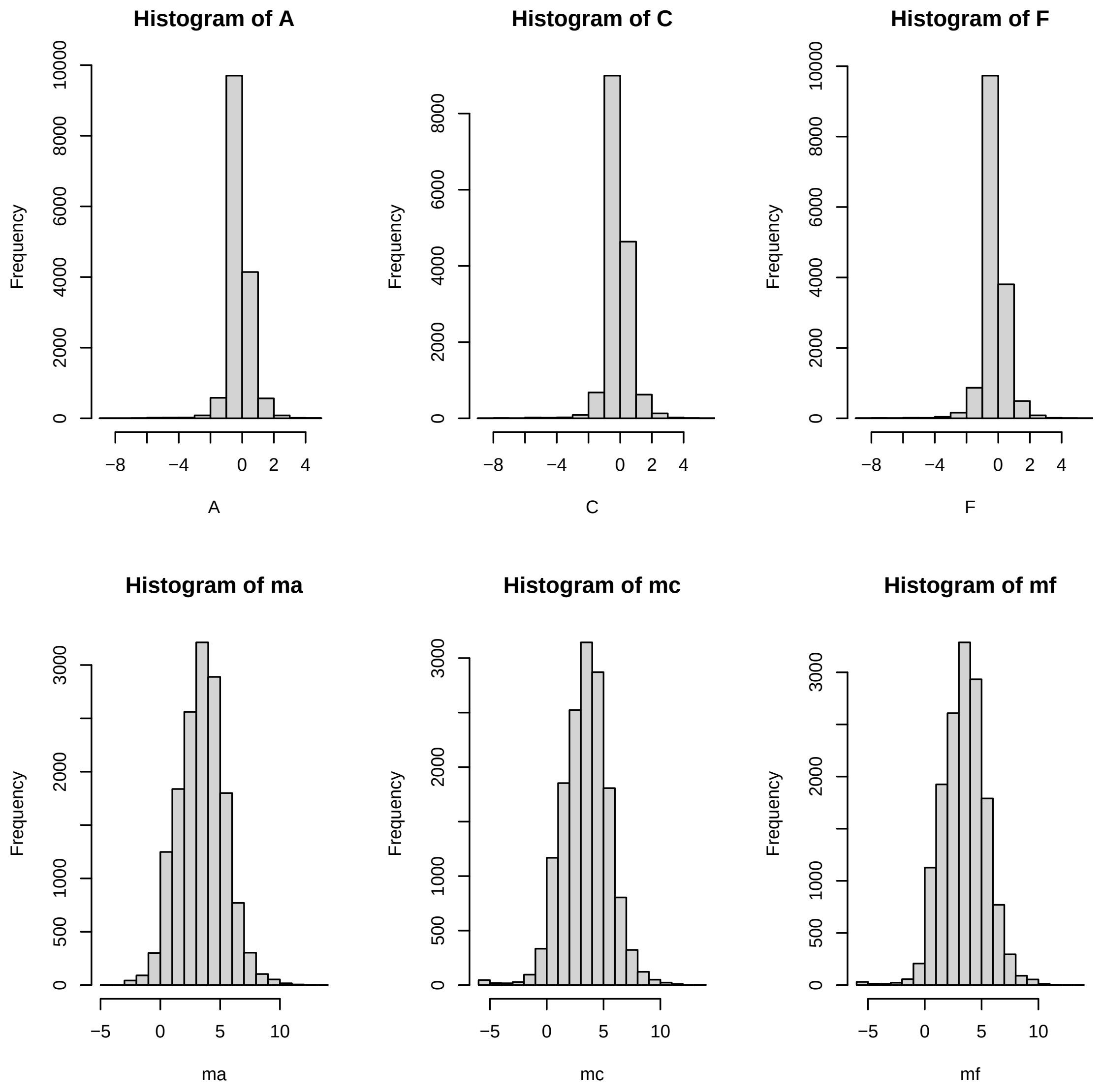
```
> A <- fit1$coefficients[,2]
> C <- fit2$coefficients[,2]
> F <- fit2$coefficients[,2]+fit2$coefficients[,4]
> ma <- macf[,"ma"]
> mc <- fit3$coefficients[,1]
> mf <- fit3$coefficients[,2]
> coefs <- data.frame(A,C,F,ma,mc,mf)
> head(coefs)
```

```
                      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
```

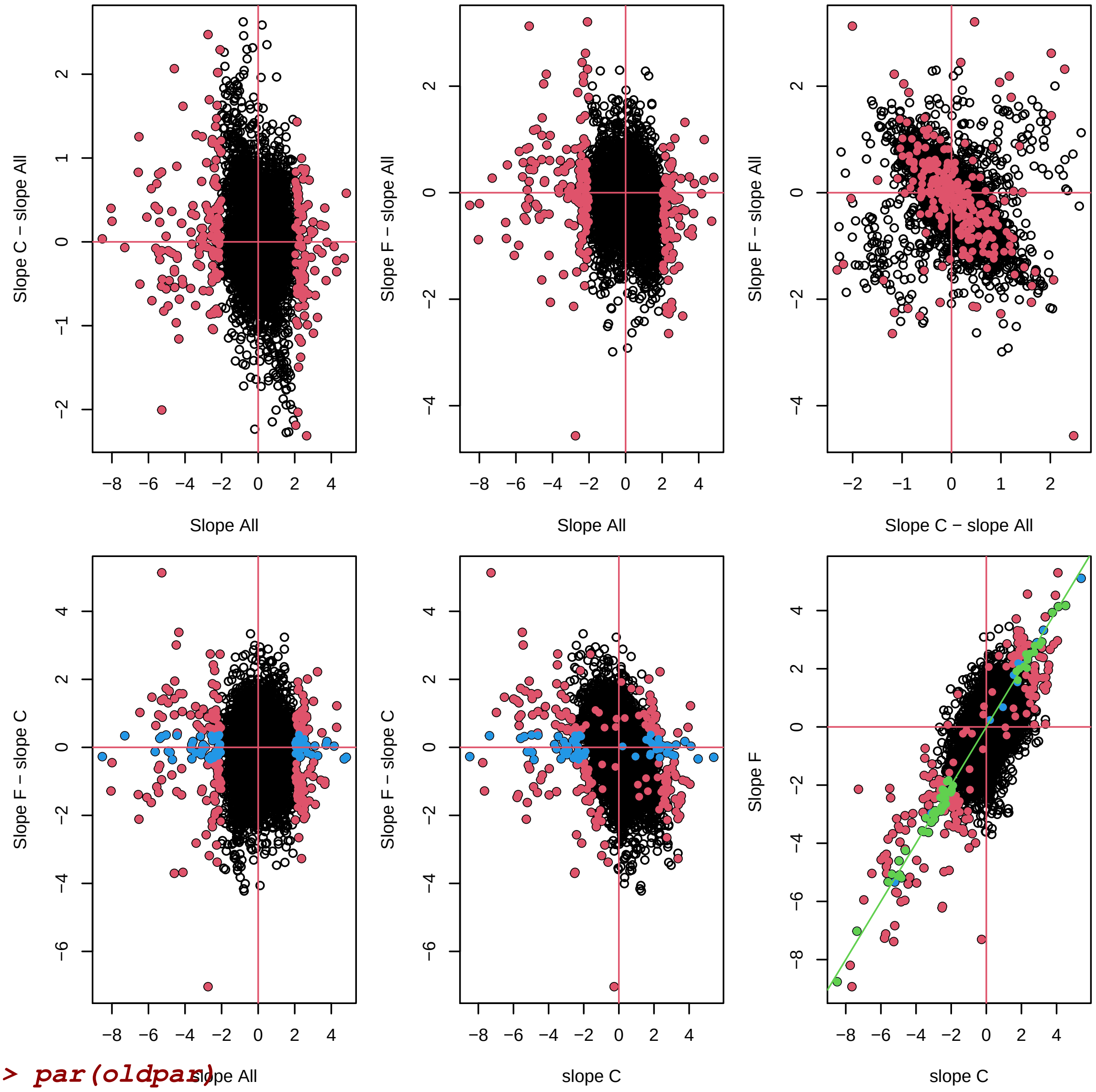
```
> par(mfrow=c(2,3))
> hist(A,xlim=range(c(A,C,F)))
> hist(C,xlim=range(c(A,C,F)))
> hist(F,xlim=range(c(A,C,F)))
> hist(ma)
> hist(mc)
> hist(mf)
```



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
  "2"
> .maxC         # <- 0.5
.maxC
"0.5"
> .minfc        # <- 1
.minfc
   "1"
> .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 2 with difference of slopes smaller than 0.5 and difference of means below 2.

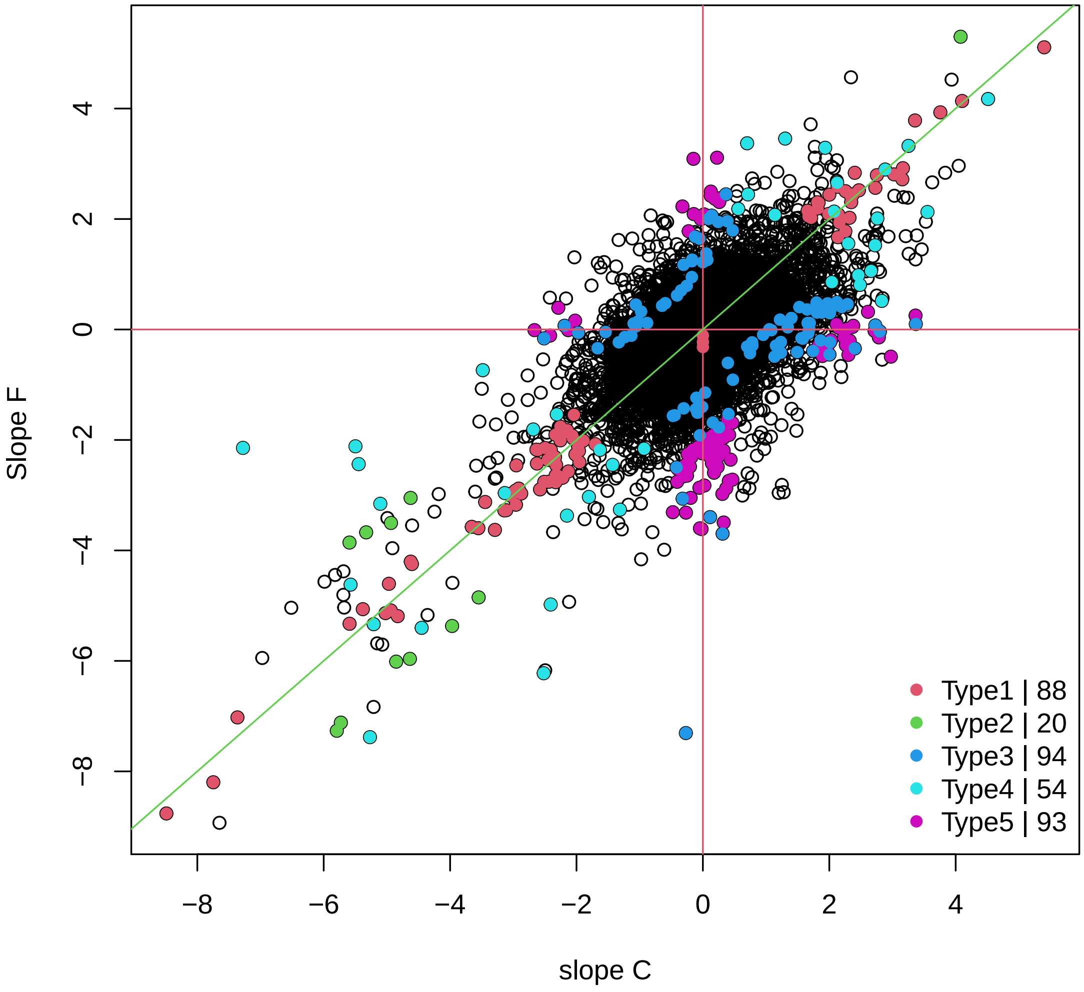
Type2

```
> #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 2 , both positive or negative, with difference of slopes larger than 1 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 15146    16
  TRUE      8    72
> 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 14136  1012
  TRUE      0    94

> 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 15055    93
  TRUE     94     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
```

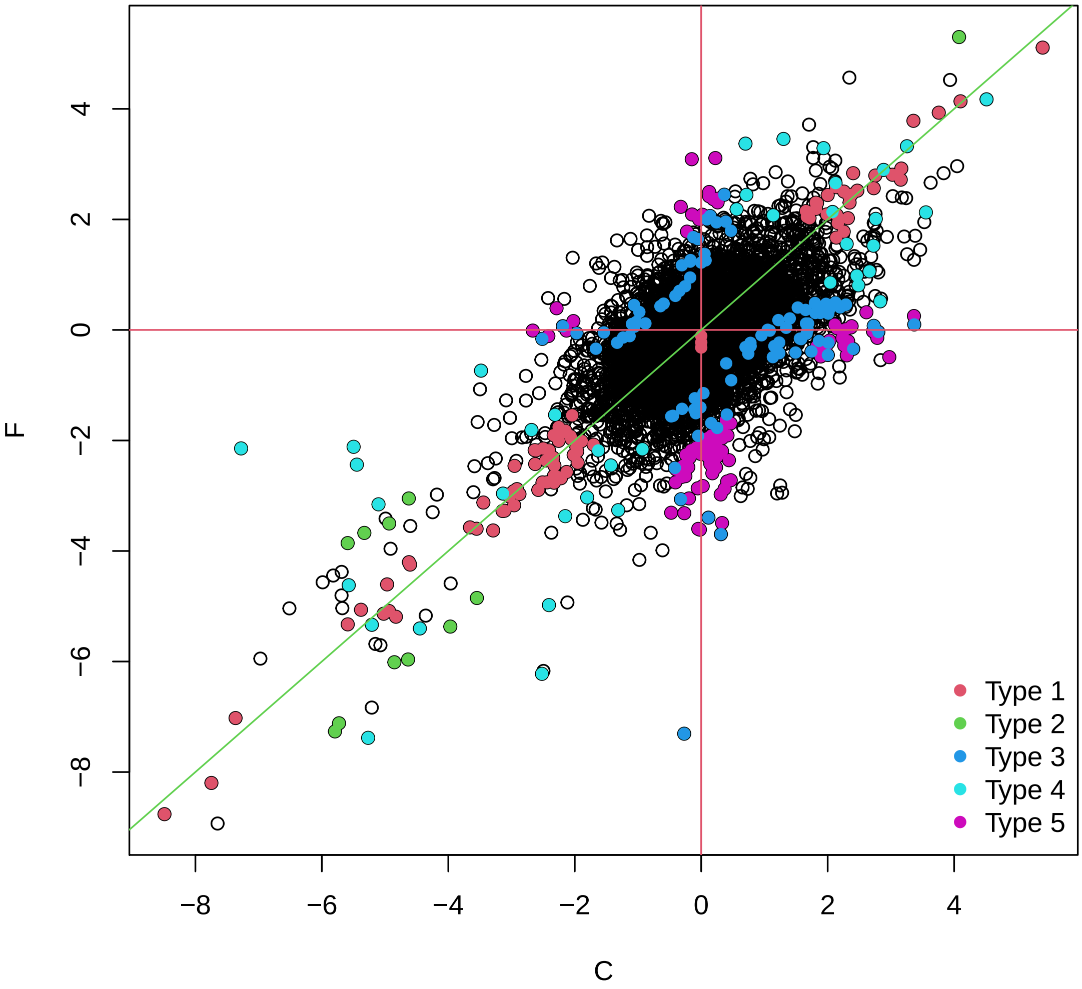


```
> head(types)
```

```
                type1 type2 type3 type4 type5
Vitvi15g01736 FALSE FALSE FALSE FALSE FALSE
Vitvi07g02832 FALSE FALSE FALSE FALSE FALSE
Vitvi07g02830 FALSE FALSE FALSE FALSE FALSE
Vitvi07g02812 FALSE FALSE FALSE FALSE FALSE
Vitvi07g02811 FALSE FALSE FALSE FALSE FALSE
Vitvi09g02033 FALSE FALSE FALSE 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]],
```

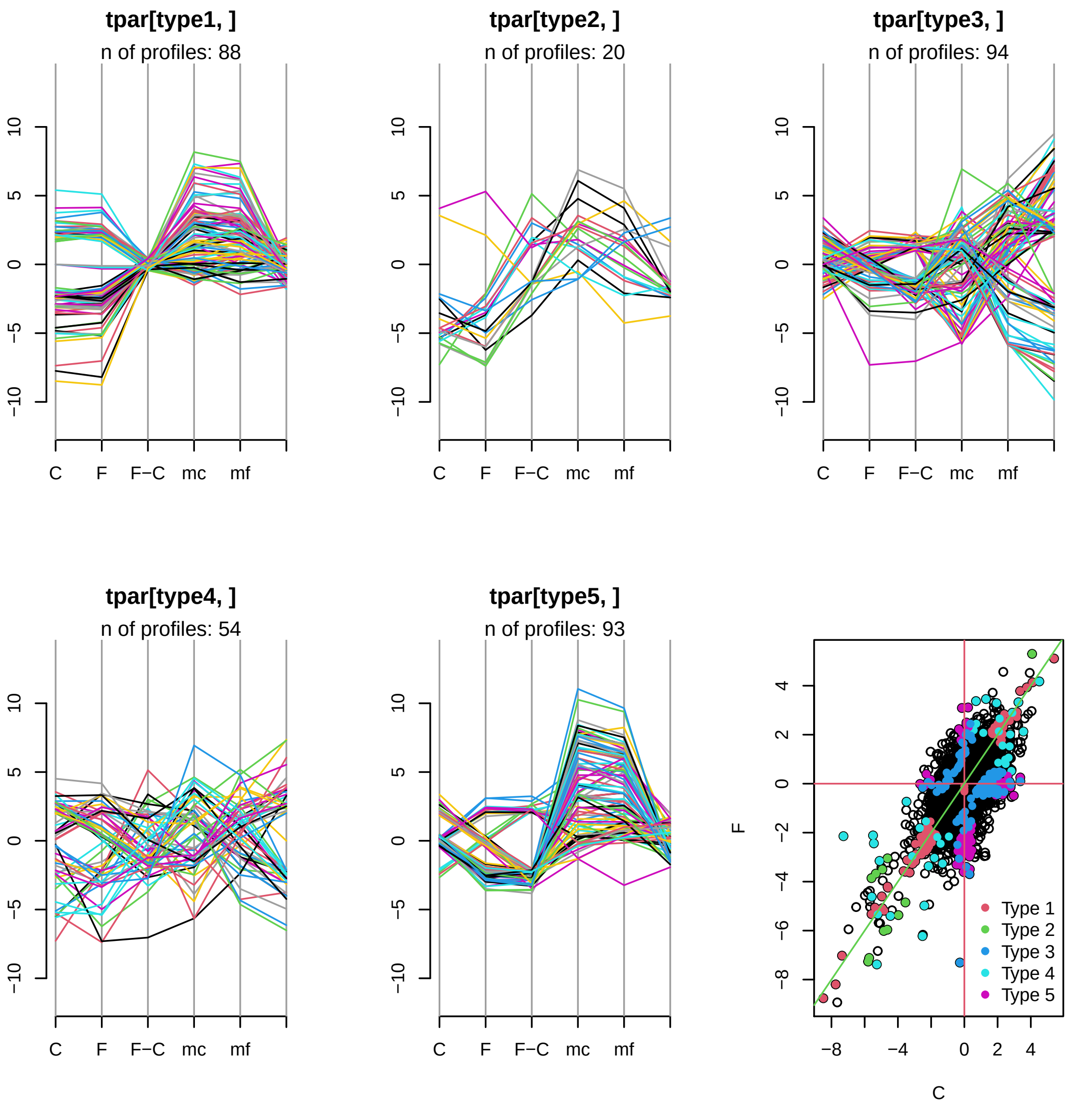
```
+    col=i+1,pch=16)
+    }
+    abline(h=0,v=0,col=2)
+ abline(c(0,1),col=3)
+ if(!missing(title)) title(title)
+ legend("bottomright",pch=rep(16,m),col=1+(1:m),legend=paste("Type",1:m),bty=
+ }
> plot.types()
```



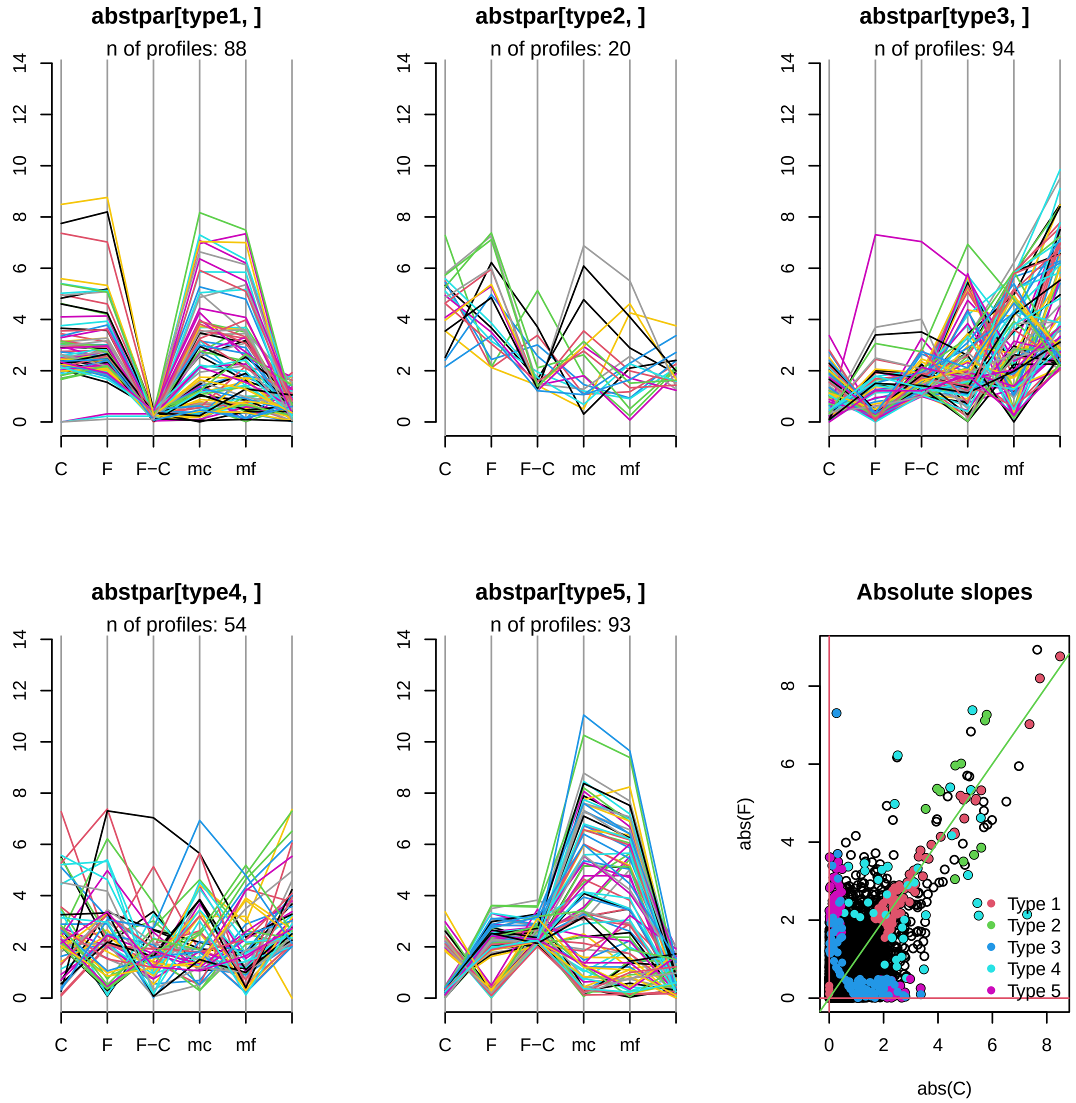
```
> x <- coefs[type1,]
> ylim <- range(x)
> my.parallelplot <- function(x, ylim = range(x), title,  ...){
+ if(missing(title)) title <- deparse(substitute(x))
+ m <- ncol(x)
+ plot(0,0, type = "n"
+     , xlim = c(1,m)
+     , ylim = ylim
+     , axes = FALSE
+     , ann=FALSE
+     )
```

```
+ 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,])
```

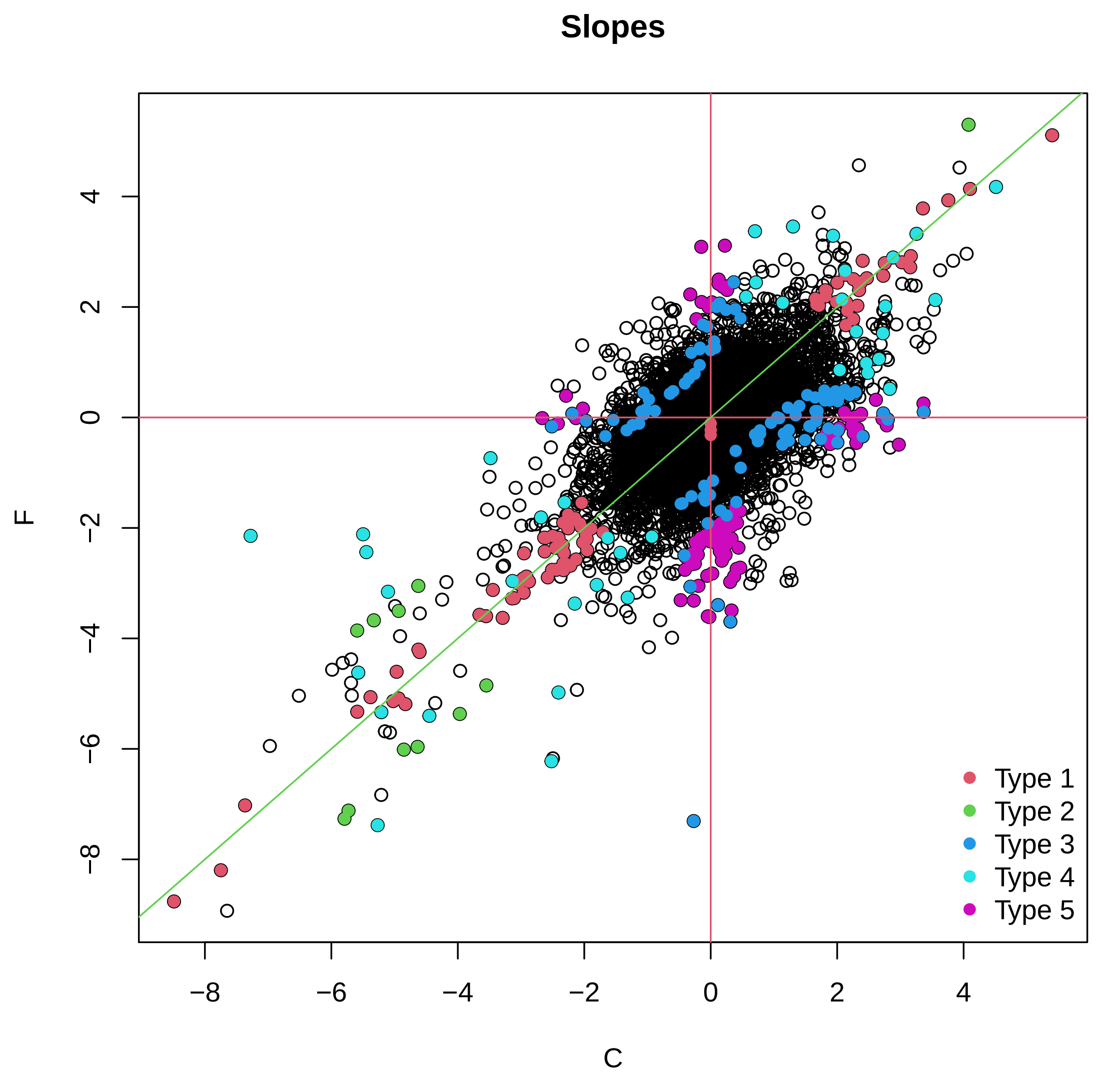
```
> par(mfrow=c(2,3))
> tpar <- data.frame(C,F,F-C,mc,mf,mf-mc)
> ylim <- range(tpar)
> my.parallelplot(tpar[type1,], ylim=ylim)
> my.parallelplot(tpar[type2,], ylim=ylim)
> my.parallelplot(tpar[type3,], ylim=ylim)
> my.parallelplot(tpar[type4,], ylim=ylim)
> my.parallelplot(tpar[type5,], ylim=ylim)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



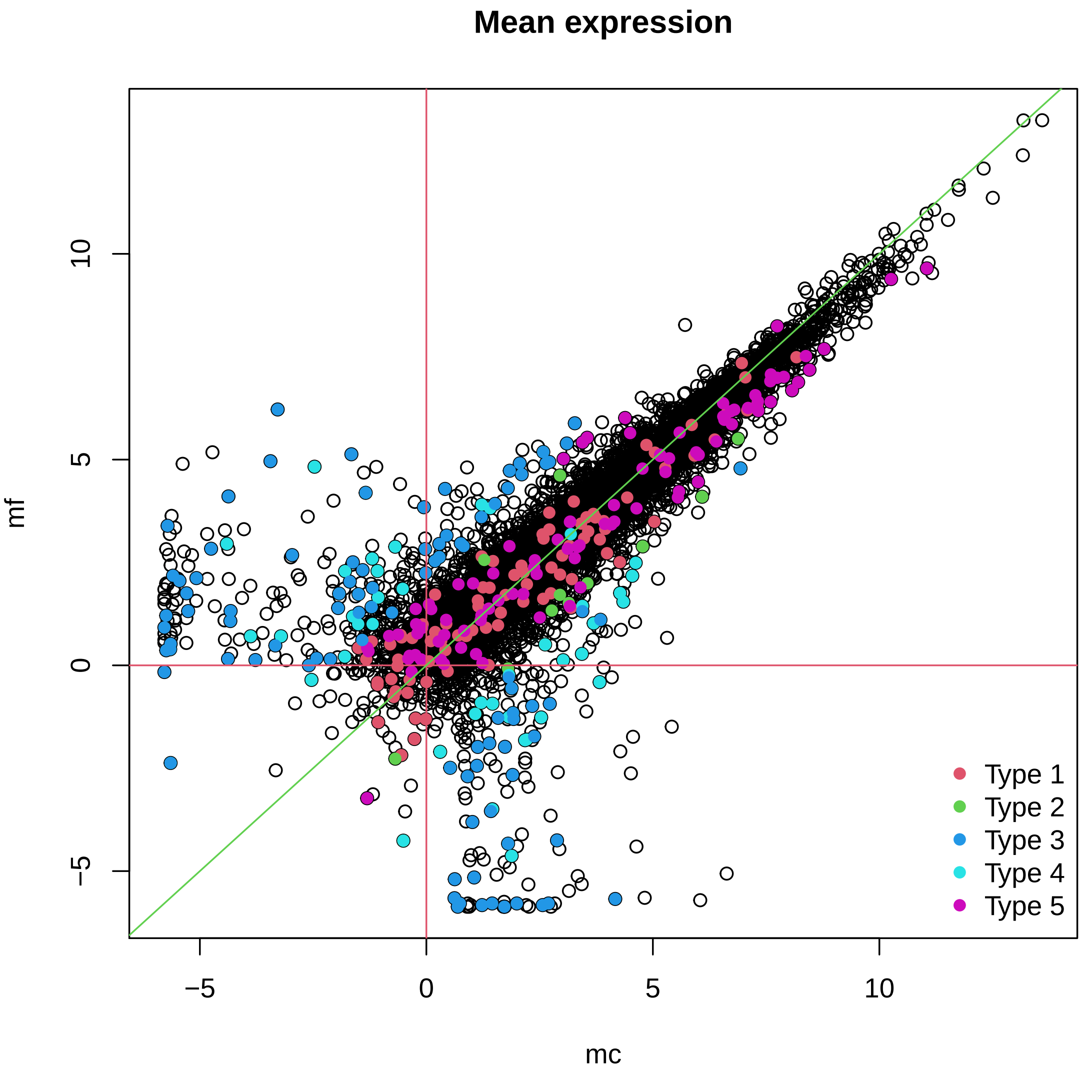
```
> par(mfrow=c(2,3))
> tpar <- data.frame(C,F,F-C,mc,mf,mf-mc)
> abstpar <- abs(tpar)
> ylim <- range(abstpar)
> my.parallelplot(abstpar[type1,], ylim=ylim)
> my.parallelplot(abstpar[type2,], ylim=ylim)
> my.parallelplot(abstpar[type3,], ylim=ylim)
> my.parallelplot(abstpar[type4,], ylim=ylim)
> my.parallelplot(abstpar[type5,],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



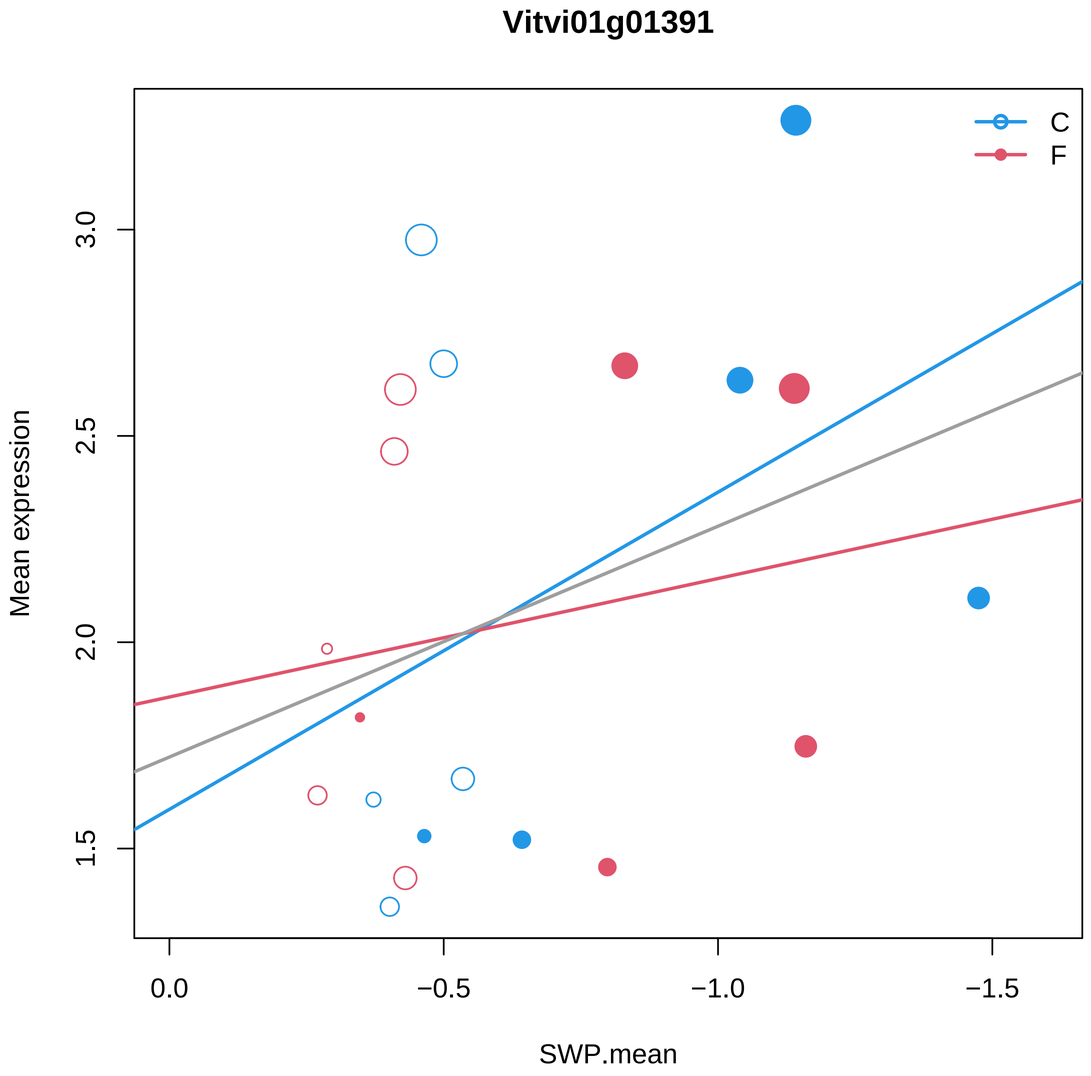
```
> plot.types(C,F,title="Slopes")
```



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

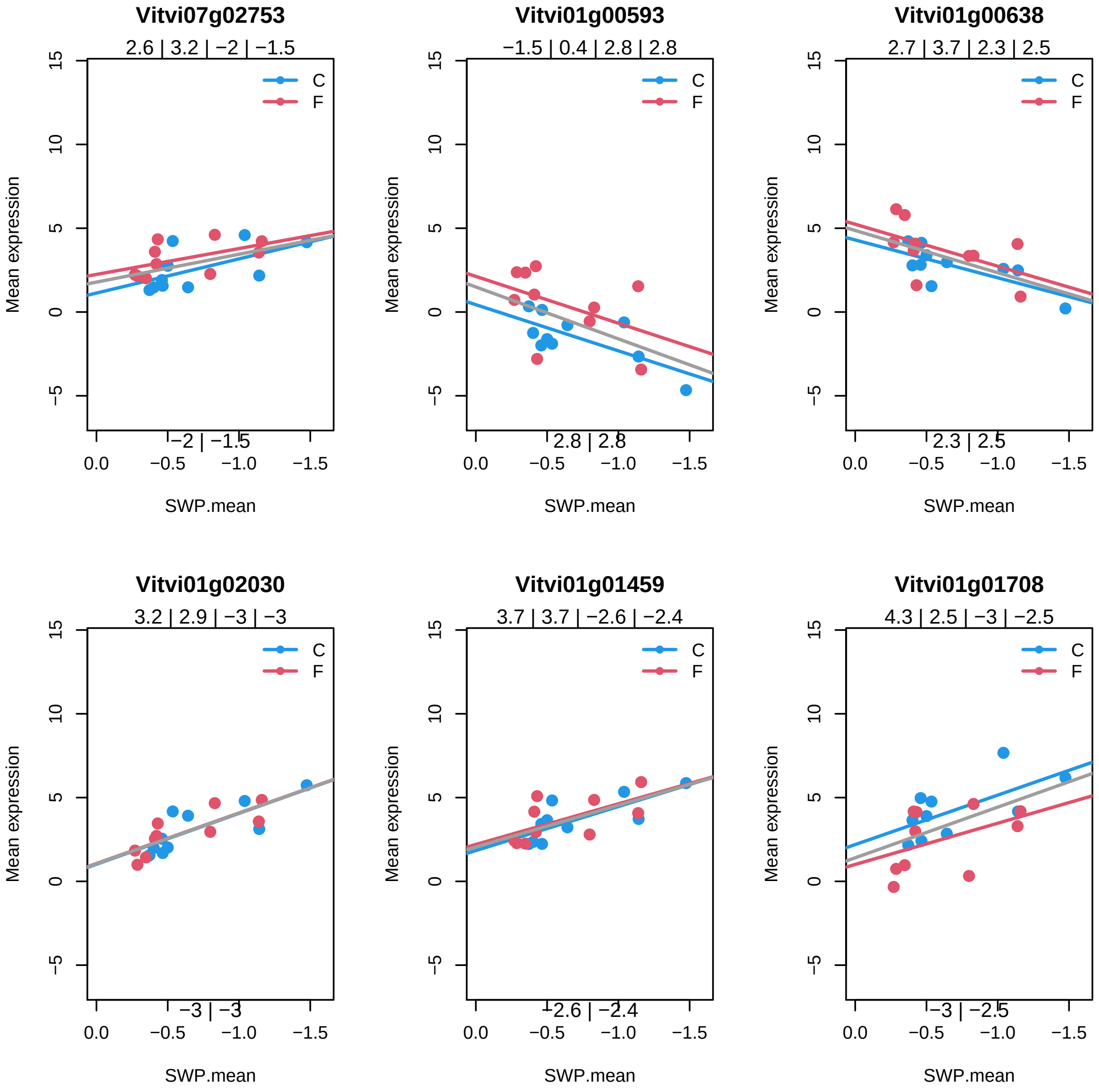


```
> varname <- testvar
> plot.ewp(varname,model="", exprs=exprs, pd=pd)
```

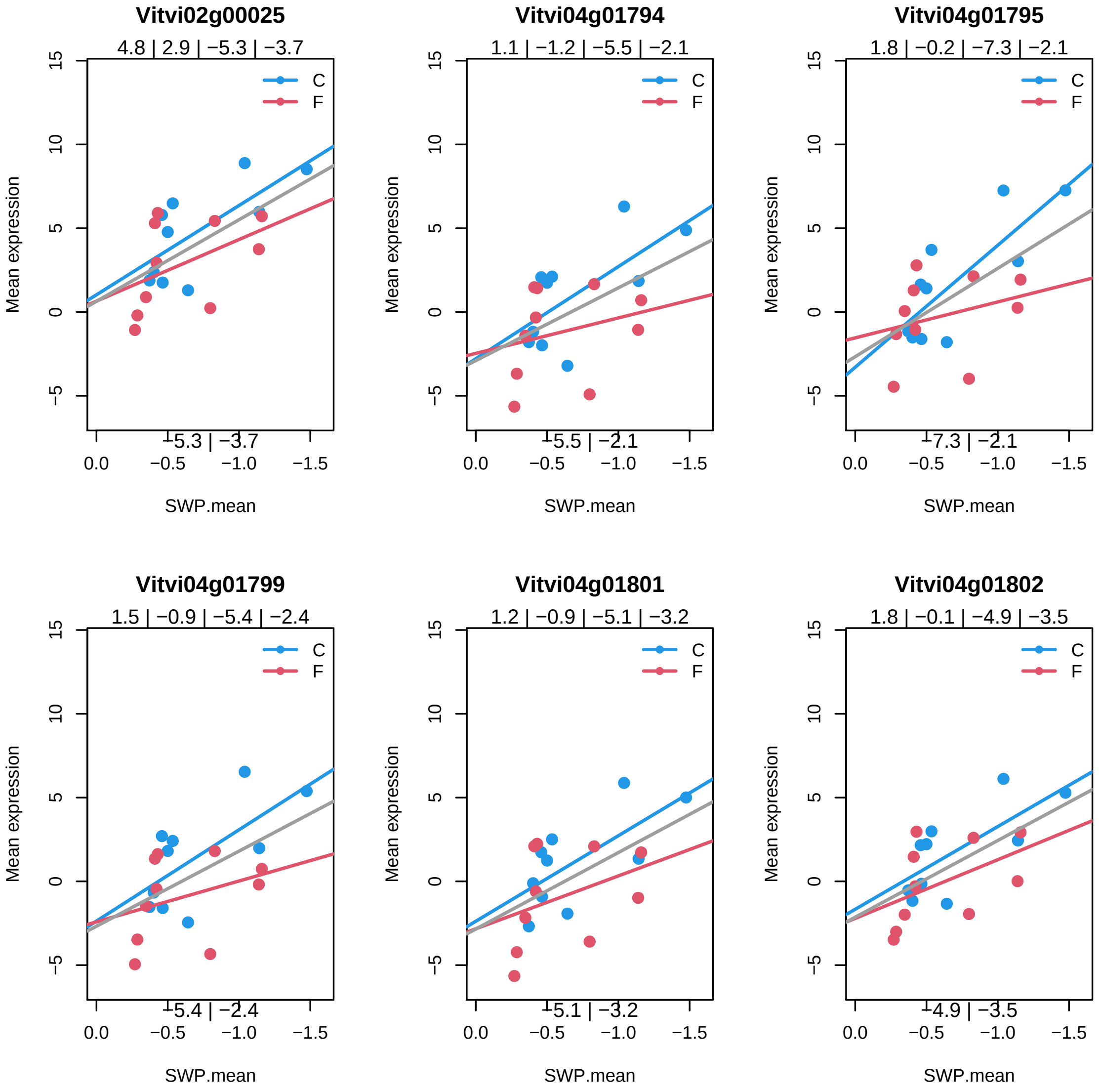


```
> apply(data.frame(type1,type2,type3,type4, type5),2,sum)
type1 type2 type3 type4 type5
   88    20    94    54    93
```

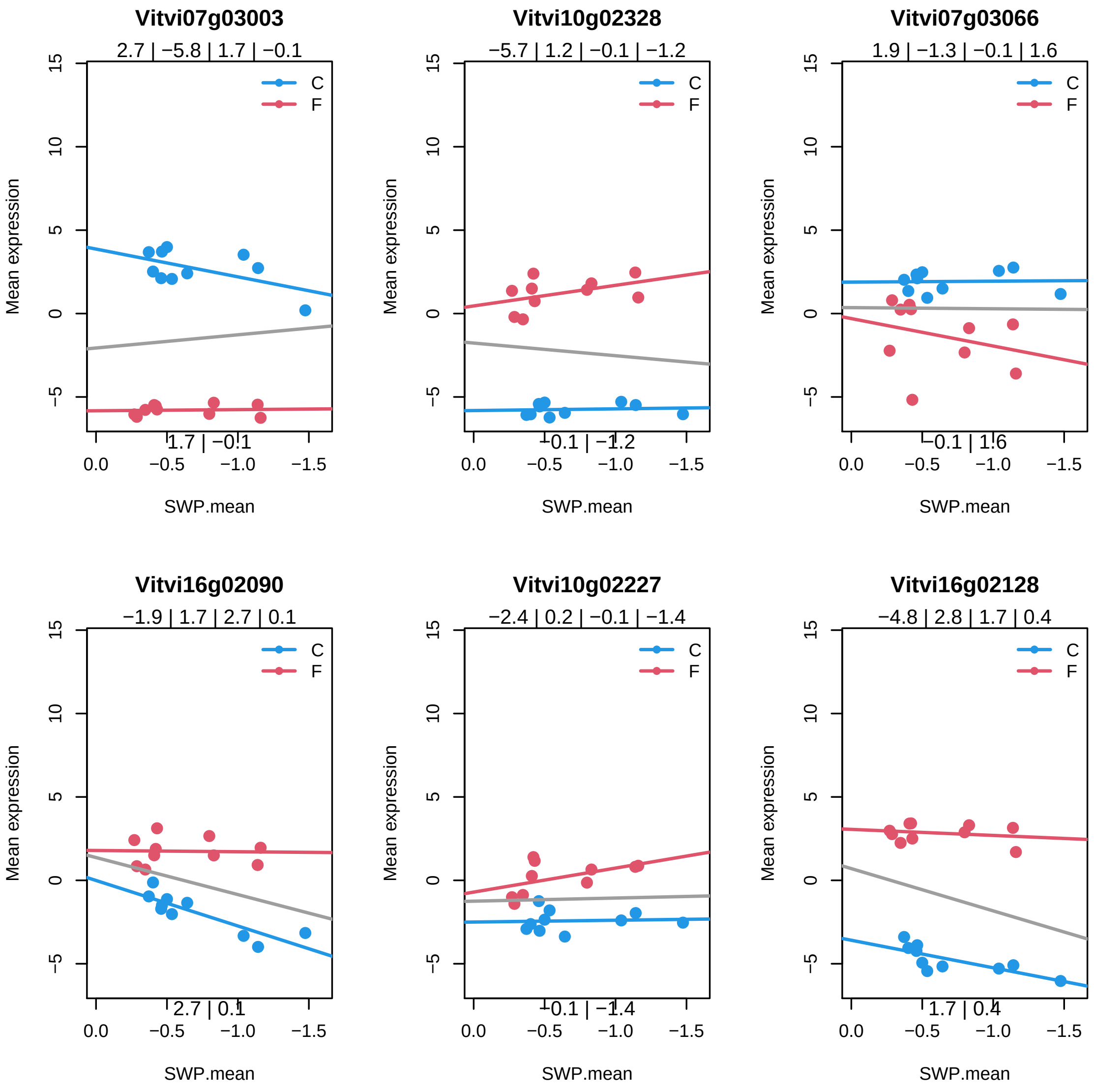
```
> par(mfrow=c(2,3))
> filt <- type1
> print(sum(filt))
[1] 88
> for(i in 1:min(sum(filt),6)){
+ varname <- rownames(exprs)[filt][i]
+ p <- plot.ewp(varname,model="", exprs=exprs, pd=pd, ylim=range(exprs)
+       , cex= 1.5
+       , pch = c(16,16)
+       )
+ mtext(paste(round(coefs[varname,],1),collapse=" | "),cex=0.75)
+ mtext(paste(round(c(p$C$coefficients[2],p$F$coefficients[2]),1)
+ ,collapse=" | "),1,cex=0.75)
+ }
```



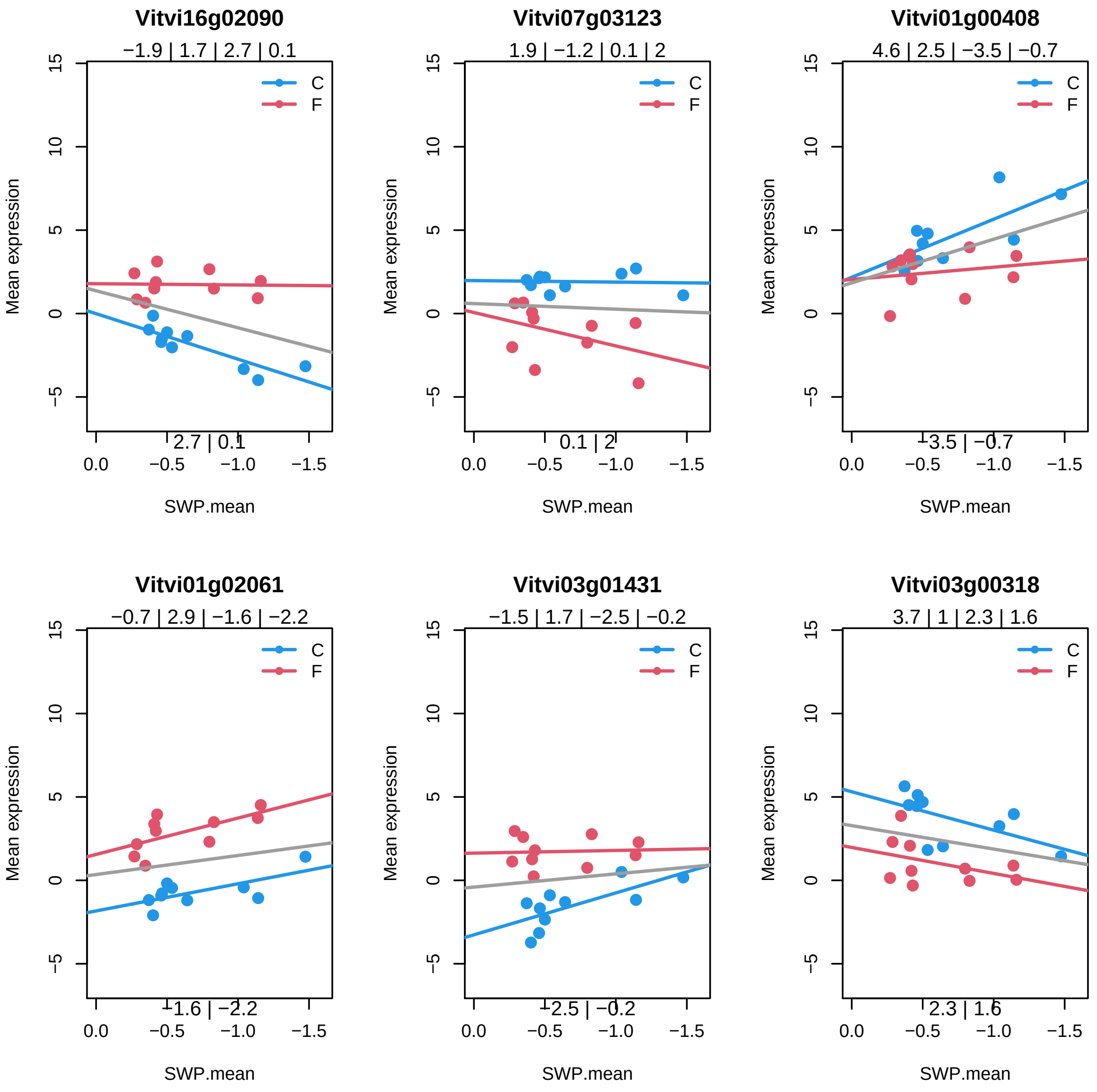
```
> par(mfrow=c(2,3))
> filt <- type2
> print(sum(filt))
[1] 20
> for(i in 1:min(sum(filt),6)){
+ varname <- rownames(exprs)[filt][i]
+ p <- plot.ewp(varname,model="", exprs=exprs, pd=pd, ylim=range(exprs)
+      , cex= 1.5
+      , pch = c(16,16)
+      )
+ mtext(paste(round(coefs[varname,],1),collapse=" | "),cex=0.75)
+ mtext(paste(round(c(p$C$coefficients[2],p$F$coefficients[2]),1)
+ ,collapse=" | "),1,cex=0.75)
+ }
```



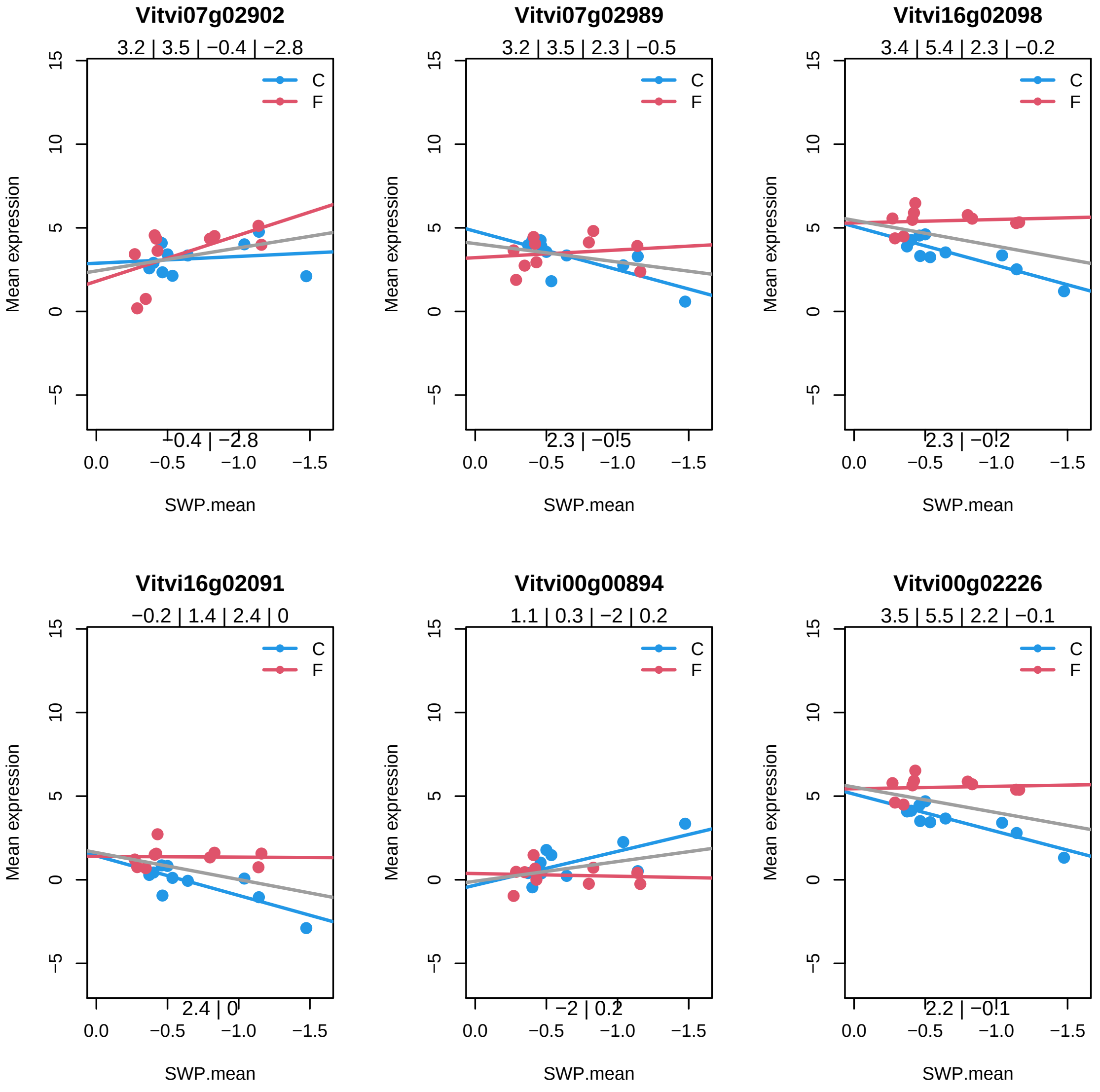
```
> par(mfrow=c(2,3))
> filt <- type3
> print(sum(filt))
[1] 94
> for(i in 1:min(sum(filt),6)){
+ varname <- rownames(exprs)[filt][i]
+ p <- plot.ewp(varname,model="", exprs=exprs, pd=pd, ylim=range(exprs)
+       , cex= 1.5
+       , pch = c(16,16)
+       )
+ mtext(paste(round(coefs[varname,],1),collapse=" | "),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] 54
> 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] 93
> 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          0.56626956
Vitvi09g02033          -0.78732802375         -2.84283707706586          0.41956448
```

```
> 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-2-2-0.5-1-0.5-1/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
```

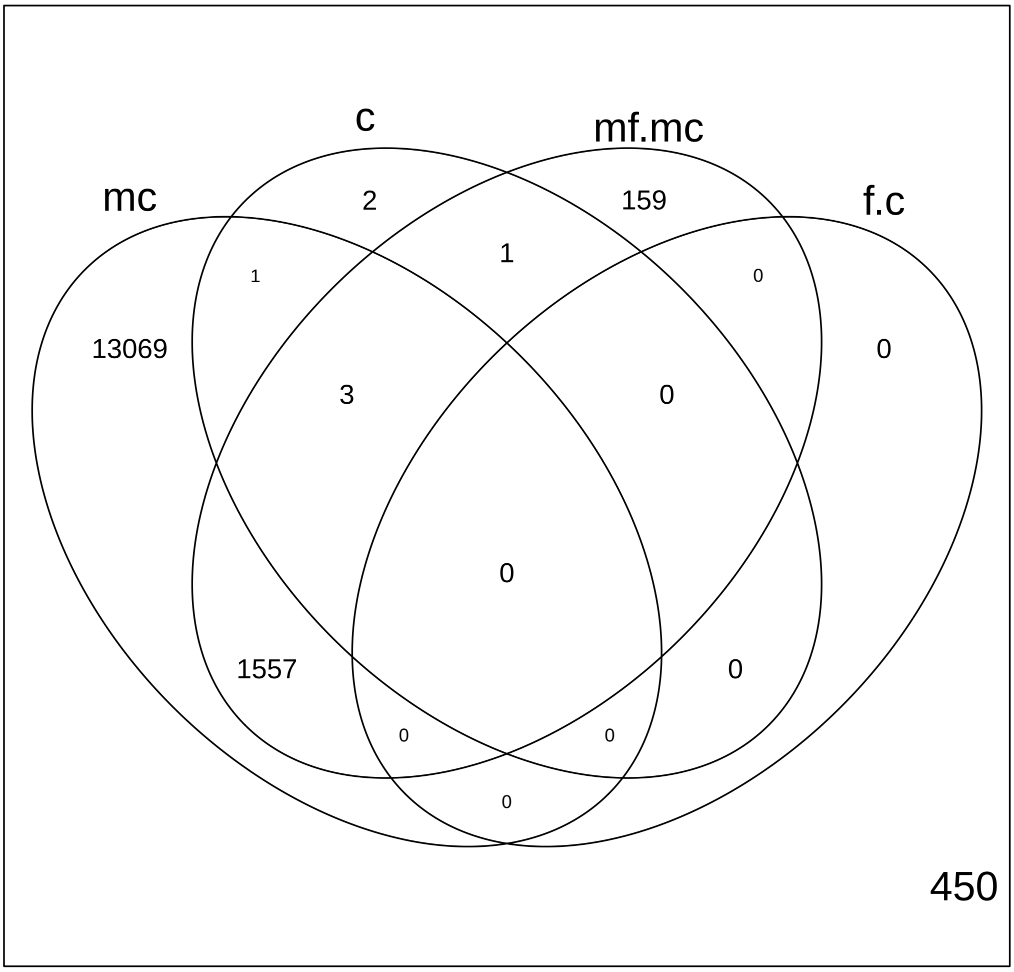
```
$qr
  (Intercept)         swp   varietyF swp:varietyF
1  -4.4721360  2.93478215 -2.2360680   1.36240911
2   0.2236068 -1.54891442 -0.3031114  -0.50167273
3   0.2236068  0.04473752  2.2154285  -1.44373971
4   0.2236068  0.06733399  0.1816105   0.76367769
5   0.2236068  0.09365515  0.1805019   0.08777677
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
 15154     88

       |type1 |type2
 15134     88     20

       |type1 |type2 |type3
 15040     88     20     94

                   |type1       |type2 |type2|type4
       15009           88           11            9
      |type3 |type3|type4       |type4
          80           14           31

                   |type1       |type2 |type2|type4
       14916           88           11            9
      |type3 |type3|type4       |type4       |type5
          80           14           31           93
> 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]
            14916
type1          88
type2          11
type2|type4     9
type3          80
type3|type4    14
type4          31
type5          93
```

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

	Count
	14916
type1	88
type2	11
type2|type4	9
type3	80
type3|type4	14
type4	31
type5	93

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-2-2-0.5-1-0.5-1/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
 1218   276
> table(indp,large_abs_C)
       large_abs_C
indp    FALSE  TRUE
  FALSE 13711    37
  TRUE   1218   276
```

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

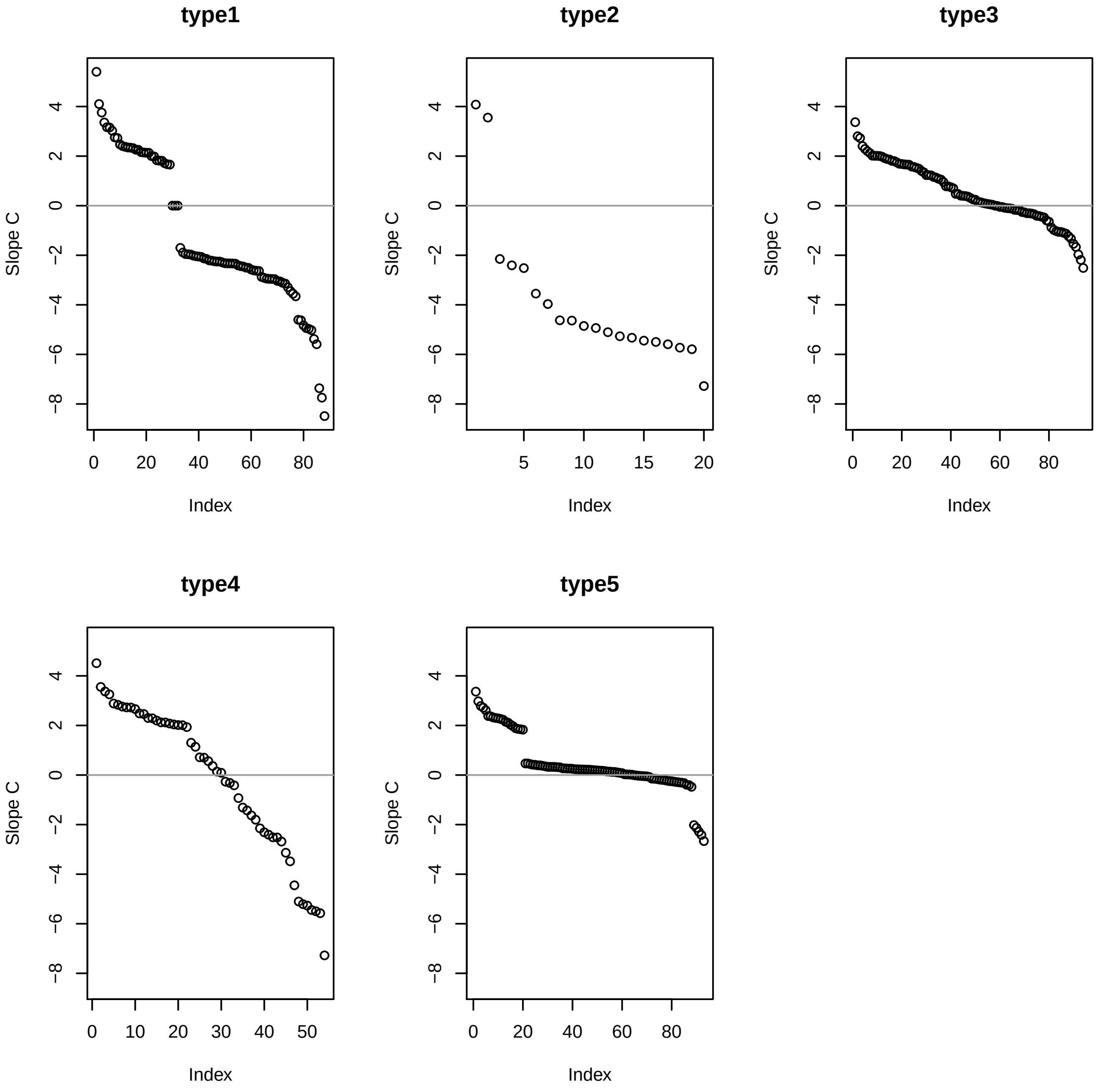
Plots of situation for genes in determined types. Significance can be checked in individual plots.

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

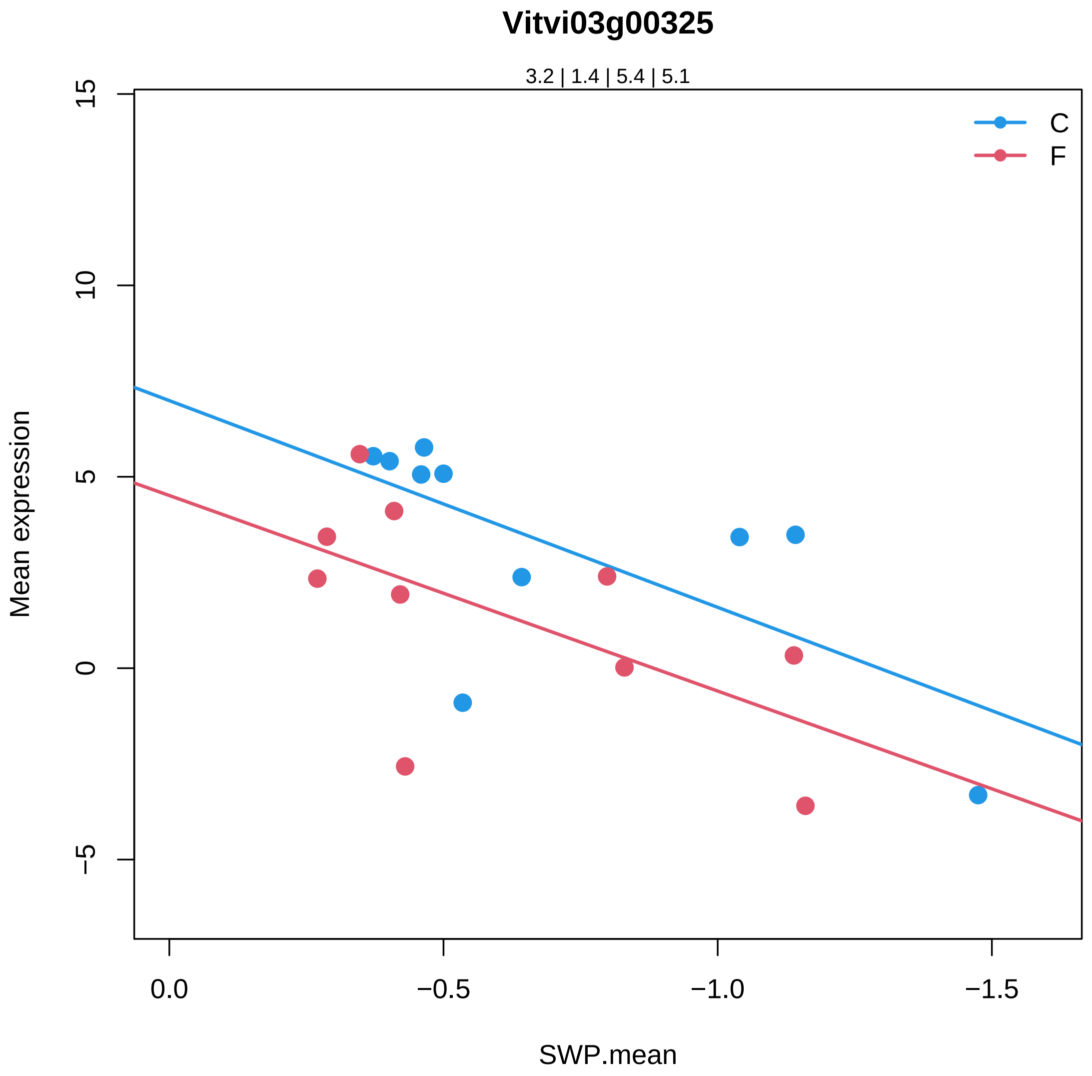
7.2.1 Vitvi03g00325: * type1

```
> 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
```



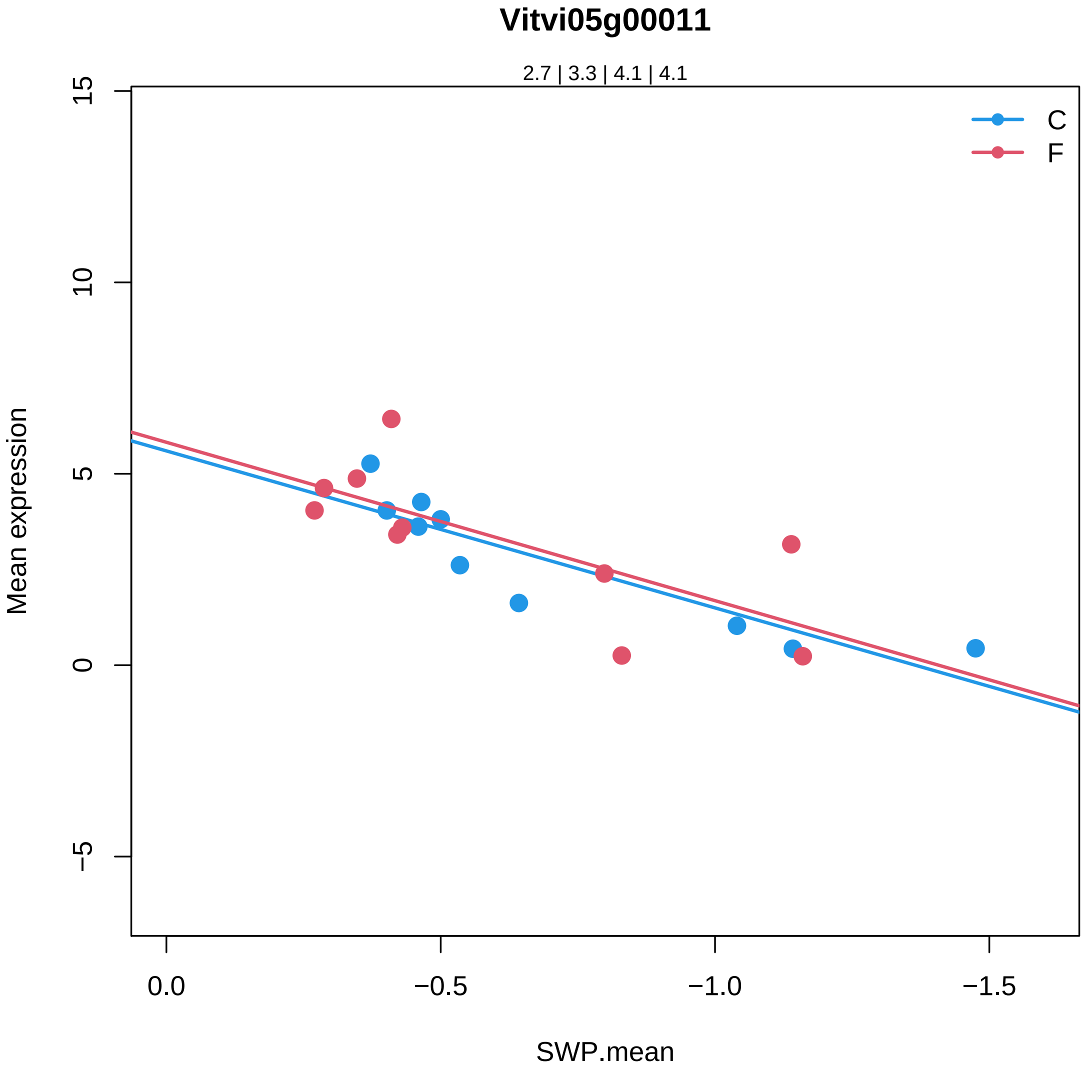
7.2.2 Vitvi05g00011: * type1

```
> 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
```



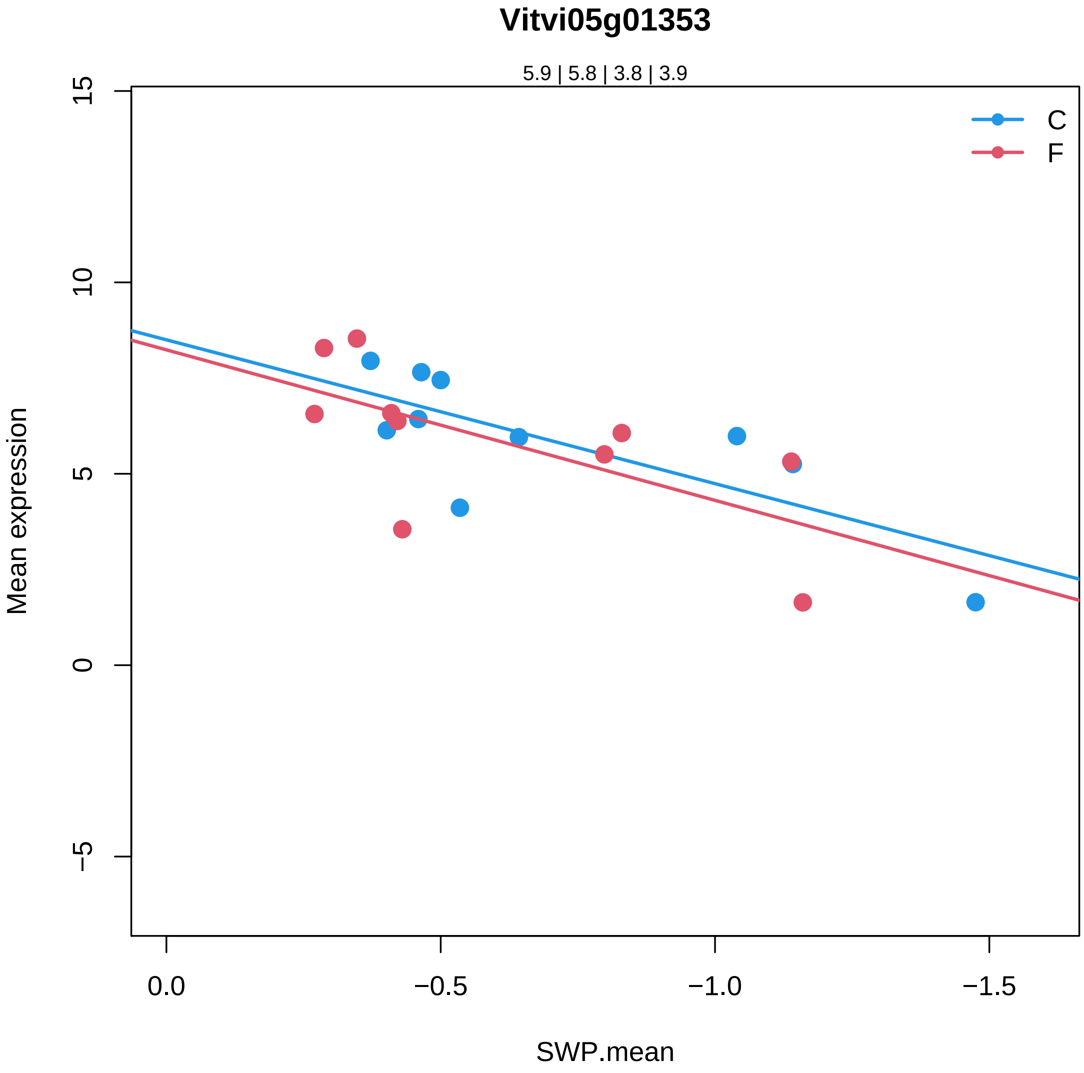
7.2.3 Vitvi05g01353: * type1

```
> 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
```



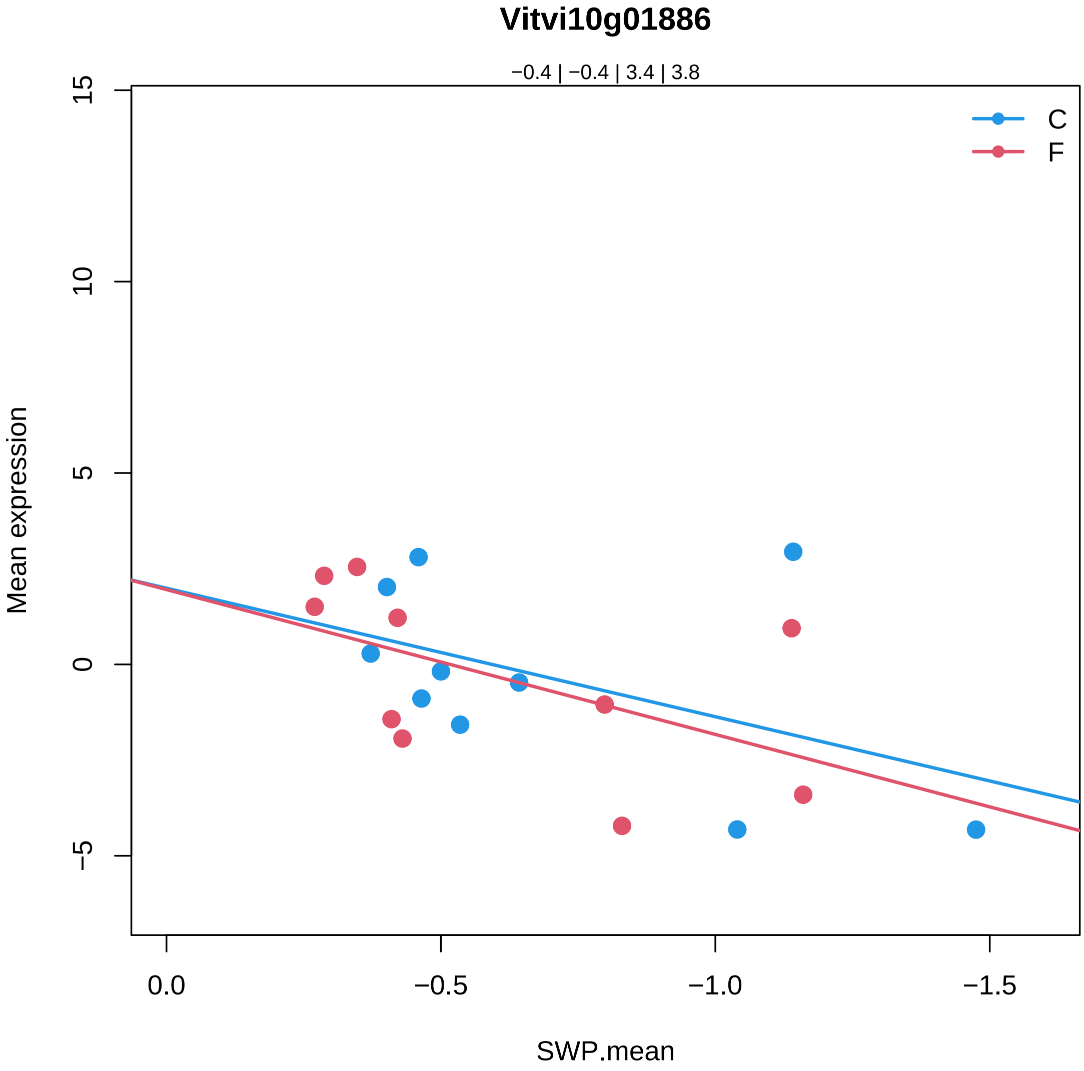
7.2.4 Vitvi10g01886: type1

```
> 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
```



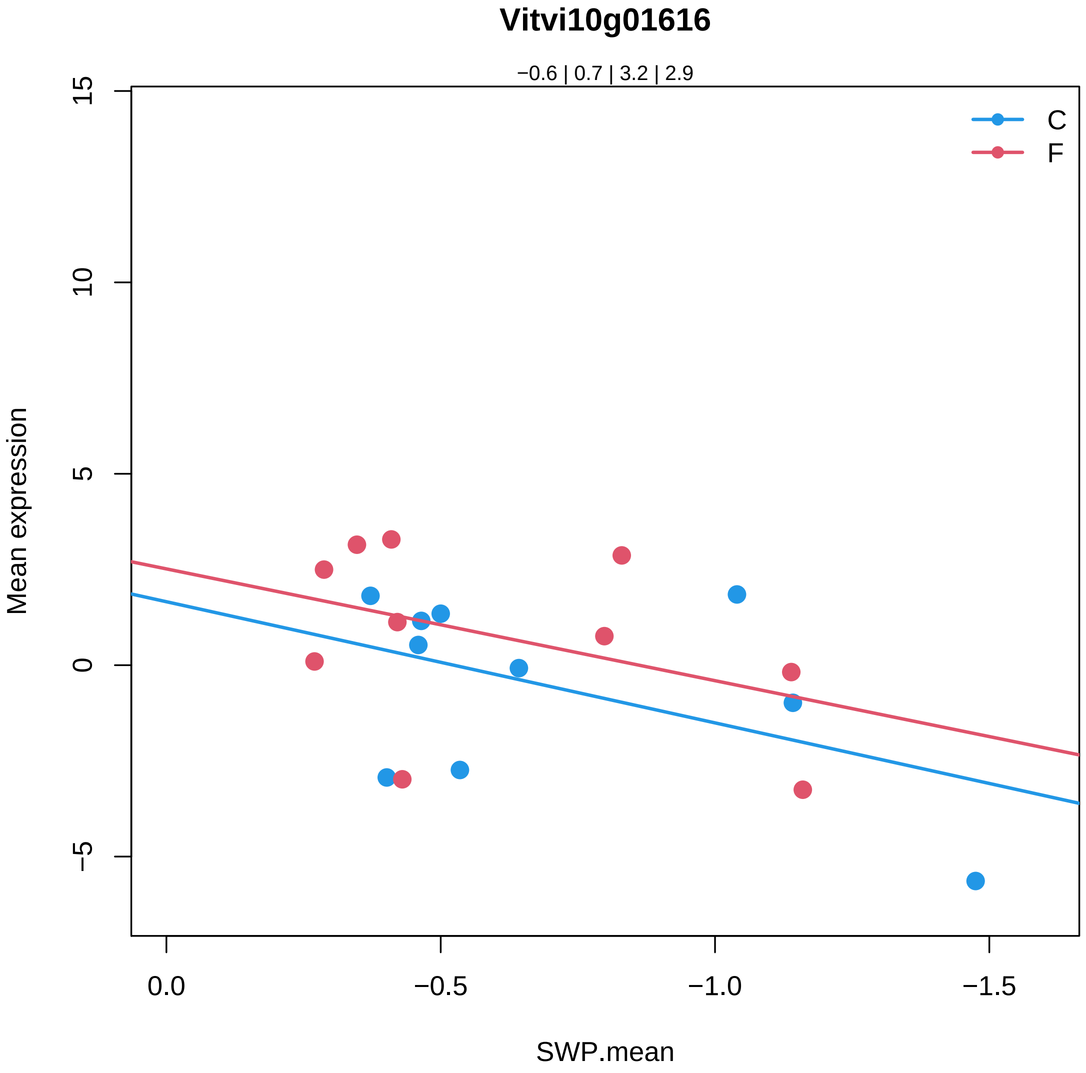
7.2.5 Vitvi10g01616: type1

```
> 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
```



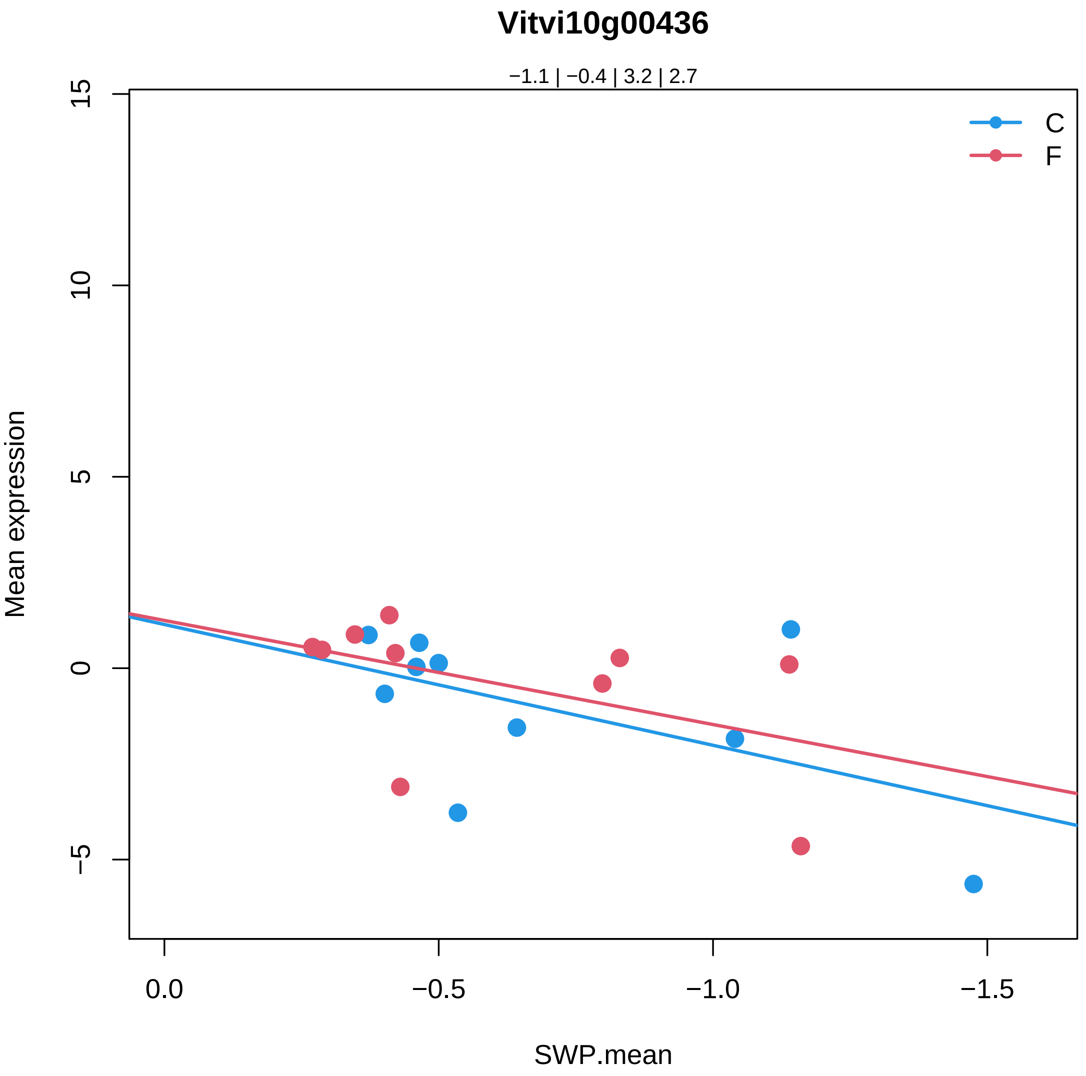
7.2.6 Vitvi10g00436: * type1

```
> 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
```



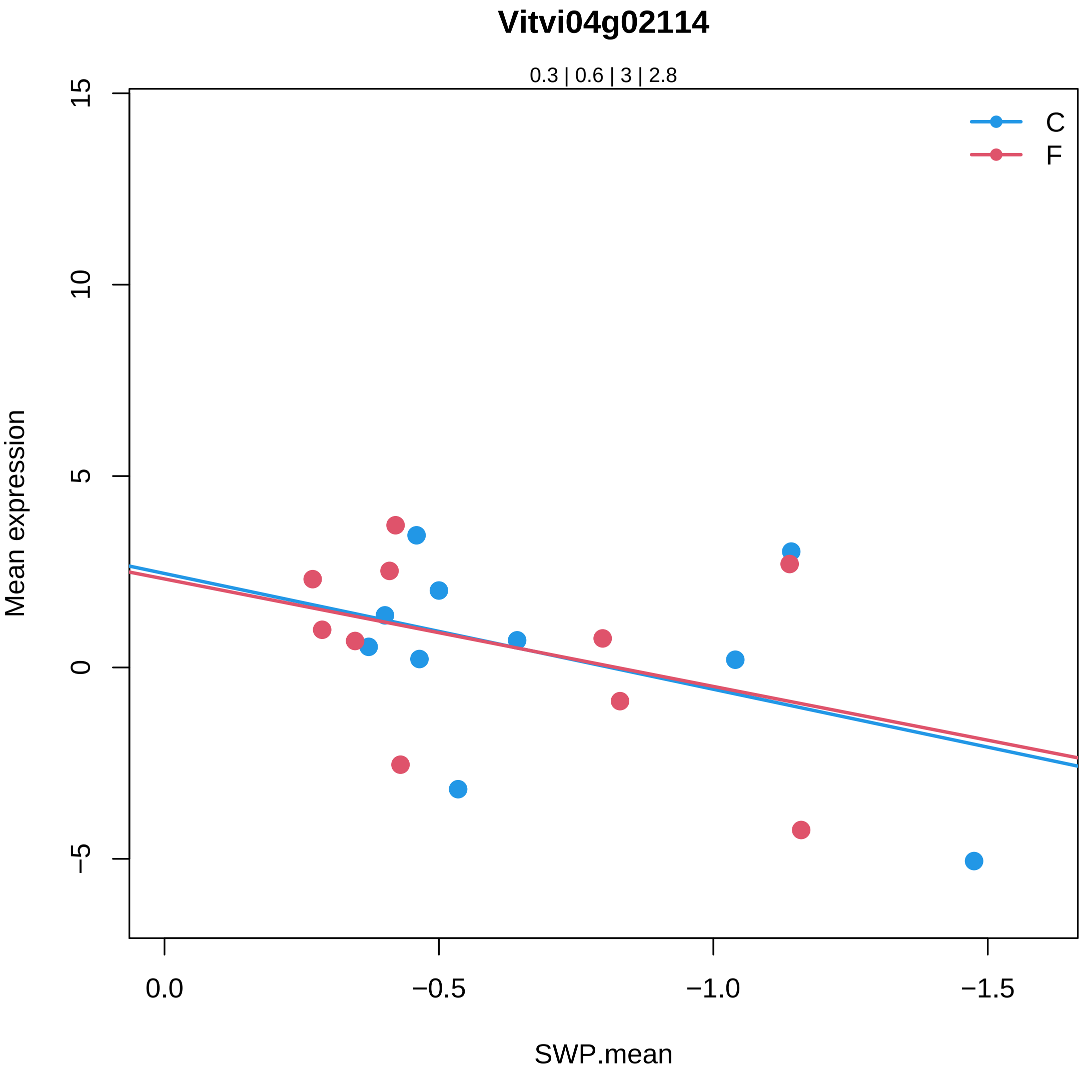
7.2.7 Vitvi04g02114: type1

```
> 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

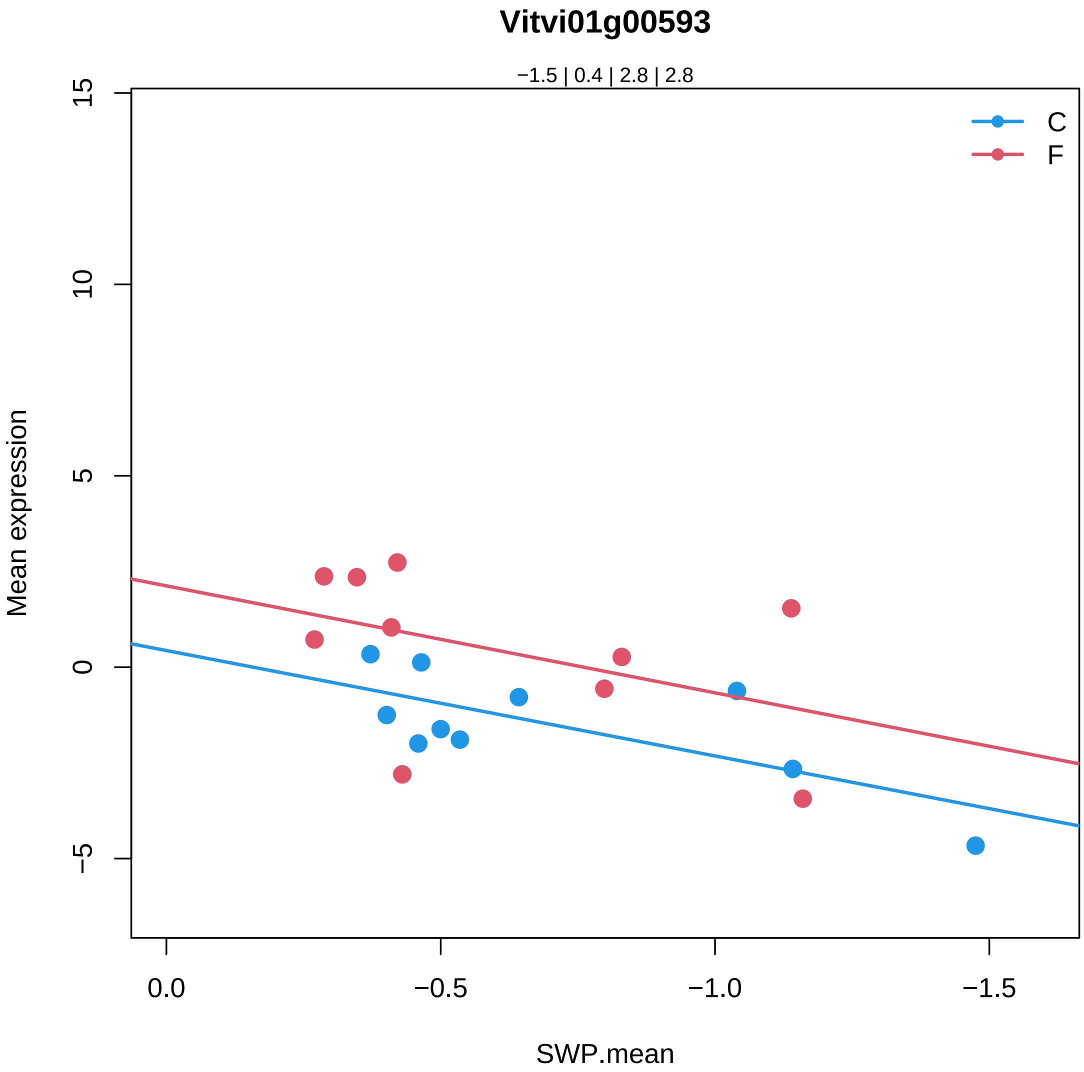
7.2.8 Vitvi01g00593: * type1

```
> 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
```



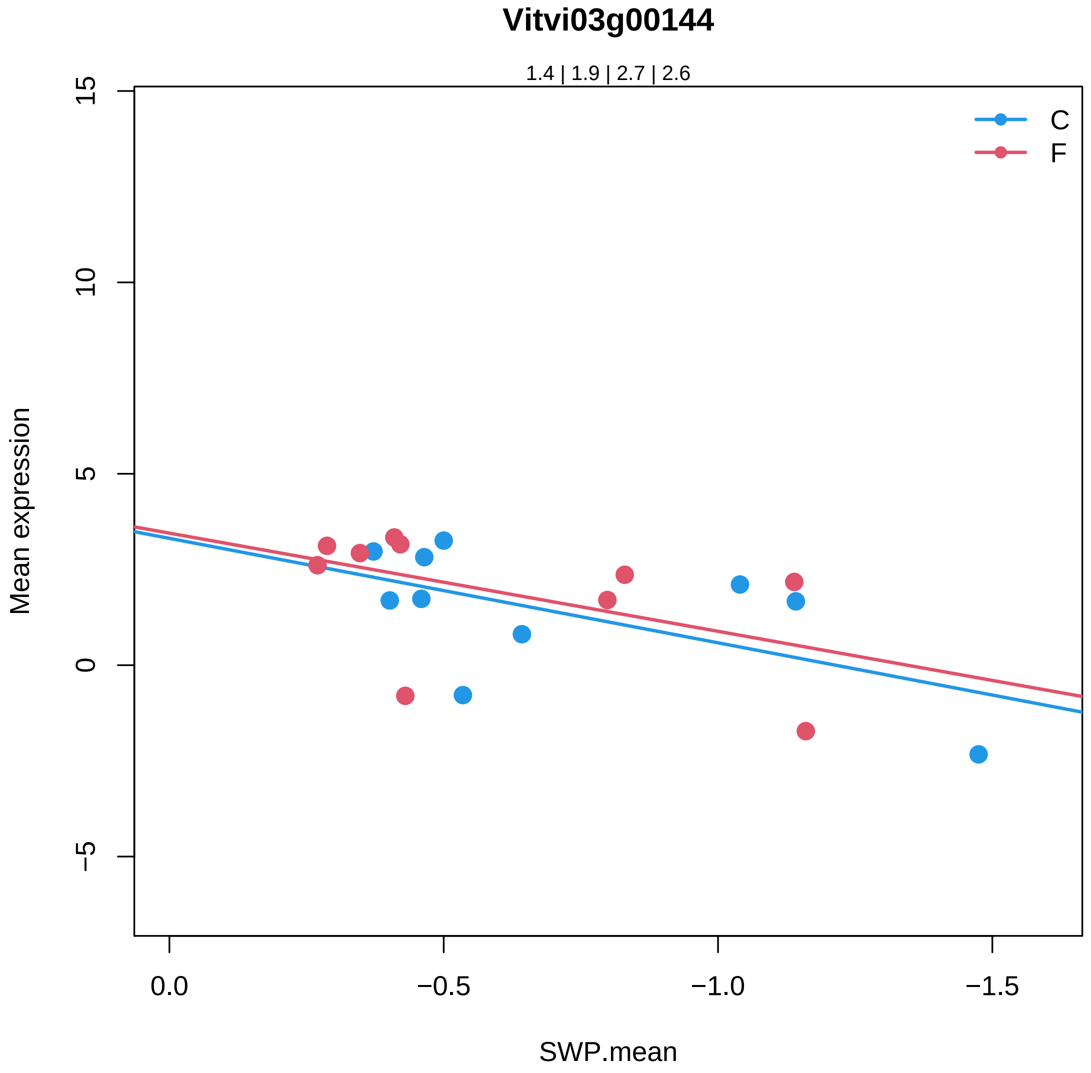
7.2.9 Vitvi03g00144: * type1

```
> 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
```



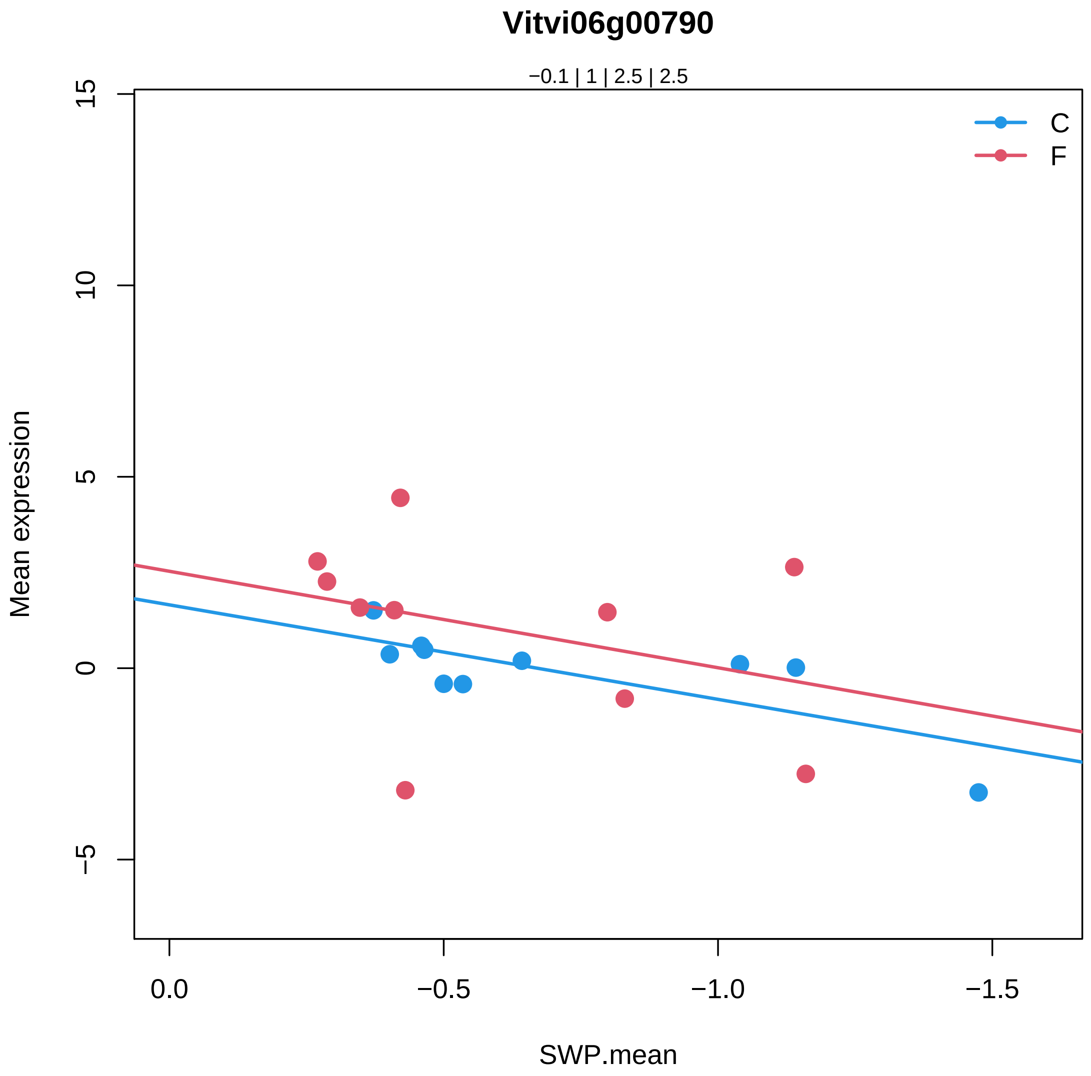
7.2.10 Vitvi06g00790: type1

```
> 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
```



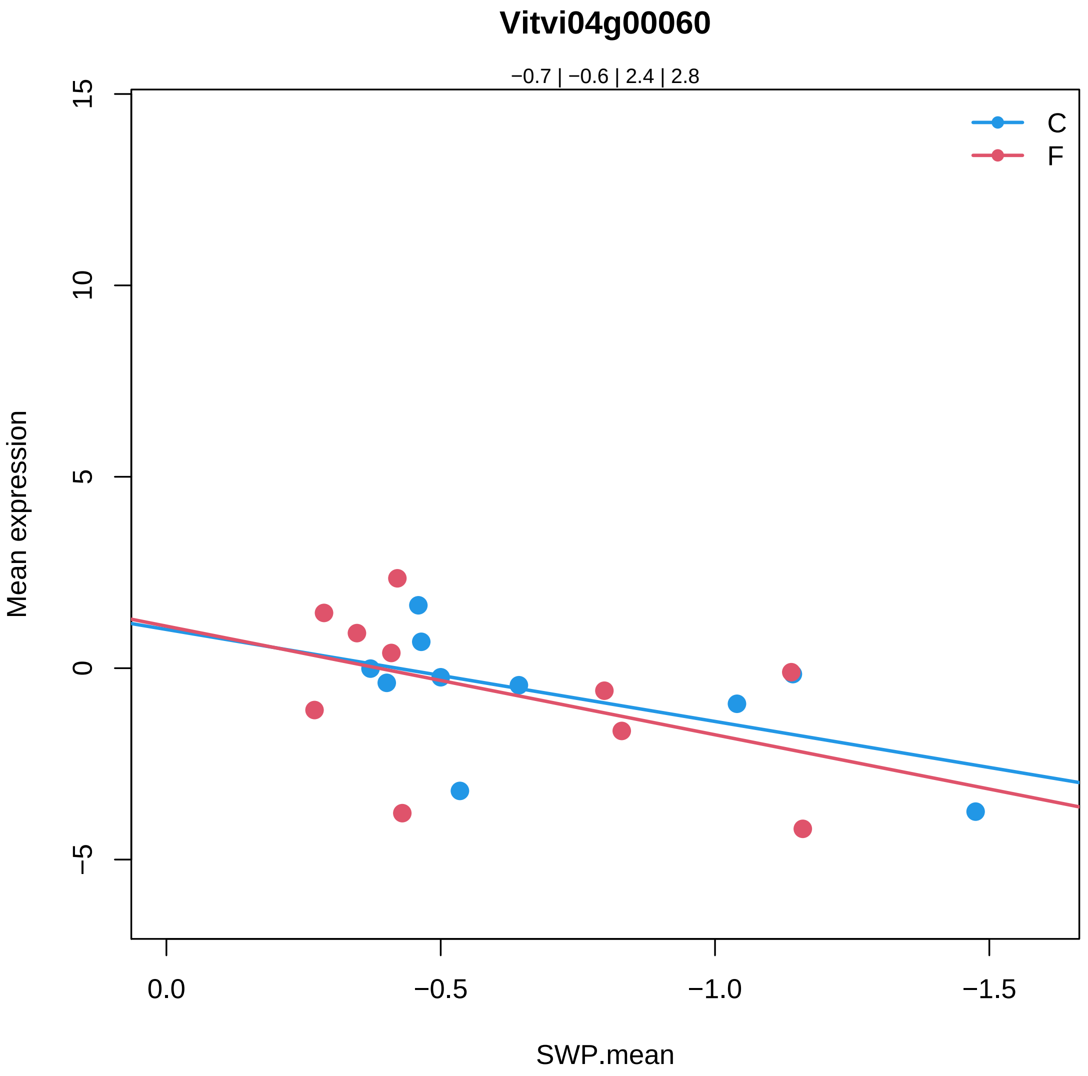
7.2.11 Vitvi04g00060: type1

```
> 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
```



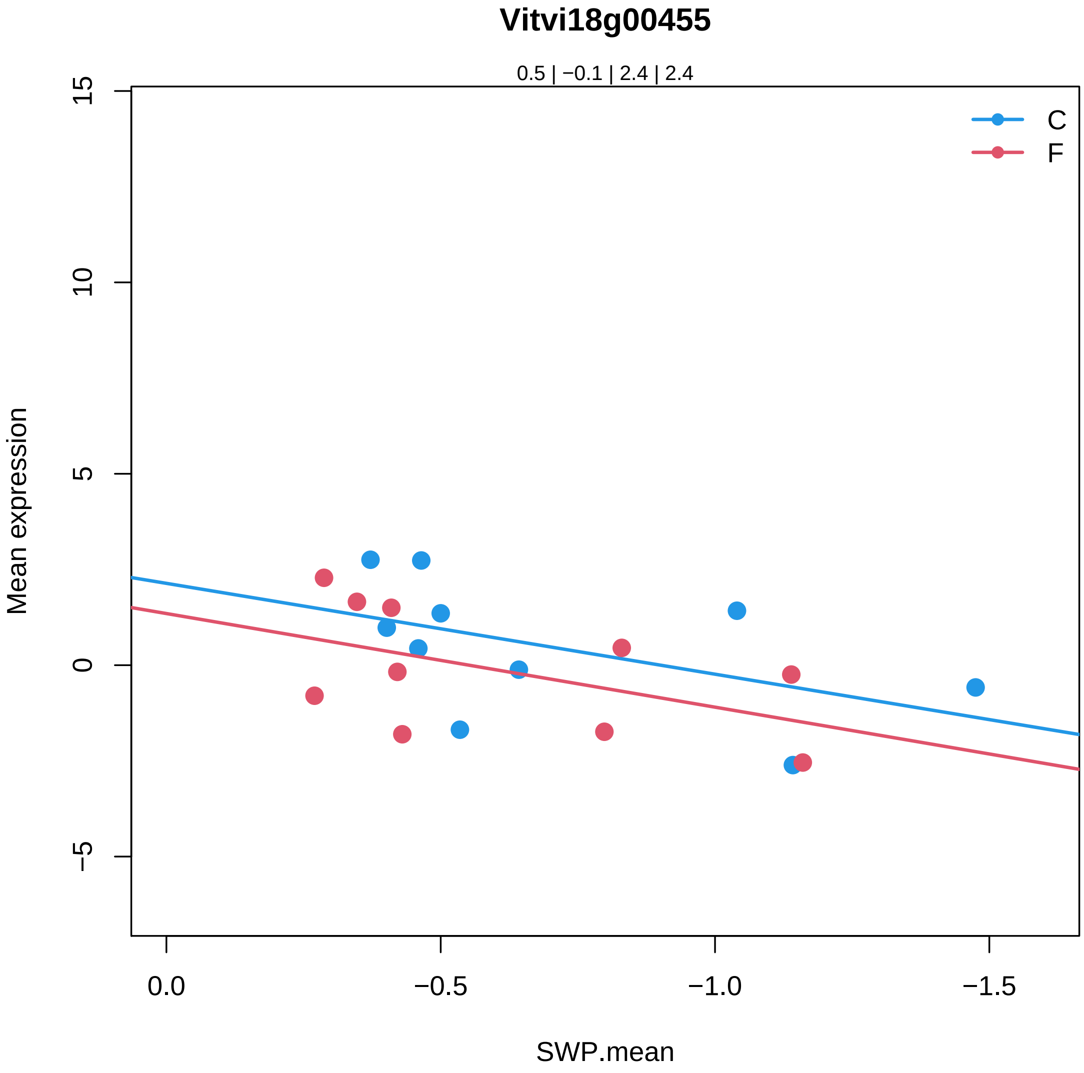
7.2.12 Vitvi18g00455: type1

```
> 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
```



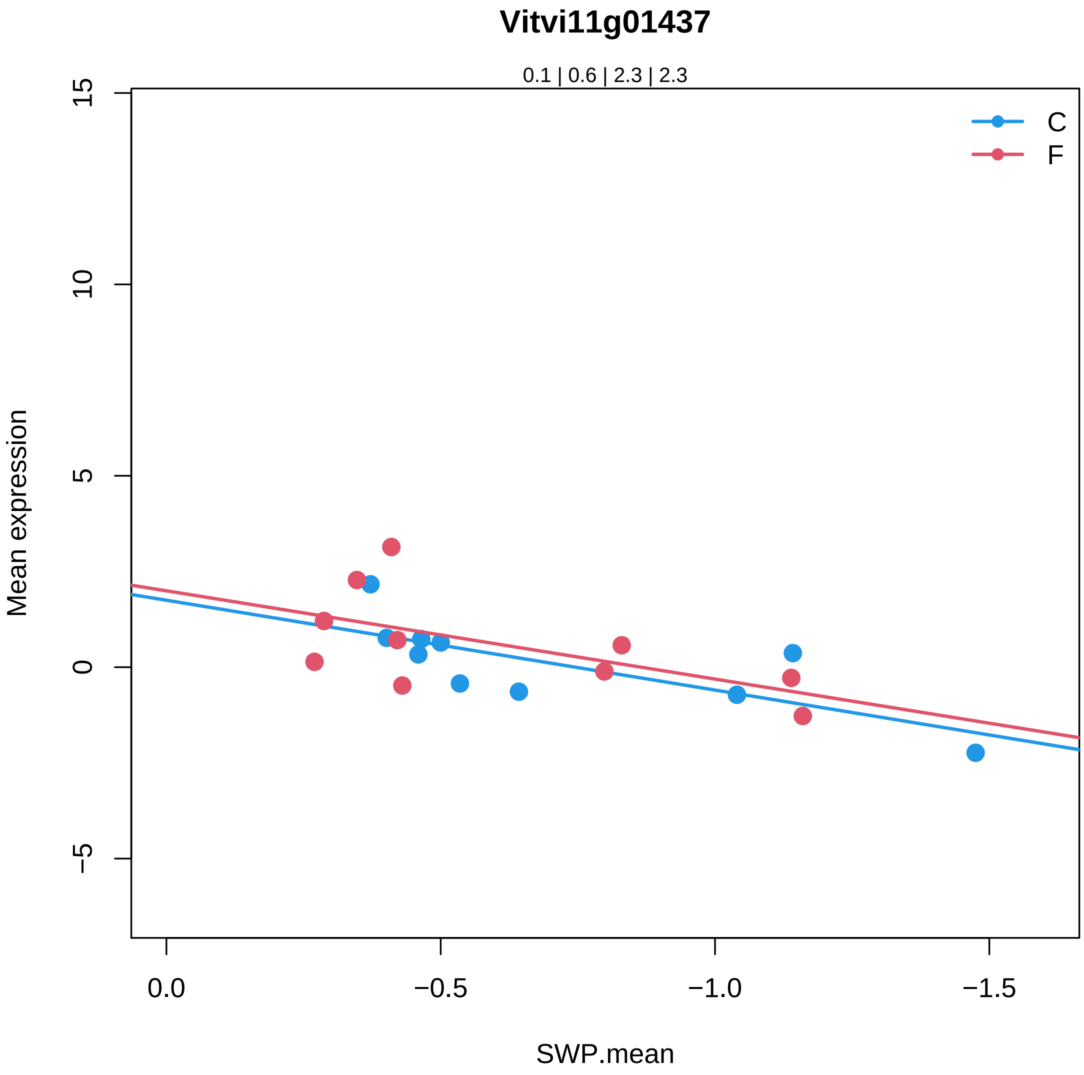
7.2.13 Vitvi11g01437: * type1

```
> 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
```



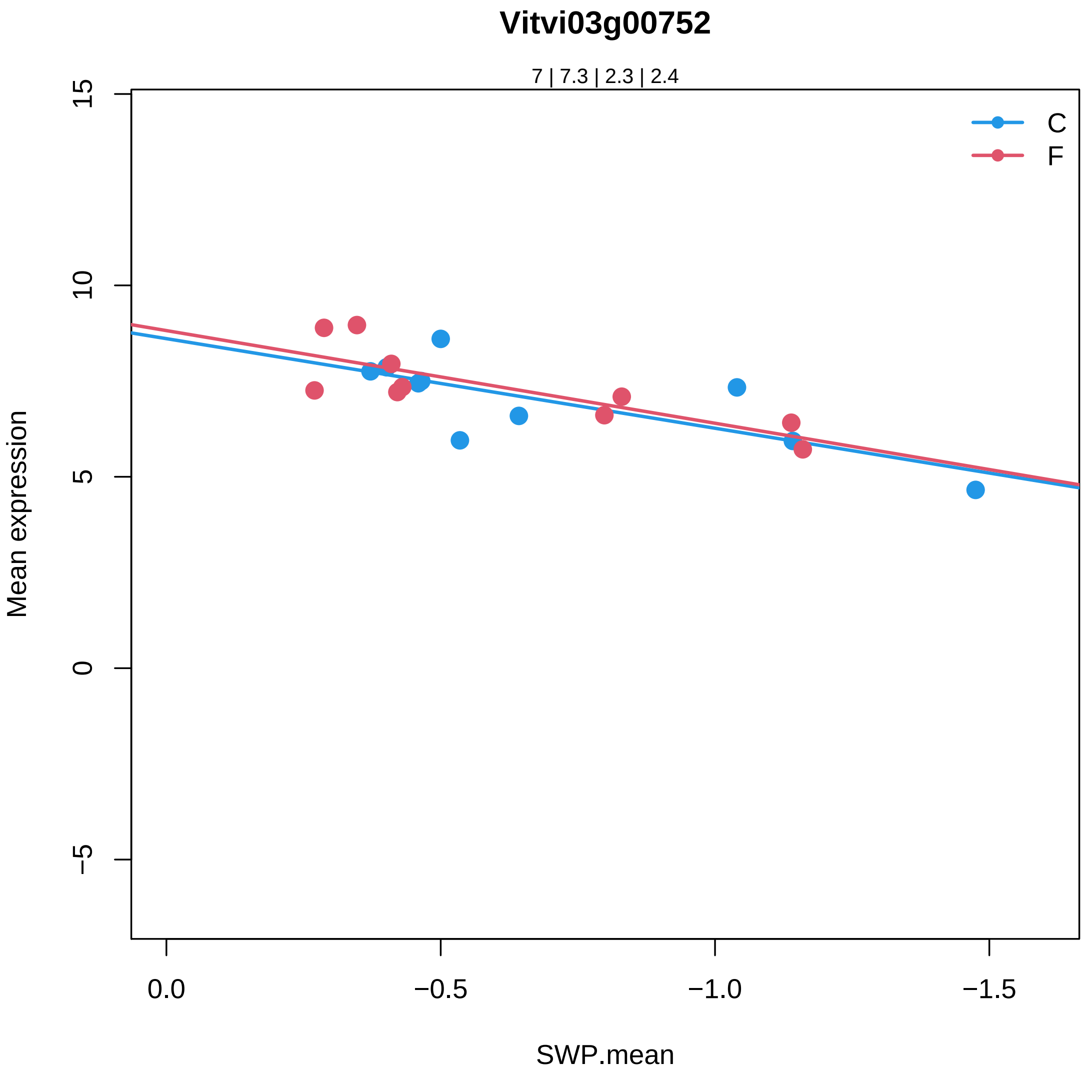
7.2.14 Vitvi03g00752: * type1

```
> 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        
```



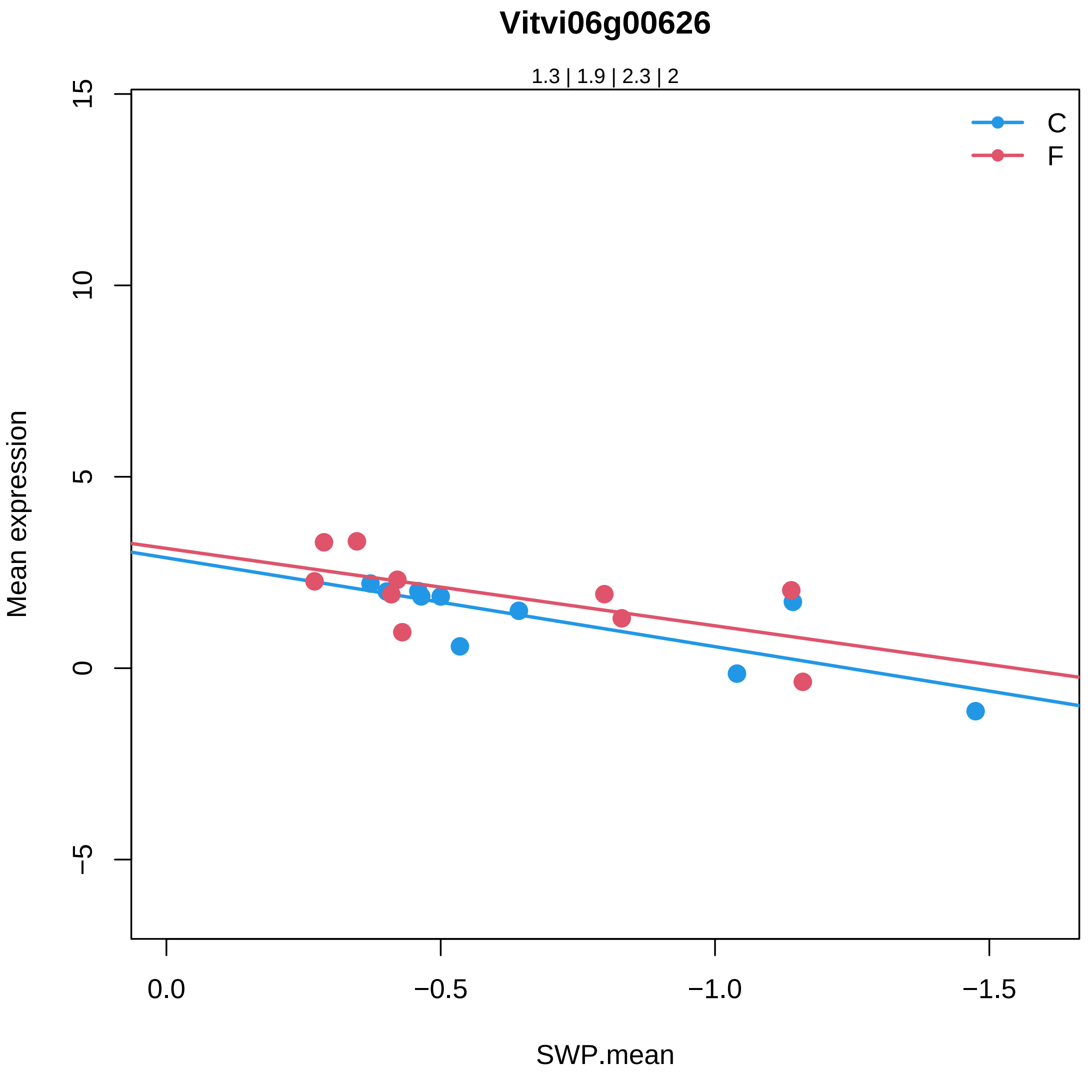
7.2.15 Vitvi06g00626: * type1

```
> 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
```



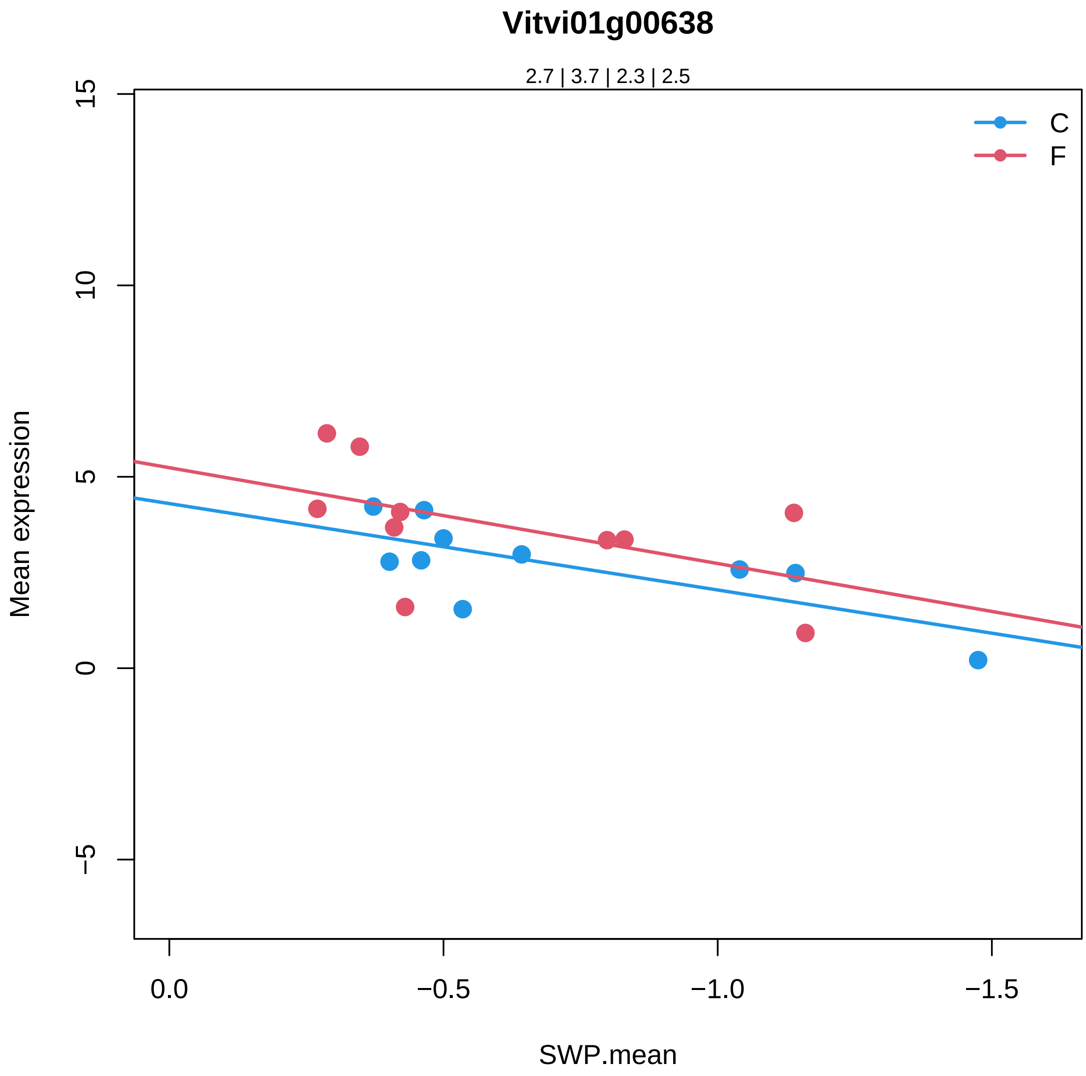
7.2.16 Vitvi01g00638: * type1

```
> 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
```



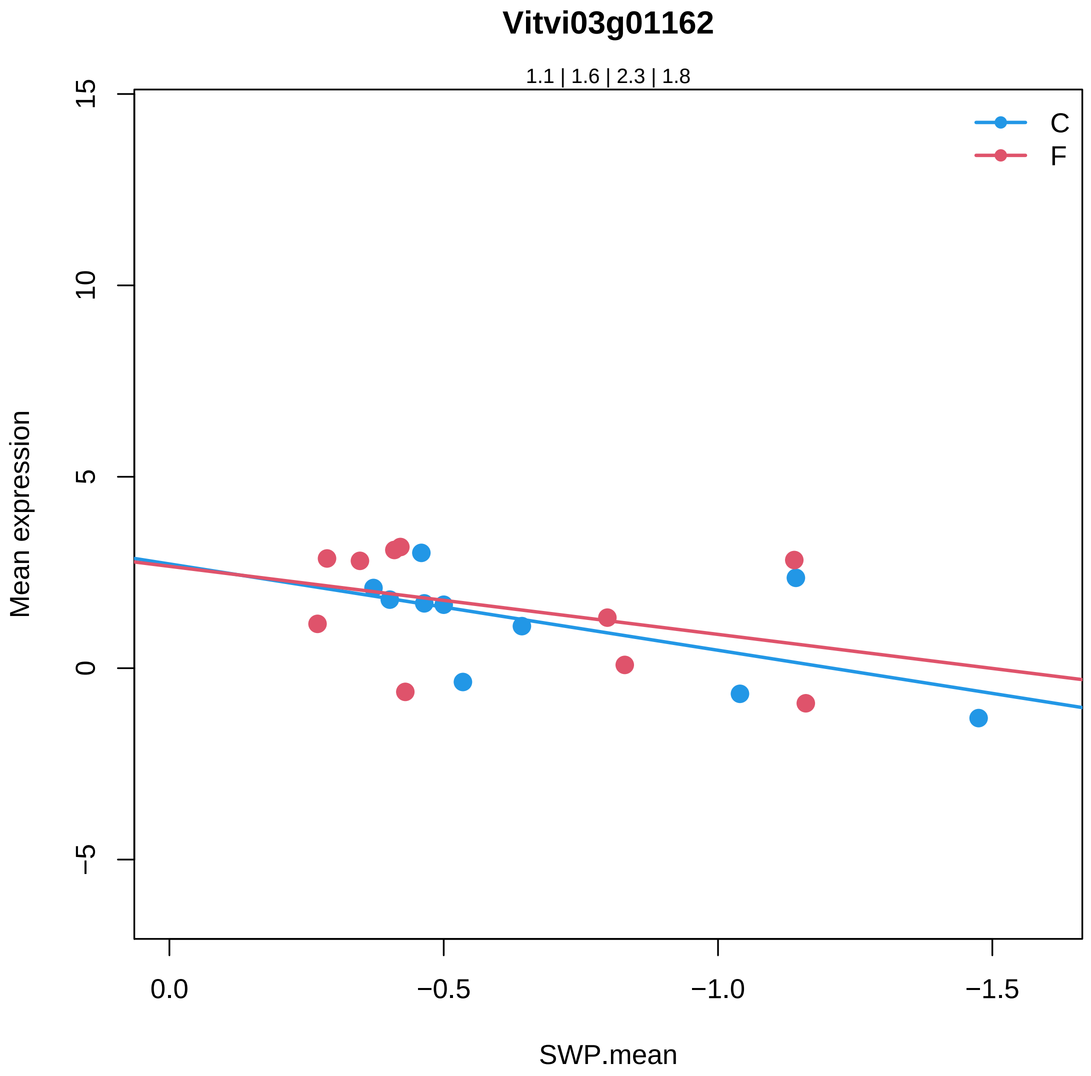
7.2.17 Vitvi03g01162: type1

```
> 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
```



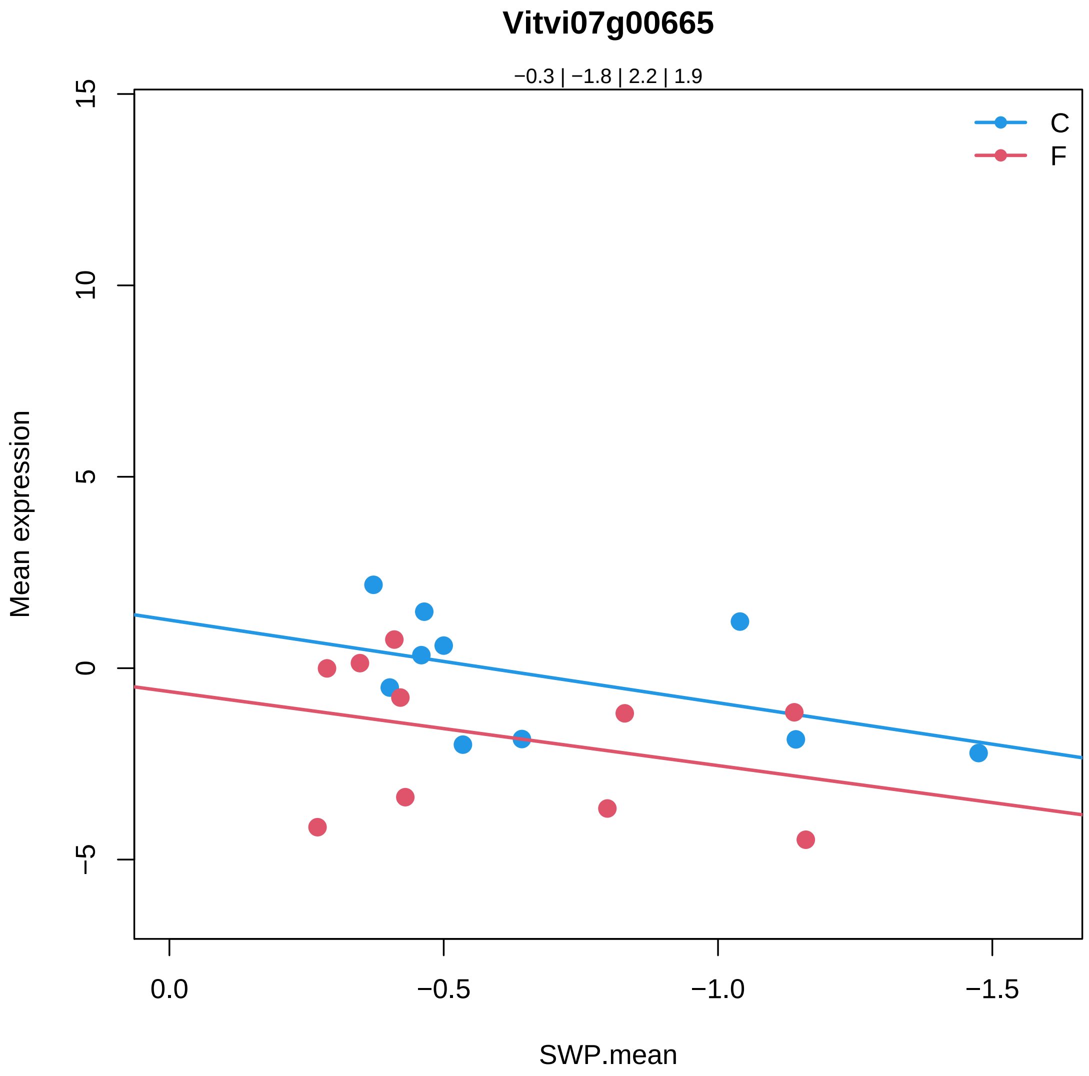
7.2.18 Vitvi07g00665: type1

```
> 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
```



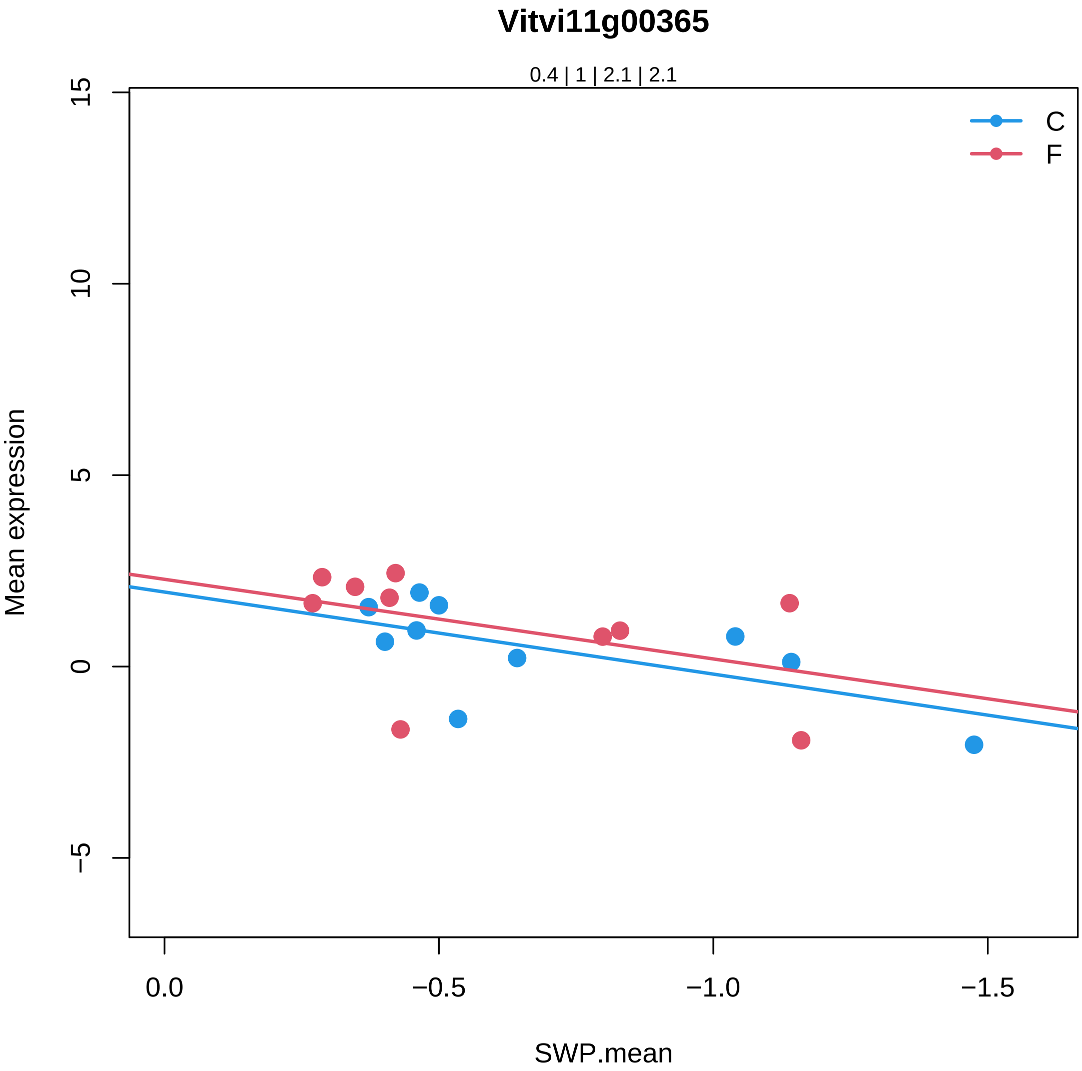
7.2.19 Vitvi11g00365: * type1

```
> 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
```



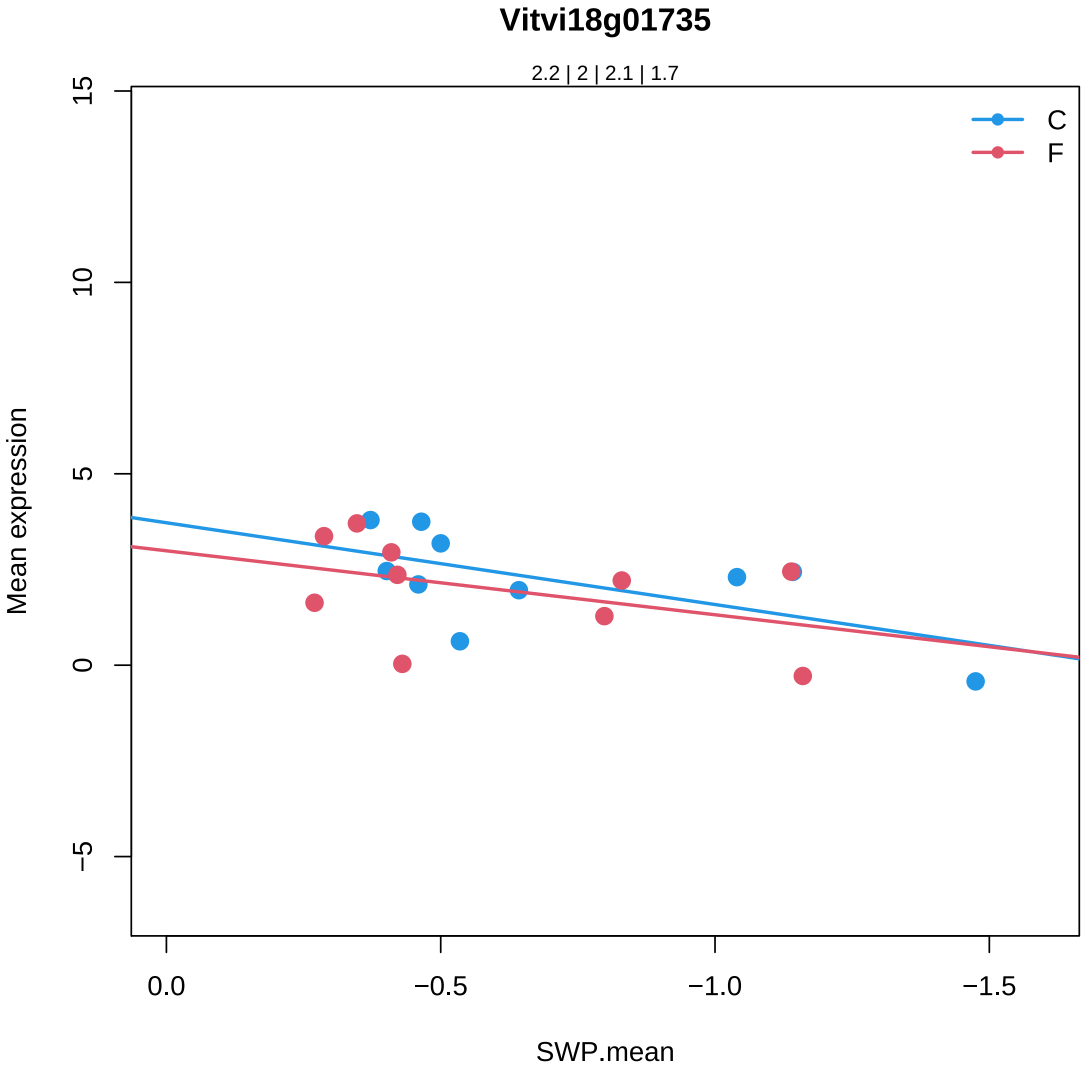
7.2.20 Vitvi18g01735: * type1

```
> 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
```



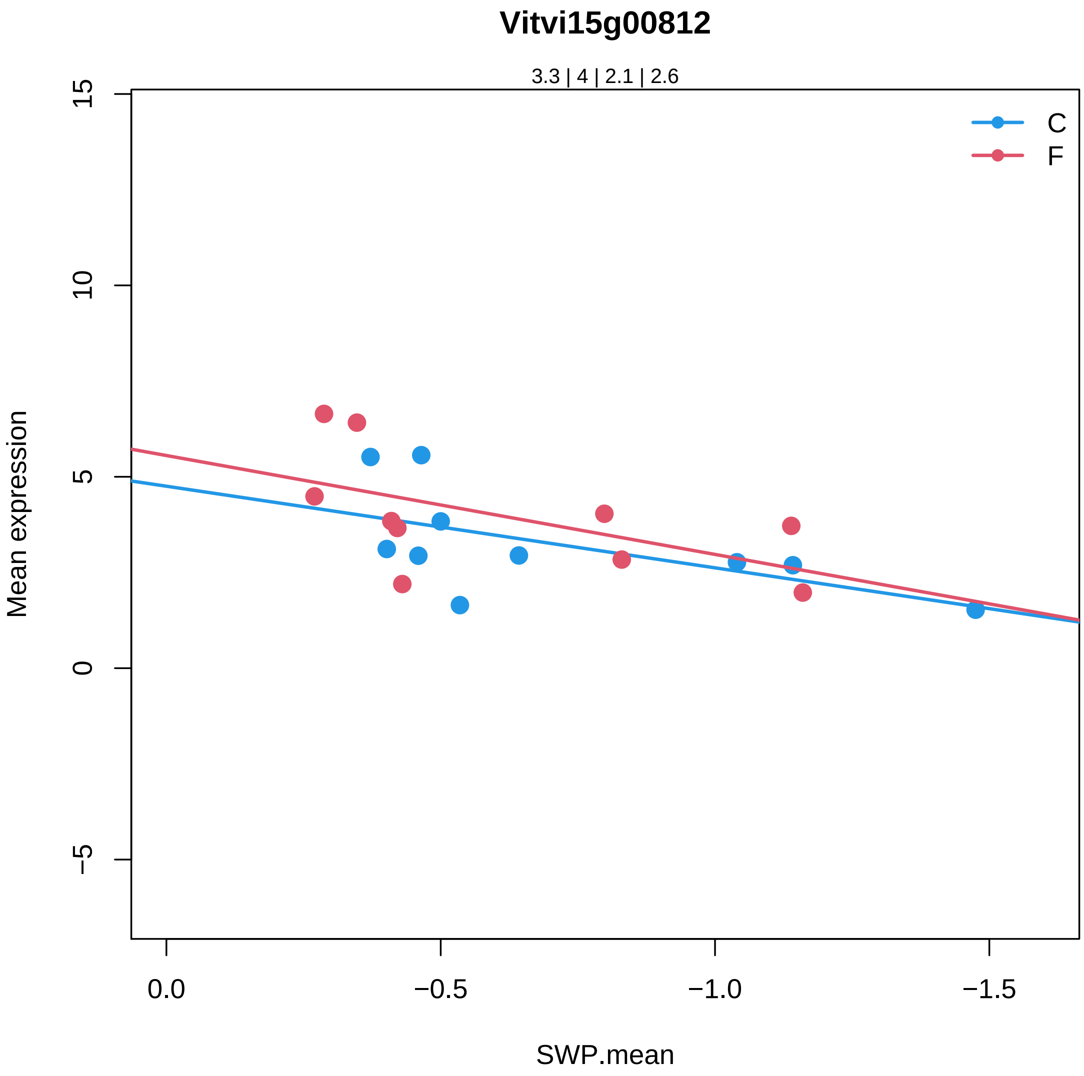
7.2.21 Vitvi15g00812: * type1

```
> 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
```



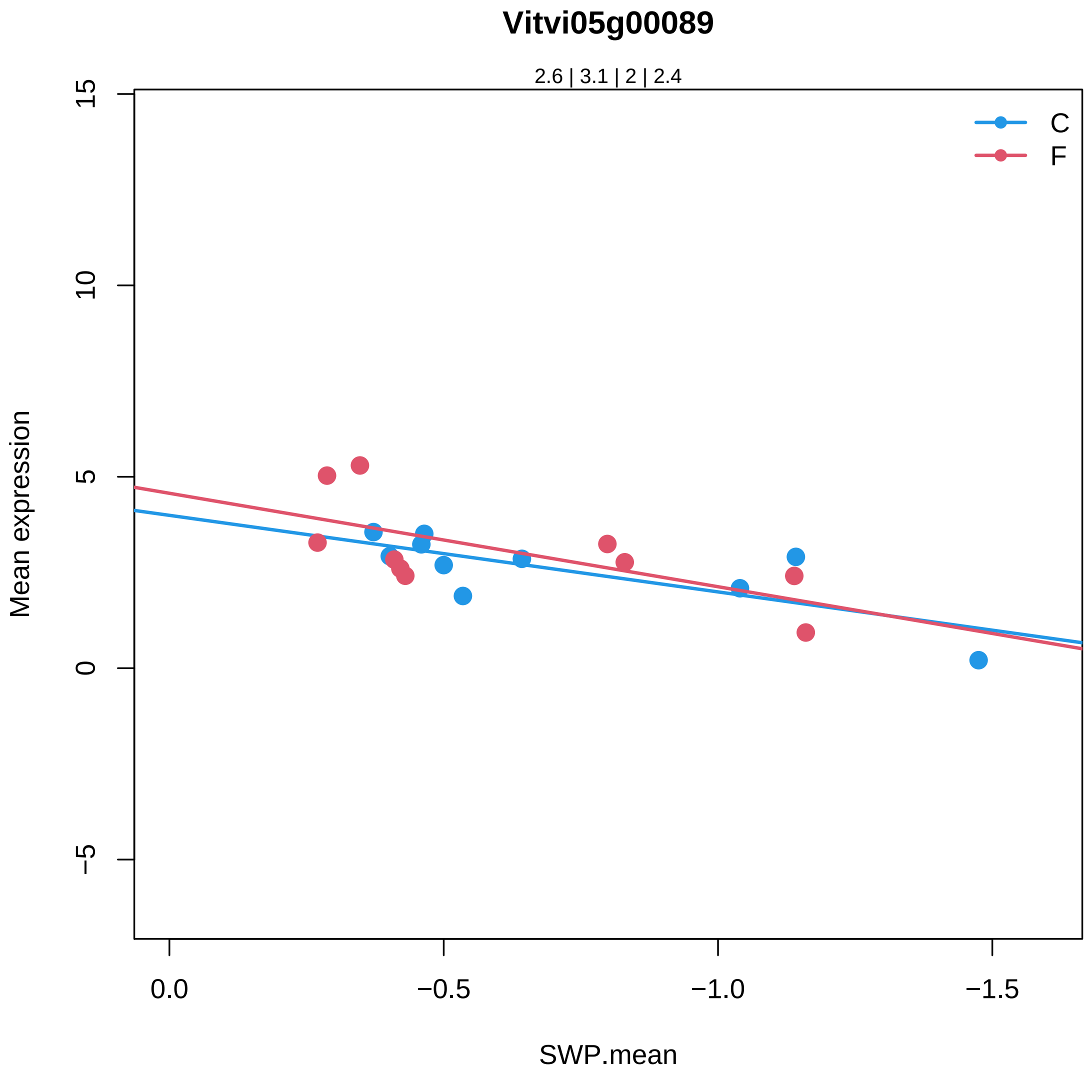
7.2.22 Vitvi05g00089: * type1

```
> 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
```



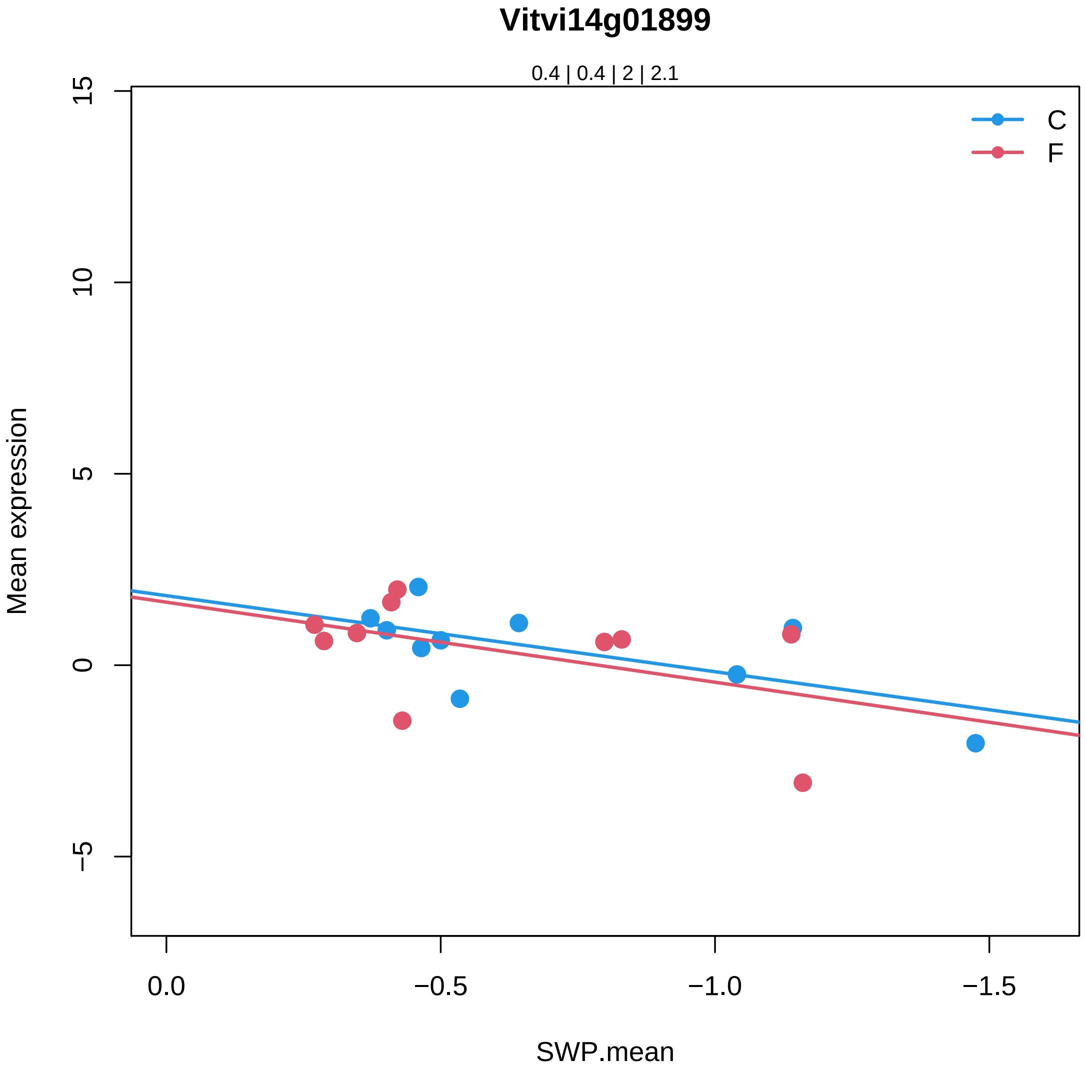
7.2.23 Vitvi14g01899: * type1

```
> 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
```



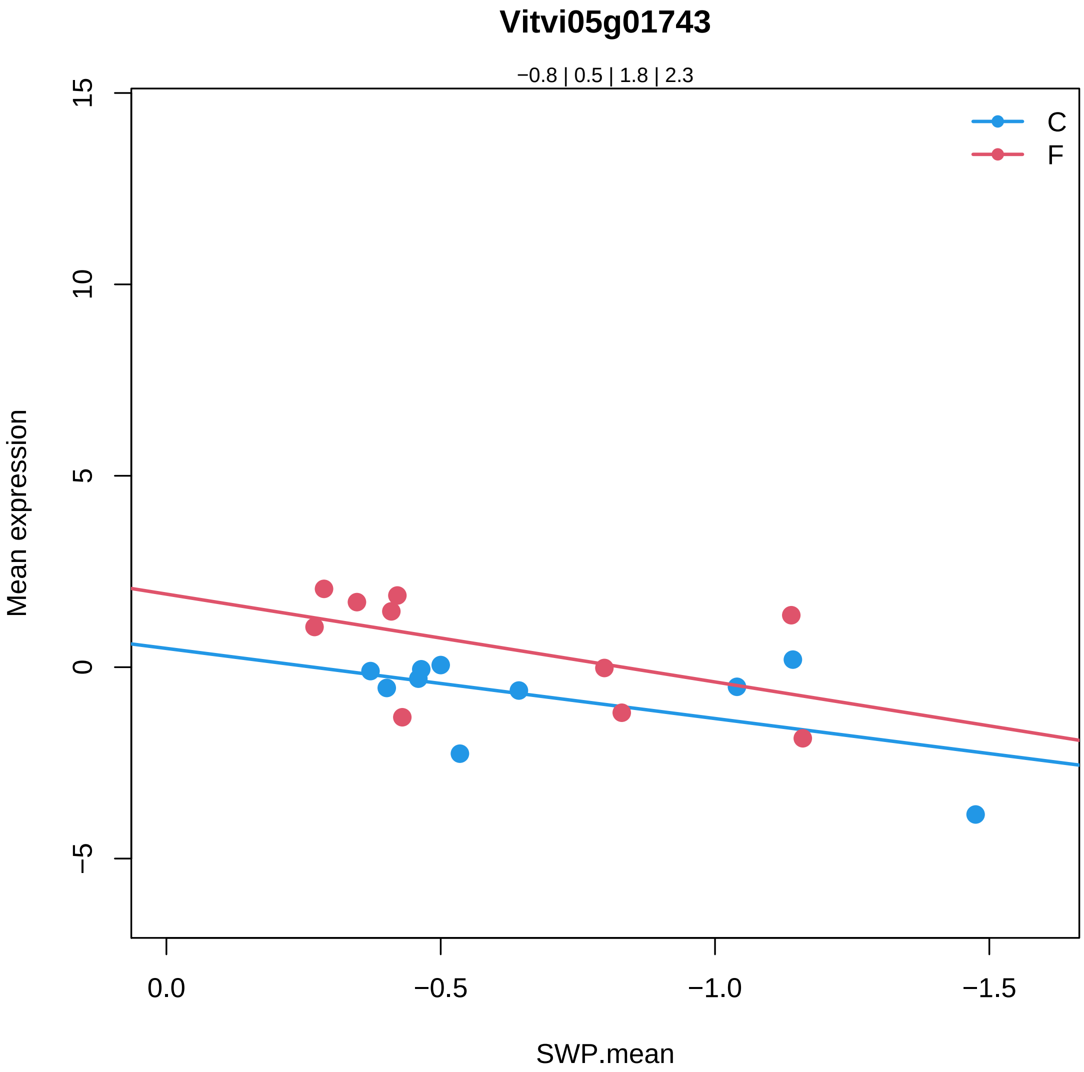
7.2.24 Vitvi05g01743: type1

```
> 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
```



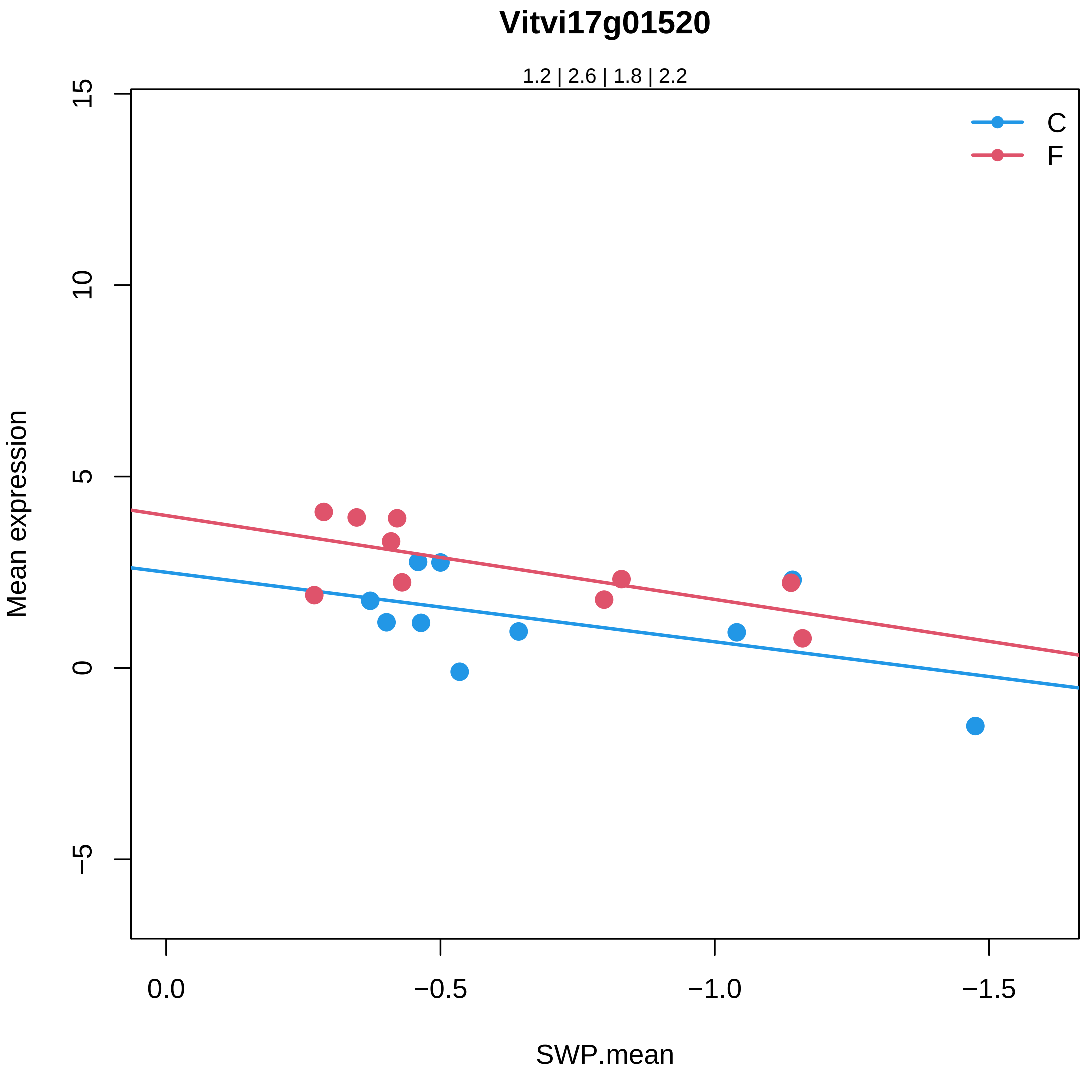
7.2.25 Vitvi17g01520: * type1

```
> 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
```



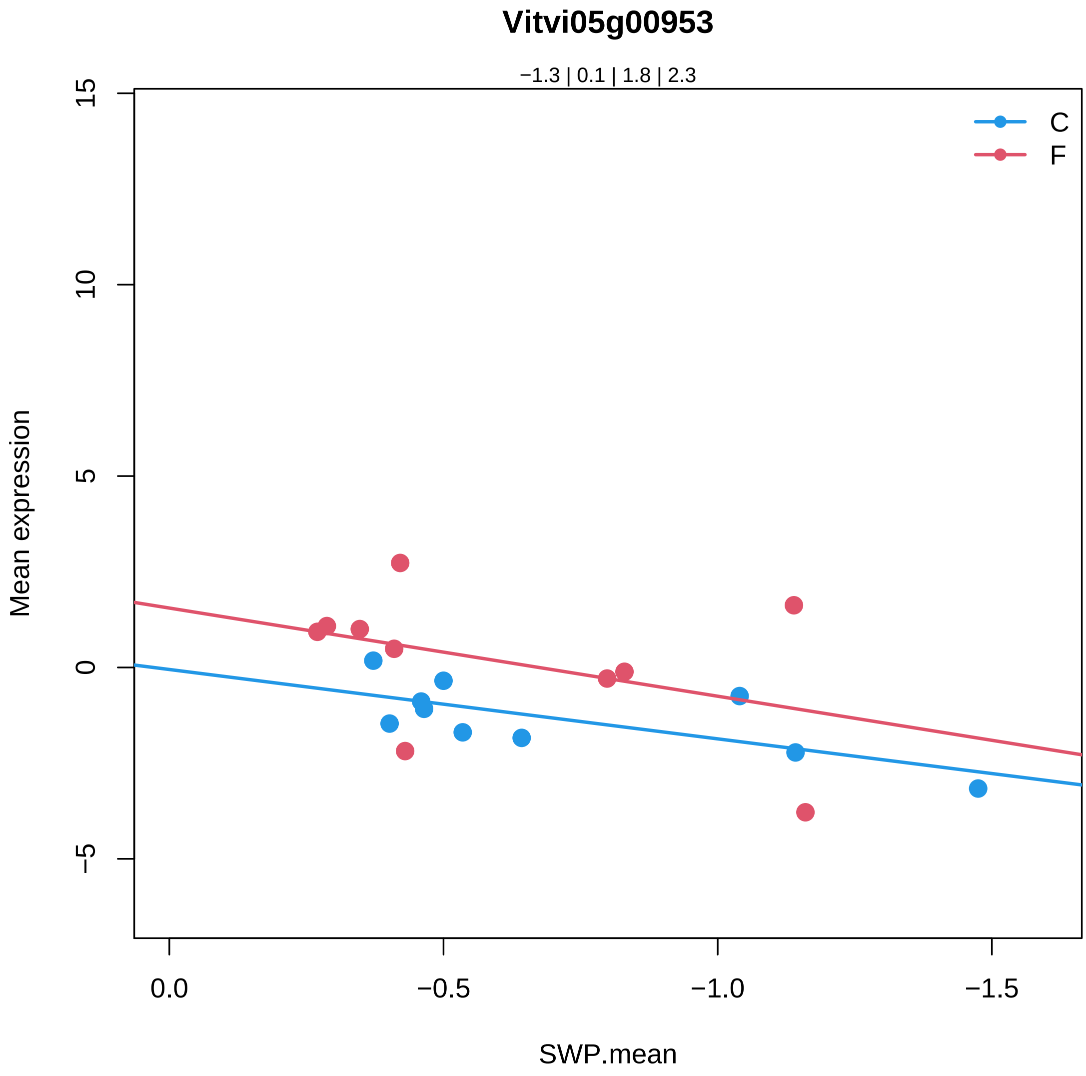
7.2.26 Vitvi05g00953: type1

```
> 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

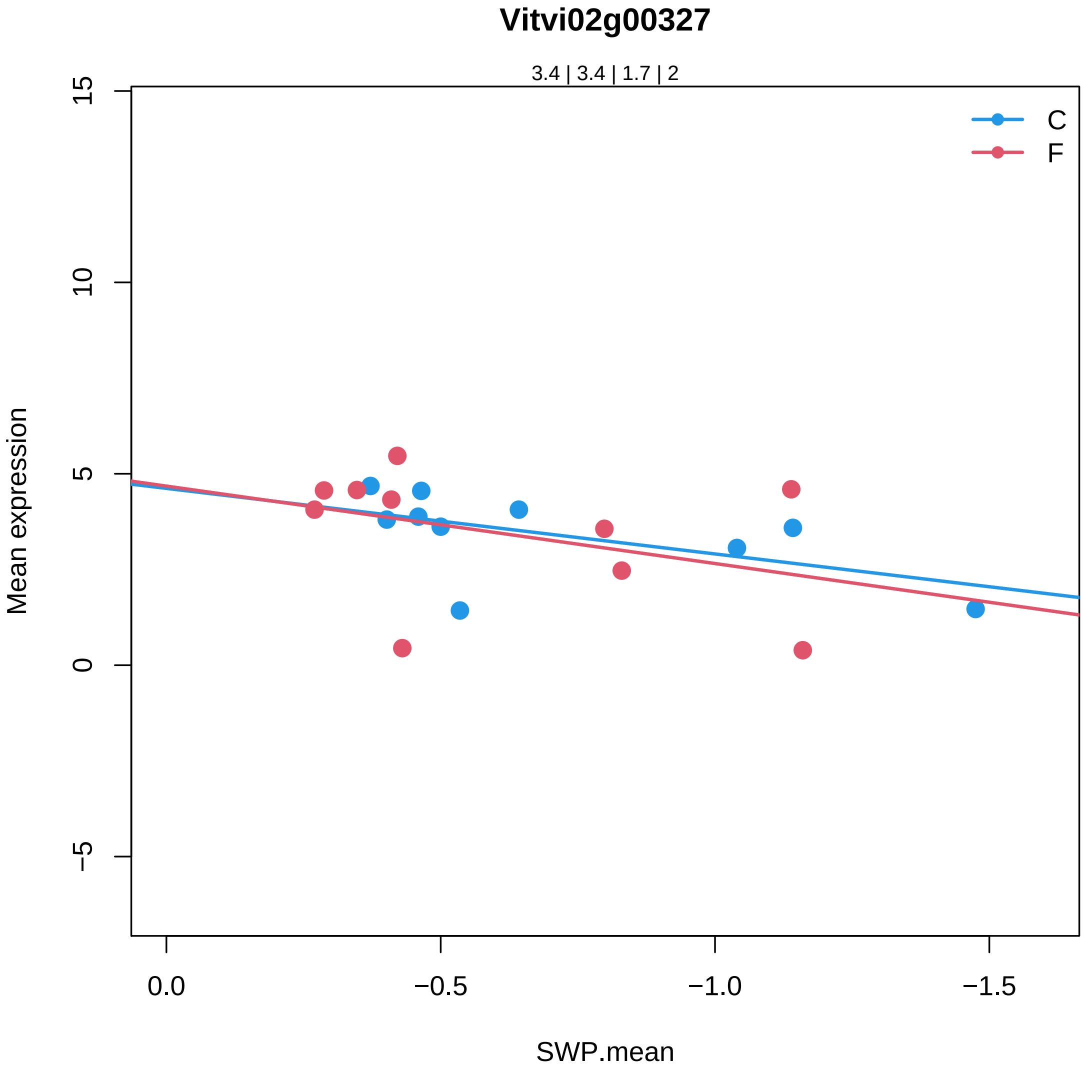
7.2.27 Vitvi02g00327: type1

```
> 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
```



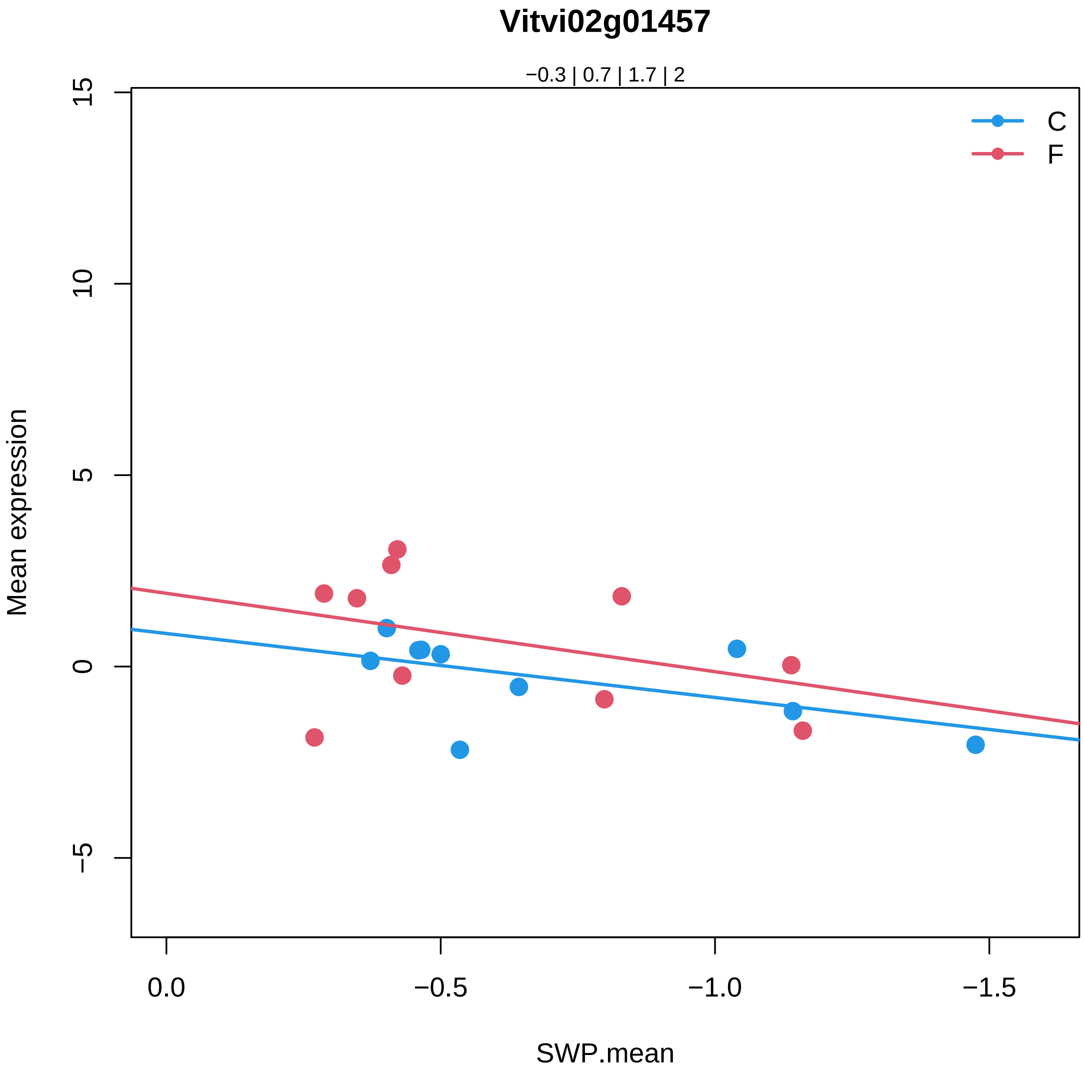
7.2.28 Vitvi02g01457: type1

```
> 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
```



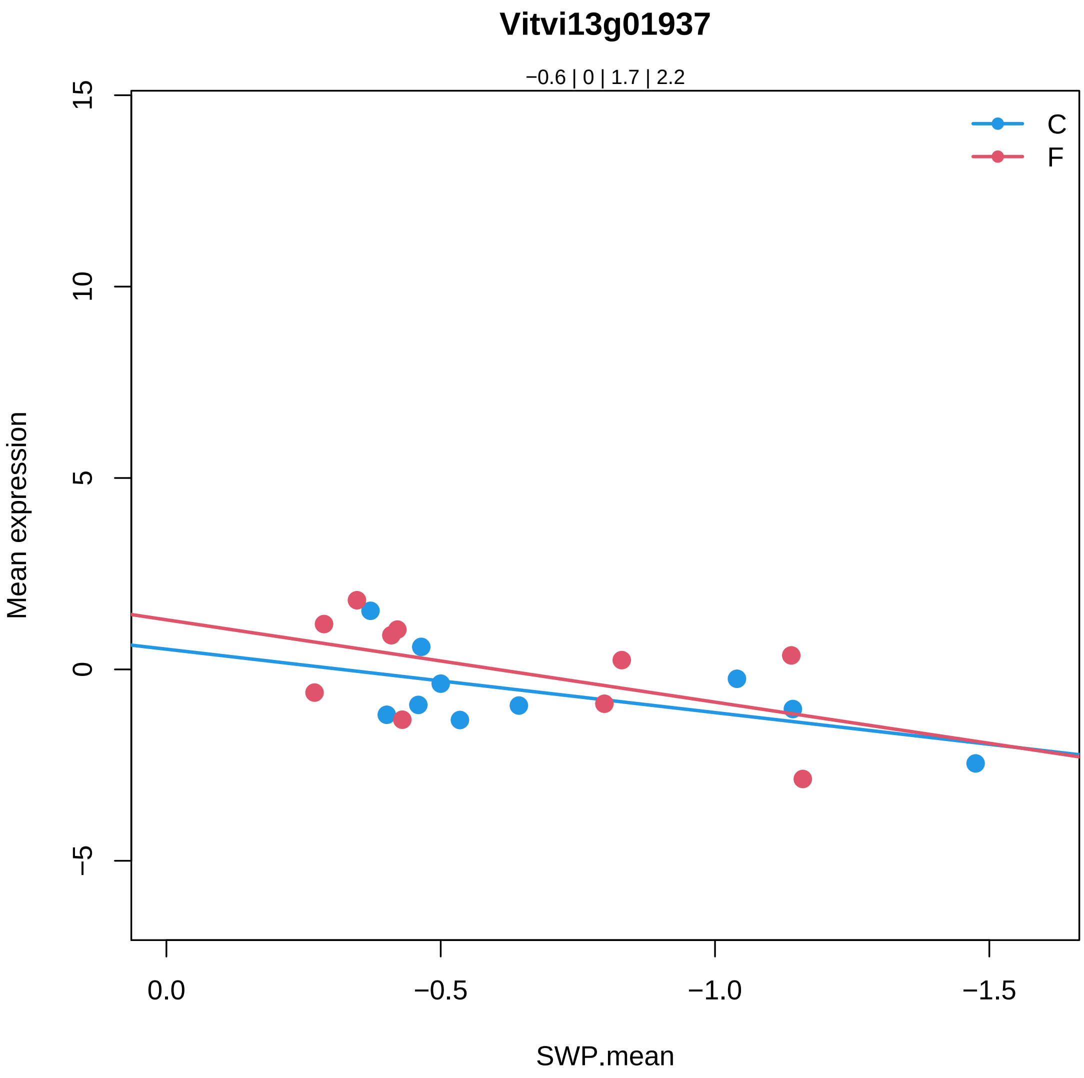
7.2.29 Vitvi13g01937: type1

```
> 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
```



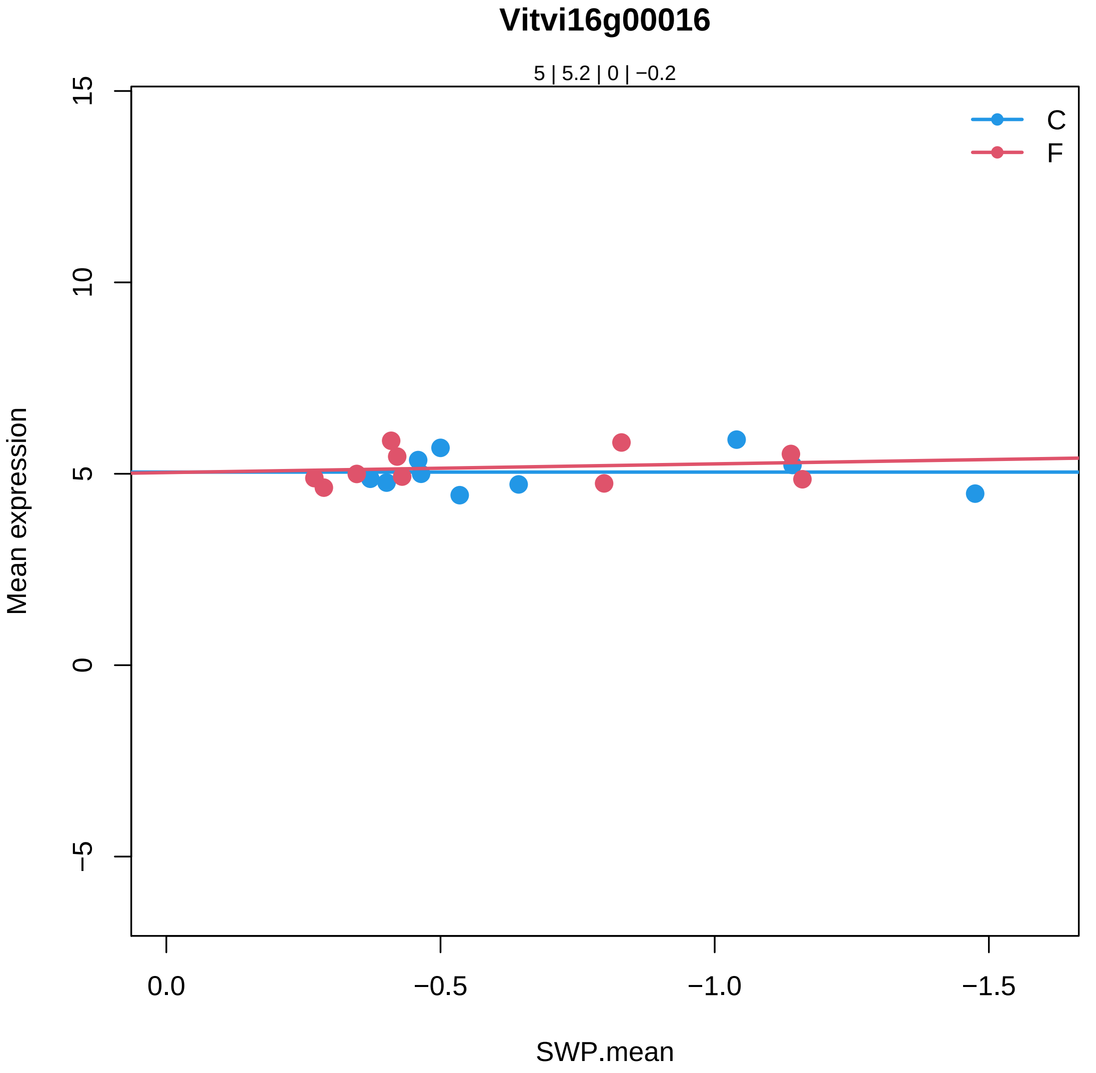
7.2.30 Vitvi16g00016: type1

```
> 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
```

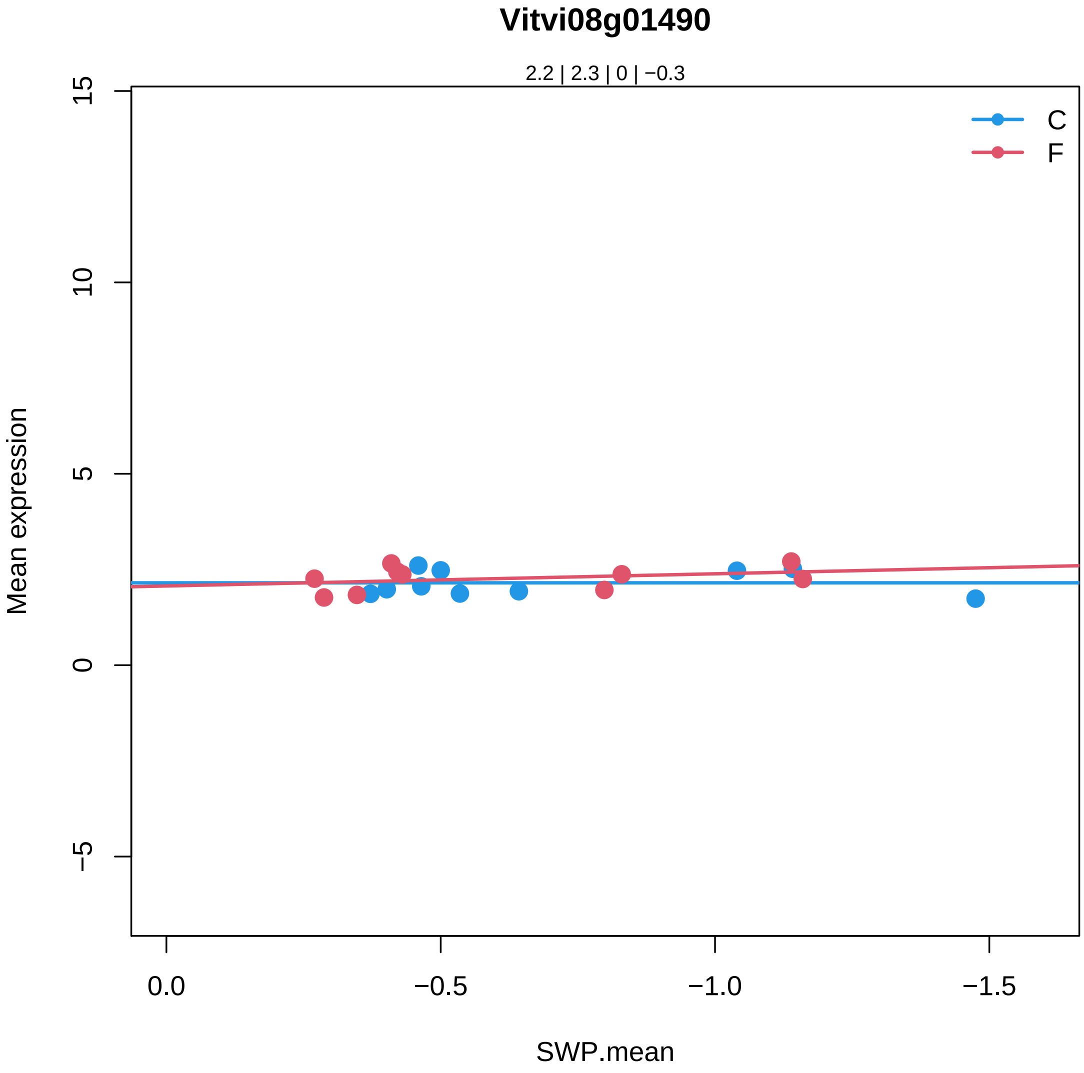


7.2.31 Vitvi08g01490: type1

```
> 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
```



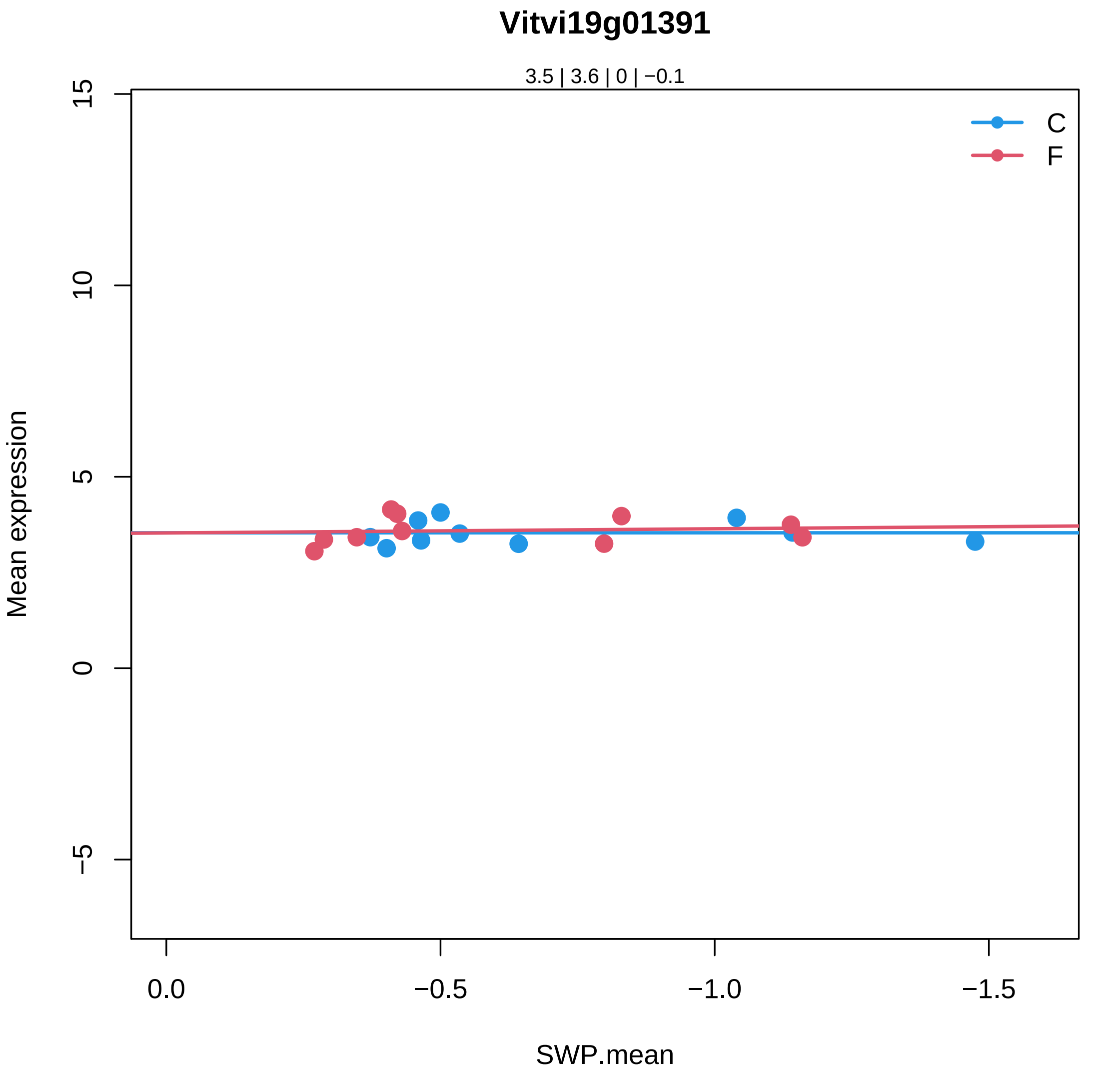
7.2.32 Vitvi19g01391: type1

```
> 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
```



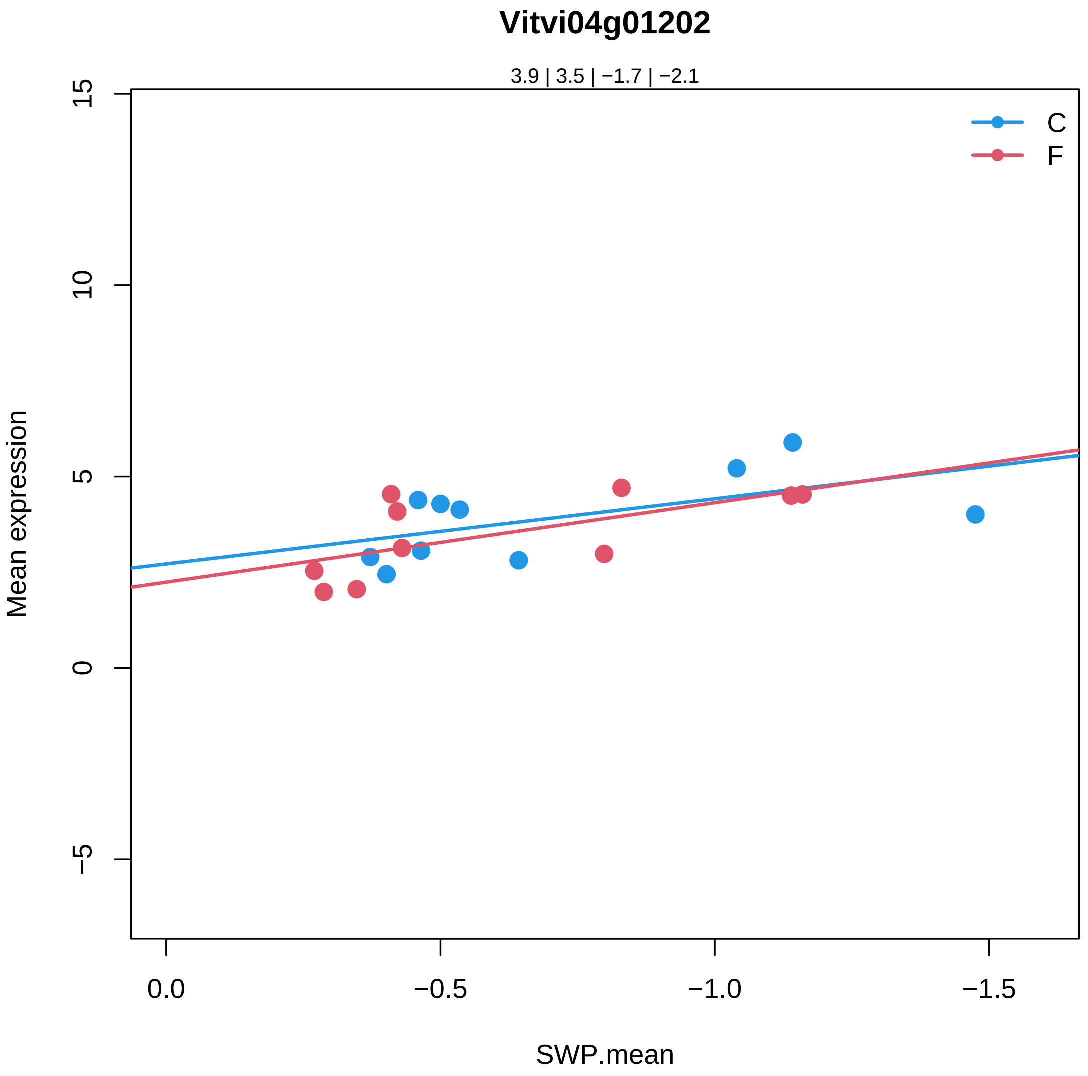
7.2.33 Vitvi04g01202: * type1

```
> 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
```



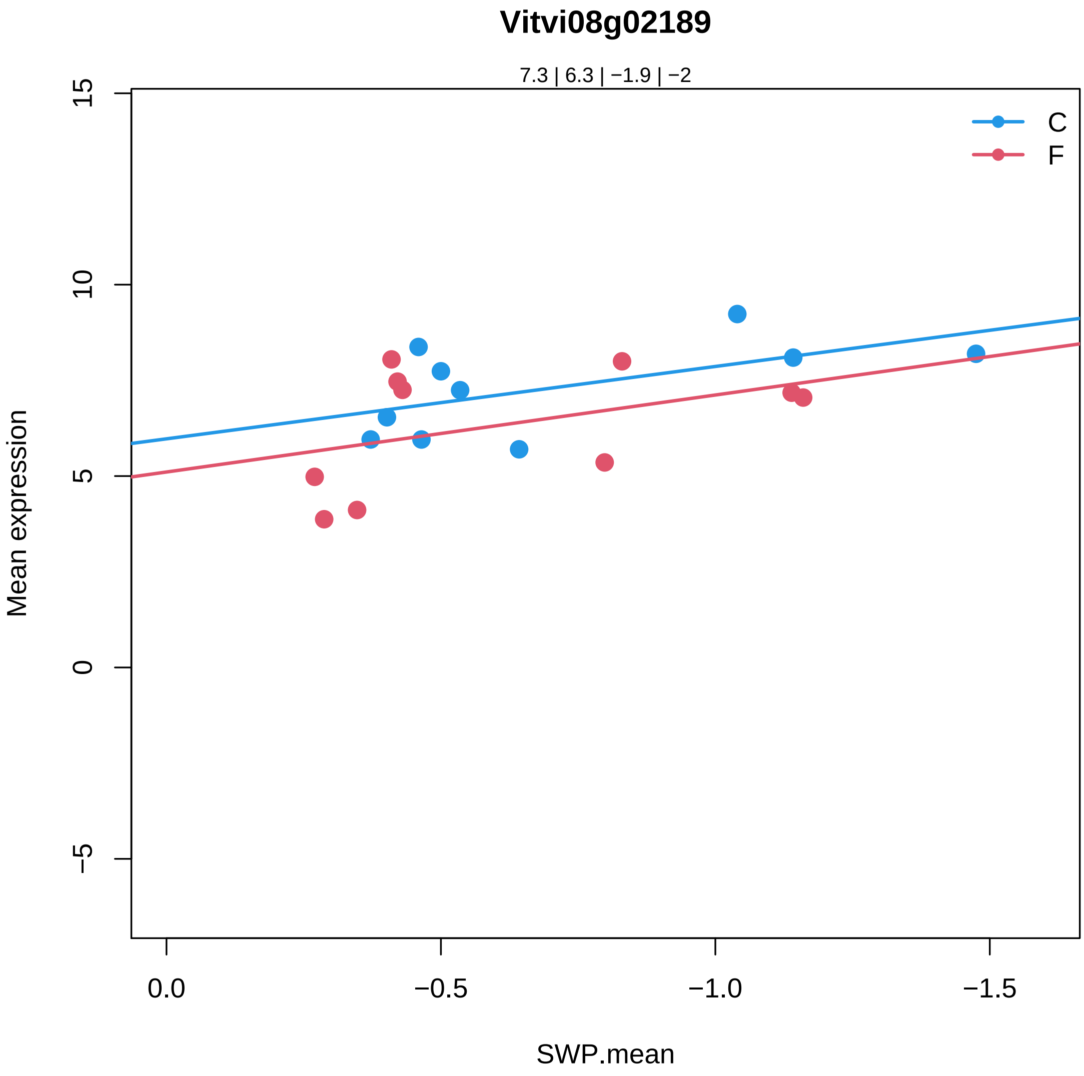
7.2.34 Vitvi08g02189: type1

```
> 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

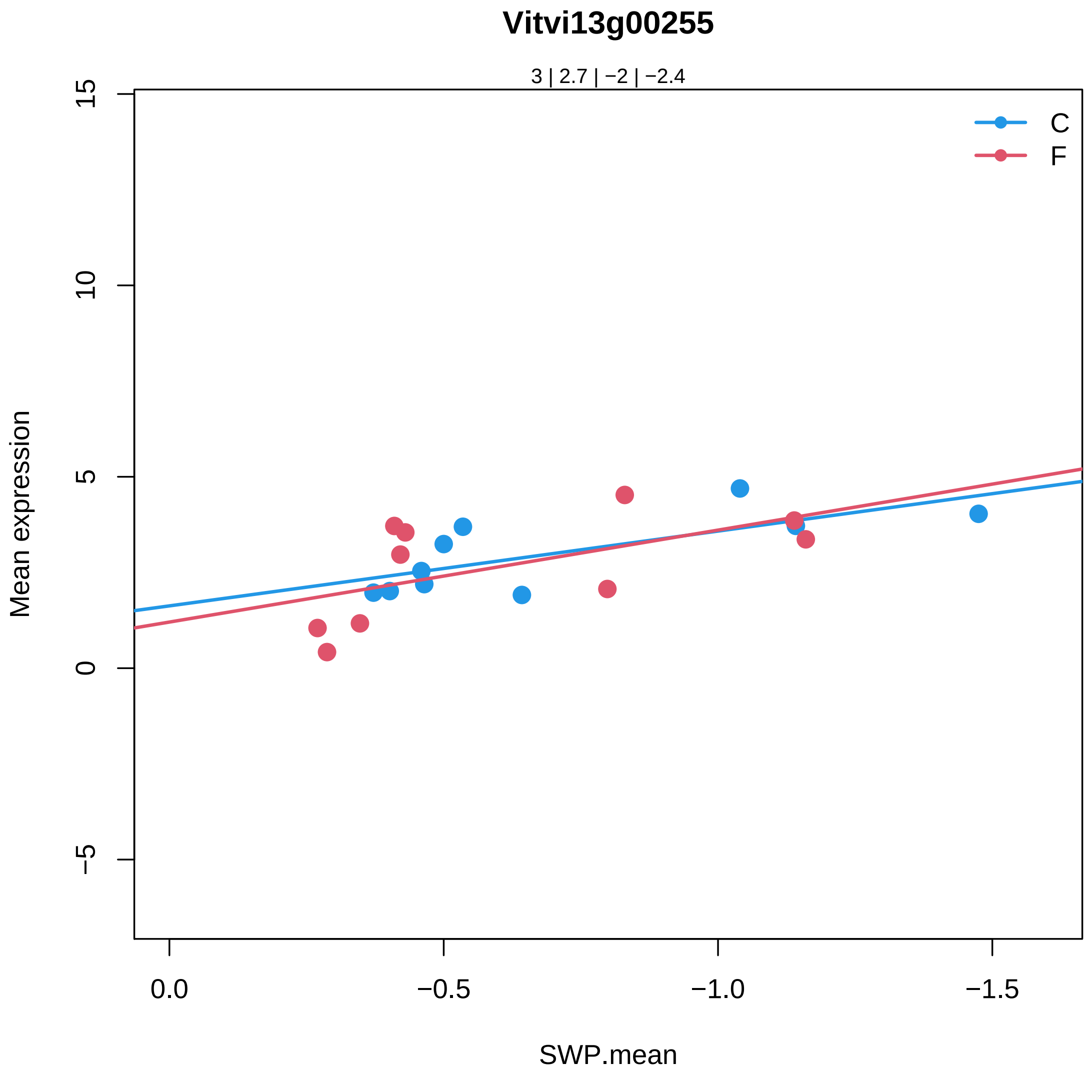
7.2.35 Vitvi13g00255: * type1

```
> 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
```



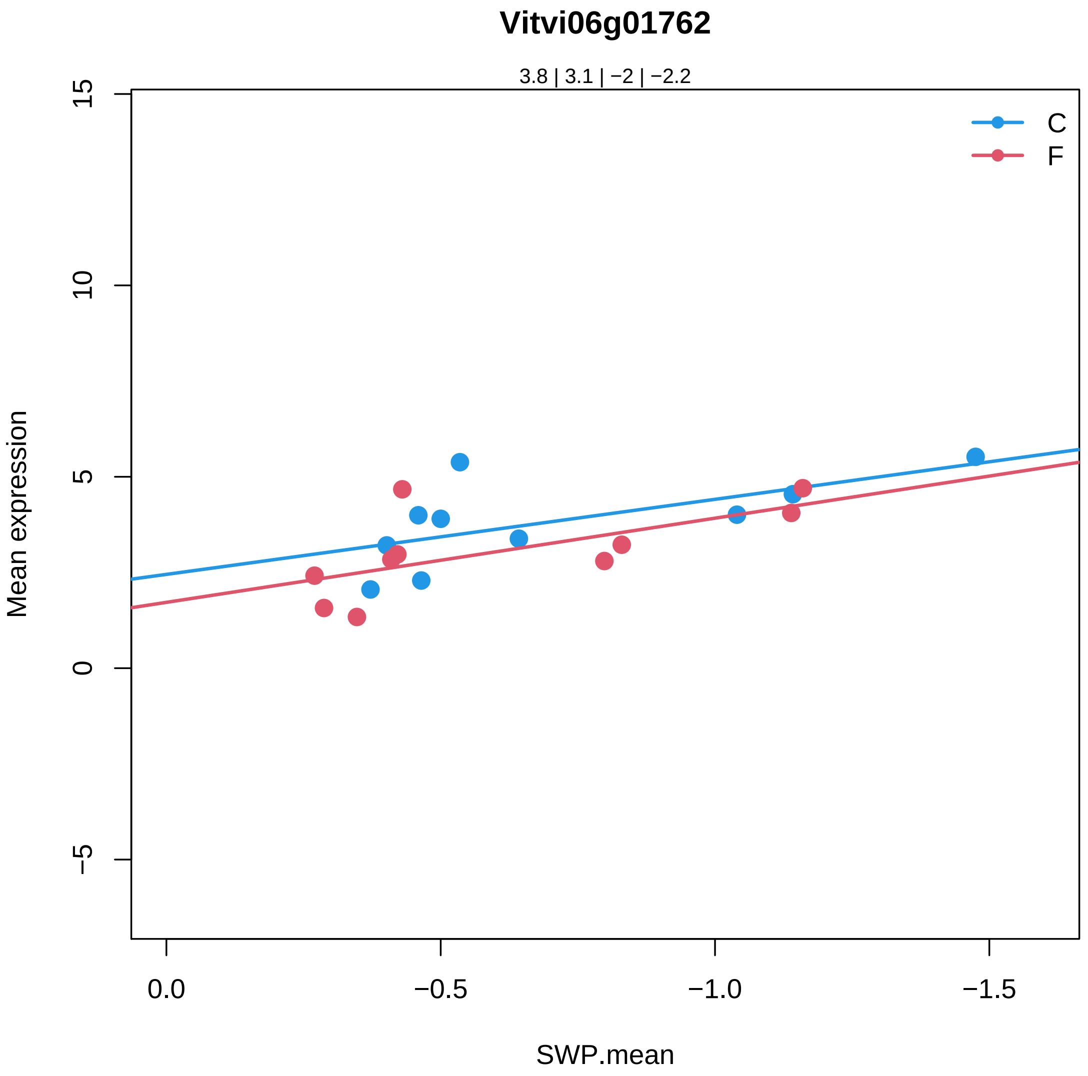
7.2.36 Vitvi06g01762: * type1

```
> 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
```



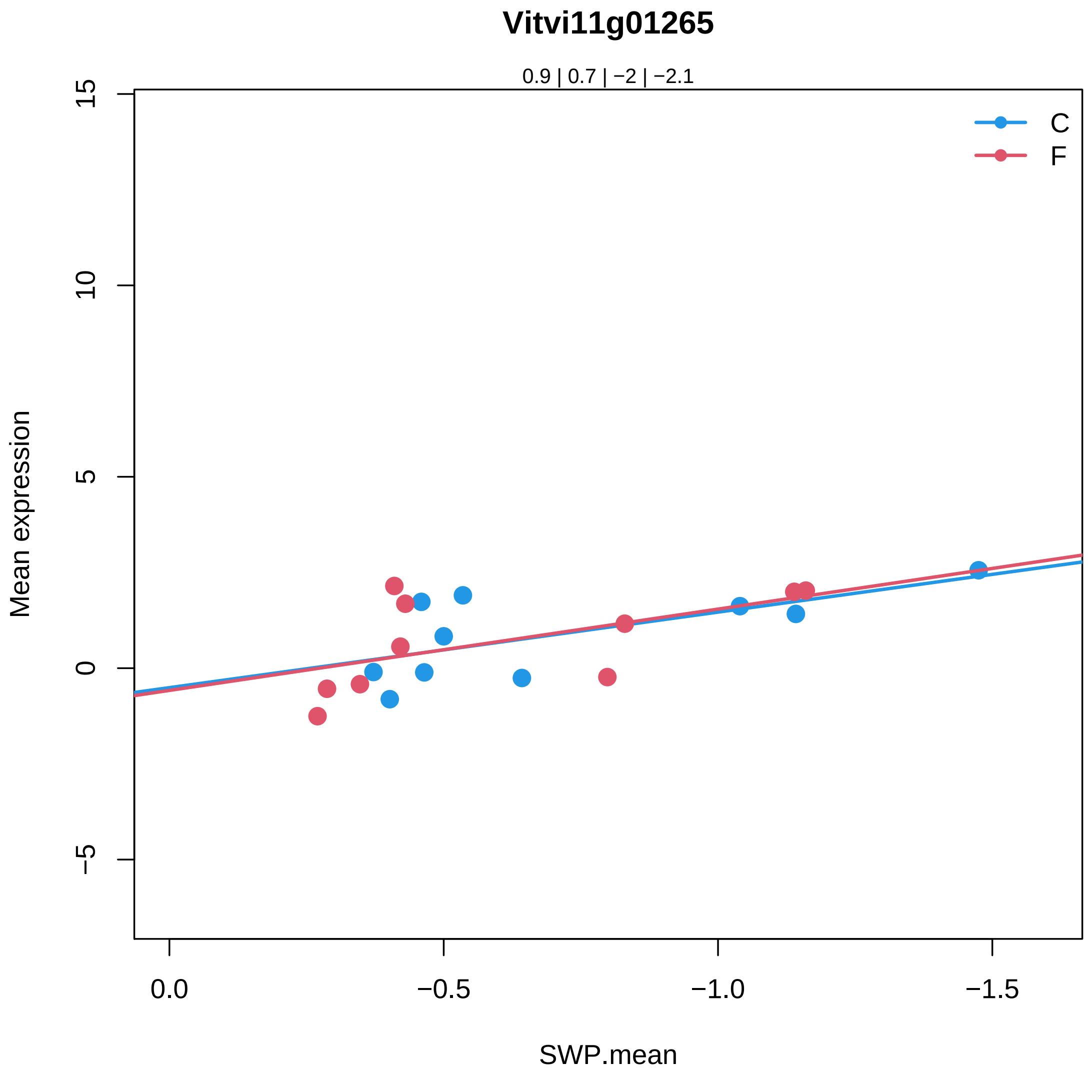
7.2.37 Vitvi11g01265: * type1

```
> 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
```



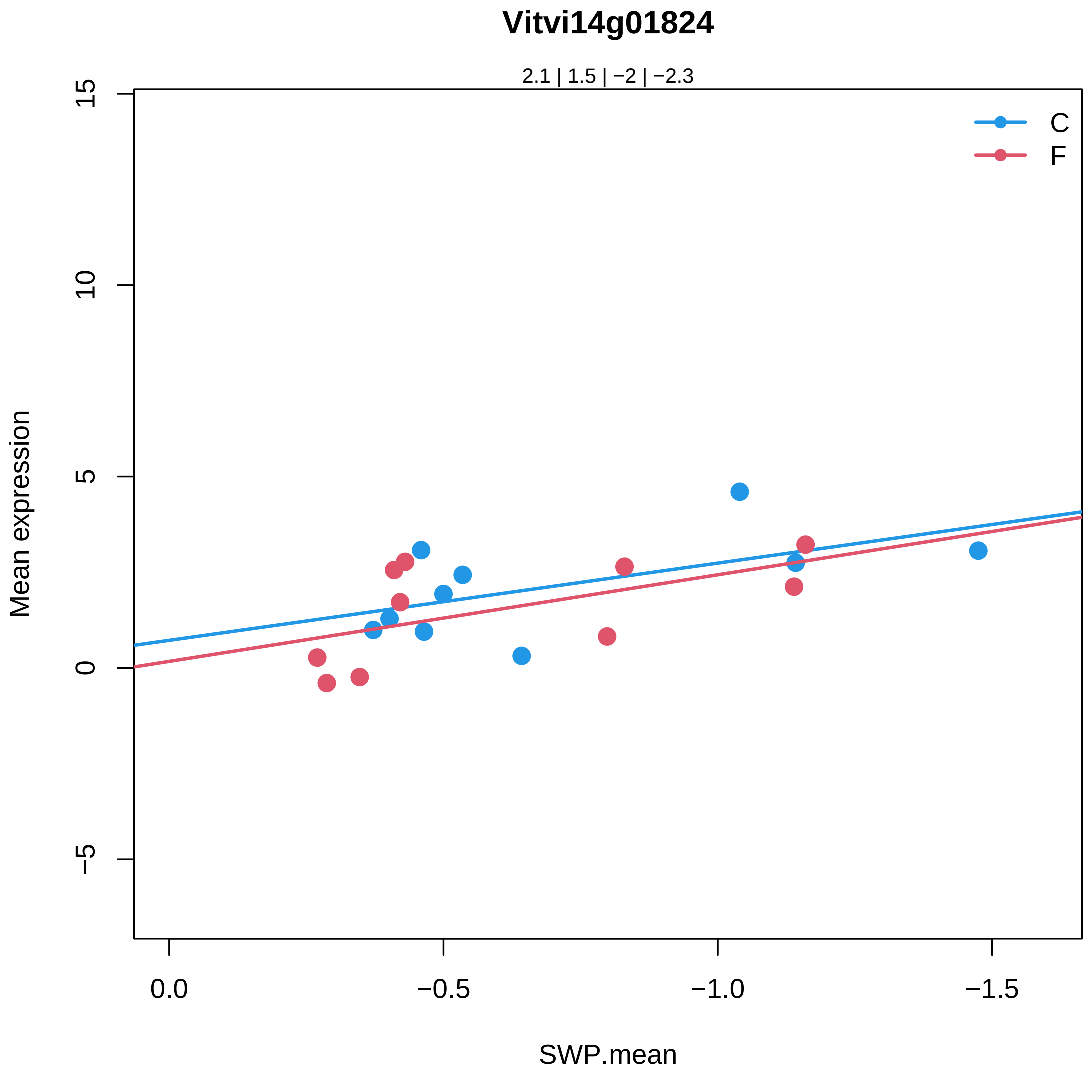
7.2.38 Vitvi14g01824: * type1

```
> 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
```



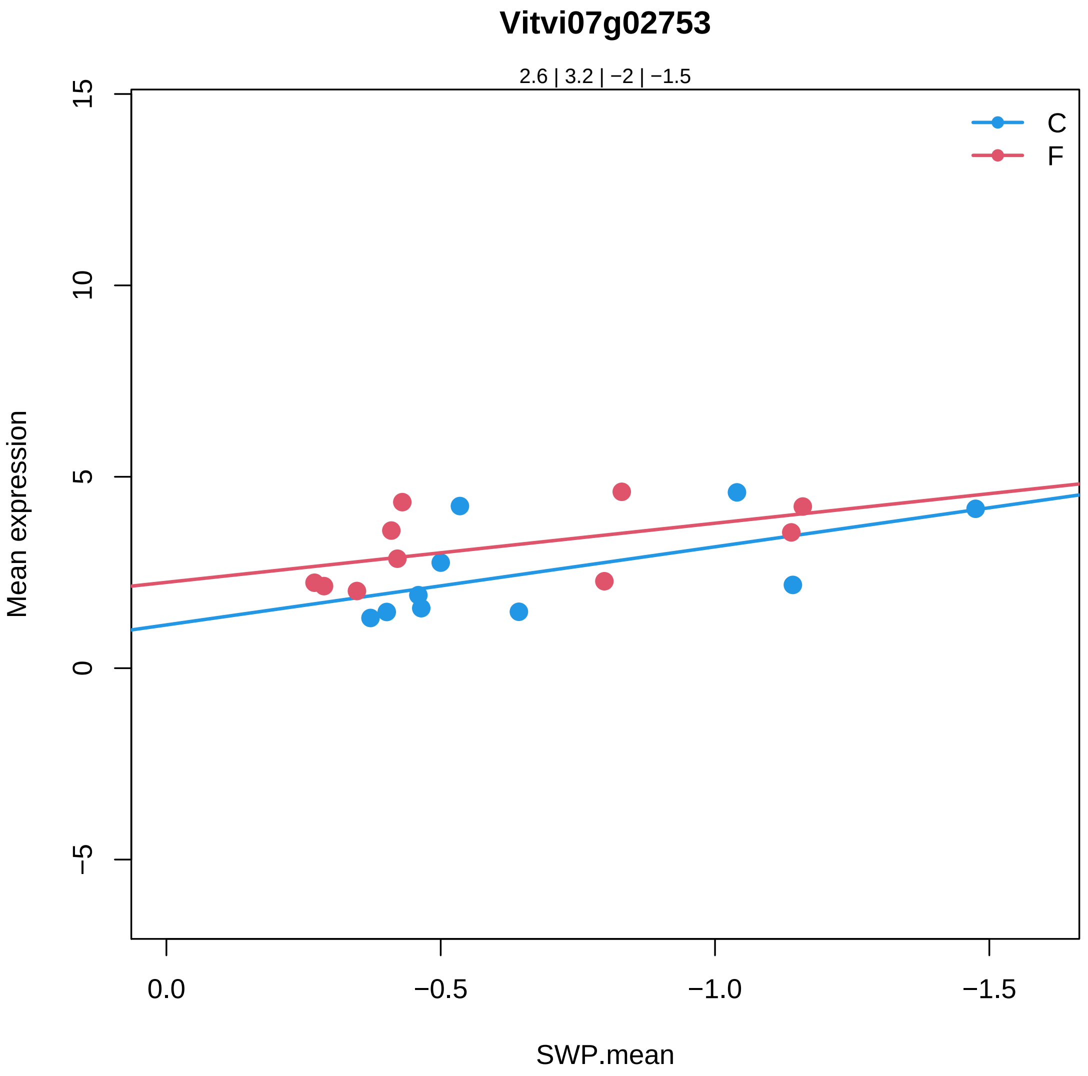
7.2.39 Vitvi07g02753: * type1

```
> 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
```



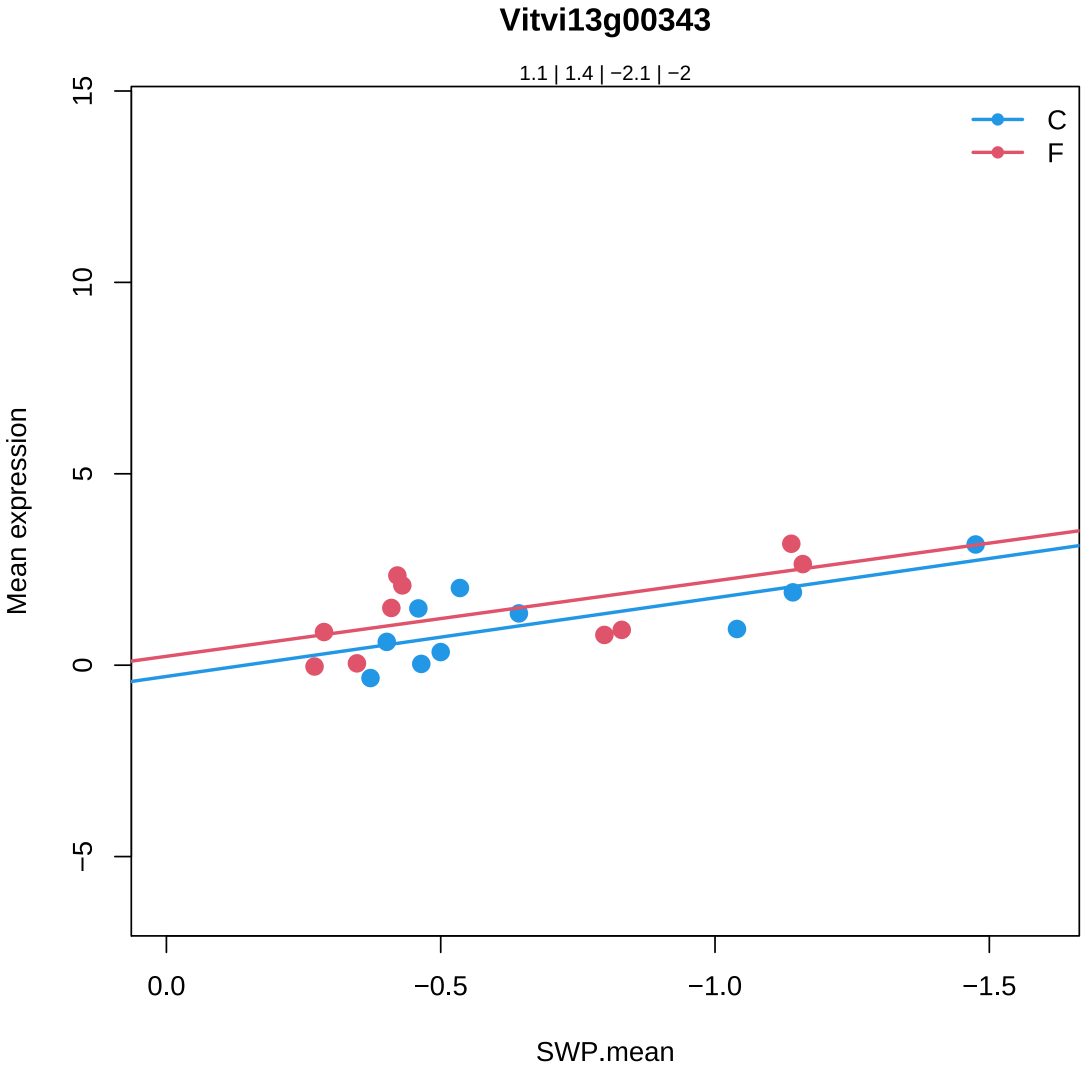
7.2.40 Vitvi13g00343: * type1

```
> 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
```



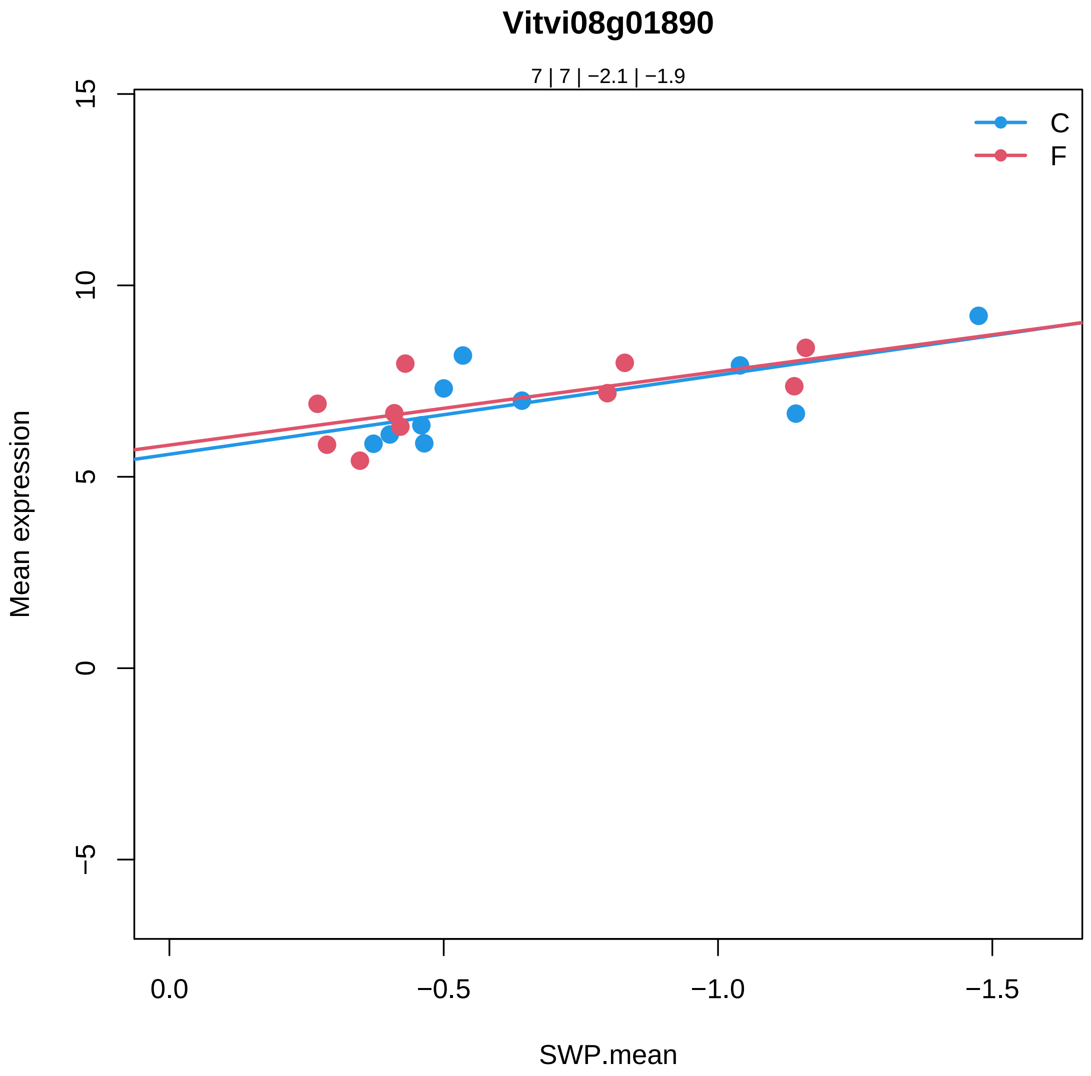
7.2.41 Vitvi08g01890: * type1

```
> 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
```



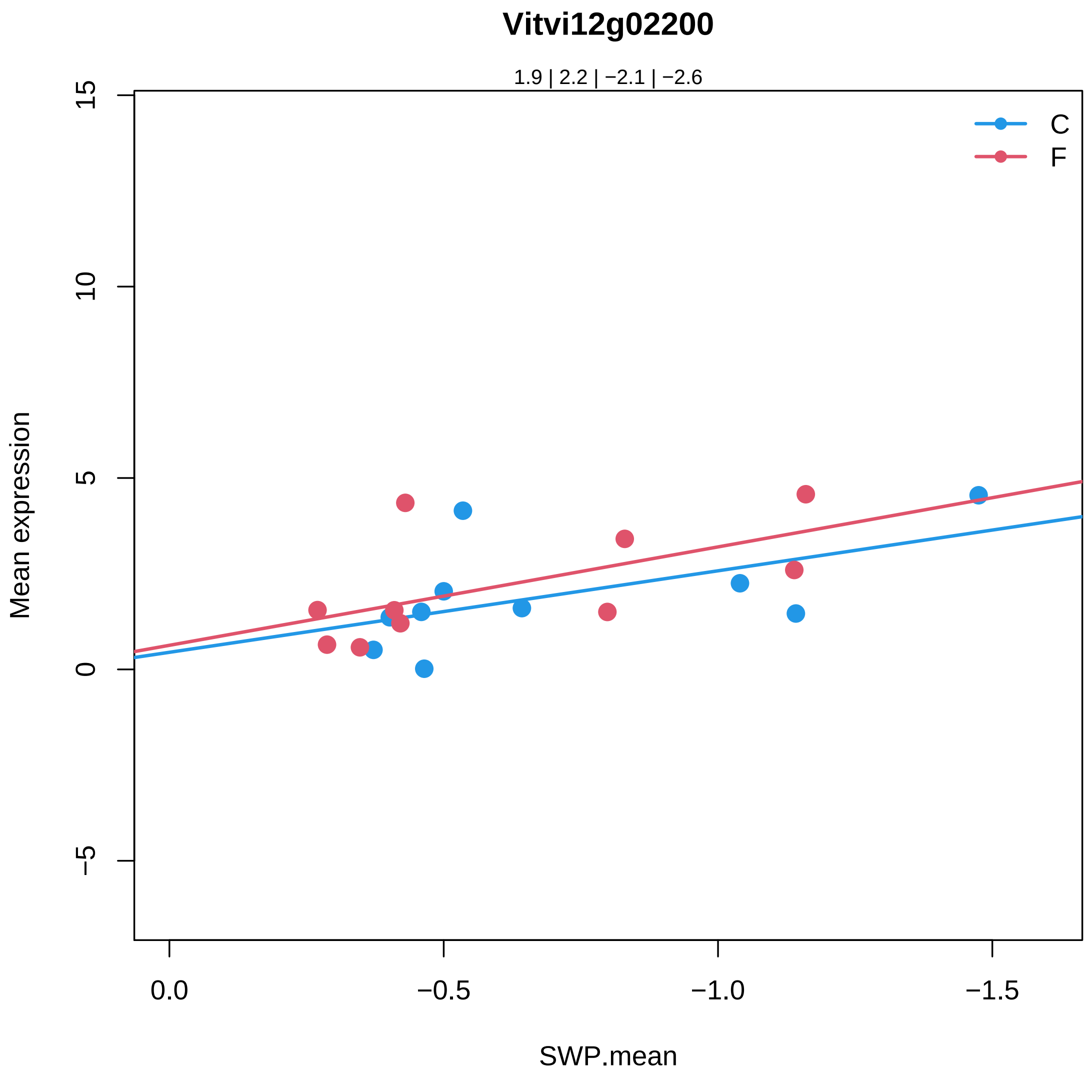
7.2.42 Vitvi12g02200: * type1

```
> 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
```



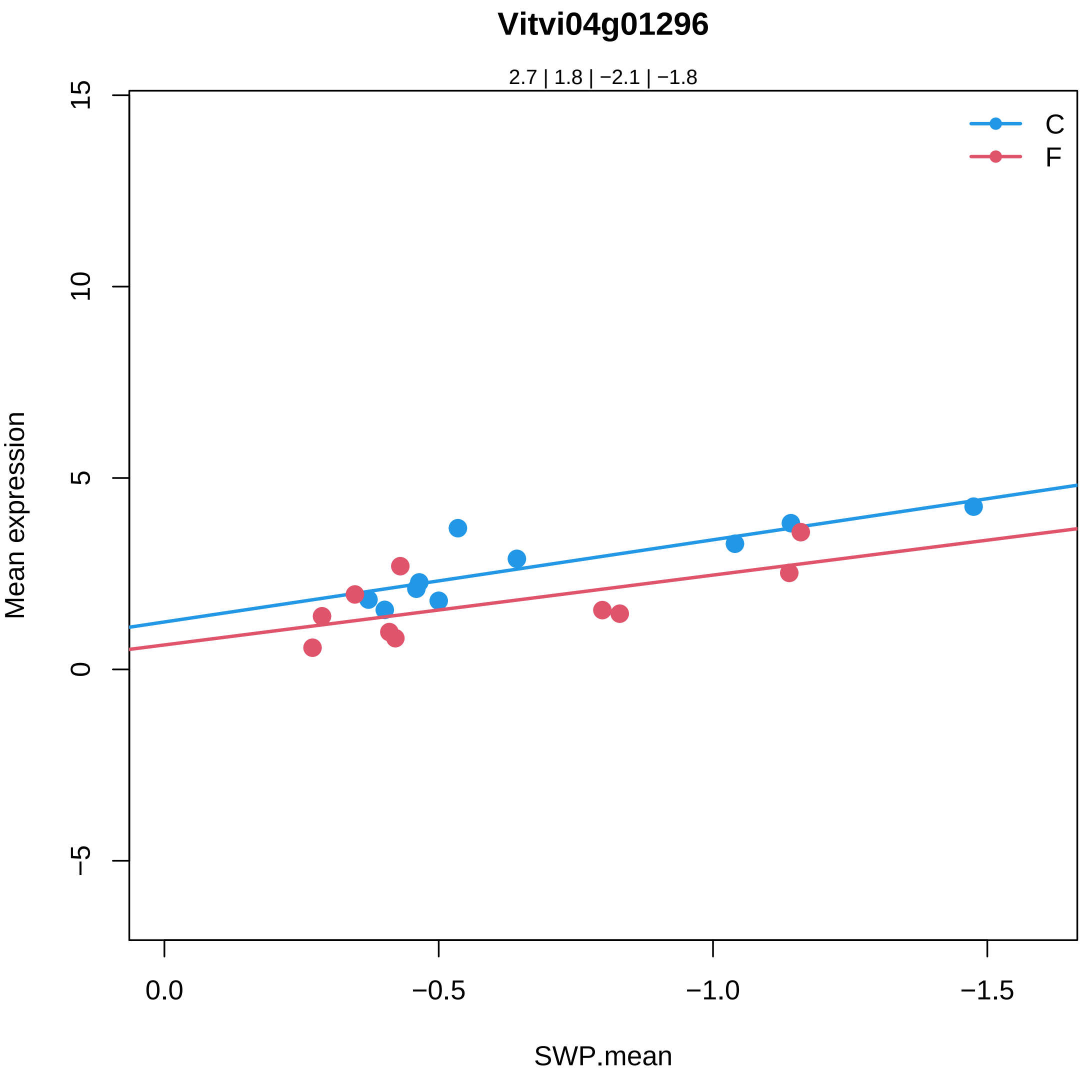
7.2.43 Vitvi04g01296: * type1

```
> 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
```



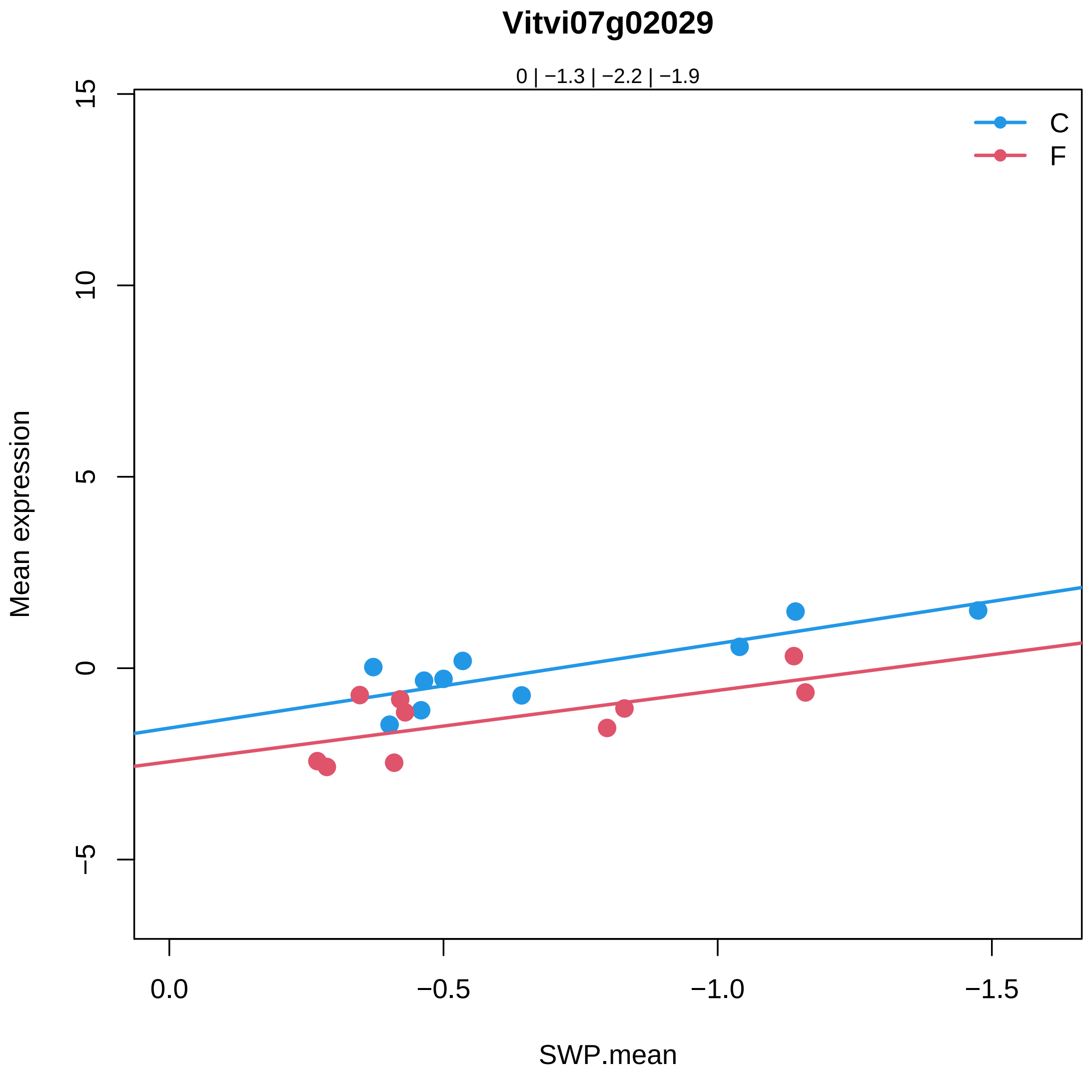
7.2.44 Vitvi07g02029: * type1

```
> 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
```



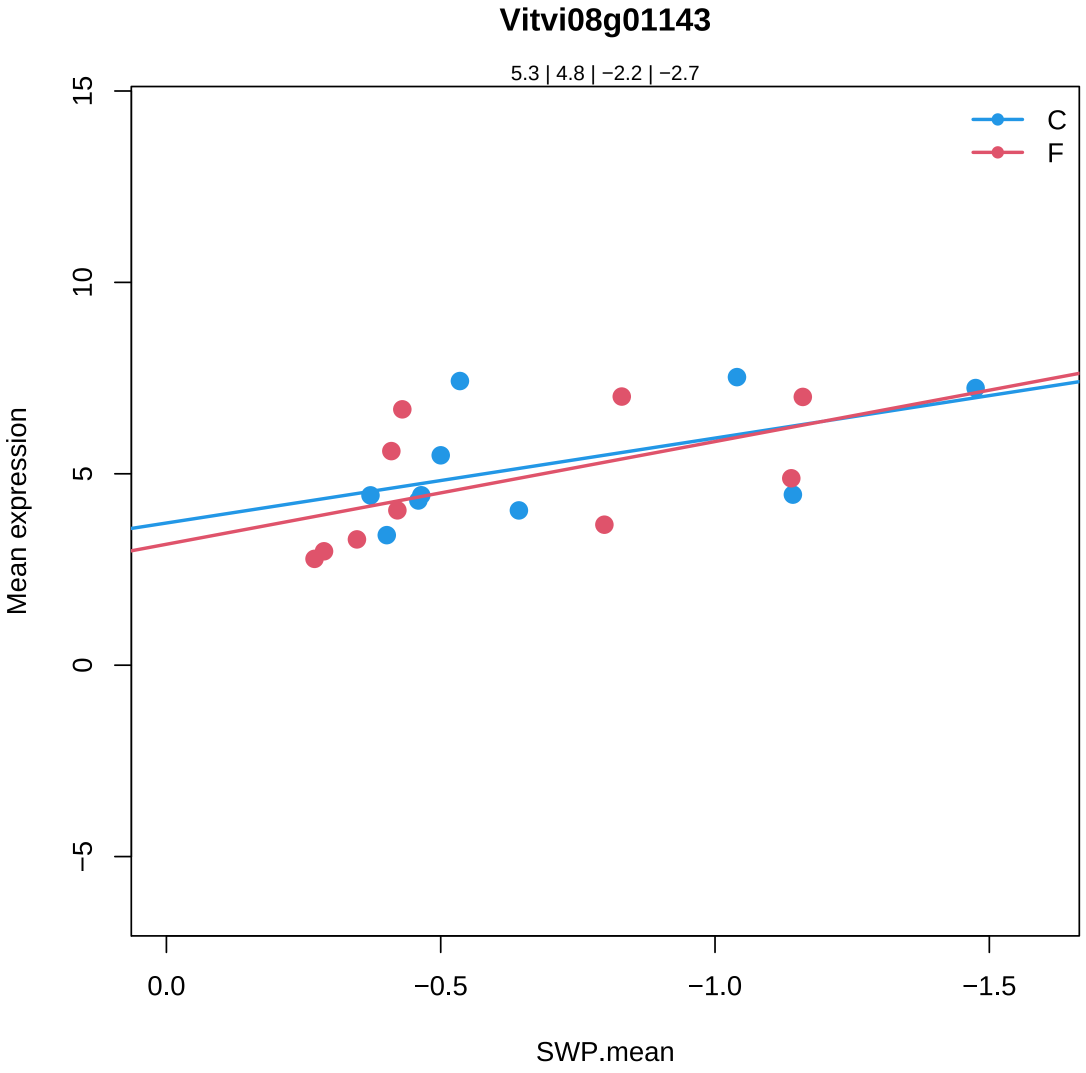
7.2.45 Vitvi08g01143: type1

```
> 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
```



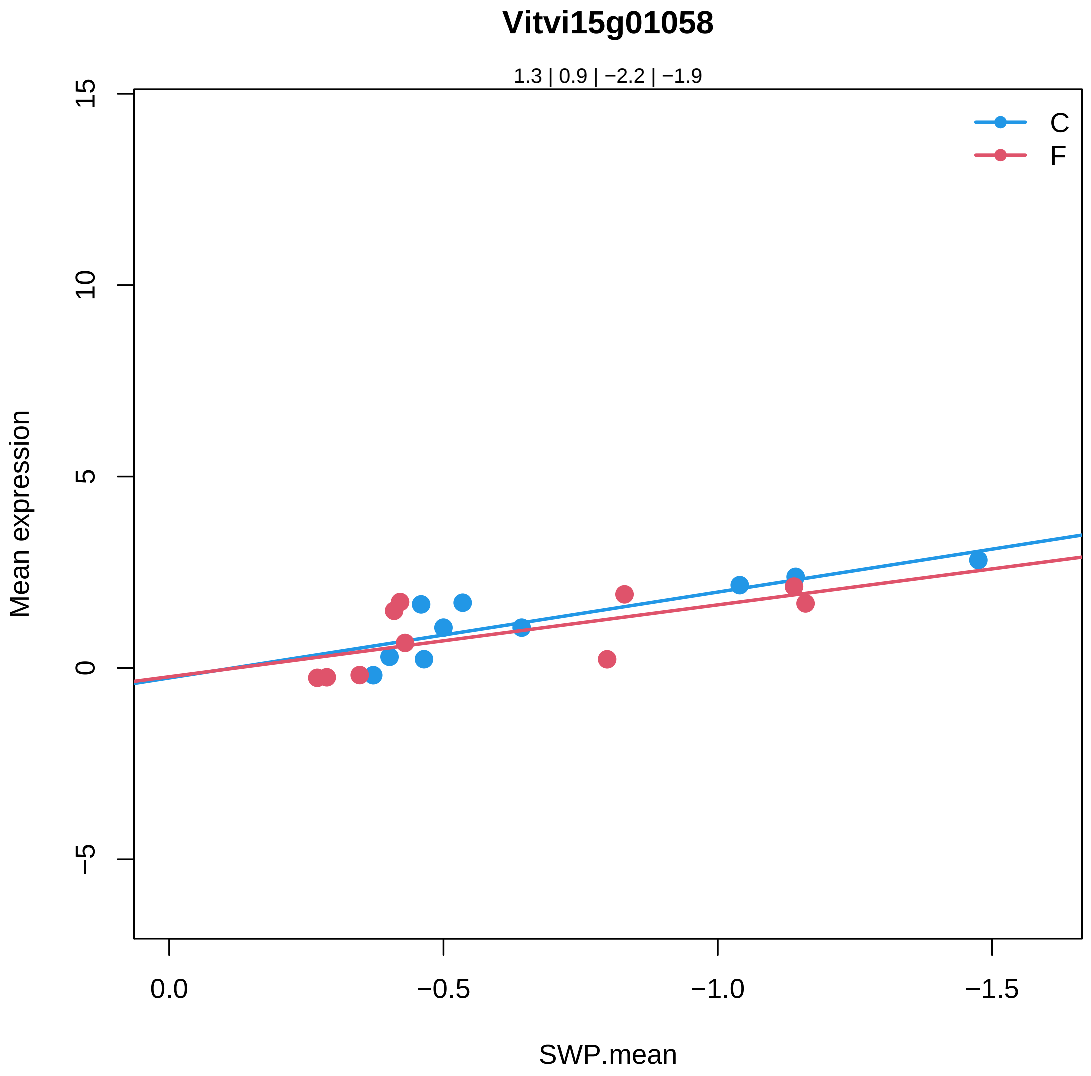
7.2.46 Vitvi15g01058: * type1

```
> 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
```



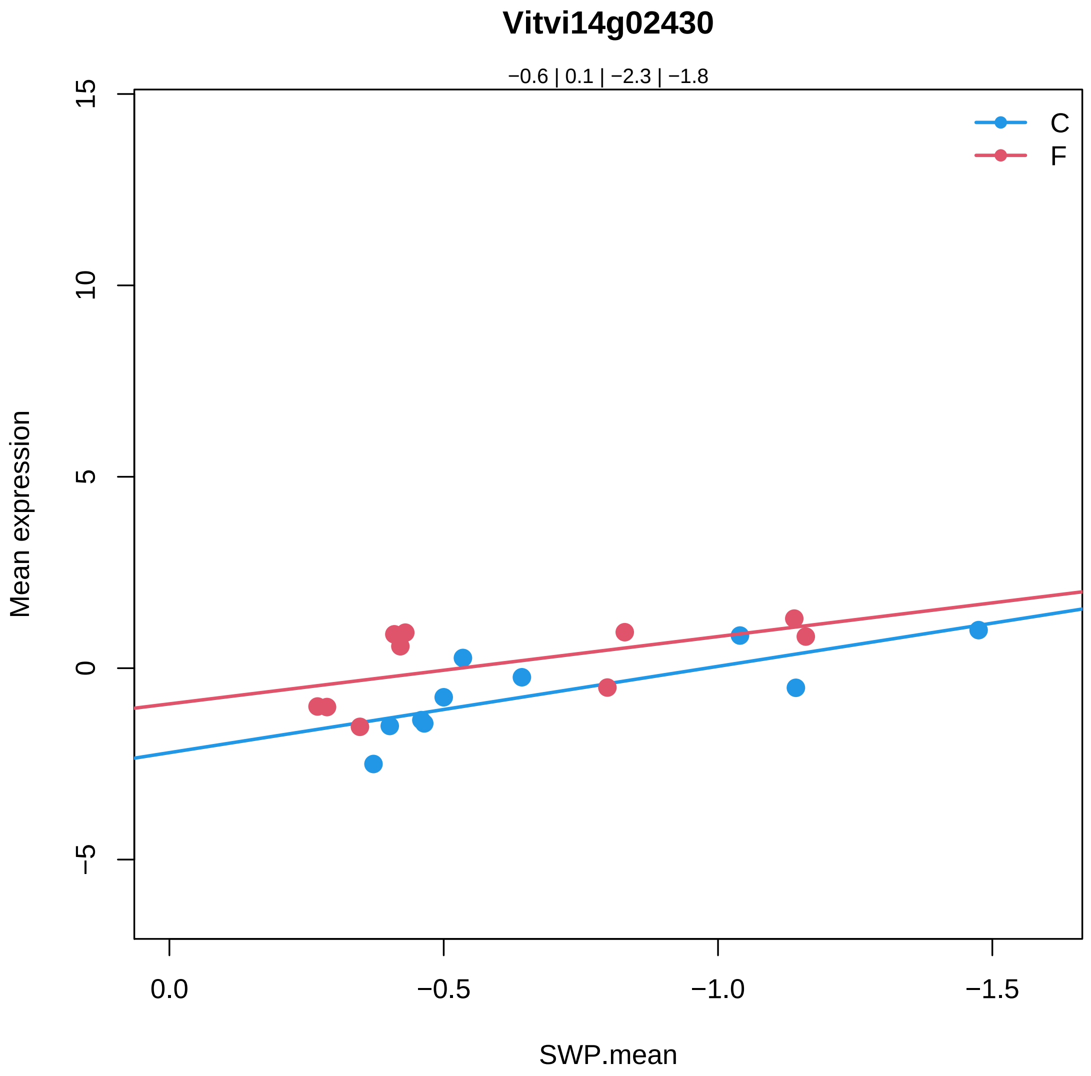
7.2.47 Vitvi14g02430: * type1

```
> 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
```



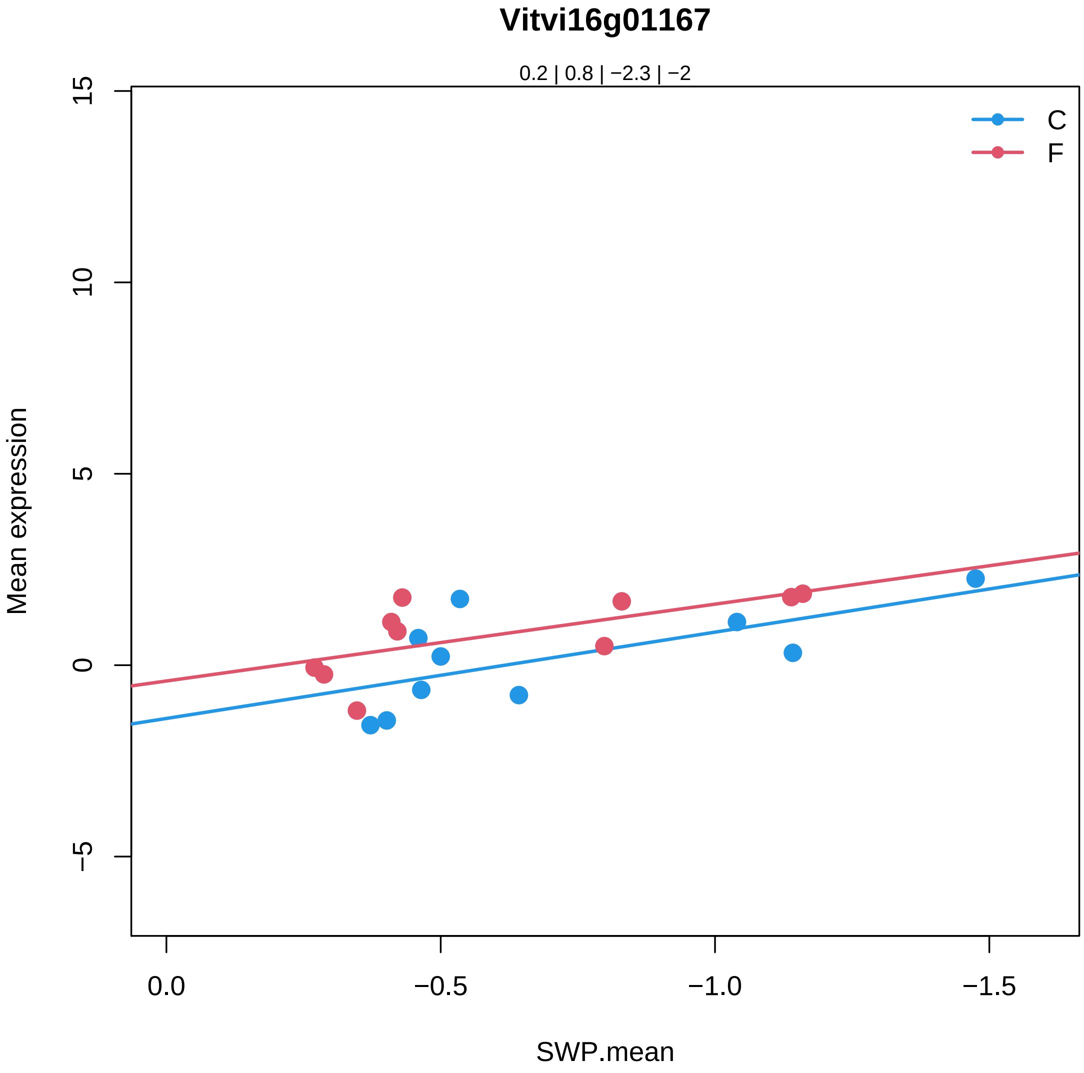
7.2.48 Vitvi16g01167: * type1

```
> 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
```



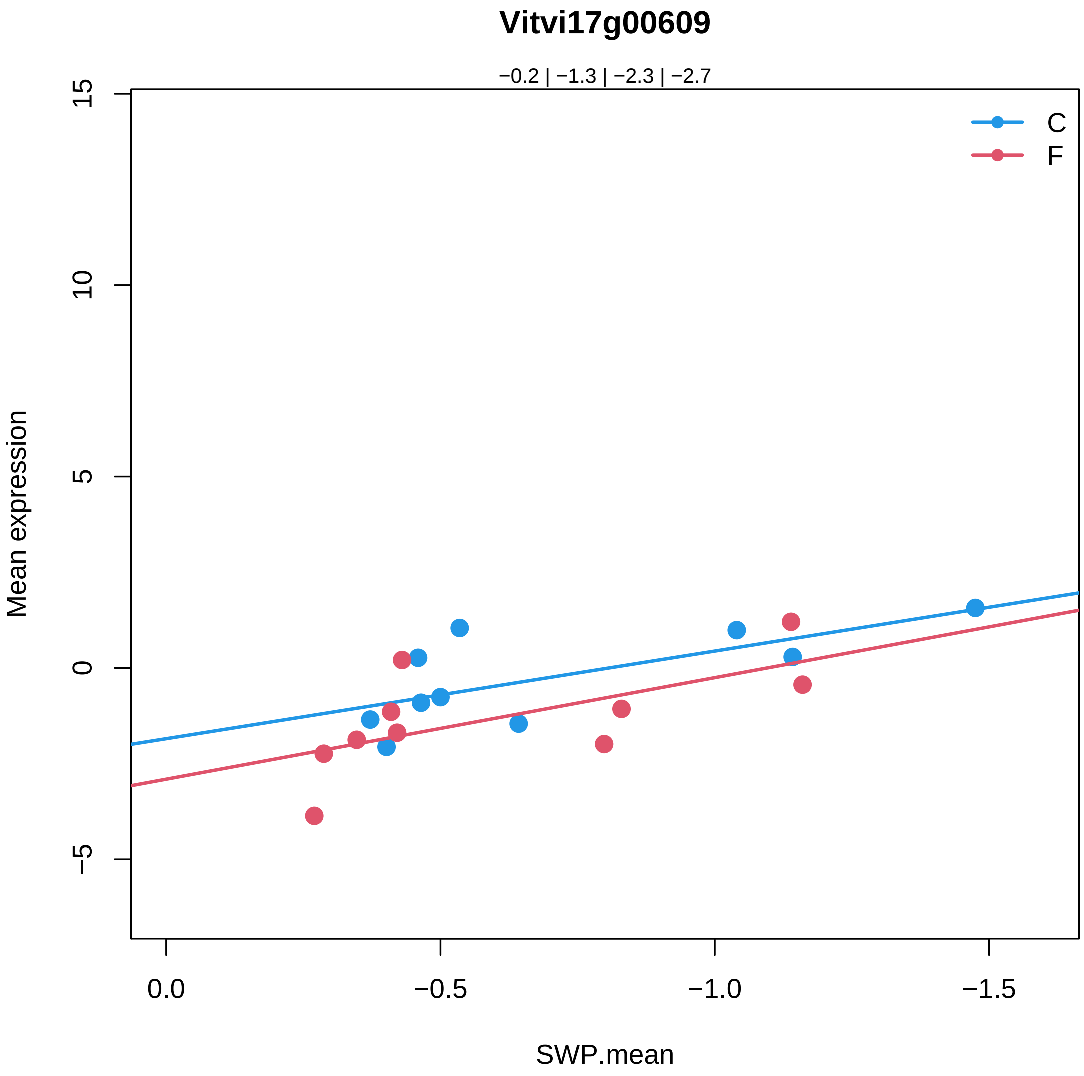
7.2.49 Vitvi17g00609: * type1

```
> 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
```



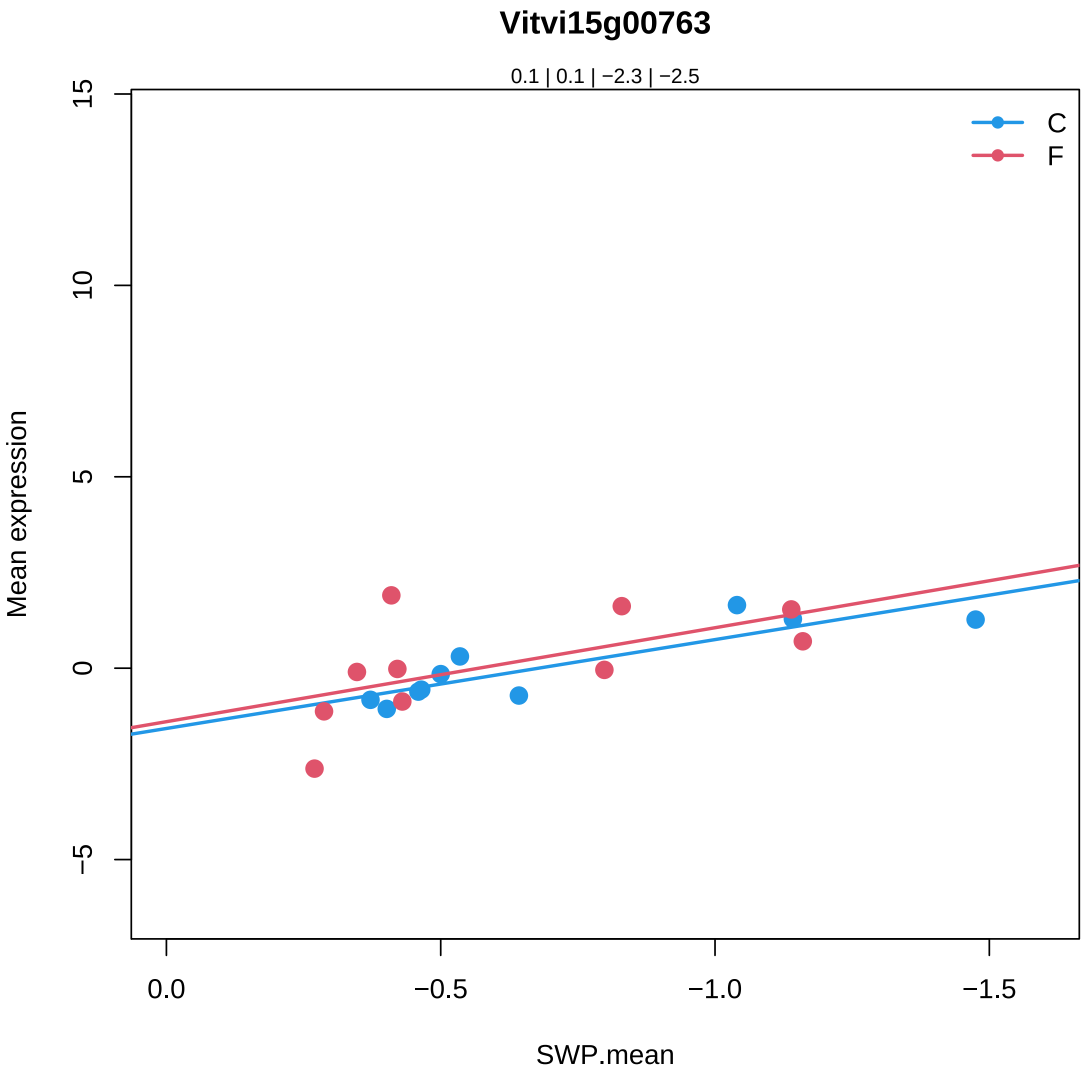
7.2.50 Vitvi15g00763: * type1

```
> 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
```



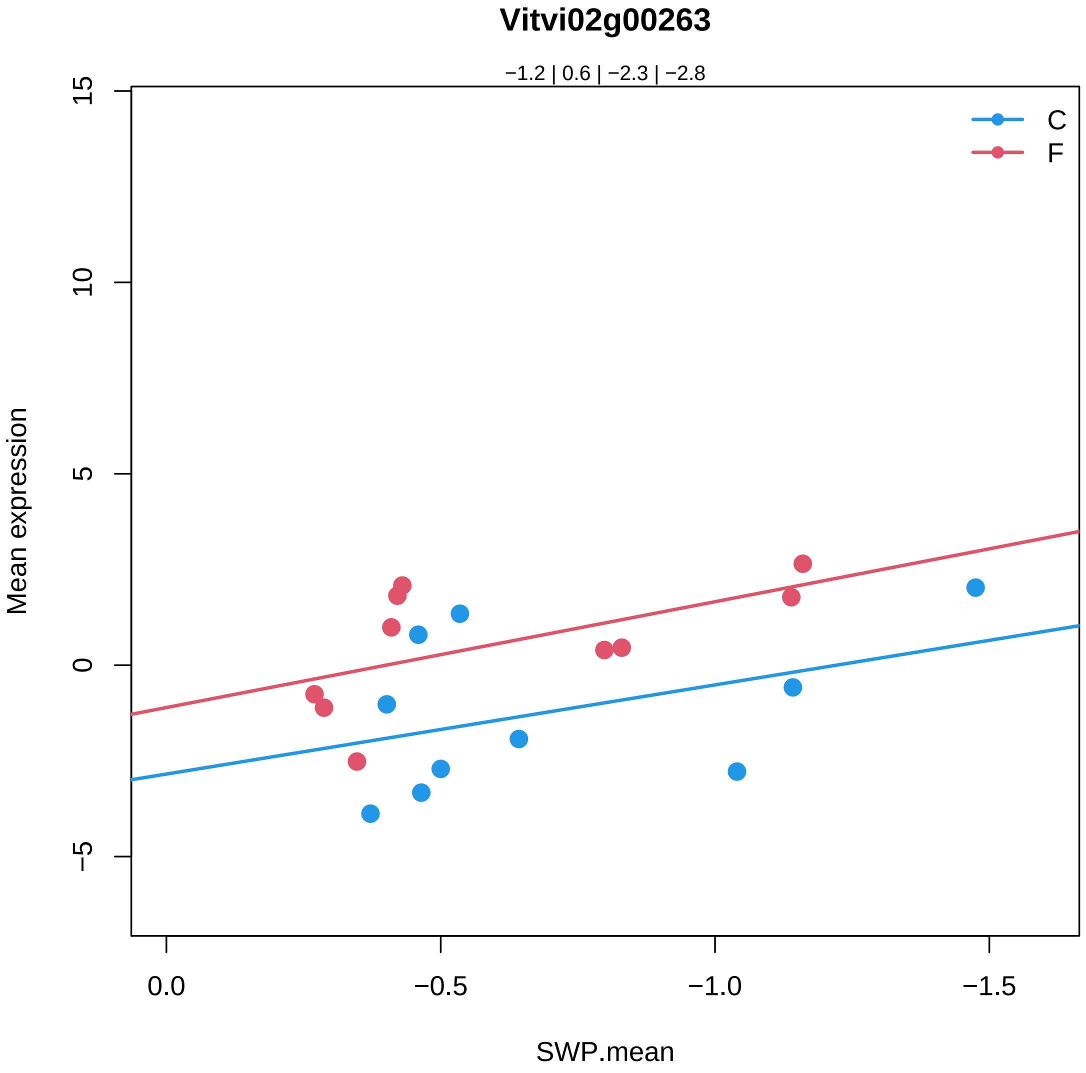
7.2.51 Vitvi02g00263: type1

```
> 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
```



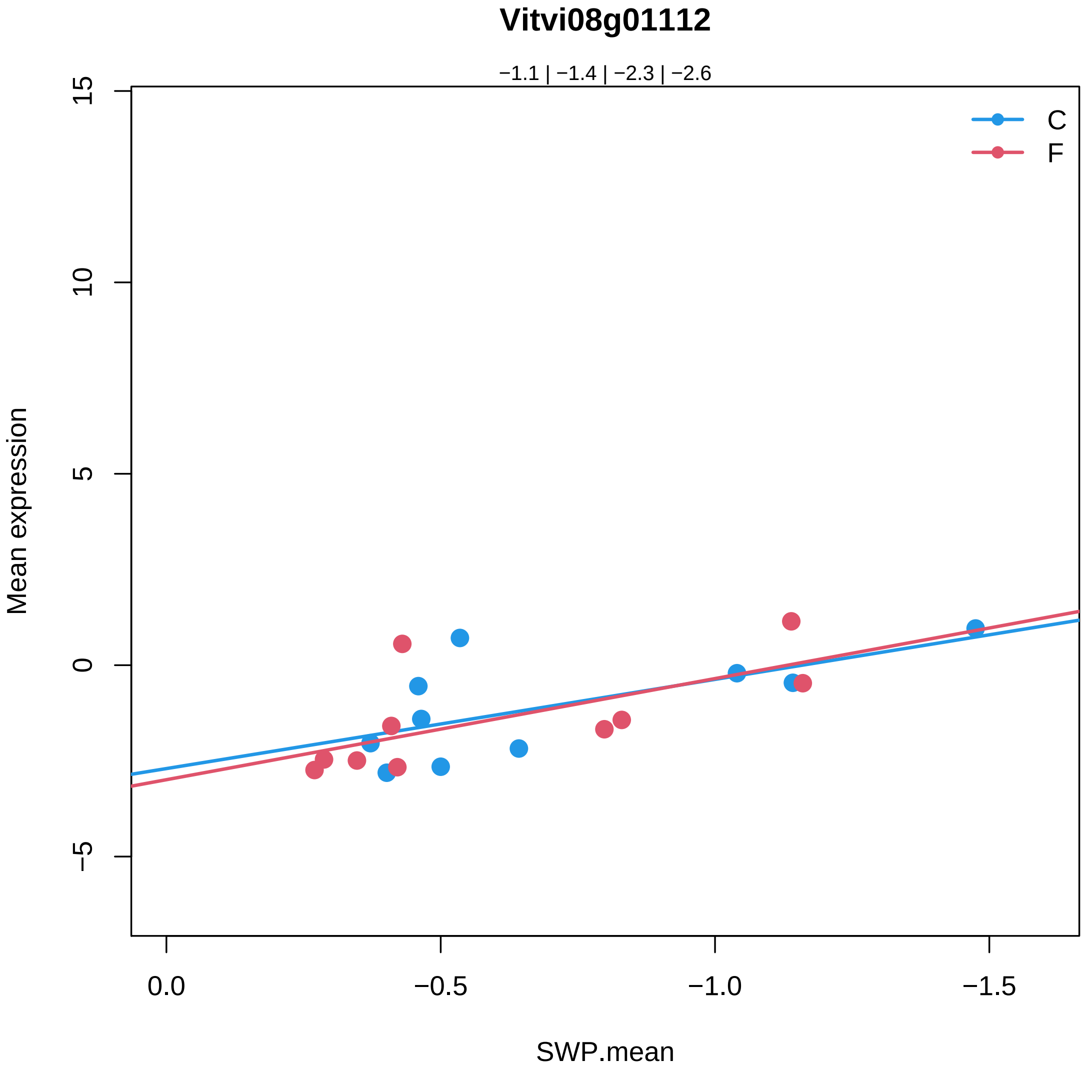
7.2.52 Vitvi08g01112: * type1

```
> 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
```



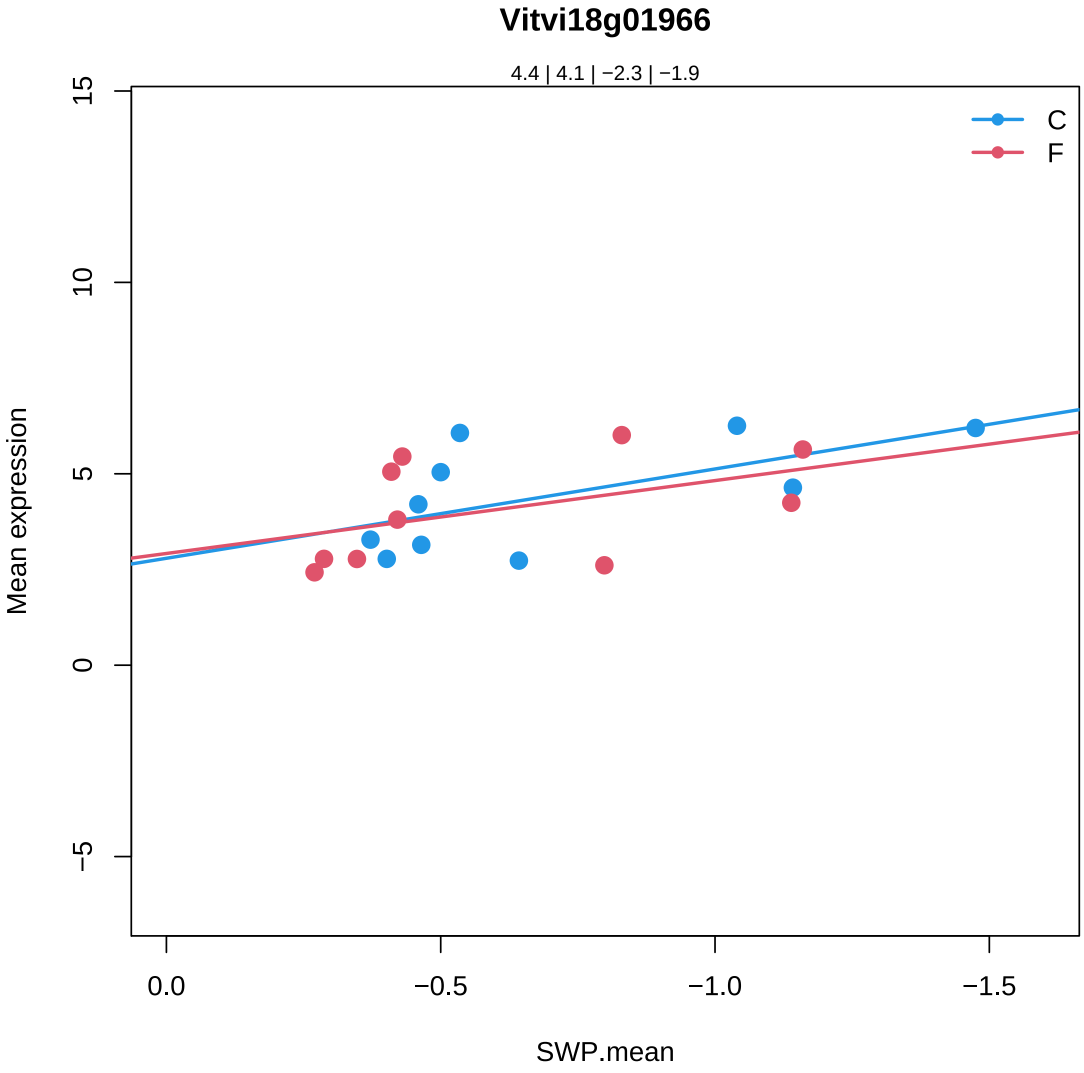
7.2.53 Vitvi18g01966: * type1

```
> 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
```



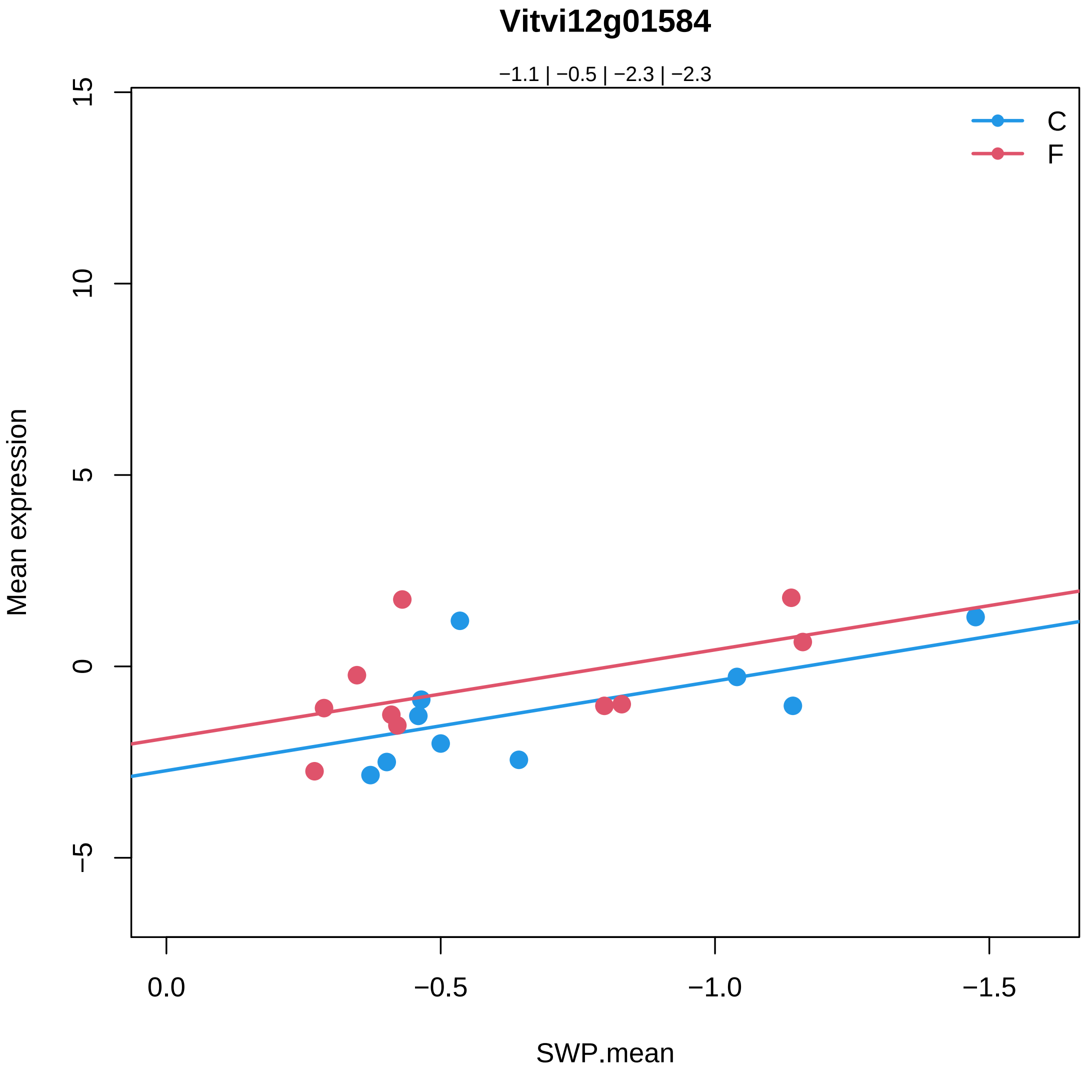
7.2.54 Vitvi12g01584: * type1

```
> 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
```



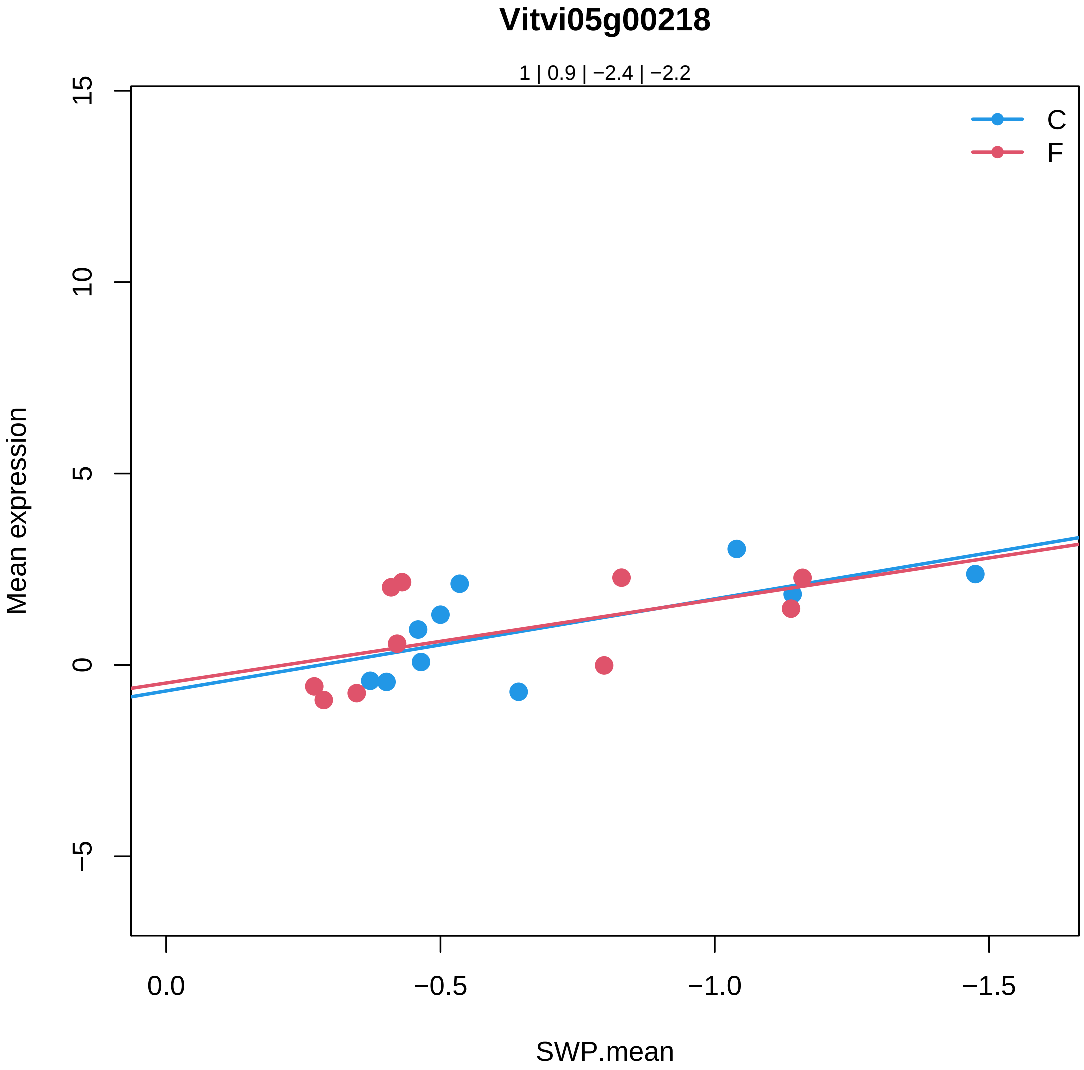
7.2.55 Vitvi05g00218: * type1

```
> 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
```



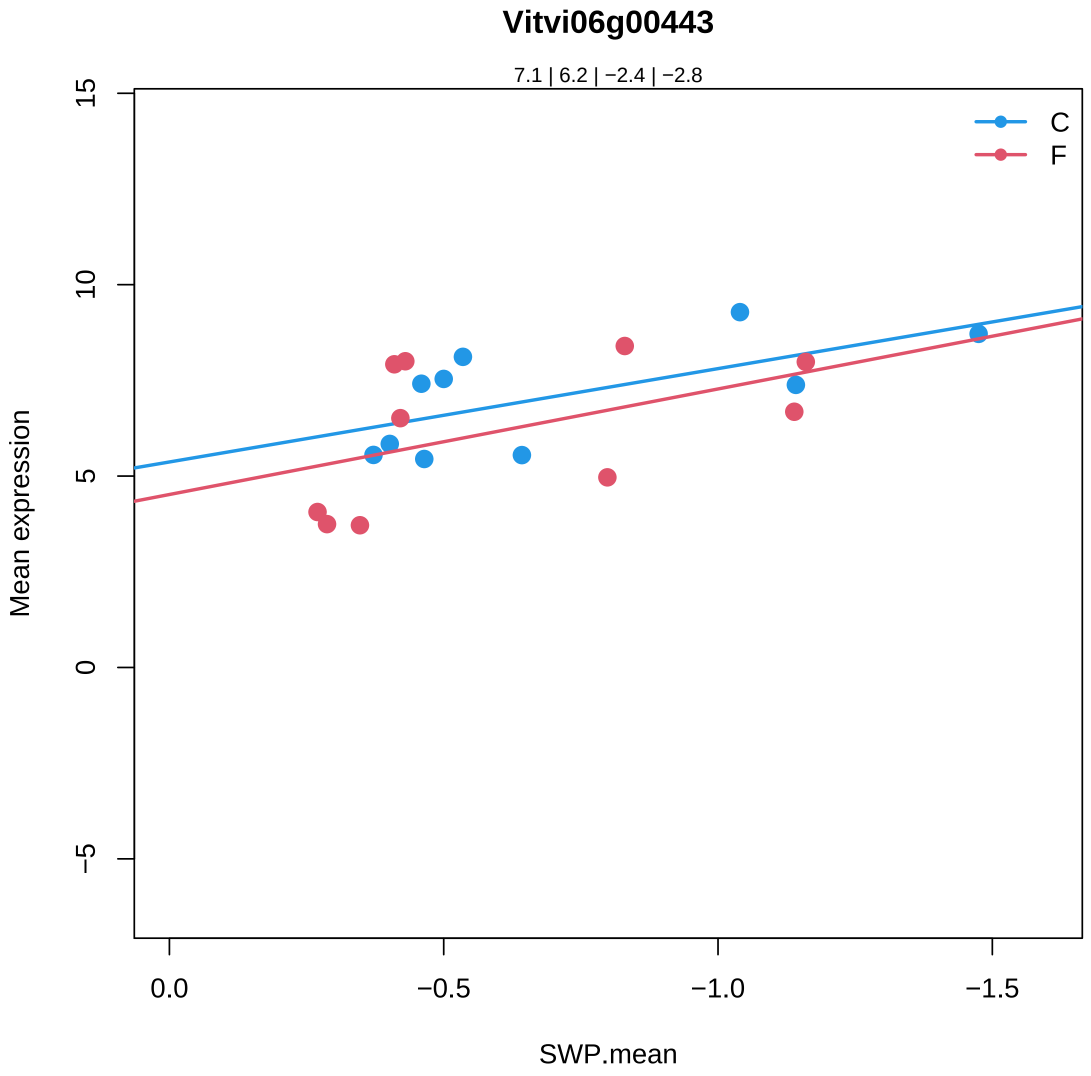
7.2.56 Vitvi06g00443: * type1

```
> 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
SWP.mean
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5

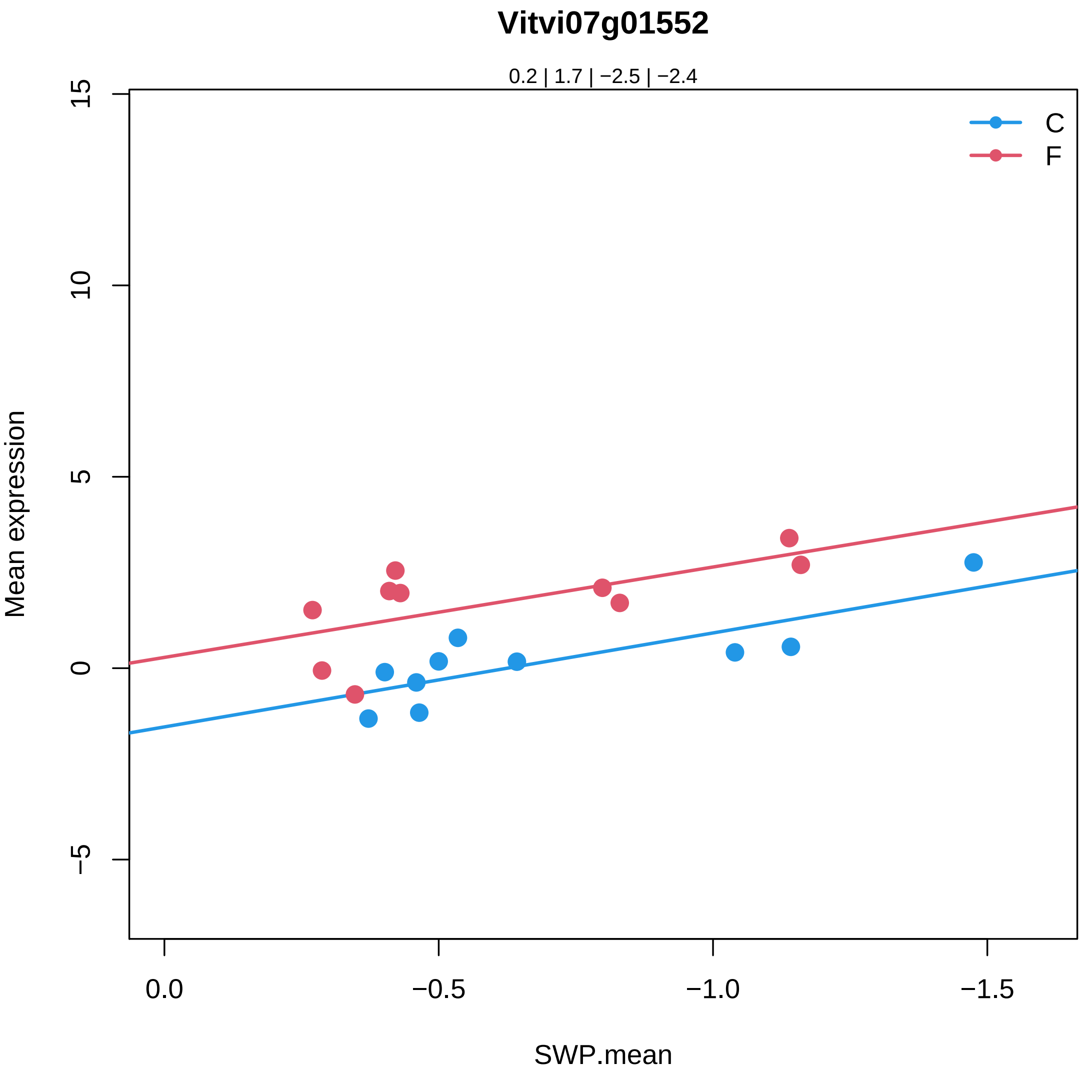
7.2.57 Vitvi07g01552: * type1

```
> 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
```



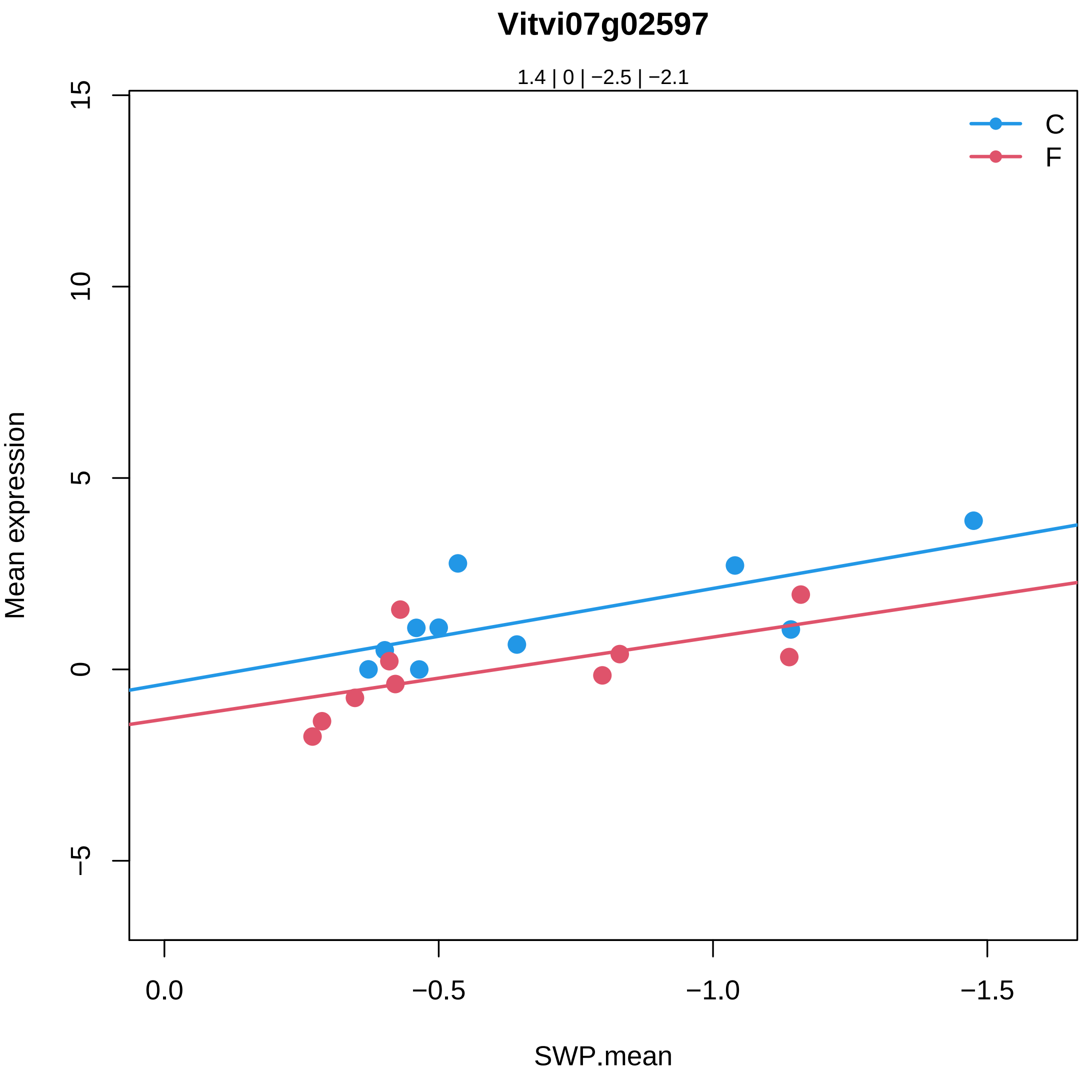
7.2.58 Vitvi07g02597: * type1

```
> 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
```



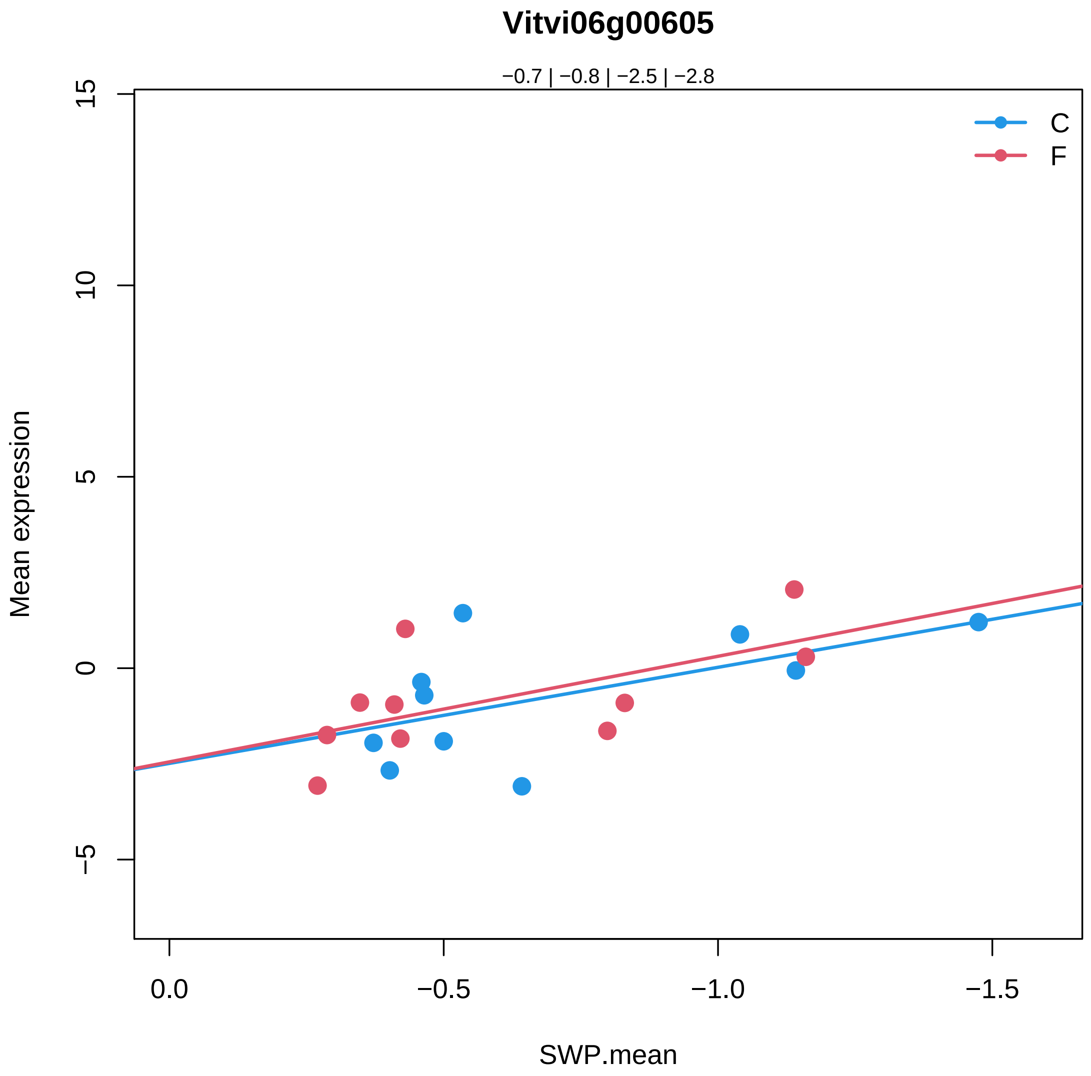
7.2.59 Vitvi06g00605: * type1

```
> 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
```



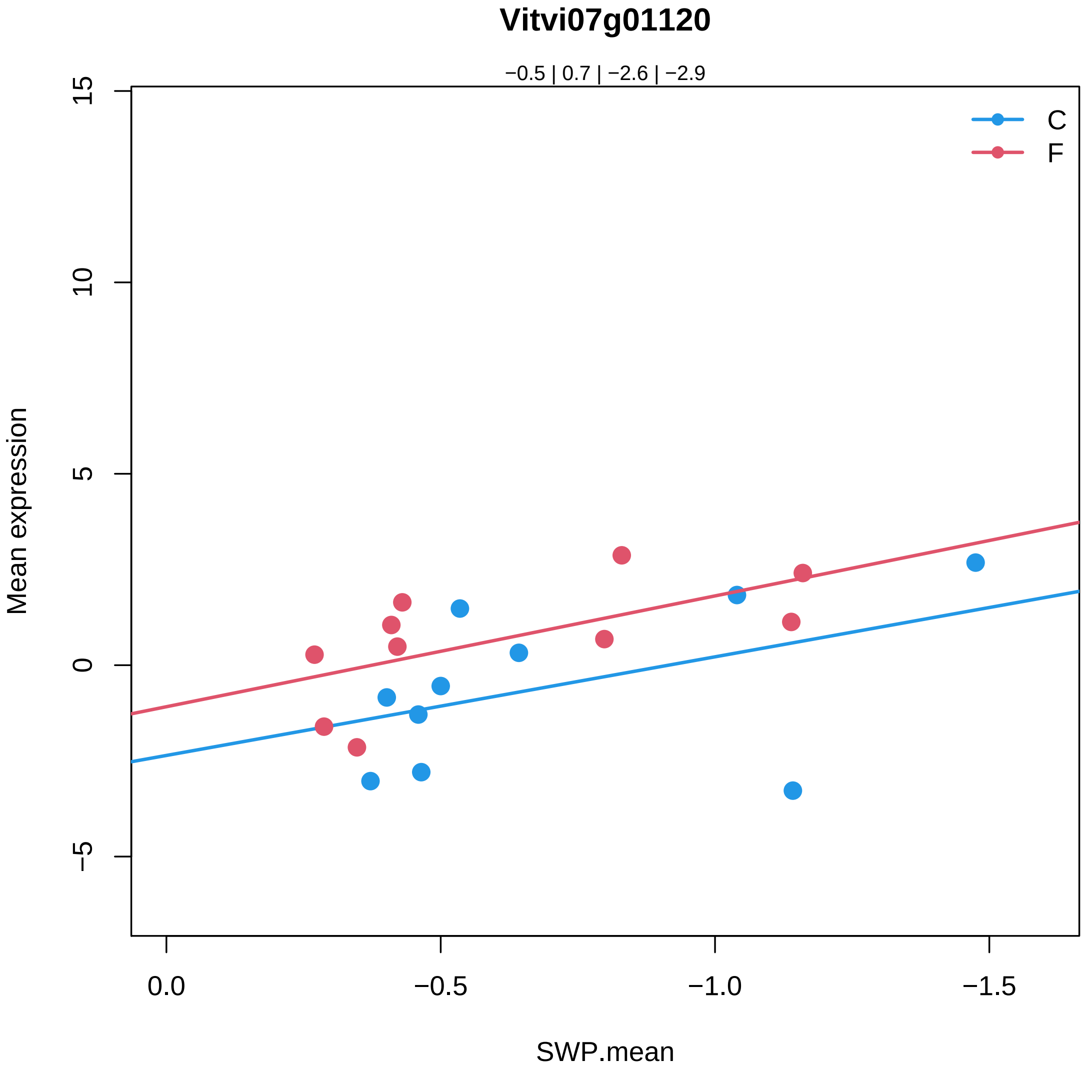
7.2.60 Vitvi07g01120: type1

```
> 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
```



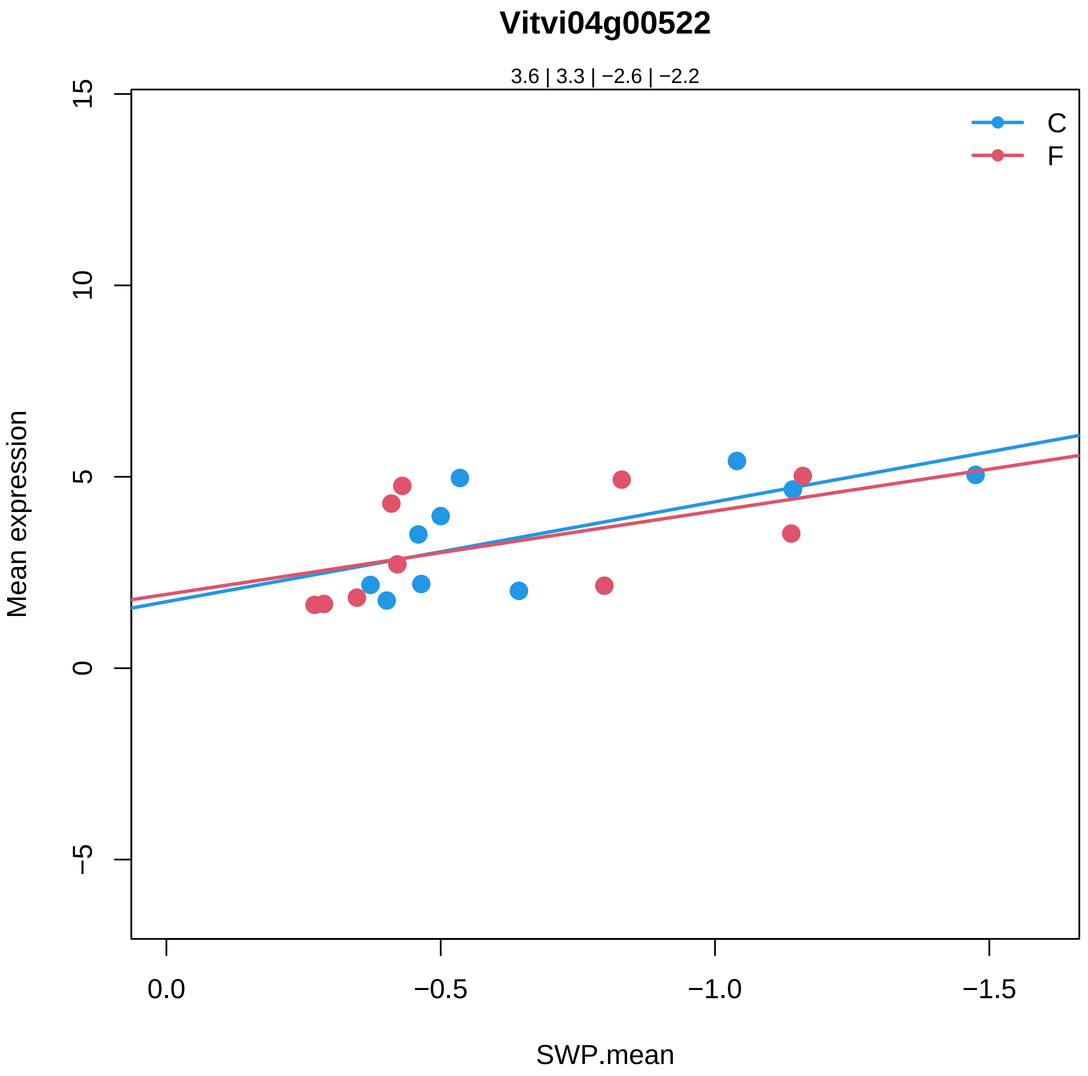
7.2.61 Vitvi04g00522: * type1

```
> 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
```



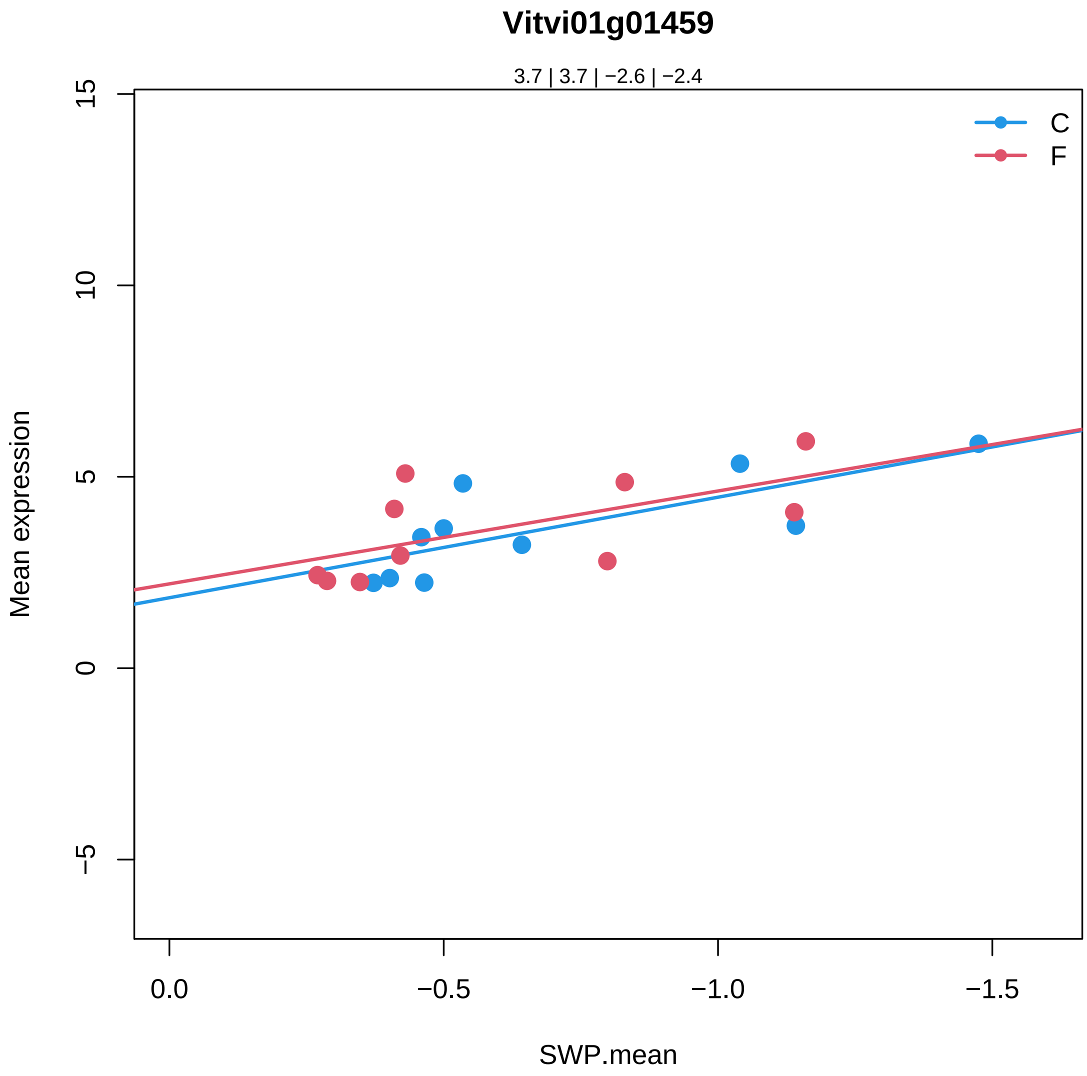
7.2.62 Vitvi01g01459: * type1

```
> 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
```



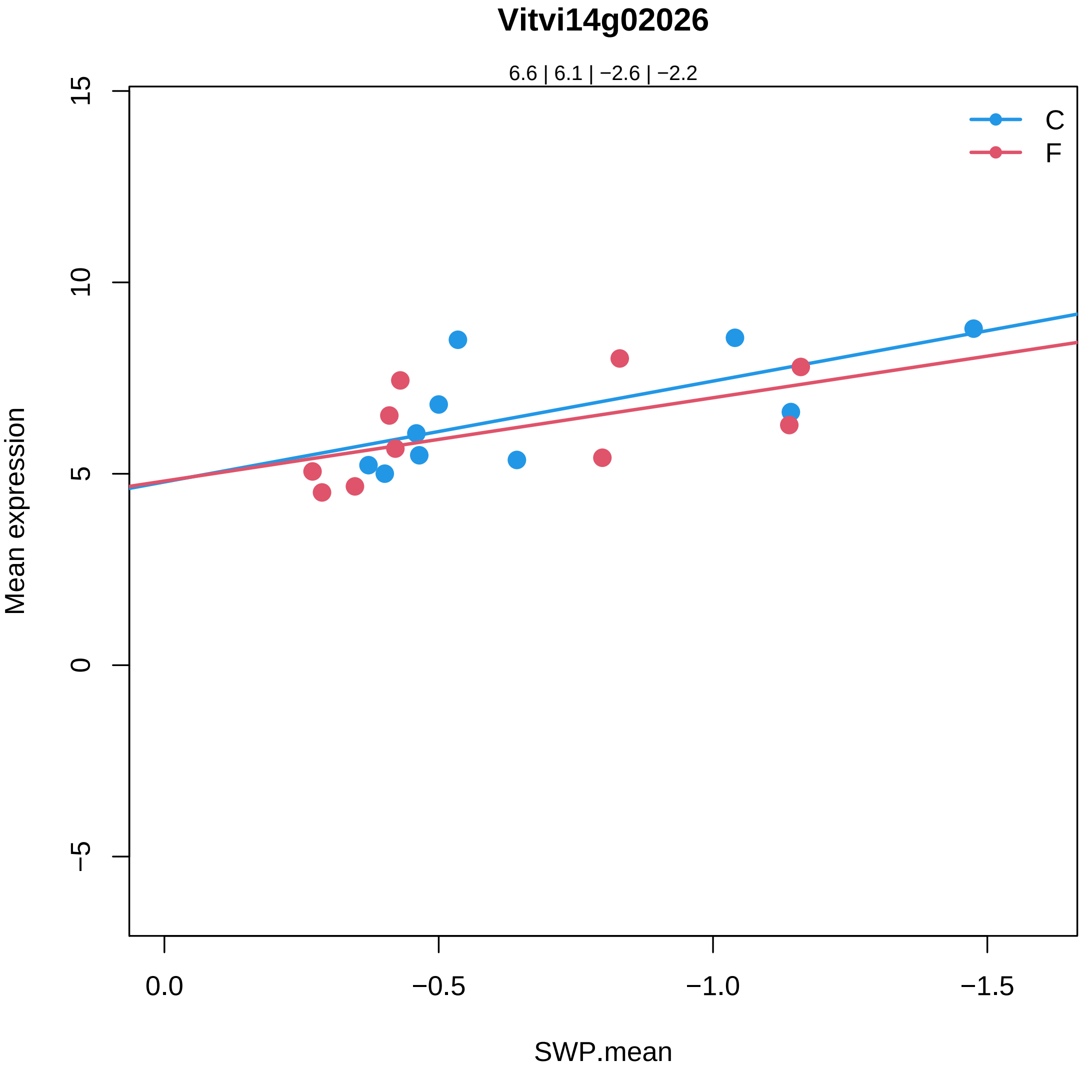
7.2.63 Vitvi14g02026: * type1

```
> 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
```



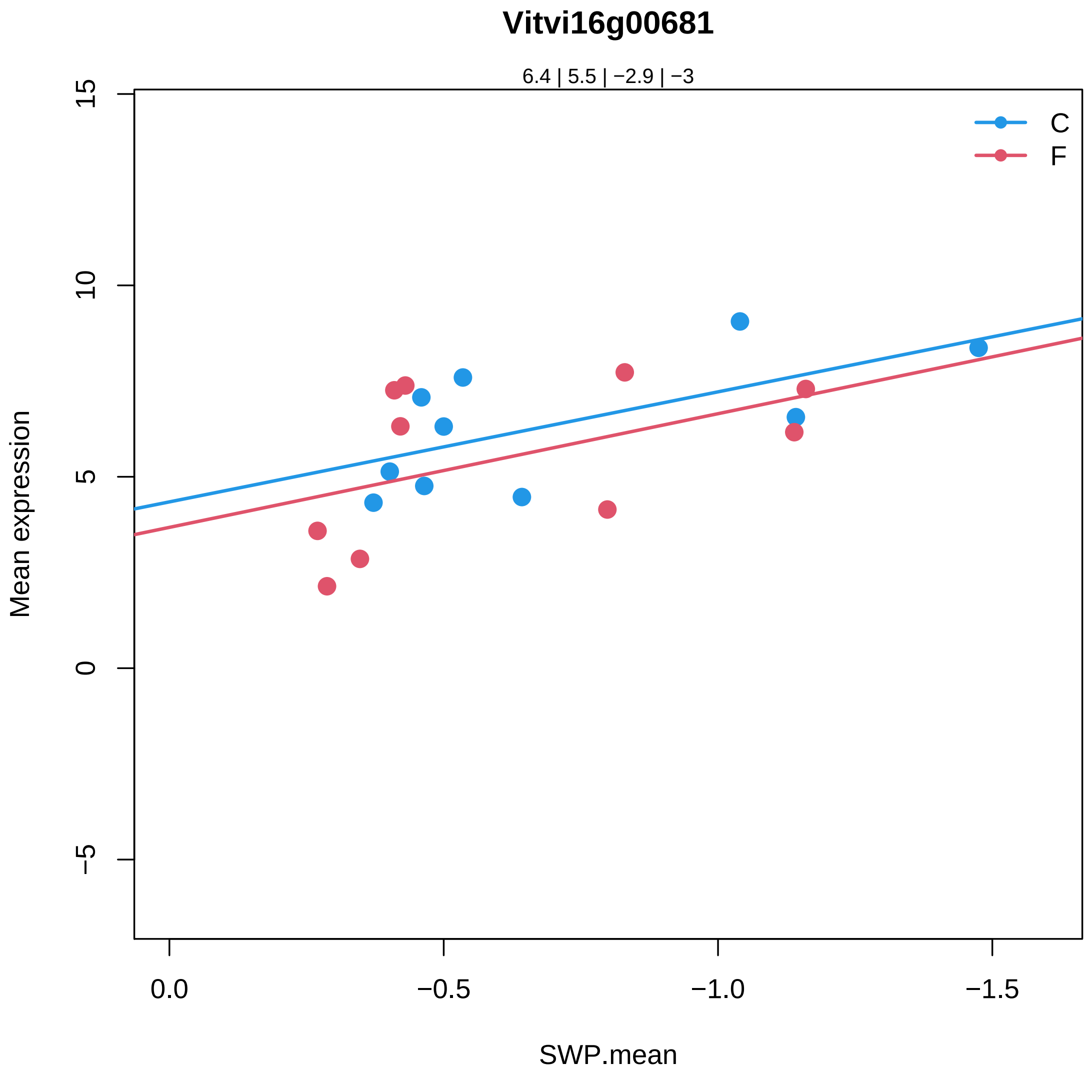
7.2.64 Vitvi16g00681: * type1

```
> 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
```



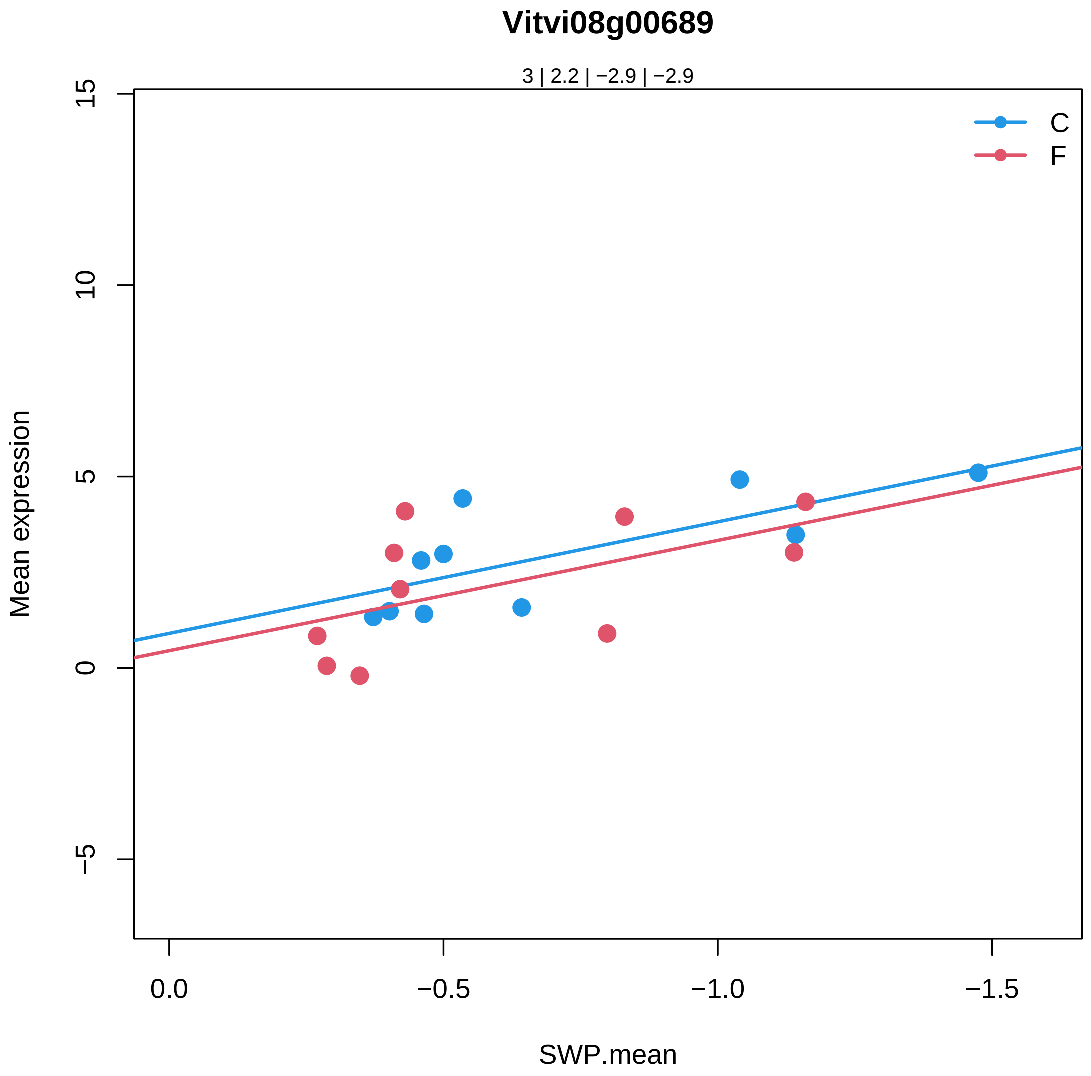
7.2.65 Vitvi08g00689: * type1

```
> 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
```



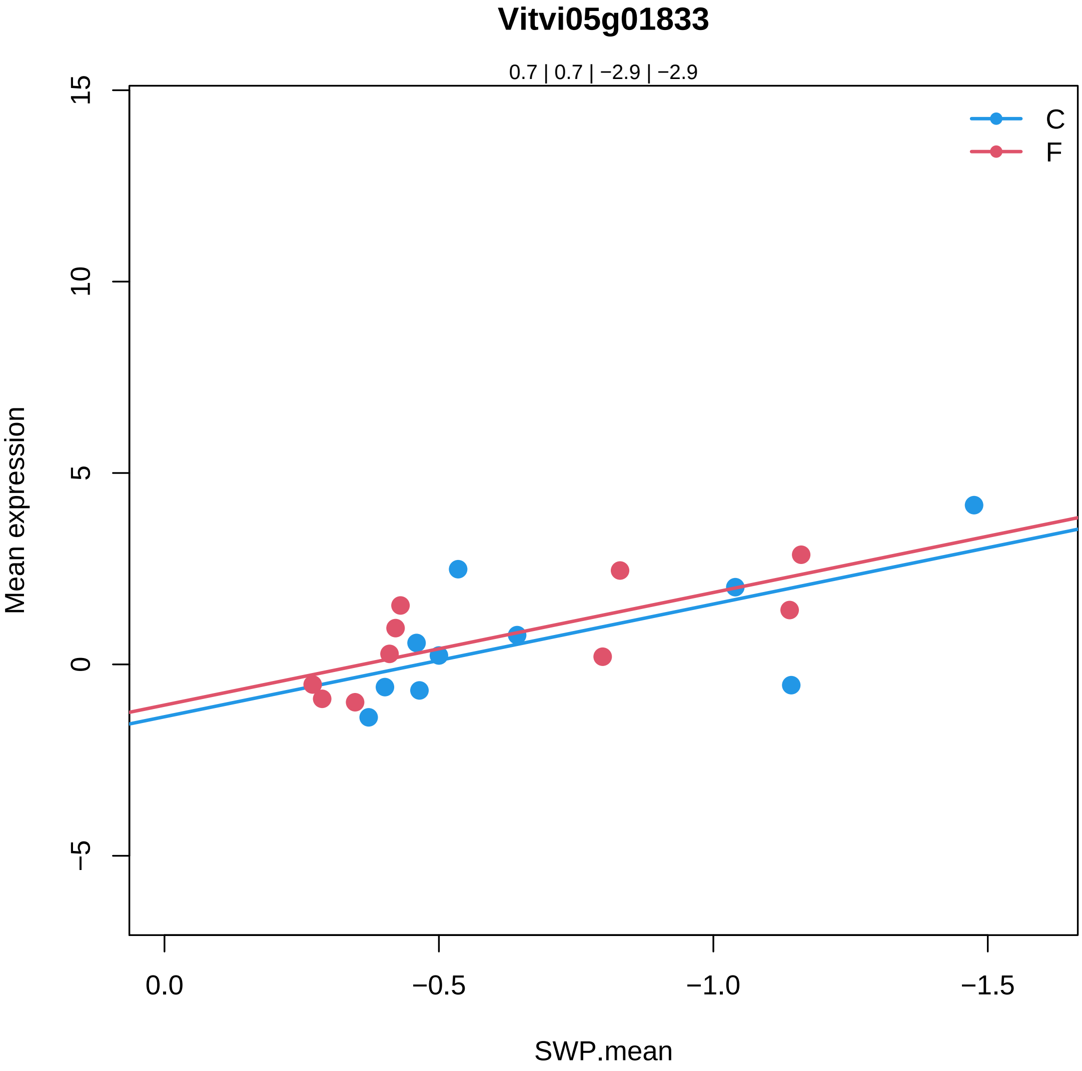
7.2.66 Vitvi05g01833: * type1

```
> 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
```



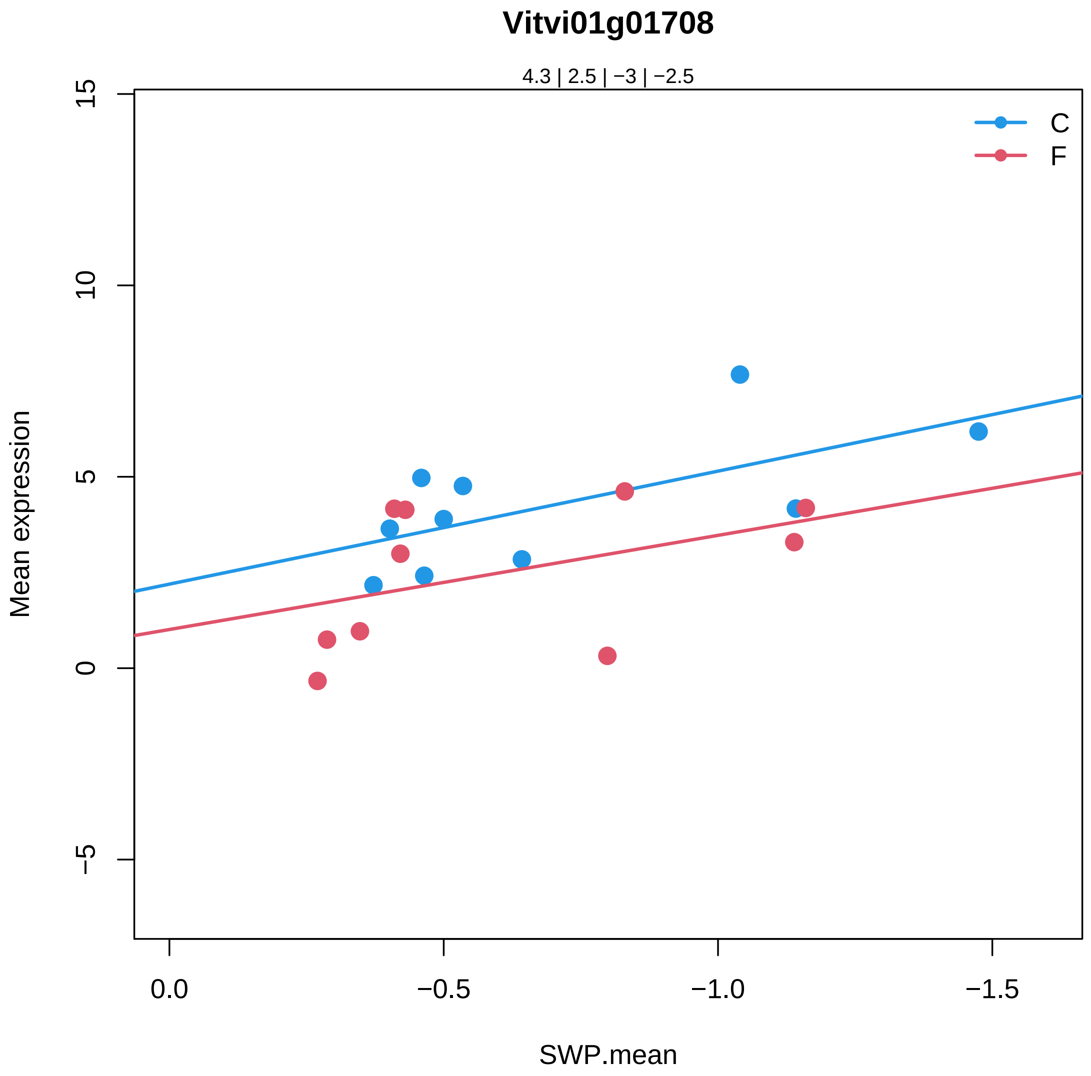
7.2.67 Vitvi01g01708: * type1

```
> 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
```



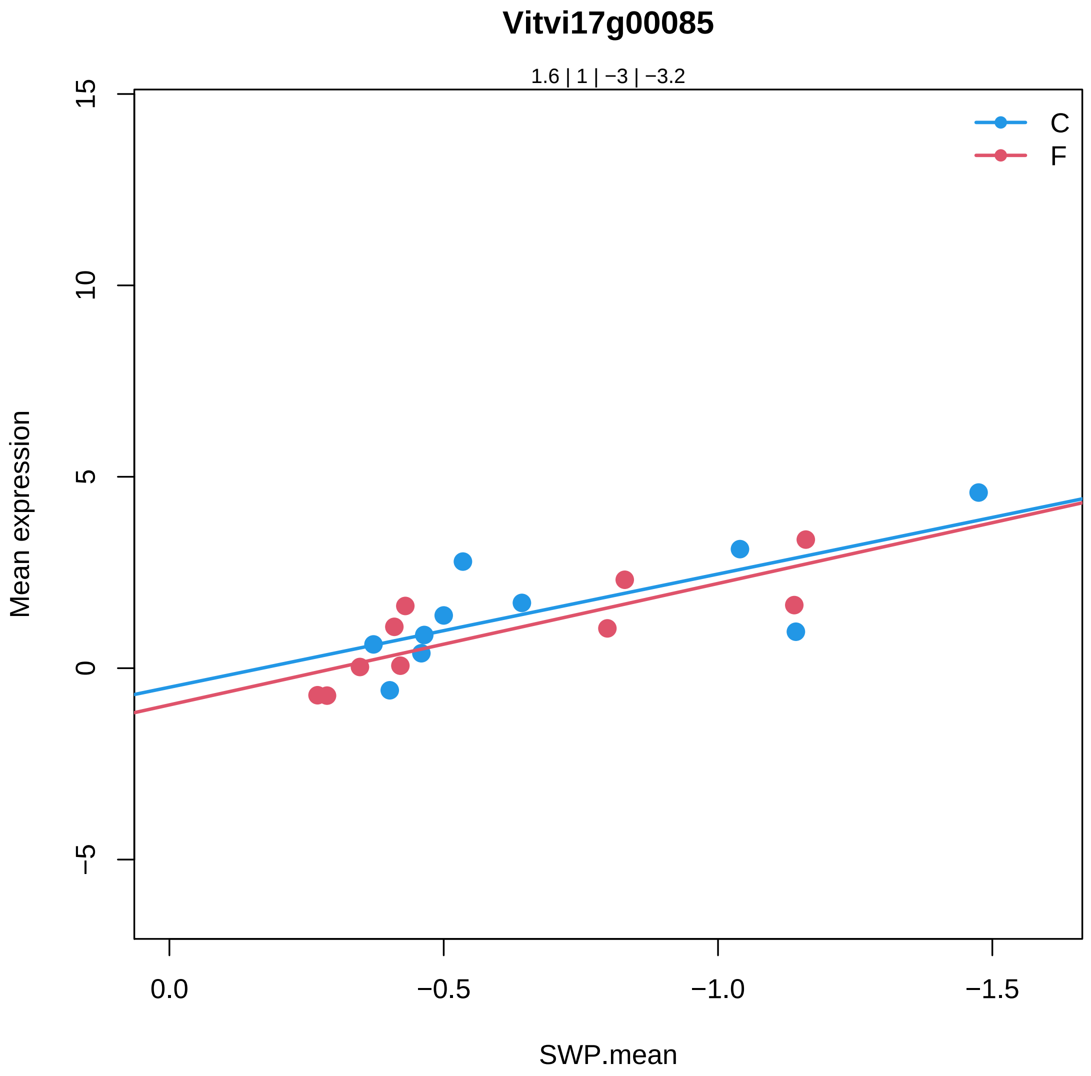
7.2.68 Vitvi17g00085: * type1

```
> 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
```



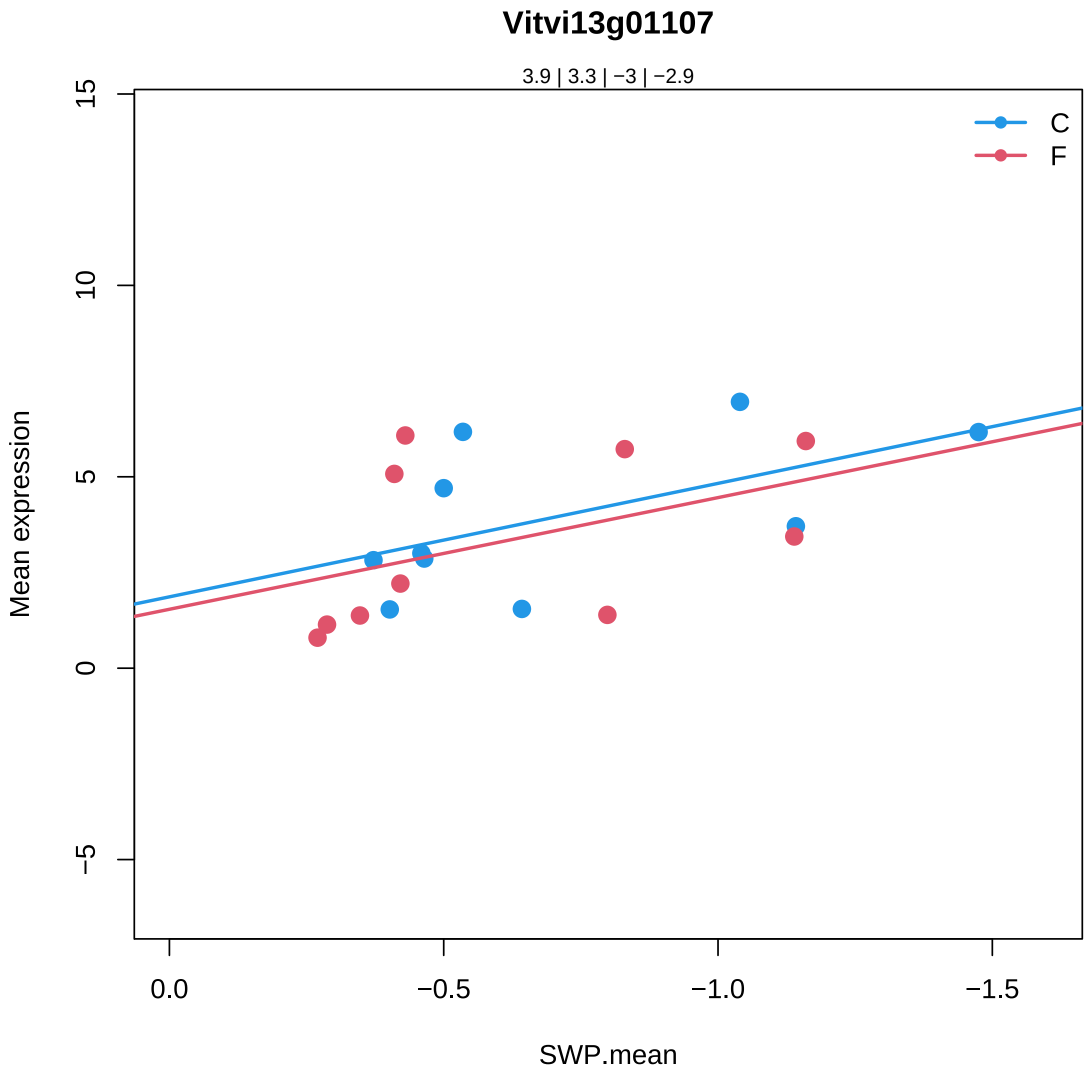
7.2.69 Vitvi13g01107: type1

```
> 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
```



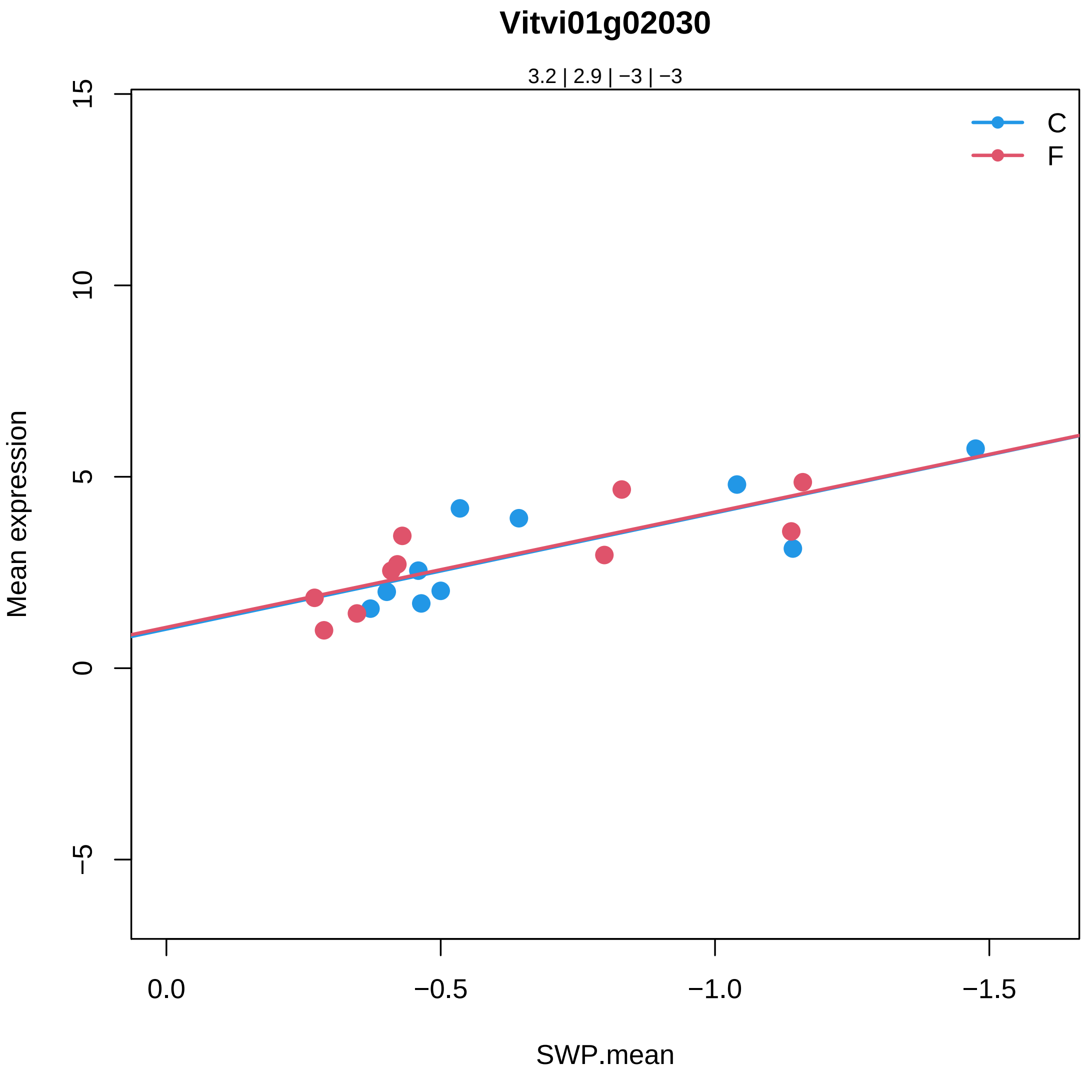
7.2.70 Vitvi01g02030: * type1

```
> 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
```



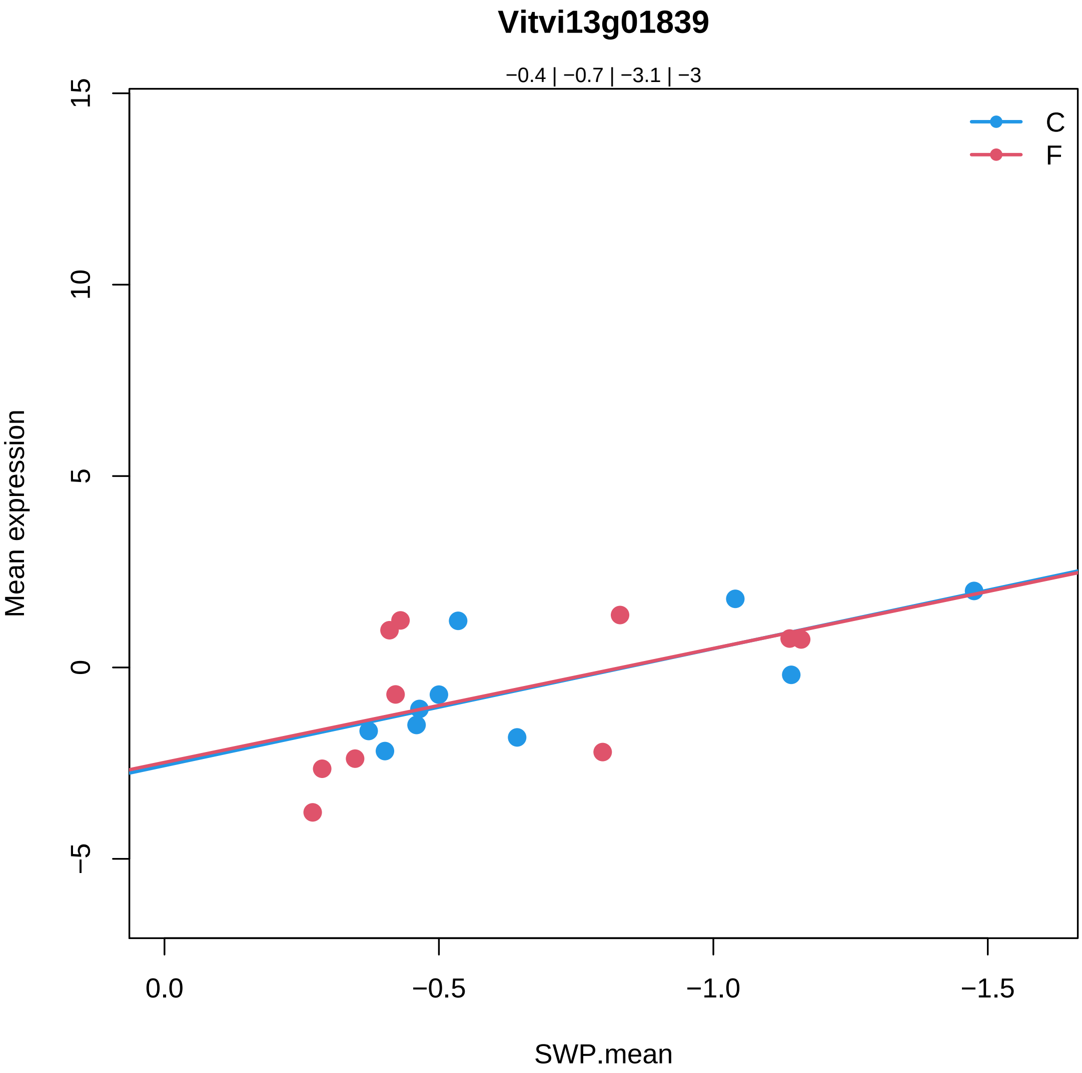
7.2.71 Vitvi13g01839: * type1

```
> 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

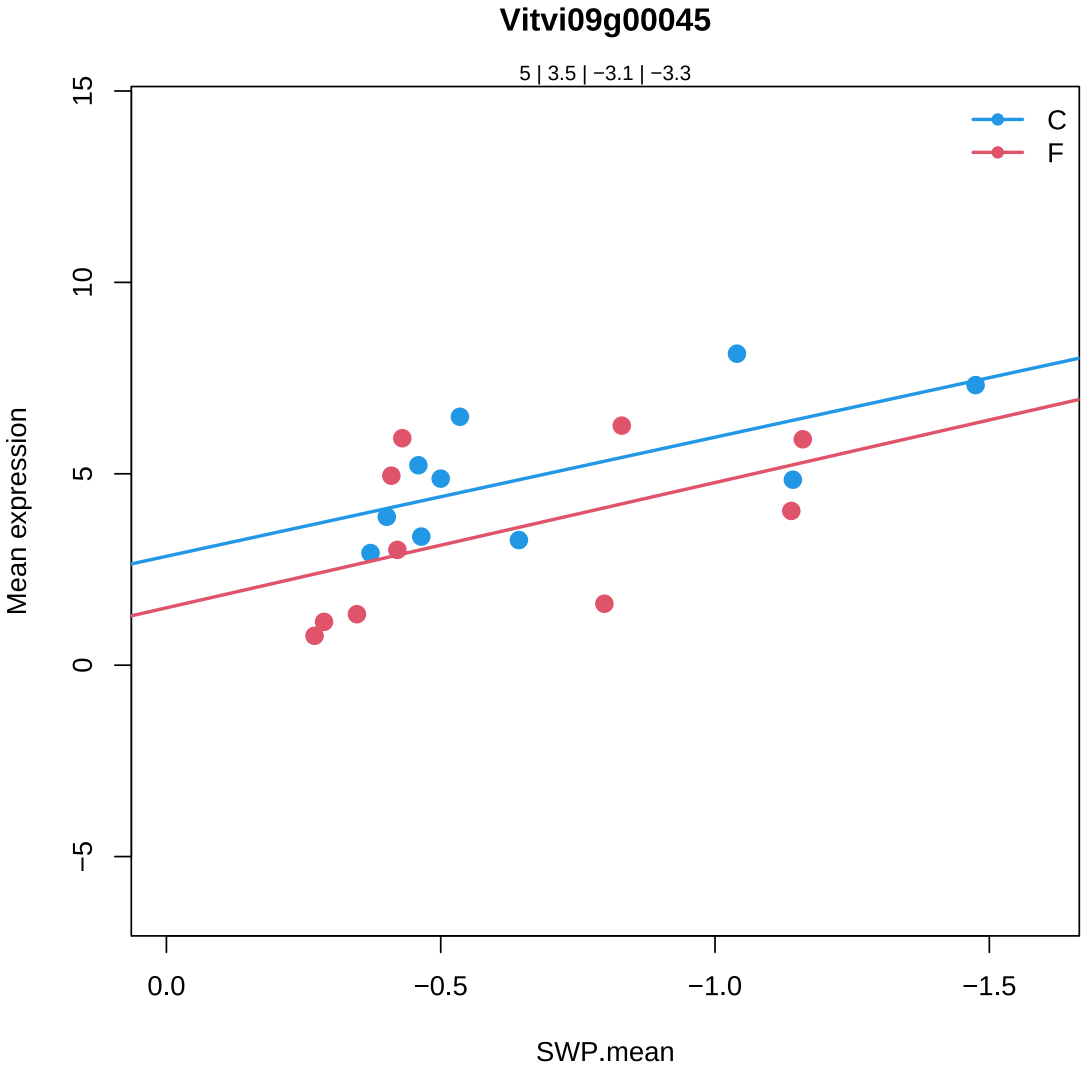
7.2.72 Vitvi09g00045: * type1

```
> 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
```



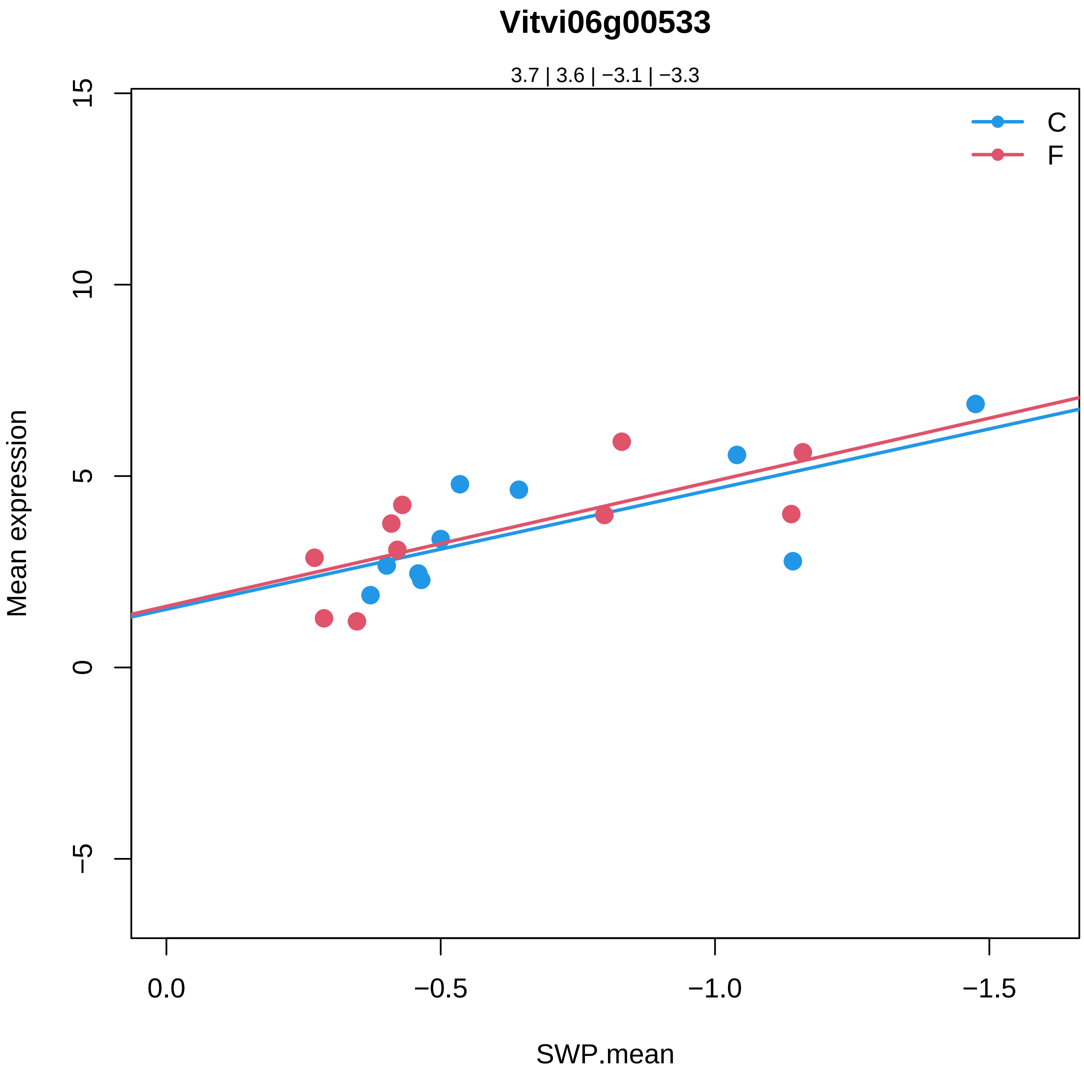
7.2.73 Vitvi06g00533: * type1

```
> 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

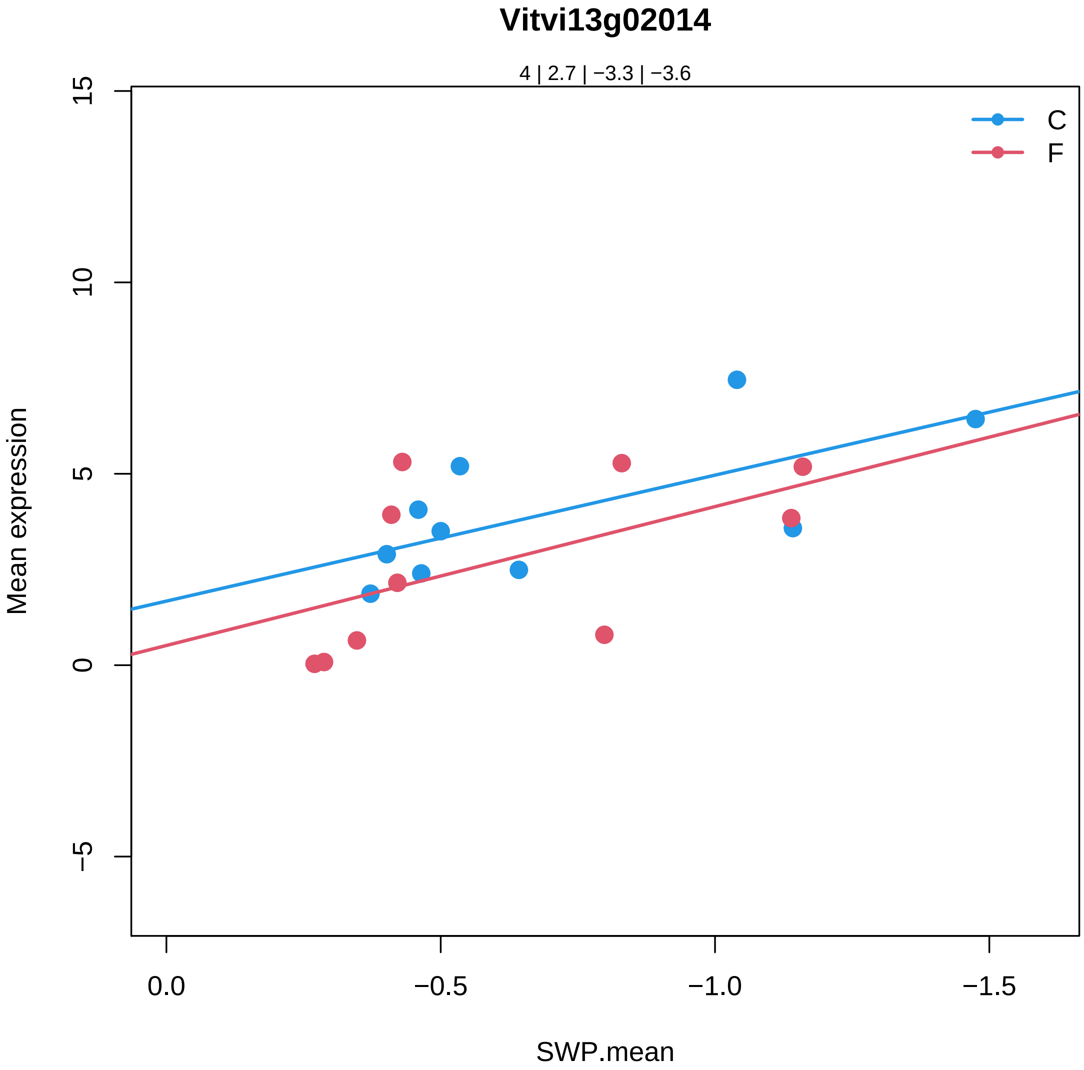
7.2.74 Vitvi13g02014: * type1

```
> 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
```



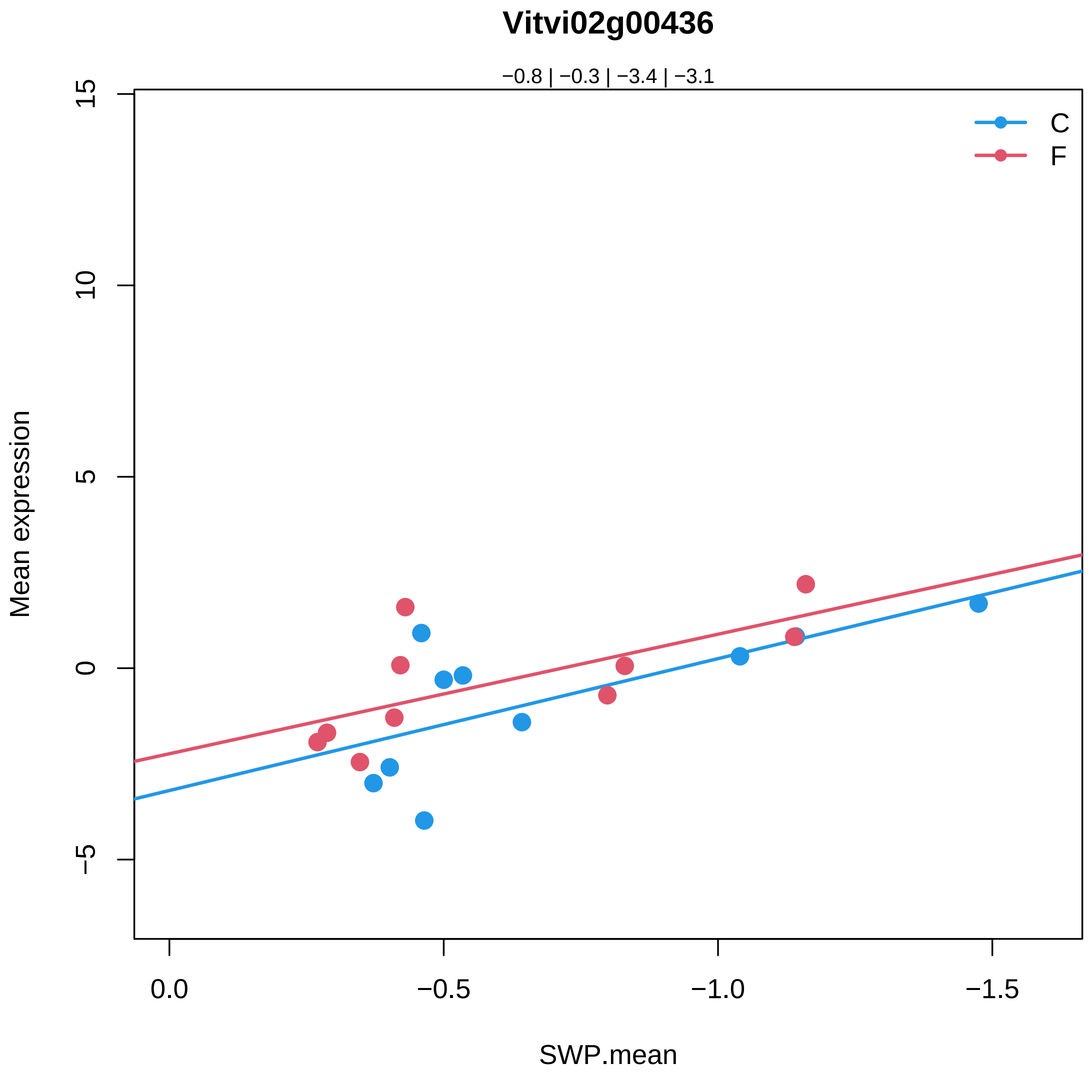
7.2.75 Vitvi02g00436: * type1

```
> 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
```



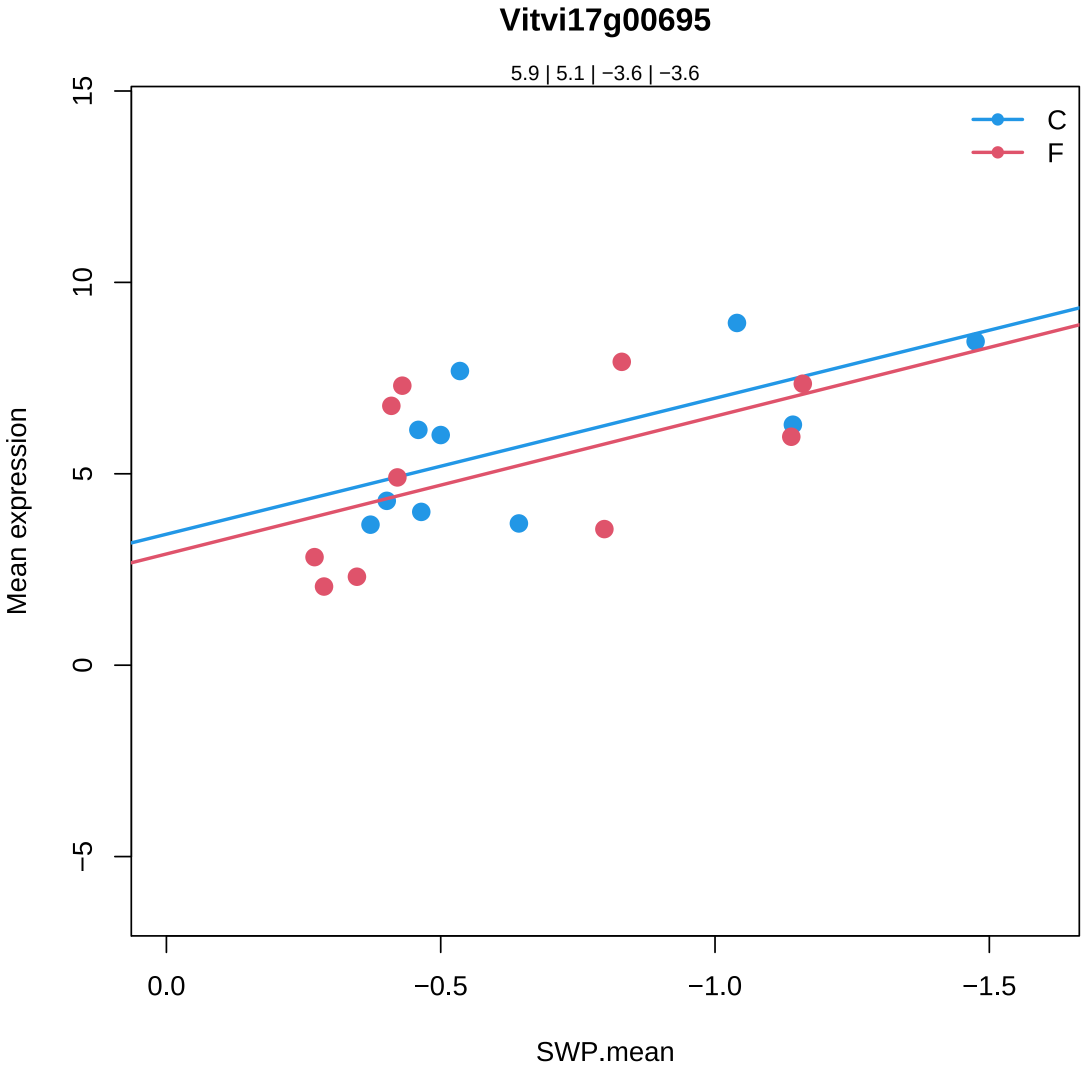
7.2.76 Vitvi17g00695: * type1

```
> 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
```



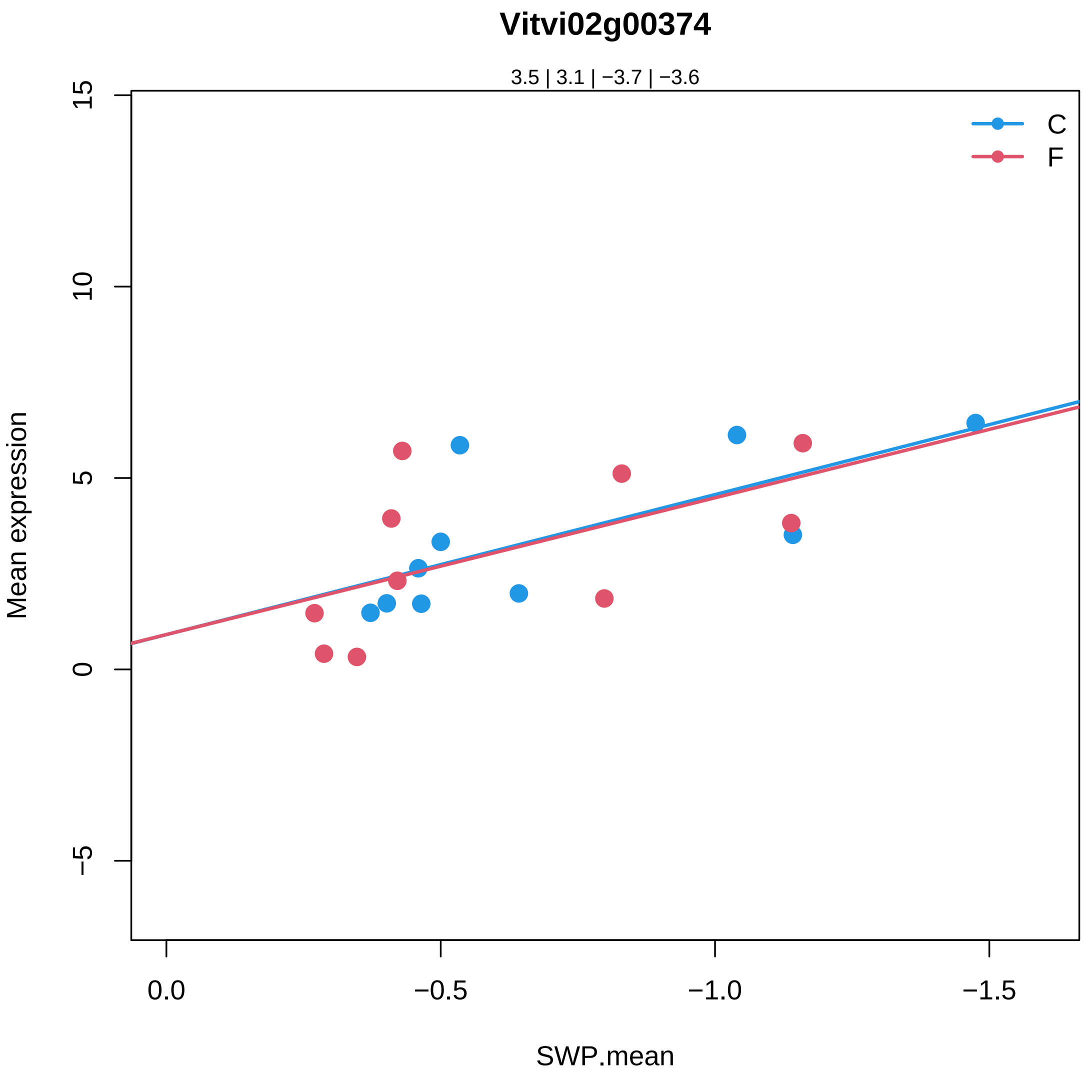
7.2.77 Vitvi02g00374: * type1

```
> 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
```



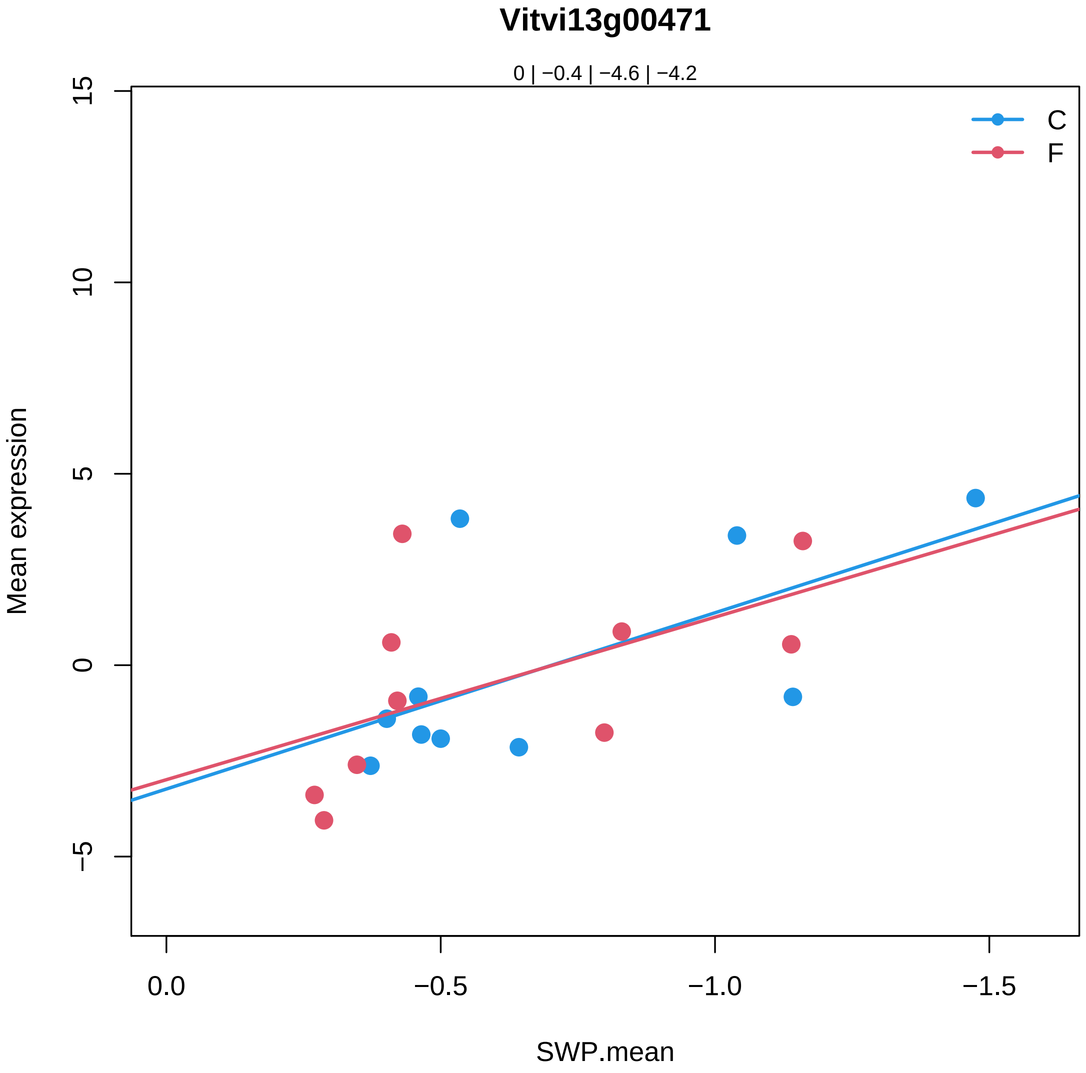
7.2.78 Vitvi13g00471: * type1

```
> 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
```



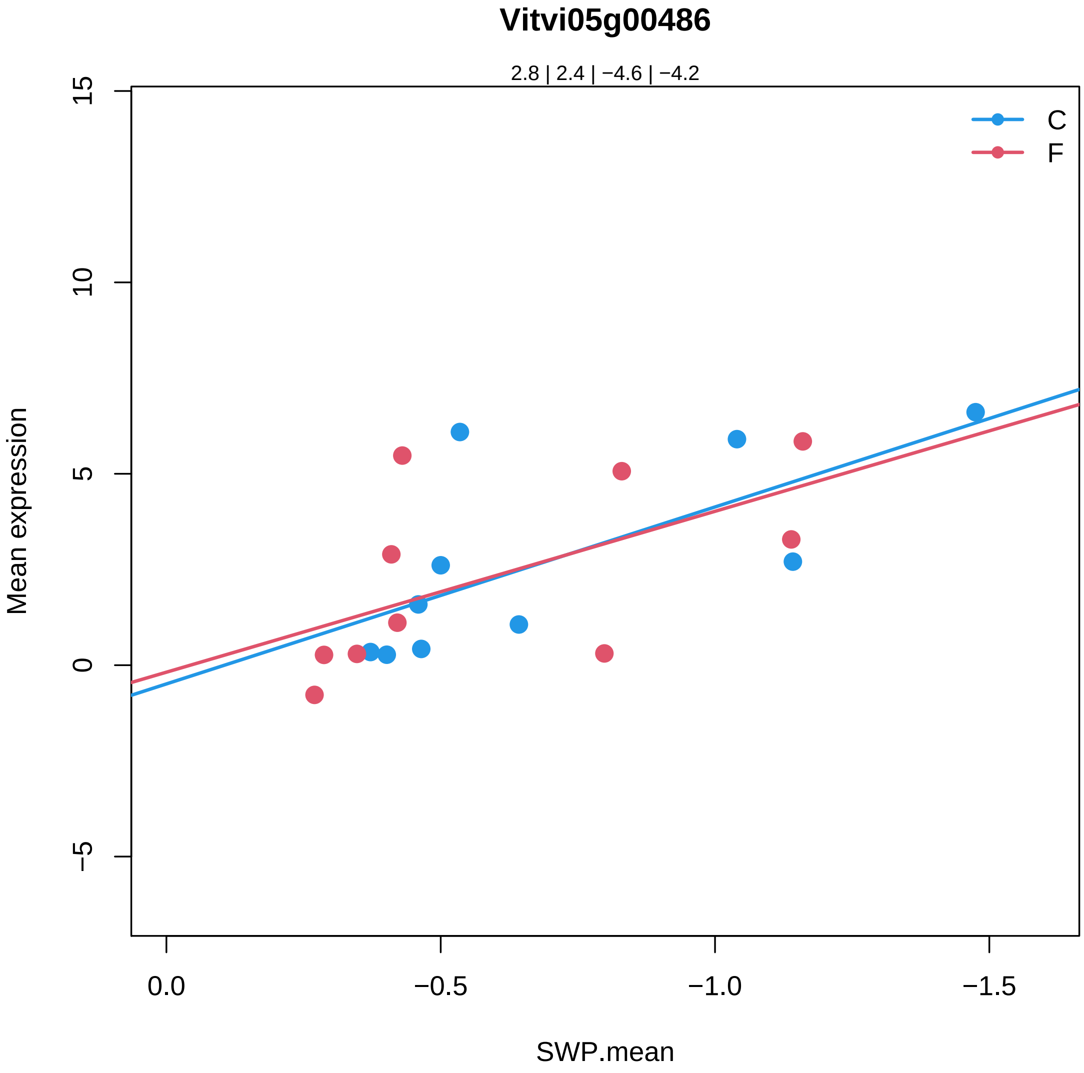
7.2.79 Vitvi05g00486: * type1

```
> 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
```



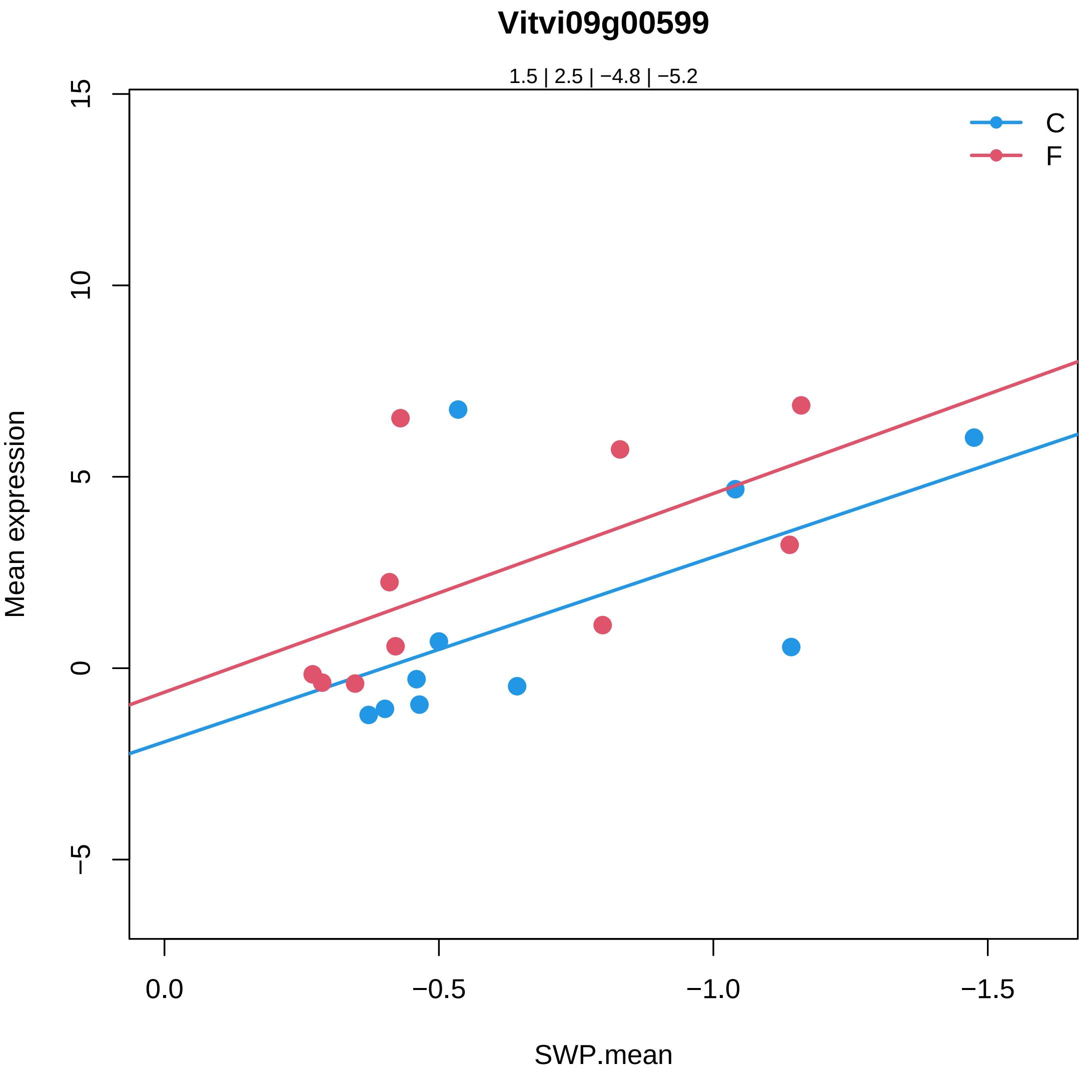
7.2.80 Vitvi09g00599: * type1

```
> 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
```



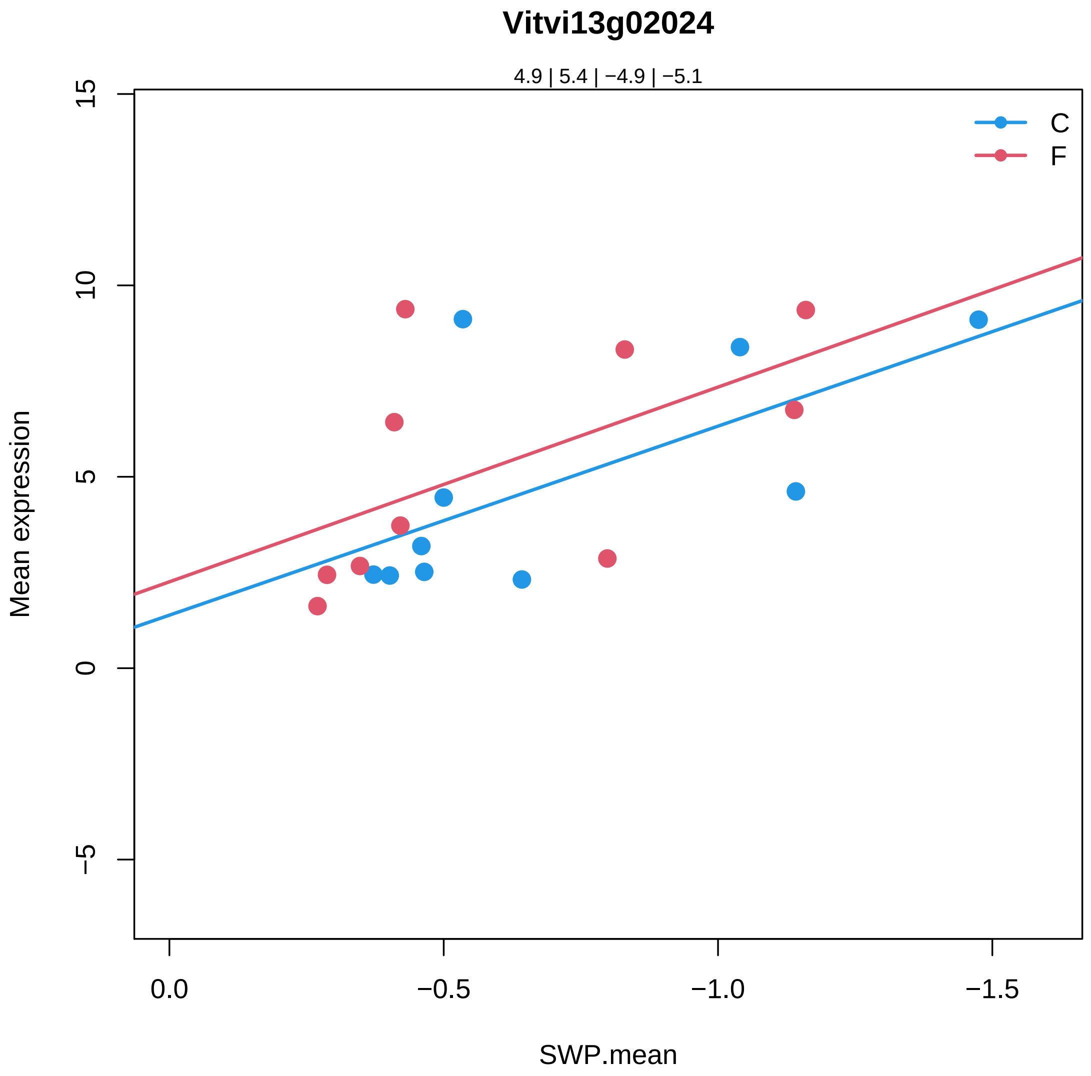
7.2.81 Vitvi13g02024: * type1

```
> 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
```



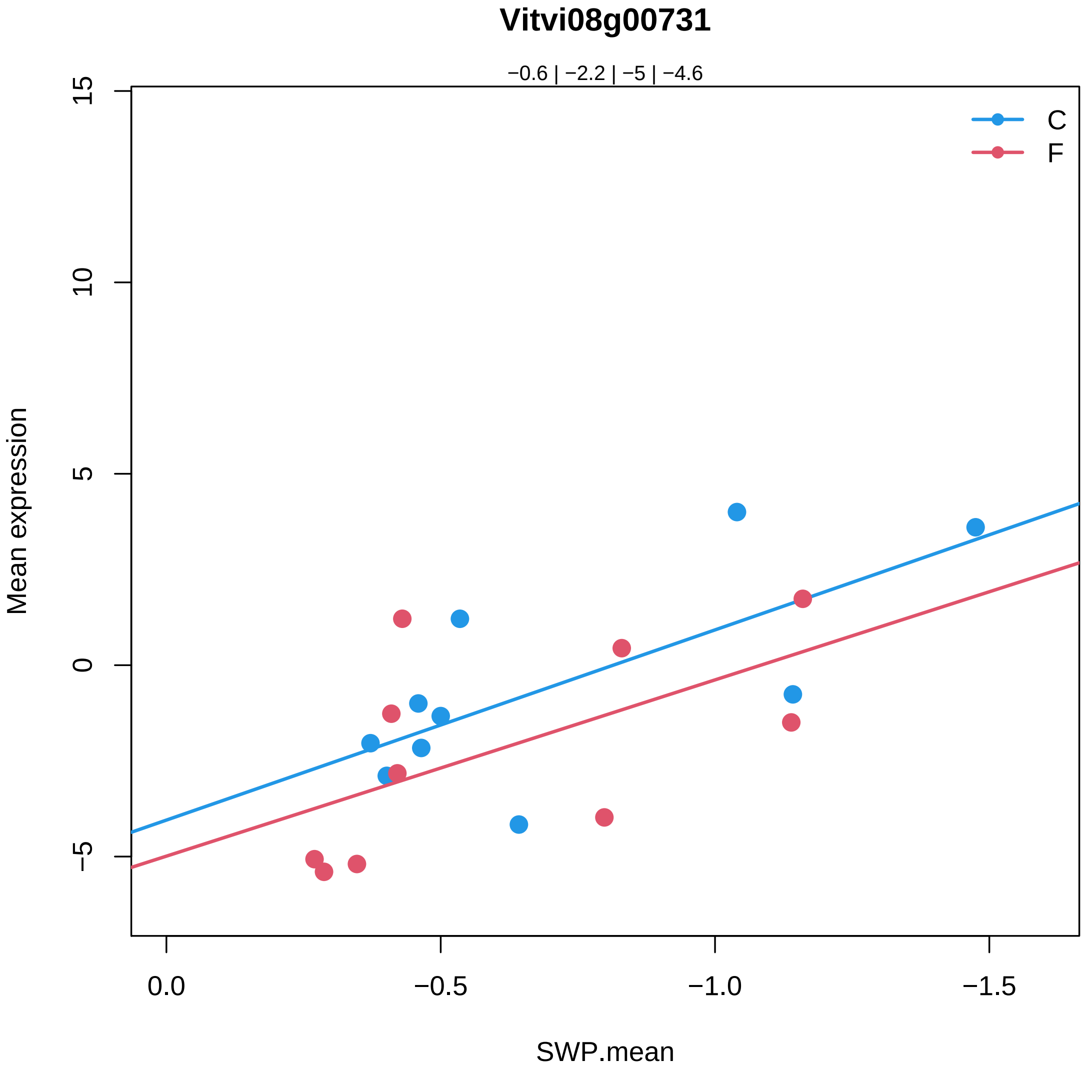
7.2.82 Vitvi08g00731: * type1

```
> 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
```



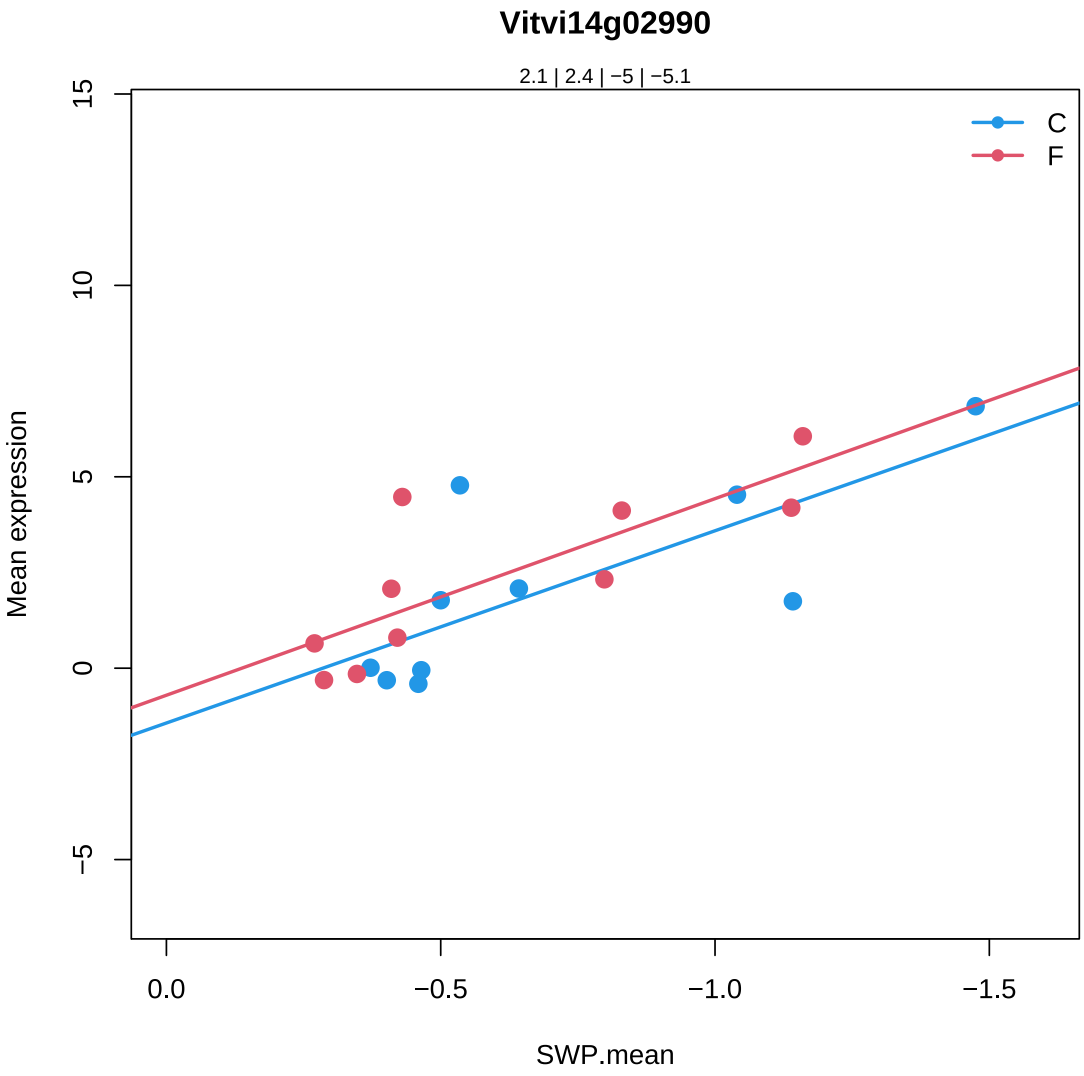
7.2.83 Vitvi14g02990: * type1

```
> 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
```



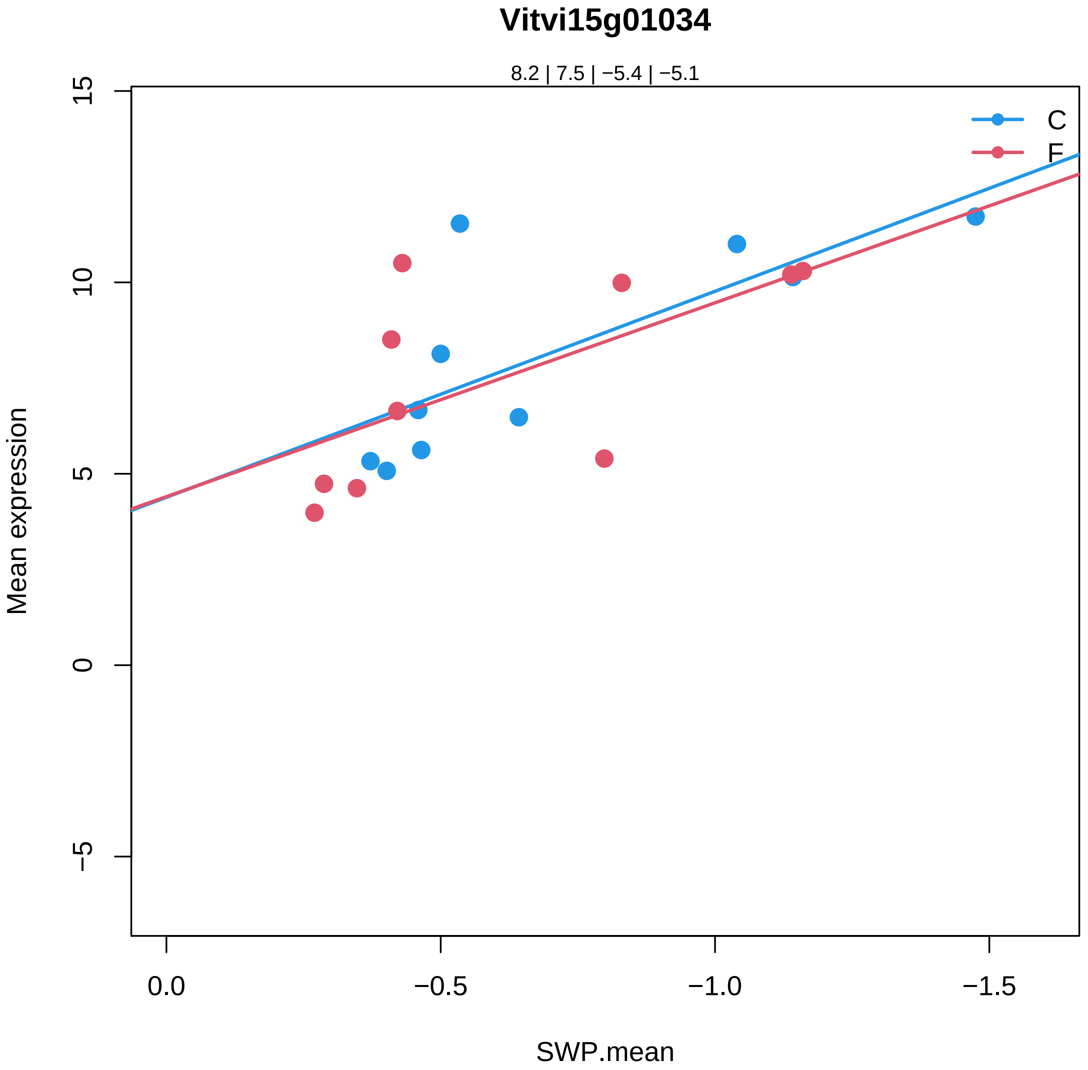
7.2.84 Vitvi15g01034: * type1

```
> 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
```



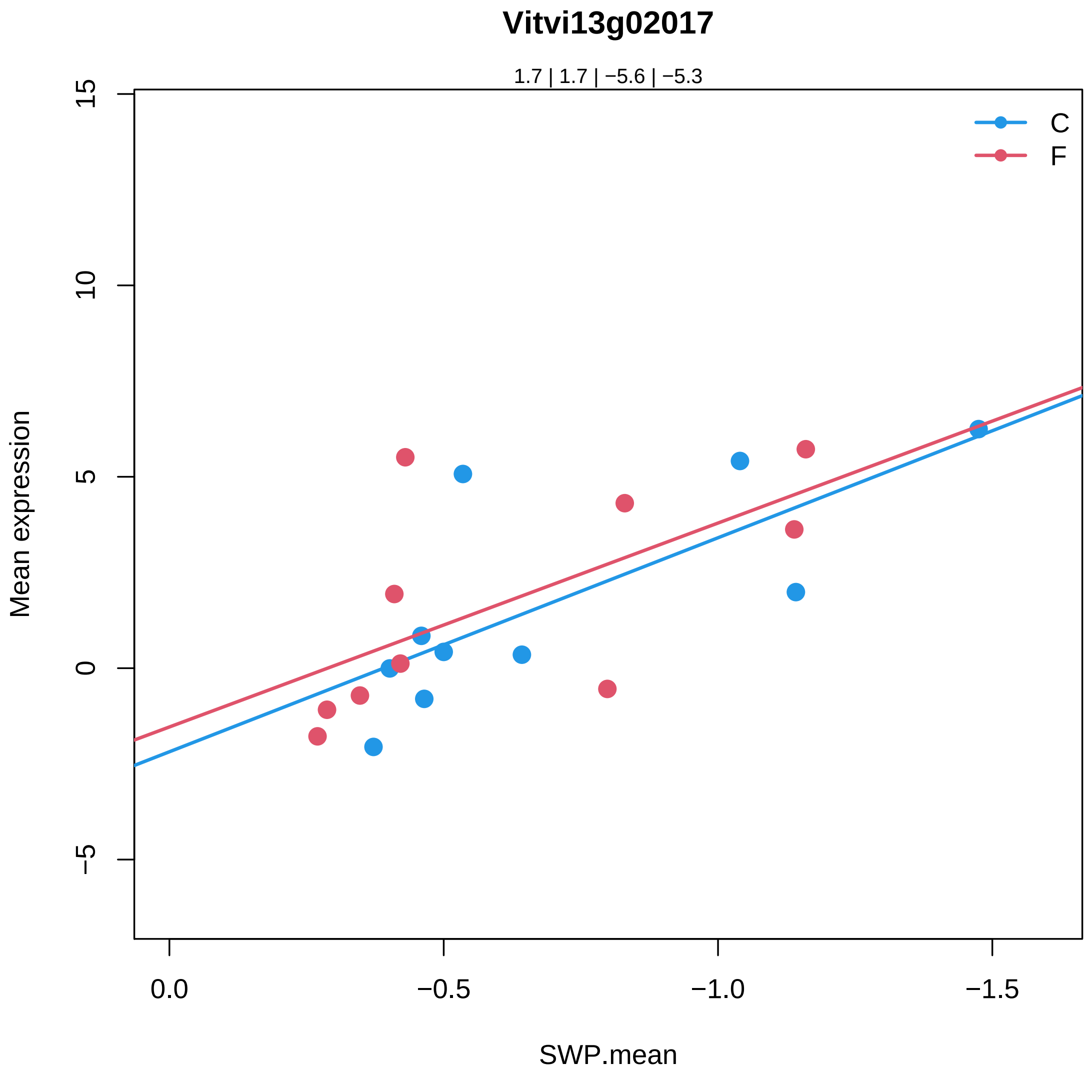
7.2.85 Vitvi13g02017: * type1

```
> 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
```



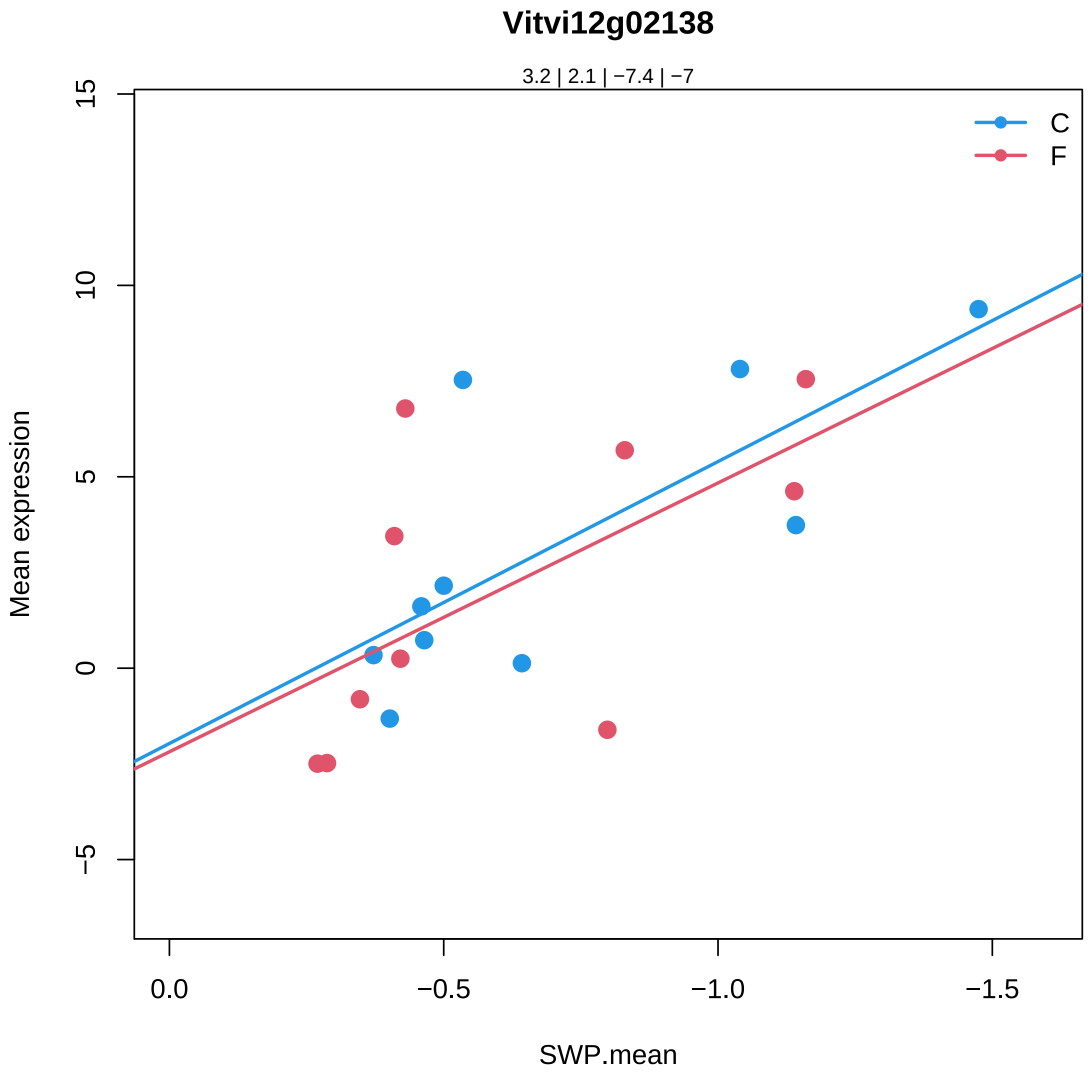
7.2.86 Vitvi12g02138: * type1

```
> 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
```



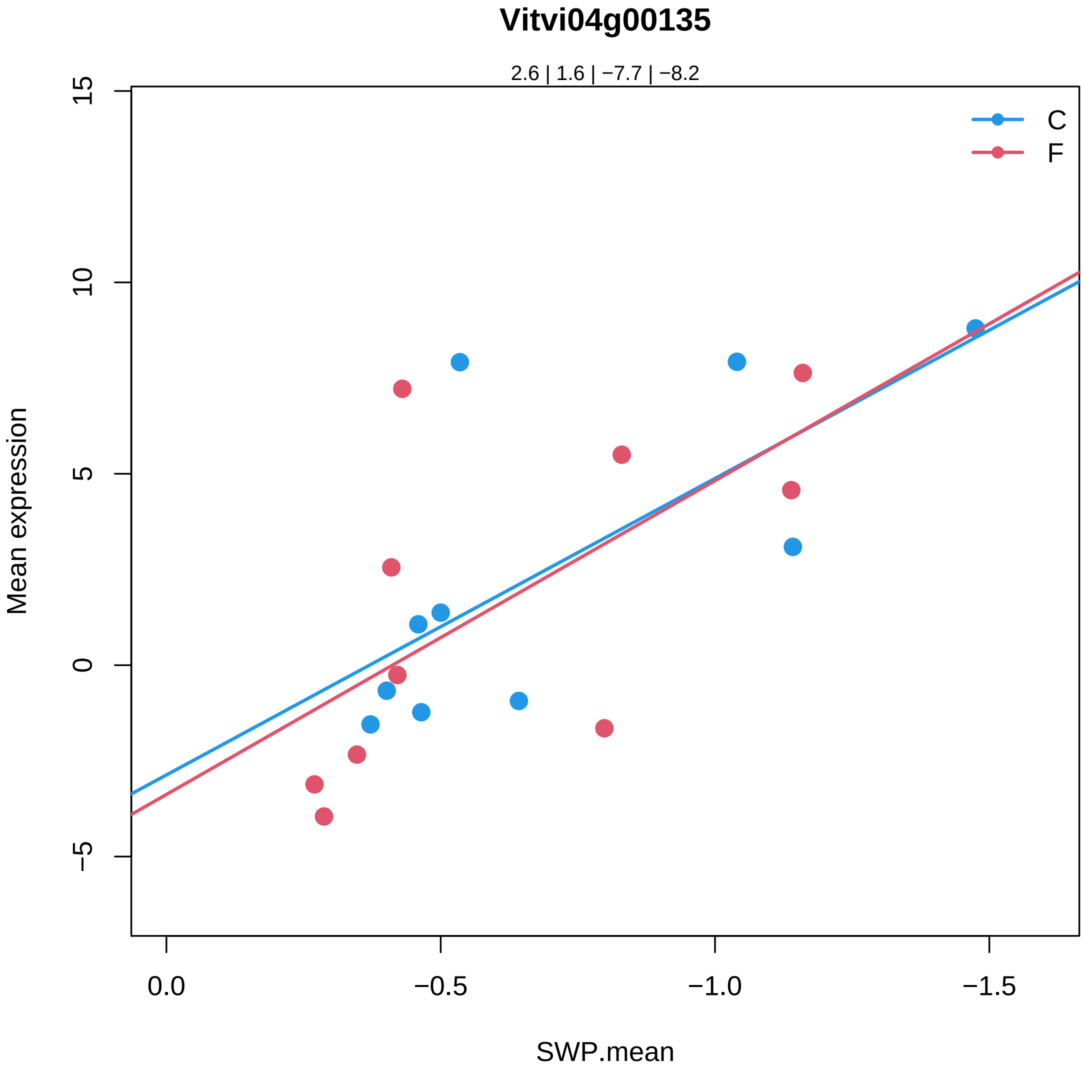
7.2.87 Vitvi04g00135: * type1

```
> 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
```



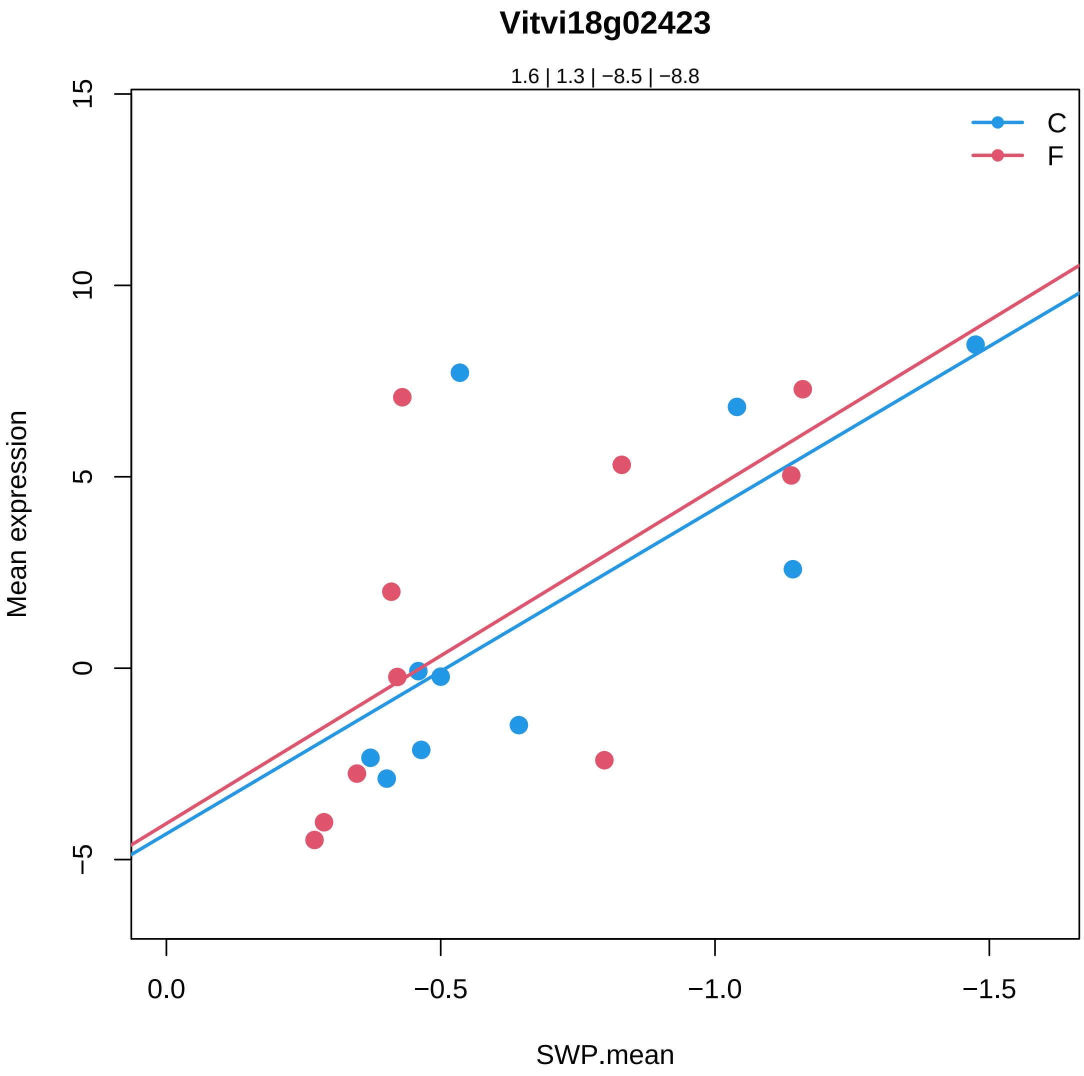
7.2.88 Vitvi18g02423: * type1

```
> 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

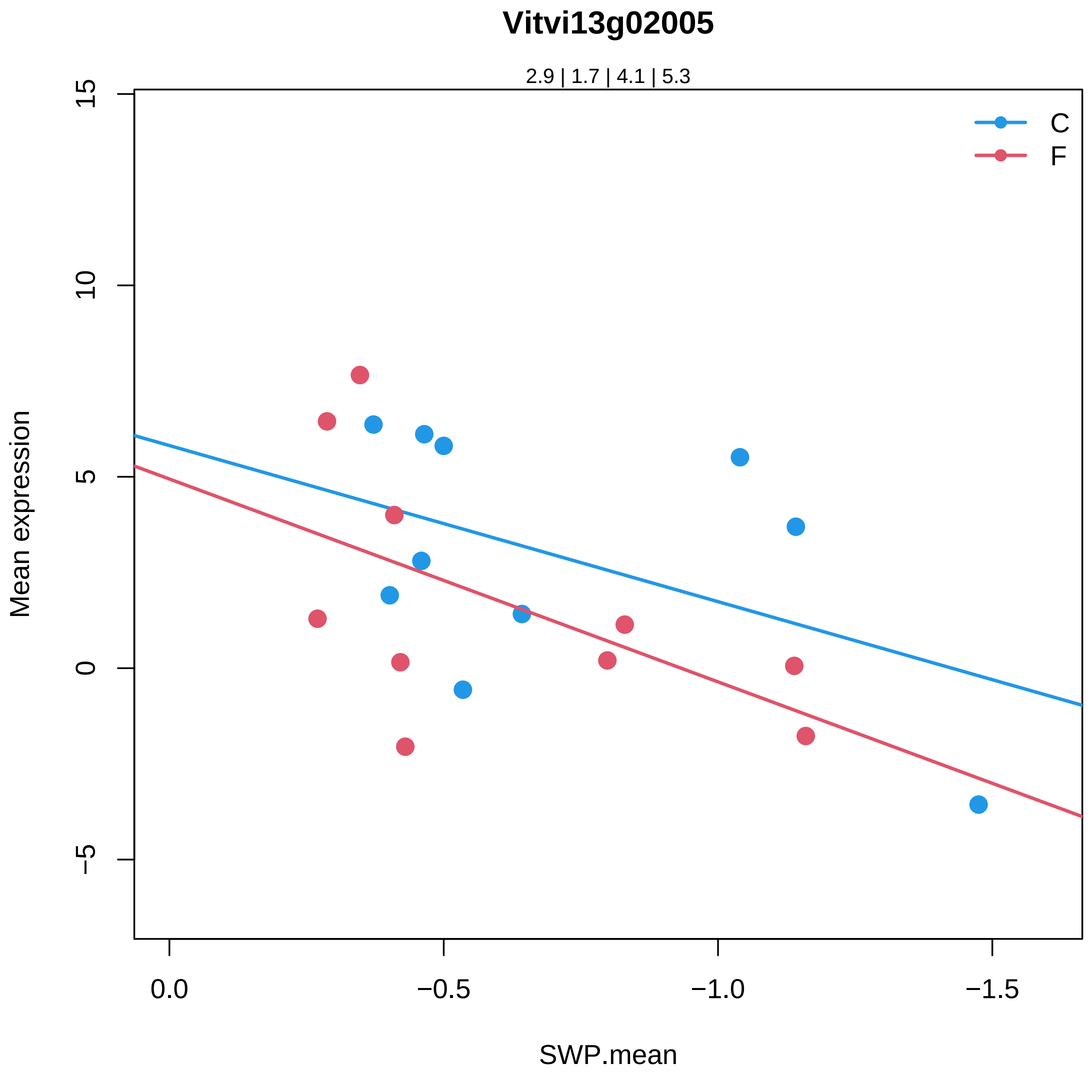
7.3.1 Vitvi13g02005: type2

```
> 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
```



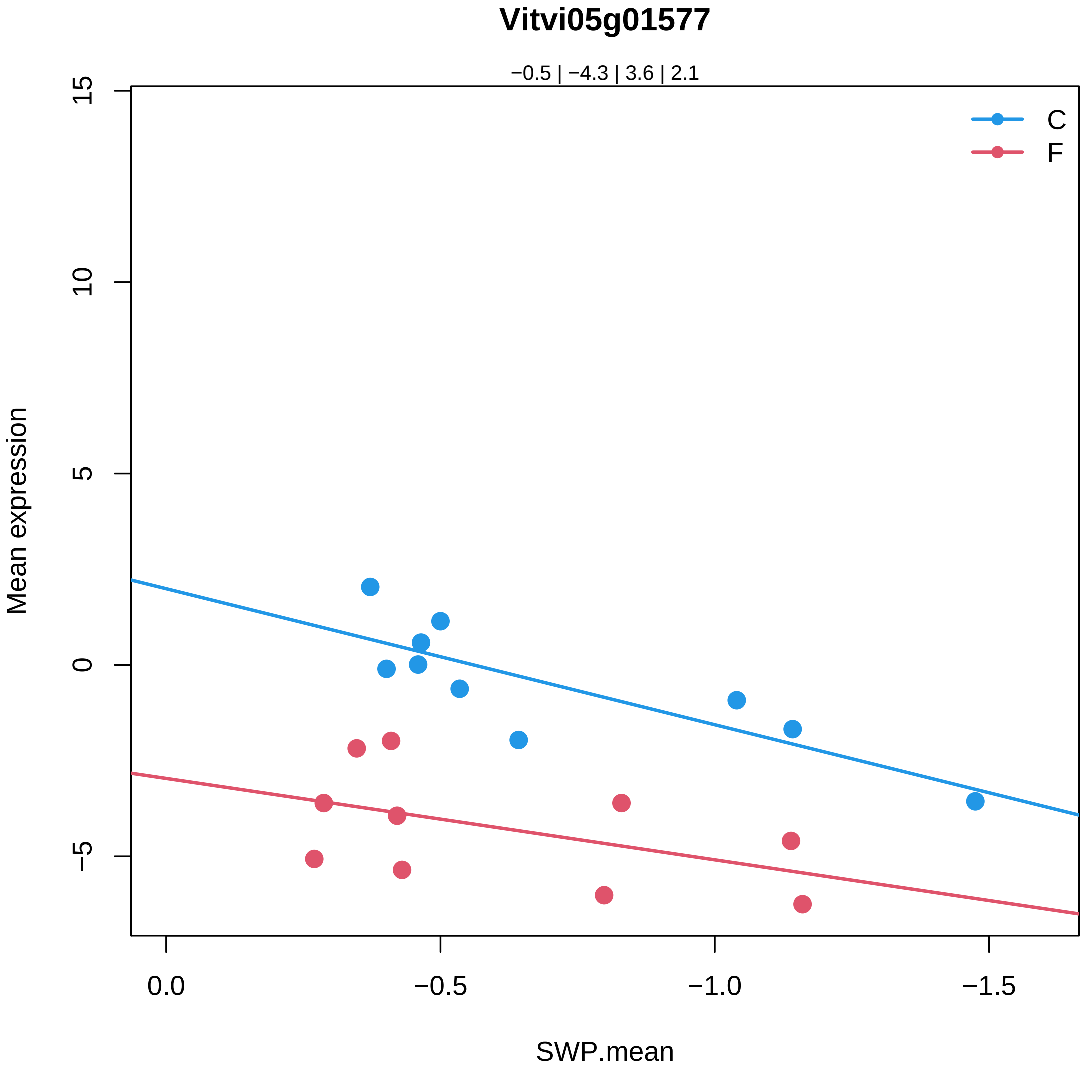
7.3.2 Vitvi05g01577: * type2 | type4

```
> 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
```



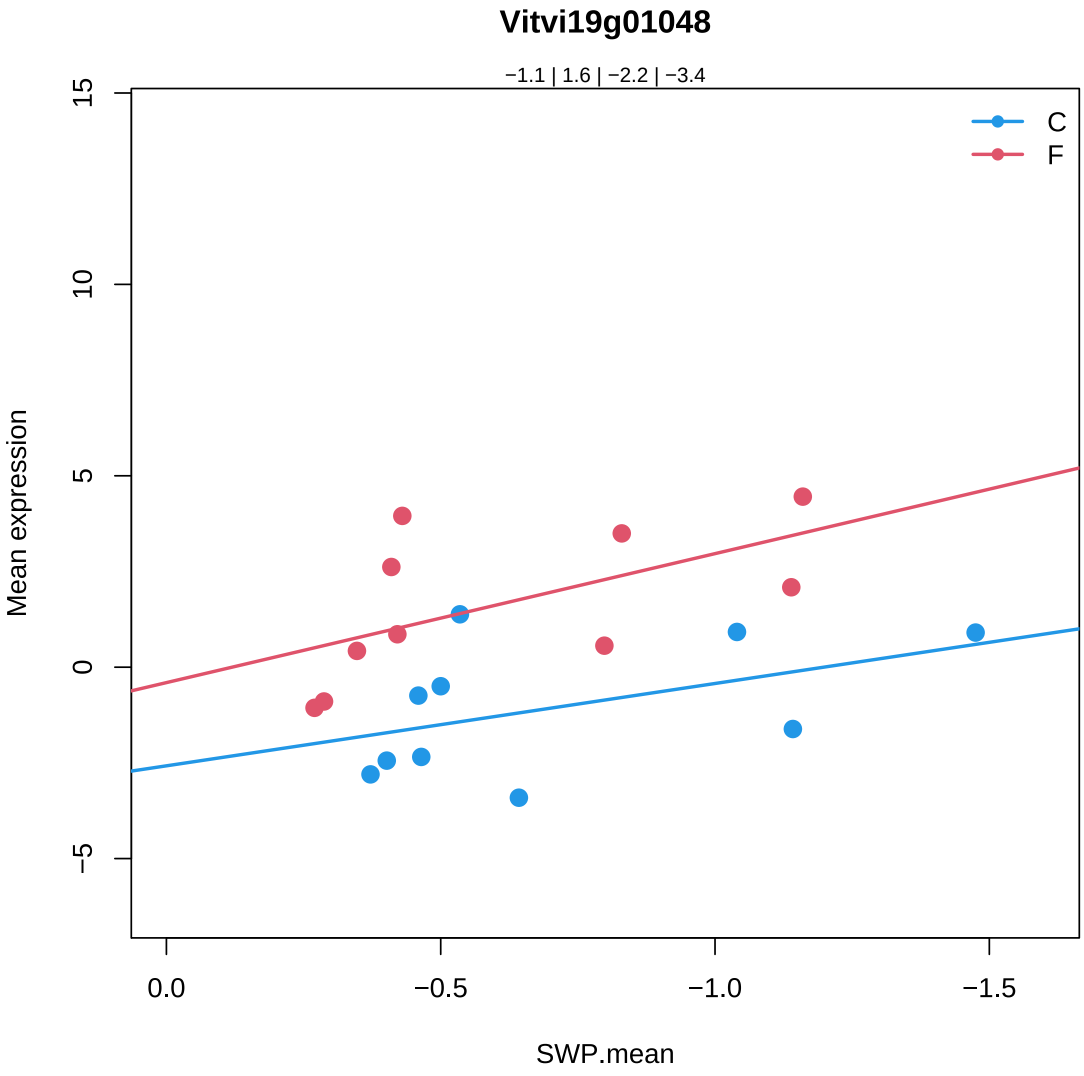
7.3.3 Vitvi19g01048: type2 | type4

```
> 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
```



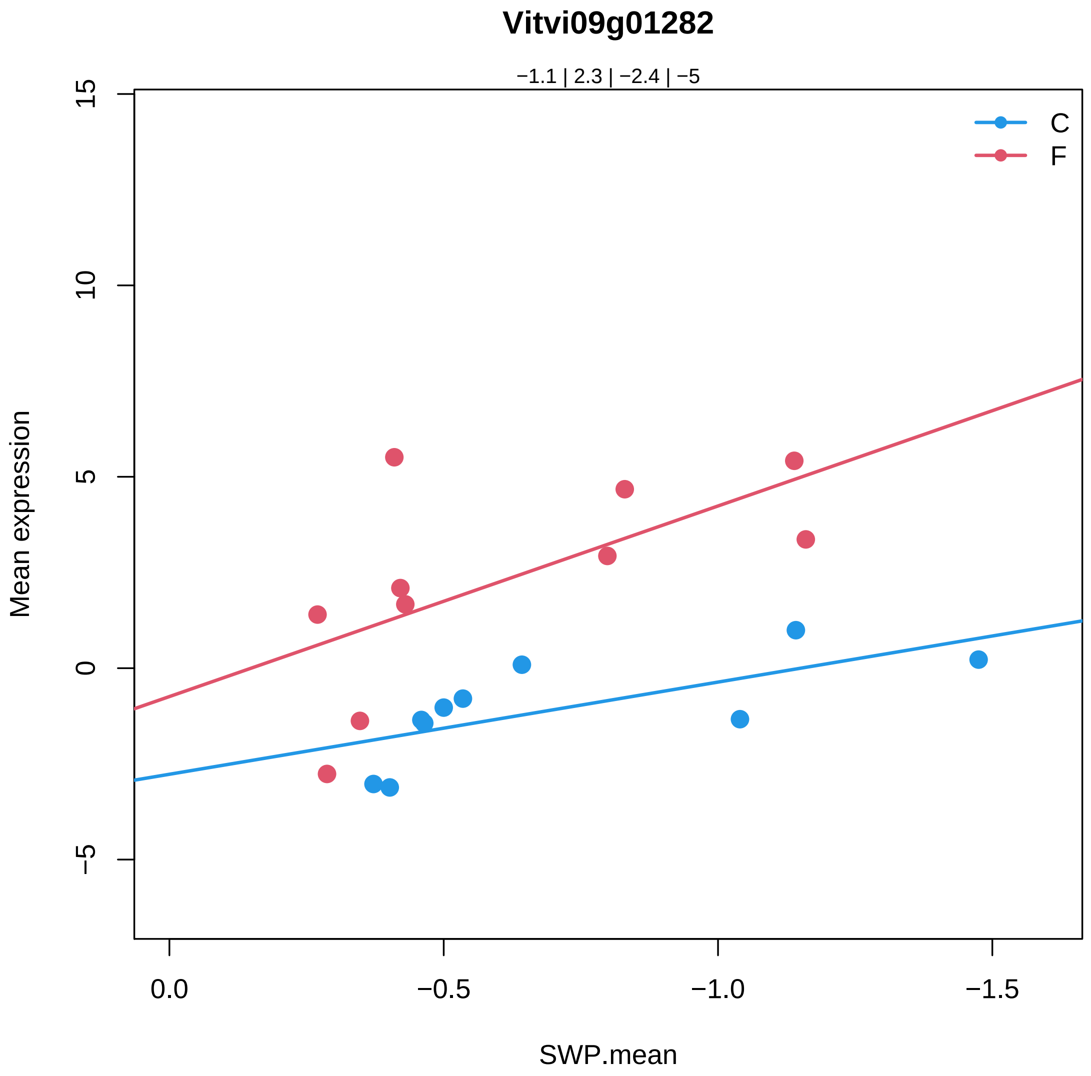
7.3.4 Vitvi09g01282: type2 | type4

```
> 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        
```



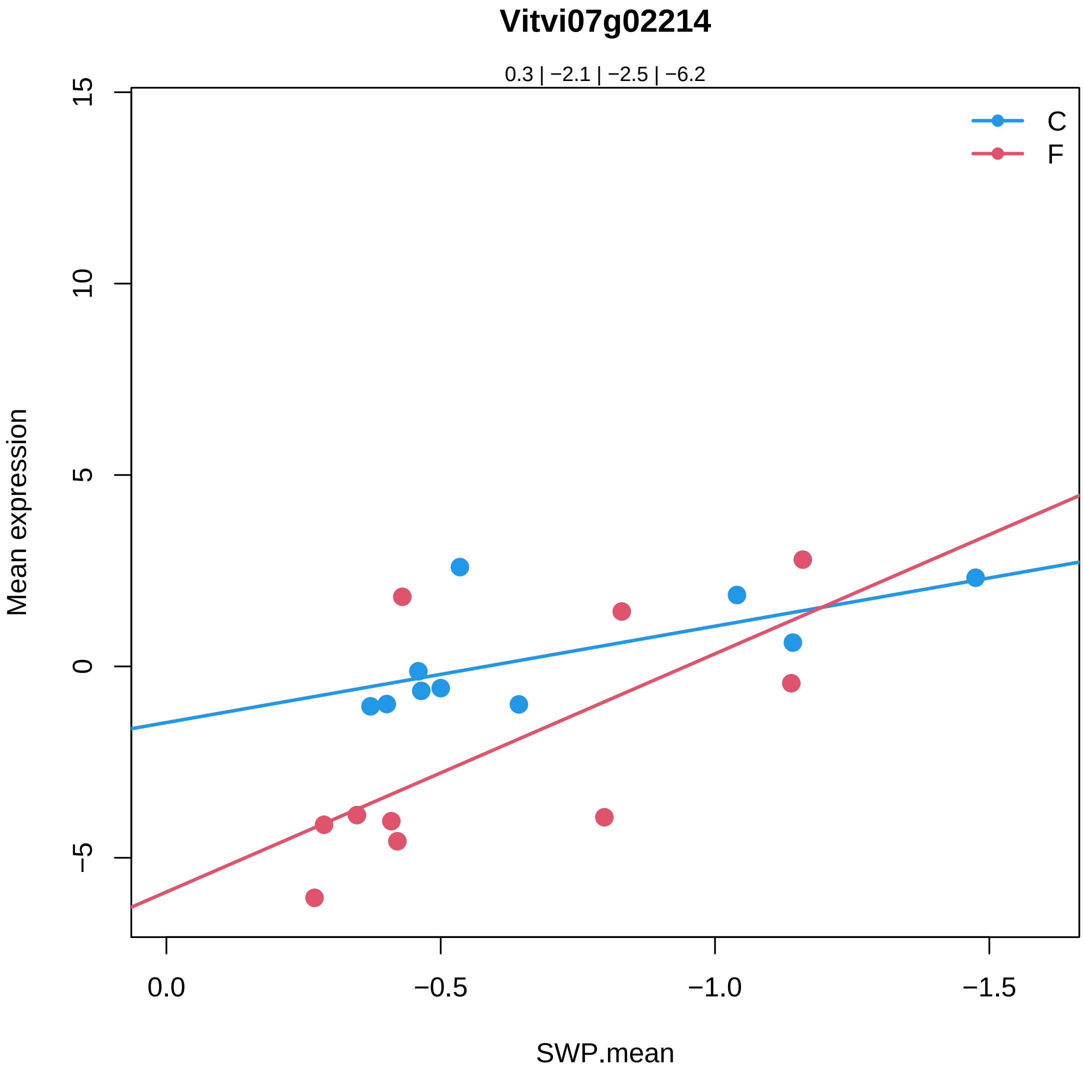
7.3.5 Vitvi07g02214: type2 | type4

```
> 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
```



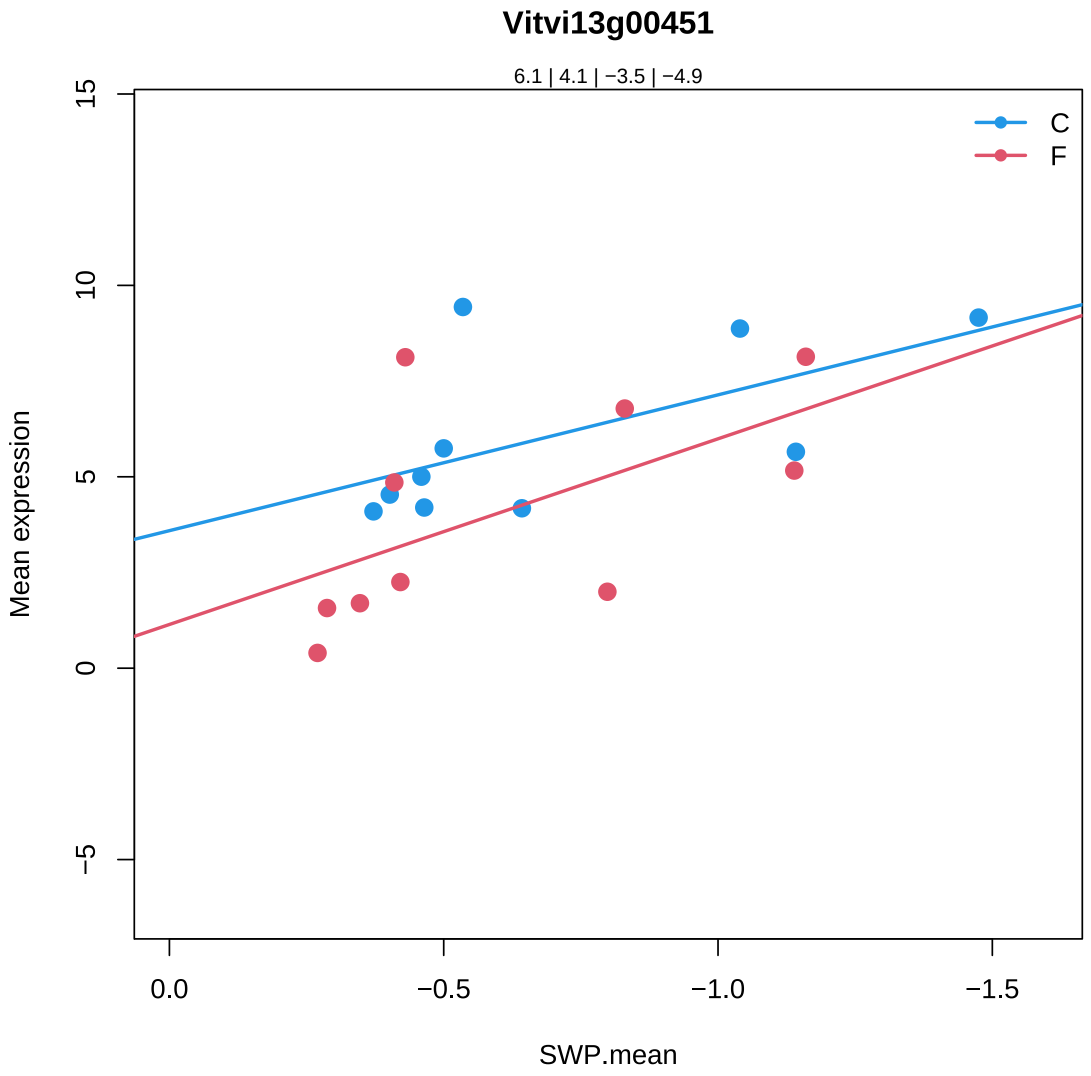
7.3.6 Vitvi13g00451: * type2

```
> 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
```



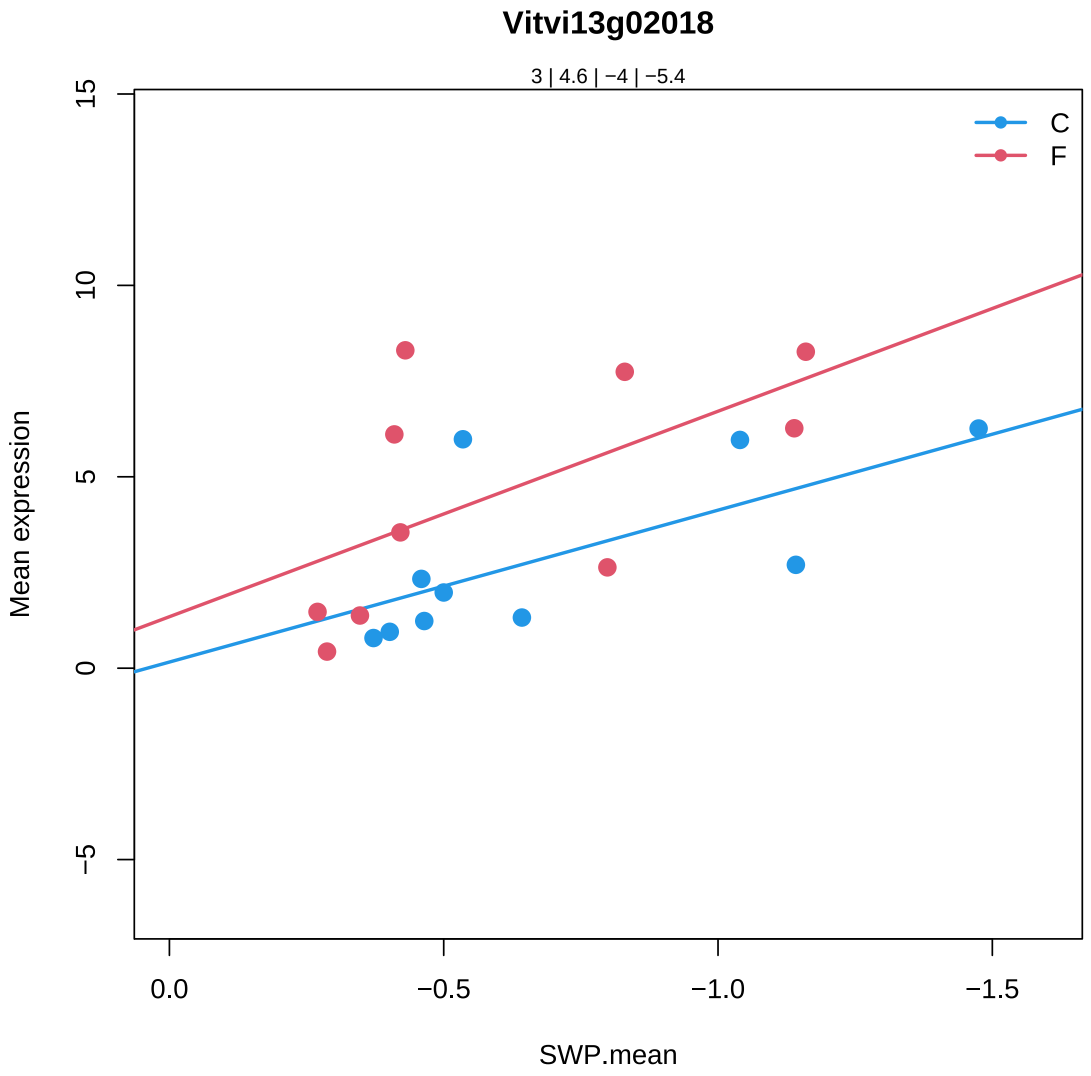
7.3.7 Vitvi13g02018: * type2

```
> 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
```



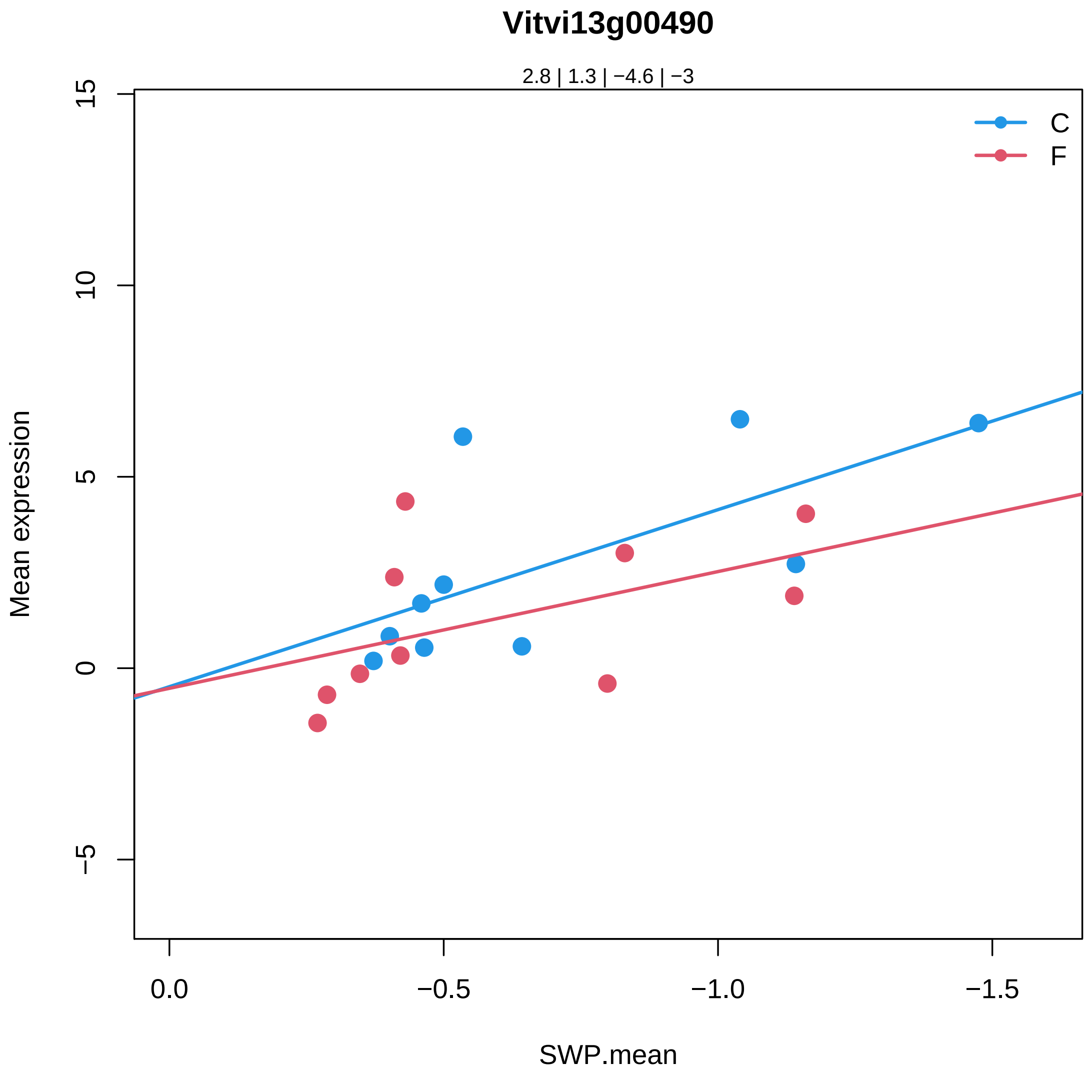
7.3.8 Vitvi13g00490: * type2

```
> 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
```



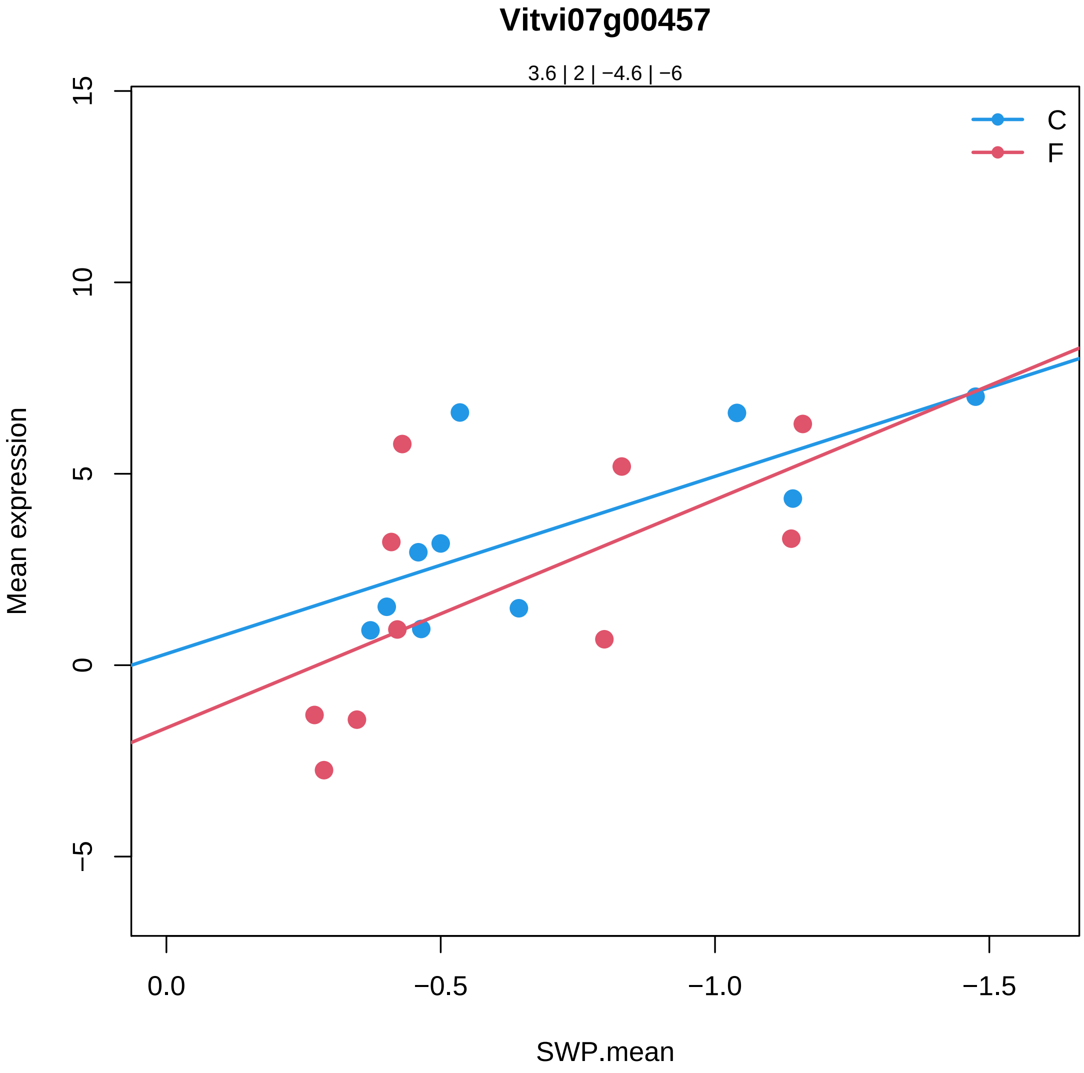
7.3.9 Vitvi07g00457: * type2

```
> 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
```



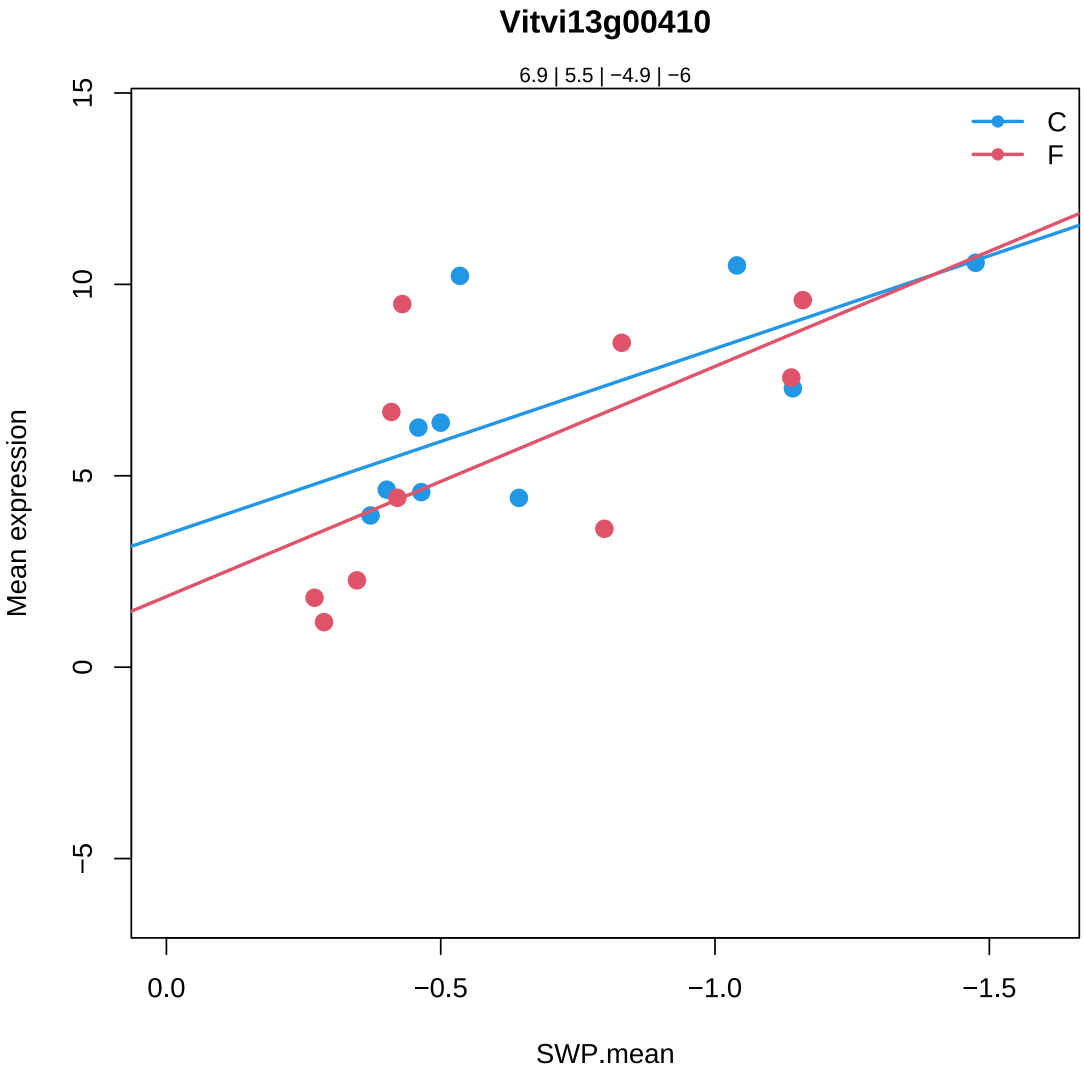
7.3.10 Vitvi13g00410: * type2

```
> 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
```



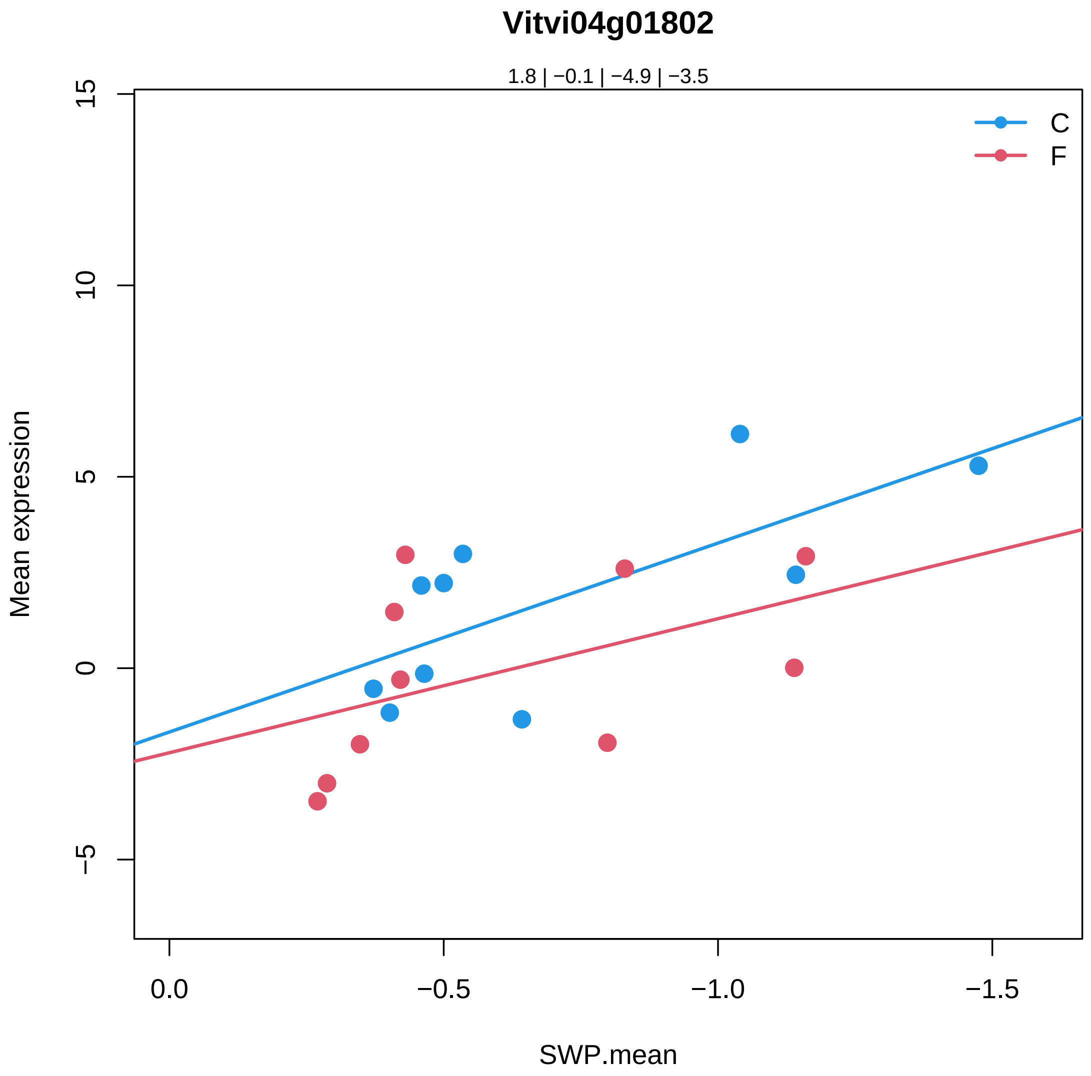
7.3.11 Vitvi04g01802: * type2

```
> 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
```



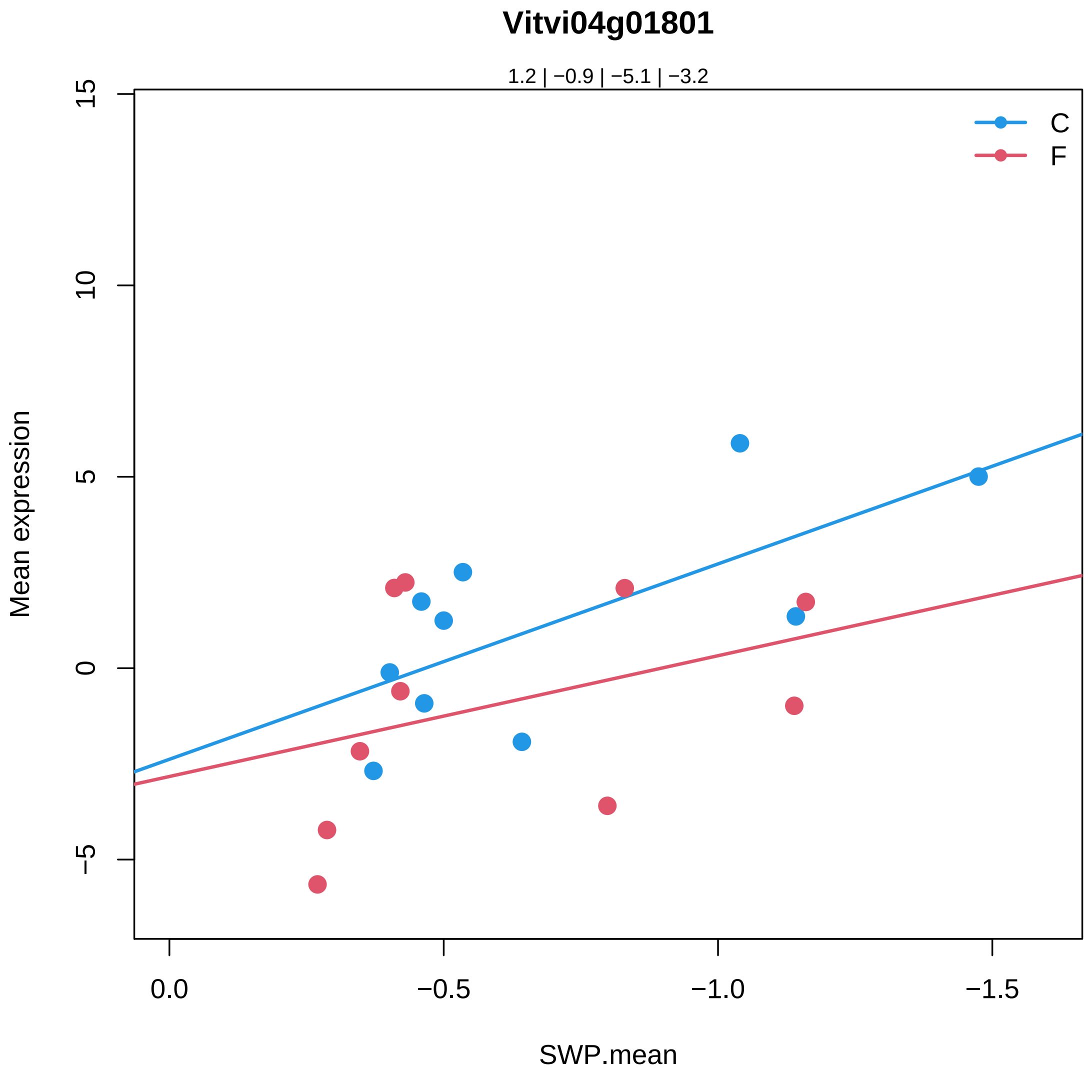
7.3.12 Vitvi04g01801: * type2 | type4

```
> 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
```



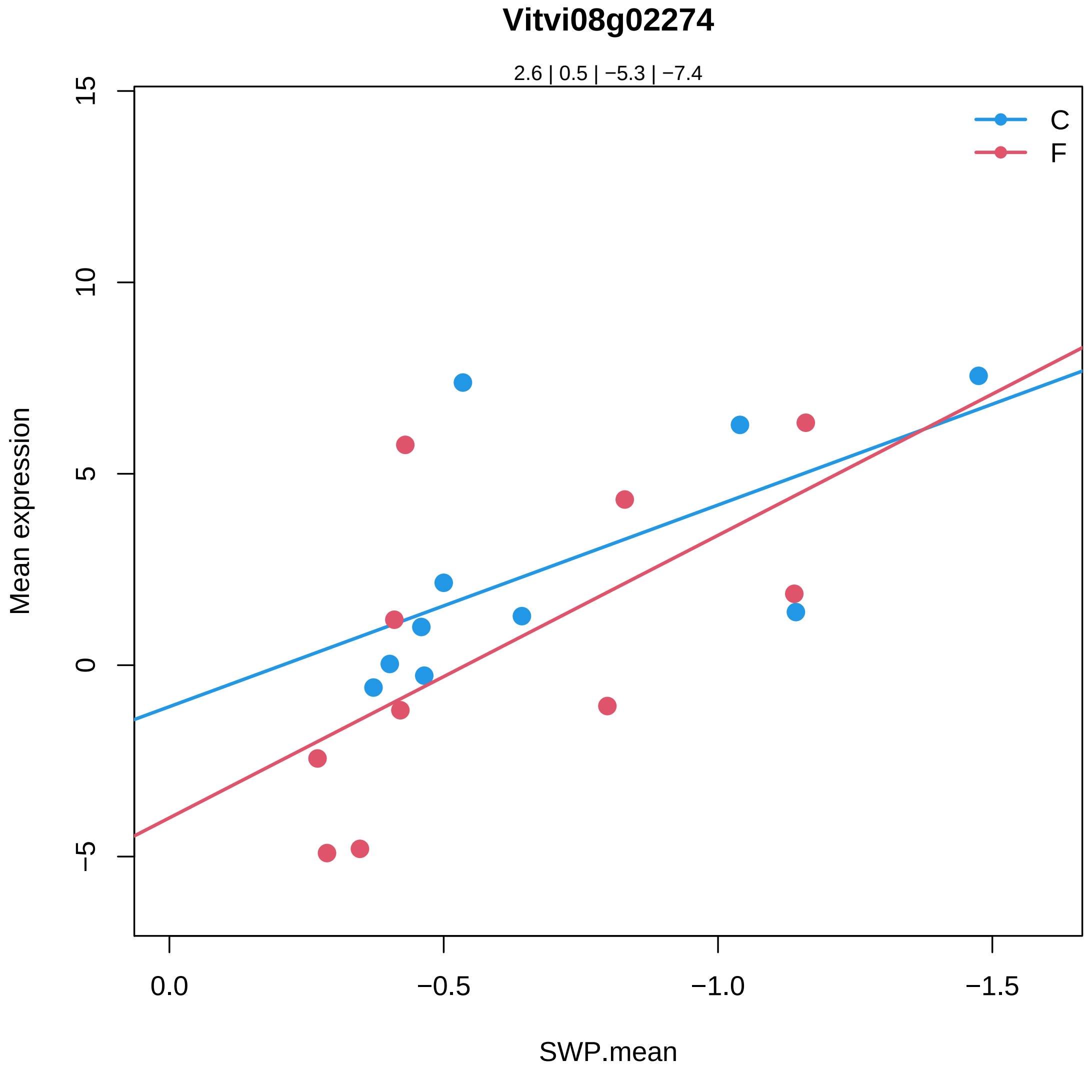
7.3.13 Vitvi08g02274: * type2 | type4

```
> 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        
```



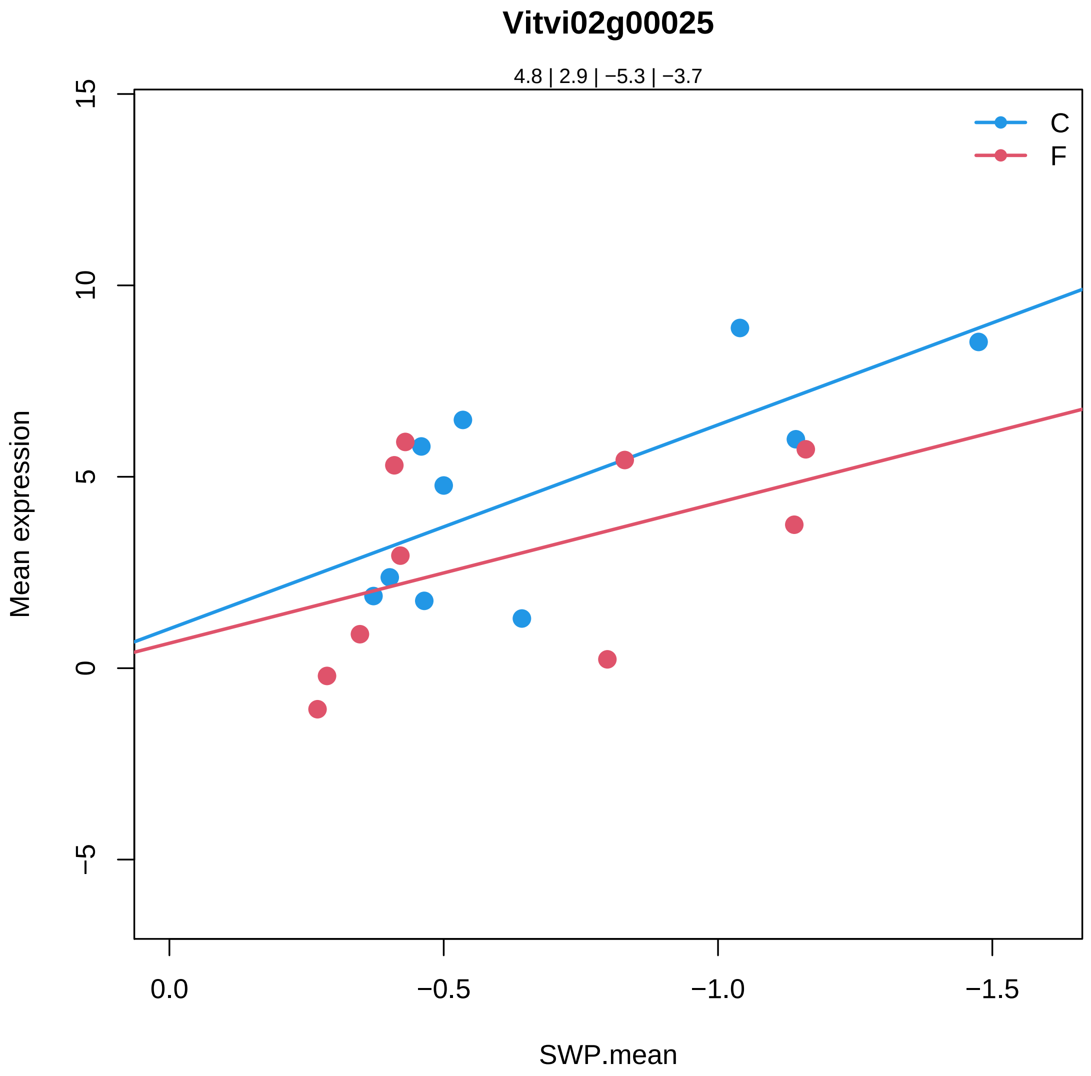
7.3.14 Vitvi02g00025: * type2

```
> 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
```



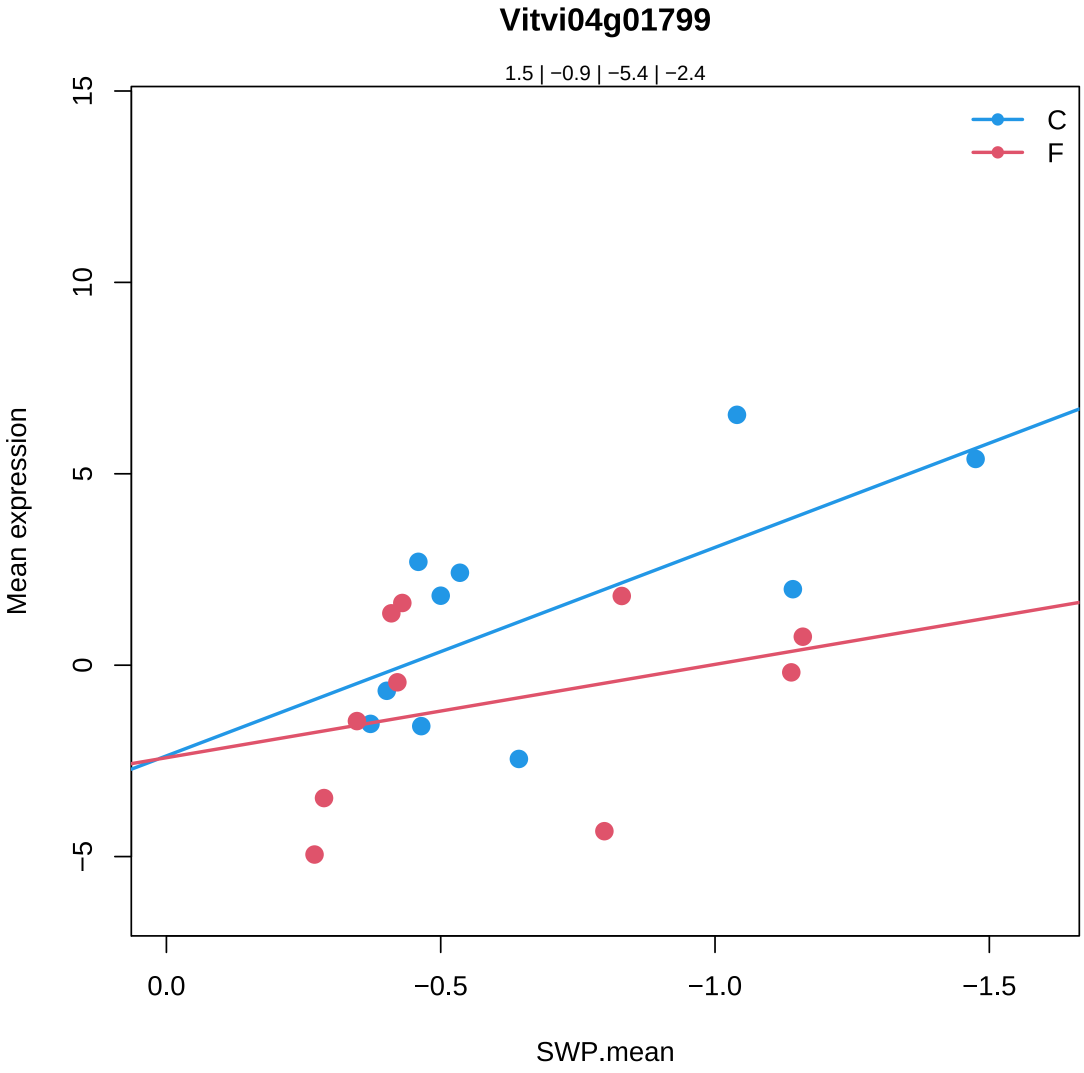
7.3.15 Vitvi04g01799: * type2 | type4

```
> 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
```



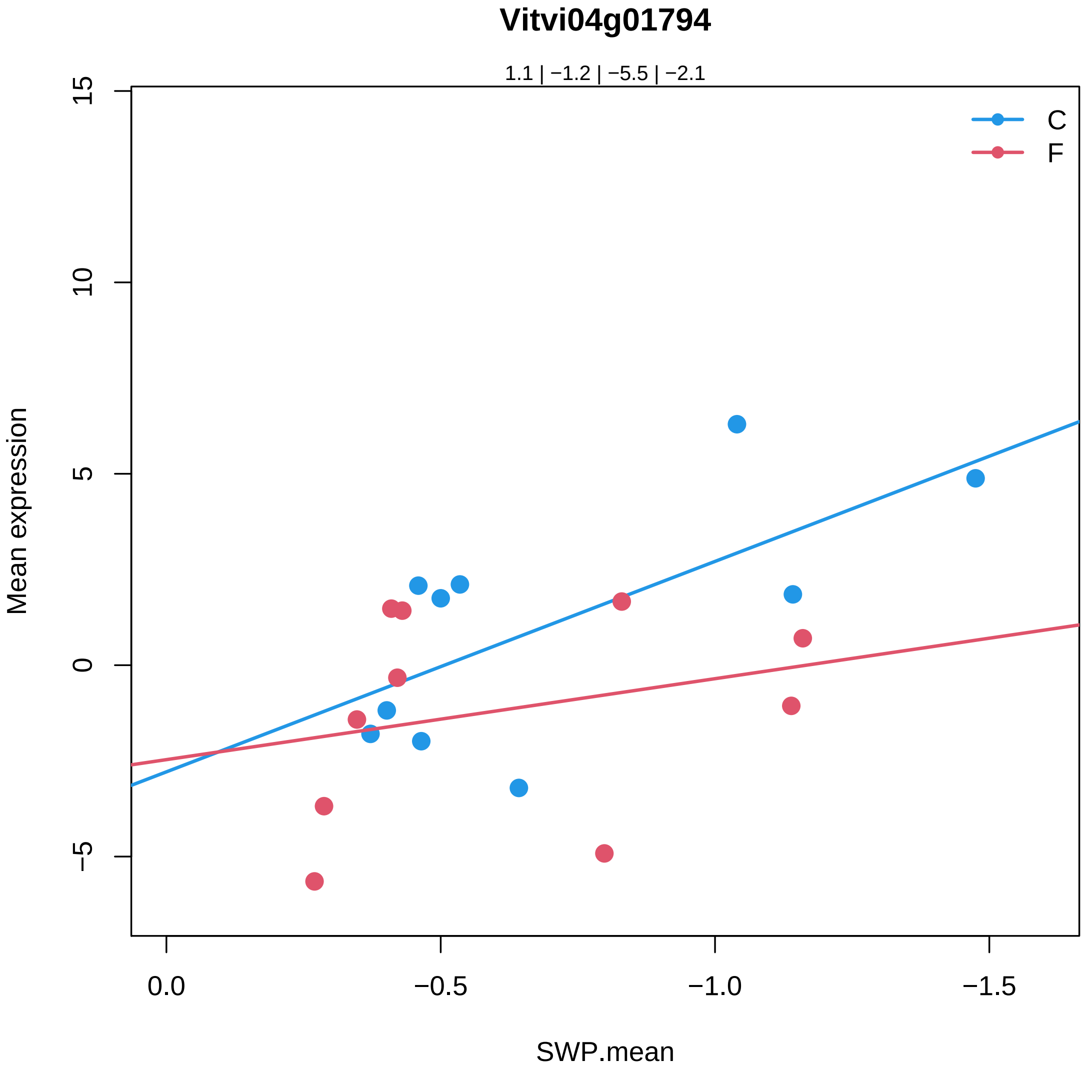
7.3.16 Vitvi04g01794: * type2 | type4

```
> 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
```



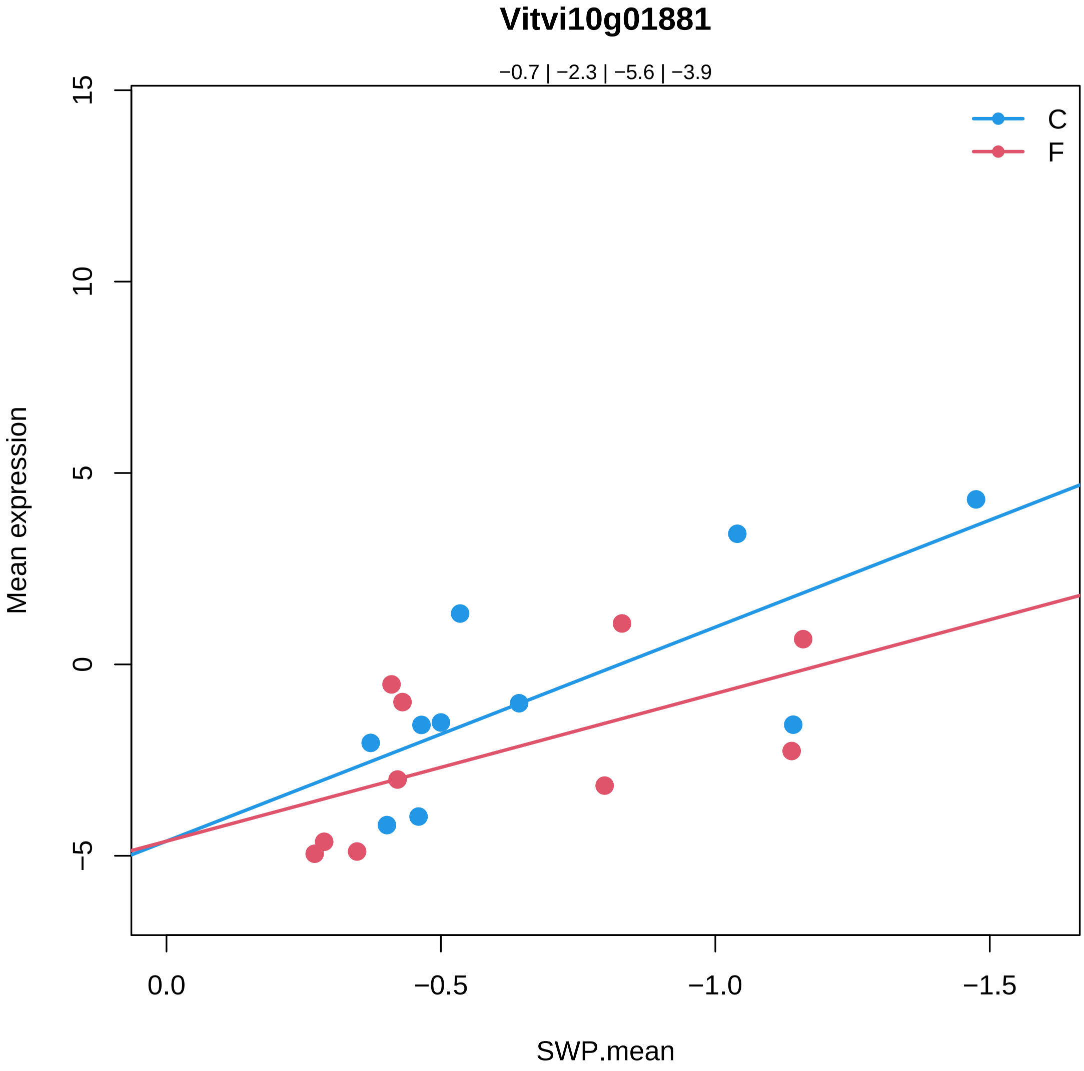
7.3.17 Vitvi10g01881: * type2

```
> 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
```



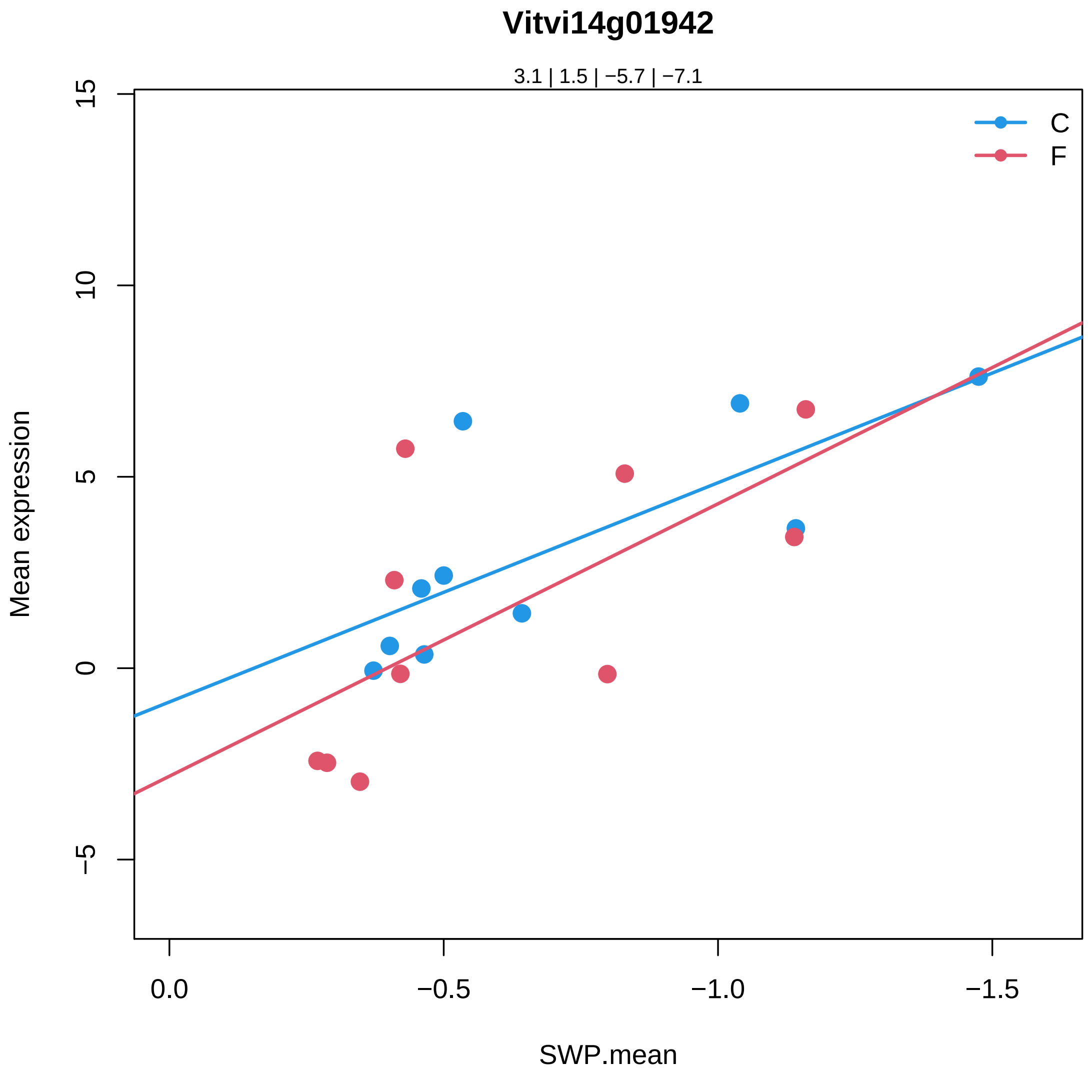
7.3.18 Vitvi14g01942: * type2

```
> 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
```



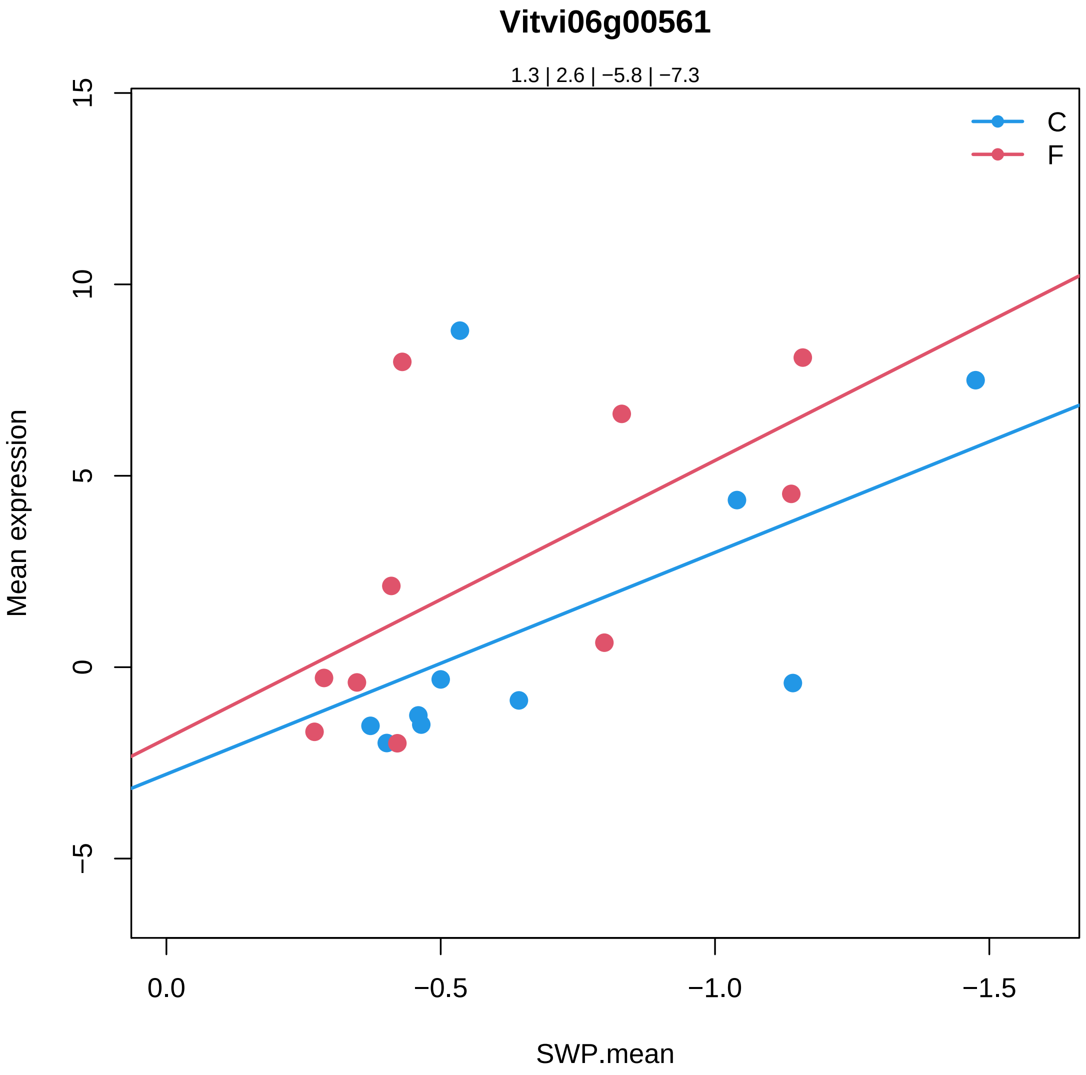
7.3.19 Vitvi06g00561: * type2

```
> 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
```



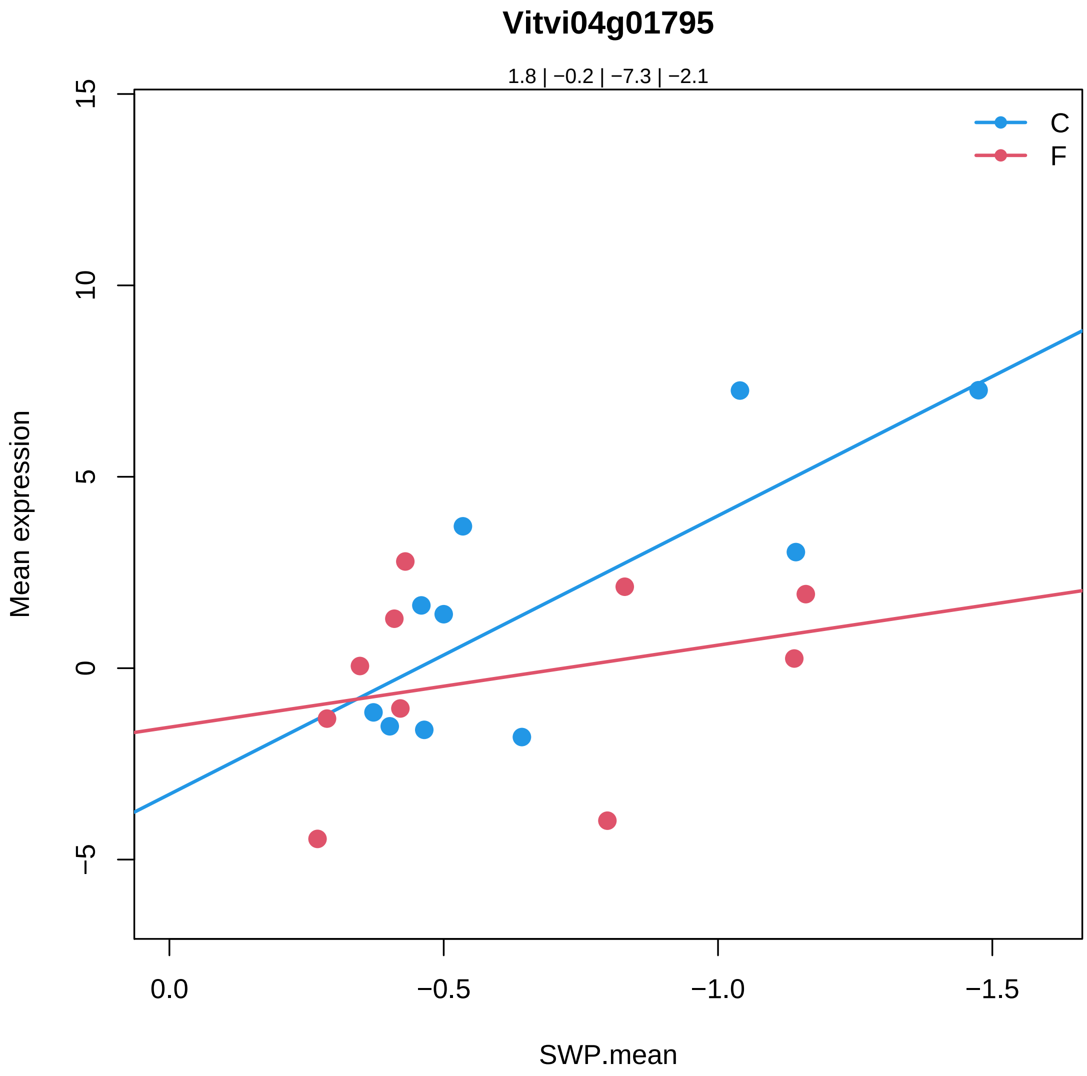
7.3.20 Vitvi04g01795: * type2 | type4

```
> 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

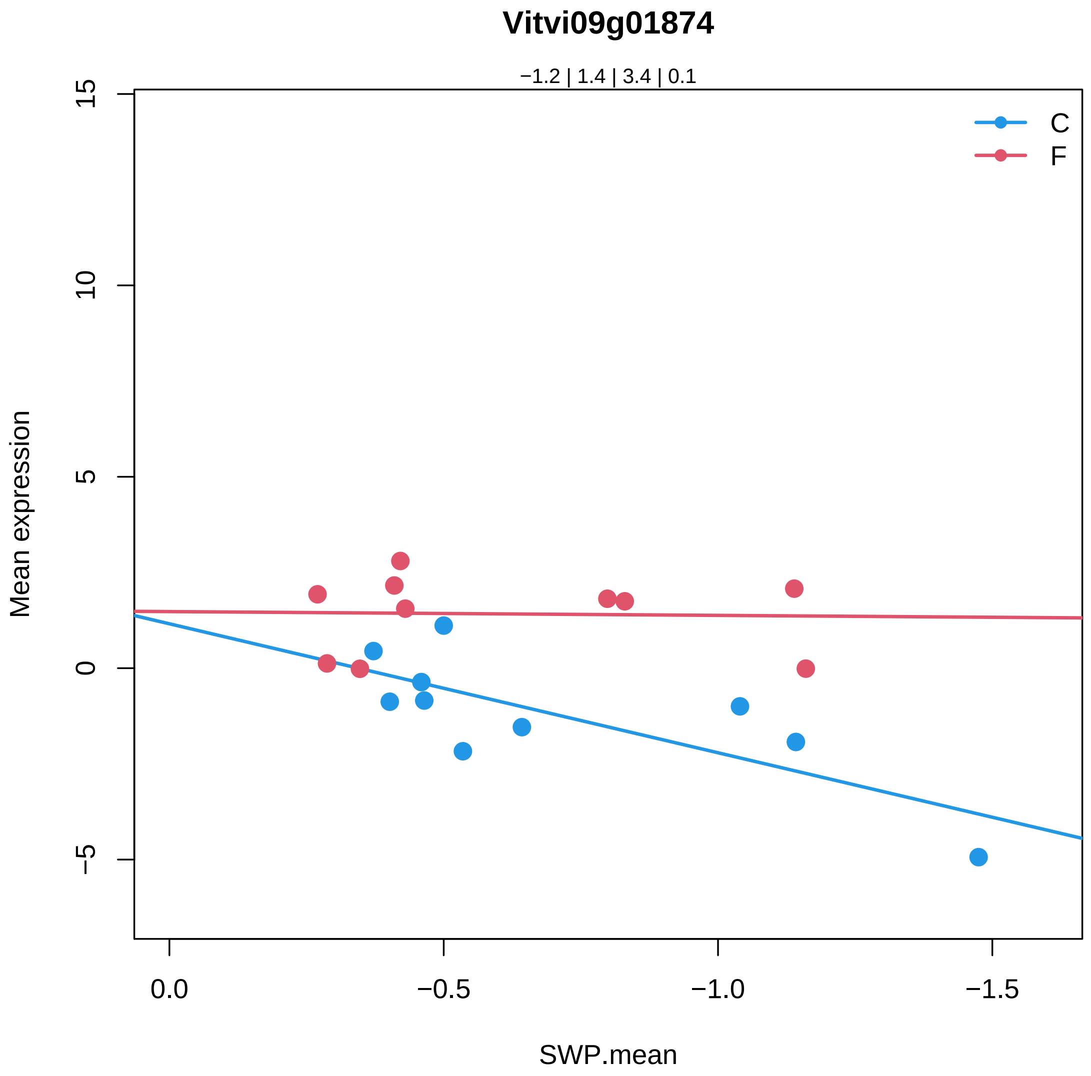
7.4.1 Vitvi09g01874: * type3 | type4

```
> 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
```



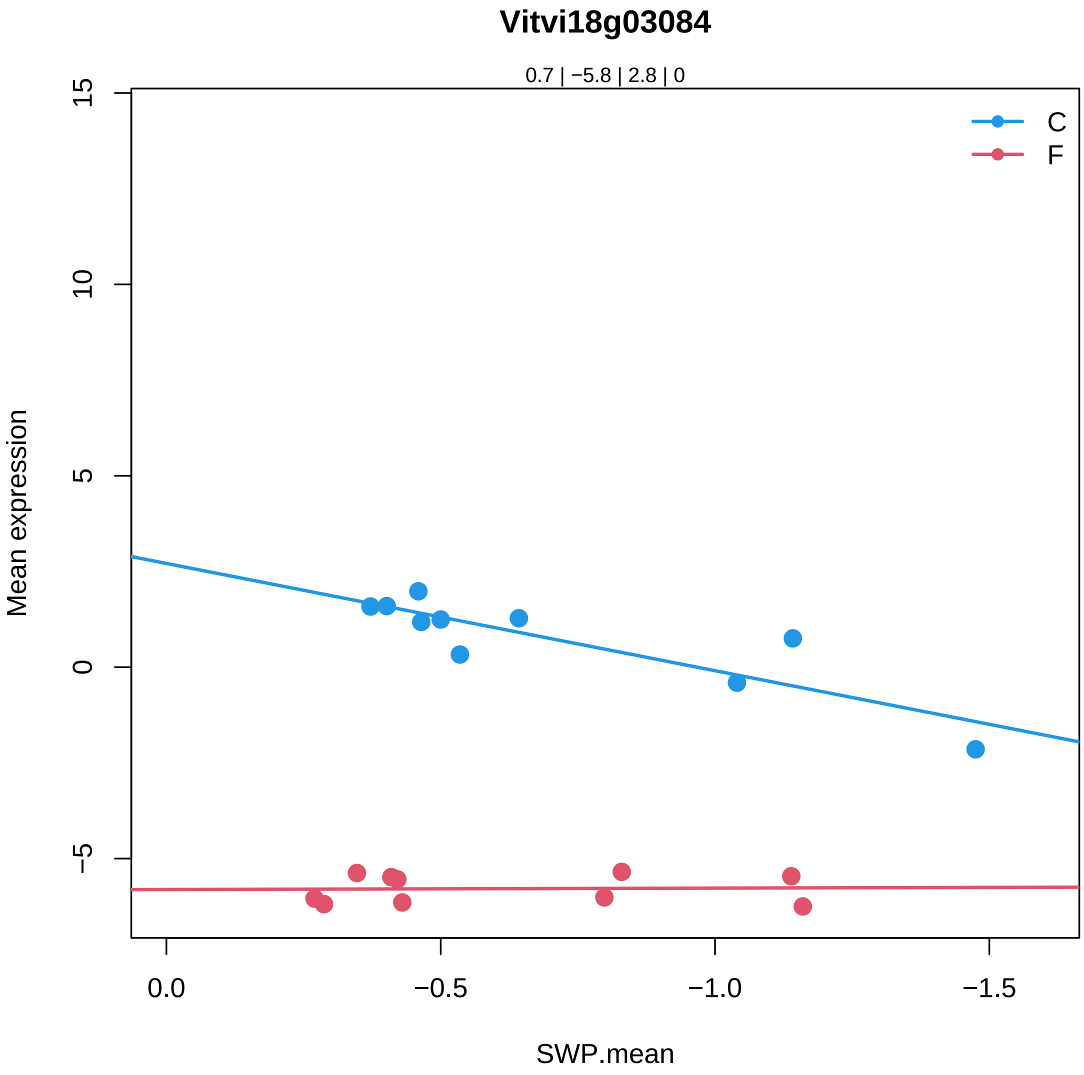
7.4.2 Vitvi18g03084: * type3

```
> 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
```



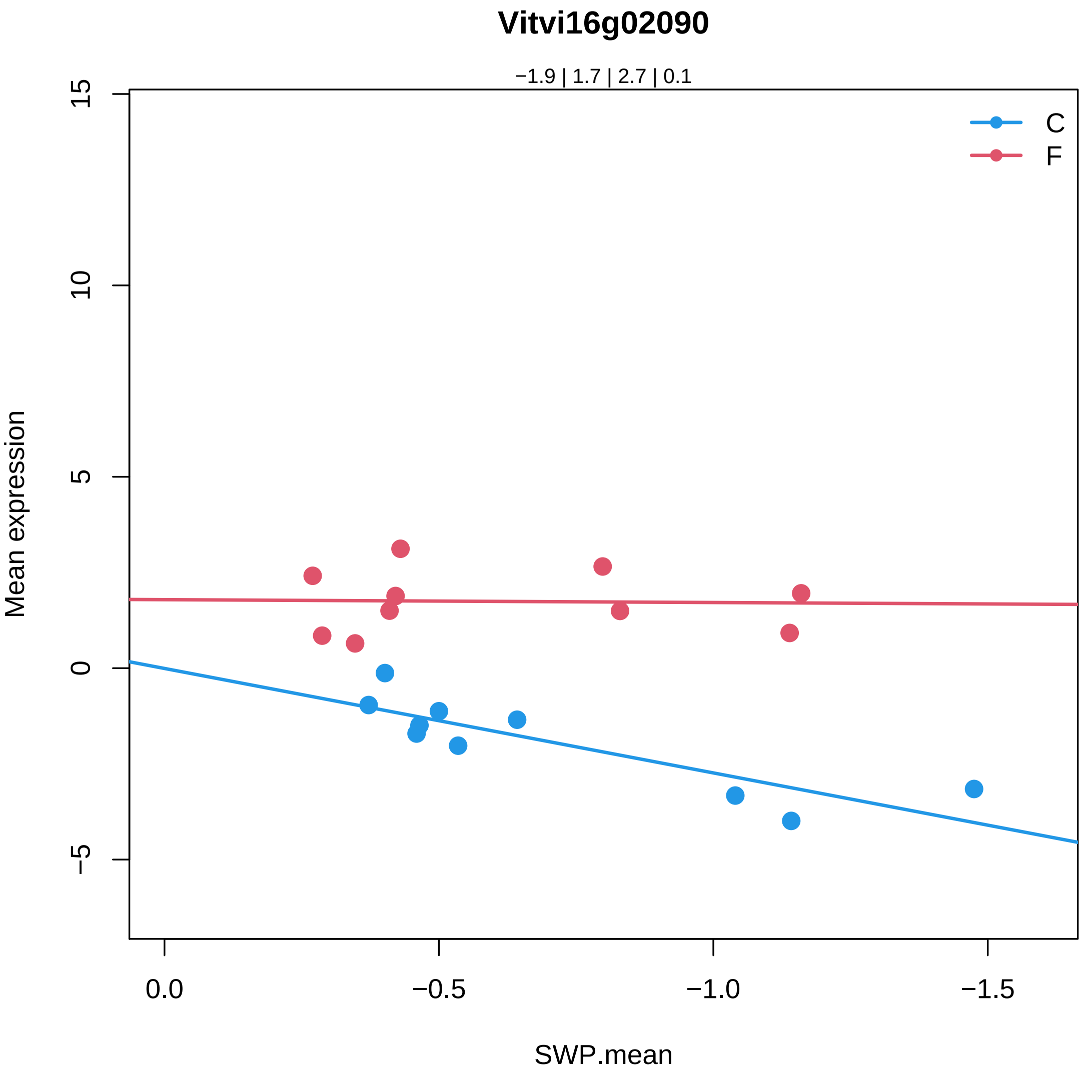
7.4.3 Vitvi16g02090: * type3 | type4

```
> 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
```



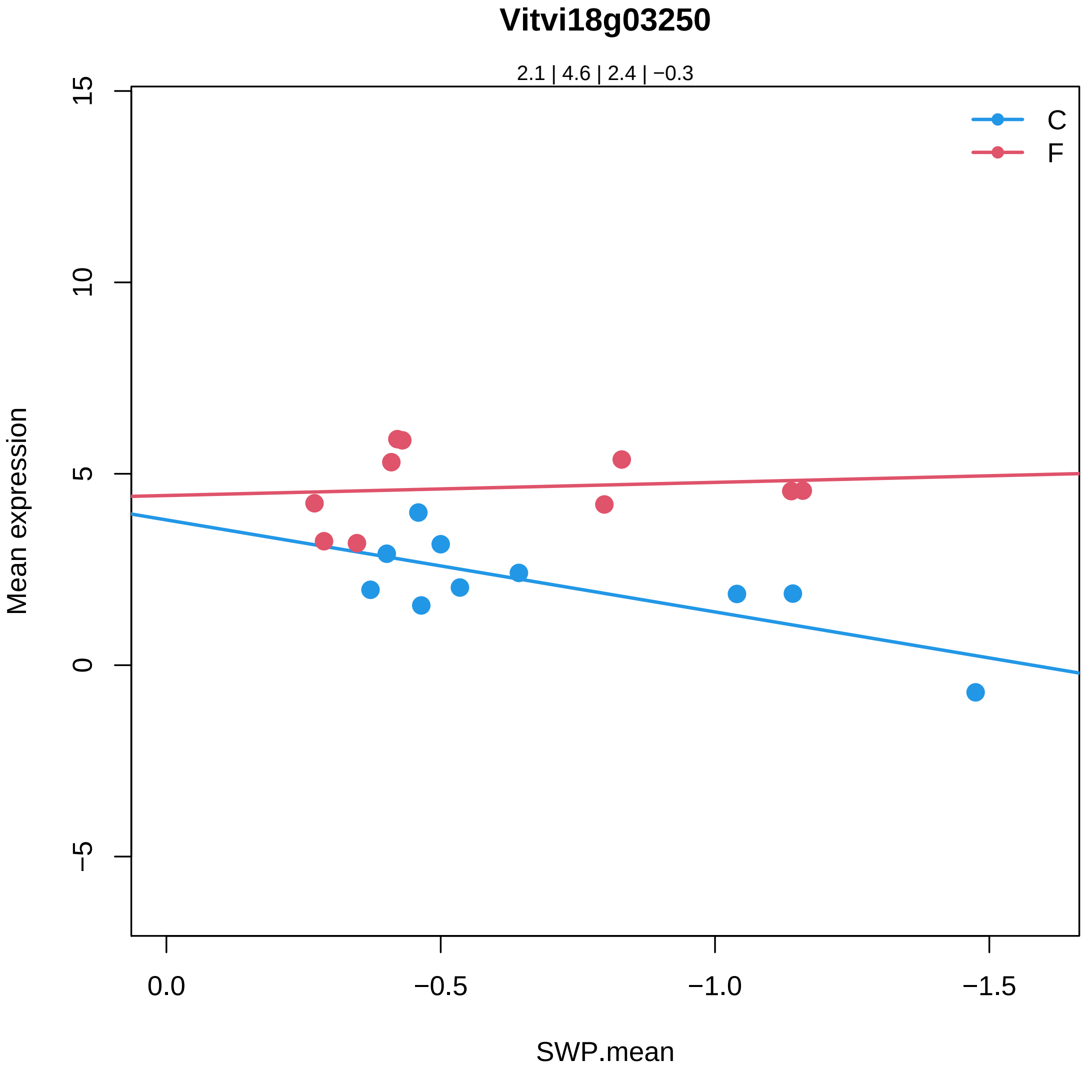
7.4.4 Vitvi18g03250: * type3

```
> 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
```



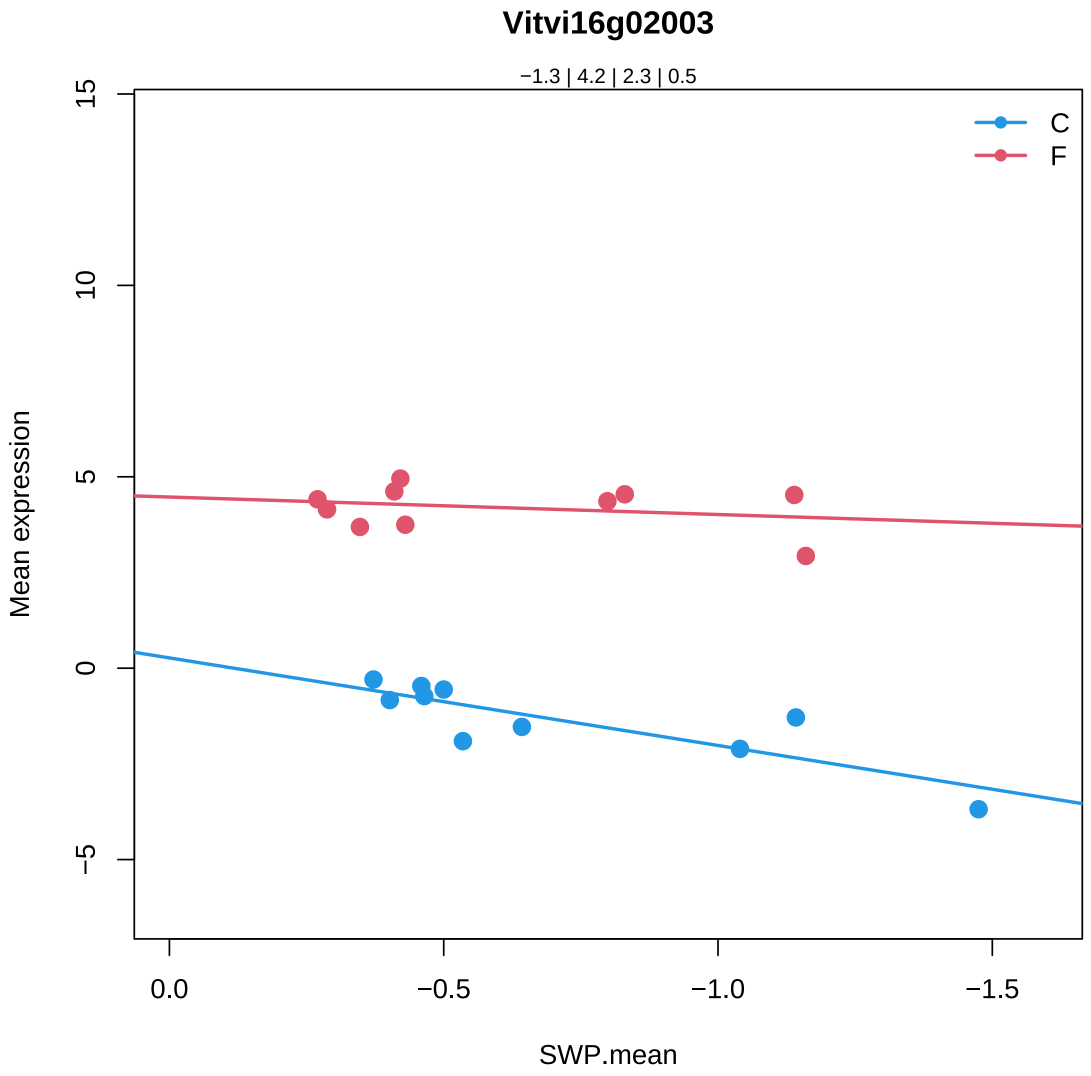
7.4.5 Vitvi16g02003: * type3 | type4

```
> 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
```



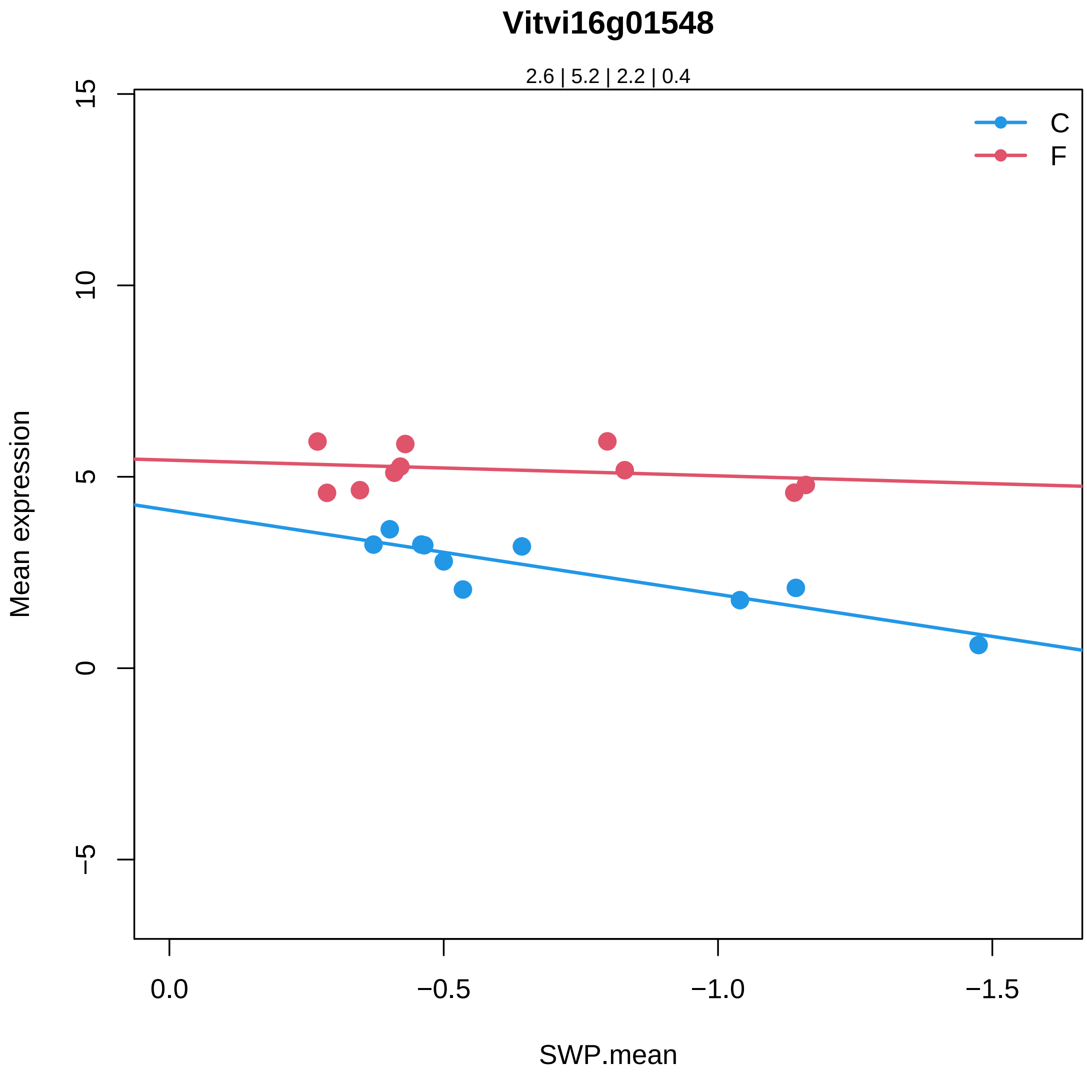
7.4.6 Vitvi16g01548: * type3 | type4

```
> 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
```



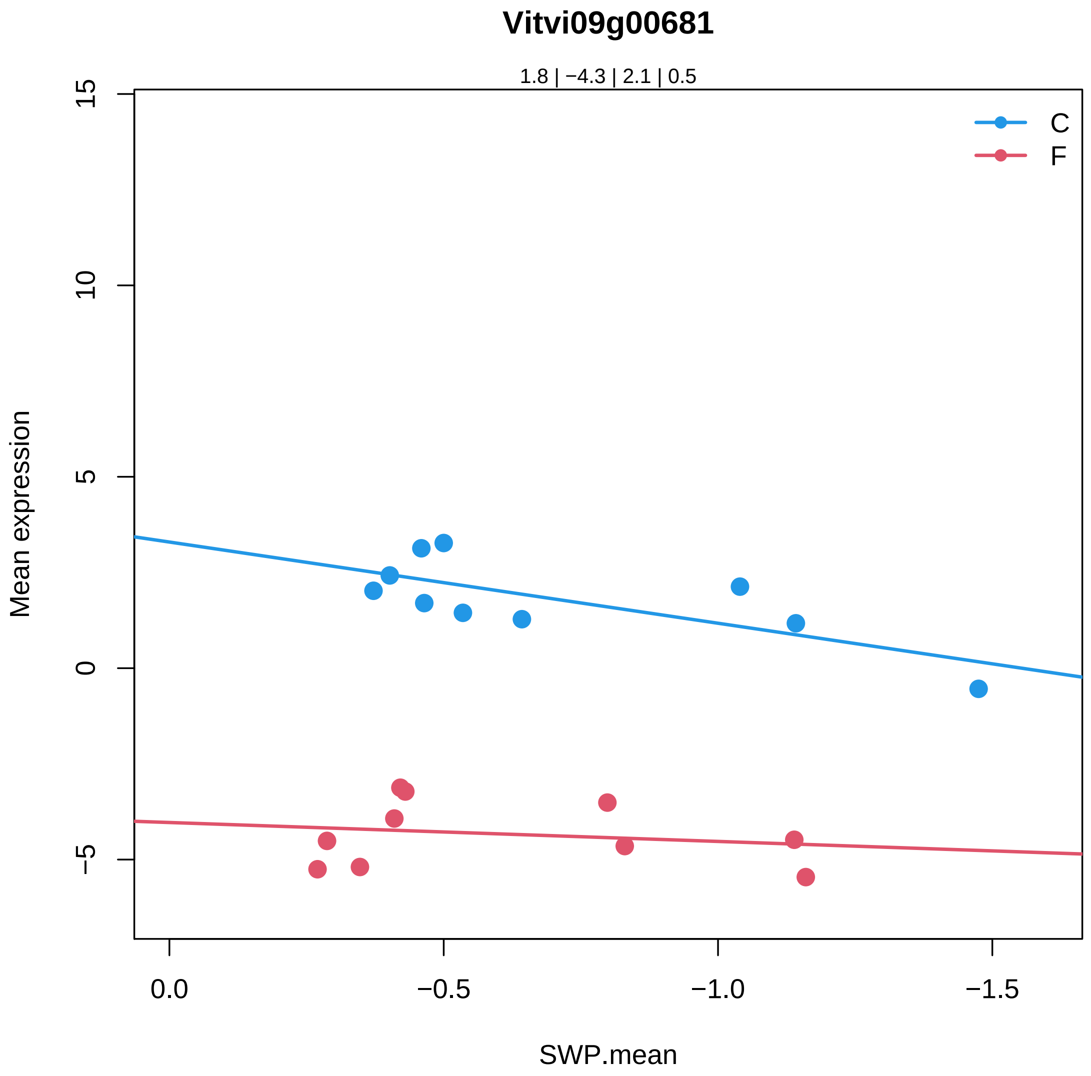
7.4.7 Vitvi09g00681: * type3 | type4

```
> 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        
```



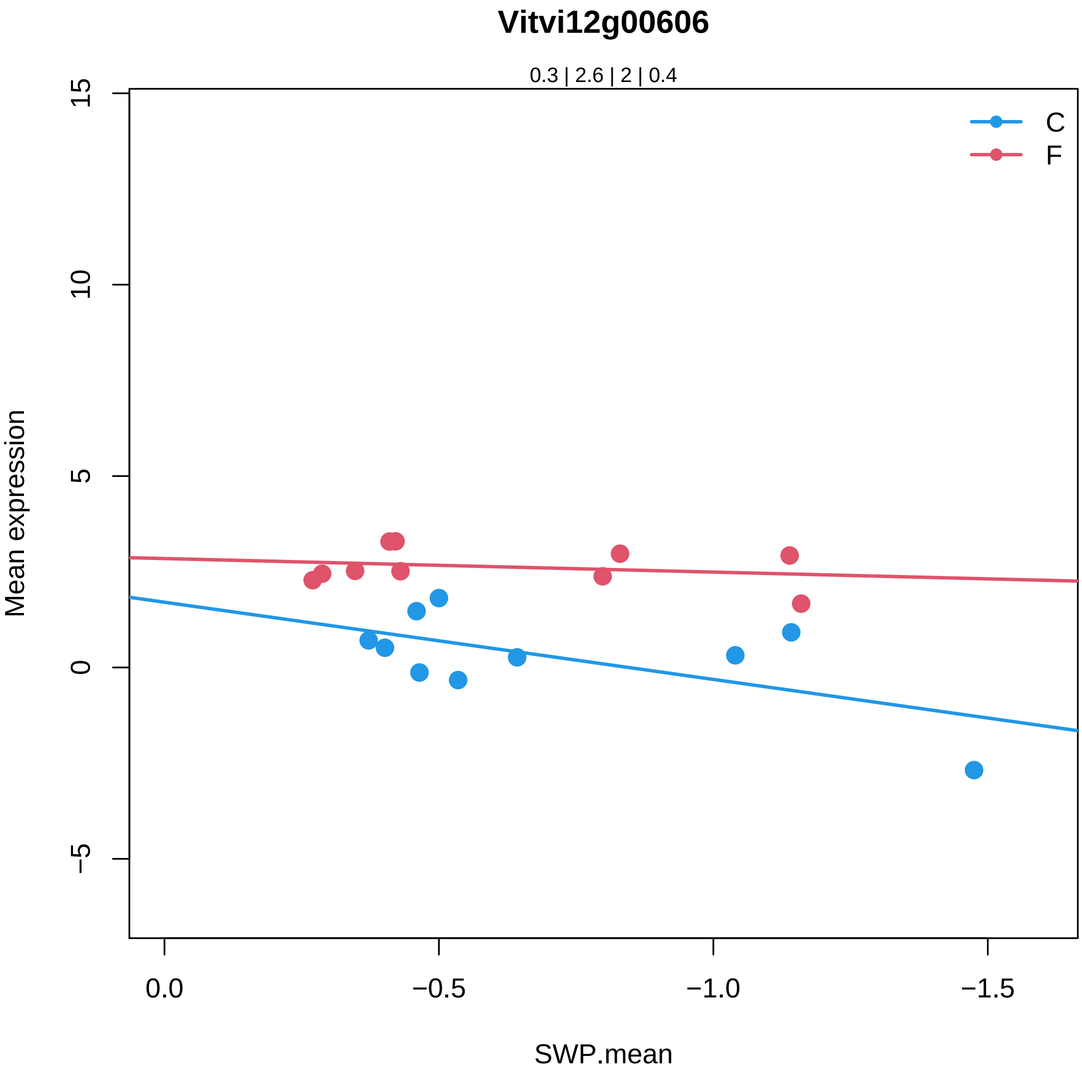
7.4.8 Vitvi12g00606: * type3 | type4

```
> 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

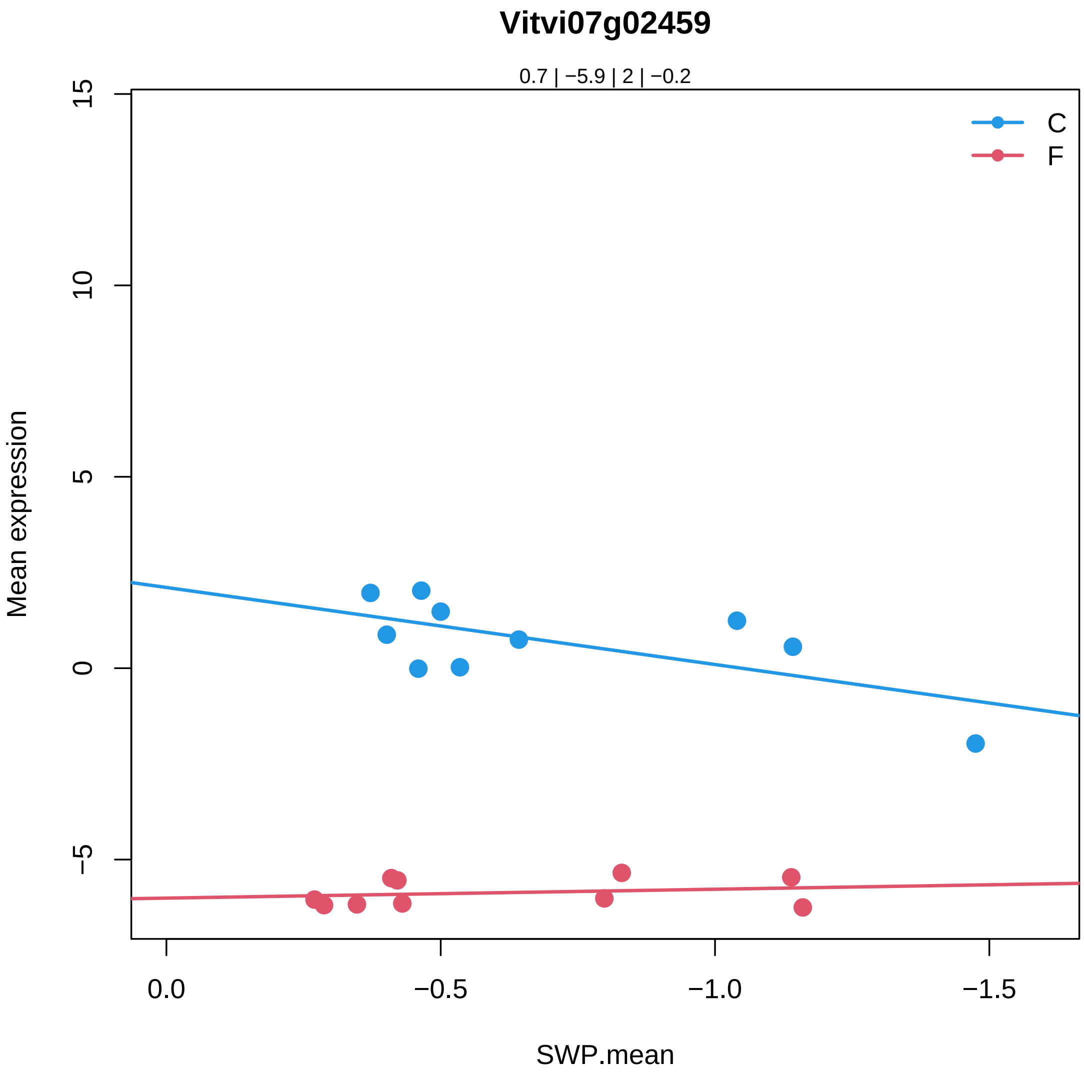
7.4.9 Vitvi07g02459: * type3

```
> 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
```



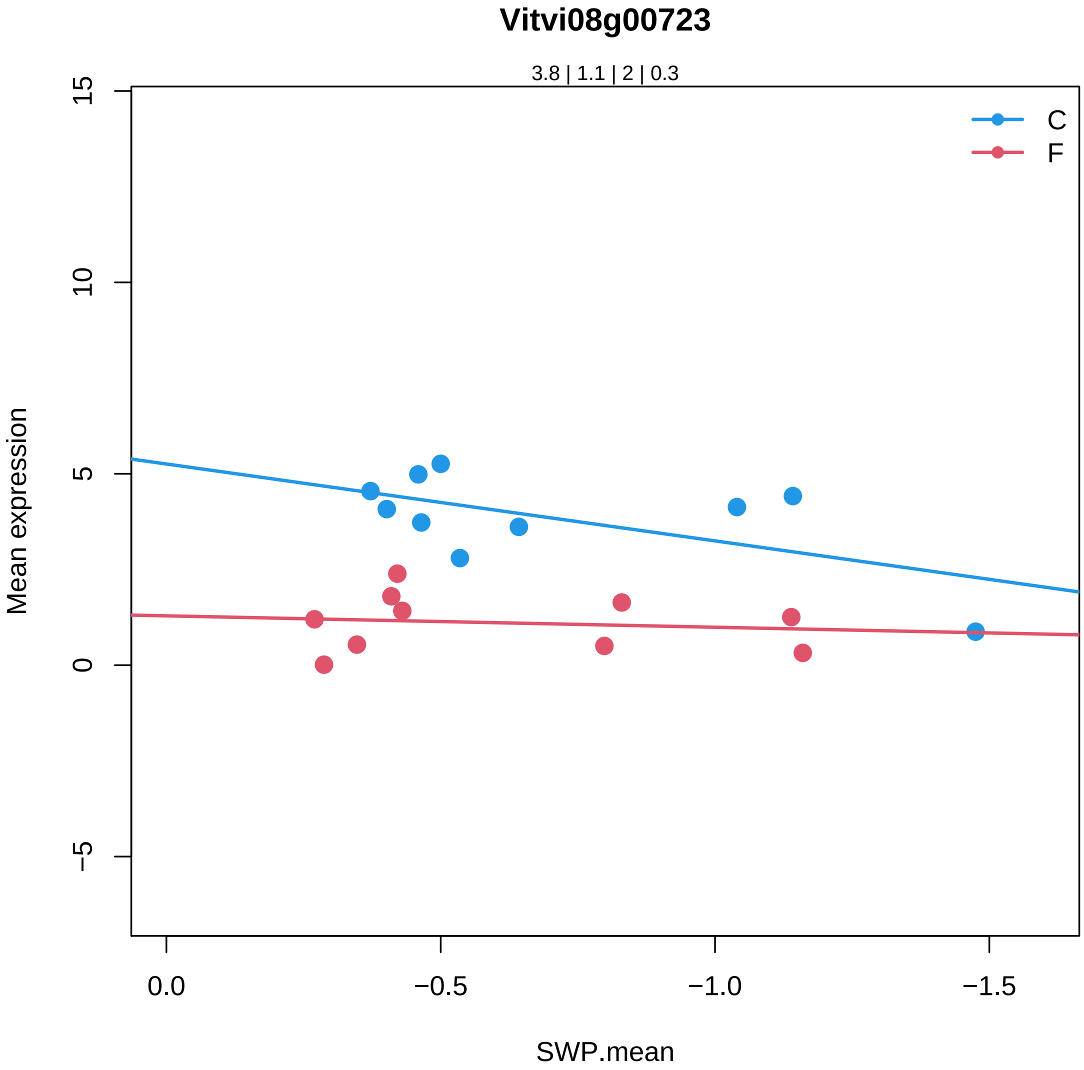
7.4.10 Vitvi08g00723: * type3 | type4

```
> 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        
```



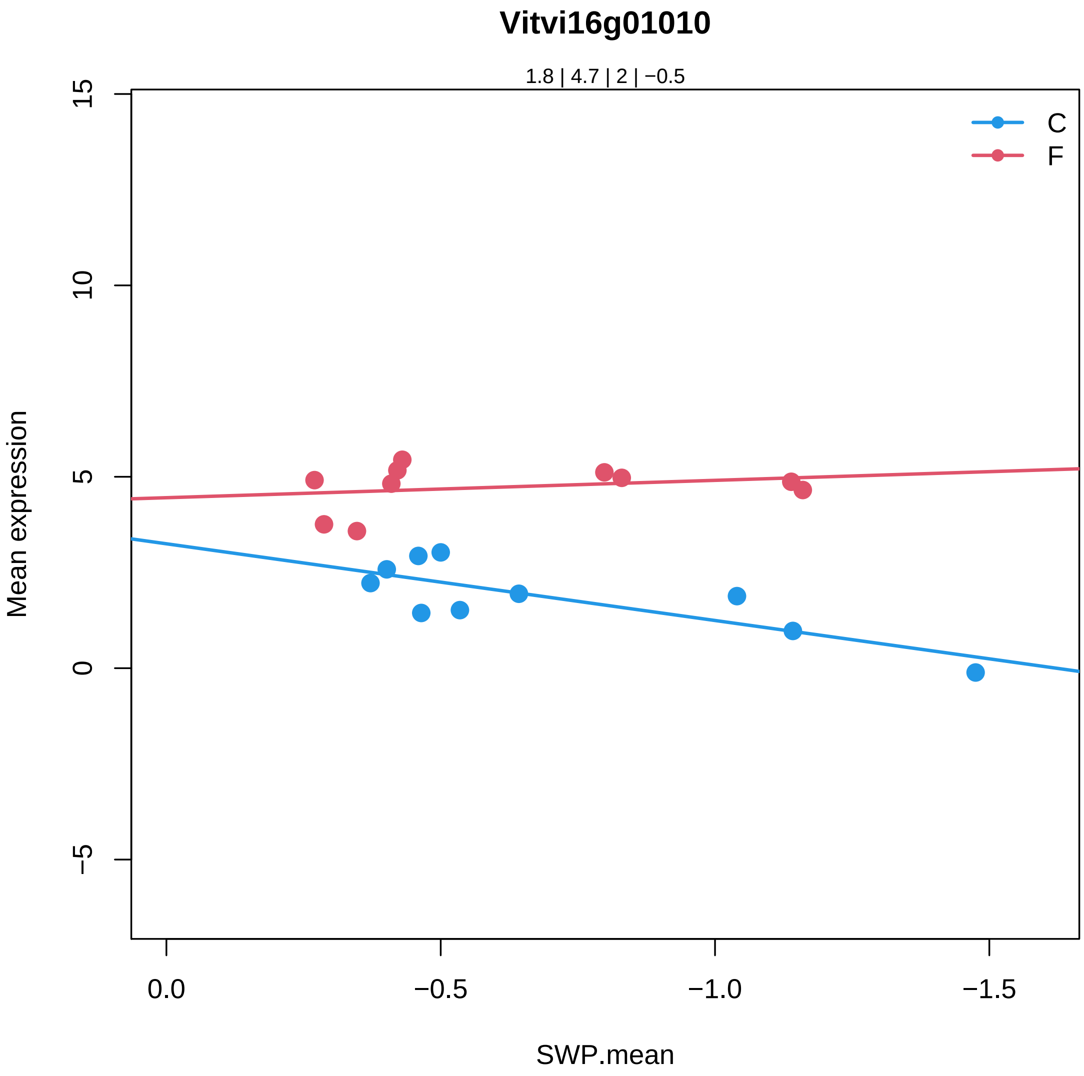
7.4.11 Vitvi16g01010: * type3

```
> 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
```



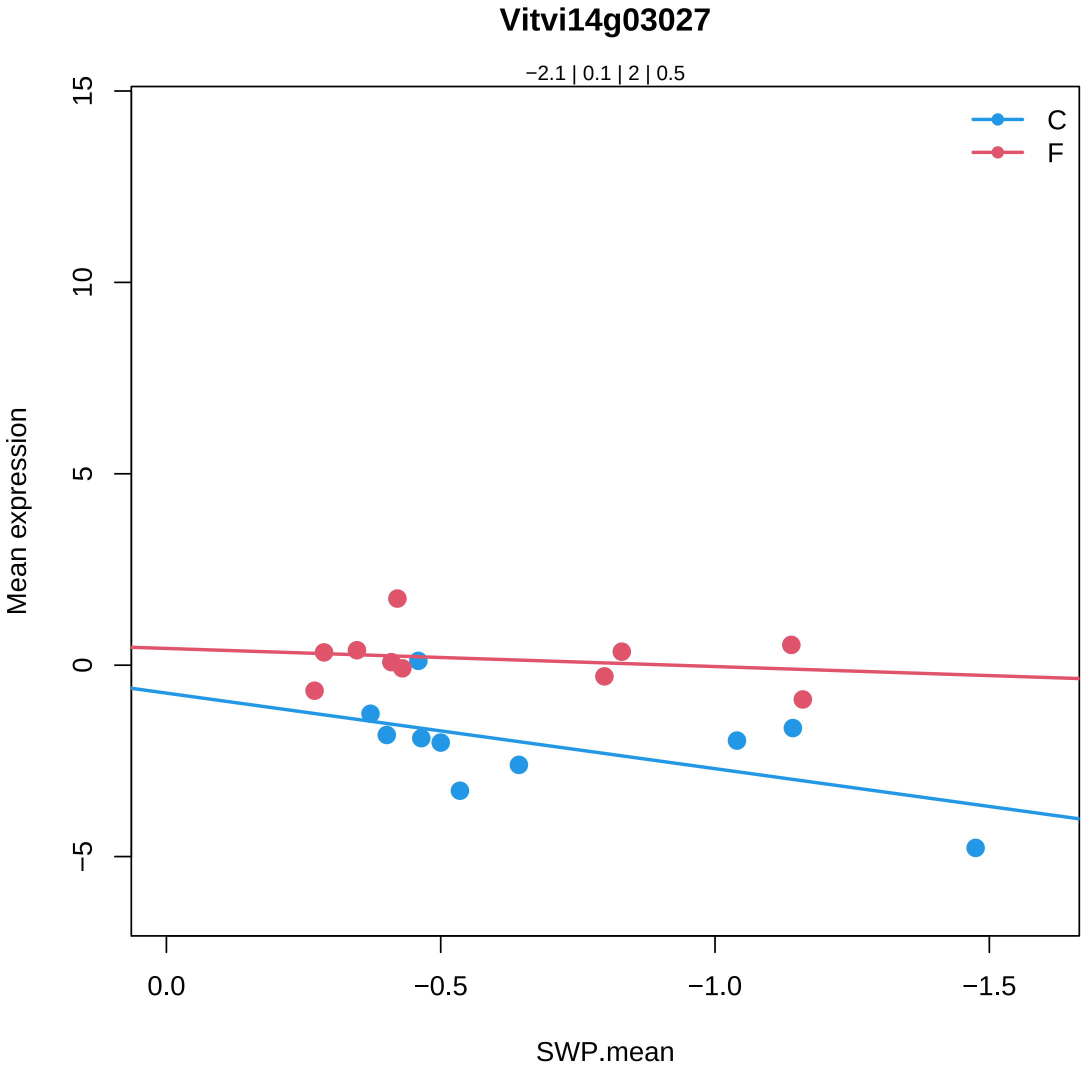
7.4.12 Vitvi14g03027: * type3

```
> 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
```



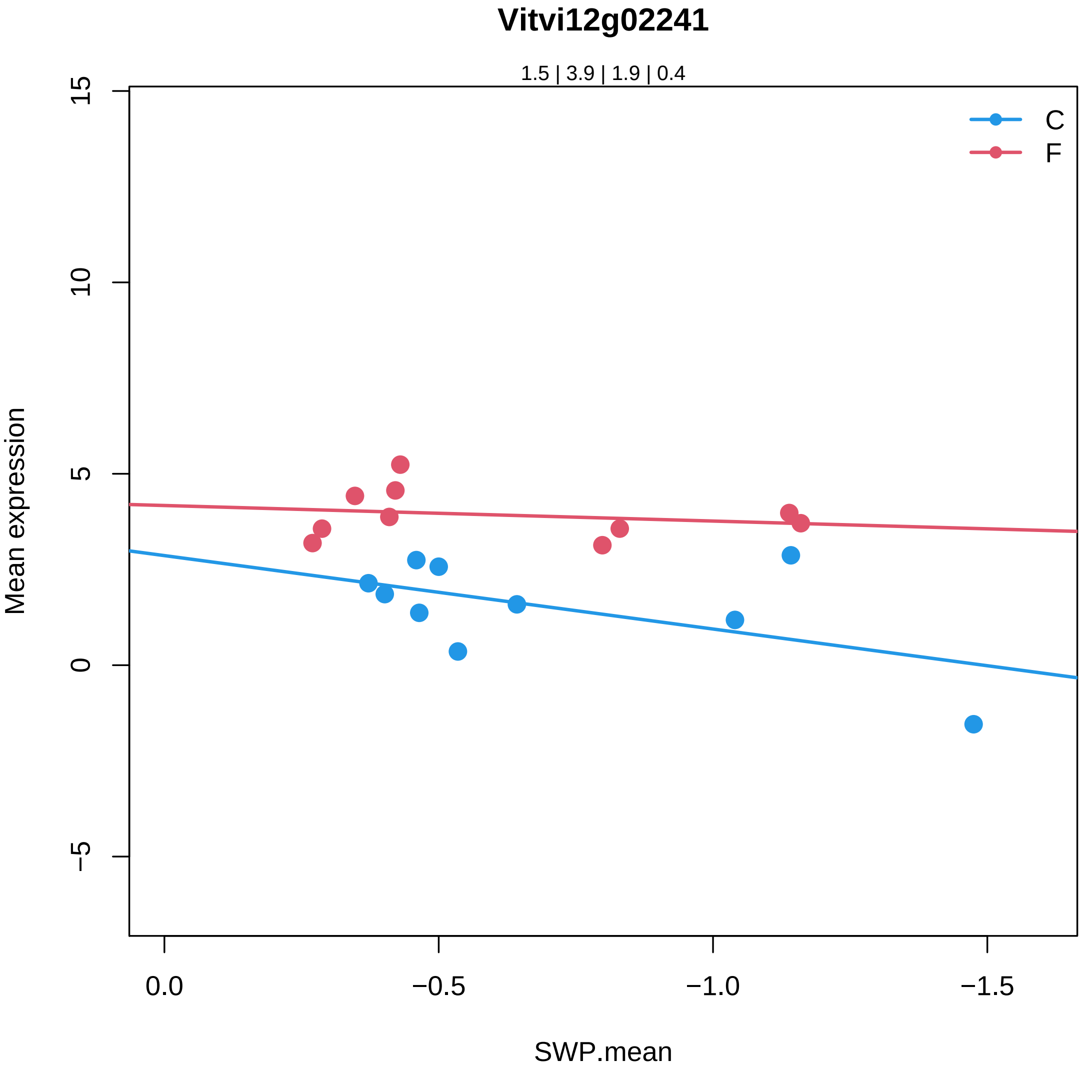
7.4.13 Vitvi12g02241: * type3

```
> 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
```



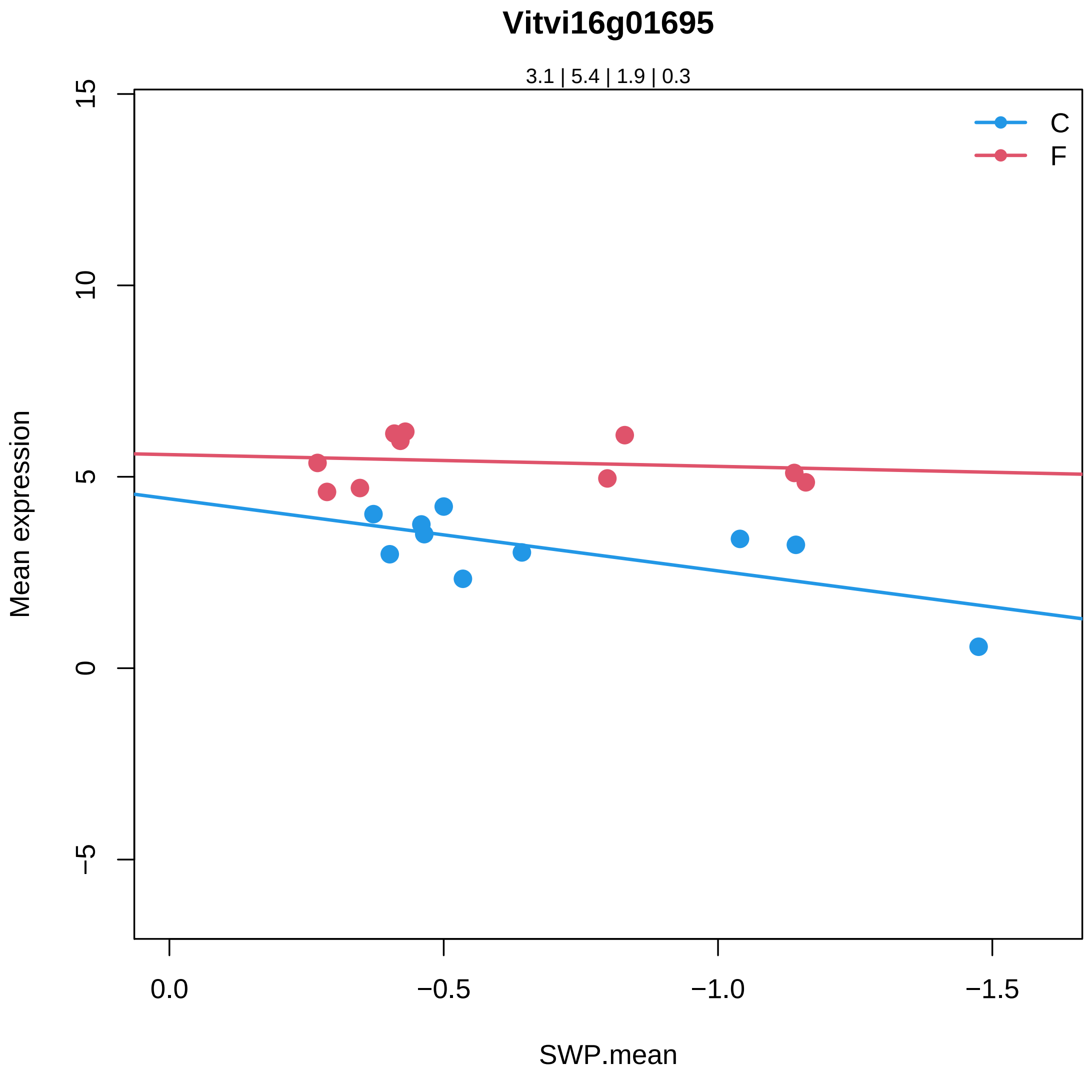
7.4.14 Vitvi16g01695: * type3

```
> 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        
```



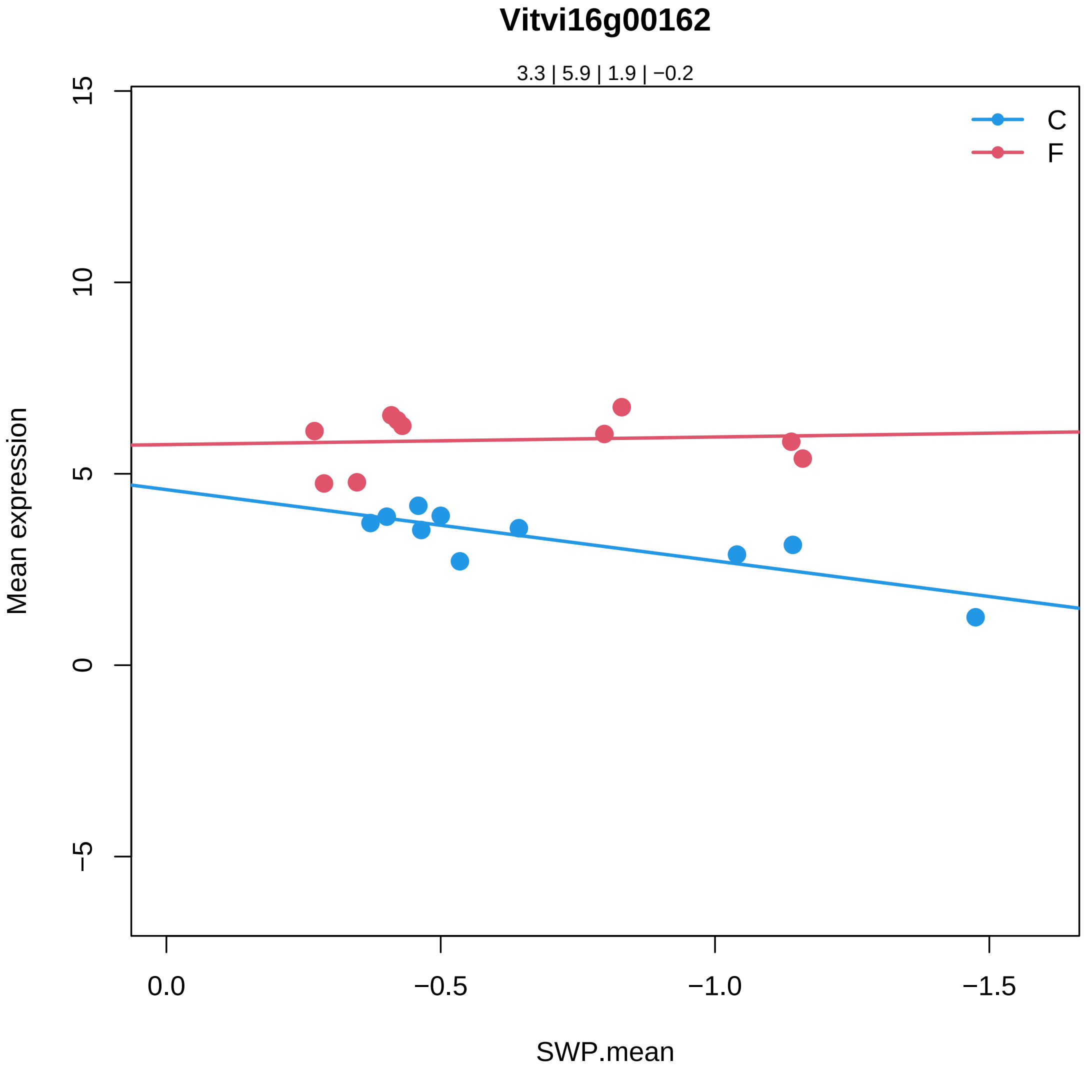
7.4.15 Vitvi16g00162: * type3

```
> 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
```



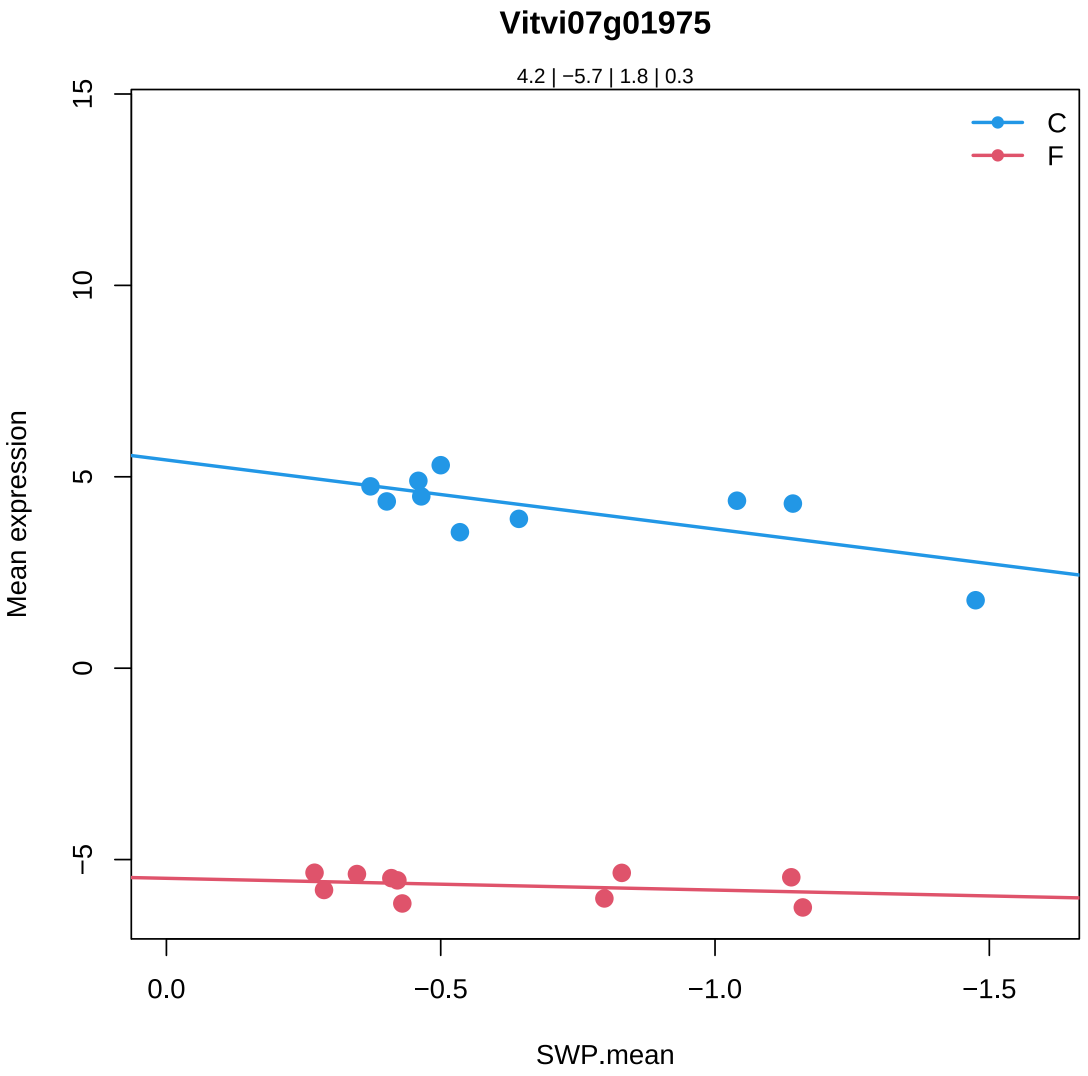
7.4.16 Vitvi07g01975: * type3

```
> 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
```



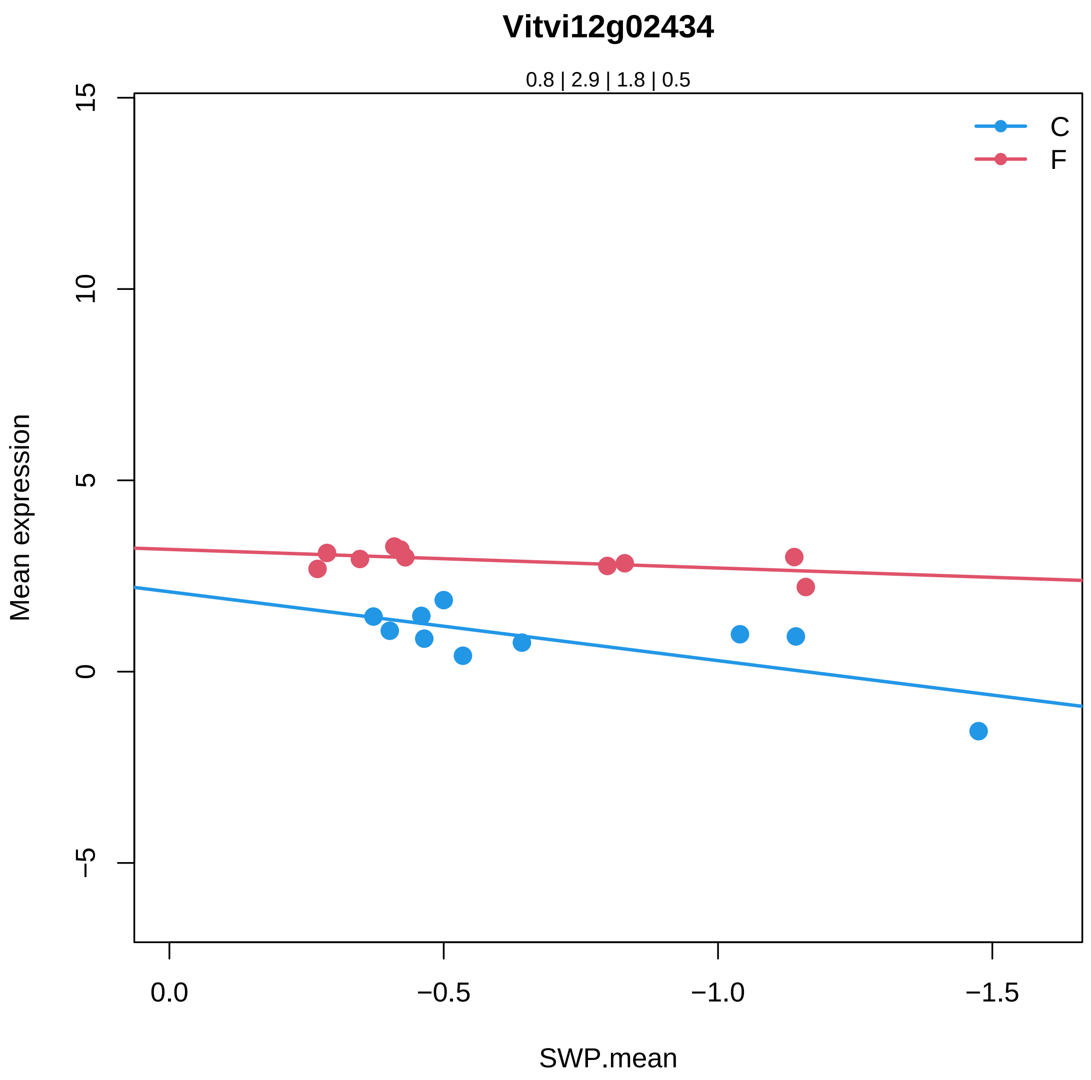
7.4.17 Vitvi12g02434: * type3

```
> 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

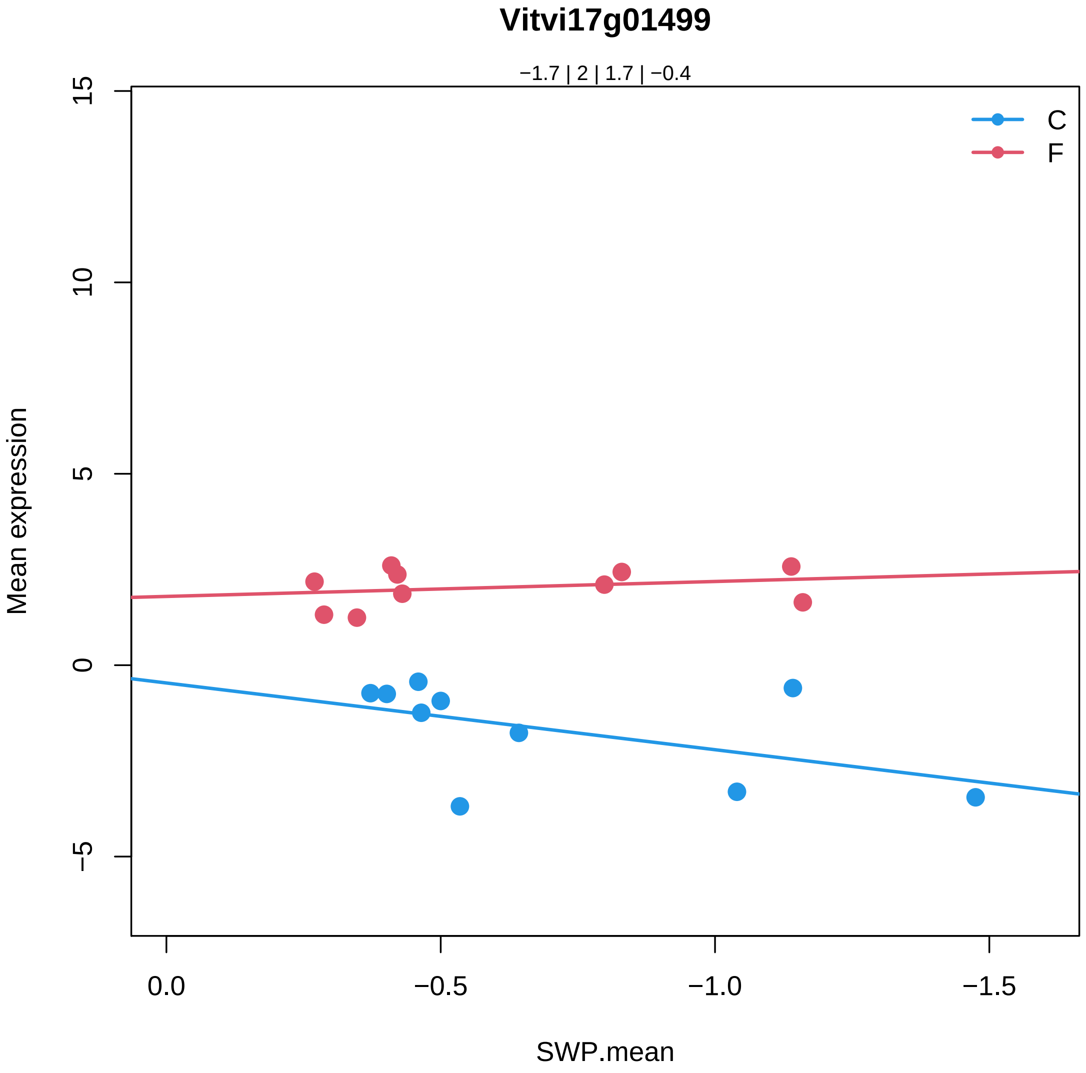
7.4.18 Vitvi17g01499: * type3

```
> 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        
```



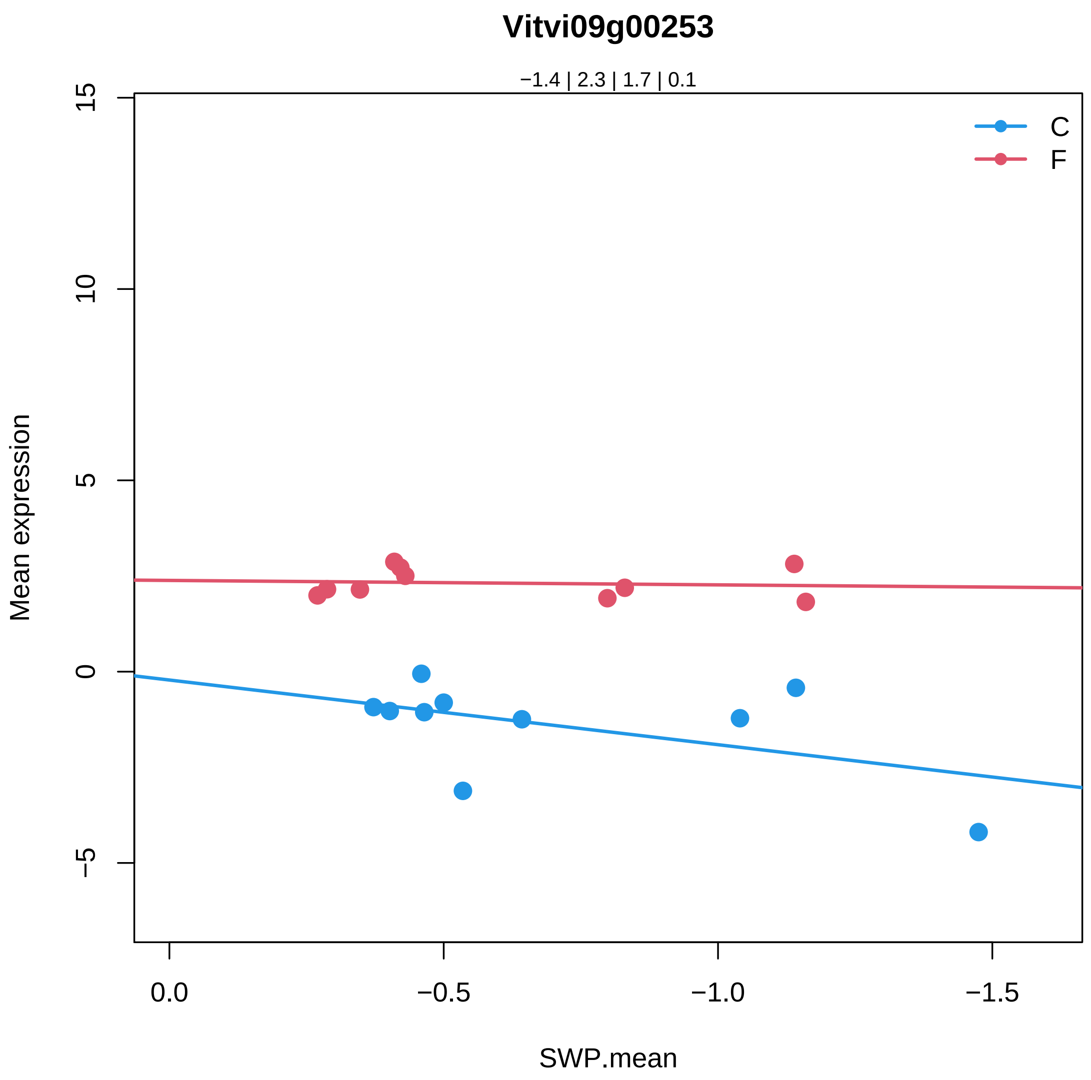
7.4.19 Vitvi09g00253: * type3

```
> 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

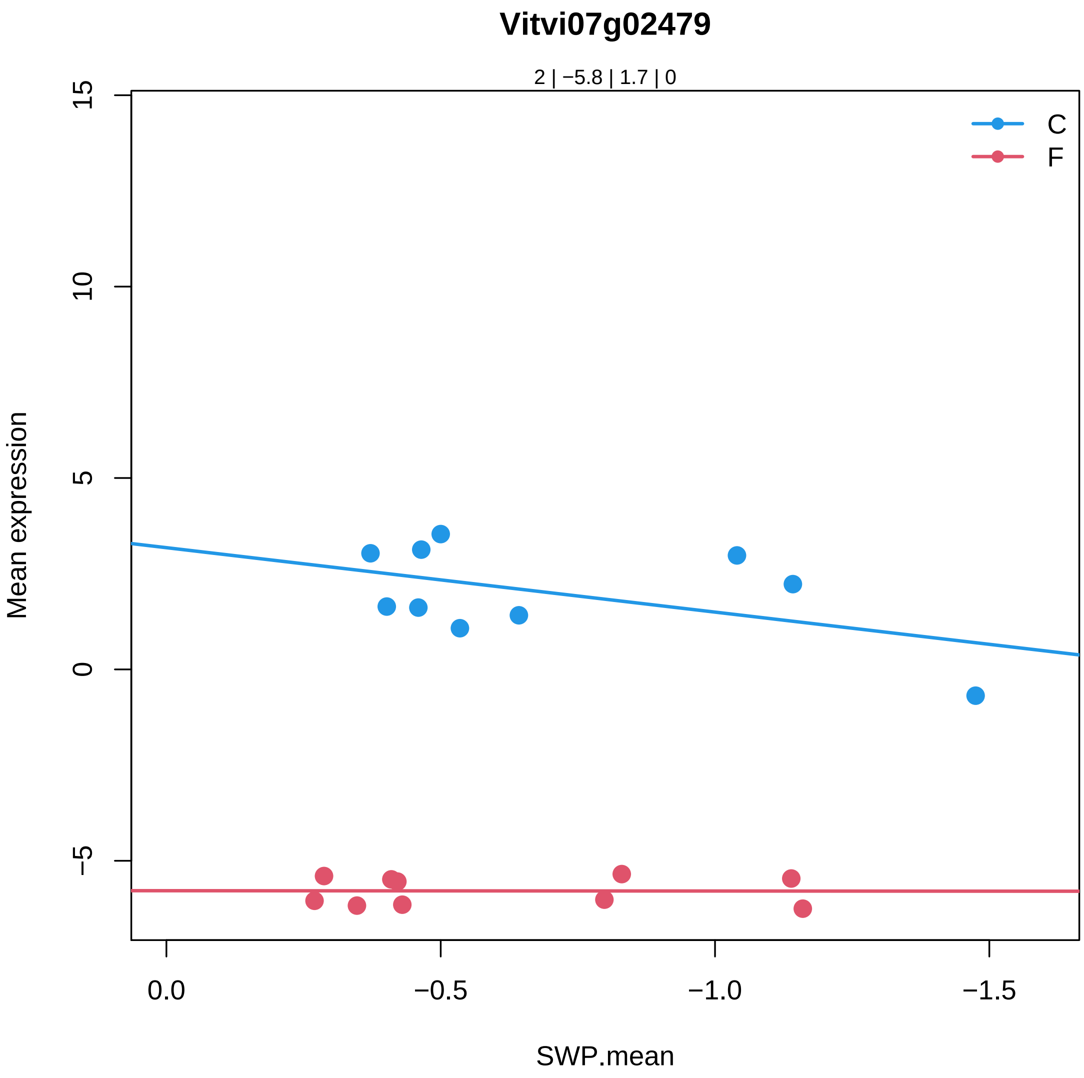
7.4.20 Vitvi07g02479: * type3

```
> 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        
```



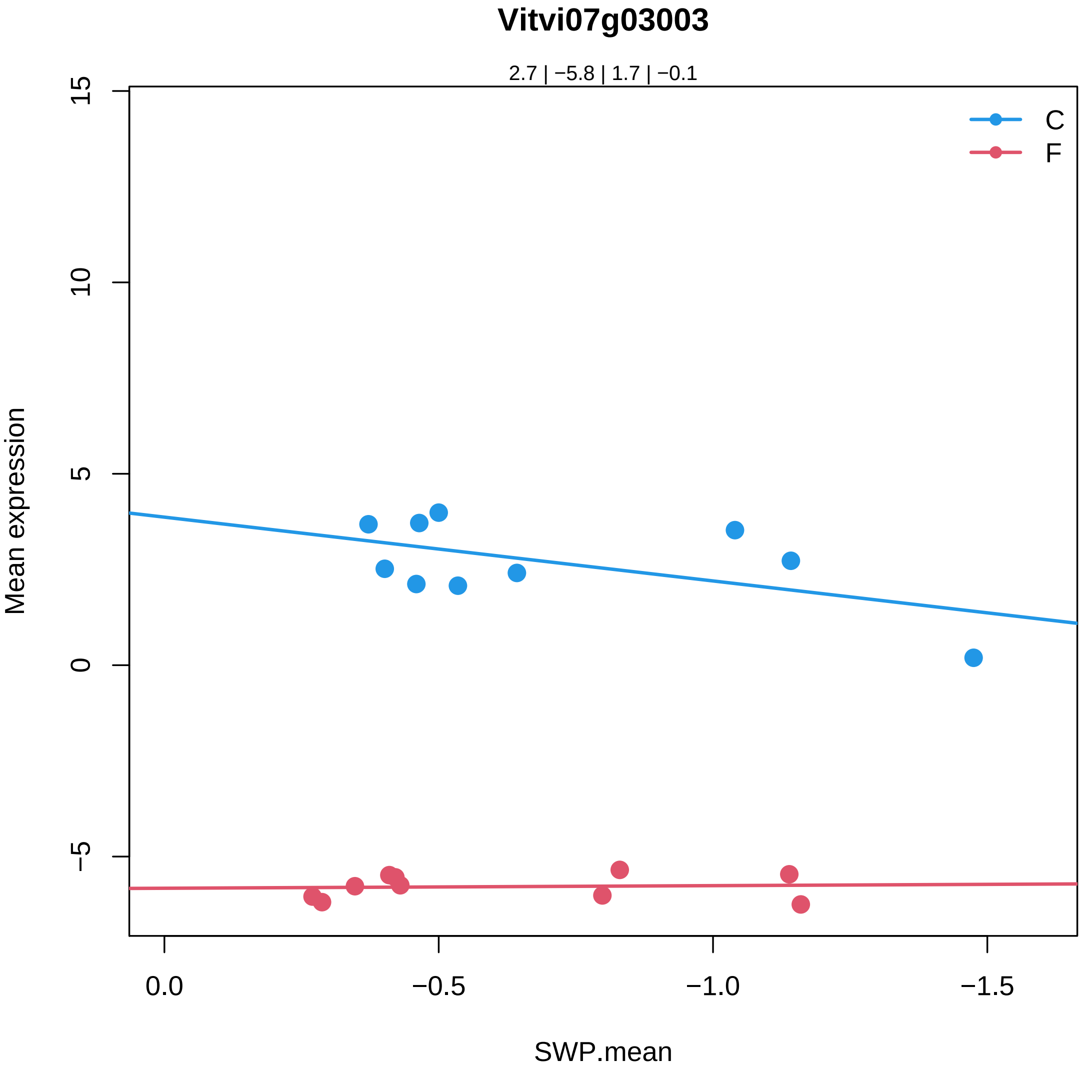
7.4.21 Vitvi07g03003: * type3

```
> 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        
```



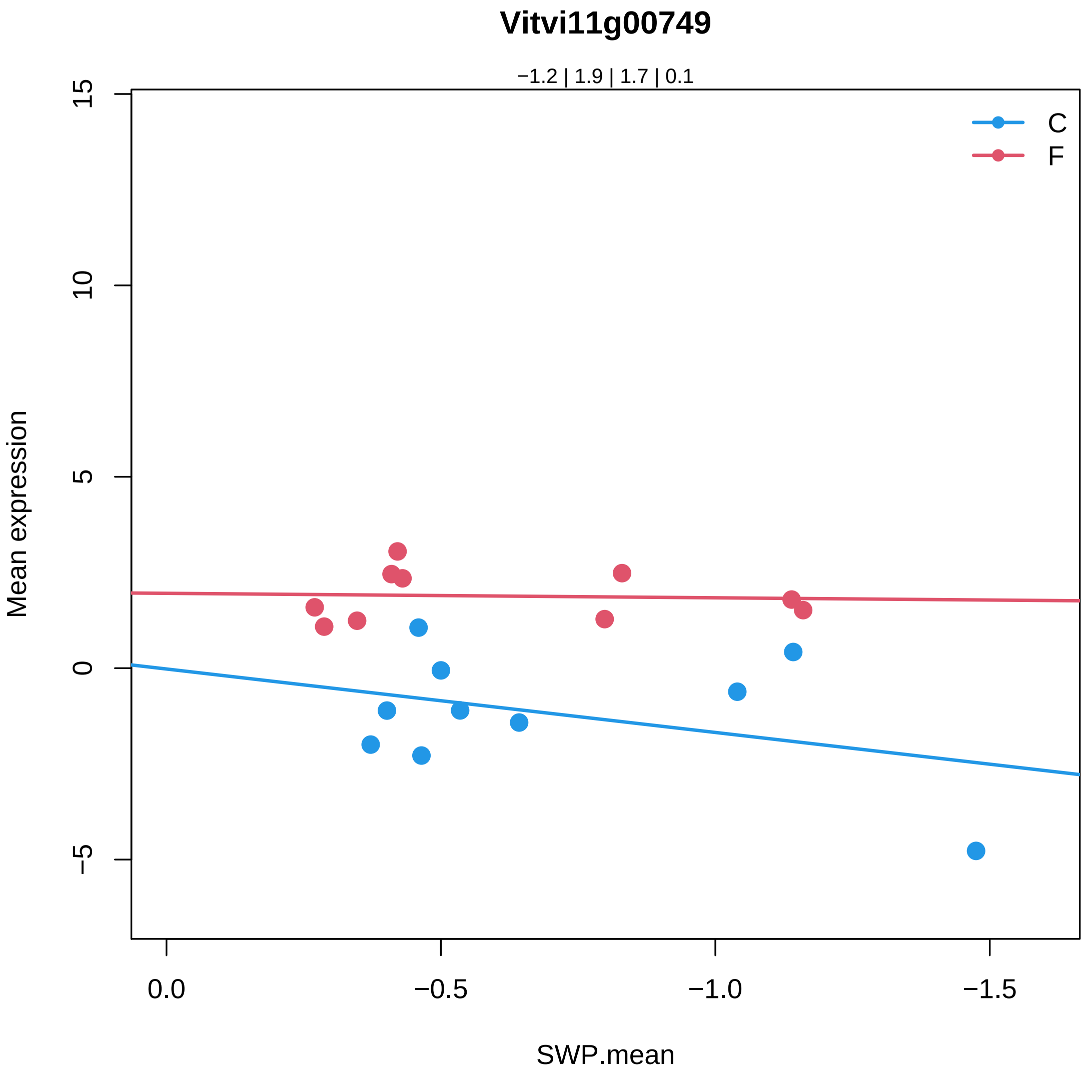
7.4.22 Vitvi11g00749: type3

```
> 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        
```



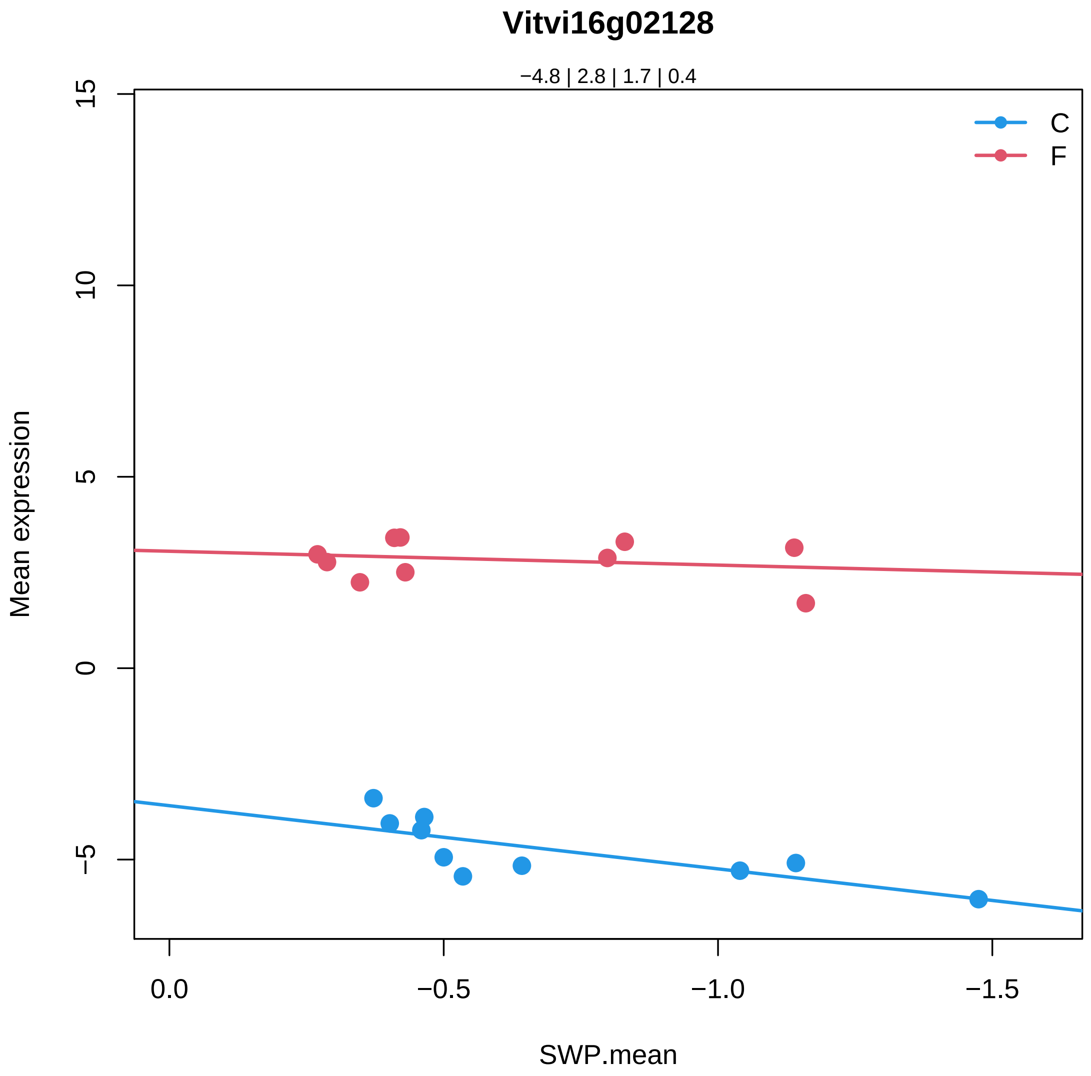
7.4.23 Vitvi16g02128: * type3

```
> 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
```



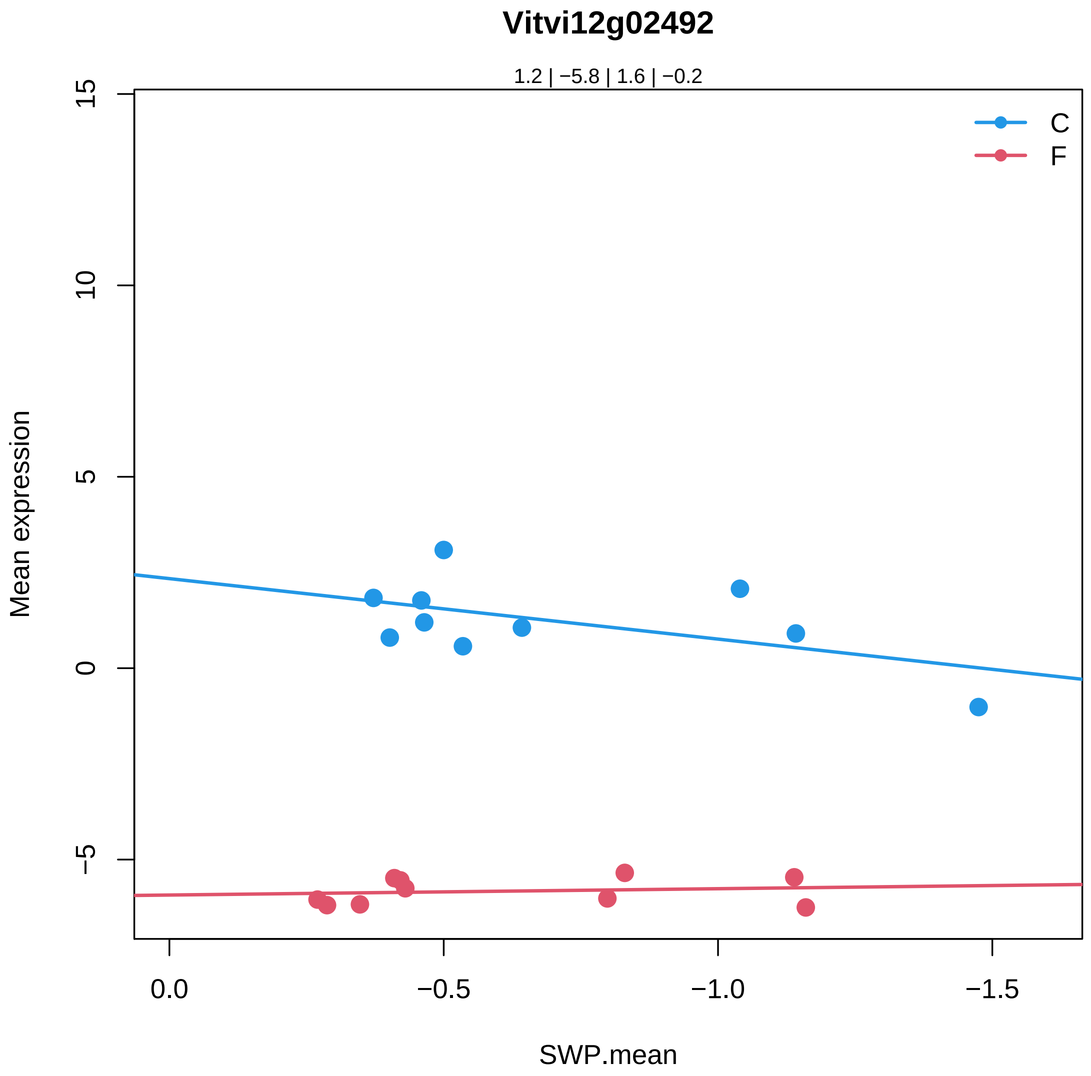
7.4.24 Vitvi12g02492: * type3

```
> 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        
```



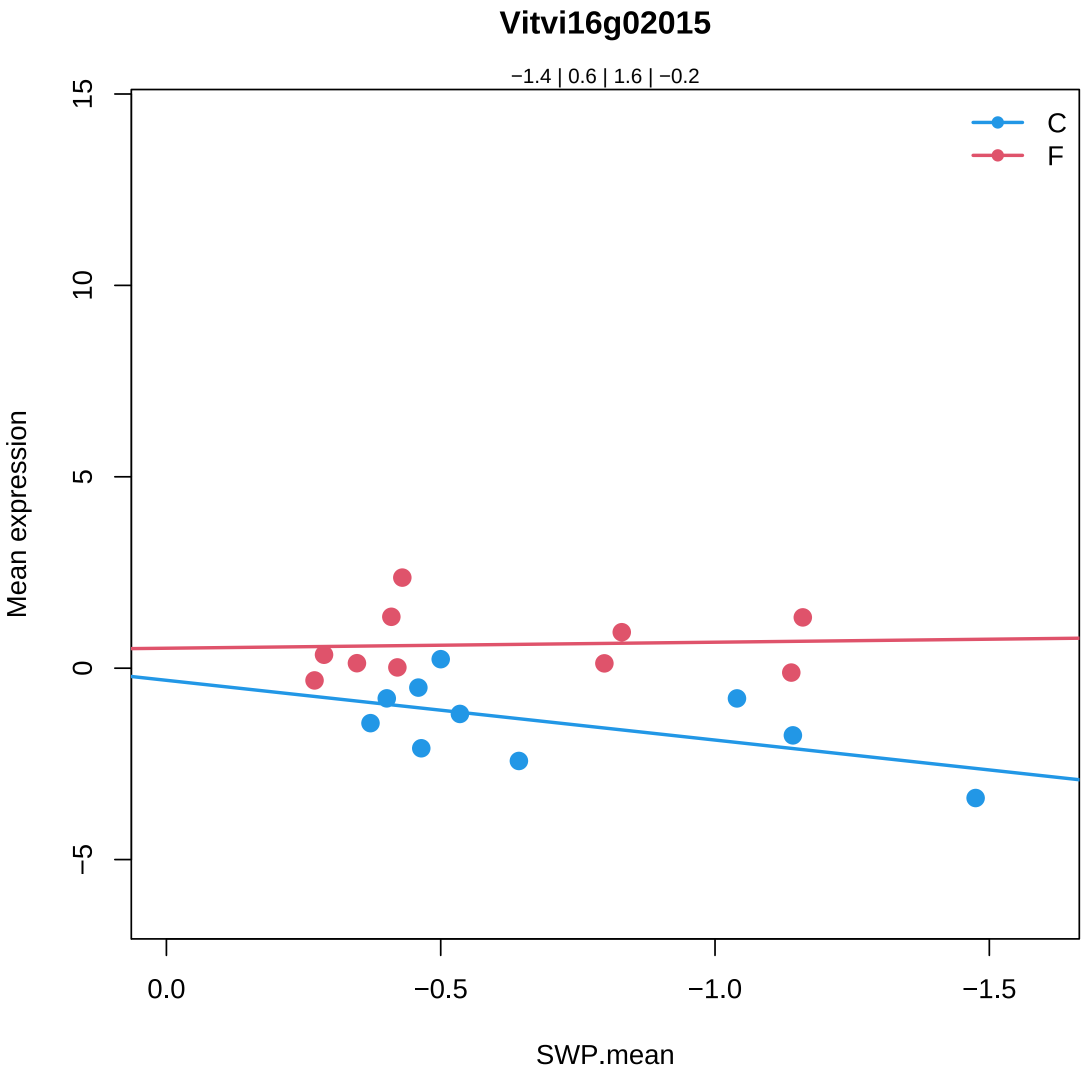
7.4.25 Vitvi16g02015: * type3

```
> 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
```



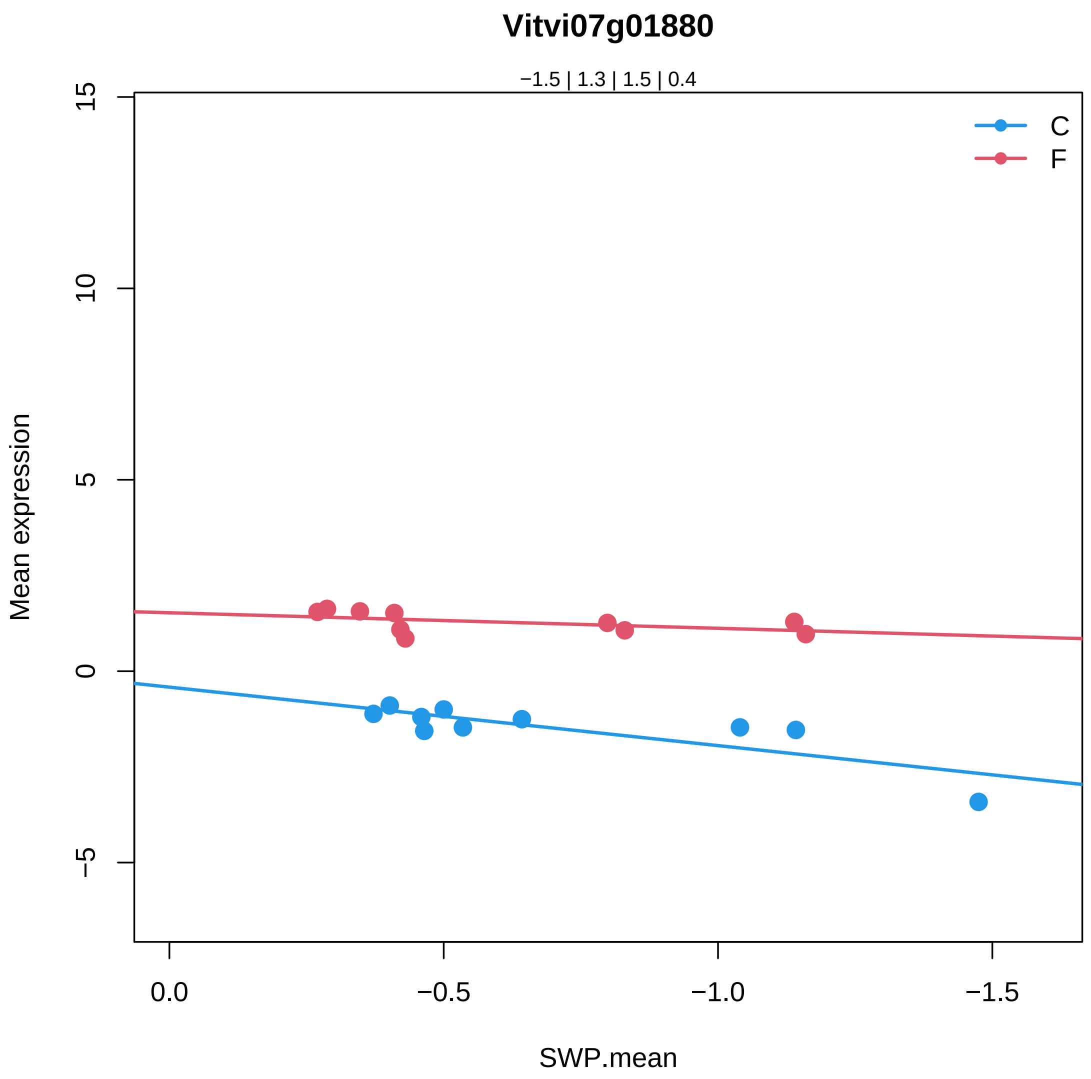
7.4.26 Vitvi07g01880: * type3

```
> 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
```



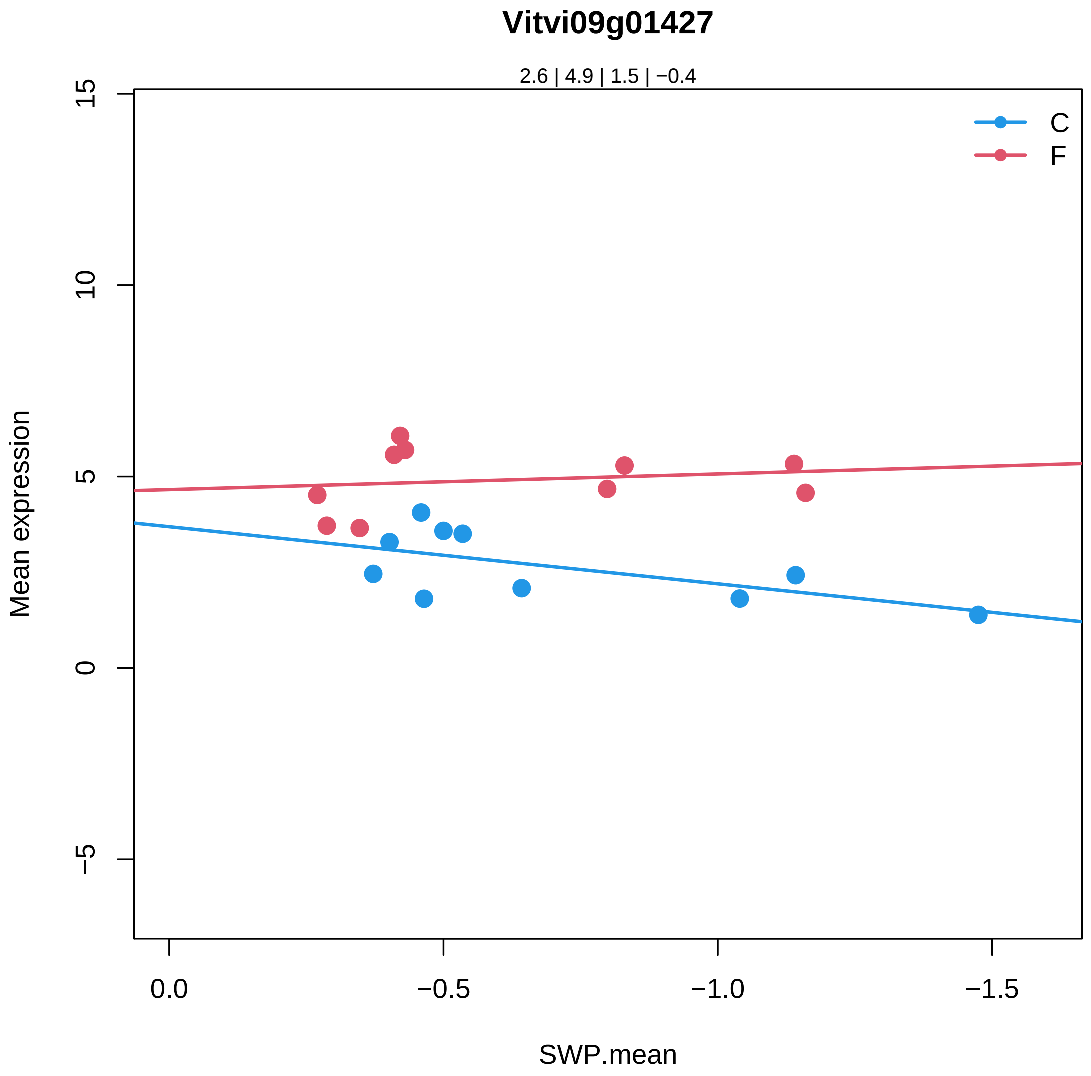
7.4.27 Vitvi09g01427: * type3

```
> 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        
```



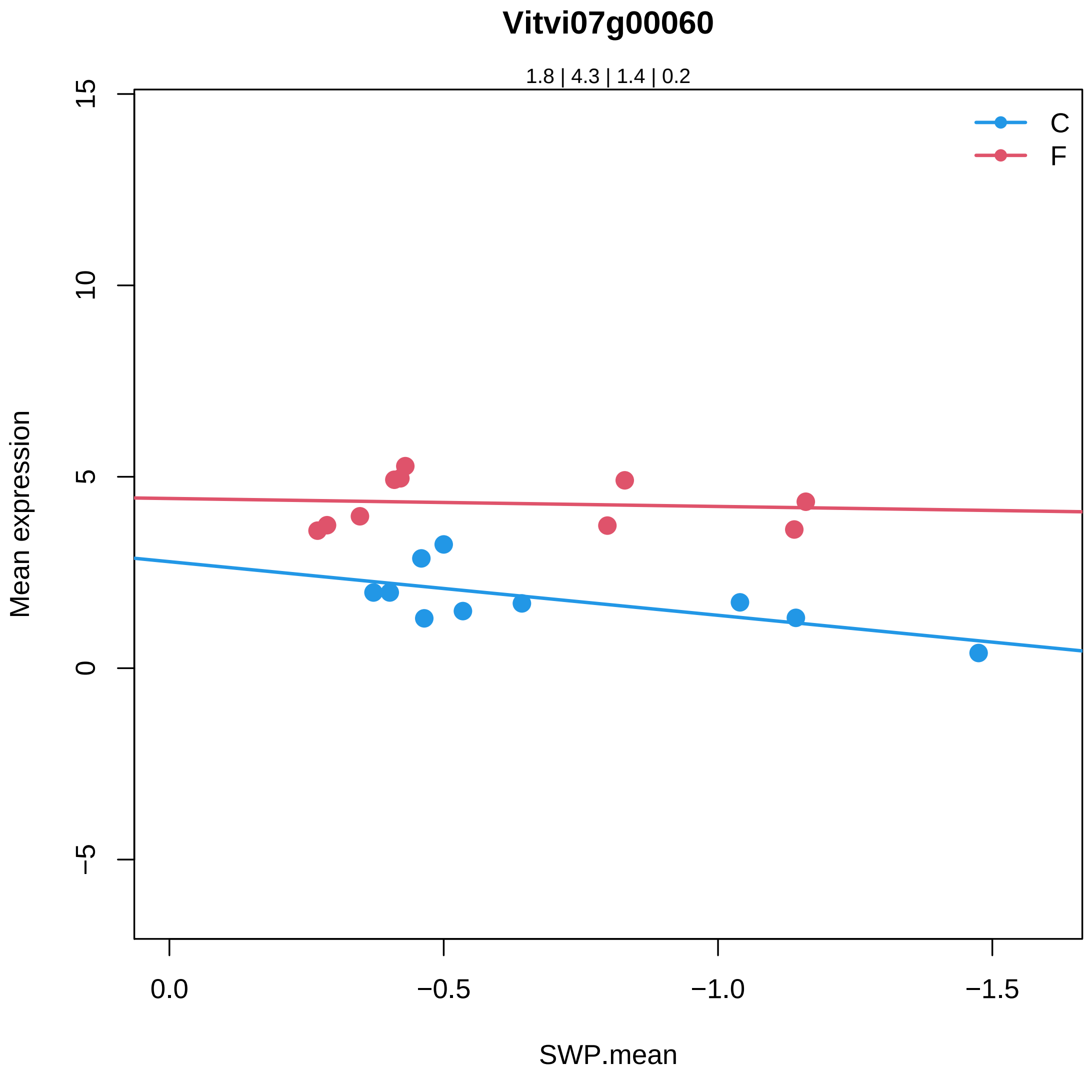
7.4.28 Vitvi07g00060: * type3

```
> 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
```



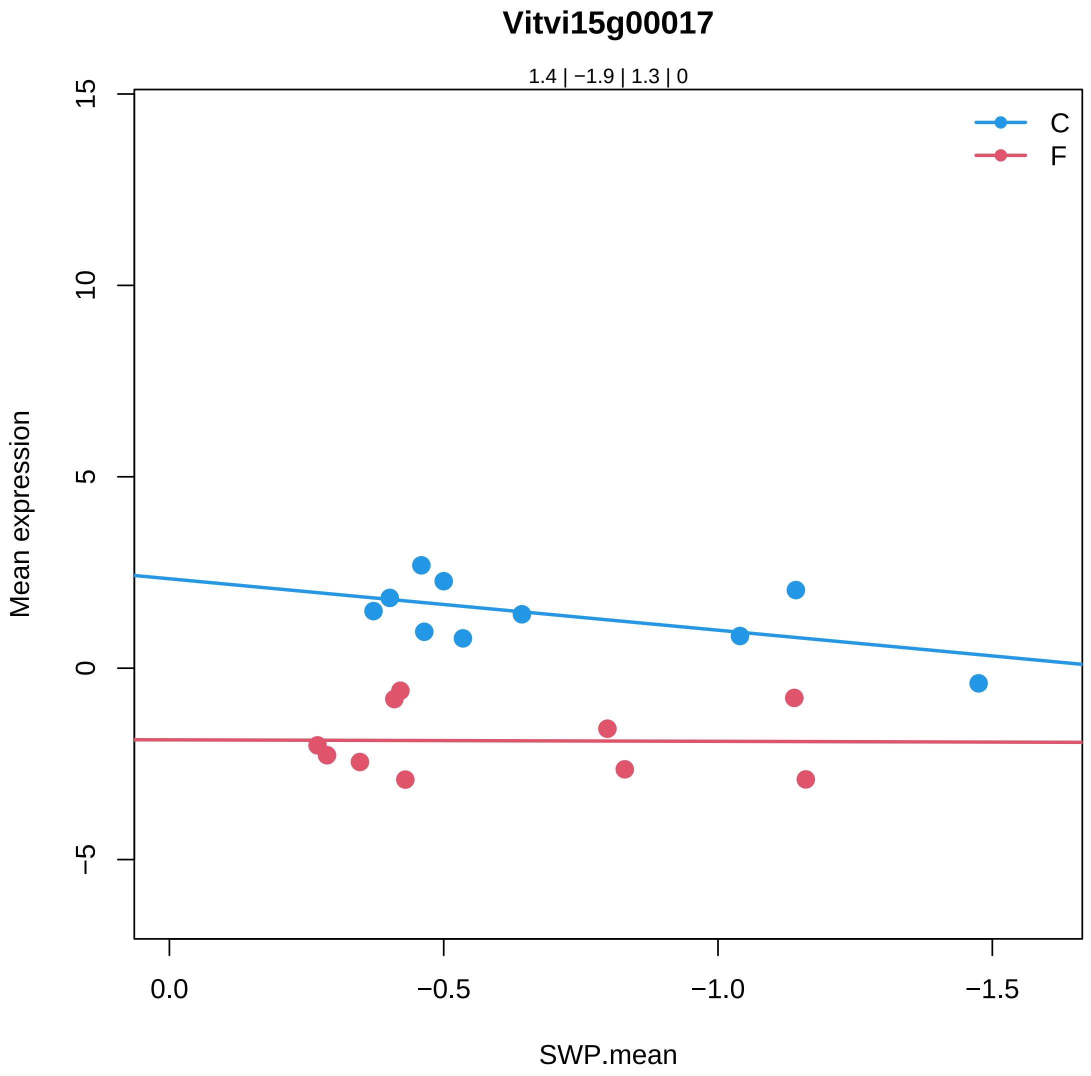
7.4.29 Vitvi15g00017: type3

```
> 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
```



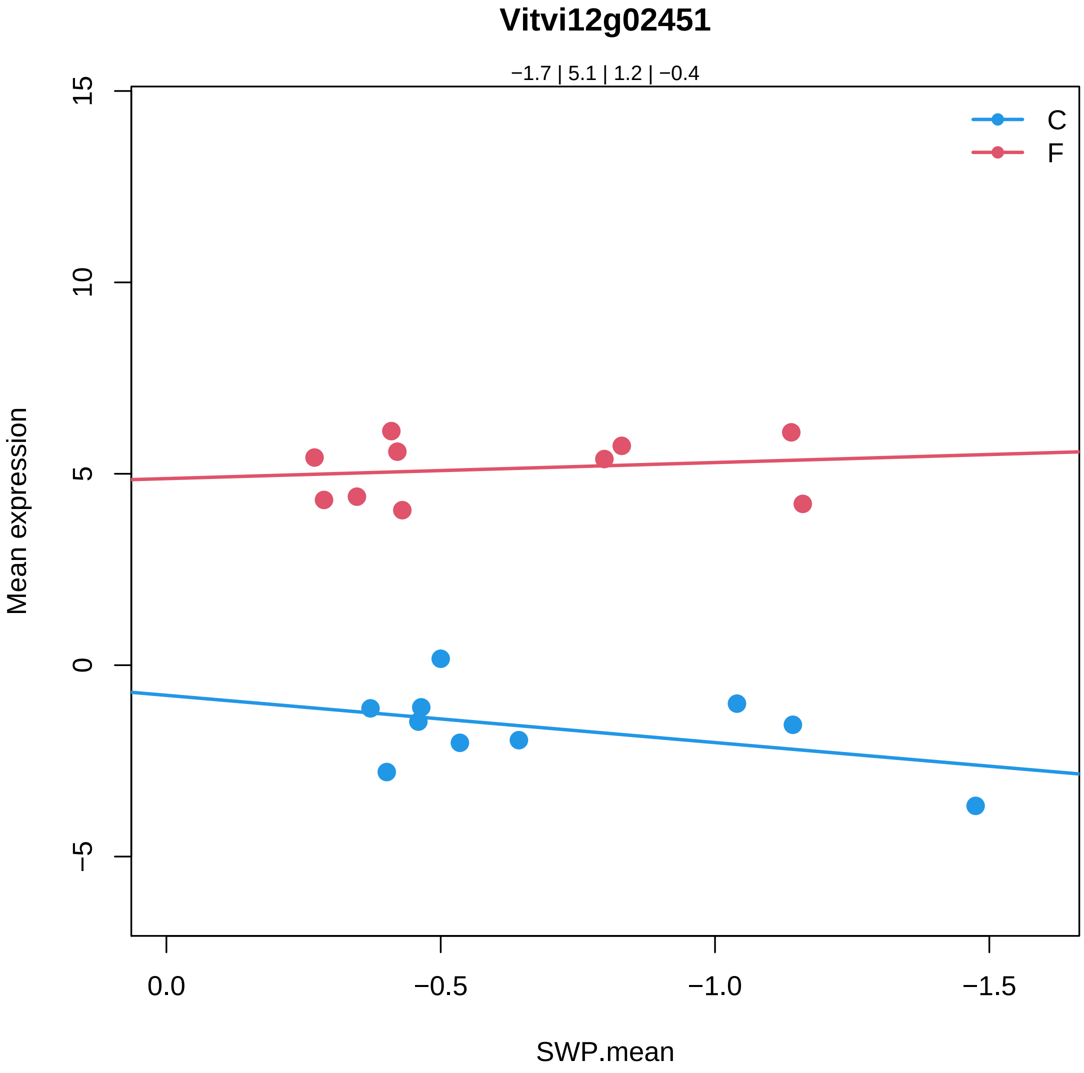
7.4.30 Vitvi12g02451: type3

```
> 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
```



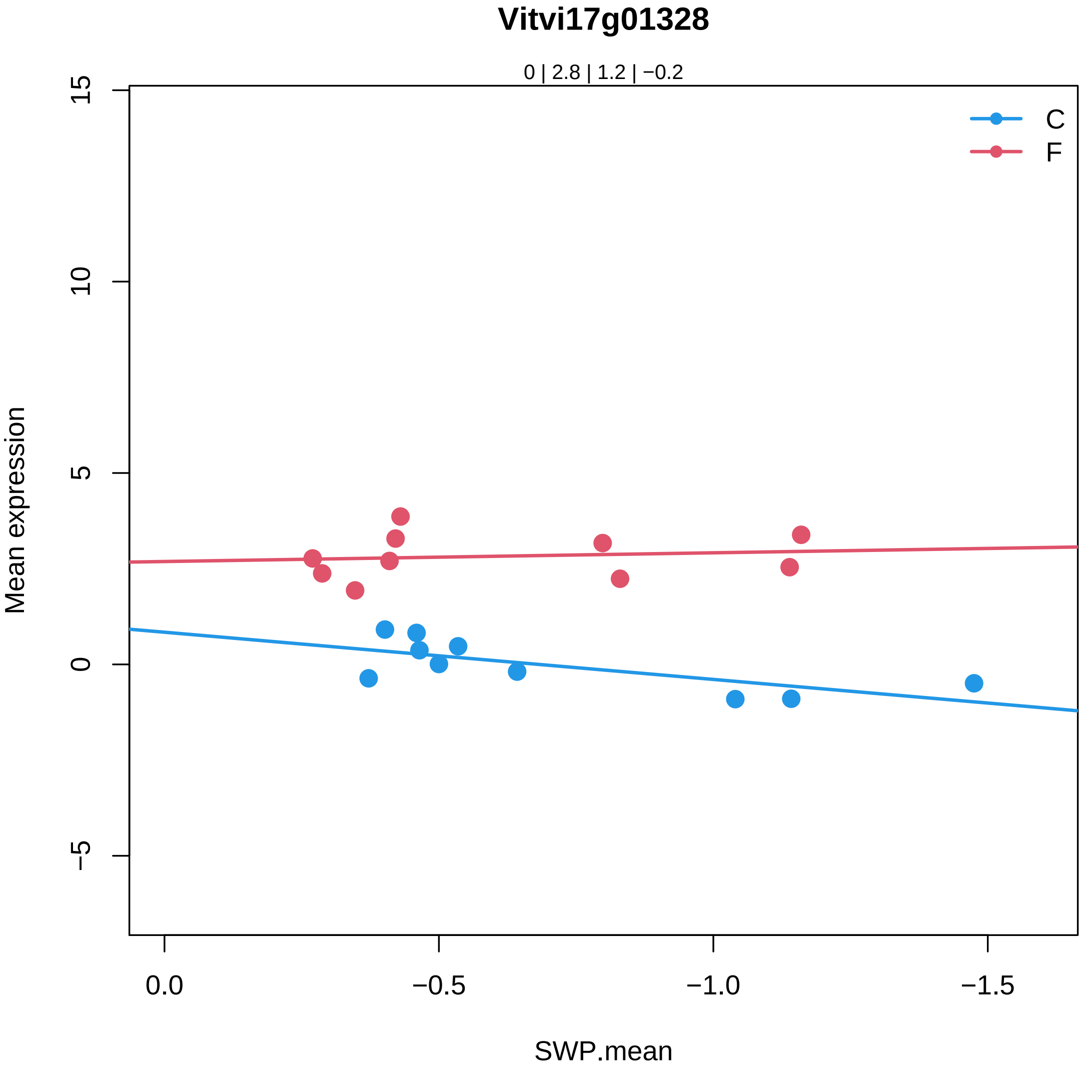
7.4.31 Vitvi17g01328: * type3

```
> 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
```



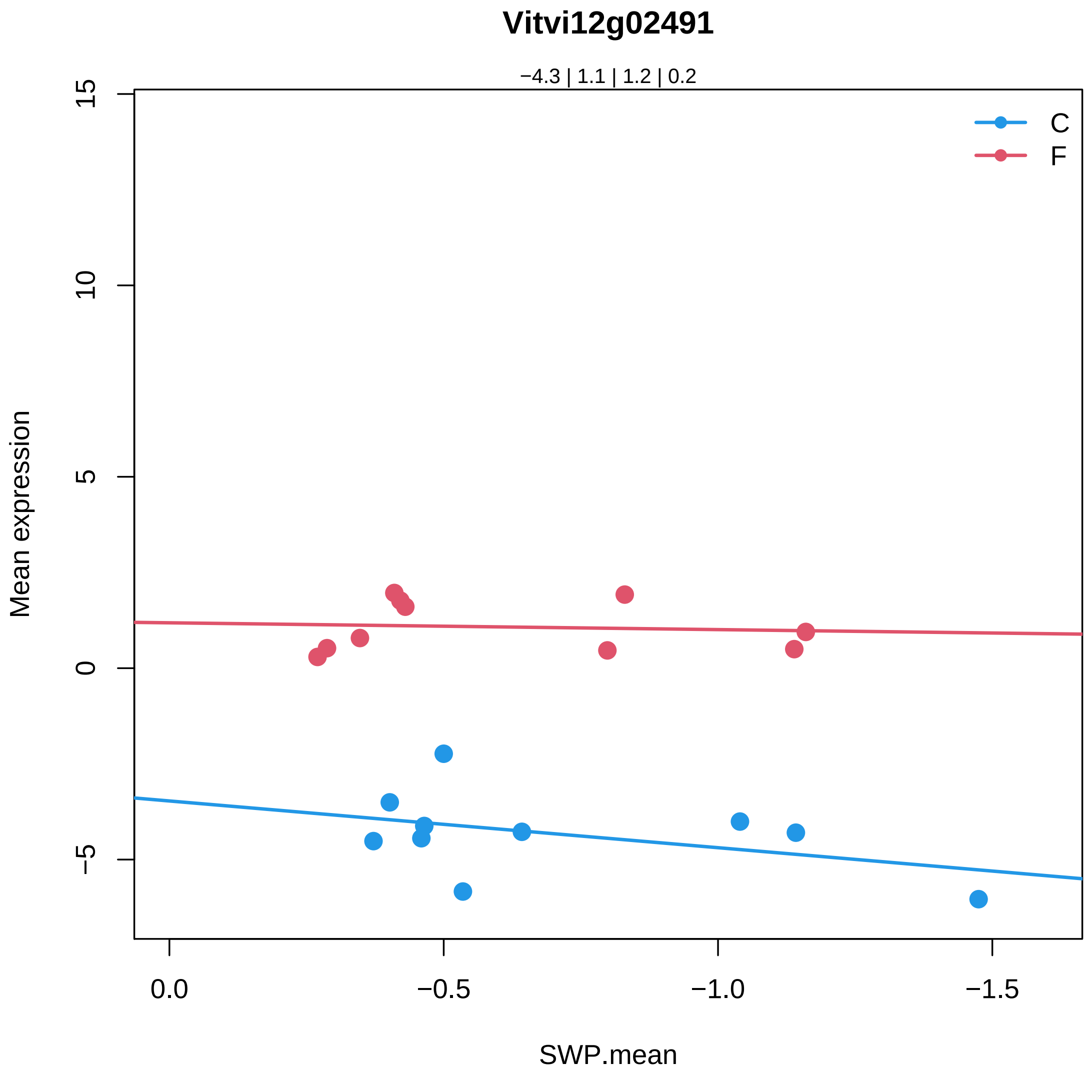
7.4.32 Vitvi12g02491: type3

```
> 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
```



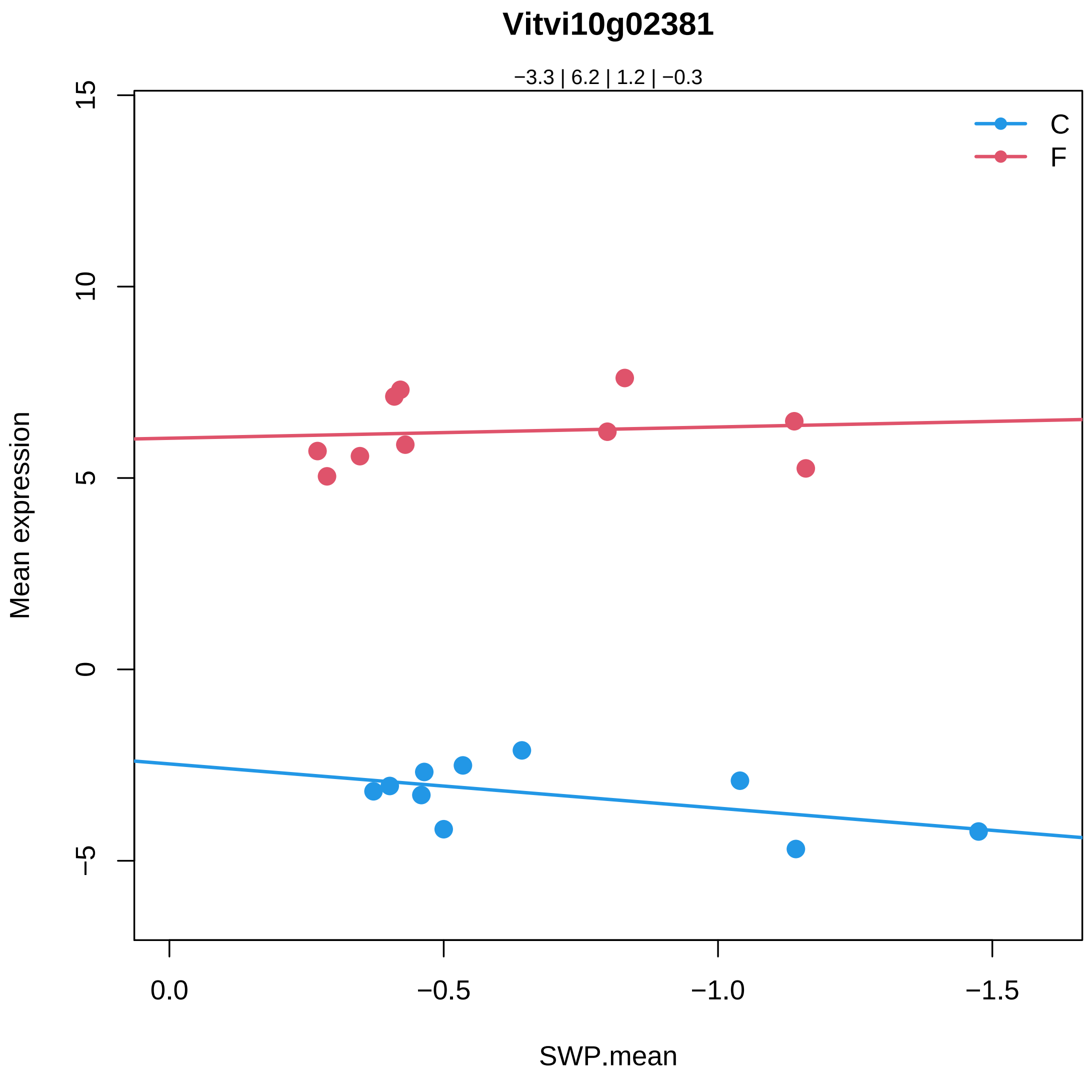
7.4.33 Vitvi10g02381: type3

```
> 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
```



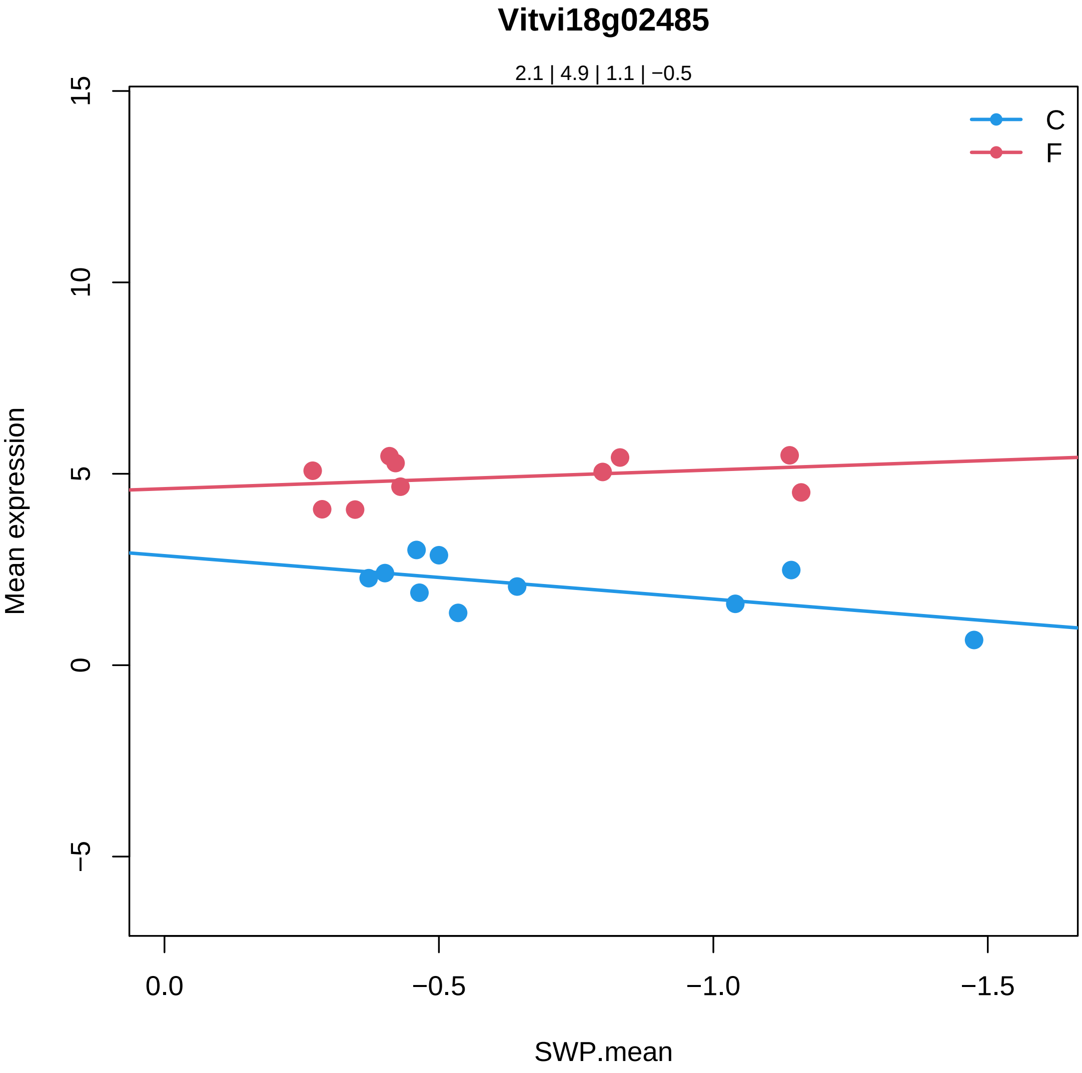
7.4.34 Vitvi18g02485: * type3

```
> 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
```



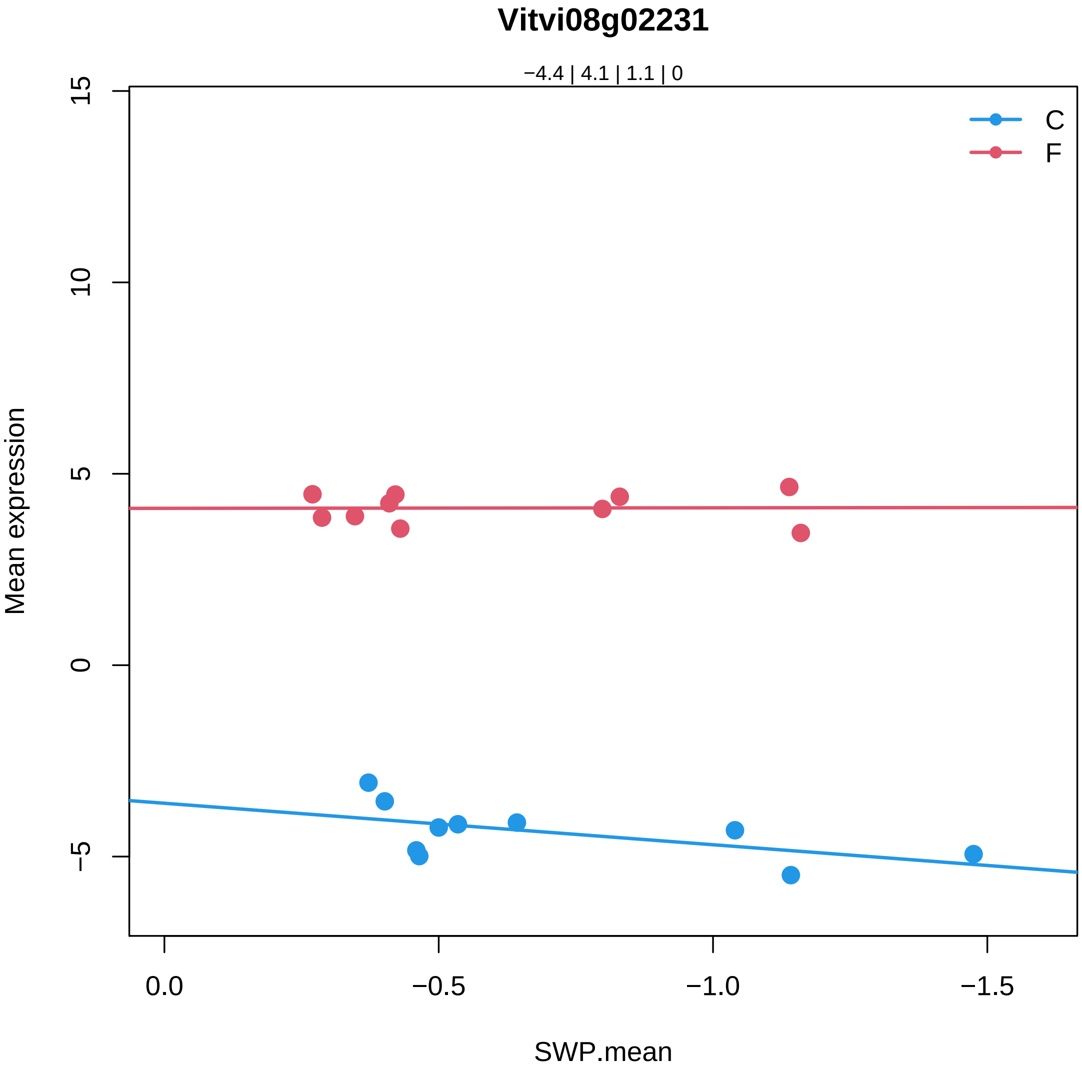
7.4.35 Vitvi08g02231: * type3

```
> 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
```



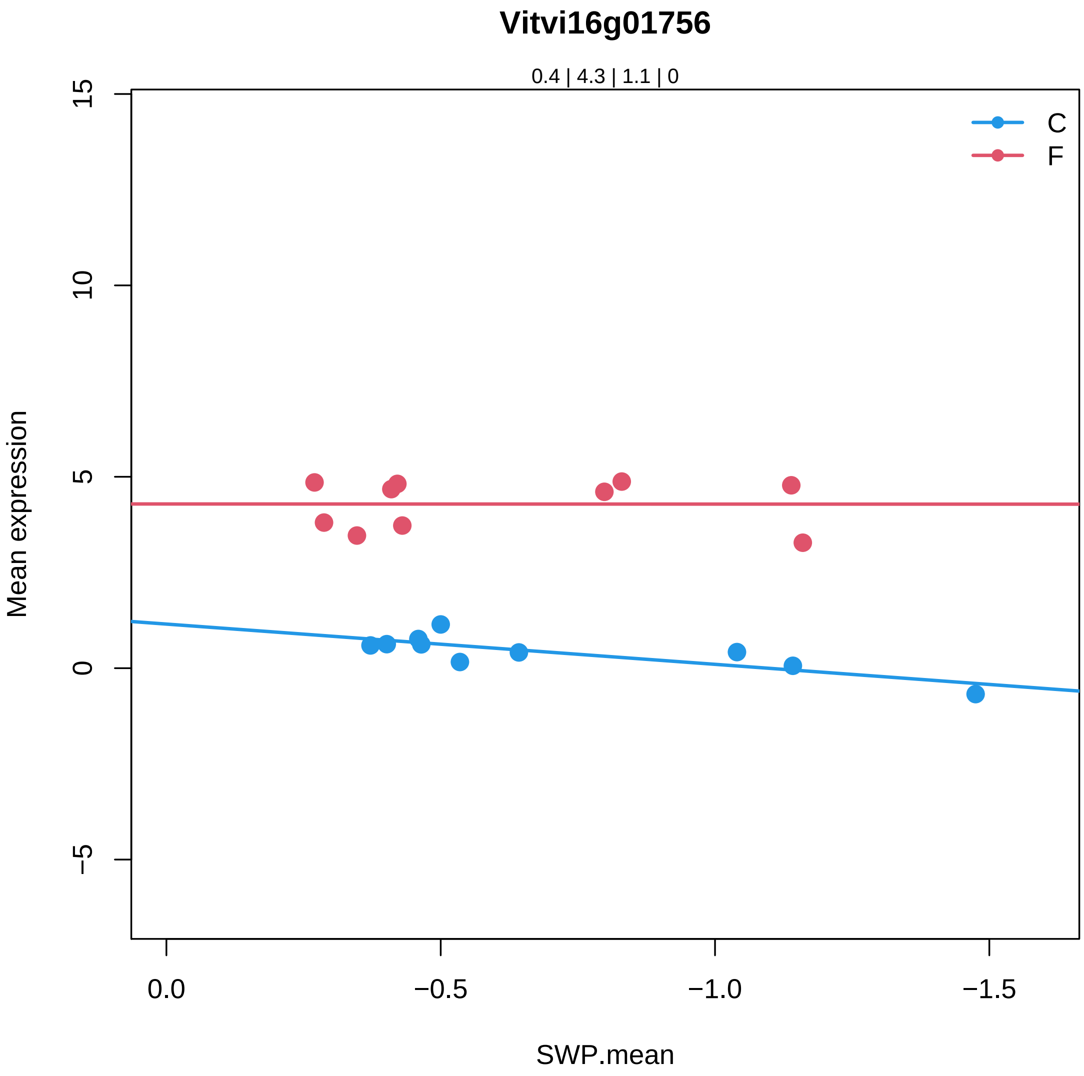
7.4.36 Vitvi16g01756: * type3

```
> 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
```



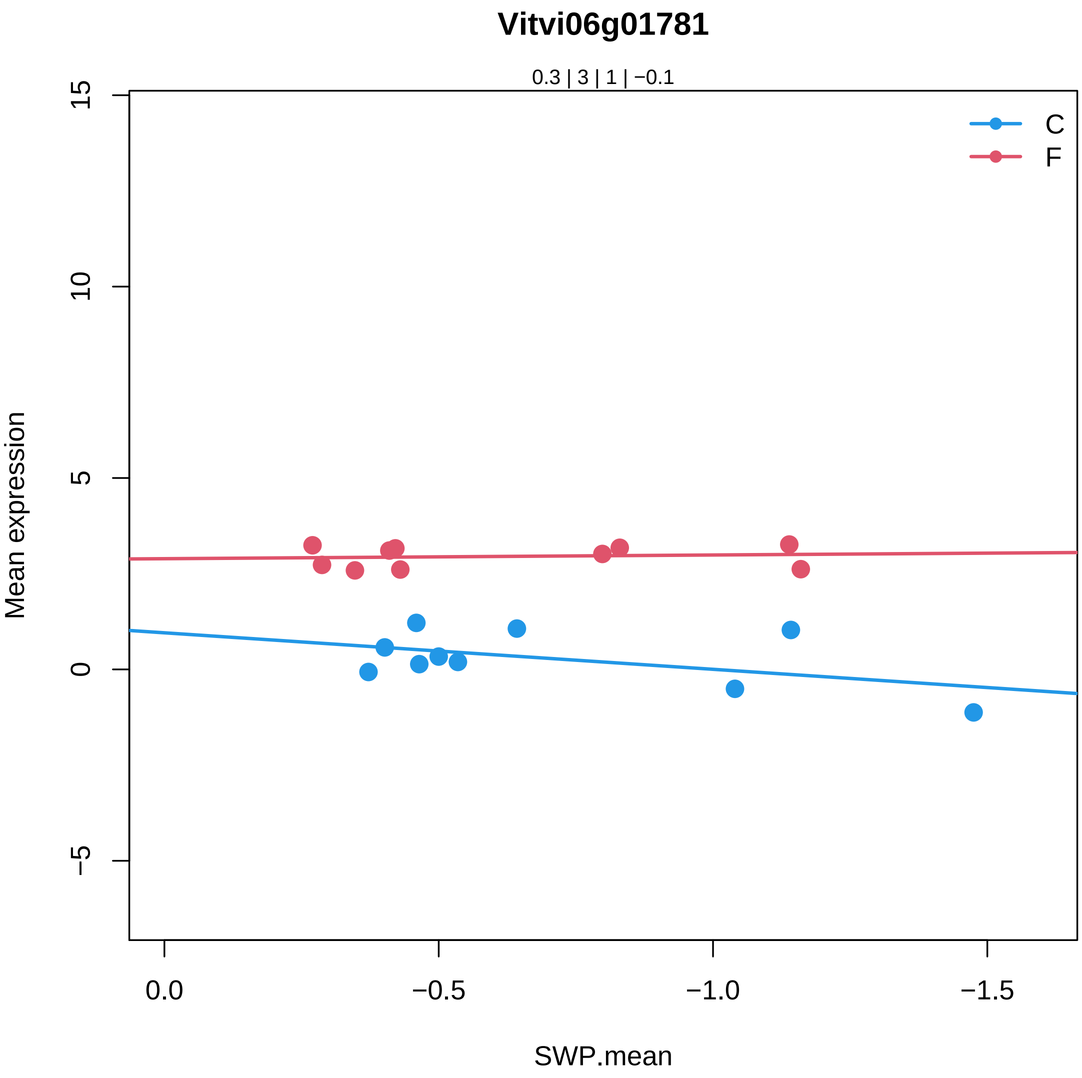
7.4.37 Vitvi06g01781: * type3

```
> 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
```



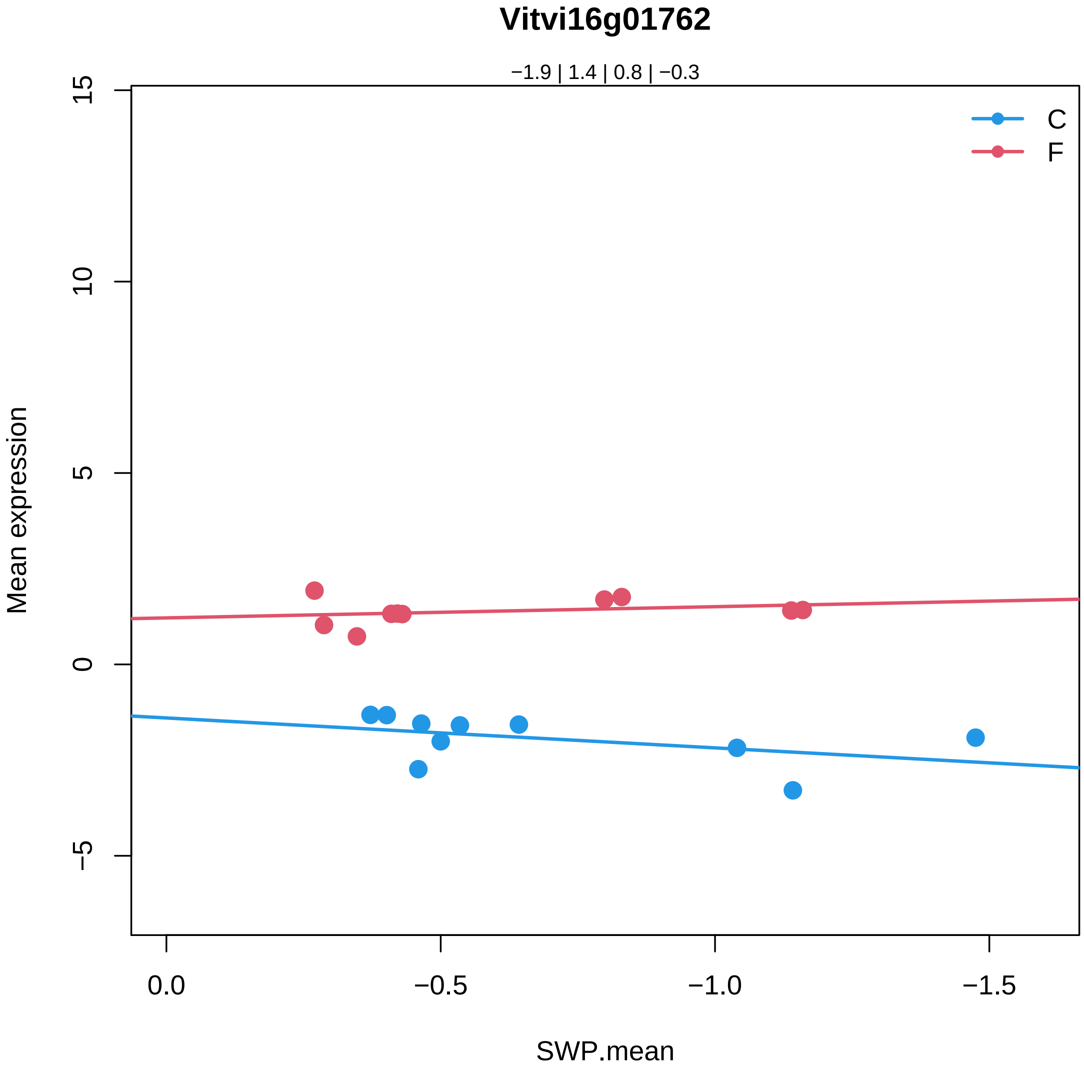
7.4.38 Vitvi16g01762: type3

```
> 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
```



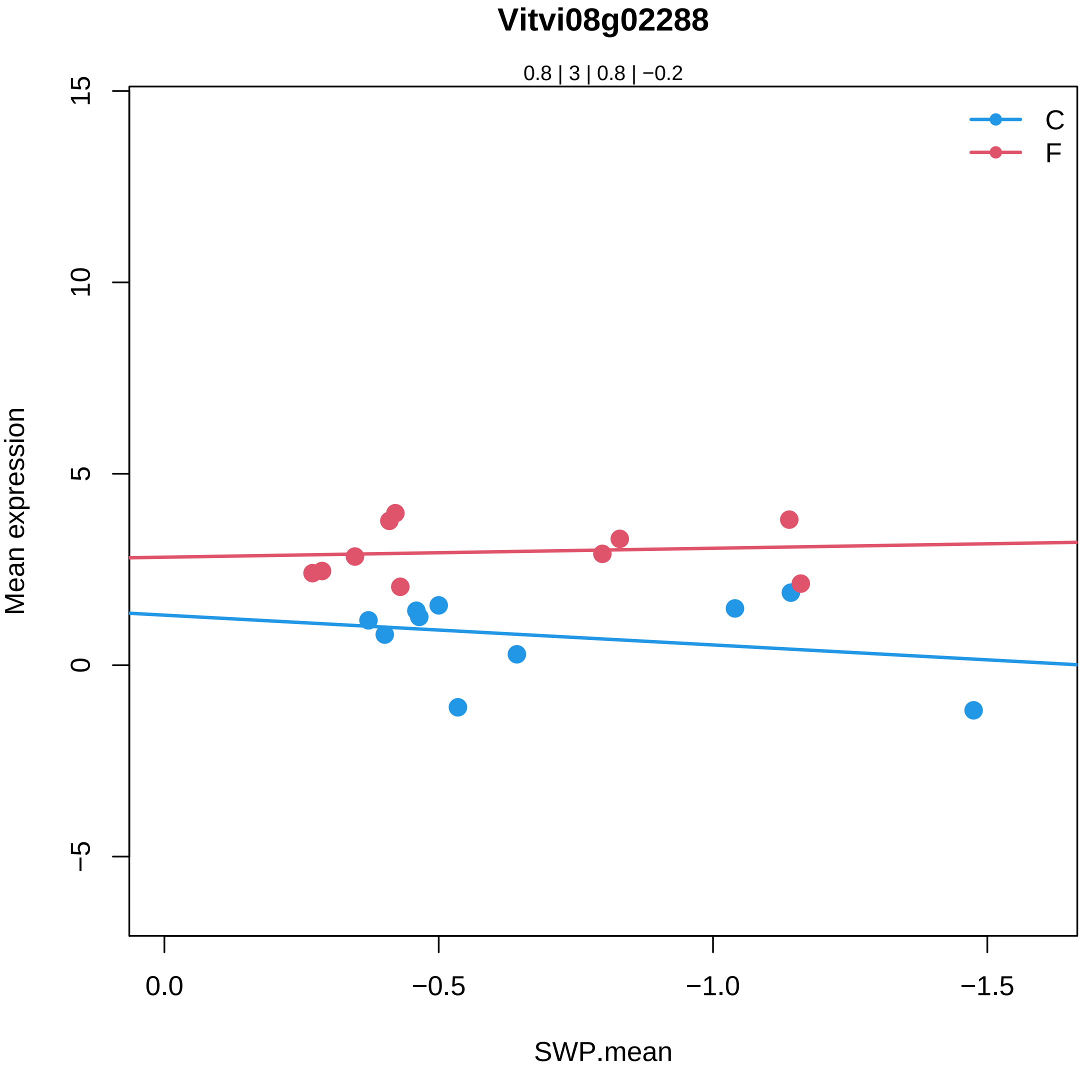
7.4.39 Vitvi08g02288: type3

```
> 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
```



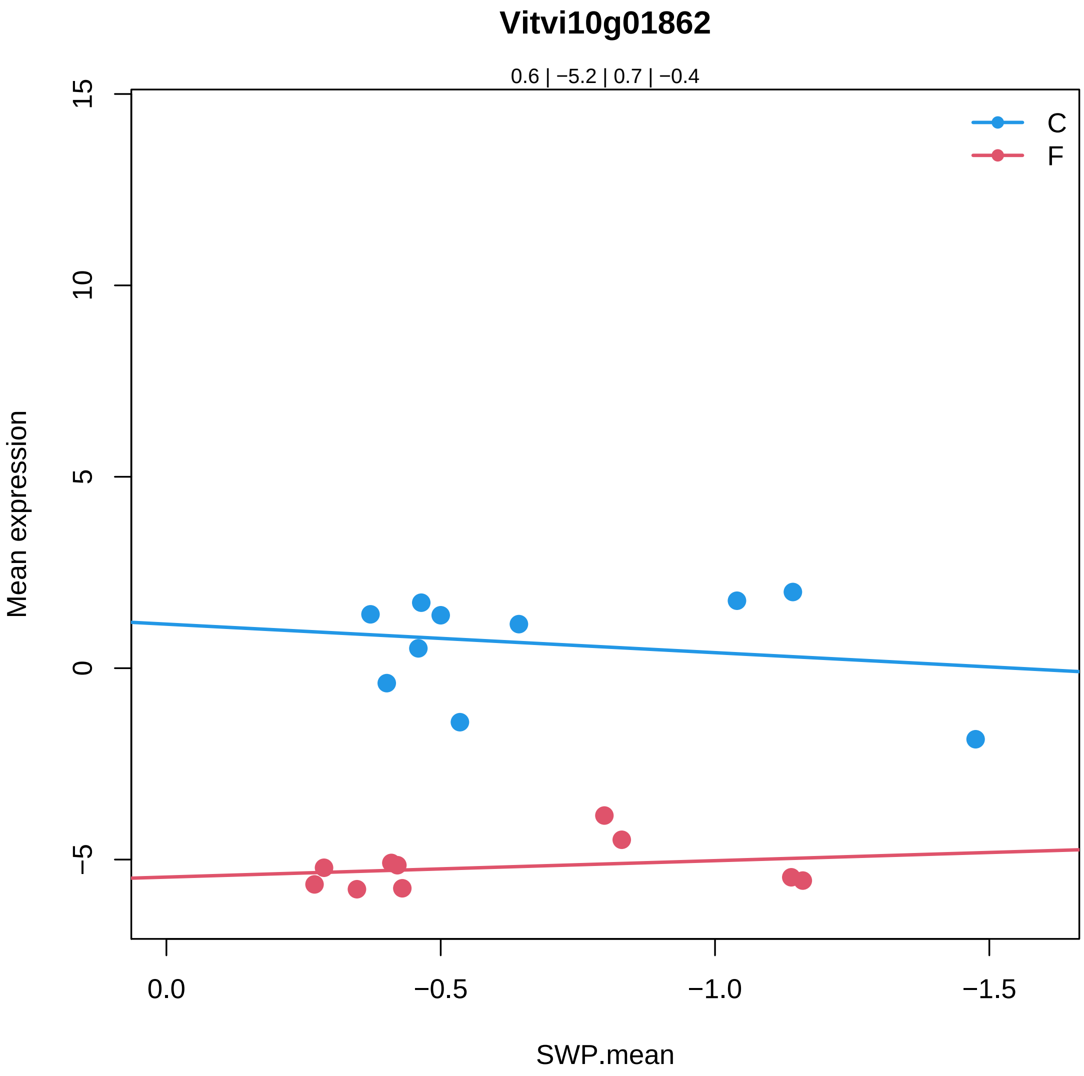
7.4.40 Vitvi10g01862: type3

```
> 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
```



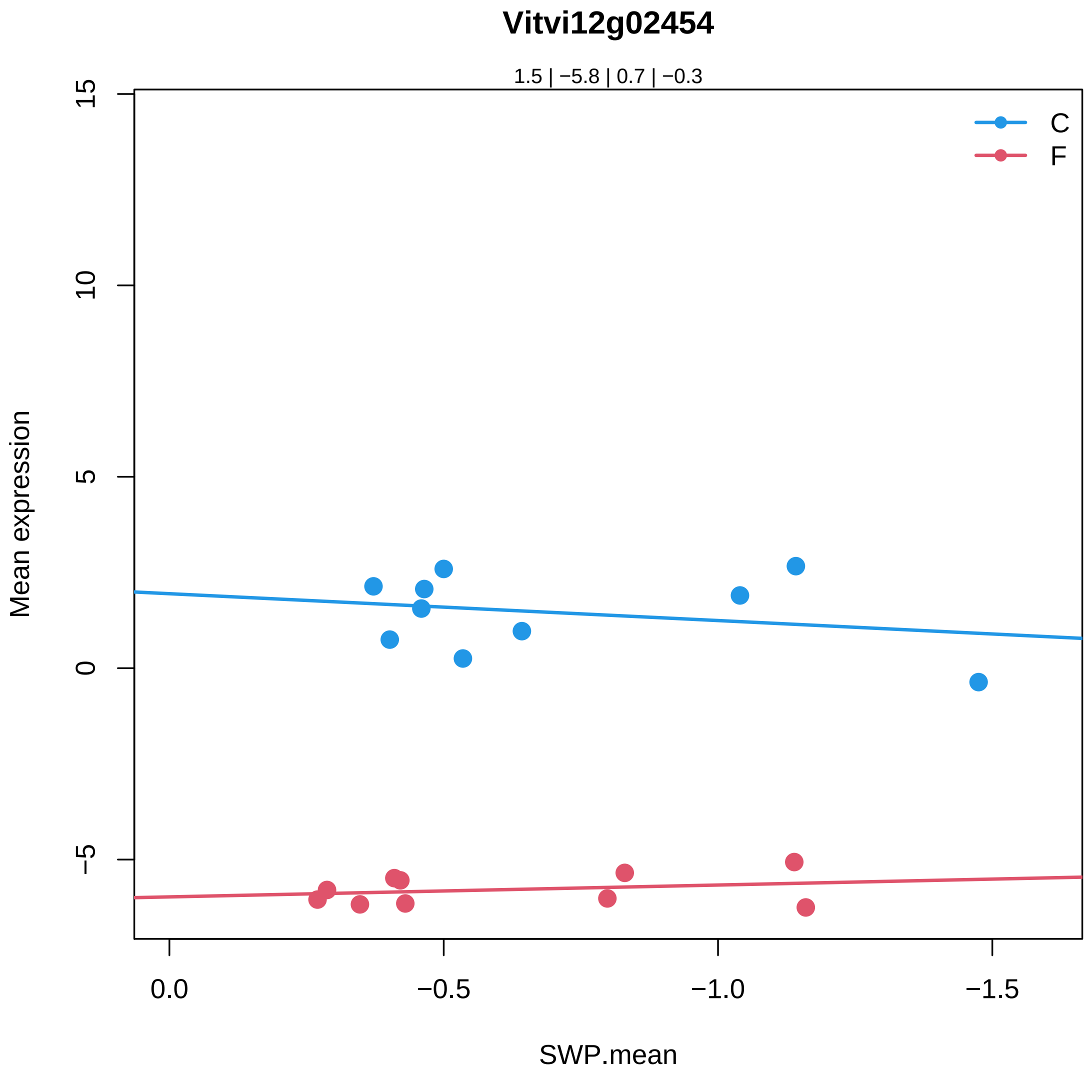
7.4.41 Vitvi12g02454: type3

```
> 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        
```



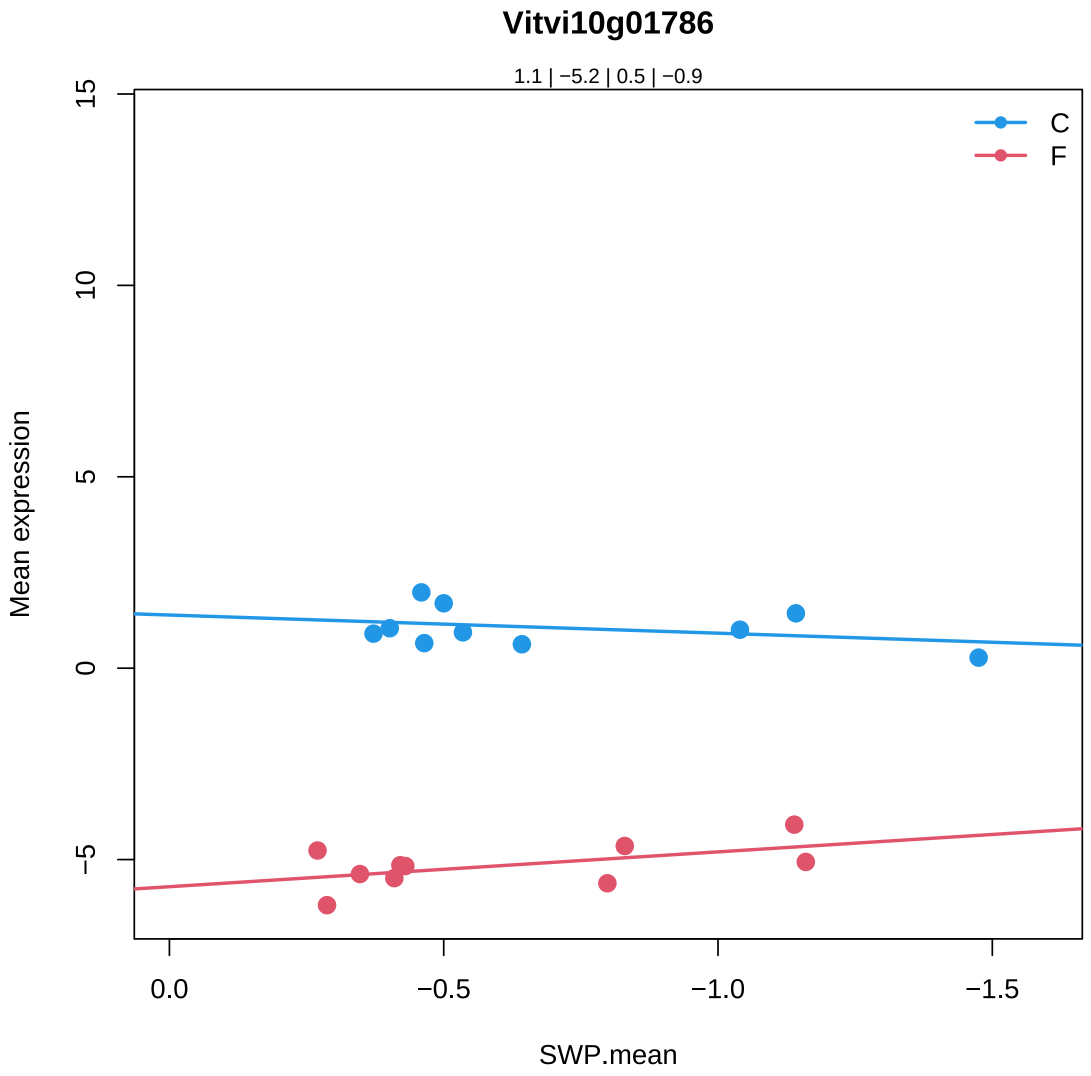
7.4.42 Vitvi10g01786: + type3

```
> 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        
```



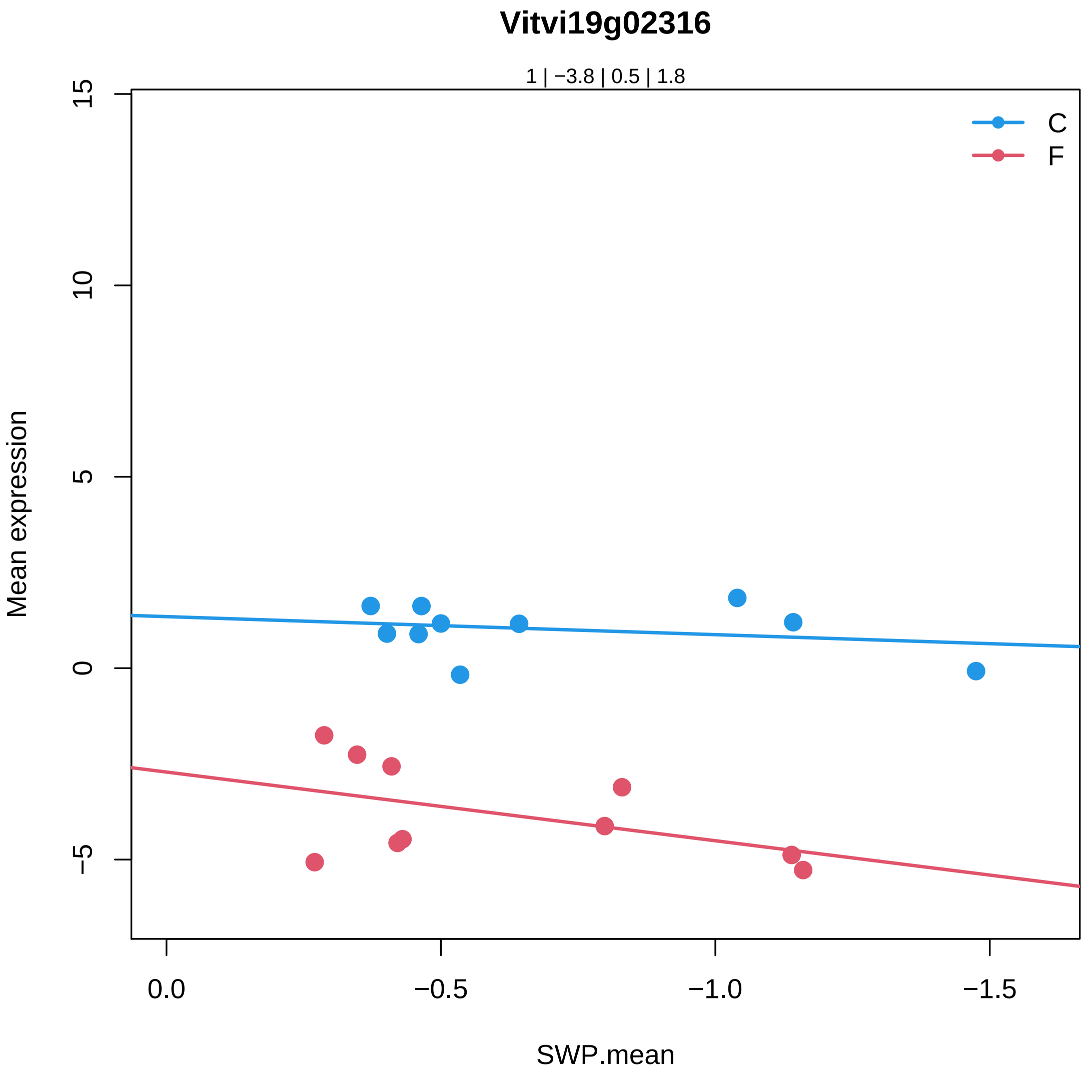
7.4.43 Vitvi19g02316: type3

```
> 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
```



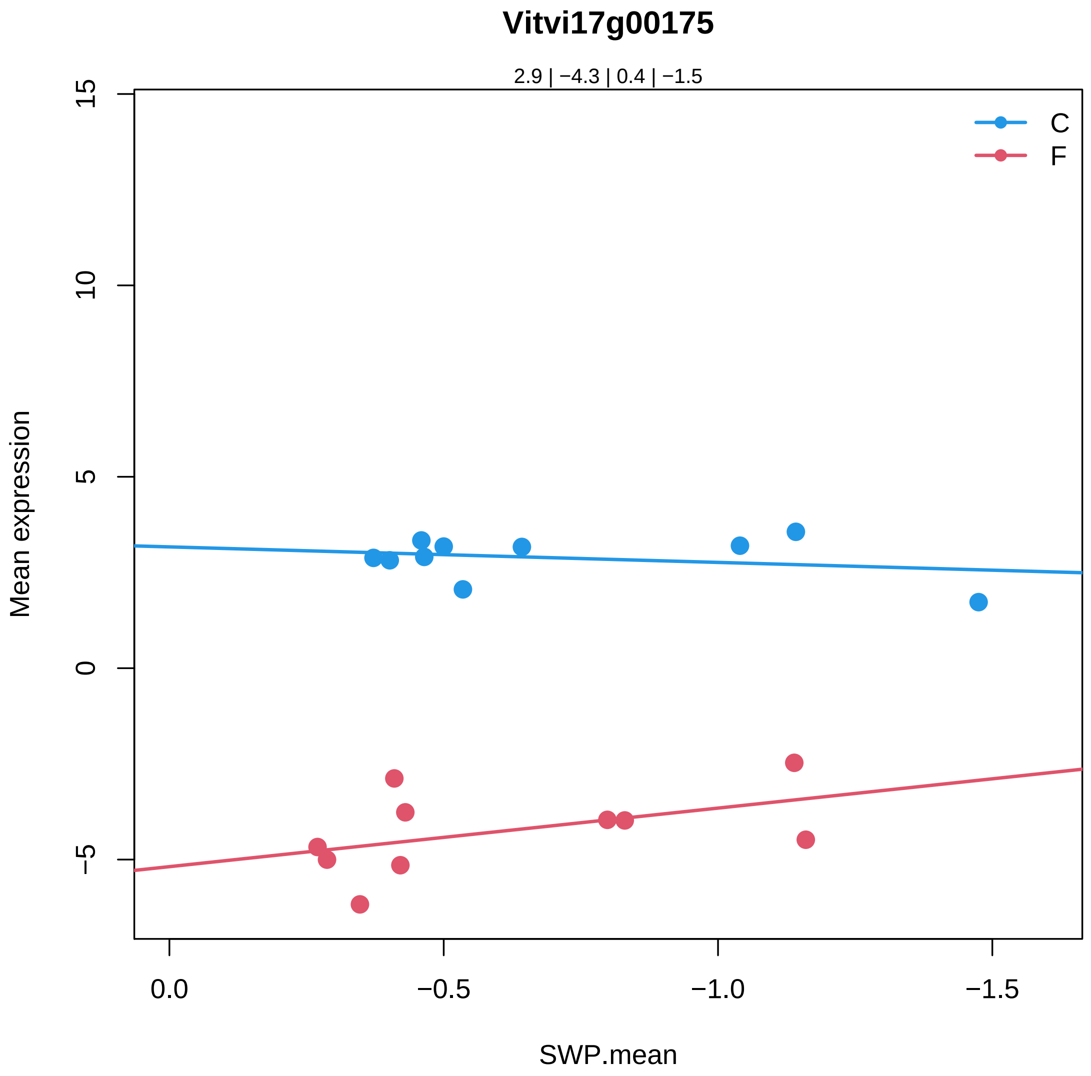
7.4.44 Vitvi17g00175: type3

```
> 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
```



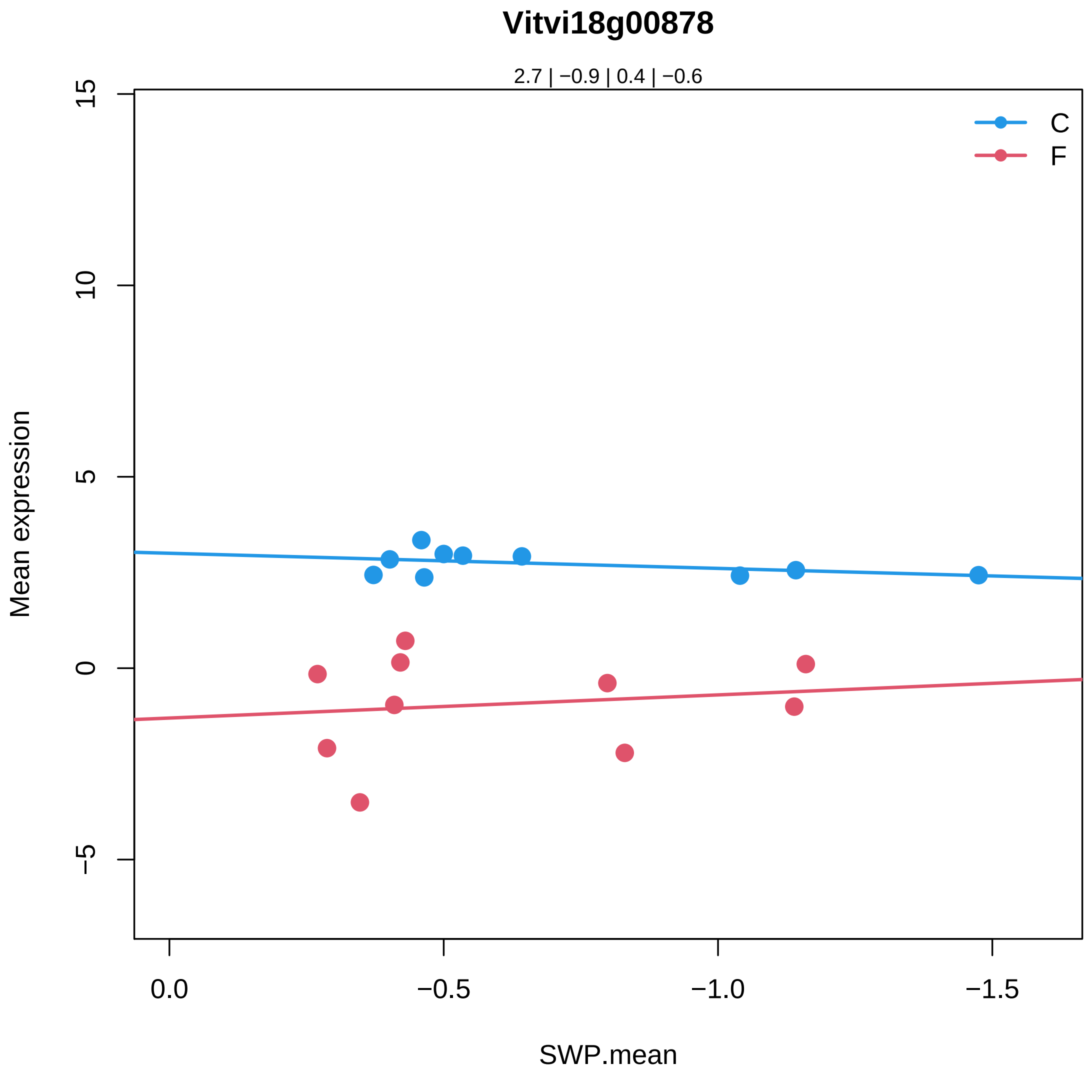
7.4.45 Vitvi18g00878: type3

```
> 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
```



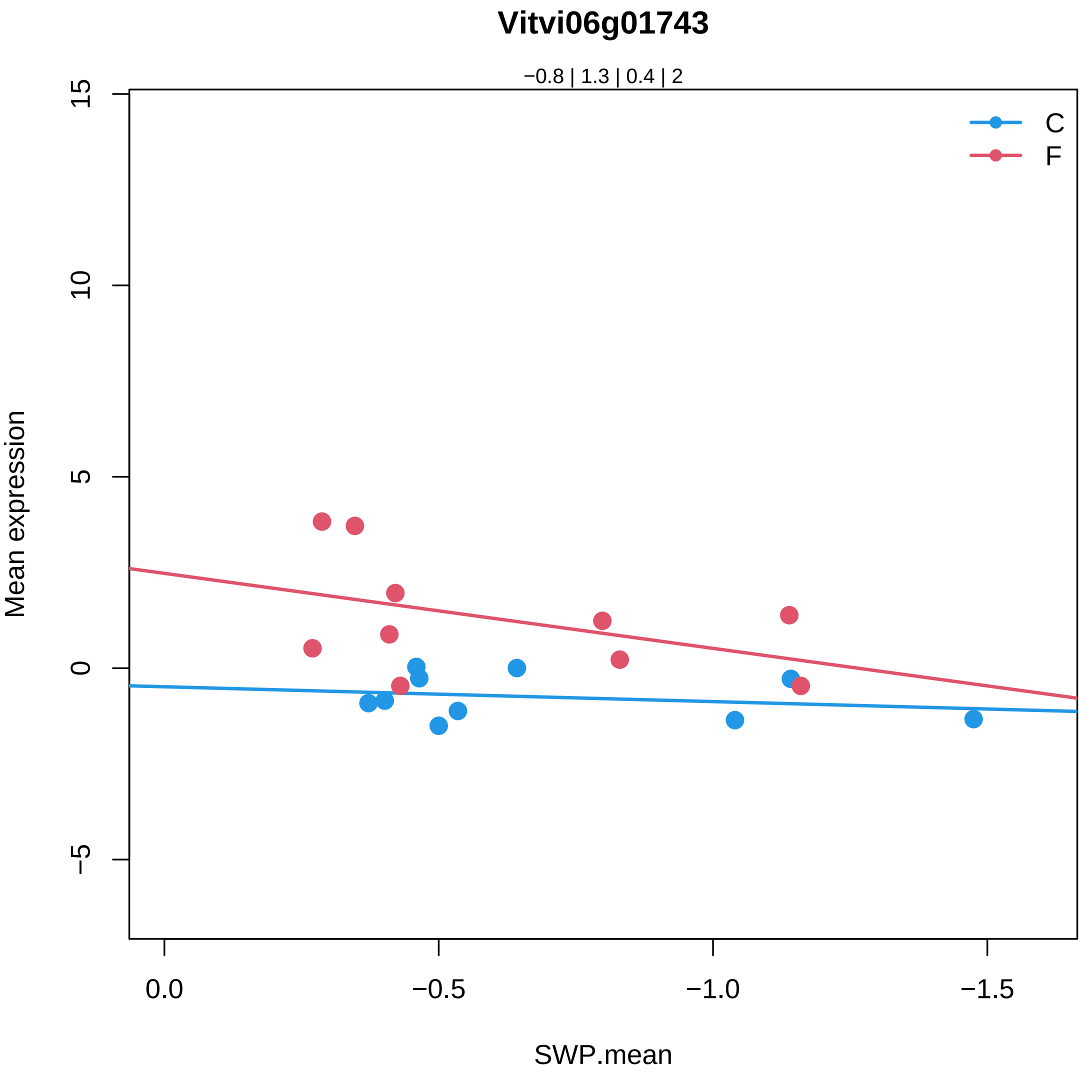
7.4.46 Vitvi06g01743: type3

```
> 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
```



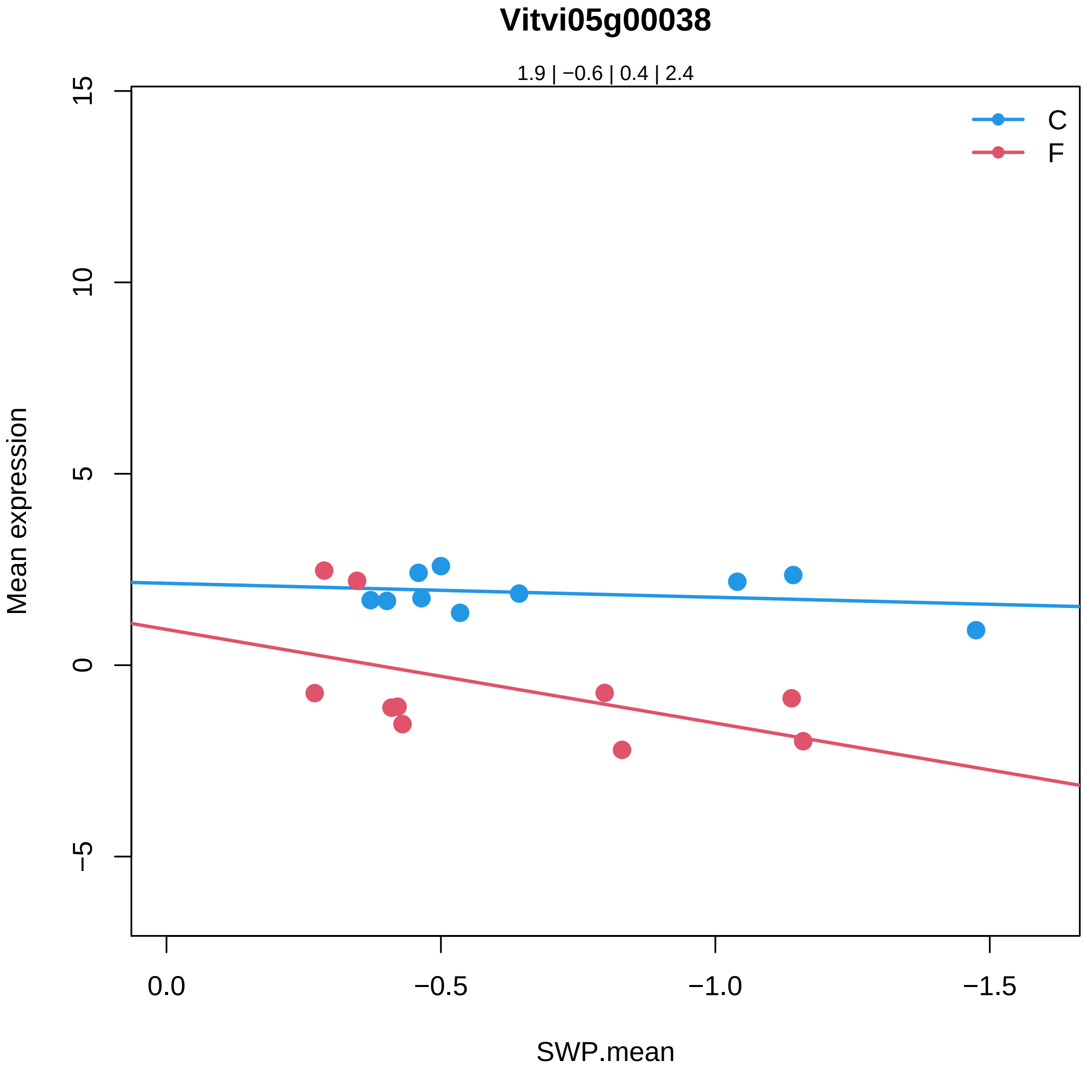
7.4.47 Vitvi05g00038: type3 | type4

```
> 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
```



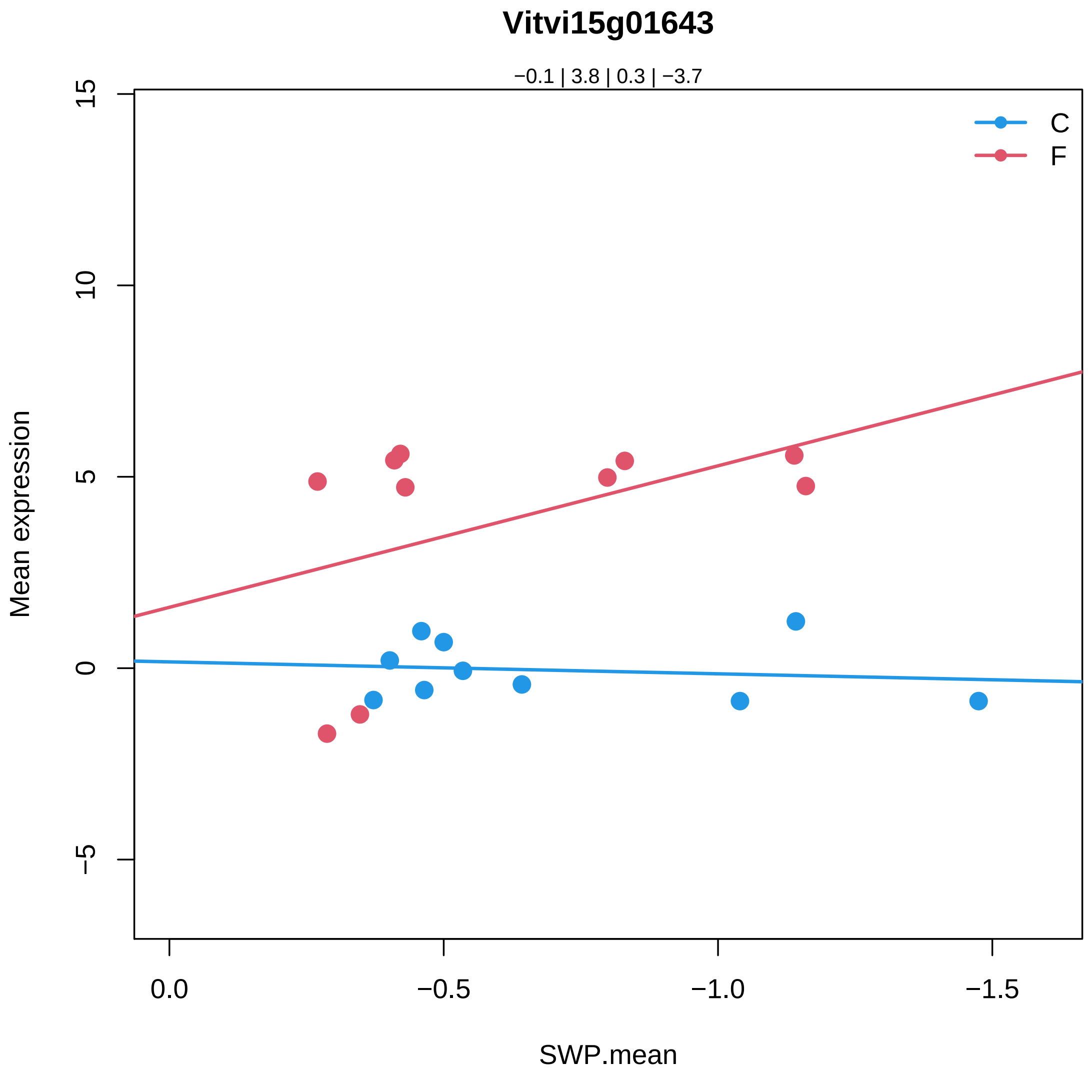
7.4.48 Vitvi15g01643: type3

```
> 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
```



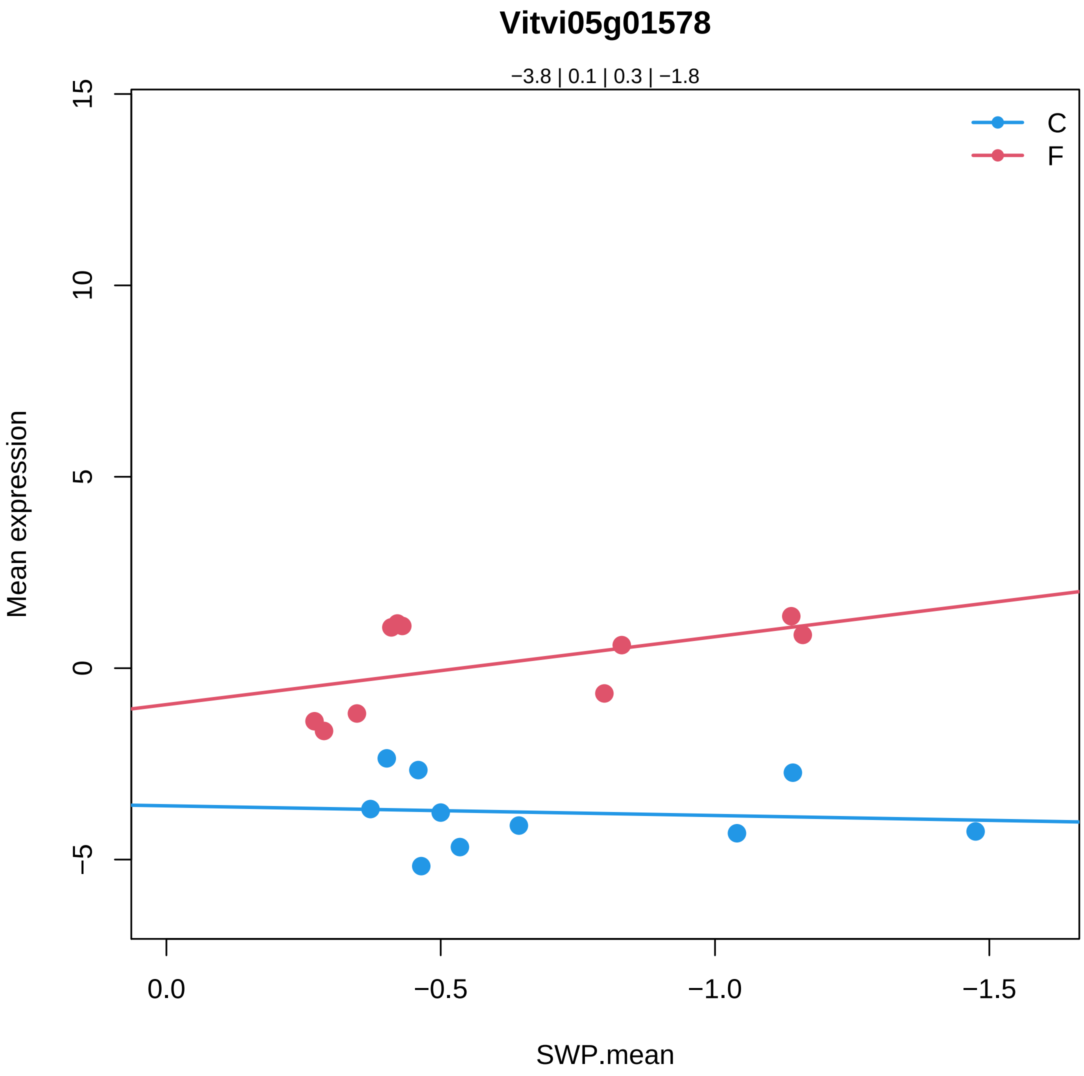
7.4.49 Vitvi05g01578: type3

```
> 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
```



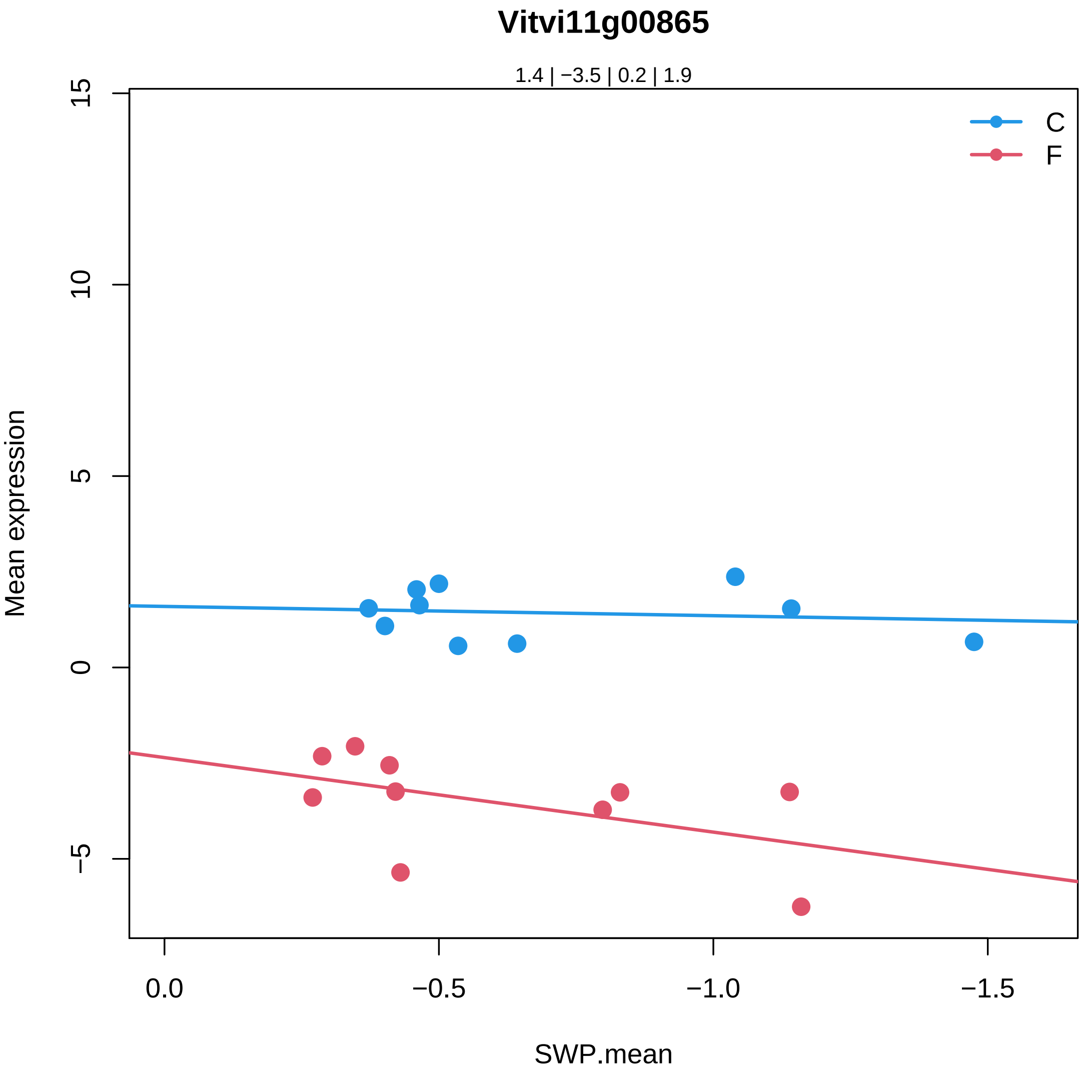
7.4.50 Vitvi11g00865: type3

```
> 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

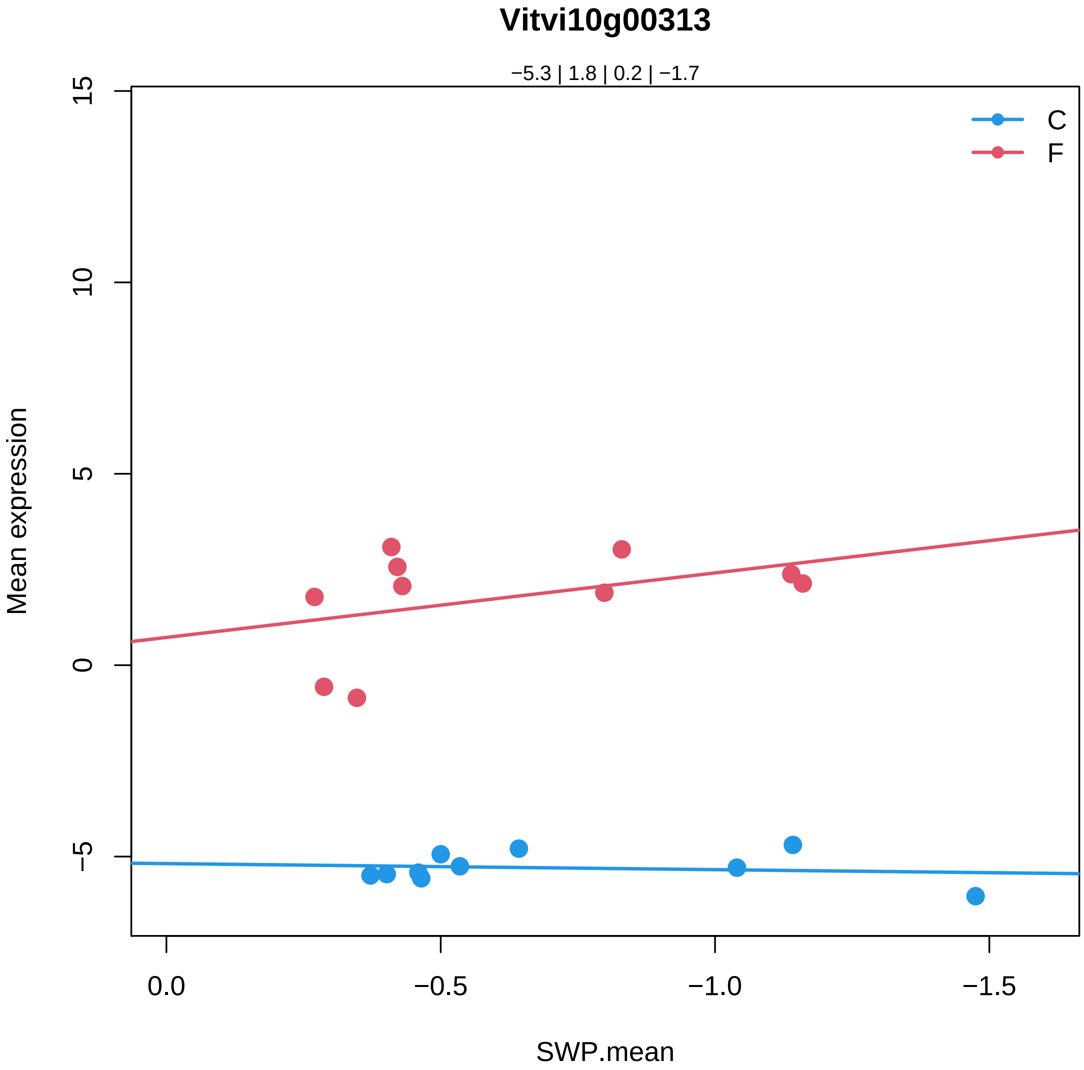
7.4.51 Vitvi10g00313: type3

```
> 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
```



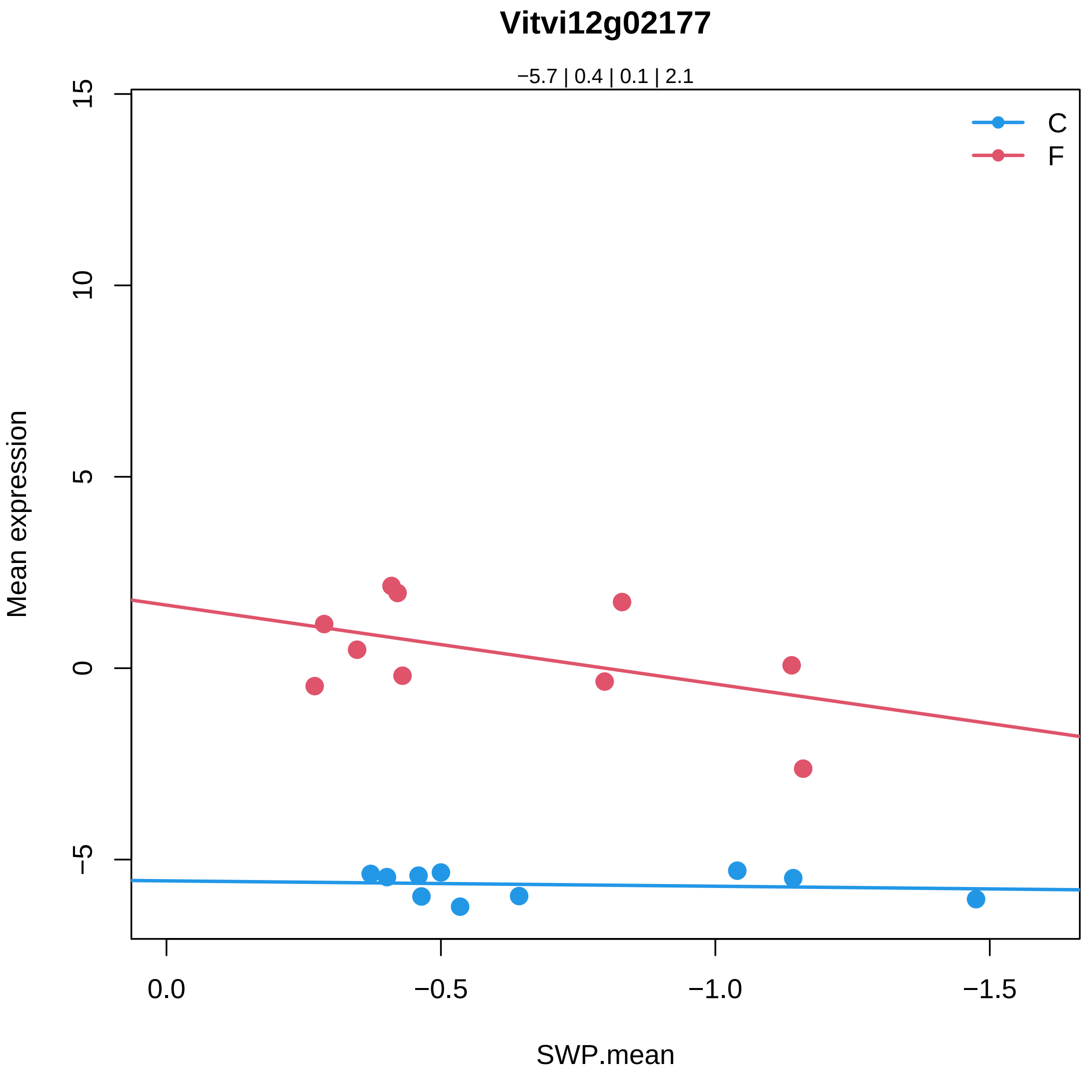
7.4.52 Vitvi12g02177: type3 | type4

```
> 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
```



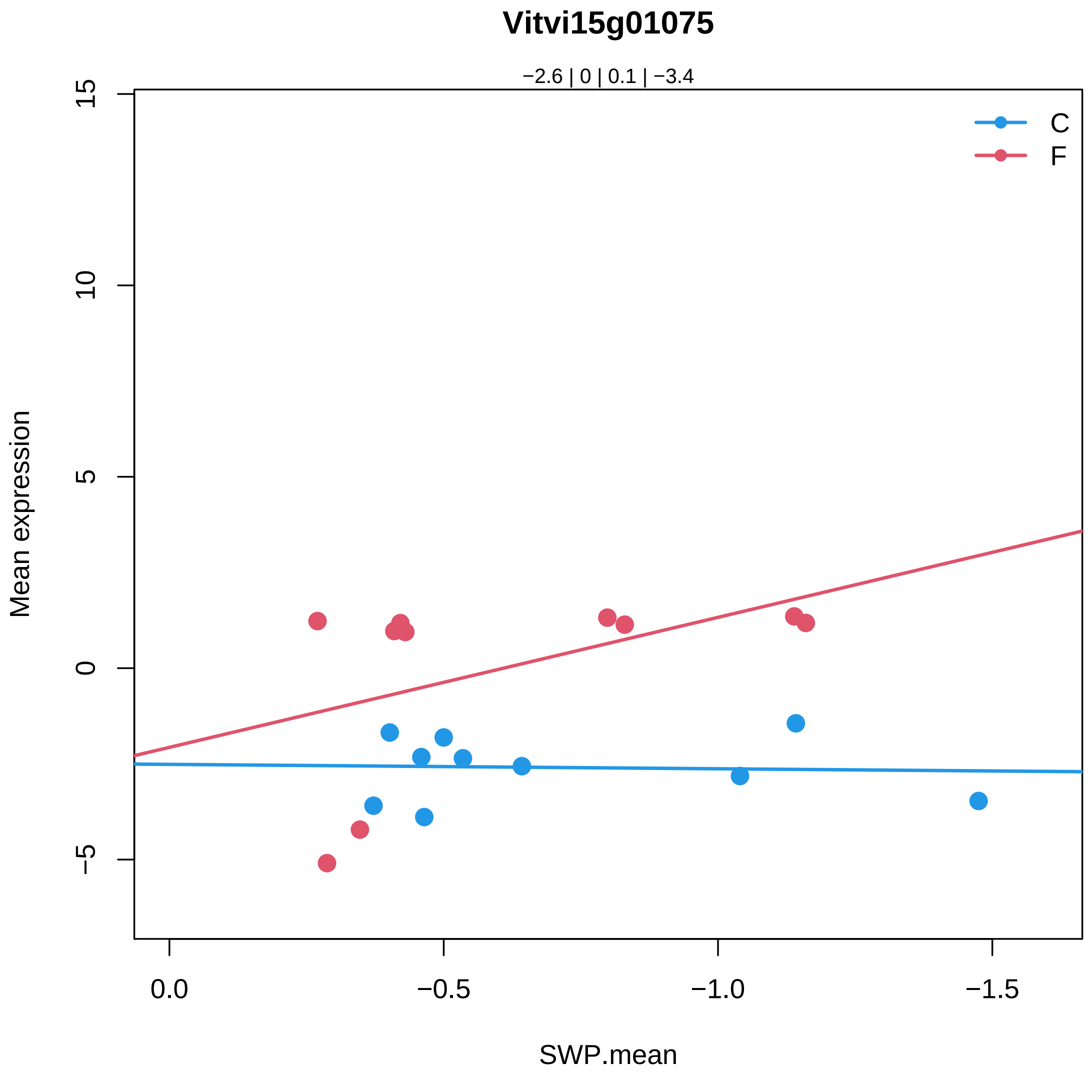
7.4.53 Vitvi15g01075: type3

```
> 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
```



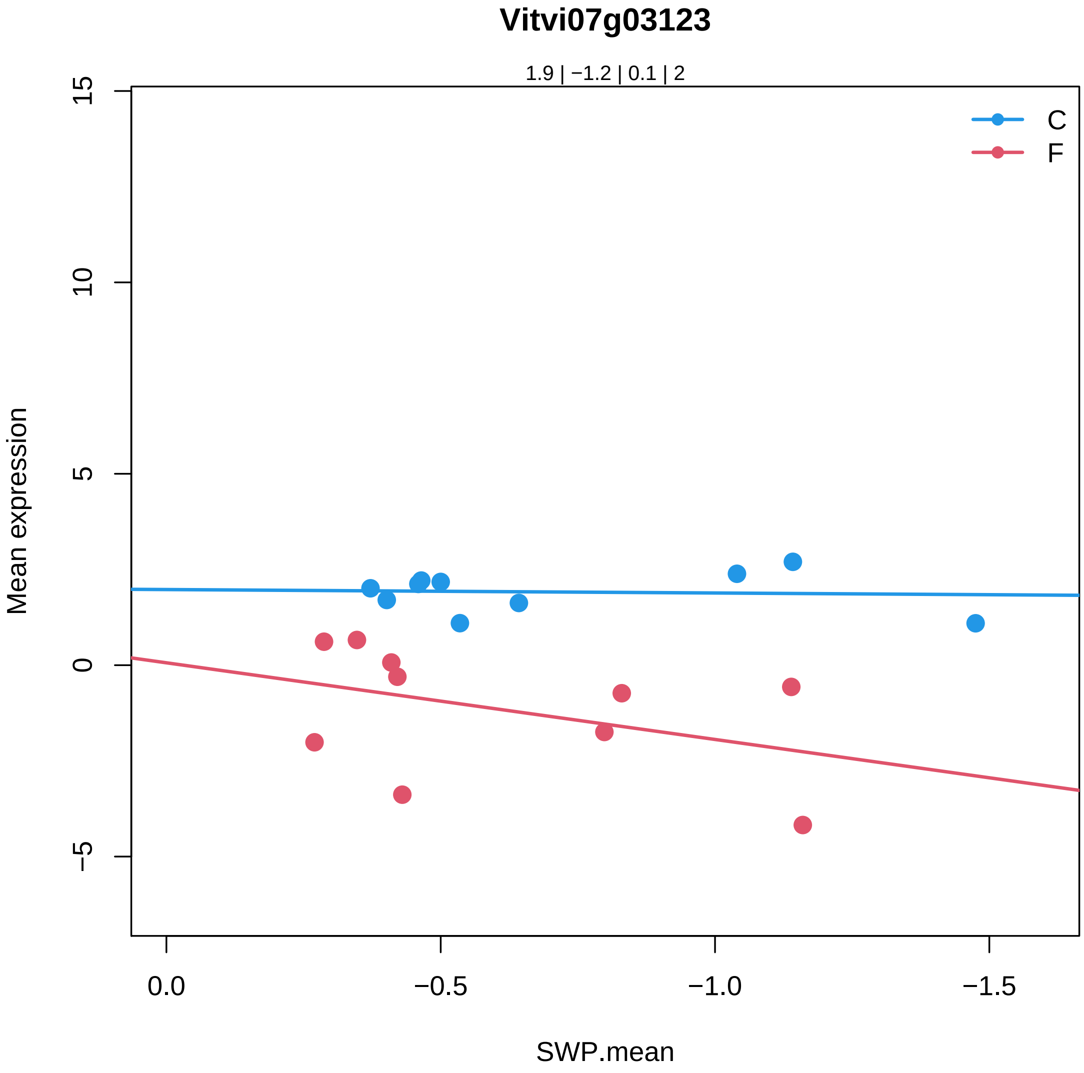
7.4.54 Vitvi07g03123: type3 | type4

```
> 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
```



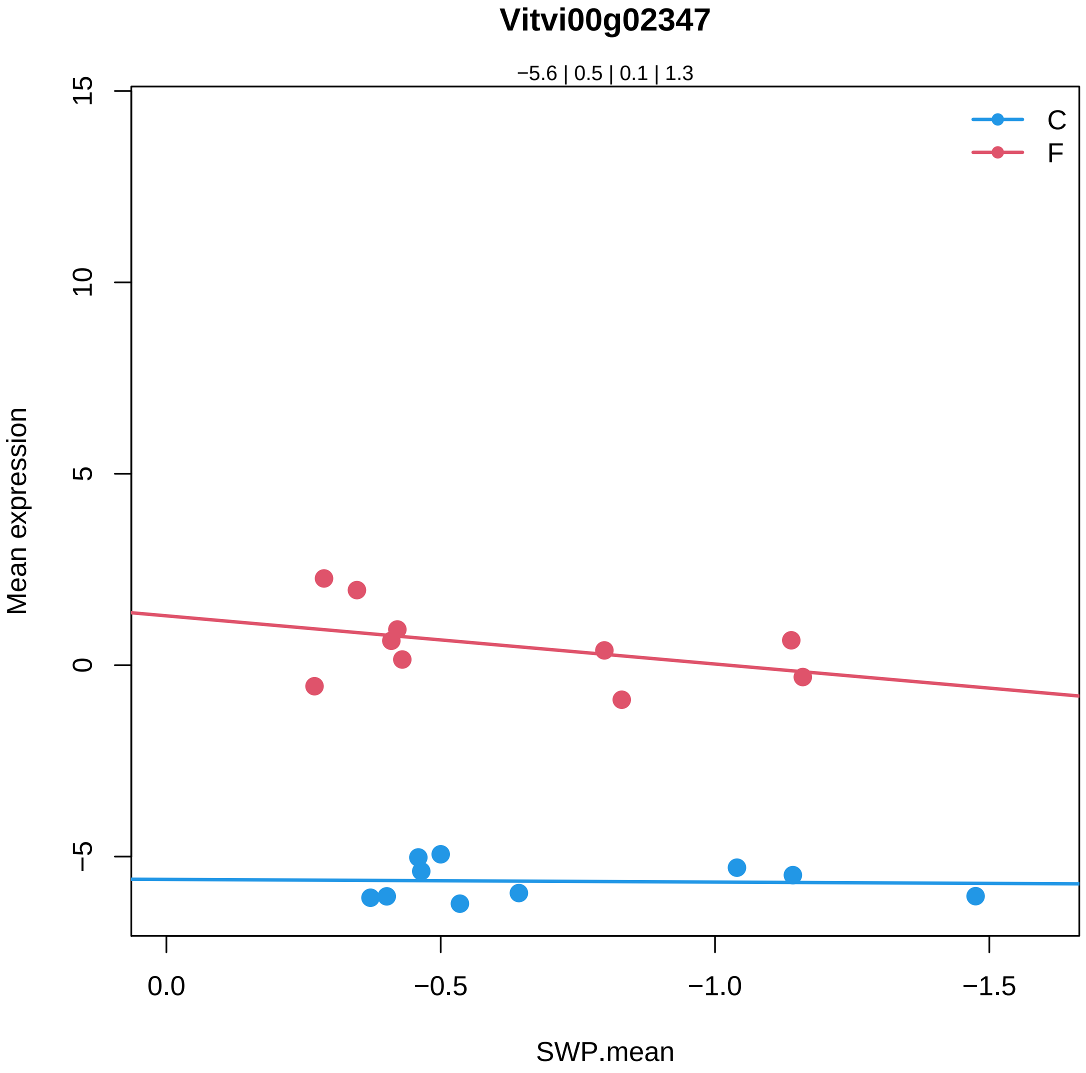
7.4.55 Vitvi00g02347: type3

```
> 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
```



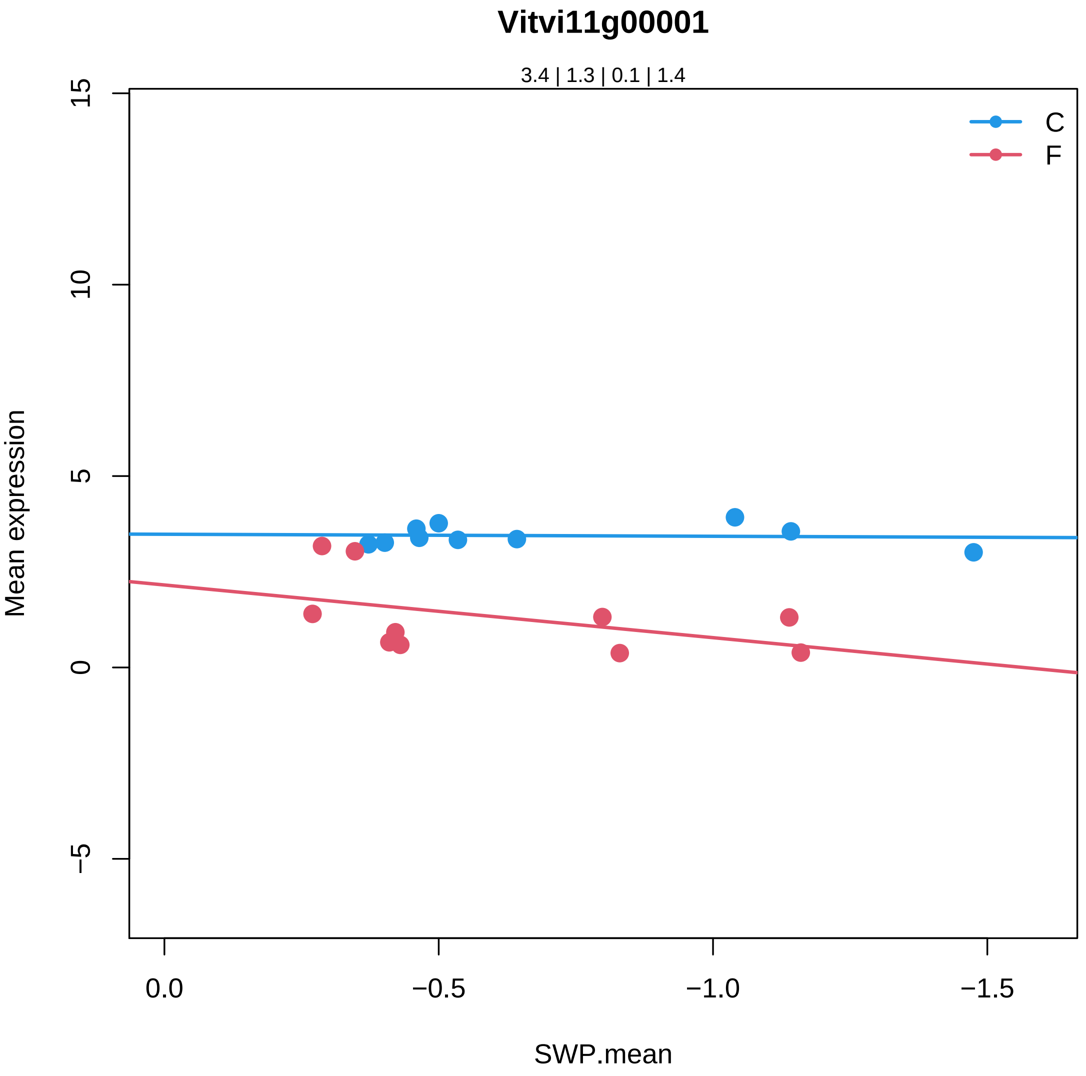
7.4.56 Vitvi11g00001: type3

```
> 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
SWP.mean
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5

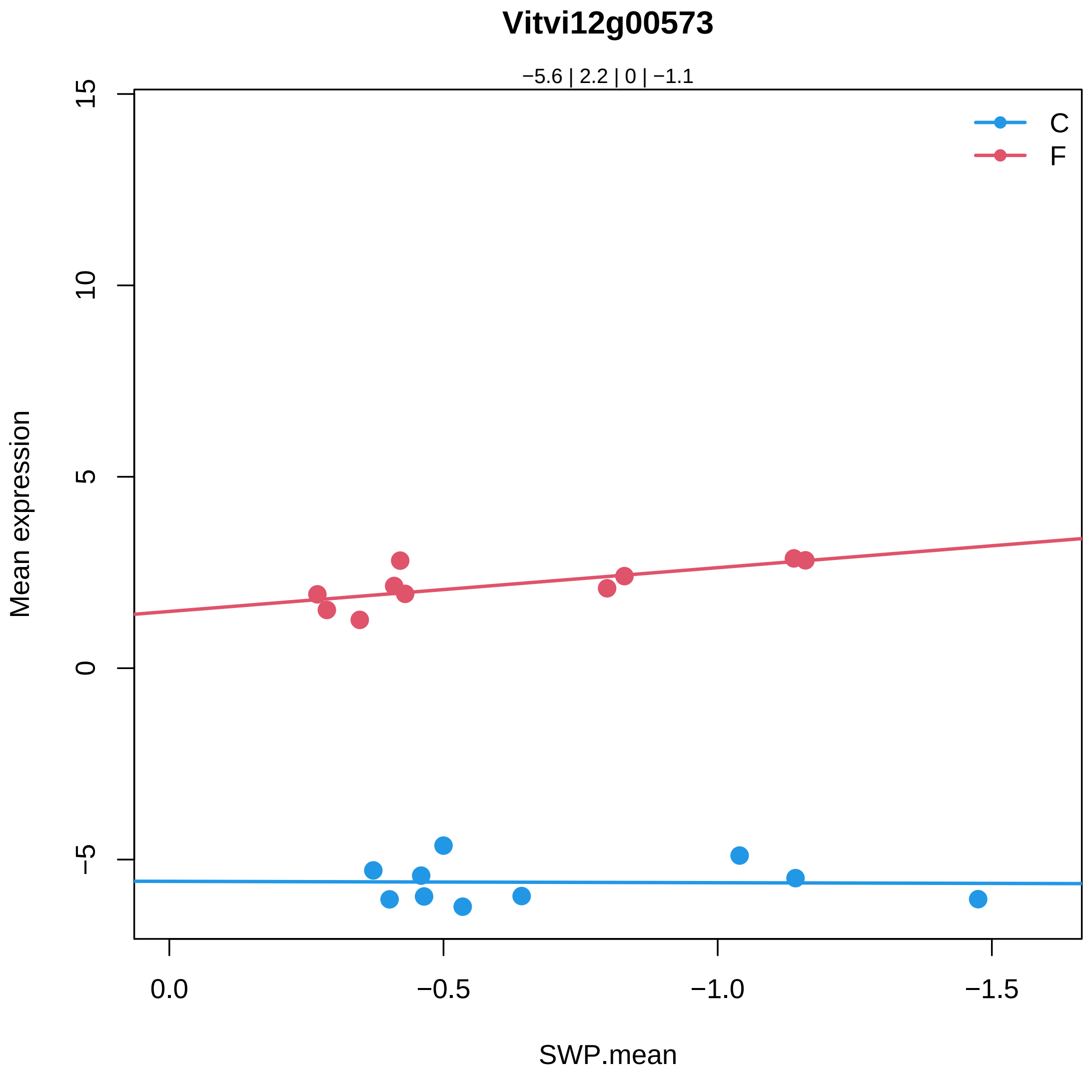
7.4.57 Vitvi12g00573: type3

```
> 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
```



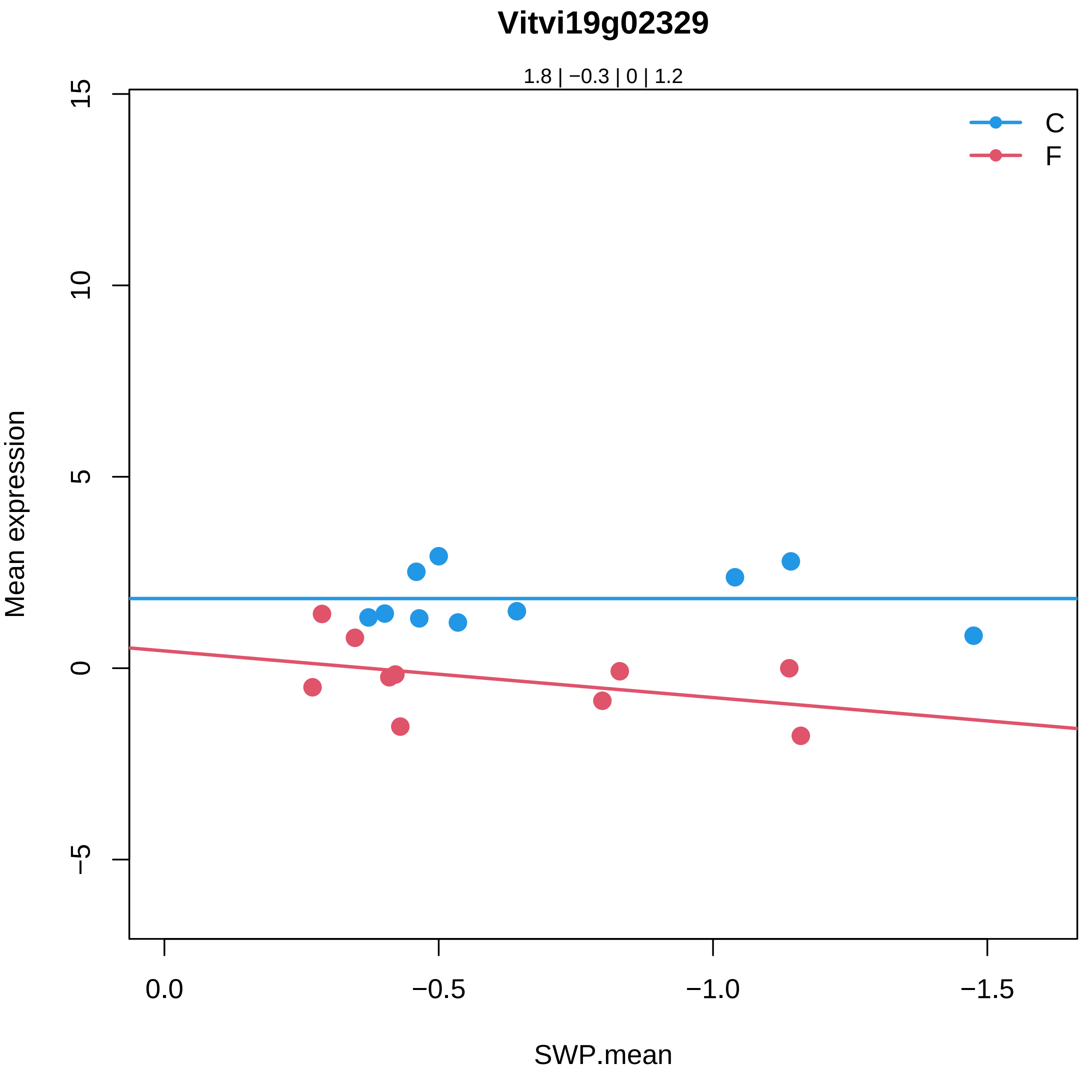
7.4.58 Vitvi19g02329: type3

```
> 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
```



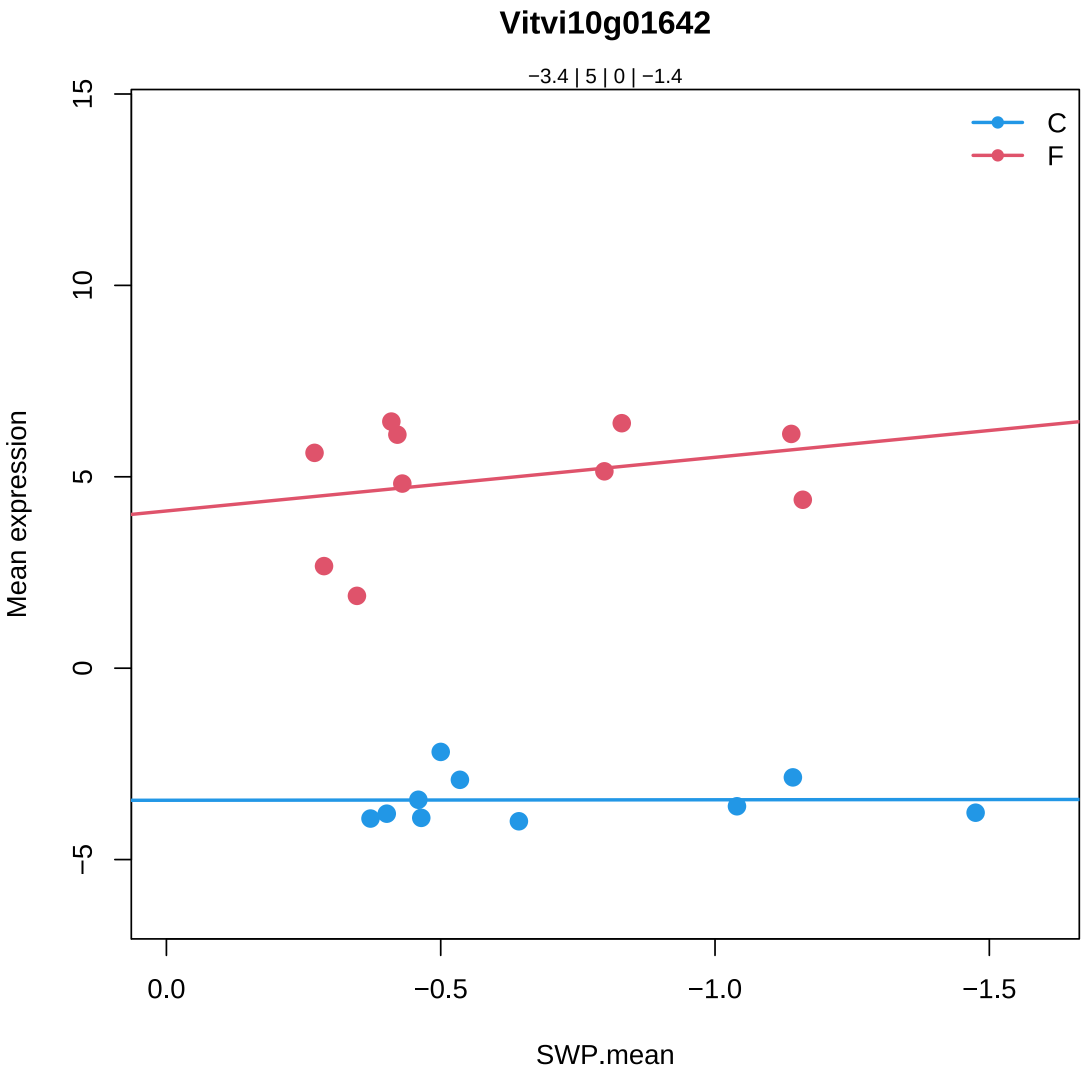
7.4.59 Vitvi10g01642: type3

```
> 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
```



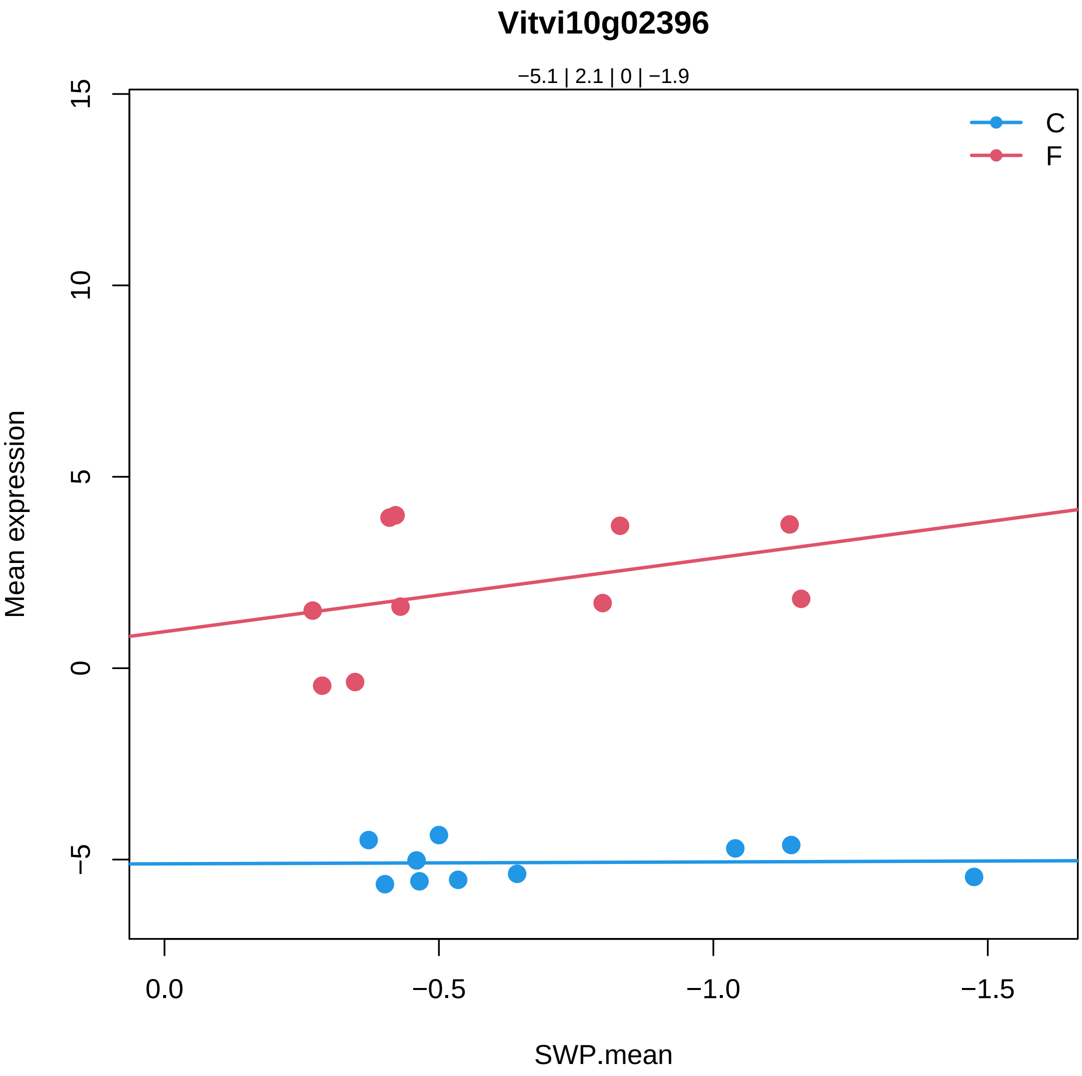
7.4.60 Vitvi10g02396: type3

```
> 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
```



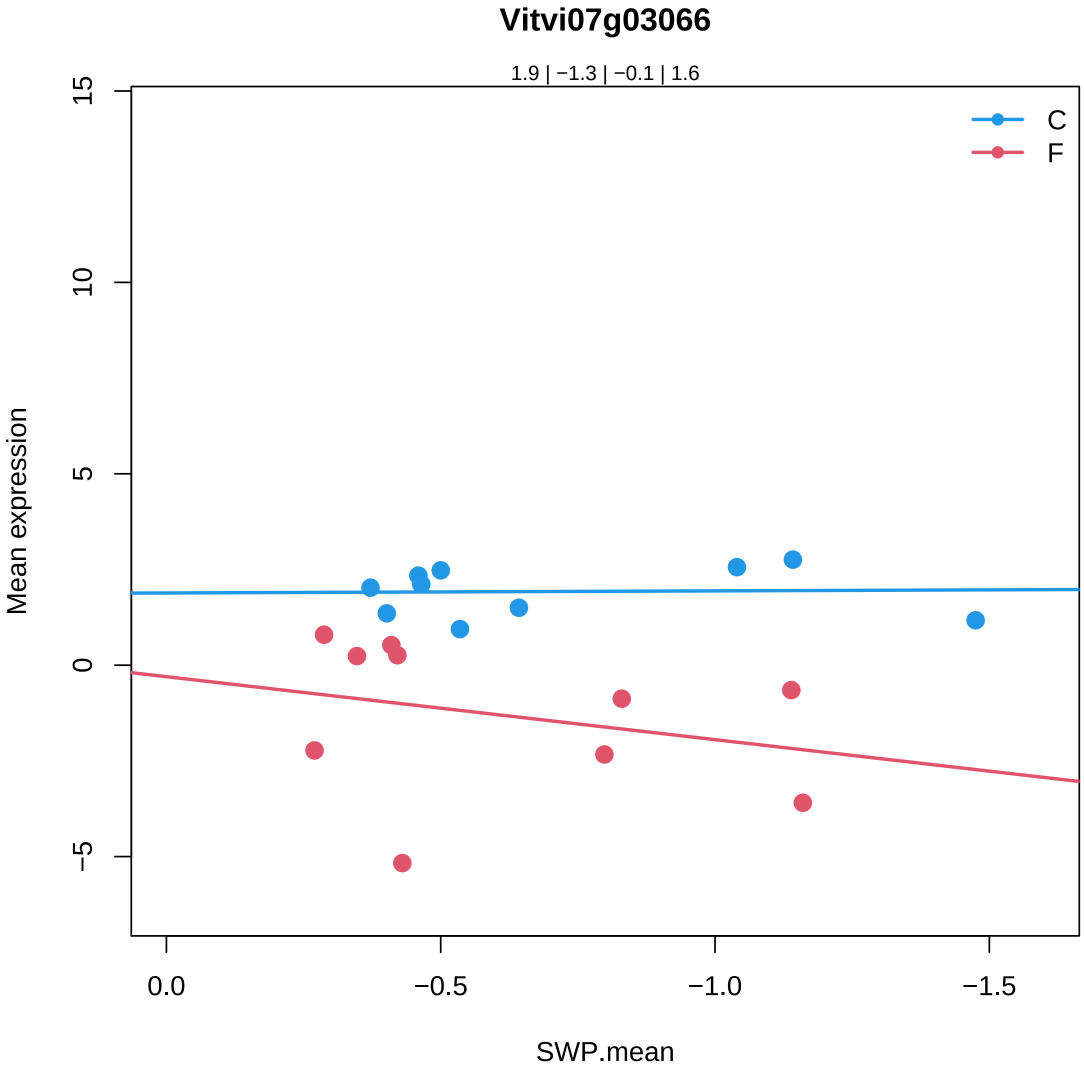
7.4.61 Vitvi07g03066: type3

```
> 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
```



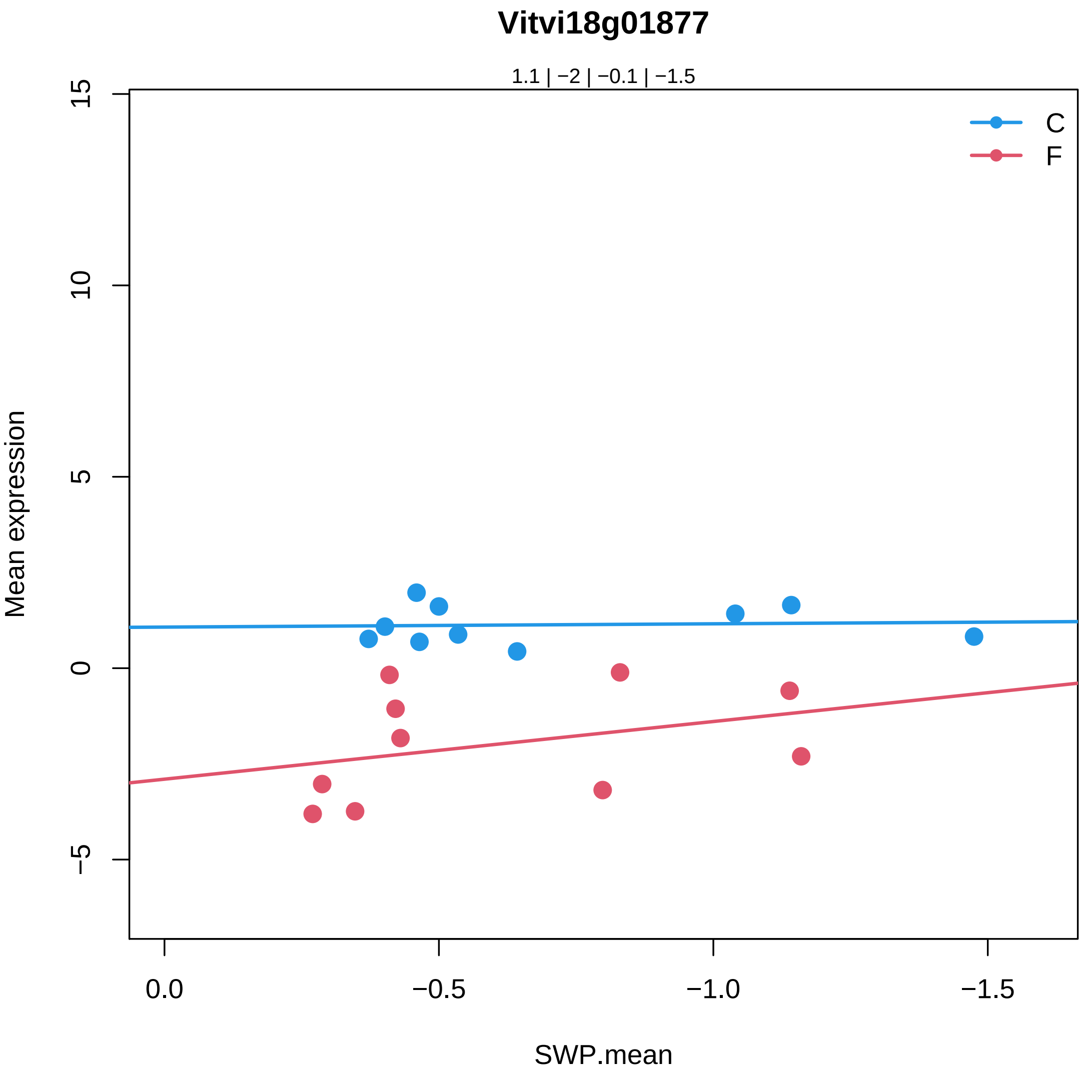
7.4.62 Vitvi18g01877: type3

```
> 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
```



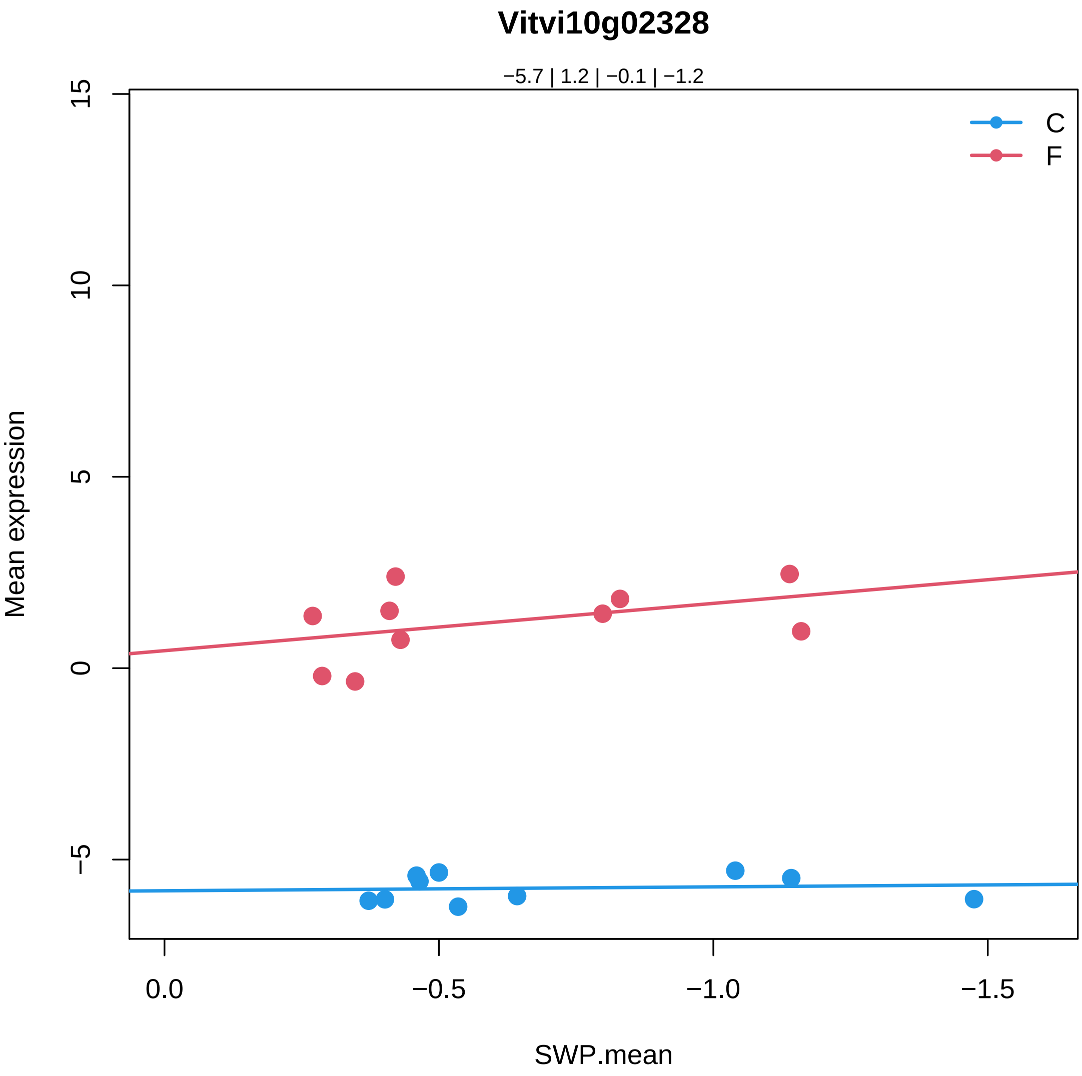
7.4.63 Vitvi10g02328: type3

```
> 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
```



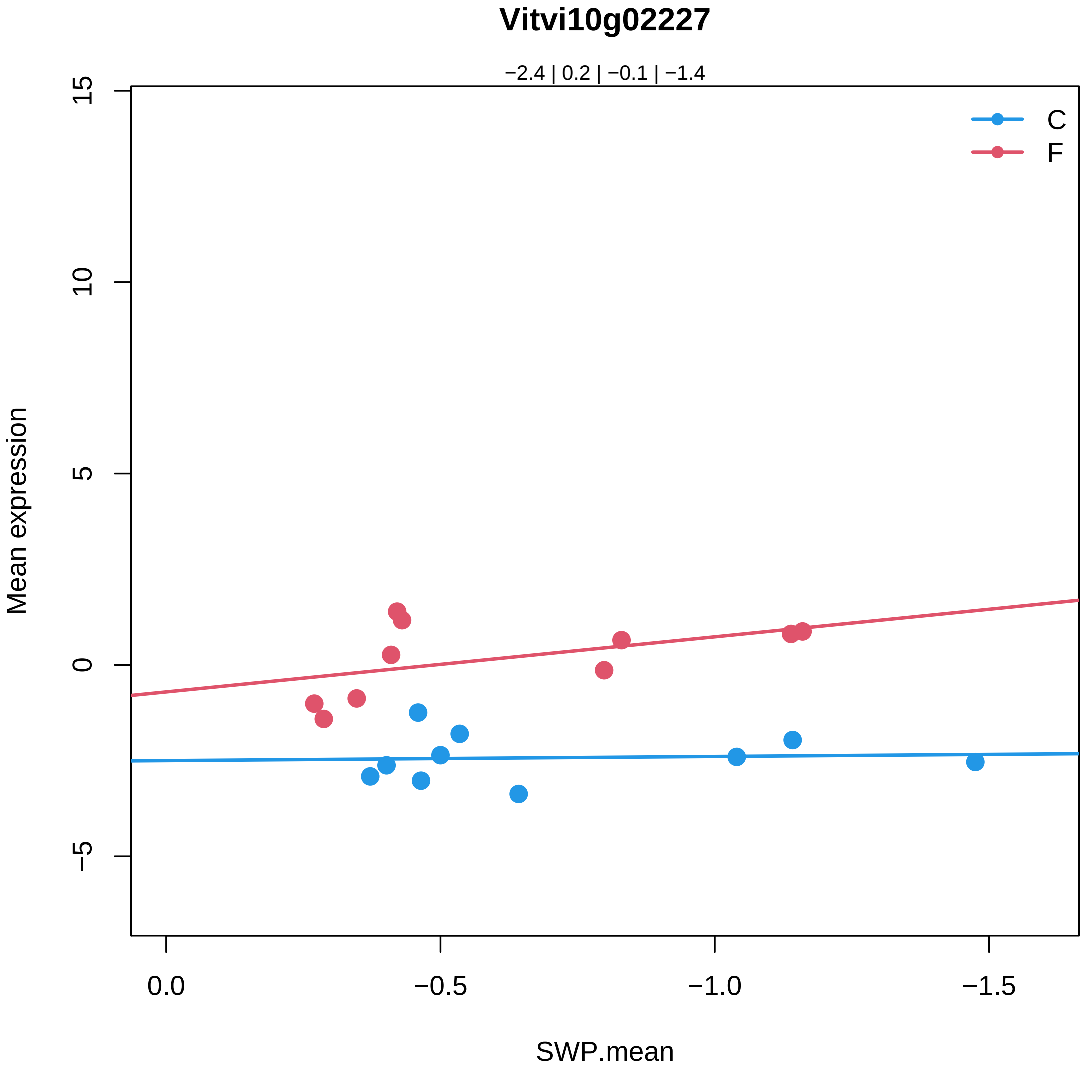
7.4.64 Vitvi10g02227: type3

```
> 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
```



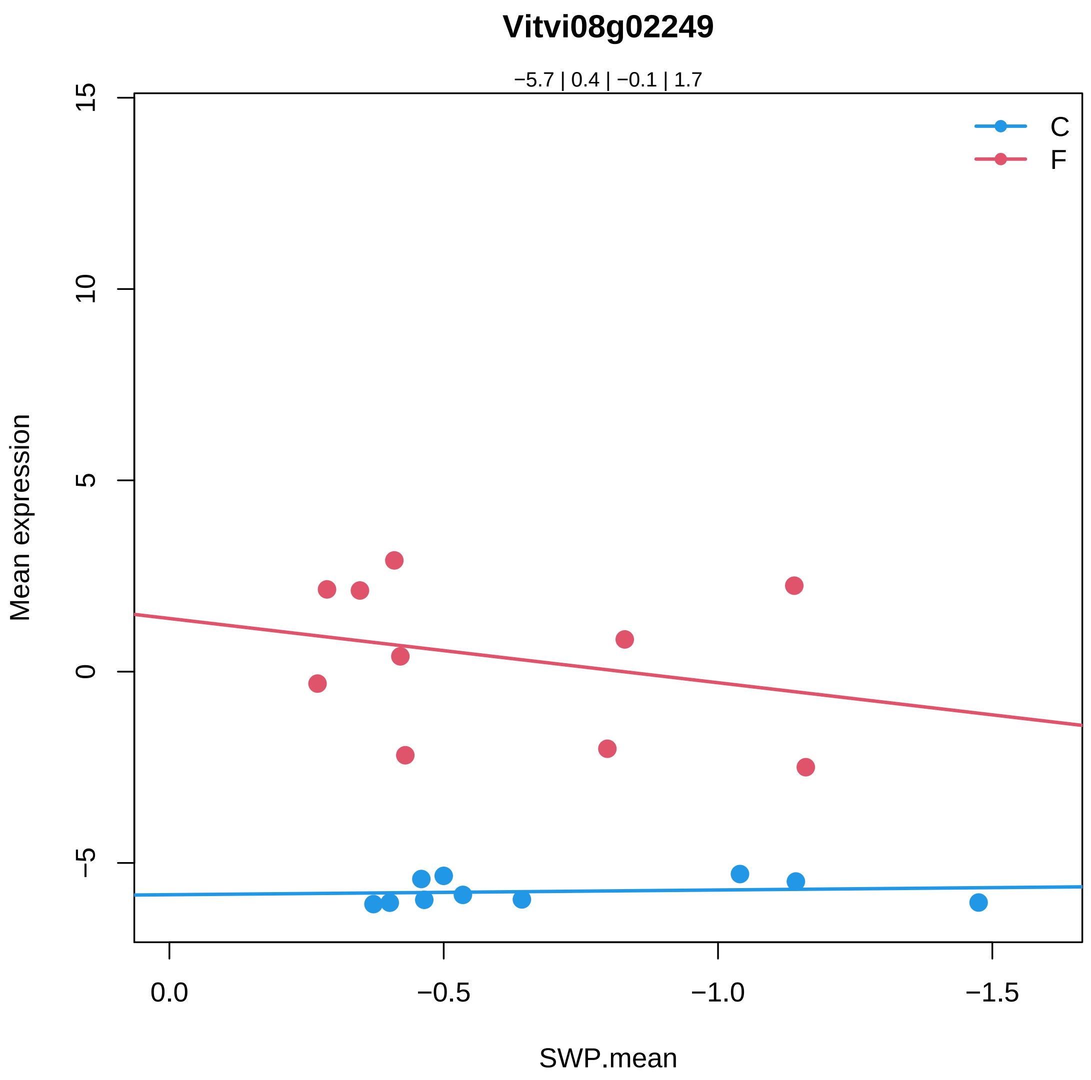
7.4.65 Vitvi08g02249: type3

```
> 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

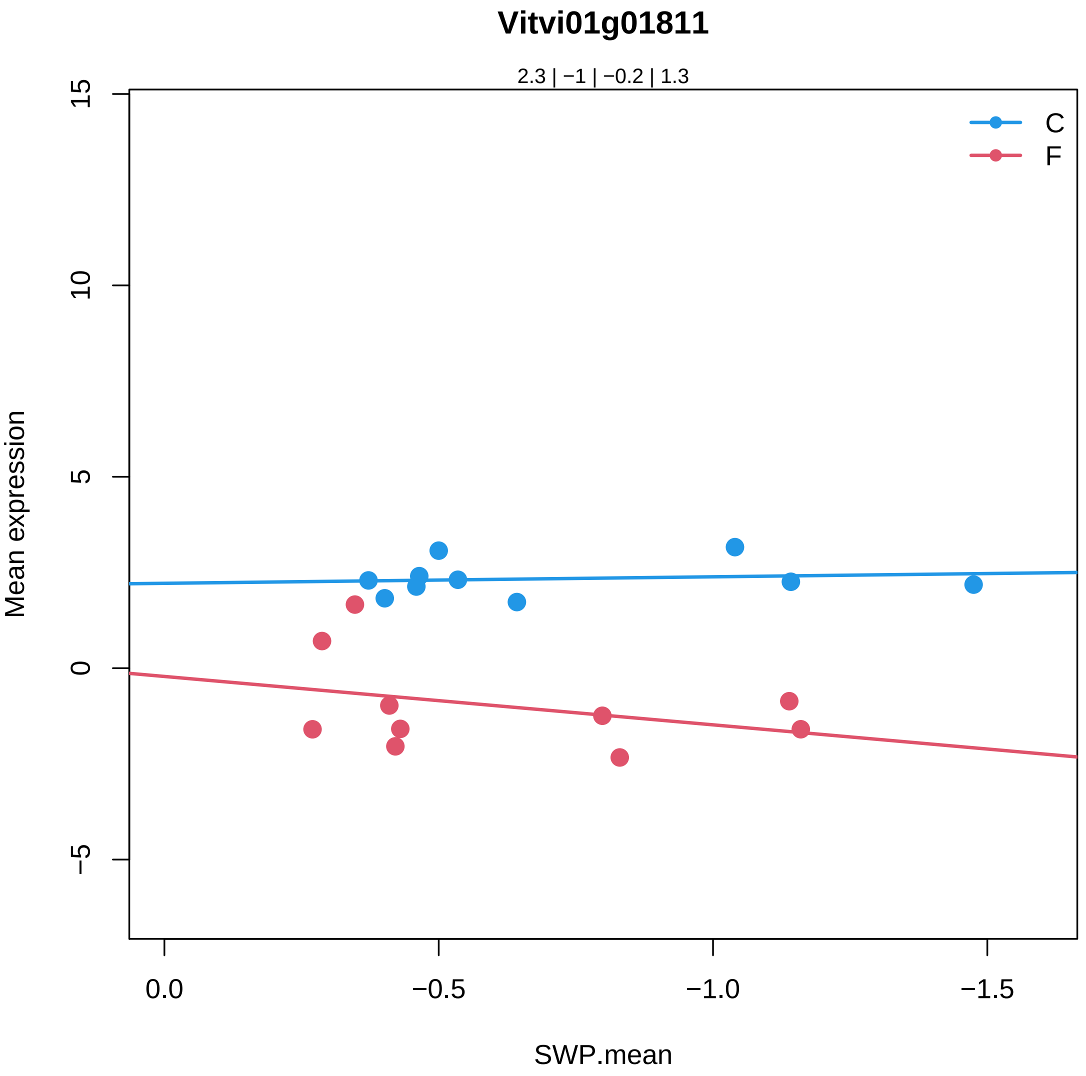
7.4.66 Vitvi01g01811: type3

```
> 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
```



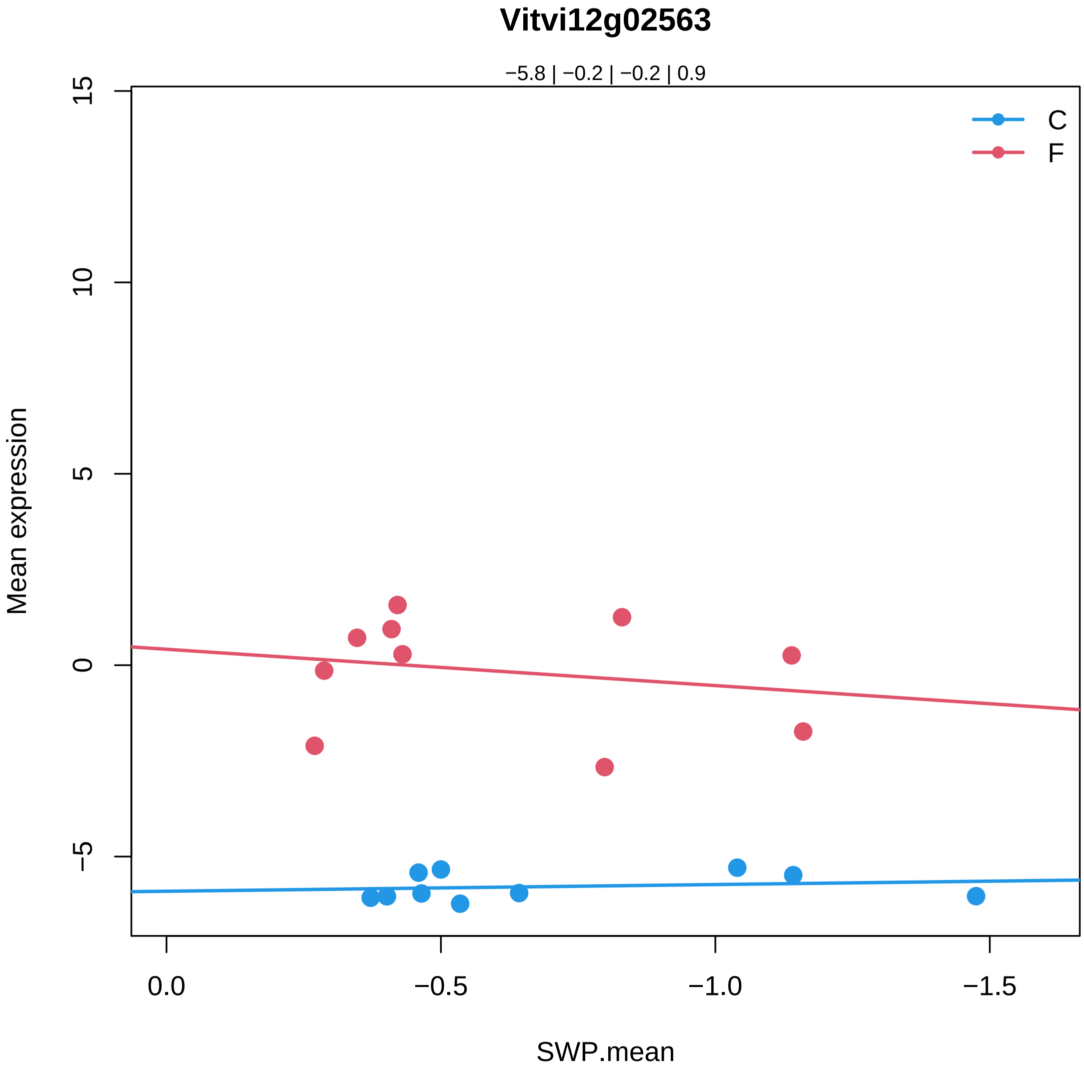
7.4.67 Vitvi12g02563: type3

```
> 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
```



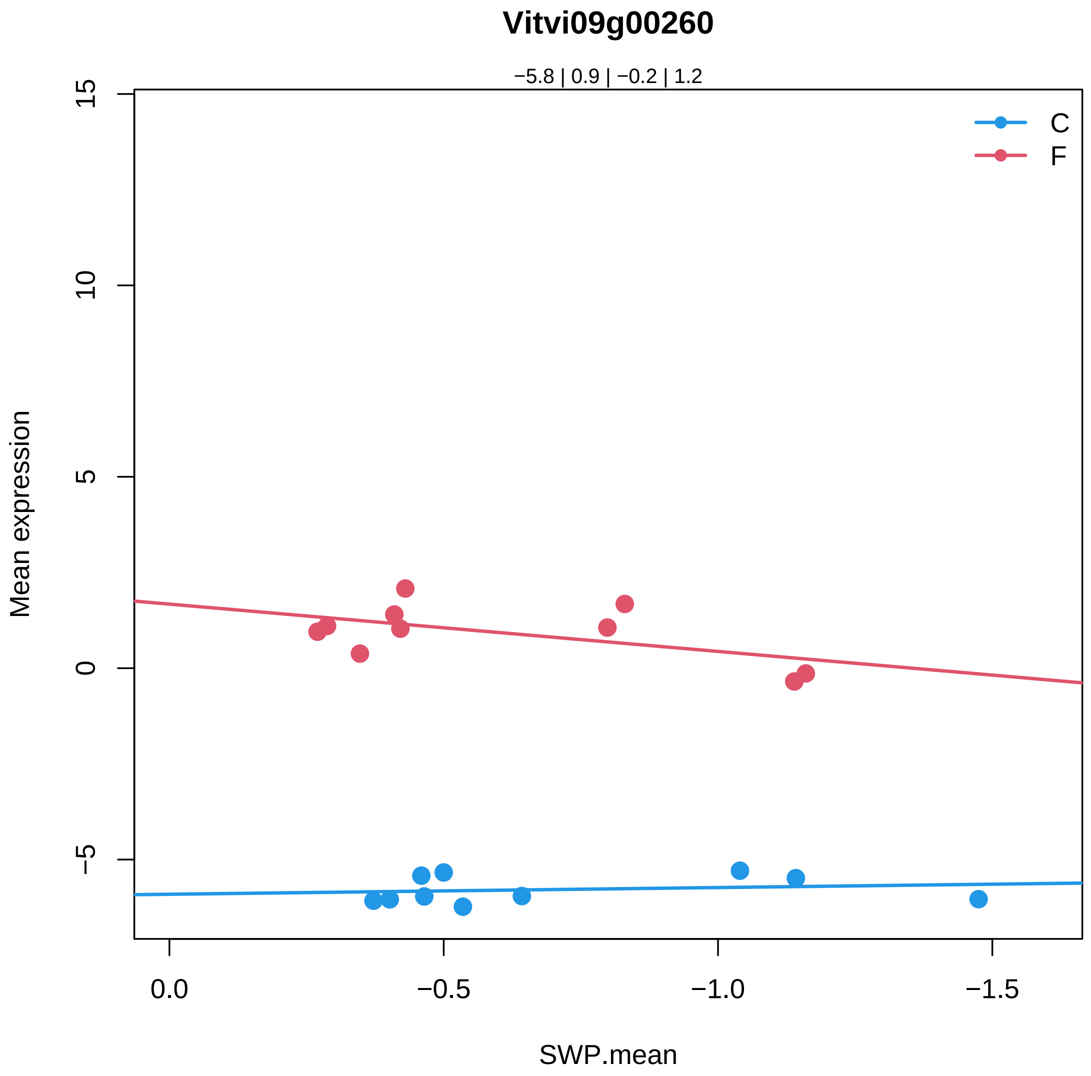
7.4.68 Vitvi09g00260: type3

```
> 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
```



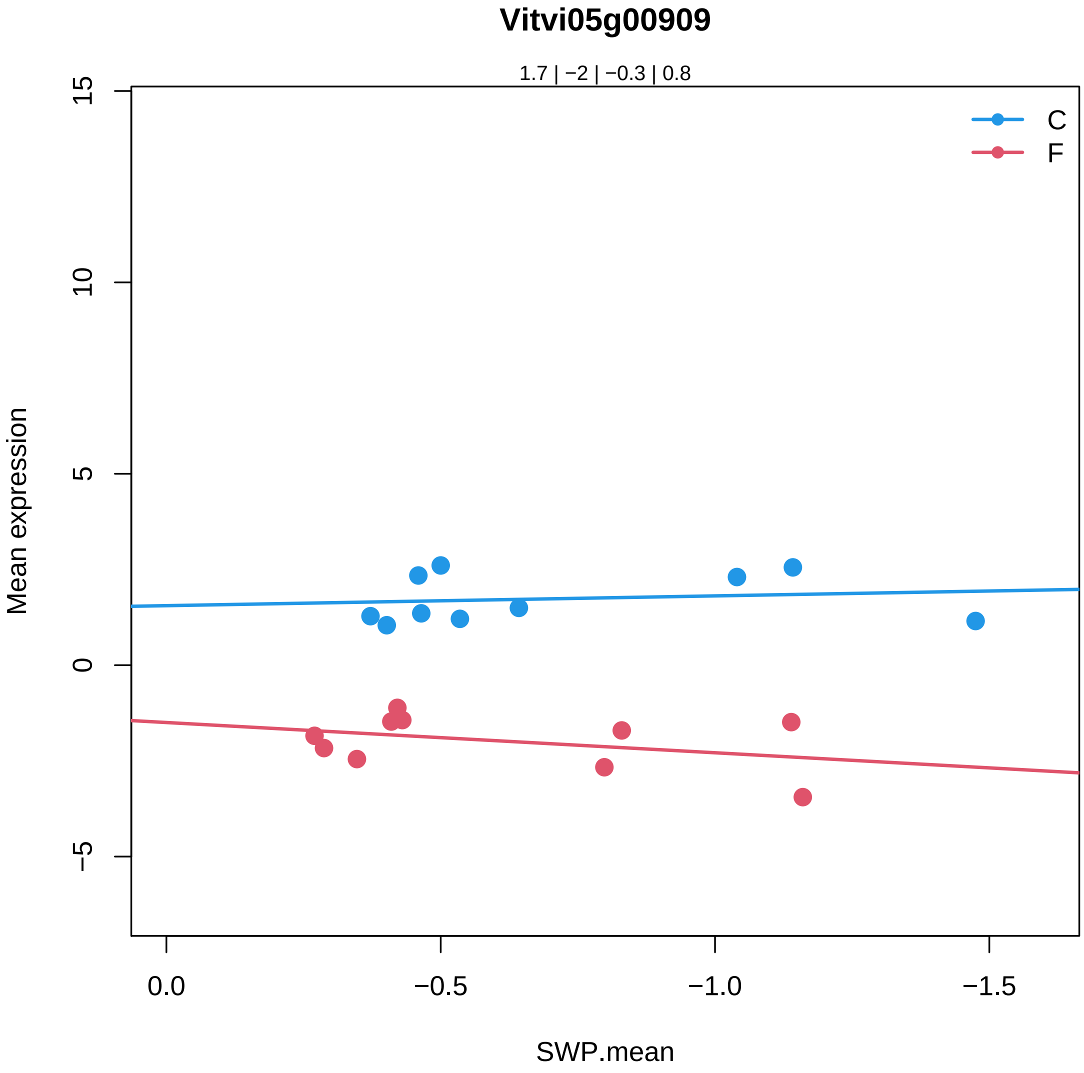
7.4.69 Vitvi05g00909: type3

```
> 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
```



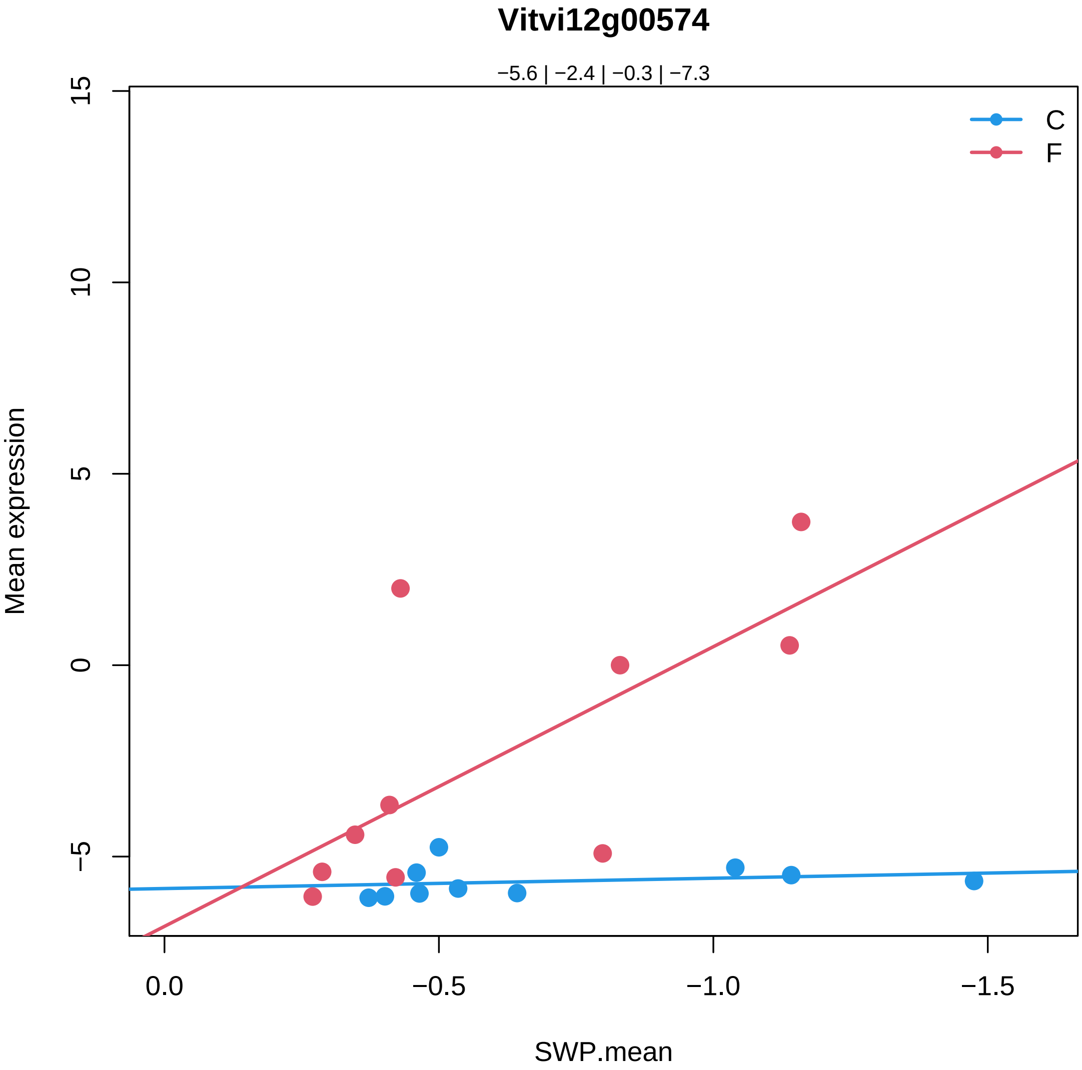
7.4.70 Vitvi12g00574: + type3 | type4

```
> 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
```



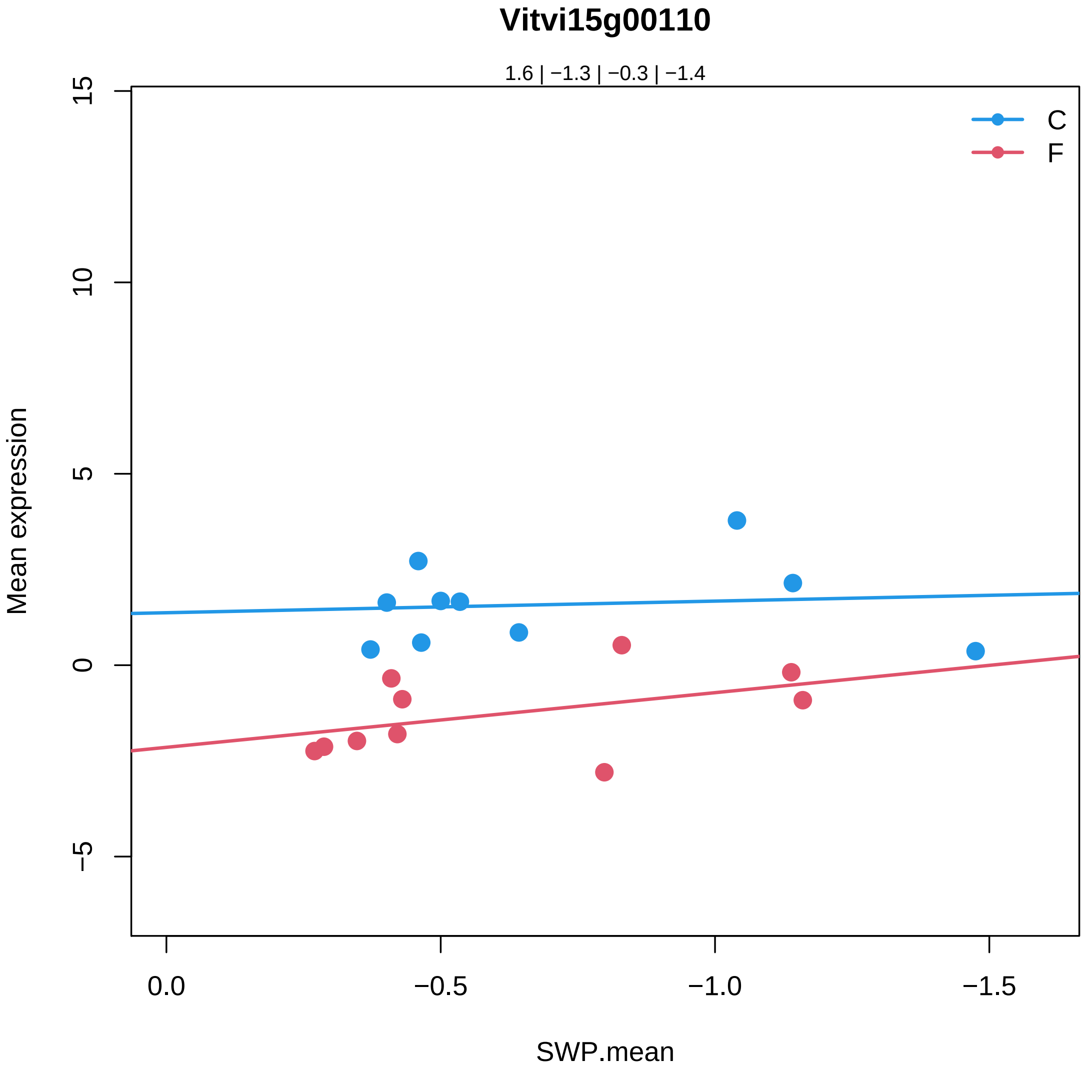
7.4.71 Vitvi15g00110: type3

```
> 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
```



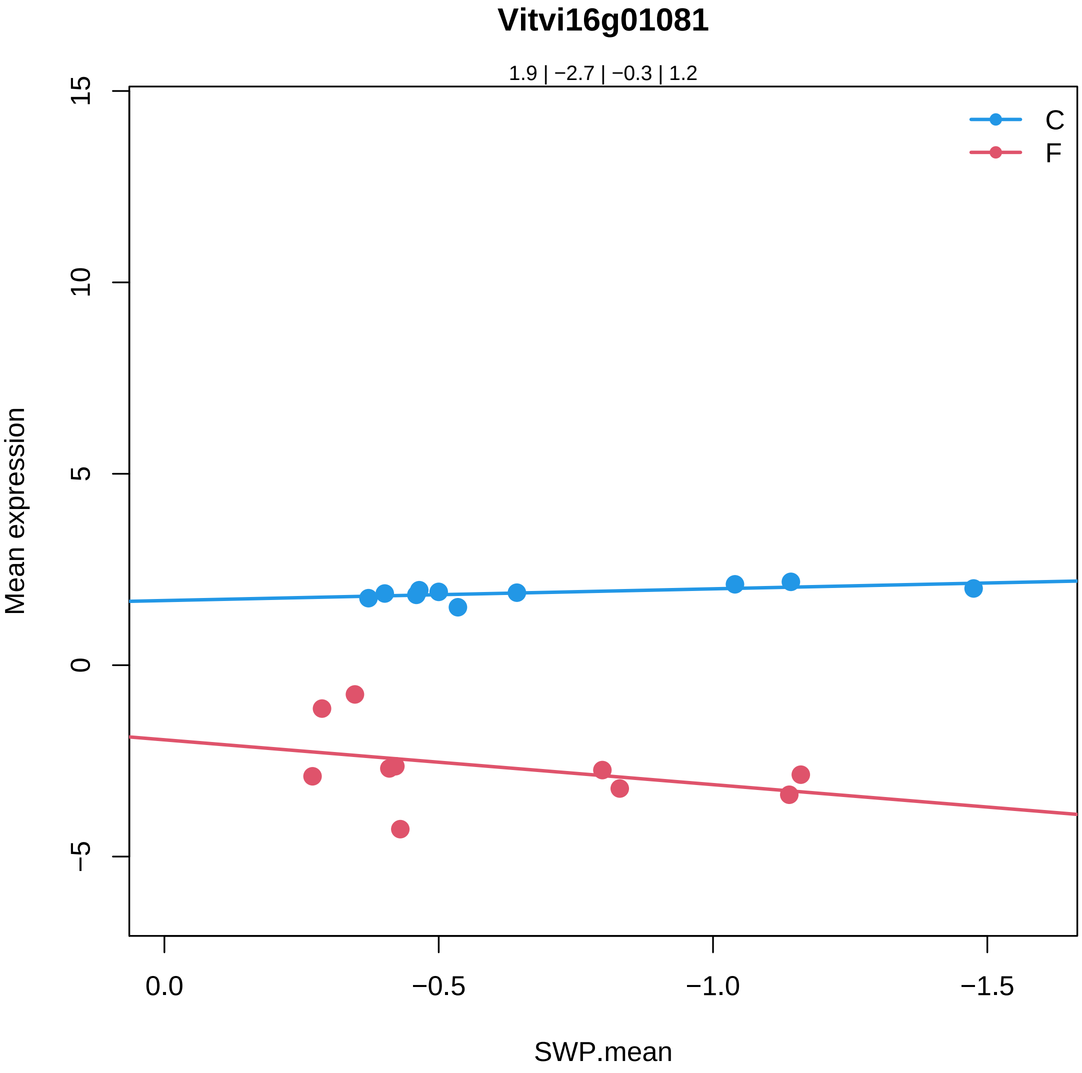
7.4.72 Vitvi16g01081: type3

```
> 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
```



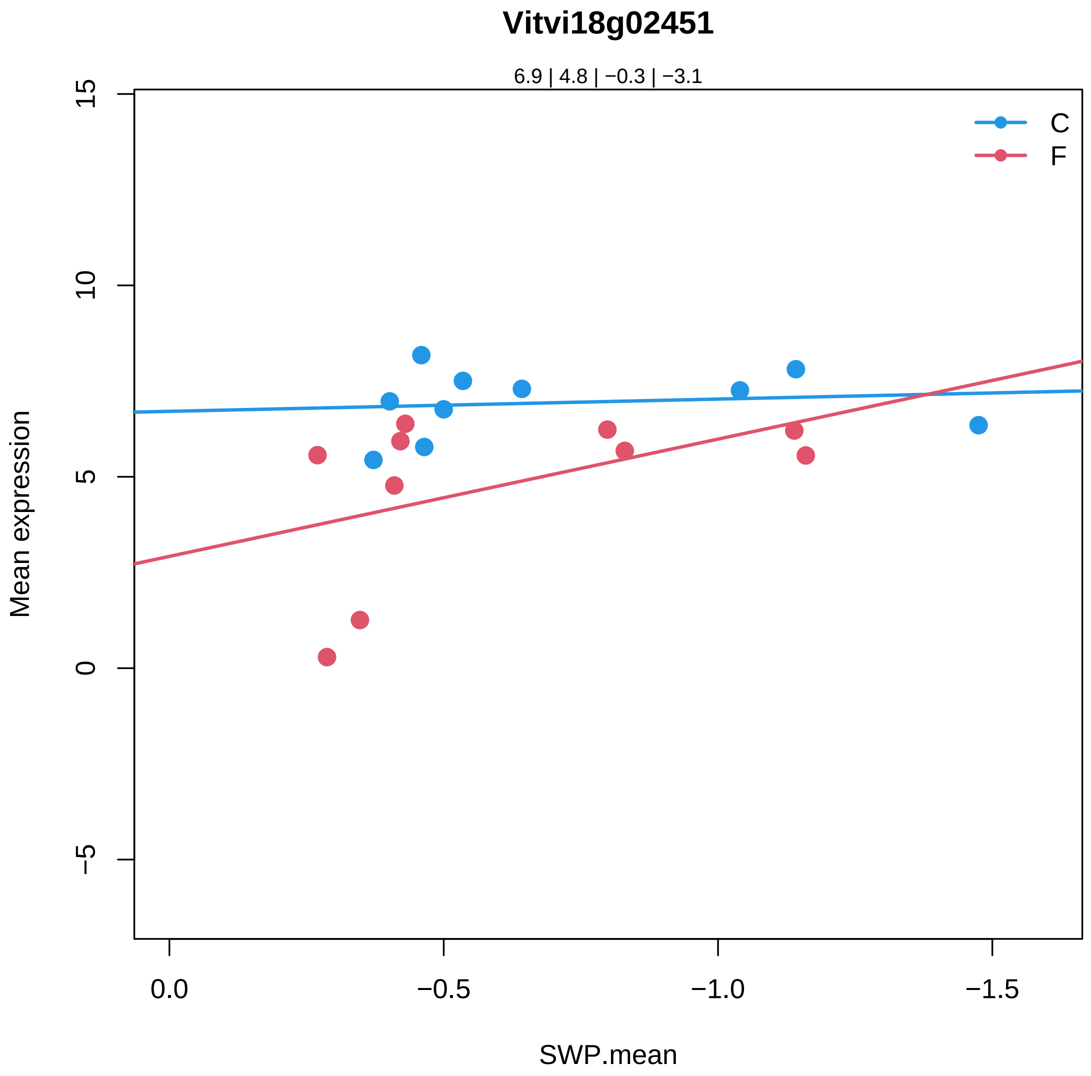
7.4.73 Vitvi18g02451: type3 | type4

```
> 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
```



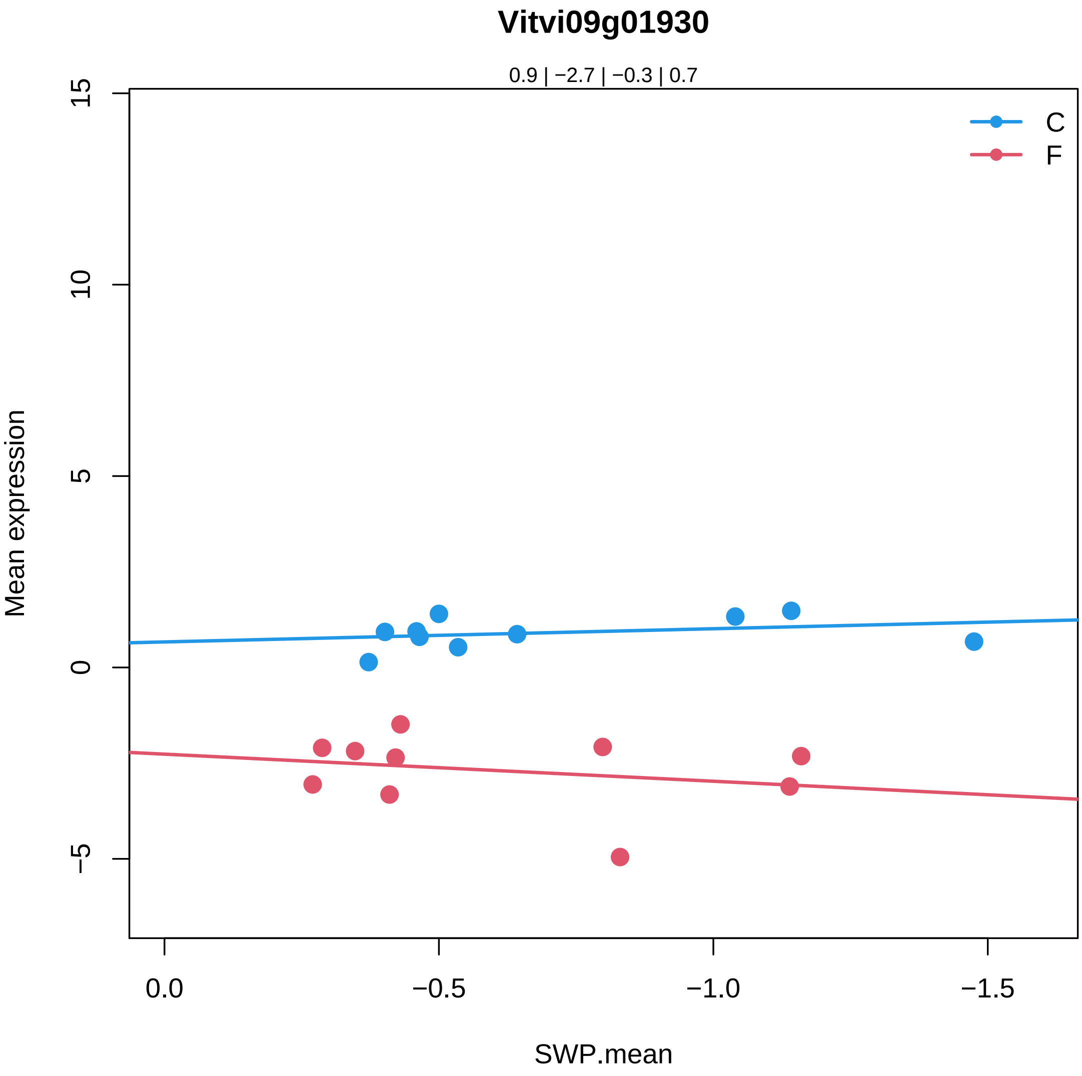
7.4.74 Vitvi09g01930: type3

```
> 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

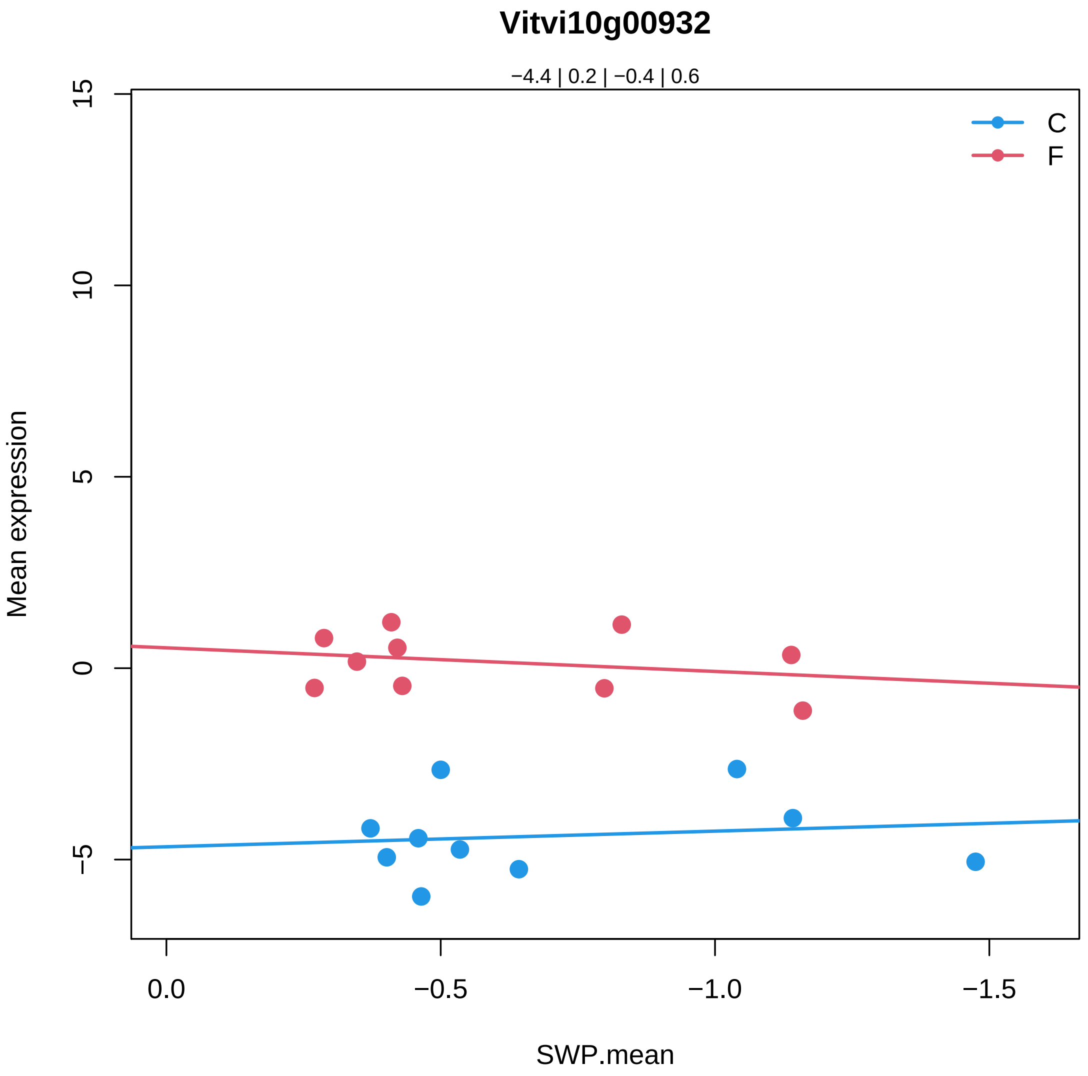
7.4.75 Vitvi10g00932: type3

```
> 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
```



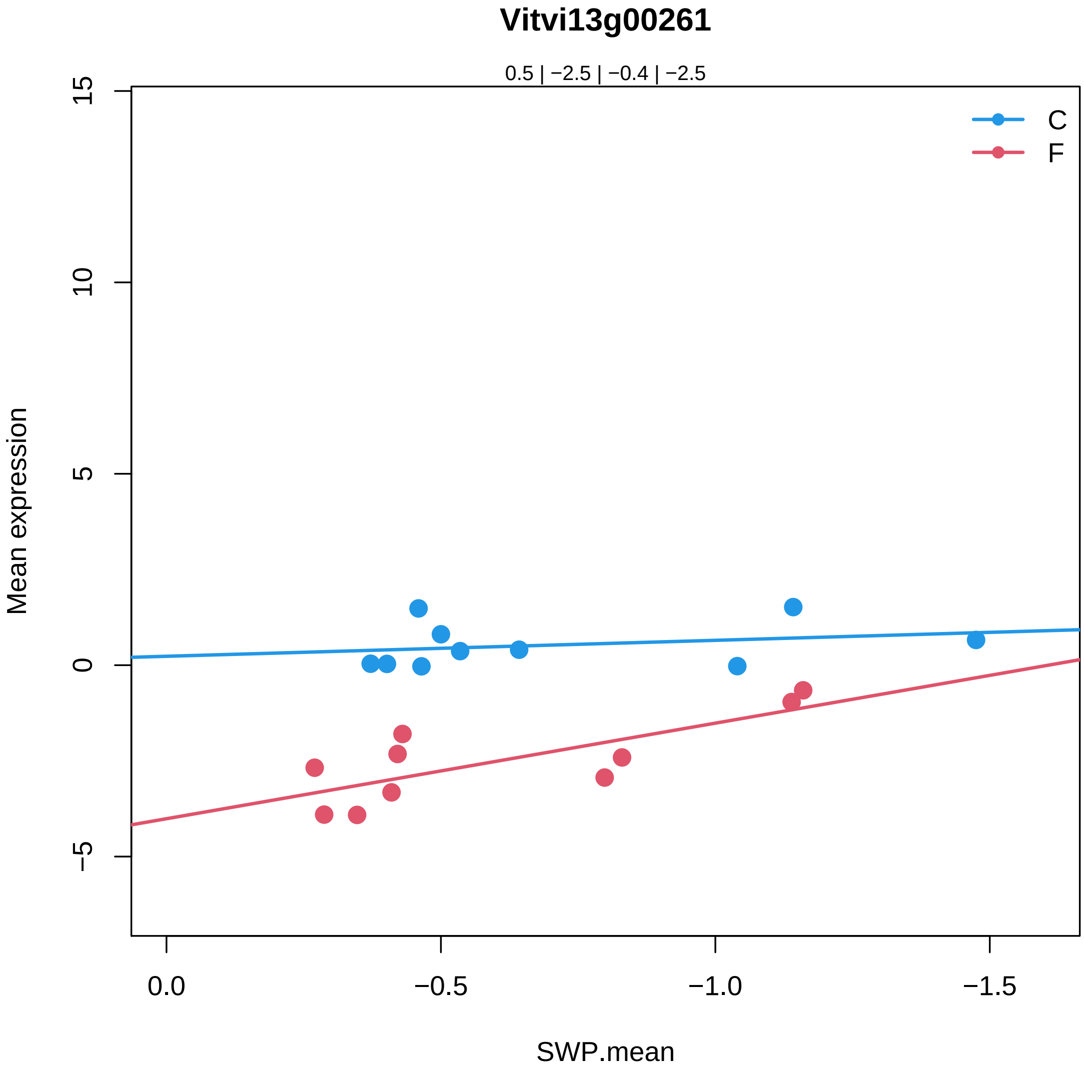
7.4.76 Vitvi13g00261: + type3 | type4

```
> 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
```



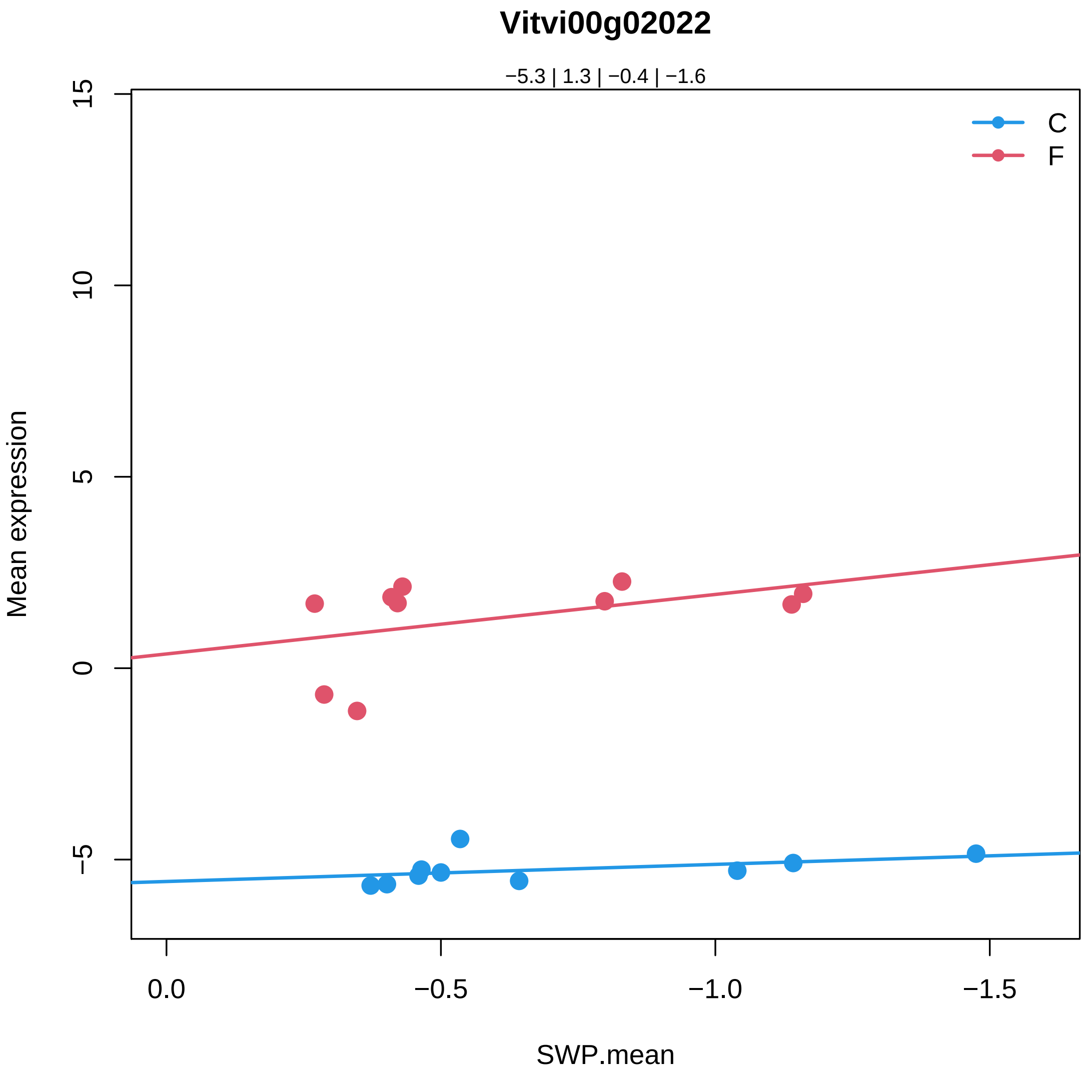
7.4.77 Vitvi00g02022: type3

```
> 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
```



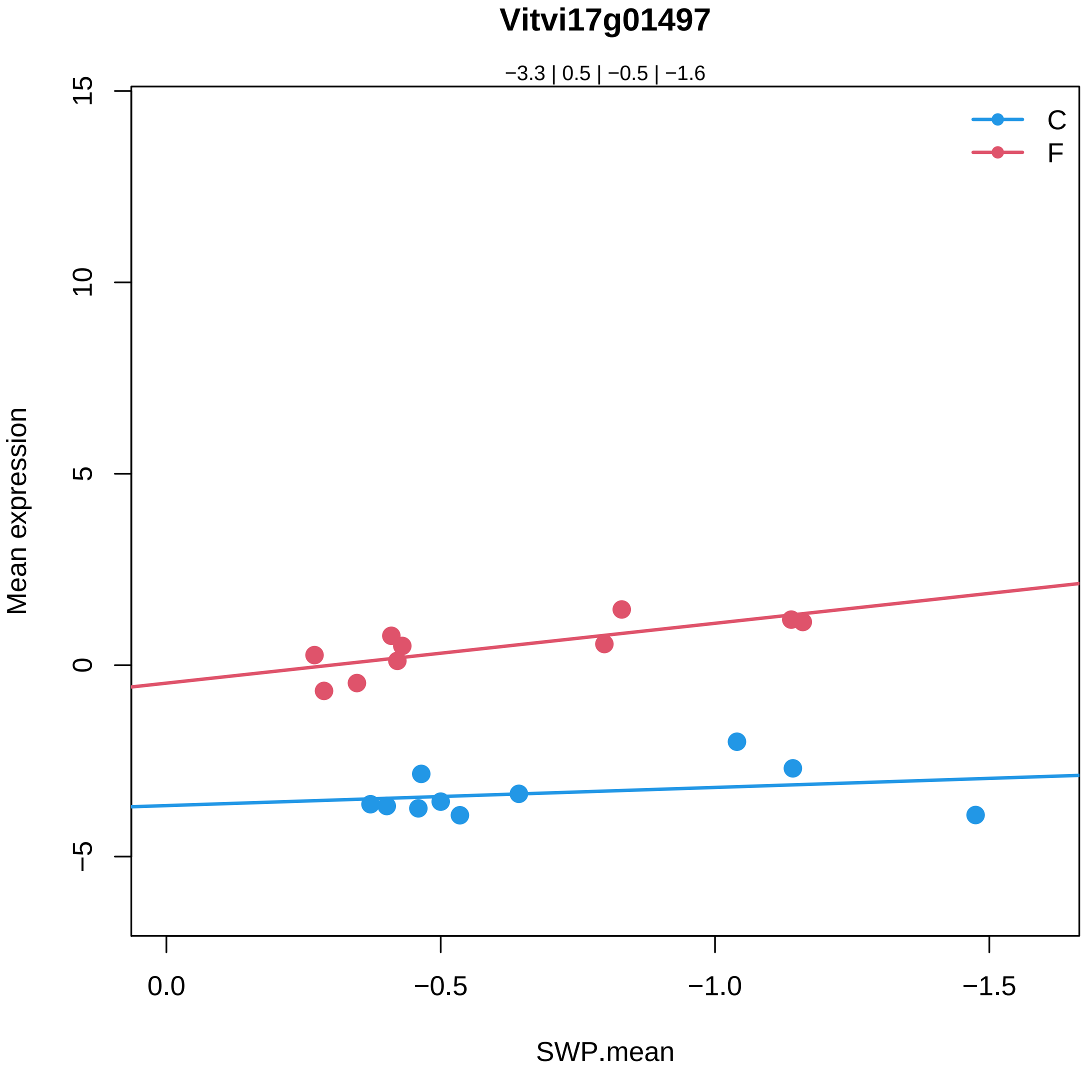
7.4.78 Vitvi17g01497: type3

```
> 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
```



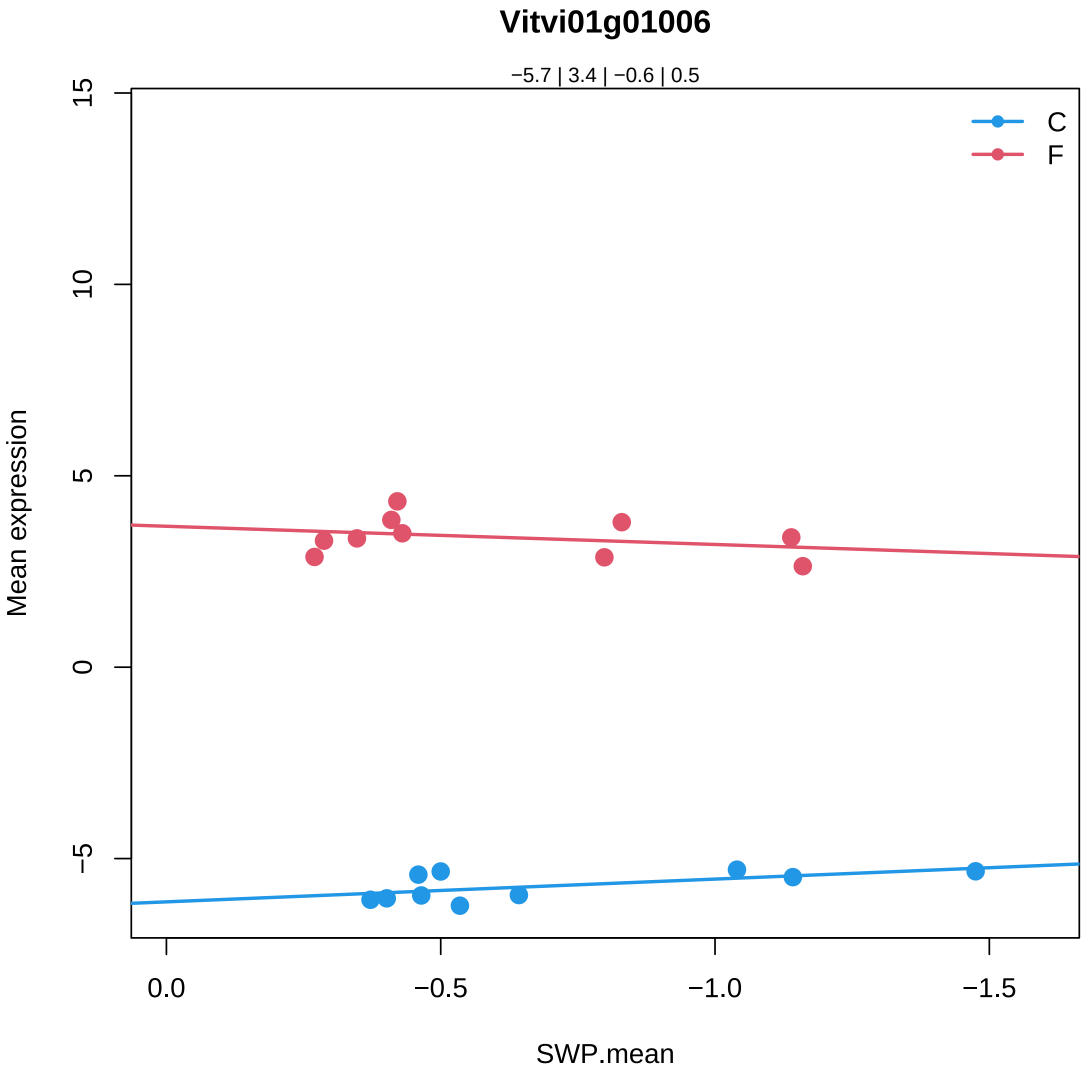
7.4.79 Vitvi01g01006: type3

```
> 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
```



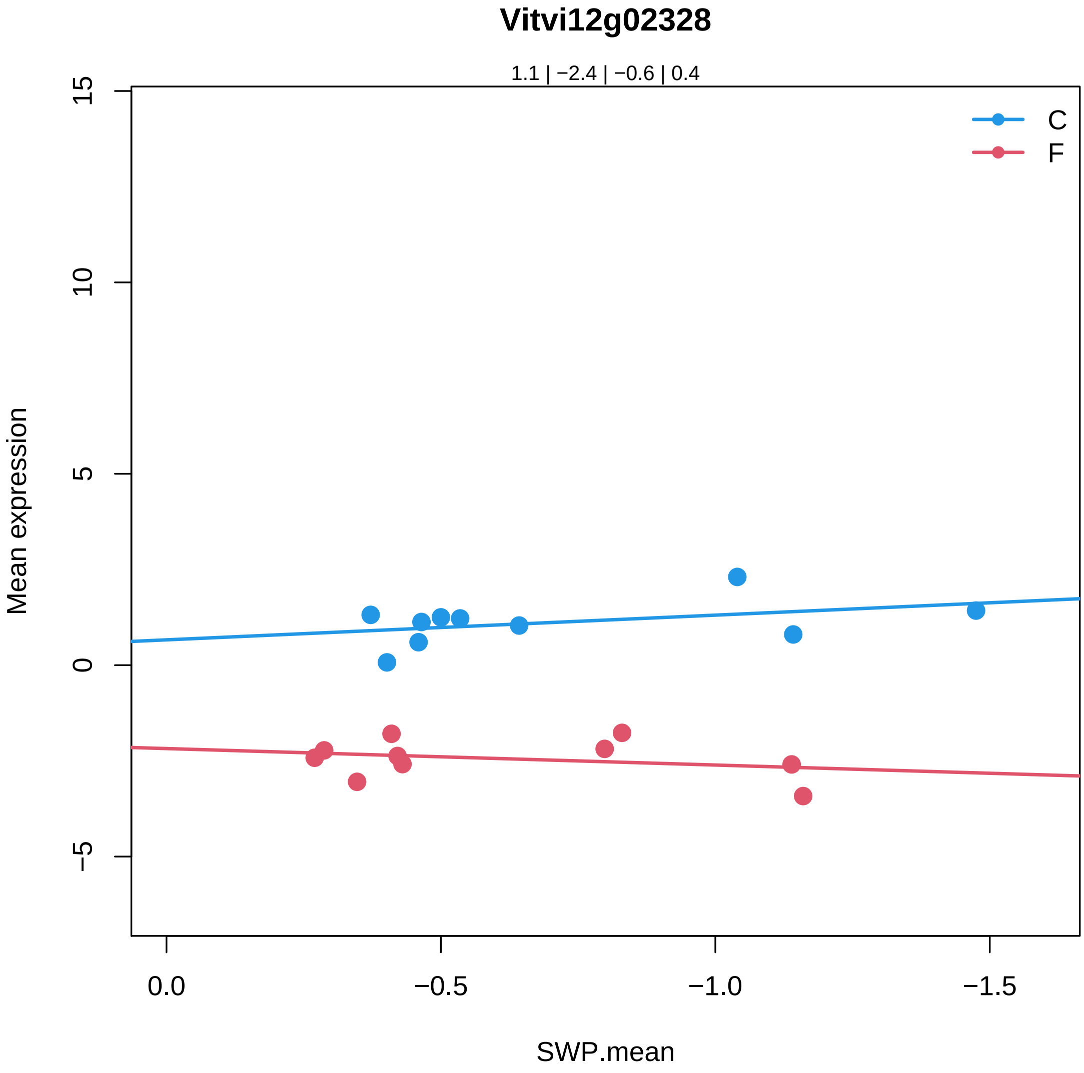
7.4.80 Vitvi12g02328: type3

```
> 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        
```



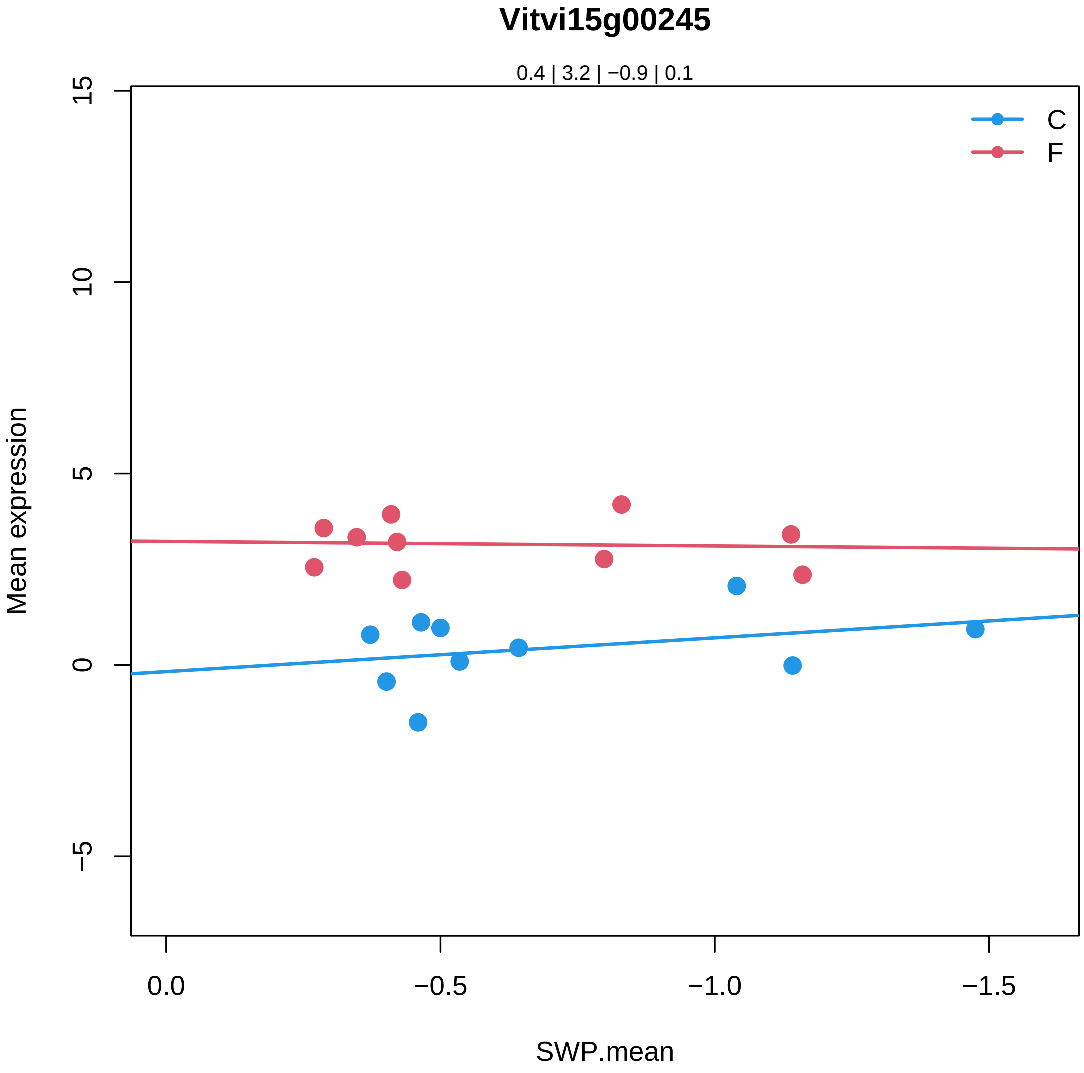
7.4.81 Vitvi15g00245: type3

```
> 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
```



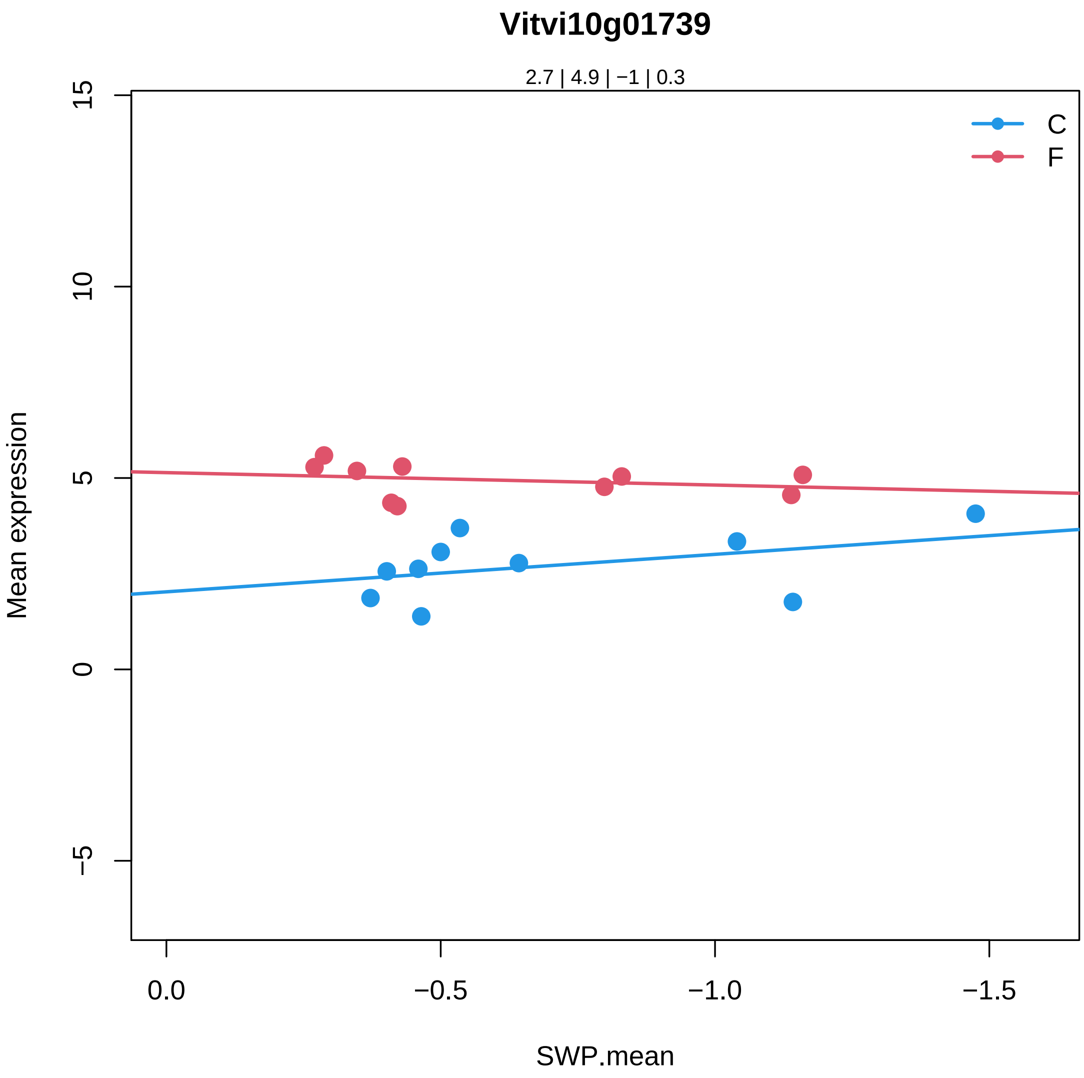
7.4.82 Vitvi10g01739: type3

```
> 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
```



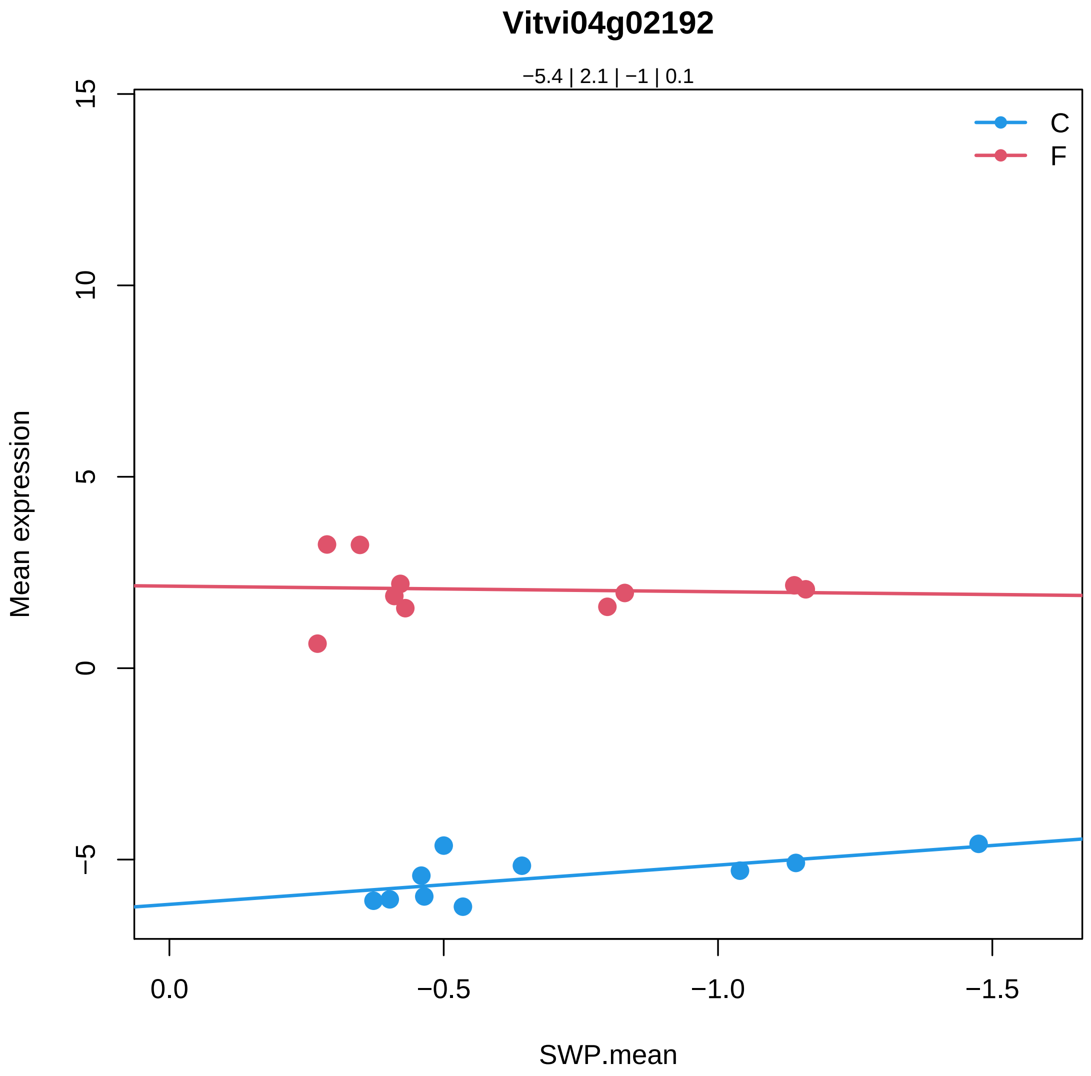
7.4.83 Vitvi04g02192: type3

```
> 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
```



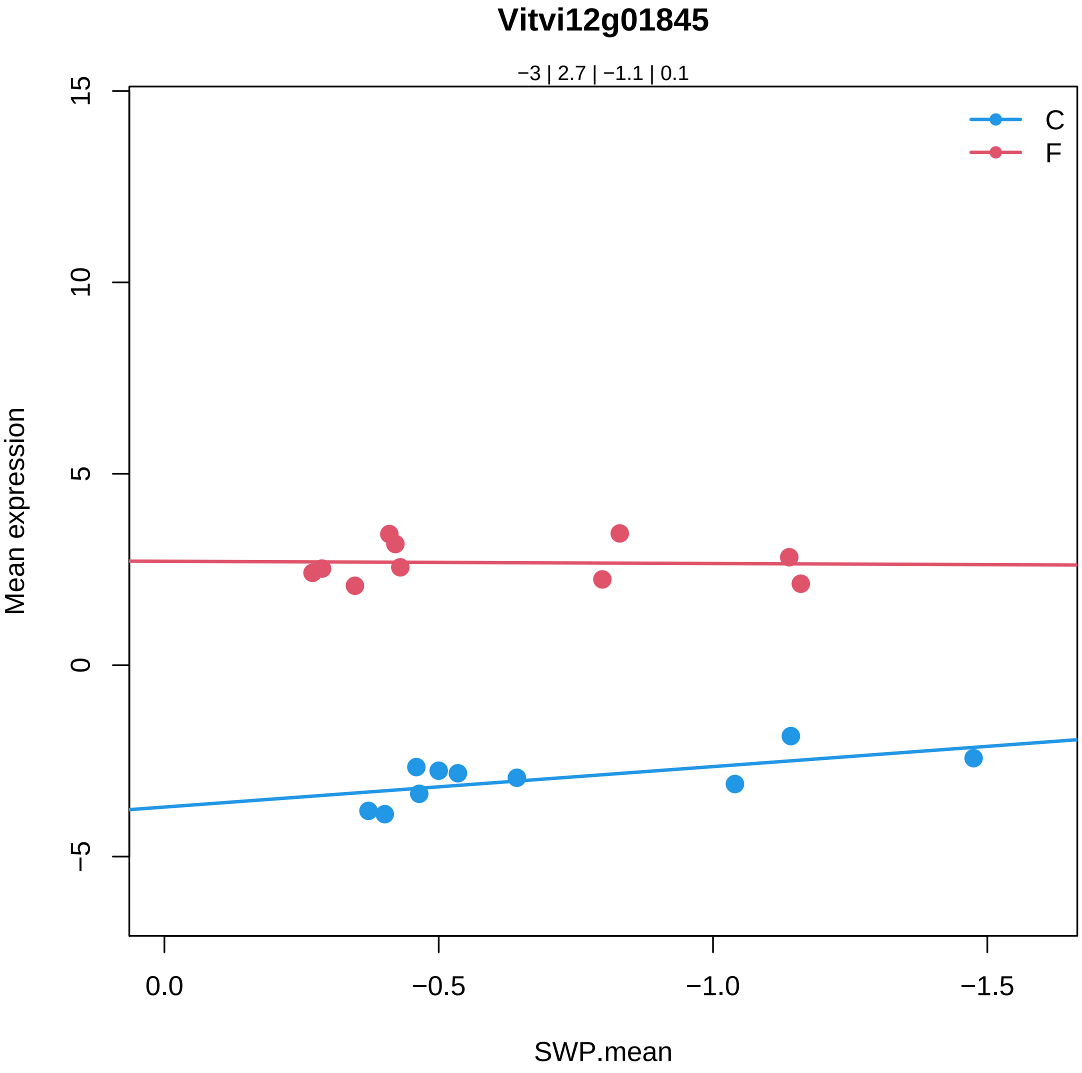
7.4.84 Vitvi12g01845: * type3

```
> 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        
```



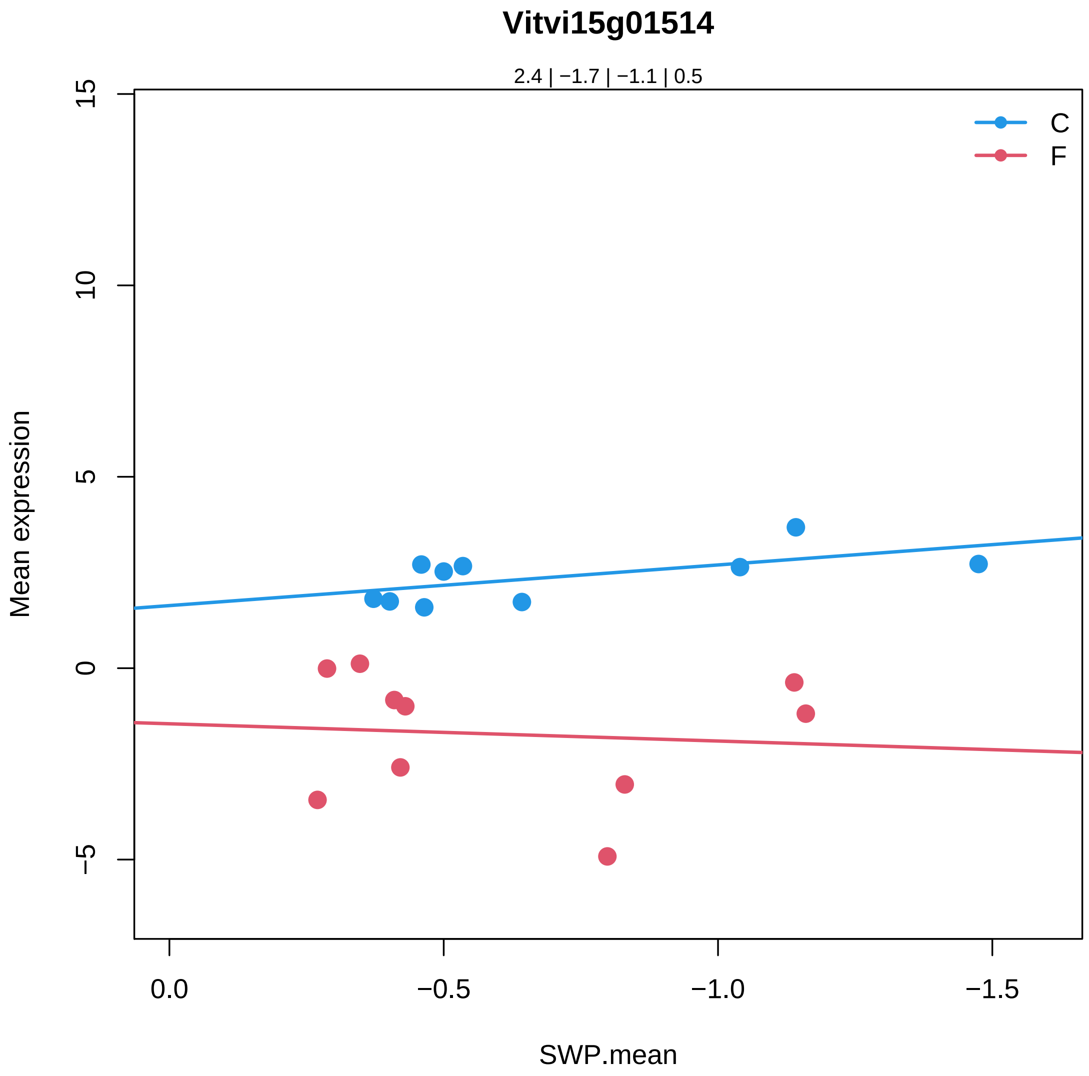
7.4.85 Vitvi15g01514: type3

```
> 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
```



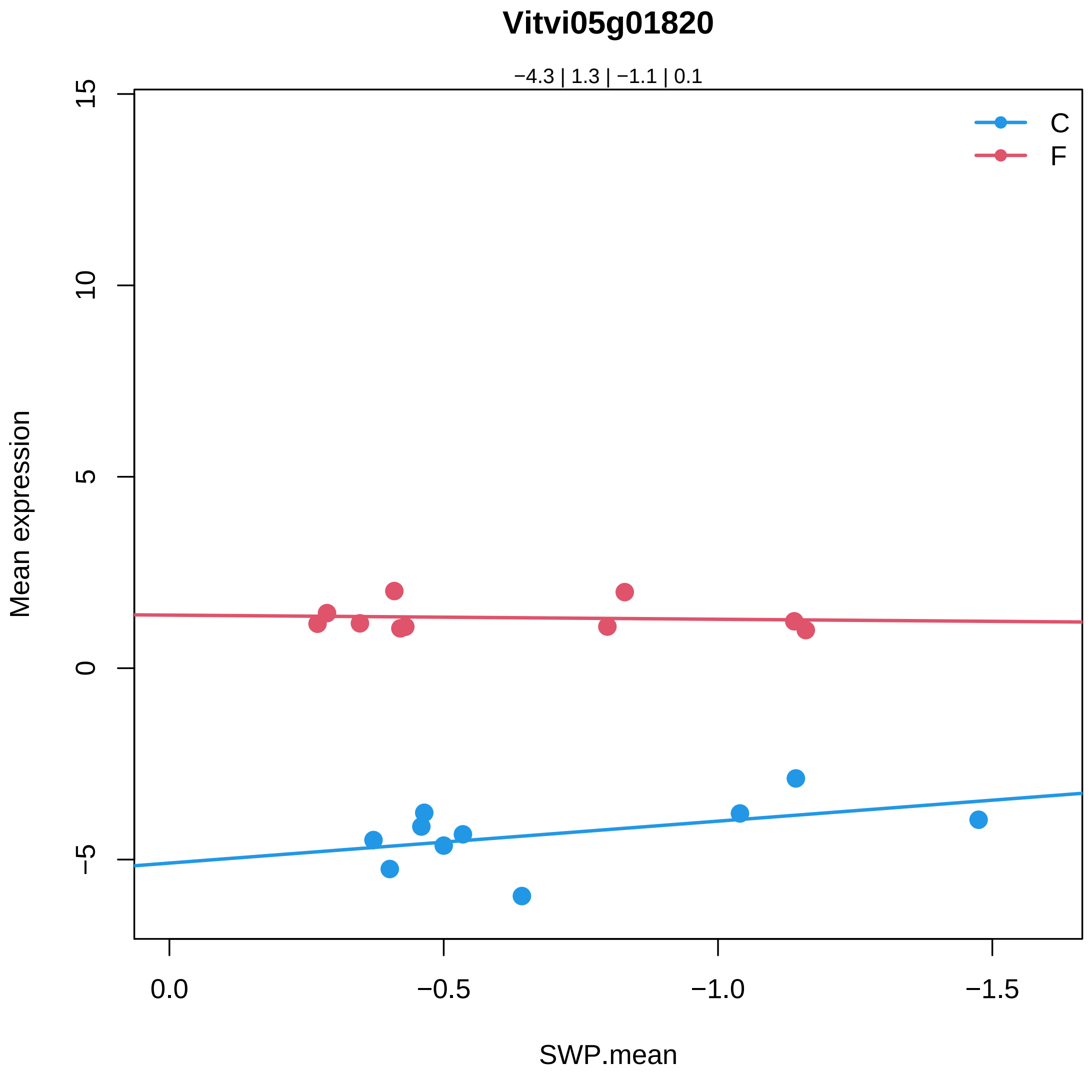
7.4.86 Vitvi05g01820: * type3

```
> 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
```



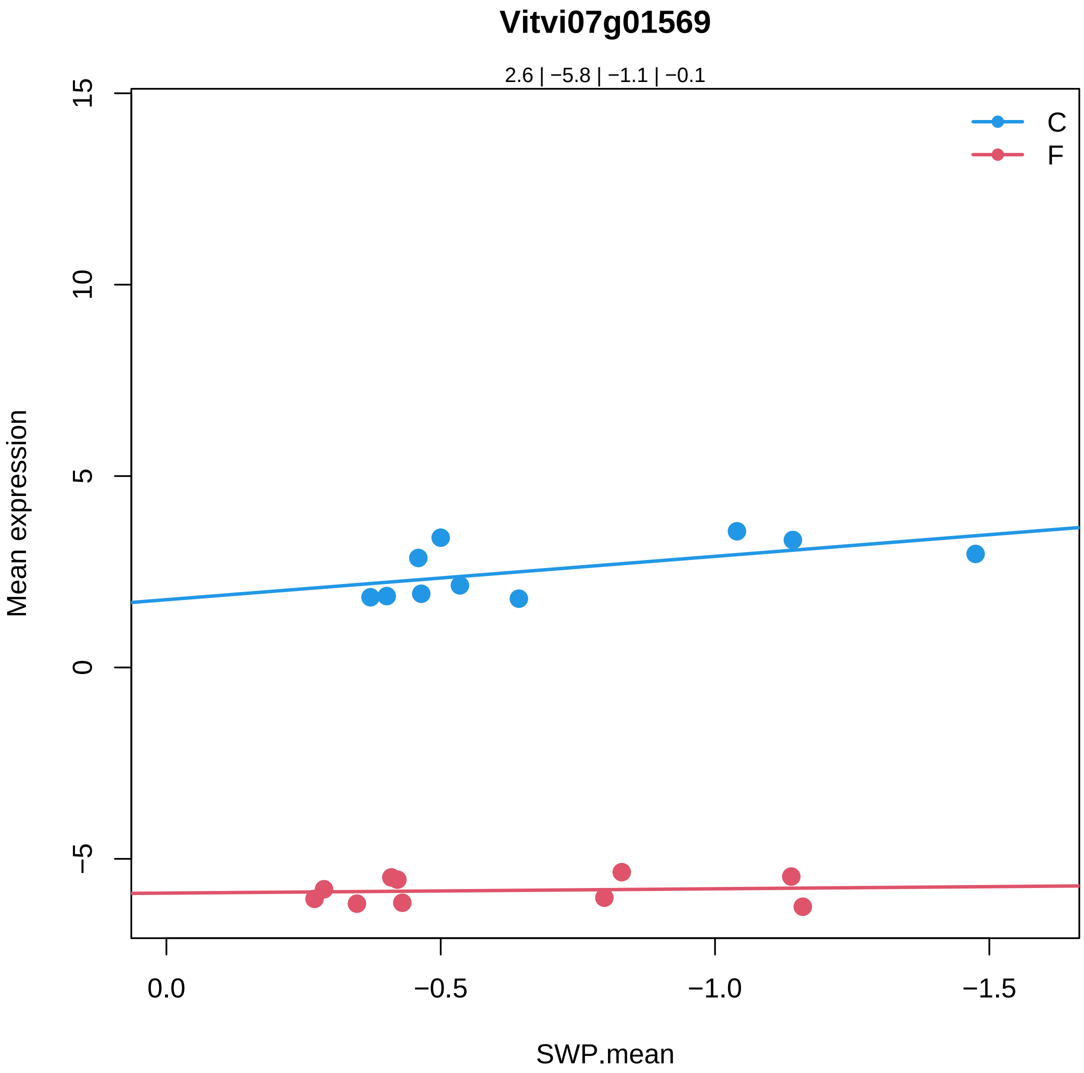
7.4.87 Vitvi07g01569: * type3

```
> 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

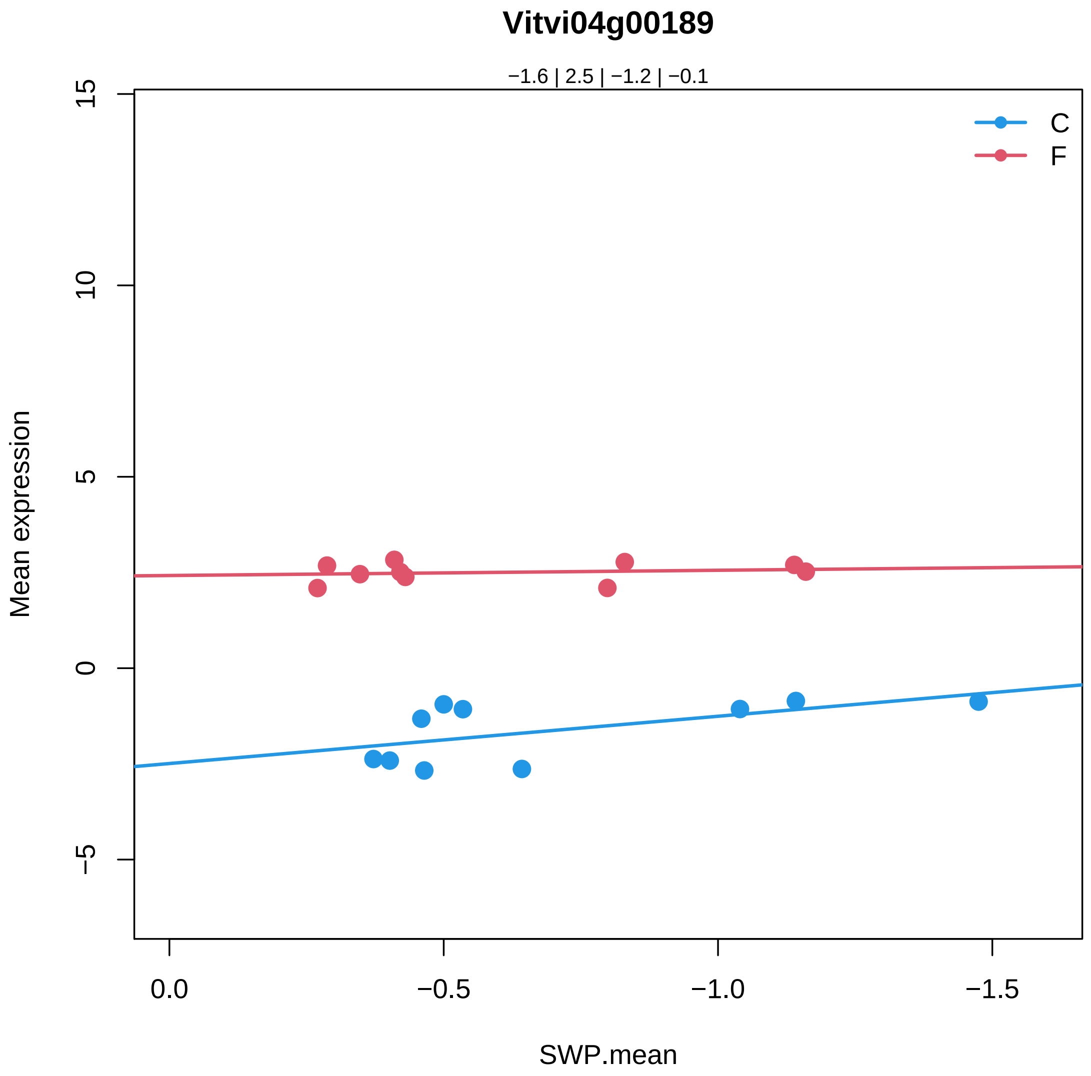
7.4.88 Vitvi04g00189: * type3

```
> 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
```



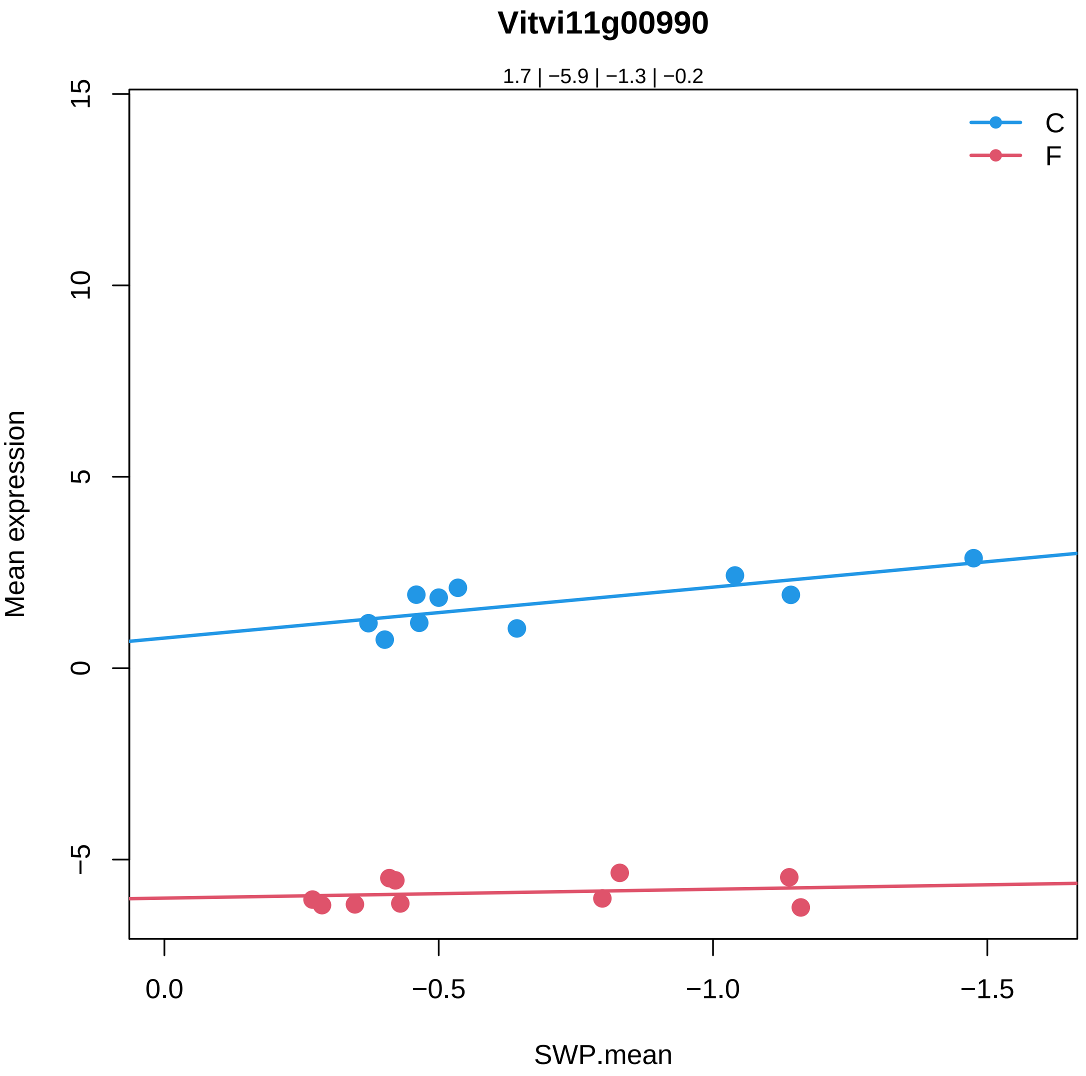
7.4.89 Vitvi11g00990: * type3

```
> 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        
```



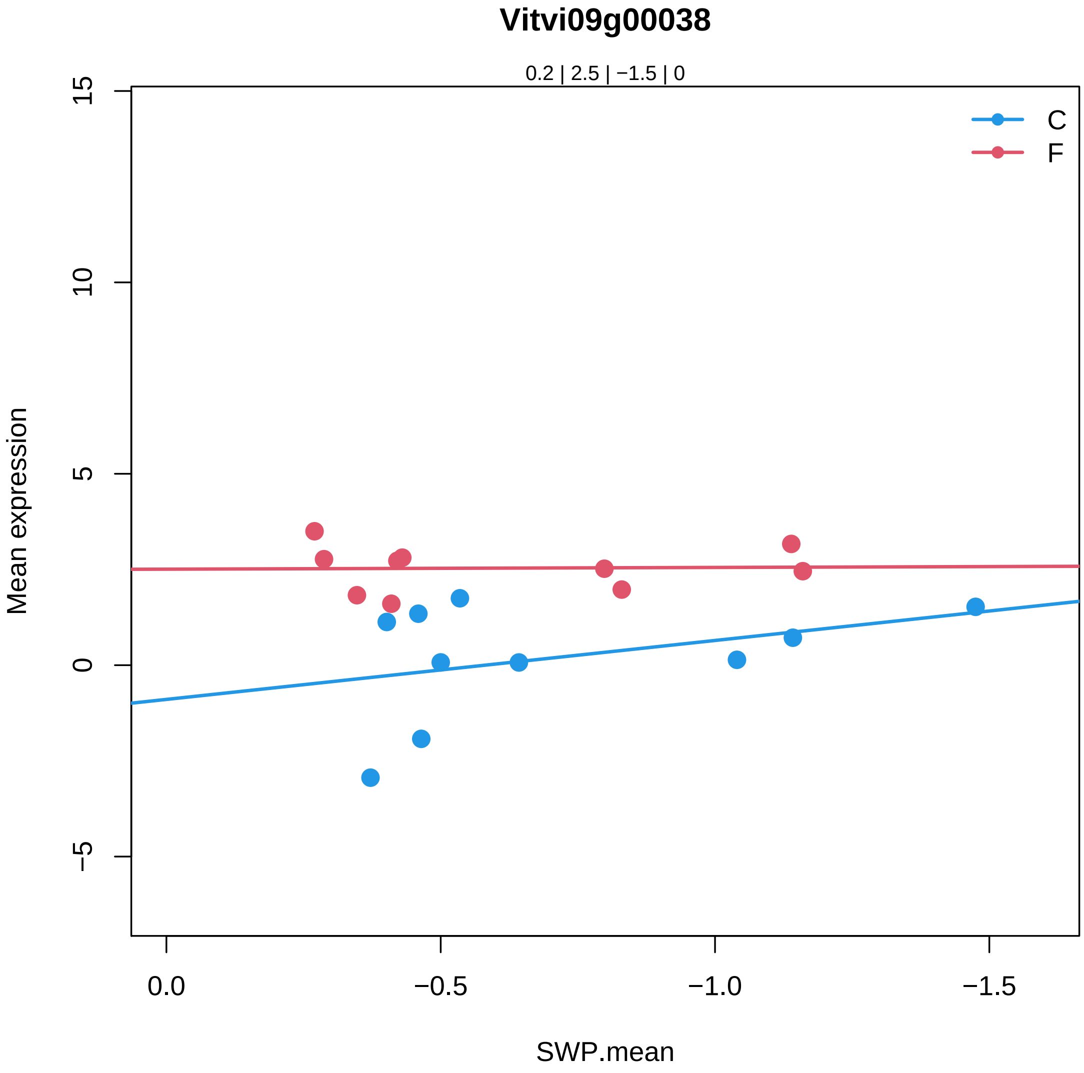
7.4.90 Vitvi09g00038: type3

```
> 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
```



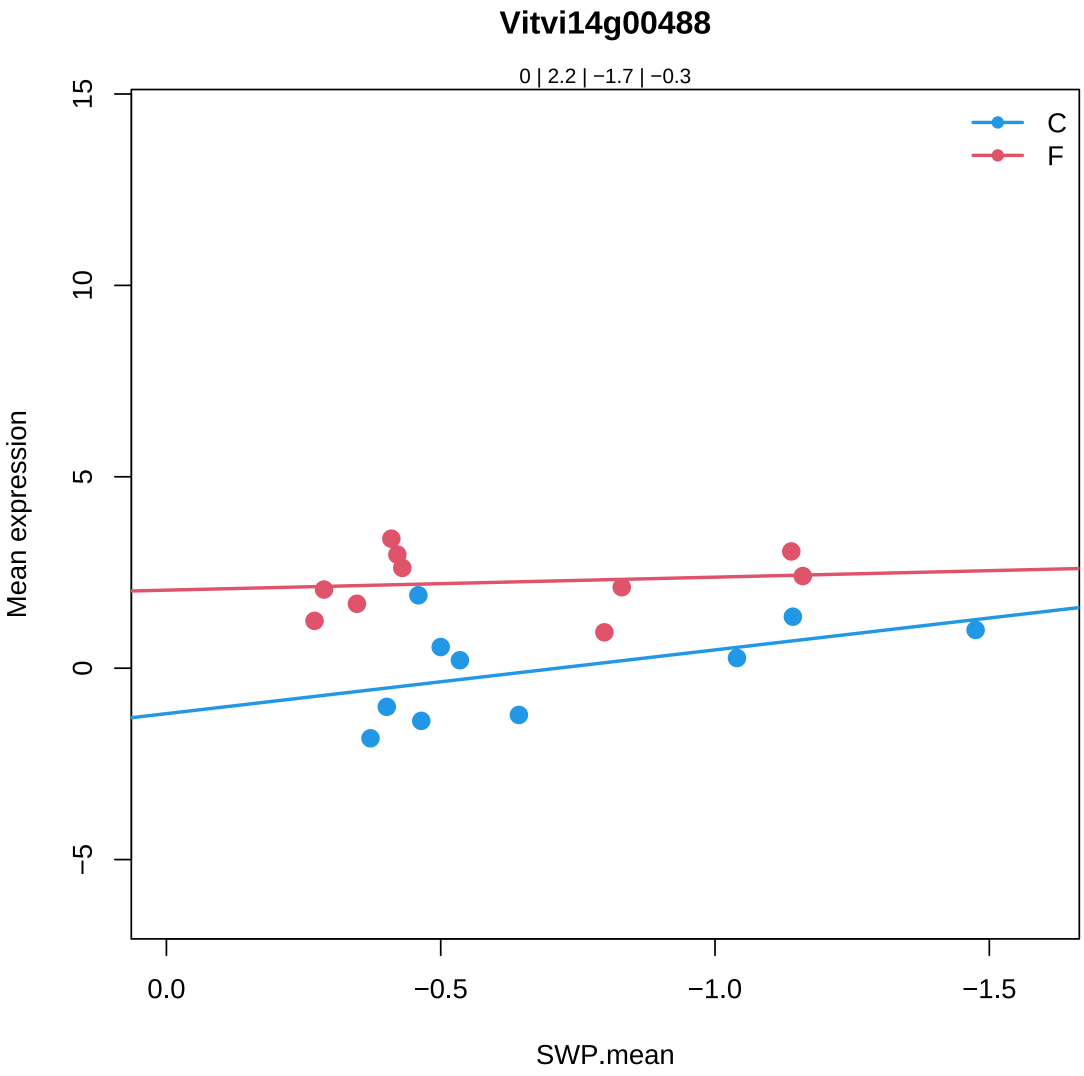
7.4.91 Vitvi14g00488: type3

```
> 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
```



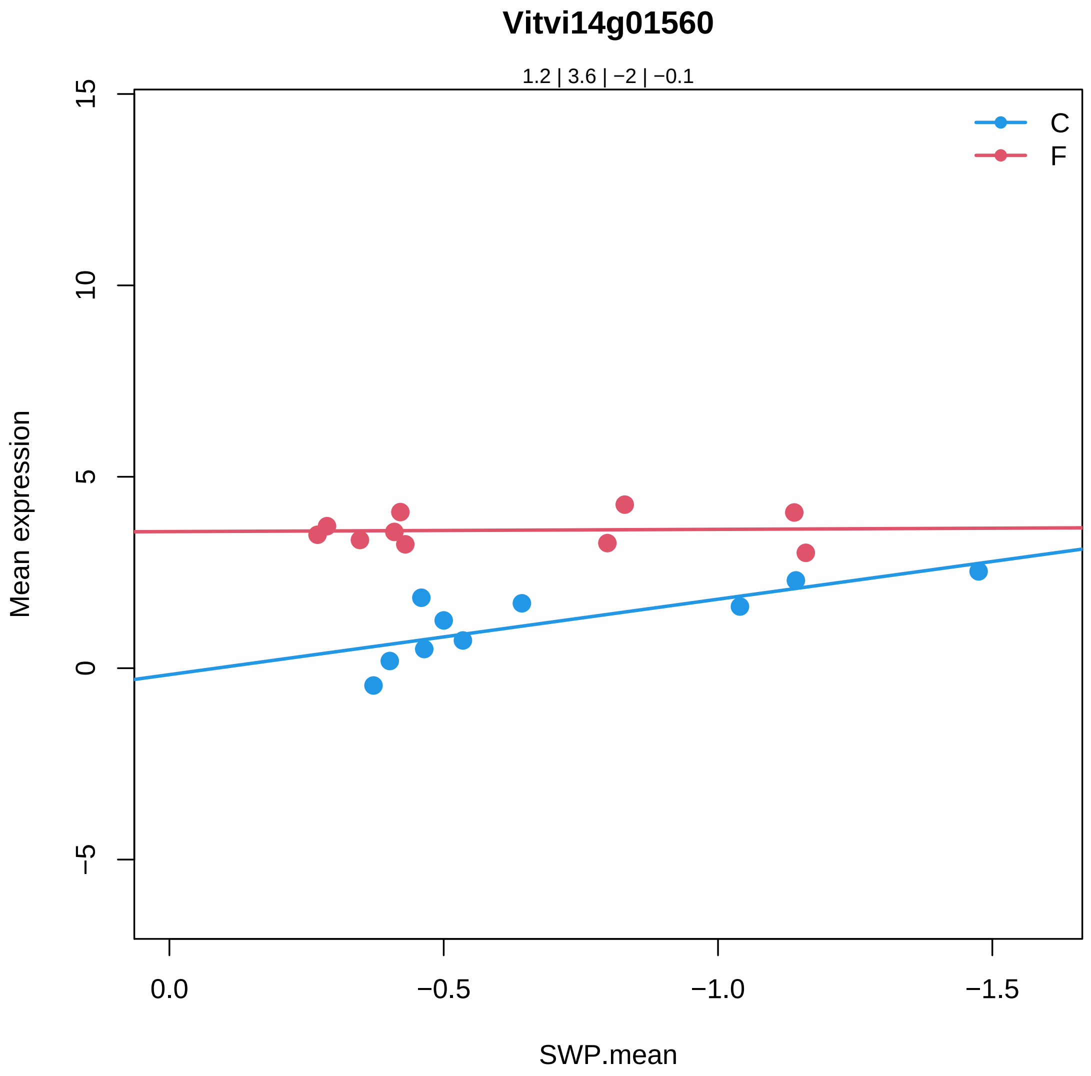
7.4.92 Vitvi14g01560: * type3

```
> 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
```



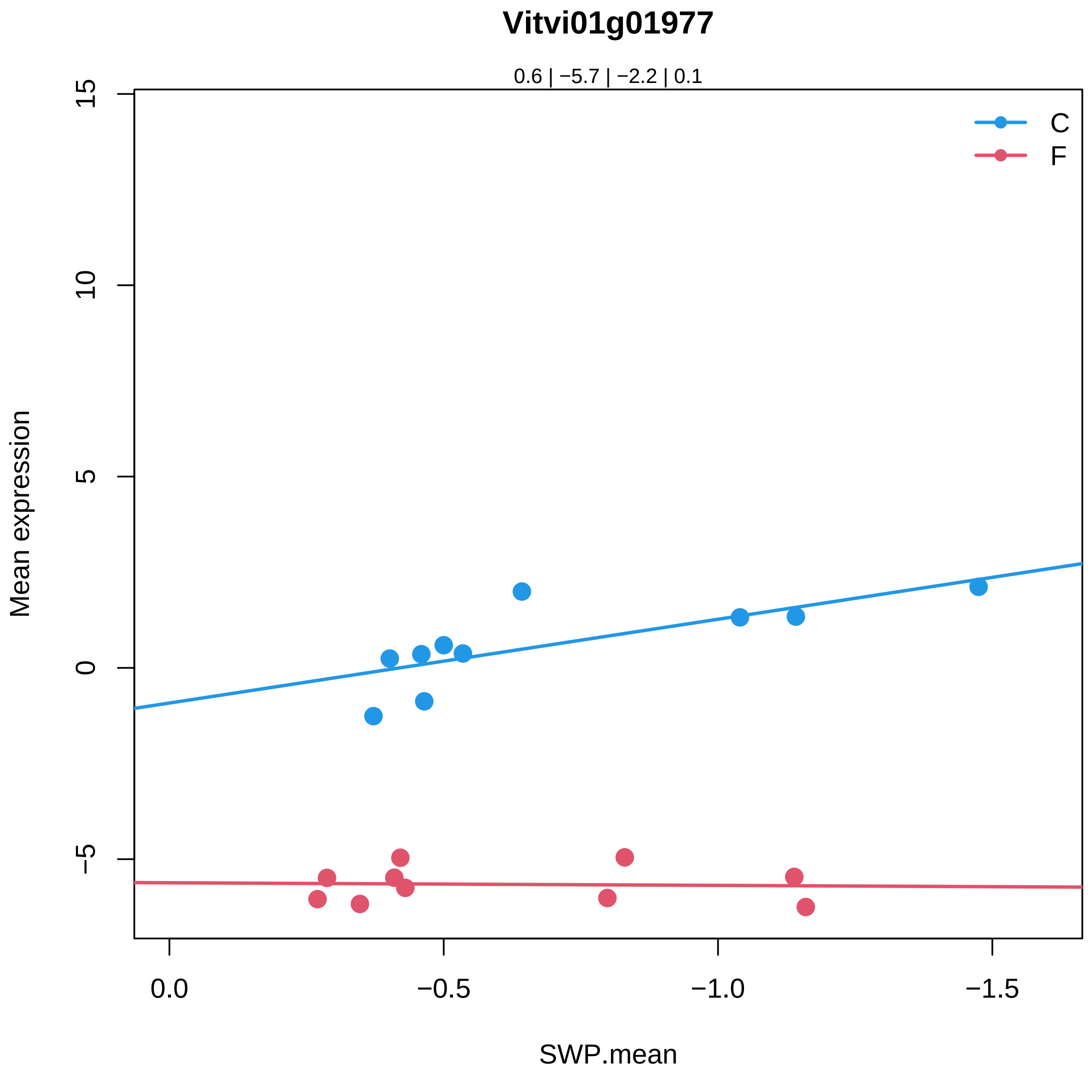
7.4.93 Vitvi01g01977: * type3

```
> 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
```



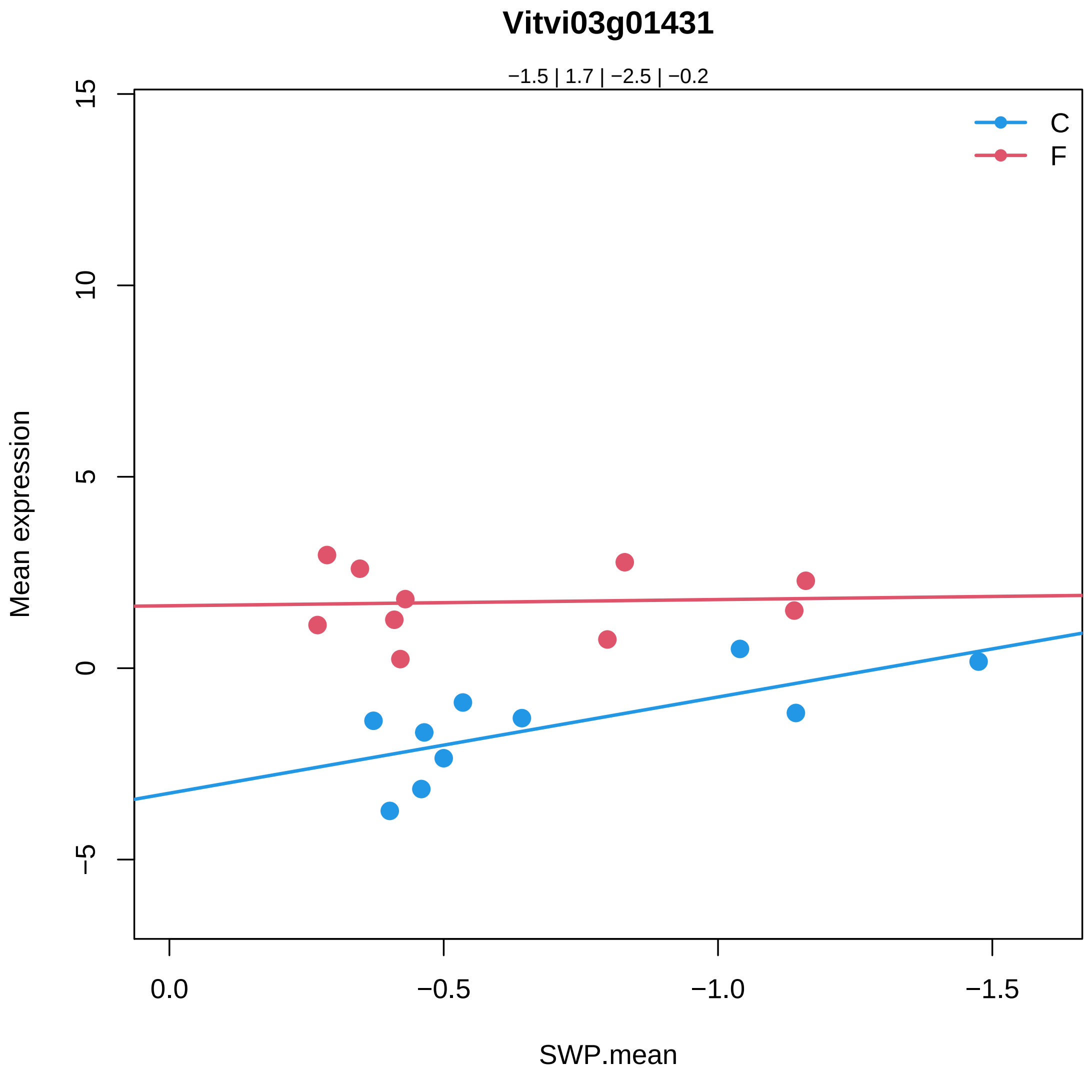
7.4.94 Vitvi03g01431: * type3 | type4

```
> 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

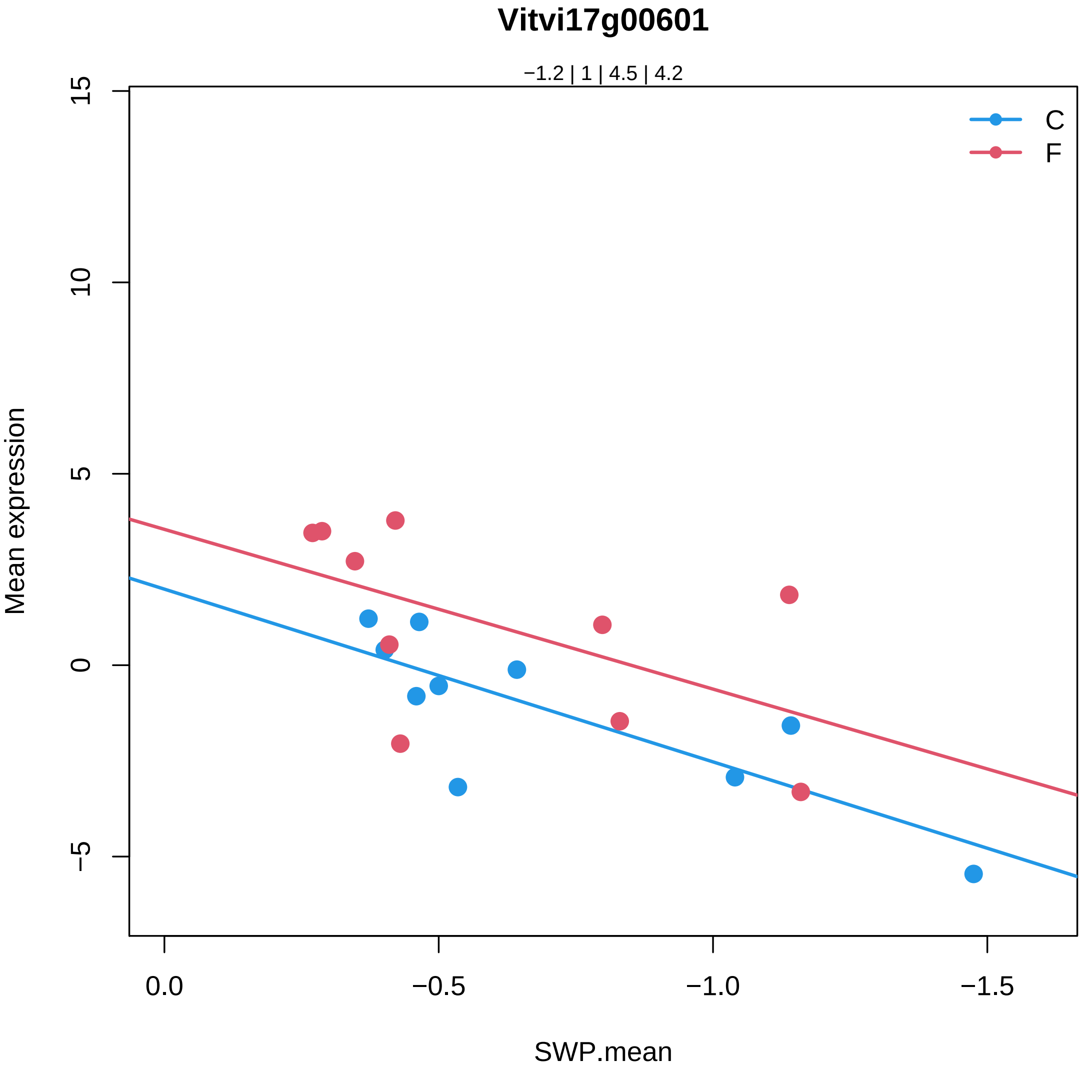
7.5.1 Vitvi17g00601: * type4

```
> 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
```



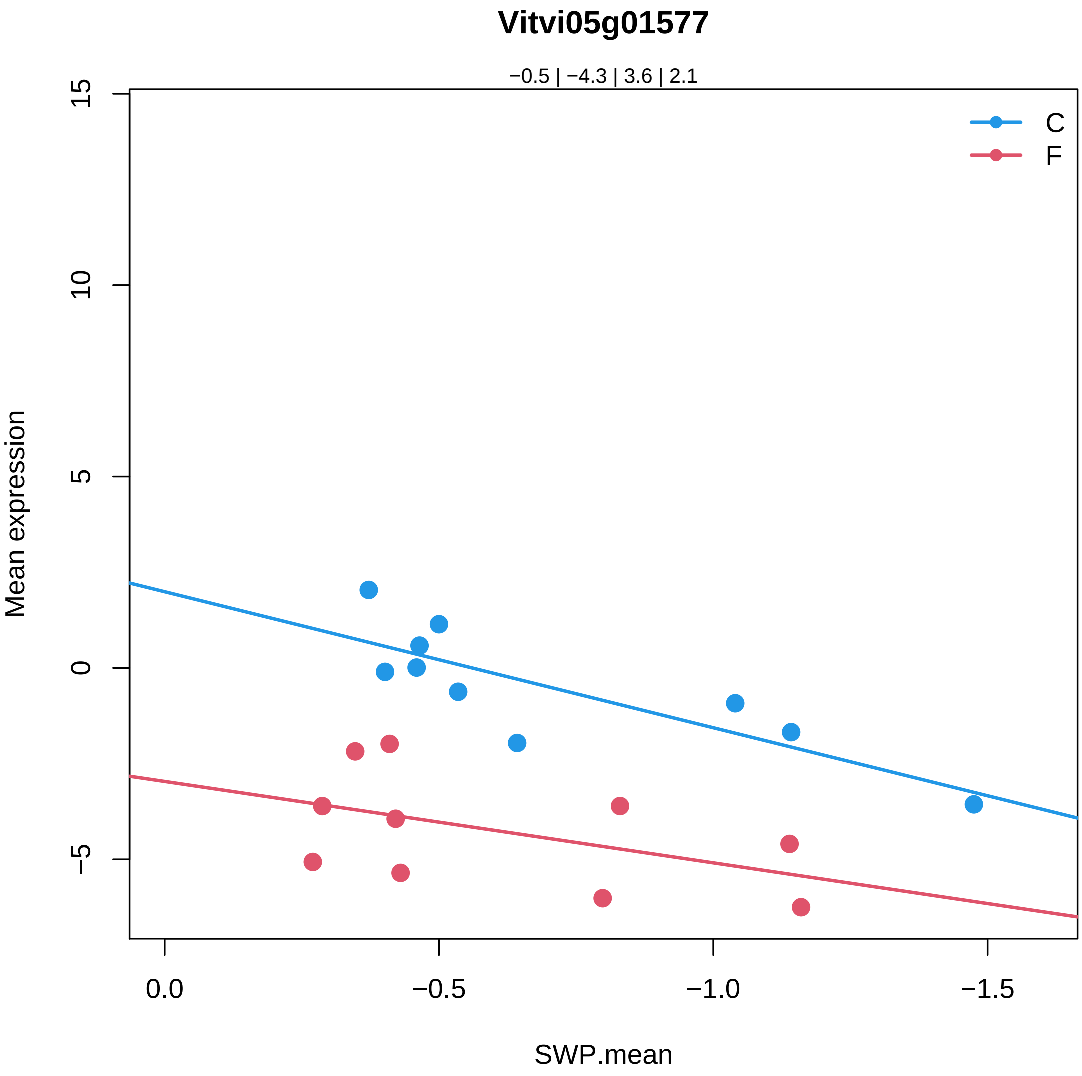
7.5.2 Vitvi05g01577: * type2 | type4

```
> 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
```



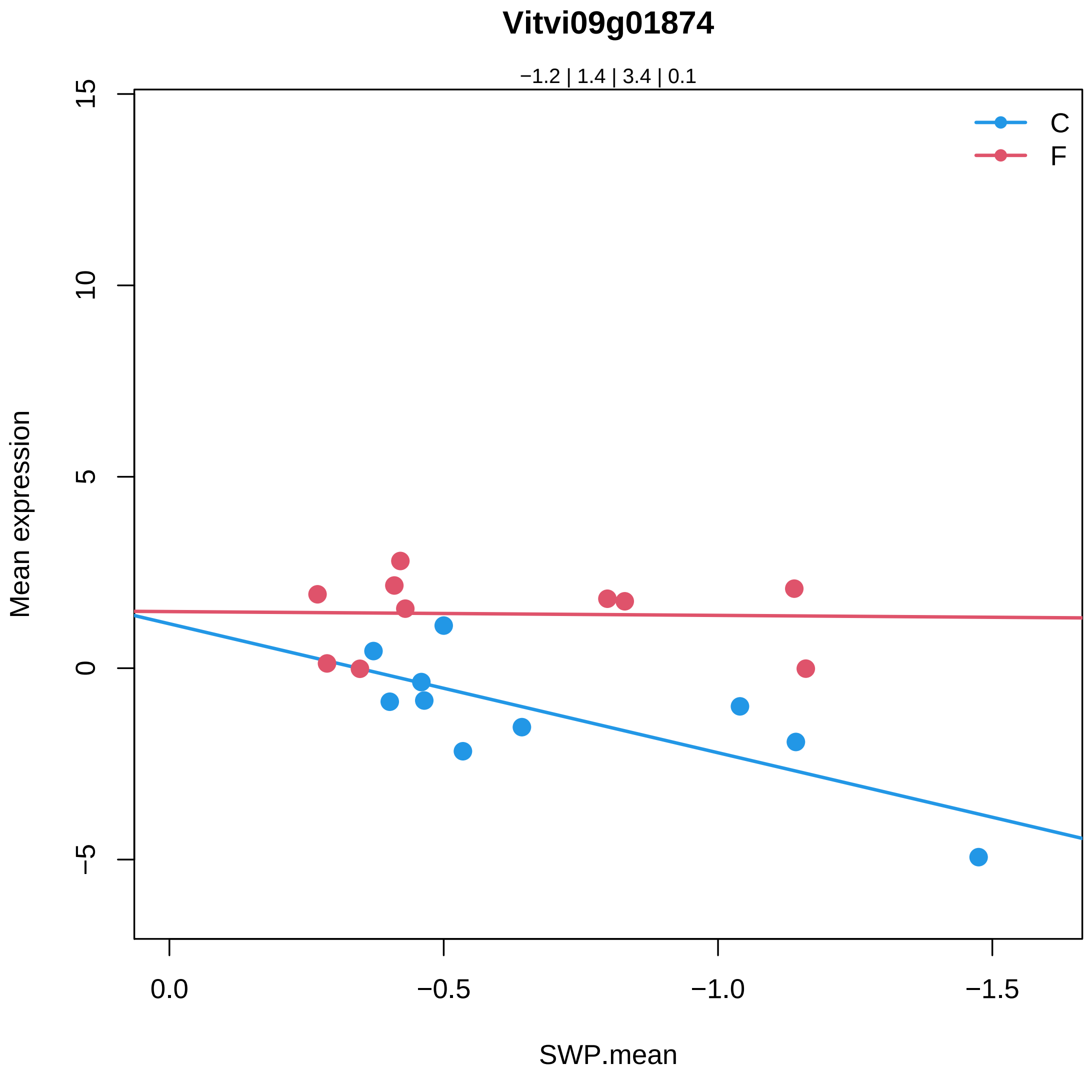
7.5.3 Vitvi09g01874: * type3 | type4

```
> 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
```



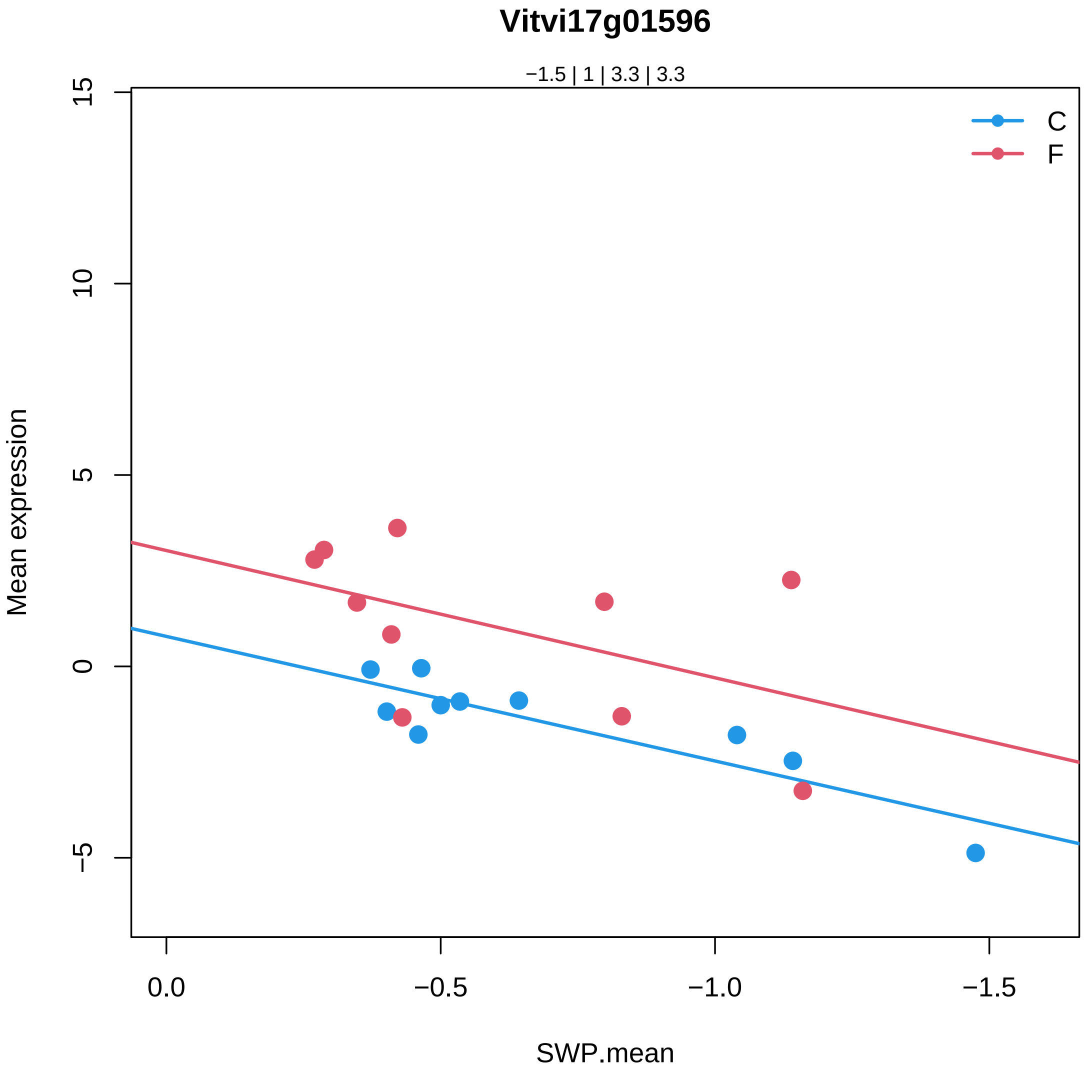
7.5.4 Vitvi17g01596: * type4

```
> 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
```



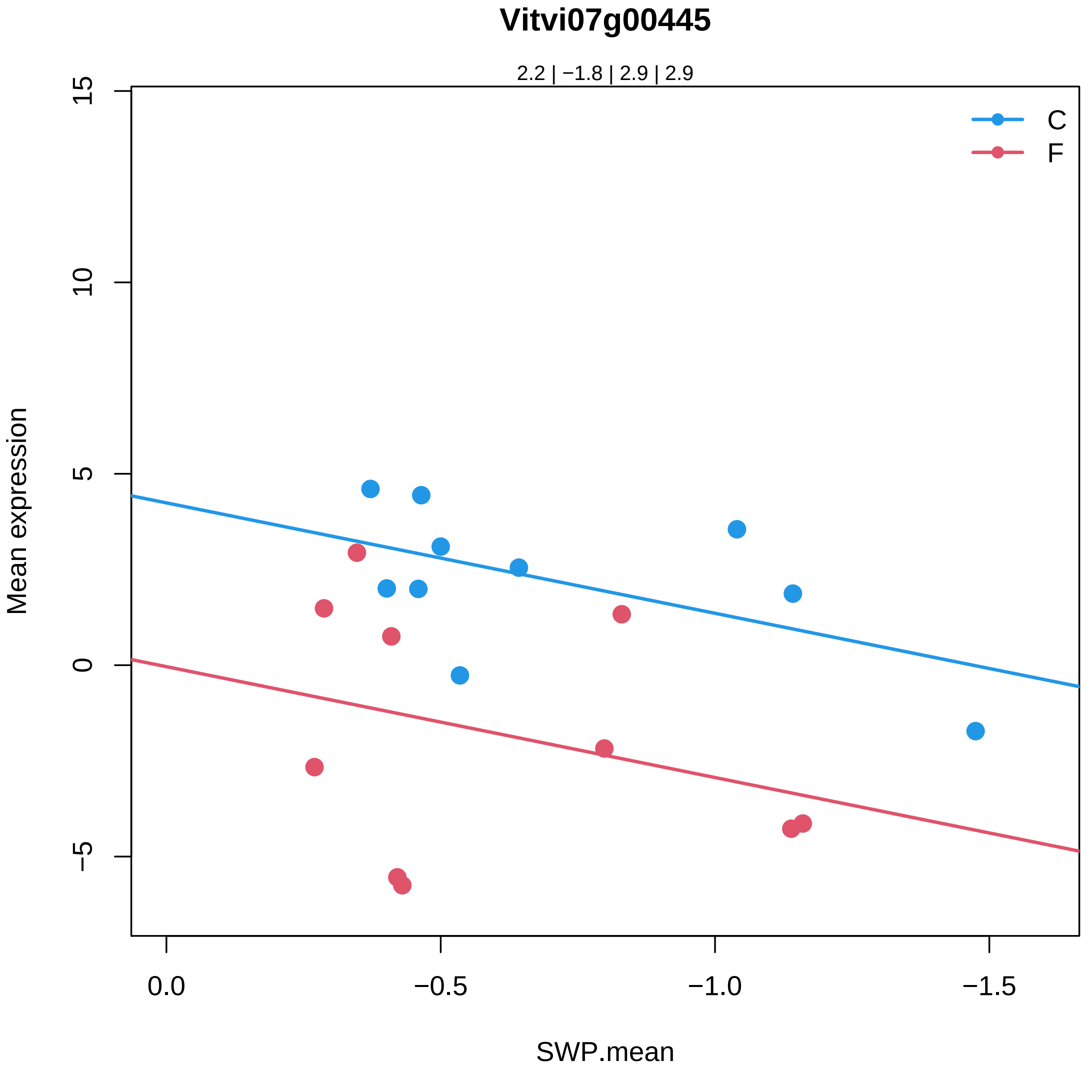
7.5.5 Vitvi07g00445: type4

```
> 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        
```



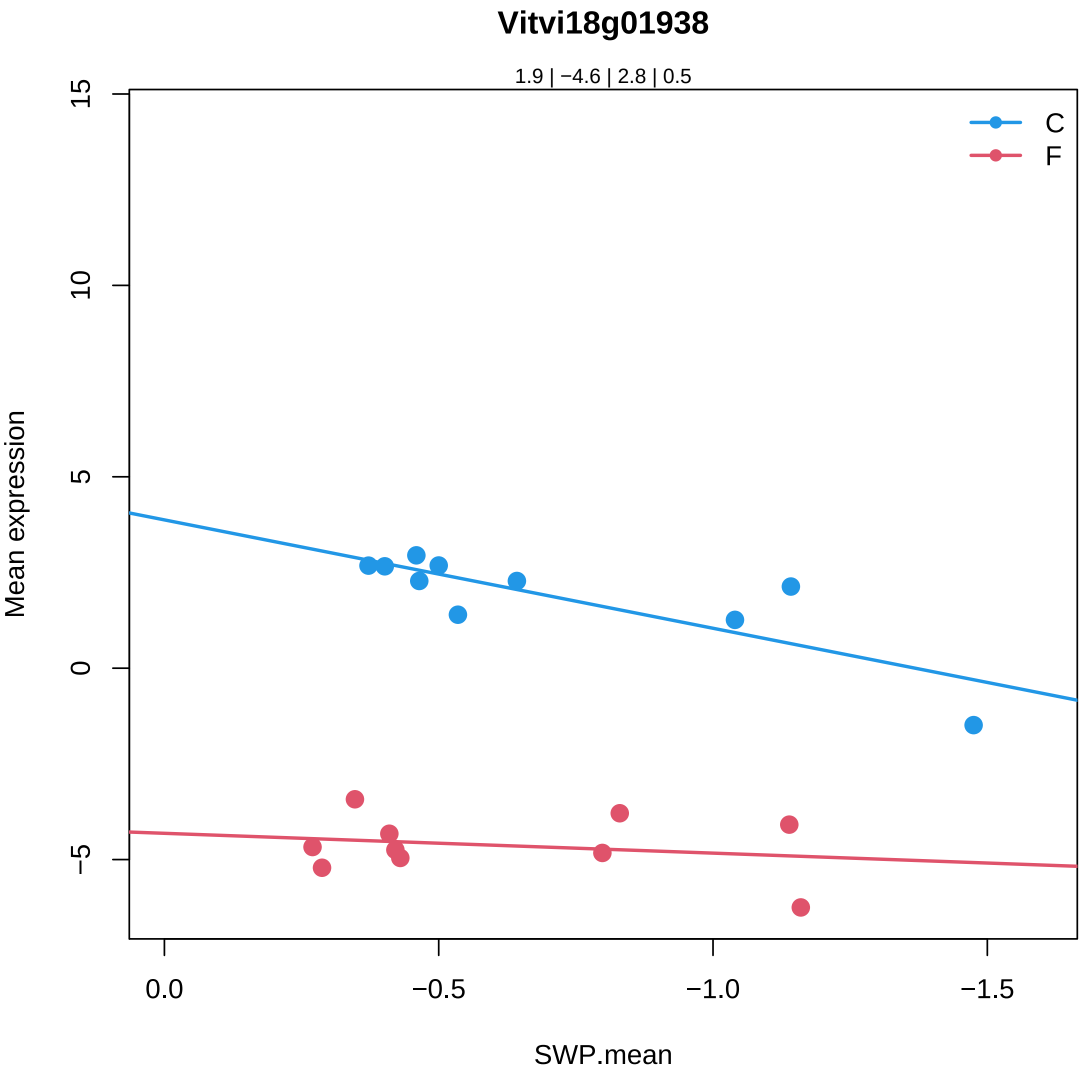
7.5.6 Vitvi18g01938: * type4

```
> 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
```



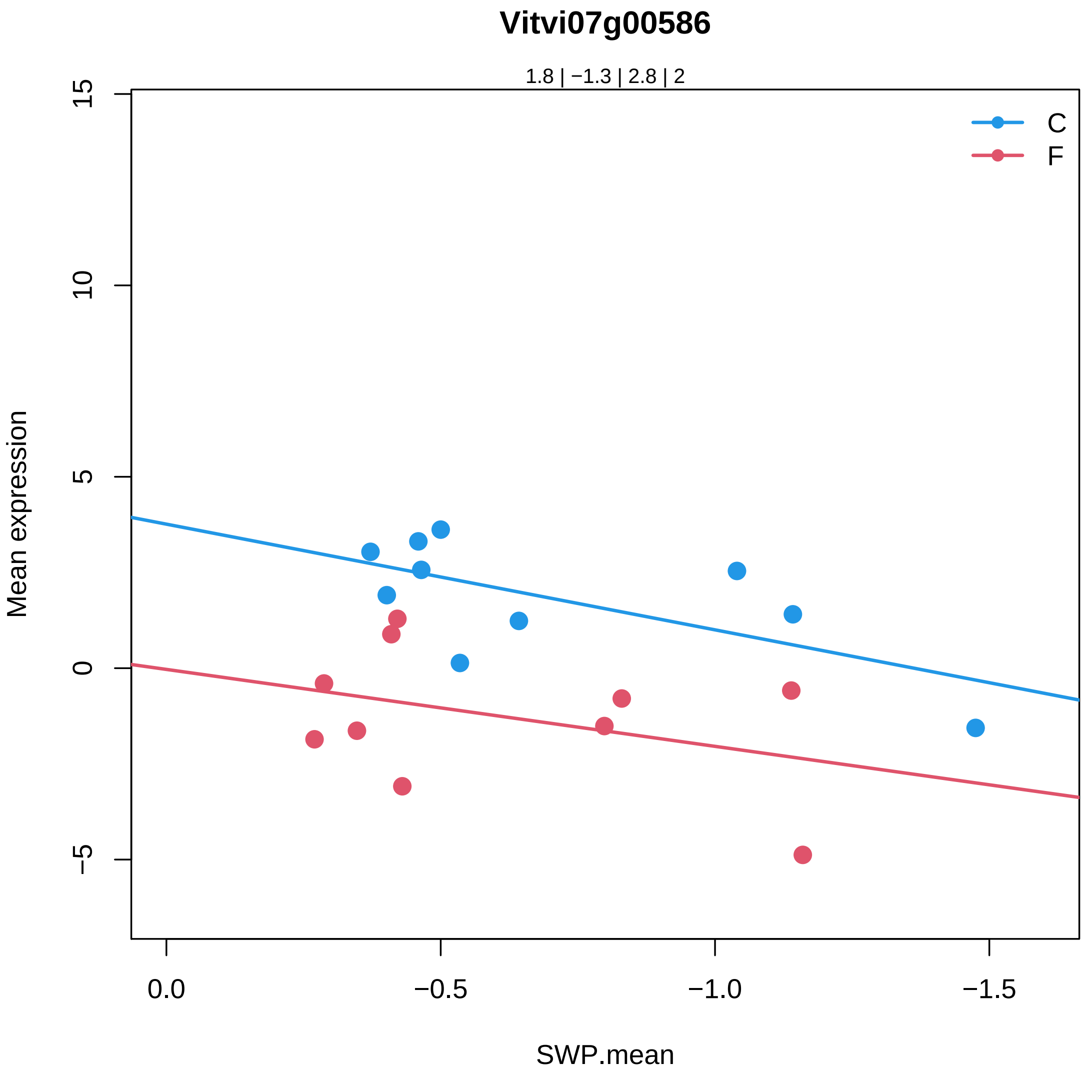
7.5.7 Vitvi07g00586: * type4

```
> 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
```



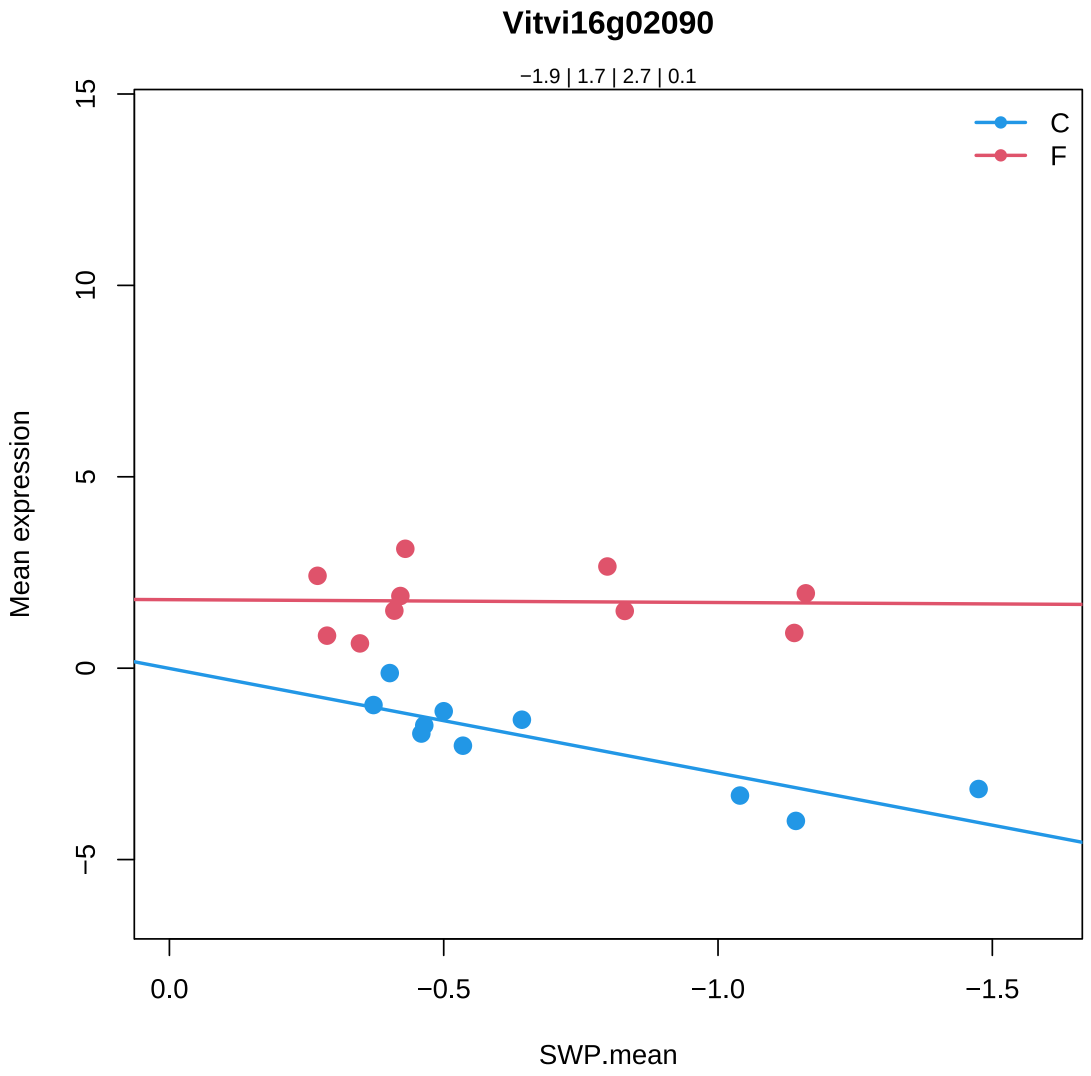
7.5.8 Vitvi16g02090: * type3 | type4

```
> 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
```



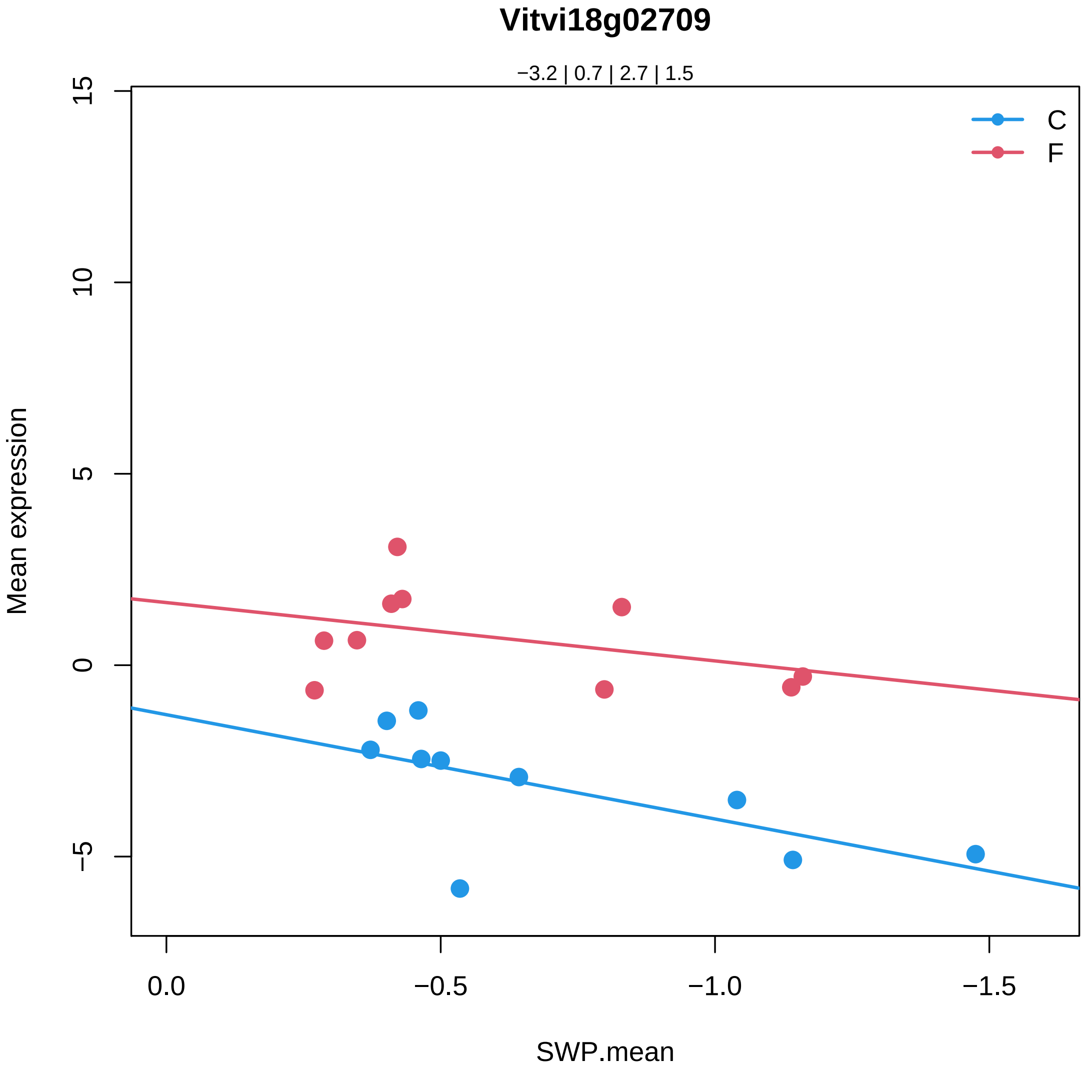
7.5.9 Vitvi18g02709: * type4

```
> 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
```



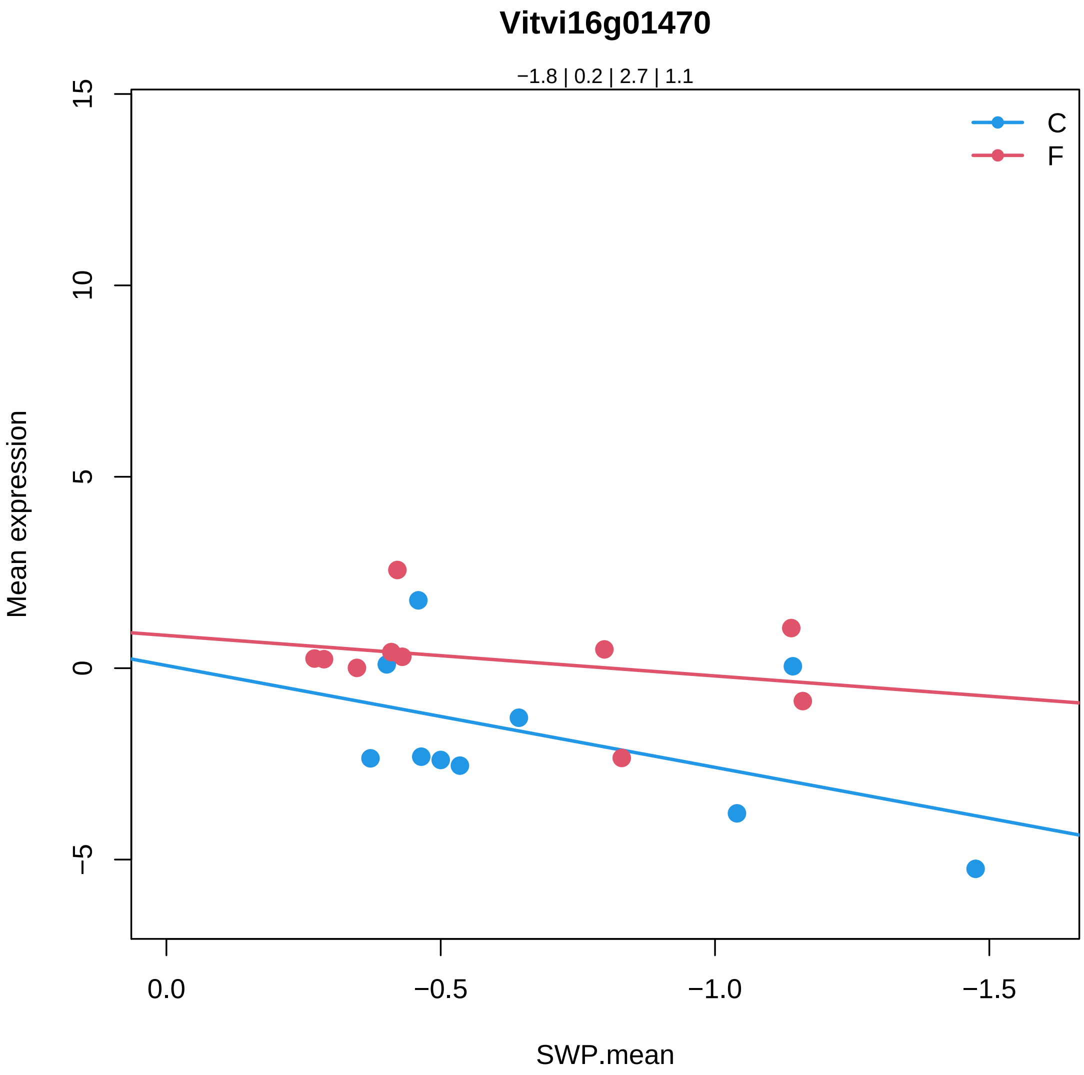
7.5.10 Vitvi16g01470: * type4

```
> 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        
```



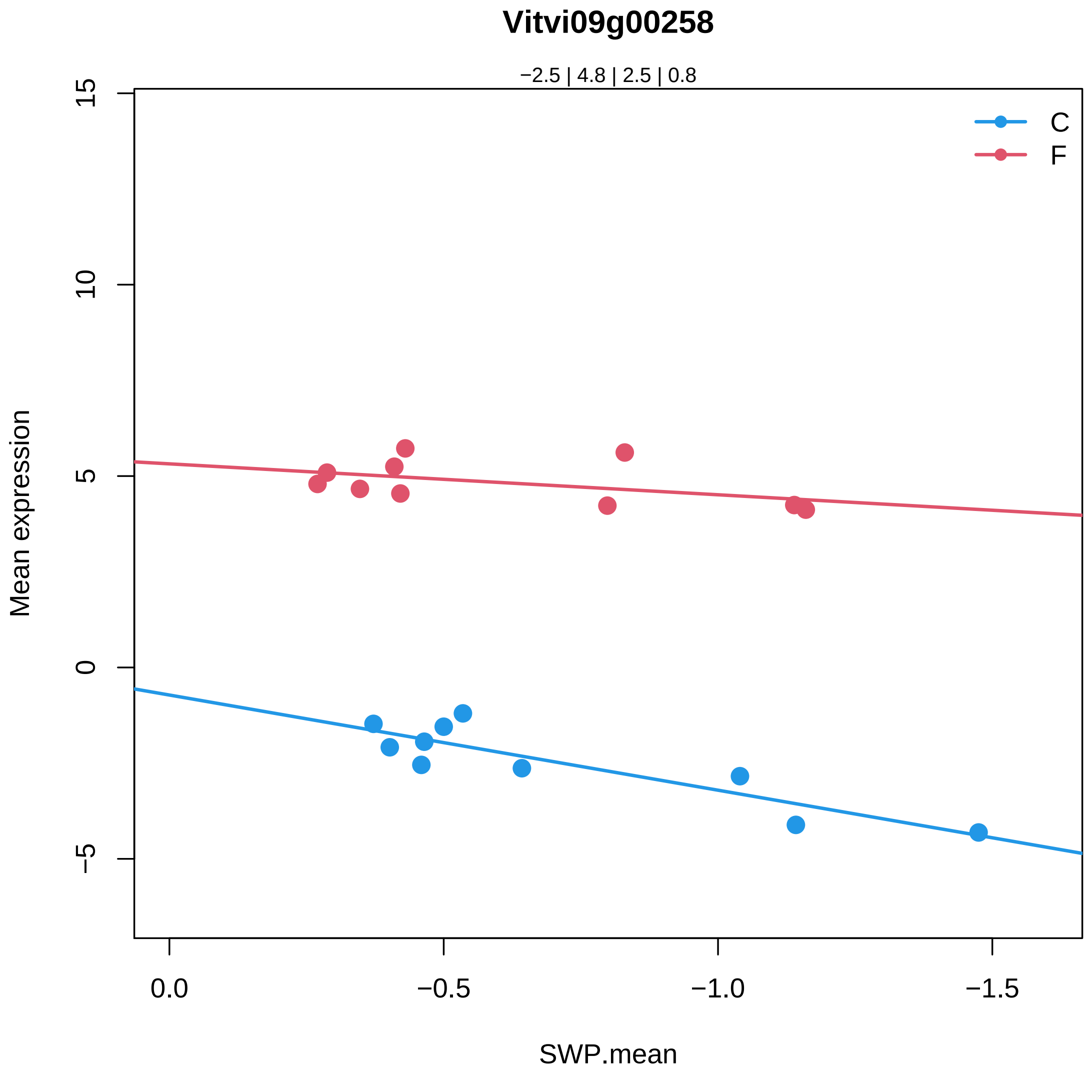
7.5.11 Vitvi09g00258: * type4

```
> 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

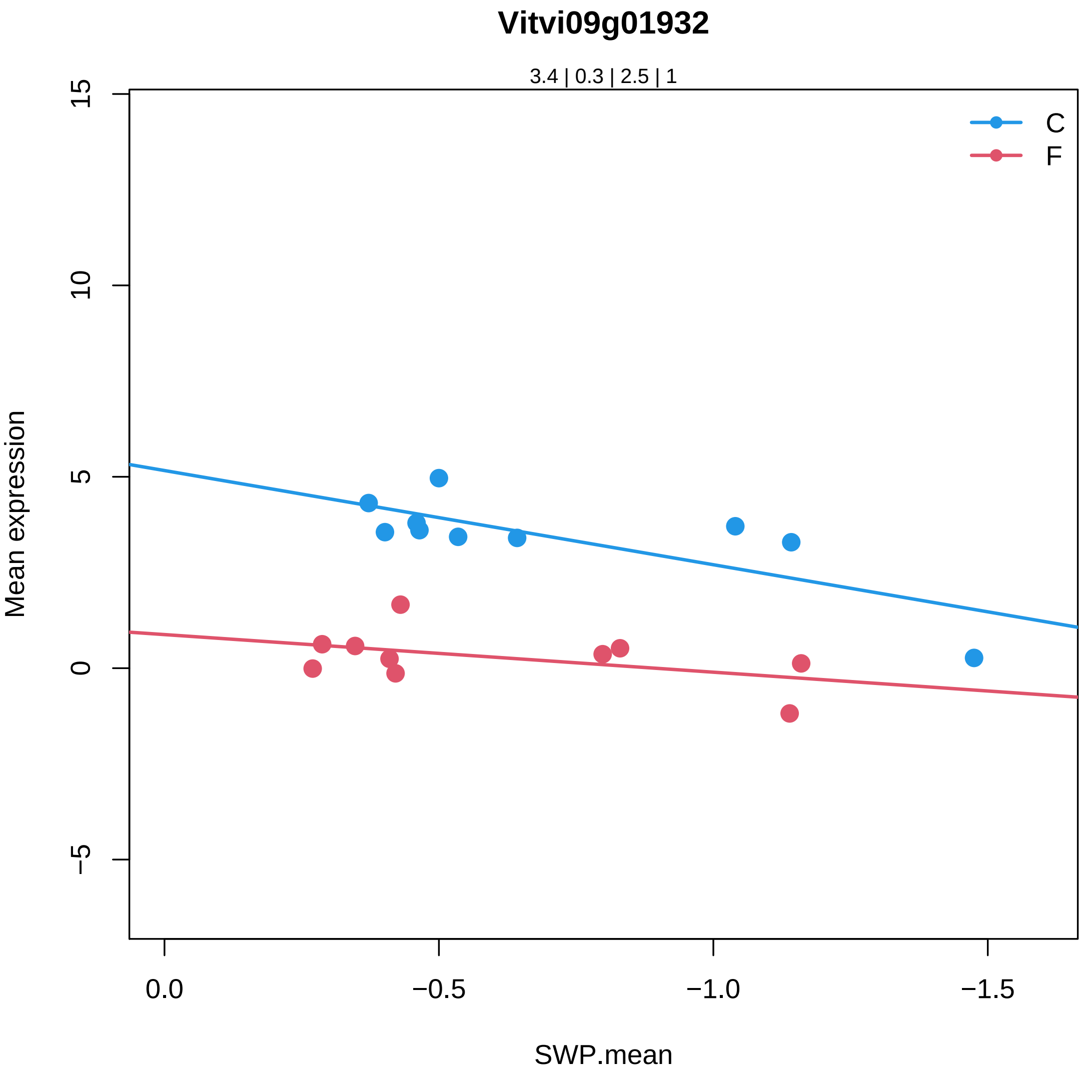
7.5.12 Vitvi09g01932: * type4

```
> 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
```



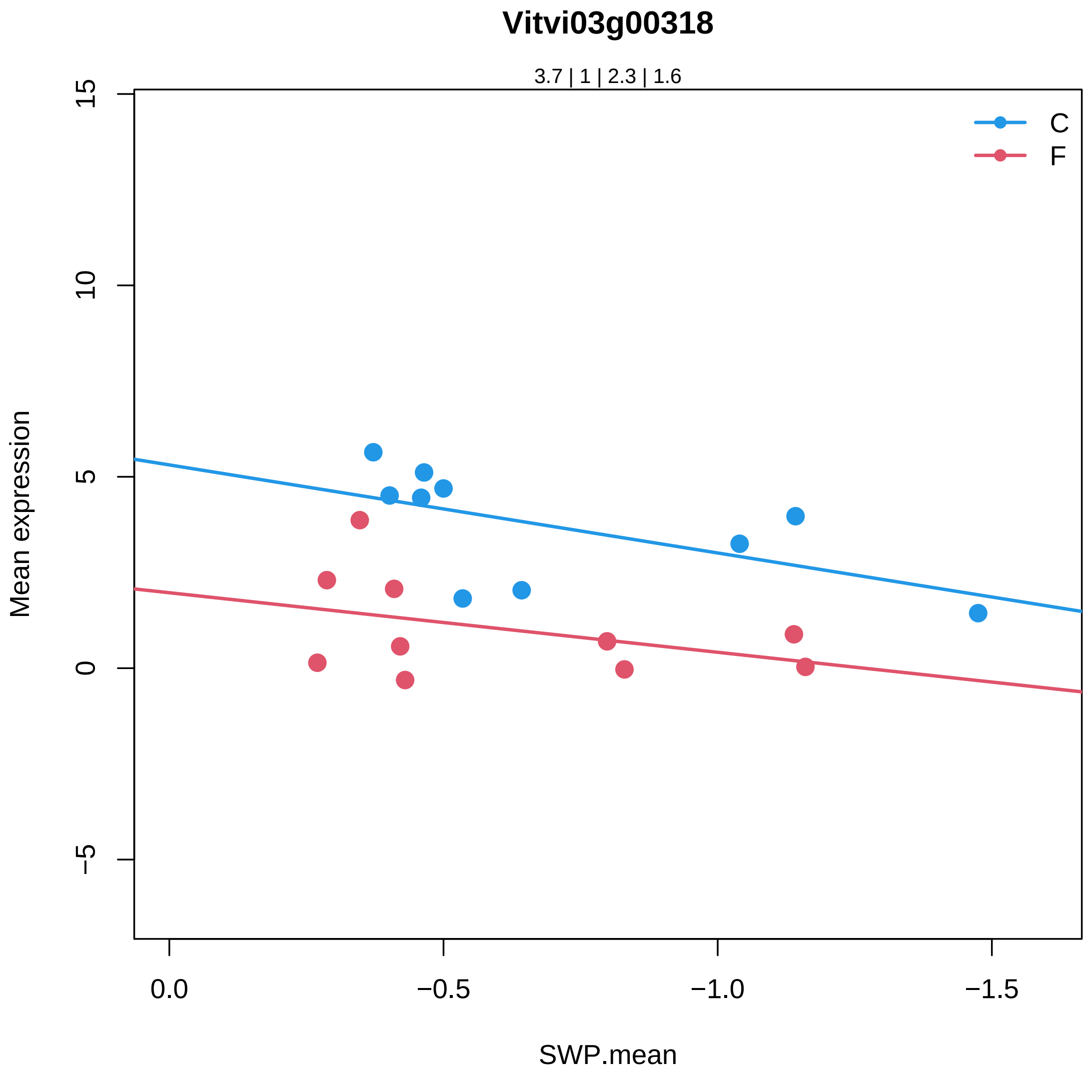
7.5.13 Vitvi03g00318: * type4

```
> 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
```



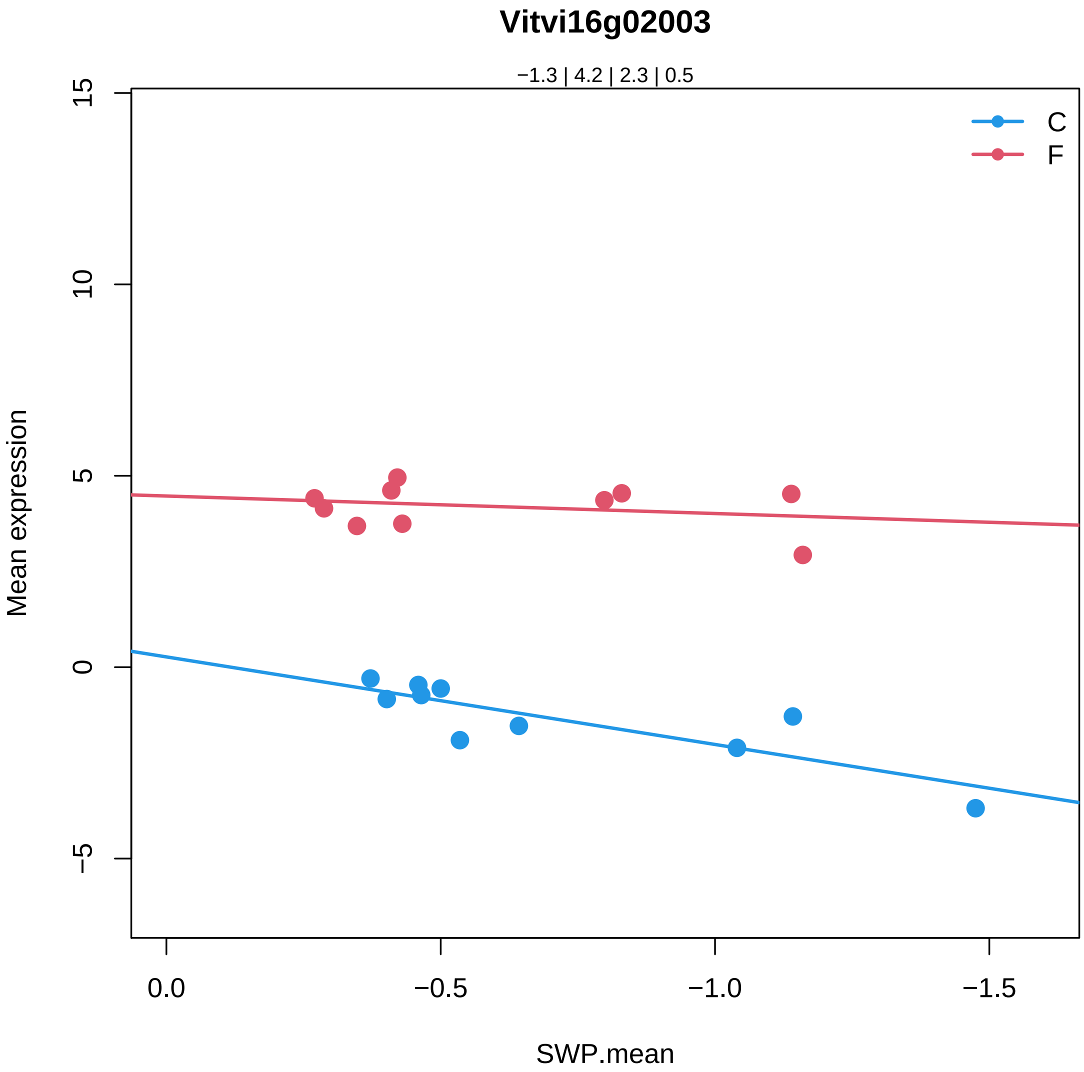
7.5.14 Vitvi16g02003: * type3 | type4

```
> 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
```

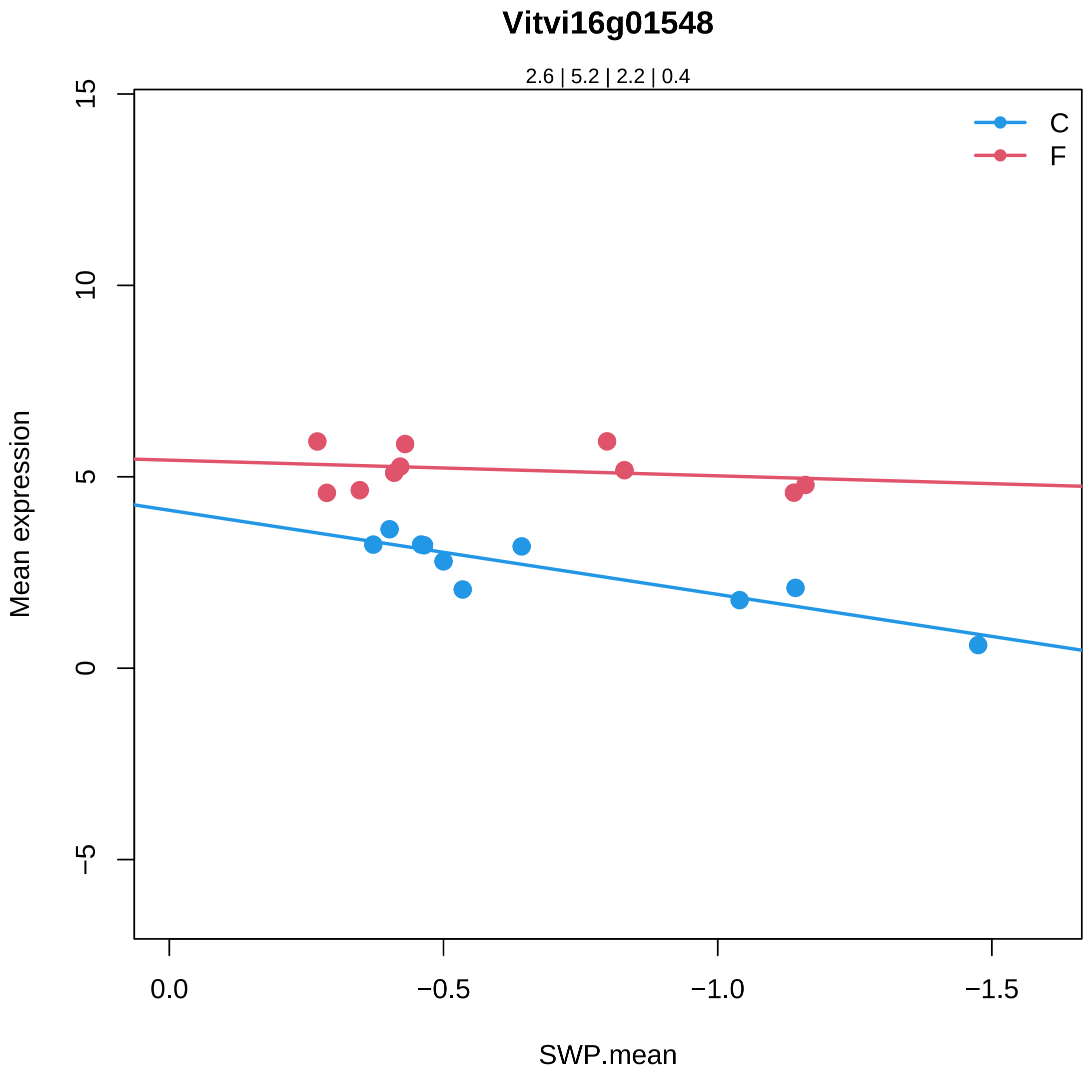


7.5.15 Vitvi16g01548: * type3 | type4

```
> 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
```



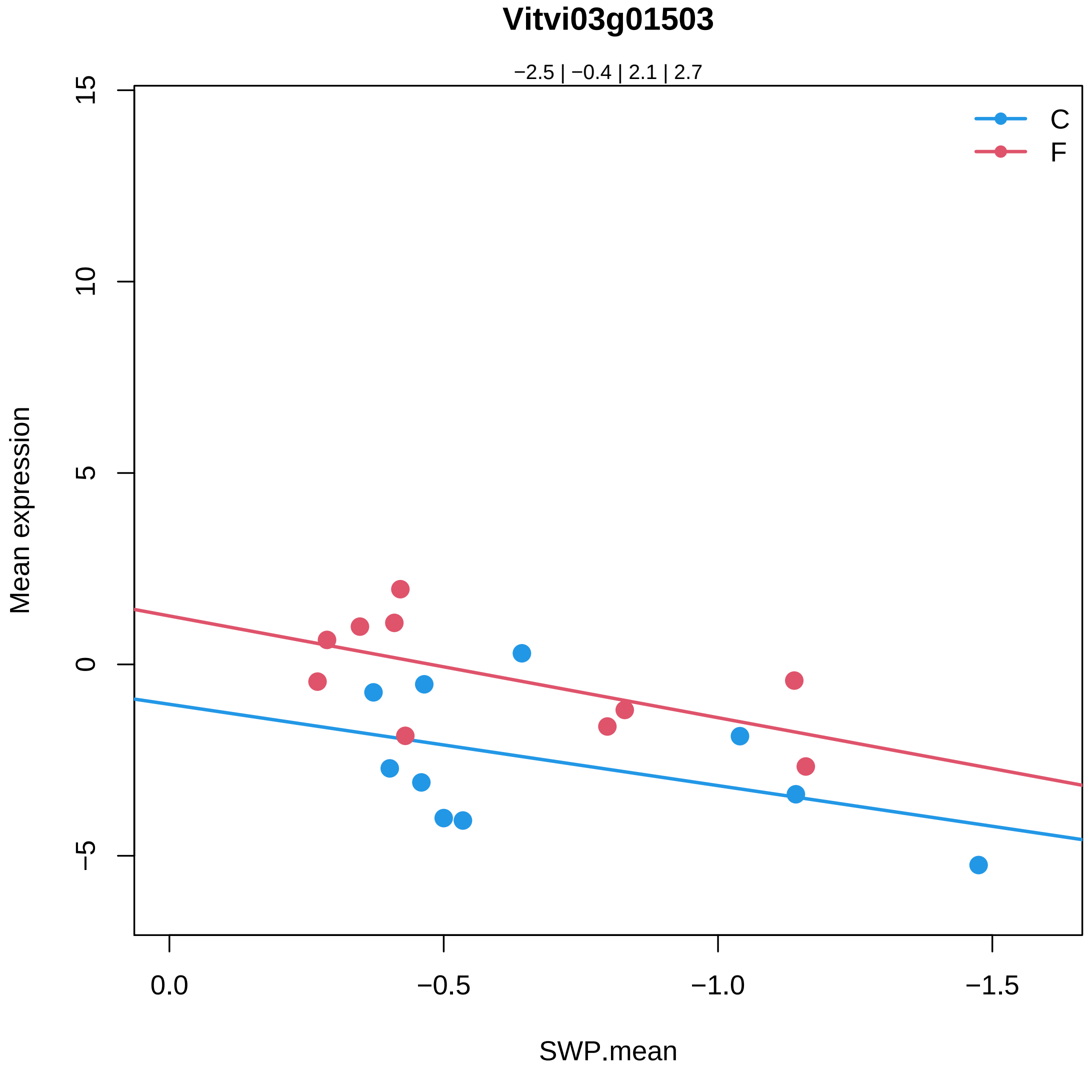
7.5.16 Vitvi03g01503: type4

```
> 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
```



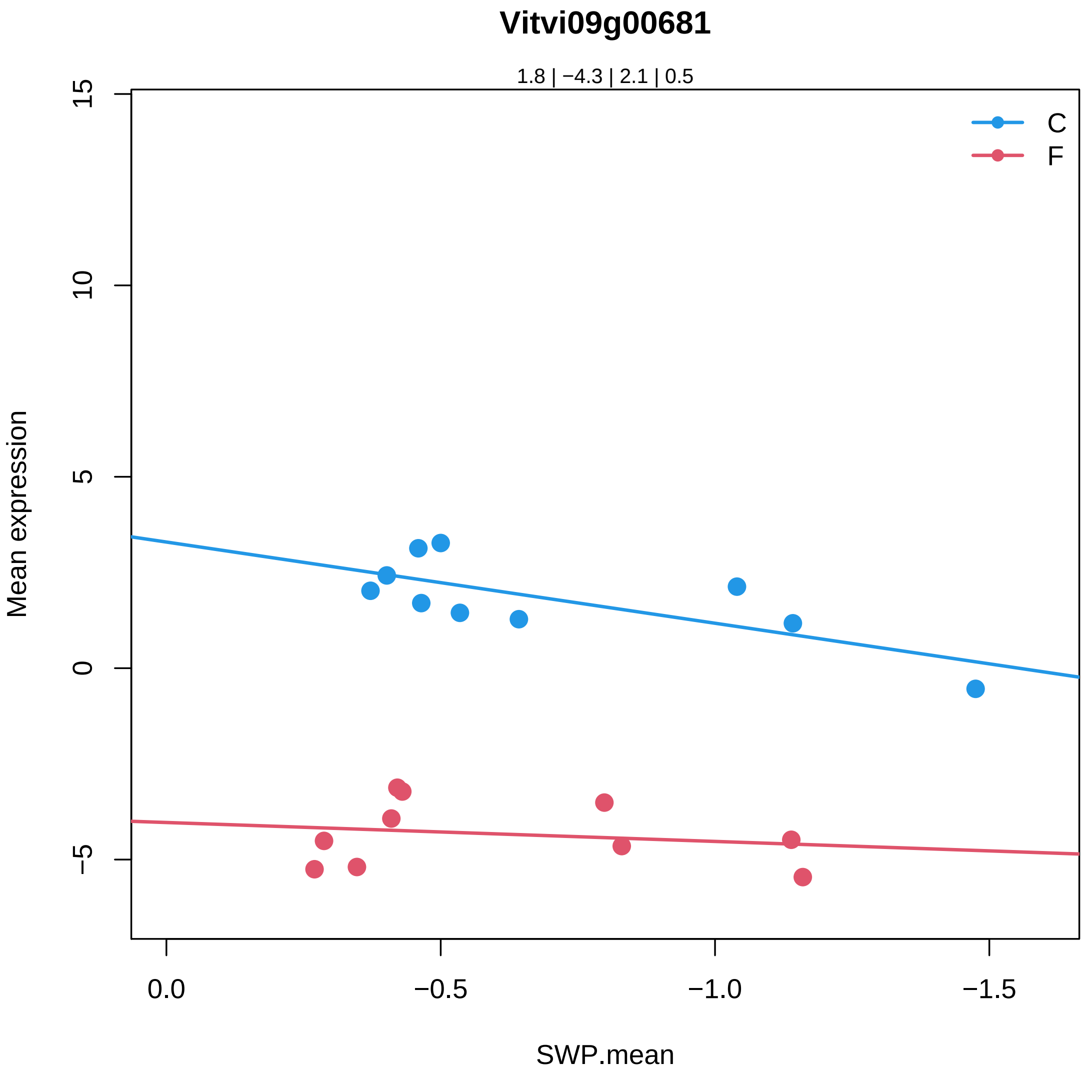
7.5.17 Vitvi09g00681: * type3 | type4

```
> 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
```



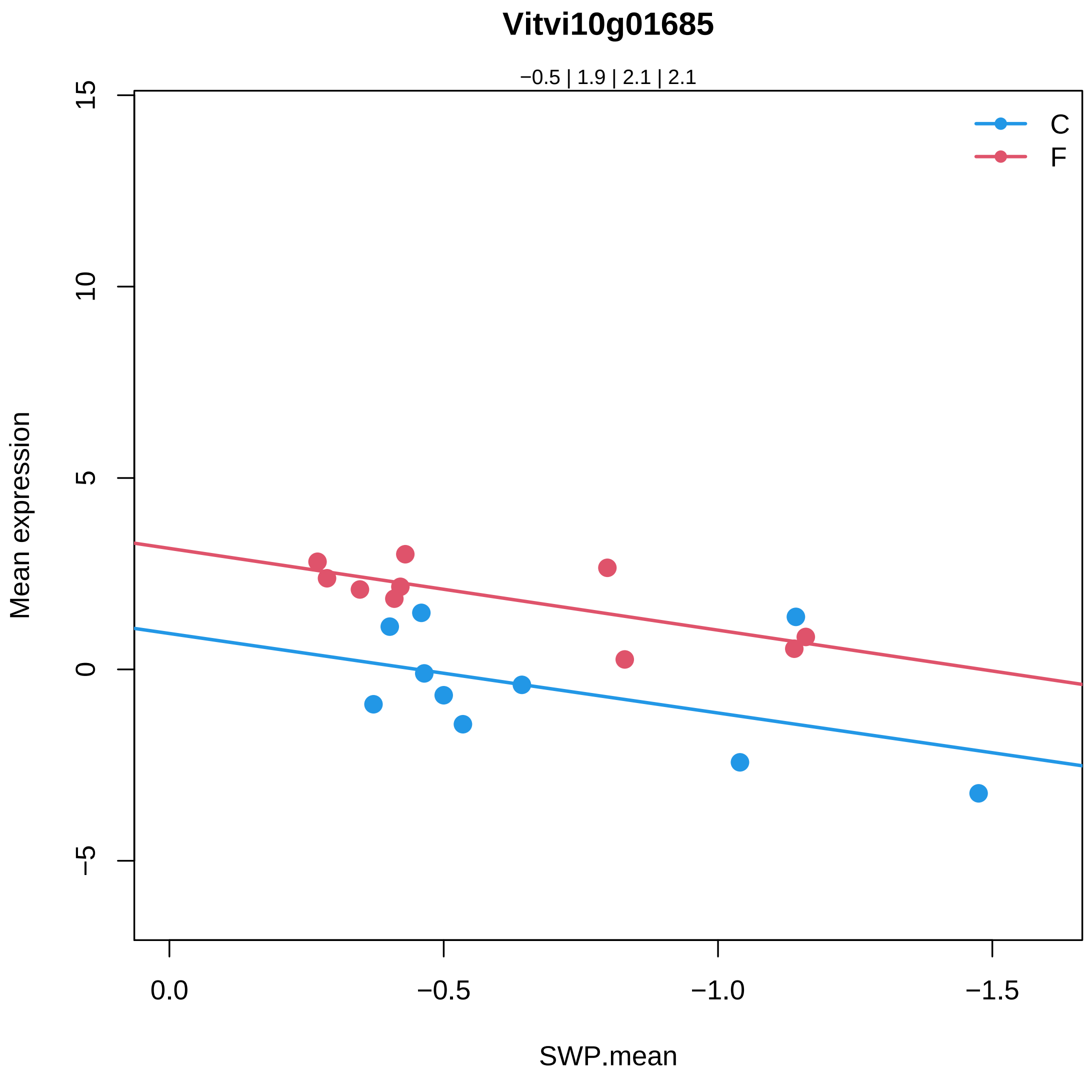
7.5.18 Vitvi10g01685: * type4

```
> 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
```



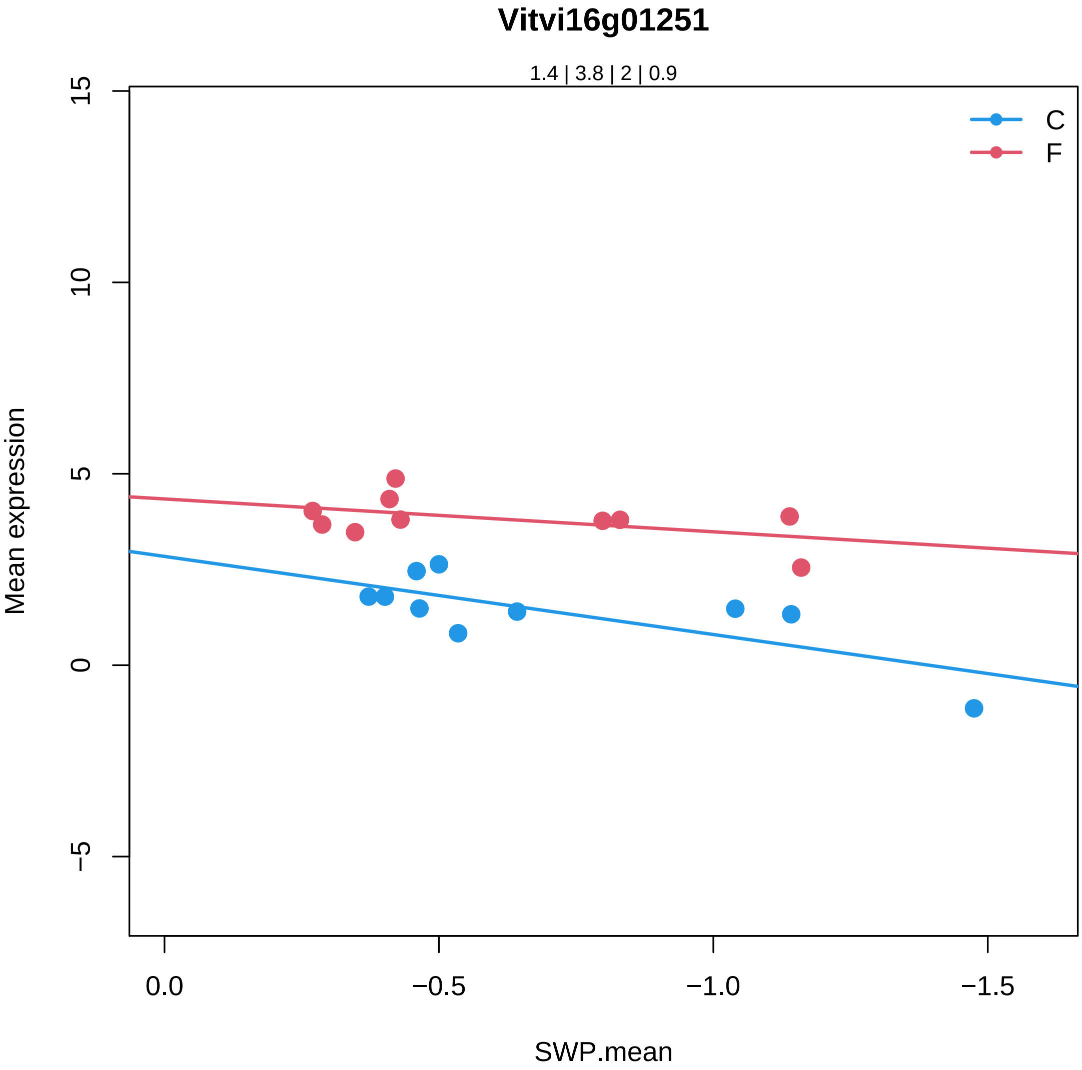
7.5.19 Vitvi16g01251: * type4

```
> 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        
```



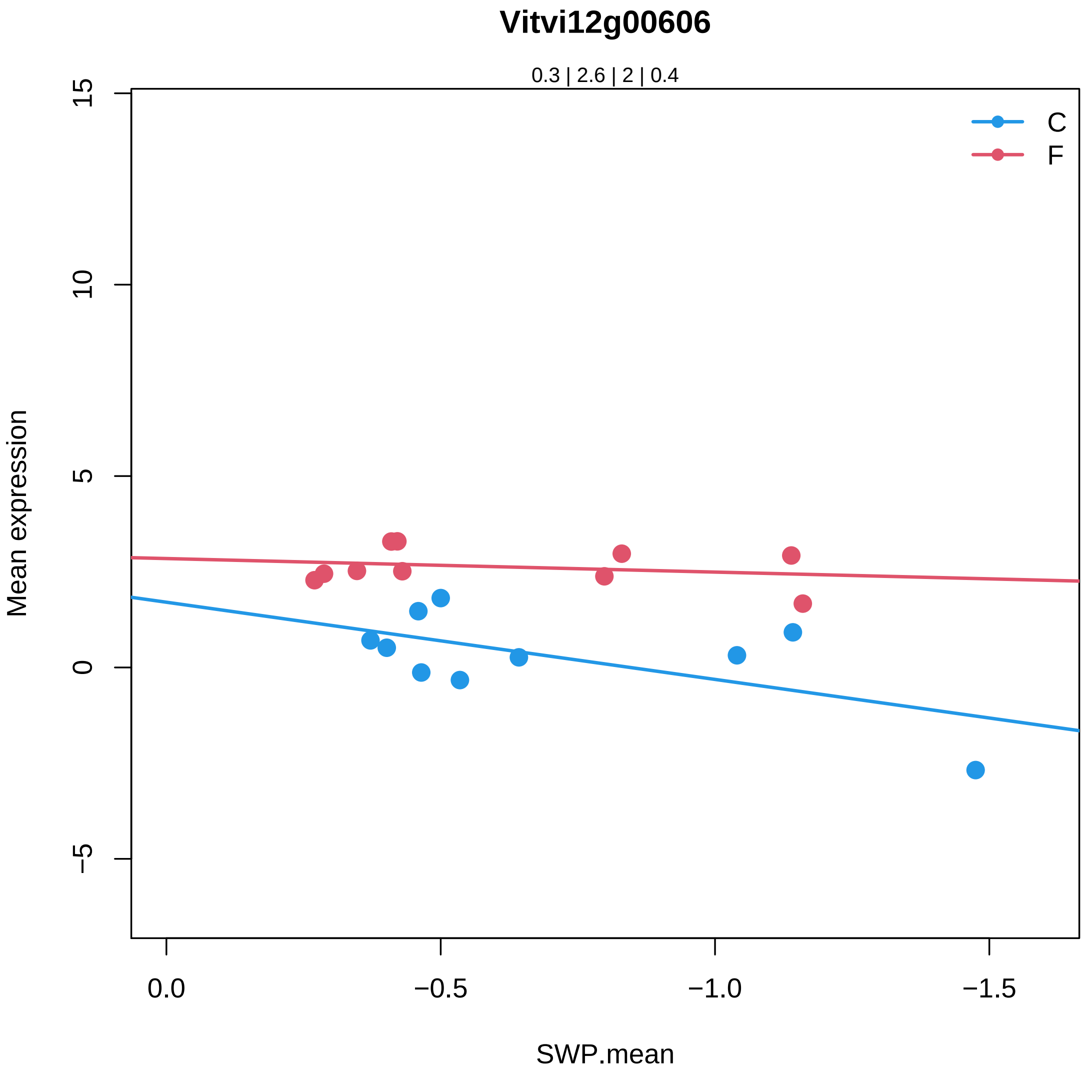
7.5.20 Vitvi12g00606: * type3 | type4

```
> 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

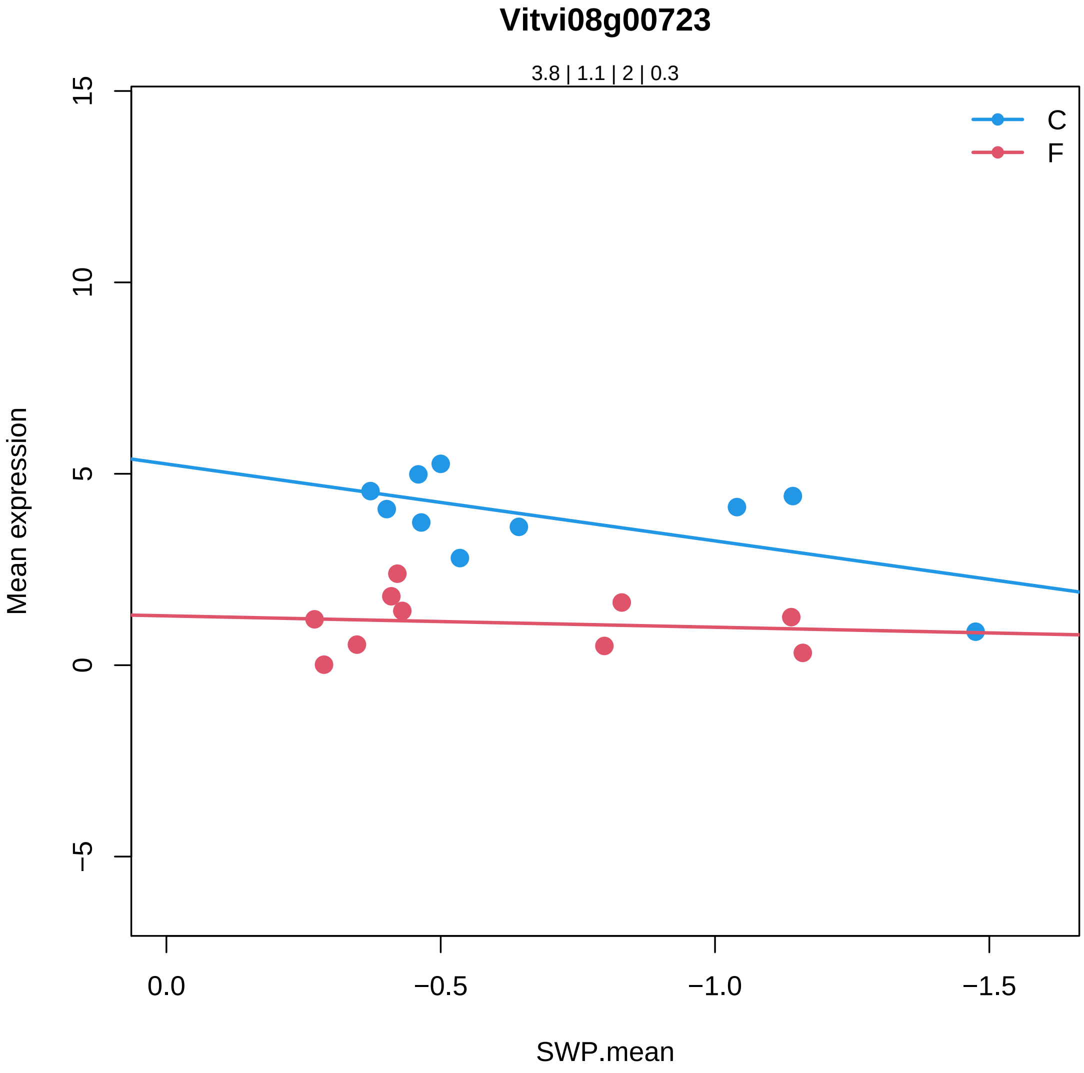
7.5.21 Vitvi08g00723: * type3 | type4

```
> 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
```



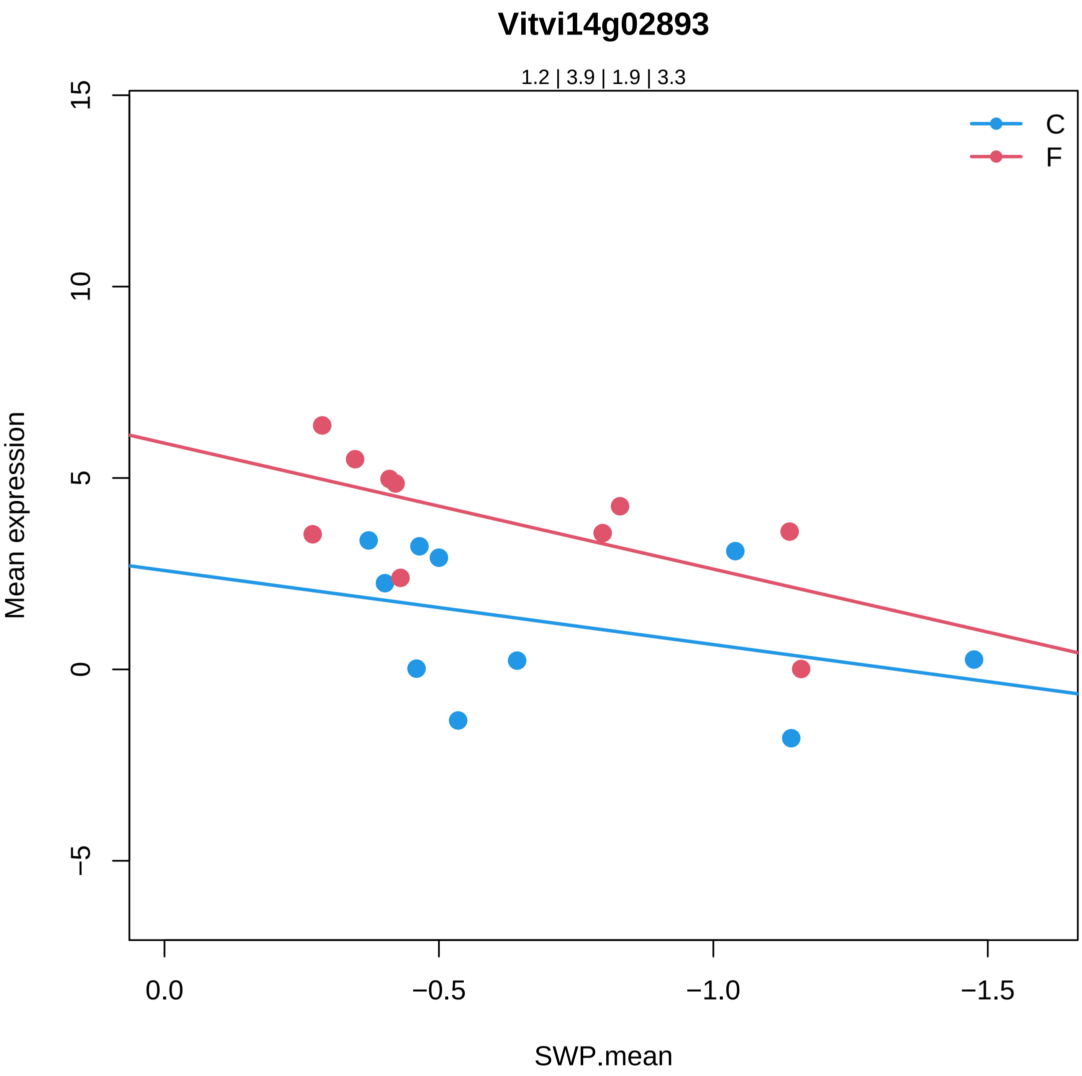
7.5.22 Vitvi14g02893: type4

```
> 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
```



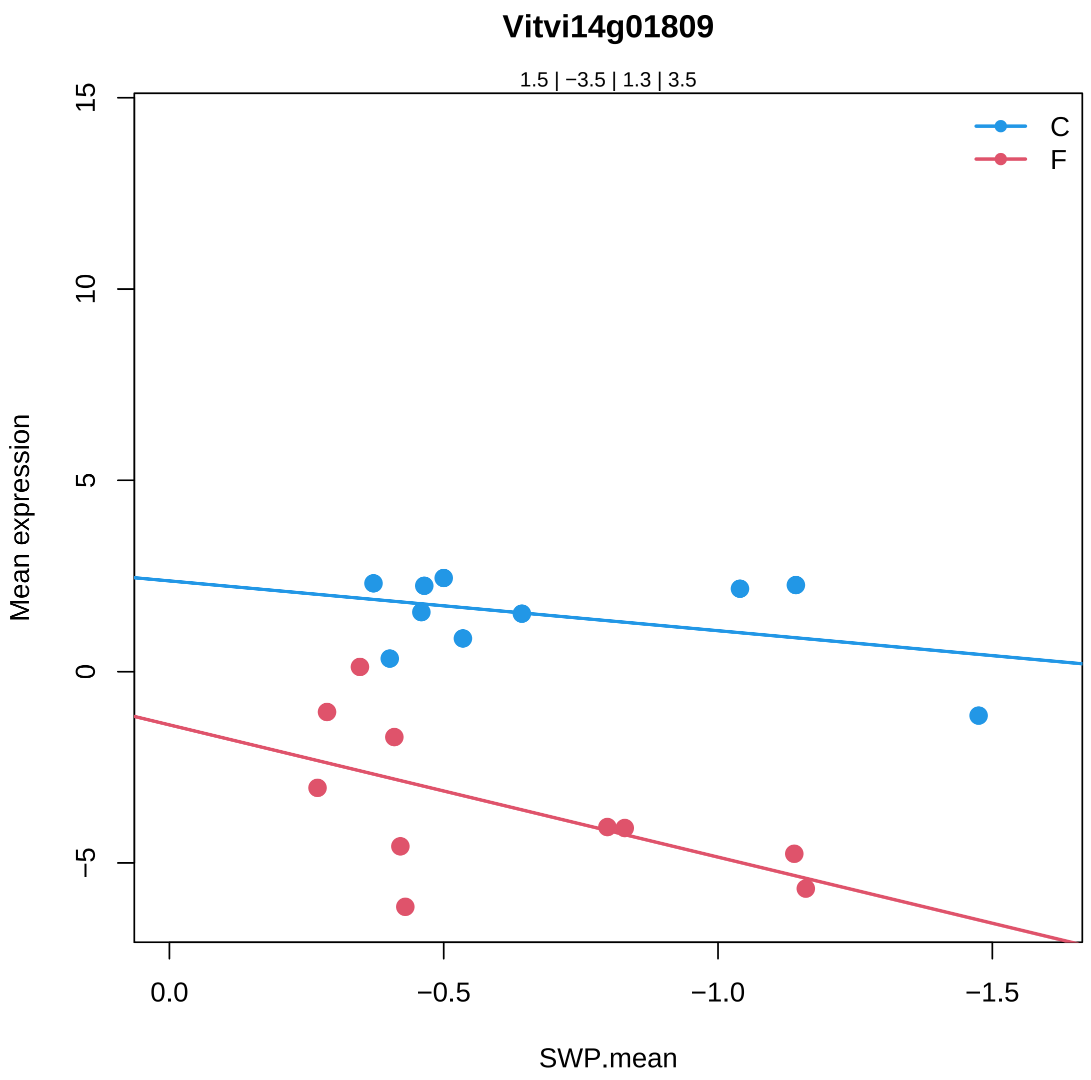
7.5.23 Vitvi14g01809: type4

```
> 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

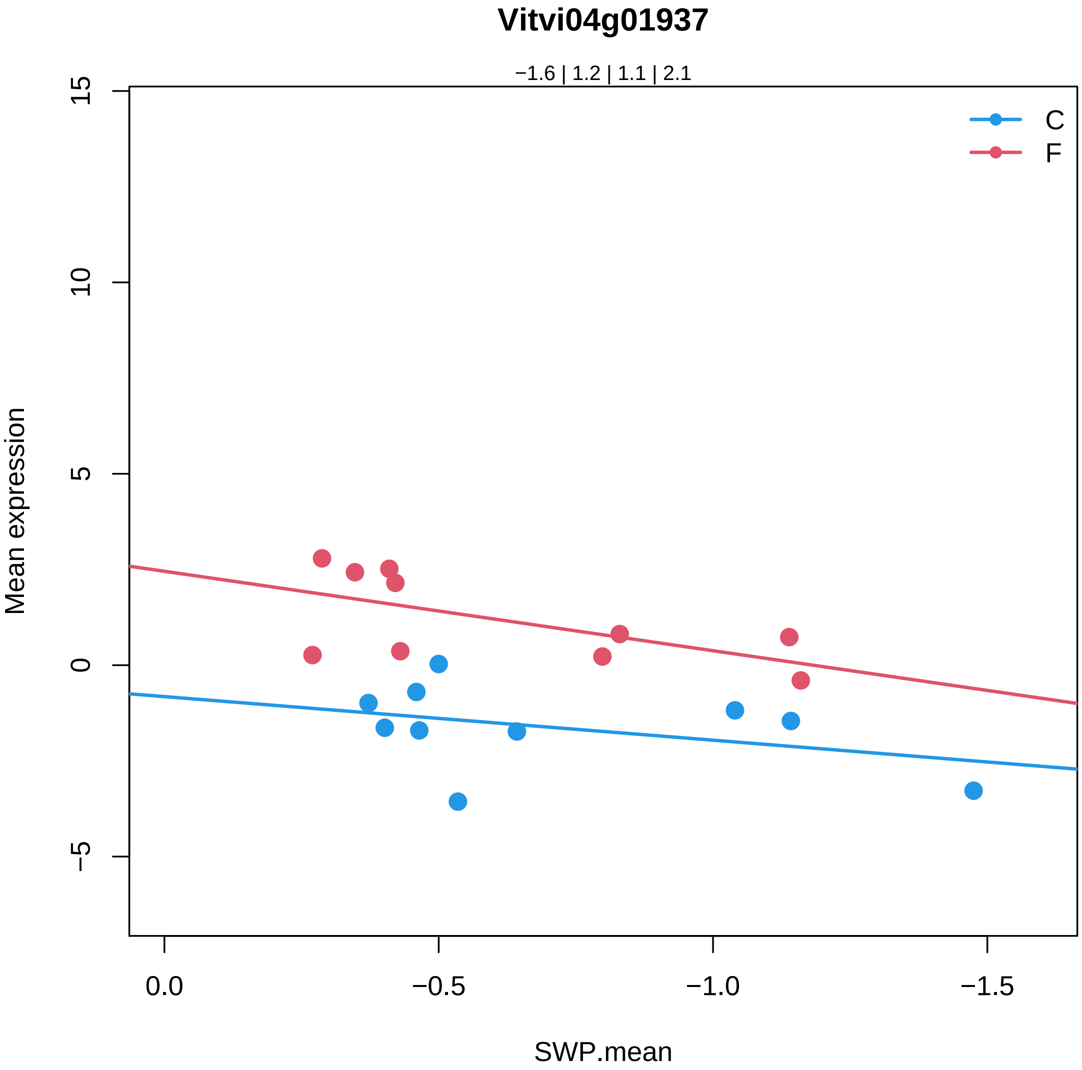
7.5.24 Vitvi04g01937: type4

```
> 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        
```



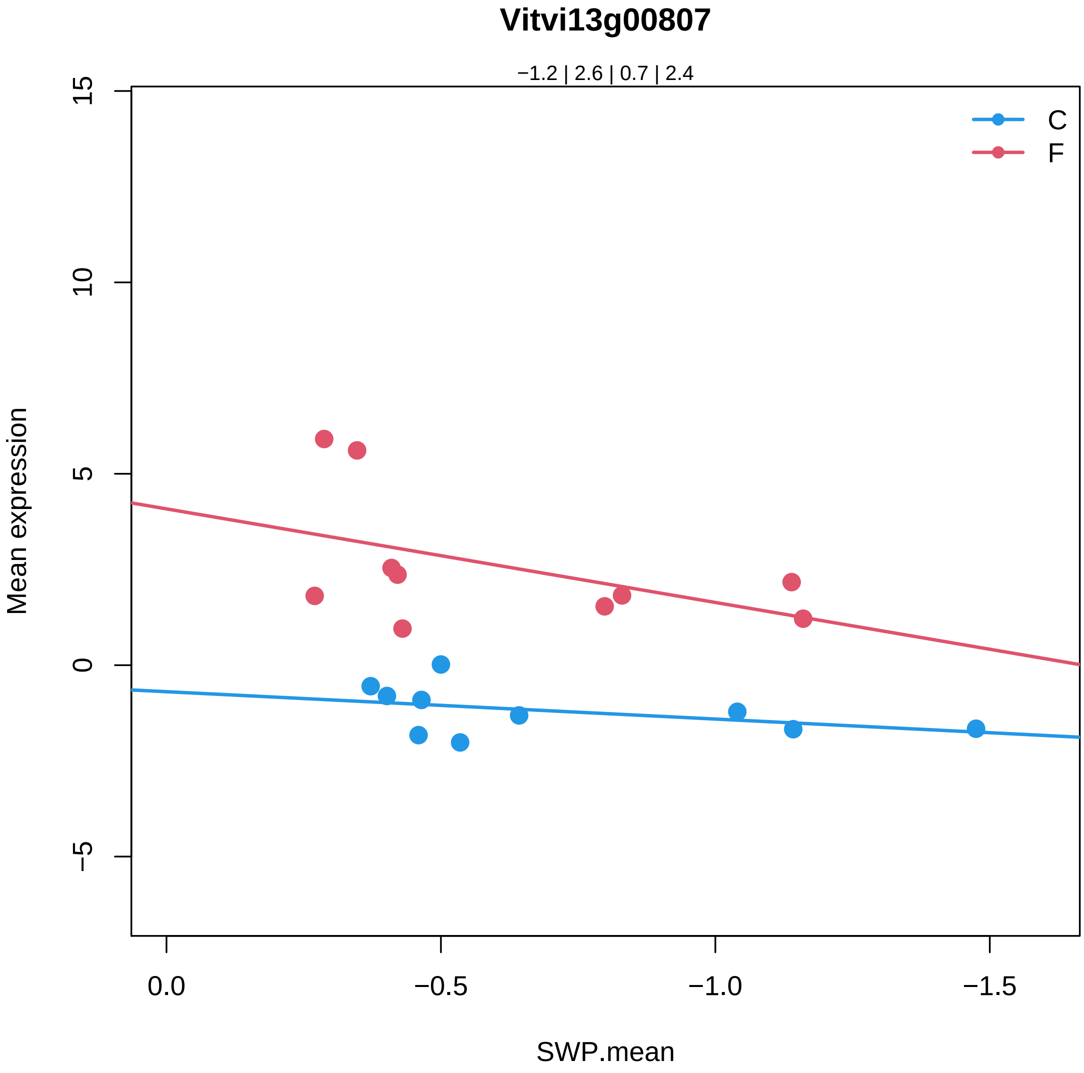
7.5.25 Vitvi13g00807: type4

```
> 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
```



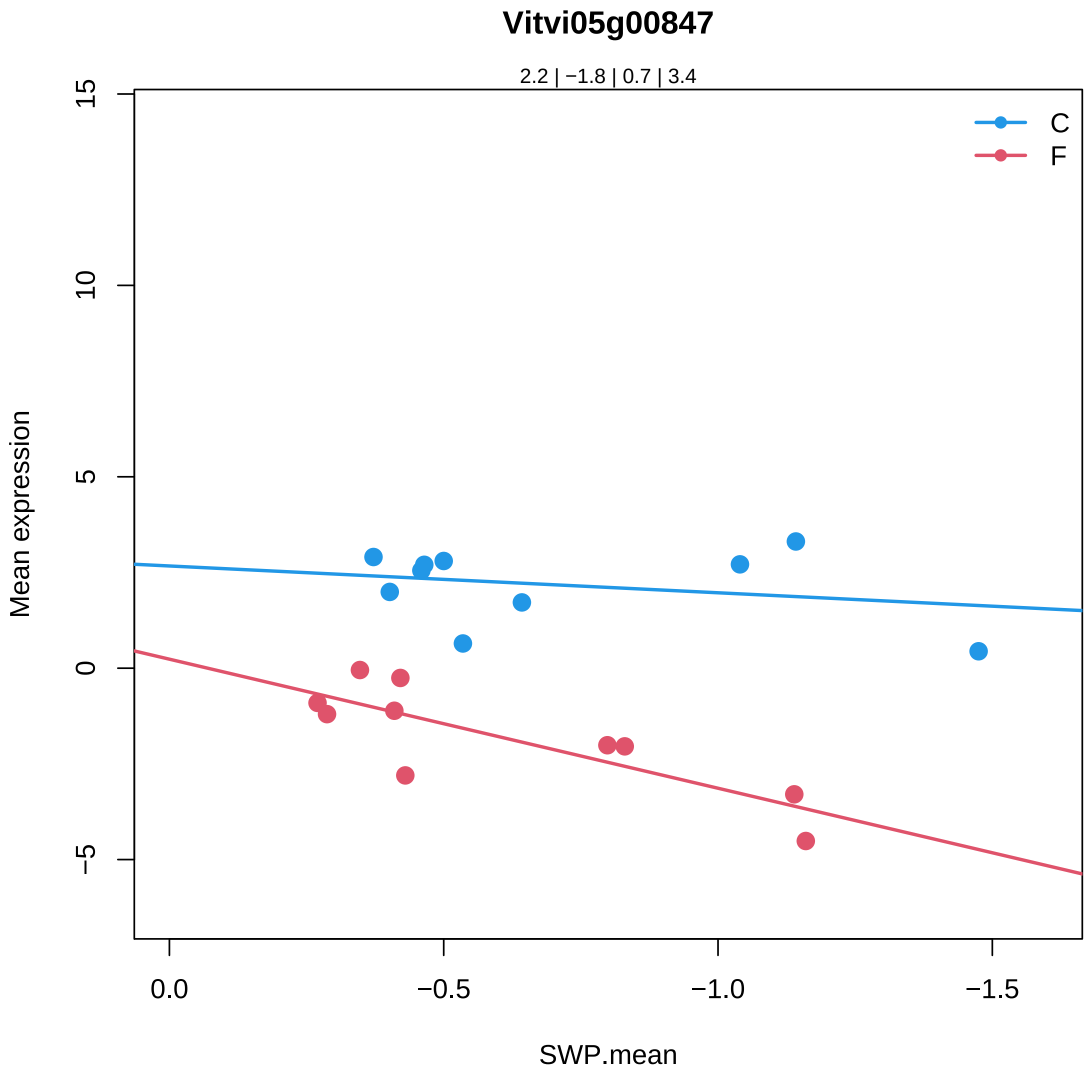
7.5.26 Vitvi05g00847: + type4

```
> 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
```



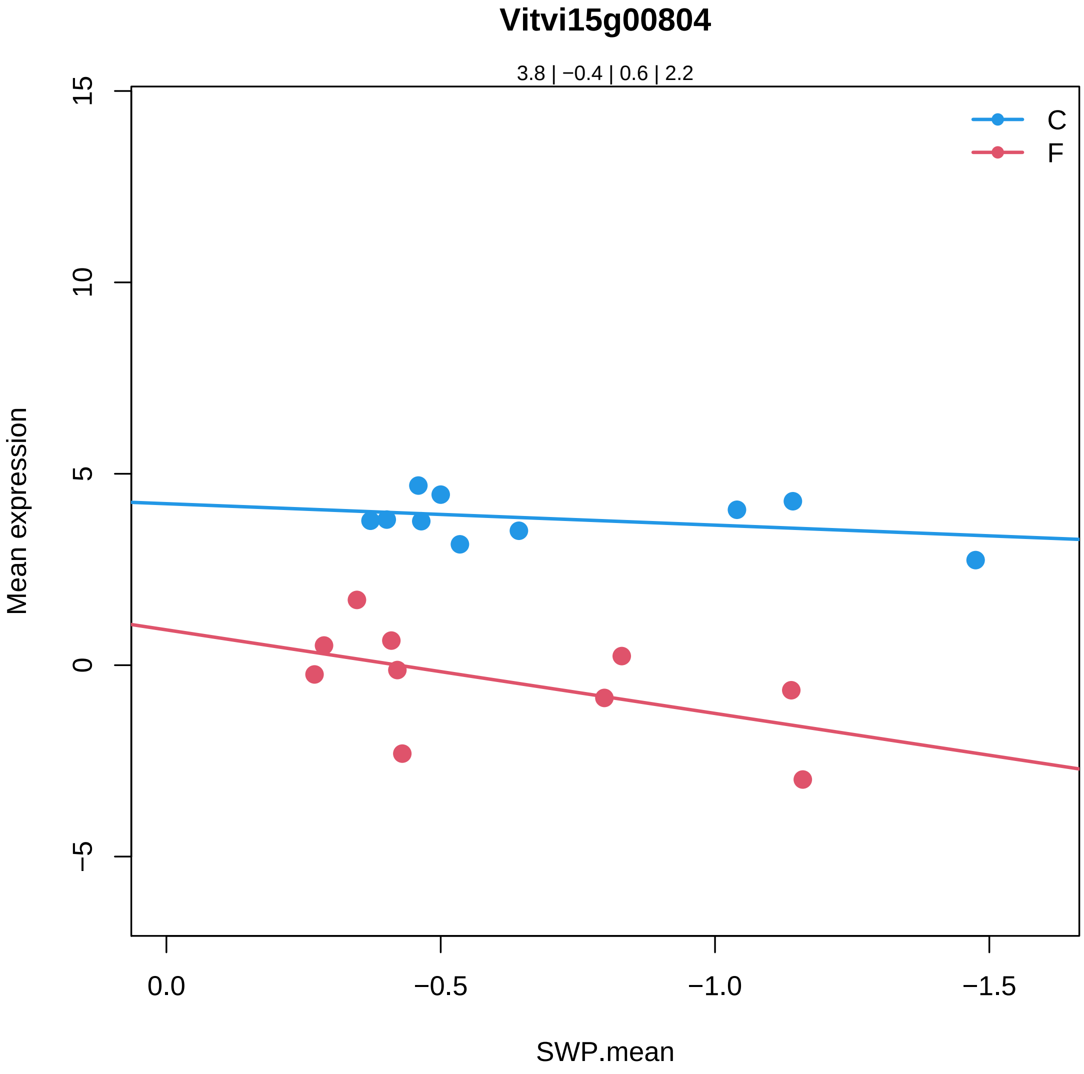
7.5.27 Vitvi15g00804: type4

```
> 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
```



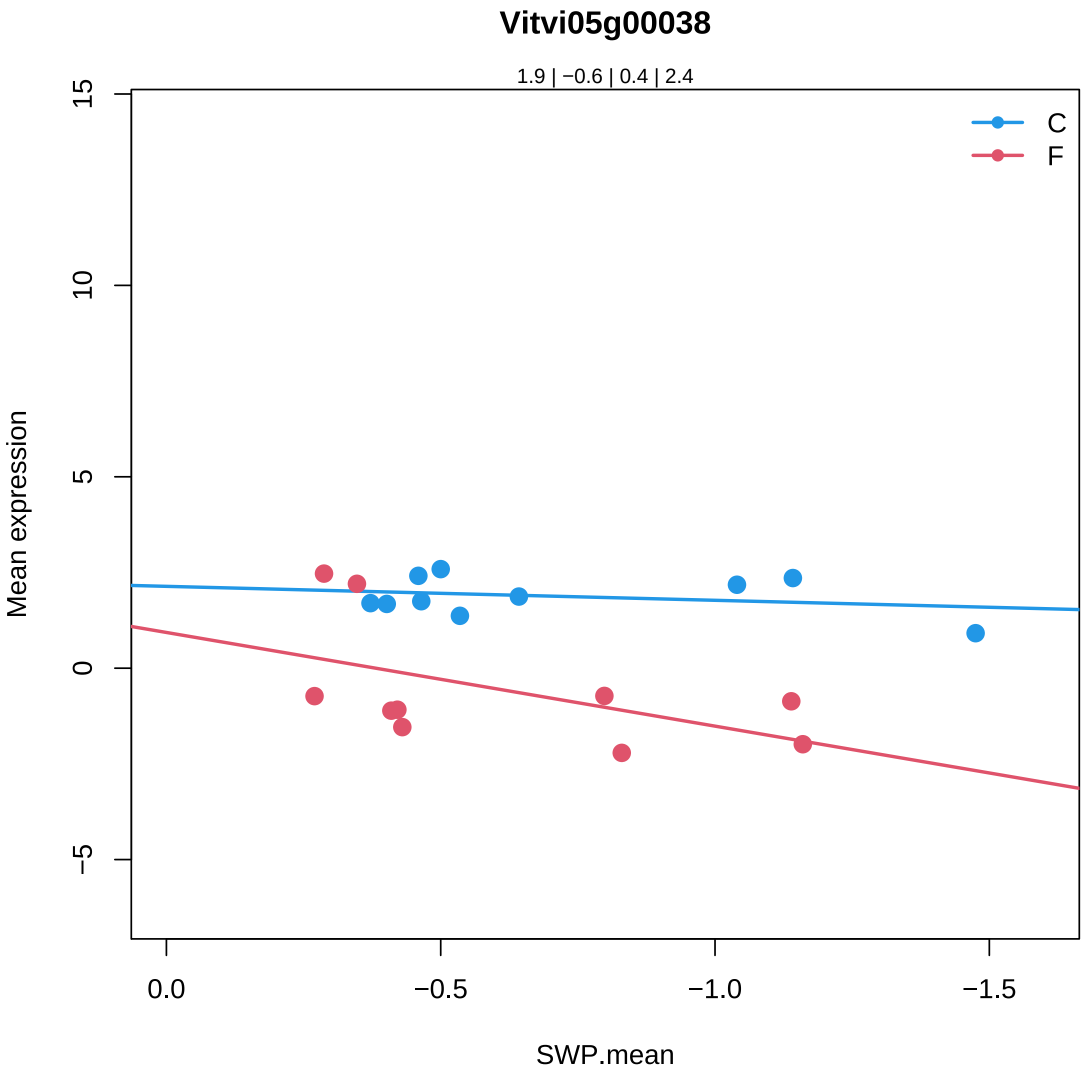
7.5.28 Vitvi05g00038: type3 | type4

```
> 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
```



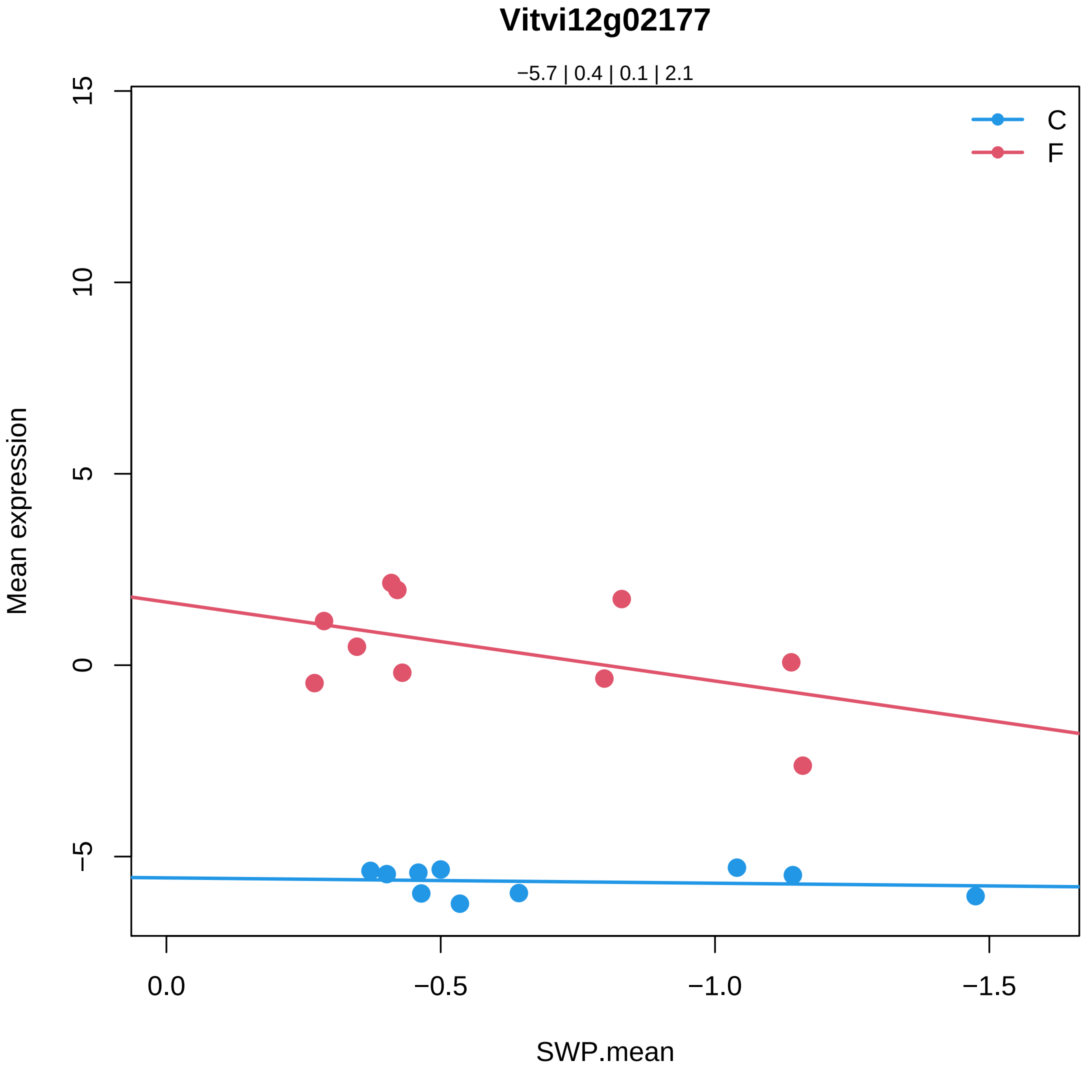
7.5.29 Vitvi12g02177: type3 | type4

```
> 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
```



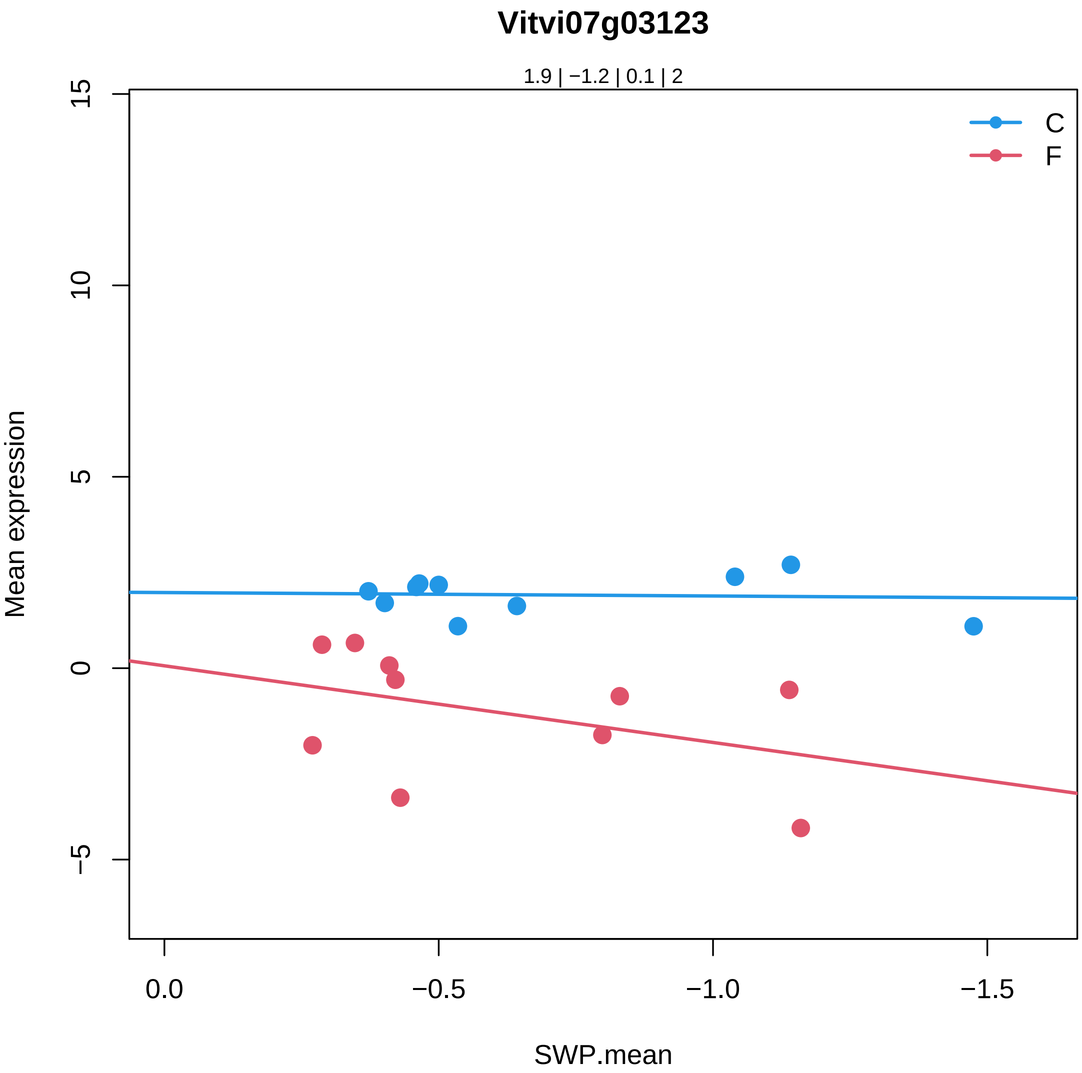
7.5.30 Vitvi07g03123: type3 | type4

```
> 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
```



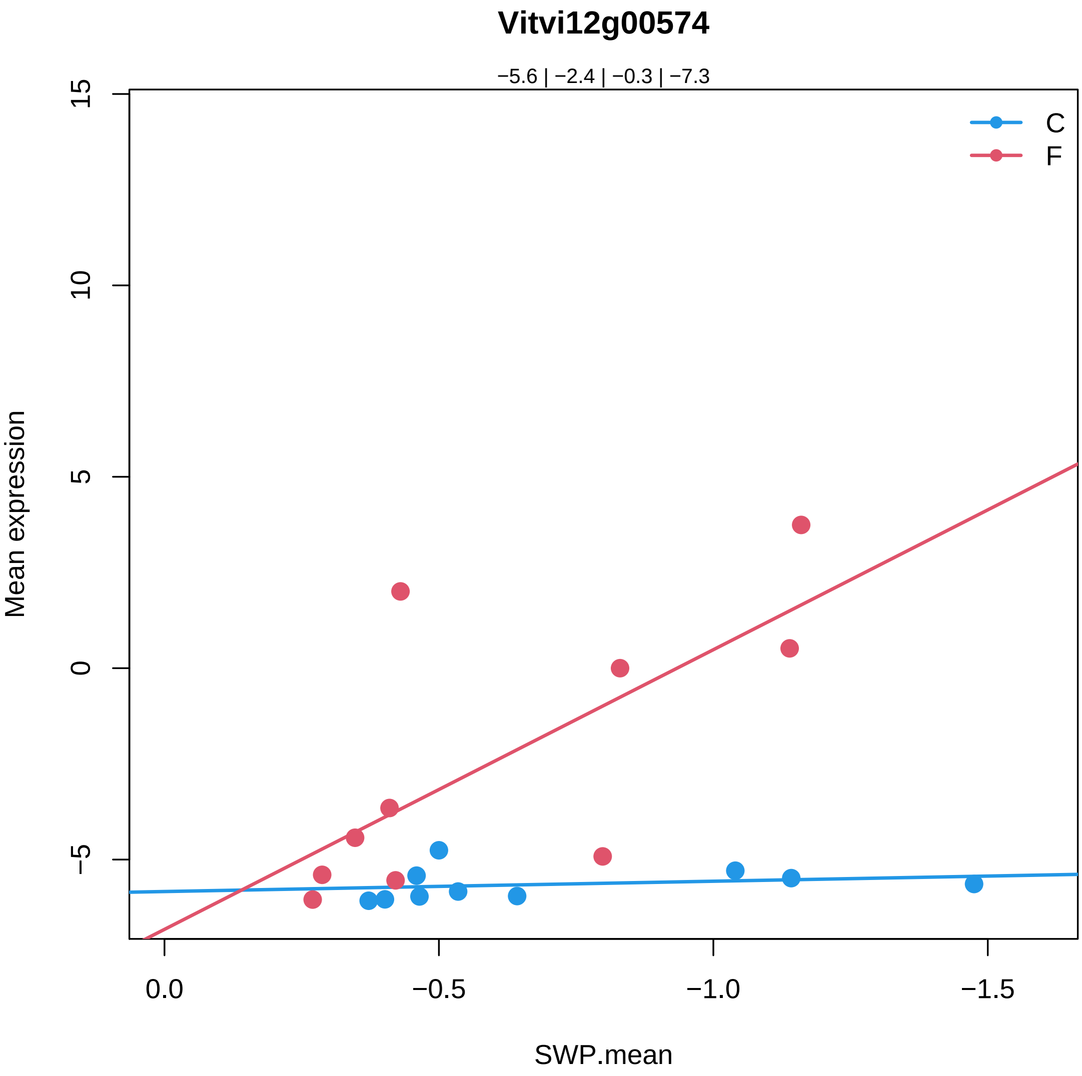
7.5.31 Vitvi12g00574: + type3 | type4

```
> 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
```



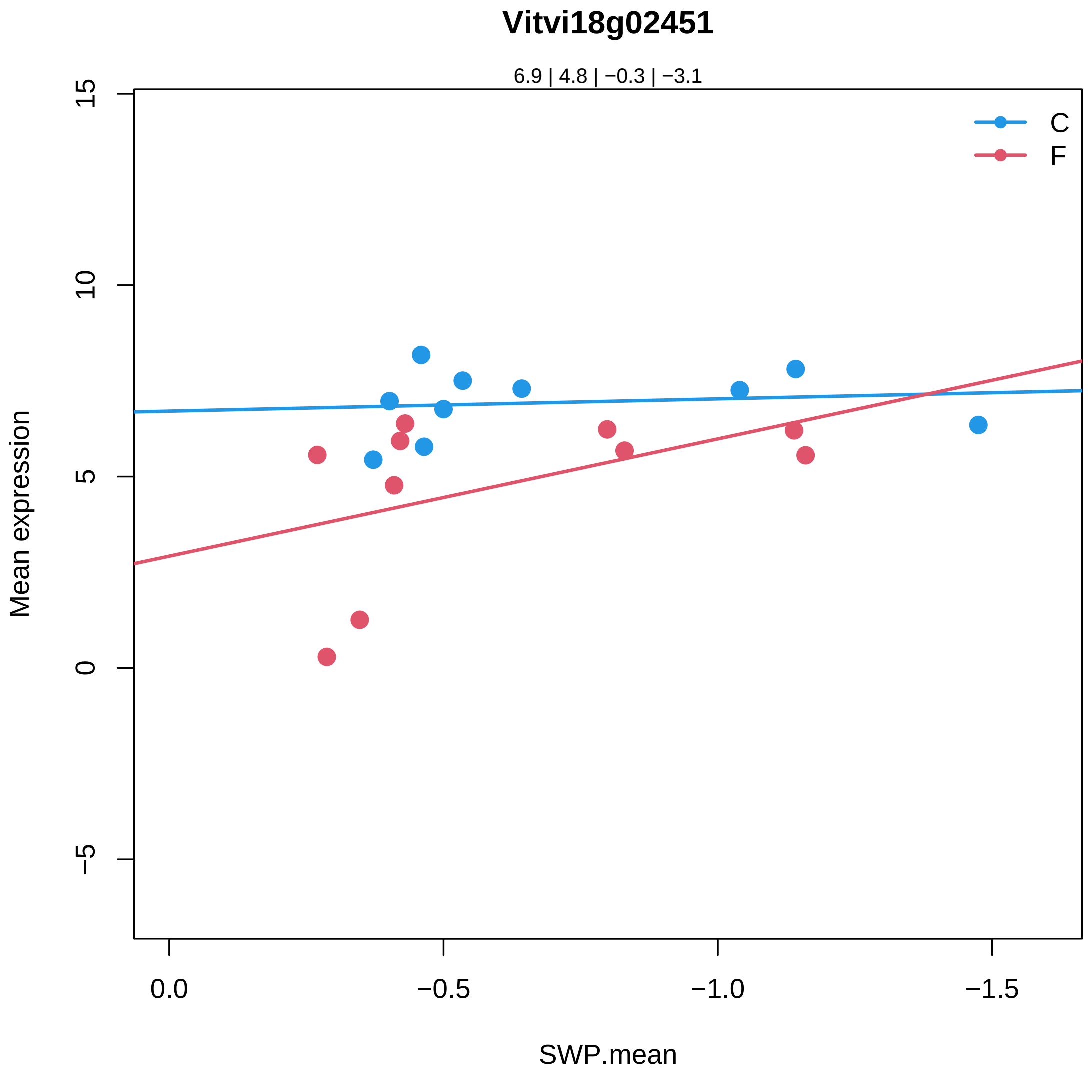
7.5.32 Vitvi18g02451: type3 | type4

```
> 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
```



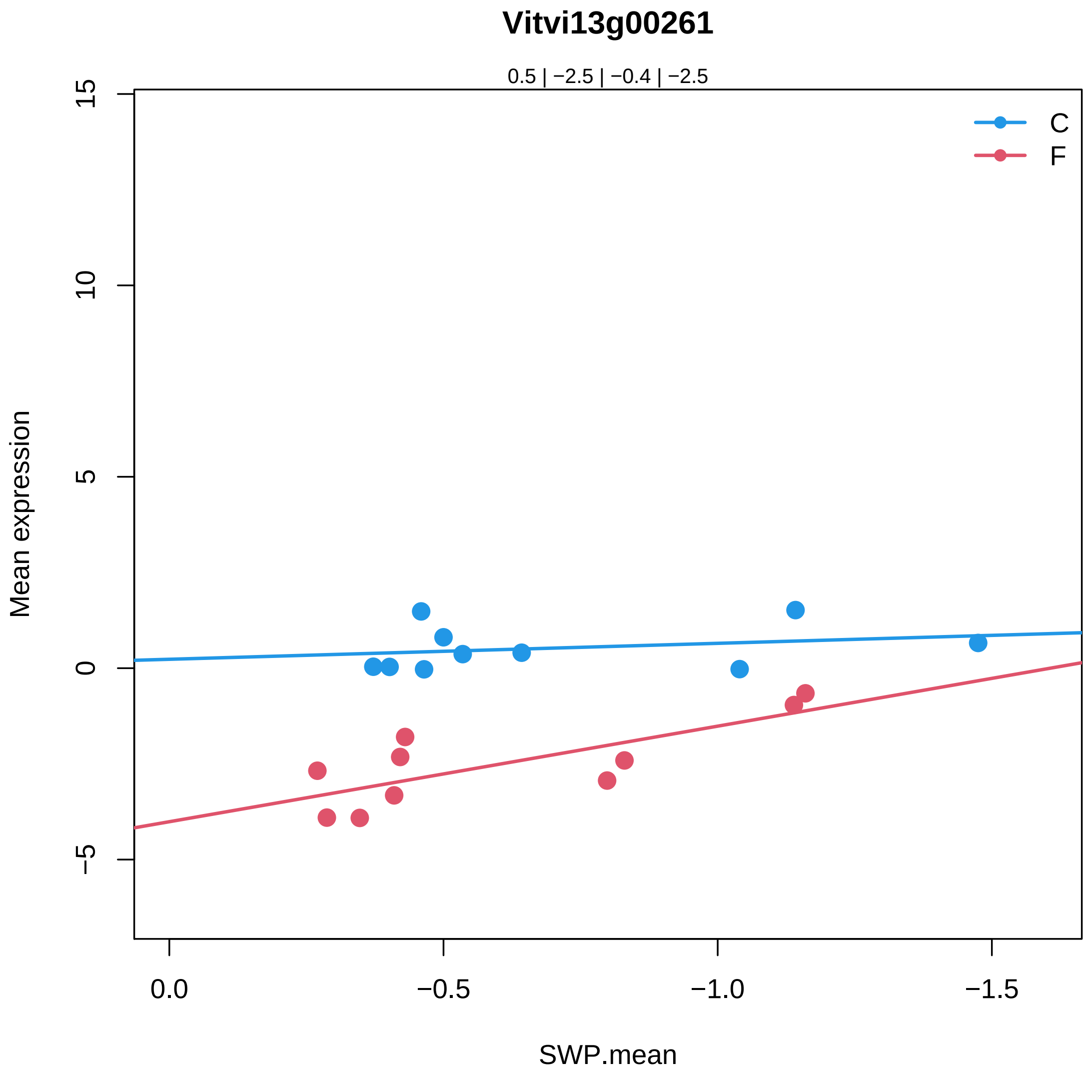
7.5.33 Vitvi13g00261: + type3 | type4

```
> 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
```



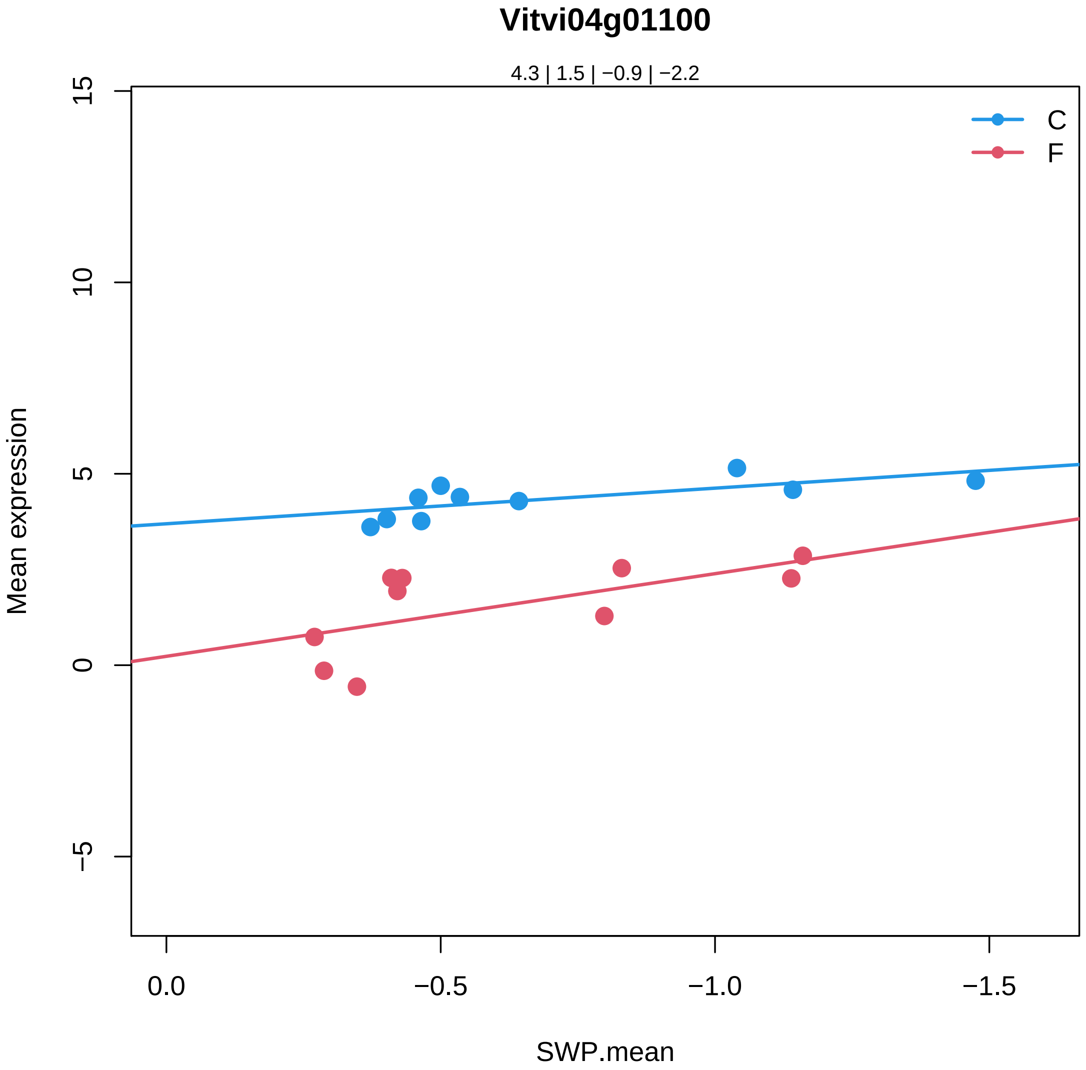
7.5.34 Vitvi04g01100: type4

```
> 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
```



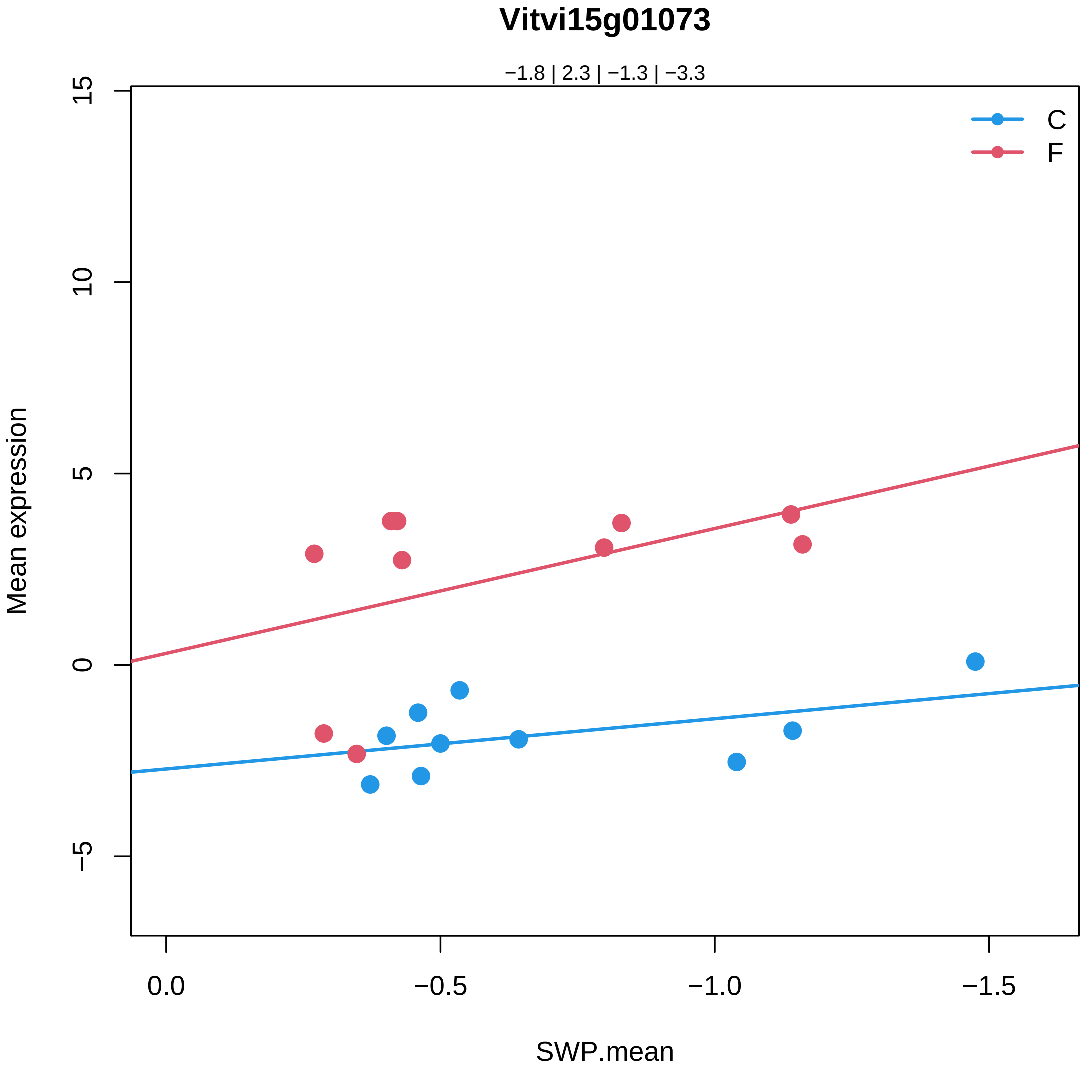
7.5.35 Vitvi15g01073: type4

```
> 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
```



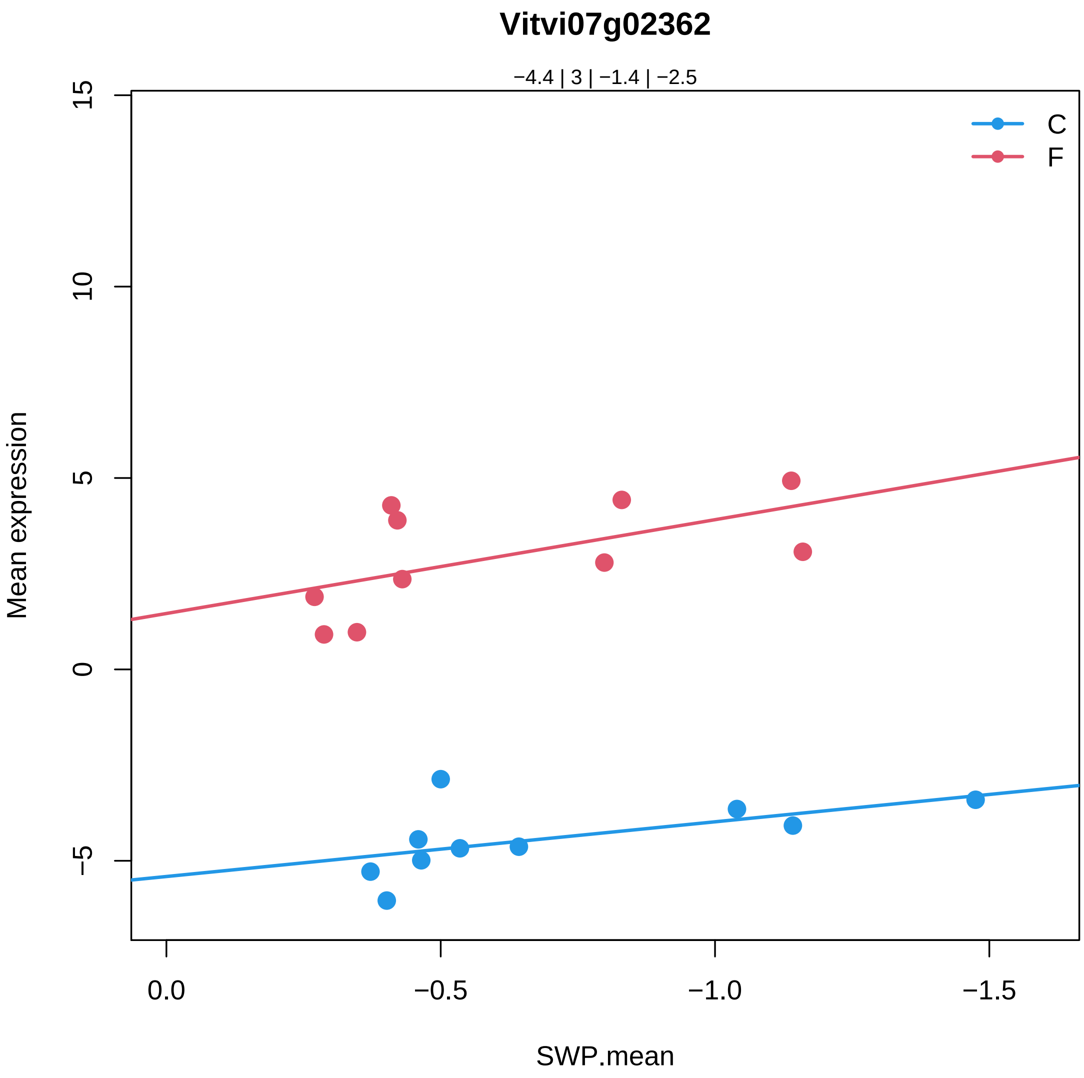
7.5.36 Vitvi07g02362: type4

```
> 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
```



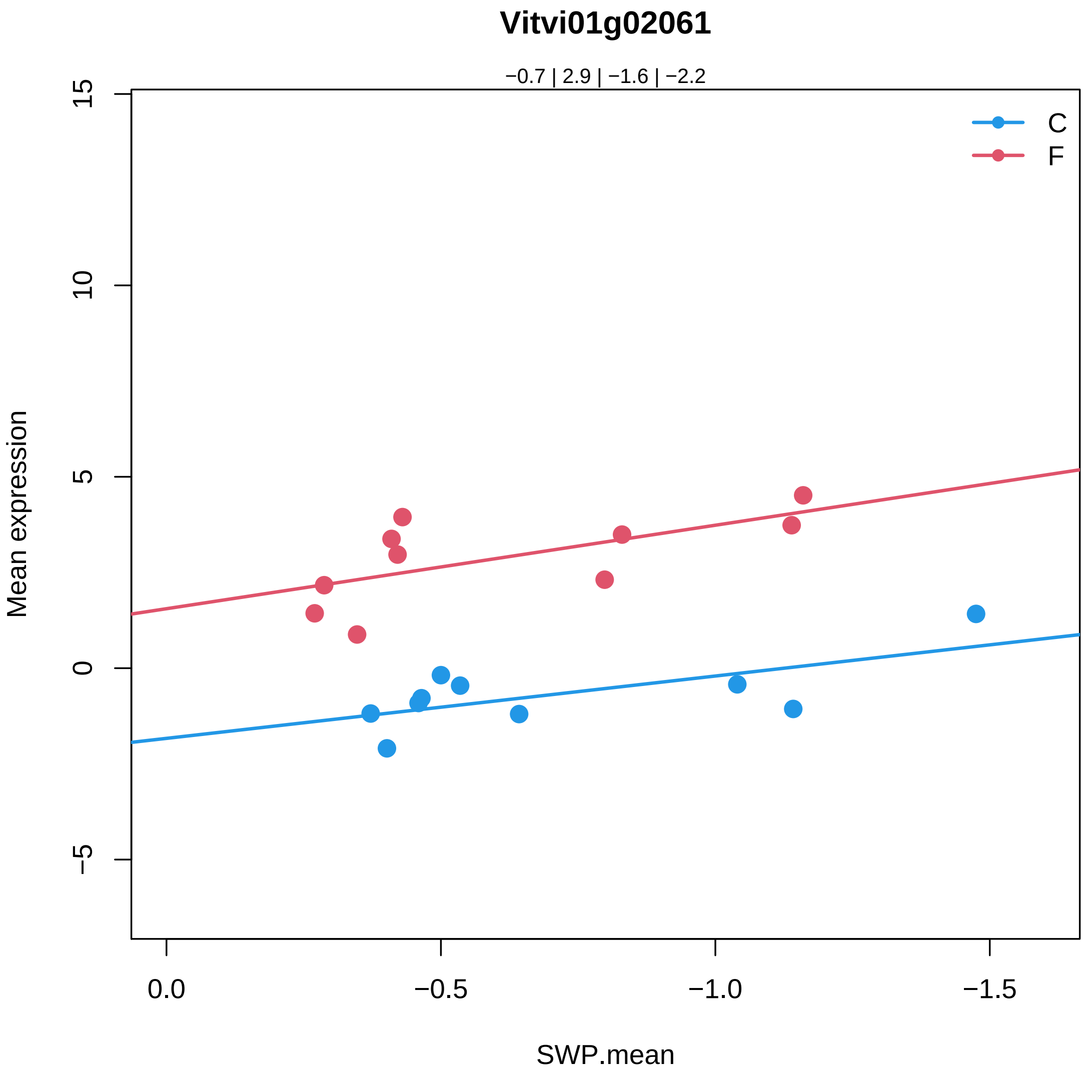
7.5.37 Vitvi01g02061: * type4

```
> 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
```



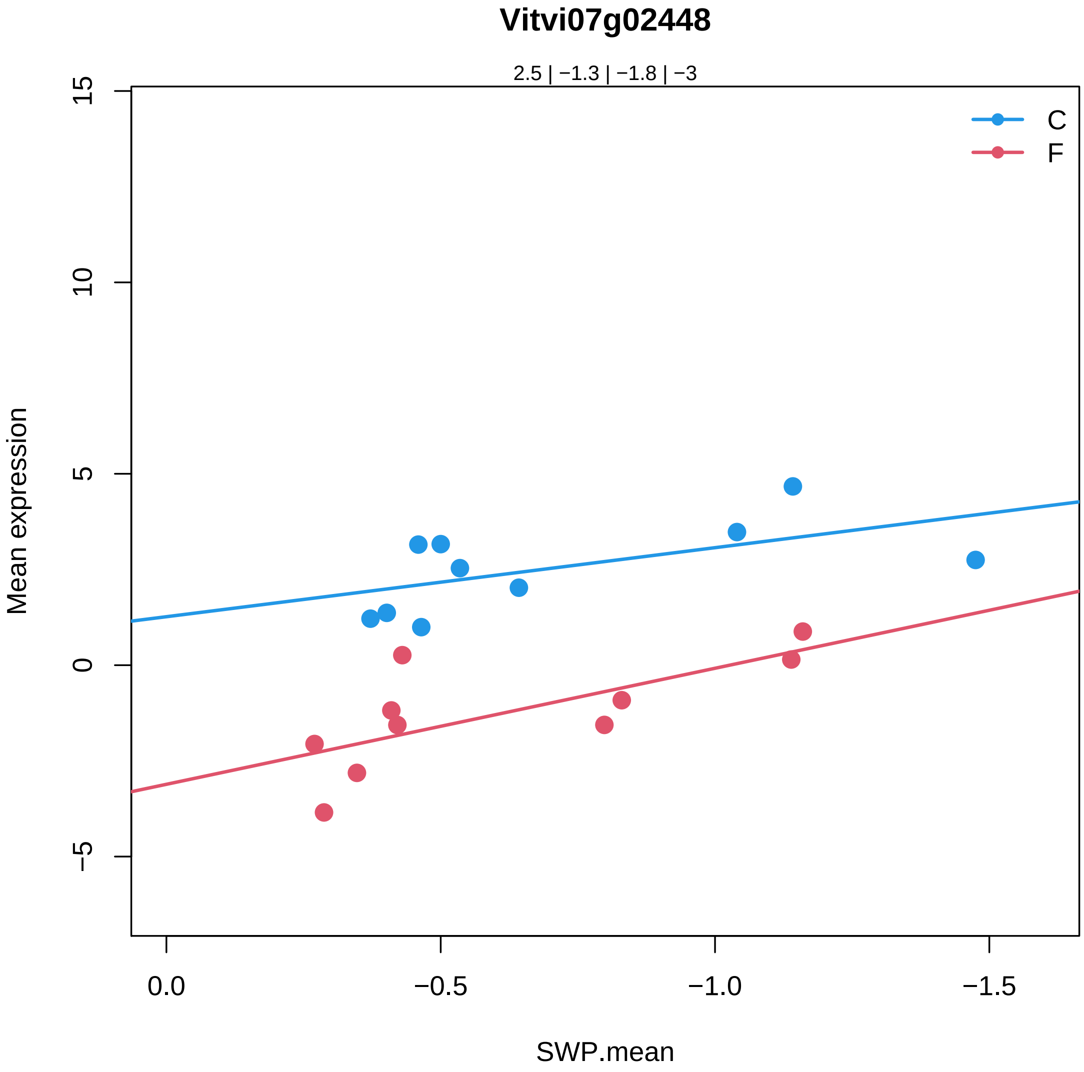
7.5.38 Vitvi07g02448: * type4

```
> 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        
```



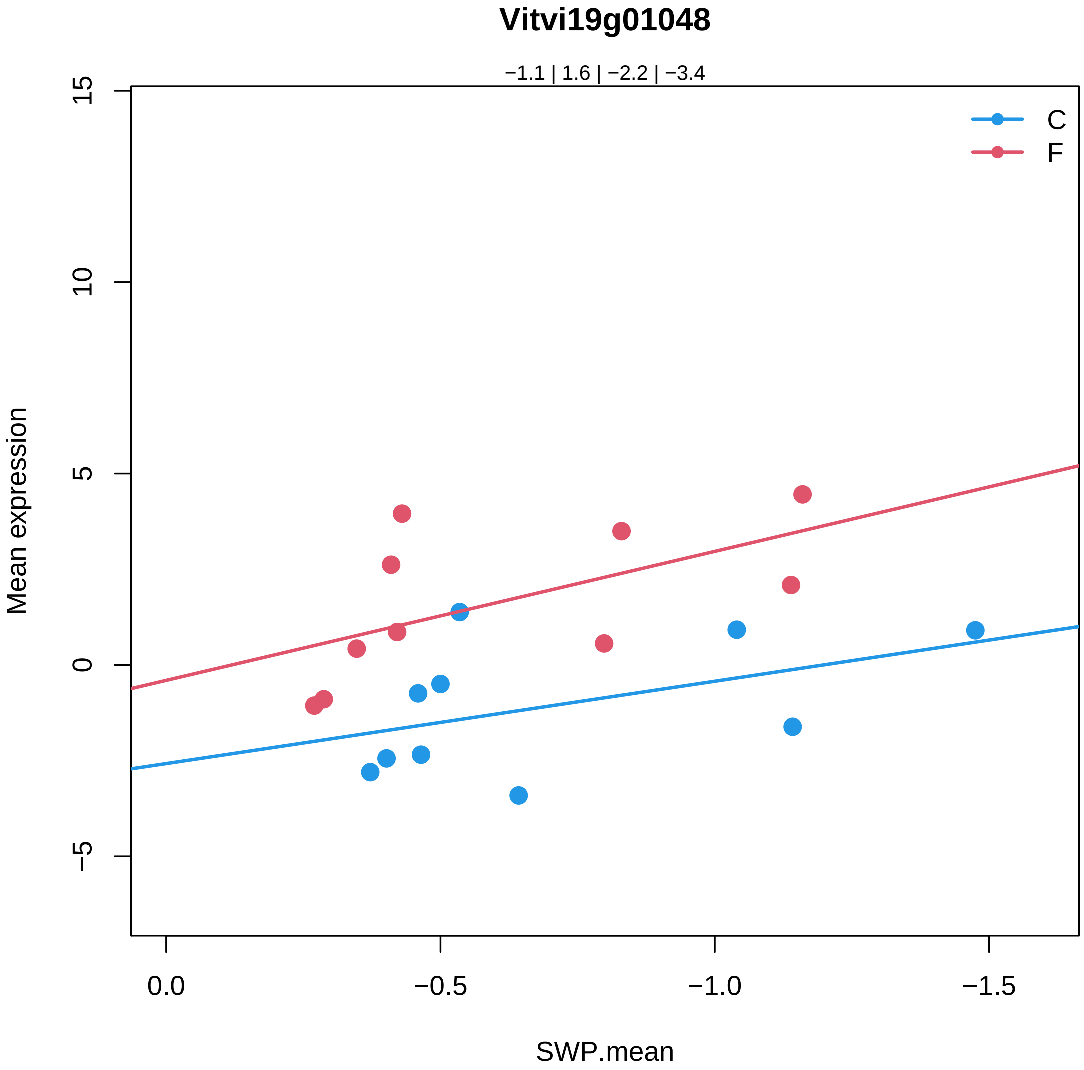
7.5.39 Vitvi19g01048: type2 | type4

```
> 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
```



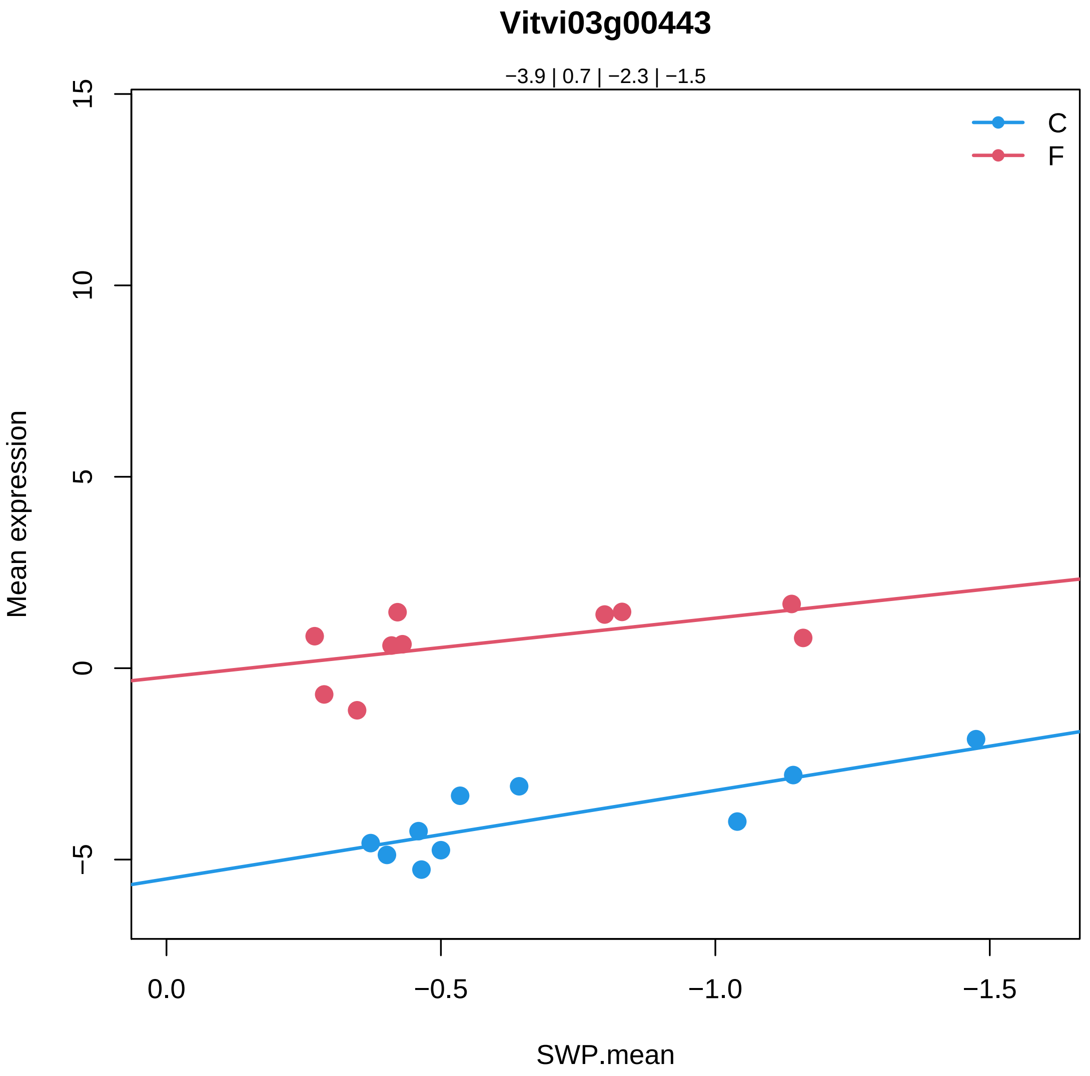
7.5.40 Vitvi03g00443: * type4

```
> 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
```



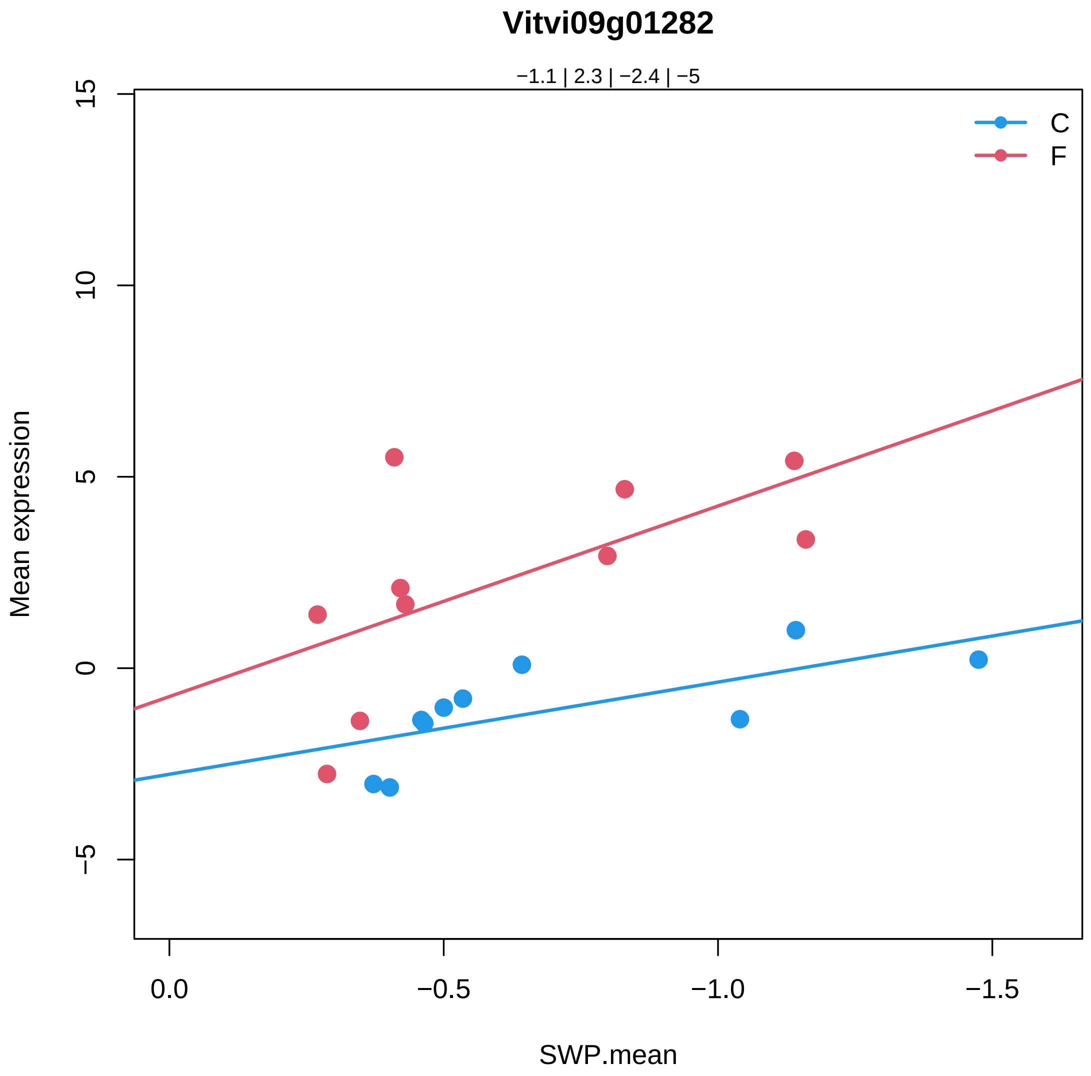
7.5.41 Vitvi09g01282: type2 | type4

```
> 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        
```



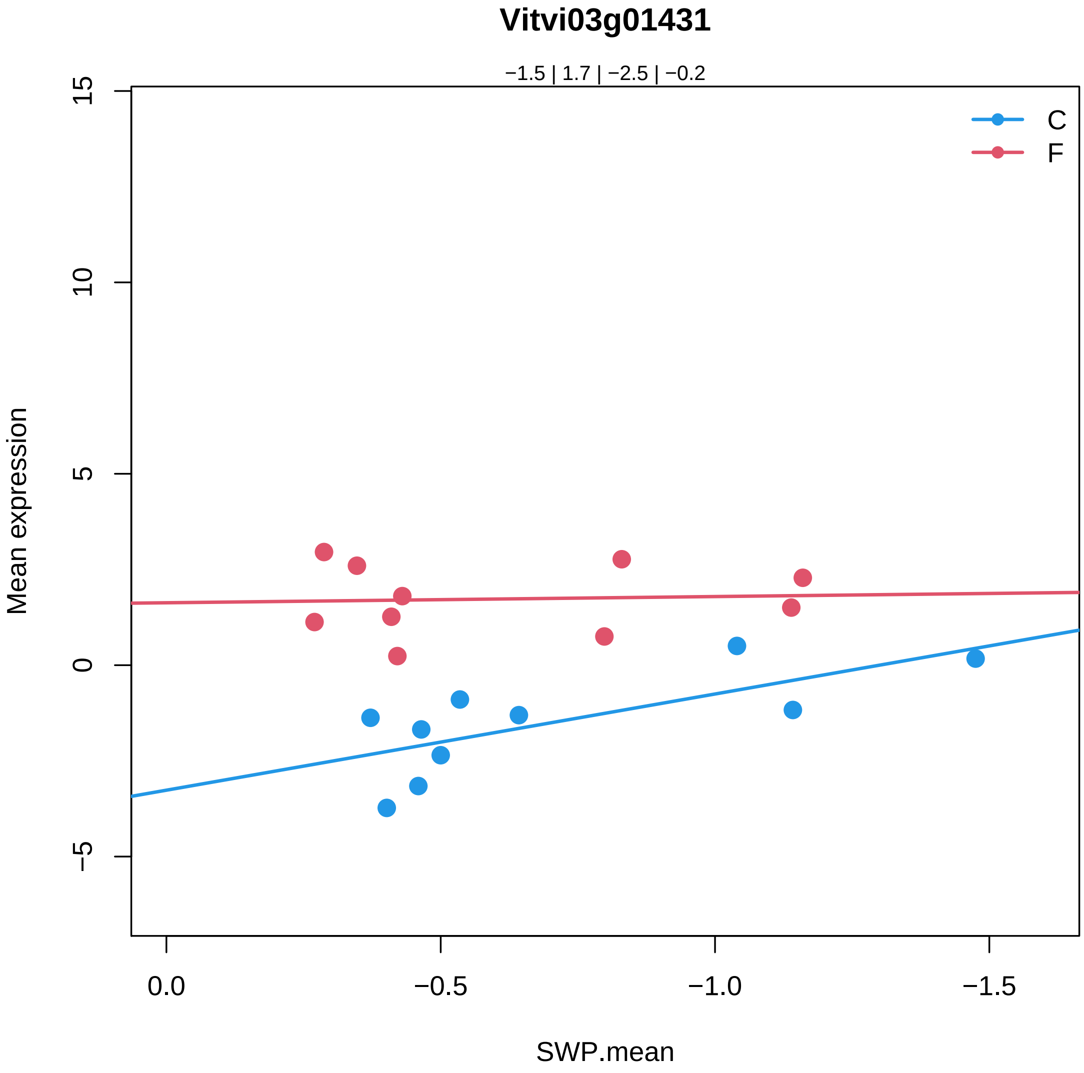
7.5.42 Vitvi03g01431: * type3 | type4

```
> 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
```



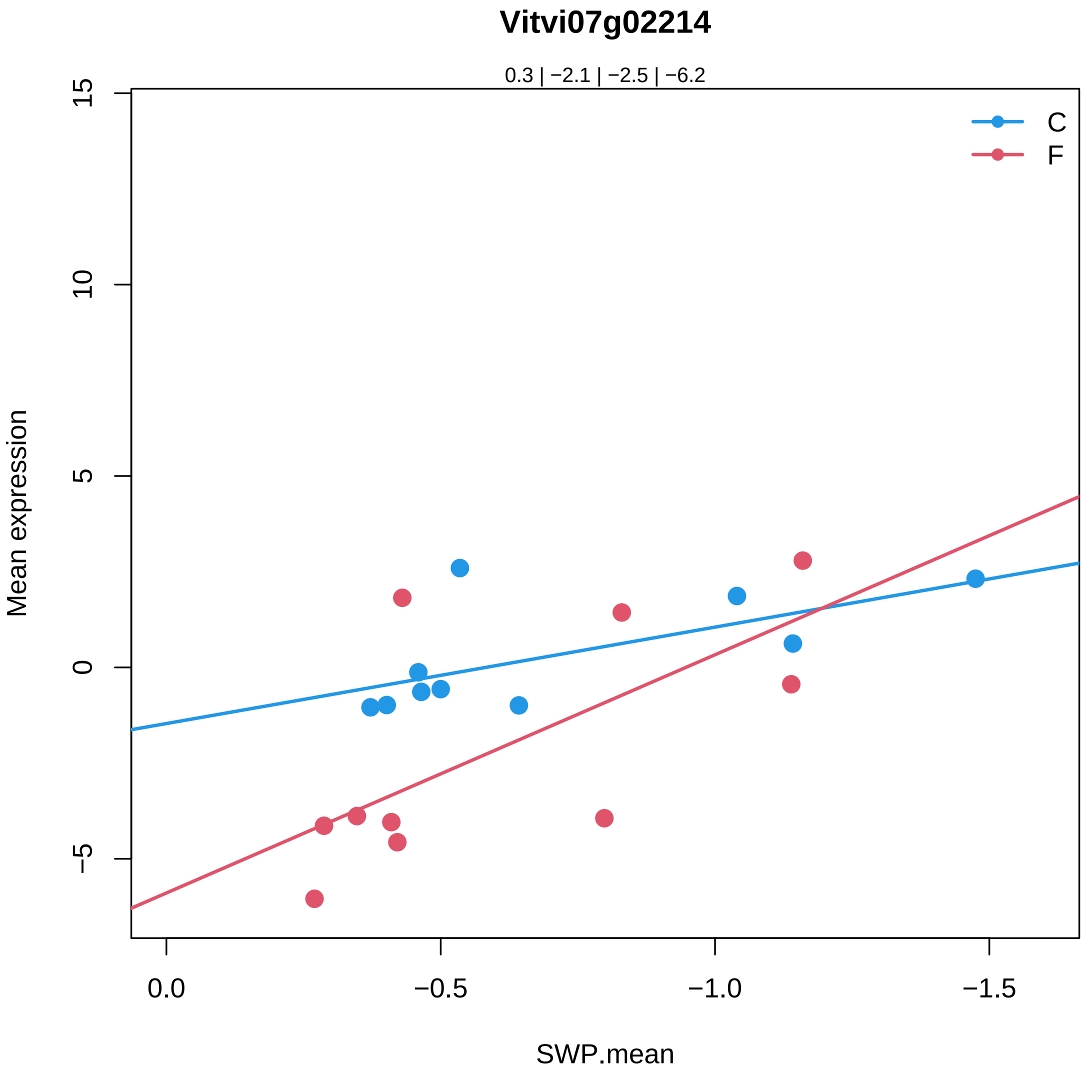
7.5.43 Vitvi07g02214: type2 | type4

```
> 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        
```



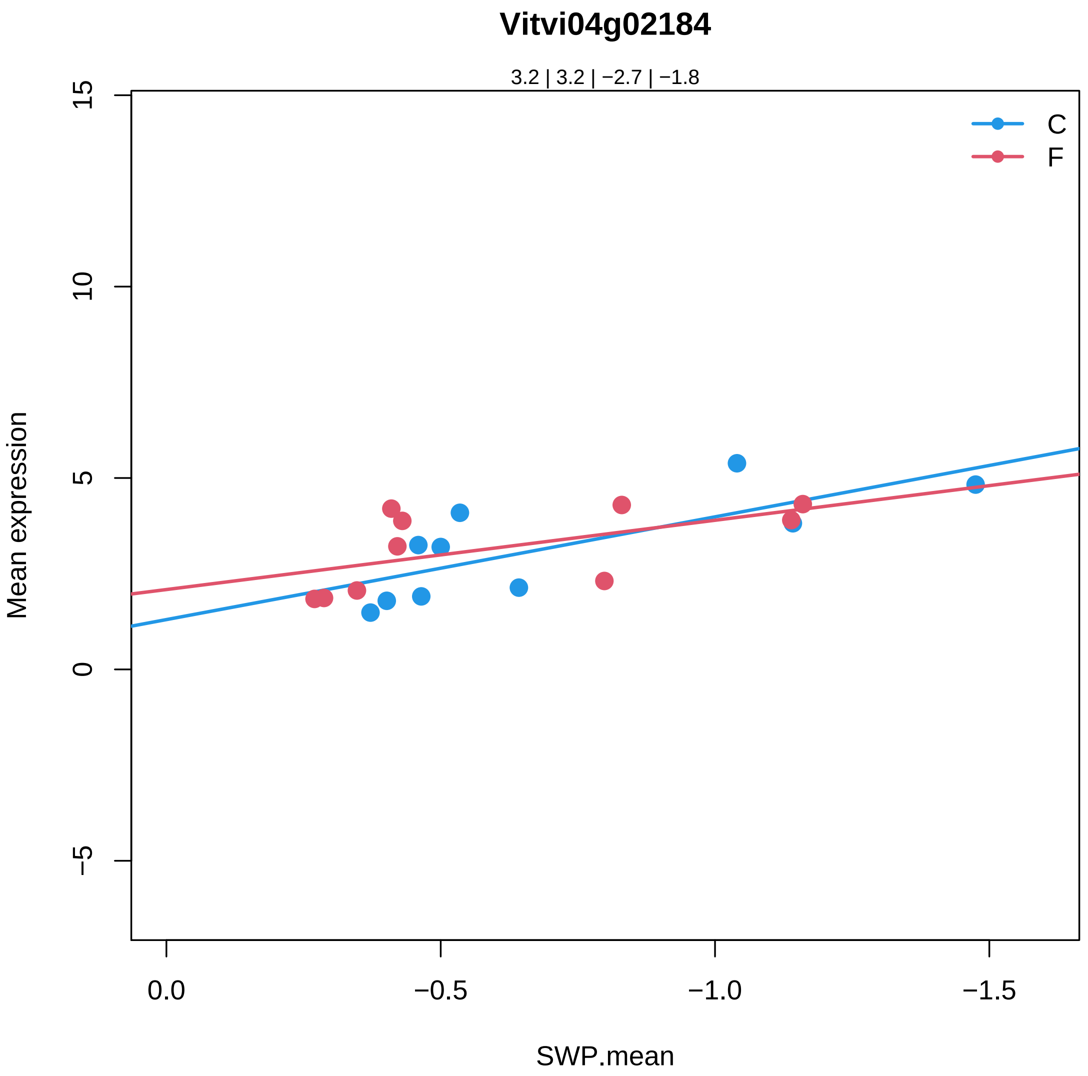
7.5.44 Vitvi04g02184: * type4

```
> 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
```



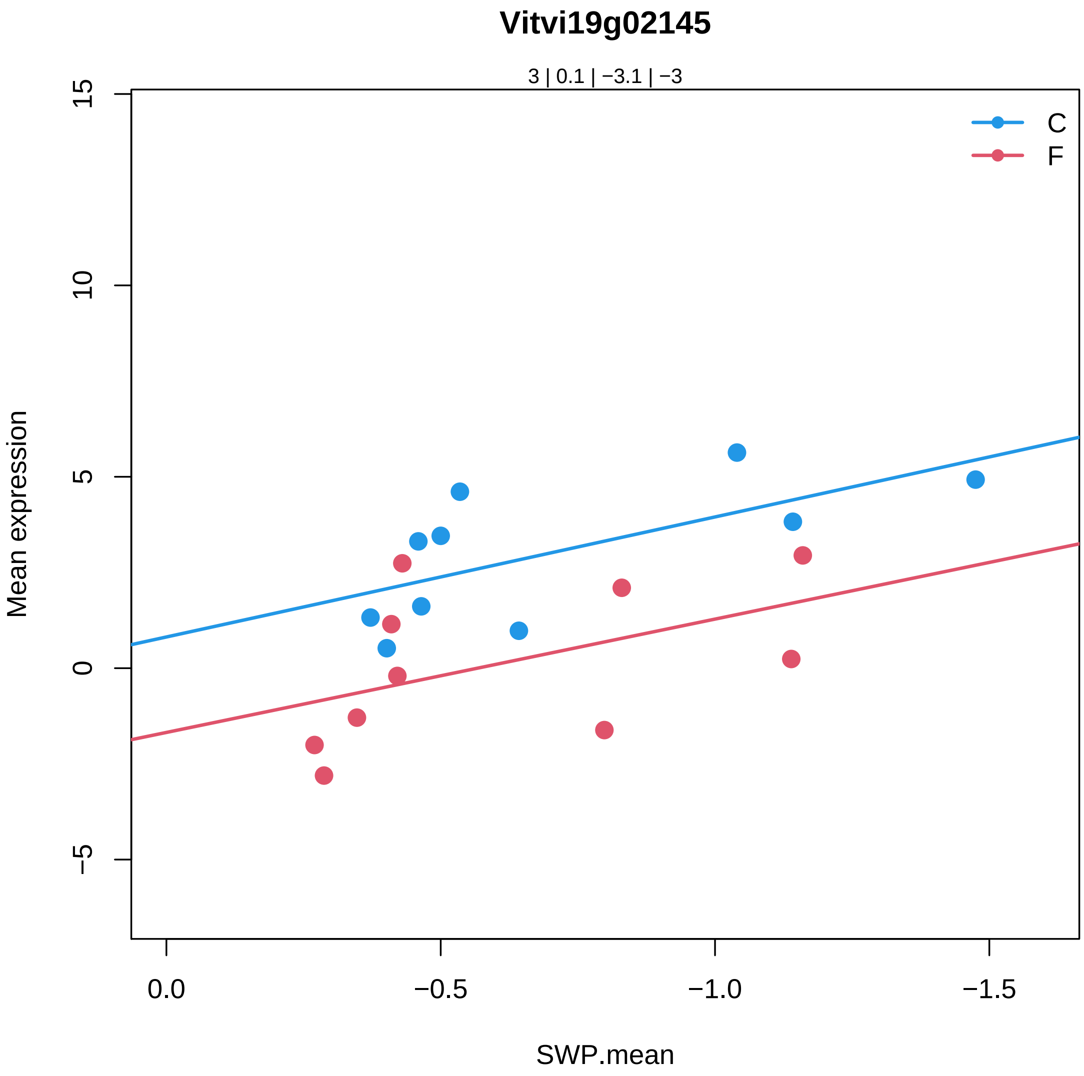
7.5.45 Vitvi19g02145: * type4

```
> 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
```



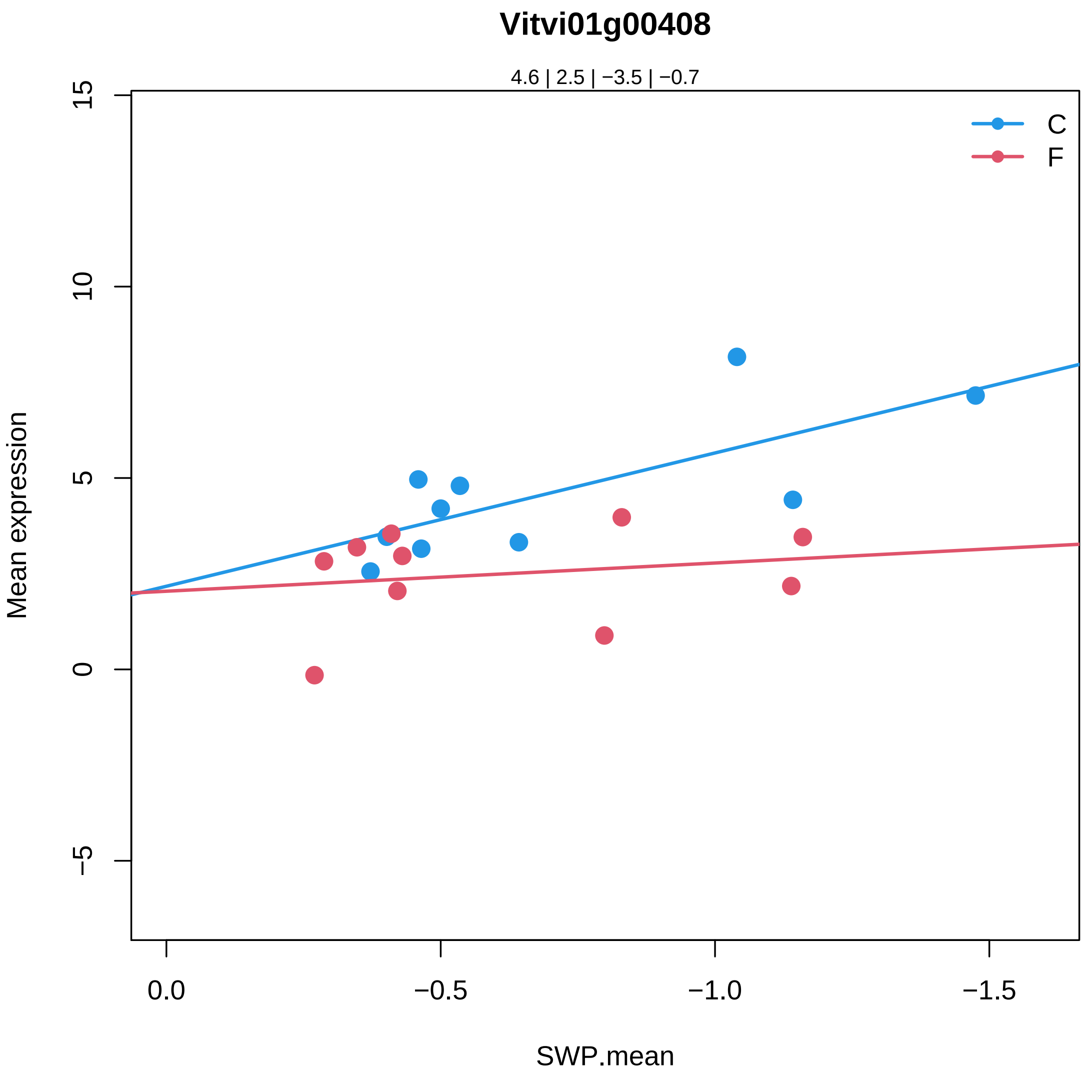
7.5.46 Vitvi01g00408: * type4

```
> 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        
```



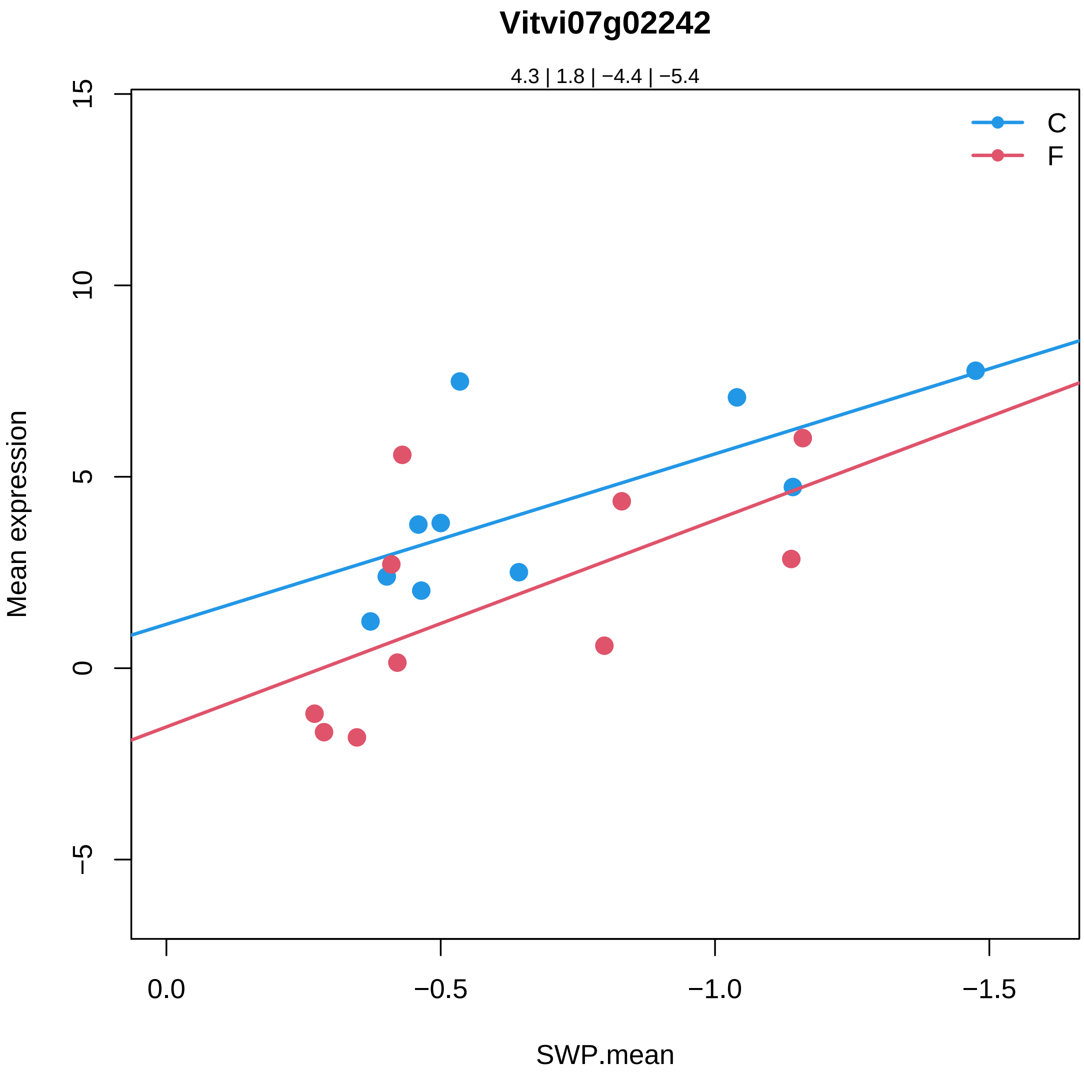
7.5.47 Vitvi07g02242: * type4

```
> 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        
```



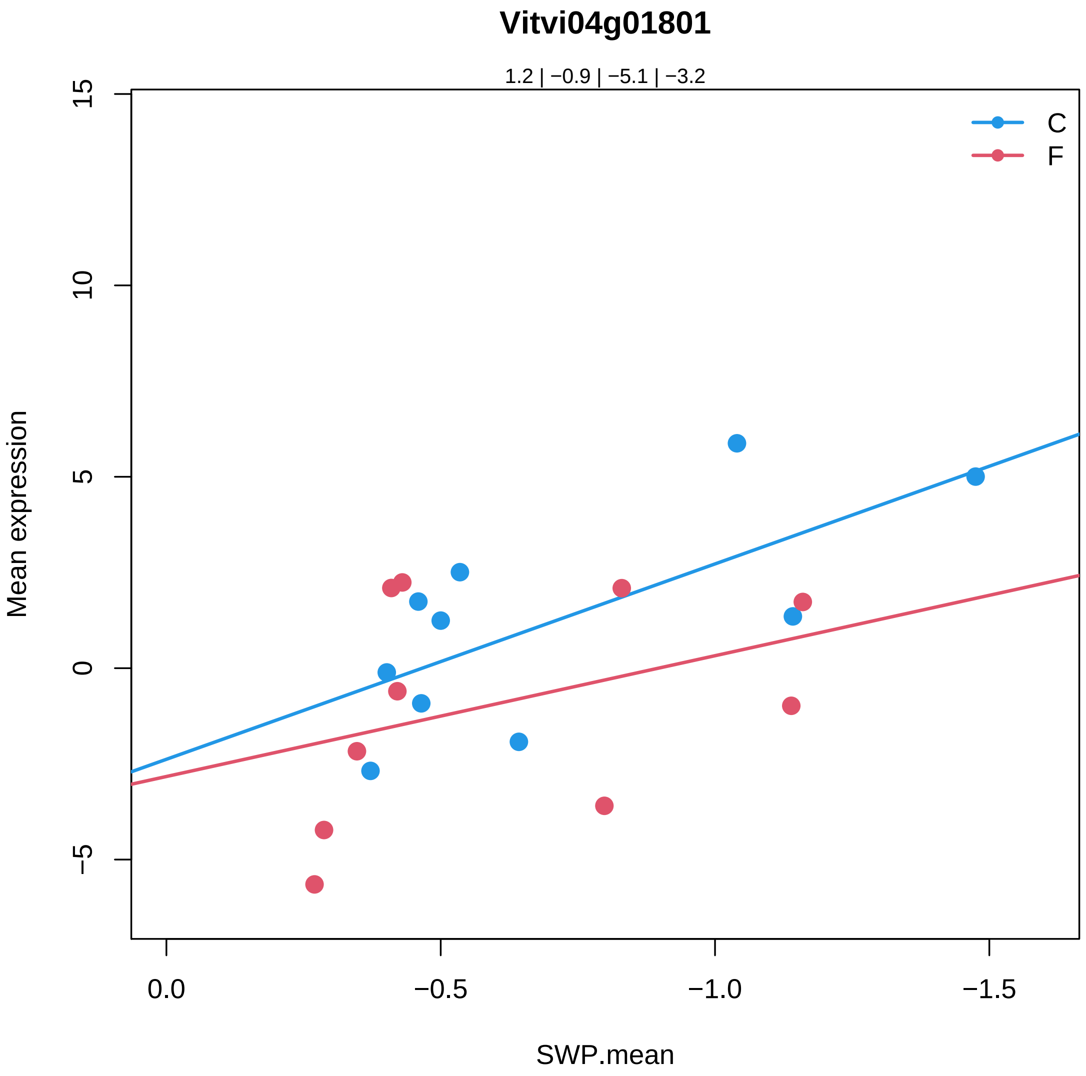
7.5.48 Vitvi04g01801: * type2 | type4

```
> 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
```



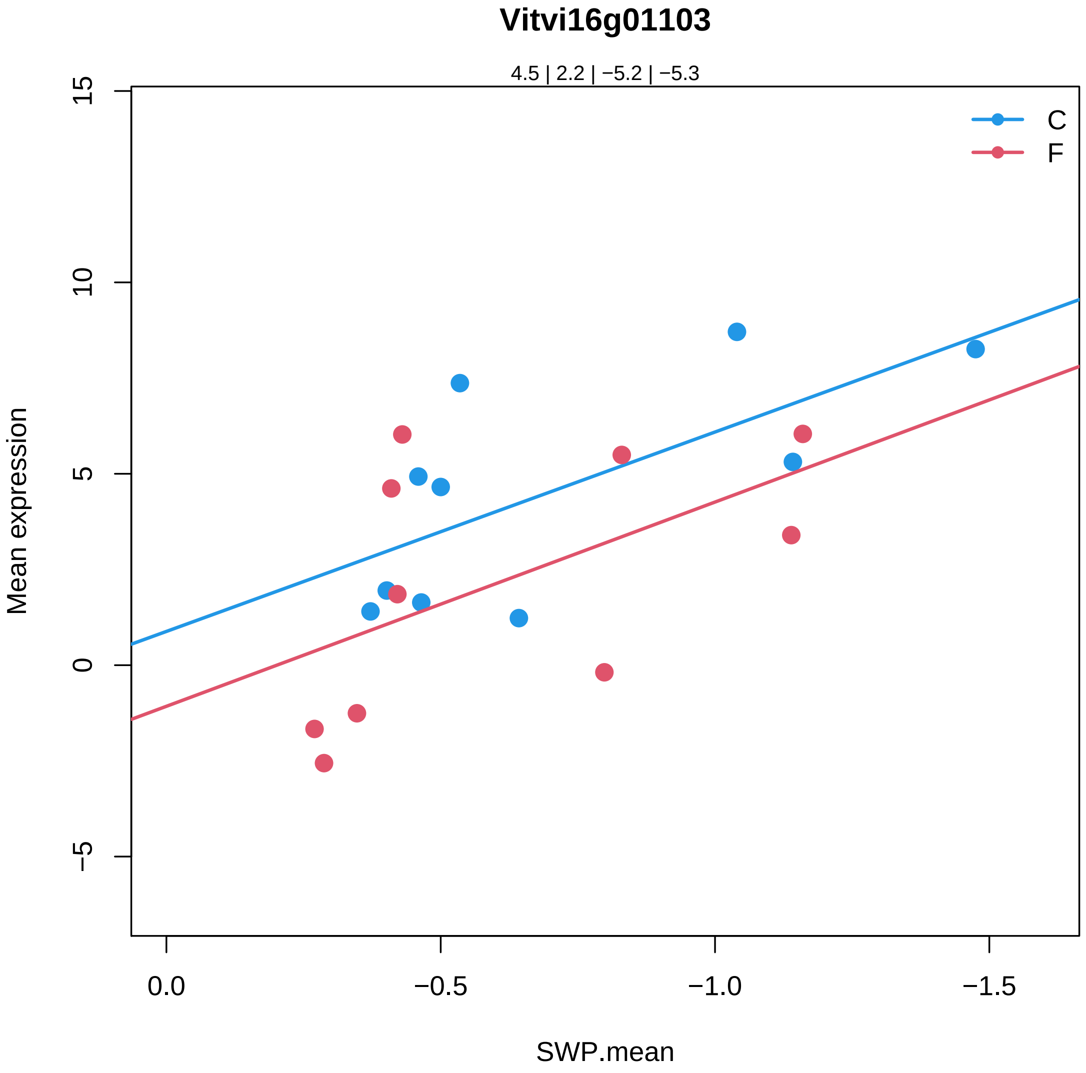
7.5.49 Vitvi16g01103: * type4

```
> 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
```



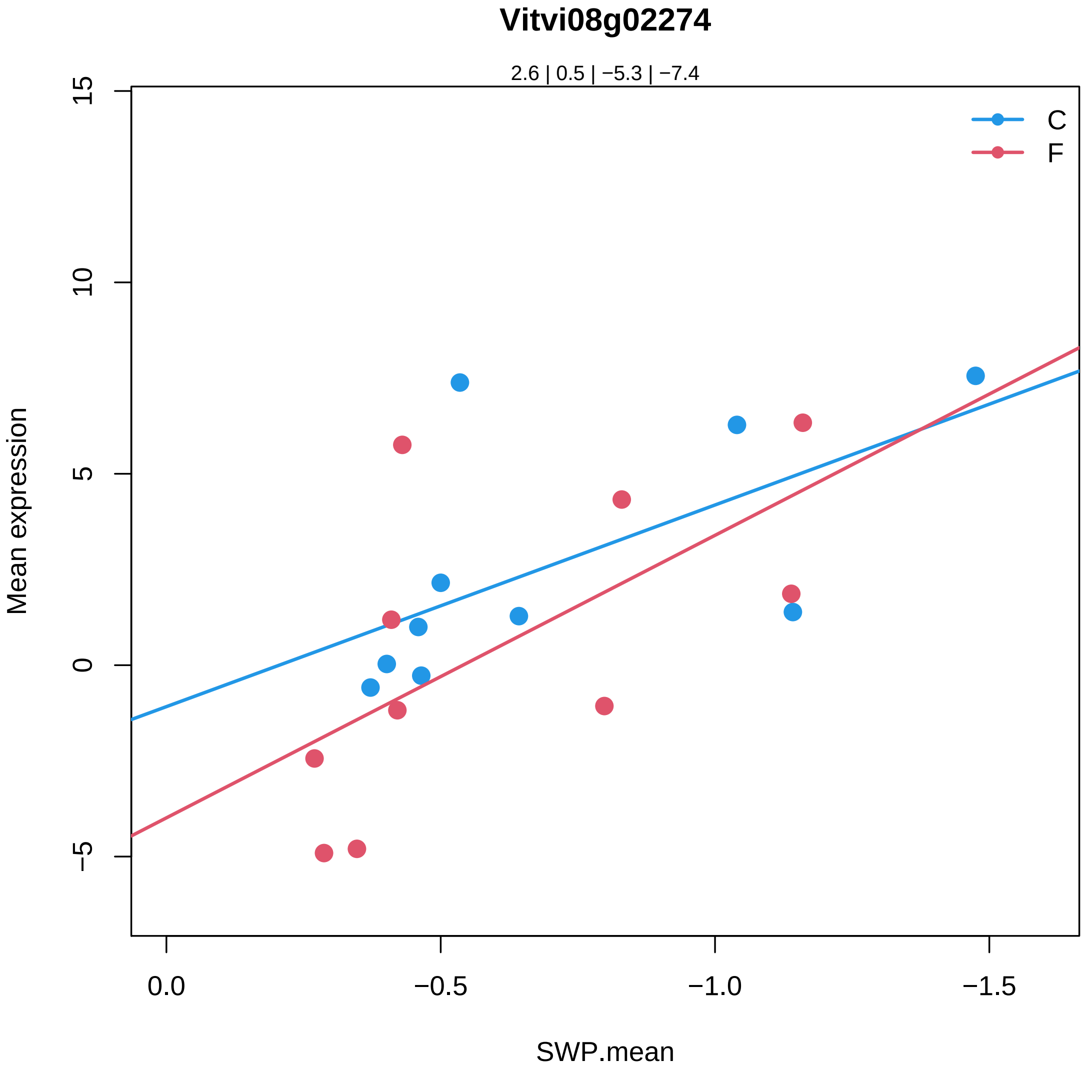
7.5.50 Vitvi08g02274: * type2 | type4

```
> 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        
```



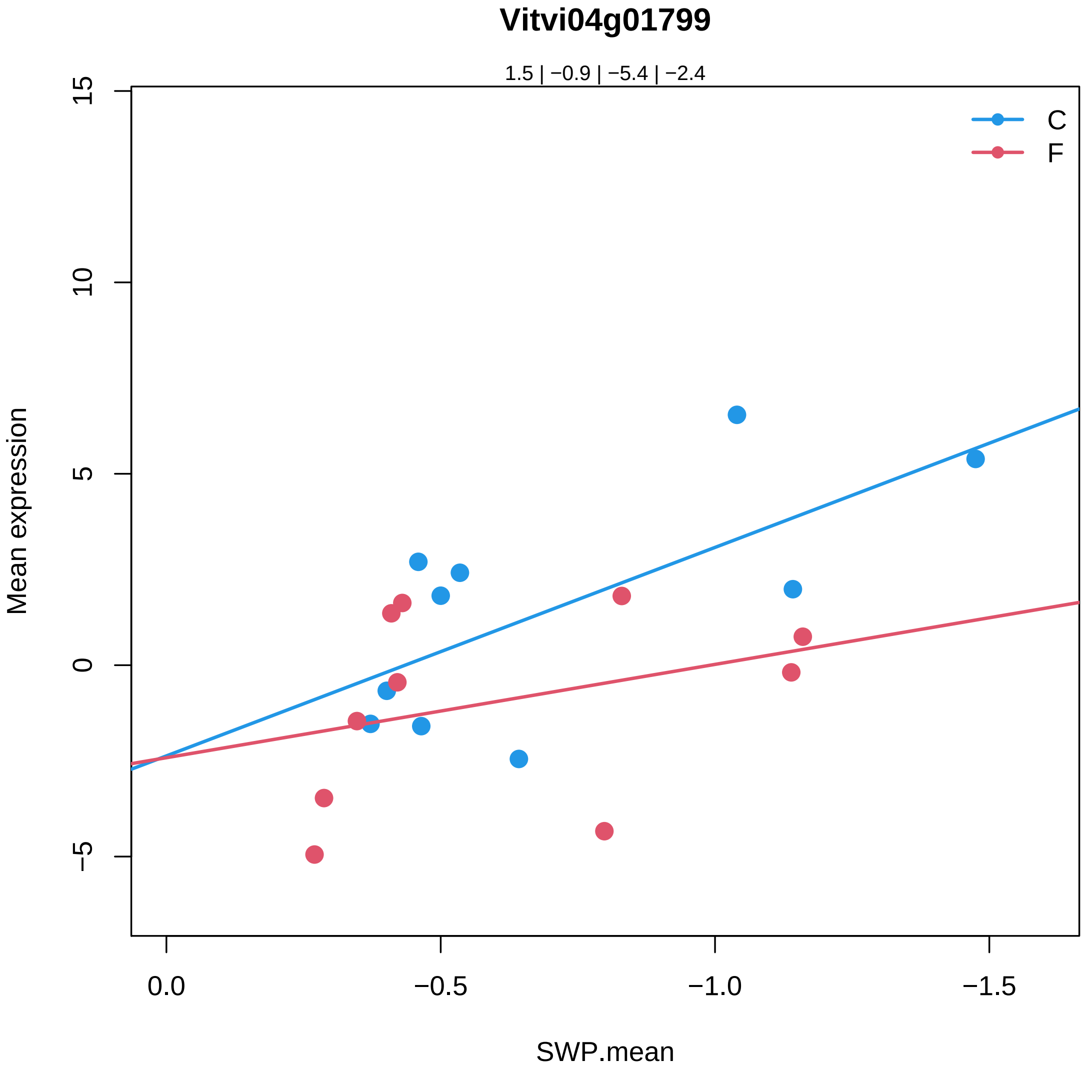
7.5.51 Vitvi04g01799: * type2 | type4

```
> 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
```



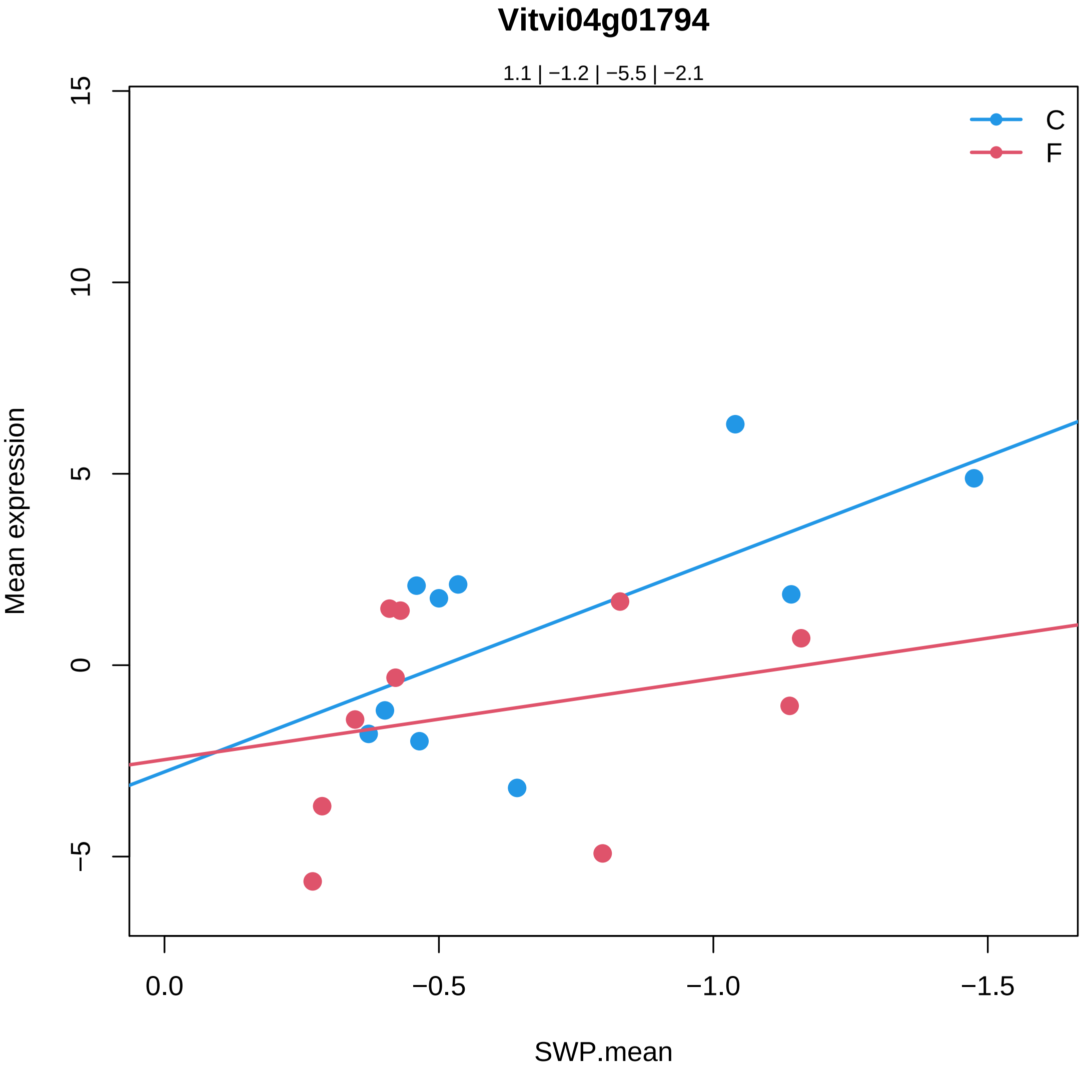
7.5.52 Vitvi04g01794: * type2 | type4

```
> 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
```



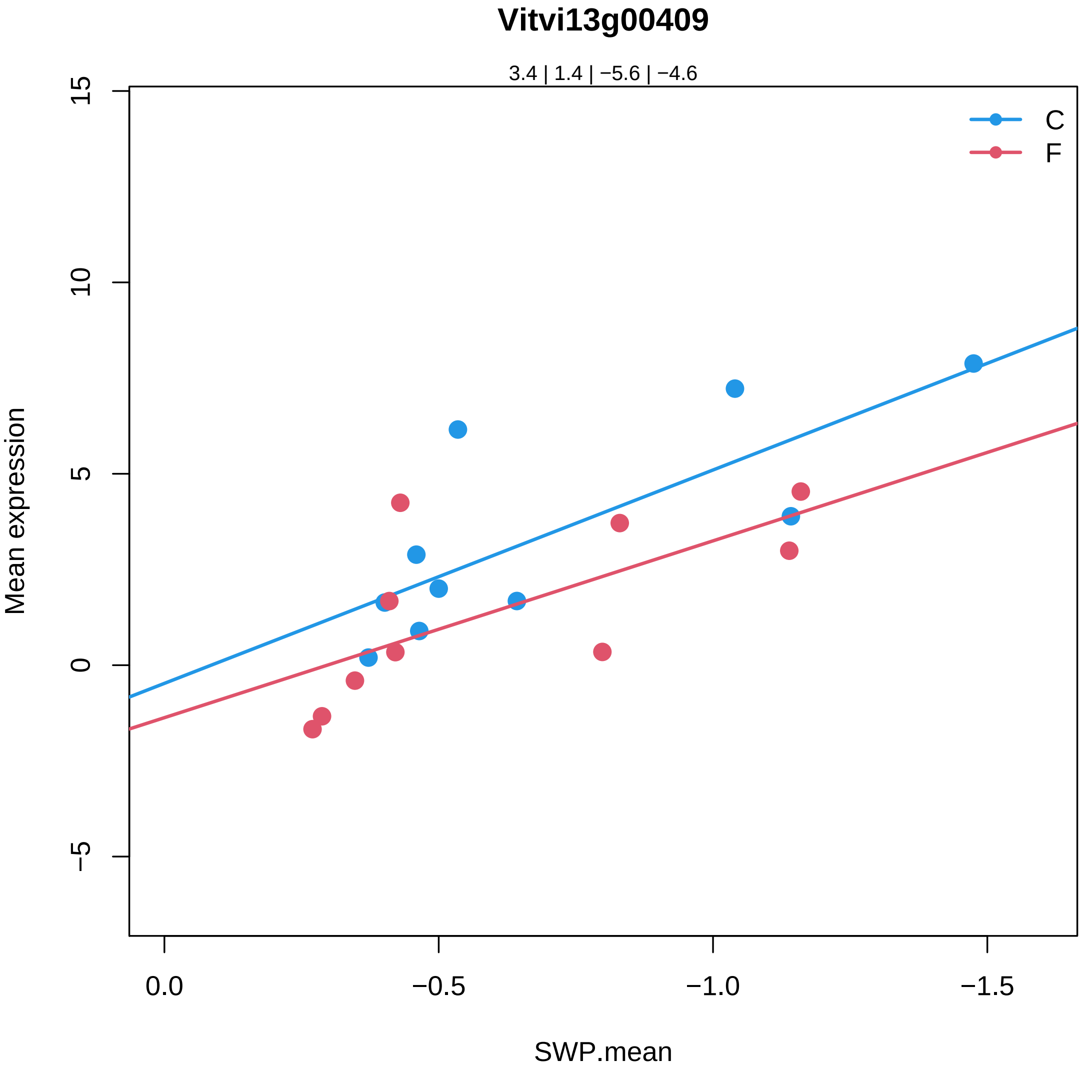
7.5.53 Vitvi13g00409: * type4

```
> 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
```



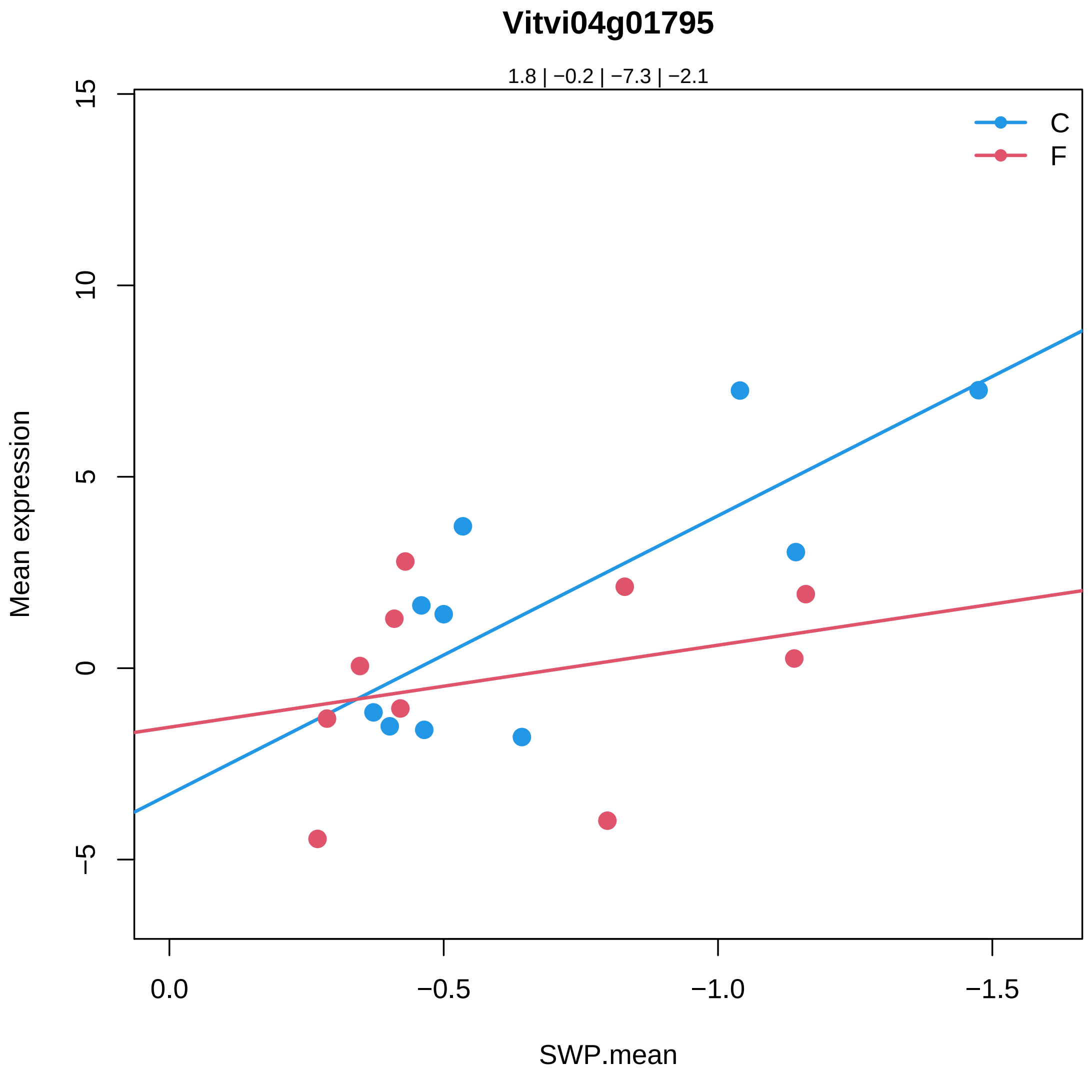
7.5.54 Vitvi04g01795: * type2 | type4

```
> 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

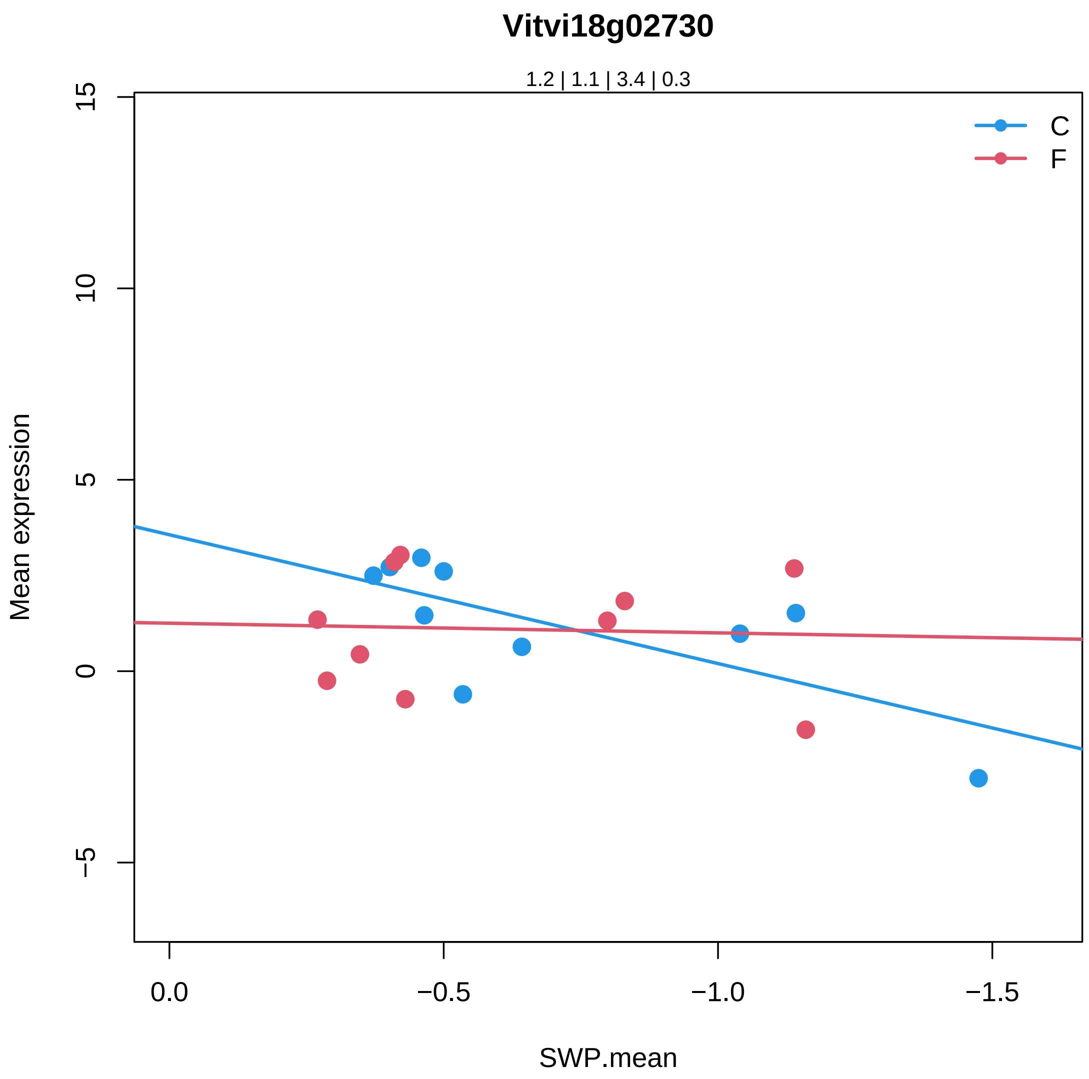
7.6.1 Vitvi18g02730: * type5

```
> 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
```



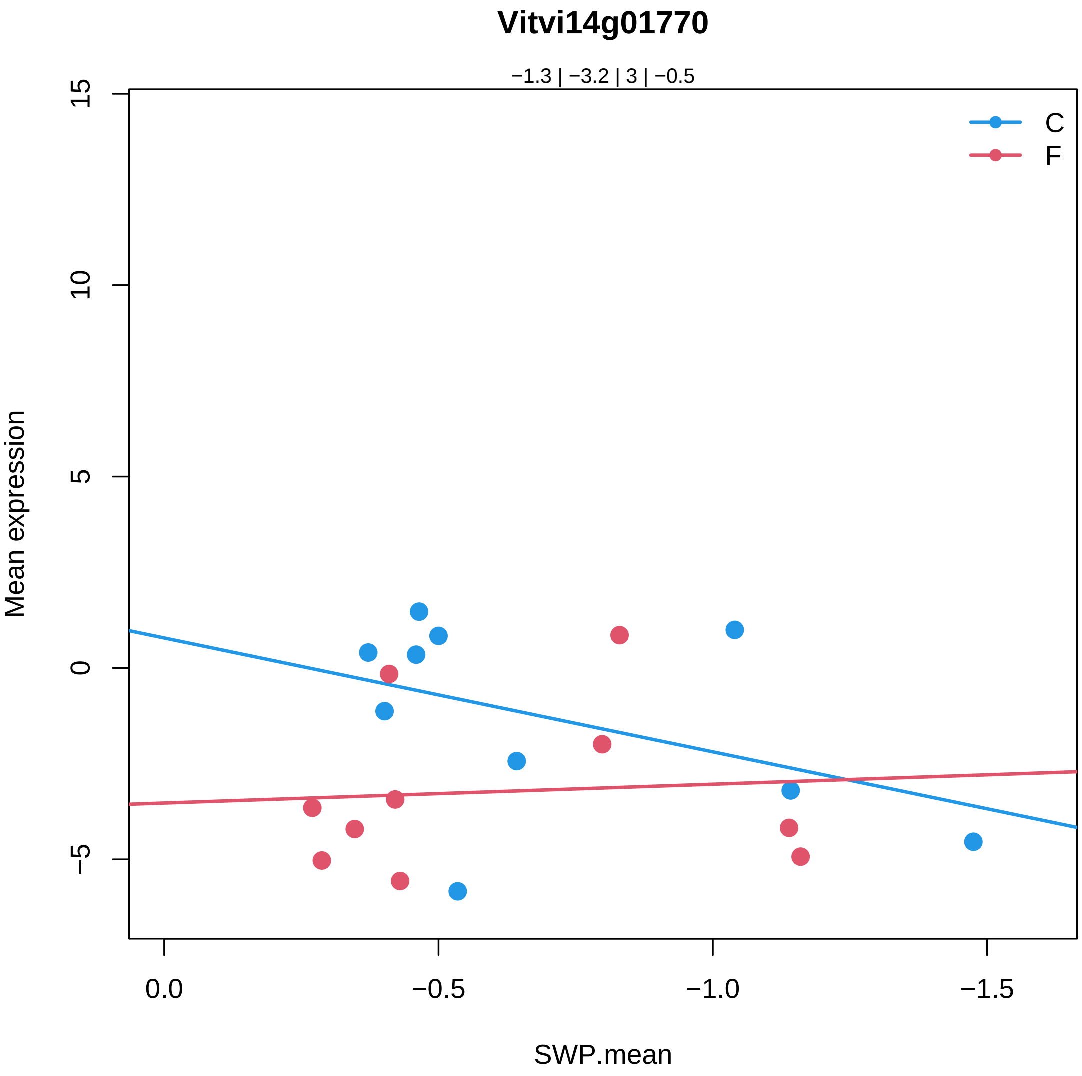
7.6.2 Vitvi14g01770: type5

```
> 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
```



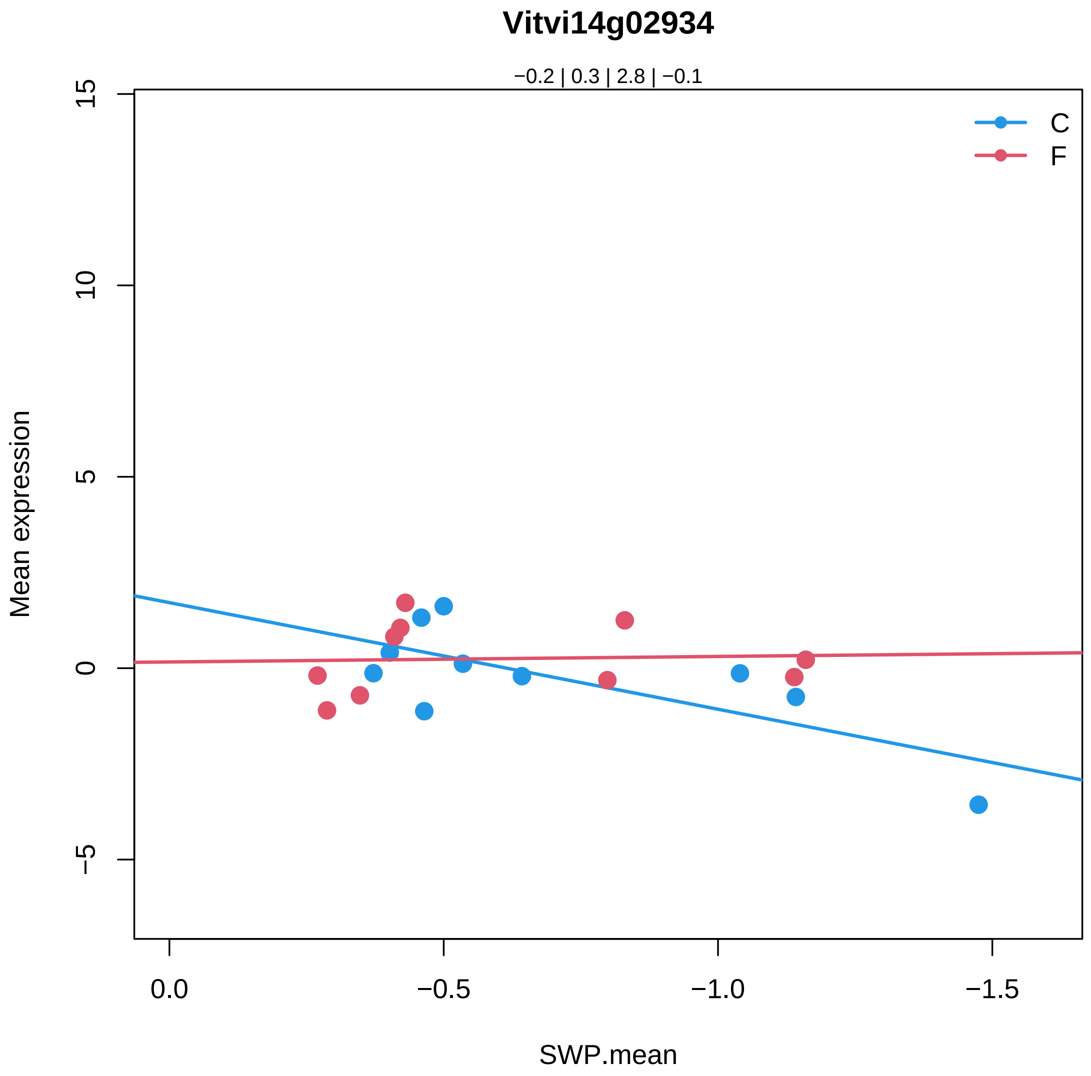
7.6.3 Vitvi14g02934: * type5

```
> 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
```



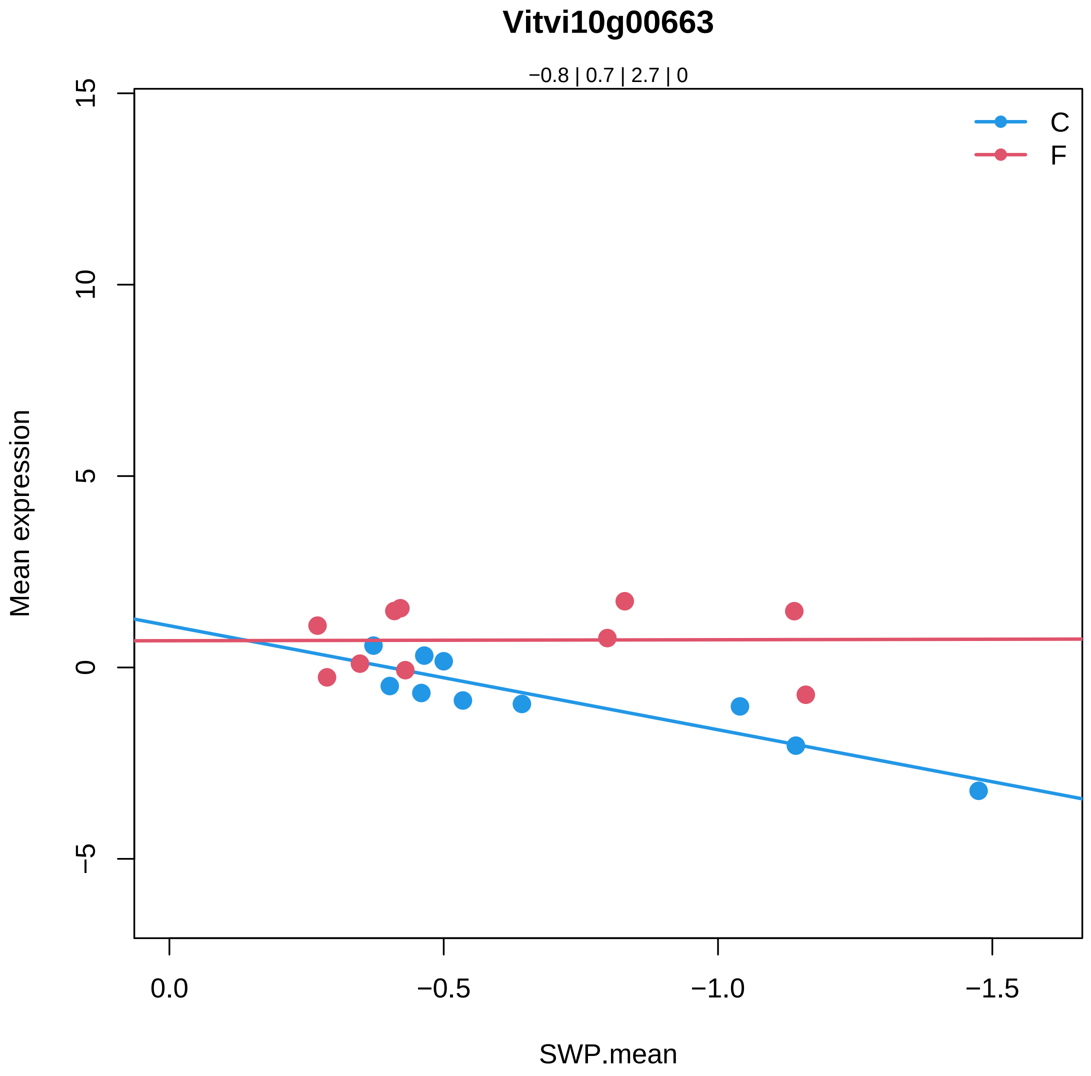
7.6.4 Vitvi10g00663: * type5

```
> 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

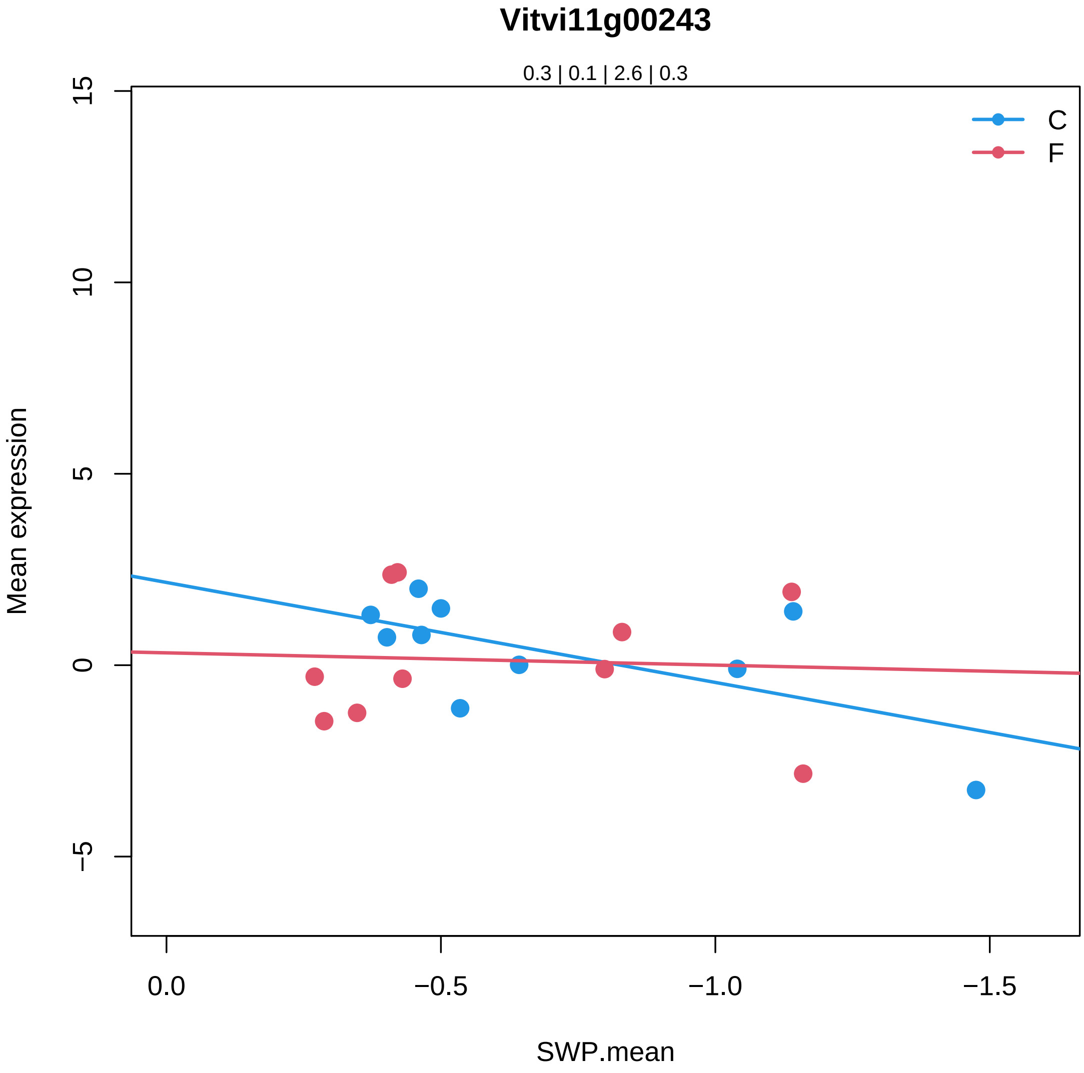
7.6.5 Vitvi11g00243: * type5

```
> 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
```



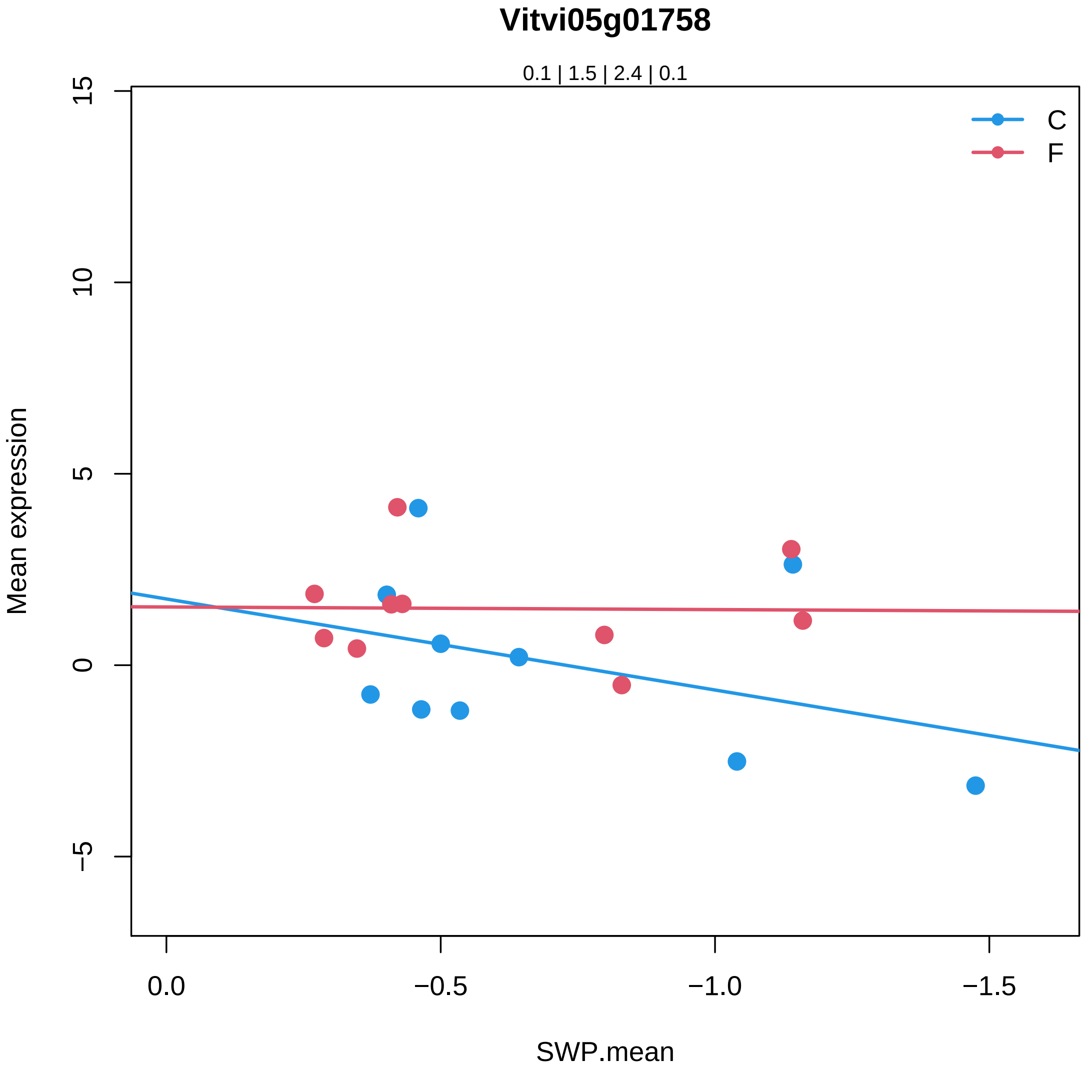
7.6.6 Vitvi05g01758: type5

```
> 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
```



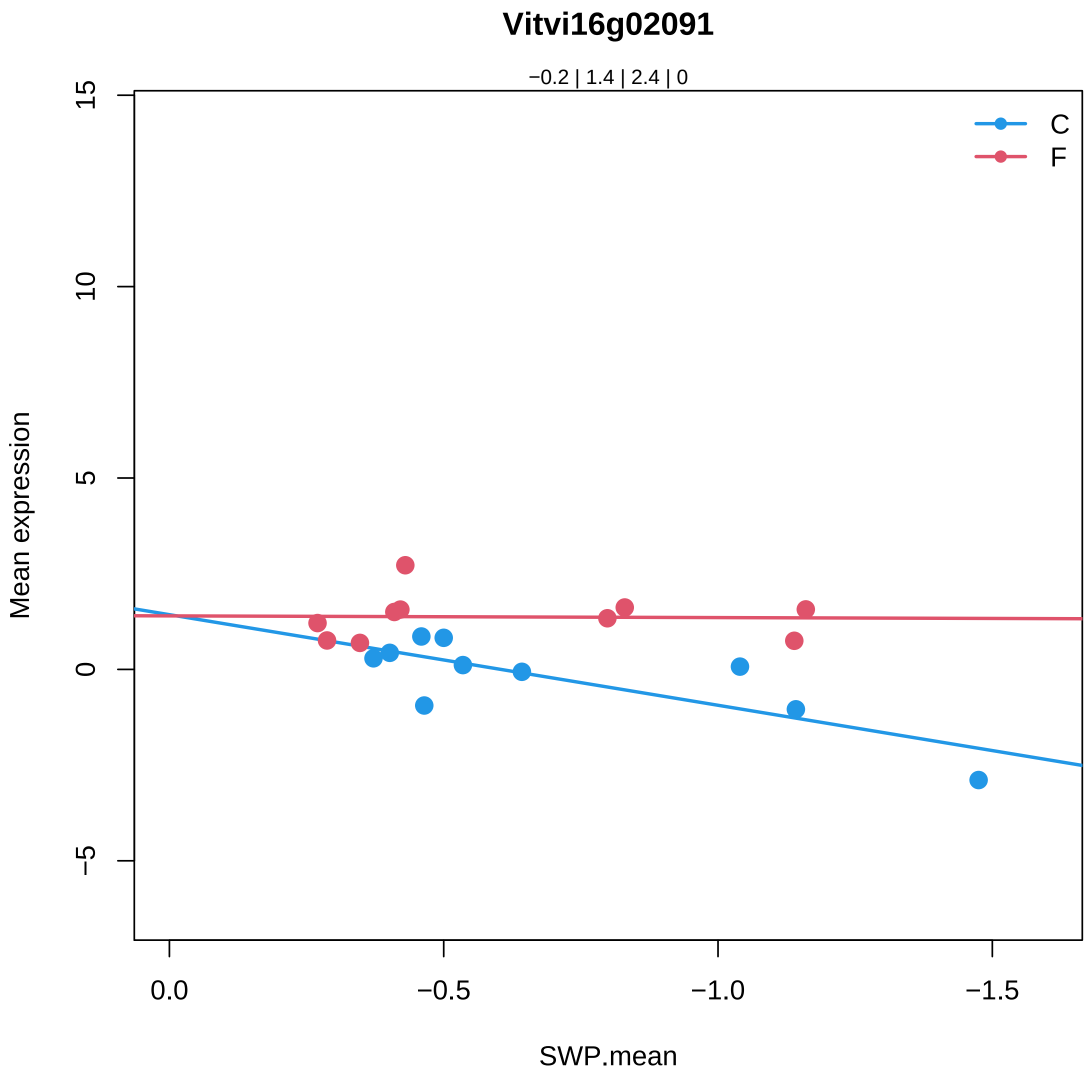
7.6.7 Vitvi16g02091: * type5

```
> 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        
```



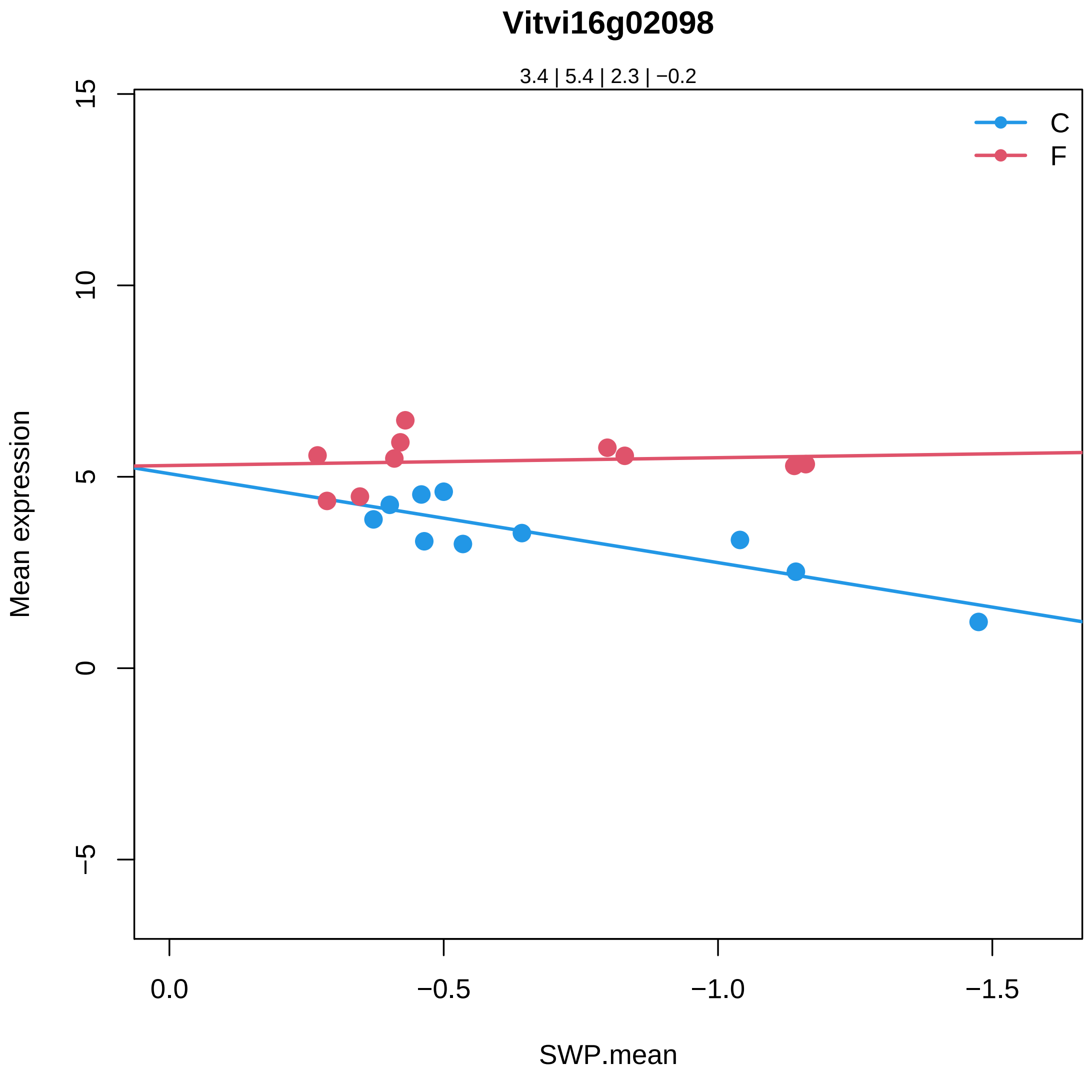
7.6.8 Vitvi16g02098: * type5

```
> 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
```



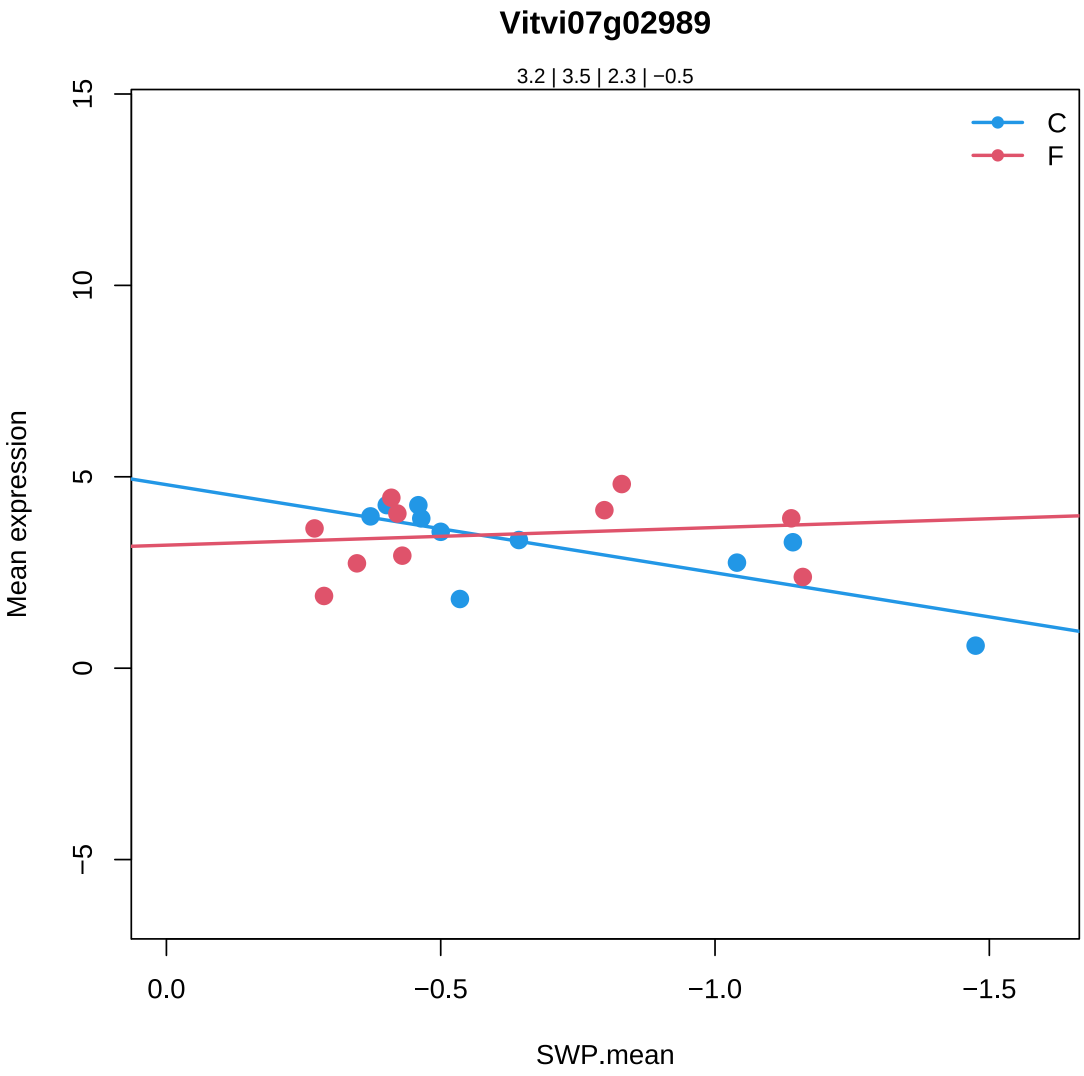
7.6.9 Vitvi07g02989: * type5

```
> 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
```



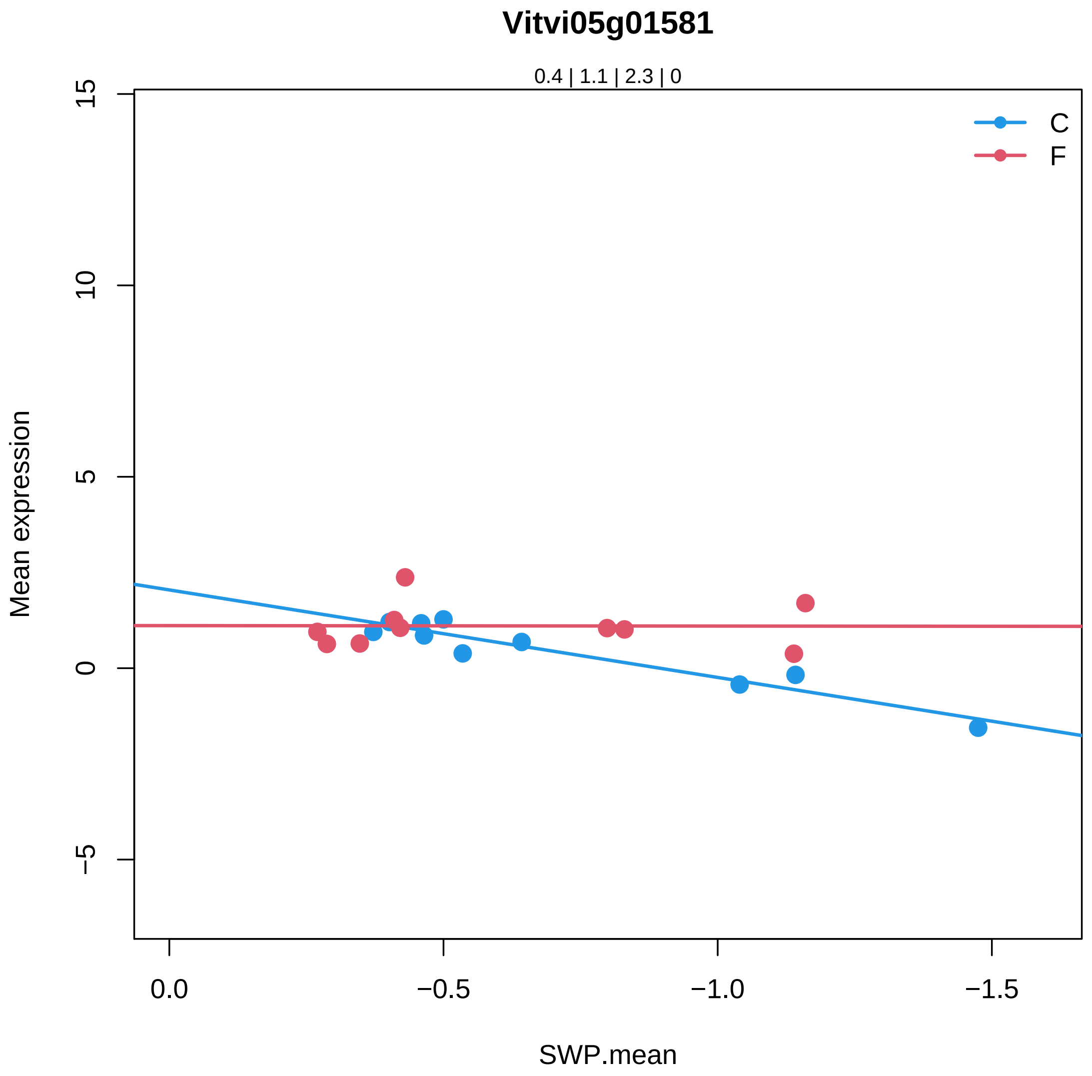
7.6.10 Vitvi05g01581: * type5

```
> 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
```



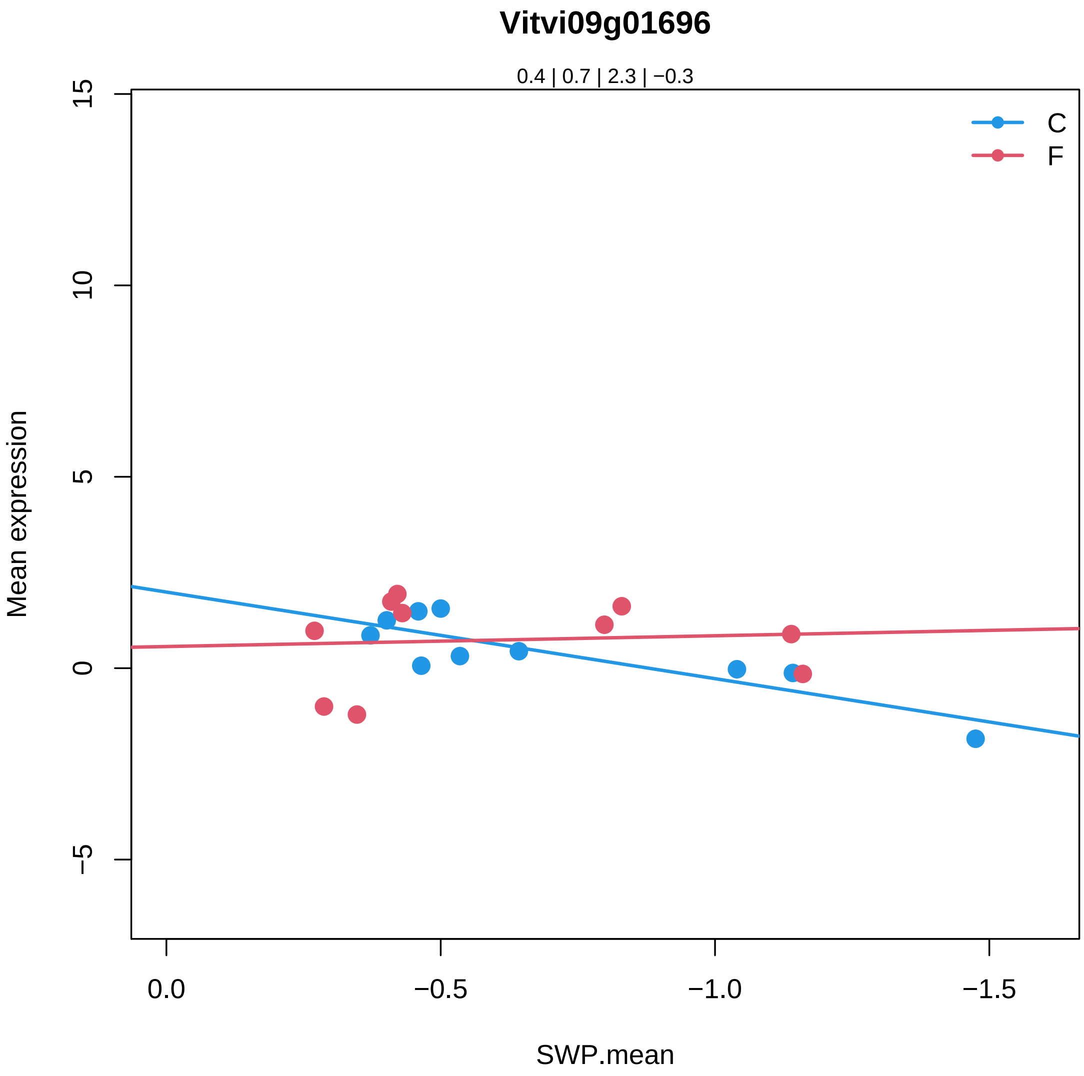
7.6.11 Vitvi09g01696: * type5

```
> 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
```



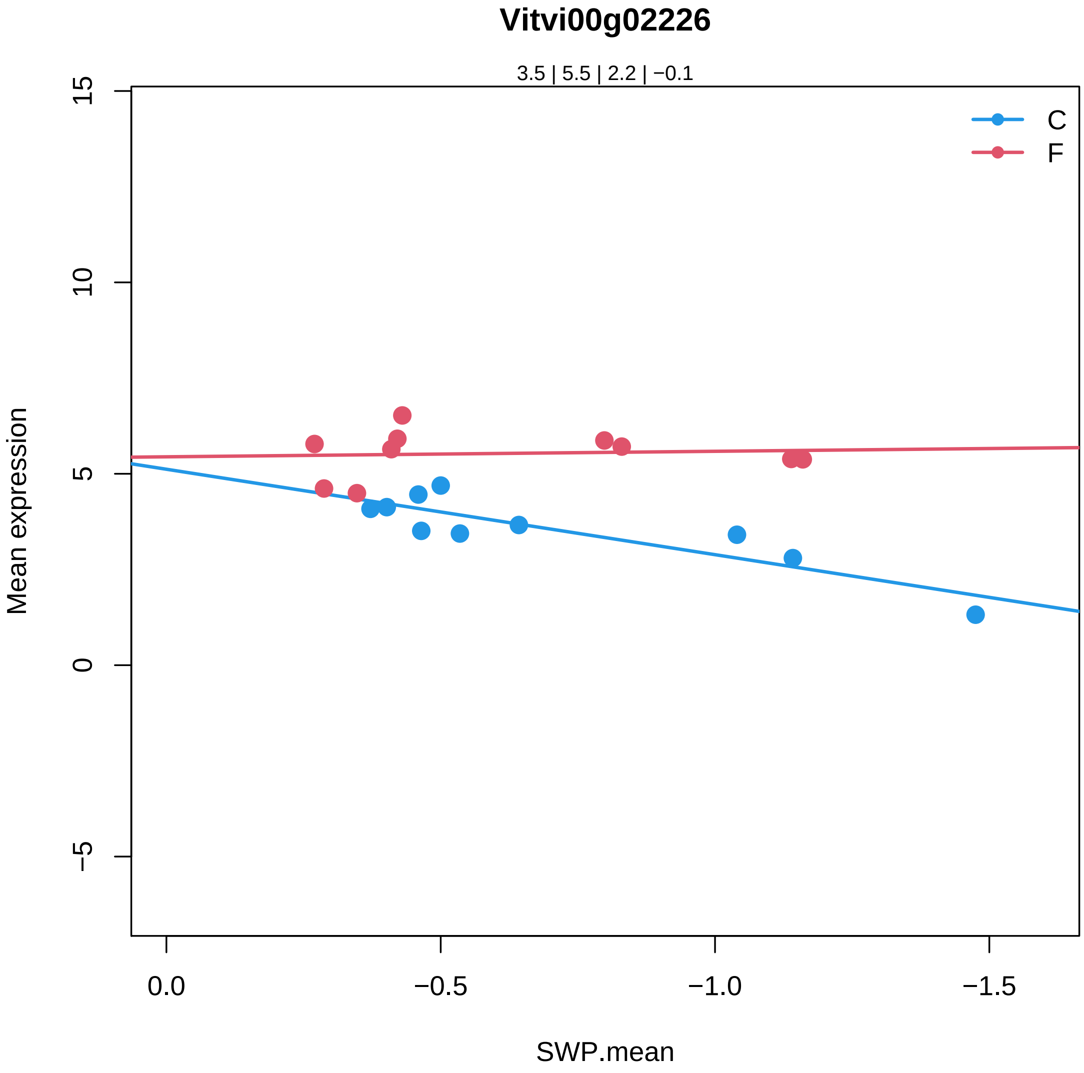
7.6.12 Vitvi00g02226: * type5

```
> 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
```



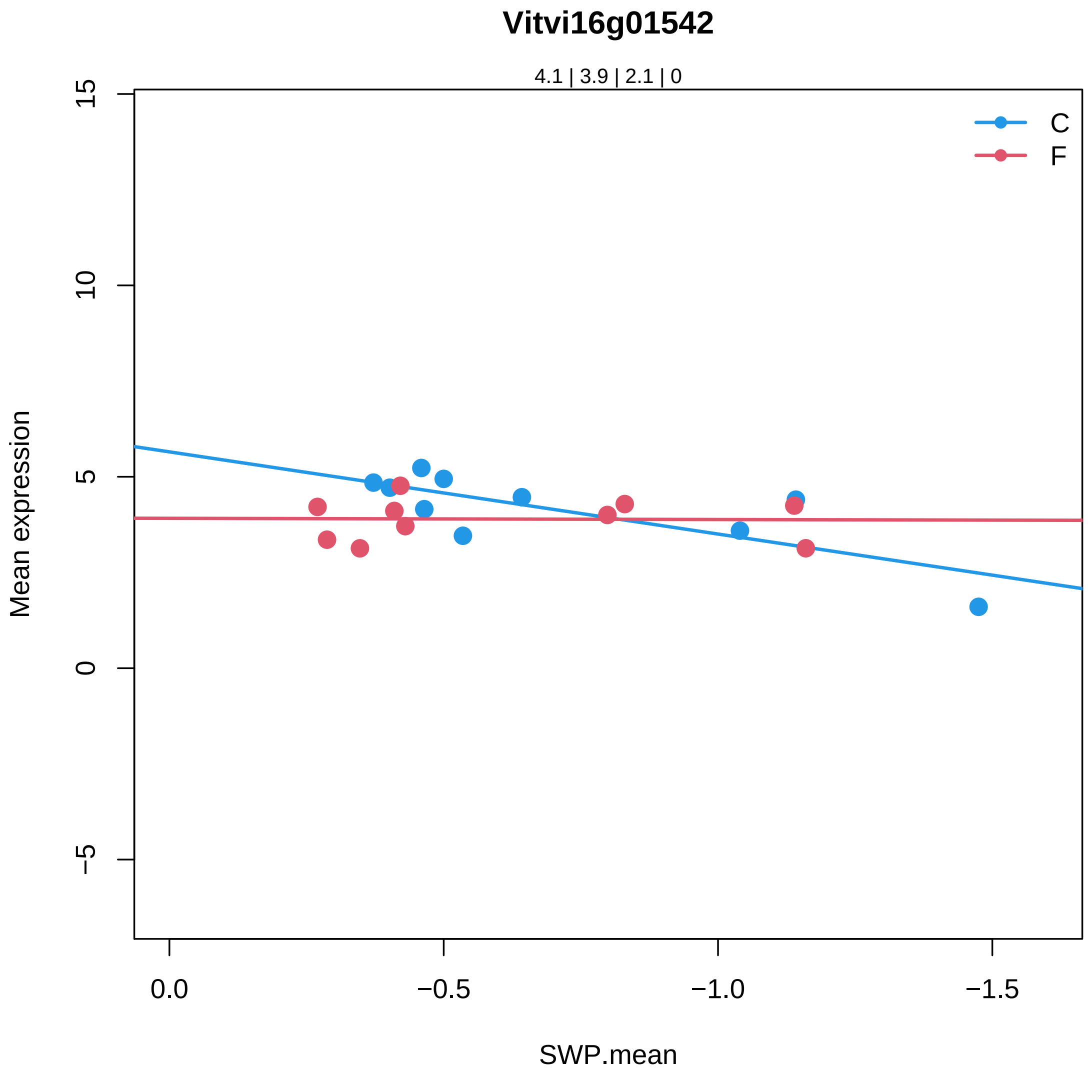
7.6.13 Vitvi16g01542: * type5

```
> 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
```



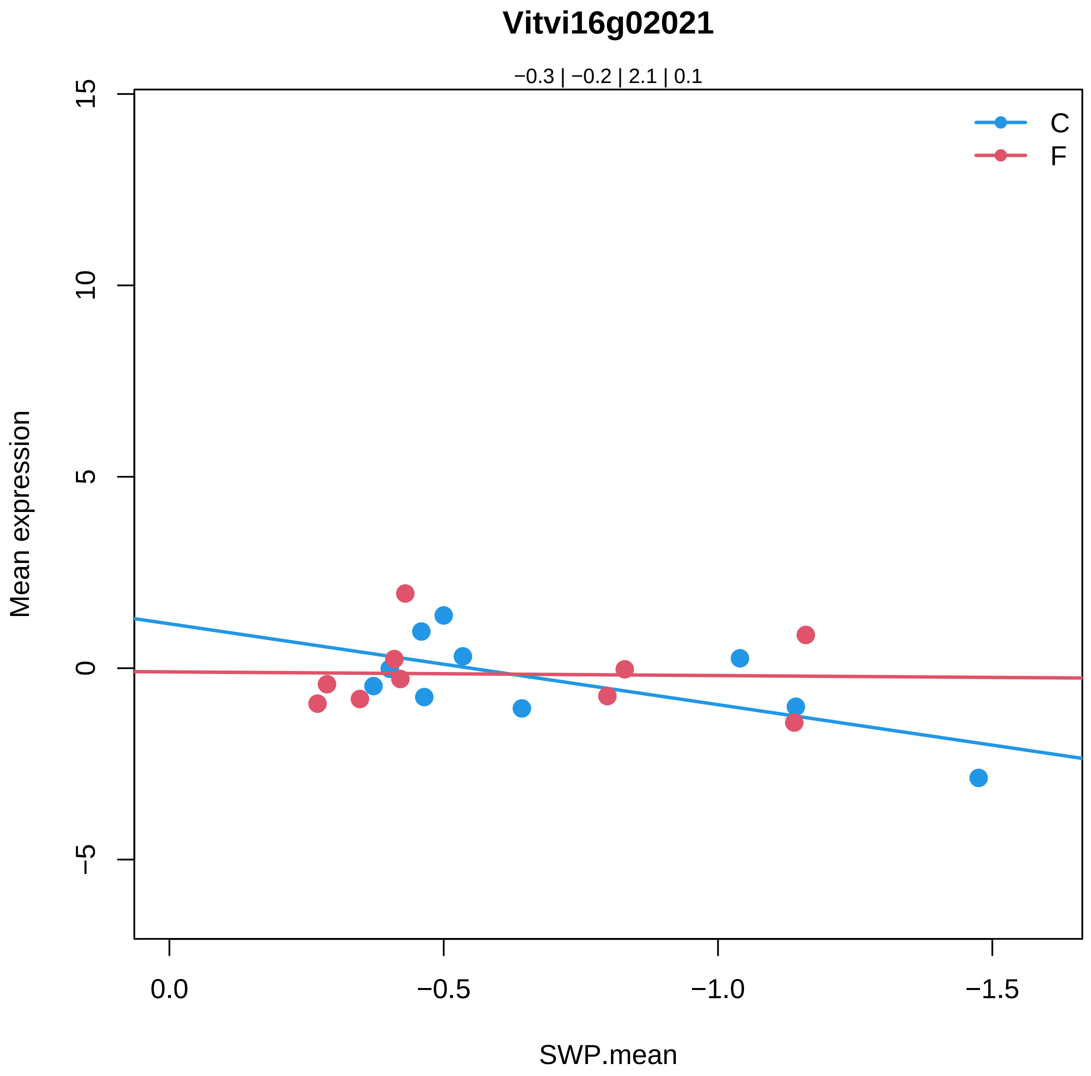
7.6.14 Vitvi16g02021: * type5

```
> 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
```



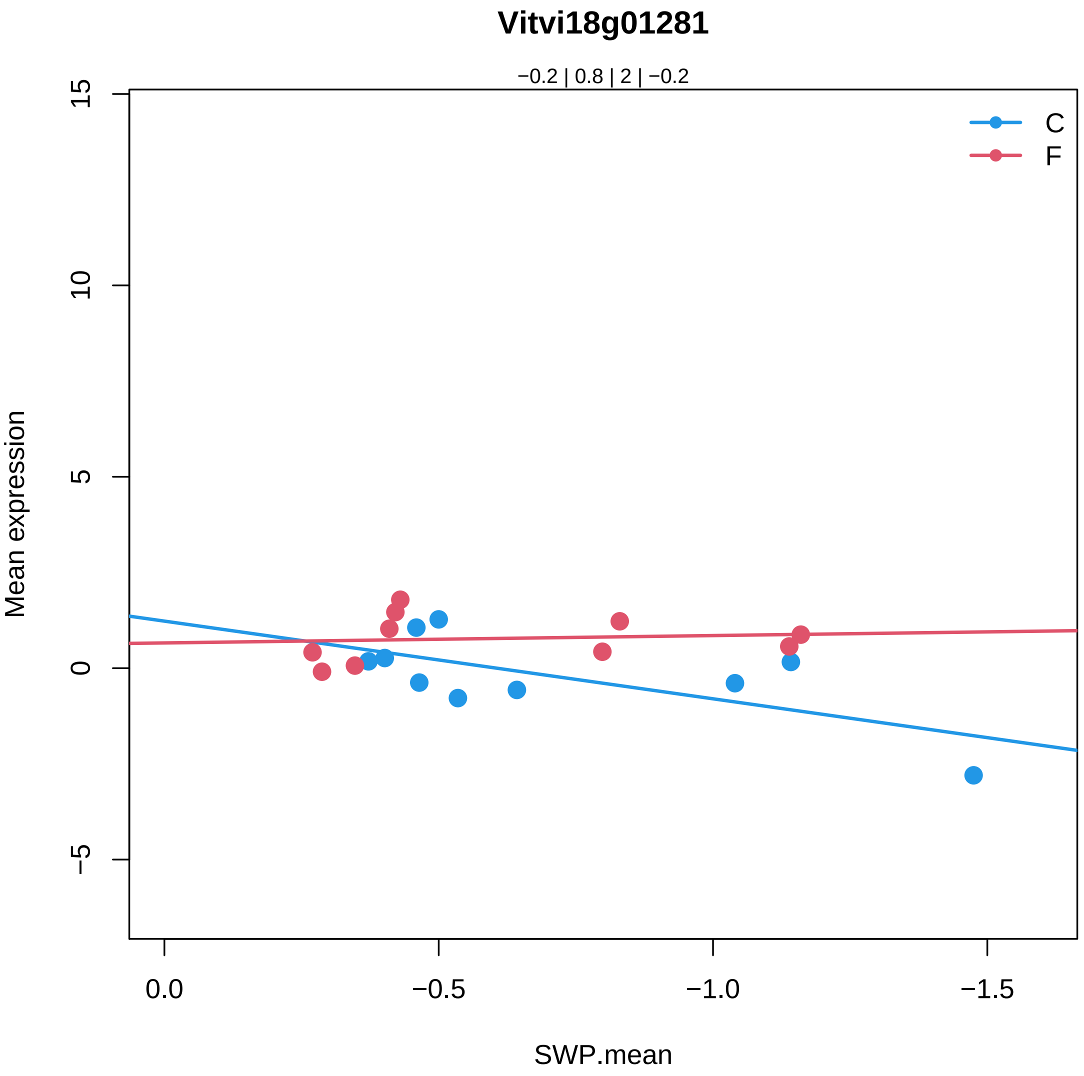
7.6.15 Vitvi18g01281: * type5

```
> 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
```



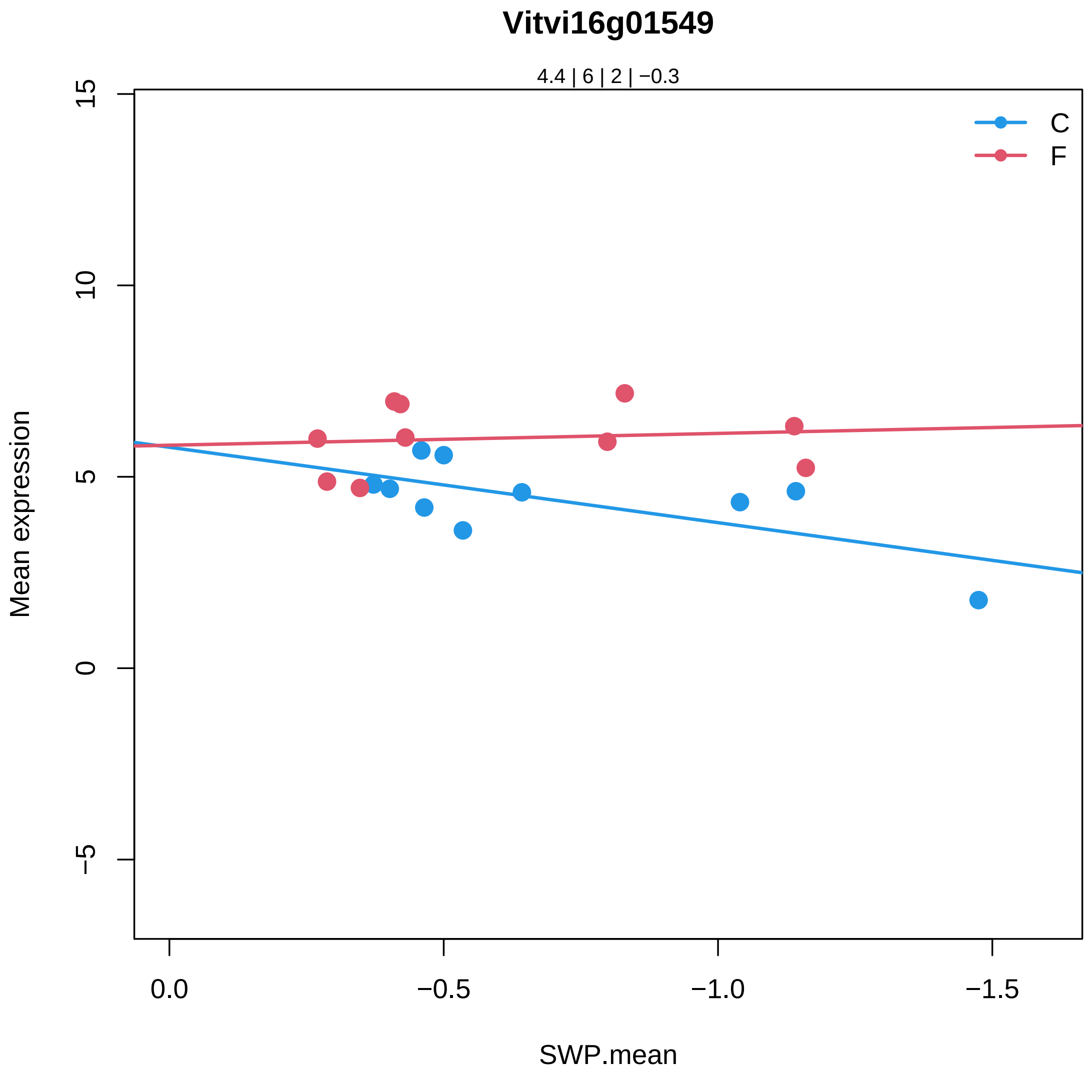
7.6.16 Vitvi16g01549: * type5

```
> 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        
```



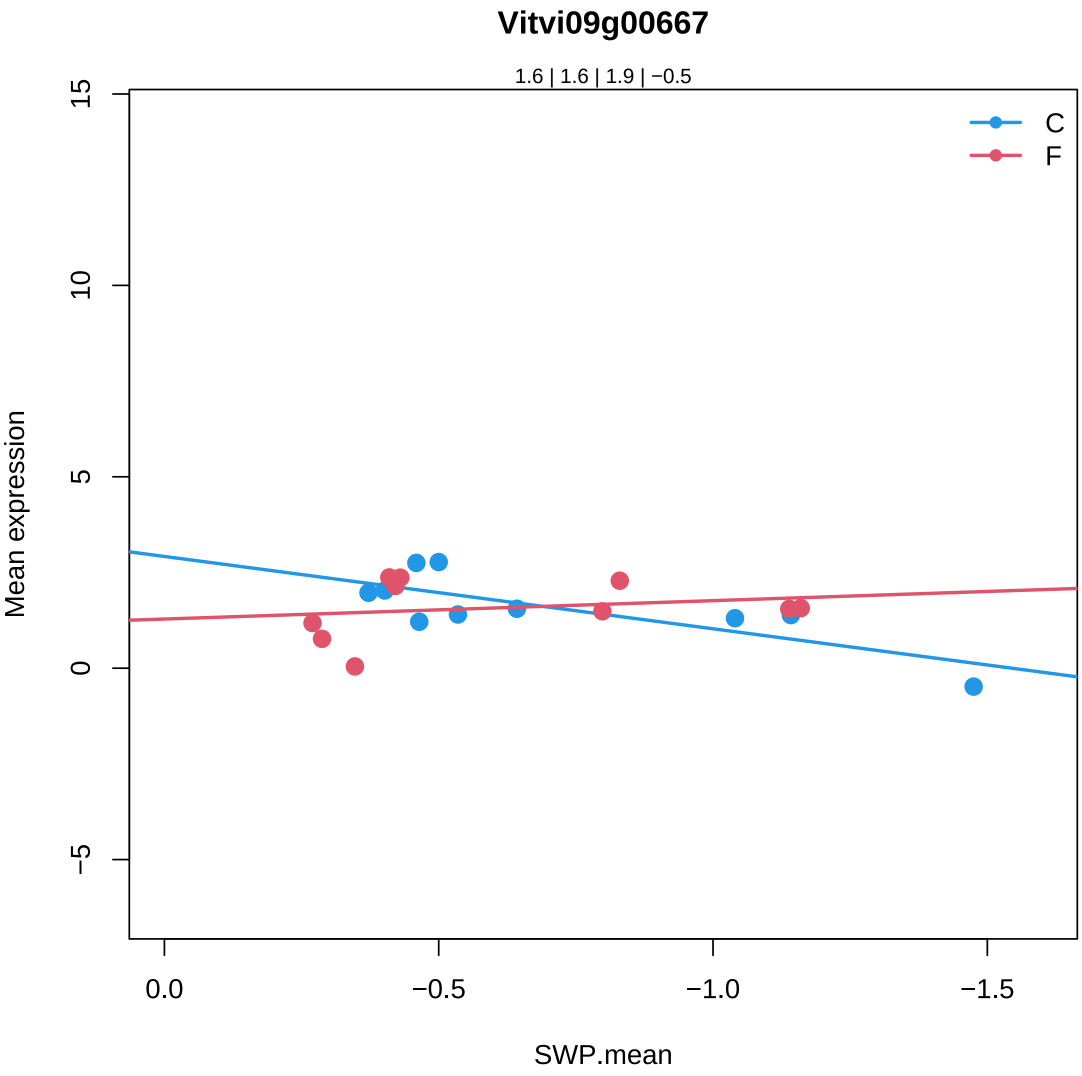
7.6.17 Vitvi09g00667: * type5

```
> 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        
```



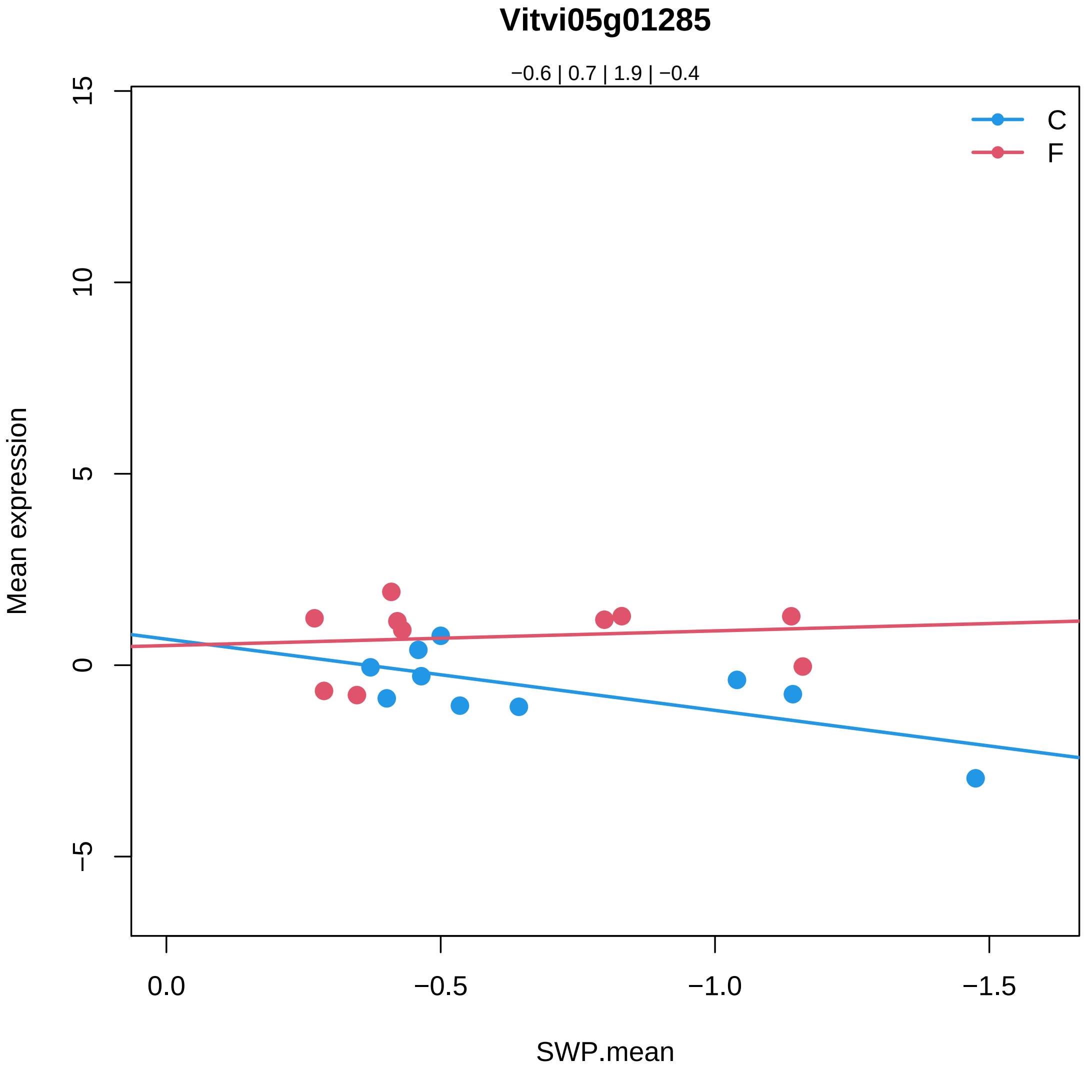
7.6.18 Vitvi05g01285: * type5

```
> 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
```



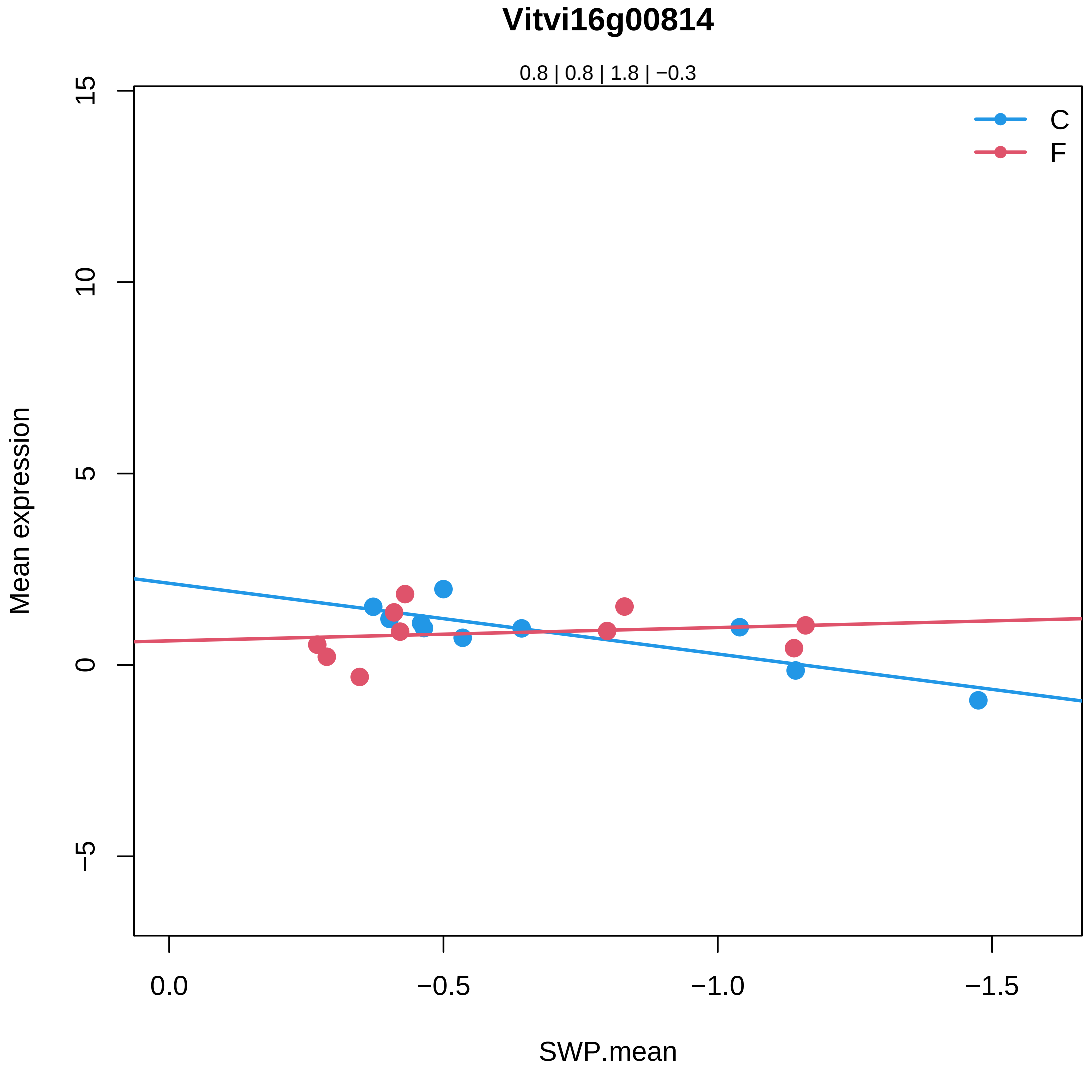
7.6.19 Vitvi16g00814: * type5

```
> 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
```



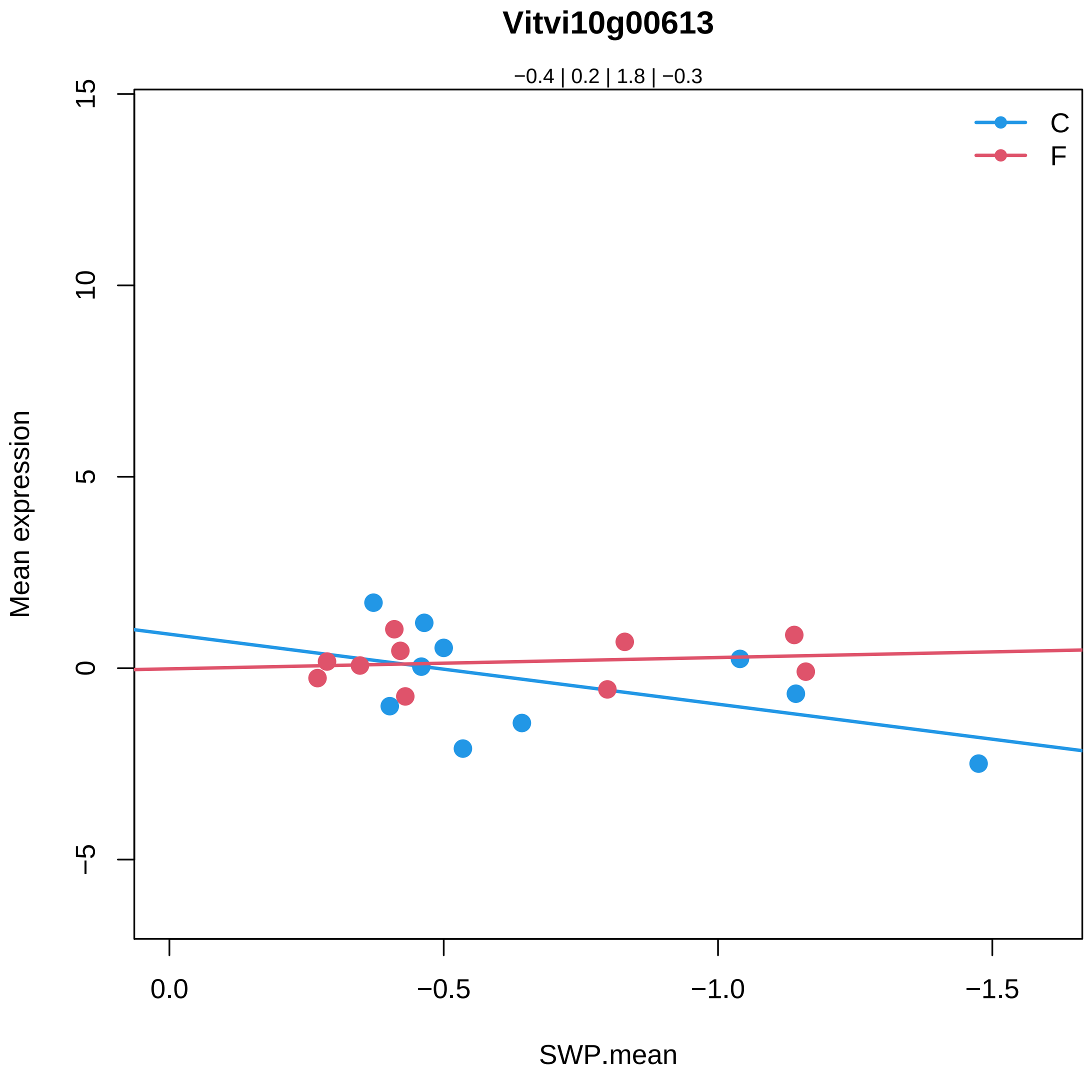
7.6.20 Vitvi10g00613: * type5

```
> 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        
```



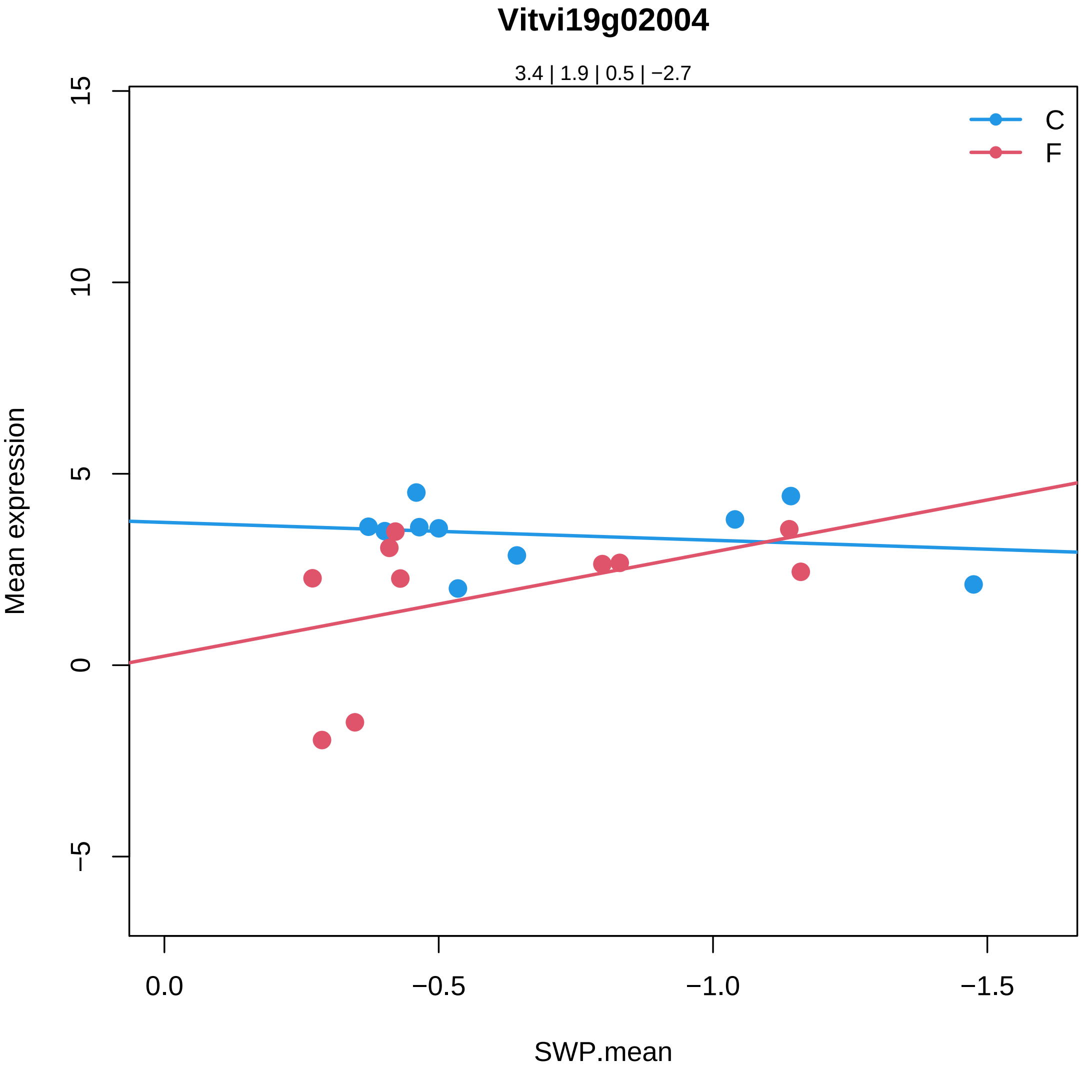
7.6.21 Vitvi19g02004: type5

```
> 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
```



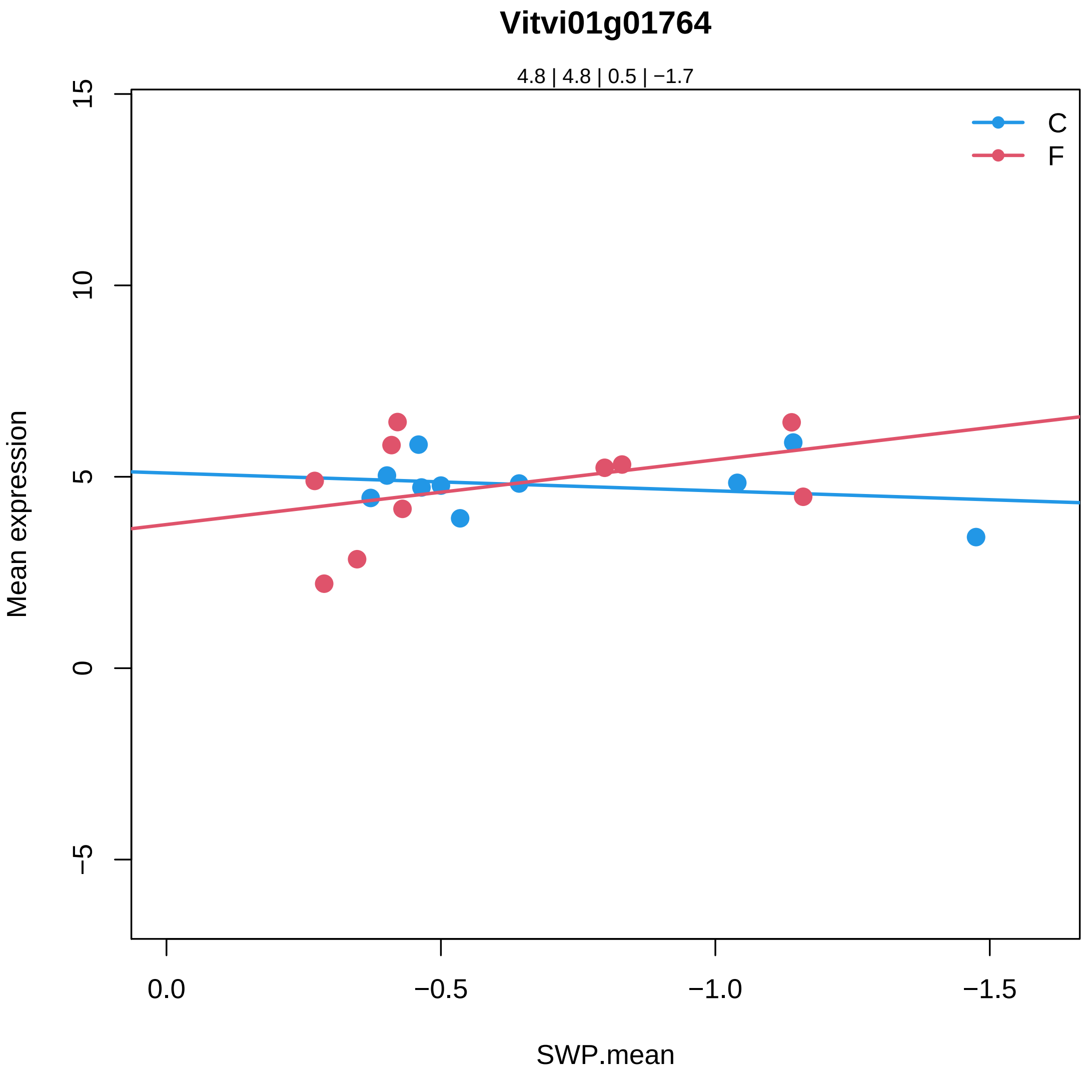
7.6.22 Vitvi01g01764: type5

```
> 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
```



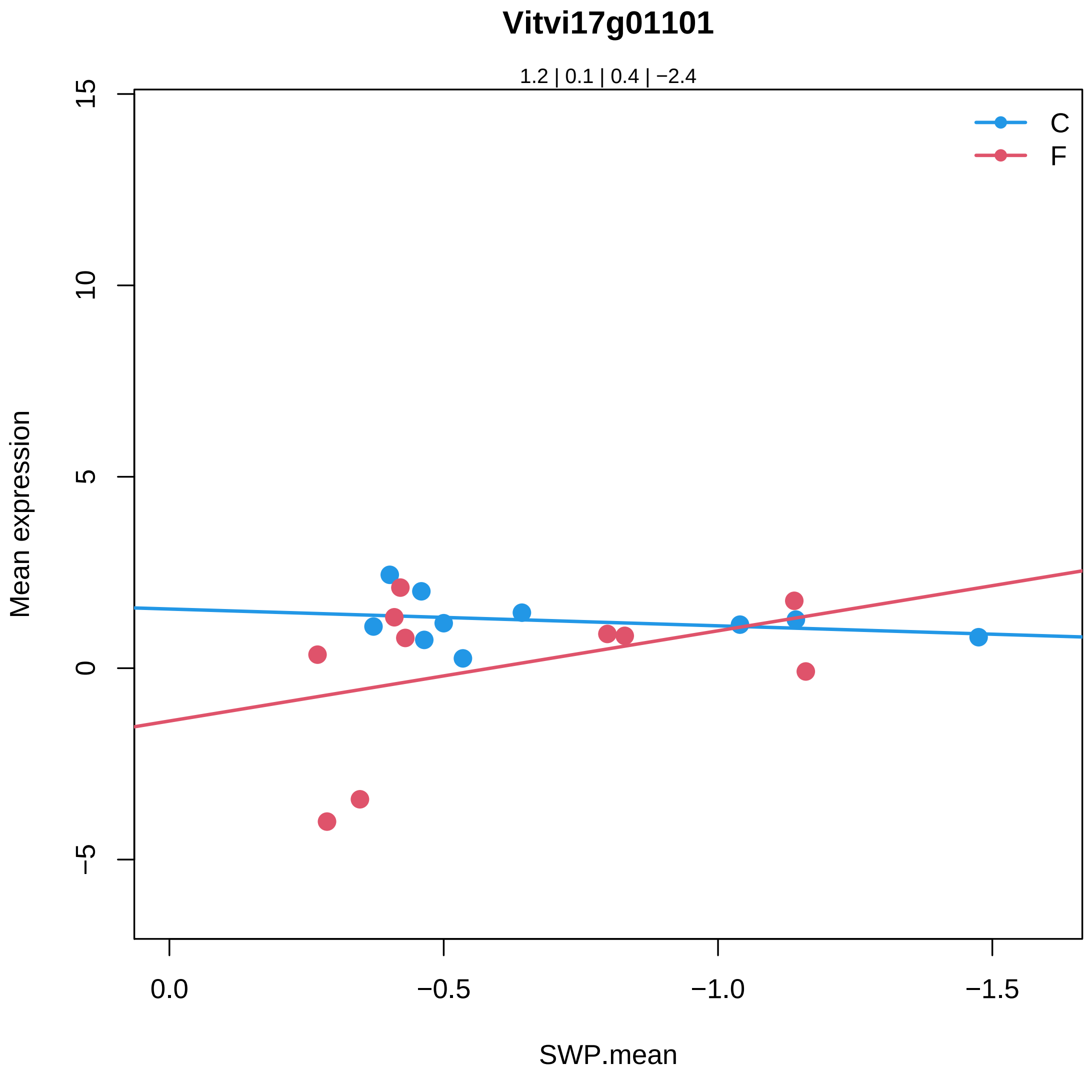
7.6.23 Vitvi17g01101: type5

```
> 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
```



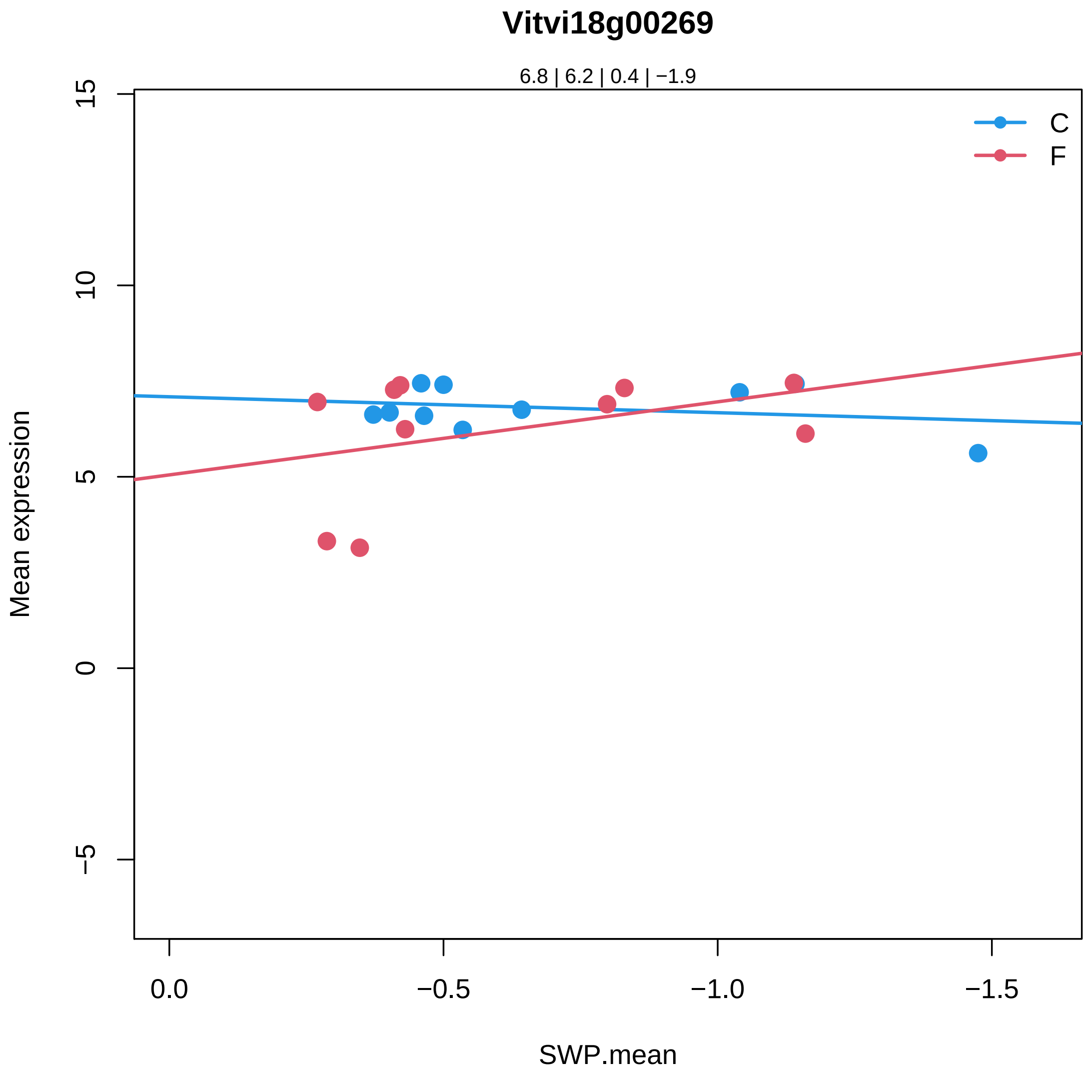
7.6.24 Vitvi18g00269: type5

```
> 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
```



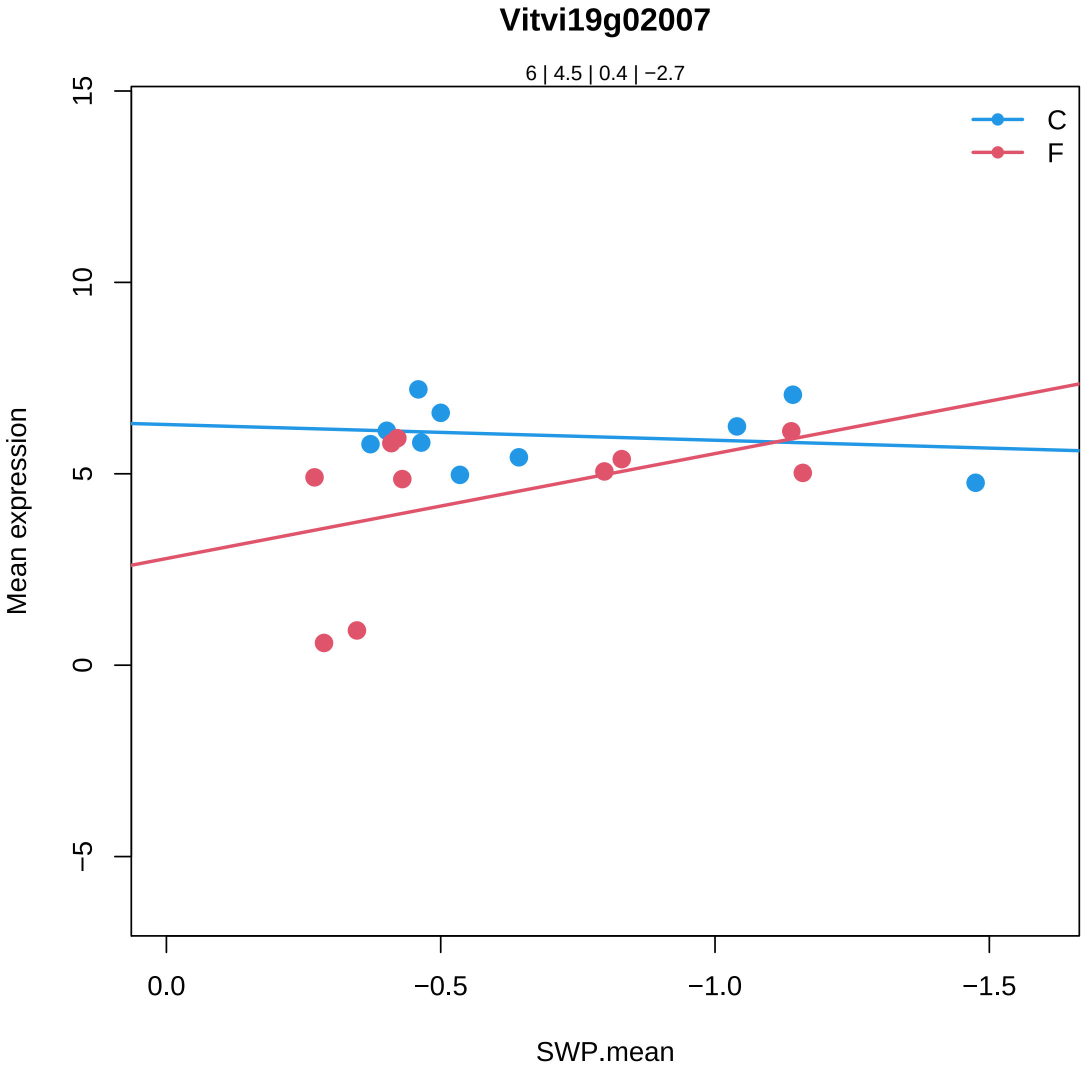
7.6.25 Vitvi19g02007: type5

```
> 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
```



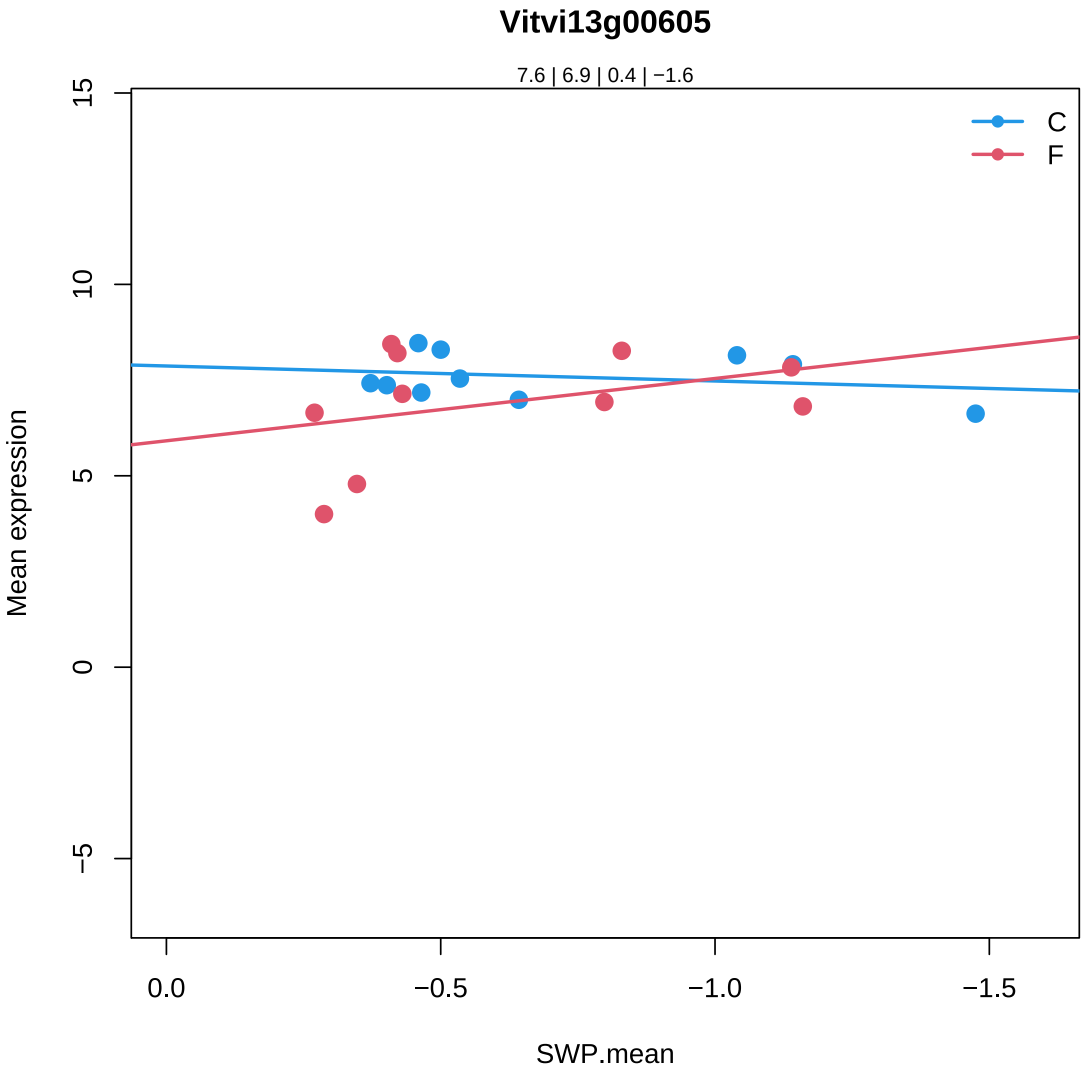
7.6.26 Vitvi13g00605: type5

```
> 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
```



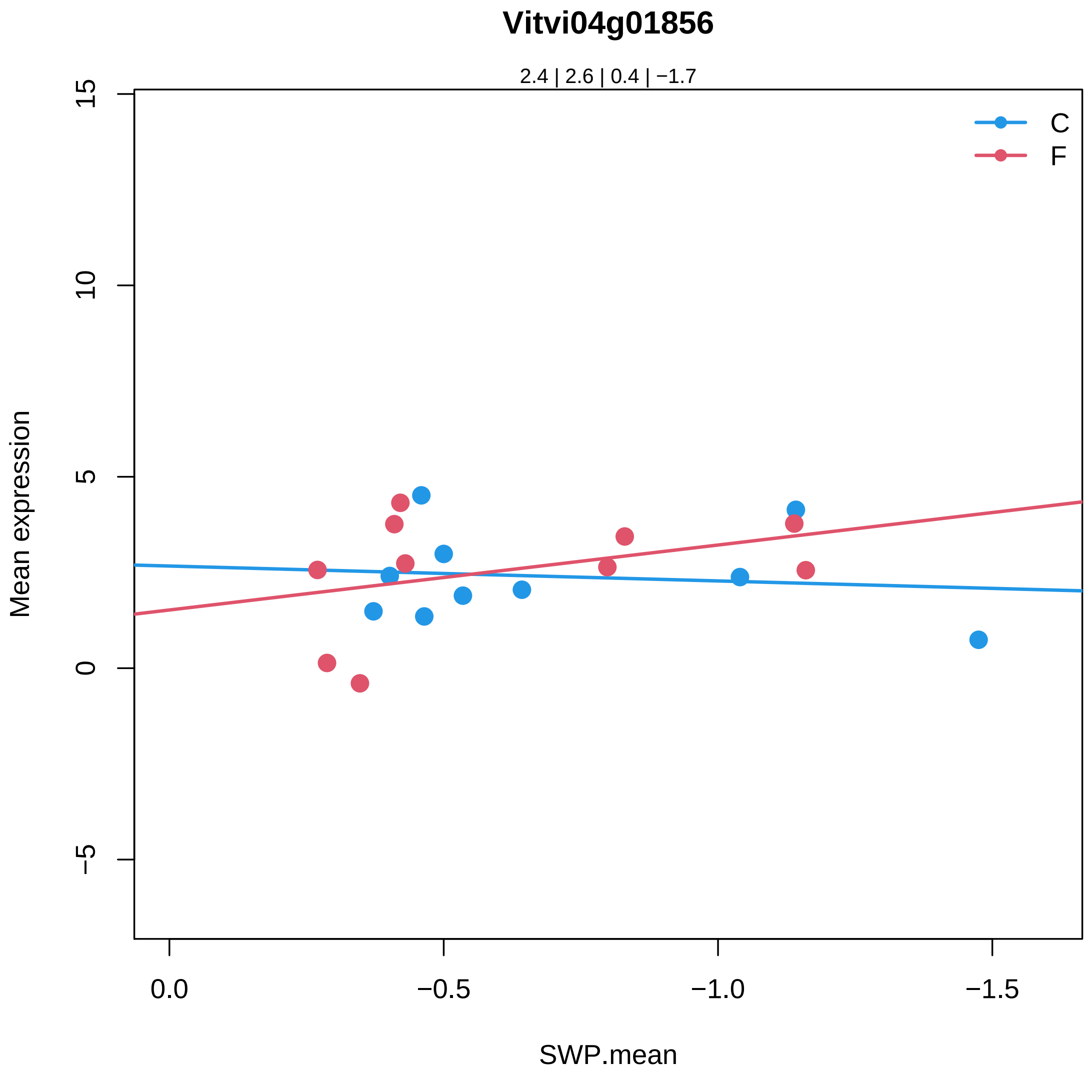
7.6.27 Vitvi04g01856: type5

```
> 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
```



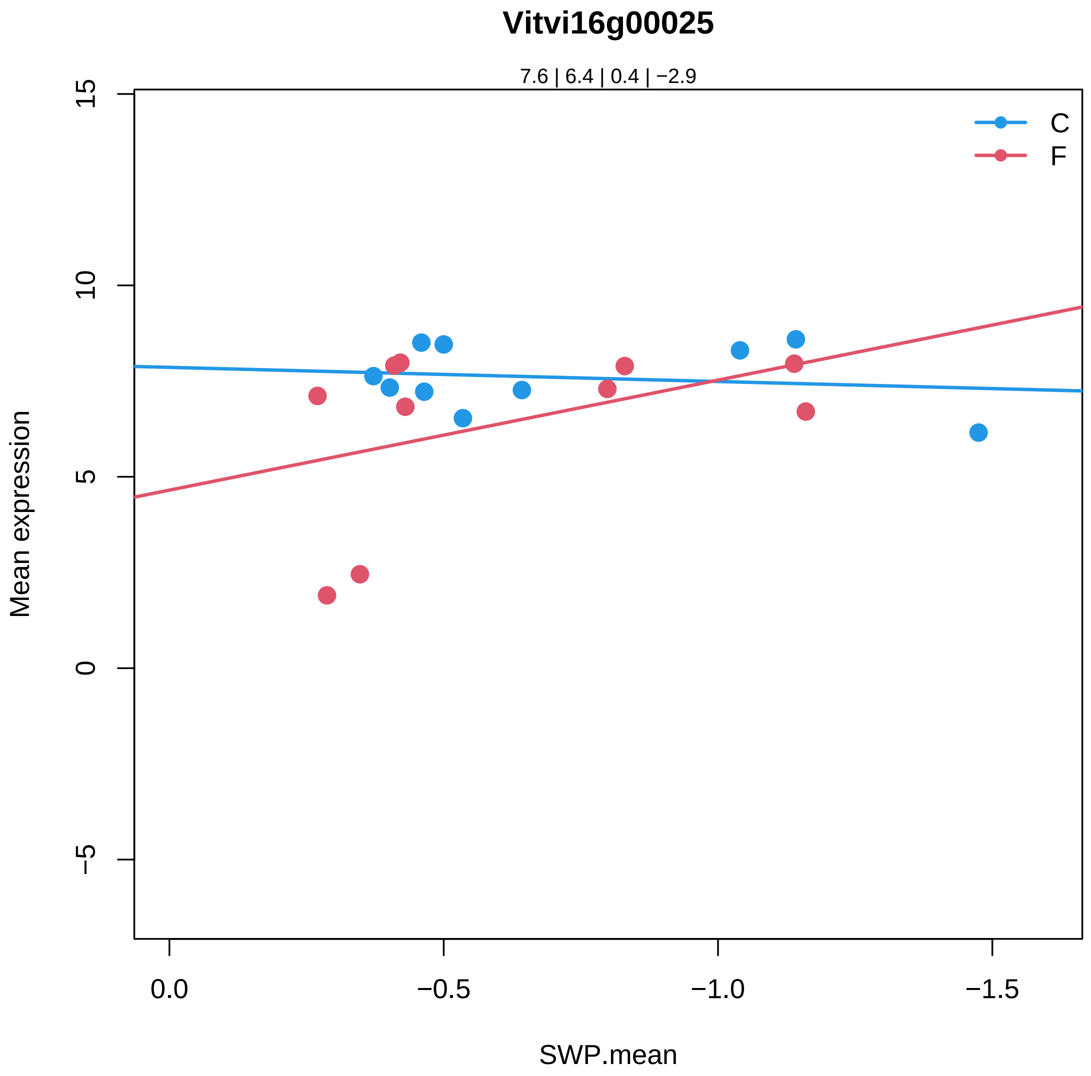
7.6.28 Vitvi16g00025: type5

```
> 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
```



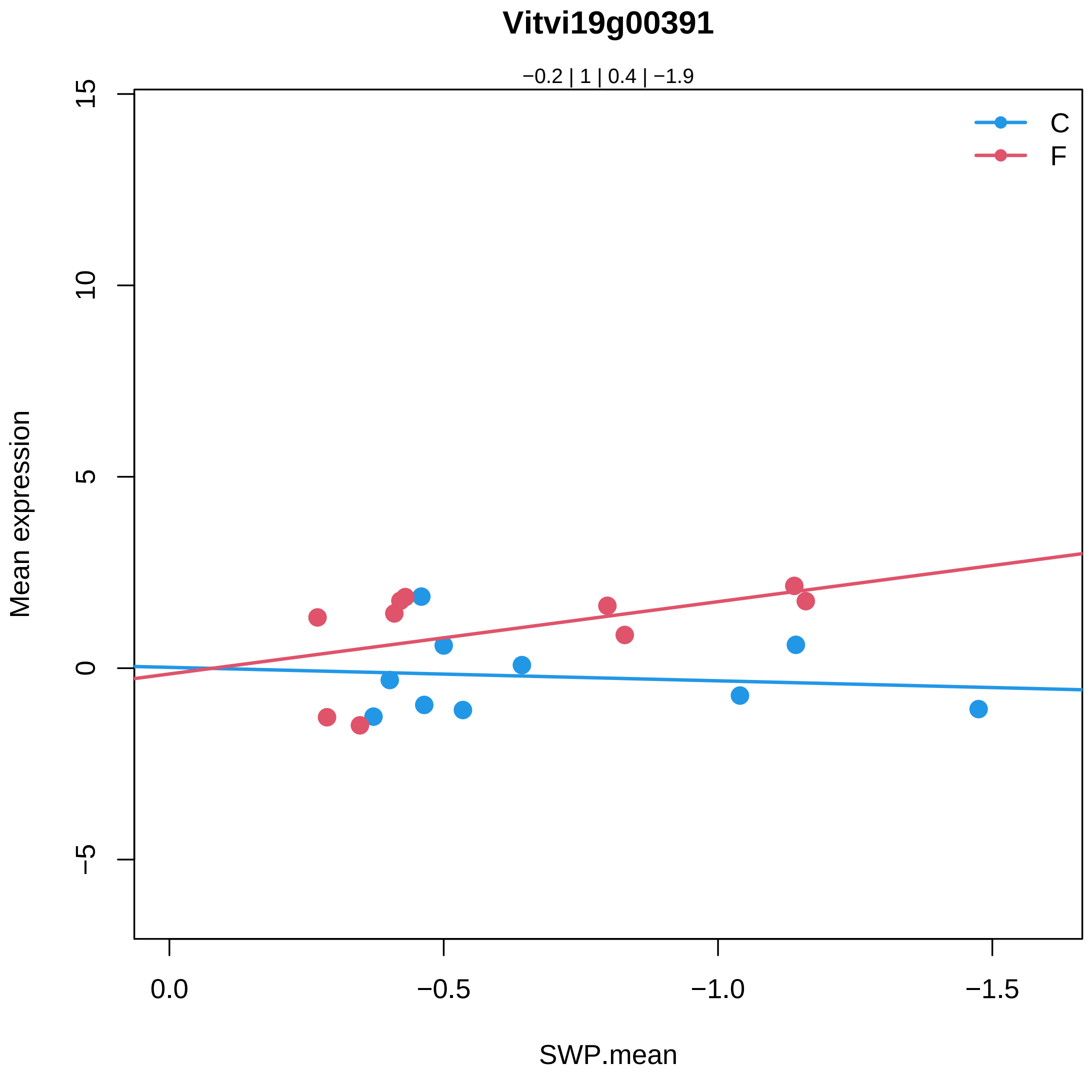
7.6.29 Vitvi19g00391: type5

```
> 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
```



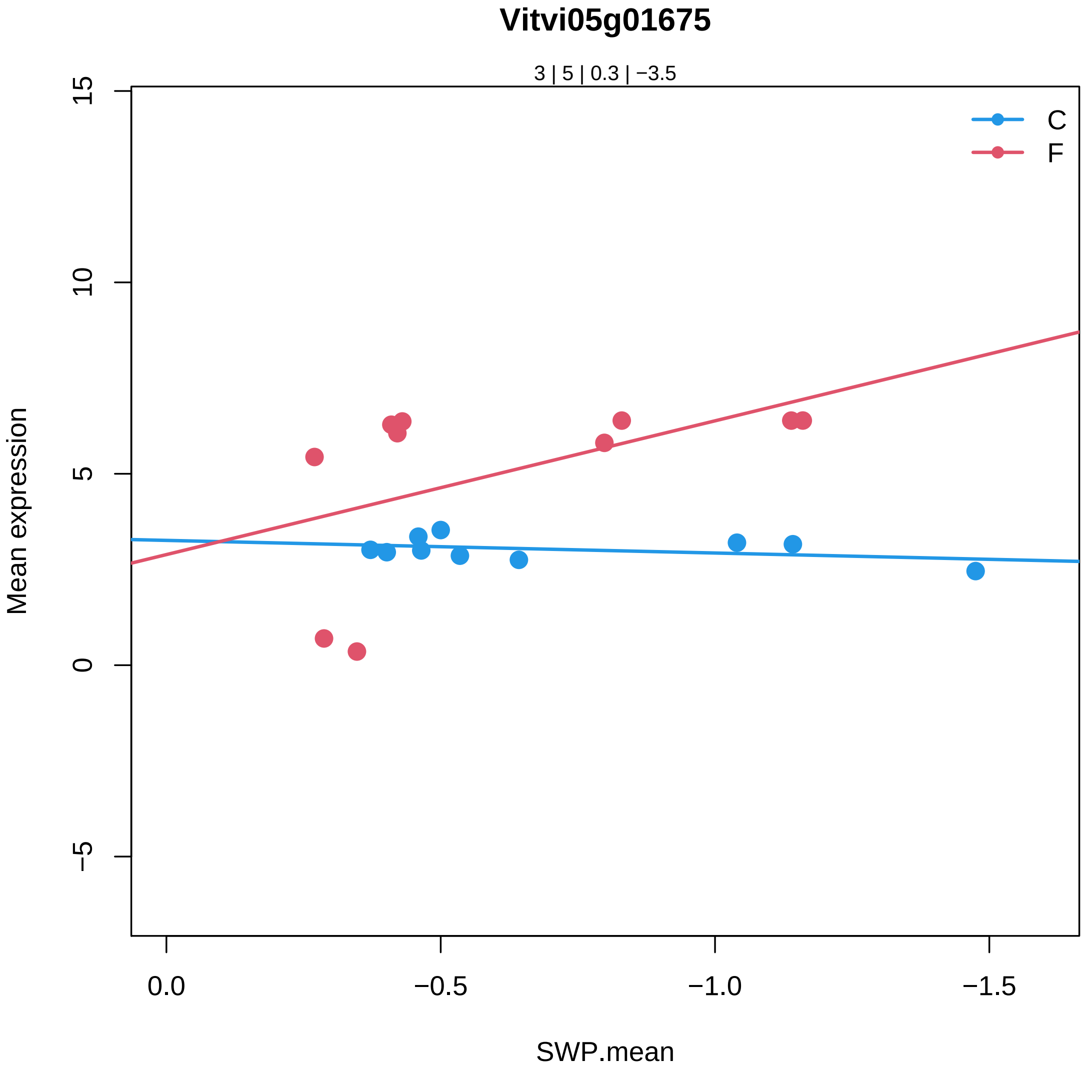
7.6.30 Vitvi05g01675: + type5

```
> 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
```



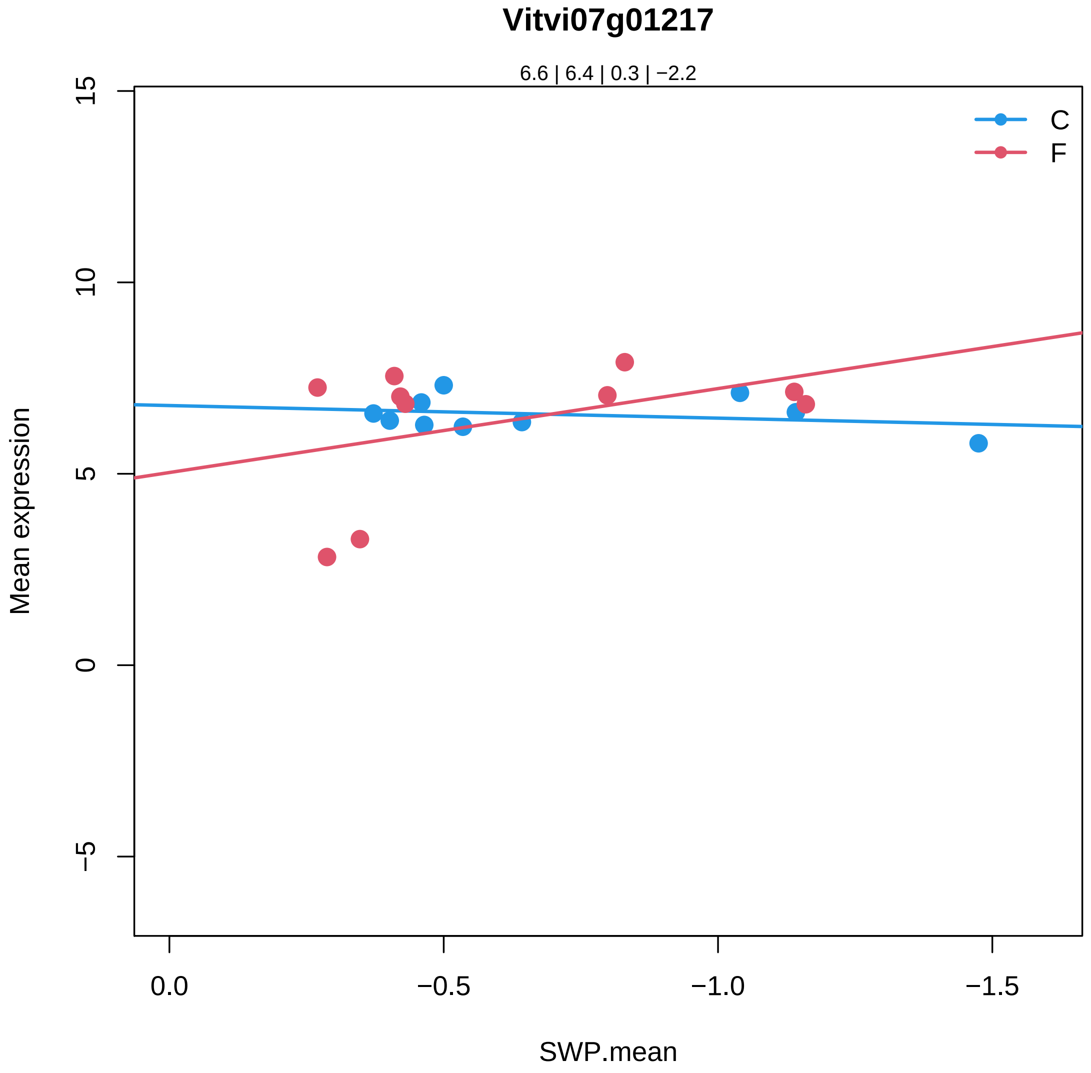
7.6.31 Vitvi07g01217: type5

```
> 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
```



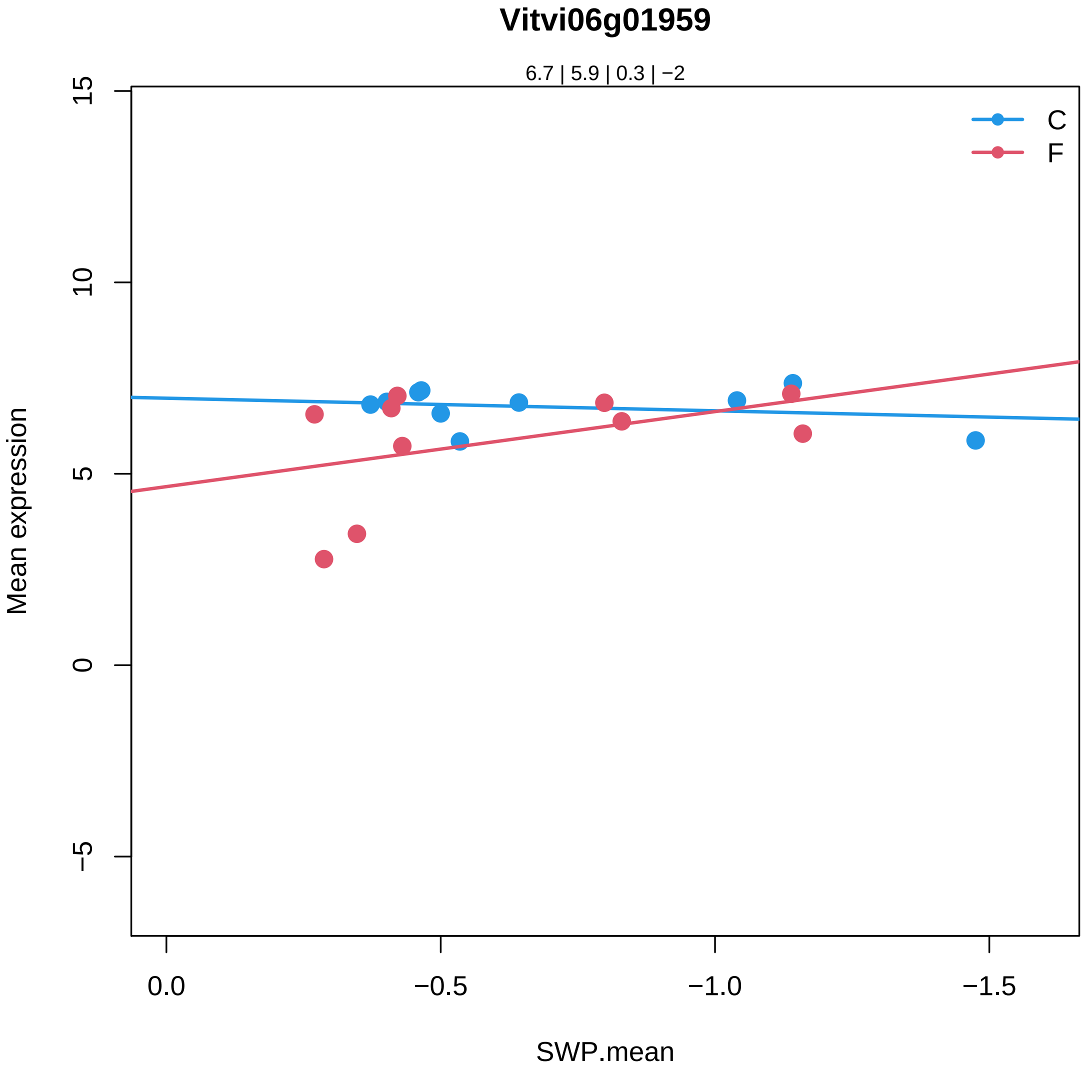
7.6.32 Vitvi06g01959: type5

```
> 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
```



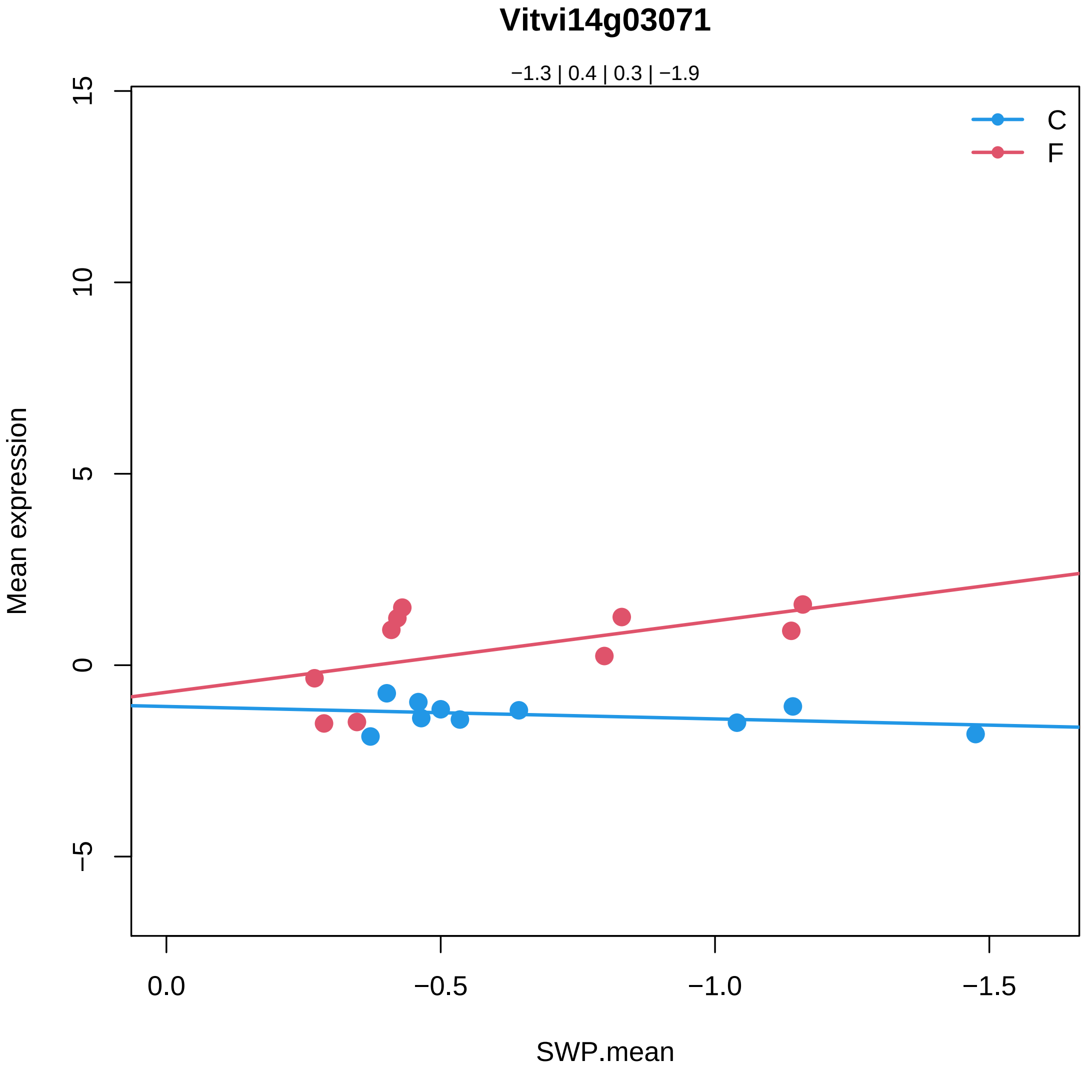
7.6.33 Vitvi14g03071: + type5

```
> 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
```



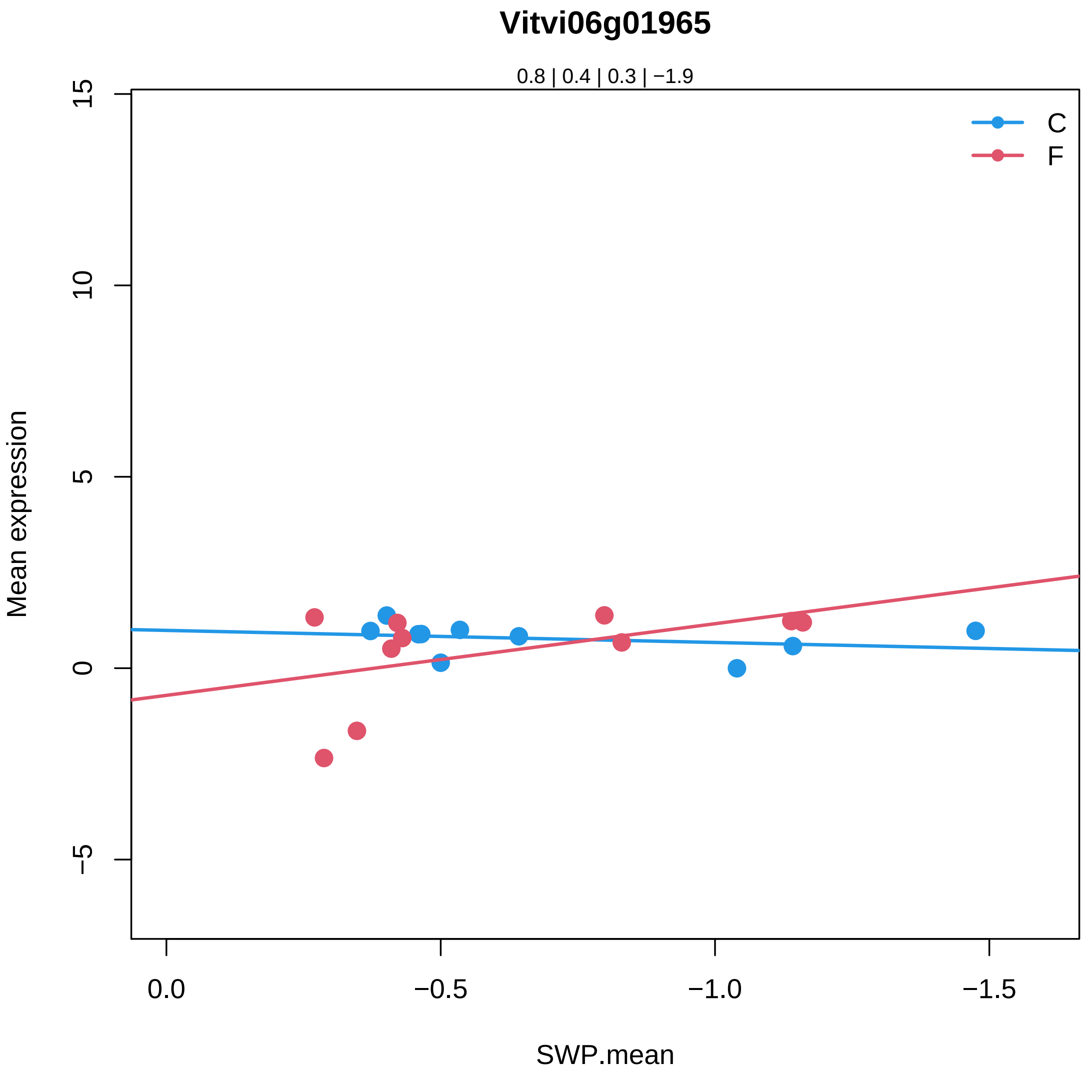
7.6.34 Vitvi06g01965: type5

```
> 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
```



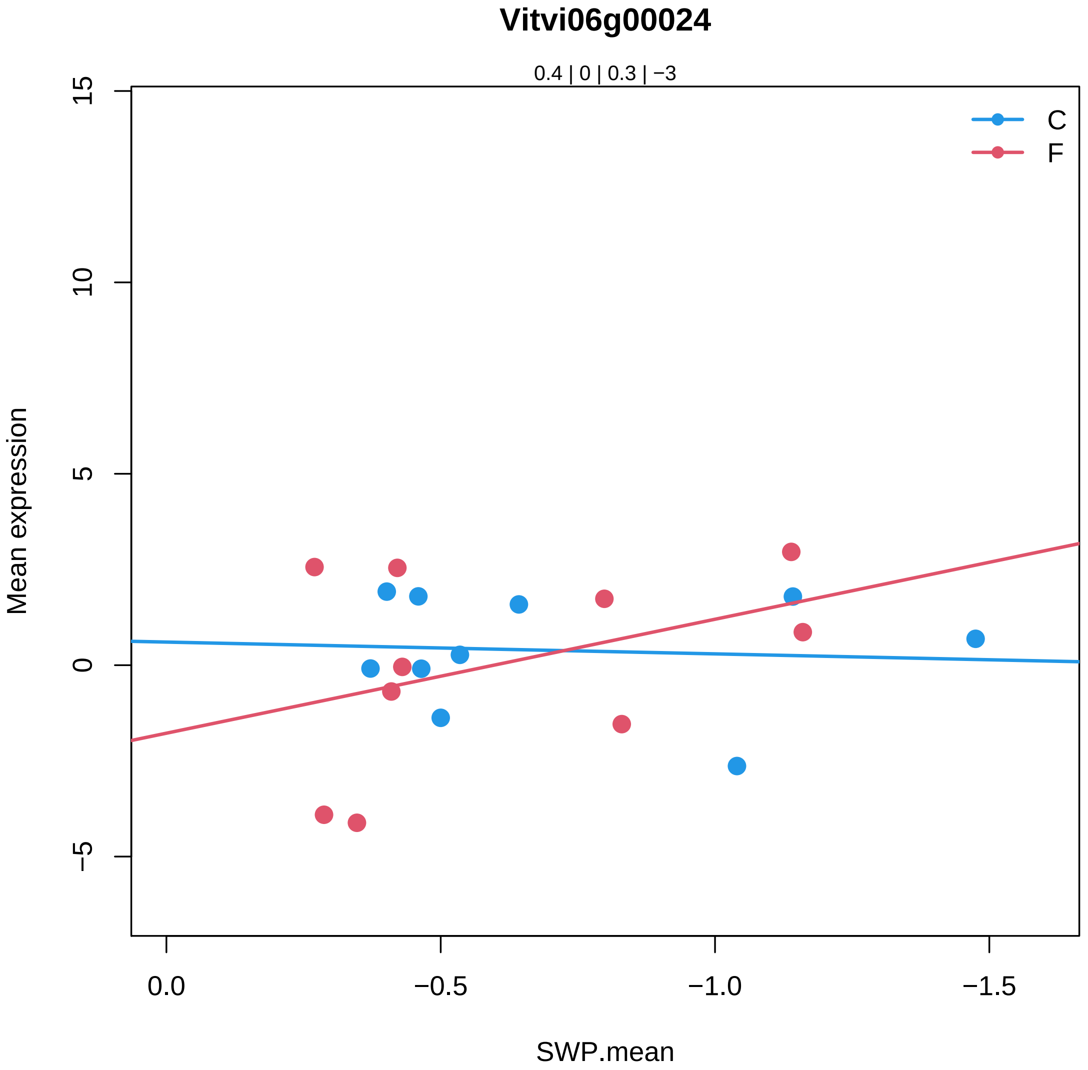
7.6.35 Vitvi06g00024: type5

```
> 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
```



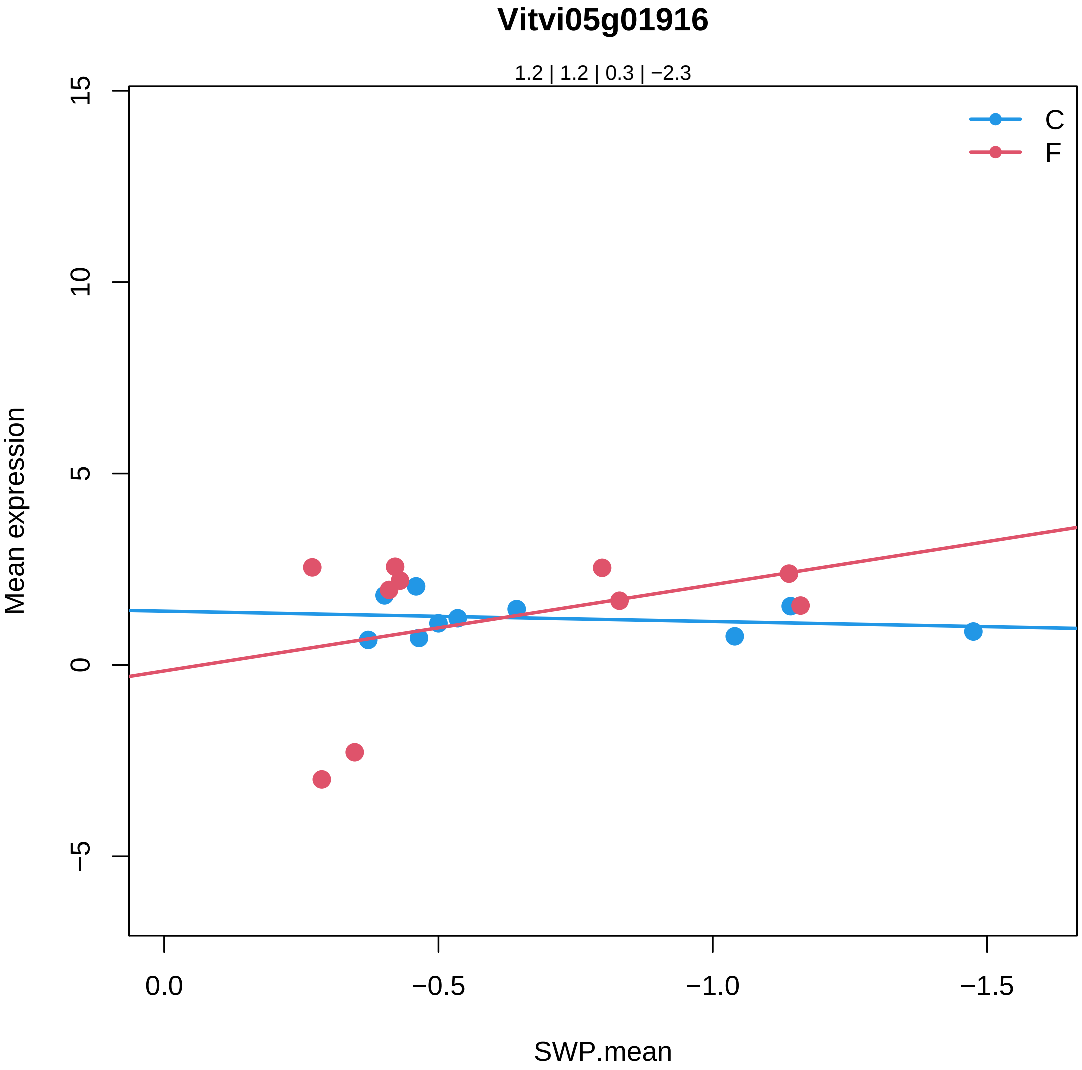
7.6.36 Vitvi05g01916: type5

```
> 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
```



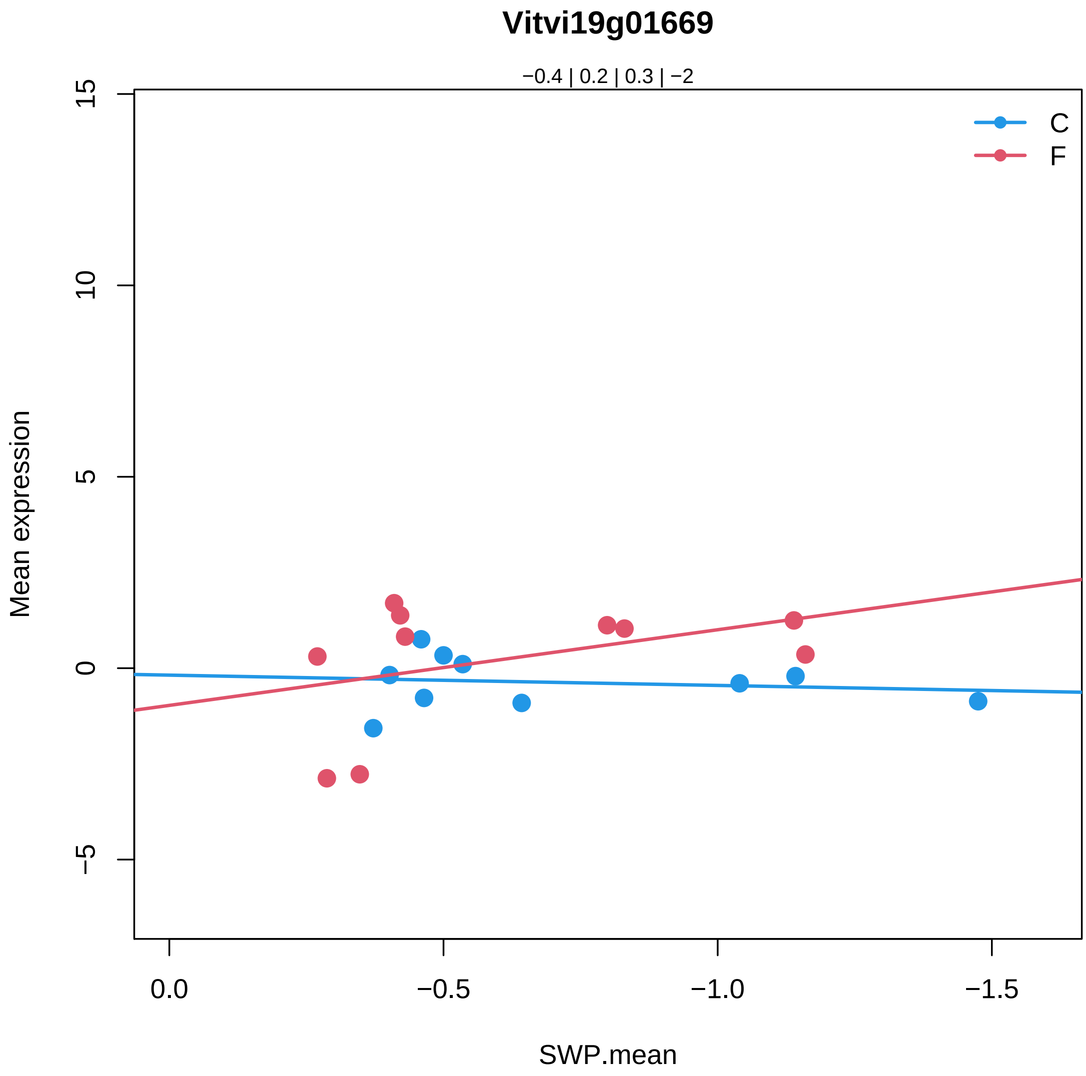
7.6.37 Vitvi19g01669: type5

```
> 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
```



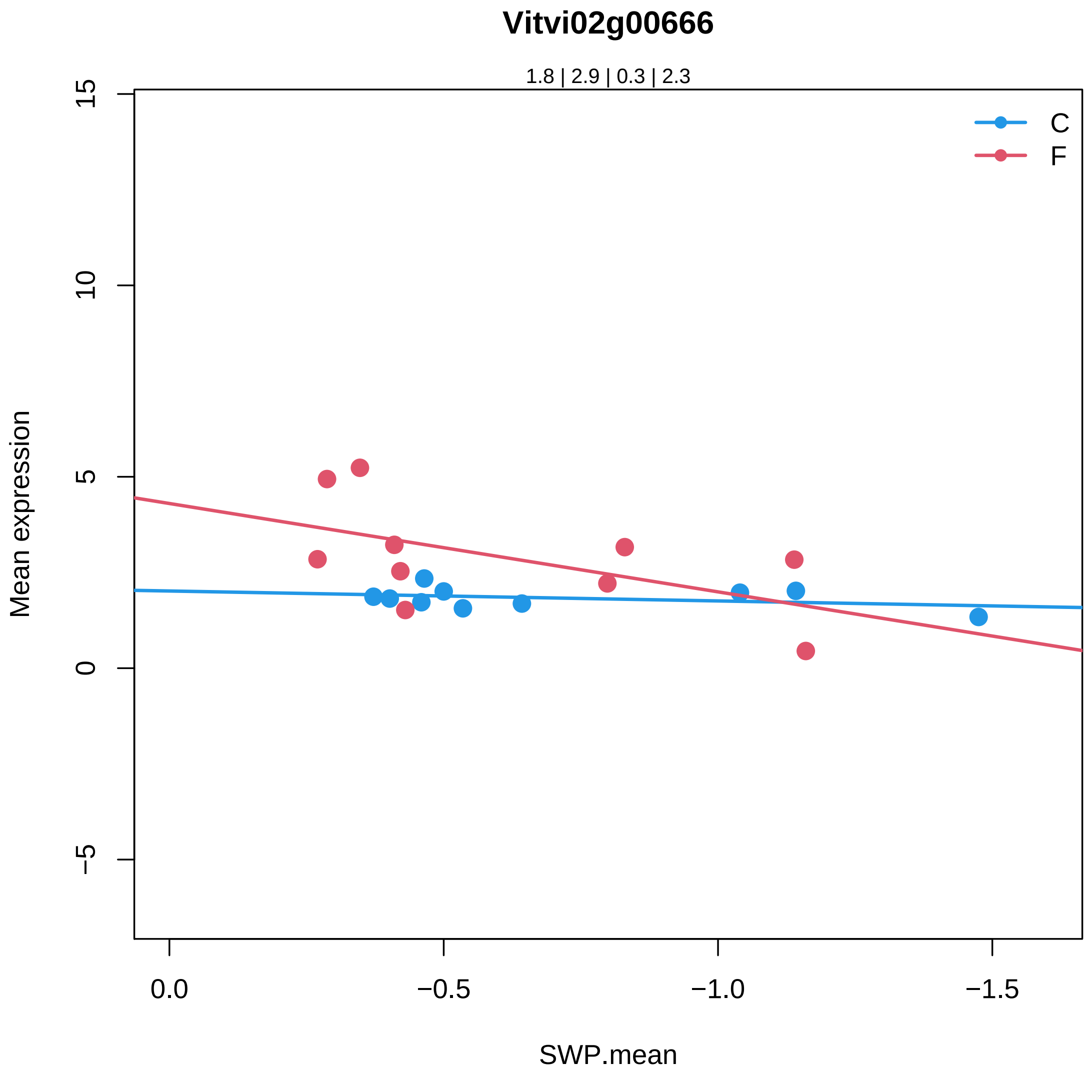
7.6.38 Vitvi02g00666: type5

```
> 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
```



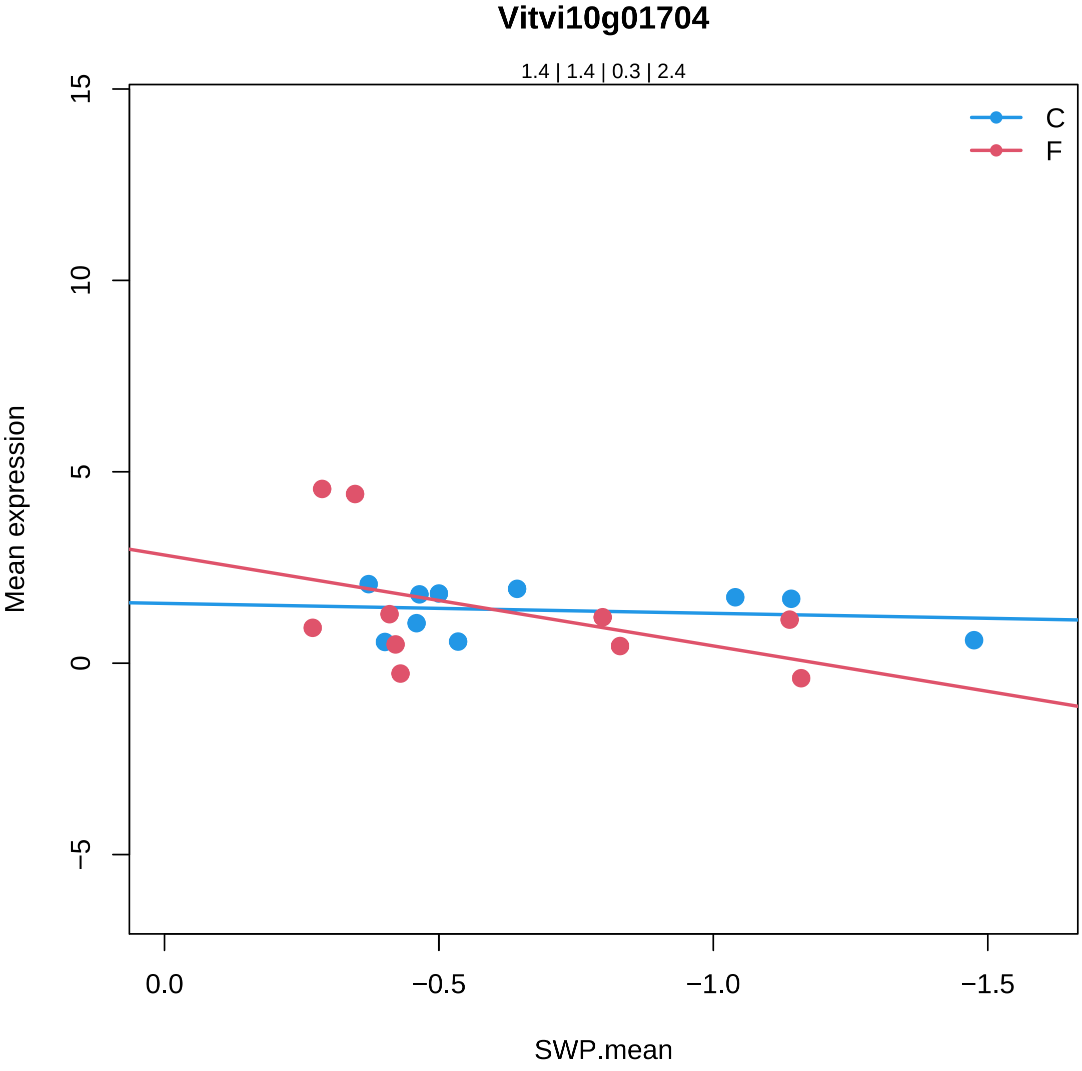
7.6.39 Vitvi10g01704: type5

```
> 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
```



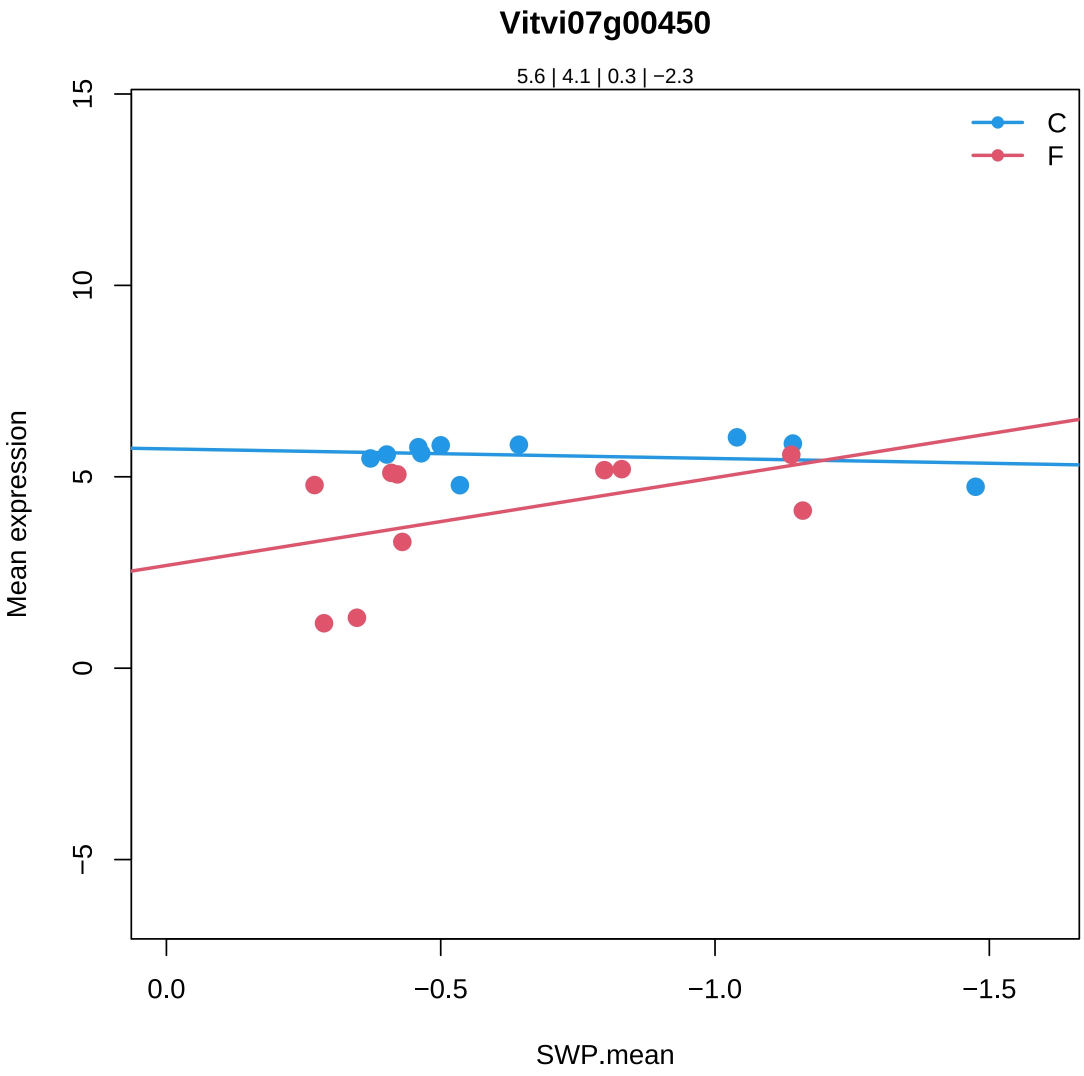
7.6.40 Vitvi07g00450: type5

```
> 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        
```



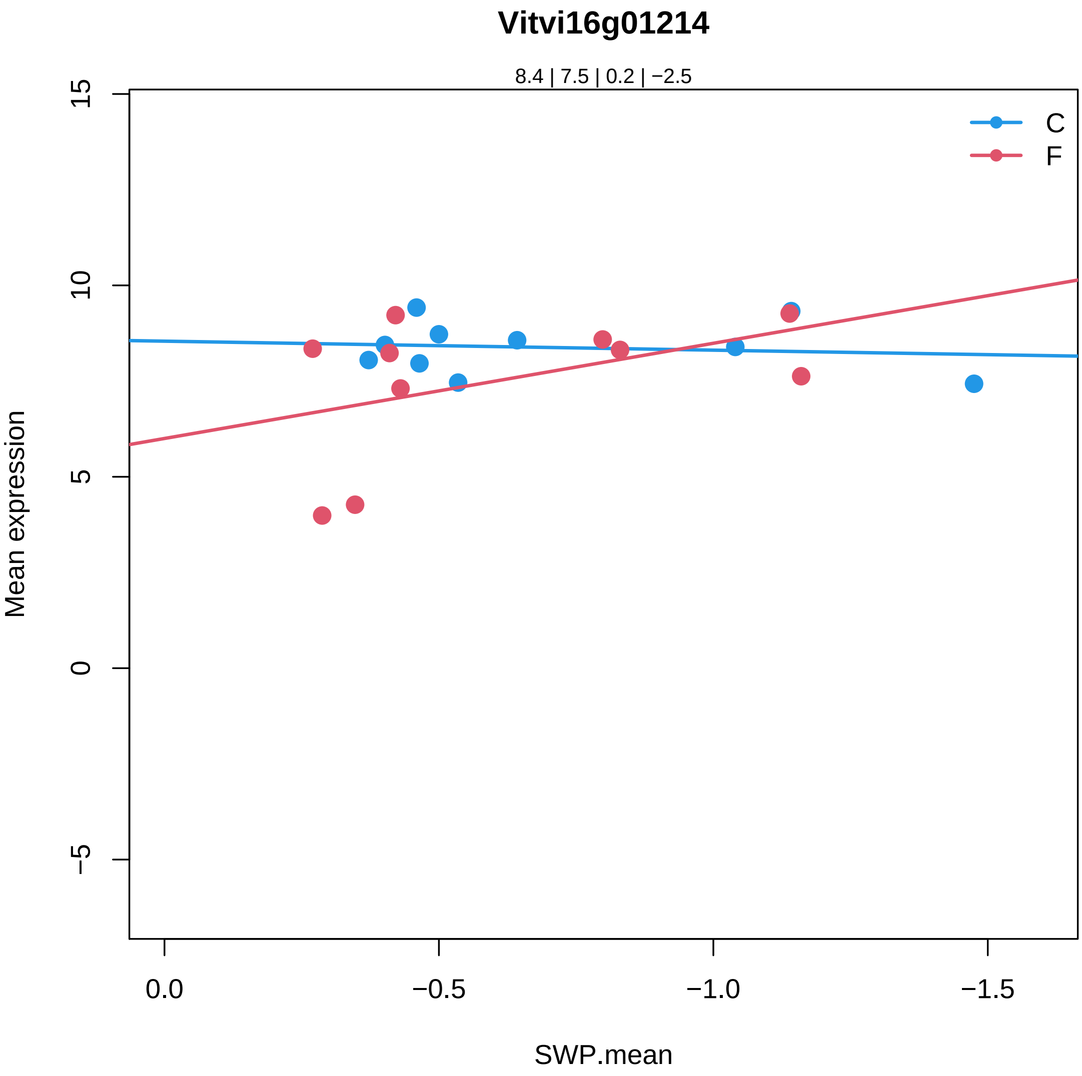
7.6.41 Vitvi16g01214: type5

```
> 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
```



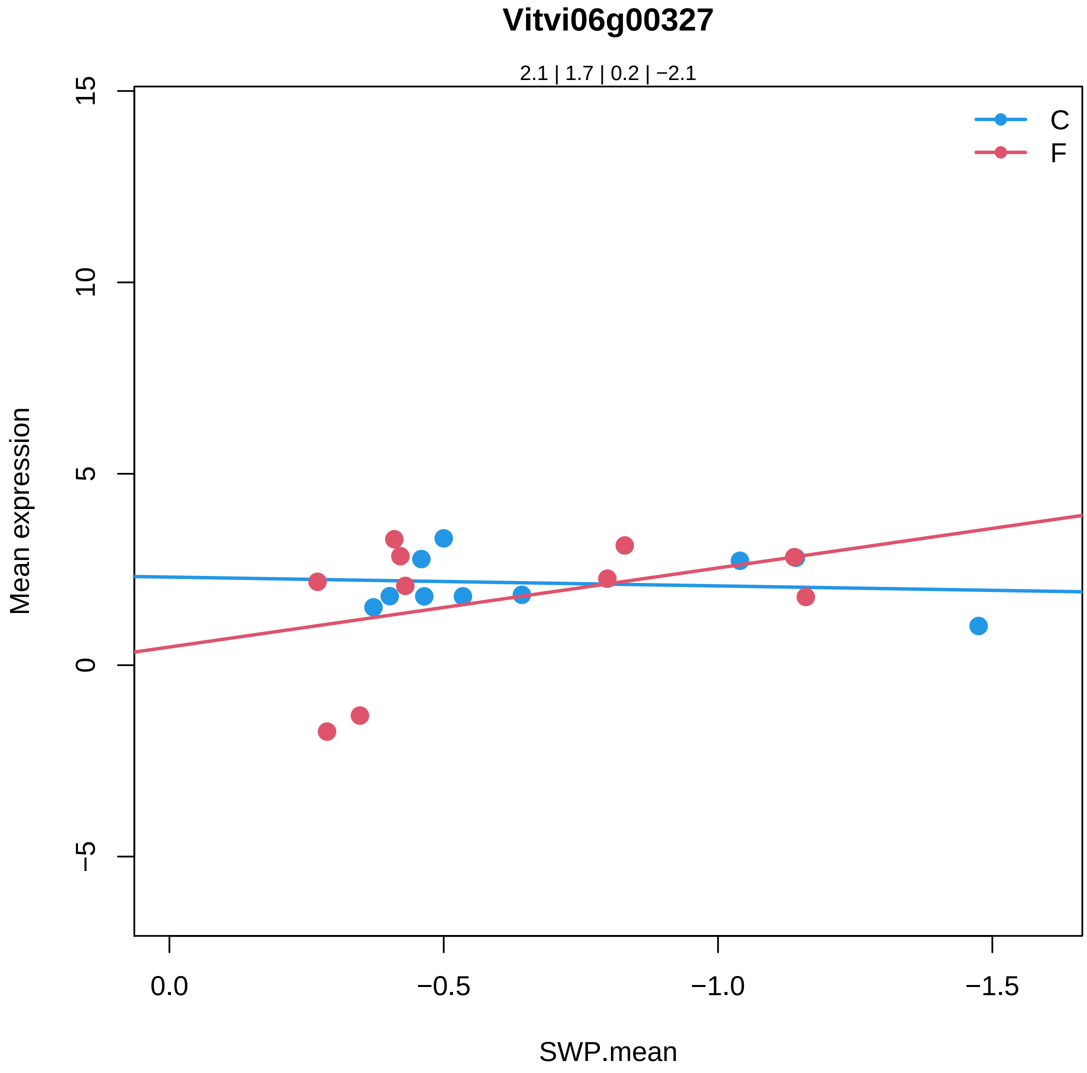
7.6.42 Vitvi06g00327: type5

```
> 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
```



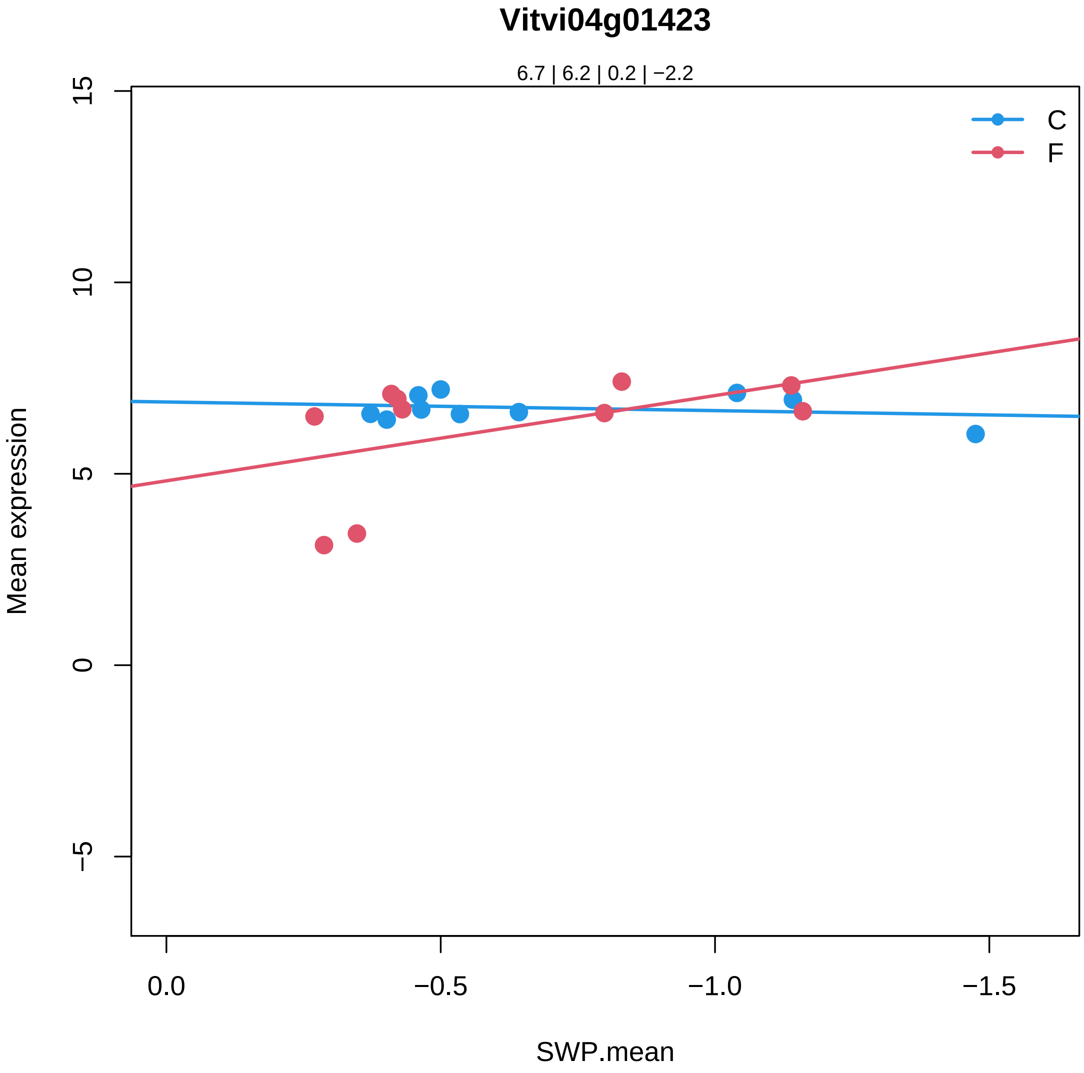
7.6.43 Vitvi04g01423: type5

```
> 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
```



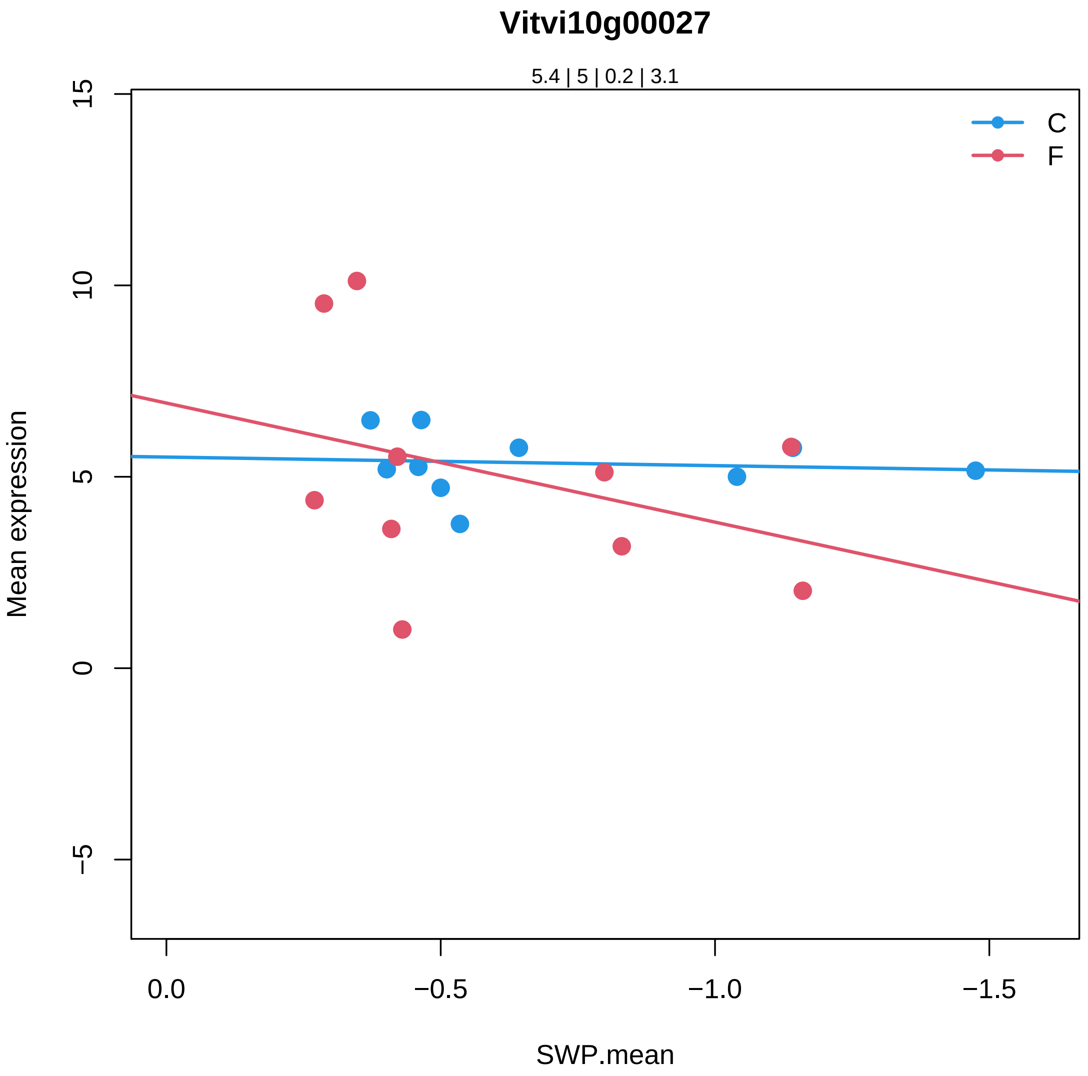
7.6.44 Vitvi10g00027: type5

```
> 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
```



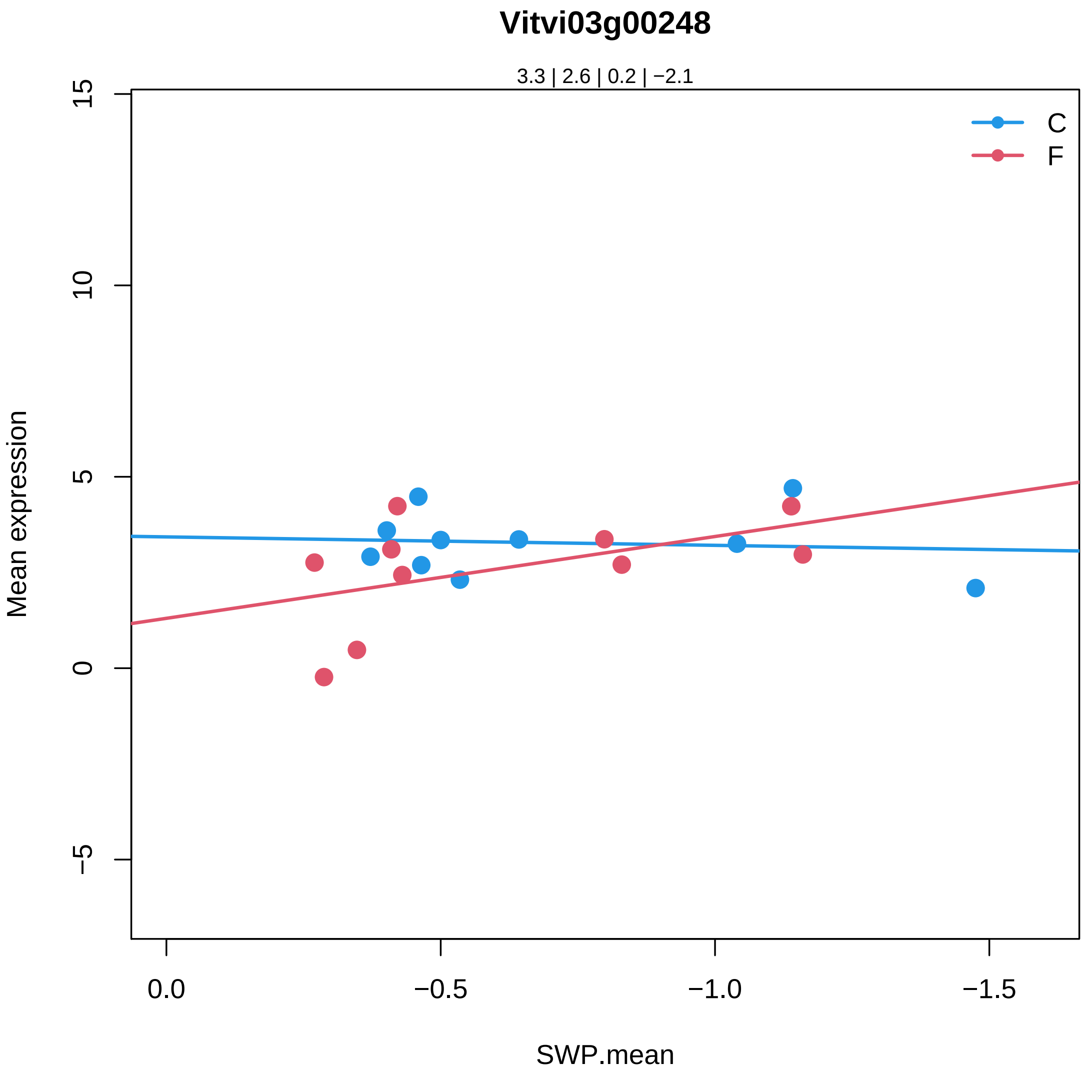
7.6.45 Vitvi03g00248: type5

```
> 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
```



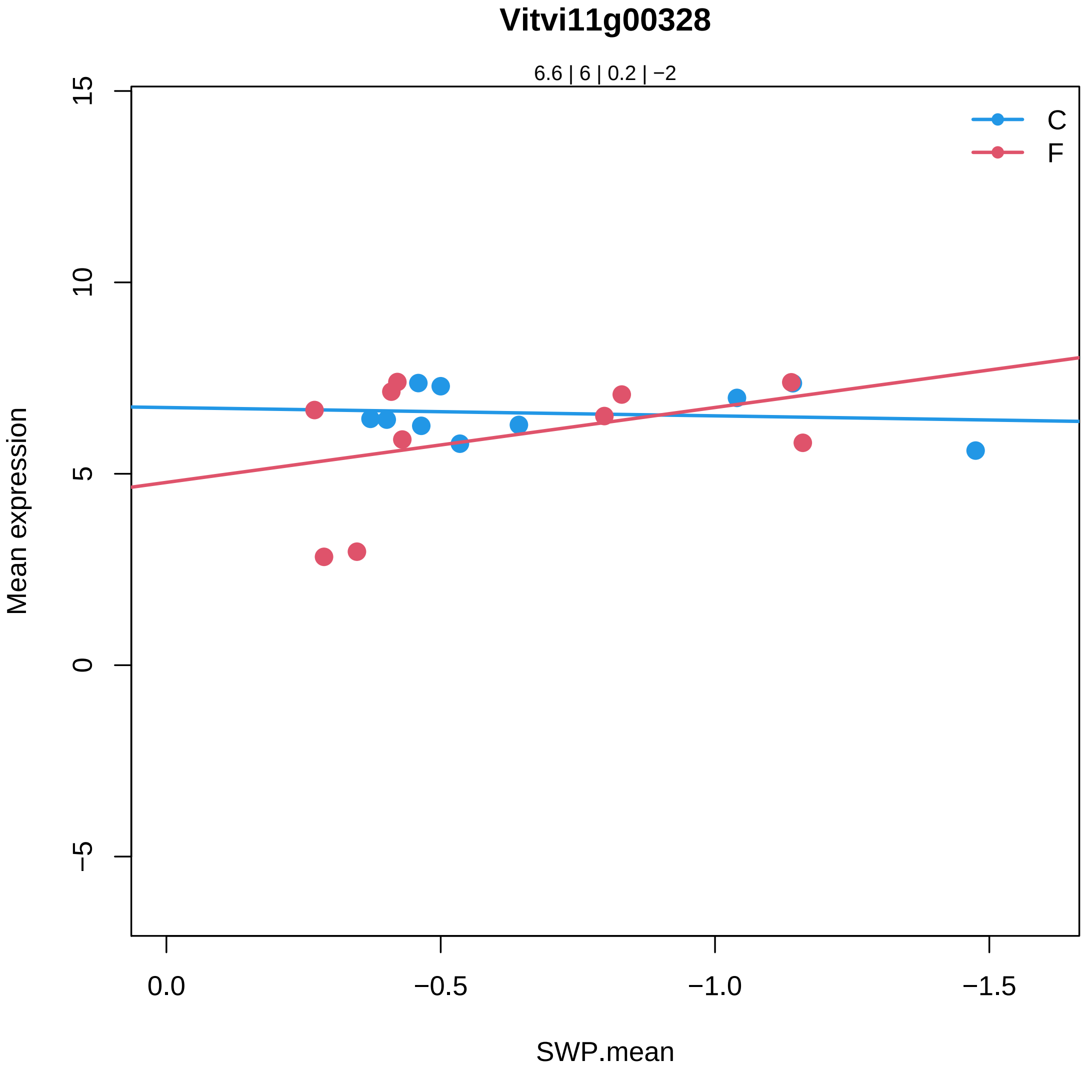
7.6.46 Vitvi11g00328: type5

```
> 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
```



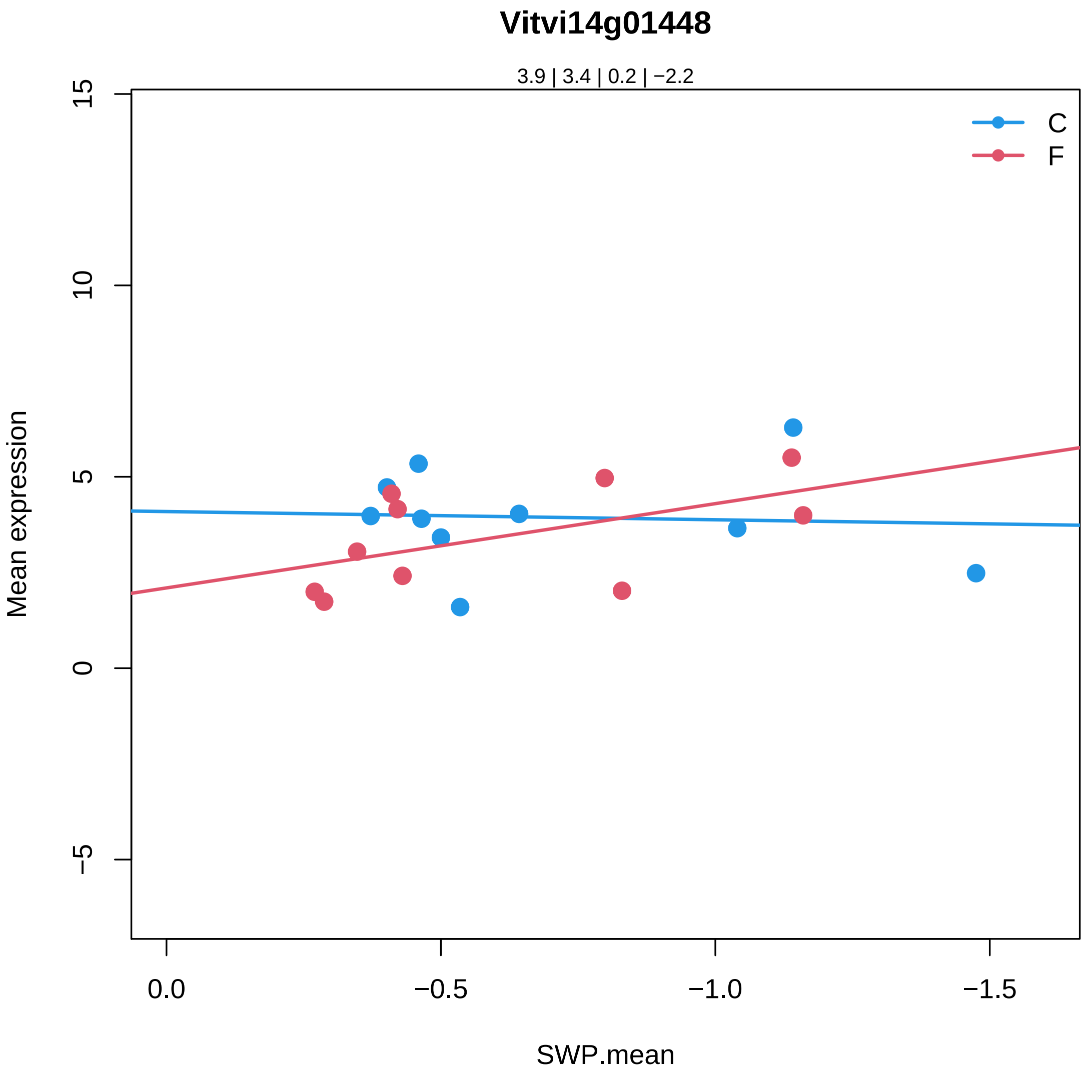
7.6.47 Vitvi14g01448: type5

```
> 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
```



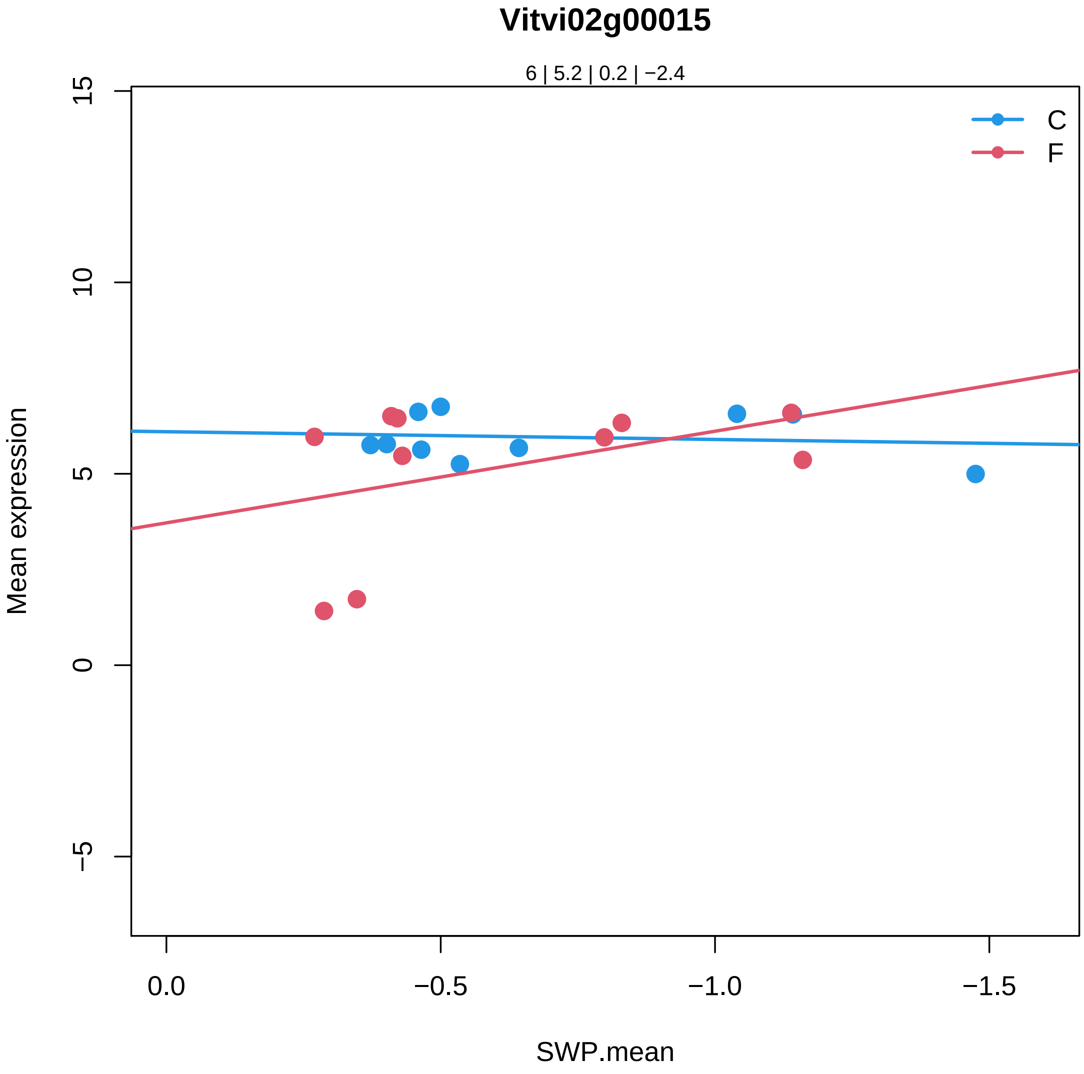
7.6.48 Vitvi02g00015: type5

```
> 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
```



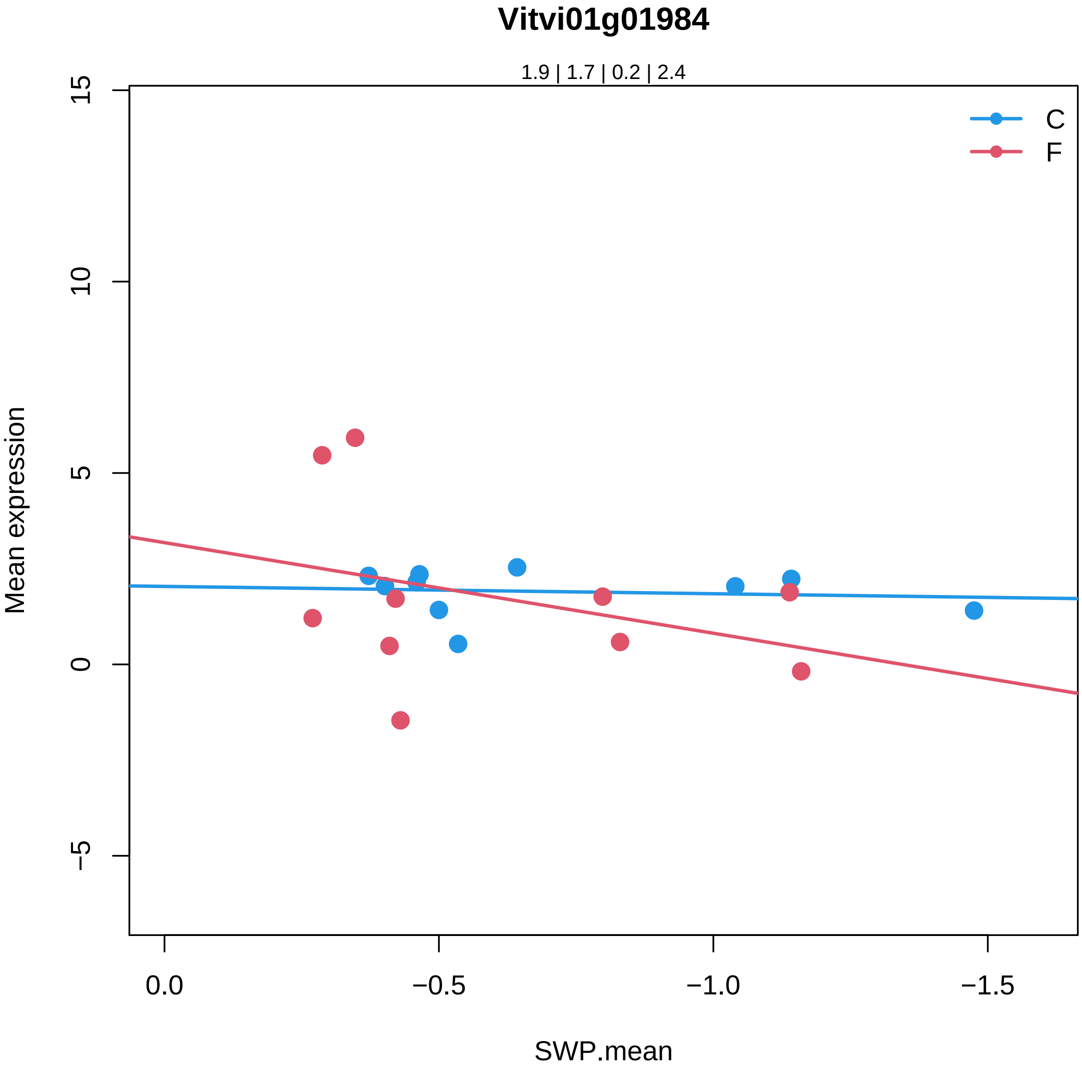
7.6.49 Vitvi01g01984: type5

```
> 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
```



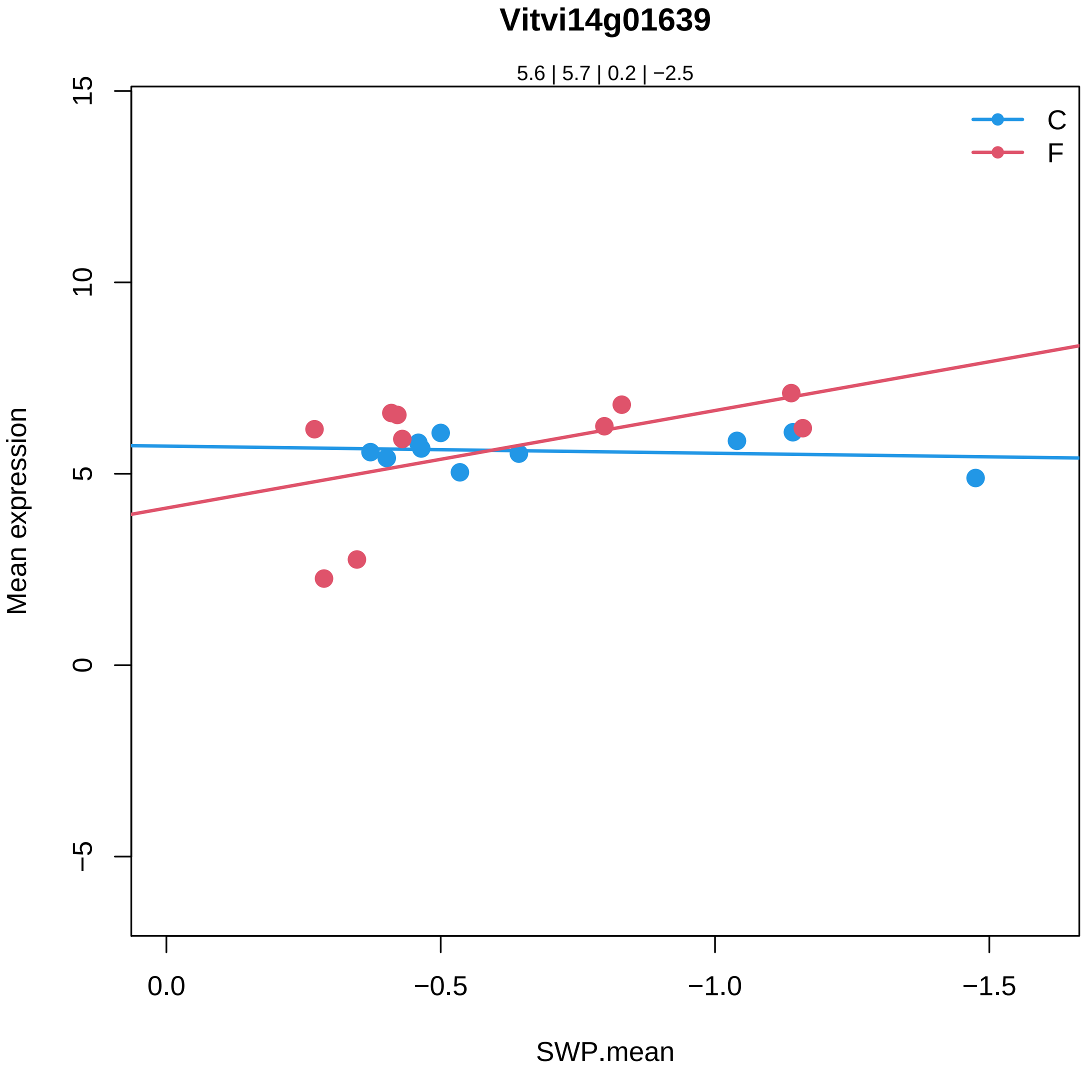
7.6.50 Vitvi14g01639: type5

```
> 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
```



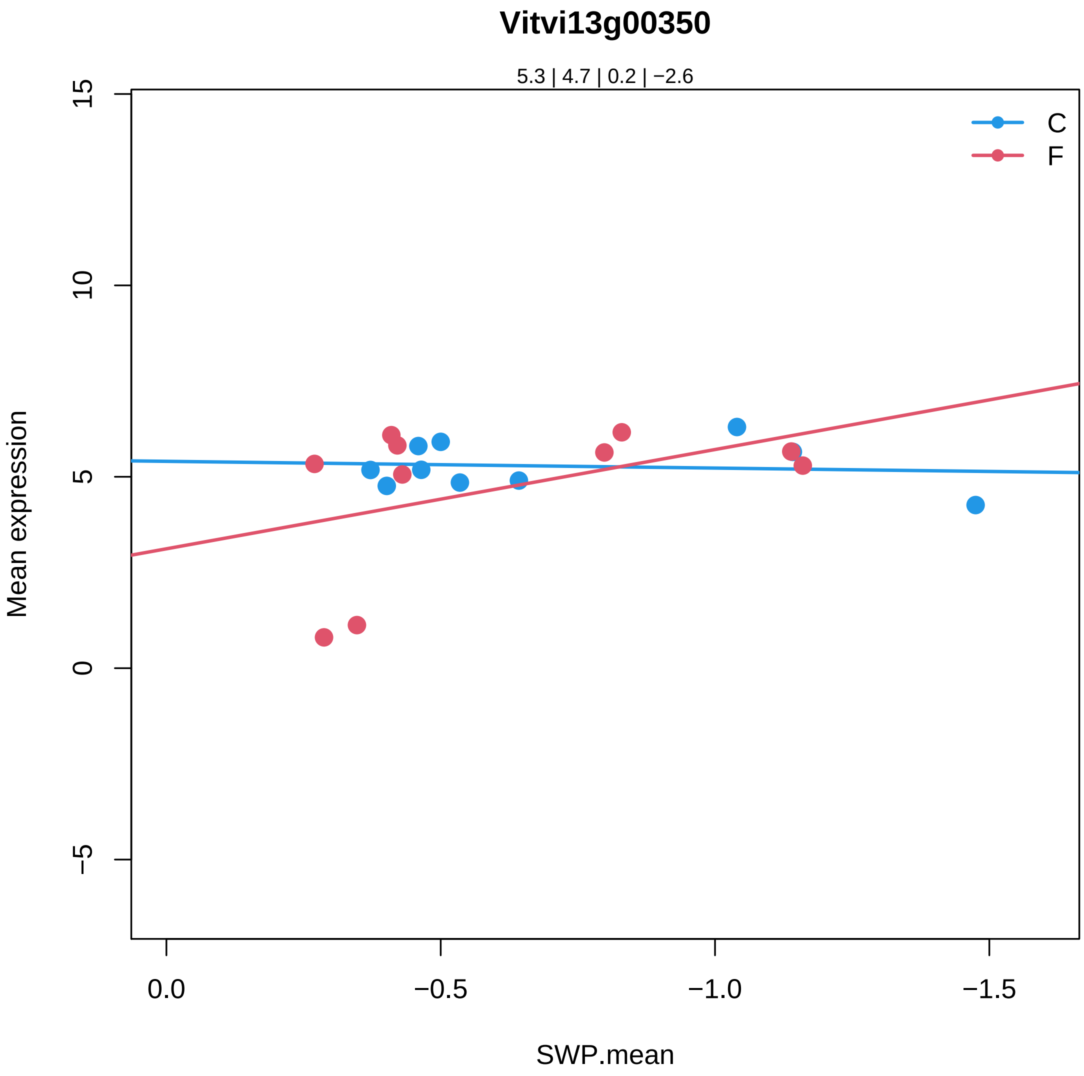
7.6.51 Vitvi13g00350: type5

```
> 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
```



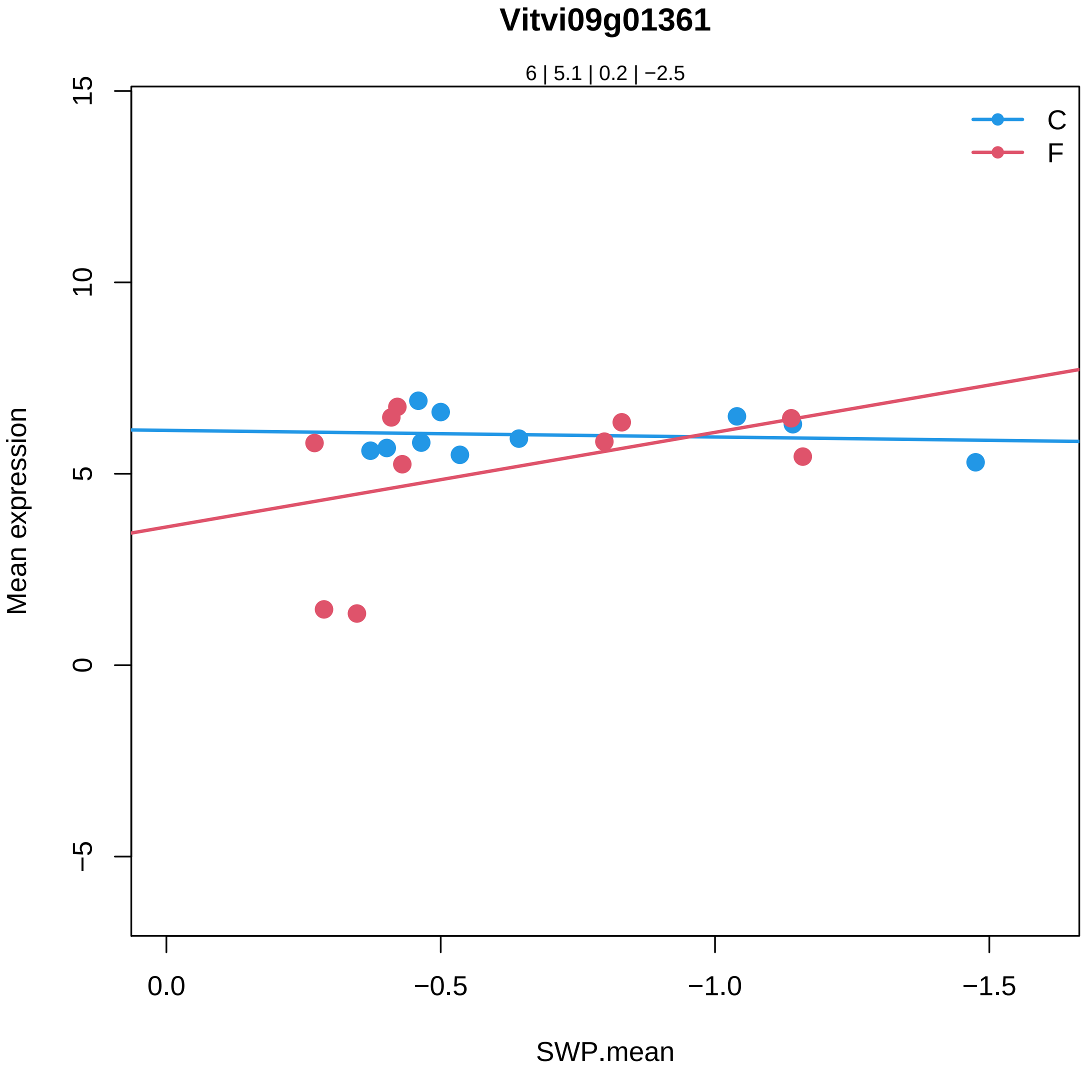
7.6.52 Vitvi09g01361: type5

```
> 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
```



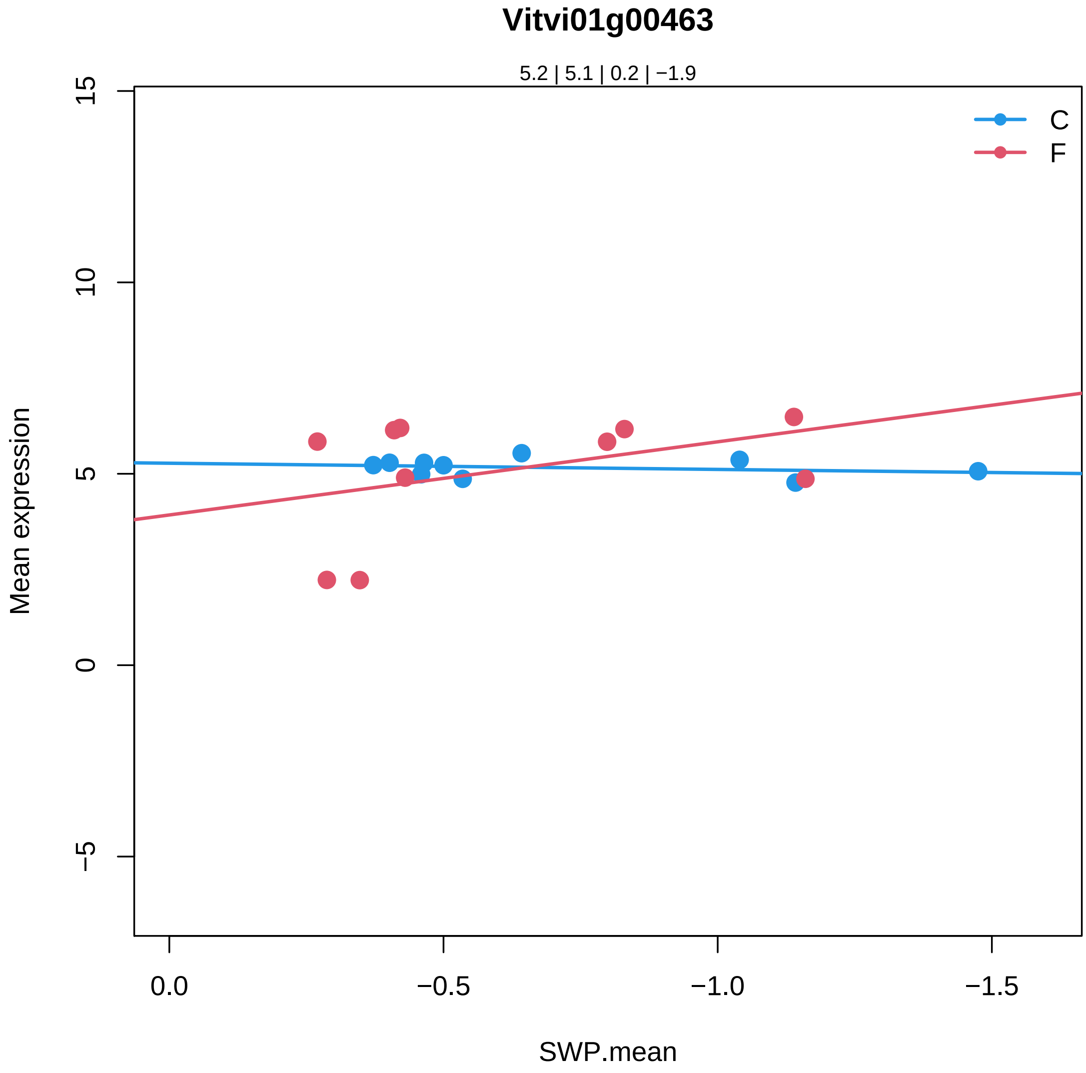
7.6.53 Vitvi01g00463: type5

```
> 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
```



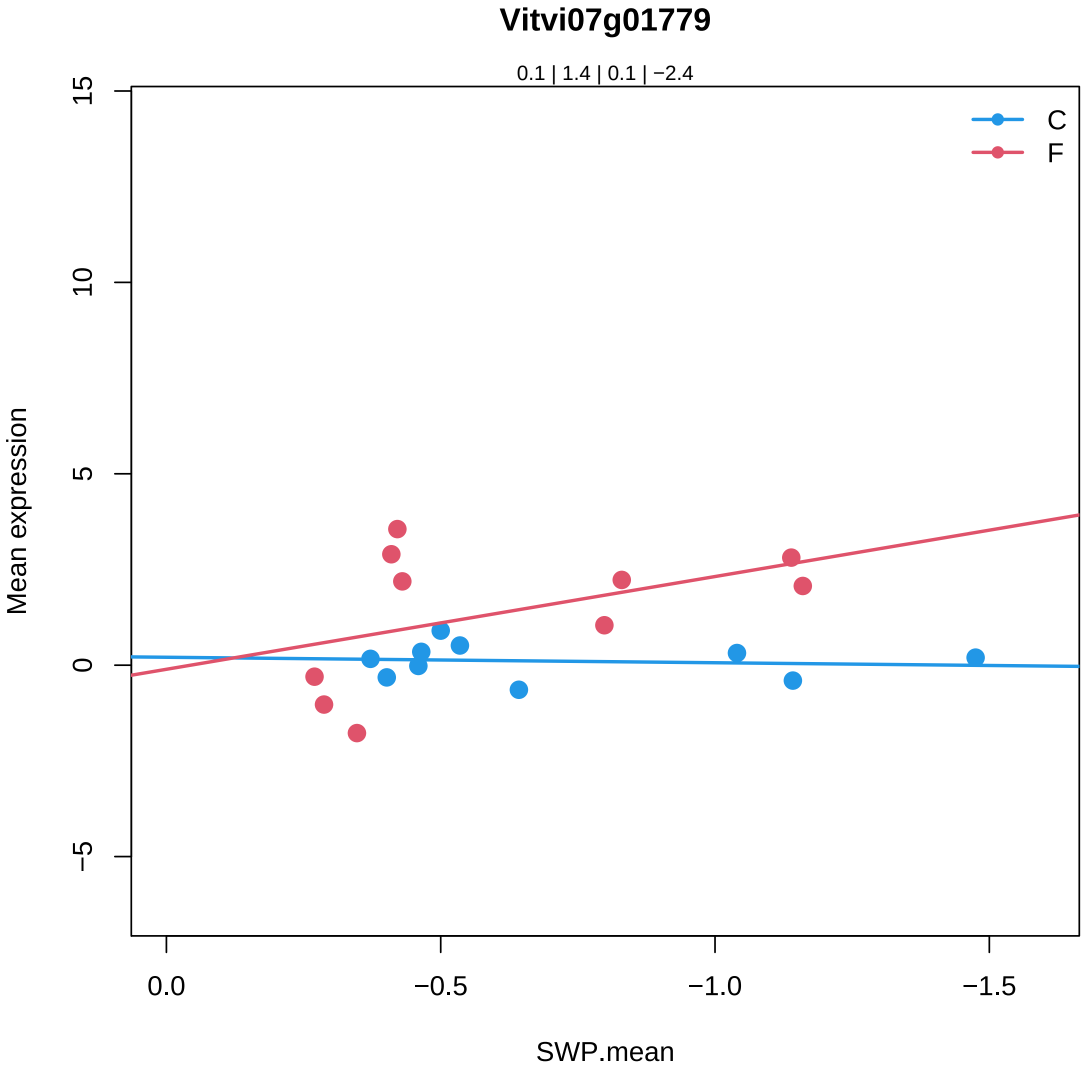
7.6.54 Vitvi07g01779: type5

```
> 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
```



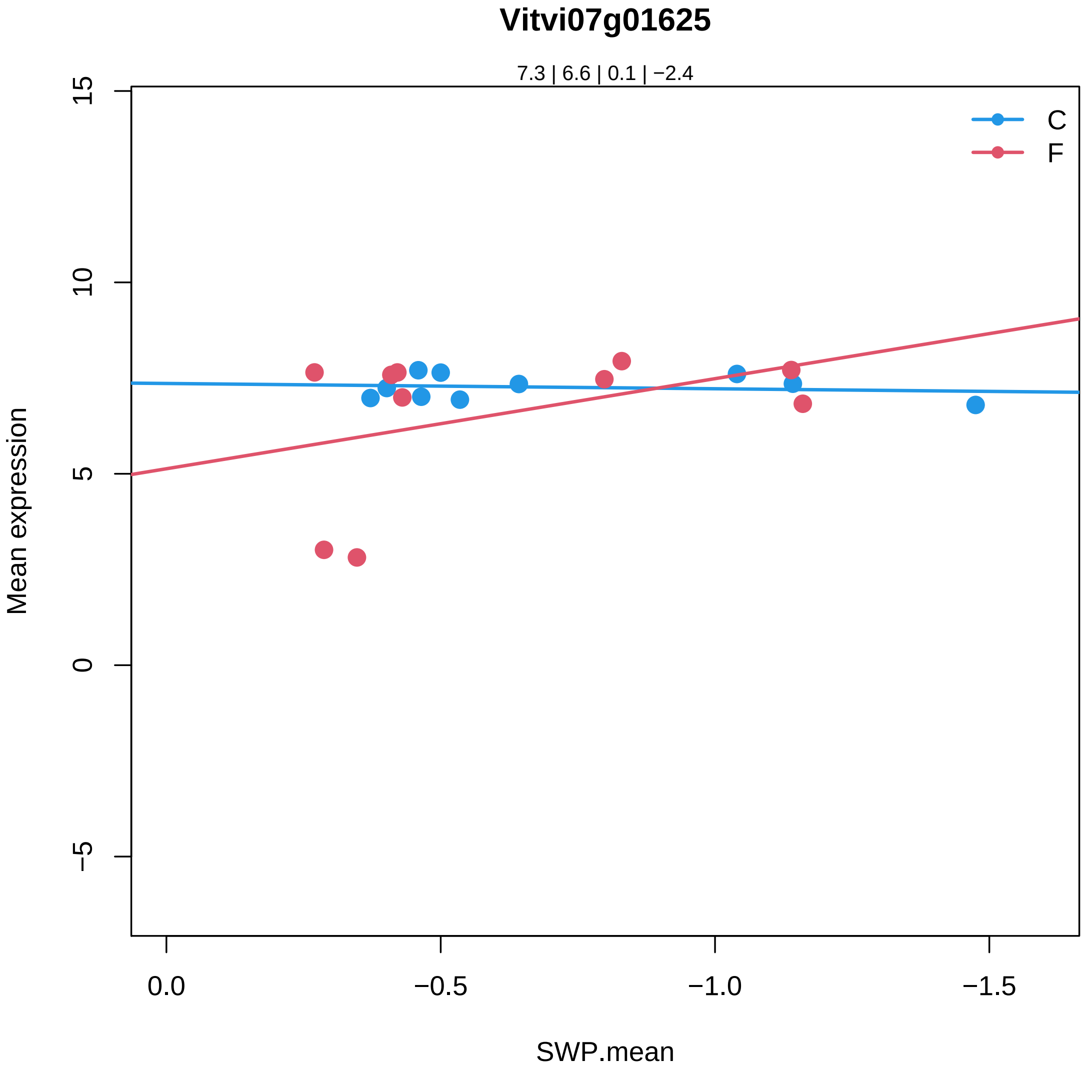
7.6.55 Vitvi07g01625: type5

```
> 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
```



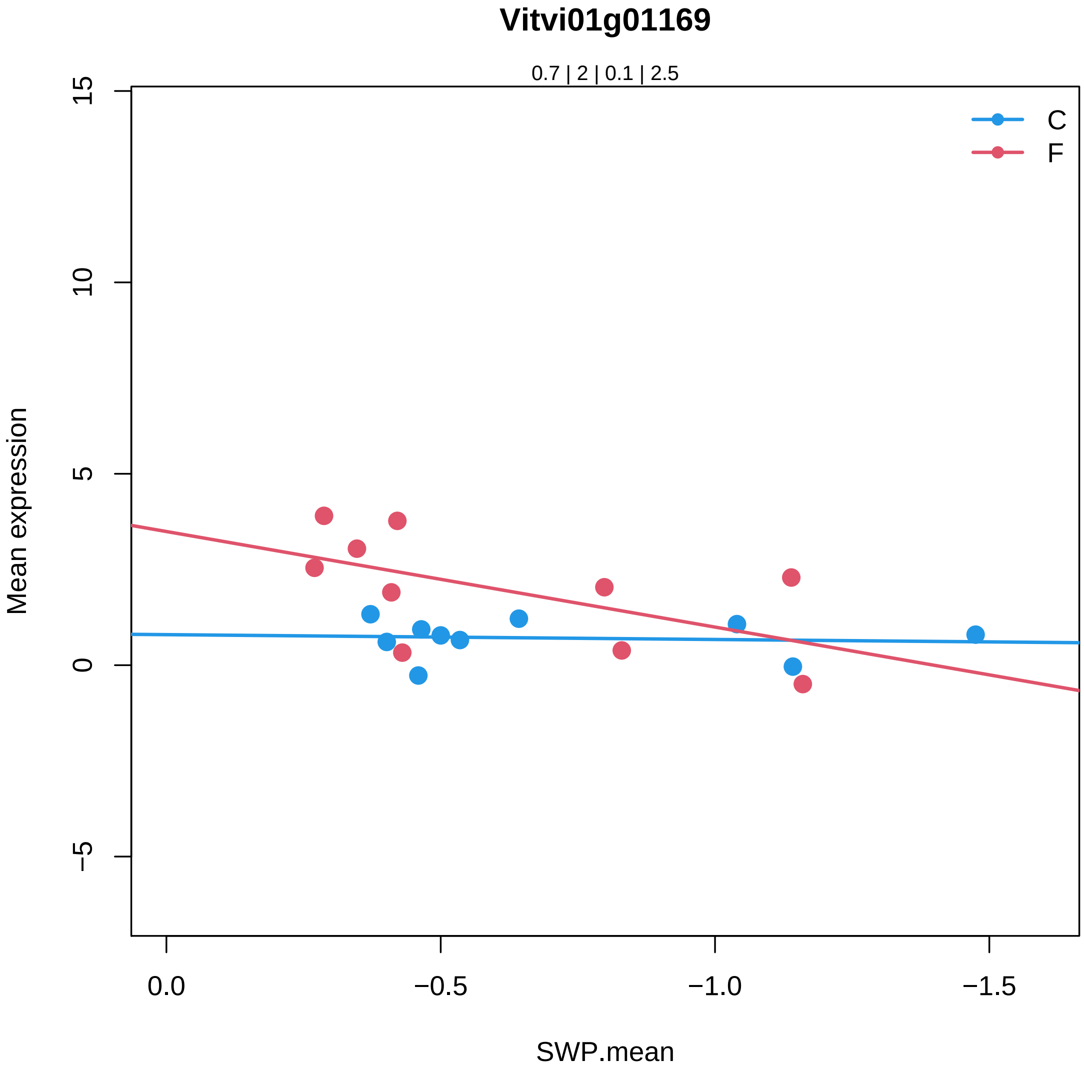
7.6.56 Vitvi01g01169: type5

```
> 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
```



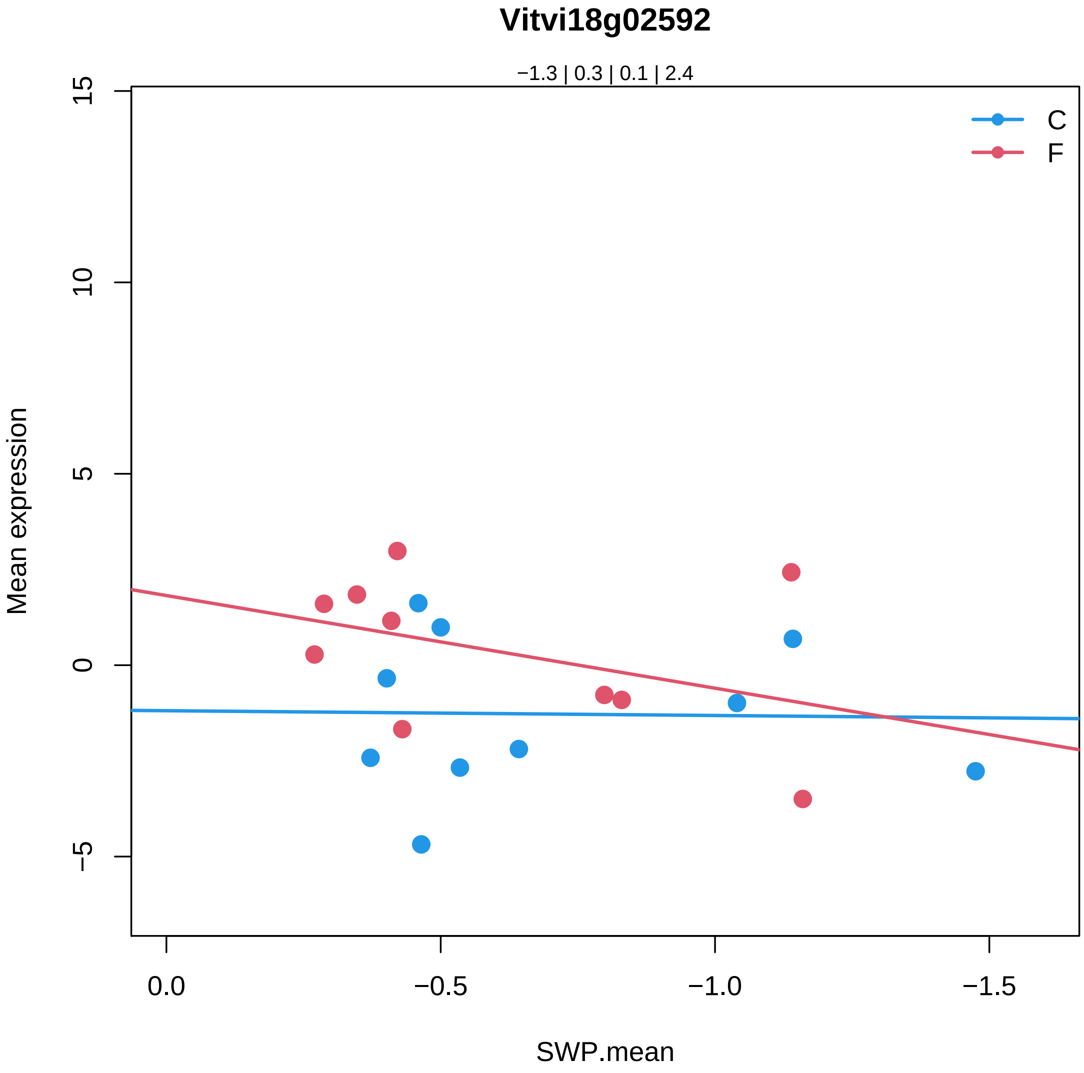
7.6.57 Vitvi18g02592: type5

```
> 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
```



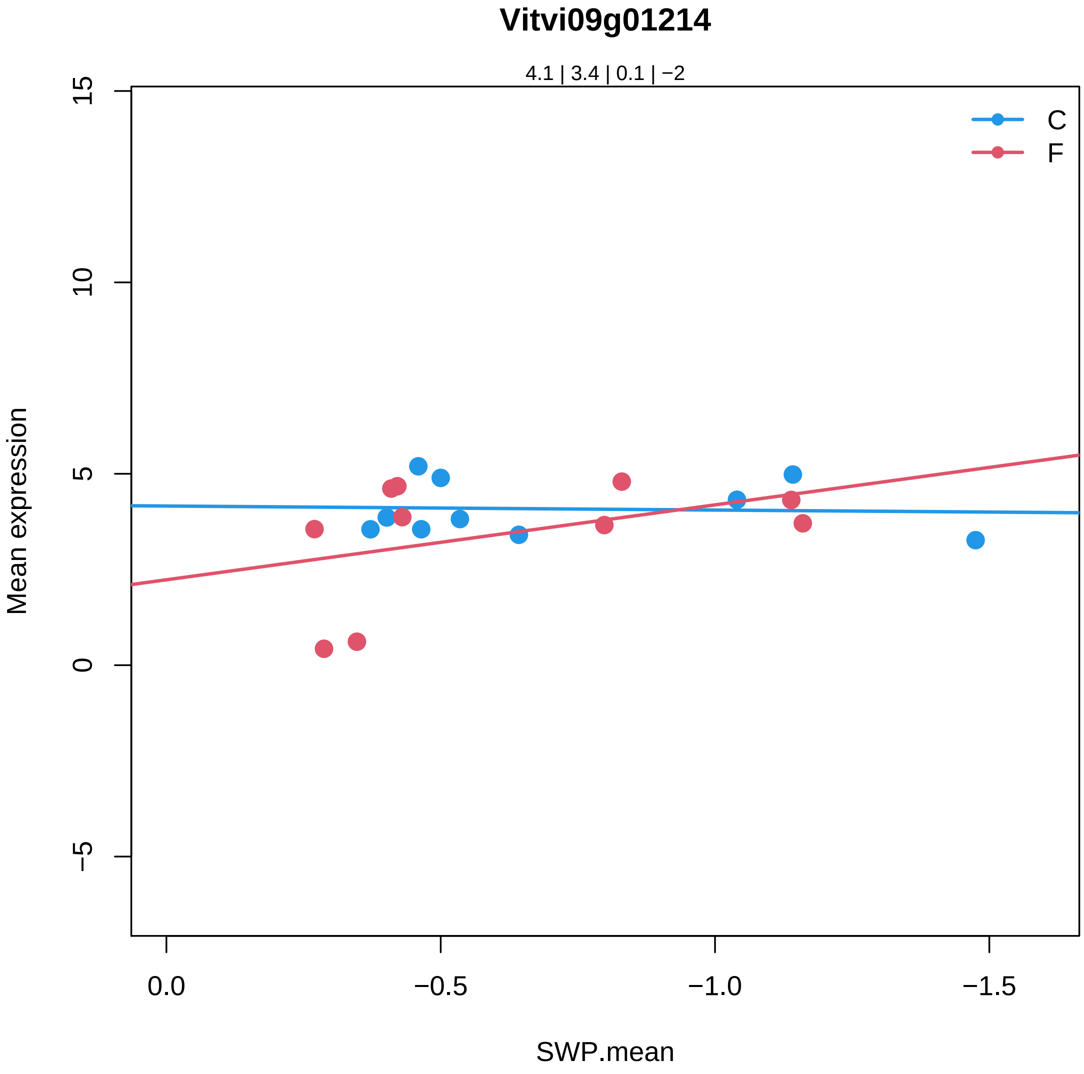
7.6.58 Vitvi09g01214: type5

```
> 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
```



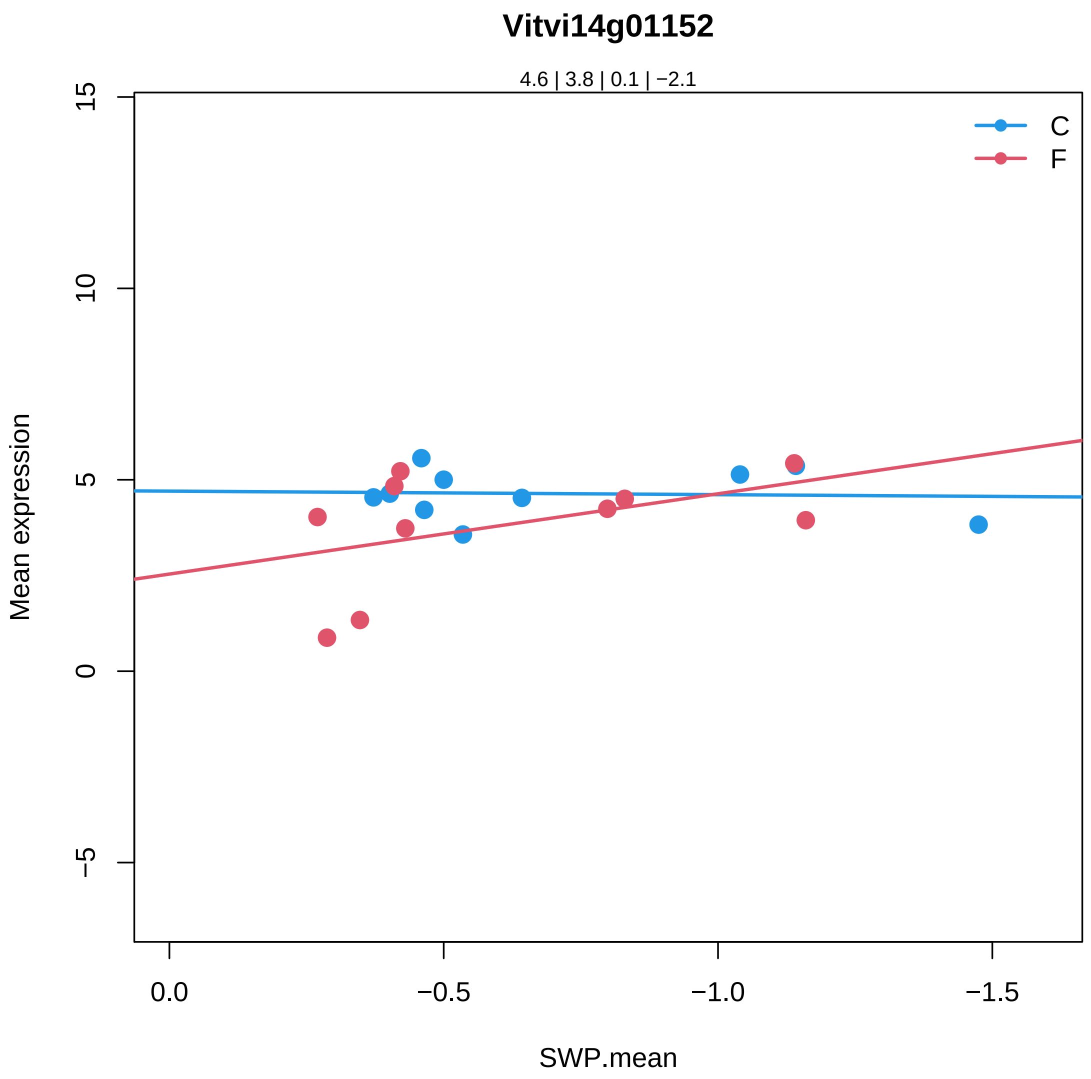
7.6.59 Vitvi14g01152: type5

```
> 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
```



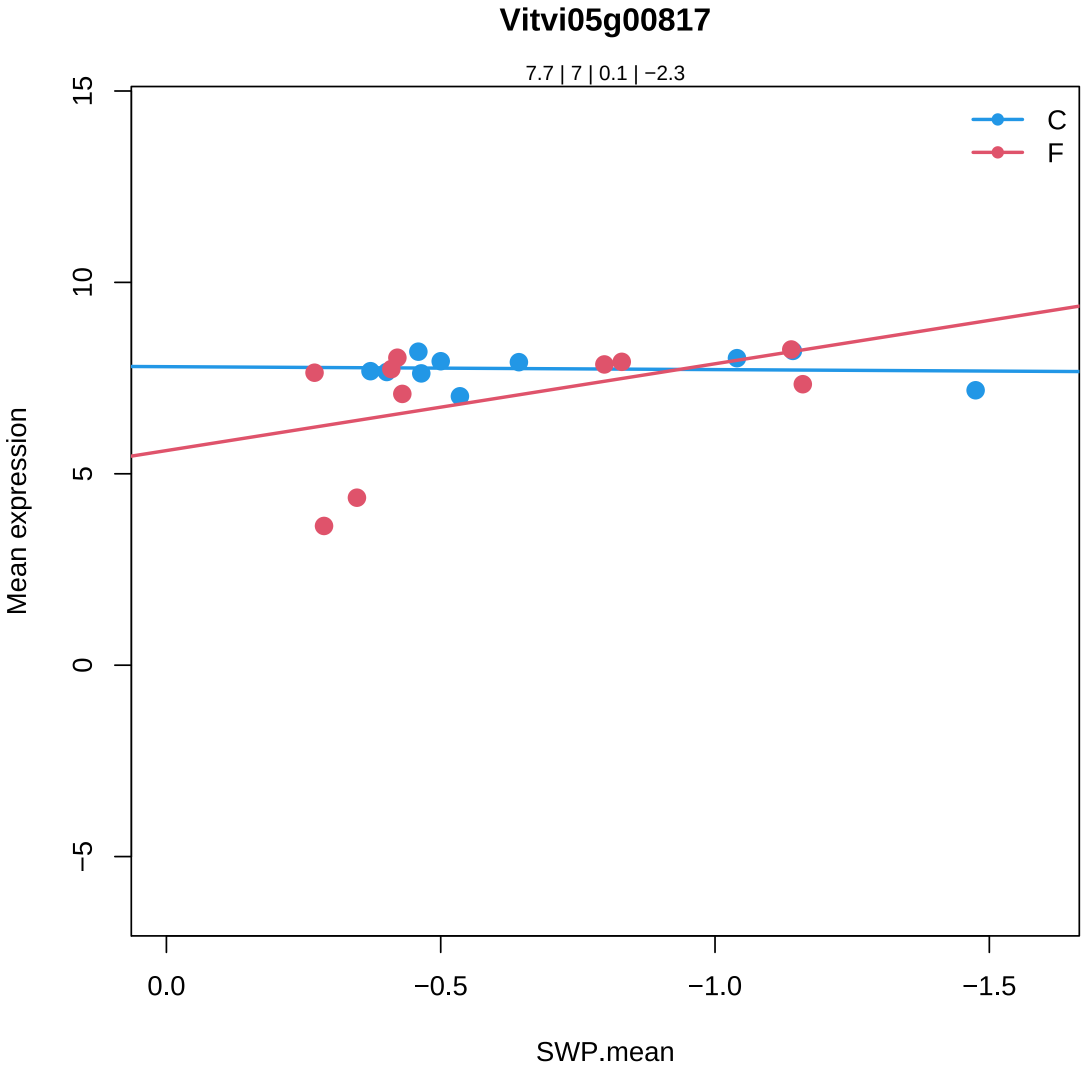
7.6.60 Vitvi05g00817: type5

```
> 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
```



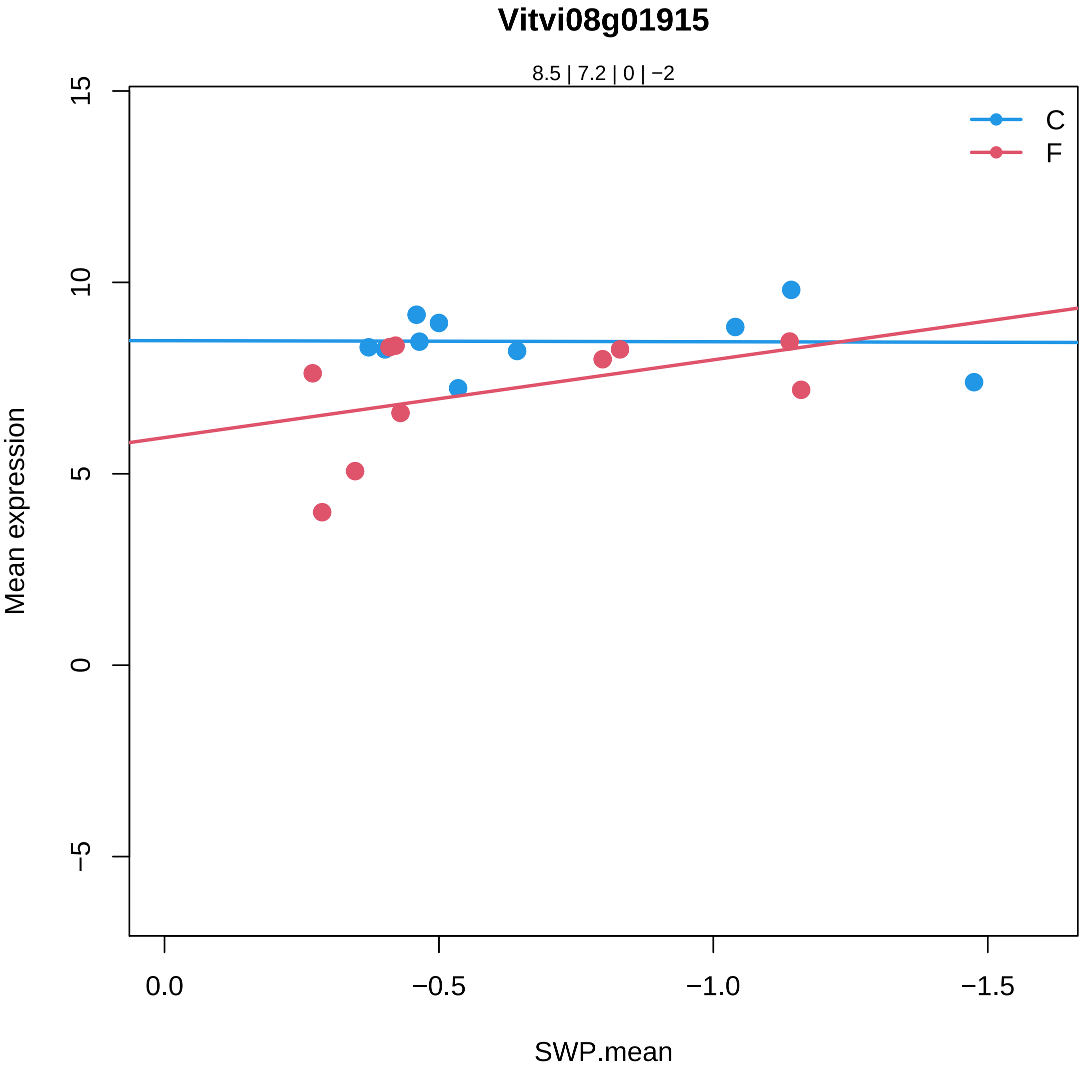
7.6.61 Vitvi08g01915: type5

```
> 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
```



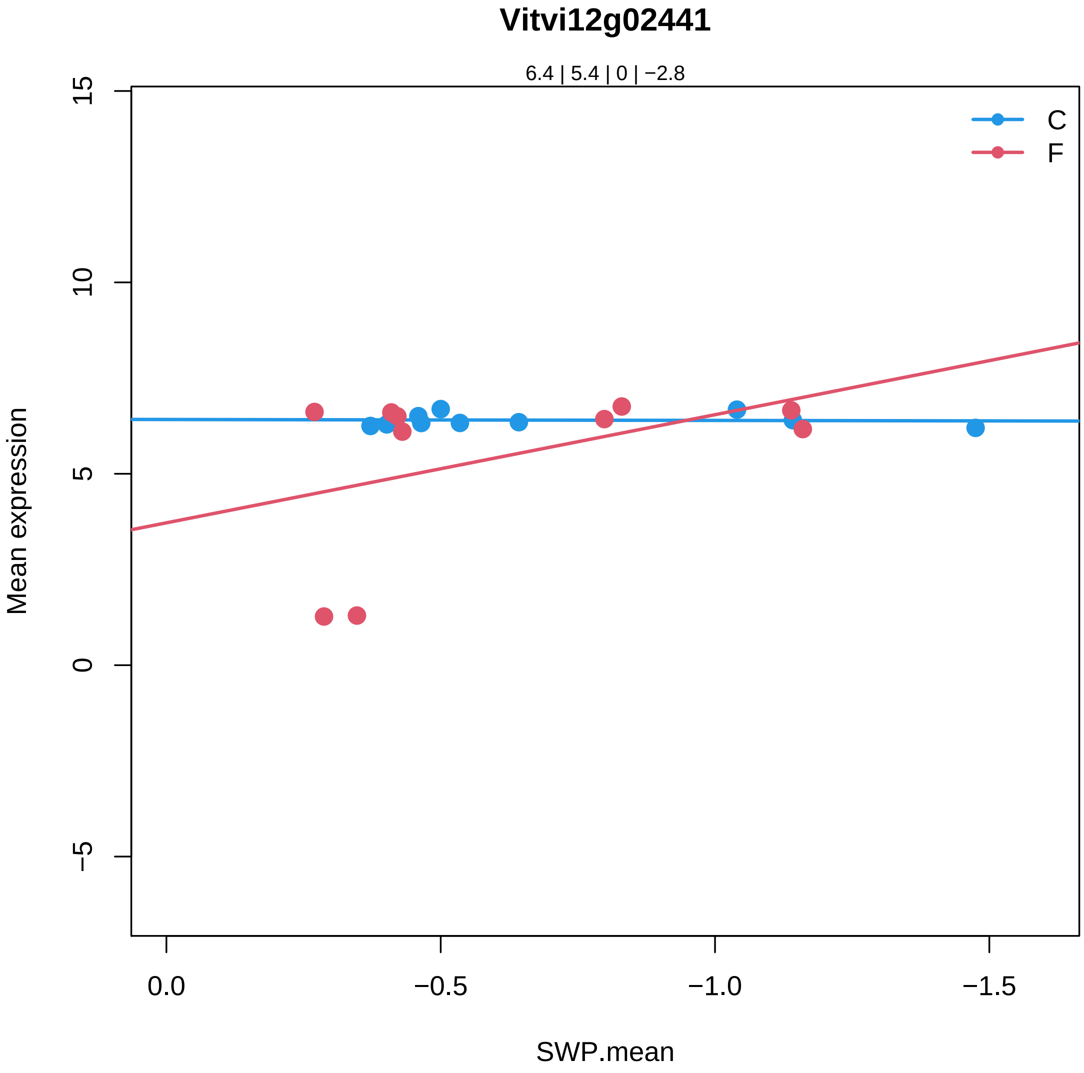
7.6.62 Vitvi12g02441: type5

```
> 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
```



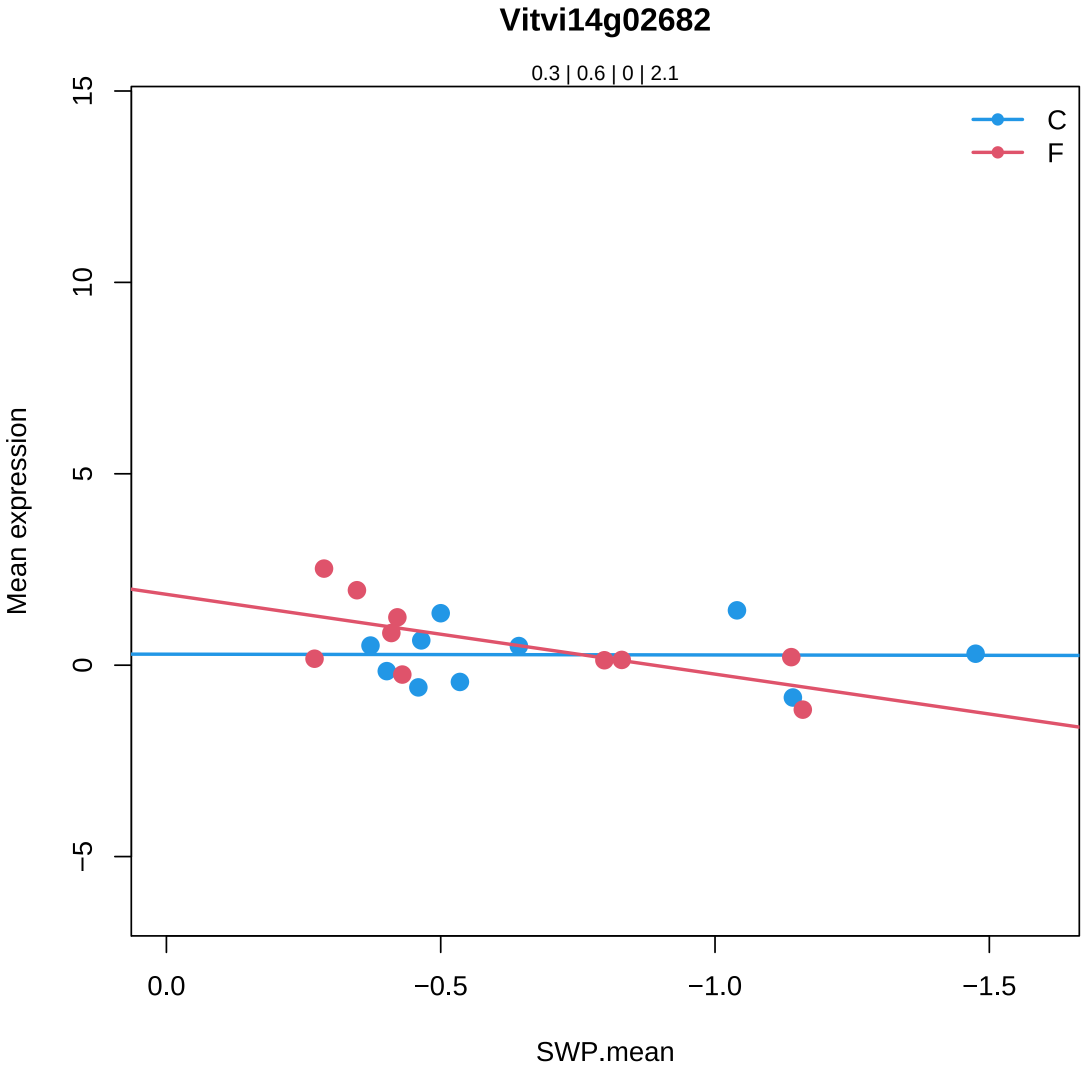
7.6.63 Vitvi14g02682: type5

```
> 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
```



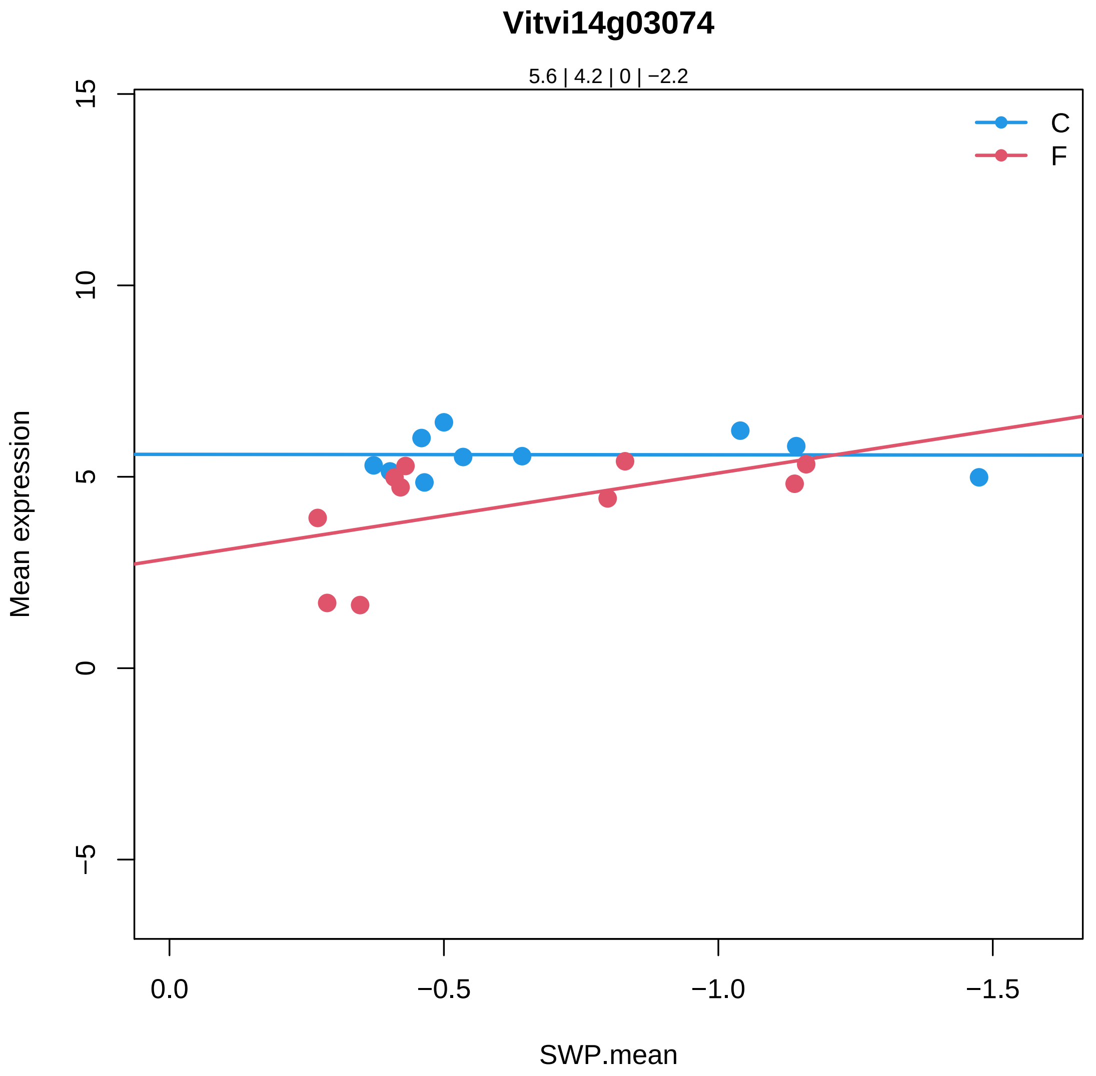
7.6.64 Vitvi14g03074: type5

```
> 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
```



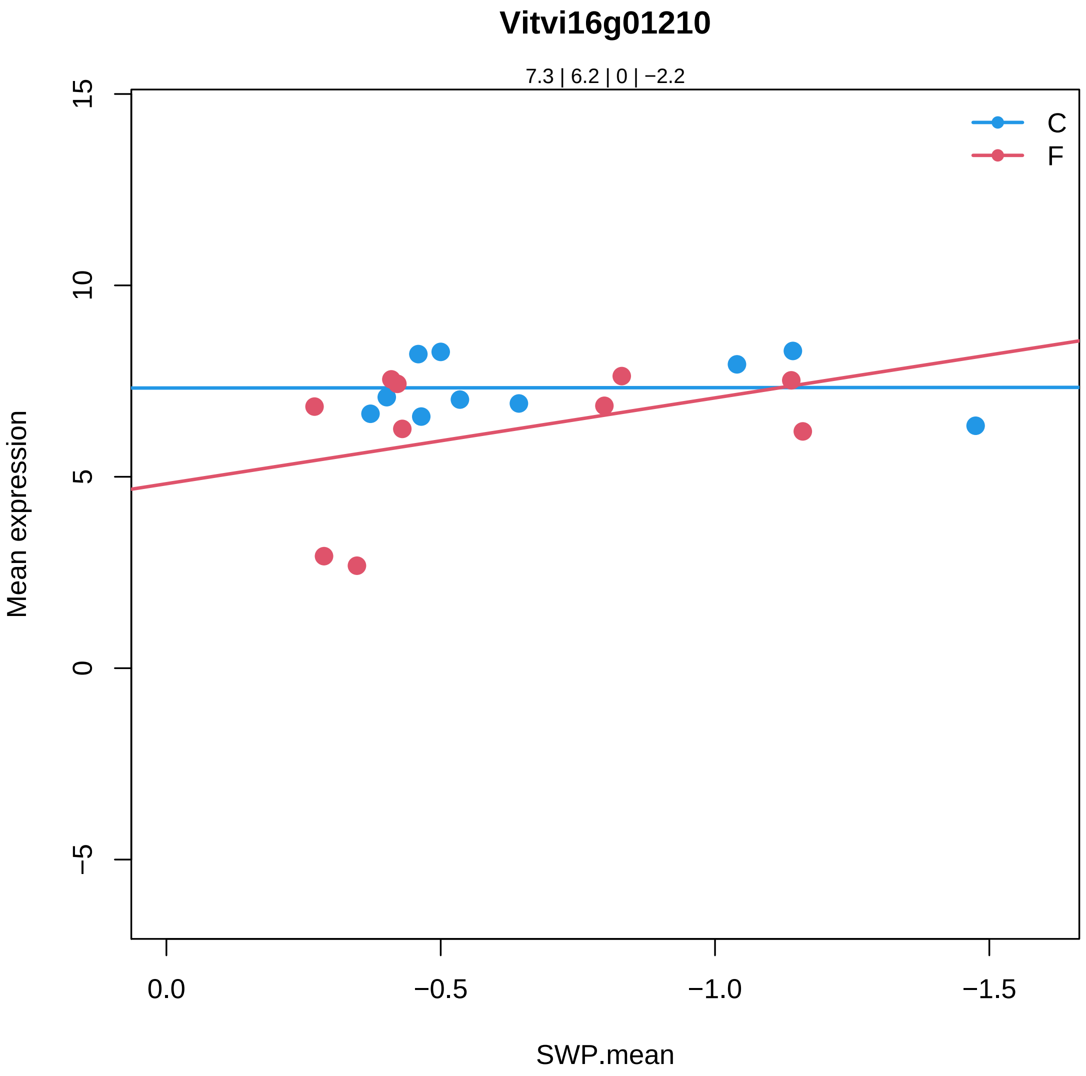
7.6.65 Vitvi16g01210: type5

```
> 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
```



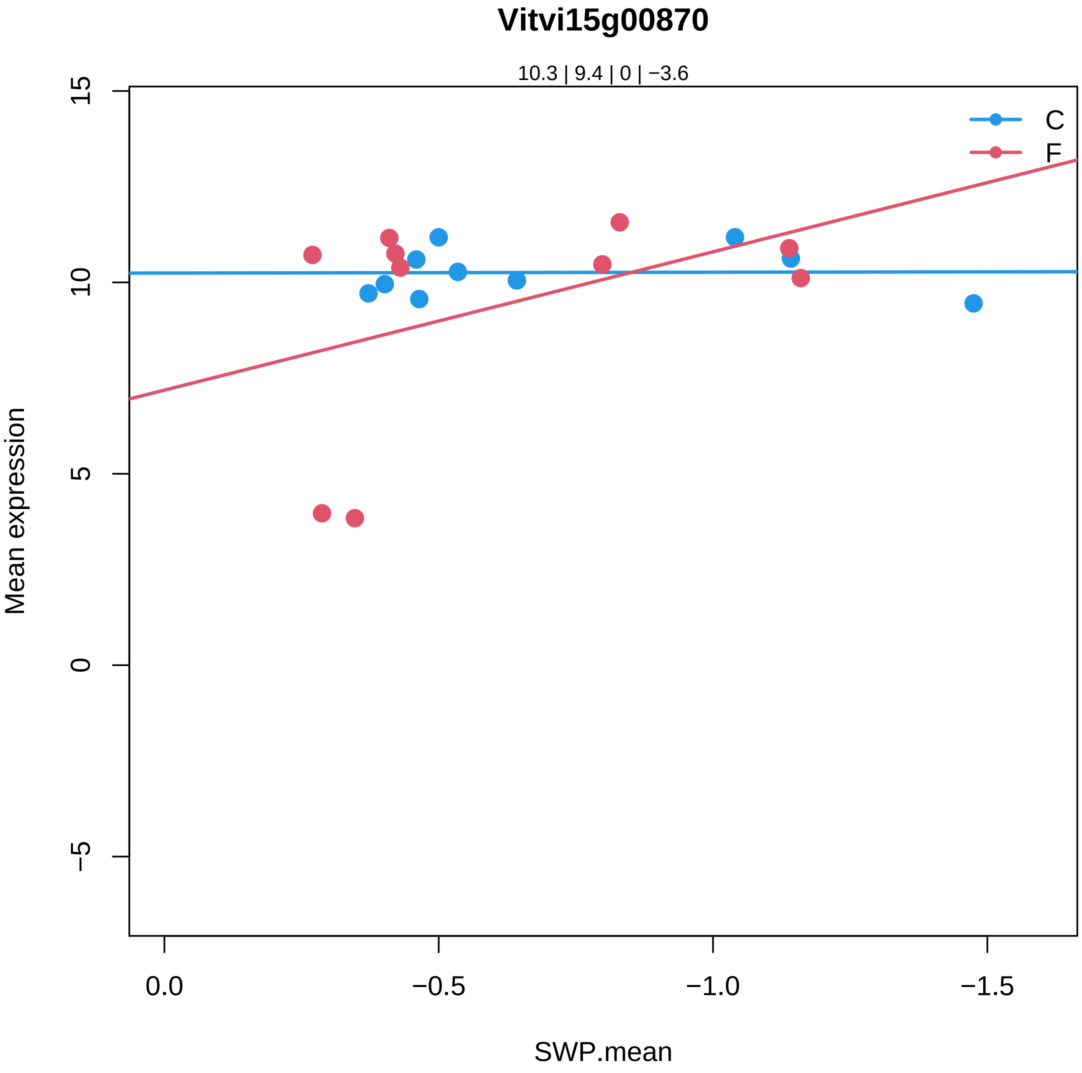
7.6.66 Vitvi15g00870: type5

```
> 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
```



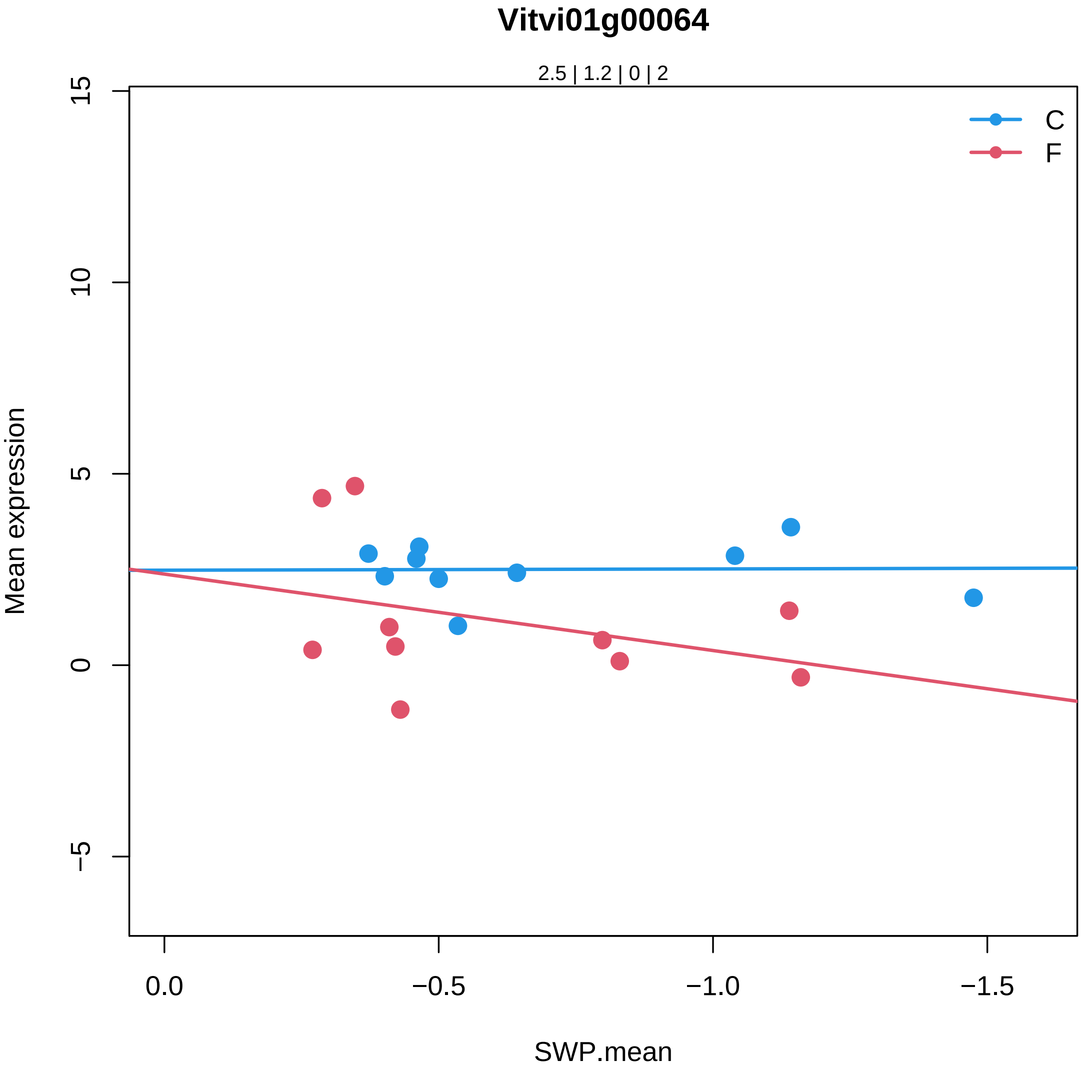
7.6.67 Vitvi01g00064: type5

```
> 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
```



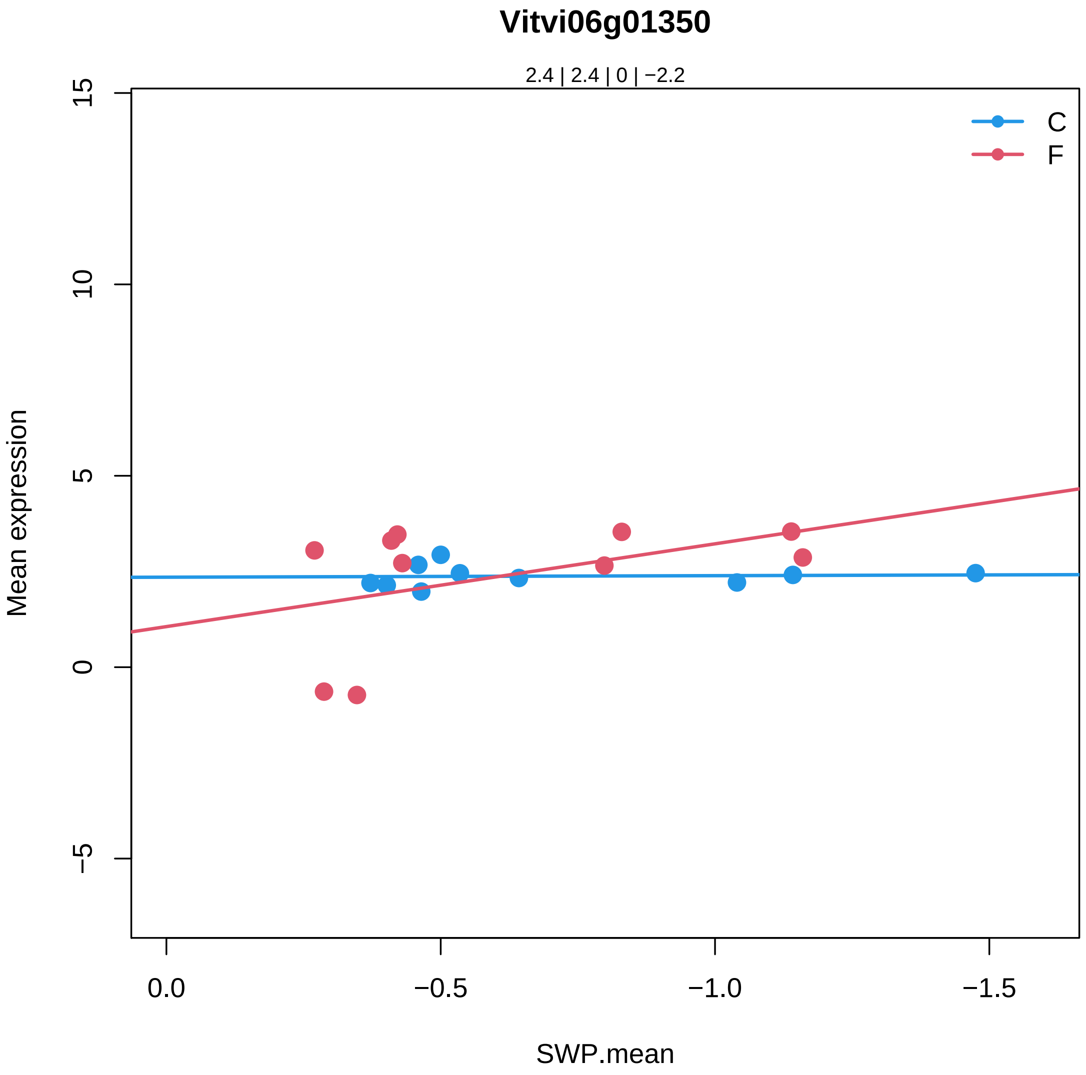
7.6.68 Vitvi06g01350: type5

```
> 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
```



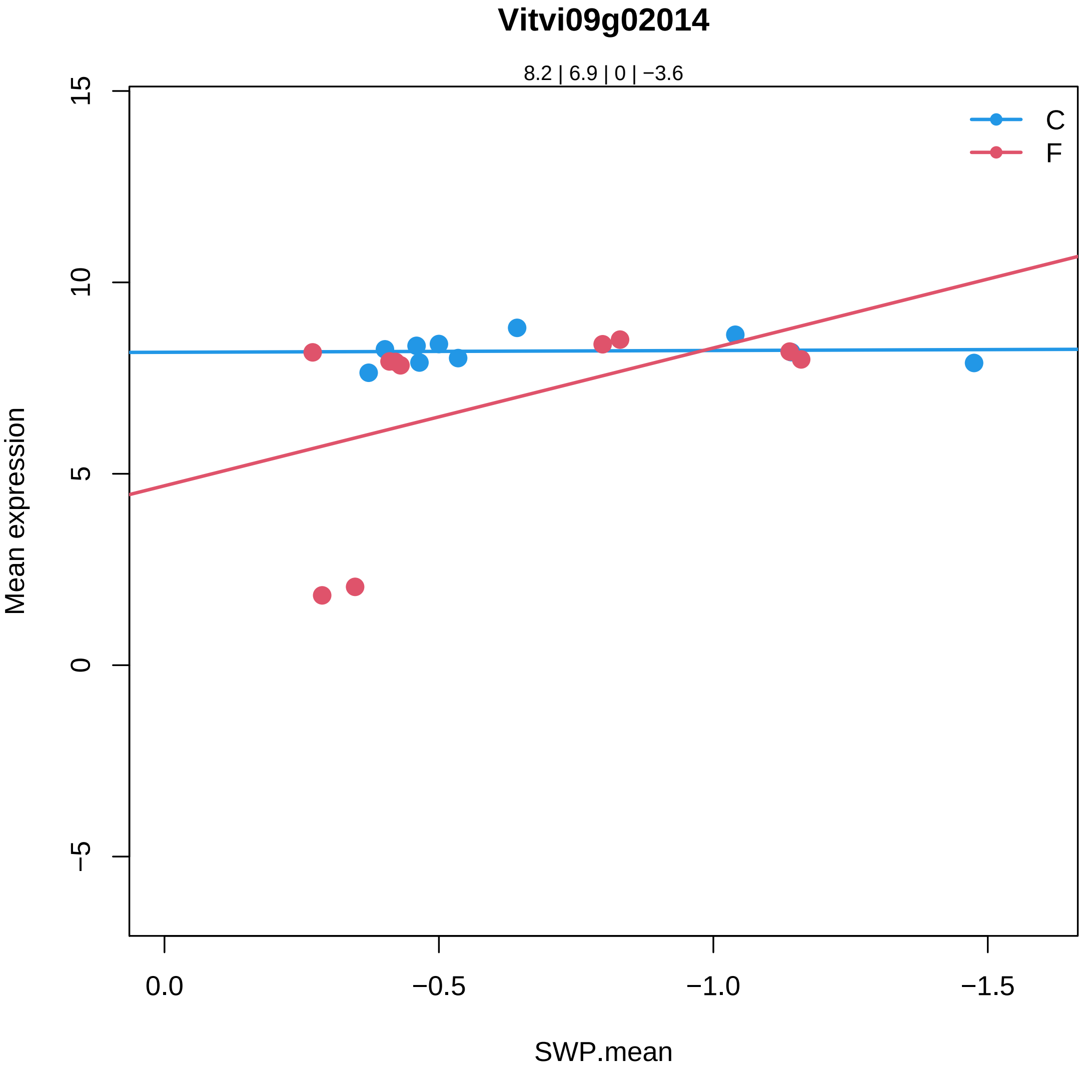
7.6.69 Vitvi09g02014: type5

```
> 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
```



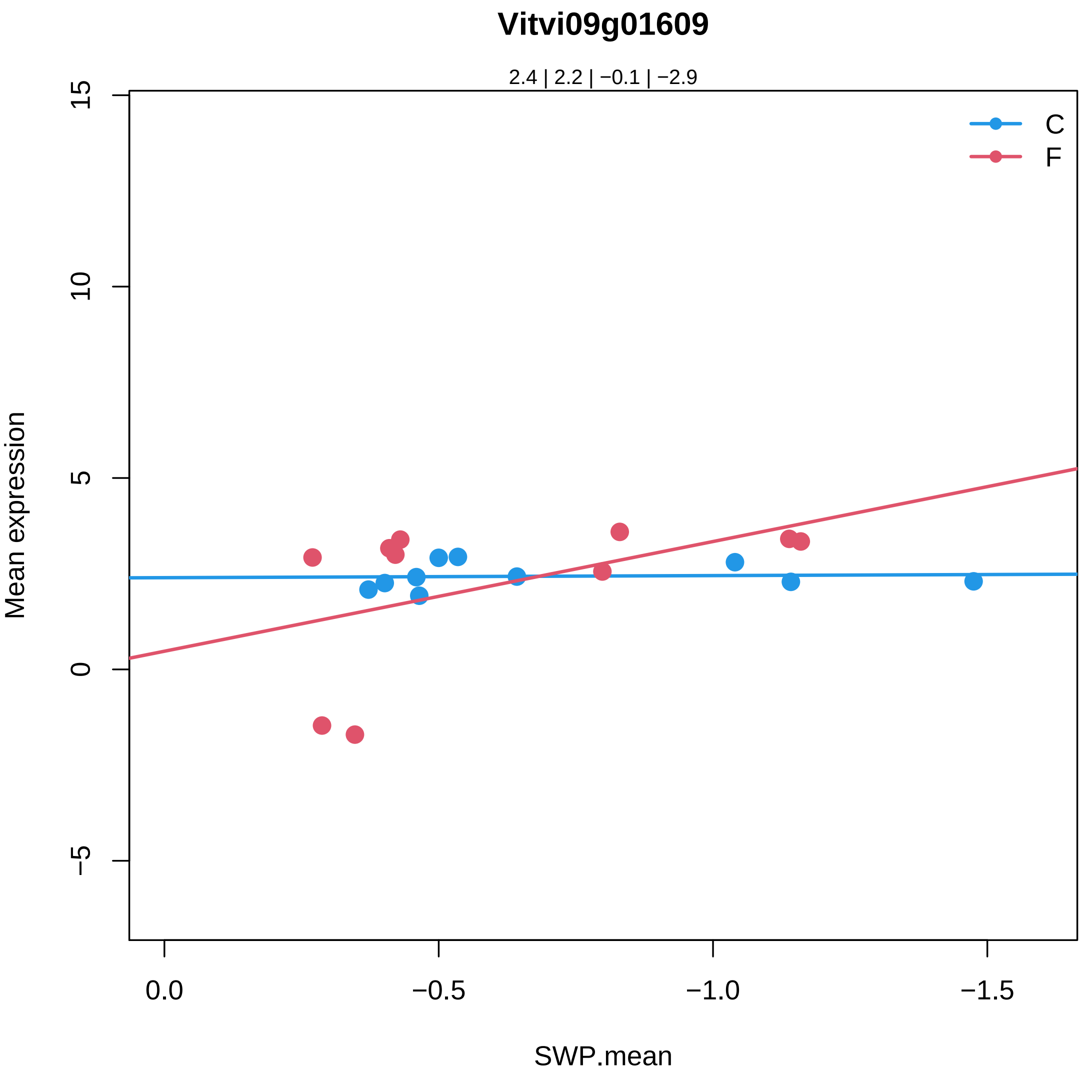
7.6.70 Vitvi09g01609: type5

```
> 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
```



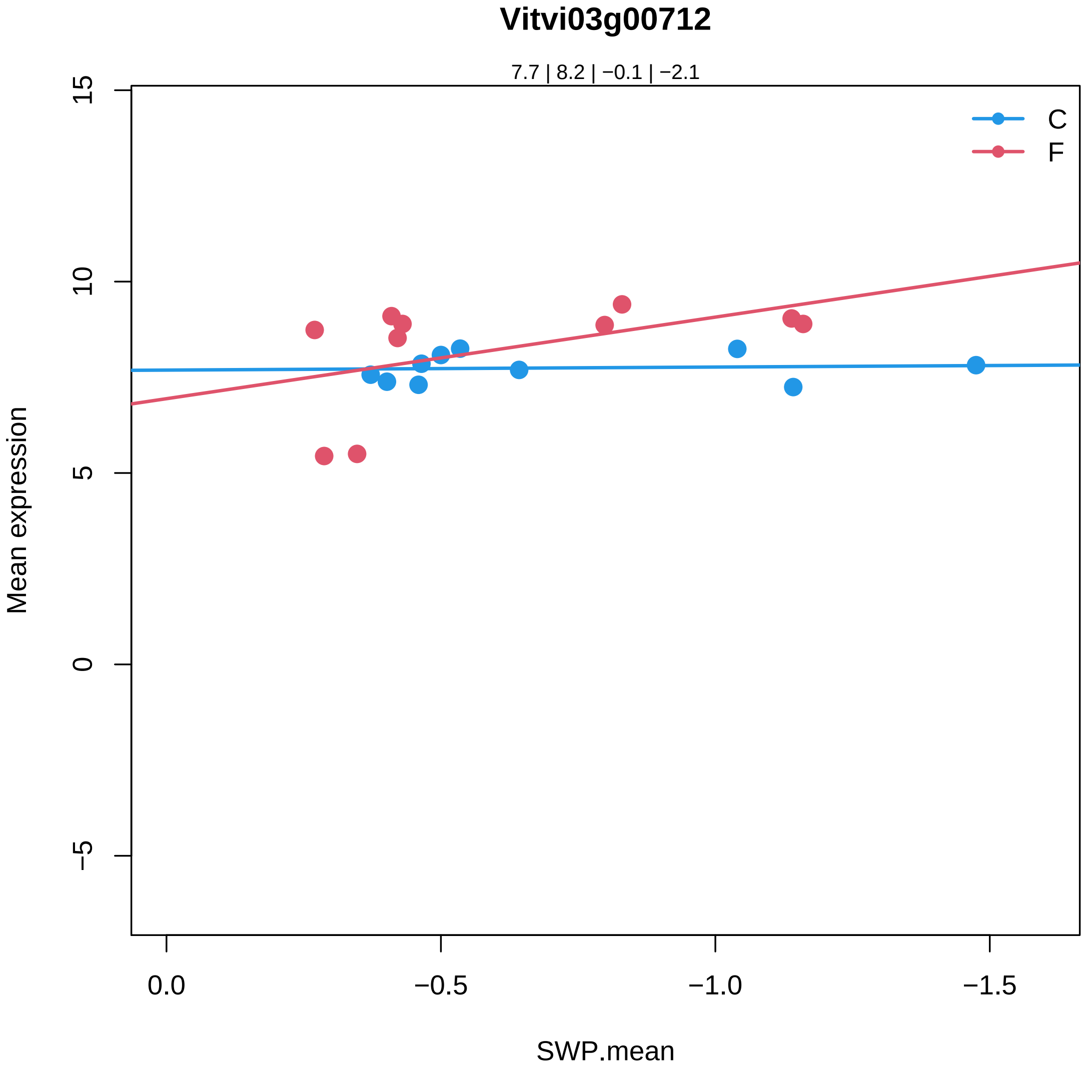
7.6.71 Vitvi03g00712: type5

```
> 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
```



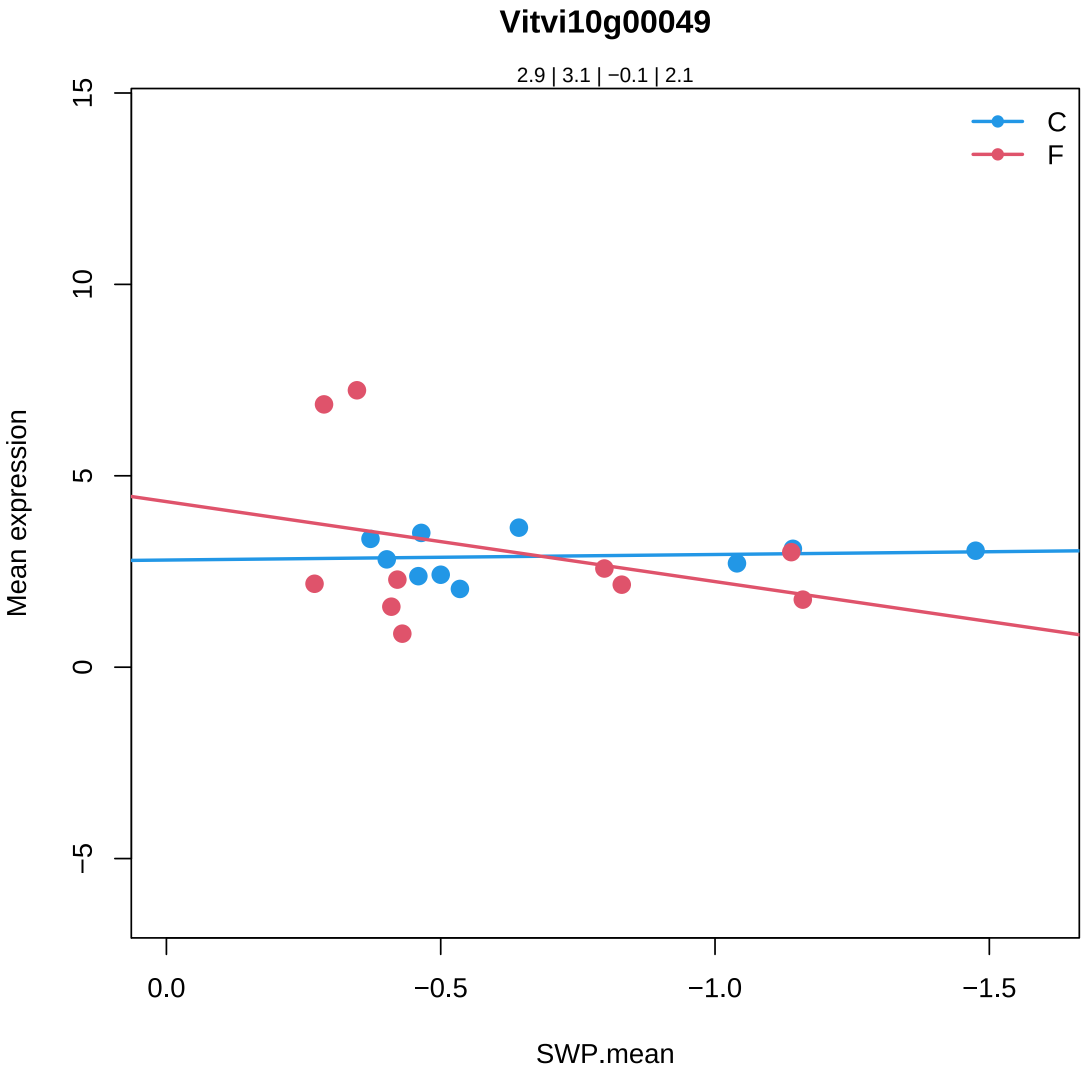
7.6.72 Vitvi10g00049: type5

```
> 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
```



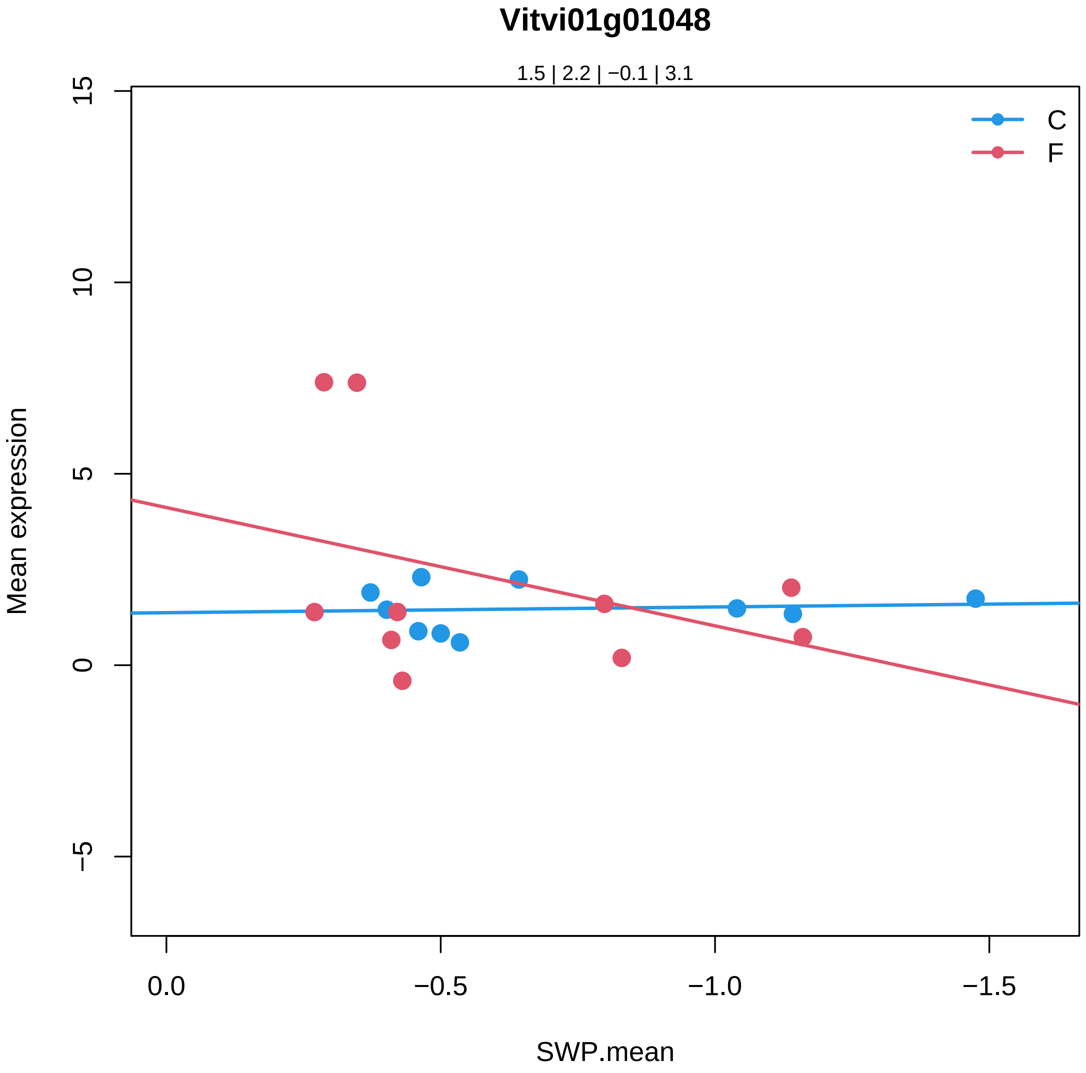
7.6.73 Vitvi01g01048: type5

```
> 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
```



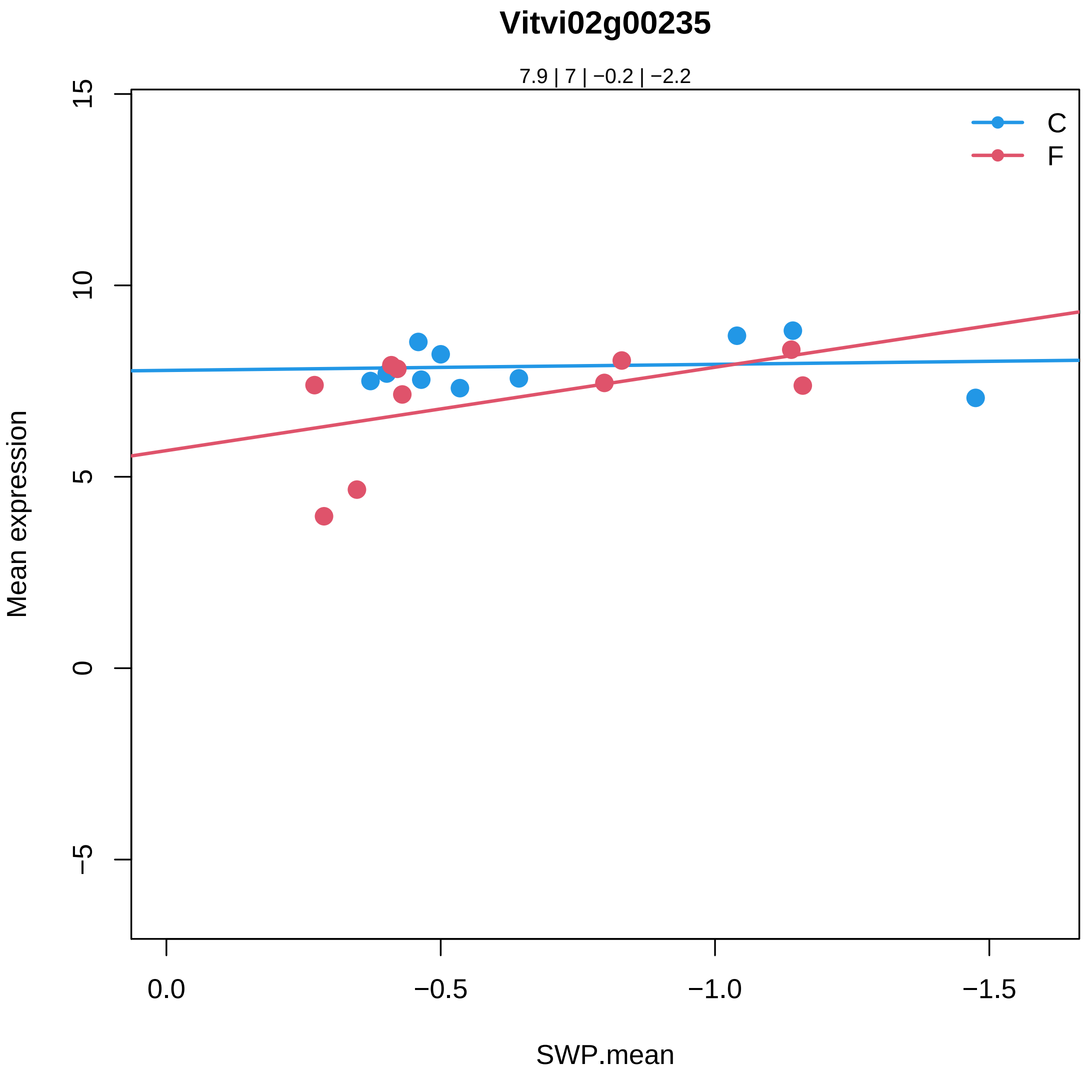
7.6.74 Vitvi02g00235: type5

```
> 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
```



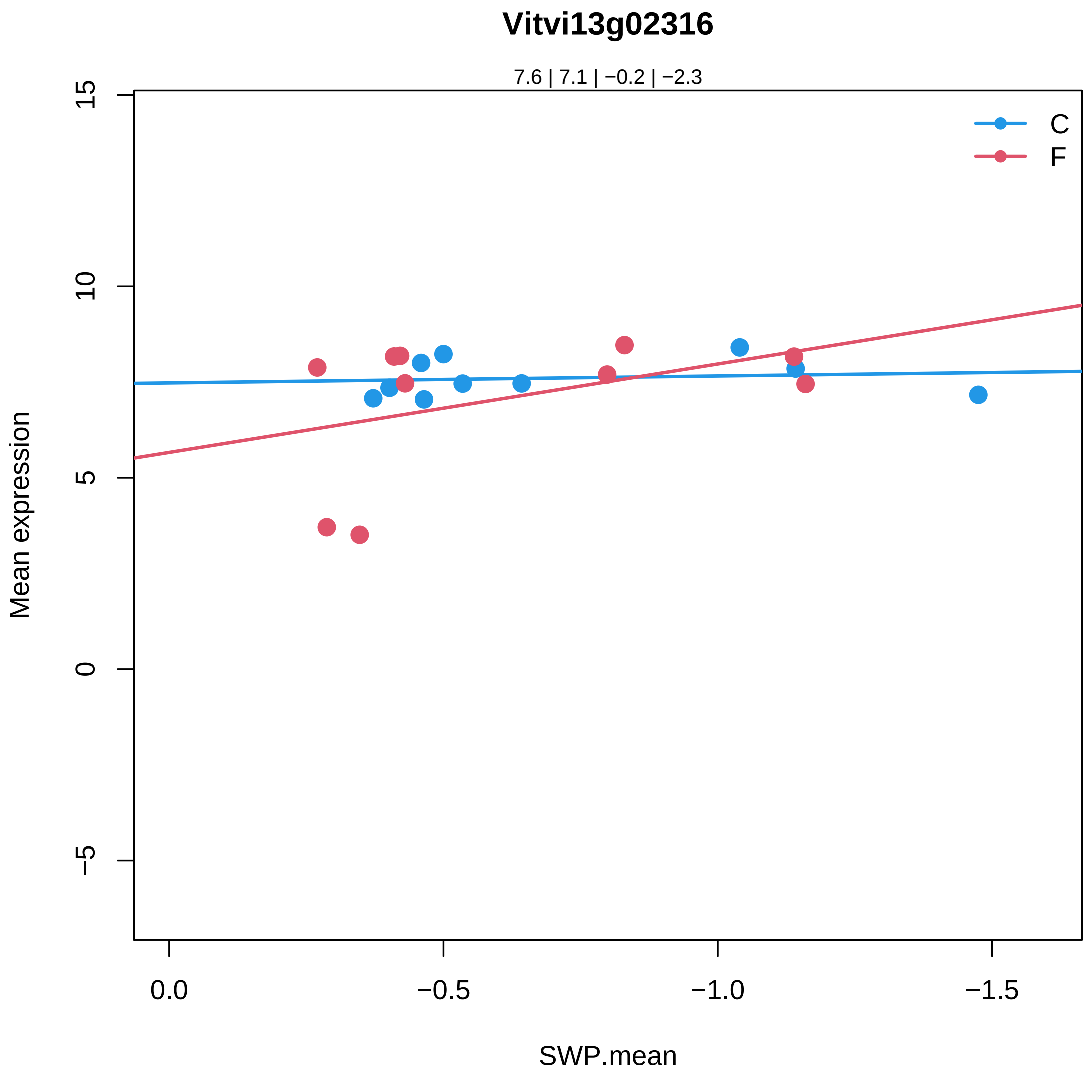
7.6.75 Vitvi13g02316: type5

```
> 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
```



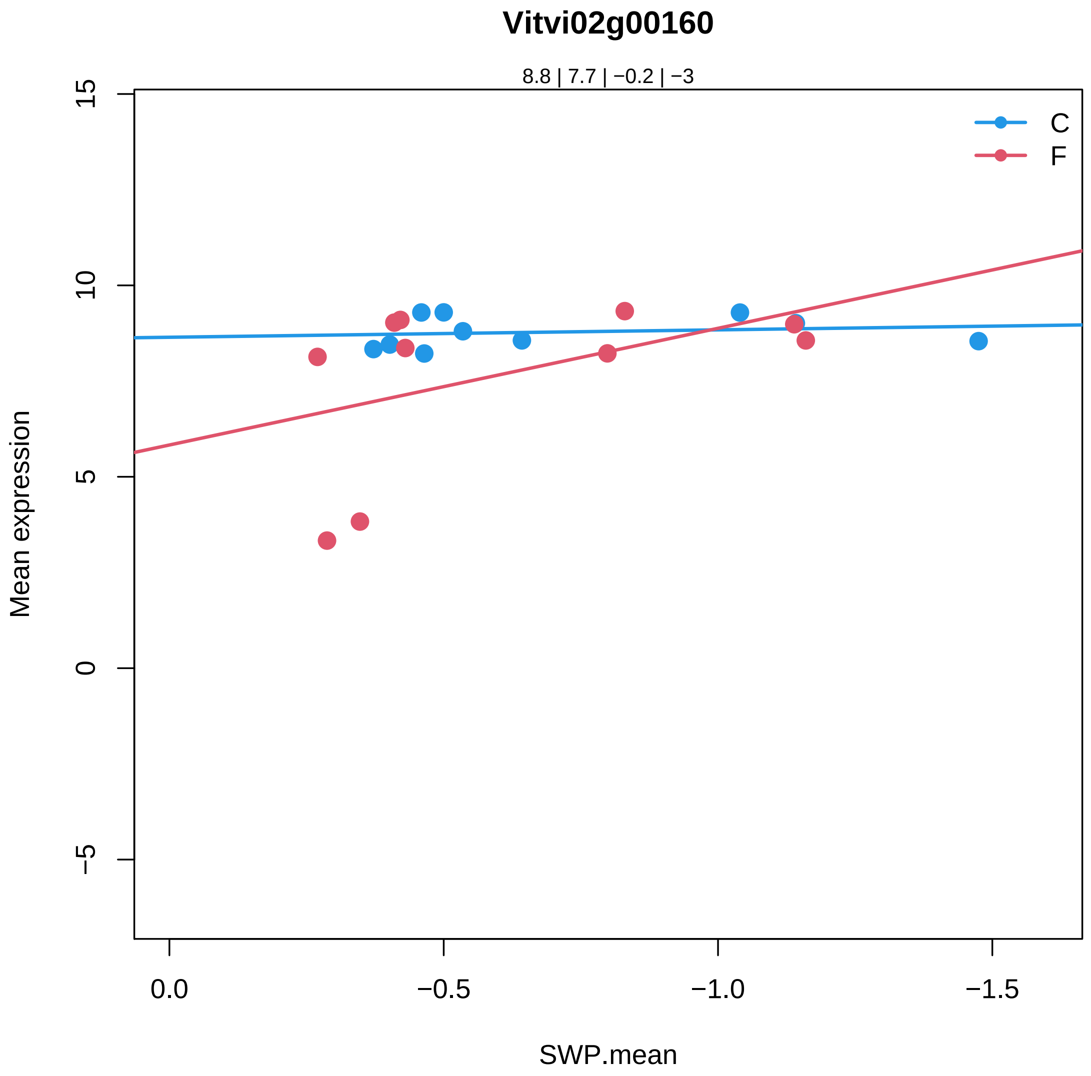
7.6.76 Vitvi02g00160: type5

```
> 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
```



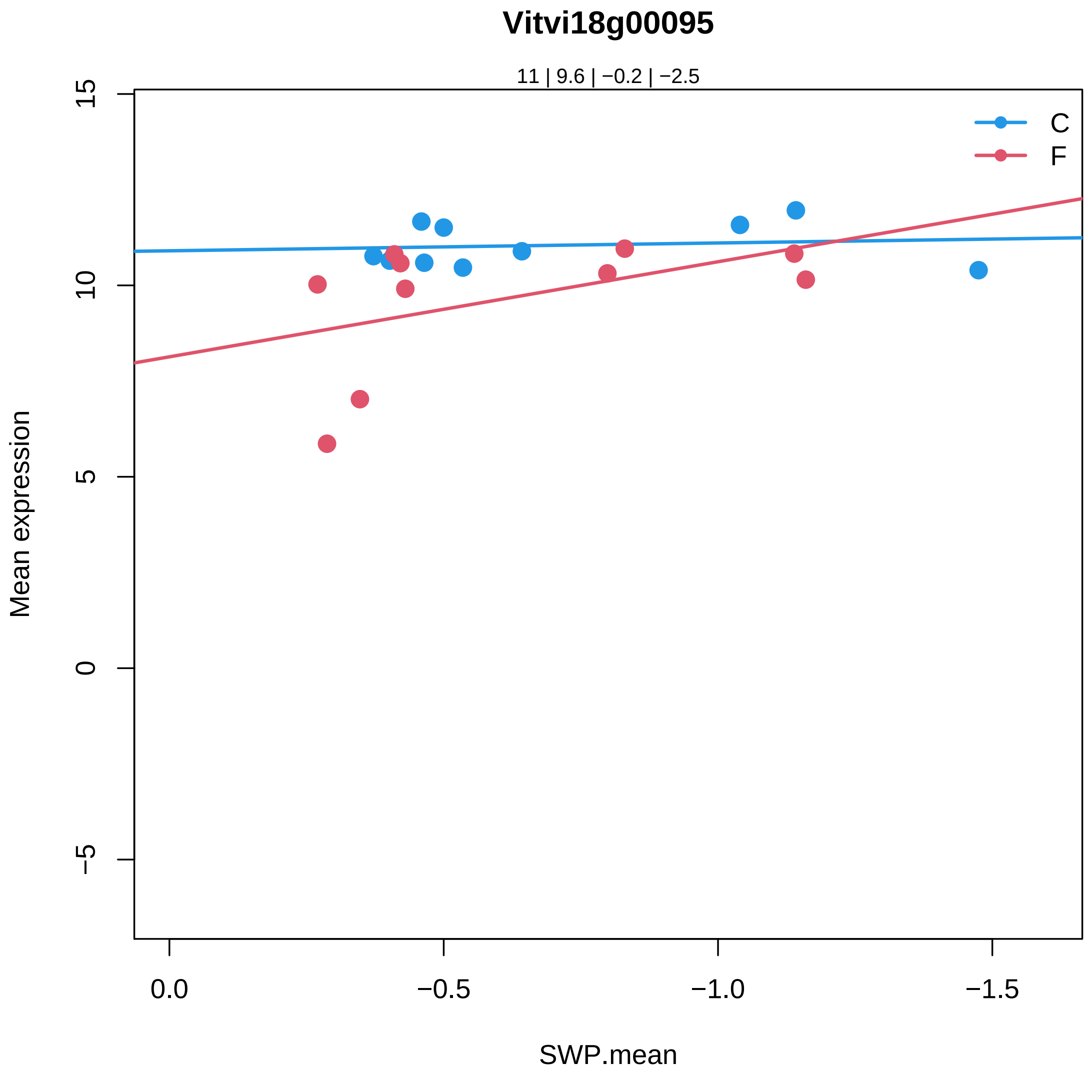
7.6.77 Vitvi18g00095: type5

```
> 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
```



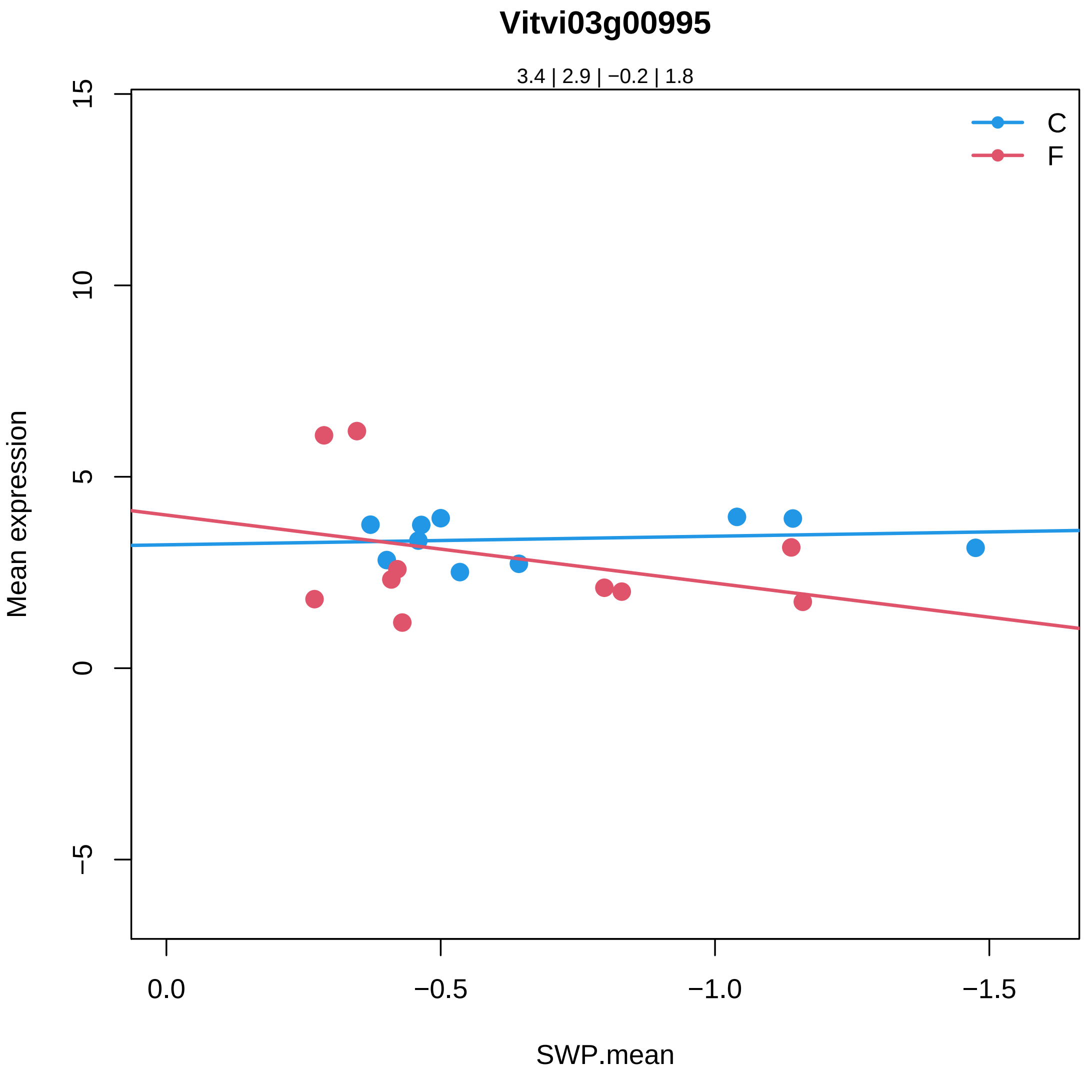
7.6.78 Vitvi03g00995: type5

```
> 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
```



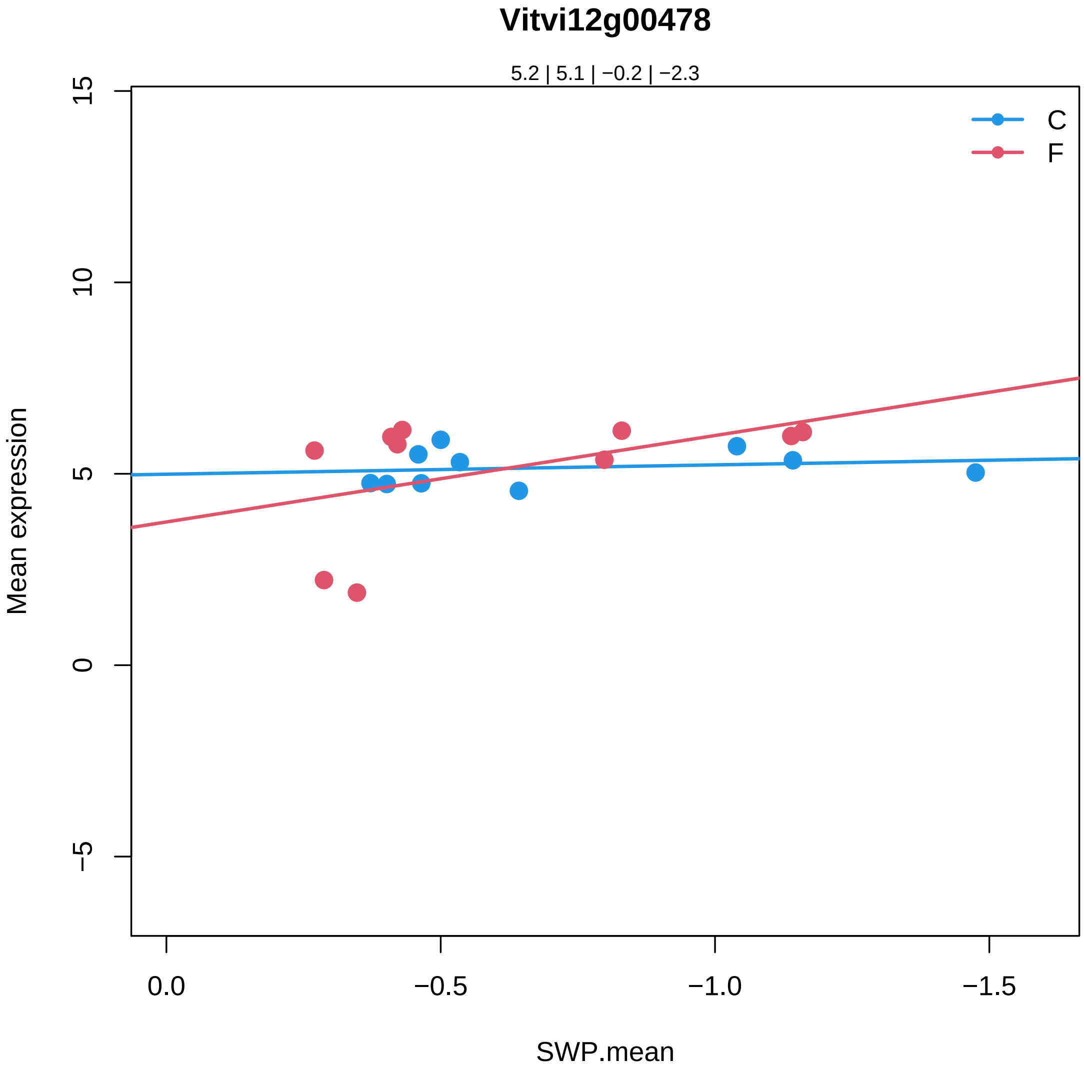
7.6.79 Vitvi12g00478: type5

```
> 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
```



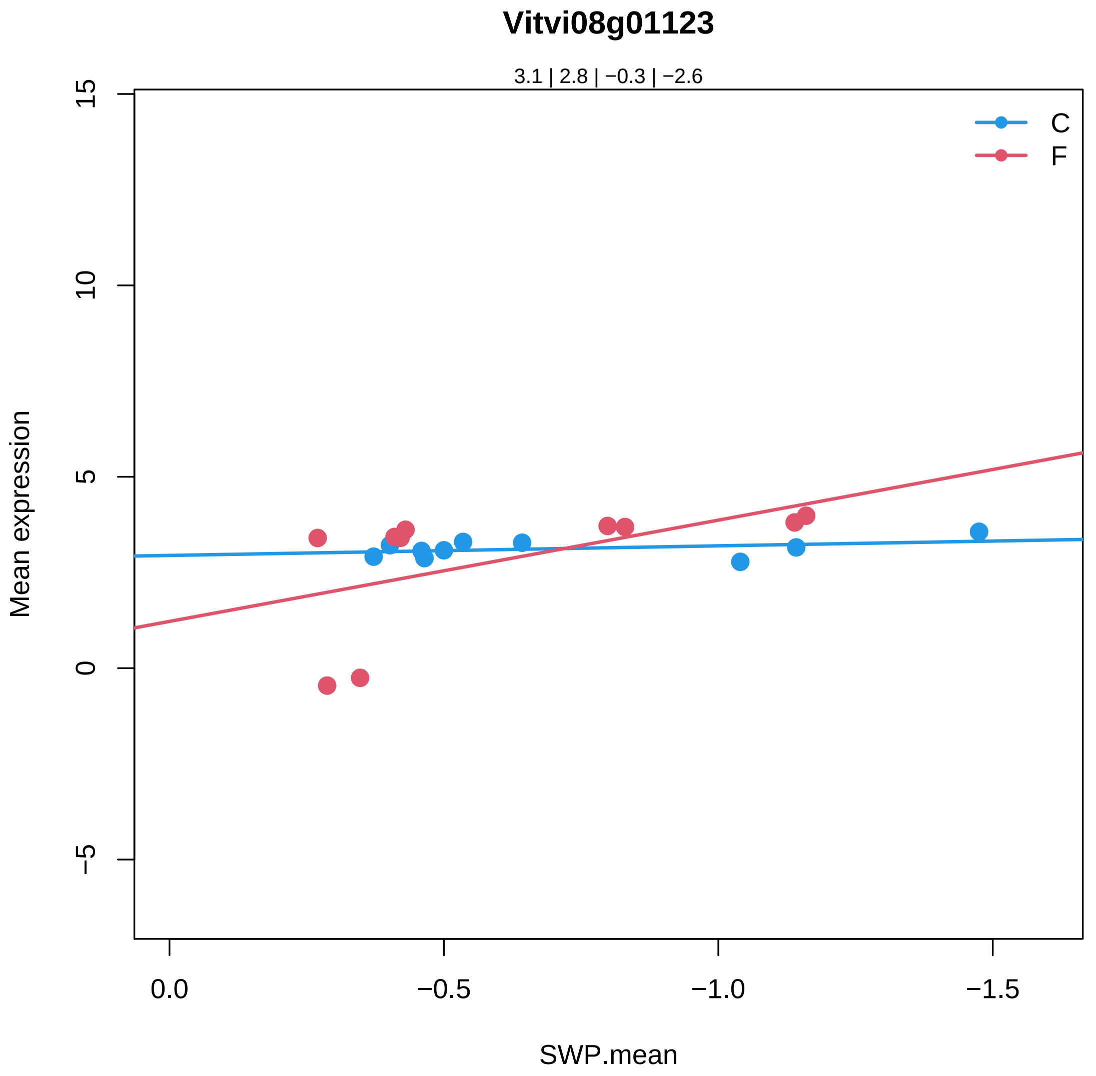
7.6.80 Vitvi08g01123: type5

```
> 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
```



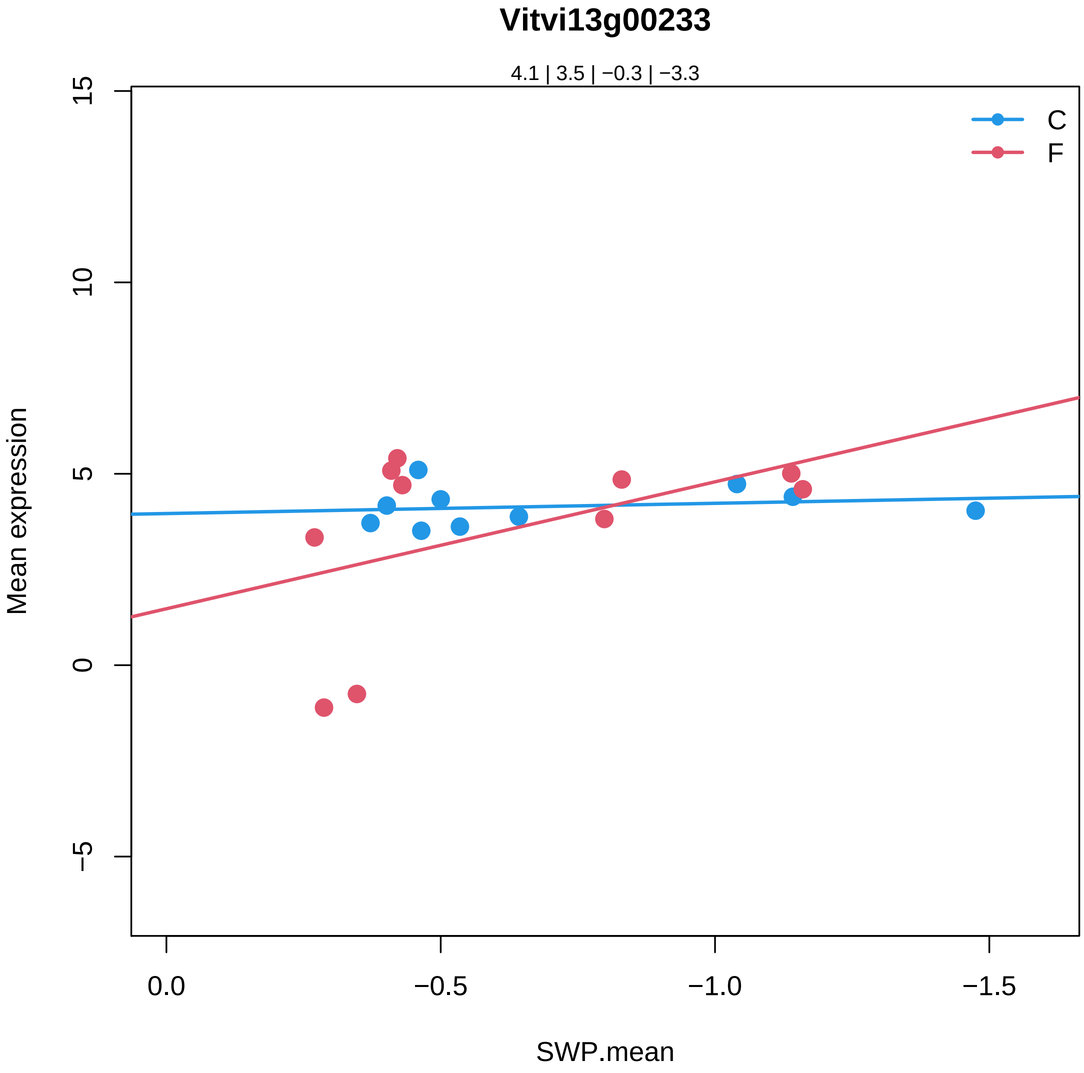
7.6.81 Vitvi13g00233: type5

```
> 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
```



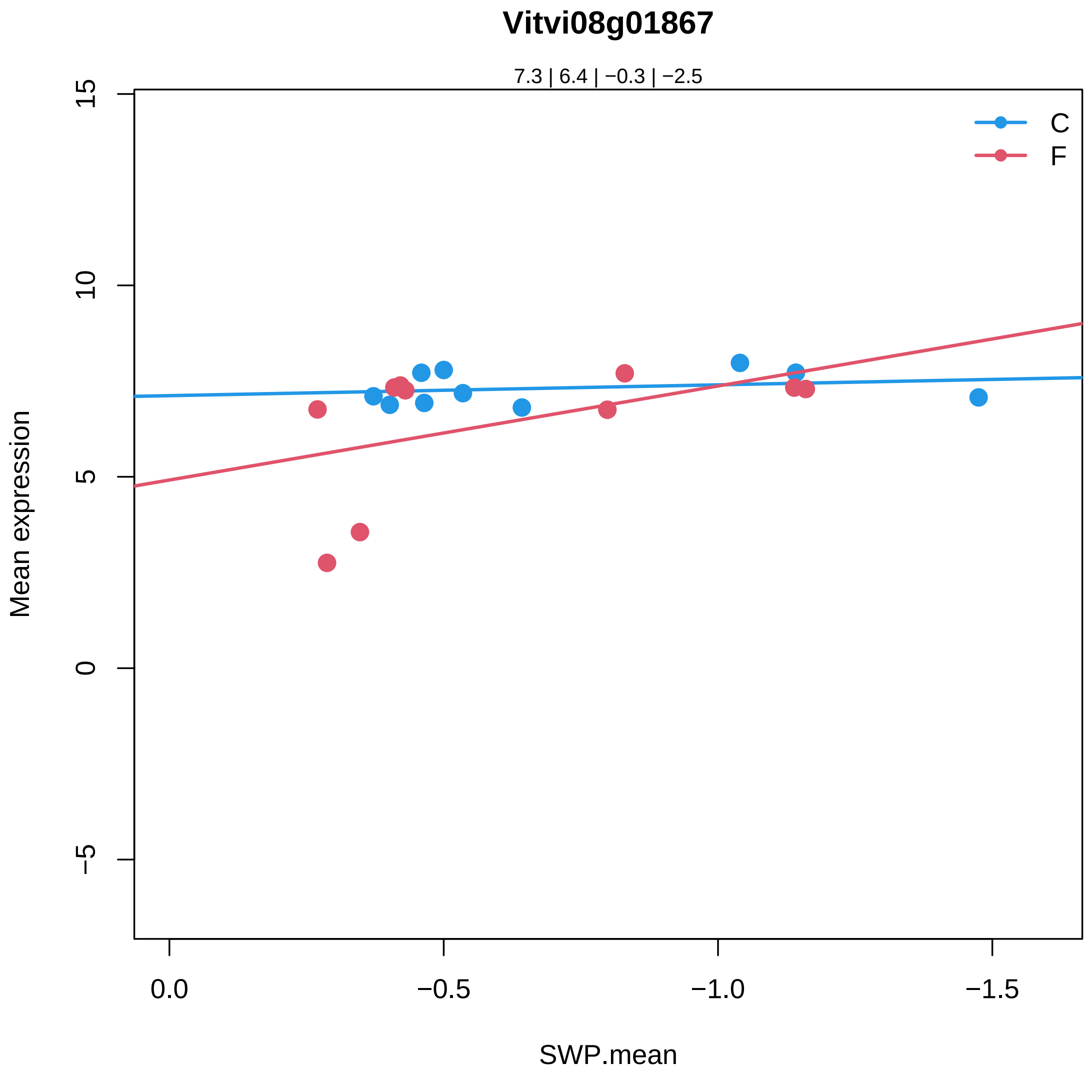
7.6.82 Vitvi08g01867: type5

```
> 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
```



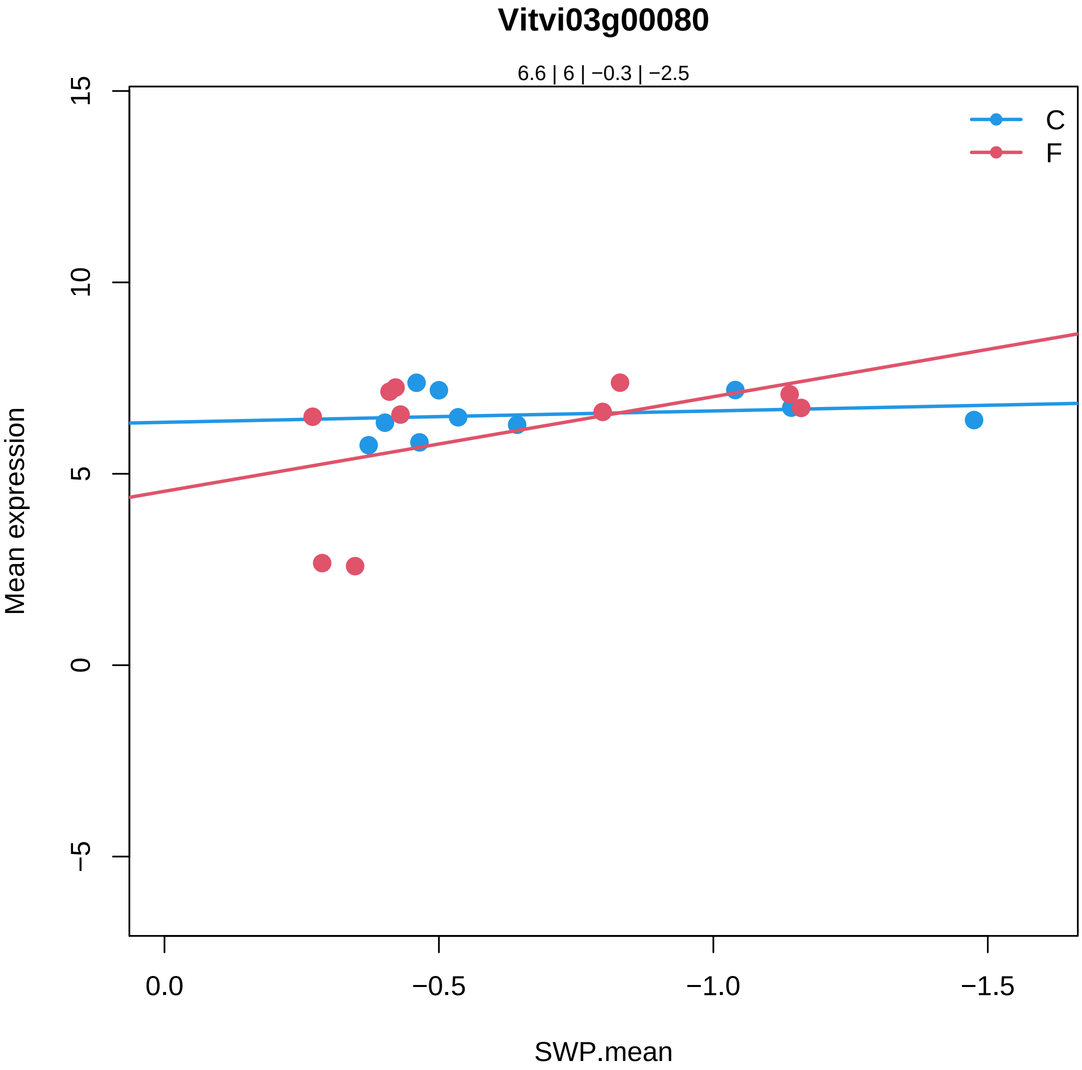
7.6.83 Vitvi03g00080: type5

```
> 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
```



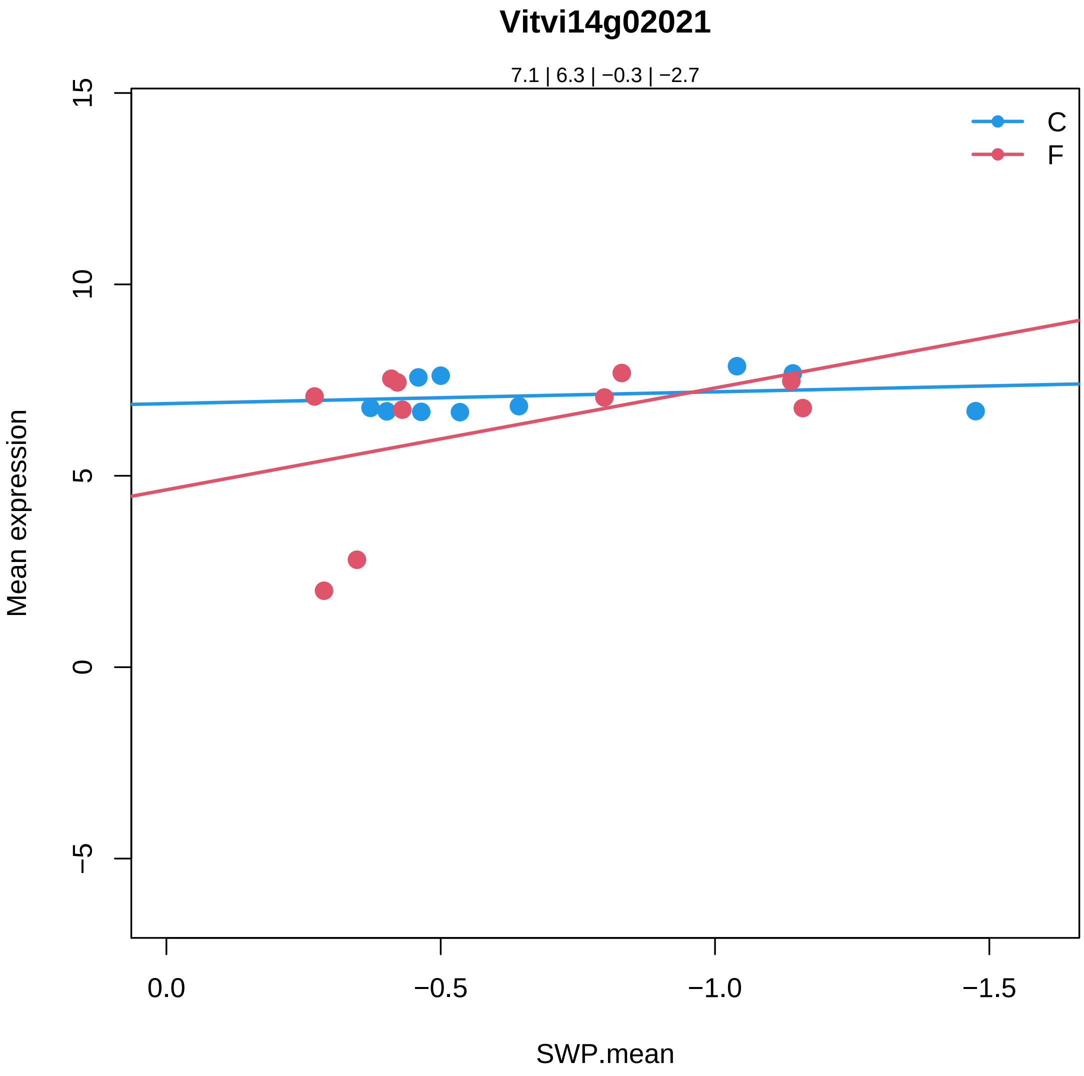
7.6.84 Vitvi14g02021: type5

```
> 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
```



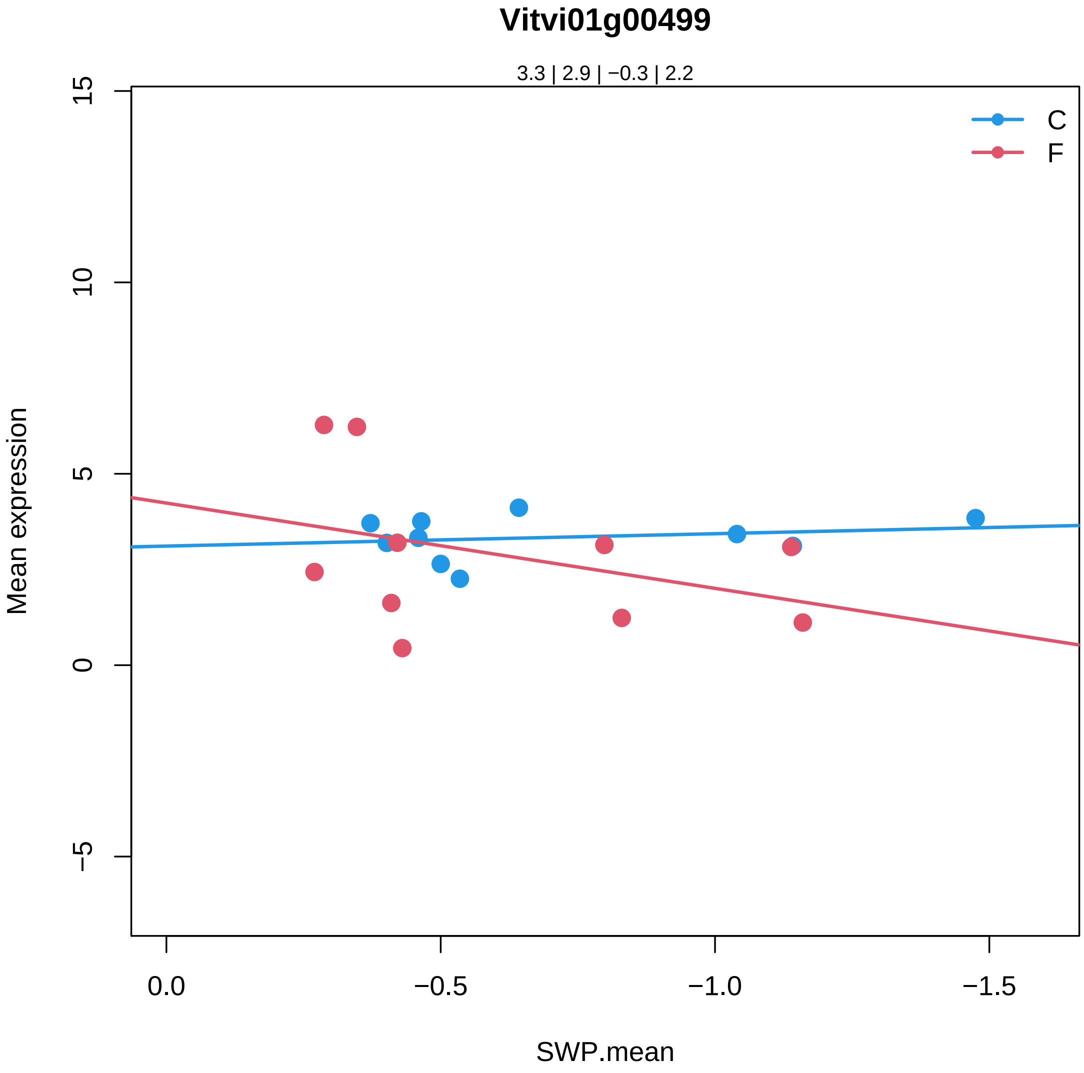
7.6.85 Vitvi01g00499: type5

```
> 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
```



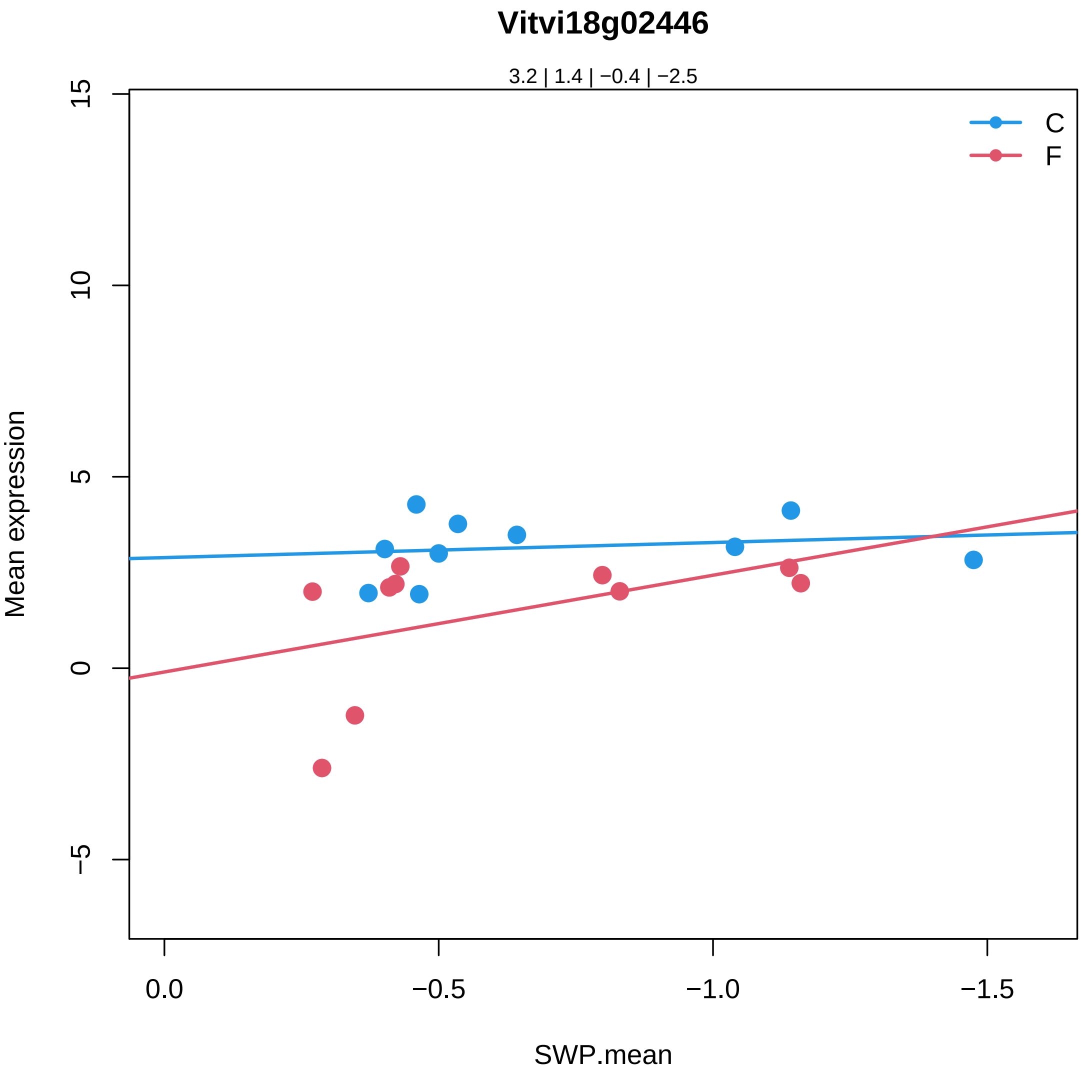
7.6.86 Vitvi18g02446: type5

```
> 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
```



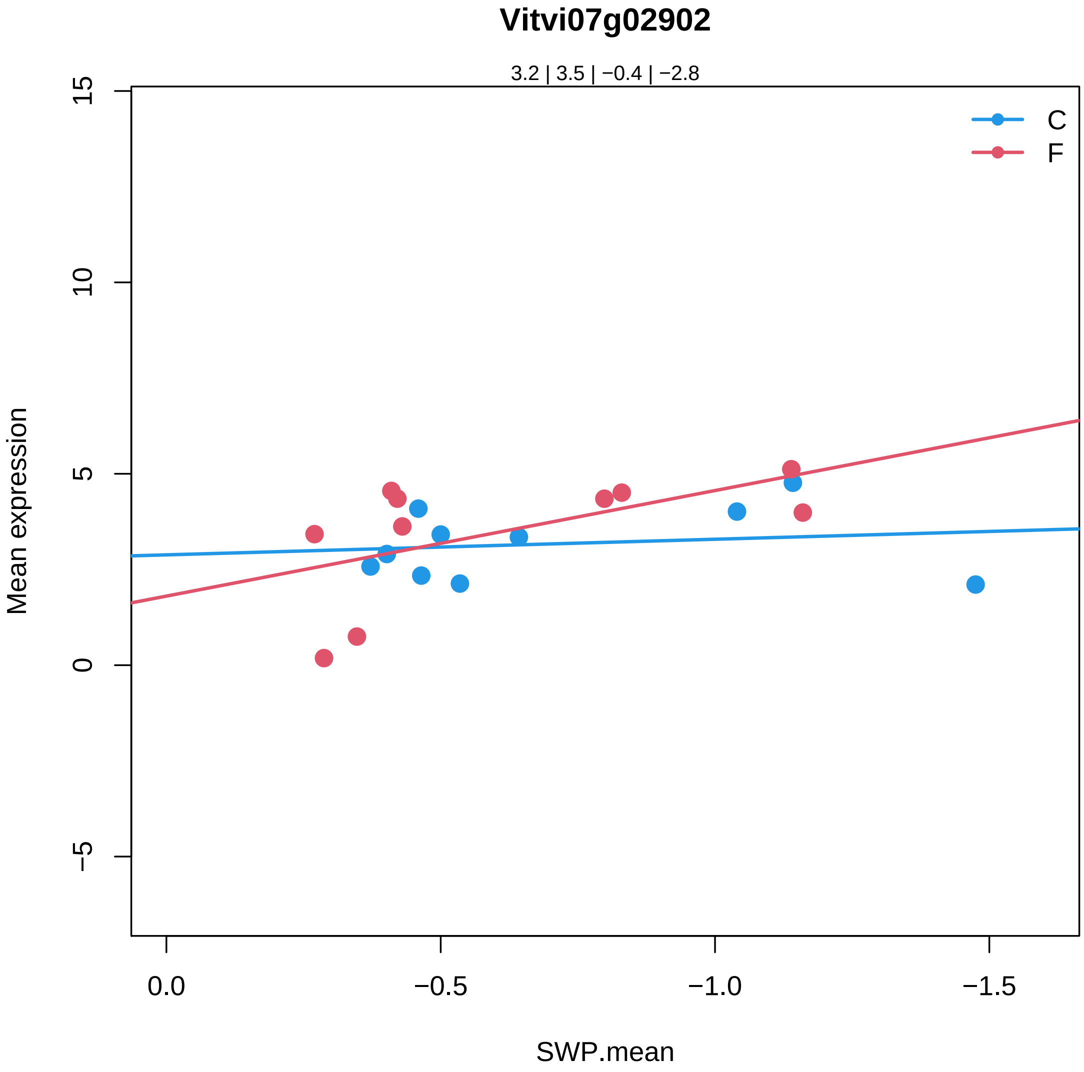
7.6.87 Vitvi07g02902: type5

```
> 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        
```



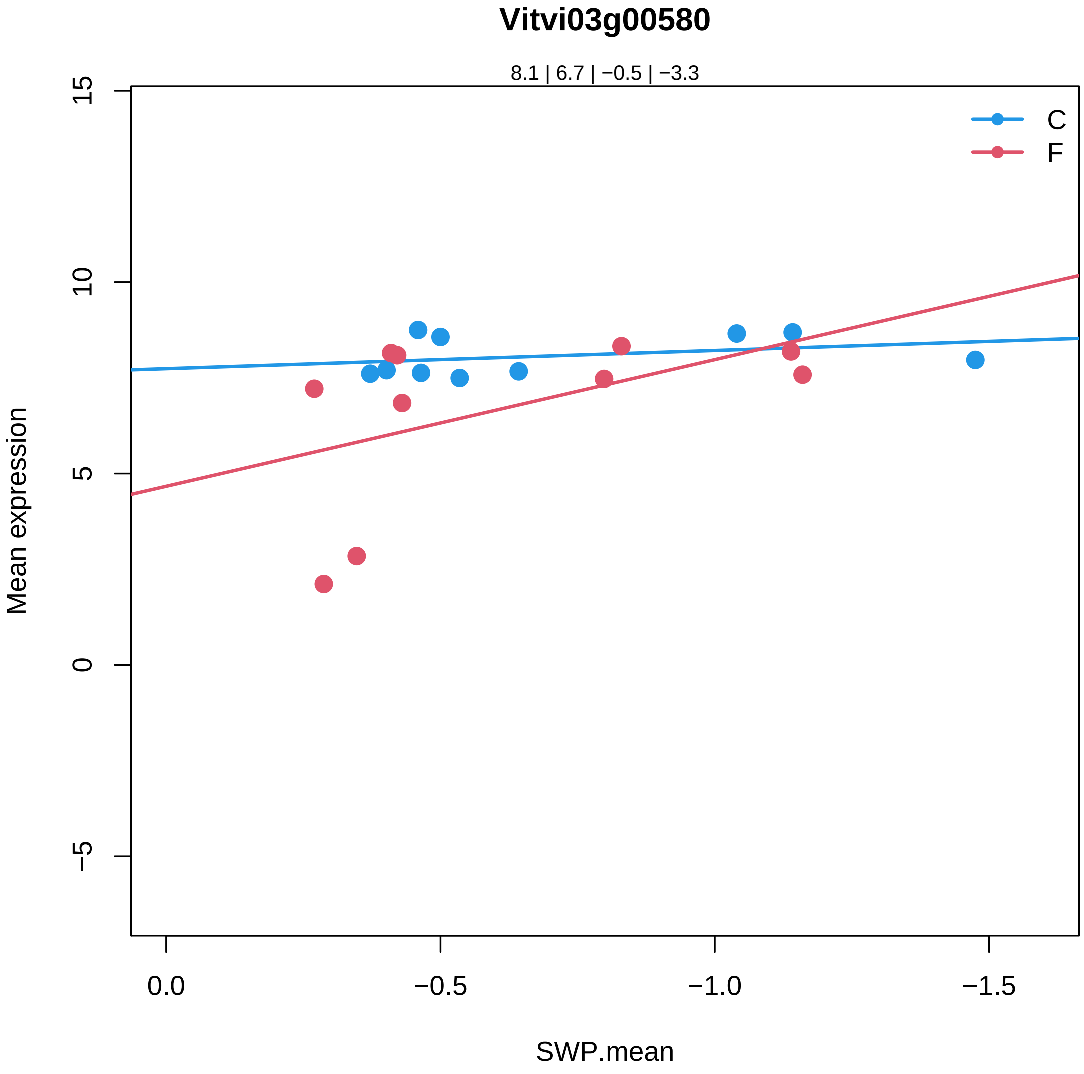
7.6.88 Vitvi03g00580: type5

```
> 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
```



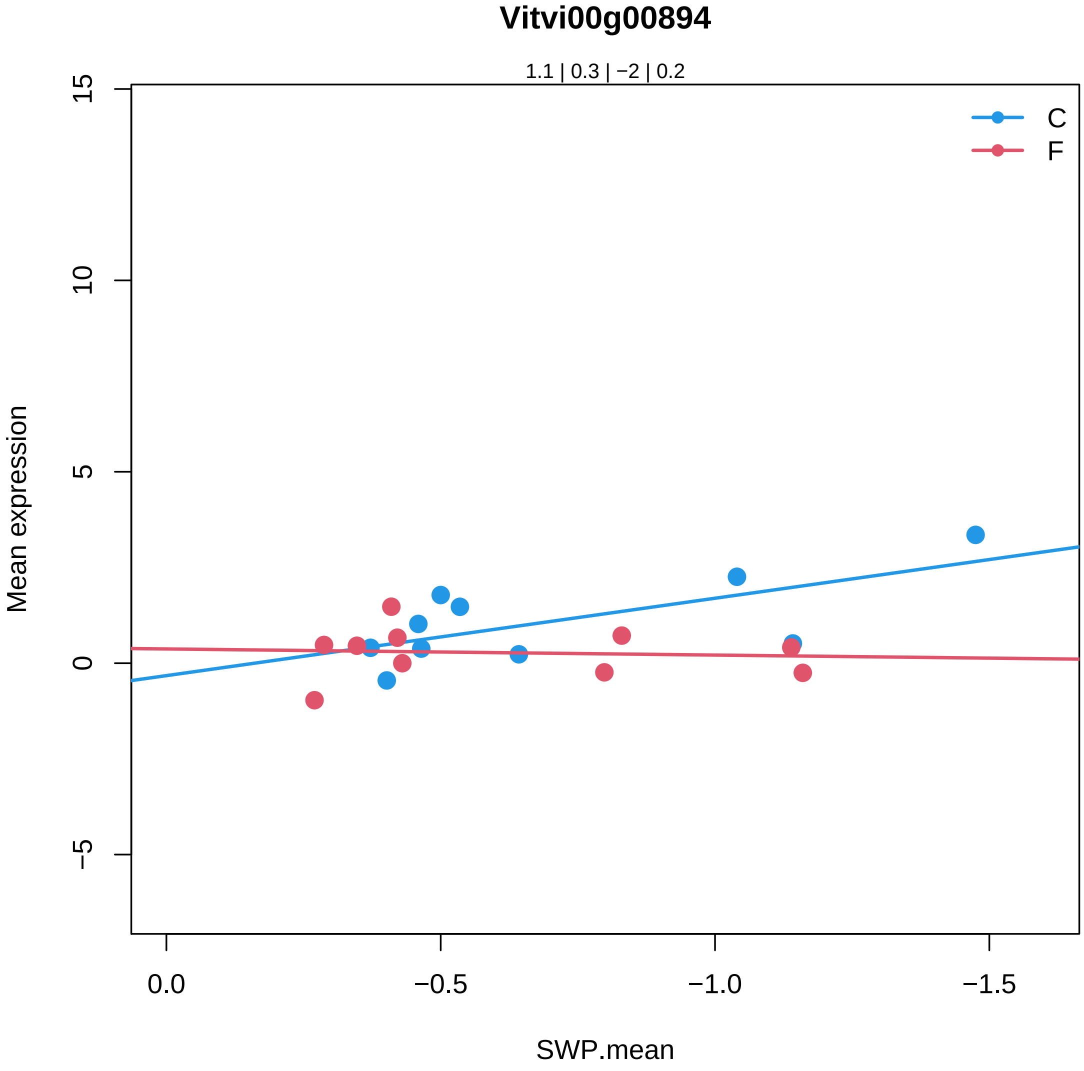
7.6.89 Vitvi00g00894: * type5

```
> 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
```



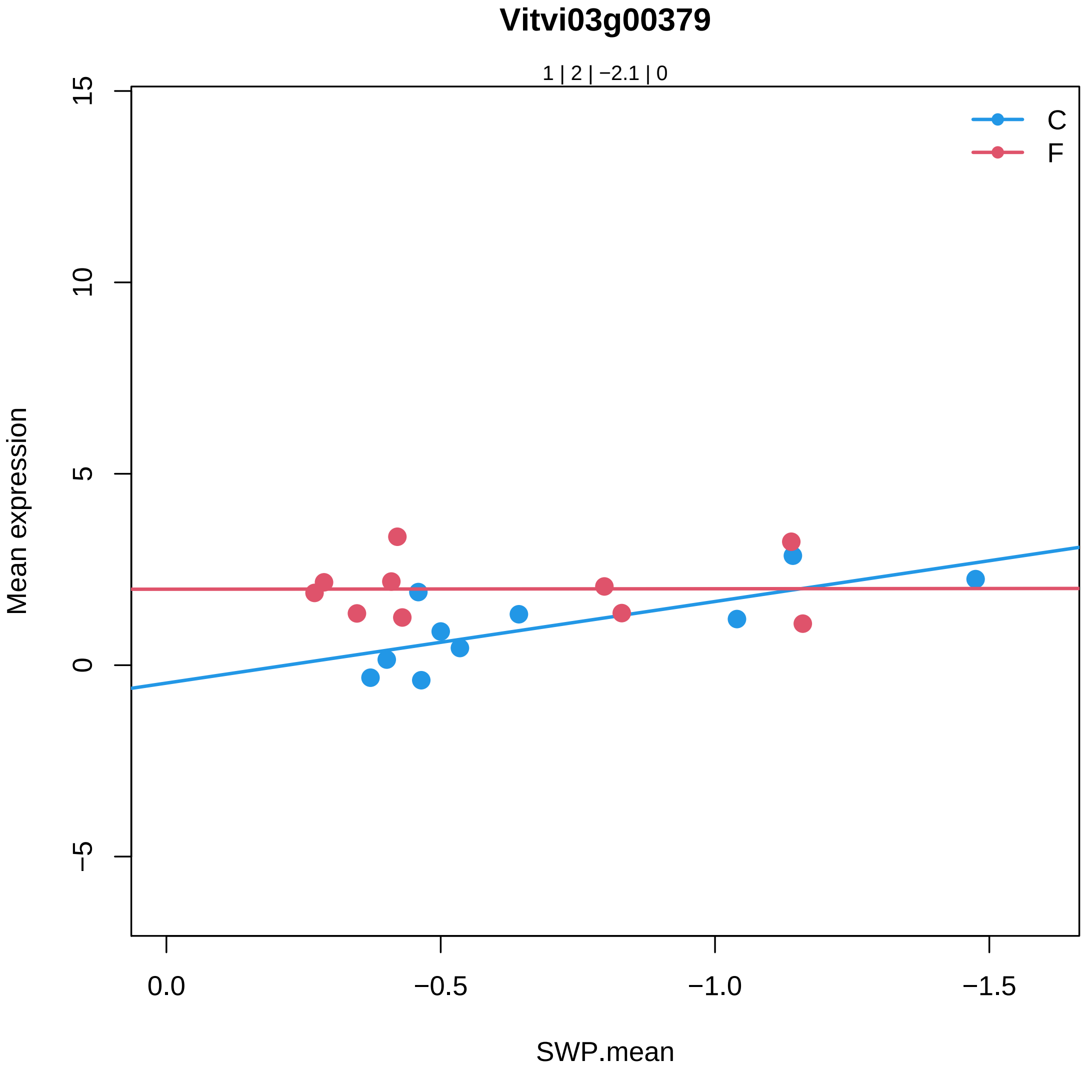
7.6.90 Vitvi03g00379: * type5

```
> 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
```



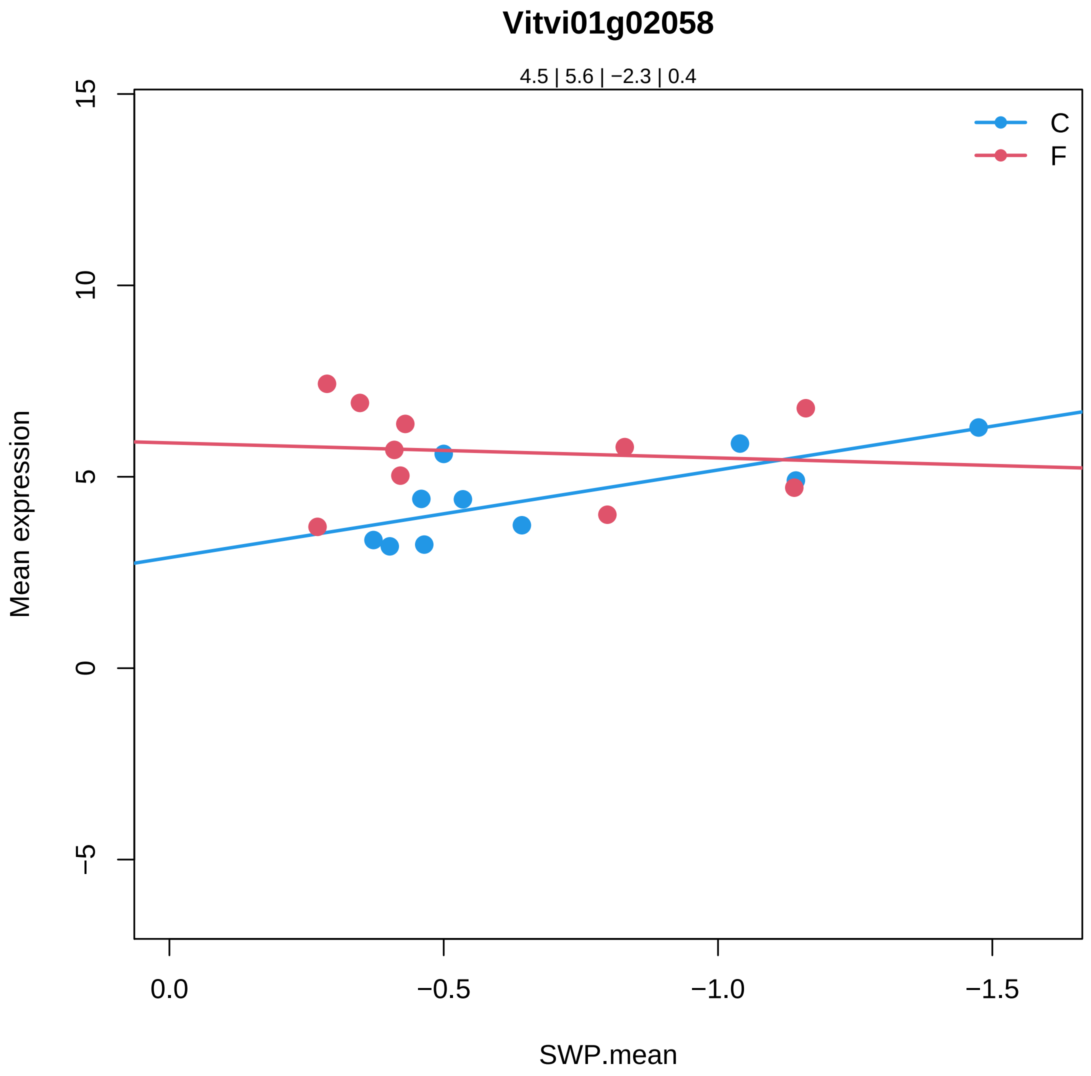
7.6.91 Vitvi01g02058: * type5

```
> 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
```



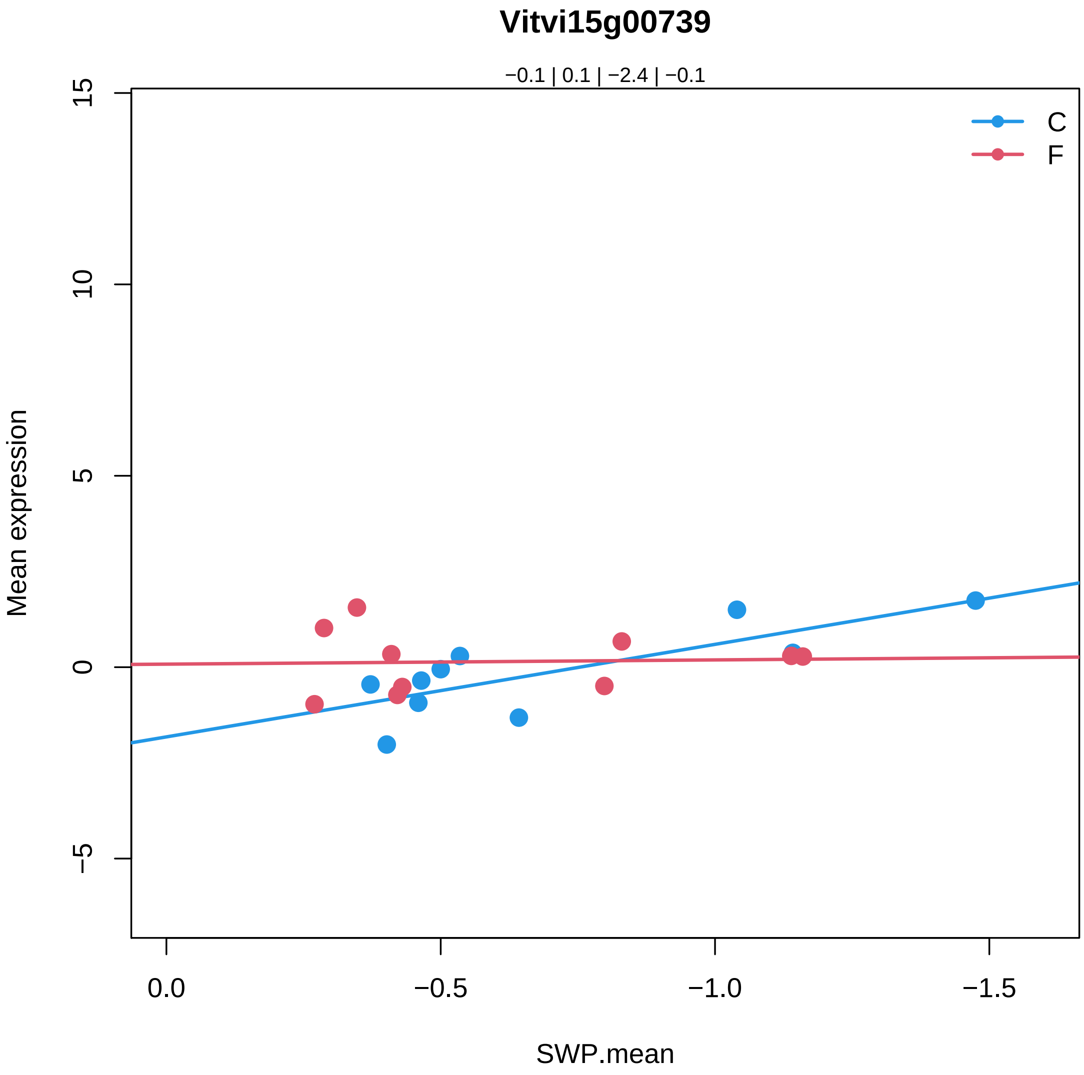
7.6.92 Vitvi15g00739: * type5

```
> 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     0.267912 6 0.4334342       0.7672943
SlopeF-SlopeC   2.306901  0.02855227   *   0.9999488
```



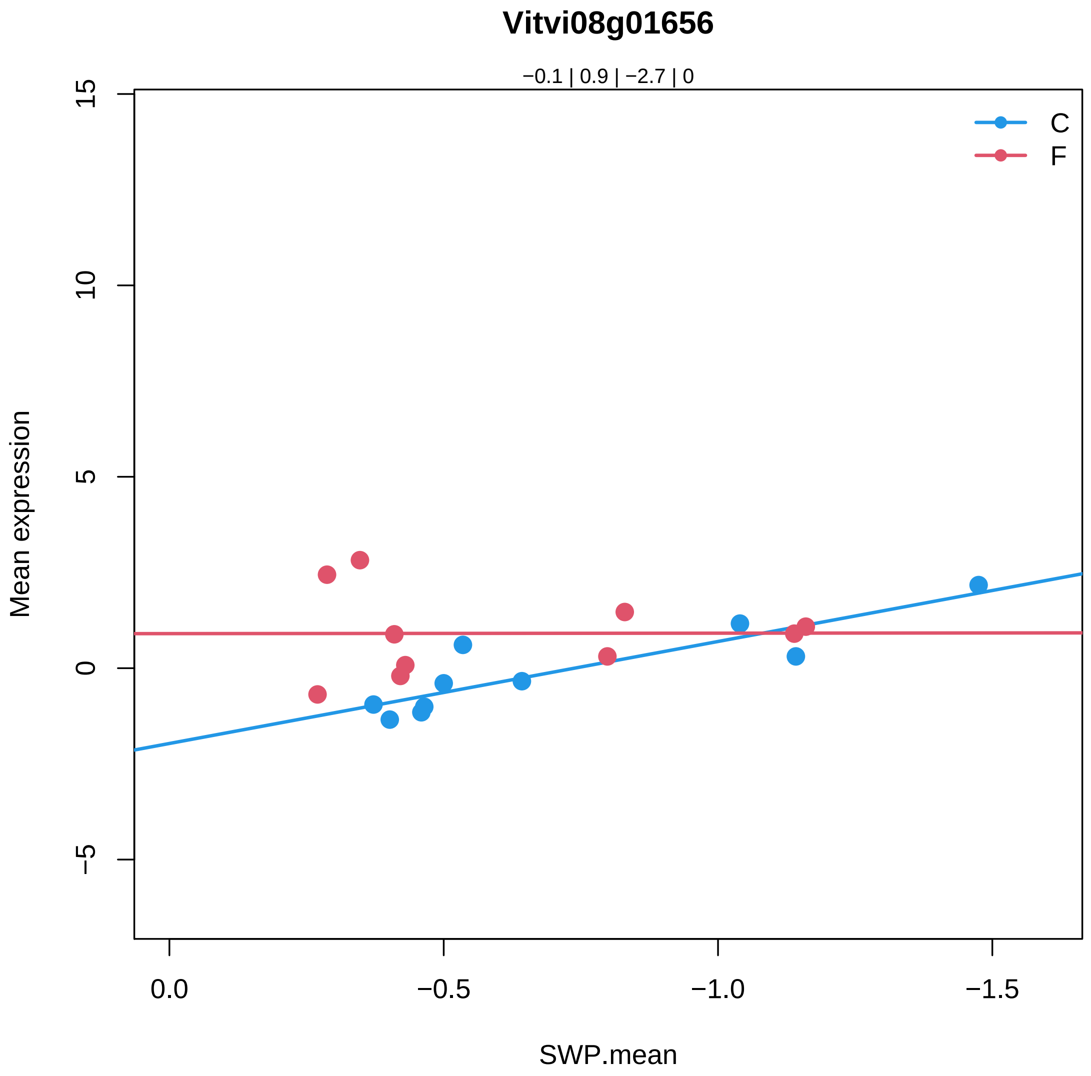
7.6.93 Vitvi08g01656: * type5

```
> 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=".")))
```