

Expression analysis - water potential

A. Blejec

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Parameters:

.alpha = 0.05
.min.slope = 1.5
.max.slope = 0.5
.diff.slope = 1
.diff01 = 1
.ver = 3

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8.4.18	Vitvi10g01685: Type5.0 *	952
8.4.19	Vitvi16g01251: Type5.0 *	953
8.4.20	Vitvi11g00726: Type5.0	954
8.4.21	Vitvi14g02893: Type5.0	955

8.4.22	Vitvi16g02004: Type5.0 *	956
8.4.23	Vitvi13g01997: Type5.0 *	957
8.4.24	Vitvi01g00784: Type5.0	958
8.4.25	Vitvi18g01019: Type5.0	959
8.4.26	Vitvi04g00644: Type5.0 *	961
8.4.27	Vitvi16g01994: Type5.0 *	962
8.4.28	Vitvi16g01118: Type5.0 *	963
8.4.29	Vitvi16g02033: Type5.0 *	964
8.4.30	Vitvi13g01760: Type5.0	965
8.4.31	Vitvi04g02118: Type5.0	966
8.4.32	Vitvi16g02116: Type5.0 *	967
8.4.33	Vitvi09g00112: Type5.0	968
8.4.34	Vitvi10g00650: Type5.0 *	969
8.4.35	Vitvi07g02830: Type5.0 *	970
8.4.36	Vitvi05g01951: Type5.0	971
8.4.37	Vitvi12g00036: Type5.0	972
8.4.38	Vitvi12g02245: Type5.0	973
8.4.39	Vitvi14g02924: Type5.0	974
8.4.40	Vitvi14g01809: Type5.0	975
8.4.41	Vitvi04g01937: Type5.0	977
8.4.42	Vitvi11g00097: Type5.0	978
8.4.43	Vitvi07g00283: Type5.0	979
8.4.44	Vitvi13g00807: Type5.0	980
8.4.45	Vitvi05g00847: Type5.0 +	981
8.4.46	Vitvi15g00804: Type5.0	982
8.4.47	Vitvi13g01724: Type5.0	983
8.4.48	Vitvi03g01524: Type5.0	984
8.4.49	Vitvi13g00829: Type5.0	985
8.4.50	Vitvi04g01100: Type5.0	986
8.4.51	Vitvi07g01150: Type5.0	987
8.4.52	Vitvi14g01128: Type5.0	988
8.4.53	Vitvi15g01073: Type5.0	990
8.4.54	Vitvi07g02362: Type5.0	991
8.4.55	Vitvi03g00432: Type5.0 *	992
8.4.56	Vitvi12g00101: Type5.0 *	994
8.4.57	Vitvi01g02061: Type5.0 *	995
8.4.58	Vitvi05g01116: Type5.0 *	996
8.4.59	Vitvi14g01919: Type5.0 *	997
8.4.60	Vitvi18g00508: Type5.0 *	998
8.4.61	Vitvi07g02448: Type5.0 *	999
8.4.62	Vitvi15g01396: Type5.0	1000
8.4.63	Vitvi05g02185: Type5.0 *	1001
8.4.64	Vitvi19g01048: Type5.0	1002
8.4.65	Vitvi03g00443: Type5.0 *	1003
8.4.66	Vitvi02g00263: Type5.0	1004
8.4.67	Vitvi09g01282: Type5.0	1005
8.4.68	Vitvi07g01552: Type5.0 *	1006
8.4.69	Vitvi07g01120: Type5.0	1007
8.4.70	Vitvi05g00421: Type5.0 *	1008
8.4.71	Vitvi01g01708: Type5.0 *	1009

8.4.72	Vitvi09g00045: Type5.0 *	1010
8.4.73	Vitvi19g02145: Type5.0 *	1011
8.4.74	Vitvi11g01516: Type5.0 *	1012
8.4.75	Vitvi05g00857: Type5.0 *	1013
8.4.76	Vitvi13g02018: Type5.0 *	1014
8.4.77	Vitvi07g02242: Type5.0 *	1015
8.4.78	Vitvi09g00599: Type5.0 *	1016
8.4.79	Vitvi16g01103: Type5.0 *	1017
8.5	Type6.C	1018
8.5.1	Vitvi18g03084: Type6.C *	1019
8.5.2	Vitvi16g02090: Type6.C *	1020
8.5.3	Vitvi16g02003: Type6.C *	1021
8.5.4	Vitvi16g01548: Type6.C *	1022
8.5.5	Vitvi09g00681: Type6.C *	1023
8.5.6	Vitvi12g00606: Type6.C *	1024
8.5.7	Vitvi07g02459: Type6.C *	1026
8.5.8	Vitvi08g00723: Type6.C *	1027
8.5.9	Vitvi16g01010: Type6.C *	1028
8.5.10	Vitvi14g03027: Type6.C *	1029
8.5.11	Vitvi12g02241: Type6.C *	1030
8.5.12	Vitvi16g01695: Type6.C *	1031
8.5.13	Vitvi16g00162: Type6.C *	1032
8.5.14	Vitvi07g01975: Type6.C *	1033
8.5.15	Vitvi12g02434: Type6.C *	1034
8.5.16	Vitvi17g01499: Type6.C *	1036
8.5.17	Vitvi09g00253: Type6.C *	1037
8.5.18	Vitvi07g02479: Type6.C *	1039
8.5.19	Vitvi07g03003: Type6.C *	1040
8.5.20	Vitvi11g00749: Type6.C *	1041
8.5.21	Vitvi16g02128: Type6.C *	1042
8.5.22	Vitvi12g02492: Type6.C *	1043
8.5.23	Vitvi07g01880: Type6.C *	1044
8.5.24	Vitvi09g00038: Type6.C *	1045
8.5.25	Vitvi14g00488: Type6.C *	1046
8.5.26	Vitvi01g01977: Type6.C *	1047
8.5.27	Vitvi03g01431: Type6.C *	1048
8.6	Type6.F	1049
8.6.1	Vitvi19g02316: Type6.F	1050
8.6.2	Vitvi17g00175: Type6.F	1051
8.6.3	Vitvi05g00038: Type6.F	1052
8.6.4	Vitvi15g01643: Type6.F	1053
8.6.5	Vitvi05g01578: Type6.F	1054
8.6.6	Vitvi11g00865: Type6.F	1055
8.6.7	Vitvi10g00313: Type6.F	1057
8.6.8	Vitvi12g02177: Type6.F	1058
8.6.9	Vitvi07g03123: Type6.F	1059
8.6.10	Vitvi10g02396: Type6.F	1060
8.6.11	Vitvi07g03066: Type6.F	1061
8.6.12	Vitvi18g01877: Type6.F	1062
8.6.13	Vitvi08g02249: Type6.F	1063

8.6.14	Vitvi13g00261: Type6.F +	1065
8.6.15	Vitvi00g02022: Type6.F	1066
8.6.16	Vitvi17g01497: Type6.F	1067
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1 Task

Final document in folder /reports:

```
> fileName(outputFile)
```

```
[1] "50_Expression-water-stress_0.05-1.5-0.5-1-1-3"
```

2 Information from pISA

Data directory

```
> .inroot
```

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

Results directory

```
> .oroot
```

```
[1] "../..output/50_Expression-water-stress-0.05-1.5-0.5-1-1-3"
```

```
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	Fleurtaï :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 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 -80°C ; 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 | Chr2:12618111-12618871
2 Disease resistance protein (TIR-NBS-LRR class) family | Chr4:7197325-7201393
3
4
5
```

```
6 Disease resistance protein (CC-NBS-LRR class) family | Chr1:4145374-4147680
```

```
> 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..H2O." "Glucopyranose..H2O."
[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

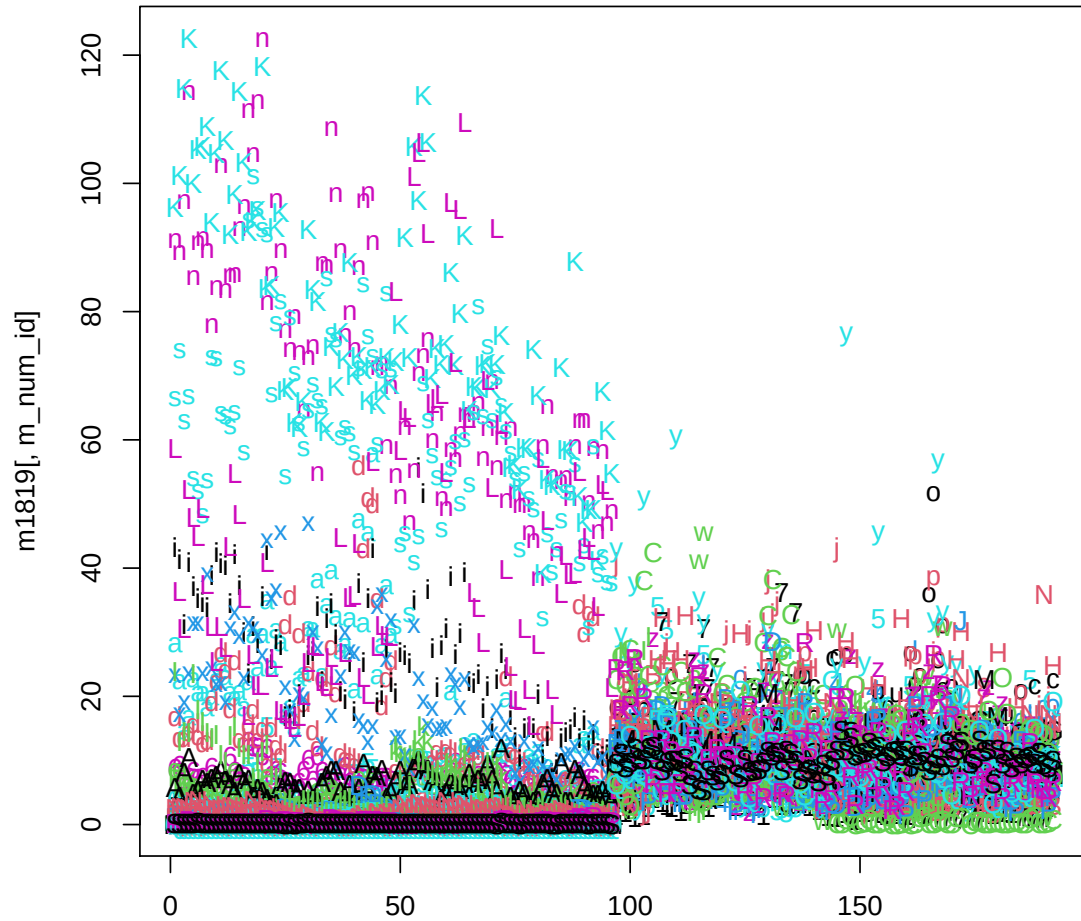
> m_num_id <- 6:ncol(m1819)
> colnames(m1819)[-m_num_id]
[1] "ID"          "Variety" "Date"      "Treat"     "Rep"
```

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.

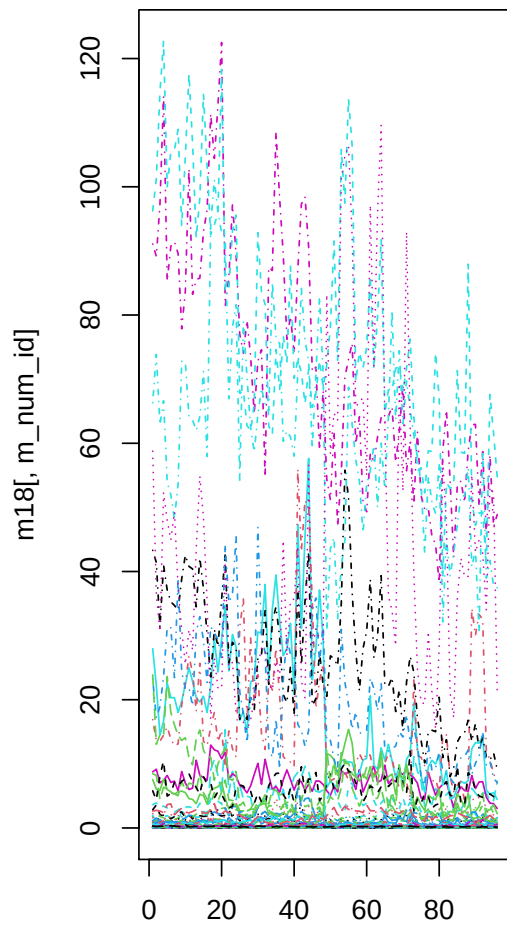
3.7 Visualize metabolites

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

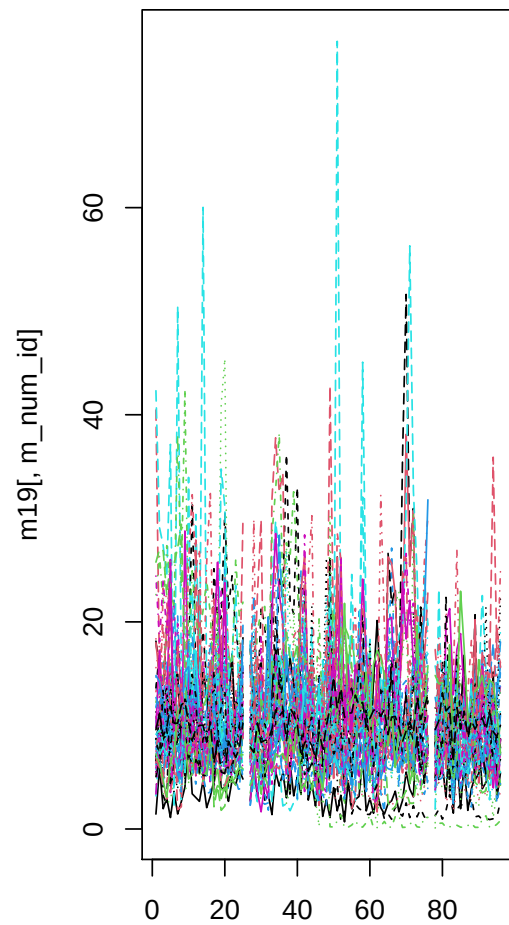


```
> par(mfrow=c(1,2))
> matplot(m18[,m_num_id], main="2018", type="l")
> matplot(m19[,m_num_id], main="2019", type="l")
```

2018



2019



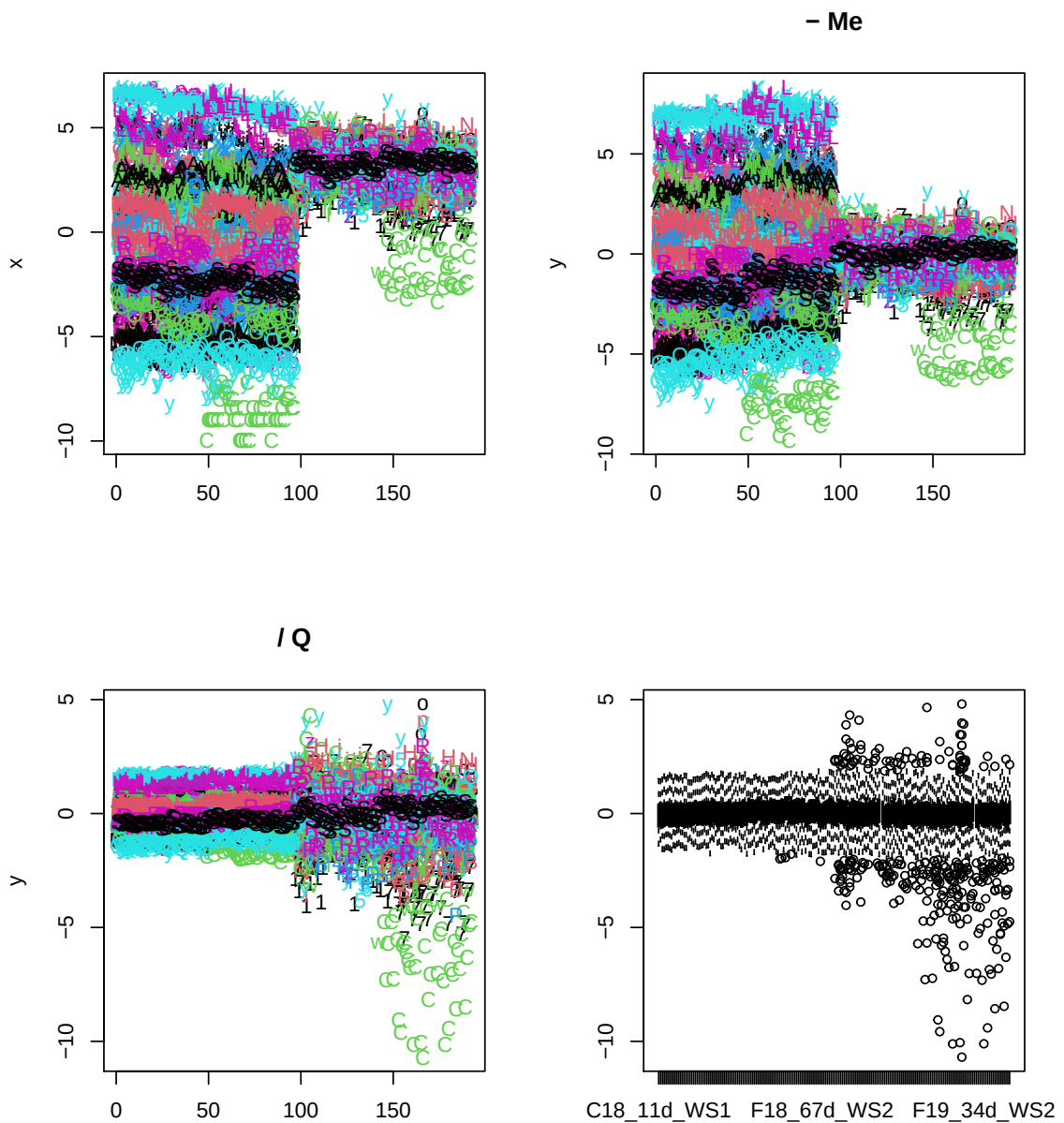
Median standardization of samples

```
> 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
```

```

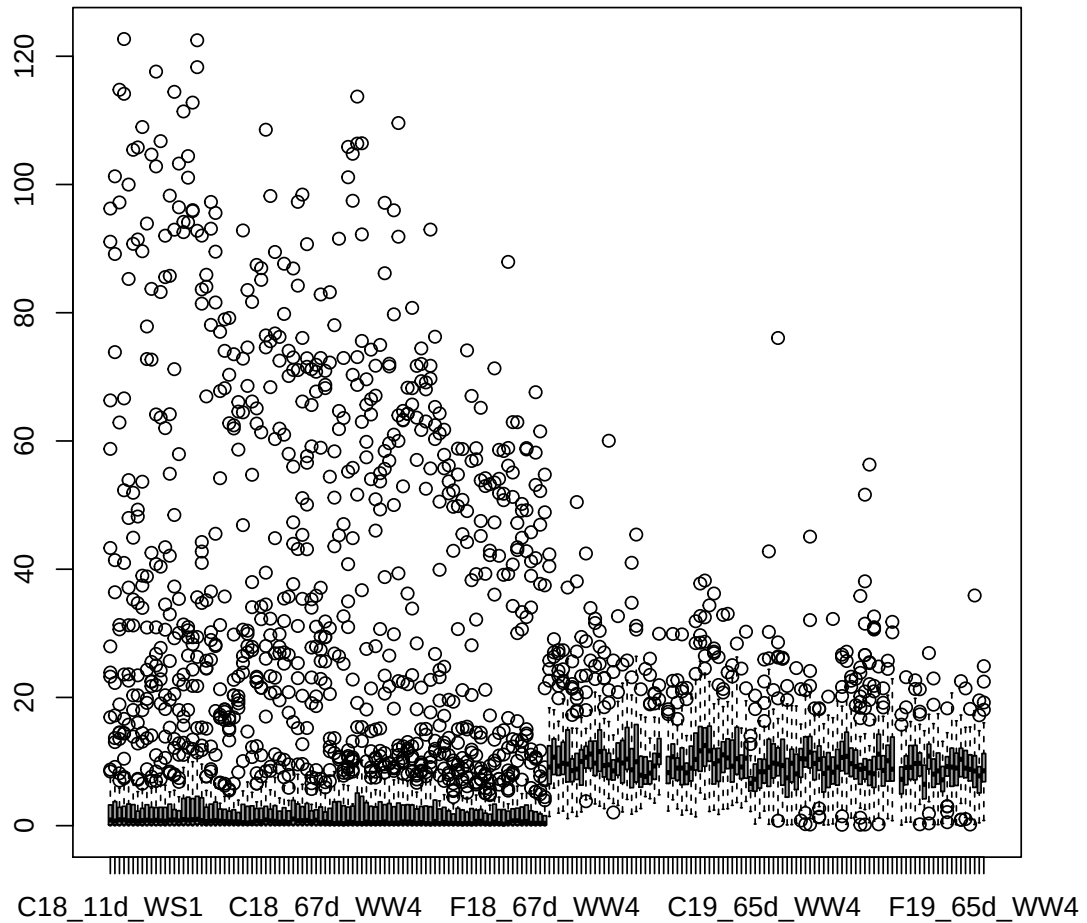
> for(k in seq(1,ncol(x),10)) {
+ if(interactive()) windows()
+   my.parallel( x, k:(k+9))
+ }
Error in h(simpleError(msg, call)): error in evaluating the argument 'x' in se
> par(mfrow=c(2,2))
> x <- log2(m1819[,m_num_id])
> matplot(x)
}1 dim(x) 55
Me <- apply(x,1,median, na.rm=TRUE)
> Q <- apply(x,1,function(x) 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))

```



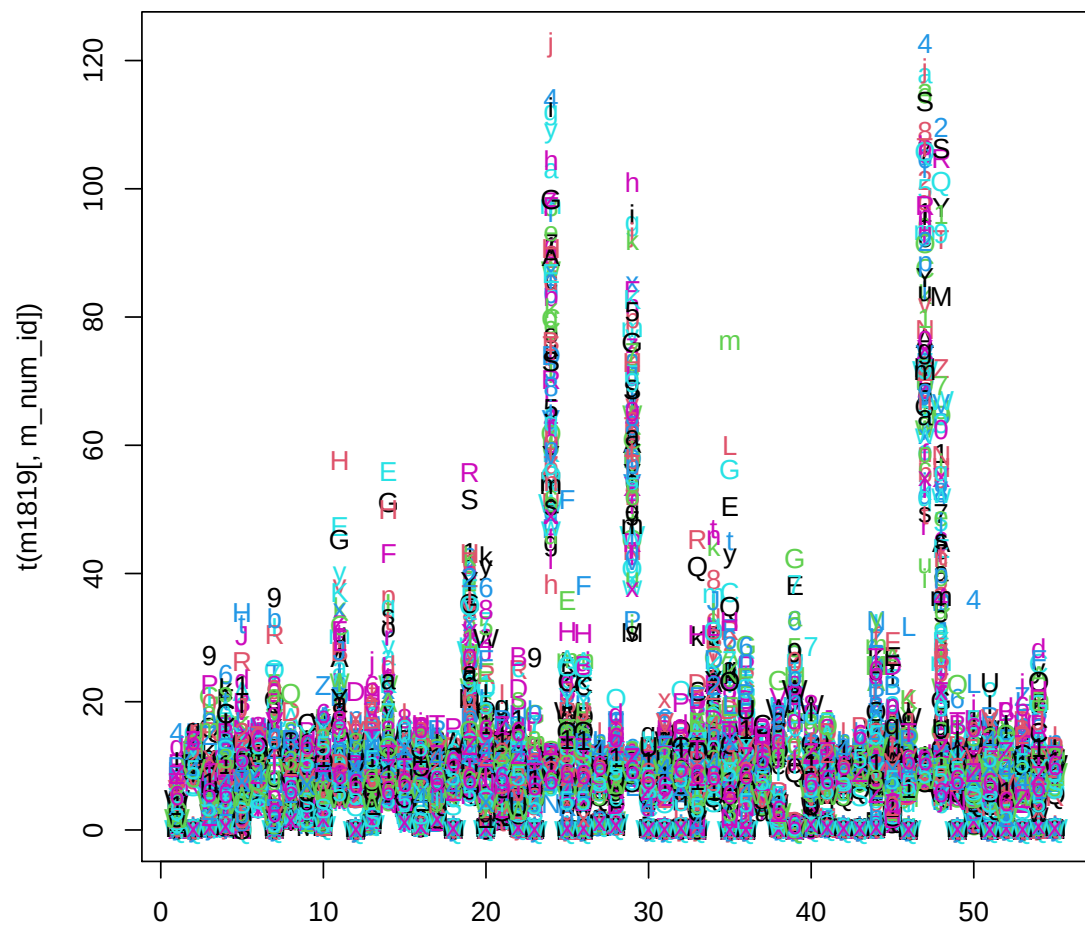
Data are highly skewed with marked differences between years

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

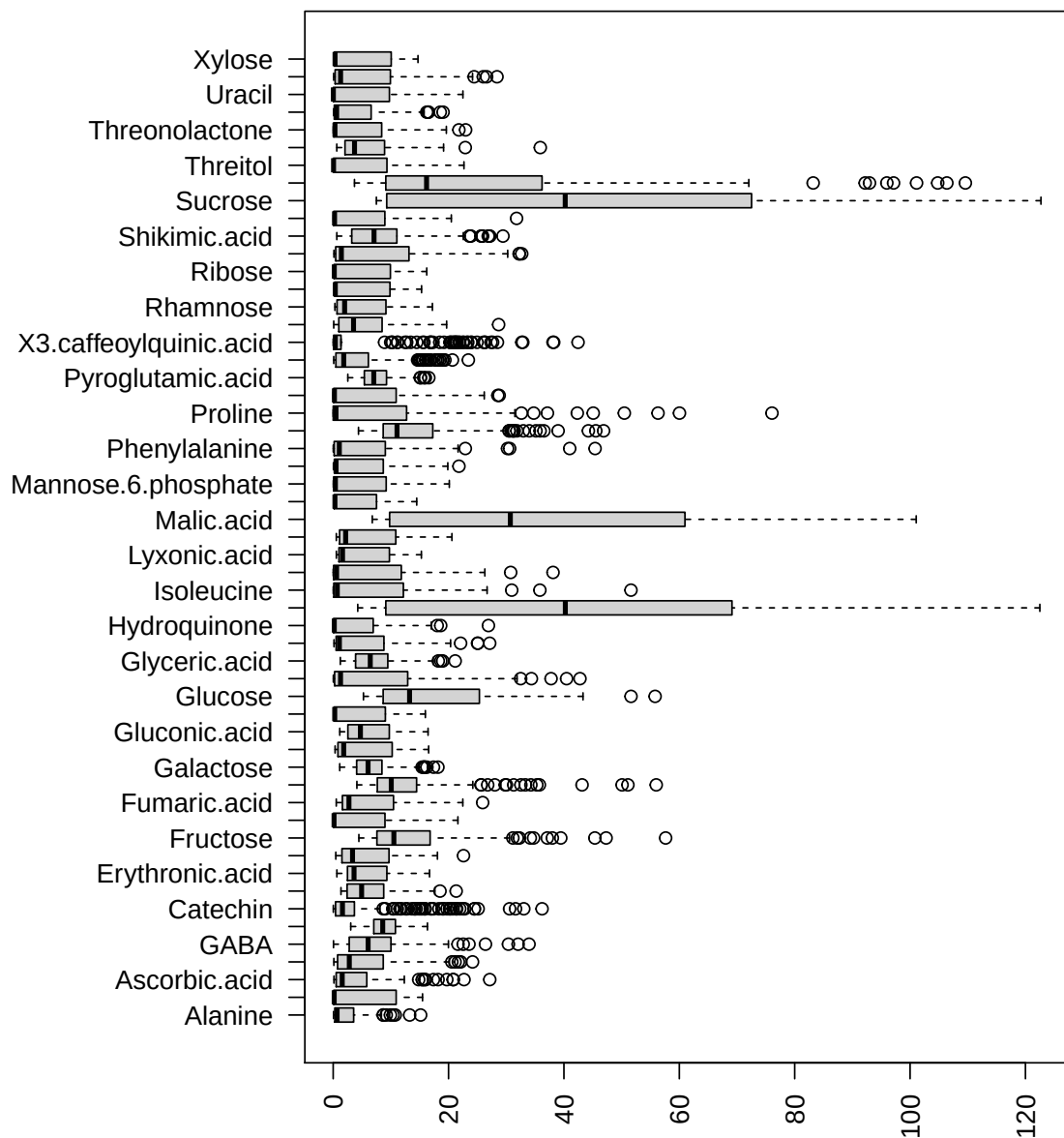


```
> matplot(t(m1819[,m_num_id]))
```

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



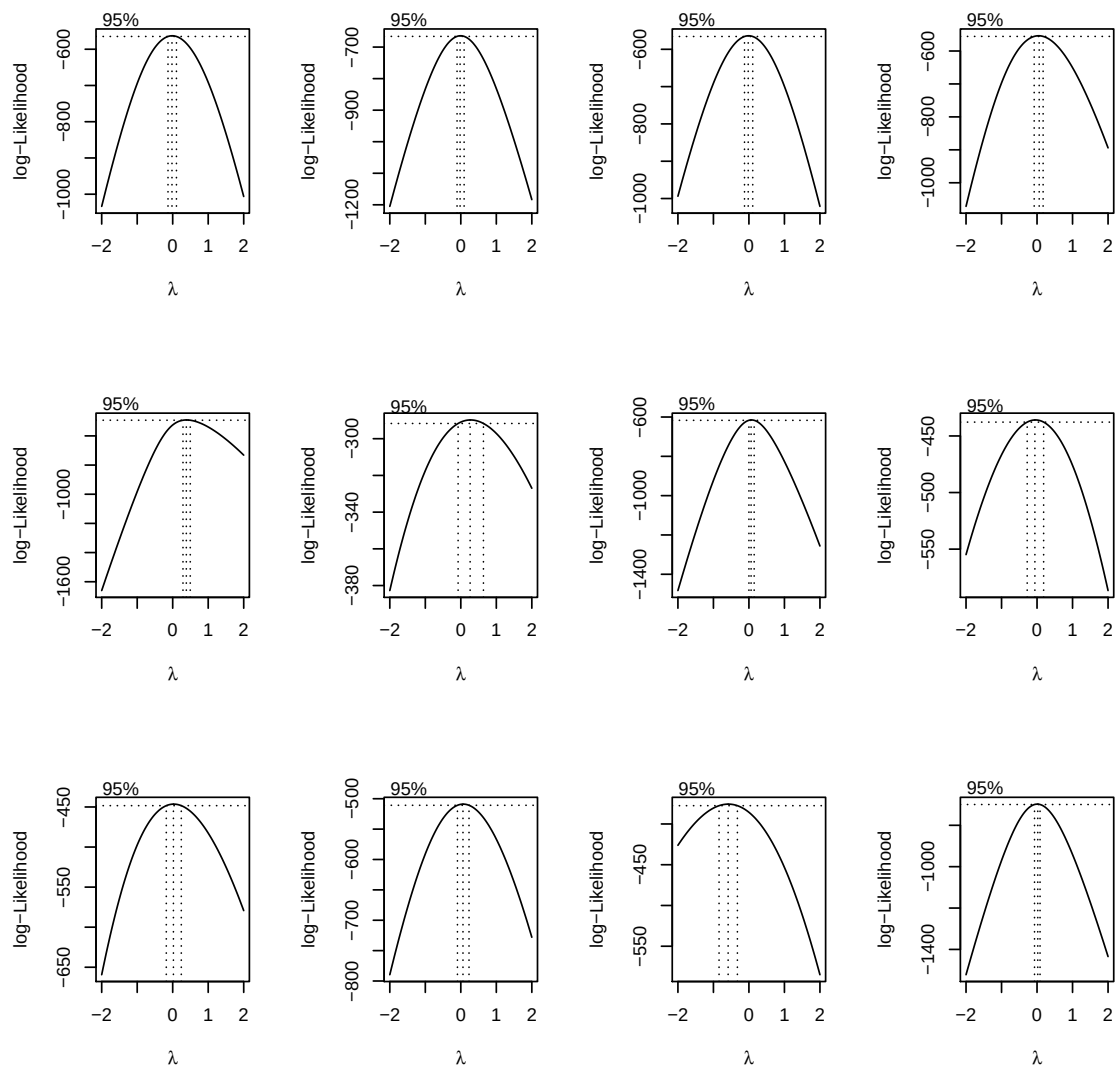
```
> par(mar=c(4,10,3,1))
> boxplot(m1819[,m_num_id], horizontal=TRUE, las=2)
```



Box-Cox transformation

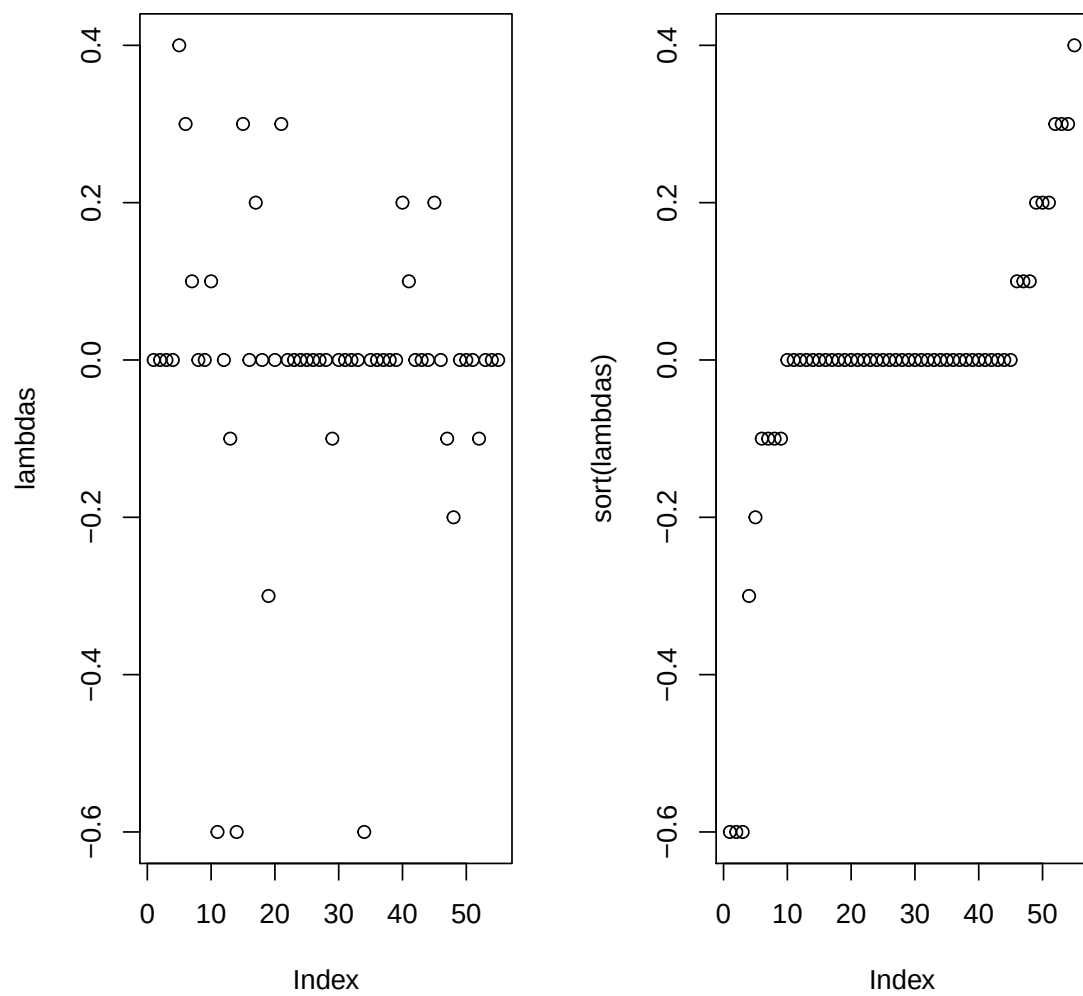
```
> library(MASS)
> par(mfrow=c(3,2))
> my.boxcox <- function(x, plotit=FALSE,...) {
+   require(MASS)
+   bc <- boxcox(x ~1, plotit=plotit, ...)
+   bc$x[which.max(bc$y)]
+ }

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



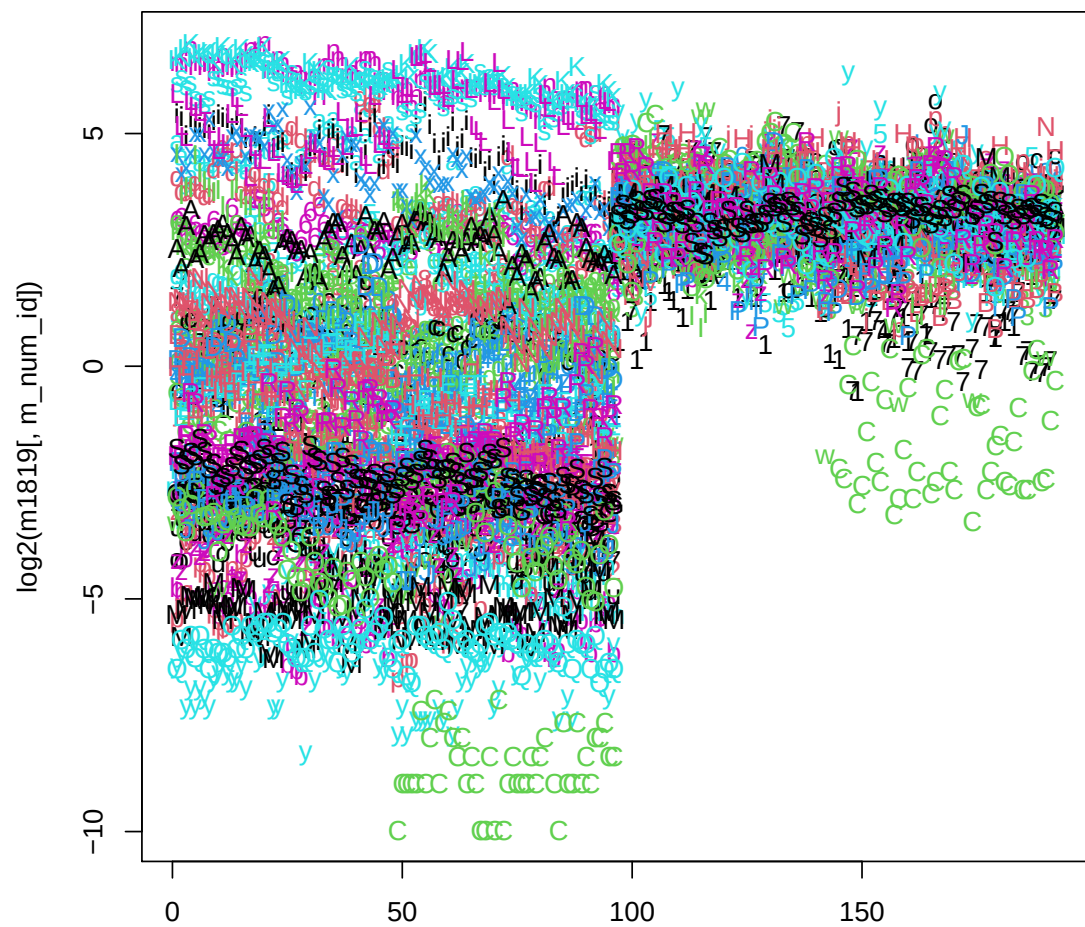
Alanine	Arabinose	Ascorbic.acid
-0.02020202	-0.02020202	-0.02020202
Aspartic.acid	GABA	Trans.Caffeic.acid
0.06060606	0.38383838	0.26262626
Catechin	Citric.acid	Erythronic.acid
0.06060606	-0.06060606	0.02020202
Ethanolamine	Fructose	Fructose.6.phosphate
0.06060606	-0.58585859	0.02020202

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

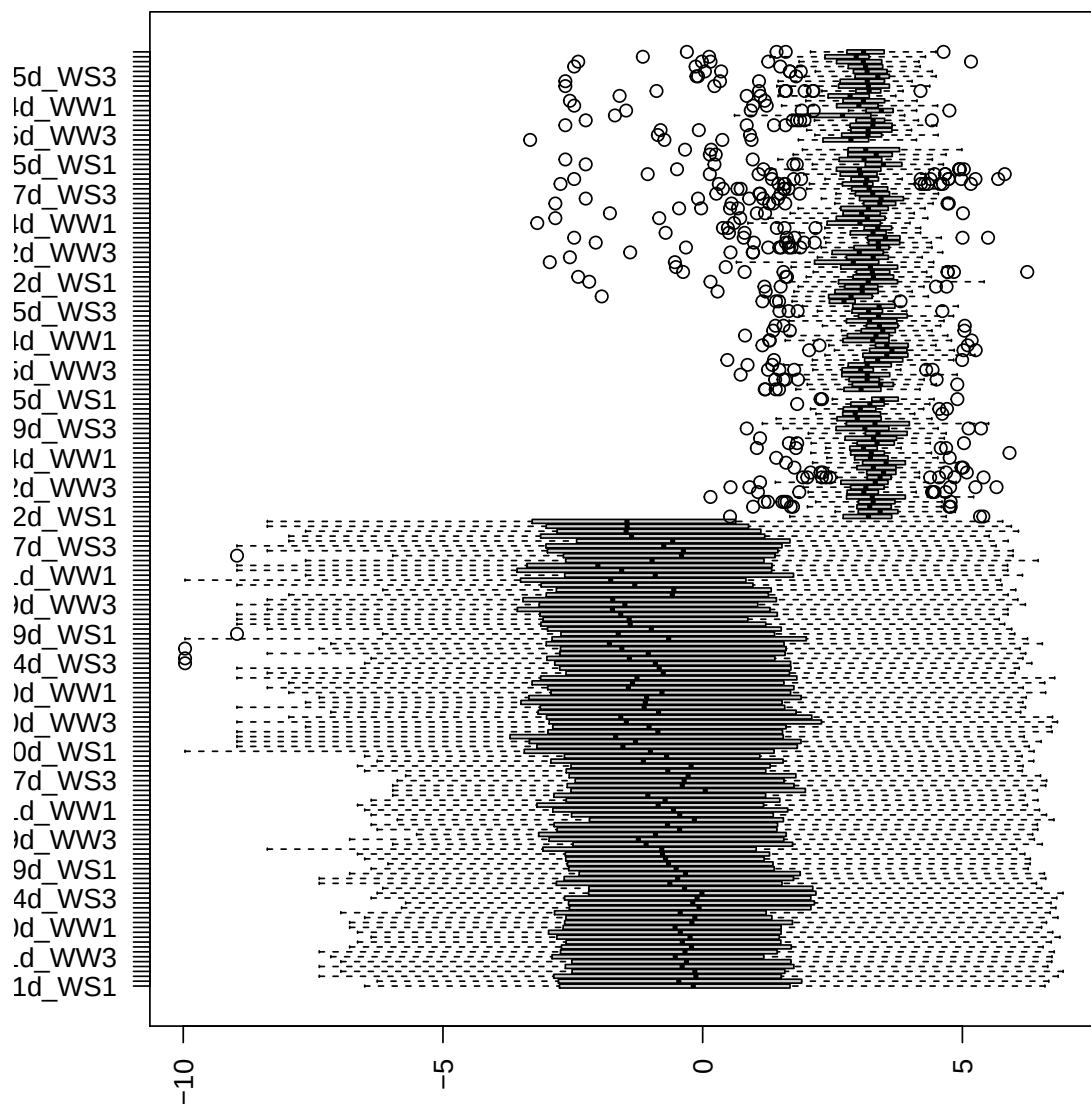
It seems that logarithm is adequate.

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



Data are highly skewed with marked differences between years

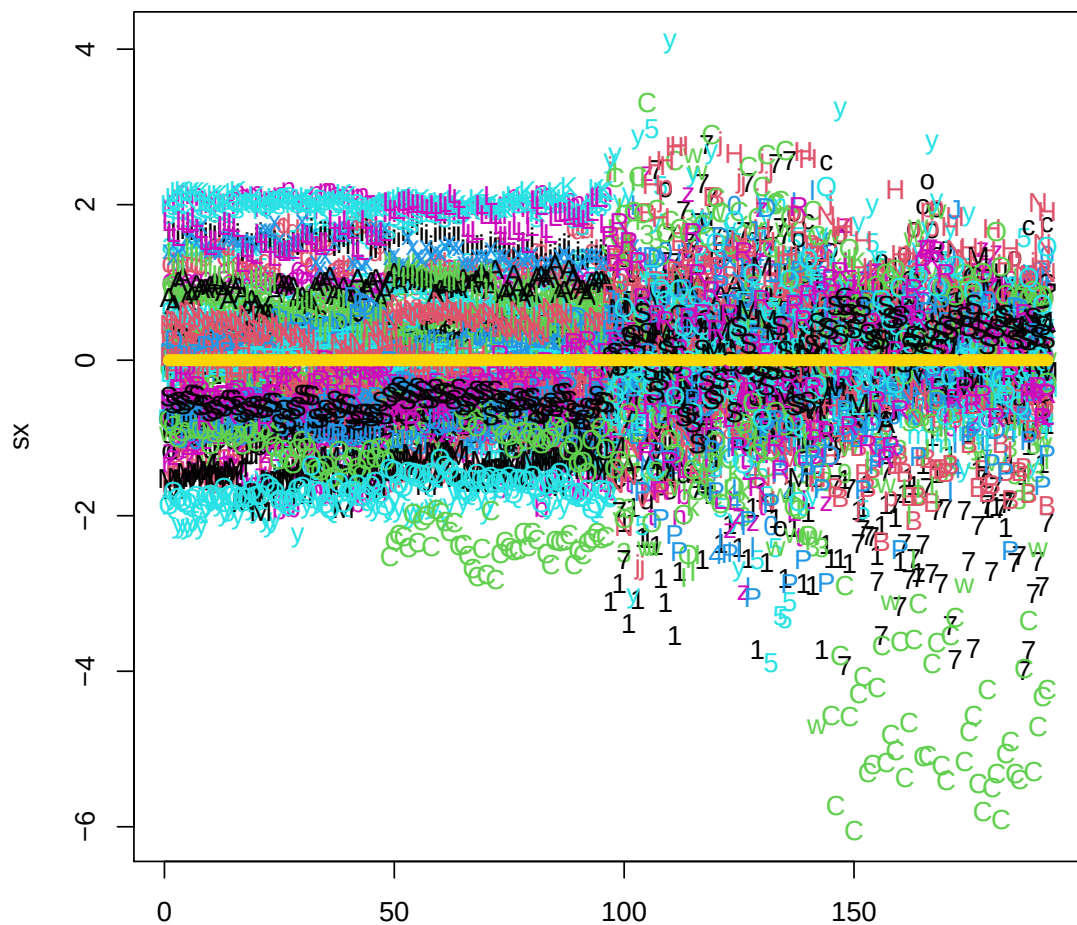
```
> boxplot(t(log2(m1819[,m_num_id])))
+ , horizontal=TRUE, las=2)
```



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)
```

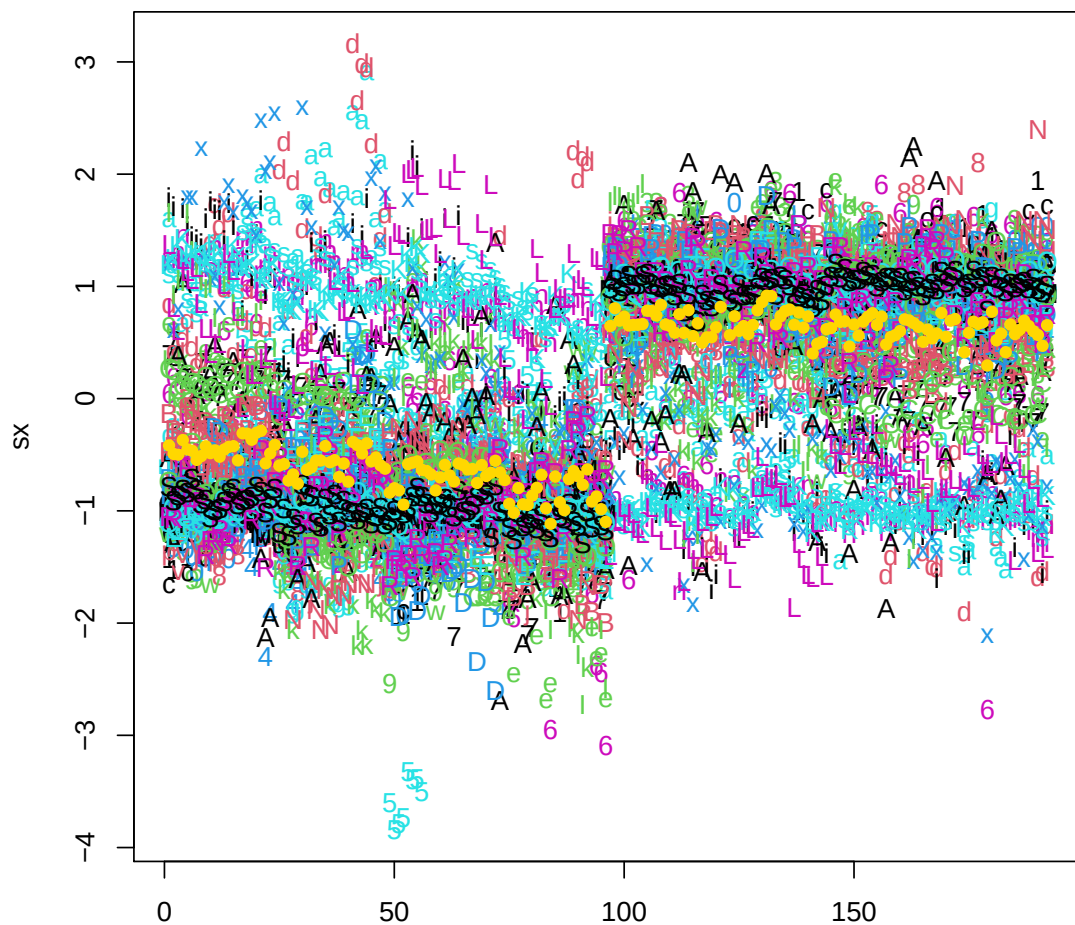


```
> head(apply(sx,1,mean, na.rm=TRUE))
  C18_11d_WS1  C18_11d_WS2  C18_11d_WS3  C18_11d_WS4  C18_11d_WW1
3.156507e-18 2.714645e-17 -5.391442e-19 2.231091e-17 9.791331e-18
  C18_11d_WW2
-2.039877e-17

> 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

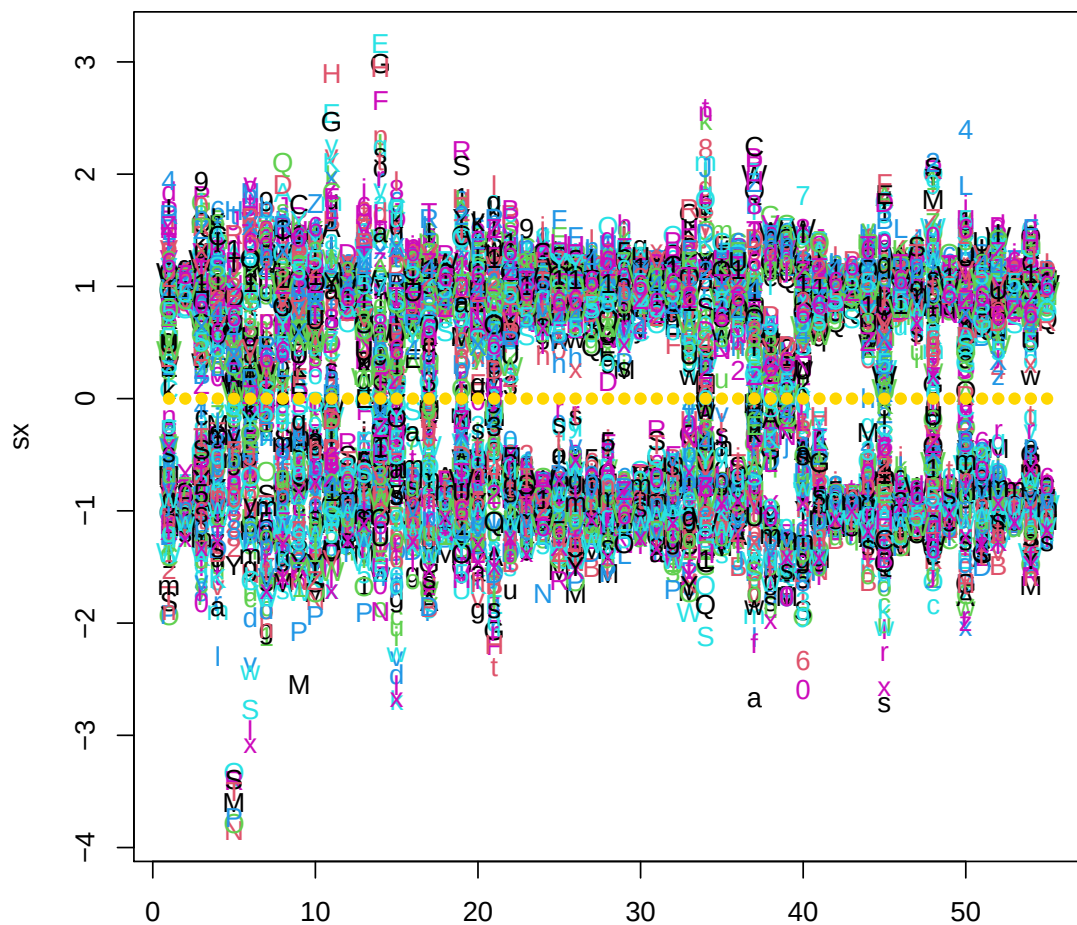
```
> x <- log2(m1819[,m_num_id])
```

```
> 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
```

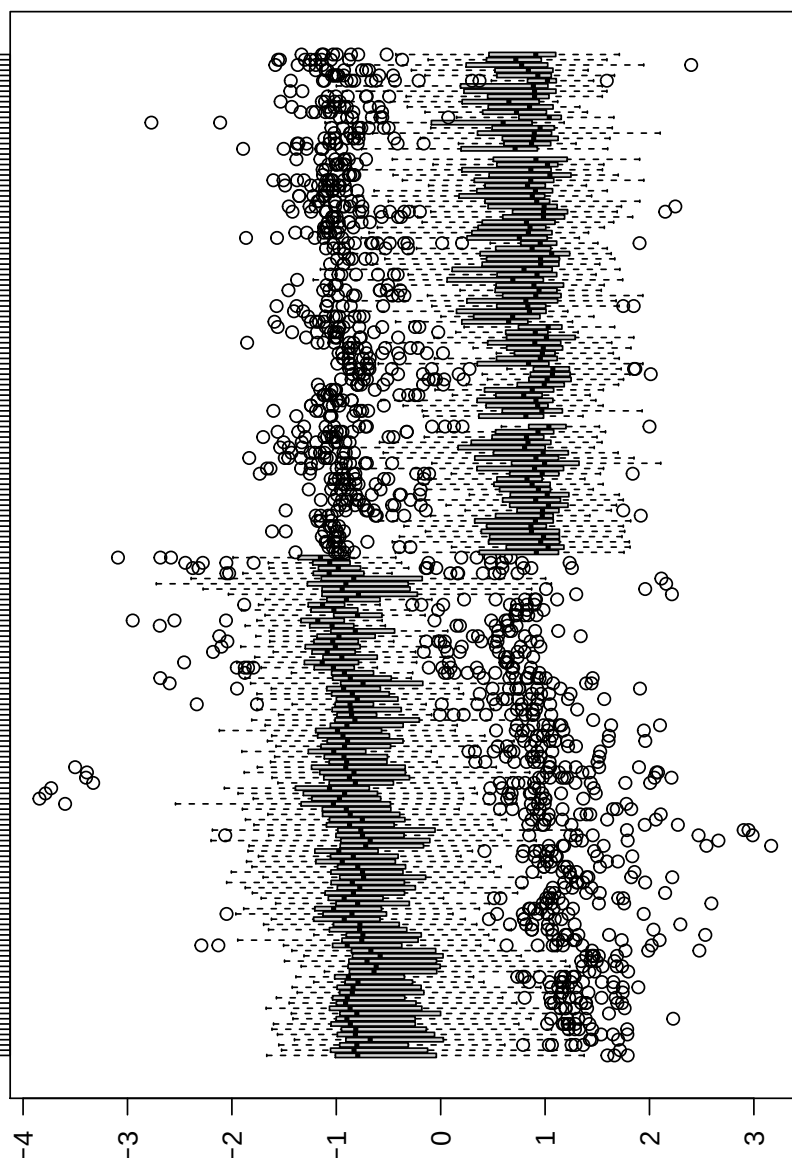
```
> head(apply(sx, 2, sd, na.rm=TRUE))
```

```
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)
```

F19_65d_WW3
 F19_65d_WS2
 F19_34d_WW1
 F19_55d_WW4
 F19_55d_WS3
 F19_47d_WW2
 F19_47d_WS1
 F19_44d_WS4
 F19_22d_WW3
 F19_22d_WS2
 C19_65d_WW1
 C19_34d_WW4
 C19_34d_WS3
 C19_55d_WW2
 C19_55d_WS1
 C19_49d_WS4
 C19_44d_WW3
 C19_44d_WS2
 C19_22d_WW1
 F18_67d_WW4
 F18_67d_WS3
 F18_61d_WW2
 F18_61d_WS1
 F18_49d_WS4
 F18_34d_WW3
 F18_34d_WS2
 F18_20d_WW1
 F18_10d_WW4
 F18_10d_WS3
 C18_67d_WW2
 C18_67d_WS1
 C18_61d_WS4
 C18_49d_WW3
 C18_49d_WS2
 C18_34d_WW1
 C18_20d_WW4
 C18_20d_WS3
 C18_11d_WW2
 C18_11d_WS1



```

> 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"
> mfddata <- read.table(file.path(.iroot, fmfn), sep="\t", header=TRUE)
> cbind(rownames(sm1819), make.names(mfddata[,1]), mfddata[,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..H2O."	"Glucopyranose..H2O."
[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-Inositol"	
[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
```

```
Ascorbic.acid
```

```
Aspartic.acid
```

```
GABA
```

```
Trans.Caffeic.acid
```

```
cell wall
```

```
hormone metabol
```

```
amino acid metabolism.synthesis.central amino acid metaboli
```

```
pol
```

```
secondary metabolism.phenylpropanoids.lignin
```


3.10 Interesting bins

For Canonical Correlation Analysis (CCA) we will need to restrict the 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:

```
1) (bfn <- getMeta(aDesc, "Interesting bins"))
2) 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
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$bin
[1] "1.2" "1.3" "2.1" "2.2" "3.1" "3.3" "3.4" "3.99" "5"
[10] "6" "8.1" "10.6" "11" "12.2" "13.1" "16.1" "16.2" "16.8"
[19] "17.5" "21" "22"
1) paste0("1", bindata$bin[1])
2) ind <- grep(paste0("1", 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]
      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("^(x)",
> 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, ncol=NA)
+ 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	mfddata	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	mfddata	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	mfddata	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

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

----- 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

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	
5	
6	Disease resistance protein (CC-NBS-LRR class) family Chr1:4145374-414768

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

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

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

C18_11d_WS1	1.052	27.962		0.037	0.683
C18_11d_WS2	0.865	22.260		0.035	1.069
C18_11d_WS3	1.335	14.477		0.058	1.907
C18_11d_WS4	0.901	16.651		0.079	2.009
C18_11d_WW1	0.861	22.621		0.033	0.760
C18_11d_WW2	0.805	20.318		0.089	1.094
Galactinol Galactose Gallic.acid Gluconic.acid					
C18_11d_WS1	16.908	8.455	1.002	3.640	
C18_11d_WS2	13.660	8.218	0.958	3.911	
C18_11d_WS3	13.524	4.445	0.936	3.079	
C18_11d_WS4	14.463	6.358	0.905	3.421	
C18_11d_WW1	15.754	6.071	1.143	3.133	
C18_11d_WW2	13.891	5.467	0.917	2.805	
Glucopyranose..H2O. Glucose Glutamic.acid Glyceric.acid					
C18_11d_WS1		0.143	43.309	0.491	7.540
C18_11d_WS2		0.155	41.412	0.298	6.082
C18_11d_WS3		0.178	31.305	0.140	5.876
C18_11d_WS4		0.153	40.981	0.202	7.596
C18_11d_WW1		0.169	37.135	0.303	6.008
C18_11d_WW2		0.156	35.269	0.263	5.638
Glycine Hydroquinone Myo.Inostol Isoleucine Leucine					
C18_11d_WS1	0.742	0.161	91.071	0.055	0.022
C18_11d_WS2	0.727	0.208	89.166	0.054	0.027
C18_11d_WS3	0.913	0.099	97.202	0.072	0.033
C18_11d_WS4	0.742	0.176	114.143	0.150	0.079
C18_11d_WW1	1.031	0.101	85.266	0.146	0.077
C18_11d_WW2	0.847	0.161	90.745	0.096	0.050
Lyxonic.acid Maleic.acid Malic.acid Malonic.acid					
C18_11d_WS1	1.028	1.093	66.326	0.166	
C18_11d_WS2	1.187	1.486	73.855	0.140	
C18_11d_WS3	1.237	1.108	62.877	0.183	
C18_11d_WS4	1.020	1.084	66.638	0.233	
C18_11d_WW1	1.205	0.879	53.894	0.156	
C18_11d_WW2	1.096	1.202	51.917	0.170	
Mannose.6.phosphate Melibiose Phenylalanine					
C18_11d_WS1		0.088	0.227	0.095	
C18_11d_WS2		0.102	0.204	0.116	
C18_11d_WS3		0.134	0.069	0.103	
C18_11d_WS4		0.174	0.092	0.203	
C18_11d_WW1		0.082	0.178	0.104	
C18_11d_WW2		0.198	0.164	0.179	
Phosphoric.acid Proline Putrescine Pyroglutamic.acid					
C18_11d_WS1	23.244	0.011	0.054		5.790
C18_11d_WS2	17.190	0.013	0.046		4.354
C18_11d_WS3	18.909	0.006	0.104		8.169
C18_11d_WS4	23.579	0.008	0.111		10.445
C18_11d_WW1	31.264	0.006	0.066		4.966
C18_11d_WW2	31.233	0.008	0.058		5.408
Quinic.acid X3.caffeoylquinic.acid Raffinose Rhamnose					
C18_11d_WS1	1.615		0.677	1.117	0.603
C18_11d_WS2	1.304		0.635	1.544	0.472
C18_11d_WS3	1.254		0.378	0.961	0.516
C18_11d_WS4	1.106		0.423	1.164	0.634

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

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

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

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

C19_22d_WS2	10.69	12.24		7.71	8.39
C19_22d_WS3	8.34	10.82		8.21	4.05
C19_22d_WS4	5.94	10.75		9.73	11.80
C19_22d_WW1	8.68	14.73		13.54	3.79
C19_22d_WW2	6.65	15.20		21.62	5.53
Galactinol Galactose Gallic.acid Gluconic.acid					
C19_22d_WS1	18.37	12.24	8.35	10.27	
C19_22d_WS2	14.63	13.59	6.97	11.45	
C19_22d_WS3	19.87	11.75	4.26	9.88	
C19_22d_WS4	12.76	12.42	11.59	8.80	
C19_22d_WW1	11.17	15.85	8.83	8.55	
C19_22d_WW2	12.18	14.85	10.23	7.69	
Glucopyranose..H2O. 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

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

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..H2O. Glucose Glutamic.acid Glyceric.acid					
C18_11d_WS1		0.143	43.309	0.491	7.540
C18_11d_WS2		0.155	41.412	0.298	6.082
C18_11d_WS3		0.178	31.305	0.140	5.876
C18_11d_WS4		0.153	40.981	0.202	7.596
C18_11d_WW1		0.169	37.135	0.303	6.008
C18_11d_WW2		0.156	35.269	0.263	5.638
Glycine Hydroquinone Myo.Inostol Isoleucine Leucine					
C18_11d_WS1	0.742	0.161	91.071	0.055	0.022
C18_11d_WS2	0.727	0.208	89.166	0.054	0.027
C18_11d_WS3	0.913	0.099	97.202	0.072	0.033
C18_11d_WS4	0.742	0.176	114.143	0.150	0.079
C18_11d_WW1	1.031	0.101	85.266	0.146	0.077
C18_11d_WW2	0.847	0.161	90.745	0.096	0.050
Lyxonic.acid Maleic.acid Malic.acid Malonic.acid					
C18_11d_WS1	1.028	1.093	66.326	0.166	
C18_11d_WS2	1.187	1.486	73.855	0.140	
C18_11d_WS3	1.237	1.108	62.877	0.183	
C18_11d_WS4	1.020	1.084	66.638	0.233	
C18_11d_WW1	1.205	0.879	53.894	0.156	
C18_11d_WW2	1.096	1.202	51.917	0.170	
Mannose.6.phosphate Melibiose Phenylalanine					
C18_11d_WS1		0.088	0.227	0.095	
C18_11d_WS2		0.102	0.204	0.116	
C18_11d_WS3		0.134	0.069	0.103	
C18_11d_WS4		0.174	0.092	0.203	
C18_11d_WW1		0.082	0.178	0.104	
C18_11d_WW2		0.198	0.164	0.179	
Phosphoric.acid Proline Putrescine Pyroglutamic.acid					
C18_11d_WS1	23.244	0.011	0.054	5.790	
C18_11d_WS2	17.190	0.013	0.046	4.354	
C18_11d_WS3	18.909	0.006	0.104	8.169	
C18_11d_WS4	23.579	0.008	0.111	10.445	
C18_11d_WW1	31.264	0.006	0.066	4.966	
C18_11d_WW2	31.233	0.008	0.058	5.408	
Quinic.acid X3.caffeoylquinic.acid Raffinose Rhamnose					
C18_11d_WS1	1.615		0.677	1.117	0.603
C18_11d_WS2	1.304		0.635	1.544	0.472
C18_11d_WS3	1.254		0.378	0.961	0.516
C18_11d_WS4	1.106		0.423	1.164	0.634
C18_11d_WW1	1.985		0.576	0.870	0.534
C18_11d_WW2	1.513		0.462	1.001	0.747

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

----- 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

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

----- mldata: Metabolites featuredata 18/19 -----

name	description	class	nrow	ncol
12 mldata 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:
 $ variety      : 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	Fleurta
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 >
```

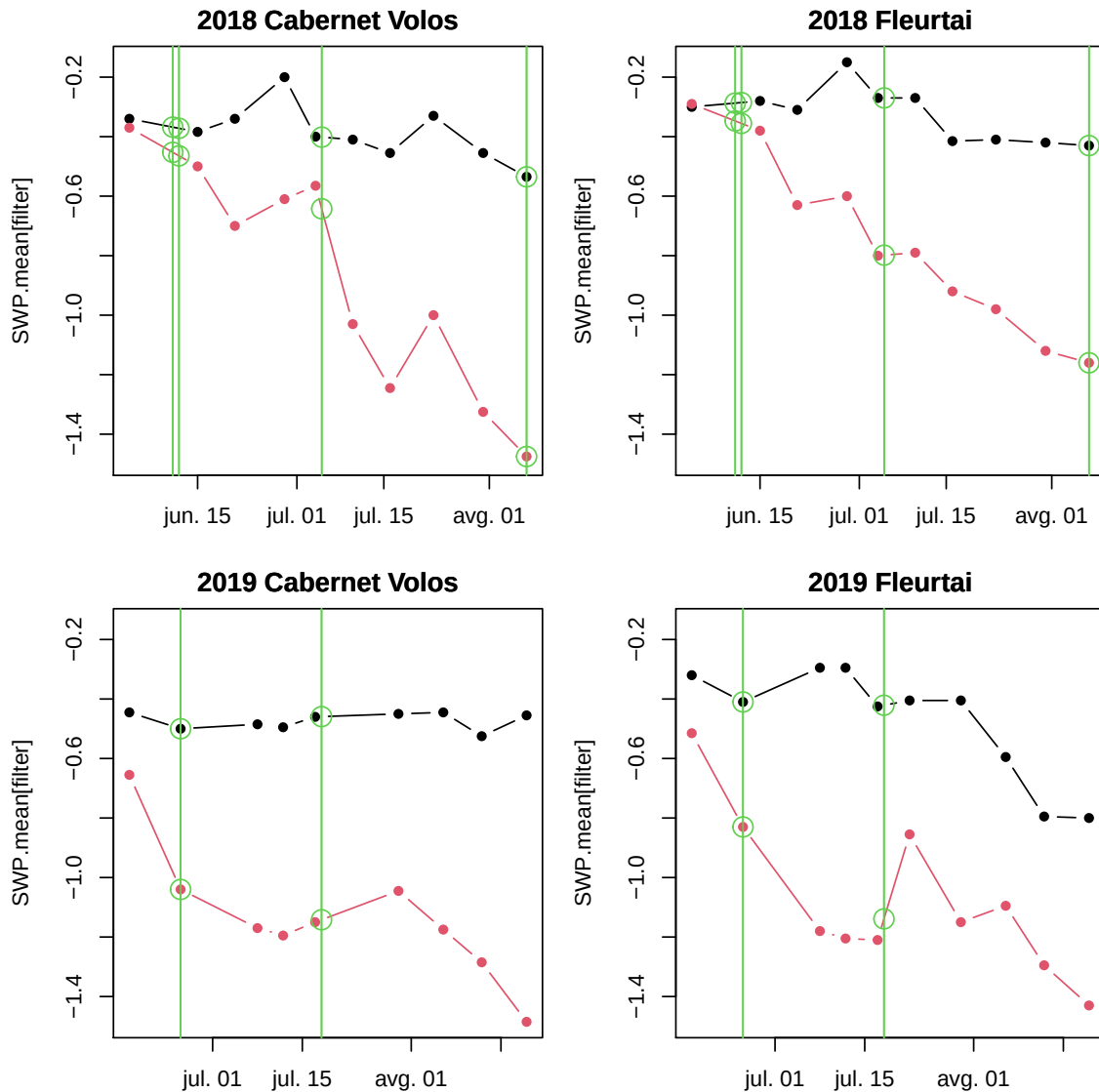
```
> pdata1819$date <- as_date(pdata1819$Date, format="%d.%m.%Y")
> table(pdata1819$date)
```

```
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"))
> wpa <- wpas[,1:2]
```

@@

Order water potential data by date

```
> diff(wpas$date)
```

Time differences in days

```
[1] 23 33 -57 1 23 33 -57 1 23 33 -57 380
[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
[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))
```

yr	variety	treat	date 2018-06-11	2018-06-12	2018-07-05	2018-08-07	2019-06-26
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  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"
```

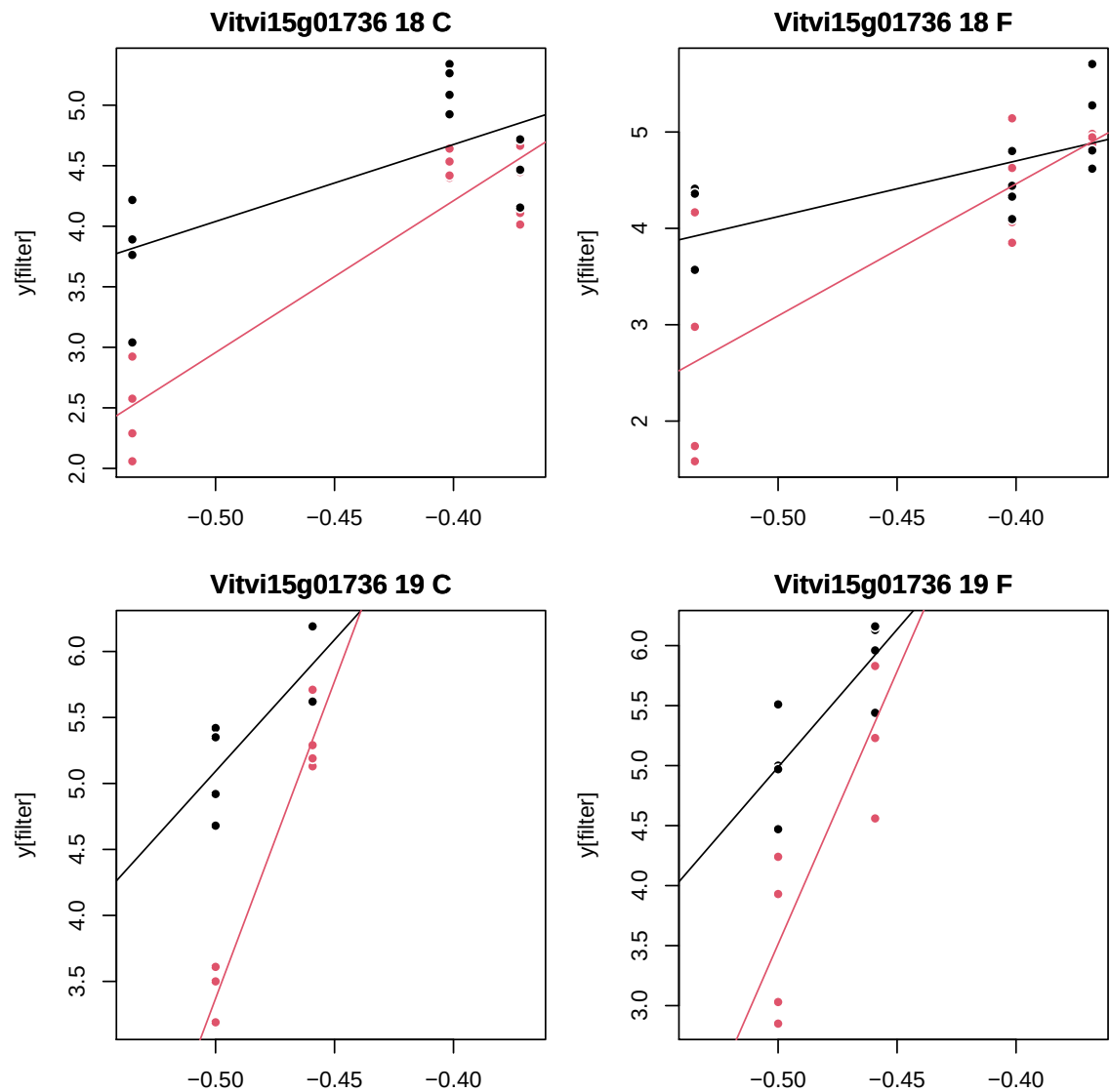
```
Call:
lm(formula = y[select] ~ pd$swp[select])
```

```
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 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(tl1819)[10]
```

```
> pd <- pdata1819
```

```
> (y <- unlist(tl1819[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(wpas$swp, wpas[, c("date", "treat", "variety")], unique)
> 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

```

```

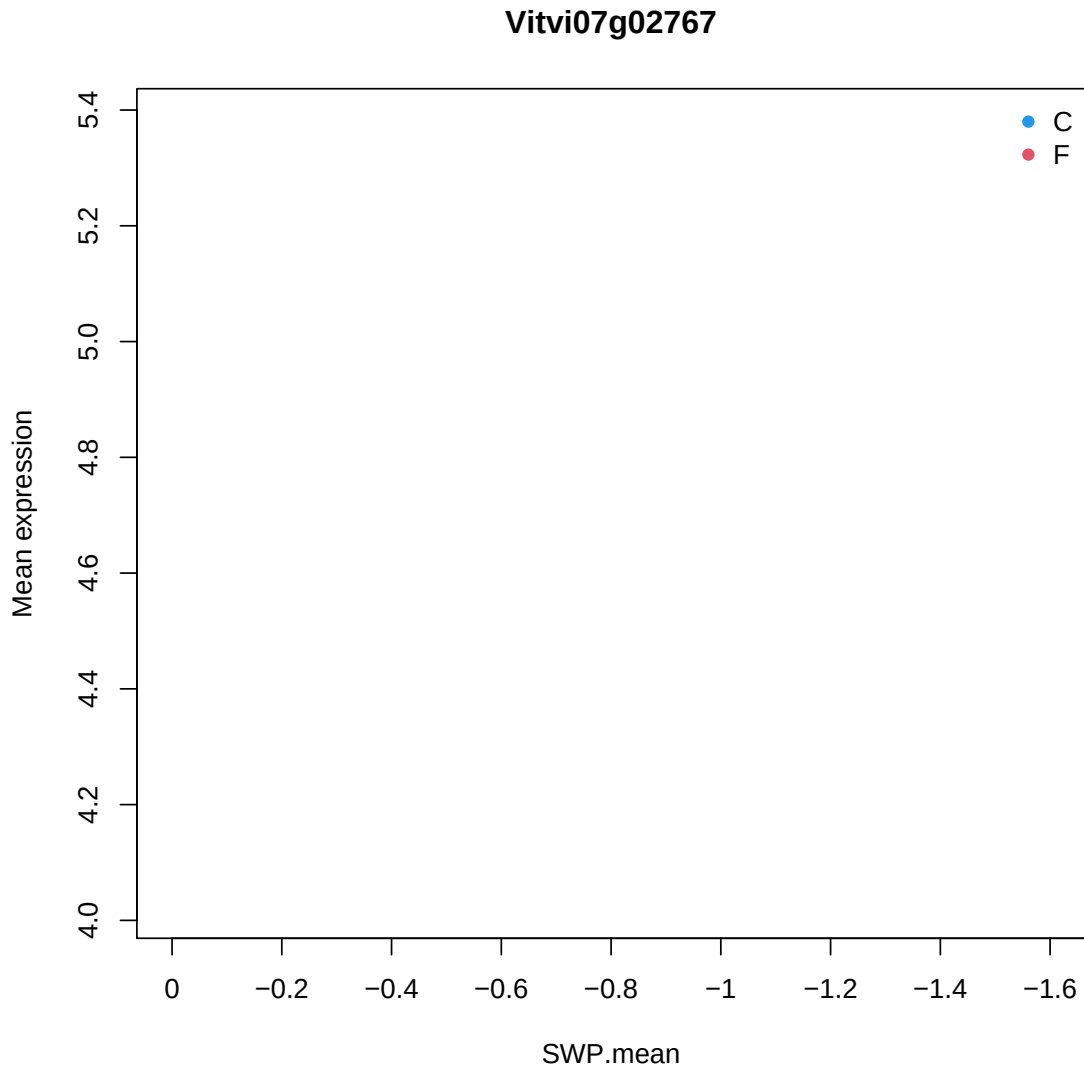
> ylim <- range(means, na.rm=TRUE)
> xlim <- c(min(wpas$swp, -1.6, na.rm=TRUE), max(wpas$swp, 0, na.rm=TRUE))
> vlvs <- unique(wpas$variety)
> tlvs <- rev(unique(wpas$treat))
> cols <- c(4, 2)
> pchs <- c(16, 16)
> plot(1, 1, #wpas$swp[tfilter & vfilter], means[, "WS", vlvs[i]],
+      ylim=ylim,
+      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 = vlvs)

```



```

> #
> for(i in 1:length(vlvs)){
+ for( j in 1:length(tlvls)){
+ tfilter <- wpas$treat %in% tlvls[j]
+ vfilter <- wpas$variety %in% vlvs[i]
+ yy <- means[as.character(wpa$date),tlvls[j],vlvs[i]]
+ wpa <- wpa[tfilter & vfilter,]
+ all(wpa$date==names(yy))
+ points(-wpa$swp, yy,
+       col = cols[j],
+       pch = pchs[j]
+     )
+   }
+ }
Error in xy.coords(x, y): 'x' and 'y' lengths differ

```

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=NULL, all=TRUE){
+   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$swp,0, na.rm=TRUE))
+   vlvs <- levels(wpas$variety)
+   tlvs <- levels(wpas$treat)
+   #cols <- c(4,2)
+   #pchs <- c(1,16)
+   plot(1,1, #wpas$swp[tfilter & vfilter], means[, "WS",vlvs[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= vlvs)
+   } else {
+     legend("topright", bty="n", pch=pchs, col=rep(cols,each=2),lwd=lwd,
+       legend= outer(tlvs,vlvs,paste))
+   }
+   #
+   allx <- NULL
+   ally <- NULL
+   fits <- list(name=varname)
+   for(i in 1:length(vlvs)){
+     #for( j in 1:length(tlvs)){
+     #tfilter <- wpas$treat %in% tlvs[j]
+     vfilter <- wpas$variety %in% vlvs[i]
+     wpa <- wpas[vfilter,]
+     means[, ,vlvs[i]]
+     mns <- melt(means[, ,vlvs[i]])
+     mns
+     wp <- melt(swps[, ,vlvs[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,
```



```

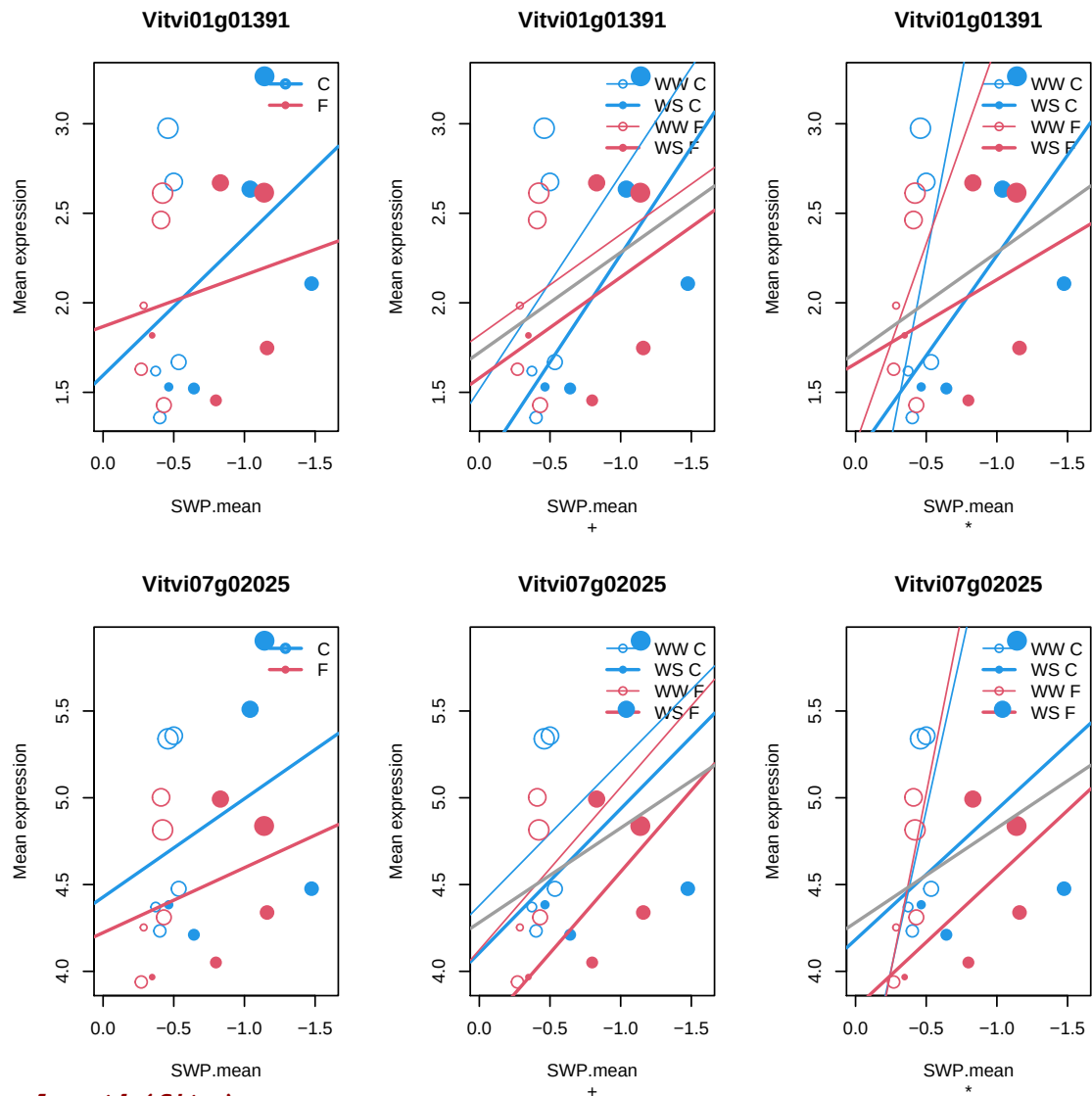
+       col = cols[i],
+       pch = pchs[as.numeric(mns$treat)]
+       , cex=cex
+     )
+ #   }
+   xx <- xx
+   if(model=="") fit <- lm(yy~xx)
+   if(model=="+") fit <- lm(yy~xx+mns$treat)
+   if(model=="*") fit <- lm(yy~xx*mns$treat)
+   if(verbose) print(summary(fit))
+   coef <- fit$coefficients
+ #   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[[v1vls[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$swp, 0, na.rm=TRUE))
+   vlvs <- levels(wpas$variety)
+   tlvs <- 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

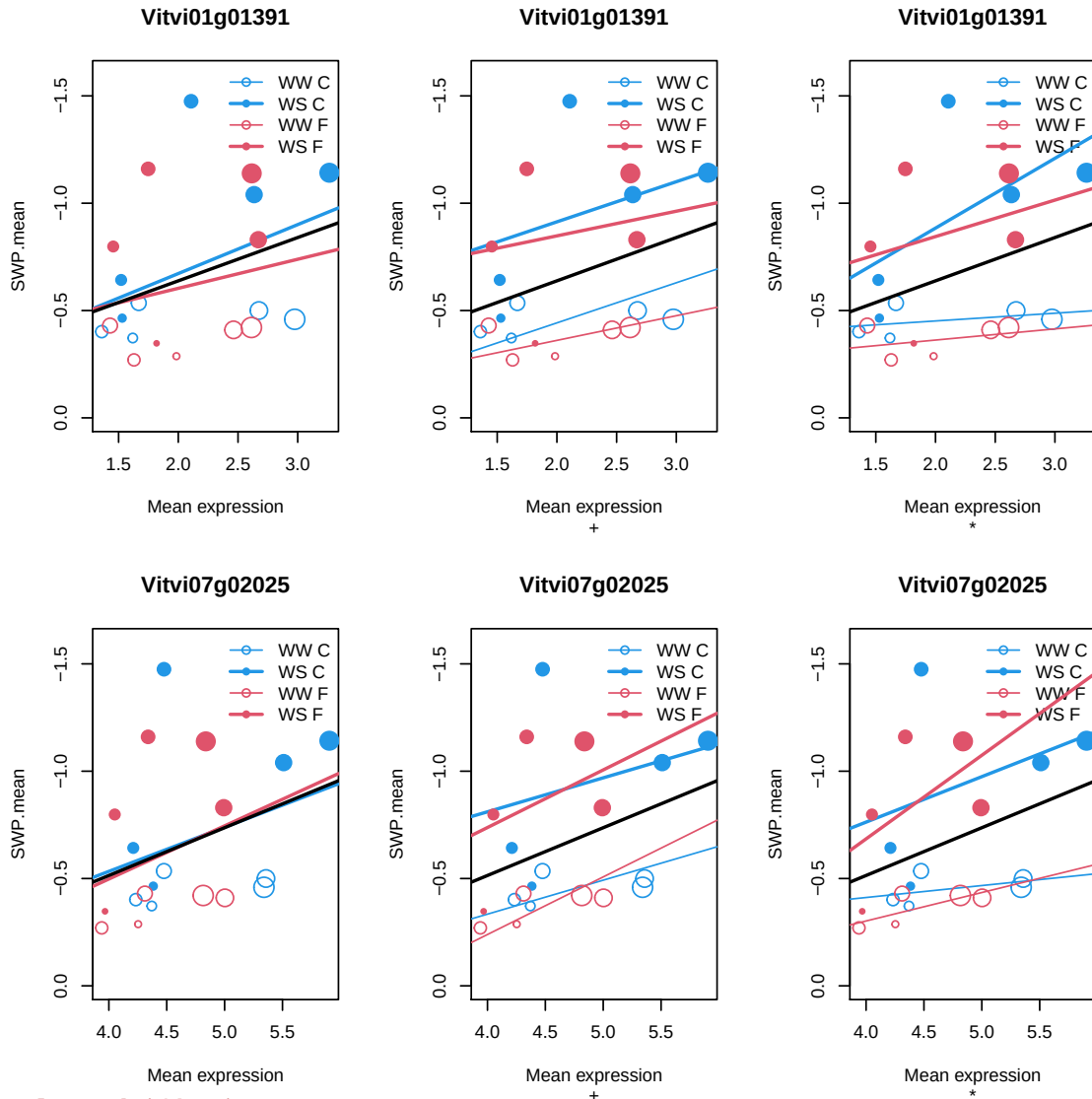
```

```

+ 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

```

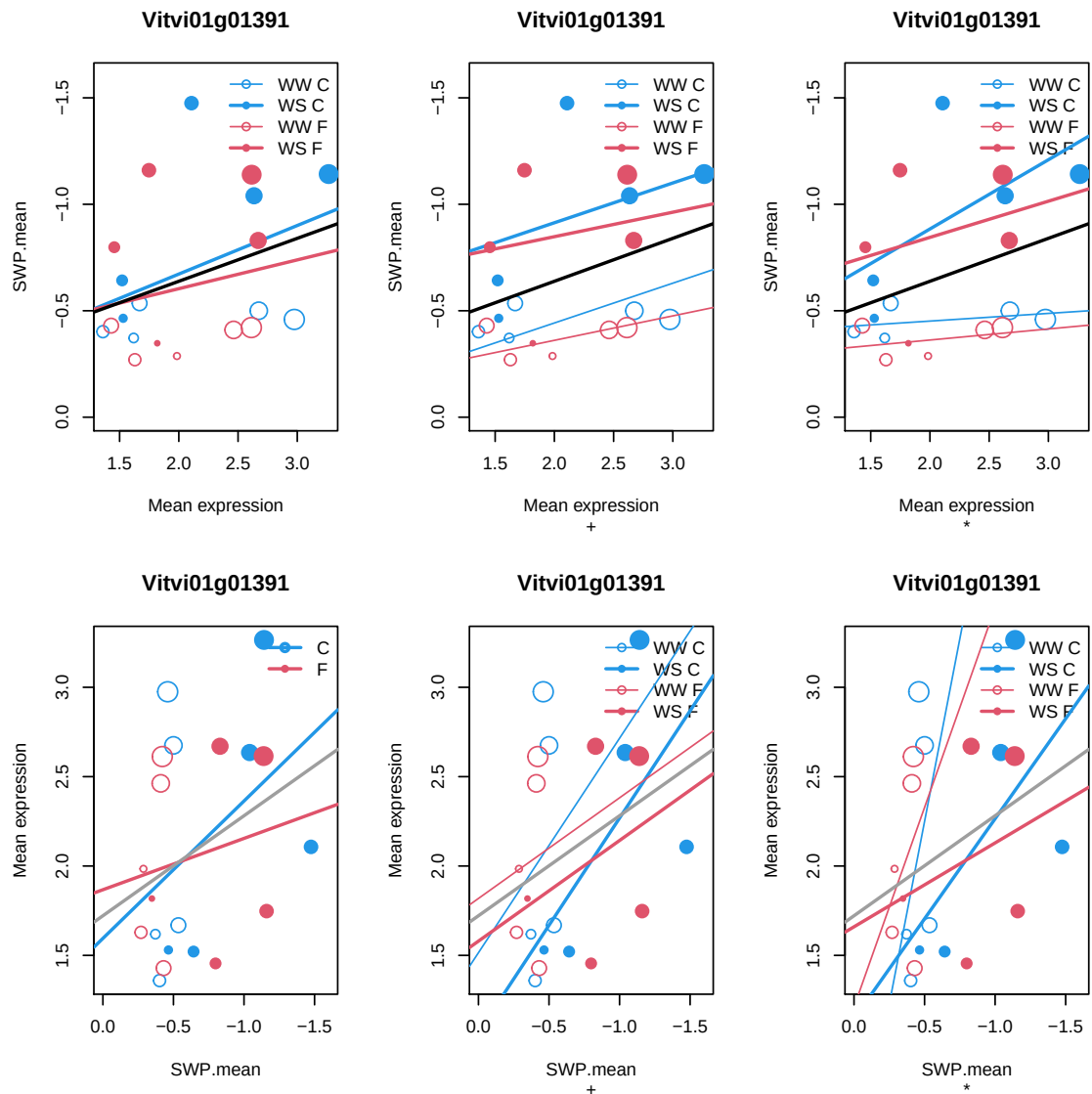
```

> 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)]

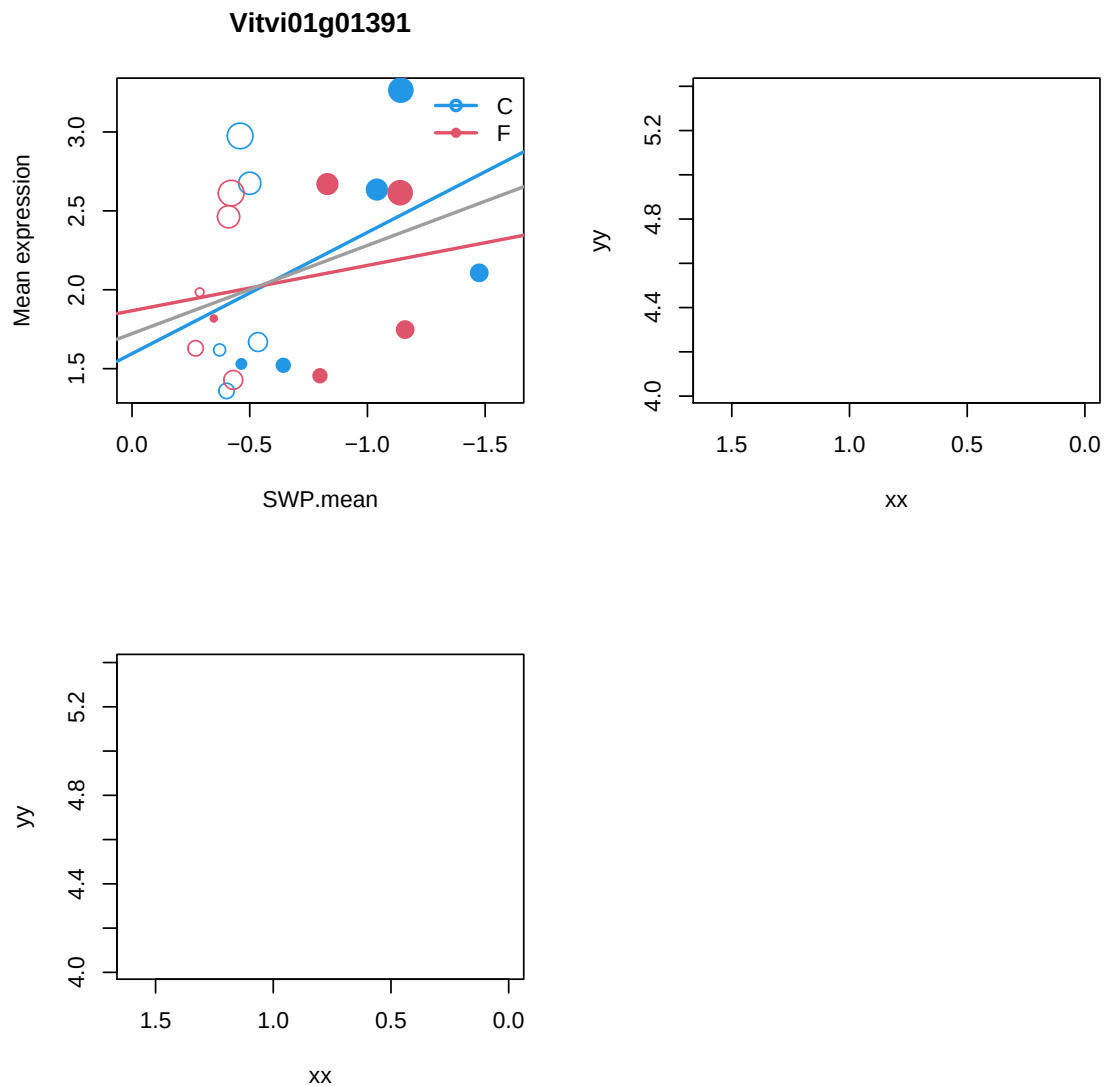
```



```

+ plot(xx, yy, pch=16, col=cols[i], xlim=-xlim, ylim=ylim)
+ fit <- lm(yy ~ xx)
+ abline(fit, col=cols[i])
+ }

```



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(tl1819[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
```

	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

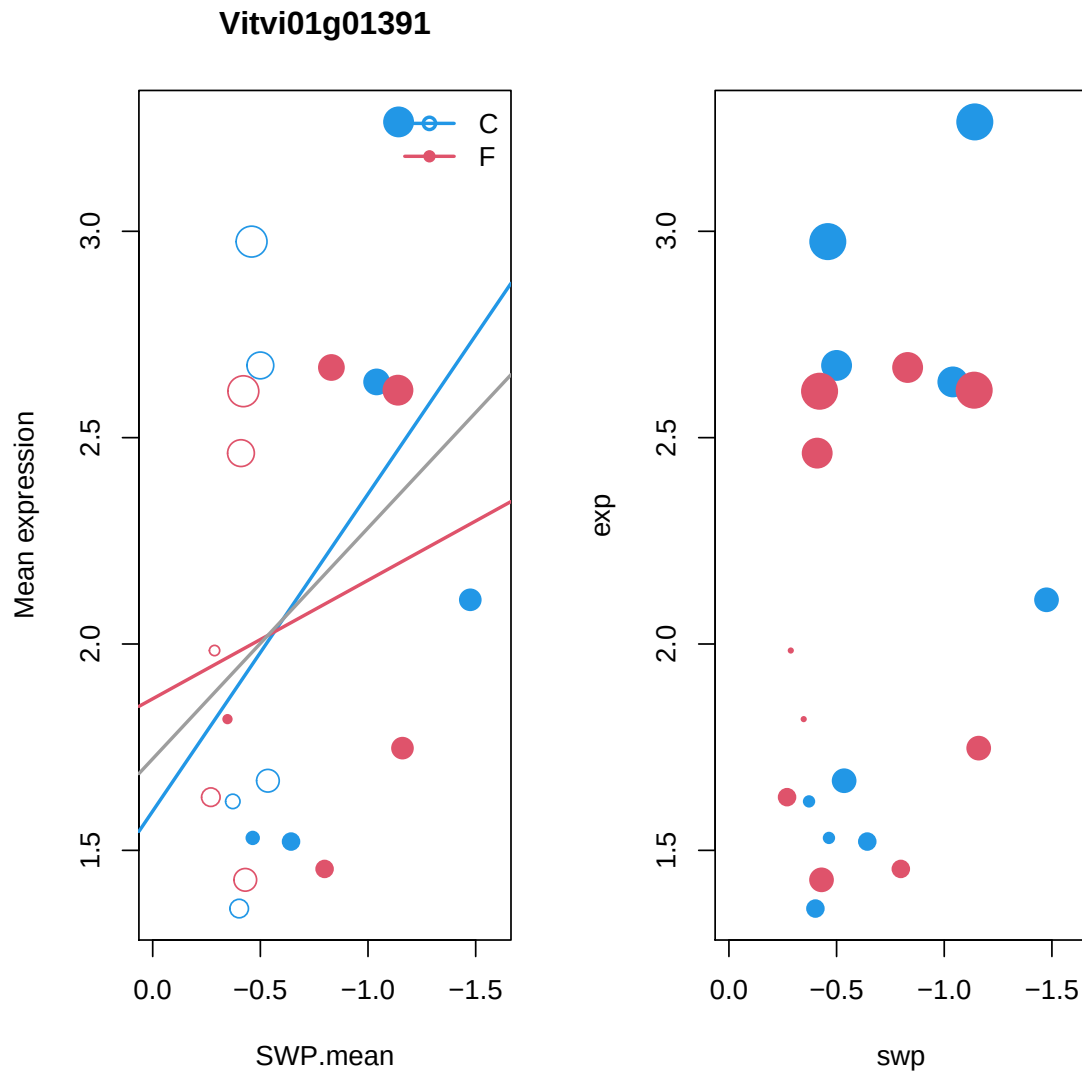
Label: Interpolated swp data, considered as phenodata when swp is used.

File :

[../..output/50_Expression-water-stress-0.05-1.5-0.5-1-1-3/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" "Vitvi07g02830" ...
..$ : 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" "Vitvi07g02830" ...
..$ : 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" ...

```

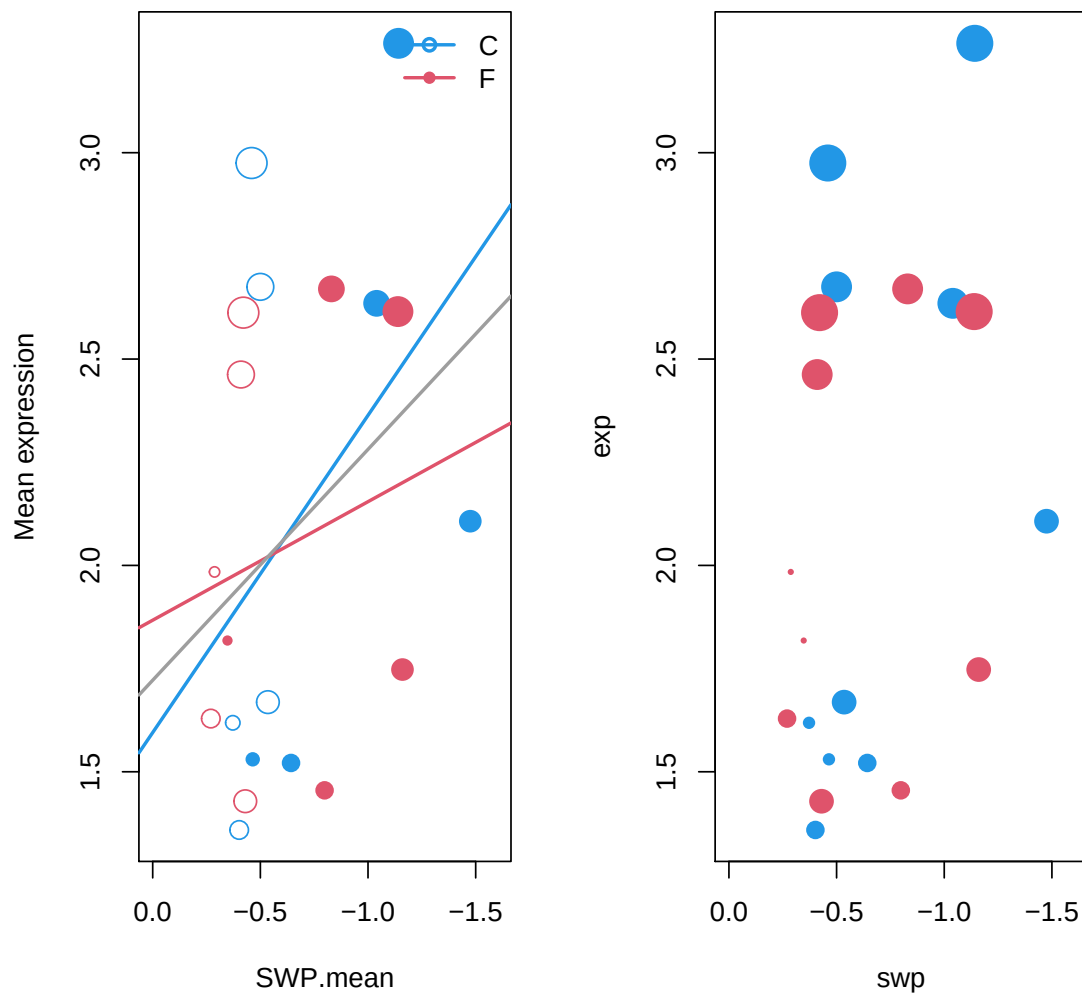
Check regressions

```

> 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)

```

Vitvi01g01391



```

> 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/", "50c_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

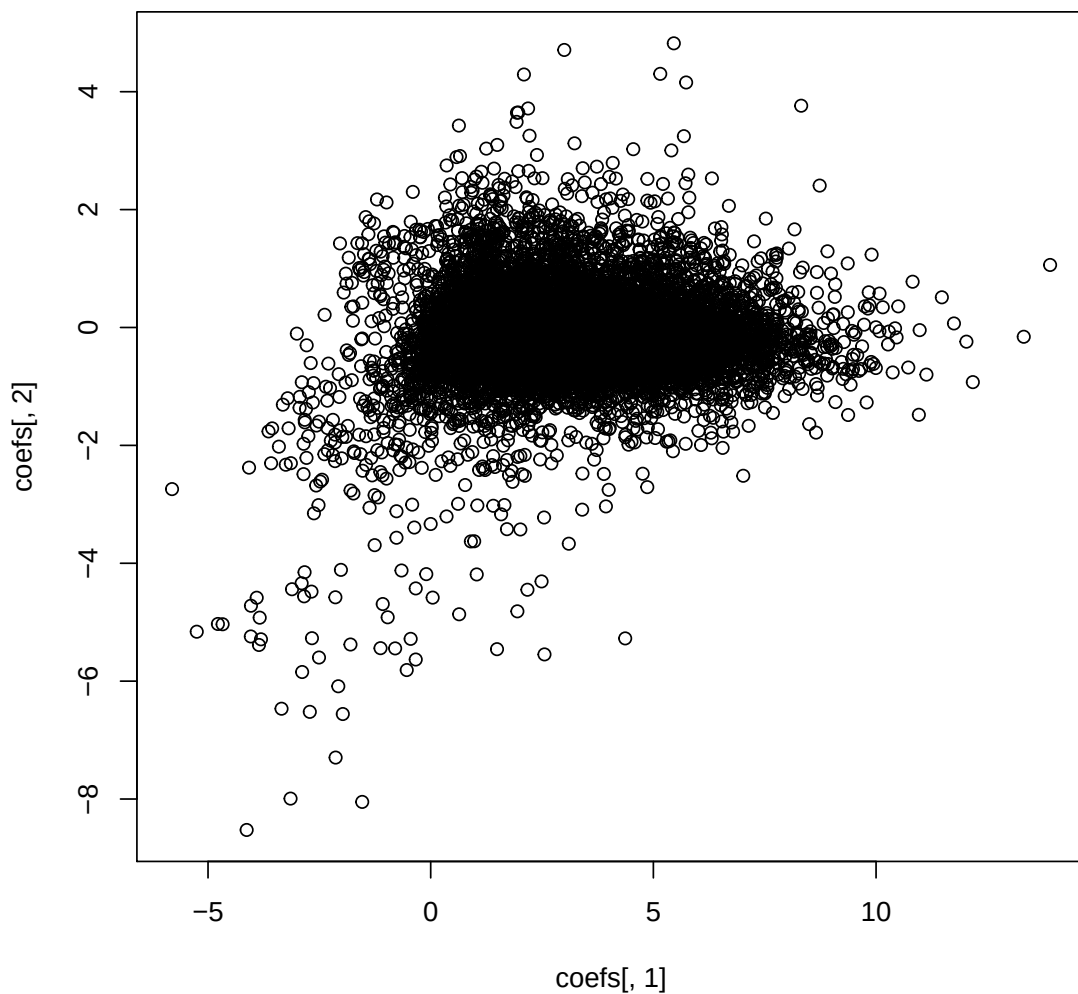
> fit1 <- eBayes(fit1)
> fit1[testvar,]$coefficients
      (Intercept)      swp
Vitvi01g01391    1.721772 -0.5593981

> 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

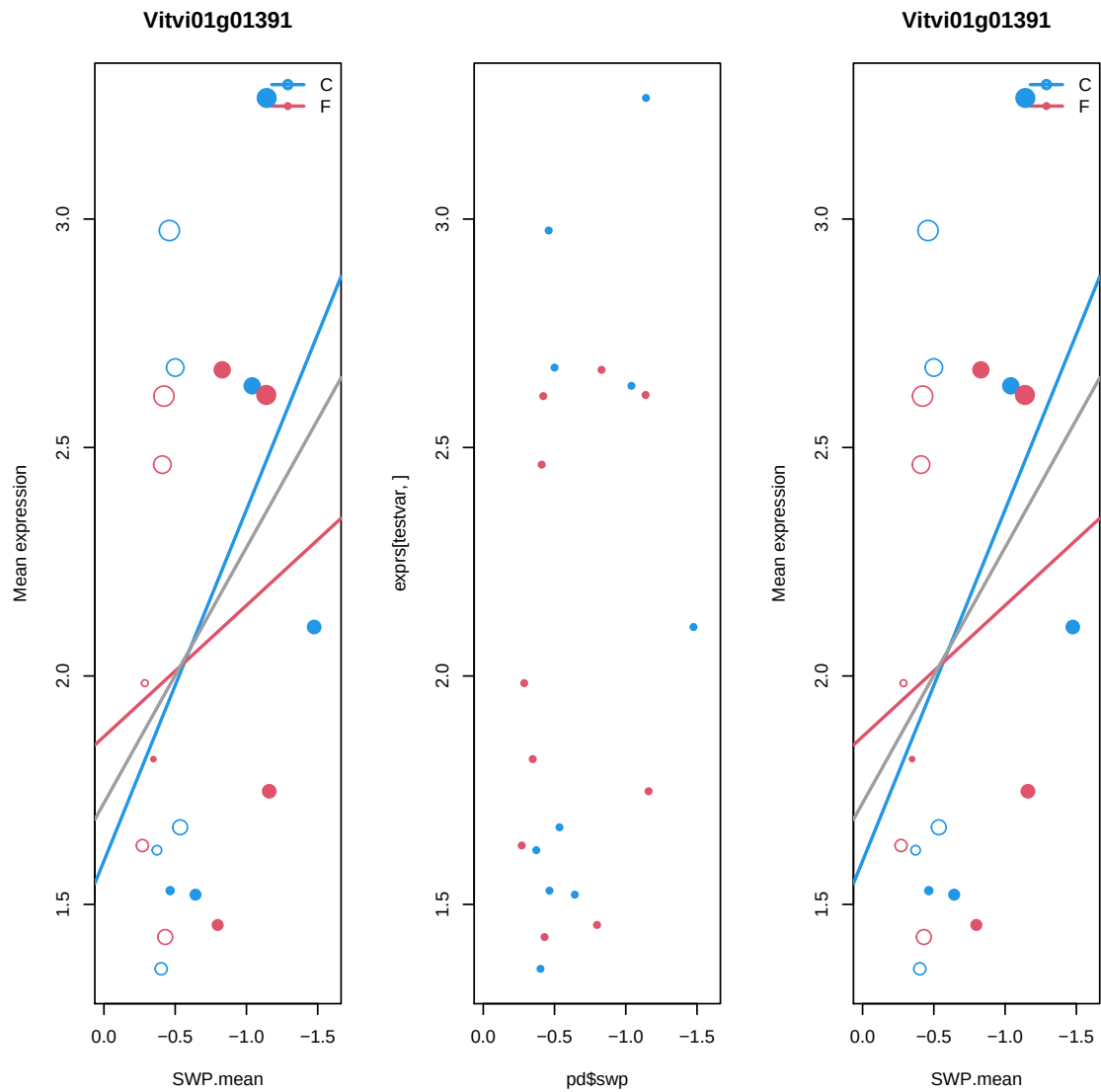
```
> varname <- testvar
> par(mfrow=c(1,3))
> p <- plot.ewp(varname,model="")
> plot(pd$swp,exprs[testvar,], xlim=c(0,-1.6),
+      ,pch=16, col=6-as.numeric(pd$variety)*2,cex=pd$day/2)
> c(p$C$coef[2],p$F$coef[2])
```

	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

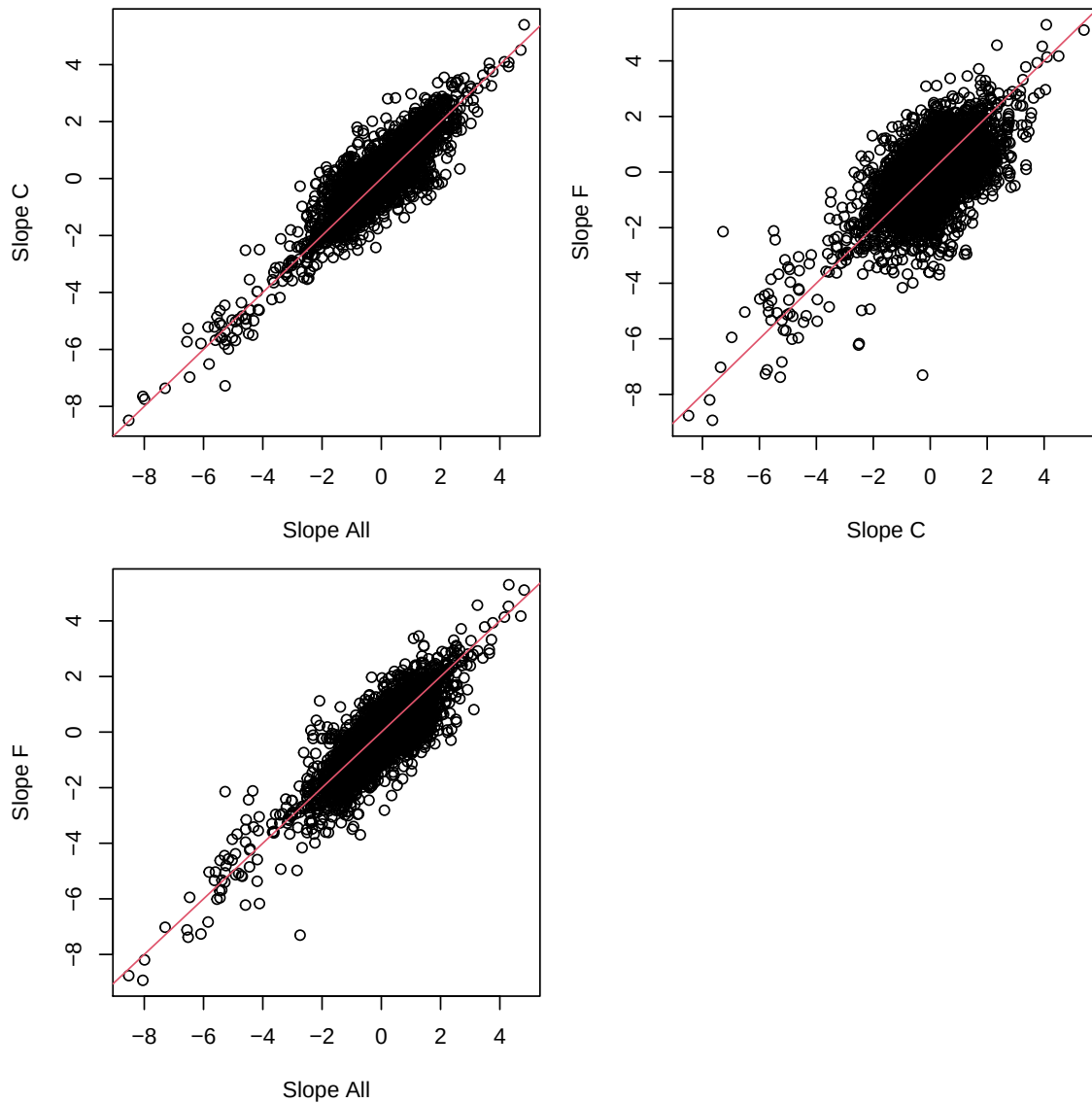
> fit2[testvar,]$coefficients[2]
[1] -0.7685916

> 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

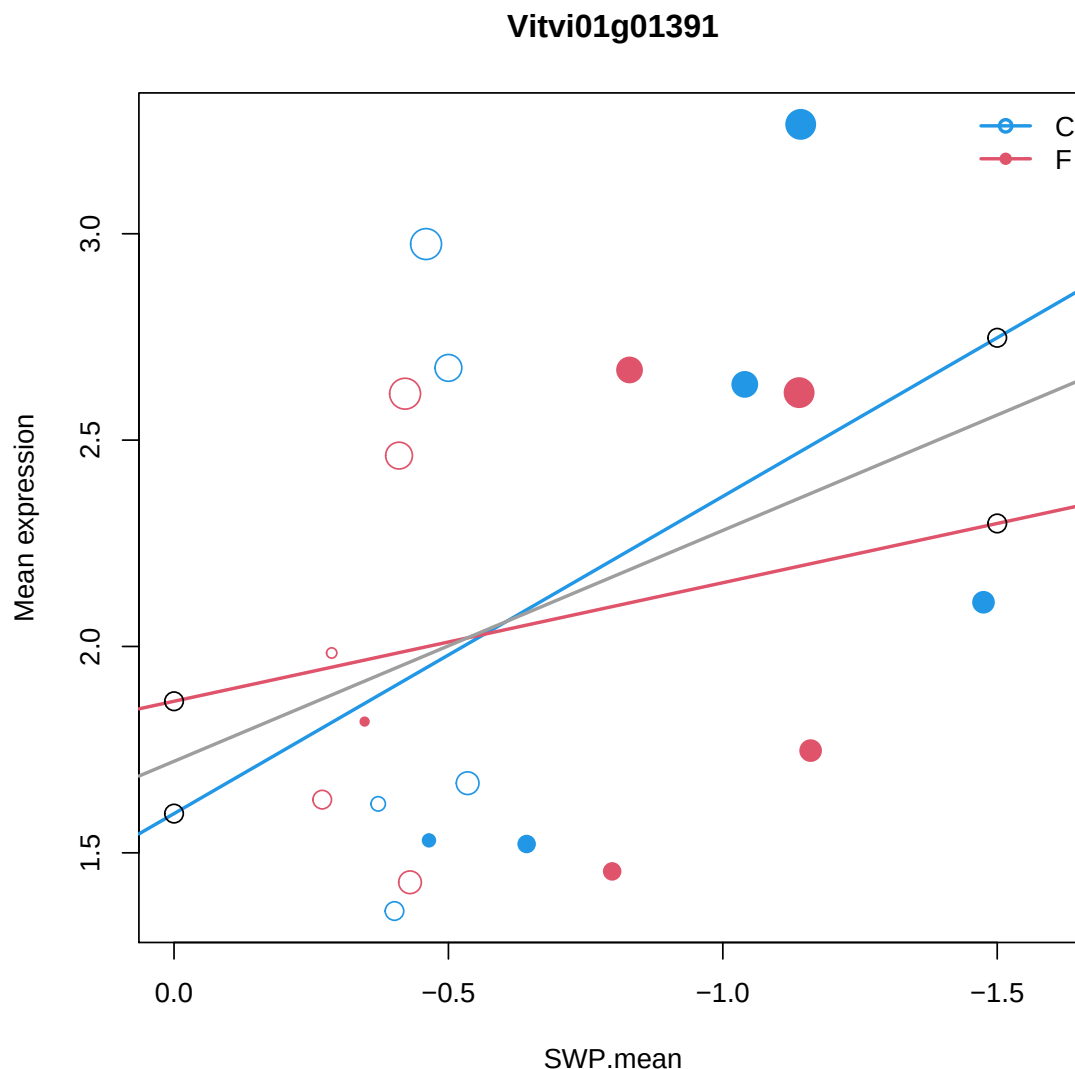
```

Object fit3 holds mean expressions for varieties.
Predicting expression for given SWP value

```

> p <- plot.ewp(varname,model="", exprs=exprs, pd=pd)
> x <- 0
> points(rep(x,2) ,my.predict(fit2,x=x)[varname,], cex=1.5)
> x <- -1.5
> points(rep(x,2) ,my.predict(fit2,x=x)[varname,], cex=1.5)

```



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

```

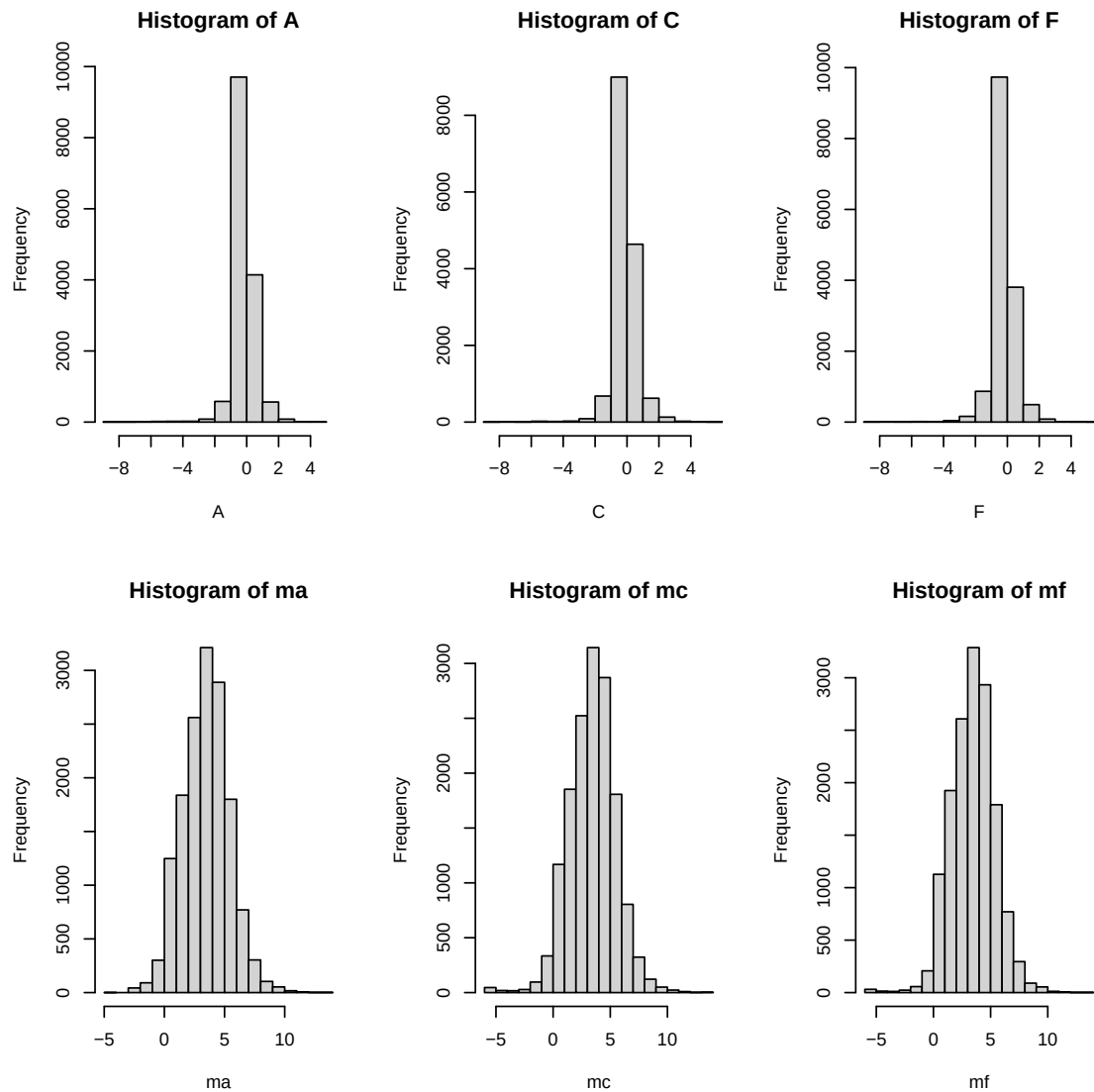
      mc      mf
Vitvi15g01736  4.430191 4.5232904
Vitvi07g02832 -2.991443 2.6259591
Vitvi07g02830 -2.839209 2.1903769
Vitvi07g02812 -1.374475 0.6817977
Vitvi07g02811  1.837984 3.1363800
Vitvi09g02033 -3.137869 1.5632132

> 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)
```



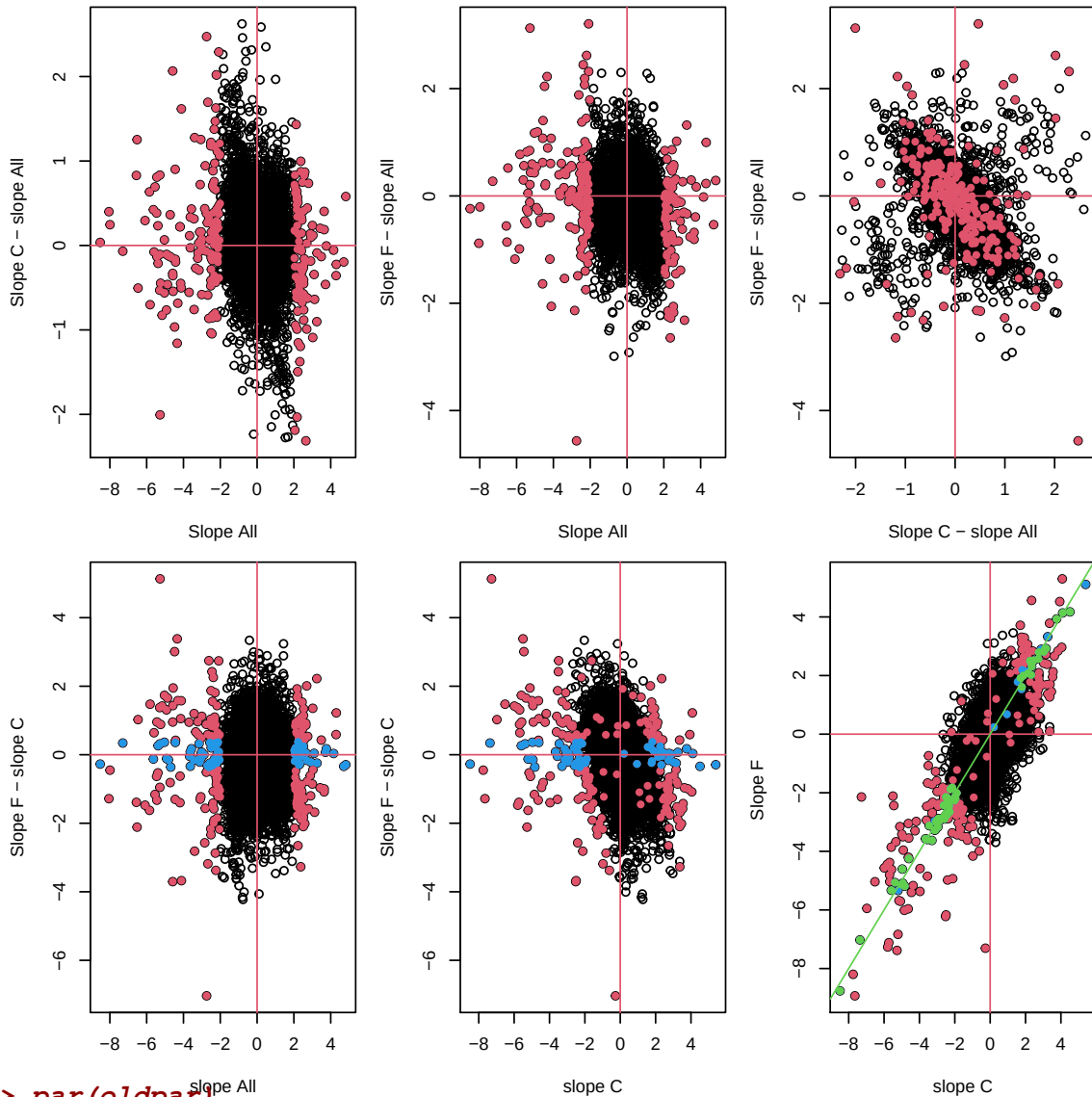
5.4.2 Types by effects

```
> 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 ... ($<$)

deltax difference of mean x-y treshold ($<$)

```
> .deltam      # <- 2
[1] 2
> .min.slope    # <- 2
.min.slope
1.5
> .max.slope    # <- 0.5
.max.slope
0.5
> .diff.slope   # <- 1
.diff.slope
1
> .maxfc        # <- 0.5
[1] 1
> .diff01
.diff01
1
> .deltam2      # <- .deltam/2
[1] 1
```

6.1 Old Types

Type1

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

Absolute slope C or F larger than 1.5 with difference of slopes smaller than 1 and difference of means below 2.

Type2

```
> #type2 <- (large_abs_C & large_abs_F) & (abs(fc) > diff.slope) & (abs(mc-mf)>0)
> #type2 <- type2 & ( (C*F >0) )
```

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

```
> #
> delta <- 2
> #
> (deltam <- as.numeric(.deltam)) #2
[1] 2
> (deltam2 <- as.numeric(.deltam2)) # delta mean for type 2
[1] 1
> (min.slope <- as.numeric(.min.slope)) # 2 # slope C larger
```

```

[1] 1.5
> (max.slope <- as.numeric(.max.slope))      # slope C smaller
[1] 0.5
> min.slope <- min.slope      # slope F larger
> max.slope <- max.slope      # slope F smaller
> minA <- min.slope      # slope A larger
> (diff.slope <- as.numeric(.diff.slope)) # 1      # difference F - C larger
[1] 1
> (diff.slope5 <- as.numeric(.diff.slope5)) # difference for F - C larger for
[1] 2
> (maxfc <- as.numeric(.maxfc))      # difference F - C smaller
[1] 1
> maxca <- maxfc      # difference C - A smaller
> maxfa <- maxfc      # difference F - A smaller
> #
> large_abs_A <- abs(A) > minA
> large_abs_C <- abs(C) > min.slope
> large_abs_F <- abs(F) > min.slope
> #
> 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 14775  146
TRUE    28  293

> points(
+   C[type1],
+   F[type1],
+   col=2, pch=16)
> #
> type2 <- (large_abs_C & large_abs_F) & (abs(fc) > diff.slope) & (abs(mc-mf)>de
> type2 <- type2 & ( (C*F >0) )
> points(
+   C[type2],
+   F[type2],
+   col=3,pch=16)
> #
> type30 <- ((abs(C)<max.slope) | (abs(F)<max.slope)) & (abs(fc)> diff.slope)
> type3 <- ((abs(C)<max.slope) | (abs(F)<max.slope)) & (abs(fc)> diff.slope) & (ab
> table(type3,type30)

```

```

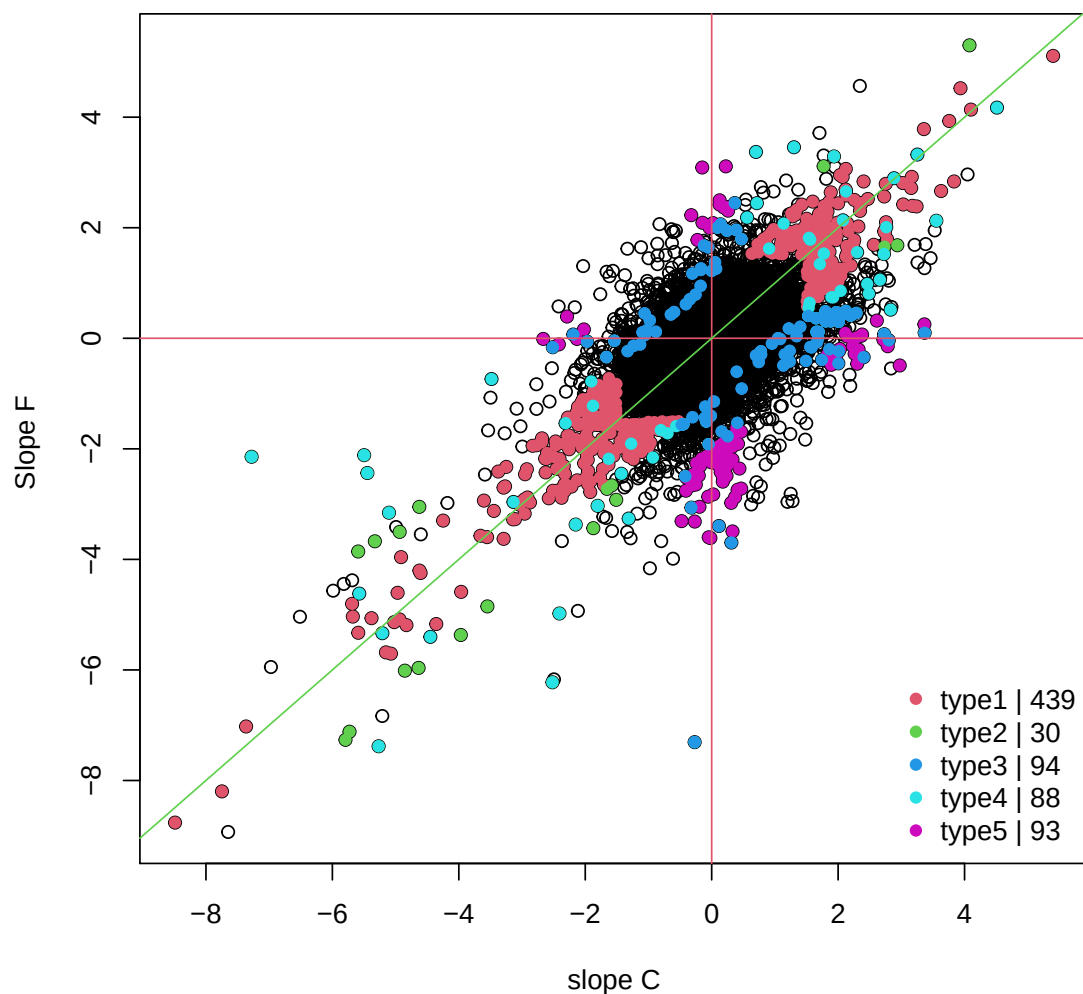
      type30
type3  FALSE  TRUE
      FALSE 14139 1009
      TRUE   0    94

> 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)<max.slope) | (abs(F)<max.slope)) & (abs(fc)> diff.slope5) & (a
> 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

```



6.2 New type definitions

After discussion with Maruša on Feb 3, new type definitions were summarized in the excel file.

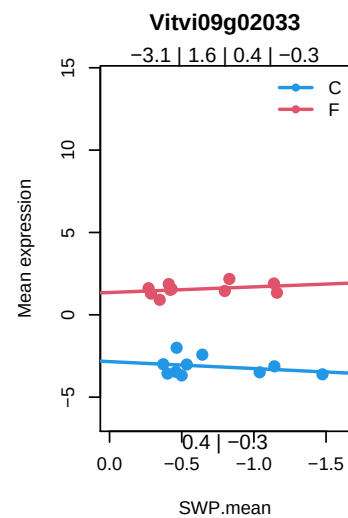
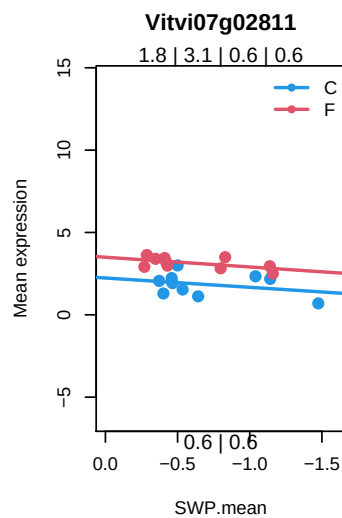
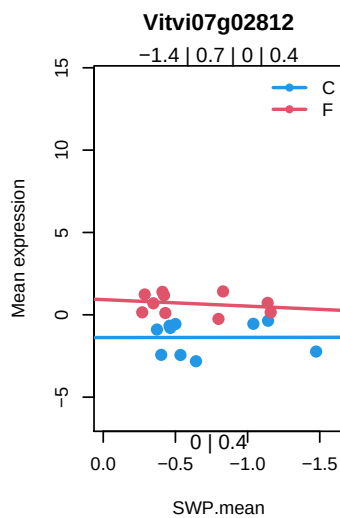
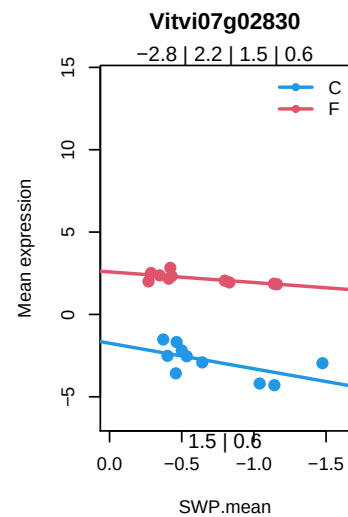
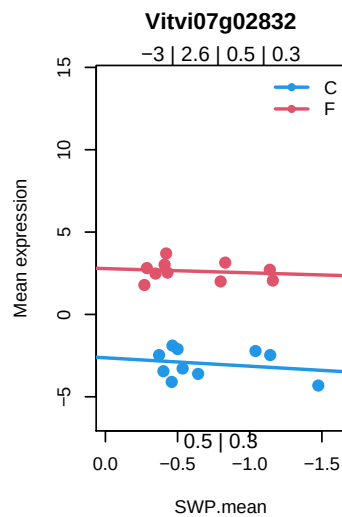
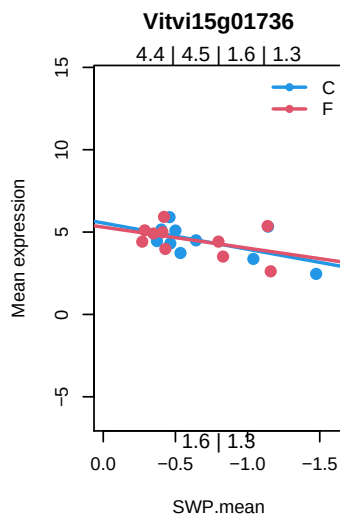
Function to plot the overview for types

```
> #' Plot selected expression swp graphs for selected genes
> #'
> #' @param filt logical vector to select genes, typically type identification
> #' @param
> #' @return Plot first six exprs-swp situations
> #' @export
> #' @seealso \code{\link{funkcija}}
> #' @note
> #' @references
> #' @keywords package
> #' @title
> #' @author Andrej Blejec \email{andrej.blejec@nib.si}
> #' @examples
```

```

> #' plot.type() # TRUE most of the time
>
> plot.type <- function( filt=rep(TRUE,6), ... ){
+ par(mfrow=c(2,3), oma=c(0,0,1,0))
+ #filt <- type1
+ print(sum(filt))
+ 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)
+ , all = FALSE
+ )
+ 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)
+ }
+ }
> plot.type()
[1] 6

```




```
> (min.slope <- as.numeric(.min.slope))      # slope C larger
[1] 1.5
> (max.slope <- as.numeric(.max.slope))      # slope C smaller
[1] 0.5
> (diff.slope <- as.numeric(.diff.slope))    # difference of slopes
[1] 1
> (diff01 <- as.numeric(.diff01))           # difference at extremes
[1] 1
```

6.2.1 Parameter explanation

.min.slope (1.5) Lower level for large slope

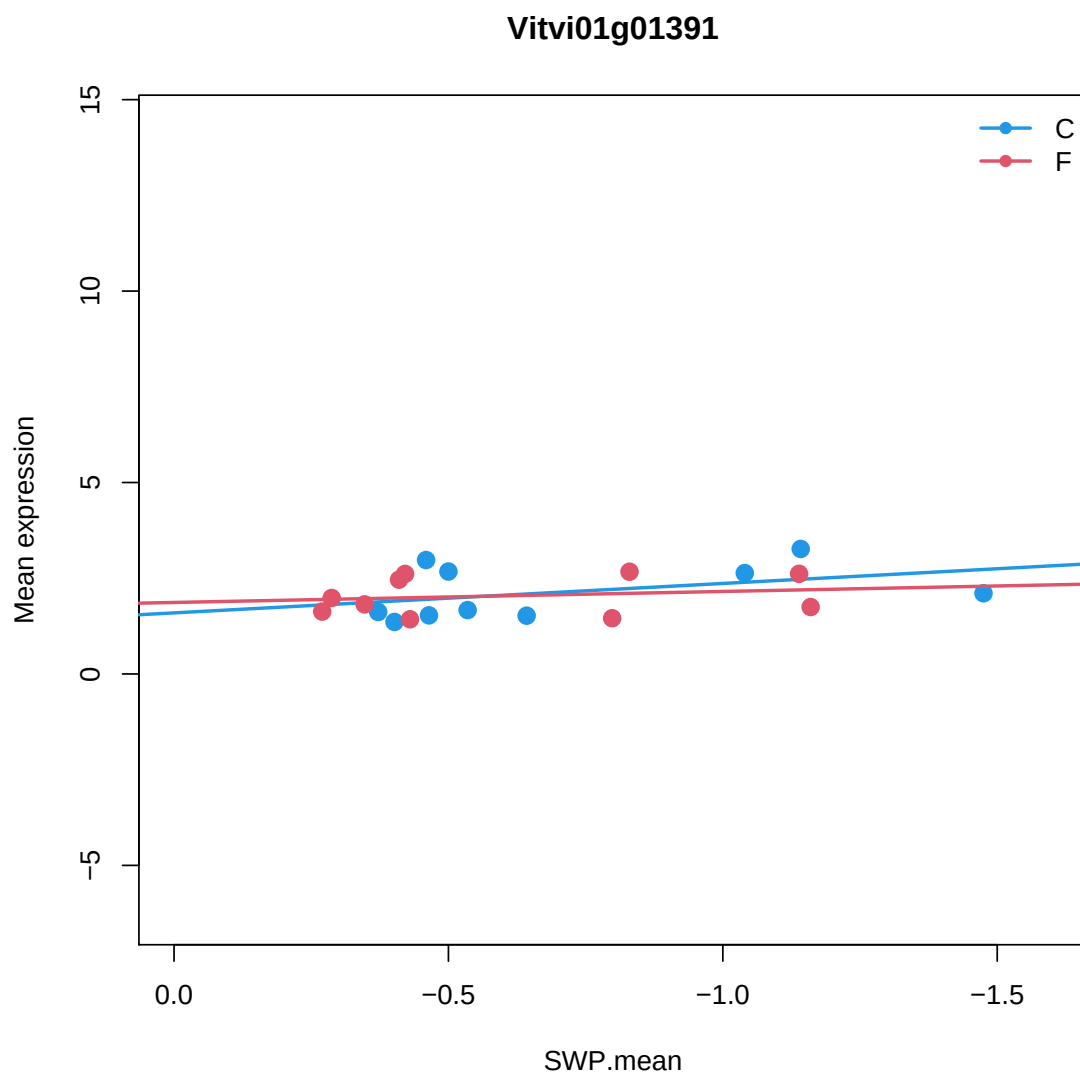
.max.slope (0.5) Upper level for small slope

.diff.slope (1) Threshold for slope difference

.diff01 (1) Threshold for differences of predicted values at 0 and -1.5

Preparation for decision rules

```
> # predicted values
> left <- my.predict(fit2, x = -0.2)
> right <- my.predict(fit2, x = -1.4)
> left[varname,]
               mc               mf
Vitvi01g01391 1.74876 1.924696
> right[varname,]
               mc               mf
Vitvi01g01391 2.671069 2.269314
> p <- plot.ewp(varname,model="", exprs=exprs, pd=pd, ylim=range(exprs)
+           , cex= 1.5
+           , pch = c(16,16)
+           , all = FALSE
+           )
```

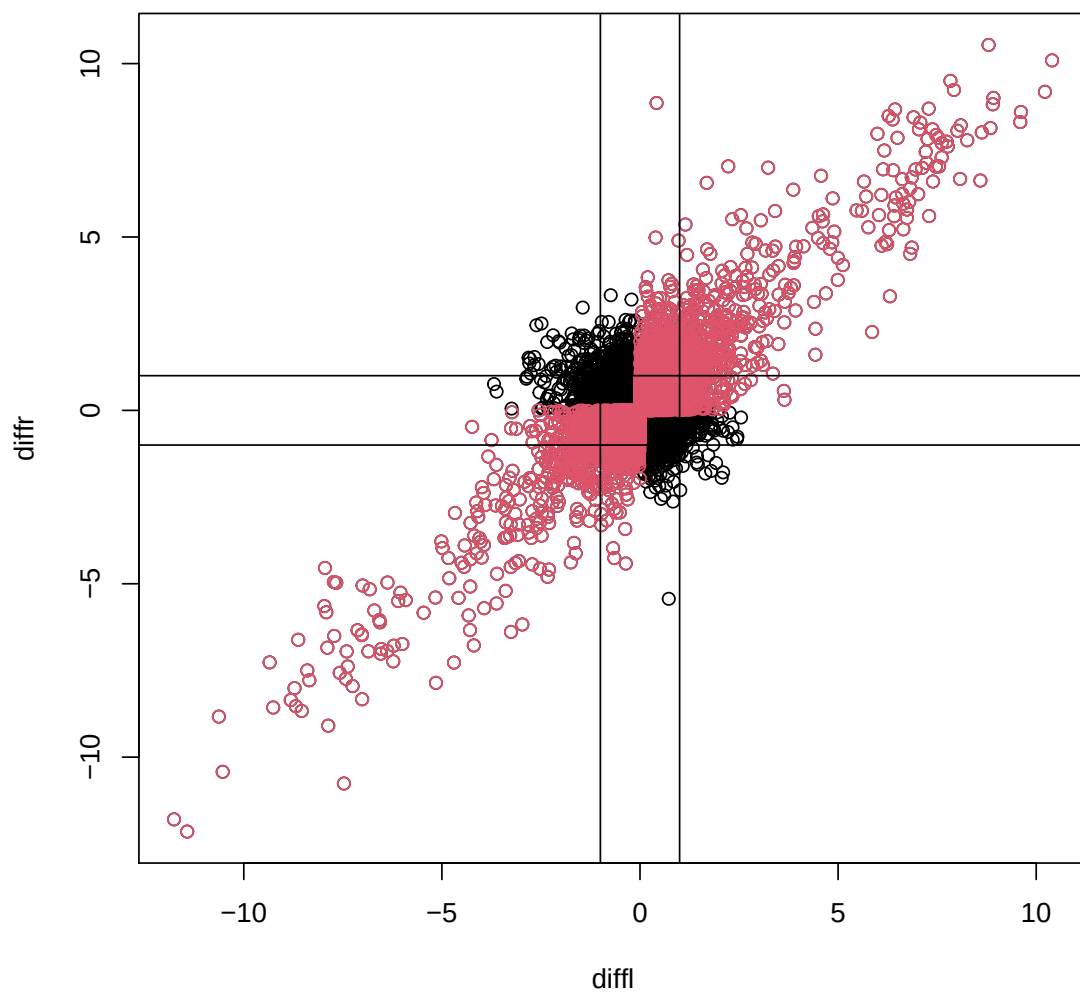


```

> # differences at the no-crossing borders
> diff1 <- apply(left,1,diff)
> diff2 <- apply(right,1,diff)
> nocross <- (diff1*diff2>0)
> # differences of predicted values at extremes
> diff0 <- apply(my.predict(fit2,x=0),1,diff)
> diff1 <- apply(my.predict(fit2,x=-1.5),1,diff)

> plot(diff1,diff2)
> points(diff1[nocross],diff2[nocross], col=2)
> abline(h=c(-.diff01,.diff01),v=c(-.diff01,.diff01))

```

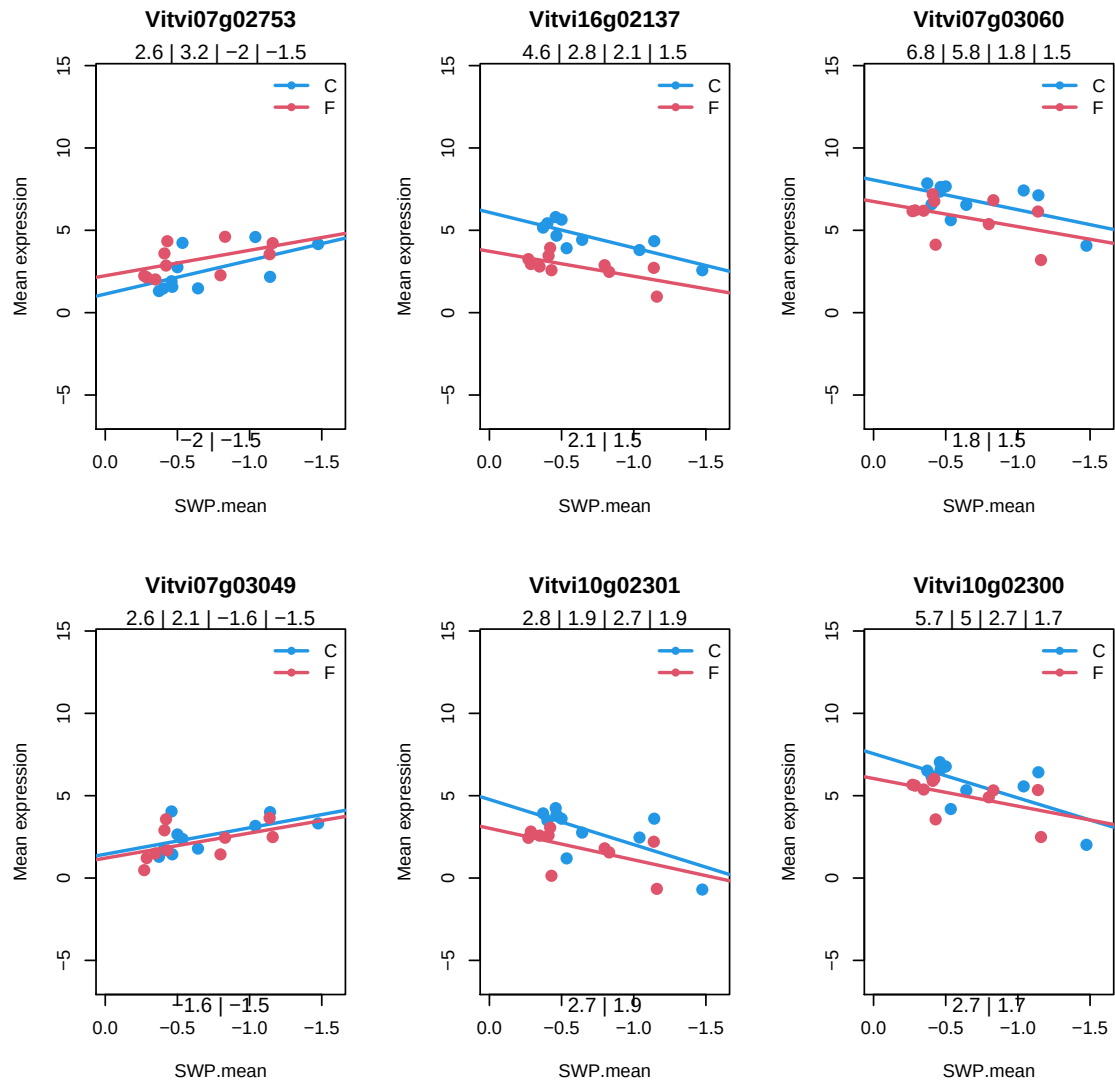


Function to plot coefficients for types

```

> largeslope <- ( abs(C) > min.slope) & (abs(F) > min.slope)
> plot.type(largeslope&nocross)
[1] 206

```



```
> head(types)
```

```

      type1 type2 type3 type4 type5
Vitvi15g01736 TRUE FALSE FALSE FALSE FALSE
Vitvi07g02832 FALSE FALSE FALSE FALSE FALSE
Vitvi07g02830 FALSE FALSE FALSE TRUE FALSE
Vitvi07g02812 FALSE FALSE FALSE FALSE FALSE
Vitvi07g02811 FALSE FALSE FALSE FALSE FALSE
Vitvi09g02033 FALSE FALSE 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, type="n", ...)
+   abline(h=0,v=0,col=2, lty=2)
+   abline(c(0,1),col=3)
+   points(x,y,col=8)
+   m <- ncol(type)
+   sek <- 1:ncol(type)
+
+   for( i in sek){

```

```

+ points(
+   x[type[,i]],
+   y[type[,i]],
+   col=i+1,pch=16)
+ }
+
+ if(!missing(title)) title(title)
+ nt <- apply(type,2,sum)
+ pre <- "" # substr(rep(" ",length(nt)),1,(3-nchar(nt))*2.3)
+ legend("bottomright",pch=rep(16,m),col=2:(m+1),legend=paste0(colnames(type),
+ )
> #plot.types(type=Types)

```

6.2.2 Type1

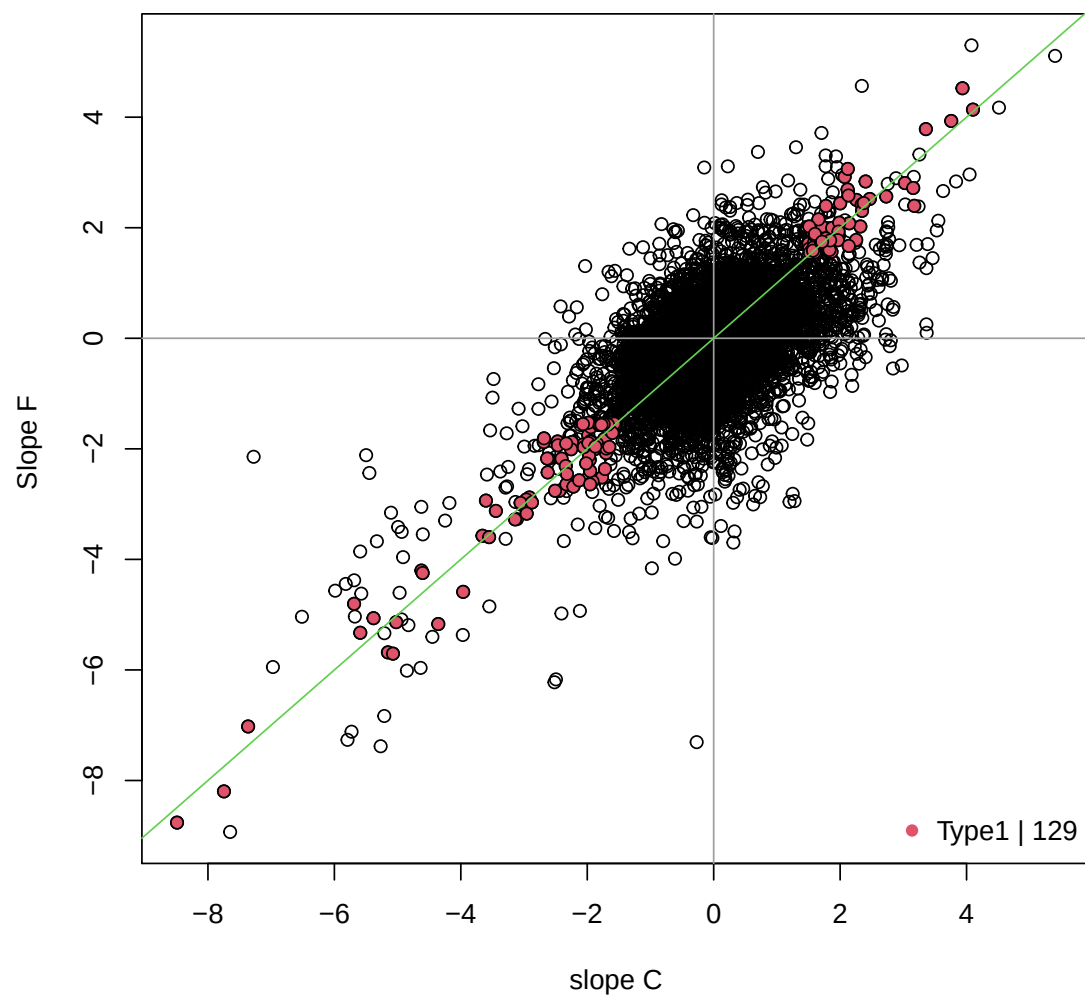
```

> plot(C,F, xlab="slope C",ylab="Slope F ")
> abline(h=0,v=0,col=8)
> #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)
> #
> Type1 <- C*F > 0
> Type1 <- Type1 & ( abs(C) > min.slope) & (abs(F) > min.slope)
> Type1 <- Type1 & ( abs(F-C) < diff.slope)
> Type1 <- Type1 & ((abs(diff0) < diff01) & (abs(diff1) < diff01))
> #
> table(Type1,type1)

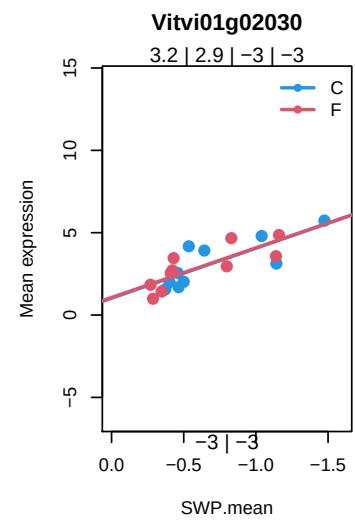
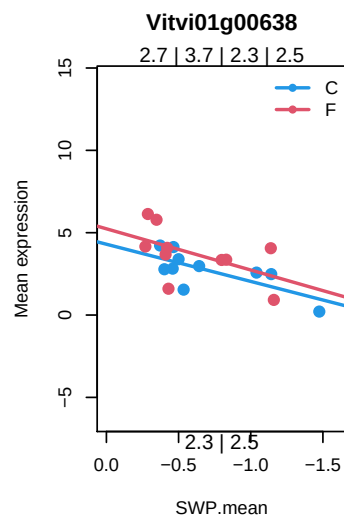
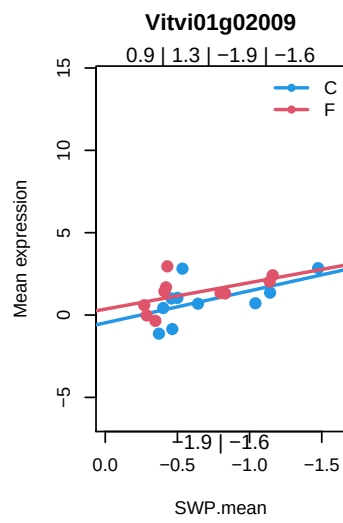
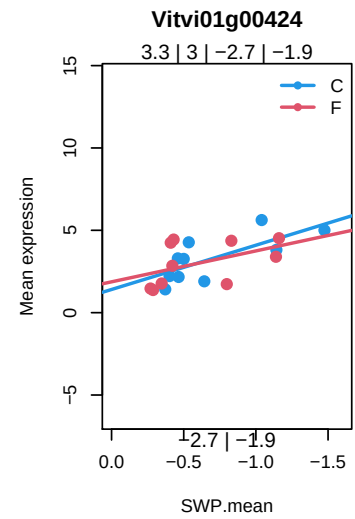
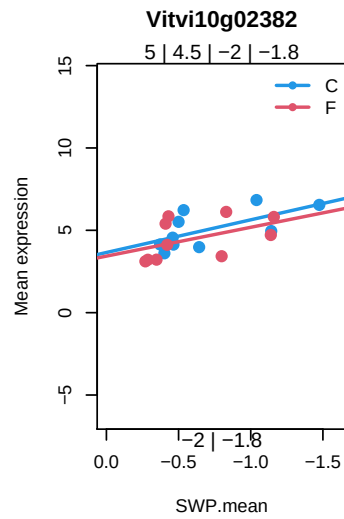
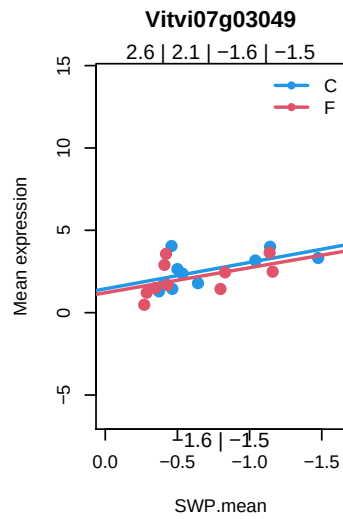
      type1
Type1  FALSE  TRUE
FALSE 14803   310
TRUE     0   129

> points(
+   C[Type1],
+   F[Type1],
+   bg=2, pch=21, col=1)
> abline(c(0,1),col=3)
> Types <- data.frame(Type1)
> nt <- apply(Types,2,sum)
> legend("bottomright",pch=rep(16,5),col=2:7,legend=paste0("Type",1:ncol(Types

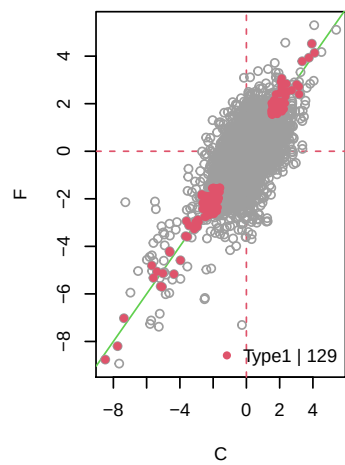
```



```
> nt
Type1
129
> plot.type(Type1)
[1] 129
```



> plot.types (type=Types)



6.2.3 Type1, extended

After manual inspection, Maruša extended the definition of Type1.

- Both slopes > 1.5 (Type1.0)
- One slope > 1.5, the other between 0.5 and 1.5 (Type1.0C and Type1.0F)

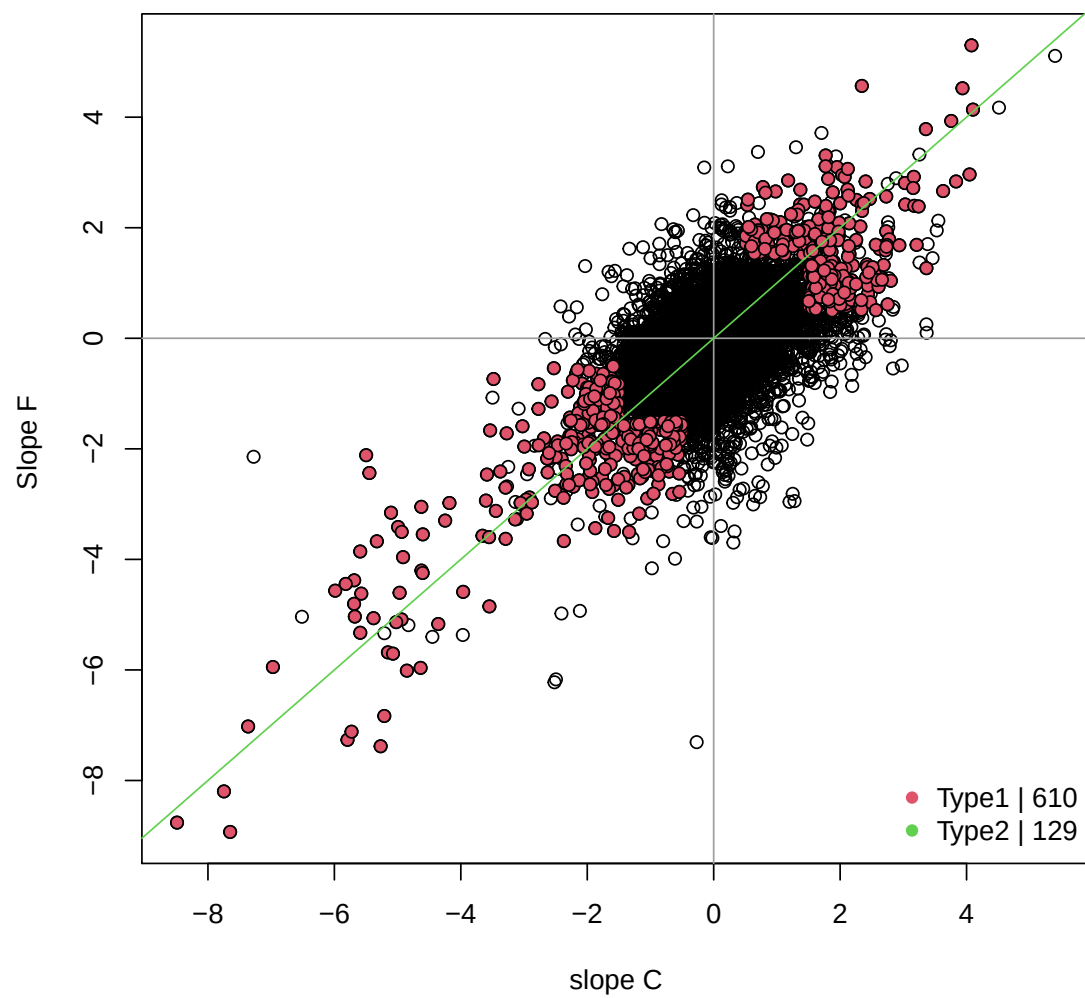
```
> plot(C,F, xlab="slope C",ylab="Slope F ")
> abline(h=0,v=0,col=8)
> #points(C[large_abs_A],F[large_abs_A],col=2,pch=16)
> #
> type10 <- large_abs_A & small_fc & small_ca
> type1 <- (large_abs_C/large_abs_F) & small_fc & (abs(mc-mf)<deltam)
> #
> Type1.0 <- C*F > 0
> sum(Type1.0)
[1] 11042
> Type1.0CF <- ( abs(C) > min.slope) & (abs(F) > min.slope)
> sum(Type1.0CF)
[1] 281
> Type1.0C <- (abs(C) > min.slope) & (abs(F) > max.slope & abs(F) < min.slope)
> sum(Type1.0C)
[1] 236
> Type1.0F <- (abs(F) > min.slope) & (abs(C) > max.slope & abs(C) < min.slope)
> sum(Type1.0F)
[1] 254
> Type1.0CF <- Type1.0CF | Type1.0C | Type1.0F
> sum(Type1.0CF)
[1] 771
> Type1.0diff <- ((abs(diff0) < diff01) | (abs(diff1) < diff01))
> sum(Type1.0diff)
[1] 14323
> #
> Type1.0 <- Type1.0 & Type1.0CF & Type1.0diff
> #
> table(Type1,Type1.0)

```

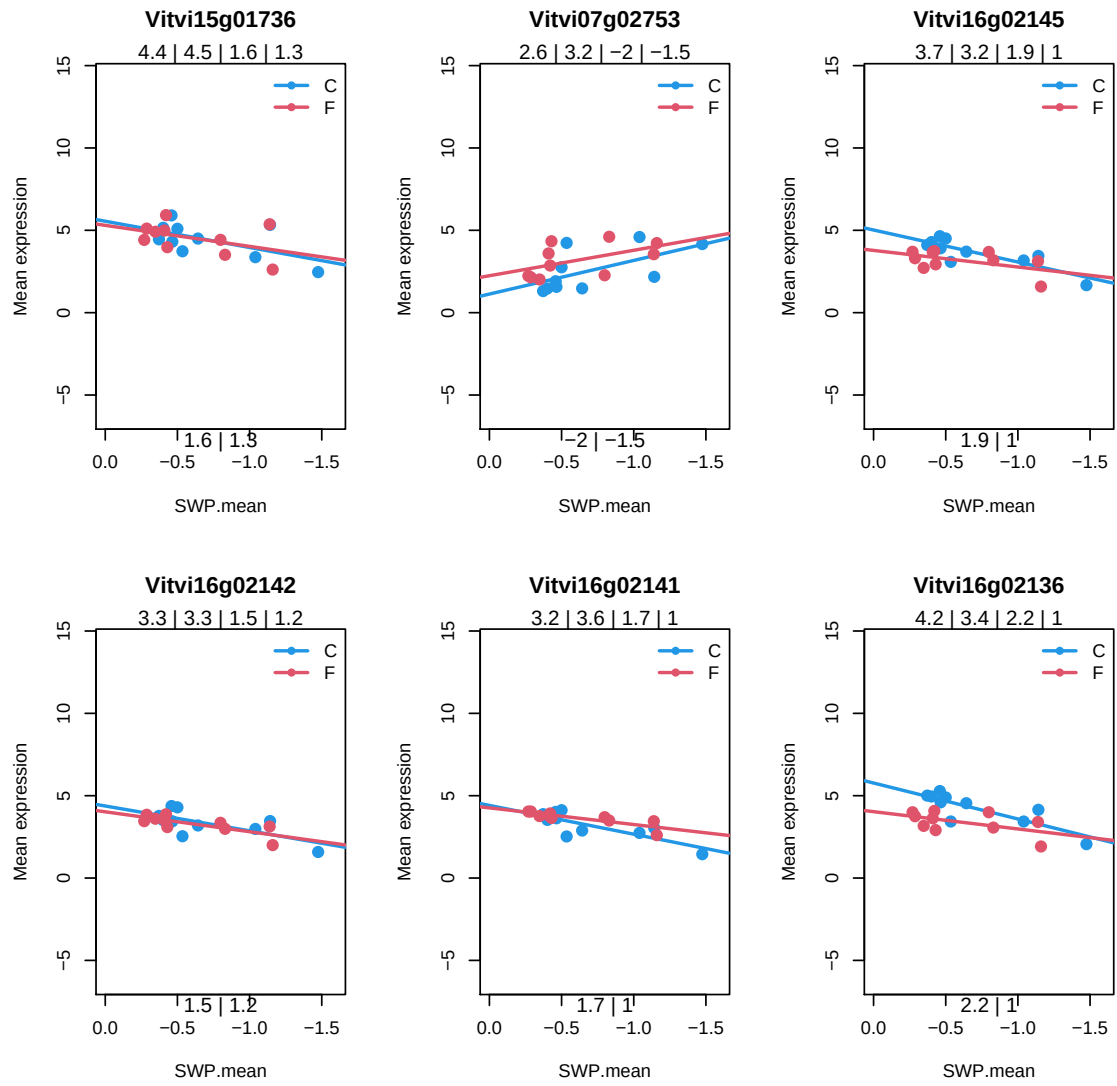
	Type1.0	
Type1	FALSE	TRUE
FALSE	14632	481
TRUE	0	129

```

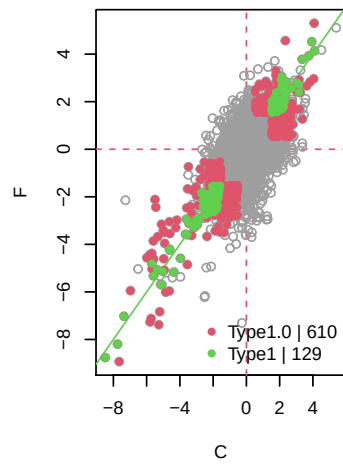
> points(
+   C[Type1.0],
+   F[Type1.0],
+   bg=2, pch=21, col=1)
> abline(c(0,1),col=3)
> Types <- data.frame(Type1.0, Type1)
> nt <- apply(Types,2,sum)
> legend("bottomright",pch=rep(16,5),col=2:7,legend=paste0("Type",1:ncol(Types
```



```
> nt
Type1.0  Type1
    610    129
> plot.type(Type1.0)
[1] 610
```



> plot.types (type=Types)



```
> table(Type1, Type1.0)
```

	Type1.0	
Type1	FALSE	TRUE
FALSE	14632	481
TRUE	0	129

6.2.4 Type2

```

> plot(C,F, xlab="slope C",ylab="Slope F ")
>       abline(h=0,v=0,col=8)
> #
> type2 <- (large_abs_C & large_abs_F) & (abs(fc) > diff.slope)&(abs(mc-mf)>de
> type2 <- type2 & ( (C*F >0) )
> #
>
> #
> Type2 <- C*F > 0
> Type2 <- Type2 & ( abs(C) > min.slope) & (abs(F) > min.slope )
> Type2 <- Type2 & ( abs(F-C) > diff.slope )
> Type2 <- Type2 & ( abs(diff1) < diff01 )
> Type2 <- Type2 & nocross
> #
> table(Type2,type2)

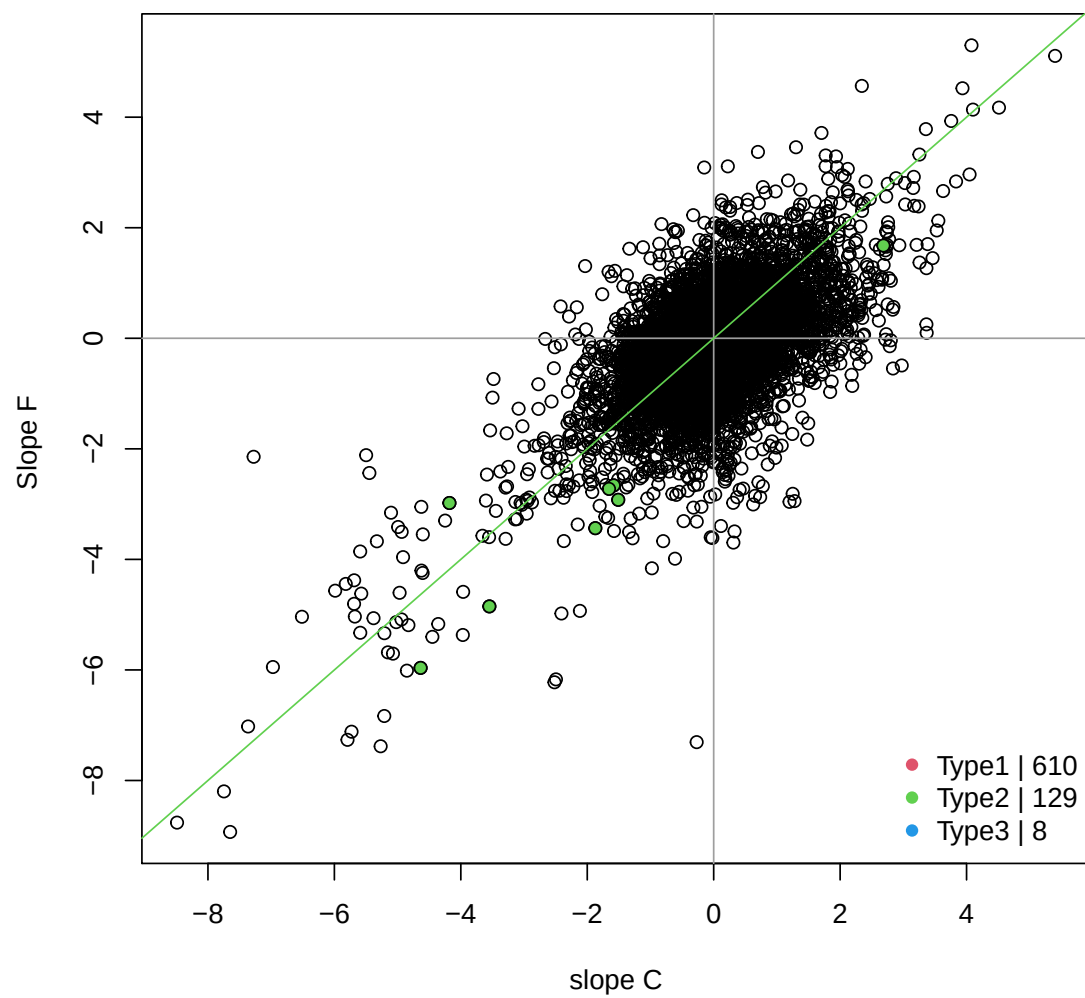
      type2
Type2  FALSE  TRUE
  FALSE 15210   24
  TRUE     2    6

> points(
+   C[Type2],
+   F[Type2],
+   bg=3, pch=21, col=1)
>       abline(c(0,1),col=3)
> Type1.2 <- Type2
> Types <- data.frame(Types,Type1.2)
> (nt <- apply(Types,2,sum))

Type1.0  Type1 Type1.2
      610     129      8

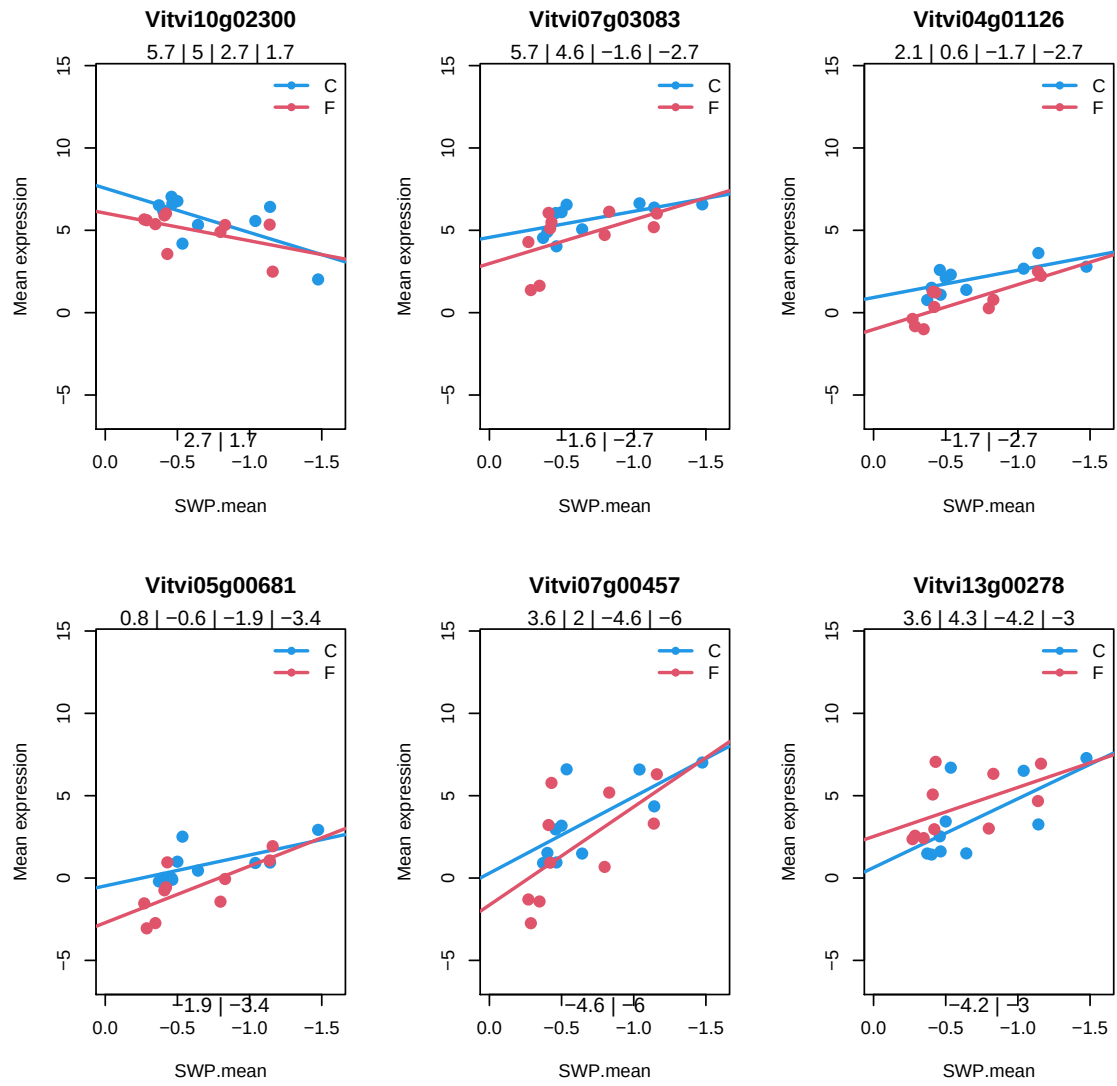
> legend("bottomright",pch=rep(16,5),col=2:7,legend=paste0("Type",1:ncol(Types

```

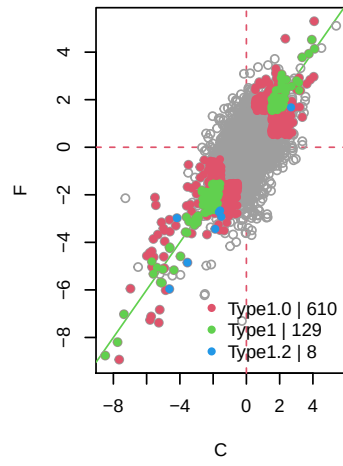


```
> nt
Type1.0  Type1 Type1.2
    610    129     8

> #
>
> plot.type(Type1.2)
[1] 8
```



> plot.types (type=Types)



6.2.5 Type3

```
> plot(C,F, xlab="slope C",ylab="Slope F ")
> abline(h=0,v=0,col=8)
> type30 <- ((abs(C)<max.slope)|(abs(F)<max.slope)) & (abs(fc)> diff.slope)
> type3 <- ((abs(C)<max.slope)|(abs(F)<max.slope)) & (abs(fc)> diff.slope)&(ab
> #
> table(( abs(C) > min.slope) , (abs(F) < max.slope))

      FALSE TRUE
FALSE  5011 9572
TRUE   517  142

> Type3 <- ((abs(diff0) < diff01) | (abs(diff1) < diff01))
> Type3 <- Type3 & nocross
> Type3.C <- Type3 & (( abs(C) > min.slope) & (abs(F) < max.slope))
> Type3.F <- Type3 & (( abs(F) > min.slope) & (abs(C) < max.slope))
> Type3 <- Type3 & ((( abs(C) > min.slope) & (abs(F) < max.slope)) |
+                   (( abs(F) > min.slope) & (abs(C) < max.slope)))
> all(Type3==(Type3.C|Type3.F))

[1] TRUE

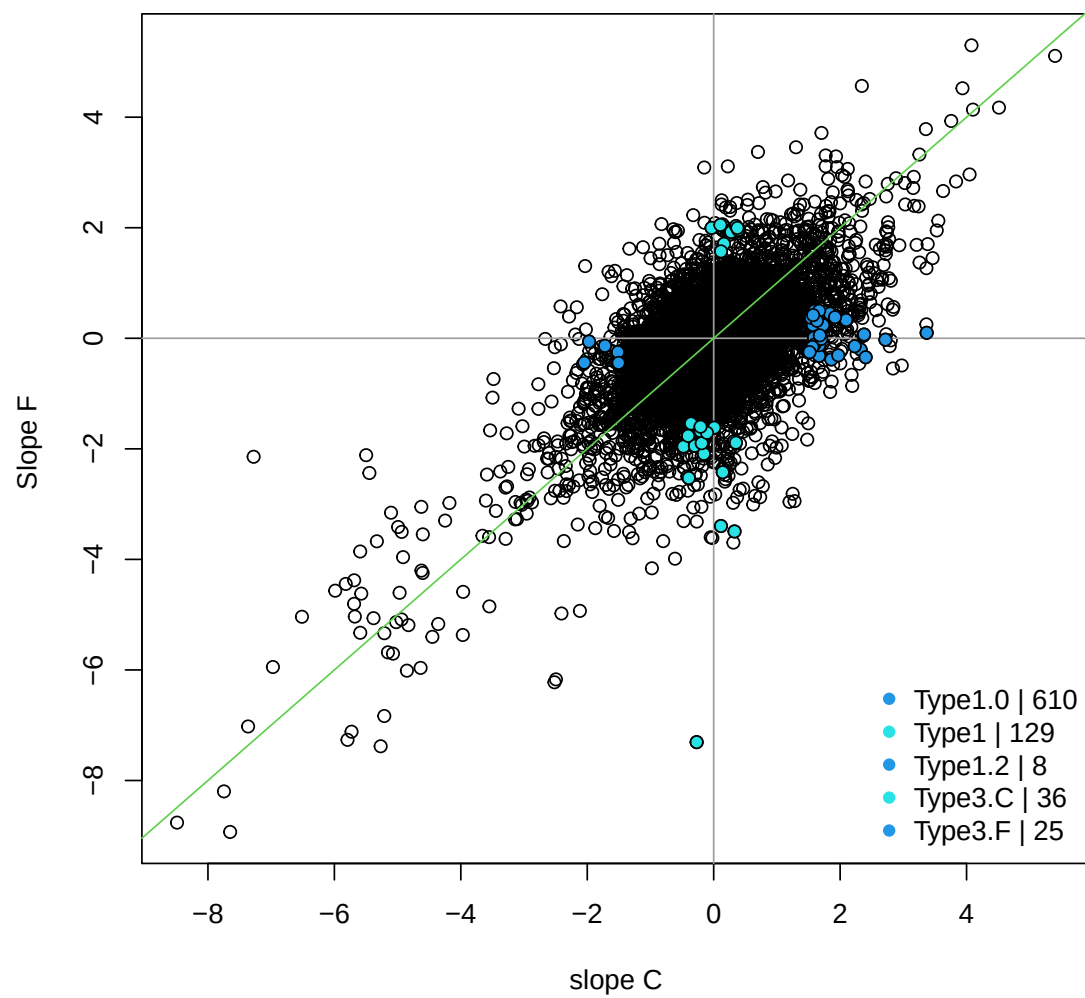
> cbind(Type3,Type3.C,Type3.F)[((Type3 != (Type3.C|Type3.F))),]

      Type3 Type3.C Type3.F
Type3  FALSE  TRUE
FALSE 15094    87
TRUE   54     7

> points(
+   C[Type3.C],
+   F[Type3.C],
+   bg=4, pch=21, col=1)
> points(
+   C[Type3.F],
+   F[Type3.F],
+   bg=5, pch=21, col=1)
> abline(c(0,1),col=3)
> Types <- data.frame(Types,Type3.C, Type3.F)
> (nt <- apply(Types,2,sum))

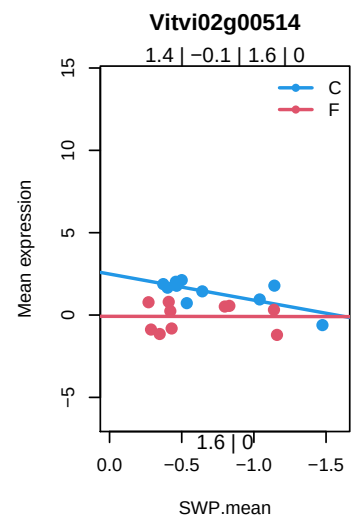
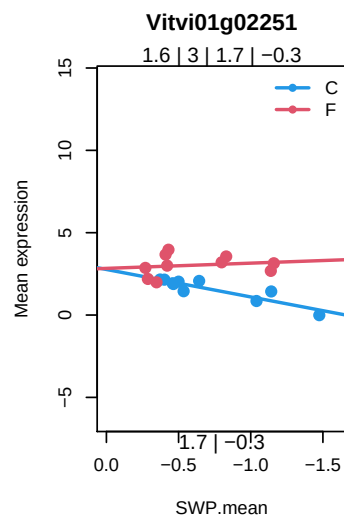
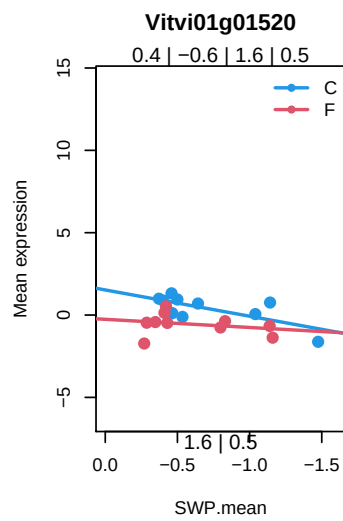
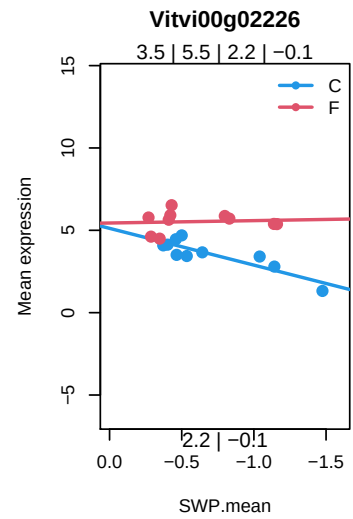
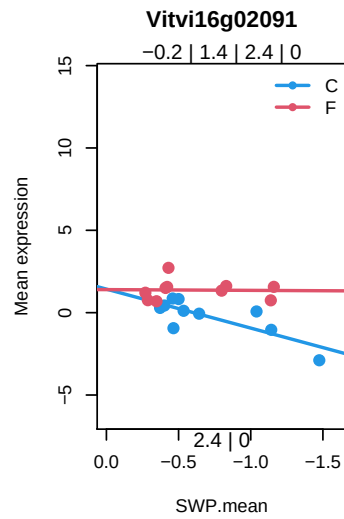
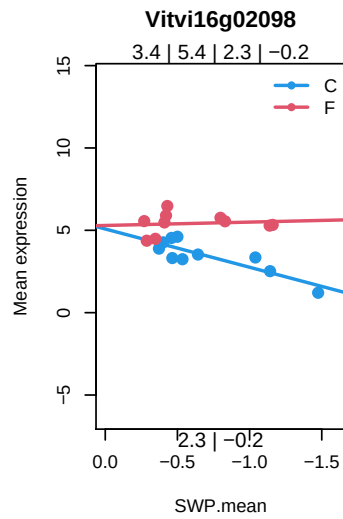
Type1.0  Type1 Type1.2 Type3.C Type3.F
      610    129      8     36     25

> legend("bottomright",pch=rep(16,ncol(Types)),col=c(4,5),legend=paste0(colnam
```



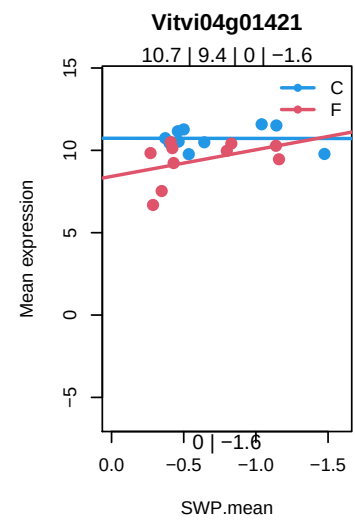
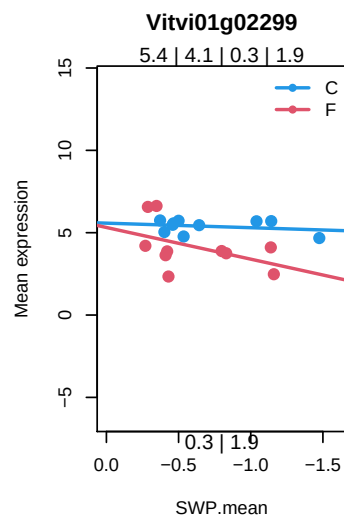
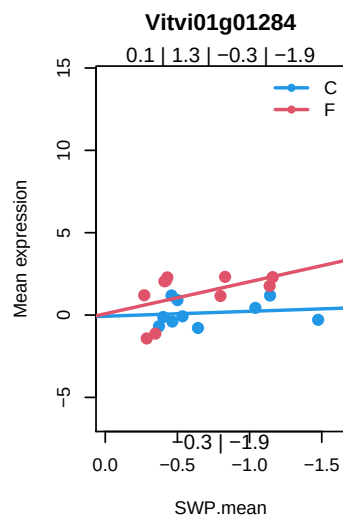
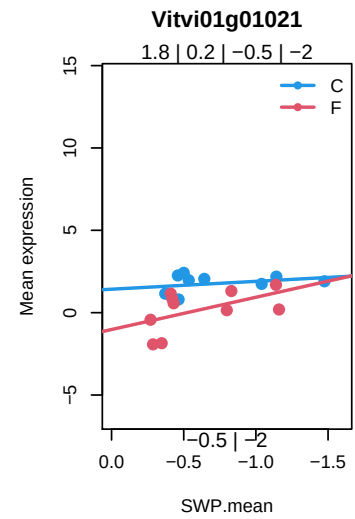
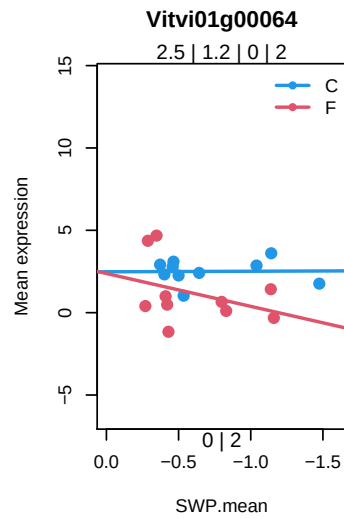
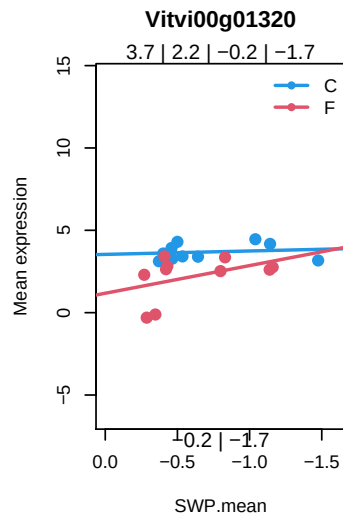
```
> nt
Type1.0   Type1 Type1.2 Type3.C Type3.F
    610    129     8    36    25

> #
>
> plot.type(Type3.C)
[1] 36
```

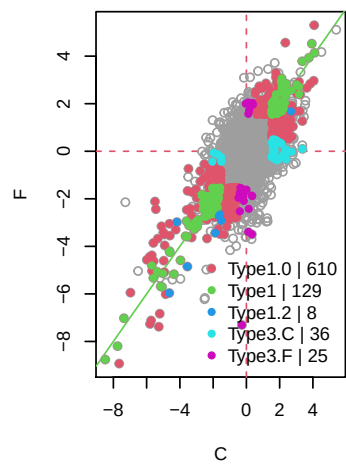


> plot.type(Type3.F)

[1] 25



> plot.types (type=Types)



6.2.6 Type4

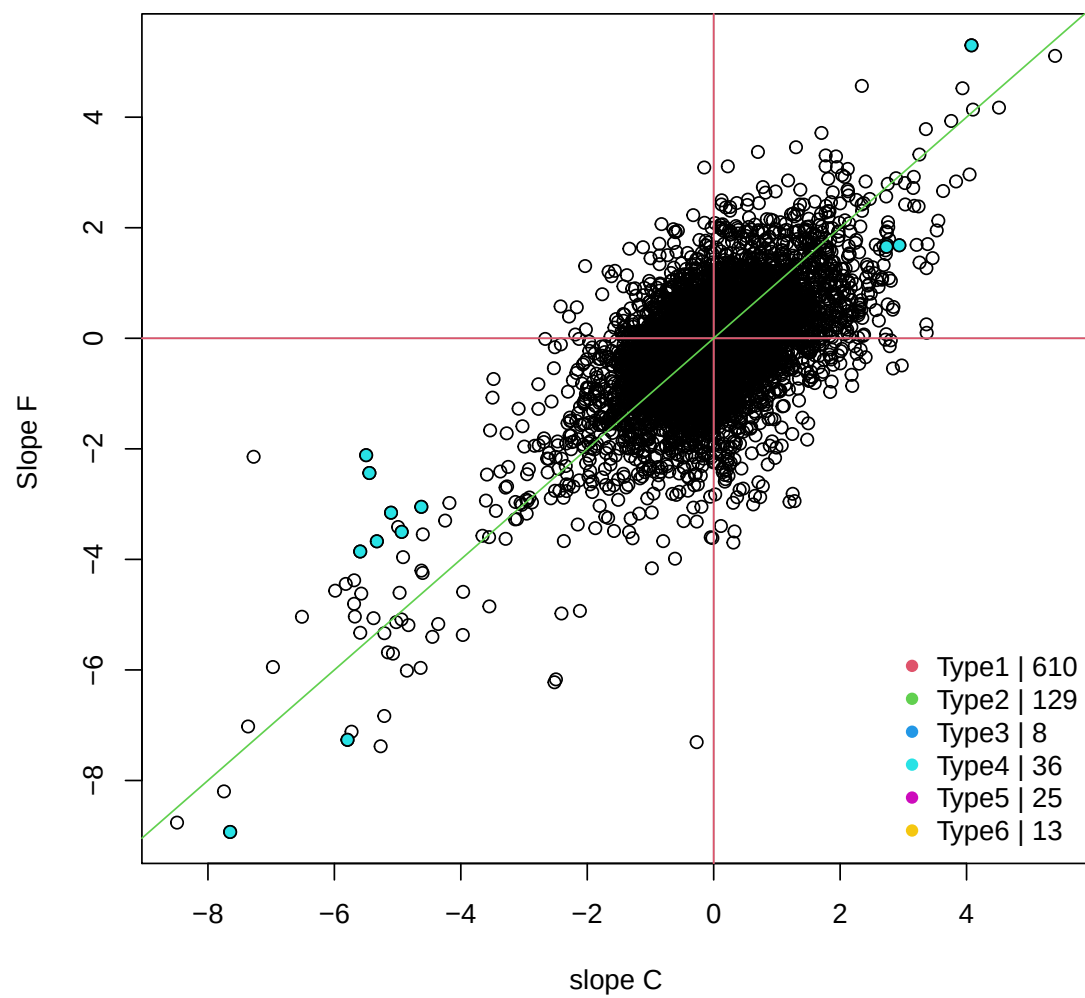
```
> plot(C,F, xlab="slope C",ylab="Slope F ")
>       abline(h=0,v=0,col=8)
> #
> type4 <- (large_abs_C/large_abs_F) & (abs(mc-mf)>deltam) & (C*F>0)
> #
> Type4 <- C*F > 0
> Type4 <- Type4 & ( abs(C) > min.slope) & (abs(F) > min.slope )
> Type4 <- Type4 & ( abs(F-C) > diff.slope )
> Type4 <- Type4 & ( abs(diff0) < diff01 )
> Type4 <- Type4 & nocross
> #
> Type1.4 <- Type4
> table(Type4,type4)
```

	type4	
Type4	FALSE	TRUE
FALSE	15144	85
TRUE	10	3

```
> points(
+   C[Type4],
+   F[Type4],
+   bg=5, pch=21, col=1)
>       abline(h=0,v=0,col=2)
>       abline(c(0,1),col=3)
> Types <- data.frame(Types, Type1.4)
> (nt <- apply(Types,2,sum))
```

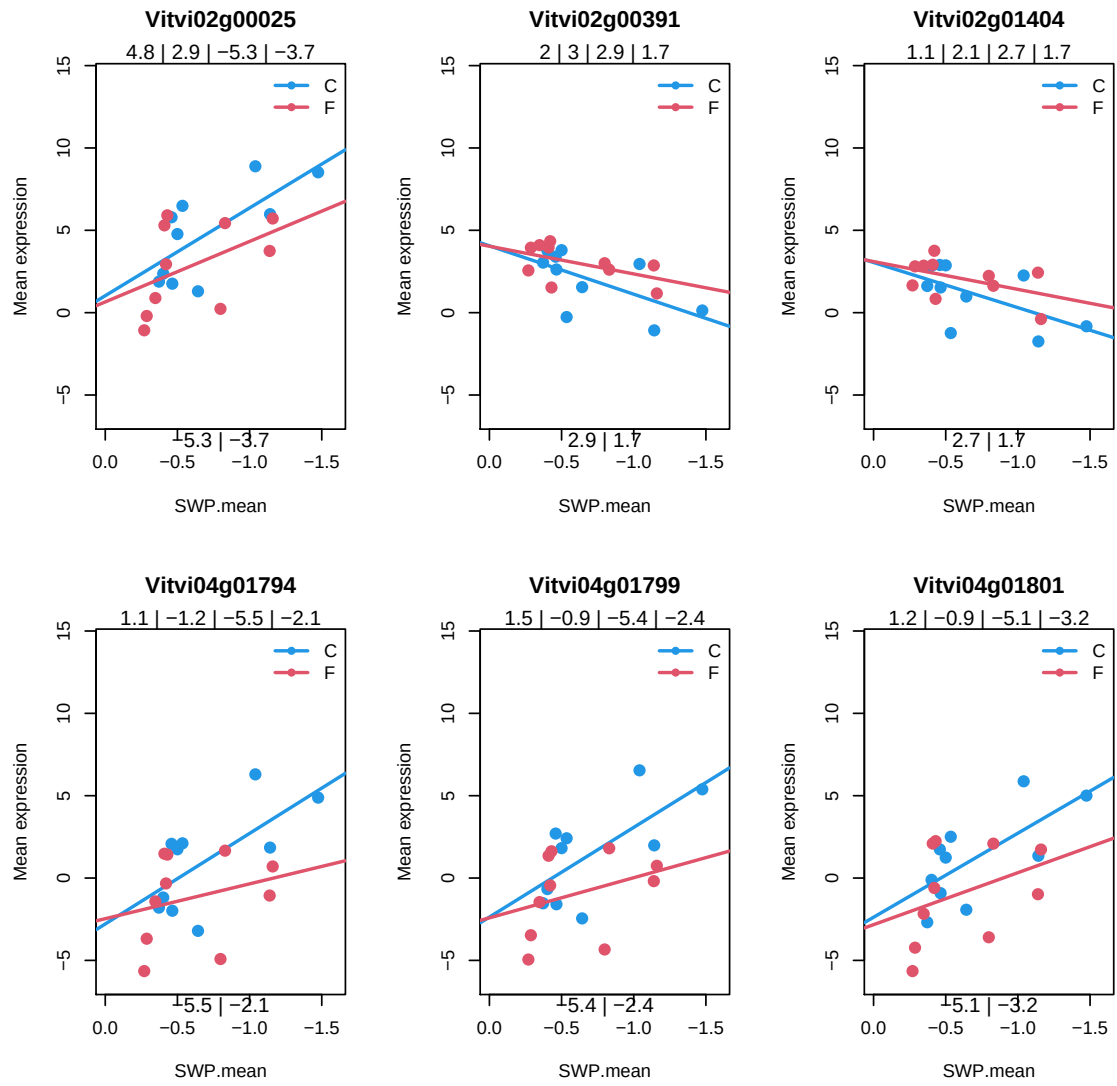
Type1.0	Type1	Type1.2	Type3.C	Type3.F	Type1.4
610	129	8	36	25	13

```
> legend("bottomright",pch=rep(16,5),col=2:7,legend=paste0("Type",1:ncol(Types
```

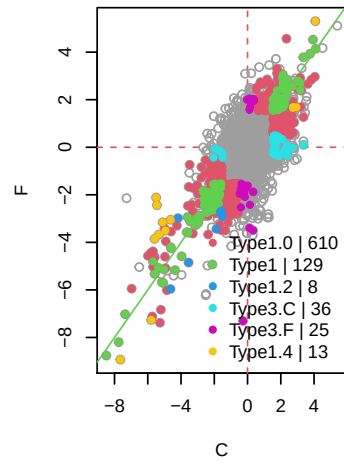
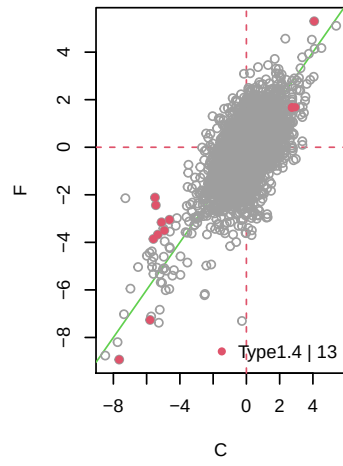


```
> nt
Type1.0   Type1 Type1.2 Type3.C Type3.F Type1.4
    610     129      8     36     25      13

> plot.type(Type1.4)
[1] 13
```

```
> plot.types (type=data.frame (Type1.4) )
> plot.types (type=Types)
```



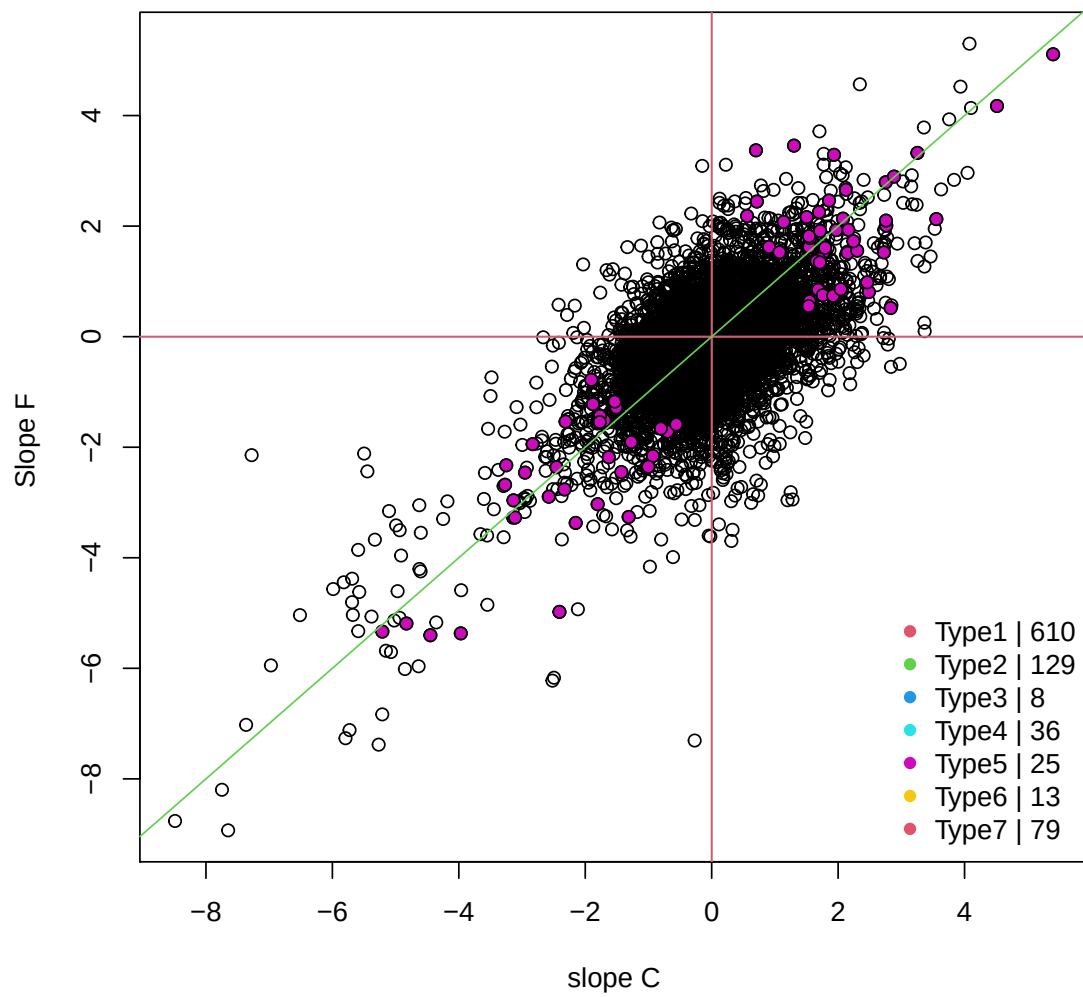
6.2.7 Type5

```

> plot(C,F, xlab="slope C",ylab="Slope F ")
> abline(h=0,v=0,col=8)
> #
> type5 <- ((abs(C)<max.slope)|(abs(F)<max.slope)) & (abs(fc)> diff.slope5)&(a
> #
> Type5 <- C*F > 0
> Type5 <- Type5 & ( abs(C) > min.slope) & (abs(F) > min.slope )
> Type5 <- Type5 & ( ( abs(diff0) > diff01 ) & ( abs(diff1) > diff01 ) )
> Type5 <- Type5 & nocross
> #
> Type5.0 <- C*F > 0
> sum(Type5.0)
[1] 11042
> Type5.0CF <- ( abs(C) > min.slope) & (abs(F) > min.slope)
> sum(Type5.0CF)
[1] 281
> Type5.0C <- (abs(C) > min.slope) & (abs(F) > max.slope & abs(F) < min.slope)
> sum(Type5.0C)
[1] 236
> Type5.0F <- (abs(F) > min.slope) & (abs(C) > max.slope & abs(C) < min.slope)
> sum(Type5.0F)
[1] 254
> Type5.0CF <- Type5.0CF | Type5.0C | Type5.0F
> sum(Type5.0CF)
[1] 771
> Type5.0diff <- ((abs(diff0) > diff01) & (abs(diff1) > diff01))
> sum(Type5.0diff)
[1] 919
> #
> Type5.0 <- Type5.0 & Type5.0CF & Type5.0diff & nocross
> #
> table(Type5,Type5.0)
      Type5.0
Type5  FALSE  TRUE
  FALSE 15163   33
   TRUE     0   46
> # type 3 is a subset of type5, type3 & large mean difference
> points(
+   C[Type5.0],
+   F[Type5.0],
+   bg=6, pch=21, col=1)
> #
> abline(h=0,v=0,col=2)
> abline(c(0,1),col=3)
> Types <- data.frame(Types, Type5.0)
> (nt <- apply(Types,2,sum))
Type1.0  Type1  Type1.2  Type3.C  Type3.F  Type1.4  Type5.0
    610    129      8      36      25      13      79

```

```
> legend("bottomright",pch=rep(16,5),col=2:7,legend=paste0("Type",1:ncol(Types
```



```
> nt
```

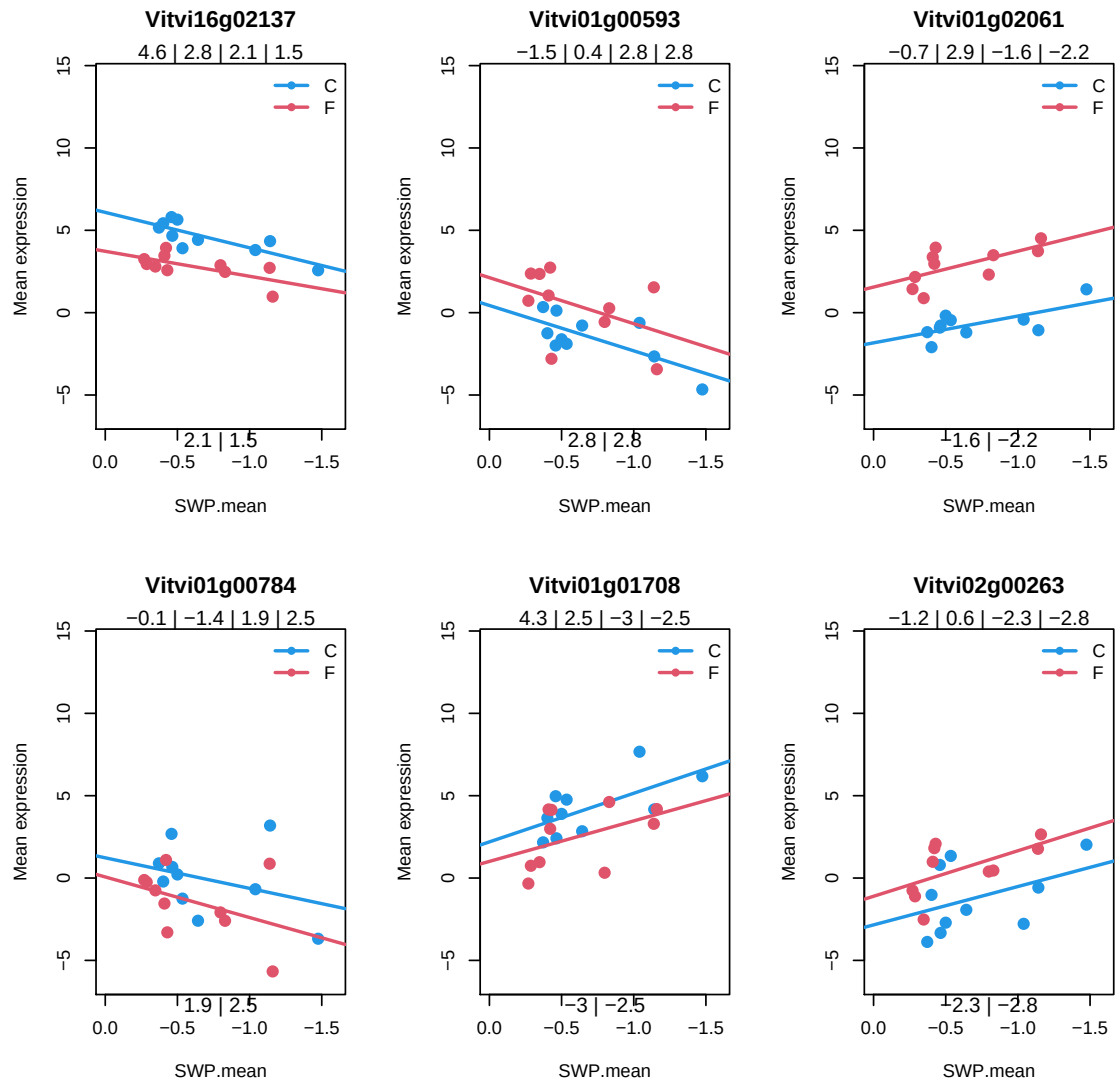
```

Type1.0   Type1 Type1.2 Type3.C Type3.F Type1.4 Type5.0
    610     129      8      36      25      13      79

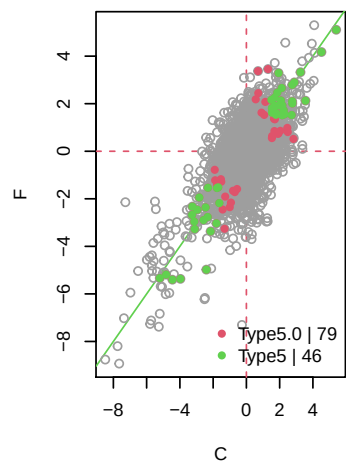
```

```
> plot.type(Type5)
```

```
[1] 46
```



> plot.types (type=data.frame (Type5.0, Type5))



6.2.8 Type6

```
> plot(C,F, xlab="slope C",ylab="Slope F ")
> abline(h=0,v=0,col=8)
> #
> #
> Type6 <- ((abs(diff0) > diff01) & (abs(diff1) > diff01))
> Type6 <- Type6 & nocross
> Type6.C <- Type6 & (( abs(C) > min.slope) & (abs(F) < max.slope))
> Type6.F <- Type6 & (( abs(F) > min.slope) & (abs(C) < max.slope))
> Type6 <- Type6 & ((( abs(C) > min.slope) & (abs(F) < max.slope)) |
+ (( abs(F) > min.slope) & (abs(C) < max.slope)))
> #
> table(Type6,Type6.C, Type6.F)

      Type6.C
Type6  FALSE  TRUE
  FALSE 15199    0
   TRUE     0   27

      Type6.F = FALSE

      Type6.C
Type6  FALSE  TRUE
  FALSE     0    0
   TRUE    16    0

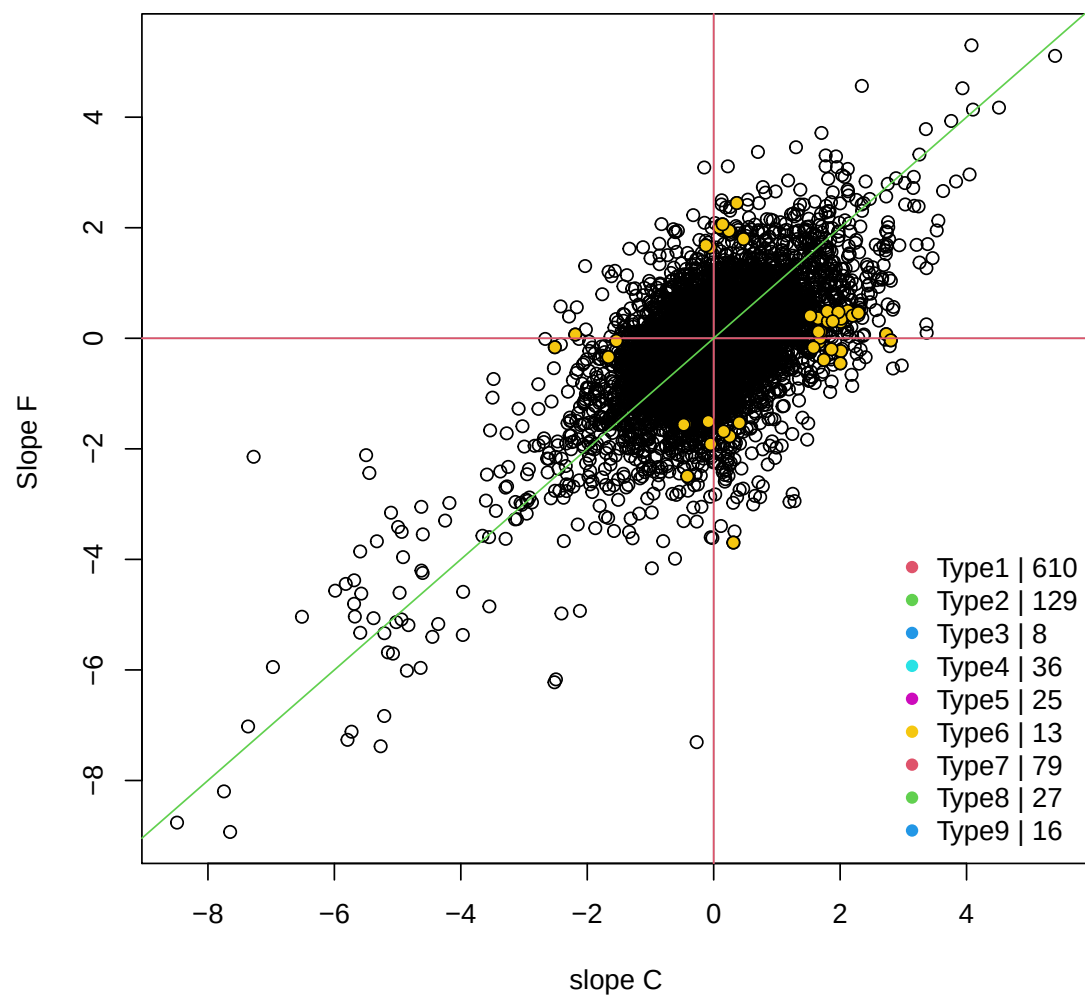
> # type 3 is a subset of Type6, type3 & large mean difference
> table(Type3,Type6)

      Type6
Type3  FALSE  TRUE
  FALSE 15138   43
   TRUE   61    0

> points(
+   C[Type6.C],
+   F[Type6.C],
+   bg=7, pch=21, col=1)
> points(
+   C[Type6.F],
+   F[Type6.F],
+   bg=7, pch=21, col=1)
> #
> abline(h=0,v=0,col=2)
> abline(c(0,1),col=3)
> Types <- data.frame(Types, Type6.C, Type6.F)
> (nt <- apply(Types,2,sum))

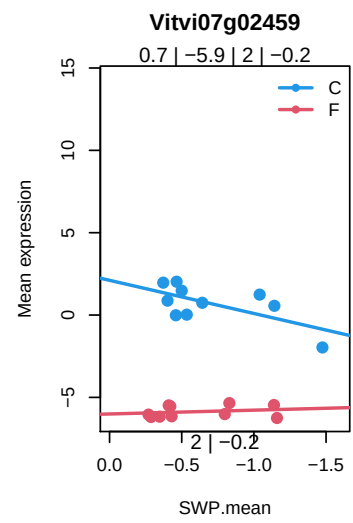
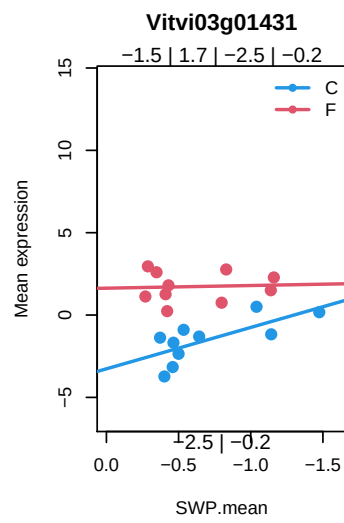
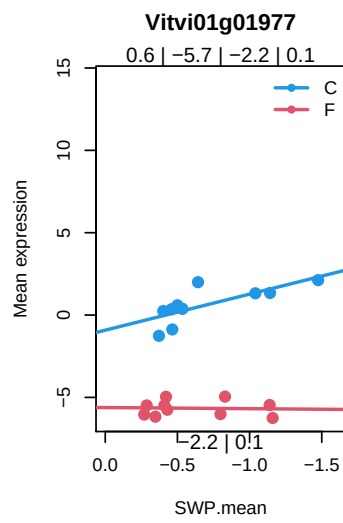
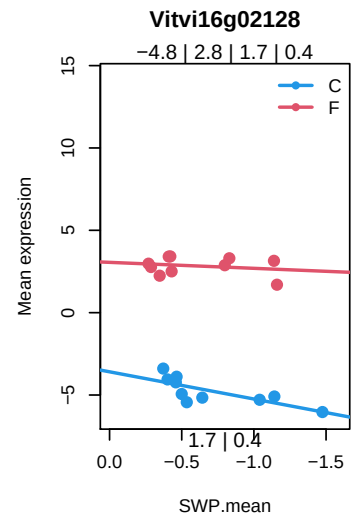
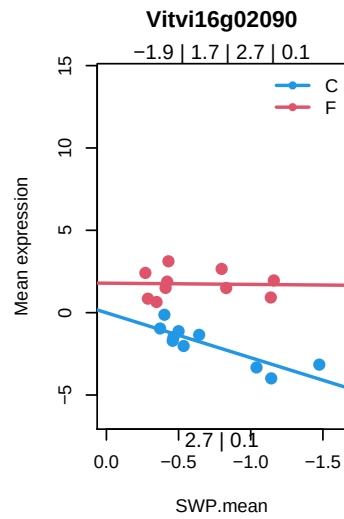
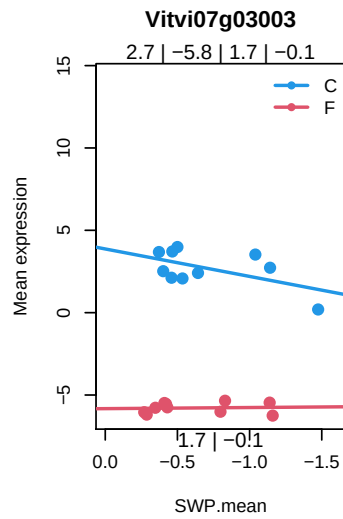
Type1.0  Type1 Type1.2 Type3.C Type3.F Type1.4 Type5.0
      610      129         8      36      25      13      79
Type6.C Type6.F
      27      16

> legend("bottomright",pch=rep(16,5),col=2:7,legend=paste0("Type",1:ncol(Types
```

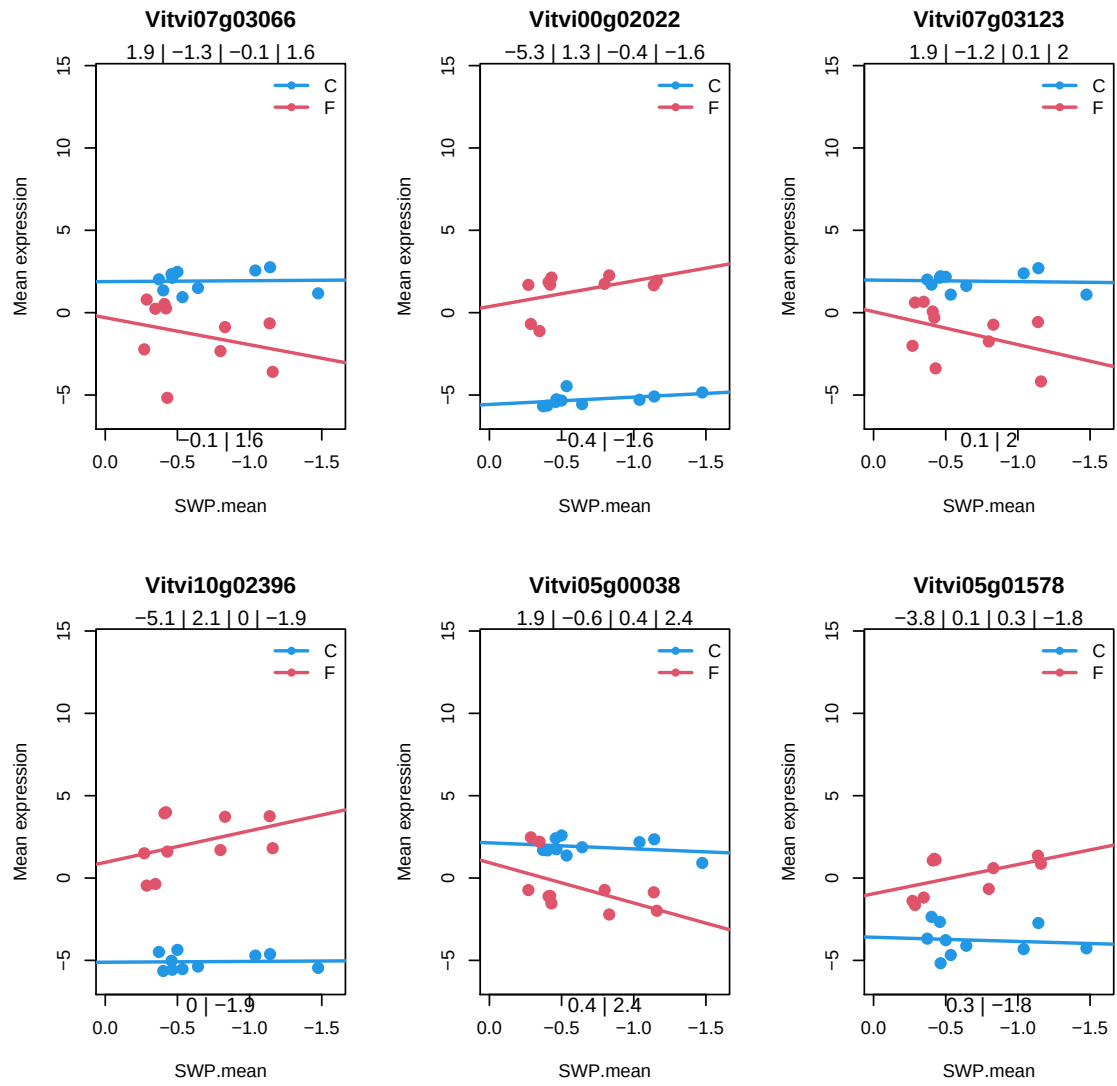


```
> nt
Type1.0   Type1 Type1.2 Type3.C Type3.F Type1.4 Type5.0
      610      129       8      36      25      13      79
Type6.C Type6.F
      27      16

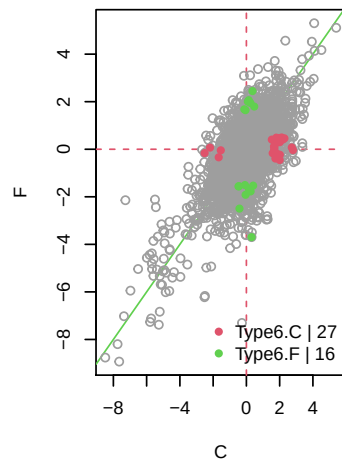
> plot.type(Type6.C)
[1] 27
```

```
> plot.type(Type6.F)
[1] 16
```



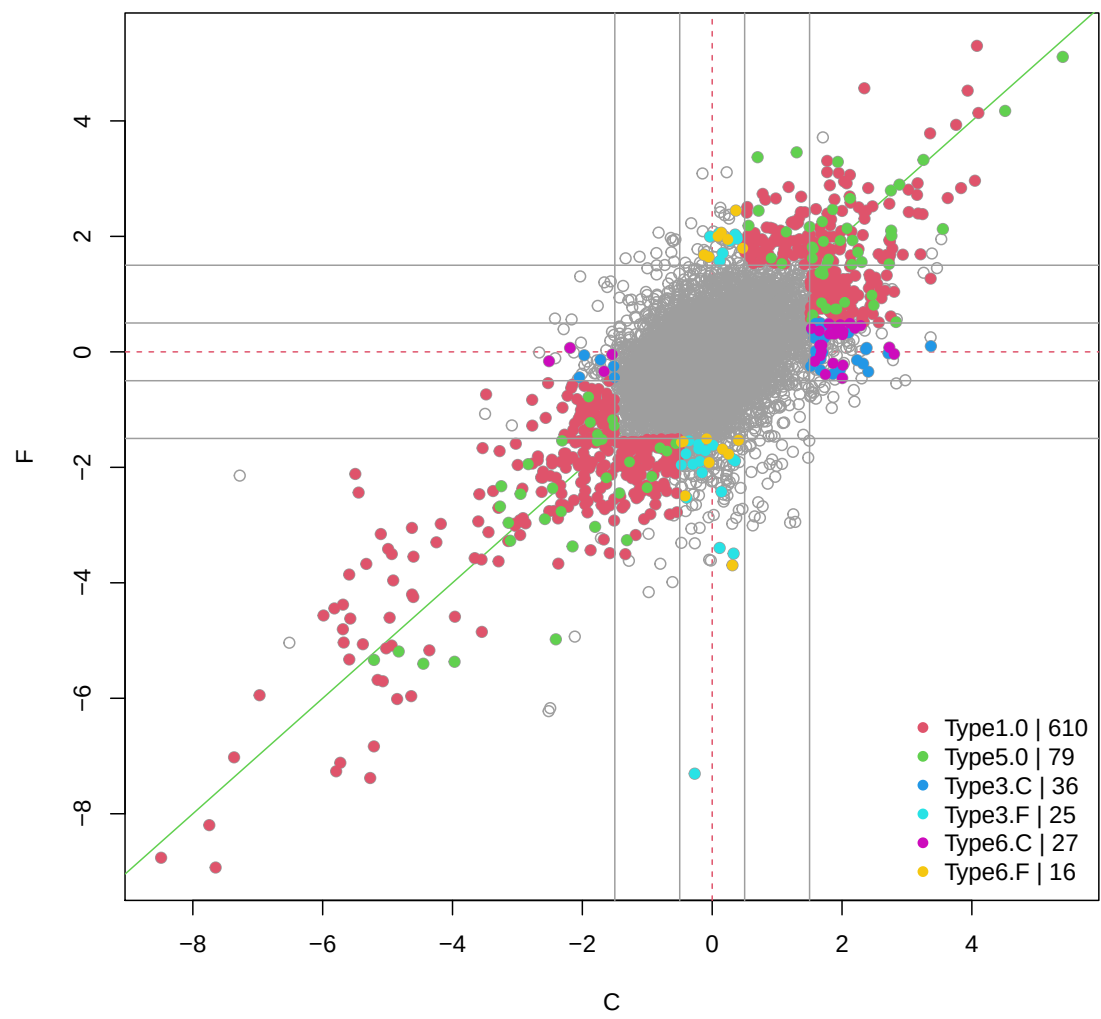
> plot.types(type=cbind(Type6.C, Type6.F))



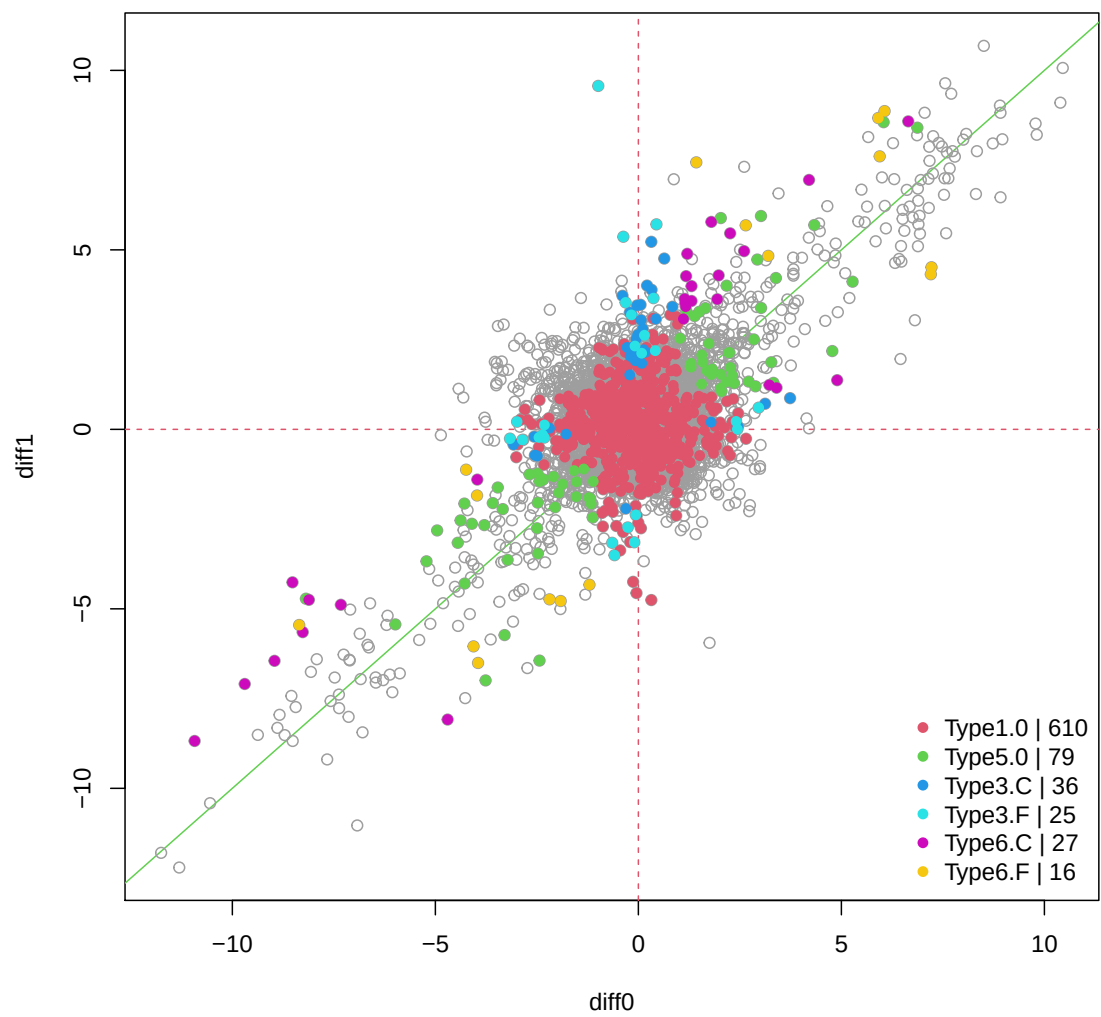
Type2 and Type4 are merged with Type1 + some mixed types

```
> Types <- data.frame(Type1.0, Type5.0, Type3.C, Type3.F,
+                      Type6.C, Type6.F)

> plot.types(type=Types, pty="s")
> abline(v=c(min.slope,max.slope),h=c(min.slope,max.slope), col=8)
> abline(v=-c(min.slope,max.slope),h=-c(min.slope,max.slope), col=8)
```



```
> plot.types(diff0, diff1, type=Types, pty="s")
```



```
> nts <- apply (Types, 2, sum)
> sum(nts)
[1] 793
> xtable( data.frame(Count=t(t(addmargins(apply(Types, 2, table), 2)[2, ]))), auto
```

	Count
Type1.0	610
Type5.0	79
Type3.C	36
Type3.F	25
Type6.C	27
Type6.F	16
Sum	793

Table 1: Table of new types.

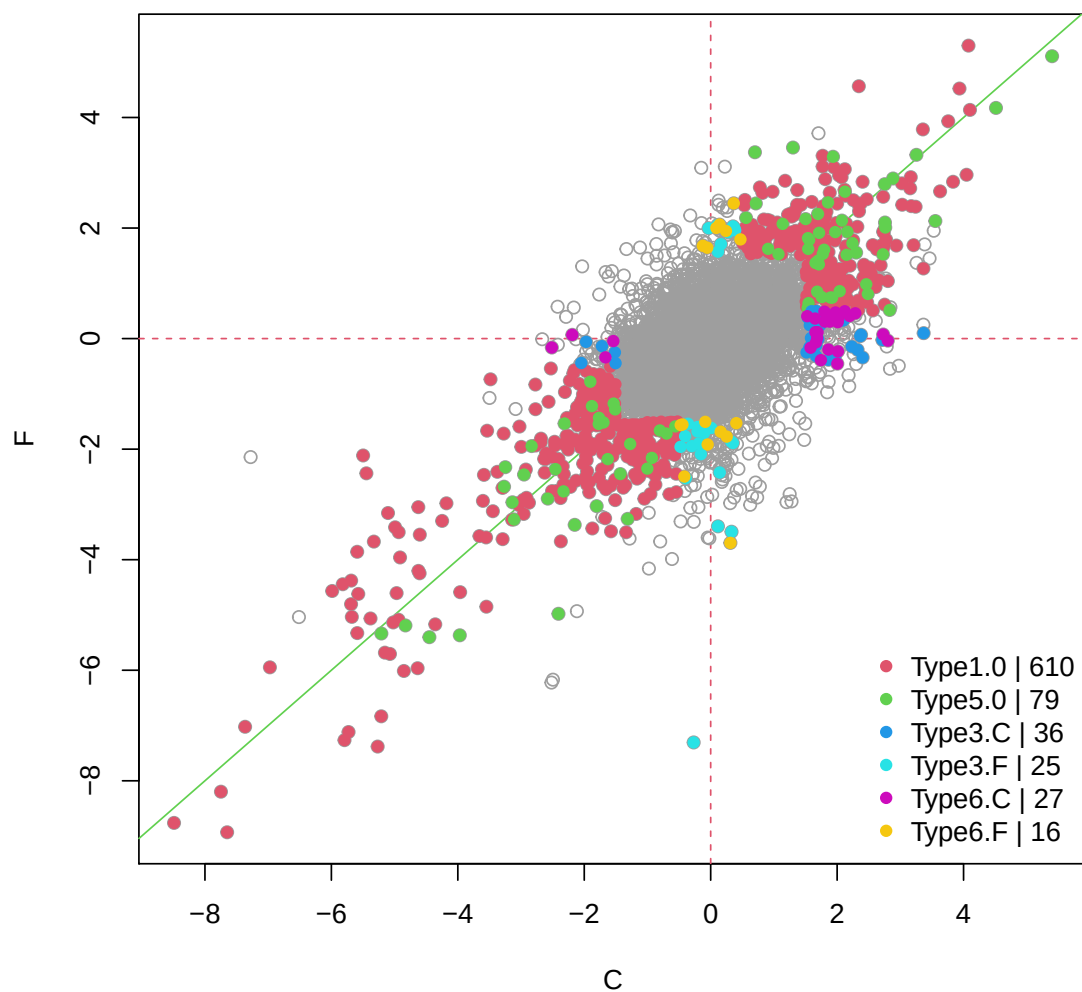
Override old types

```

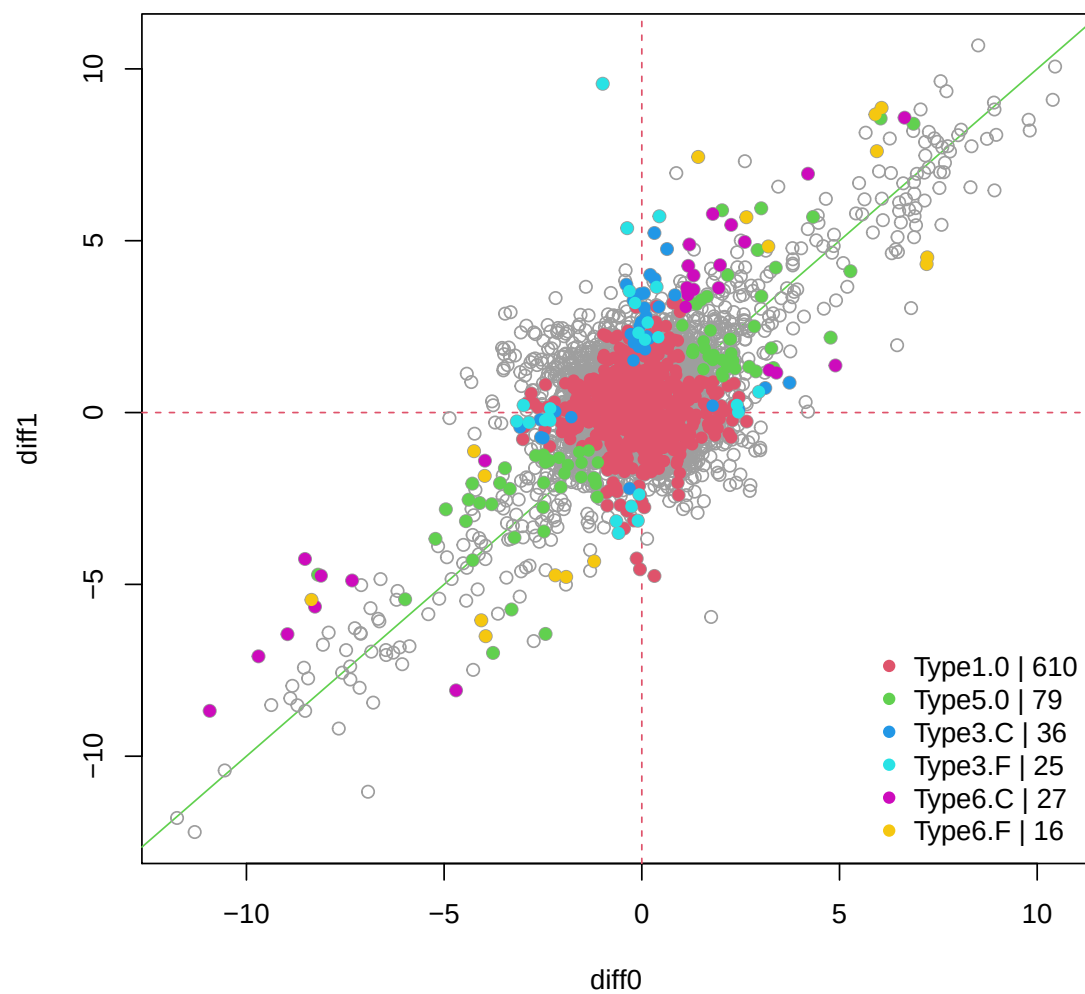
> types.old <- types
> types.new <- Types
> types <- types.new

> head(types)
      Type1.0 Type5.0 Type3.C Type3.F Type6.C
Vitvi15g01736   TRUE  FALSE  FALSE  FALSE  FALSE
Vitvi07g02832   FALSE  FALSE  FALSE  FALSE  FALSE
Vitvi07g02830   FALSE   TRUE  FALSE  FALSE  FALSE
Vitvi07g02812   FALSE  FALSE  FALSE  FALSE  FALSE
Vitvi07g02811   FALSE  FALSE  FALSE  FALSE  FALSE
Vitvi09g02033   FALSE  FALSE  FALSE  FALSE  FALSE
      Type6.F
Vitvi15g01736   FALSE
Vitvi07g02832   FALSE
Vitvi07g02830   FALSE
Vitvi07g02812   FALSE
Vitvi07g02811   FALSE
Vitvi09g02033   FALSE
> plot.types()

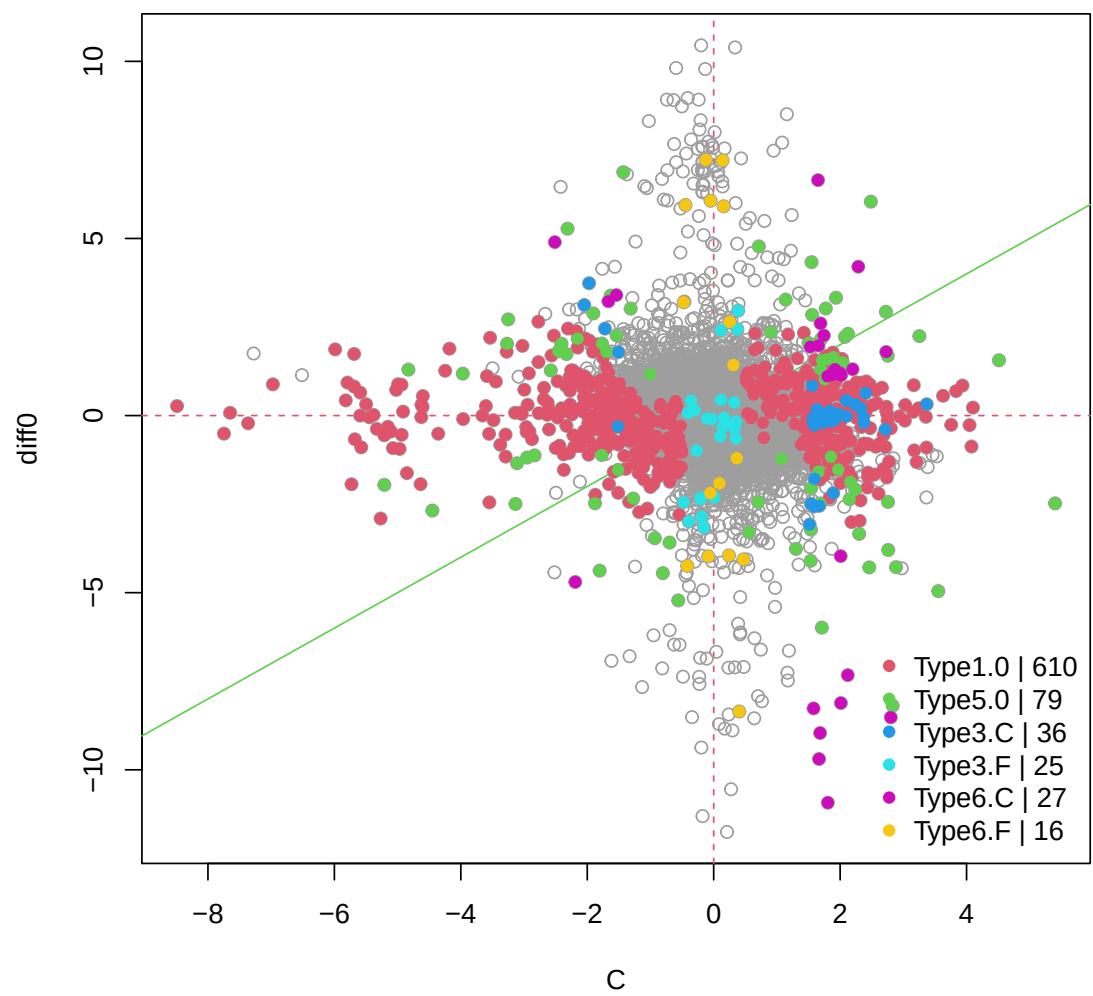
```



```
> plot.types(diff0, diff1)
```



```
> plot.types(C, diff0)
```



```
> plot.types(C+F, diff0-diff1)
```

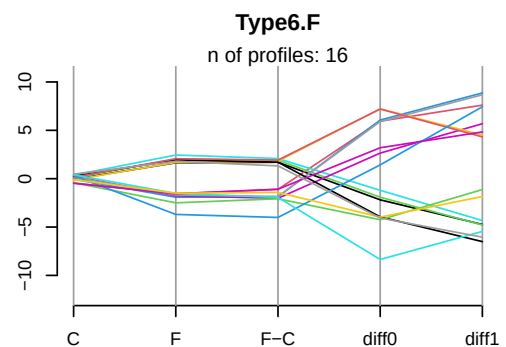
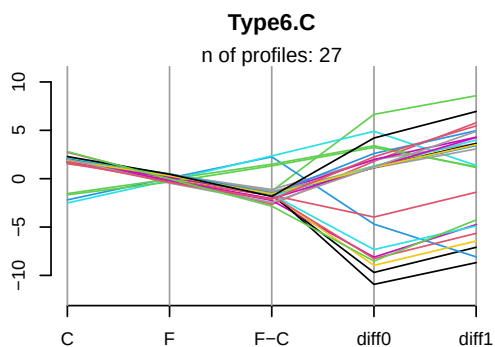
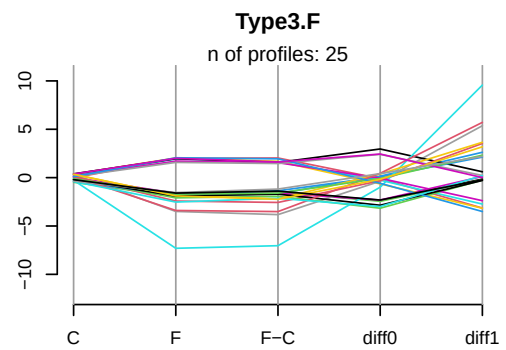
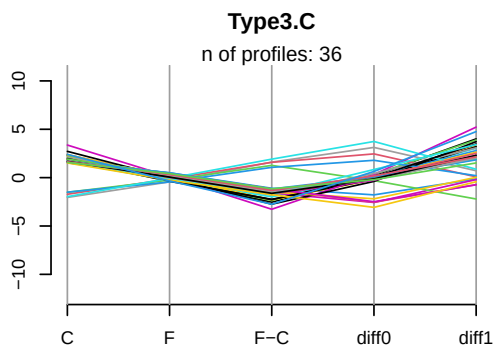
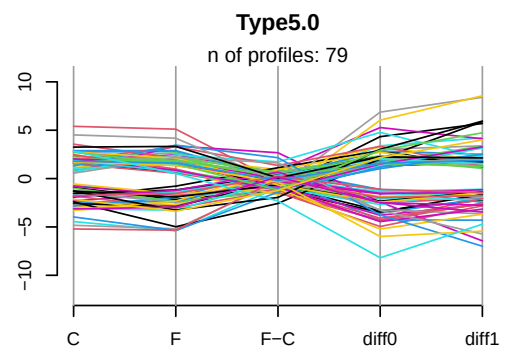
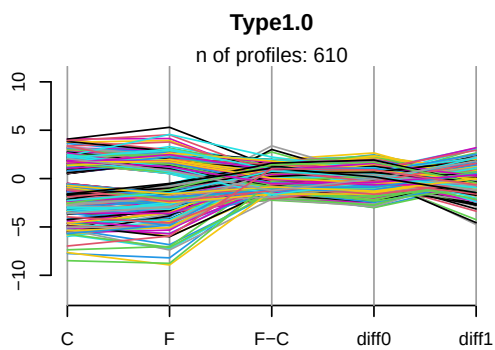


```

+ 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(3,2))
> tpar <- data.frame(C,F,F-C,diff0,diff1)
> ylim <- range(tpar)
> for(tip in colnames(types))
+ my.parallelplot(tpar[types[,tip],], ylim=ylim, title=tip)

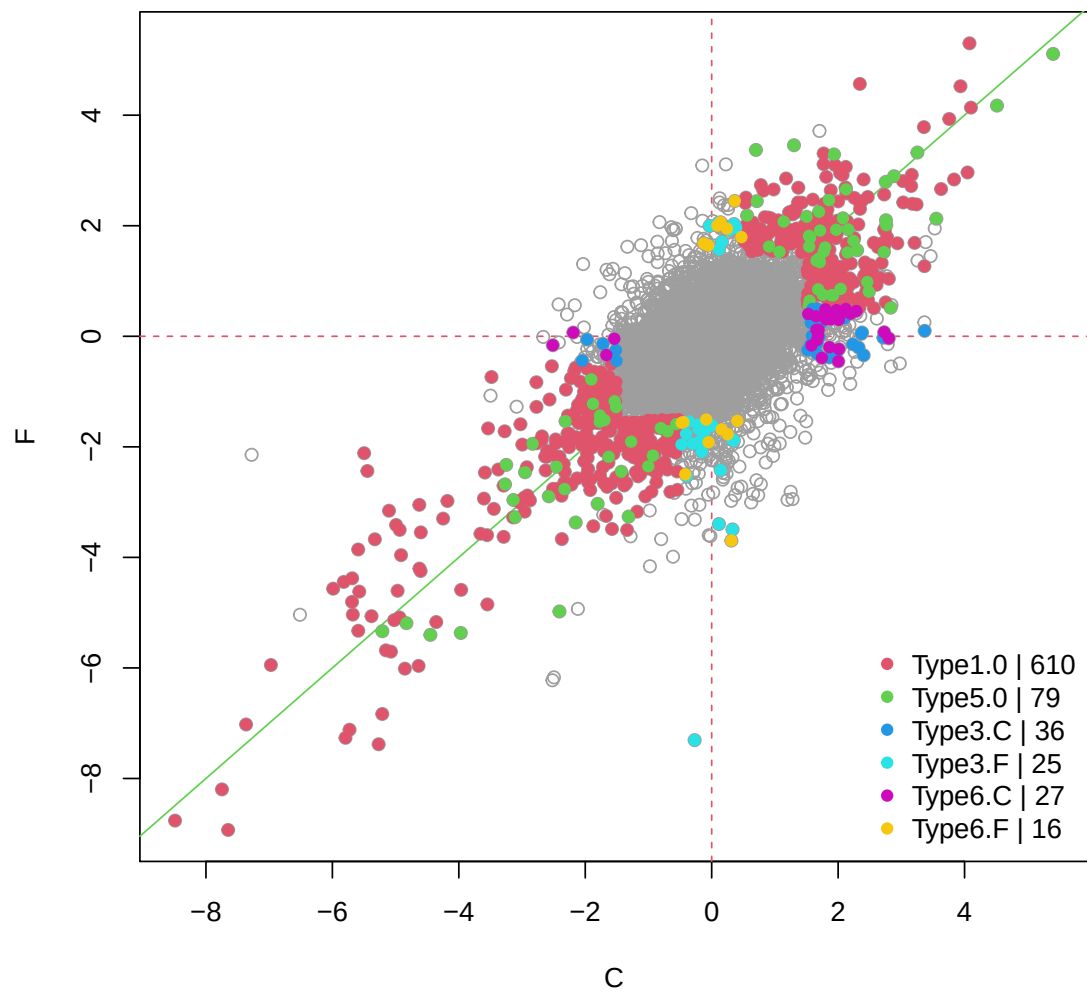
```



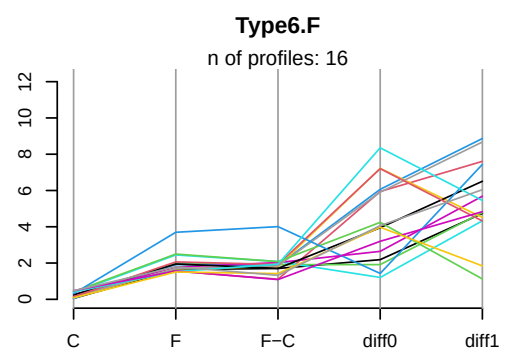
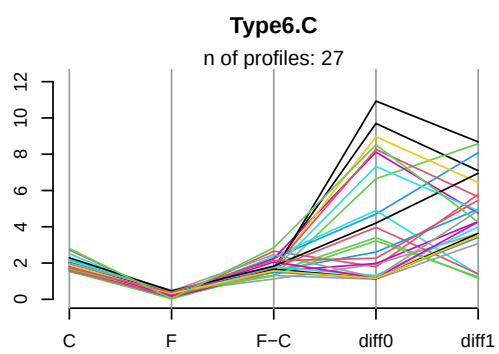
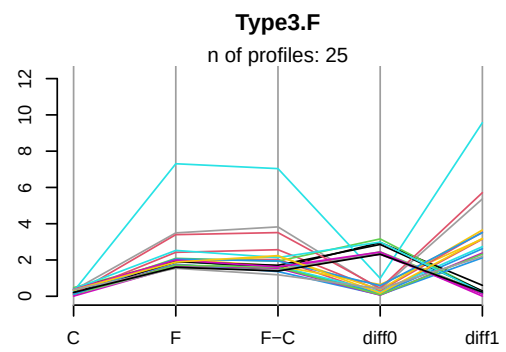
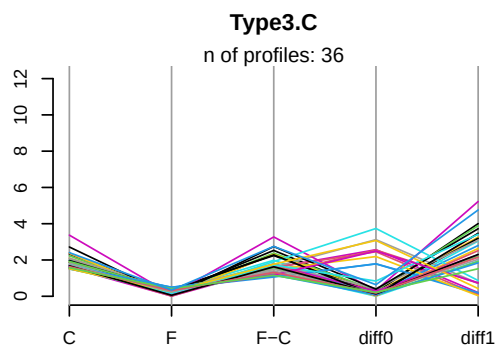
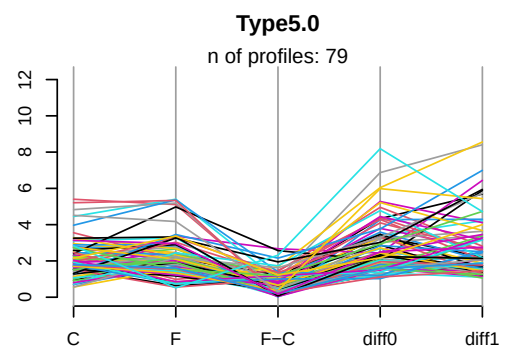
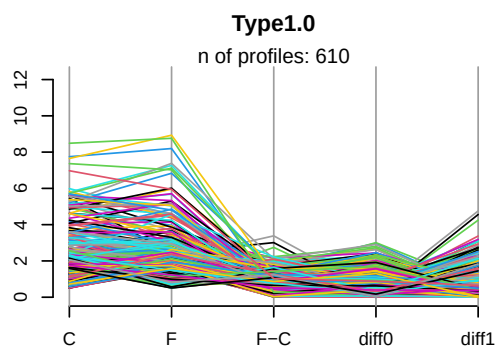
```

> plot.types()

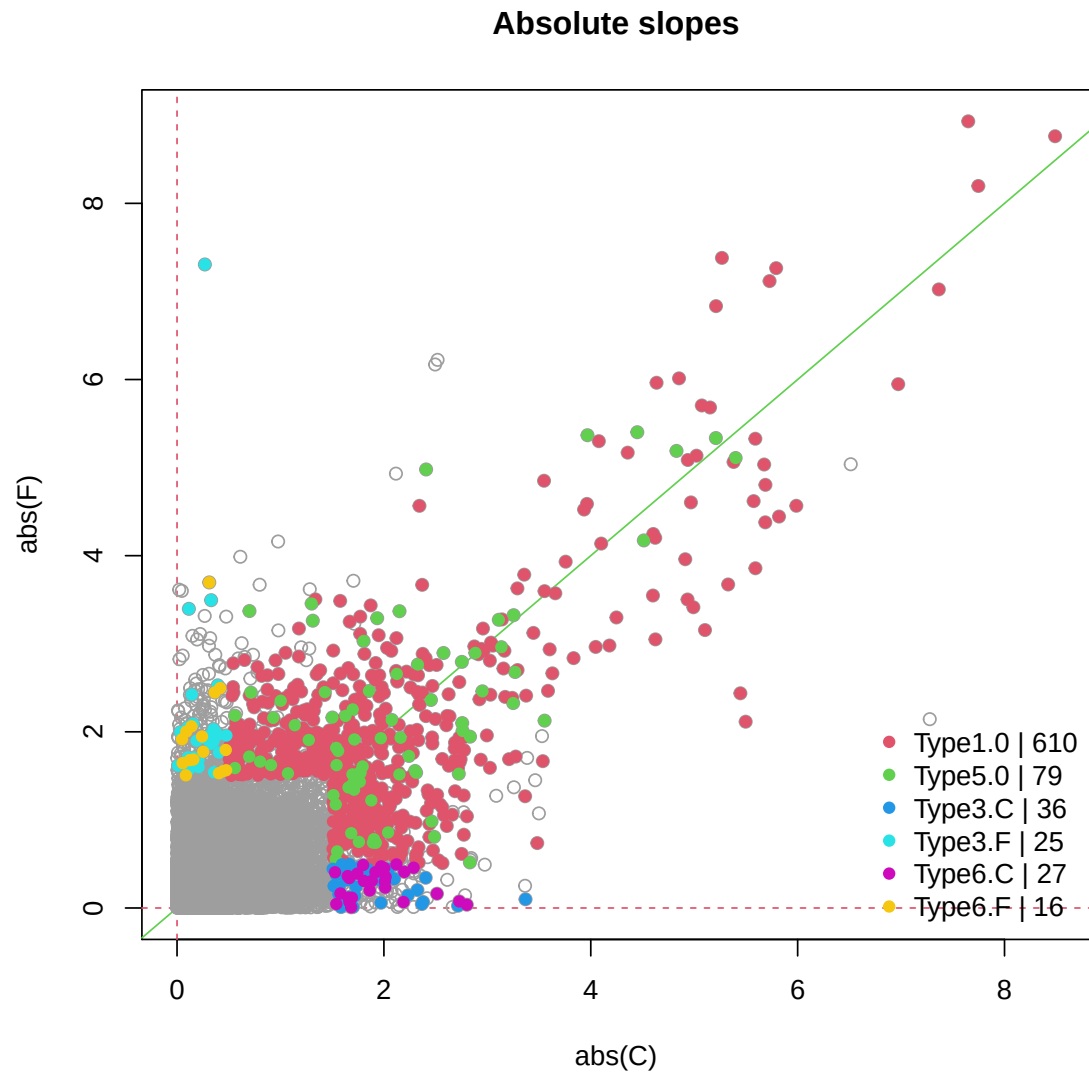
```



```
> par(mfrow=c(3,2))
> tpar <- data.frame(C,F,F-C,diff0,diff1)
> abstpar <- abs(tpar)
> ylim <- range(abstpar)
> for(tip in colnames(types))
+ my.parallelplot(abstpar[types[,tip],], ylim=ylim, title=tip)
```

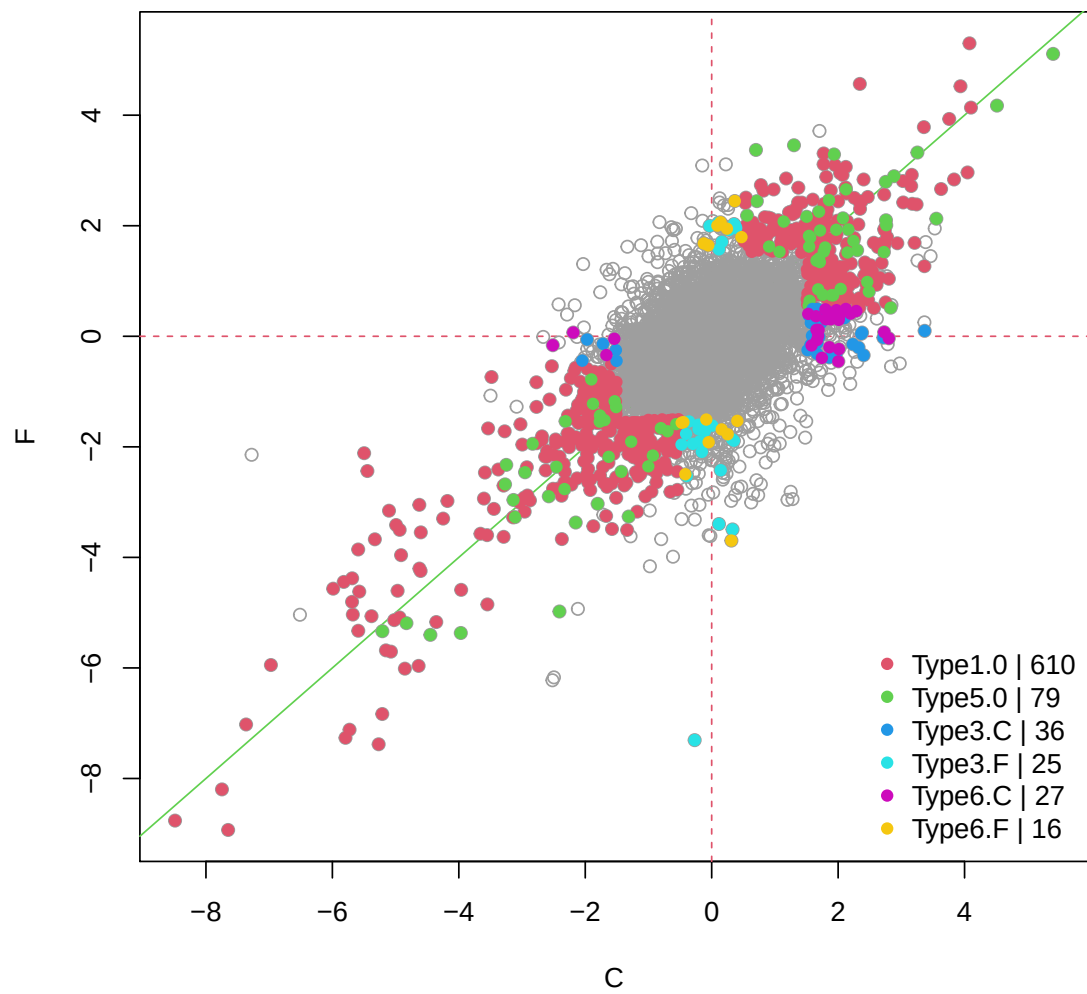


> plot.types(abs(C),abs(F),title="Absolute slopes")

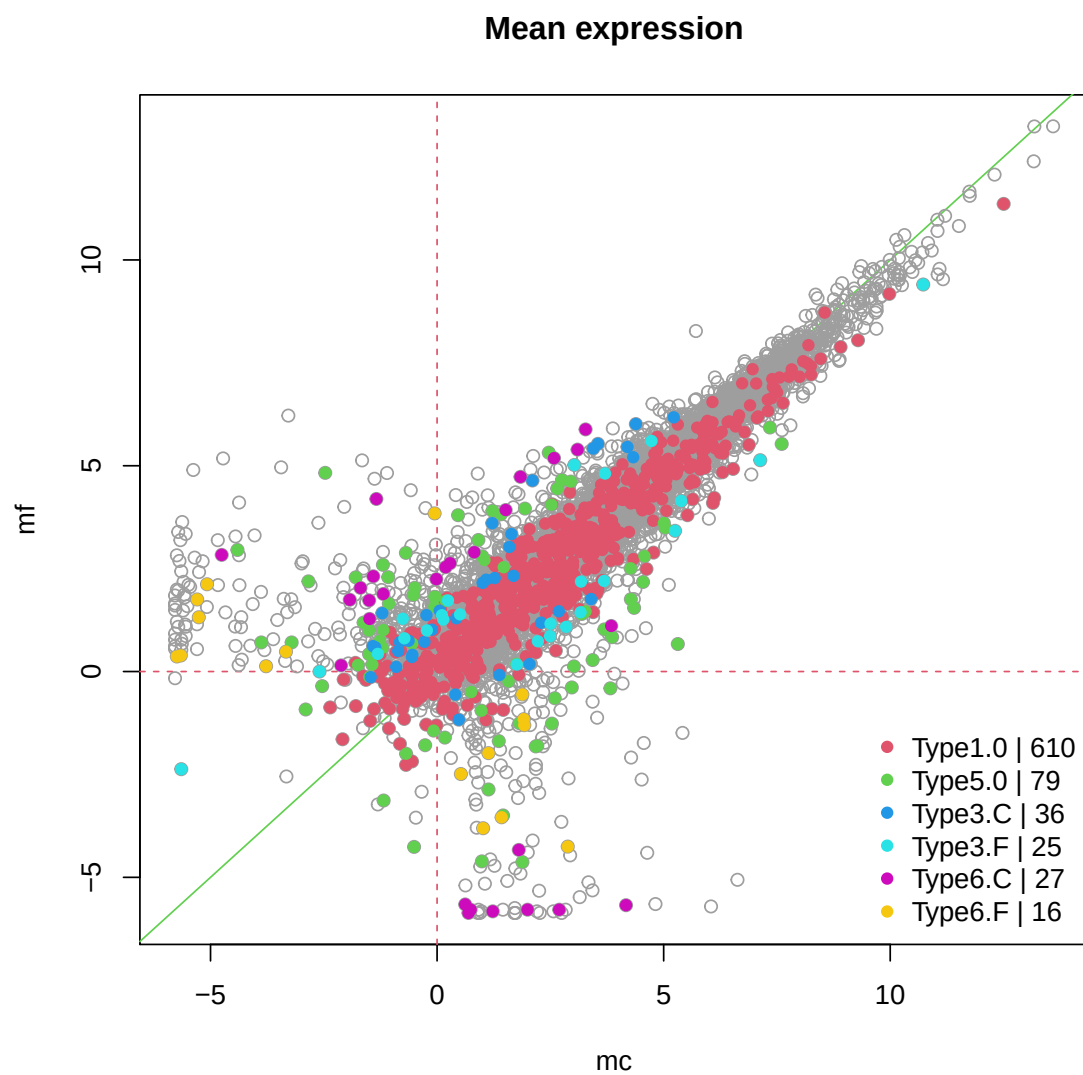


```
> plot.types(C,F,title="Slopes")
```

Slopes

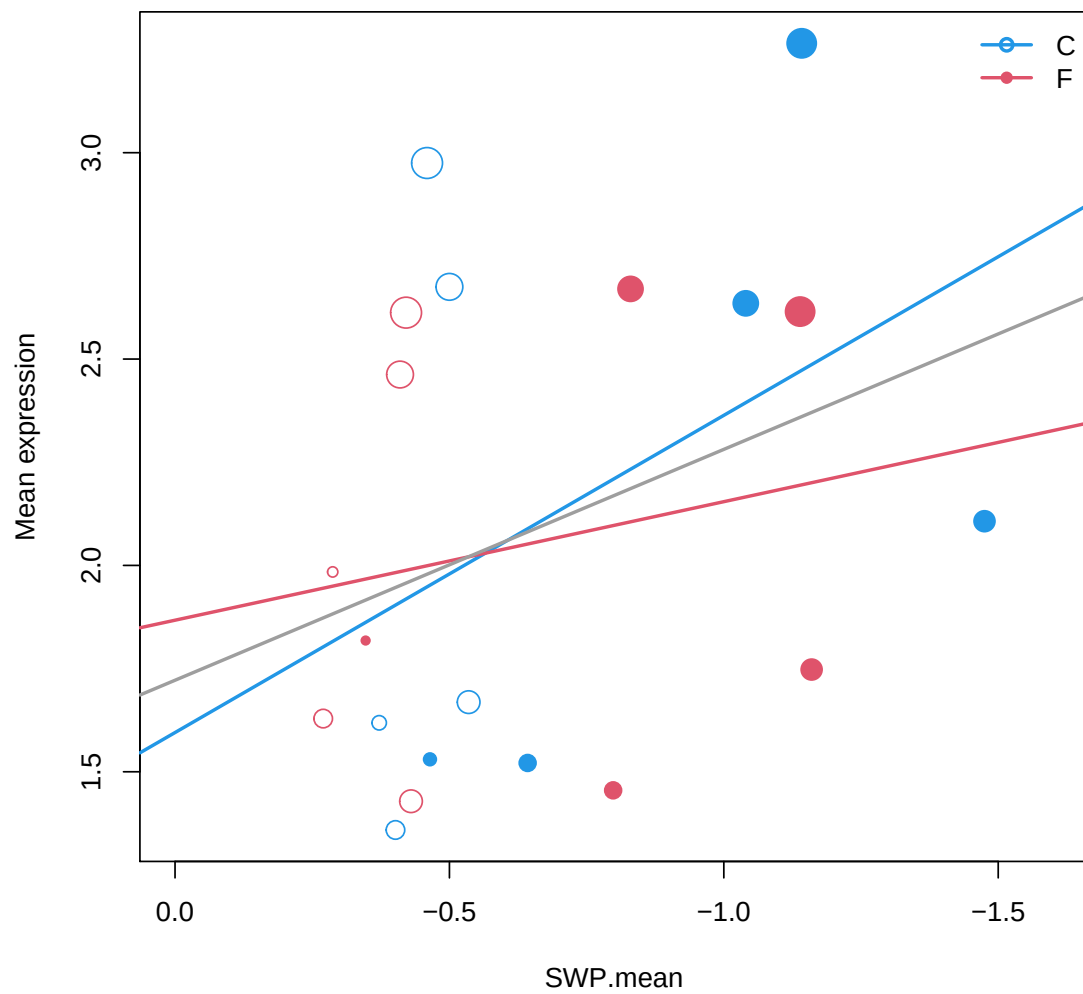


```
> plot.types(mc,mf,title="Mean expression")
```



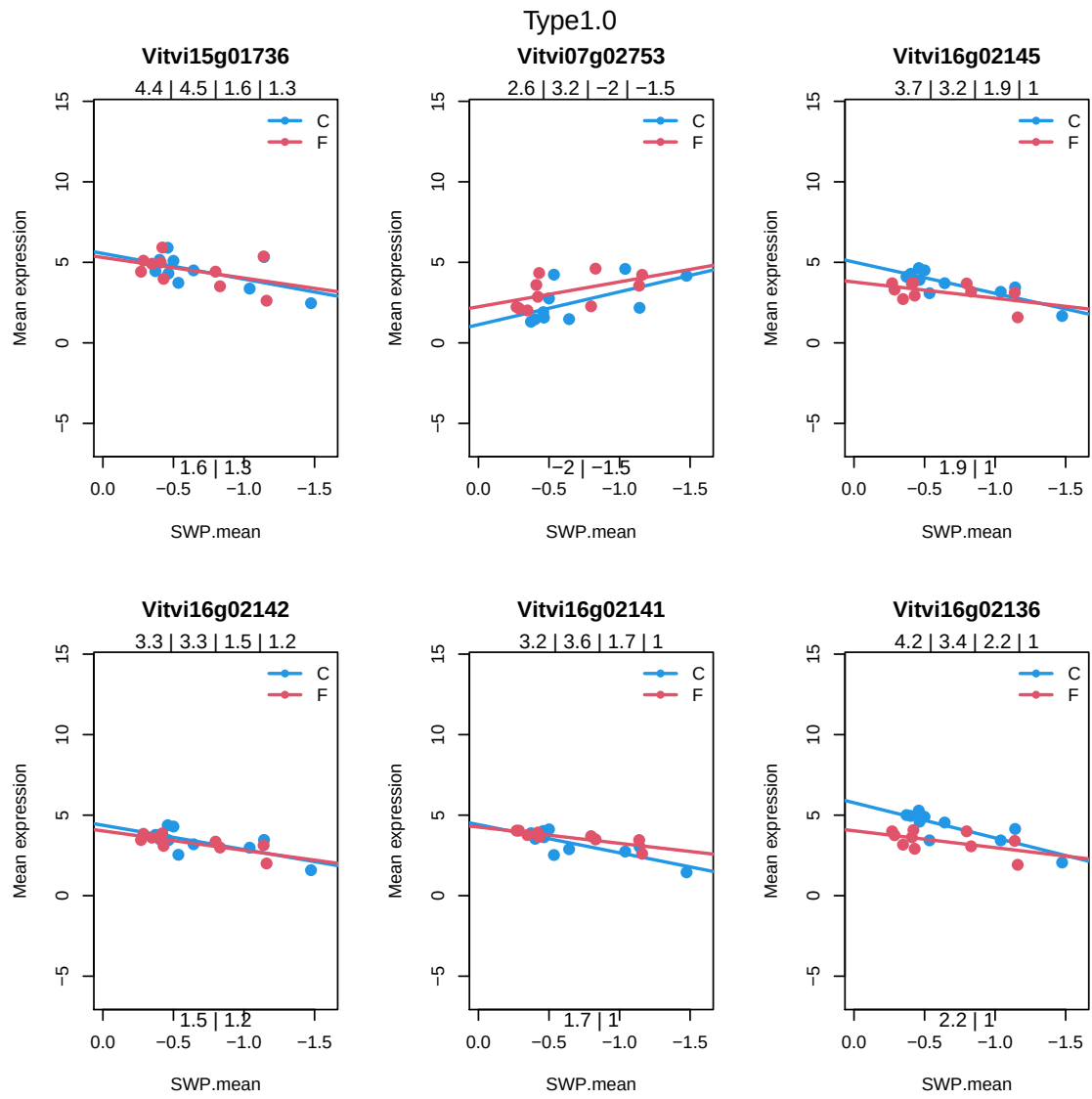
```
> varname <- testvar  
> plot.ewp(varname,model="", exprs=exprs, pd=pd)
```

Vitvi01g01391



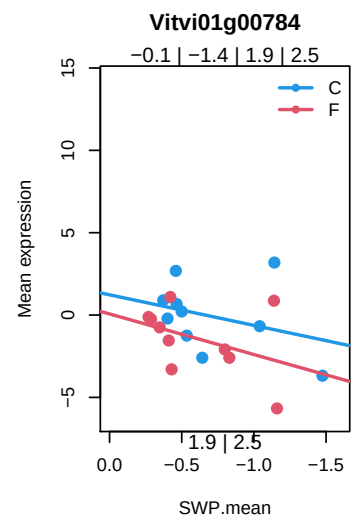
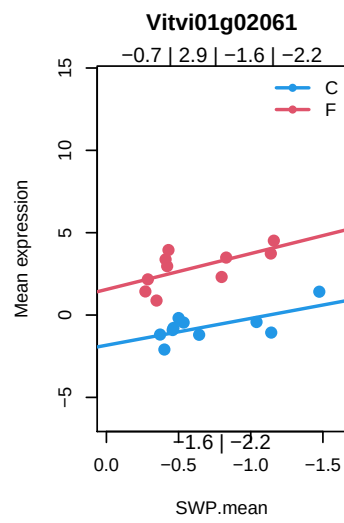
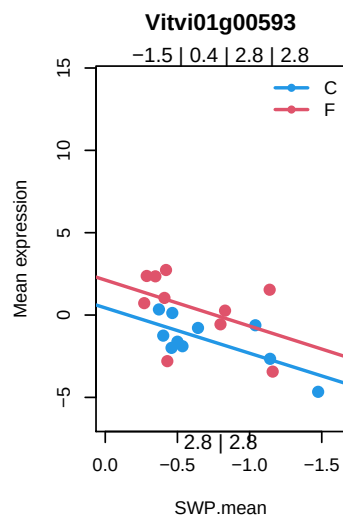
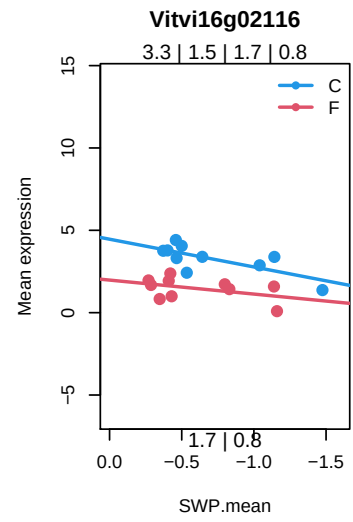
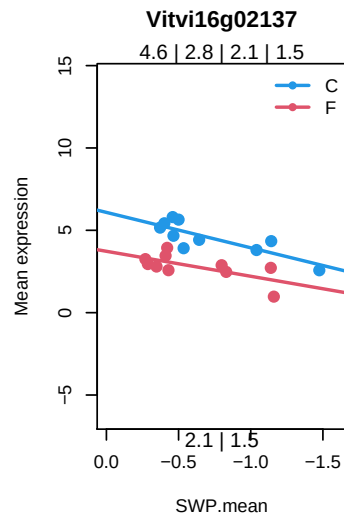
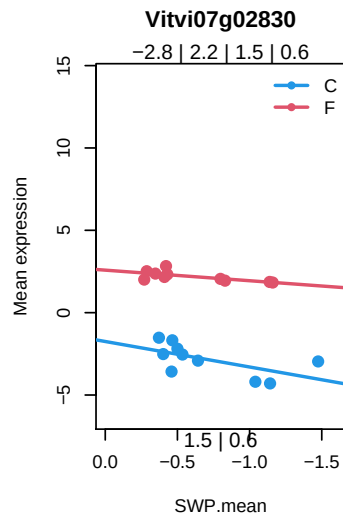
```
> apply(types, 2, sum)
Type1.0 Type5.0 Type3.C Type3.F Type6.C Type6.F
610      79      36      25      27      16

> for(i in 1:ncol(types)) {
+ plot.type(types[,i])
+ mtext(names(types[i]), outer=TRUE, line=-1)
+ }
[1] 610
```

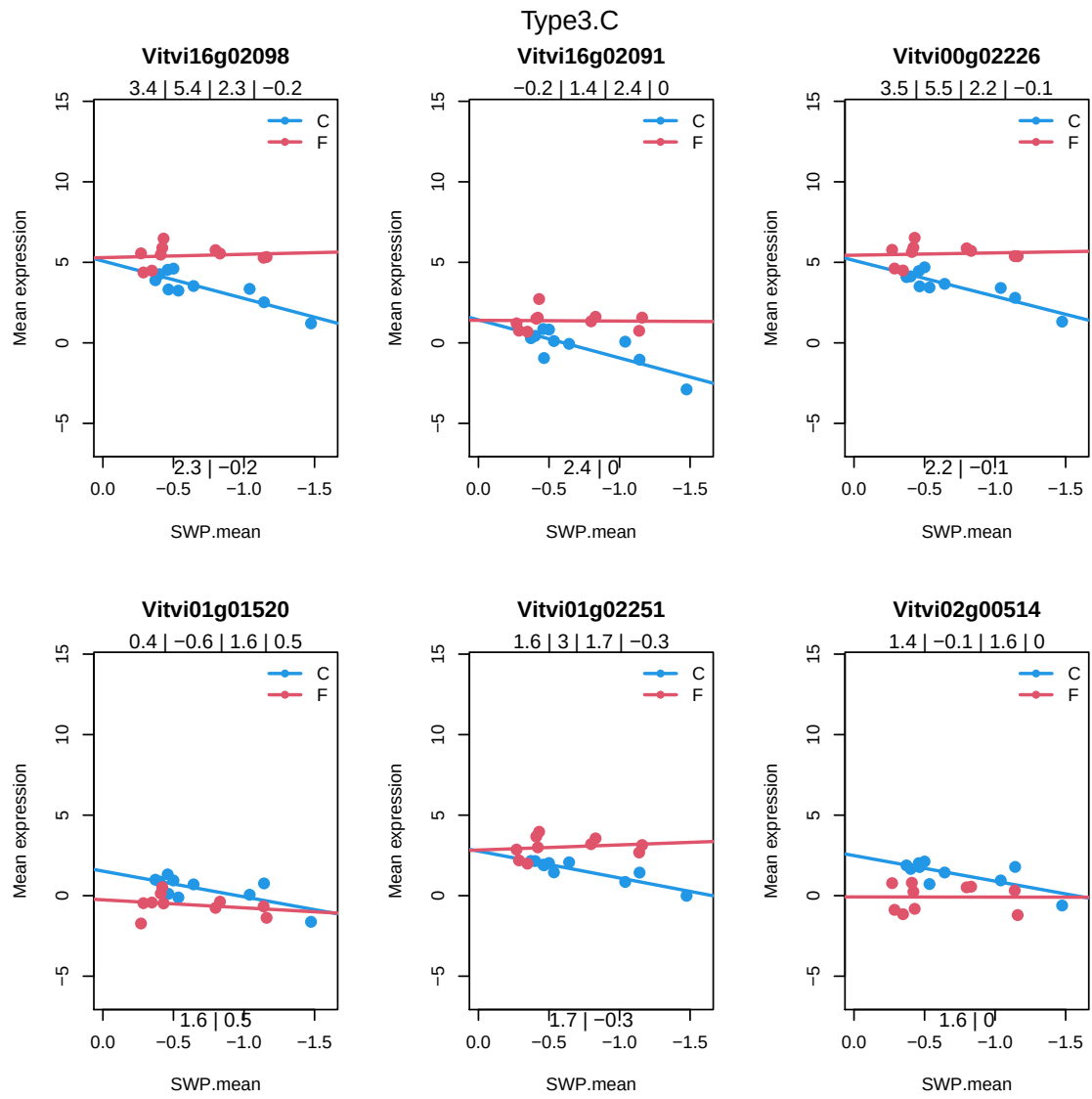



[1] 79

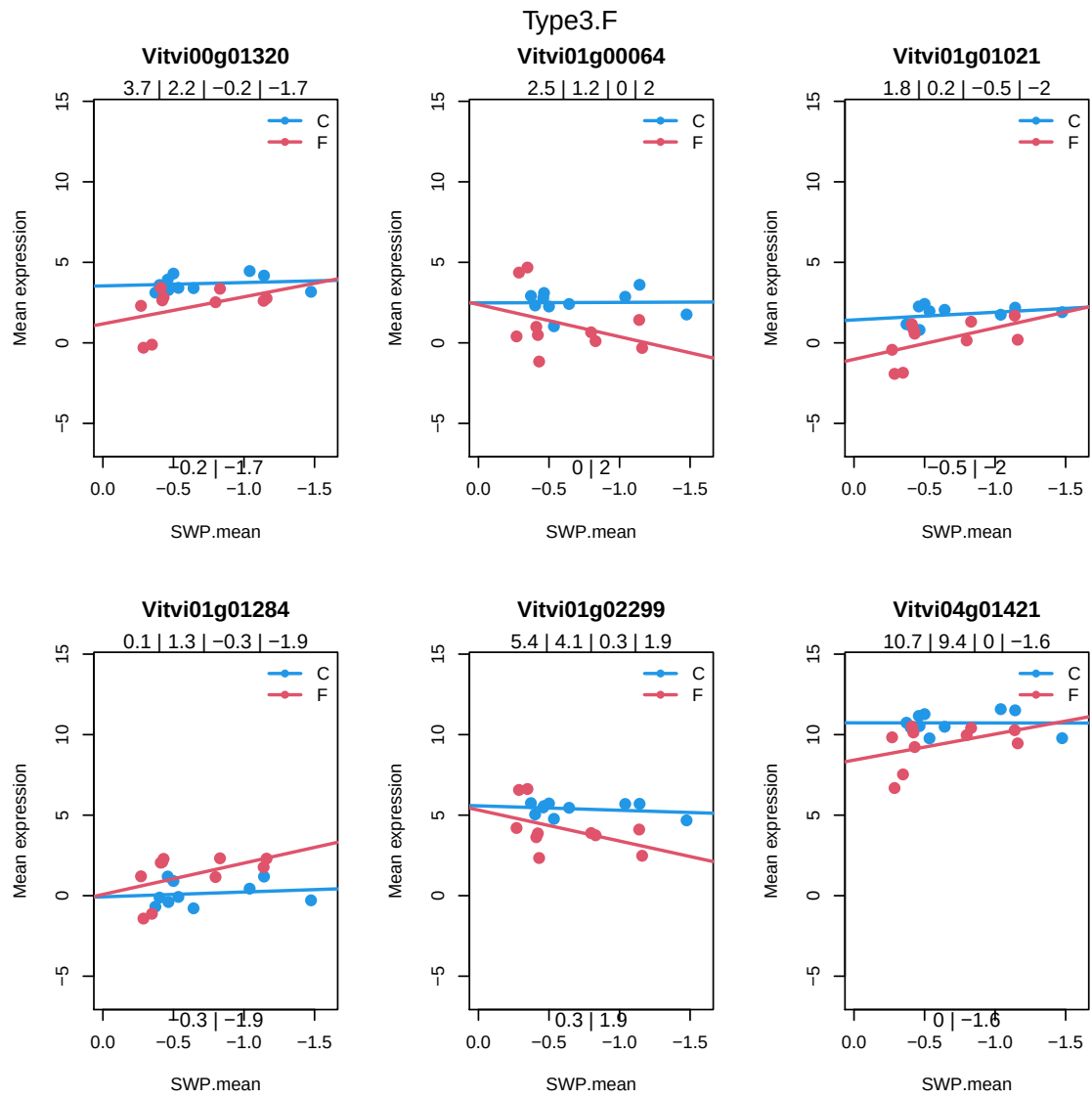
Type5.0



[1] 36

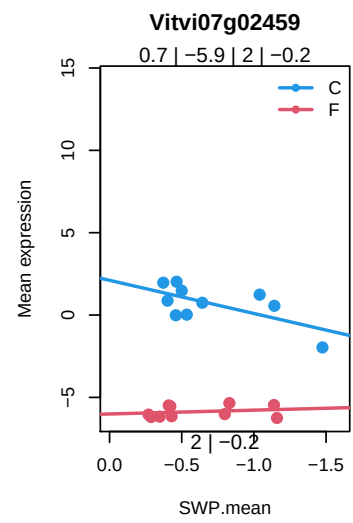
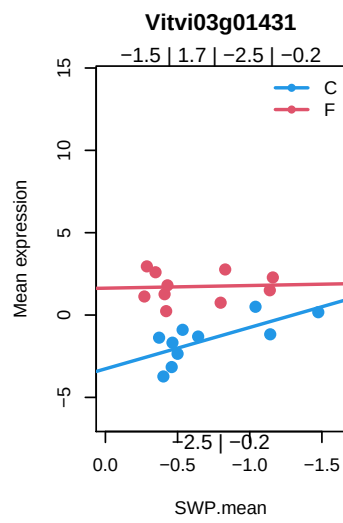
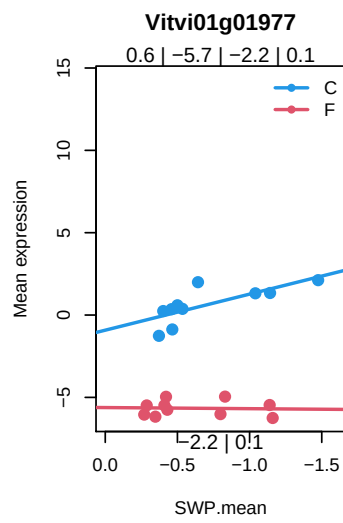
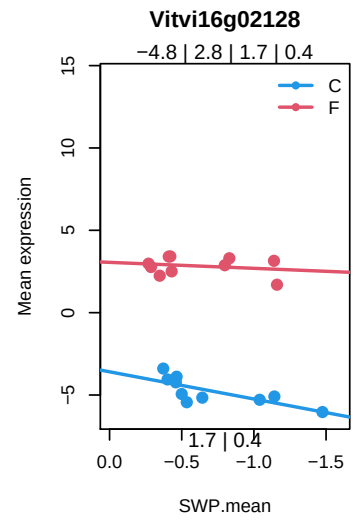
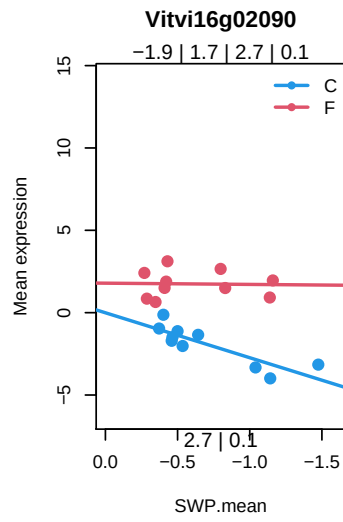
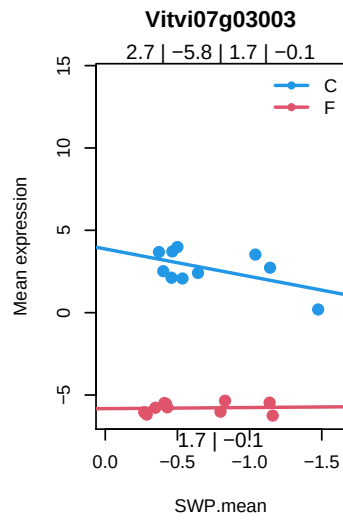


[1] 25

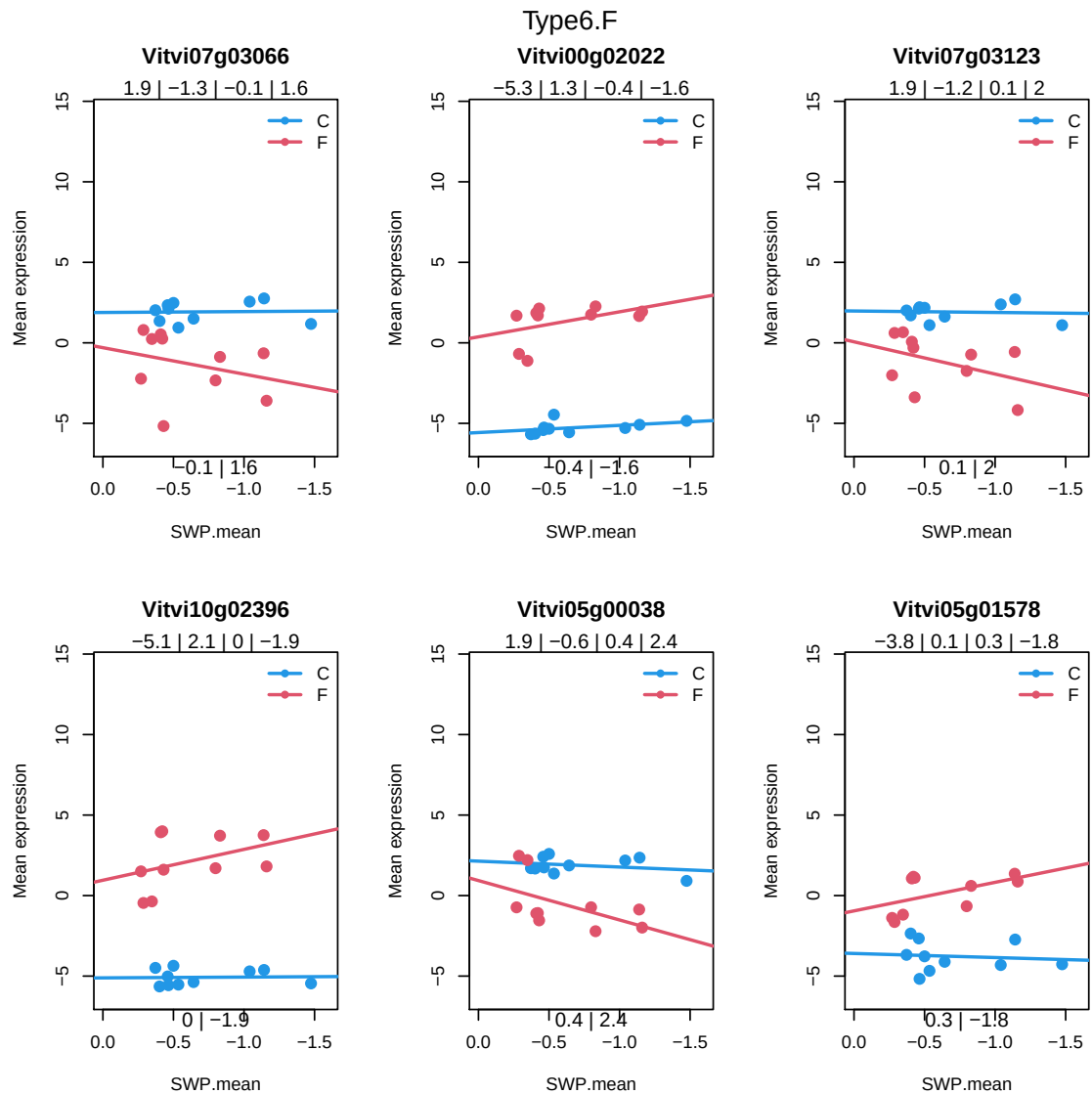


[1] 27

Type6.C



[1] 16



```
> 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

6.3 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

```
> #
> types <- types.new
> 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-0.05-1.5-0.5-1-1-3/TopTable.txt

```
> types <- types.new

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

7 Types and 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 intercepts 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

$qqr
$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      fl.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
      fl.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              cl              mf              fl.cl
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 ...

$sraux
[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

\$stddev.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	0
2	1 -0.4016667	0	0	0
3	1 -0.5350000	0	0	0
4	1 -0.5000000	0	0	0
5	1 -0.4592308	0	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 ...

\$sraux

[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 ...

$graux
[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

$scov.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))

```

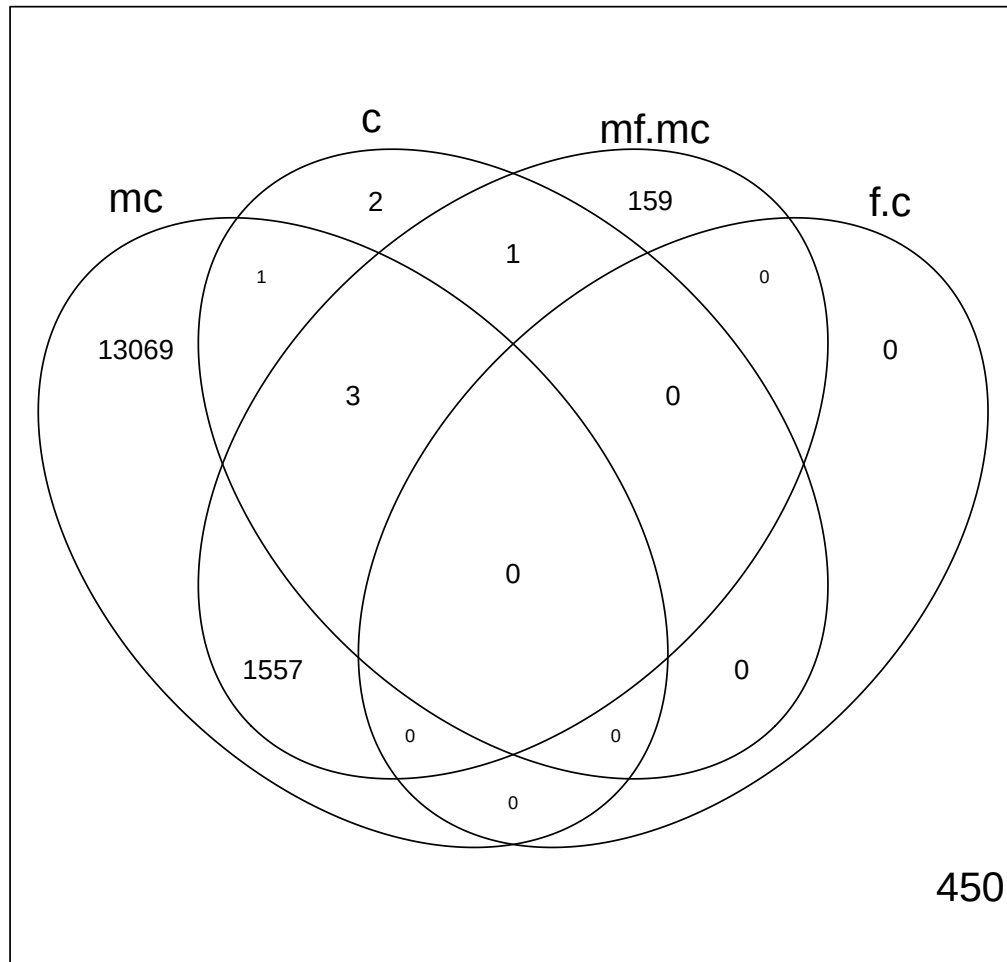
```

[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

```

7.1 Export fit statistics, types and descriptions

```
> 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, diff0, diff1, df4[, ins:ncol(df4)])
> #
> ## df4$type <- ""
> ## types <- types.old
> ## types <- types[rownames(df4),]
> ## all(rownames(df4)==rownames(types))
> ## #ind <- sapply(rownames(tt), FUN=function(x) match(x, rownames(types)))
> ## for(i in 1:ncol(types)) {
> ##     df4$type[types[,i]] <- paste(df4$type[types[,i]], colnames(types)[i],
> ##     print(table(df4$type))
> ##     }
> ## df4$type <- gsub("^\\|", "", df4$type)
> #
> df4$Type <- ""
> types <- types.new
> 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))
+     }

      |Type1.0
14632      610

      |Type1.0 |Type5.0
14553      610      79

      |Type1.0 |Type3.C |Type5.0
14517      610      36      79

      |Type1.0 |Type3.C |Type3.F |Type5.0
14492      610      36      25      79

      |Type1.0 |Type3.C |Type3.F |Type5.0 |Type6.C
14465      610      36      25      79      27

      |Type1.0 |Type3.C |Type3.F |Type5.0 |Type6.C
14449      610      36      25      79      27
|Type6.F
      16

> df4$Type <- gsub("^\\|", "", df4$Type)
> types <- types.new
> #
> # 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
> #print(table(stat4$type, stat4$Type), zero.print=".")

```

Some genes are classified into two types:

```

> t(t(table(df4$Type)))

      [,1]
14449
Type1.0   610
Type3.C    36
Type3.F    25
Type5.0    79
Type6.C    27
Type6.F    16

> summary(types)

Type1.0      Type5.0      Type3.C
Mode :logical Mode :logical Mode :logical
FALSE:14632  FALSE:15163  FALSE:15206
TRUE :610    TRUE :79      TRUE :36
Type3.F      Type6.C      Type6.F
Mode :logical Mode :logical Mode :logical
FALSE:15217  FALSE:15215  FALSE:15226
TRUE :25     TRUE :27     TRUE :16

```

Order stat4 and types by decreasing coefficient for C

```

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

```

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-0.05-1.5-0.5-1-1-3/lm-fit-means-swpXvariety-statistics.txt

Comparison with effects.

Large abs slope C

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

FALSE TRUE
  954   540
> table(indp, large_abs_C)
      large_abs_C
indp  FALSE  TRUE
  FALSE 13629  119
   TRUE   954  540
```

Small difference of slopes

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

FALSE TRUE
 1482 13601
> table(indp, small_fc)
      small_fc
indp  FALSE  TRUE
  FALSE   157    2
   TRUE  1482 13601
```

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
  410  2779
> table(indp, large.diff.means=(abs(mc-mf)<deltam))
      large.diff.means
indp  FALSE  TRUE
  FALSE    1 12052
   TRUE   410  2779
```


8 Detailed plots, stats and info of Genes by types

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

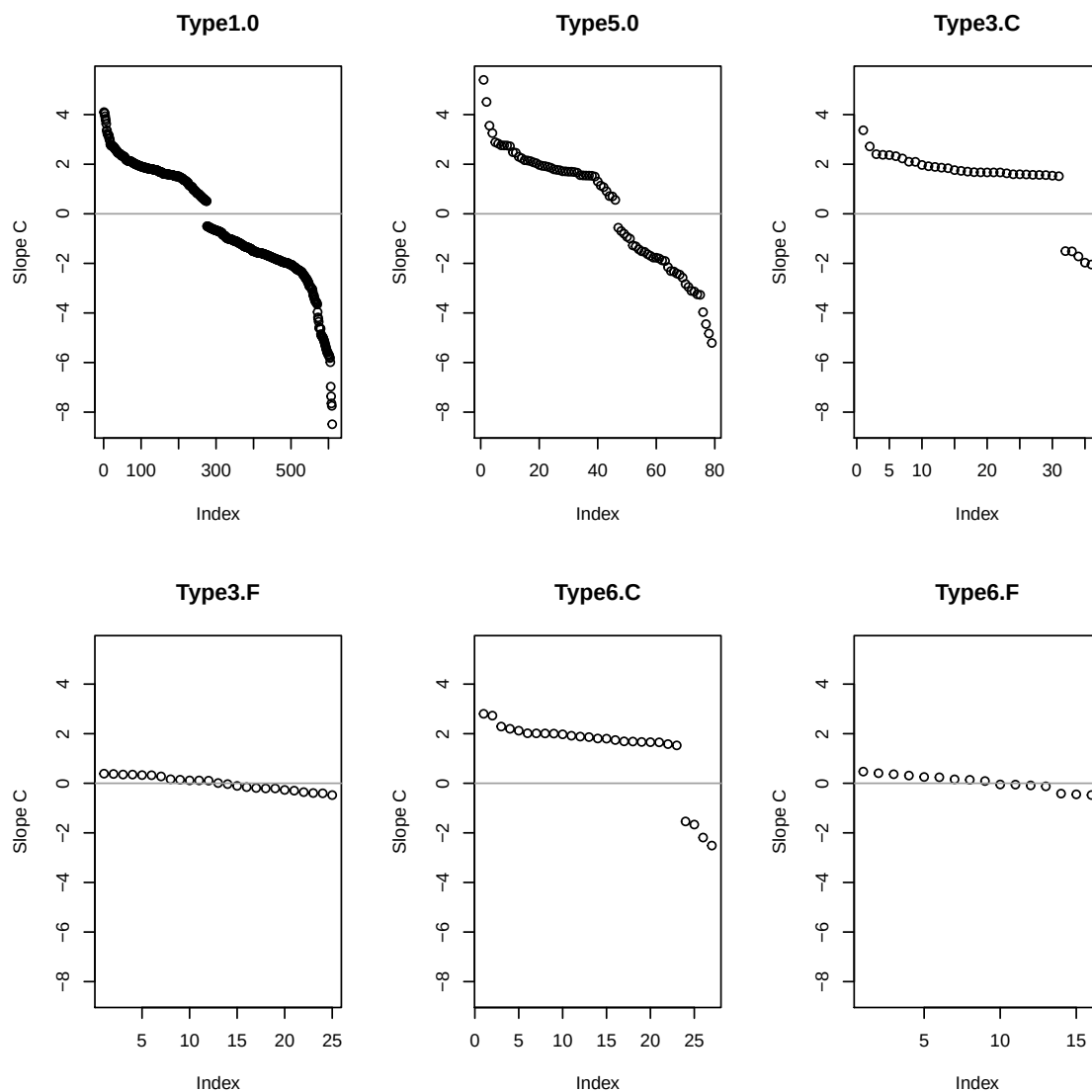
Figures caption:

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

Order stat4 and types by decreasing coefficient for C

```
> 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] "diff0"            "diff1"
[9] "t.mc"             "t.c"
[11] "t.mf.mc"          "t.f.c"
[13] "P.value.mc"       "P.value.c"
[15] "P.value.mf.mc"    "P.value.f.c"
[17] "P.value.adj.mc"   "P.value.adj.c"
[19] "P.value.adj.mf.mc" "P.value.adj.f.c"
[21] "F"                "F.p.value"
[23] "Type"             "interestingC"
[25] "interestingFC"     "geneID"
[27] "BINCODE"          "NAME"
[29] "DESCRIPTION"

> i <- 1
> (typevar <- substr(names(types)[1],1,4))

[1] "Type"

> tipi <- sort(unique(stat4[,typevar]))[-1]
> # reorder type names
> types <- types[,sort(colnames(types))]
> for(i in 1:ncol(types)){
+ type.name <- colnames(types)[i]
+ out <- paste(out, "
+ \\clearpage
+ \\subsection{",type.name,"}\\")
+ 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"),
+ }

```

8.1 Type1.0

8.1.1 Vitvi05g00011: Type1.0 *

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

```
Vitvi05g00011
```

```
35.2
```

```
not assigned.unknown
```

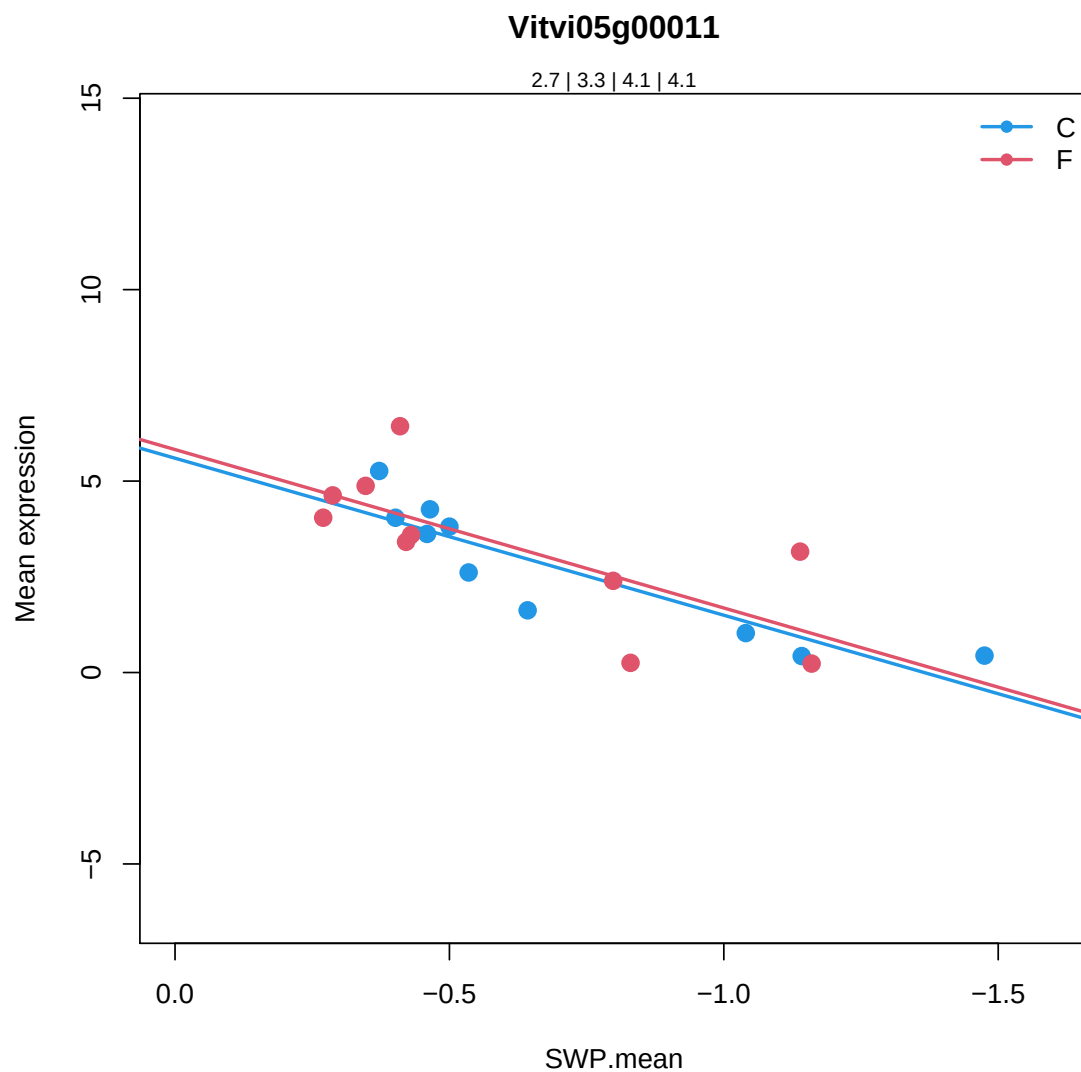
```
Pollen Ole e 1 allergen and extensin family protein |
```

```
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	



8.1.2 Vitvi13g02005: Type1.0

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

Vitvi13g02005

29.5.1

protein.degradation.subtilases

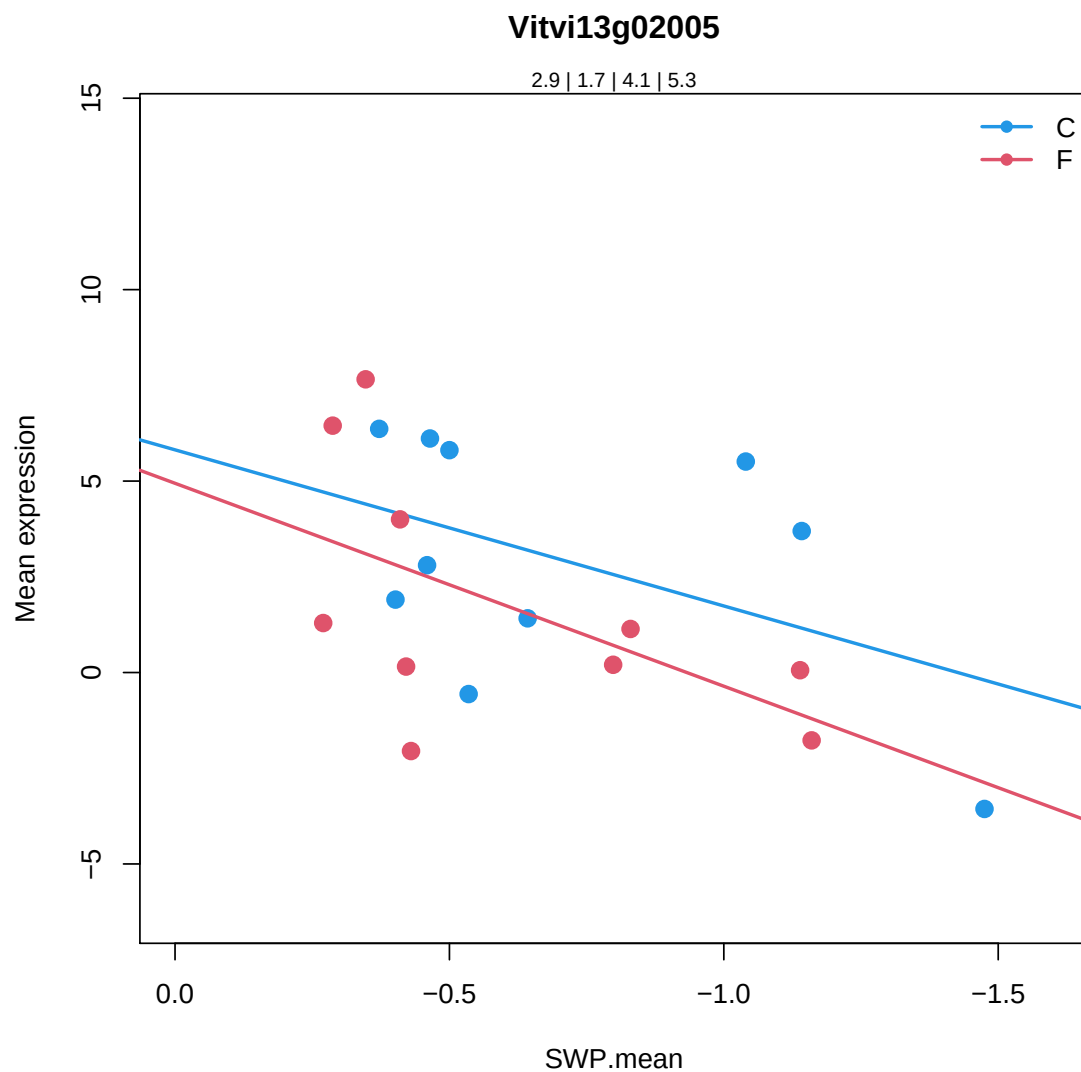
Subtilisin-like serine endopeptidase family protein |

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	



8.1.3 Vitvi02g00695: Type1.0 *

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

Vitvi02g00695

20.1

stress.biotic

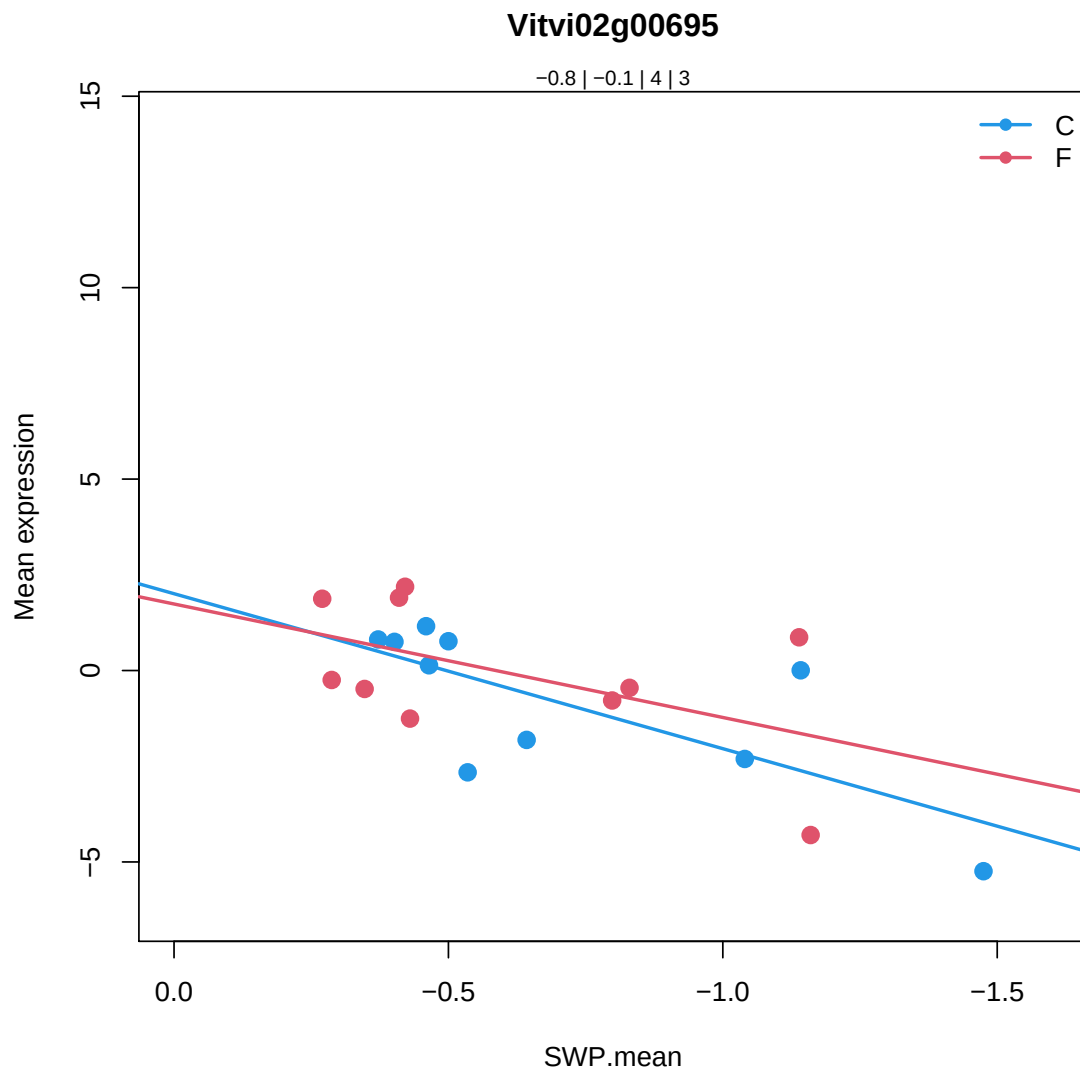
Polyketide cyclase/dehydrase and lipid transport superfamily protein |

Chr4:9928792-9929367 FORWARD LENGTH=191 |

201606

Coefficients for Vitvi02g00695.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.8399601	0.07705364	.	0.07988693	.
SlopeC	4.04752	0.00406135	**	0.2328828	
MeanF-MeanC	0.7715056	0.2408449		0.5983631	
SlopeF-SlopeC	-1.083729	0.5688147		0.9999488	



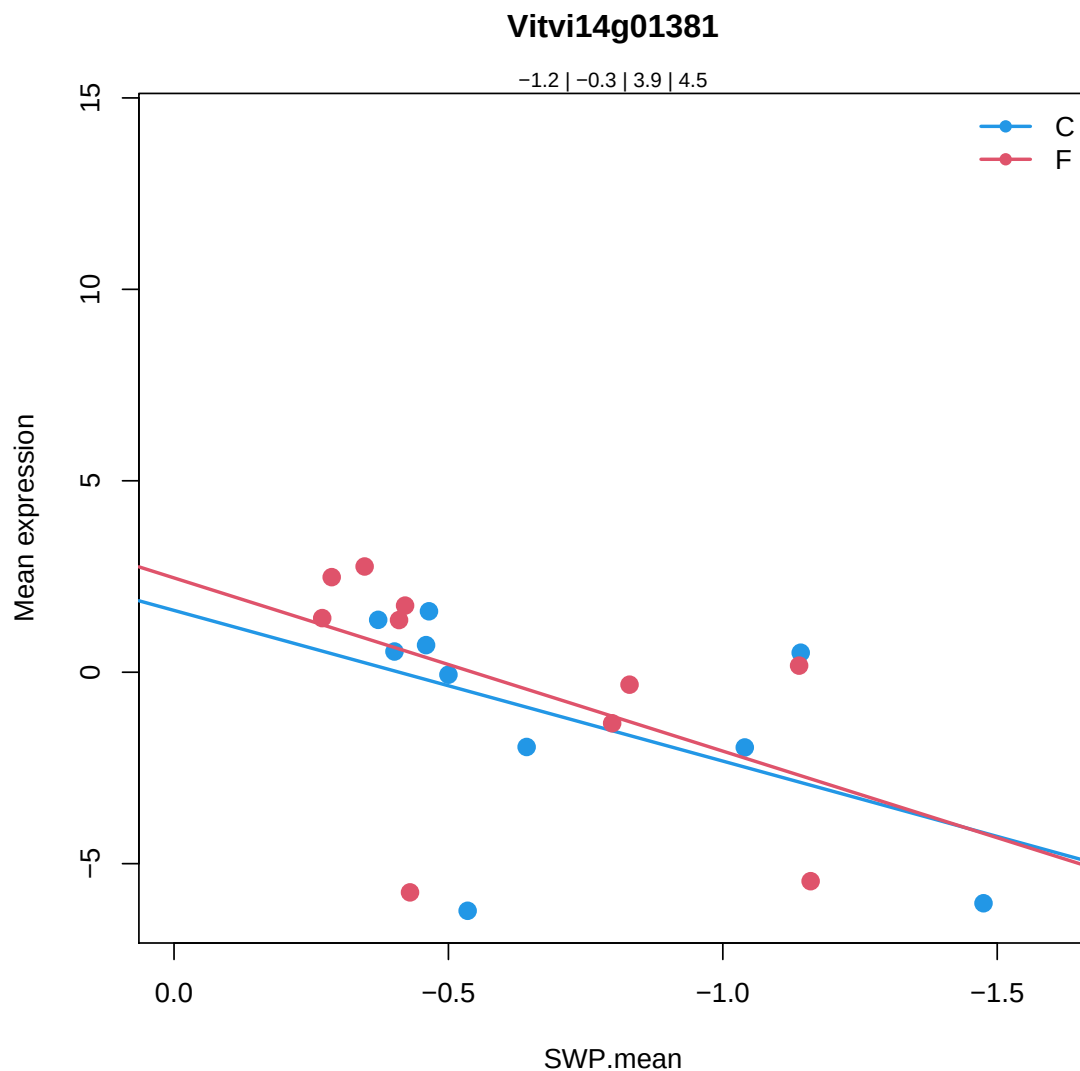
8.1.4 Vitvi14g01381: Type1.0

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

```
Vitvi14g01381
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi14g01381.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.153067	0.1366212		0.1407775	
SlopeC	3.935431	0.07135627	.	0.5630621	
MeanF-MeanC	0.8596946	0.4238626		0.7605433	
SlopeF-SlopeC	0.588279	0.8506793		0.9999488	



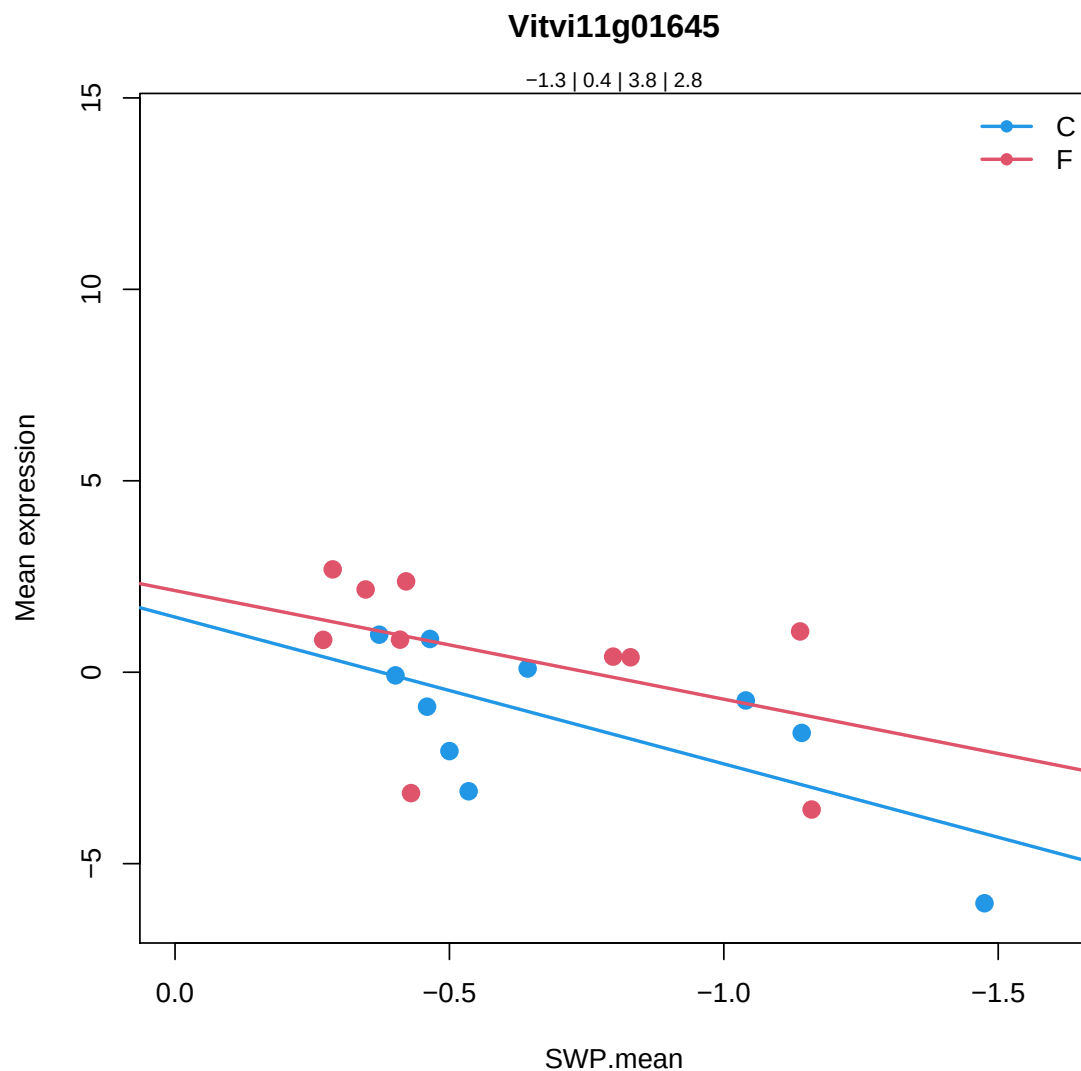
8.1.5 Vitvi11g01645: Type1.0 *

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

```
Vitvi11g01645
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi11g01645.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.256387	0.0220056	*	0.02311893	*
SlopeC	3.833904	0.01301173	*	0.3305597	
MeanF-MeanC	1.659781	0.03113549	*	0.1738341	
SlopeF-SlopeC	-0.9971111	0.6408022		0.9999488	



8.1.6 Vitvi05g01353: Type1.0 *

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

Vitvi05g01353

10.8.1

cell wall.pectinesterases.PME

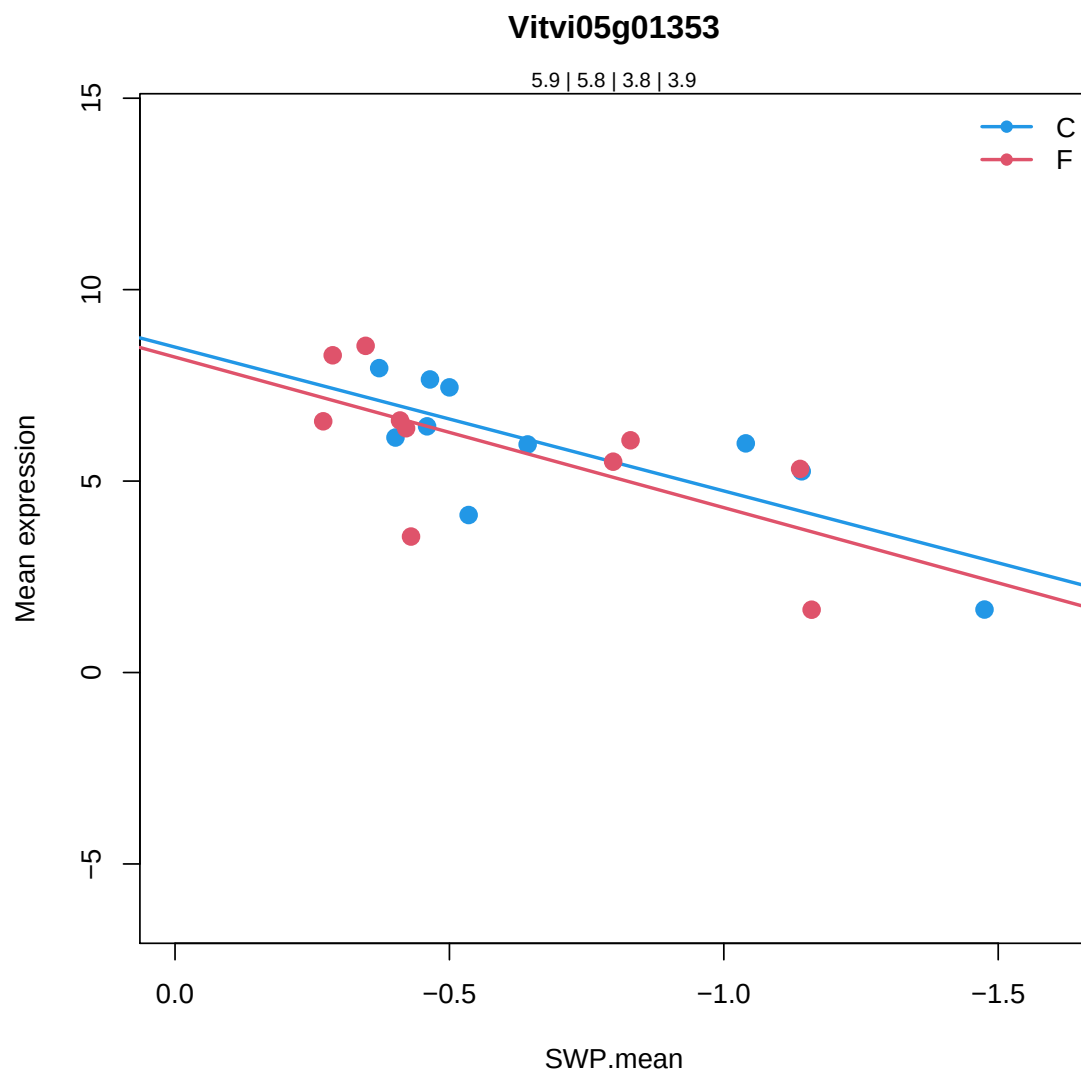
pectin methylesterase 61 |

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	



8.1.7 Vitvi01g02286: Type1.0 *

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

Vitvi01g02286

17.2.3

hormone metabolism.auxin.induced-regulated-responsive-activated

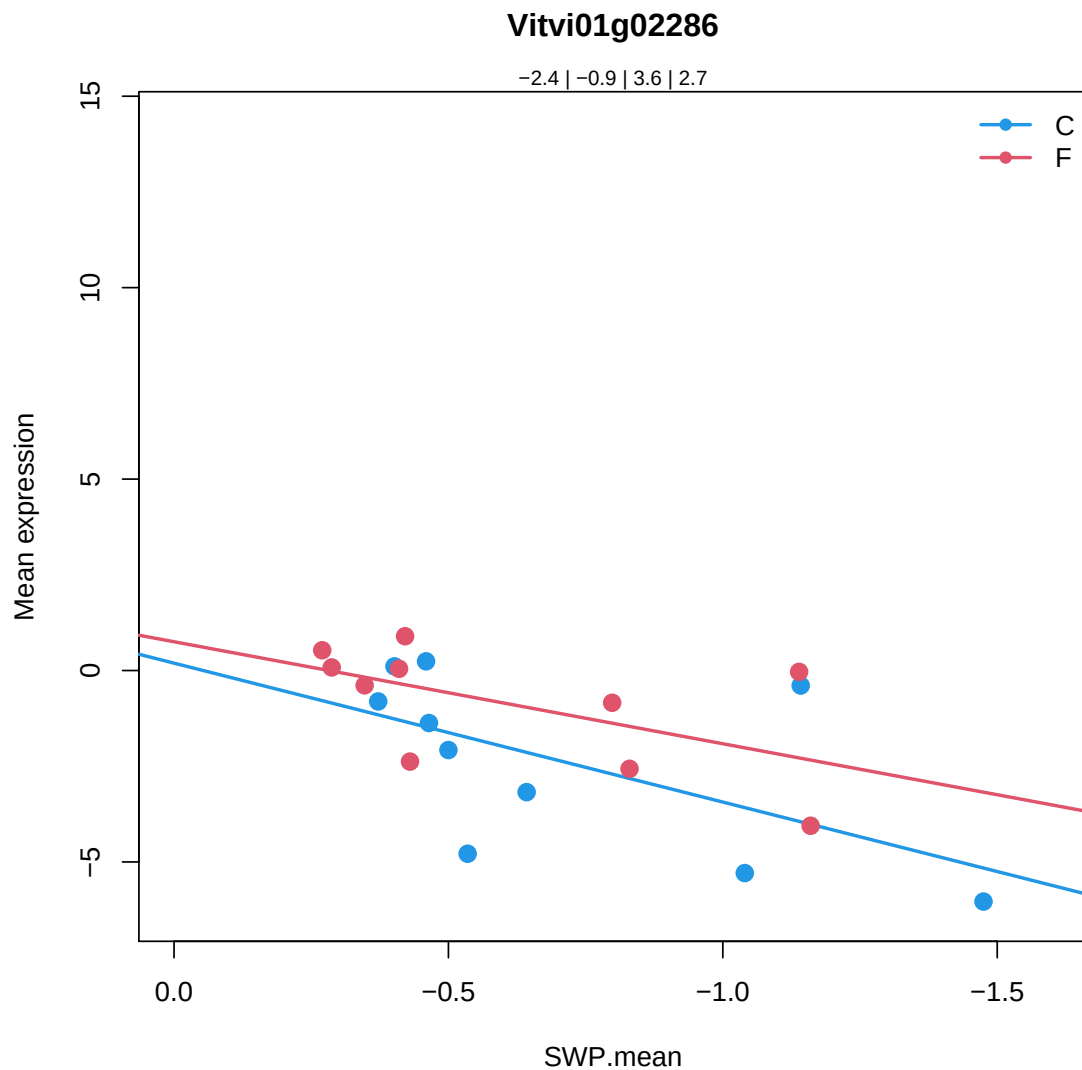
SAUR-like auxin-responsive protein family |

Chr5:20644780-20645331 FORWARD LENGTH=183 |

201606

Coefficients for Vitvi01g02286.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-2.35875	6.3206e-05	***	7.006952e-05	***
SlopeC	3.628699	0.01215037	*	0.3229093	
MeanF-MeanC	1.487141	0.03823163	*	0.1999748	
SlopeF-SlopeC	-0.9648213	0.6295866		0.9999488	



8.1.8 Vitvi14g01926: Type1.0 *

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

Vitvi14g01926

27.3.6

RNA.regulation of transcription.basic helix-loop-helix family (bHLH)

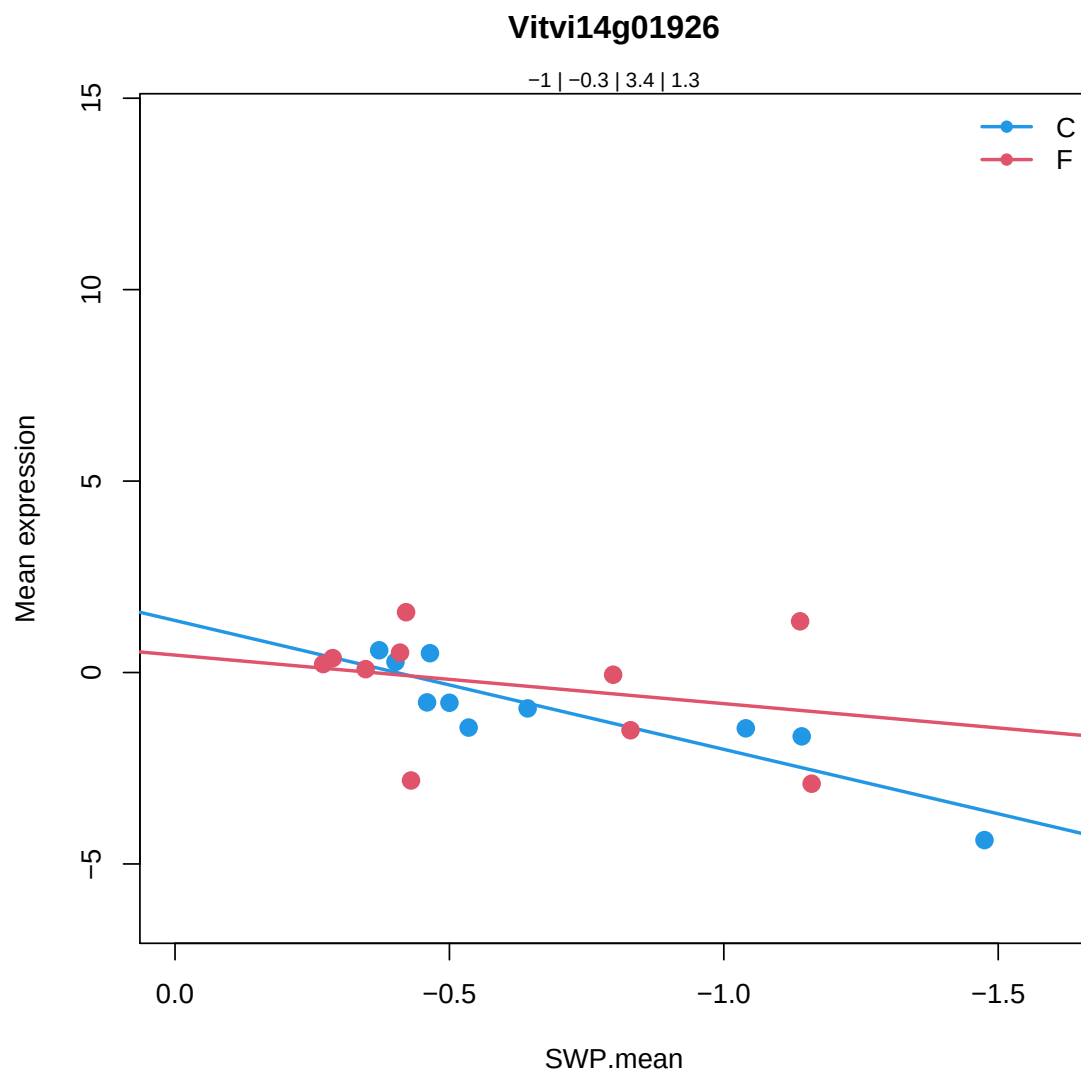
basic helix-loop-helix (bHLH) DNA-binding family protein |

Chr3:10855781-10856313 REVERSE LENGTH=92 |

201606

Coefficients for Vitvi14g01926.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.008442	0.008635654	**	0.009162871	**
SlopeC	3.365317	0.002253335	**	0.1816214	
MeanF-MeanC	0.6912249	0.1755638		0.507769	
SlopeF-SlopeC	-2.096888	0.1611547		0.9999488	



8.1.9 Vitvi10g01886: Type1.0

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

Vitvi10g01886

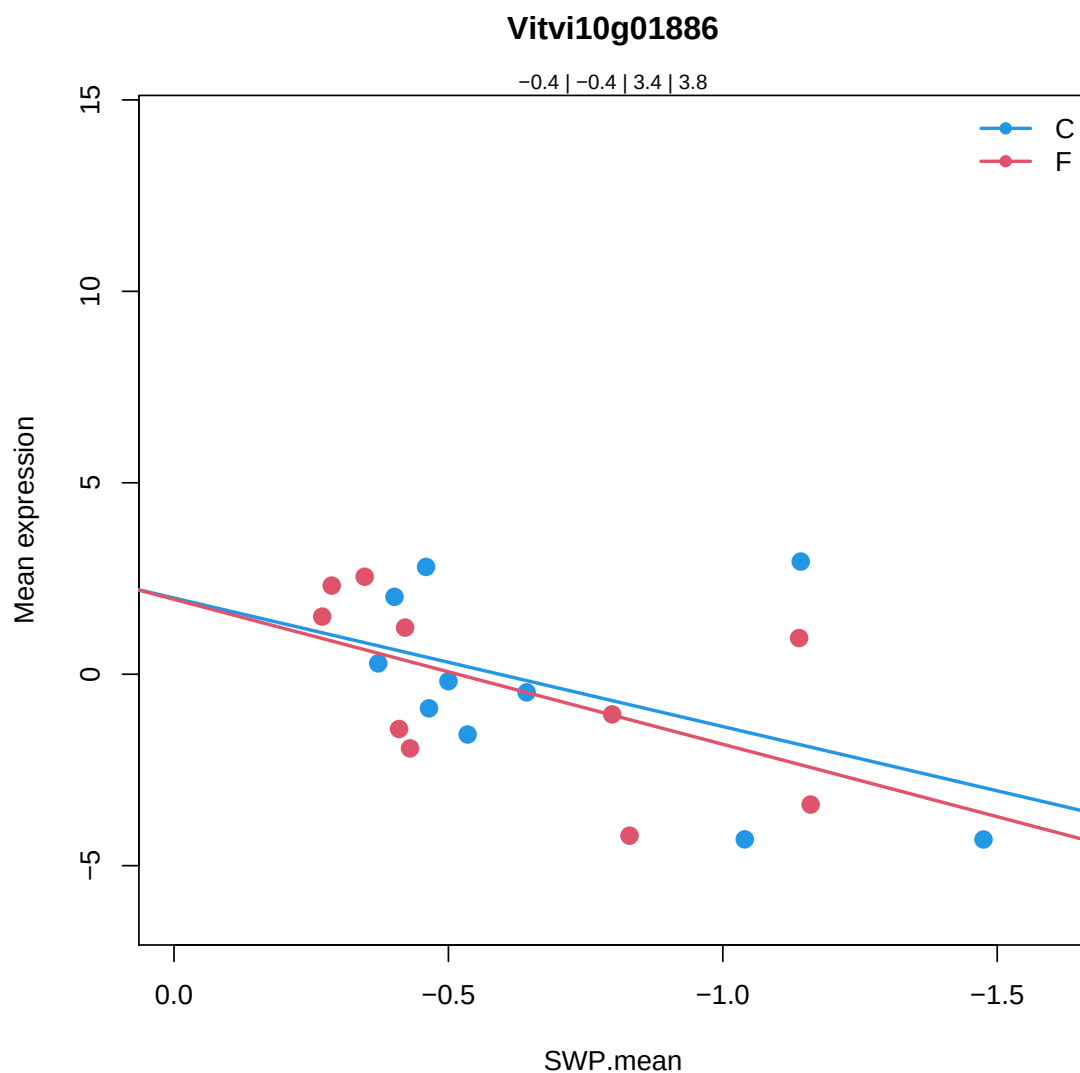
35.2

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	



8.1.10 Vitvi13g00172: Type1.0 *

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

Vitvi13g00172

10.7

cell wall.modification

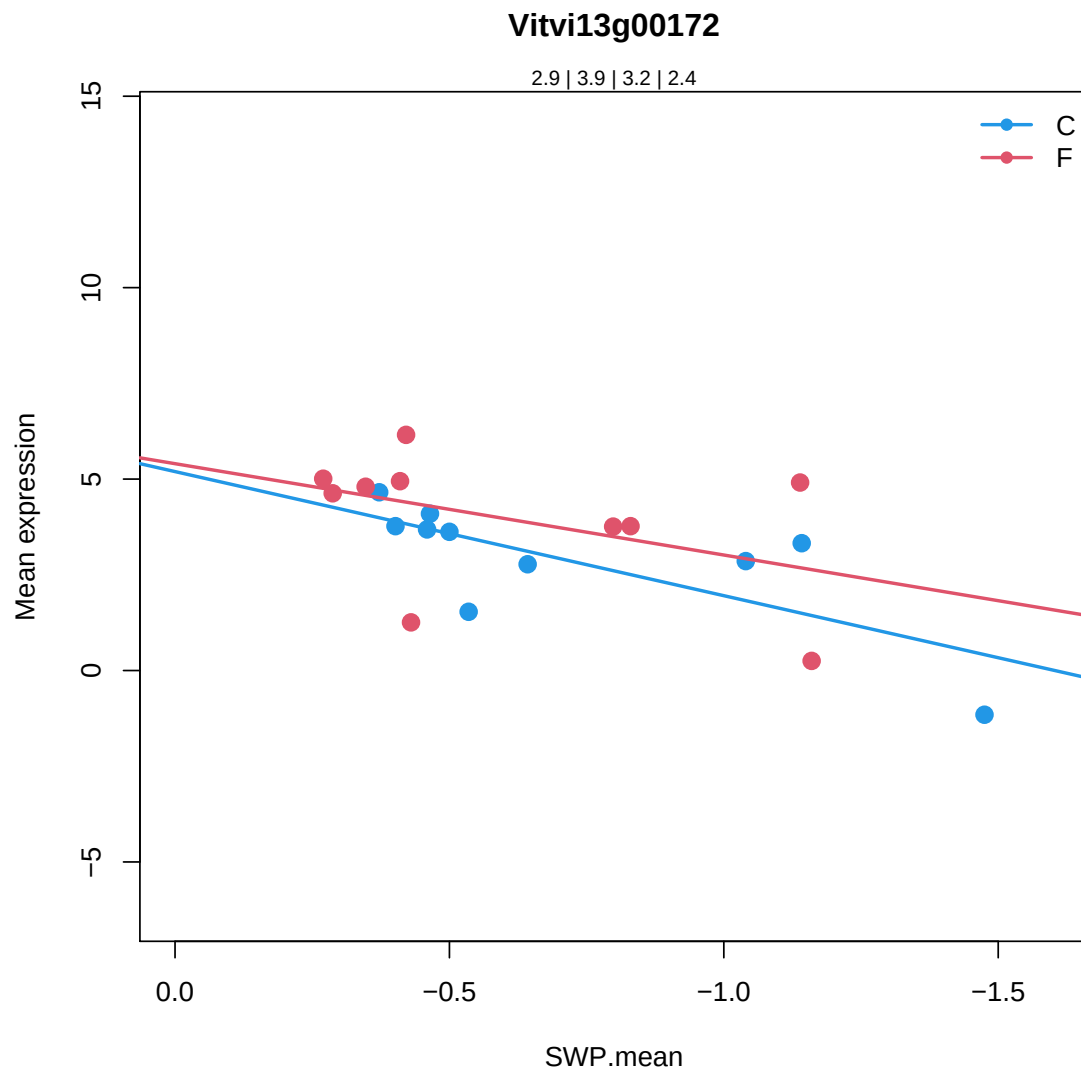
expansin A8 |

Chr2:16949121-16950472 REVERSE LENGTH=253 |

201606

Coefficients for Vitvi13g00172.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.916449	5.190381e-07	***	6.037224e-07	***
SlopeC	3.240978	0.01020129	*	0.3054776	
MeanF-MeanC	1.032131	0.09184968	.	0.3470433	
SlopeF-SlopeC	-0.8556393	0.6224147		0.9999488	



8.1.11 Vitvi08g00219: Type1.0 *

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

Vitvi08g00219

35.2

not assigned.unknown

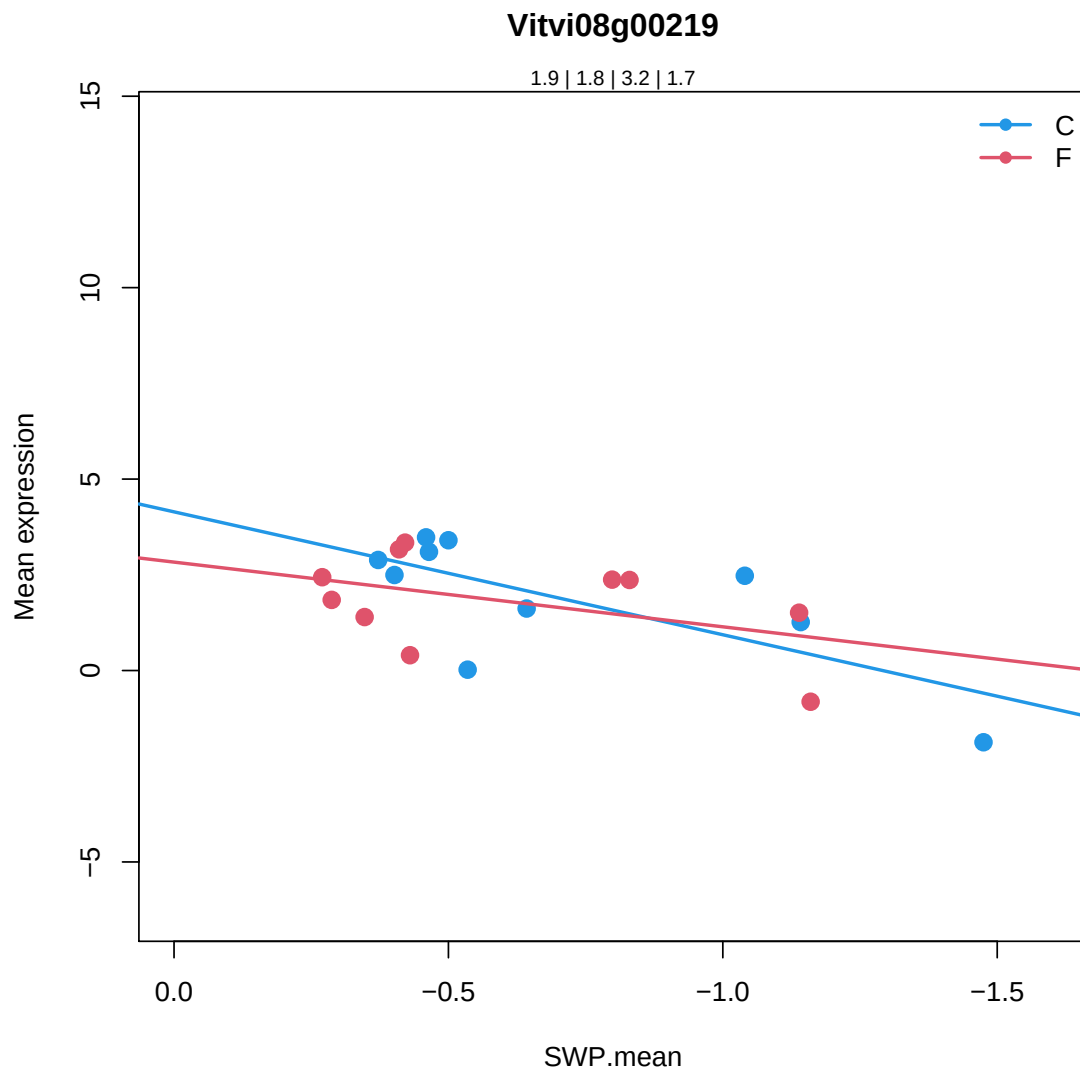
LURP-one-like protein (DUF567) |

Chr2:16157725-16158474 REVERSE LENGTH=196 |

201606

Coefficients for Vitvi08g00219.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.886935	1.799297e-05	***	2.020101e-05	***
SlopeC	3.210113	0.002950206	**	0.2074322	
MeanF-MeanC	-0.08529526	0.8625147		0.9642219	
SlopeF-SlopeC	-1.520202	0.2979077		0.9999488	



8.1.12 Vitvi08g00768: Type1.0 *

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

Vitvi08g00768

35.2

not assigned.unknown

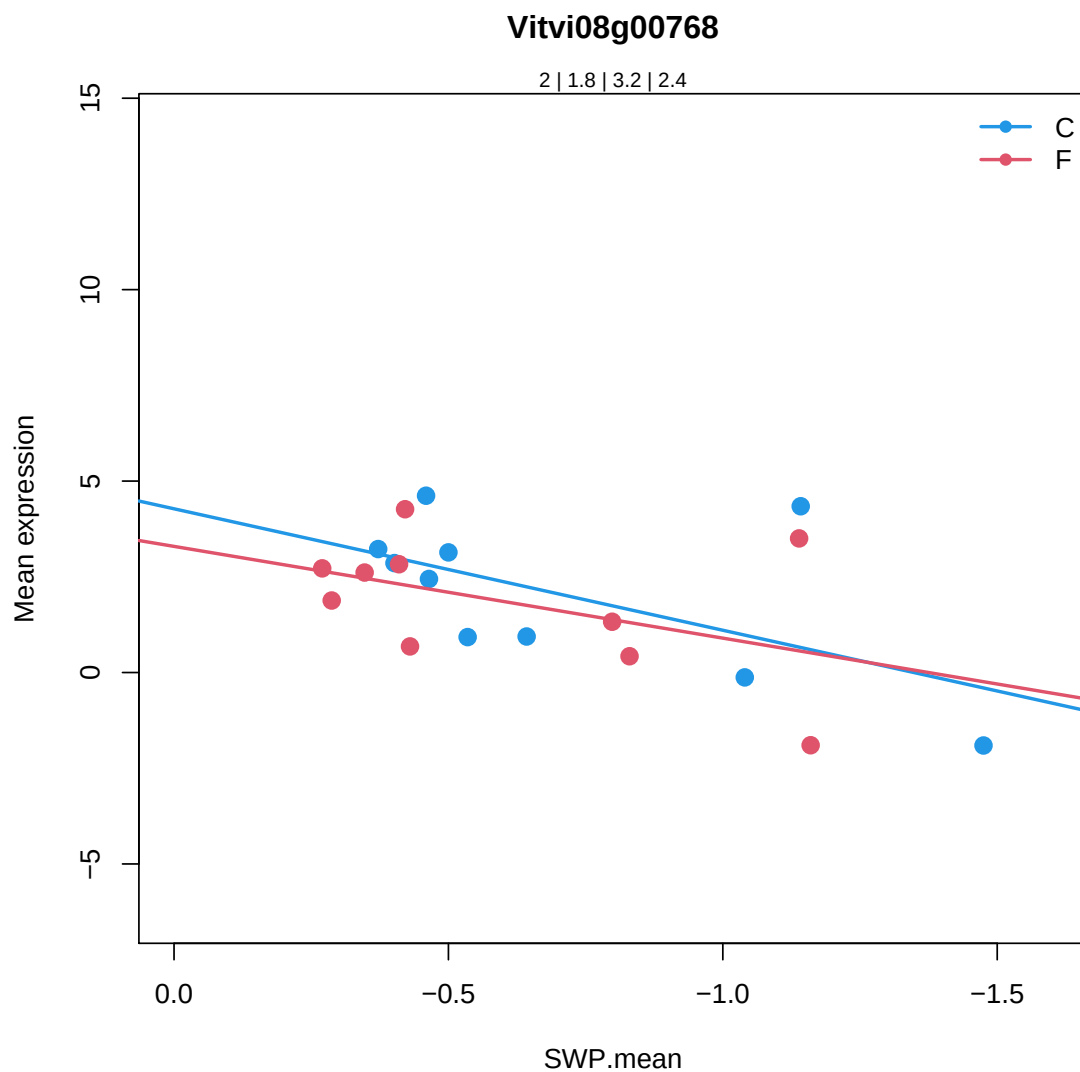
PYR1-like 4 |

Chr2:16050251-16050874 FORWARD LENGTH=207 |

201606

Coefficients for Vitvi08g00768.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.045597	0.0003165141	***	0.0003459029	***
SlopeC	3.172254	0.0262084	*	0.4118231	
MeanF-MeanC	-0.211544	0.7571003		0.9293433	
SlopeF-SlopeC	-0.7760365	0.6985702		0.9999488	



8.1.13 Vitvi10g01616: Type1.0

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

Vitvi10g01616

35.2

not assigned.unknown

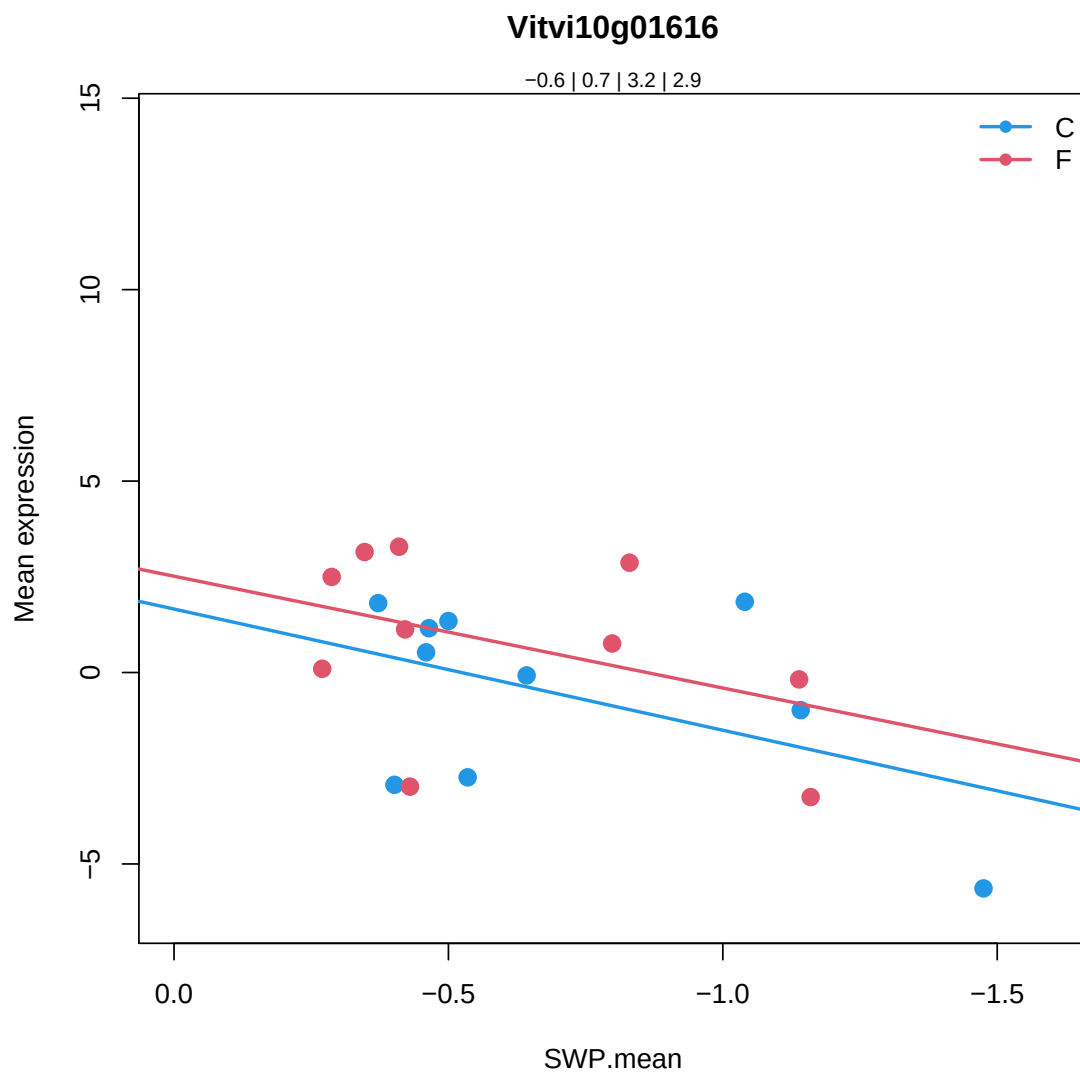
Stigma-specific Stig1 family protein |

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	



8.1.14 Vitvi10g00436: Type1.0 *

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

Vitvi10g00436

3.8.2

minor CHO metabolism.galactose.alpha-galactosidases

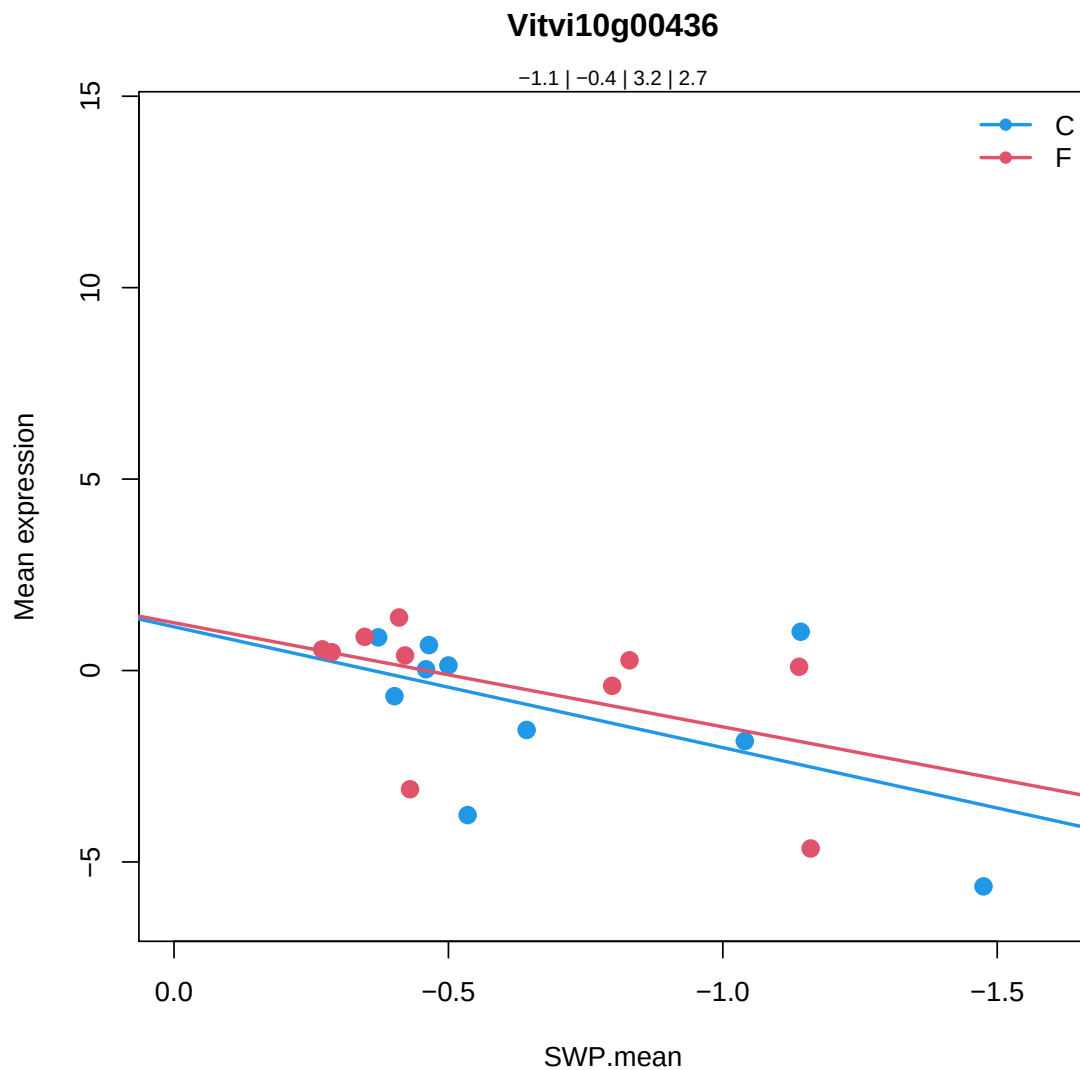
Melibiase family protein |

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	



8.1.15 Vitvi07g00352: Type1.0 *

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

Vitvi07g00352

10.6.1

cell wall.degradation.cellulases and beta-1,4-glucanases

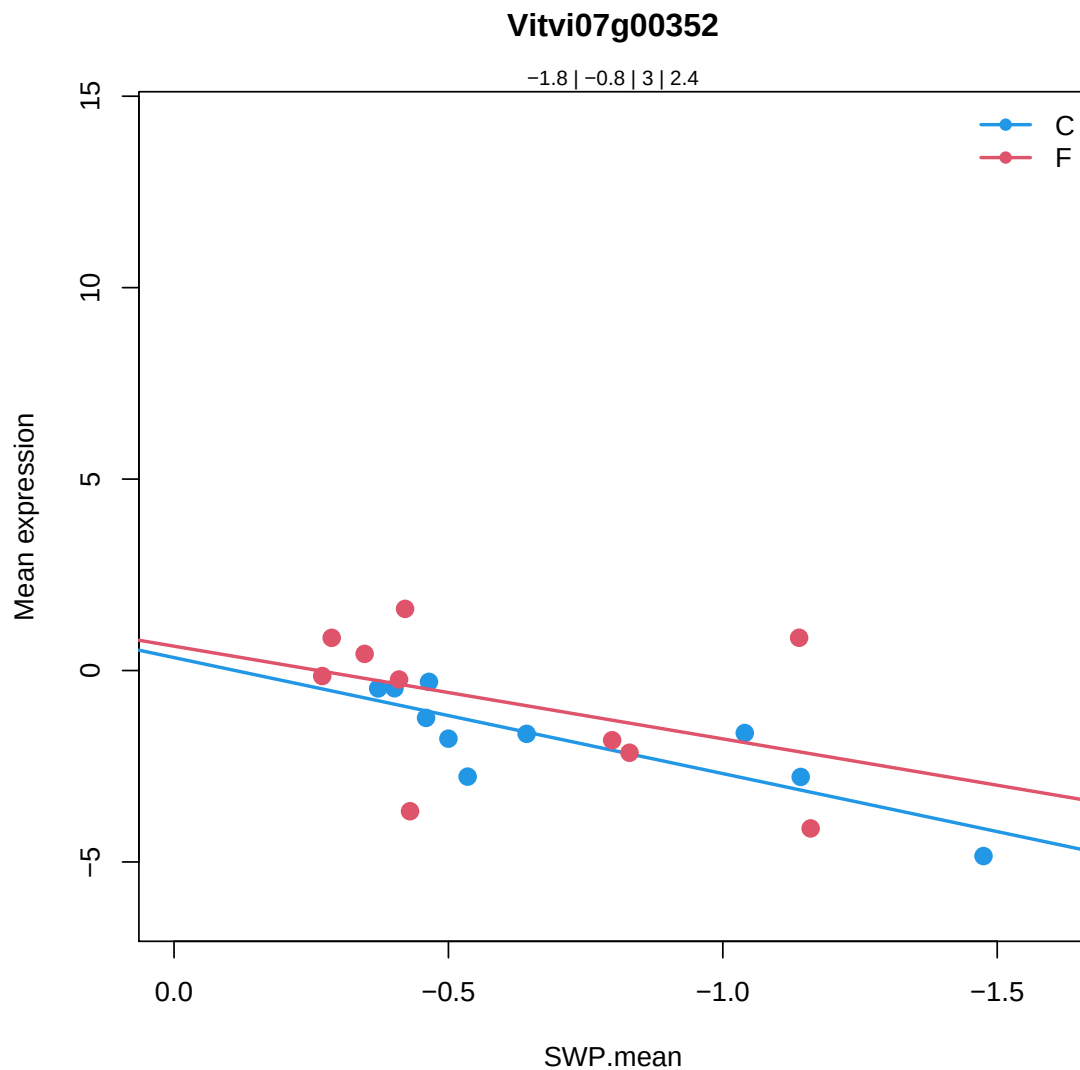
cellulase 3 |

Chr1:26899989-26901749 REVERSE LENGTH=484 |

201606

Coefficients for Vitvi07g00352.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.792996	0.0002651206	***	0.000290362	***
SlopeC	3.029361	0.01494198	*	0.337401	
MeanF-MeanC	0.9535039	0.1158978		0.3986716	
SlopeF-SlopeC	-0.6081053	0.7246576		0.9999488	



8.1.16 Vitvi04g02114: Type1.0

```
> 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
```

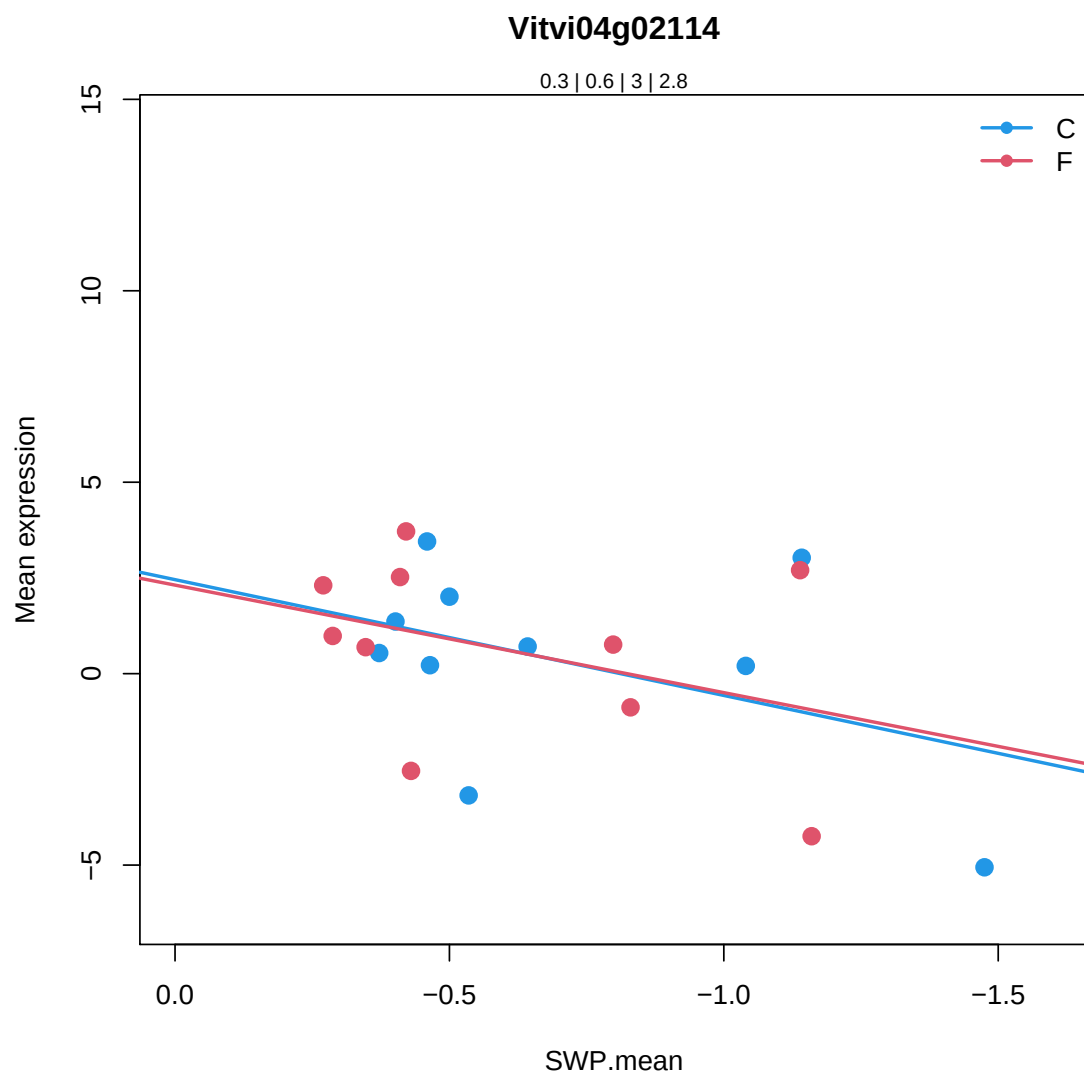
```
S-adenosyl-L-methionine-dependent methyltransferases superfamily prote
```

```
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	

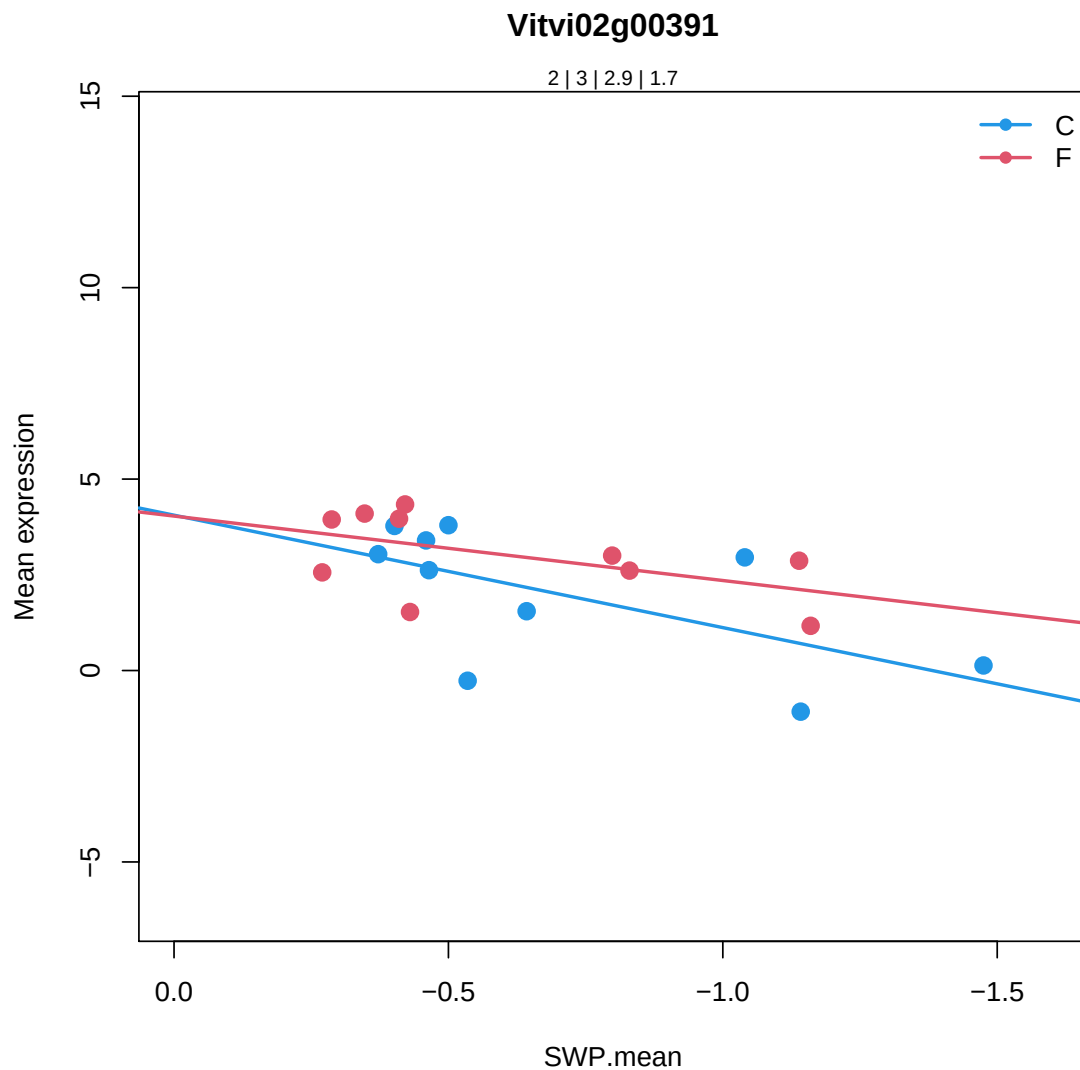


8.1.17 Vitvi02g00391: Type1.0 *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
Vitvi02g00391
20.1.7.5
stress.biotic.PR-proteins.PR5 (thaumatin-like proteins)
osmotin 34 |
Chr4:7025127-7026113 REVERSE LENGTH=244 |
201606
```

Coefficients for Vitvi02g00391.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.992013	1.280131e-05	***	1.441791e-05	***
SlopeC	2.936439	0.00699603	**	0.2775469	
MeanF-MeanC	1.016364	0.05486513	.	0.253872	
SlopeF-SlopeC	-1.253394	0.4018436		0.9999488	



8.1.18 Vitvi05g00544: Type1.0 *

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

Vitvi05g00544

10.5.3

cell wall.cell wall proteins.LRR

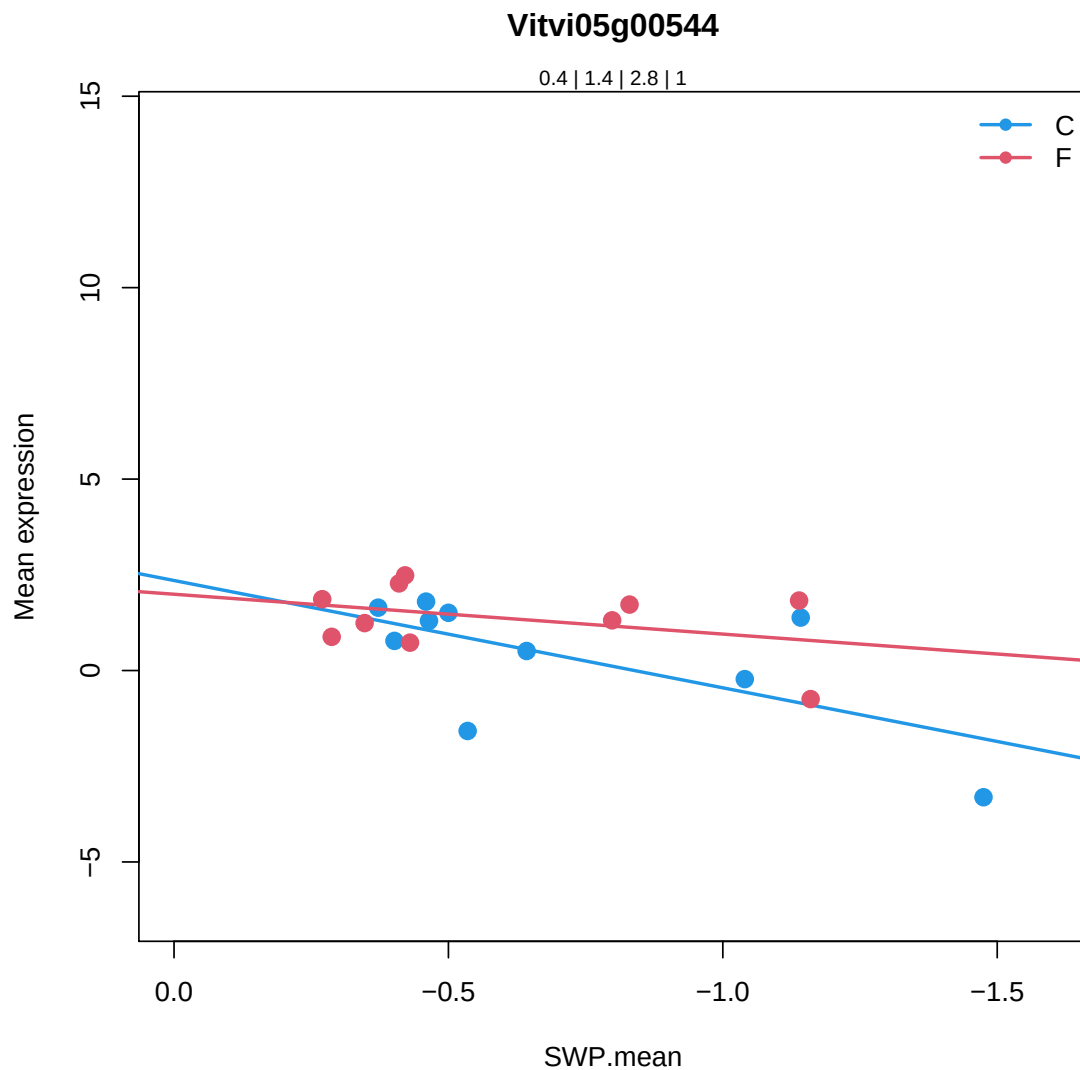
Leucine-rich repeat (LRR) family protein |

Chr3:8063063-8064475 REVERSE LENGTH=470 |

201606

Coefficients for Vitvi05g00544.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3799313	0.2537996		0.2591729	
SlopeC	2.802707	0.005218877	**	0.2566004	
MeanF-MeanC	0.9784327	0.04441472	*	0.2215213	
SlopeF-SlopeC	-1.761653	0.2030328		0.9999488	



8.1.19 Vitvi00g01146: Type1.0 *

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

```
Vitvi00g01146
```

```
35.2
```

```
not assigned.unknown
```

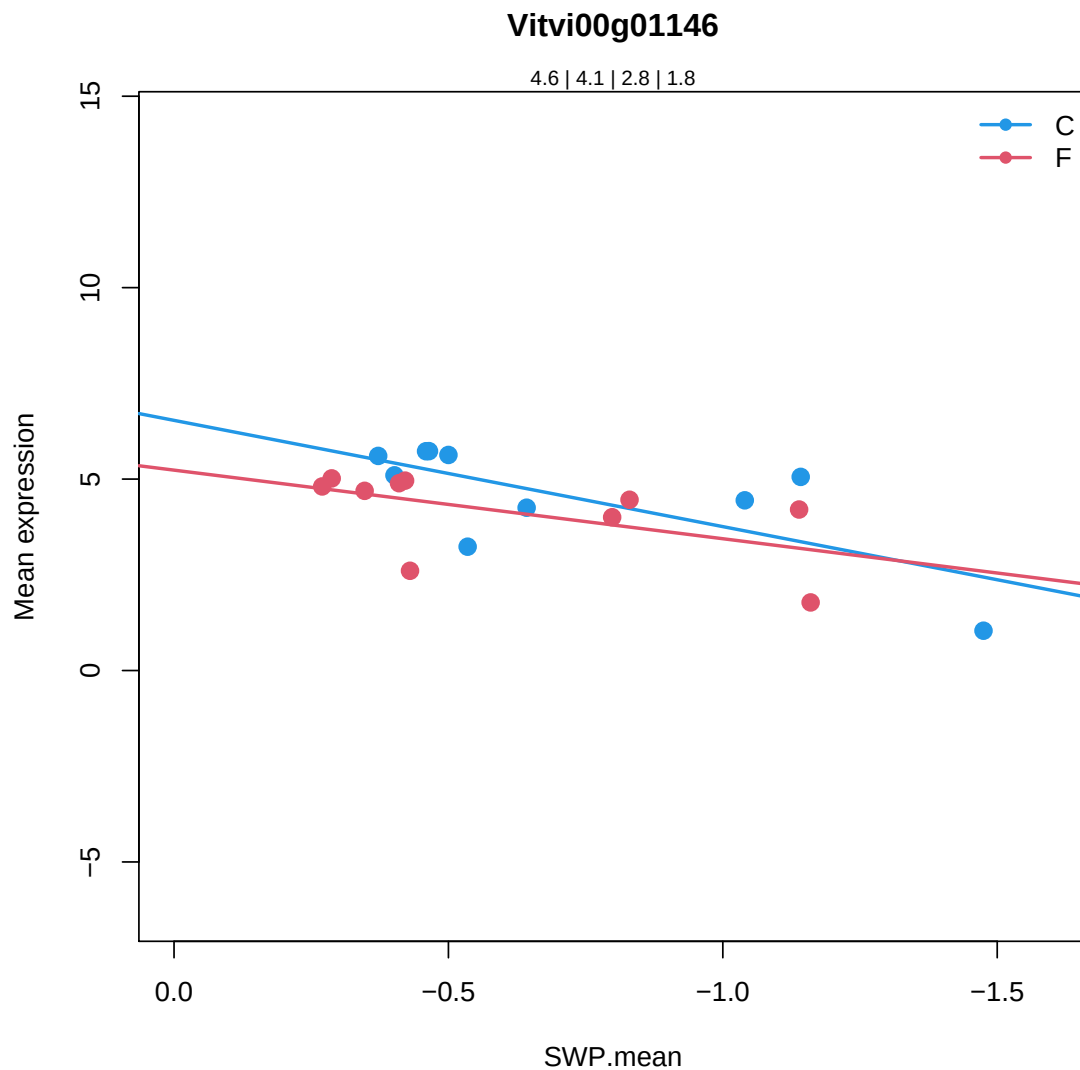
```
Subtilisin-like serine endopeptidase family protein |
```

```
Chr2:1401450-1407694 REVERSE LENGTH=772 |
```

```
201606
```

Coefficients for Vitvi00g01146.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.581812	3.55502e-13	***	5.253598e-13	***
SlopeC	2.775057	0.00268109	**	0.1974163	
MeanF-MeanC	-0.4396028	0.3020336		0.6671976	
SlopeF-SlopeC	-0.983617	0.4278834		0.9999488	



8.1.20 Vitvi09g01928: Type1.0 *

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

```
Vitvi09g01928
```

```
35.2
```

```
not assigned.unknown
```

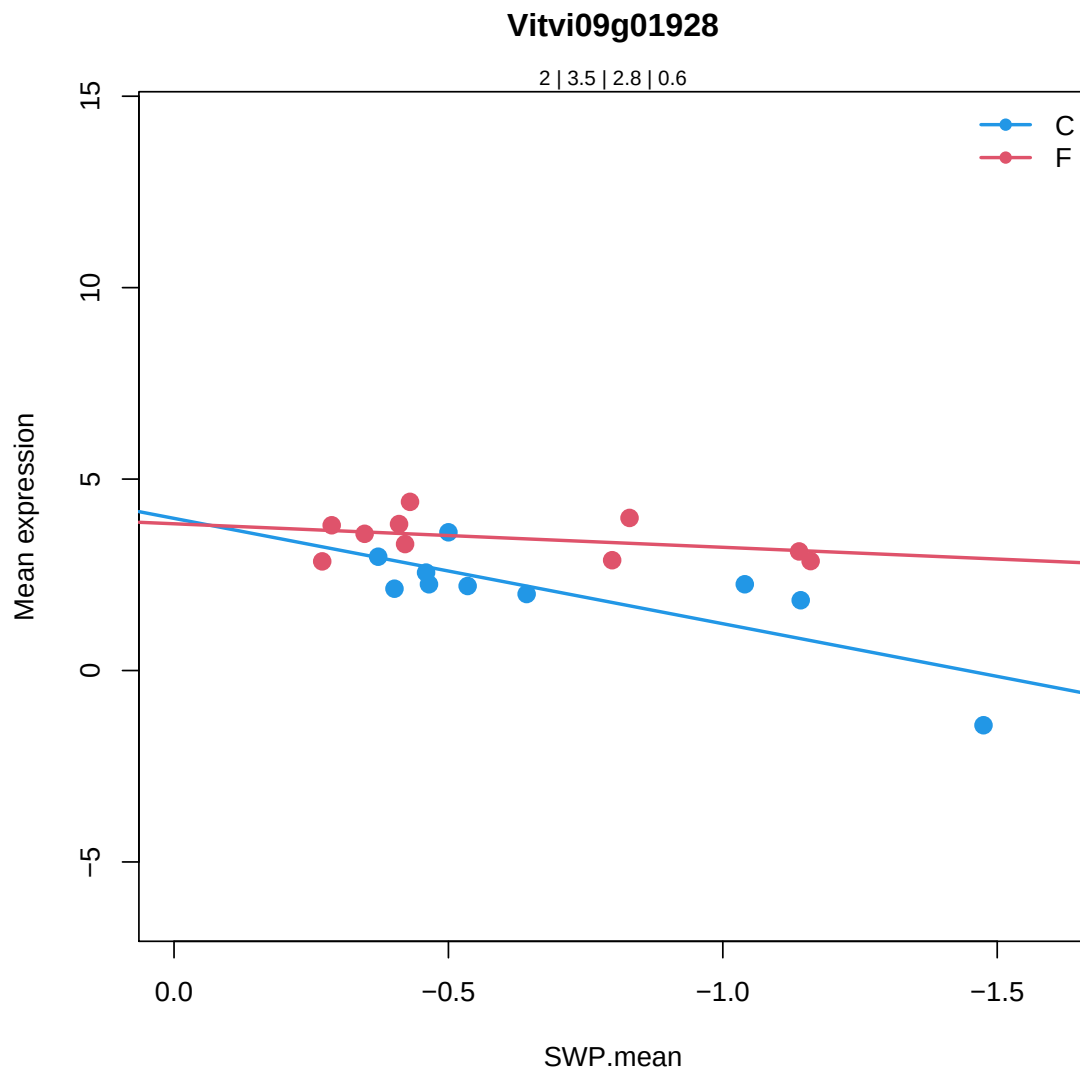
```
disease resistance family protein / LRR family protein |
```

```
Chr2:14737169-14739886 REVERSE LENGTH=905 |
```

```
201606
```

Coefficients for Vitvi09g01928.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.039141	2.944912e-09	***	3.657623e-09	***
SlopeC	2.751808	0.0001215222	***	0.07644173	.
MeanF-MeanC	1.418945	0.0001033386	***	0.001853043	**
SlopeF-SlopeC	-2.137842	0.02327414	*	0.9999488	

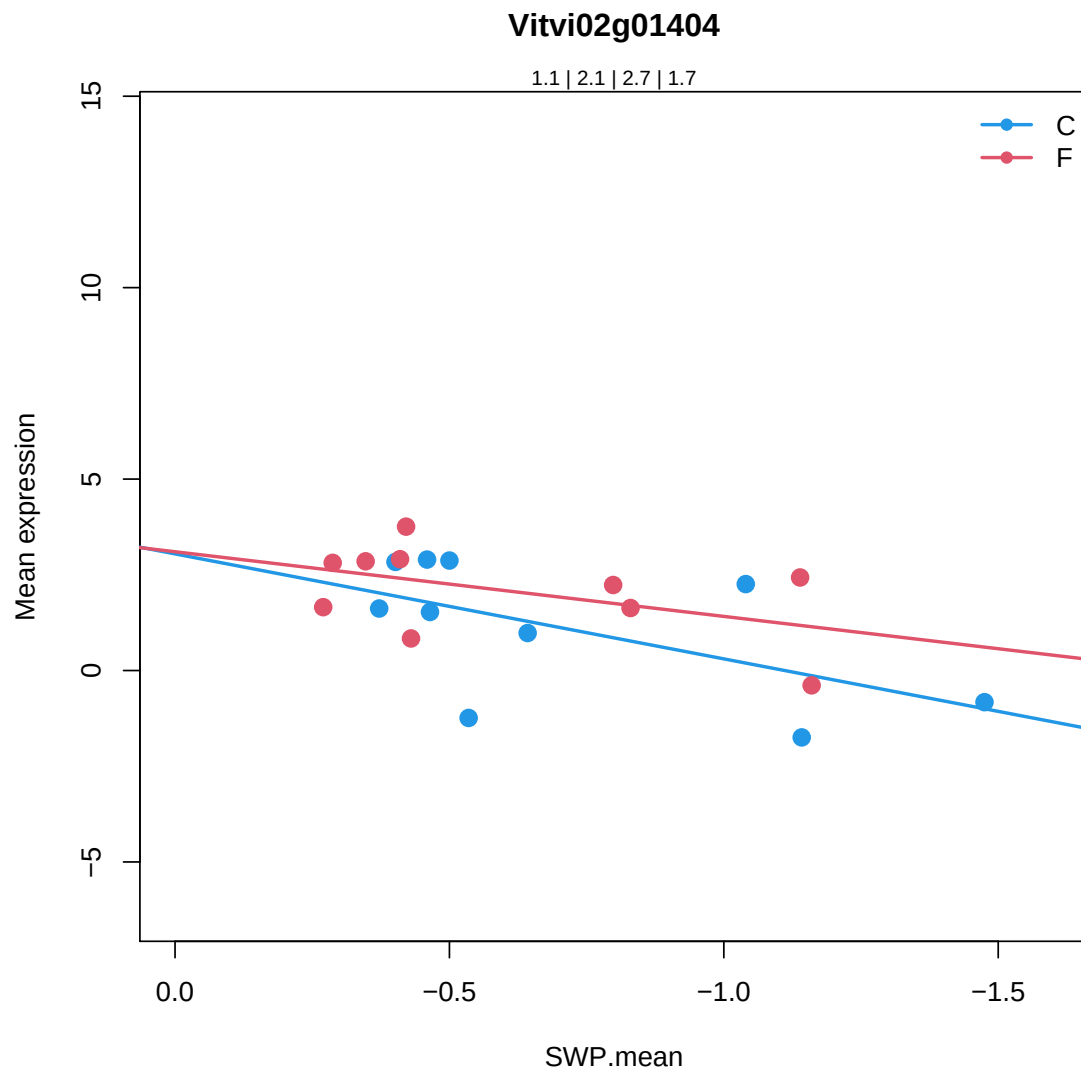


8.1.21 Vitvi02g01404: Type1.0 *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
Vitvi02g01404
20.1.7.5
stress.biotic.PR-proteins.PR5 (thaumatin-like proteins)
osmotin 34 |
Chr4:7025127-7026113 REVERSE LENGTH=244 |
201606
```

Coefficients for Vitvi02g01404.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.117841	0.006769827	**	0.007198166	**
SlopeC	2.741969	0.01508005	*	0.3381314	
MeanF-MeanC	0.9551072	0.08425637	.	0.3288695	
SlopeF-SlopeC	-1.05361	0.5024767		0.9999488	



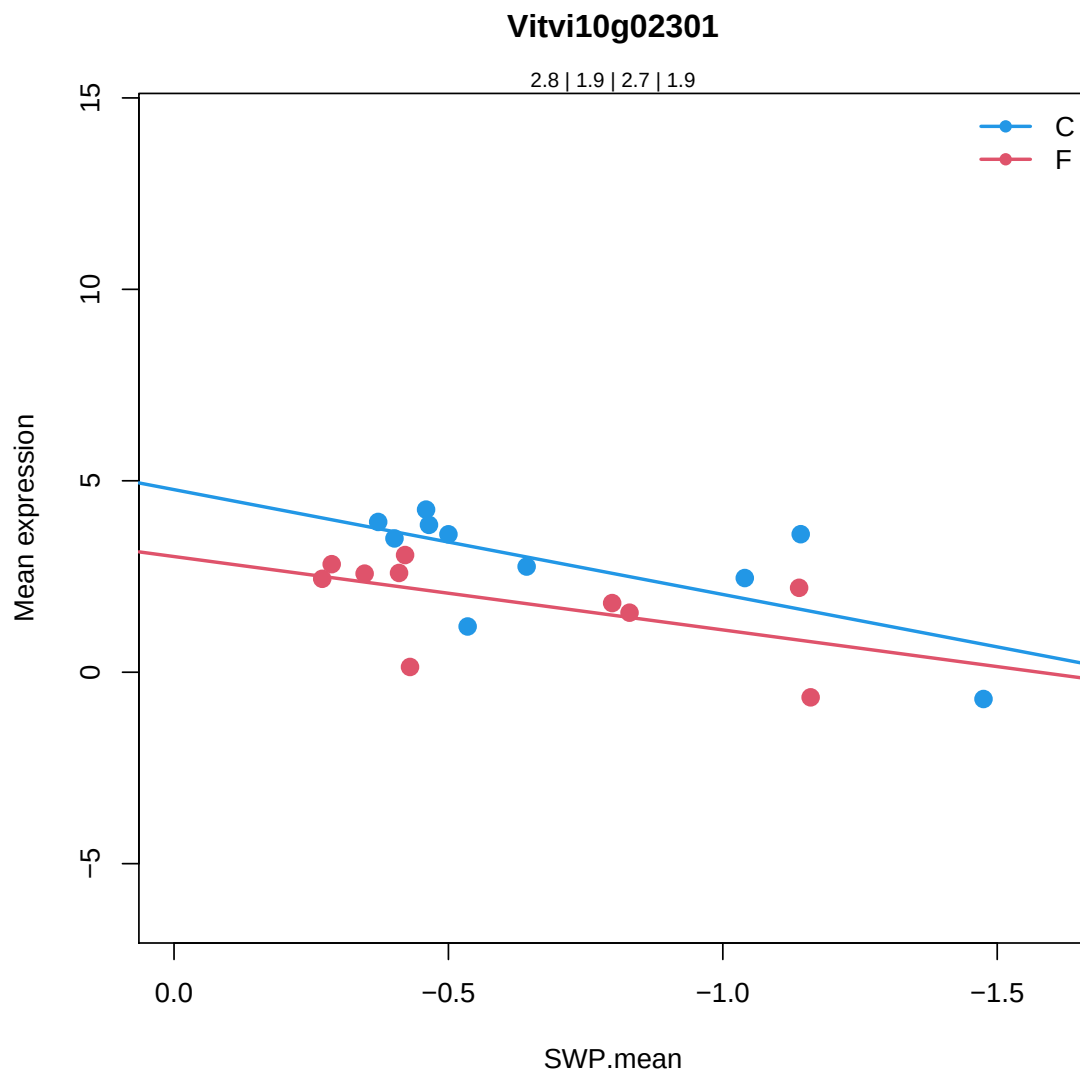
8.1.22 Vitvi10g02301: Type1.0 *

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

```
Vitvi10g02301
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi10g02301.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.843656	1.317328e-08	***	1.60194e-08	***
SlopeC	2.738514	0.005801276	**	0.2626746	
MeanF-MeanC	-0.9901192	0.04061255	*	0.2085588	
SlopeF-SlopeC	-0.8220594	0.5431535		0.9999488	



8.1.23 Vitvi12g02414: Type1.0 *

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

Vitvi12g02414

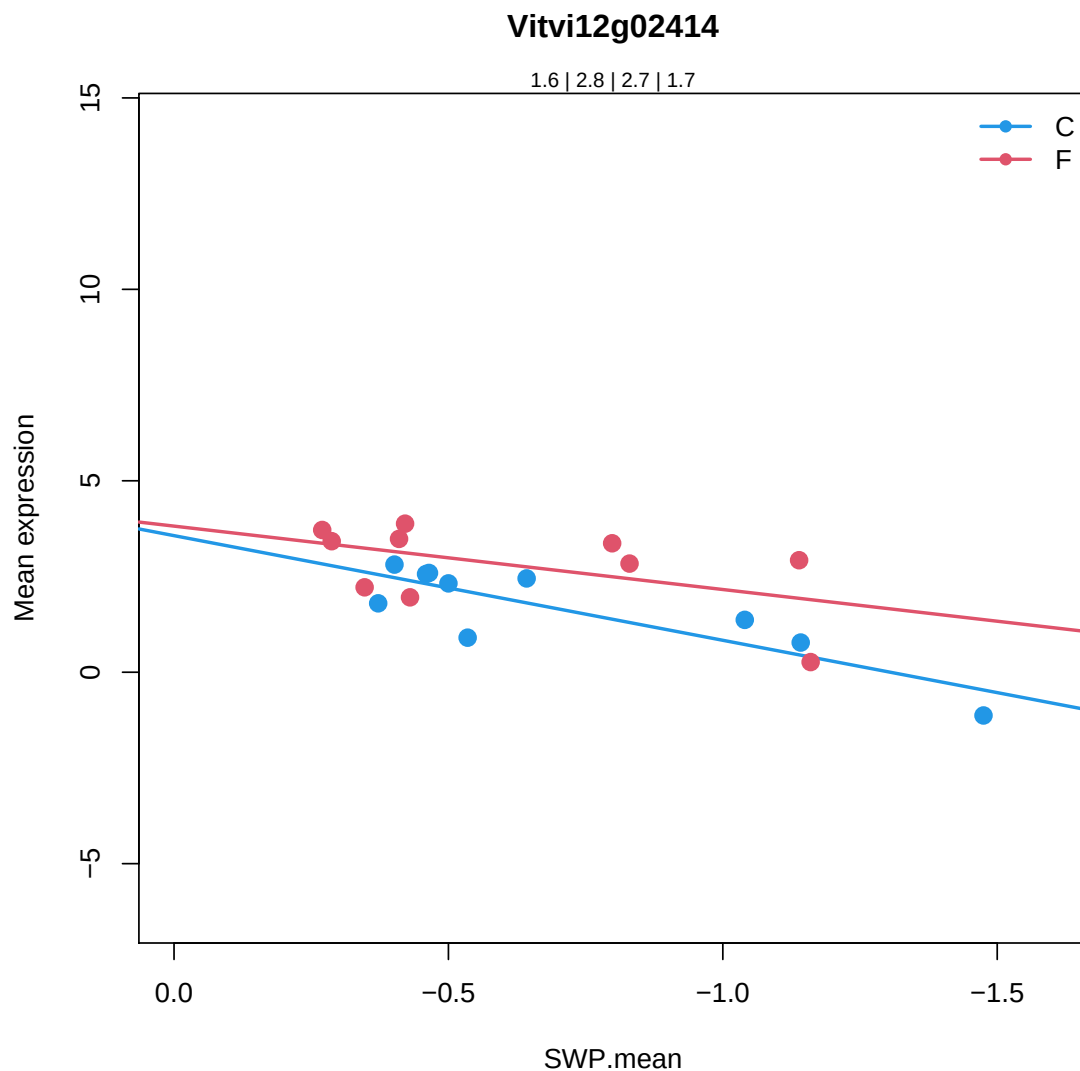
35.2

not assigned.unknown

Genomic DNA chromosome 3 P1 clone MSD21

Coefficients for Vitvi12g02414.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.645198	1.000115e-06	***	1.155267e-06	***
SlopeC	2.733097	0.0005824794	***	0.1005065	
MeanF-MeanC	1.161642	0.002828531	**	0.02929549	*
SlopeF-SlopeC	-1.077144	0.2976229		0.9999488	



8.1.24 Vitvi10g02298: Type1.0 *

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

Vitvi10g02298

29.5.1

protein.degradation.subtilases

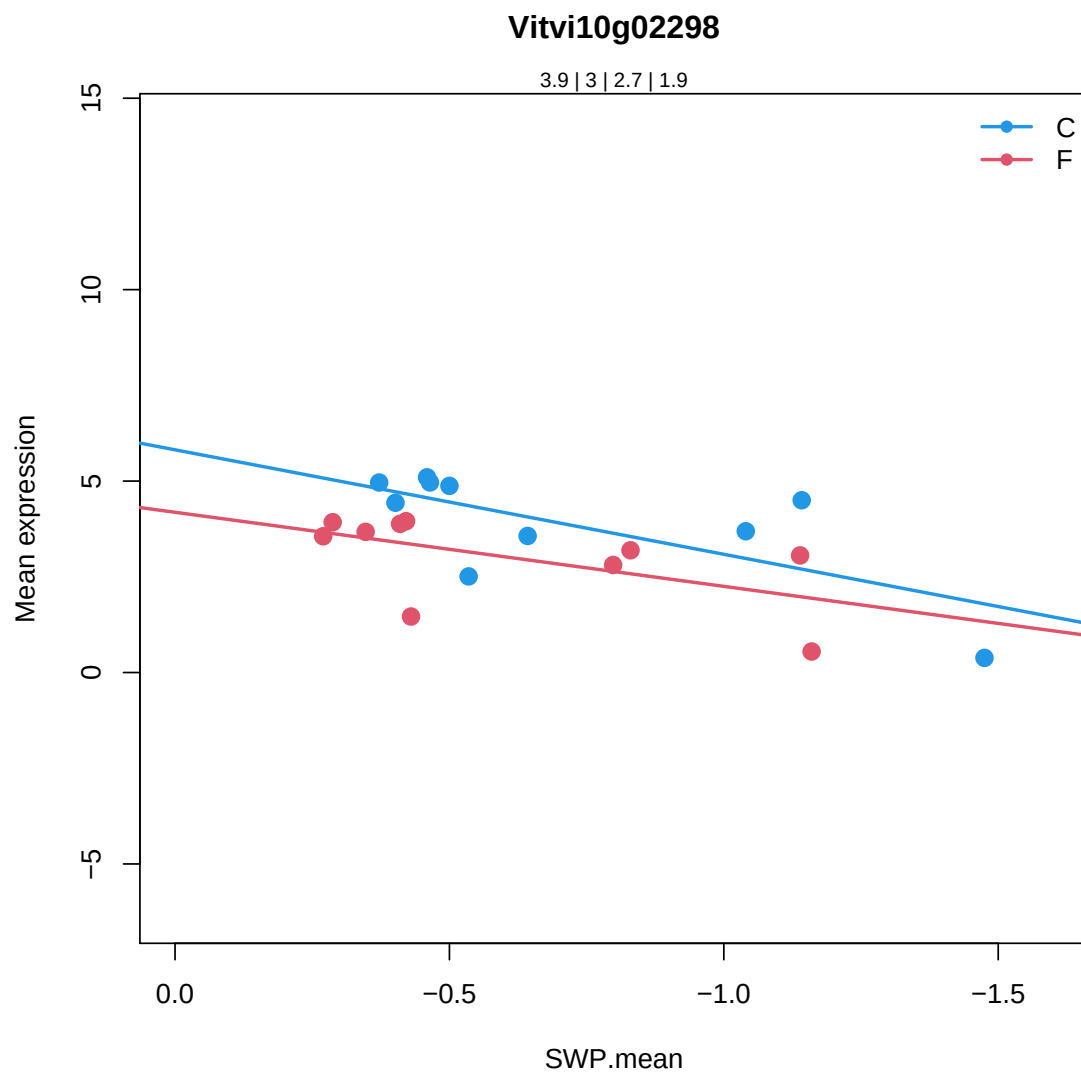
Subtilase family protein |

Chr5:24096895-24100387 REVERSE LENGTH=778 |

201606

Coefficients for Vitvi10g02298.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.898138	1.183268e-11	***	1.609725e-11	***
SlopeC	2.728815	0.003535614	**	0.2245324	
MeanF-MeanC	-0.8918327	0.04712082	*	0.2302711	
SlopeF-SlopeC	-0.793757	0.5287874		0.9999488	



8.1.25 Vitvi03g00144: Type1.0 *

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

Vitvi03g00144

29.4.1.56

protein.postranslational modification.kinase.receptor like cytoplasmat

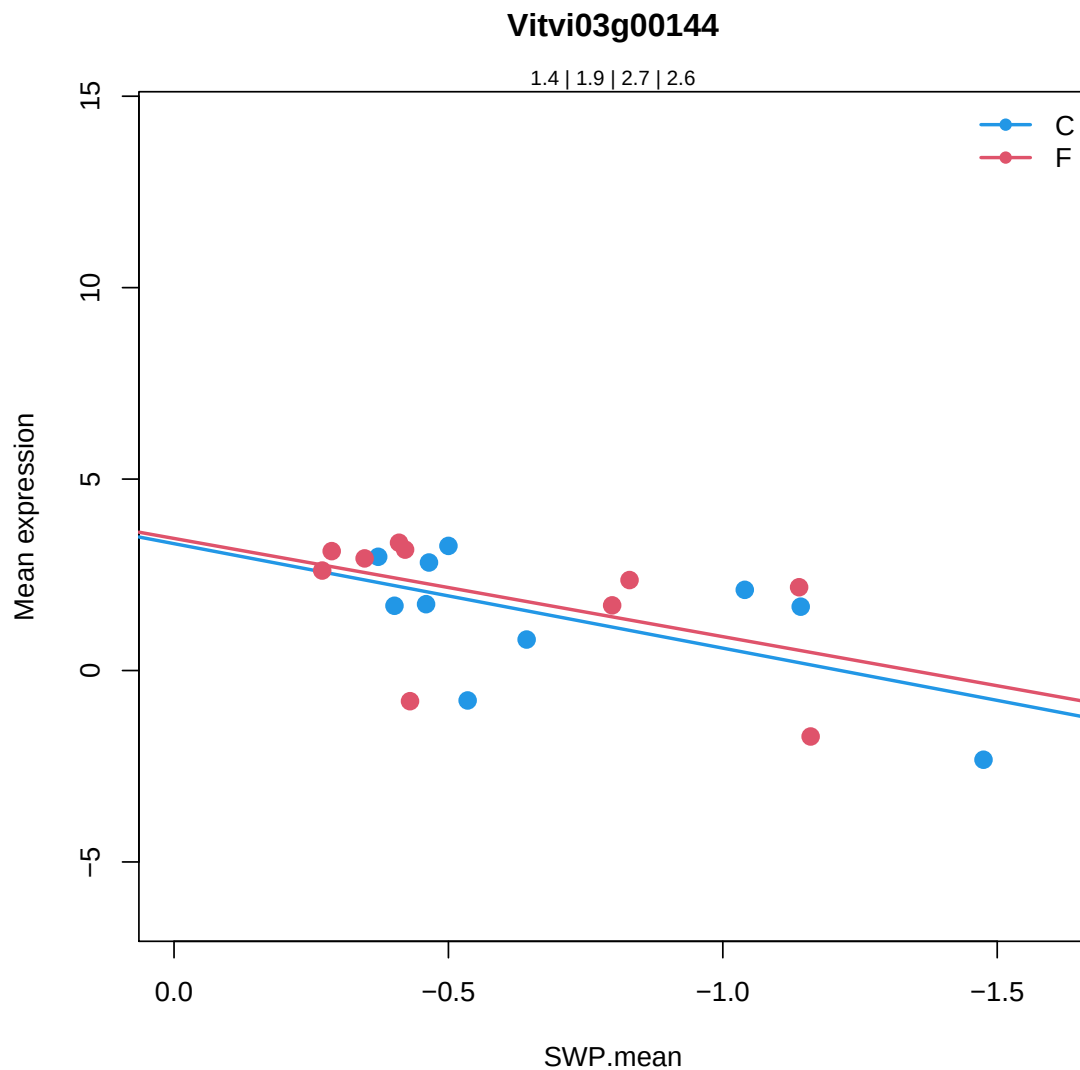
Protein kinase superfamily protein |

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	



8.1.26 Vitvi09g01581: Type1.0 *

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

```
Vitvi09g01581
```

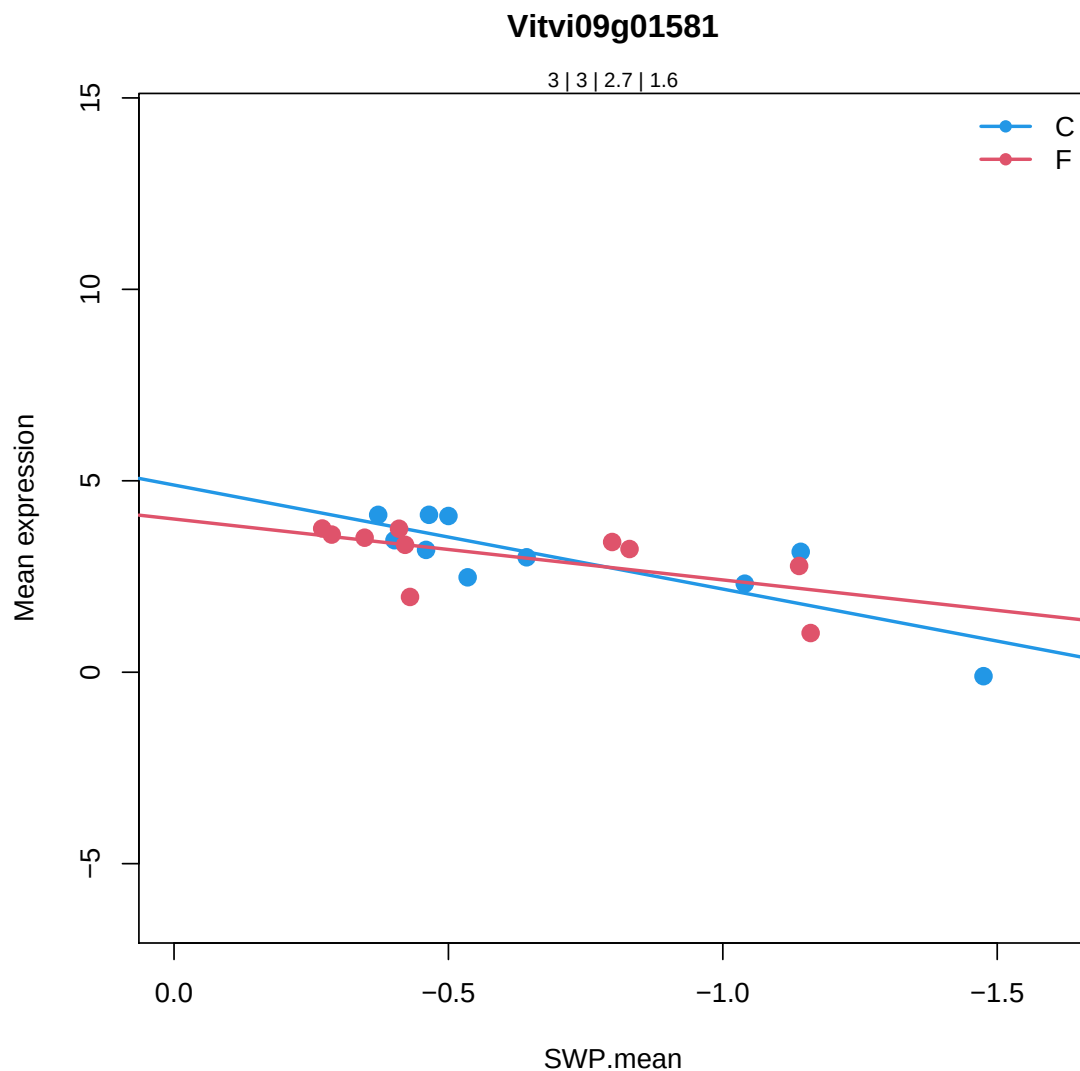
```
35.1
```

```
not assigned.no ontology
```

```
NA
```

Coefficients for Vitvi09g01581.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.977797	5.836364e-12	***	8.046844e-12	***
SlopeC	2.717208	0.0002223154	***	0.08109226	.
MeanF-MeanC	0.05414971	0.8637371		0.964386	
SlopeF-SlopeC	-1.126599	0.2304934		0.9999488	



8.1.27 Vitvi01g00682: Type1.0 *

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

Vitvi01g00682

34.4

transport.nitrate

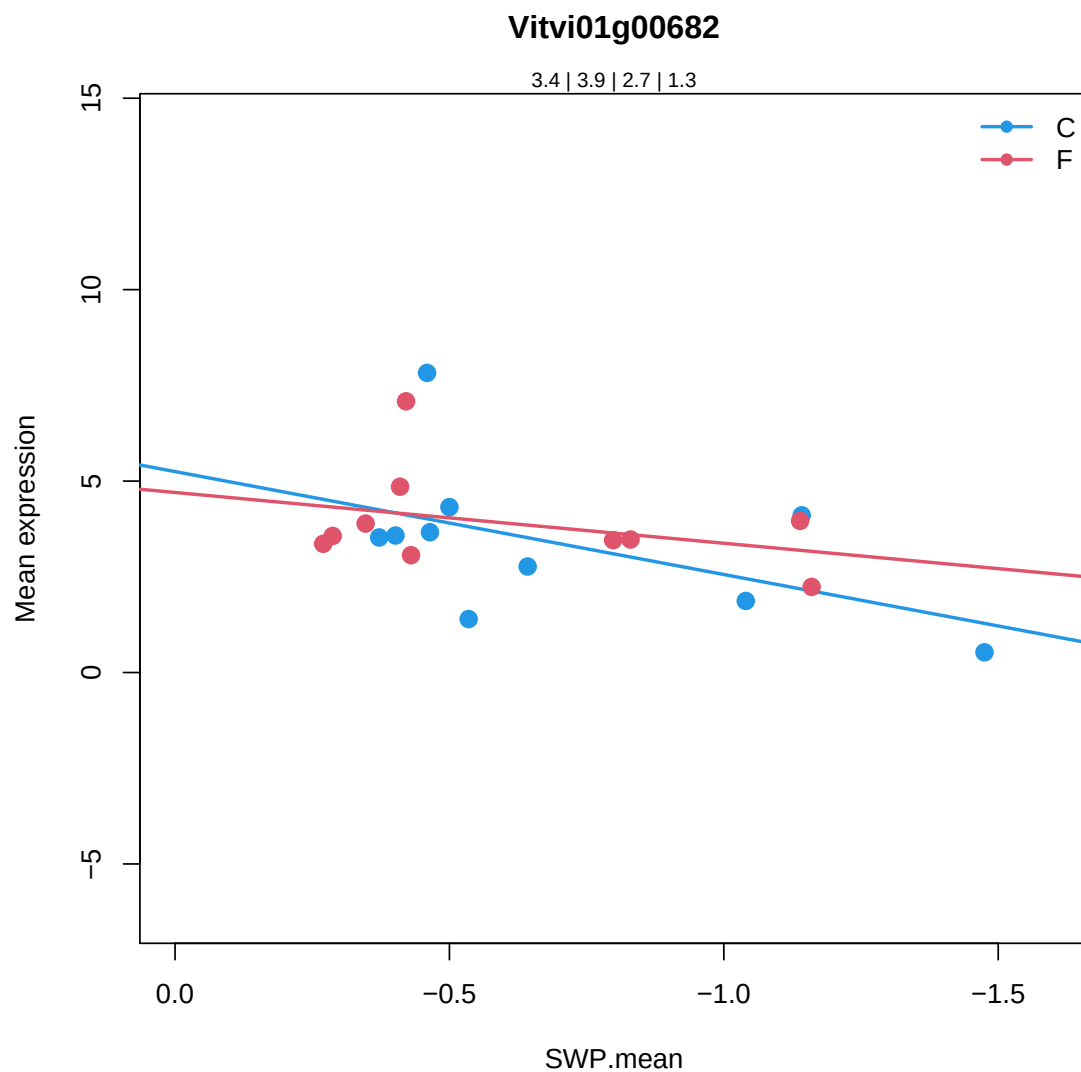
nitrate transporter2.5 |

Chr1:4416405-4418337 FORWARD LENGTH=502 |

201606

Coefficients for Vitvi01g00682.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.358203	1.486375e-07	***	1.755274e-07	***
SlopeC	2.688368	0.03900773	*	0.4699262	
MeanF-MeanC	0.5361088	0.3979344		0.7436631	
SlopeF-SlopeC	-1.362444	0.4622103		0.9999488	



8.1.28 Vitvi10g02300: Type1.0 *

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

Vitvi10g02300

35.2

not assigned.unknown

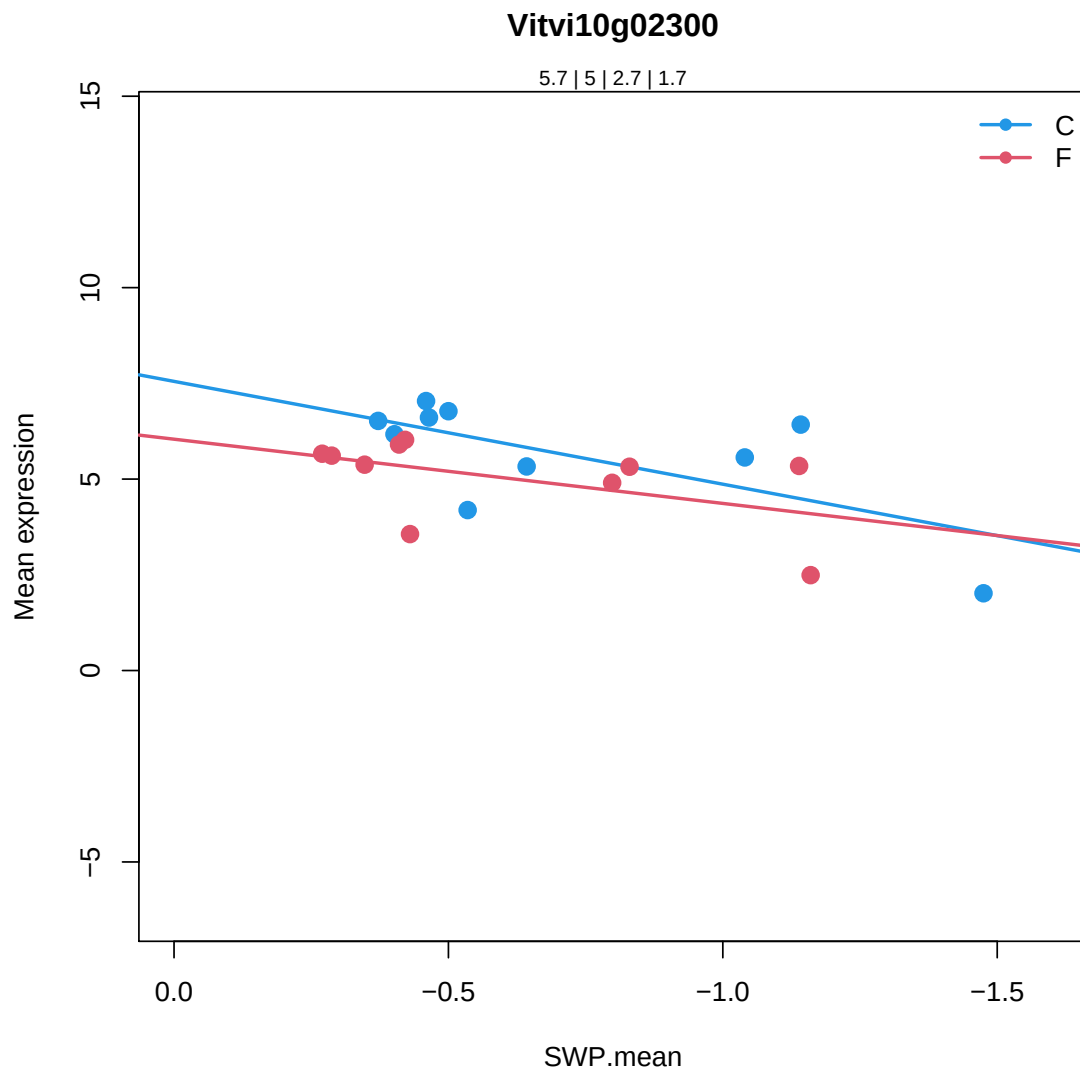
Subtilase family protein |

Chr5:24096895-24100387 REVERSE LENGTH=778 |

201606

Coefficients for Vitvi10g02300.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.663357	2.361803e-14	***	3.819886e-14	***
SlopeC	2.685016	0.006089369	**	0.2647742	
MeanF-MeanC	-0.6434342	0.1658799		0.4945328	
SlopeF-SlopeC	-1.00753	0.4513861		0.9999488	



8.1.29 Vitvi16g01470: Type1.0 *

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

Vitvi16g01470

35.2

not assigned.unknown

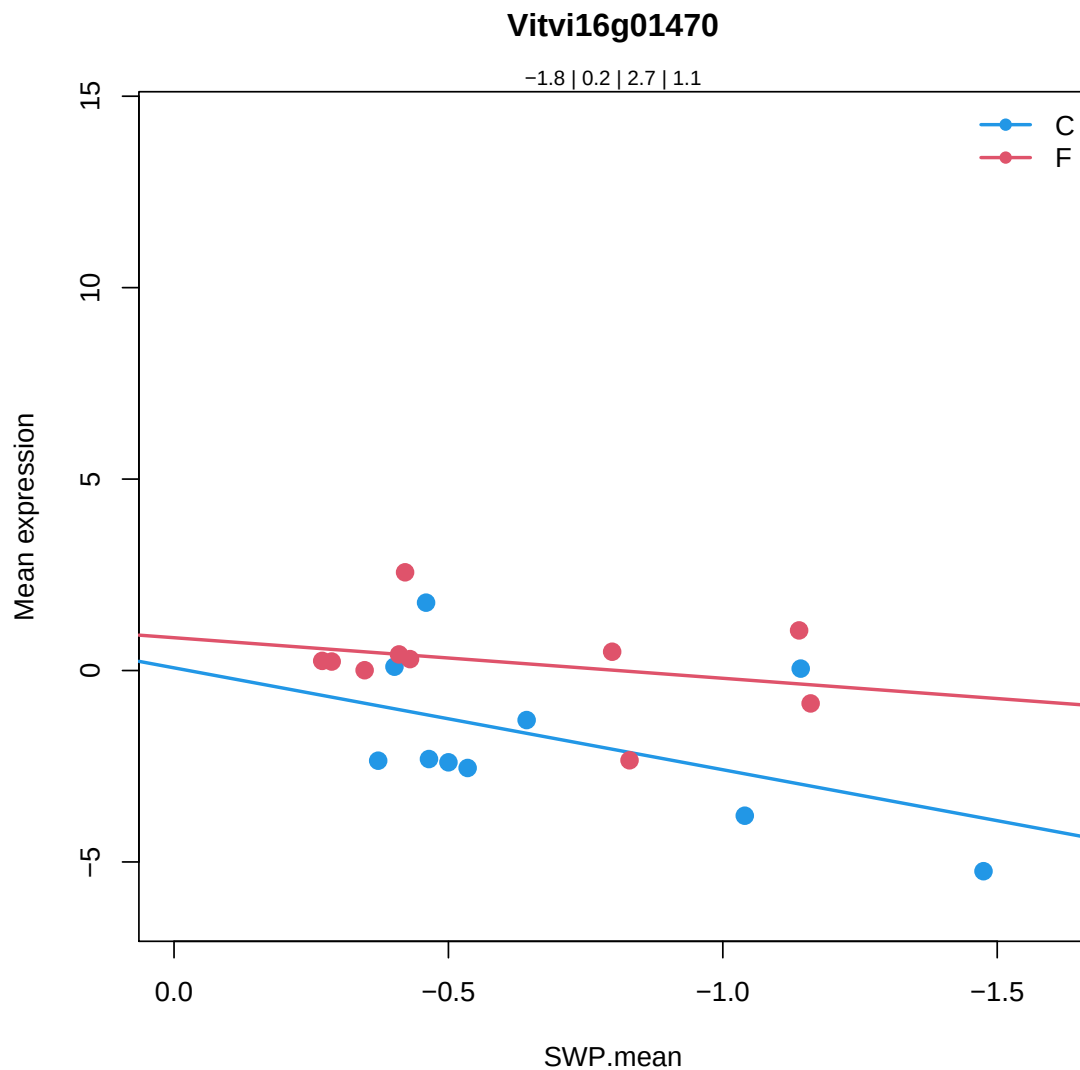
Chalcone and stilbene synthase family protein |

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	



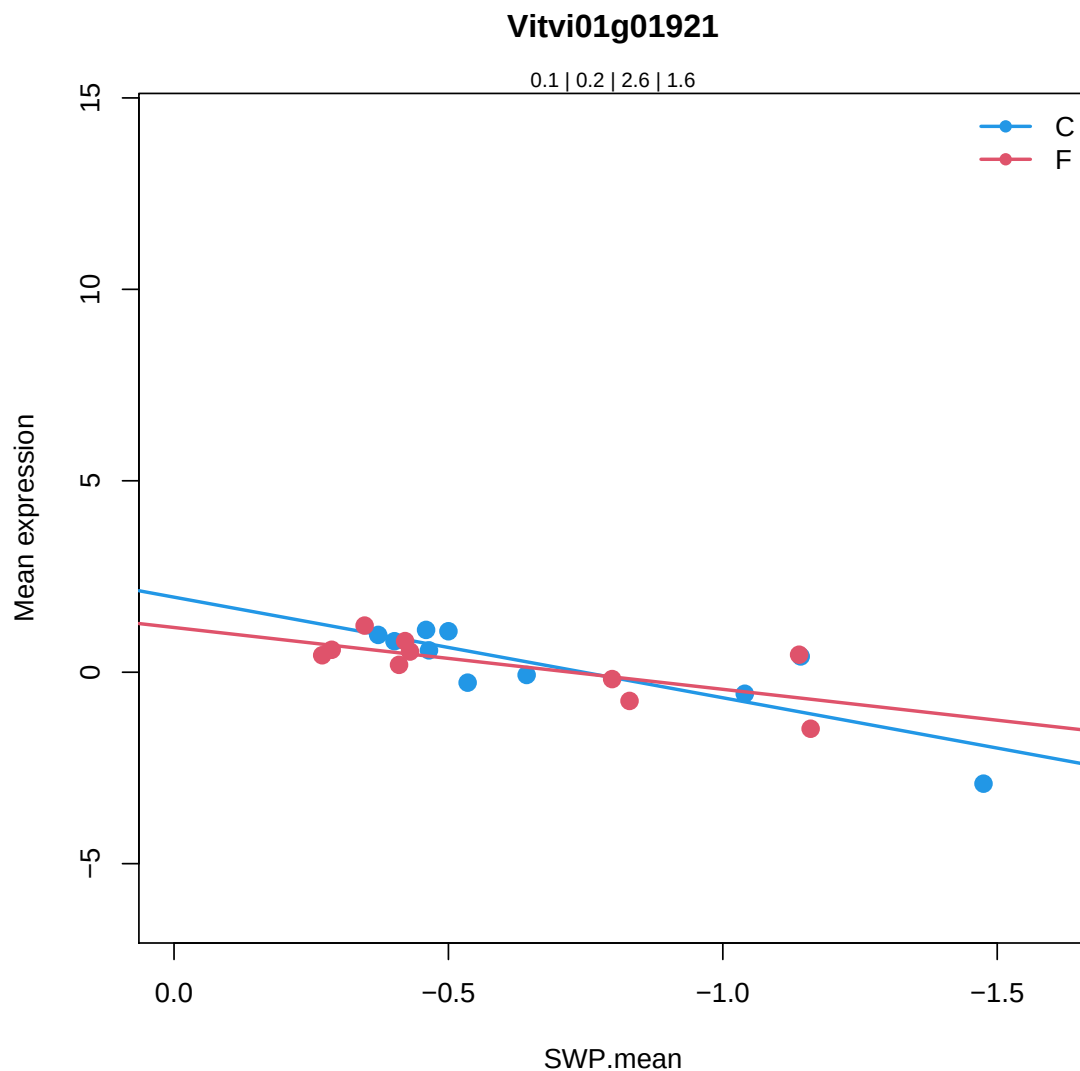
8.1.30 Vitvi01g01921: Type1.0 *

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

```
Vitvi01g01921
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi01g01921.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1124485	0.5776061		0.5830765	
SlopeC	2.627557	0.0001030679	***	0.07644173	.
MeanF-MeanC	0.07201238	0.800333		0.9440396	
SlopeF-SlopeC	-1.013117	0.2318755		0.9999488	



8.1.31 Vitvi07g01697: Type1.0 *

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

Vitvi07g01697

30.2.3

signalling.receptor kinases.leucine rich repeat III

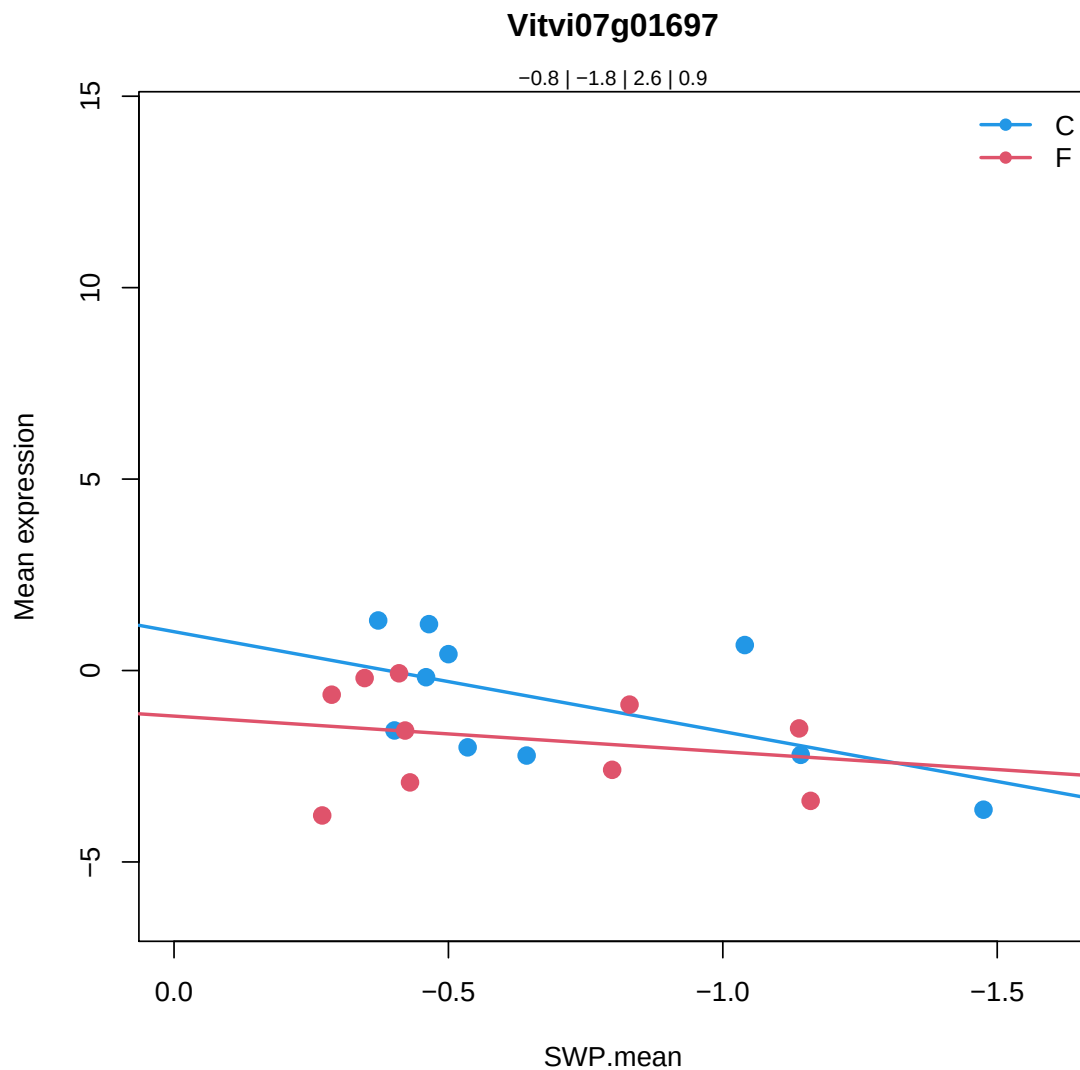
IRREGULAR XYLEM protein (DUF579) |

Chr5:26819019-26819972 FORWARD LENGTH=317 |

201606

Coefficients for Vitvi07g01697.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.8195669	0.05338584	.	0.05555452	.
SlopeC	2.608045	0.02912017	*	0.4288878	
MeanF-MeanC	-0.9381943	0.1125195		0.3917364	
SlopeF-SlopeC	-1.677237	0.3235785		0.9999488	



8.1.32 Vitvi08g02336: Type1.0 *

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

Vitvi08g02336

26.4.1

misc.beta 1,3 glucan hydrolases.glucan endo-1,3-beta-glucosidase

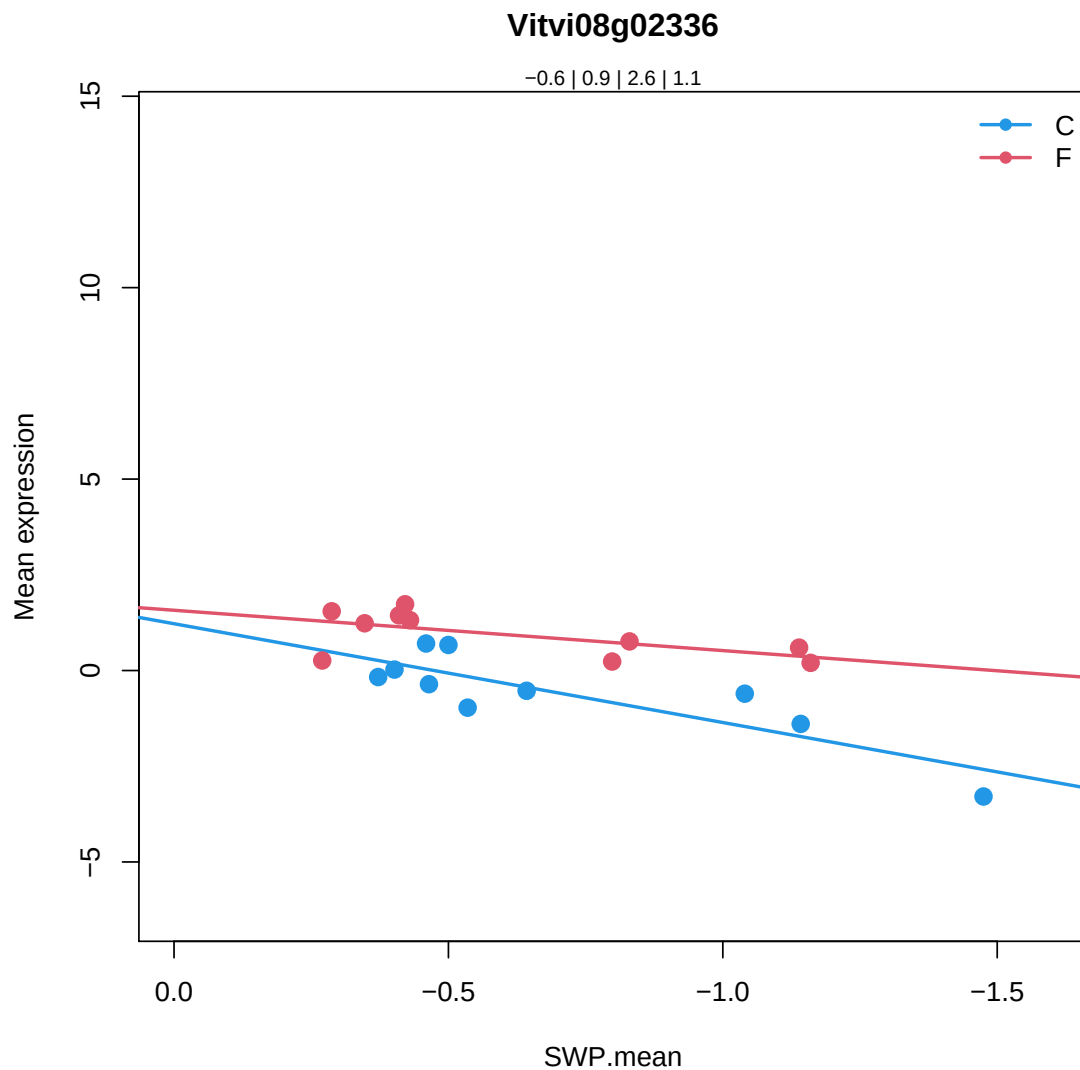
beta-1%2C3-glucanase 1 |

Chr3:21191336-21193118 REVERSE LENGTH=340 |

201606

Coefficients for Vitvi08g02336.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.5921284	0.002810534	**	0.003012529	**
SlopeC	2.580033	2.882805e-05	***	0.05492465	.
MeanF-MeanC	1.524056	3.937337e-06	***	0.0001085224	***
SlopeF-SlopeC	-1.526918	0.04764719	*	0.9999488	



8.1.33 Vitvi11g00099: Type1.0

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

Vitvi11g00099

27.3.25

RNA.regulation of transcription.MYB domain transcription factor family

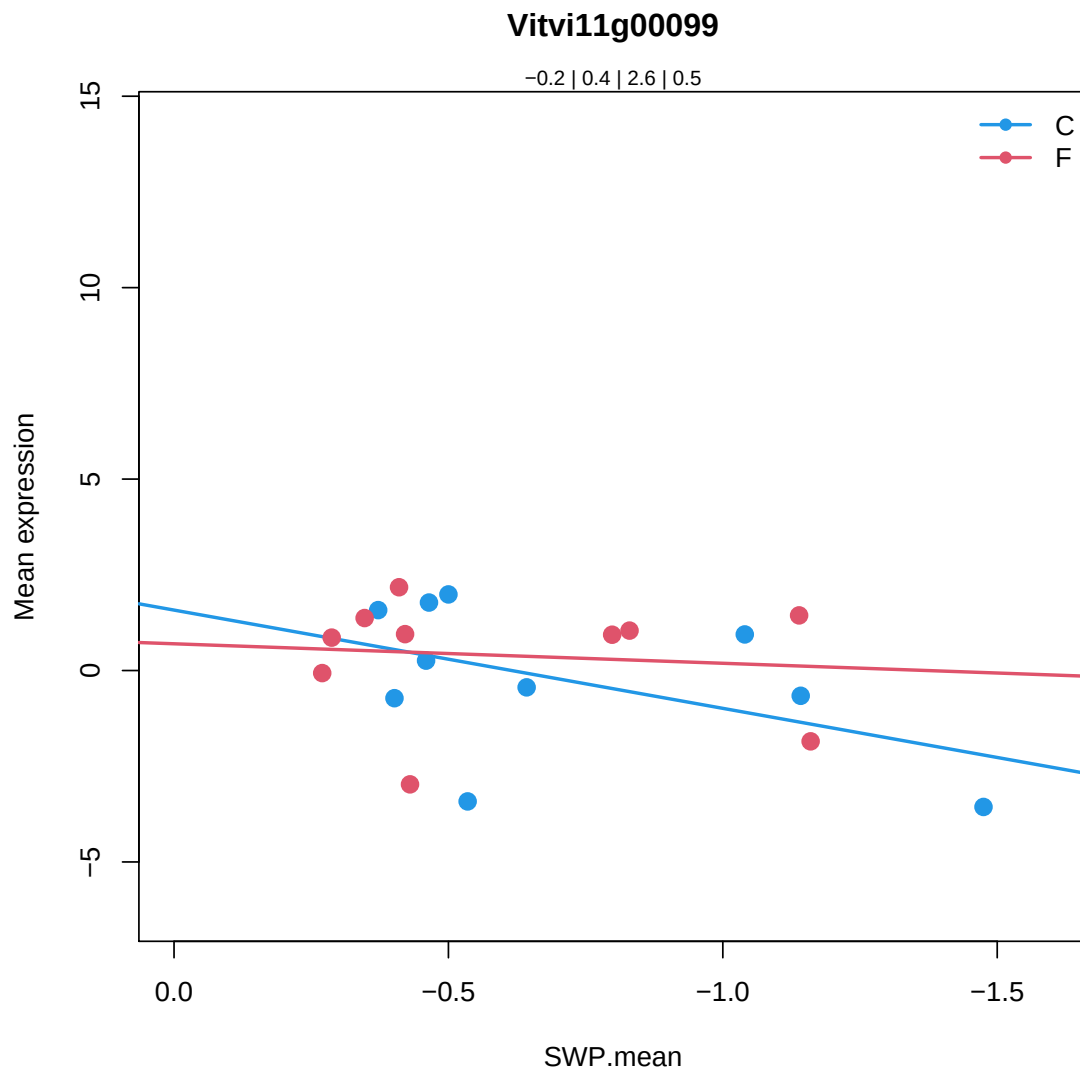
myb domain protein 13 |

Chr1:1889510-1891089 FORWARD LENGTH=246 |

201606

Coefficients for Vitvi11g00099.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.2264991	0.6474752		0.6524838	
SlopeC	2.566253	0.07252928	.	0.563271	
MeanF-MeanC	0.6145939	0.3834143		0.7339597	
SlopeF-SlopeC	-2.057179	0.3203705		0.9999488	



8.1.34 Vitvi11g00016: Type1.0 *

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

Vitvi11g00016

35.2

not assigned.unknown

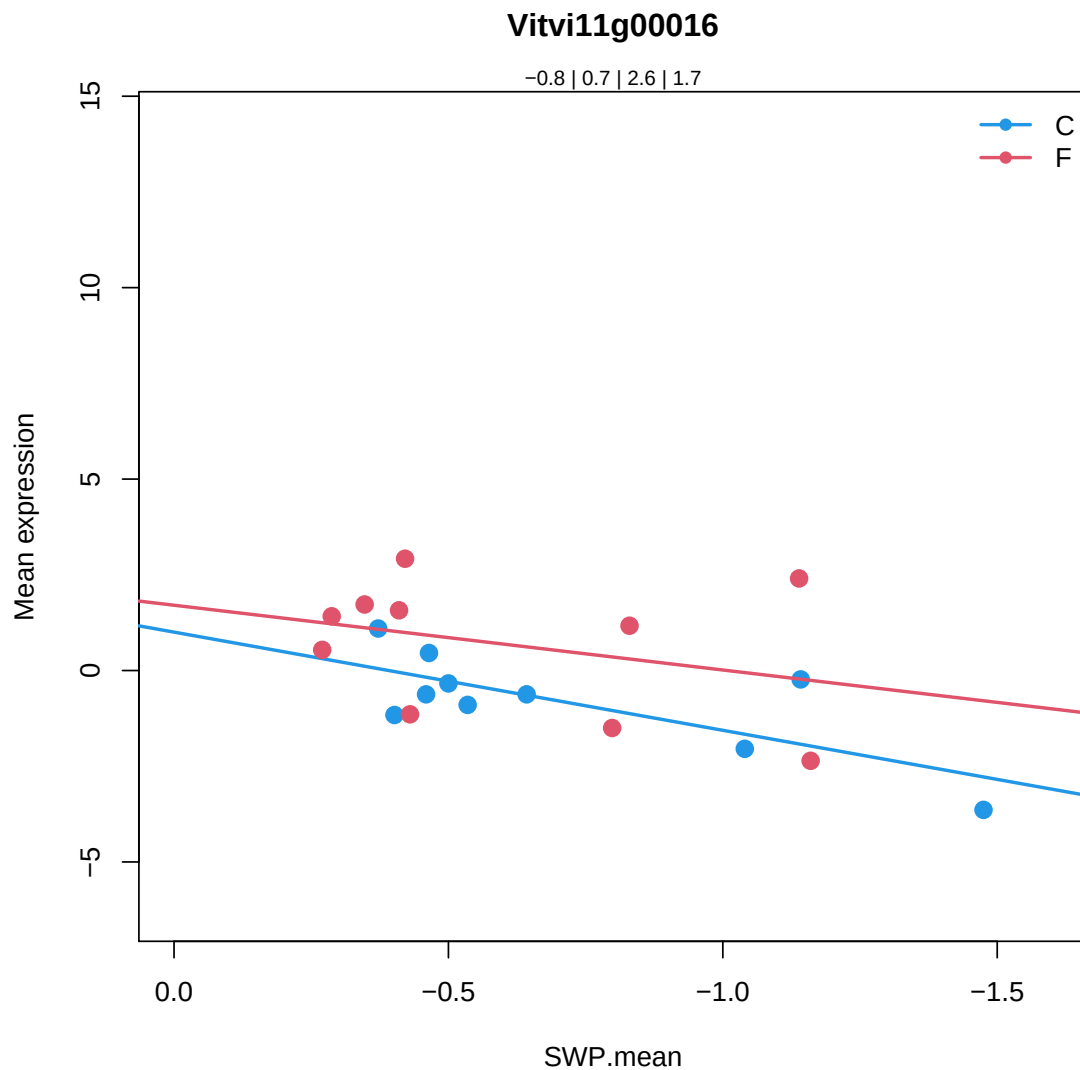
Plant invertase/pectin methylesterase inhibitor superfamily |

Chr5:7076971-7079077 REVERSE LENGTH=538 |

201606

Coefficients for Vitvi11g00016.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.8004064	0.0548222	.	0.05704143	.
SlopeC	2.564374	0.02908345	*	0.4288878	
MeanF-MeanC	1.474787	0.01493928	*	0.1015631	
SlopeF-SlopeC	-0.8725008	0.5983658		0.9999488	



8.1.35 Vitvi00g02313: Type1.0 *

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

Vitvi00g02313

35.2

not assigned.unknown

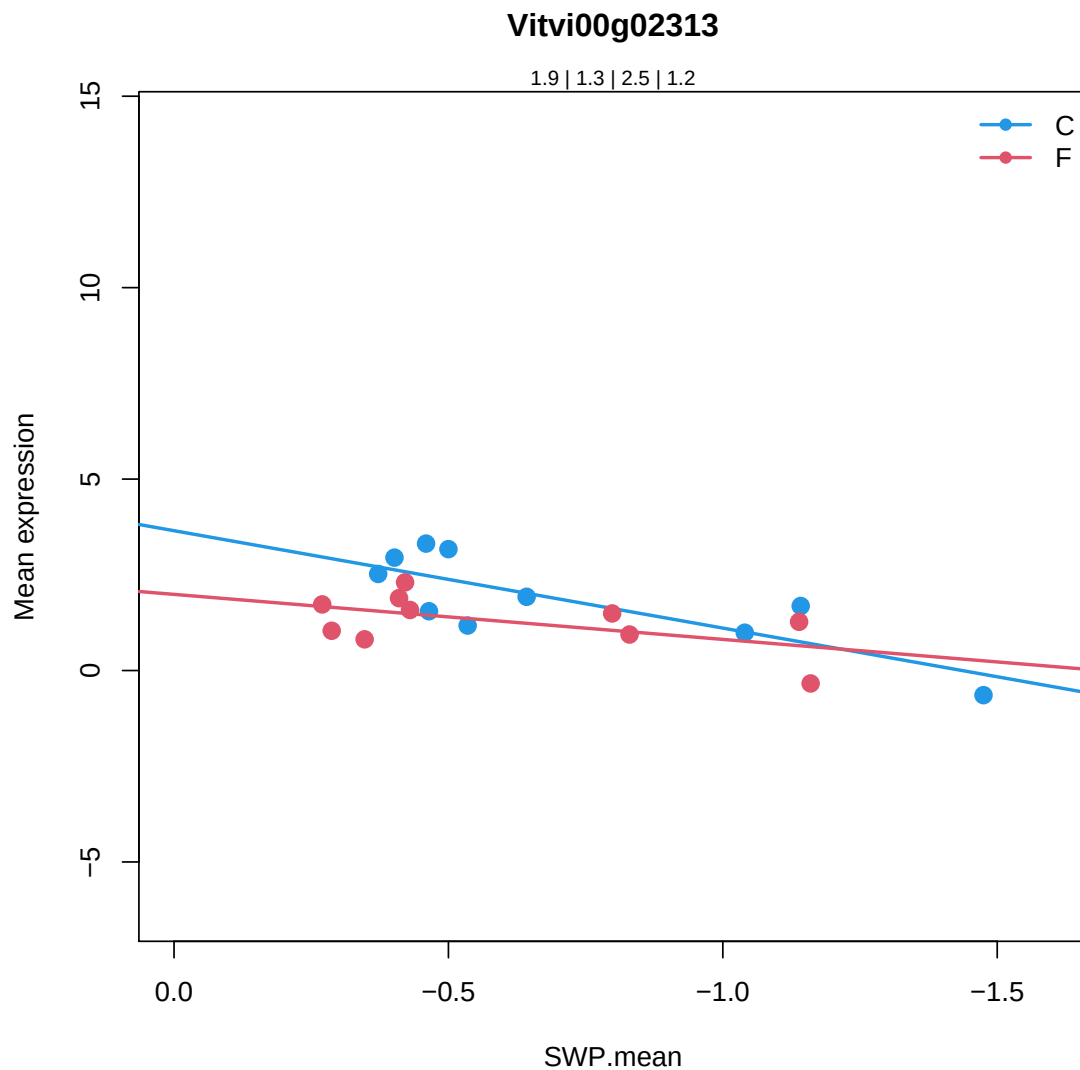
PR5-like receptor kinase |

Chr5:15293325-15295838 REVERSE LENGTH=665 |

201606

Coefficients for Vitvi00g02313.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.863229	1.123844e-08	***	1.369823e-08	***
SlopeC	2.543145	0.0002494031	***	0.08263916	.
MeanF-MeanC	-0.5914233	0.05773703	.	0.2619131	
SlopeF-SlopeC	-1.367169	0.1280553		0.9999488	



8.1.36 Vitvi10g00342: Type1.0 *

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

Vitvi10g00342

35.2

not assigned.unknown

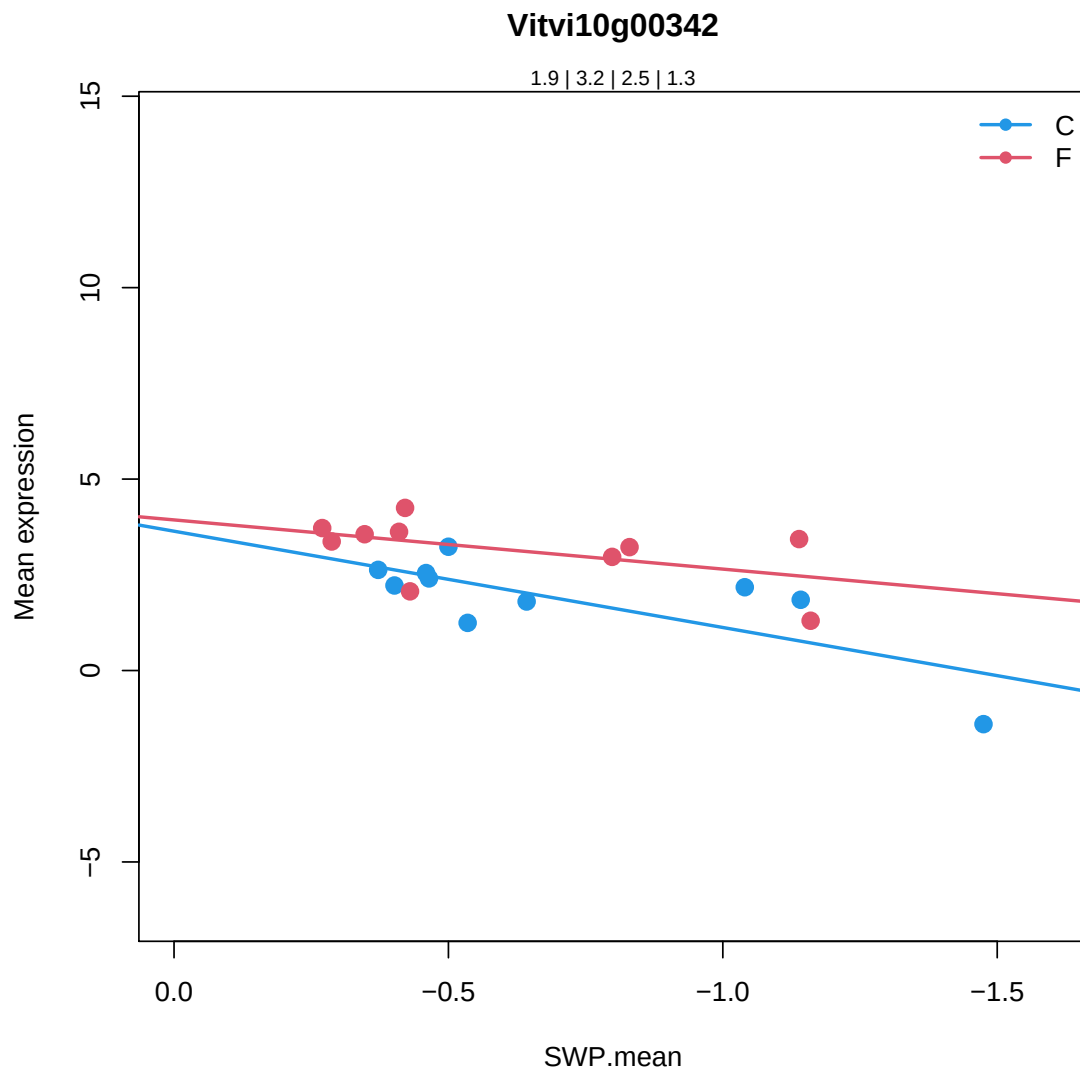
Major facilitator superfamily protein |

Chr4:2632886-2634824 REVERSE LENGTH=418 |

201606

Coefficients for Vitvi10g00342.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.870078	1.236738e-07	***	1.463879e-07	***
SlopeC	2.514567	0.00118631	**	0.136563	
MeanF-MeanC	1.280912	0.001164015	**	0.01427347	*
SlopeF-SlopeC	-1.229844	0.2329113		0.9999488	



8.1.37 Vitvi05g01759: Type1.0 *

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

Vitvi05g01759

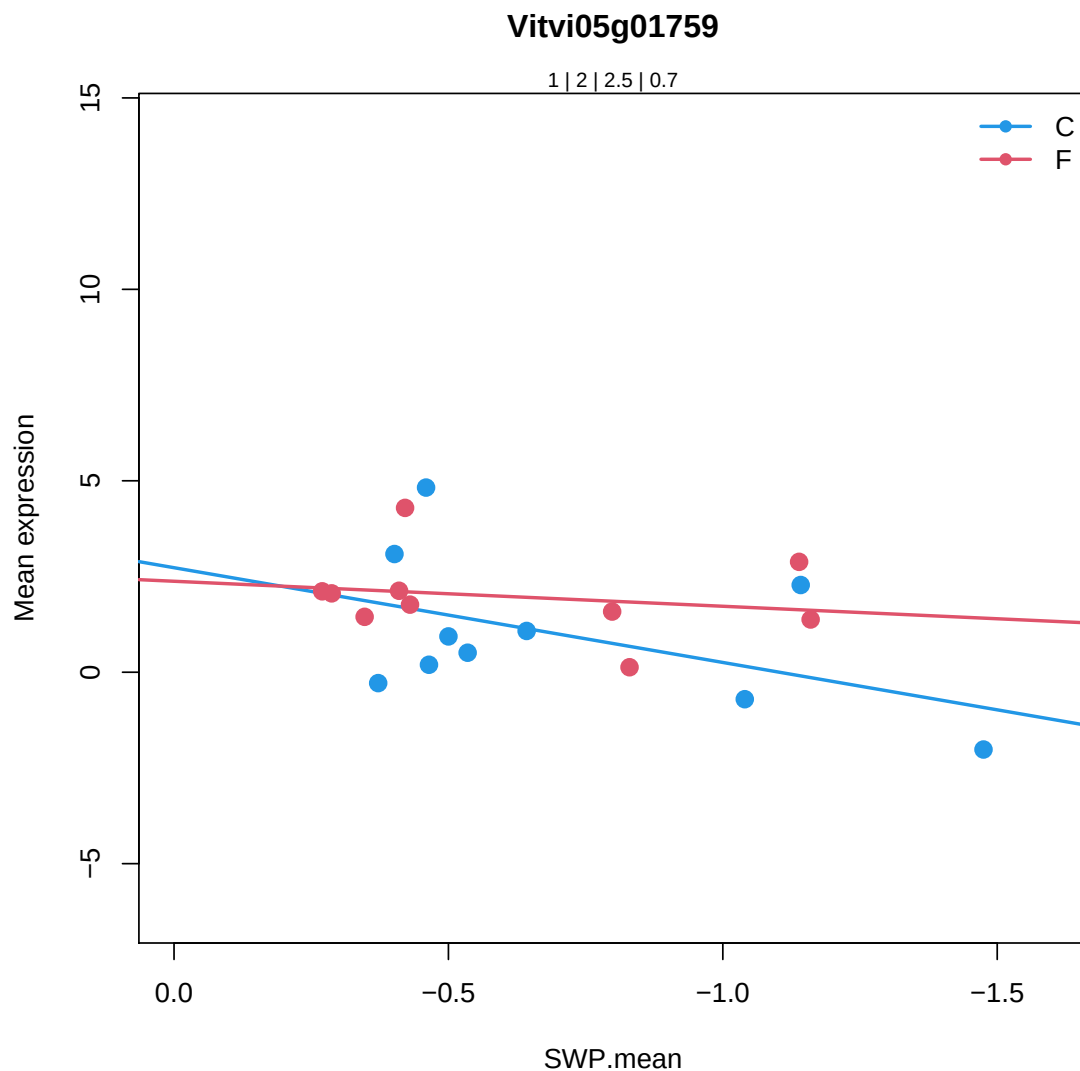
35.2

not assigned.unknown

Major allergen Mal d 1 IPR000916 Bet v I allergen

Coefficients for Vitvi05g01759.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.9895296	0.02948639	*	0.03087392	*
SlopeC	2.474581	0.04805918	*	0.5013813	
MeanF-MeanC	0.9883512	0.1140625		0.3950331	
SlopeF-SlopeC	-1.821369	0.3113755		0.9999488	



8.1.38 Vitvi06g00790: Type1.0

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

Vitvi06g00790

10.7

cell wall.modification

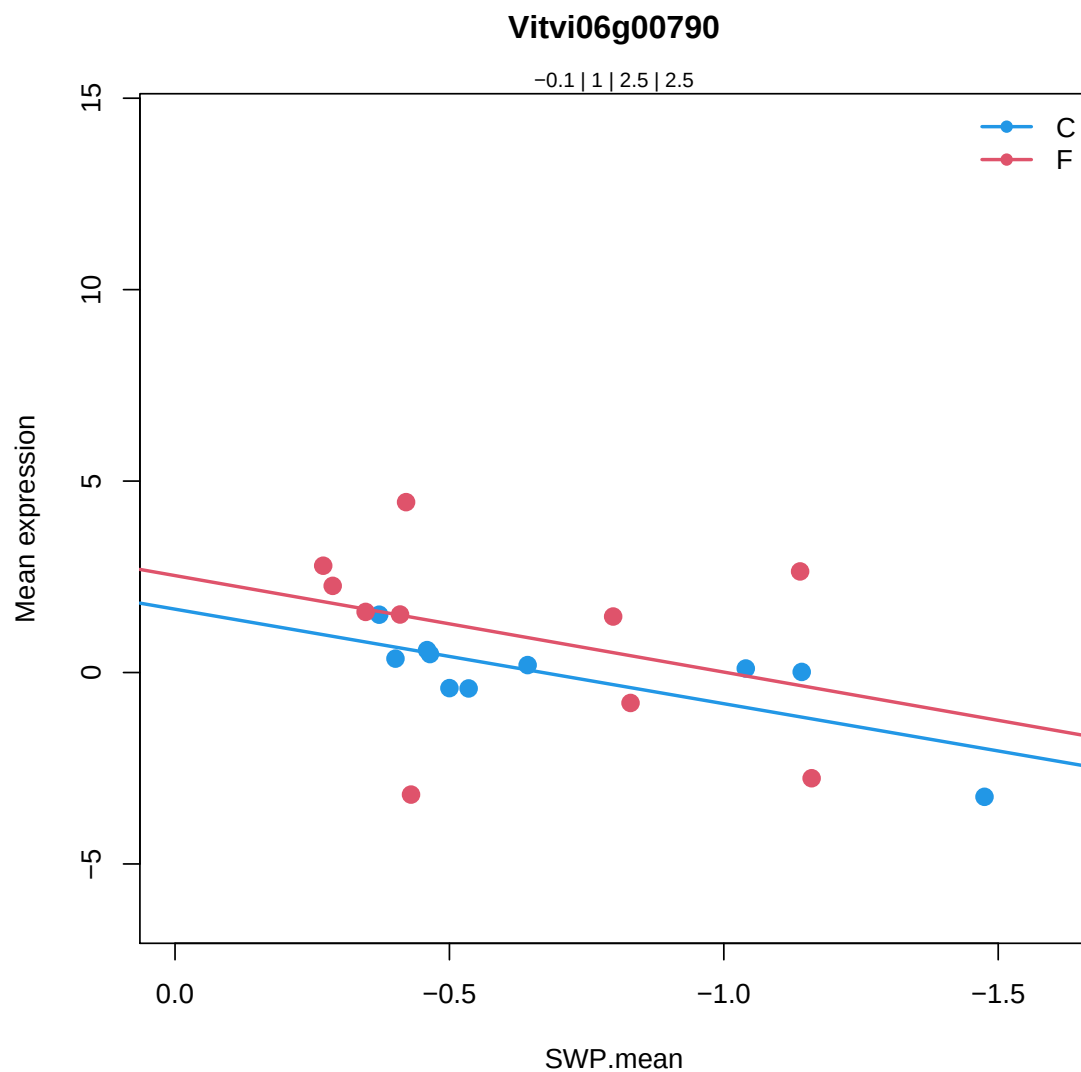
expansin A8 |

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	



8.1.39 Vitvi18g01937: Type1.0 *

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

Vitvi18g01937

30.2.25

signalling.receptor kinases.wall associated kinase

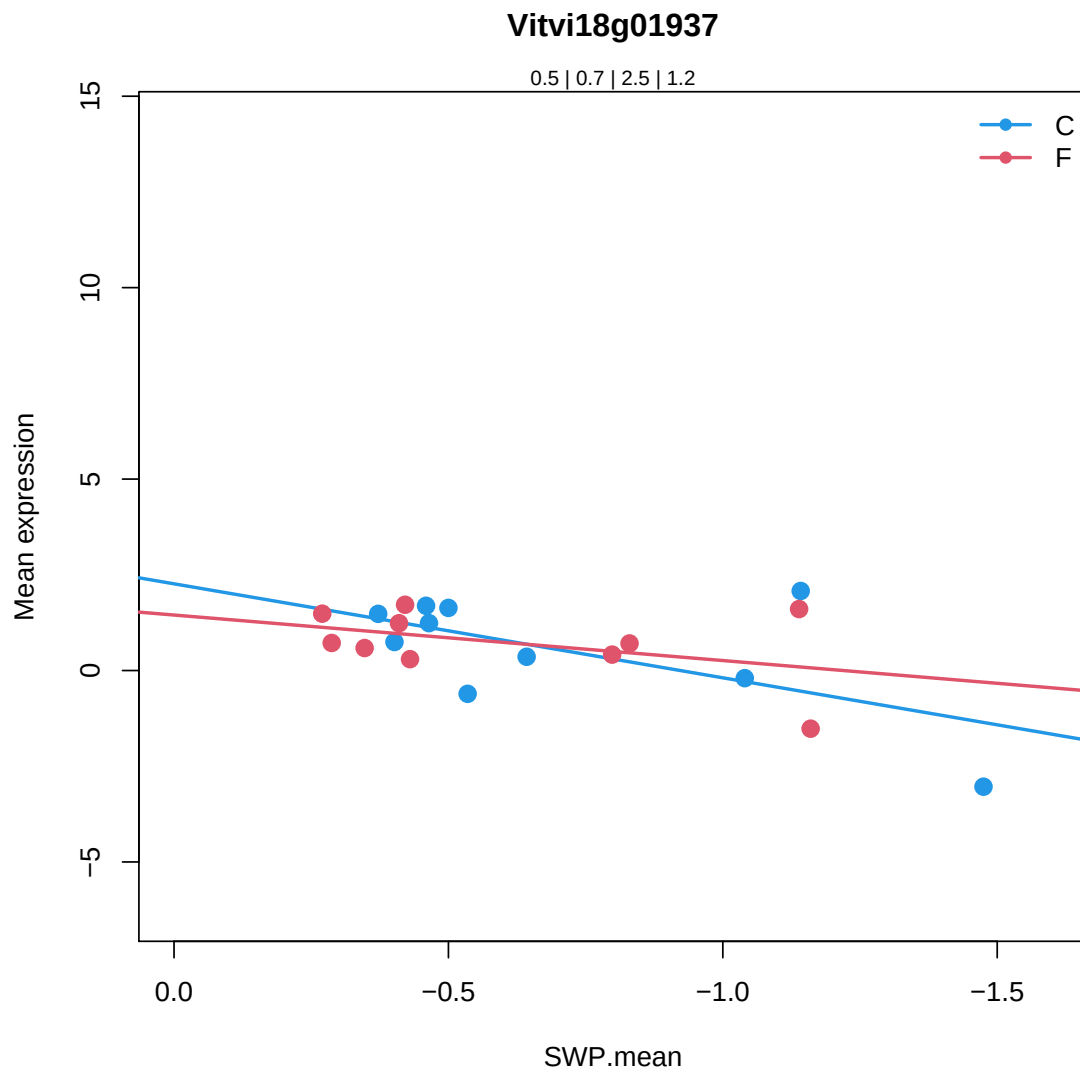
wall associated kinase 3 |

Chr1:7434303-7436702 FORWARD LENGTH=741 |

201606

Coefficients for Vitvi18g01937.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.5380126	0.09941263	.	0.1027913	
SlopeC	2.455009	0.01001862	*	0.3042249	
MeanF-MeanC	0.1868549	0.6765337		0.8951087	
SlopeF-SlopeC	-1.266487	0.3384522		0.9999488	



8.1.40 Vitvi02g01317: Type1.0 *

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

Vitvi02g01317

35.2

not assigned.unknown

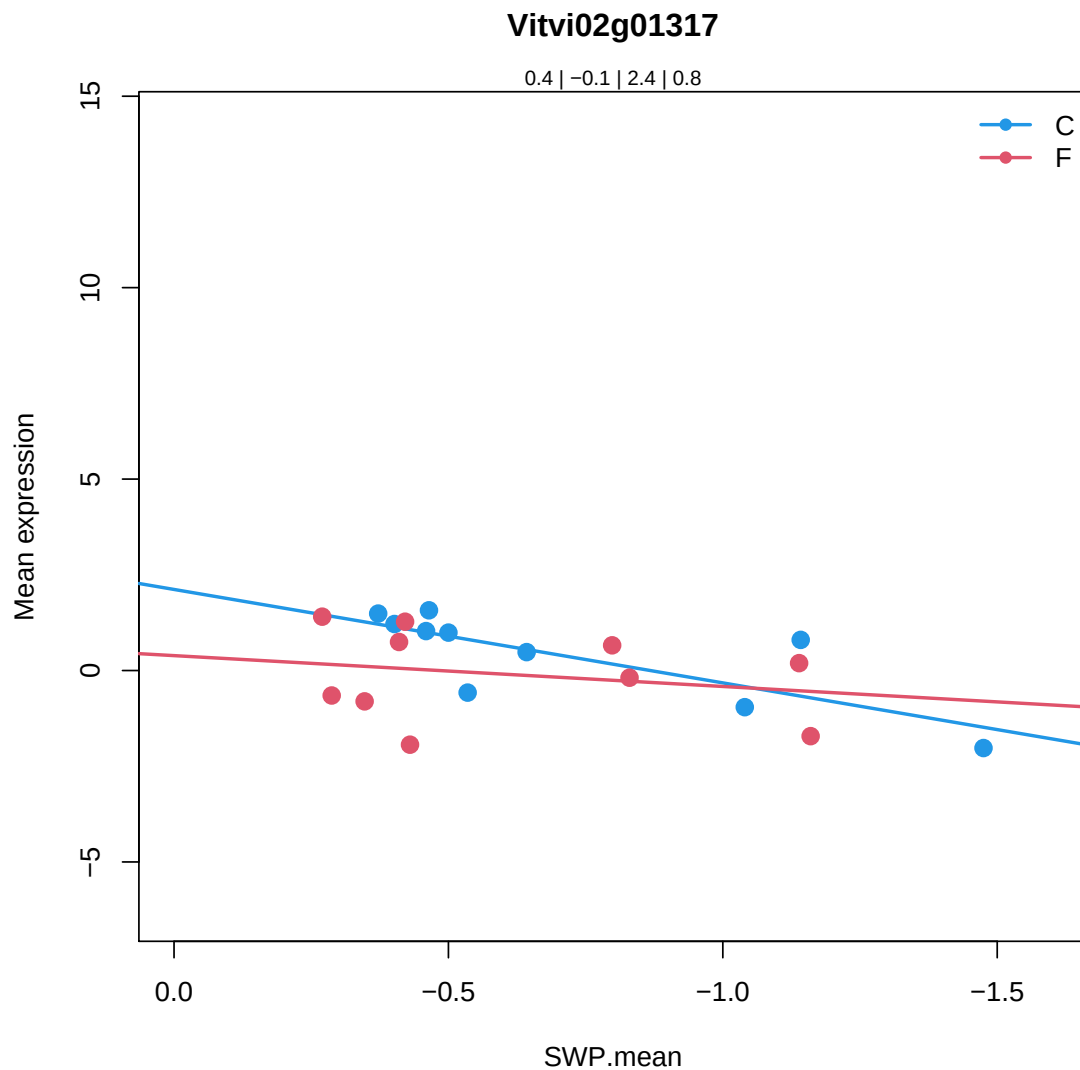
Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein fam

Chr2:18961424-18962089 FORWARD LENGTH=221 |

201606

Coefficients for Vitvi02g01317.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4014866	0.1807803		0.1855899	
SlopeC	2.440462	0.006378977	**	0.2661465	
MeanF-MeanC	-0.5035401	0.2331788		0.5881143	
SlopeF-SlopeC	-1.635035	0.187791		0.9999488	



8.1.41 Vitvi04g01941: Type1.0 *

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

Vitvi04g01941

35.2

not assigned.unknown

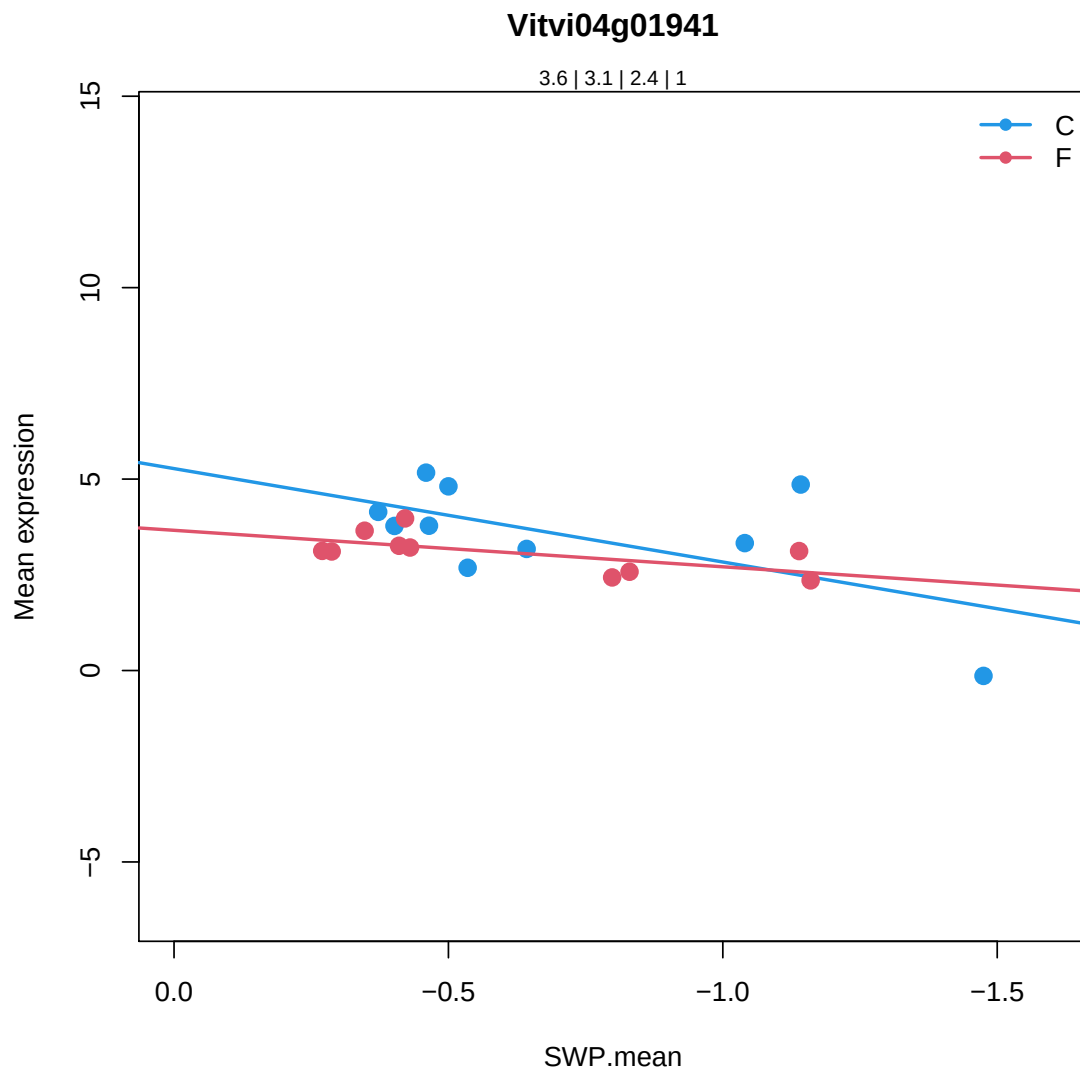
Eukaryotic aspartyl protease family protein |

Chr5:3403331-3405331 REVERSE LENGTH=474 |

201606

Coefficients for Vitvi04g01941.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.558254	1.143666e-11	***	1.556268e-11	***
SlopeC	2.439719	0.004084534	**	0.2328828	
MeanF-MeanC	-0.4770416	0.2296485		0.583151	
SlopeF-SlopeC	-1.486574	0.2020793		0.9999488	



8.1.42 Vitvi03g01495: Type1.0 *

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

Vitvi03g01495

35.2

not assigned.unknown

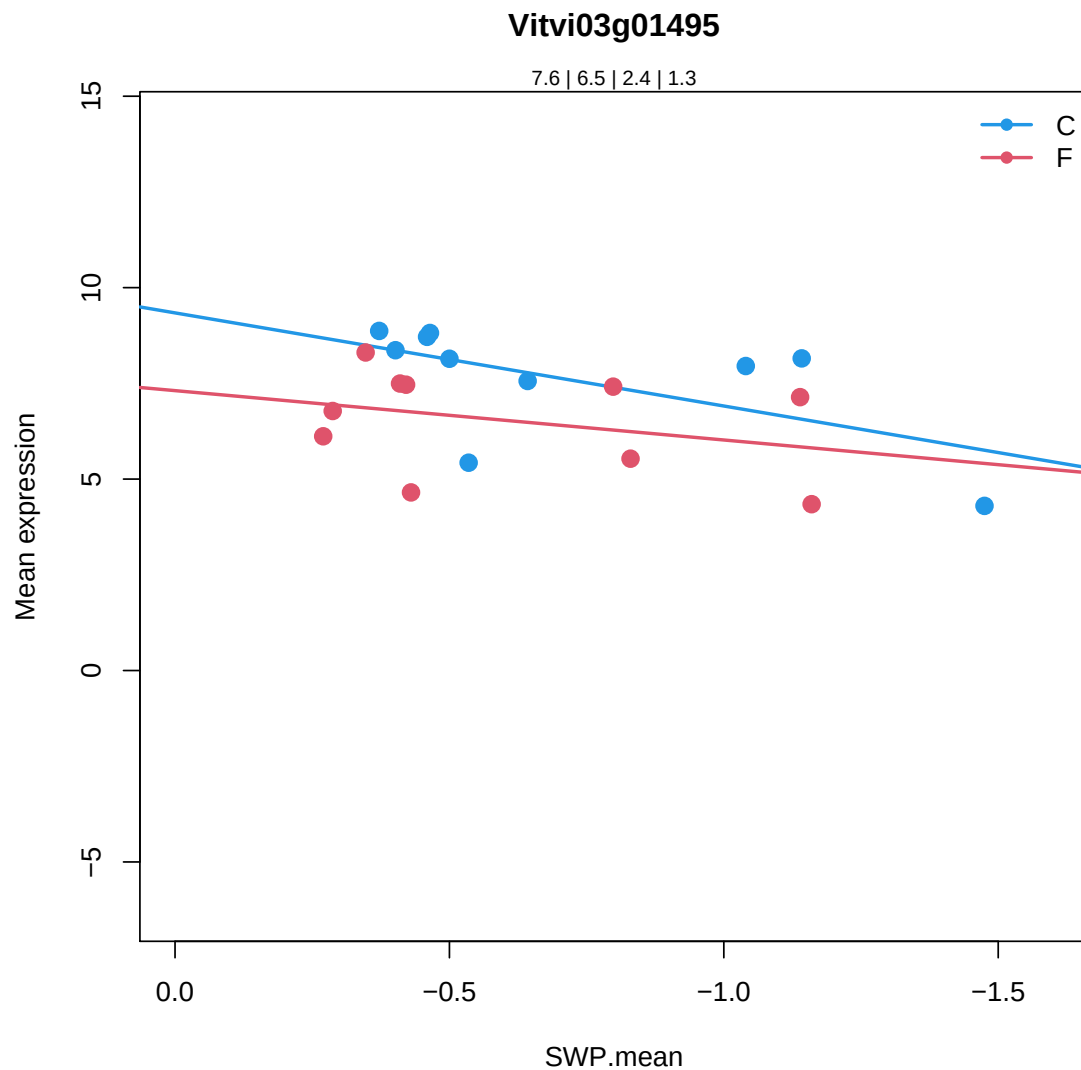
RAD-like 6 |

Chr1:28245073-28245453 REVERSE LENGTH=126 |

201606

Coefficients for Vitvi03g01495.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.630314	1.037714e-15	***	1.939526e-15	***
SlopeC	2.431909	0.0263468	*	0.4131461	
MeanF-MeanC	-1.105936	0.04452893	*	0.2219457	
SlopeF-SlopeC	-1.142729	0.4595701		0.9999488	



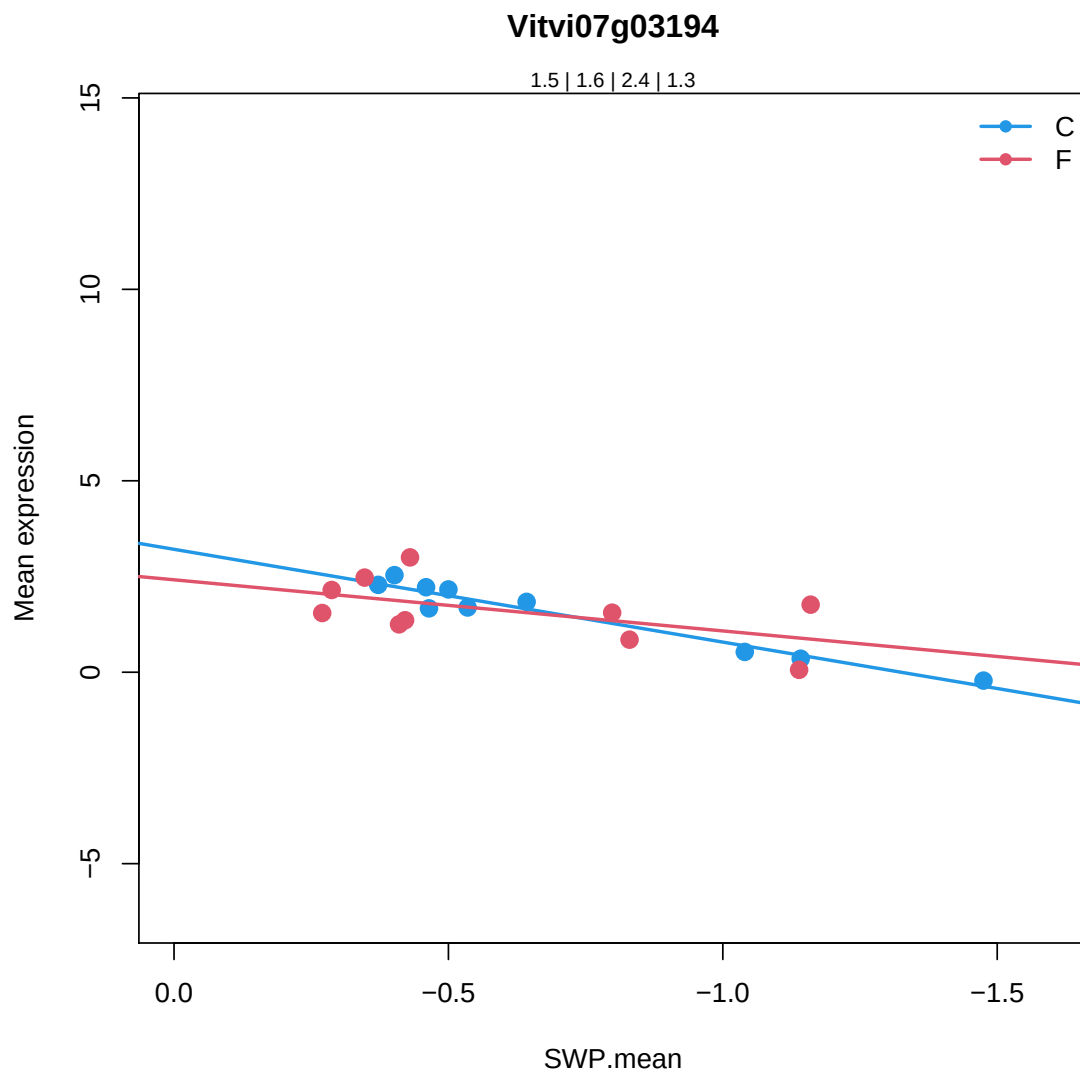
8.1.43 Vitvi07g03194: Type1.0 *

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

```
Vitvi07g03194
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi07g03194.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.505922	1.003209e-08	***	1.224645e-08	***
SlopeC	2.423515	3.496776e-05	***	0.05641797	.
MeanF-MeanC	0.09446766	0.6939088		0.903615	
SlopeF-SlopeC	-1.088143	0.1312265		0.9999488	



8.1.44 Vitvi16g01997: Type1.0 *

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

```
Vitvi16g01997
```

```
35.2
```

```
not assigned.unknown
```

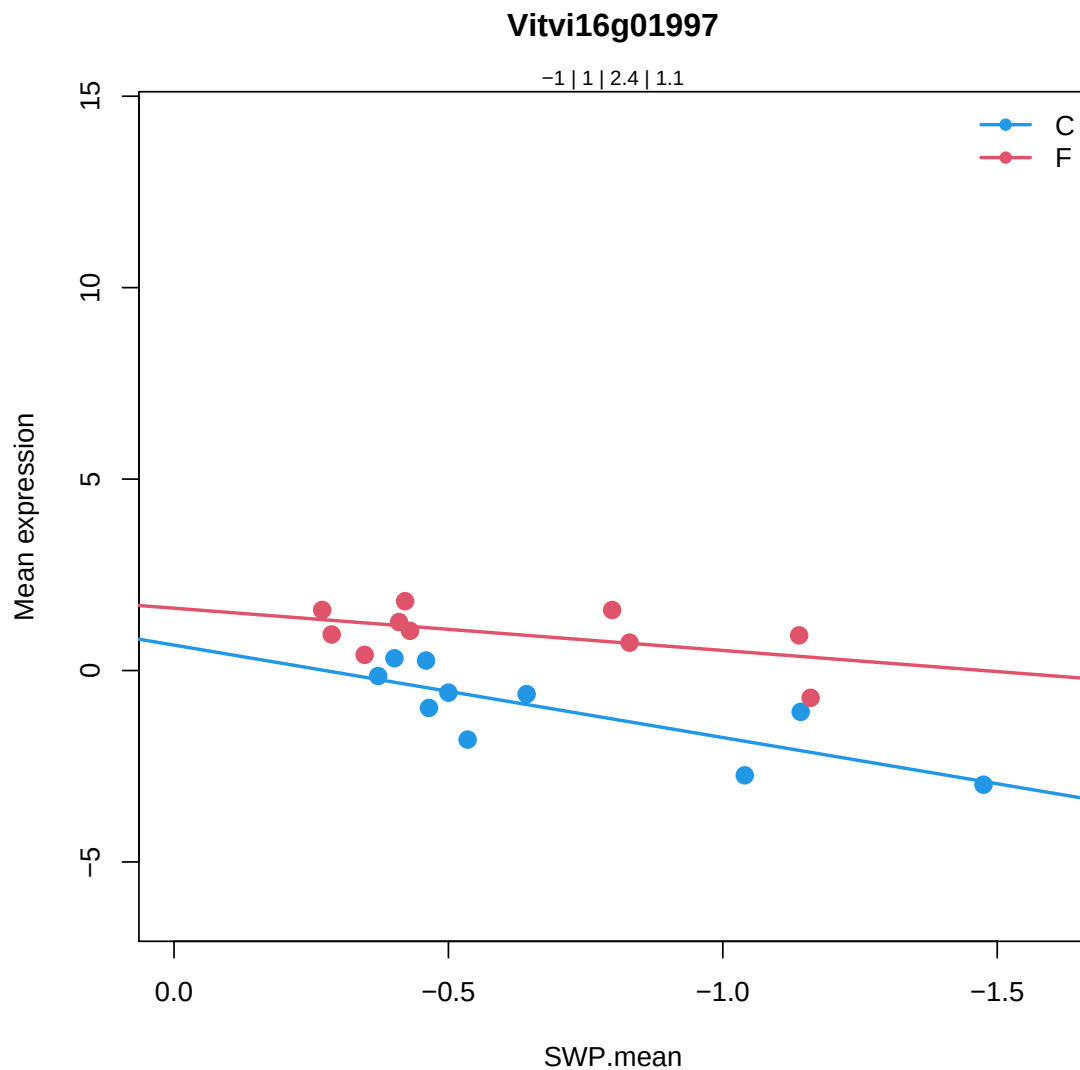
```
Protein kinase superfamily protein |
```

```
Chr1:24961634-24963941 REVERSE LENGTH=663 |
```

```
201606
```

Coefficients for Vitvi16g01997.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.034148	5.836645e-05	***	6.475154e-05	***
SlopeC	2.413916	0.0004030742	***	0.09599463	.
MeanF-MeanC	1.989554	9.310868e-07	***	3.05854e-05	***
SlopeF-SlopeC	-1.310402	0.1416231		0.9999488	



8.1.45 Vitvi04g00060: Type1.0

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

Vitvi04g00060

29.4

protein.postranslational modification

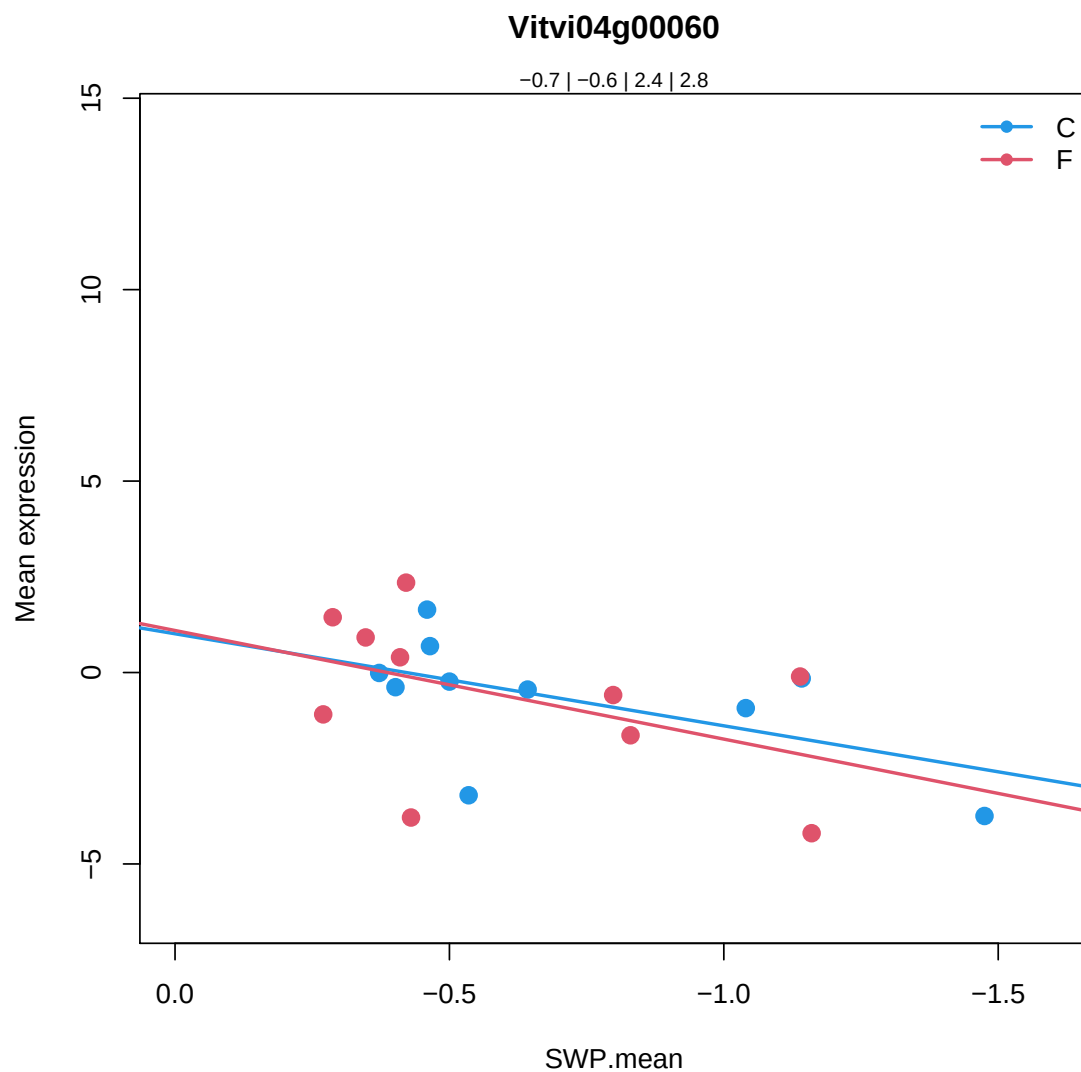
Protein phosphatase 2C family protein |

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	



8.1.46 Vitvi18g00455: Type1.0

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

Vitvi18g00455

26.7

misc.oxidases - copper, flavone etc

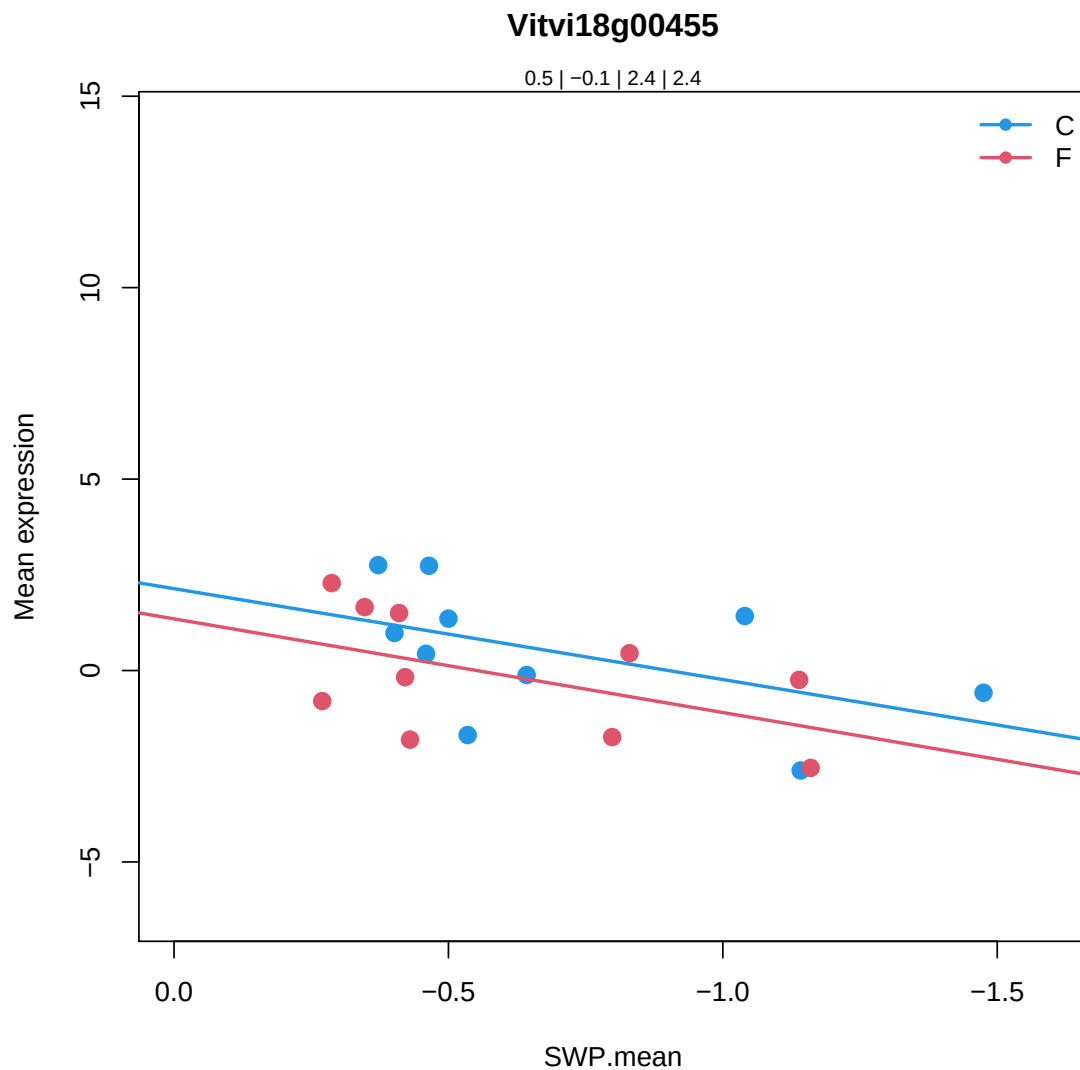
Cupredoxin superfamily protein |

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	



8.1.47 Vitvi11g01437: Type1.0 *

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

Vitvi11g01437

26.12

misc.peroxidases

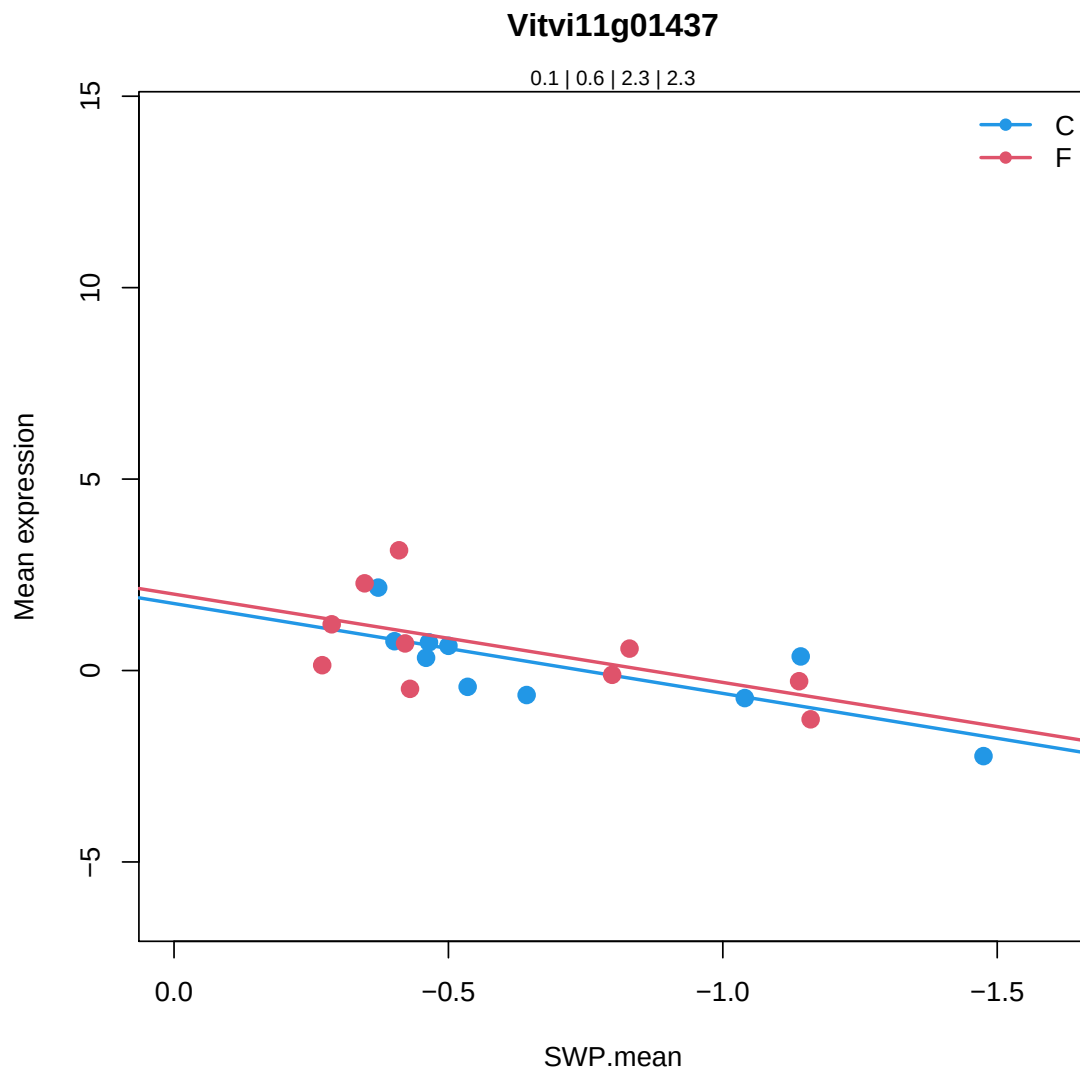
peroxidase superfamily protein |

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	



8.1.48 Vitvi14g01469: Type1.0

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

Vitvi14g01469

30.11

signalling.light

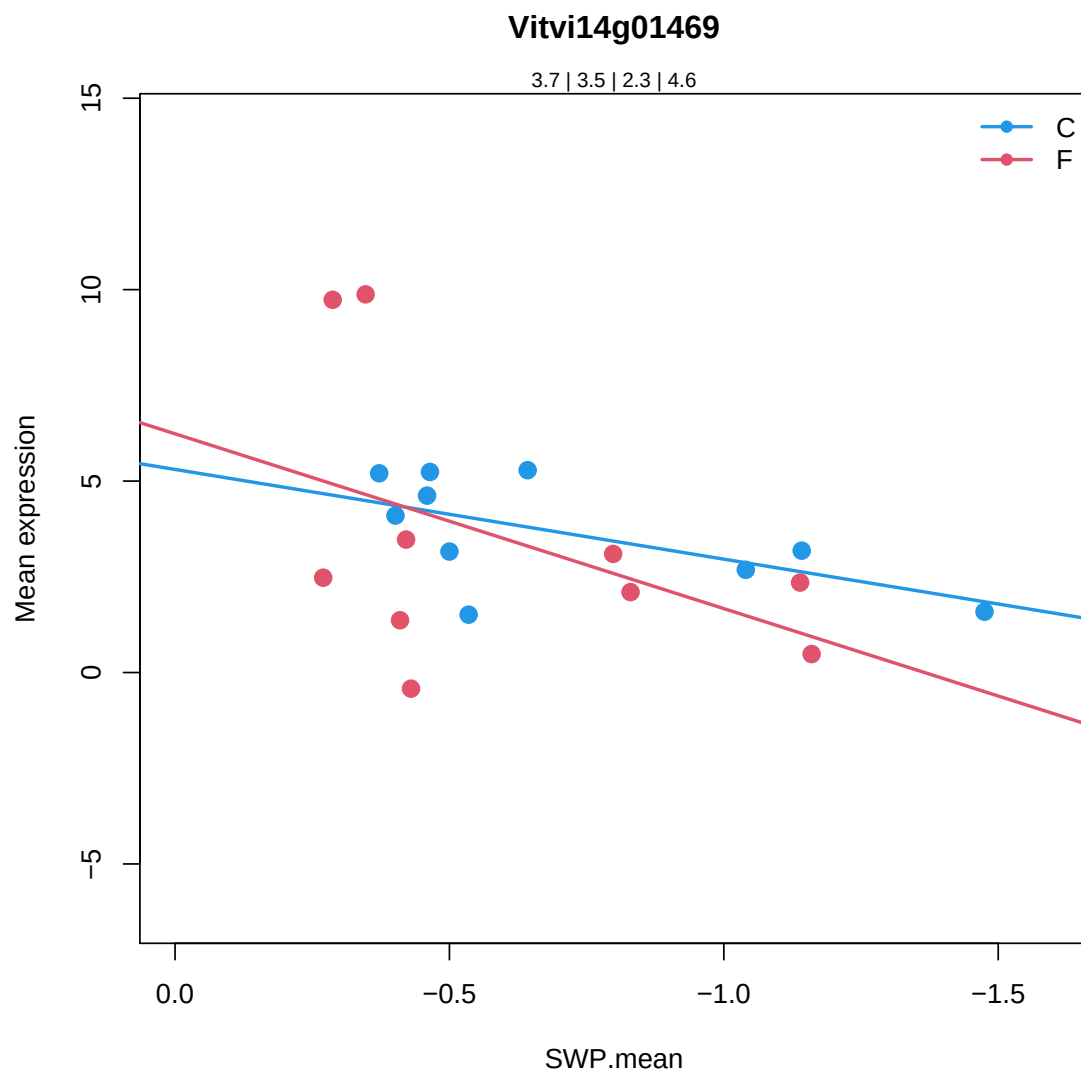
CCR-like protein |

Chr3:9827868-9828461 FORWARD LENGTH=141 |

201606

Coefficients for Vitvi14g01469.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.656865	3.127355e-05	***	3.489542e-05	***
SlopeC	2.343466	0.2397977		0.7540013	
MeanF-MeanC	-0.2034828	0.8383248		0.9564181	
SlopeF-SlopeC	2.222219	0.4495166		0.9999488	



8.1.49 Vitvi03g00752: Type1.0 *

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

Vitvi03g00752

20.1.7.1

stress.biotic.PR-proteins.PR1 (antifungal)

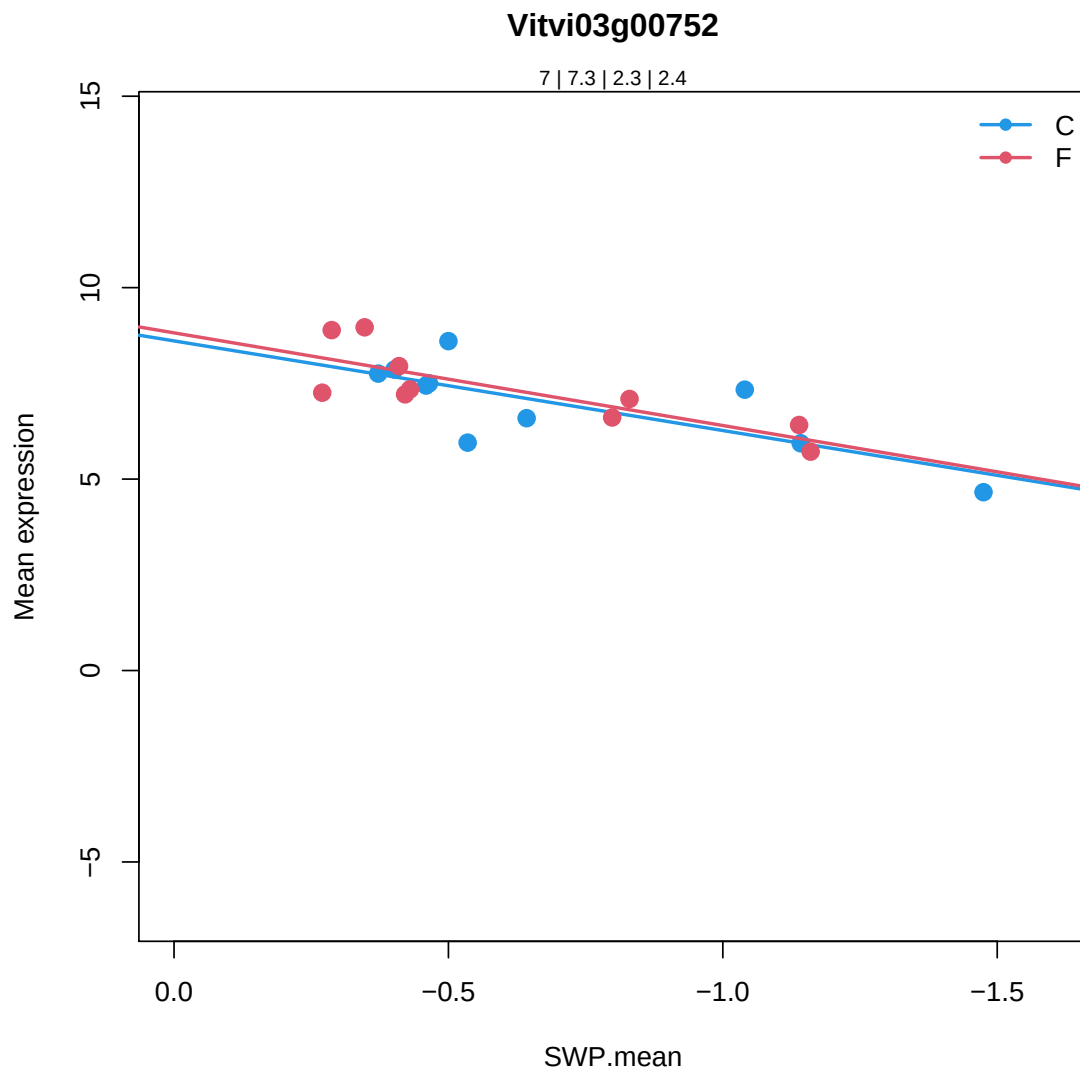
pathogenesis-related protein 1 |

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	



8.1.50 Vitvi13g01977: Type1.0 *

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

Vitvi13g01977

35.2

not assigned.unknown

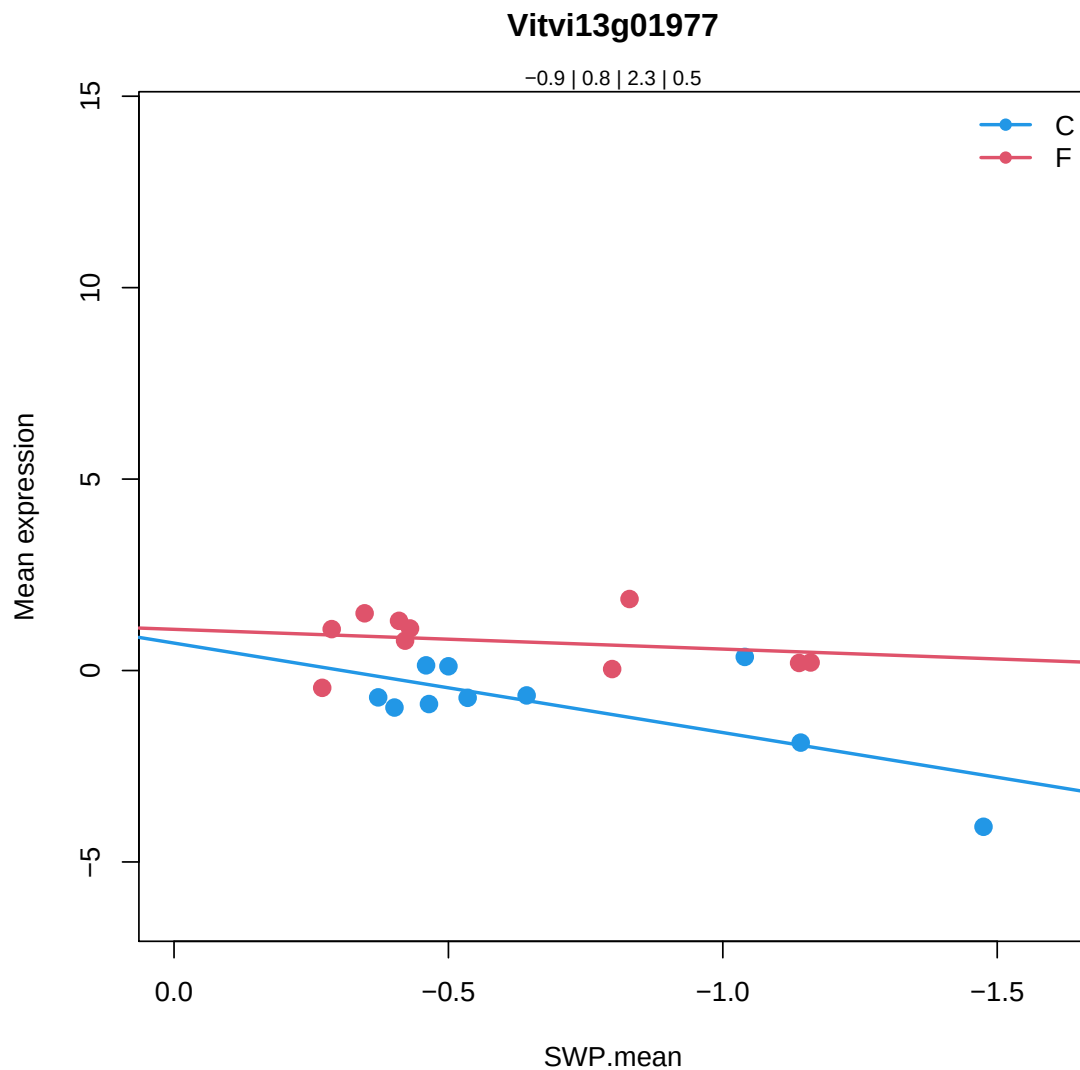
Cysteine/Histidine-rich C1 domain family protein |

Chr2:6980450-6981939 FORWARD LENGTH=243 |

201606

Coefficients for Vitvi13g01977.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.9271232	0.001411657	**	0.001524369	**
SlopeC	2.336916	0.003197938	**	0.2103859	
MeanF-MeanC	1.688268	0.00011153	***	0.001978975	**
SlopeF-SlopeC	-1.820621	0.0967028	.	0.9999488	



8.1.51 Vitvi19g01959: Type1.0 *

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

Vitvi19g01959

29.4

protein.postranslational modification

S-locus lectin protein kinase family protein |

Chr4:13669308-13672348 REVERSE LENGTH=815 |

201606

Vitvi19g01959

30.2.24

signalling.receptor kinases.S-locus glycoprotein like

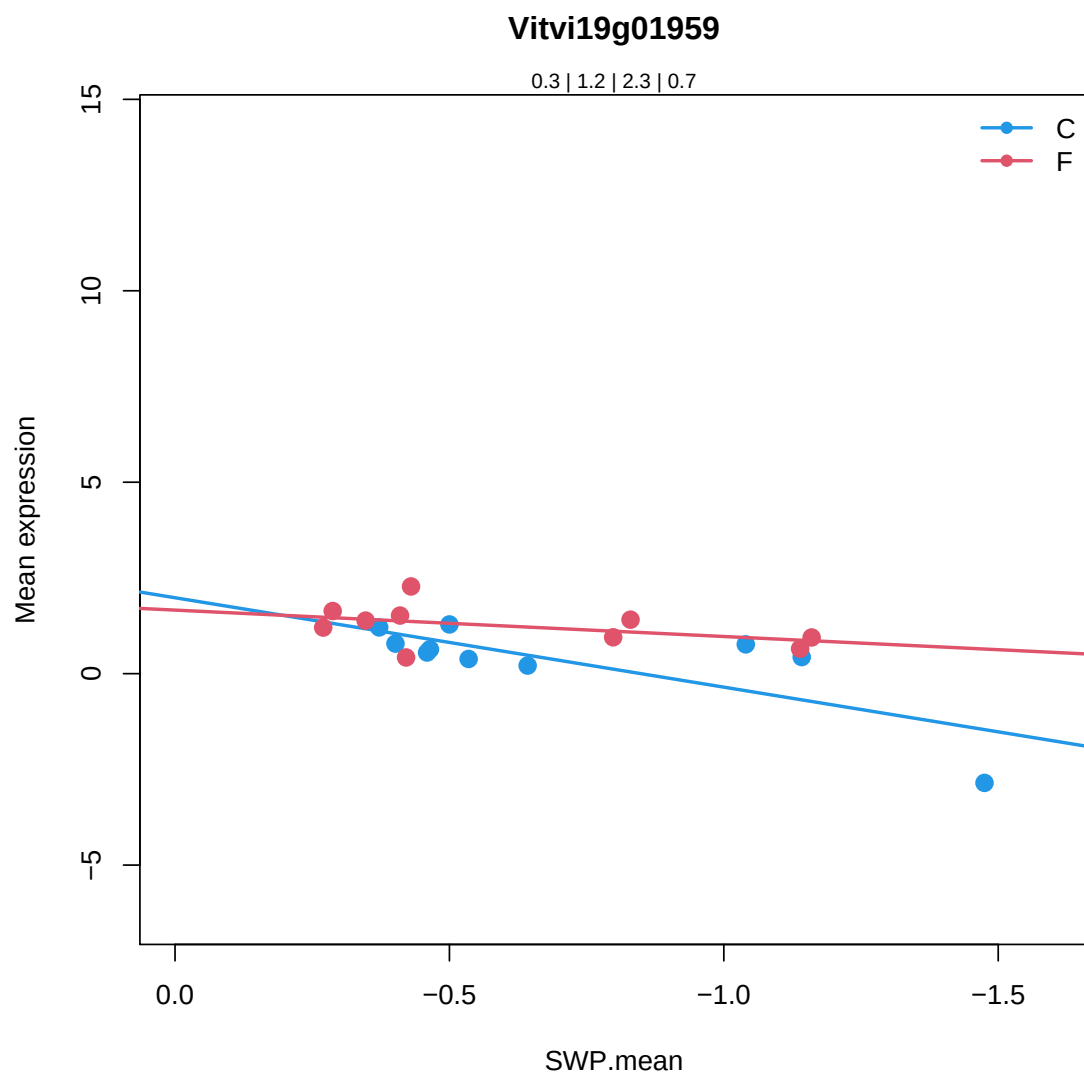
S-locus lectin protein kinase family protein |

Chr4:13669308-13672348 REVERSE LENGTH=815 |

201606

Coefficients for Vitvi19g01959.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.340466	0.1052773		0.1087889	
SlopeC	2.334968	0.0004178903	***	0.09737206	.
MeanF-MeanC	0.8991398	0.00465786	**	0.04325824	*
SlopeF-SlopeC	-1.645257	0.06144402	.	0.9999488	



8.1.52 Vitvi09g01859: Type1.0 *

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

Vitvi09g01859

20.1.2

stress.biotic.receptors

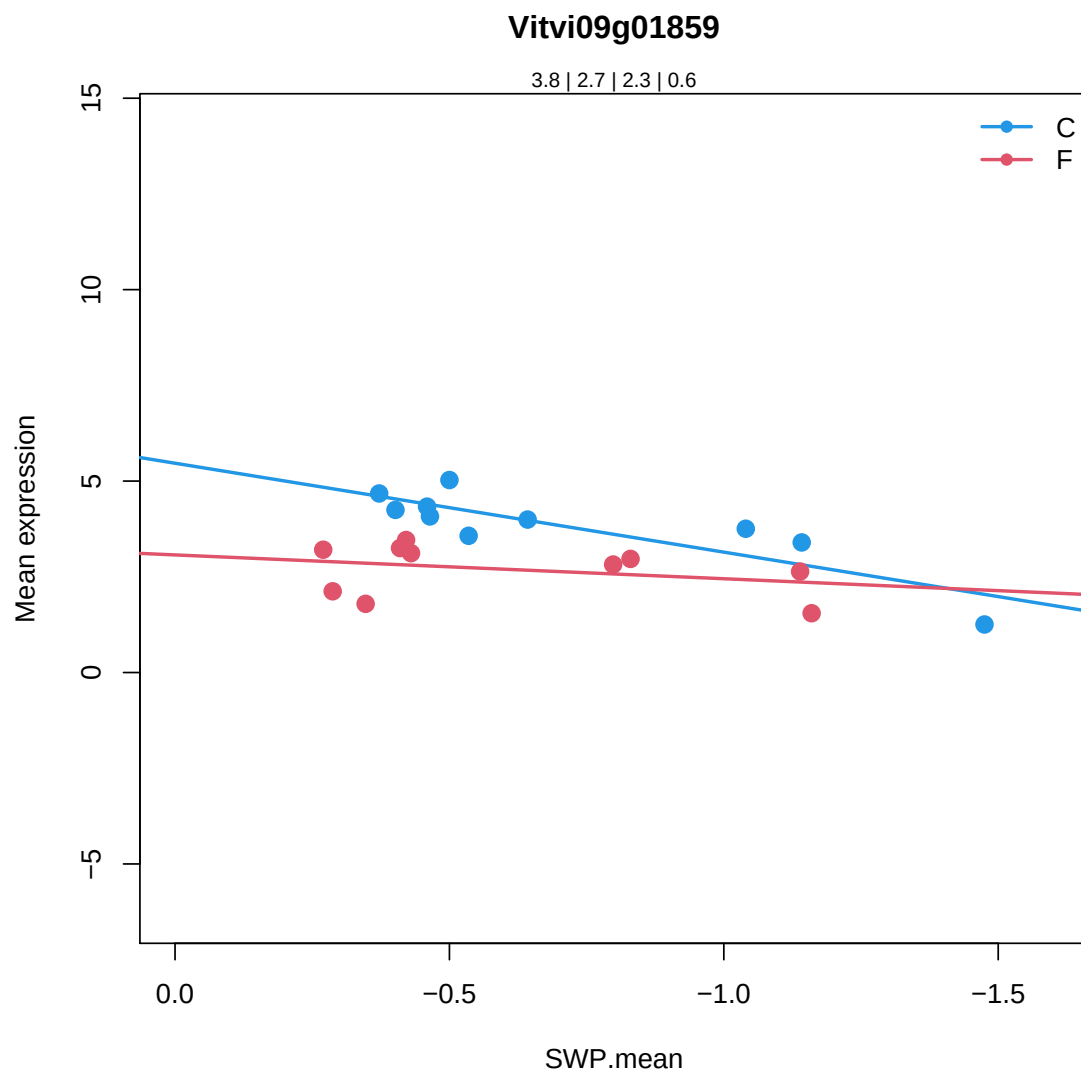
disease resistance family protein / LRR family protein |

Chr2:14737169-14739886 REVERSE LENGTH=905 |

201606

Coefficients for Vitvi09g01859.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.833324	1.199232e-15	***	2.223685e-15	***
SlopeC	2.322169	0.0001869698	***	0.07916093	.
MeanF-MeanC	-1.140958	0.0002688179	***	0.004196963	**
SlopeF-SlopeC	-1.699955	0.03775724	*	0.9999488	



8.1.53 Vitvi06g00626: Type1.0 *

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

Vitvi06g00626

30.2.8.2

signalling.receptor kinases.leucine rich repeat VIII.type 2

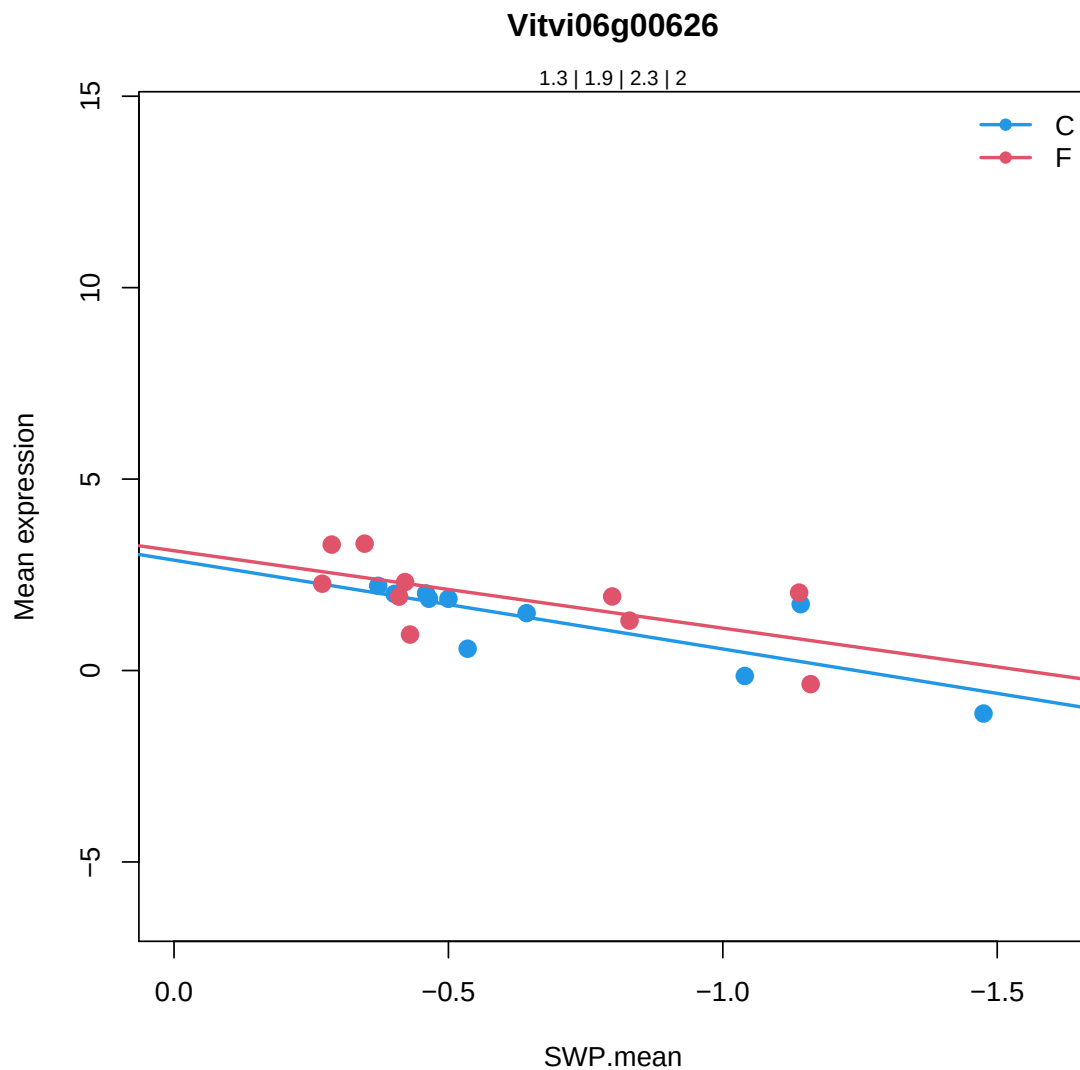
Protein kinase superfamily protein |

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	



8.1.54 Vitvi00g02268: Type1.0 *

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

Vitvi00g02268

35.2

not assigned.unknown

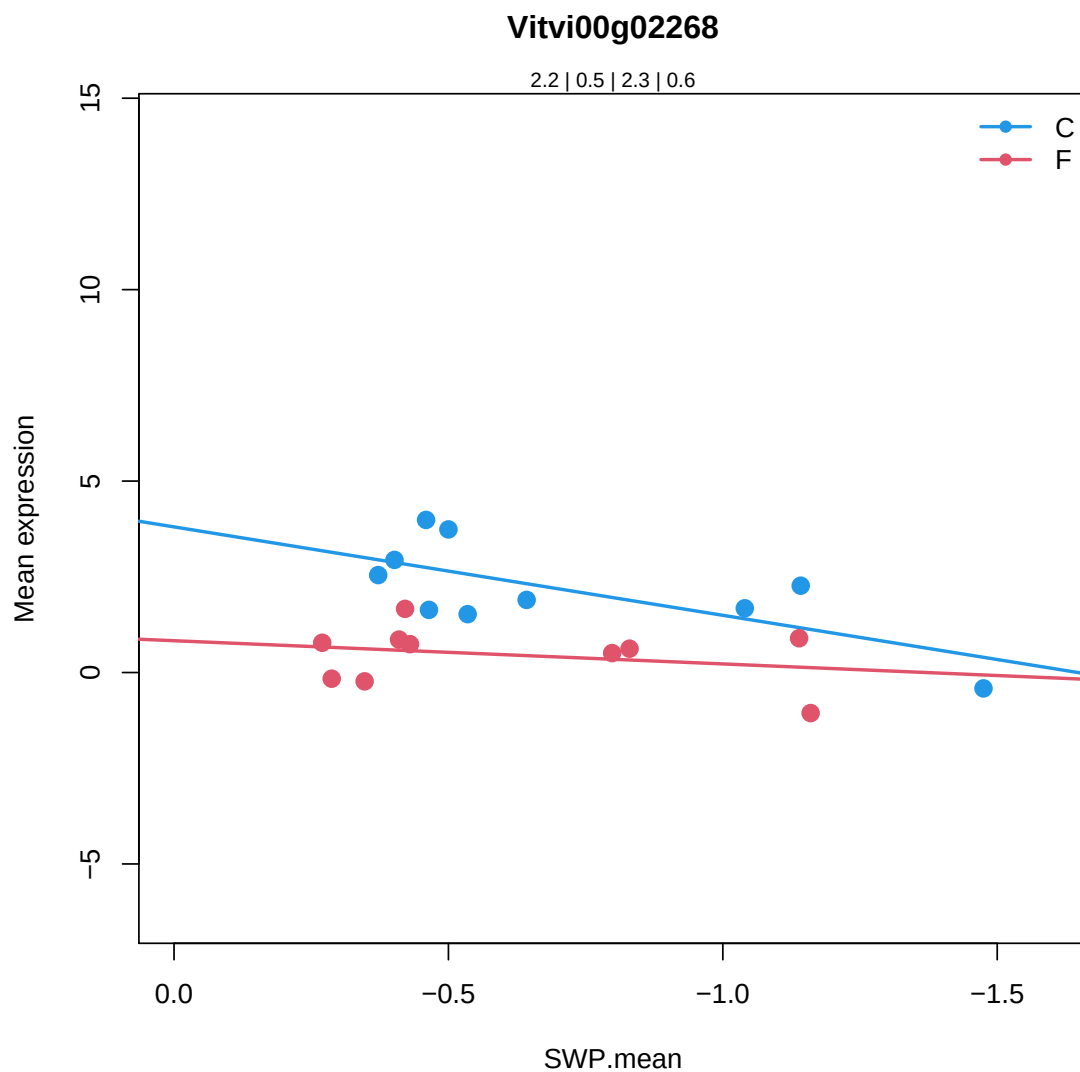
PR5-like receptor kinase |

Chr5:15293325-15295838 REVERSE LENGTH=665 |

201606

Coefficients for Vitvi00g02268.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.179517	1.699587e-08	***	2.061524e-08	***
SlopeC	2.30912	0.003187033	**	0.2103859	
MeanF-MeanC	-1.71824	7.900095e-05	***	0.001464881	**
SlopeF-SlopeC	-1.703039	0.1144988		0.9999488	



8.1.55 Vitvi01g01853: Type1.0 *

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

Vitvi01g01853

35.2

not assigned.unknown

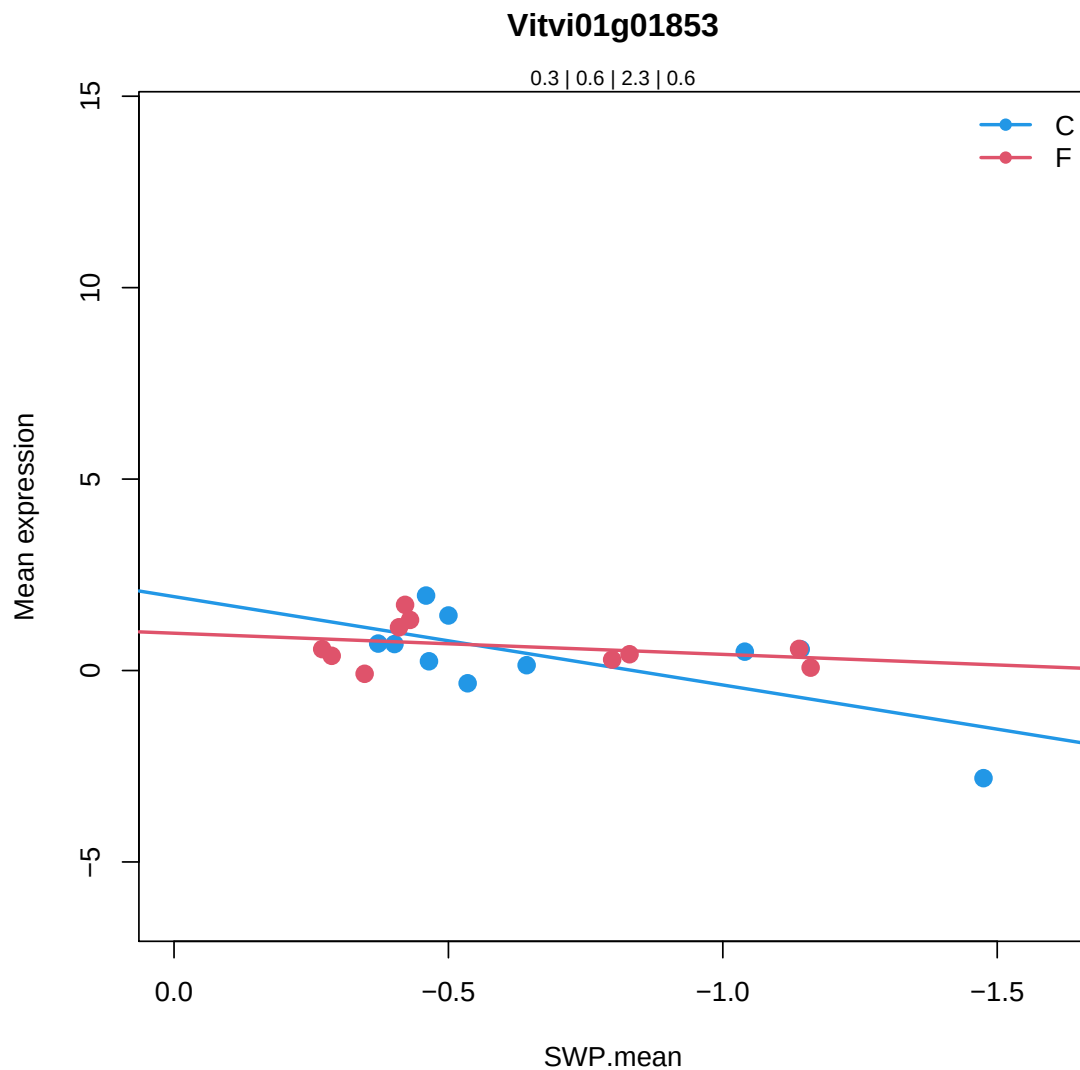
NB-ARC domain-containing disease resistance protein |

Chr3:2226244-2229024 REVERSE LENGTH=926 |

201606

Coefficients for Vitvi01g01853.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3072778	0.2009004		0.2059817	
SlopeC	2.307748	0.001796639	**	0.160246	
MeanF-MeanC	0.3301637	0.3272533		0.6873017	
SlopeF-SlopeC	-1.755036	0.08273476	.	0.9999488	



8.1.56 Vitvi01g00638: Type1.0 *

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

Vitvi01g00638

35.2

not assigned.unknown

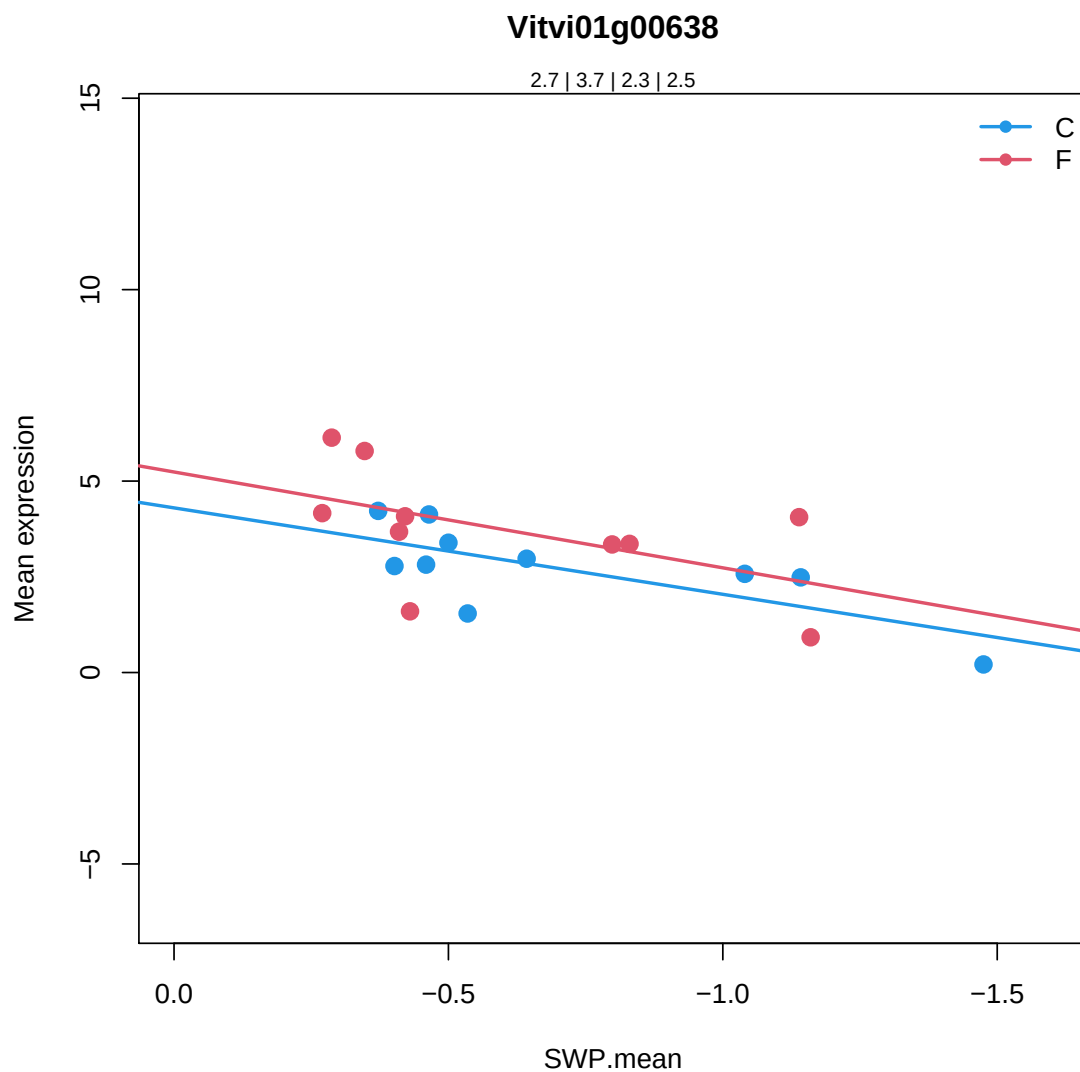
DUF868 family protein (DUF868) |

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	



8.1.57 Vitvi03g01162: Type1.0

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

Vitvi03g01162

26.2

misc.UDP glucosyl and glucoronyl transferases

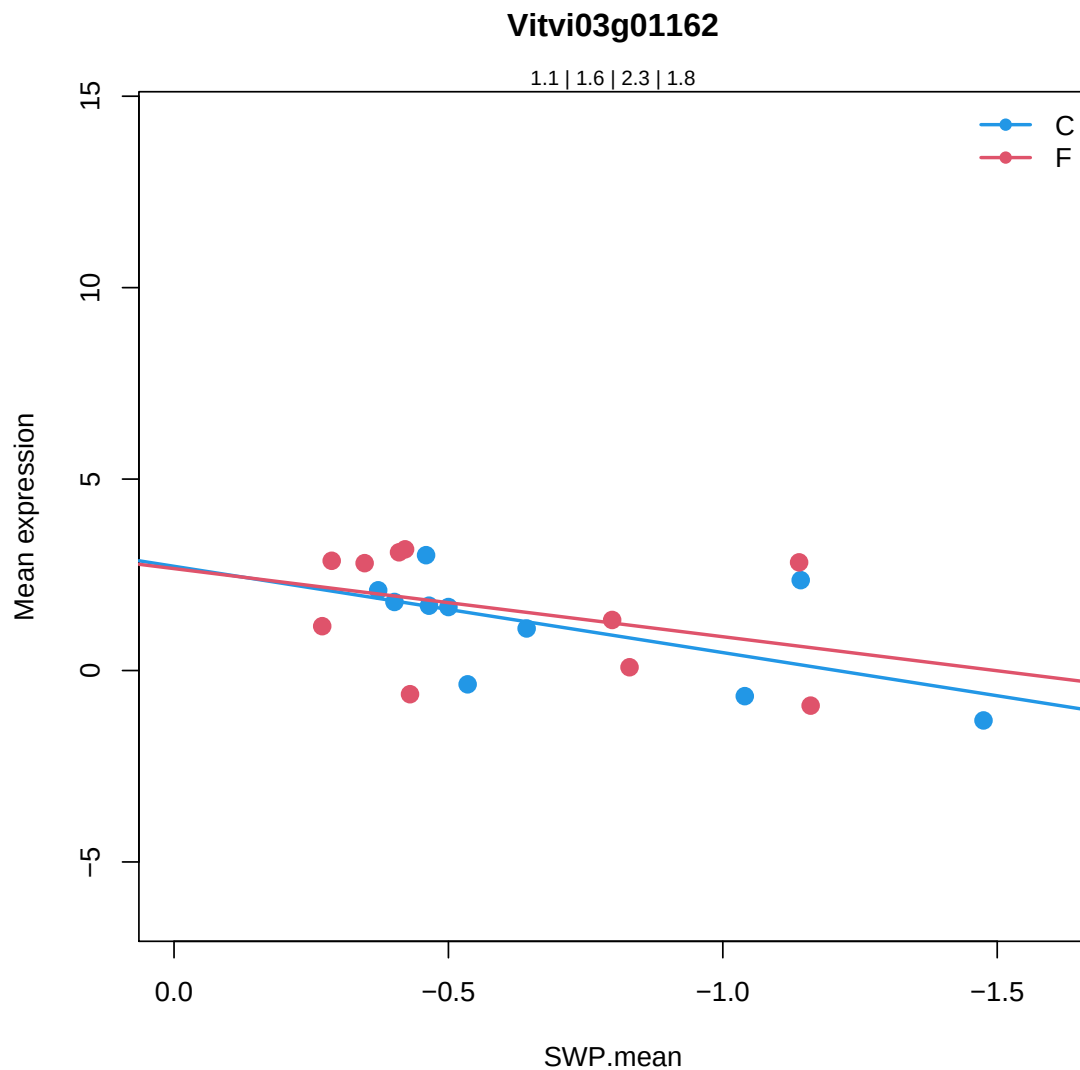
UDP-glucosyl transferase 85A3 |

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	



8.1.58 Vitvi18g00260: Type1.0 *

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

Vitvi18g00260

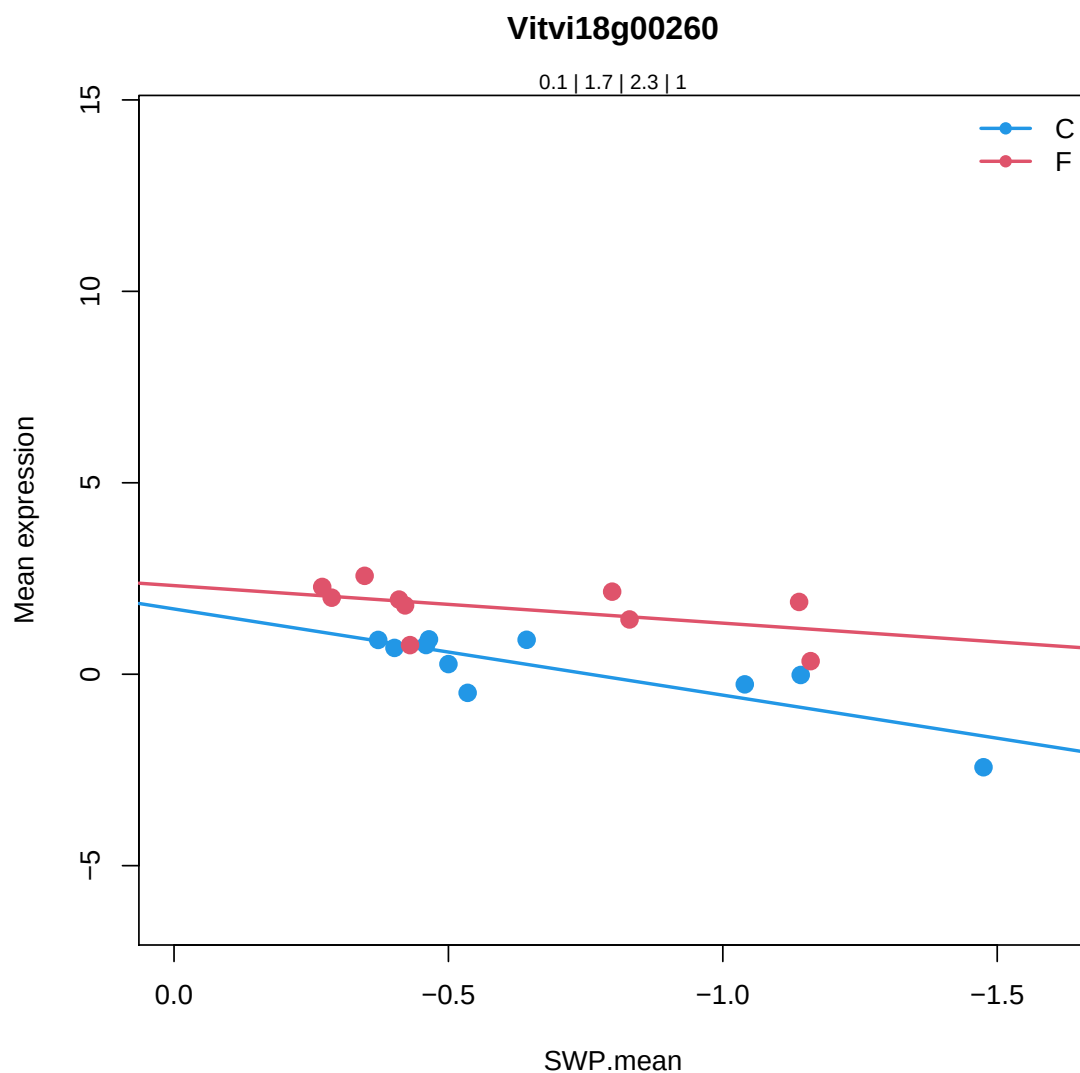
27.3.5

RNA.regulation of transcription.ARR

NA

Coefficients for Vitvi18g00260.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1218865	0.5260369		0.5320055	
SlopeC	2.250526	0.0003213001	***	0.09068993	.
MeanF-MeanC	1.595202	5.871944e-06	***	0.0001545771	***
SlopeF-SlopeC	-1.269808	0.1194824		0.9999488	



8.1.59 Vitvi03g01347: Type1.0 *

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

Vitvi03g01347

35.2

not assigned.unknown

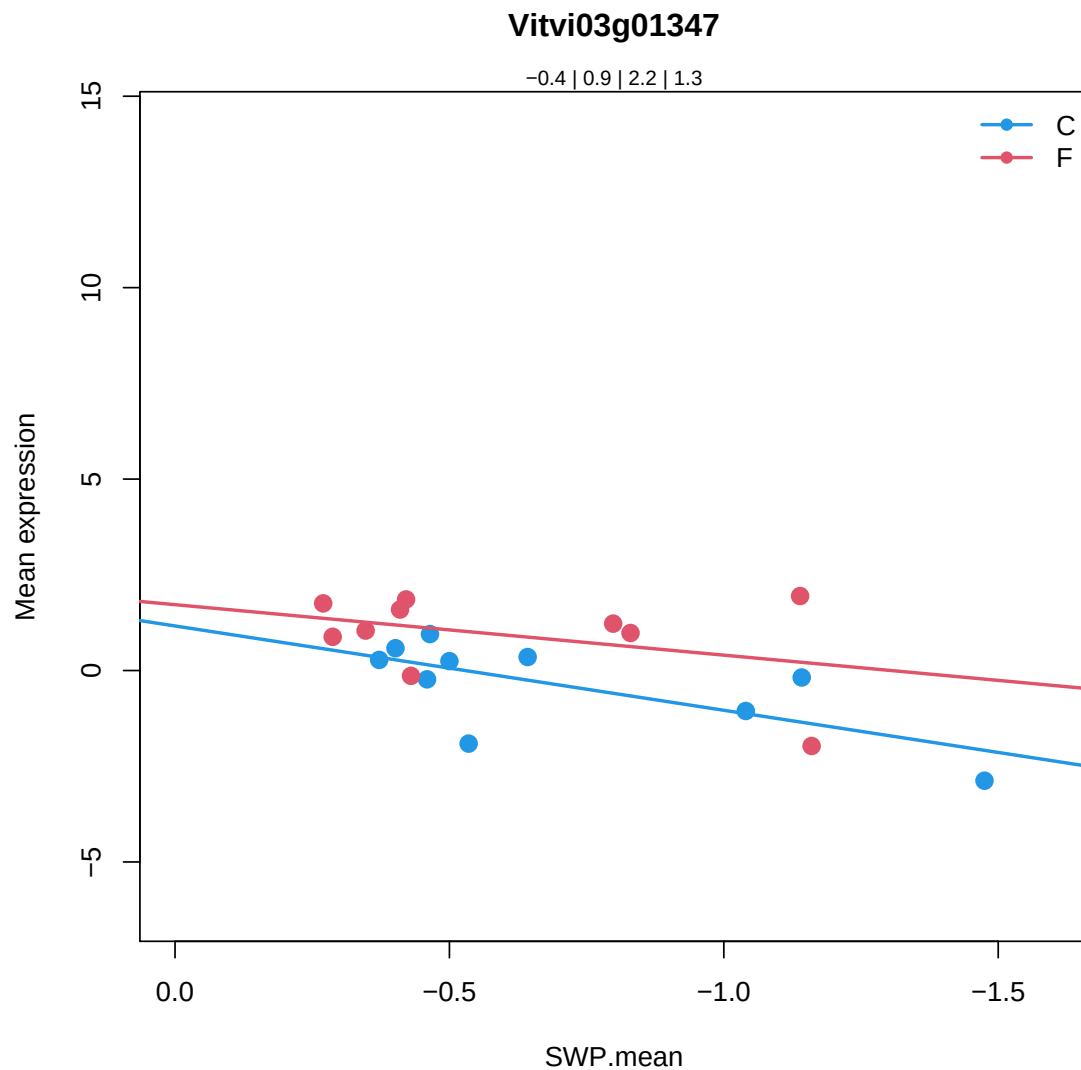
SAUR-like auxin-responsive protein family |

Chr4:16596860-16597144 FORWARD LENGTH=94 |

201606

Coefficients for Vitvi03g01347.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.3848892	0.2099805		0.2151323	
SlopeC	2.202621	0.01454504	*	0.3359386	
MeanF-MeanC	1.301538	0.005454453	**	0.04893277	*
SlopeF-SlopeC	-0.8844935	0.4809727		0.9999488	



8.1.60 Vitvi16g02136: Type1.0 *

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

Vitvi16g02136

35.2

not assigned.unknown

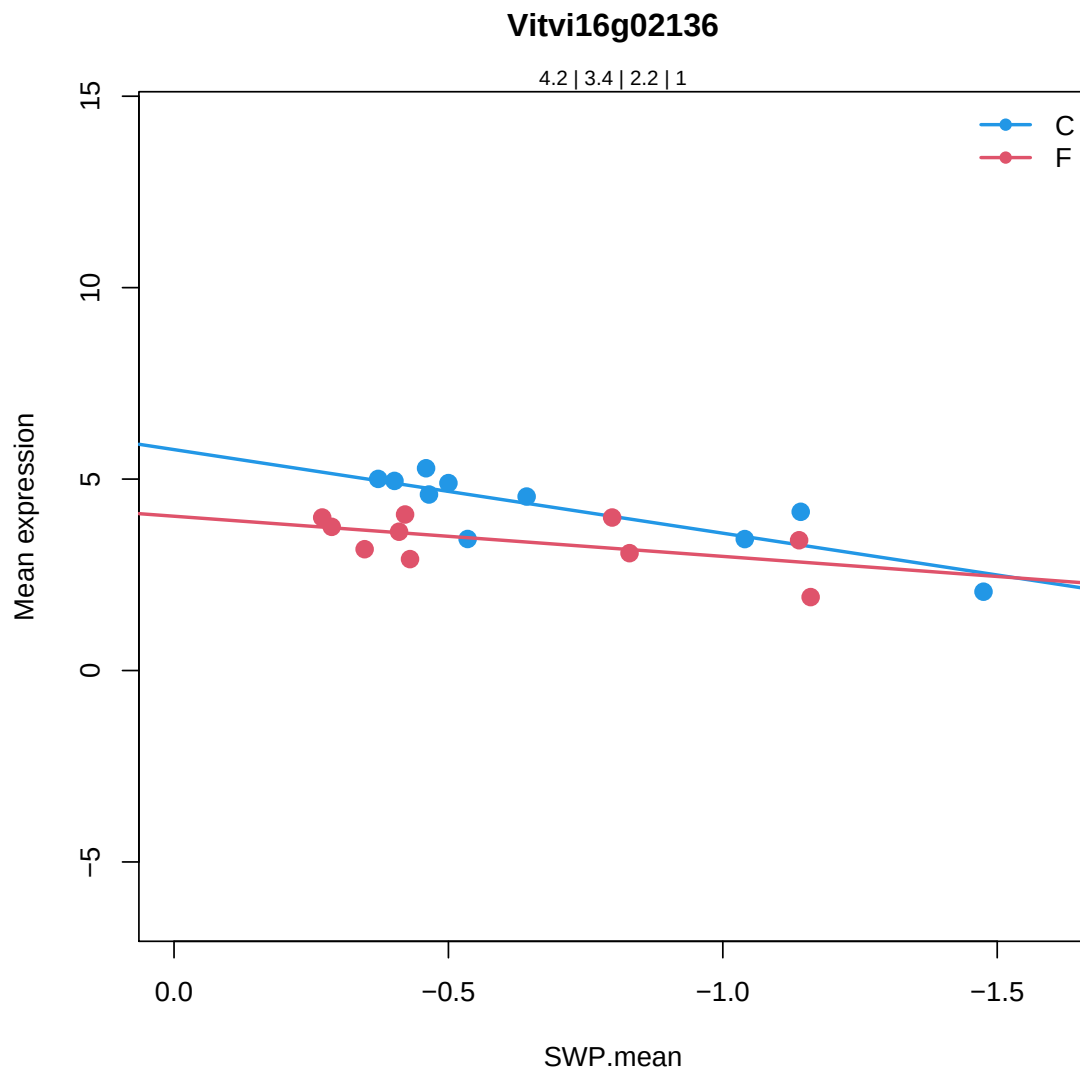
Protein kinase superfamily protein |

Chr1:24961634-24963941 REVERSE LENGTH=663 |

201606

Coefficients for Vitvi16g02136.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.23459	6.924551e-17	***	1.548702e-16	***
SlopeC	2.183464	0.0002382865	***	0.08263916	.
MeanF-MeanC	-0.8438638	0.002994902	**	0.03067762	*
SlopeF-SlopeC	-1.134268	0.1390927		0.9999488	



8.1.61 Vitvi01g02275: Type1.0 *

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

Vitvi01g02275

35.2

not assigned.unknown

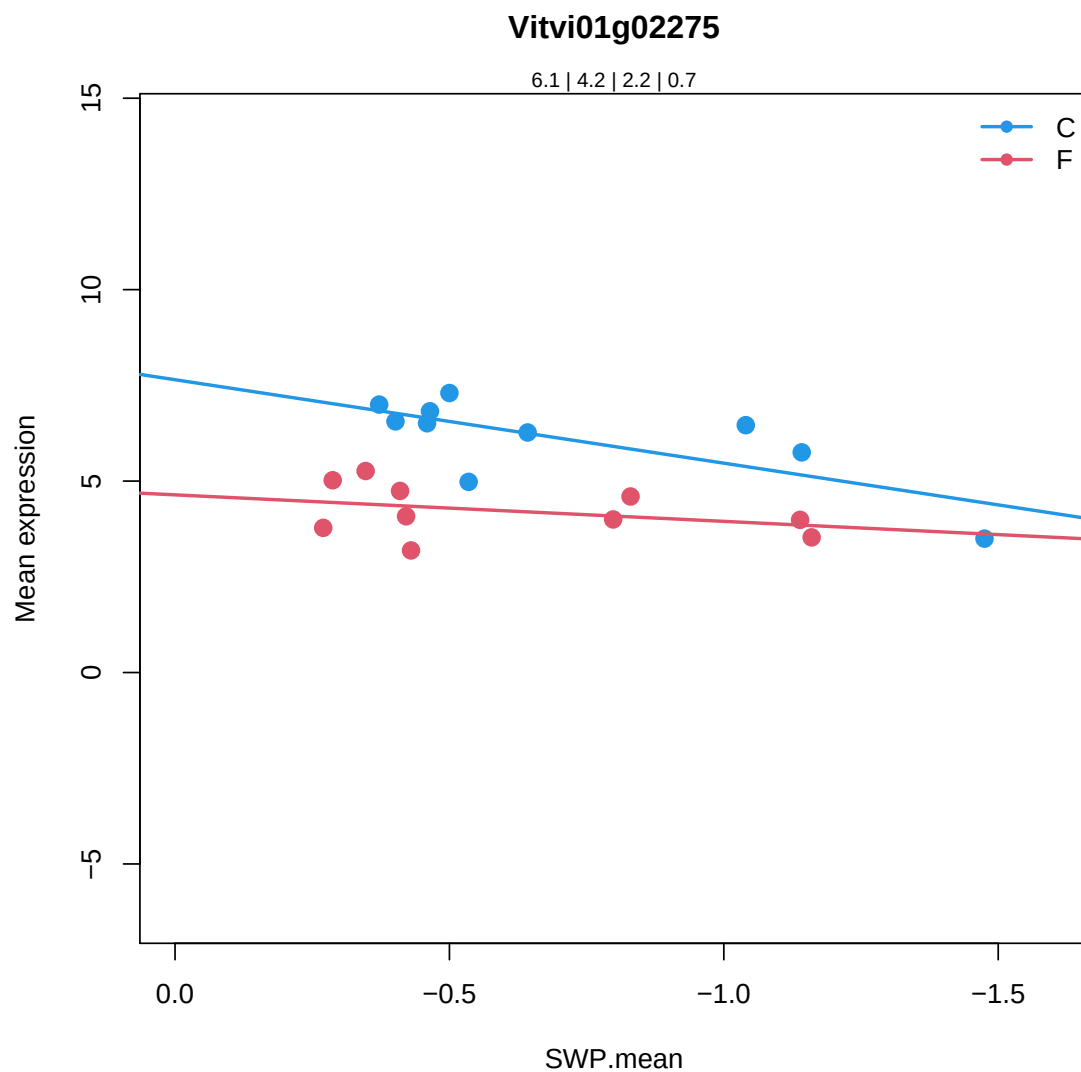
transmembrane protein%2C putative (DUF 3339) |

Chr3:18029659-18030133 FORWARD LENGTH=89 |

201606

Coefficients for Vitvi01g02275.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.114522	2.035831e-18	***	6.413836e-18	***
SlopeC	2.17951	0.001621765	**	0.1556102	
MeanF-MeanC	-1.895997	3.679847e-06	***	0.0001031034	***
SlopeF-SlopeC	-1.48696	0.1130043		0.9999488	



8.1.62 Vitvi16g01932: Type1.0 *

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

Vitvi16g01932

35.2

not assigned.unknown

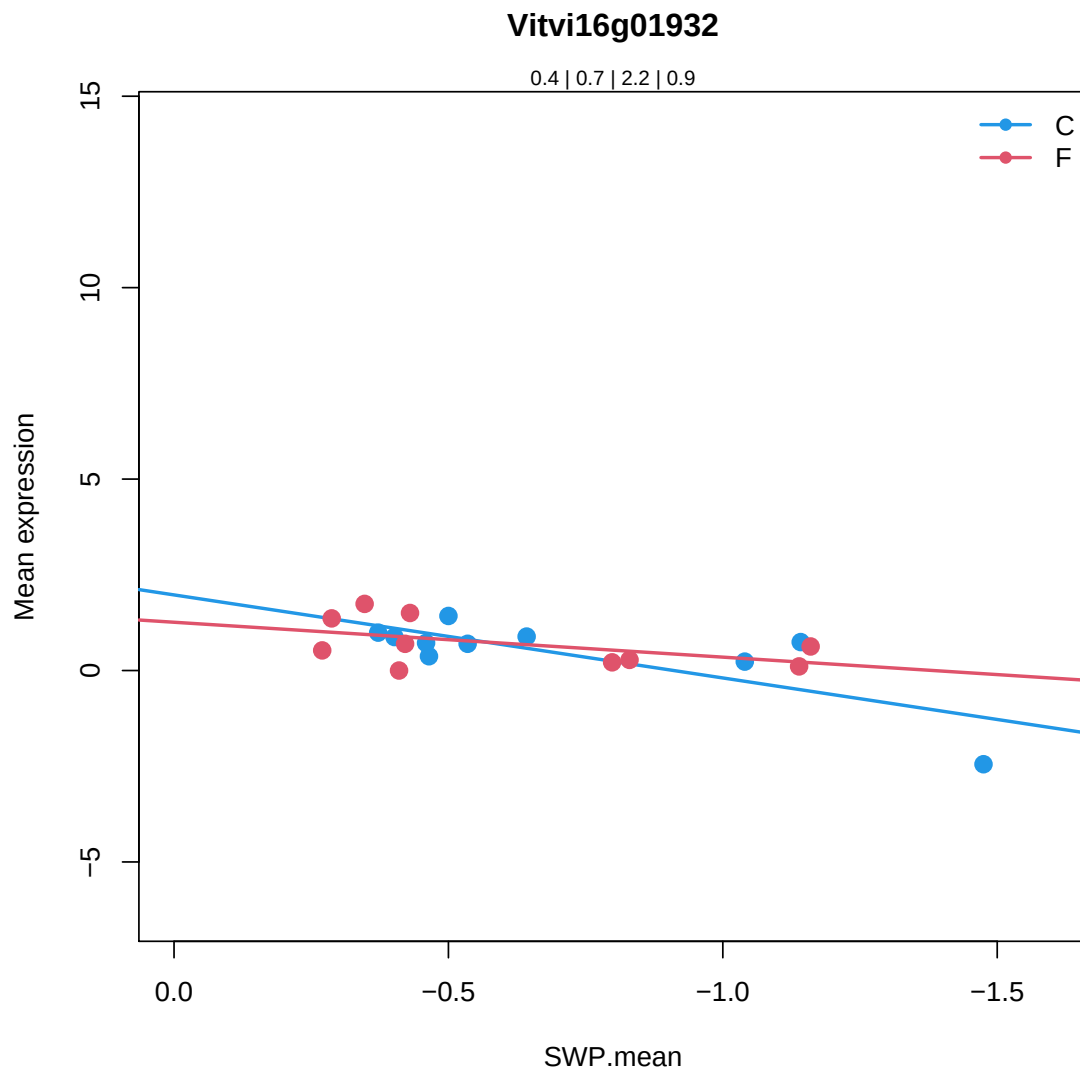
Calcium-dependent lipid-binding (CaLB domain) family protein |

Chr3:5617112-5618194 REVERSE LENGTH=360 |

201606

Coefficients for Vitvi16g01932.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4493167	0.03068247	*	0.03210863	*
SlopeC	2.168808	0.0006072705	***	0.1005065	
MeanF-MeanC	0.2561215	0.361428		0.7197395	
SlopeF-SlopeC	-1.25724	0.1325933		0.9999488	



8.1.63 Vitvi11g00365: Type1.0 *

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

Vitvi11g00365

15.2

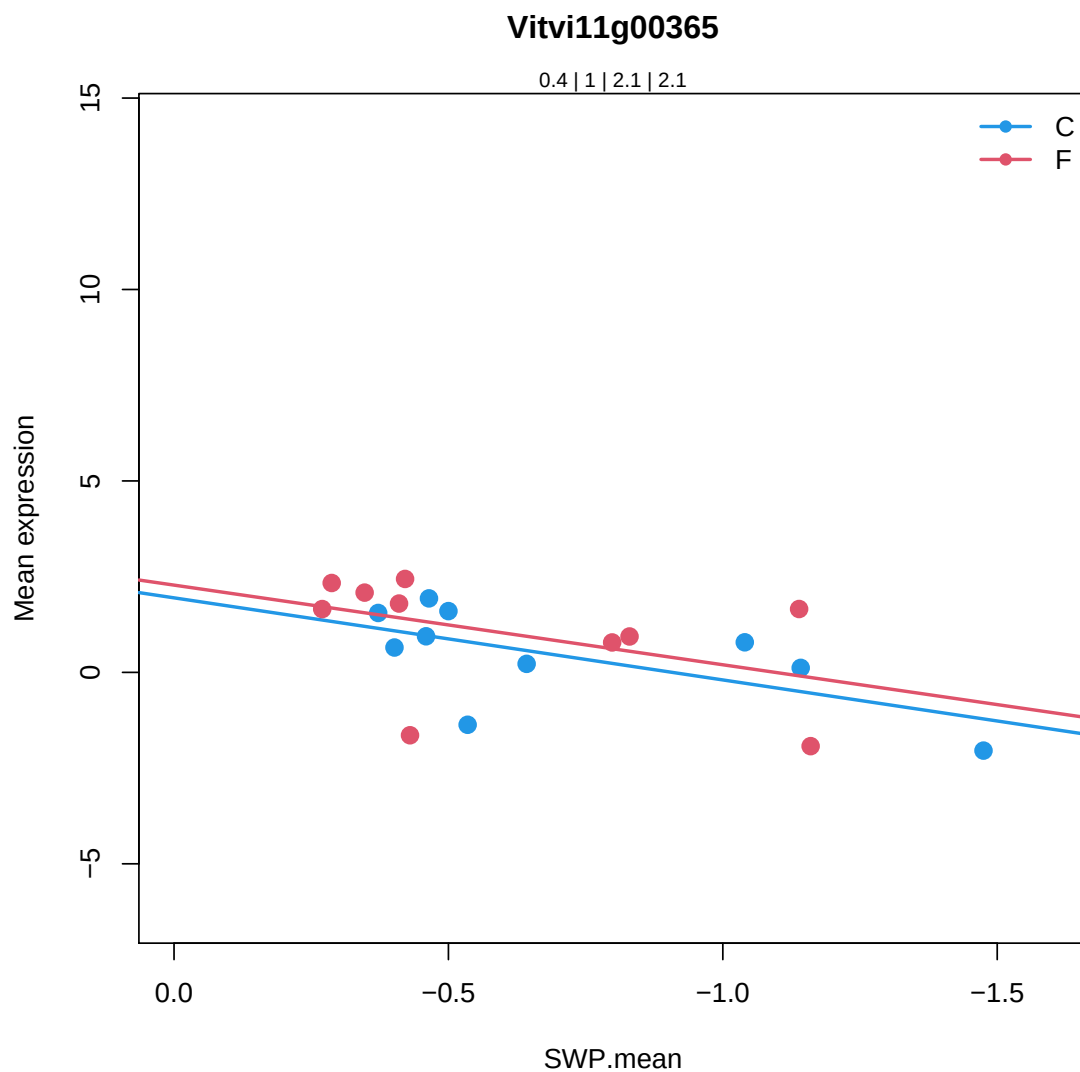
metal handling.binding, chelation and storage

[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	



8.1.64 Vitvi14g01960: Type1.0 *

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

Vitvi14g01960

27.3.25

RNA.regulation of transcription.MYB domain transcription factor family

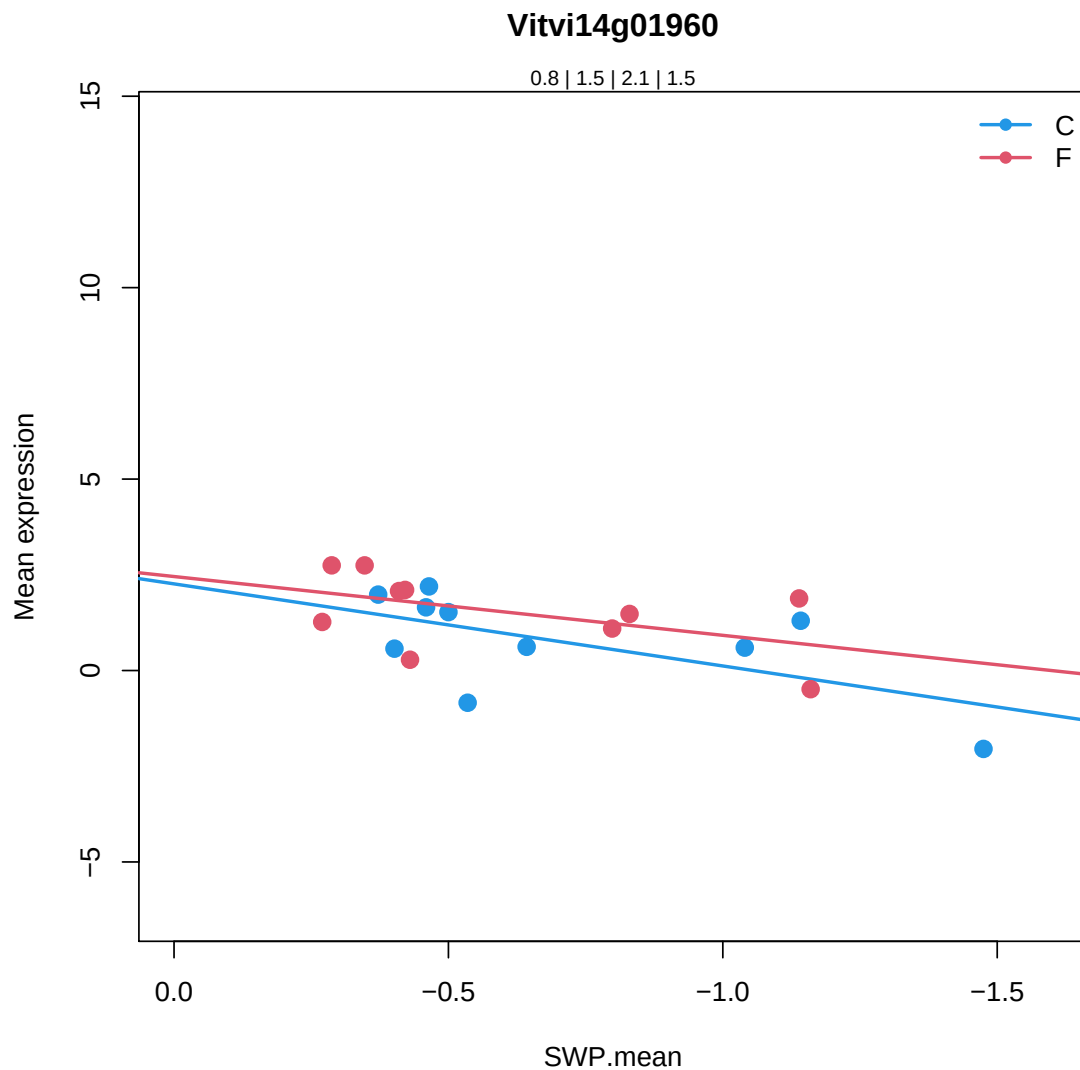
myb domain protein 94 |

Chr3:17539627-17540734 REVERSE LENGTH=327 |

201606

Coefficients for Vitvi14g01960.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.7551105	0.01688501	*	0.01778954	*
SlopeC	2.143962	0.01501475	*	0.3380427	
MeanF-MeanC	0.7640243	0.07760449	.	0.3141693	
SlopeF-SlopeC	-0.6082318	0.61942		0.9999488	



8.1.65 Vitvi18g01735: Type1.0 *

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

Vitvi18g01735

35.2

not assigned.unknown

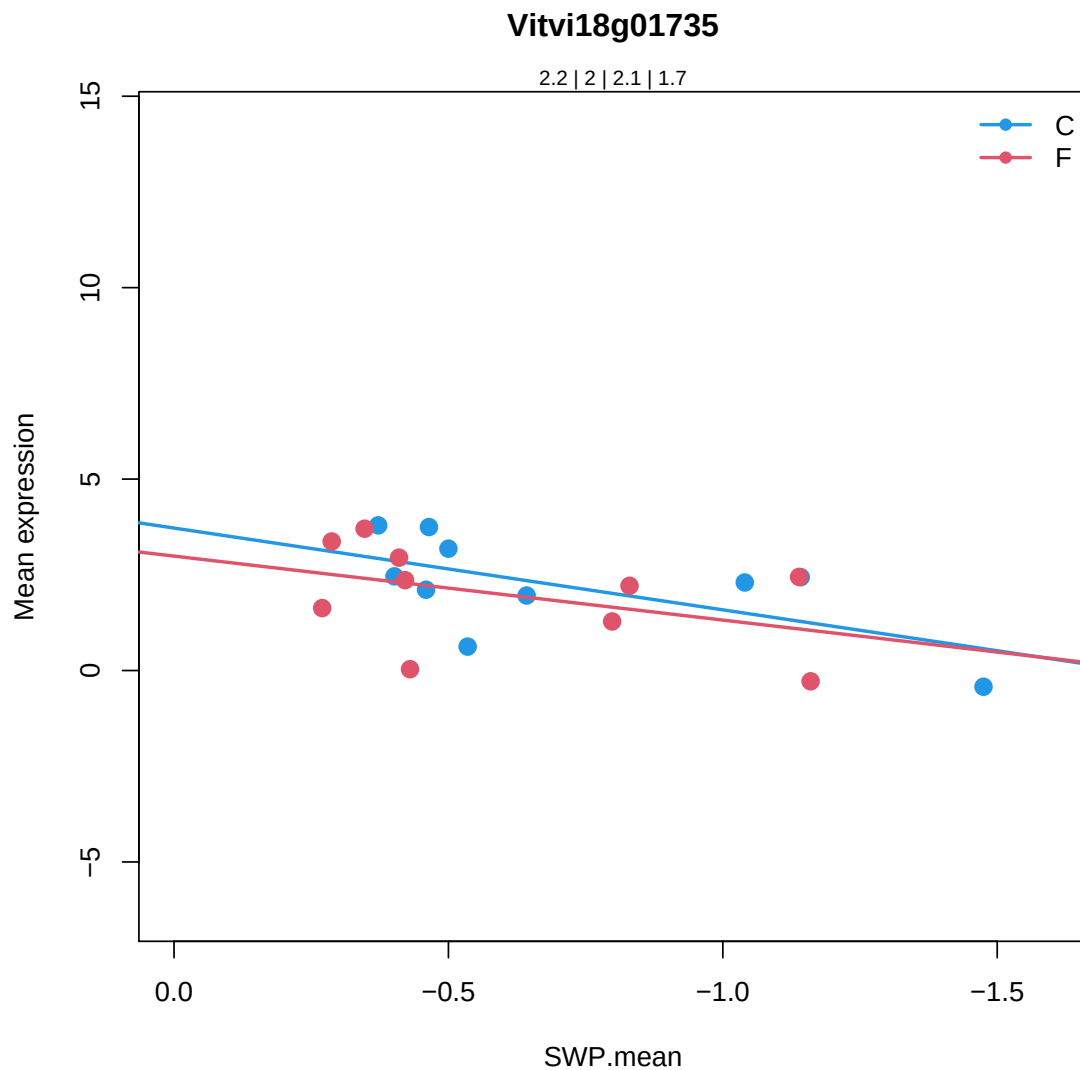
hypothetical protein |

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	



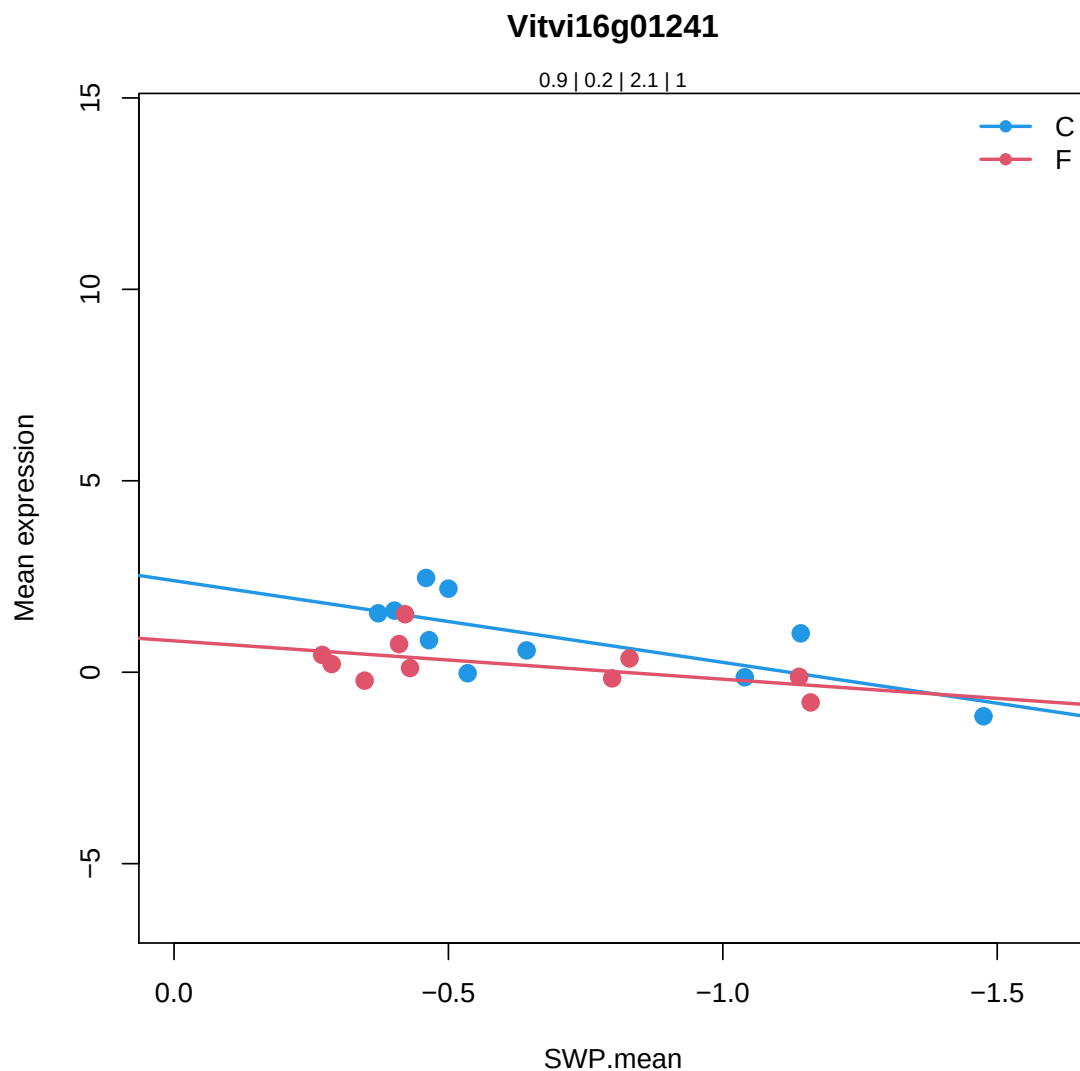
8.1.66 Vitvi16g01241: Type1.0 *

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

```
Vitvi16g01241
35.2
not assigned.unknown
Receptor-like kinase
```

Coefficients for Vitvi16g01241.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8902816	0.000291581	***	0.0003189291	***
SlopeC	2.133483	0.00123368	**	0.1365704	
MeanF-MeanC	-0.6808863	0.02931937	*	0.1663141	
SlopeF-SlopeC	-1.131978	0.1988273		0.9999488	



8.1.67 Vitvi14g01967: Type1.0 *

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

Vitvi14g01967

29.2.1.2.2.34

protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L34

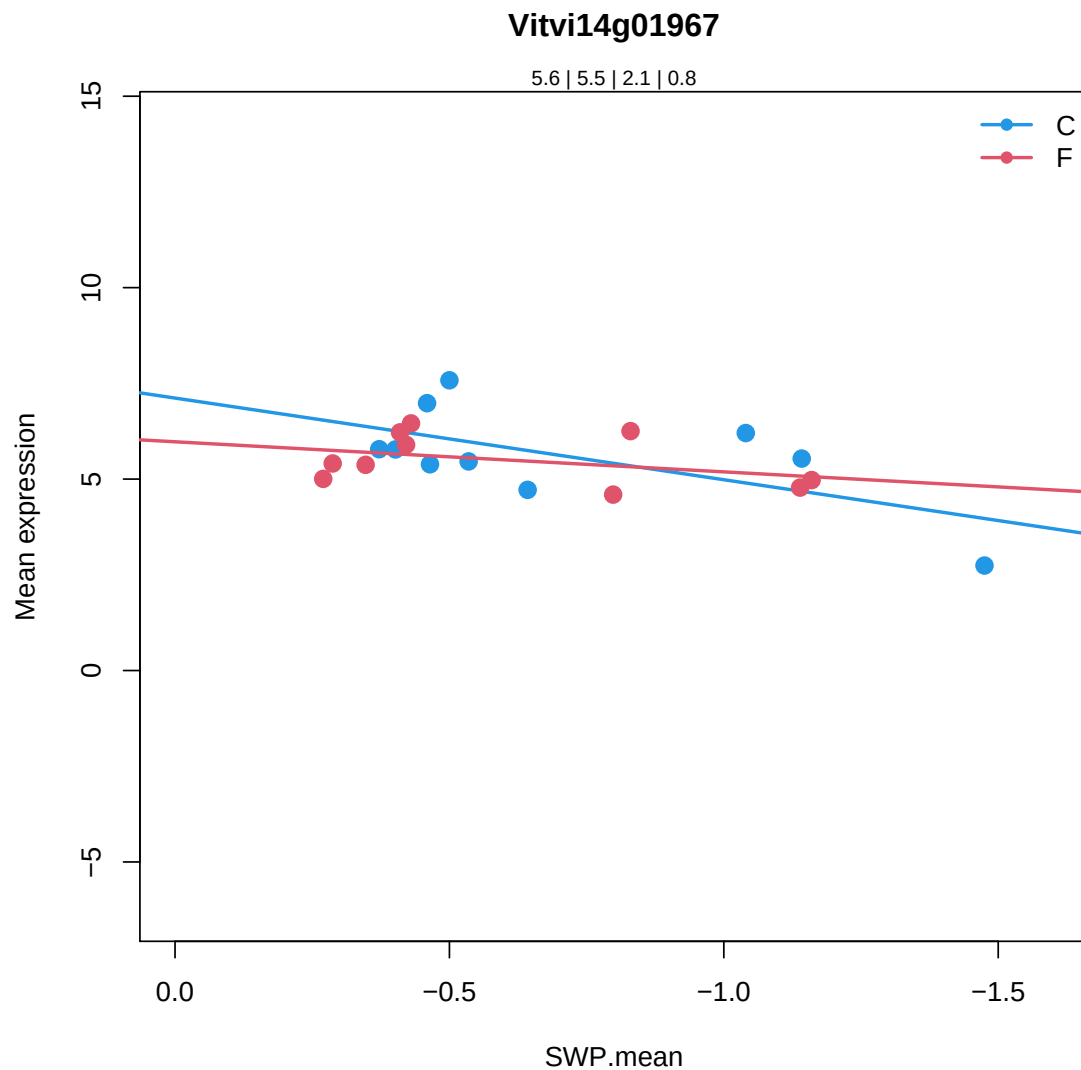
transmembrane protein |

Chr3:59484-62202 FORWARD LENGTH=577 |

201606

Coefficients for Vitvi14g01967.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.616174	3.638103e-16	***	7.243889e-16	***
SlopeC	2.132616	0.00685747	**	0.2765121	
MeanF-MeanC	-0.1209943	0.7417406		0.9235101	
SlopeF-SlopeC	-1.346918	0.2179593		0.9999488	



8.1.68 Vitvi15g00812: Type1.0 *

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

Vitvi15g00812

26.7

misc.oxidases - copper, flavone etc

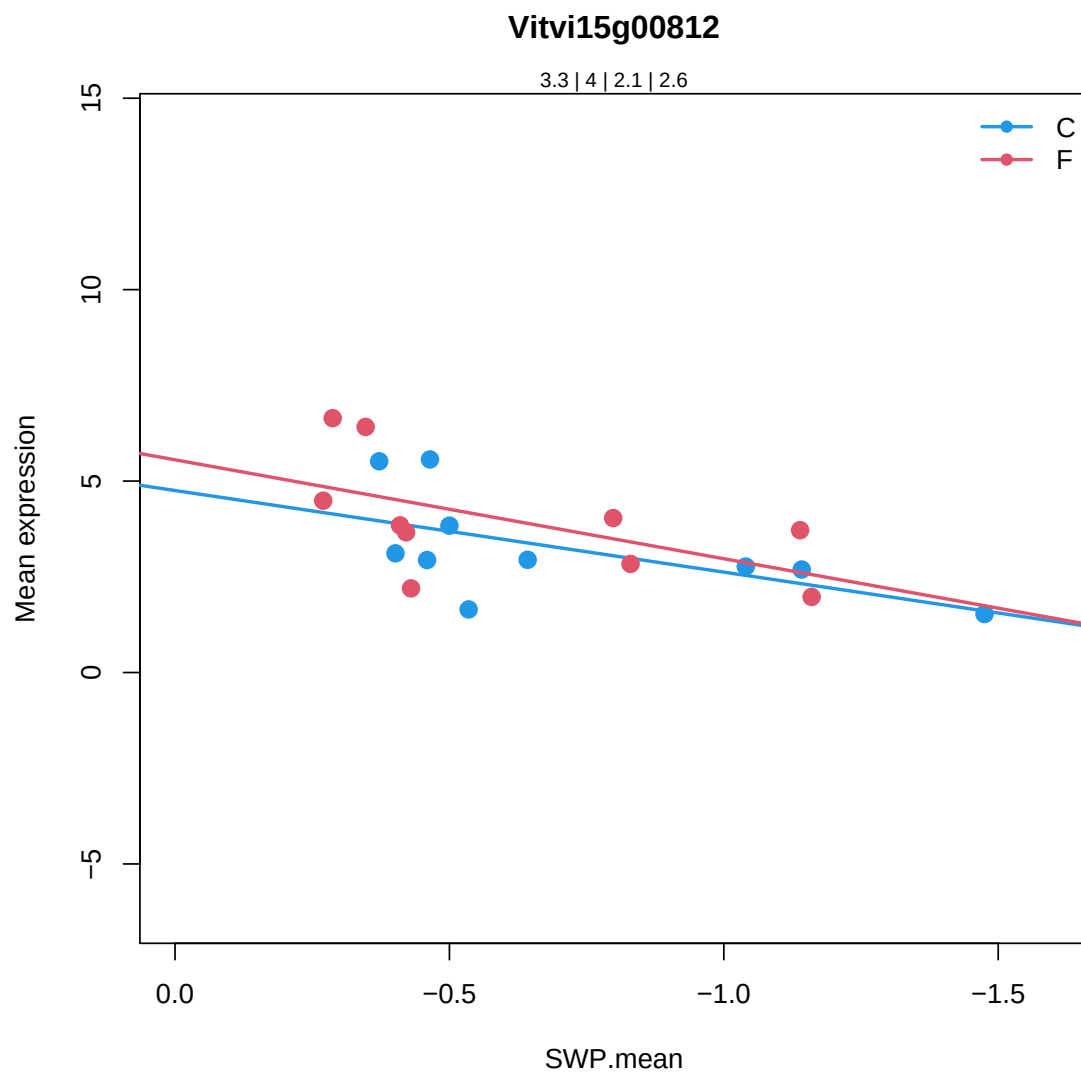
Oxidoreductase%2C zinc-binding dehydrogenase family protein |

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	



8.1.69 Vitvi08g00886: Type1.0

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

Vitvi08g00886

15.2

metal handling.binding, chelation and storage

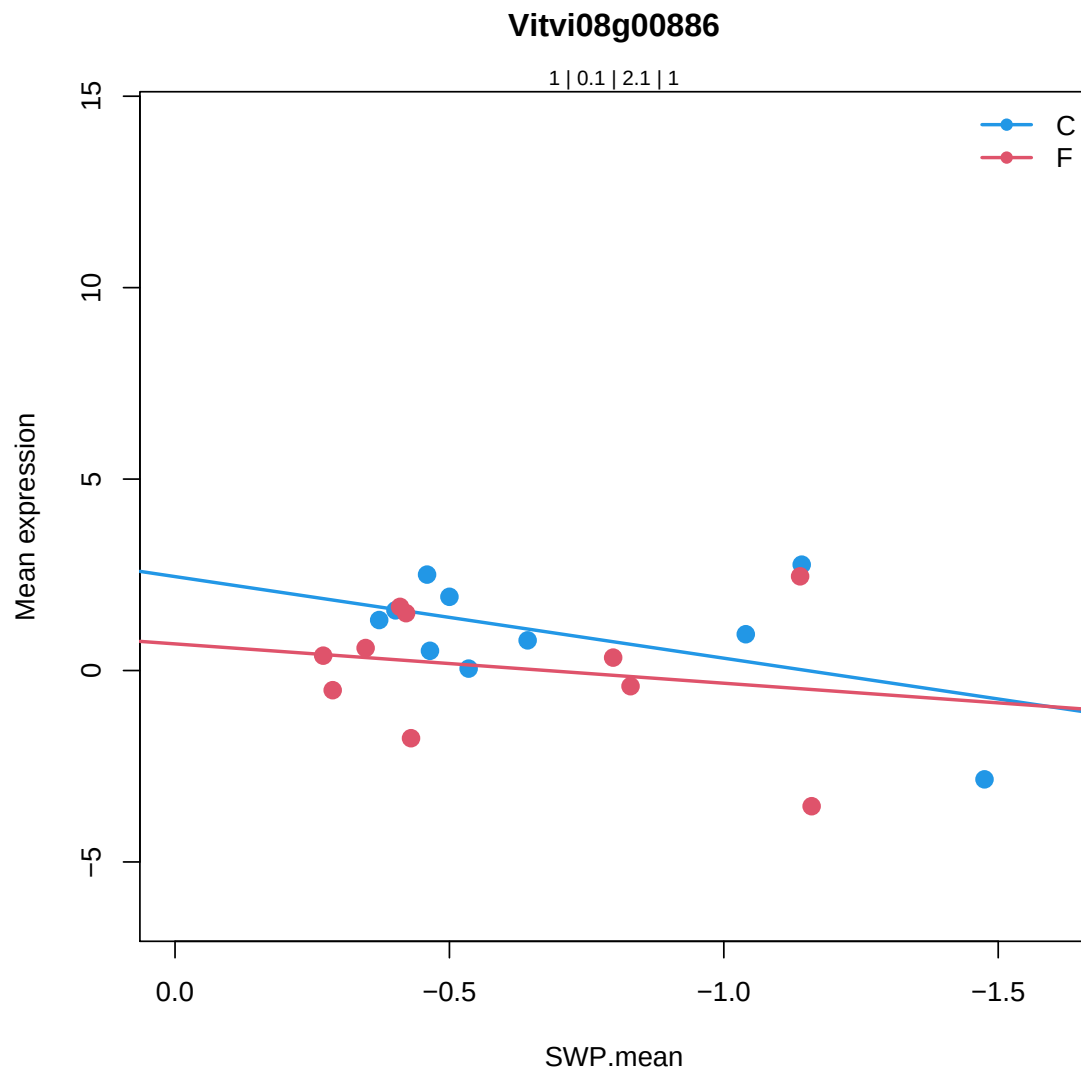
Heavy metal transport/detoxification superfamily protein |

Chr3:21064199-21064922 REVERSE LENGTH=166 |

201606

Coefficients for Vitvi08g00886.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.9541938	0.04859923	*	0.05061493	.
SlopeC	2.131099	0.1077369		0.6223948	
MeanF-MeanC	-0.8845265	0.1846603		0.5211243	
SlopeF-SlopeC	-1.104132	0.5650905		0.9999488	



8.1.70 Vitvi18g00882: Type1.0 *

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

Vitvi18g00882

30.5

signalling.G-proteins

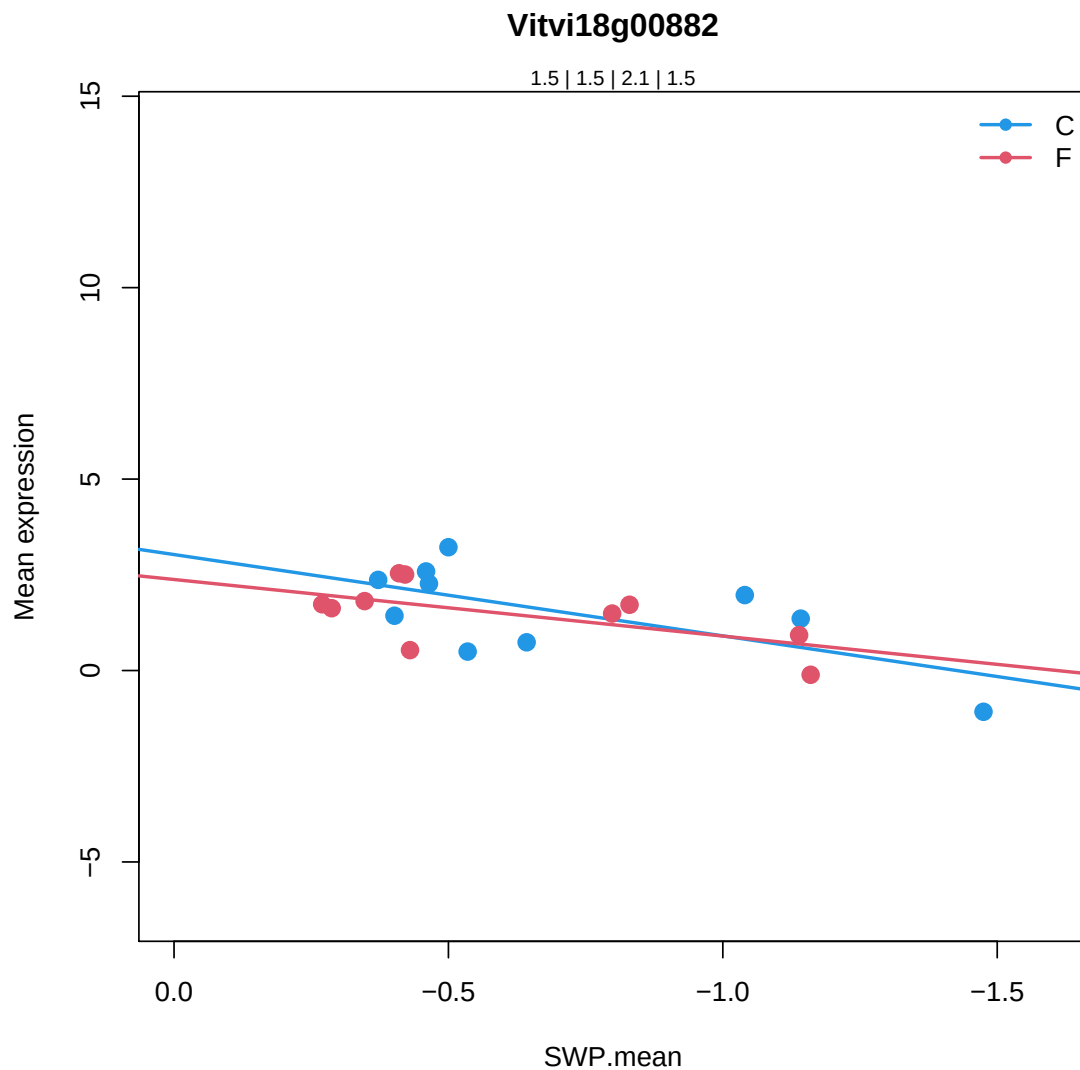
Transducin/WD40 repeat-like superfamily protein |

Chr2:11268035-11269432 FORWARD LENGTH=465 |

201606

Coefficients for Vitvi18g00882.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.535236	3.692787e-06	***	4.209203e-06	***
SlopeC	2.123839	0.005756511	**	0.2626746	
MeanF-MeanC	-0.05830412	0.8699959		0.9657933	
SlopeF-SlopeC	-0.6461071	0.5373577		0.9999488	



8.1.71 Vitvi19g00041: Type1.0

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

Vitvi19g00041

35.2

not assigned.unknown

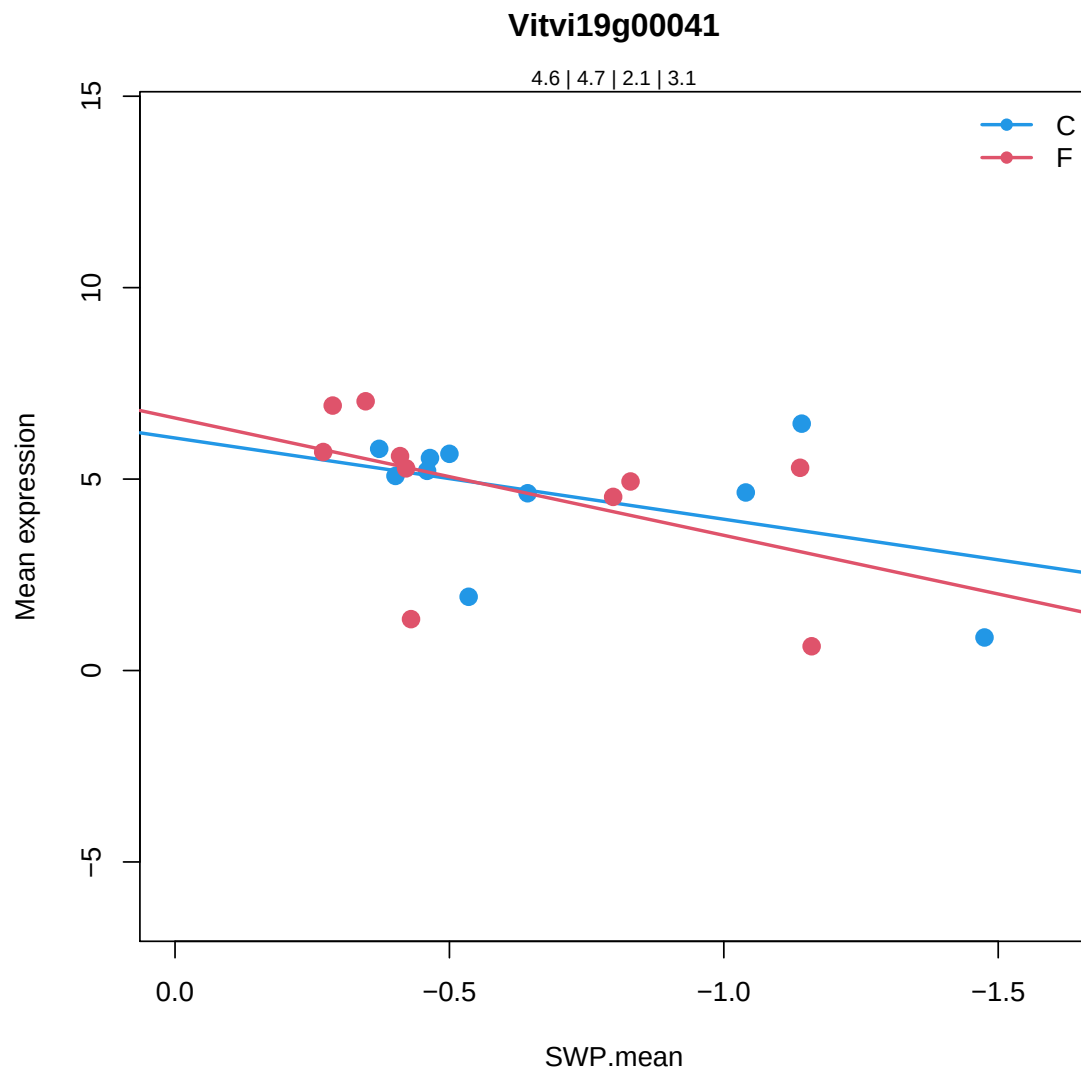
TRICHOME BIREFRINGENCE-LIKE 42 |

Chr1:29602708-29604557 FORWARD LENGTH=359 |

201606

Coefficients for Vitvi19g00041.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.581181	8.893459e-09	***	1.087042e-08	***
SlopeC	2.121266	0.1463336		0.6722139	
MeanF-MeanC	0.1469577	0.8391785		0.9568387	
SlopeF-SlopeC	0.942772	0.6571693		0.9999488	



8.1.72 Vitvi13g02129: Type1.0

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

Vitvi13g02129

26.28

misc.GDSL-motif lipase

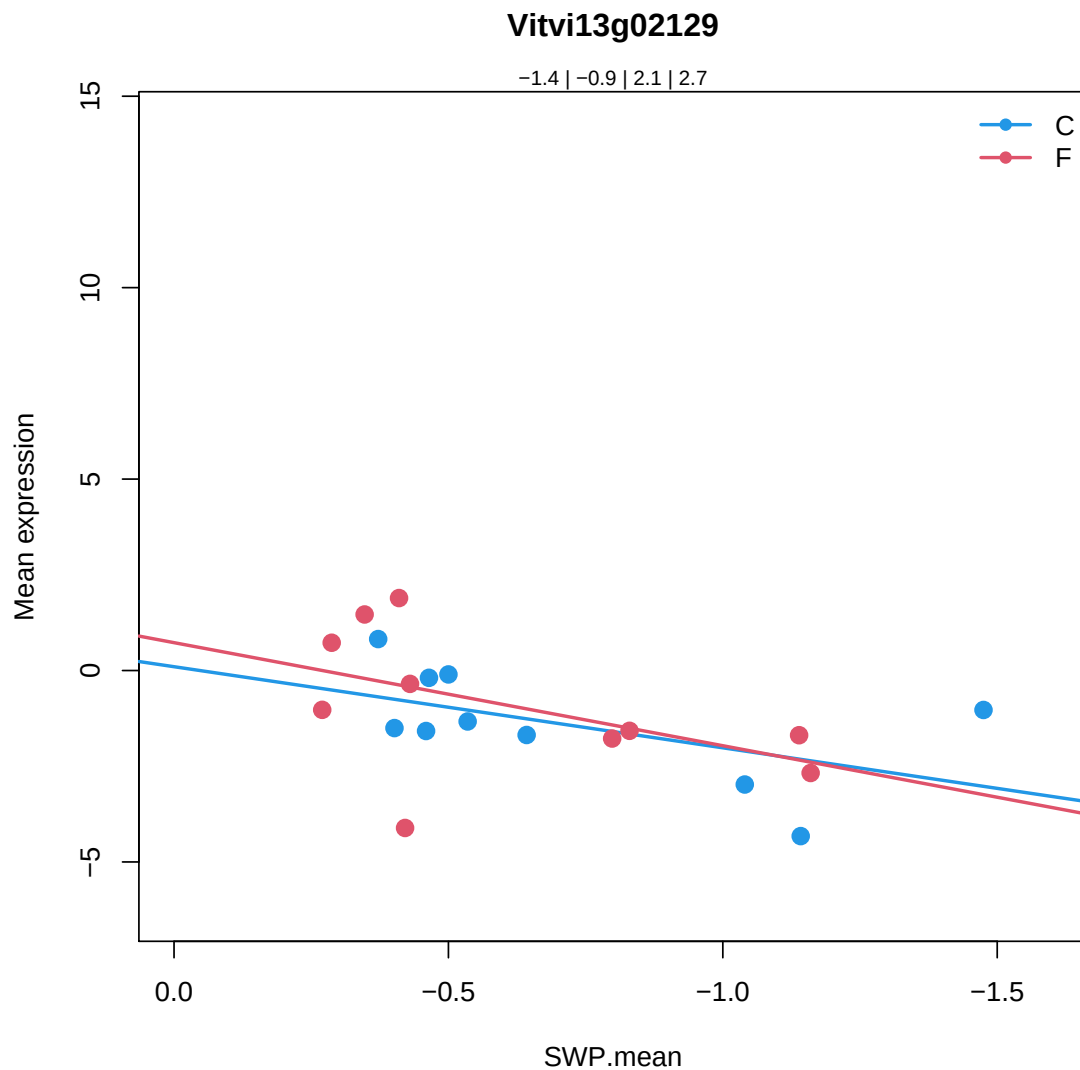
GDSL-like Lipase/Acylhydrolase superfamily protein |

Chr5:915650-918326 FORWARD LENGTH=359 |

201606

Coefficients for Vitvi13g02129.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.390348	0.003622918	**	0.003875668	**
SlopeC	2.118294	0.08785555	.	0.5932372	
MeanF-MeanC	0.477883	0.4360649		0.7679378	
SlopeF-SlopeC	0.5732464	0.7482085		0.9999488	



8.1.73 Vitvi16g02117: Type1.0 *

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

Vitvi16g02117

35.2

not assigned.unknown

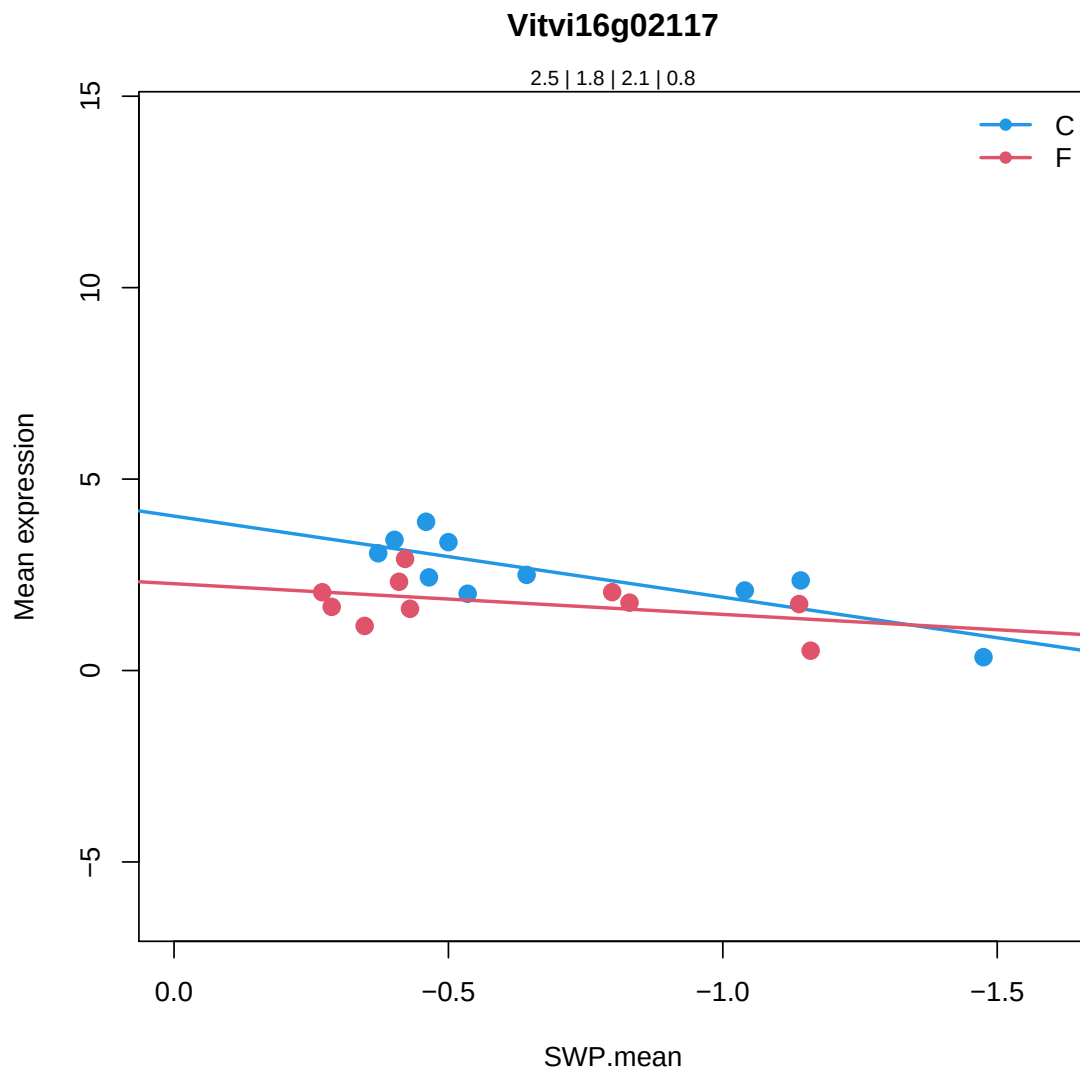
PR5-like receptor kinase |

Chr5:15293325-15295838 REVERSE LENGTH=665 |

201606

Coefficients for Vitvi16g02117.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.543924	4.528003e-12	***	6.26676e-12	***
SlopeC	2.118243	0.0004980193	***	0.1005065	
MeanF-MeanC	-0.7651143	0.008241535	**	0.06594094	.
SlopeF-SlopeC	-1.317351	0.1013931		0.9999488	



8.1.74 Vitvi10g02253: Type1.0 *

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

Vitvi10g02253

27.3.6

RNA.regulation of transcription.basic helix-loop-helix family (bHLH)

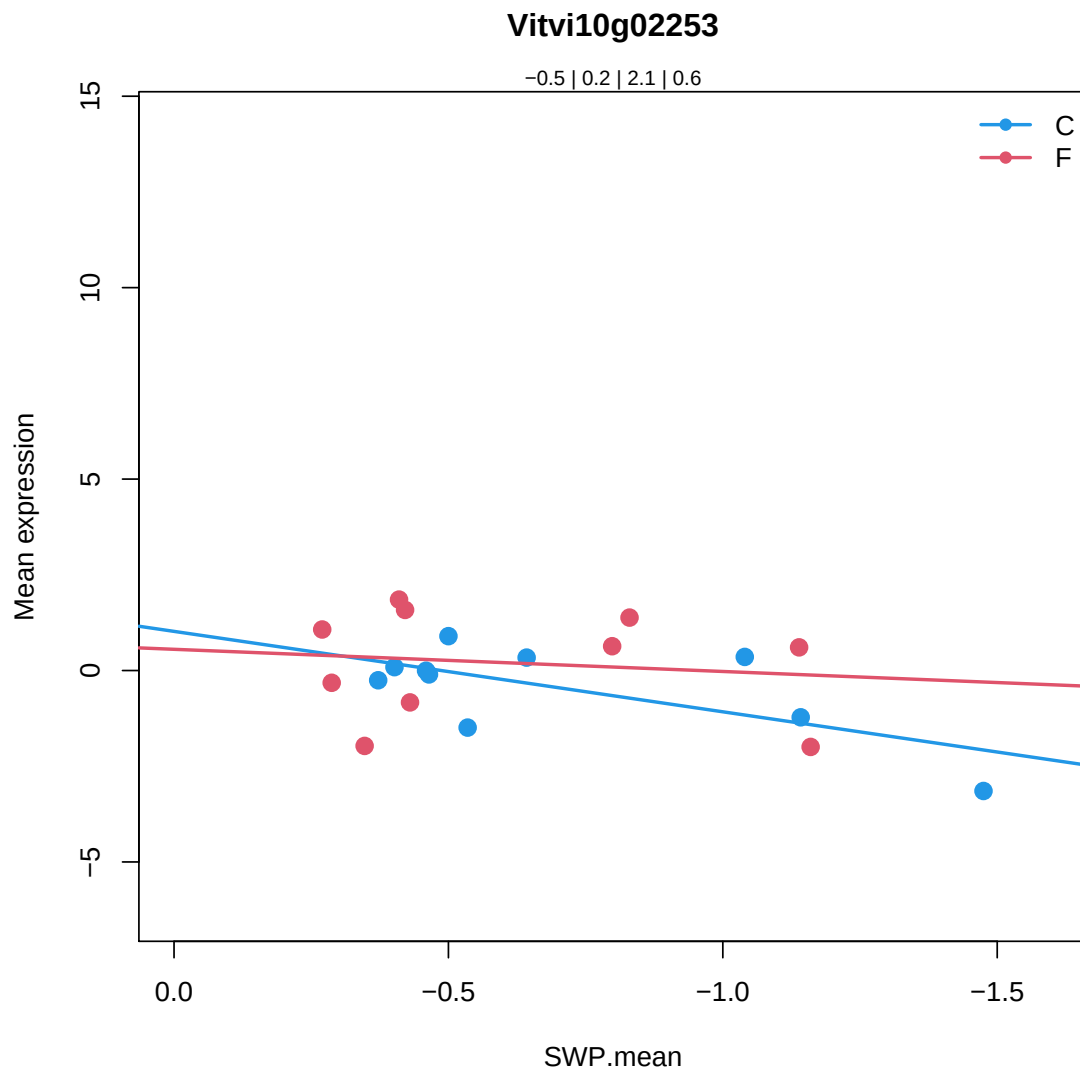
basic helix-loop-helix (bHLH) DNA-binding superfamily protein |

Chr4:11215259-11216212 FORWARD LENGTH=190 |

201606

Coefficients for Vitvi10g02253.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.4545124	0.2051877		0.2103208	
SlopeC	2.100408	0.04134974	*	0.4793992	
MeanF-MeanC	0.6555258	0.1966777		0.5382943	
SlopeF-SlopeC	-1.52142	0.3026188		0.9999488	



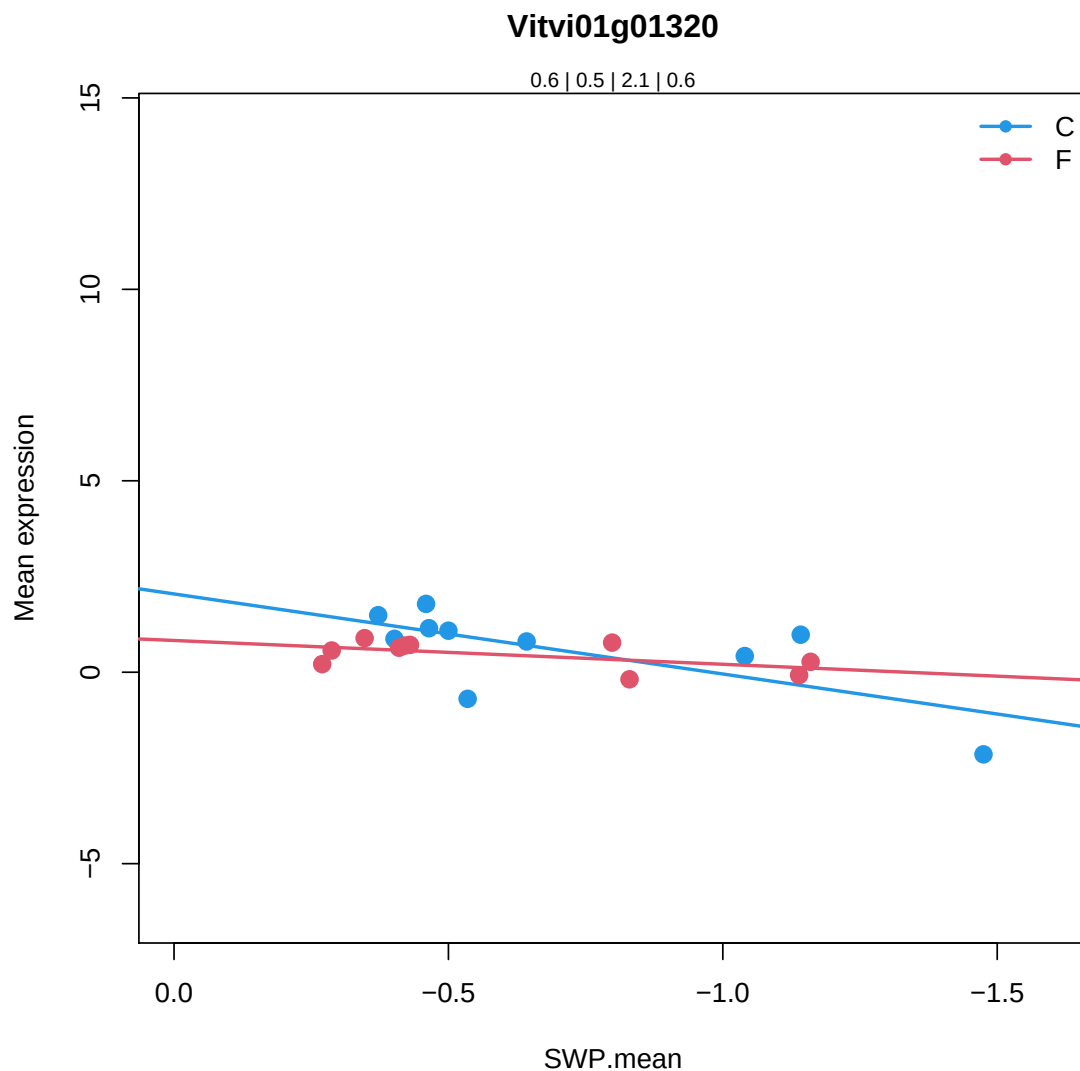
8.1.75 Vitvi01g01320: Type1.0 *

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

```
Vitvi01g01320
35.2
not assigned.unknown
Unknown Protein
```

Coefficients for Vitvi01g01320.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.574494	0.009512857	**	0.010081	*
SlopeC	2.09098	0.001215895	**	0.1365704	
MeanF-MeanC	-0.124207	0.6676597		0.8914216	
SlopeF-SlopeC	-1.469346	0.09285893	.	0.9999488	



8.1.76 Vitvi15g00617: Type1.0 *

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

Vitvi15g00617

35.2

not assigned.unknown

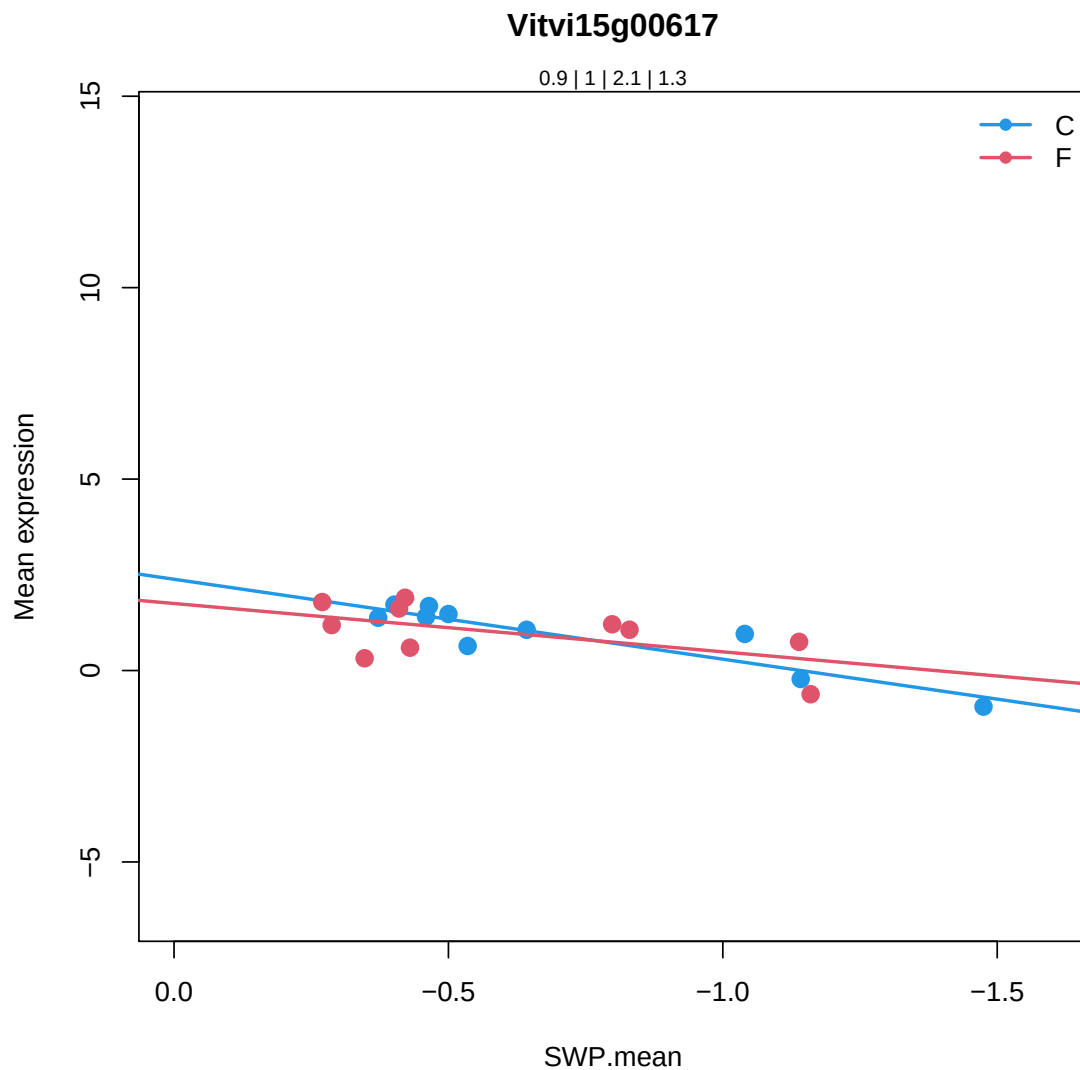
zinc ion-binding protein |

Chr3:22361751-22362323 REVERSE LENGTH=118 |

201606

Coefficients for Vitvi15g00617.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.915899	1.934159e-05	***	2.169275e-05	***
SlopeC	2.087425	0.0002036597	***	0.08109226	.
MeanF-MeanC	0.06515175	0.7865075		0.9397152	
SlopeF-SlopeC	-0.8251147	0.2484975		0.9999488	



8.1.77 Vitvi15g00641: Type1.0

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

Vitvi15g00641

31.3

cell.cycle

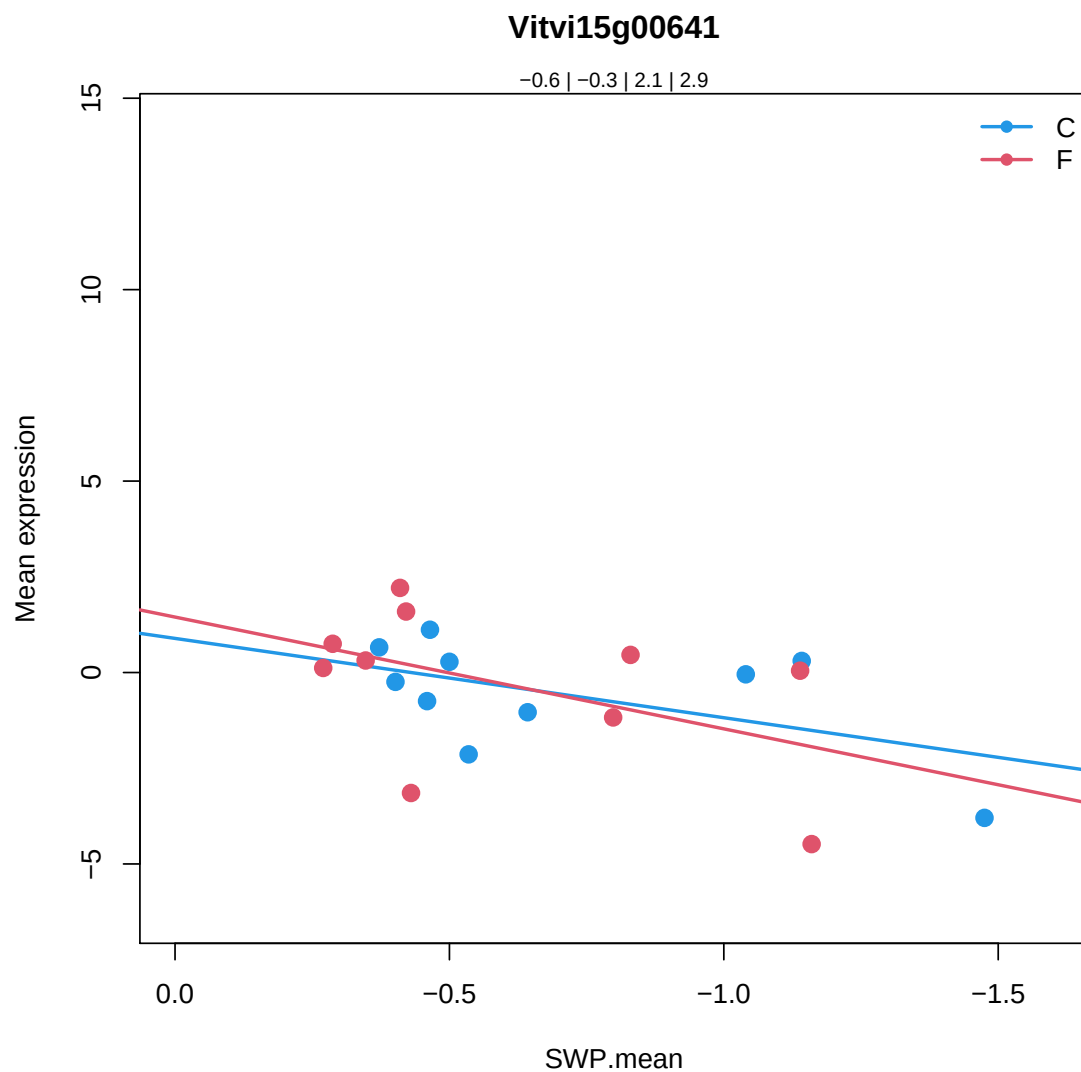
cyclin p3%3B1 |

Chr2:18591688-18592443 FORWARD LENGTH=222 |

201606

Coefficients for Vitvi15g00641.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.565473	0.2284777		0.2338004	
SlopeC	2.071382	0.1172227		0.6341652	
MeanF-MeanC	0.2347244	0.719514		0.9141312	
SlopeF-SlopeC	0.847936	0.6579831		0.9999488	



8.1.78 Vitvi19g02292: Type1.0 *

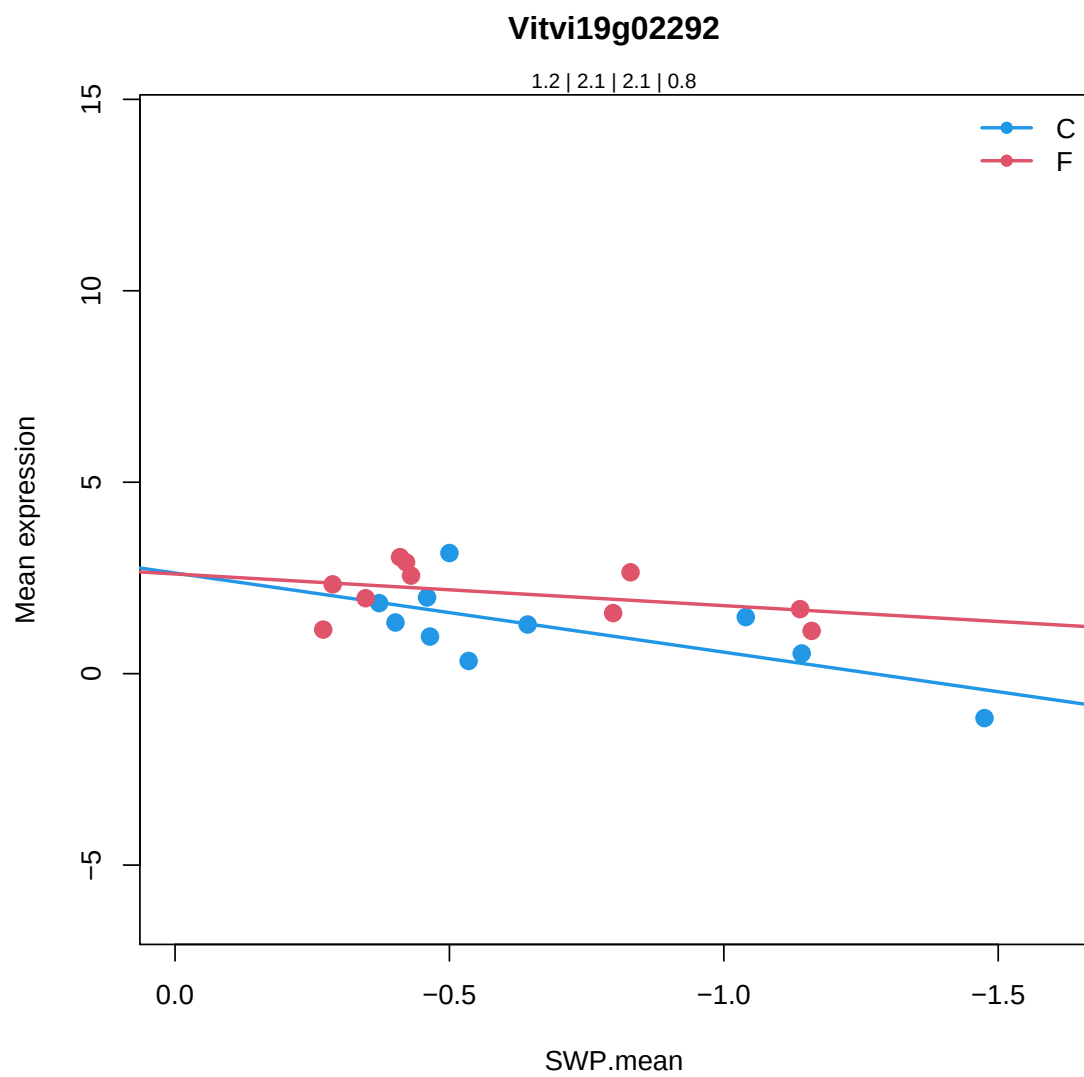
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi19g02292
  30.2.99
  signalling.receptor kinases.misc
  receptor like protein 34 |
  Chr3:3450988-3453861 REVERSE LENGTH=957 |
  201606
```

```
Vitvi19g02292
  20.1.2
  stress.biotic.receptors
  receptor like protein 34 |
  Chr3:3450988-3453861 REVERSE LENGTH=957 |
  201606
```

Coefficients for Vitvi19g02292.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.174513	4.198572e-05	***	4.671823e-05	***
SlopeC	2.066362	0.003839738	**	0.2269459	
MeanF-MeanC	0.9249743	0.009378075	**	0.0724851	.
SlopeF-SlopeC	-1.239063	0.2054939		0.9999488	



8.1.79 Vitvi16g01239: Type1.0 *

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

Vitvi16g01239

35.2

not assigned.unknown

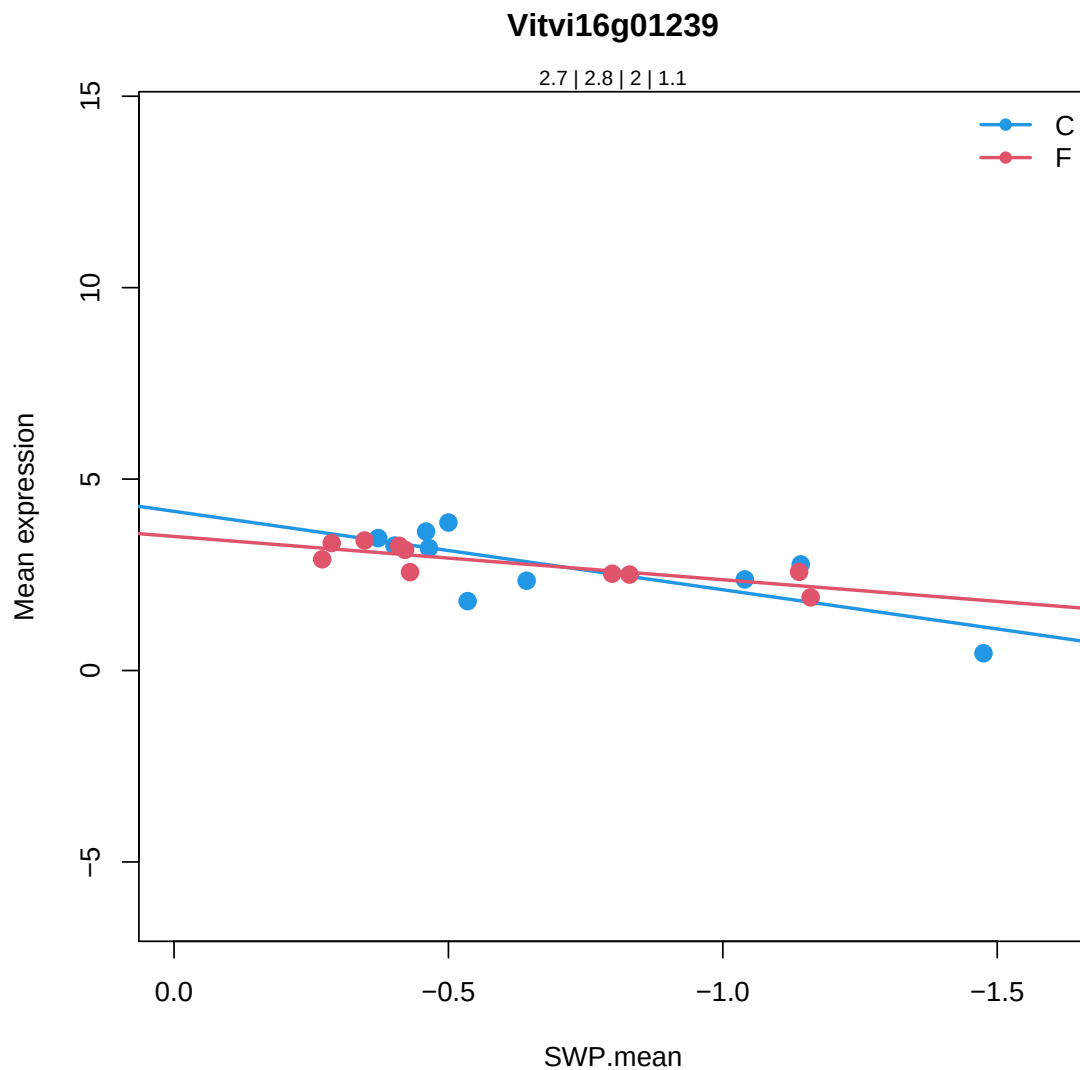
PR5-like receptor kinase |

Chr5:15293325-15295838 REVERSE LENGTH=665 |

201606

Coefficients for Vitvi16g01239.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.717611	1.58588e-13	***	2.399205e-13	***
SlopeC	2.047716	0.0002409246	***	0.08263916	.
MeanF-MeanC	0.09525423	0.691383		0.9015976	
SlopeF-SlopeC	-0.9169868	0.1997844		0.9999488	



8.1.80 Vitvi15g00537: Type1.0 *

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

Vitvi15g00537

31.3

cell.cycle

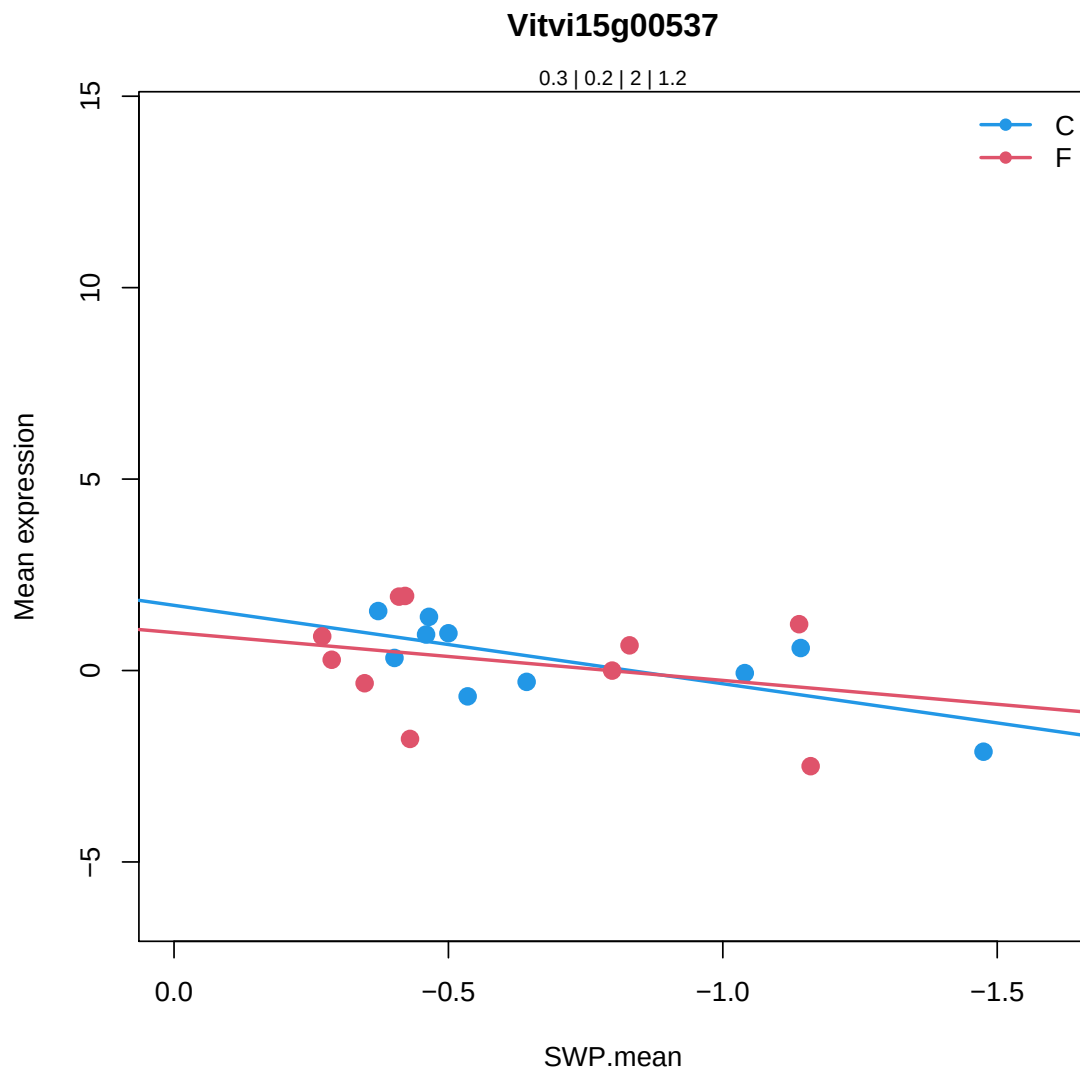
cyclin p4%3B1 |

Chr2:18442287-18443304 REVERSE LENGTH=202 |

201606

Coefficients for Vitvi15g00537.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.262389	0.4465972		0.4527459	
SlopeC	2.047416	0.04098653	*	0.477587	
MeanF-MeanC	-0.03238648	0.9466744		0.986373	
SlopeF-SlopeC	-0.798659	0.5746443		0.9999488	



8.1.81 Vitvi16g02100: Type1.0 *

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

Vitvi16g02100

35.2

not assigned.unknown

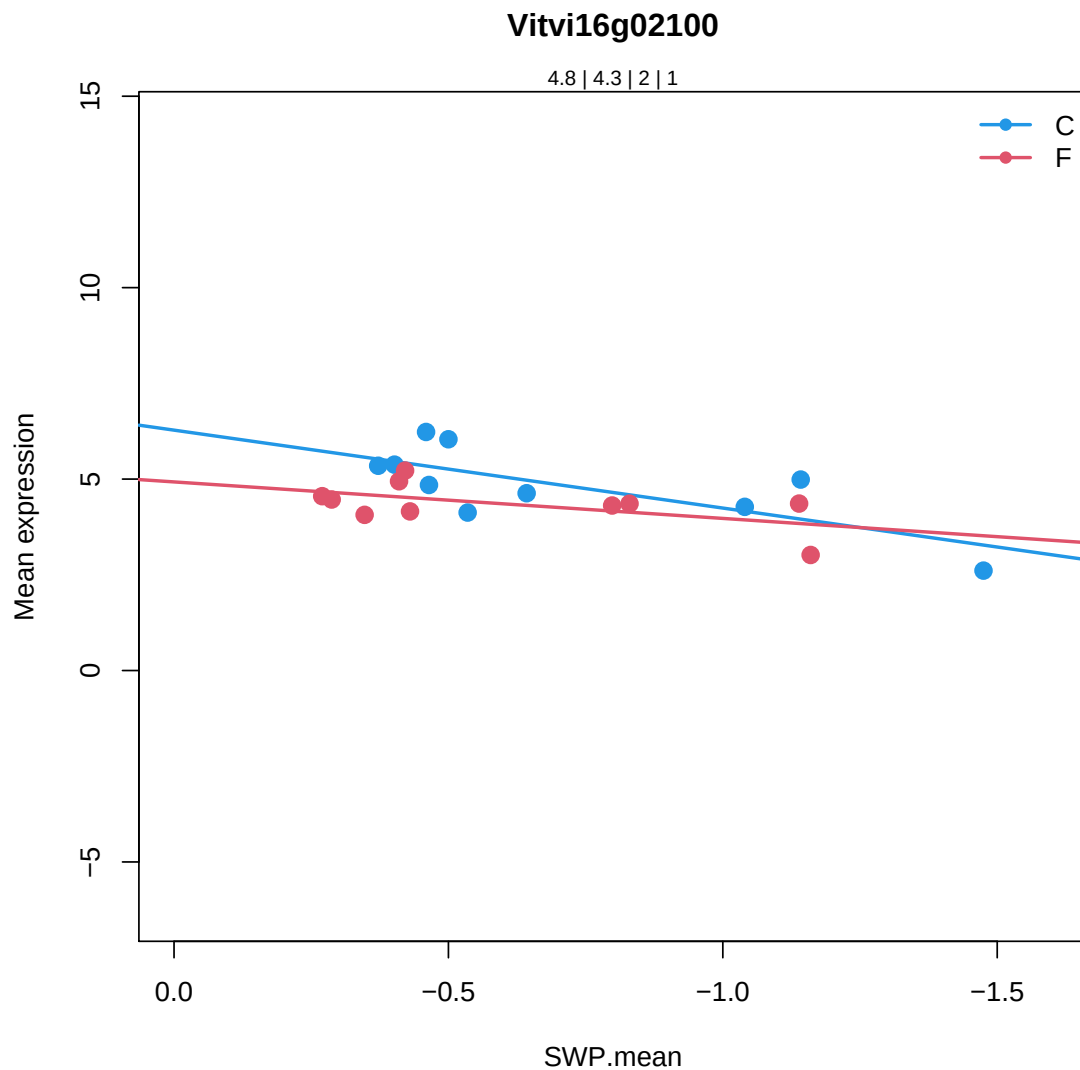
PR5-like receptor kinase |

Chr5:15293325-15295838 REVERSE LENGTH=665 |

201606

Coefficients for Vitvi16g02100.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.846865	1.805215e-17	***	4.51437e-17	***
SlopeC	2.035174	0.0009585373	***	0.1259485	
MeanF-MeanC	-0.5019092	0.07732123	.	0.313753	
SlopeF-SlopeC	-1.081723	0.1861631		0.9999488	



8.1.82 Vitvi07g02226: Type1.0 *

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

Vitvi07g02226

10.6.3

cell wall.degradation.pectate lyases and polygalacturonases

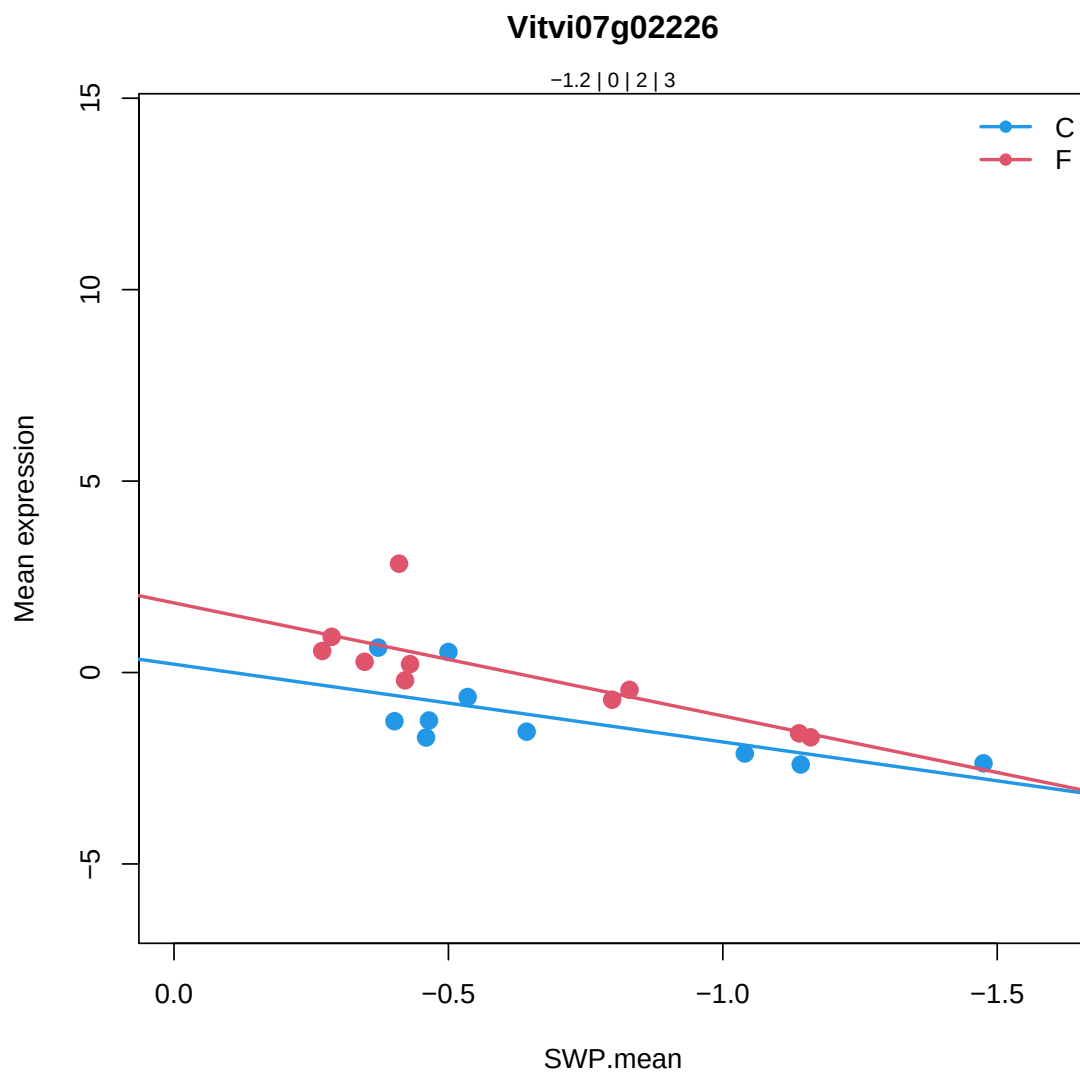
Pectin lyase-like superfamily protein |

Chr3:9777025-9780267 FORWARD LENGTH=470 |

201606

Coefficients for Vitvi07g02226.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.210898	6.960267e-05	***	7.708231e-05	***
SlopeC	2.030632	0.007339062	**	0.2775732	
MeanF-MeanC	1.22983	0.001946382	**	0.02159152	*
SlopeF-SlopeC	0.9218452	0.3764086		0.9999488	



8.1.83 Vitvi16g00731: Type1.0

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

Vitvi16g00731

26.18

misc.invertase/pectin methylesterase inhibitor family protein

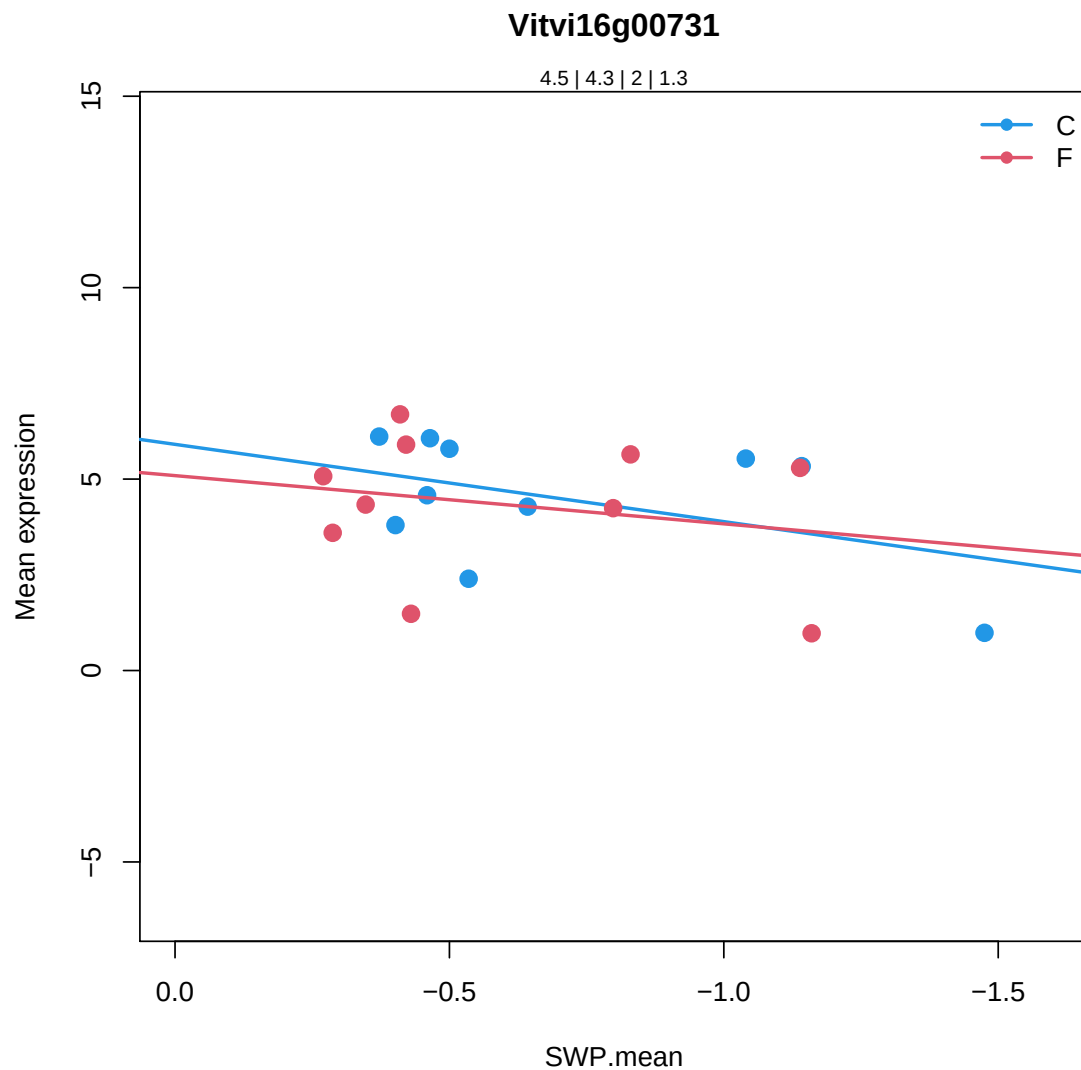
Plant invertase/pectin methylesterase inhibitor superfamily protein |

Chr5:25040699-25041310 FORWARD LENGTH=203 |

201606

Coefficients for Vitvi16g00731.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.487949	7.165939e-09	***	8.787774e-09	***
SlopeC	2.018225	0.1528053		0.6839811	
MeanF-MeanC	-0.1651427	0.8136718		0.9483566	
SlopeF-SlopeC	-0.7590483	0.7116623		0.9999488	



8.1.84 Vitvi07g01737: Type1.0 *

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

```
Vitvi07g01737
```

```
30.6
```

```
signalling.MAP kinases
```

```
mitogen-activated protein kinase kinase kinase 21 |
```

```
Chr4:17422834-17423844 REVERSE LENGTH=336 |
```

```
201606
```

```
Vitvi07g01737
```

```
29.4
```

```
protein.postranslational modification
```

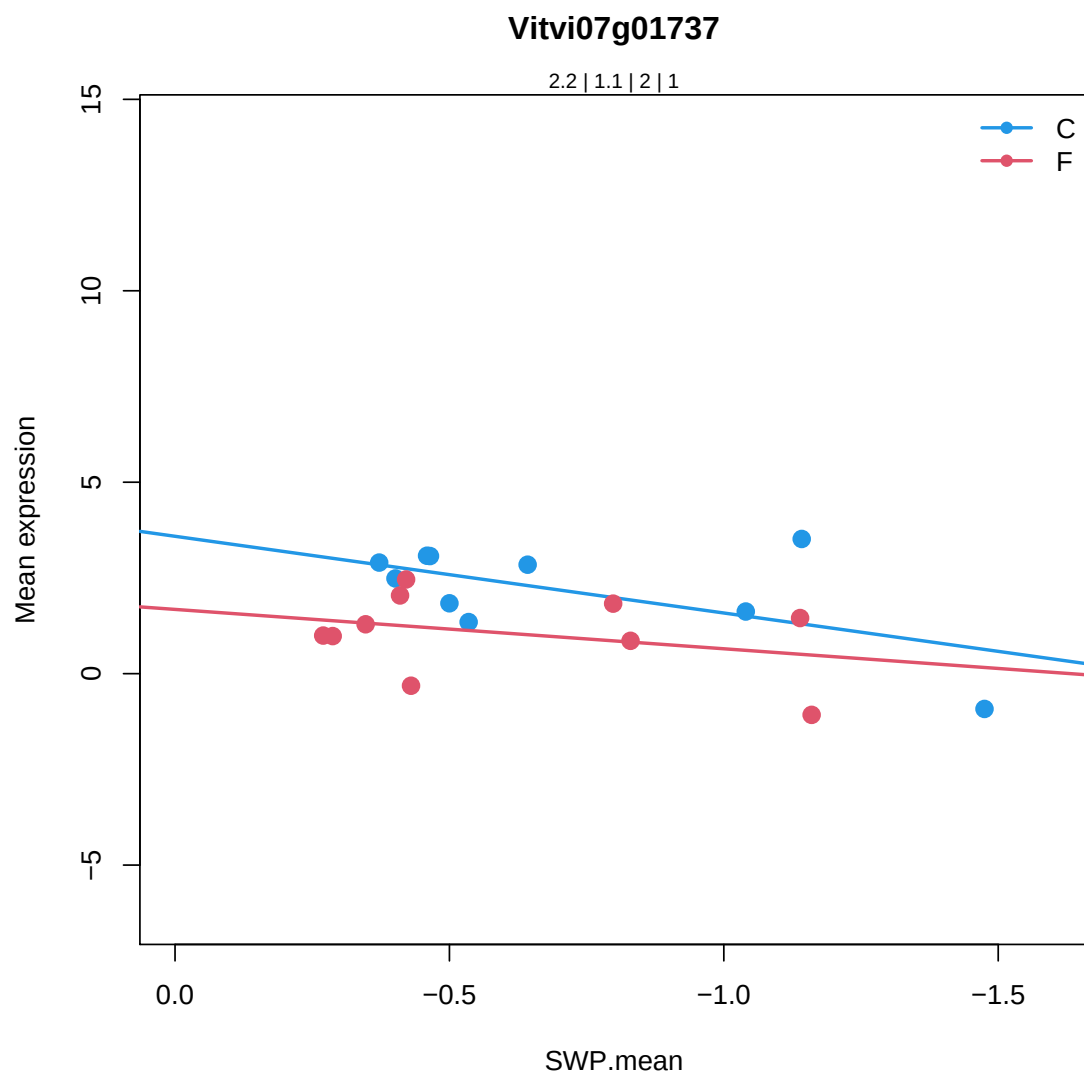
```
mitogen-activated protein kinase kinase kinase 21 |
```

```
Chr4:17422834-17423844 REVERSE LENGTH=336 |
```

```
201606
```

Coefficients for Vitvi07g01737.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.178708	5.096694e-07	***	5.929157e-07	***
SlopeC	2.003894	0.02938282	*	0.4298647	
MeanF-MeanC	-1.127269	0.01717298	*	0.112513	
SlopeF-SlopeC	-0.9756038	0.4534768		0.9999488	



8.1.85 Vitvi09g01945: Type1.0 *

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

Vitvi09g01945

35.2

not assigned.unknown

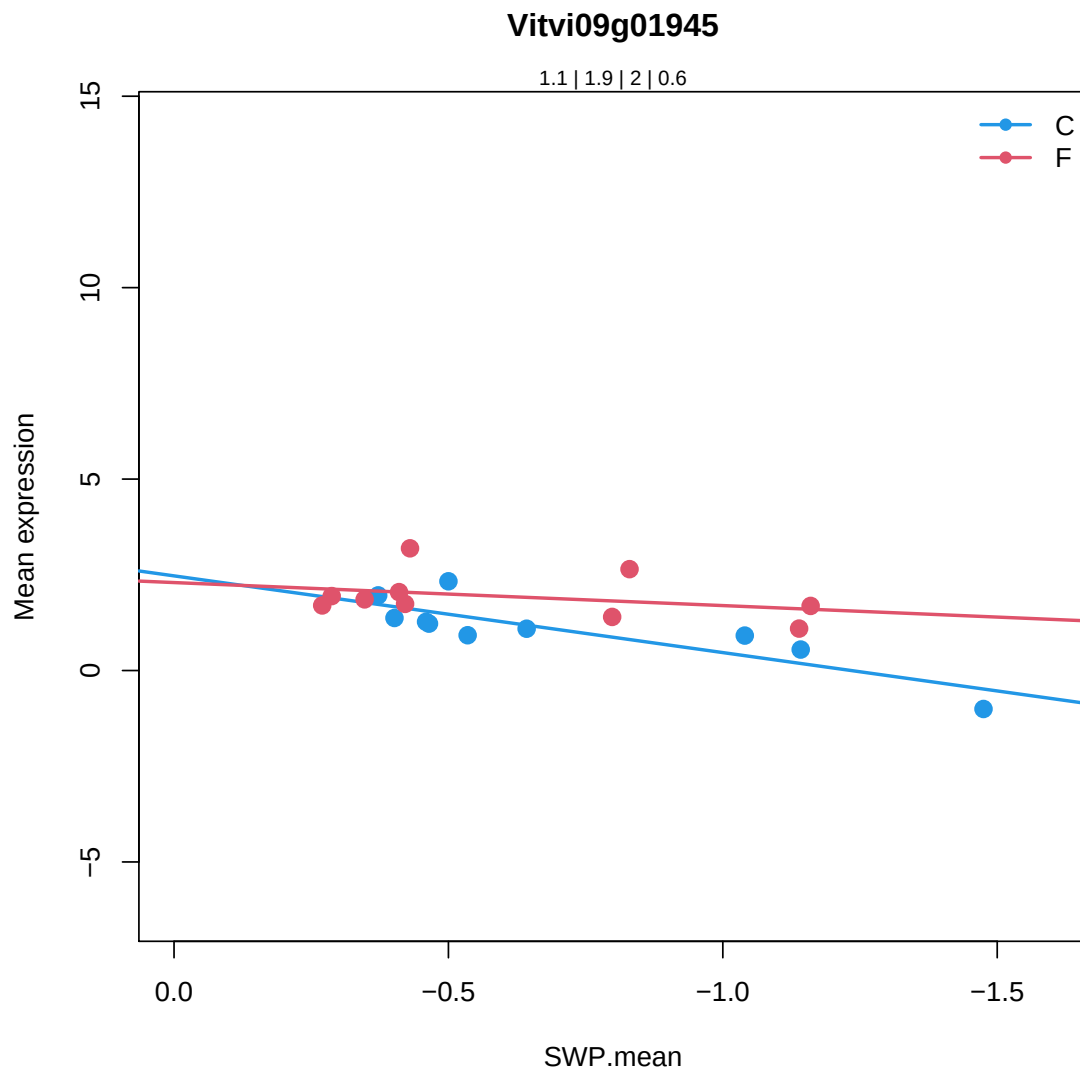
disease resistance family protein / LRR family protein |

Chr2:14737169-14739886 REVERSE LENGTH=905 |

201606

Coefficients for Vitvi09g01945.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.062901	2.897787e-06	***	3.309709e-06	***
SlopeC	2.003646	0.0003423184	***	0.09461517	.
MeanF-MeanC	0.8680532	0.001551389	**	0.01792742	*
SlopeF-SlopeC	-1.402389	0.05840037	.	0.9999488	



8.1.86 Vitvi05g00089: Type1.0 *

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

Vitvi05g00089

10.6.2

cell wall.degradation.mannan-xylose-arabinose-fucose

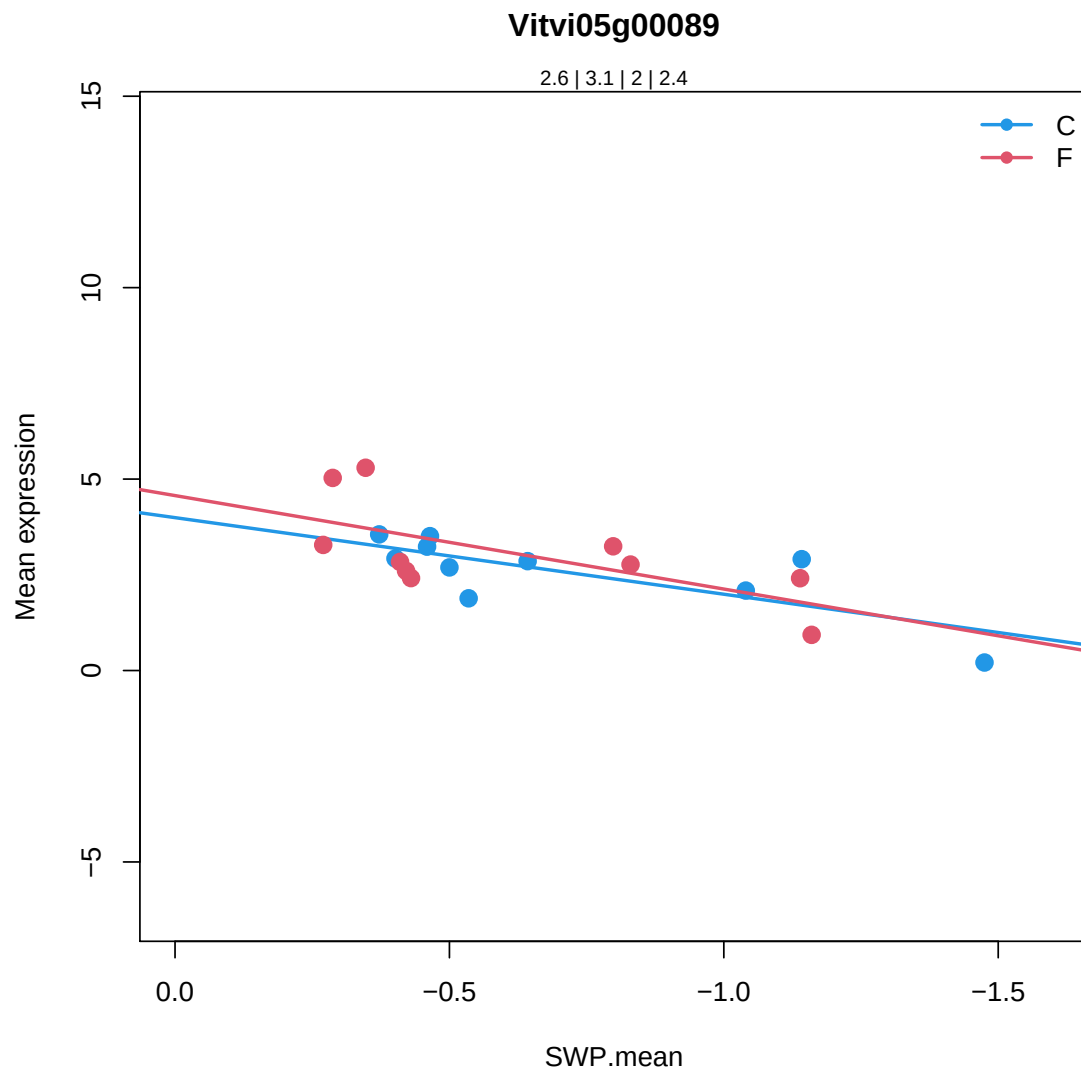
beta-xylosidase 1 |

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	



8.1.87 Vitvi14g01899: Type1.0 *

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

Vitvi14g01899

17.2.2

hormone metabolism.auxin.signal transduction

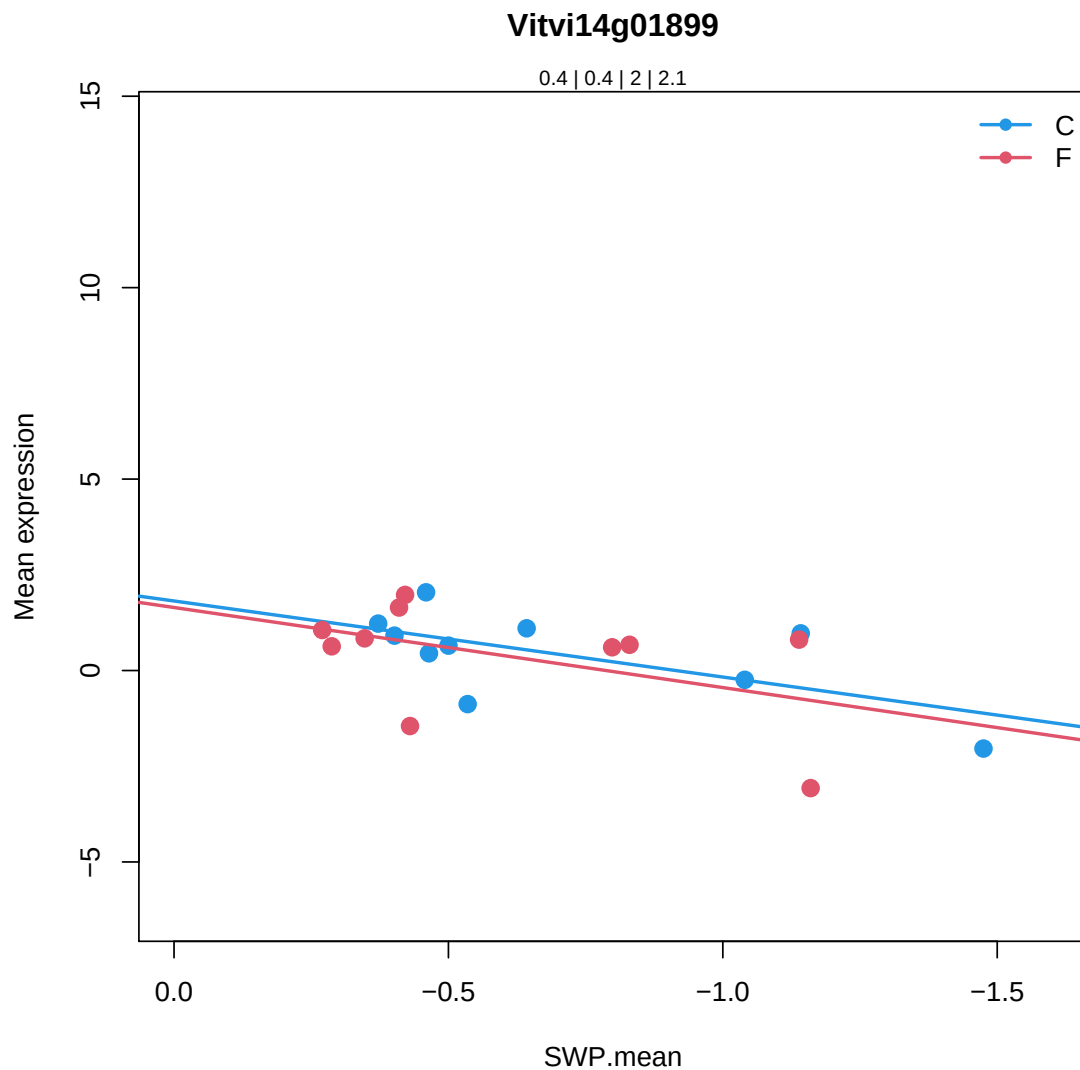
Auxin efflux carrier family protein |

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	



8.1.88 Vitvi18g02589: Type1.0 *

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

Vitvi18g02589

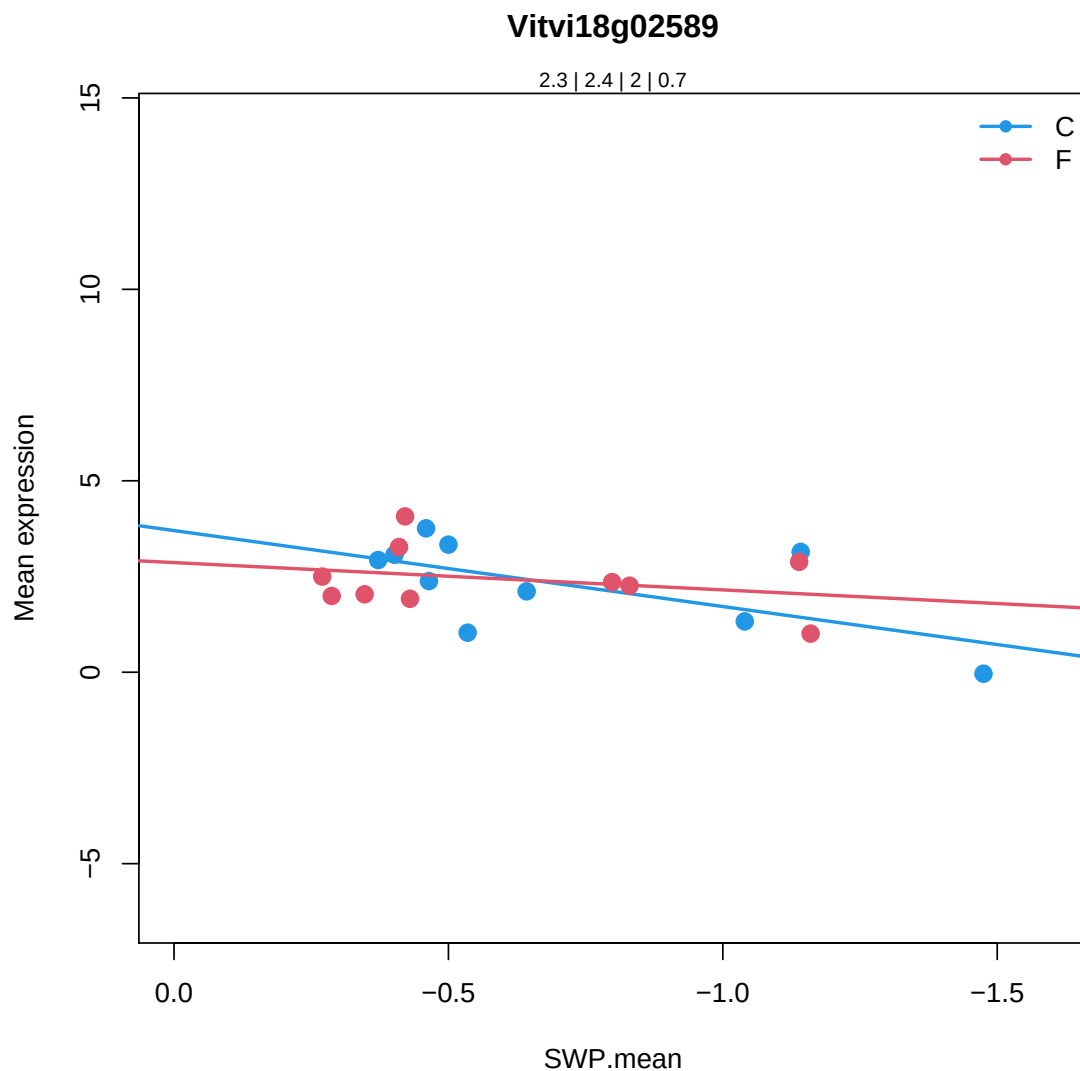
35.2

not assigned.unknown

Unknown Protein

Coefficients for Vitvi18g02589.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.304588	1.623262e-08	***	1.969885e-08	***
SlopeC	1.984255	0.01309462	*	0.3305597	
MeanF-MeanC	0.1242884	0.7420741		0.9238499	
SlopeF-SlopeC	-1.271205	0.2569828		0.9999488	



8.1.89 Vitvi08g01702: Type1.0 *

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

Vitvi08g01702

26.4.1

misc.beta 1,3 glucan hydrolases.glucan endo-1,3-beta-glucosidase

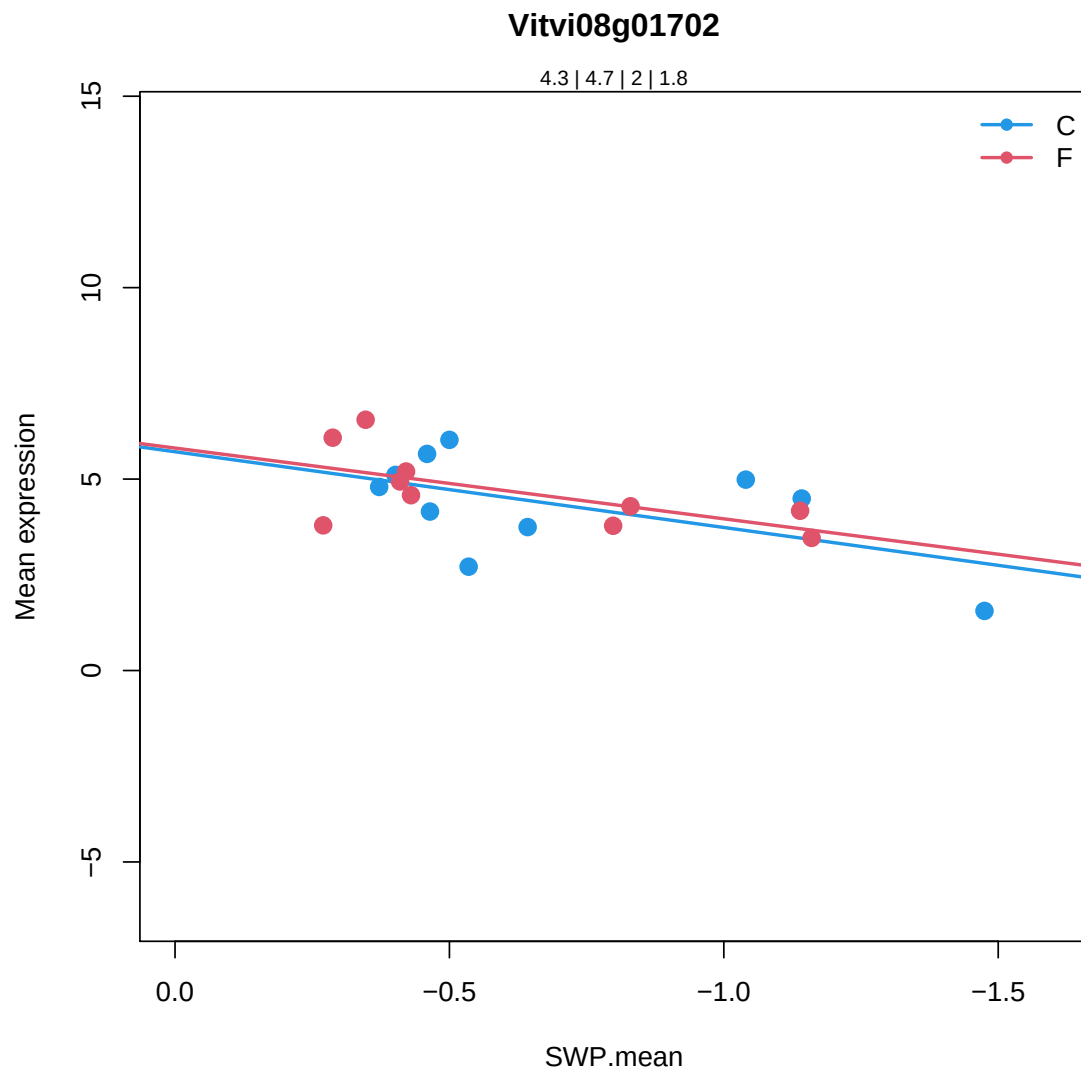
beta-1%2C3-glucanase 3 |

Chr3:21181916-21183045 REVERSE LENGTH=341 |

201606

Coefficients for Vitvi08g01702.

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



8.1.90 Vitvi18g00739: Type1.0

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

Vitvi18g00739

35.2

not assigned.unknown

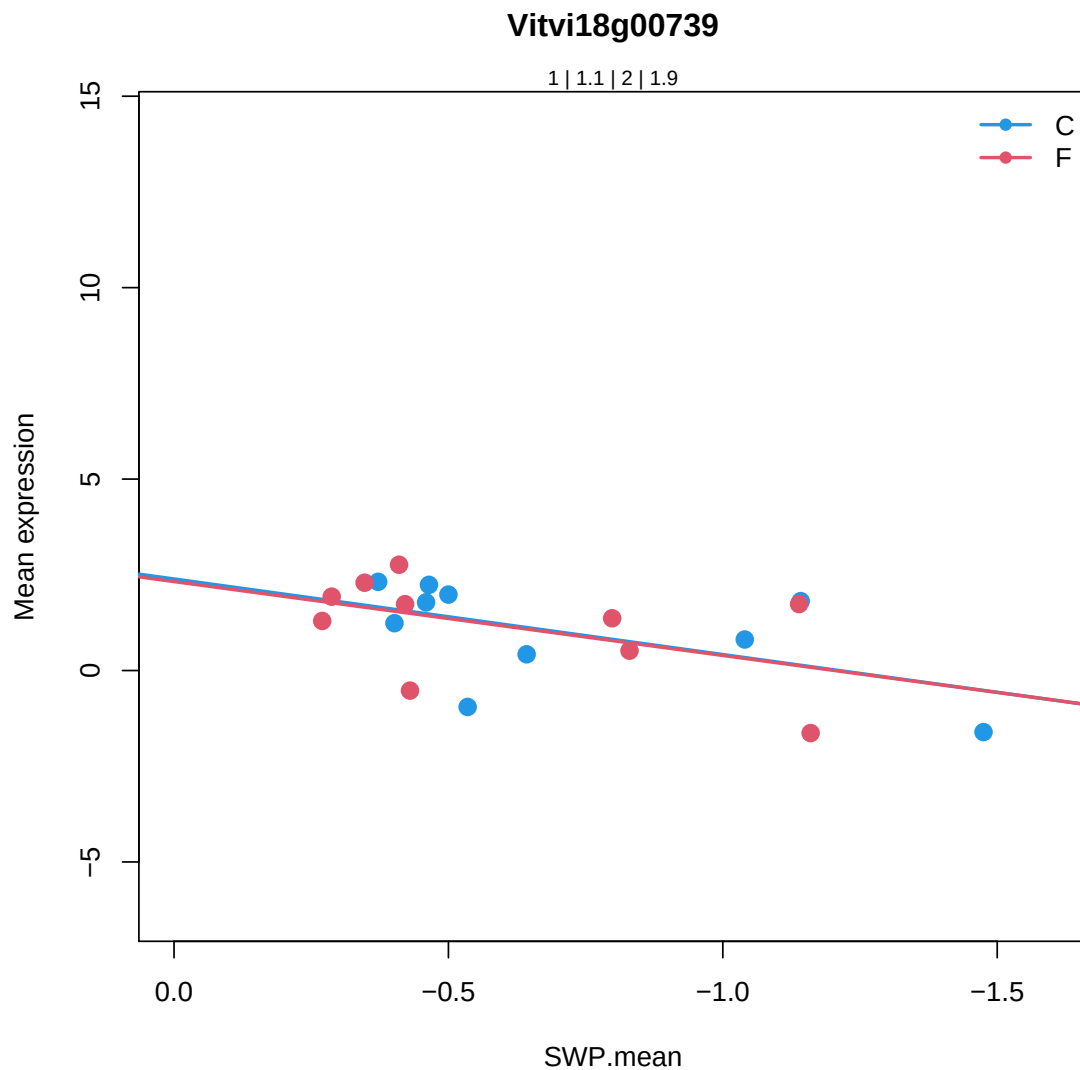
Serine/threonine-protein kinase WNK (With No Lysine)-like protein |

Chr1:22139282-22141585 FORWARD LENGTH=386 |

201606

Coefficients for Vitvi18g00739.

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



8.1.91 Vitvi18g02692: Type1.0 *

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

Vitvi18g02692

33.1

development.storage proteins

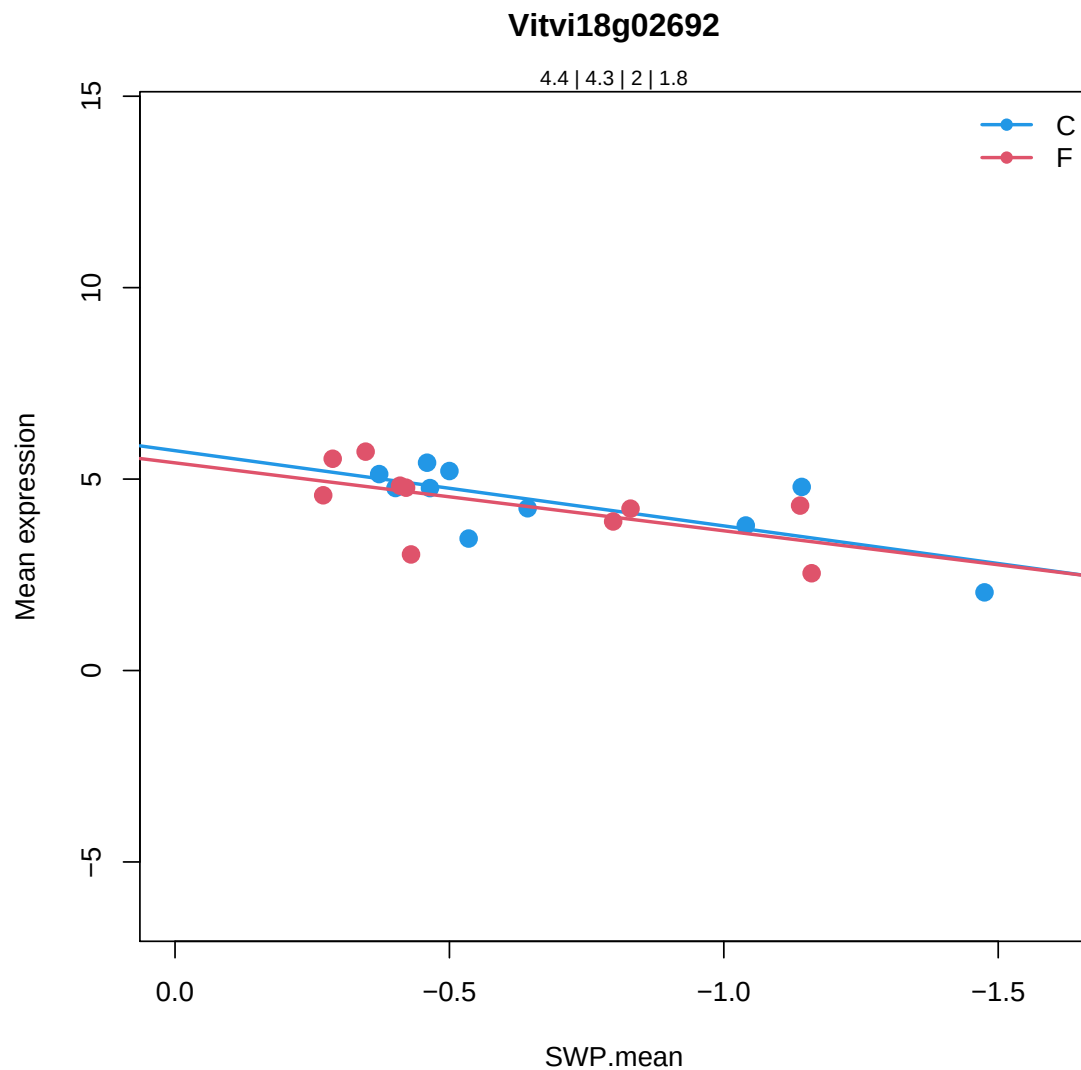
phospholipase A 2A |

Chr2:11293912-11295708 REVERSE LENGTH=407 |

201606

Coefficients for Vitvi18g02692.

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



8.1.92 Vitvi16g02101: Type1.0 *

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

```
Vitvi16g02101
```

```
35.2
```

```
not assigned.unknown
```

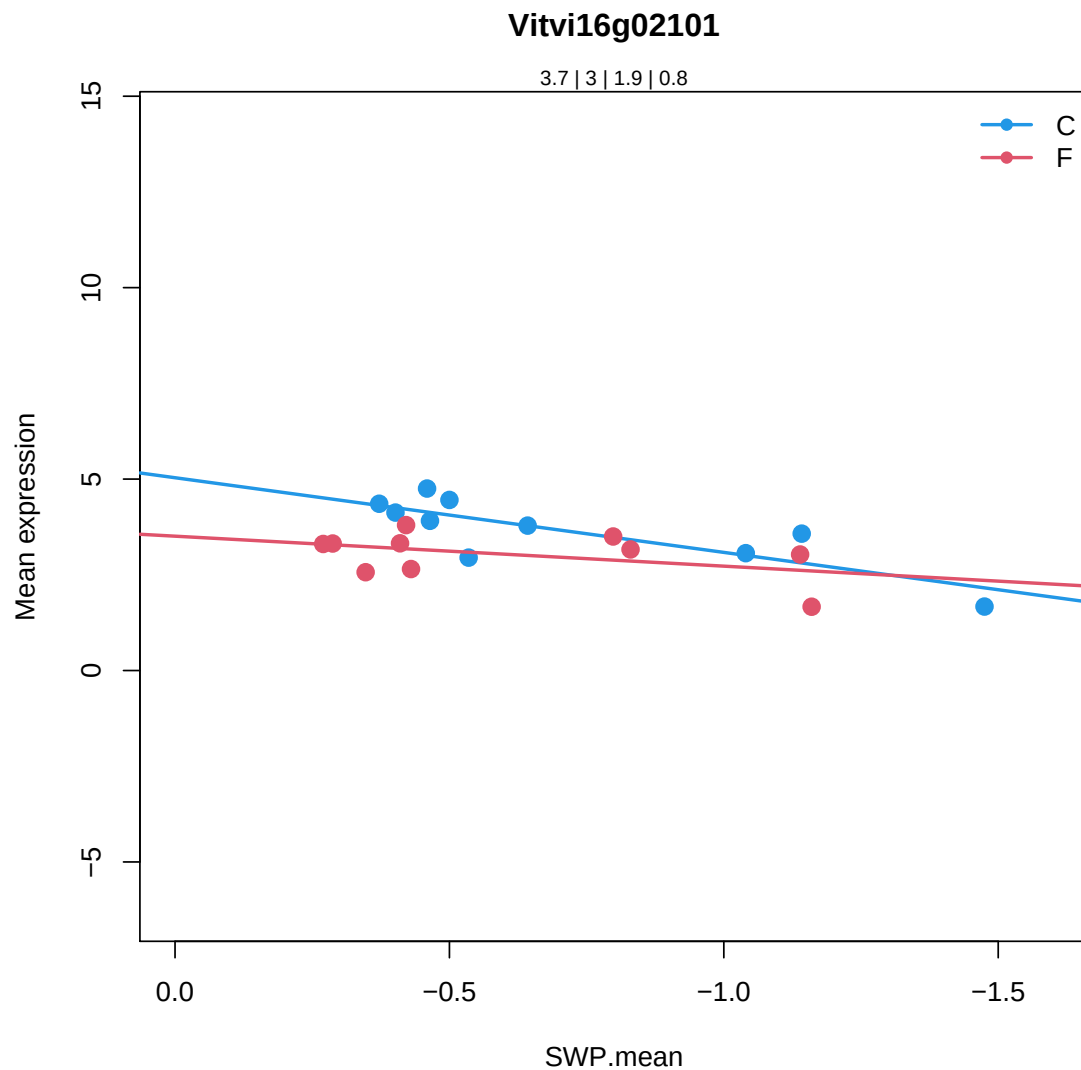
```
Protein kinase superfamily protein |
```

```
Chr1:24961634-24963941 REVERSE LENGTH=663 |
```

```
201606
```

Coefficients for Vitvi16g02101.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.66414	7.864672e-16	***	1.493377e-15	***
SlopeC	1.949956	0.0005741122	***	0.1005065	
MeanF-MeanC	-0.6322727	0.01746672	*	0.1139673	
SlopeF-SlopeC	-1.166934	0.1191261		0.9999488	



8.1.93 Vitvi06g01346: Type1.0

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

Vitvi06g01346

35.2

not assigned.unknown

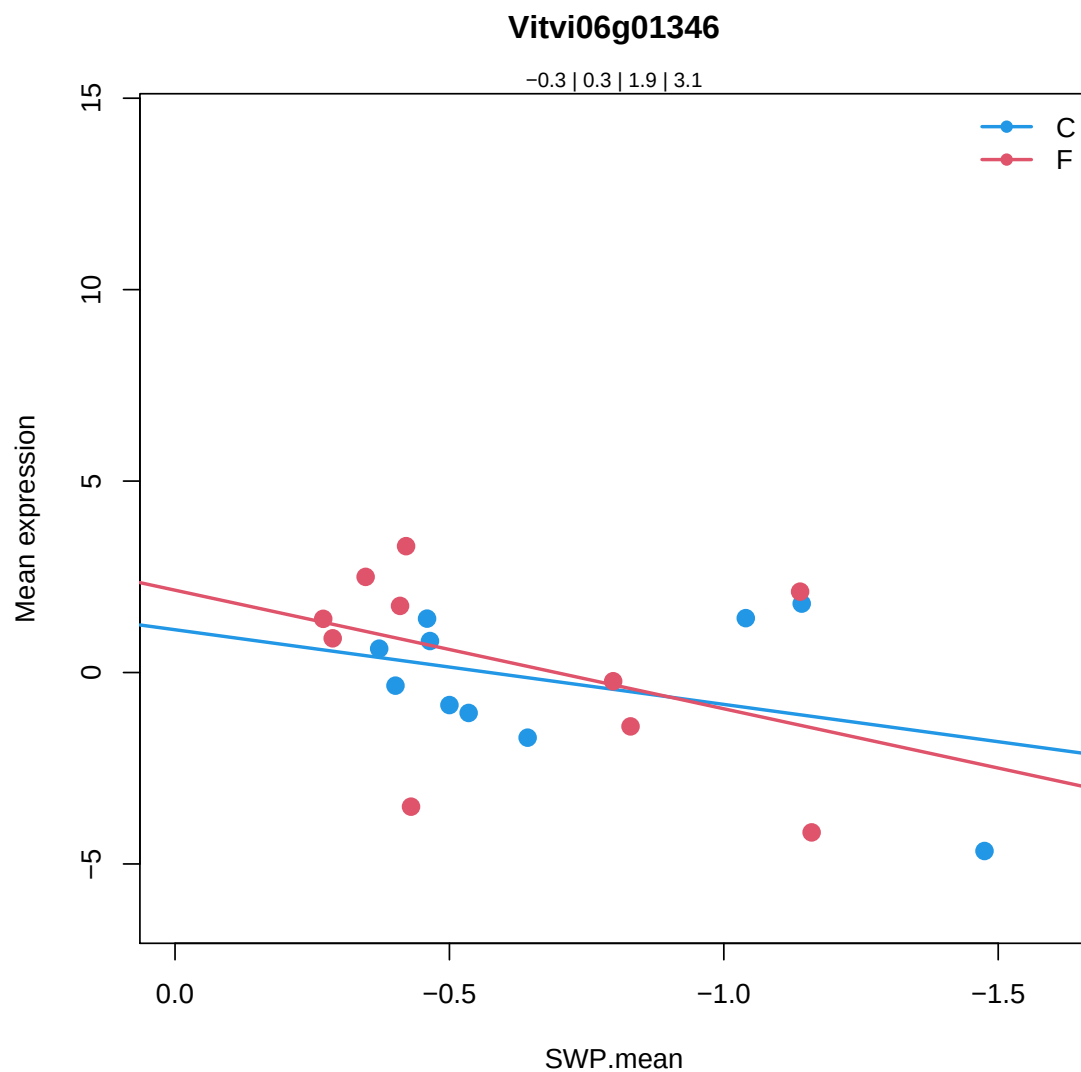
tonoplast intrinsic protein 1%3B3 |

Chr4:625092-625850 REVERSE LENGTH=252 |

201606

Coefficients for Vitvi06g01346.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.253913	0.6796358		0.6843954	
SlopeC	1.949631	0.2606311		0.7688128	
MeanF-MeanC	0.5169893	0.5530014		0.835201	
SlopeF-SlopeC	1.14708	0.6524505		0.9999488	



8.1.94 Vitvi04g01585: Type1.0 *

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

Vitvi04g01585

16.2.1.10

secondary metabolism.phenylpropanoids.lignin biosynthesis.CAD

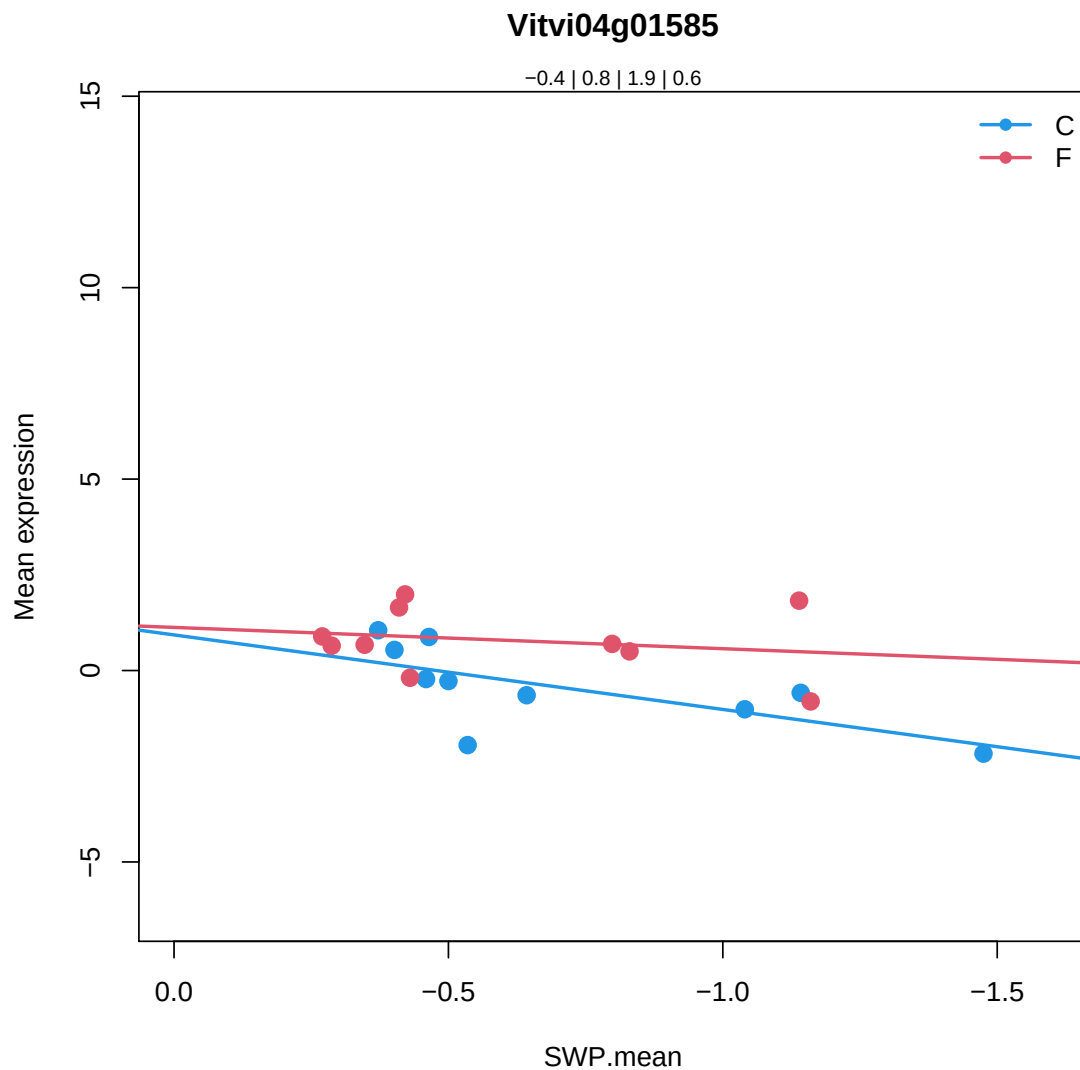
cinnamyl alcohol dehydrogenase 9 |

Chr4:18291268-18292740 FORWARD LENGTH=311 |

201606

Coefficients for Vitvi04g01585.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.4389963	0.09581086	.	0.0991075	.
SlopeC	1.946457	0.01117285	*	0.3143947	
MeanF-MeanC	1.226111	0.002397998	**	0.02541744	*
SlopeF-SlopeC	-1.390109	0.1967688		0.9999488	



8.1.95 Vitvi16g02145: Type1.0 *

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

Vitvi16g02145

35.2

not assigned.unknown

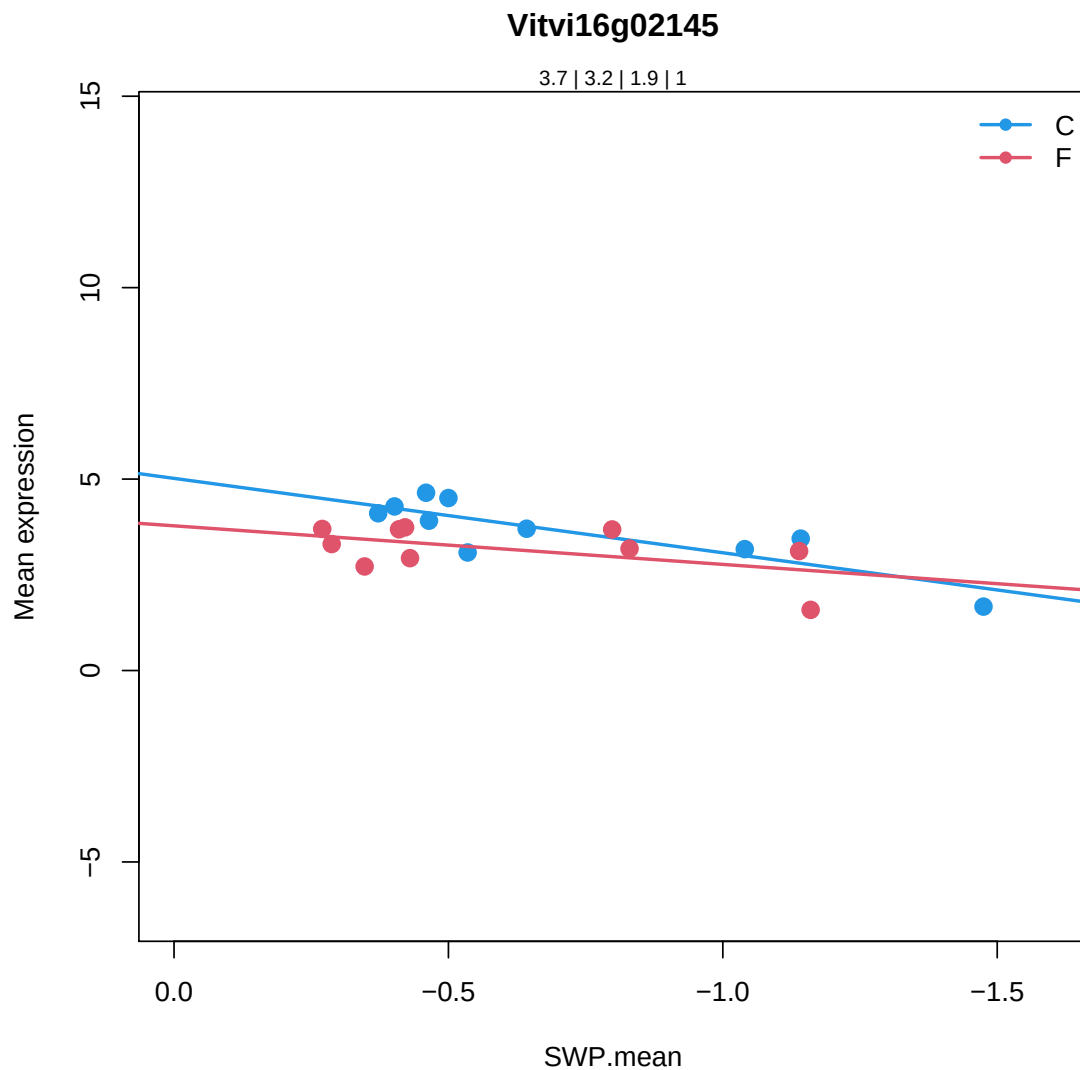
Protein kinase superfamily protein |

Chr1:24961634-24963941 REVERSE LENGTH=663 |

201606

Coefficients for Vitvi16g02145.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.652252	5.506751e-16	***	1.065692e-15	***
SlopeC	1.942658	0.0004864165	***	0.1005065	
MeanF-MeanC	-0.4870218	0.05548594	.	0.256018	
SlopeF-SlopeC	-0.9351712	0.1981273		0.9999488	



8.1.96 Vitvi04g00284: Type1.0 *

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

Vitvi04g00284

35.2

not assigned.unknown

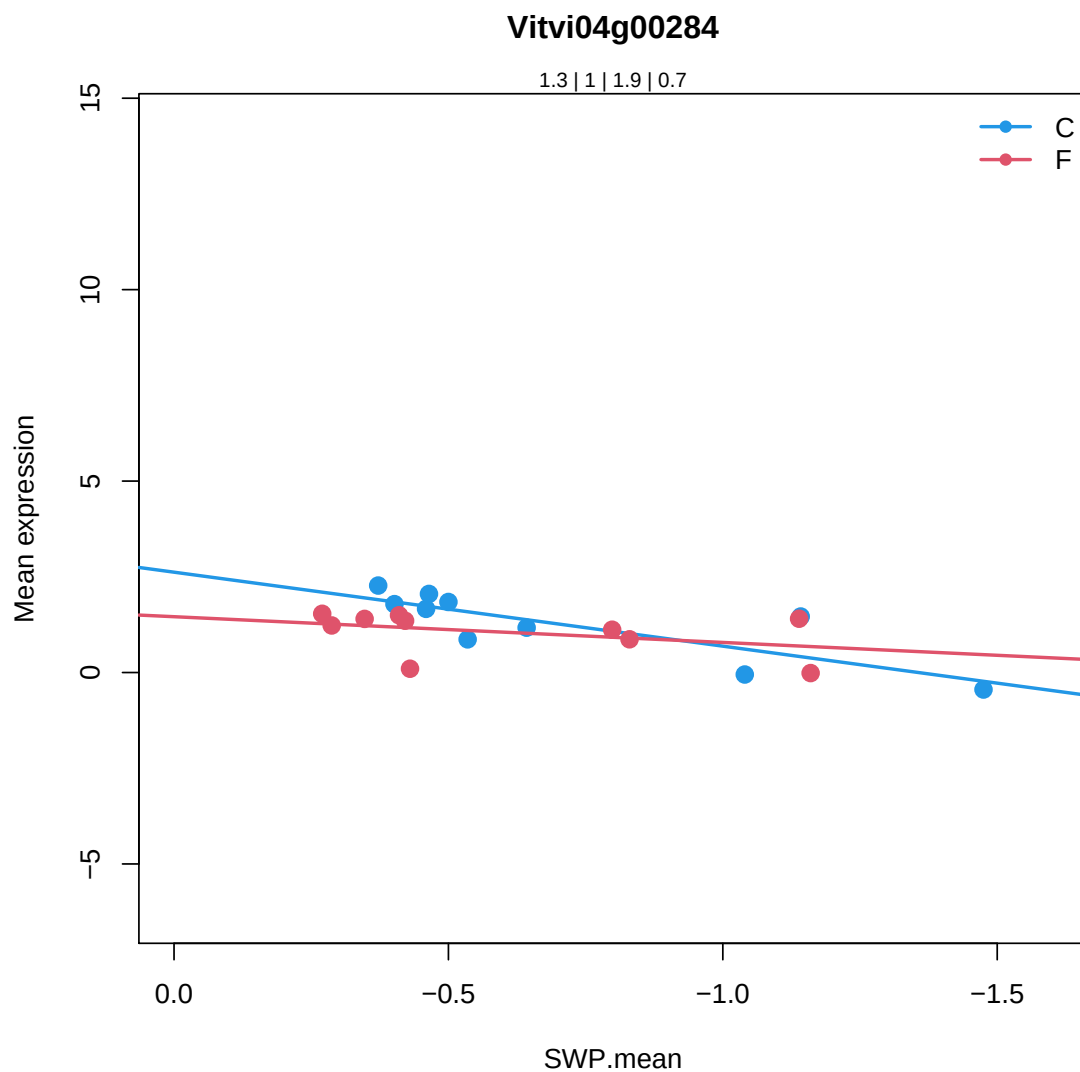
DUF1677 family protein (DUF1677) |

Chr5:9010909-9011430 REVERSE LENGTH=173 |

201606

Coefficients for Vitvi04g00284.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.261699	2.205957e-07	***	2.591983e-07	***
SlopeC	1.932209	0.0004908684	***	0.1005065	
MeanF-MeanC	-0.2132044	0.3830786		0.733924	
SlopeF-SlopeC	-1.260301	0.08630779	.	0.9999488	



8.1.97 Vitvi01g00437: Type1.0 *

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

Vitvi01g00437

35.2

not assigned.unknown

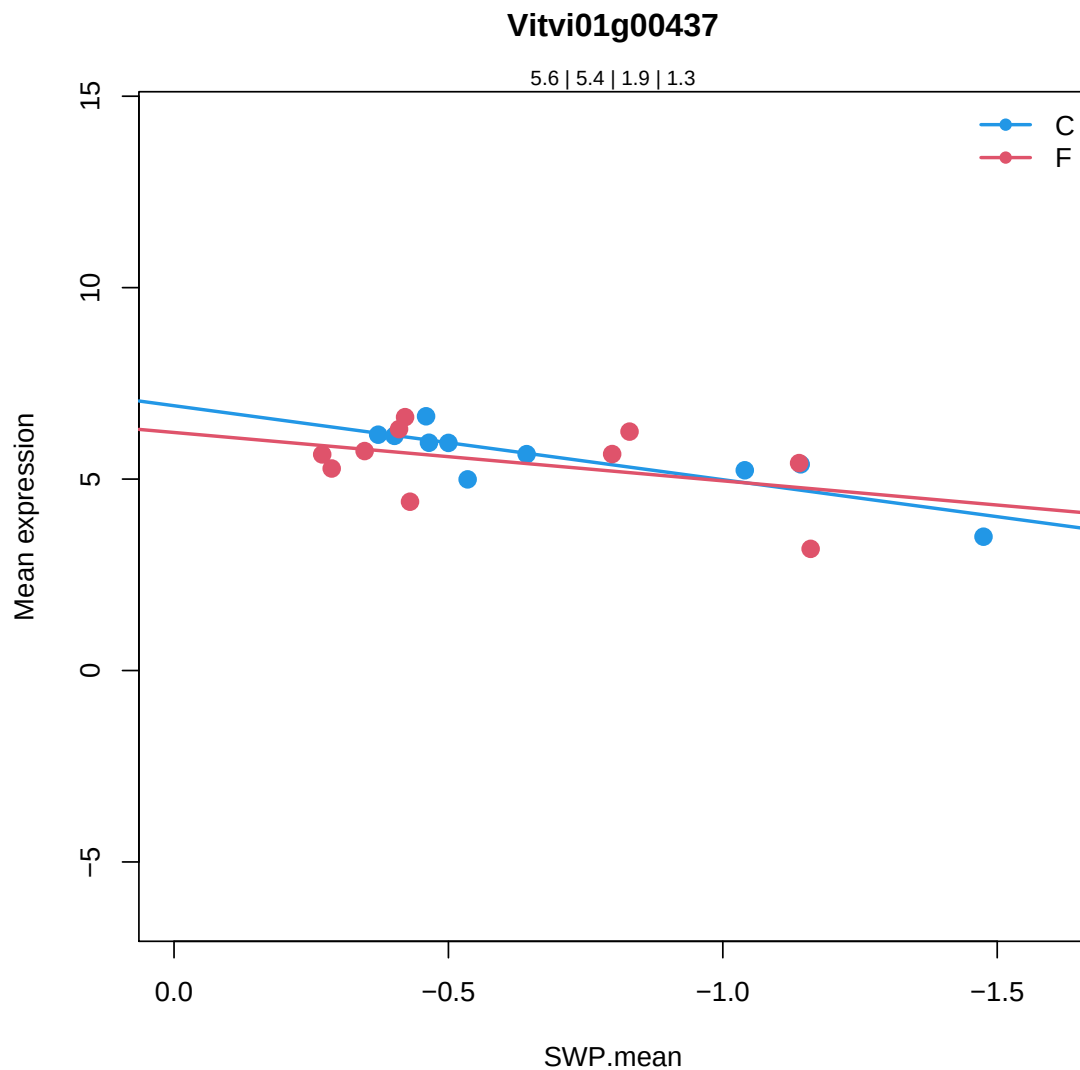
MLP-like protein 34 |

Chr1:26715429-26716744 REVERSE LENGTH=316 |

201606

Coefficients for Vitvi01g00437.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.557522	2.990641e-17	***	7.159314e-17	***
SlopeC	1.932154	0.005450458	**	0.2577627	
MeanF-MeanC	-0.1104175	0.7316363		0.918522	
SlopeF-SlopeC	-0.6690955	0.4798581		0.9999488	



8.1.98 Vitvi04g00029: Type1.0 *

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

Vitvi04g00029

30.2.11

signalling.receptor kinases.leucine rich repeat XI

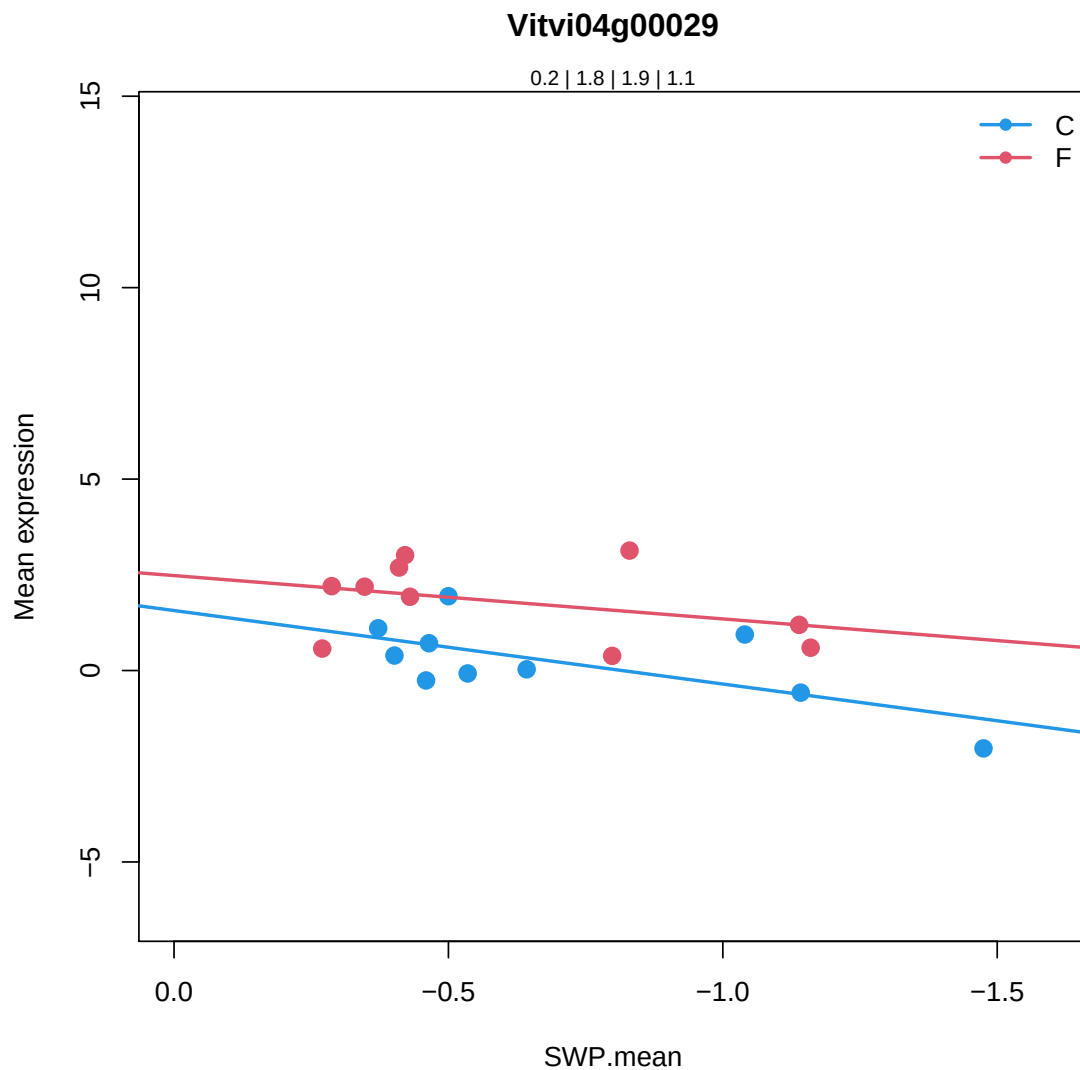
kinase family with leucine-rich repeat domain-containing protein |

Chr5:9050880-9053978 FORWARD LENGTH=1005 |

201606

Coefficients for Vitvi04g00029.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.2169475	0.4283702		0.4344413	
SlopeC	1.919174	0.01779611	*	0.3578474	
MeanF-MeanC	1.572964	0.0004495255	***	0.006450919	**
SlopeF-SlopeC	-0.7874491	0.4868005		0.9999488	



8.1.99 Vitvi09g01122: Type1.0

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

Vitvi09g01122

27.3.32

RNA.regulation of transcription.WRKY domain transcription factor famil

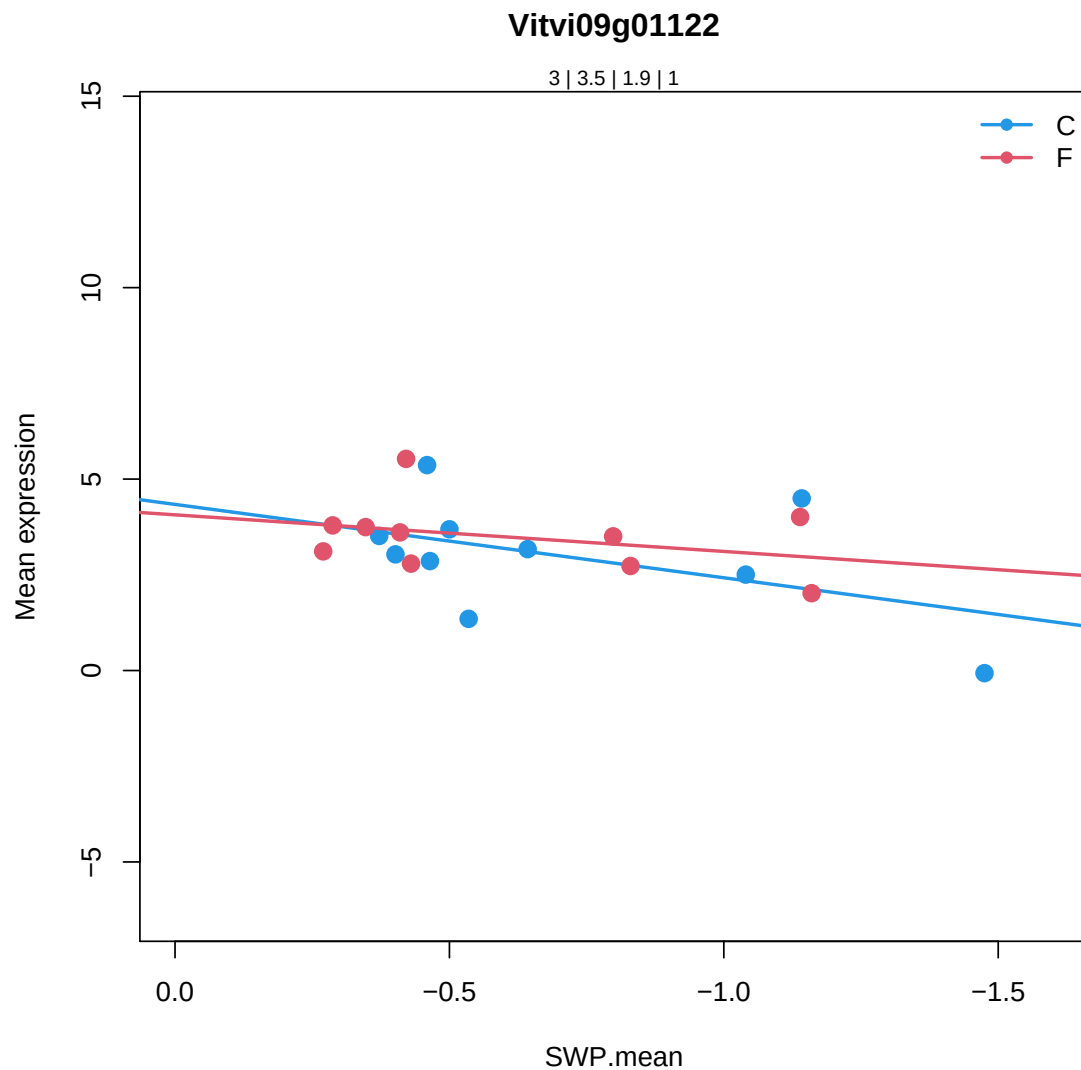
WRKY DNA-binding protein 40 |

Chr1:30383834-30385356 FORWARD LENGTH=302 |

201606

Coefficients for Vitvi09g01122.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.991055	1.347534e-08	***	1.638018e-08	***
SlopeC	1.91616	0.05436682	.	0.5212455	
MeanF-MeanC	0.4927082	0.3146938		0.6767544	
SlopeF-SlopeC	-0.9601498	0.5005529		0.9999488	



8.1.100 Vitvi16g01247: Type1.0 *

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

Vitvi16g01247

35.2

not assigned.unknown

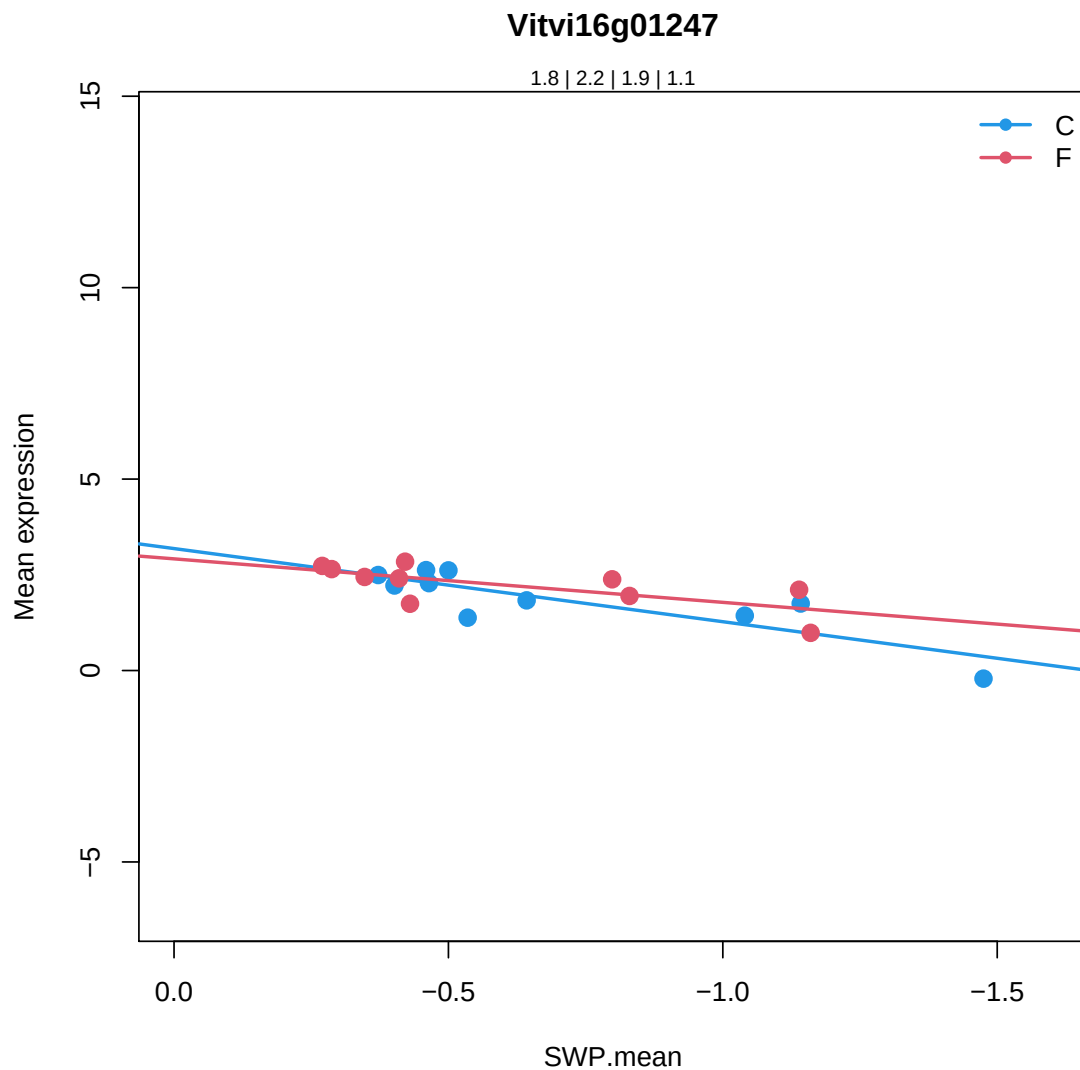
PR5-like receptor kinase |

Chr5:15293325-15295838 REVERSE LENGTH=665 |

201606

Coefficients for Vitvi16g01247.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.841615	2.228104e-11	***	2.996098e-11	***
SlopeC	1.910334	0.0001172076	***	0.07644173	.
MeanF-MeanC	0.3826072	0.07810066	.	0.3151735	
SlopeF-SlopeC	-0.7742674	0.2146354		0.9999488	



8.1.101 Vitvi06g00674: Type1.0 *

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

Vitvi06g00674

35.1.41

not assigned.no ontology.hydroxyproline rich proteins

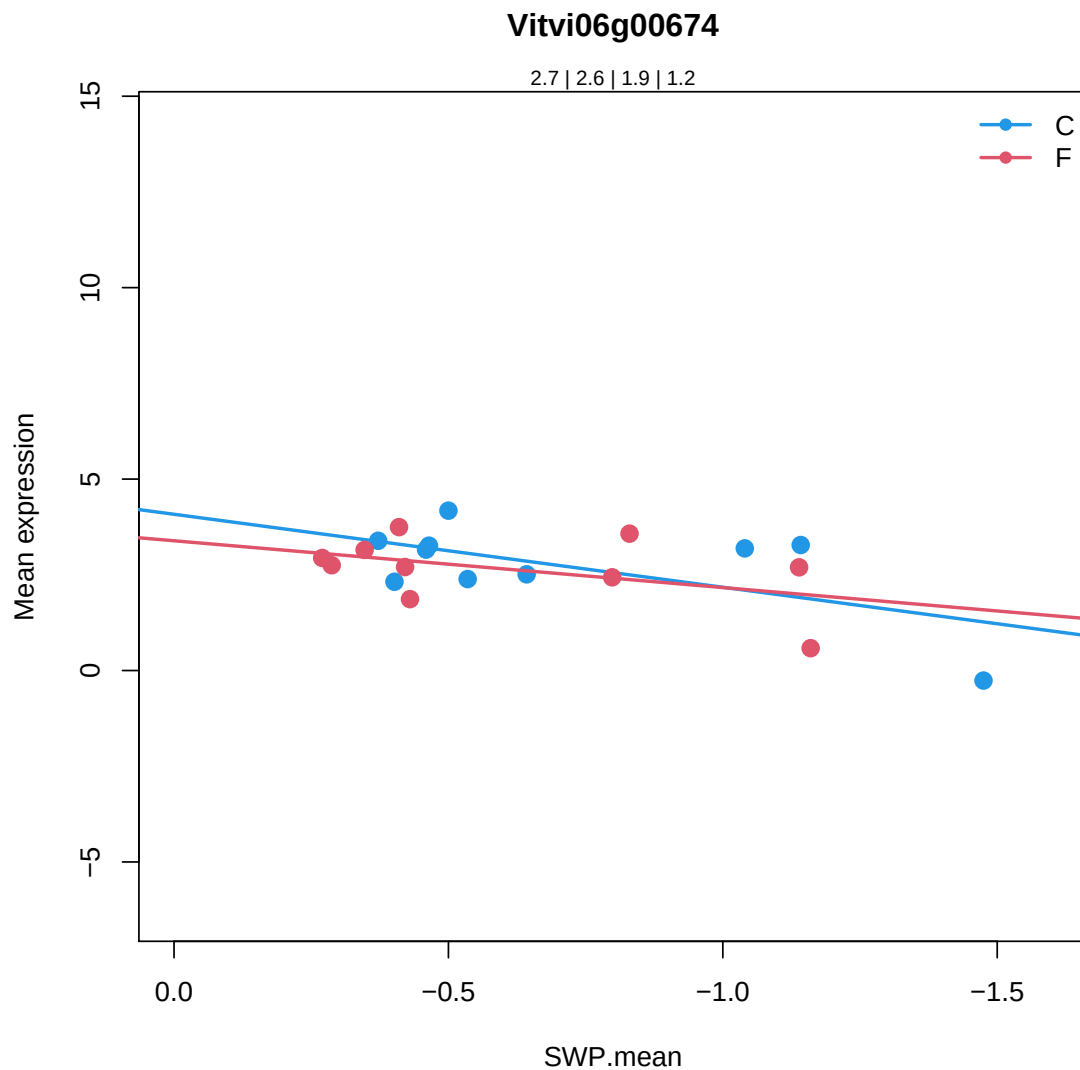
CHUP1-like protein |

Chr1:2185387-2186580 REVERSE LENGTH=325 |

201606

Coefficients for Vitvi06g00674.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.740557	9.065915e-10	***	1.144654e-09	***
SlopeC	1.906005	0.0173858	*	0.3551322	
MeanF-MeanC	-0.0966843	0.799465		0.9439496	
SlopeF-SlopeC	-0.6838882	0.5409062		0.9999488	



8.1.102 Vitvi16g02148: Type1.0 *

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

Vitvi16g02148

35.2

not assigned.unknown

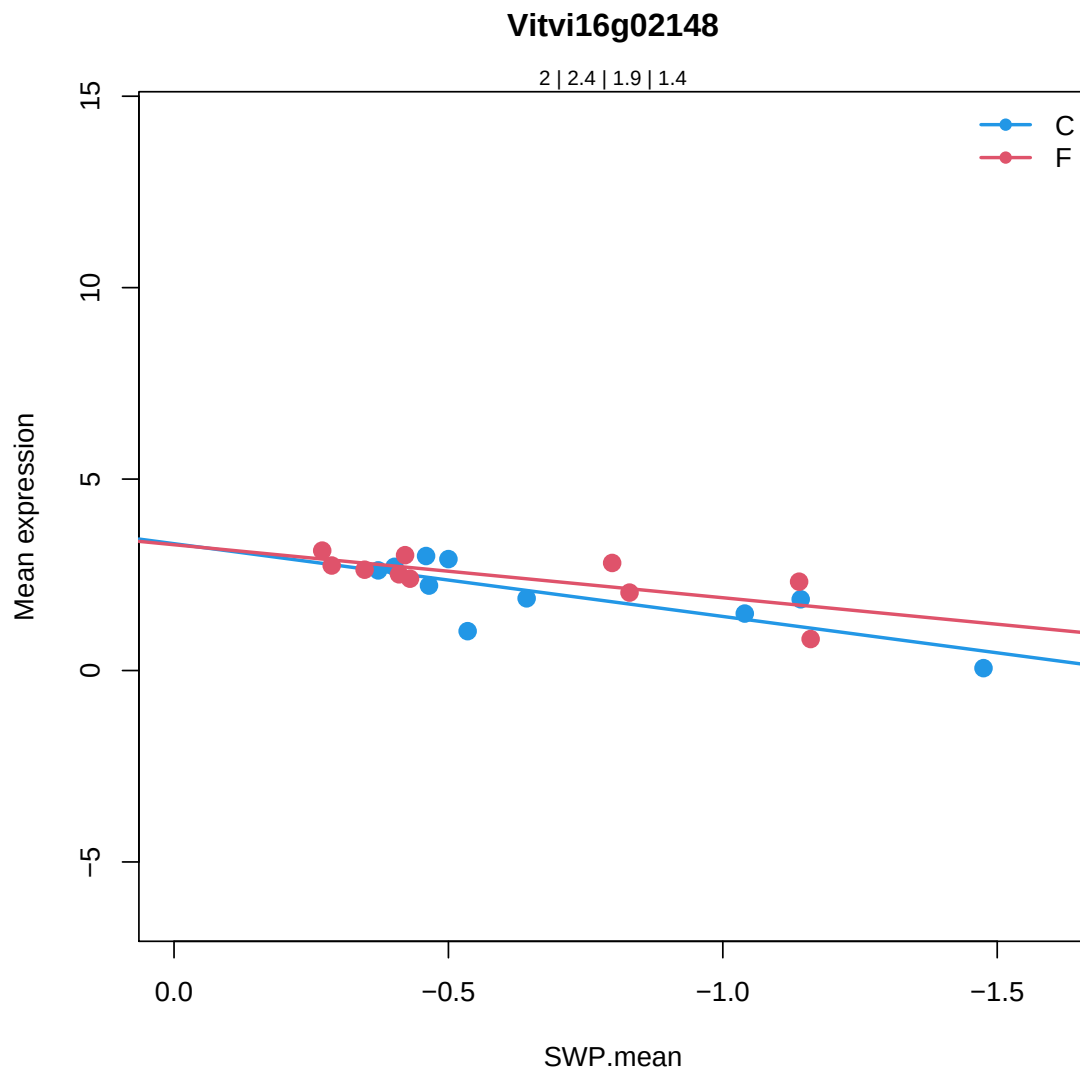
PR5-like receptor kinase |

Chr5:15293325-15295838 REVERSE LENGTH=665 |

201606

Coefficients for Vitvi16g02148.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.976338	1.019381e-10	***	1.33311e-10	***
SlopeC	1.900285	0.000606049	***	0.1005065	
MeanF-MeanC	0.4653611	0.06638624	.	0.2859081	
SlopeF-SlopeC	-0.5159112	0.4718784		0.9999488	



8.1.103 Vitvi16g01249: Type1.0 *

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

Vitvi16g01249

35.2

not assigned.unknown

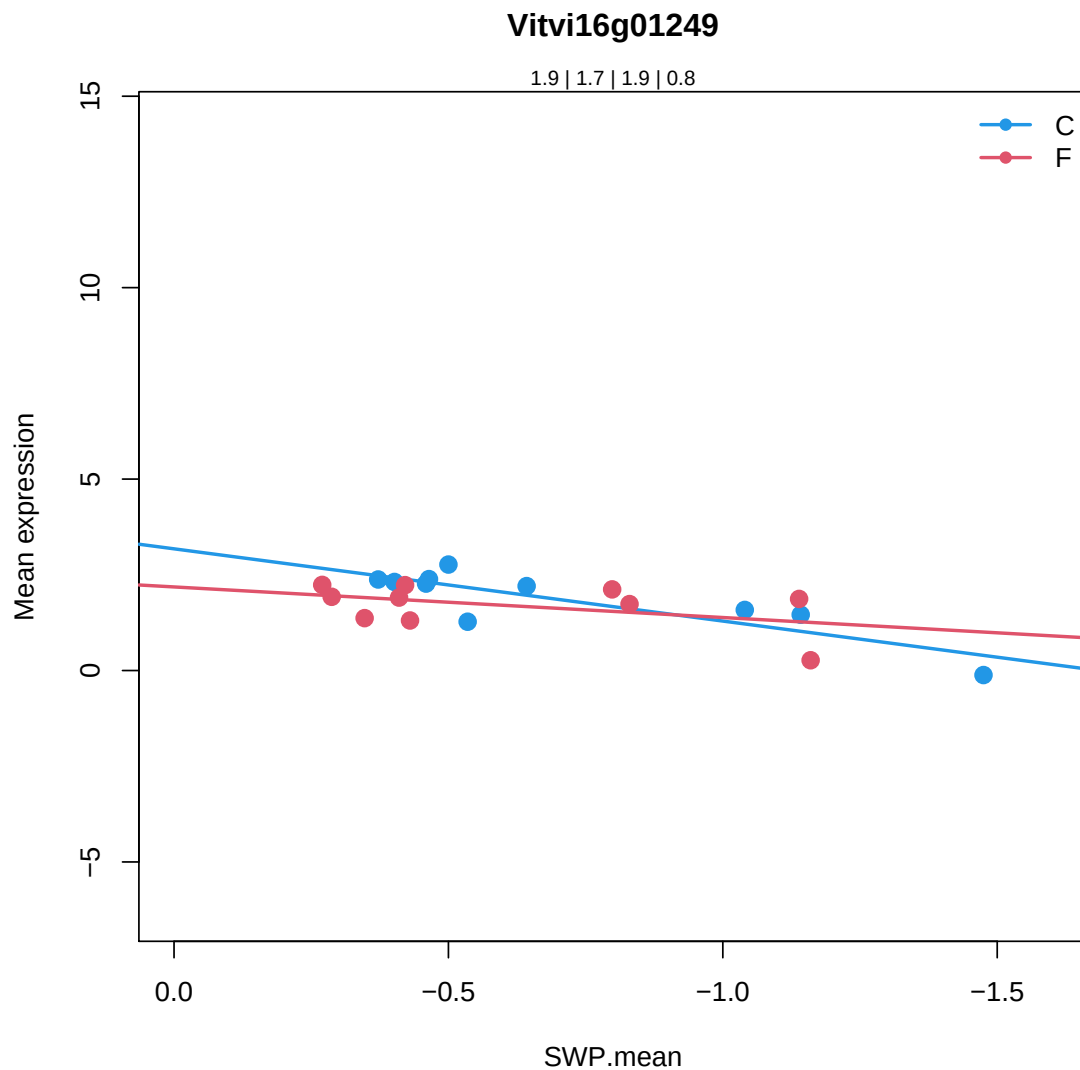
Protein kinase family protein |

Chr5:15277239-15279317 REVERSE LENGTH=578 |

201606

Coefficients for Vitvi16g01249.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.851625	1.251007e-10	***	1.630985e-10	***
SlopeC	1.886861	0.000379866	***	0.09467692	.
MeanF-MeanC	-0.1553033	0.5028818		0.8079107	
SlopeF-SlopeC	-1.087785	0.1176784		0.9999488	



8.1.104 Vitvi09g00971: Type1.0

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

Vitvi09g00971

34.19.3

transport.major intrinsic proteins.NIP

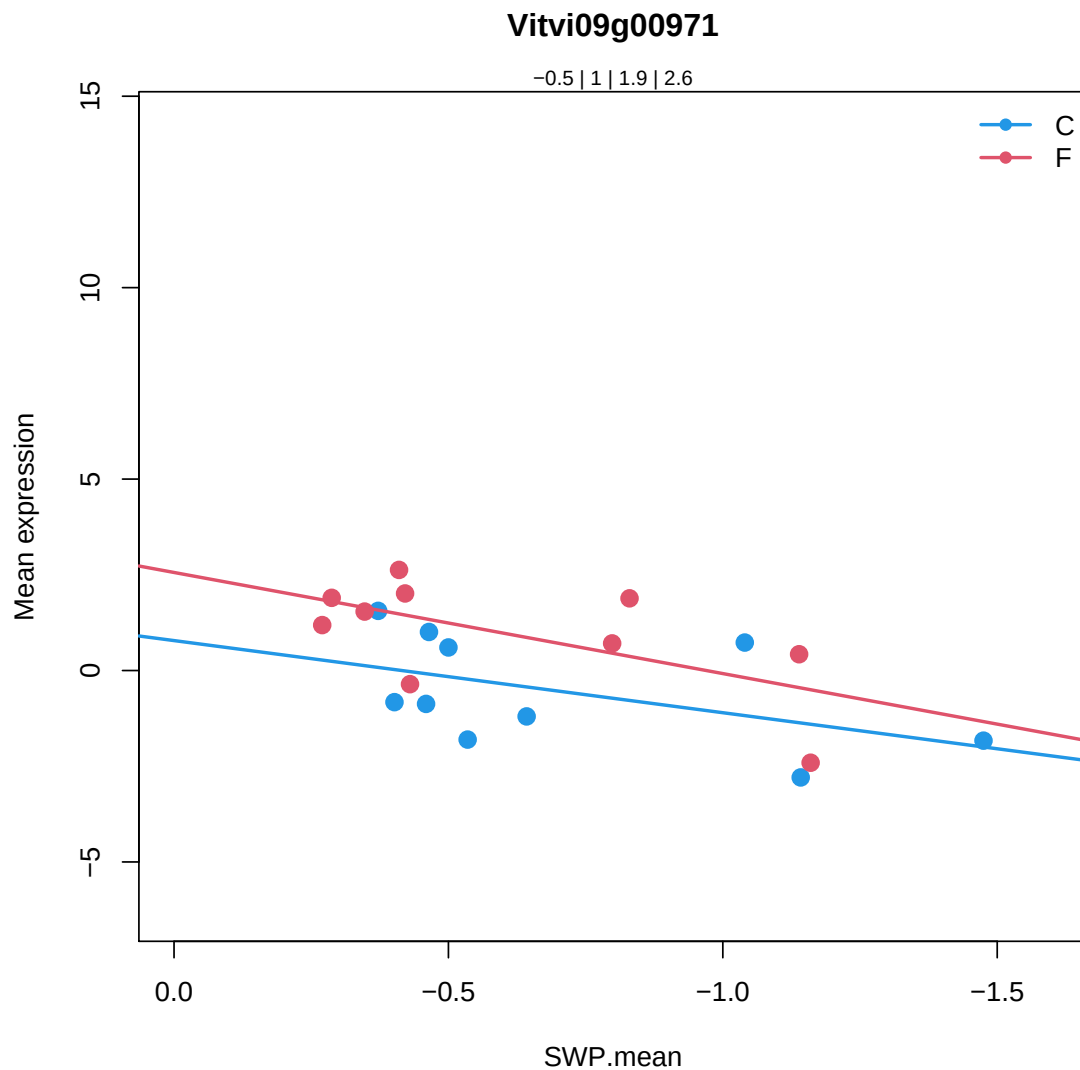
NOD26-like intrinsic protein 6%3B1 |

Chr1:30350640-30352015 REVERSE LENGTH=305 |

201606

Coefficients for Vitvi09g00971.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.5429204	0.1436317		0.1479012	
SlopeC	1.883775	0.071919	.	0.5630621	
MeanF-MeanC	1.494678	0.007449359	**	0.06123152	.
SlopeF-SlopeC	0.7567378	0.6146061		0.9999488	



8.1.105 Vitvi18g00214: Type1.0 *

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

Vitvi18g00214

35.2

not assigned.unknown

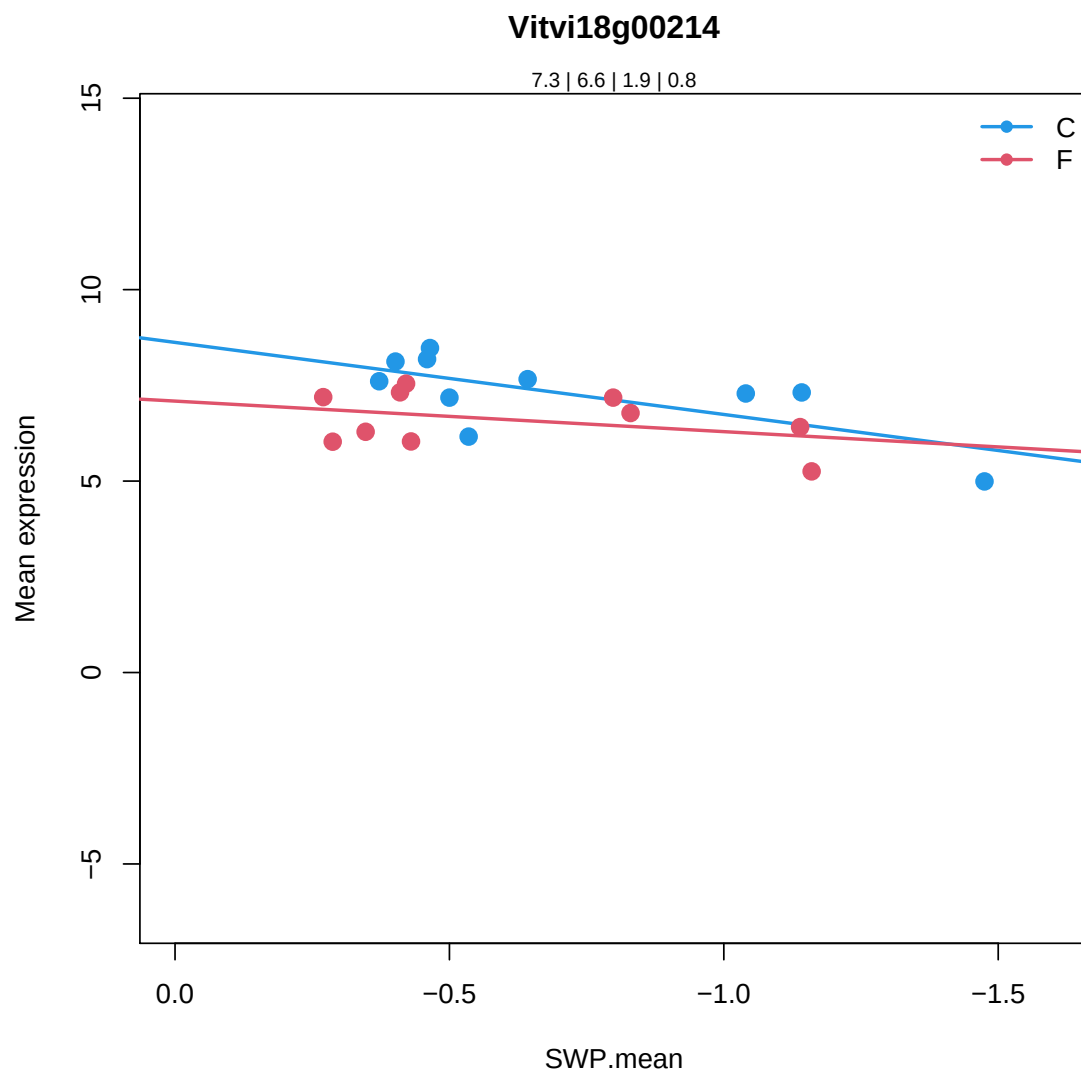
Calcium-binding EF-hand family protein |

Chr1:7553317-7553784 REVERSE LENGTH=155 |

201606

Coefficients for Vitvi18g00214.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.298562	7.12722e-20	***	3.579344e-19	***
SlopeC	1.881986	0.005852975	**	0.263938	
MeanF-MeanC	-0.6958849	0.03687791	*	0.1943614	
SlopeF-SlopeC	-1.084216	0.2492372		0.9999488	



8.1.106 Vitvi09g00528: Type1.0 *

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

Vitvi09g00528

27.4

RNA.RNA binding

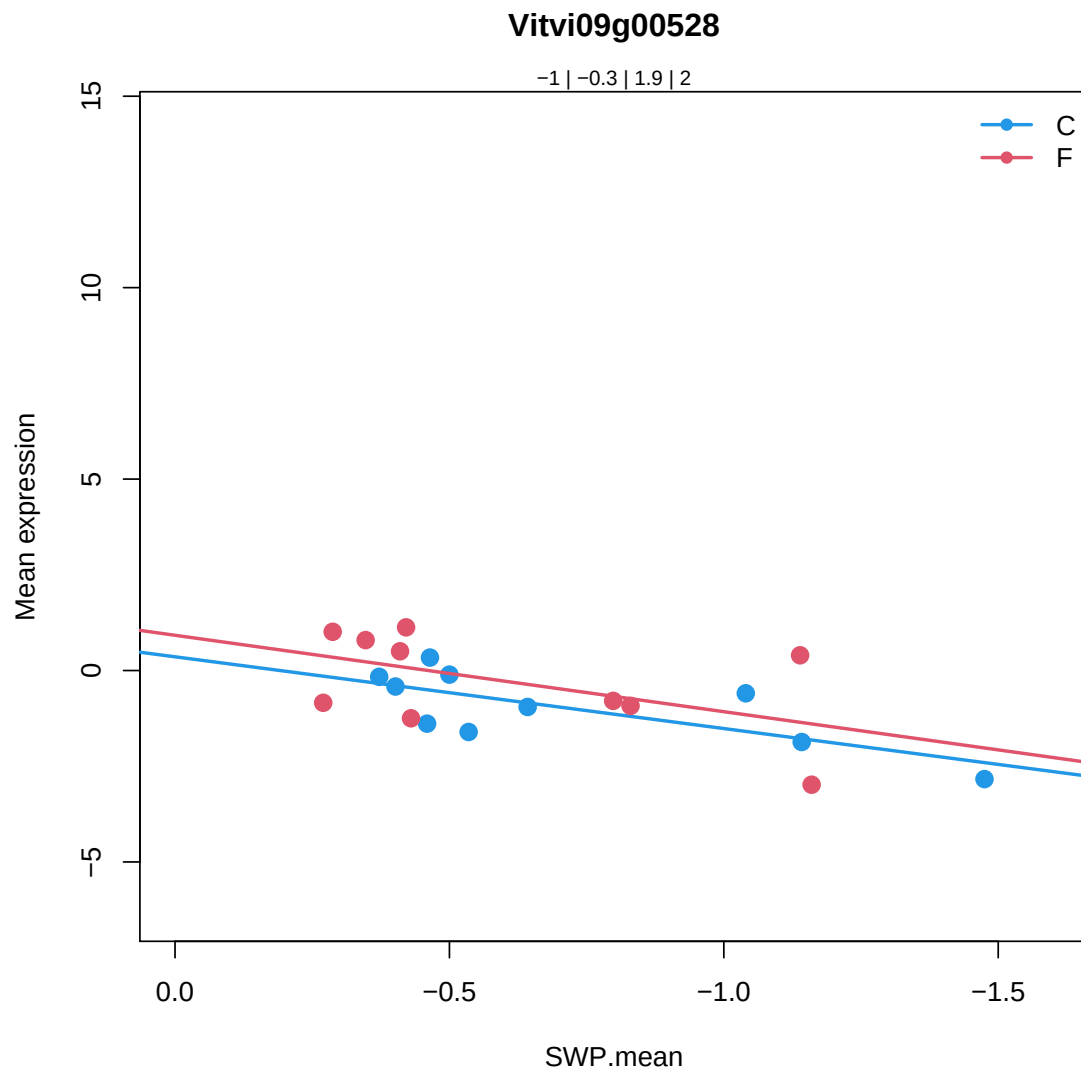
Ran BP2/NZF zinc finger-like superfamily protein |

Chr3:5315437-5316048 FORWARD LENGTH=164 |

201606

Coefficients for Vitvi09g00528.

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



8.1.107 Vitvi06g01410: Type1.0 *

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

Vitvi06g01410

35.2

not assigned.unknown

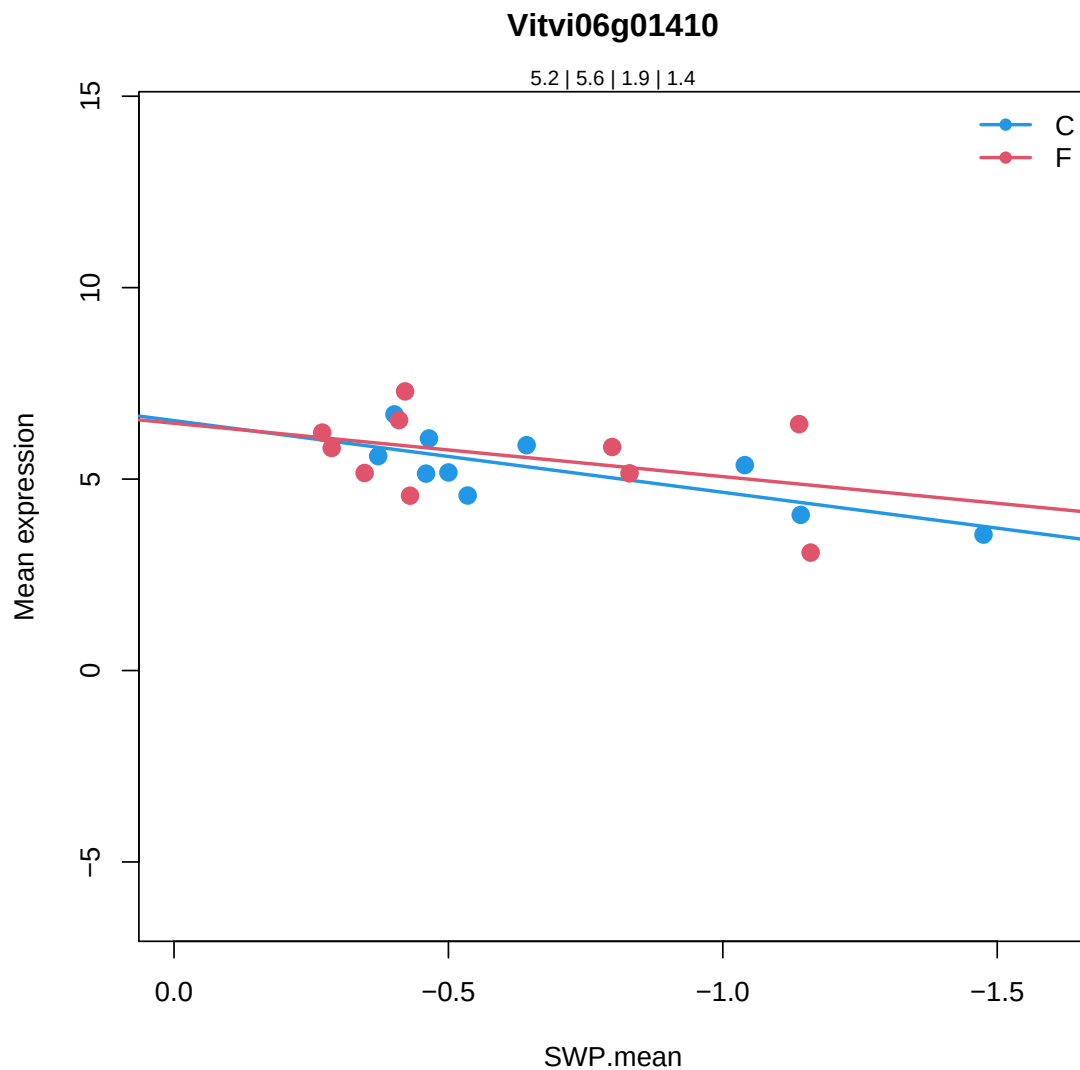
Stress responsive A/B Barrel Domain-containing protein |

Chr5:7502709-7503137 FORWARD LENGTH=111 |

201606

Coefficients for Vitvi06g01410.

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



8.1.108 Vitvi07g02064: Type1.0

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

Vitvi07g02064

17.5.2

hormone metabolism.ethylene.signal transduction

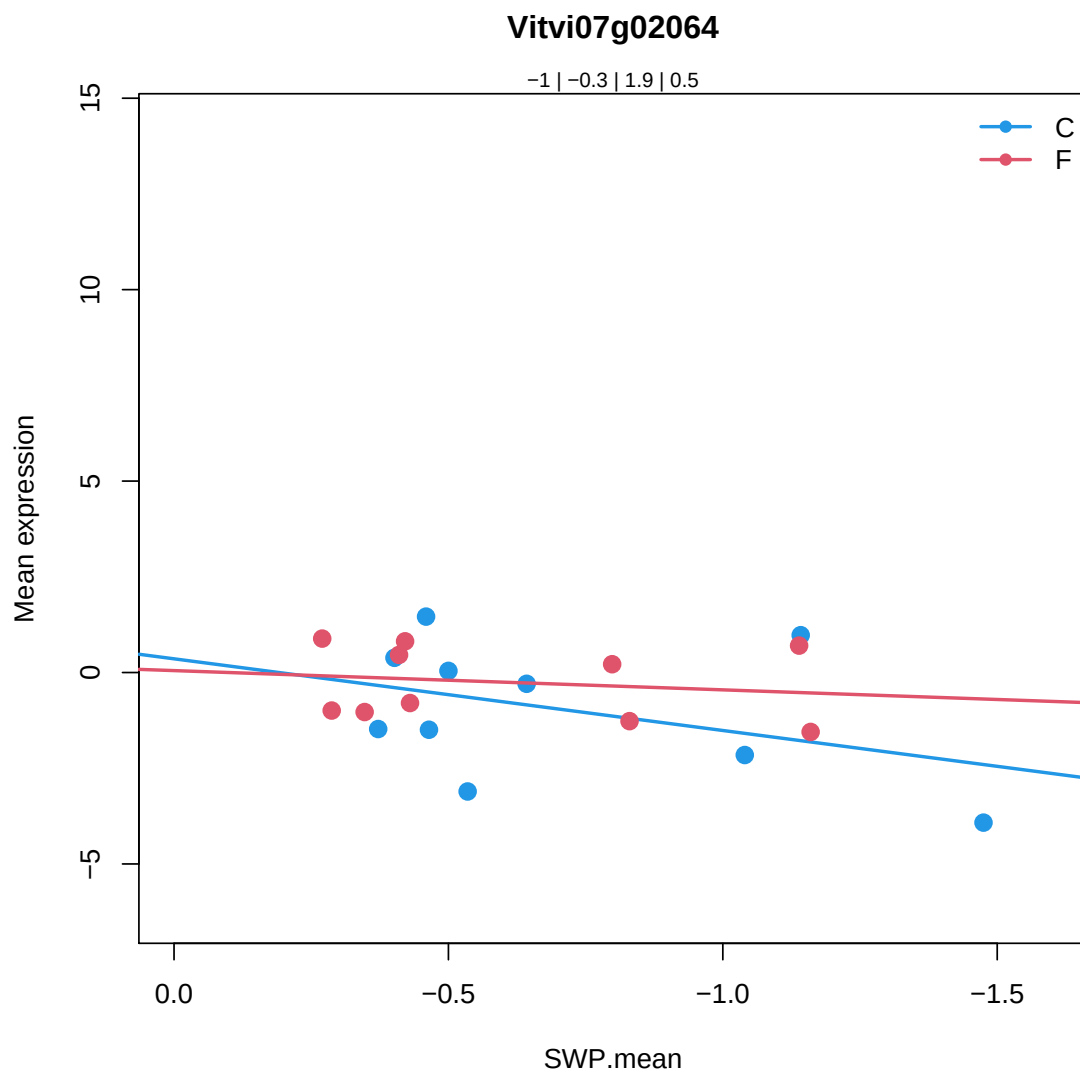
Integrase-type DNA-binding superfamily protein |

Chr3:8289647-8290066 REVERSE LENGTH=139 |

201606

Coefficients for Vitvi07g02064.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.9586707	0.02320606	*	0.02436333	*
SlopeC	1.872117	0.1005798		0.612269	
MeanF-MeanC	0.7022142	0.2190144		0.5690773	
SlopeF-SlopeC	-1.369523	0.4083109		0.9999488	



8.1.109 Vitvi18g01385: Type1.0 *

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

Vitvi18g01385

26.28

misc.GDSL-motif lipase

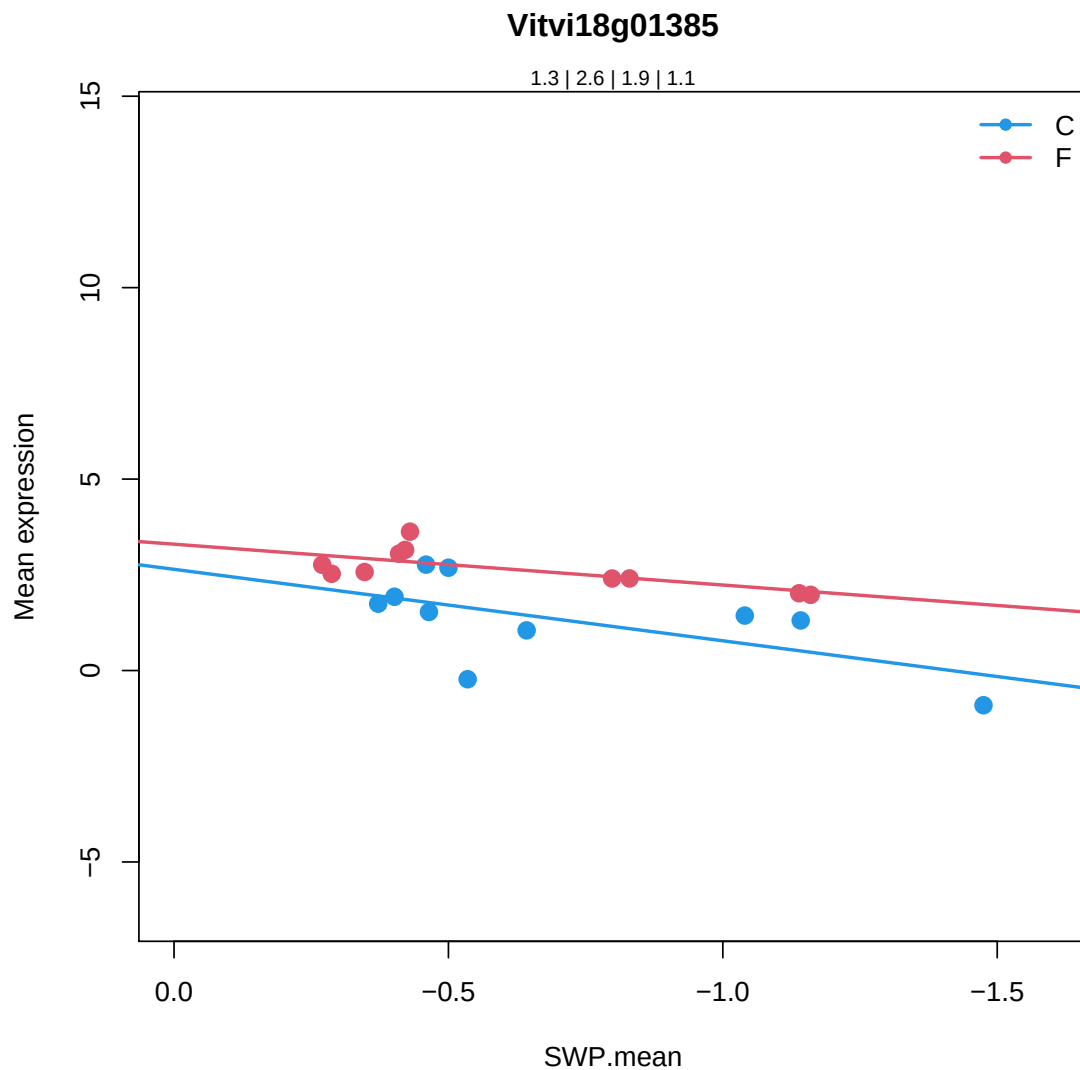
GDSL-like Lipase/Acylhydrolase superfamily protein |

Chr1:26860125-26861582 FORWARD LENGTH=374 |

201606

Coefficients for Vitvi18g01385.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.330609	3.620138e-06	***	4.12732e-06	***
SlopeC	1.866834	0.005152298	**	0.2549719	
MeanF-MeanC	1.31882	0.0002840403	***	0.004397825	**
SlopeF-SlopeC	-0.8000174	0.3797615		0.9999488	



8.1.110 Vitvi18g02632: Type1.0 *

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

Vitvi18g02632

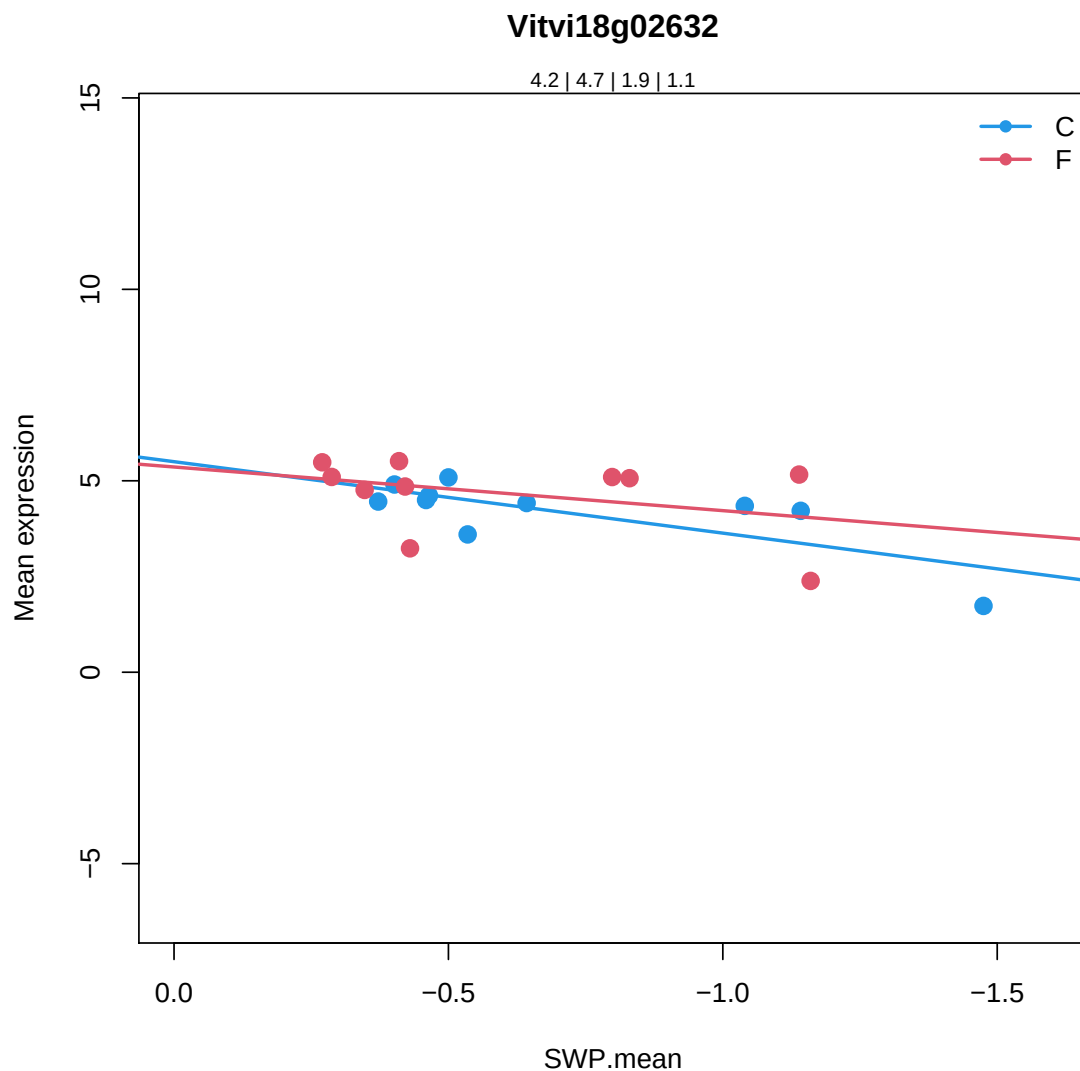
35.2

not assigned.unknown

NA

Coefficients for Vitvi18g02632.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.186783	6.373766e-14	***	9.938511e-14	***
SlopeC	1.865594	0.01263008	*	0.3271124	
MeanF-MeanC	0.4786933	0.1836661		0.519569	
SlopeF-SlopeC	-0.7256556	0.4845644		0.9999488	



8.1.111 Vitvi05g01949: Type1.0

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

Vitvi05g01949

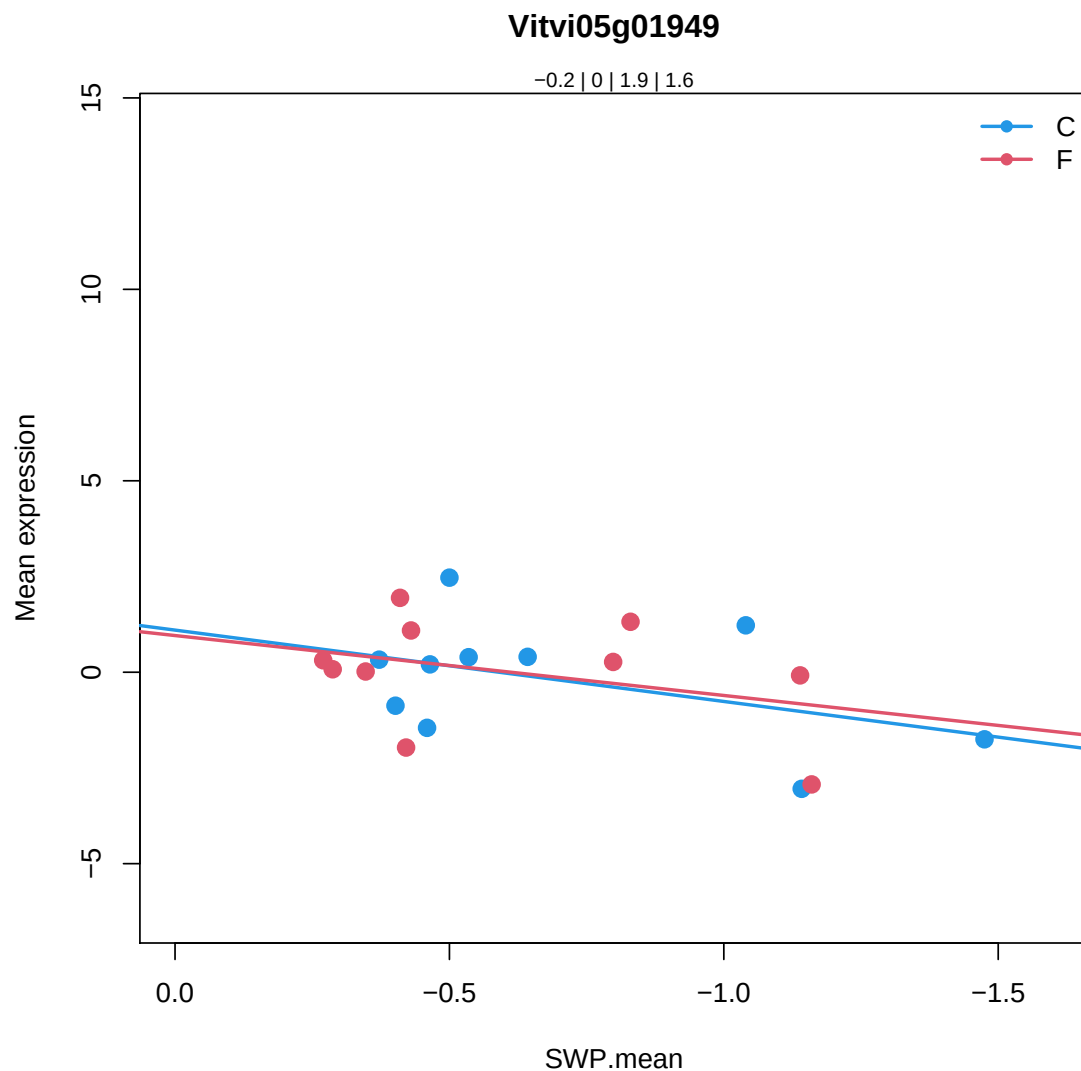
35.2

not assigned.unknown

NA

Coefficients for Vitvi05g01949.

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



8.1.112 Vitvi14g02493: Type1.0

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

Vitvi14g02493

35.2

not assigned.unknown

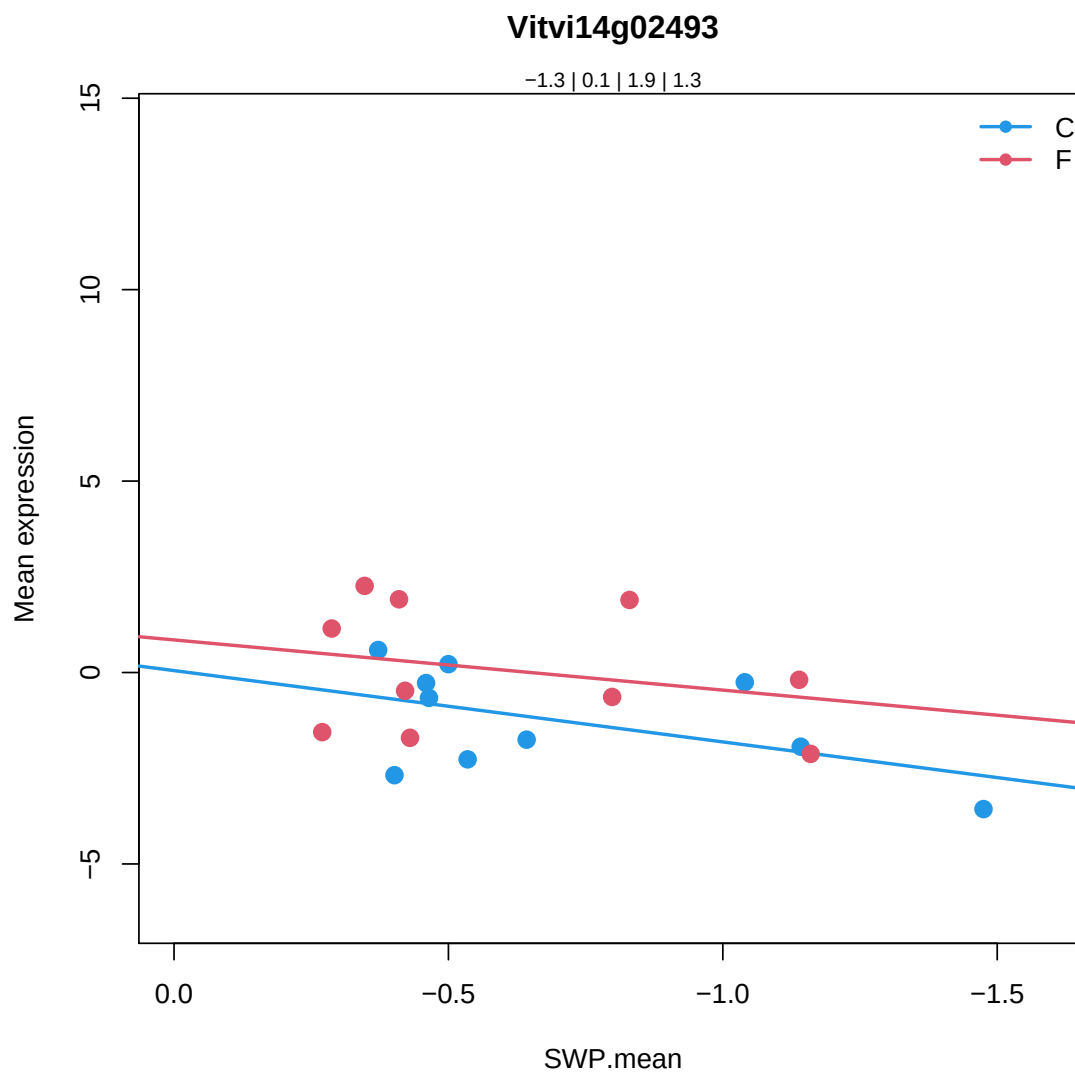
pectinesterase (Protein of unknown function%2C DUF538) |

Chr1:621637-622137 FORWARD LENGTH=166 |

201606

Coefficients for Vitvi14g02493.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.259589	0.005766001	**	0.00614025	**
SlopeC	1.862561	0.1177628		0.6341652	
MeanF-MeanC	1.312154	0.03443542	*	0.1857928	
SlopeF-SlopeC	-0.5519093	0.7487345		0.9999488	



8.1.113 Vitvi16g02005: Type1.0 *

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

Vitvi16g02005

35.2

not assigned.unknown

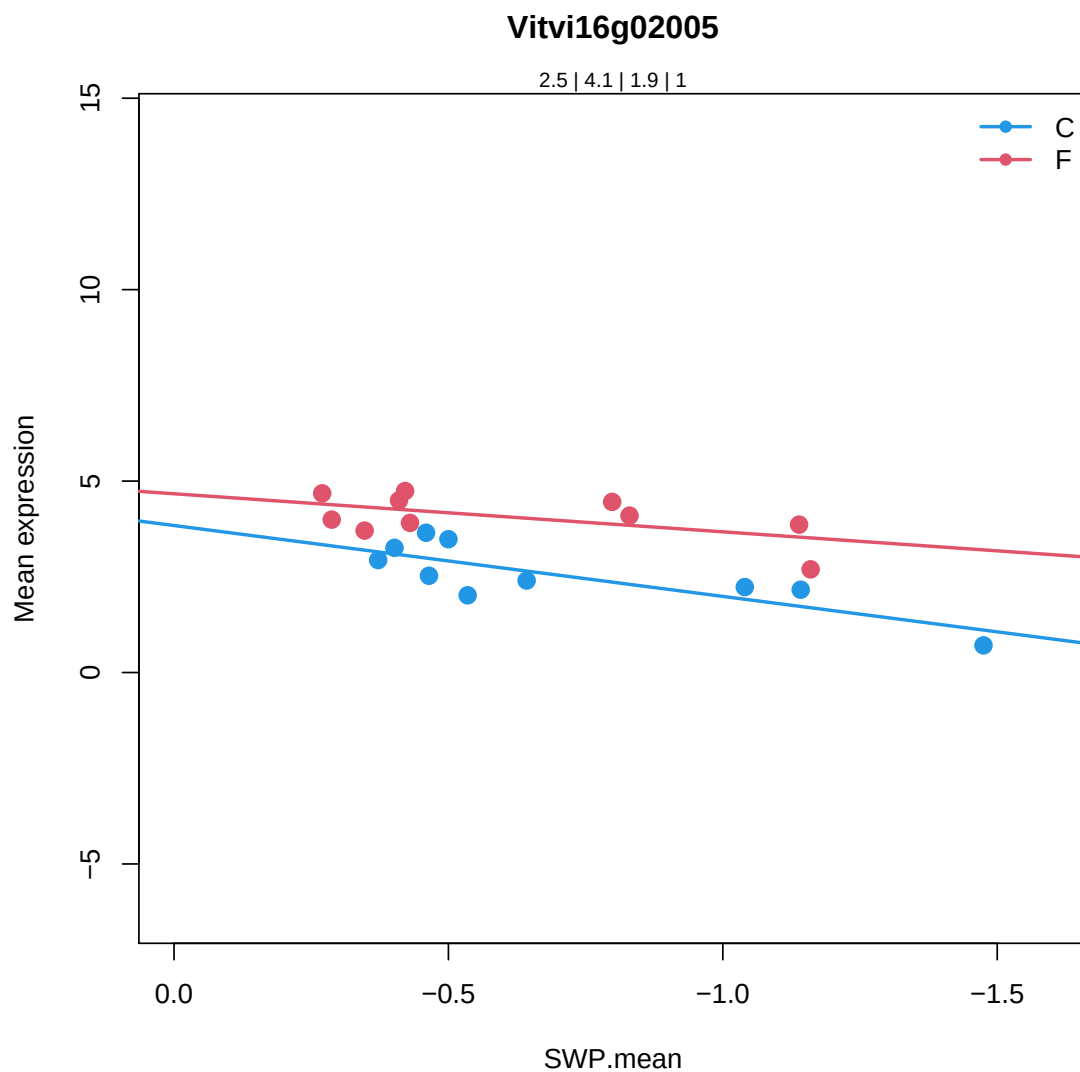
PR5-like receptor kinase |

Chr5:15293122-15295838 REVERSE LENGTH=672 |

201606

Coefficients for Vitvi16g02005.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.537556	3.988805e-13	***	5.873948e-13	***
SlopeC	1.85145	0.0005381335	***	0.1005065	
MeanF-MeanC	1.525691	1.433772e-06	***	4.522889e-05	***
SlopeF-SlopeC	-0.8573839	0.2196113		0.9999488	



8.1.114 Vitvi19g01964: Type1.0 *

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

Vitvi19g01964

29.4

protein.postranslational modification

S-locus lectin protein kinase family protein |

Chr4:13666281-13669202 FORWARD LENGTH=829 |

201606

Vitvi19g01964

35.2

not assigned.unknown

S-locus lectin protein kinase family protein |

Chr4:13666281-13669202 FORWARD LENGTH=829 |

201606

Vitvi19g01964

30.2.24

signalling.receptor kinases.S-locus glycoprotein like

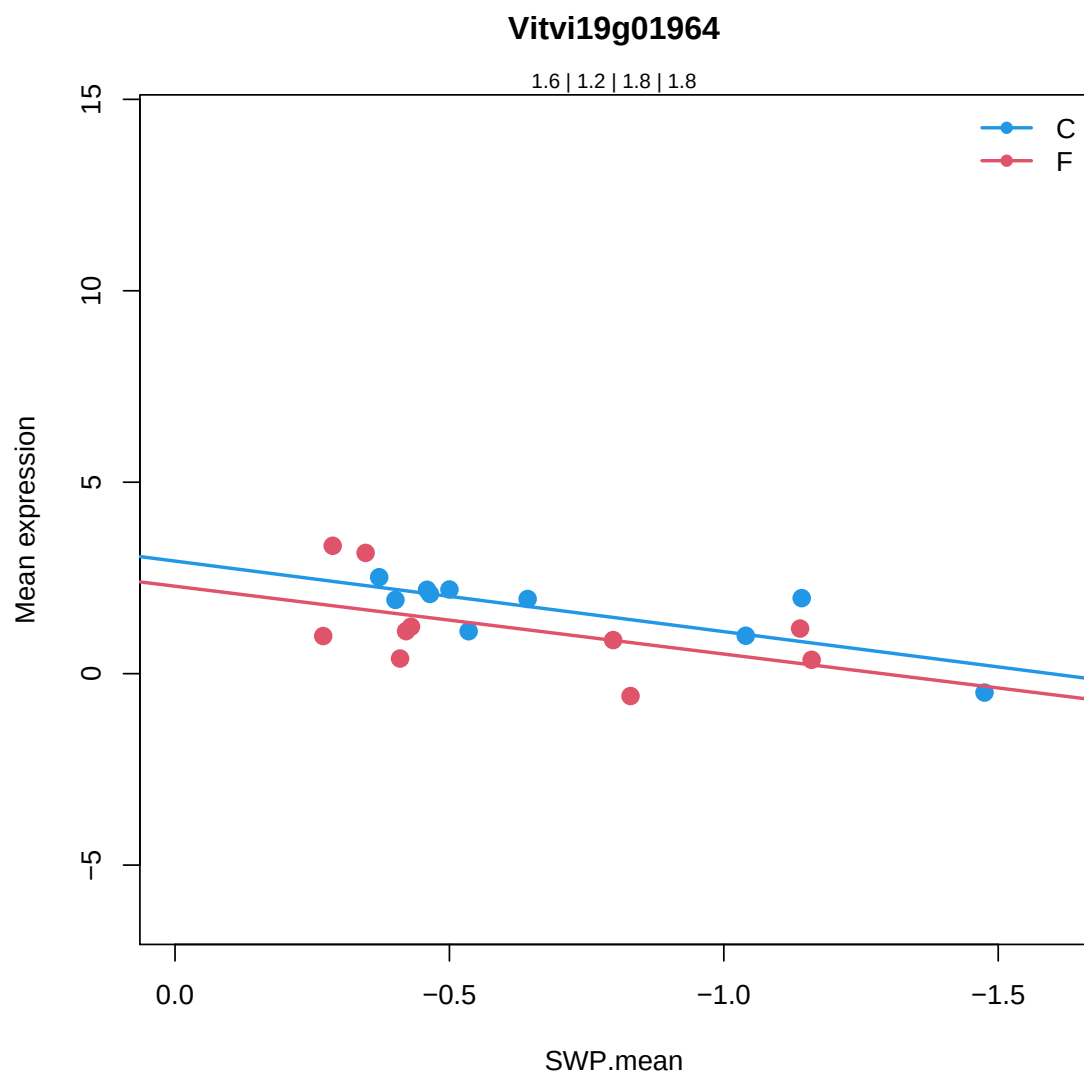
S-locus lectin protein kinase family protein |

Chr4:13666281-13669202 FORWARD LENGTH=829 |

201606

Coefficients for Vitvi19g01964.

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



8.1.115 Vitvi02g00114: Type1.0 *

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

Vitvi02g00114

27.3.32

RNA.regulation of transcription.WRKY domain transcription factor famil

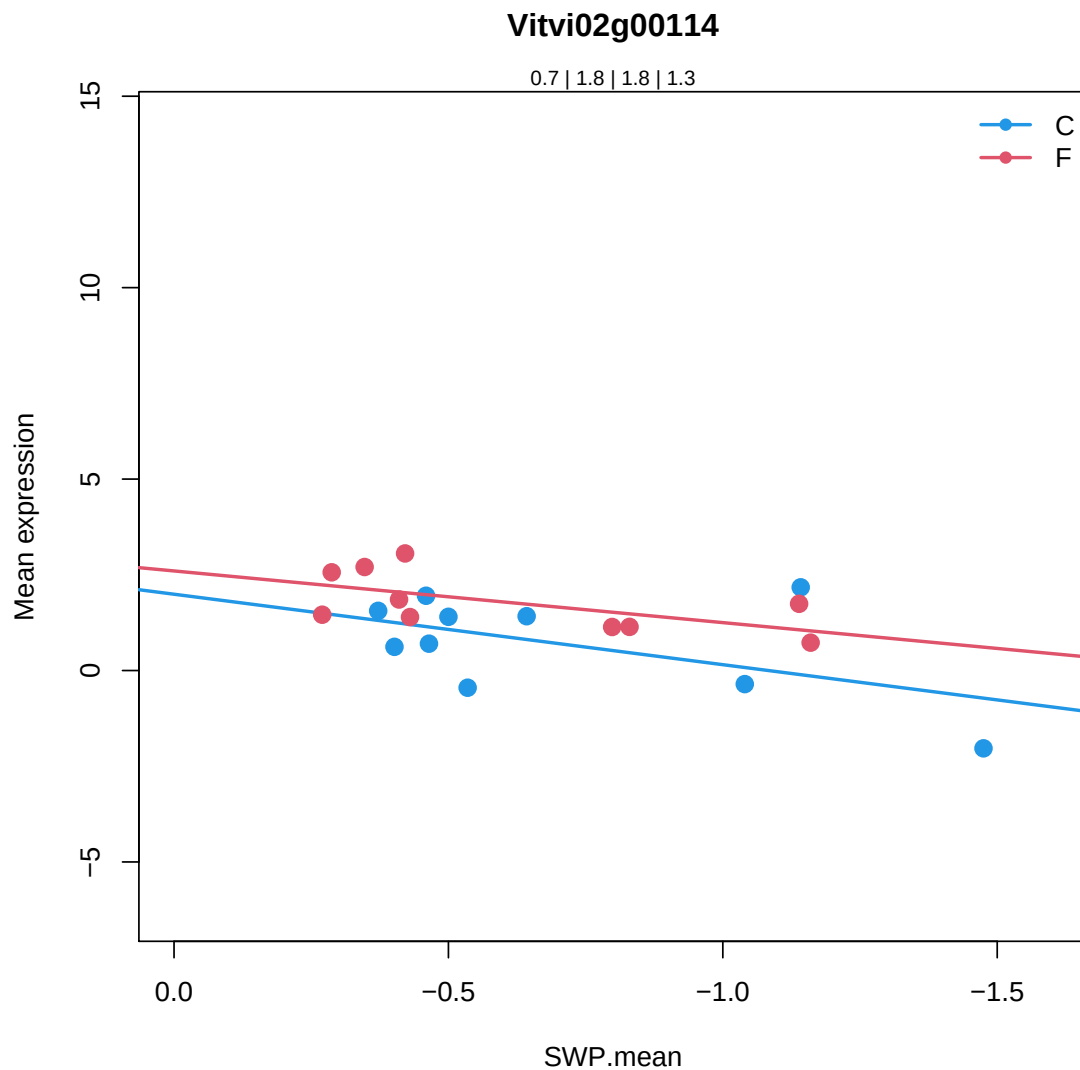
WRKY family transcription factor |

Chr4:12392666-12393739 REVERSE LENGTH=324 |

201606

Coefficients for Vitvi02g00114.

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



8.1.116 Vitvi16g02002: Type1.0 *

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

Vitvi16g02002

35.2

not assigned.unknown

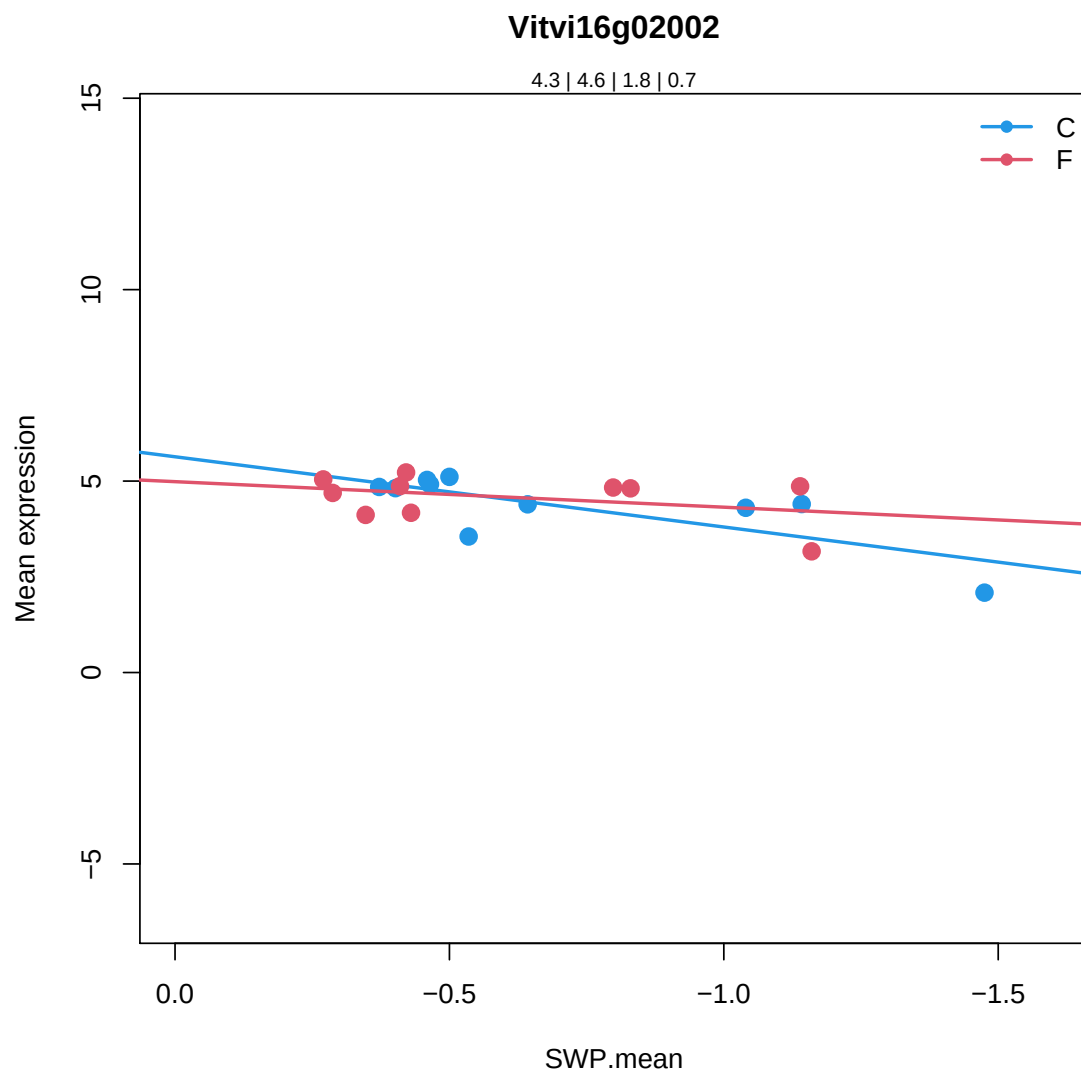
suppressor of npr1-1 constitutive 4 |

Chr1:24997491-25001961 REVERSE LENGTH=1101 |

201606

Coefficients for Vitvi16g02002.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.345001	9.313224e-17	***	2.036324e-16	***
SlopeC	1.83438	0.001837421	**	0.160246	
MeanF-MeanC	0.2334813	0.3835662		0.7340008	
SlopeF-SlopeC	-1.167749	0.1432418		0.9999488	



8.1.117 Vitvi16g01418: Type1.0

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

Vitvi16g01418

10.8.1

cell wall.pectinesterases.PME

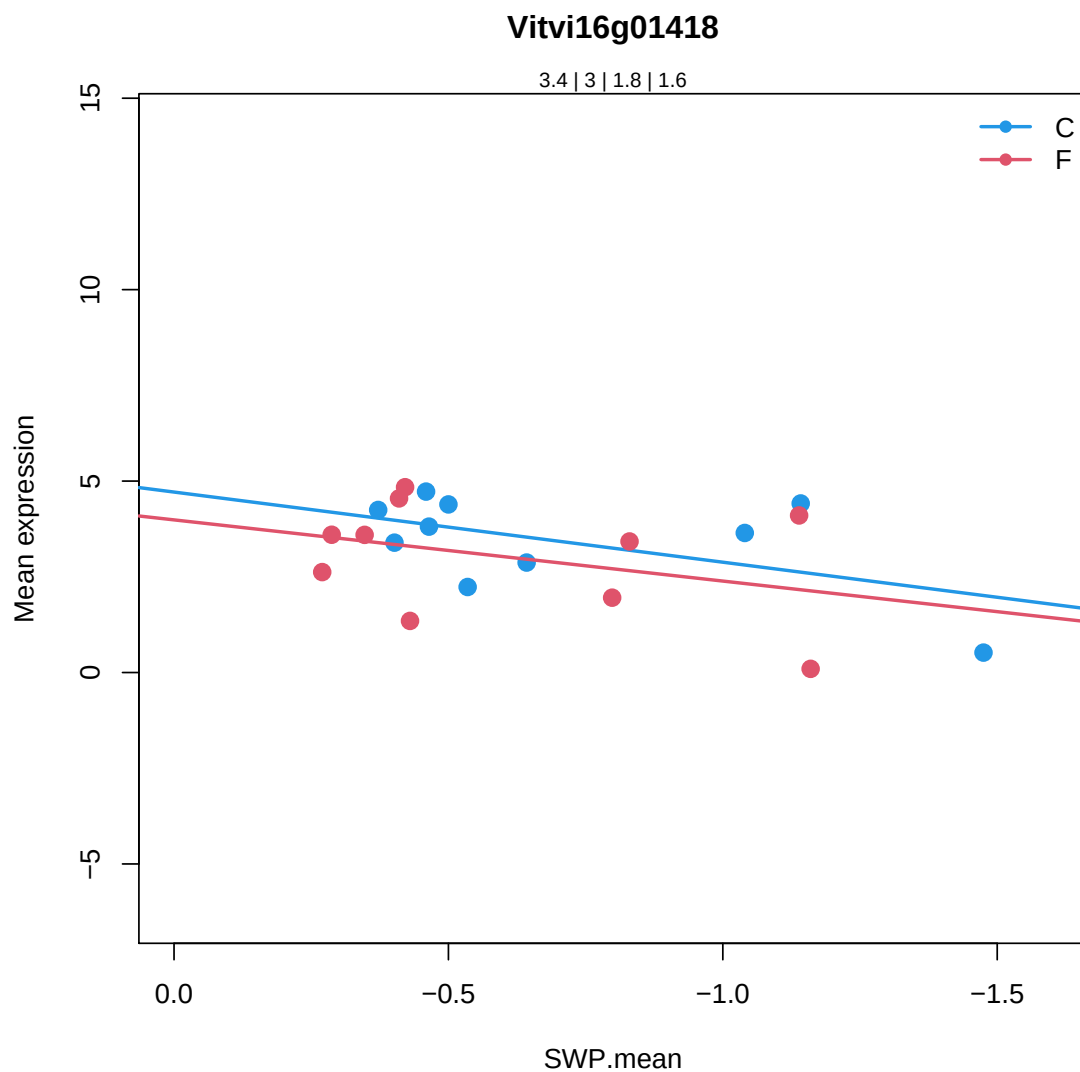
Plant invertase/pectin methylesterase inhibitor superfamily |

Chr3:18249840-18253647 FORWARD LENGTH=598 |

201606

Coefficients for Vitvi16g01418.

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



8.1.118 Vitvi05g01743: Type1.0

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

Vitvi05g01743

35.2

not assigned.unknown

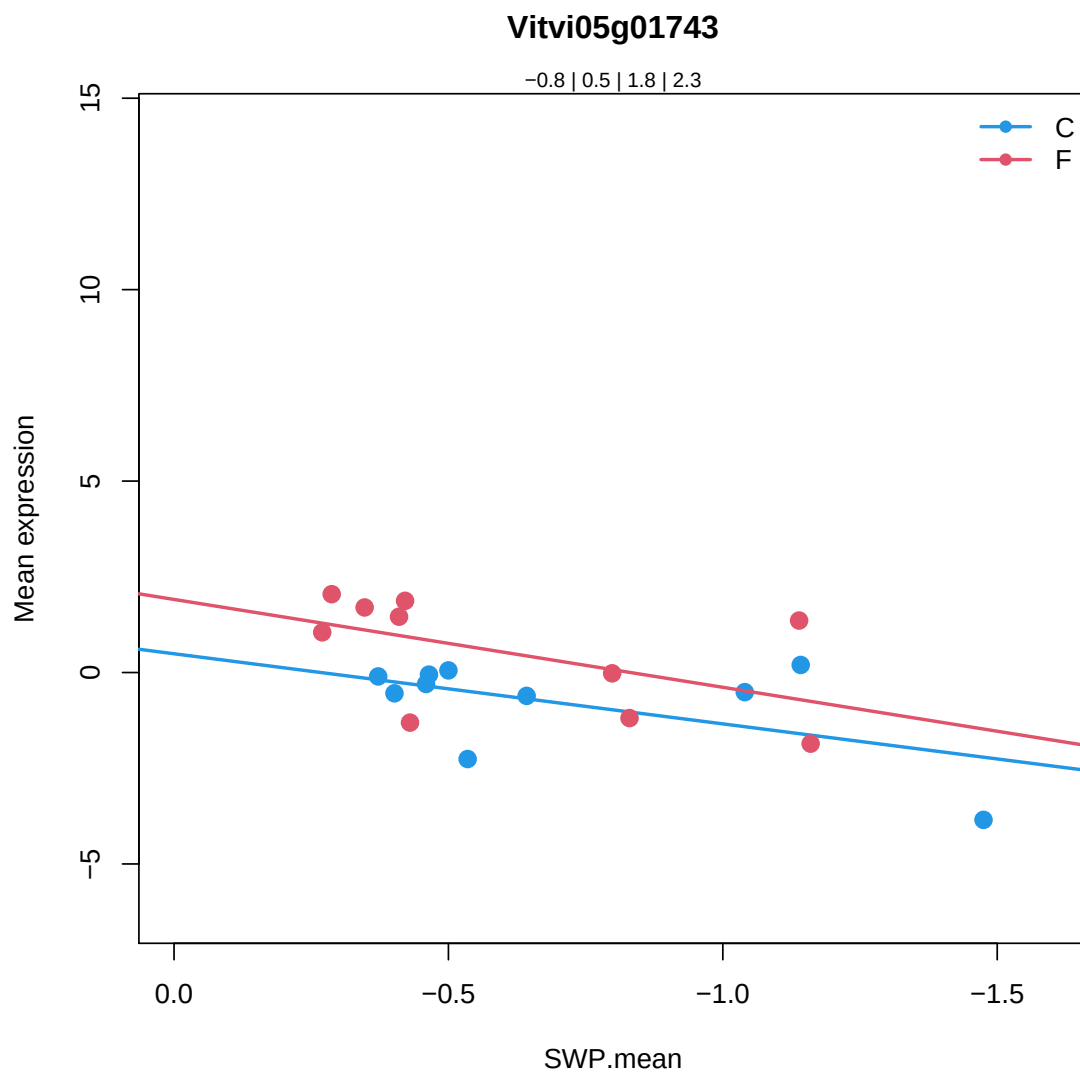
hypothetical protein |

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	



8.1.119 Vitvi16g01999: Type1.0 *

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

Vitvi16g01999

35.2

not assigned.unknown

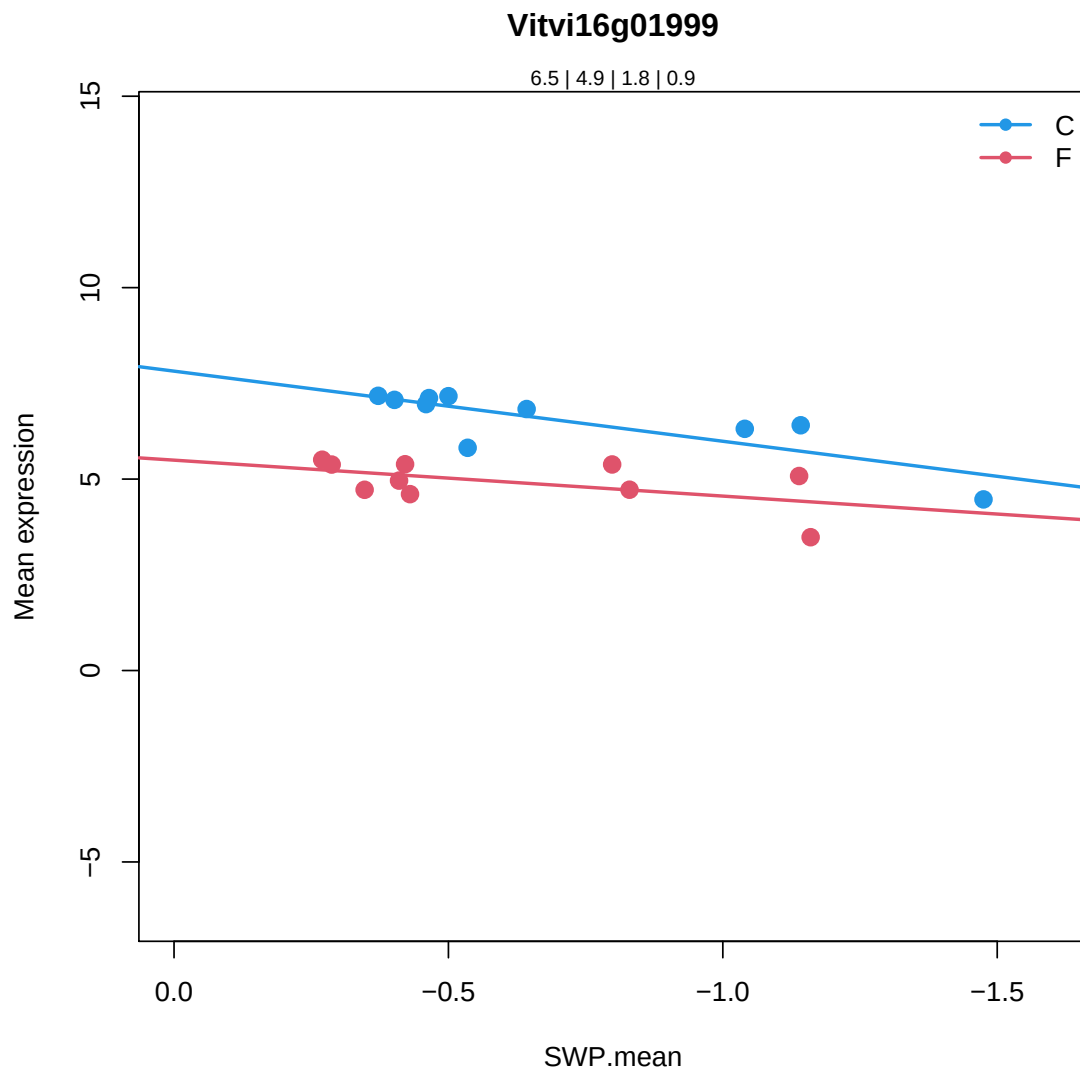
suppressor of npr1-1 constitutive 4 |

Chr1:24997491-25001961 REVERSE LENGTH=1101 |

201606

Coefficients for Vitvi16g01999.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.531361	1.551435e-21	***	1.603185e-20	***
SlopeC	1.831231	0.0006461652	***	0.1015345	
MeanF-MeanC	-1.608841	7.327582e-07	***	2.465497e-05	***
SlopeF-SlopeC	-0.8927148	0.2052796		0.9999488	



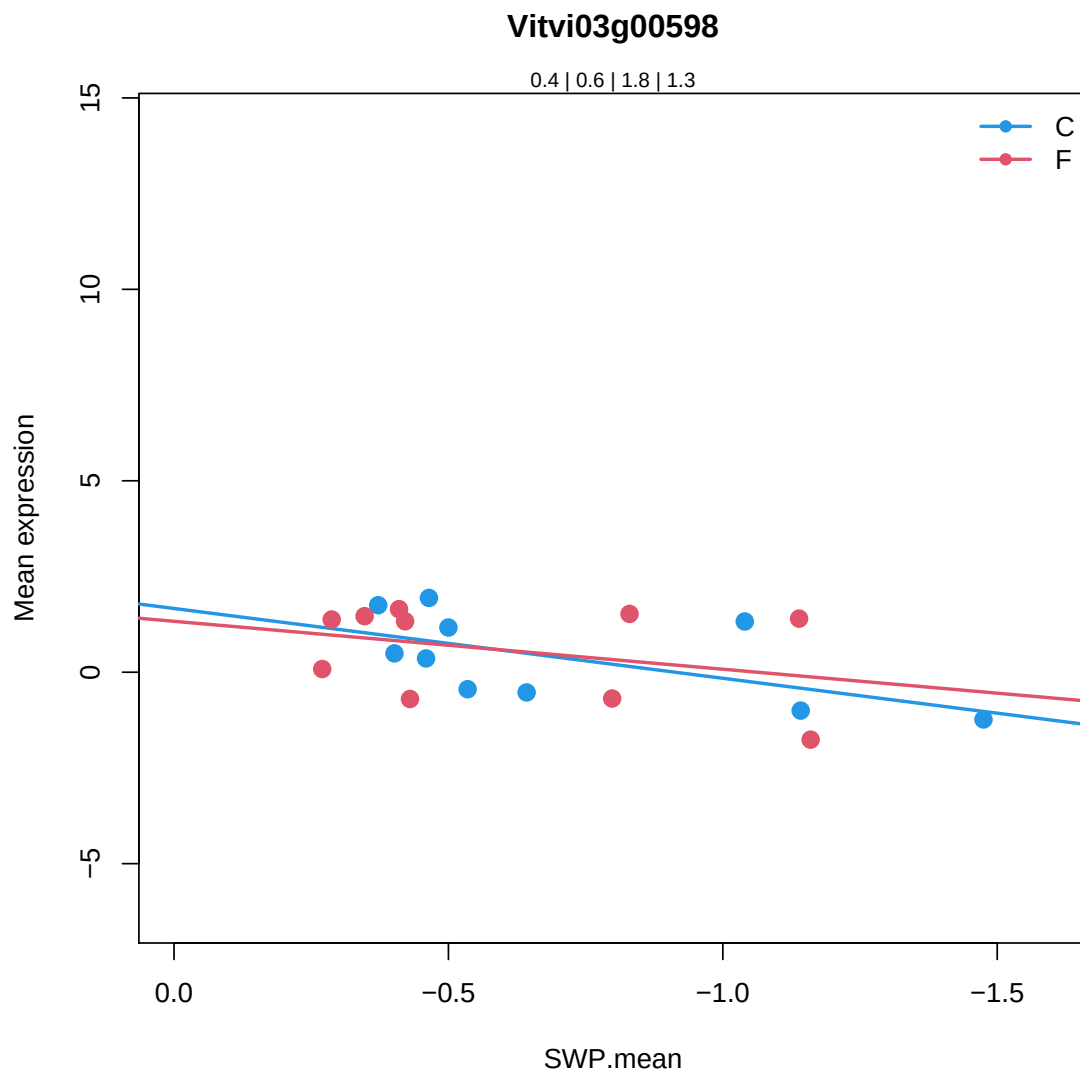
8.1.120 Vitvi03g00598: Type1.0 *

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

```
Vitvi03g00598
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi03g00598.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3827826	0.2329315		0.238246	
SlopeC	1.82289	0.04761637	*	0.4998407	
MeanF-MeanC	0.1848456	0.6792737		0.8960957	
SlopeF-SlopeC	-0.5715636	0.6624575		0.9999488	



8.1.121 Vitvi17g01520: Type1.0 *

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

Vitvi17g01520

20.1.7.1

stress.biotic.PR-proteins.PR1 (antifungal)

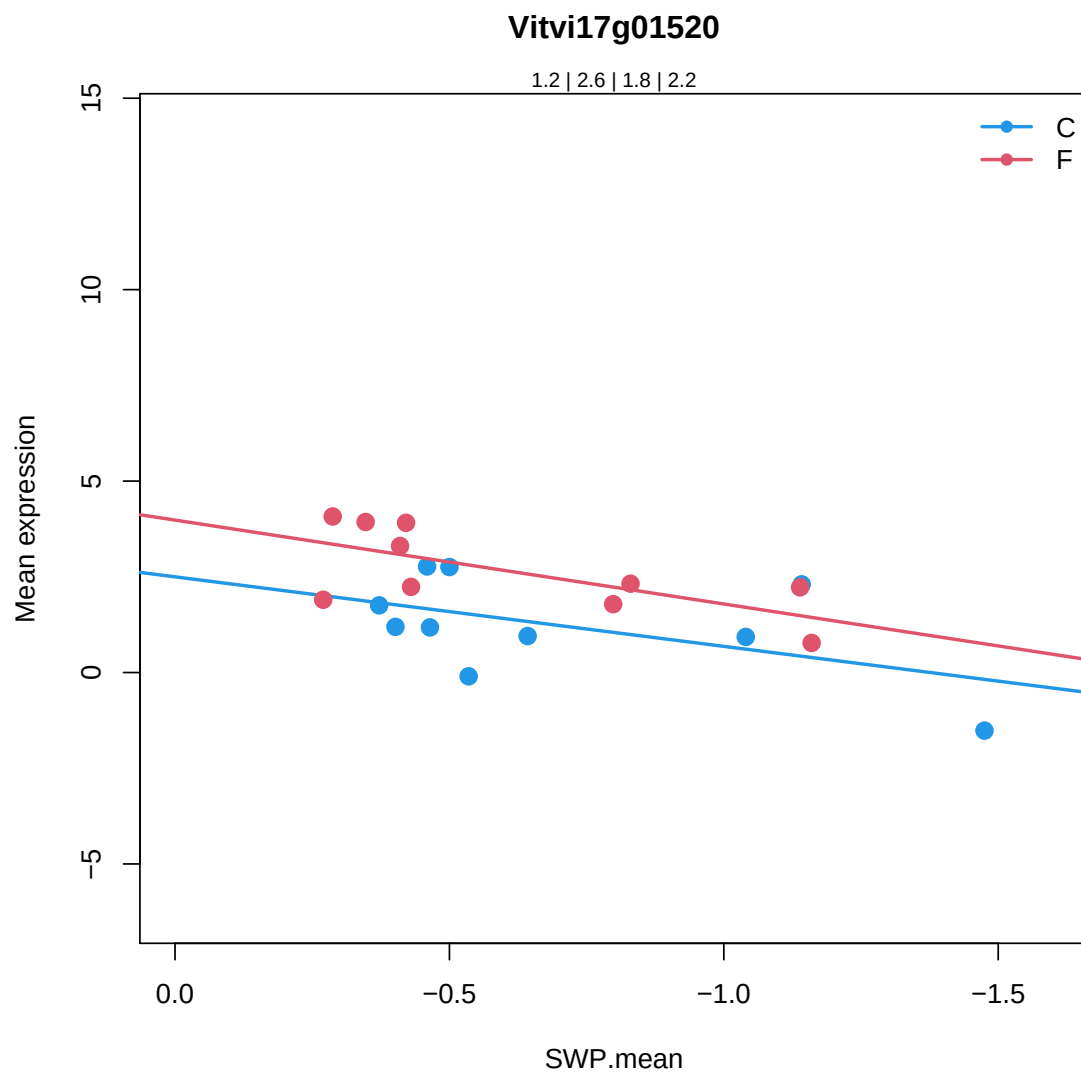
alpha/beta-Hydrolases superfamily protein |

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	



8.1.122 Vitvi06g00665: Type1.0 *

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

Vitvi06g00665

35.2

not assigned.unknown

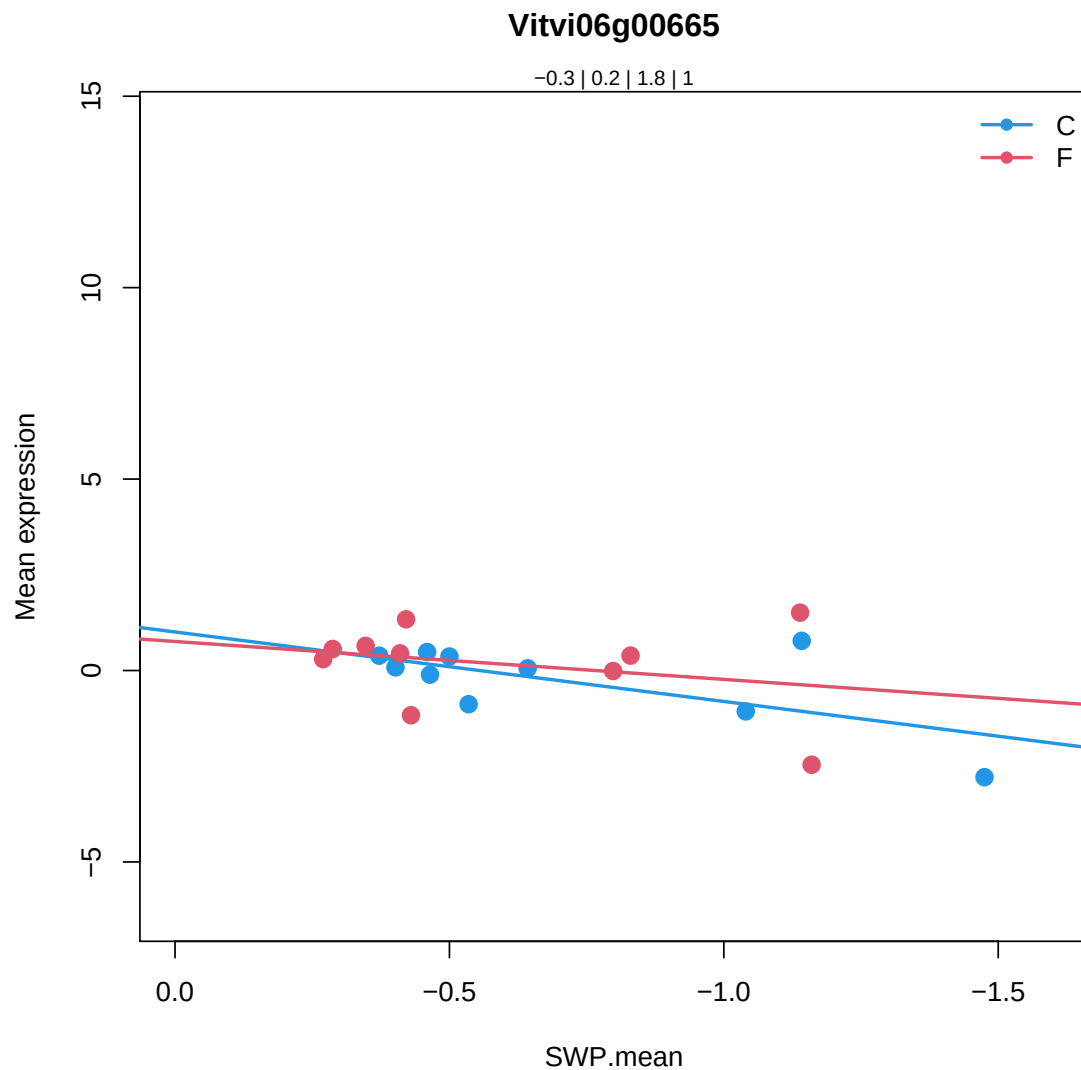
Pmr5/Cas1p GDSL/SGNH-like acyl-esterase family protein (DUF828) |

Chr5:23684372-23685679 REVERSE LENGTH=291 |

201606

Coefficients for Vitvi06g00665.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.2691995	0.3700074		0.3761273	
SlopeC	1.815095	0.0373806	*	0.4623401	
MeanF-MeanC	0.4240484	0.3191214		0.6800376	
SlopeF-SlopeC	-0.8248166	0.505297		0.9999488	



8.1.123 Vitvi05g00953: Type1.0

```
> 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

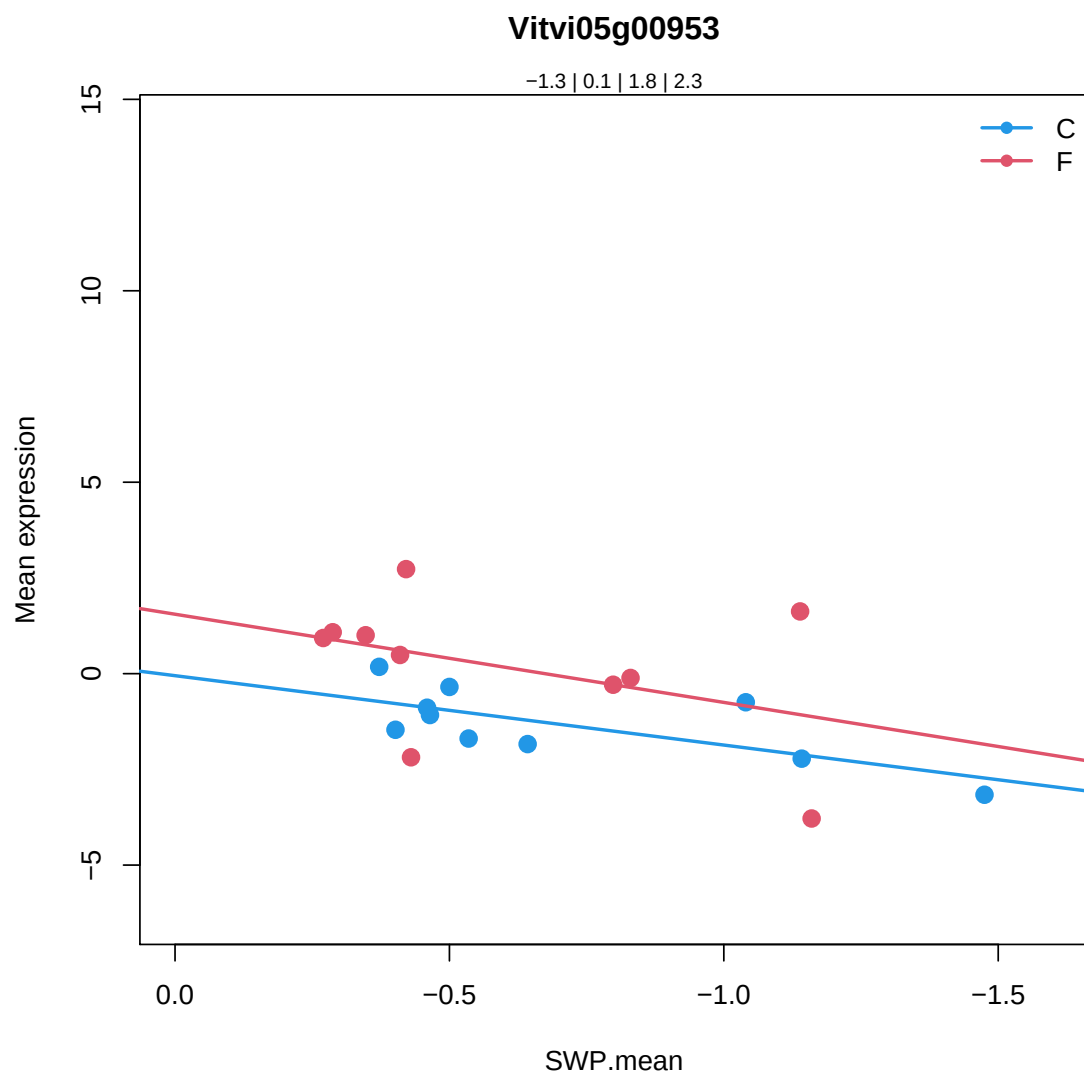
Pectin lyase-like superfamily protein |

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	



8.1.124 Vitvi02g00220: Type1.0

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

```
Vitvi02g00220
```

```
34.12
```

```
transport.metal
```

```
YELLOW STRIPE like 3 |
```

```
Chr5:21756081-21758776 FORWARD LENGTH=675 |
```

```
201606
```

```
Vitvi02g00220
```

```
34.13
```

```
transport.peptides and oligopeptides
```

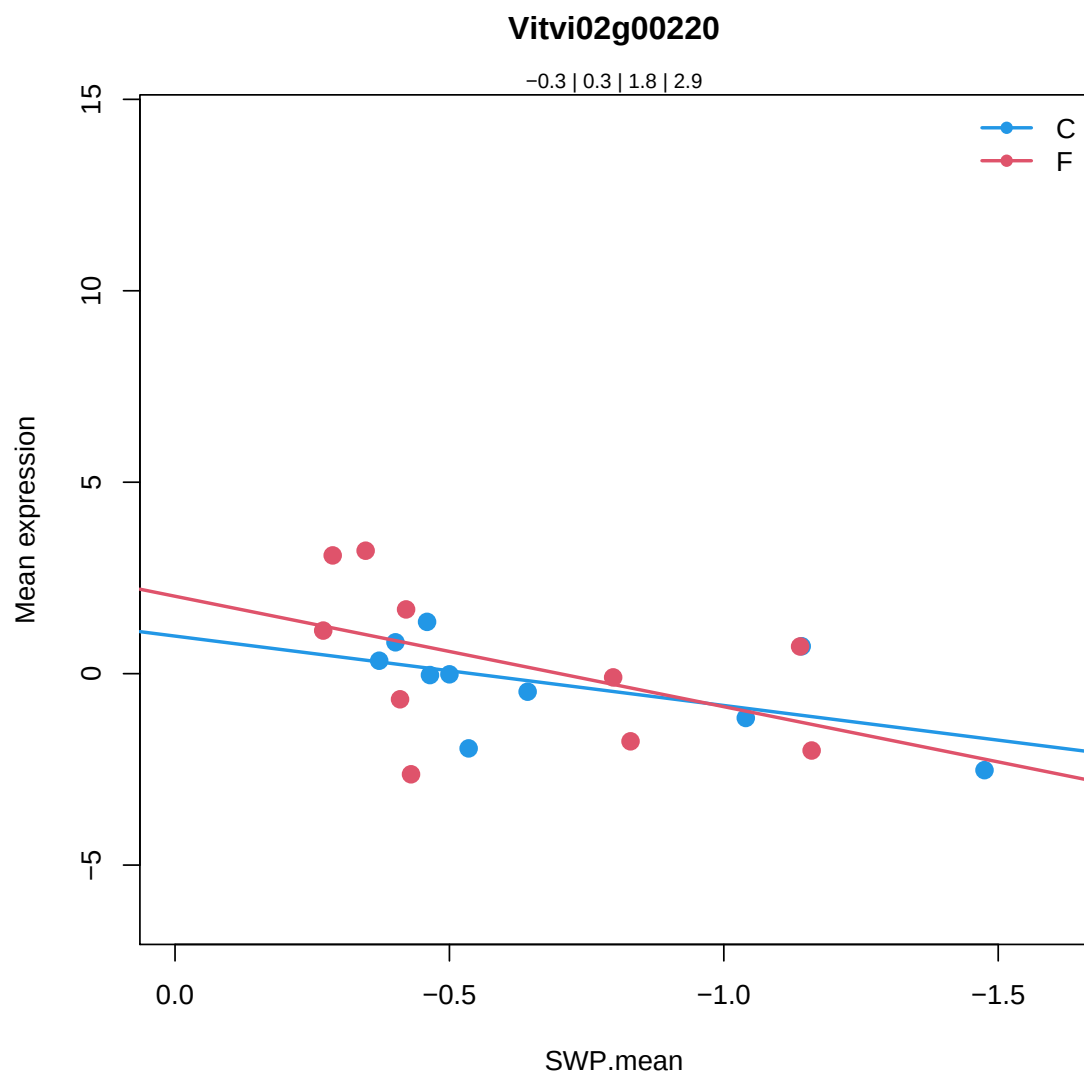
```
YELLOW STRIPE like 3 |
```

```
Chr5:21756081-21758776 FORWARD LENGTH=675 |
```

```
201606
```

Coefficients for Vitvi02g00220.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.293284	0.5068504		0.5130098	
SlopeC	1.811976	0.1484275		0.6739149	
MeanF-MeanC	0.5573513	0.3744198		0.7276434	
SlopeF-SlopeC	1.072524	0.557301		0.9999488	



8.1.125 Vitvi16g00890: Type1.0

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

Vitvi16g00890

17.6.1.11

hormone metabolism.gibberelin.synthesis-degradation.GA20 oxidase

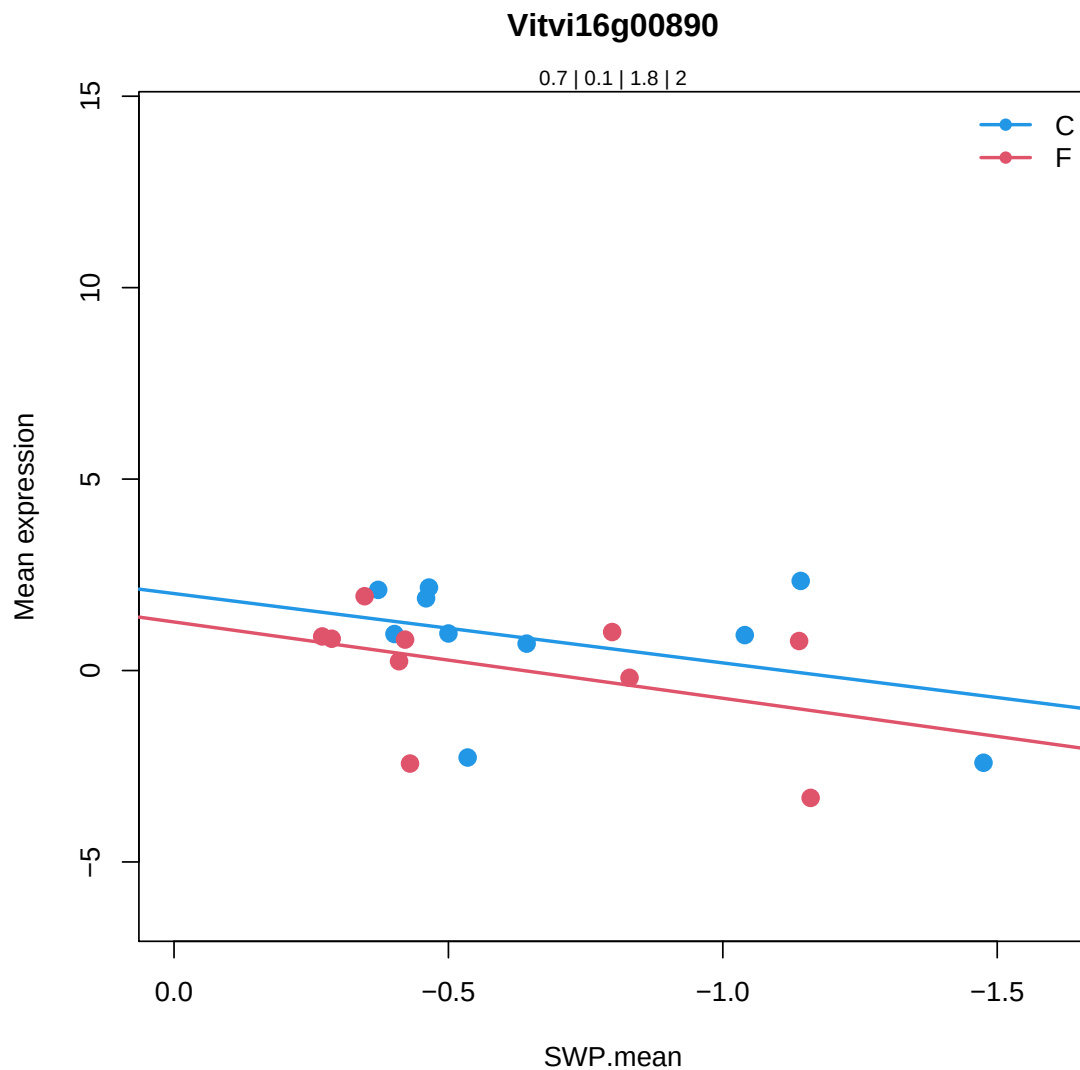
2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein

Chr4:12991325-12992409 REVERSE LENGTH=297 |

201606

Coefficients for Vitvi16g00890.

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



8.1.126 Vitvi16g01989: Type1.0 *

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

Vitvi16g01989

35.2

not assigned.unknown

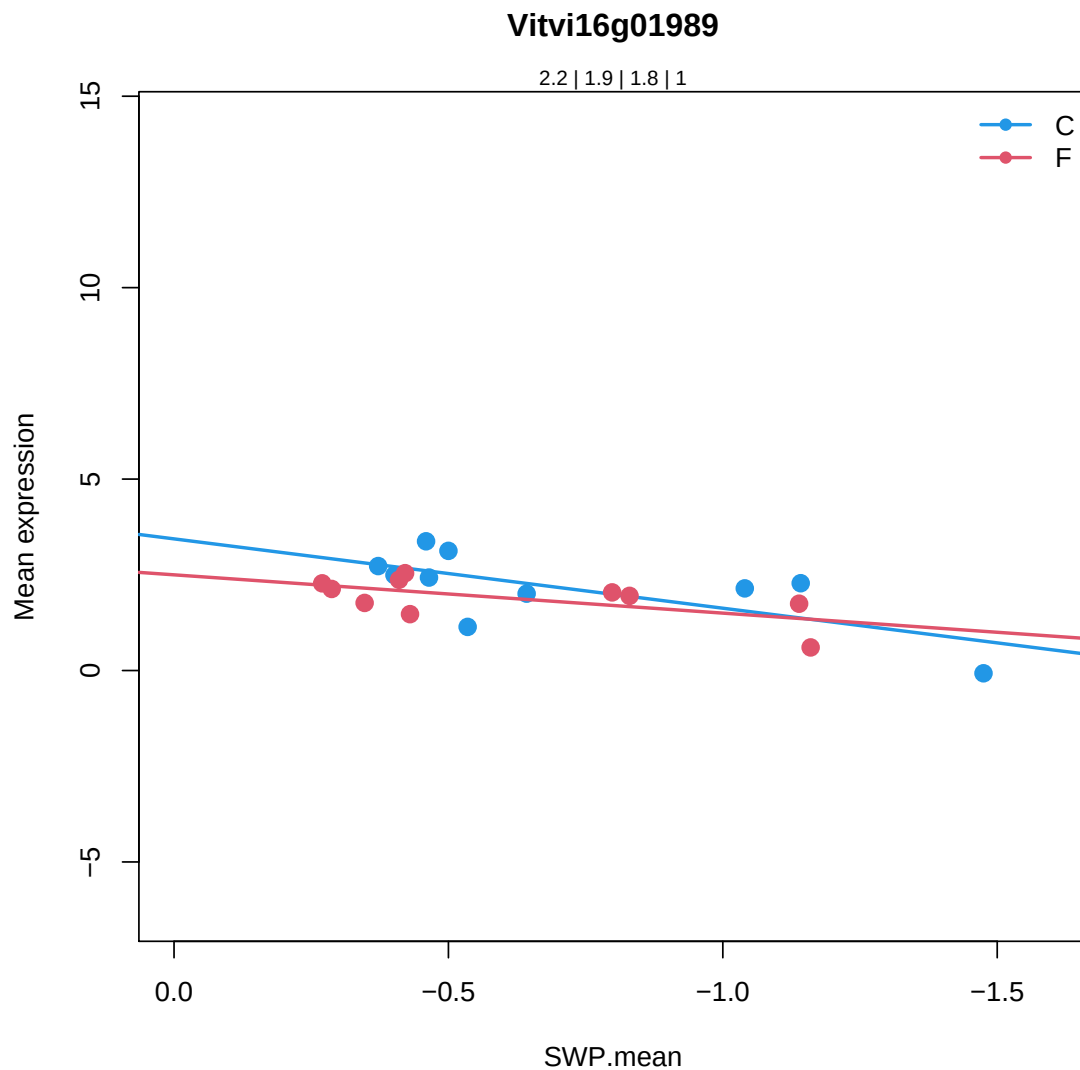
Protein kinase superfamily protein |

Chr1:24961634-24963941 REVERSE LENGTH=663 |

201606

Coefficients for Vitvi16g01989.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.164844	1.461984e-10	***	1.901977e-10	***
SlopeC	1.810698	0.002485977	**	0.1896965	
MeanF-MeanC	-0.2752542	0.3170707		0.6785233	
SlopeF-SlopeC	-0.8103771	0.314483		0.9999488	



8.1.127 Vitvi16g01257: Type1.0 *

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

Vitvi16g01257

35.2

not assigned.unknown

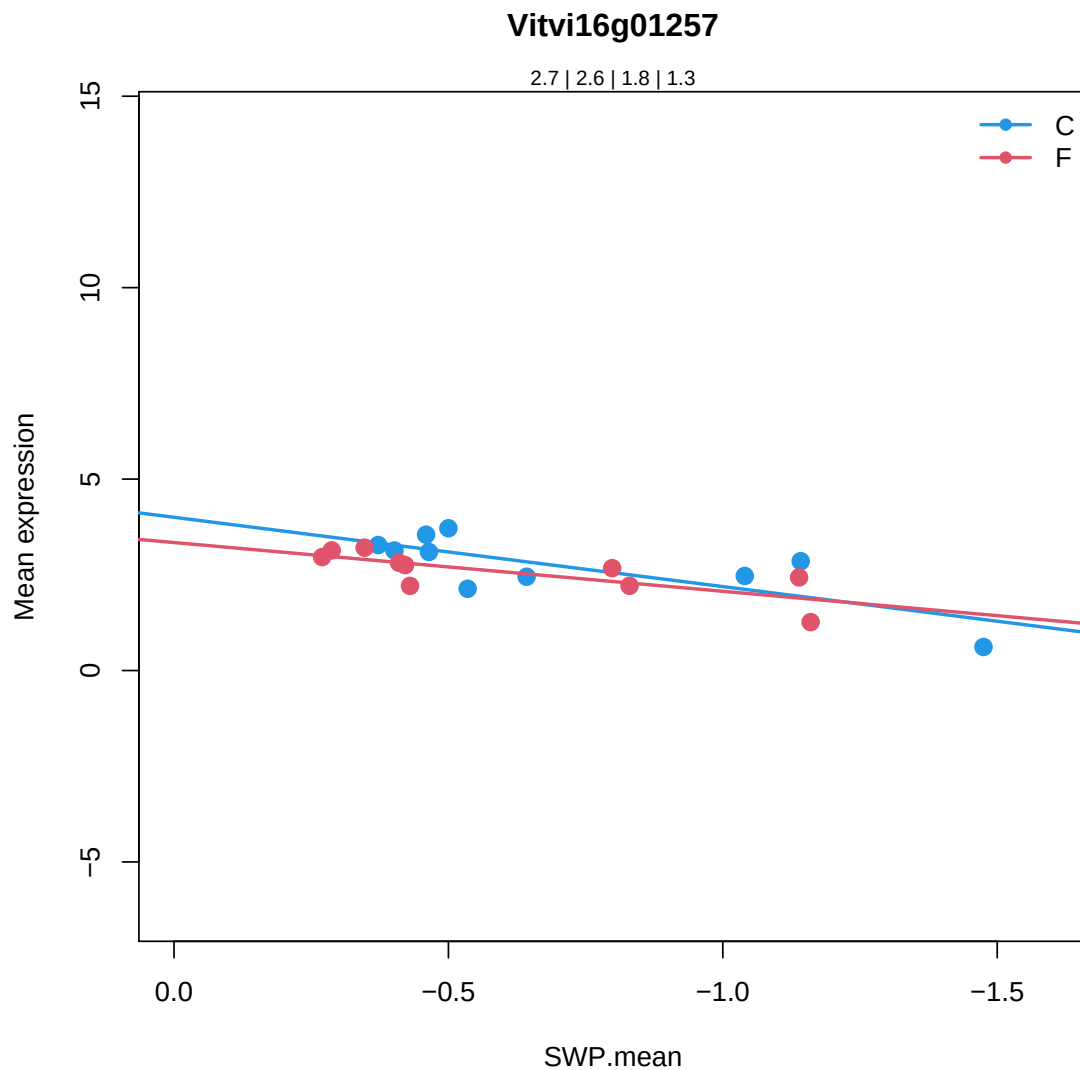
PR5-like receptor kinase |

Chr5:15293325-15295838 REVERSE LENGTH=665 |

201606

Coefficients for Vitvi16g01257.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.729406	6.572807e-14	***	1.023526e-13	***
SlopeC	1.809774	0.000565135	***	0.1005065	
MeanF-MeanC	-0.1625724	0.4825374		0.7965813	
SlopeF-SlopeC	-0.5368769	0.4290832		0.9999488	



8.1.128 Vitvi18g01098: Type1.0

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

Vitvi18g01098

10.6.1

cell wall.degradation.cellulases and beta-1,4-glucanases

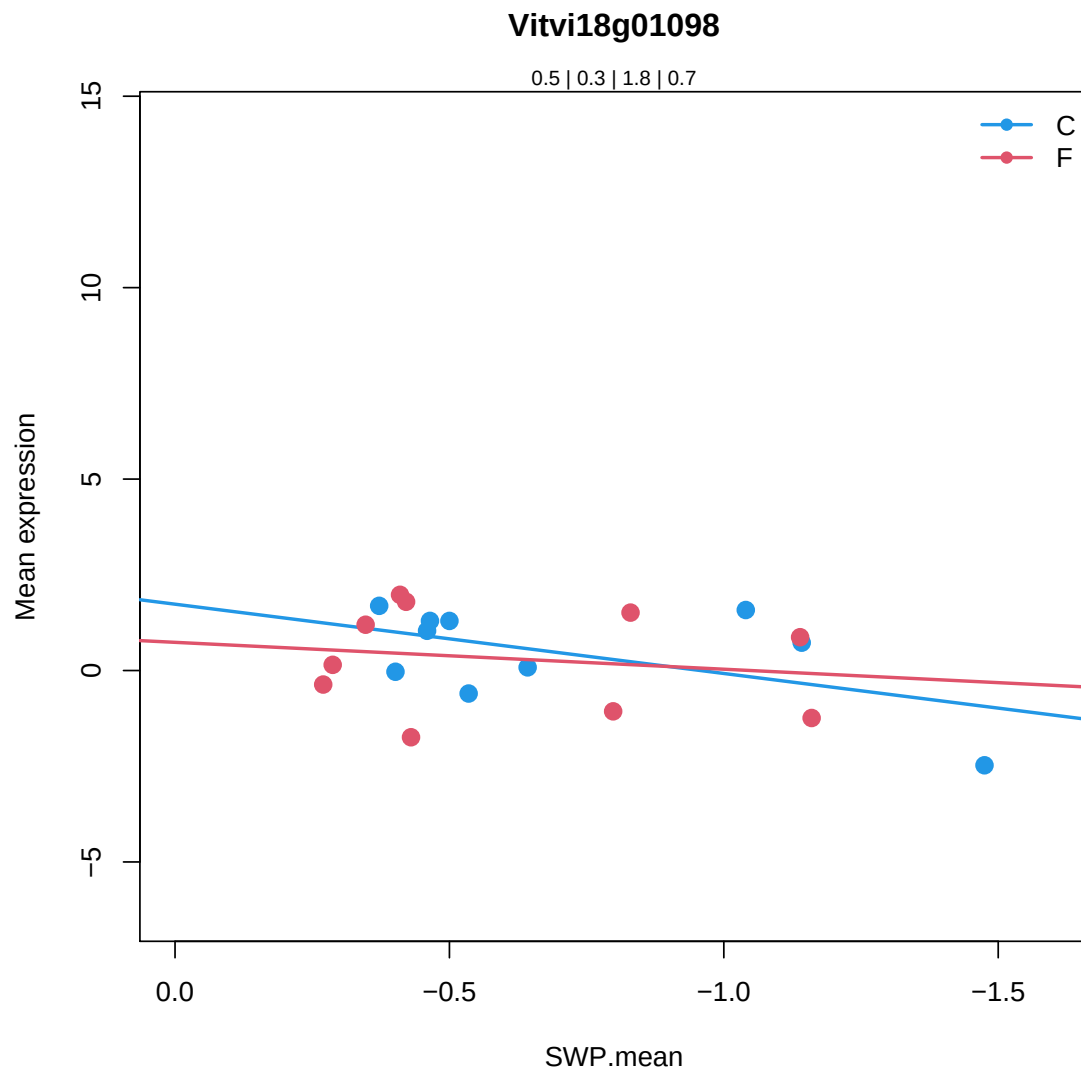
glycosyl hydrolase 9B5 |

Chr1:6918323-6920268 REVERSE LENGTH=515 |

201606

Coefficients for Vitvi18g01098.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4597451	0.2151043		0.2203226	
SlopeC	1.809645	0.08476099	.	0.5859079	
MeanF-MeanC	-0.1513939	0.7689834		0.932817	
SlopeF-SlopeC	-1.107637	0.4653993		0.9999488	



8.1.129 Vitvi07g03060: Type1.0

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

Vitvi07g03060

35.2

not assigned.unknown

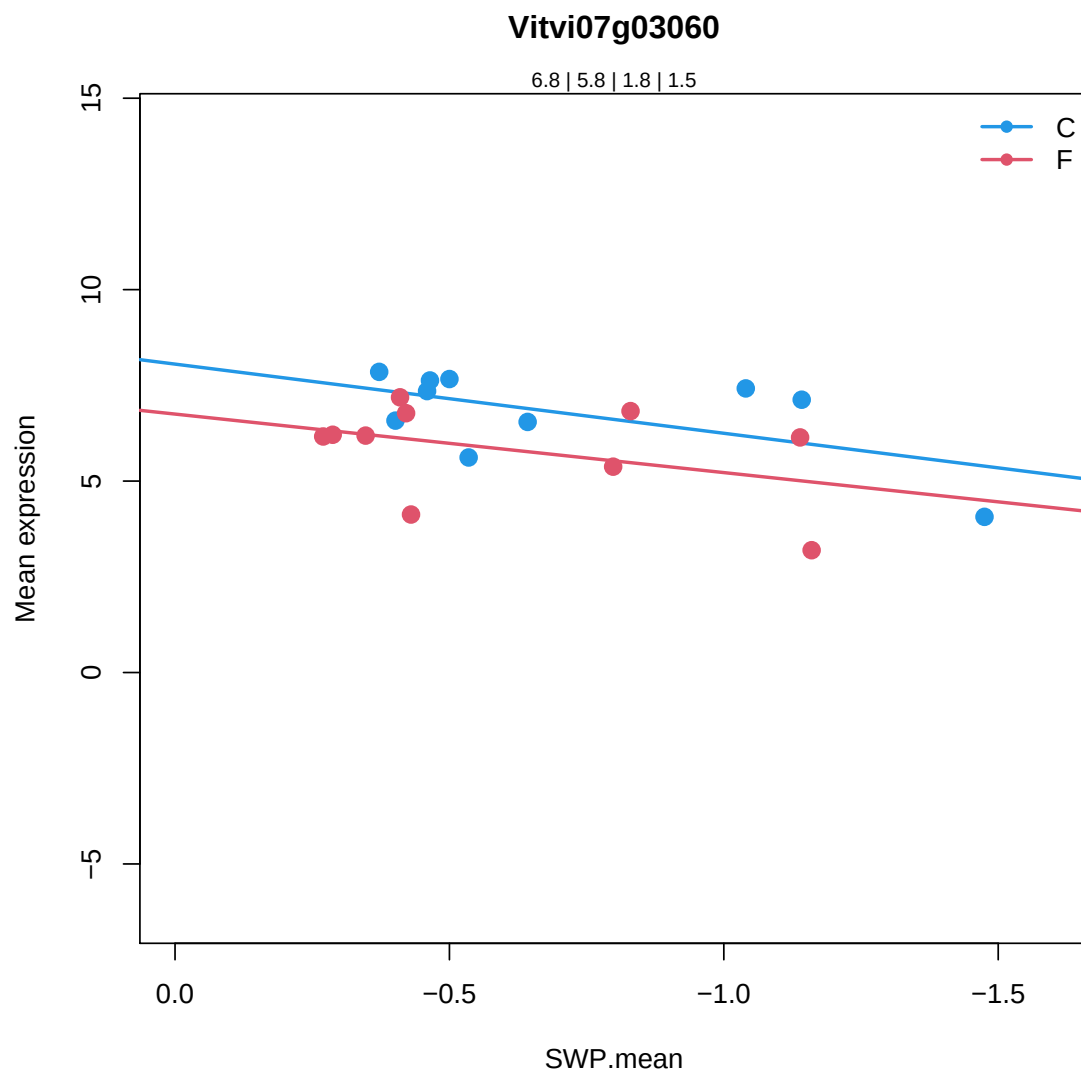
xyloglucan endotransglucosylase/hydrolase 7 |

Chr4:17775703-17777372 REVERSE LENGTH=293 |

201606

Coefficients for Vitvi07g03060.

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



8.1.130 Vitvi02g00177: Type1.0 *

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

Vitvi02g00177

35.2

not assigned.unknown

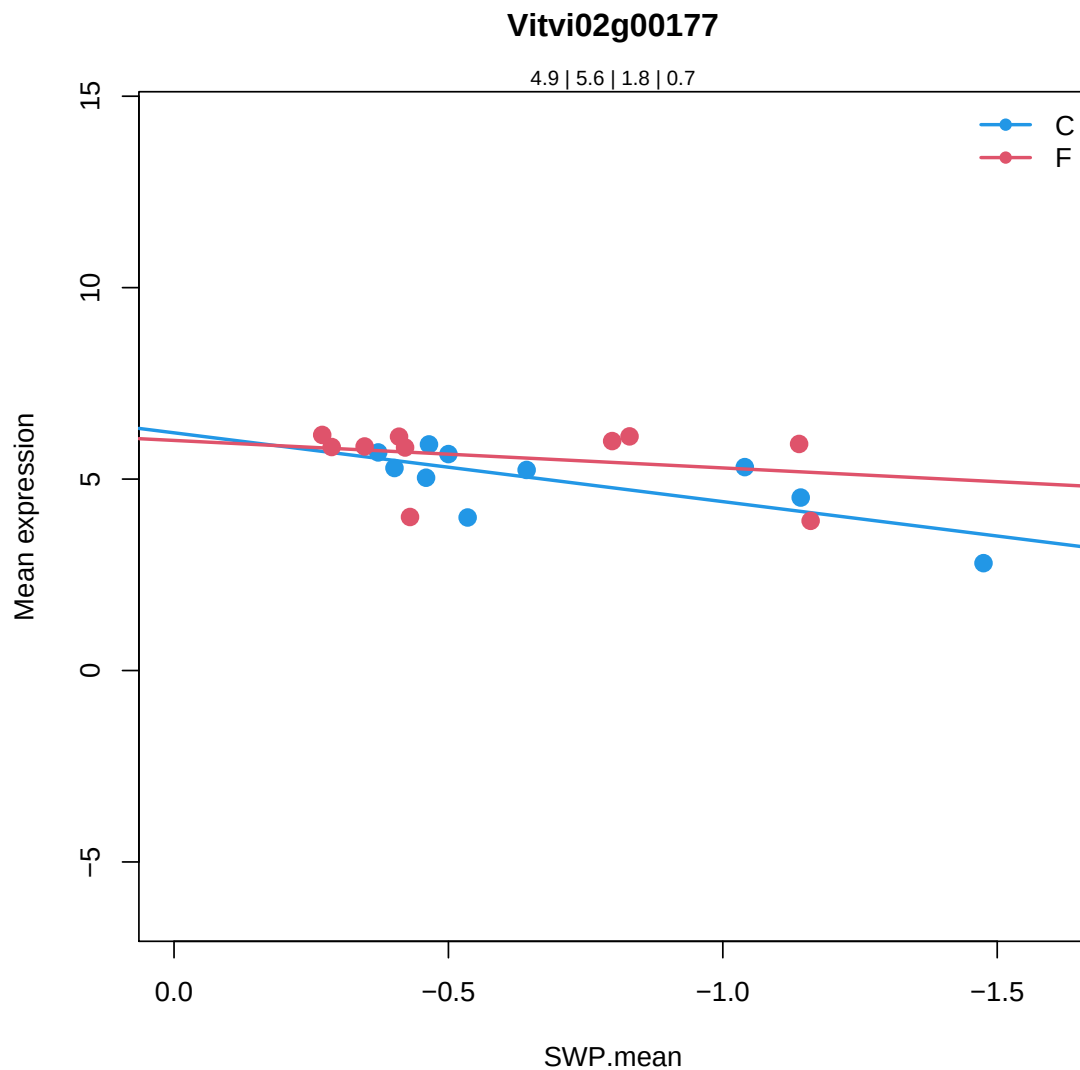
ABL interactor-like protein 3 |

Chr5:8274637-8276325 FORWARD LENGTH=307 |

201606

Coefficients for Vitvi02g00177.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.944806	4.831833e-16	***	9.434639e-16	***
SlopeC	1.797326	0.01004089	*	0.3042249	
MeanF-MeanC	0.6270961	0.06587188	.	0.2847474	
SlopeF-SlopeC	-1.078984	0.2672798		0.9999488	



8.1.131 Vitvi16g01326: Type1.0 *

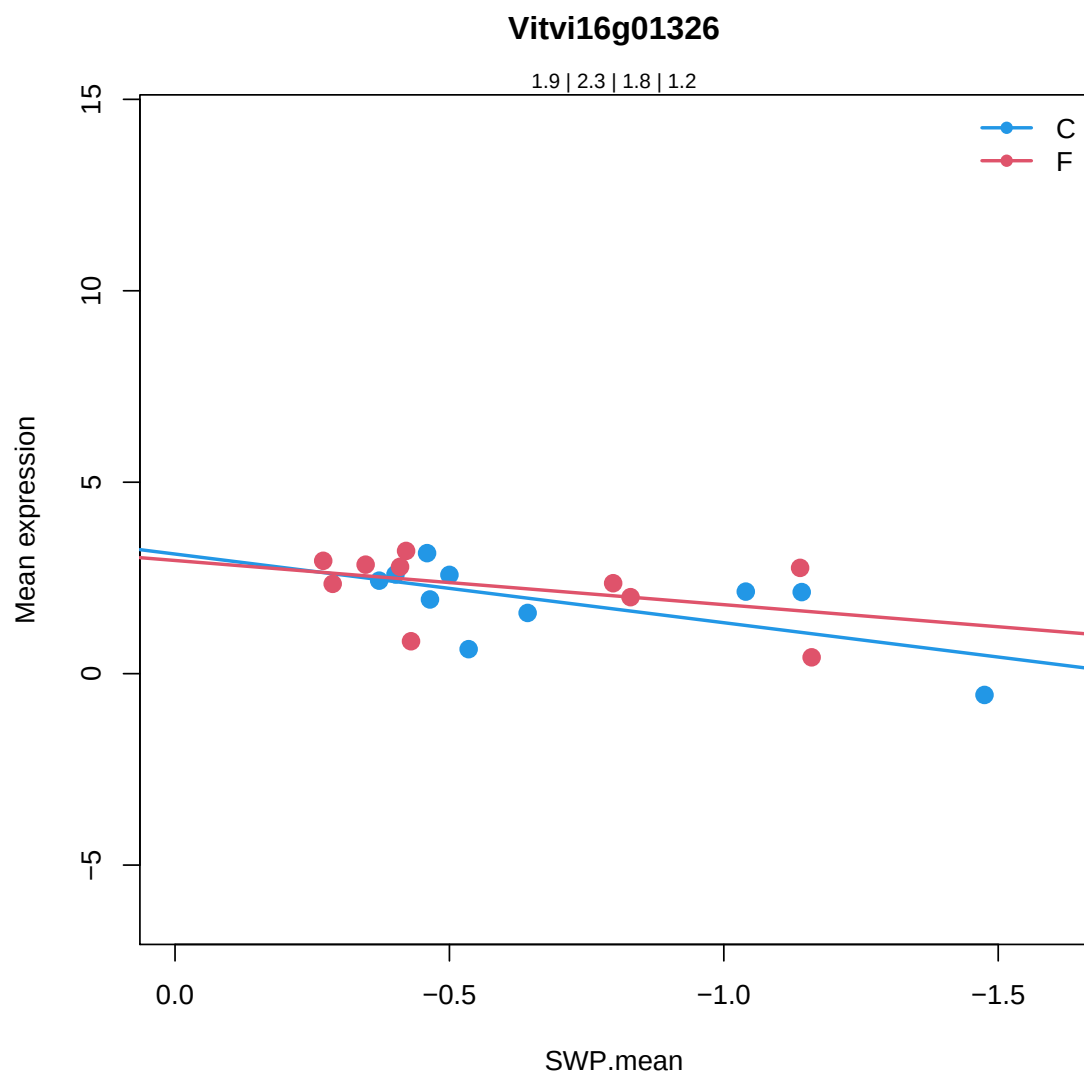
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g01326
30.3
signalling.calcium
Calcium-binding endonuclease/exonuclease/phosphatase family |
Chr5:21962900-21965279 FORWARD LENGTH=436 |
201606
```

```
Vitvi16g01326
35.2
not assigned.unknown
Calcium-binding endonuclease/exonuclease/phosphatase family |
Chr5:21962900-21965279 FORWARD LENGTH=436 |
201606
```

Coefficients for Vitvi16g01326.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.862557	3.164321e-07	***	3.699515e-07	***
SlopeC	1.793607	0.01968534	*	0.374907	
MeanF-MeanC	0.3902039	0.2926564		0.6592771	
SlopeF-SlopeC	-0.6395583	0.5522498		0.9999488	



8.1.132 Vitvi08g01423: Type1.0

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

Vitvi08g01423

33.99

development.unspecified

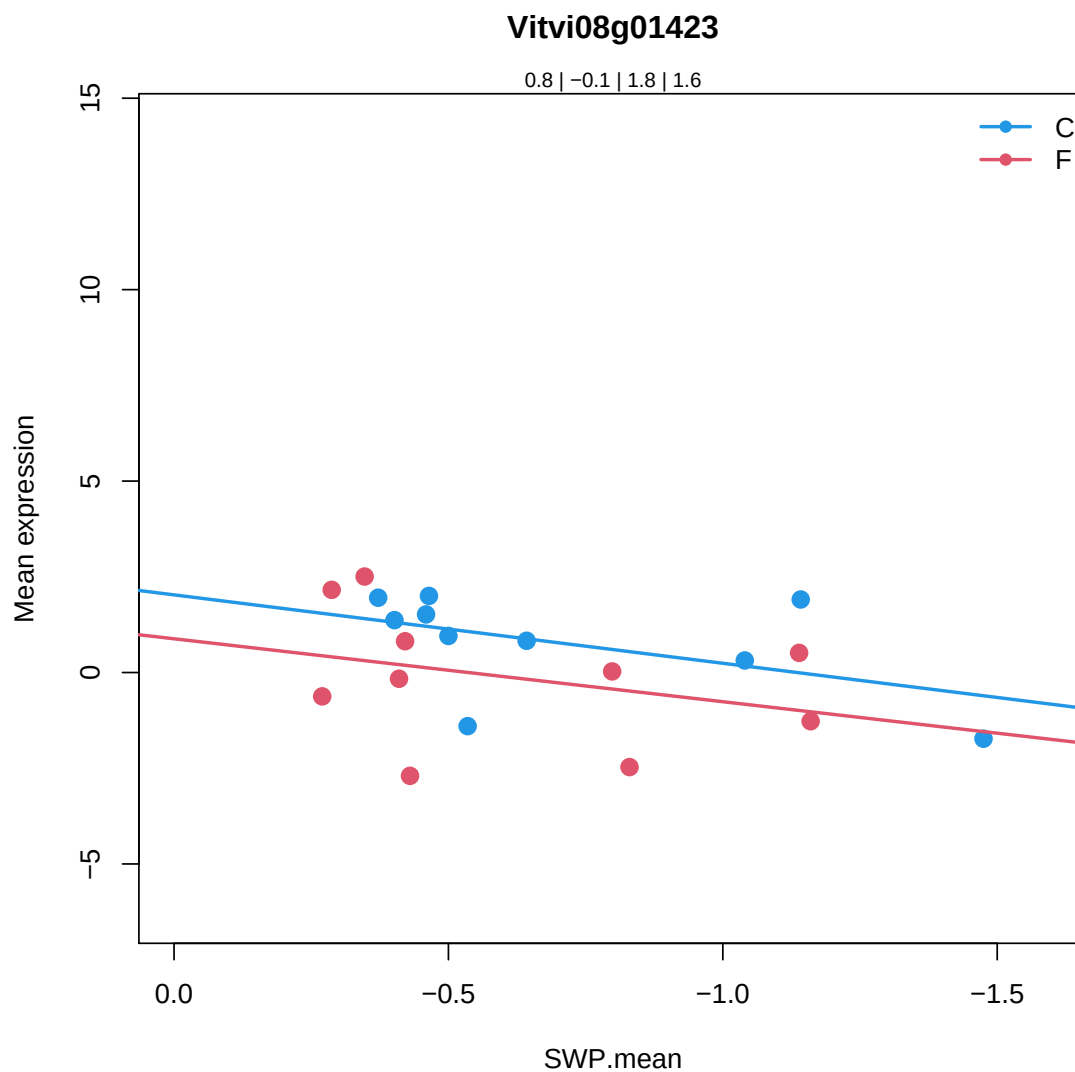
Transducin/WD40 repeat-like superfamily protein |

Chr1:4395114-4396154 REVERSE LENGTH=346 |

201606

Coefficients for Vitvi08g01423.

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



8.1.133 Vitvi14g01164: Type1.0 *

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

Vitvi14g01164

35.2

not assigned.unknown

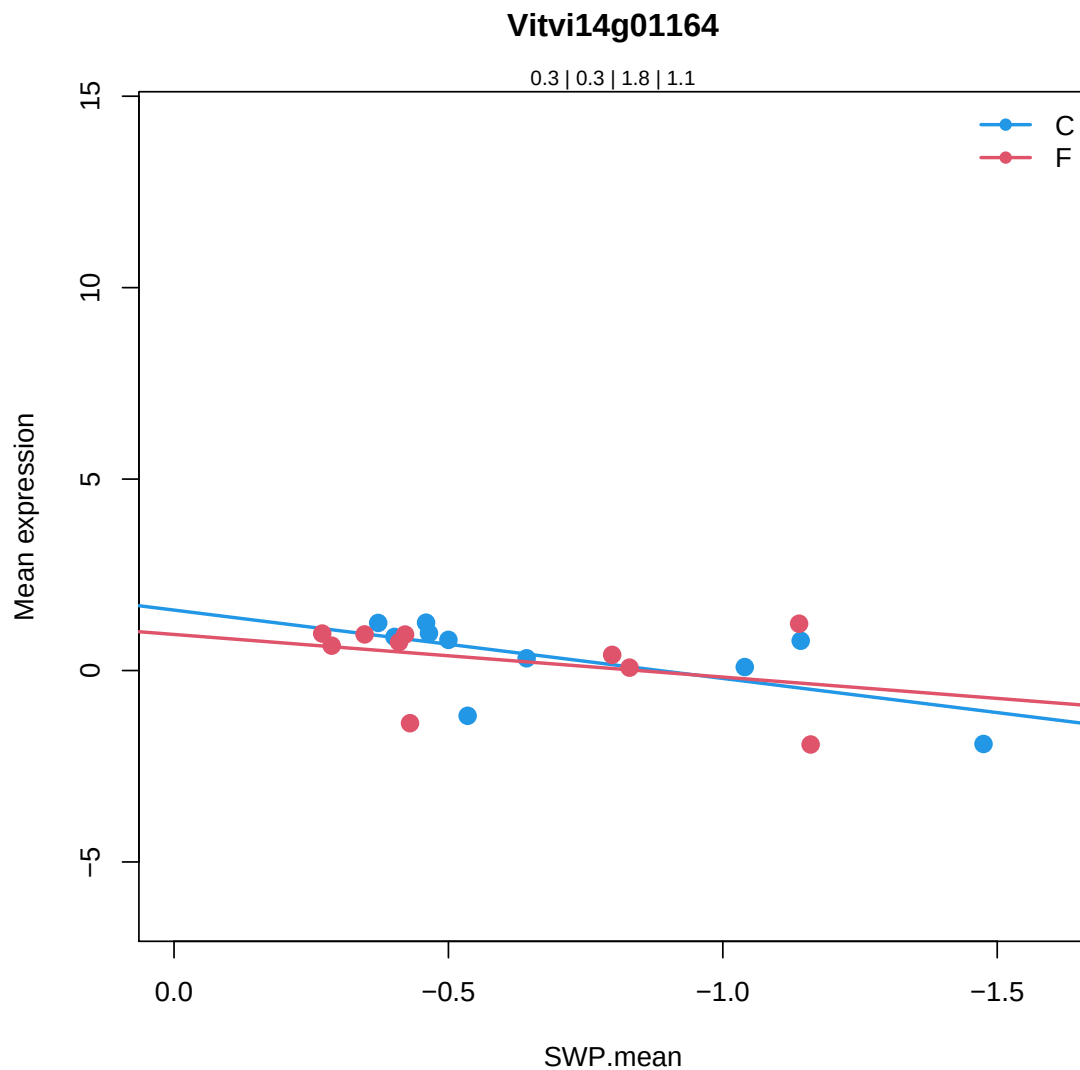
membrane-associated kinase regulator |

Chr1:25028862-25029656 REVERSE LENGTH=264 |

201606

Coefficients for Vitvi14g01164.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3229337	0.2552259		0.2606118	
SlopeC	1.784924	0.03011681	*	0.431429	
MeanF-MeanC	-0.0593902	0.8805899		0.9689711	
SlopeF-SlopeC	-0.671136	0.5635185		0.9999488	



8.1.134 Vitvi01g01859: Type1.0 *

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

Vitvi01g01859

34.3

transport.amino acids

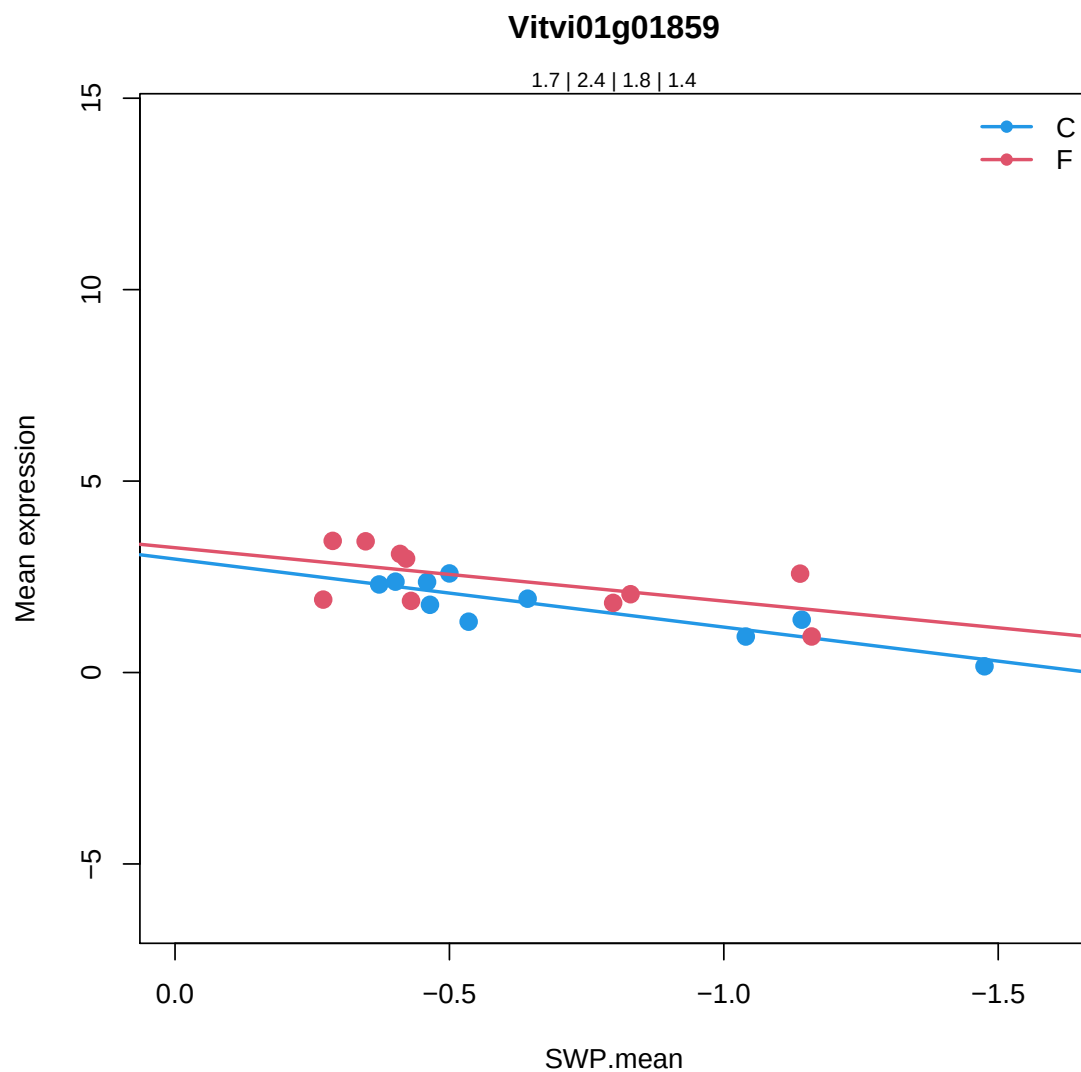
cationic amino acid transporter 5 |

Chr2:14744175-14745884 REVERSE LENGTH=569 |

201606

Coefficients for Vitvi01g01859.

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



8.1.135 Vitvi11g00708: Type1.0

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

Vitvi11g00708

35.2

not assigned.unknown

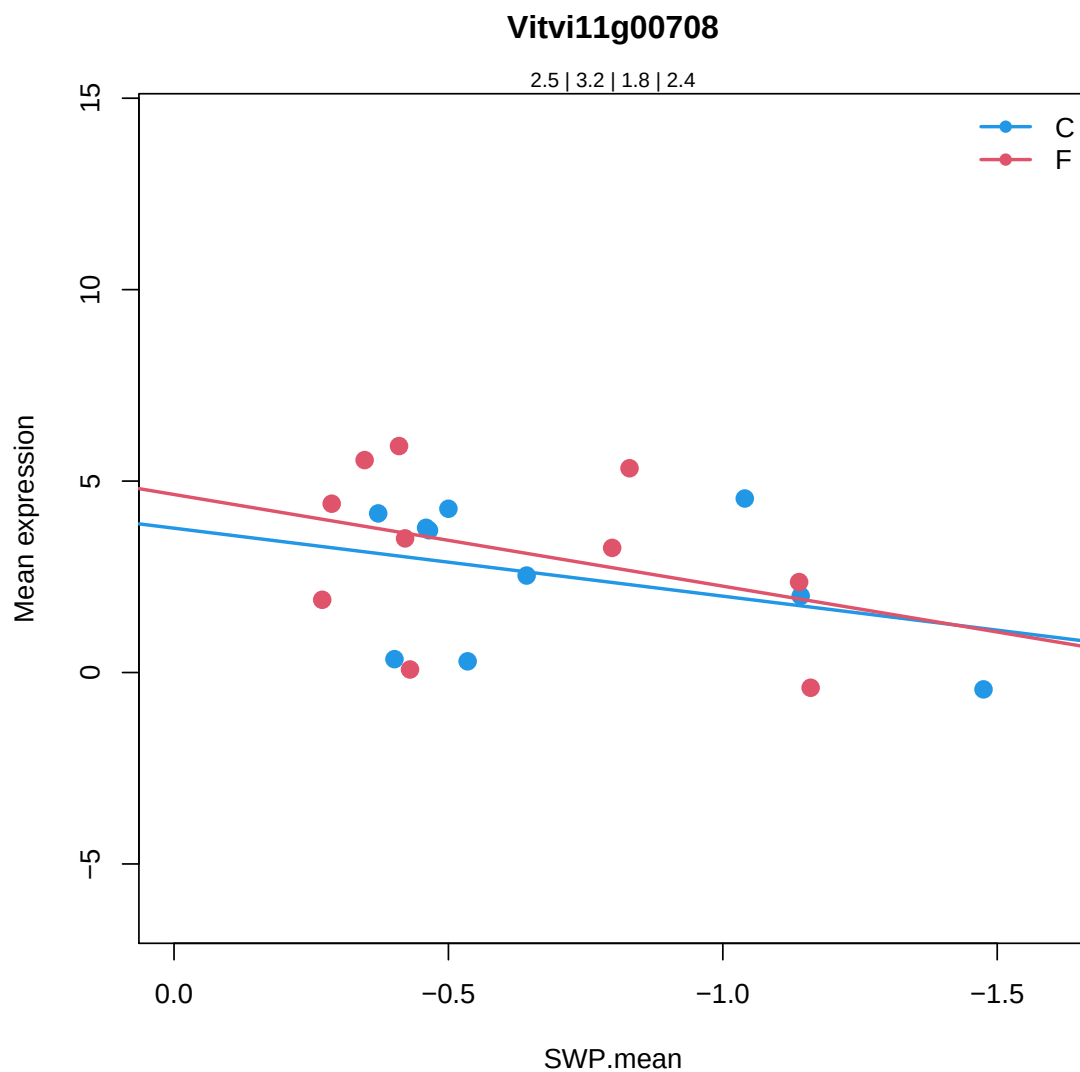
early nodulin-like protein 15 |

Chr4:15401798-15402426 FORWARD LENGTH=177 |

201606

Coefficients for Vitvi11g00708.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.520695	0.0001809839	***	0.0001988579	***
SlopeC	1.775499	0.2655362		0.7701943	
MeanF-MeanC	0.6701617	0.4053051		0.7481666	
SlopeF-SlopeC	0.6186164	0.7915426		0.9999488	



8.1.136 Vitvi14g02920: Type1.0 *

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

Vitvi14g02920

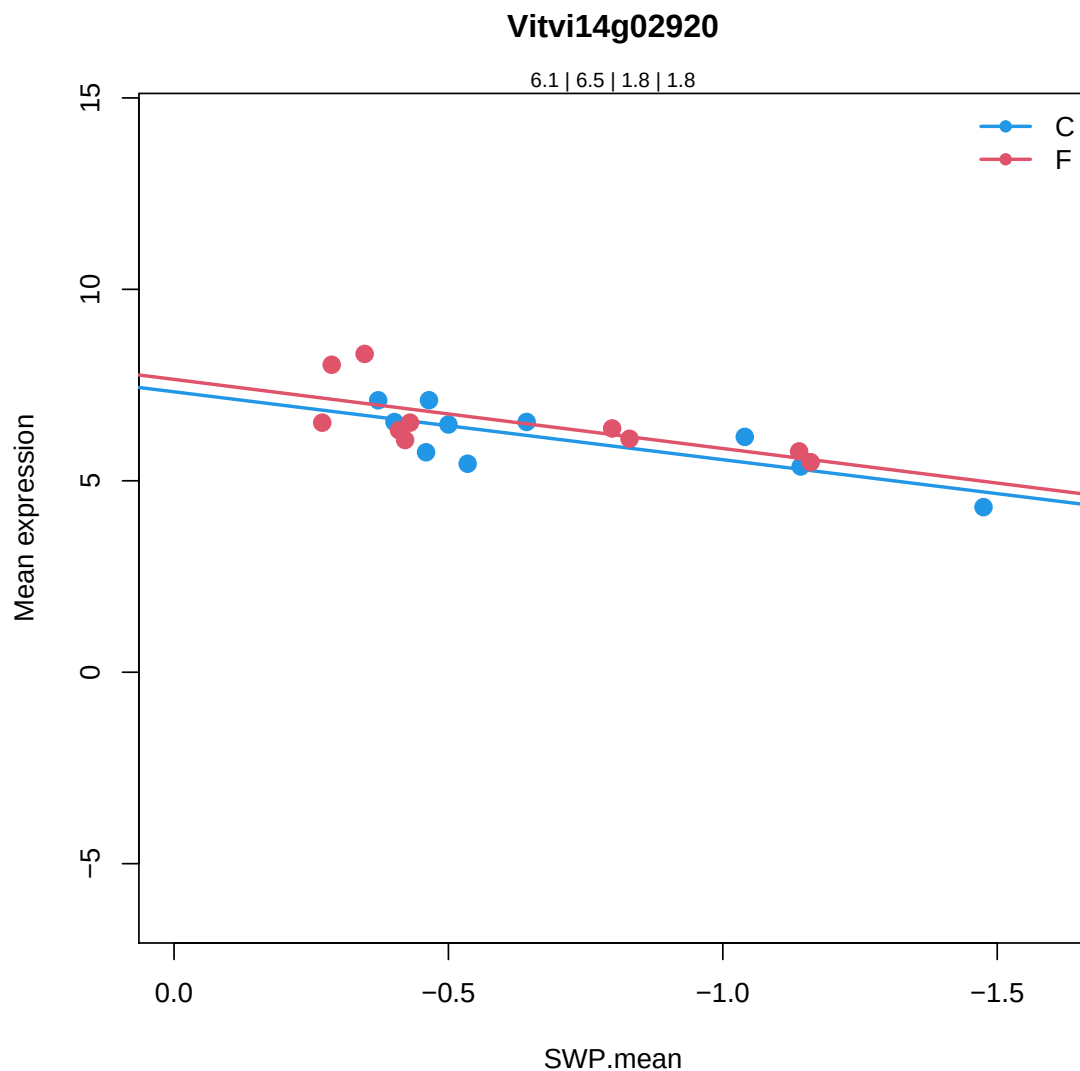
35.2

not assigned.unknown

NA

Coefficients for Vitvi14g02920.

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



8.1.137 Vitvi10g02309: Type1.0

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

Vitvi10g02309

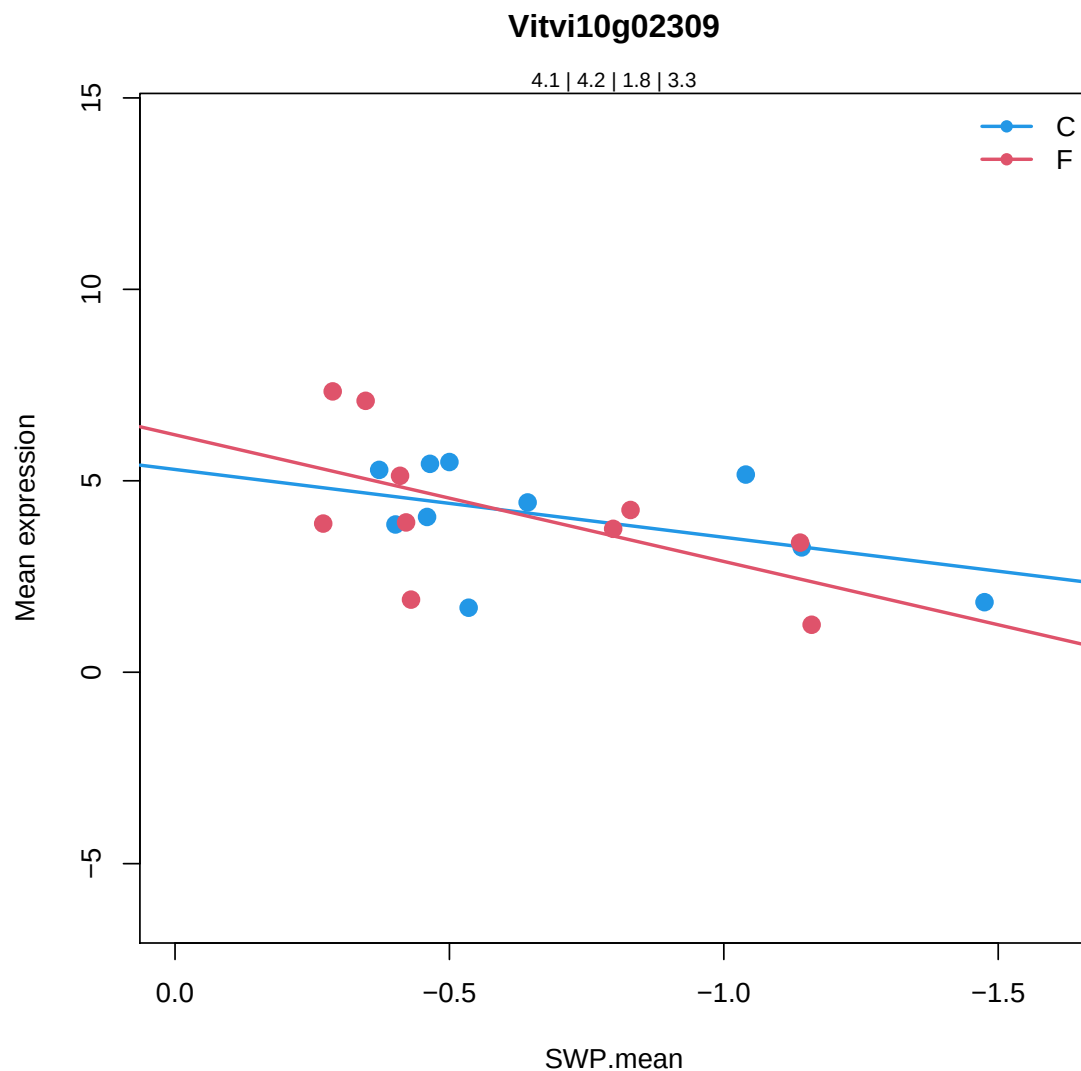
34.12

transport.metal

NA

Coefficients for Vitvi10g02309.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.050203	3.029903e-09	***	3.762263e-09	***
SlopeC	1.771519	0.1444425		0.6693663	
MeanF-MeanC	0.1348607	0.8226891		0.9503527	
SlopeF-SlopeC	1.536101	0.3873108		0.9999488	



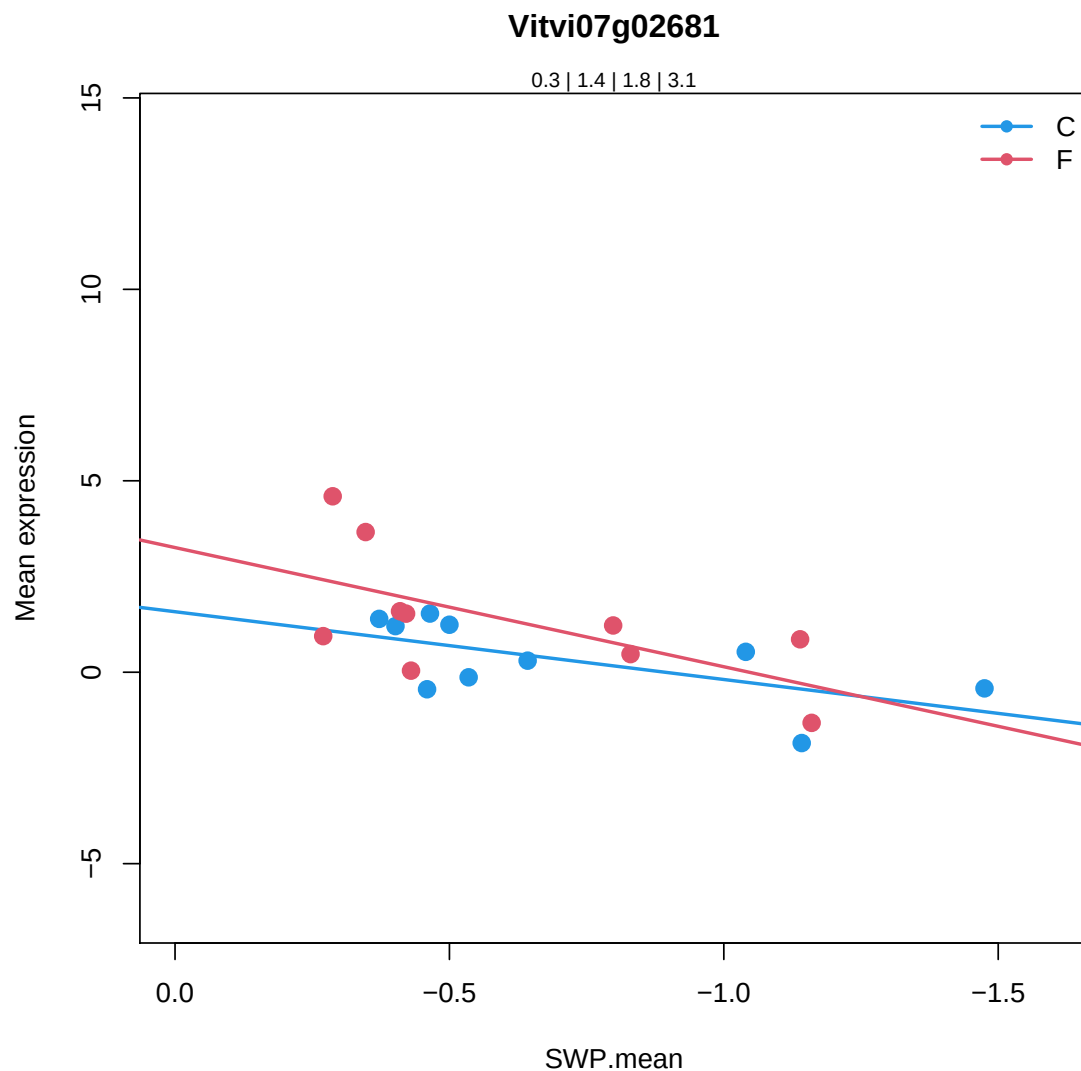
8.1.138 Vitvi07g02681: Type1.0

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

```
Vitvi07g02681
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi07g02681.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3353629	0.3204223		0.3261789	
SlopeC	1.770583	0.06691152	.	0.5548906	
MeanF-MeanC	1.023932	0.03922308	*	0.2038273	
SlopeF-SlopeC	1.342068	0.3365688		0.9999488	



8.1.139 Vitvi05g01779: Type1.0 *

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

Vitvi05g01779

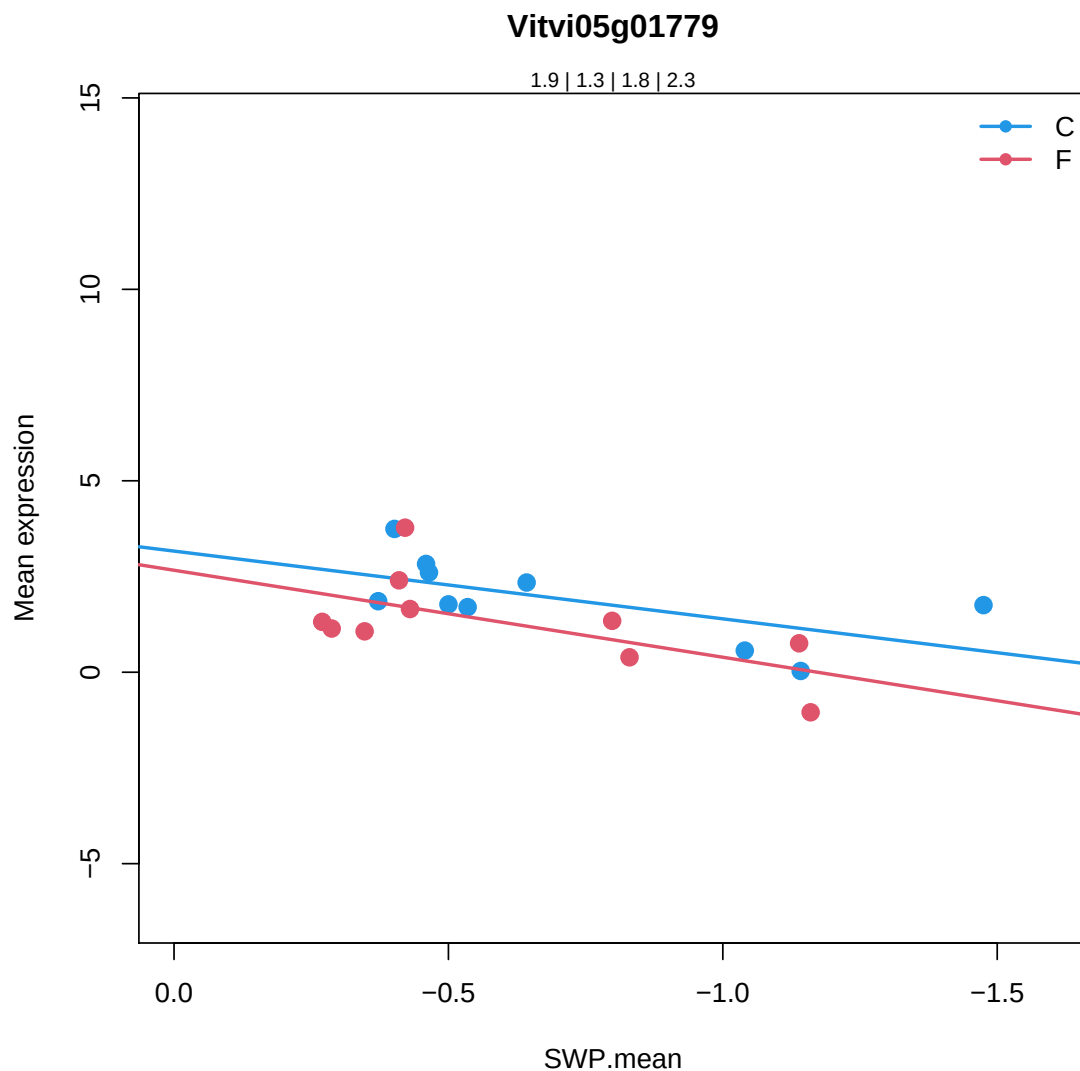
35.2

not assigned.unknown

NA

Coefficients for Vitvi05g01779.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.919505	6.134533e-07	***	7.122376e-07	***
SlopeC	1.769027	0.03088751	*	0.4322019	
MeanF-MeanC	-0.6404011	0.1144564		0.395678	
SlopeF-SlopeC	0.5028954	0.6634111		0.9999488	



8.1.140 Vitvi16g02008: Type1.0 *

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

Vitvi16g02008

35.2

not assigned.unknown

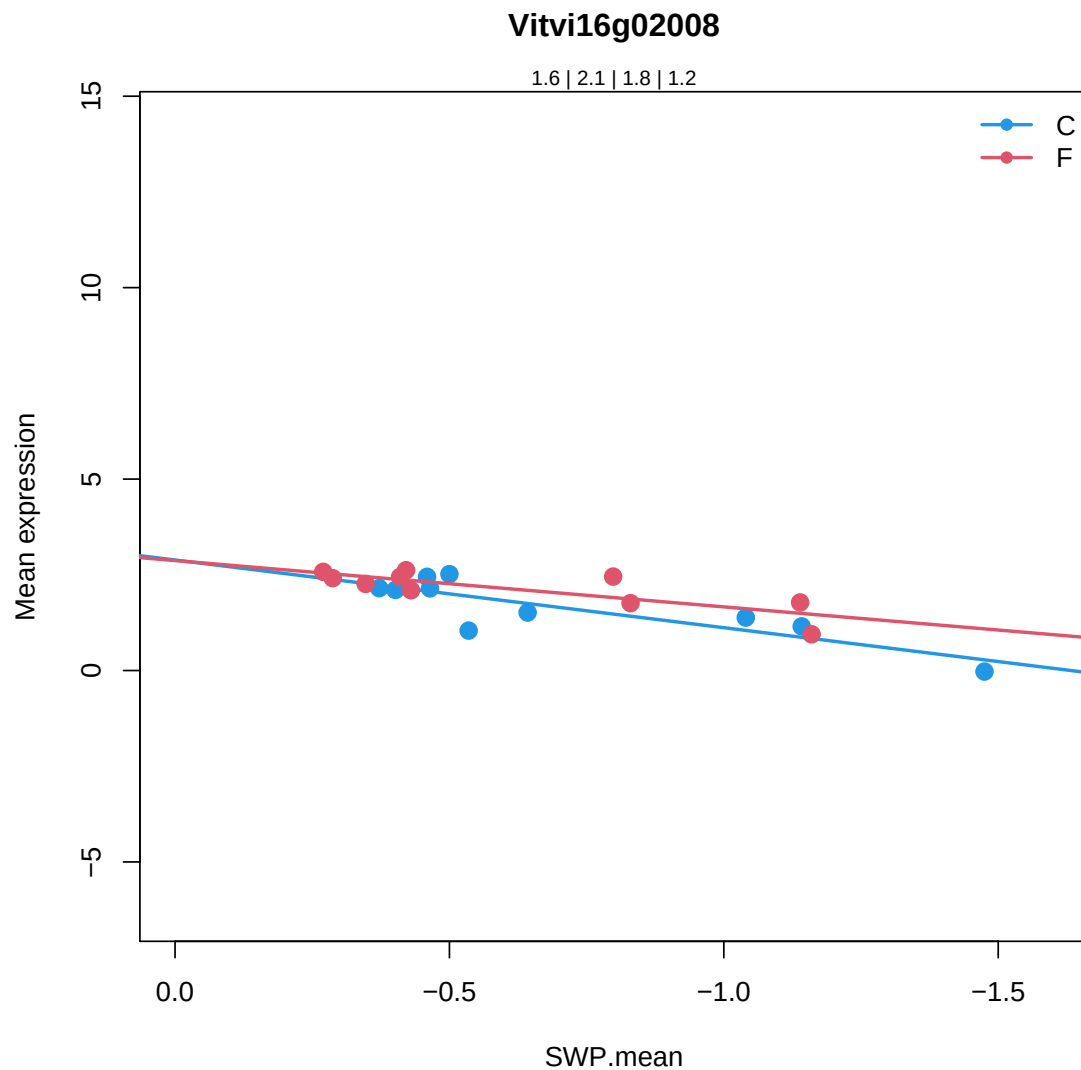
Protein kinase superfamily protein |

Chr1:24961634-24963941 REVERSE LENGTH=663 |

201606

Coefficients for Vitvi16g02008.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.643262	2.733125e-11	***	3.661301e-11	***
SlopeC	1.768253	8.717221e-05	***	0.07644173	.
MeanF-MeanC	0.4914276	0.01532163	*	0.1034435	
SlopeF-SlopeC	-0.5591352	0.3173104		0.9999488	



8.1.141 Vitvi11g00417: Type1.0 *

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

Vitvi11g00417

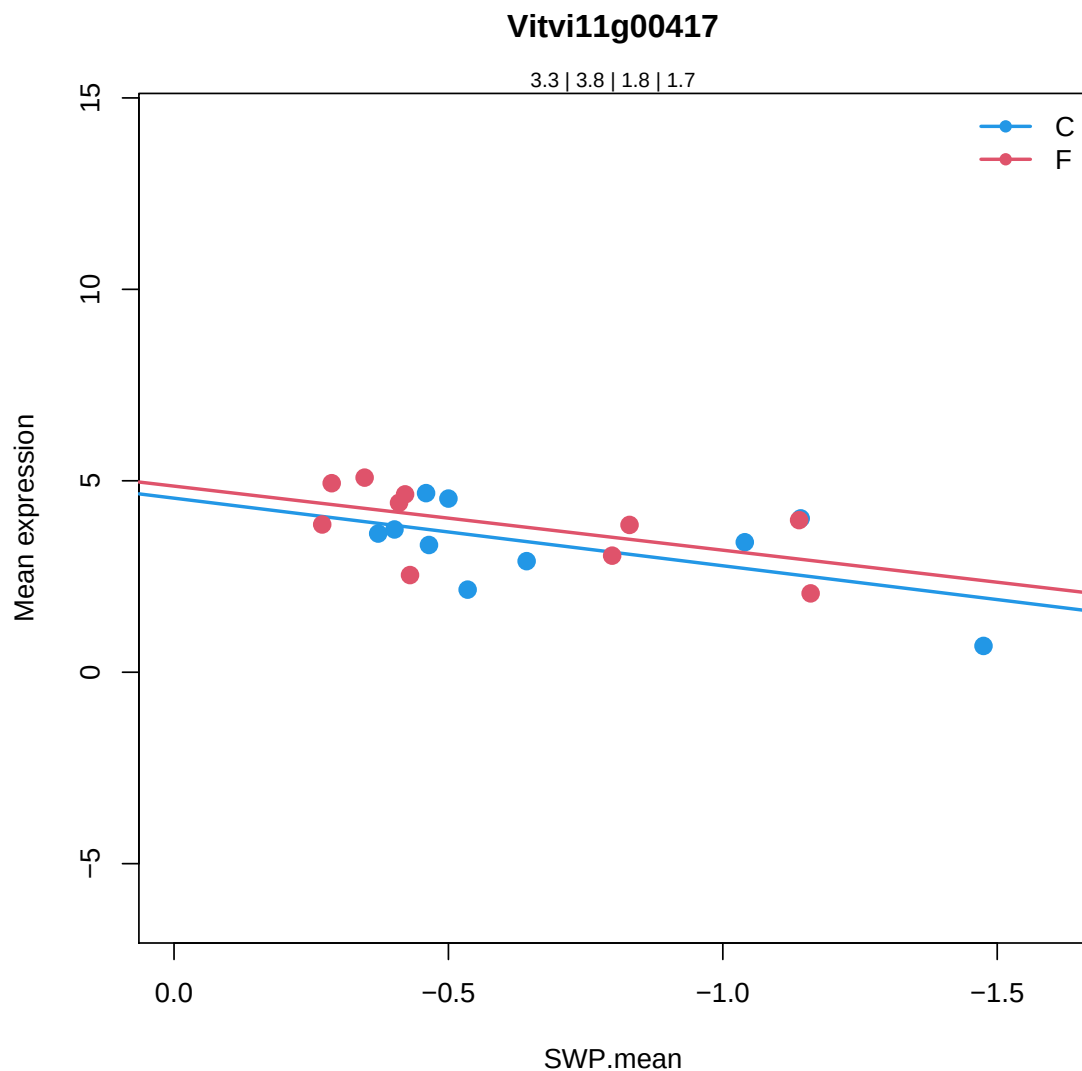
35.2

not assigned.unknown

Blight-associated protein P12 (Fragment) IPR007112 Expansin 45, endogl

Coefficients for Vitvi11g00417.

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



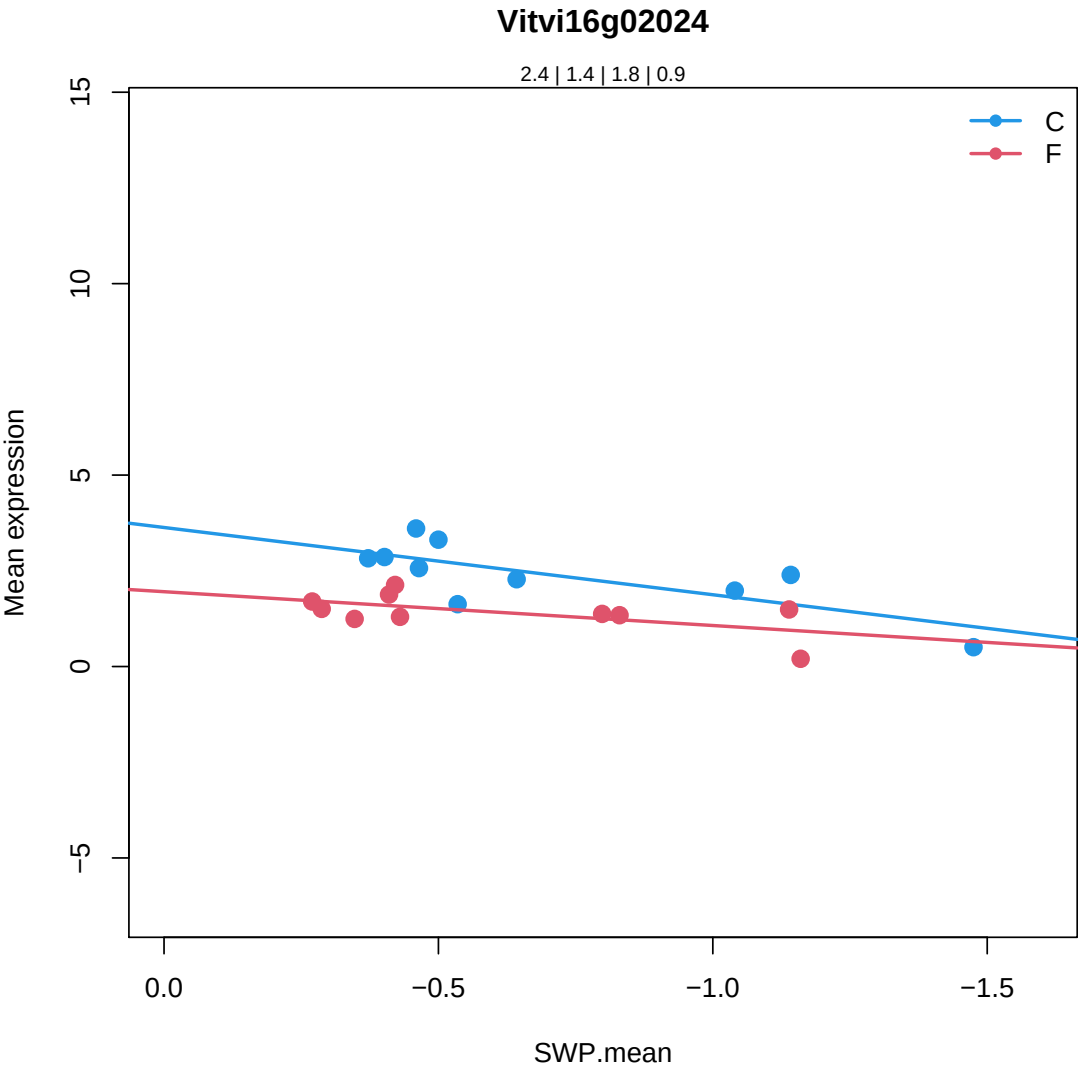
8.1.142 Vitvi16g02024: Type1.0 *

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

```
Vitvi16g02024
35.2
not assigned.unknown
Protein kinase superfamily protein |
Chr1:24961634-24963941 REVERSE LENGTH=663 |
201606
```

Coefficients for Vitvi16g02024.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.39609	1.635379e-12	***	2.317662e-12	***
SlopeC	1.756184	0.001017369	**	0.1271346	
MeanF-MeanC	-0.9800343	0.0004154175	***	0.006030279	**
SlopeF-SlopeC	-0.8729691	0.2180335		0.9999488	



8.1.143 Vitvi16g02141: Type1.0 *

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

Vitvi16g02141

35.2

not assigned.unknown

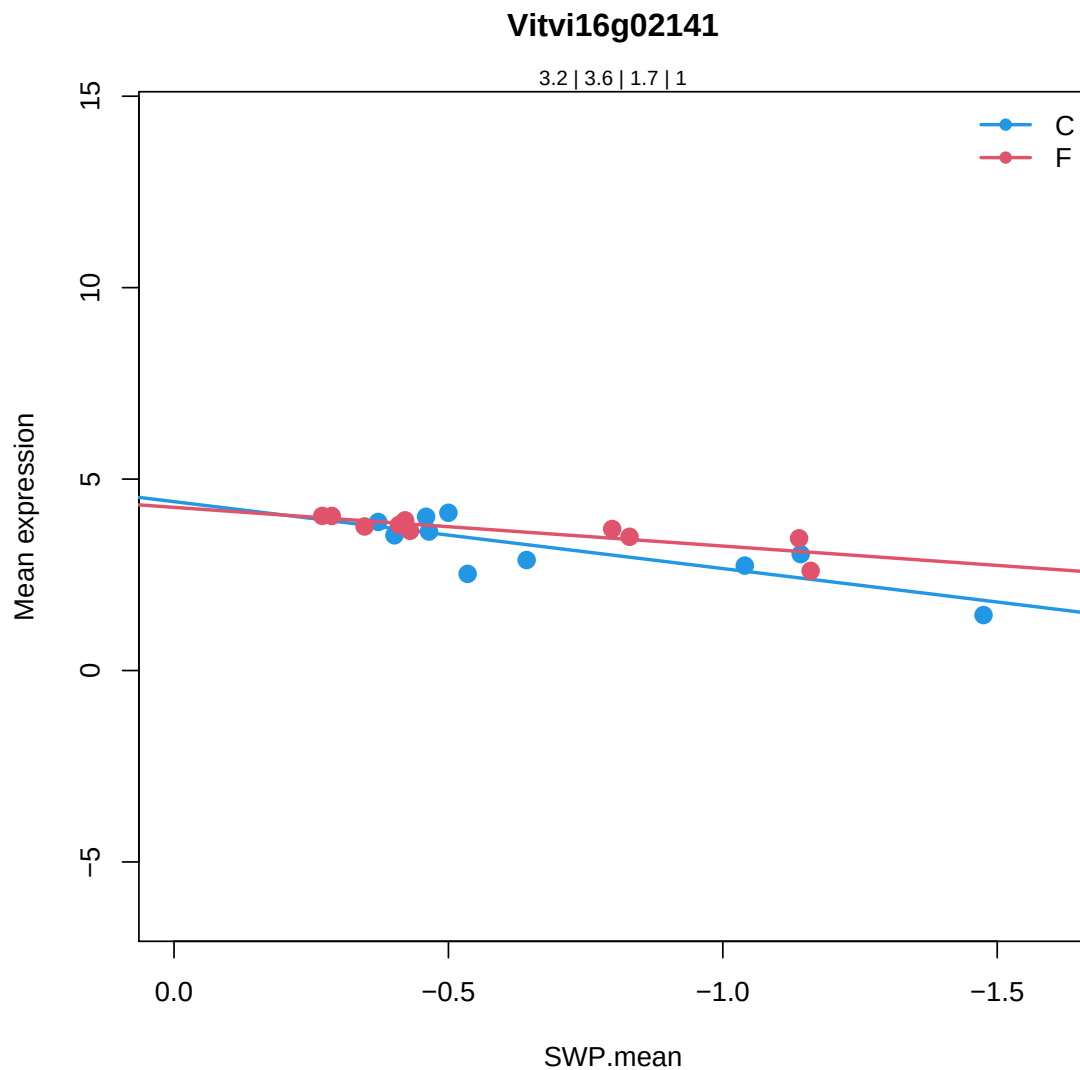
Protein kinase superfamily protein |

Chr1:24961634-24963941 REVERSE LENGTH=663 |

201606

Coefficients for Vitvi16g02141.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.181323	9.615205e-17	***	2.097538e-16	***
SlopeC	1.747491	0.0001423717	***	0.07644173	.
MeanF-MeanC	0.4644224	0.02484255	*	0.1477371	
SlopeF-SlopeC	-0.7369854	0.2048051		0.9999488	



8.1.144 Vitvi19g02230: Type1.0

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

Vitvi19g02230

17.6.1.13

hormone metabolism.gibberelin.synthesis-degradation.GA2 oxidase

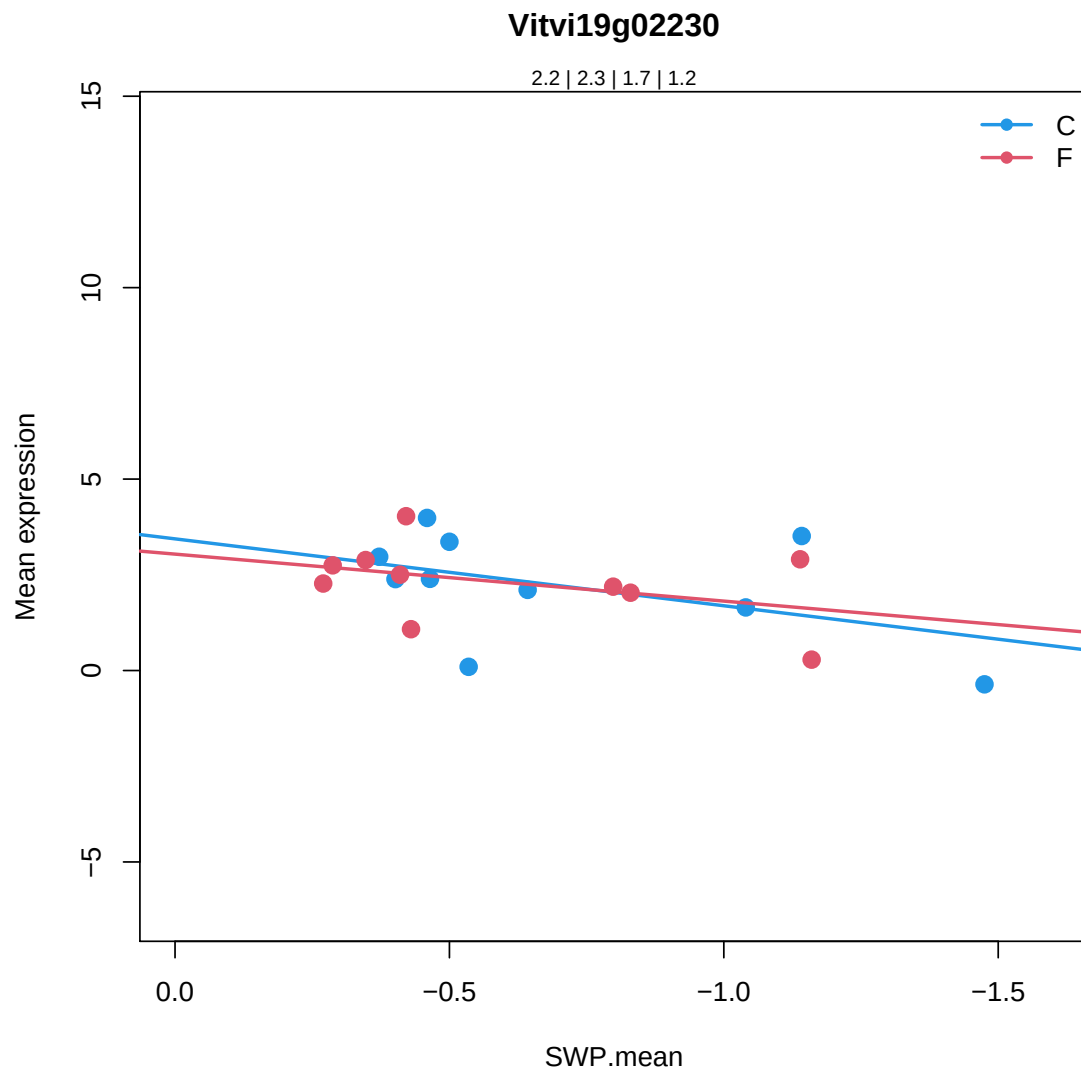
gibberellin 2-beta-dioxygenase |

Chr1:29511772-29512990 REVERSE LENGTH=329 |

201606

Coefficients for Vitvi19g02230.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.210147	1.206936e-06	***	1.390591e-06	***
SlopeC	1.747299	0.07175031	.	0.5630621	
MeanF-MeanC	0.08256185	0.8618777		0.964024	
SlopeF-SlopeC	-0.5202282	0.7084605		0.9999488	



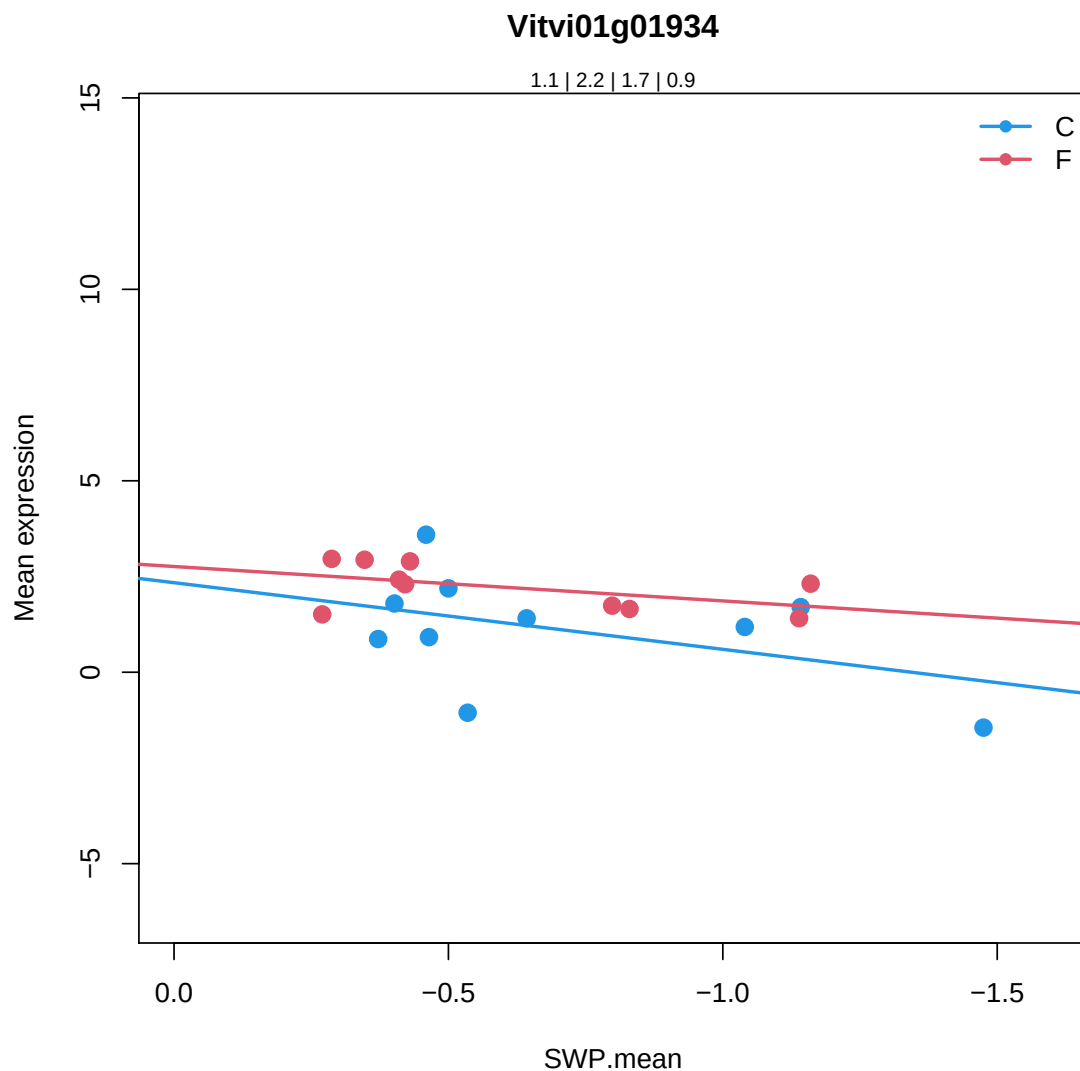
8.1.145 Vitvi01g01934: Type1.0 *

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

```
Vitvi01g01934
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi01g01934.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.114597	0.001274472	**	0.001377304	**
SlopeC	1.740554	0.04969294	*	0.5087769	
MeanF-MeanC	1.09869	0.01717739	*	0.112513	
SlopeF-SlopeC	-0.8415438	0.5064549		0.9999488	



8.1.146 Vitvi19g00445: Type1.0

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

Vitvi19g00445

26.19

misc.plastocyanin-like

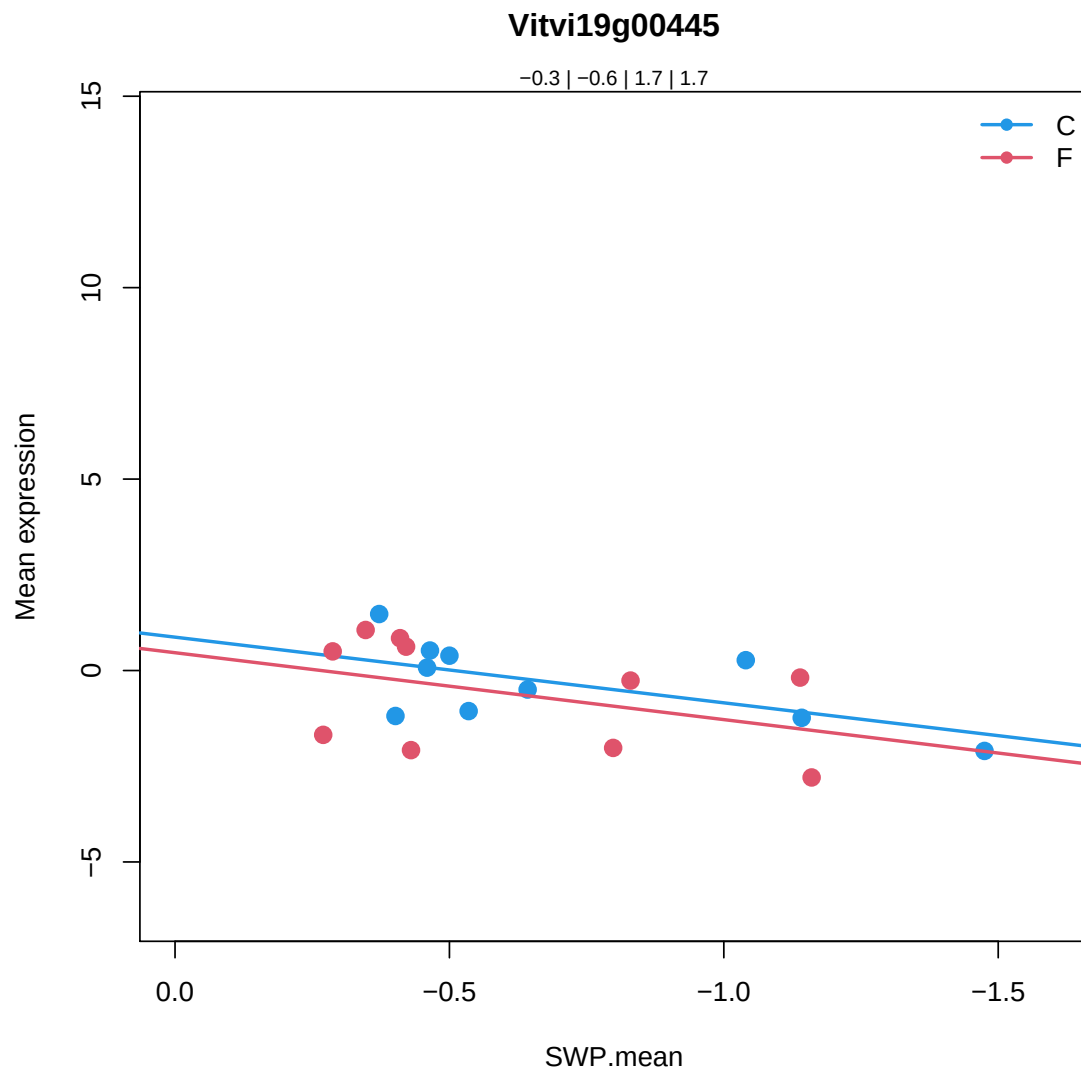
early nodulin-like protein 9 |

Chr3:7186754-7187453 REVERSE LENGTH=203 |

201606

Coefficients for Vitvi19g00445.

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



8.1.147 Vitvi02g00327: Type1.0

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

Vitvi02g00327

31.1

cell.organisation

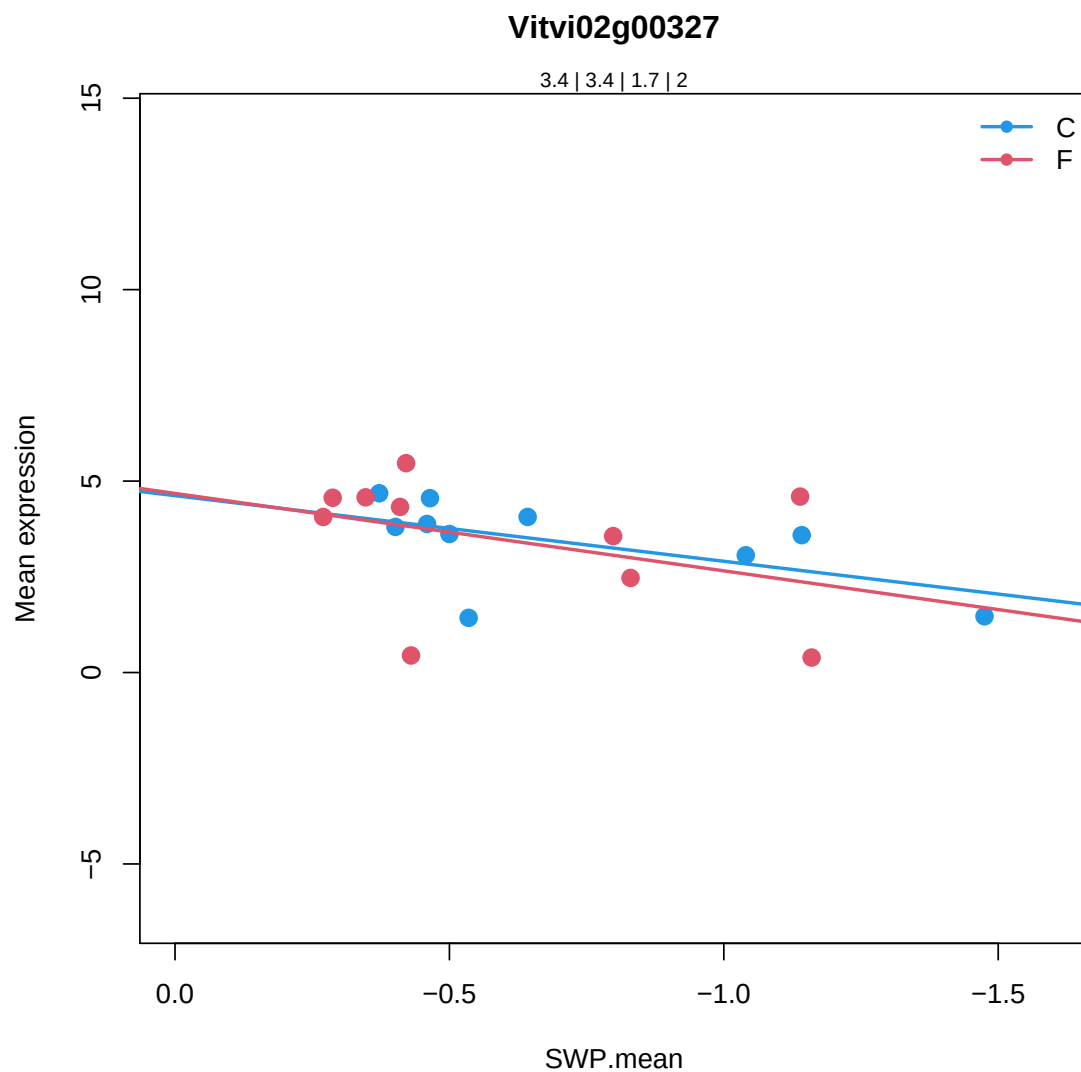
tubulin beta 8 |

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	



8.1.148 Vitvi14g00483: Type1.0

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

Vitvi14g00483

27.3.40

RNA.regulation of transcription.AUX/IAA family

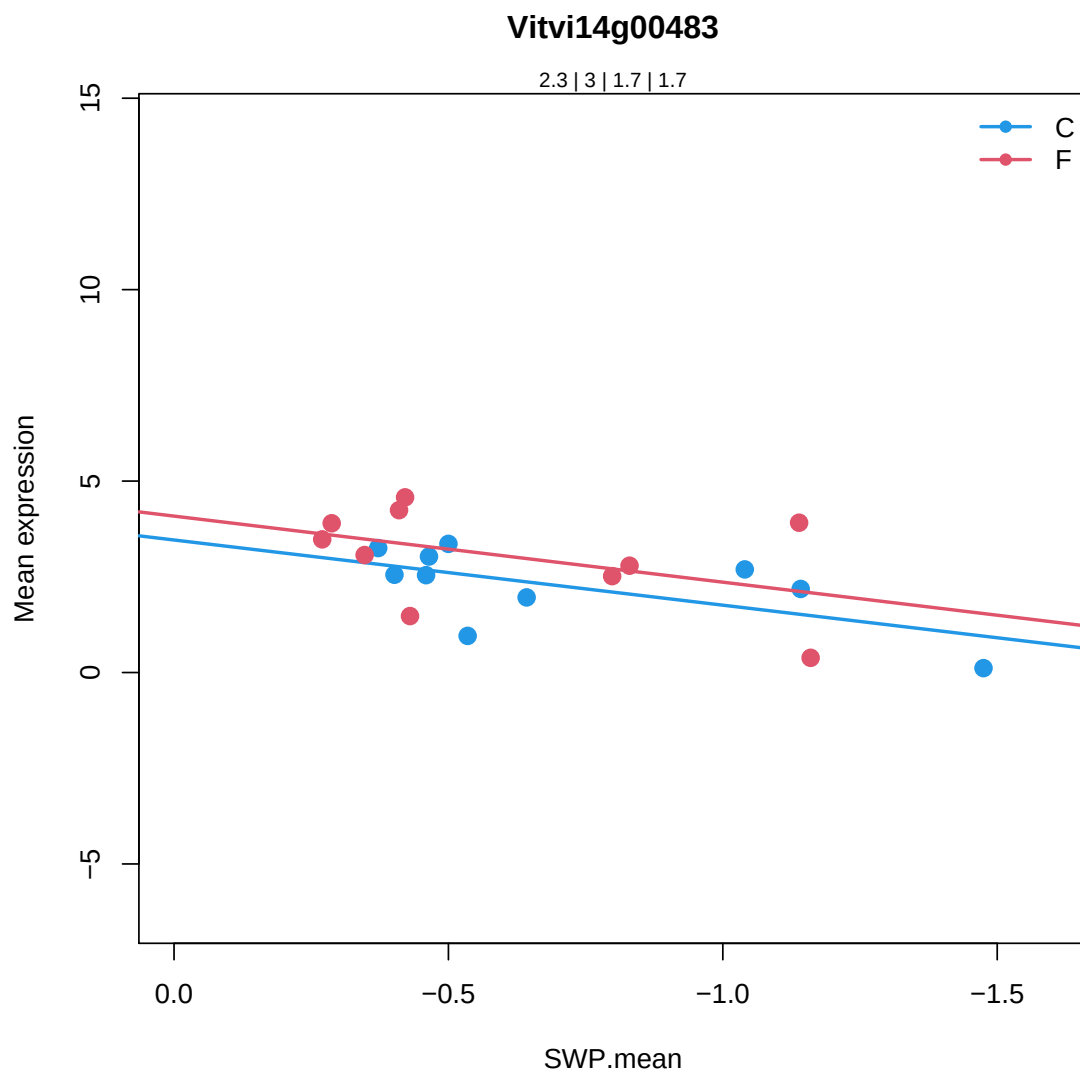
AUX/IAA transcriptional regulator family protein |

Chr5:17550465-17551206 FORWARD LENGTH=186 |

201606

Coefficients for Vitvi14g00483.

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



8.1.149 Vitvi12g02680: Type1.0

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

Vitvi12g02680

27.3.46

RNA.regulation of transcription.DNA methyltransferases

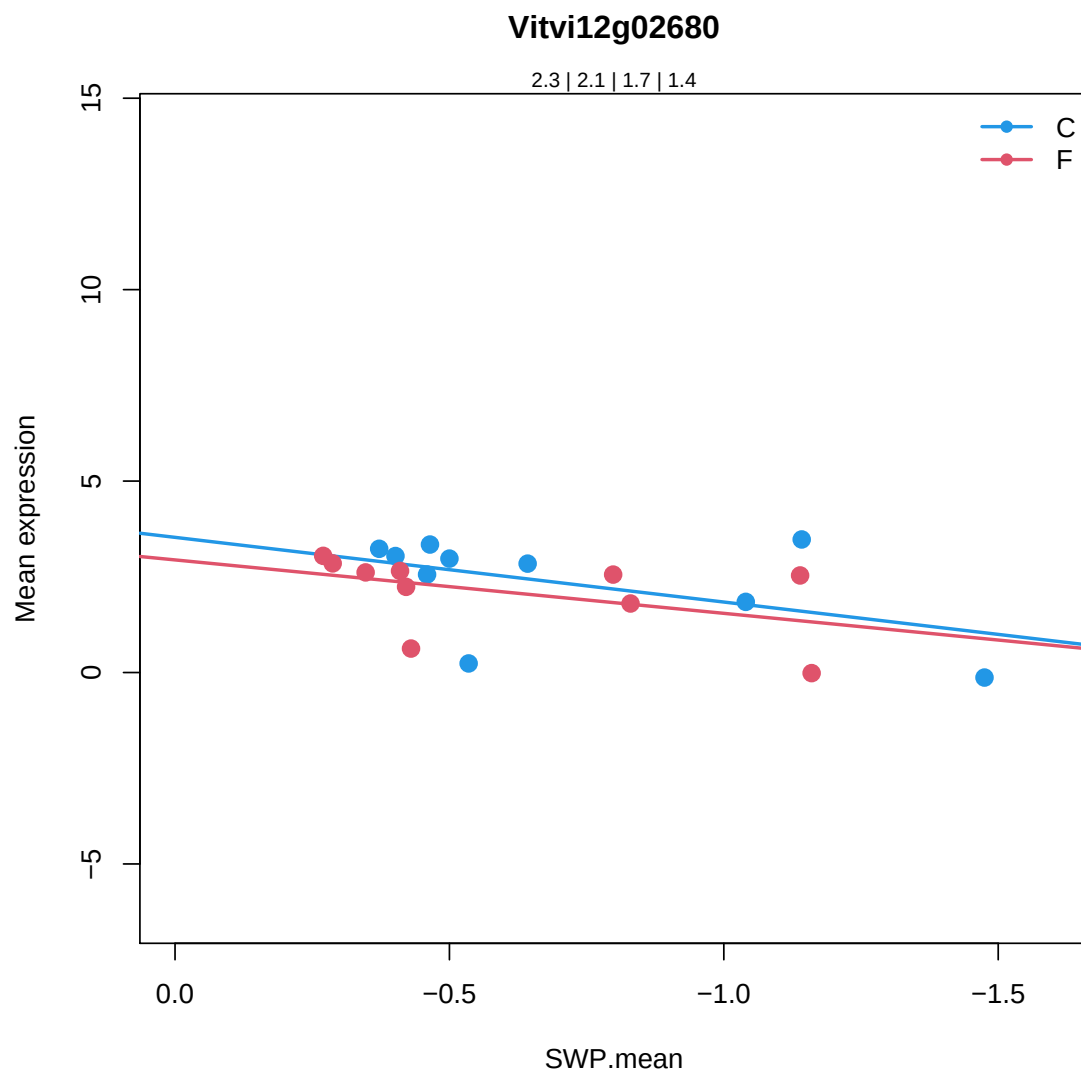
methyltransferase 1 |

Chr5:19932501-19938186 FORWARD LENGTH=1534 |

201606

Coefficients for Vitvi12g02680.

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



8.1.150 Vitvi04g00024: Type1.0 *

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

Vitvi04g00024

30.2.11

signalling.receptor kinases.leucine rich repeat XI

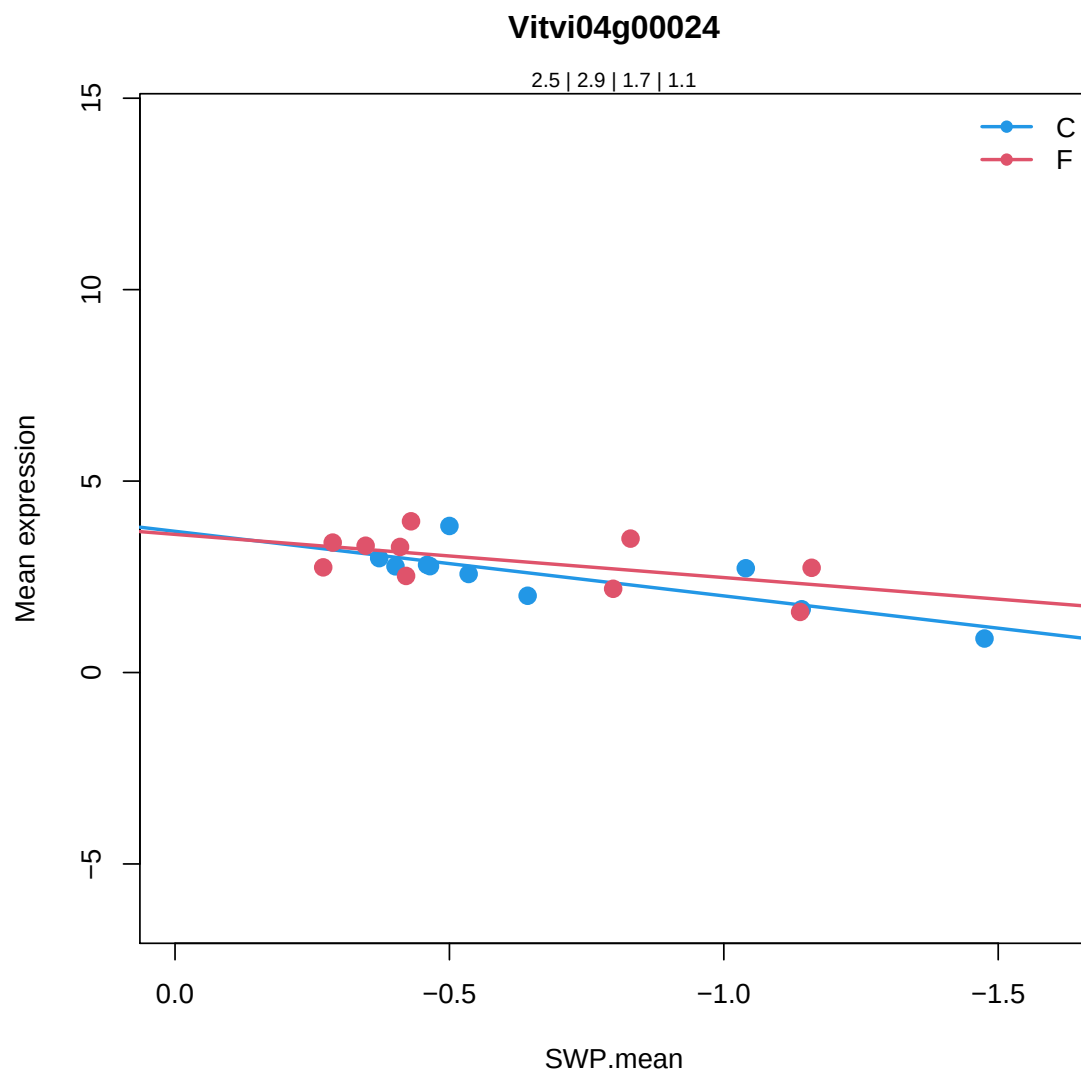
kinase family with leucine-rich repeat domain-containing protein |

Chr5:9050880-9053978 FORWARD LENGTH=1005 |

201606

Coefficients for Vitvi04g00024.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.501928	2.021967e-12	***	2.850164e-12	***
SlopeC	1.686835	0.00230403	**	0.1817854	
MeanF-MeanC	0.4185721	0.1059431		0.3781732	
SlopeF-SlopeC	-0.5591009	0.4497254		0.9999488	



8.1.151 Vitvi18g00388: Type1.0 *

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

Vitvi18g00388

35.2

not assigned.unknown

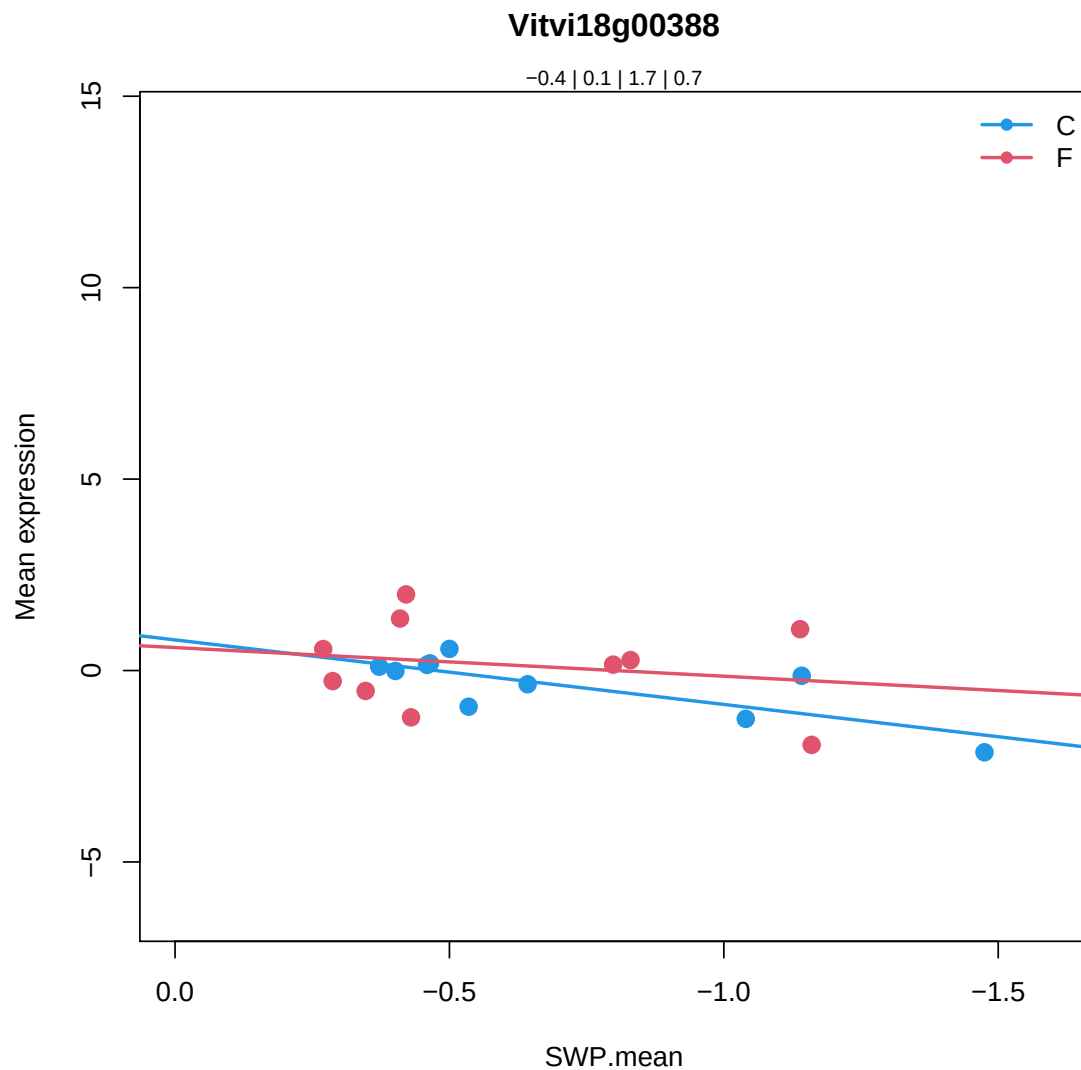
nucleolar GTP-binding protein |

Chr1:29391879-29392907 FORWARD LENGTH=342 |

201606

Coefficients for Vitvi18g00388.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.3855522	0.1716263		0.1763349	
SlopeC	1.685645	0.03712377	*	0.4620709	
MeanF-MeanC	0.529216	0.1840285		0.5202294	
SlopeF-SlopeC	-0.9378064	0.4152529		0.9999488	



8.1.152 Vitvi07g01951: Type1.0 *

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

Vitvi07g01951

35.2

not assigned.unknown

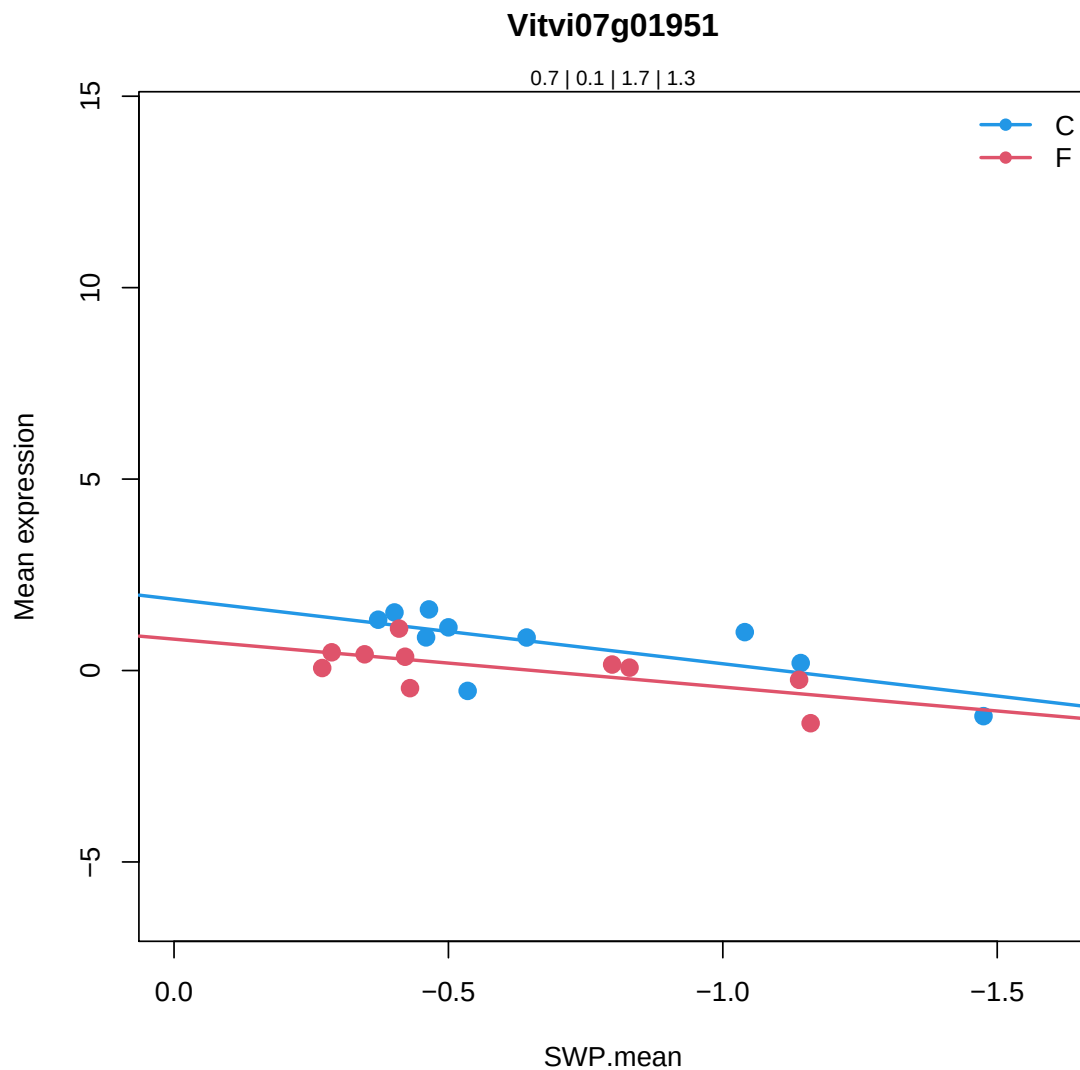
SAUR-like auxin-responsive protein family |

Chr5:21772107-21772535 FORWARD LENGTH=142 |

201606

Coefficients for Vitvi07g01951.

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



8.1.153 Vitvi08g00793: Type1.0 *

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

Vitvi08g00793

27.3.32

RNA.regulation of transcription.WRKY domain transcription factor famil

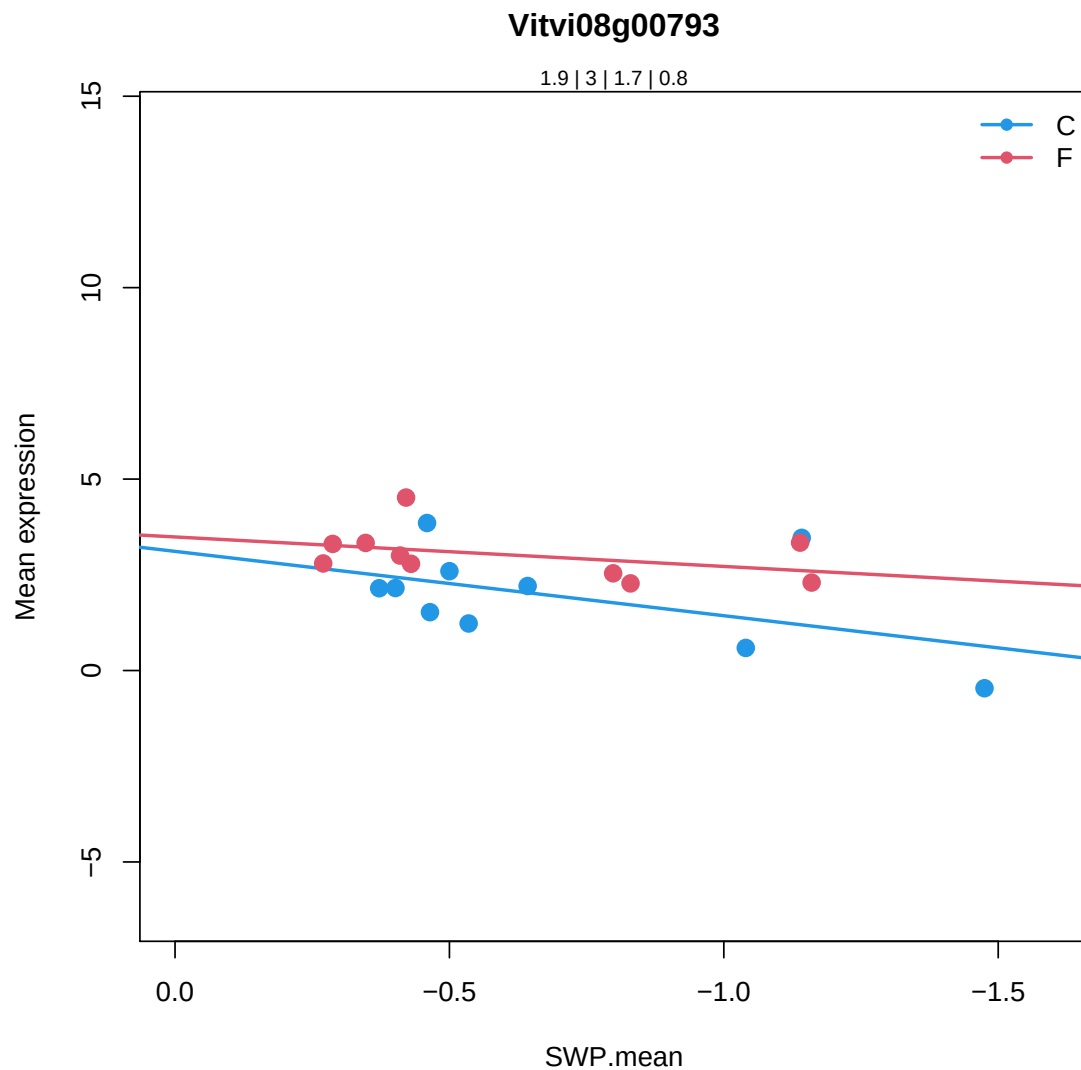
WRKY DNA-binding protein 33 |

Chr2:16108476-16110539 FORWARD LENGTH=519 |

201606

Coefficients for Vitvi08g00793.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.930135	4.61146e-07	***	5.369175e-07	***
SlopeC	1.680358	0.03702164	*	0.4620709	
MeanF-MeanC	1.089323	0.009764866	**	0.07460456	.
SlopeF-SlopeC	-0.9099544	0.42733		0.9999488	



8.1.154 Vitvi16g02026: Type1.0 *

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

Vitvi16g02026

35.2

not assigned.unknown

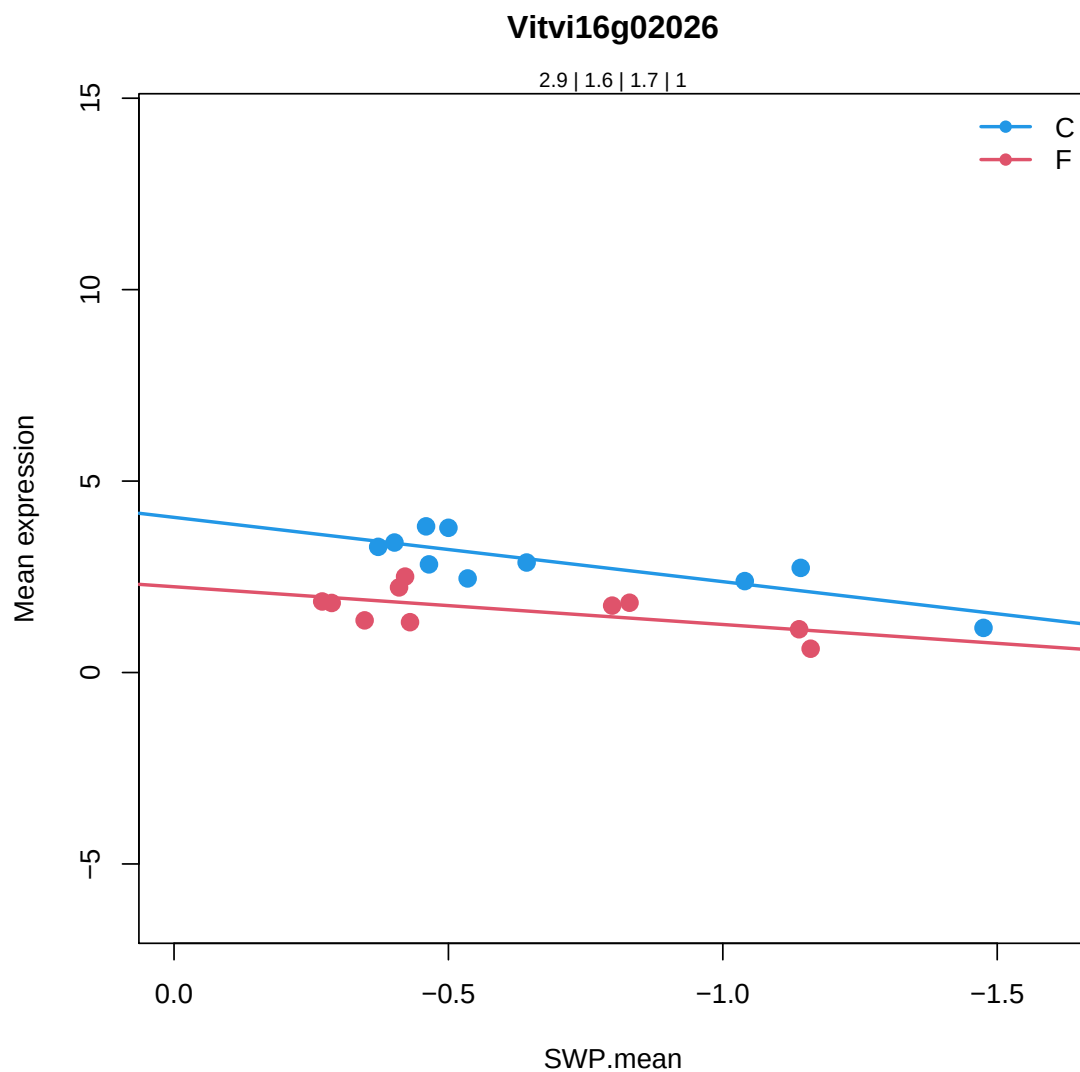
PR5-like receptor kinase |

Chr5:15293325-15295838 REVERSE LENGTH=665 |

201606

Coefficients for Vitvi16g02026.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.871416	5.778696e-15	***	9.912097e-15	***
SlopeC	1.678848	0.0005948157	***	0.1005065	
MeanF-MeanC	-1.231718	8.475631e-06	***	0.0002153093	***
SlopeF-SlopeC	-0.6929079	0.2769802		0.9999488	



8.1.155 Vitvi02g01457: Type1.0

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

Vitvi02g01457

35.2

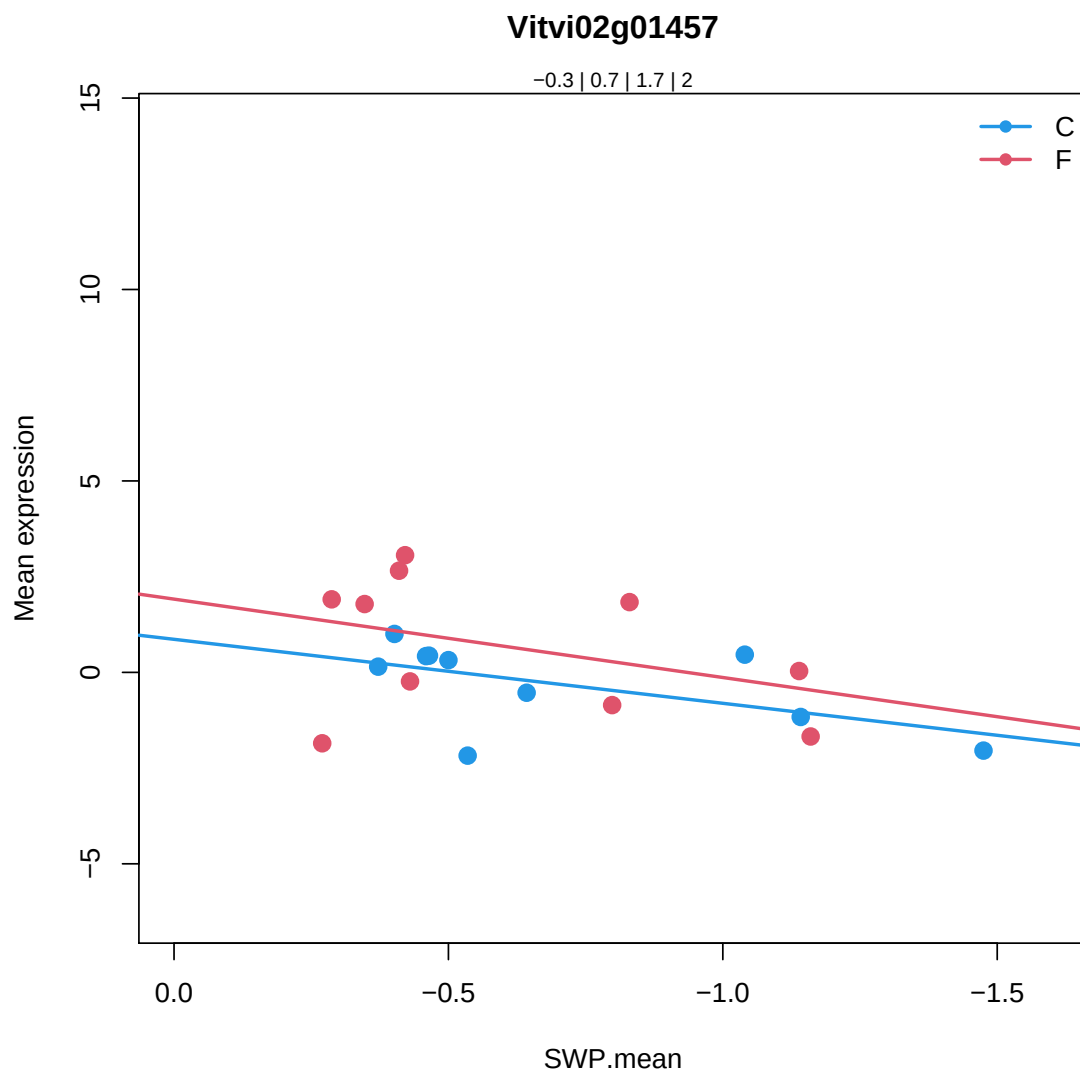
not assigned.unknown

[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	



8.1.156 Vitvi04g00005: Type1.0 *

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

Vitvi04g00005

35.2

not assigned.unknown

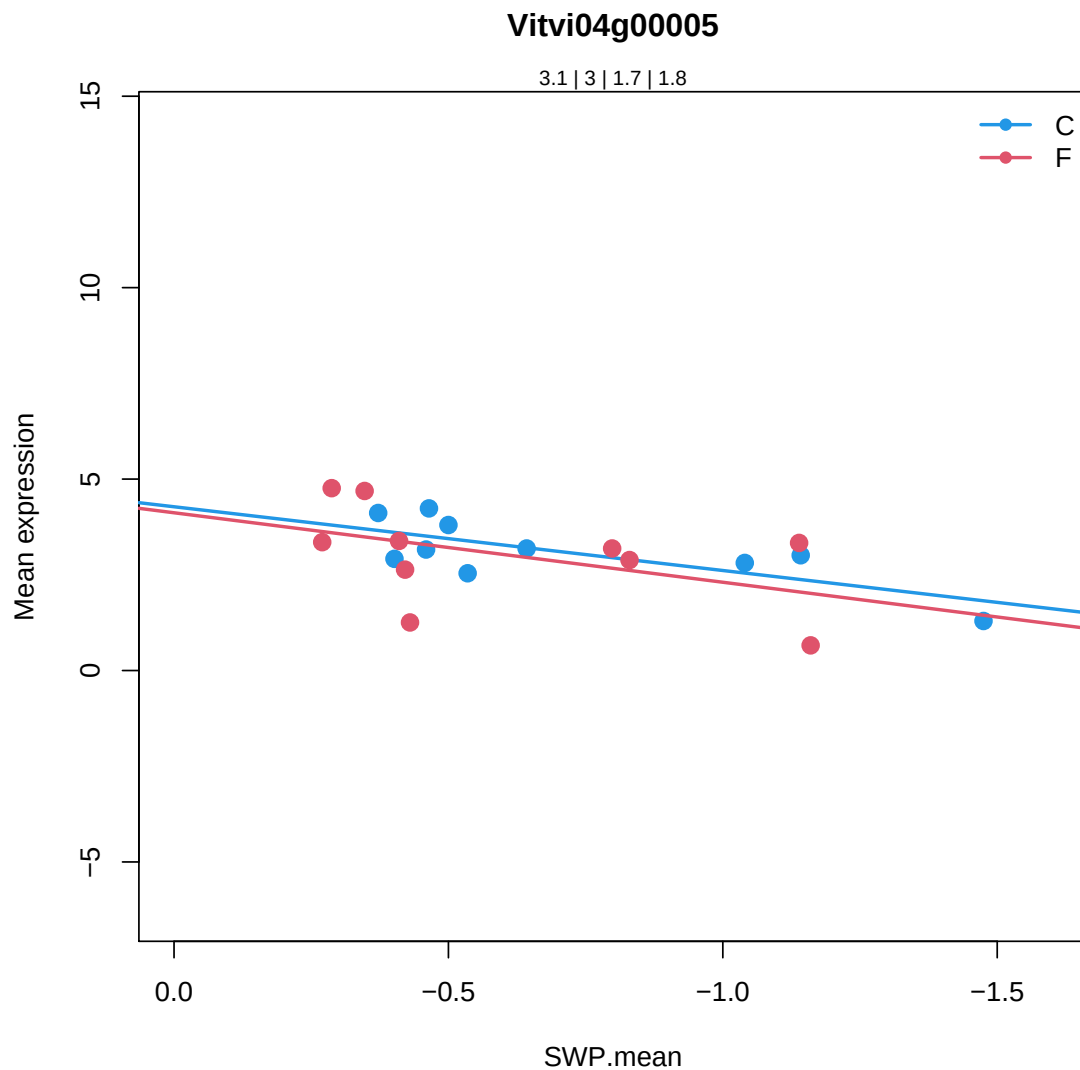
Avr9/Cf-9 rapidly elicited protein |

Chr1:19407559-19408185 REVERSE LENGTH=208 |

201606

Coefficients for Vitvi04g00005.

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



8.1.157 Vitvi13g01937: Type1.0

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

Vitvi13g01937

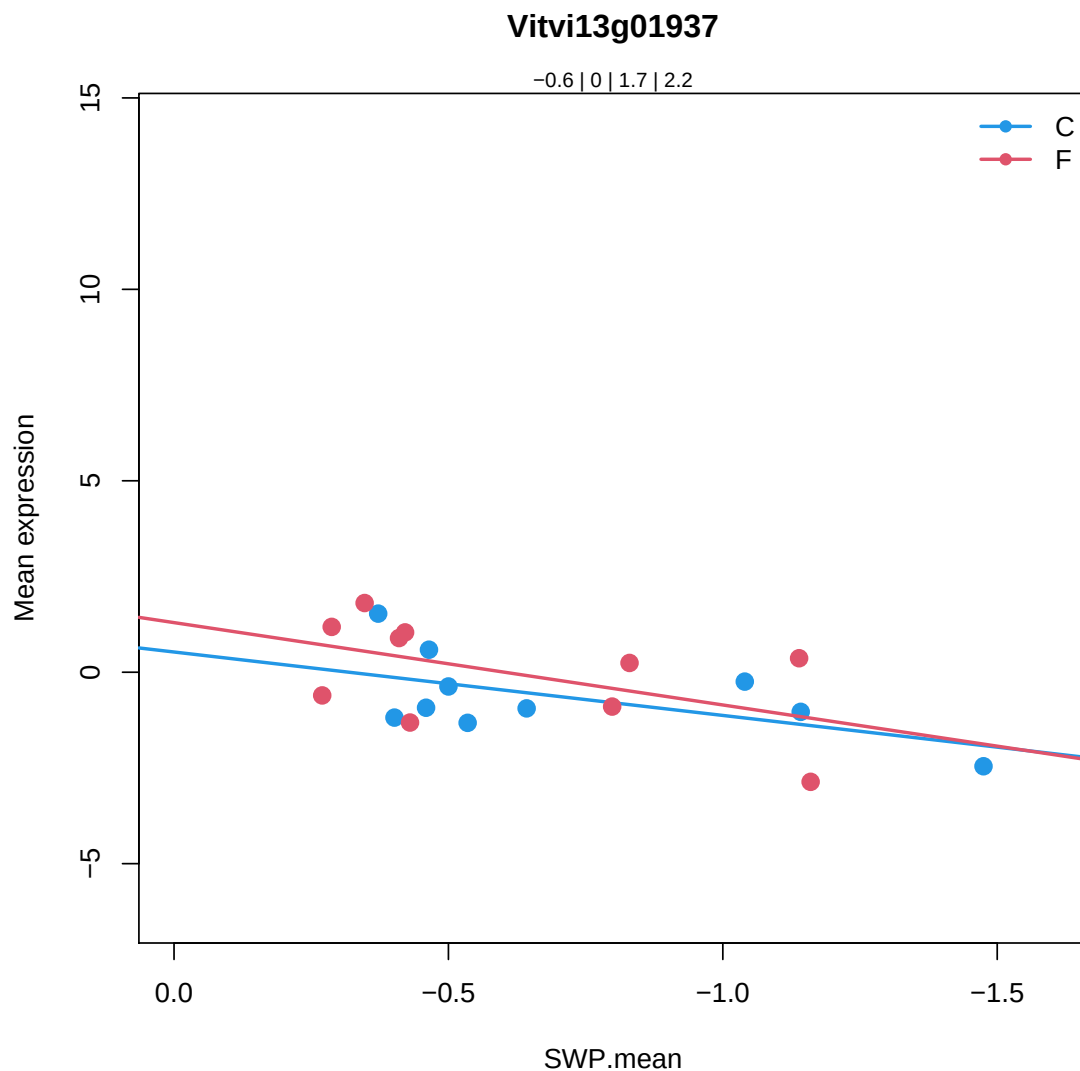
35.2

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	



8.1.158 Vitvi09g01557: Type1.0 *

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

Vitvi09g01557

30.2.1

signalling.receptor kinases.leucine rich repeat I

root hair specific 16 |

Chr4:14385631-14389524 FORWARD LENGTH=910 |

201606

Vitvi09g01557

29.4

protein.postranslational modification

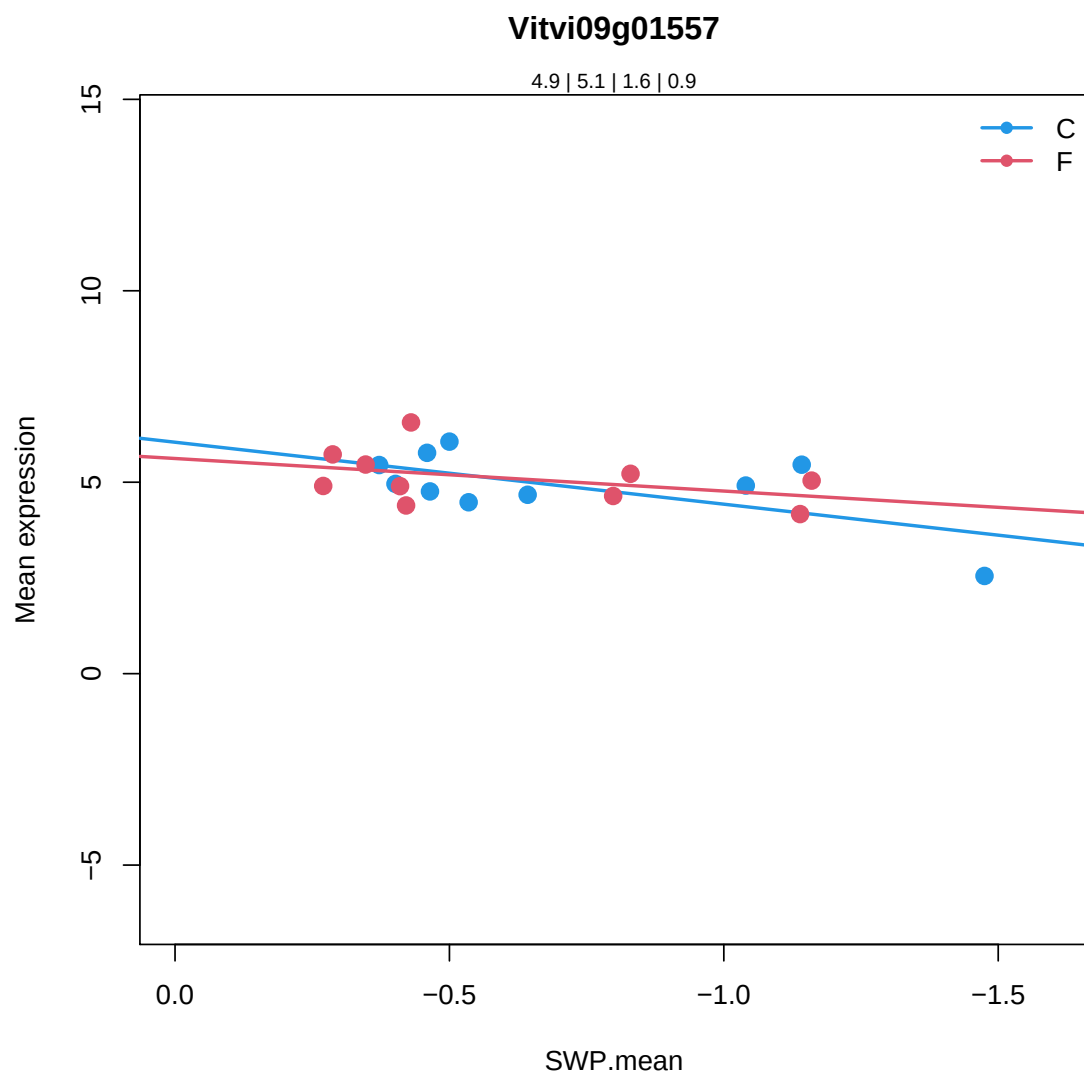
root hair specific 16 |

Chr4:14385631-14389524 FORWARD LENGTH=910 |

201606

Coefficients for Vitvi09g01557.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.90615	1.680973e-16	***	3.516042e-16	***
SlopeC	1.618247	0.01333708	*	0.3305597	
MeanF-MeanC	0.1948871	0.5295521		0.8241195	
SlopeF-SlopeC	-0.7679779	0.3992665		0.9999488	



8.1.159 Vitvi08g01905: Type1.0 *

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

Vitvi08g01905

17.3.1.2.2

hormone metabolism.brassinosteroid.synthesis-degradation.sterols.SMT2

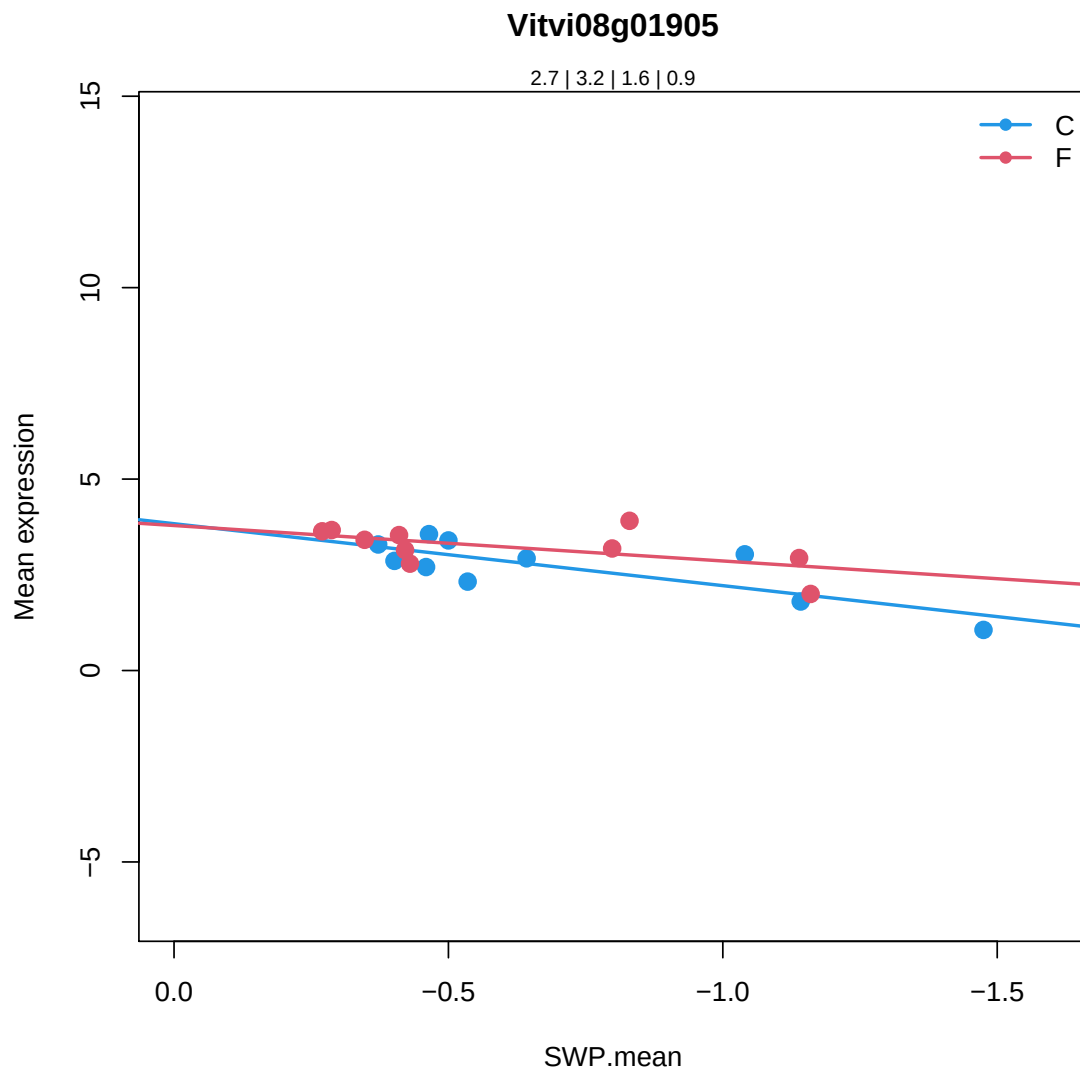
sterol methyltransferase 1 |

Chr5:4424048-4426866 REVERSE LENGTH=336 |

201606

Coefficients for Vitvi08g01905.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.696728	4.136032e-14	***	6.553841e-14	***
SlopeC	1.617844	0.001161907	**	0.1351892	
MeanF-MeanC	0.5260214	0.02581563	*	0.1522763	
SlopeF-SlopeC	-0.6919492	0.2938912		0.9999488	



8.1.160 Vitvi10g02015: Type1.0 *

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

Vitvi10g02015

30.2.12

signalling.receptor kinases.leucine rich repeat XII

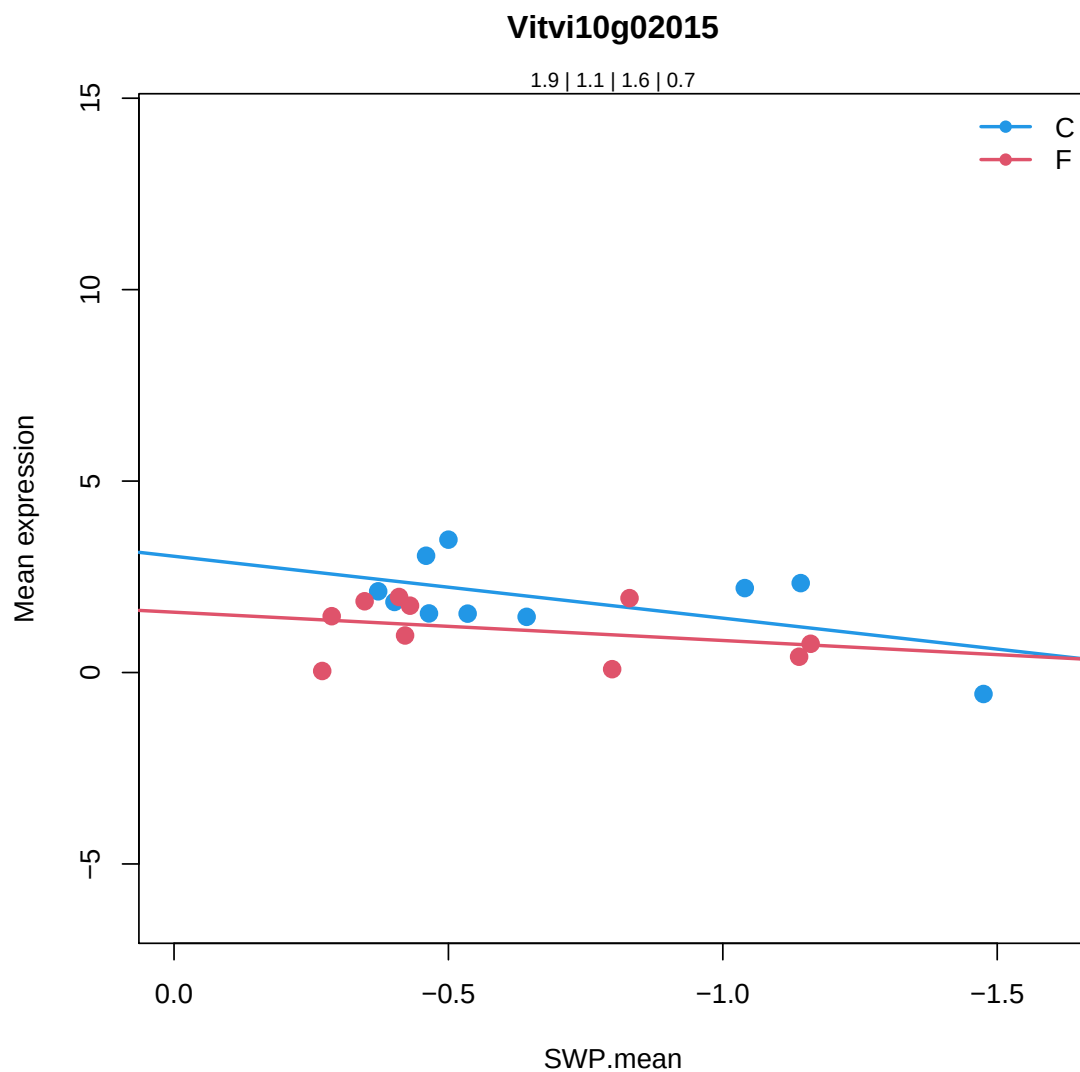
Leucine-rich repeat receptor-like protein kinase family protein |

Chr4:5637467-5640496 REVERSE LENGTH=1009 |

201606

Coefficients for Vitvi10g02015.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.899736	1.570681e-07	***	1.853827e-07	***
SlopeC	1.616306	0.02973003	*	0.4299803	
MeanF-MeanC	-0.7747487	0.03923561	*	0.2038273	
SlopeF-SlopeC	-0.8771358	0.4052406		0.9999488	



8.1.161 Vitvi18g00534: Type1.0 *

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

Vitvi18g00534

30.6

signalling.MAP kinases

Protein kinase superfamily protein |

Chr4:12650410-12654755 FORWARD LENGTH=956 |

201606

Vitvi18g00534

29.4

protein.postranslational modification

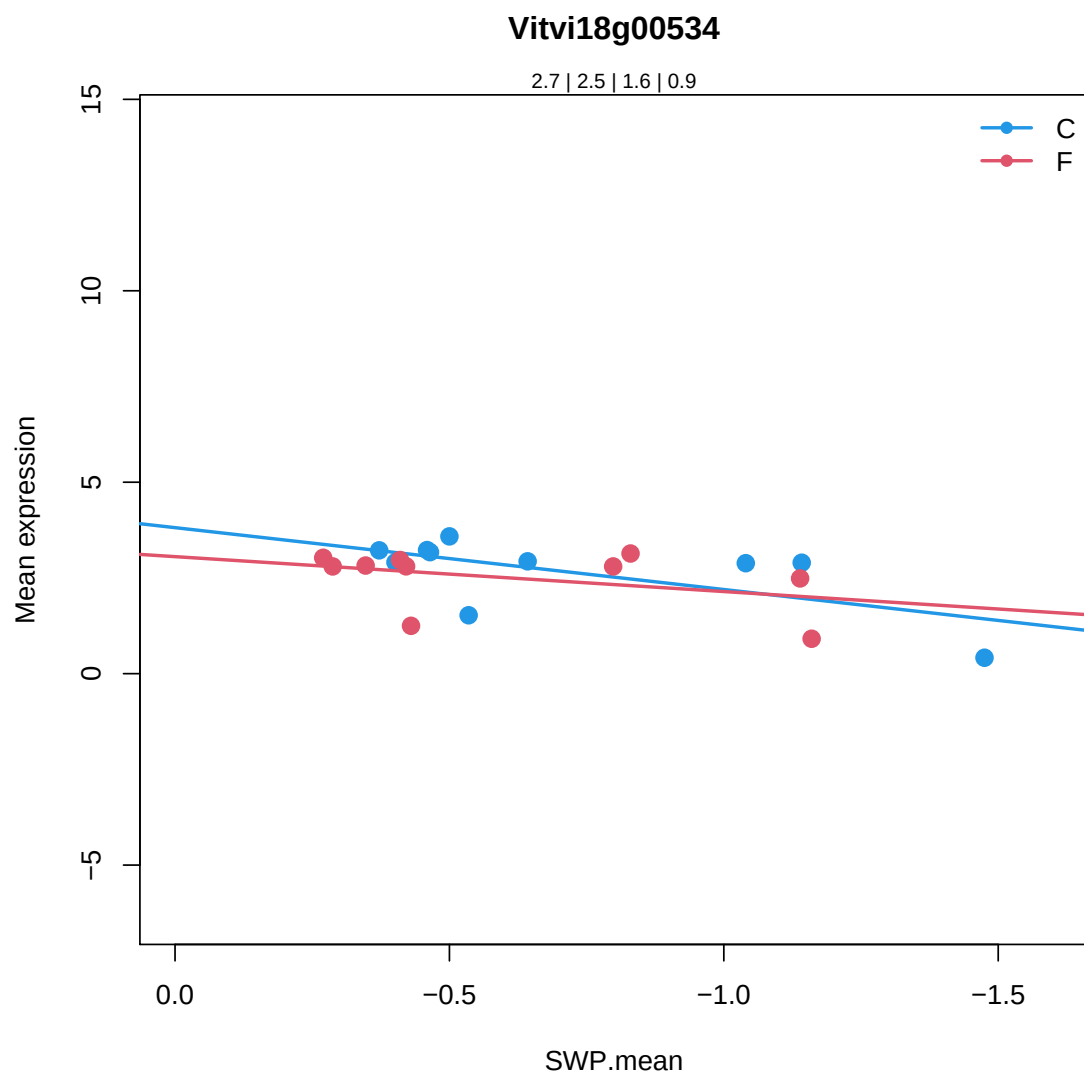
Protein kinase superfamily protein |

Chr4:12650410-12654755 FORWARD LENGTH=956 |

201606

Coefficients for Vitvi18g00534.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.677041	5.893699e-11	***	7.778315e-11	***
SlopeC	1.615536	0.01673619	*	0.3523917	
MeanF-MeanC	-0.1764632	0.5829017		0.8533617	
SlopeF-SlopeC	-0.7035348	0.4559857		0.9999488	



8.1.162 Vitvi15g01003: Type1.0 *

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

Vitvi15g01003

27.3.32

RNA.regulation of transcription.WRKY domain transcription factor famil

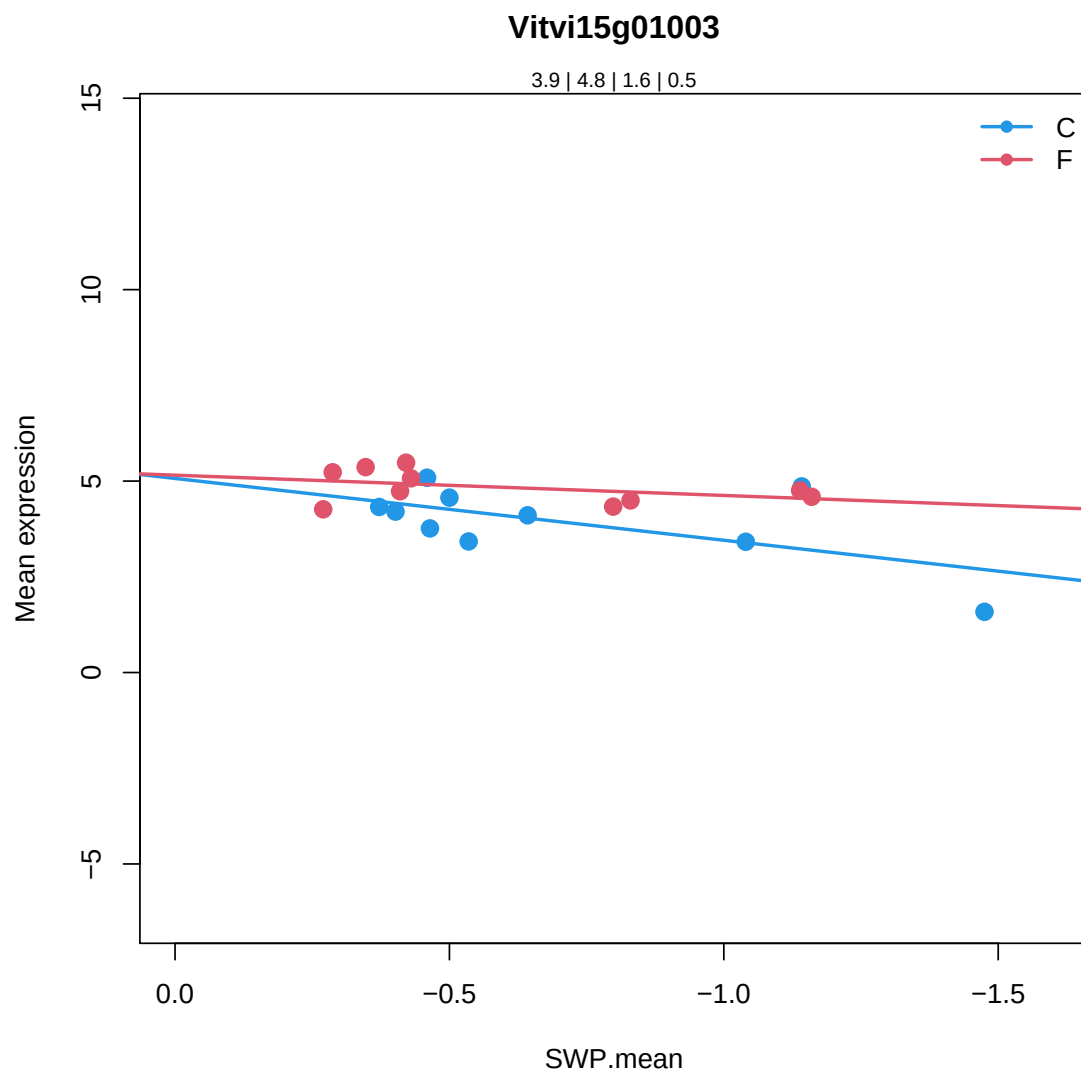
WRKY DNA-binding protein 46 |

Chr2:19043676-19044754 REVERSE LENGTH=295 |

201606

Coefficients for Vitvi15g01003.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.933475	2.219351e-15	***	4.003237e-15	***
SlopeC	1.614216	0.007374271	**	0.2777732	
MeanF-MeanC	0.8982111	0.003851808	**	0.03725207	*
SlopeF-SlopeC	-1.084787	0.1954872		0.9999488	



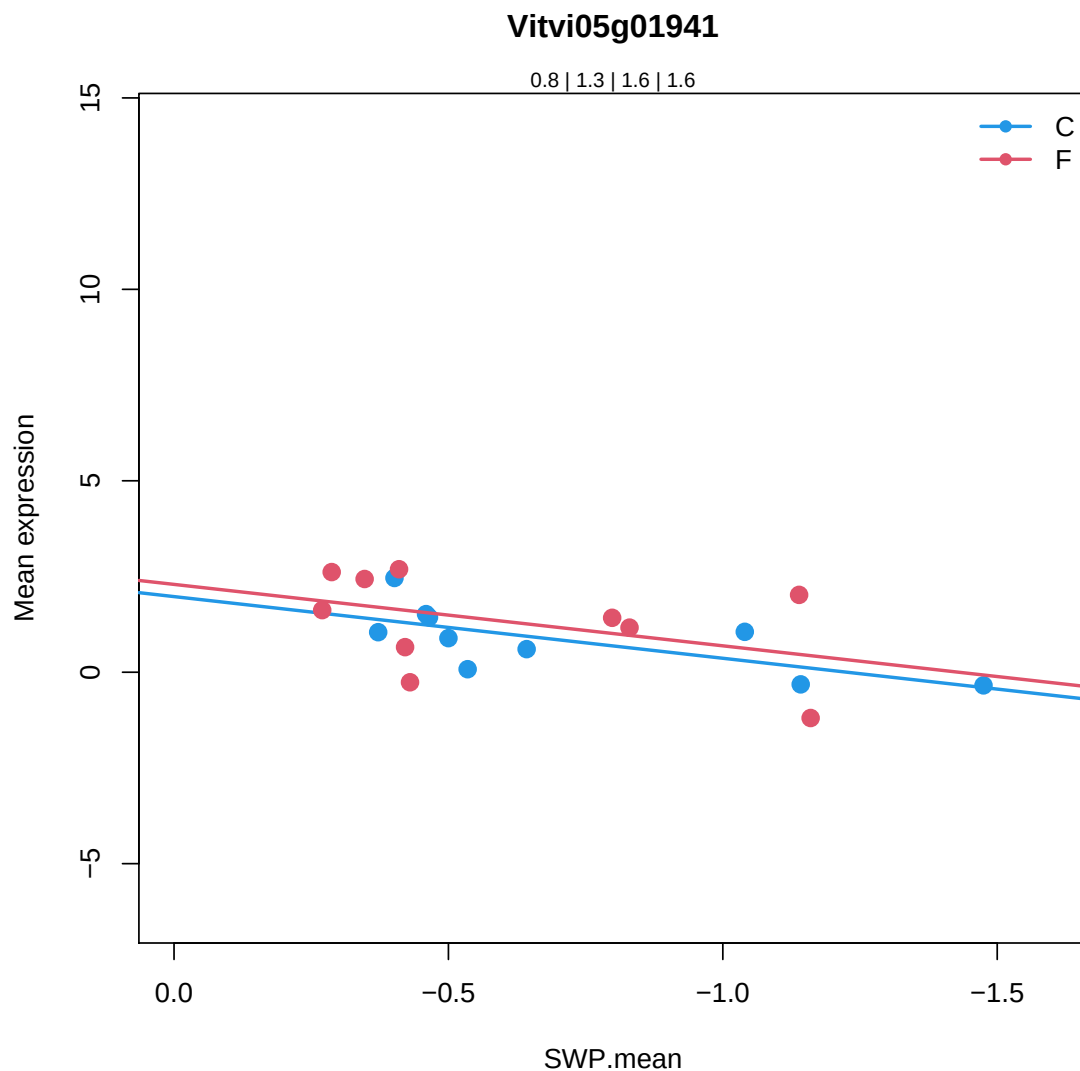
8.1.163 Vitvi05g01941: Type1.0

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

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

Coefficients for Vitvi05g01941.

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



8.1.164 Vitvi16g02034: Type1.0 *

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

Vitvi16g02034

35.2

not assigned.unknown

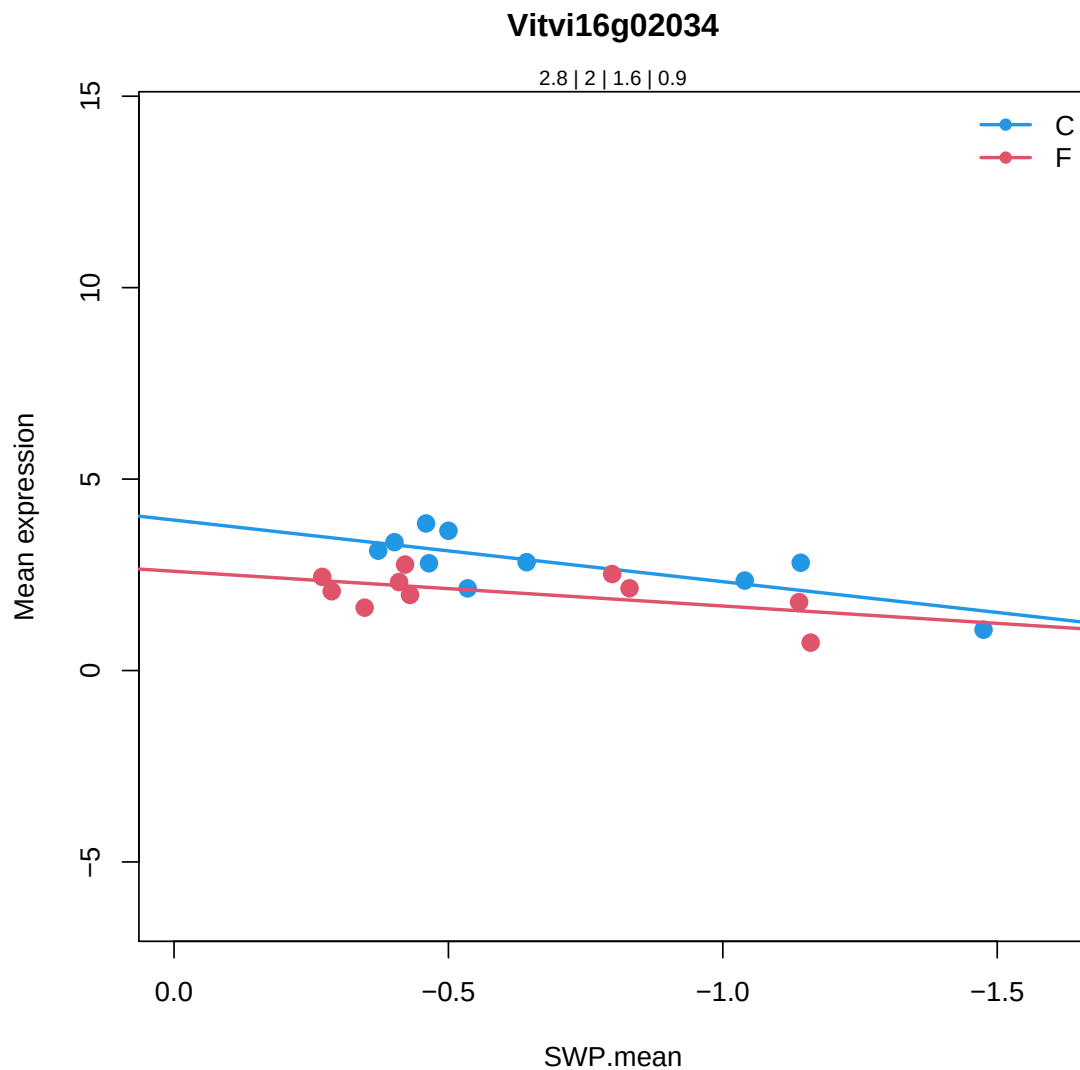
Protein kinase superfamily protein |

Chr1:24961634-24963941 REVERSE LENGTH=663 |

201606

Coefficients for Vitvi16g02034.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.797958	7.456936e-14	***	1.156007e-13	***
SlopeC	1.608045	0.002168125	**	0.1776697	
MeanF-MeanC	-0.7586639	0.003913123	**	0.03767771	*
SlopeF-SlopeC	-0.7017667	0.3185023		0.9999488	



8.1.165 Vitvi07g00256: Type1.0 *

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

Vitvi07g00256

29.5.3

protein.degradation.cysteine protease

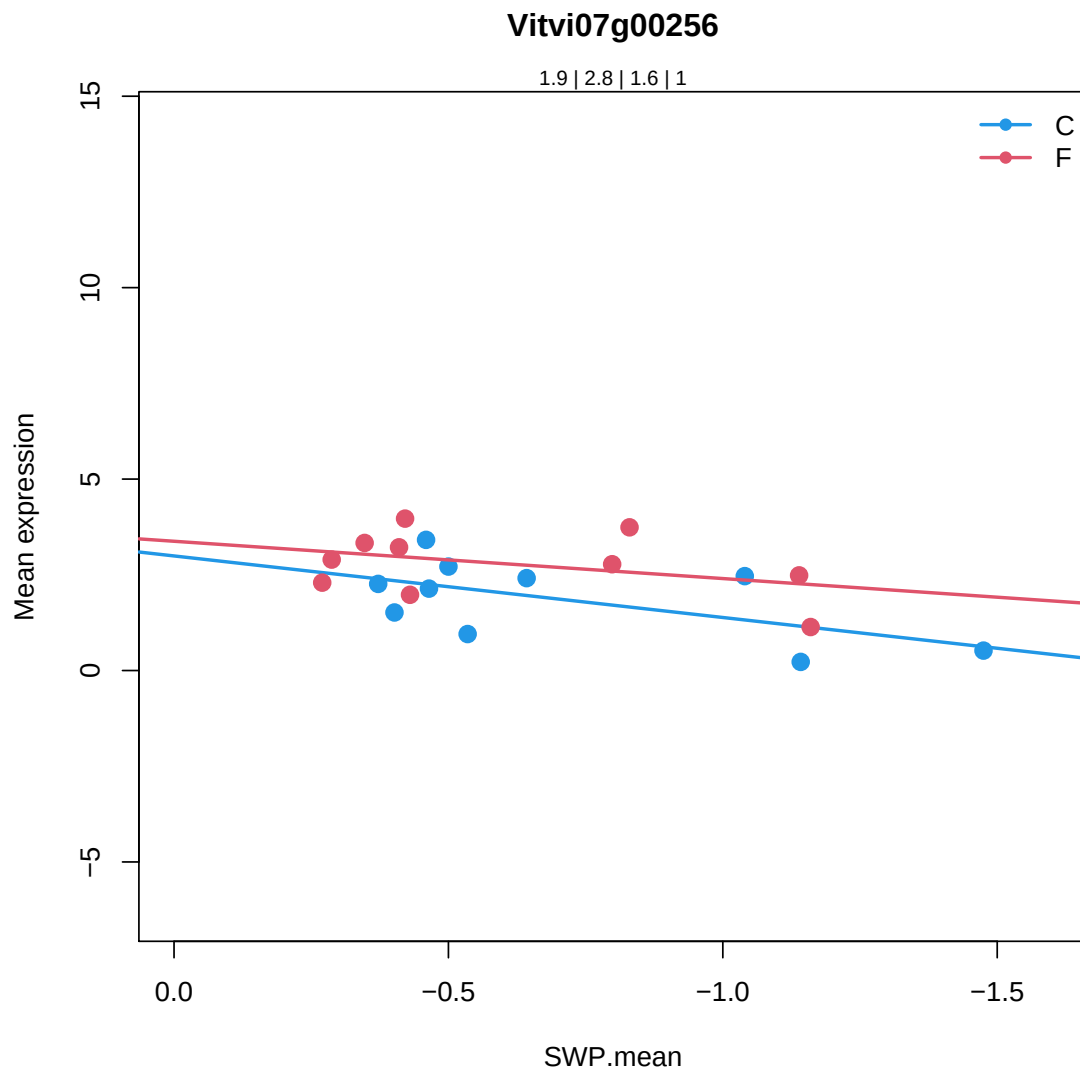
Thioredoxin superfamily protein |

Chr3:23266303-23266614 FORWARD LENGTH=103 |

201606

Coefficients for Vitvi07g00256.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.861934	1.683609e-07	***	1.984961e-07	***
SlopeC	1.607692	0.02823847	*	0.4274188	
MeanF-MeanC	0.9203376	0.01482444	*	0.1010076	
SlopeF-SlopeC	-0.6337991	0.5397133		0.9999488	



8.1.166 Vitvi18g02815: Type1.0

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

Vitvi18g02815

26.28

misc.GDSL-motif lipase

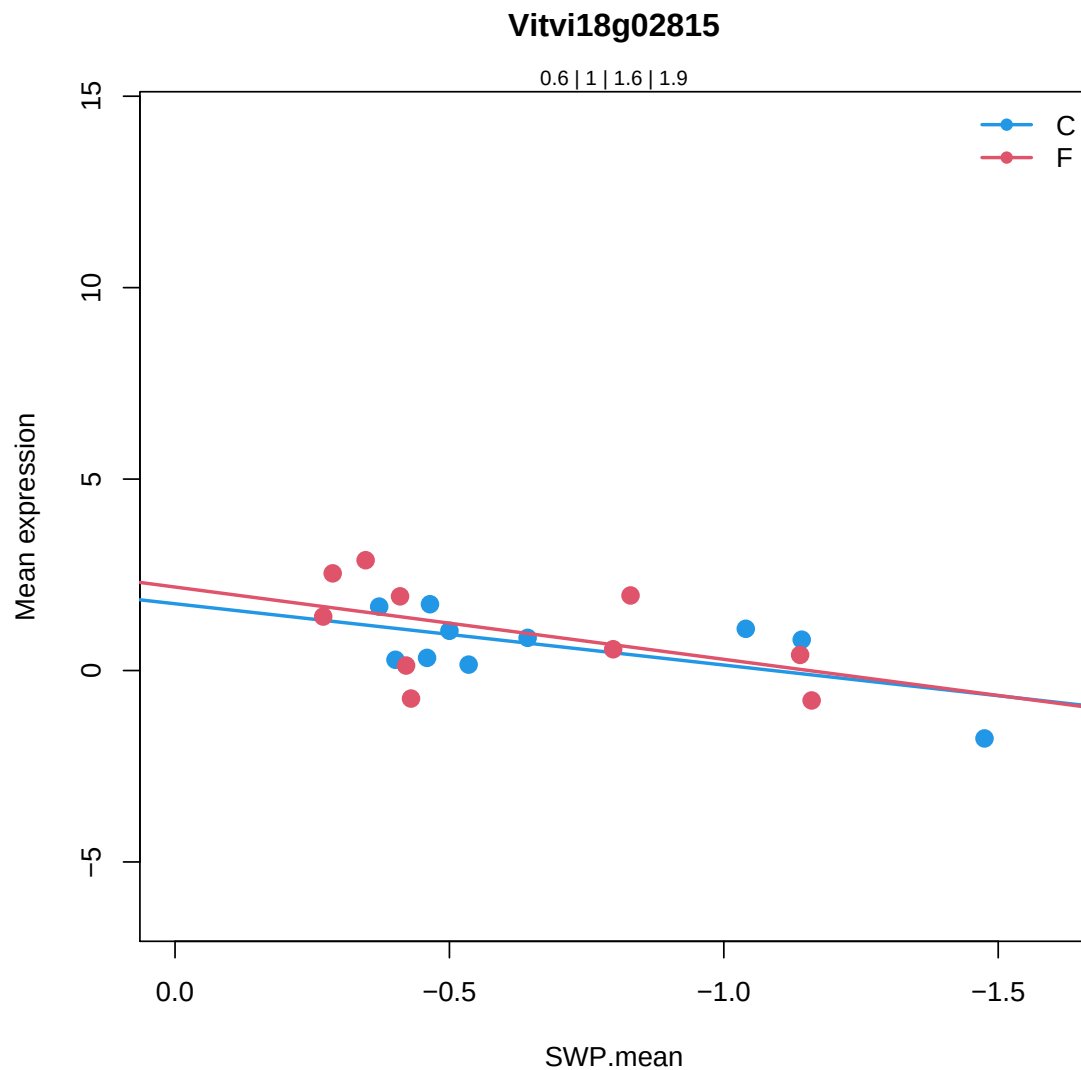
GDSL-like Lipase/Acylhydrolase superfamily protein |

Chr1:28499179-28500943 FORWARD LENGTH=364 |

201606

Coefficients for Vitvi18g02815.

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



8.1.167 Vitvi19g00094: Type1.0

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

Vitvi19g00094

20.1.7

stress.biotic.PR-proteins

pathogenesis-related family protein |

Chr1:29621447-29622431 REVERSE LENGTH=238 |

201606

Vitvi19g00094

35.2

not assigned.unknown

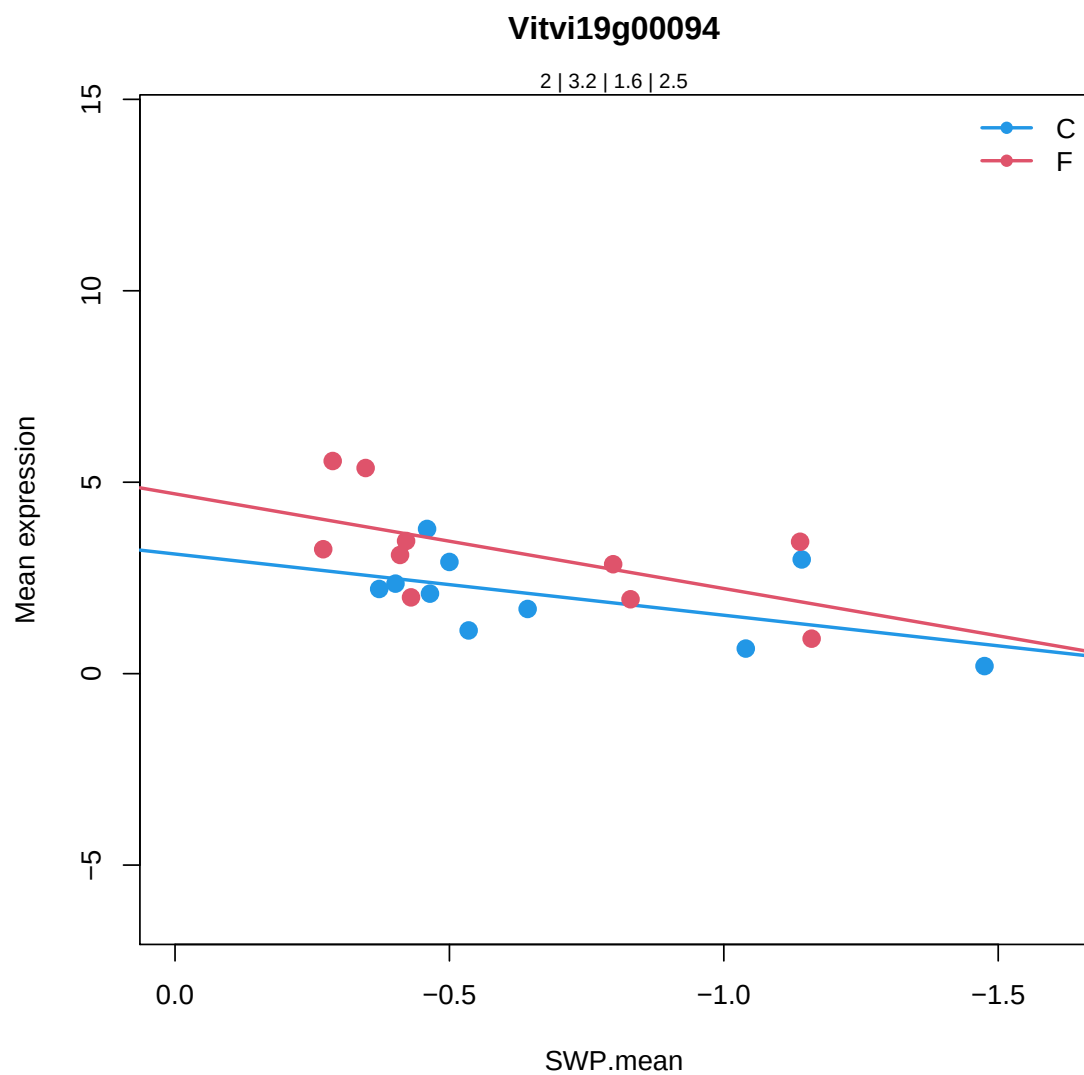
pathogenesis-related family protein |

Chr1:29621447-29622431 REVERSE LENGTH=238 |

201606

Coefficients for Vitvi19g00094.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.000287	2.504844e-06	***	2.864343e-06	***
SlopeC	1.598781	0.08255374	.	0.5797186	
MeanF-MeanC	1.188635	0.01437332	*	0.09904078	.
SlopeF-SlopeC	0.8735558	0.5108944		0.9999488	



8.1.168 Vitvi11g00178: Type1.0 *

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

Vitvi11g00178

26.3.2

misc.gluco-, galacto- and mannosidases.beta-galactosidase

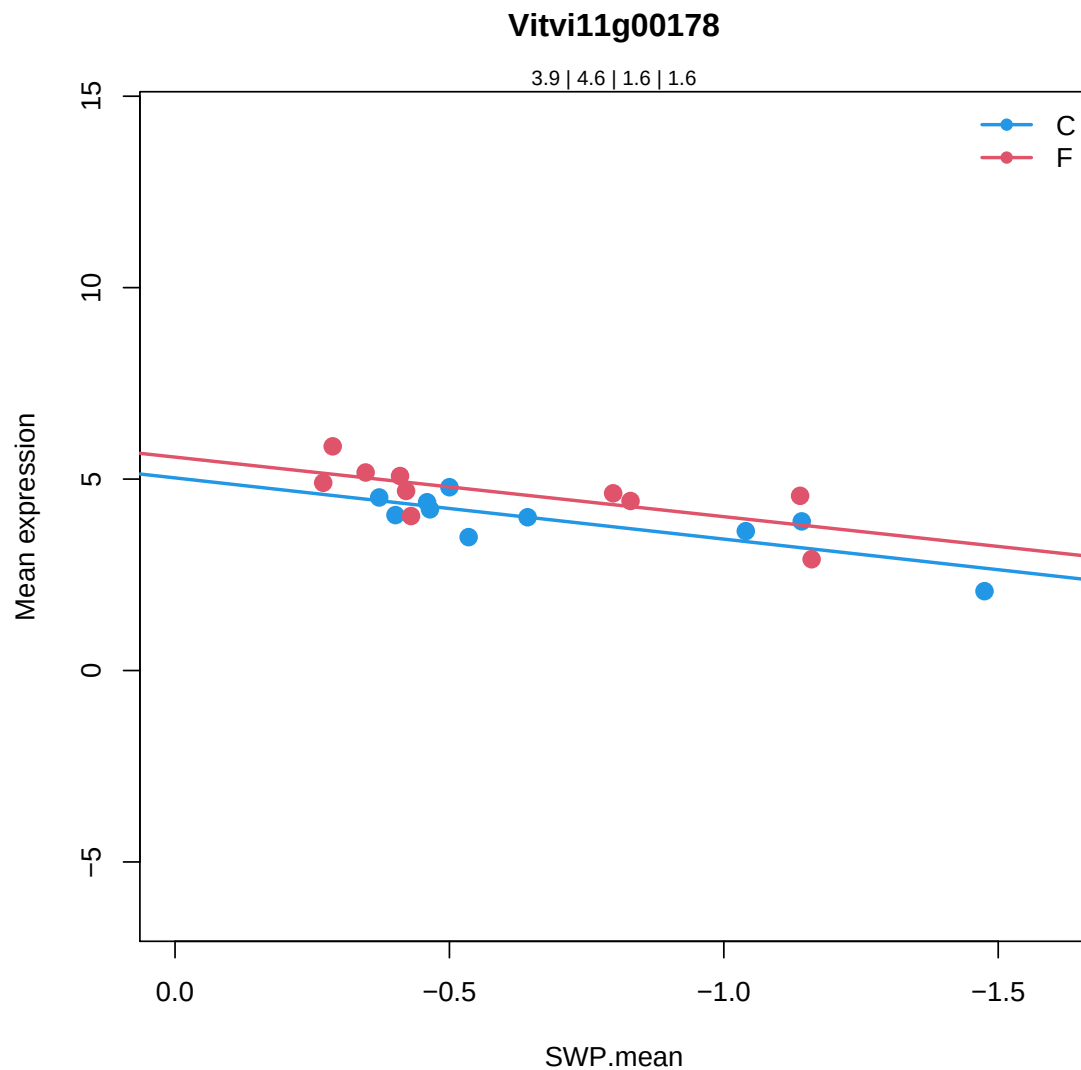
beta galactosidase 1 |

Chr3:4511192-4515756 FORWARD LENGTH=847 |

201606

Coefficients for Vitvi11g00178.

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



8.1.169 Vitvi07g01847: Type1.0 *

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

Vitvi07g01847

27.3.32

RNA.regulation of transcription.WRKY domain transcription factor famil

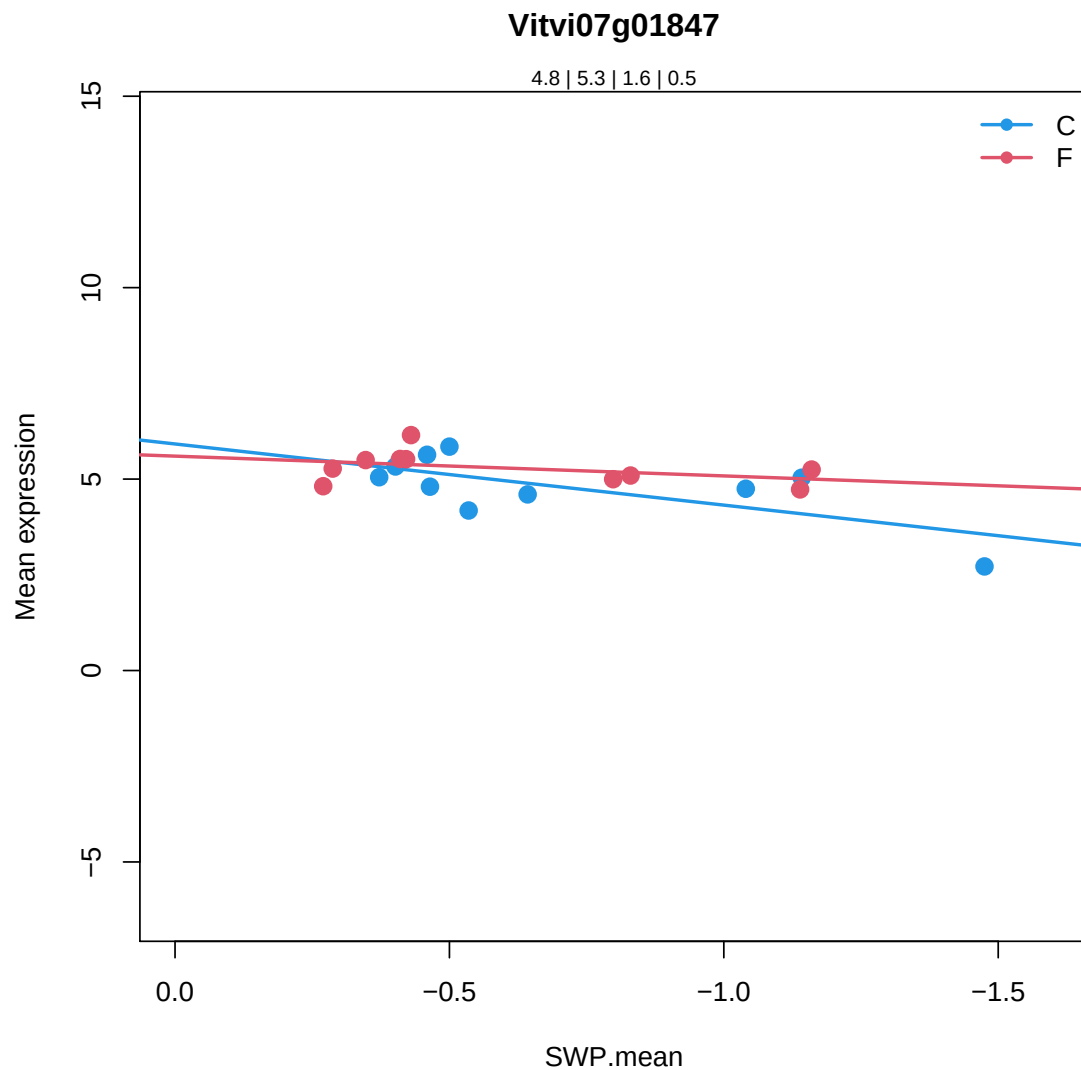
WRKY DNA-binding protein 51 |

Chr5:25908415-25909687 FORWARD LENGTH=194 |

201606

Coefficients for Vitvi07g01847.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.794137	2.072061e-18	***	6.514511e-18	***
SlopeC	1.597241	0.002856106	**	0.2035467	
MeanF-MeanC	0.4903821	0.05456768	.	0.2531104	
SlopeF-SlopeC	-1.080431	0.1406106		0.9999488	



8.1.170 Vitvi17g00217: Type1.0

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

Vitvi17g00217

20.1.7.5

stress.biotic.PR-proteins.PR5 (thaumatin-like proteins)

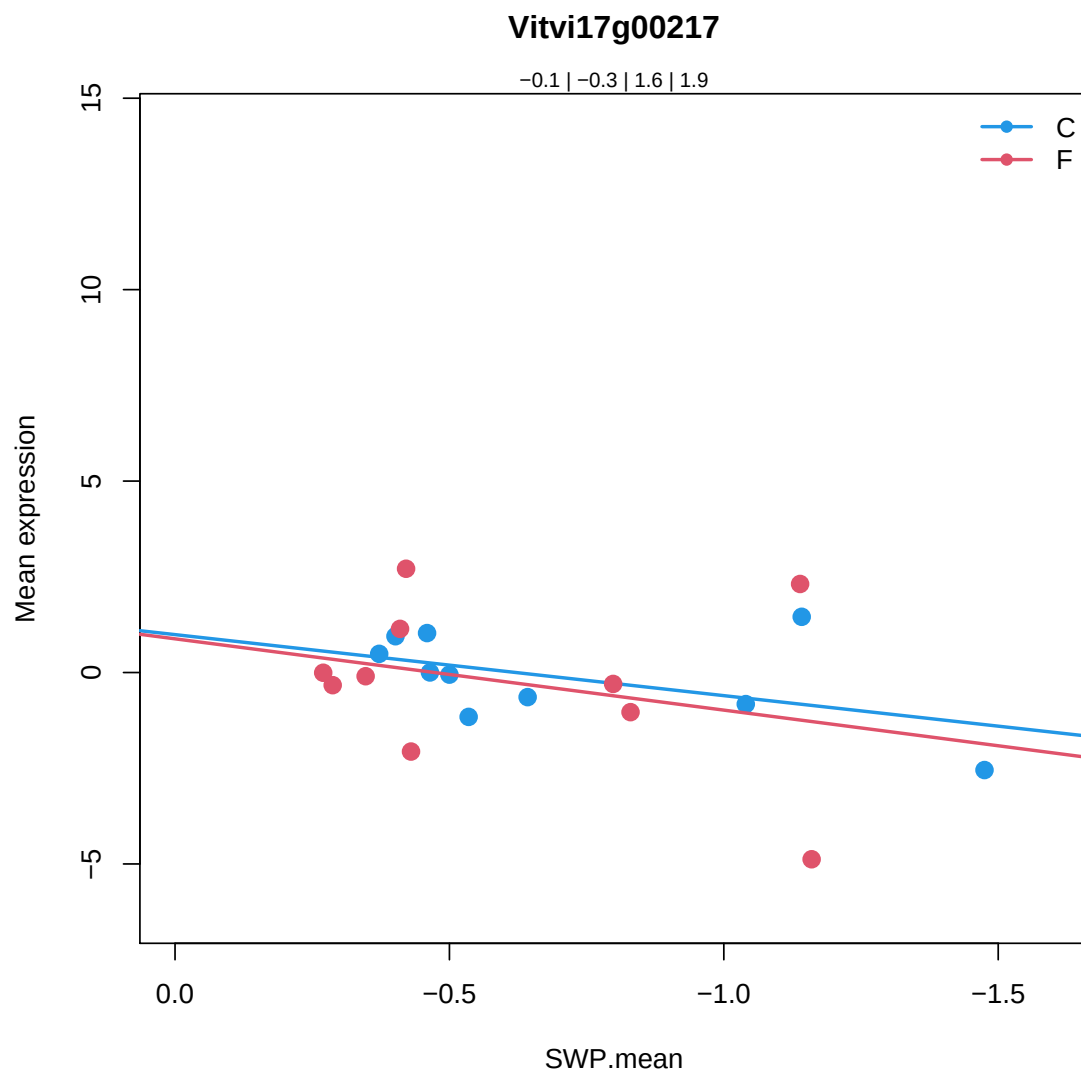
Pathogenesis-related thaumatin superfamily protein |

Chr1:6277024-6278005 REVERSE LENGTH=243 |

201606

Coefficients for Vitvi17g00217.

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



8.1.171 Vitvi15g01736: Type1.0 *

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

Vitvi15g01736

26.9

misc.glutathione S transferases

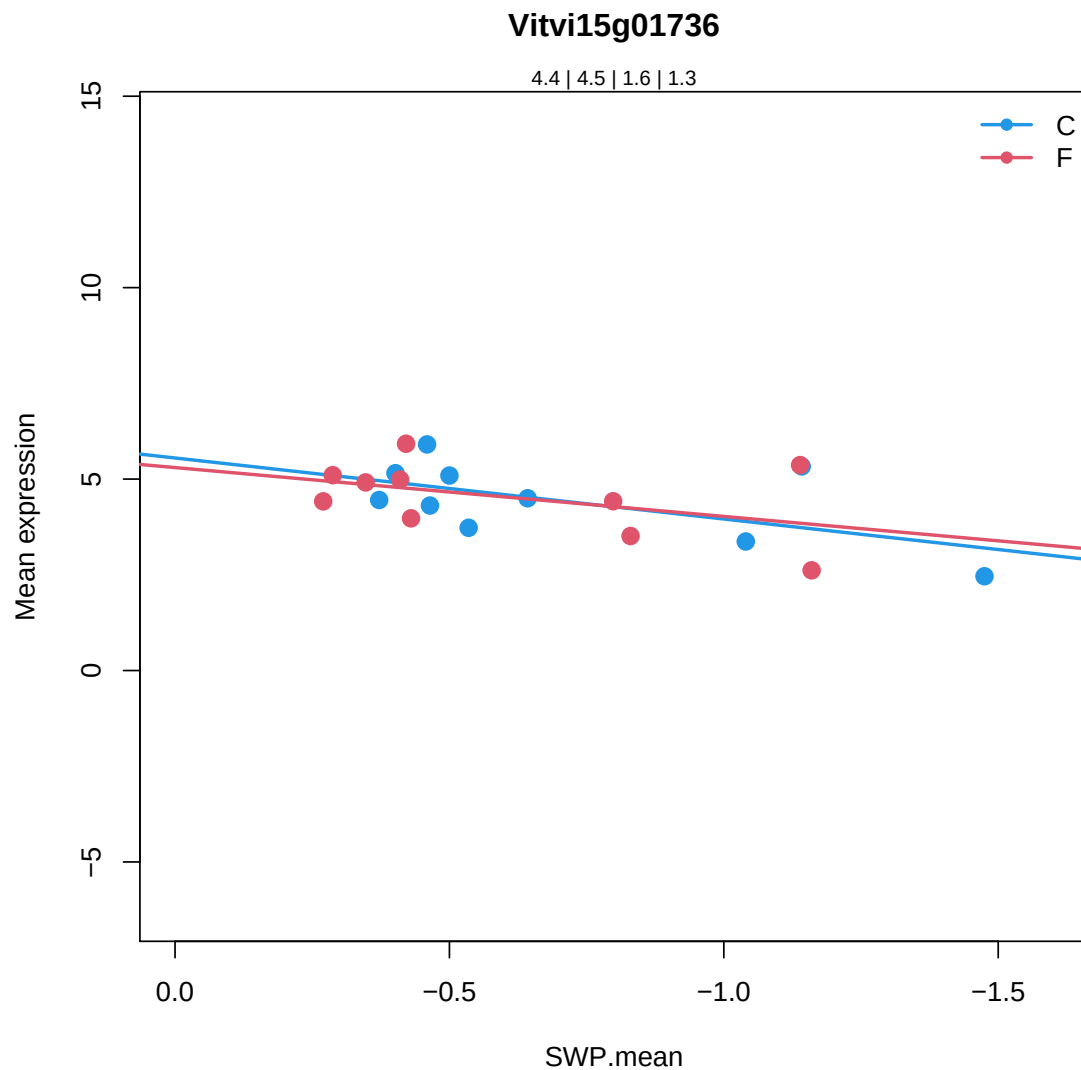
glutathione S-transferase tau 7 |

Chr2:12618111-12618871 REVERSE LENGTH=227 |

201606

Coefficients for Vitvi15g01736.

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



8.1.172 Vitvi17g00670: Type1.0

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

Vitvi17g00670

27.3.11

RNA.regulation of transcription.C2H2 zinc finger family

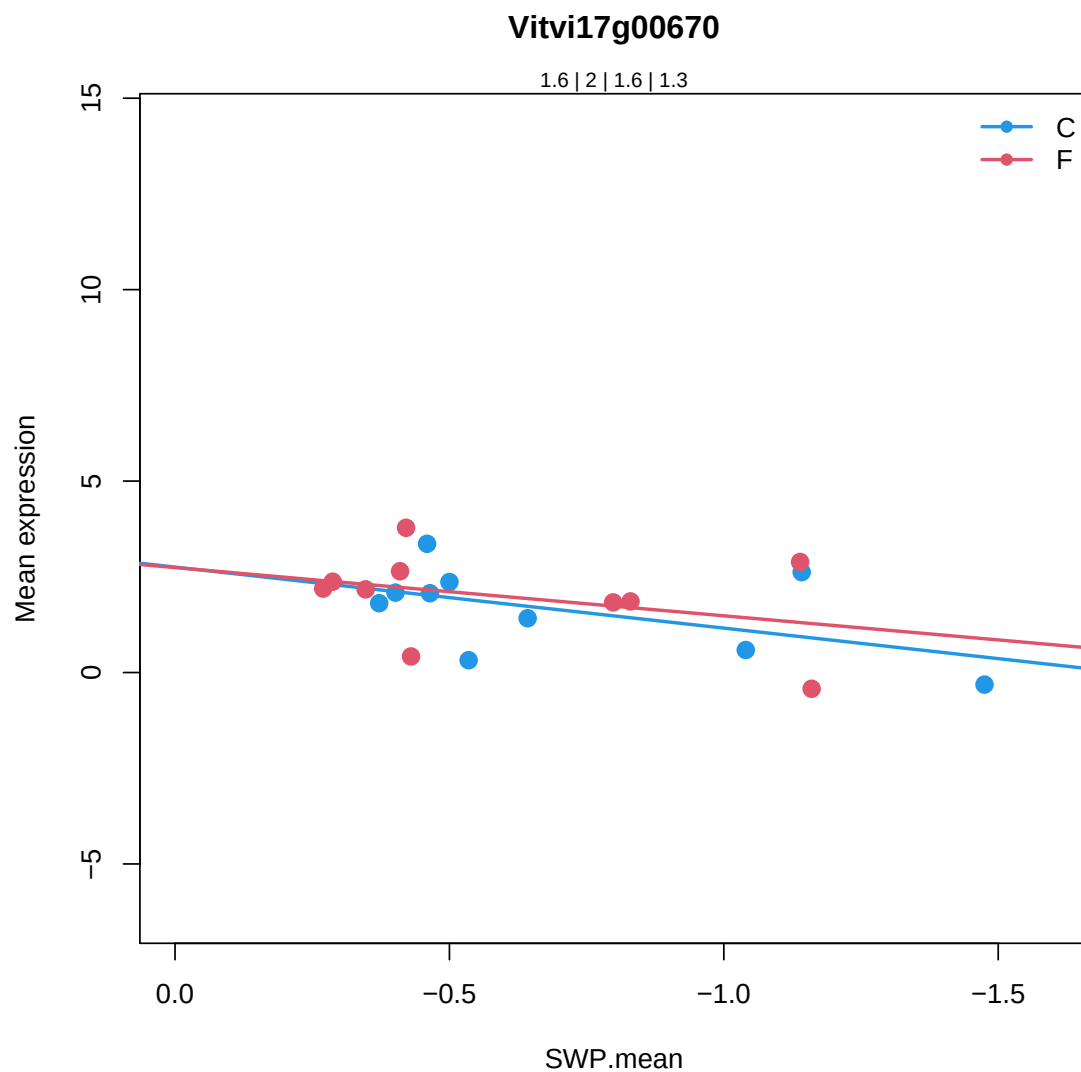
C2H2-like zinc finger protein |

Chr1:9193735-9195102 FORWARD LENGTH=455 |

201606

Coefficients for Vitvi17g00670.

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



8.1.173 Vitvi08g01789: Type1.0

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

Vitvi08g01789

26.3.5

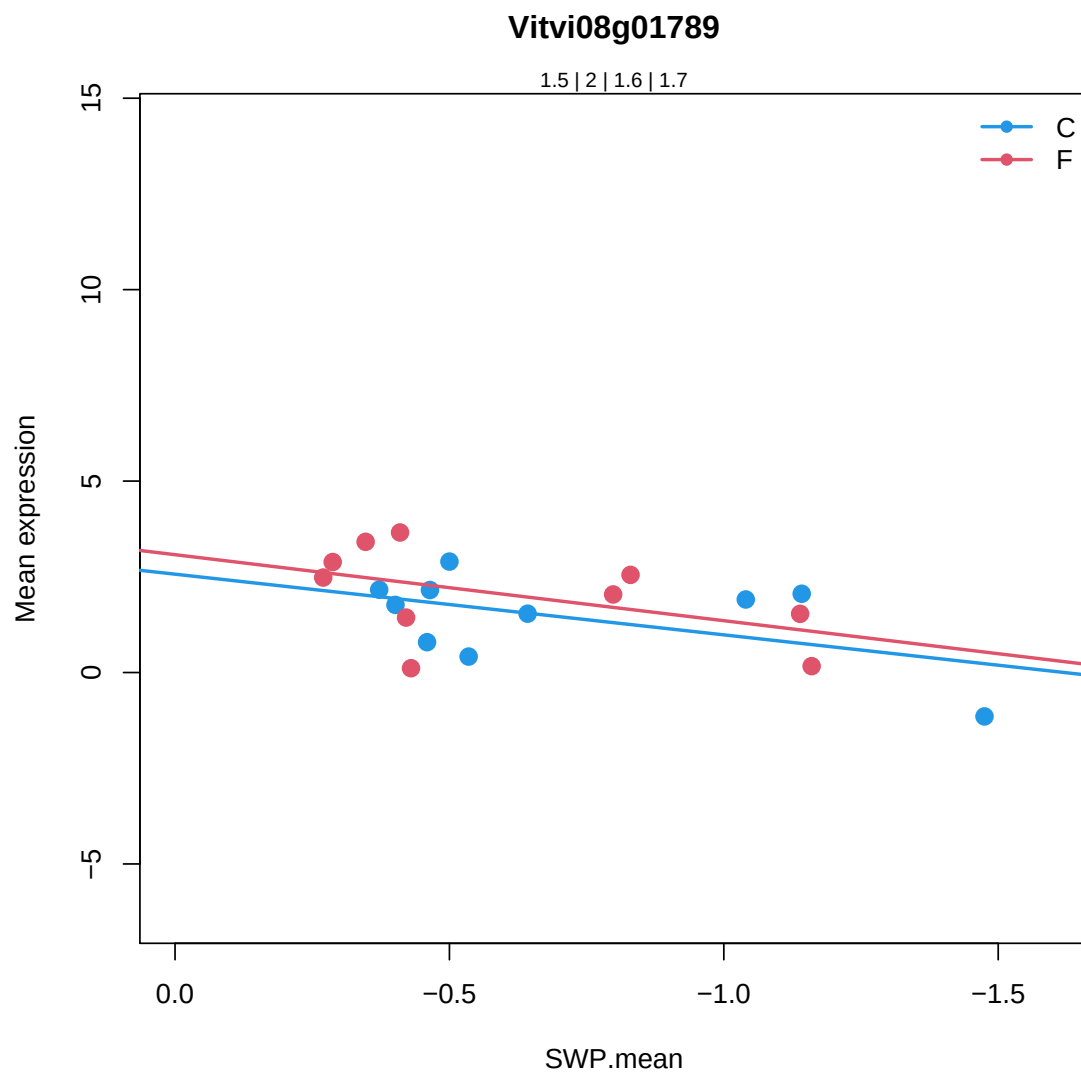
misc.gluco-, galacto- and mannosidases.glycosyl hydrolase family 5
alpha/beta-Hydrolases superfamily protein |

Chr3:1033788-1034591 FORWARD LENGTH=267 |

201606

Coefficients for Vitvi08g01789.

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



8.1.174 Vitvi18g02684: Type1.0 *

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

Vitvi18g02684

35.2

not assigned.unknown

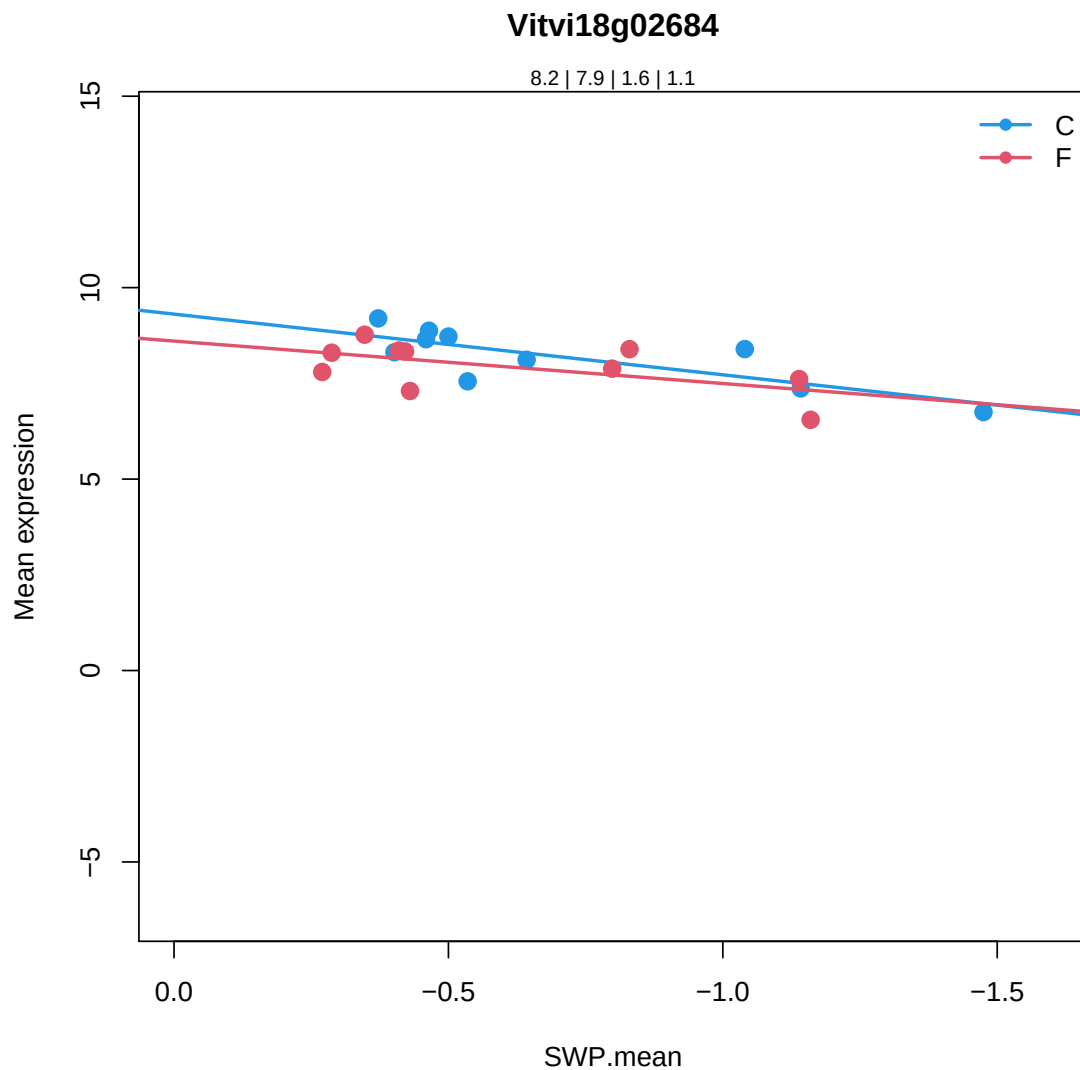
cysteine-rich RECEPTOR-like kinase |

Chr4:12129485-12133157 FORWARD LENGTH=1043 |

201606

Coefficients for Vitvi18g02684.

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



8.1.175 Vitvi09g00573: Type1.0 *

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

Vitvi09g00573

26.4.1

misc.beta 1,3 glucan hydrolases.glucan endo-1,3-beta-glucosidase

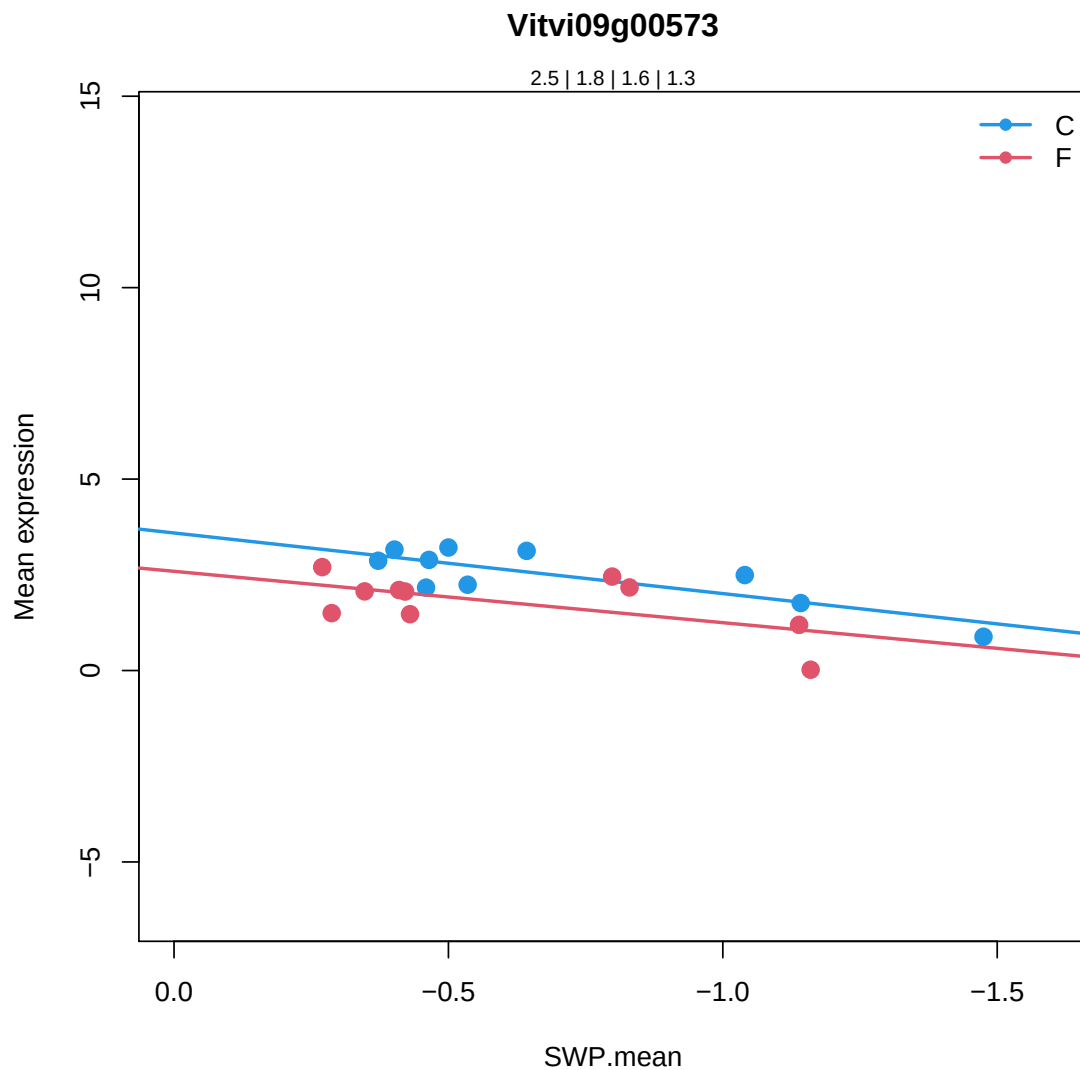
plant natriuretic peptide A |

Chr2:8091032-8091644 REVERSE LENGTH=130 |

201606

Coefficients for Vitvi09g00573.

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



8.1.176 Vitvi09g00050: Type1.0 *

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

Vitvi09g00050

17.2.3

hormone metabolism.auxin.induced-regulated-responsive-activated

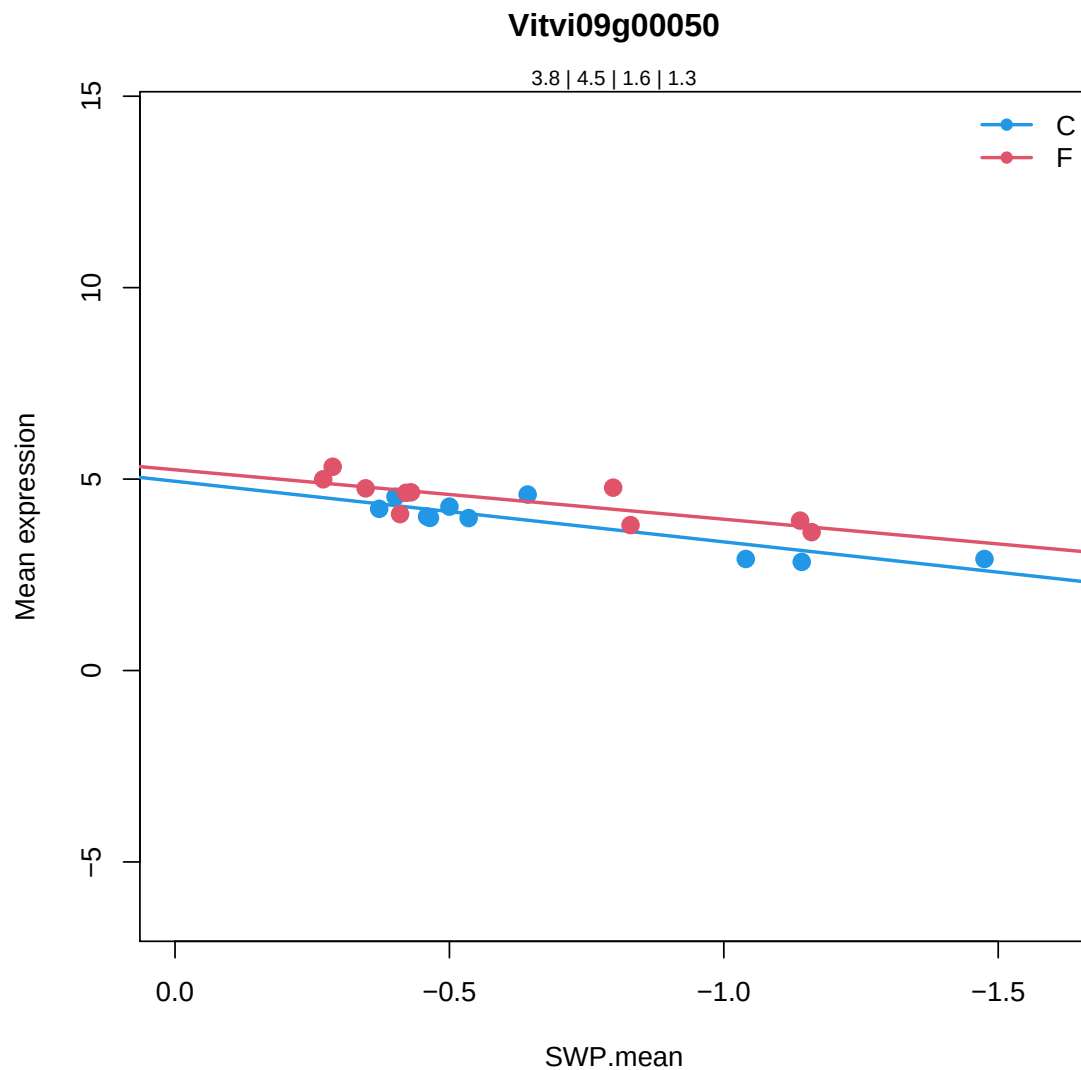
Dormancy/auxin associated family protein |

Chr1:20182683-20183242 FORWARD LENGTH=123 |

201606

Coefficients for Vitvi09g00050.

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



8.1.177 Vitvi02g00605: Type1.0

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

Vitvi02g00605

2.2.2.1.2

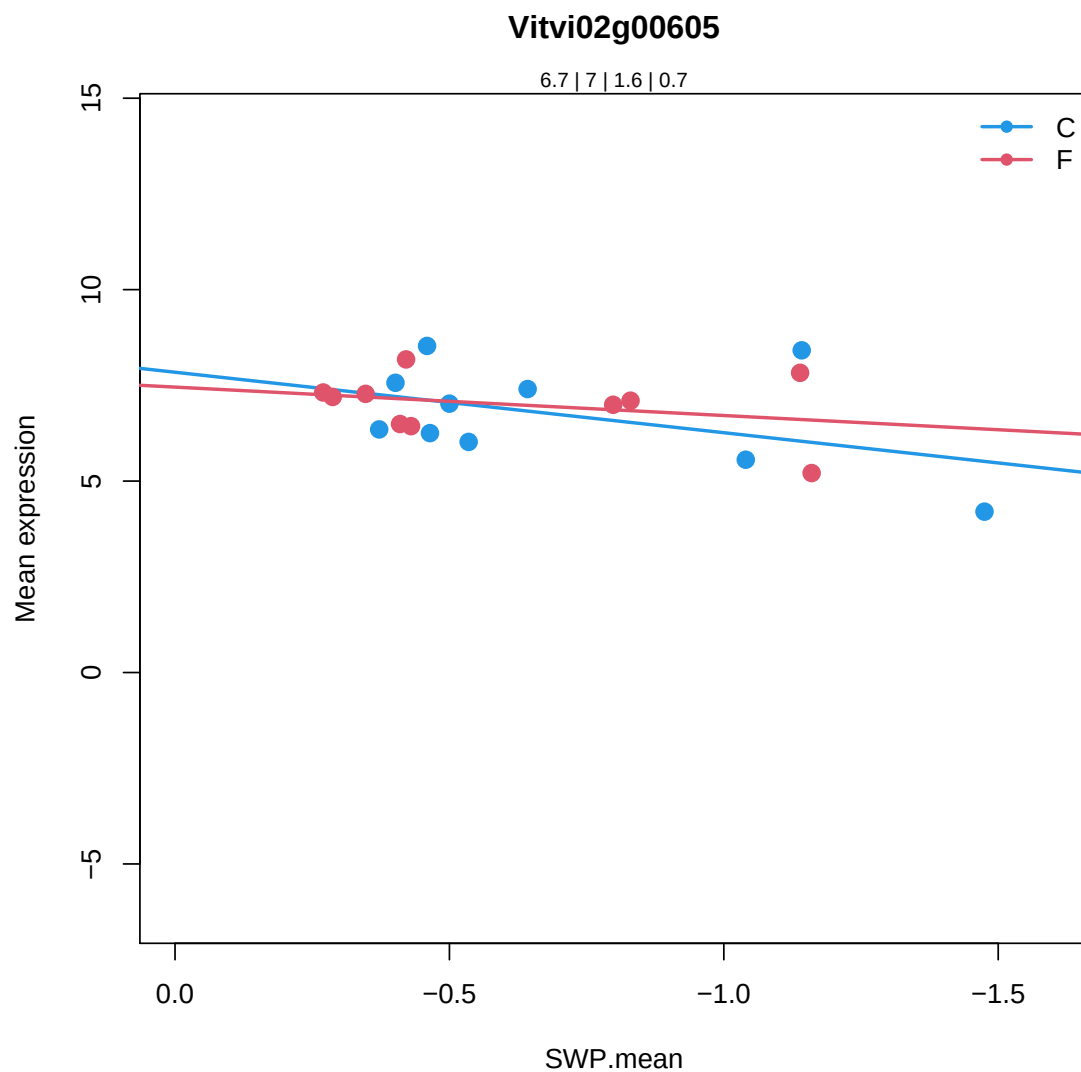
major CHO metabolism.degradation.starch.starch cleavage.beta amylase
chloroplast beta-amylase |

Chr4:9605266-9607250 REVERSE LENGTH=548 |

201606

Coefficients for Vitvi02g00605.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.73224	2.541592e-16	***	5.170019e-16	***
SlopeC	1.579216	0.07373382	.	0.5667824	
MeanF-MeanC	0.2699331	0.5339119		0.8262547	
SlopeF-SlopeC	-0.8374027	0.5100936		0.9999488	



8.1.178 Vitvi13g00367: Type1.0 *

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

Vitvi13g00367

34.13

transport.peptides and oligopeptides

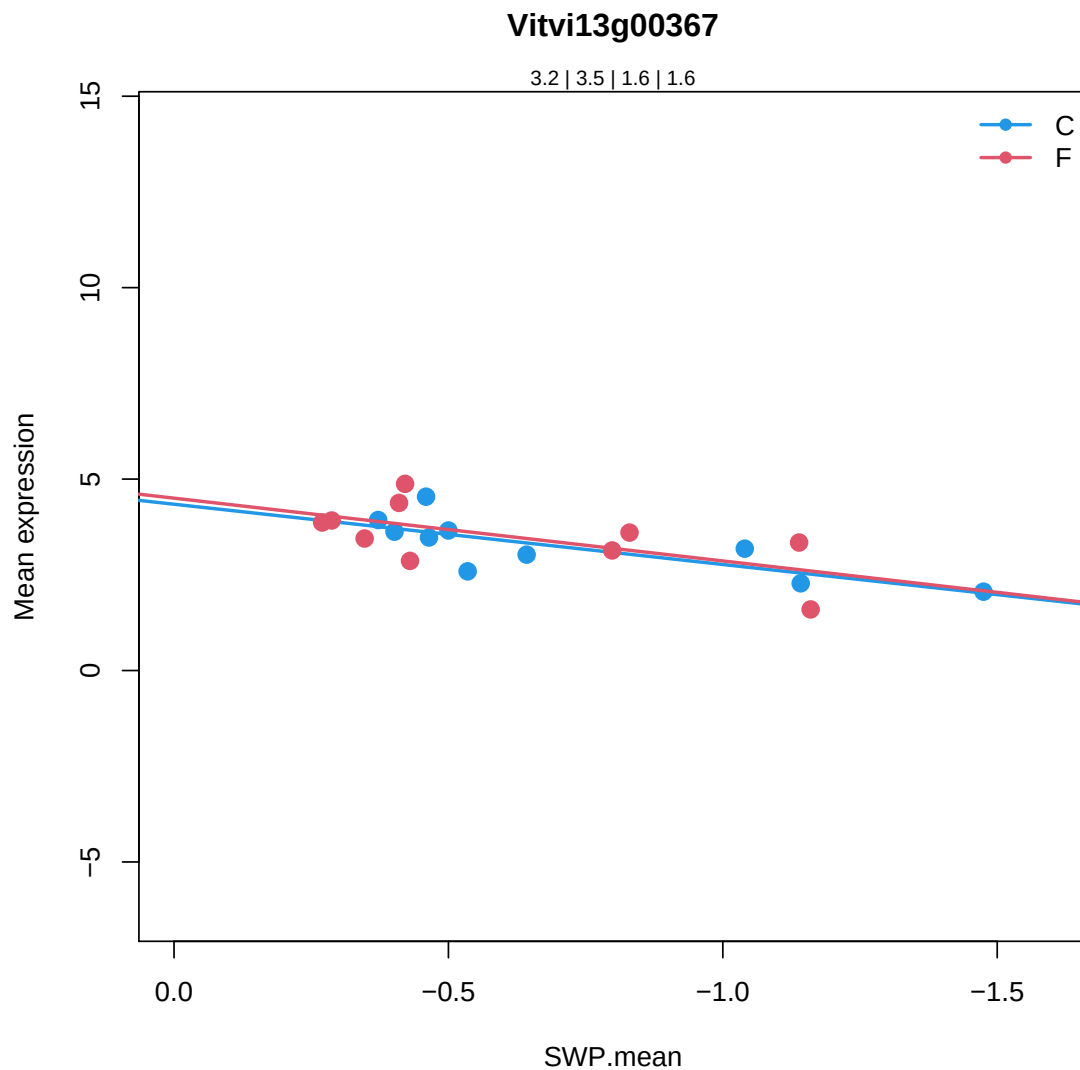
Major facilitator superfamily protein |

Chr2:15864396-15866408 REVERSE LENGTH=575 |

201606

Coefficients for Vitvi13g00367.

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



8.1.179 Vitvi16g02105: Type1.0 *

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

Vitvi16g02105

35.2

not assigned.unknown

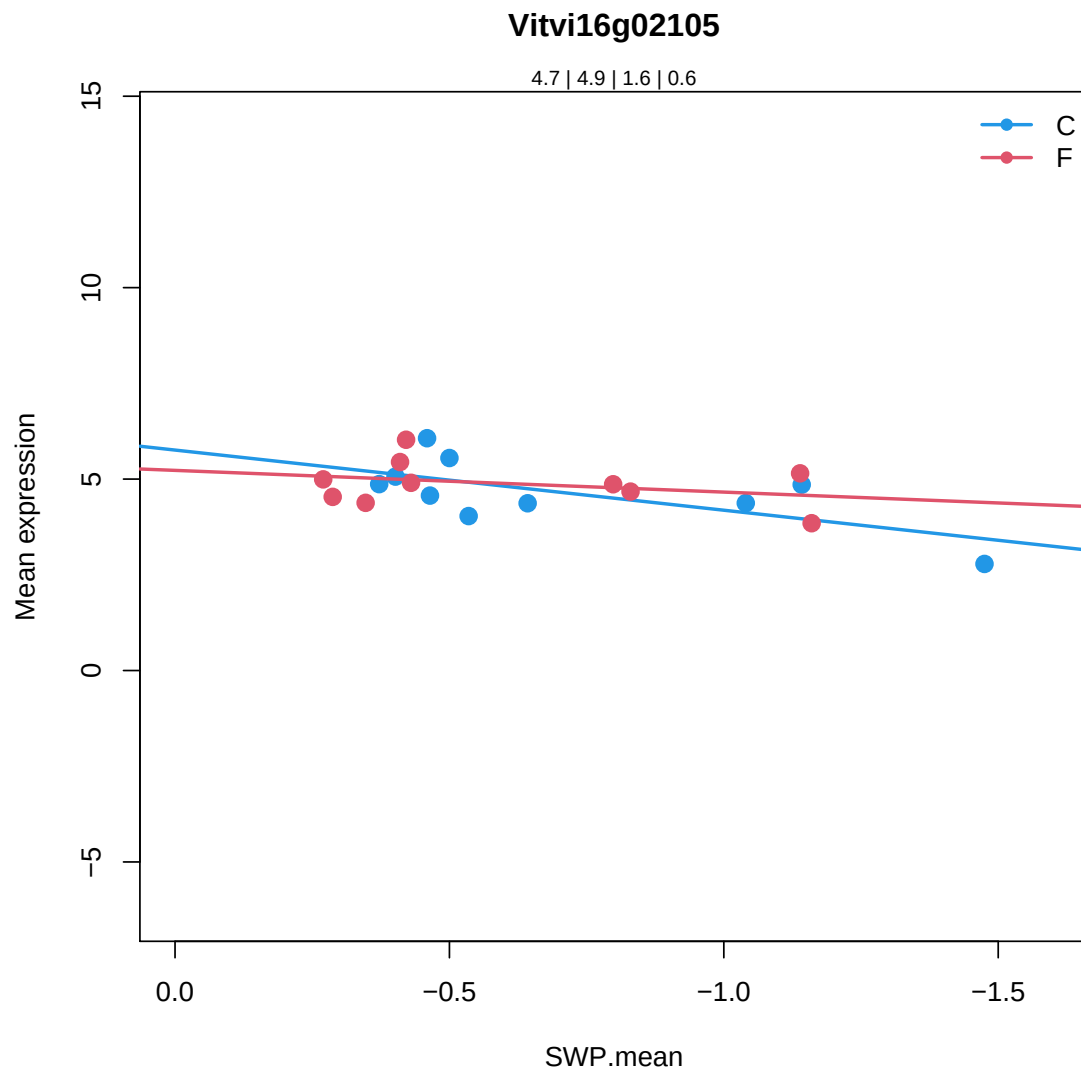
PR5-like receptor kinase |

Chr5:15293325-15295838 REVERSE LENGTH=665 |

201606

Coefficients for Vitvi16g02105.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.653122	5.755141e-17	***	1.306522e-16	***
SlopeC	1.571153	0.0082886	**	0.2862911	
MeanF-MeanC	0.2285062	0.4145201		0.7535921	
SlopeF-SlopeC	-1.004073	0.2252228		0.9999488	



8.1.180 Vitvi13g02006: Type1.0

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

Vitvi13g02006

35.2

not assigned.unknown

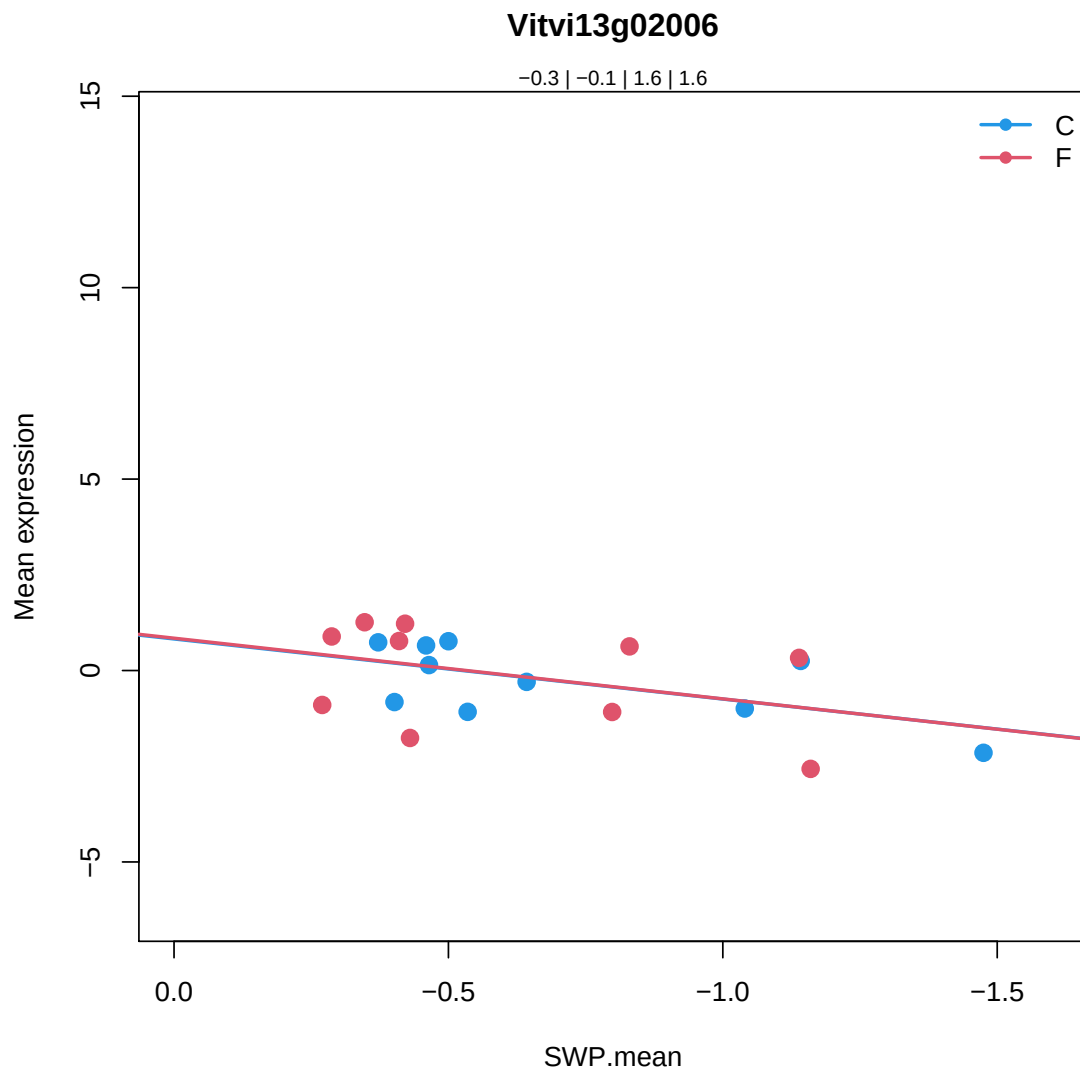
Subtilisin-like serine endopeptidase family protein |

Chr5:23858951-23862087 REVERSE LENGTH=741 |

201606

Coefficients for Vitvi13g02006.

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



8.1.181 Vitvi04g00021: Type1.0 *

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

Vitvi04g00021

30.2.11

signalling.receptor kinases.leucine rich repeat XI

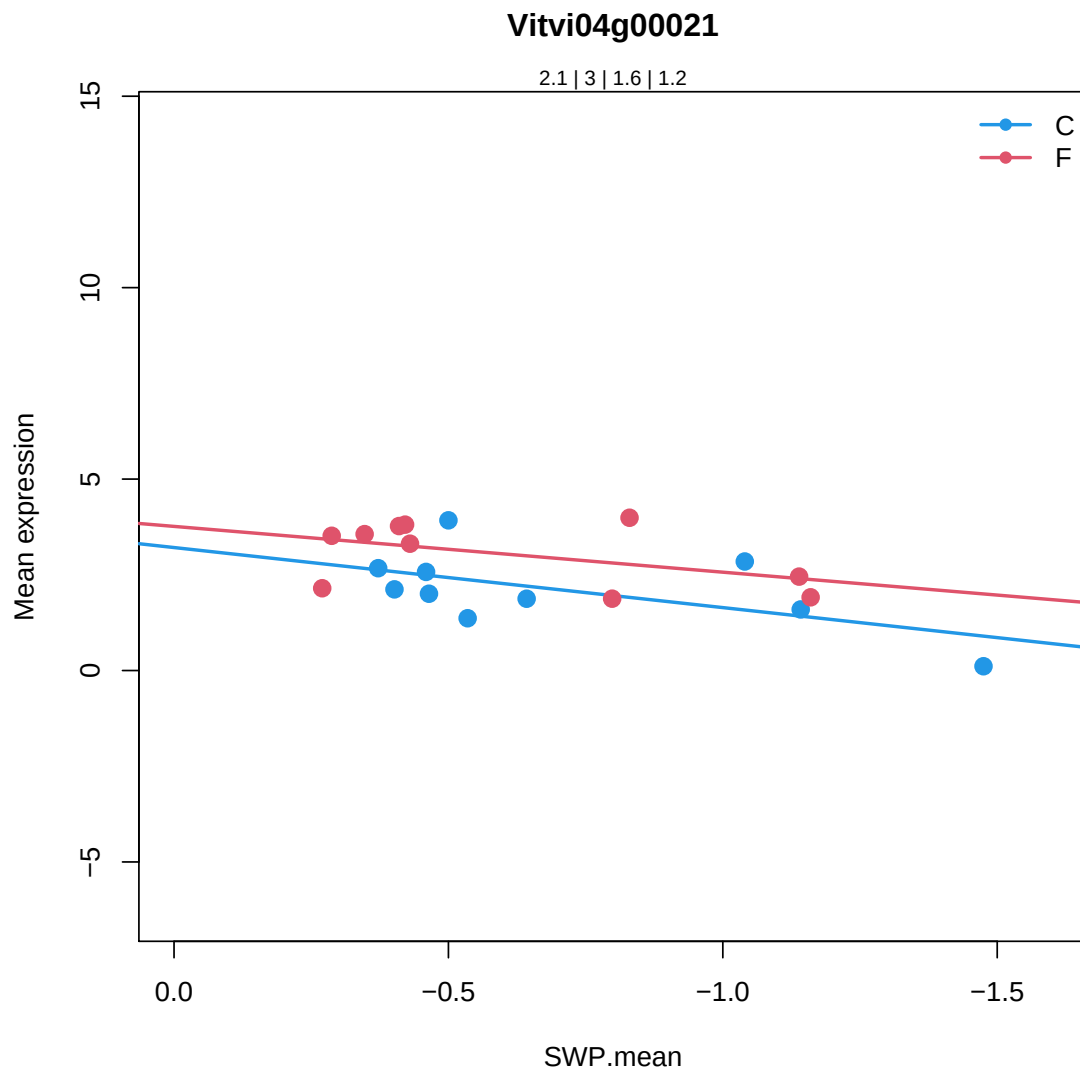
kinase family with leucine-rich repeat domain-containing protein |

Chr5:9050880-9053978 FORWARD LENGTH=1005 |

201606

Coefficients for Vitvi04g00021.

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



8.1.182 Vitvi06g01744: Type1.0 *

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

Vitvi06g01744

35.2

not assigned.unknown

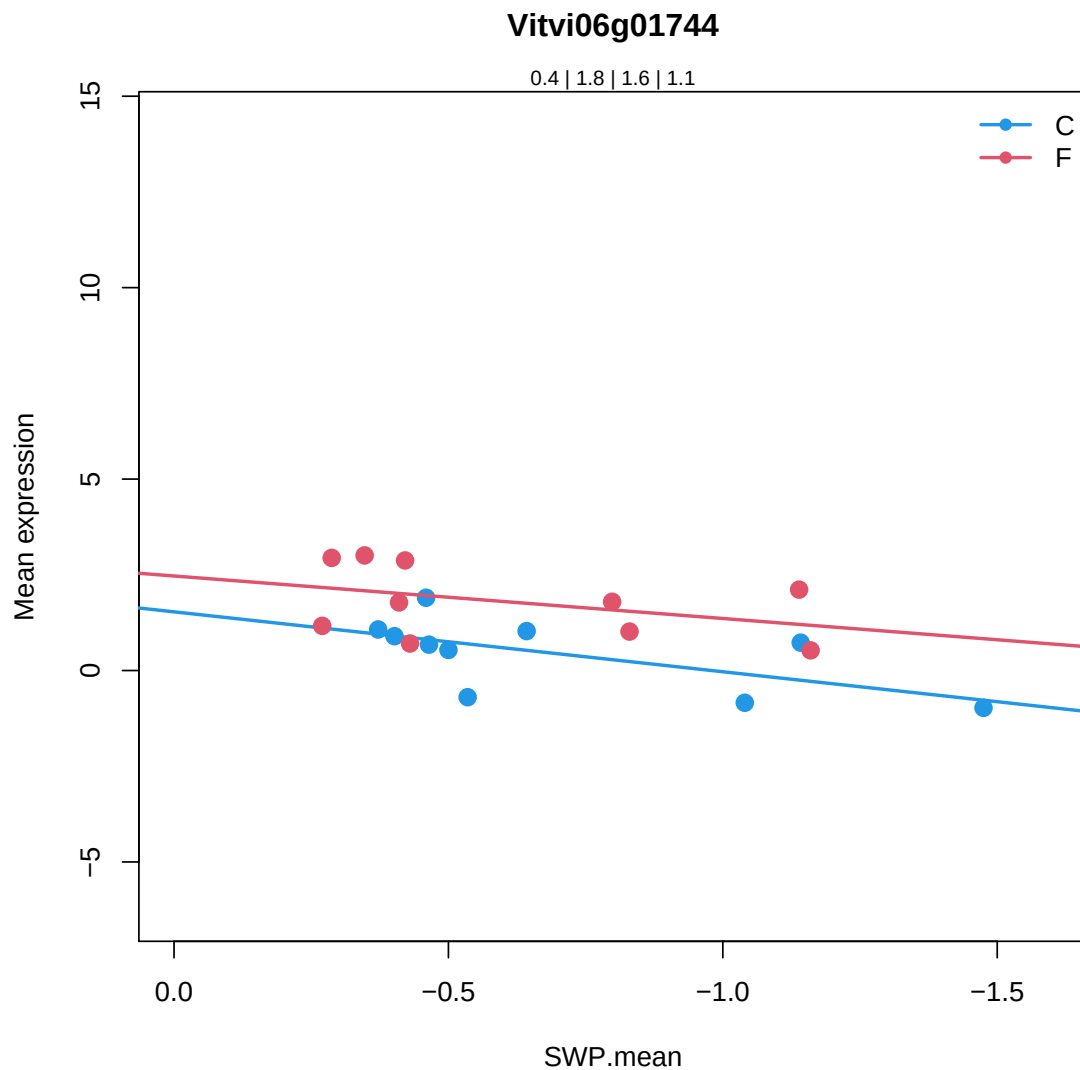
UDP-glucosyl transferase 71C4 |

Chr1:2225963-2227402 FORWARD LENGTH=479 |

201606

Coefficients for Vitvi06g01744.

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



8.1.183 Vitvi10g01746: Type1.0 *

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

Vitvi10g01746

35.2

not assigned.unknown

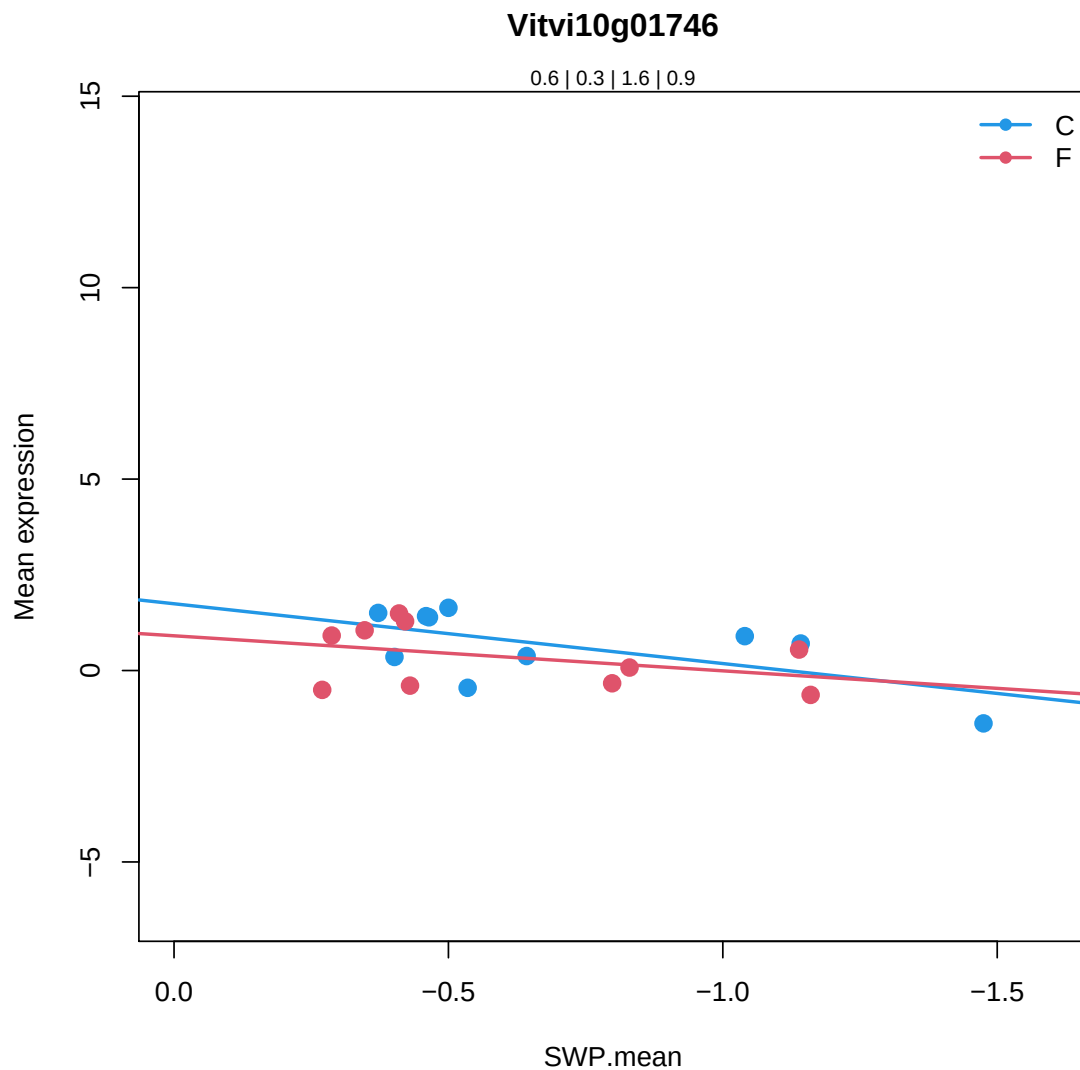
transmembrane protein |

Chr4:11441065-11441712 REVERSE LENGTH=215 |

201606

Coefficients for Vitvi10g01746.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6453909	0.01092222	*	0.01156087	*
SlopeC	1.561435	0.02430495	*	0.4035469	
MeanF-MeanC	-0.2961199	0.3760126		0.7284392	
SlopeF-SlopeC	-0.6463097	0.5075783		0.9999488	



8.1.184 Vitvi13g00669: Type1.0 *

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

Vitvi13g00669

10.6.3

cell wall.degradation.pectate lyases and polygalacturonases

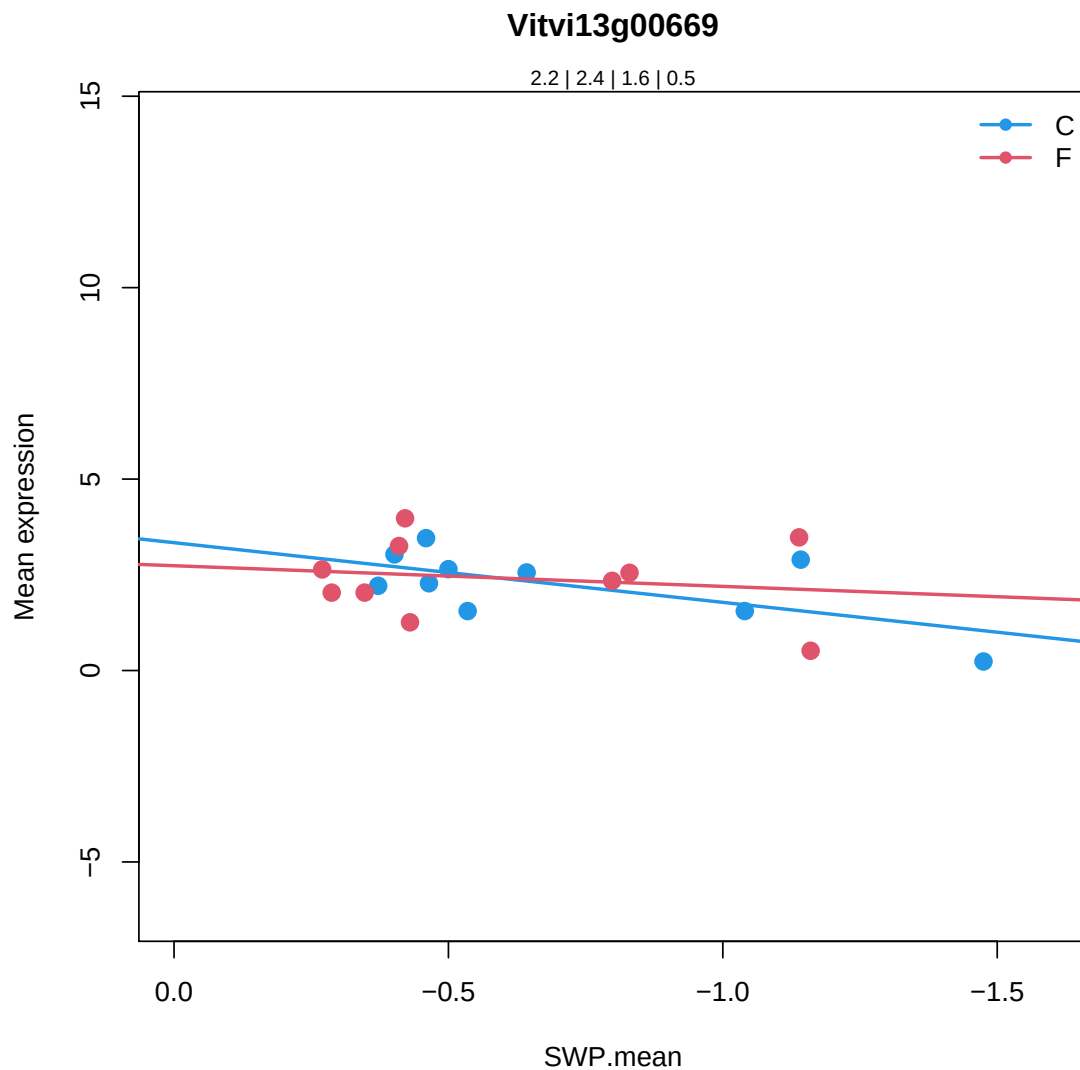
Pectin lyase-like superfamily protein |

Chr3:19714171-19717537 FORWARD LENGTH=483 |

201606

Coefficients for Vitvi13g00669.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.242726	3.037106e-08	***	3.653059e-08	***
SlopeC	1.558798	0.04732526	*	0.4997782	
MeanF-MeanC	0.1656203	0.6644704		0.8894229	
SlopeF-SlopeC	-1.01932	0.3655275		0.9999488	



8.1.185 Vitvi07g00905: Type1.0

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

Vitvi07g00905

30.11

signalling.light

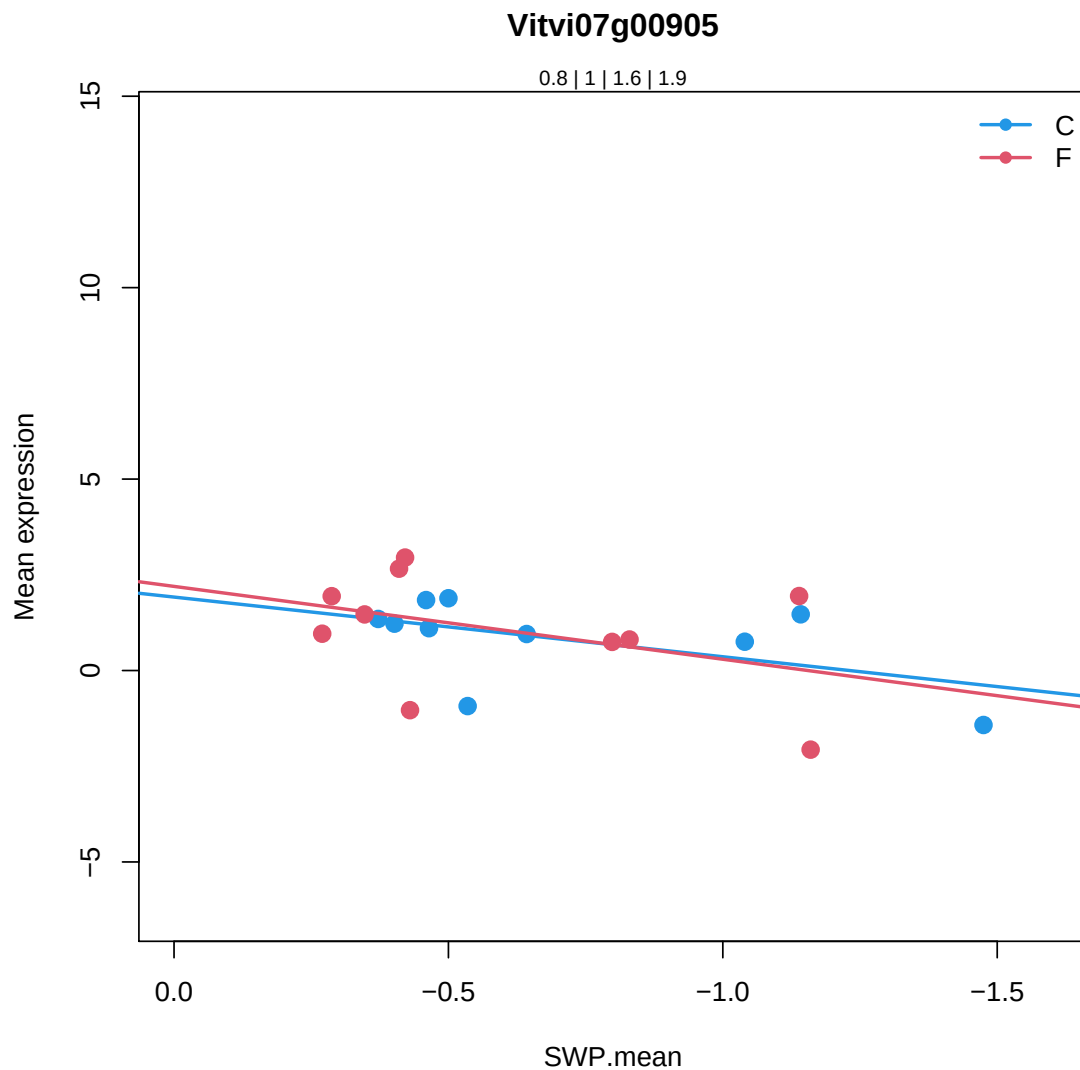
Phototropic-responsive NPH3 family protein |

Chr5:19786881-19789003 FORWARD LENGTH=614 |

201606

Coefficients for Vitvi07g00905.

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



8.1.186 Vitvi09g00177: Type1.0 *

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

Vitvi09g00177

26.3.2

misc.gluco-, galacto- and mannosidases.beta-galactosidase

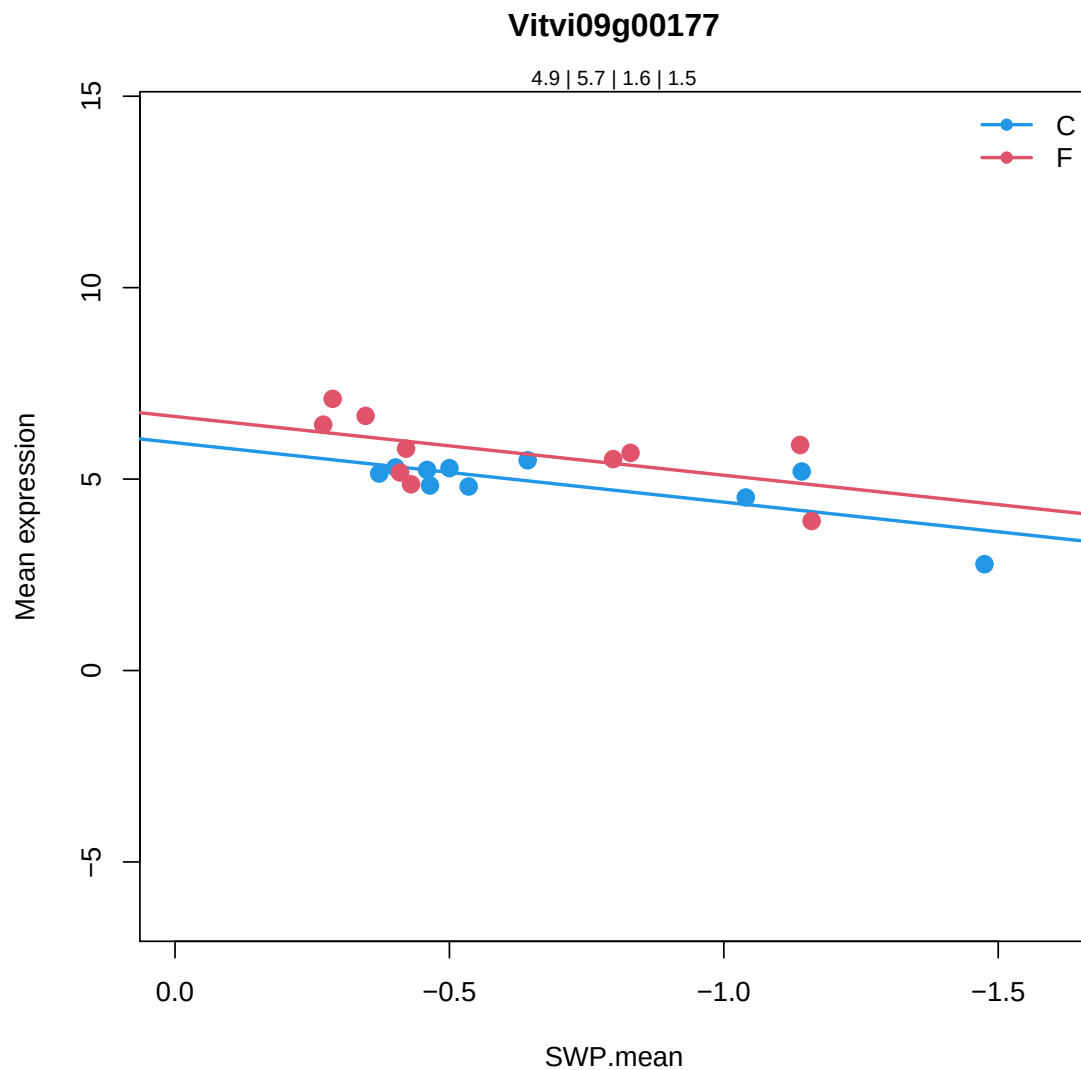
beta galactosidase 1 |

Chr3:4511192-4515756 FORWARD LENGTH=847 |

201606

Coefficients for Vitvi09g00177.

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



8.1.187 Vitvi18g02685: Type1.0 *

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

Vitvi18g02685

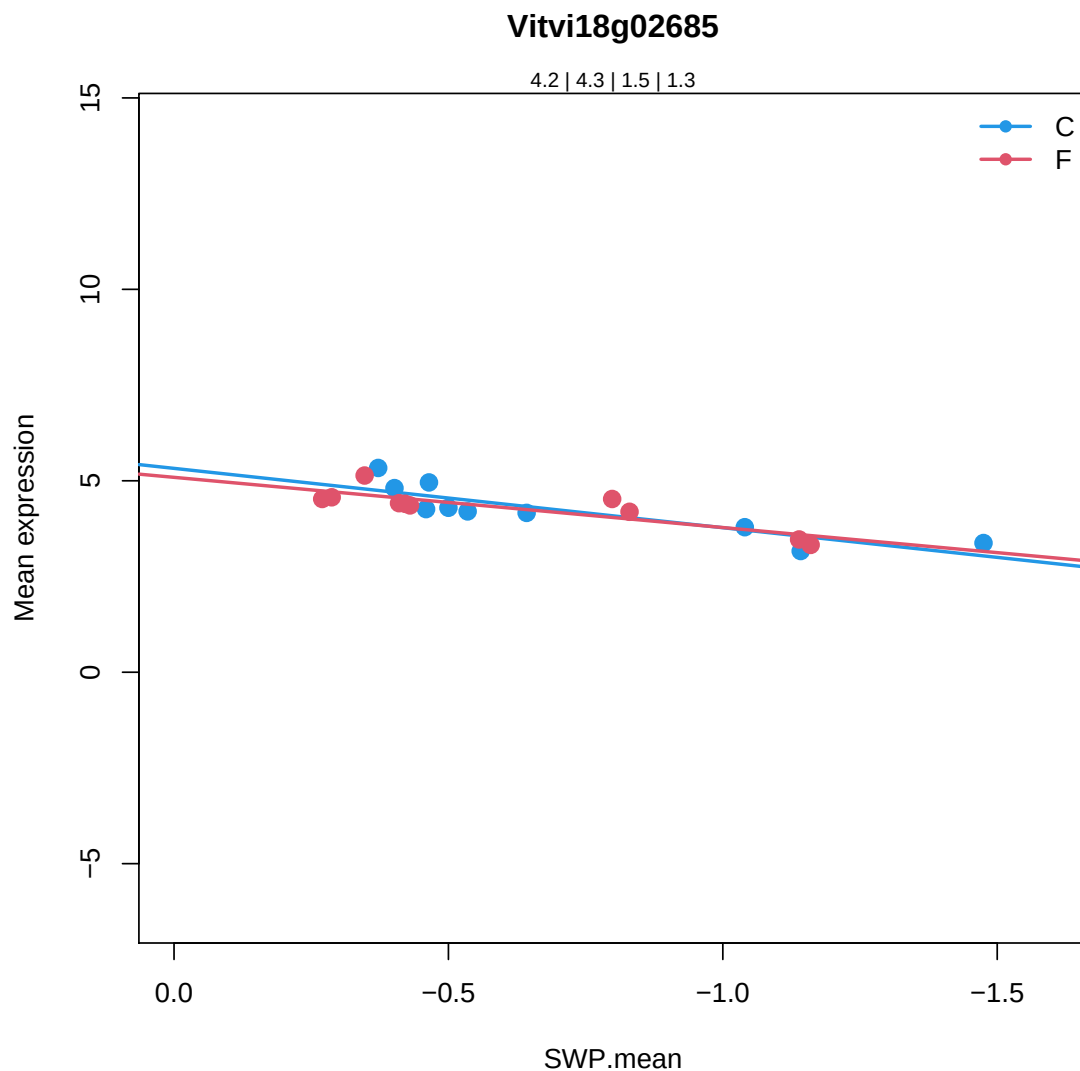
35.2

not assigned.unknown

Calmodulin IPR011992 EF-Hand type

Coefficients for Vitvi18g02685.

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



8.1.188 Vitvi16g00732: Type1.0

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

Vitvi16g00732

26.18

misc.invertase/pectin methylesterase inhibitor family protein

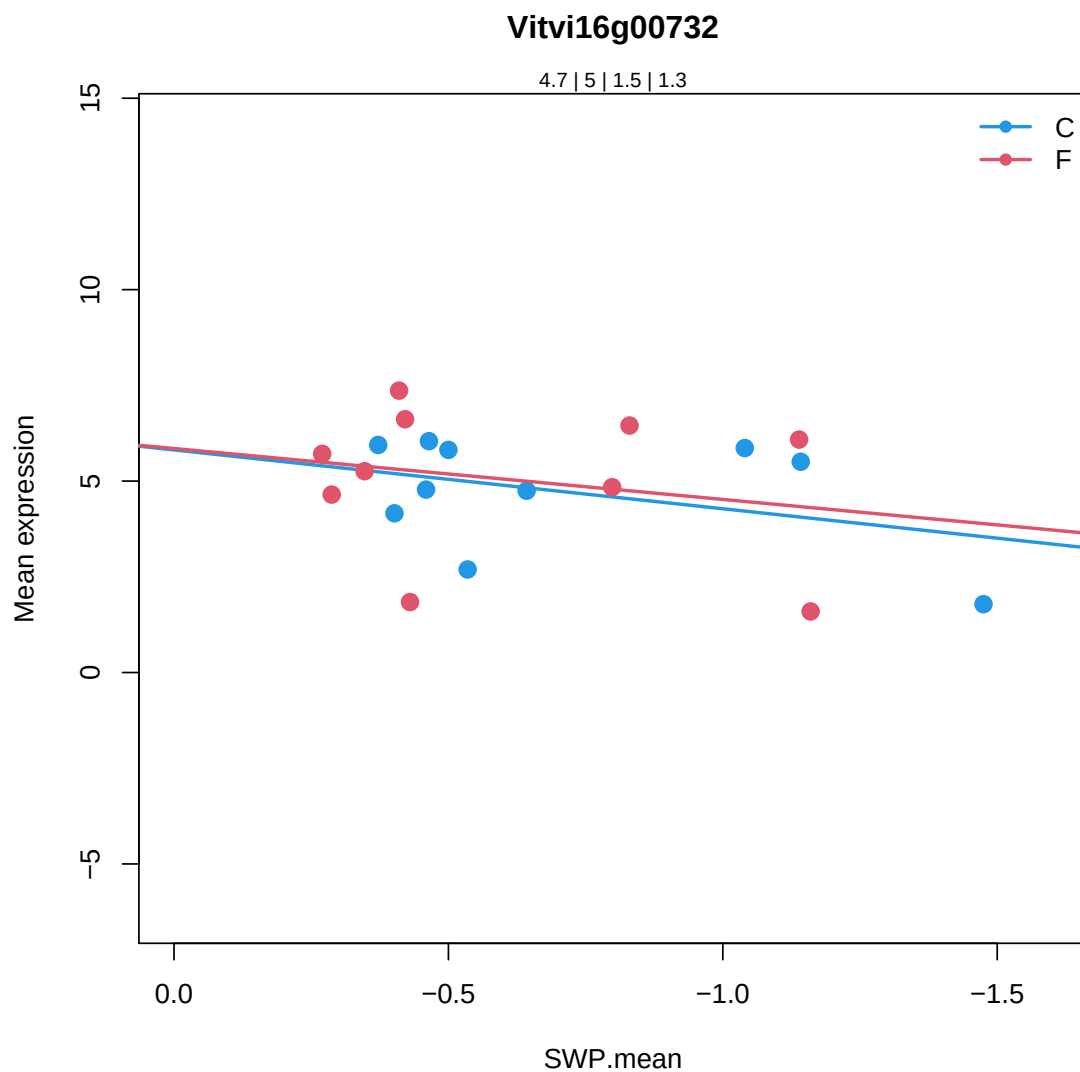
Plant invertase/pectin methylesterase inhibitor superfamily protein |

Chr5:25040699-25041310 FORWARD LENGTH=203 |

201606

Coefficients for Vitvi16g00732.

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



8.1.189 Vitvi11g01623: Type1.0 *

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

Vitvi11g01623

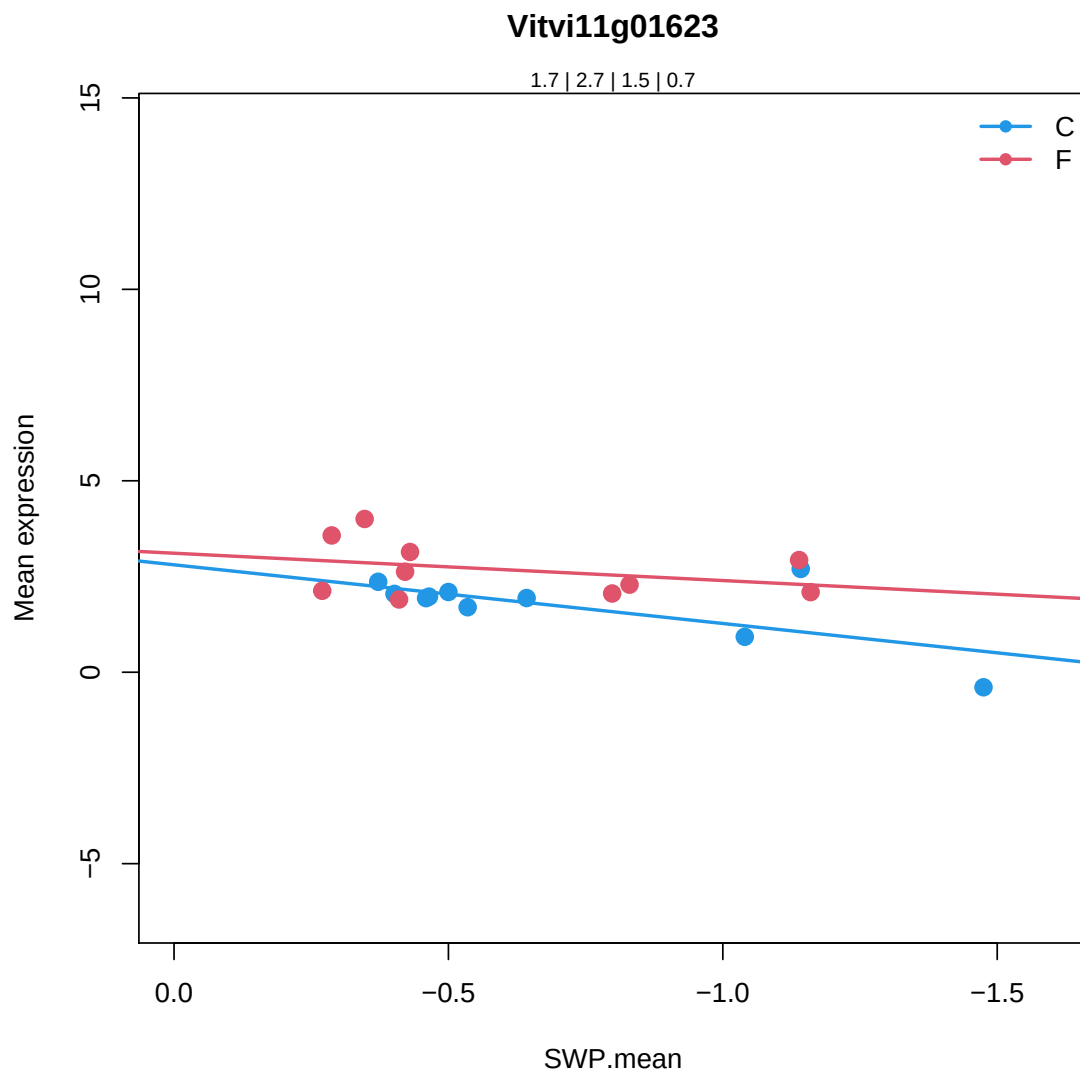
31.4

cell.vesicle transport

Unknown Protein

Coefficients for Vitvi11g01623.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.727671	3.664575e-08	***	4.399452e-08	***
SlopeC	1.532528	0.01464409	*	0.3359386	
MeanF-MeanC	0.9455967	0.004002956	**	0.03821293	*
SlopeF-SlopeC	-0.8187872	0.3511308		0.9999488	



8.1.190 Vitvi16g01237: Type1.0 *

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

Vitvi16g01237

35.2

not assigned.unknown

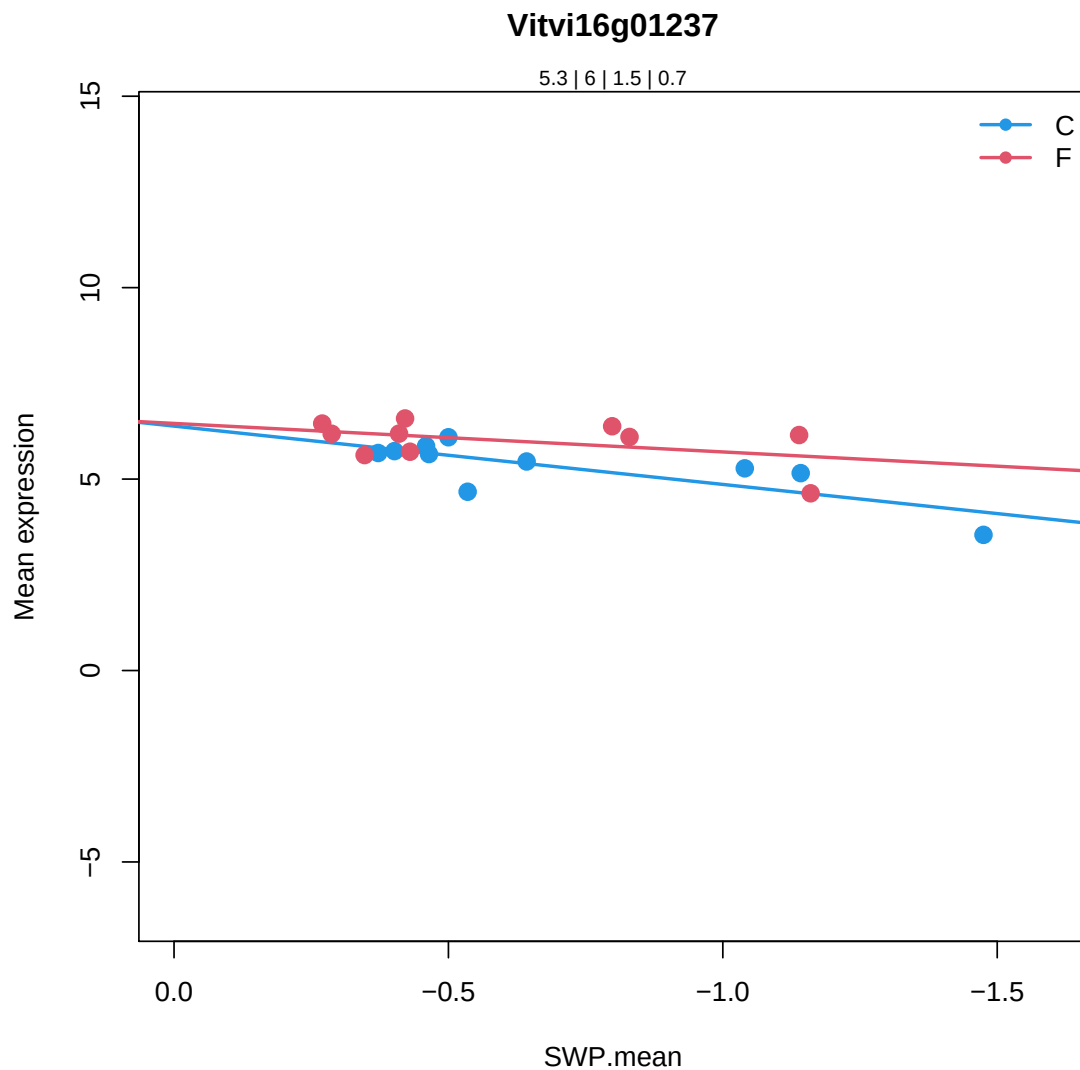
Protein kinase superfamily protein |

Chr1:24961634-24963941 REVERSE LENGTH=666 |

201606

Coefficients for Vitvi16g01237.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.31253	6.934396e-20	***	3.49633e-19	***
SlopeC	1.523417	0.002595568	**	0.1939296	
MeanF-MeanC	0.6876223	0.006335814	**	0.05413143	.
SlopeF-SlopeC	-0.7786715	0.254805		0.9999488	



8.1.191 Vitvi12g02375: Type1.0

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

Vitvi12g02375

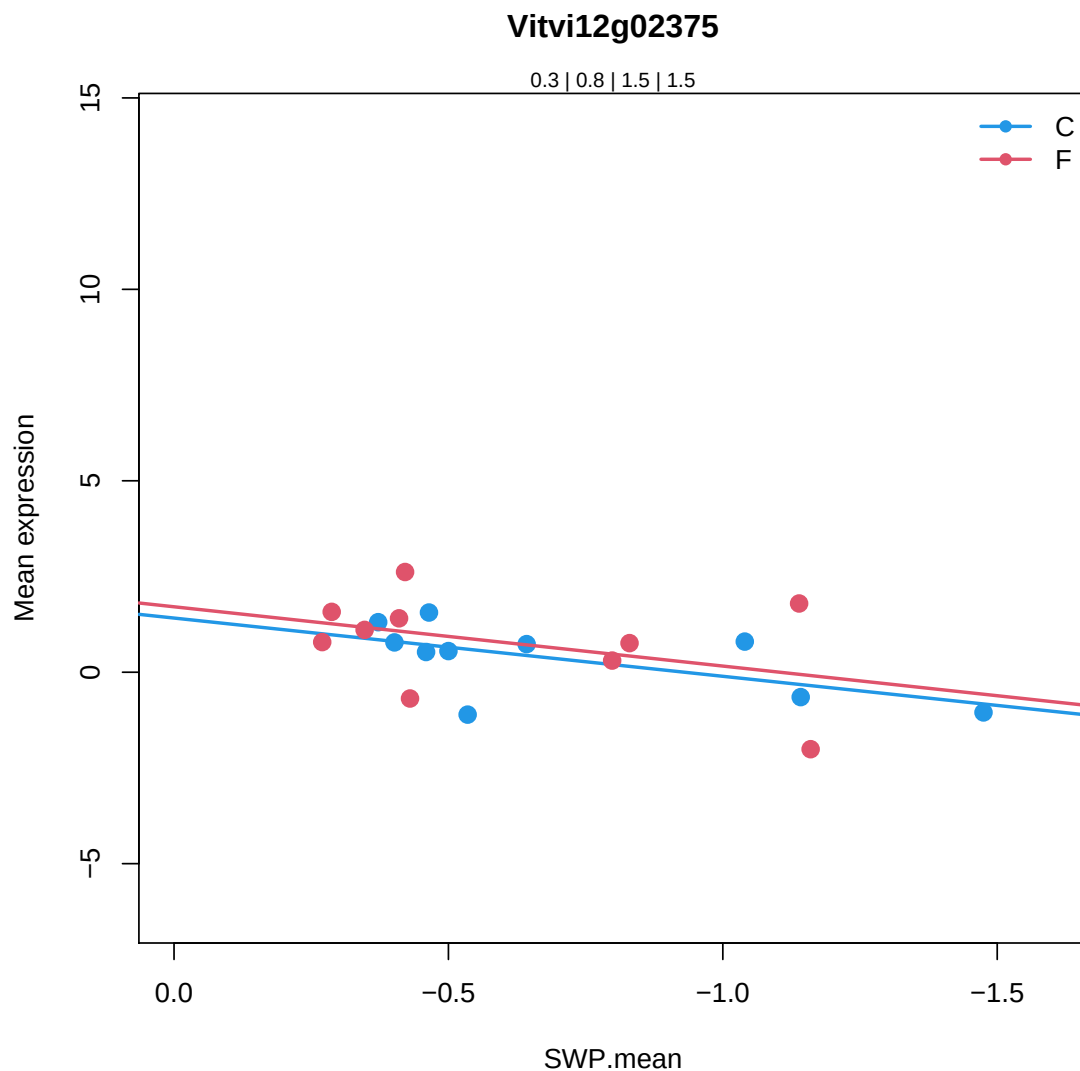
26.10

misc.cytochrome P450

NA

Coefficients for Vitvi12g02375.

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



8.1.192 Vitvi03g00480: Type1.0 *

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

Vitvi03g00480

35.2

not assigned.unknown

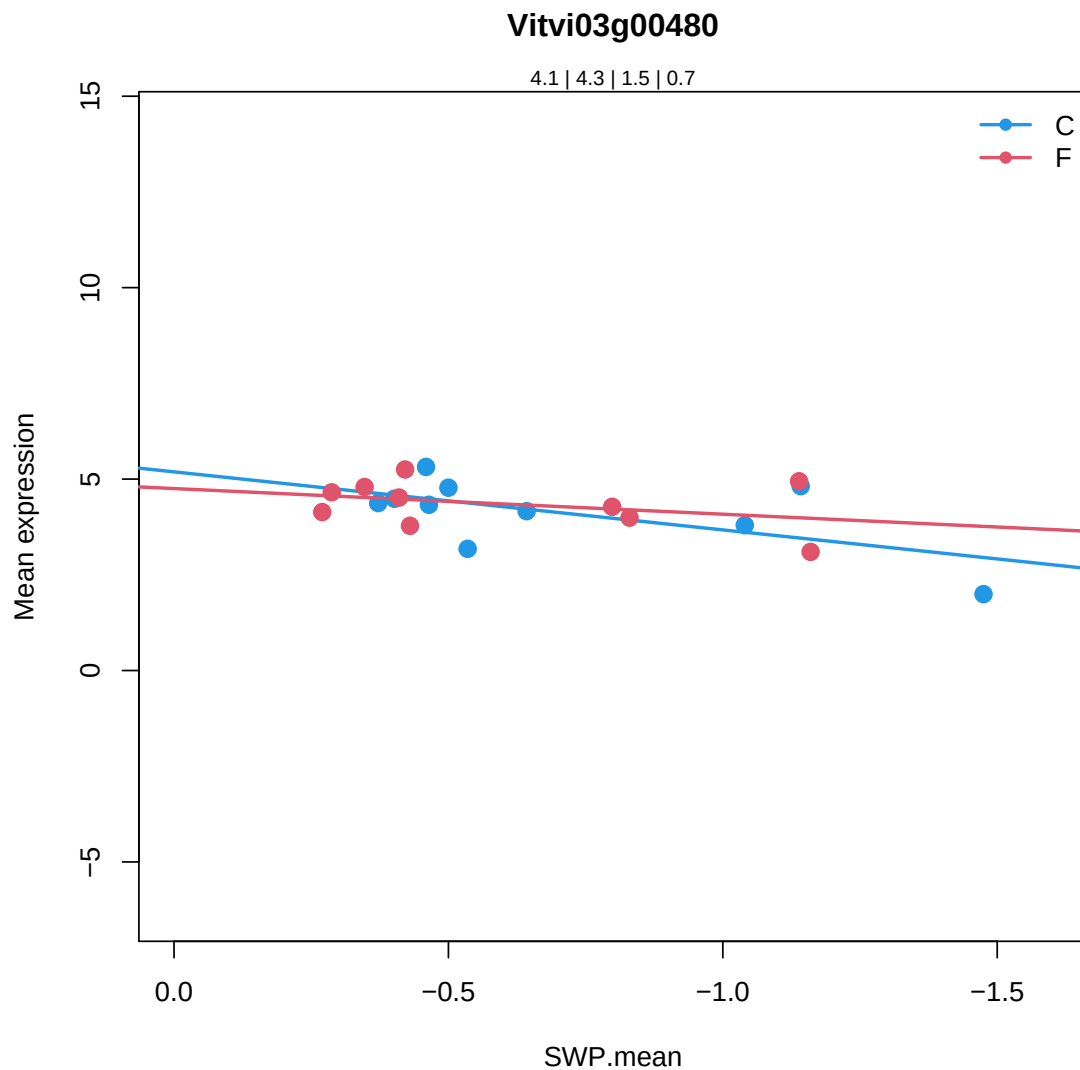
alpha/beta-Hydrolases superfamily protein |

Chr2:1077080-1078018 FORWARD LENGTH=312 |

201606

Coefficients for Vitvi03g00480.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.122657	3.65181e-15	***	6.422163e-15	***
SlopeC	1.515876	0.01700565	*	0.3539708	
MeanF-MeanC	0.2216408	0.4647792		0.7865176	
SlopeF-SlopeC	-0.8466649	0.3423628		0.9999488	



8.1.193 Vitvi13g01395: Type1.0

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

Vitvi13g01395

33.99

development.unspecified

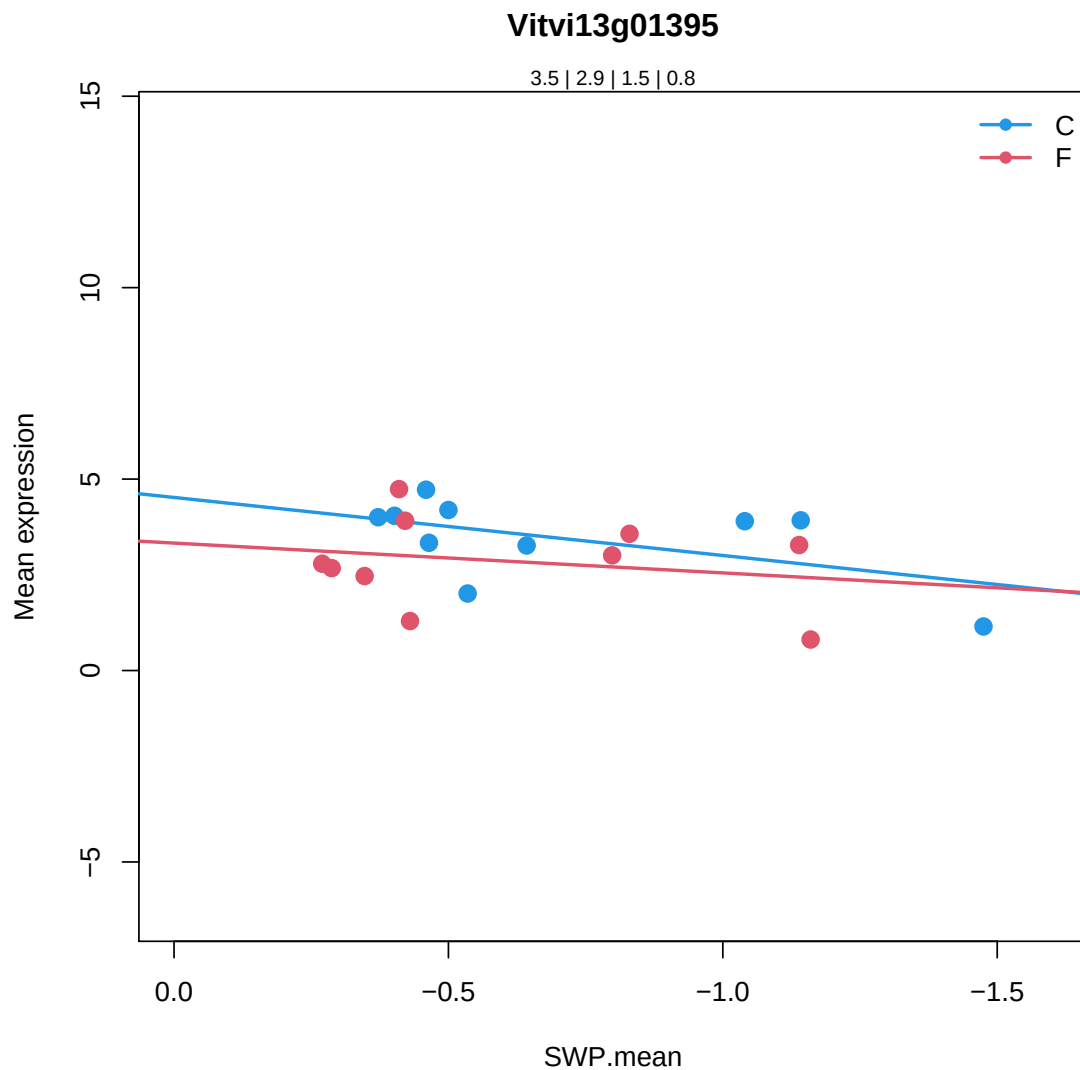
nodulin MtN21 /EamA-like transporter family protein |

Chr5:2191533-2193416 REVERSE LENGTH=402 |

201606

Coefficients for Vitvi13g01395.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.454613	2.139164e-10	***	2.763616e-10	***
SlopeC	1.515635	0.0926458	.	0.6008919	
MeanF-MeanC	-0.600843	0.184036		0.5202294	
SlopeF-SlopeC	-0.7367804	0.5713573		0.9999488	



8.1.194 Vitvi01g02051: Type1.0 *

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

```
Vitvi01g02051
```

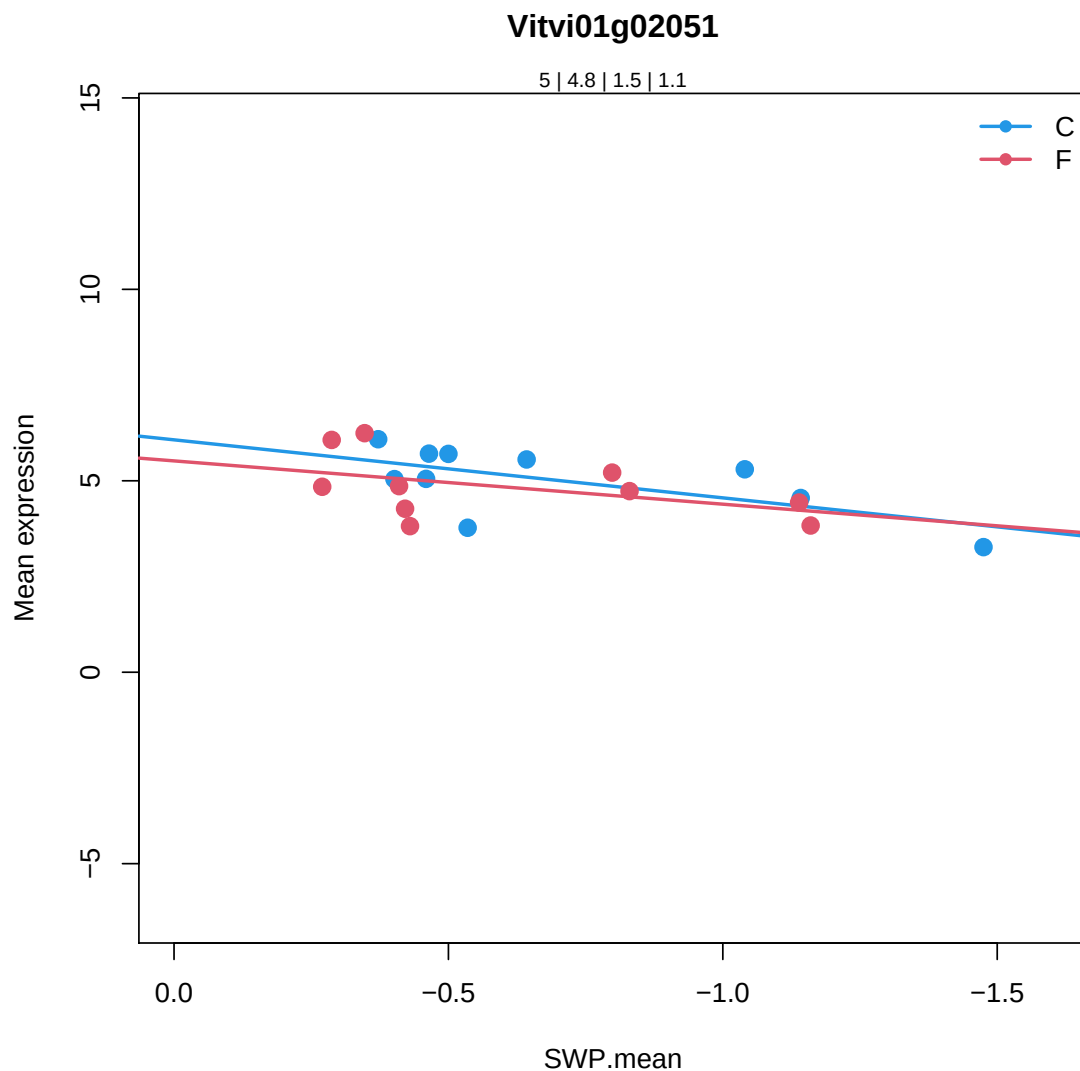
```
35.1
```

```
not assigned.no ontology
```

```
NA
```

Coefficients for Vitvi01g02051.

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



8.1.195 Vitvi16g01988: Type1.0 *

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

Vitvi16g01988

35.2

not assigned.unknown

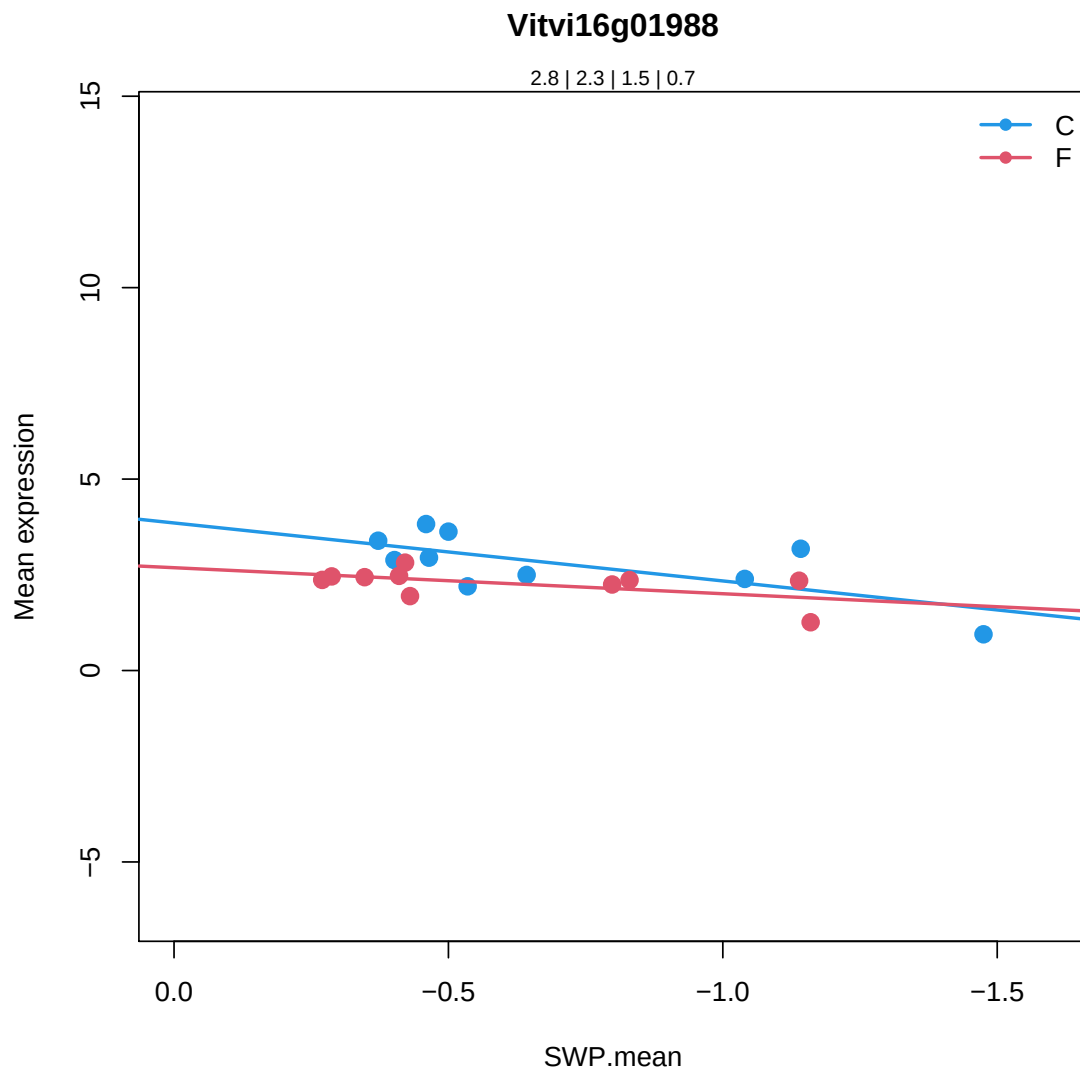
RING/U-box superfamily protein |

Chr5:21529022-21533008 FORWARD LENGTH=382 |

201606

Coefficients for Vitvi16g01988.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.788878	5.80382e-14	***	9.072077e-14	***
SlopeC	1.514231	0.003099592	**	0.2103859	
MeanF-MeanC	-0.5177726	0.03569776	*	0.1899809	
SlopeF-SlopeC	-0.8349165	0.2304198		0.9999488	



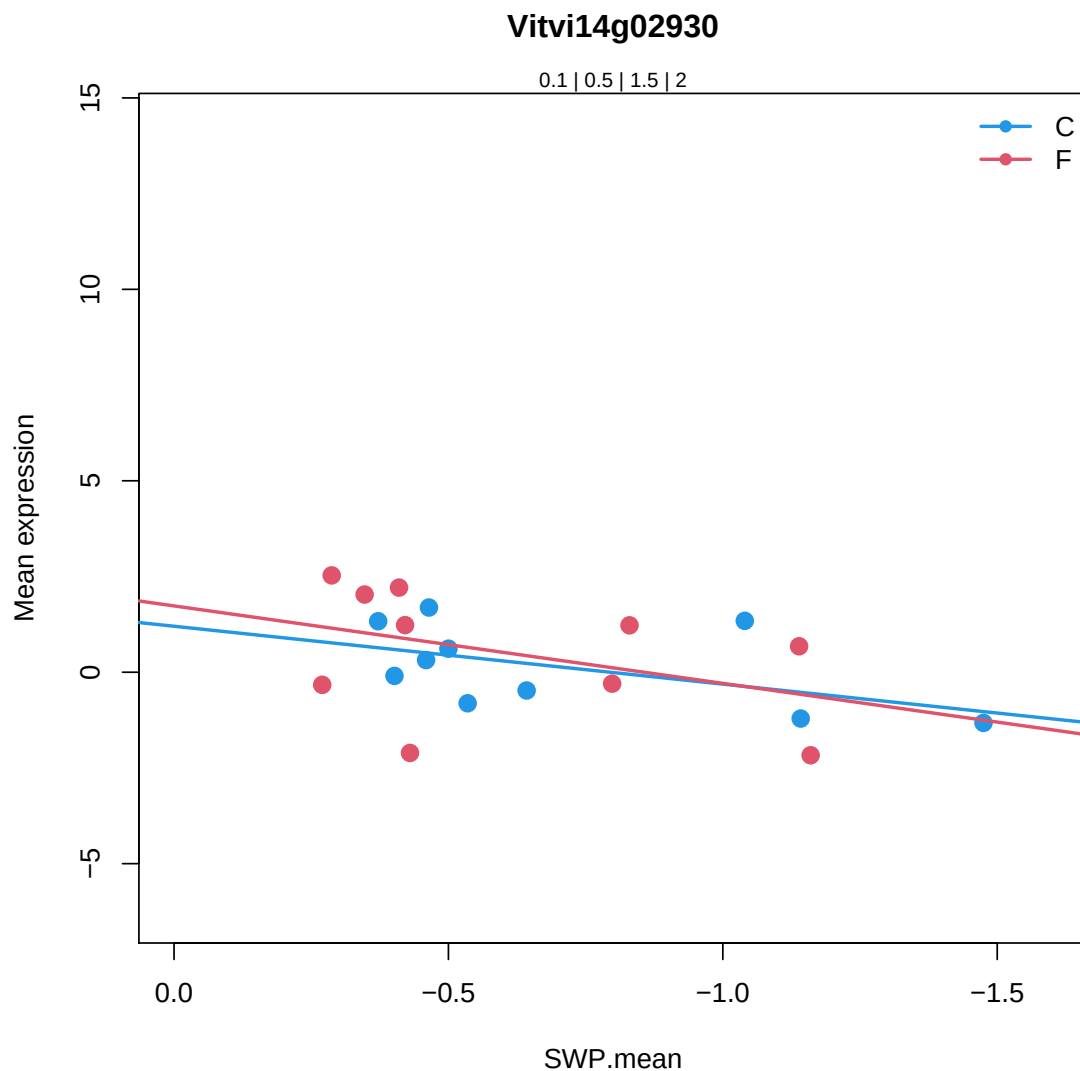
8.1.196 Vitvi14g02930: Type1.0

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

```
Vitvi14g02930
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi14g02930.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1378459	0.7185972		0.7231997	
SlopeC	1.511351	0.1646165		0.6944601	
MeanF-MeanC	0.3616838	0.5053835		0.8092239	
SlopeF-SlopeC	0.5109768	0.7469466		0.9999488	



8.1.197 Vitvi07g00255: Type1.0 *

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

Vitvi07g00255

29.5.3

protein.degradation.cysteine protease

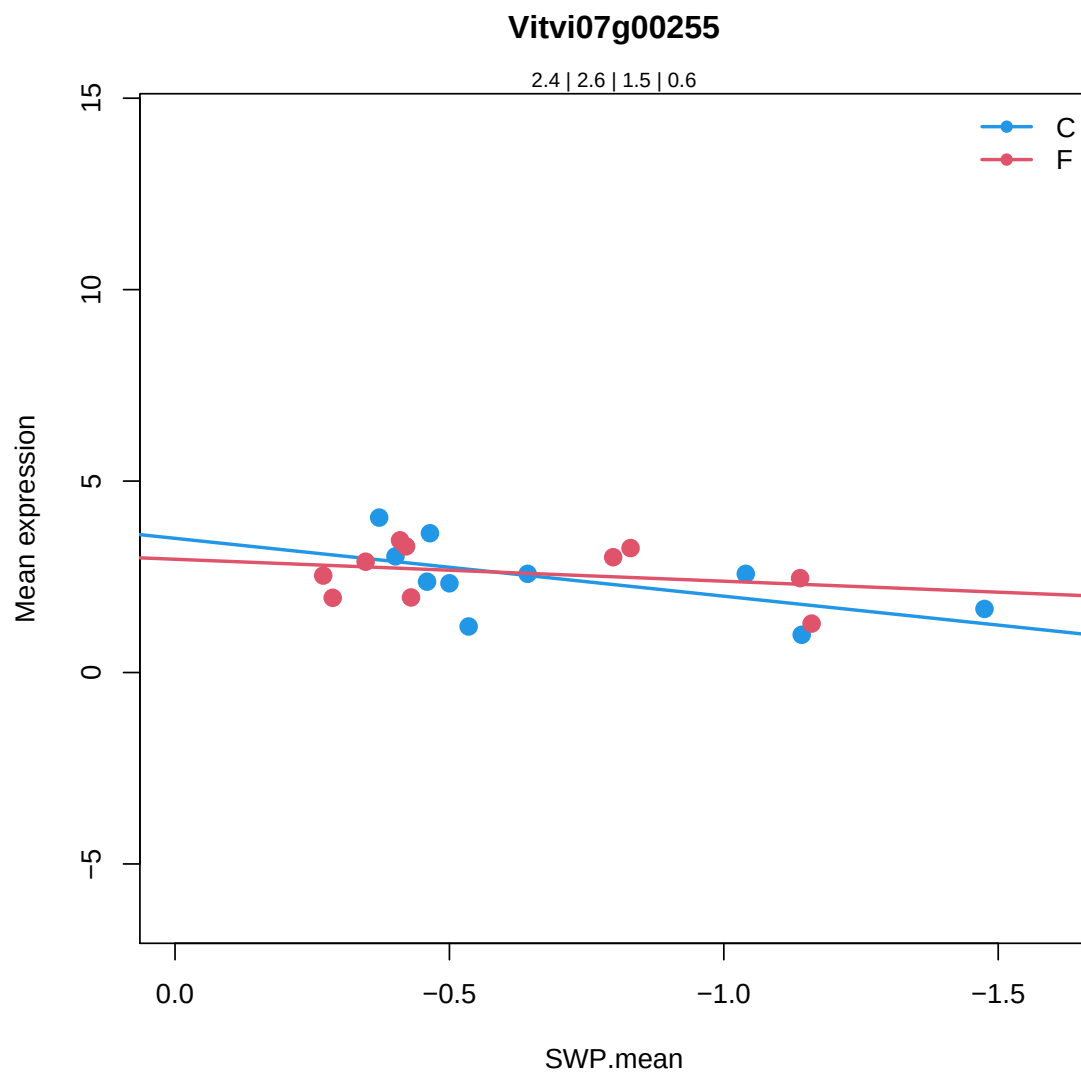
Glutaredoxin family protein |

Chr2:19605124-19605432 FORWARD LENGTH=102 |

201606

Coefficients for Vitvi07g00255.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.442342	4.637365e-10	***	5.918338e-10	***
SlopeC	1.510808	0.02671081	*	0.4162844	
MeanF-MeanC	0.1668123	0.6106148		0.8643119	
SlopeF-SlopeC	-0.9374504	0.3323478		0.9999488	



8.1.198 Vitvi06g00266: Type1.0

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

Vitvi06g00266

26.2

misc.UDP glucosyl and glucoronyl transferases

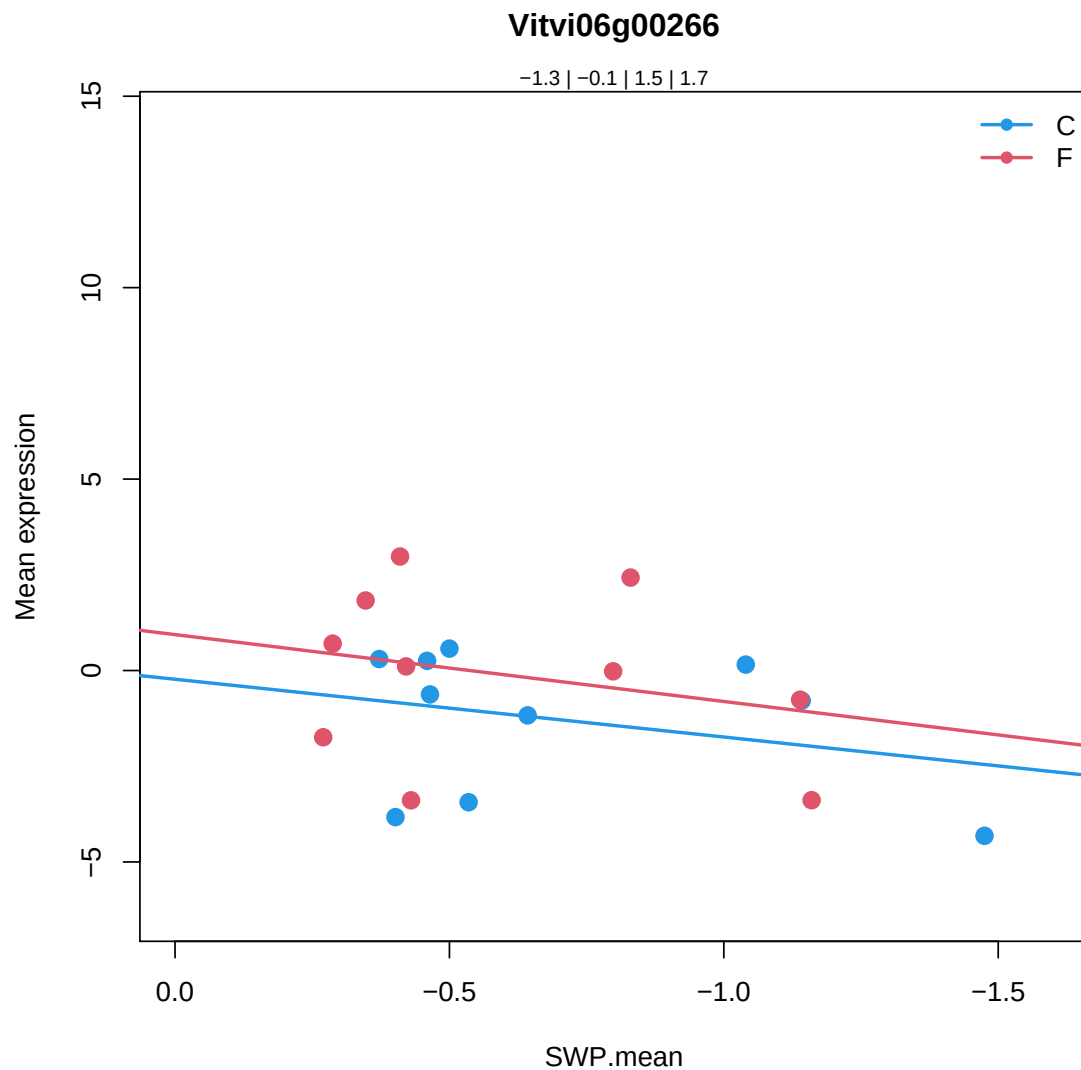
glycosyltransferase family protein 2 |

Chr5:24402329-24405521 REVERSE LENGTH=932 |

201606

Coefficients for Vitvi06g00266.

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



8.1.199 Vitvi07g00421: Type1.0

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

Vitvi07g00421

27.3.32

RNA.regulation of transcription.WRKY domain transcription factor famil

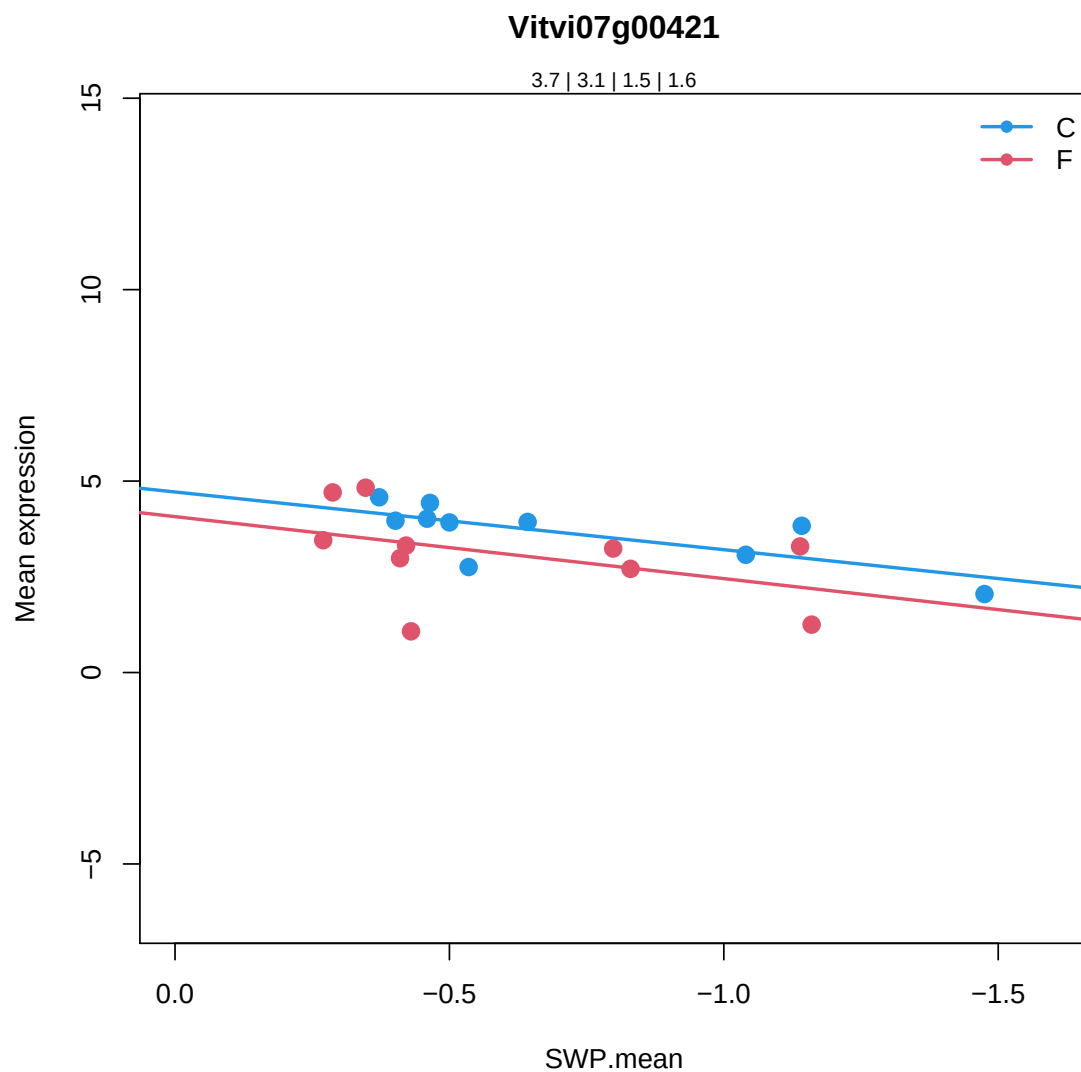
WRKY DNA-binding protein 35 |

Chr2:14693839-14696378 REVERSE LENGTH=427 |

201606

Coefficients for Vitvi07g00421.

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



8.1.200 Vitvi16g02142: Type1.0 *

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

Vitvi16g02142

35.2

not assigned.unknown

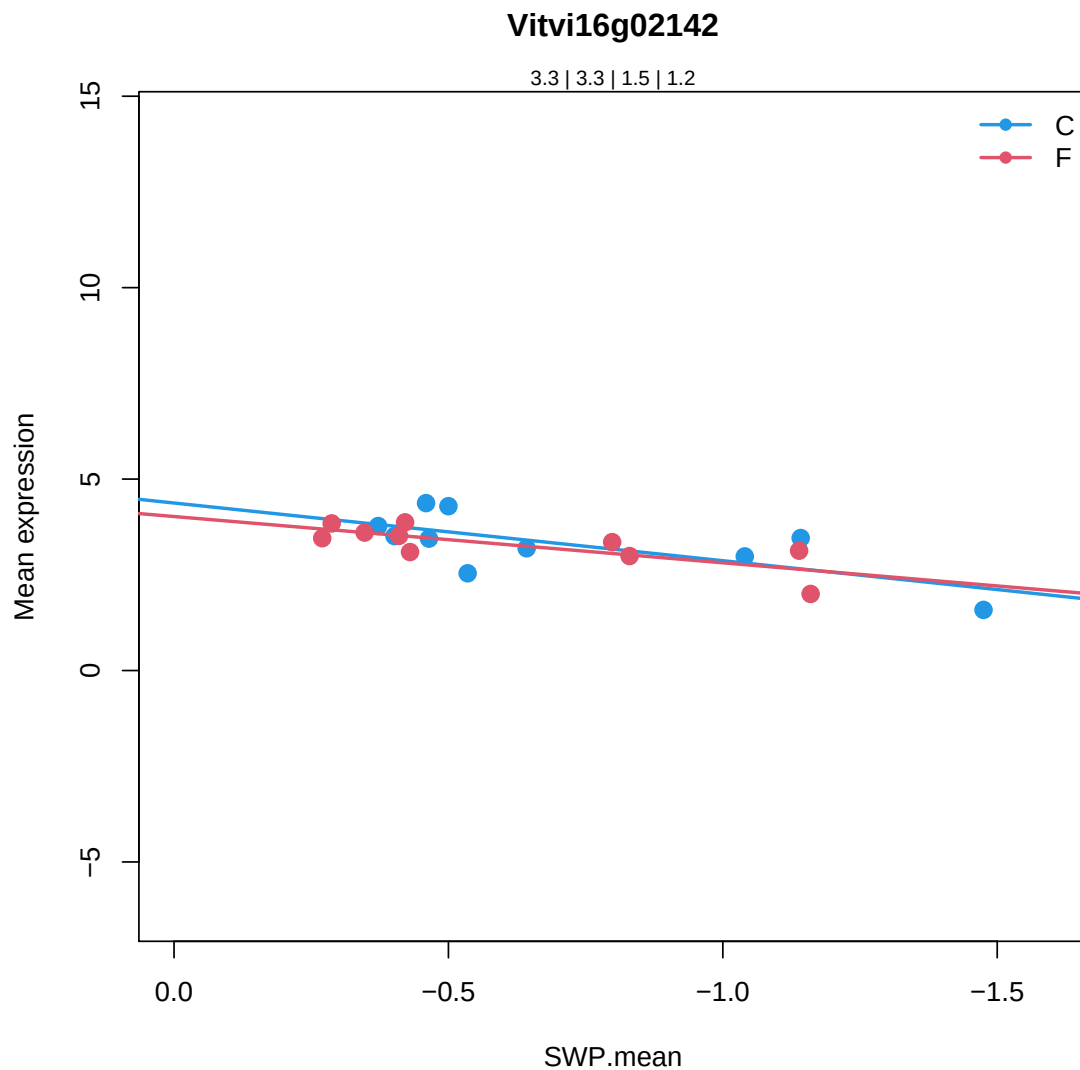
PR5-like receptor kinase |

Chr5:15293325-15295838 REVERSE LENGTH=665 |

201606

Coefficients for Vitvi16g02142.

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



8.1.201 Vitvi18g01675: Type1.0 *

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

Vitvi18g01675

30.2.10

signalling.receptor kinases.leucine rich repeat X

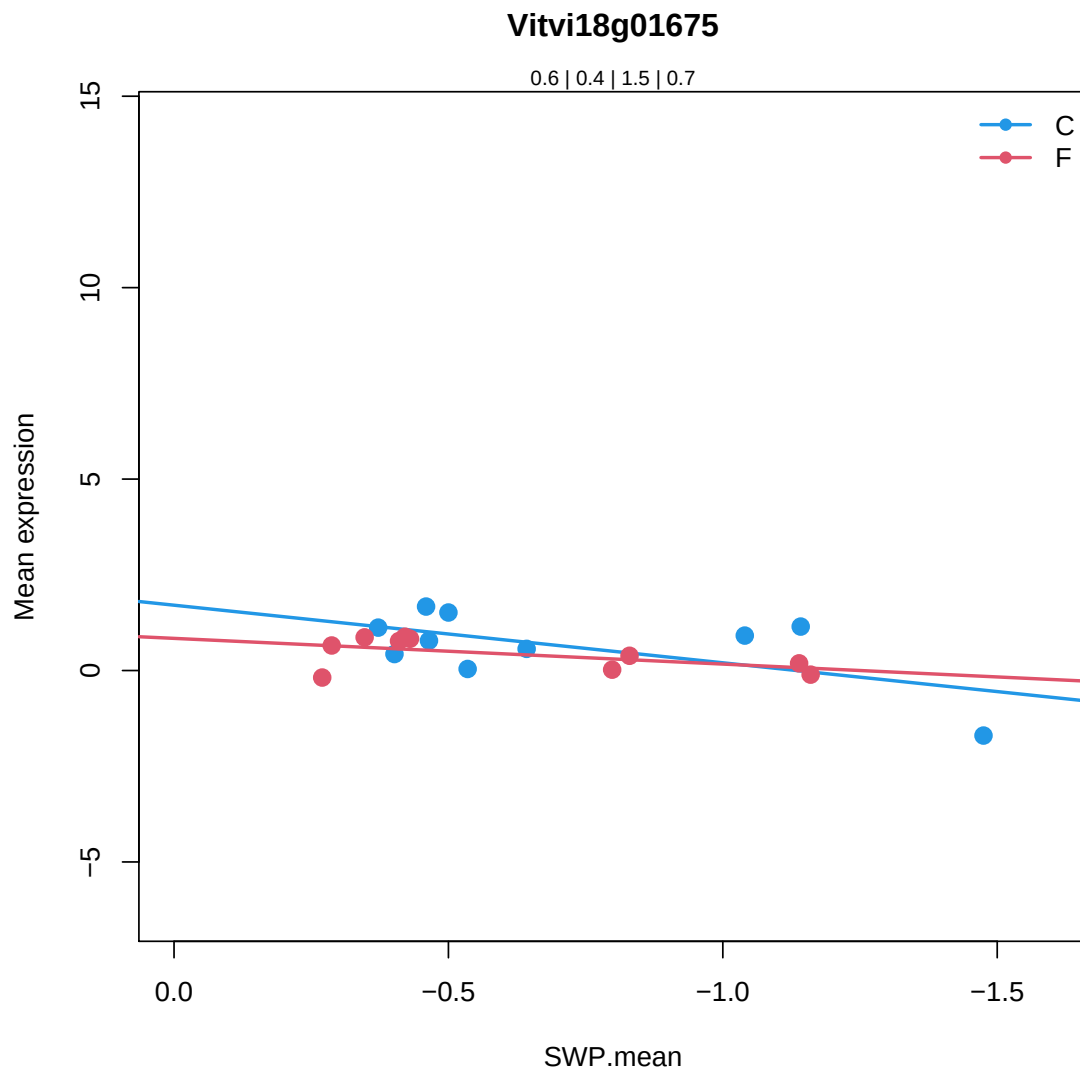
leucine-rich repeat transmembrane protein kinase family protein |

Chr1:12584587-12587570 FORWARD LENGTH=966 |

201606

Coefficients for Vitvi18g01675.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6481574	0.002657168	**	0.002848741	**
SlopeC	1.504081	0.009820452	**	0.3011737	
MeanF-MeanC	-0.2177073	0.4285956		0.7636958	
SlopeF-SlopeC	-0.8322673	0.3038511		0.9999488	



8.1.202 Vitvi05g01314: Type1.0 *

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

Vitvi05g01314

35.2

not assigned.unknown

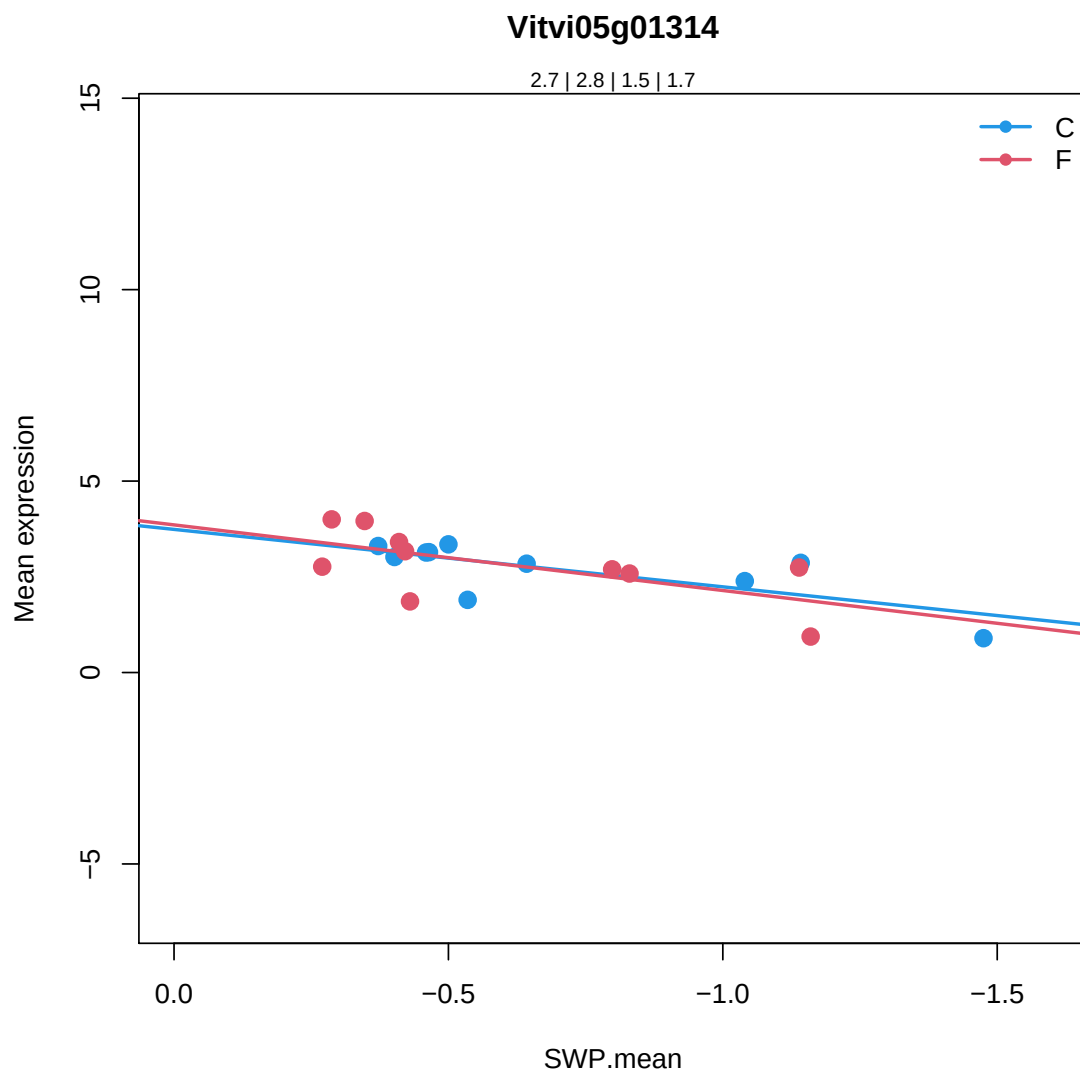
dCTP pyrophosphatase-like protein |

Chr3:9213236-9214144 FORWARD LENGTH=141 |

201606

Coefficients for Vitvi05g01314.

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



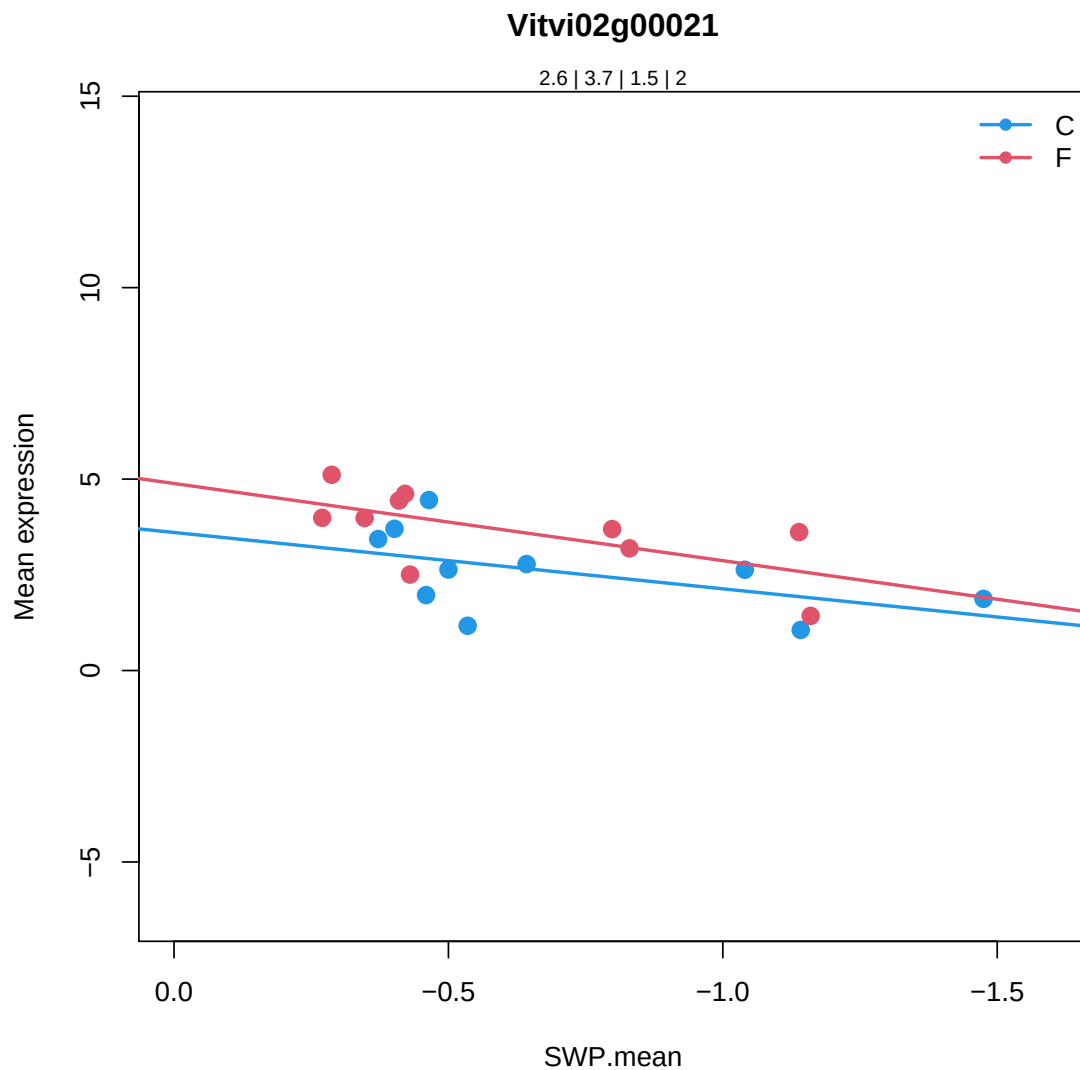
8.1.203 Vitvi02g00021: Type1.0

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

```
Vitvi02g00021
33.99
development.unspecified
SPIRAL1-like5 |
Chr4:12257914-12258297 REVERSE LENGTH=99 |
201606
```

Coefficients for Vitvi02g00021.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.570993	3.059559e-09	***	3.79816e-09	***
SlopeC	1.471451	0.06056797	.	0.5420886	
MeanF-MeanC	1.085863	0.008924126	**	0.06985418	.
SlopeF-SlopeC	0.5440579	0.6276447		0.9999488	



8.1.204 Vitvi11g00579: Type1.0

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

Vitvi11g00579

30.3

signalling.calcium

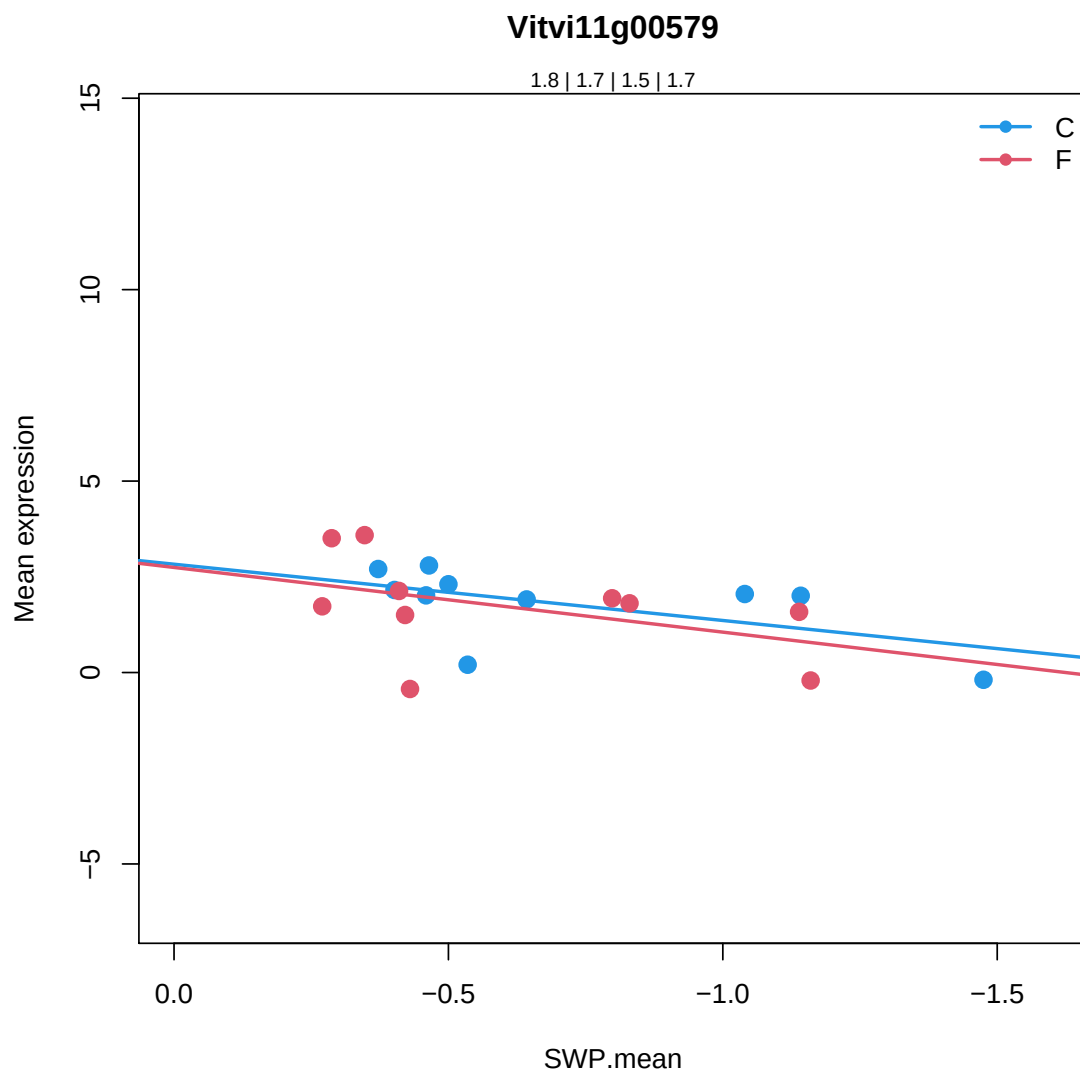
calcium-binding EF hand family protein |

Chr4:15501134-15503321 FORWARD LENGTH=498 |

201606

Coefficients for Vitvi11g00579.

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



8.1.205 Vitvi12g00710: Type1.0

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

Vitvi12g00710

35.1

not assigned.no ontology

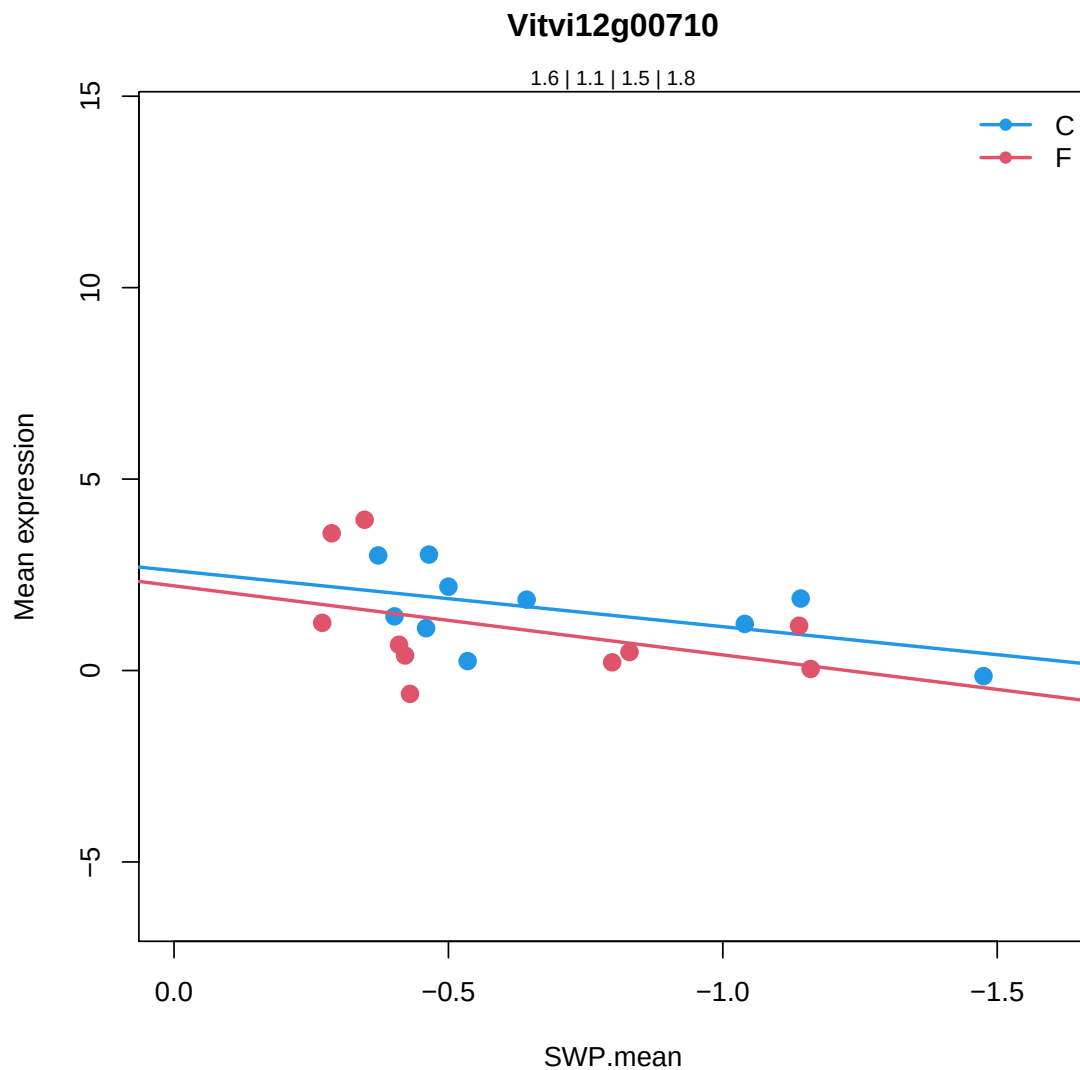
HXXXD-type acyl-transferase family protein |

Chr5:16431448-16433086 FORWARD LENGTH=457 |

201606

Coefficients for Vitvi12g00710.

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



8.1.206 Vitvi07g00578: Type1.0

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

Vitvi07g00578

33.99

development.unspecified

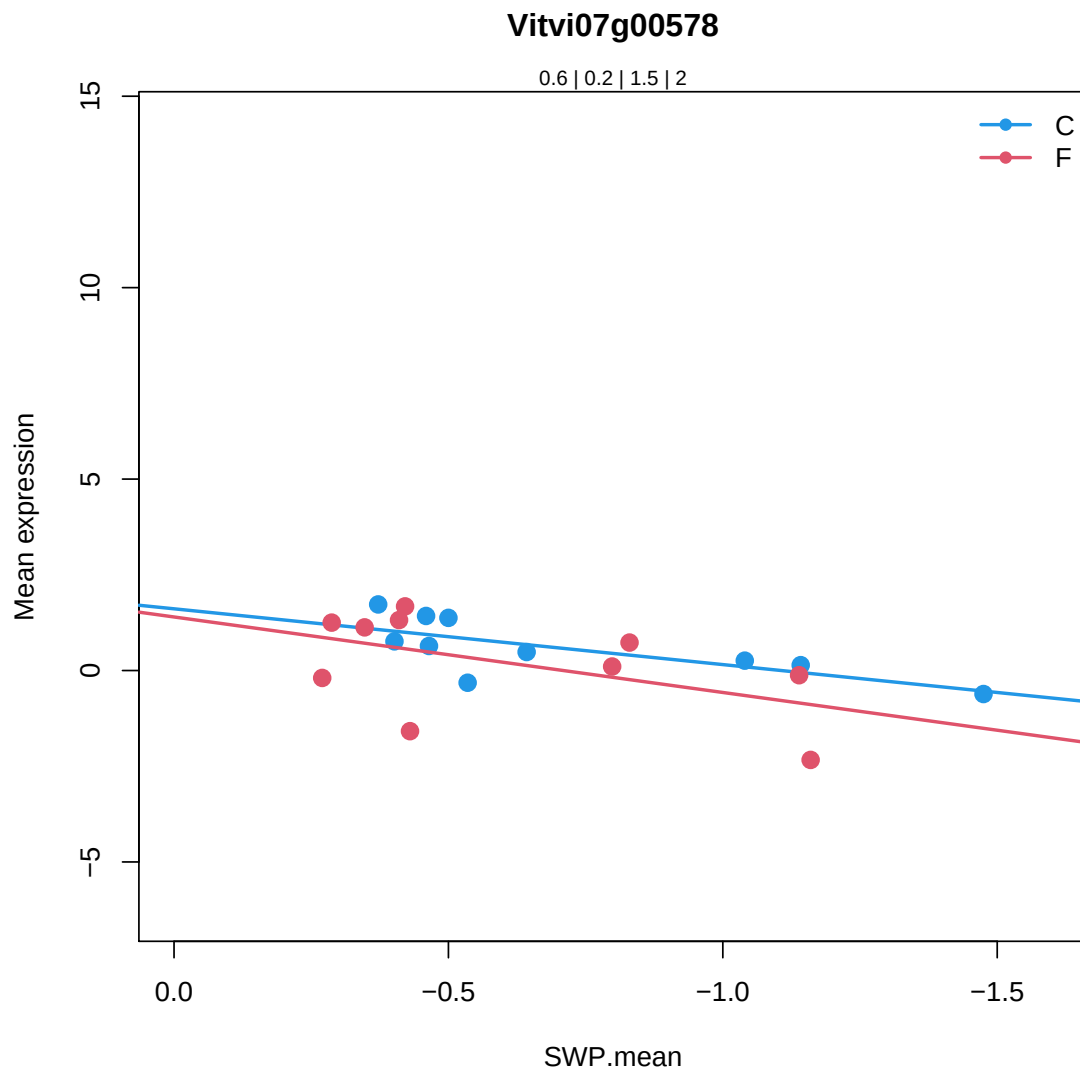
nodulin MtN21 /EamA-like transporter family protein |

Chr2:17063396-17065514 REVERSE LENGTH=394 |

201606

Coefficients for Vitvi07g00578.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.5874801	0.03845343	*	0.04014708	*
SlopeC	1.456916	0.06237985	.	0.5462034	
MeanF-MeanC	-0.3905416	0.3113994		0.6755408	
SlopeF-SlopeC	0.5147619	0.6454184		0.9999488	



8.1.207 Vitvi10g01138: Type1.0

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

Vitvi10g01138

26.10

misc.cytochrome P450

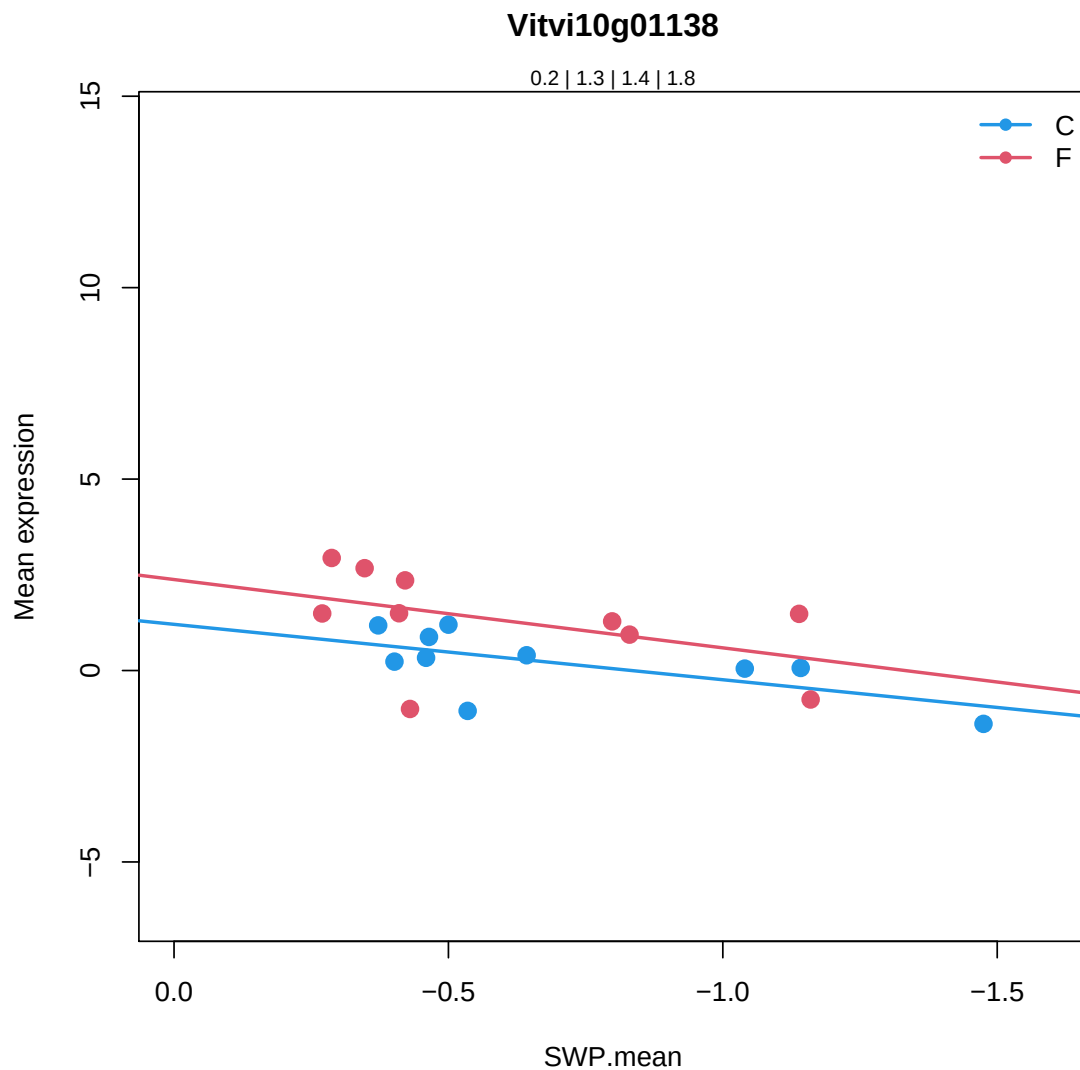
cytochrome P450%2C family 71%2C subfamily B%2C polypeptide 34 |

Chr3:9639199-9640866 REVERSE LENGTH=500 |

201606

Coefficients for Vitvi10g01138.

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



8.1.208 Vitvi04g01309: Type1.0

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

Vitvi04g01309

27.3.25

RNA.regulation of transcription.MYB domain transcription factor family

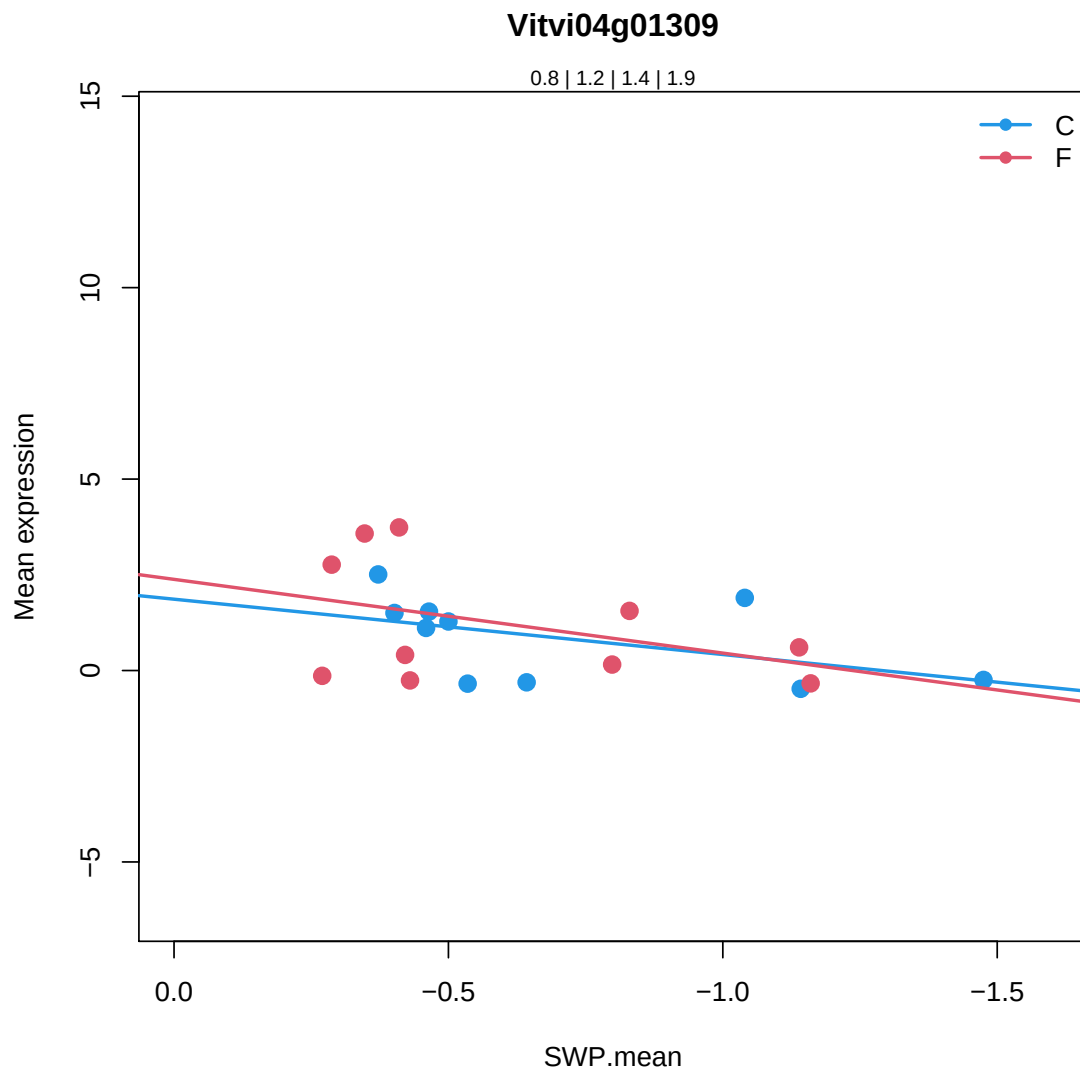
RAD-like 6 |

Chr1:28244463-28245453 REVERSE LENGTH=97 |

201606

Coefficients for Vitvi04g01309.

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



8.1.209 Vitvi14g02997: Type1.0

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

Vitvi14g02997

35.2

not assigned.unknown

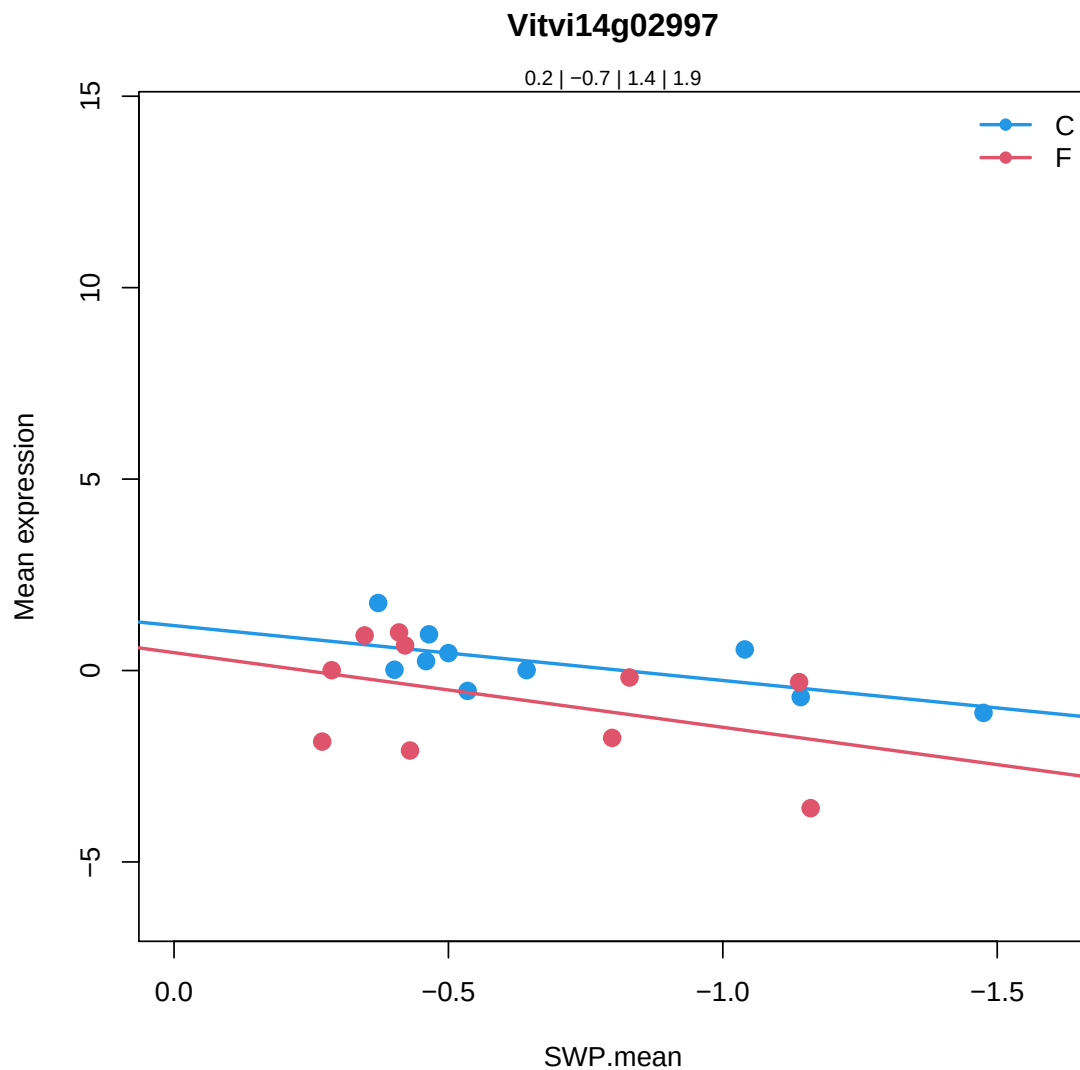
sieve element occlusion amino-terminus protein |

Chr3:252033-255246 FORWARD LENGTH=740 |

201606

Coefficients for Vitvi14g02997.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1654385	0.6101192		0.6154899	
SlopeC	1.433471	0.1216638		0.6432185	
MeanF-MeanC	-0.8865813	0.06300563	.	0.2774724	
SlopeF-SlopeC	0.5164558	0.7002951		0.9999488	



8.1.210 Vitvi13g02416: Type1.0

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

Vitvi13g02416

31.1

cell.organisation

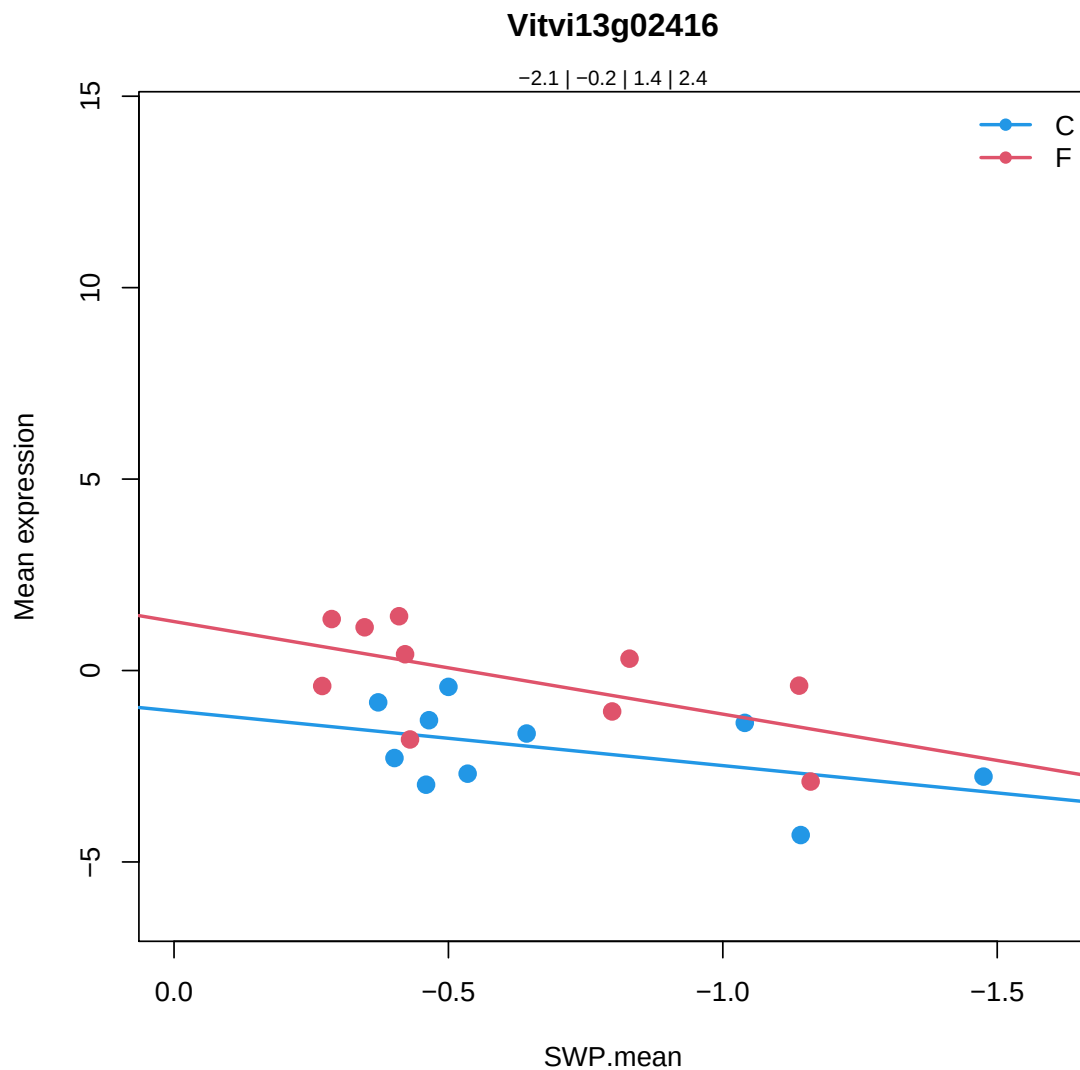
annexin 4 |

Chr2:16196582-16198273 REVERSE LENGTH=302 |

201606

Coefficients for Vitvi13g02416.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-2.060222	2.61879e-06	***	2.99352e-06	***
SlopeC	1.426257	0.1304665		0.6531879	
MeanF-MeanC	1.86576	0.0005611289	***	0.007733026	**
SlopeF-SlopeC	0.9919442	0.470413		0.9999488	



8.1.211 Vitvi03g00780: Type1.0

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

Vitvi03g00780

17.3.1.2.99

hormone metabolism.brassinosteroid.synthesis-degradation.sterols.other

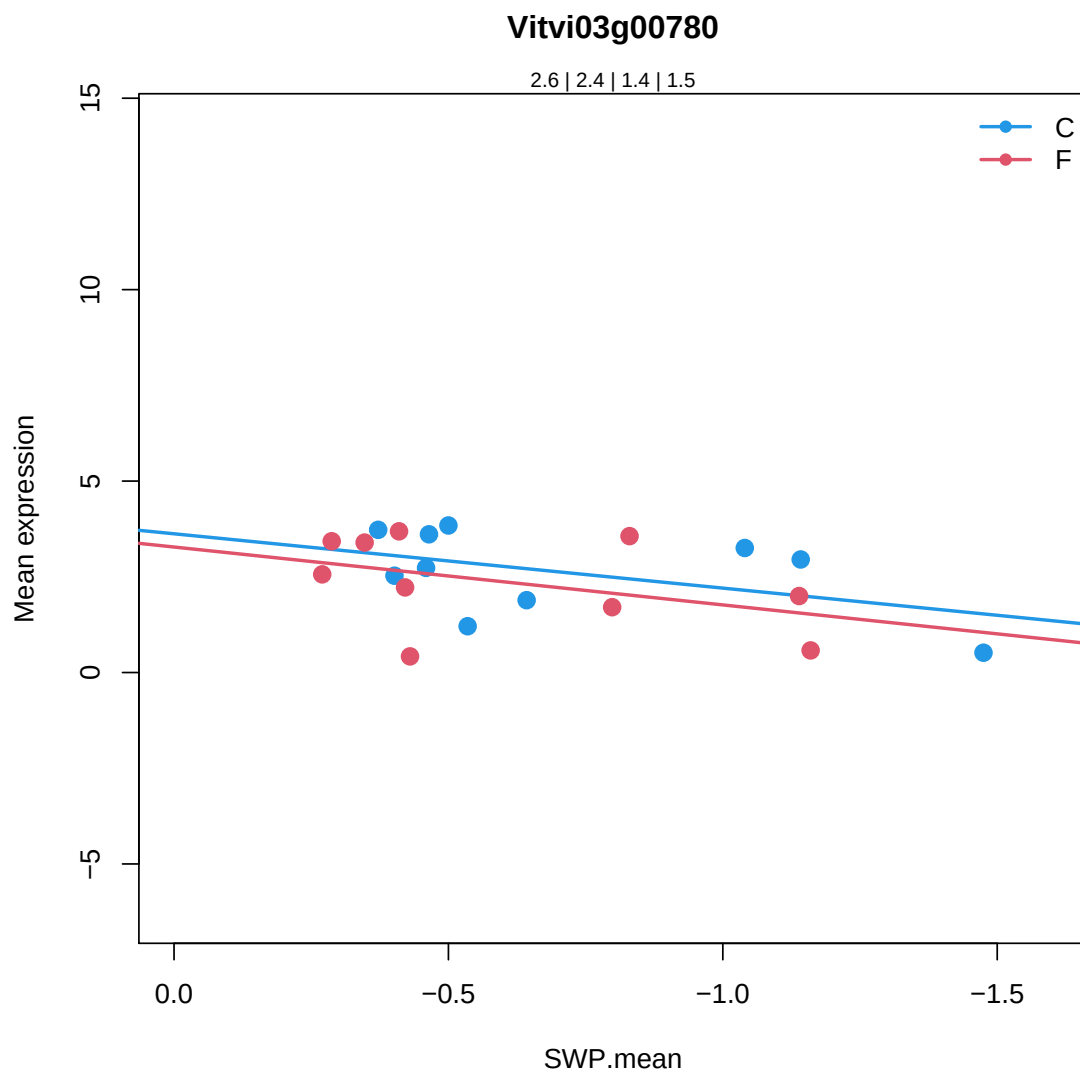
FAD/NAD(P)-binding oxidoreductase family protein |

Chr1:21714094-21717246 REVERSE LENGTH=531 |

201606

Coefficients for Vitvi03g00780.

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



8.1.212 Vitvi04g02075: Type1.0

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

Vitvi04g02075

35.2

not assigned.unknown

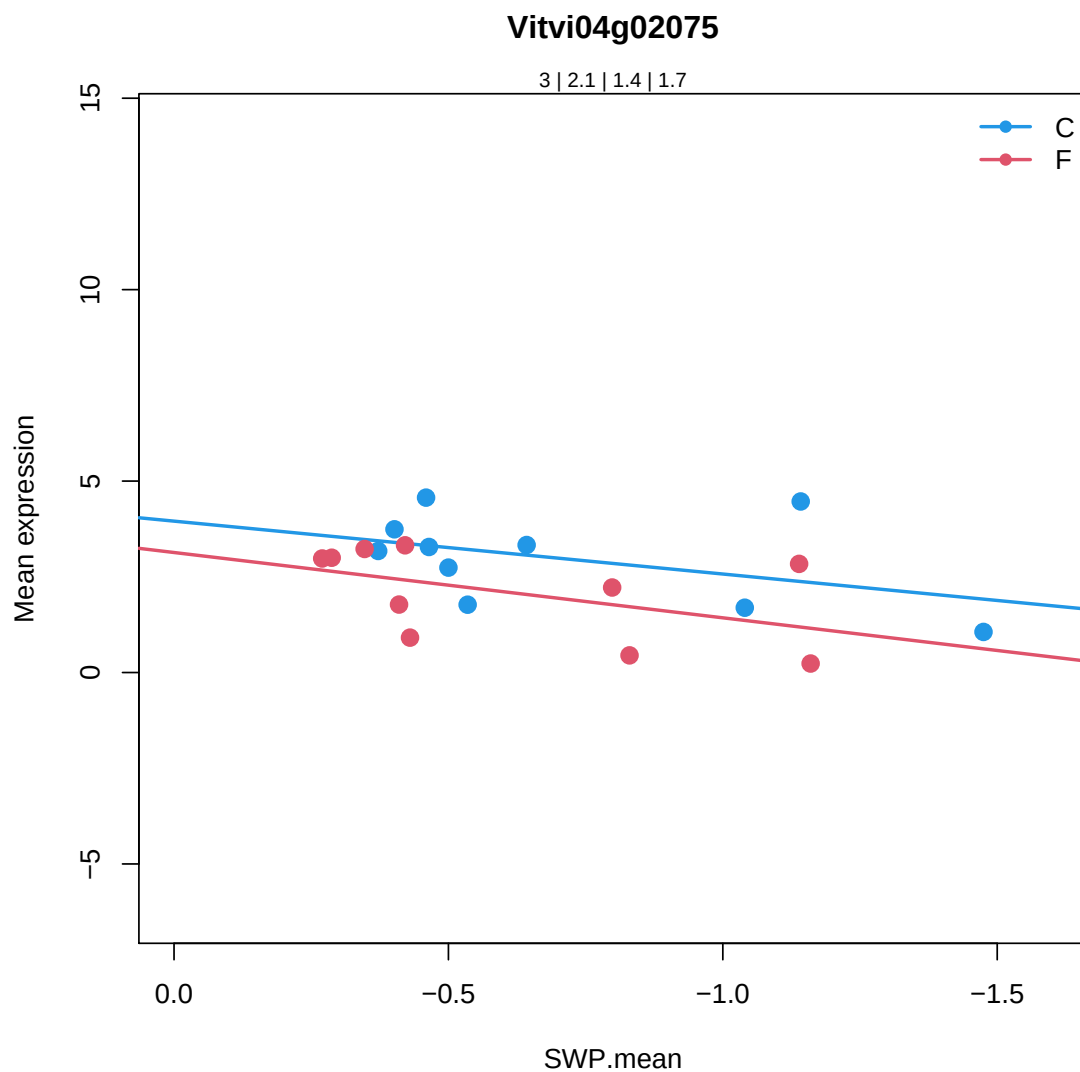
SAUR-like auxin-responsive protein family |

Chr4:16596860-16597144 FORWARD LENGTH=94 |

201606

Coefficients for Vitvi04g02075.

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



8.1.213 Vitvi04g01475: Type1.0

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

Vitvi04g01475

20.1.3.1

stress.biotic.signalling.MLO-like

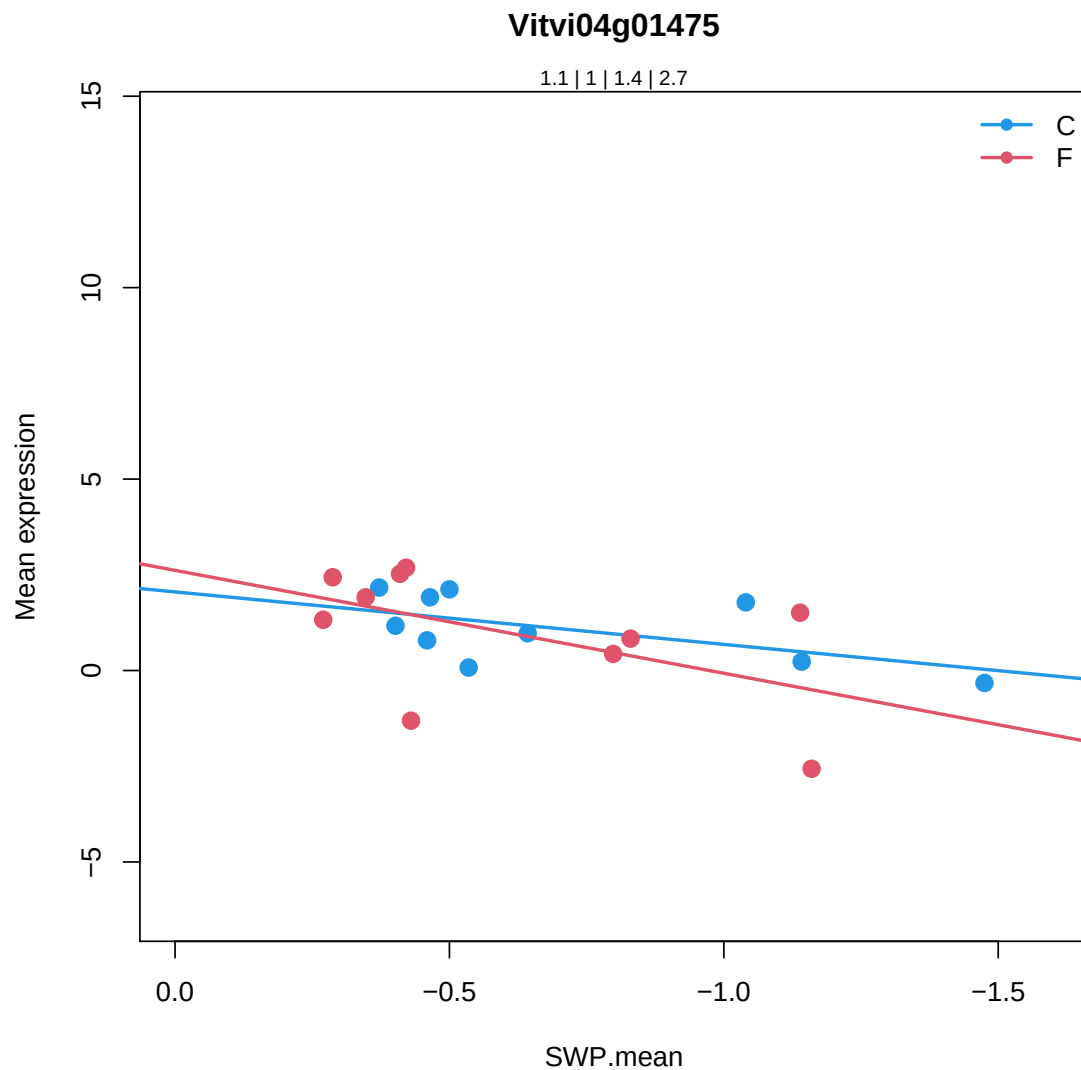
Seven transmembrane MLO family protein |

Chr1:3671935-3675909 REVERSE LENGTH=573 |

201606

Coefficients for Vitvi04g01475.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.08928	0.004506471	**	0.004811069	**
SlopeC	1.370647	0.165766		0.6963267	
MeanF-MeanC	-0.1110502	0.8212749		0.9503527	
SlopeF-SlopeC	1.31695	0.3646259		0.9999488	



8.1.214 Vitvi06g00379: Type1.0

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

Vitvi06g00379

35.2

not assigned.unknown

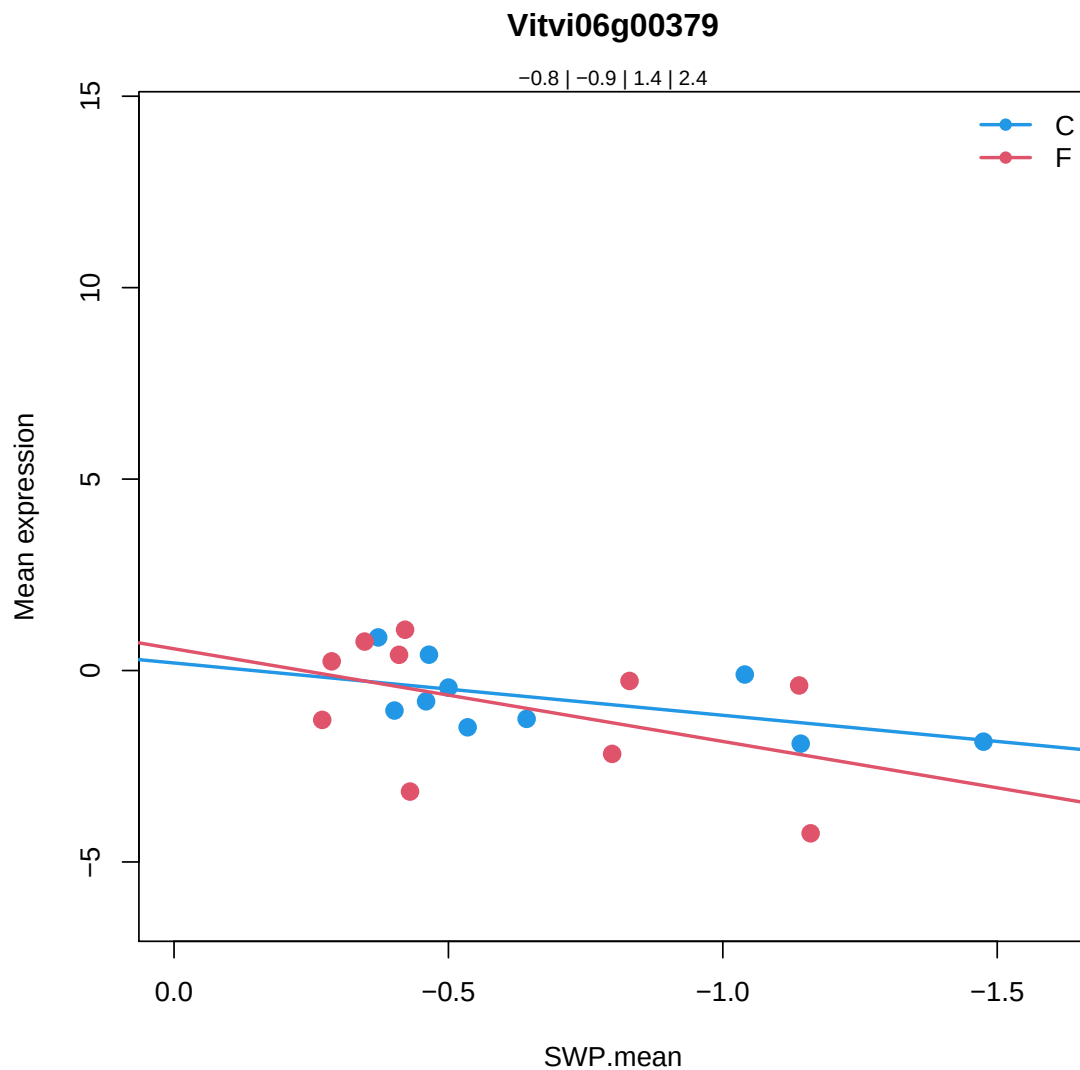
Embryo-specific protein 3%2C (ATS3) |

Chr2:17295259-17296329 REVERSE LENGTH=179 |

201606

Coefficients for Vitvi06g00379.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.7637726	0.05004379	.	0.05210872	.
SlopeC	1.36578	0.1959731		0.7250708	
MeanF-MeanC	-0.1435373	0.7852276		0.9392905	
SlopeF-SlopeC	1.054433	0.4961613		0.9999488	



8.1.215 Vitvi14g00952: Type1.0

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

Vitvi14g00952

29.4.1.56

protein.postranslational modification.kinase.receptor like cytoplasmat

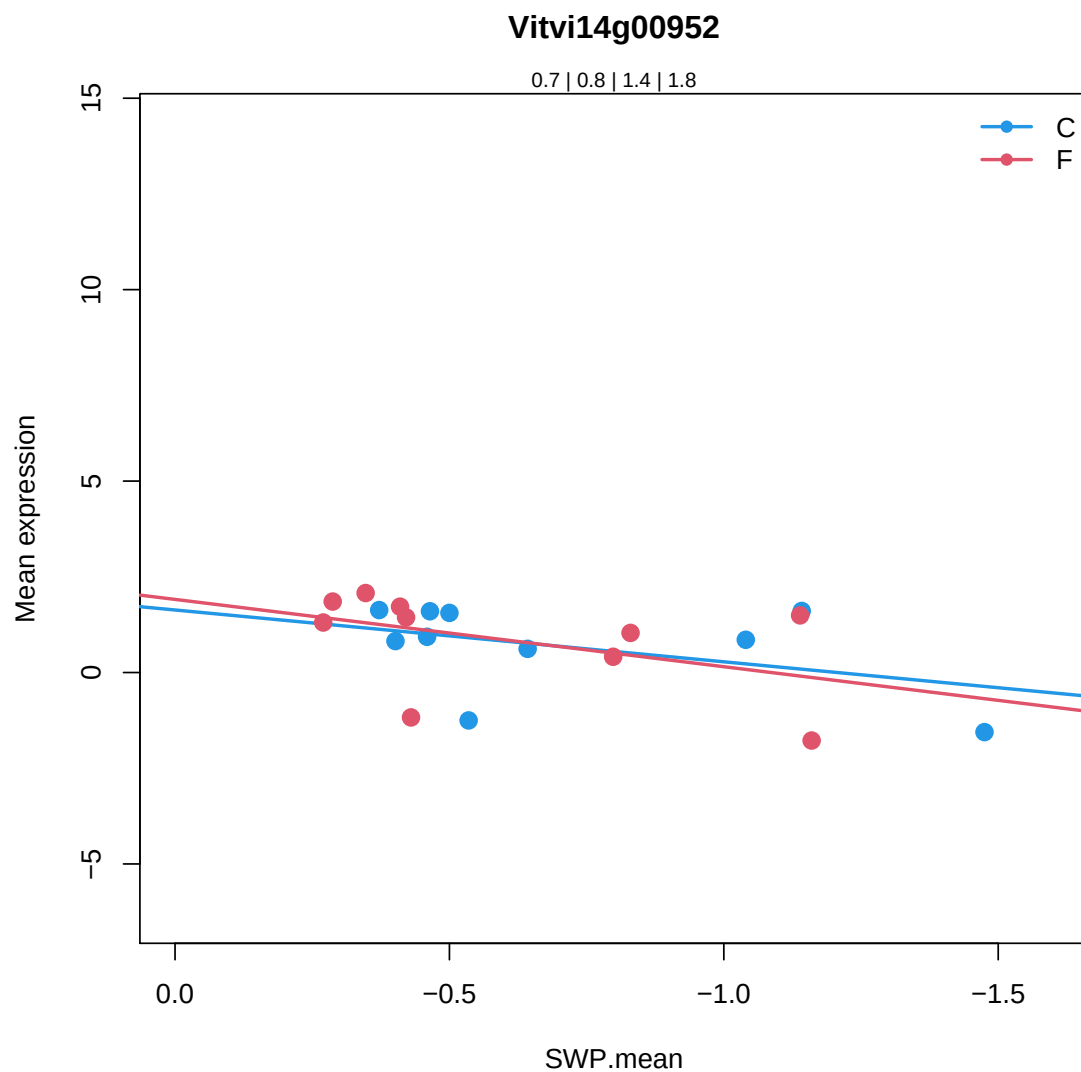
Protein kinase superfamily protein |

Chr5:15008433-15011025 REVERSE LENGTH=552 |

201606

Coefficients for Vitvi14g00952.

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



8.1.216 Vitvi16g00349: Type1.0

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

Vitvi16g00349

17.5.2

hormone metabolism.ethylene.signal transduction

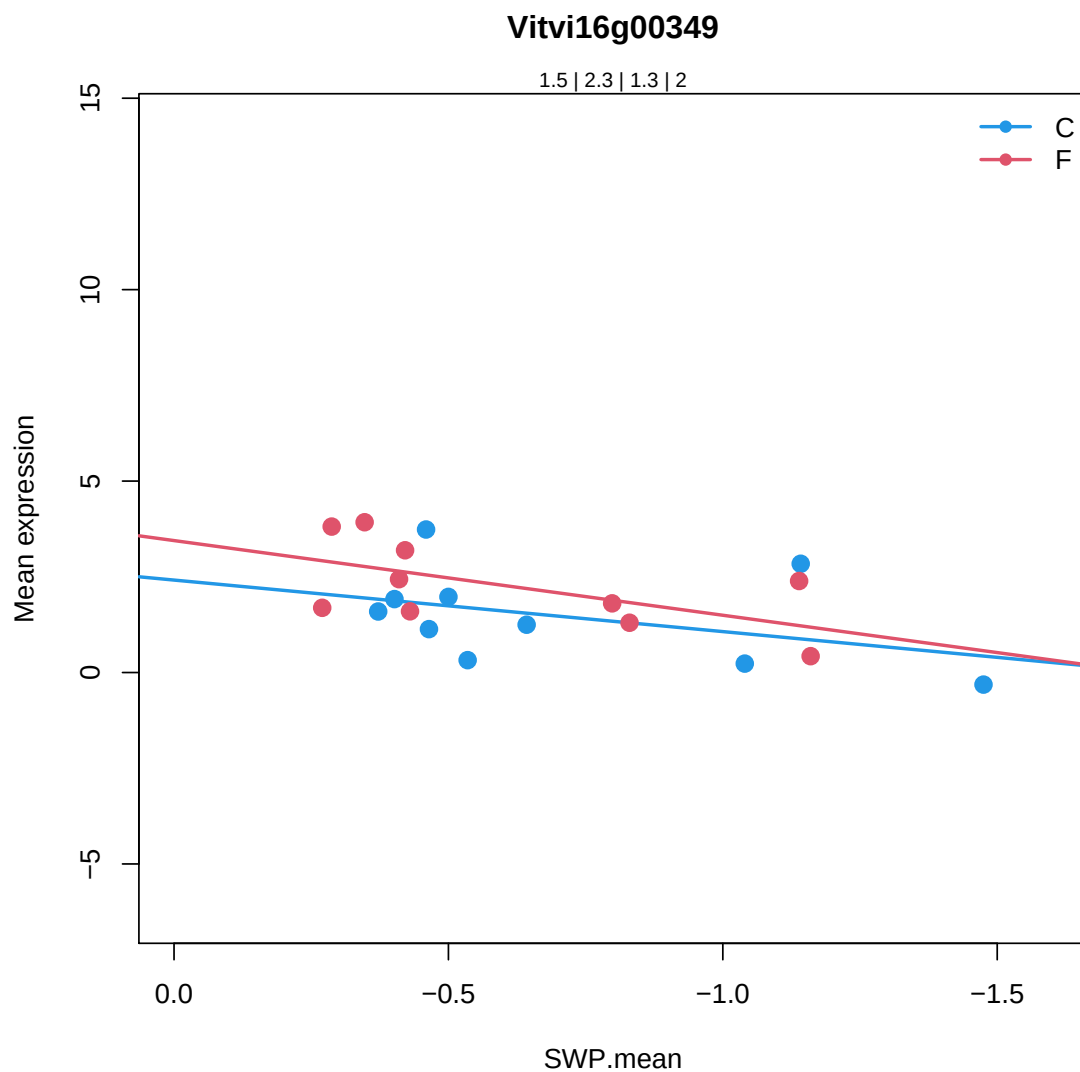
ethylene responsive element binding factor 1 |

Chr4:9759405-9760211 FORWARD LENGTH=268 |

201606

Coefficients for Vitvi16g00349.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.468392	8.827956e-05	***	9.757484e-05	***
SlopeC	1.345486	0.1274888		0.6480866	
MeanF-MeanC	0.7893419	0.08120993	.	0.3229329	
SlopeF-SlopeC	0.6046809	0.636966		0.9999488	



8.1.217 Vitvi14g00087: Type1.0

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

Vitvi14g00087

35.1

not assigned.no ontology

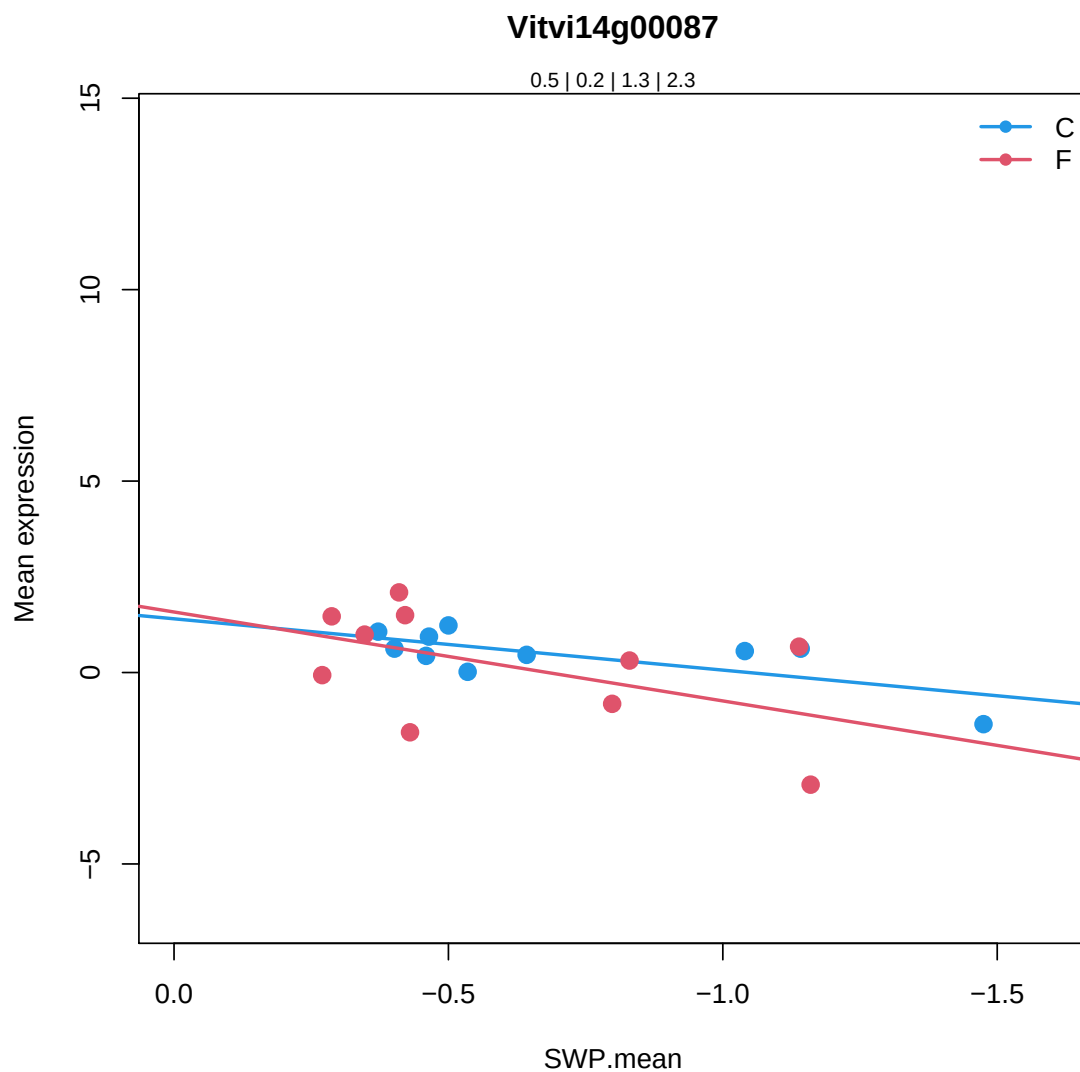
Galactose oxidase/kelch repeat superfamily protein |

Chr1:27880528-27883626 FORWARD LENGTH=569 |

201606

Coefficients for Vitvi14g00087.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.460657	0.1431602		0.1474456	
SlopeC	1.34012	0.1266458		0.6480866	
MeanF-MeanC	-0.2948699	0.49888		0.8053304	
SlopeF-SlopeC	0.9826353	0.44223		0.9999488	



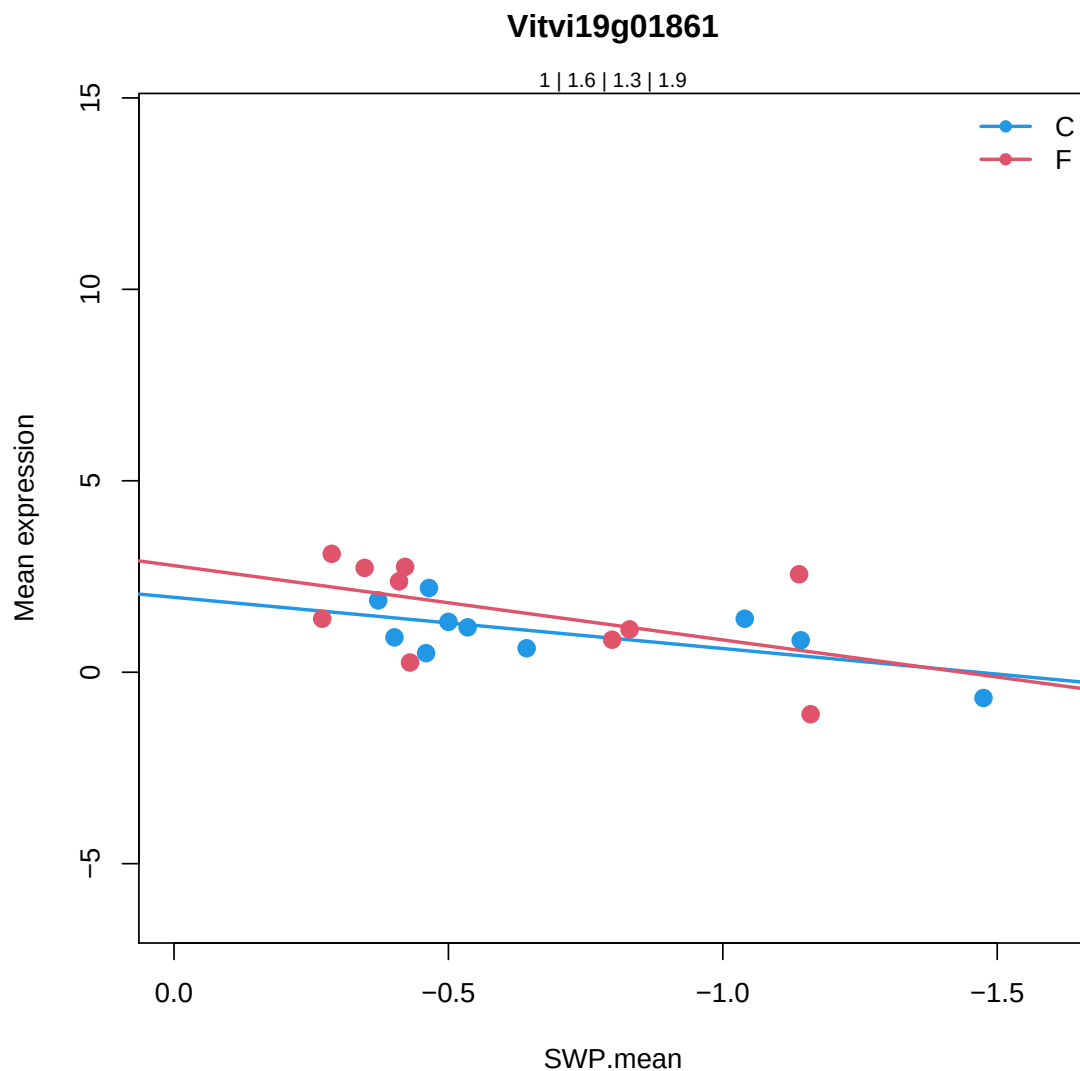
8.1.218 Vitvi19g01861: Type1.0

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

```
Vitvi19g01861
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi19g01861.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.015686	0.001605385	**	0.001731235	**
SlopeC	1.337273	0.1020627		0.6138959	
MeanF-MeanC	0.5860897	0.1553622		0.4755329	
SlopeF-SlopeC	0.603086	0.610071		0.9999488	



8.1.219 Vitvi14g00113: Type1.0

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

Vitvi14g00113

35.2

not assigned.unknown

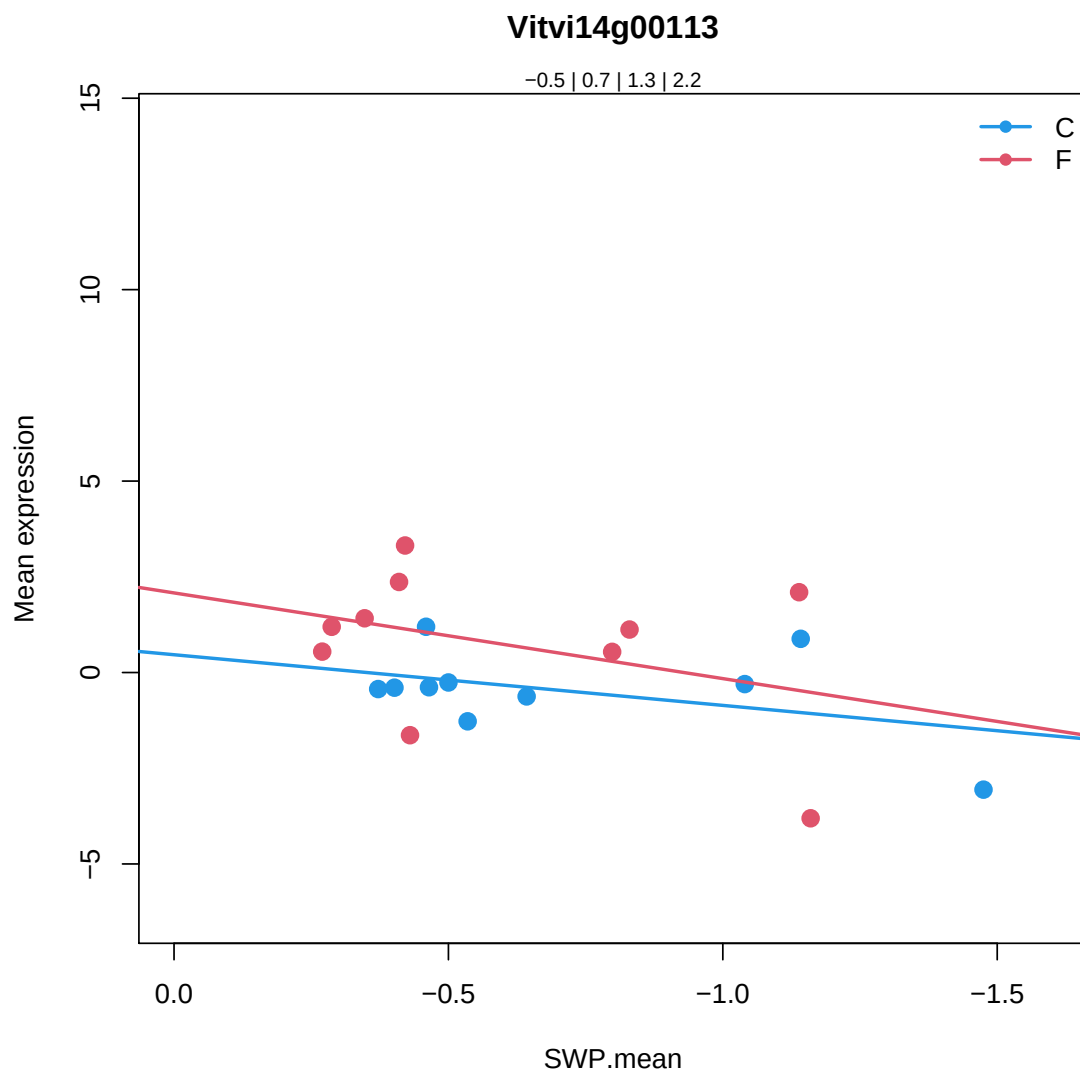
stress response NST1-like protein (DUF1645) |

Chr3:23163937-23165079 REVERSE LENGTH=380 |

201606

Coefficients for Vitvi14g00113.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.4658979	0.3158072		0.3215239	
SlopeC	1.322791	0.3062141		0.7901329	
MeanF-MeanC	1.181322	0.07941481	.	0.3186842	
SlopeF-SlopeC	0.9151976	0.6310191		0.9999488	



8.1.220 Vitvi01g00864: Type1.0

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

Vitvi01g00864

35.2

not assigned.unknown

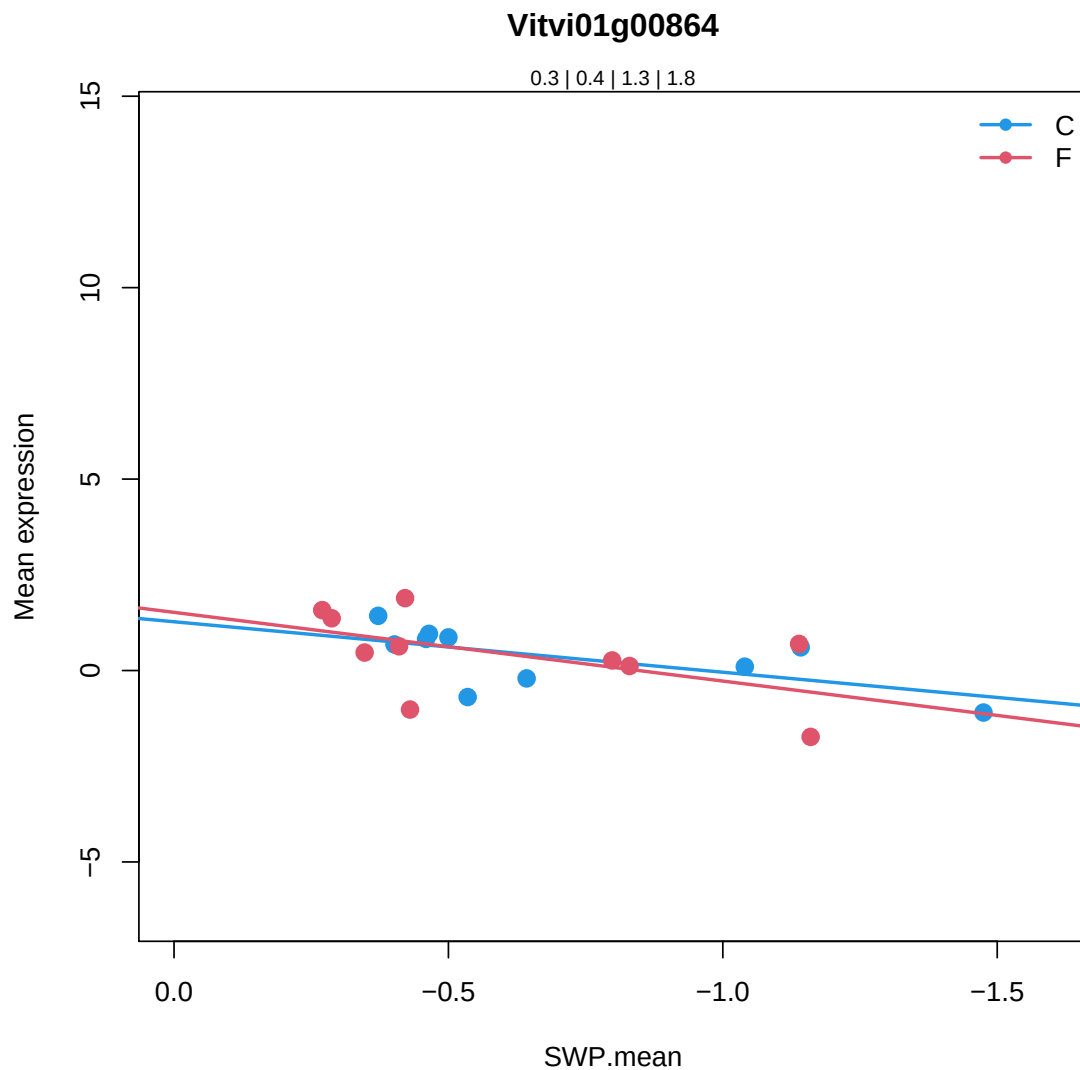
ARM repeat superfamily protein |

Chr1:9455669-9457917 REVERSE LENGTH=625 |

201606

Coefficients for Vitvi01g00864.

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



8.1.221 Vitvi18g02514: Type1.0

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

Vitvi18g02514

35.2

not assigned.unknown

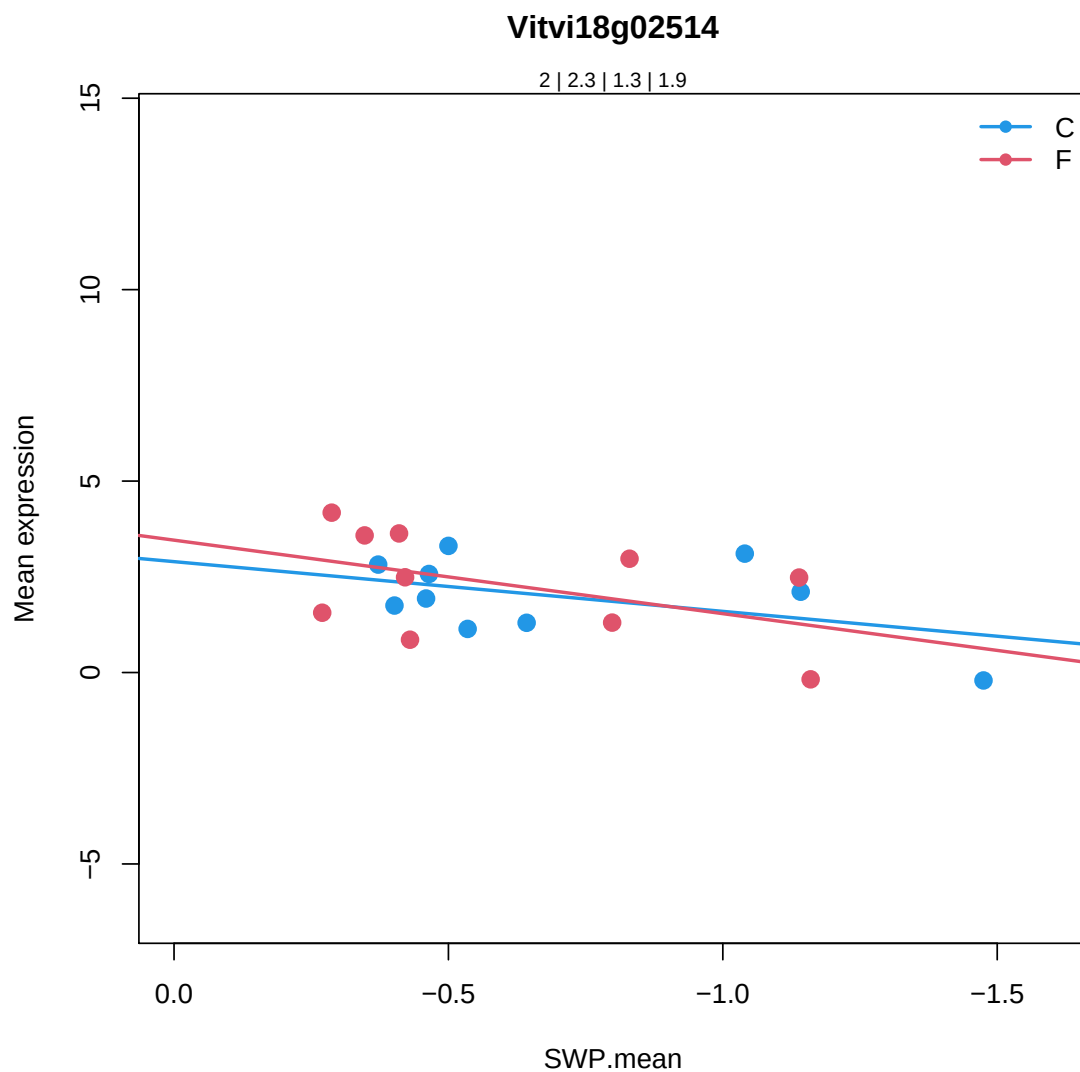
wall associated kinase 5 |

Chr1:7429980-7432346 FORWARD LENGTH=733 |

201606

Coefficients for Vitvi18g02514.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.982612	4.166939e-06	***	4.742923e-06	***
SlopeC	1.298413	0.1644691		0.6941016	
MeanF-MeanC	0.304681	0.5134628		0.8144764	
SlopeF-SlopeC	0.6211479	0.6482701		0.9999488	



8.1.222 Vitvi06g00801: Type1.0

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

Vitvi06g00801

35.2

not assigned.unknown

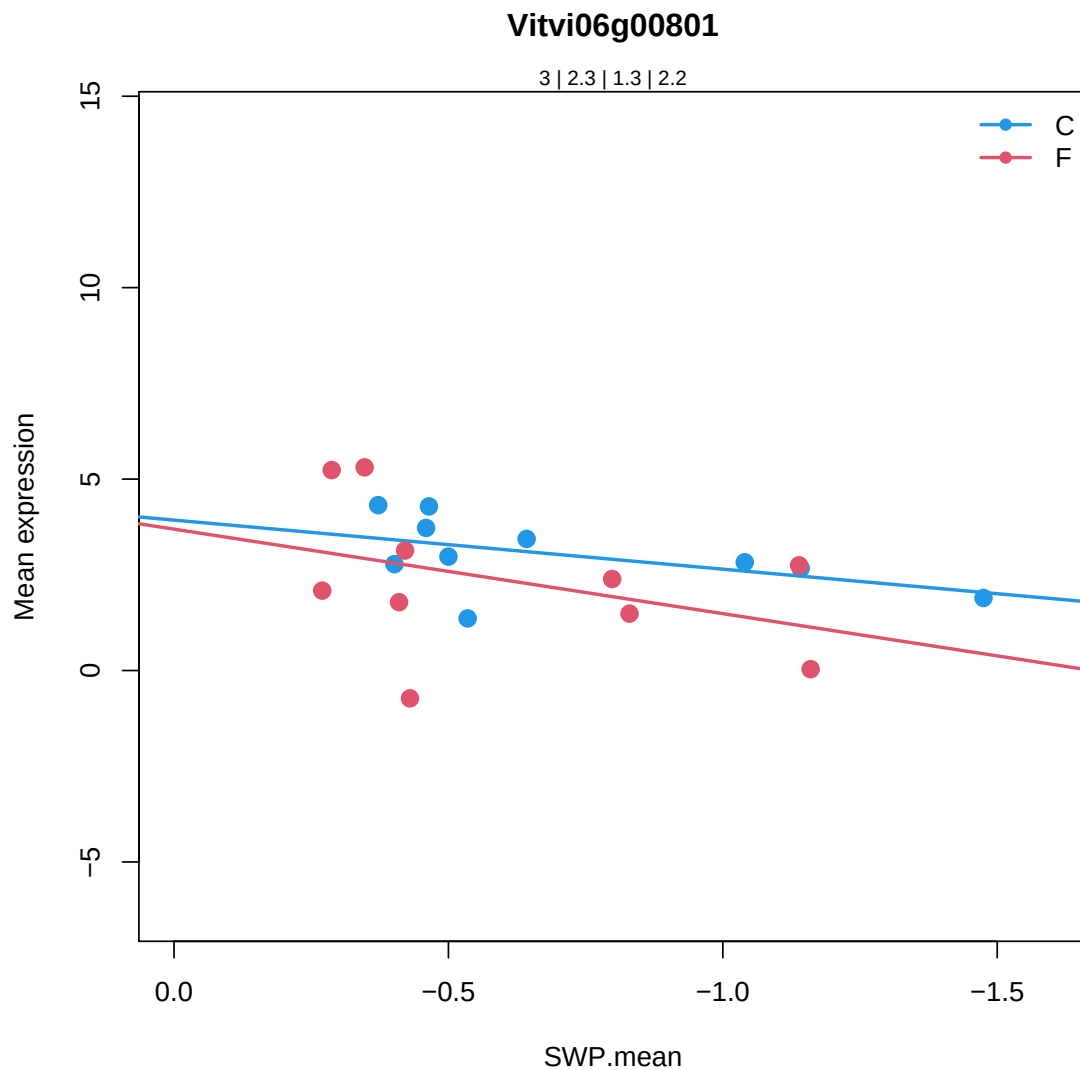
RING/U-box superfamily protein |

Chr3:3413068-3413613 REVERSE LENGTH=181 |

201606

Coefficients for Vitvi06g00801.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.027437	2.53117e-07	***	2.9677e-07	***
SlopeC	1.281227	0.2735377		0.7744772	
MeanF-MeanC	-0.679575	0.2538203		0.6140839	
SlopeF-SlopeC	0.9250071	0.5913054		0.9999488	



8.1.223 Vitvi02g01355: Type1.0

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

Vitvi02g01355

10.2.1

cell wall.cellulose synthesis.cellulose synthase

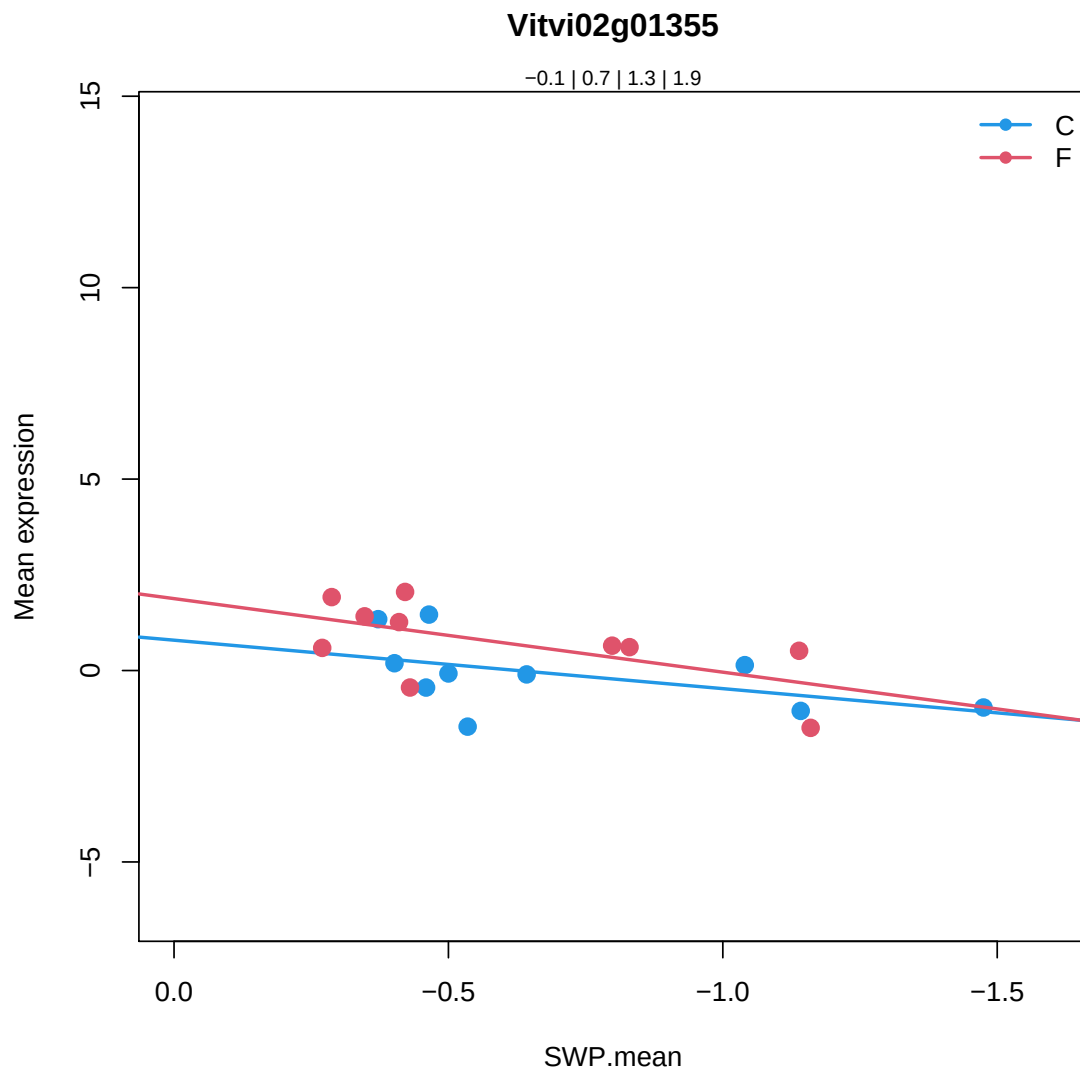
cellulose synthase like G3 |

Chr4:12456491-12460498 FORWARD LENGTH=751 |

201606

Coefficients for Vitvi02g01355.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.09790373	0.7049488		0.7096513	
SlopeC	1.265094	0.08886511	.	0.5949341	
MeanF-MeanC	0.8052468	0.03641827	*	0.1923379	
SlopeF-SlopeC	0.6559593	0.5412056		0.9999488	



8.1.224 Vitvi07g02123: Type1.0

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

```
Vitvi07g02123
```

```
20
```

```
stress
```

```
chlorophyllase 1 |
```

```
Chr1:6803796-6804923 REVERSE LENGTH=324 |
```

```
201606
```

```
Vitvi07g02123
```

```
19.99
```

```
tetrapyrrole synthesis.unspecified
```

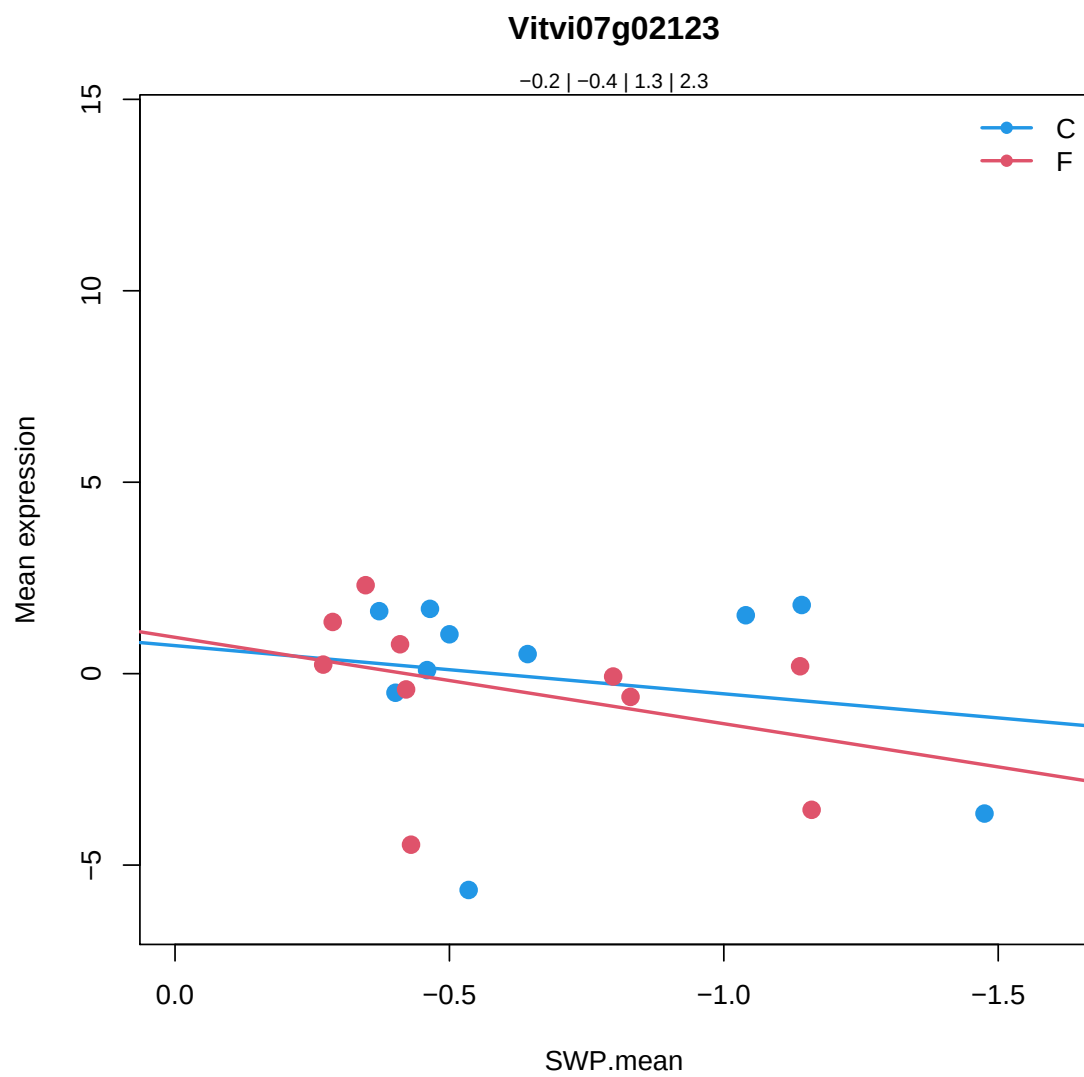
```
chlorophyllase 1 |
```

```
Chr1:6803796-6804923 REVERSE LENGTH=324 |
```

```
201606
```

Coefficients for Vitvi07g02123.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.1530994	0.8161393		0.8197967	
SlopeC	1.258572	0.4941933		0.8687743	
MeanF-MeanC	-0.2732232	0.7692929		0.9328212	
SlopeF-SlopeC	0.9980726	0.7145826		0.9999488	



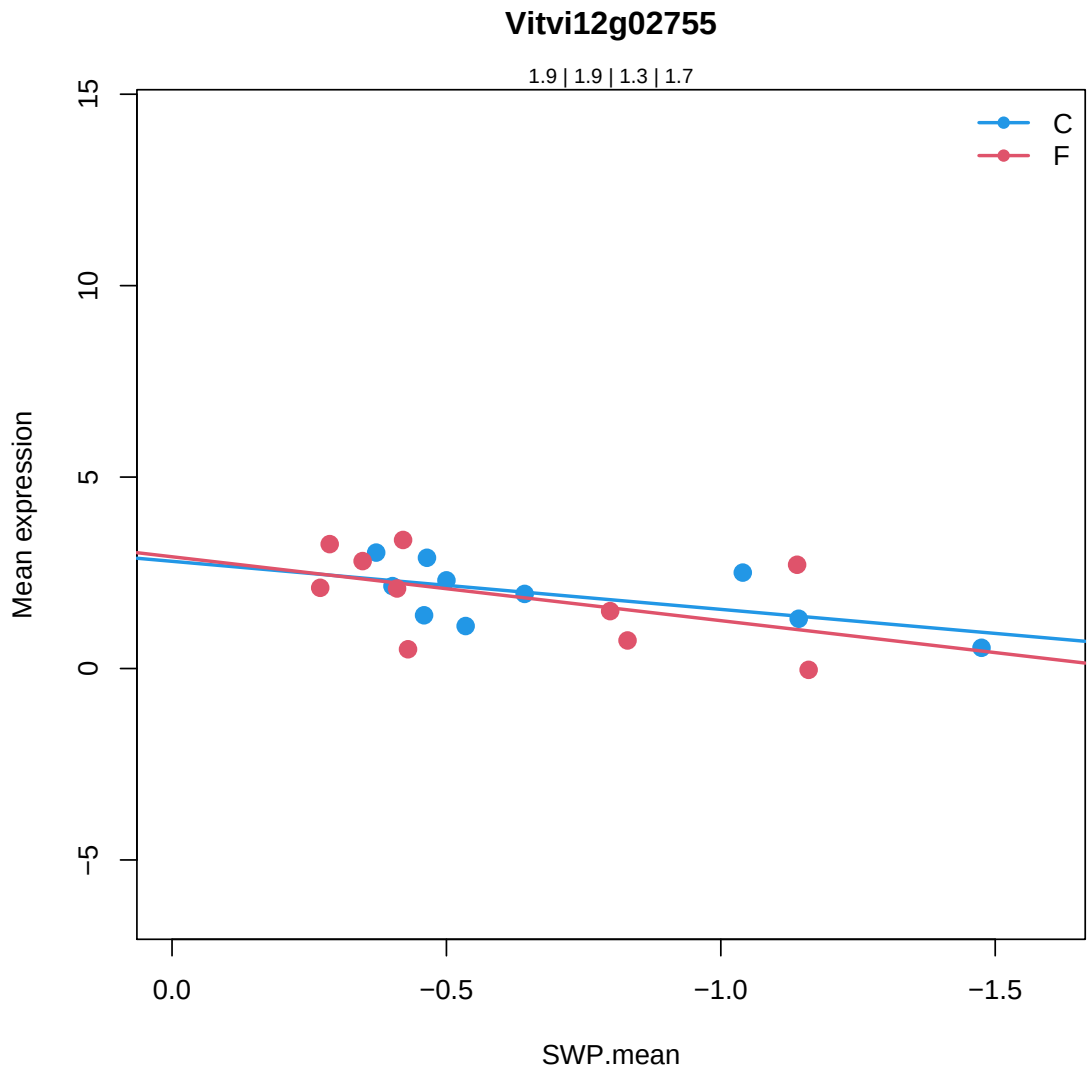
8.1.225 Vitvi12g02755: Type1.0

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

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

Coefficients for Vitvi12g02755.

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



8.1.226 Vitvi18g02776: Type1.0

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

Vitvi18g02776

35.2

not assigned.unknown

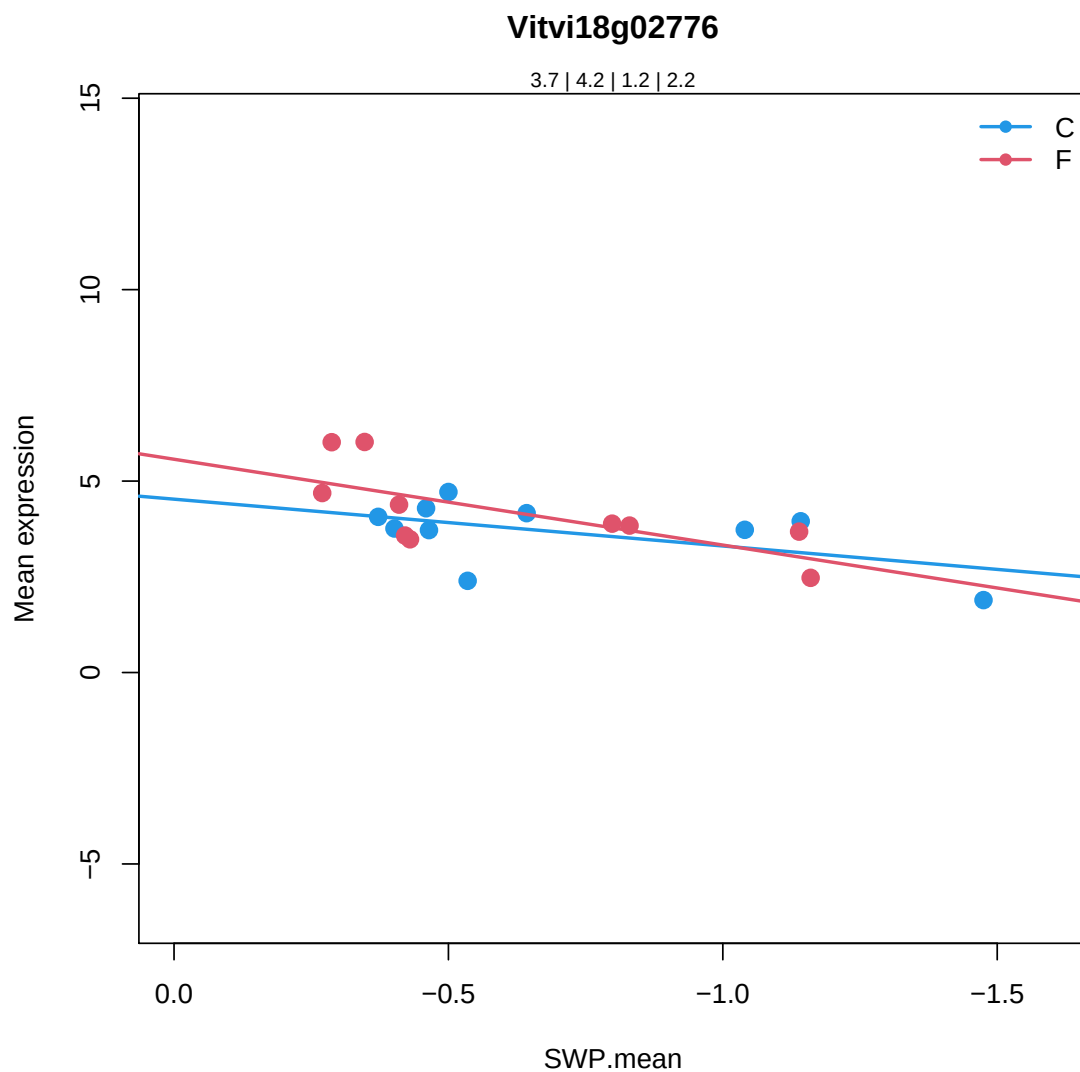
maternal effect embryo arrest protein |

Chr3:2393895-2394464 REVERSE LENGTH=189 |

201606

Coefficients for Vitvi18g02776.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.667748	4.164975e-13	***	6.127659e-13	***
SlopeC	1.222926	0.07765932	.	0.5717559	
MeanF-MeanC	0.5366427	0.1242624		0.4169985	
SlopeF-SlopeC	1.018596	0.3112418		0.9999488	



8.1.227 Vitvi13g00387: Type1.0

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

Vitvi13g00387

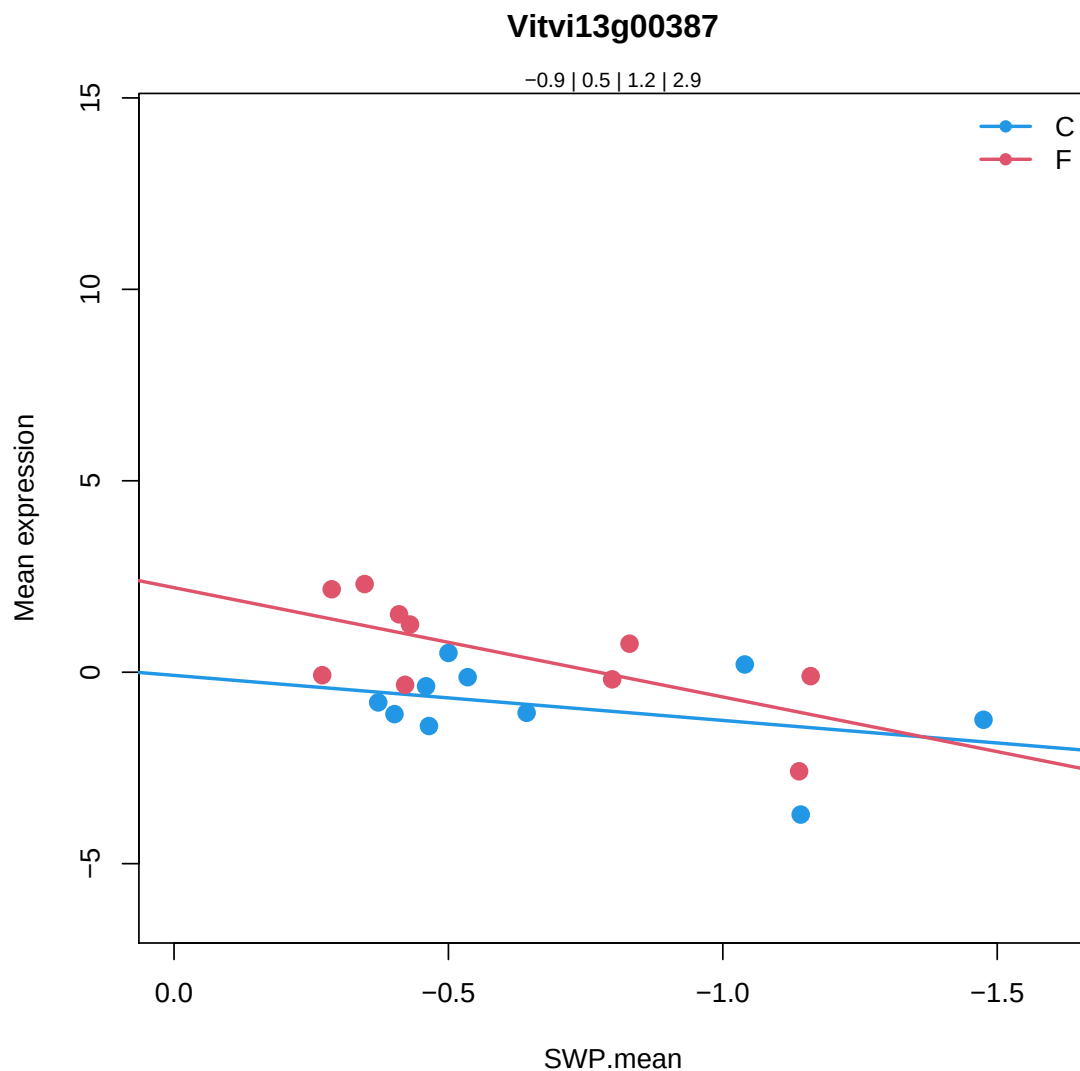
35.2

not assigned.unknown

NA

Coefficients for Vitvi13g00387.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.9099844	0.0101519	*	0.01075147	*
SlopeC	1.17744	0.2037122		0.7293041	
MeanF-MeanC	1.378832	0.006411463	**	0.05474707	.
SlopeF-SlopeC	1.677457	0.2230135		0.9999488	



8.1.228 Vitvi05g01596: Type1.0

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

Vitvi05g01596

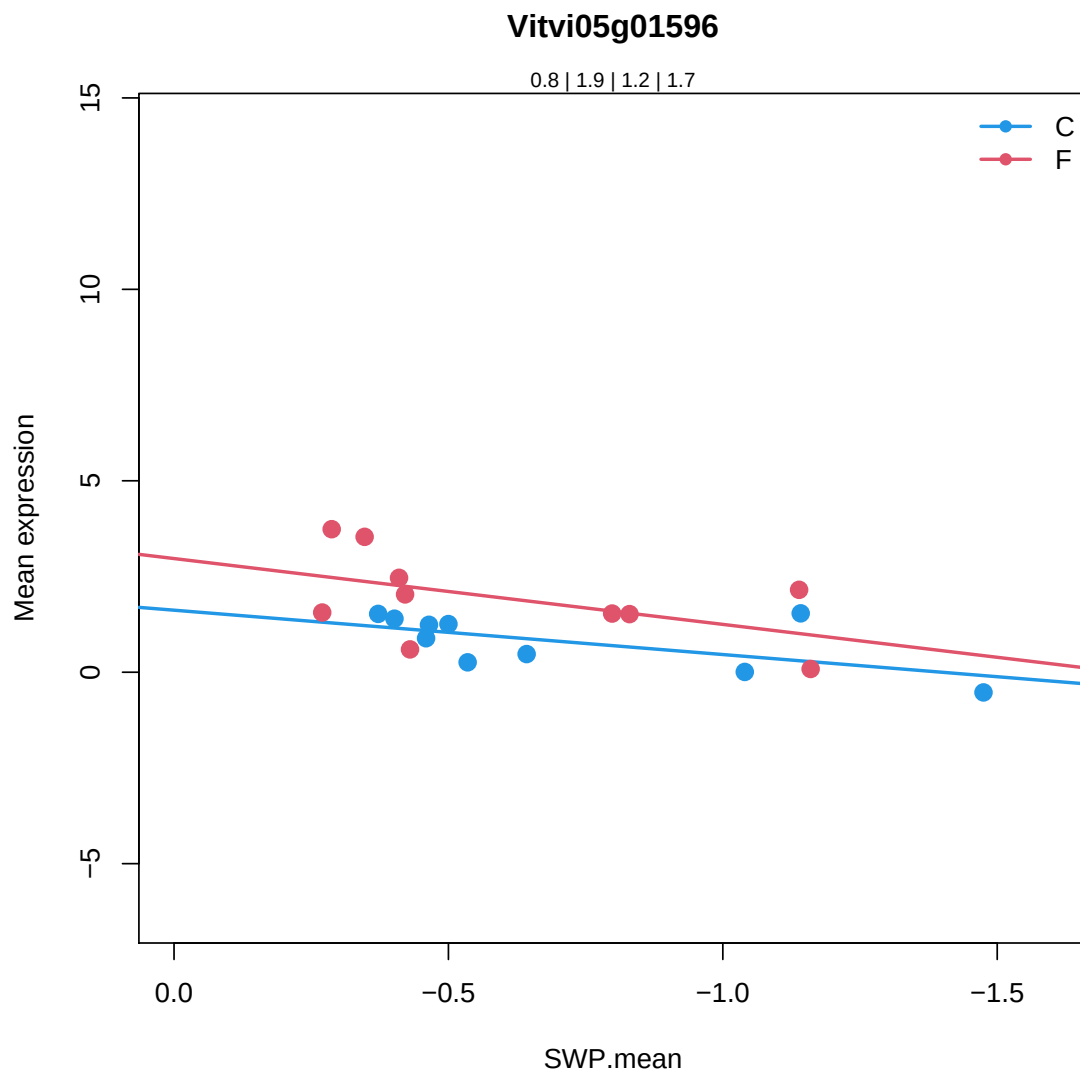
29.5.11.4.2

protein.degradation.ubiquitin.E3.RING

E3 ubiquitin-protein ligase MARCH3 IPR011016 Zinc finger, RING-CH-type

Coefficients for Vitvi05g01596.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8054442	0.003465145	**	0.00370845	**
SlopeC	1.158025	0.1040826		0.6160882	
MeanF-MeanC	1.115718	0.004057699	**	0.0386064	*
SlopeF-SlopeC	0.5611028	0.5862565		0.9999488	



8.1.229 Vitvi12g00572: Type1.0

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

Vitvi12g00572

30.11

signalling.light

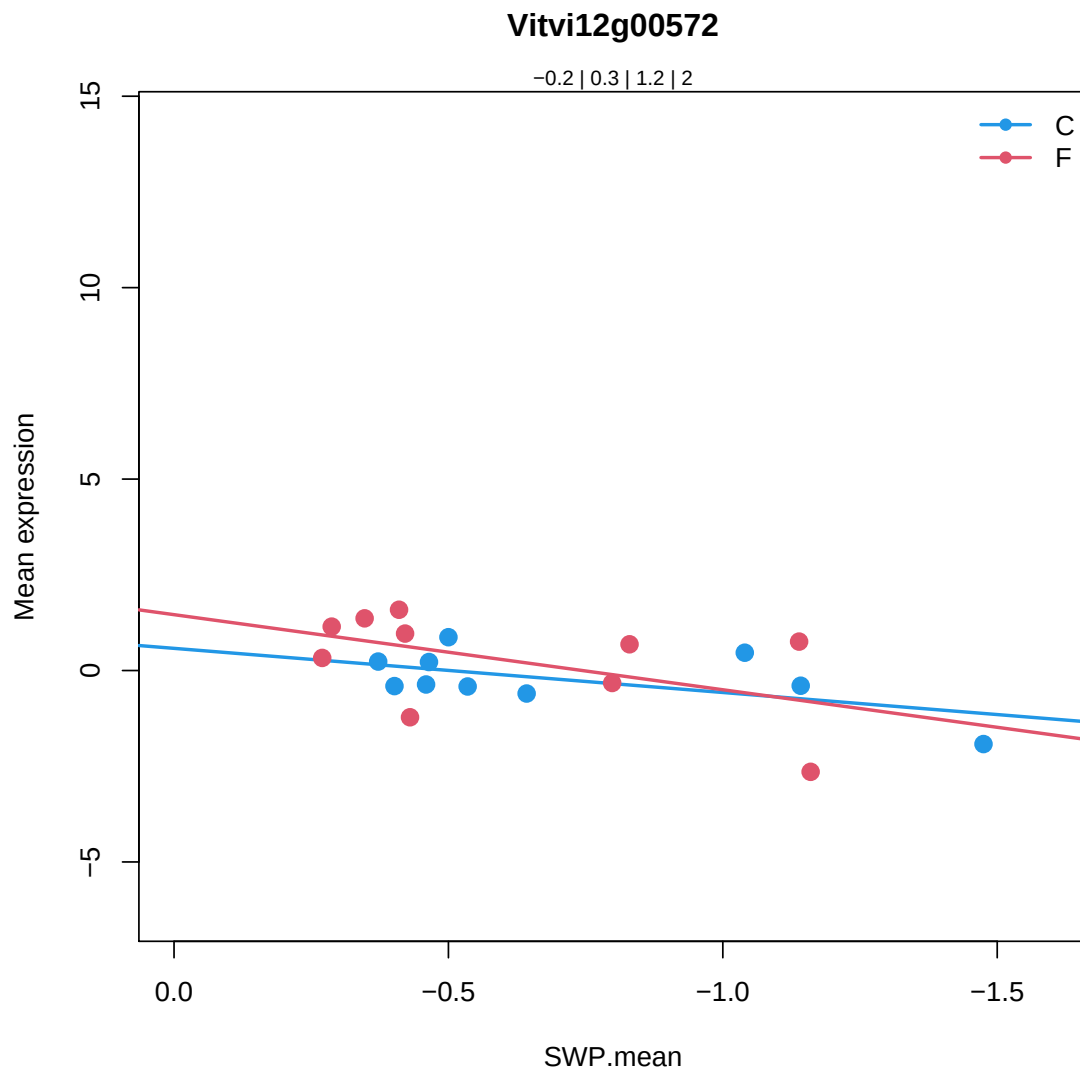
Phototropic-responsive NPH3 family protein |

Chr3:7789814-7792179 FORWARD LENGTH=506 |

201606

Coefficients for Vitvi12g00572.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.2317676	0.4112213		0.4173271	
SlopeC	1.152685	0.1486554		0.6741002	
MeanF-MeanC	0.4955185	0.2187343		0.5685241	
SlopeF-SlopeC	0.8082272	0.4879069		0.9999488	



8.1.230 Vitvi01g00958: Type1.0

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

Vitvi01g00958

27.3.35

RNA.regulation of transcription.bZIP transcription factor family

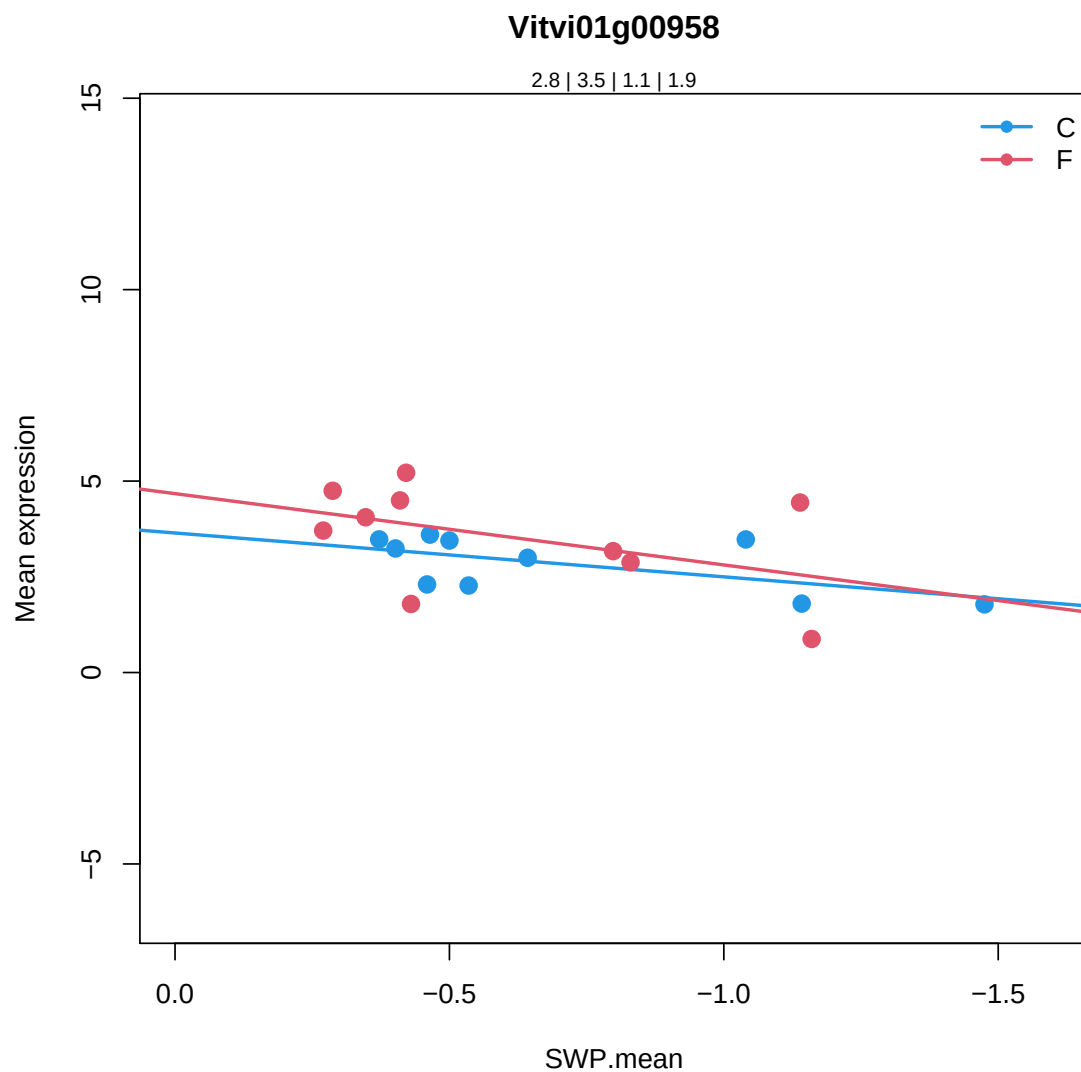
Homeobox-leucine zipper protein family |

Chr1:26259166-26260465 FORWARD LENGTH=294 |

201606

Coefficients for Vitvi01g00958.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.83892	1.946959e-09	***	2.432422e-09	***
SlopeC	1.145533	0.1663259		0.6963267	
MeanF-MeanC	0.6985561	0.100038		0.36417	
SlopeF-SlopeC	0.7161665	0.5535843		0.9999488	



8.1.231 Vitvi05g01308: Type1.0

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

Vitvi05g01308

30.5

signalling.G-proteins

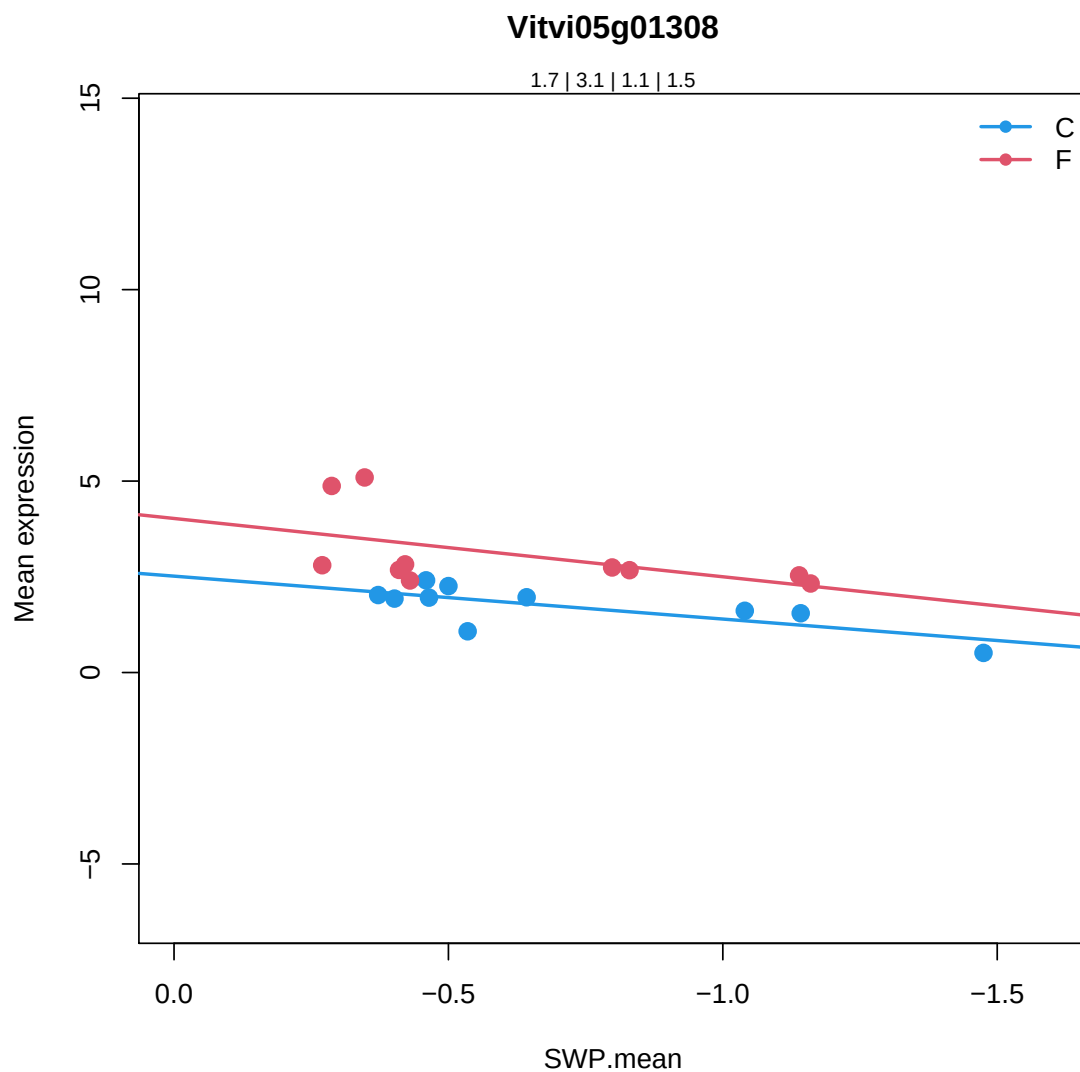
Immunoglobulin E-set superfamily protein |

Chr3:2514175-2515544 FORWARD LENGTH=240 |

201606

Coefficients for Vitvi05g01308.

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



8.1.232 Vitvi10g00030: Type1.0

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

Vitvi10g00030

35.2

not assigned.unknown

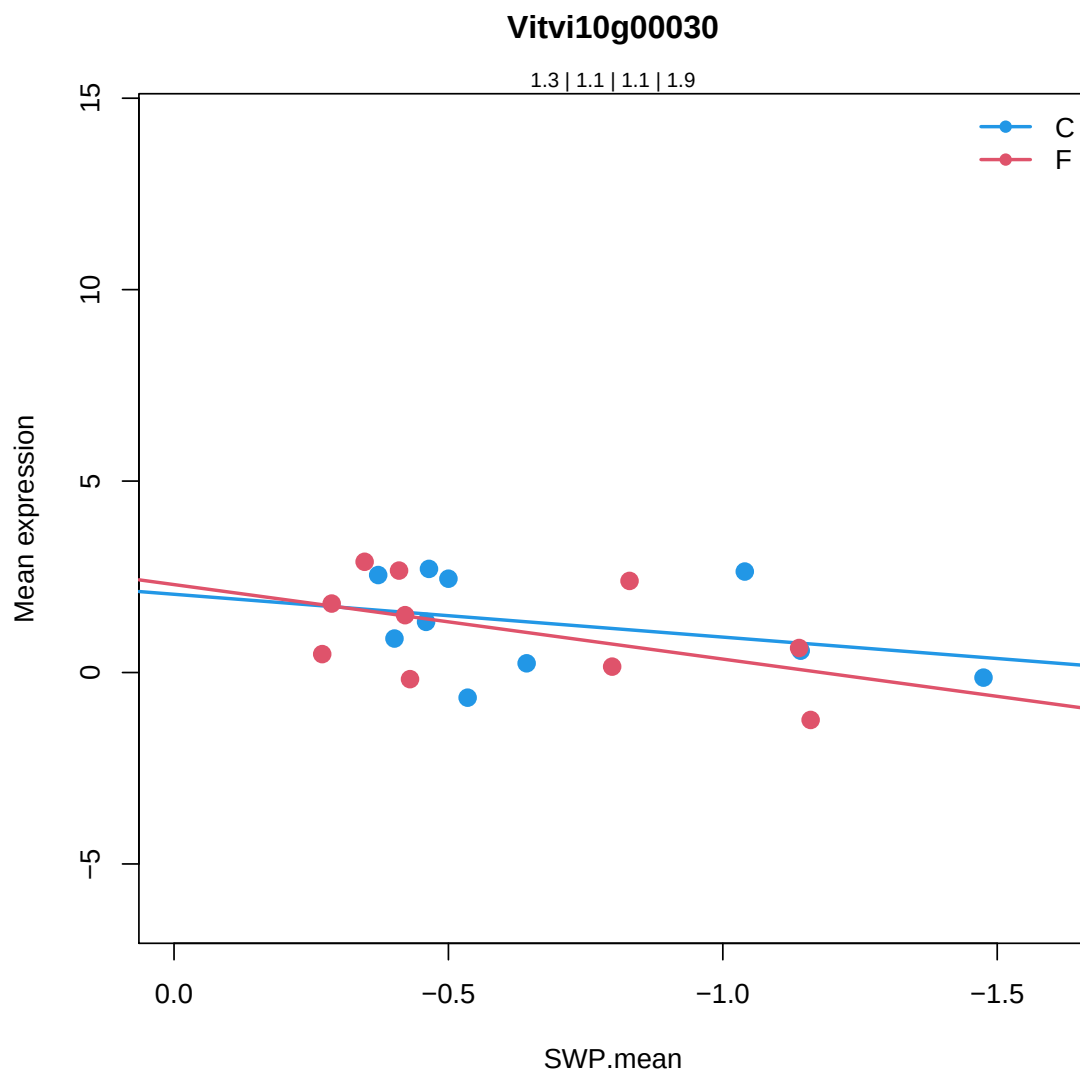
NTF2-like protein |

Chr1:3883280-3883663 FORWARD LENGTH=127 |

201606

Coefficients for Vitvi10g00030.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.256944	0.00175586	**	0.001890564	**
SlopeC	1.118878	0.2657234		0.7701943	
MeanF-MeanC	-0.1460935	0.7719256		0.9348236	
SlopeF-SlopeC	0.8269105	0.5762981		0.9999488	



8.1.233 Vitvi11g00838: Type1.0

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

Vitvi11g00838

27.3.99

RNA.regulation of transcription.unclassified

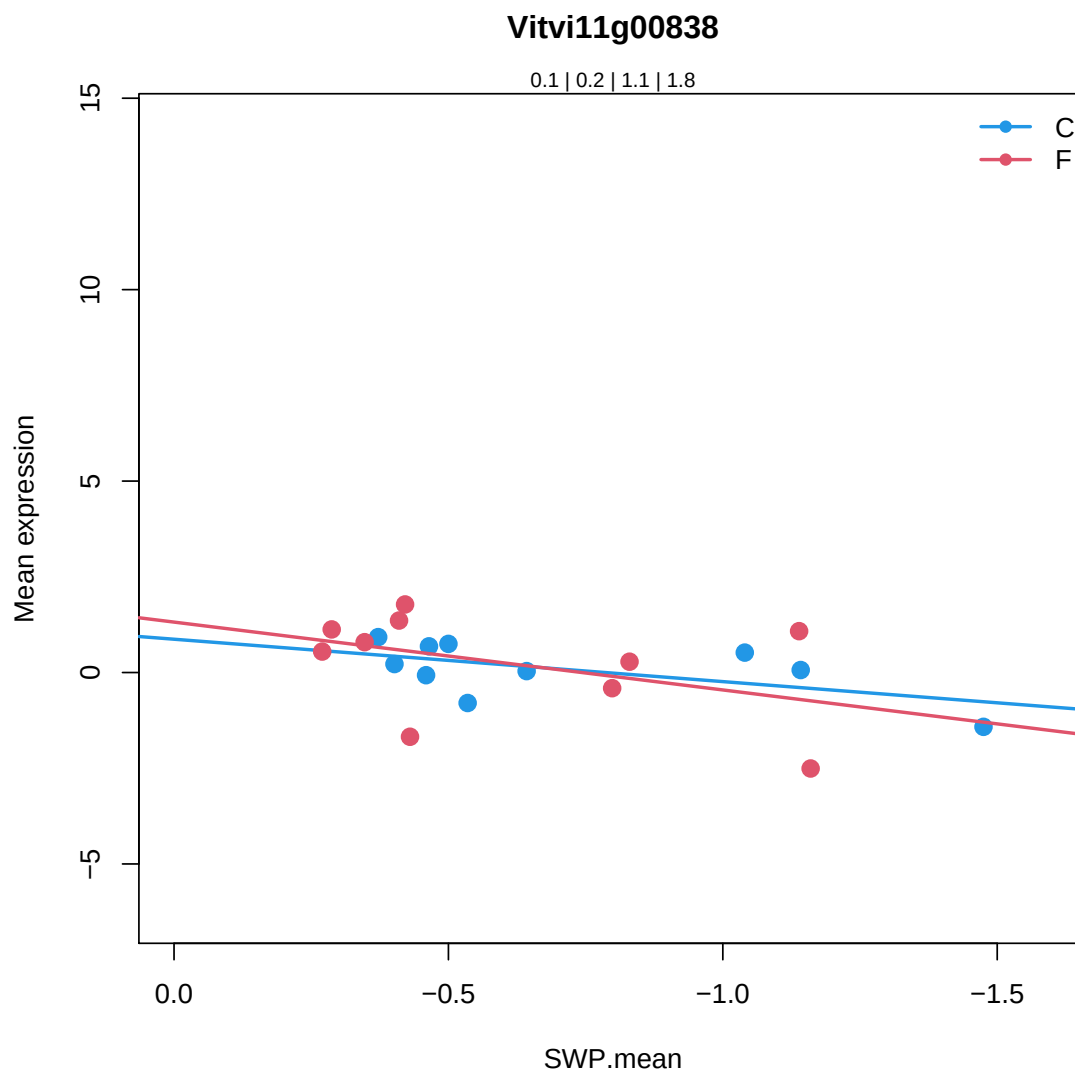
sequence-specific DNA binding transcription factor |

Chr4:14871309-14871851 REVERSE LENGTH=180 |

201606

Coefficients for Vitvi11g00838.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.09128743	0.7577569		0.7622579	
SlopeC	1.107109	0.1874038		0.7189549	
MeanF-MeanC	0.1455646	0.7280982		0.9177699	
SlopeF-SlopeC	0.6648361	0.588381		0.9999488	



8.1.234 Vitvi15g00429: Type1.0

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

Vitvi15g00429

35.2

not assigned.unknown

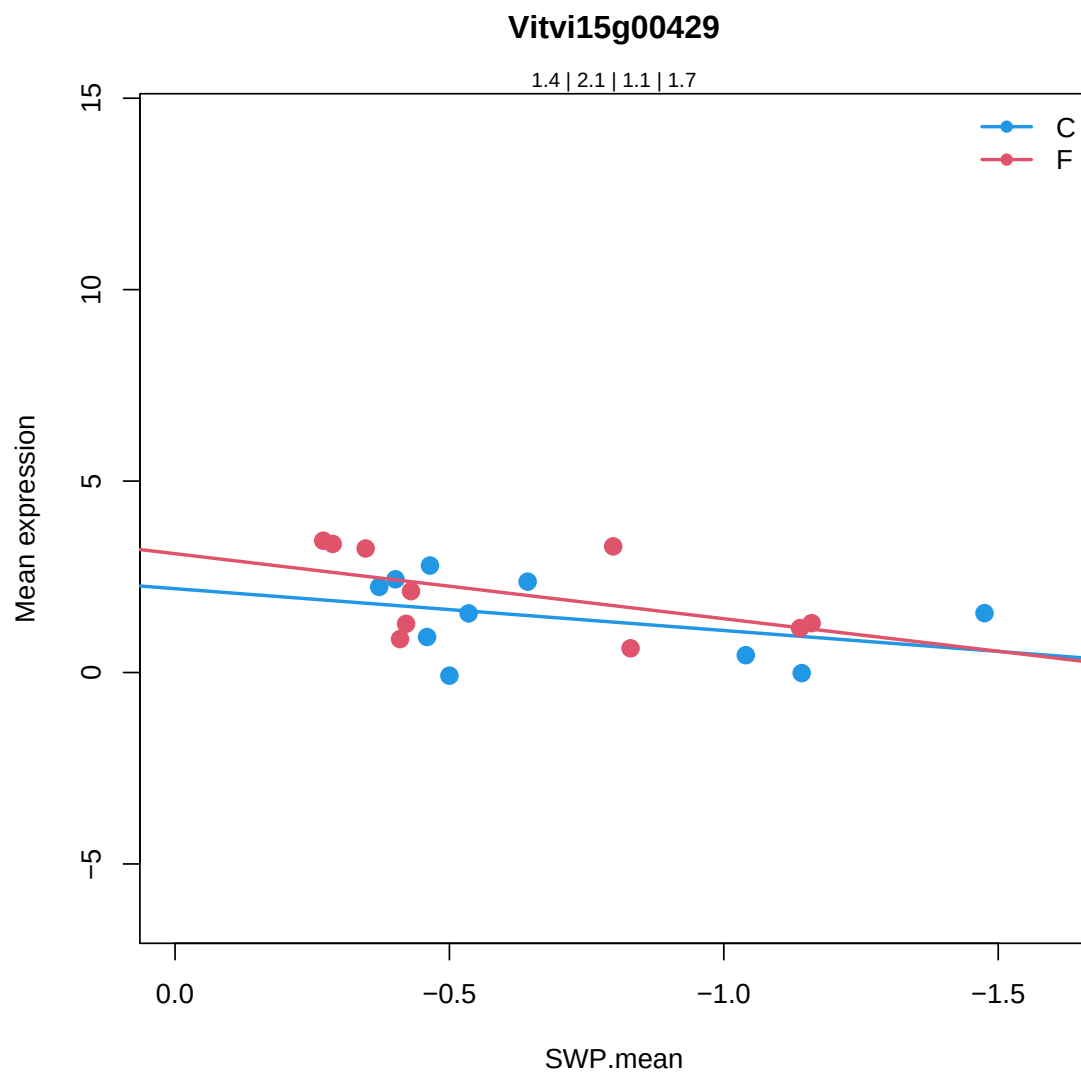
chloroplast ribosomal protein S14 |

ChrC:36938-37240 REVERSE LENGTH=100 |

201606

Coefficients for Vitvi15g00429.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.421475	8.856504e-05	***	9.788328e-05	***
SlopeC	1.092425	0.1976806		0.7250708	
MeanF-MeanC	0.6471251	0.1359553		0.4410877	
SlopeF-SlopeC	0.606105	0.6252371		0.9999488	



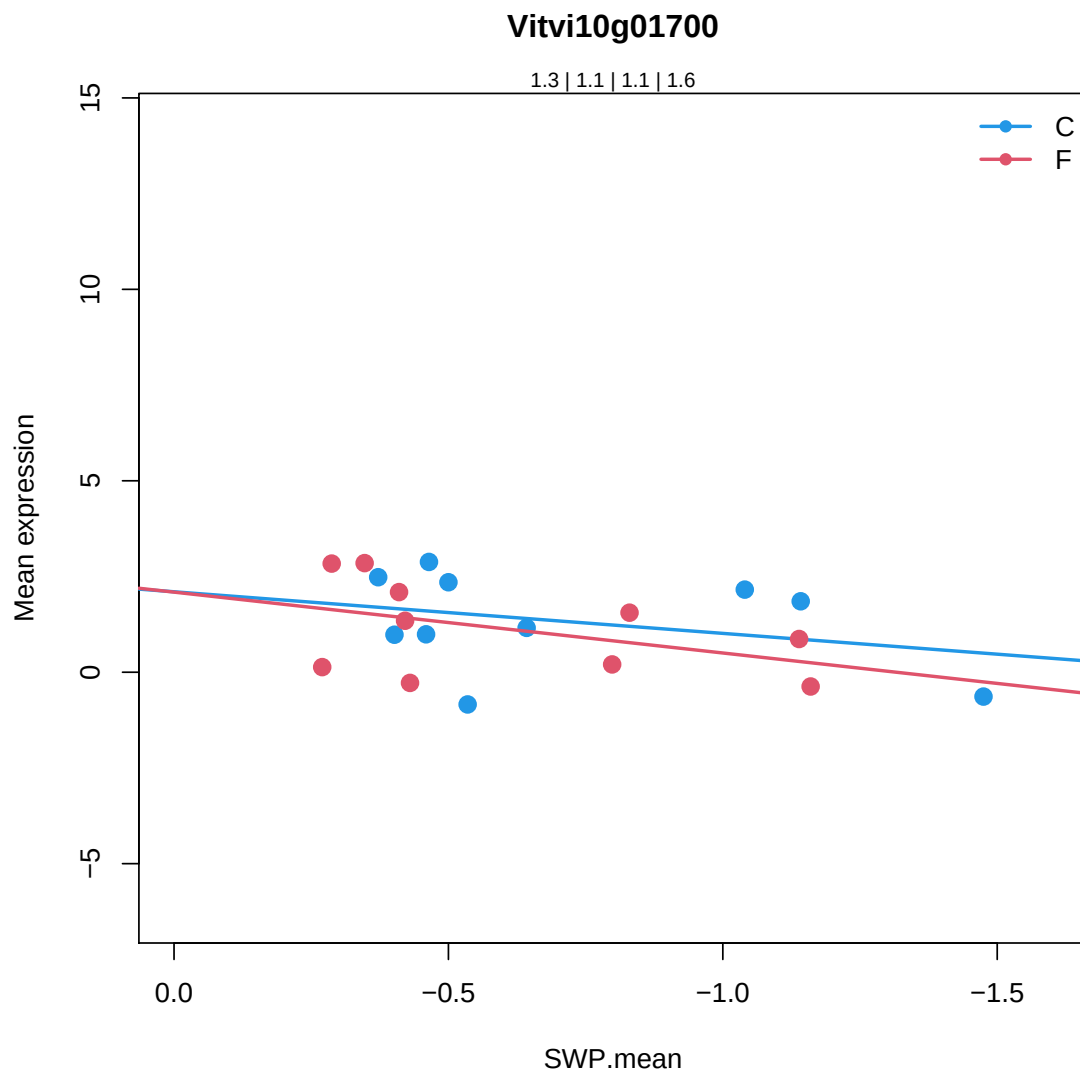
8.1.235 Vitvi10g01700: Type1.0

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

```
Vitvi10g01700
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi10g01700.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.33714	0.0007495182	***	0.0008139182	***
SlopeC	1.086546	0.2640545		0.7701943	
MeanF-MeanC	-0.2139433	0.6613008		0.8873544	
SlopeF-SlopeC	0.5032011	0.7246758		0.9999488	



8.1.236 Vitvi18g00757: Type1.0

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

Vitvi18g00757

27.3.22

RNA.regulation of transcription.homeobox transcription factor family (

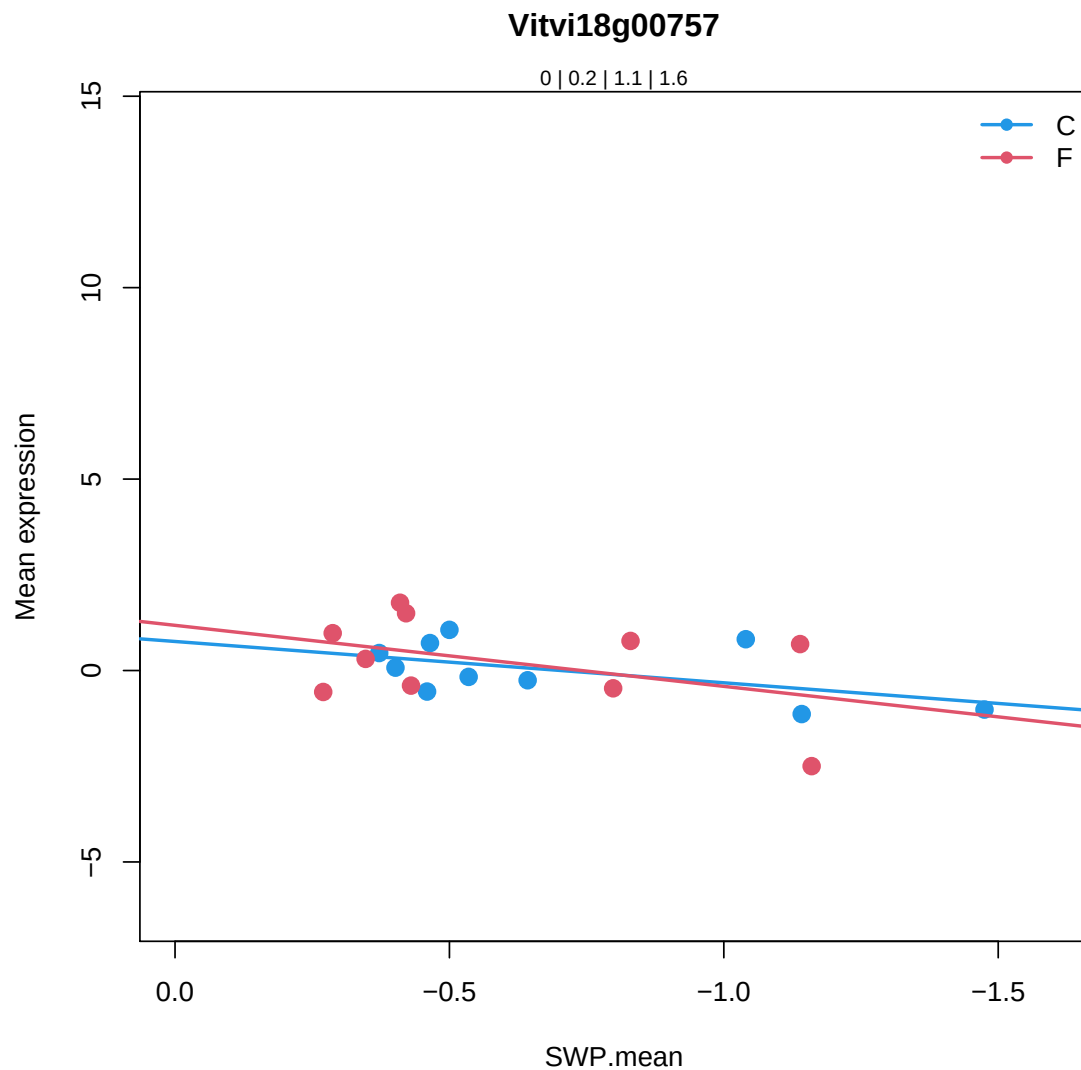
WUSCHEL related homeobox 4 |

Chr1:17237162-17237953 REVERSE LENGTH=190 |

201606

Coefficients for Vitvi18g00757.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-4.83948e-05	0.9998617		0.9998719	
SlopeC	1.079069	0.1741874		0.7069798	
MeanF-MeanC	0.2089792	0.5978166		0.8601581	
SlopeF-SlopeC	0.5144477	0.6570736		0.9999488	



8.1.237 Vitvi09g01499: Type1.0

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

Vitvi09g01499

1.2.2

PS.photorespiration.glycolate oxydase

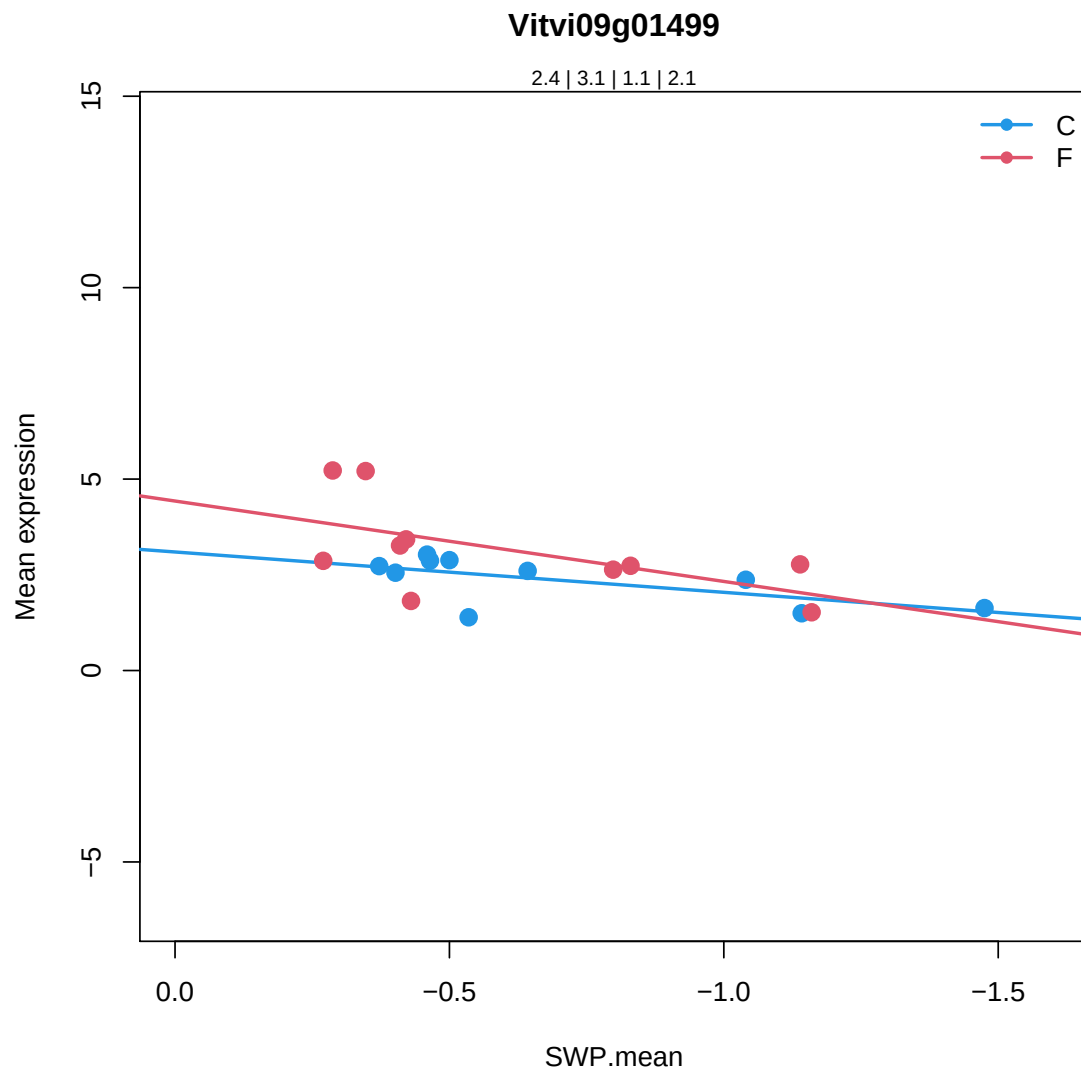
Aldolase-type TIM barrel family protein |

Chr3:4690667-4692679 REVERSE LENGTH=363 |

201606

Coefficients for Vitvi09g01499.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.354812	2.179061e-09	***	2.717497e-09	***
SlopeC	1.053663	0.1290226		0.6505958	
MeanF-MeanC	0.791984	0.0293583	*	0.166411	
SlopeF-SlopeC	1.046397	0.3038675		0.9999488	



8.1.238 Vitvi01g01796: Type1.0

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

Vitvi01g01796

27.3.99

RNA.regulation of transcription.unclassified

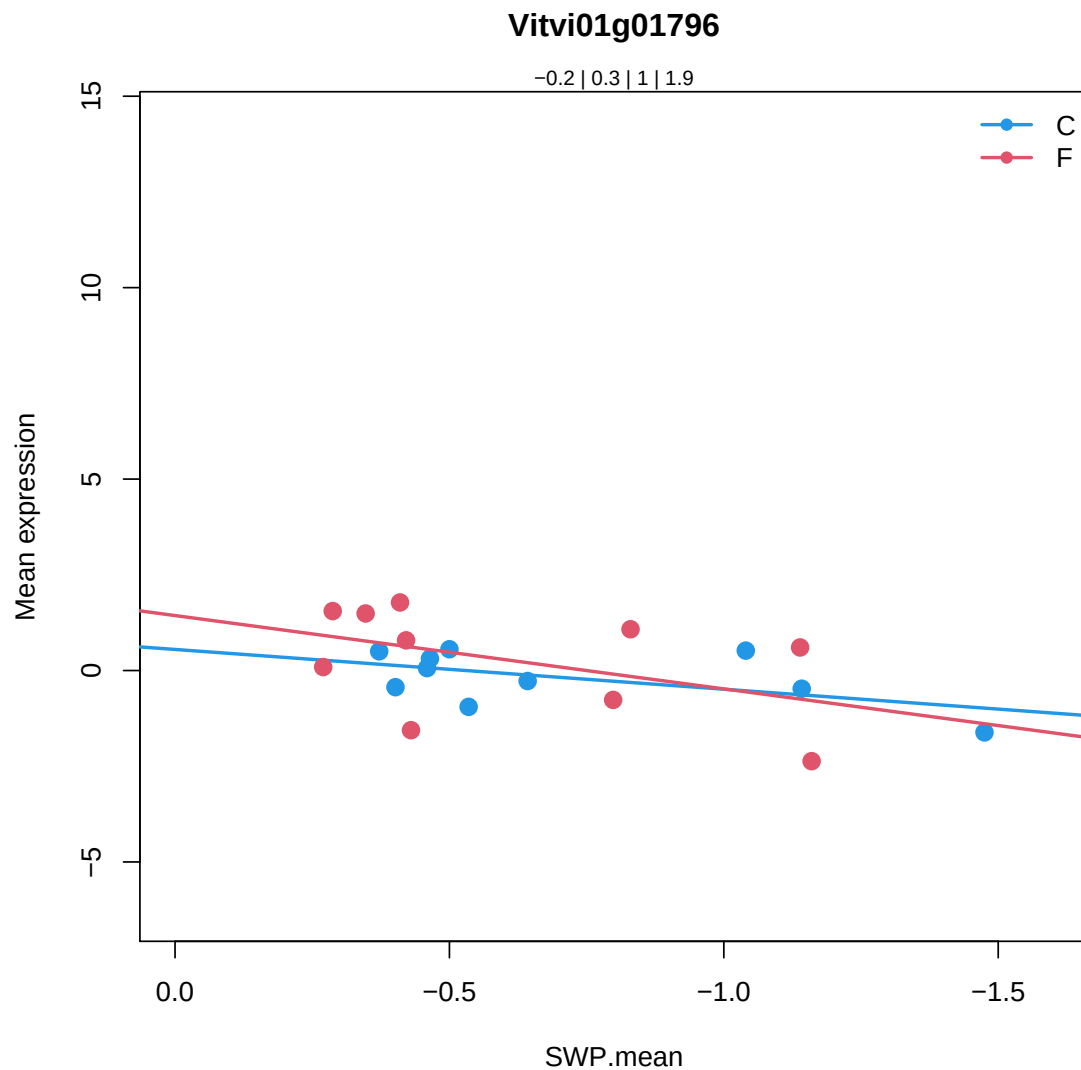
DHHC-type zinc finger family protein |

Chr3:9933001-9935218 REVERSE LENGTH=443 |

201606

Coefficients for Vitvi01g01796.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.1800098	0.5461188		0.551949	
SlopeC	1.038521	0.2170585		0.7389959	
MeanF-MeanC	0.4483911	0.2920256		0.6580505	
SlopeF-SlopeC	0.8764992	0.4785828		0.9999488	



8.1.239 Vitvi14g01525: Type1.0

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

Vitvi14g01525

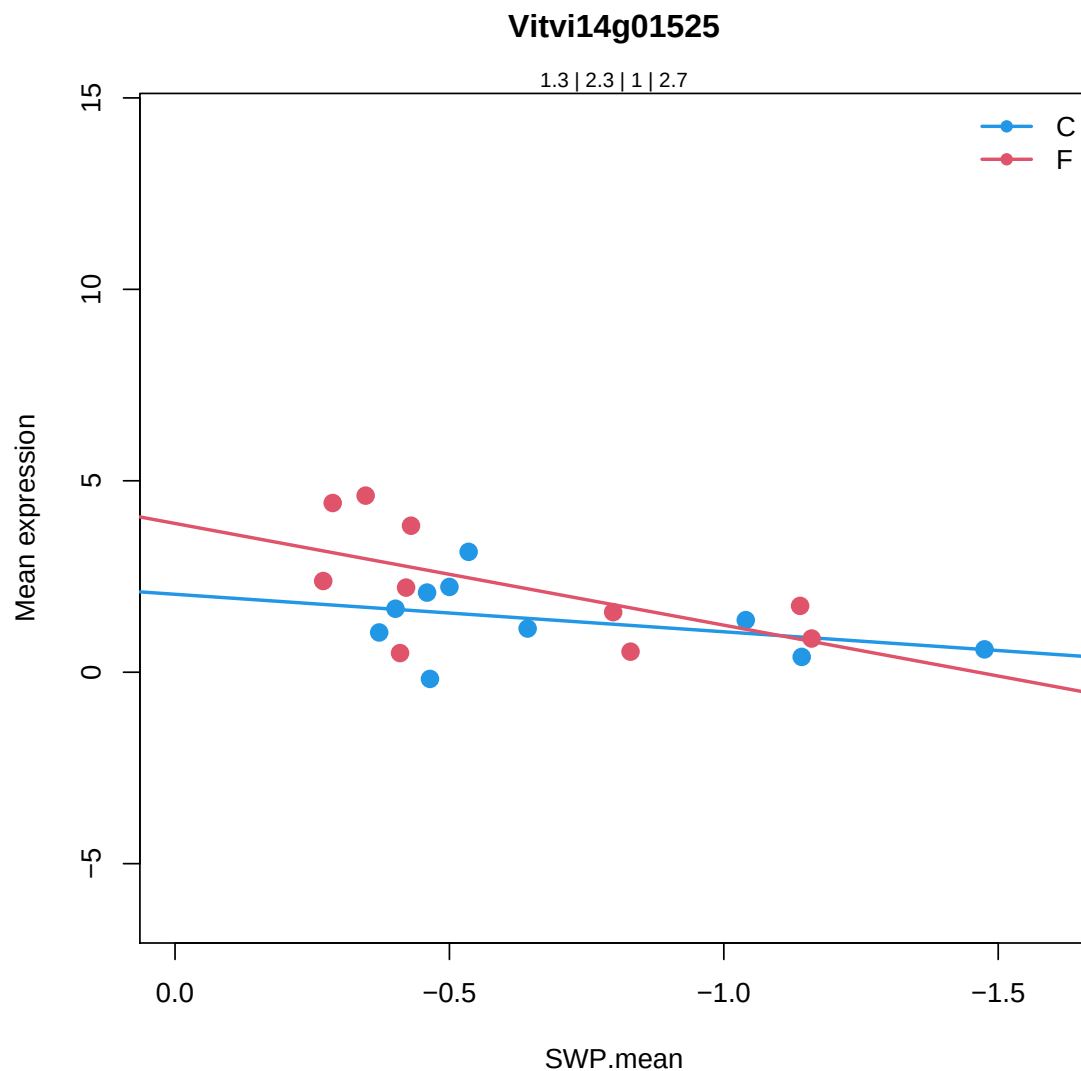
35.2

not assigned.unknown

Unknown Protein

Coefficients for Vitvi14g01525.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.347055	0.0004296441	***	0.00046863	***
SlopeC	0.9798375	0.2891099		0.7809644	
MeanF-MeanC	0.9198305	0.05747086	.	0.261172	
SlopeF-SlopeC	1.676665	0.2248785		0.9999488	



8.1.240 Vitvi05g01945: Type1.0

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

Vitvi05g01945

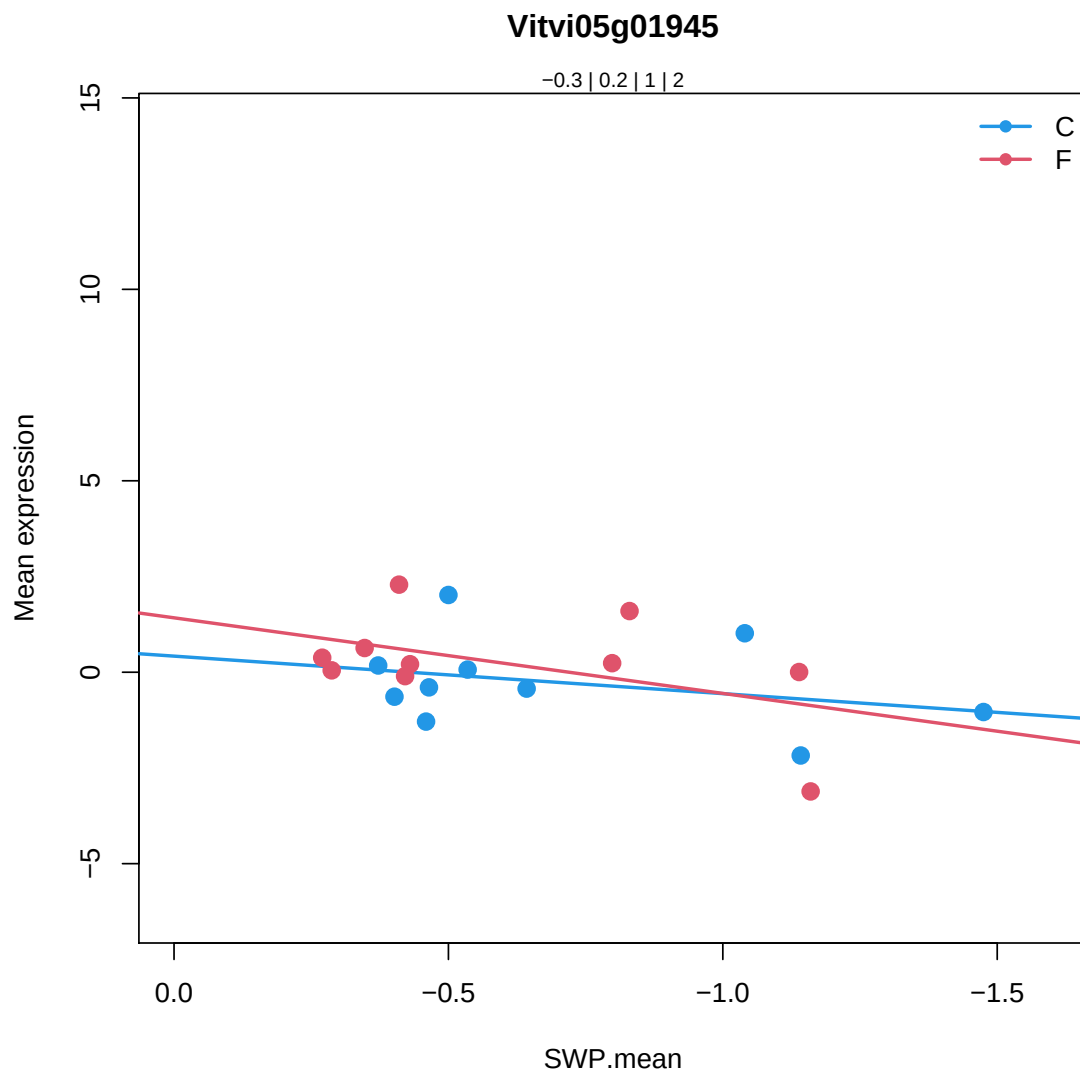
35.2

not assigned.unknown

NA

Coefficients for Vitvi05g01945.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.268782	0.4505569		0.456669	
SlopeC	0.979546	0.3252991		0.7999692	
MeanF-MeanC	0.4866703	0.3361075		0.695595	
SlopeF-SlopeC	0.9945871	0.4995882		0.9999488	



8.1.241 Vitvi17g00906: Type1.0

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

Vitvi17g00906

35.1

not assigned.no ontology

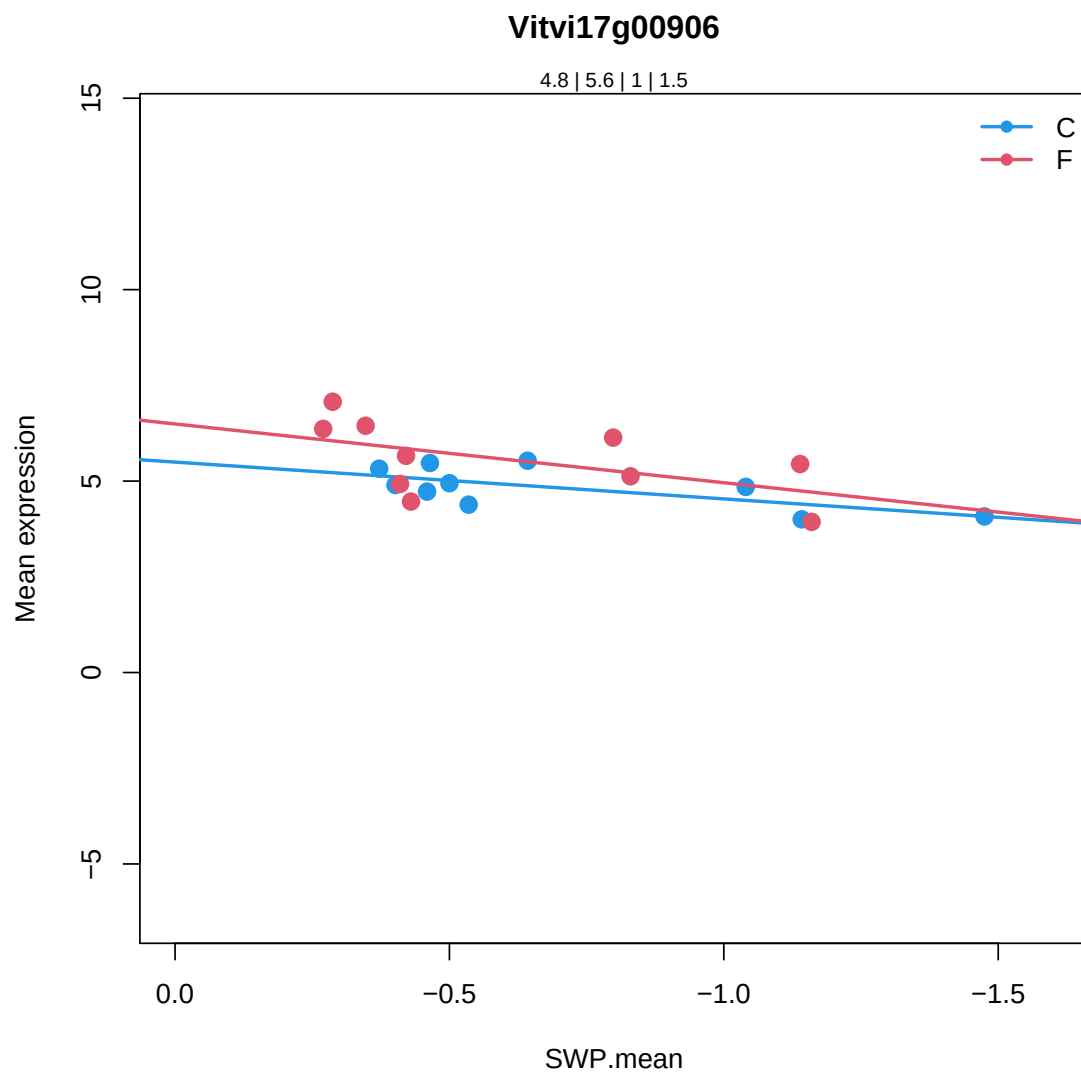
Octicosapeptide/Phox/Bemlp family protein |

Chr3:9711886-9712588 REVERSE LENGTH=196 |

201606

Coefficients for Vitvi17g00906.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.820205	6.263717e-17	***	1.41251e-16	***
SlopeC	0.9614251	0.1015215		0.6135572	
MeanF-MeanC	0.7370332	0.01727985	*	0.1130384	
SlopeF-SlopeC	0.5729909	0.5006183		0.9999488	



8.1.242 Vitvi17g00046: Type1.0

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

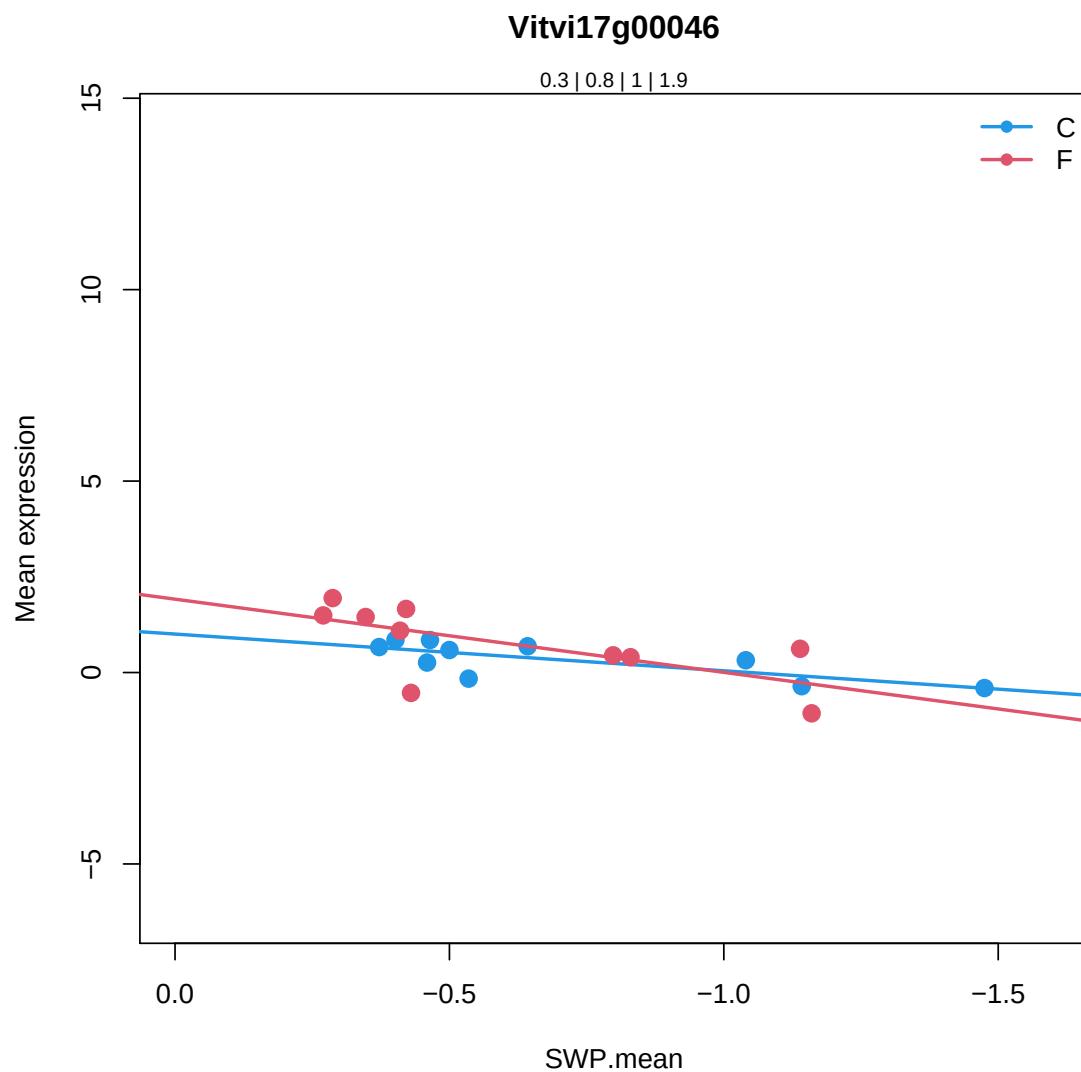
Vitvi17g00046

27.3.6

RNA.regulation of transcription.basic helix-loop-helix family (bHLH)
basic helix-loop-helix (bHLH) DNA-binding superfamily protein |
Chr5:20710936-20712252 REVERSE LENGTH=268 |
201606

Coefficients for Vitvi17g00046.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3297109	0.0804075	.	0.08333251	.
SlopeC	0.9597241	0.06826792	.	0.5569429	
MeanF-MeanC	0.4211883	0.1119582		0.390764	
SlopeF-SlopeC	0.9519066	0.2144112		0.9999488	



8.1.243 Vitvi07g01698: Type1.0

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

Vitvi07g01698

30.2.3

signalling.receptor kinases.leucine rich repeat III

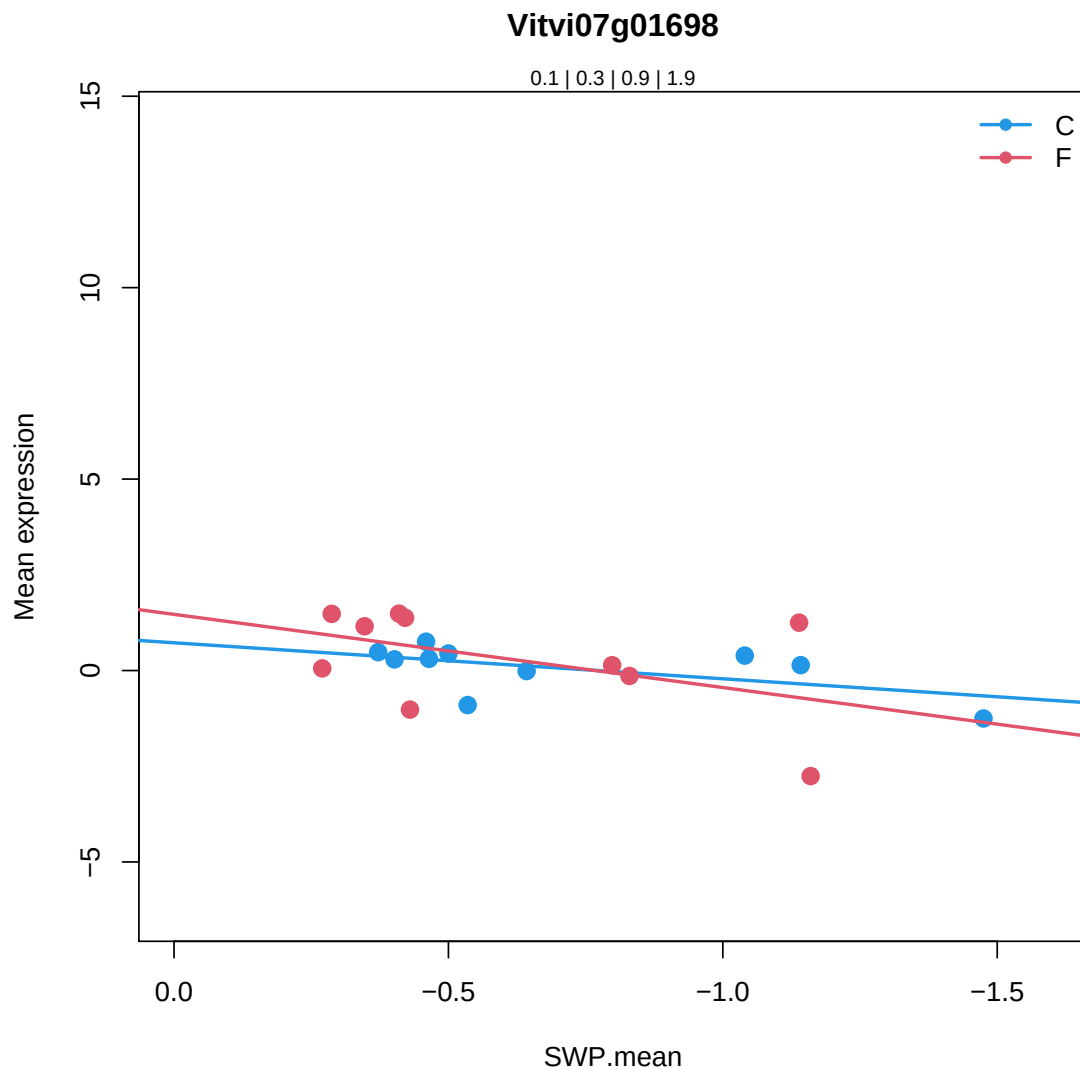
Leucine-rich repeat protein kinase family protein |

Chr5:26813893-26816555 REVERSE LENGTH=669 |

201606

Coefficients for Vitvi07g01698.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.06337883	0.8237086		0.8272364	
SlopeC	0.9400718	0.2423406		0.7560552	
MeanF-MeanC	0.2386271	0.5545247		0.8359309	
SlopeF-SlopeC	0.9711072	0.4132045		0.9999488	



8.1.244 Vitvi12g02440: Type1.0

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

Vitvi12g02440

29.4

protein.postranslational modification

G-type lectin S-receptor-like Serine/Threonine-kinase |

Chr4:1419278-1422719 REVERSE LENGTH=910 |

201606

Vitvi12g02440

30.2.24

signalling.receptor kinases.S-locus glycoprotein like

G-type lectin S-receptor-like Serine/Threonine-kinase |

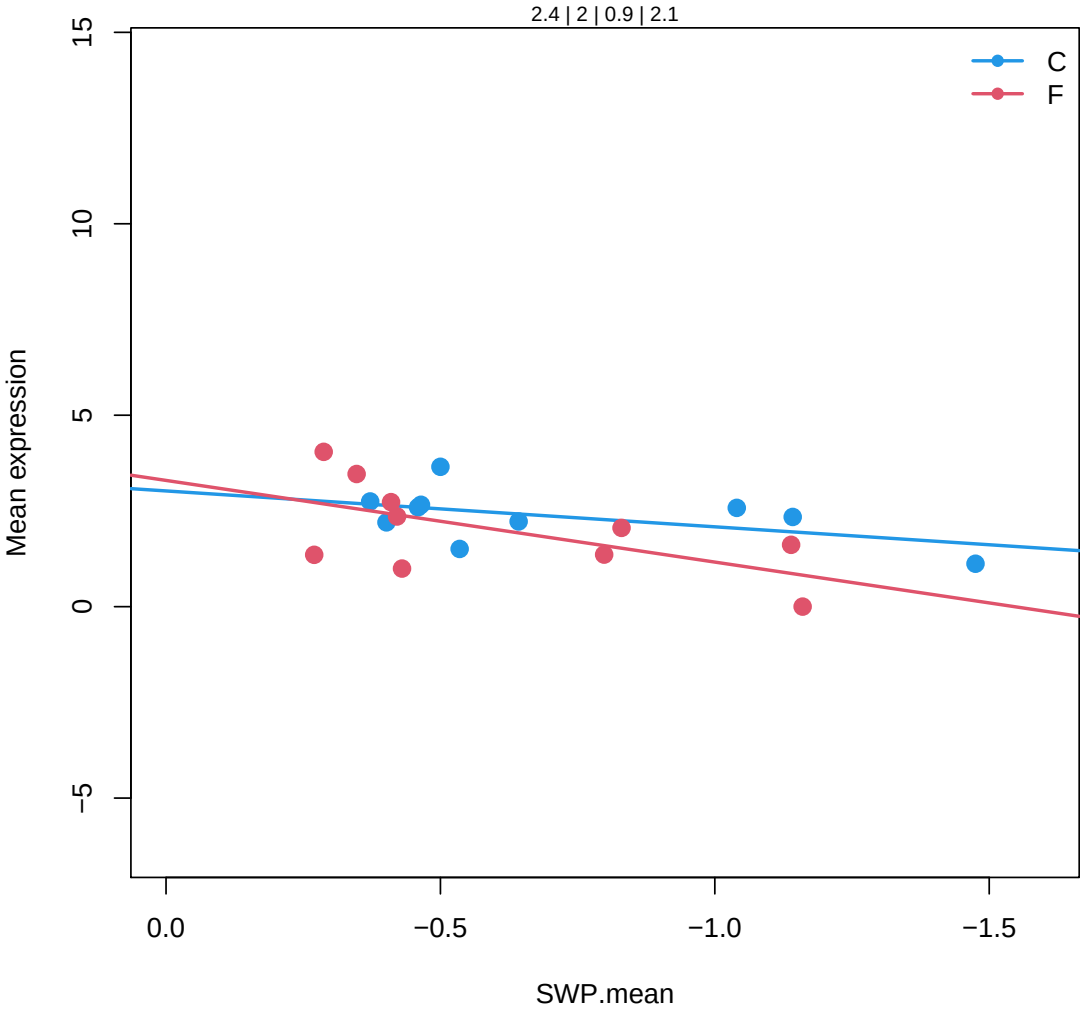
Chr4:1419278-1422719 REVERSE LENGTH=910 |

201606

Coefficients for Vitvi12g02440.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.363208	2.501224e-09	***	3.113406e-09	***
SlopeC	0.9369838	0.1793591		0.711889	
MeanF-MeanC	-0.3658604	0.2981584		0.6646965	
SlopeF-SlopeC	1.196179	0.2468152		0.9999488	

Vitvi12g02440



8.1.245 Vitvi16g00350: Type1.0

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

Vitvi16g00350

17.5.2

hormone metabolism.ethylene.signal transduction

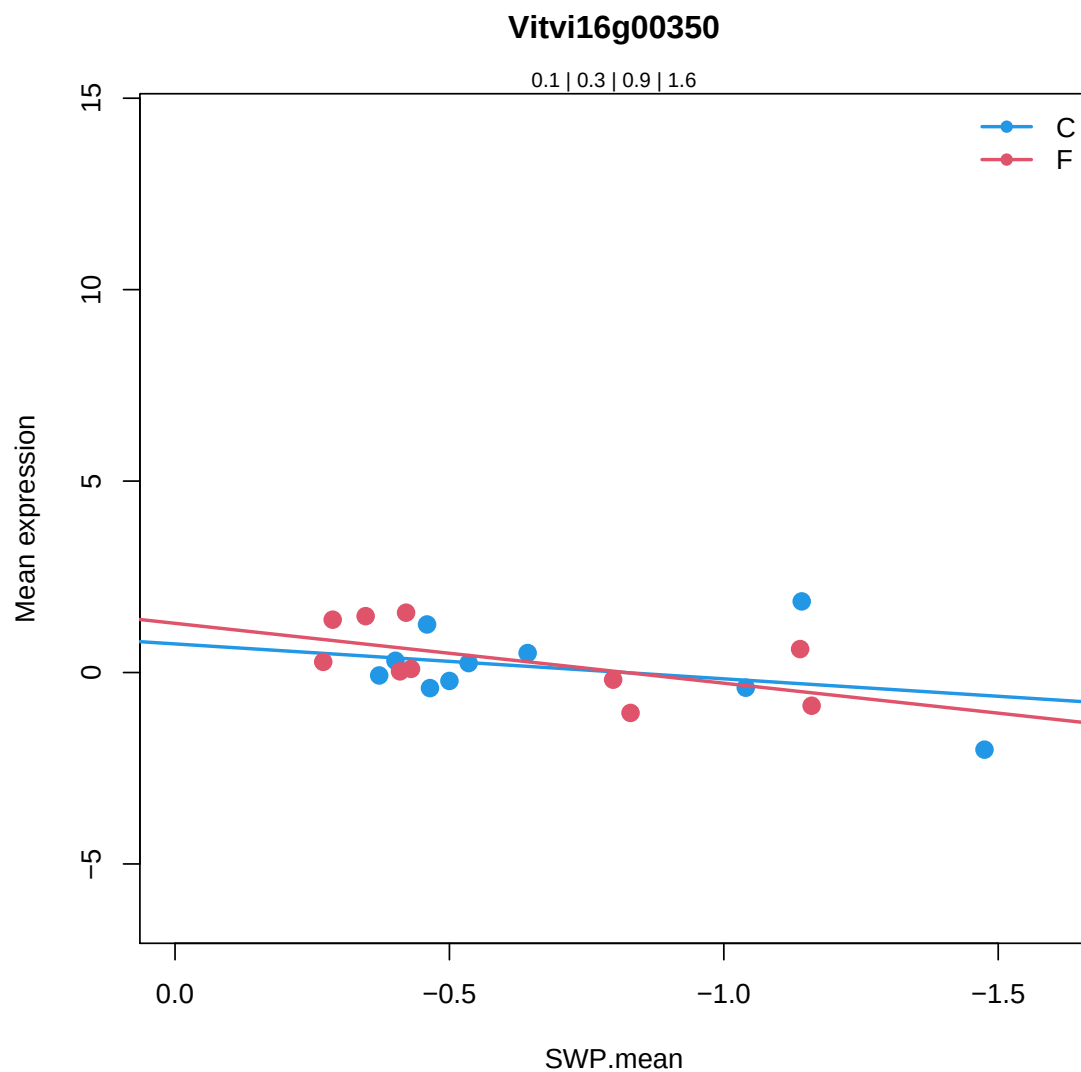
Integrase-type DNA-binding superfamily protein |

Chr5:20800708-20801373 REVERSE LENGTH=221 |

201606

Coefficients for Vitvi16g00350.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1057739	0.6948271		0.6995544	
SlopeC	0.9116913	0.2313204		0.7493698	
MeanF-MeanC	0.2260283	0.5542459		0.8358382	
SlopeF-SlopeC	0.6525092	0.5597857		0.9999488	



8.1.246 Vitvi01g01071: Type1.0

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

Vitvi01g01071

34.7

transport.phosphate

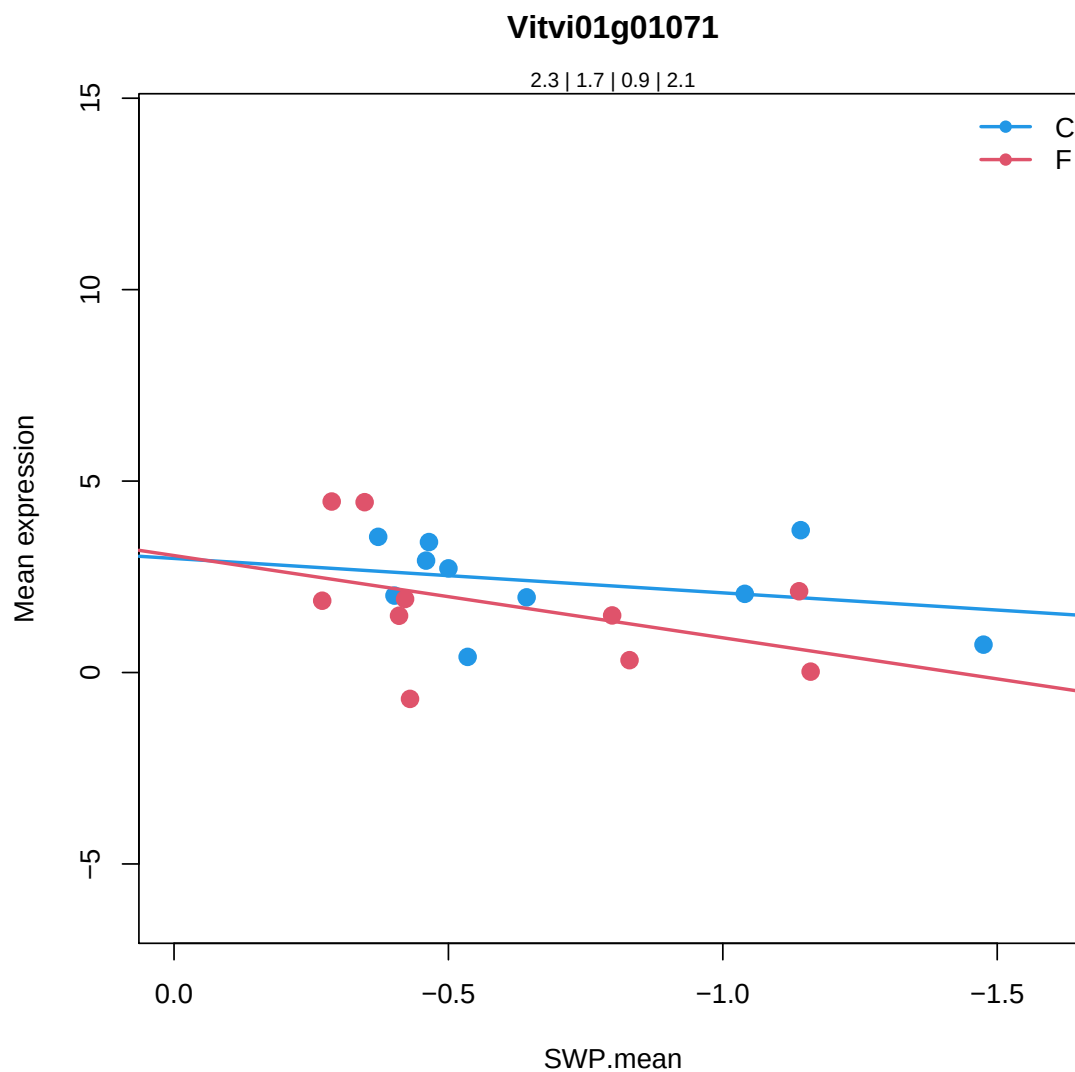
EXS (ERD1/XPR1/SYG1) family protein |

Chr1:9241435-9244325 FORWARD LENGTH=700 |

201606

Coefficients for Vitvi01g01071.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.347276	5.564051e-06	***	6.317585e-06	***
SlopeC	0.8985644	0.4190061		0.8427244	
MeanF-MeanC	-0.601019	0.2902905		0.6556916	
SlopeF-SlopeC	1.249171	0.4499044		0.9999488	



8.1.247 Vitvi04g01389: Type1.0

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

Vitvi04g01389

26.3.2

misc.gluco-, galacto- and mannosidases.beta-galactosidase

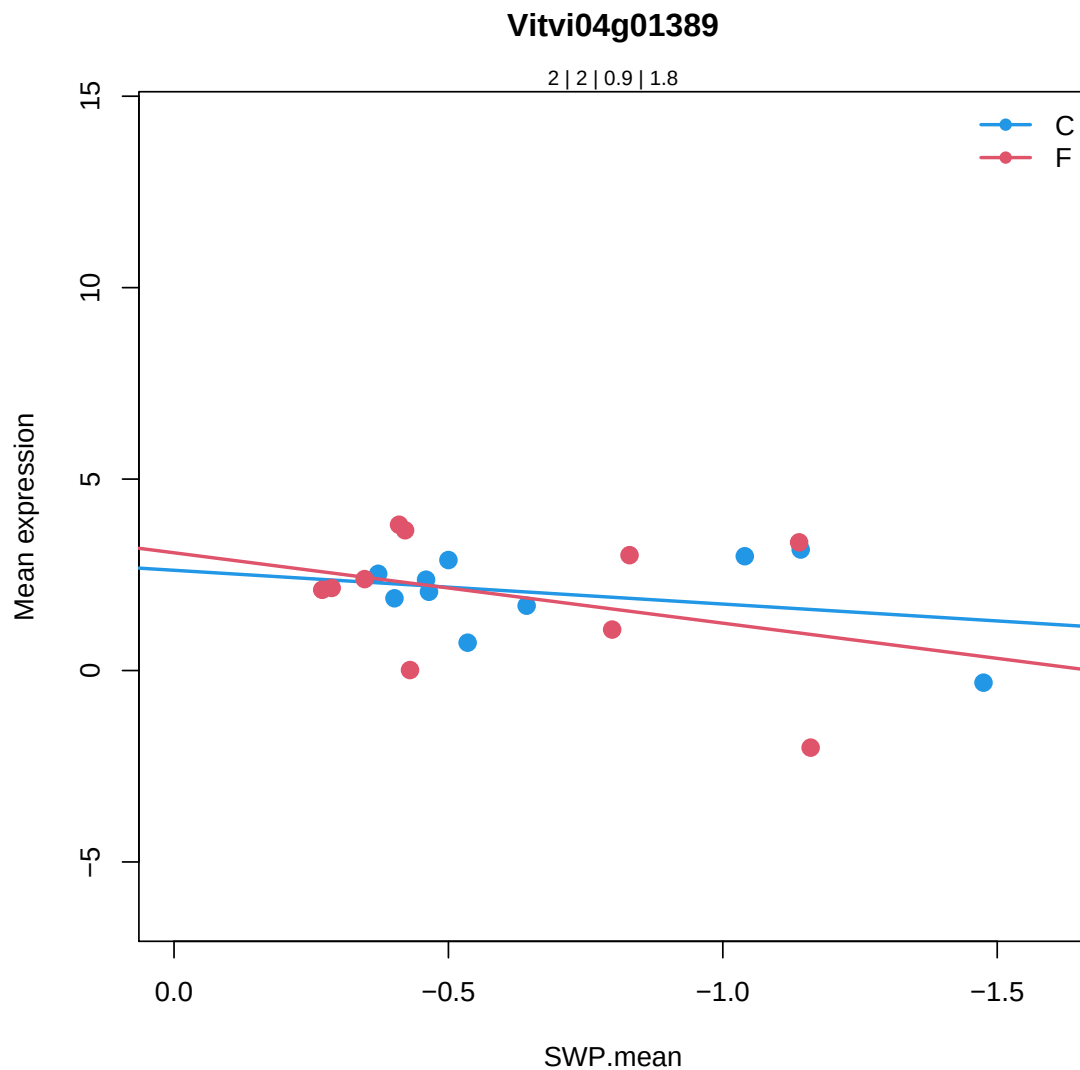
beta-galactosidase 3 |

Chr4:17176840-17181143 REVERSE LENGTH=856 |

201606

Coefficients for Vitvi04g01389.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.997471	9.359027e-05	***	0.0001033848	***
SlopeC	0.8818588	0.455494		0.8579805	
MeanF-MeanC	-0.04249229	0.9432314		0.9853726	
SlopeF-SlopeC	0.9567788	0.5852768		0.9999488	



8.1.248 Vitvi07g00515: Type1.0

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

Vitvi07g00515

27.3.25

RNA.regulation of transcription.MYB domain transcription factor family

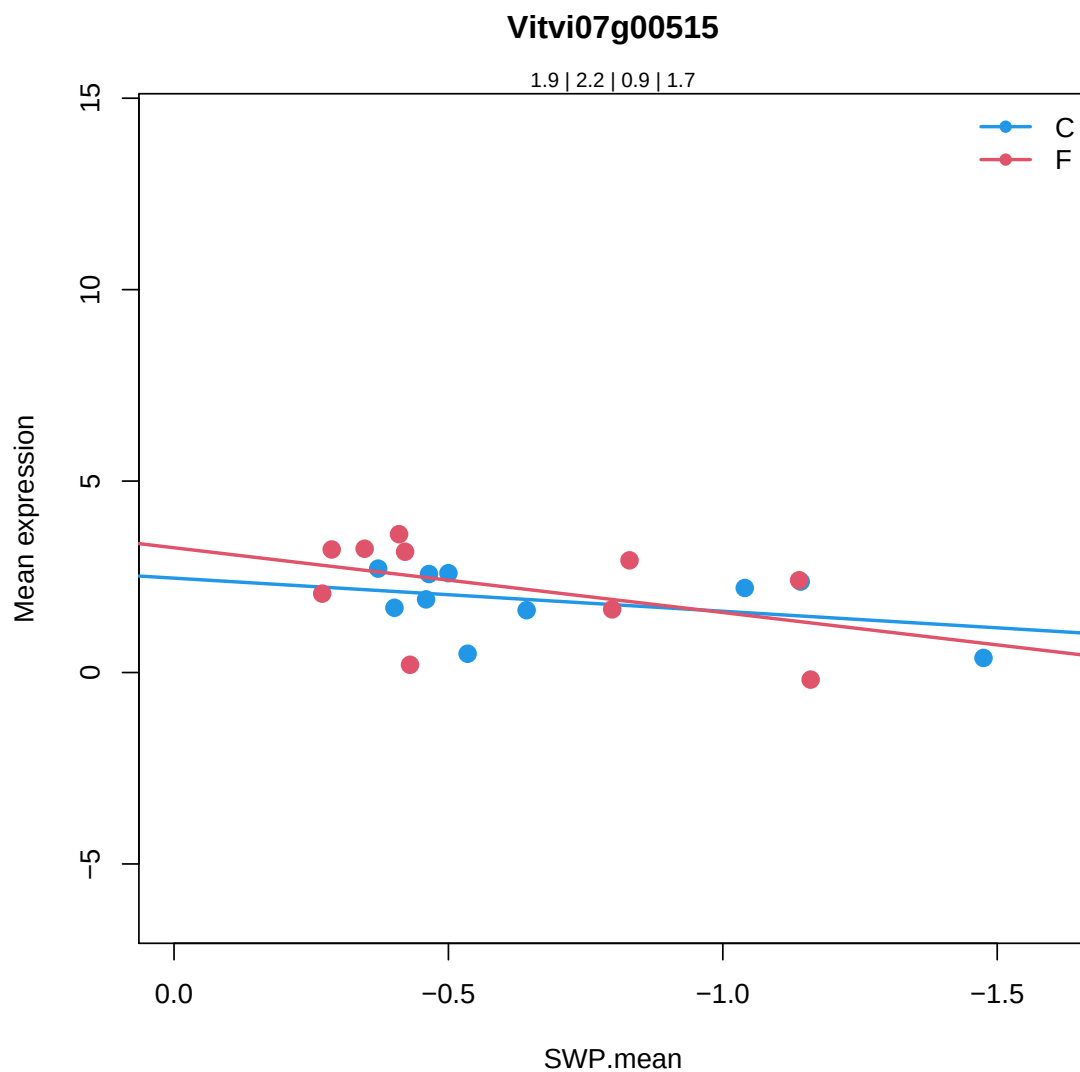
myb domain protein 61 |

Chr1:3086333-3087689 FORWARD LENGTH=366 |

201606

Coefficients for Vitvi07g00515.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.856286	3.394417e-06	***	3.871423e-06	***
SlopeC	0.8650731	0.3102055		0.7925436	
MeanF-MeanC	0.371641	0.3894456		0.7378593	
SlopeF-SlopeC	0.8262021	0.5119142		0.9999488	



8.1.249 Vitvi18g02581: Type1.0

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

Vitvi18g02581

26.2

misc.UDP glucosyl and glucoronyl transferases

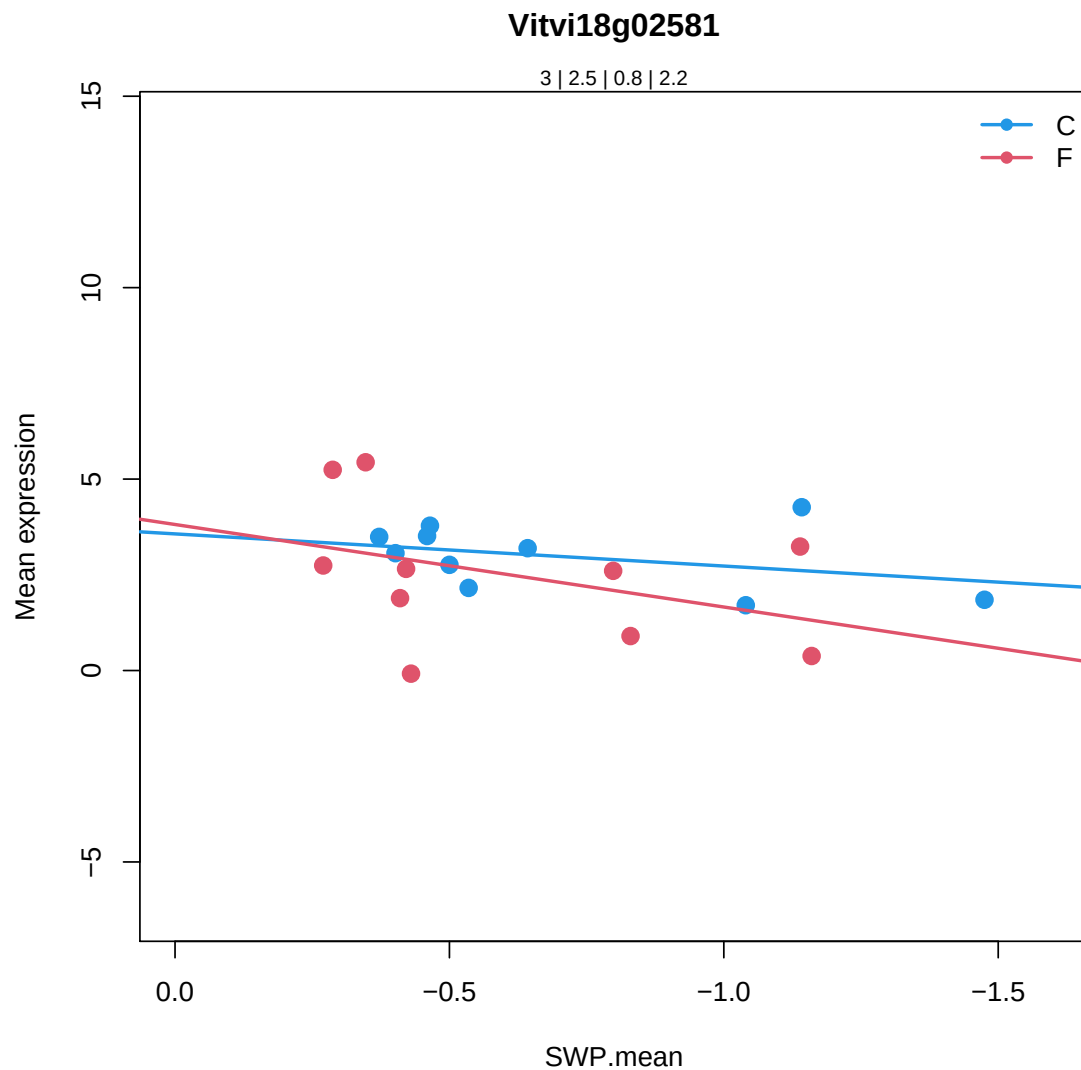
UDP-glucosyl transferase 85A2 |

Chr1:7895068-7897527 REVERSE LENGTH=481 |

201606

Coefficients for Vitvi18g02581.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.977955	1.600602e-07	***	1.888265e-07	***
SlopeC	0.8399546	0.4490865		0.8555685	
MeanF-MeanC	-0.4772917	0.3982571		0.7439014	
SlopeF-SlopeC	1.315211	0.4261783		0.9999488	



8.1.250 Vitvi15g00526: Type1.0

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

Vitvi15g00526

35.2

not assigned.unknown

RAC-like 9 |

Chr2:18429276-18430636 FORWARD LENGTH=209 |

201606

Vitvi15g00526

30.5

signalling.G-proteins

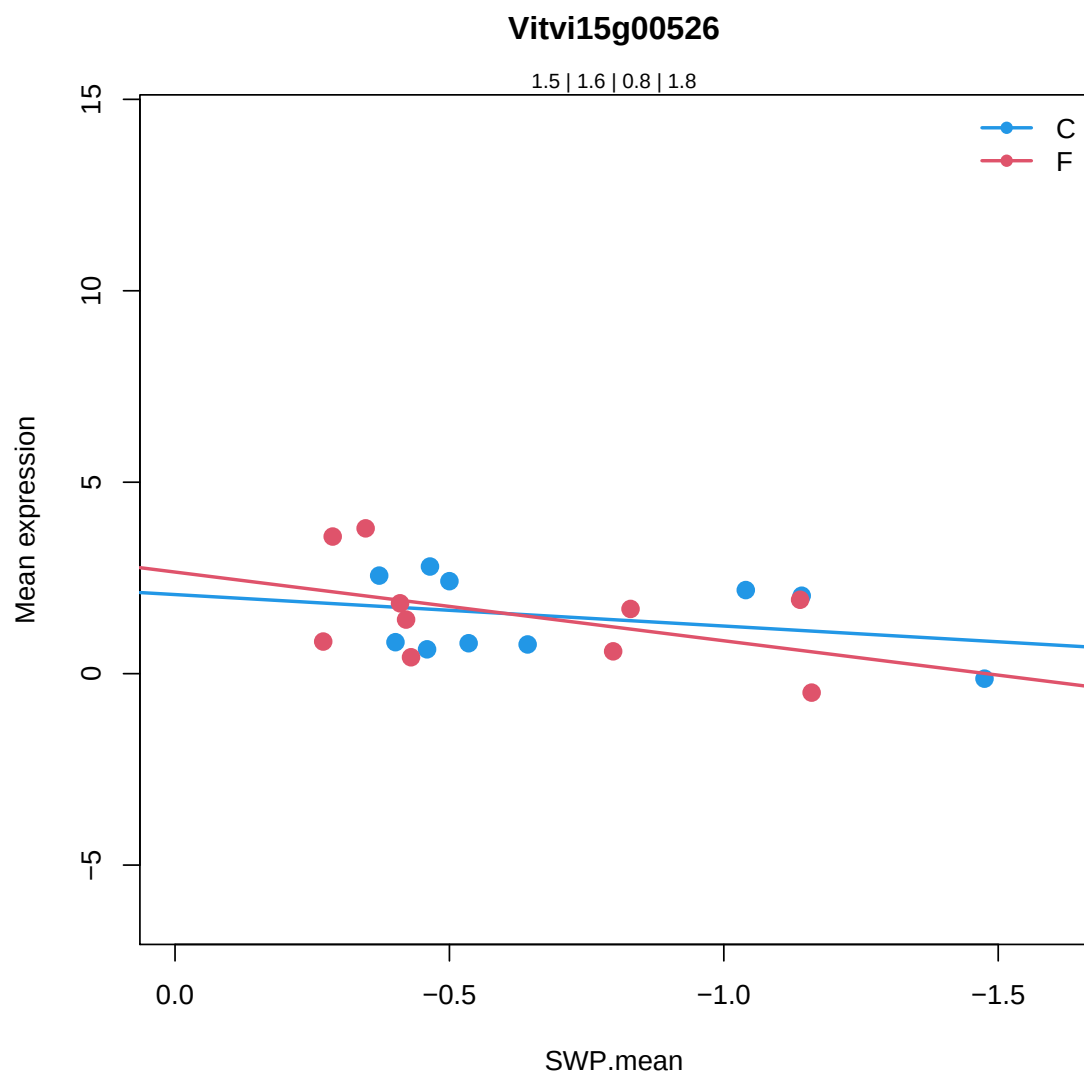
RAC-like 9 |

Chr2:18429276-18430636 FORWARD LENGTH=209 |

201606

Coefficients for Vitvi15g00526.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.487387	0.0001555967	***	0.0001711733	***
SlopeC	0.8221935	0.3731104		0.8234798	
MeanF-MeanC	0.07256401	0.8759819		0.9674455	
SlopeF-SlopeC	0.9724678	0.4775597		0.9999488	



8.1.251 Vitvi18g02476: Type1.0

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

Vitvi18g02476

16.8.3.1

secondary metabolism.flavonoids.dihydroflavonols.dihydroflavonol 4-red

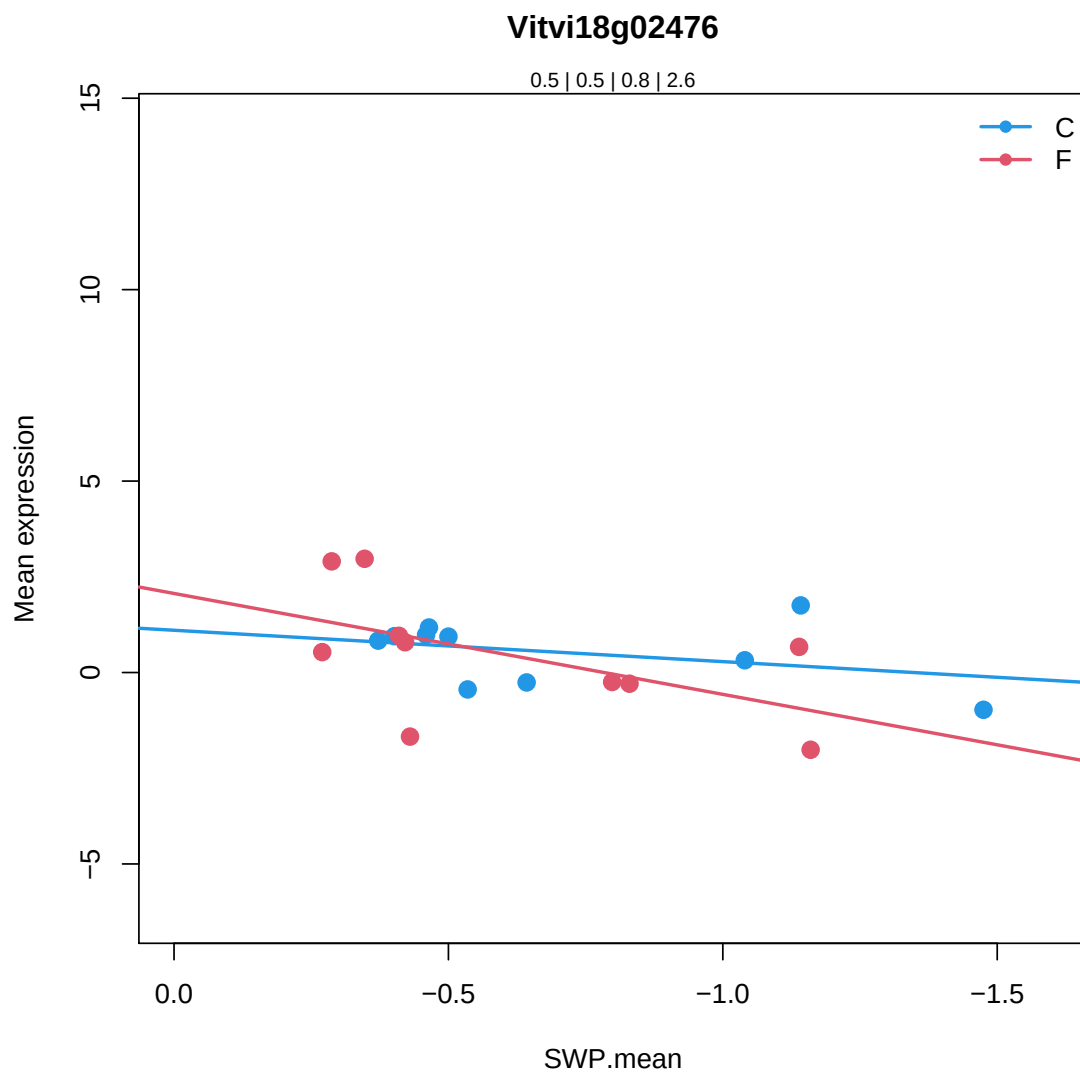
NAD(P)-binding Rossmann-fold superfamily protein |

Chr2:14224622-14226365 FORWARD LENGTH=321 |

201606

Coefficients for Vitvi18g02476.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.5275177	0.1288808		0.1329094	
SlopeC	0.8189022	0.387939		0.8295407	
MeanF-MeanC	-0.06826584	0.8864345		0.9704088	
SlopeF-SlopeC	1.816103	0.203017		0.9999488	



8.1.252 Vitvi14g03084: Type1.0

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

Vitvi14g03084

17.6.3

hormone metabolism.gibberelin.induced-regulated-responsive-activated

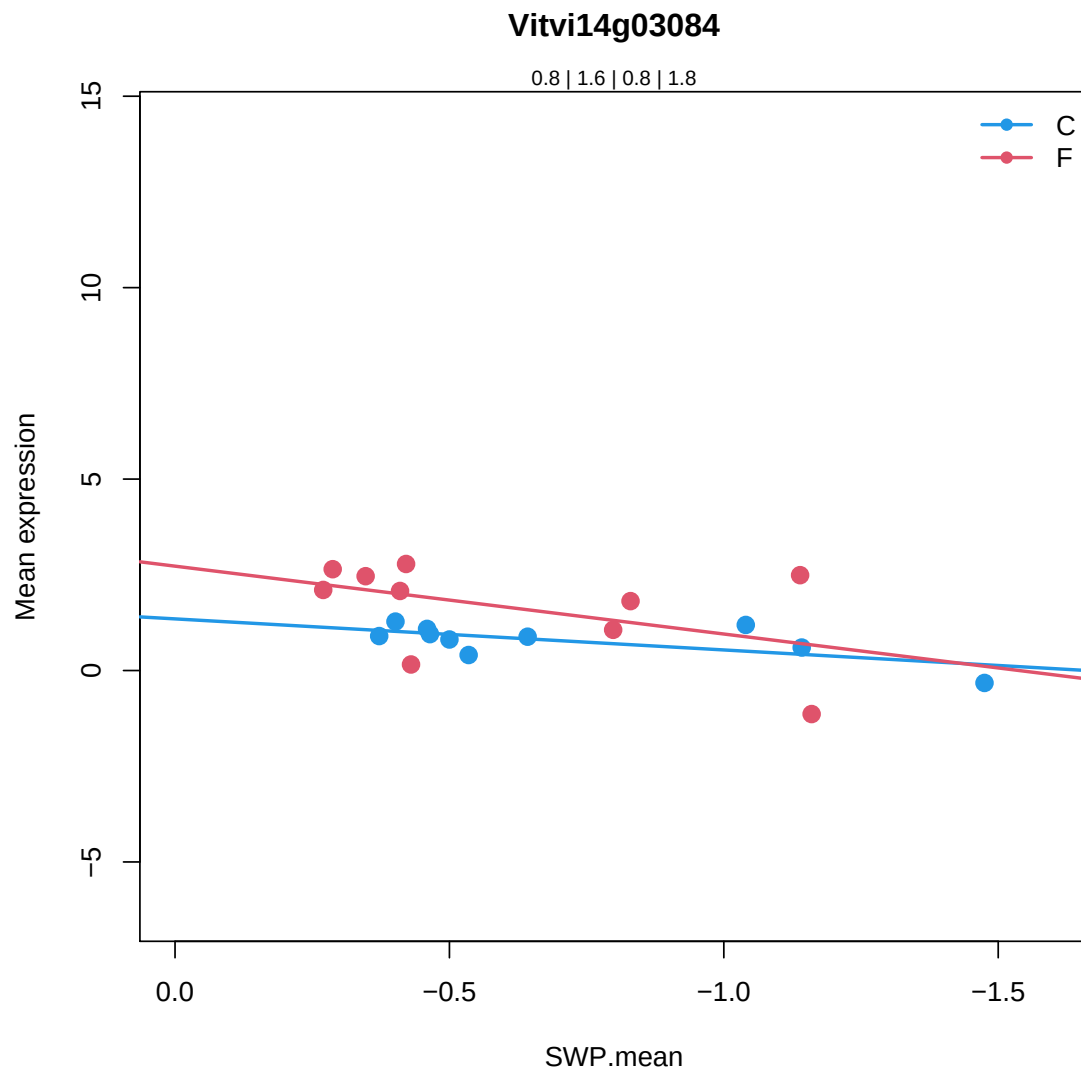
GAST1 protein homolog 4 |

Chr5:4945017-4946025 FORWARD LENGTH=106 |

201606

Coefficients for Vitvi14g03084.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.7778319	0.005297618	**	0.00564541	**
SlopeC	0.8111778	0.2575737		0.7667562	
MeanF-MeanC	0.8681824	0.02299767	*	0.1398765	
SlopeF-SlopeC	0.9612854	0.3647228		0.9999488	



8.1.253 Vitvi18g02636: Type1.0

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

Vitvi18g02636

35.2

not assigned.unknown

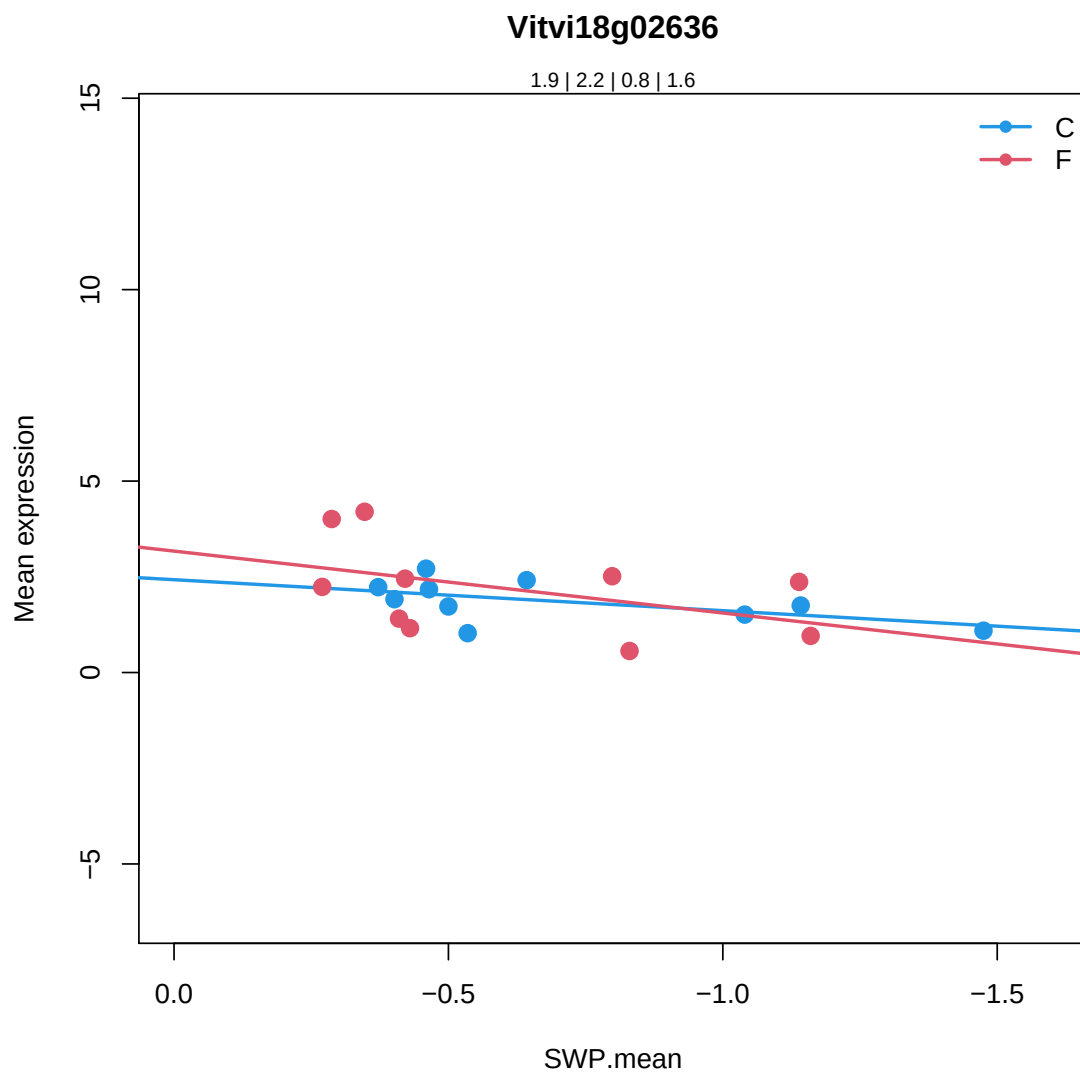
Uncharacterized conserved protein UCP031279 |

Chr1:3322970-3323473 REVERSE LENGTH=167 |

201606

Coefficients for Vitvi18g02636.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.855121	2.937817e-07	***	3.43813e-07	***
SlopeC	0.8091286	0.263956		0.7701943	
MeanF-MeanC	0.3309606	0.3662311		0.7224758	
SlopeF-SlopeC	0.8075936	0.4501168		0.9999488	



8.1.254 Vitvi04g01338: Type1.0

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

Vitvi04g01338

17.8.1.1.7

hormone metabolism.salicylic acid.synthesis-degradation.synthesis.meth

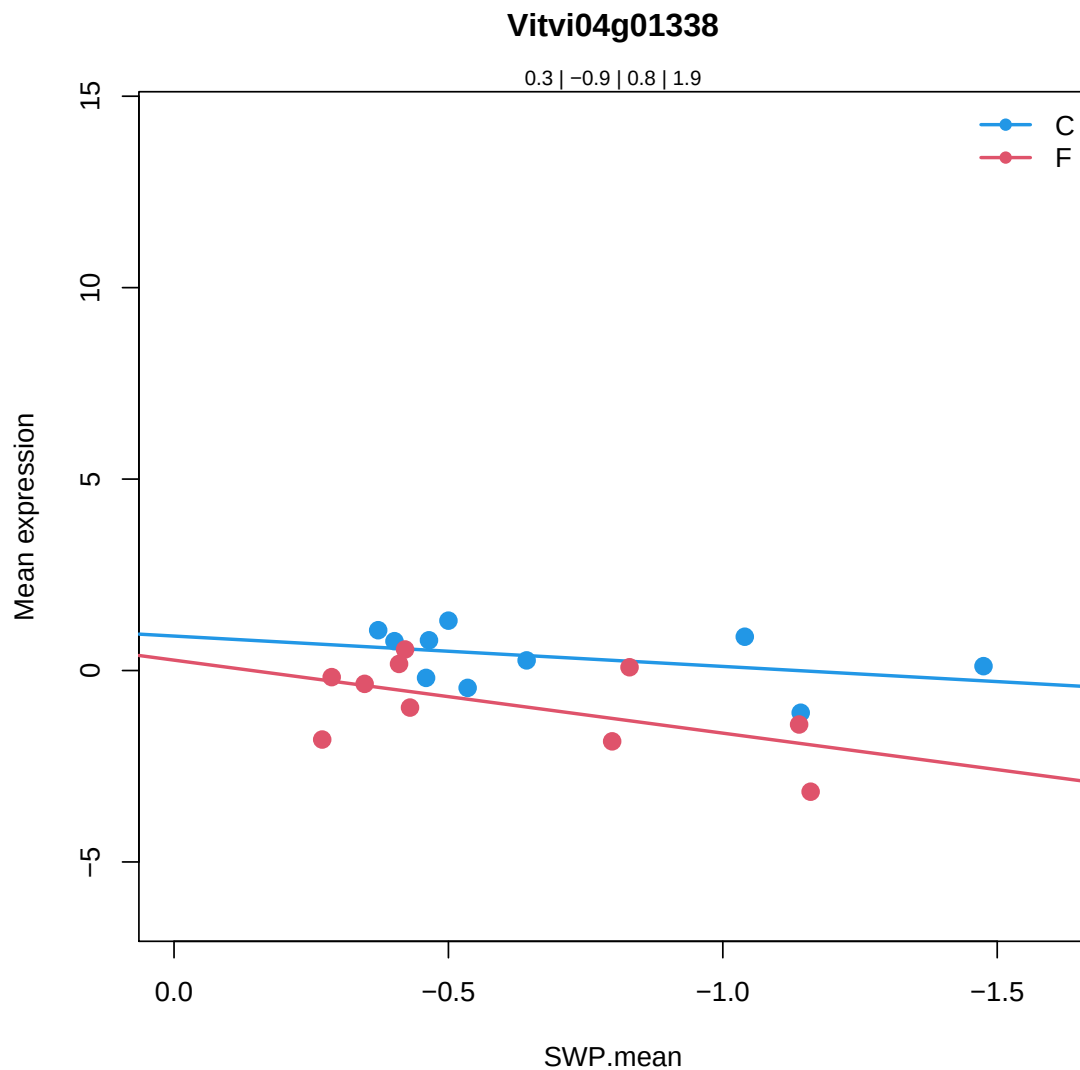
S-adenosyl-L-methionine-dependent methyltransferases superfamily prote

Chr4:17215128-17216475 REVERSE LENGTH=371 |

201606

Coefficients for Vitvi04g01338.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3422048	0.1939619		0.1988945	
SlopeC	0.7926799	0.2765681		0.7754618	
MeanF-MeanC	-1.233159	0.002536334	**	0.02666124	*
SlopeF-SlopeC	1.113932	0.303547		0.9999488	



8.1.255 Vitvi04g00433: Type1.0

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

Vitvi04g00433

16.5.1.1.1.11

secondary metabolism.sulfur-containing.glucosinolates.synthesis.alpha

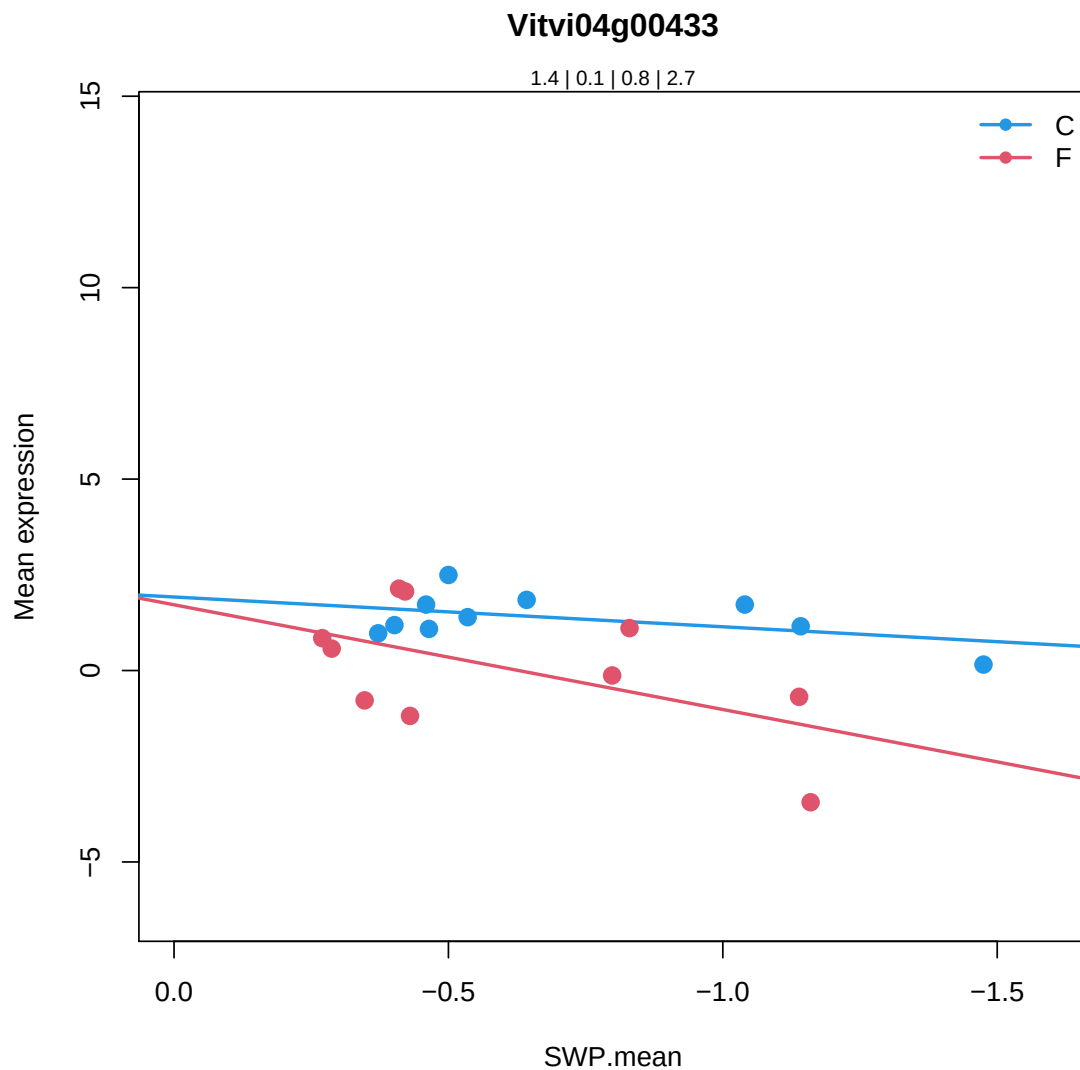
2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protei

Chr4:1358442-1359620 FORWARD LENGTH=322 |

201606

Coefficients for Vitvi04g00433.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.373288	0.0002804157	***	0.0003069149	***
SlopeC	0.778262	0.3870968		0.8290193	
MeanF-MeanC	-1.322872	0.007496407	**	0.06152947	.
SlopeF-SlopeC	1.957266	0.1503196		0.9999488	



8.1.256 Vitvi05g01108: Type1.0

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

Vitvi05g01108

35.2

not assigned.unknown

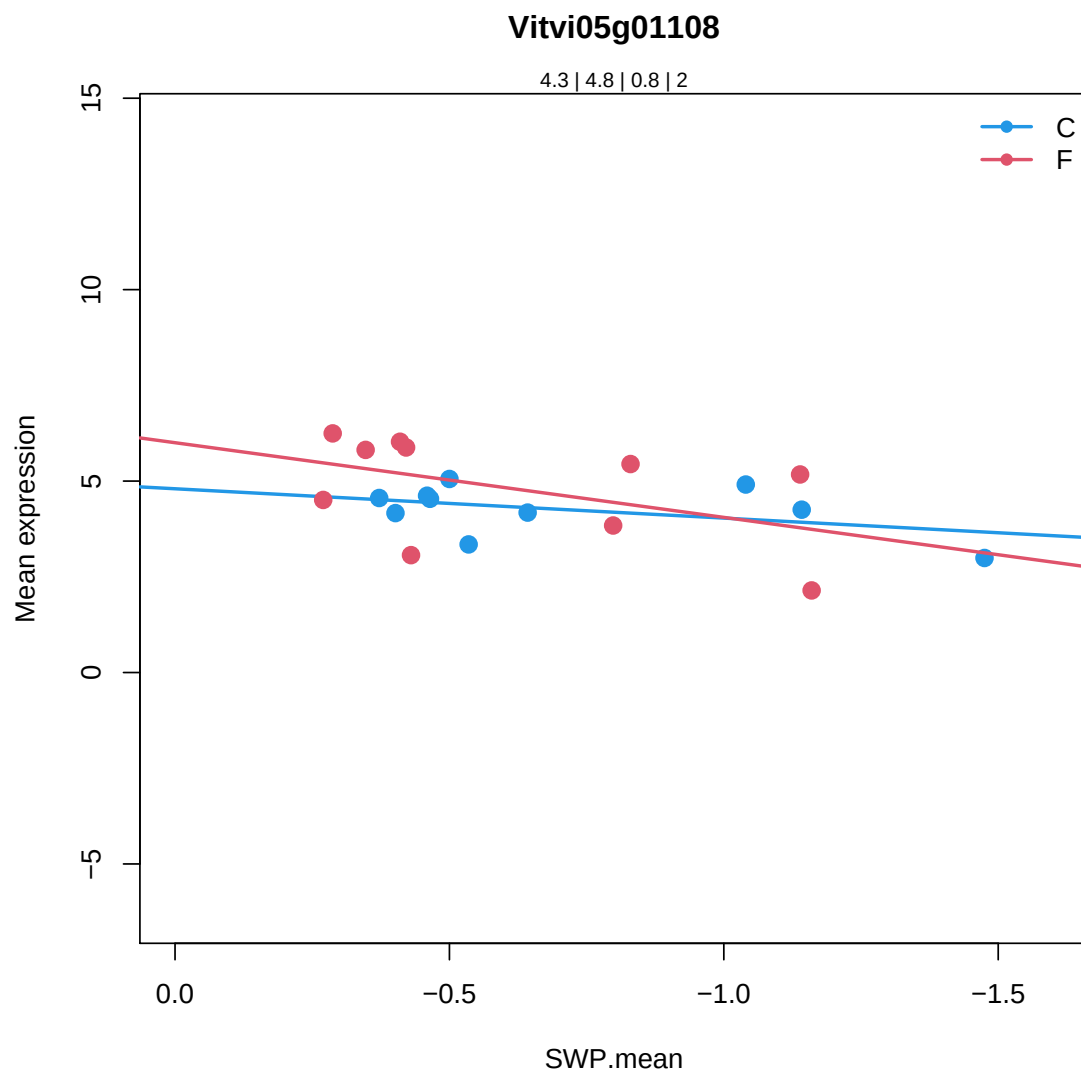
UDP-D-glucuronate 4-epimerase 6 |

Chr3:8603645-8605027 FORWARD LENGTH=460 |

201606

Coefficients for Vitvi05g01108.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.260653	9.651259e-13	***	1.386601e-12	***
SlopeC	0.7656202	0.3492156		0.811889	
MeanF-MeanC	0.5531759	0.1878588		0.5258391	
SlopeF-SlopeC	1.184646	0.3308669		0.9999488	



8.1.257 Vitvi07g02478: Type1.0

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

Vitvi07g02478

31.1

cell.organisation

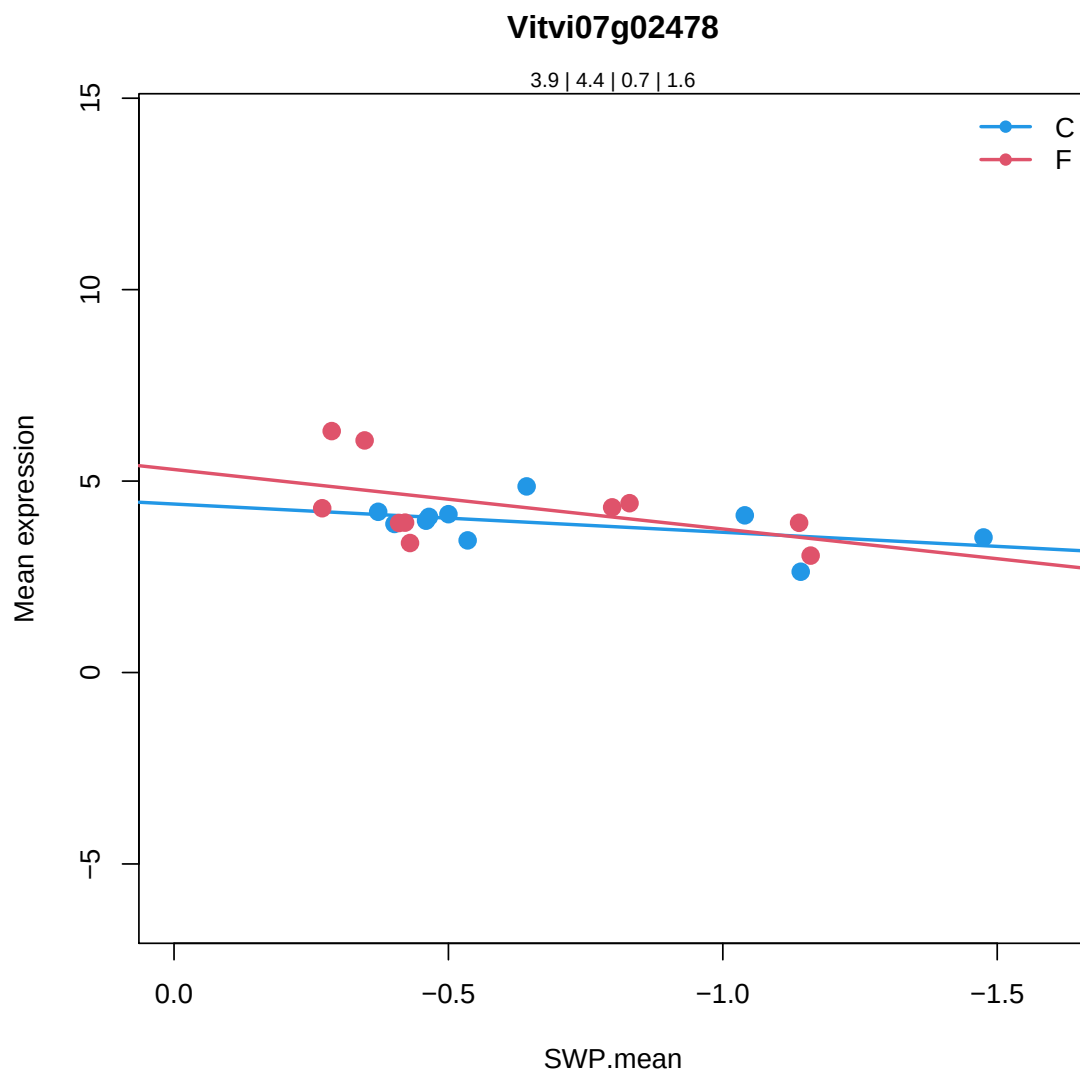
Ankyrin-repeat containing protein |

Chr5:1364101-1367303 REVERSE LENGTH=603 |

201606

Coefficients for Vitvi07g02478.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.882014	5.804596e-14	***	9.072359e-14	***
SlopeC	0.737293	0.256603		0.7658397	
MeanF-MeanC	0.4739643	0.1550146		0.475043	
SlopeF-SlopeC	0.8163619	0.3955		0.9999488	

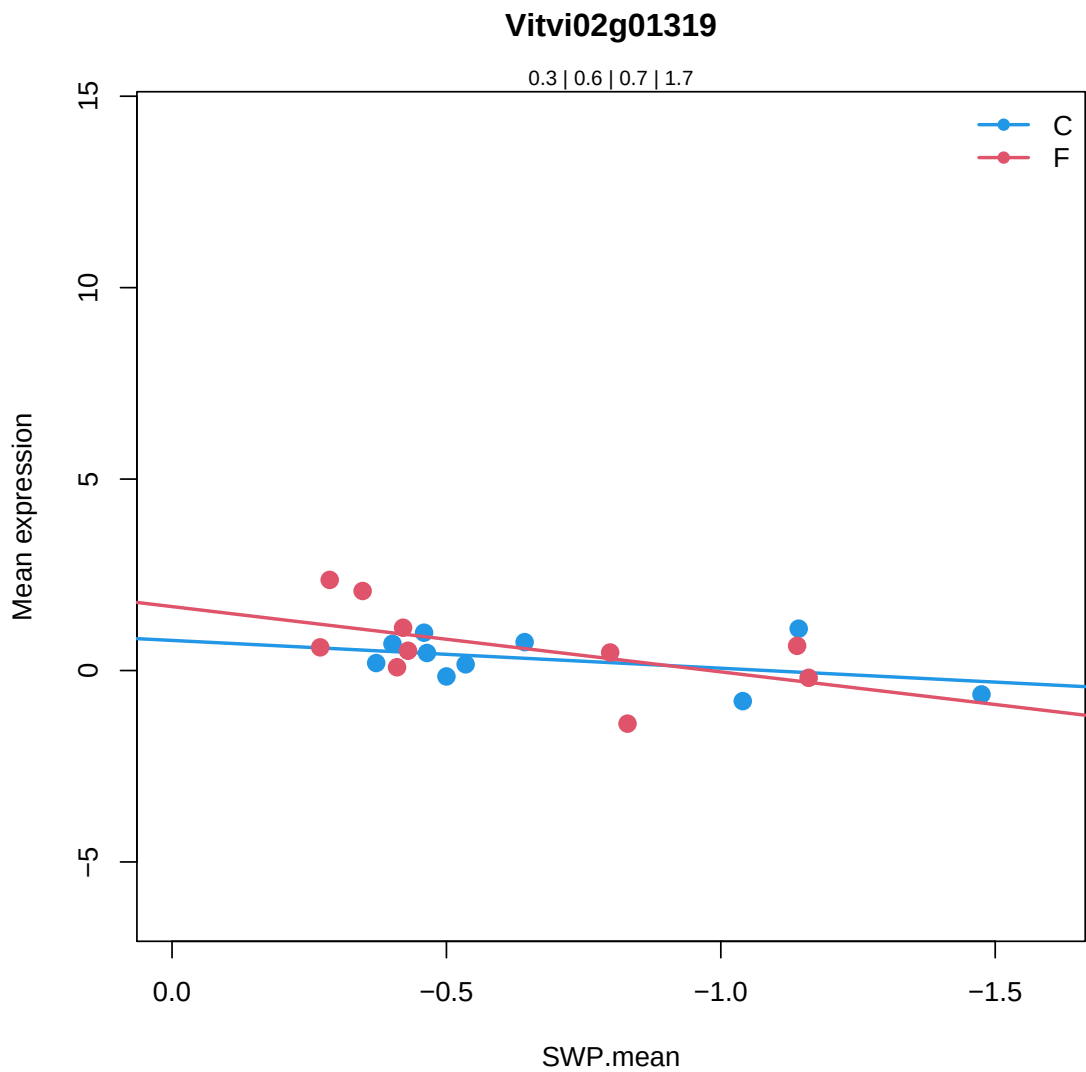


8.1.258 Vitvi02g01319: Type1.0

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
Vitvi02g01319
35.2
not assigned.unknown
Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein fam
Chr1:23778628-23779272 FORWARD LENGTH=214 |
201606
```

Coefficients for Vitvi02g01319.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.2755047	0.2519544		0.2573575	
SlopeC	0.7259749	0.2771378		0.7754618	
MeanF-MeanC	0.3549365	0.2953971		0.6616374	
SlopeF-SlopeC	0.9785907	0.3237891		0.9999488	



8.1.259 Vitvi07g02682: Type1.0

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

Vitvi07g02682

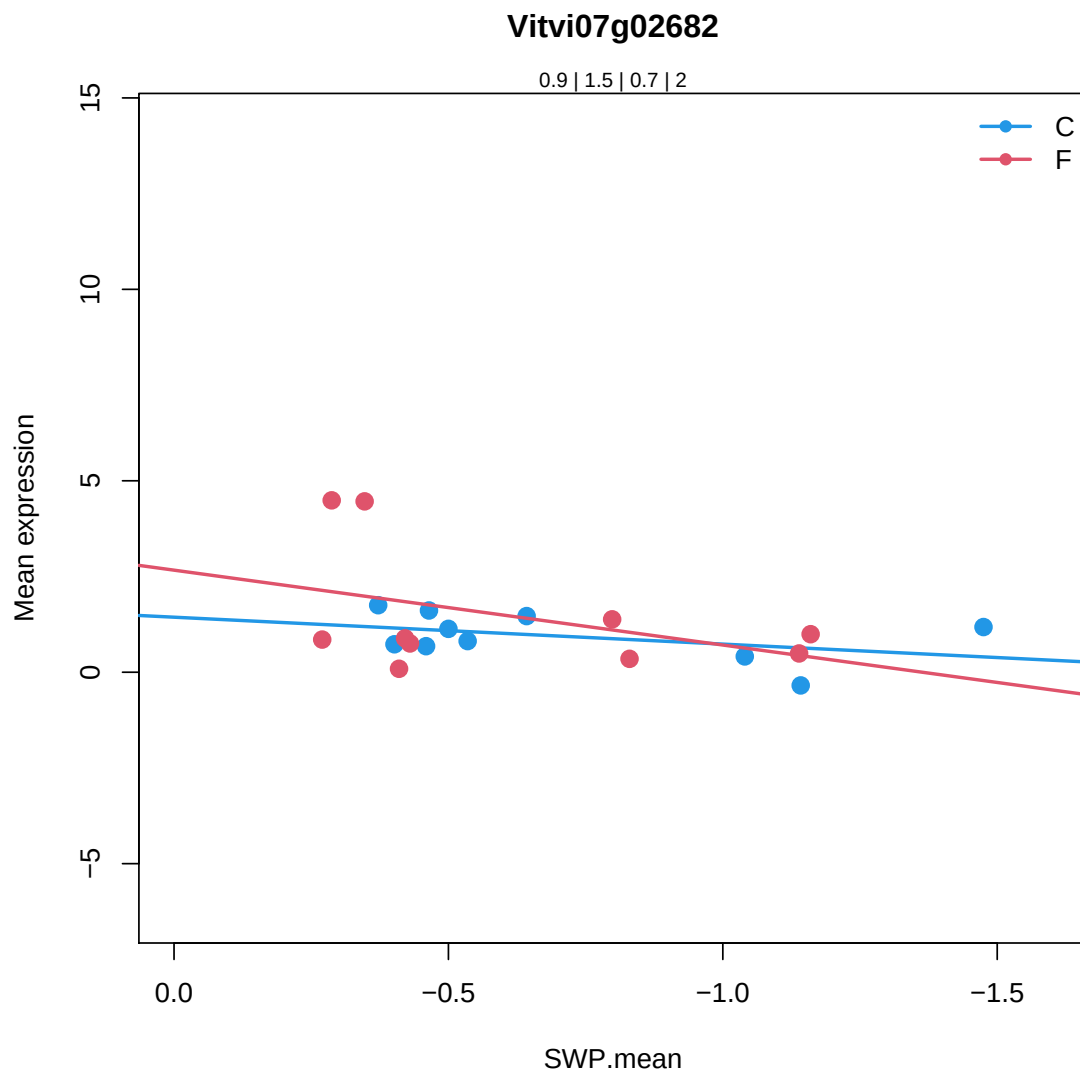
35.2

not assigned.unknown

Unknown Protein

Coefficients for Vitvi07g02682.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.9431016	0.009891269	**	0.01047764	*
SlopeC	0.7027648	0.4566385		0.8582289	
MeanF-MeanC	0.5313927	0.2719016		0.6352826	
SlopeF-SlopeC	1.252449	0.3740969		0.9999488	



8.1.260 Vitvi11g01428: Type1.0

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

Vitvi11g01428

27.4

RNA.RNA binding

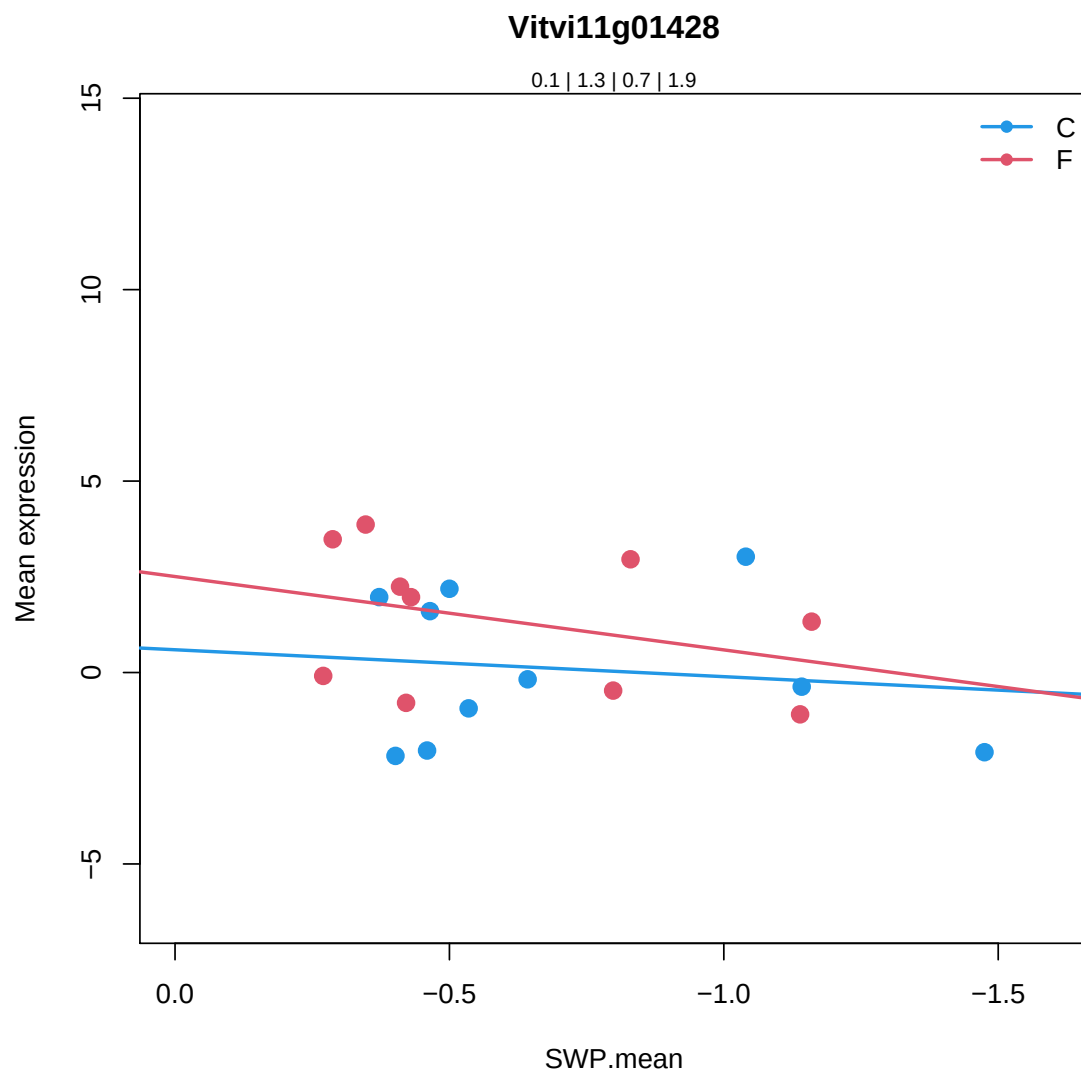
Ran BP2/NZF zinc finger-like superfamily protein |

Chr2:11365275-11365789 FORWARD LENGTH=138 |

201606

Coefficients for Vitvi11g01428.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1003848	0.8535352		0.8564571	
SlopeC	0.7024627	0.6431214		0.9162886	
MeanF-MeanC	1.239152	0.1175085		0.4025964	
SlopeF-SlopeC	1.213608	0.5910246		0.9999488	



8.1.261 Vitvi03g00666: Type1.0

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

Vitvi03g00666

27.3.50

RNA.regulation of transcription.general transcription

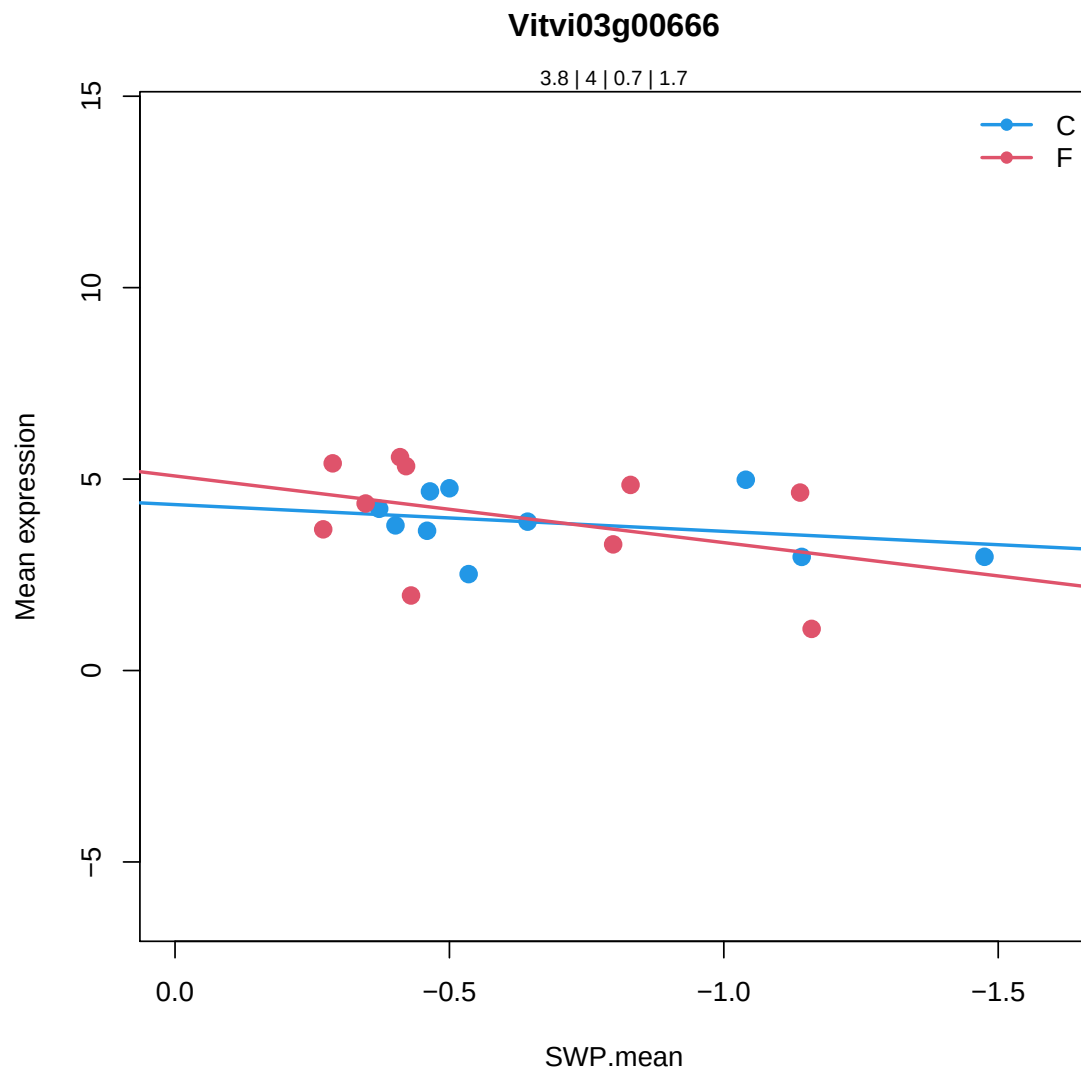
GATA type zinc finger transcription factor family protein |

Chr1:3346677-3347763 REVERSE LENGTH=190 |

201606

Coefficients for Vitvi03g00666.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.842762	1.538888e-10	***	2.000659e-10	***
SlopeC	0.6986815	0.4658092		0.8617488	
MeanF-MeanC	0.1778654	0.7136318		0.9117247	
SlopeF-SlopeC	1.041411	0.4651692		0.9999488	



8.1.262 Vitvi04g02117: Type1.0

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

Vitvi04g02117

17.8.1.1.7

hormone metabolism.salicylic acid.synthesis-degradation.synthesis.meth

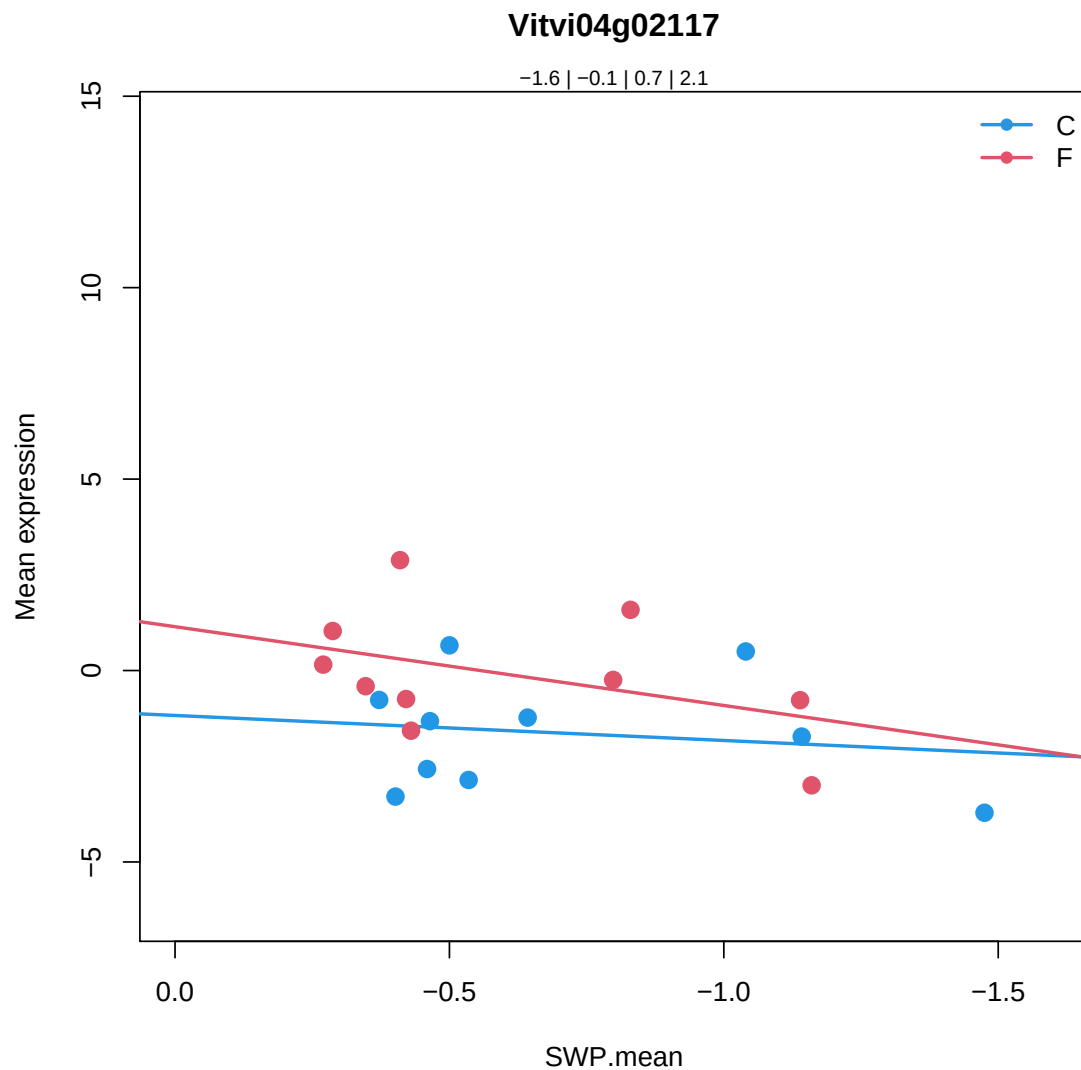
S-adenosyl-L-methionine-dependent methyltransferases superfamily prote

Chr5:26525410-26526799 REVERSE LENGTH=354 |

201606

Coefficients for Vitvi04g02117.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.633026	0.001211469	**	0.001310054	**
SlopeC	0.6531659	0.5976063		0.9029217	
MeanF-MeanC	1.5237	0.02250533	*	0.1373204	
SlopeF-SlopeC	1.404465	0.447337		0.9999488	



8.1.263 Vitvi10g00902: Type1.0

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

Vitvi10g00902

34.3

transport.amino acids

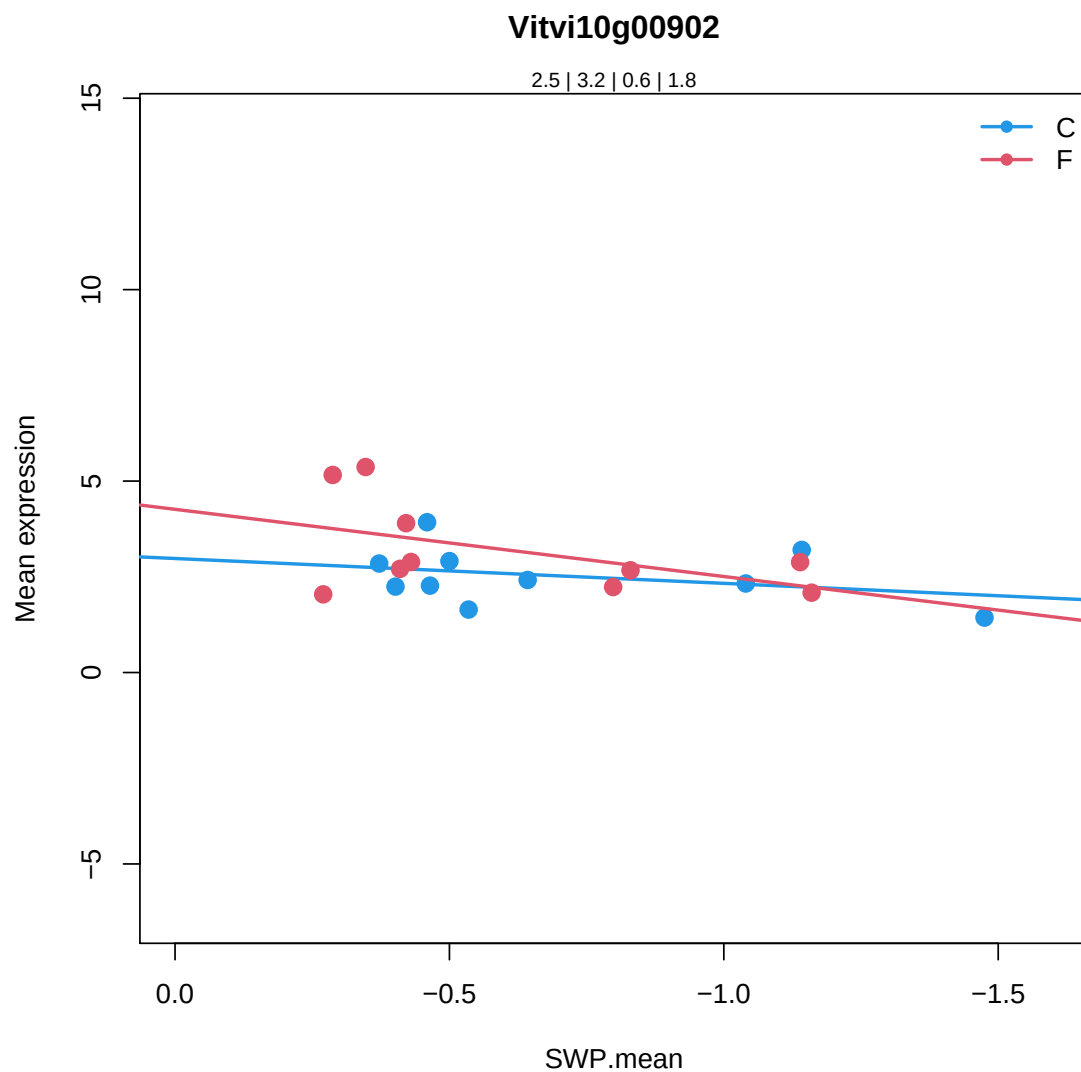
amino acid transporter 1 |

Chr4:11270318-11273775 FORWARD LENGTH=594 |

201606

Coefficients for Vitvi10g00902.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.521716	5.108008e-09	***	6.29294e-09	***
SlopeC	0.6485782	0.3968795		0.8324742	
MeanF-MeanC	0.671678	0.09244586	.	0.3485586	
SlopeF-SlopeC	1.106254	0.3328751		0.9999488	



8.1.264 Vitvi13g00122: Type1.0

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

Vitvi13g00122

35.2

not assigned.unknown

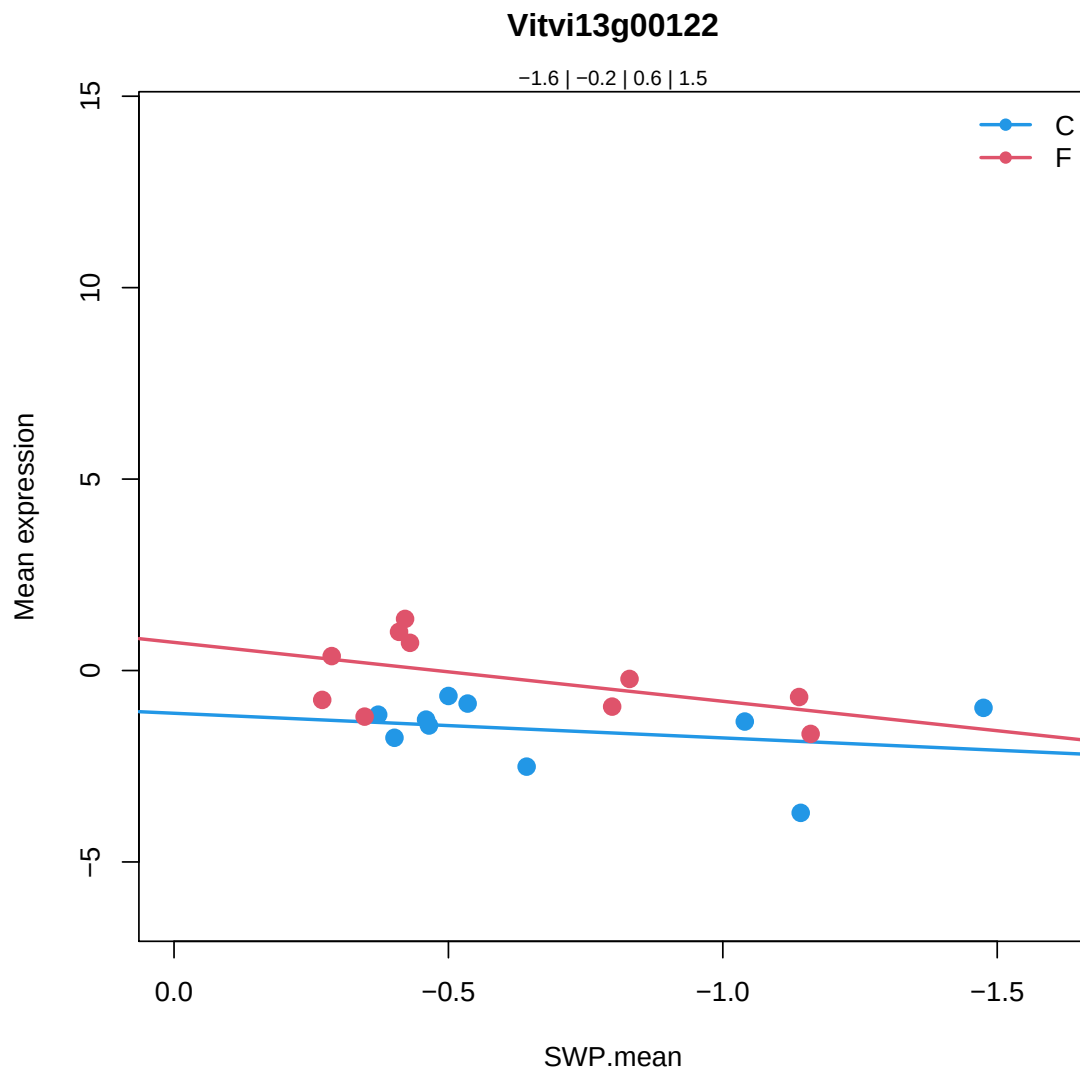
neuronal PAS domain protein |

Chr2:16867385-16868961 FORWARD LENGTH=496 |

201606

Coefficients for Vitvi13g00122.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.569322	6.547987e-06	***	7.420954e-06	***
SlopeC	0.6440993	0.3923264		0.8309601	
MeanF-MeanC	1.366734	0.001476524	**	0.01720579	*
SlopeF-SlopeC	0.8942126	0.4244105		0.9999488	



8.1.265 Vitvi03g00597: Type1.0

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

Vitvi03g00597

35.2

not assigned.unknown

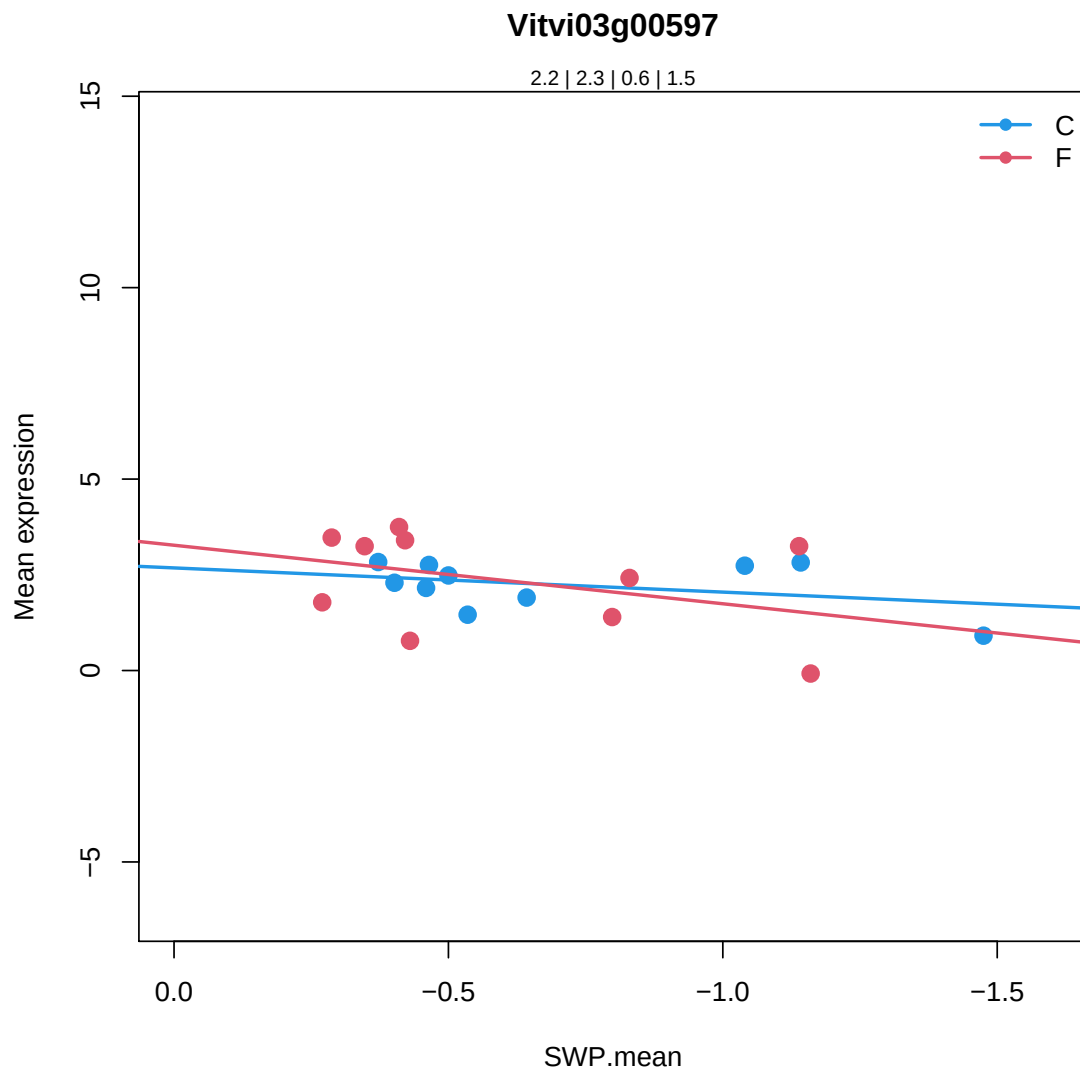
glutamyl-tRNA (Gln) amidotransferase subunit A (DUF620) |

Chr3:6780762-6782633 FORWARD LENGTH=485 |

201606

Coefficients for Vitvi03g00597.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.235526	1.07164e-07	***	1.270135e-07	***
SlopeC	0.6317979	0.4369085		0.8502756	
MeanF-MeanC	0.1053089	0.7975155		0.9432553	
SlopeF-SlopeC	0.8968689	0.458116		0.9999488	



8.1.266 Vitvi05g01885: Type1.0

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

Vitvi05g01885

35.2

not assigned.unknown

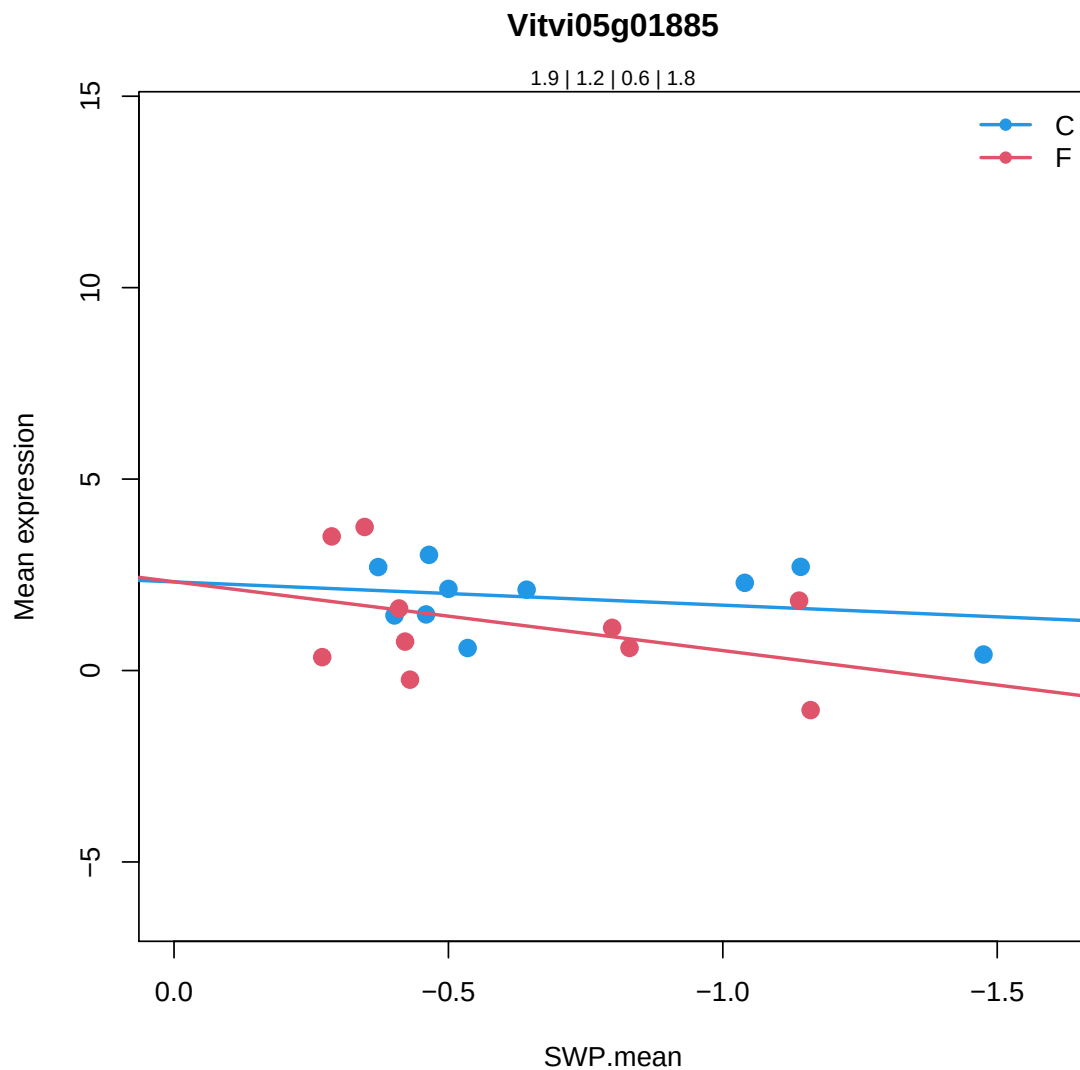
hypothetical protein (DUF868) |

Chr5:10135826-10136695 FORWARD LENGTH=289 |

201606

Coefficients for Vitvi05g01885.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.887177	1.726214e-05	***	1.938763e-05	***
SlopeC	0.6079153	0.530909		0.878432	
MeanF-MeanC	-0.6640838	0.1852341		0.5221907	
SlopeF-SlopeC	1.190904	0.4110915		0.9999488	



8.1.267 Vitvi18g00590: Type1.0

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

Vitvi18g00590

31.1

cell.organisation

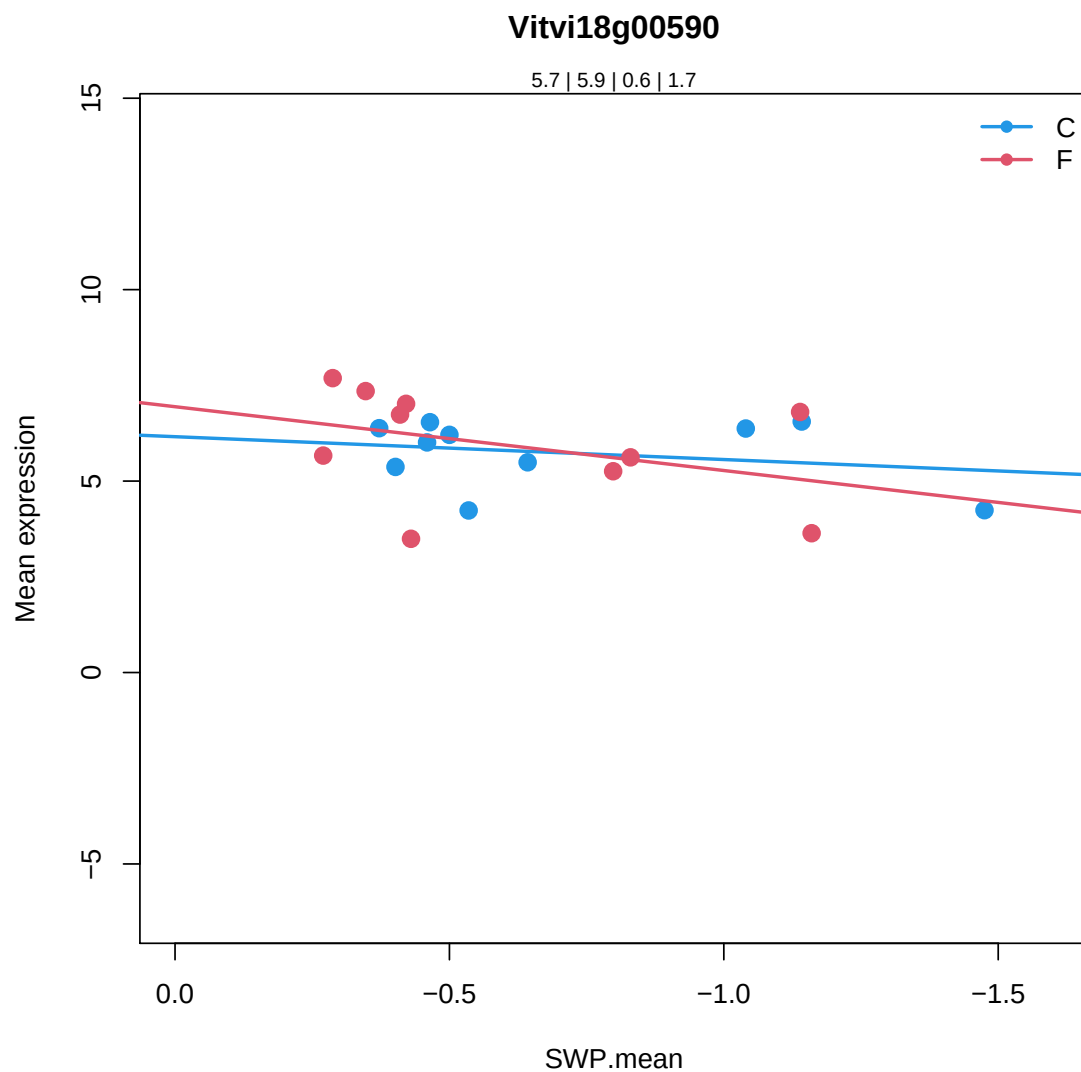
alpha-1 tubulin |

Chr1:24050114-24052296 FORWARD LENGTH=450 |

201606

Coefficients for Vitvi18g00590.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.739694	6.599185e-14	***	1.027319e-13	***
SlopeC	0.5966689	0.5328641		0.8796574	
MeanF-MeanC	0.1874849	0.6990481		0.9060081	
SlopeF-SlopeC	1.069877	0.4533969		0.9999488	



8.1.268 Vitvi17g00600: Type1.0

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

Vitvi17g00600

35.2

not assigned.unknown

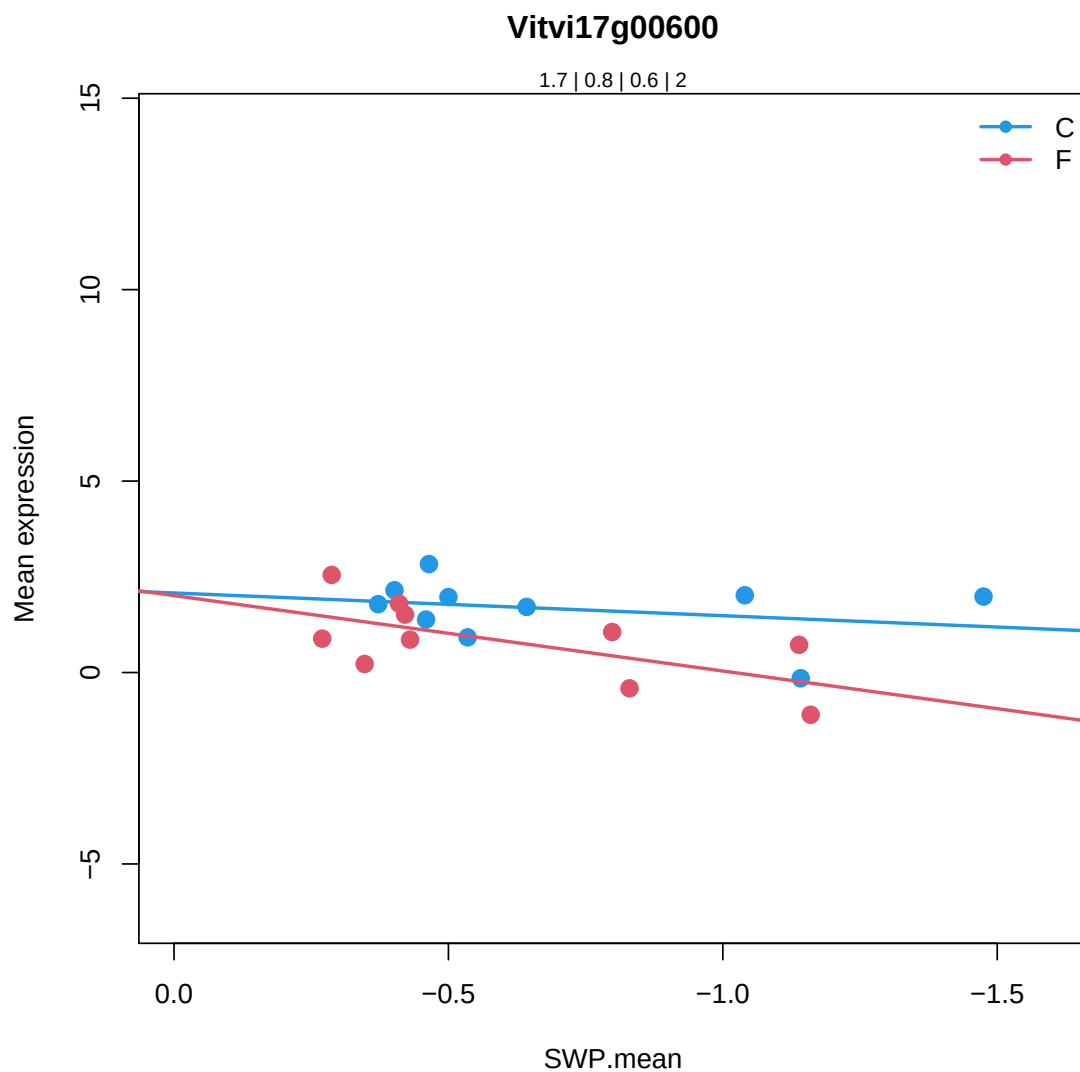
mini zinc finger 1 |

Chr1:28047742-28048050 REVERSE LENGTH=102 |

201606

Coefficients for Vitvi17g00600.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.660287	8.421129e-07	***	9.740824e-07	***
SlopeC	0.5930129	0.3903061		0.8308722	
MeanF-MeanC	-0.8512128	0.02169253	*	0.1336449	
SlopeF-SlopeC	1.375607	0.1859265		0.9999488	



8.1.269 Vitvi07g01805: Type1.0

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

Vitvi07g01805

35.2

not assigned.unknown

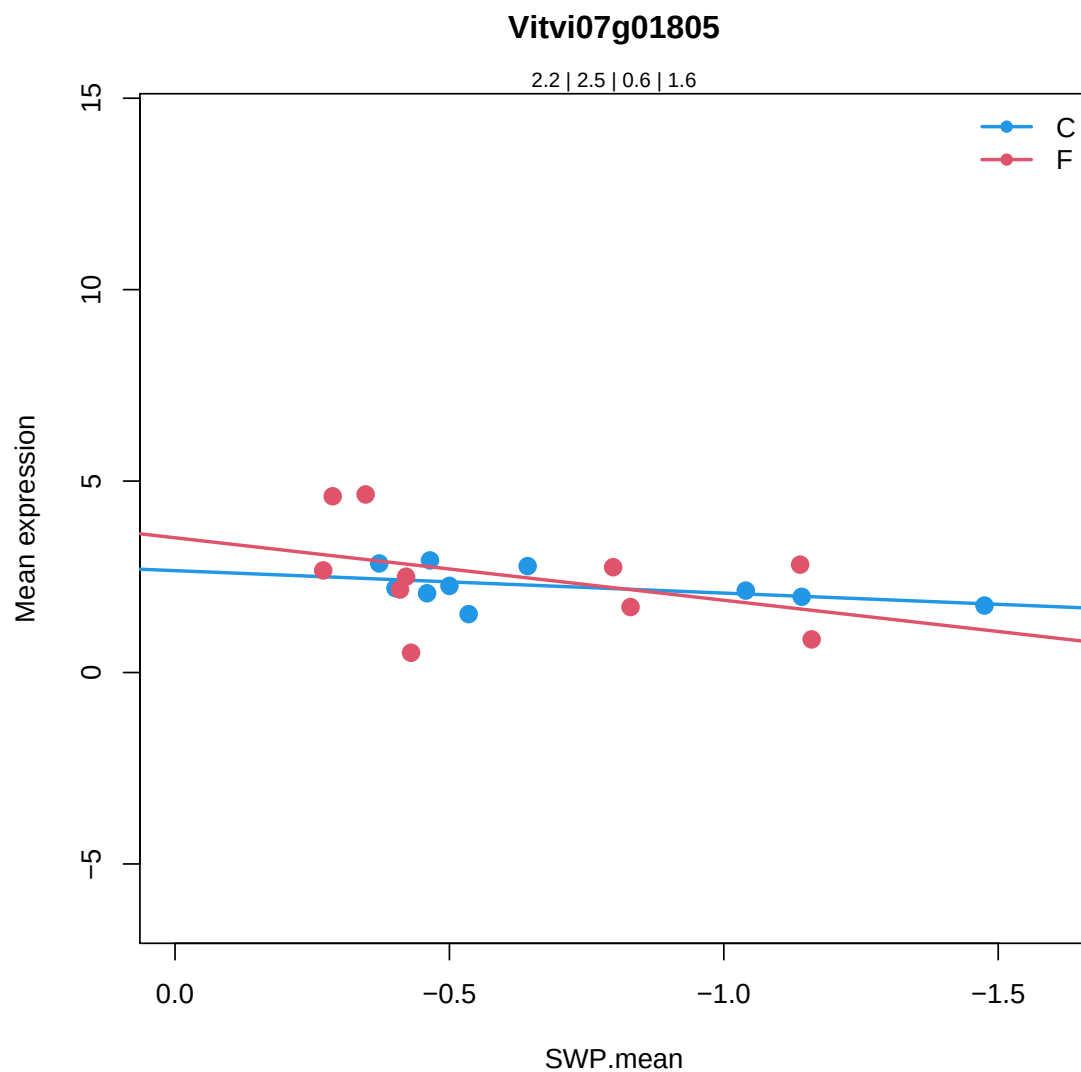
RING-H2 finger A2A |

Chr1:5193703-5194170 REVERSE LENGTH=155 |

201606

Coefficients for Vitvi07g01805.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.248352	6.018225e-08	***	7.178728e-08	***
SlopeC	0.5865647	0.4568294		0.8582289	
MeanF-MeanC	0.2765933	0.4896411		0.8001618	
SlopeF-SlopeC	1.045538	0.3742188		0.9999488	



8.1.270 Vitvi18g00448: Type1.0

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

Vitvi18g00448

27.3.35

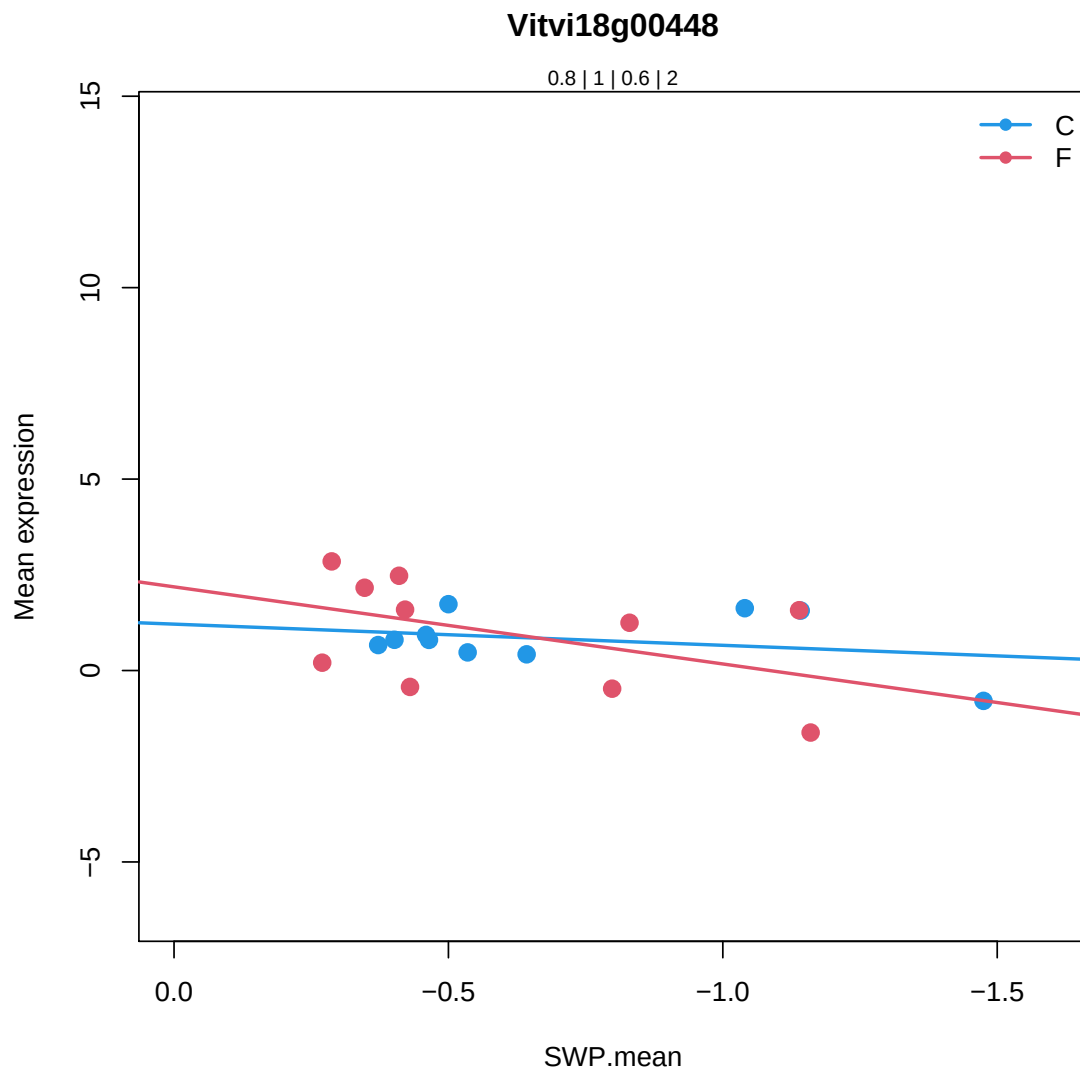
RNA.regulation of transcription.bZIP transcription factor family
homeobox protein 16 |

Chr4:18571682-18572774 REVERSE LENGTH=294 |

201606

Coefficients for Vitvi18g00448.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8225952	0.0154003	*	0.01624326	*
SlopeC	0.5531167	0.5313425		0.8785769	
MeanF-MeanC	0.1354842	0.7621078		0.9306501	
SlopeF-SlopeC	1.461107	0.2712723		0.9999488	



8.1.271 Vitvi14g01805: Type1.0

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

Vitvi14g01805

33.99

development.unspecified

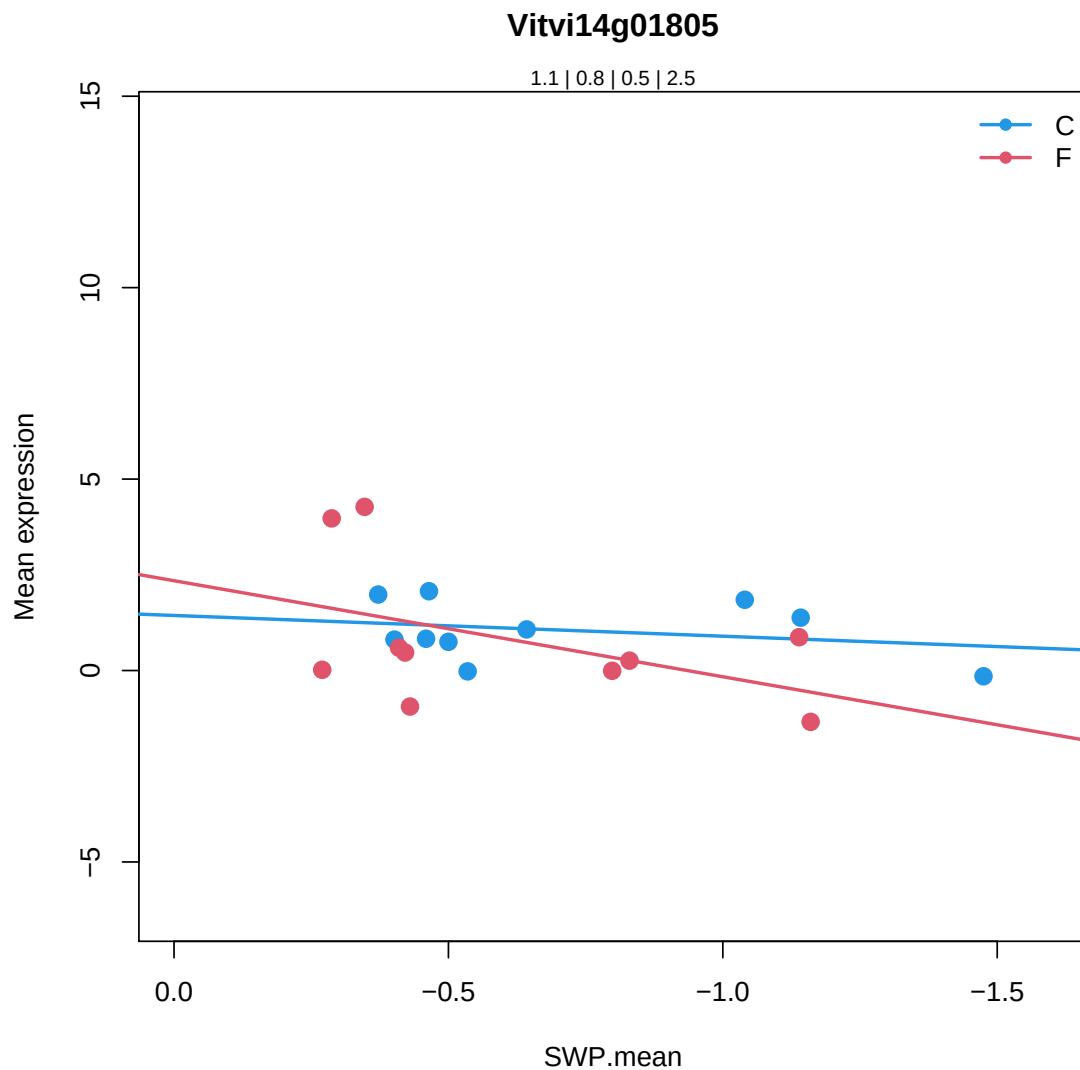
nodulin MtN21 /EamA-like transporter family protein |

Chr5:16079814-16081735 REVERSE LENGTH=370 |

201606

Coefficients for Vitvi14g01805.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.057056	0.01125574	*	0.01191058	*
SlopeC	0.5414053	0.6148951		0.9074064	
MeanF-MeanC	-0.24011	0.6604784		0.8870954	
SlopeF-SlopeC	1.966964	0.2261385		0.9999488	



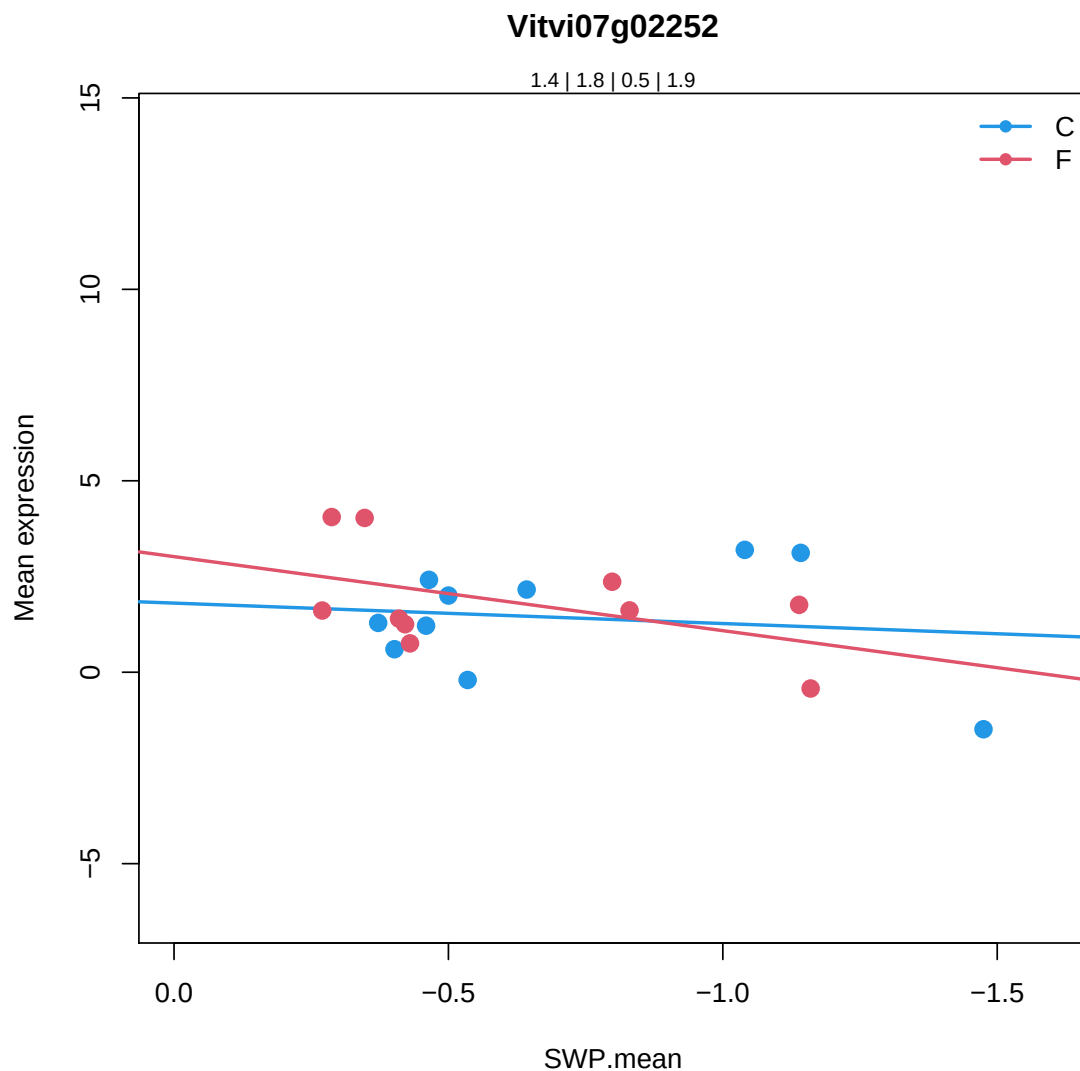
8.1.272 Vitvi07g02252: Type1.0

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

```
Vitvi07g02252
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi07g02252.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.429907	0.001597659	**	0.001723025	**
SlopeC	0.5338287	0.6328749		0.912027	
MeanF-MeanC	0.4112074	0.4706901		0.7894788	
SlopeF-SlopeC	1.400071	0.4025883		0.9999488	



8.1.273 Vitvi12g02718: Type1.0

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

Vitvi12g02718

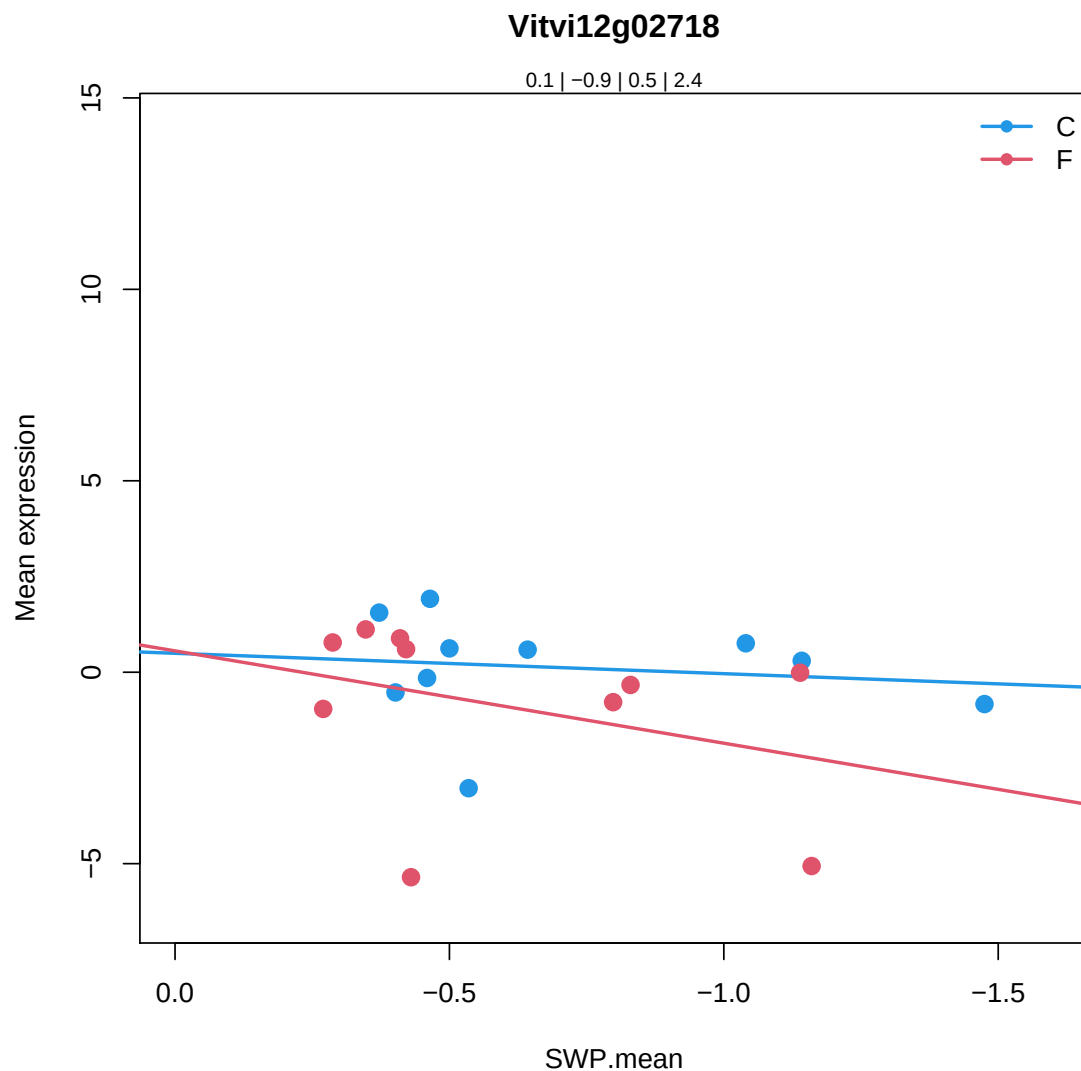
17.7.2

hormone metabolism.jasmonate.signal transduction

NA

Coefficients for Vitvi12g02718.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1198652	0.8269394		0.8303715	
SlopeC	0.5323722	0.7273034		0.9398478	
MeanF-MeanC	-1.03172	0.1920432		0.5316242	
SlopeF-SlopeC	1.878685	0.4114418		0.9999488	



8.1.274 Vitvi09g00340: Type1.0

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

Vitvi09g00340

34.13

transport.peptides and oligopeptides

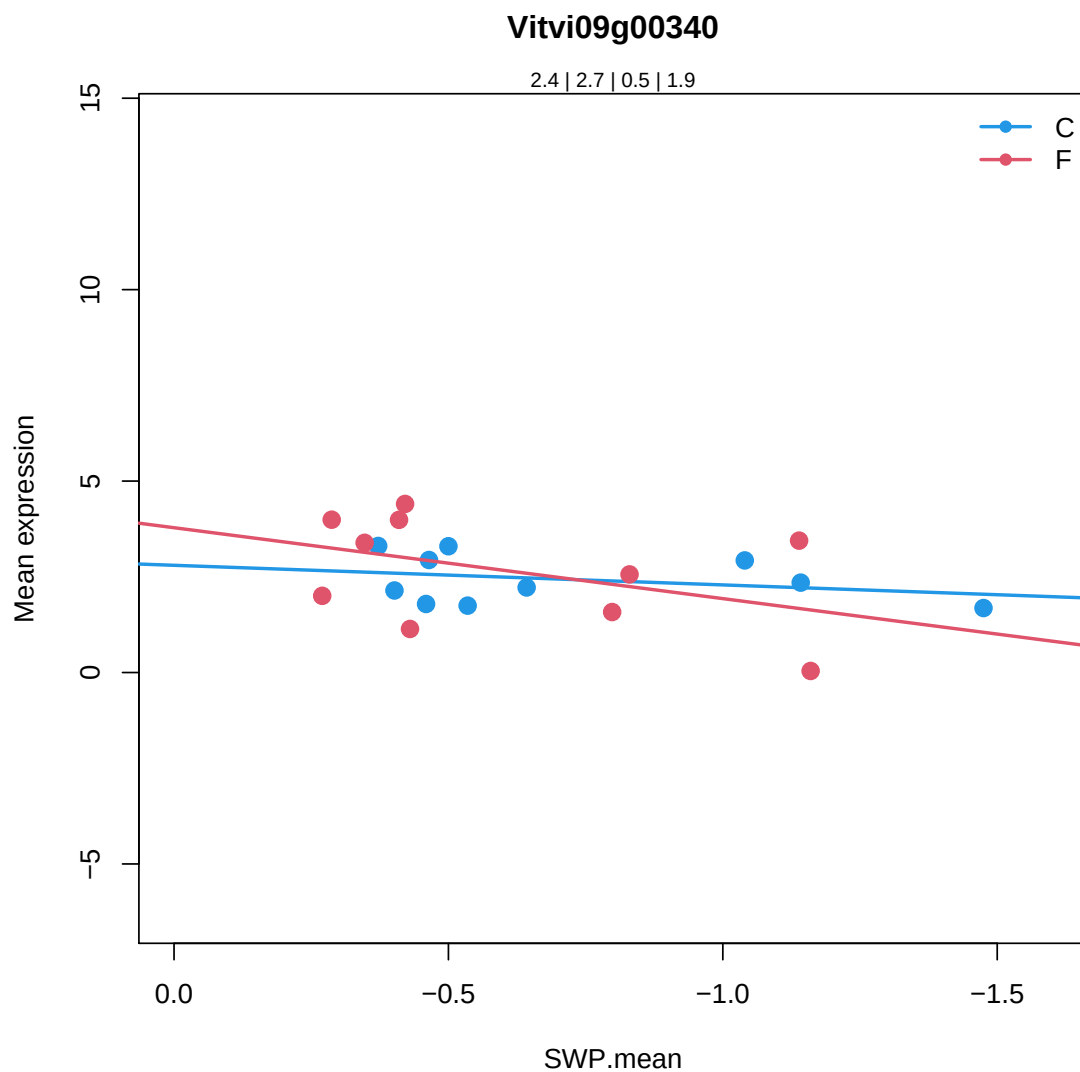
Major facilitator superfamily protein |

Chr1:19434671-19438673 FORWARD LENGTH=607 |

201606

Coefficients for Vitvi09g00340.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.44005	5.694118e-08	***	6.797975e-08	***
SlopeC	0.511981	0.5472799		0.886252	
MeanF-MeanC	0.2136163	0.620819		0.8691217	
SlopeF-SlopeC	1.339883	0.2942054		0.9999488	



8.1.275 Vitvi03g00315: Type1.0

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

Vitvi03g00315

27.3.6

RNA.regulation of transcription.basic helix-loop-helix family (bHLH)

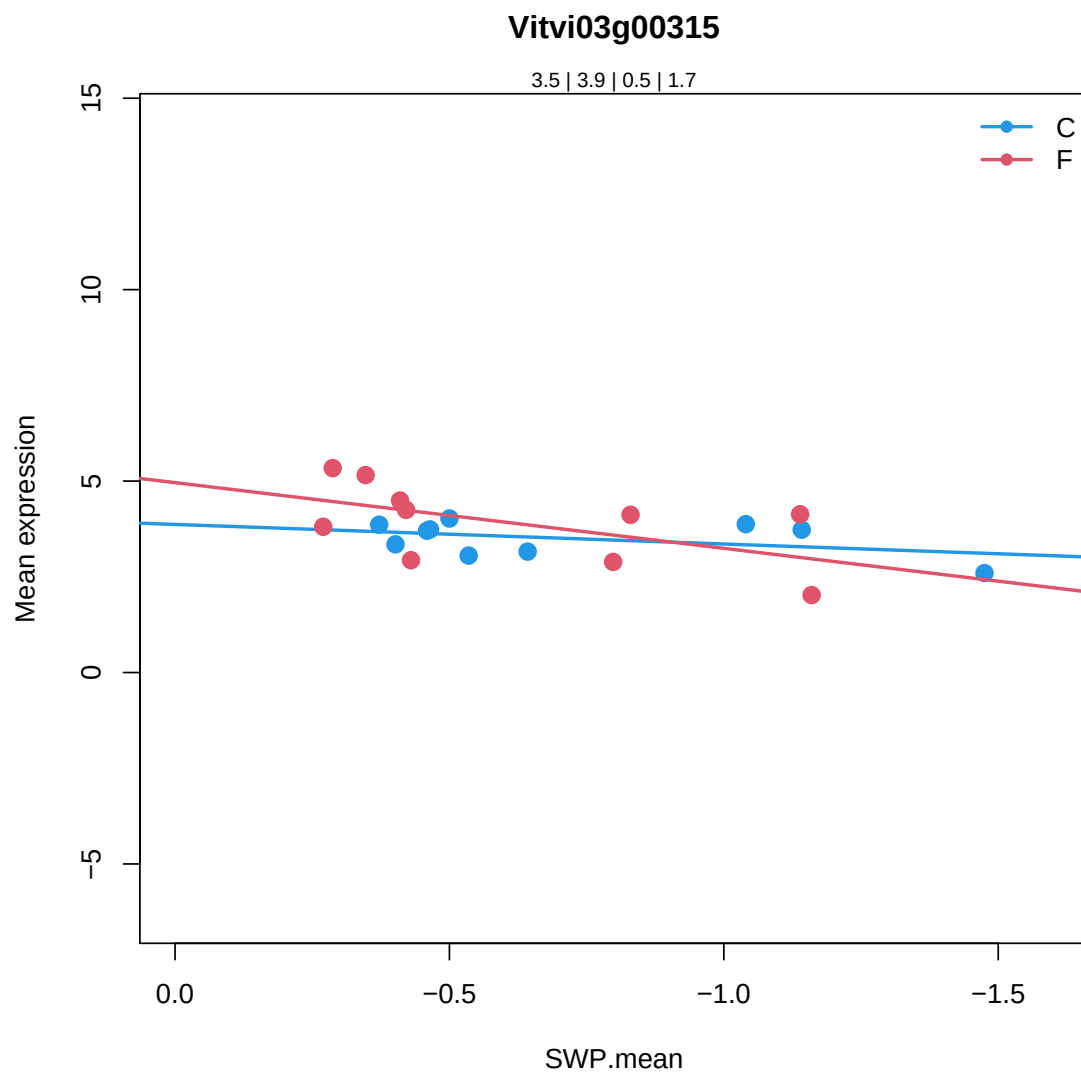
cryptochrome-interacting basic-helix-loop-helix 1 |

Chr4:16498466-16499946 FORWARD LENGTH=335 |

201606

Coefficients for Vitvi03g00315.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.508446	8.397489e-14	***	1.296804e-13	***
SlopeC	0.5108647	0.3900773		0.8308493	
MeanF-MeanC	0.4055045	0.1849088		0.5216401	
SlopeF-SlopeC	1.204615	0.1788531		0.9999488	



8.1.276 Vitvi05g02017: Type1.0

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

Vitvi05g02017

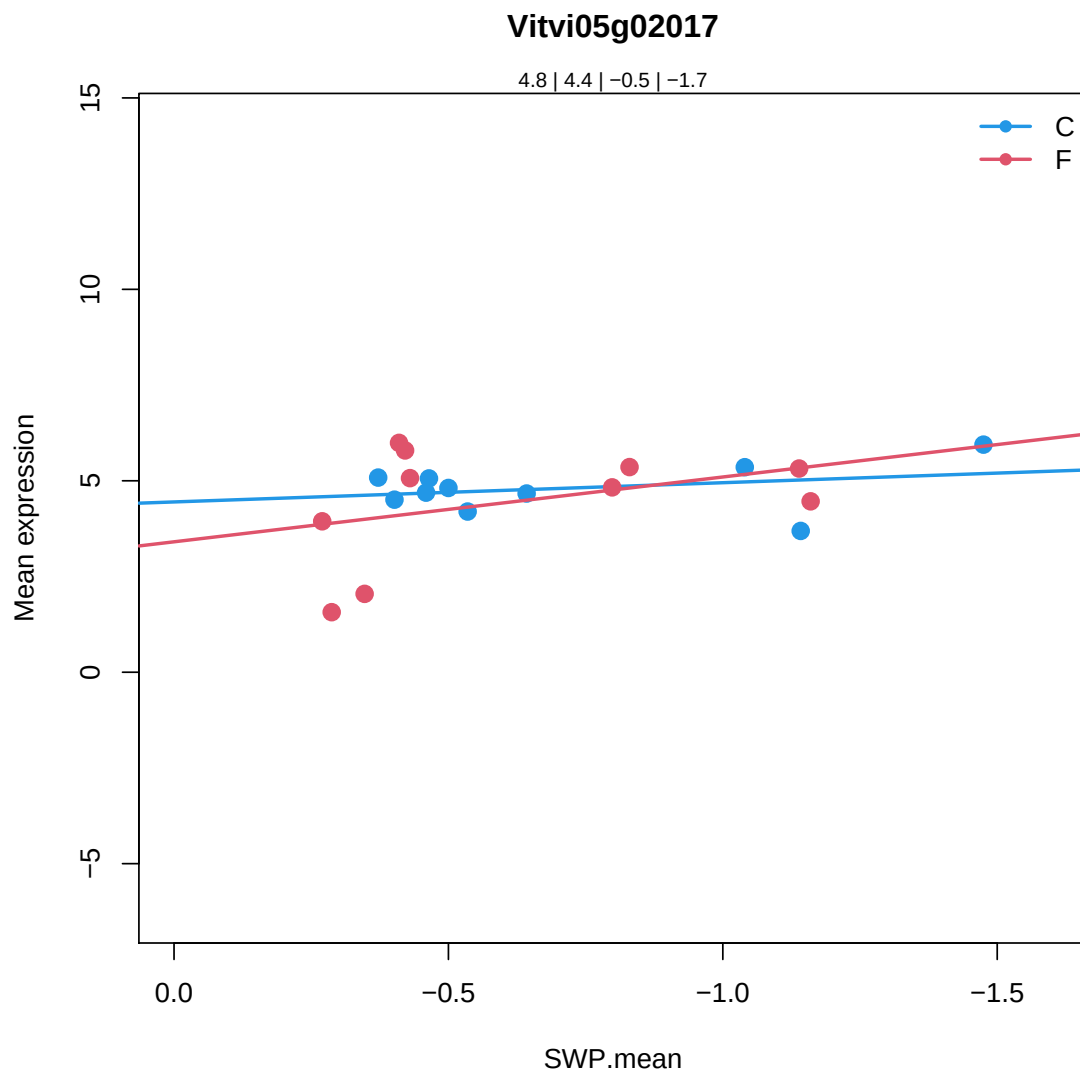
35.2

not assigned.unknown

NA

Coefficients for Vitvi05g02017.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.800732	7.827281e-13	***	1.131804e-12	***
SlopeC	-0.5022915	0.5791317		0.8944184	
MeanF-MeanC	-0.3630565	0.4319997		0.7662677	
SlopeF-SlopeC	-1.190326	0.3798102		0.9999488	



8.1.277 Vitvi07g01818: Type1.0

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

Vitvi07g01818

29.4.1

protein.postranslational modification.kinase

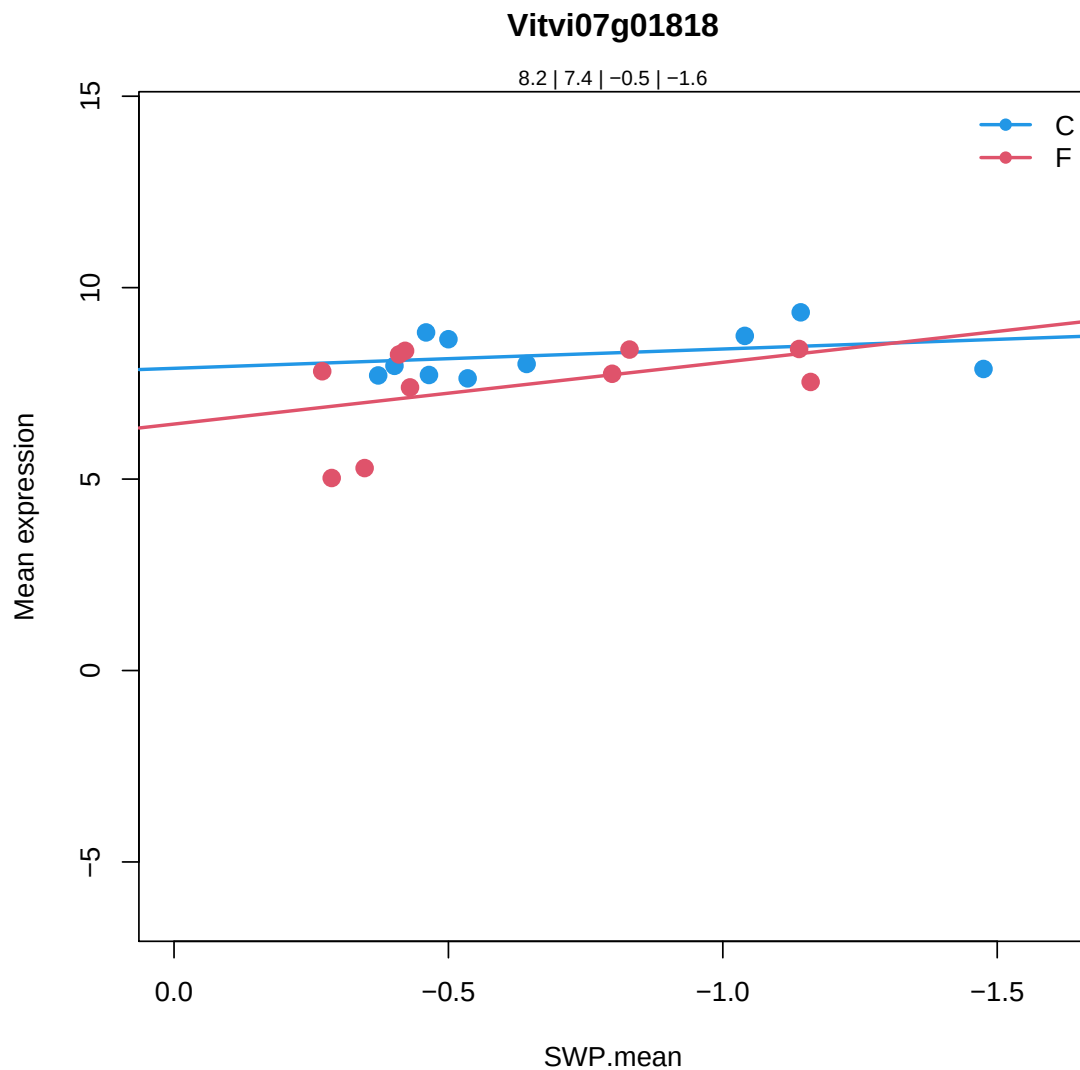
ABC2 homolog 13 |

Chr5:25949116-25953326 FORWARD LENGTH=761 |

201606

Coefficients for Vitvi07g01818.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	8.247314	3.148048e-19	***	1.269715e-18	***
SlopeC	-0.5044974	0.5060549		0.8709231	
MeanF-MeanC	-0.8275675	0.04031958	*	0.2074084	
SlopeF-SlopeC	-1.108519	0.3291837		0.9999488	



8.1.278 Vitvi14g00167: Type1.0

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

Vitvi14g00167

35.1

not assigned.no ontology

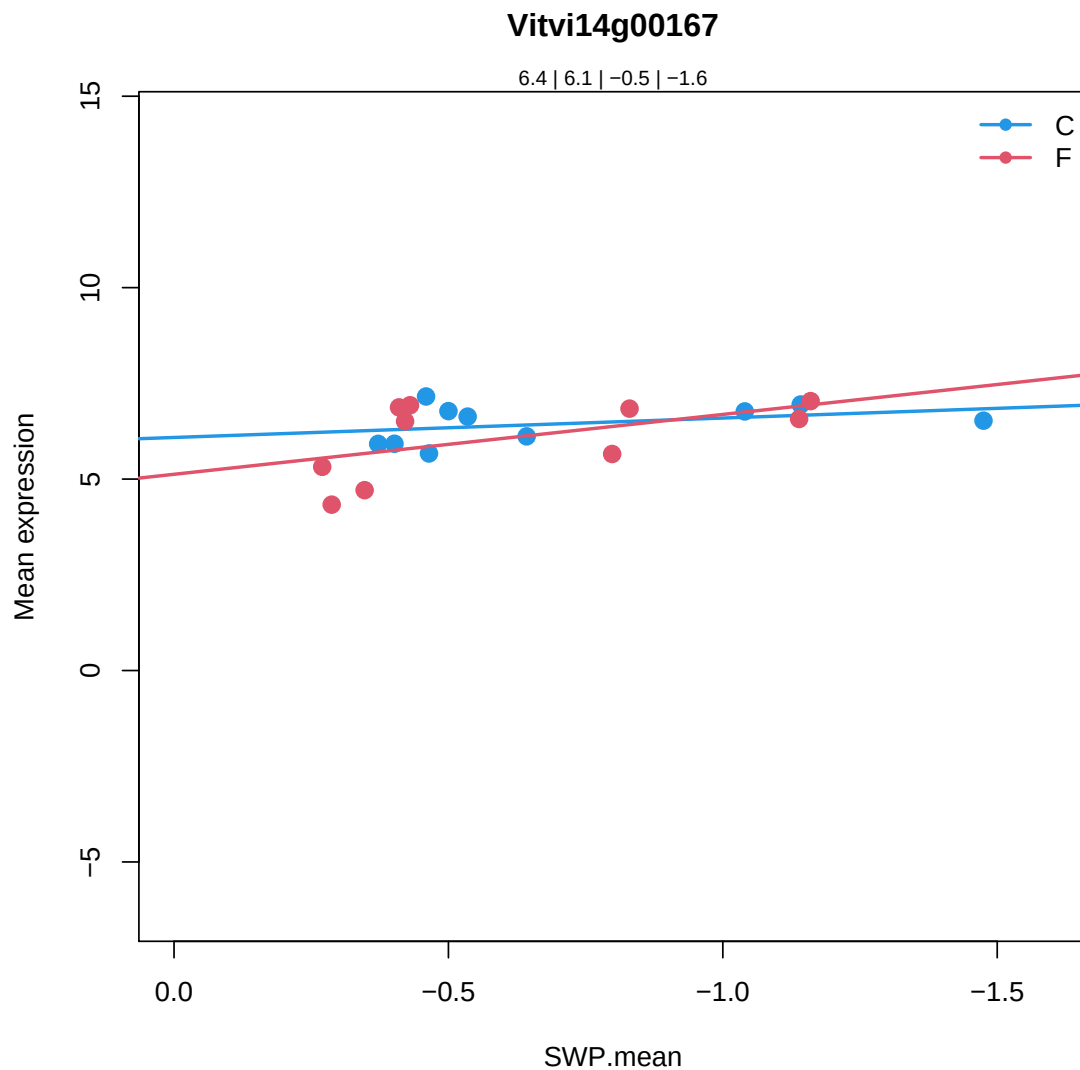
Rubber elongation factor protein (REF) |

Chr3:1593803-1594802 FORWARD LENGTH=174 |

201606

Coefficients for Vitvi14g00167.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.443315	3.895976e-19	***	1.526006e-18	***
SlopeC	-0.5076561	0.3980543		0.8337418	
MeanF-MeanC	-0.3658707	0.2347455		0.590038	
SlopeF-SlopeC	-1.055807	0.2413523		0.9999488	



8.1.279 Vitvi01g00803: Type1.0

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

Vitvi01g00803

33.99

development.unspecified

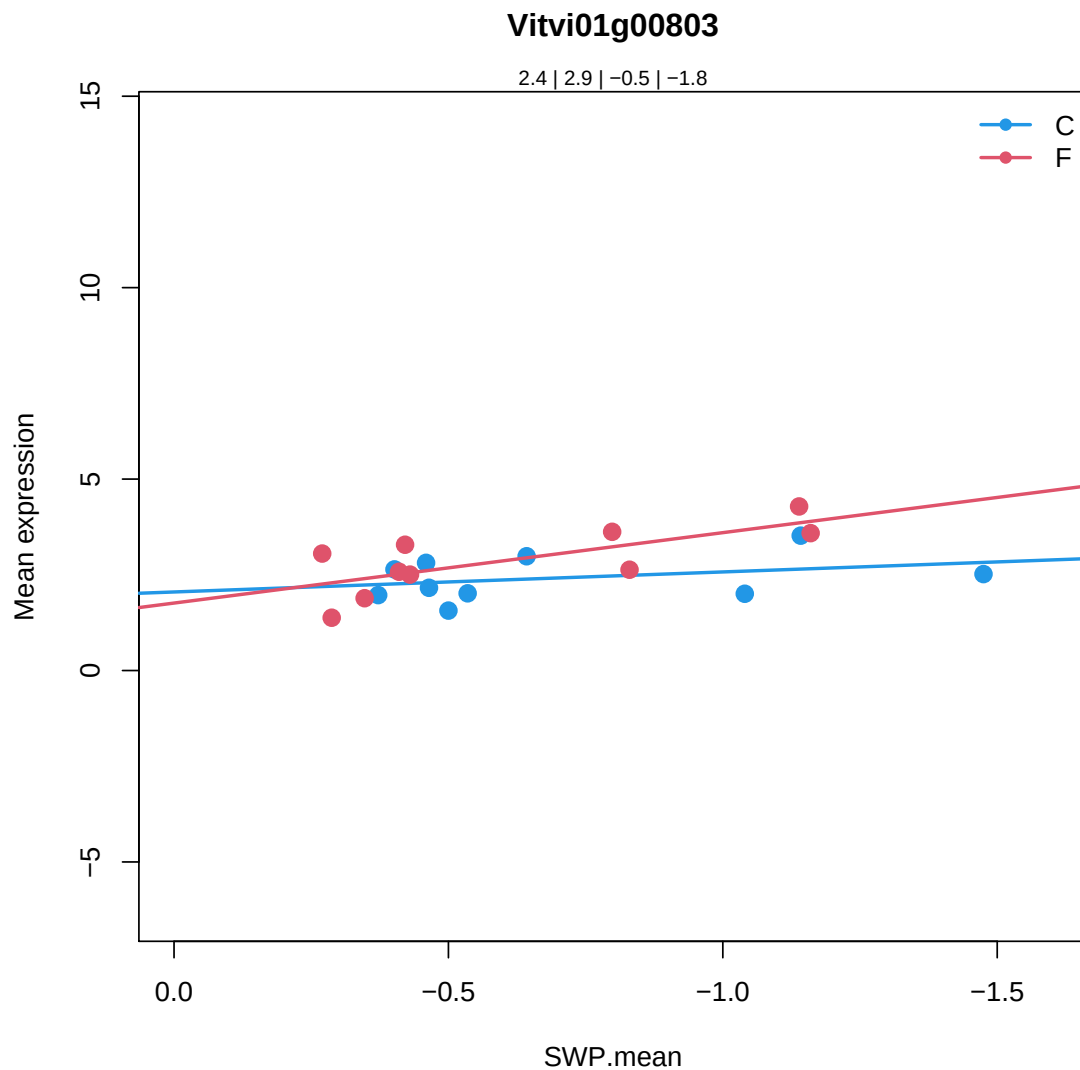
nodulin MtN21 /EamA-like transporter family protein |

Chr5:16082325-16084466 REVERSE LENGTH=368 |

201606

Coefficients for Vitvi01g00803.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.419448	8.972957e-12	***	1.228362e-11	***
SlopeC	-0.523193	0.3159965		0.7958391	
MeanF-MeanC	0.4626168	0.08825541	.	0.3390704	
SlopeF-SlopeC	-1.315434	0.09720379	.	0.9999488	



8.1.280 Vitvi02g00691: Type1.0

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

Vitvi02g00691

27.3.99

RNA.regulation of transcription.unclassified

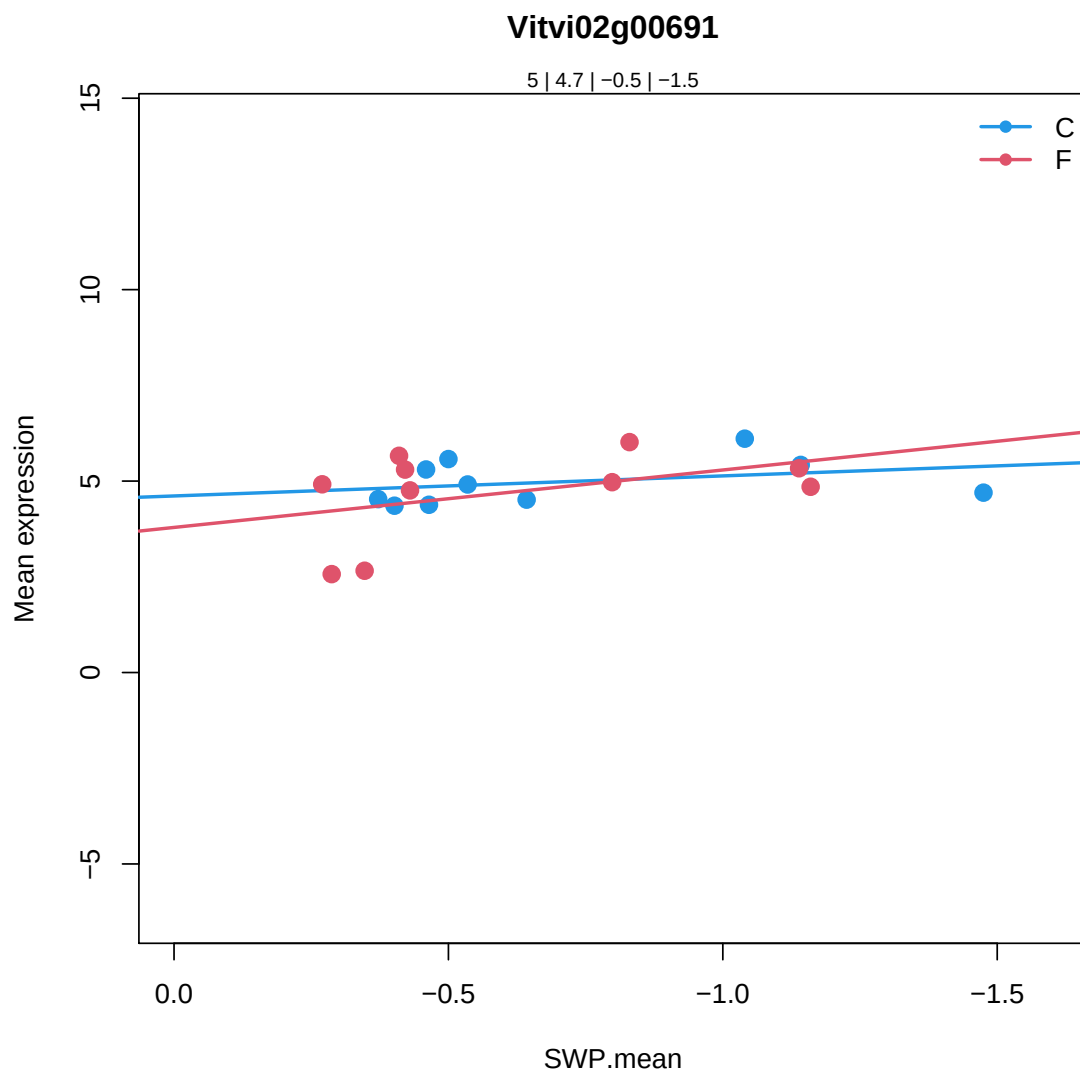
RING/FYVE/PHD zinc finger superfamily protein |

Chr3:640828-645303 FORWARD LENGTH=994 |

201606

Coefficients for Vitvi02g00691.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.97982	4.042779e-15	***	7.079509e-15	***
SlopeC	-0.5237659	0.4694202		0.8618199	
MeanF-MeanC	-0.2762012	0.4531737		0.77969	
SlopeF-SlopeC	-0.9766363	0.3664477		0.9999488	



8.1.281 Vitvi14g00887: Type1.0

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

Vitvi14g00887

33.99

development.unspecified

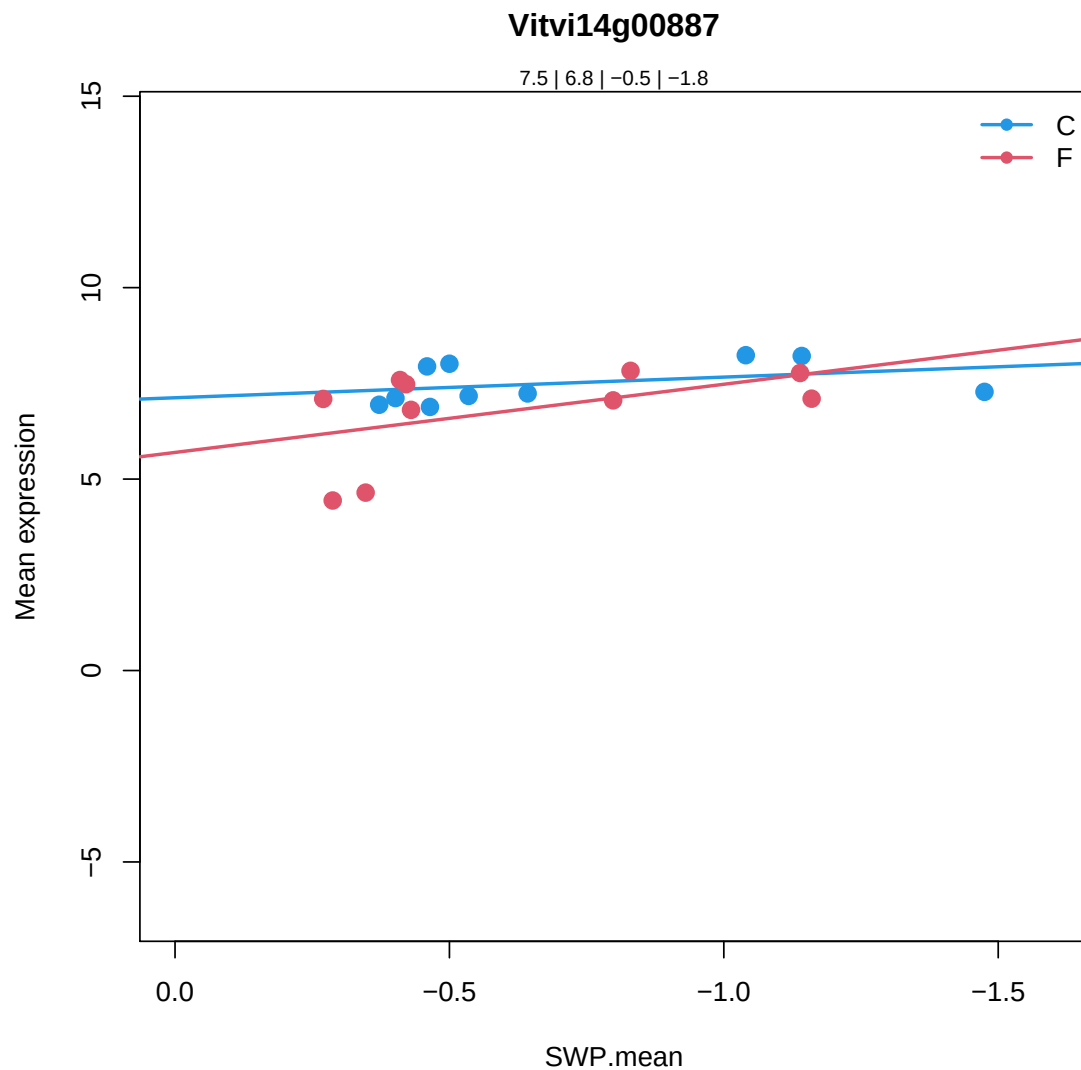
cysteine-rich RECEPTOR-like kinase |

Chr4:12129485-12133157 FORWARD LENGTH=1043 |

201606

Coefficients for Vitvi14g00887.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.503167	6.433942e-19	***	2.343277e-18	***
SlopeC	-0.539557	0.4506074		0.8555685	
MeanF-MeanC	-0.7226466	0.05552941	.	0.256018	
SlopeF-SlopeC	-1.240955	0.2480377		0.9999488	



8.1.282 Vitvi07g01354: Type1.0

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

Vitvi07g01354

35.2

not assigned.unknown

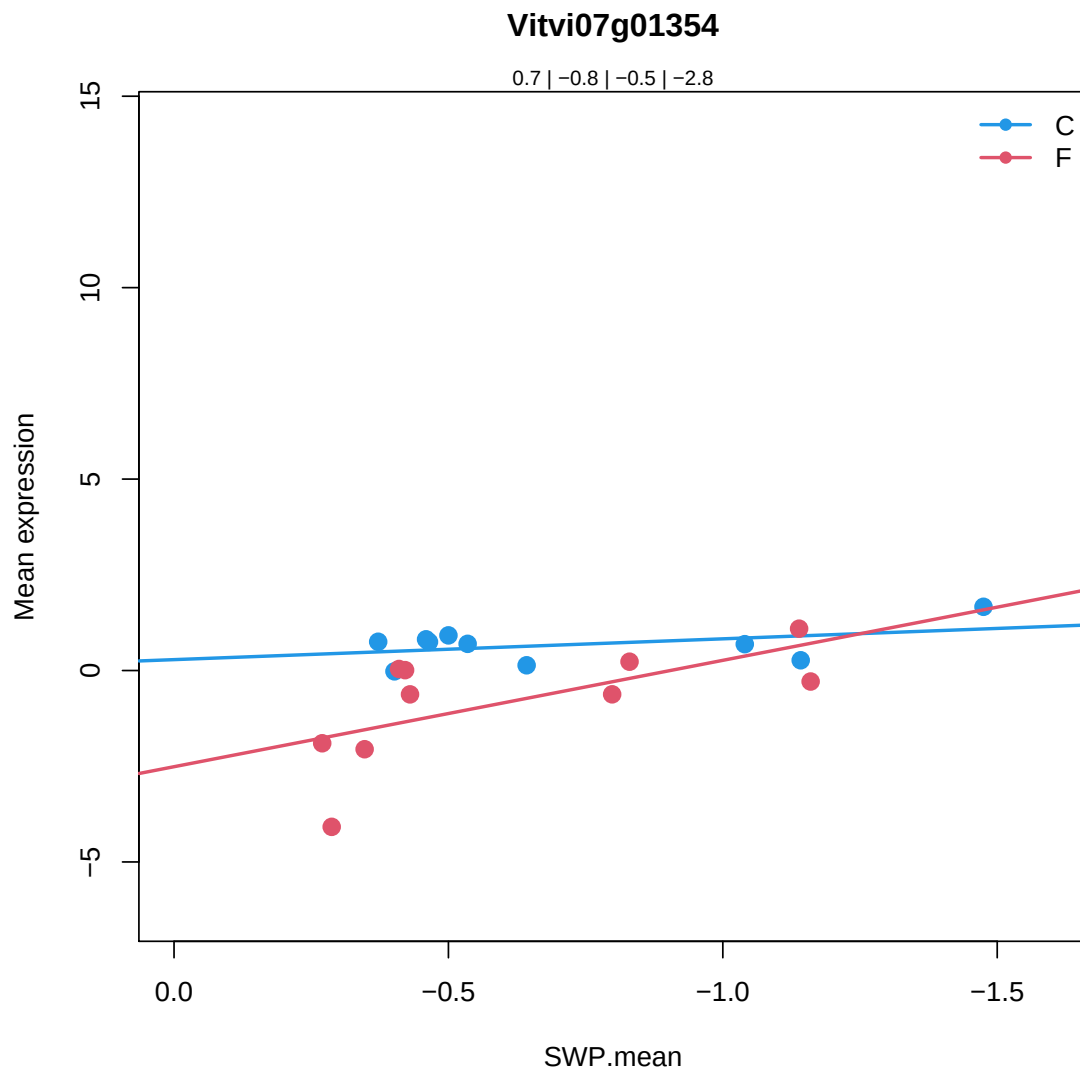
annexin 8 |

Chr5:4009223-4010687 FORWARD LENGTH=316 |

201606

Coefficients for Vitvi07g01354.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6662462	0.01840968	*	0.01937179	*
SlopeC	-0.5435793	0.4624567		0.8604478	
MeanF-MeanC	-1.486166	0.0005924781	***	0.008113703	**
SlopeF-SlopeC	-2.234707	0.05105037	.	0.9999488	



8.1.283 Vitvi18g00115: Type1.0

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

Vitvi18g00115

35.2

not assigned.unknown

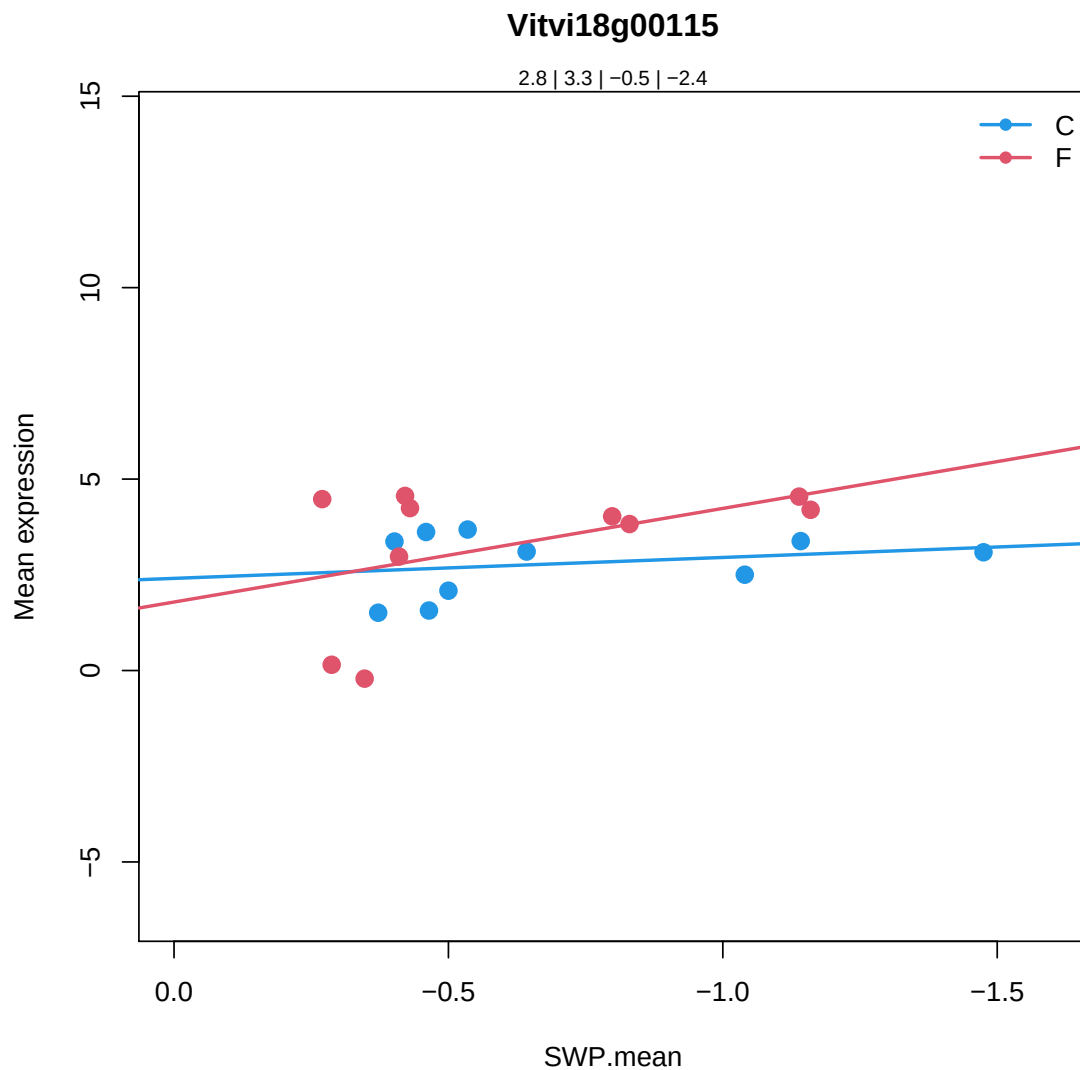
inactive purple acid phosphatase-like protein |

Chr1:15891512-15894322 FORWARD LENGTH=426 |

201606

Coefficients for Vitvi18g00115.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.790765	2.169364e-07	***	2.549969e-07	***
SlopeC	-0.54633	0.6049968		0.9047128	
MeanF-MeanC	0.4876239	0.3669079		0.7230942	
SlopeF-SlopeC	-1.899325	0.2334225		0.9999488	



8.1.284 Vitvi08g01888: Type1.0

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

Vitvi08g01888

29.2.4

protein.synthesis.elongation

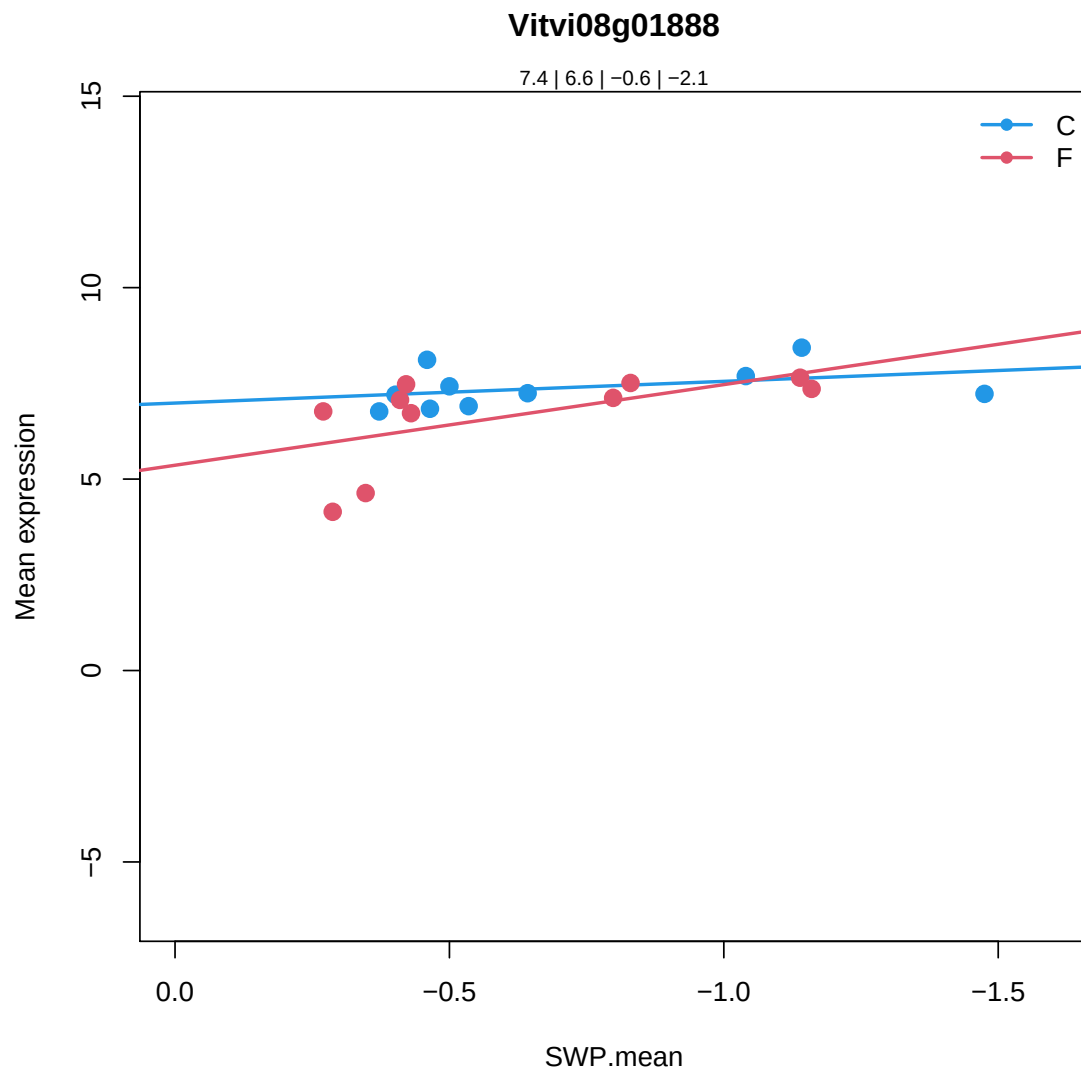
cysteine-rich RECEPTOR-like kinase |

Chr4:12129485-12133157 FORWARD LENGTH=1043 |

201606

Coefficients for Vitvi08g01888.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.383914	3.721311e-19	***	1.466018e-18	***
SlopeC	-0.56744	0.4085737		0.8377166	
MeanF-MeanC	-0.7394282	0.04215998	*	0.2138622	
SlopeF-SlopeC	-1.538998	0.1391596		0.9999488	



8.1.285 Vitvi13g01649: Type1.0

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

Vitvi13g01649

35.2

not assigned.unknown

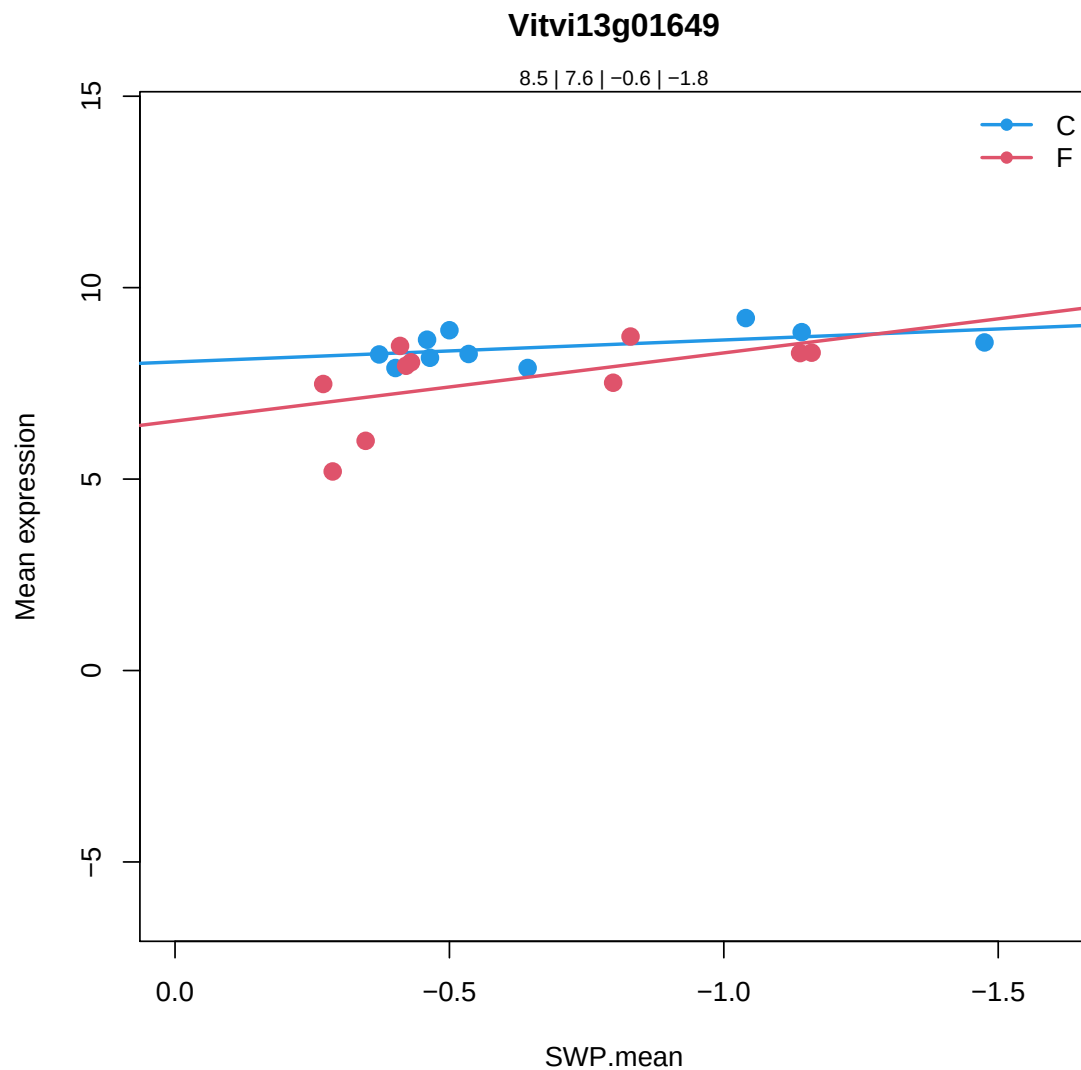
UvrABC system C protein%2C putative (DUF3411) |

Chr5:4044950-4047290 REVERSE LENGTH=386 |

201606

Coefficients for Vitvi13g01649.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	8.463107	4.77601e-21	***	3.920083e-20	***
SlopeC	-0.5740754	0.370383		0.8225965	
MeanF-MeanC	-0.8630673	0.01307976	*	0.092706	.
SlopeF-SlopeC	-1.205823	0.2103658		0.9999488	



8.1.286 Vitvi12g00649: Type1.0

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

Vitvi12g00649

17.2.3

hormone metabolism.auxin.induced-regulated-responsive-activated

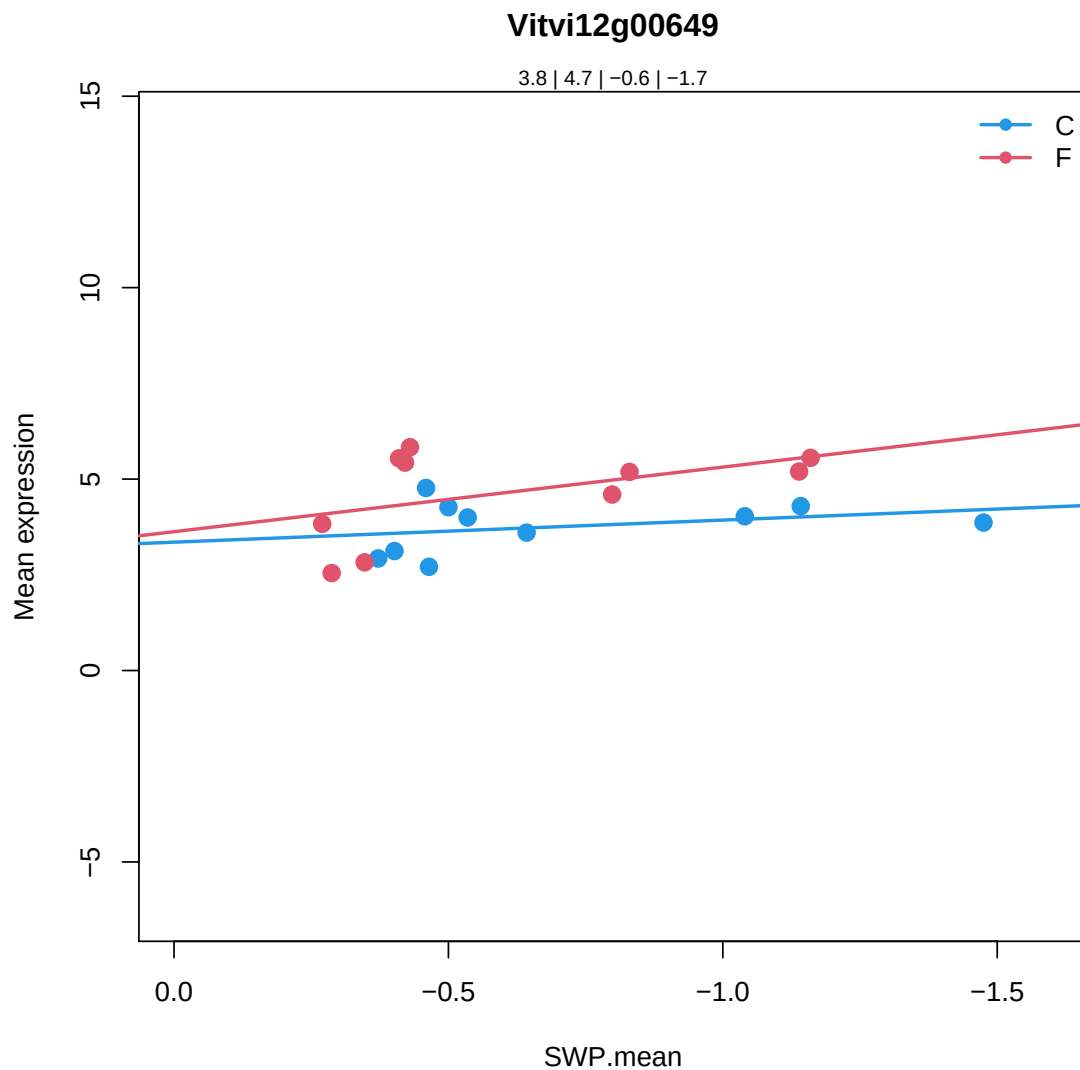
Auxin-responsive family protein |

Chr5:13900913-13902934 REVERSE LENGTH=404 |

201606

Coefficients for Vitvi12g00649.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.757271	1.492363e-12	***	2.119117e-12	***
SlopeC	-0.5765194	0.4329296		0.8483989	
MeanF-MeanC	0.8970007	0.02312794	*	0.1402212	
SlopeF-SlopeC	-1.110625	0.3124565		0.9999488	



8.1.287 Vitvi15g01035: Type1.0

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

Vitvi15g01035

20.1.7.3

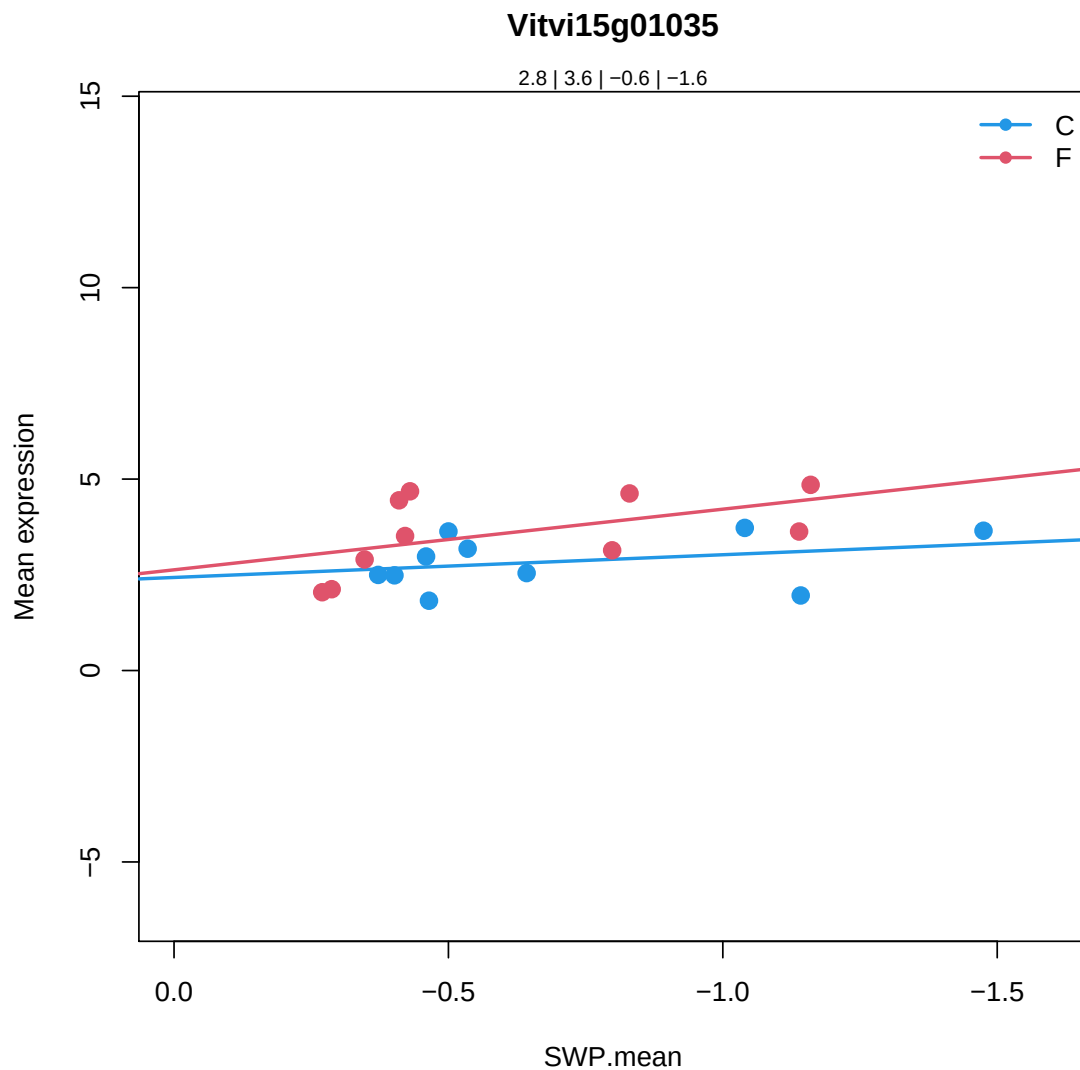
stress.biotic.PR-proteins.PR3/4/8/11 (chitinases and chitin binding pr
chitinase A |

Chr5:8143805-8145153 REVERSE LENGTH=302 |

201606

Coefficients for Vitvi15g01035.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.847872	6.751736e-11	***	8.891478e-11	***
SlopeC	-0.5934209	0.3836072		0.82771	
MeanF-MeanC	0.7471841	0.03863413	*	0.2015958	
SlopeF-SlopeC	-0.9906941	0.3295416		0.9999488	



8.1.288 Vitvi08g01217: Type1.0

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

Vitvi08g01217

35.1

not assigned.no ontology

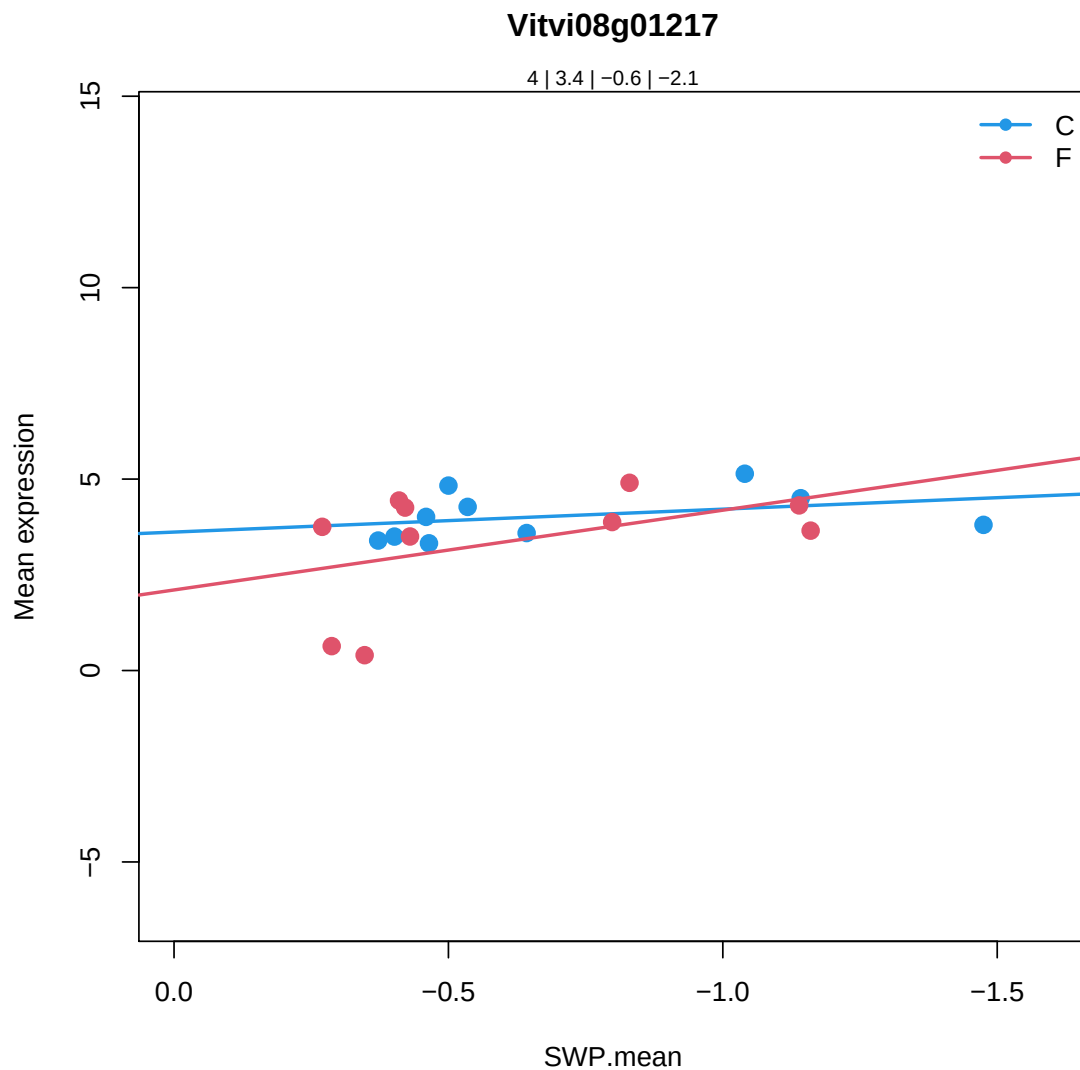
Haloacid dehalogenase-like hydrolase (HAD) superfamily protein |

Chr5:448293-450507 FORWARD LENGTH=317 |

201606

Coefficients for Vitvi08g01217.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.036566	1.993734e-11	***	2.686395e-11	***
SlopeC	-0.5983268	0.506905		0.8711742	
MeanF-MeanC	-0.6633628	0.1554967		0.4756778	
SlopeF-SlopeC	-1.484579	0.2729302		0.9999488	



8.1.289 Vitvi19g00749: Type1.0

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

Vitvi19g00749

33.99

development.unspecified

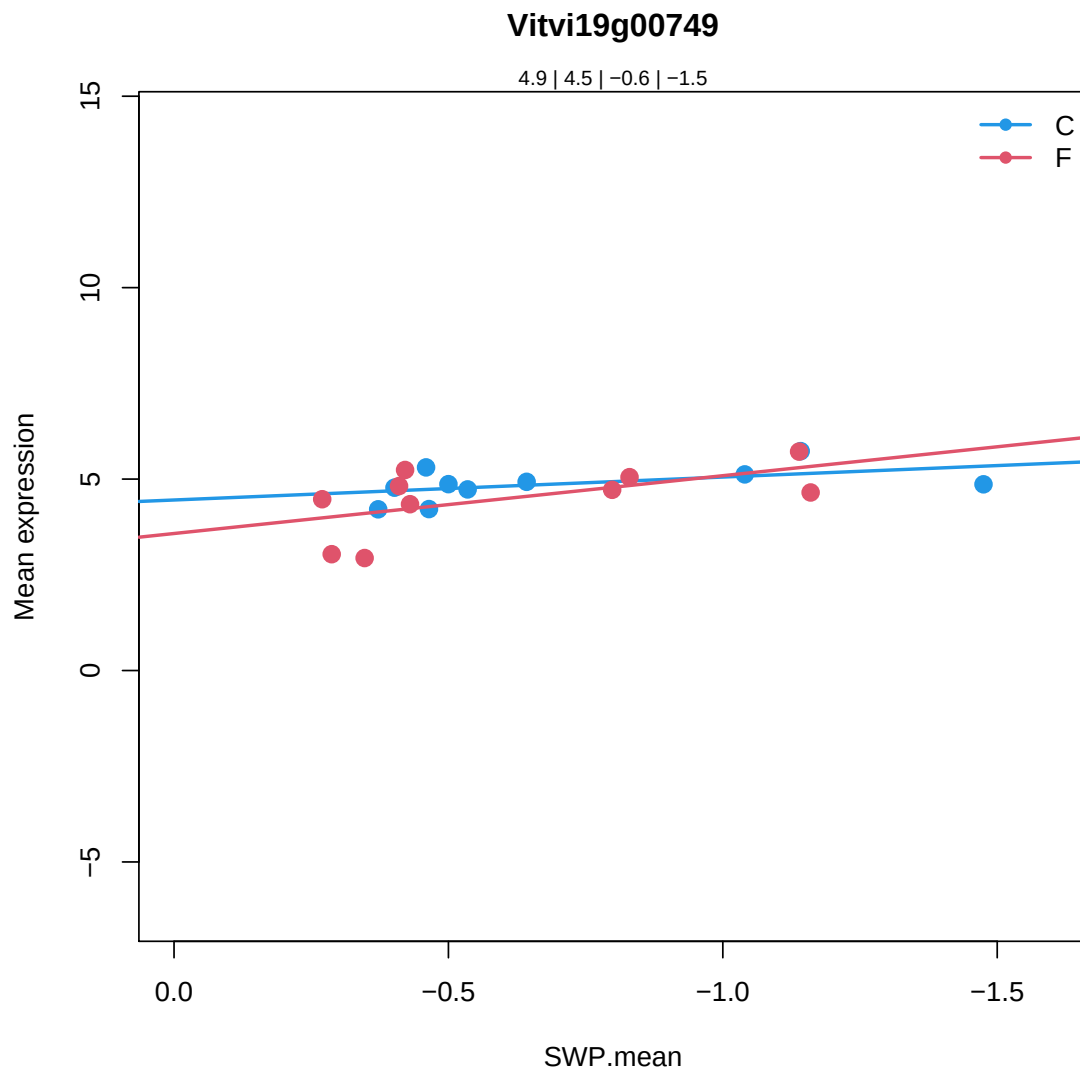
Transducin/WD40 repeat-like superfamily protein |

Chr5:22722755-22725065 REVERSE LENGTH=315 |

201606

Coefficients for Vitvi19g00749.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.87479	8.849403e-18	***	2.363873e-17	***
SlopeC	-0.5993603	0.2592304		0.7673704	
MeanF-MeanC	-0.3761706	0.1668663		0.4954895	
SlopeF-SlopeC	-0.9105462	0.2497889		0.9999488	



8.1.290 Vitvi15g00084: Type1.0

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

Vitvi15g00084

33.99

development.unspecified

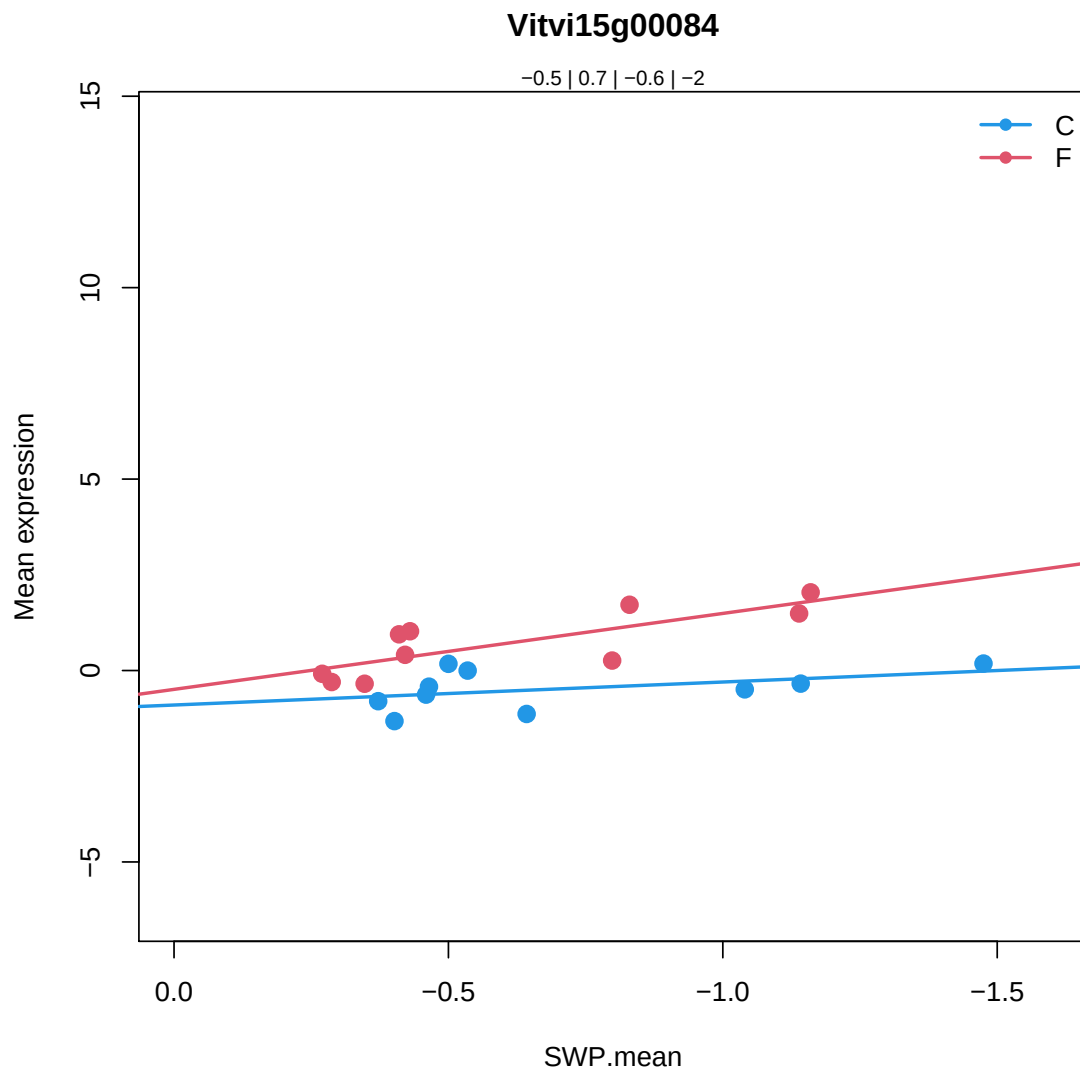
Major facilitator superfamily protein |

Chr5:18334476-18337240 REVERSE LENGTH=570 |

201606

Coefficients for Vitvi15g00084.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.4789442	0.007524357	**	0.007994859	**
SlopeC	-0.6008635	0.1973199		0.7250708	
MeanF-MeanC	1.194793	3.473196e-05	***	0.000726179	***
SlopeF-SlopeC	-1.382961	0.05199729	.	0.9999488	



8.1.291 Vitvi01g00674: Type1.0

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

Vitvi01g00674

31.2

cell.division

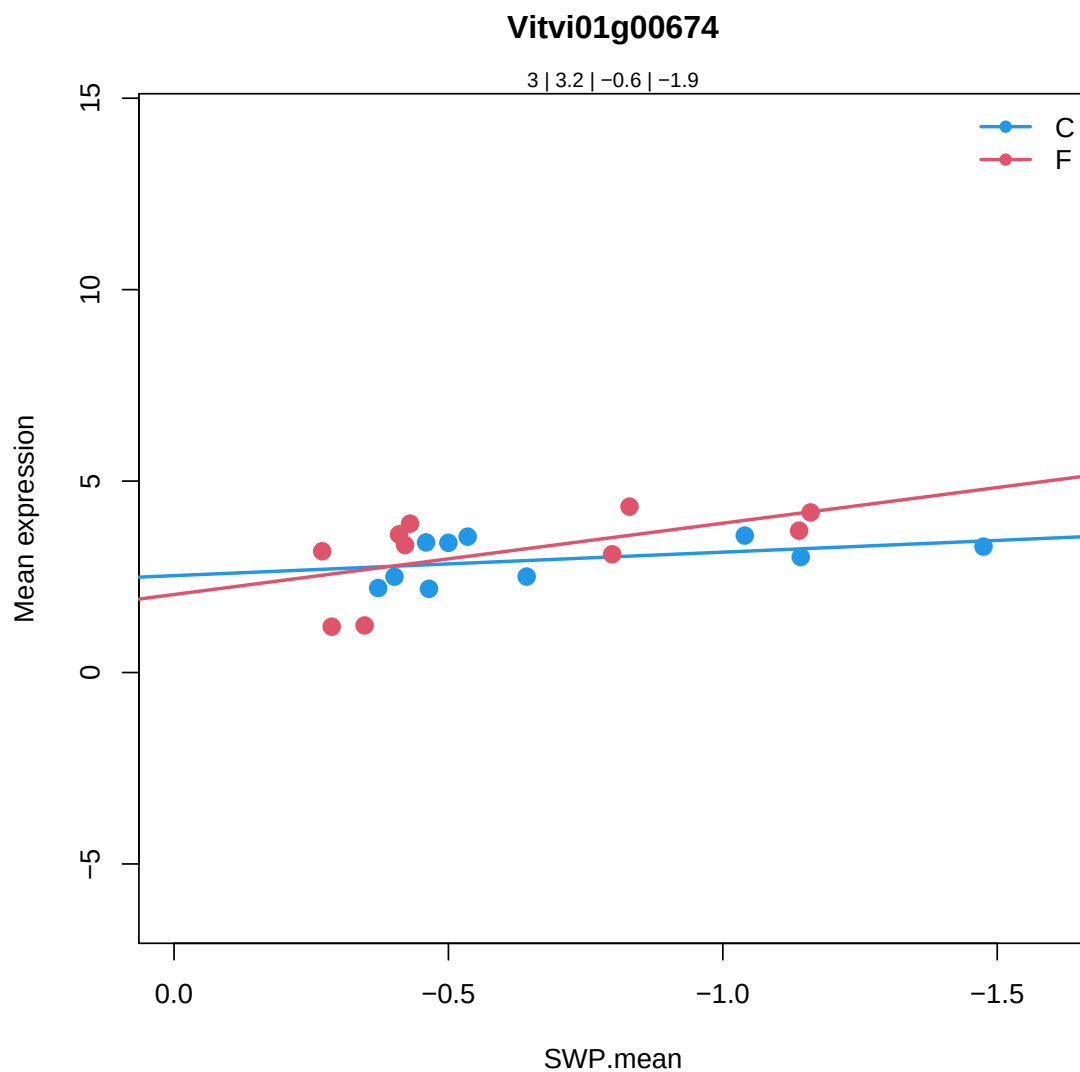
alpha/beta-Hydrolases superfamily protein |

Chr1:3568612-3570466 REVERSE LENGTH=406 |

201606

Coefficients for Vitvi01g00674.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.961661	1.070839e-11	***	1.4586e-11	***
SlopeC	-0.6134074	0.340747		0.804724	
MeanF-MeanC	0.2106152	0.5174521		0.816539	
SlopeF-SlopeC	-1.249407	0.1963959		0.9999488	



8.1.292 Vitvi16g00863: Type1.0

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

Vitvi16g00863

35.2

not assigned.unknown

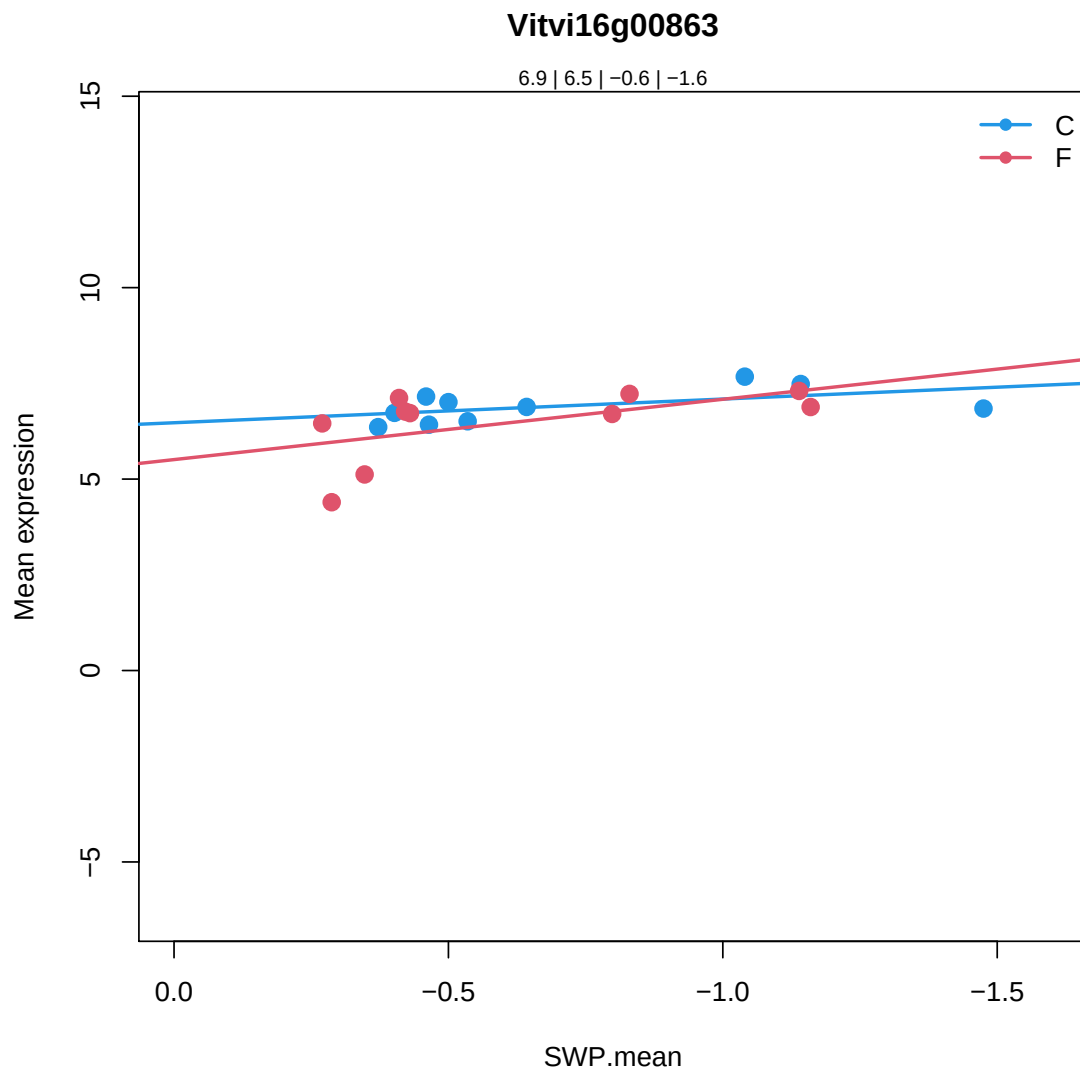
2 iron%2C 2 sulfur cluster binding protein |

Chr5:21009645-21010227 FORWARD LENGTH=108 |

201606

Coefficients for Vitvi16g00863.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.906561	1.471445e-20	***	9.675482e-20	***
SlopeC	-0.6187618	0.264527		0.7701943	
MeanF-MeanC	-0.4379308	0.1252872		0.4189659	
SlopeF-SlopeC	-0.9567573	0.2469424		0.9999488	



8.1.293 Vitvi16g00139: Type1.0

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

Vitvi16g00139

16.2.1.3

secondary metabolism.phenylpropanoids.lignin biosynthesis.4CL

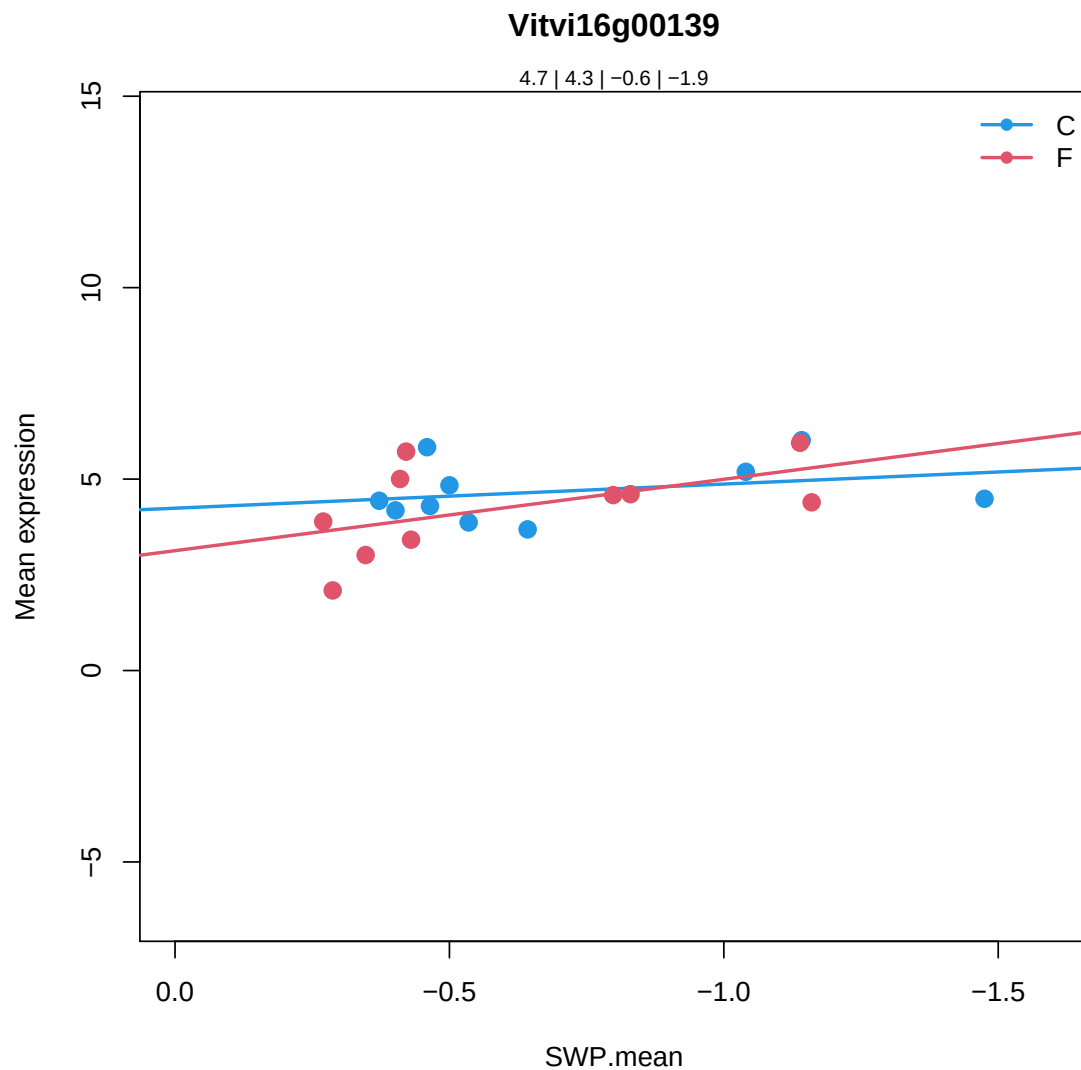
4-coumarate:CoA ligase 3 |

Chr1:24167927-24171457 REVERSE LENGTH=495 |

201606

Coefficients for Vitvi16g00139.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.682616	3.886032e-14	***	6.169242e-14	***
SlopeC	-0.630287	0.4086905		0.8377166	
MeanF-MeanC	-0.4164862	0.285458		0.6507885	
SlopeF-SlopeC	-1.234384	0.2797695		0.9999488	



8.1.294 Vitvi10g00544: Type1.0

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

Vitvi10g00544

16.2

secondary metabolism.phenylpropanoids

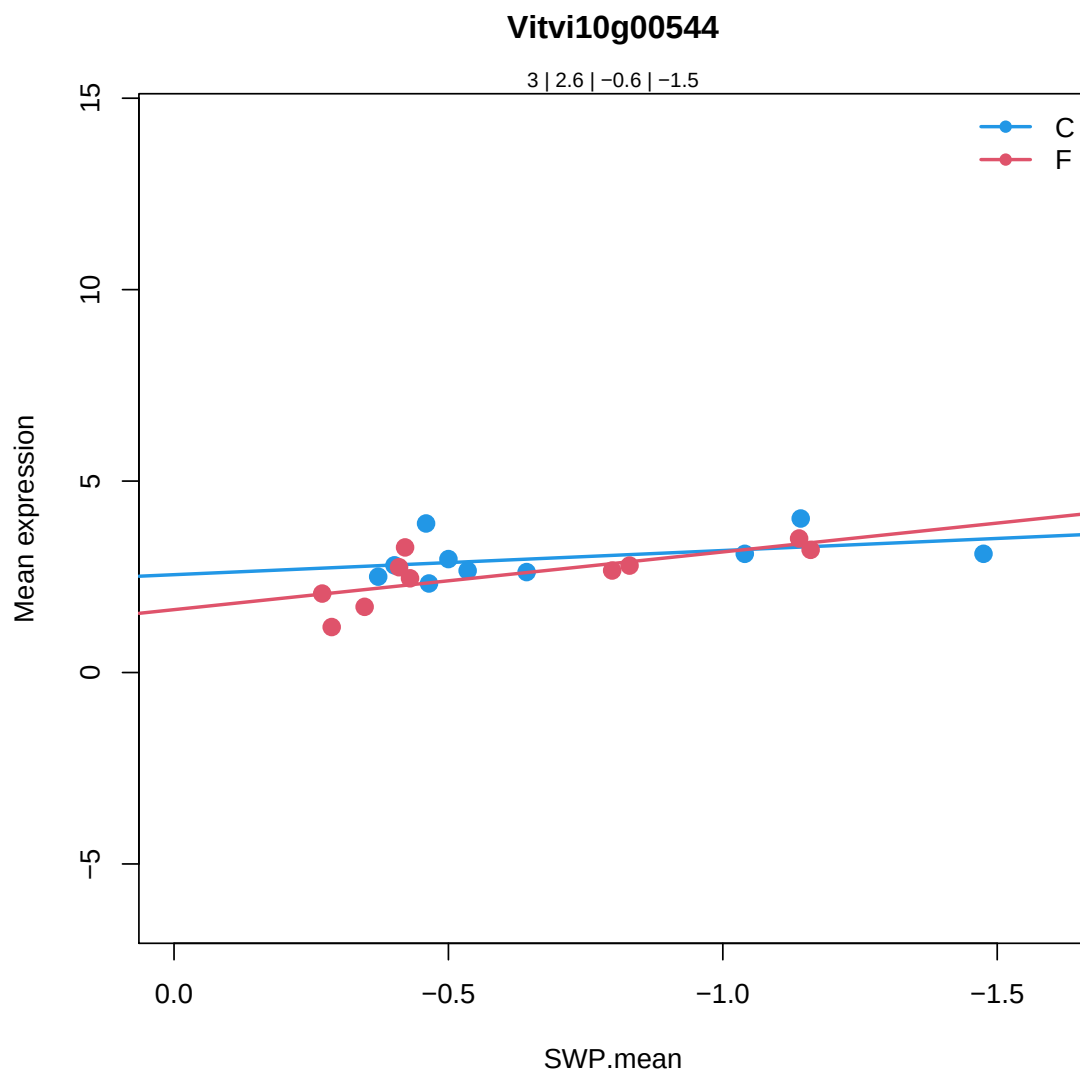
HXXXD-type acyl-transferase family protein |

Chr1:10078222-10079492 FORWARD LENGTH=394 |

201606

Coefficients for Vitvi10g00544.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.998883	2.155876e-14	***	3.497218e-14	***
SlopeC	-0.6313792	0.1888007		0.7197362	
MeanF-MeanC	-0.4384792	0.0774908	.	0.3141263	
SlopeF-SlopeC	-0.8757221	0.2194979		0.9999488	



8.1.295 Vitvi18g00792: Type1.0

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

Vitvi18g00792

26.10

misc.cytochrome P450

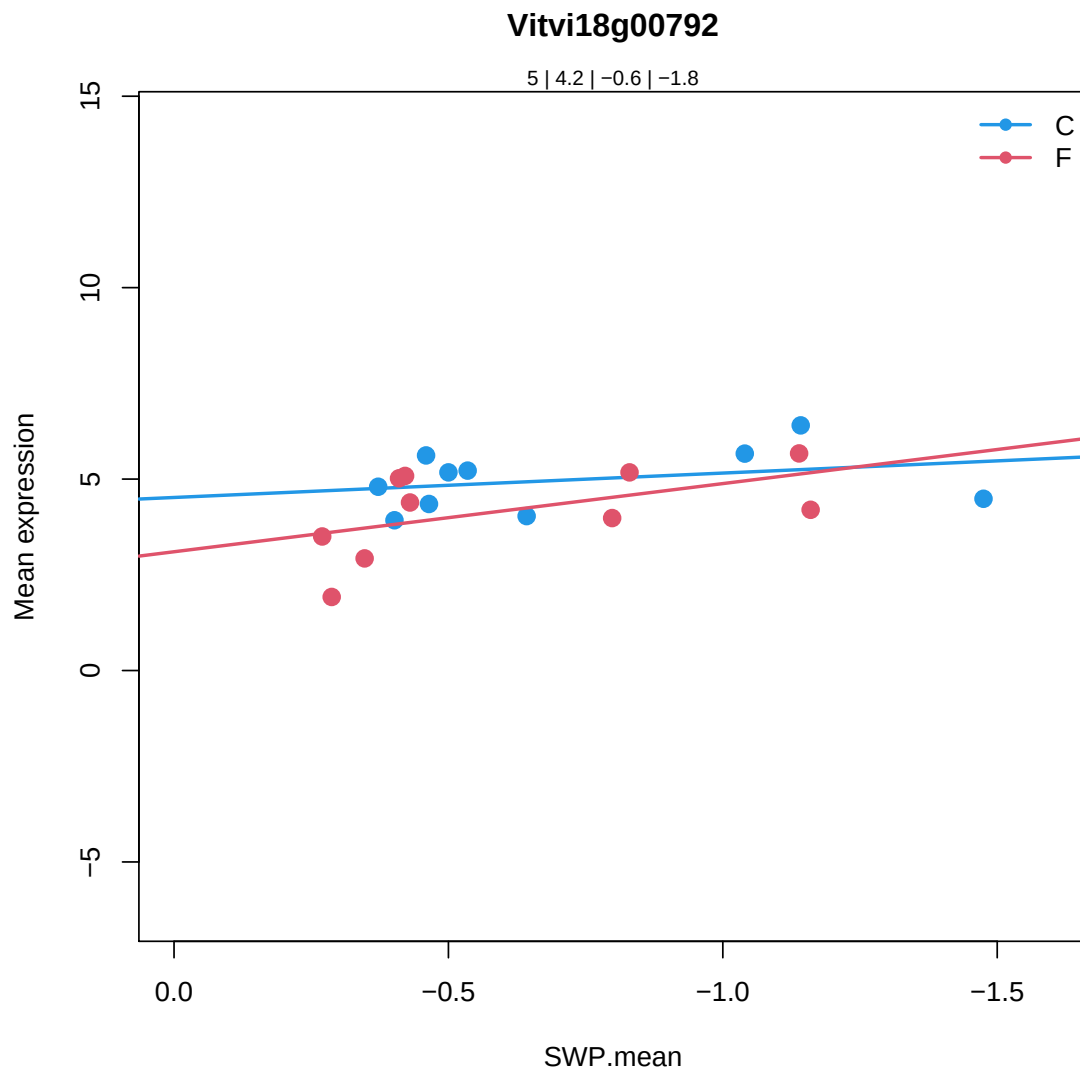
cytochrome P450%2C family 707%2C subfamily A%2C polypeptide 2 |

Chr2:12496875-12499080 REVERSE LENGTH=345 |

201606

Coefficients for Vitvi18g00792.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.967387	8.703297e-15	***	1.464675e-14	***
SlopeC	-0.6372864	0.3965843		0.8323371	
MeanF-MeanC	-0.7807856	0.04920108	*	0.2361962	
SlopeF-SlopeC	-1.142883	0.3088766		0.9999488	



8.1.296 Vitvi03g00676: Type1.0

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

Vitvi03g00676

35.2

not assigned.unknown

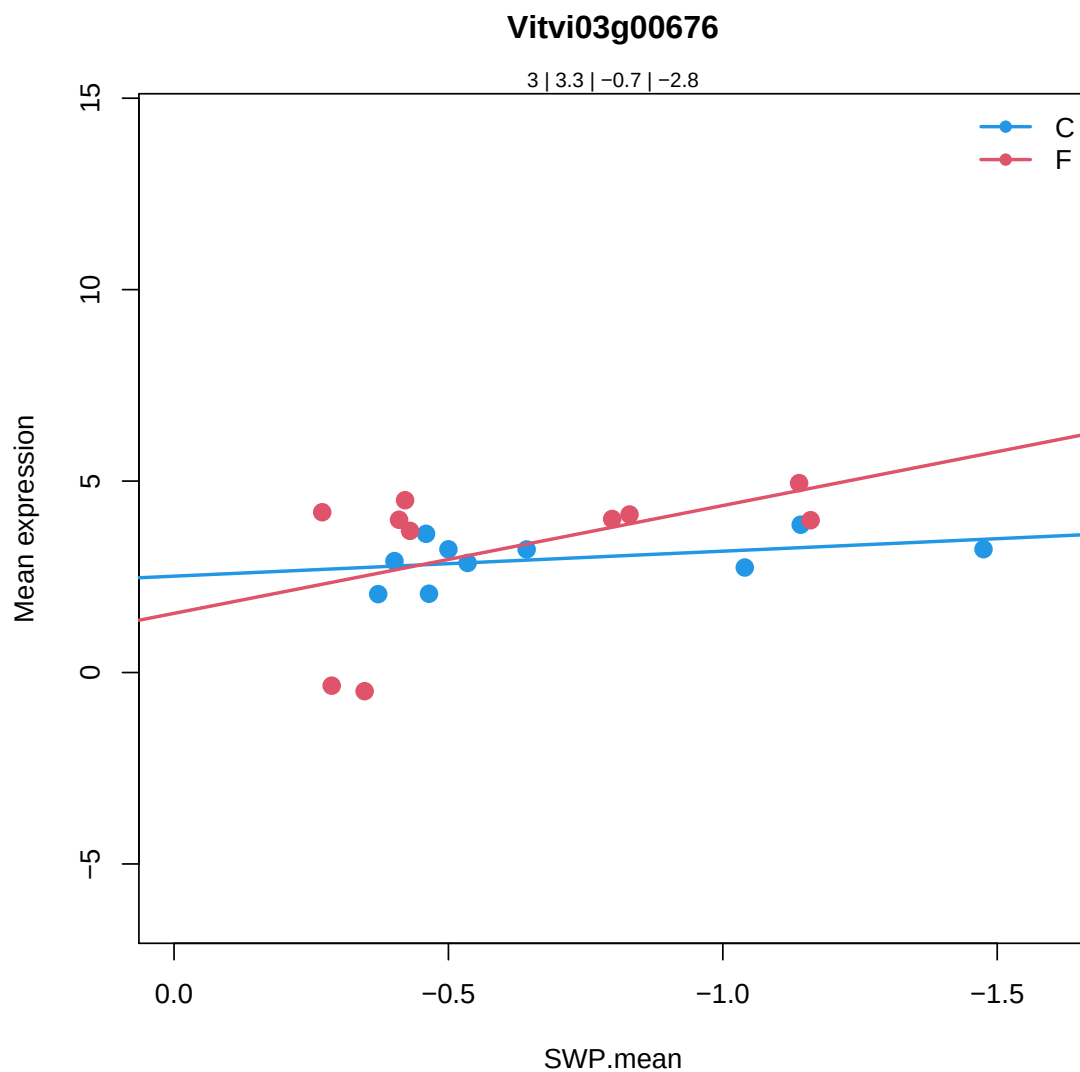
2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein

Chr1:29545031-29546041 REVERSE LENGTH=278 |

201606

Coefficients for Vitvi03g00676.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.975489	8.47516e-08	***	1.007632e-07	***
SlopeC	-0.65251	0.5393904		0.883204	
MeanF-MeanC	0.2852641	0.5971837		0.8596783	
SlopeF-SlopeC	-2.162774	0.1790919		0.9999488	



8.1.297 Vitvi02g01408: Type1.0

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

Vitvi02g01408

20.1.7.5

stress.biotic.PR-proteins.PR5 (thaumatin-like proteins)

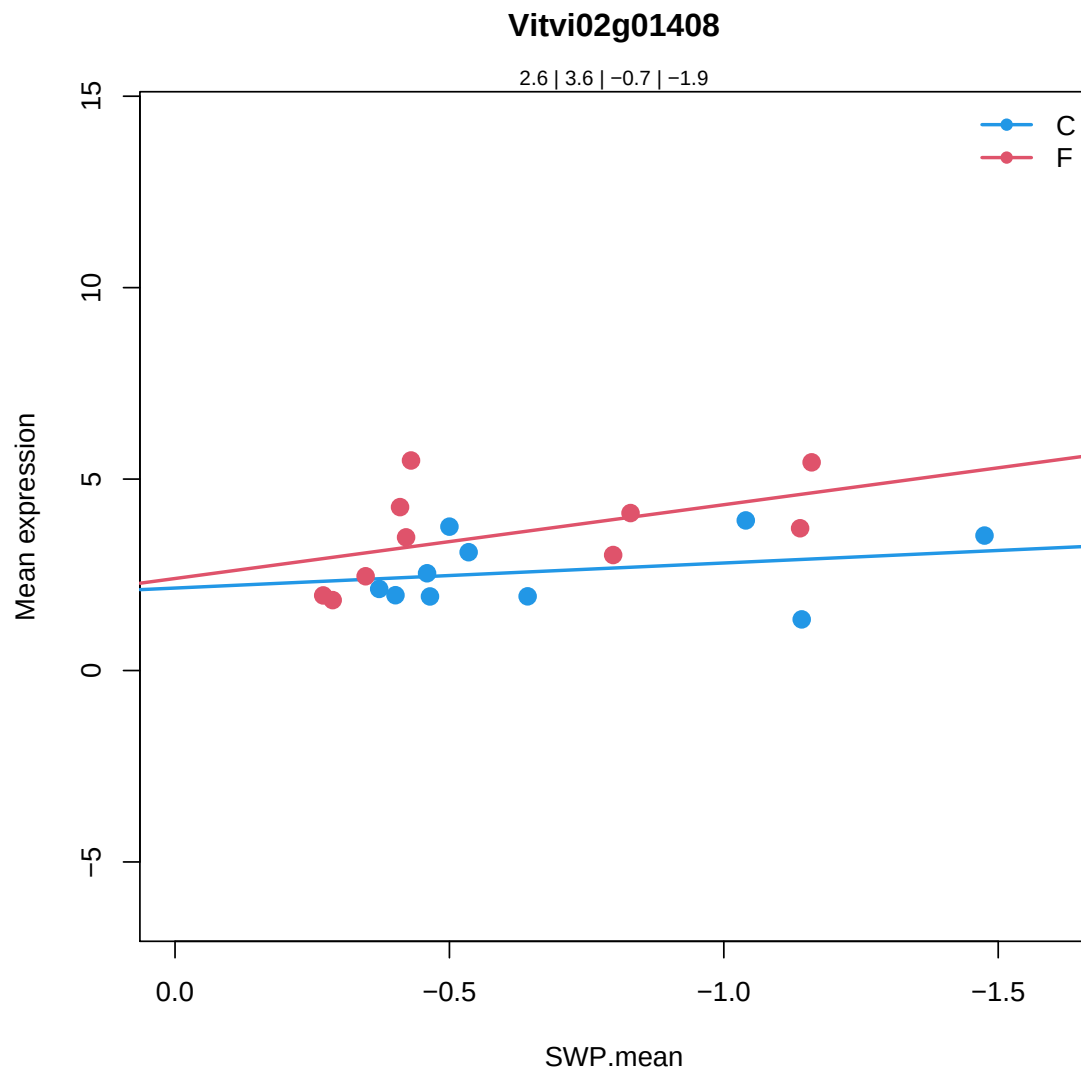
osmotin 34 |

Chr4:7025127-7026113 REVERSE LENGTH=244 |

201606

Coefficients for Vitvi02g01408.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.613612	1.631969e-08	***	1.980136e-08	***
SlopeC	-0.6546022	0.440015		0.8507652	
MeanF-MeanC	0.9636557	0.03302993	*	0.1803349	
SlopeF-SlopeC	-1.272797	0.3154781		0.9999488	



8.1.298 Vitvi03g01392: Type1.0

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

Vitvi03g01392

26.8

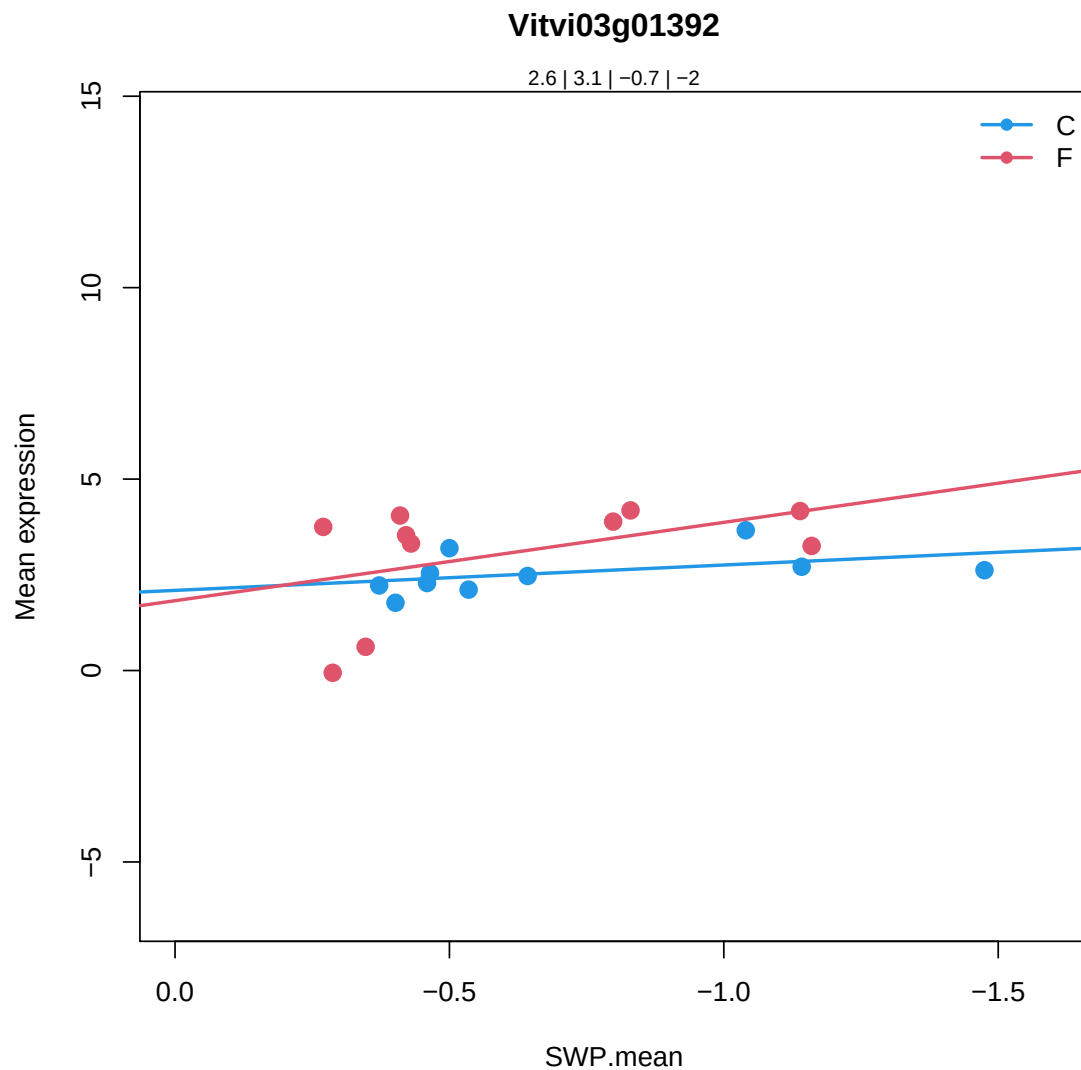
misc.nitrilases, nitrile lyases, berberine bridge enzymes, reticuline
Amidase family protein |

Chr4:16615549-16617424 FORWARD LENGTH=512 |

201606

Coefficients for Vitvi03g01392.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.558863	2.798517e-08	***	3.369805e-08	***
SlopeC	-0.6628284	0.4392916		0.8505602	
MeanF-MeanC	0.5110158	0.24505		0.6046708	
SlopeF-SlopeC	-1.382729	0.2816026		0.9999488	



8.1.299 Vitvi11g00075: Type1.0

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

Vitvi11g00075

29.4.1.57

protein.postranslational modification.kinase.receptor like cytoplasmat

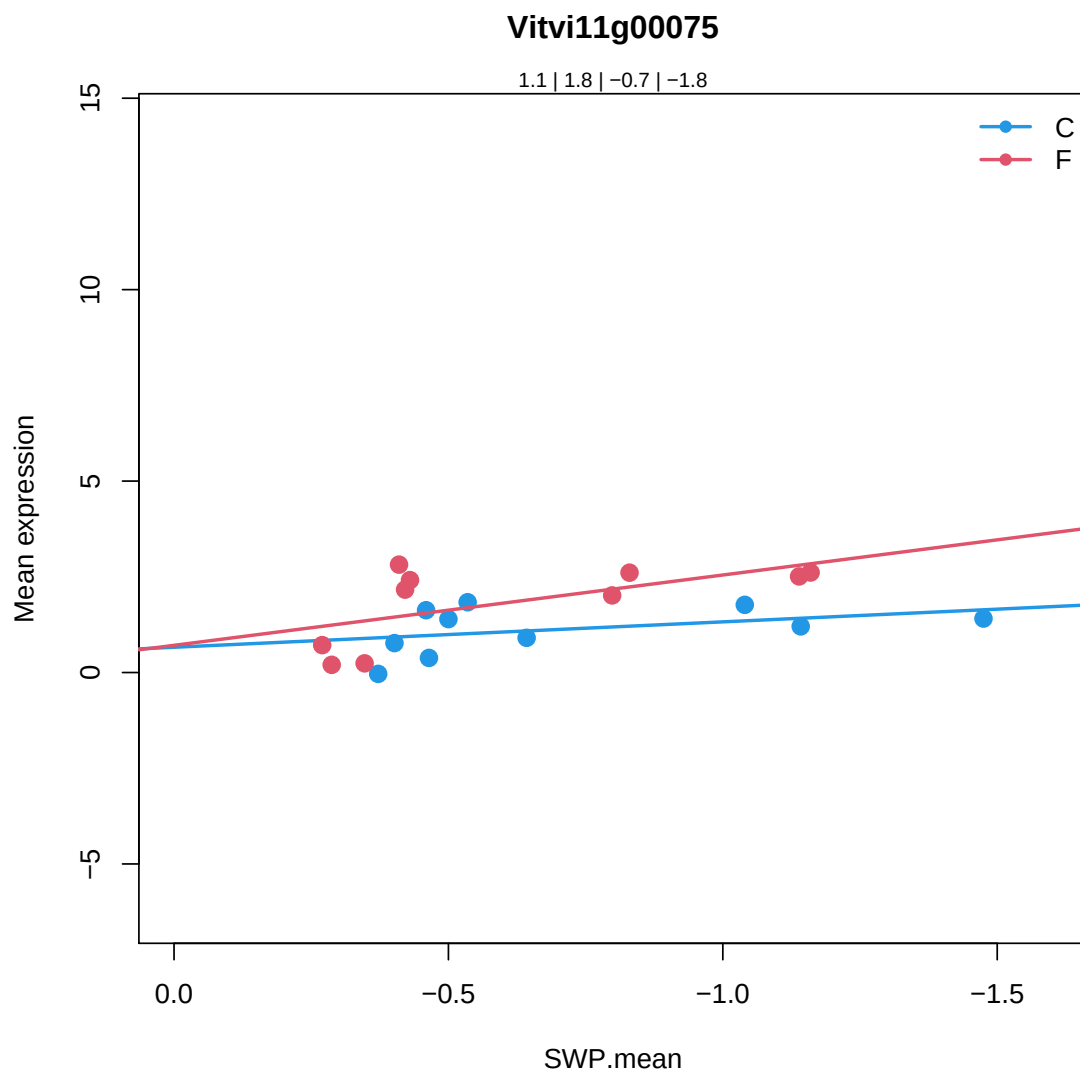
Protein kinase superfamily protein |

Chr2:2287514-2289270 REVERSE LENGTH=462 |

201606

Coefficients for Vitvi11g00075.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.125922	3.679766e-05	***	4.100826e-05	***
SlopeC	-0.6632429	0.2848623		0.7782526	
MeanF-MeanC	0.7035067	0.03232727	*	0.1782034	
SlopeF-SlopeC	-1.173116	0.2062245		0.9999488	



8.1.300 Vitvi01g00300: Type1.0

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

Vitvi01g00300

28.1

DNA.synthesis/chromatin structure

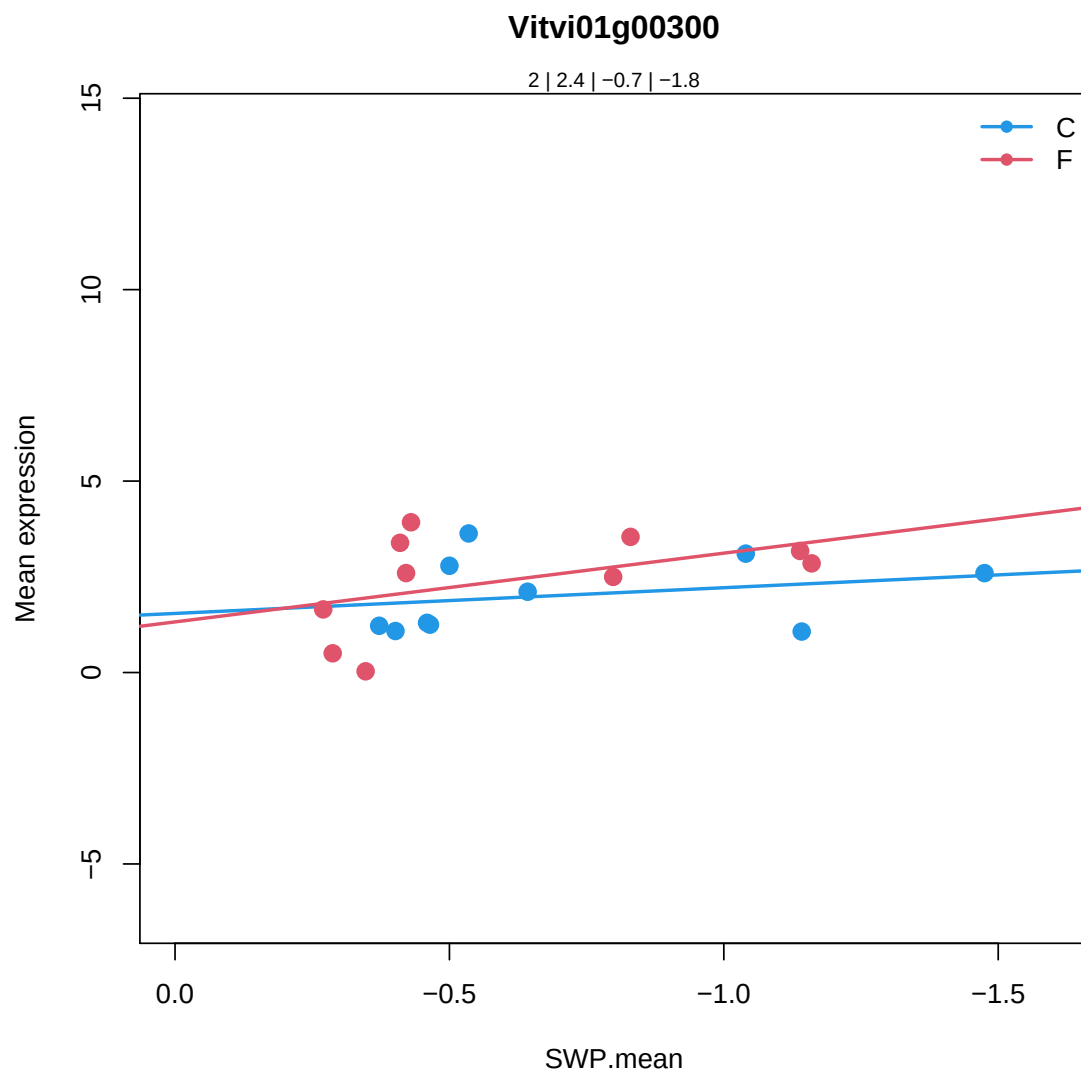
endonuclease 2 |

Chr1:25596718-25598264 FORWARD LENGTH=290 |

201606

Coefficients for Vitvi01g00300.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.015288	1.84356e-06	***	2.115452e-06	***
SlopeC	-0.6716536	0.4463591		0.8546992	
MeanF-MeanC	0.400427	0.3730137		0.7266712	
SlopeF-SlopeC	-1.124188	0.3926578		0.9999488	



8.1.301 Vitvi12g01916: Type1.0

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

Vitvi12g01916

35.1

not assigned.no ontology

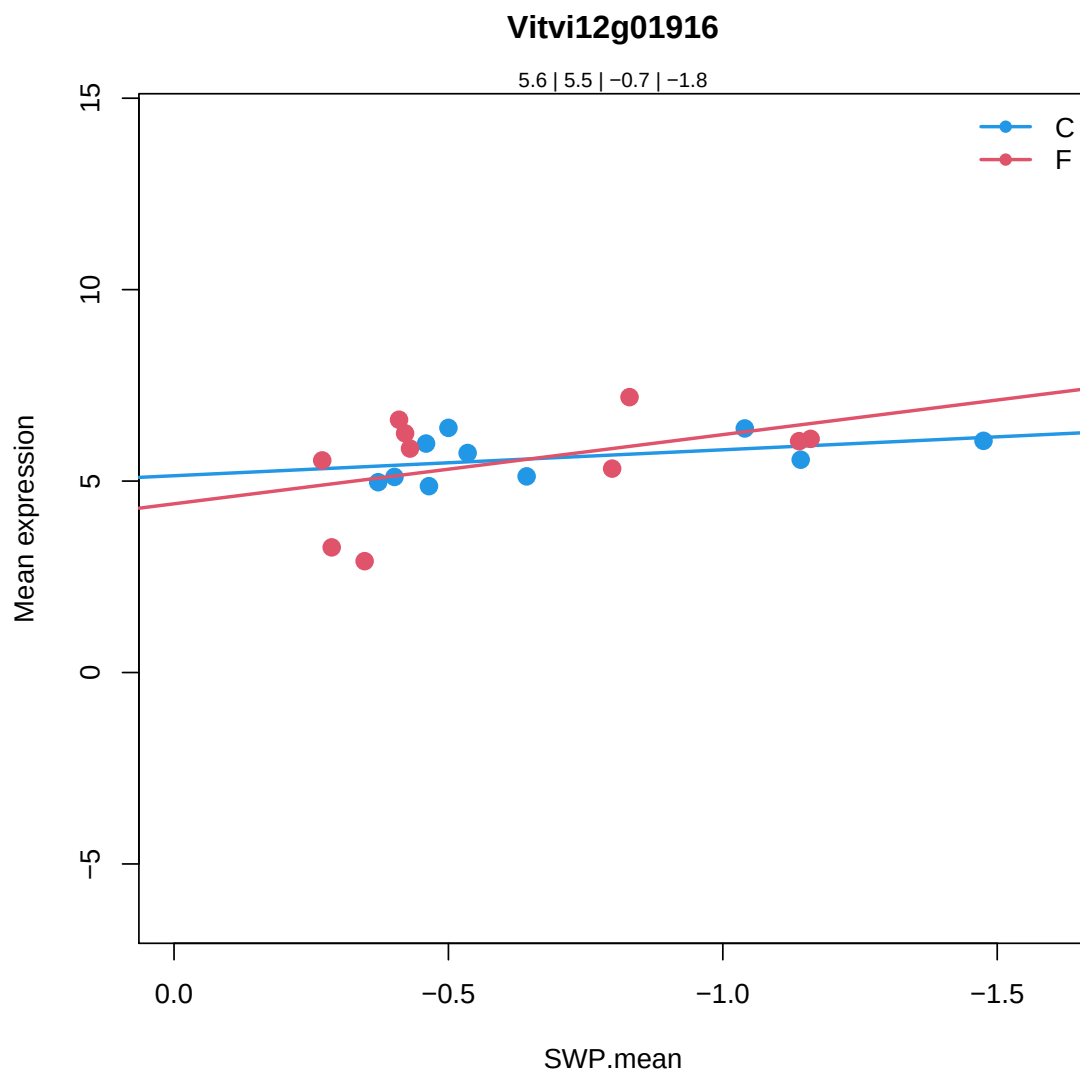
T-complex protein 11 |

Chr1:8118049-8121854 FORWARD LENGTH=1020 |

201606

Coefficients for Vitvi12g01916.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.61564	3.142432e-15	***	5.56747e-15	***
SlopeC	-0.6775159	0.4018266		0.8354442	
MeanF-MeanC	-0.1077605	0.7915415		0.9410089	
SlopeF-SlopeC	-1.12947	0.3487299		0.9999488	



8.1.302 Vitvi18g00216: Type1.0

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

Vitvi18g00216

1.1.6

PS.lightreaction.NADH DH

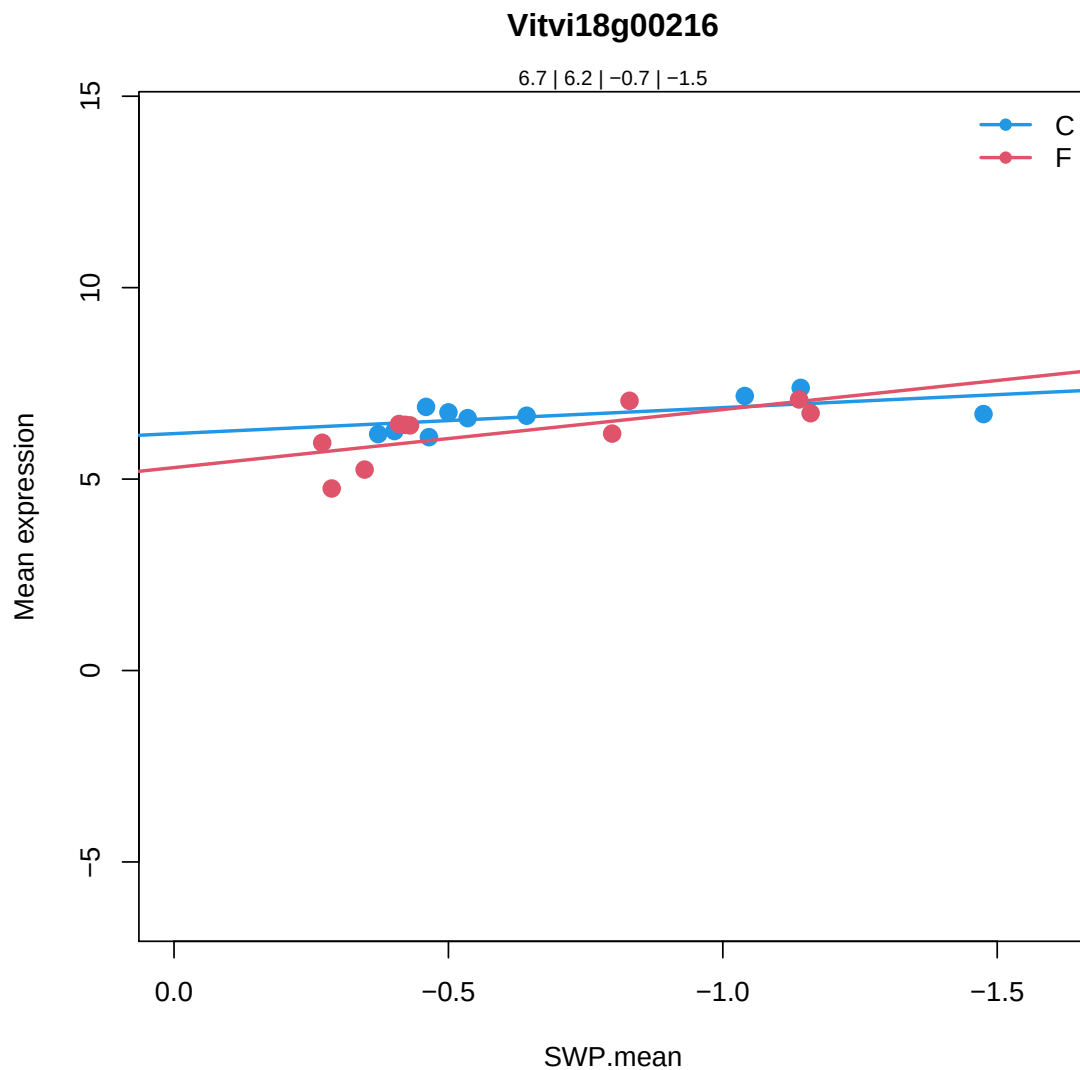
subunit NDH-M of NAD(P)H:plastoquinone dehydrogenase complex |

Chr4:17830748-17831485 REVERSE LENGTH=217 |

201606

Coefficients for Vitvi18g00216.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.664826	1.238085e-22	***	2.214447e-21	***
SlopeC	-0.6782539	0.1174851		0.6341652	
MeanF-MeanC	-0.4408549	0.04914097	*	0.2361826	
SlopeF-SlopeC	-0.8387039	0.1894946		0.9999488	



8.1.303 Vitvi07g01840: Type1.0

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

Vitvi07g01840

34.16

transport.ABC transporters and multidrug resistance systems

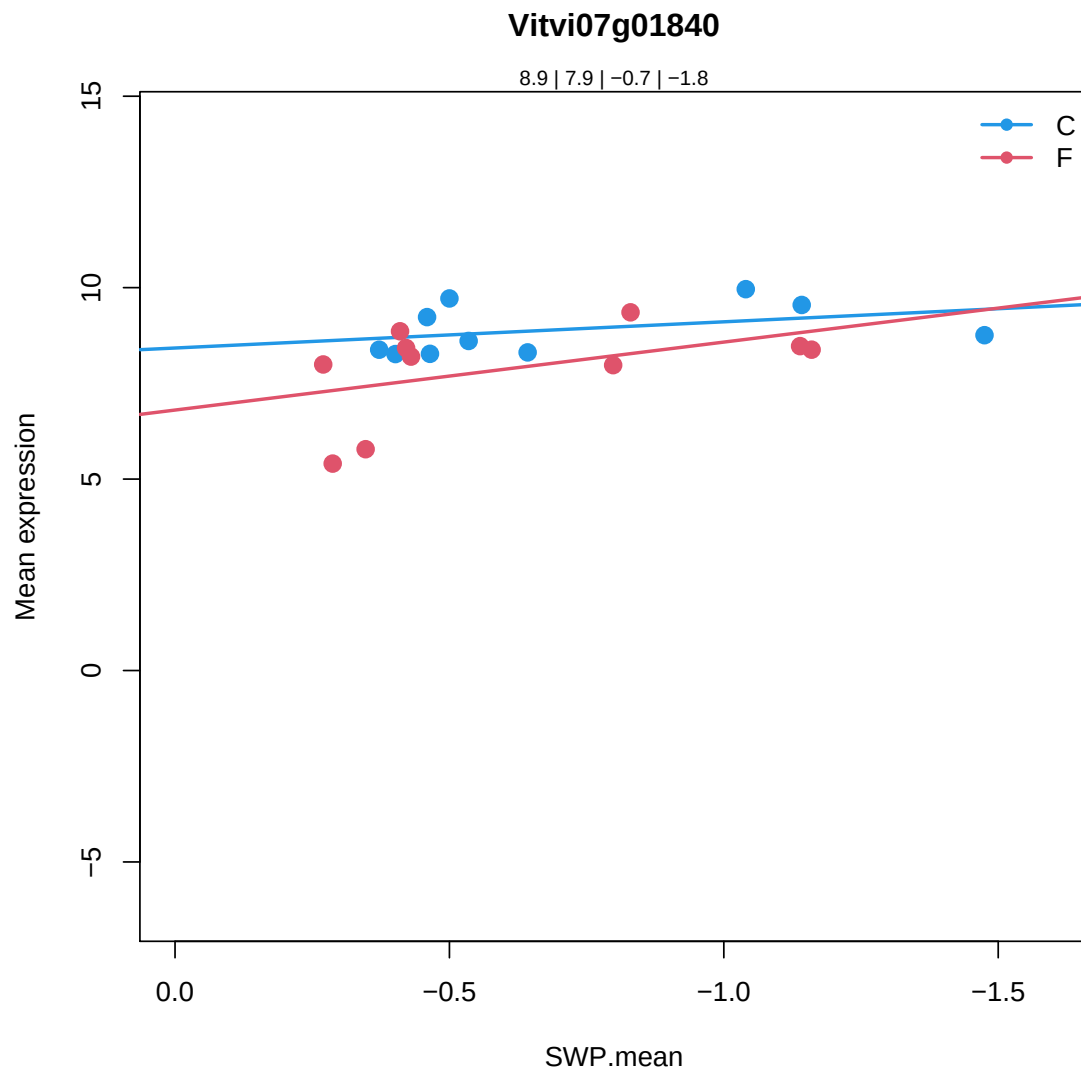
general control non-repressible 5 |

Chr5:25916956-25919693 REVERSE LENGTH=692 |

201606

Coefficients for Vitvi07g01840.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	8.904386	8.666675e-20	***	4.232536e-19	***
SlopeC	-0.6842502	0.3763423		0.8249251	
MeanF-MeanC	-1.020234	0.01481947	*	0.1010076	
SlopeF-SlopeC	-1.09106	0.3439079		0.9999488	



8.1.304 Vitvi19g00007: Type1.0

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

Vitvi19g00007

17.3.1.1.1

hormone metabolism.brassinosteroid.synthesis-degradation.BRs.DET2

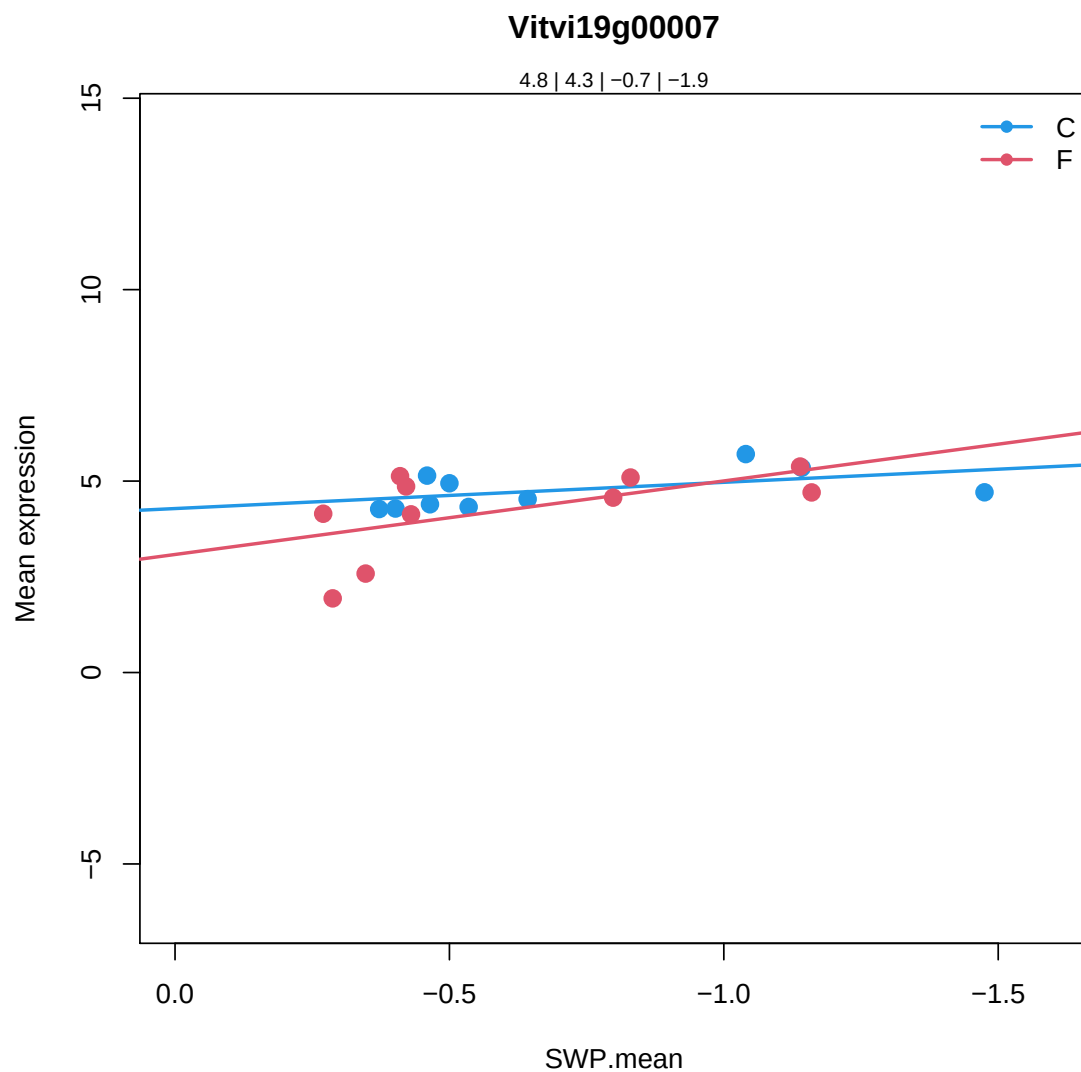
3-oxo-5-alpha-steroid 4-dehydrogenase family protein |

Chr5:5227982-5229012 FORWARD LENGTH=268 |

201606

Coefficients for Vitvi19g00007.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.764474	5.933318e-16	***	1.143452e-15	***
SlopeC	-0.6854411	0.2807485		0.7773135	
MeanF-MeanC	-0.5115055	0.1188835		0.4054152	
SlopeF-SlopeC	-1.235582	0.1942187		0.9999488	



8.1.305 Vitvi03g00048: Type1.0

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

Vitvi03g00048

1.3.6

PS.calvin cycle.aldolase

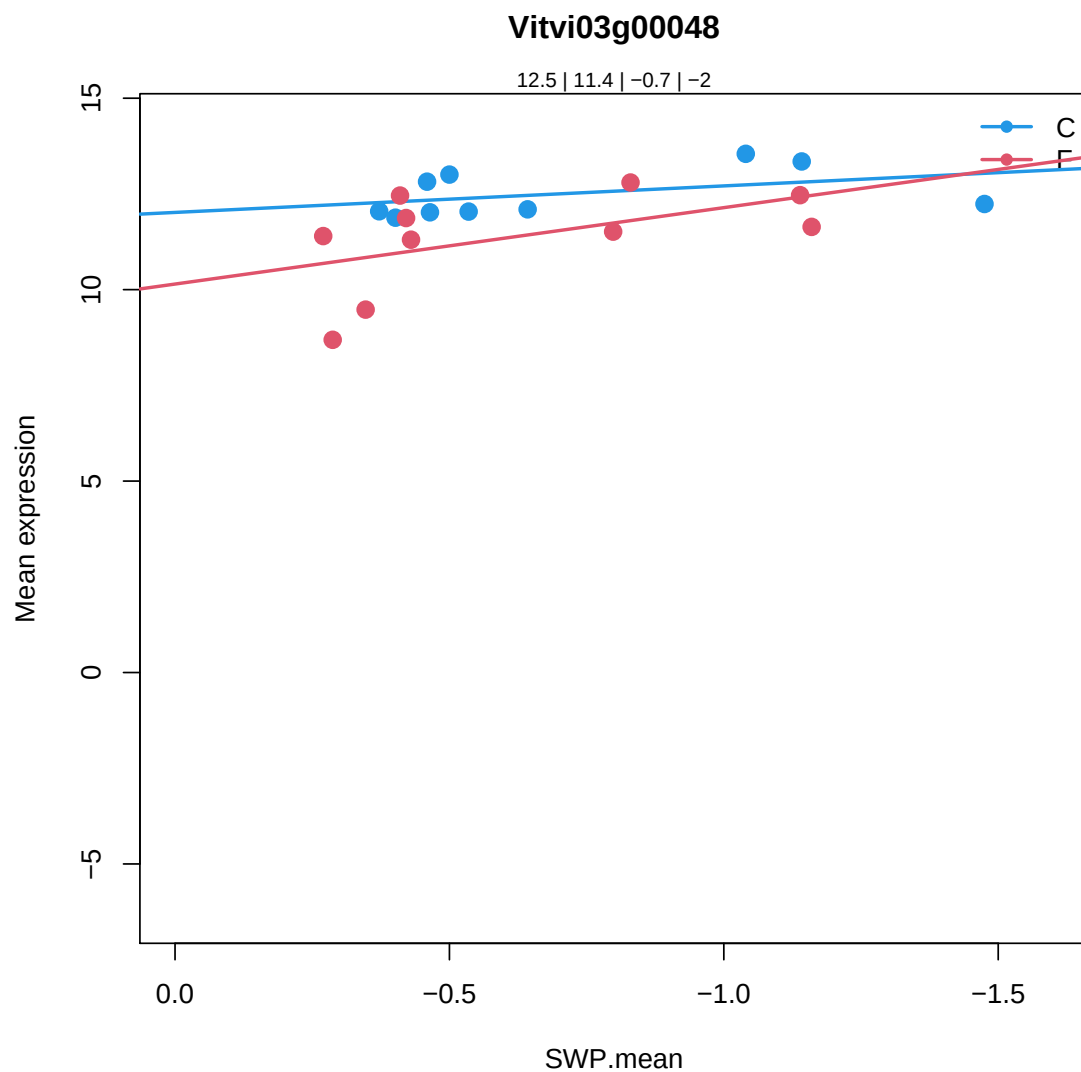
fructose-bisphosphate aldolase 1 |

Chr2:9128416-9130152 REVERSE LENGTH=399 |

201606

Coefficients for Vitvi03g00048.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	12.50365	4.821409e-23	***	1.067779e-21	***
SlopeC	-0.6929189	0.363469		0.8192699	
MeanF-MeanC	-1.14188	0.006562371	**	0.05566147	.
SlopeF-SlopeC	-1.302864	0.2536607		0.9999488	



8.1.306 Vitvi09g00596: Type1.0

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

Vitvi09g00596

26.10

misc.cytochrome P450

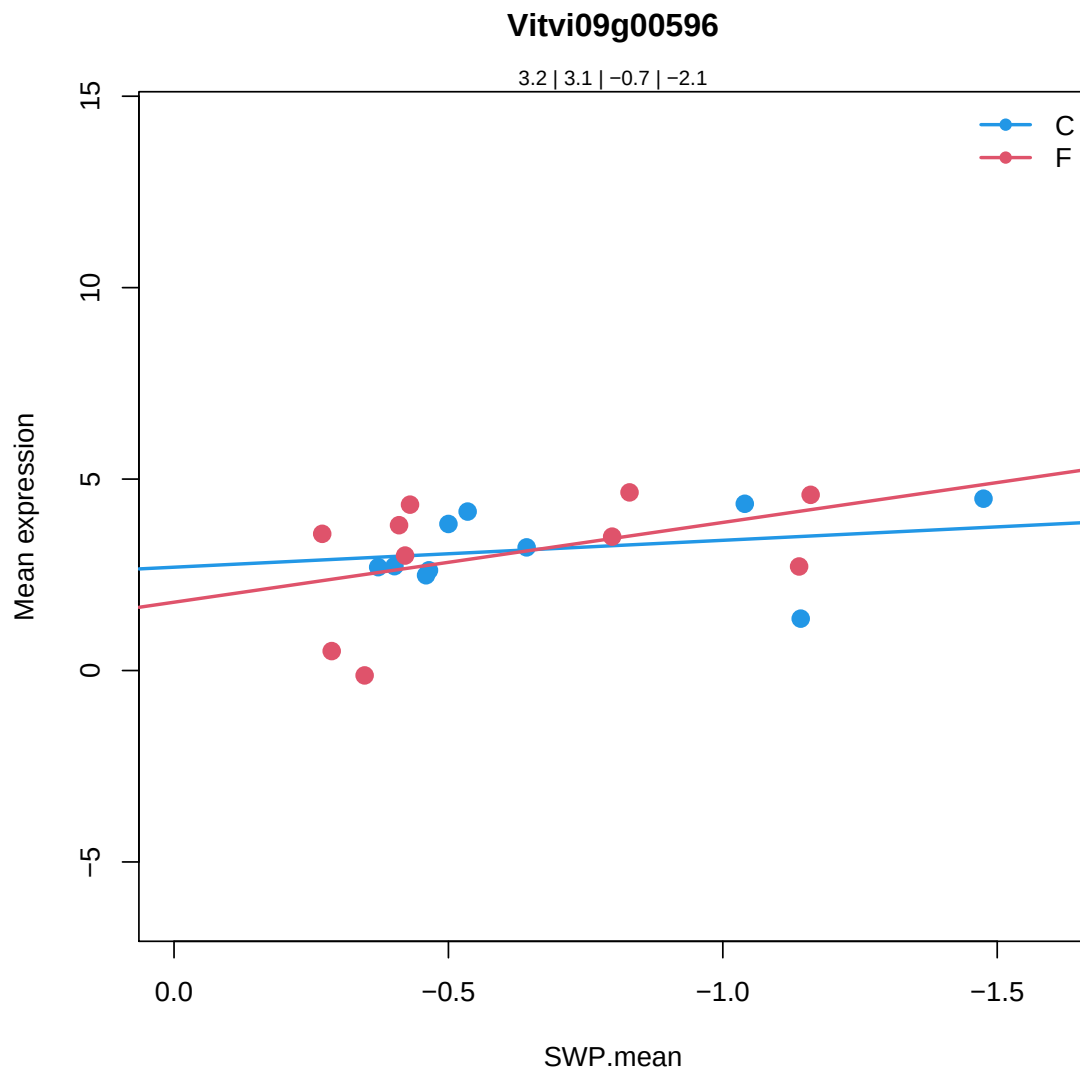
cytochrome P450 family protein |

Chr1:19580061-19580511 REVERSE LENGTH=129 |

201606

Coefficients for Vitvi09g00596.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.192205	2.030225e-08	***	2.455148e-08	***
SlopeC	-0.7020554	0.5025355		0.8703103	
MeanF-MeanC	-0.1387562	0.793407		0.9417915	
SlopeF-SlopeC	-1.381154	0.3773568		0.9999488	



8.1.307 Vitvi06g00216: Type1.0

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

Vitvi06g00216

34.16

transport.ABC transporters and multidrug resistance systems

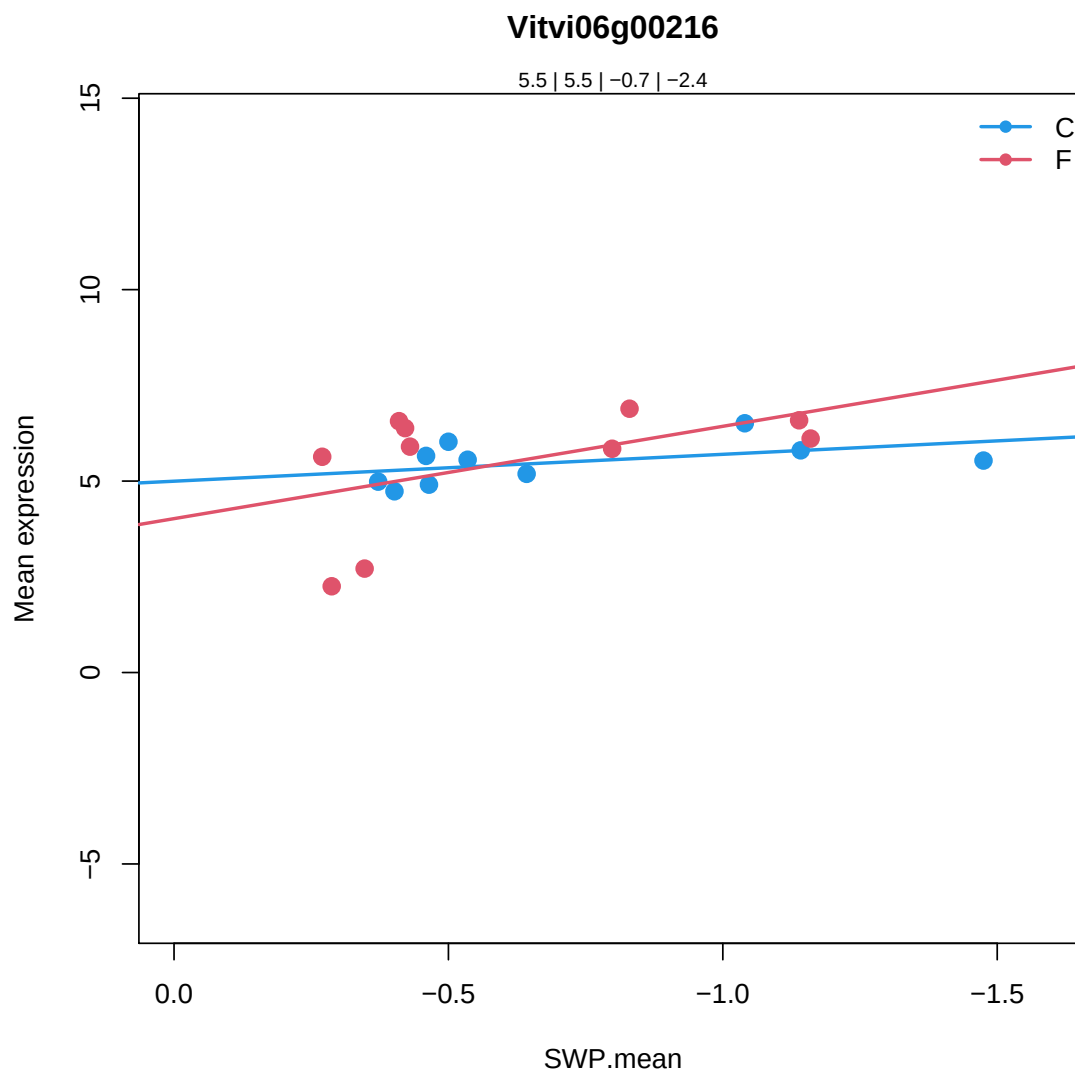
MATE efflux family protein |

Chr1:19032021-19034362 FORWARD LENGTH=397 |

201606

Coefficients for Vitvi06g00216.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.490292	3.717691e-14	***	5.912464e-14	***
SlopeC	-0.7024498	0.4308991		0.8481624	
MeanF-MeanC	-0.002195493	0.9961072		0.9993198	
SlopeF-SlopeC	-1.709172	0.203261		0.9999488	



8.1.308 Vitvi16g01036: Type1.0

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

Vitvi16g01036

11.1.8

lipid metabolism.FA synthesis and FA elongation.acyl CoA ligase

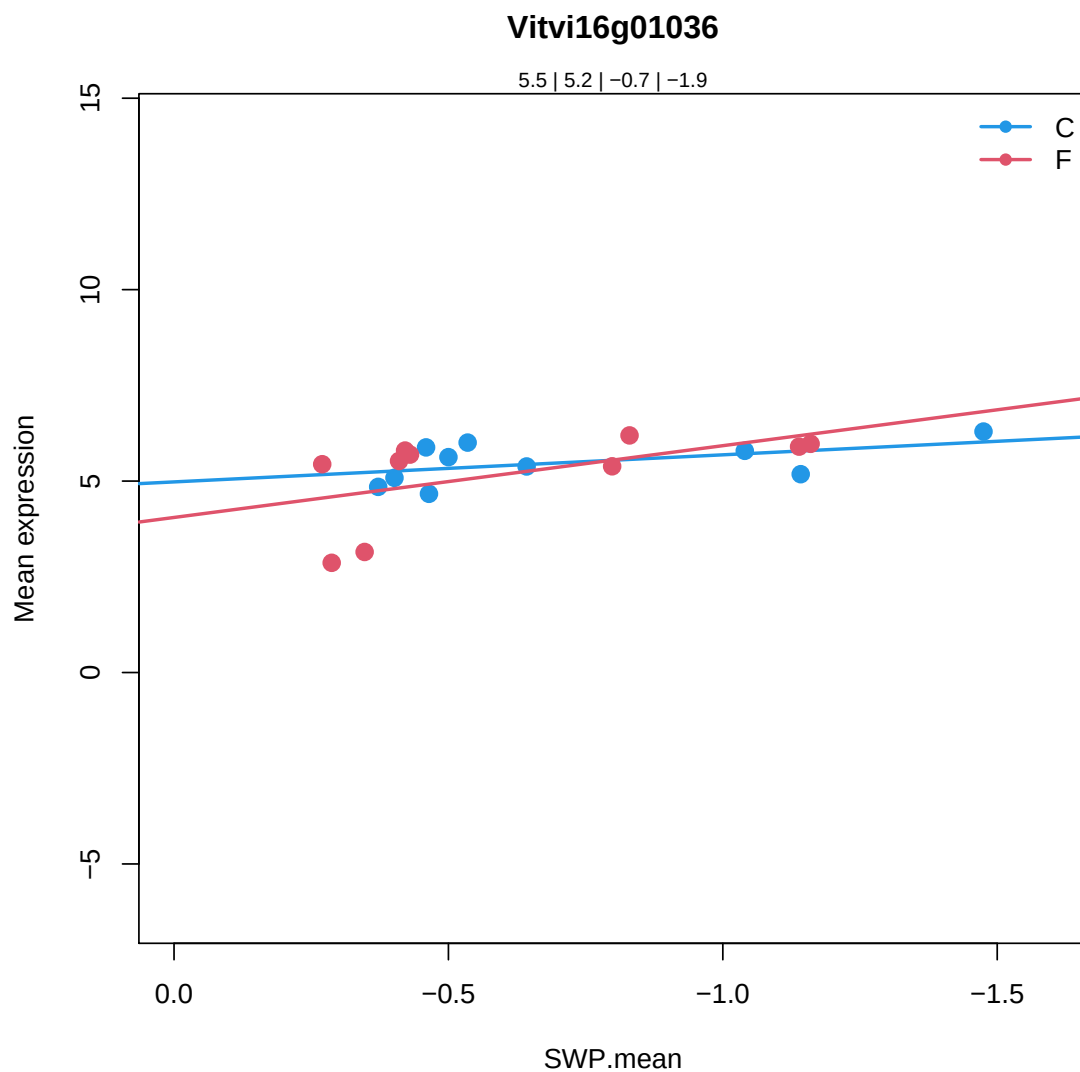
AMP-dependent synthetase and ligase family protein |

Chr3:18159031-18161294 REVERSE LENGTH=514 |

201606

Coefficients for Vitvi16g01036.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.47561	1.160853e-16	***	2.494885e-16	***
SlopeC	-0.7069463	0.2943531		0.7823247	
MeanF-MeanC	-0.2837694	0.405351		0.7481666	
SlopeF-SlopeC	-1.16768	0.2459398		0.9999488	



8.1.309 Vitvi04g00870: Type1.0

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

Vitvi04g00870

13.1.1.1.1

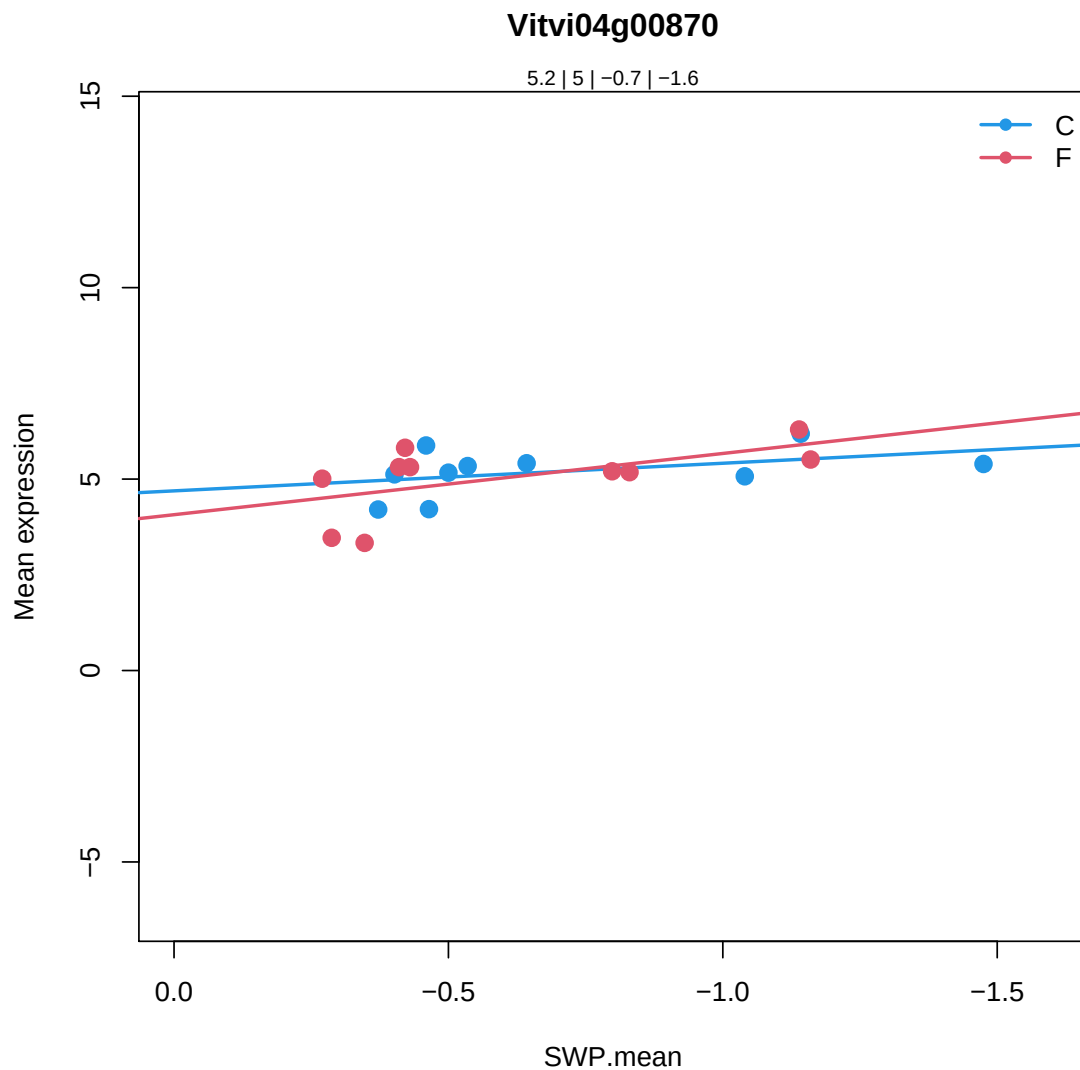
amino acid metabolism.synthesis.central amino acid metabolism.GABA.glu
glutamate decarboxylase |

Chr5:5711141-5714839 FORWARD LENGTH=502 |

201606

Coefficients for Vitvi04g00870.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.19925	2.797379e-17	***	6.725182e-17	***
SlopeC	-0.7213133	0.229369		0.748457	
MeanF-MeanC	-0.1551375	0.6059948		0.8617806	
SlopeF-SlopeC	-0.87807	0.3228505		0.9999488	



8.1.310 Vitvi19g01471: Type1.0

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

Vitvi19g01471

29.2.3

protein.synthesis.initiation

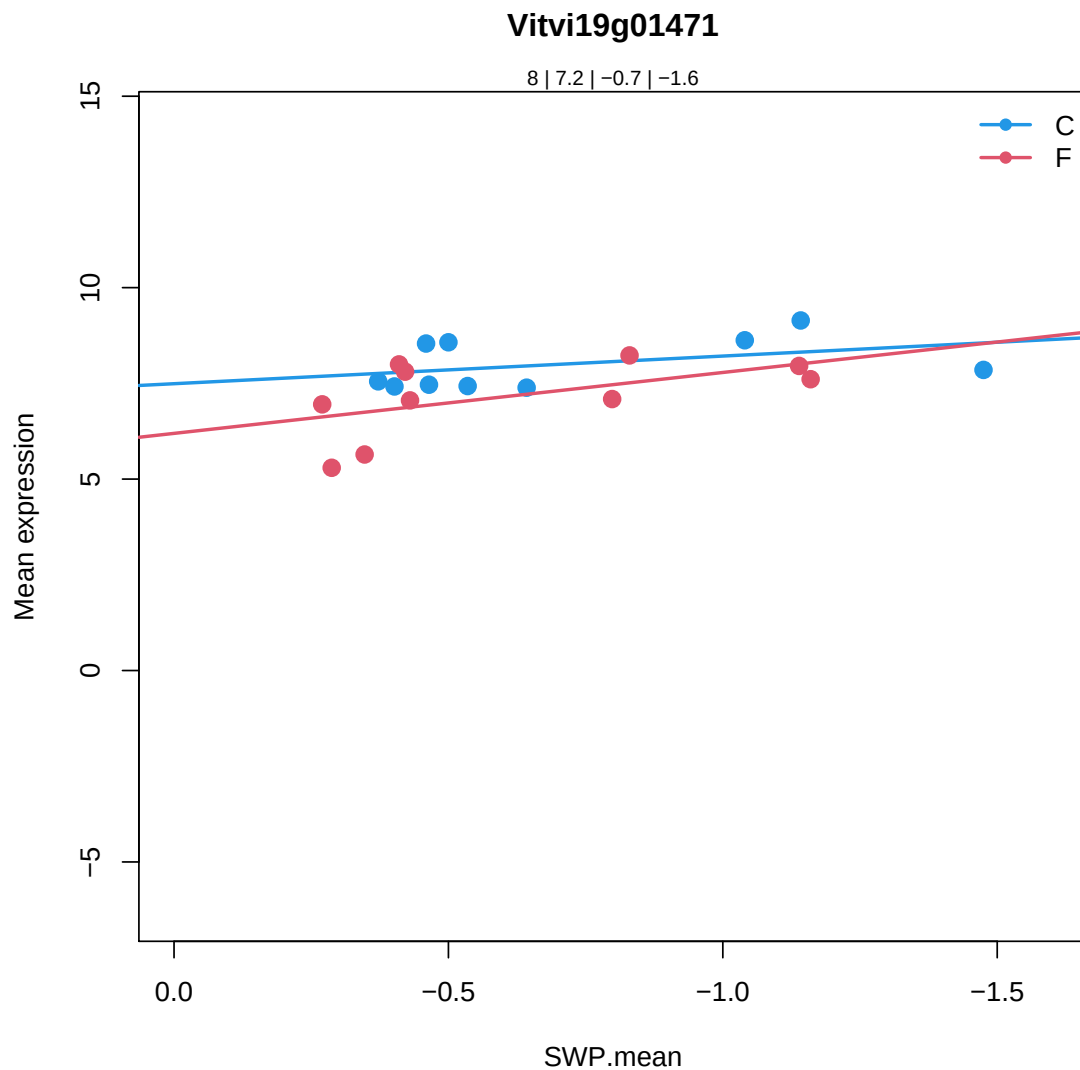
Translation initiation factor 2%2C small GTP-binding protein |

Chr1:5885383-5890165 FORWARD LENGTH=1026 |

201606

Coefficients for Vitvi19g01471.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.998427	1.339695e-20	***	9.035234e-20	***
SlopeC	-0.7220523	0.2589479		0.767187	
MeanF-MeanC	-0.8357314	0.01513334	*	0.1026036	
SlopeF-SlopeC	-0.8685094	0.3591113		0.9999488	



8.1.311 Vitvi08g00940: Type1.0

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

Vitvi08g00940

26.10

misc.cytochrome P450

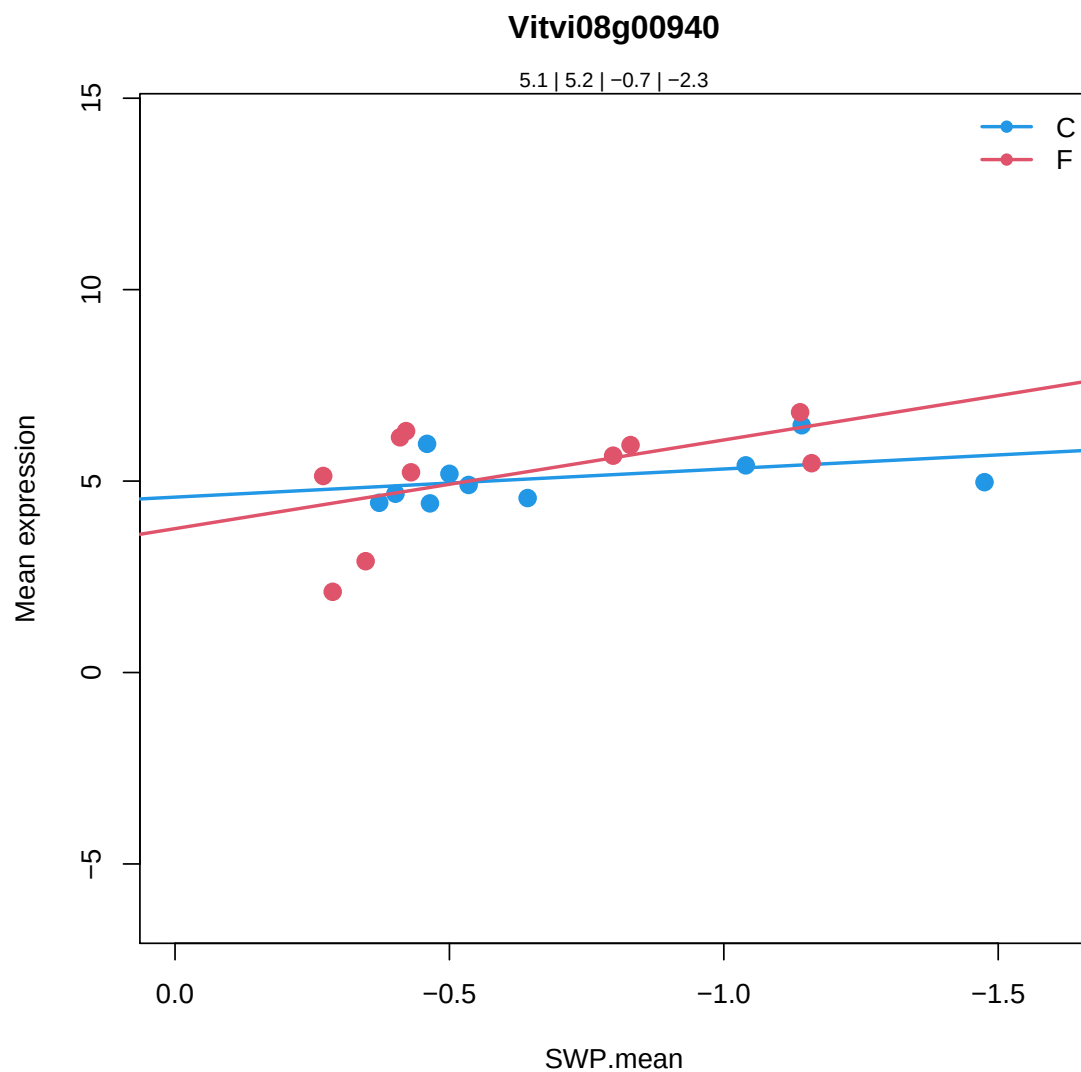
cytochrome P450%2C family 98%2C subfamily A%2C polypeptide 3 |

Chr2:17058291-17060532 REVERSE LENGTH=508 |

201606

Coefficients for Vitvi08g00940.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.097576	6.632575e-14	***	1.032411e-13	***
SlopeC	-0.7352094	0.389027		0.8306423	
MeanF-MeanC	0.07159846	0.867813		0.9650959	
SlopeF-SlopeC	-1.580882	0.2176205		0.9999488	



8.1.312 Vitvi13g01614: Type1.0

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

Vitvi13g01614

17.4.1

hormone metabolism.cytokinin.synthesis-degradation

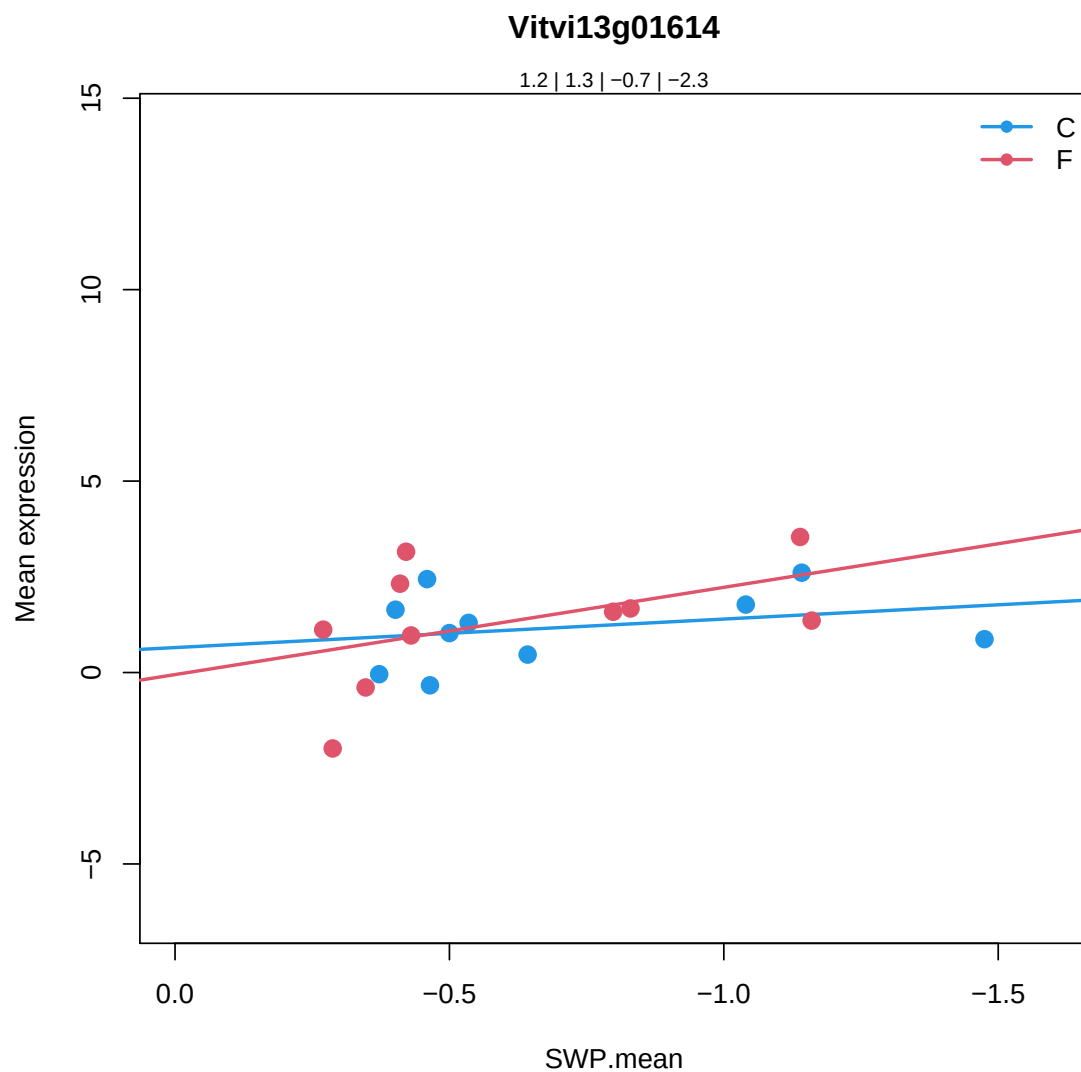
cytokinin oxidase/dehydrogenase 1 |

Chr2:17314440-17316861 FORWARD LENGTH=637 |

201606

Coefficients for Vitvi13g01614.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.174997	0.003343477	**	0.003579244	**
SlopeC	-0.7451578	0.4601135		0.8600853	
MeanF-MeanC	0.1594451	0.754585		0.9282231	
SlopeF-SlopeC	-1.533252	0.3099812		0.9999488	



8.1.313 Vitvi05g00548: Type1.0

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

Vitvi05g00548

34.6

transport.sulphate

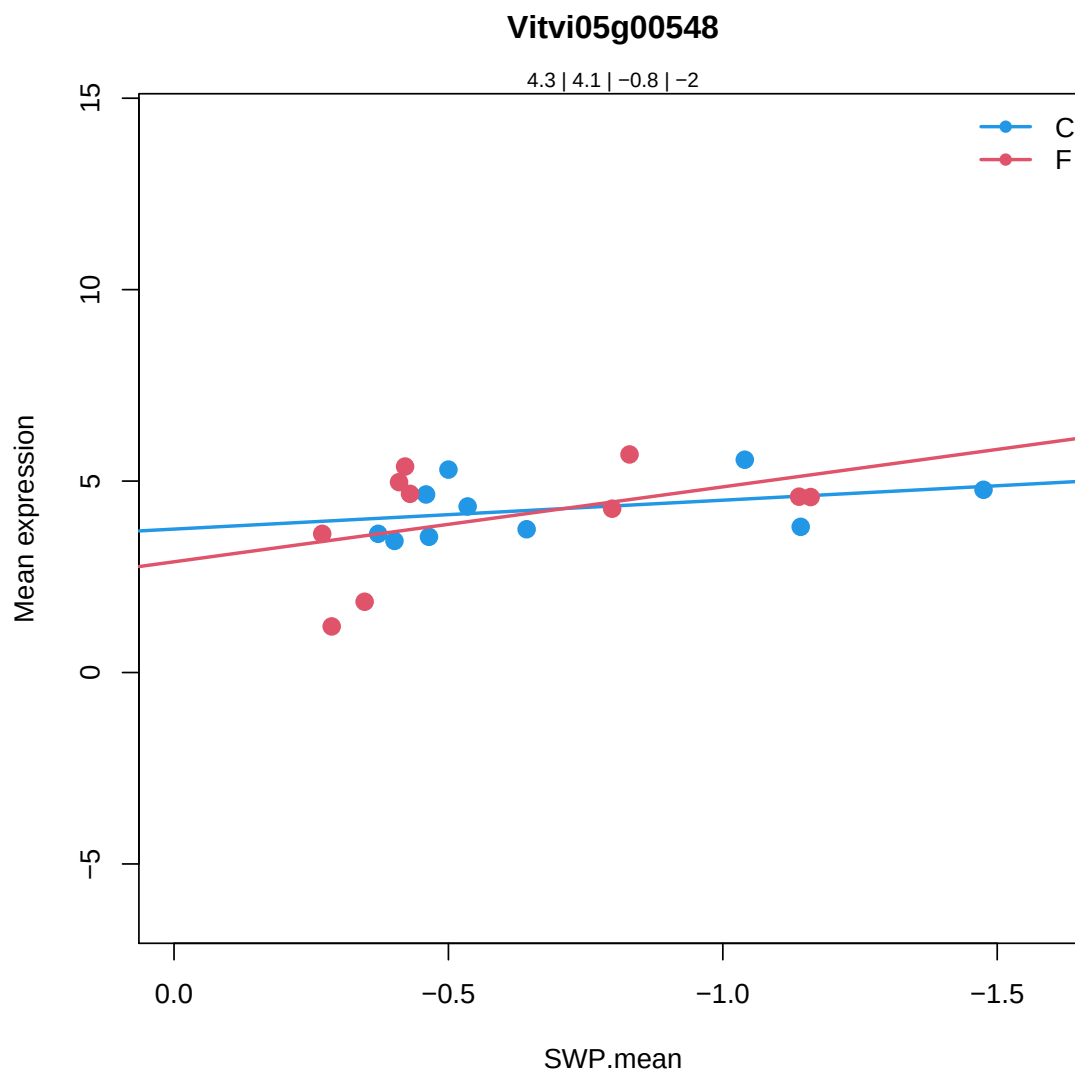
sulfate transporter 3%3B1 |

Chr3:19251503-19255812 REVERSE LENGTH=703 |

201606

Coefficients for Vitvi05g00548.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.276674	5.134969e-12	***	7.093275e-12	***
SlopeC	-0.7548136	0.3978804		0.8334926	
MeanF-MeanC	-0.1924661	0.6695388		0.8923321	
SlopeF-SlopeC	-1.201965	0.3663115		0.9999488	



8.1.314 Vitvi18g02824: Type1.0

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

Vitvi18g02824

35.2

not assigned.unknown

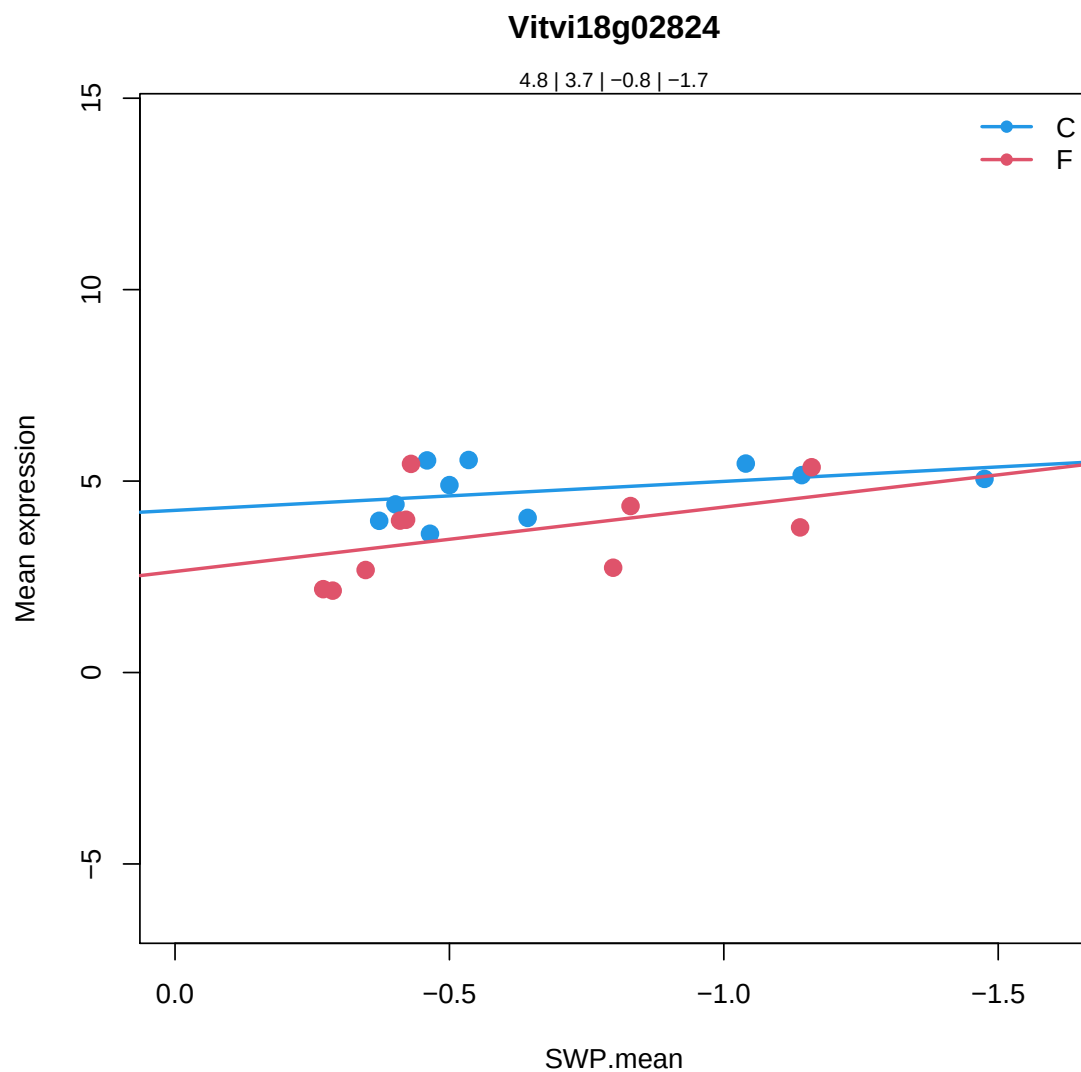
polyadenylate-binding protein 1-B-binding protein |

Chr4:10809977-10810942 FORWARD LENGTH=321 |

201606

Coefficients for Vitvi18g02824.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.767125	2.295777e-14	***	3.715857e-14	***
SlopeC	-0.7565228	0.3191469		0.7967625	
MeanF-MeanC	-1.103587	0.007944251	**	0.06410073	.
SlopeF-SlopeC	-0.9268909	0.410419		0.9999488	



8.1.315 Vitvi19g00341: Type1.0

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

```
Vitvi19g00341
```

```
29.4
```

```
protein.postranslational modification
```

```
S-locus lectin protein kinase family protein |
```

```
Chr4:13666281-13669202 FORWARD LENGTH=783 |
```

```
201606
```

```
Vitvi19g00341
```

```
30.2.24
```

```
signalling.receptor kinases.S-locus glycoprotein like
```

```
S-locus lectin protein kinase family protein |
```

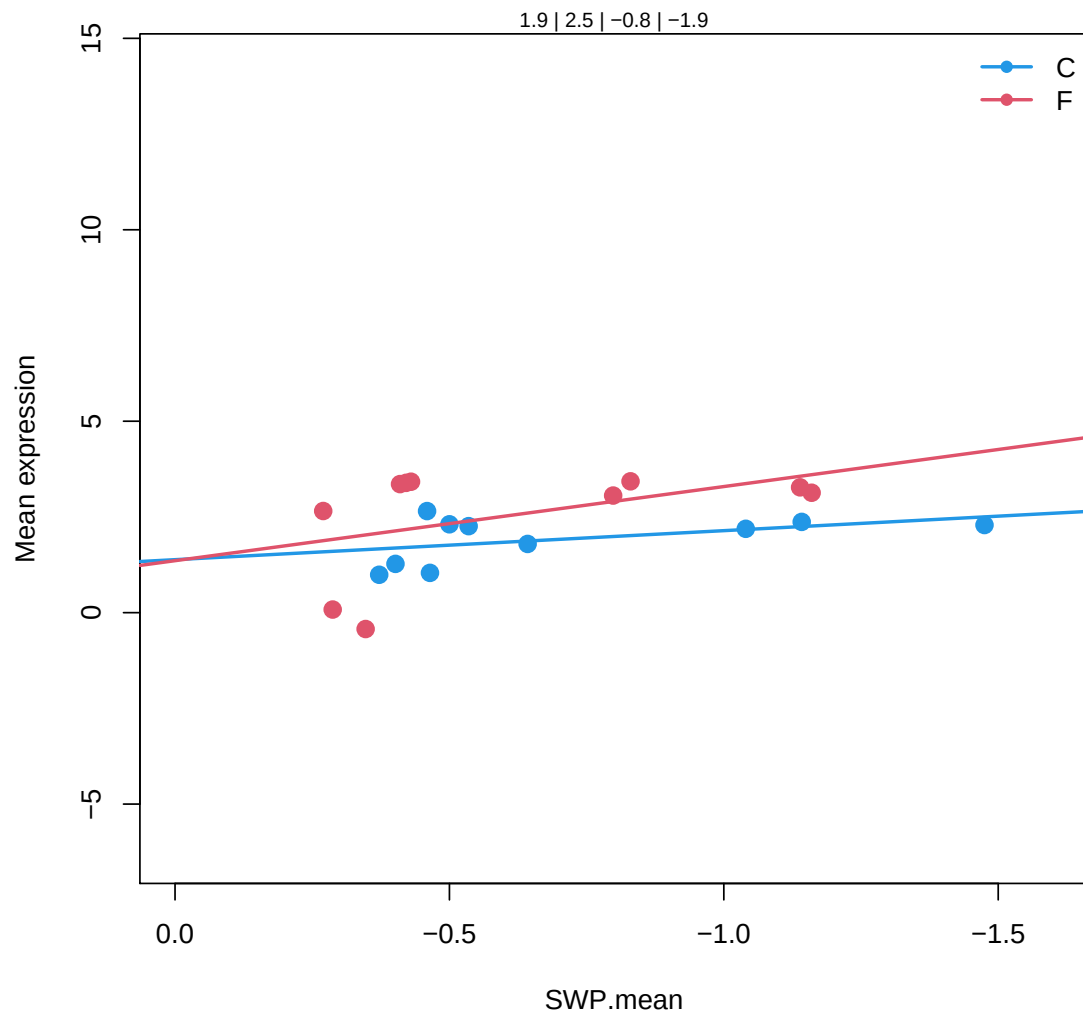
```
Chr4:13666281-13669202 FORWARD LENGTH=783 |
```

```
201606
```

Coefficients for Vitvi19g00341.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.916459	1.892208e-06	***	2.170784e-06	***
SlopeC	-0.7577334	0.3684884		0.8217265	
MeanF-MeanC	0.6202836	0.1535674		0.4724816	
SlopeF-SlopeC	-1.178453	0.3477876		0.9999488	

Vitvi19g00341



8.1.316 Vitvi14g01614: Type1.0

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

Vitvi14g01614

29.5.11.4.2

protein.degradation.ubiquitin.E3.RING

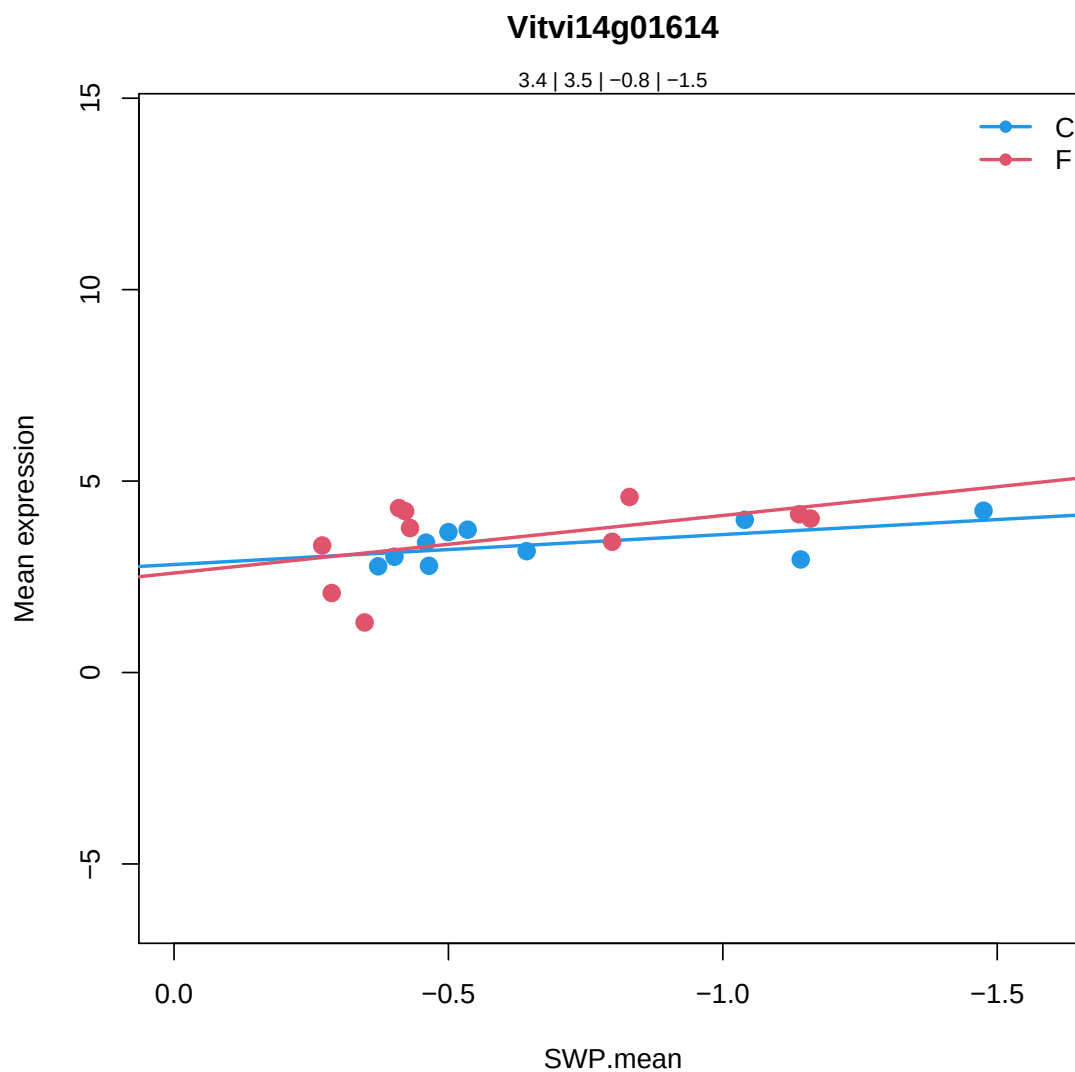
zinc finger (C3HC4-type RING finger) family protein |

Chr3:10116950-10120516 REVERSE LENGTH=913 |

201606

Coefficients for Vitvi14g01614.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.371074	5.13488e-13	***	7.514724e-13	***
SlopeC	-0.7835057	0.2148421		0.7381588	
MeanF-MeanC	0.142602	0.6517982		0.8831922	
SlopeF-SlopeC	-0.7196801	0.4388454		0.9999488	



8.1.317 Vitvi08g01245: Type1.0

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

Vitvi08g01245

1.3.13

PS.calvin cycle.rubisco interacting

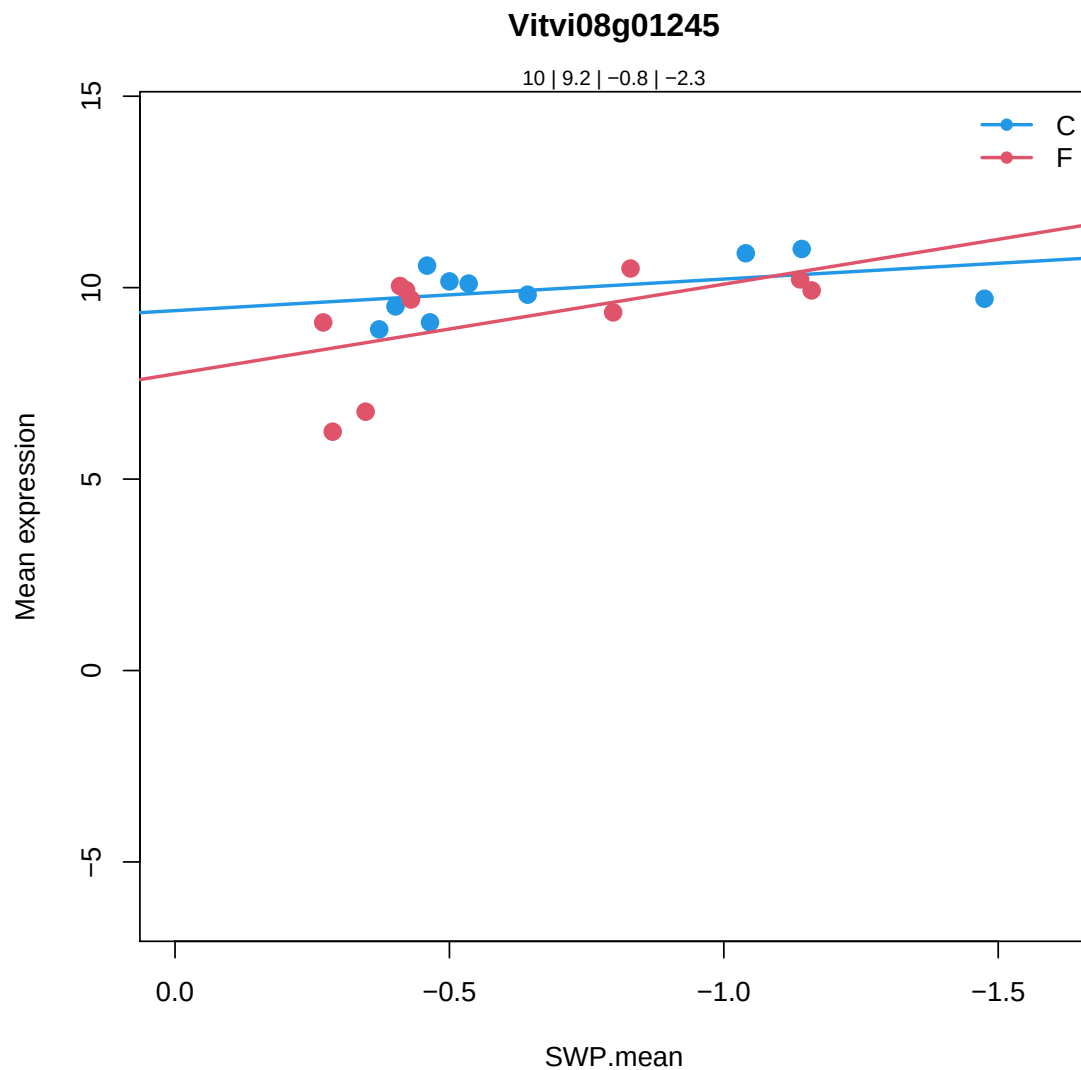
rubisco activase |

Chr2:16571174-16573345 REVERSE LENGTH=441 |

201606

Coefficients for Vitvi08g01245.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	9.97905	4.22624e-20	***	2.293213e-19	***
SlopeC	-0.8253309	0.3255969		0.8000183	
MeanF-MeanC	-0.8040715	0.06717145	.	0.2883208	
SlopeF-SlopeC	-1.517285	0.2274047		0.9999488	



8.1.318 Vitvi07g01723: Type1.0

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

Vitvi07g01723

29.2.2.3.3

protein.synthesis.ribosome biogenesis.pre-rRNA processing and modifica

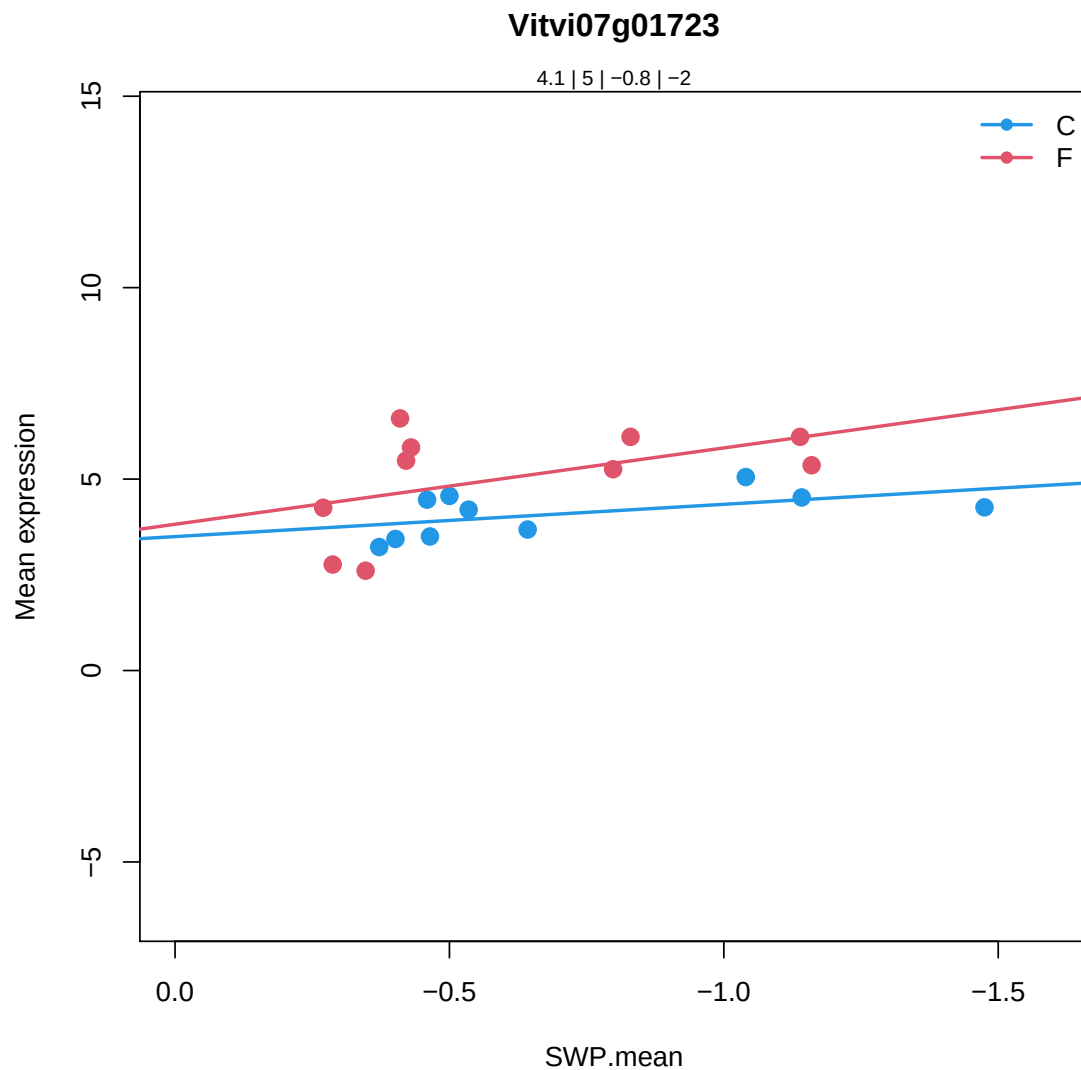
S-adenosyl-L-methionine-dependent methyltransferases superfamily prote

Chr4:16310763-16311973 FORWARD LENGTH=286 |

201606

Coefficients for Vitvi07g01723.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.090361	1.177945e-12	***	1.682369e-12	***
SlopeC	-0.8428274	0.2894048		0.7810036	
MeanF-MeanC	0.9438532	0.02591612	*	0.1526327	
SlopeF-SlopeC	-1.151025	0.3300014		0.9999488	



8.1.319 Vitvi02g01288: Type1.0

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

Vitvi02g01288

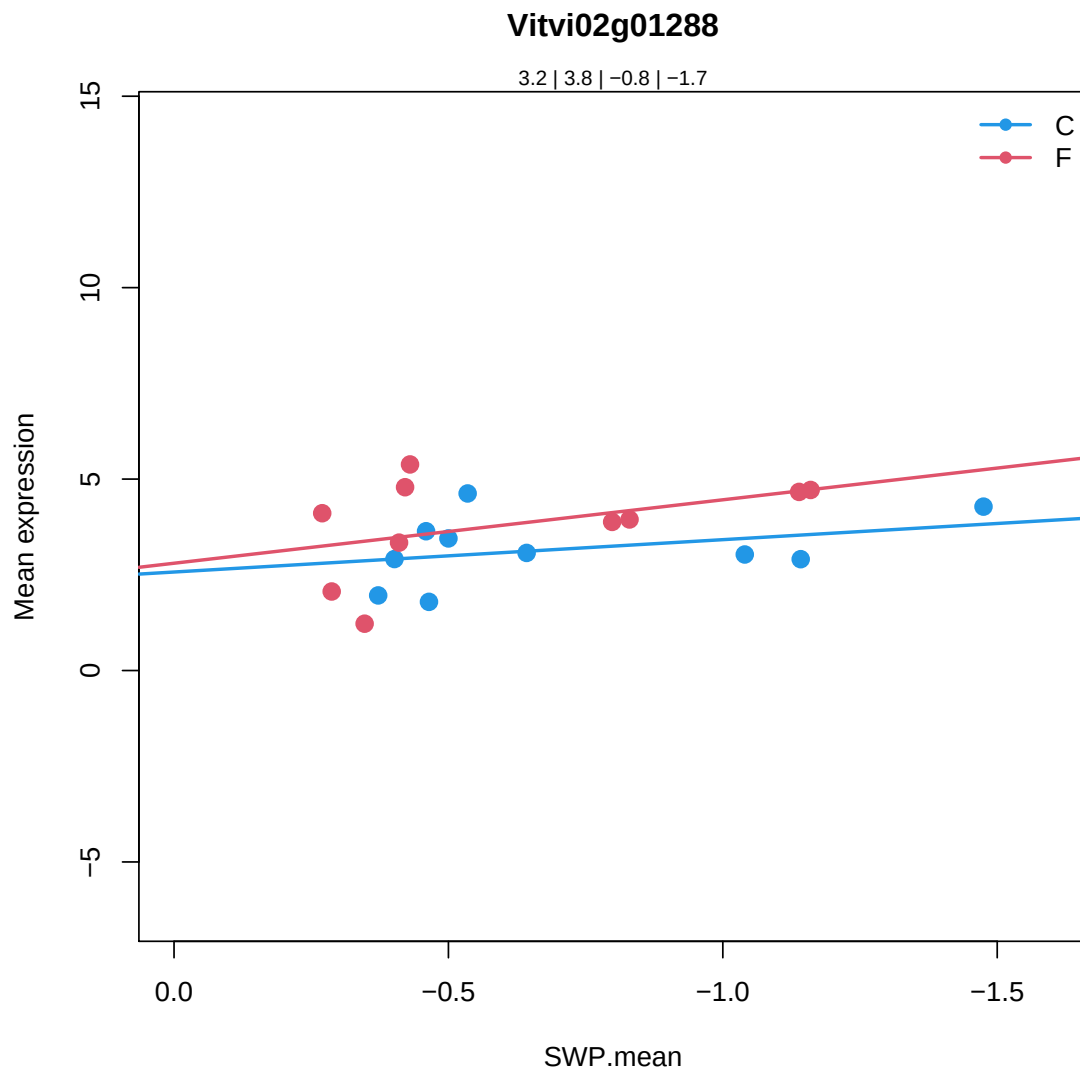
17.1.1.1.10

hormone metabolism.abscisic acid.synthesis-degradation.synthesis.9-cis-
nine-cis-epoxycarotenoid dioxygenase 4 |

Chr4:10481835-10483622 FORWARD LENGTH=595 |
201606

Coefficients for Vitvi02g01288.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.166684	7.107552e-10	***	9.00676e-10	***
SlopeC	-0.8451787	0.327242		0.800028	
MeanF-MeanC	0.6444604	0.1471834		0.4618606	
SlopeF-SlopeC	-0.811713	0.5245375		0.9999488	



8.1.320 Vitvi04g02011: Type1.0

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

Vitvi04g02011

16.1.4.1

secondary metabolism.isoprenoids.carotenoids.phytoene synthase

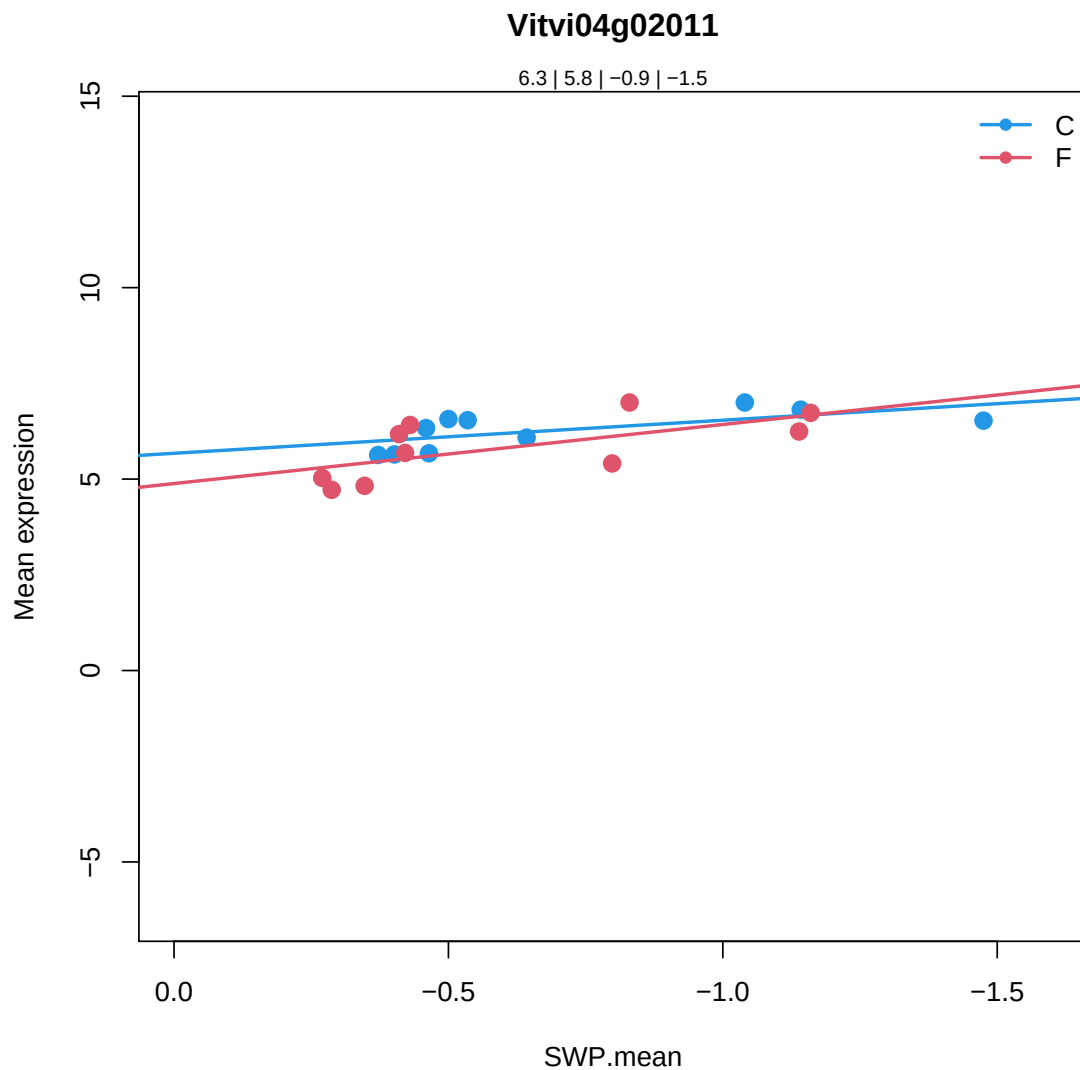
PHYTOENE SYNTHASE |

Chr5:5659839-5662087 REVERSE LENGTH=422 |

201606

Coefficients for Vitvi04g02011.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.280701	4.352122e-21	***	3.644783e-20	***
SlopeC	-0.8635469	0.07625521	.	0.5694531	
MeanF-MeanC	-0.4580989	0.06513618	.	0.28277	
SlopeF-SlopeC	-0.6784864	0.3364124		0.9999488	



8.1.321 Vitvi18g03125: Type1.0

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

Vitvi18g03125

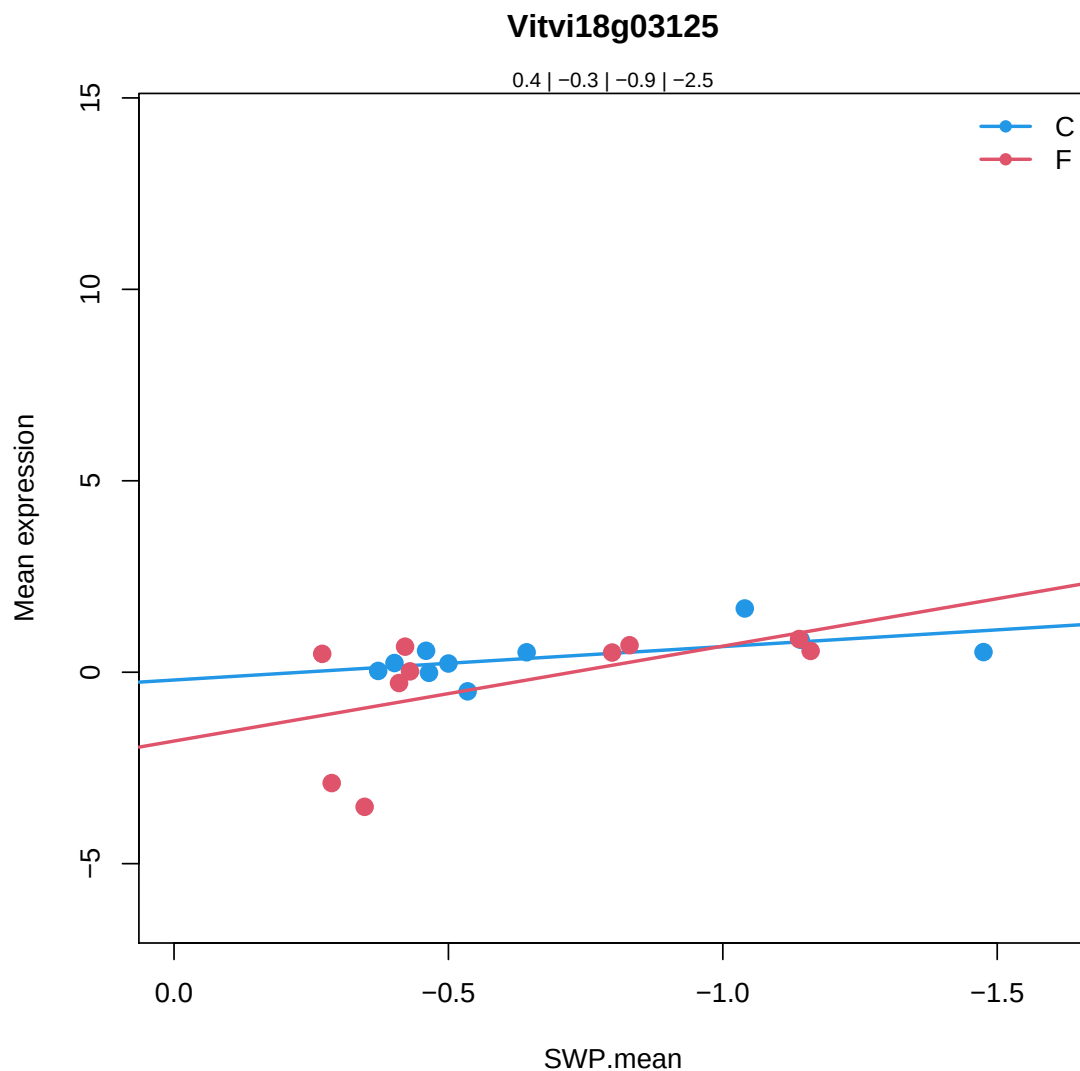
30.2.19

signalling.receptor kinases.legume-lectin

GCN5-related N-acetyltransferase IPR000182 GCN5-related N-acetyltransferase

Coefficients for Vitvi18g03125.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4105219	0.1854161		0.190285	
SlopeC	-0.8732097	0.3071847		0.7904743	
MeanF-MeanC	-0.6986146	0.1142598		0.3954469	
SlopeF-SlopeC	-1.605675	0.2099886		0.9999488	



8.1.322 Vitvi07g02940: Type1.0

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

Vitvi07g02940

29.5.11.4.2

protein.degradation.ubiquitin.E3.RING

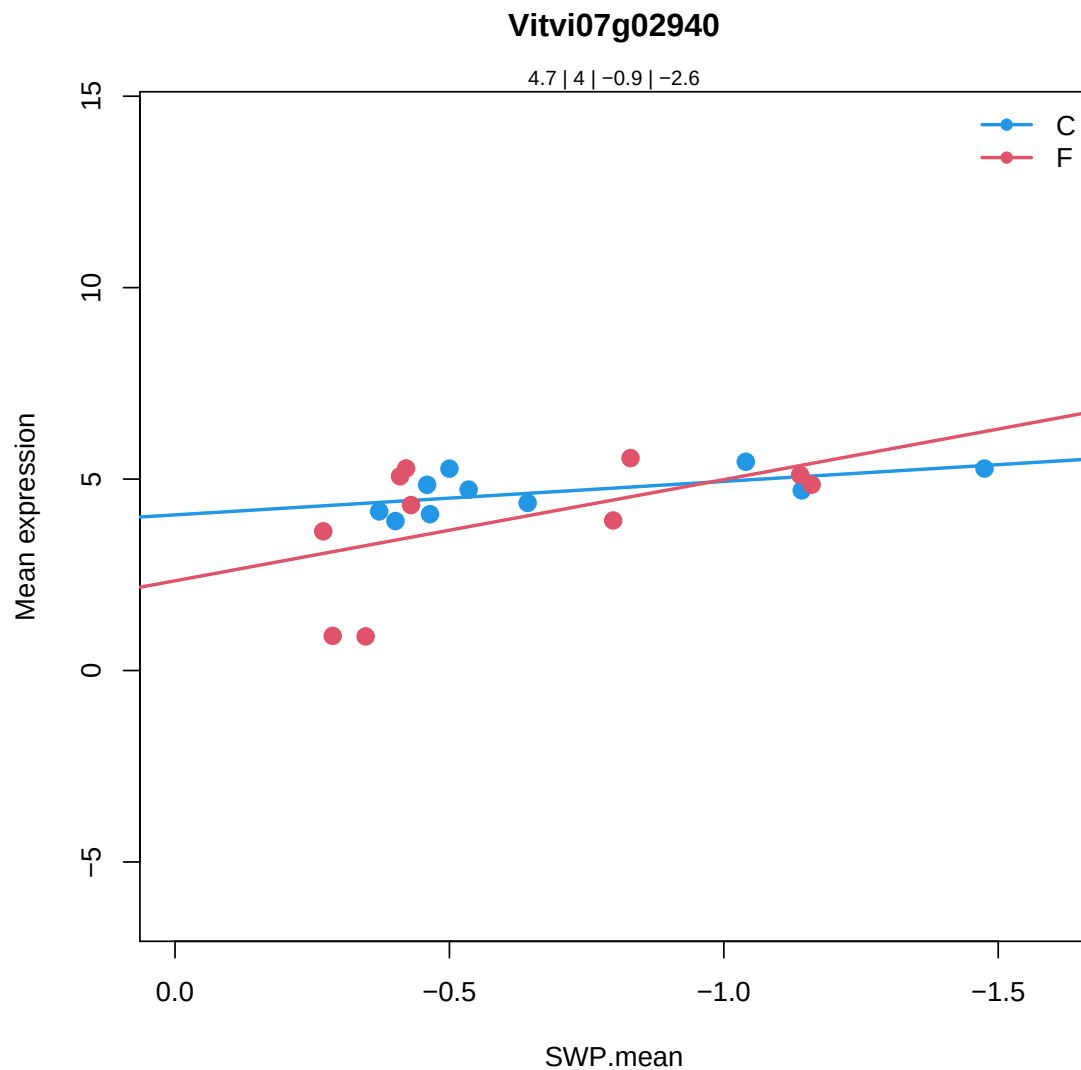
plant U-box 9 |

Chr3:2354884-2356613 FORWARD LENGTH=460 |

201606

Coefficients for Vitvi07g02940.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.679928	1.368884e-12	***	1.948135e-12	***
SlopeC	-0.8742332	0.3393167		0.8047182	
MeanF-MeanC	-0.7264877	0.1247443		0.4180469	
SlopeF-SlopeC	-1.767867	0.1981997		0.9999488	



8.1.323 Vitvi06g00063: Type1.0

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

Vitvi06g00063

31.5.1

cell.cell death.plants

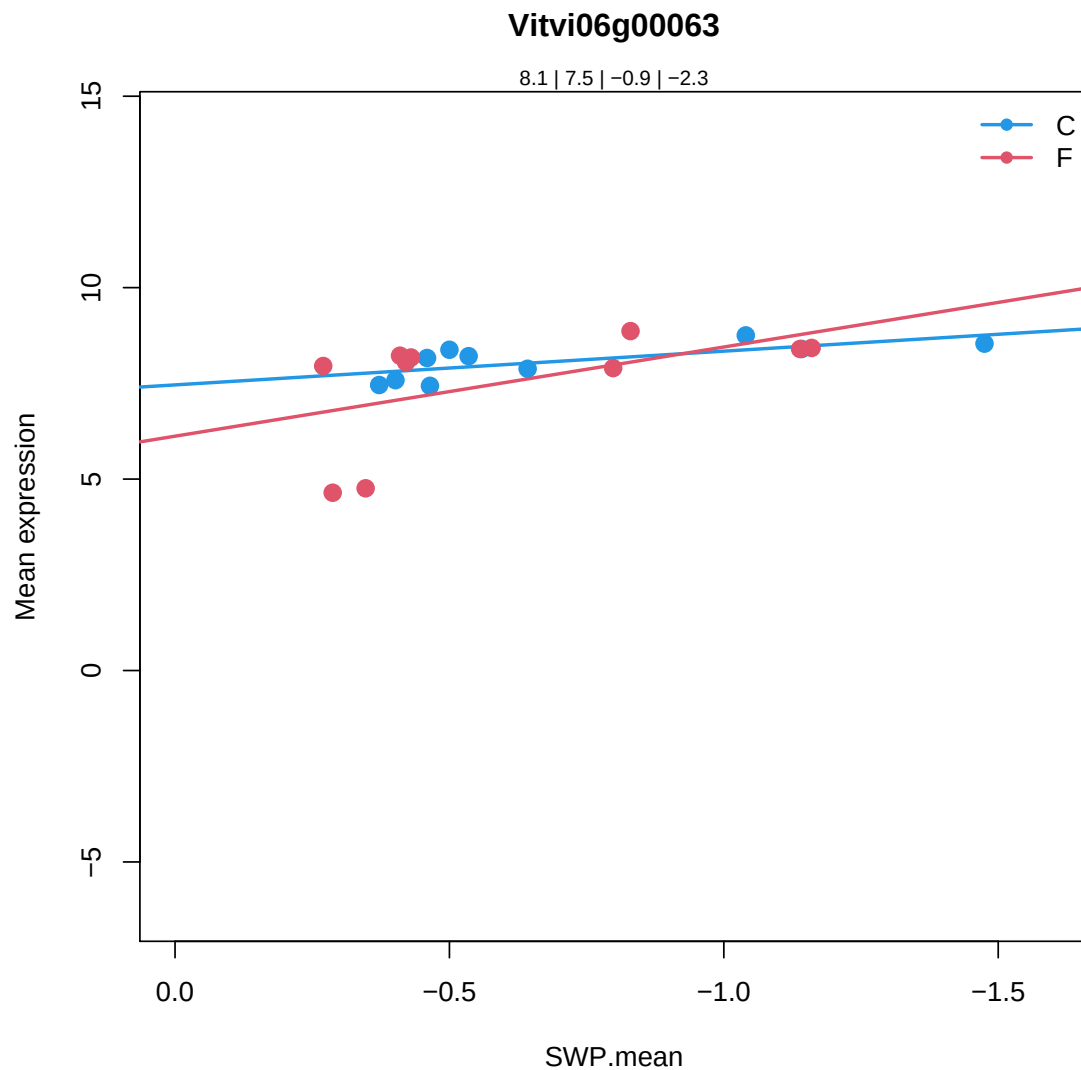
ACD1-like protein |

Chr4:13081021-13083153 REVERSE LENGTH=536 |

201606

Coefficients for Vitvi06g00063.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	8.079392	1.651658e-18	***	5.340384e-18	***
SlopeC	-0.8812793	0.2774951		0.7756987	
MeanF-MeanC	-0.5400838	0.1931906		0.533734	
SlopeF-SlopeC	-1.448207	0.2319256		0.9999488	



8.1.324 Vitvi04g00845: Type1.0

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

Vitvi04g00845

27.3.25

RNA.regulation of transcription.MYB domain transcription factor family

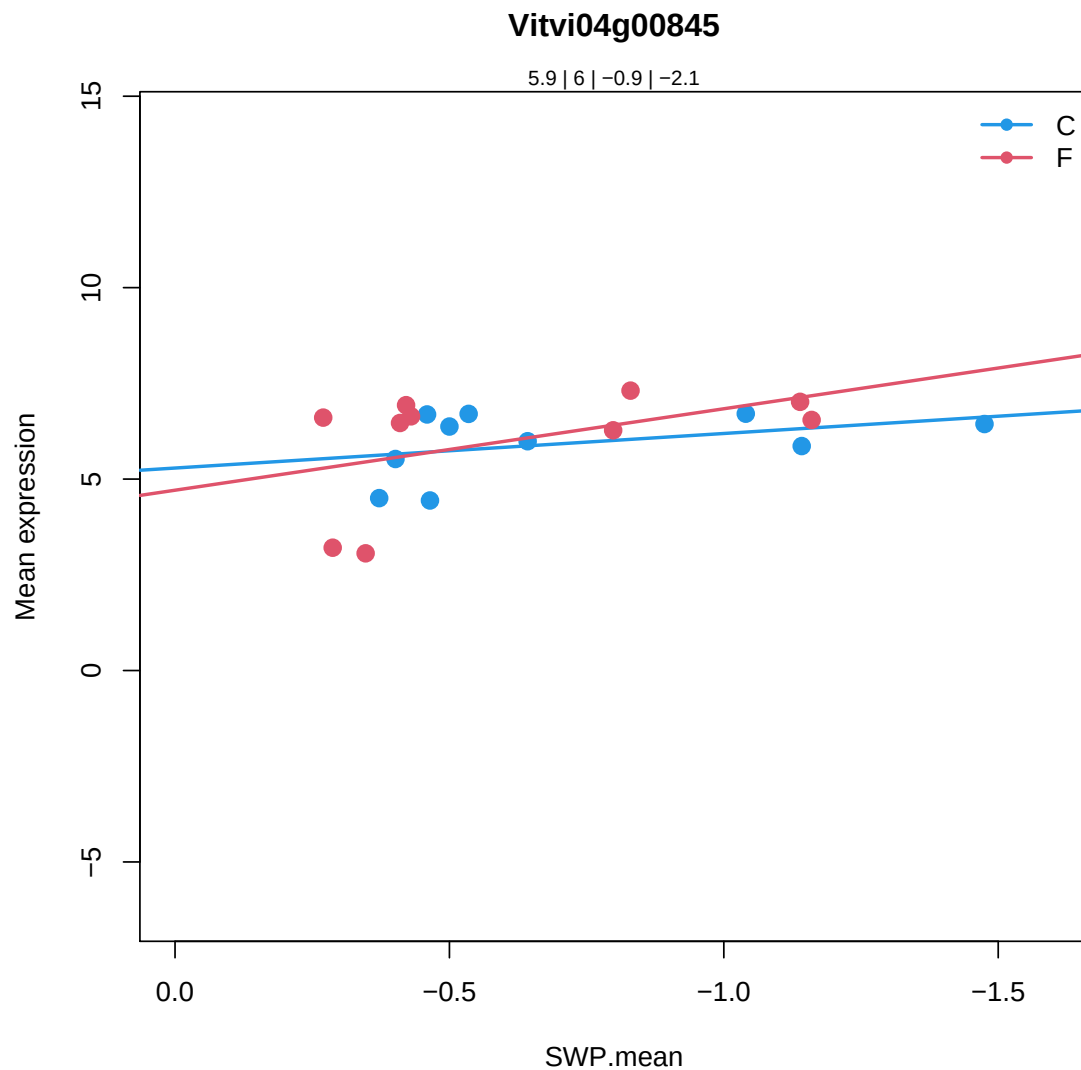
Homeodomain-like superfamily protein |

Chr5:5690435-5692435 REVERSE LENGTH=387 |

201606

Coefficients for Vitvi04g00845.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.922683	2.28485e-14	***	3.698957e-14	***
SlopeC	-0.9025401	0.3382148		0.8045998	
MeanF-MeanC	0.08259513	0.8616685		0.9640011	
SlopeF-SlopeC	-1.224721	0.3817174		0.9999488	



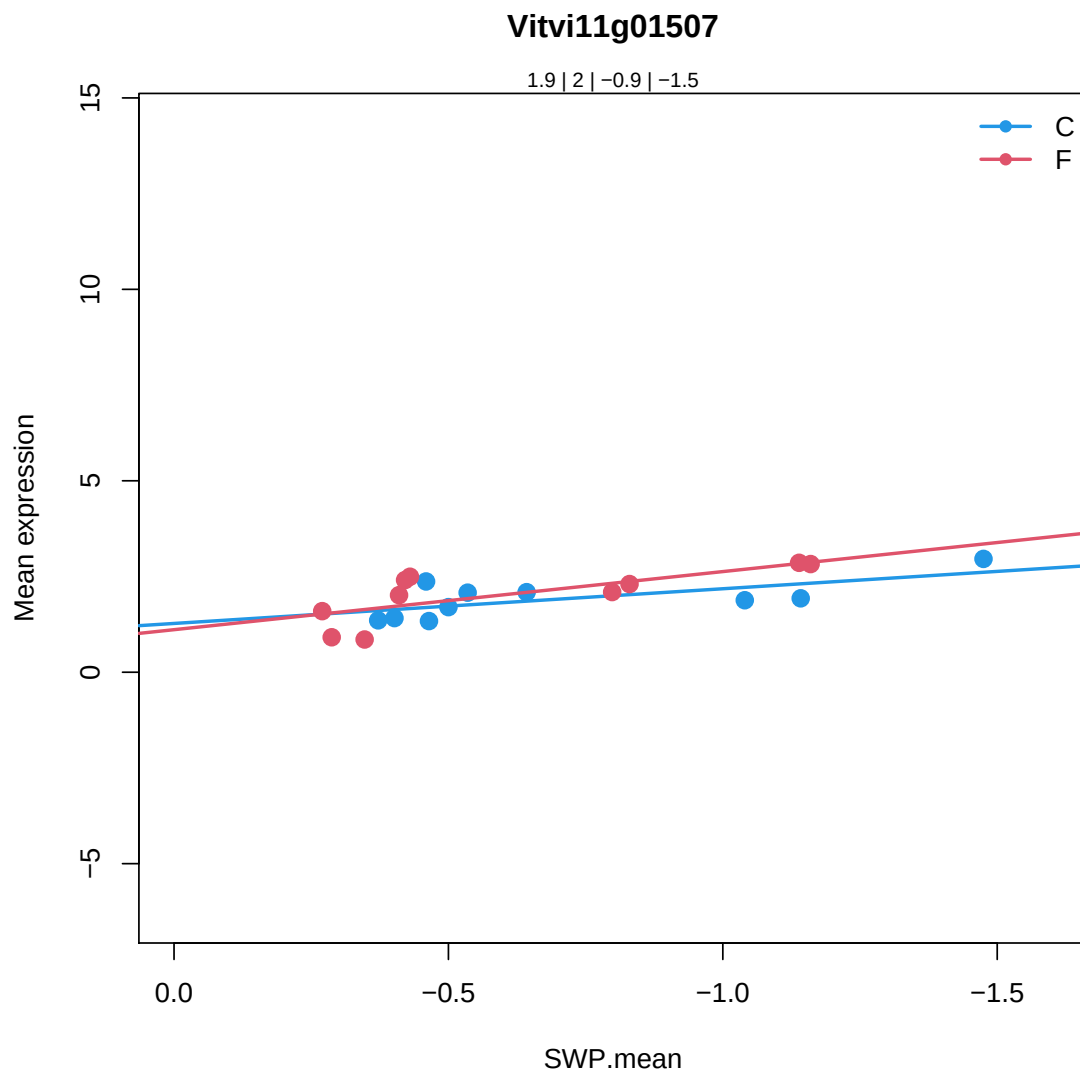
8.1.325 Vitvi11g01507: Type1.0 *

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

```
Vitvi11g01507
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi11g01507.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.911178	1.324316e-11	***	1.798559e-11	***
SlopeC	-0.9063475	0.03839096	*	0.4670907	
MeanF-MeanC	0.1243569	0.5577161		0.8379714	
SlopeF-SlopeC	-0.6108351	0.3289084		0.9999488	



8.1.326 Vitvi05g00883: Type1.0

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

Vitvi05g00883

35.2

not assigned.unknown

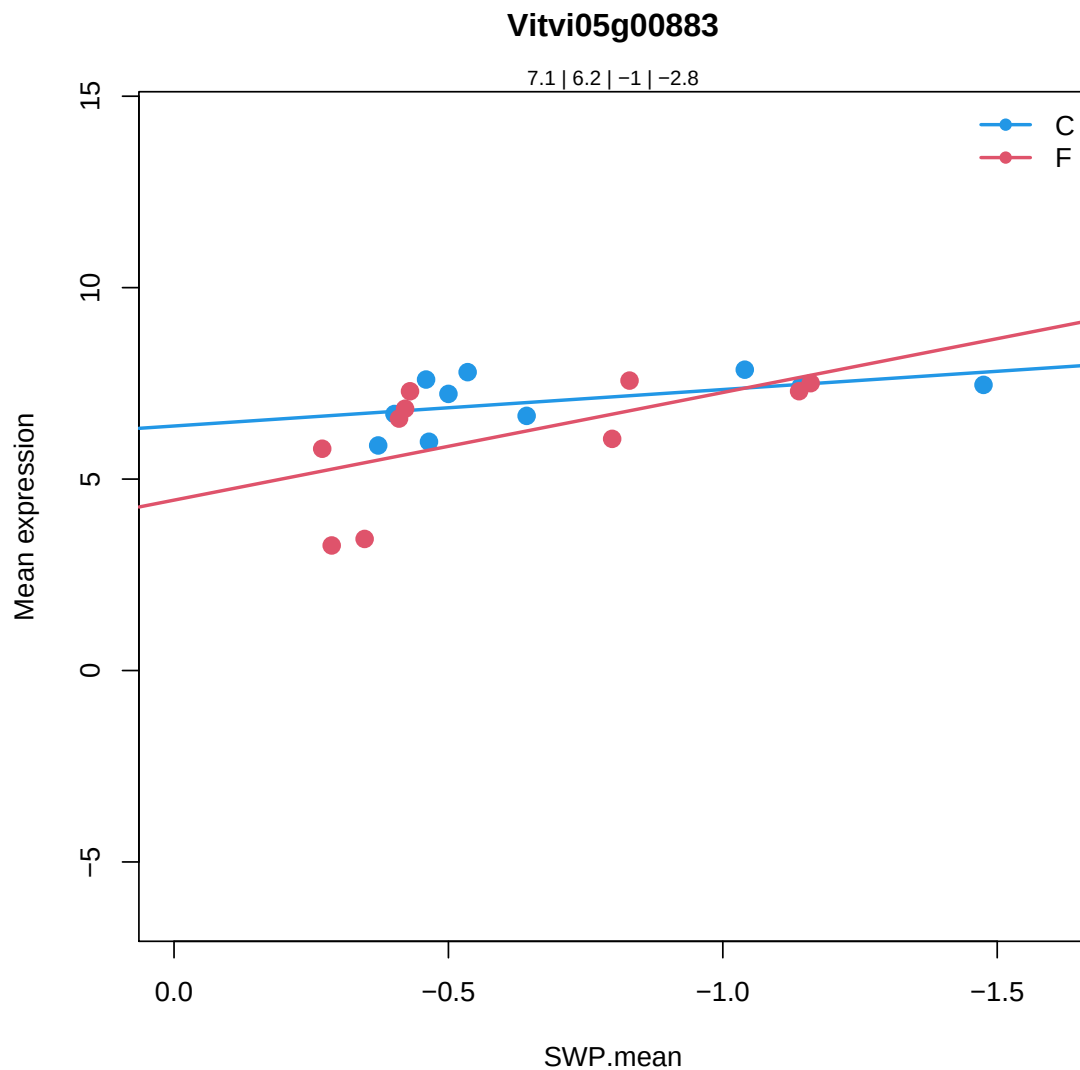
beta-amylase 1 |

Chr3:8641722-8644199 FORWARD LENGTH=575 |

201606

Coefficients for Vitvi05g00883.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.055827	8.660386e-17	***	1.903412e-16	***
SlopeC	-0.9526328	0.2667999		0.7710589	
MeanF-MeanC	-0.8929404	0.04749483	*	0.2316427	
SlopeF-SlopeC	-1.858615	0.149601		0.9999488	



8.1.327 Vitvi06g00495: Type1.0

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

Vitvi06g00495

35.1

not assigned.no ontology

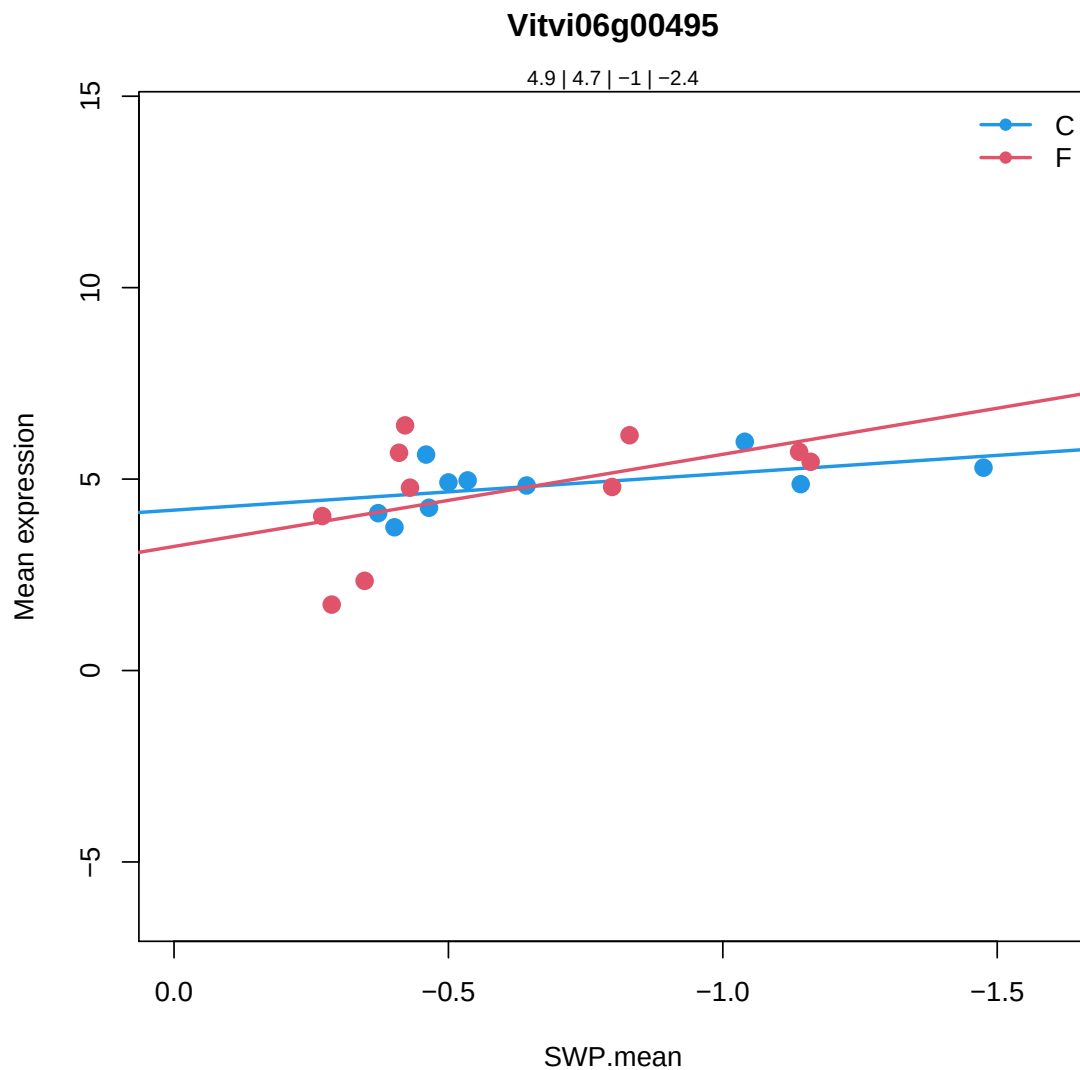
Haloacid dehalogenase-like hydrolase (HAD) superfamily protein |

Chr5:23979619-23981156 REVERSE LENGTH=282 |

201606

Coefficients for Vitvi06g00495.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.859213	3.264894e-13	***	4.843164e-13	***
SlopeC	-0.9531694	0.2819197		0.7773135	
MeanF-MeanC	-0.1526442	0.731424		0.918522	
SlopeF-SlopeC	-1.453674	0.2705395		0.9999488	



8.1.328 Vitvi17g00473: Type1.0

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

Vitvi17g00473

35.2

not assigned.unknown

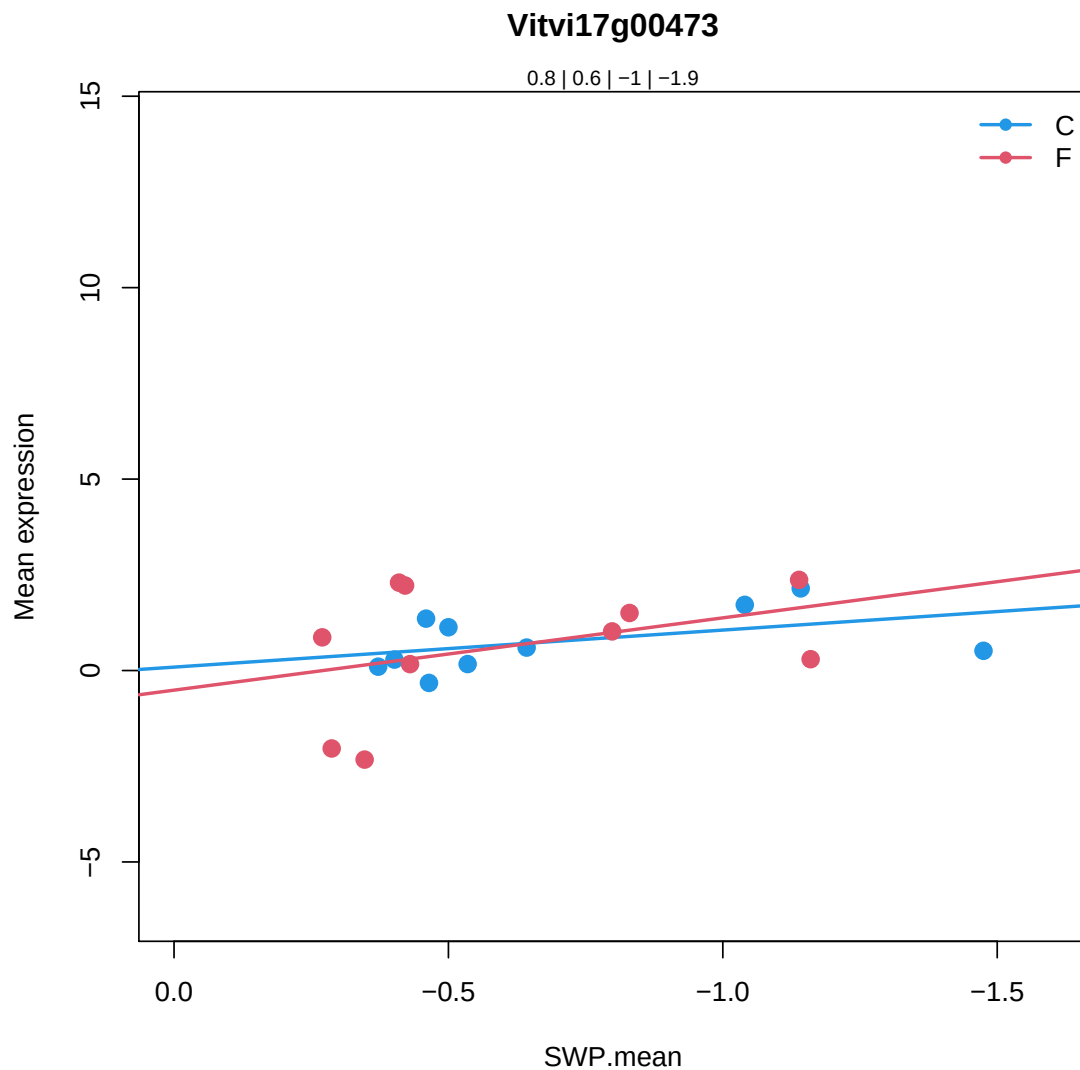
Squamosa promoter-binding protein-like (SBP domain) transcription fact

Chr1:26005626-26007041 FORWARD LENGTH=405 |

201606

Coefficients for Vitvi17g00473.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.7688096	0.04293221	*	0.04478325	*
SlopeC	-0.967168	0.3413622		0.8049123	
MeanF-MeanC	-0.1315192	0.7971039		0.9429813	
SlopeF-SlopeC	-0.9213217	0.539985		0.9999488	



8.1.329 Vitvi15g00653: Type1.0

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

Vitvi15g00653

35.1

not assigned.no ontology

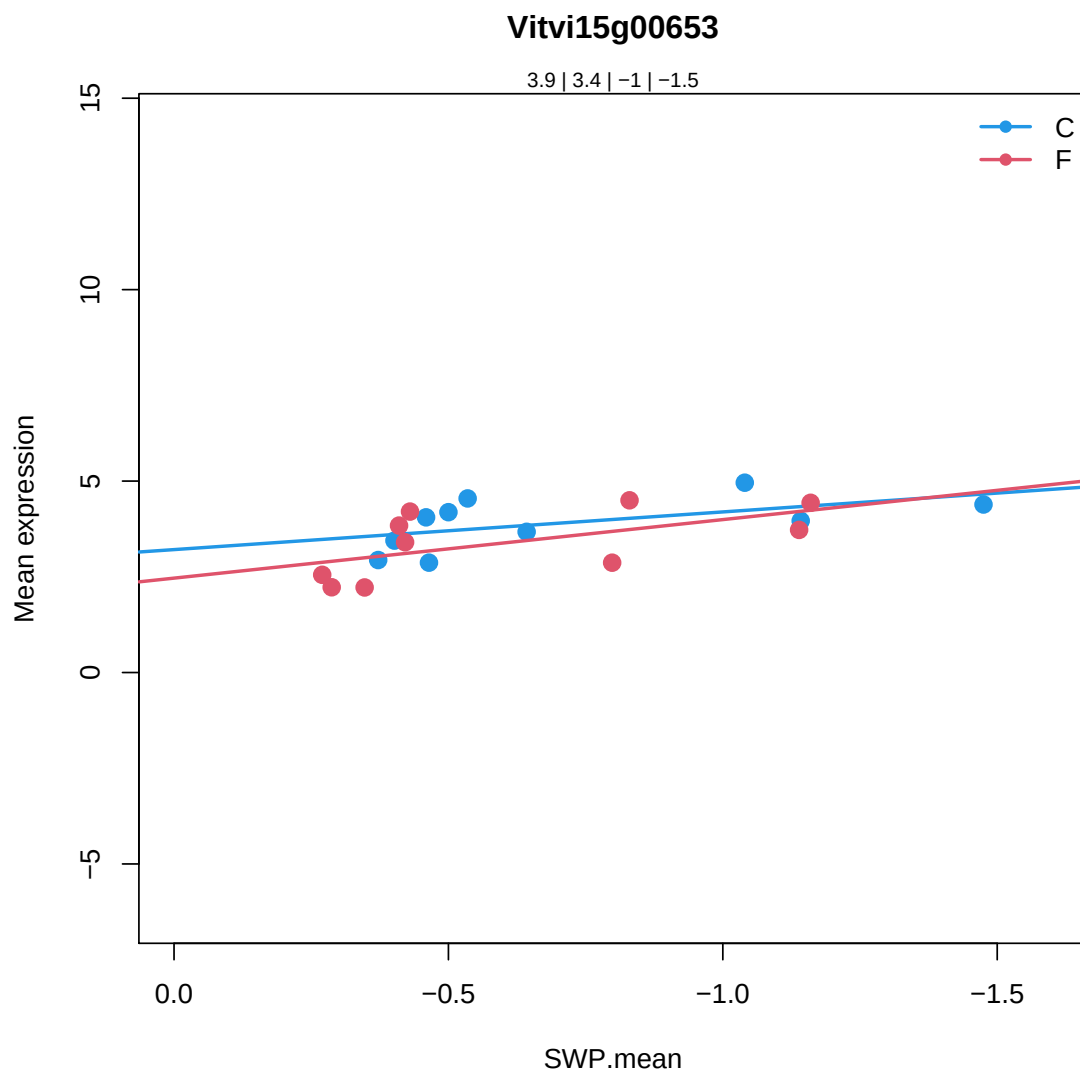
ELCH-like protein |

Chr5:4473212-4474318 REVERSE LENGTH=368 |

201606

Coefficients for Vitvi15g00653.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.9021	4.446624e-15	***	7.74488e-15	***
SlopeC	-0.9840762	0.09307482	.	0.6013762	
MeanF-MeanC	-0.5055483	0.0898663	.	0.3425335	
SlopeF-SlopeC	-0.5448595	0.5201595		0.9999488	



8.1.330 Vitvi14g01537: Type1.0

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

Vitvi14g01537

13.1.4.1.1

amino acid metabolism.synthesis.branched chain group.common.acetolacta

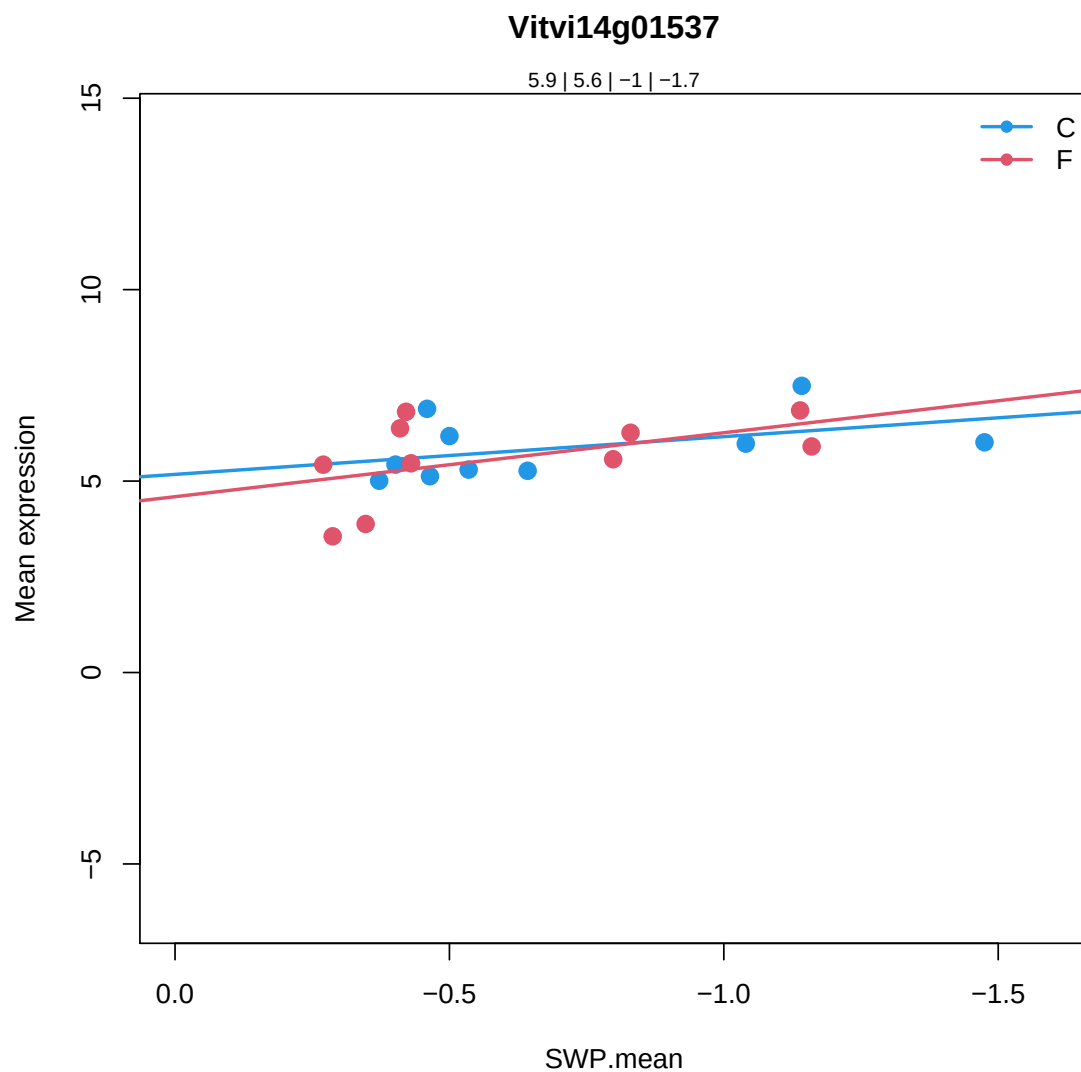
chlorsulfuron/imidazolinone resistant 1 |

Chr3:18001530-18003542 REVERSE LENGTH=670 |

201606

Coefficients for Vitvi14g01537.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.867544	1.813131e-16	***	3.773313e-16	***
SlopeC	-0.9853033	0.1854103		0.7156302	
MeanF-MeanC	-0.2576089	0.4891691		0.7997335	
SlopeF-SlopeC	-0.6849984	0.5295312		0.9999488	



8.1.331 Vitvi06g00119: Type1.0

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

Vitvi06g00119

11.2.4

lipid metabolism.FA desaturation.omega 6 desaturase

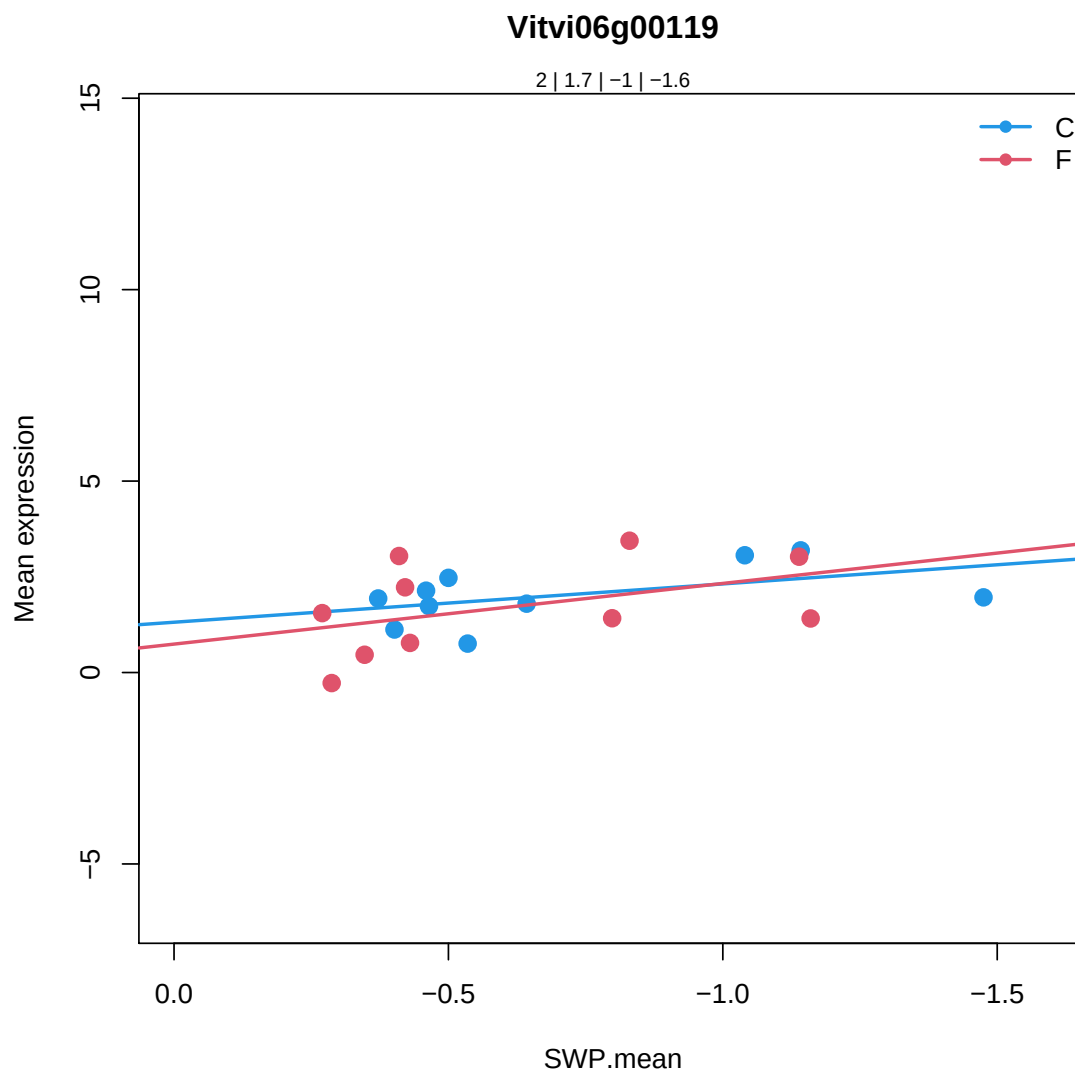
fatty acid desaturase 2 |

Chr3:3860592-3861743 REVERSE LENGTH=383 |

201606

Coefficients for Vitvi06g00119.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.016948	2.439001e-07	***	2.860735e-07	***
SlopeC	-1.000786	0.2005291		0.7274513	
MeanF-MeanC	-0.3092008	0.4309471		0.7654698	
SlopeF-SlopeC	-0.5837738	0.6100393		0.9999488	



8.1.332 Vitvi09g00603: Type1.0

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

Vitvi09g00603

34.14

transport.unspecified cations

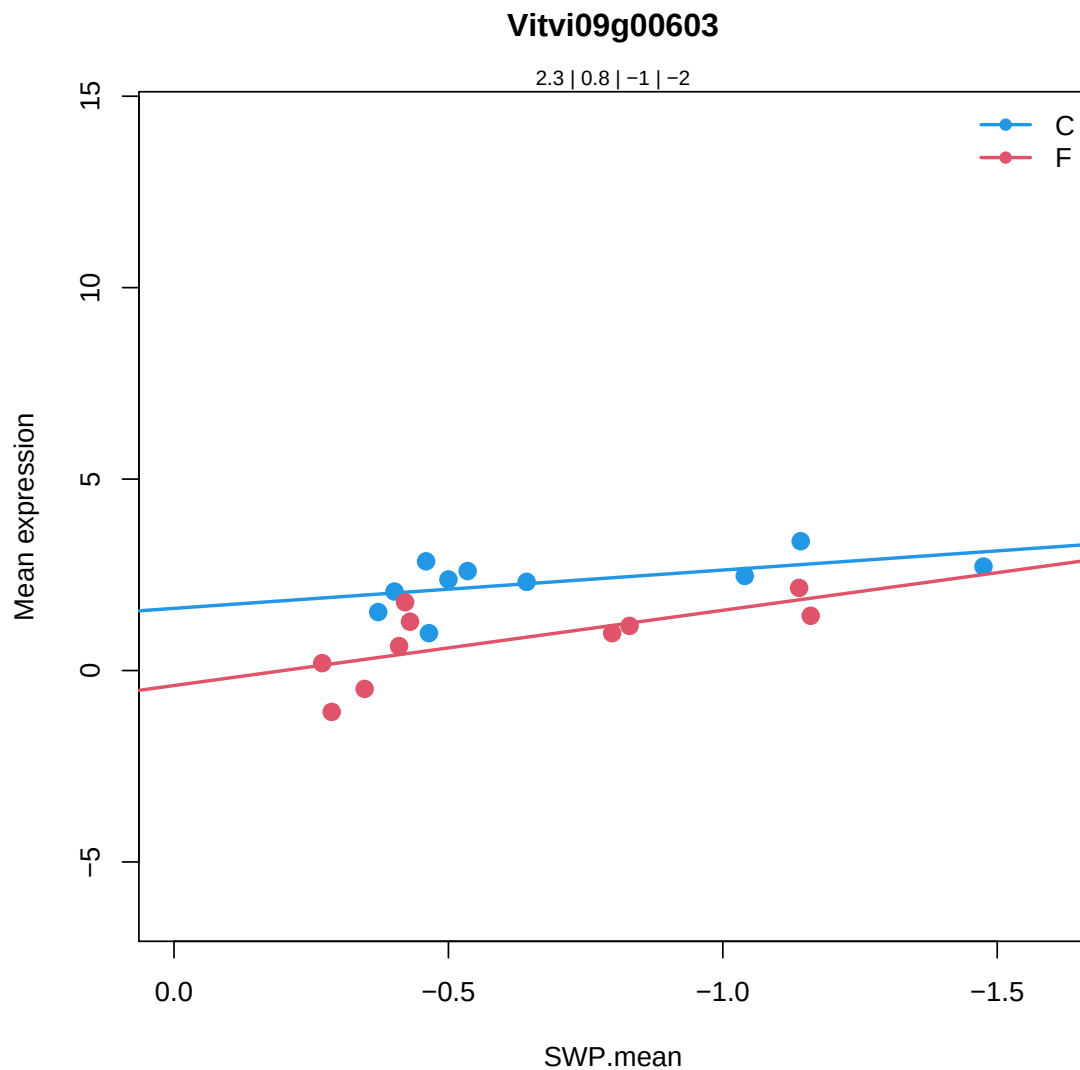
Nucleoside transporter family protein |

Chr1:561007-562382 REVERSE LENGTH=389 |

201606

Coefficients for Vitvi09g00603.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.327292	1.968874e-10	***	2.547934e-10	***
SlopeC	-1.000867	0.0974339	.	0.6084506	
MeanF-MeanC	-1.522013	3.642178e-05	***	0.000753244	***
SlopeF-SlopeC	-0.9642078	0.2743586		0.9999488	



8.1.333 Vitvi16g01320: Type1.0

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

Vitvi16g01320

35.2

not assigned.unknown

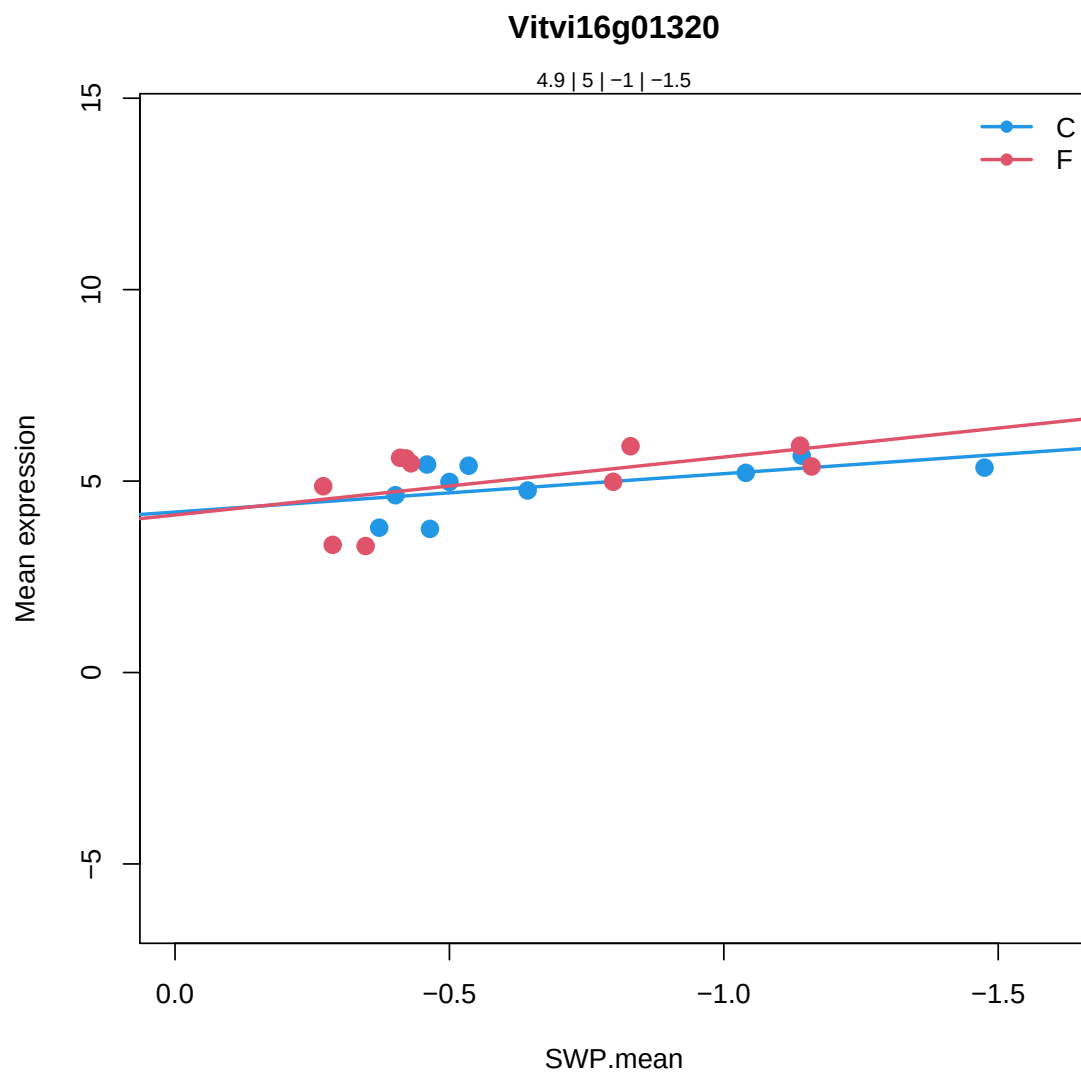
Major facilitator superfamily protein |

Chr1:6199980-6201359 FORWARD LENGTH=459 |

201606

Coefficients for Vitvi16g01320.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.895723	1.983506e-16	***	4.099891e-16	***
SlopeC	-1.001625	0.1115232		0.6258604	
MeanF-MeanC	0.1407173	0.6510534		0.8829186	
SlopeF-SlopeC	-0.5112082	0.5751744		0.9999488	



8.1.334 Vitvi12g00202: Type1.0

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

Vitvi12g00202

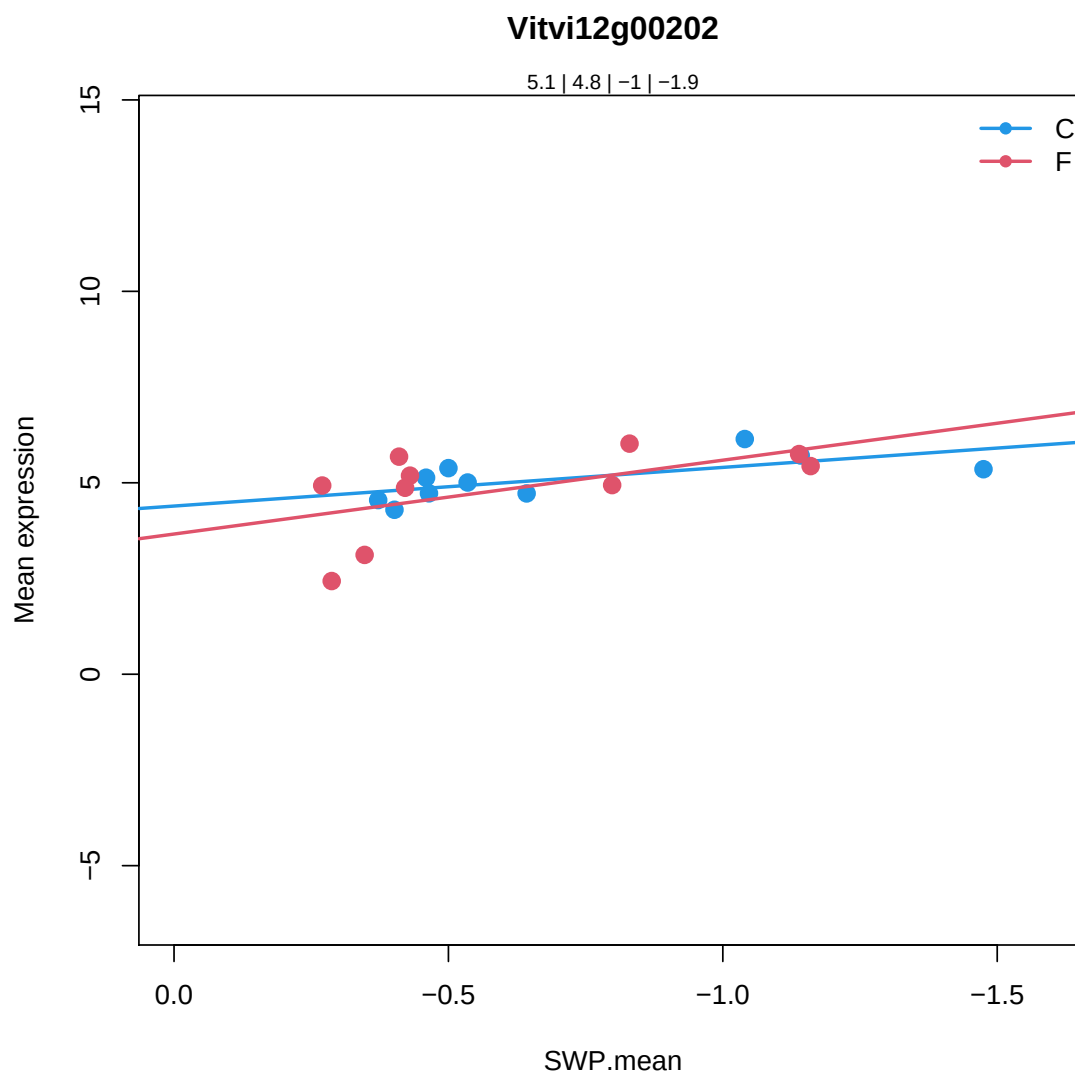
29.5.11.20

protein.degradation.ubiquitin.proteasom

Methyltransferase IPR013216 Methyltransferase type 11

Coefficients for Vitvi12g00202.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.102053	2.223297e-16	***	4.562744e-16	***
SlopeC	-1.009483	0.1250676		0.6459779	
MeanF-MeanC	-0.2655533	0.4178629		0.7561518	
SlopeF-SlopeC	-0.9197091	0.3394151		0.9999488	



8.1.335 Vitvi13g02466: Type1.0

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

Vitvi13g02466

20.1.2.1

stress.biotic.receptors.CC-NBS-LRR

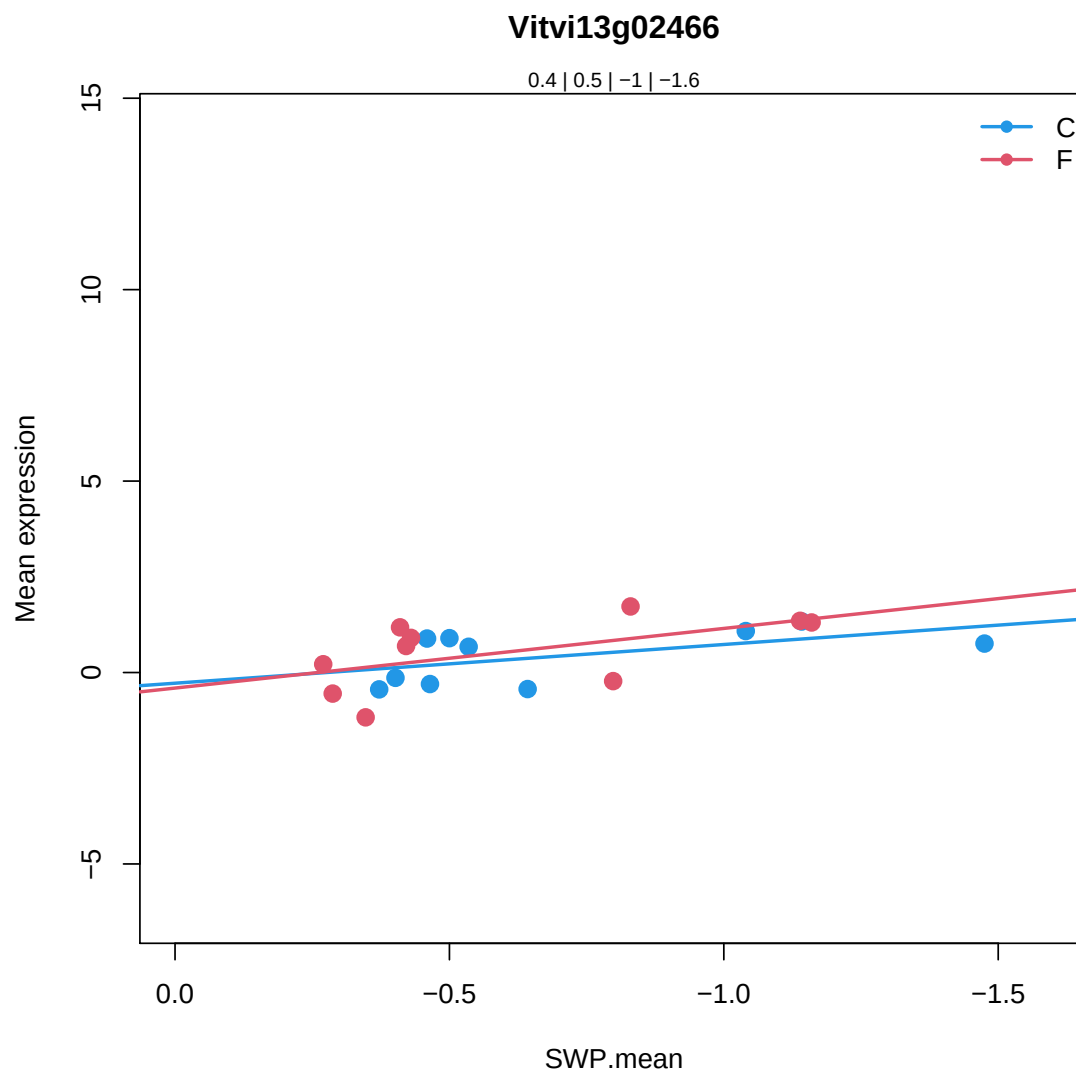
NB-ARC domain-containing disease resistance protein |

Chr3:4857940-4861104 FORWARD LENGTH=1054 |

201606

Coefficients for Vitvi13g02466.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4315664	0.05411383	.	0.05630823	.
SlopeC	-1.011474	0.1004758		0.612269	
MeanF-MeanC	0.1113024	0.7138424		0.9117897	
SlopeF-SlopeC	-0.5461617	0.5400201		0.9999488	



8.1.336 Vitvi18g02541: Type1.0

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

Vitvi18g02541

35.2

not assigned.unknown

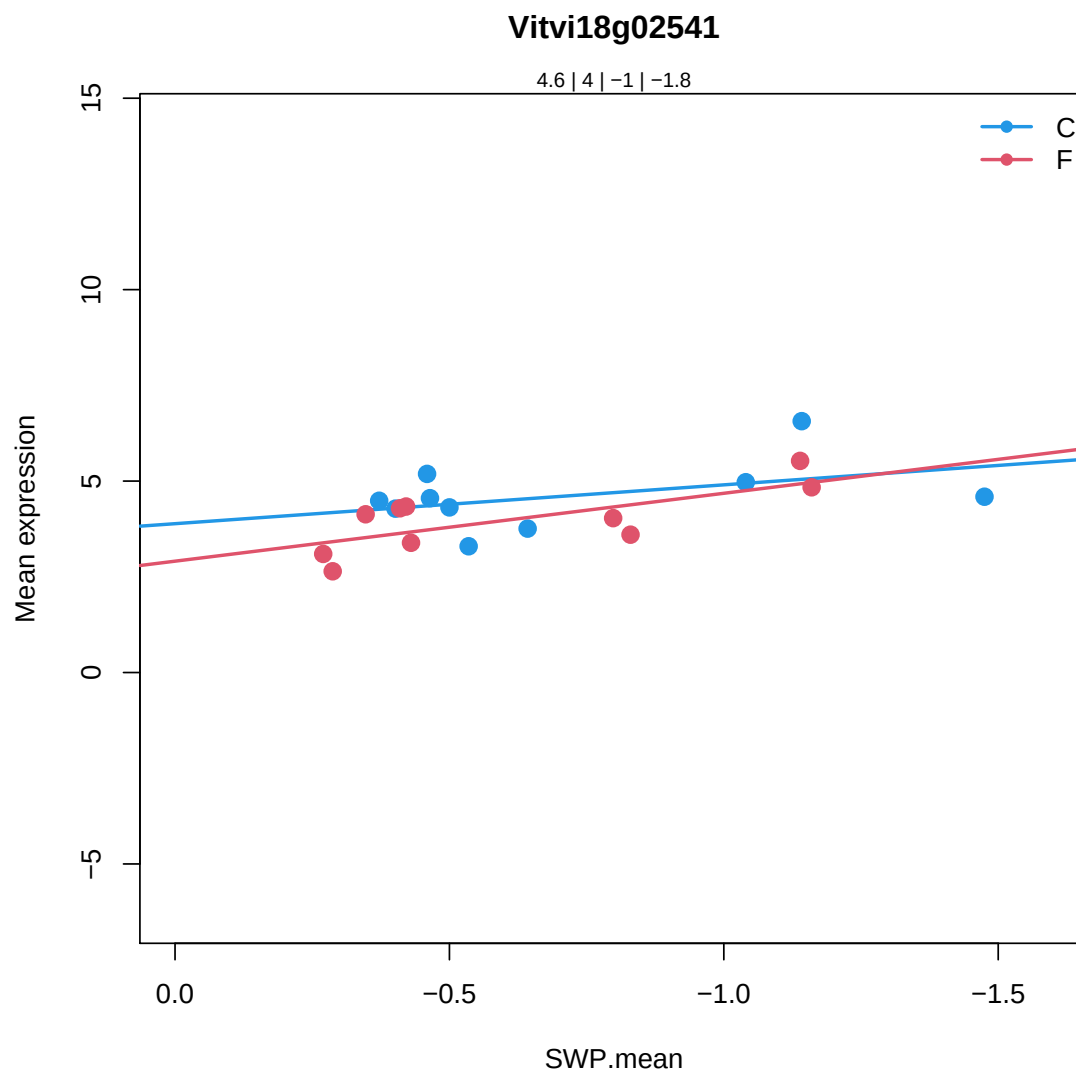
flavonol synthase 1 |

Chr5:2804009-2805175 FORWARD LENGTH=336 |

201606

Coefficients for Vitvi18g02541.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.600214	6.65143e-16	***	1.273792e-15	***
SlopeC	-1.014469	0.1061418		0.6208032	
MeanF-MeanC	-0.6118513	0.05816668	.	0.2629231	
SlopeF-SlopeC	-0.7586023	0.406096		0.9999488	



8.1.337 Vitvi02g00575: Type1.0 *

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

Vitvi02g00575

35.1

not assigned.no ontology

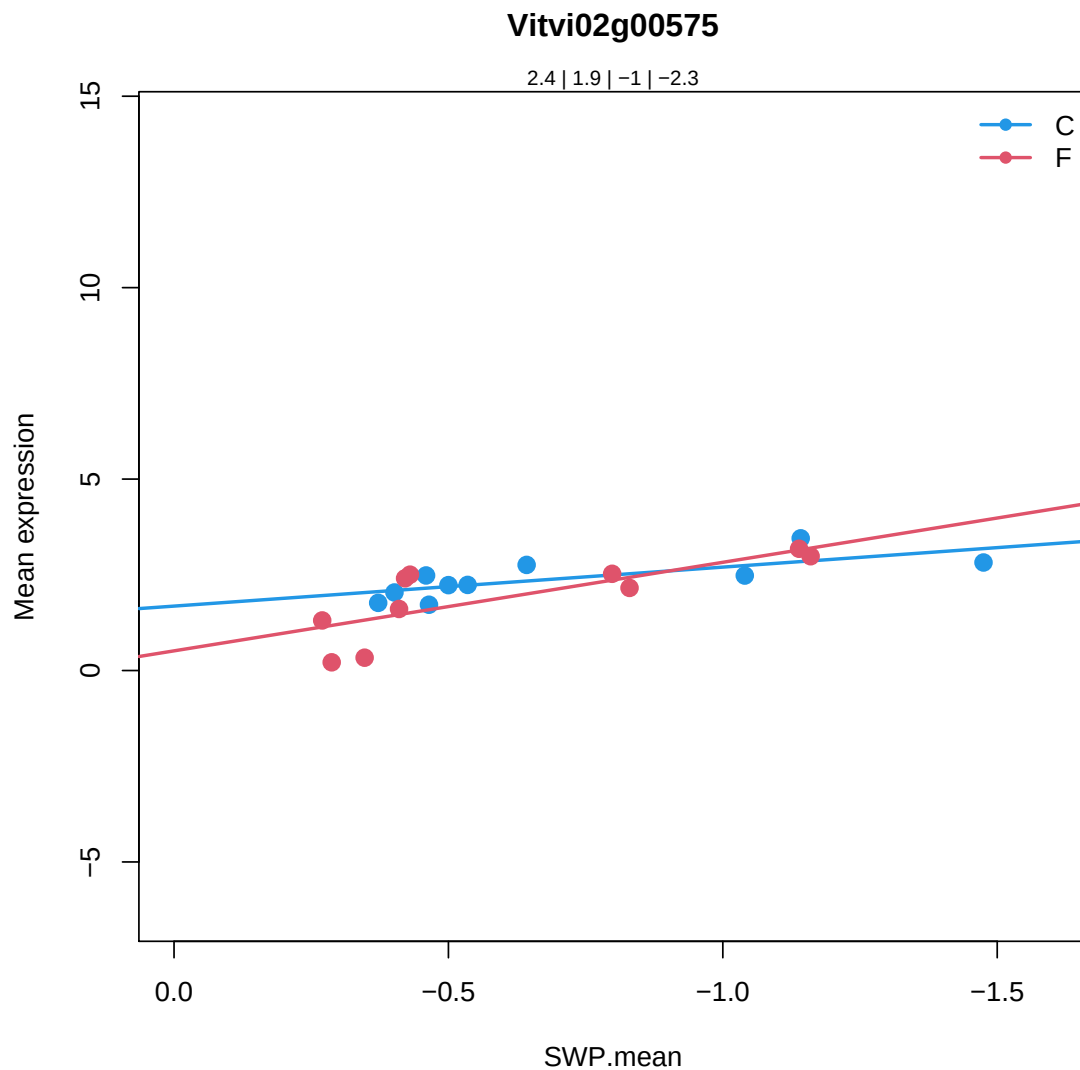
Oxidoreductase family protein |

Chr4:9706698-9708142 FORWARD LENGTH=286 |

201606

Coefficients for Vitvi02g00575.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.39837	3.323934e-12	***	4.635261e-12	***
SlopeC	-1.018044	0.04566111	*	0.4926906	
MeanF-MeanC	-0.4760438	0.06413563	.	0.2805842	
SlopeF-SlopeC	-1.295	0.08378902	.	0.9999488	



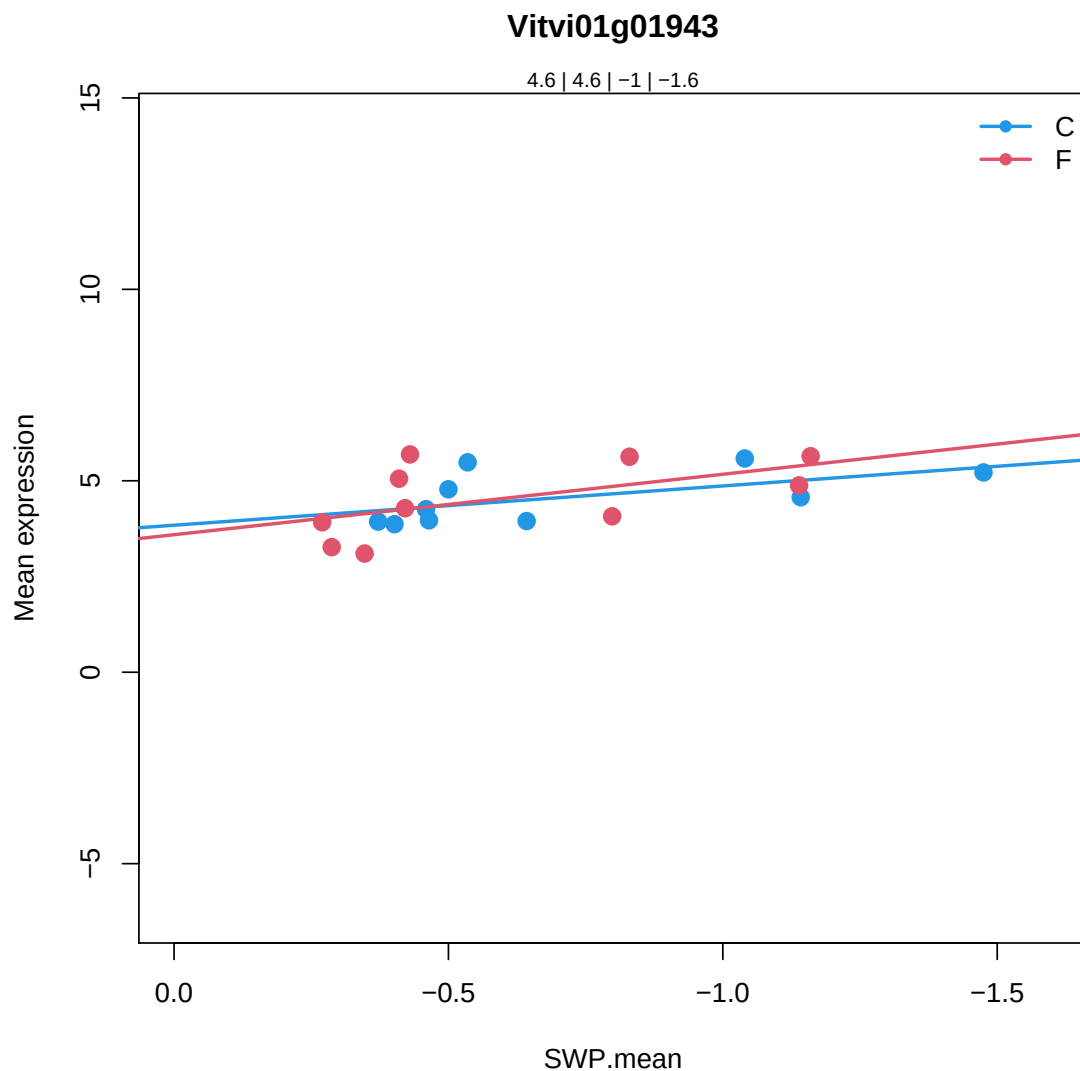
8.1.338 Vitvi01g01943: Type1.0

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

```
Vitvi01g01943
20
stress
NA
```

Coefficients for Vitvi01g01943.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.560527	6.514615e-16	***	1.249318e-15	***
SlopeC	-1.026328	0.0992638	.	0.6110181	
MeanF-MeanC	-0.007453514	0.9805876		0.9950147	
SlopeF-SlopeC	-0.5517993	0.540221		0.9999488	



8.1.339 Vitvi12g00907: Type1.0

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

Vitvi12g00907

35.2

not assigned.unknown

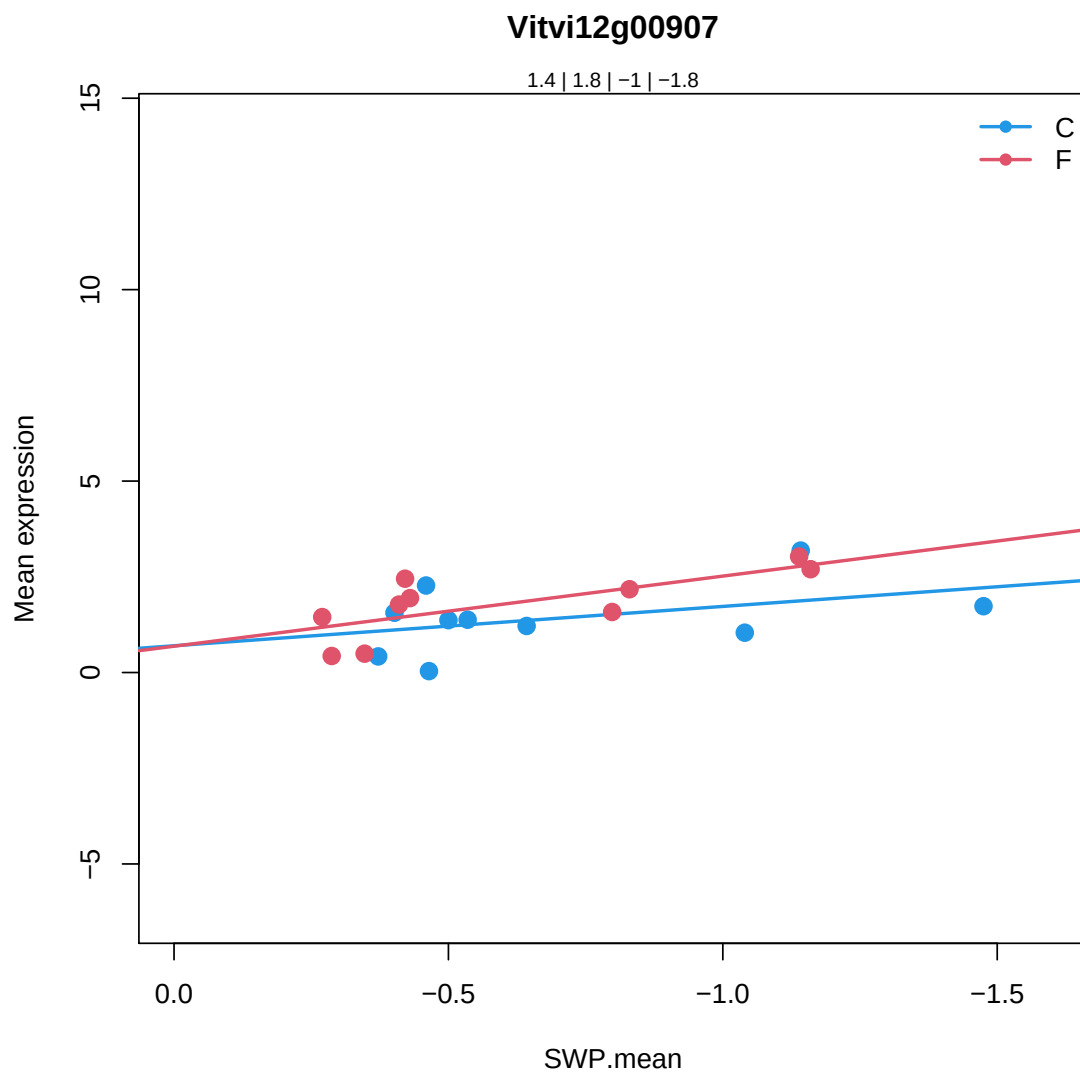
cysteine-rich RECEPTOR-like kinase |

Chr4:12129485-12133157 FORWARD LENGTH=1043 |

201606

Coefficients for Vitvi12g00907.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.420997	1.571121e-06	***	1.805415e-06	***
SlopeC	-1.027719	0.1031954		0.6146329	
MeanF-MeanC	0.3814265	0.2273823		0.5801408	
SlopeF-SlopeC	-0.8036979	0.3810854		0.9999488	



8.1.340 Vitvi08g01022: Type1.0

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

Vitvi08g01022

16.2.1.1

secondary metabolism.phenylpropanoids.lignin biosynthesis.PAL

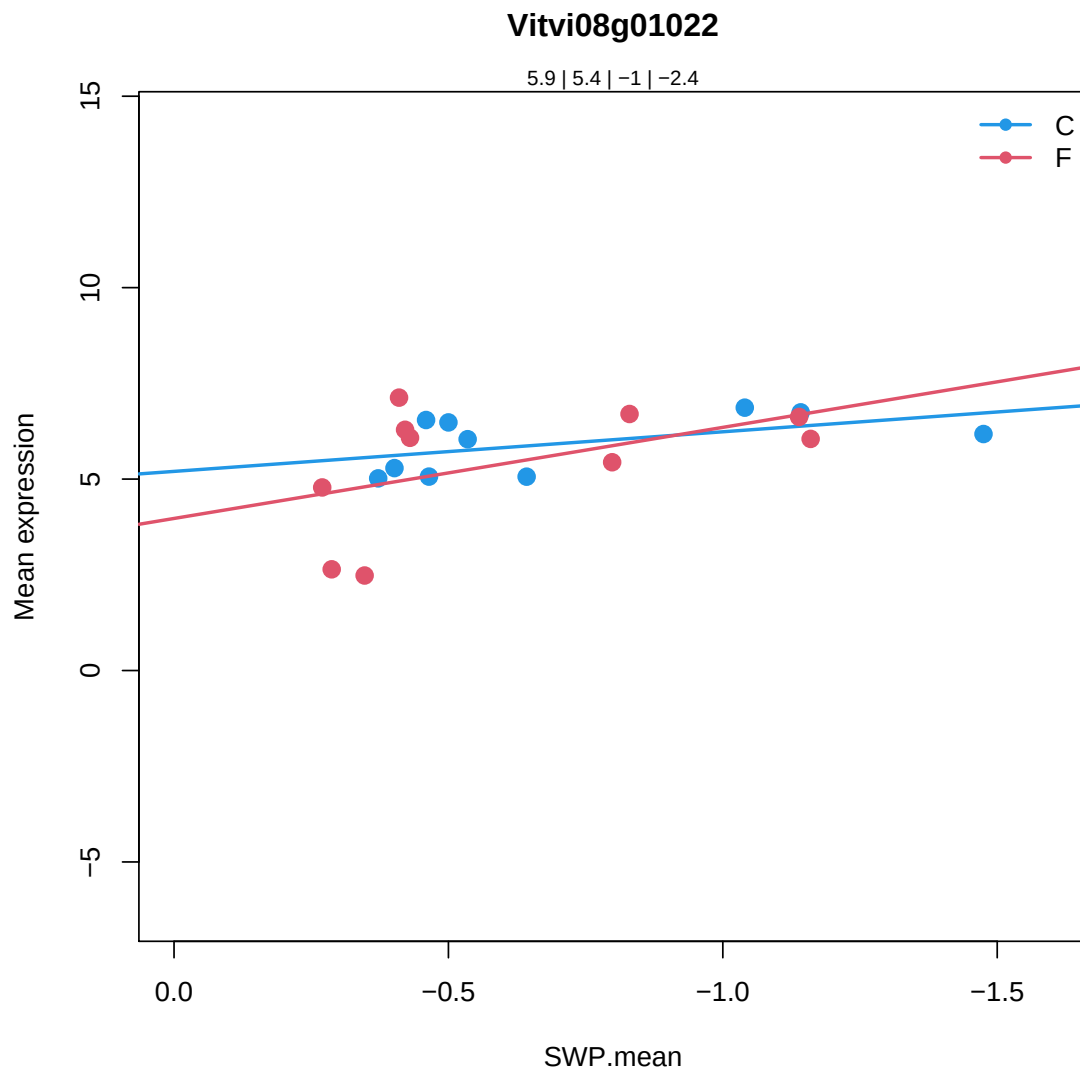
phenylalanine ammonia-lyase 2 |

Chr3:19744256-19746619 REVERSE LENGTH=717 |

201606

Coefficients for Vitvi08g01022.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.928083	2.022303e-14	***	3.286836e-14	***
SlopeC	-1.034541	0.2715179		0.773903	
MeanF-MeanC	-0.5070959	0.2885294		0.6536088	
SlopeF-SlopeC	-1.344275	0.3354466		0.9999488	



8.1.341 Vitvi15g01027: Type1.0

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

Vitvi15g01027

27.3.35

RNA.regulation of transcription.bZIP transcription factor family

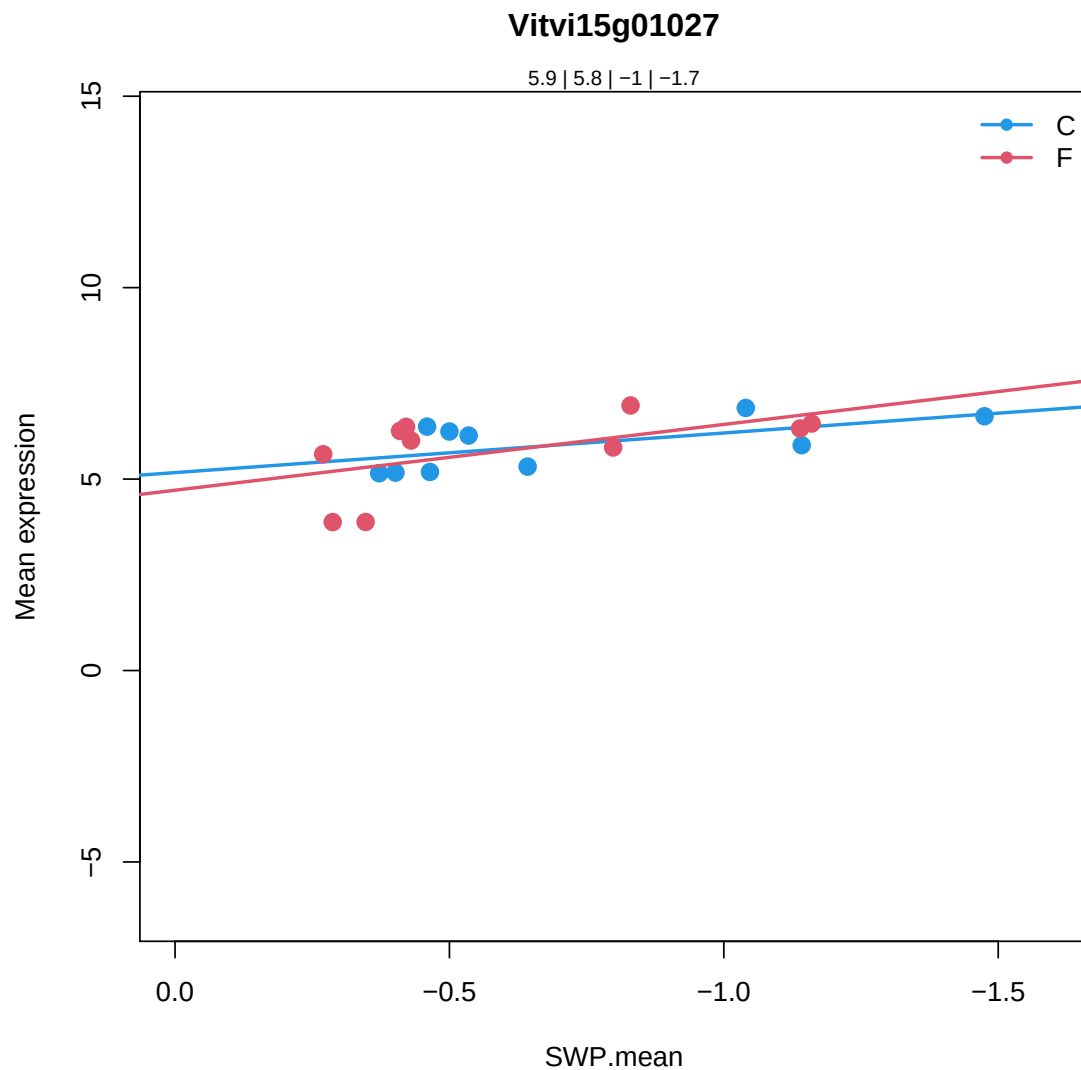
G-box binding factor 3 |

Chr2:19000859-19002901 FORWARD LENGTH=382 |

201606

Coefficients for Vitvi15g01027.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.896459	6.360836e-18	***	1.753515e-17	***
SlopeC	-1.034909	0.1073105		0.6223948	
MeanF-MeanC	-0.1408923	0.6571137		0.8855638	
SlopeF-SlopeC	-0.6839102	0.4636007		0.9999488	



8.1.342 Vitvi08g01621: Type1.0

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

Vitvi08g01621

35.2

not assigned.unknown

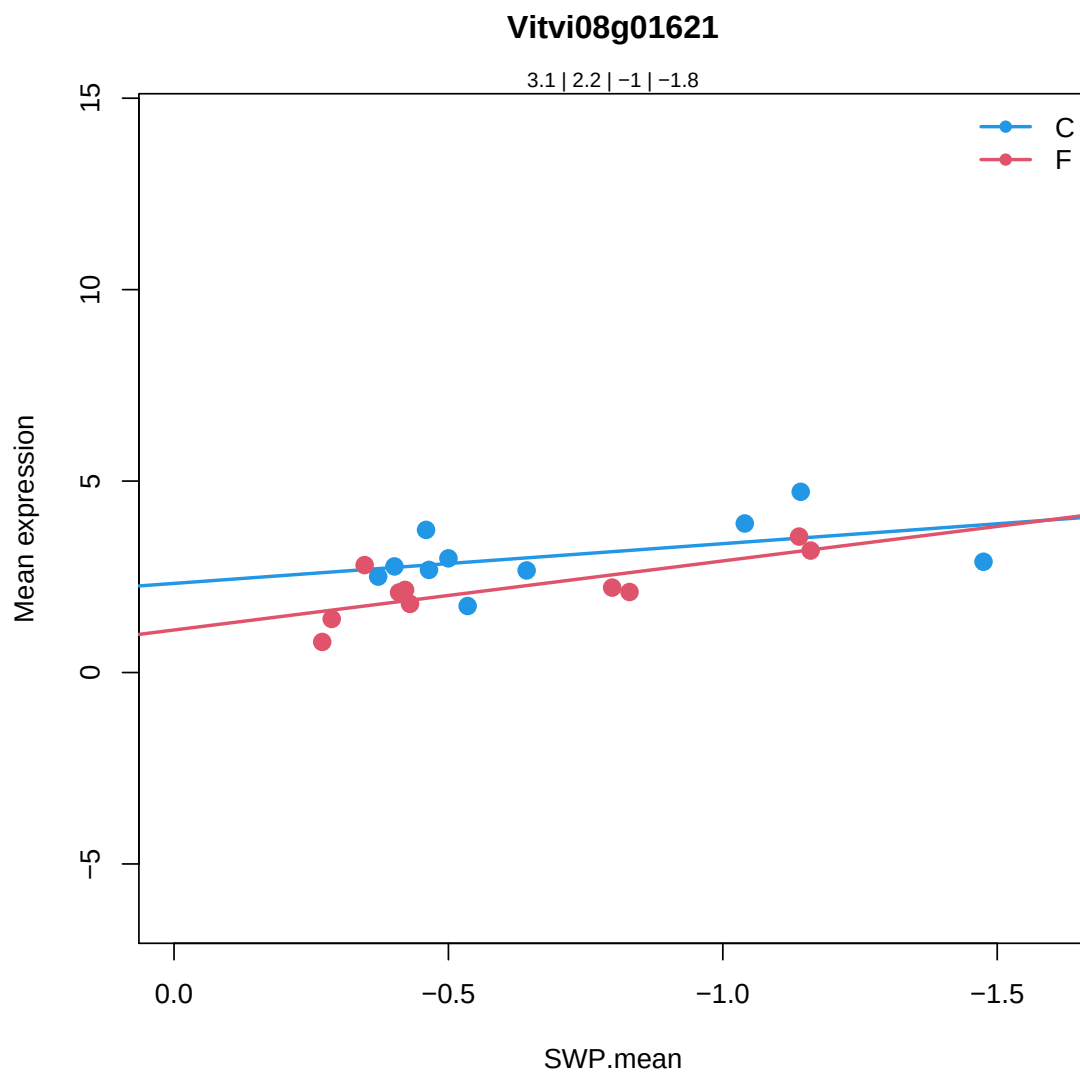
translation initiation factor |

Chr2:15482167-15483676 REVERSE LENGTH=256 |

201606

Coefficients for Vitvi08g01621.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.057216	6.575109e-13	***	9.558208e-13	***
SlopeC	-1.03827	0.07898339	.	0.5748584	
MeanF-MeanC	-0.8475412	0.007332163	**	0.06045569	.
SlopeF-SlopeC	-0.7651909	0.3712477		0.9999488	



8.1.343 Vitvi02g00466: Type1.0

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

Vitvi02g00466

35.2

not assigned.unknown

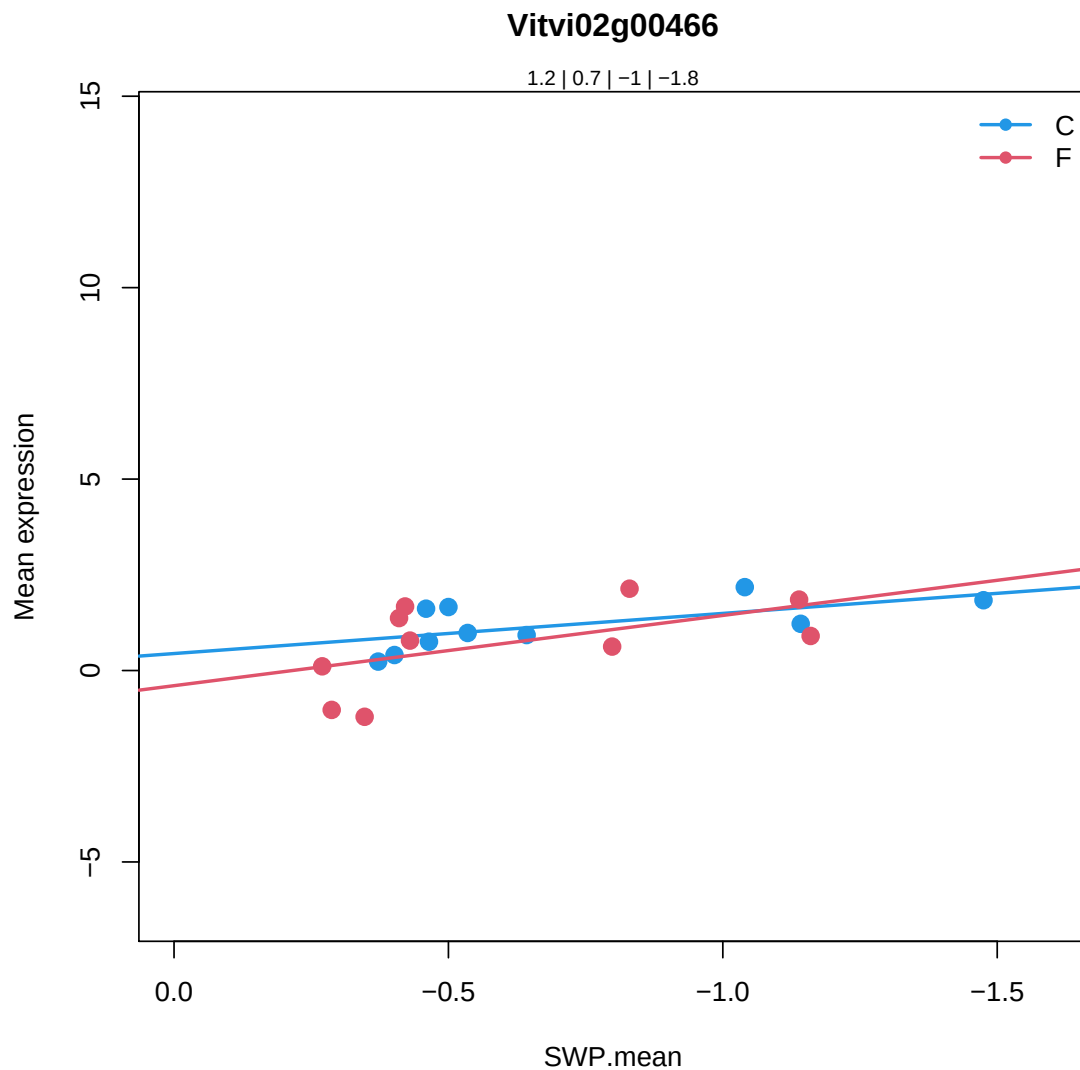
MATE efflux family protein |

Chr4:11975153-11976628 REVERSE LENGTH=491 |

201606

Coefficients for Vitvi02g00466.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.180283	5.124596e-05	***	5.692253e-05	***
SlopeC	-1.048439	0.1221037		0.64341	
MeanF-MeanC	-0.4589528	0.1799449		0.5148714	
SlopeF-SlopeC	-0.7865444	0.426095		0.9999488	



8.1.344 Vitvi03g00312: Type1.0 +

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

Vitvi03g00312

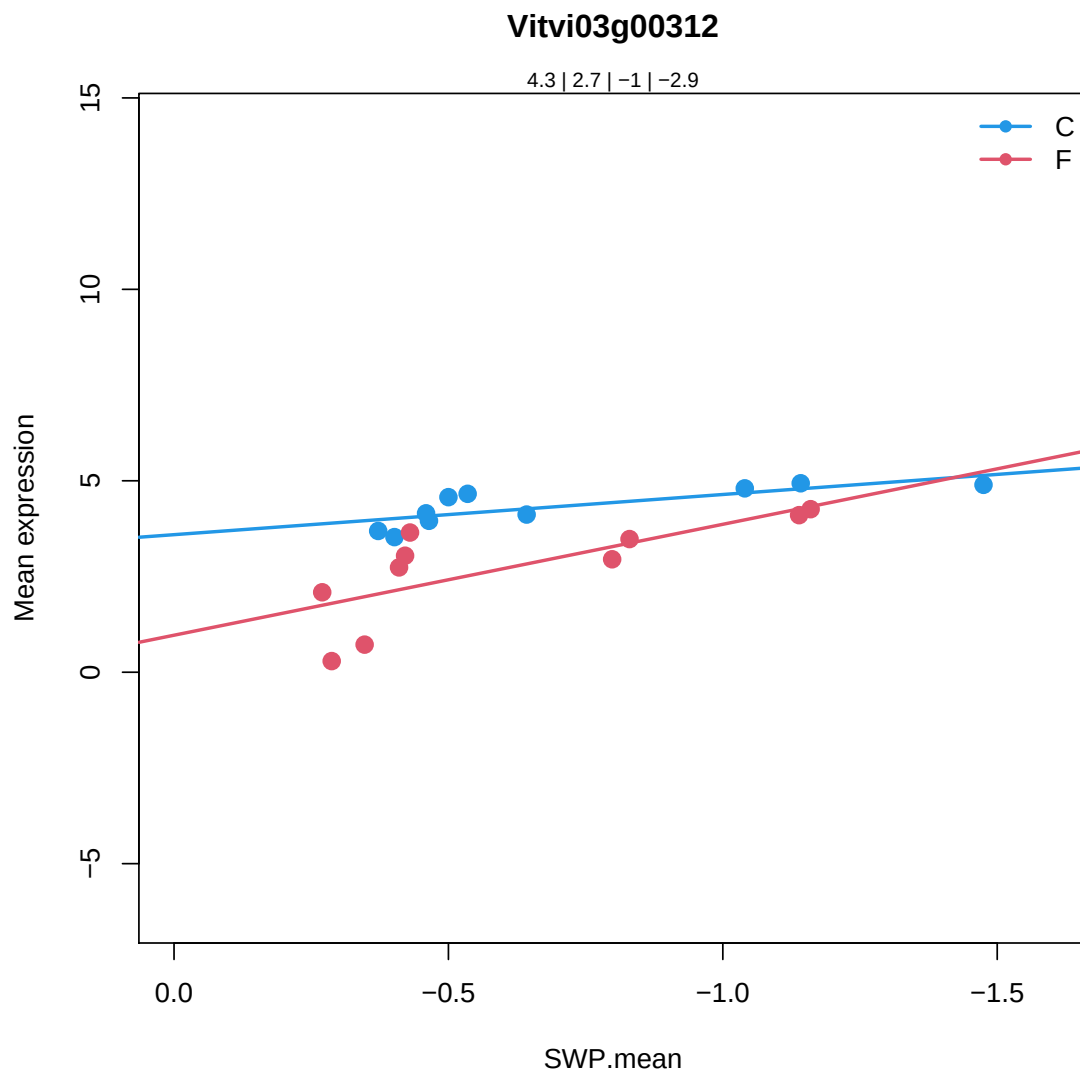
35.2

not assigned.unknown

Polyphenol oxidase IPR016213 Polyphenol oxidase, plant

Coefficients for Vitvi03g00312.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.330496	1.289442e-15	***	2.381976e-15	***
SlopeC	-1.04922	0.08688051	.	0.5919681	
MeanF-MeanC	-1.598941	2.298862e-05	***	0.0005130197	***
SlopeF-SlopeC	-1.847796	0.0455431	*	0.9999488	



8.1.345 Vitvi18g00548: Type1.0

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

Vitvi18g00548

35.2

not assigned.unknown

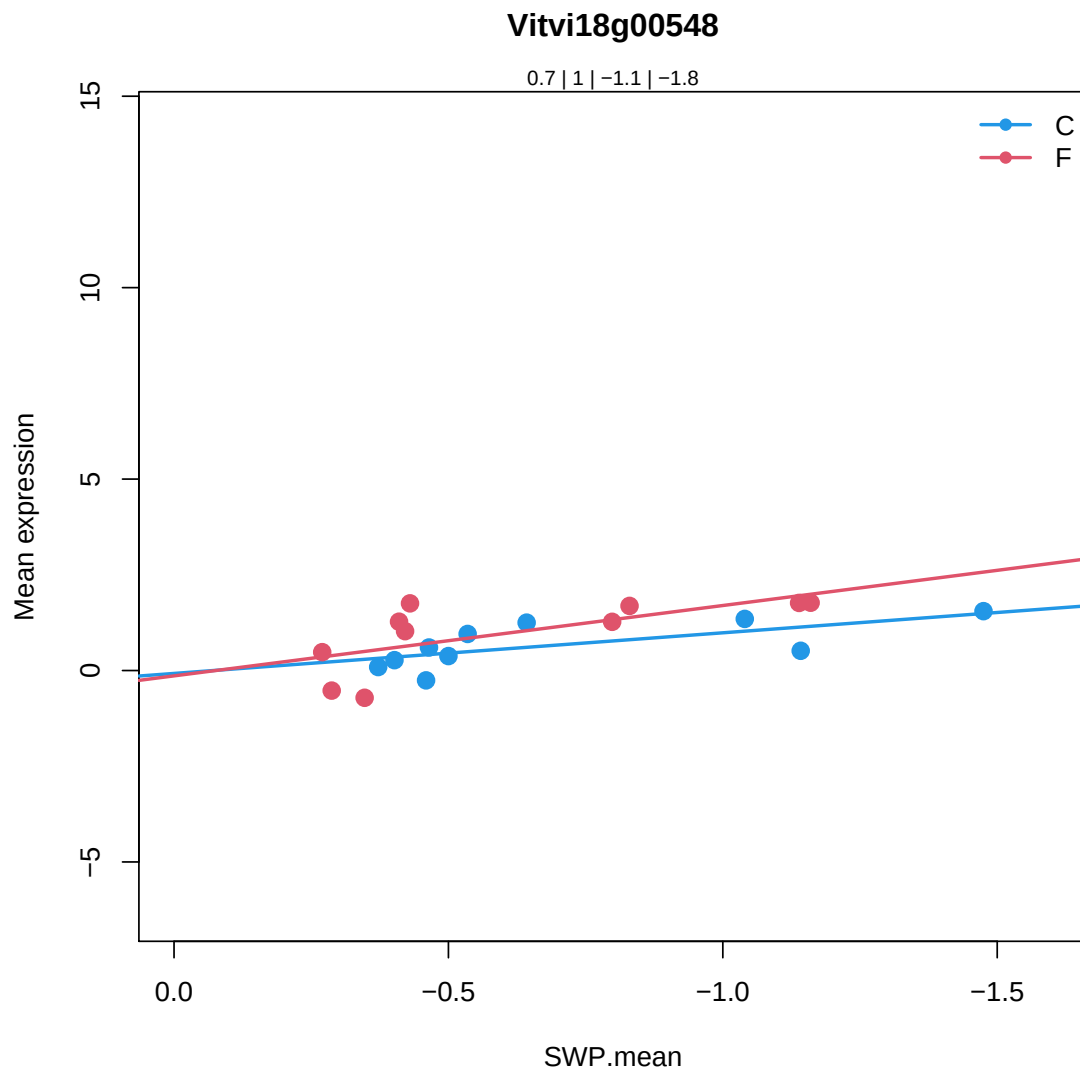
hypothetical protein |

Chr2:16106393-16106810 REVERSE LENGTH=84 |

201606

Coefficients for Vitvi18g00548.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6700423	0.001501646	**	0.001620395	**
SlopeC	-1.061023	0.05068707	.	0.5104439	
MeanF-MeanC	0.3094202	0.2479432		0.6079714	
SlopeF-SlopeC	-0.7768392	0.3198473		0.9999488	



8.1.346 Vitvi14g01798: Type1.0

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

Vitvi14g01798

34.15

transport.potassium

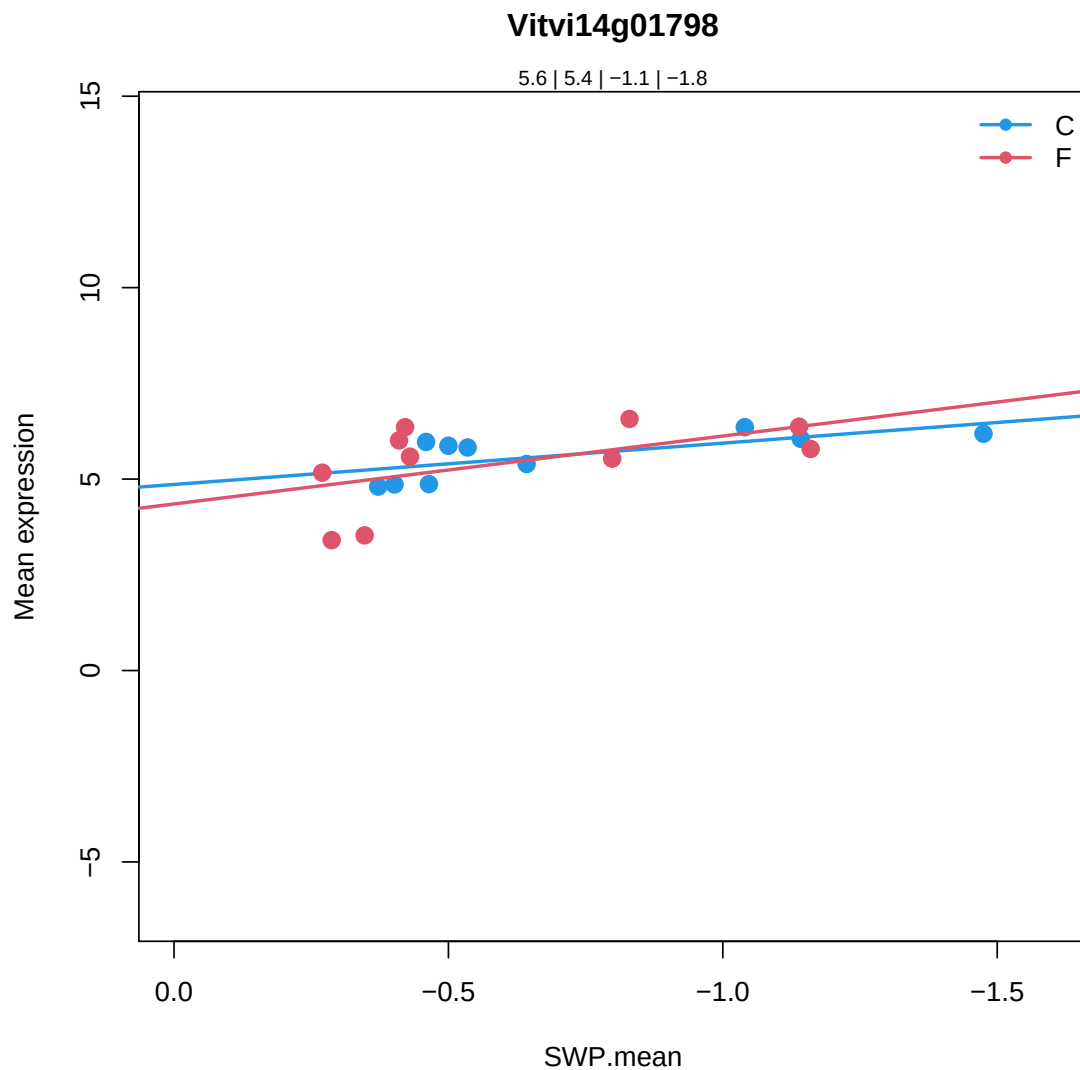
Potassium transporter family protein |

Chr5:4814244-4817667 FORWARD LENGTH=781 |

201606

Coefficients for Vitvi14g01798.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.61826	2.55935e-17	***	6.208755e-17	***
SlopeC	-1.079149	0.09976898	.	0.611697	
MeanF-MeanC	-0.1872821	0.5631037		0.8413084	
SlopeF-SlopeC	-0.6951451	0.4646195		0.9999488	



8.1.347 Vitvi13g02053: Type1.0

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

Vitvi13g02053

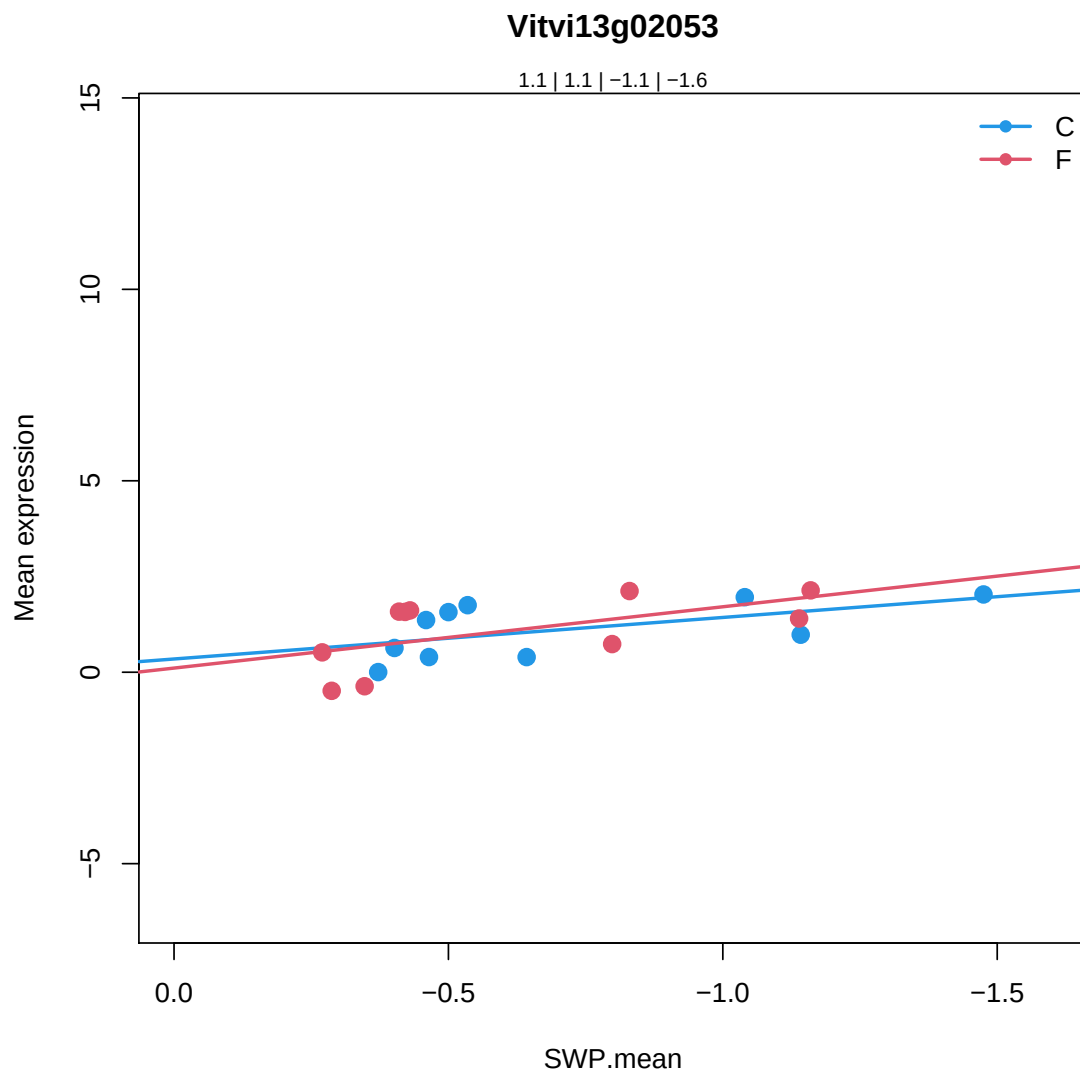
29.2.4

protein.synthesis.elongation

NA

Coefficients for Vitvi13g02053.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.108271	3.819493e-05	***	4.254675e-05	***
SlopeC	-1.084615	0.08325455	.	0.5813429	
MeanF-MeanC	-0.02485601	0.93548		0.9824739	
SlopeF-SlopeC	-0.5163267	0.5672391		0.9999488	



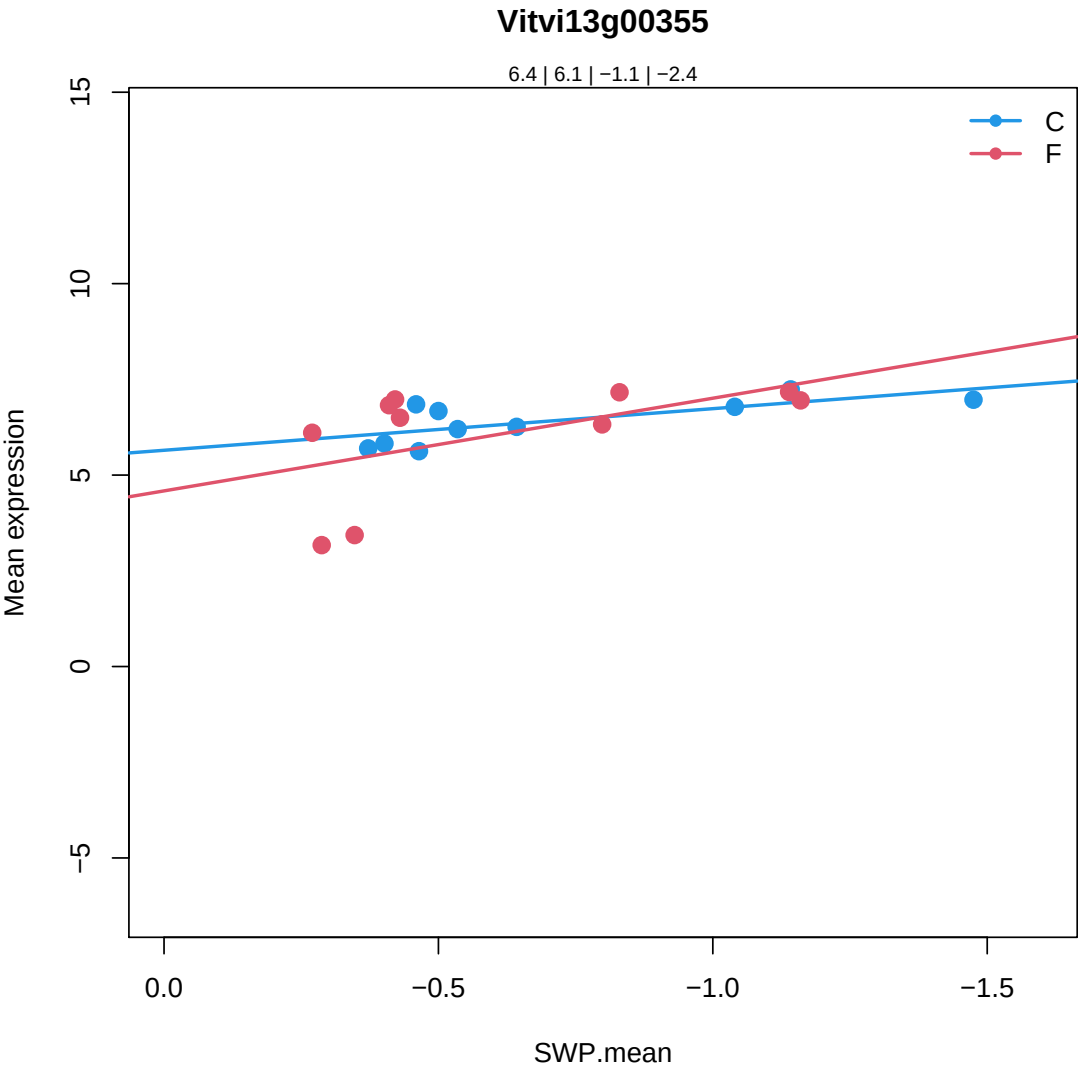
8.1.348 Vitvi13g00355: Type1.0

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

Vitvi13g00355
13.1.2.2.1
amino acid metabolism.synthesis.glutamate family.proline.delta 1-pyrro
RNA-directed DNA polymerase (reverse transcriptase)-related family pro
Chr3:8789309-8790907 FORWARD LENGTH=532 |
201606

Coefficients for Vitvi13g00355.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.411512	1.348819e-16	***	2.863728e-16	***
SlopeC	-1.086697	0.1755404		0.7086494	
MeanF-MeanC	-0.3499812	0.3846043		0.734788	
SlopeF-SlopeC	-1.333739	0.2607078		0.9999488	



8.1.349 Vitvi08g00857: Type1.0 *

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

Vitvi08g00857

35.2

not assigned.unknown

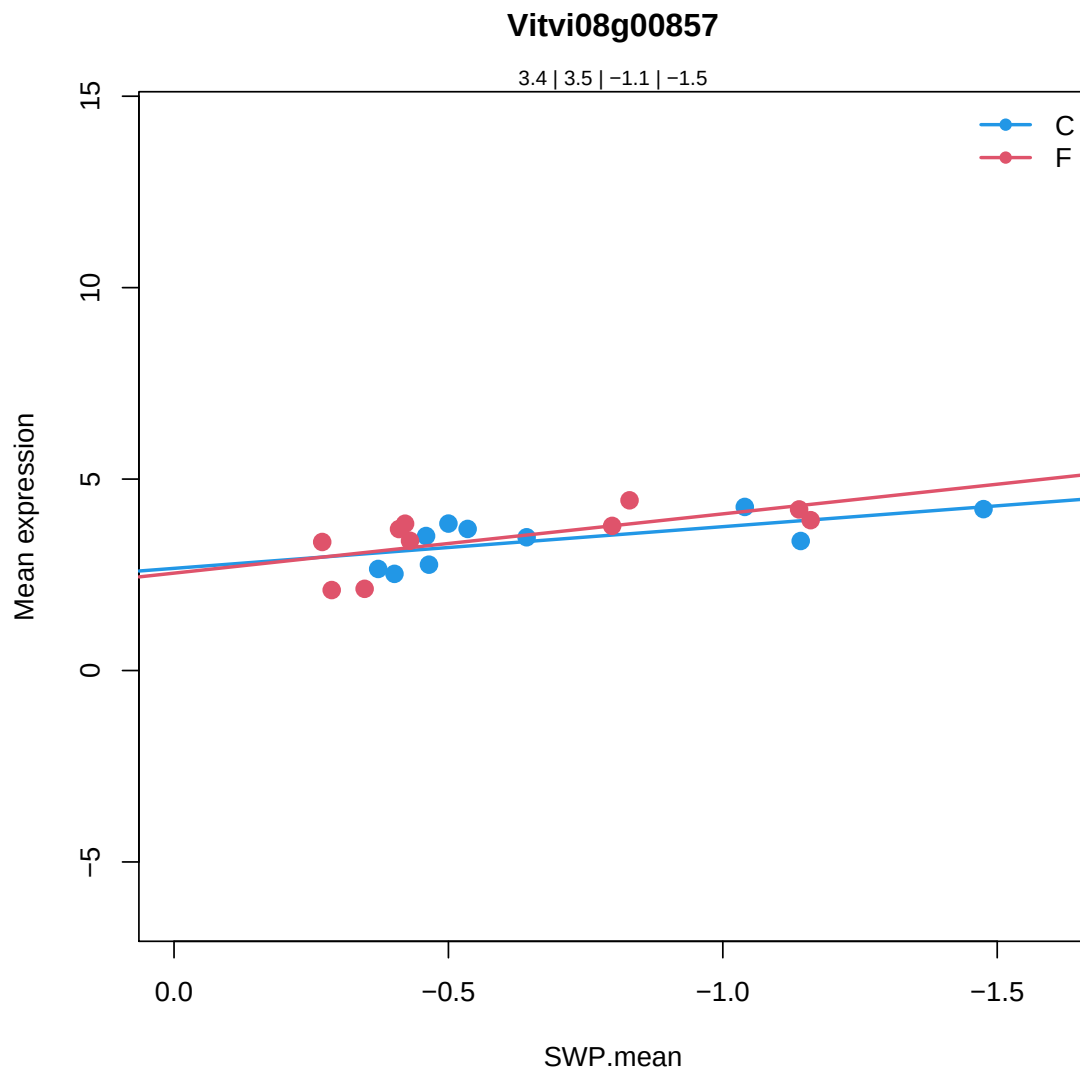
RING/U-box superfamily protein |

Chr3:3413068-3413613 REVERSE LENGTH=181 |

201606

Coefficients for Vitvi08g00857.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.433887	2.386415e-15	***	4.286322e-15	***
SlopeC	-1.08926	0.03297358	*	0.4417082	
MeanF-MeanC	0.05274916	0.8301412		0.9526501	
SlopeF-SlopeC	-0.4590712	0.5254875		0.9999488	



8.1.350 Vitvi01g00214: Type1.0

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

Vitvi01g00214

4.1.15

glycolysis.cytosolic branch.phospho-enol-pyruvate carboxylase (PEPC)

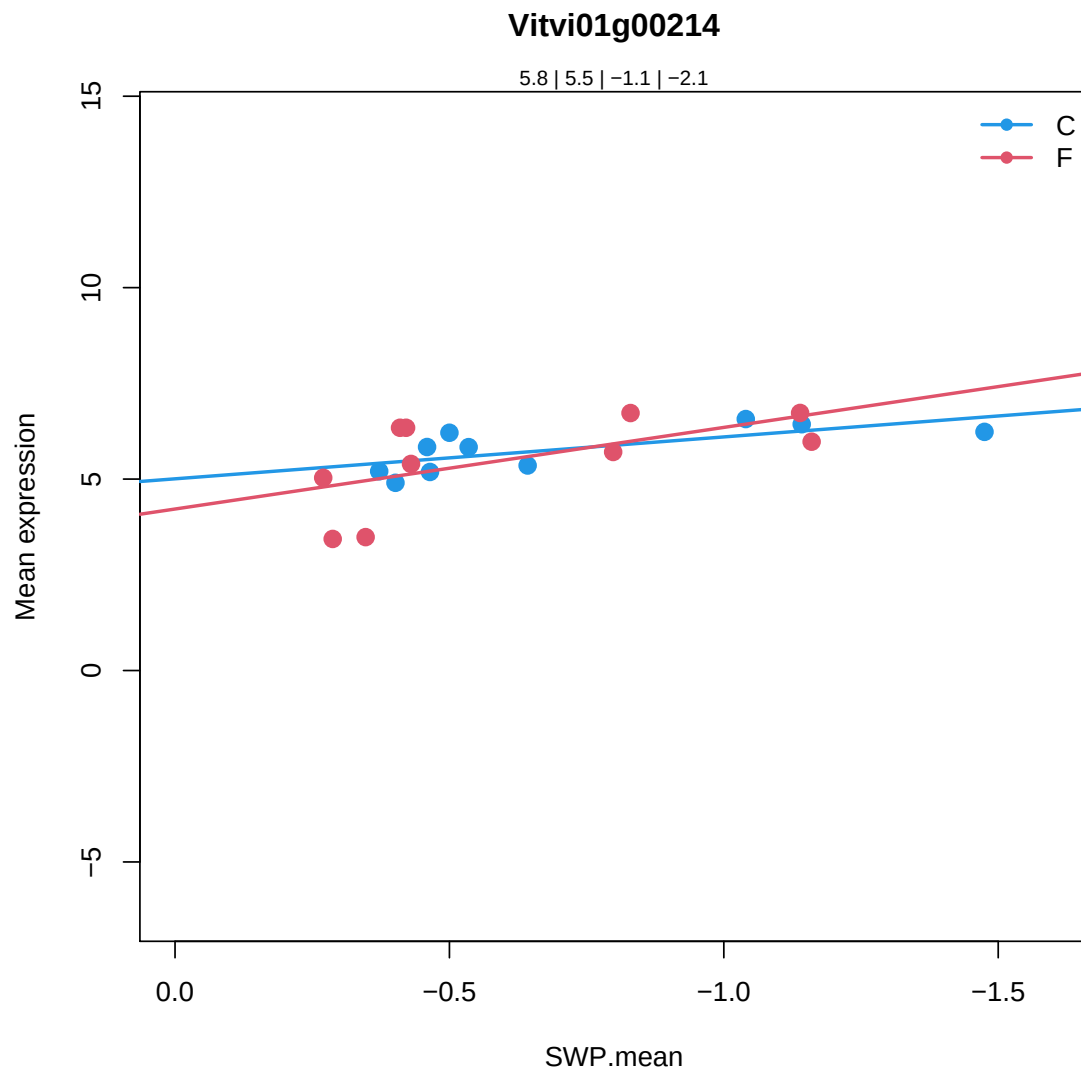
phosphoenolpyruvate carboxylase 4 |

Chr1:25822942-25828104 REVERSE LENGTH=1032 |

201606

Coefficients for Vitvi01g00214.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.776278	1.985174e-17	***	4.926413e-17	***
SlopeC	-1.094375	0.100244		0.6121177	
MeanF-MeanC	-0.2596095	0.4315471		0.7659319	
SlopeF-SlopeC	-1.037168	0.286175		0.9999488	



8.1.351 Vitvi07g01624: Type1.0

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

Vitvi07g01624

26.7

misc.oxidases - copper, flavone etc

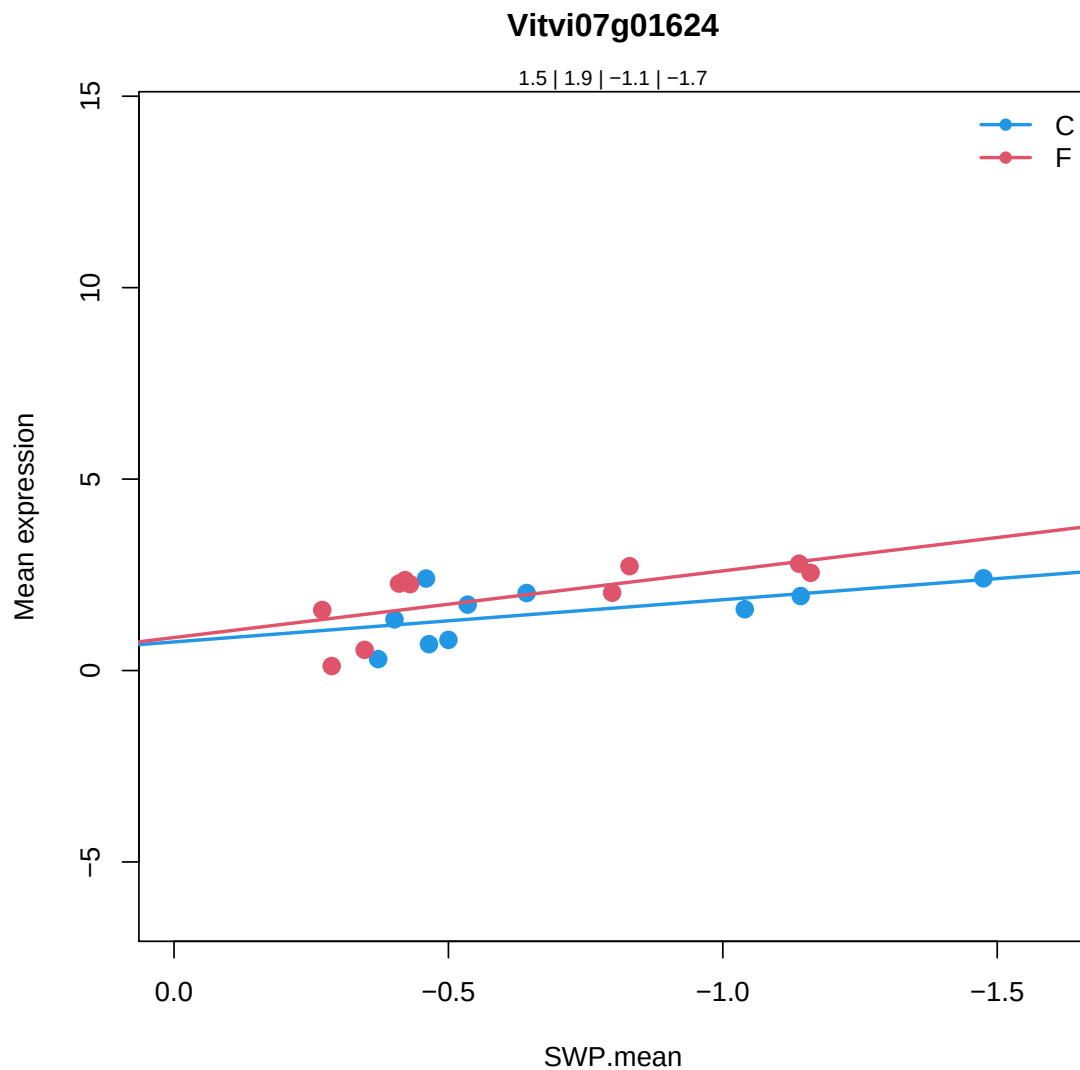
2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein

Chr4:16256943-16258614 REVERSE LENGTH=288 |

201606

Coefficients for Vitvi07g01624.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.522014	1.976298e-07	***	2.325182e-07	***
SlopeC	-1.102975	0.06376278	.	0.5471512	
MeanF-MeanC	0.3998104	0.1775967		0.5113202	
SlopeF-SlopeC	-0.6387479	0.4551719		0.9999488	



8.1.352 Vitvi19g00305: Type1.0 *

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

Vitvi19g00305

11.3.5

lipid metabolism.phospholipid synthesis.diacylglycerol kinase

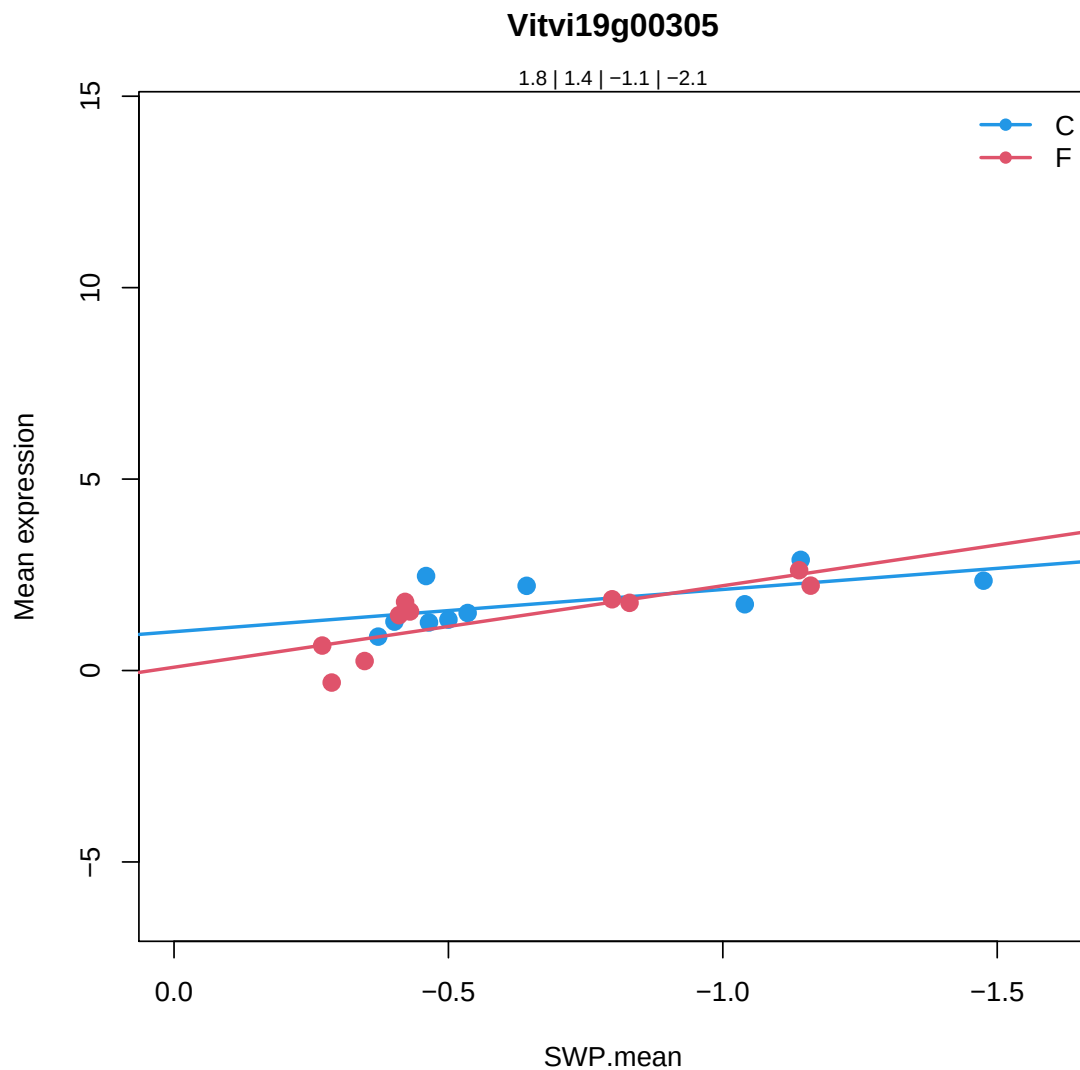
cysteine-rich RECEPTOR-like kinase |

Chr4:12129485-12133157 FORWARD LENGTH=1043 |

201606

Coefficients for Vitvi19g00305.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.789459	6.658432e-10	***	8.450277e-10	***
SlopeC	-1.103198	0.03000666	*	0.4310665	
MeanF-MeanC	-0.4065561	0.1064841		0.3791998	
SlopeF-SlopeC	-1.02601	0.1608892		0.9999488	



8.1.353 Vitvi04g00317: Type1.0

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

Vitvi04g00317

35.2

not assigned.unknown

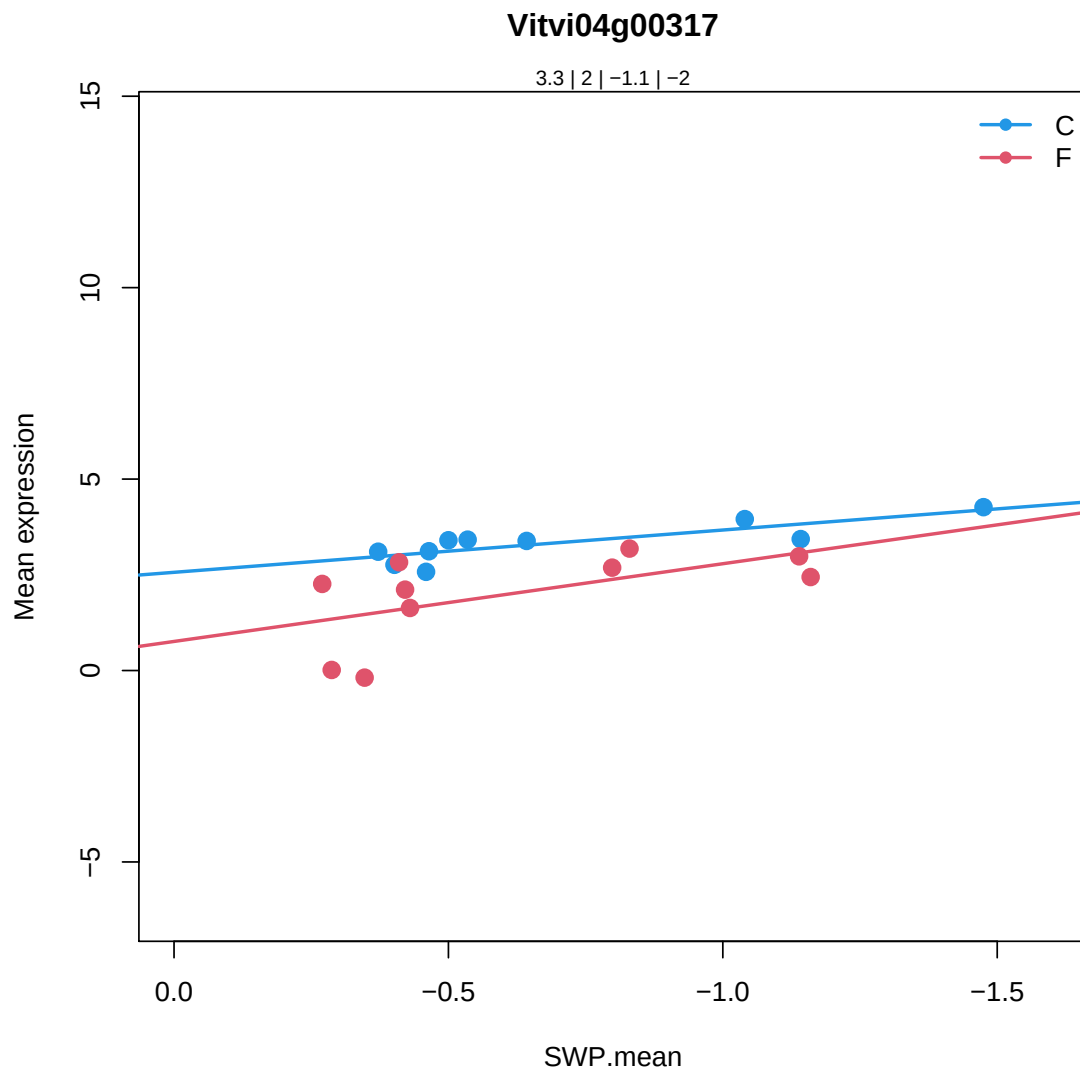
ARM repeat superfamily protein |

Chr5:3708203-3709147 REVERSE LENGTH=314 |

201606

Coefficients for Vitvi04g00317.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.341488	5.446226e-13	***	7.952804e-13	***
SlopeC	-1.104536	0.08394203	.	0.5831561	
MeanF-MeanC	-1.345506	0.0002742194	***	0.004273672	**
SlopeF-SlopeC	-0.9252681	0.3190515		0.9999488	



8.1.354 Vitvi18g00542: Type1.0

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

Vitvi18g00542

35.2

not assigned.unknown

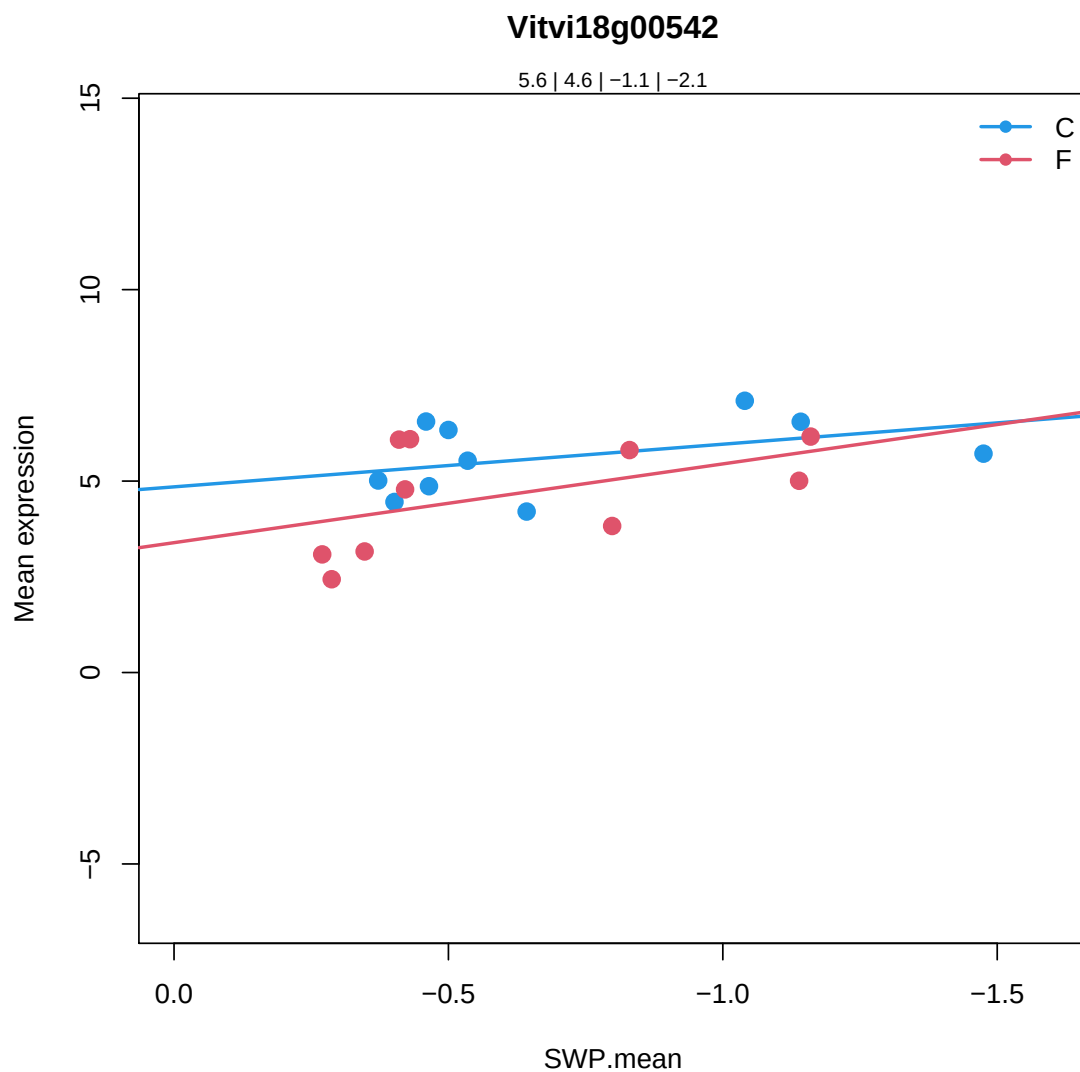
CHCH domain protein |

Chr5:25749468-25749947 FORWARD LENGTH=118 |

201606

Coefficients for Vitvi18g00542.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.632541	3.37013e-14	***	5.376546e-14	***
SlopeC	-1.113816	0.2258975		0.7454275	
MeanF-MeanC	-0.9877184	0.04093725	*	0.209525	
SlopeF-SlopeC	-0.943492	0.4855811		0.9999488	



8.1.355 Vitvi19g00557: Type1.0 *

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

Vitvi19g00557

26.4.1

misc.beta 1,3 glucan hydrolases.glucan endo-1,3-beta-glucosidase

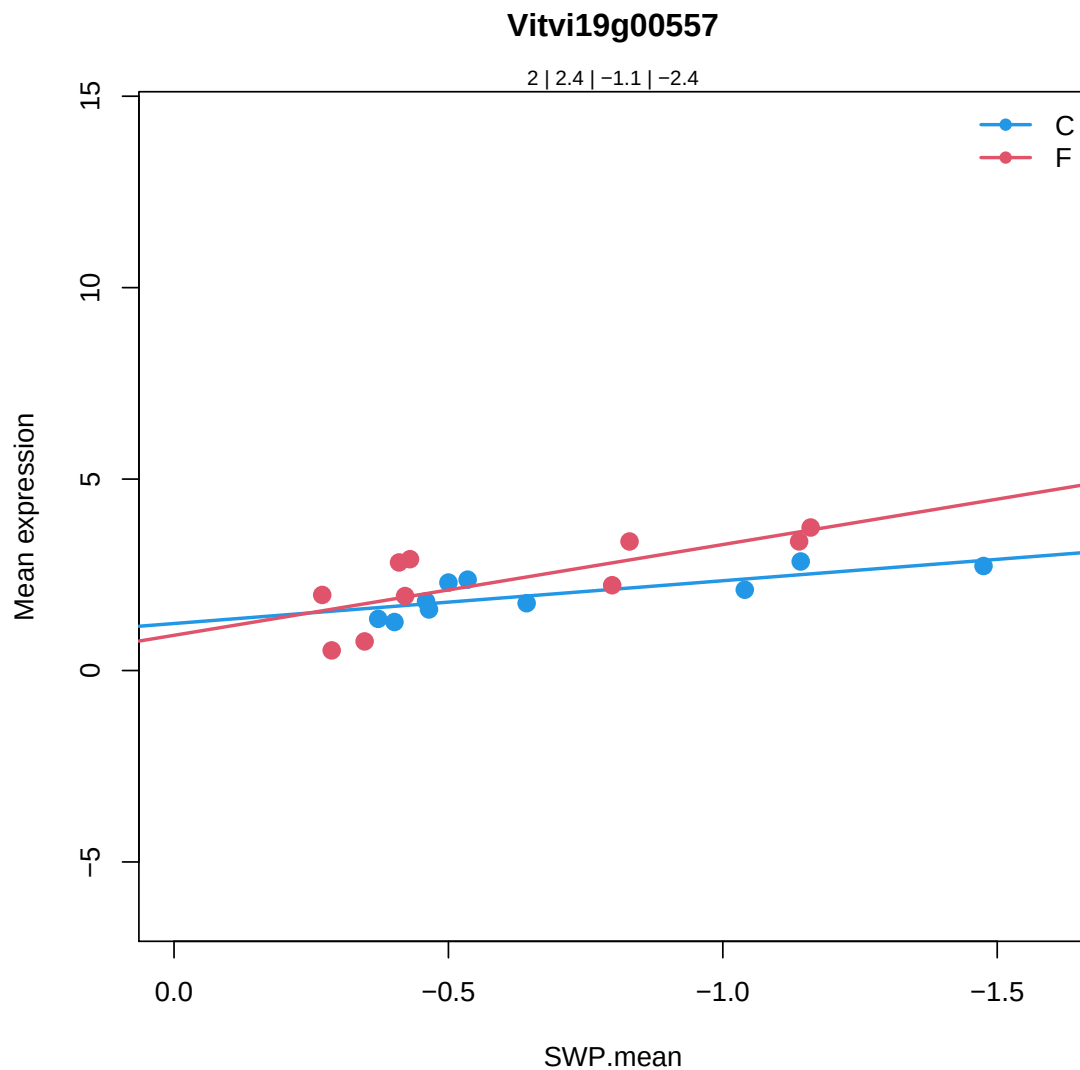
O-Glycosyl hydrolases family 17 protein |

Chr5:22388834-22390561 FORWARD LENGTH=465 |

201606

Coefficients for Vitvi19g00557.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.013379	2.656671e-10	***	3.418571e-10	***
SlopeC	-1.117552	0.03883533	*	0.4697654	
MeanF-MeanC	0.3504861	0.1886394		0.5267939	
SlopeF-SlopeC	-1.253149	0.1118654		0.9999488	



8.1.356 Vitvi15g00919: Type1.0 *

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

Vitvi15g00919

35.2

not assigned.unknown

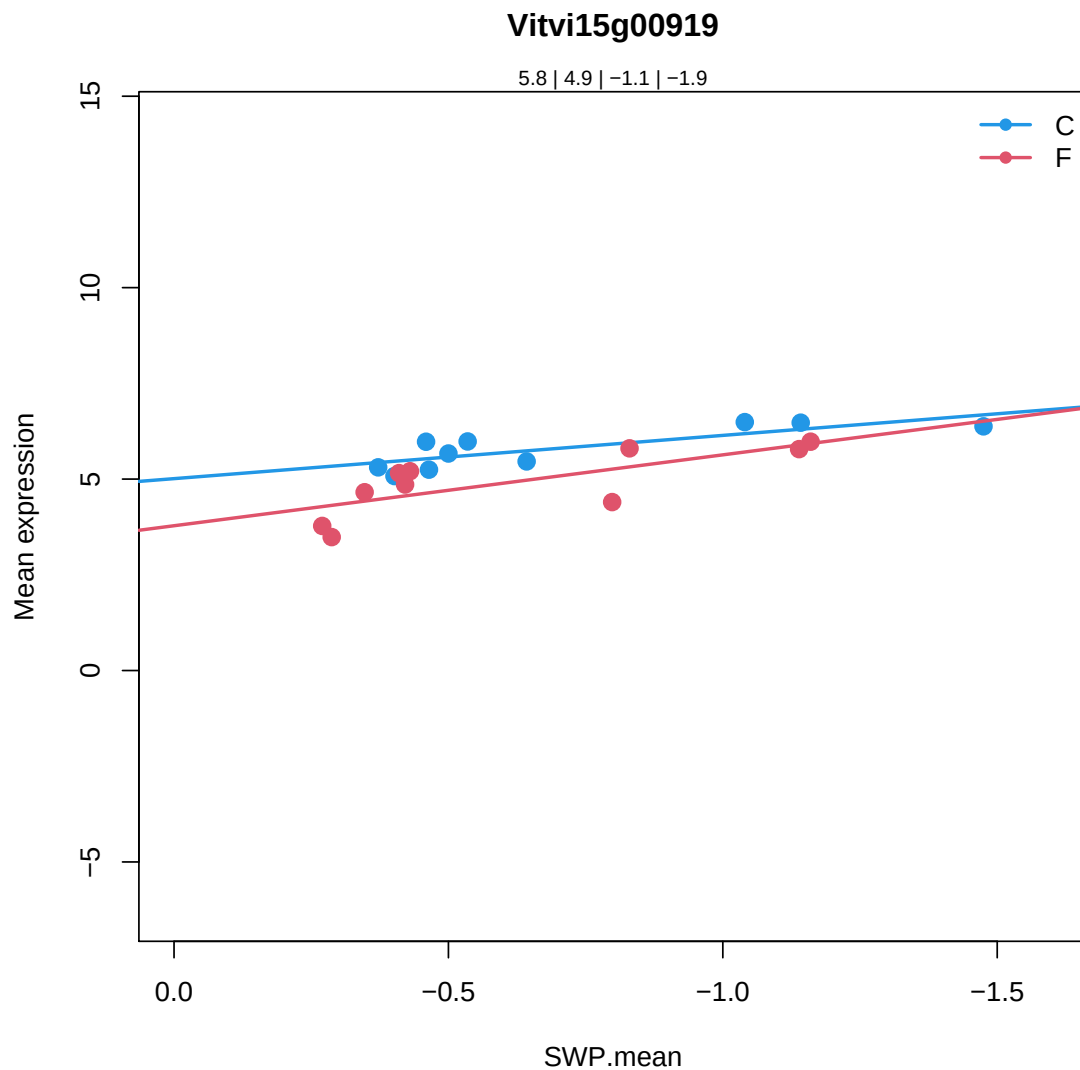
plant/protein |

Chr3:22902702-22903561 FORWARD LENGTH=254 |

201606

Coefficients for Vitvi15g00919.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.805406	3.847127e-21	***	3.303544e-20	***
SlopeC	-1.129453	0.01477732	*	0.336203	
MeanF-MeanC	-0.8959377	0.0004511165	***	0.006460007	**
SlopeF-SlopeC	-0.7219616	0.2674218		0.9999488	



8.1.357 Vitvi07g02937: Type1.0

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

Vitvi07g02937

29.5.11.4.2

protein.degradation.ubiquitin.E3.RING

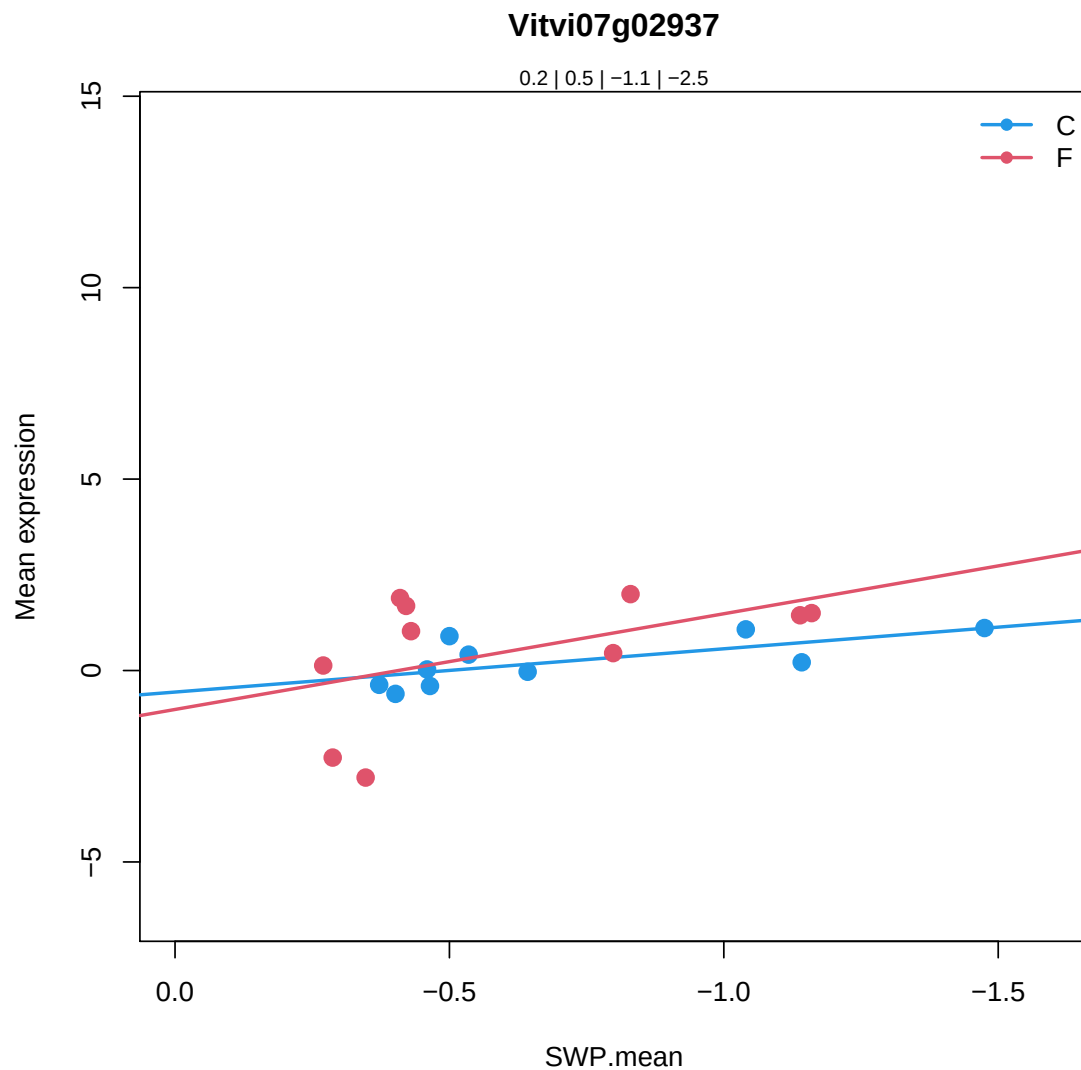
plant U-box 9 |

Chr3:2354884-2356613 FORWARD LENGTH=460 |

201606

Coefficients for Vitvi07g02937.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.2319439	0.486539		0.492746	
SlopeC	-1.130183	0.2283416		0.7477218	
MeanF-MeanC	0.2740437	0.5603413		0.8393005	
SlopeF-SlopeC	-1.369699	0.3238707		0.9999488	



8.1.358 Vitvi11g01257: Type1.0

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

Vitvi11g01257

16.2.1.3

secondary metabolism.phenylpropanoids.lignin biosynthesis.4CL

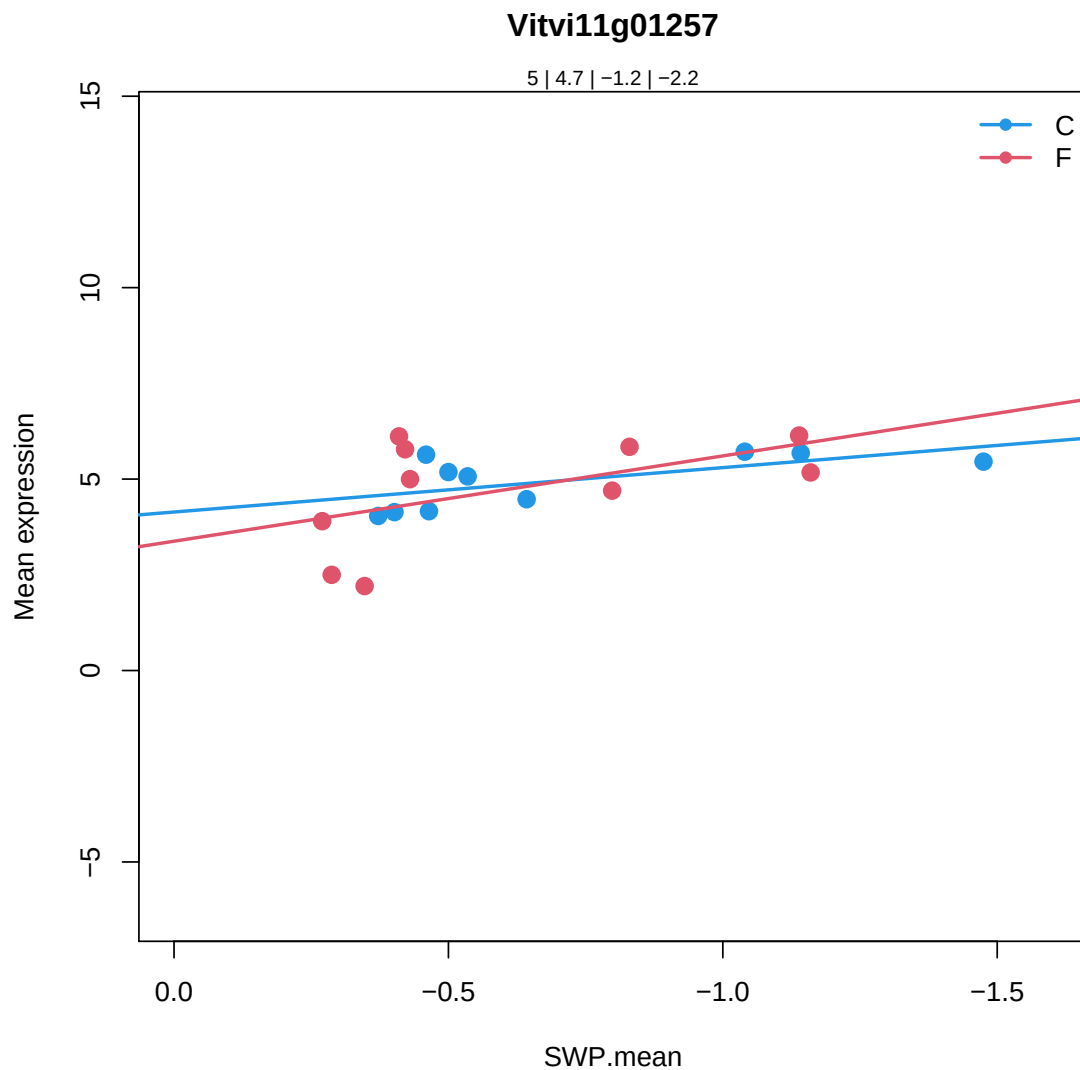
4-coumarate:CoA ligase 1 |

Chr1:19159647-19161464 REVERSE LENGTH=490 |

201606

Coefficients for Vitvi11g01257.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.954874	3.339703e-14	***	5.328562e-14	***
SlopeC	-1.15957	0.1544045		0.6857741	
MeanF-MeanC	-0.2202599	0.5868862		0.8550296	
SlopeF-SlopeC	-1.068427	0.3709254		0.9999488	



8.1.359 Vitvi04g00633: Type1.0

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

Vitvi04g00633

29.3.3

protein.targeting.chloroplast

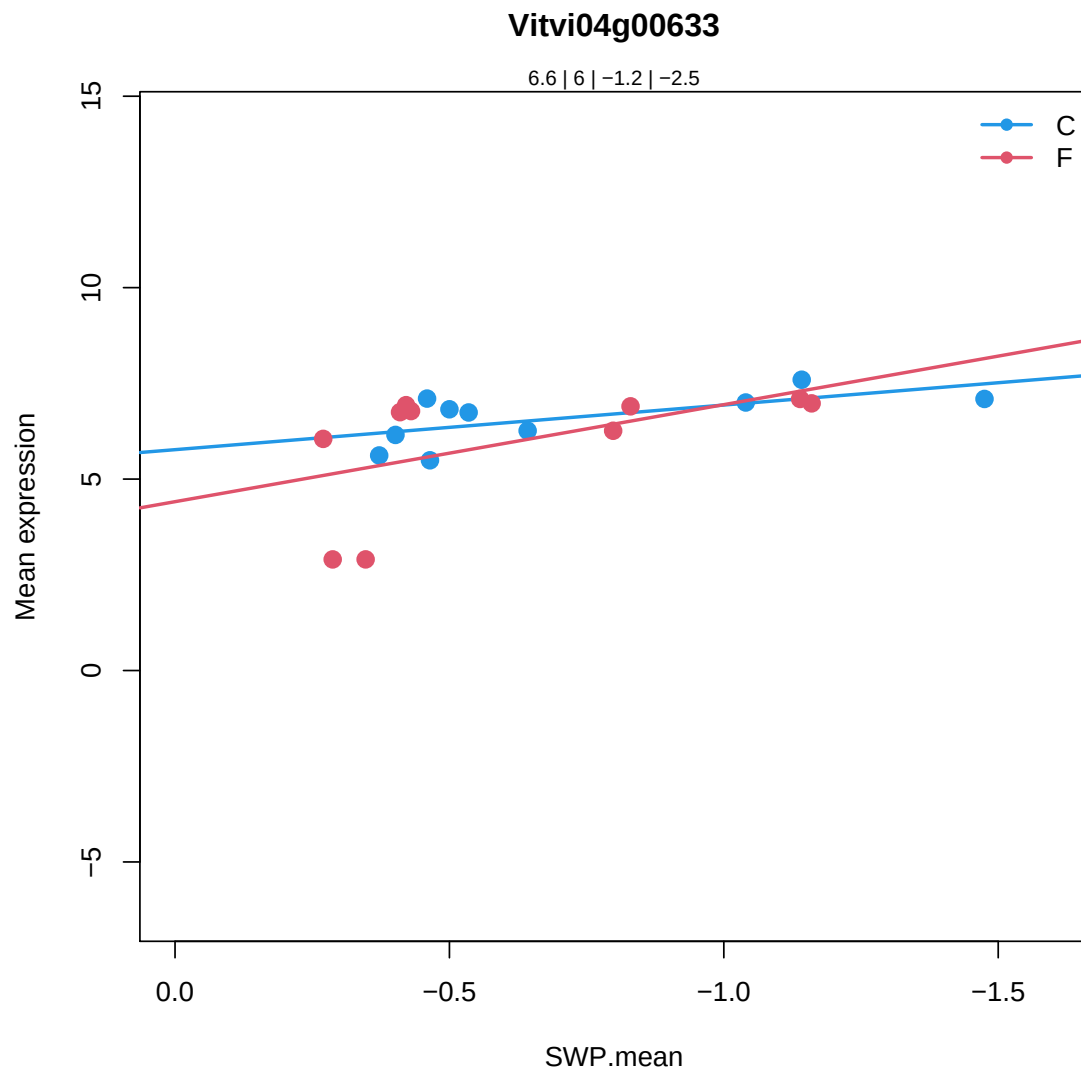
translocon at the inner envelope membrane of chloroplasts 55-II |

Chr2:10575038-10576829 FORWARD LENGTH=539 |

201606

Coefficients for Vitvi04g00633.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.587571	9.056057e-16	***	1.703894e-15	***
SlopeC	-1.165574	0.1964784		0.7250708	
MeanF-MeanC	-0.6335636	0.1683888		0.4973032	
SlopeF-SlopeC	-1.368874	0.304543		0.9999488	



8.1.360 Vitvi07g00934: Type1.0 *

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

Vitvi07g00934

35.2

not assigned.unknown

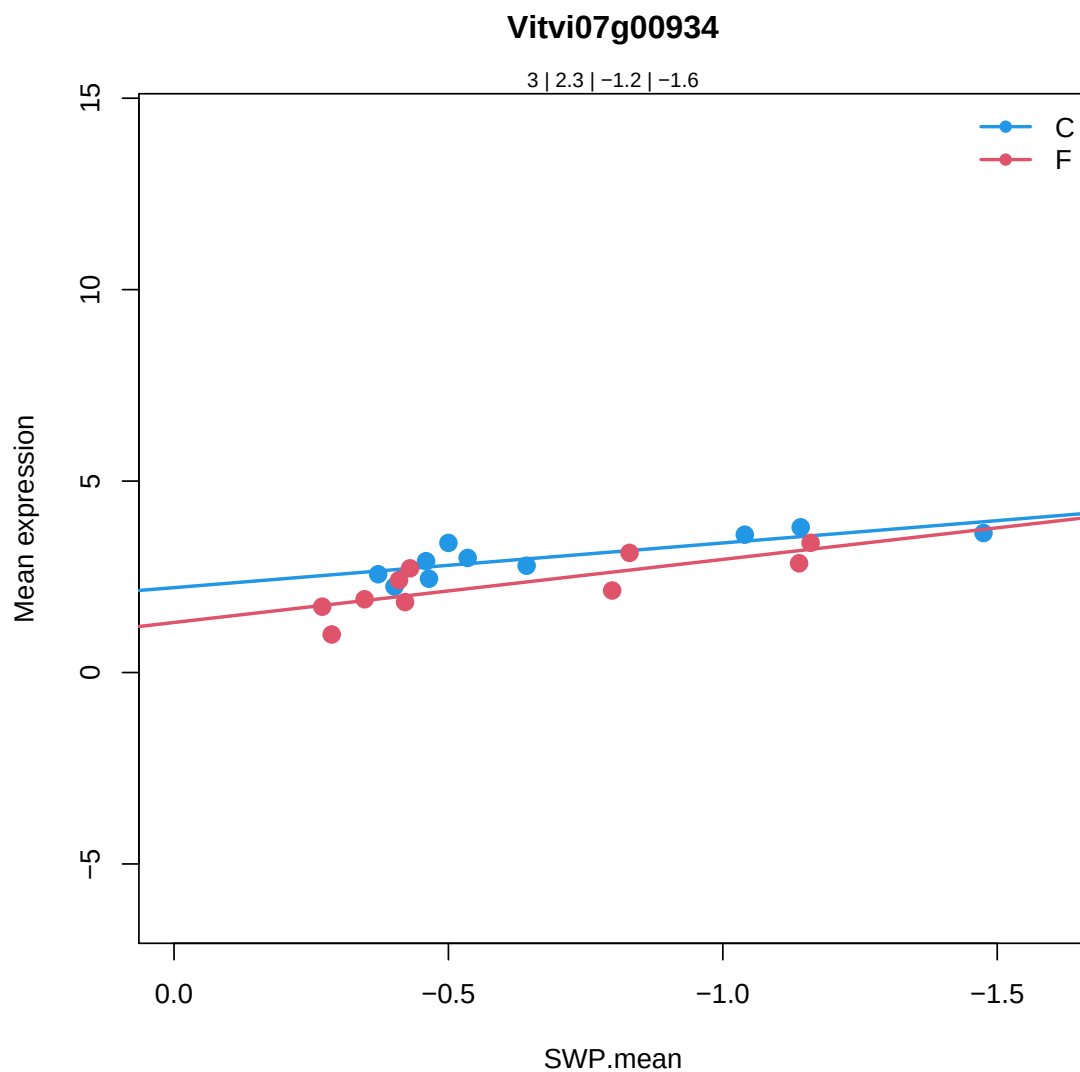
cysteine-rich RECEPTOR-like kinase |

Chr4:12129485-12133157 FORWARD LENGTH=1043 |

201606

Coefficients for Vitvi07g00934.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.037176	3.481848e-16	***	6.948197e-16	***
SlopeC	-1.16672	0.006235914	**	0.2647742	
MeanF-MeanC	-0.7264405	0.001248858	**	0.01503561	*
SlopeF-SlopeC	-0.4809399	0.4102702		0.9999488	



8.1.361 Vitvi18g00020: Type1.0

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

Vitvi18g00020

35.2

not assigned.unknown

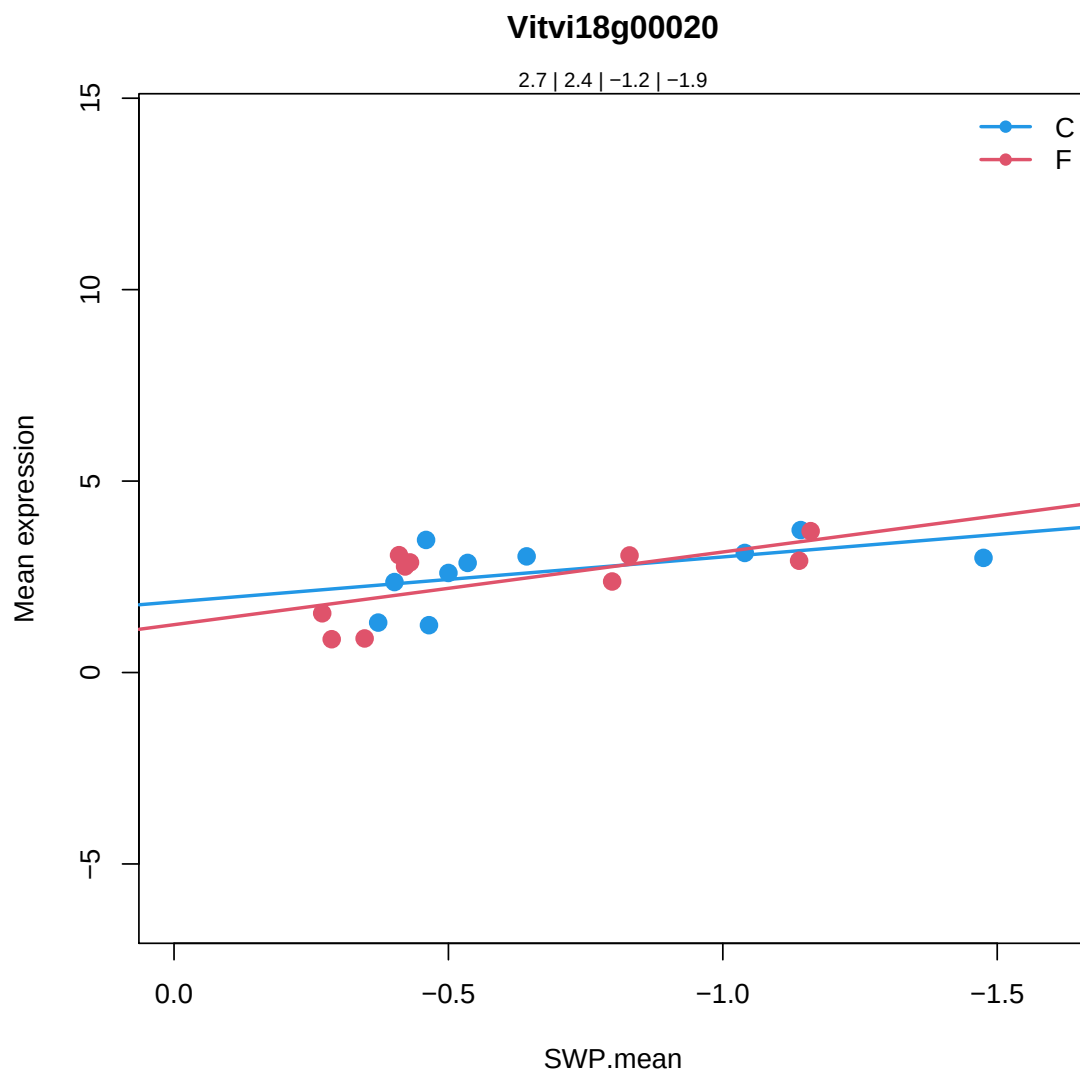
poly polymerase |

Chr1:7346239-7346871 FORWARD LENGTH=210 |

201606

Coefficients for Vitvi18g00020.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.669801	4.818591e-11	***	6.386518e-11	***
SlopeC	-1.174367	0.06936493	.	0.5582027	
MeanF-MeanC	-0.2635426	0.4079901		0.7494209	
SlopeF-SlopeC	-0.7242934	0.4369278		0.9999488	



8.1.362 Vitvi16g00034: Type1.0 *

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

Vitvi16g00034

34.99

transport.misc

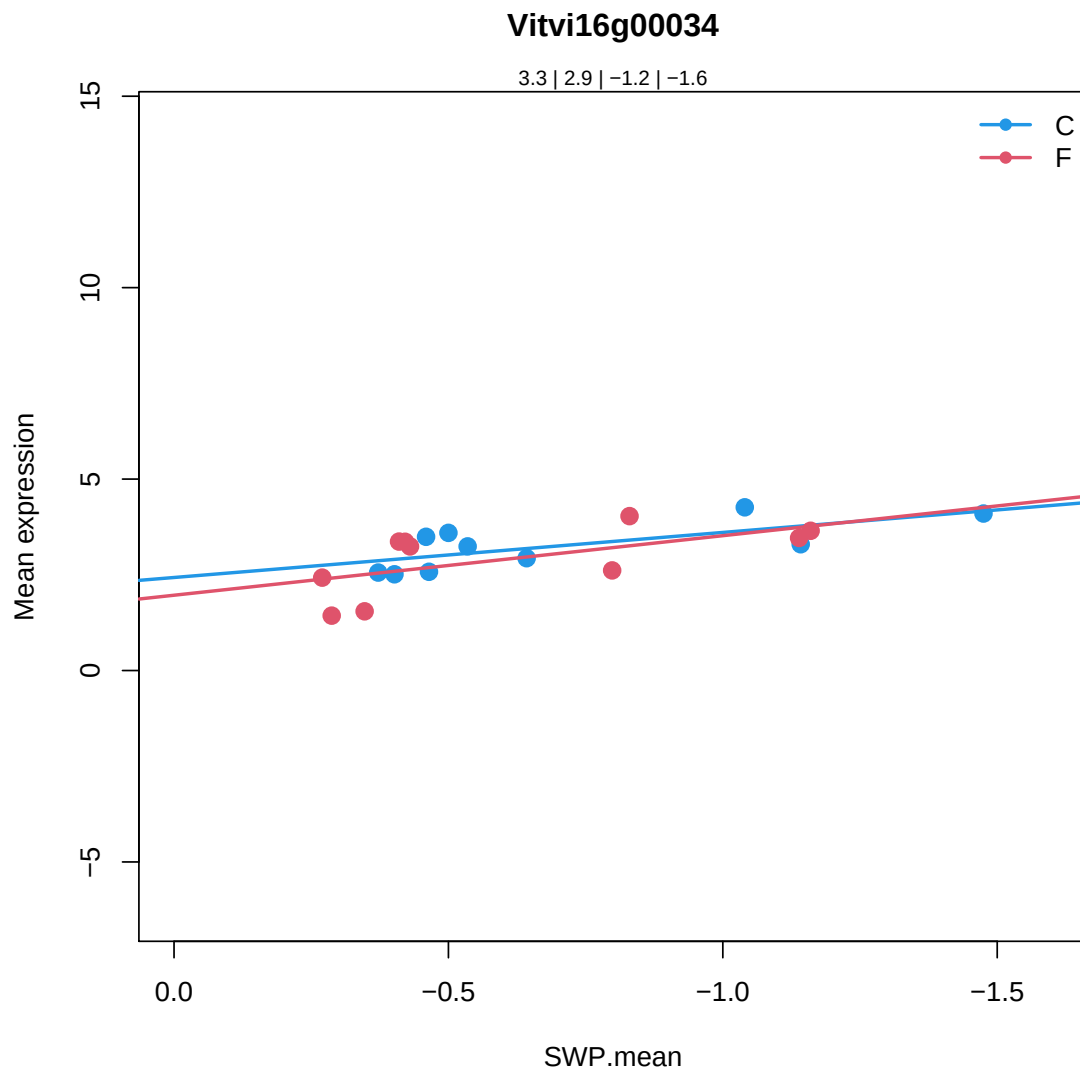
Major facilitator superfamily protein |

Chr1:24109752-24111165 FORWARD LENGTH=442 |

201606

Coefficients for Vitvi16g00034.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.25725	3.617753e-14	***	5.75713e-14	***
SlopeC	-1.176826	0.03362483	*	0.4433084	
MeanF-MeanC	-0.3437019	0.2059661		0.550148	
SlopeF-SlopeC	-0.3782124	0.6289896		0.9999488	



8.1.363 Vitvi13g00432: Type1.0

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

Vitvi13g00432

26.2

misc.UDP glucosyl and glucoronyl transferases

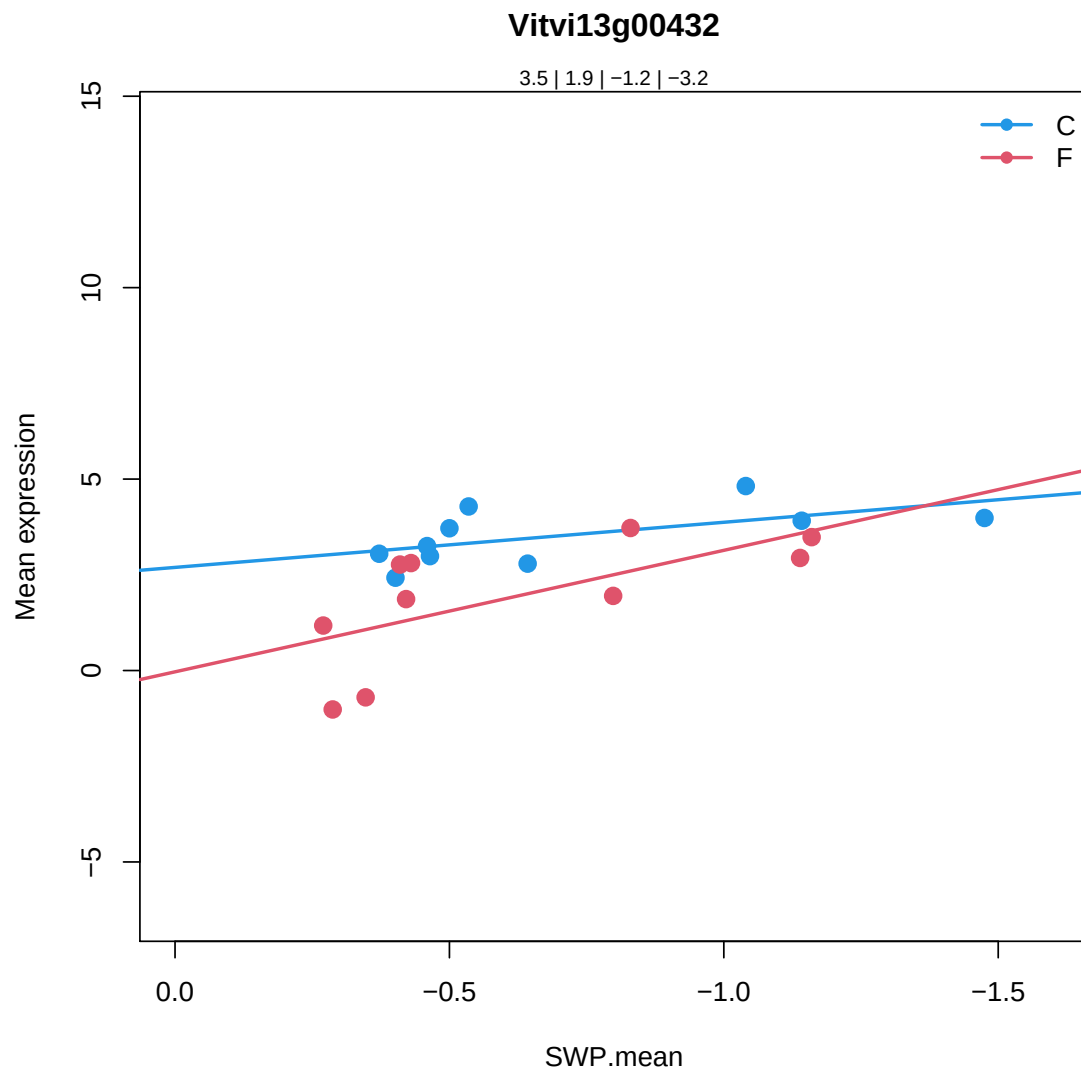
UDP-Glycosyltransferase superfamily protein |

Chr1:7903851-7906607 REVERSE LENGTH=489 |

201606

Coefficients for Vitvi13g00432.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.521617	4.572677e-11	***	6.065861e-11	***
SlopeC	-1.178642	0.1591532		0.6889929	
MeanF-MeanC	-1.622561	0.0007081716	***	0.009384875	**
SlopeF-SlopeC	-1.994139	0.111853		0.9999488	



8.1.364 Vitvi18g03266: Type1.0

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

Vitvi18g03266

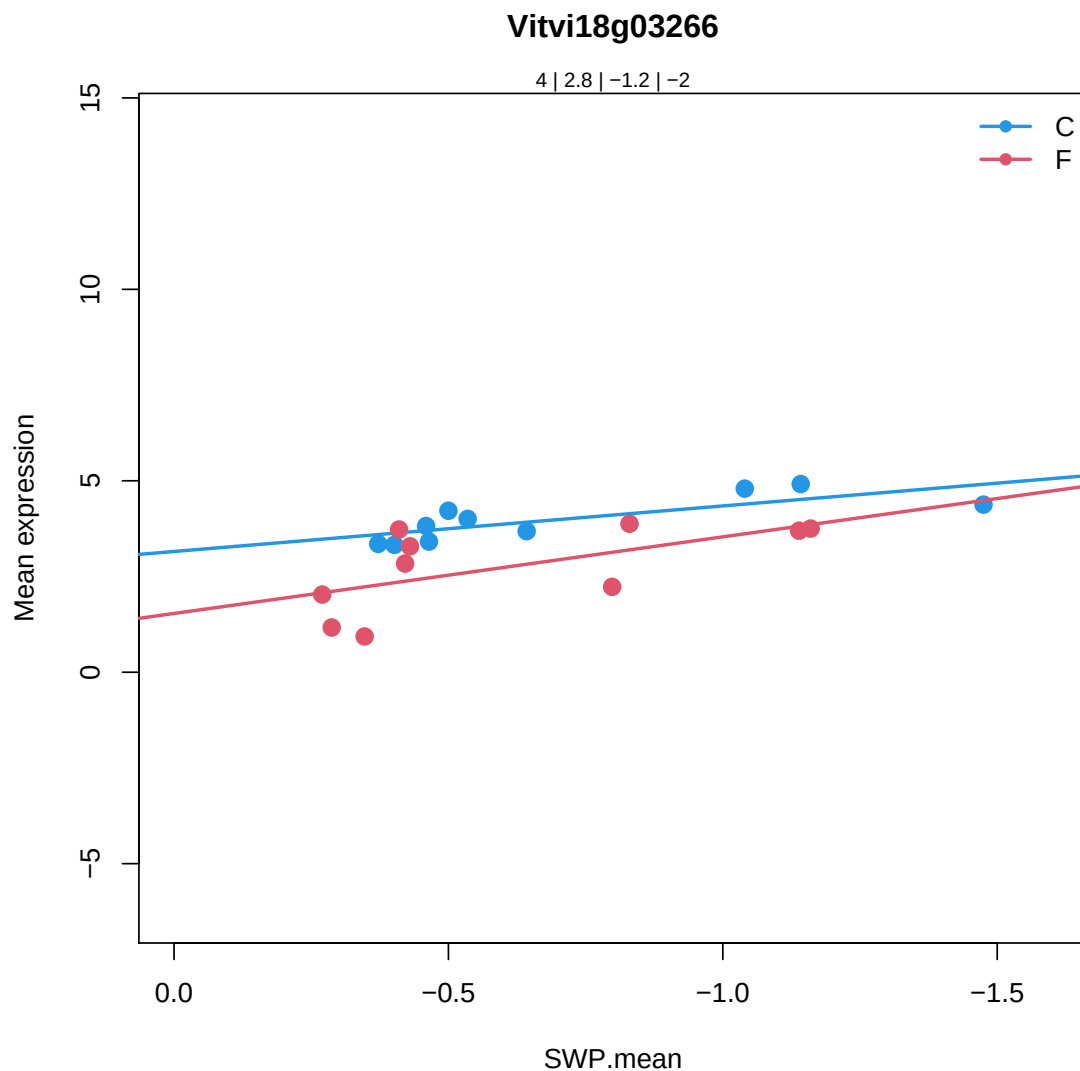
35.2

not assigned.unknown

F-box protein-like IPR001810 Cyclin-like F-box

Coefficients for Vitvi18g03266.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.990282	5.38599e-15	***	9.282368e-15	***
SlopeC	-1.189767	0.05188903	.	0.5134996	
MeanF-MeanC	-1.236333	0.0003800958	***	0.005596572	**
SlopeF-SlopeC	-0.8106258	0.3565088		0.9999488	



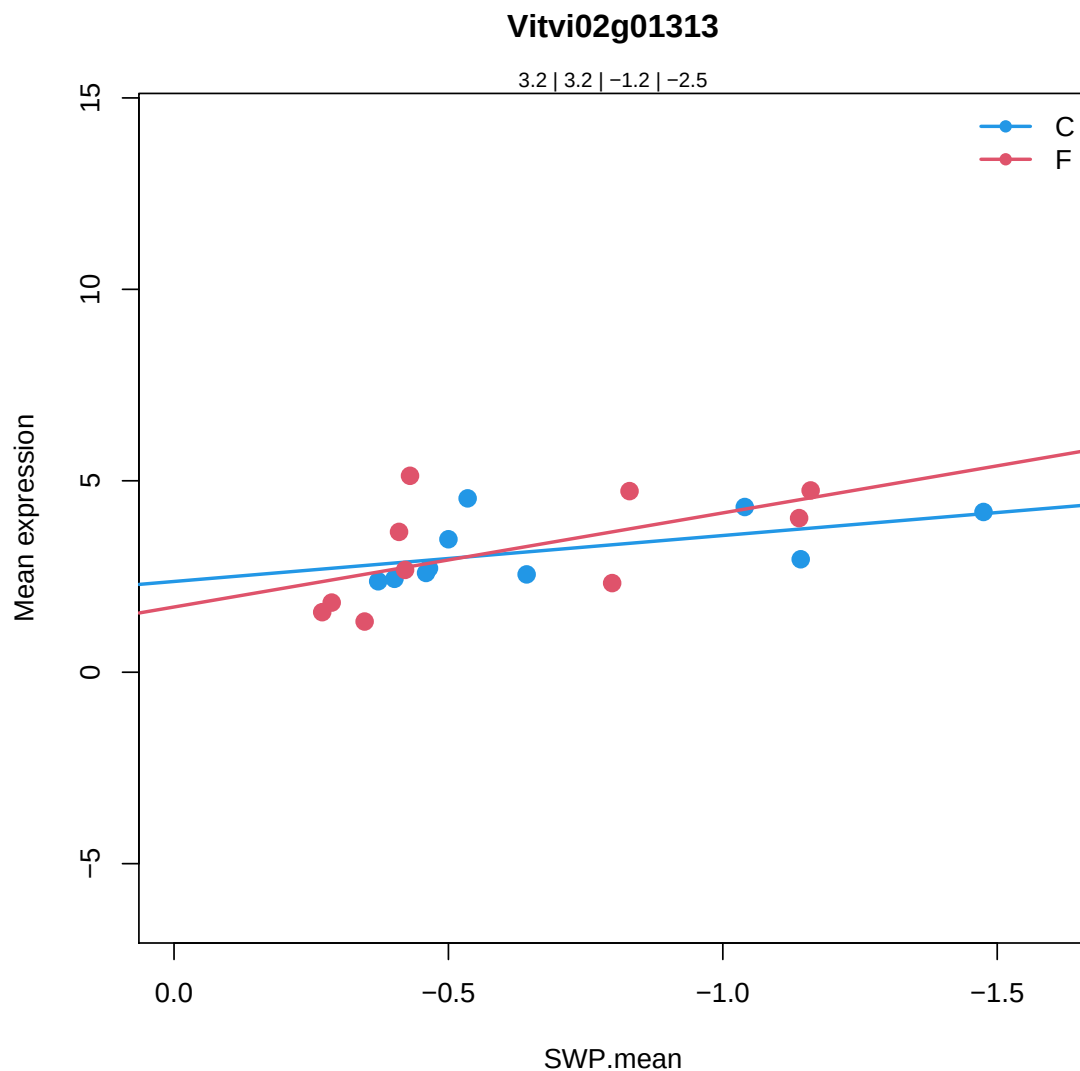
8.1.365 Vitvi02g01313: Type1.0

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

```
Vitvi02g01313
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi02g01313.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.214156	2.319783e-10	***	2.992142e-10	***
SlopeC	-1.200346	0.1503489		0.6773924	
MeanF-MeanC	-0.01323087	0.9744953		0.9940651	
SlopeF-SlopeC	-1.257262	0.3055236		0.9999488	



8.1.366 Vitvi00g01018: Type1.0 *

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

Vitvi00g01018

26.3.5

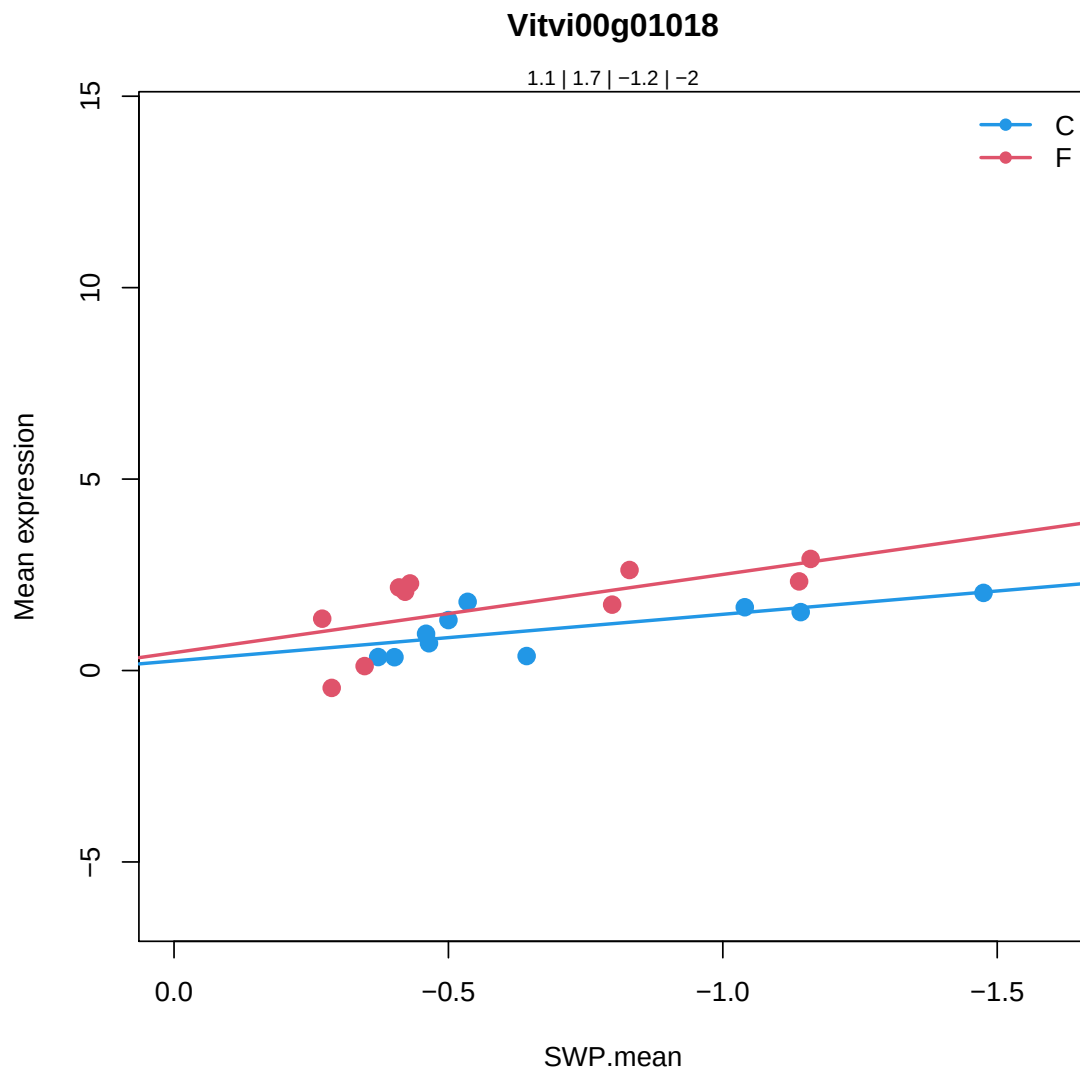
misc.gluco-, galacto- and mannosidases.glycosyl hydrolase family 5
alpha/beta-Hydrolases superfamily protein |

Chr5:2932162-2933362 FORWARD LENGTH=311 |

201606

Coefficients for Vitvi00g01018.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.106446	2.729344e-05	***	3.049455e-05	***
SlopeC	-1.217557	0.04783441	*	0.5004518	
MeanF-MeanC	0.6039517	0.0529819	.	0.248477	
SlopeF-SlopeC	-0.8252452	0.349816		0.9999488	



8.1.367 Vitvi12g02659: Type1.0

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

Vitvi12g02659

33.1

development.storage proteins

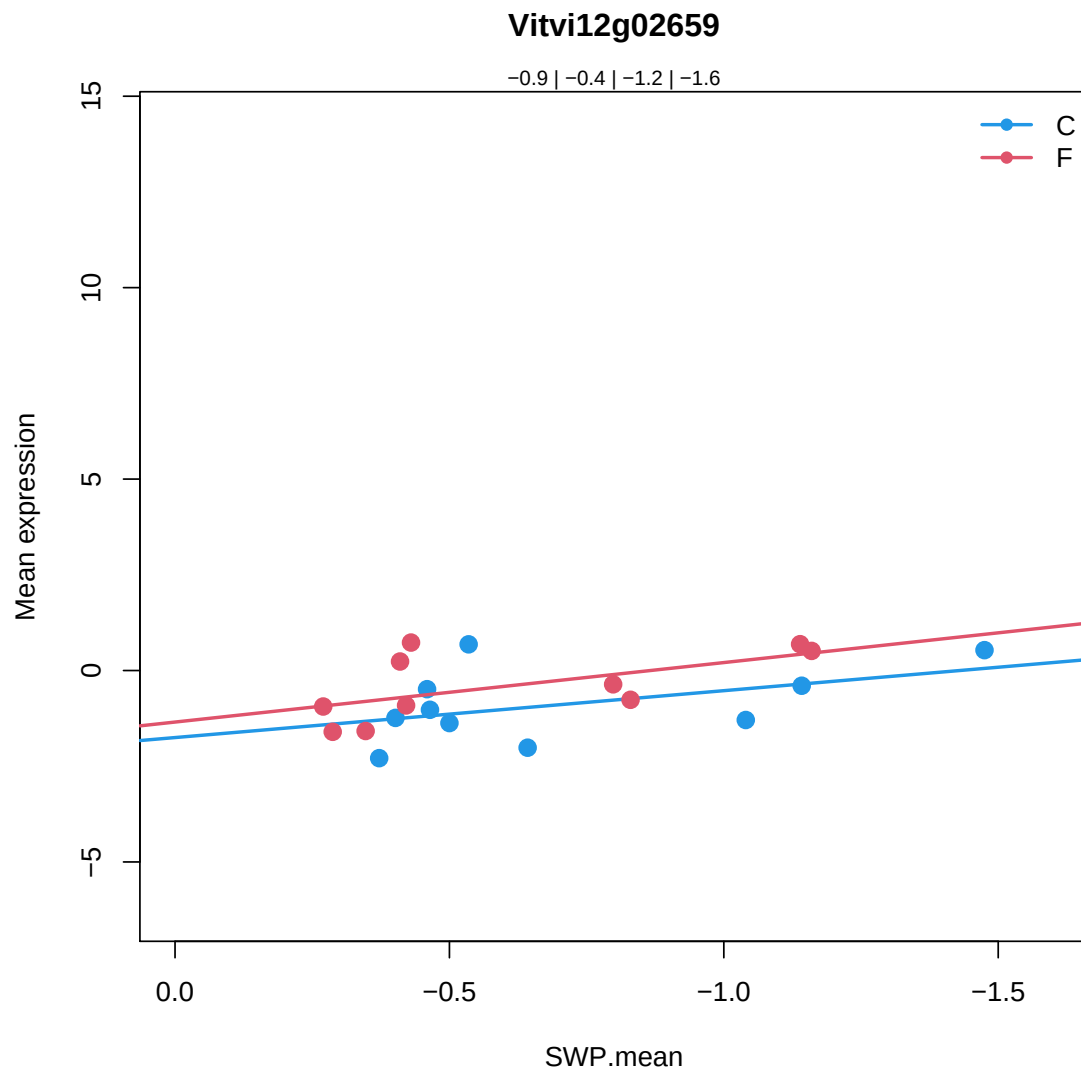
RmlC-like cupins superfamily protein |

Chr1:2404300-2405863 REVERSE LENGTH=356 |

201606

Coefficients for Vitvi12g02659.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.8903097	0.001420755	**	0.001534085	**
SlopeC	-1.224612	0.08438042	.	0.5848879	
MeanF-MeanC	0.4908415	0.167988		0.4965043	
SlopeF-SlopeC	-0.3289884	0.7471009		0.9999488	



8.1.368 Vitvi12g00429: Type1.0

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

Vitvi12g00429

10.6.1

cell wall.degradation.cellulases and beta-1,4-glucanases

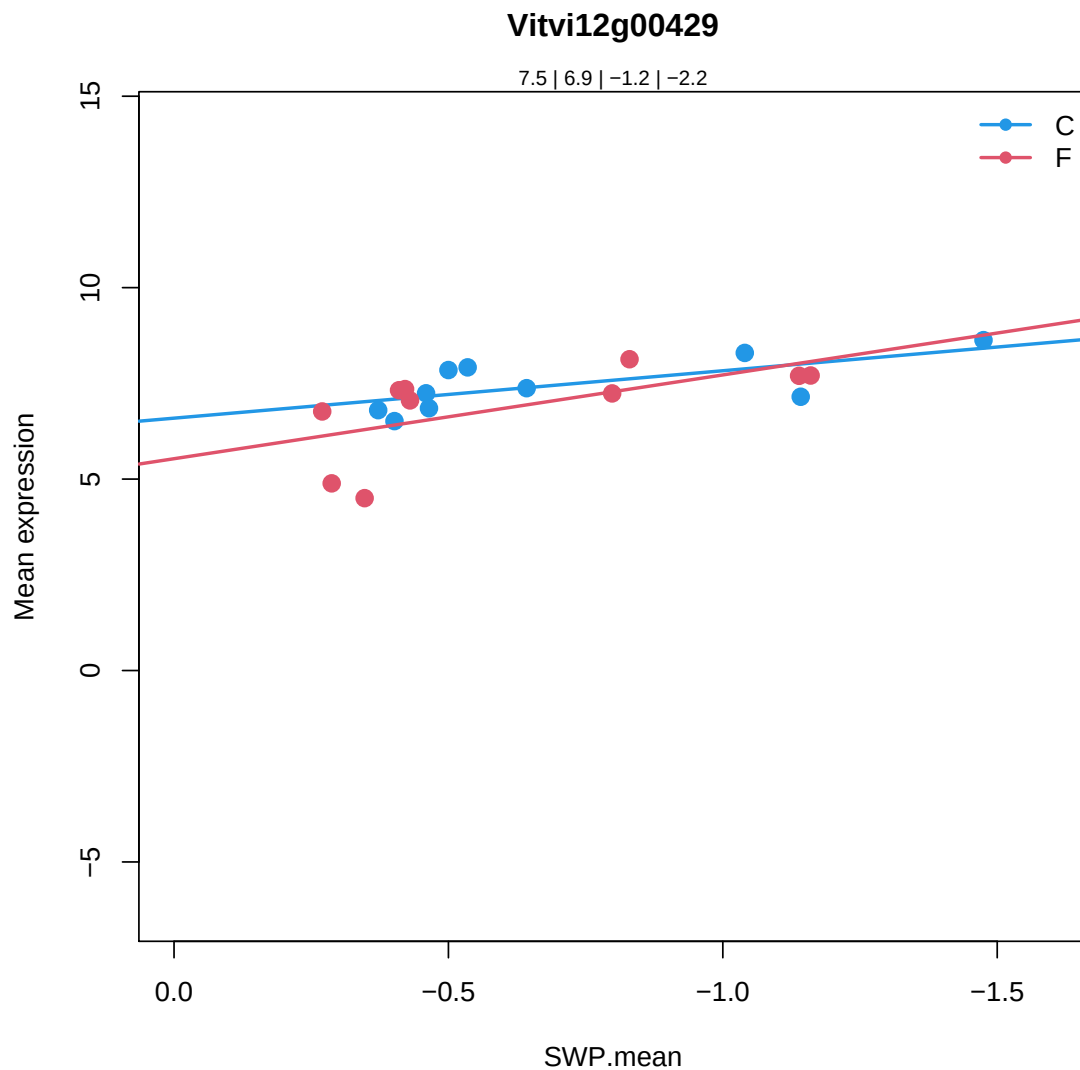
Major facilitator superfamily protein |

Chr3:7626942-7628954 REVERSE LENGTH=590 |

201606

Coefficients for Vitvi12g00429.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.461776	1.337e-19	***	6.094066e-19	***
SlopeC	-1.238376	0.06942117	.	0.5582027	
MeanF-MeanC	-0.5967013	0.08405269	.	0.328411	
SlopeF-SlopeC	-0.9499196	0.3355858		0.9999488	



8.1.369 Vitvi11g00270: Type1.0

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

```
Vitvi11g00270
```

```
17.1.2
```

```
hormone metabolism.abscisic acid.signal transduction
```

```
HYPERSENSITIVE TO ABA1 |
```

```
Chr1:27390998-27392851 FORWARD LENGTH=511 |
```

```
201606
```

```
Vitvi11g00270
```

```
29.4
```

```
protein.postranslational modification
```

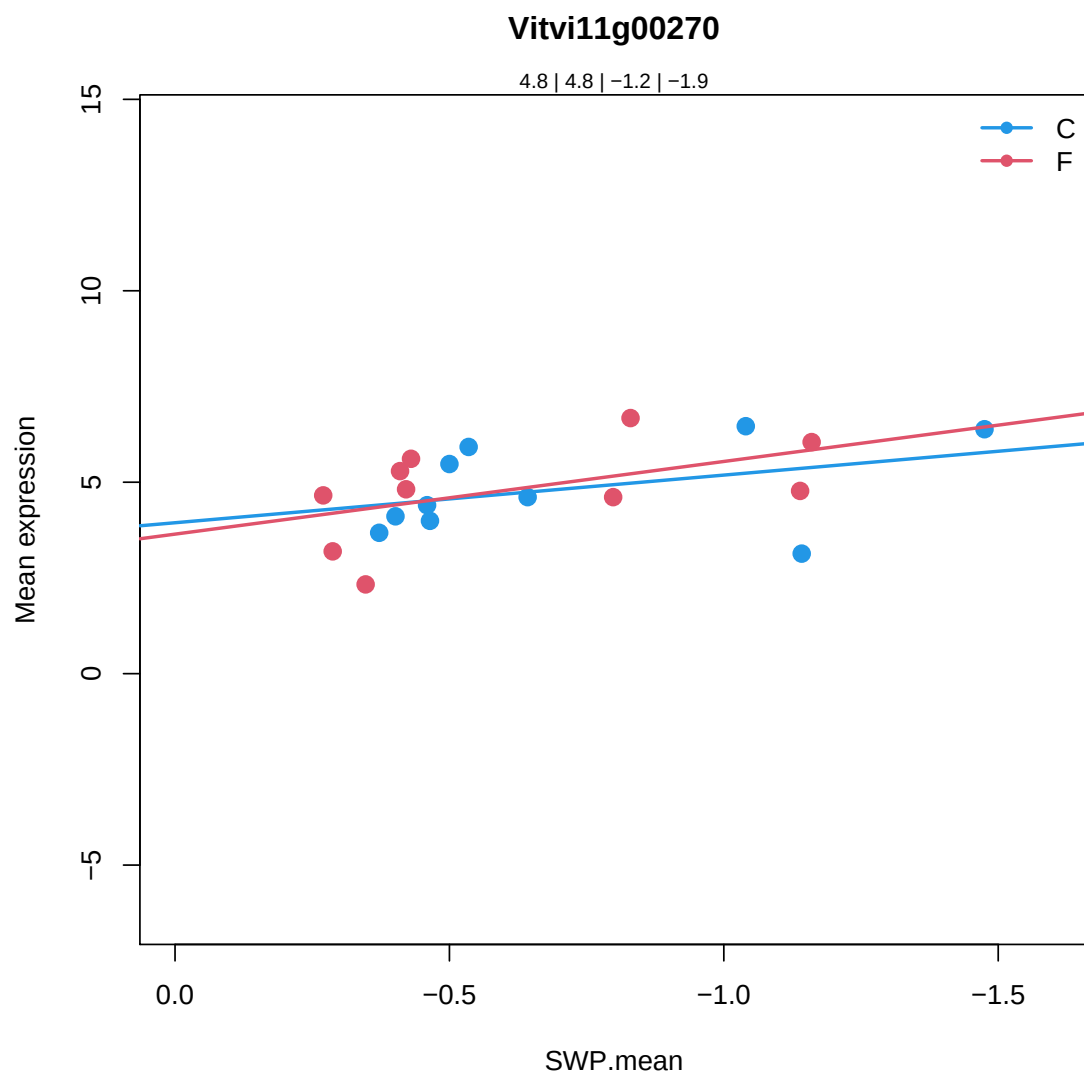
```
HYPERSENSITIVE TO ABA1 |
```

```
Chr1:27390998-27392851 FORWARD LENGTH=511 |
```

```
201606
```

Coefficients for Vitvi11g00270.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.816594	9.097417e-13	***	1.308757e-12	***
SlopeC	-1.244644	0.1816861		0.7135484	
MeanF-MeanC	-0.01636376	0.9718494		0.9934113	
SlopeF-SlopeC	-0.6533269	0.6313176		0.9999488	



8.1.370 Vitvi12g01878: Type1.0

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

Vitvi12g01878

35.2

not assigned.unknown

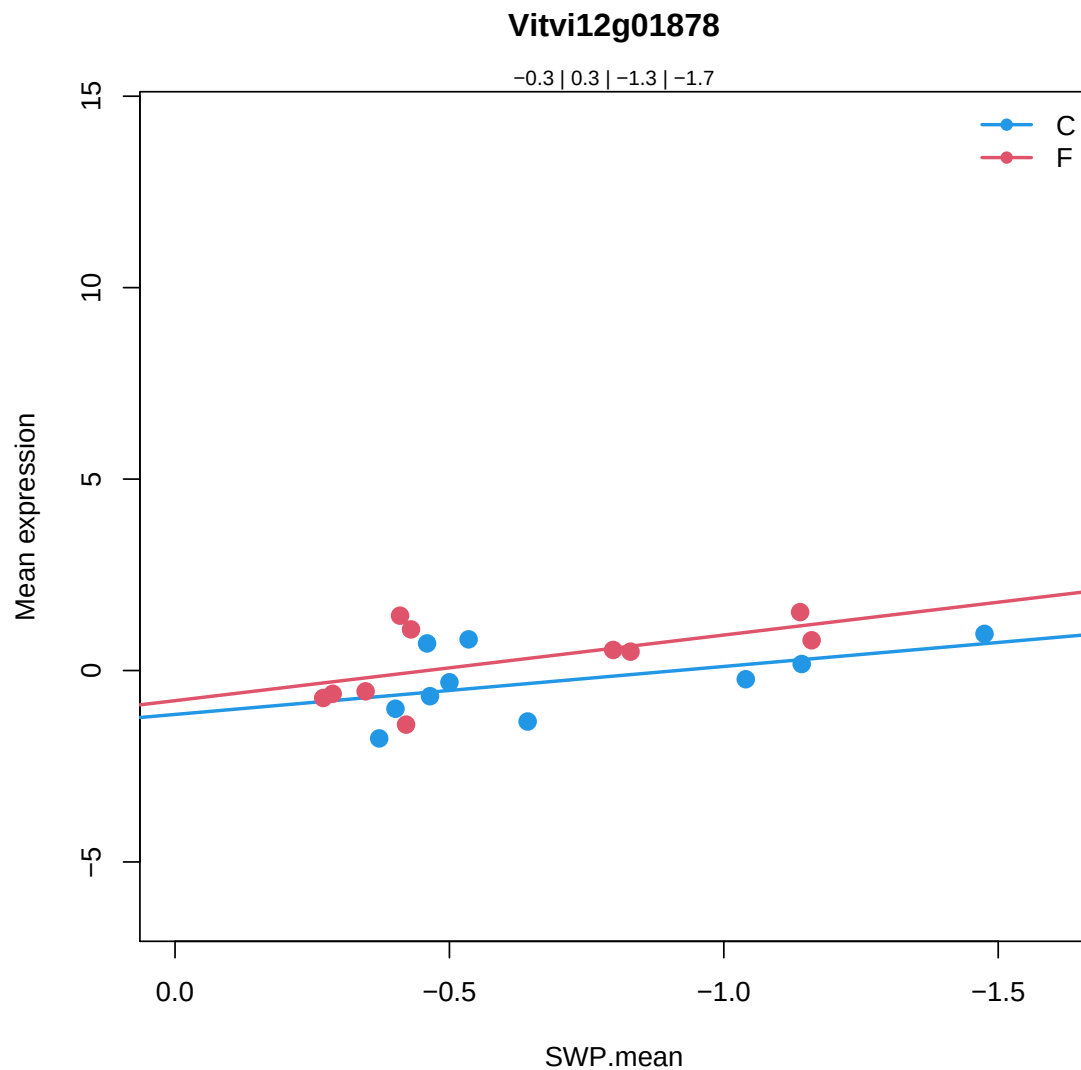
RmlC-like cupins superfamily protein |

Chr1:2404300-2405863 REVERSE LENGTH=356 |

201606

Coefficients for Vitvi12g01878.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.2661147	0.2965848		0.3022967	
SlopeC	-1.253066	0.08422197	.	0.5843019	
MeanF-MeanC	0.5229317	0.1516884		0.469258	
SlopeF-SlopeC	-0.4615107	0.6585985		0.9999488	



8.1.371 Vitvi03g01727: Type1.0 *

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

Vitvi03g01727

17.1.3

hormone metabolism.abscisic acid.induced-regulated-responsive-activate

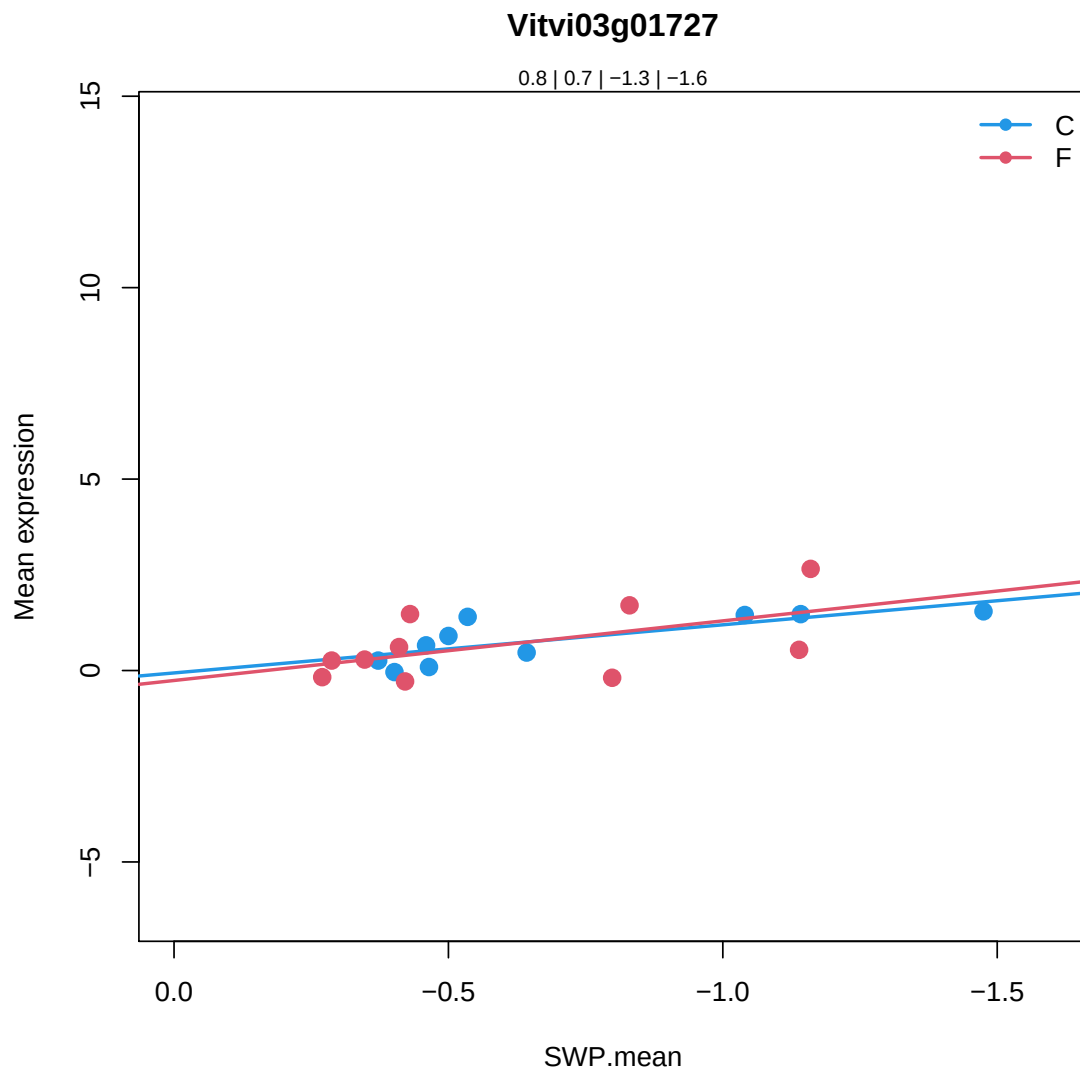
HVA22 homologue A |

Chr1:28008109-28009156 REVERSE LENGTH=177 |

201606

Coefficients for Vitvi03g01727.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8209294	0.0004568991	***	0.0004980017	***
SlopeC	-1.256935	0.03334747	*	0.4433084	
MeanF-MeanC	-0.1327742	0.6413008		0.8777751	
SlopeF-SlopeC	-0.3002579	0.7187048		0.9999488	



8.1.372 Vitvi16g01099: Type1.0

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

Vitvi16g01099

16.1.4.6

secondary metabolism.isoprenoids.carotenoids.carotenoid beta ring hydr

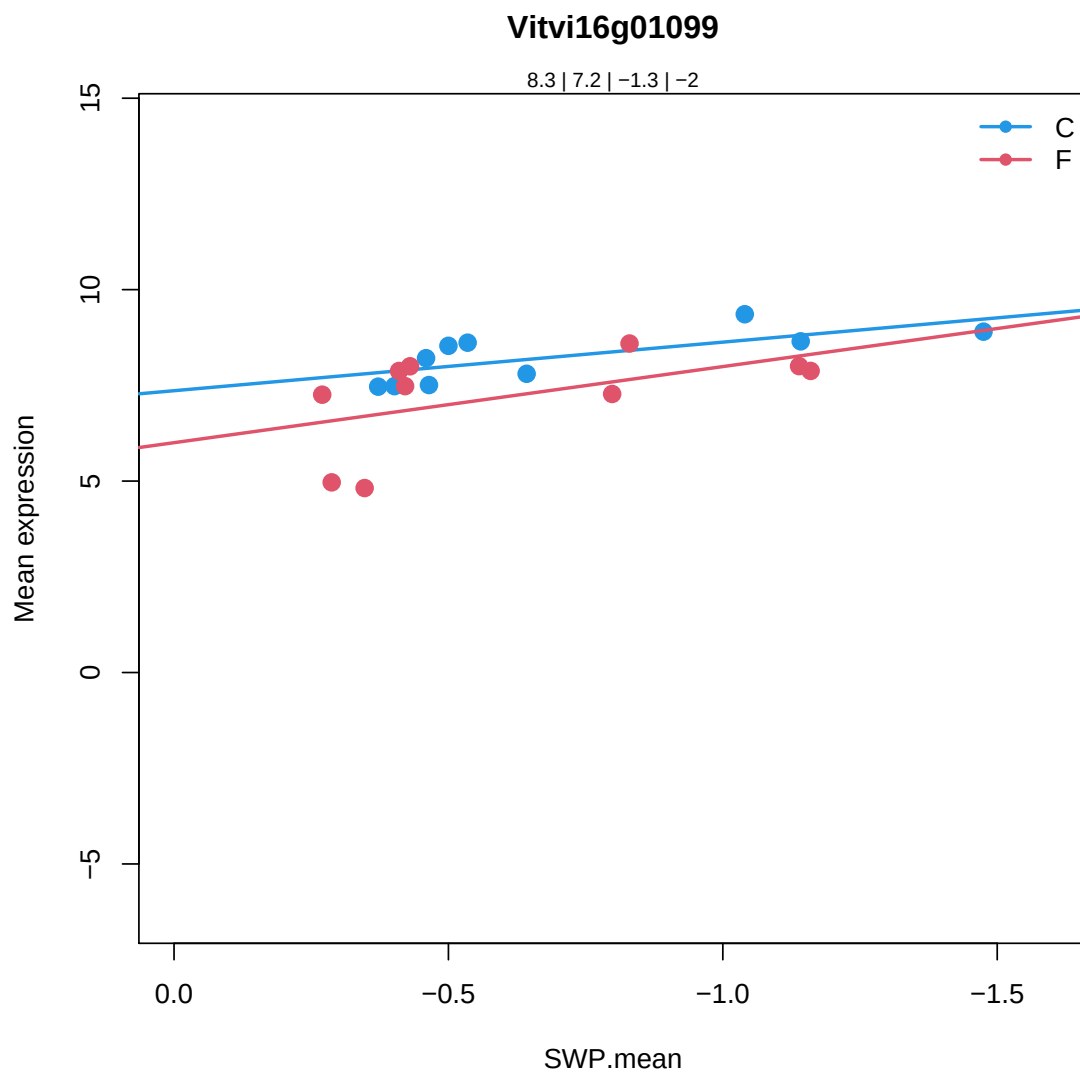
beta-carotene hydroxylase 2 |

Chr5:21334911-21336887 REVERSE LENGTH=303 |

201606

Coefficients for Vitvi16g01099.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	8.252303	1.045188e-19	***	4.952054e-19	***
SlopeC	-1.26867	0.08736169	.	0.5931255	
MeanF-MeanC	-1.03832	0.00875543	**	0.06878879	.
SlopeF-SlopeC	-0.7190535	0.5024425		0.9999488	



8.1.373 Vitvi06g01562: Type1.0

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

Vitvi06g01562

20.2.1

stress.abiotic.heat

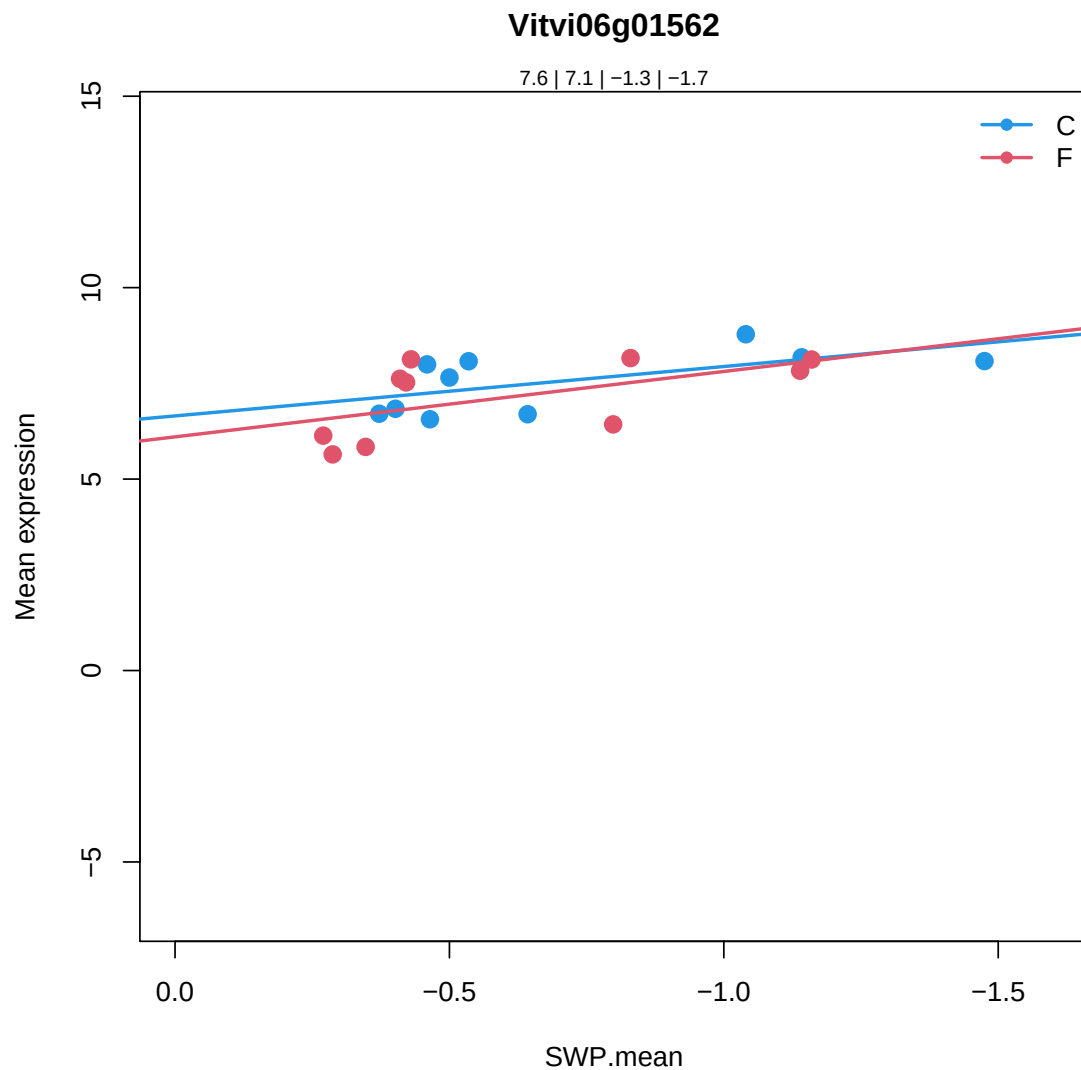
DNAJ homologue 3 |

Chr3:15869115-15871059 REVERSE LENGTH=420 |

201606

Coefficients for Vitvi06g01562.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.556709	5.440189e-20	***	2.842625e-19	***
SlopeC	-1.289769	0.05263446	.	0.5144558	
MeanF-MeanC	-0.4134006	0.2095786		0.5540716	
SlopeF-SlopeC	-0.4180297	0.6595469		0.9999488	



8.1.374 Vitvi12g01876: Type1.0

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

Vitvi12g01876

33.1

development.storage proteins

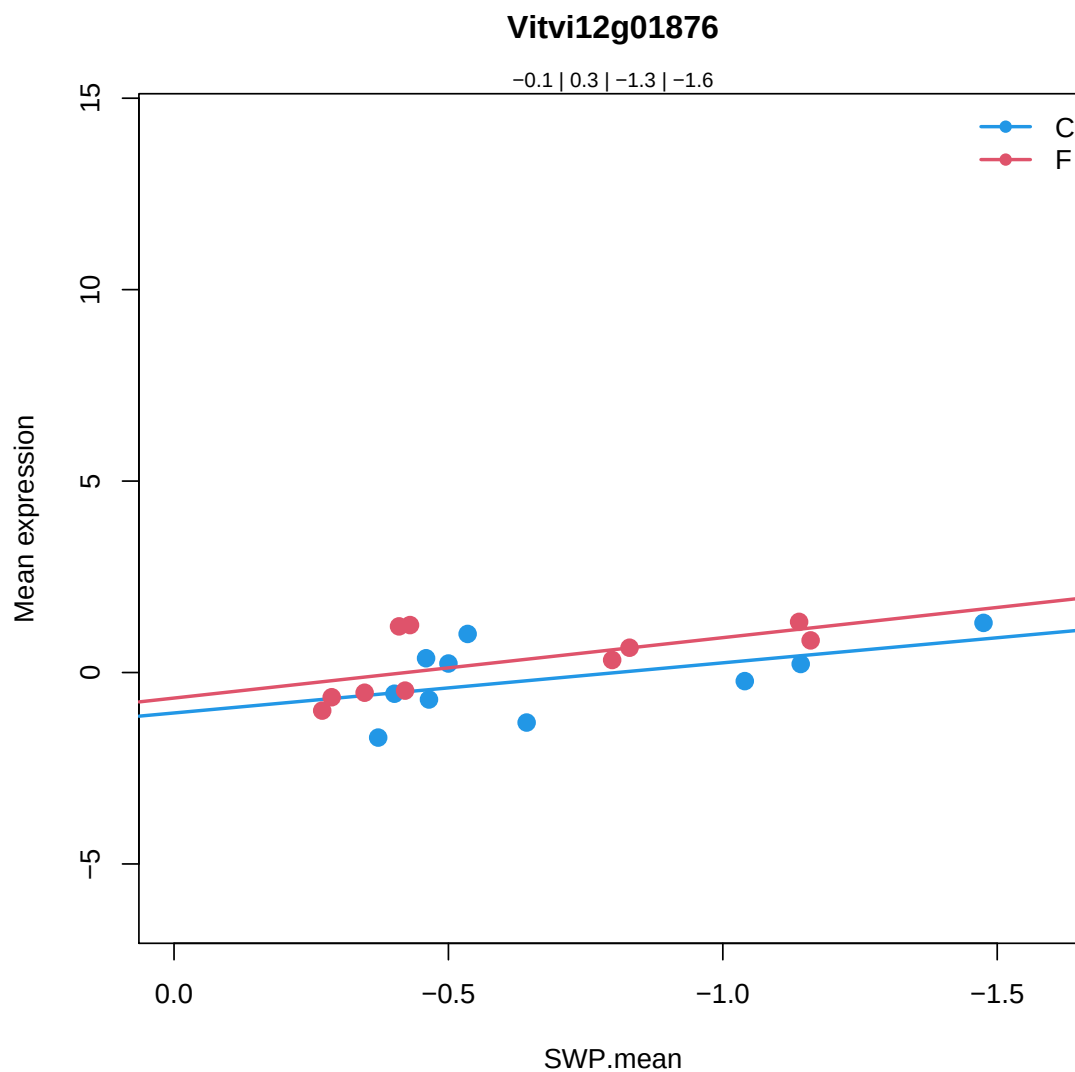
RmlC-like cupins superfamily protein |

Chr1:2404300-2405863 REVERSE LENGTH=356 |

201606

Coefficients for Vitvi12g01876.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.1356184	0.5669346		0.5727592	
SlopeC	-1.309394	0.05625572	.	0.5302719	
MeanF-MeanC	0.4295061	0.2066185		0.5512875	
SlopeF-SlopeC	-0.2685781	0.7835767		0.9999488	



8.1.375 Vitvi08g01887: Type1.0

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

Vitvi08g01887

35.2

not assigned.unknown

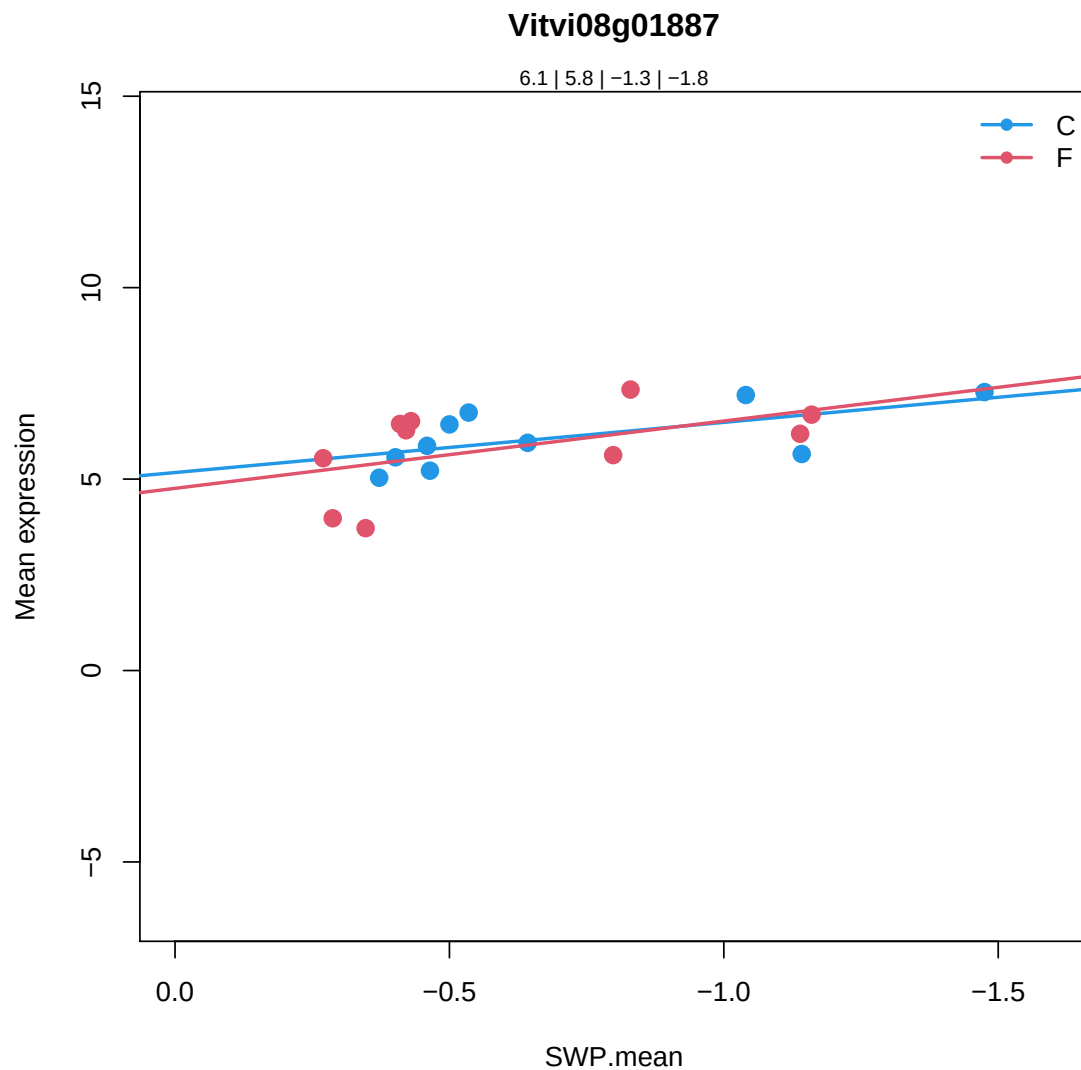
Remorin family protein |

Chr2:17471119-17472519 REVERSE LENGTH=274 |

201606

Coefficients for Vitvi08g01887.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.092284	4.484759e-17	***	1.037437e-16	***
SlopeC	-1.310628	0.07442267	.	0.5682824	
MeanF-MeanC	-0.2627953	0.4674664		0.7876703	
SlopeF-SlopeC	-0.4483446	0.6707454		0.9999488	



8.1.376 Vitvi17g00097: Type1.0

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

Vitvi17g00097

35.2

not assigned.unknown

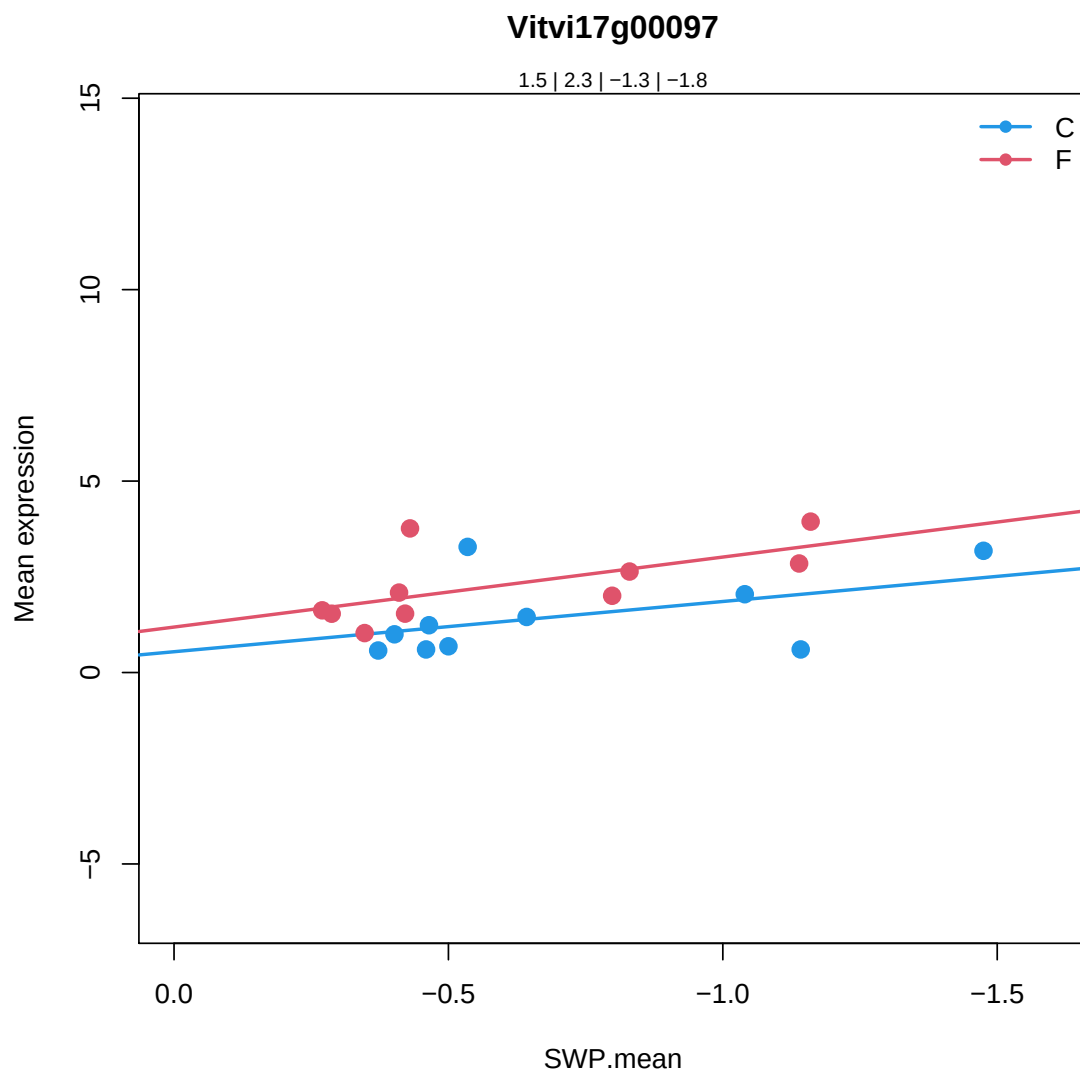
transmembrane protein%2C putative (DUF 3339) |

Chr3:18029659-18030133 FORWARD LENGTH=89 |

201606

Coefficients for Vitvi17g00097.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.465384	9.438458e-06	***	1.066506e-05	***
SlopeC	-1.311942	0.07762821	.	0.5717559	
MeanF-MeanC	0.8356345	0.03011876	*	0.1693361	
SlopeF-SlopeC	-0.5164943	0.6289334		0.9999488	



8.1.377 Vitvi14g03076: Type1.0 *

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

Vitvi14g03076

35.2

not assigned.unknown

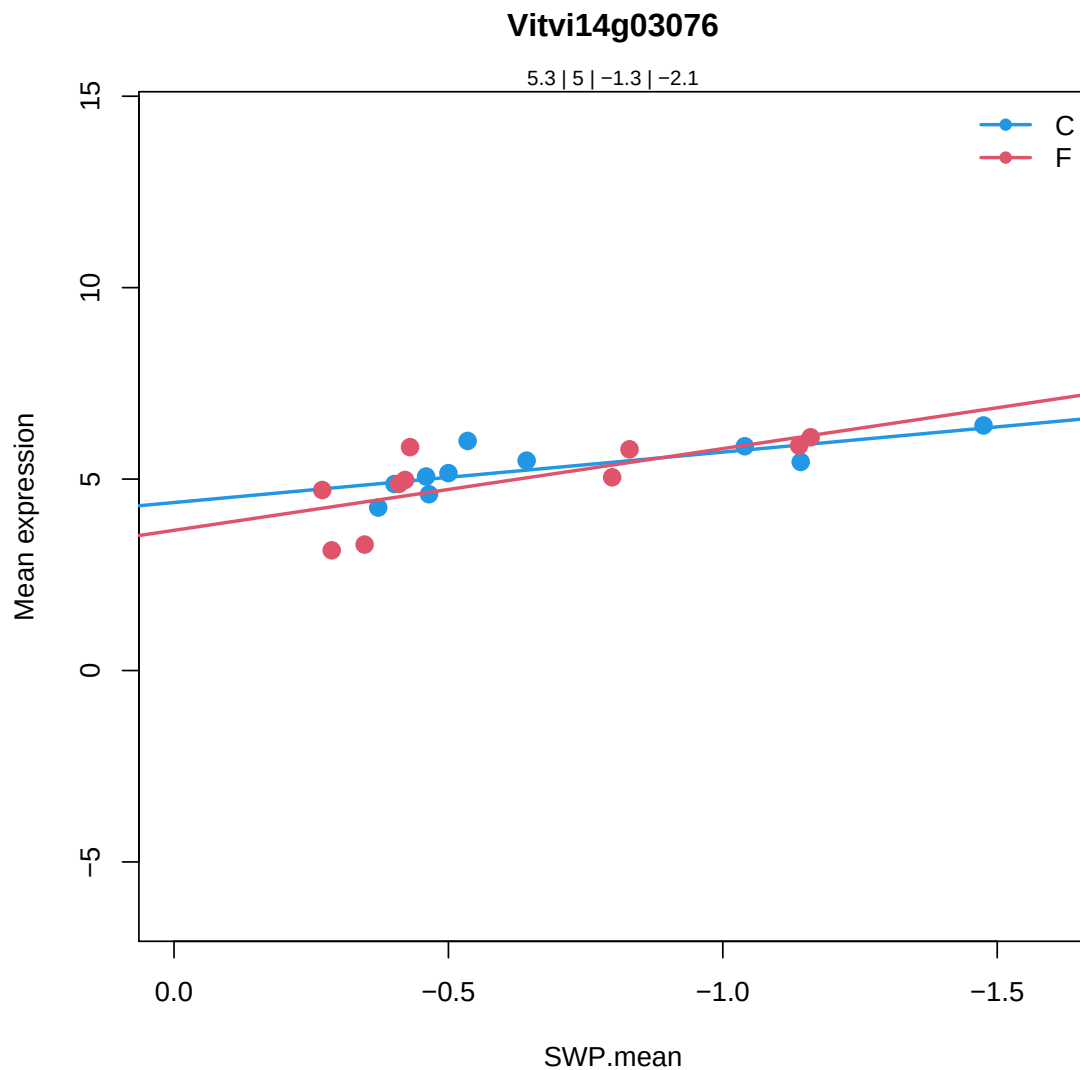
cysteine-rich RECEPTOR-like kinase |

Chr4:12129485-12133157 FORWARD LENGTH=1043 |

201606

Coefficients for Vitvi14g03076.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.313636	2.67121e-18	***	8.141288e-18	***
SlopeC	-1.317021	0.02176618	*	0.3904795	
MeanF-MeanC	-0.3515218	0.2076568		0.5524708	
SlopeF-SlopeC	-0.8171129	0.3138267		0.9999488	



8.1.378 Vitvi11g00600: Type1.0 *

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

Vitvi11g00600

29.4.1

protein.postranslational modification.kinase

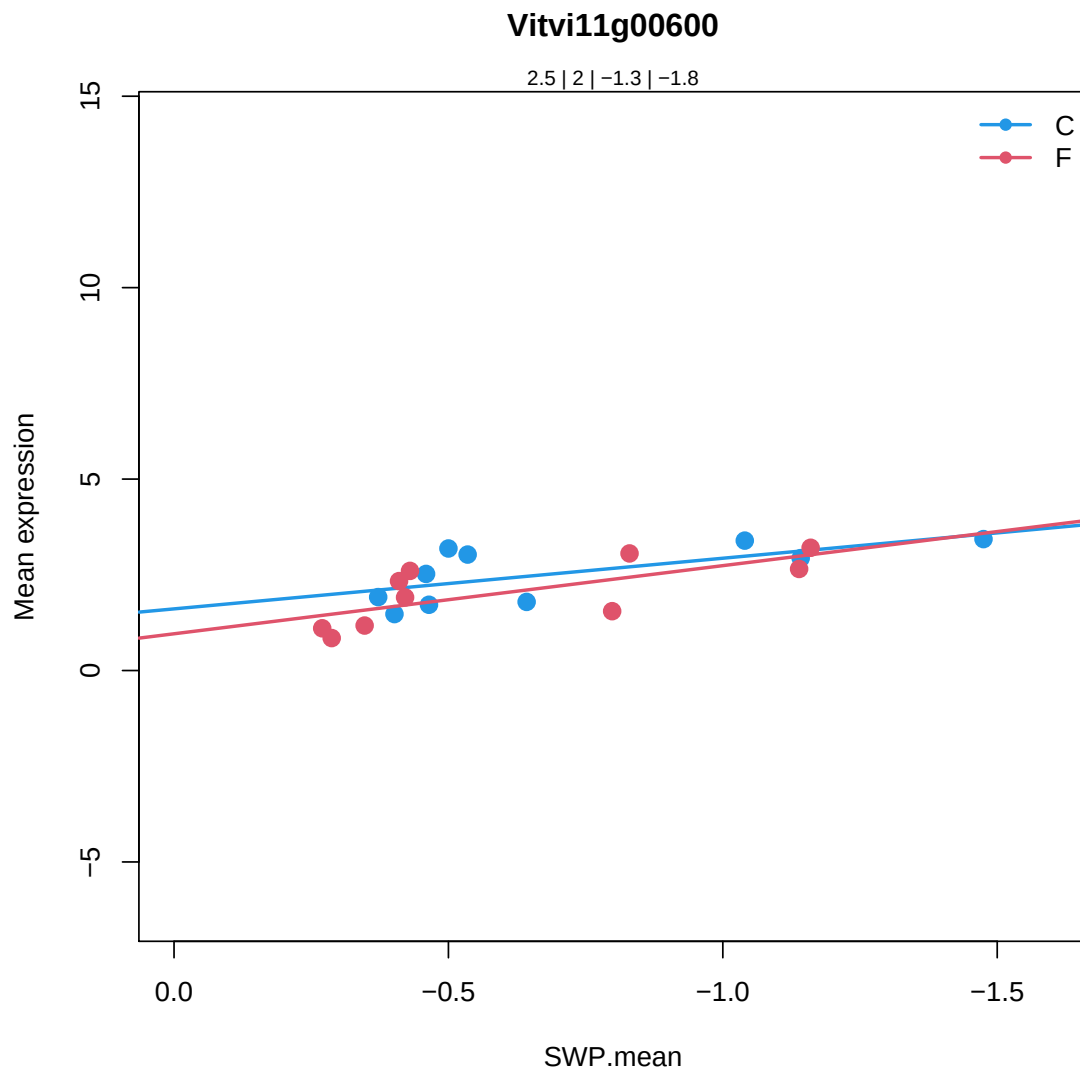
kinase superfamily with octicosapeptide/Phox/Bem1p domain-containing p

Chr3:17280430-17284857 REVERSE LENGTH=1155 |

201606

Coefficients for Vitvi11g00600.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.539925	3.820091e-12	***	5.309185e-12	***
SlopeC	-1.32255	0.01713142	*	0.3546065	
MeanF-MeanC	-0.4962363	0.06993603	.	0.2961014	
SlopeF-SlopeC	-0.4572286	0.5546237		0.9999488	



8.1.379 Vitvi05g00563: Type1.0

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

Vitvi05g00563

30.11

signalling.light

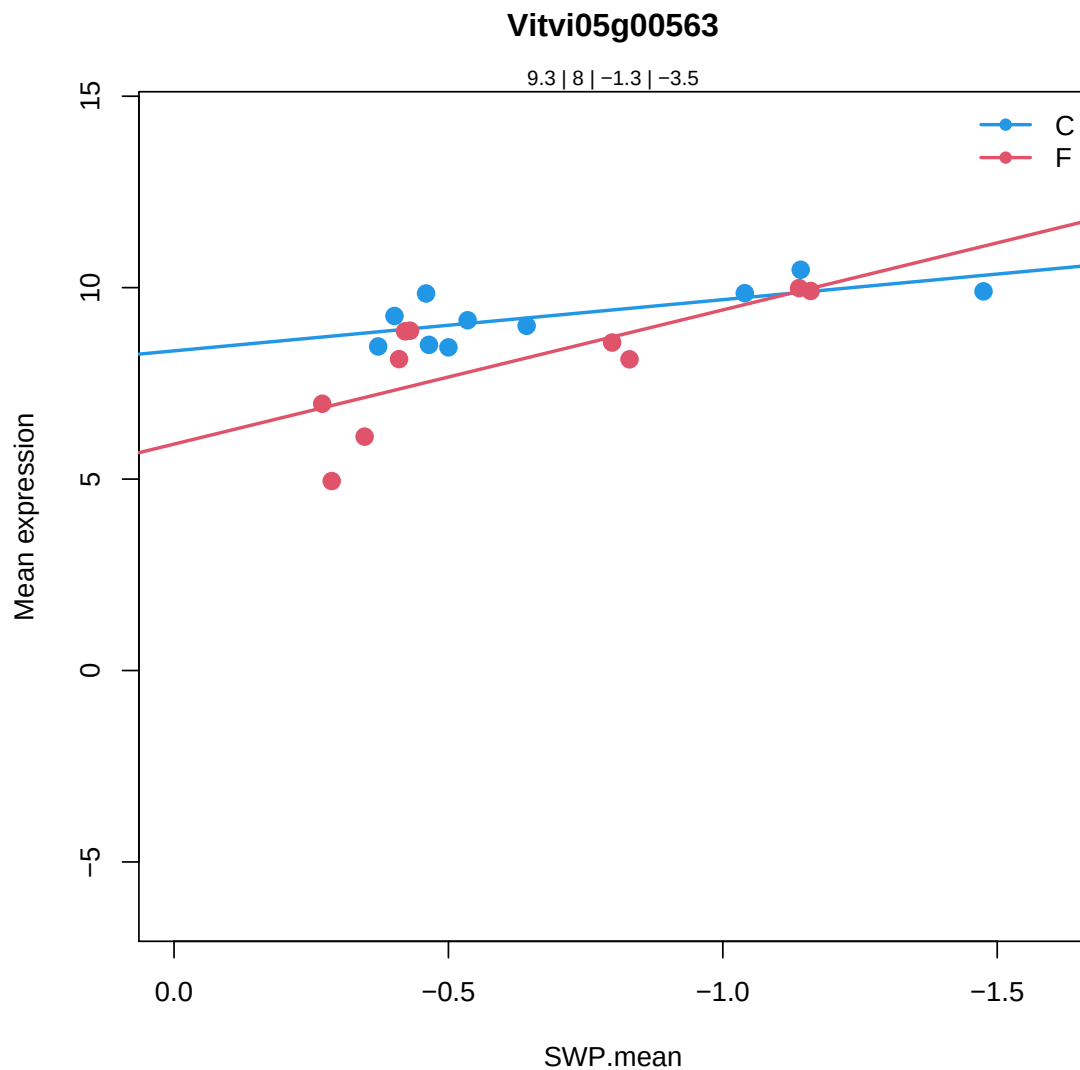
Chlorophyll A-B binding family protein |

Chr3:8084628-8085445 REVERSE LENGTH=195 |

201606

Coefficients for Vitvi05g00563.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	9.28929	8.448591e-21	***	6.229967e-20	***
SlopeC	-1.337434	0.07231022	.	0.5630621	
MeanF-MeanC	-1.240677	0.002347009	**	0.02506875	*
SlopeF-SlopeC	-2.16667	0.05200152	.	0.9999488	



8.1.380 Vitvi01g00381: Type1.0 *

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

Vitvi01g00381

29.5.11.4.2

protein.degradation.ubiquitin.E3.RING

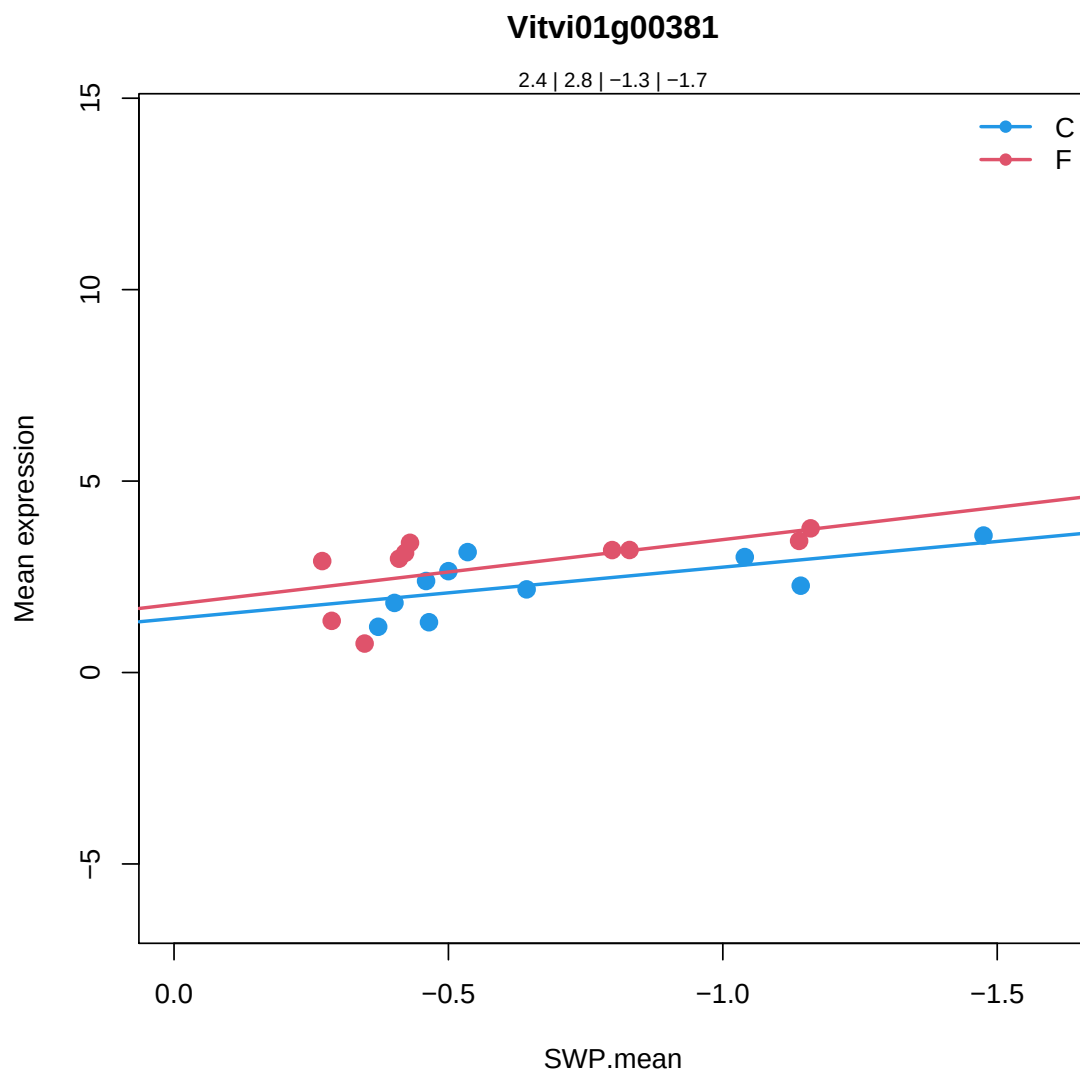
RING/FYVE/PHD zinc finger superfamily protein |

Chr2:142610-143809 REVERSE LENGTH=259 |

201606

Coefficients for Vitvi01g00381.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.353922	2.686253e-10	***	3.455762e-10	***
SlopeC	-1.341719	0.03443939	*	0.444078	
MeanF-MeanC	0.4562126	0.1454344		0.4594471	
SlopeF-SlopeC	-0.3488876	0.6970381		0.9999488	



8.1.381 Vitvi01g00299: Type1.0

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

Vitvi01g00299

35.2

not assigned.unknown

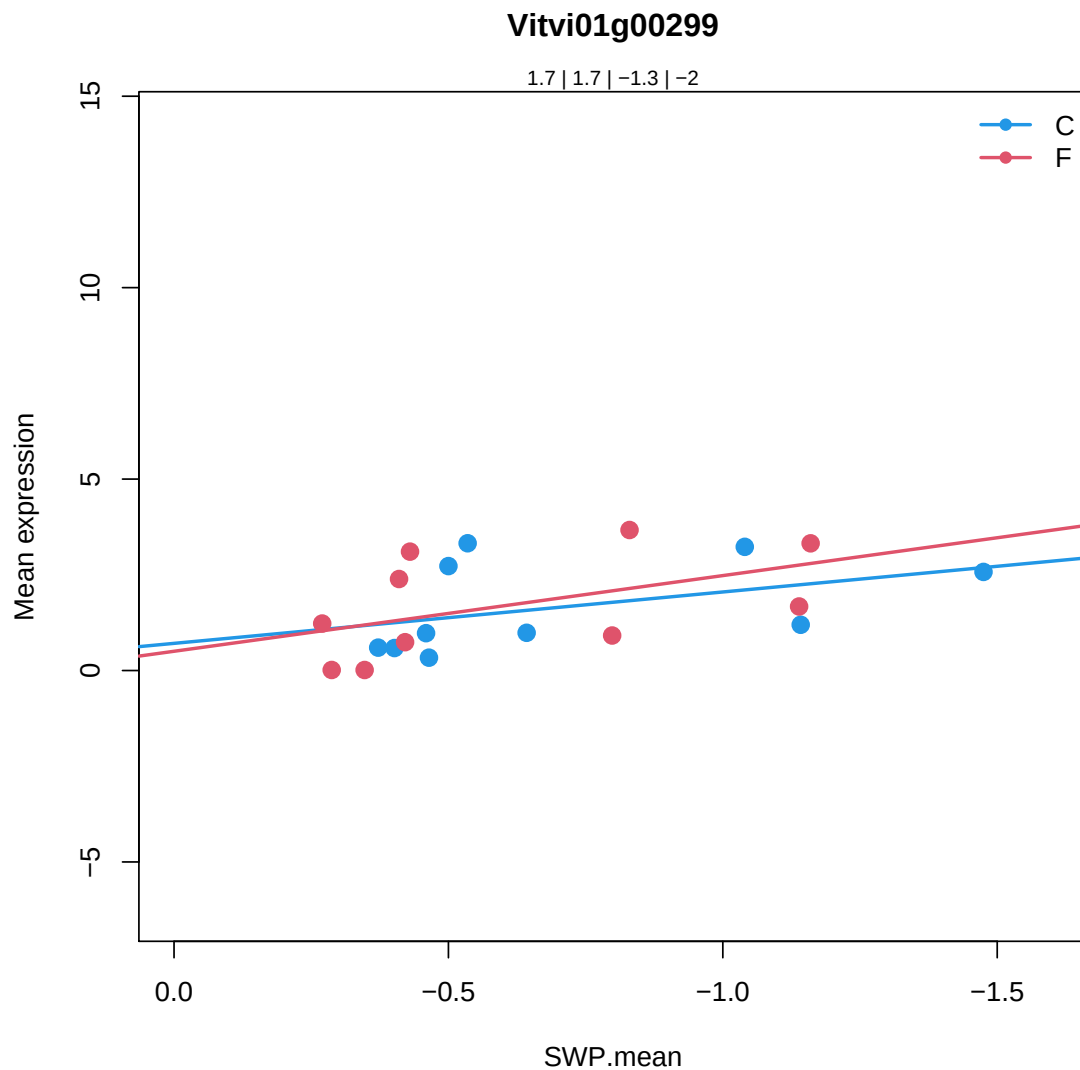
transmembrane protein |

Chr1:8911463-8912329 REVERSE LENGTH=288 |

201606

Coefficients for Vitvi01g00299.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.65308	5.926402e-05	***	6.573773e-05	***
SlopeC	-1.342104	0.160594		0.6892674	
MeanF-MeanC	0.05371794	0.9099534		0.9762703	
SlopeF-SlopeC	-0.6346585	0.6488969		0.9999488	



8.1.382 Vitvi15g01543: Type1.0

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

Vitvi15g01543

27.3.27

RNA.regulation of transcription.NAC domain transcription factor family

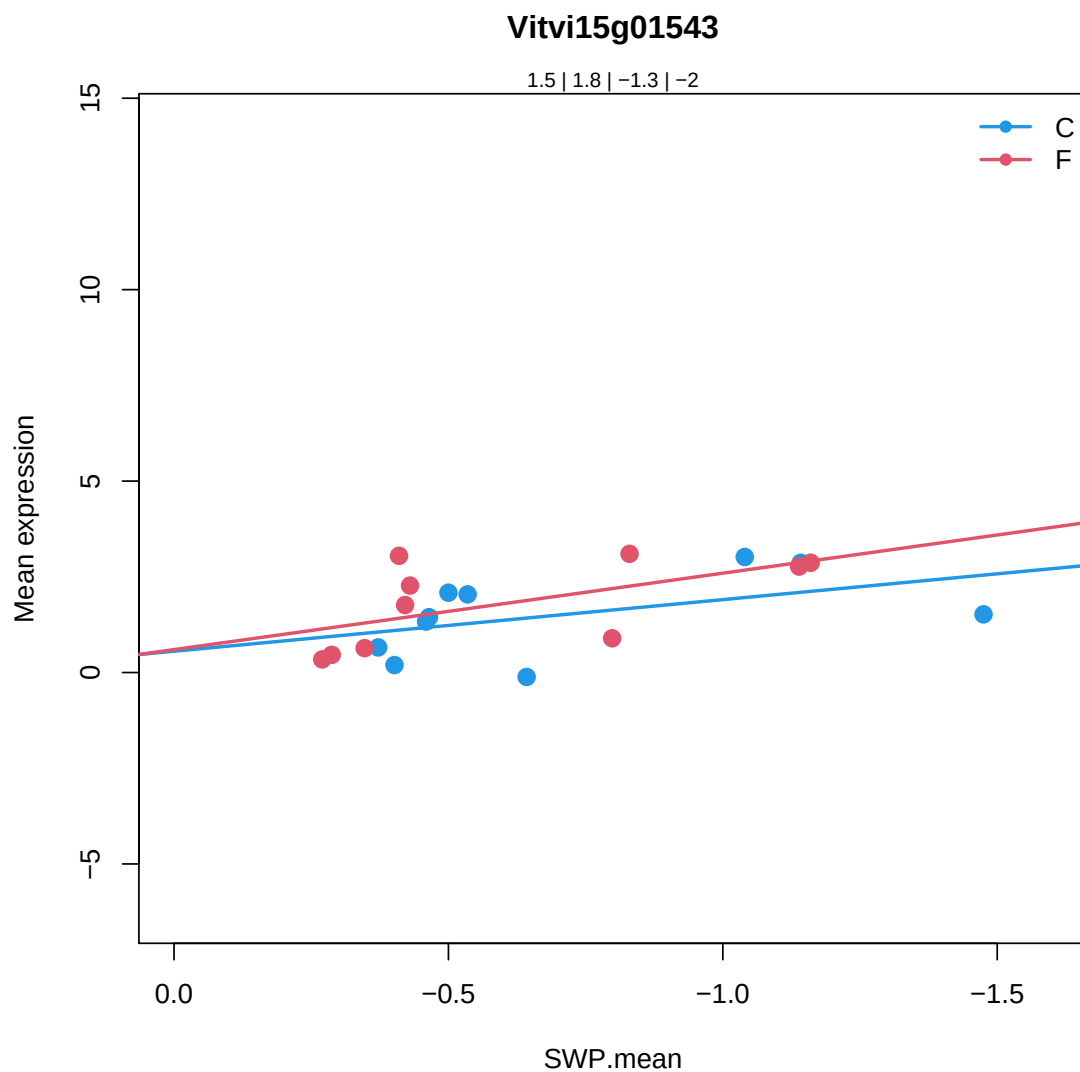
NAC transcription factor-like 9 |

Chr4:16888534-16890744 REVERSE LENGTH=534 |

201606

Coefficients for Vitvi15g01543.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.503715	1.872984e-05	***	2.101592e-05	***
SlopeC	-1.34743	0.09256855	.	0.6008919	
MeanF-MeanC	0.3111411	0.4326126		0.766636	
SlopeF-SlopeC	-0.6477273	0.5755168		0.9999488	



8.1.383 Vitvi02g00429: Type1.0

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

Vitvi02g00429

35.2

not assigned.unknown

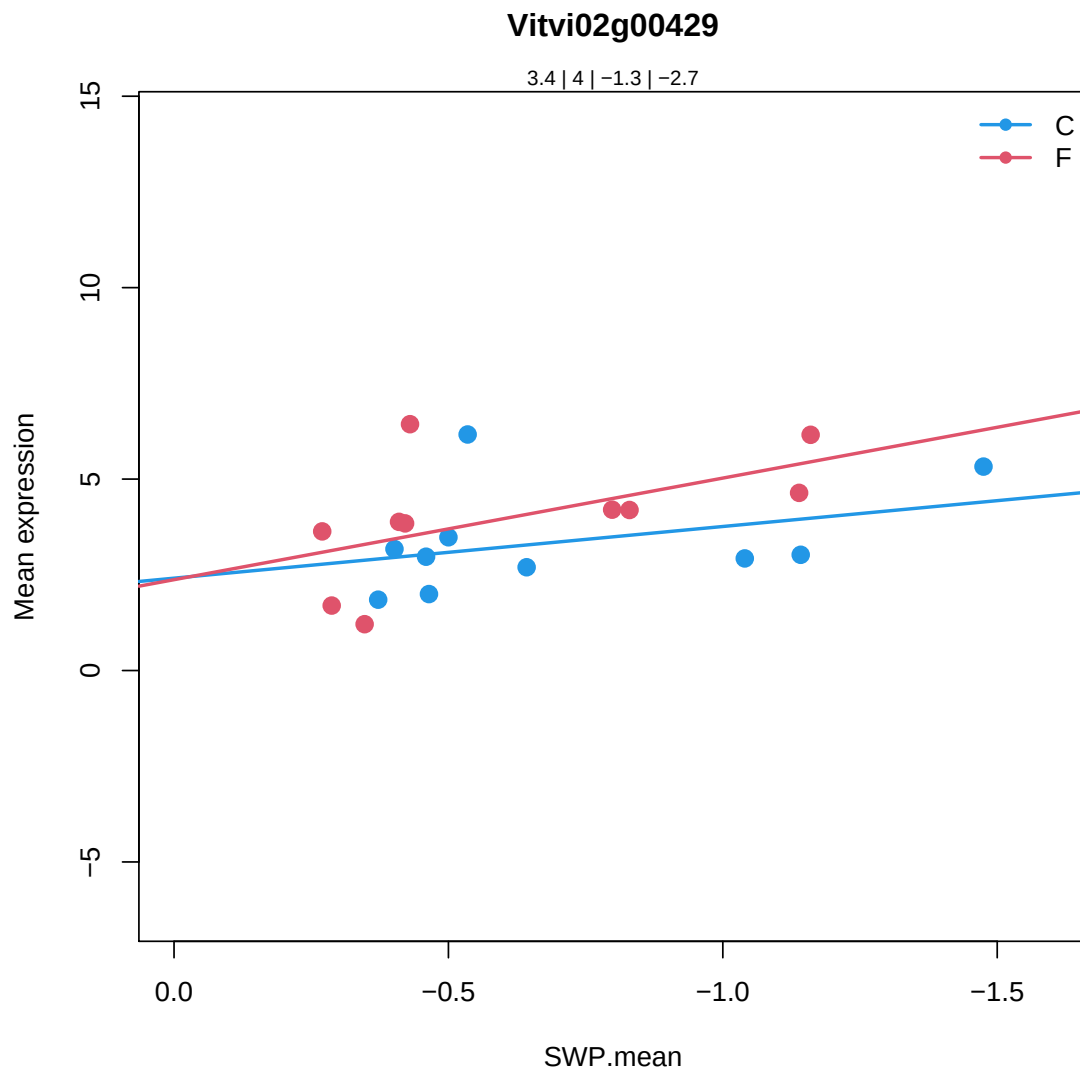
non-yellowing 1 |

Chr4:12016776-12017969 REVERSE LENGTH=268 |

201606

Coefficients for Vitvi02g00429.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.361067	2.060983e-08	***	2.49175e-08	***
SlopeC	-1.349779	0.2268388		0.7462795	
MeanF-MeanC	0.6276447	0.2675933		0.6298111	
SlopeF-SlopeC	-1.303705	0.4282791		0.9999488	



8.1.384 Vitvi13g00784: Type1.0

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

Vitvi13g00784

34.16

transport.ABC transporters and multidrug resistance systems

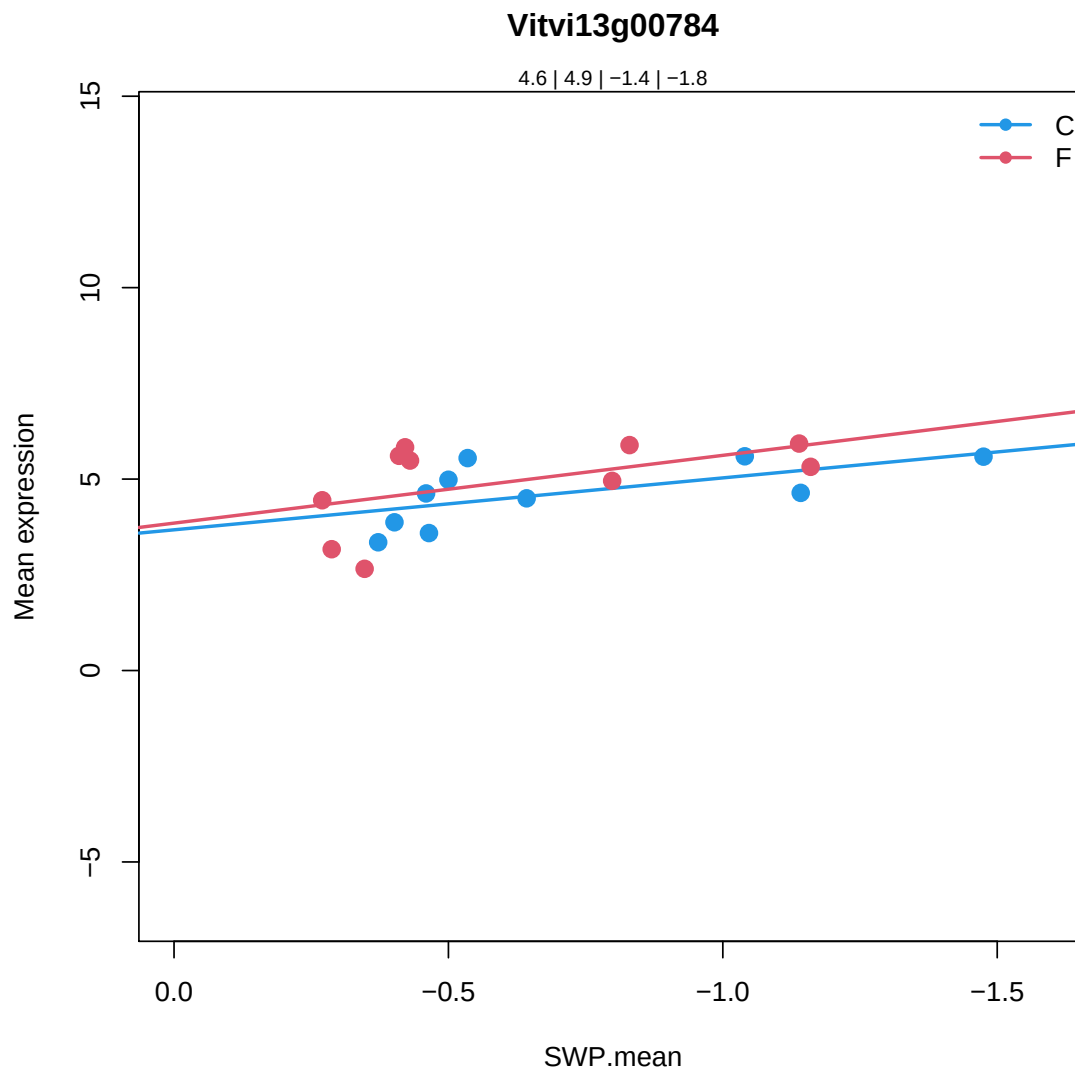
pleiotropic drug resistance 6 |

Chr2:15257583-15263627 FORWARD LENGTH=1453 |

201606

Coefficients for Vitvi13g00784.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.628324	1.615091e-14	***	2.647581e-14	***
SlopeC	-1.355593	0.06886842	.	0.5574314	
MeanF-MeanC	0.2998051	0.4138202		0.7531281	
SlopeF-SlopeC	-0.4145343	0.6978076		0.9999488	



8.1.385 Vitvi07g01395: Type1.0 *

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

Vitvi07g01395

26.2

misc.UDP glucosyl and glucoronyl transferases

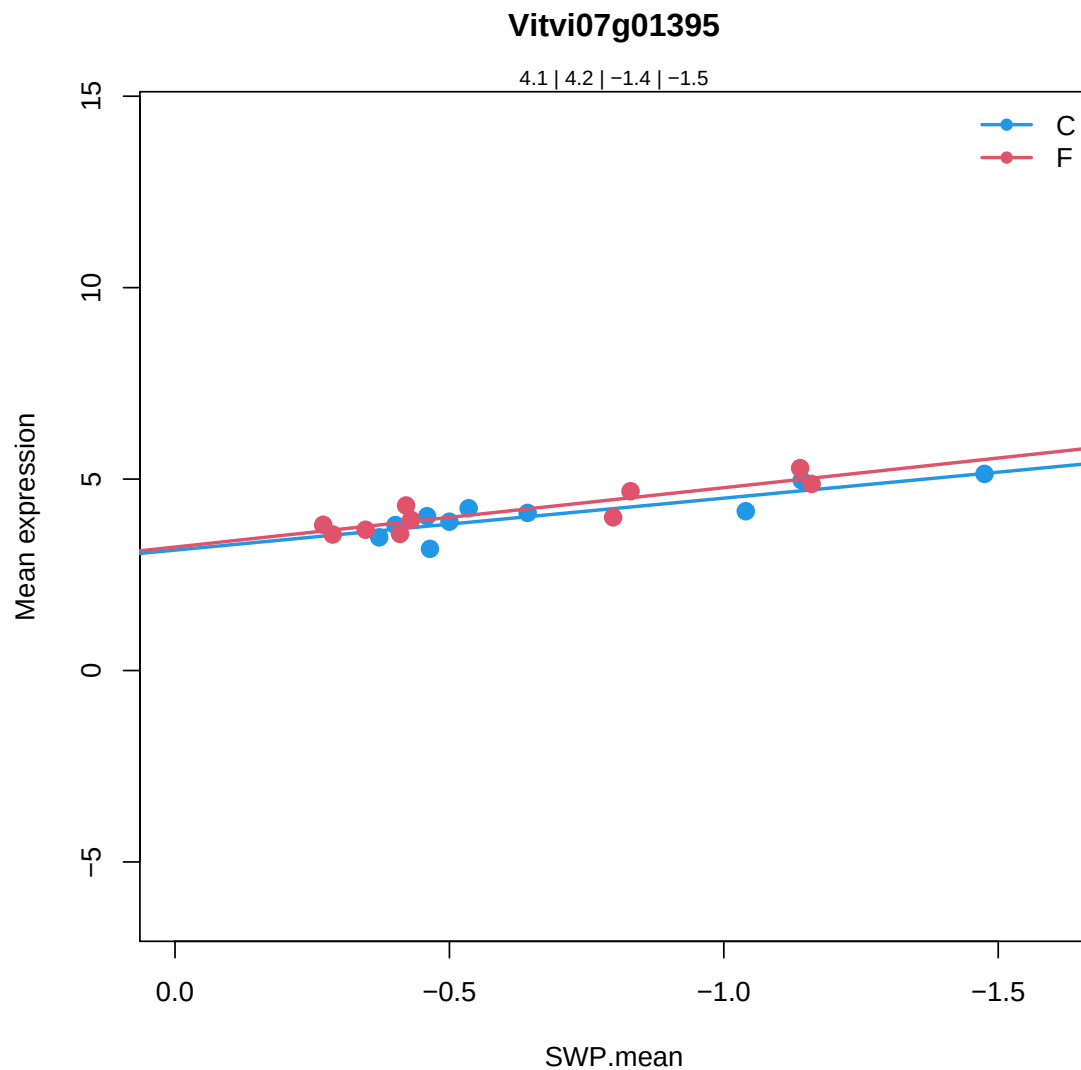
UDP-glucosyl transferase 85A2 |

Chr1:7895068-7897527 REVERSE LENGTH=481 |

201606

Coefficients for Vitvi07g01395.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.098973	1.390377e-20	***	9.307042e-20	***
SlopeC	-1.357018	0.0003476217	***	0.09461517	.
MeanF-MeanC	0.07036105	0.6693211		0.892233	
SlopeF-SlopeC	-0.1929631	0.6890673		0.9999488	



8.1.386 Vitvi02g00479: Type1.0 *

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

Vitvi02g00479

35.1.40

not assigned.no ontology.glycine rich proteins

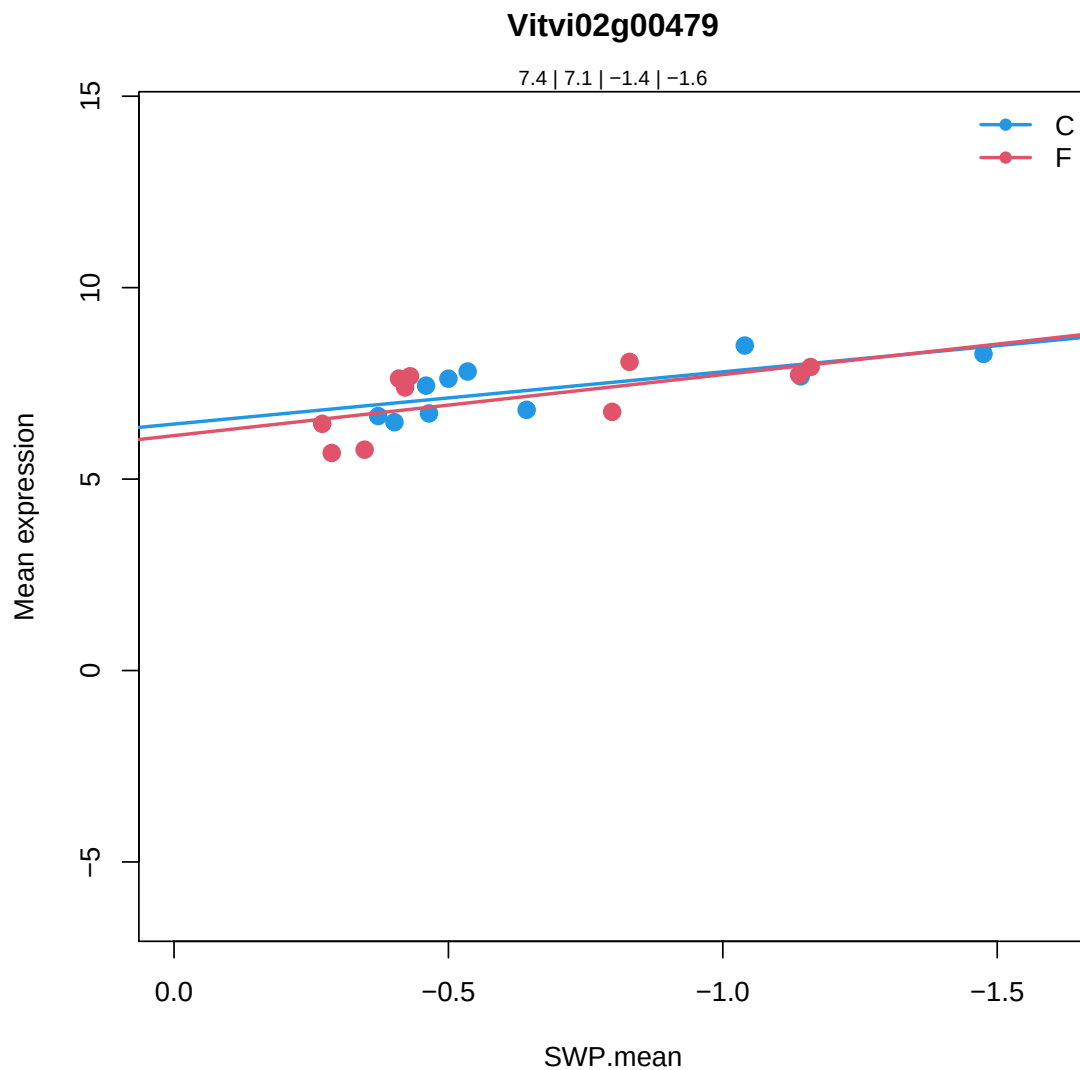
glycine-rich protein |

Chr4:11944050-11945565 REVERSE LENGTH=356 |

201606

Coefficients for Vitvi02g00479.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.396619	2.052347e-21	***	2.003963e-20	***
SlopeC	-1.364266	0.01694217	*	0.3536249	
MeanF-MeanC	-0.2907691	0.2896869		0.6552023	
SlopeF-SlopeC	-0.2291237	0.7729633		0.9999488	



8.1.387 Vitvi17g01092: Type1.0 *

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

Vitvi17g01092

26.3.5

misc.gluco-, galacto- and mannosidases.glycosyl hydrolase family 5

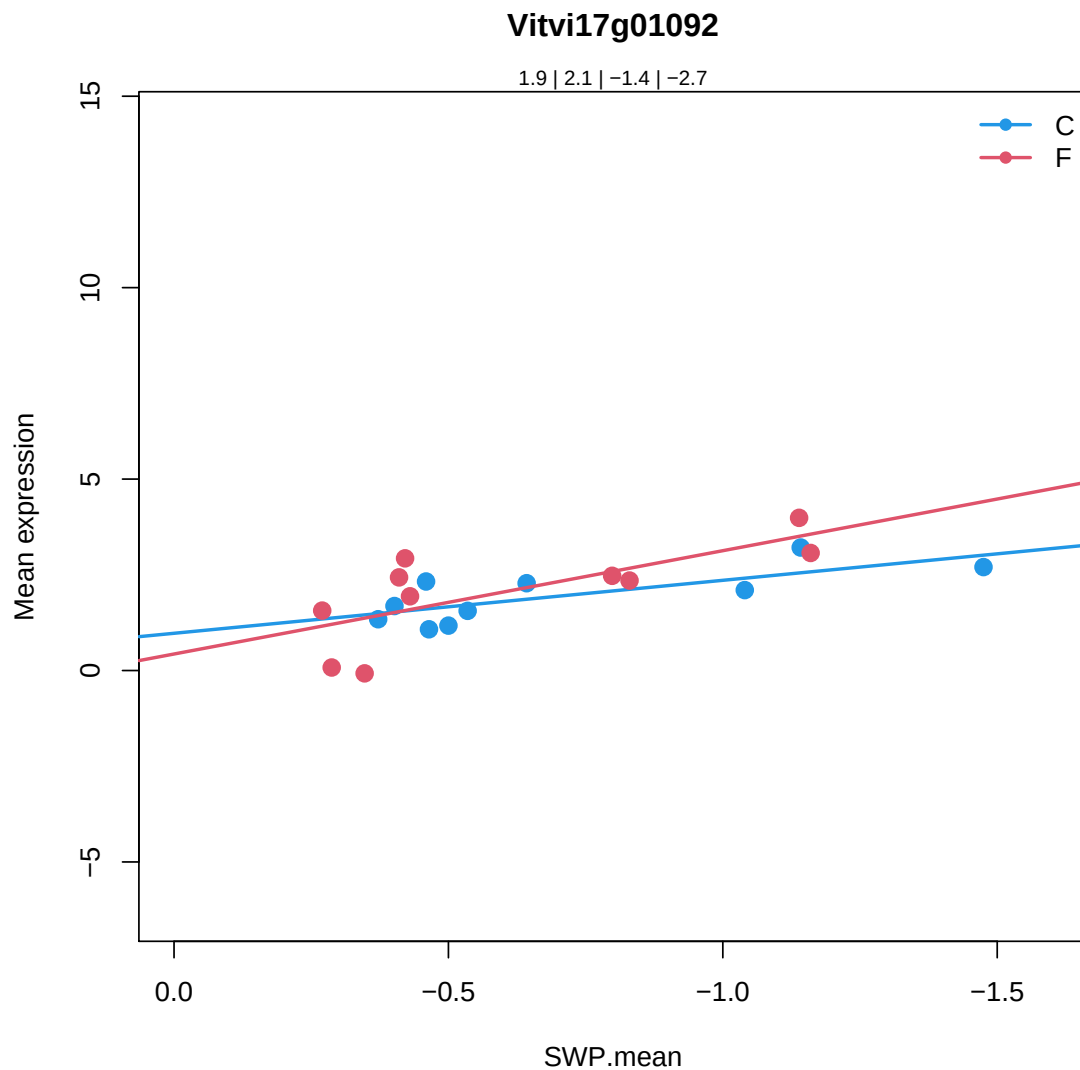
alpha/beta-Hydrolases superfamily protein |

Chr1:27629266-27632486 FORWARD LENGTH=463 |

201606

Coefficients for Vitvi17g01092.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.945062	1.077062e-08	***	1.313537e-08	***
SlopeC	-1.383799	0.03223902	*	0.4372376	
MeanF-MeanC	0.1300597	0.676189		0.8951087	
SlopeF-SlopeC	-1.314765	0.1582634		0.9999488	



8.1.388 Vitvi01g00918: Type1.0

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

Vitvi01g00918

27.3.35

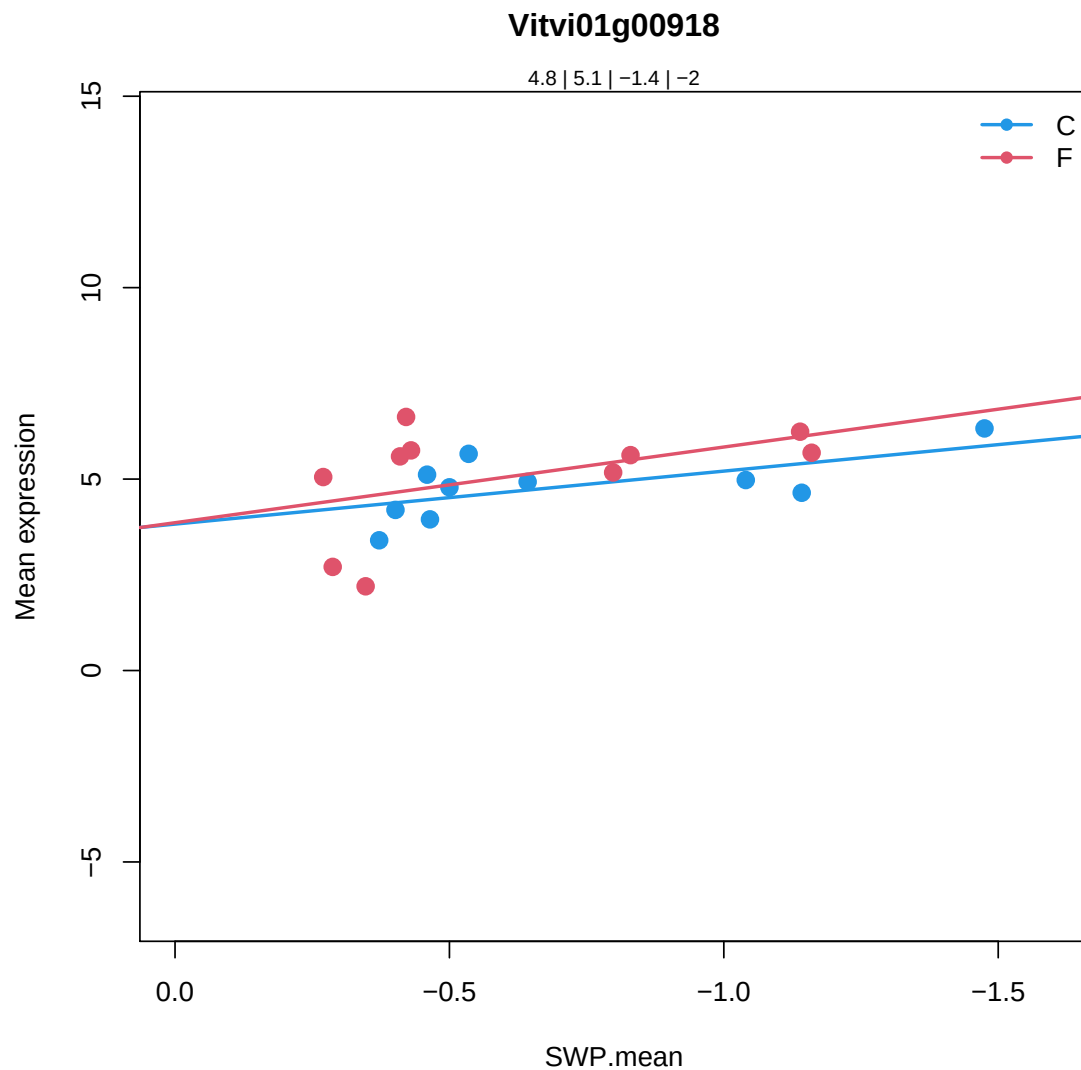
RNA.regulation of transcription.bZIP transcription factor family
homeobox 1 |

Chr3:182648-184034 REVERSE LENGTH=272 |

201606

Coefficients for Vitvi01g00918.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.797064	3.042907e-13	***	4.522229e-13	***
SlopeC	-1.384017	0.1178617		0.6341652	
MeanF-MeanC	0.2675744	0.5420075		0.8292791	
SlopeF-SlopeC	-0.5923853	0.6441302		0.9999488	

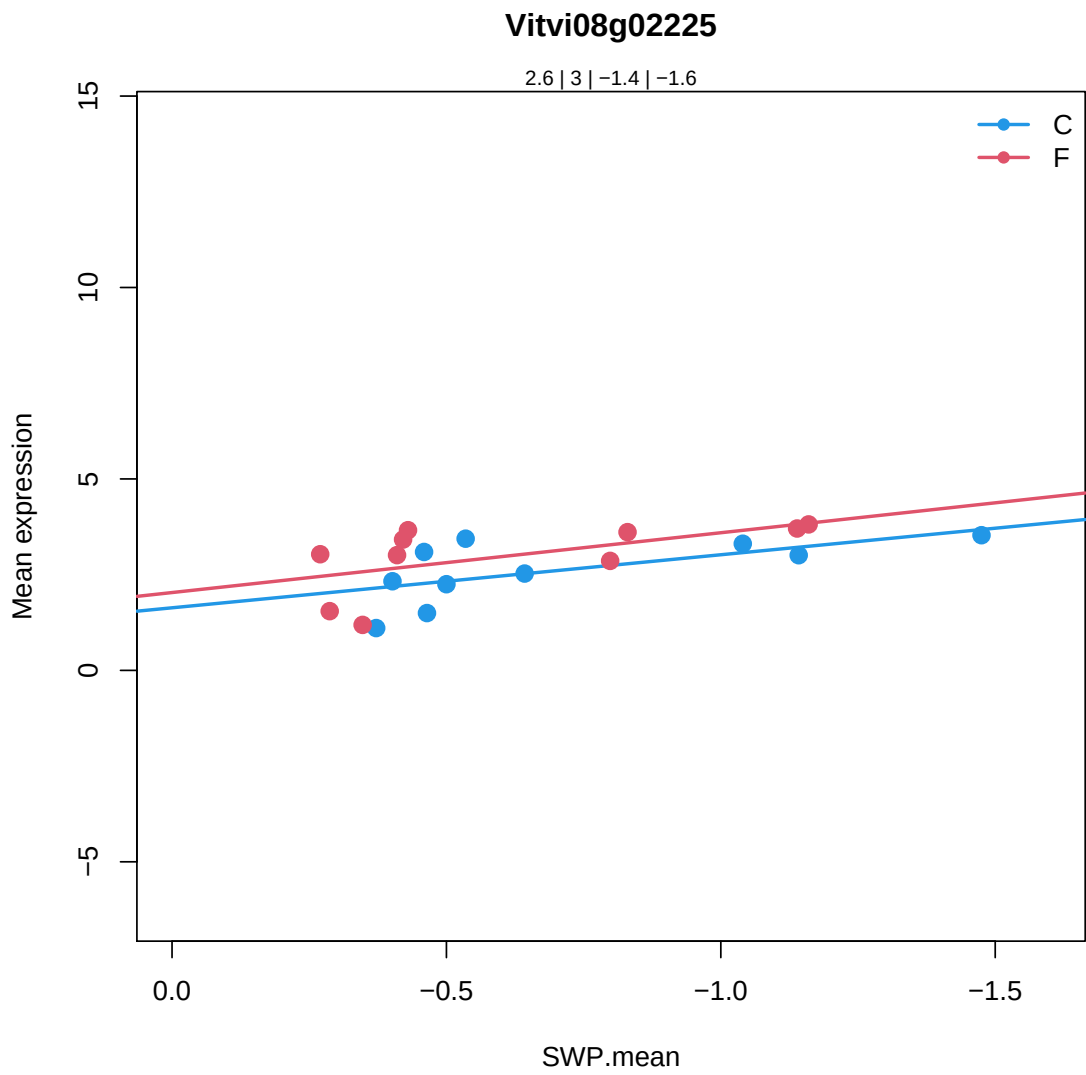


8.1.389 Vitvi08g02225: Type1.0 *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
Vitvi08g02225
35.2
not assigned.unknown
[Sotub09g012710.1.1]: Unknown Protein [Sotub09g012710.1.1]: Unknown Pr
[stNIB-v1_0001331]
```

Coefficients for Vitvi08g02225.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.608389	4.555546e-11	***	6.044714e-11	***
SlopeC	-1.385499	0.03056749	*	0.4321285	
MeanF-MeanC	0.3758626	0.2299304		0.5834191	
SlopeF-SlopeC	-0.1769986	0.8443383		0.9999488	



8.1.390 Vitvi02g01427: Type1.0 *

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

Vitvi02g01427

26.10

misc.cytochrome P450

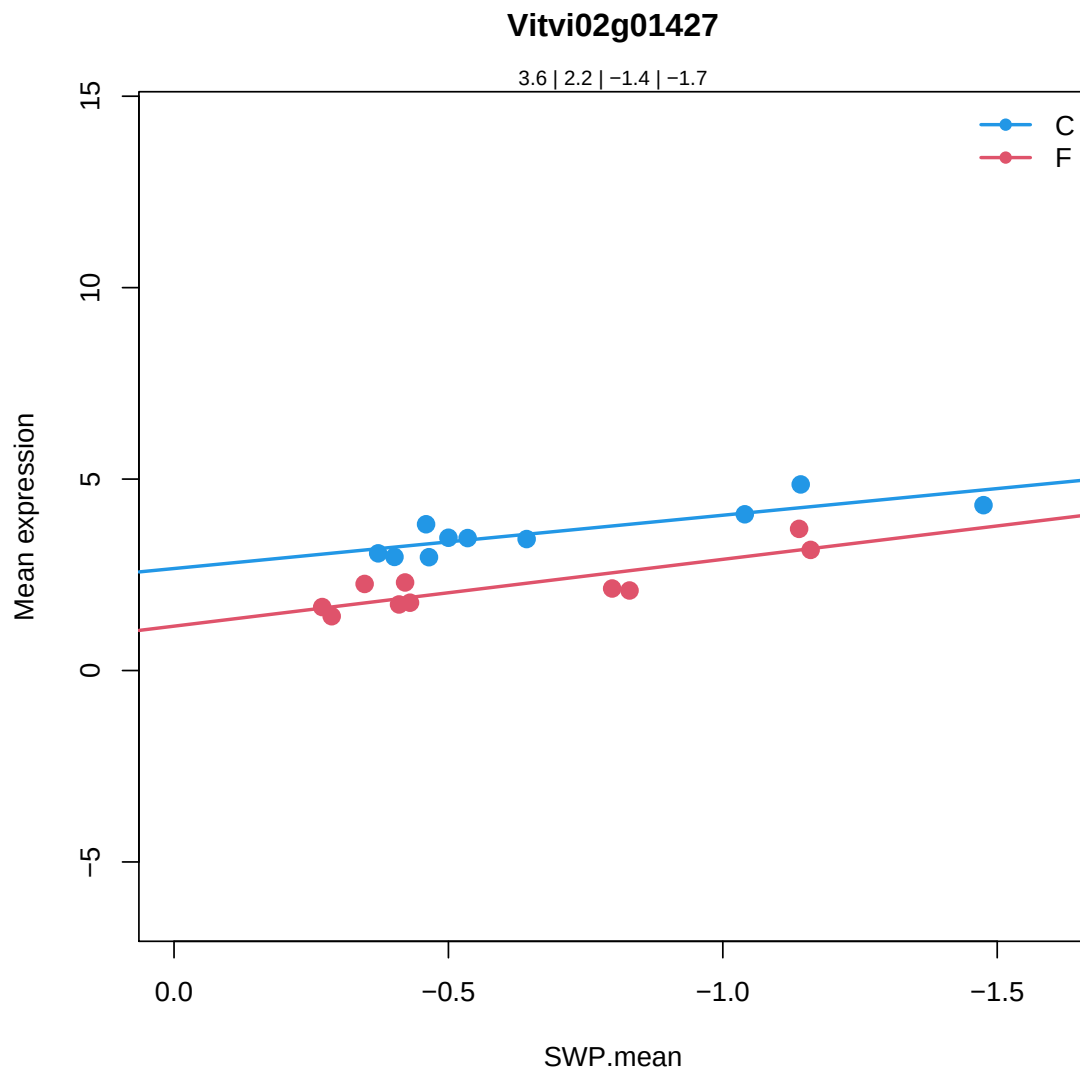
cytochrome P450%2C family 706%2C subfamily A%2C polypeptide 4 |

Chr4:7308016-7309692 REVERSE LENGTH=516 |

201606

Coefficients for Vitvi02g01427.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.642495	2.019881e-18	***	6.37017e-18	***
SlopeC	-1.392242	0.0008651745	***	0.1184327	
MeanF-MeanC	-1.420987	1.149488e-07	***	4.574544e-06	***
SlopeF-SlopeC	-0.3530263	0.5170181		0.9999488	



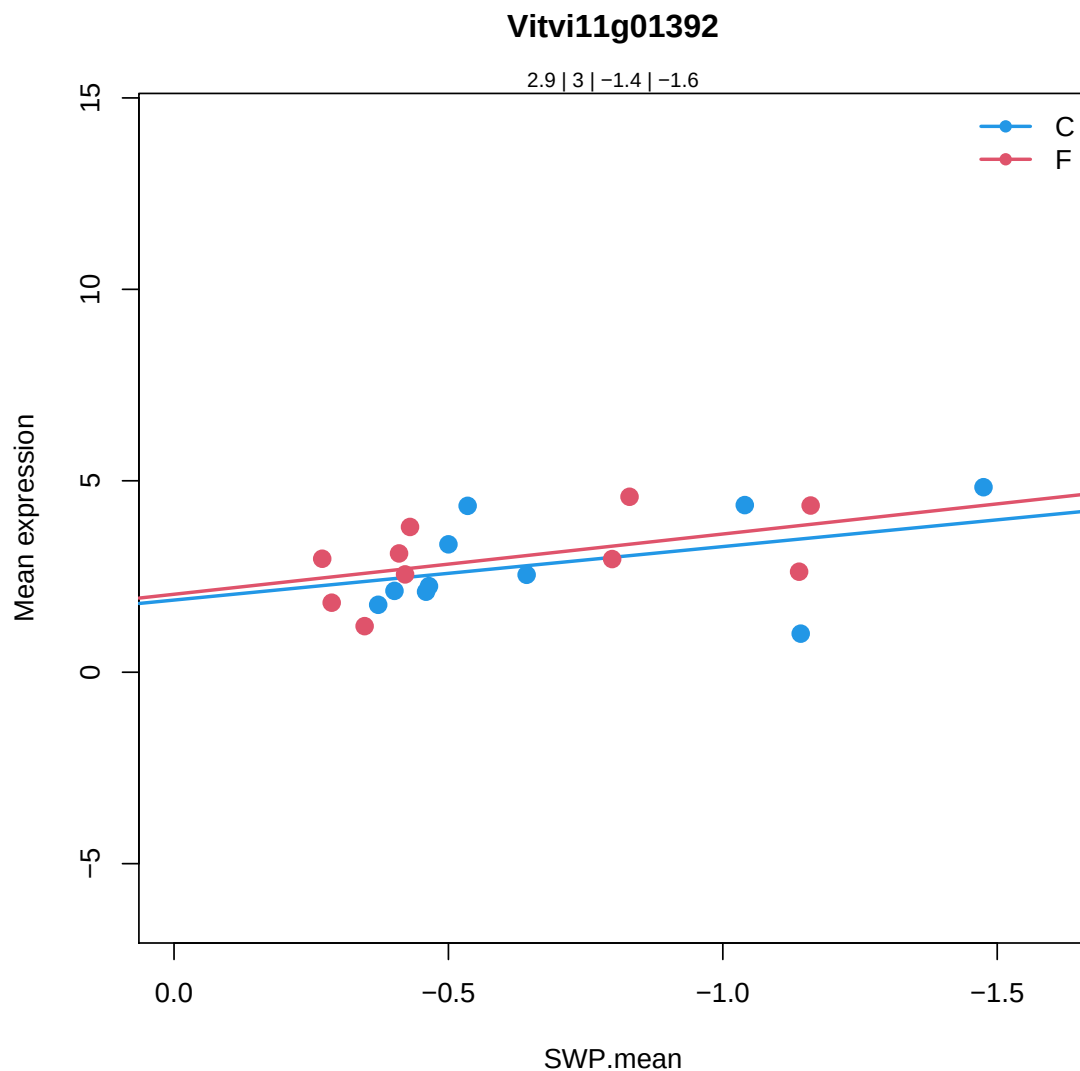
8.1.391 Vitvi11g01392: Type1.0

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

```
Vitvi11g01392
30.10
signalling.phosphorelay
NA
```

Coefficients for Vitvi11g01392.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.867044	7.063474e-09	***	8.66421e-09	***
SlopeC	-1.397001	0.1225777		0.6442513	
MeanF-MeanC	0.1280502	0.7747072		0.9355874	
SlopeF-SlopeC	-0.1768015	0.8925552		0.9999488	



8.1.392 Vitvi01g00037: Type1.0

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

Vitvi01g00037

35.2

not assigned.unknown

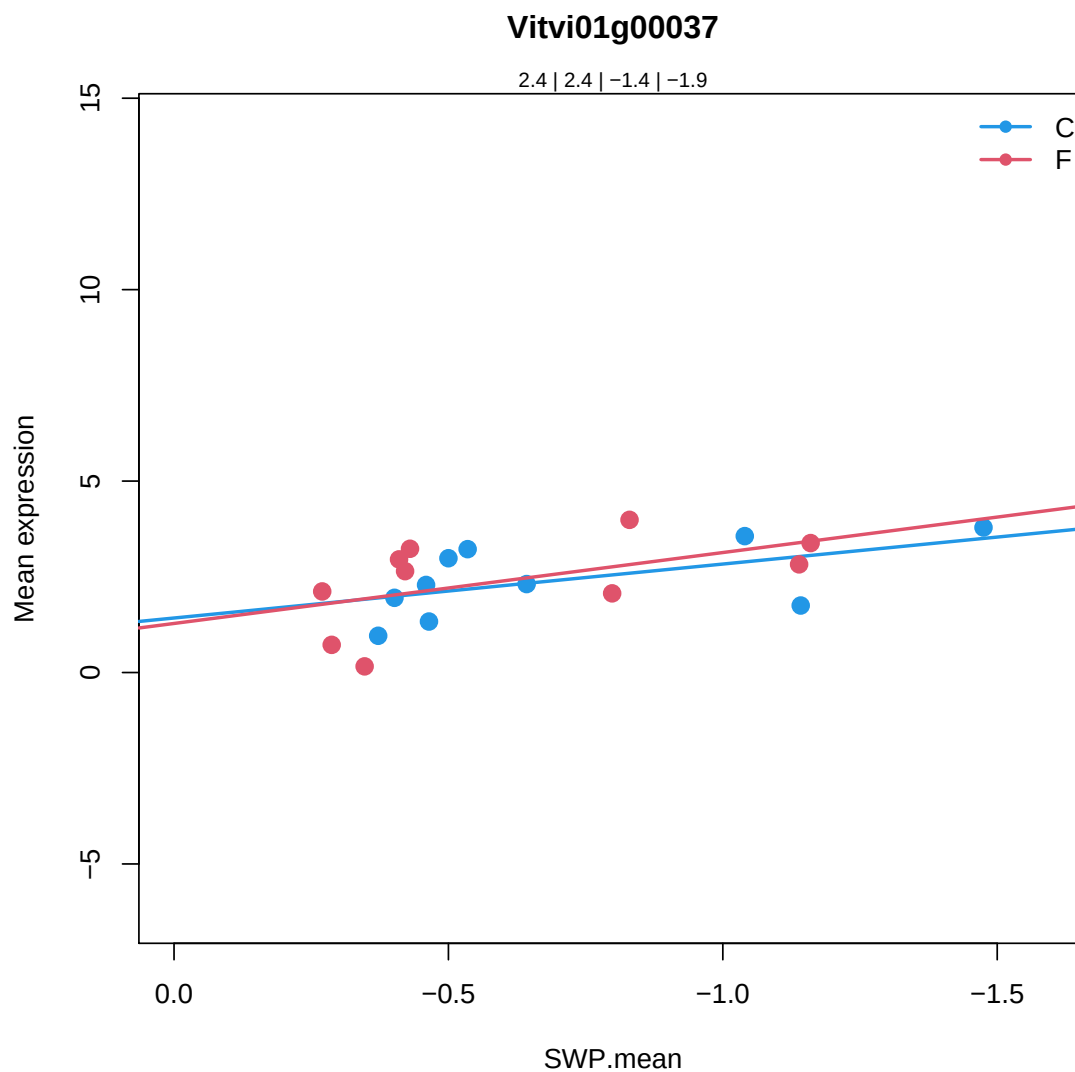
ABI five binding protein 2 |

Chr1:4713969-4715158 FORWARD LENGTH=348 |

201606

Coefficients for Vitvi01g00037.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.414563	1.341453e-08	***	1.630887e-08	***
SlopeC	-1.409016	0.07748119	.	0.5717559	
MeanF-MeanC	-0.004961904	0.9898685		0.9970642	
SlopeF-SlopeC	-0.4431473	0.6990273		0.9999488	



8.1.393 Vitvi05g00102: Type1.0 *

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

Vitvi05g00102

29.3.2

protein.targeting.mitochondria

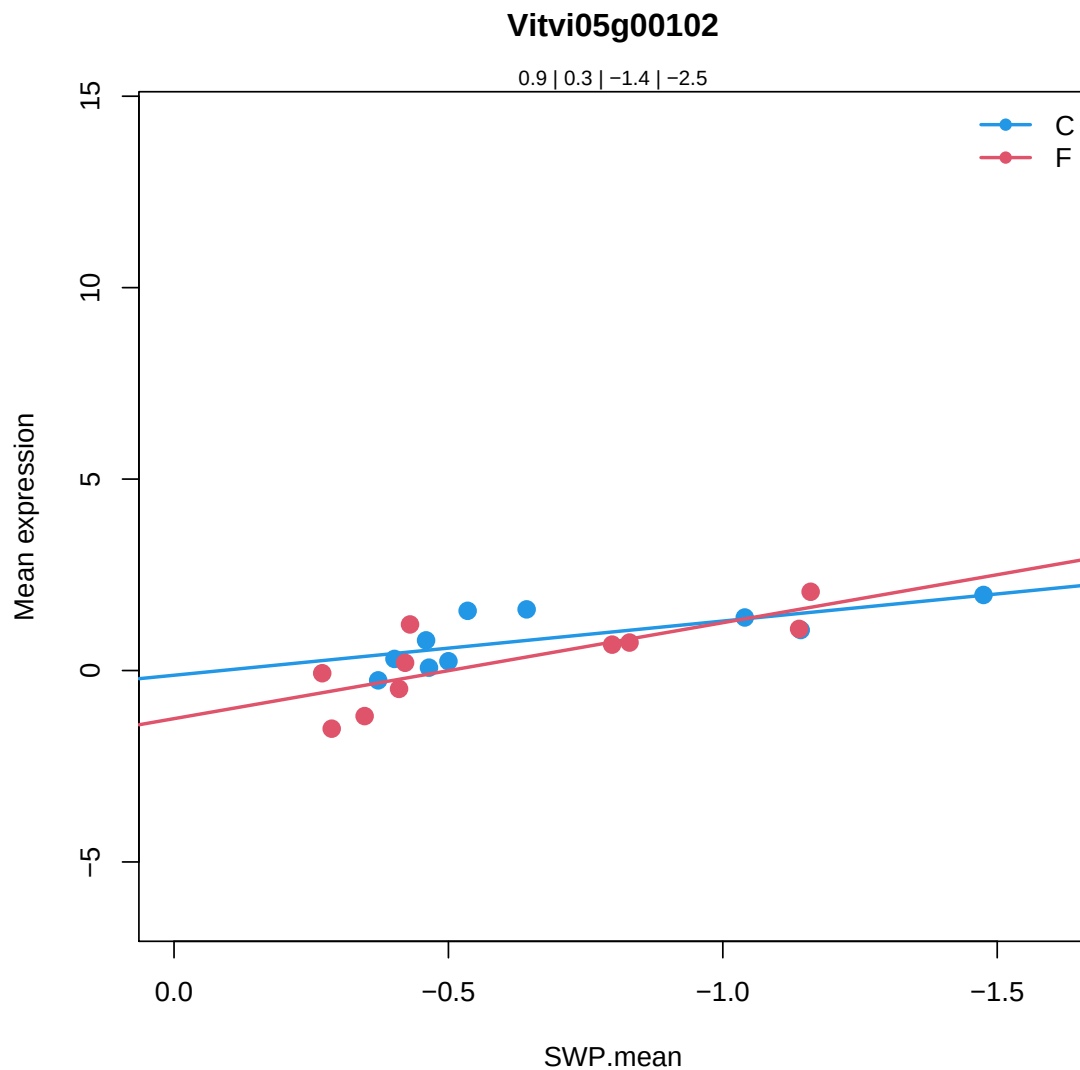
Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Ti

Chr4:9157545-9158738 FORWARD LENGTH=176 |

201606

Coefficients for Vitvi05g00102.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8722292	0.0002221683	***	0.000243653	***
SlopeC	-1.415582	0.01711681	*	0.3546065	
MeanF-MeanC	-0.6026421	0.04183624	*	0.2126978	
SlopeF-SlopeC	-1.090644	0.1949379		0.9999488	



8.1.394 Vitvi14g01811: Type1.0

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

Vitvi14g01811

35.2

not assigned.unknown

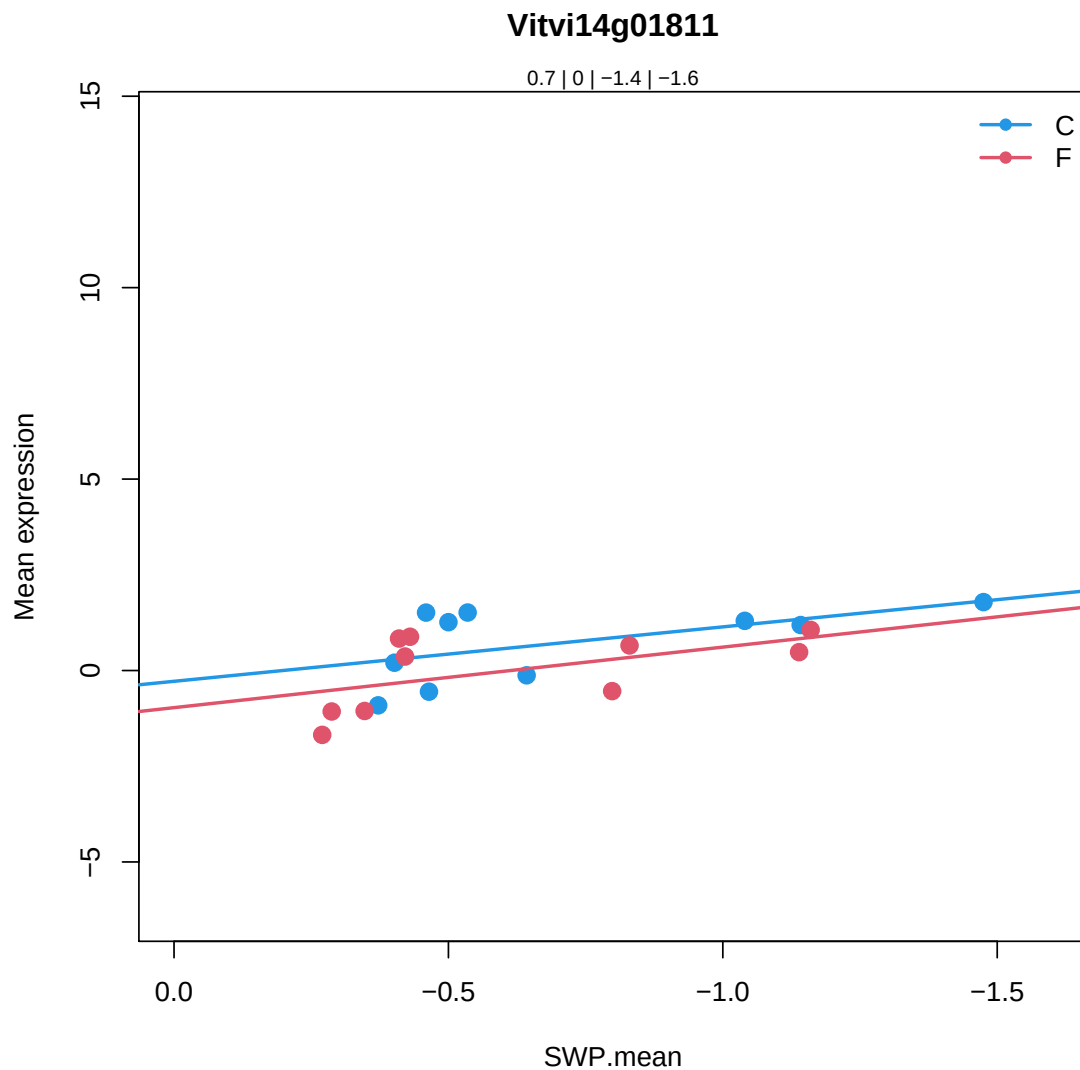
TRICHOME BIREFRINGENCE-LIKE 22 |

Chr3:10471960-10473735 REVERSE LENGTH=414 |

201606

Coefficients for Vitvi14g01811.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.7176293	0.008845858	**	0.009383295	**
SlopeC	-1.42152	0.05275518	.	0.5144558	
MeanF-MeanC	-0.7244294	0.0522048	.	0.2462722	
SlopeF-SlopeC	-0.159325	0.8787397		0.9999488	



8.1.395 Vitvi08g01816: Type1.0 *

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

Vitvi08g01816

35.1.12

not assigned.no ontology.pumilio/Puf RNA-binding domain-containing pro

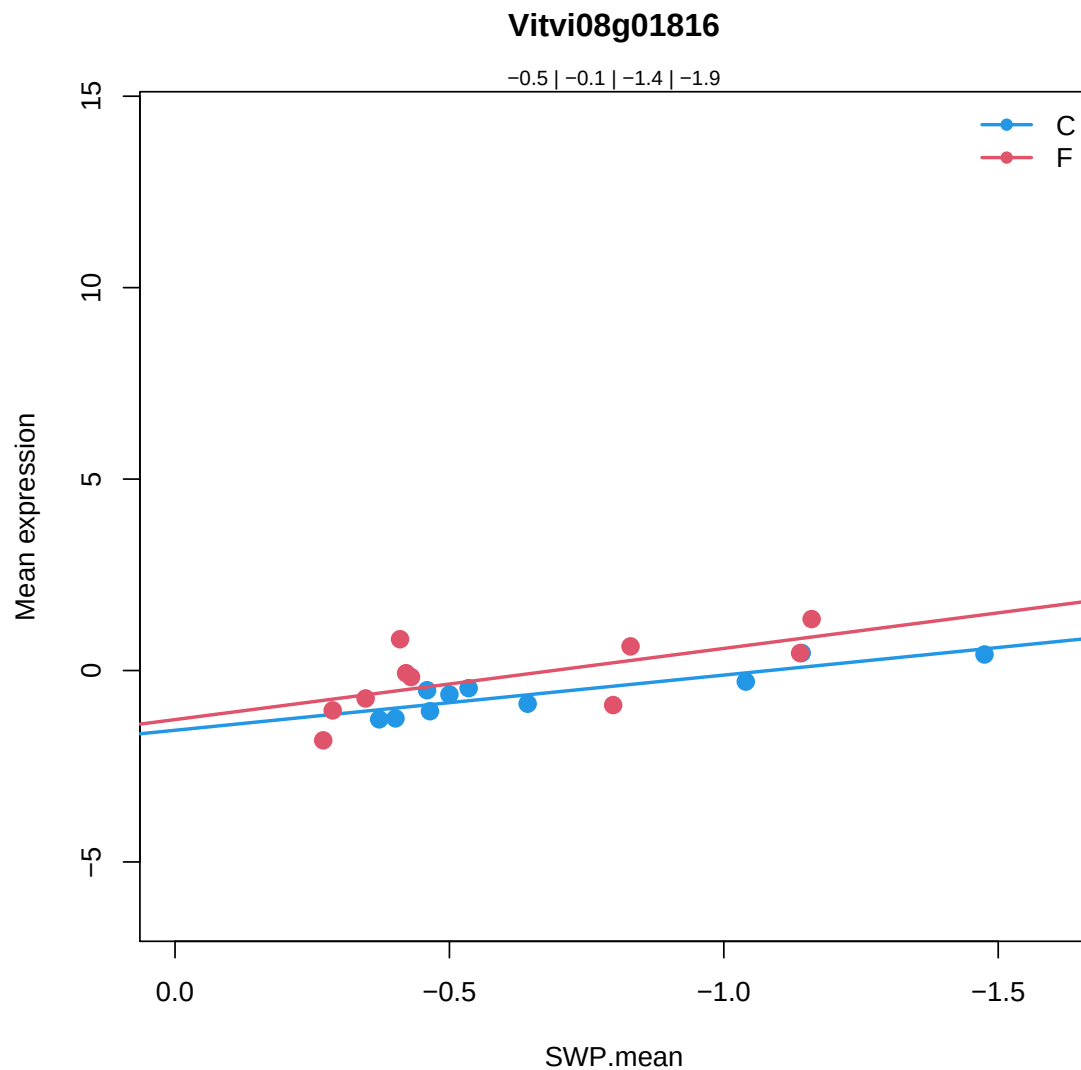
pumilio 12 |

Chr5:22881721-22883842 FORWARD LENGTH=596 |

201606

Coefficients for Vitvi08g01816.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.5471354	0.006347134	**	0.006751554	**
SlopeC	-1.441226	0.009171907	**	0.2905571	
MeanF-MeanC	0.3979652	0.1344258		0.438365	
SlopeF-SlopeC	-0.4174685	0.5830683		0.9999488	



8.1.396 Vitvi10g00444: Type1.0 *

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

Vitvi10g00444

27.3.8

RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family

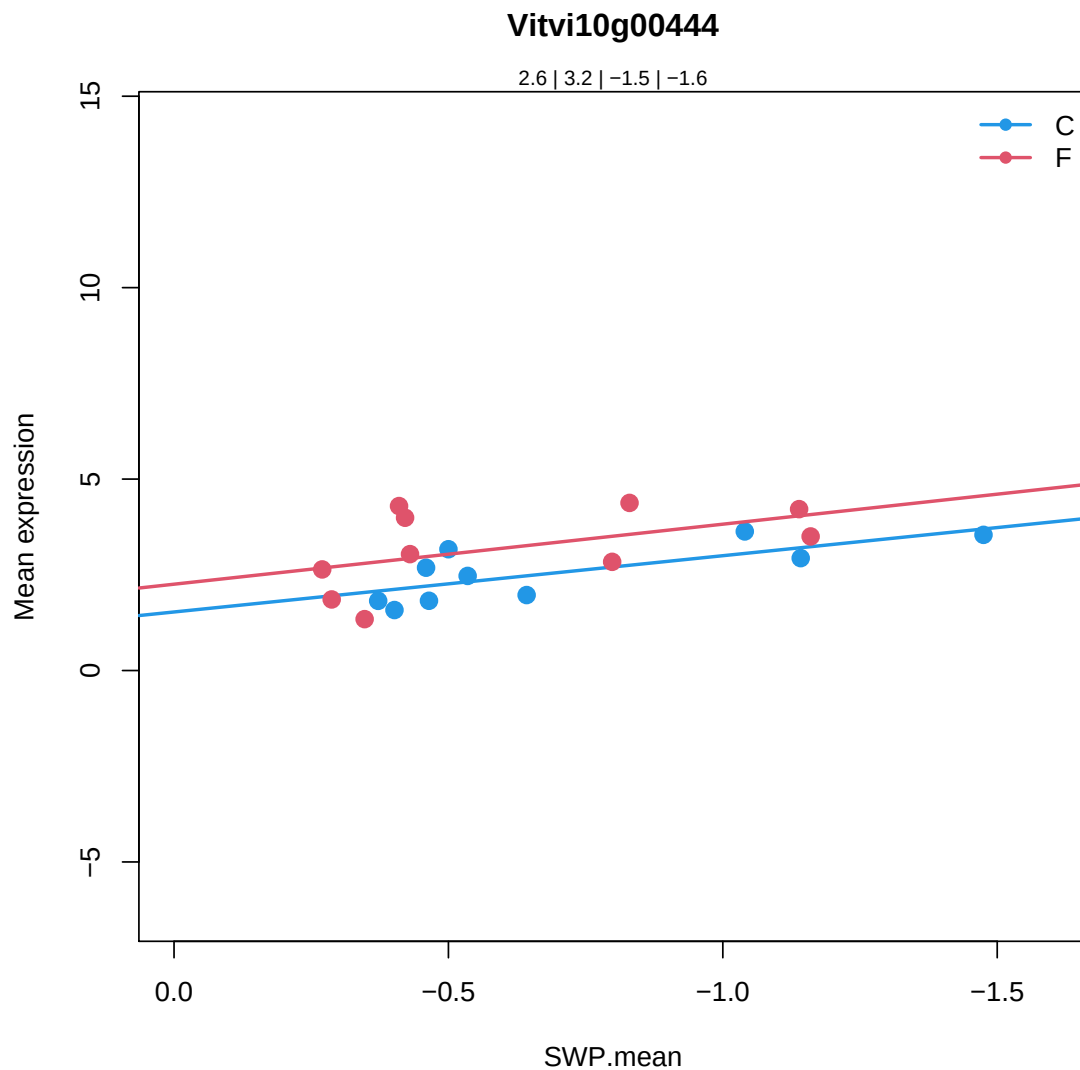
DOF zinc finger protein 1 |

Chr1:19174266-19174850 FORWARD LENGTH=194 |

201606

Coefficients for Vitvi10g00444.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.562525	1.68952e-10	***	2.19219e-10	***
SlopeC	-1.469644	0.02961247	*	0.4299803	
MeanF-MeanC	0.646972	0.0562449	.	0.2580935	
SlopeF-SlopeC	-0.09792533	0.917876		0.9999488	



8.1.397 Vitvi07g01139: Type1.0 *

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

Vitvi07g01139

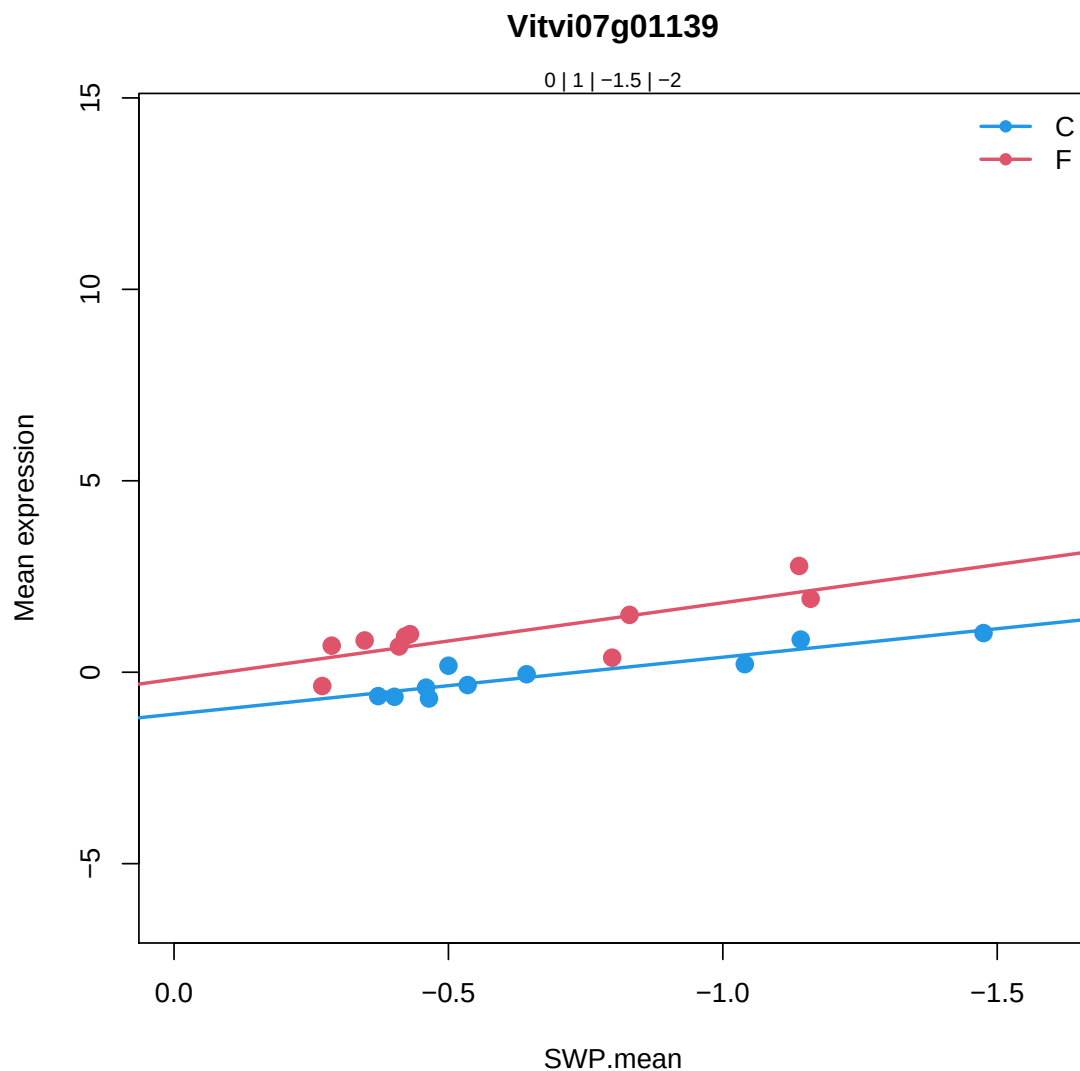
35.2

not assigned.unknown

Early tobacco anther 1

Coefficients for Vitvi07g01139.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.04879622	0.7332838		0.7377855	
SlopeC	-1.487119	0.001062304	**	0.1285051	
MeanF-MeanC	1.082316	2.115269e-05	***	0.000481208	***
SlopeF-SlopeC	-0.5087966	0.3943002		0.9999488	



8.1.398 Vitvi10g00105: Type1.0 *

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

Vitvi10g00105

35.1

not assigned.no ontology

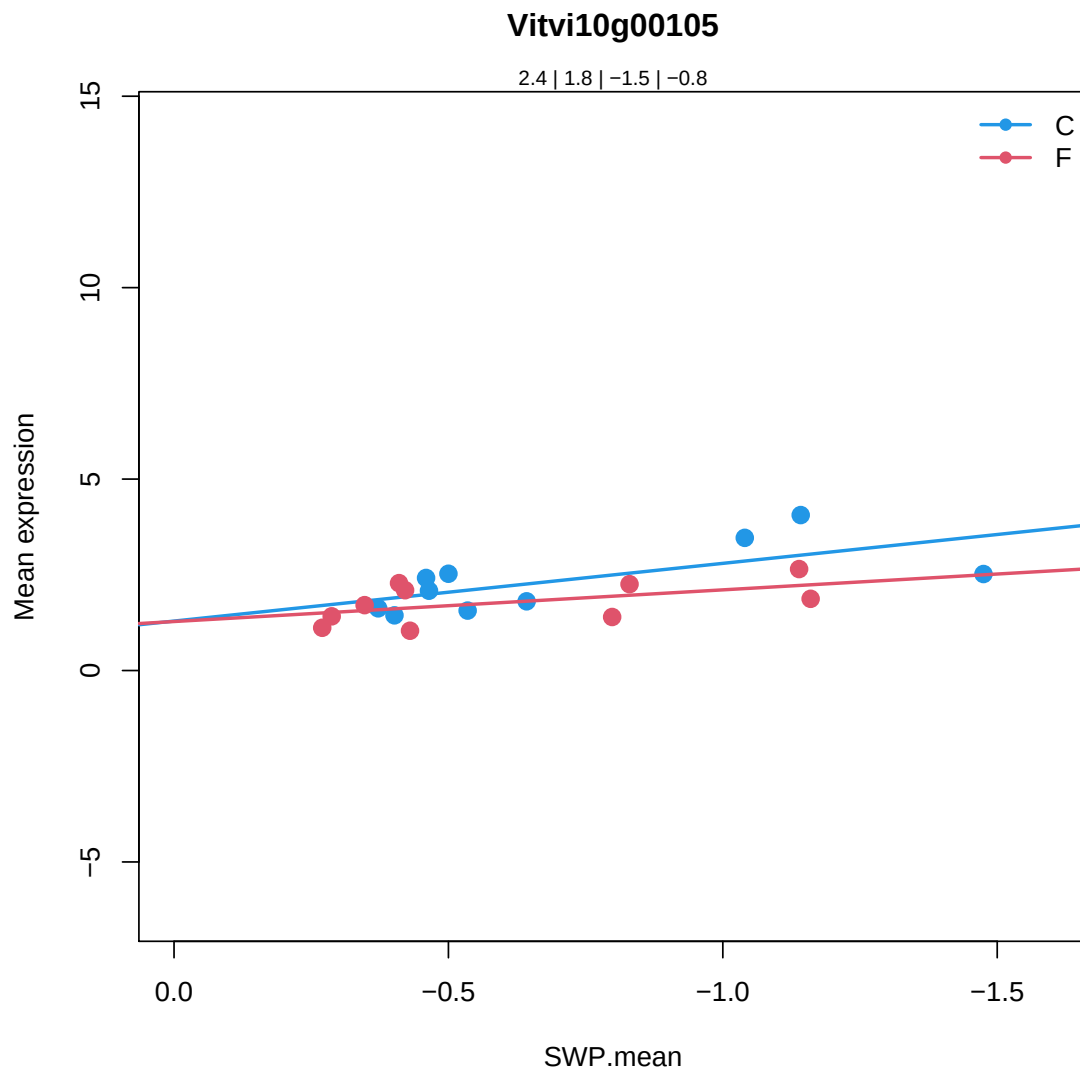
actin cytoskeleton-regulatory complex pan-like protein |

Chr1:18771386-18774385 FORWARD LENGTH=725 |

201606

Coefficients for Vitvi10g00105.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.351261	9.439819e-12	***	1.289609e-11	***
SlopeC	-1.507461	0.006183486	**	0.2647742	
MeanF-MeanC	-0.5679509	0.03504543	*	0.1876062	
SlopeF-SlopeC	0.6804577	0.3674196		0.9999488	



8.1.399 Vitvi01g00353: Type1.0 *

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

Vitvi01g00353

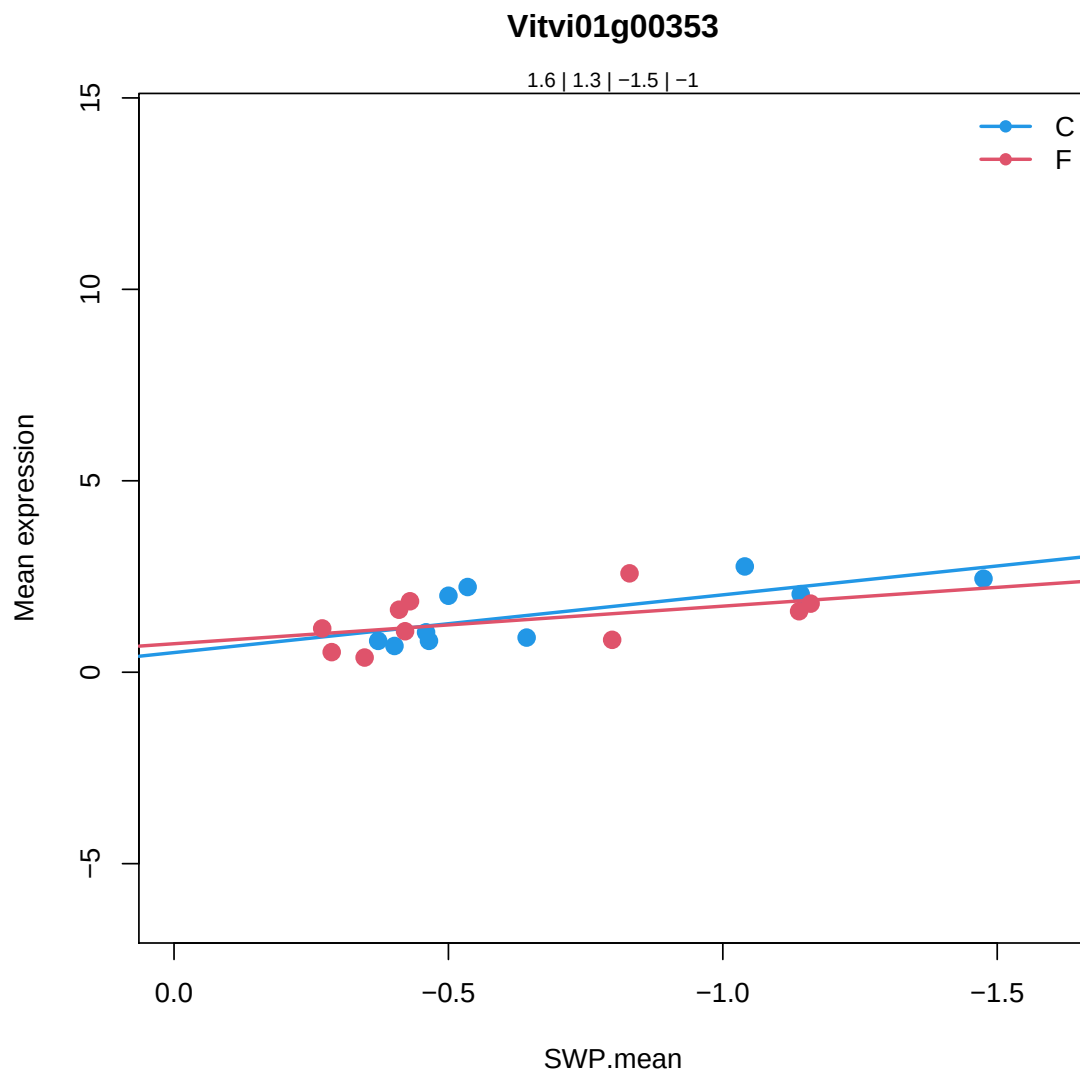
35.2

not assigned.unknown

Receptor-like kinase

Coefficients for Vitvi01g00353.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.5738	1.923832e-08	***	2.328335e-08	***
SlopeC	-1.507999	0.007019784	**	0.2775469	
MeanF-MeanC	-0.2318921	0.3771989		0.7288622	
SlopeF-SlopeC	0.5263084	0.4920685		0.9999488	



8.1.400 Vitvi03g00845: Type1.0 *

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

Vitvi03g00845

29.6

protein.folding

mitochondrial HSO70 2 |

Chr5:2975721-2978508 FORWARD LENGTH=682 |

201606

Vitvi03g00845

20.2.1

stress.abiotic.heat

mitochondrial HSO70 2 |

Chr5:2975721-2978508 FORWARD LENGTH=682 |

201606

Vitvi03g00845

35.2

not assigned.unknown

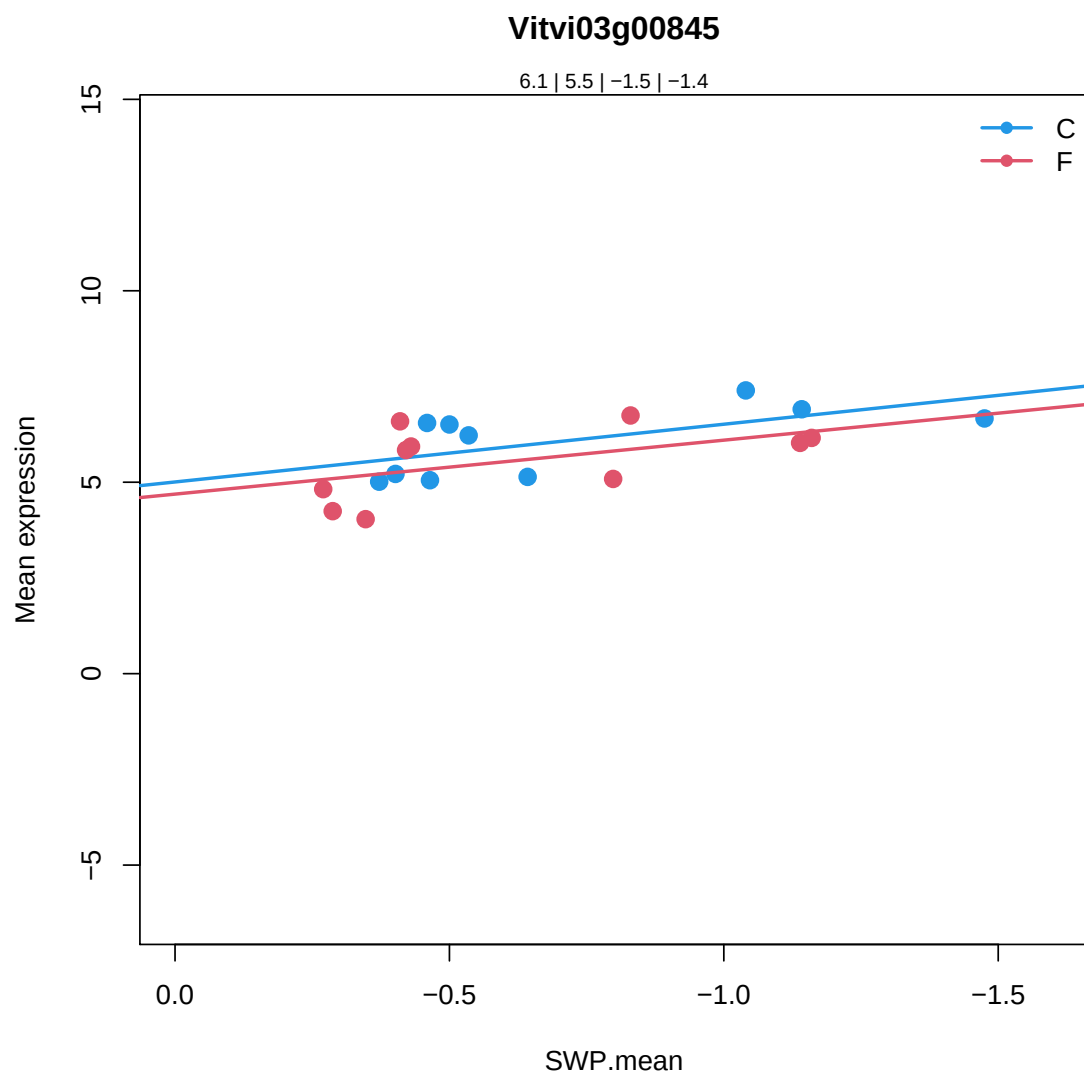
mitochondrial HSO70 2 |

Chr5:2975721-2978508 FORWARD LENGTH=682 |

201606

Coefficients for Vitvi03g00845.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.066659	7.857574e-18	***	2.123872e-17	***
SlopeC	-1.508056	0.02802278	*	0.426079	
MeanF-MeanC	-0.5194915	0.1249078		0.4183355	
SlopeF-SlopeC	0.09892301	0.9182476		0.9999488	



8.1.401 Vitvi12g01692: Type1.0

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

Vitvi12g01692

35.2

not assigned.unknown

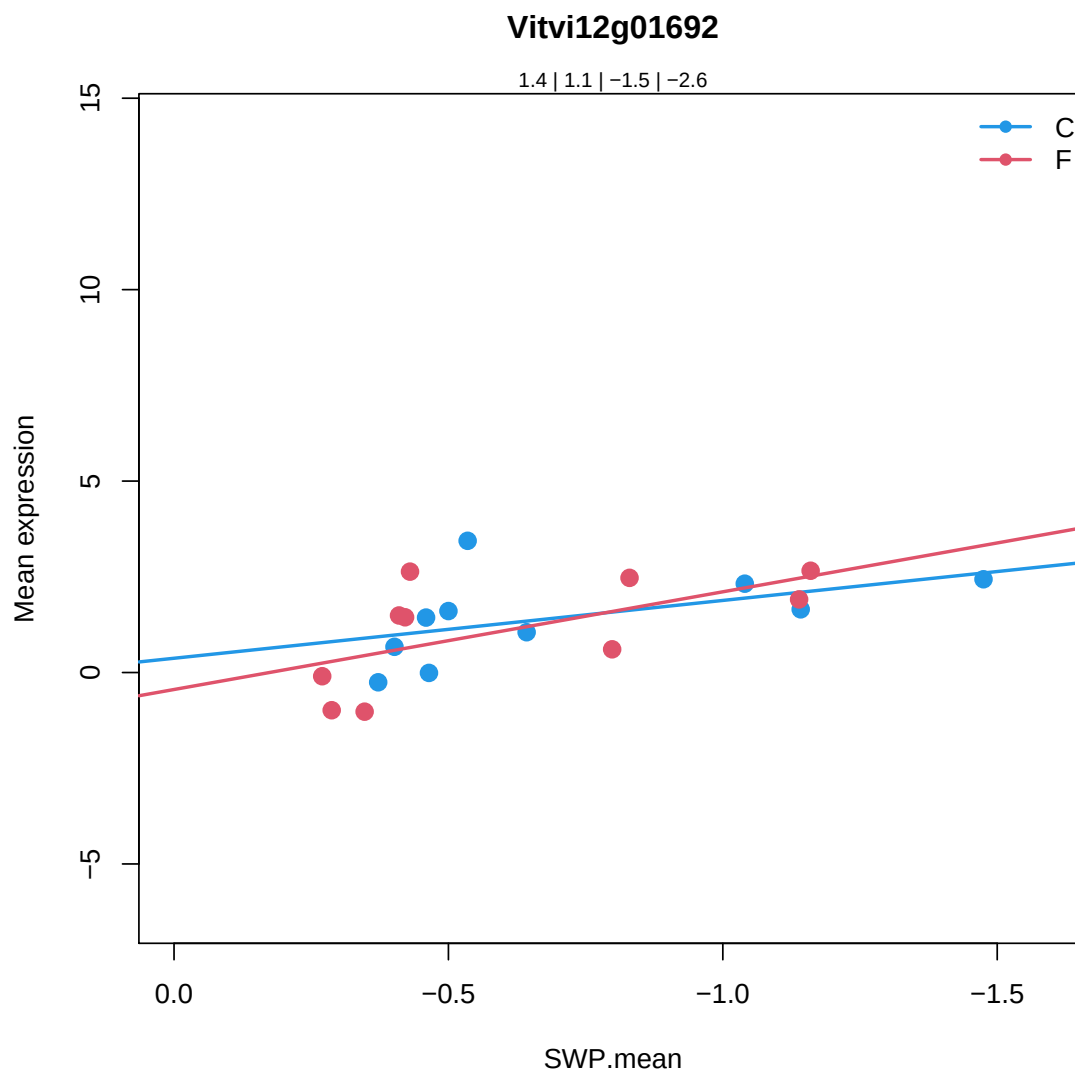
UDP-Glycosyltransferase superfamily protein |

Chr3:7667099-7668556 FORWARD LENGTH=485 |

201606

Coefficients for Vitvi12g01692.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.434333	0.0001584088	***	0.0001742292	***
SlopeC	-1.51009	0.09804829	.	0.6089862	
MeanF-MeanC	-0.3233825	0.4740621		0.7912456	
SlopeF-SlopeC	-1.041733	0.4315123		0.9999488	



8.1.402 Vitvi14g01717: Type1.0

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

Vitvi14g01717

3.1.2.2

minor CHO metabolism.raffinose family.raffinose synthases.putative

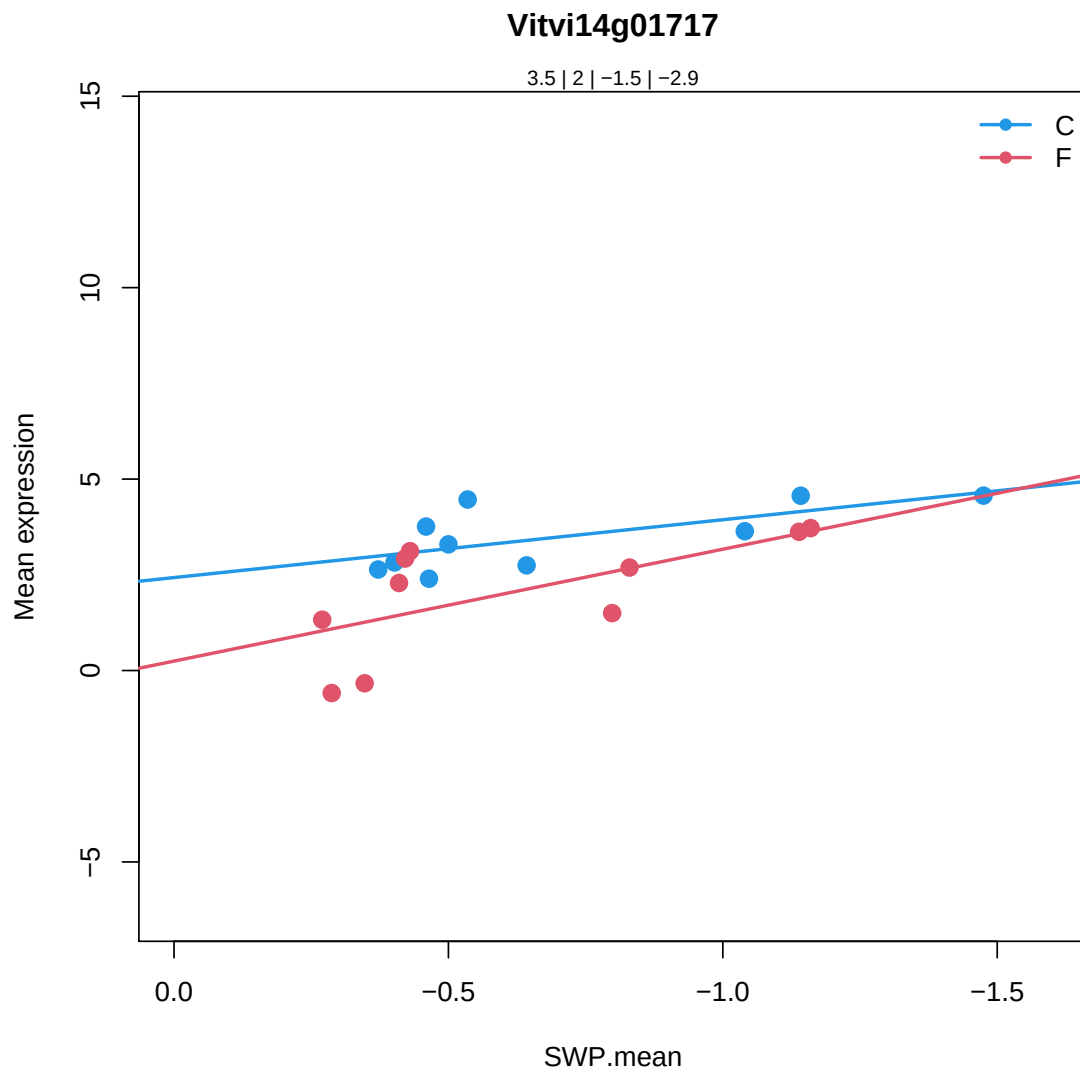
Raffinose synthase family protein |

Chr5:16161720-16165085 FORWARD LENGTH=783 |

201606

Coefficients for Vitvi14g01717.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.48977	2.551646e-11	***	3.423608e-11	***
SlopeC	-1.510356	0.06495838	.	0.5518928	
MeanF-MeanC	-1.463541	0.001266488	**	0.01523584	*
SlopeF-SlopeC	-1.411876	0.2350381		0.9999488	



8.1.403 Vitvi01g02099: Type1.0 *

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

Vitvi01g02099

29.5.11.4.2

protein.degradation.ubiquitin.E3.RING

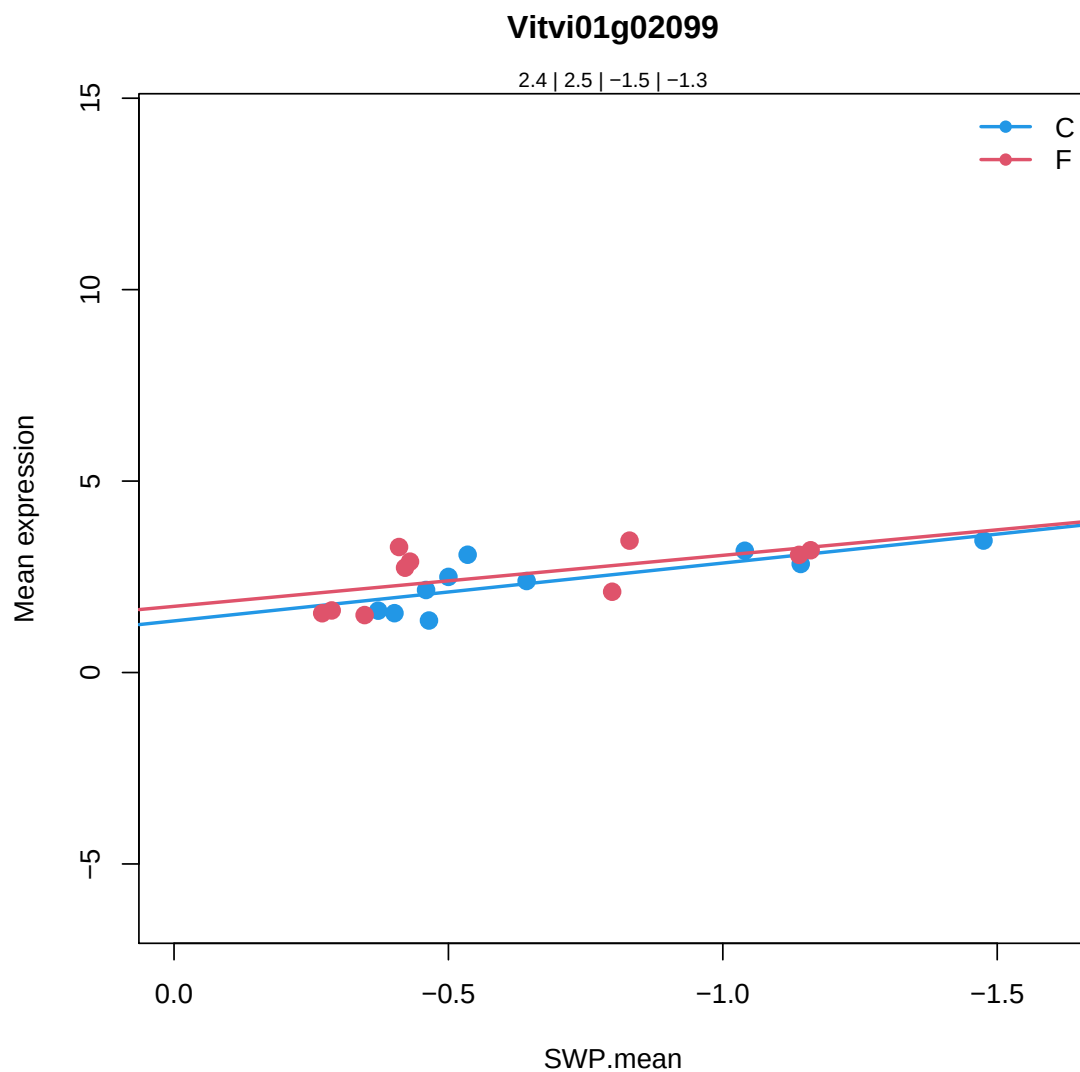
glycosyltransferase family protein (DUF23) |

Chr1:9449812-9451539 REVERSE LENGTH=575 |

201606

Coefficients for Vitvi01g02099.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.410227	4.484603e-12	***	6.208948e-12	***
SlopeC	-1.51117	0.005508617	**	0.2577627	
MeanF-MeanC	0.1298453	0.6072669		0.8620981	
SlopeF-SlopeC	0.1782757	0.8090889		0.9999488	



8.1.404 Vitvi11g00547: Type1.0 *

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

Vitvi11g00547

30.3

signalling.calcium

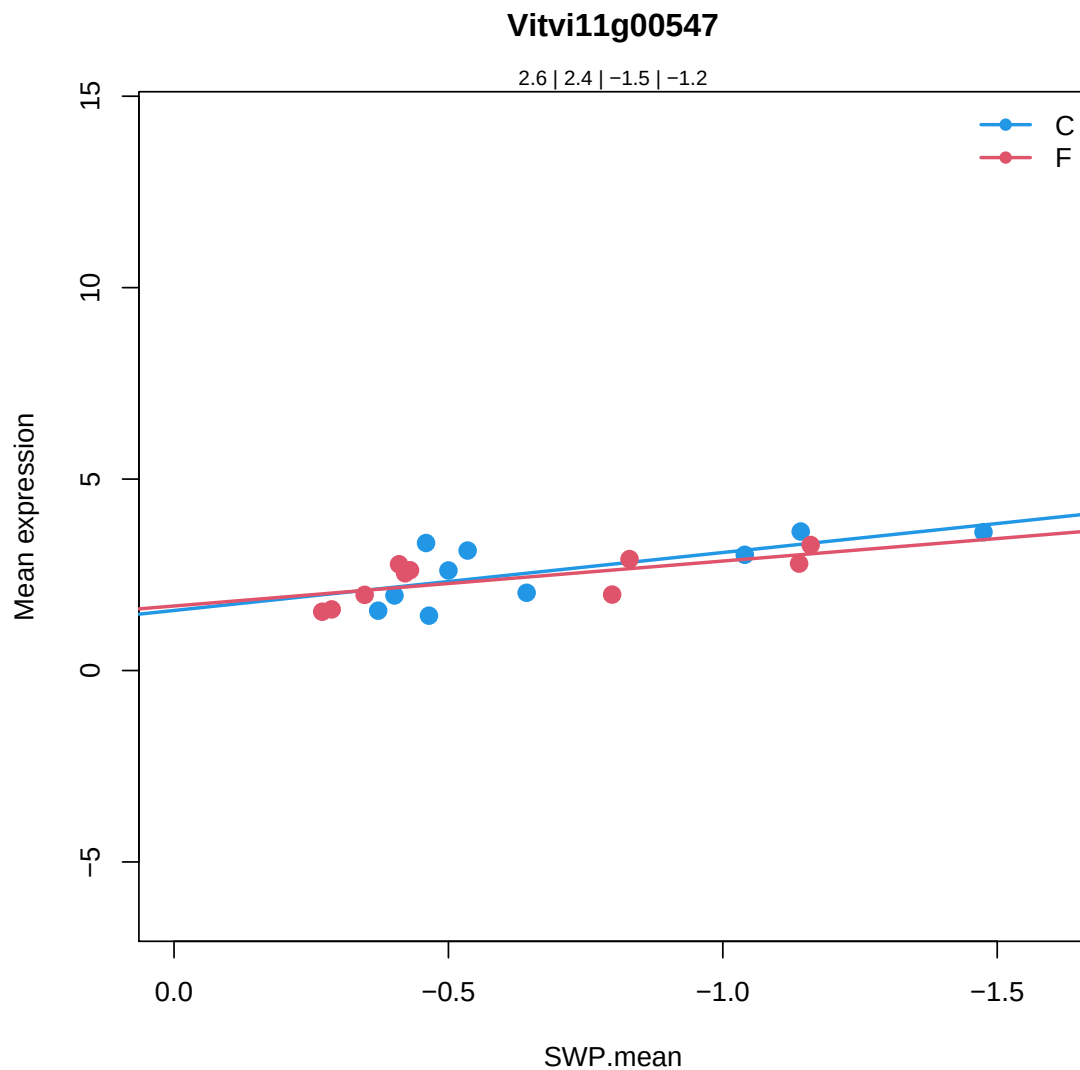
Calcium-dependent lipid-binding (CaLB domain) family protein |

Chr1:1625098-1628940 FORWARD LENGTH=560 |

201606

Coefficients for Vitvi11g00547.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.632836	4.518668e-13	***	6.635216e-13	***
SlopeC	-1.514086	0.004394116	**	0.2399107	
MeanF-MeanC	-0.2323474	0.347272		0.7068069	
SlopeF-SlopeC	0.3399814	0.6359192		0.9999488	



8.1.405 Vitvi04g00962: Type1.0 *

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

Vitvi04g00962

35.2

not assigned.unknown

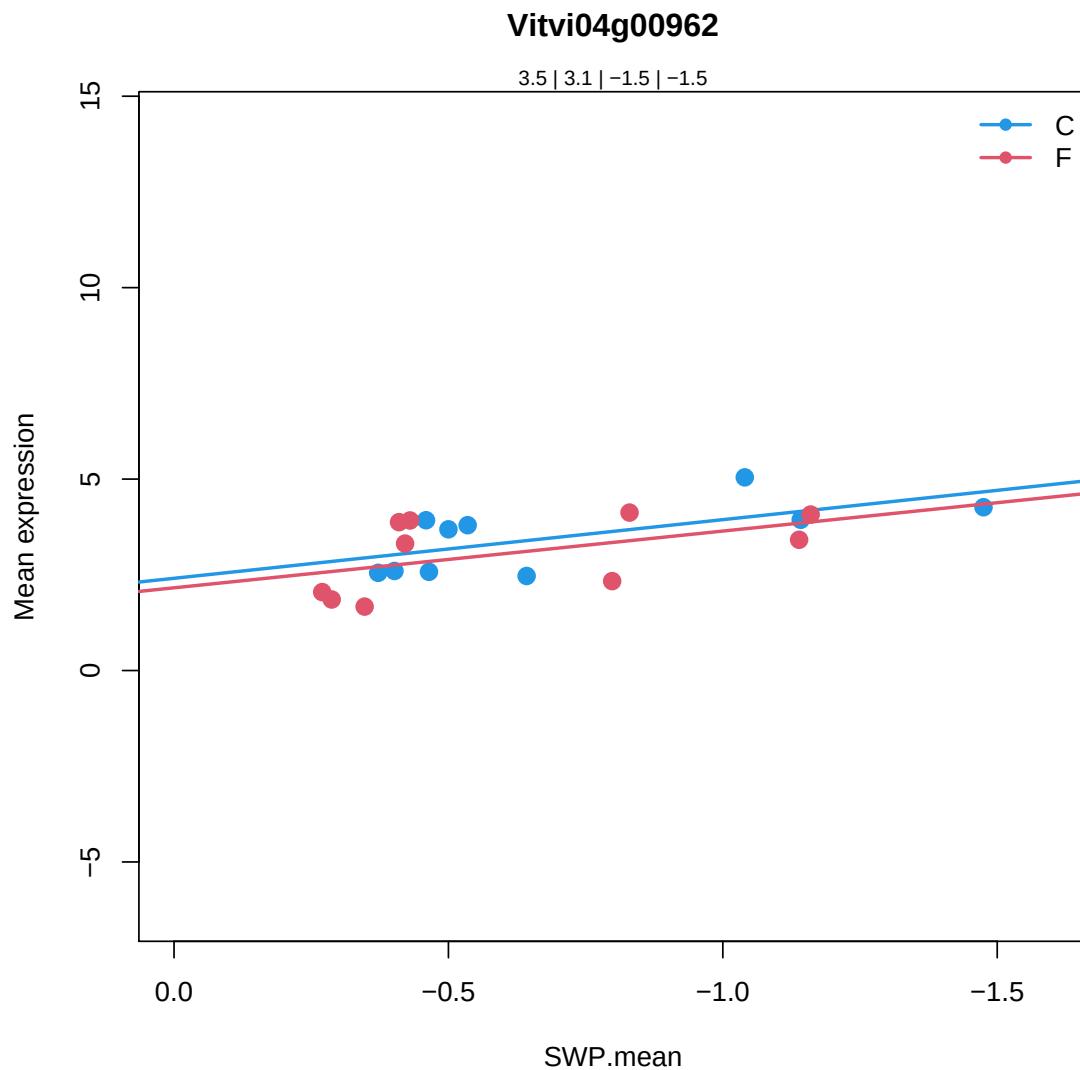
hikeshi-like protein |

Chr1:24600356-24601027 REVERSE LENGTH=190 |

201606

Coefficients for Vitvi04g00962.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.485224	8.556232e-13	***	1.233463e-12	***
SlopeC	-1.531557	0.02812359	*	0.4263731	
MeanF-MeanC	-0.4222037	0.2152382		0.5627205	
SlopeF-SlopeC	0.0494308	0.9597476		0.9999488	



8.1.406 Vitvi06g01354: Type1.0 *

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

Vitvi06g01354

31.5.1

cell.cell death.plants

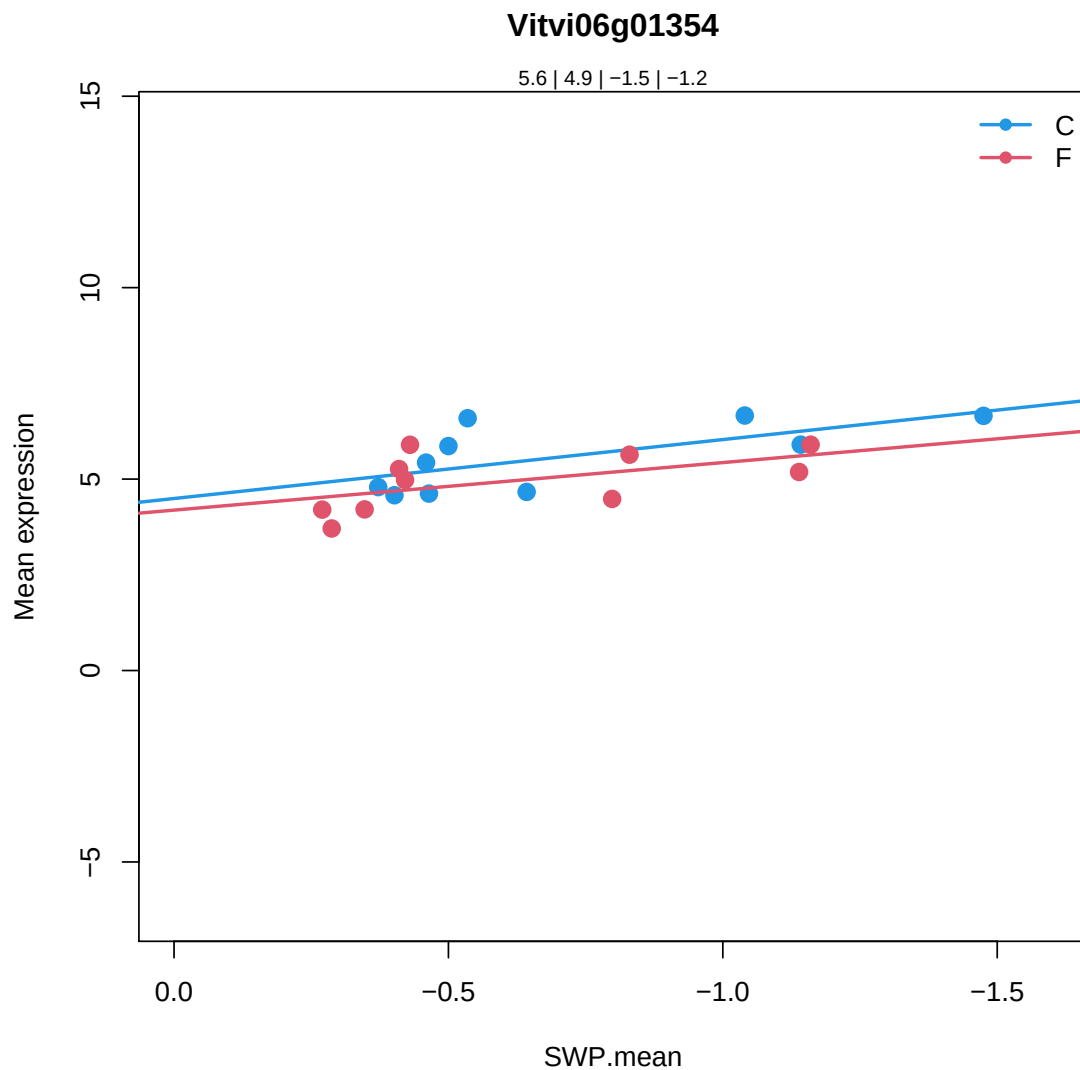
Pheophorbide a oxygenase family protein with Rieske 2Fe-2S domain-cont

Chr3:16383858-16386204 FORWARD LENGTH=537 |

201606

Coefficients for Vitvi06g01354.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.574733	3.314337e-18	***	9.858923e-18	***
SlopeC	-1.539195	0.01245439	*	0.3261682	
MeanF-MeanC	-0.6289323	0.03947009	*	0.2046966	
SlopeF-SlopeC	0.2973165	0.7267595		0.9999488	



8.1.407 Vitvi12g00913: Type1.0 *

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

Vitvi12g00913

27.1.1

RNA.processing.splicing

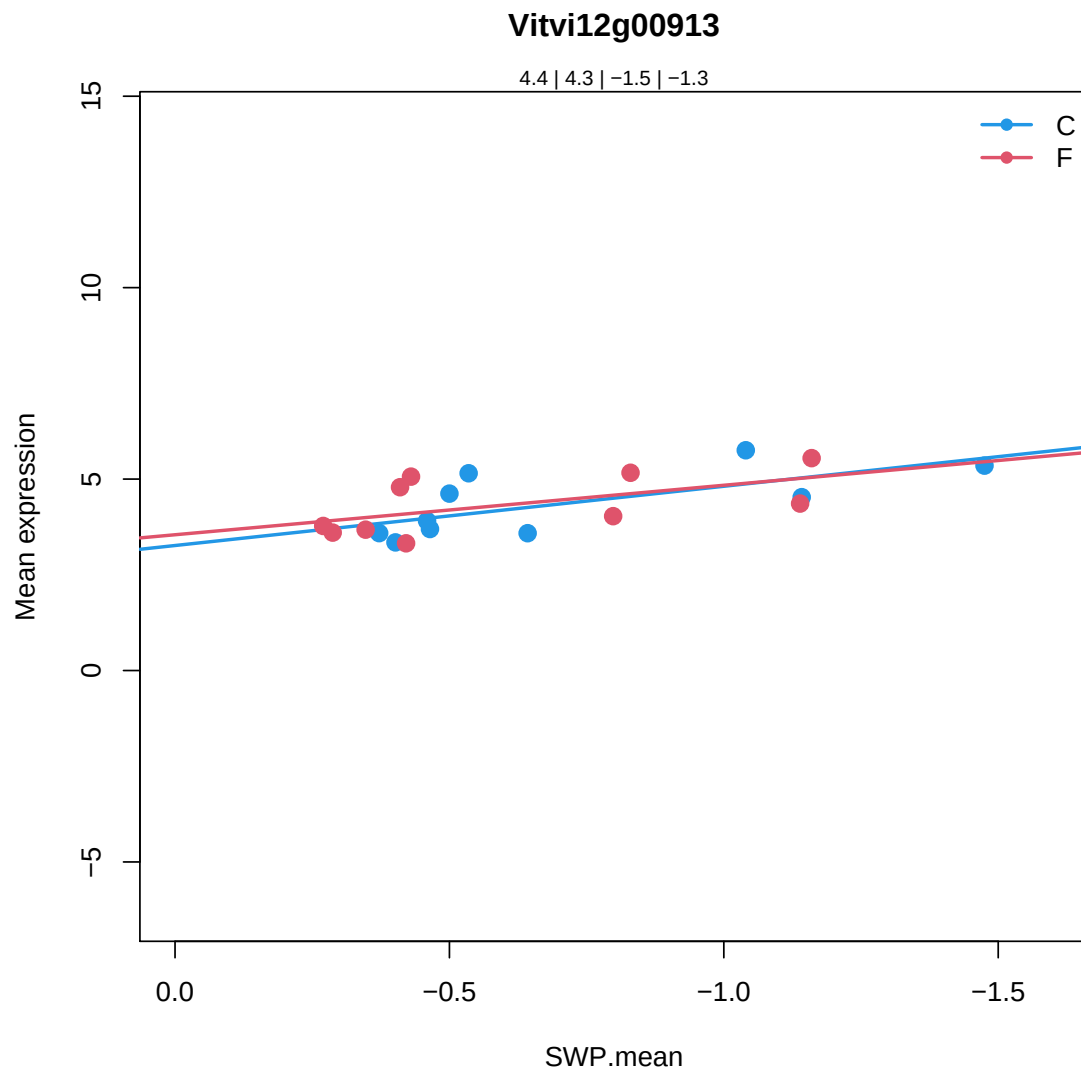
serine/arginine-rich splicing factor-like protein%2C putative |

Chr5:25681849-25683553 REVERSE LENGTH=303 |

201606

Coefficients for Vitvi12g00913.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.352667	2.795362e-16	***	5.644811e-16	***
SlopeC	-1.547135	0.00977034	**	0.3009465	
MeanF-MeanC	-0.01933659	0.9450567		0.9857335	
SlopeF-SlopeC	0.2545257	0.7569603		0.9999488	



8.1.408 Vitvi13g00062: Type1.0 *

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

Vitvi13g00062

35.2

not assigned.unknown

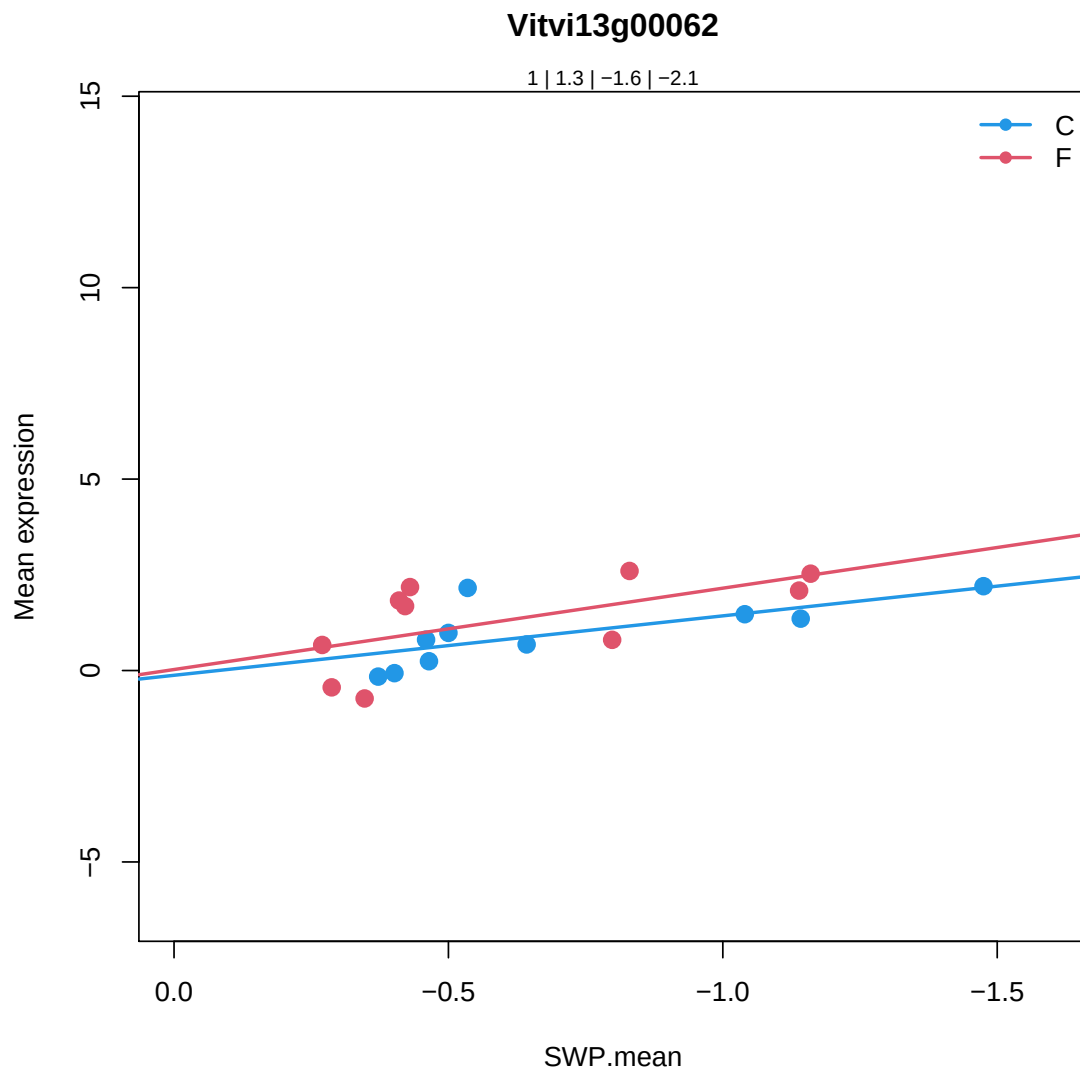
2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein

Chr3:3492986-3494599 REVERSE LENGTH=371 |

201606

Coefficients for Vitvi13g00062.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.9666478	0.0006300303	***	0.0006849934	***
SlopeC	-1.552106	0.03105912	*	0.4322019	
MeanF-MeanC	0.3537859	0.312252		0.6758693	
SlopeF-SlopeC	-0.572422	0.5733593		0.9999488	

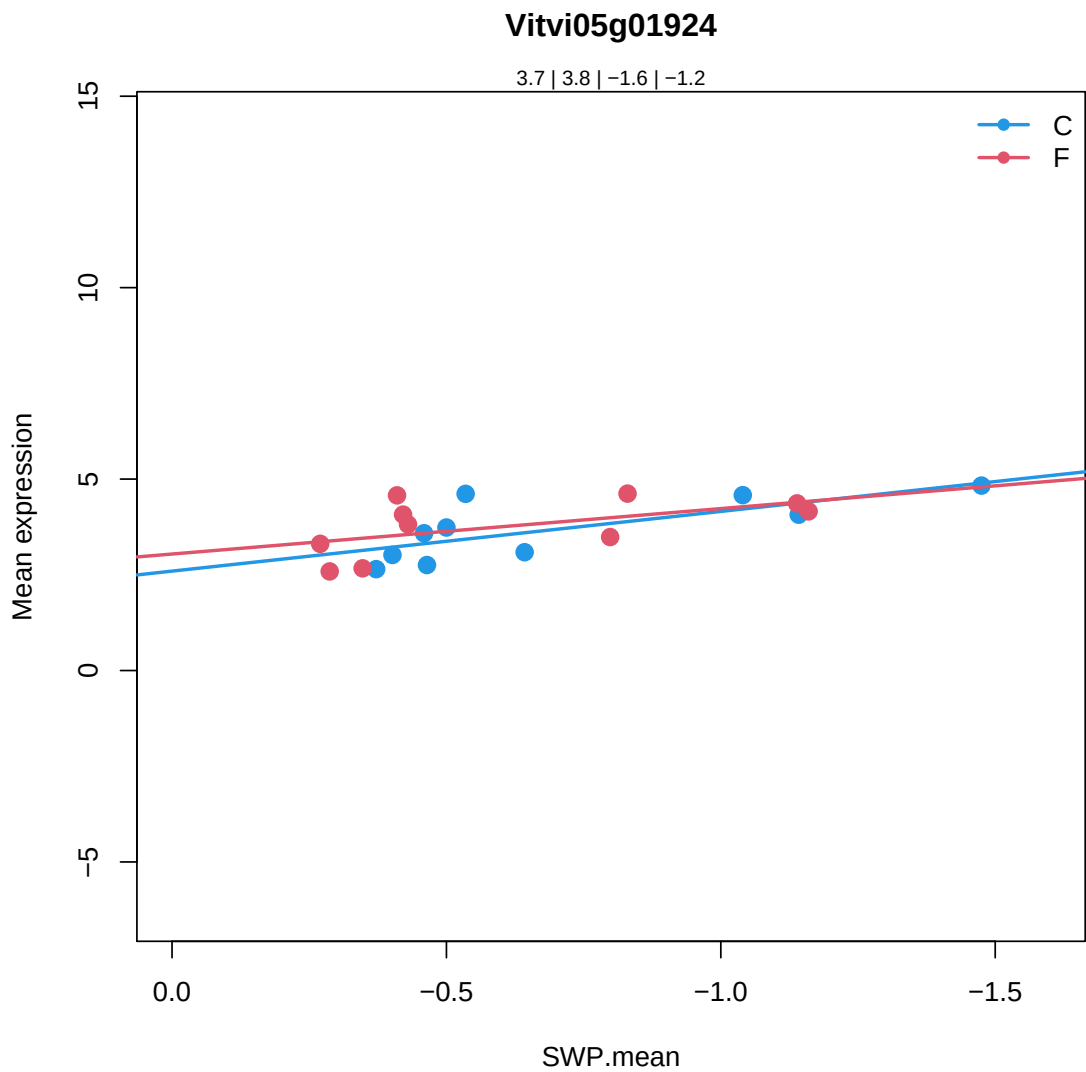


8.1.409 Vitvi05g01924: Type1.0 *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
Vitvi05g01924
17.5.1
hormone metabolism.ethylene.synthesis-degradation
2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protei
Chr1:842895-844158 REVERSE LENGTH=379 |
201606
```

Coefficients for Vitvi05g01924.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.692352	2.735716e-15	***	4.878646e-15	***
SlopeC	-1.559202	0.006502964	**	0.2686129	
MeanF-MeanC	0.07347336	0.7826008		0.9384607	
SlopeF-SlopeC	0.372102	0.633784		0.9999488	



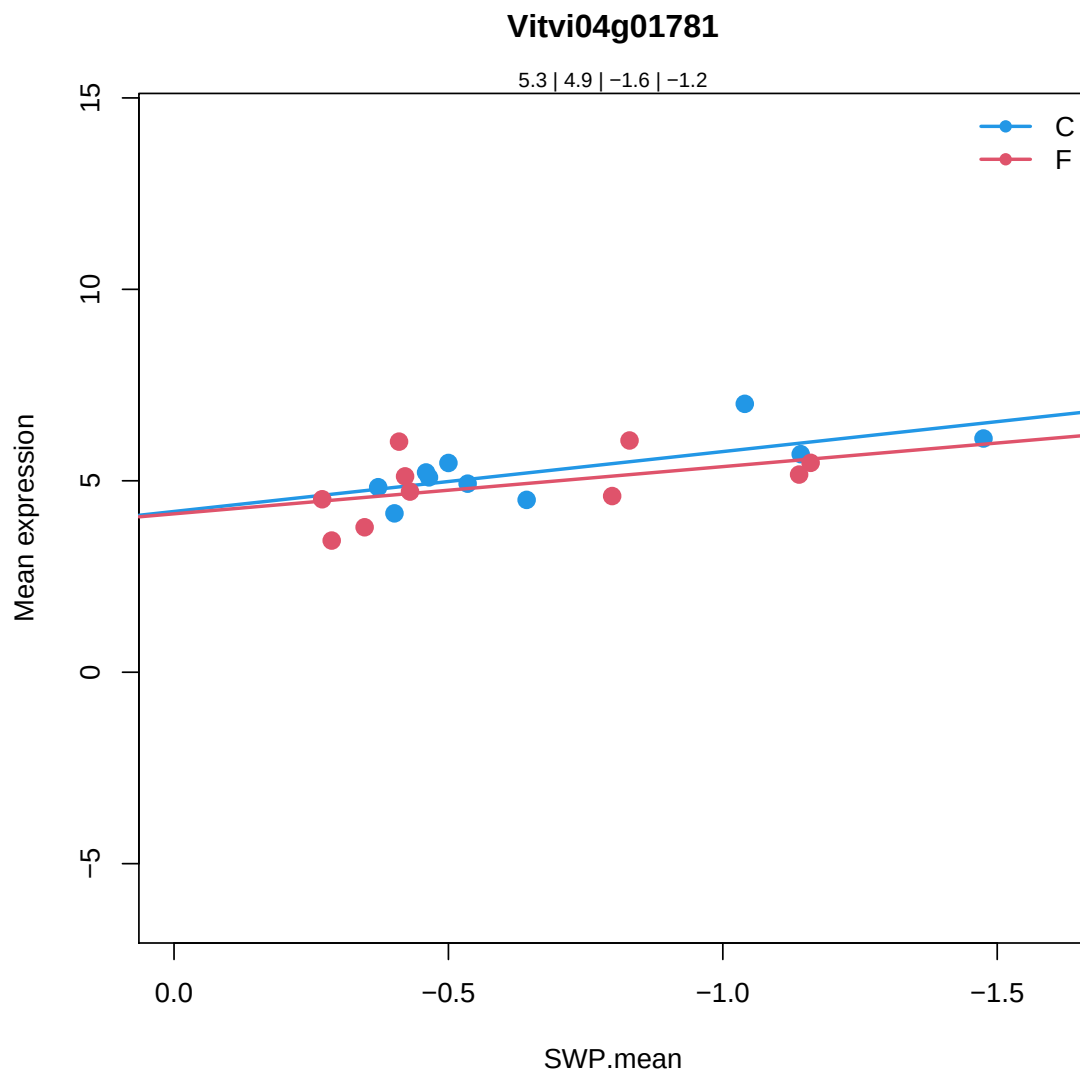
8.1.410 Vitvi04g01781: Type1.0 *

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

```
Vitvi04g01781
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi04g01781.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.298749	1.71787e-17	***	4.311506e-17	***
SlopeC	-1.56403	0.0134099	*	0.3305597	
MeanF-MeanC	-0.410543	0.1783045		0.5127769	
SlopeF-SlopeC	0.3309496	0.7053918		0.9999488	



8.1.411 Vitvi19g00206: Type1.0 *

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

Vitvi19g00206

26.19

misc.plastocyanin-like

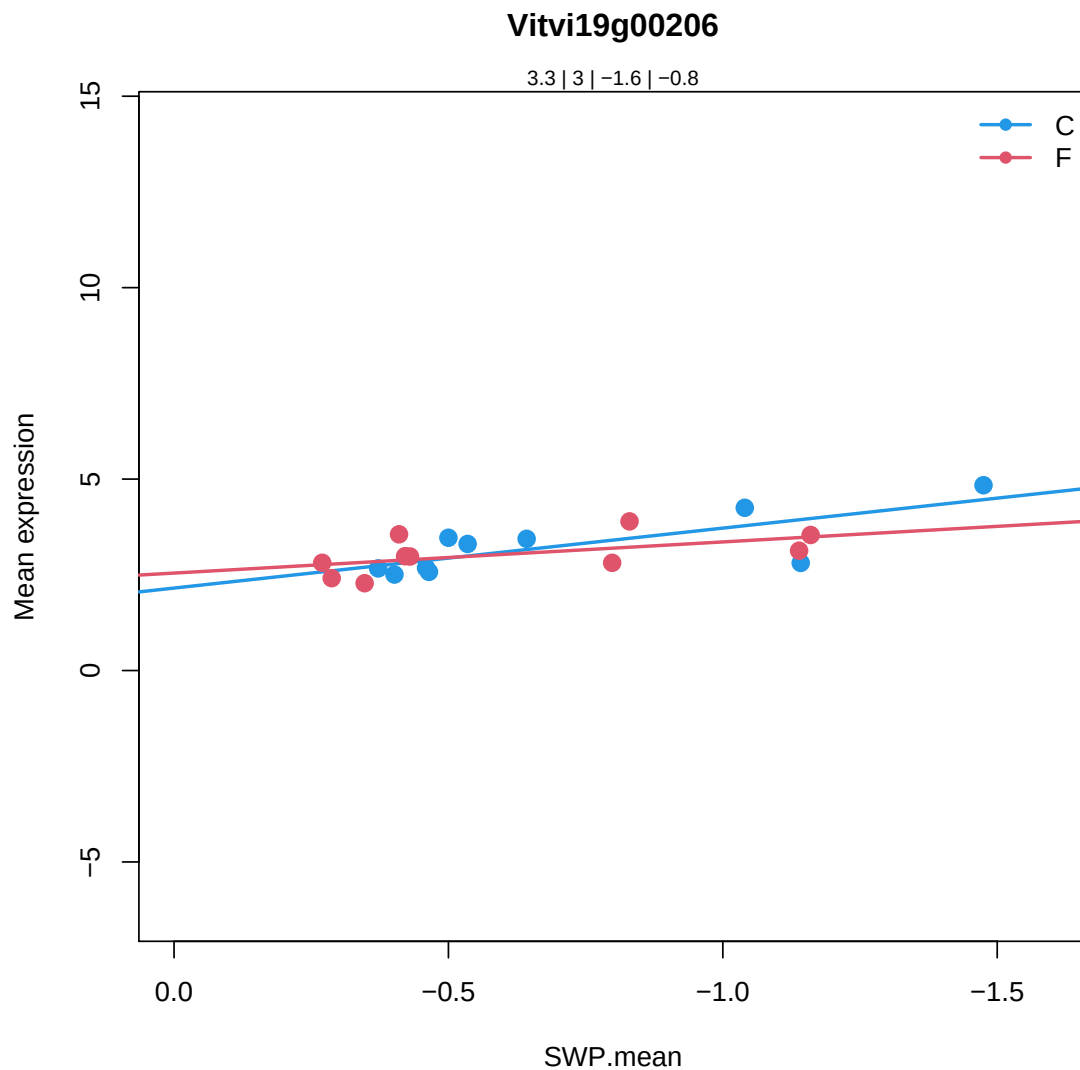
early nodulin-like protein 2 |

Chr4:13750668-13751819 REVERSE LENGTH=349 |

201606

Coefficients for Vitvi19g00206.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.25415	1.070039e-15	***	1.995782e-15	***
SlopeC	-1.565643	0.001658523	**	0.1556102	
MeanF-MeanC	-0.2137466	0.3449556		0.7046118	
SlopeF-SlopeC	0.7518545	0.258751		0.9999488	



8.1.412 Vitvi02g00991: Type1.0 *

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

Vitvi02g00991

35.2

not assigned.unknown

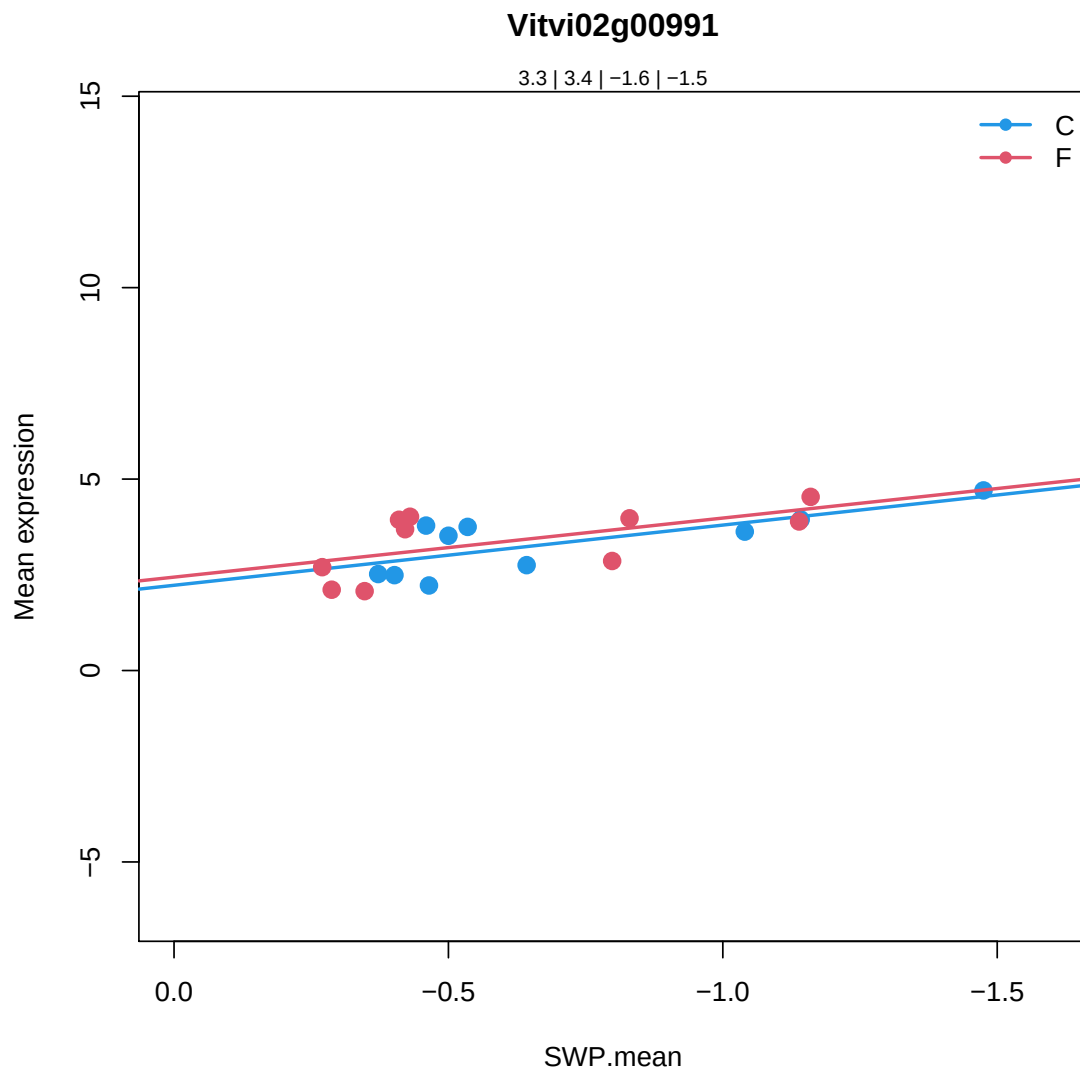
UDP-Glycosyltransferase superfamily protein |

Chr2:15417618-15419108 REVERSE LENGTH=496 |

201606

Coefficients for Vitvi02g00991.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.33156	5.382133e-14	***	8.43976e-14	***
SlopeC	-1.572287	0.008310277	**	0.2862911	
MeanF-MeanC	0.04742068	0.8646699		0.964386	
SlopeF-SlopeC	0.02977909	0.9708319		0.9999488	



8.1.413 Vitvi01g01299: Type1.0 *

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

Vitvi01g01299

30.4

signalling.phosphoinositides

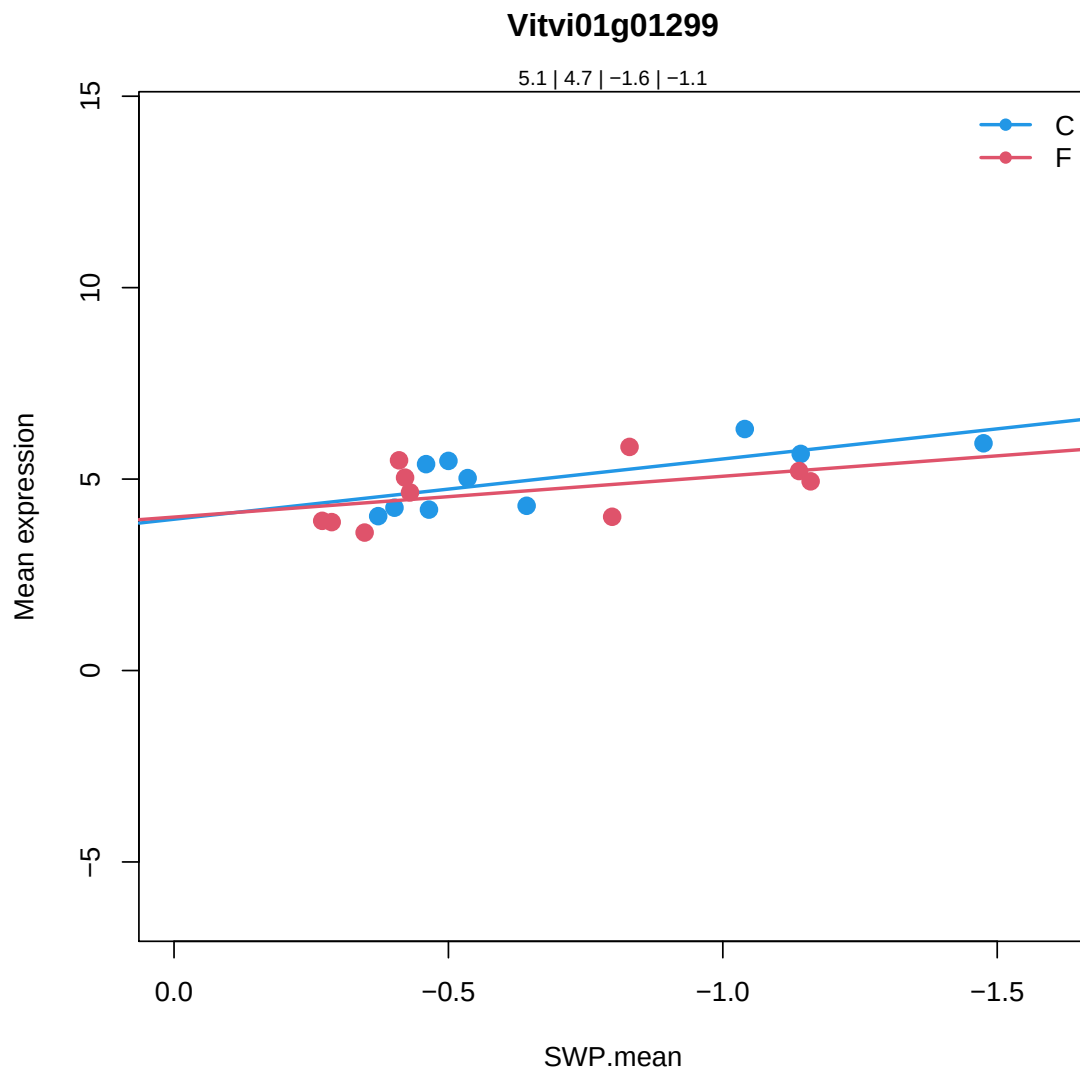
phosphoinositide 4-kinase gamma 7 |

Chr2:1186199-1188151 FORWARD LENGTH=650 |

201606

Coefficients for Vitvi01g01299.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.057904	1.172434e-17	***	3.042262e-17	***
SlopeC	-1.573904	0.008567631	**	0.2903326	
MeanF-MeanC	-0.4005521	0.1618639		0.4862297	
SlopeF-SlopeC	0.5075886	0.5372644		0.9999488	



8.1.414 Vitvi15g00816: Type1.0

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

Vitvi15g00816

35.2

not assigned.unknown

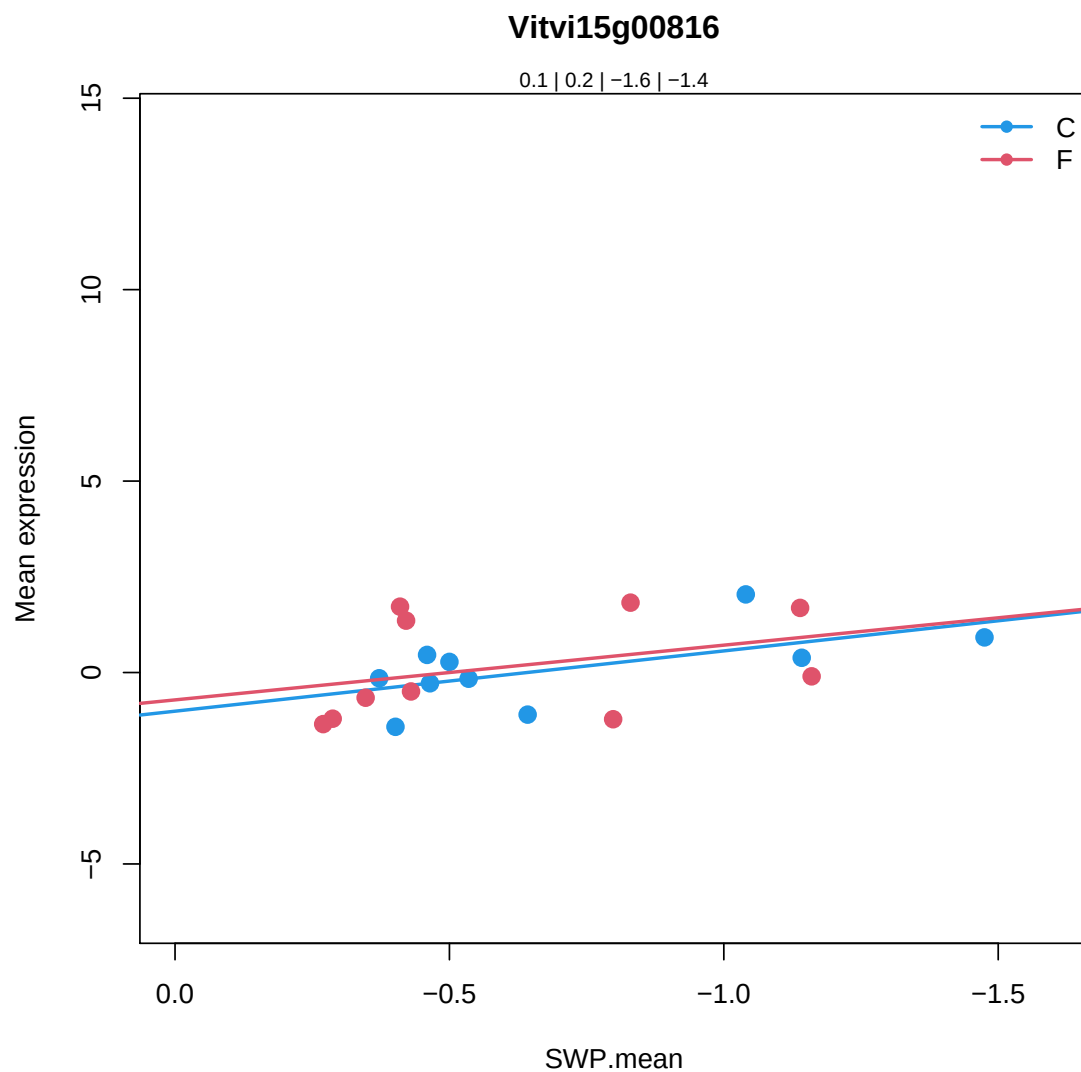
FASCICLIN-like arabinogalactan protein 8 |

Chr2:18742797-18744059 REVERSE LENGTH=420 |

201606

Coefficients for Vitvi15g00816.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.09682662	0.7589199		0.7633774	
SlopeC	-1.574329	0.08327988	.	0.5813429	
MeanF-MeanC	0.05920581	0.89434		0.9721746	
SlopeF-SlopeC	0.1447743	0.9116766		0.9999488	



8.1.415 Vitvi04g00178: Type1.0 *

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

Vitvi04g00178

26.3.5

misc.gluco-, galacto- and mannosidases.glycosyl hydrolase family 5

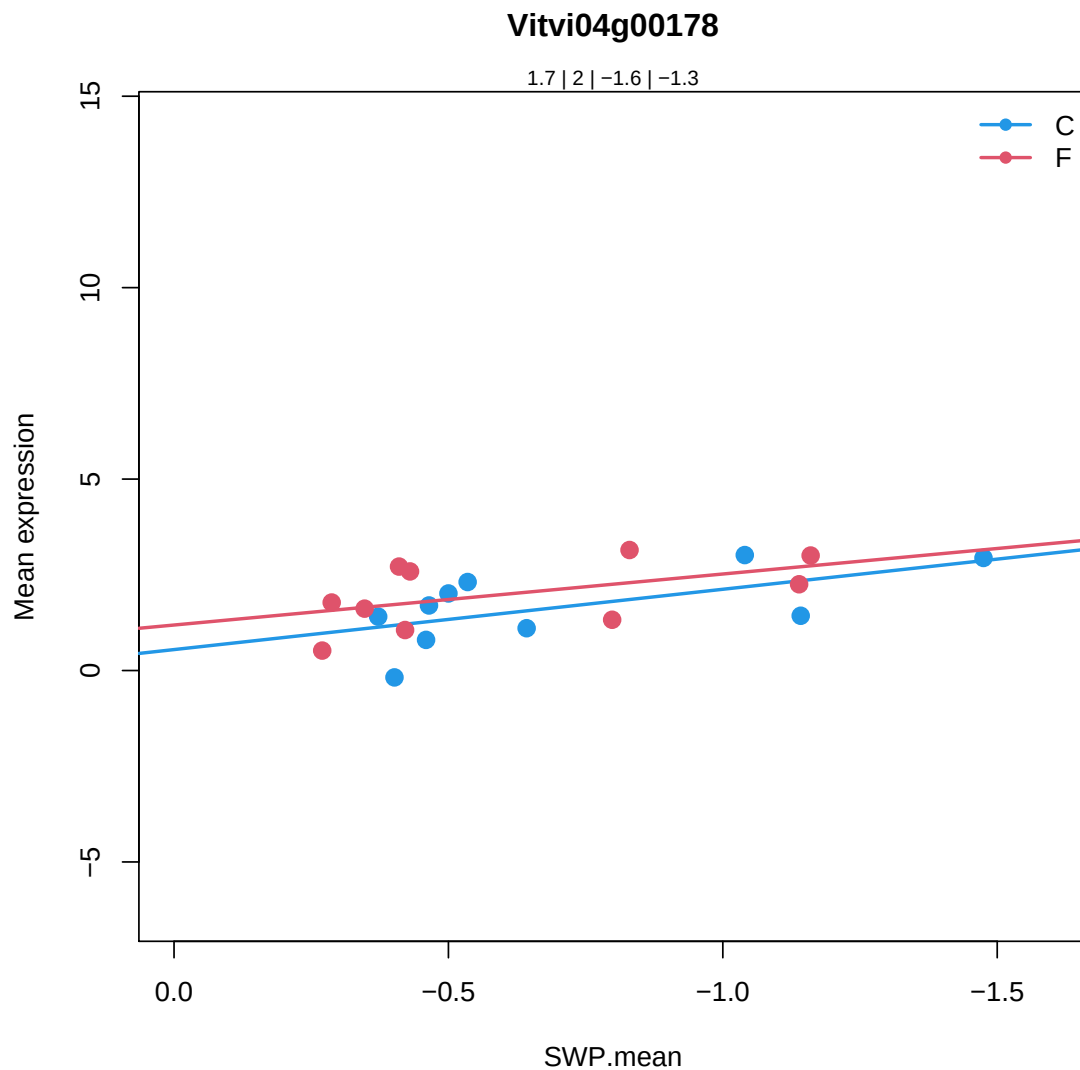
alpha/beta-Hydrolases superfamily protein |

Chr4:16000282-16001450 FORWARD LENGTH=218 |

201606

Coefficients for Vitvi04g00178.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.654019	5.082719e-07	***	5.91335e-07	***
SlopeC	-1.575118	0.02462149	*	0.4057089	
MeanF-MeanC	0.3461239	0.3076938		0.6711319	
SlopeF-SlopeC	0.2428666	0.8046557		0.9999488	



8.1.416 Vitvi12g02044: Type1.0

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

Vitvi12g02044

35.1

not assigned.no ontology

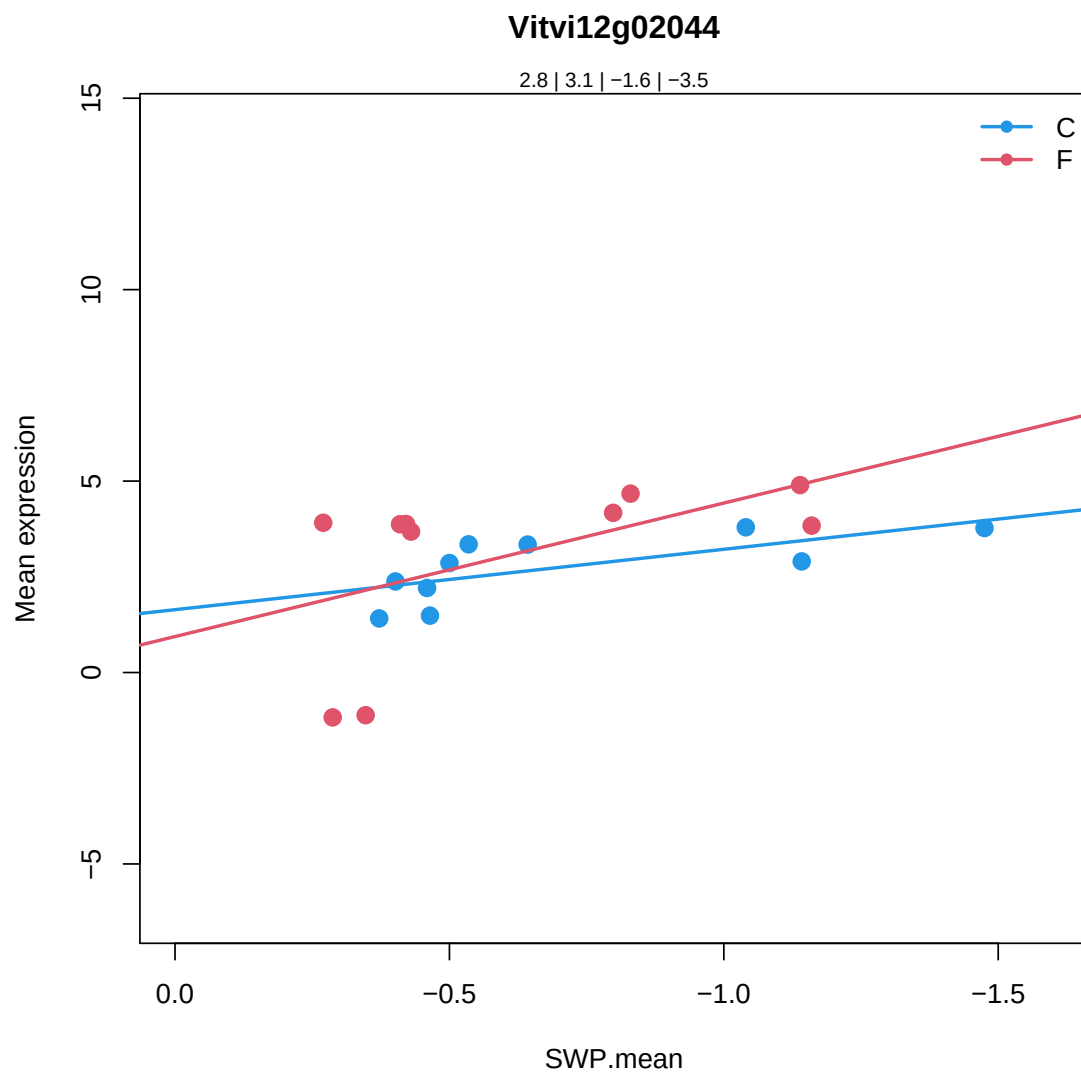
Octicosapeptide/Phox/Bemlp family protein |

Chr5:20306637-20307583 REVERSE LENGTH=288 |

201606

Coefficients for Vitvi12g02044.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.750286	1.457791e-06	***	1.676322e-06	***
SlopeC	-1.577251	0.189024		0.7197362	
MeanF-MeanC	0.3127457	0.6021179		0.8612137	
SlopeF-SlopeC	-1.909279	0.2821137		0.9999488	



8.1.417 Vitvi07g03083: Type1.0

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

Vitvi07g03083

16.2.1.10

secondary metabolism.phenylpropanoids.lignin biosynthesis.CAD

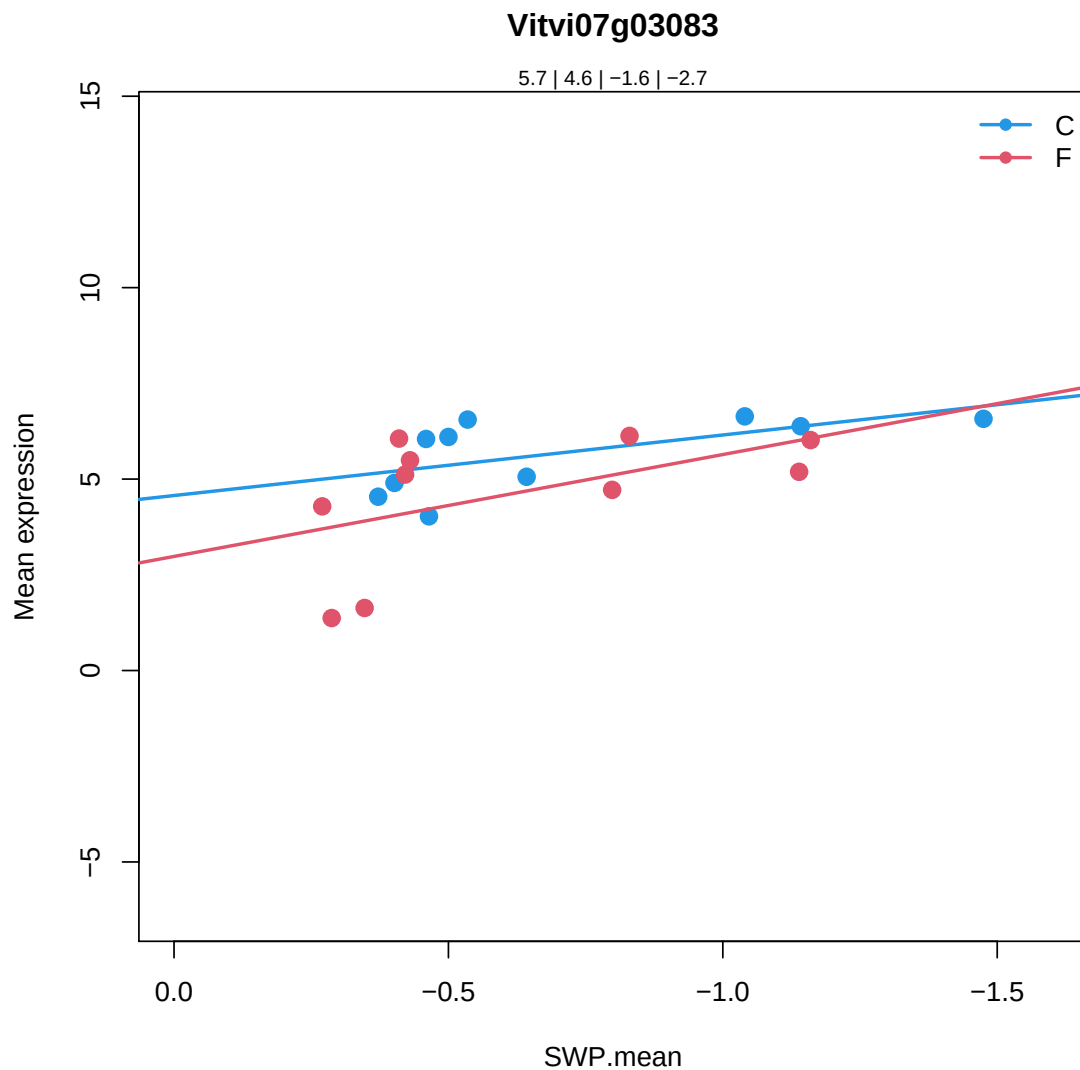
cinnamyl alcohol dehydrogenase 7 |

Chr4:17852670-17854302 FORWARD LENGTH=357 |

201606

Coefficients for Vitvi07g03083.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.681929	1.478938e-13	***	2.242536e-13	***
SlopeC	-1.581192	0.1177783		0.6341652	
MeanF-MeanC	-1.080877	0.03958276	*	0.204845	
SlopeF-SlopeC	-1.079921	0.4626984		0.9999488	



8.1.418 Vitvi10g02082: Type1.0 *

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

Vitvi10g02082

35.2

not assigned.unknown

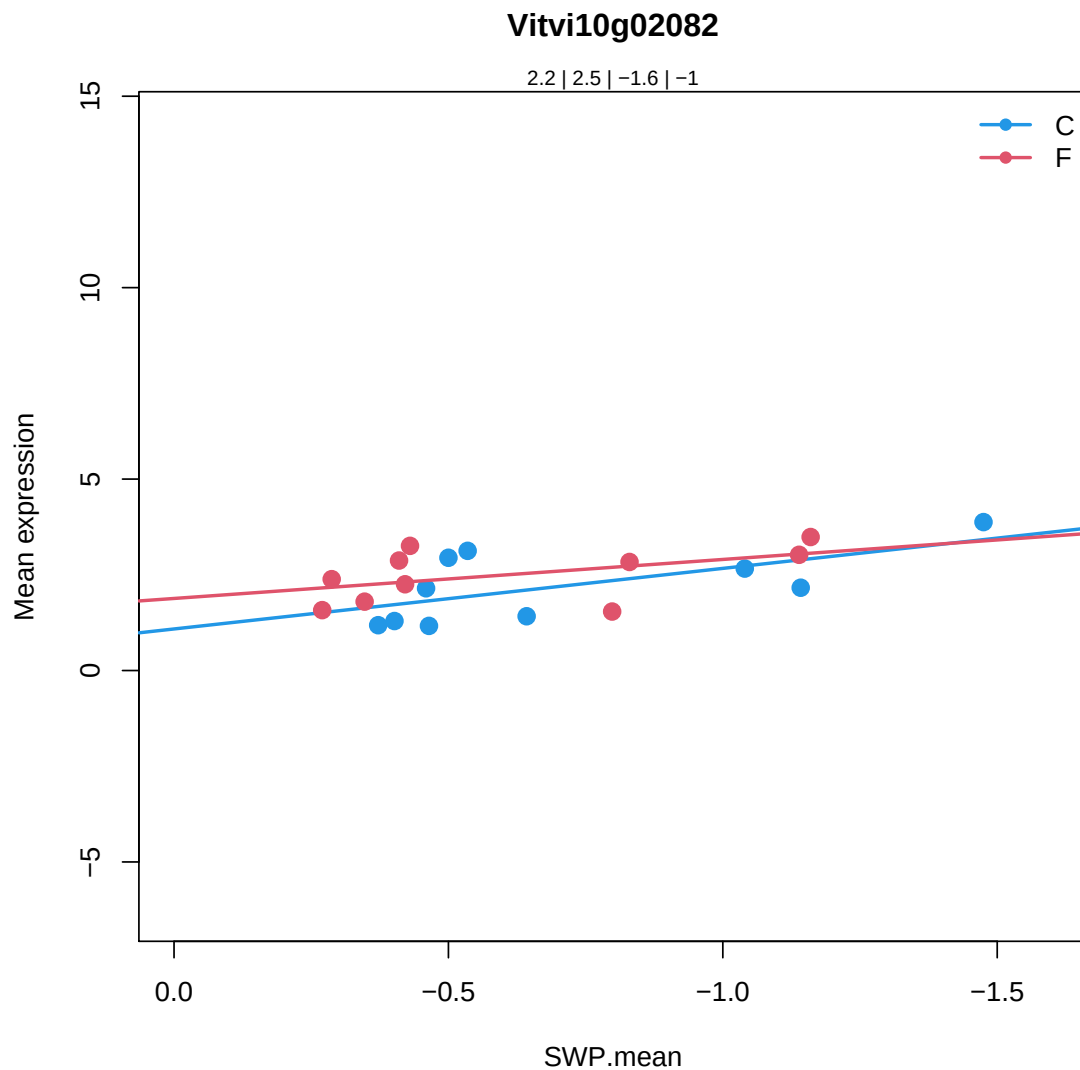
E3 ubiquitin-protein ligase |

Chr3:6965671-6967102 FORWARD LENGTH=425 |

201606

Coefficients for Vitvi10g02082.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.197741	6.31932e-10	***	8.025252e-10	***
SlopeC	-1.581865	0.01264068	*	0.3271124	
MeanF-MeanC	0.3049398	0.3135507		0.6760392	
SlopeF-SlopeC	0.5631331	0.5220186		0.9999488	



8.1.419 Vitvi14g02674: Type1.0 *

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

Vitvi14g02674

27.3.50

RNA.regulation of transcription.general transcription

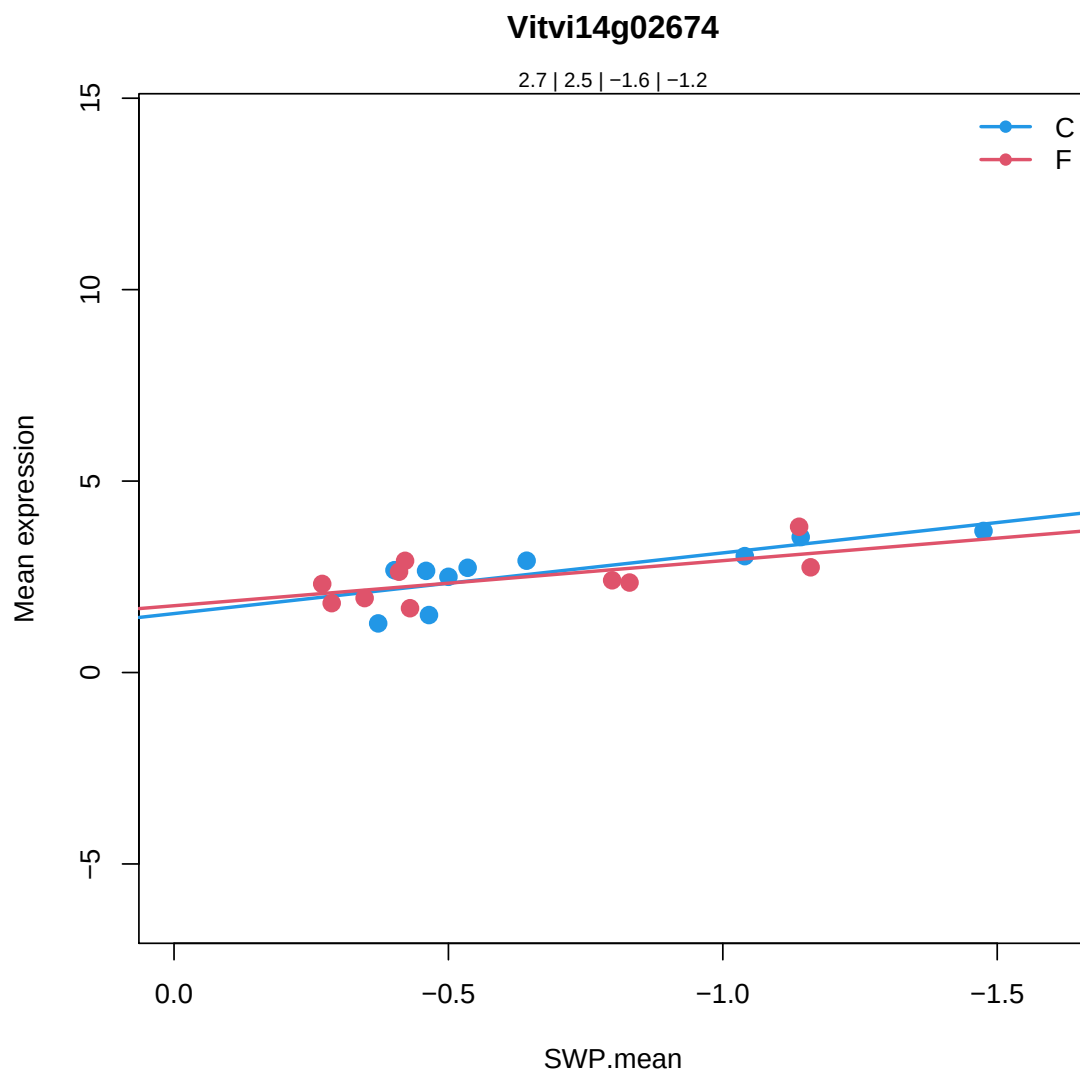
RNA-directed DNA polymerase (reverse transcriptase)-related family pro

Chr3:8789309-8790907 FORWARD LENGTH=532 |

201606

Coefficients for Vitvi14g02674.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.654027	8.609237e-14	***	1.328023e-13	***
SlopeC	-1.58514	0.00166598	**	0.1556102	
MeanF-MeanC	-0.1927377	0.3995015		0.7442687	
SlopeF-SlopeC	0.4082367	0.5405994		0.9999488	



8.1.420 Vitvi19g01702: Type1.0 *

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

Vitvi19g01702

29.5.7

protein.degradation.metalloprotease

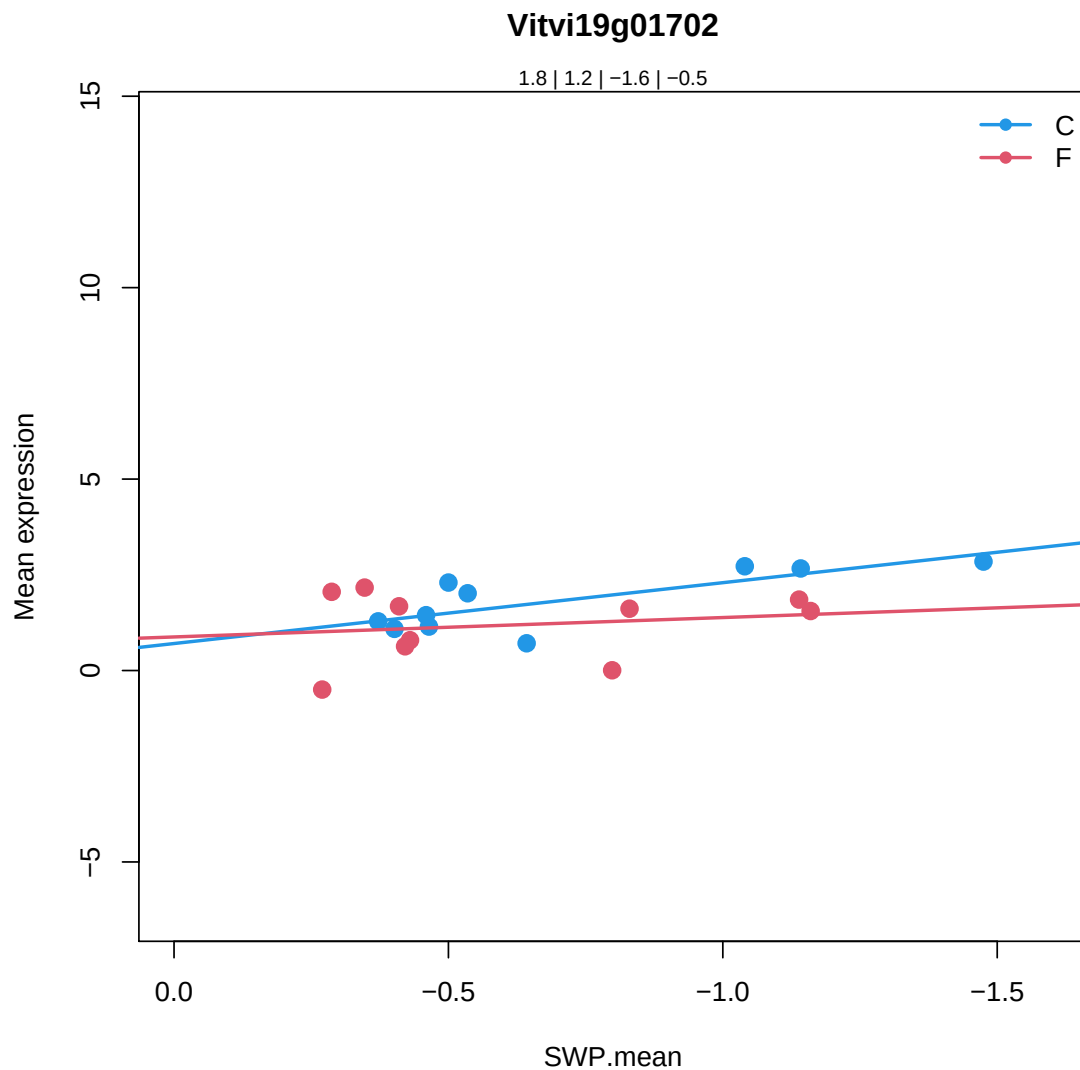
FTSH protease 12 |

Chr1:29926976-29931991 FORWARD LENGTH=963 |

201606

Coefficients for Vitvi19g01702.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.82224	5.052243e-08	***	6.040183e-08	***
SlopeC	-1.589261	0.01804896	*	0.3612388	
MeanF-MeanC	-0.636932	0.05619573	.	0.2579926	
SlopeF-SlopeC	1.082426	0.2541845		0.9999488	



8.1.421 Vitvi03g00766: Type1.0 *

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

Vitvi03g00766

35.1

not assigned.no ontology

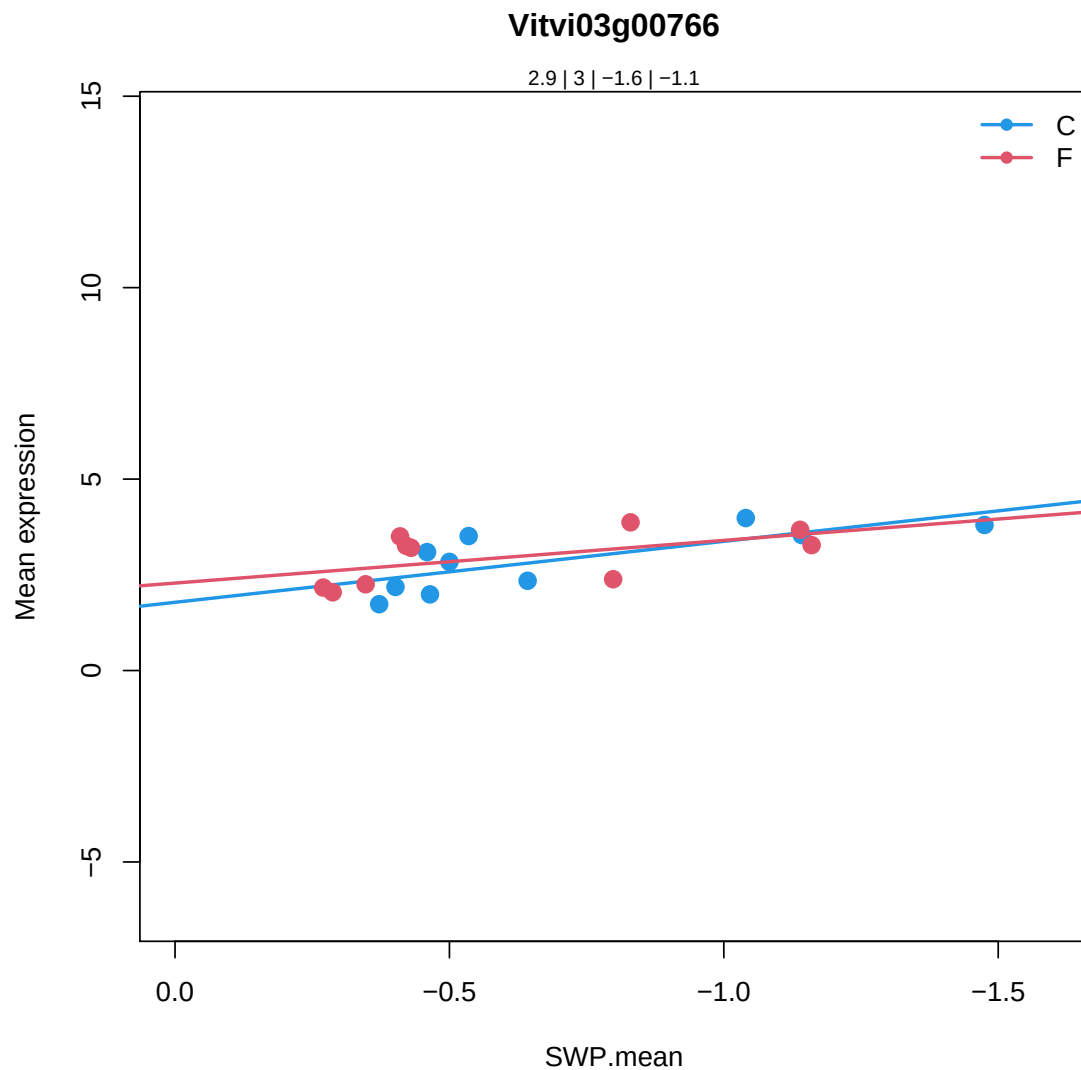
CBS domain protein (DUF21) |

Chr2:6182362-6184648 REVERSE LENGTH=423 |

201606

Coefficients for Vitvi03g00766.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.900922	1.3203e-13	***	2.007983e-13	***
SlopeC	-1.592341	0.003913092	**	0.2293975	
MeanF-MeanC	0.06199901	0.8067811		0.9464295	
SlopeF-SlopeC	0.4766948	0.522444		0.9999488	



8.1.422 Vitvi07g00315: Type1.0 *

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

Vitvi07g00315

28.1

DNA.synthesis/chromatin structure

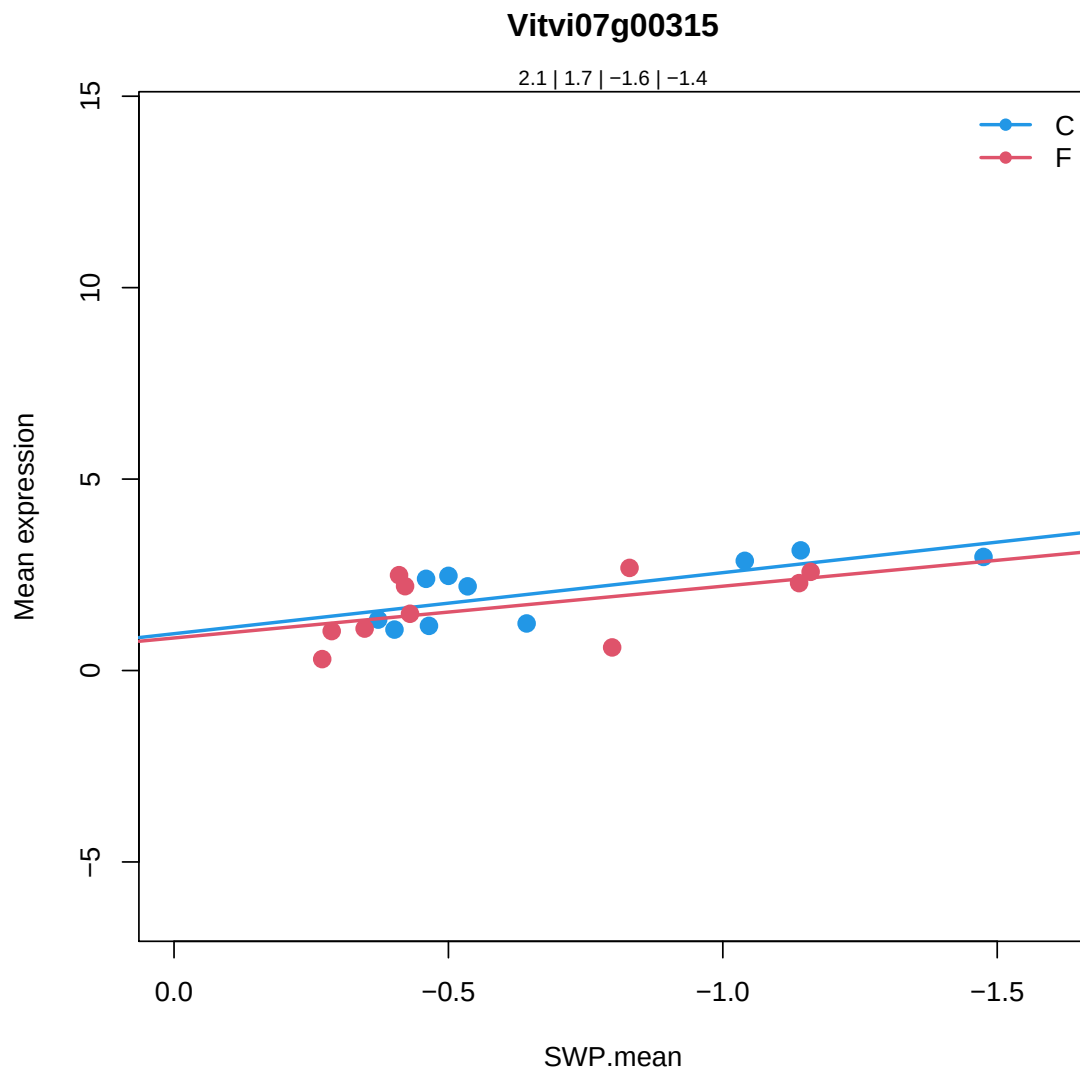
zinc finger (CCCH type) helicase family protein |

Chr2:19545828-19550871 REVERSE LENGTH=1015 |

201606

Coefficients for Vitvi07g00315.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.082814	1.151928e-09	***	1.45009e-09	***
SlopeC	-1.593846	0.01063253	*	0.3110577	
MeanF-MeanC	-0.4088765	0.1722101		0.5024667	
SlopeF-SlopeC	0.2412863	0.7786519		0.9999488	



8.1.423 Vitvi10g01544: Type1.0 *

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

Vitvi10g01544

35.2

not assigned.unknown

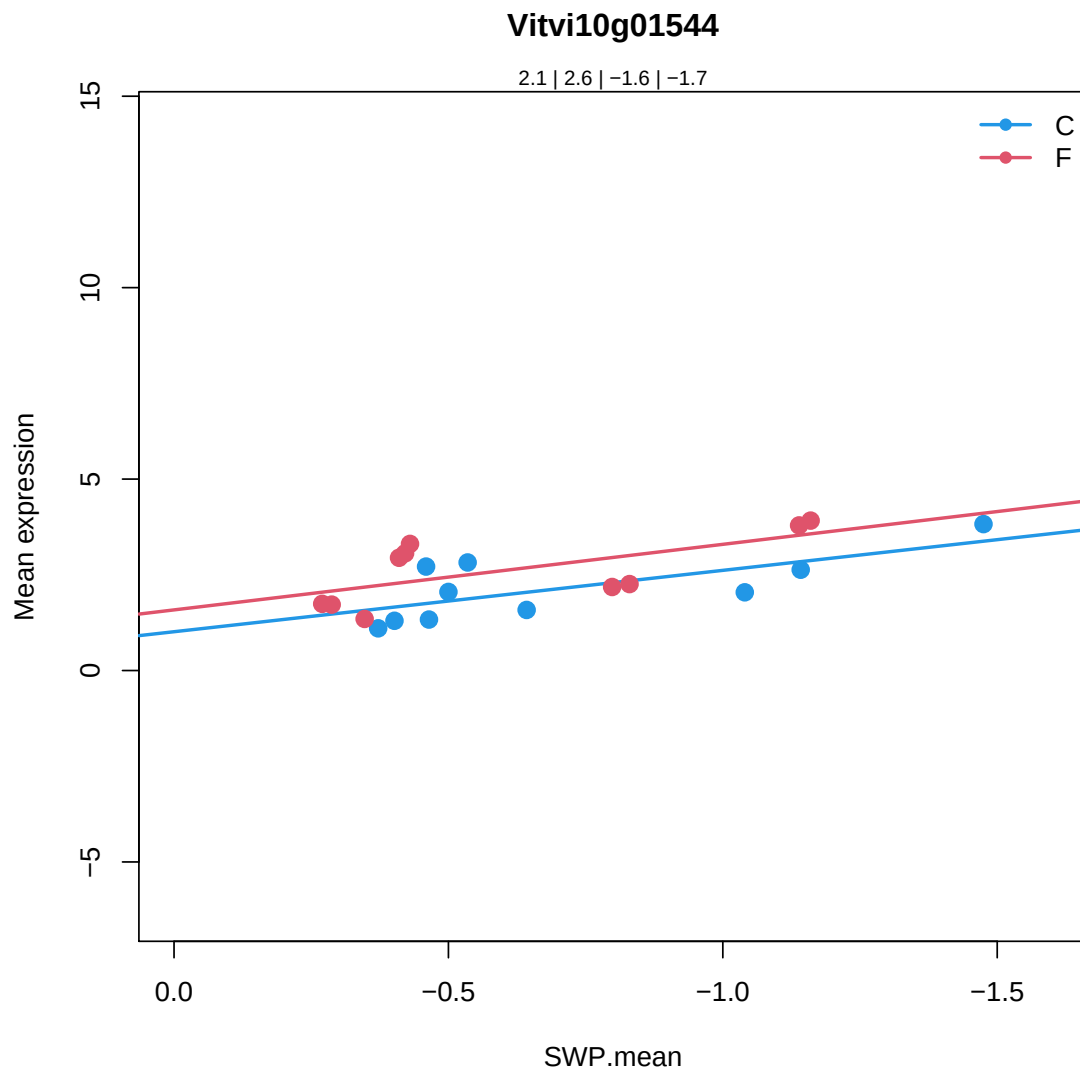
E3 ubiquitin-protein ligase |

Chr3:6965671-6967102 FORWARD LENGTH=425 |

201606

Coefficients for Vitvi10g01544.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.140199	6.191029e-10	***	7.865179e-10	***
SlopeC	-1.602621	0.009802541	**	0.3011737	
MeanF-MeanC	0.4864314	0.1050379		0.3758187	
SlopeF-SlopeC	-0.1098173	0.8973909		0.9999488	



8.1.424 Vitvi16g01094: Type1.0 *

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

Vitvi16g01094

30.2.16

signalling.receptor kinases.Catharanthus roseus-like RLK1

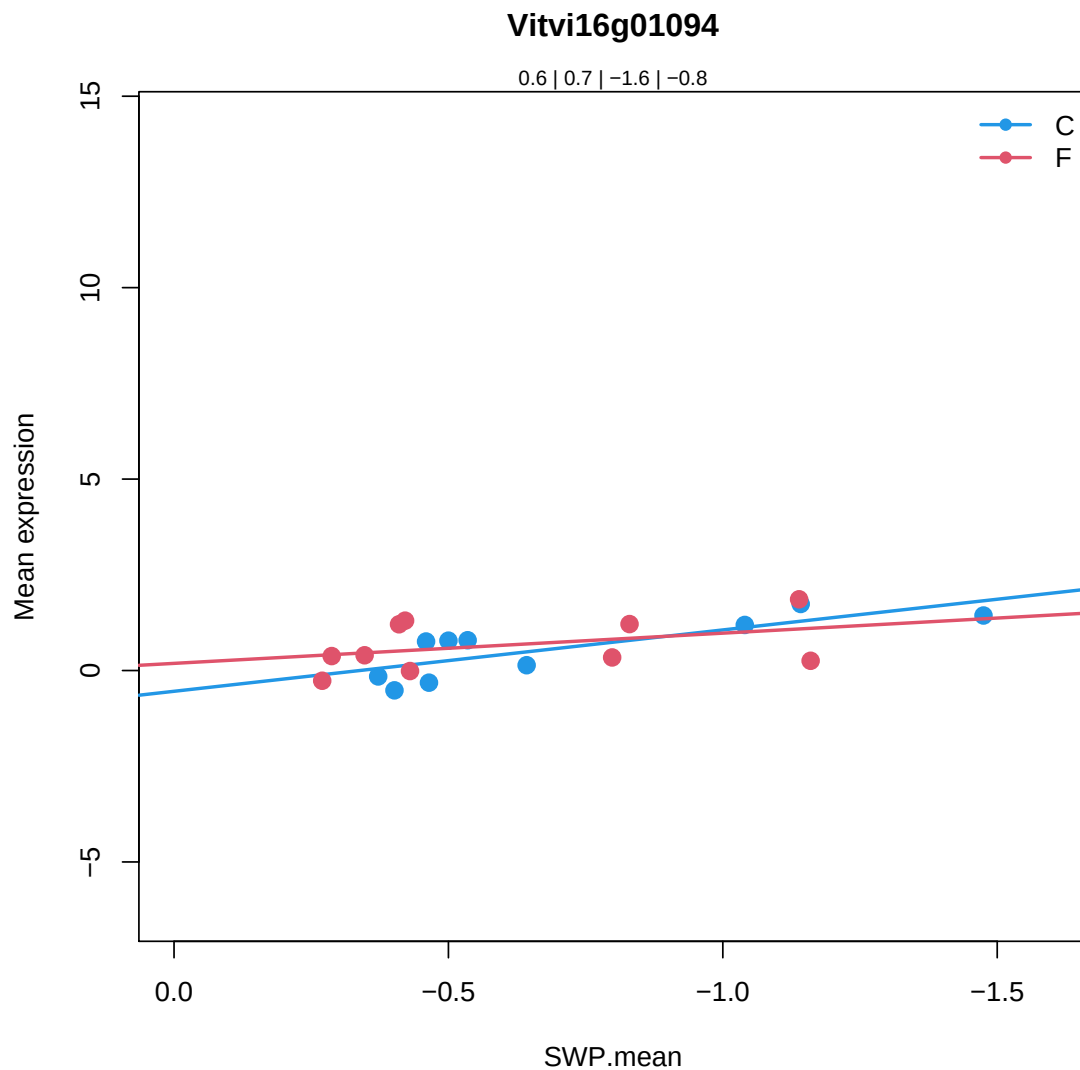
Protein kinase superfamily protein |

Chr5:8113910-8116384 FORWARD LENGTH=824 |

201606

Coefficients for Vitvi16g01094.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.5840903	0.003545671	**	0.00379383	**
SlopeC	-1.602629	0.003941288	**	0.2301652	
MeanF-MeanC	0.08308445	0.7450522		0.9249887	
SlopeF-SlopeC	0.8136283	0.2828198		0.9999488	



8.1.425 Vitvi07g03049: Type1.0 *

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

Vitvi07g03049

13.1.6.1.1

amino acid metabolism.synthesis.aromatic aa.chorismate.3-deoxy-D-arabi

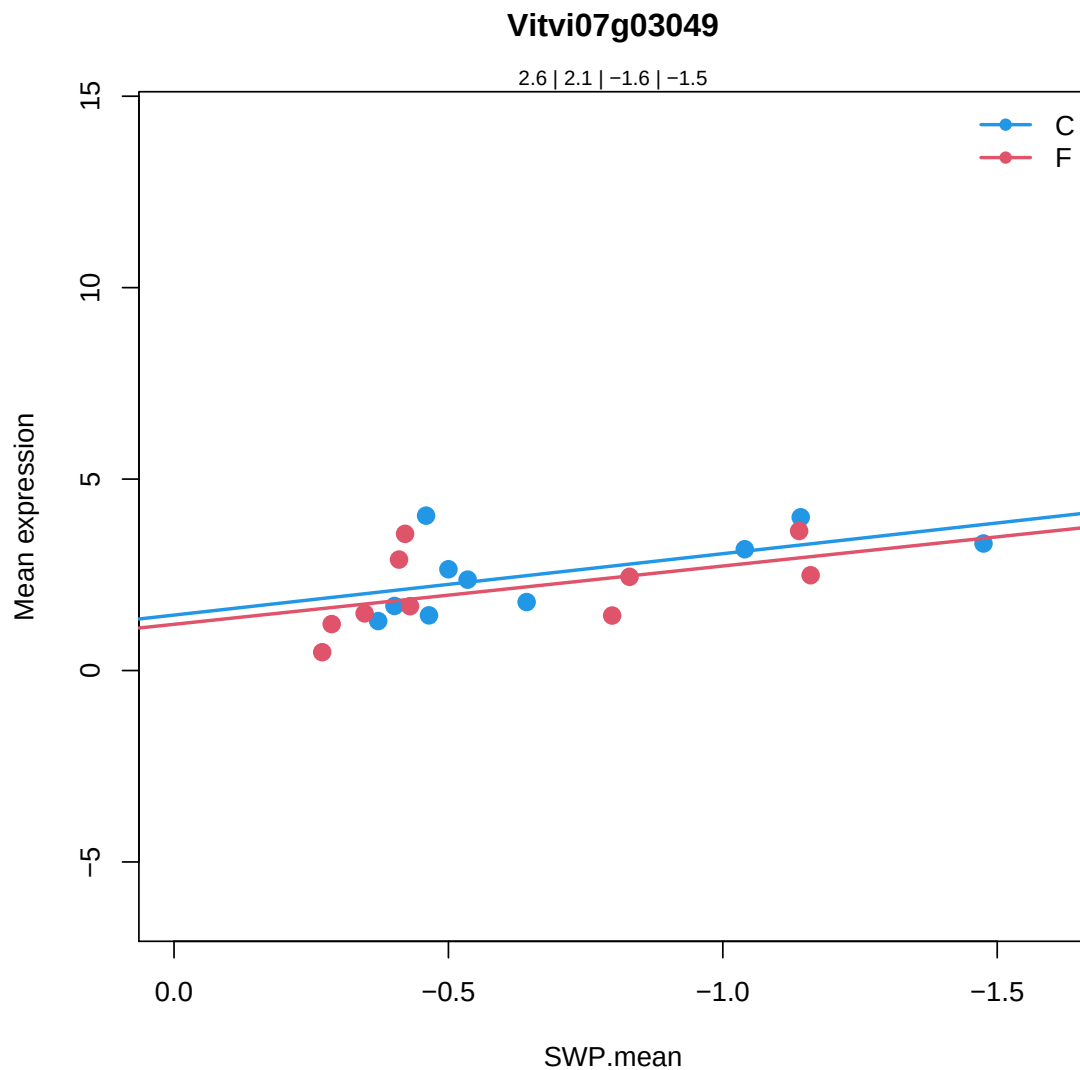
3-deoxy-D-arabino-heptulosonate 7-phosphate synthase 1 |

Chr4:18539654-18541832 FORWARD LENGTH=525 |

201606

Coefficients for Vitvi07g03049.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.575644	2.315396e-09	***	2.884451e-09	***
SlopeC	-1.603605	0.03976744	*	0.4708616	
MeanF-MeanC	-0.4410604	0.2491464		0.6091793	
SlopeF-SlopeC	0.08108974	0.9413972		0.9999488	



8.1.426 Vitvi10g00329: Type1.0 *

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

Vitvi10g00329

27.3.25

RNA.regulation of transcription.MYB domain transcription factor family

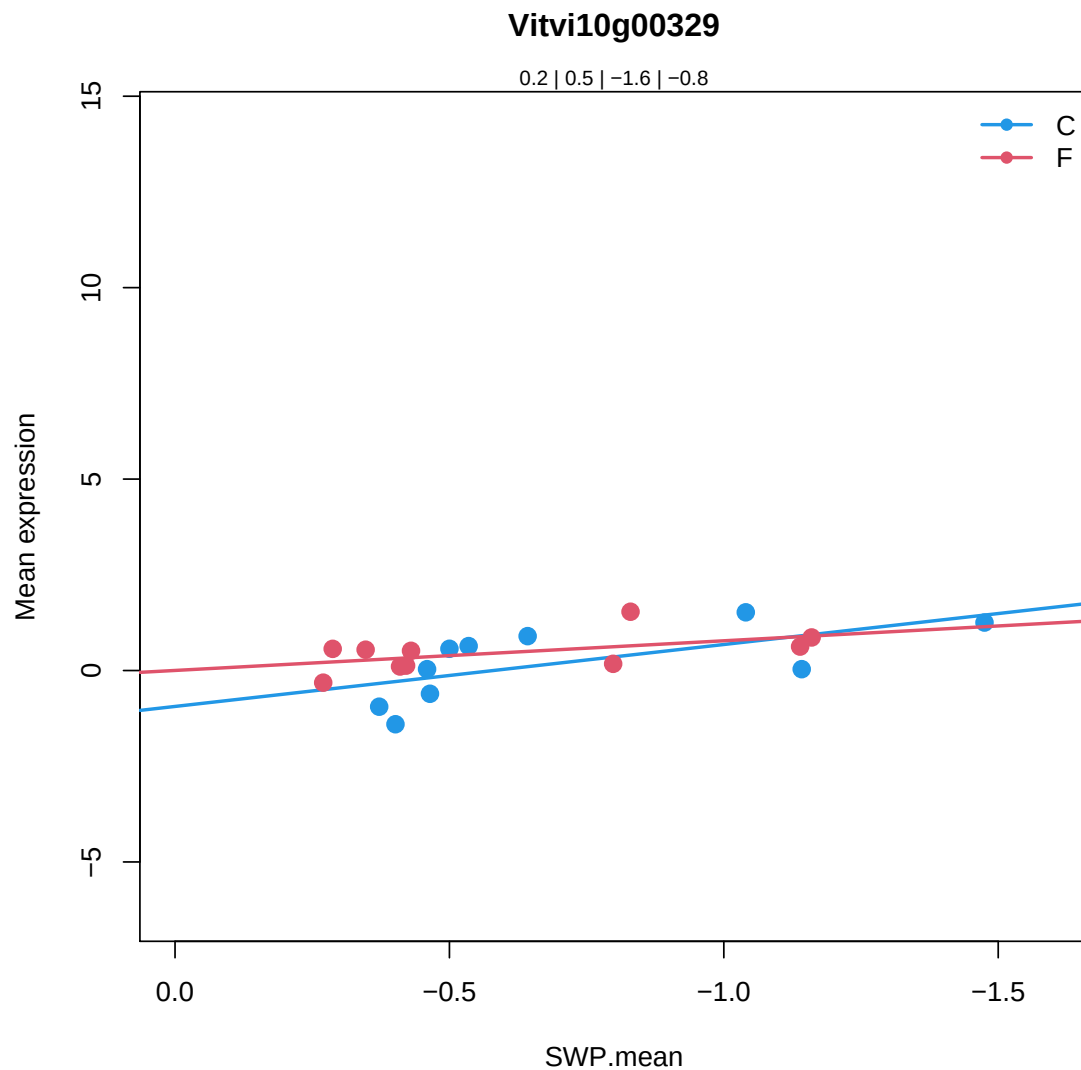
MYB-like 102 |

Chr4:11418425-11419652 REVERSE LENGTH=350 |

201606

Coefficients for Vitvi10g00329.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1990573	0.30911		0.3148527	
SlopeC	-1.617537	0.006086547	**	0.2647742	
MeanF-MeanC	0.2746456	0.3207728		0.6816197	
SlopeF-SlopeC	0.8423767	0.2988608		0.9999488	



8.1.427 Vitvi01g02001: Type1.0 *

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

Vitvi01g02001

26.6

misc.O-methyl transferases

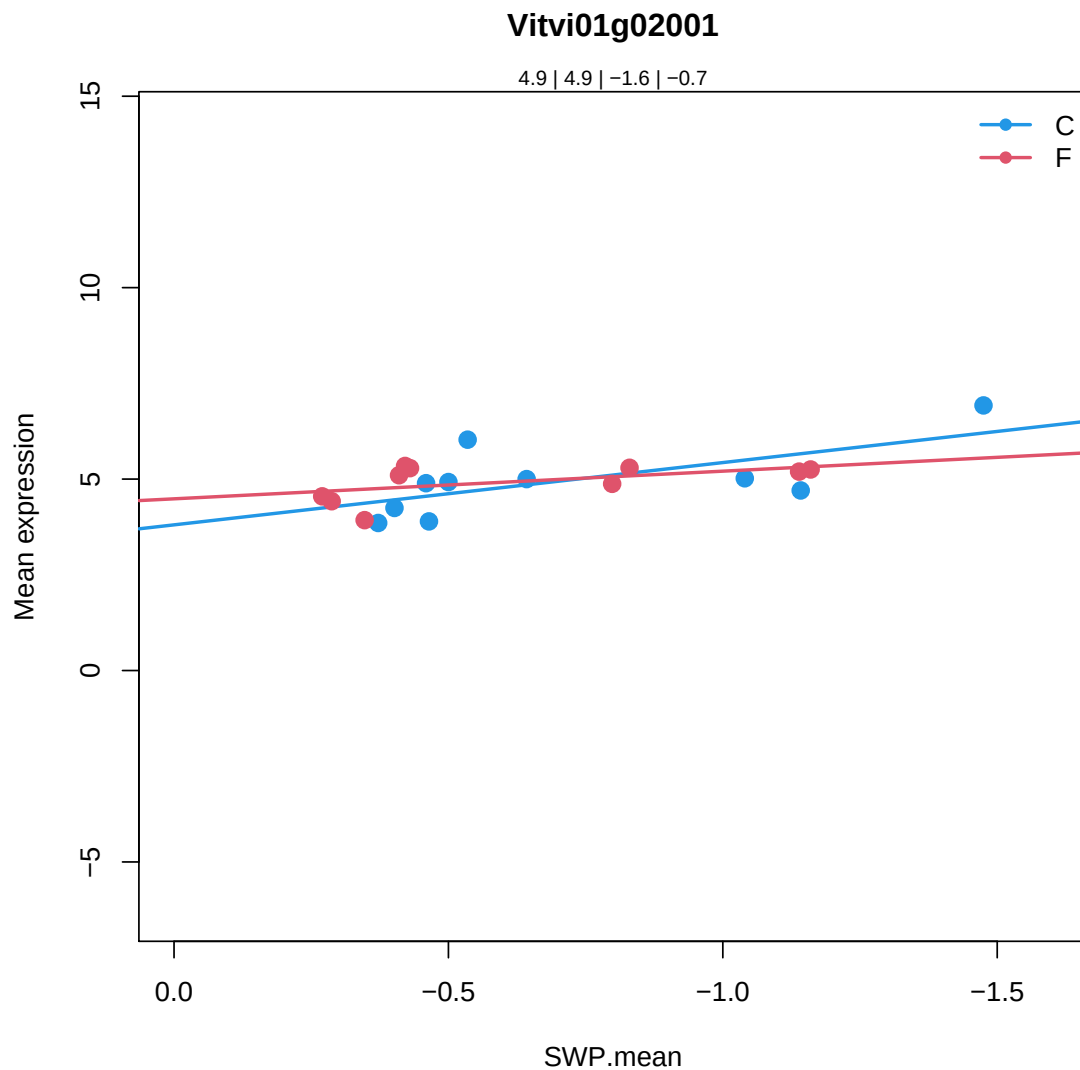
S-adenosyl-L-methionine-dependent methyltransferases superfamily prote

Chr1:25502876-25505224 FORWARD LENGTH=363 |

201606

Coefficients for Vitvi01g02001.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.948252	5.752679e-18	***	1.605022e-17	***
SlopeC	-1.626333	0.004609374	**	0.2436609	
MeanF-MeanC	-0.02396961	0.927787		0.9808107	
SlopeF-SlopeC	0.9040797	0.2504371		0.9999488	



8.1.428 Vitvi08g01602: Type1.0 *

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

Vitvi08g01602

34.19.2

transport.major intrinsic proteins.TIP

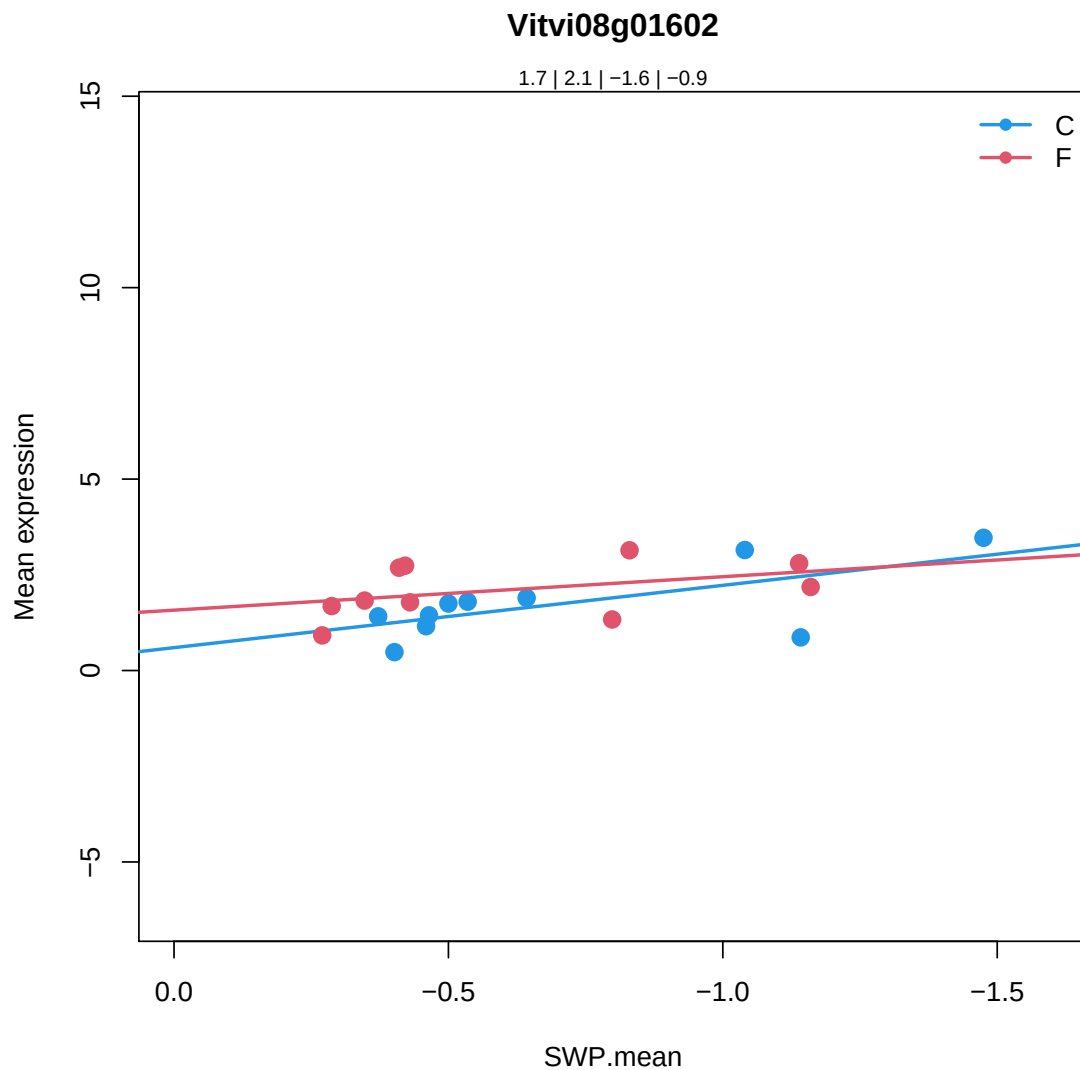
gamma tonoplast intrinsic protein |

Chr2:15445490-15446336 FORWARD LENGTH=251 |

201606

Coefficients for Vitvi08g01602.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.741569	4.517568e-08	***	5.407742e-08	***
SlopeC	-1.627435	0.01153938	*	0.318473	
MeanF-MeanC	0.3672155	0.233465		0.5882853	
SlopeF-SlopeC	0.7536191	0.3996493		0.9999488	



8.1.429 Vitvi17g00287: Type1.0 *

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

Vitvi17g00287

29.6

protein.folding

chloroplast heat shock protein 70-1 |

Chr4:12590094-12593437 FORWARD LENGTH=718 |

201606

Vitvi17g00287

20.2.1

stress.abiotic.heat

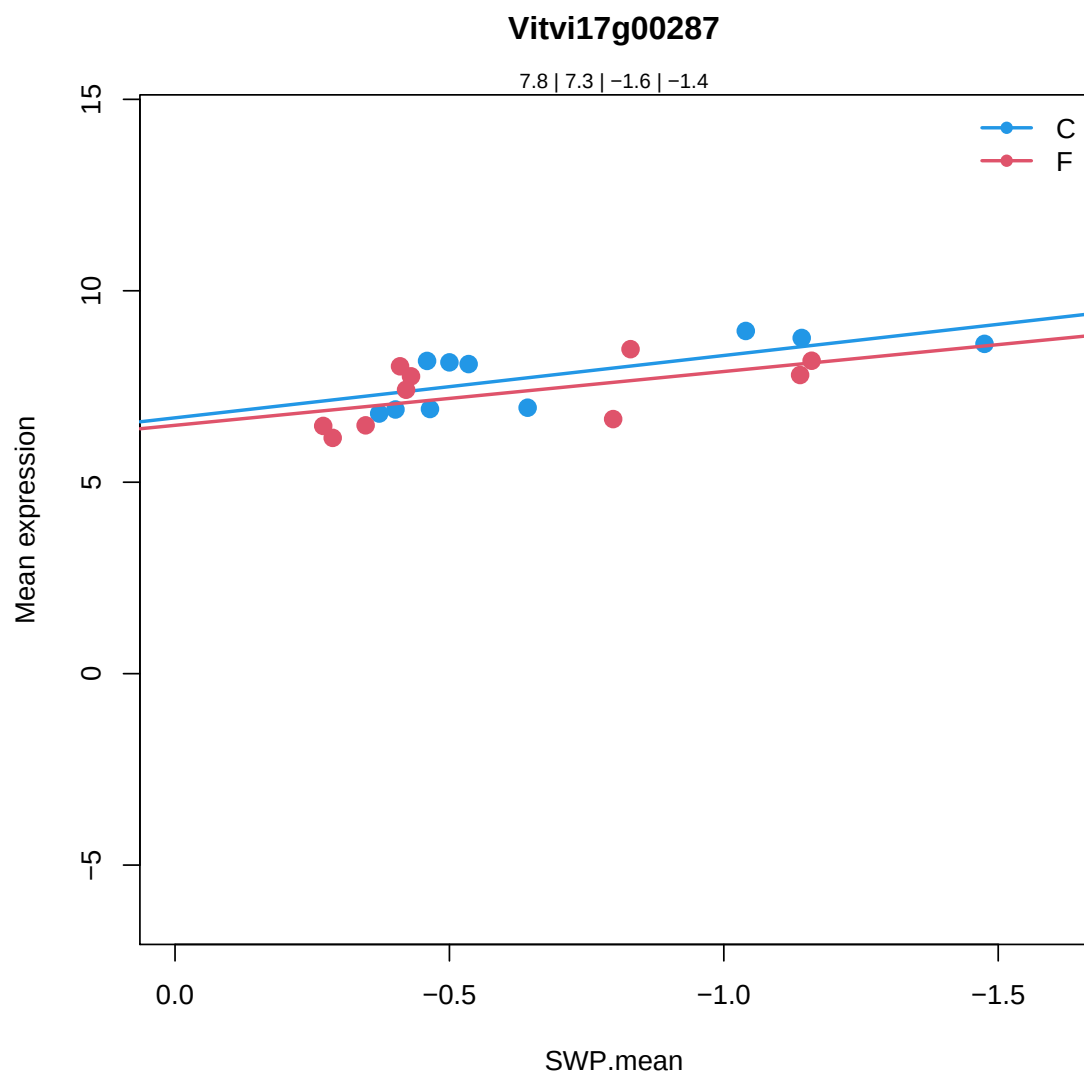
chloroplast heat shock protein 70-1 |

Chr4:12590094-12593437 FORWARD LENGTH=718 |

201606

Coefficients for Vitvi17g00287.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.826385	1.972115e-21	***	1.93679e-20	***
SlopeC	-1.628149	0.007961231	**	0.2832315	
MeanF-MeanC	-0.4846599	0.1010527		0.3663761	
SlopeF-SlopeC	0.2227912	0.7904987		0.9999488	



8.1.430 Vitvi16g00309: Type1.0

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

Vitvi16g00309

26.19

misc.plastocyanin-like

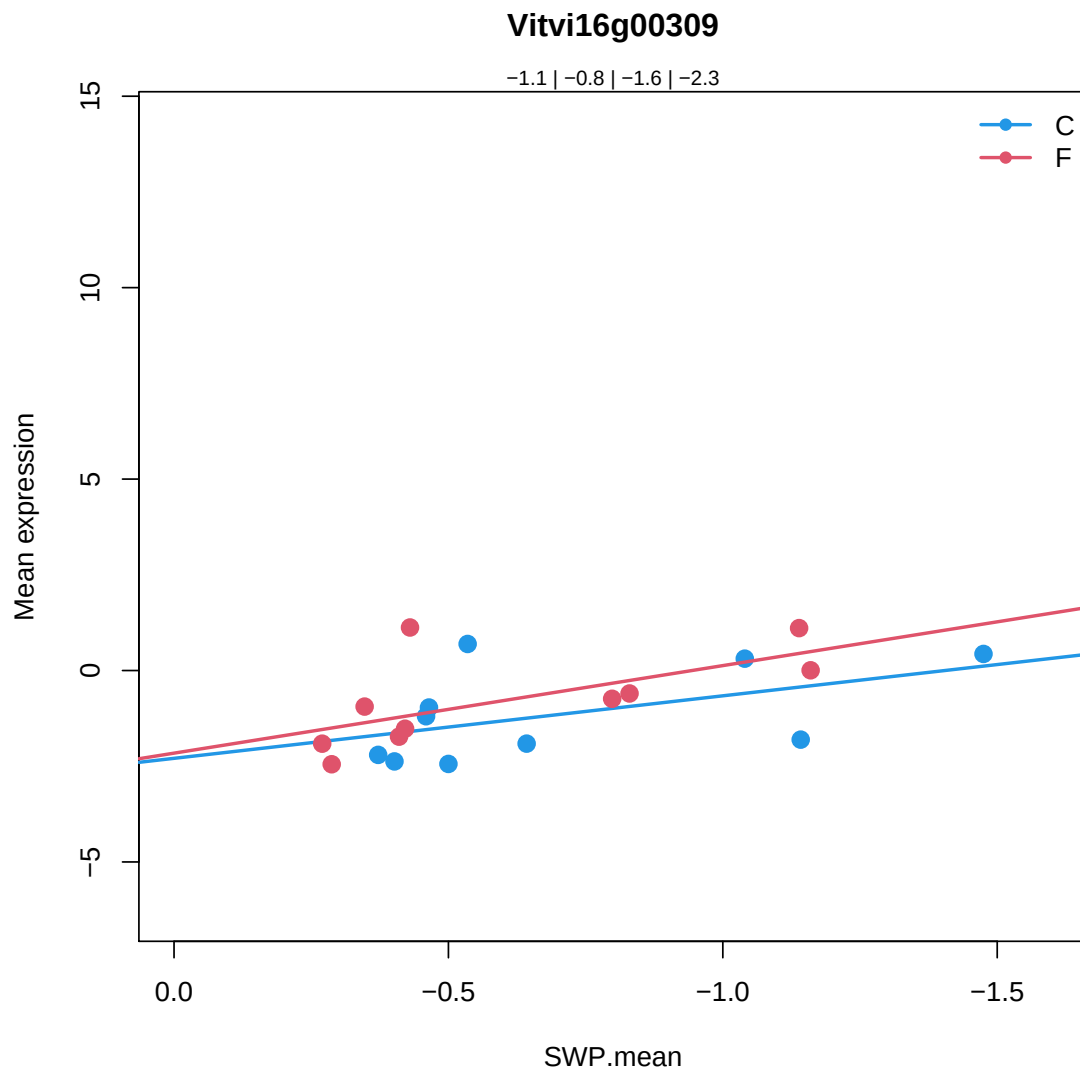
Cupredoxin superfamily protein |

Chr5:2364827-2365536 REVERSE LENGTH=192 |

201606

Coefficients for Vitvi16g00309.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.145817	0.0009091118	***	0.000985329	***
SlopeC	-1.632739	0.06187261	.	0.5446524	
MeanF-MeanC	0.3807398	0.3761449		0.7285001	
SlopeF-SlopeC	-0.6534484	0.6017208		0.9999488	



8.1.431 Vitvi19g00538: Type1.0 *

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

Vitvi19g00538

2.1.2.3

major CHO metabolism.synthesis.starch.starch branching

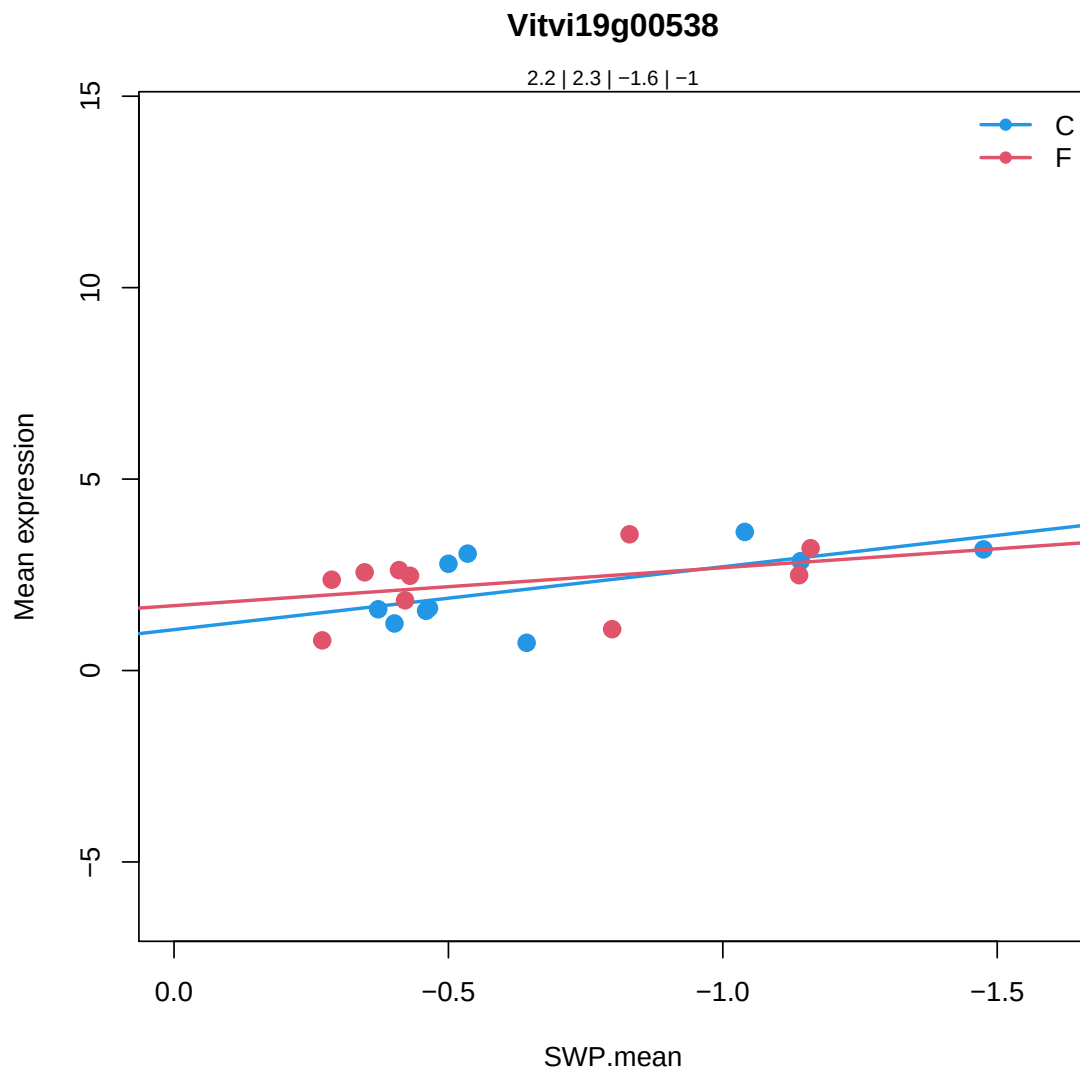
Alpha amylase family protein |

Chr3:7123603-7130364 REVERSE LENGTH=897 |

201606

Coefficients for Vitvi19g00538.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.222385	4.957828e-09	***	6.111875e-09	***
SlopeC	-1.642364	0.02112245	*	0.3832719	
MeanF-MeanC	0.07513494	0.8249241		0.9508165	
SlopeF-SlopeC	0.6516257	0.5142045		0.9999488	



8.1.432 Vitvi08g00877: Type1.0 *

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

Vitvi08g00877

10.6.2

cell wall.degradation.mannan-xylose-arabinose-fucose

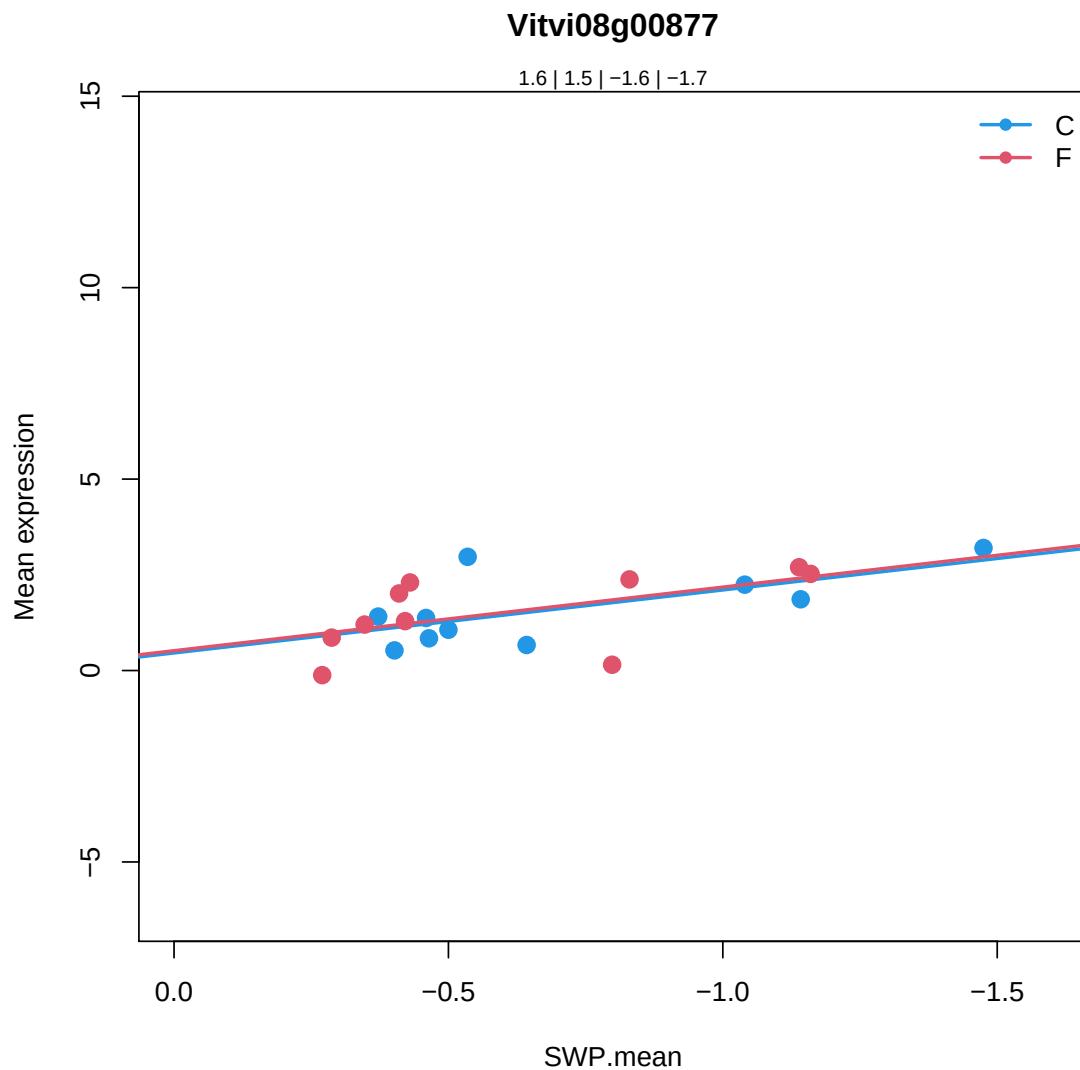
Glycosyl hydrolase superfamily protein |

Chr5:361189-362867 REVERSE LENGTH=448 |

201606

Coefficients for Vitvi08g00877.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.615209	8.009752e-07	***	9.266386e-07	***
SlopeC	-1.645206	0.0202006	*	0.3764029	
MeanF-MeanC	-0.08594045	0.7990073		0.9437748	
SlopeF-SlopeC	-0.01592818	0.9871305		0.9999488	



8.1.433 Vitvi13g00241: Type1.0 *

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

Vitvi13g00241

21.2.1

redox.ascorbate and glutathione.ascorbate

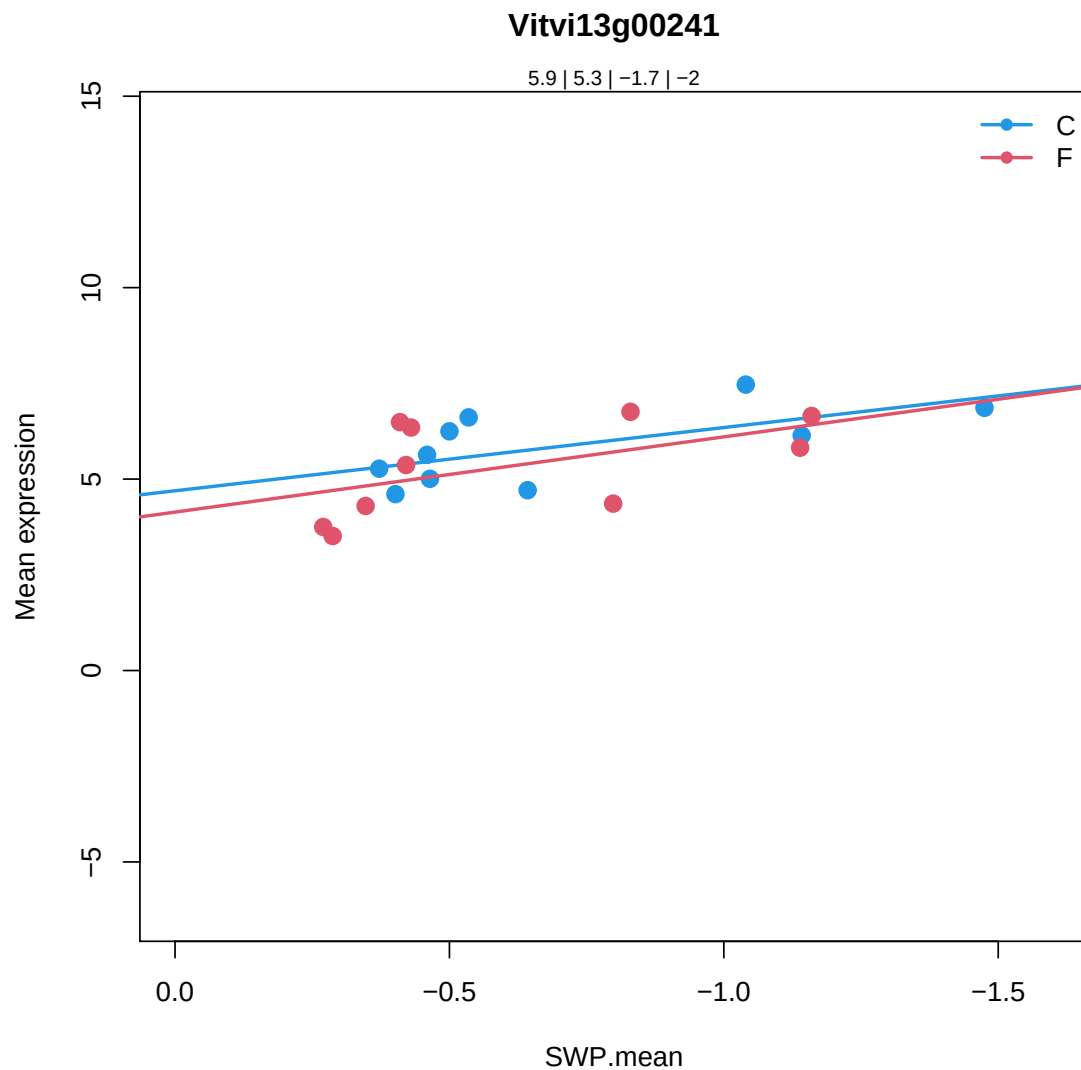
dehydroascorbate reductase 2 |

Chr1:28250255-28251237 REVERSE LENGTH=213 |

201606

Coefficients for Vitvi13g00241.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.855599	6.807616e-16	***	1.302557e-15	***
SlopeC	-1.65169	0.04266318	*	0.48214	
MeanF-MeanC	-0.5209892	0.1951408		0.5362063	
SlopeF-SlopeC	-0.3134823	0.7860909		0.9999488	



8.1.434 Vitvi04g01126: Type1.0 *

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

Vitvi04g01126

35.2

not assigned.unknown

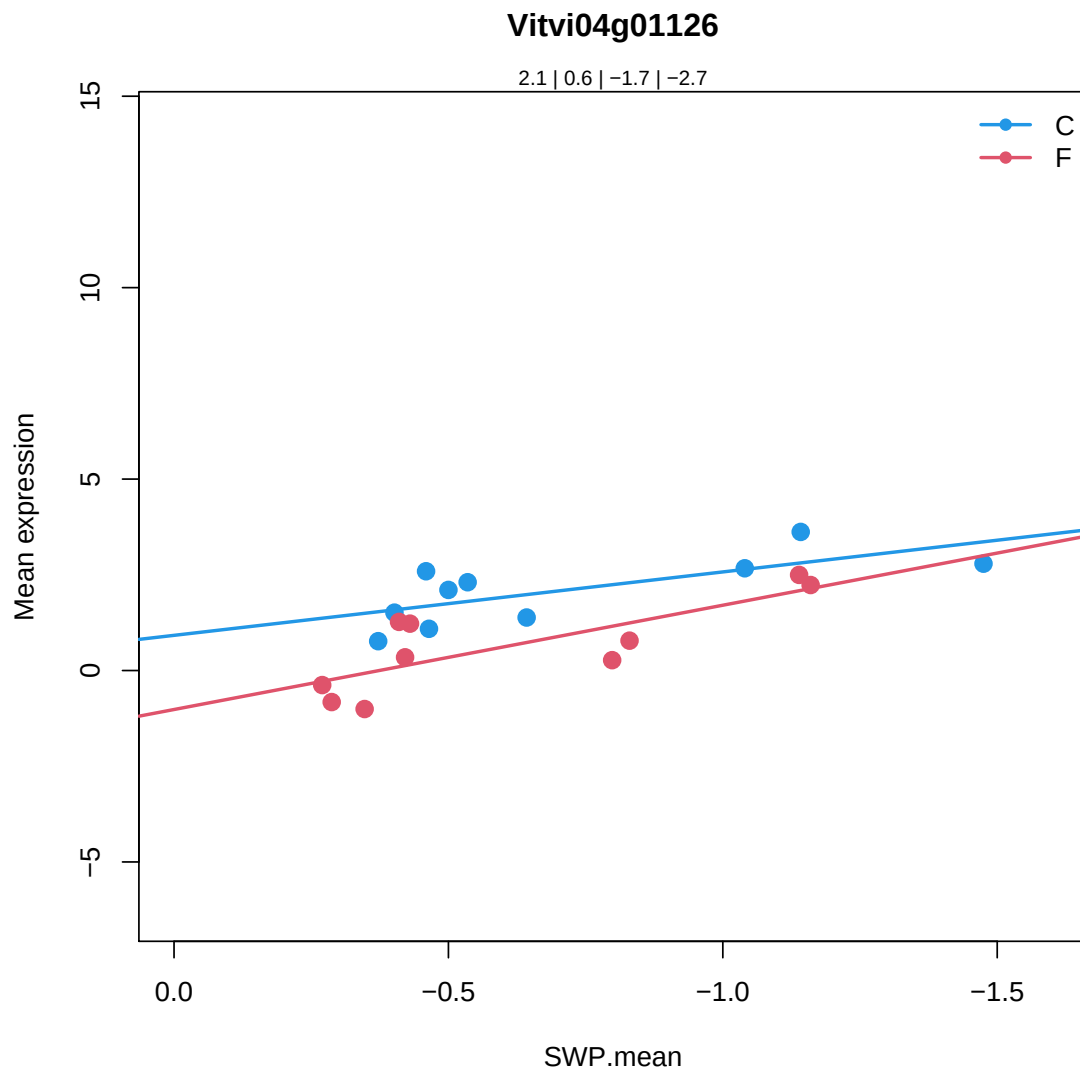
transmembrane protein |

Chr5:14191711-14193654 REVERSE LENGTH=295 |

201606

Coefficients for Vitvi04g01126.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.083353	2.456297e-09	***	3.058482e-09	***
SlopeC	-1.656076	0.01093921	*	0.3141738	
MeanF-MeanC	-1.442417	9.732007e-05	***	0.001768001	**
SlopeF-SlopeC	-1.068136	0.2404919		0.9999488	



8.1.435 Vitvi10g01366: Type1.0 *

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

Vitvi10g01366

16.2

secondary metabolism.phenylpropanoids

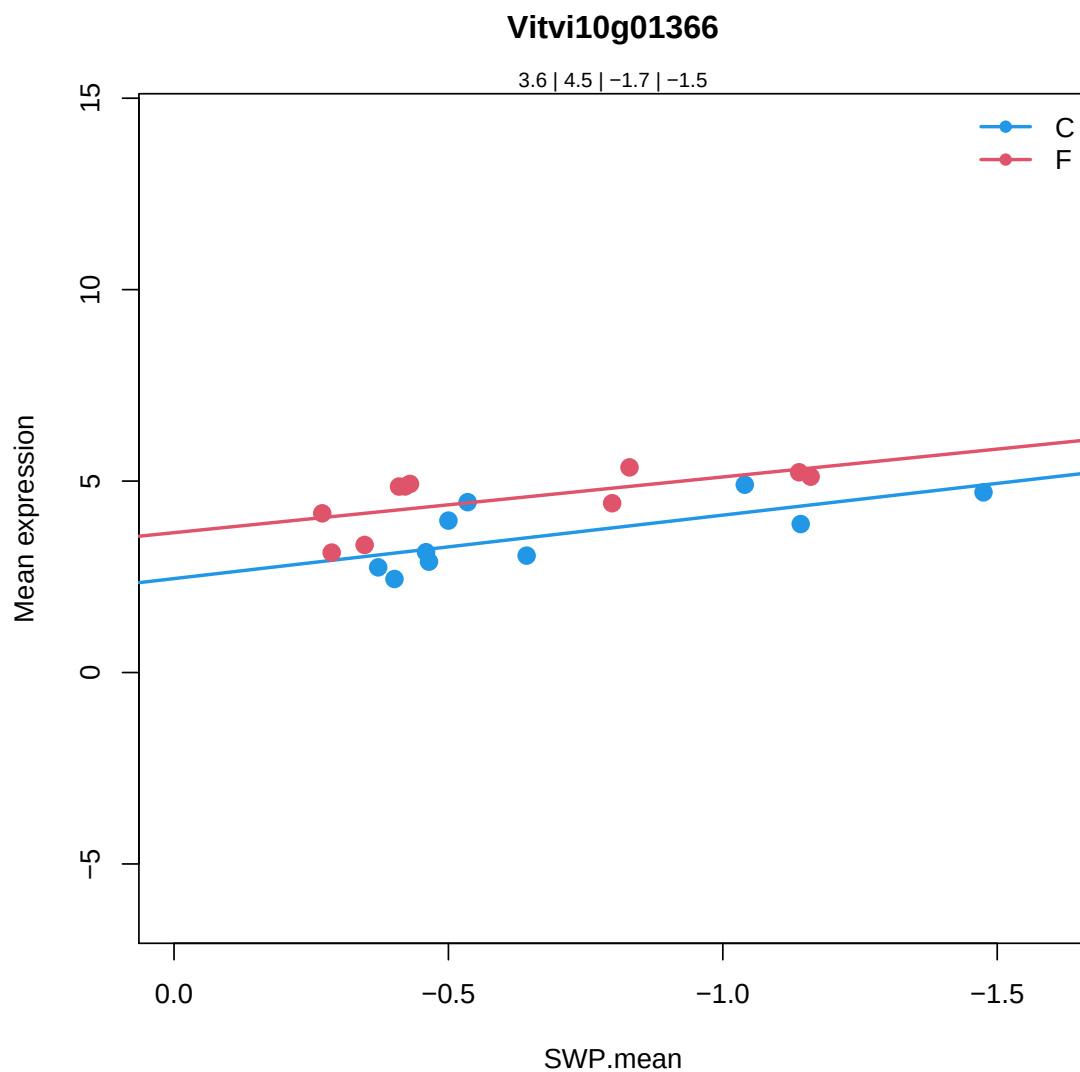
nicotinamidase 2 |

Chr5:7826005-7826601 REVERSE LENGTH=198 |

201606

Coefficients for Vitvi10g01366.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.618555	7.525381e-15	***	1.274607e-14	***
SlopeC	-1.657775	0.00519472	**	0.2562392	
MeanF-MeanC	0.9203104	0.002653097	**	0.0277356	*
SlopeF-SlopeC	0.2025806	0.8008114		0.9999488	



8.1.436 Vitvi01g02026: Type1.0

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

Vitvi01g02026

26.10

misc.cytochrome P450

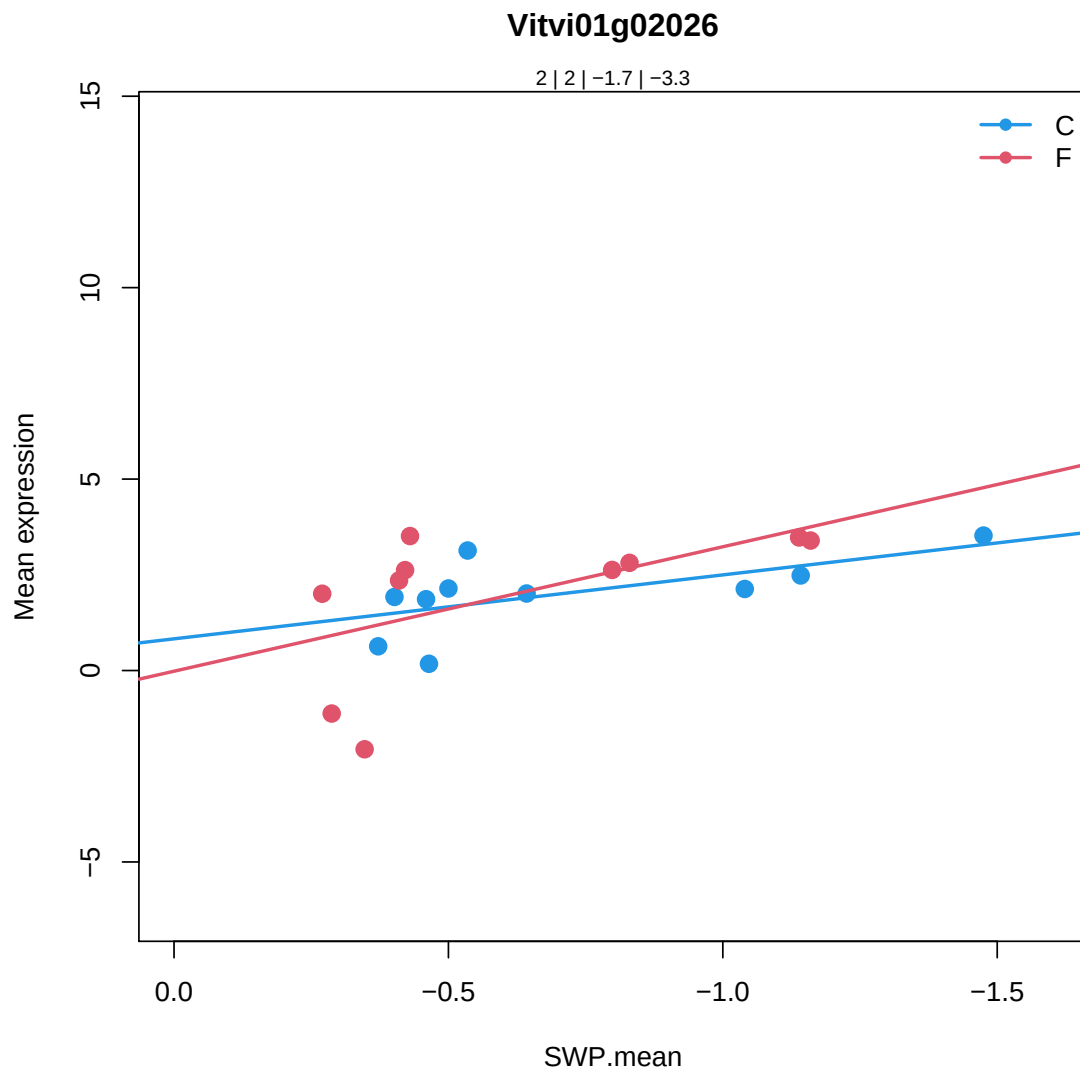
cytochrome P450%2C family 71%2C subfamily B%2C polypeptide 34 |

Chr3:9639199-9640866 REVERSE LENGTH=500 |

201606

Coefficients for Vitvi01g02026.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.001734	2.327185e-05	***	2.605668e-05	***
SlopeC	-1.669717	0.1217504		0.64341	
MeanF-MeanC	-0.03975648	0.9405385		0.9845772	
SlopeF-SlopeC	-1.580773	0.3168413		0.9999488	



8.1.437 Vitvi13g02576: Type1.0 *

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

Vitvi13g02576

35.2

not assigned.unknown

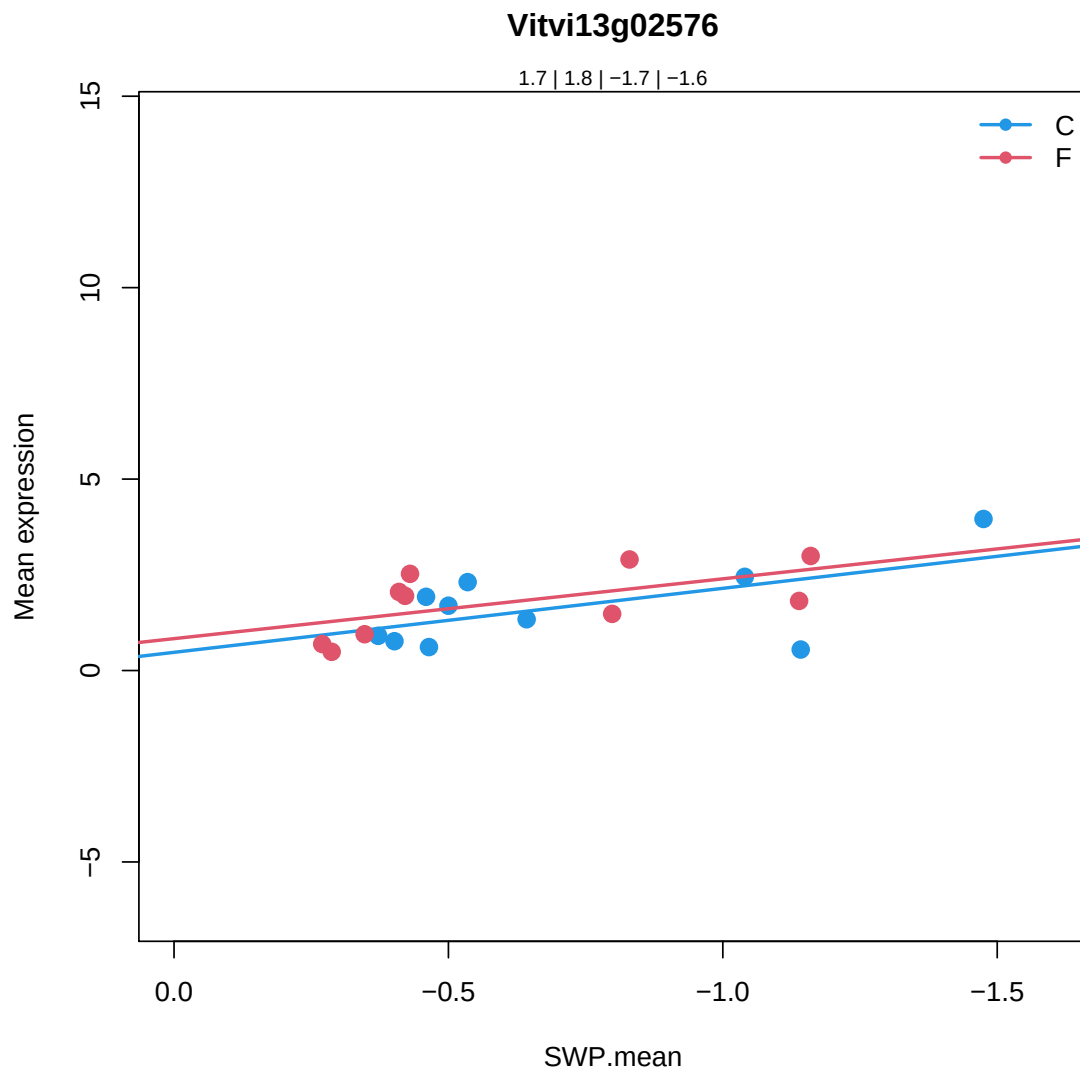
oxidoreductase/transition metal ion-binding protein |

Chr2:13580600-13580962 FORWARD LENGTH=120 |

201606

Coefficients for Vitvi13g02576.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.650056	7.486693e-07	***	8.667845e-07	***
SlopeC	-1.671749	0.02029366	*	0.3768116	
MeanF-MeanC	0.1341797	0.6961594		0.9046669	
SlopeF-SlopeC	0.1094618	0.9132158		0.9999488	



8.1.438 Vitvi09g00375: Type1.0 *

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

Vitvi09g00375

18

Co-factor and vitamine metabolism

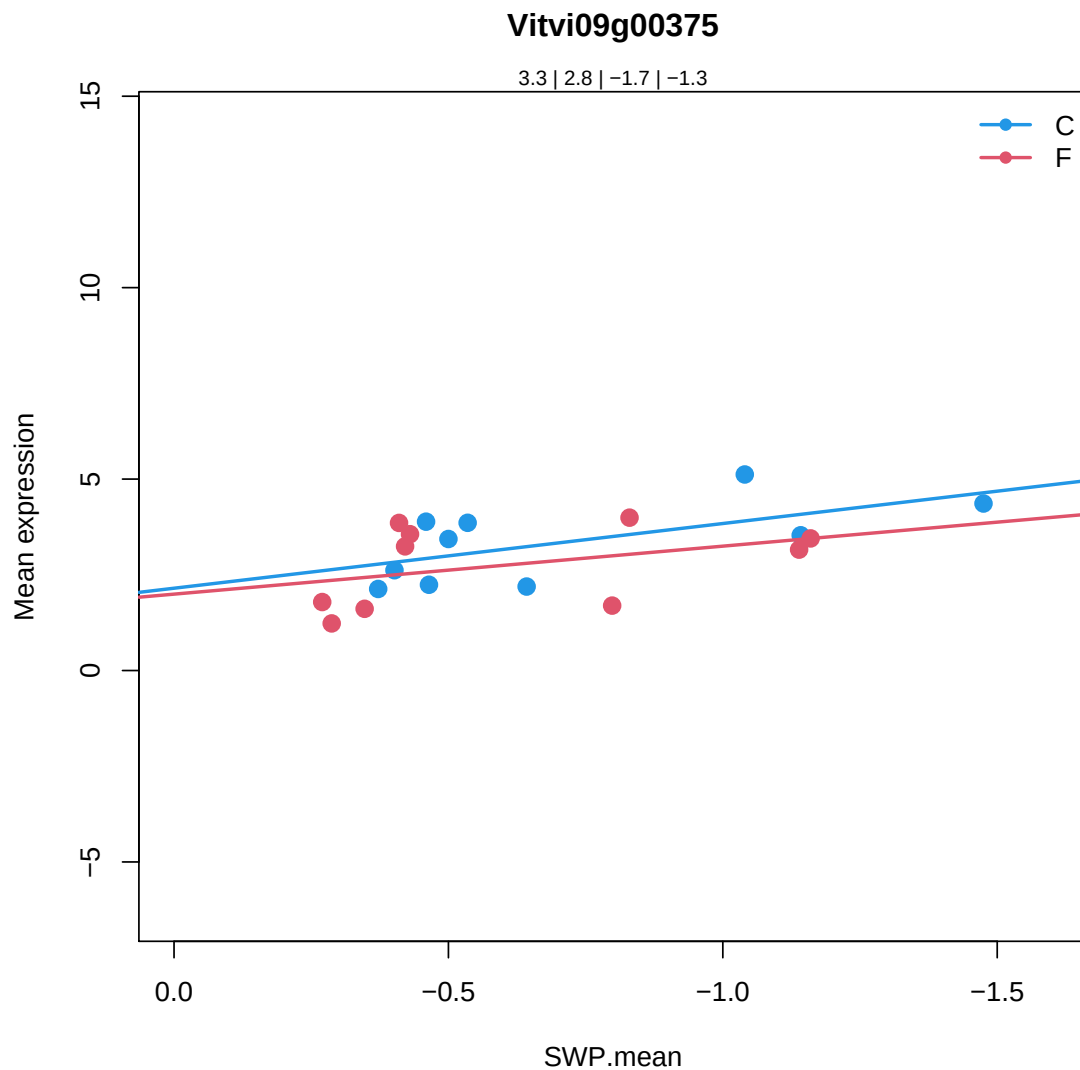
pyridoxine biosynthesis 1.2 |

Chr3:5444121-5445065 REVERSE LENGTH=314 |

201606

Coefficients for Vitvi09g00375.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.337637	2.515381e-11	***	3.376139e-11	***
SlopeC	-1.689545	0.03313431	*	0.4430116	
MeanF-MeanC	-0.5792549	0.139207		0.4466932	
SlopeF-SlopeC	0.4365358	0.6965334		0.9999488	



8.1.439 Vitvi15g01705: Type1.0 *

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

Vitvi15g01705

26.22

misc.short chain dehydrogenase/reductase (SDR)

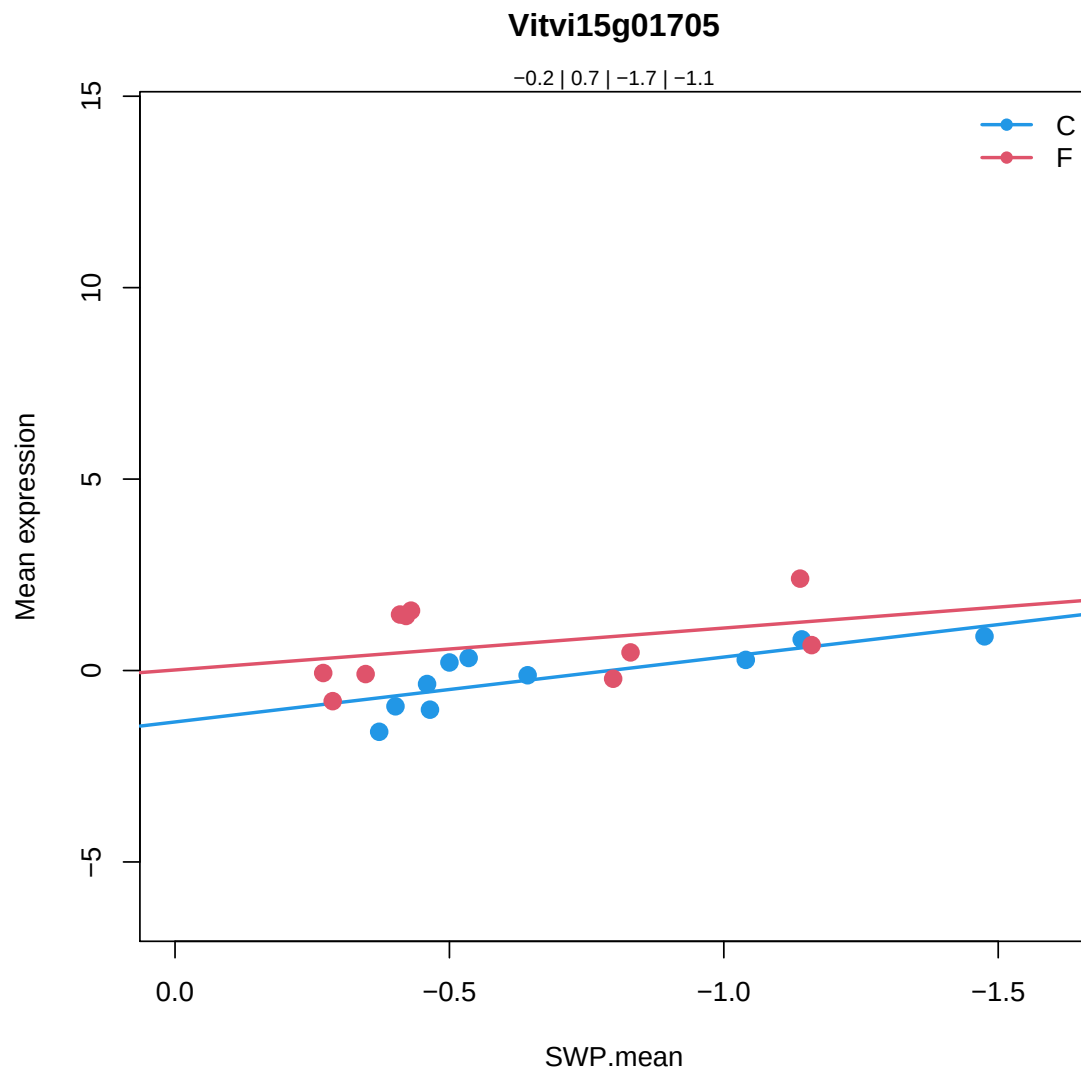
NAD(P)-binding Rossmann-fold superfamily protein |

Chr1:293595-294888 FORWARD LENGTH=260 |

201606

Coefficients for Vitvi15g01705.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.151514	0.5197104		0.5257119	
SlopeC	-1.695375	0.01539913	*	0.3393703	
MeanF-MeanC	0.8329048	0.0186952	*	0.1202838	
SlopeF-SlopeC	0.6002601	0.5377619		0.9999488	



8.1.440 Vitvi10g00798: Type1.0 *

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

Vitvi10g00798

29.5.11.4.3.3

protein.degradation.ubiquitin.E3.SCF.cullin

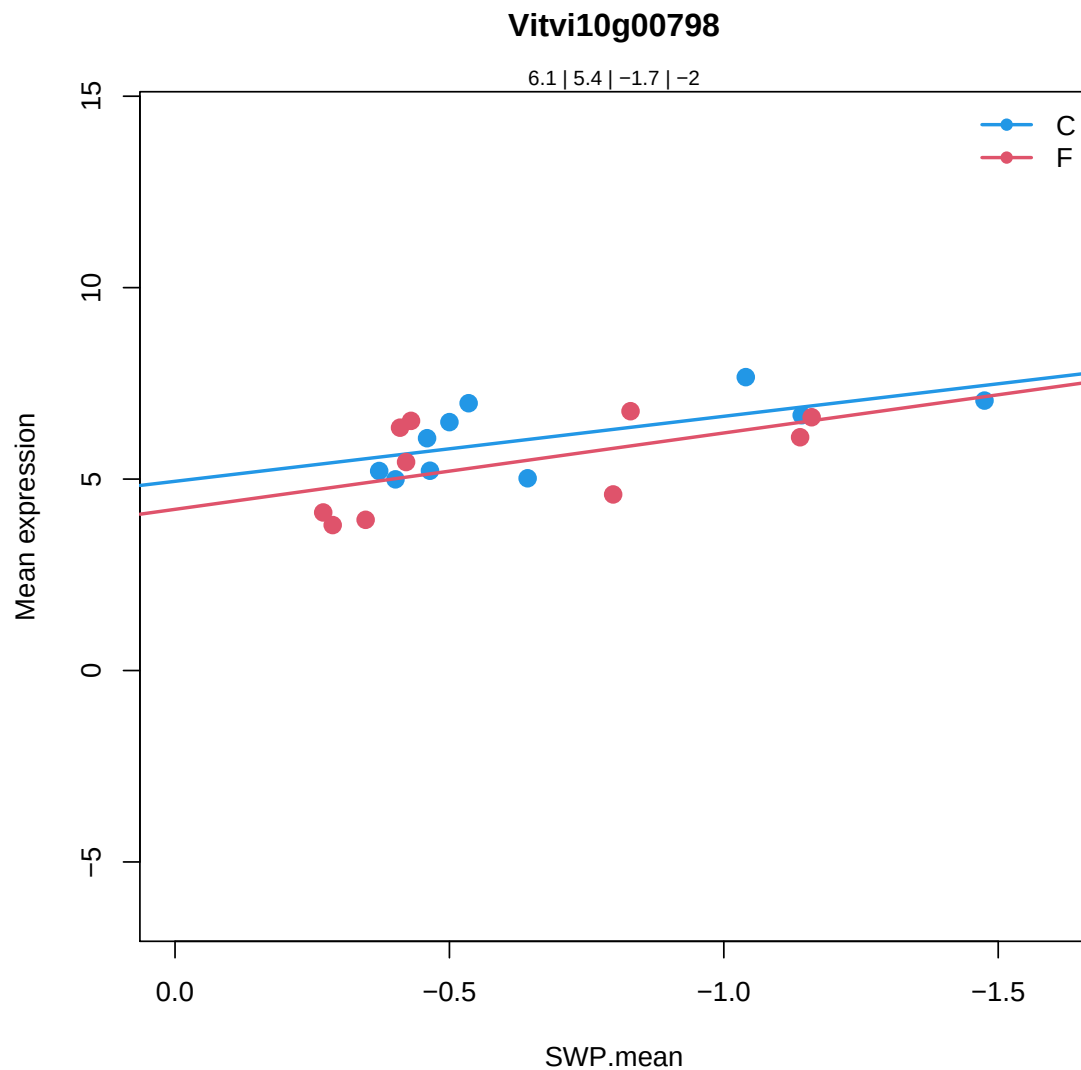
SGS domain-containing protein |

Chr1:10546794-10548072 REVERSE LENGTH=229 |

201606

Coefficients for Vitvi10g00798.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.135884	1.006157e-16	***	2.18615e-16	***
SlopeC	-1.69829	0.03024769	*	0.4320841	
MeanF-MeanC	-0.7109646	0.06946186	.	0.2947488	
SlopeF-SlopeC	-0.296639	0.7879845		0.9999488	



8.1.441 Vitvi04g01202: Type1.0 *

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

Vitvi04g01202

27.1.20

RNA.processing.degradation dicer

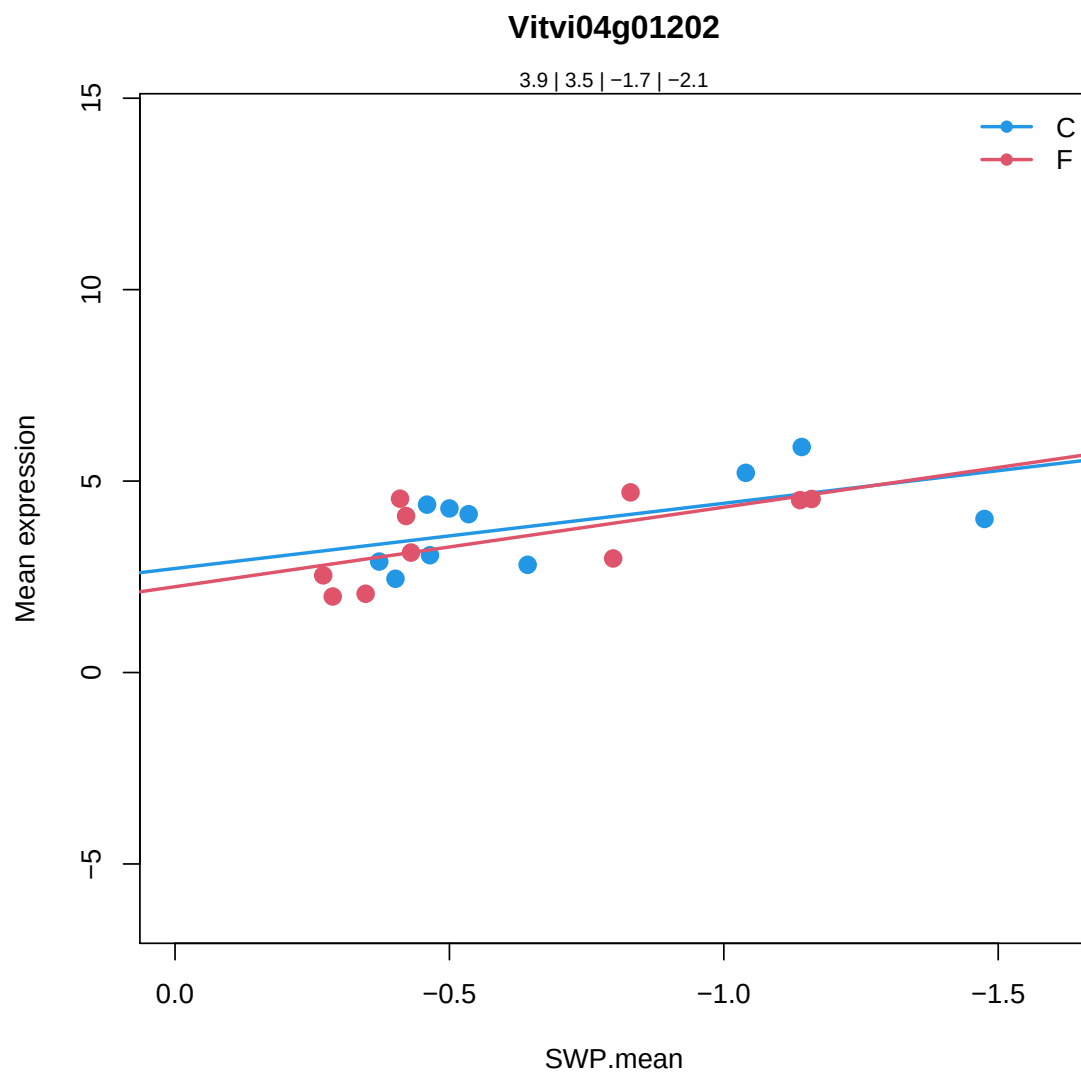
dicer-like 2 |

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	



8.1.442 Vitvi15g00912: Type1.0

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

Vitvi15g00912

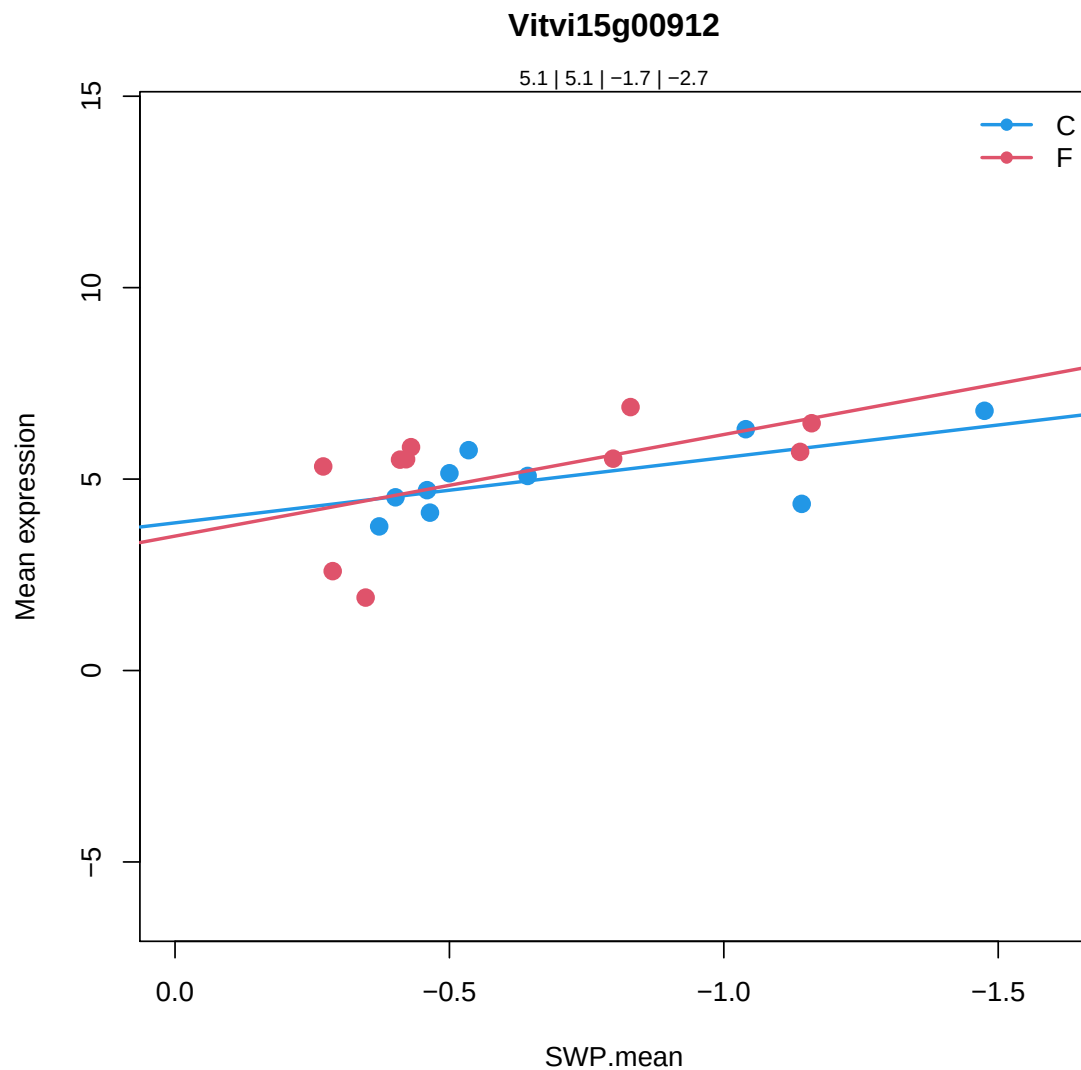
27.3.35

RNA.regulation of transcription.bZIP transcription factor family
homeobox 7 |

Chr2:19165777-19166773 REVERSE LENGTH=258 |
201606

Coefficients for Vitvi15g00912.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.054744	2.245992e-13	***	3.368767e-13	***
SlopeC	-1.703803	0.06656954	.	0.5548906	
MeanF-MeanC	0.07222379	0.8734575		0.9666187	
SlopeF-SlopeC	-0.9494001	0.4771144		0.9999488	

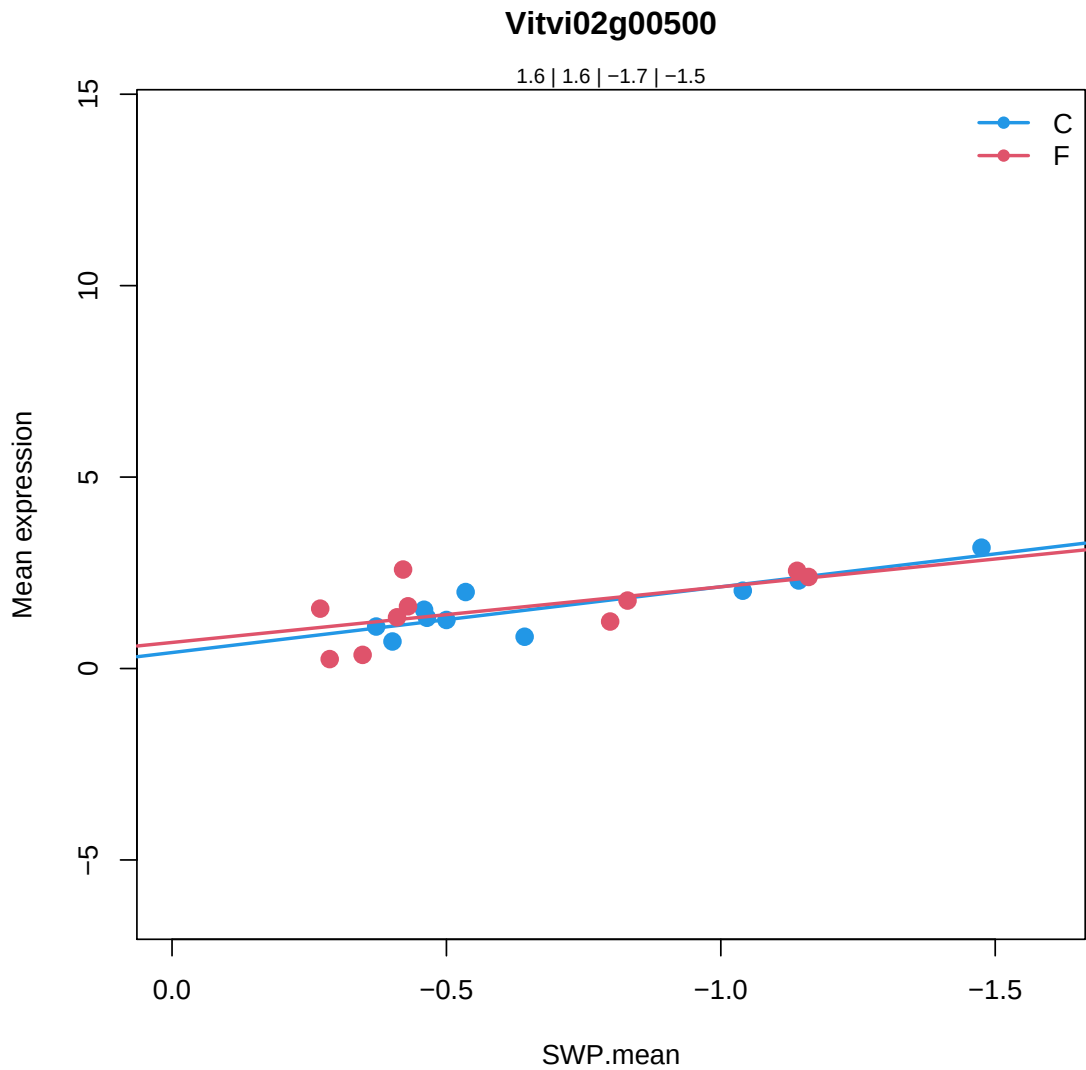


8.1.443 Vitvi02g00500: Type1.0 *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
Vitvi02g00500
35.2
not assigned.unknown
Plant invertase/pectin methylesterase inhibitor superfamily protein |
Chr5:25040699-25041310 FORWARD LENGTH=203 |
201606
```

Coefficients for Vitvi02g00500.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.62457	4.970831e-09	***	6.127409e-09	***
SlopeC	-1.71789	0.001806131	**	0.160246	
MeanF-MeanC	-0.05871081	0.8131117		0.9482333	
SlopeF-SlopeC	0.2645399	0.7162486		0.9999488	



8.1.444 Vitvi17g01012: Type1.0 *

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

Vitvi17g01012

26.28

misc.GDSL-motif lipase

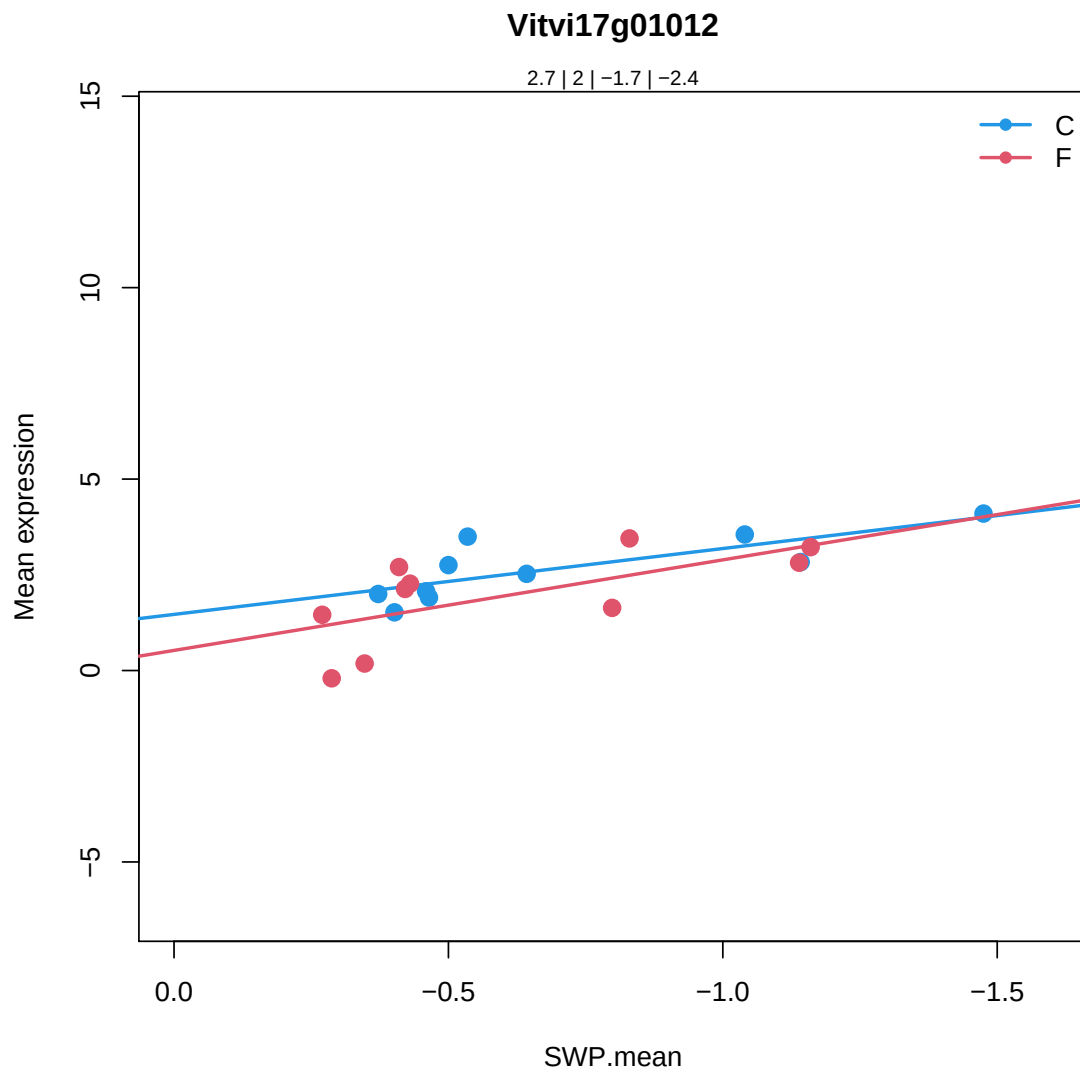
GDSL-like Lipase/Acylhydrolase superfamily protein |

Chr3:17949496-17951082 FORWARD LENGTH=381 |

201606

Coefficients for Vitvi17g01012.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.675271	9.1069e-11	***	1.193631e-10	***
SlopeC	-1.720188	0.01322339	*	0.3305597	
MeanF-MeanC	-0.7093721	0.0395954	*	0.204845	
SlopeF-SlopeC	-0.6447263	0.5036476		0.9999488	



8.1.445 Vitvi03g01396: Type1.0 *

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

Vitvi03g01396

11.9.3

lipid metabolism.lipid degradation.lysophospholipases

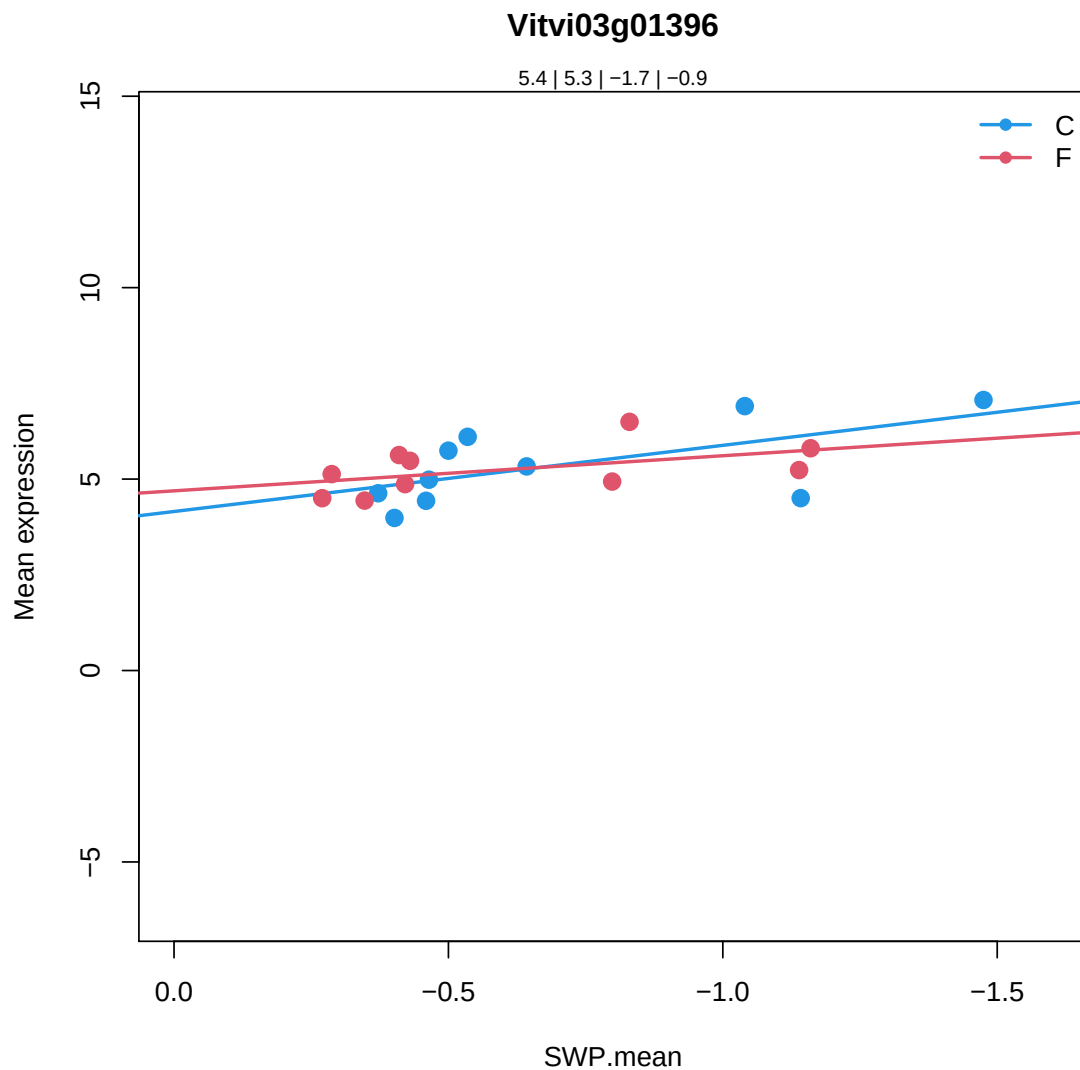
PLC-like phosphodiesterases superfamily protein |

Chr4:18074743-18075699 REVERSE LENGTH=318 |

201606

Coefficients for Vitvi03g01396.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.368151	3.467262e-17	***	8.194759e-17	***
SlopeC	-1.727573	0.009668942	**	0.2995407	
MeanF-MeanC	-0.1171447	0.7084754		0.9091945	
SlopeF-SlopeC	0.8106593	0.3804419		0.9999488	



8.1.446 Vitvi02g00983: Type1.0 *

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

Vitvi02g00983

35.2

not assigned.unknown

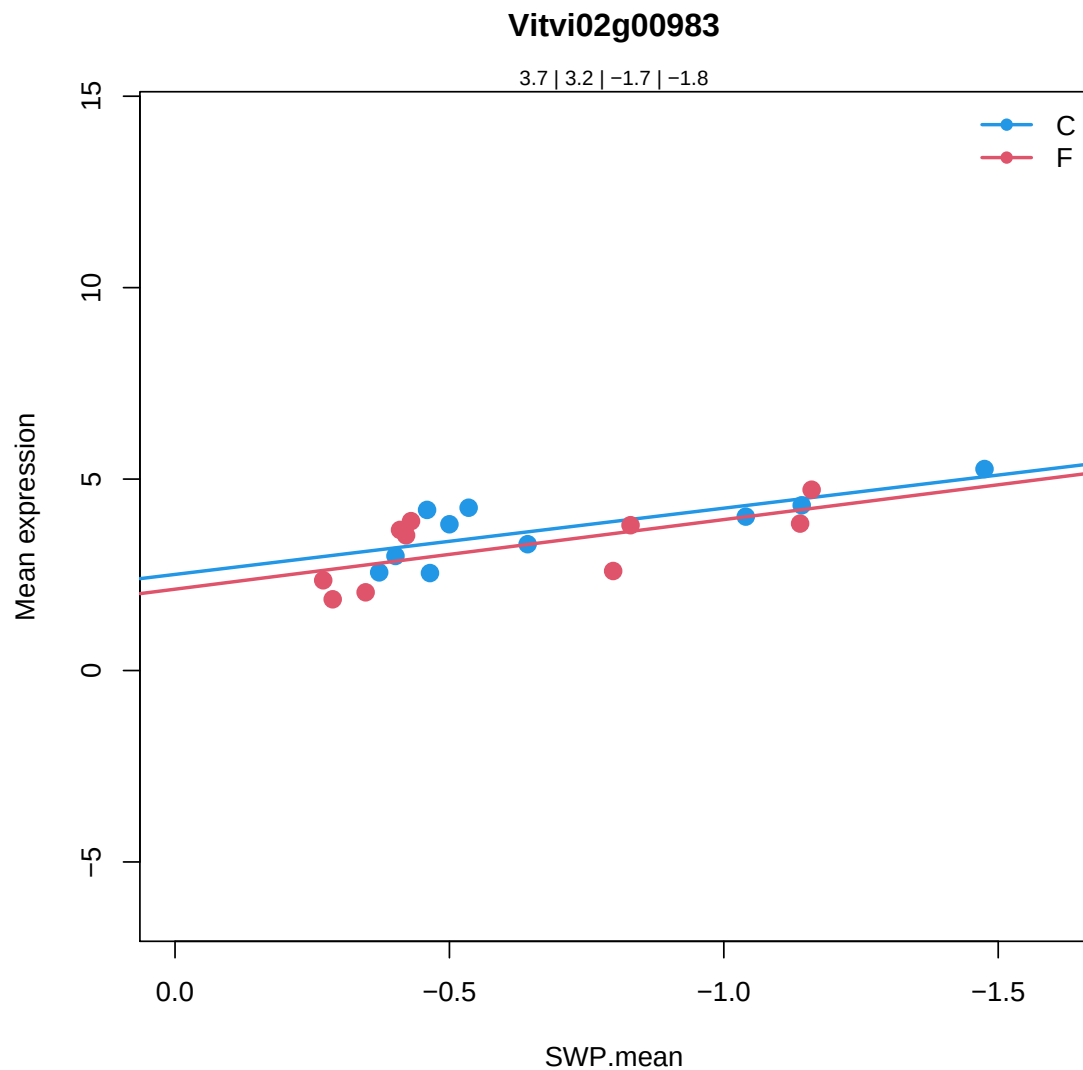
UDP-Glycosyltransferase superfamily protein |

Chr2:15417618-15419108 REVERSE LENGTH=496 |

201606

Coefficients for Vitvi02g00983.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.726364	1.280806e-14	***	2.117818e-14	***
SlopeC	-1.730352	0.005692474	**	0.2614474	
MeanF-MeanC	-0.4946906	0.0984271	.	0.3613261	
SlopeF-SlopeC	-0.08771546	0.9176478		0.9999488	



8.1.447 Vitvi17g01086: Type1.0 *

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

Vitvi17g01086

13.1.1.1.1

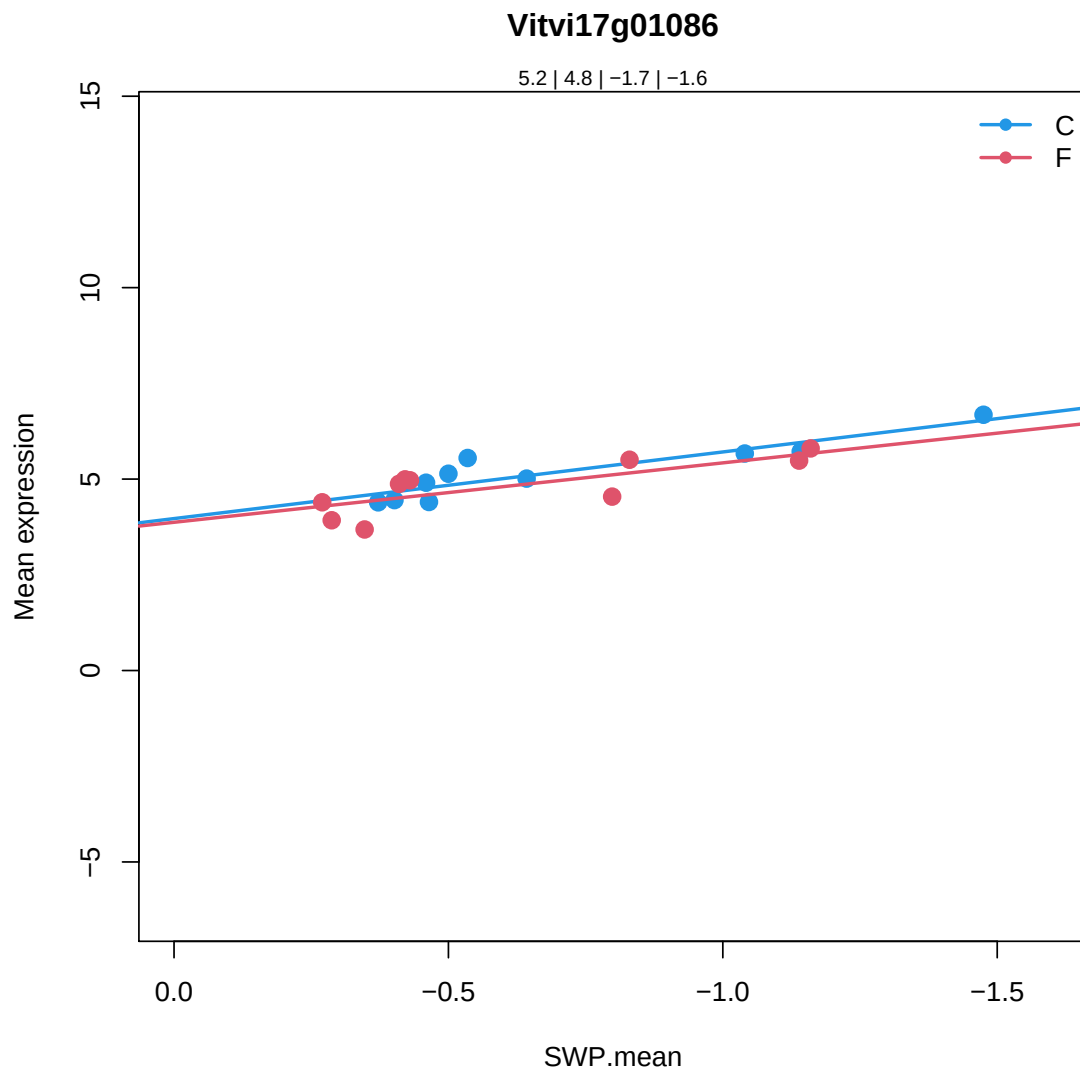
amino acid metabolism.synthesis.central amino acid metabolism.GABA.glu
glutamate decarboxylase |

Chr5:5711141-5714839 FORWARD LENGTH=502 |

201606

Coefficients for Vitvi17g01086.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.192026	2.69292e-21	***	2.468827e-20	***
SlopeC	-1.740421	0.0001322915	***	0.07644173	.
MeanF-MeanC	-0.3751626	0.06188059	.	0.2742611	
SlopeF-SlopeC	0.1882582	0.7389244		0.9999488	



8.1.448 Vitvi06g00785: Type1.0 *

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

Vitvi06g00785

35.1

not assigned.no ontology

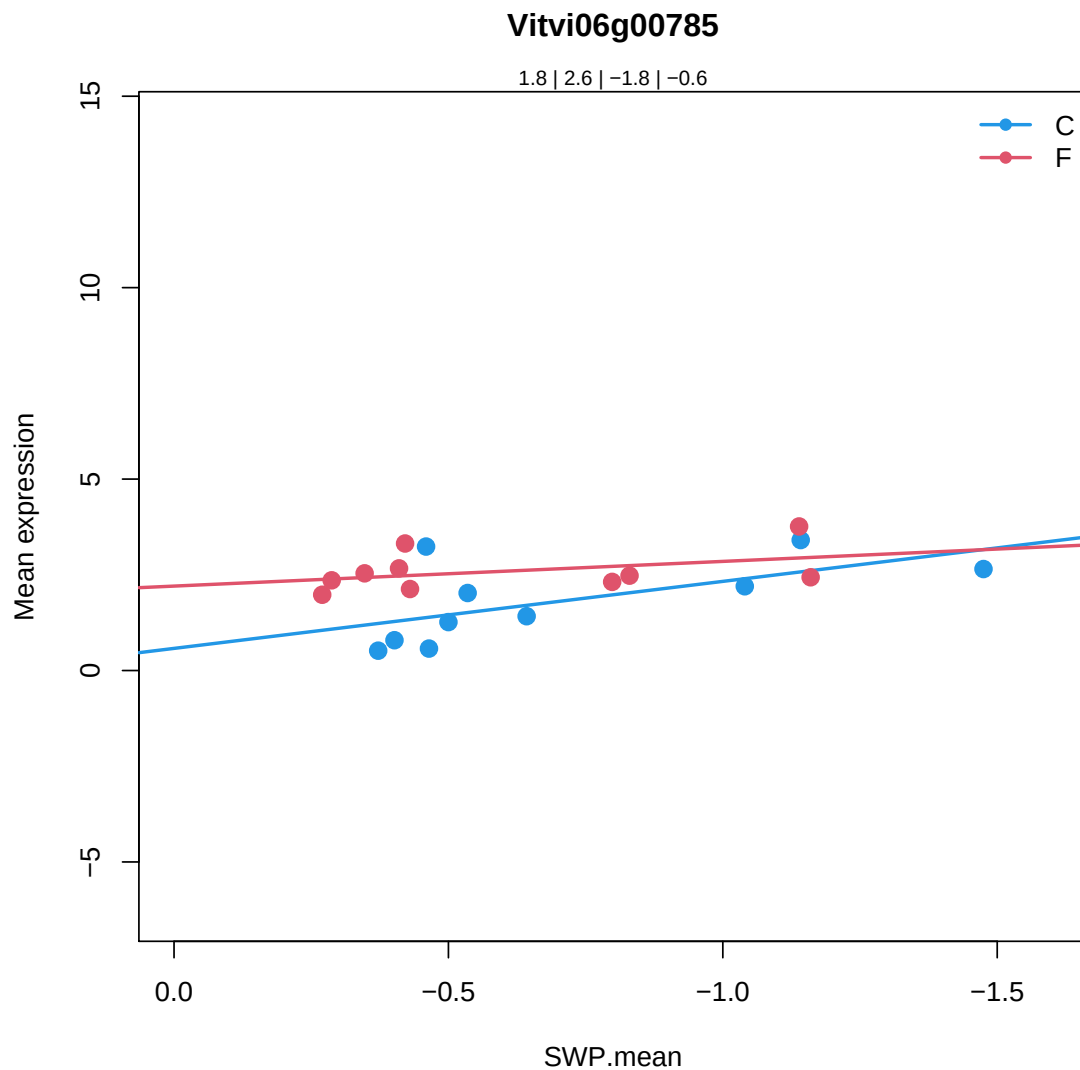
Nucleotidyltransferase family protein |

Chr2:16923541-16925675 FORWARD LENGTH=502 |

201606

Coefficients for Vitvi06g00785.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.808575	2.713846e-08	***	3.270433e-08	***
SlopeC	-1.750152	0.007544818	**	0.2777732	
MeanF-MeanC	0.7890614	0.01597452	*	0.1063712	
SlopeF-SlopeC	1.105081	0.2243224		0.9999488	



8.1.449 Vitvi16g00982: Type1.0 *

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

Vitvi16g00982

20.2.1

stress.abiotic.heat

heat shock factor 4 |

Chr4:17440660-17441706 FORWARD LENGTH=284 |

201606

Vitvi16g00982

27.3.23

RNA.regulation of transcription.heat-shock transcription factor family

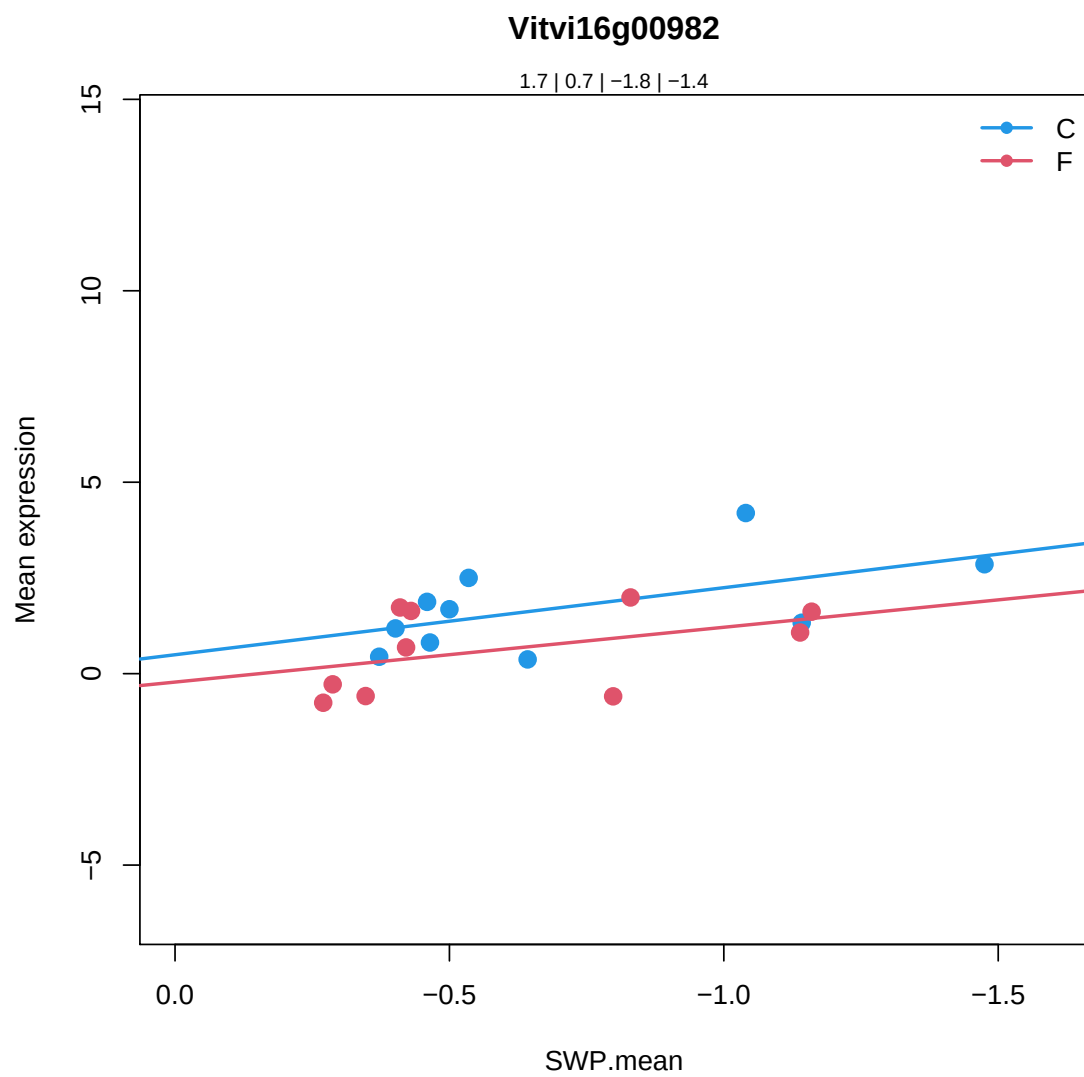
heat shock factor 4 |

Chr4:17440660-17441706 FORWARD LENGTH=284 |

201606

Coefficients for Vitvi16g00982.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.724872	8.428279e-06	***	9.534202e-06	***
SlopeC	-1.751151	0.04586852	*	0.4926906	
MeanF-MeanC	-1.073212	0.01824505	*	0.1178352	
SlopeF-SlopeC	0.319471	0.7974924		0.9999488	



8.1.450 Vitvi02g01261: Type1.0 *

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

Vitvi02g01261

29.2.1.99.99

protein.synthesis.ribosomal protein.unknown.unknown

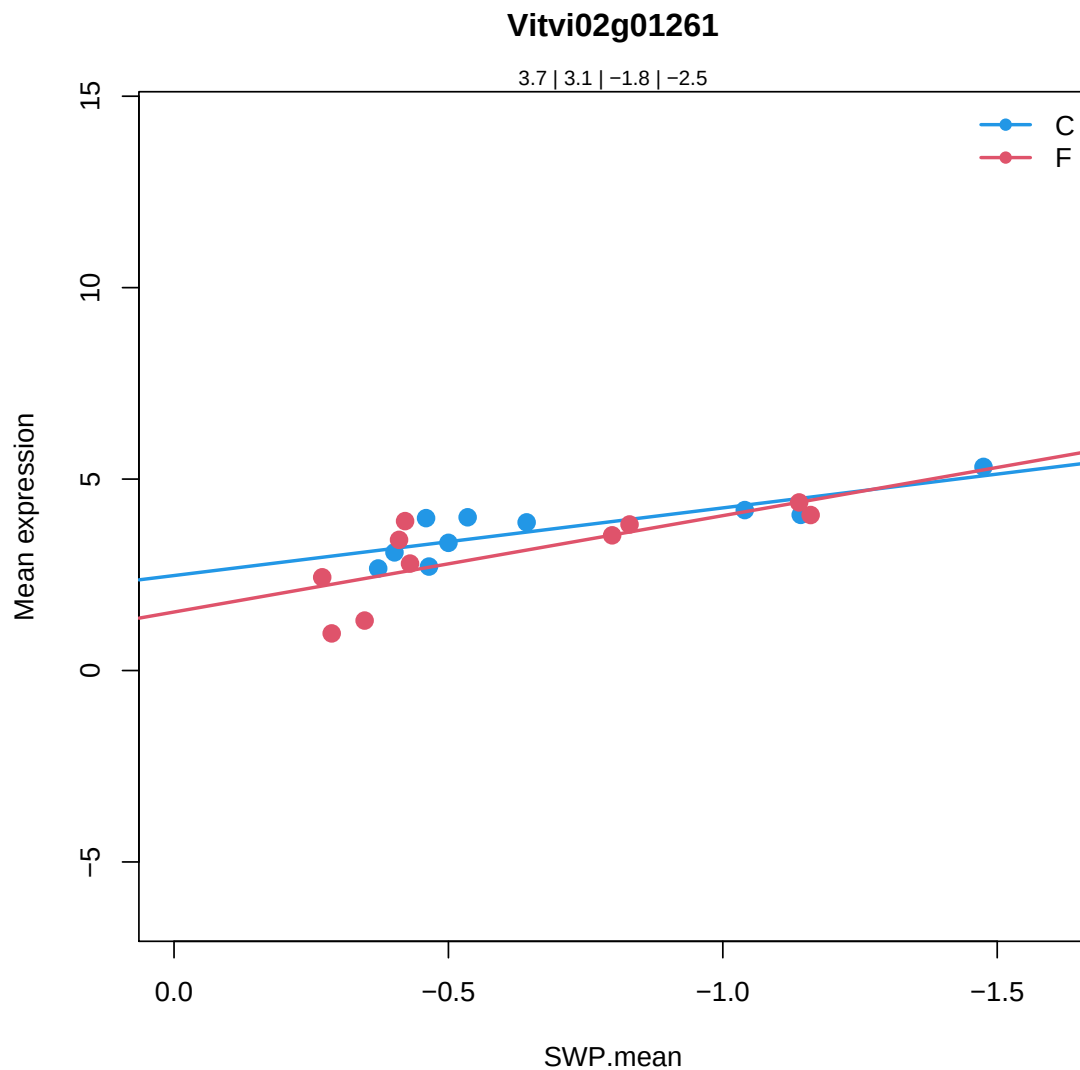
Uncharacterized protein family (UPF0114) |

Chr4:10574903-10577267 REVERSE LENGTH=185 |

201606

Coefficients for Vitvi02g01261.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.722424	1.037277e-14	***	1.731483e-14	***
SlopeC	-1.766391	0.004510503	**	0.2419697	
MeanF-MeanC	-0.6610484	0.0293114	*	0.1663141	
SlopeF-SlopeC	-0.7504356	0.3753056		0.9999488	



8.1.451 Vitvi02g01852: Type1.0 *

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

Vitvi02g01852

20.2.1

stress.abiotic.heat

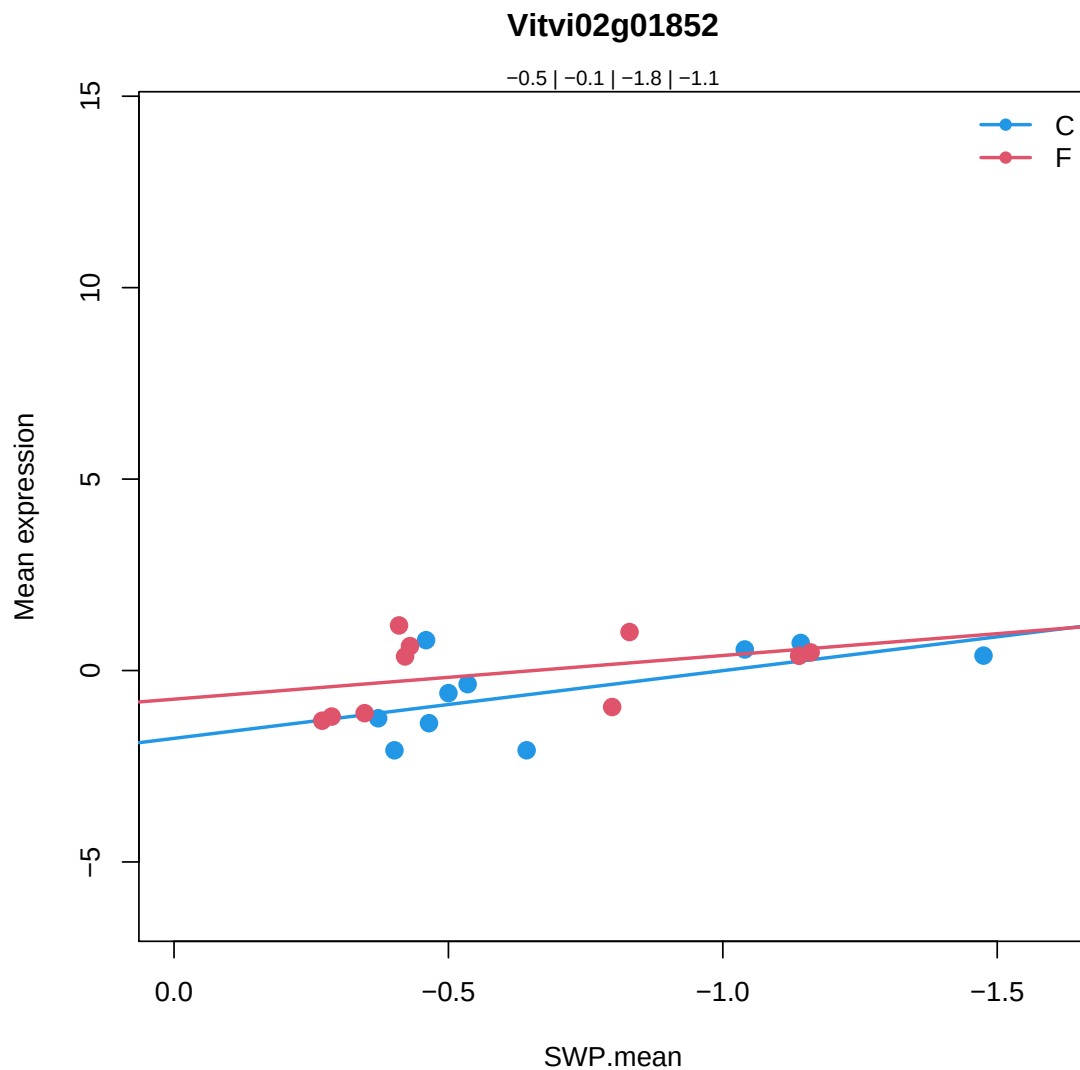
stress-inducible protein |

Chr1:23231026-23233380 FORWARD LENGTH=571 |

201606

Coefficients for Vitvi02g01852.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.5286088	0.06549246	.	0.06800436	.
SlopeC	-1.767977	0.02941536	*	0.4298647	
MeanF-MeanC	0.4750401	0.2307299		0.5845173	
SlopeF-SlopeC	0.6275276	0.5836209		0.9999488	



8.1.452 Vitvi18g02167: Type1.0

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

Vitvi18g02167

17.1.1.1.12

hormone metabolism.abscisic acid.synthesis-degradation.synthesis.absci

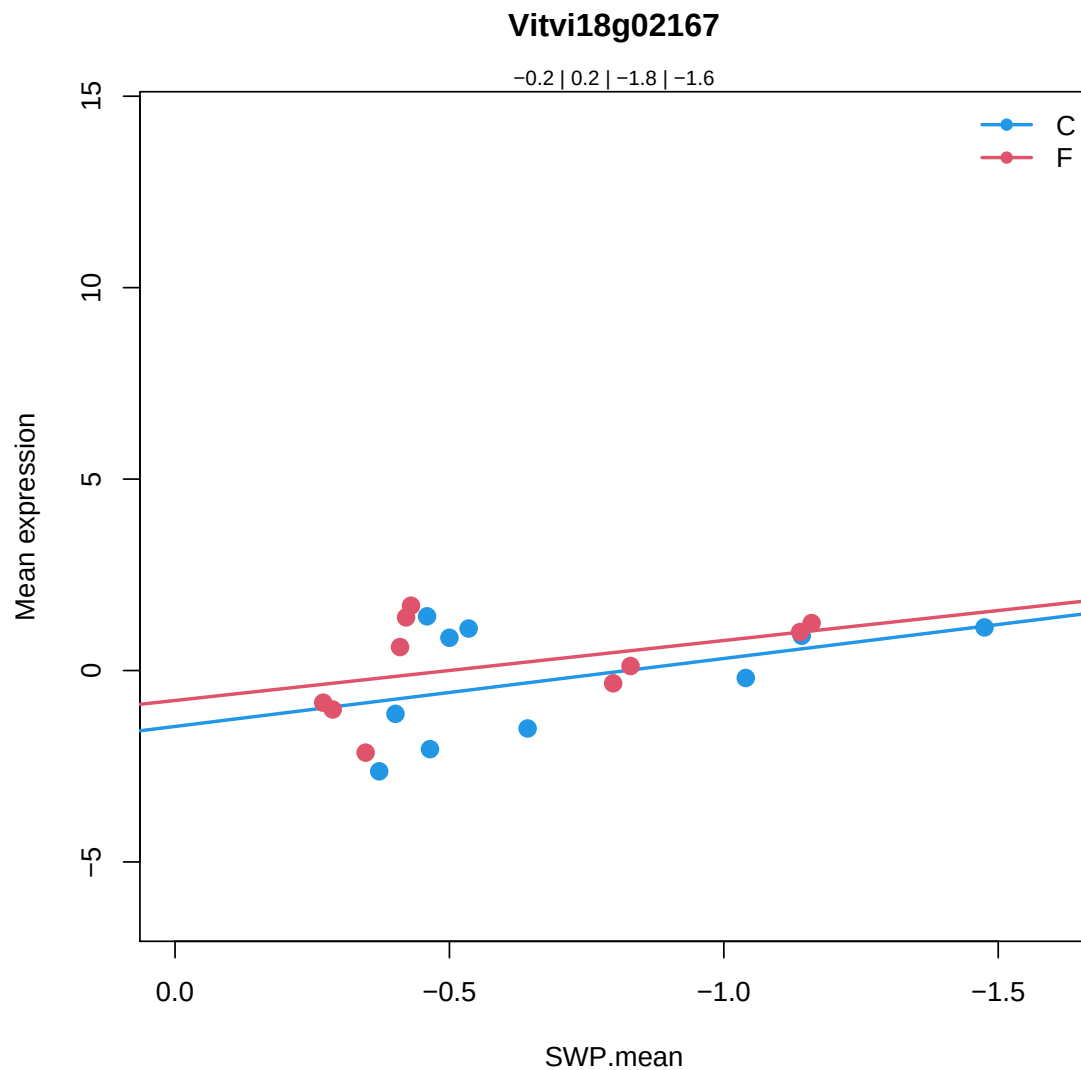
aldehyde oxidase 1 |

Chr5:7116783-7122338 FORWARD LENGTH=1368 |

201606

Coefficients for Vitvi18g02167.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.2128345	0.5677555		0.5735505	
SlopeC	-1.774895	0.09629287	.	0.6067366	
MeanF-MeanC	0.3844787	0.4665734		0.7876703	
SlopeF-SlopeC	0.2086531	0.8920053		0.9999488	



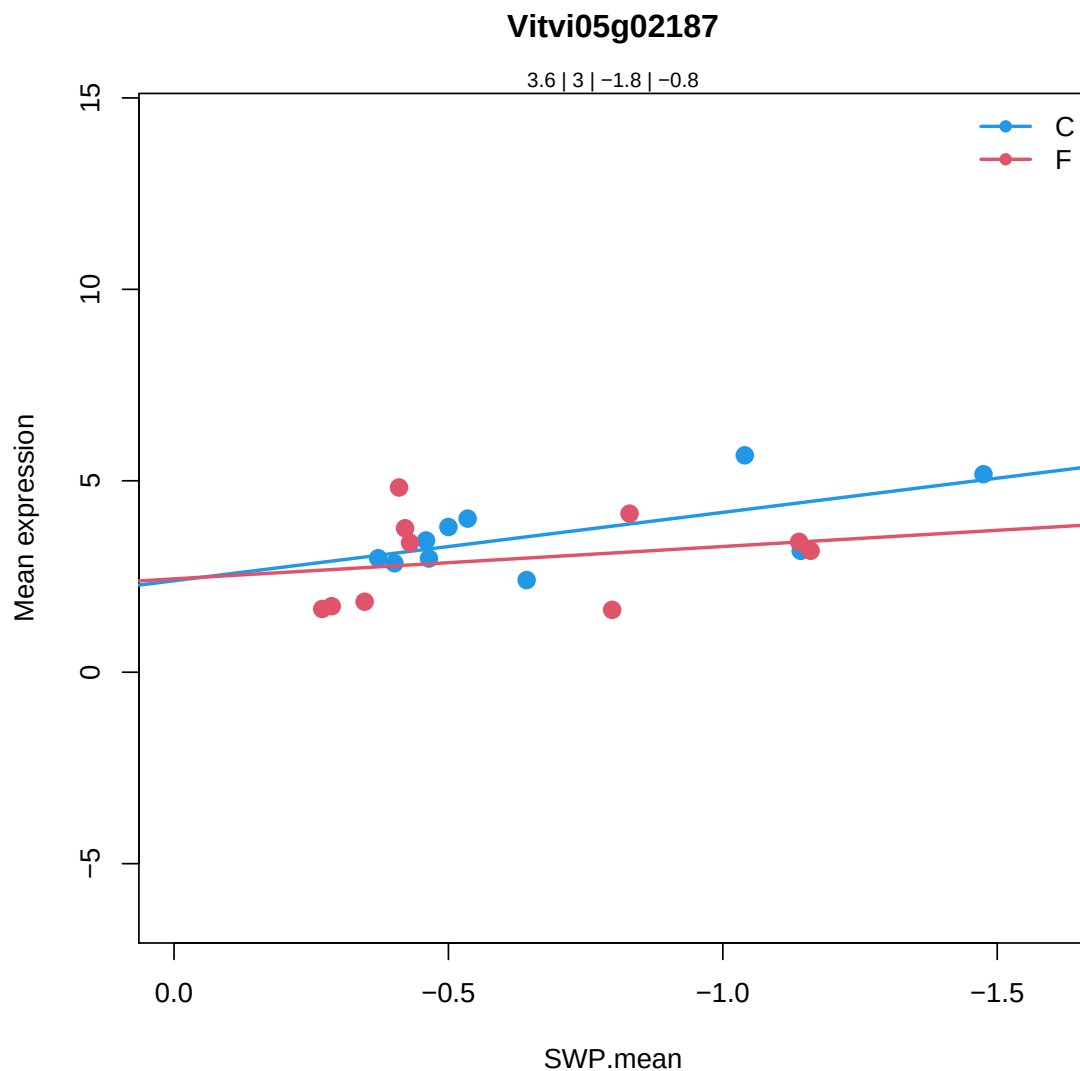
8.1.453 Vitvi05g02187: Type1.0 *

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

```
Vitvi05g02187
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi05g02187.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.644933	3.00649e-11	***	4.020082e-11	***
SlopeC	-1.785703	0.04027493	*	0.4733003	
MeanF-MeanC	-0.6916305	0.1107727		0.3883158	
SlopeF-SlopeC	0.9404973	0.4482319		0.9999488	



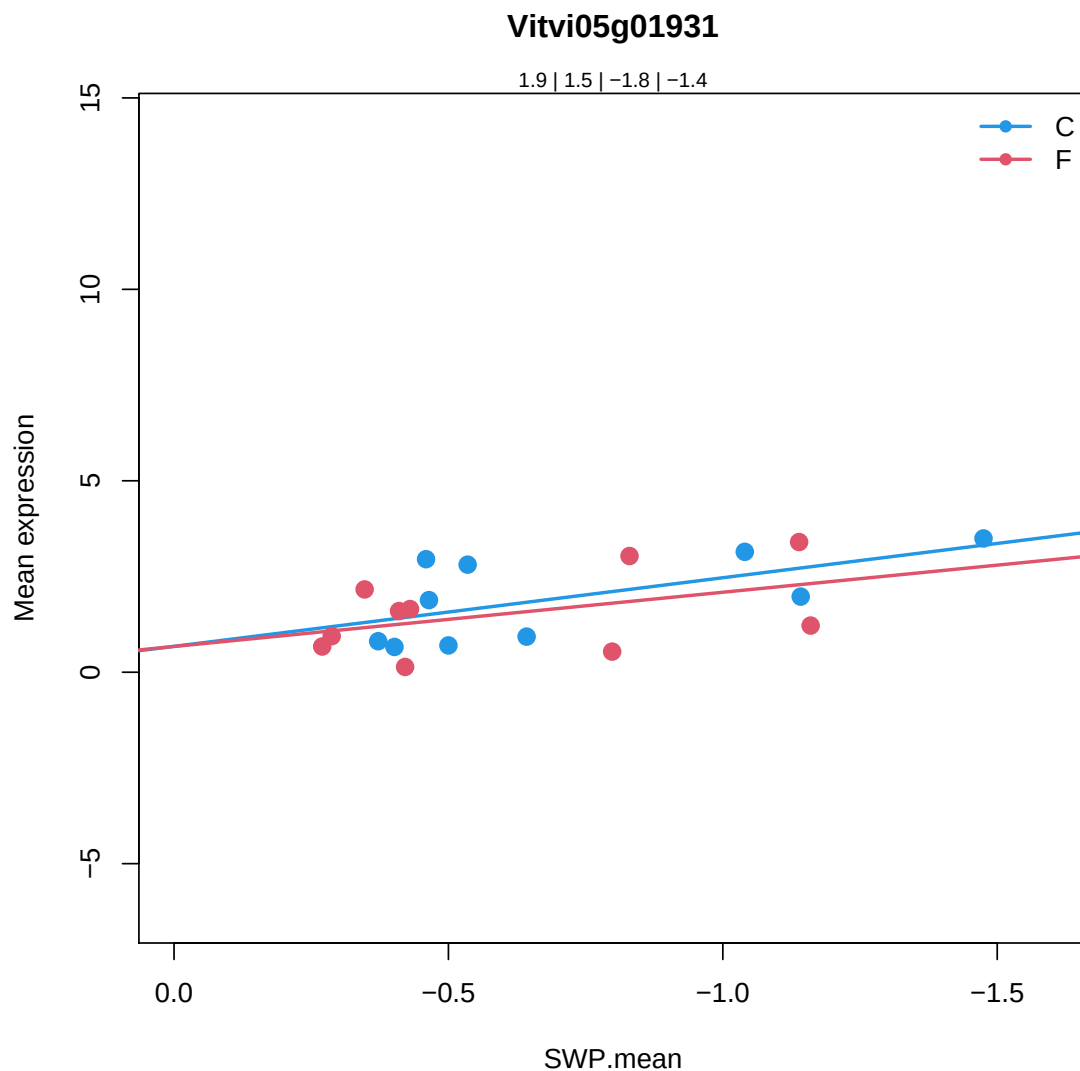
8.1.454 Vitvi05g01931: Type1.0 *

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

```
Vitvi05g01931
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi05g01931.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.935812	5.915734e-07	***	6.872532e-07	***
SlopeC	-1.79156	0.02990746	*	0.4304569	
MeanF-MeanC	-0.4005626	0.3177162		0.6790186	
SlopeF-SlopeC	0.3751086	0.7467065		0.9999488	



8.1.455 Vitvi18g00395: Type1.0 *

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

Vitvi18g00395

31.1

cell.organisation

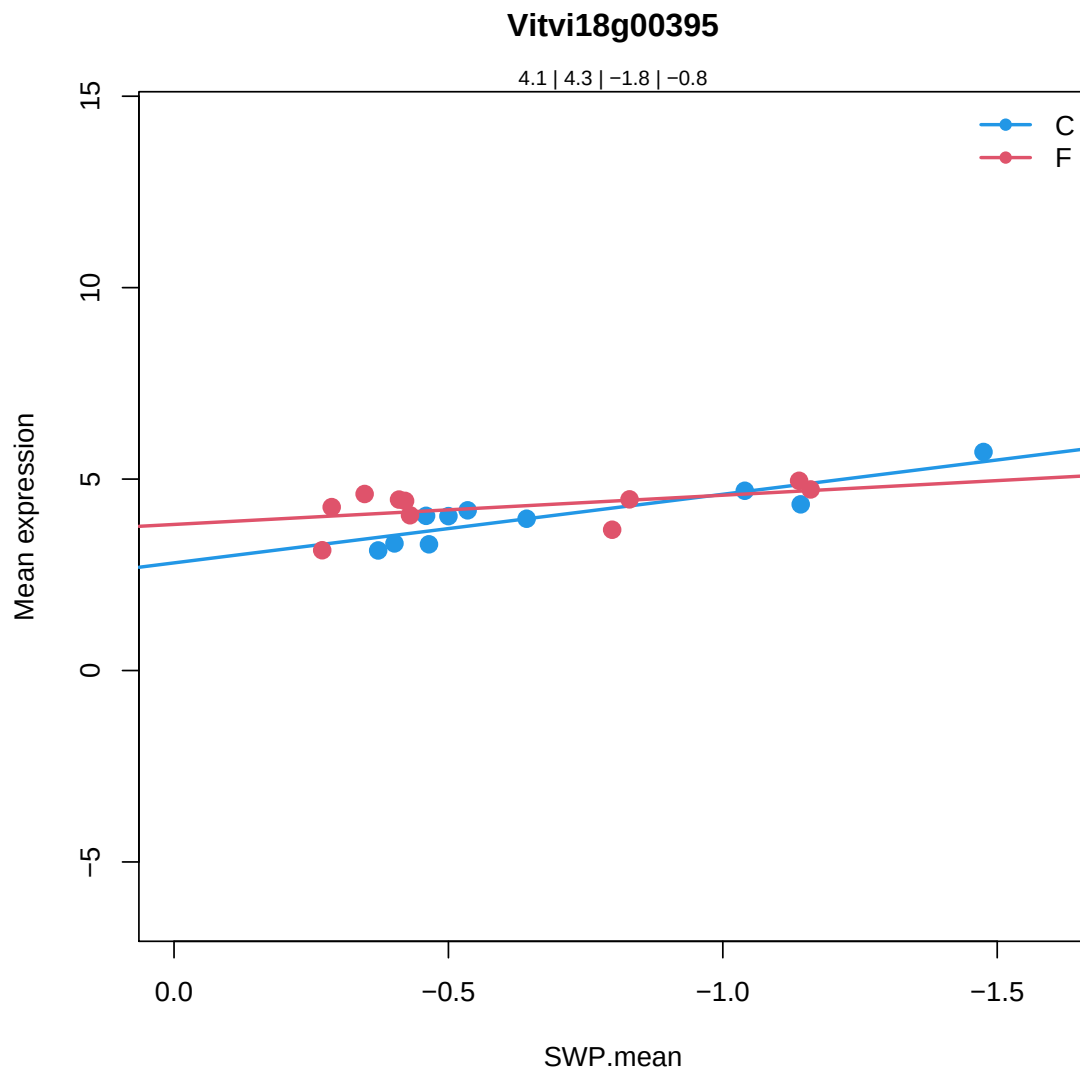
annexin 2 |

Chr5:25974366-25975554 FORWARD LENGTH=302 |

201606

Coefficients for Vitvi18g00395.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.07145	1.343893e-18	***	4.464607e-18	***
SlopeC	-1.792095	0.0001702585	***	0.07644173	.
MeanF-MeanC	0.2086388	0.3099091		0.6737853	
SlopeF-SlopeC	1.028538	0.09423197	.	0.9999488	



8.1.456 Vitvi10g01342: Type1.0 *

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

Vitvi10g01342

27.3.36

RNA.regulation of transcription.argonaute transcription factor family

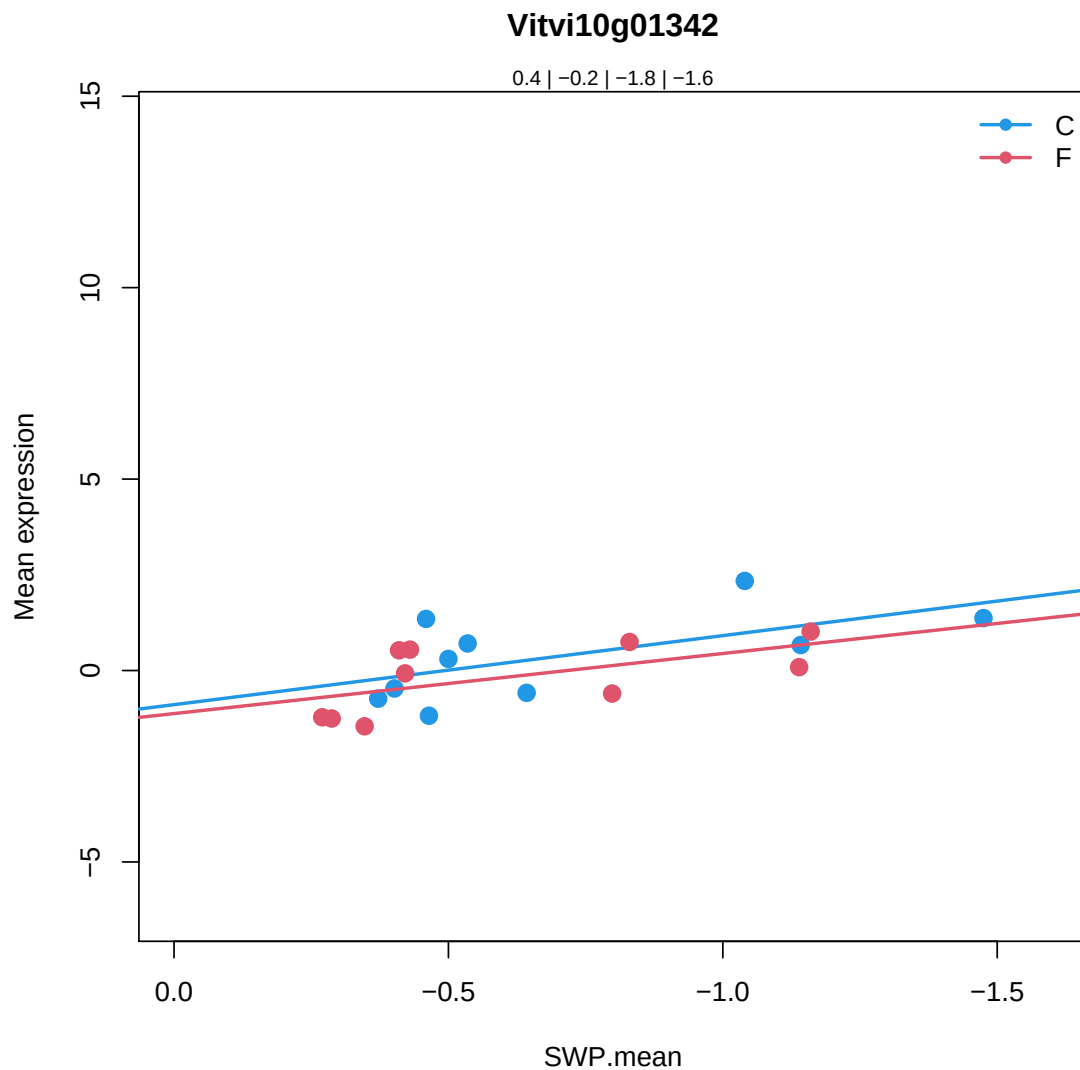
Argonaute family protein |

Chr1:11181777-11185112 FORWARD LENGTH=1014 |

201606

Coefficients for Vitvi10g01342.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3761012	0.144305		0.1485645	
SlopeC	-1.802985	0.0161523	*	0.3486596	
MeanF-MeanC	-0.5447118	0.1353421		0.4400114	
SlopeF-SlopeC	0.2340175	0.8220433		0.9999488	



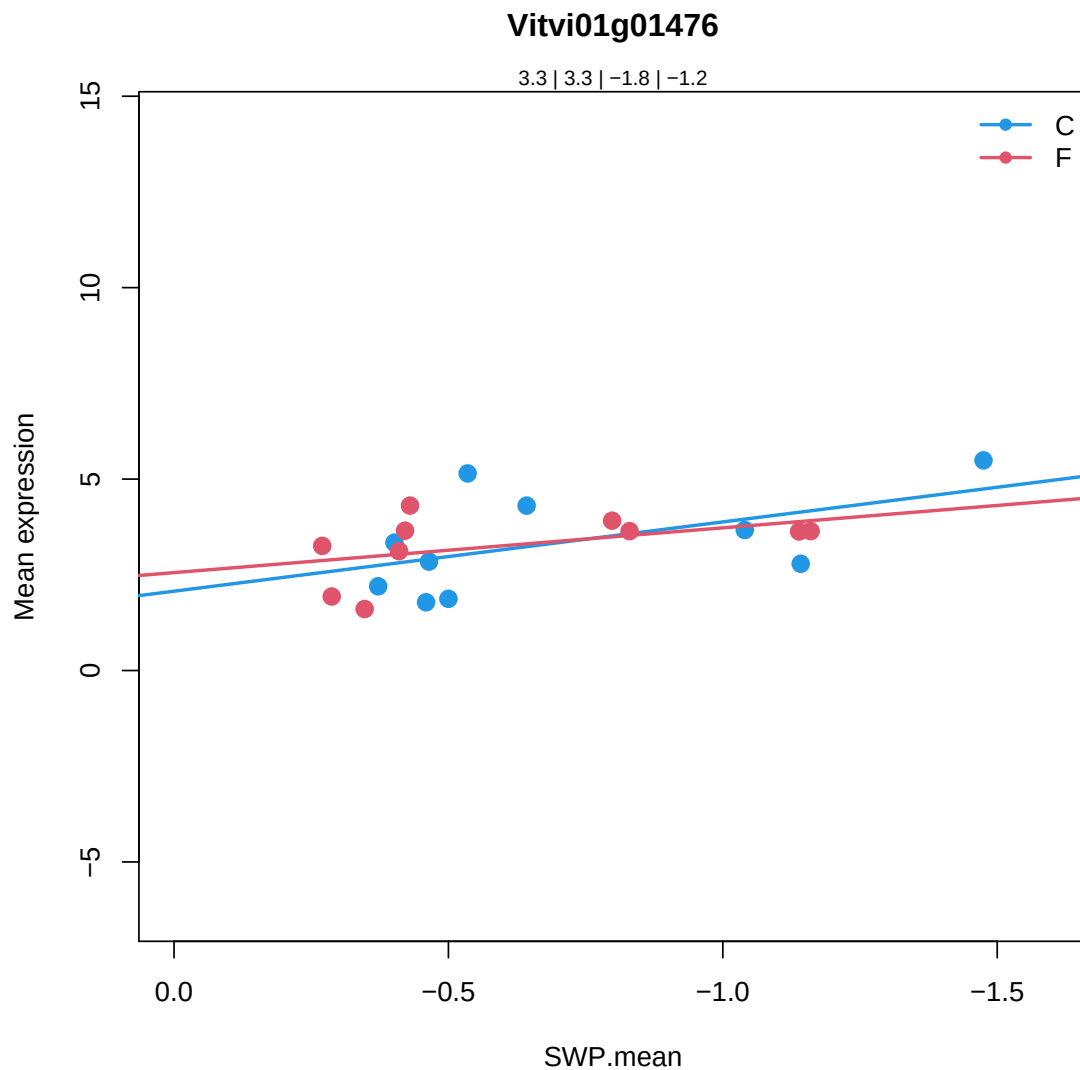
8.1.457 Vitvi01g01476: Type1.0 *

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

```
Vitvi01g01476
20.1.7
stress.biotic.PR-proteins
low-molecular-weight cysteine-rich 69 |
Chr2:528397-528885 FORWARD LENGTH=77 |
201606
```

Coefficients for Vitvi01g01476.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.344007	9.354794e-11	***	1.22549e-10	***
SlopeC	-1.809843	0.03360248	*	0.4433084	
MeanF-MeanC	-0.07433994	0.8561604		0.961934	
SlopeF-SlopeC	0.6402543	0.5950105		0.9999488	



8.1.458 Vitvi08g00764: Type1.0 *

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

Vitvi08g00764

15.2

metal handling.binding, chelation and storage

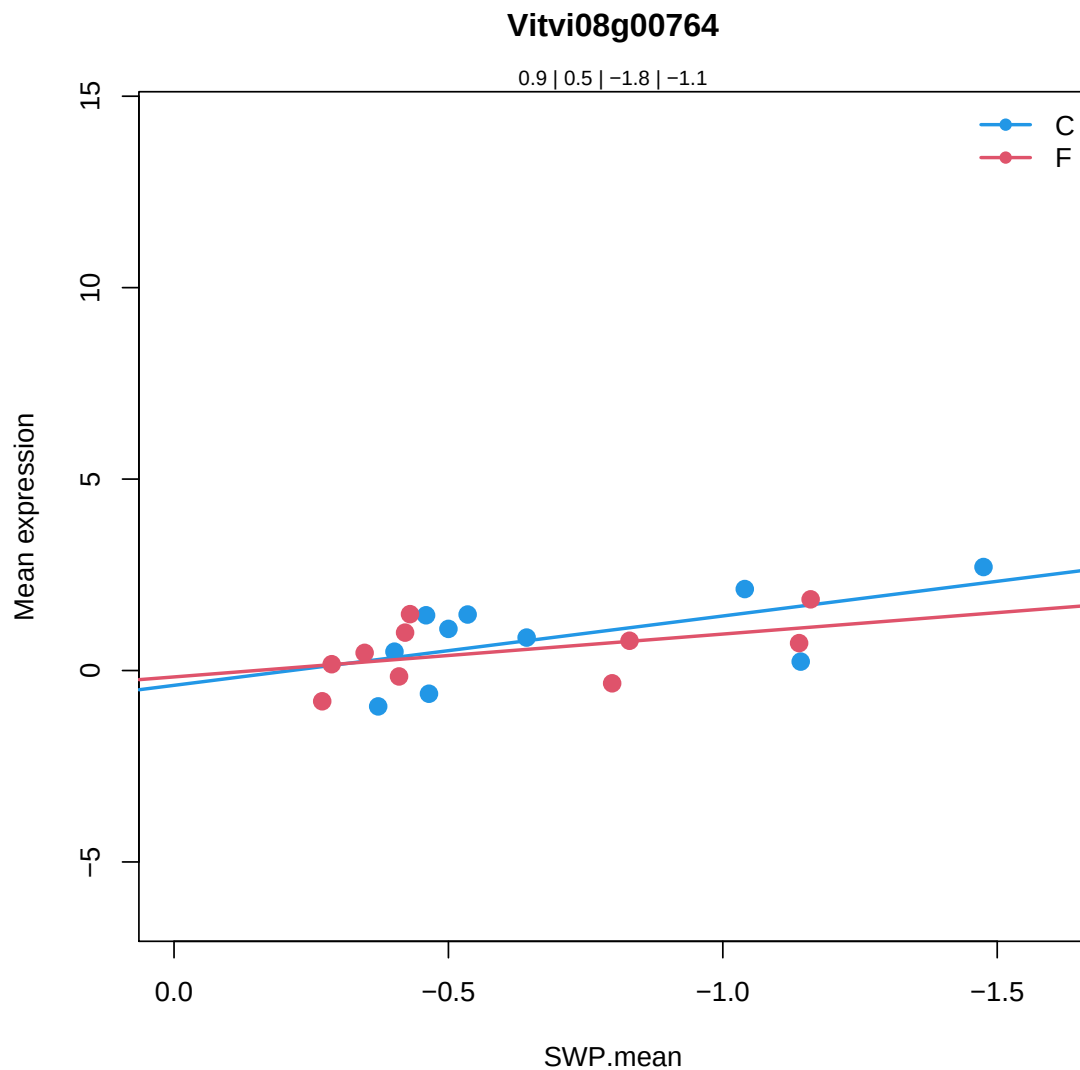
ferritin 4 |

Chr2:16831501-16833214 REVERSE LENGTH=259 |

201606

Coefficients for Vitvi08g00764.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8864719	0.001917526	**	0.002063175	**
SlopeC	-1.811376	0.01668903	*	0.3523917	
MeanF-MeanC	-0.3718117	0.3061539		0.6693361	
SlopeF-SlopeC	0.6917751	0.5124205		0.9999488	



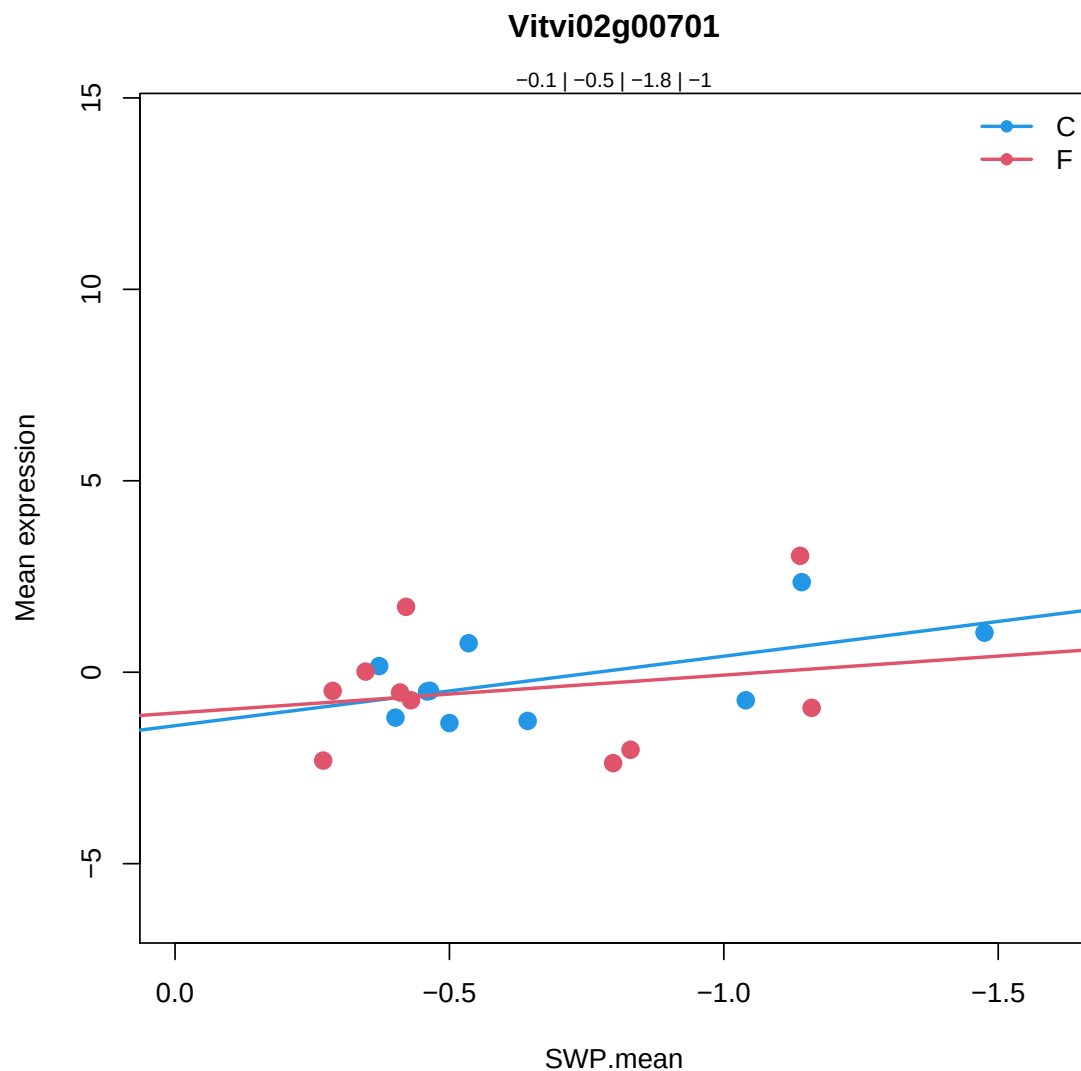
8.1.459 Vitvi02g00701: Type1.0

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

```
Vitvi02g00701
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi02g00701.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.1202513	0.7715895		0.7759165	
SlopeC	-1.815325	0.1252937		0.6460361	
MeanF-MeanC	-0.3420668	0.560469		0.8394093	
SlopeF-SlopeC	0.8241753	0.6314736		0.9999488	



8.1.460 Vitvi02g00228: Type1.0 *

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

Vitvi02g00228

27.3.35

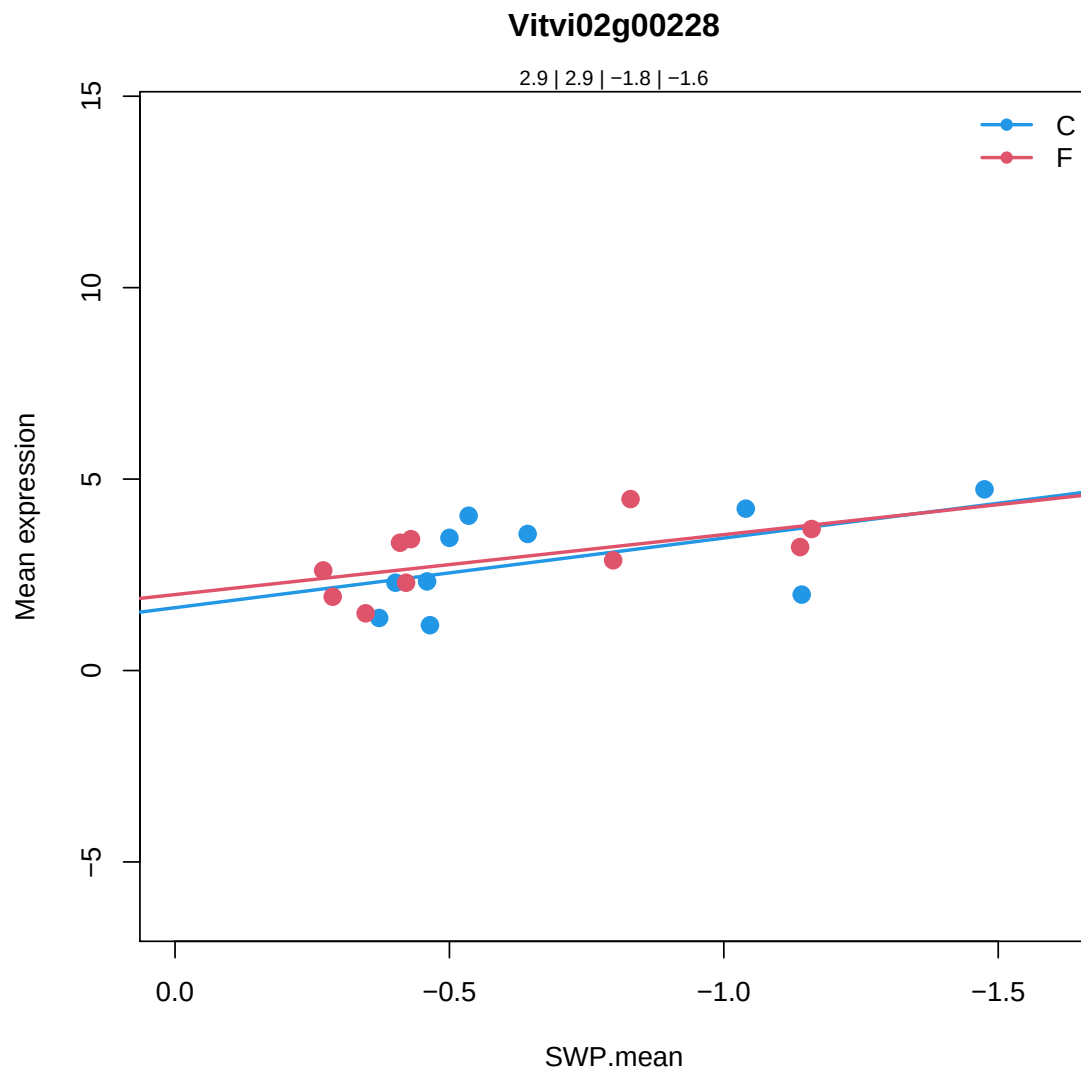
RNA.regulation of transcription.bZIP transcription factor family
homeobox 7 |

Chr2:19165777-19166773 REVERSE LENGTH=258 |

201606

Coefficients for Vitvi02g00228.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.91942	3.526112e-10	***	4.517906e-10	***
SlopeC	-1.818326	0.02386796	*	0.3984616	
MeanF-MeanC	0.01795977	0.9627522		0.9915437	
SlopeF-SlopeC	0.2522321	0.8228588		0.9999488	



8.1.461 Vitvi04g01834: Type1.0 *

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

Vitvi04g01834

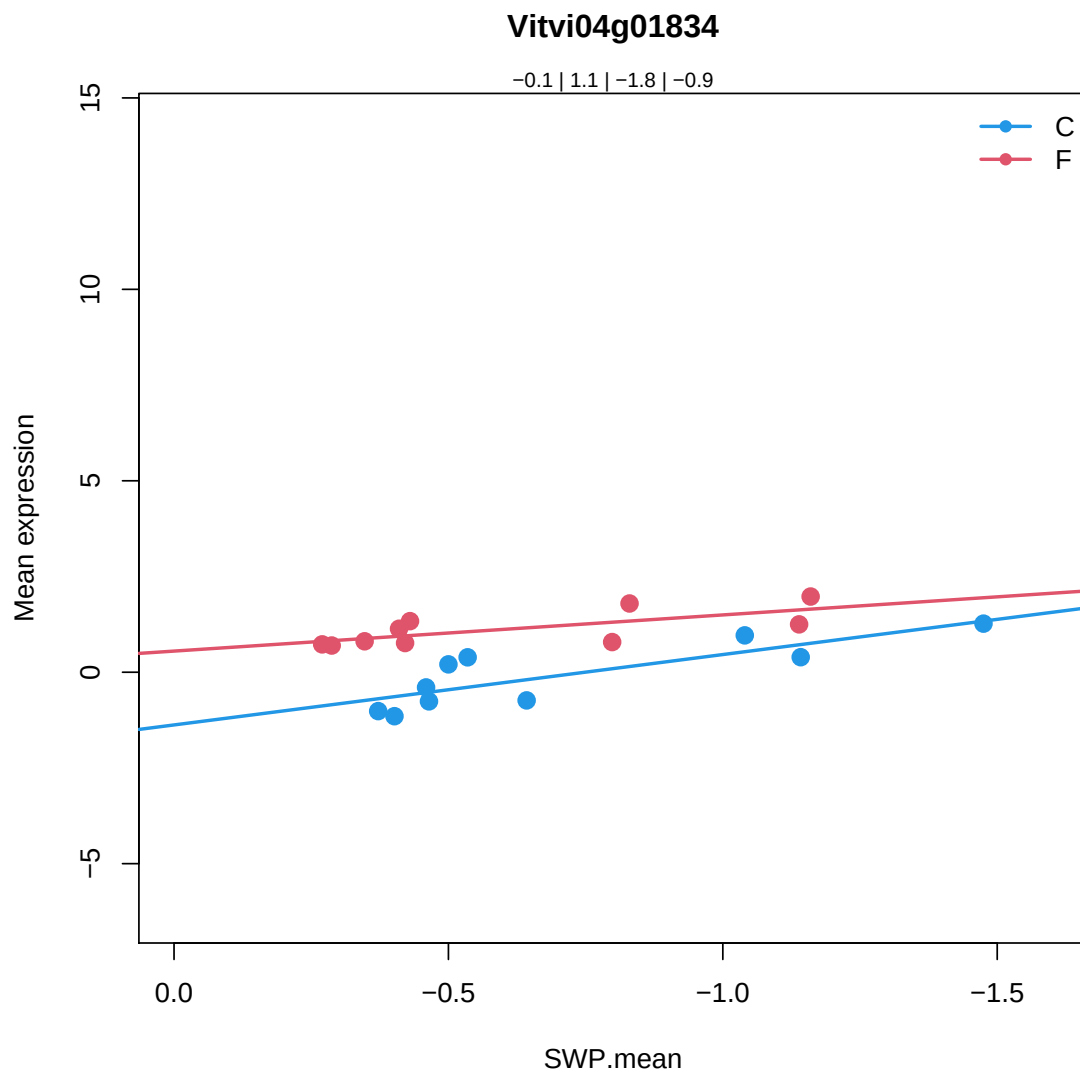
27.1

RNA.processing

NA

Coefficients for Vitvi04g01834.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.08409908	0.5614659		0.5673095	
SlopeC	-1.838155	0.0001361264	***	0.07644173	.
MeanF-MeanC	1.211348	5.327887e-06	***	0.000141552	***
SlopeF-SlopeC	0.8937189	0.1446942		0.9999488	



8.1.462 Vitvi05g01740: Type1.0 *

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

Vitvi05g01740

16.8.2

secondary metabolism.flavonoids.chalcones

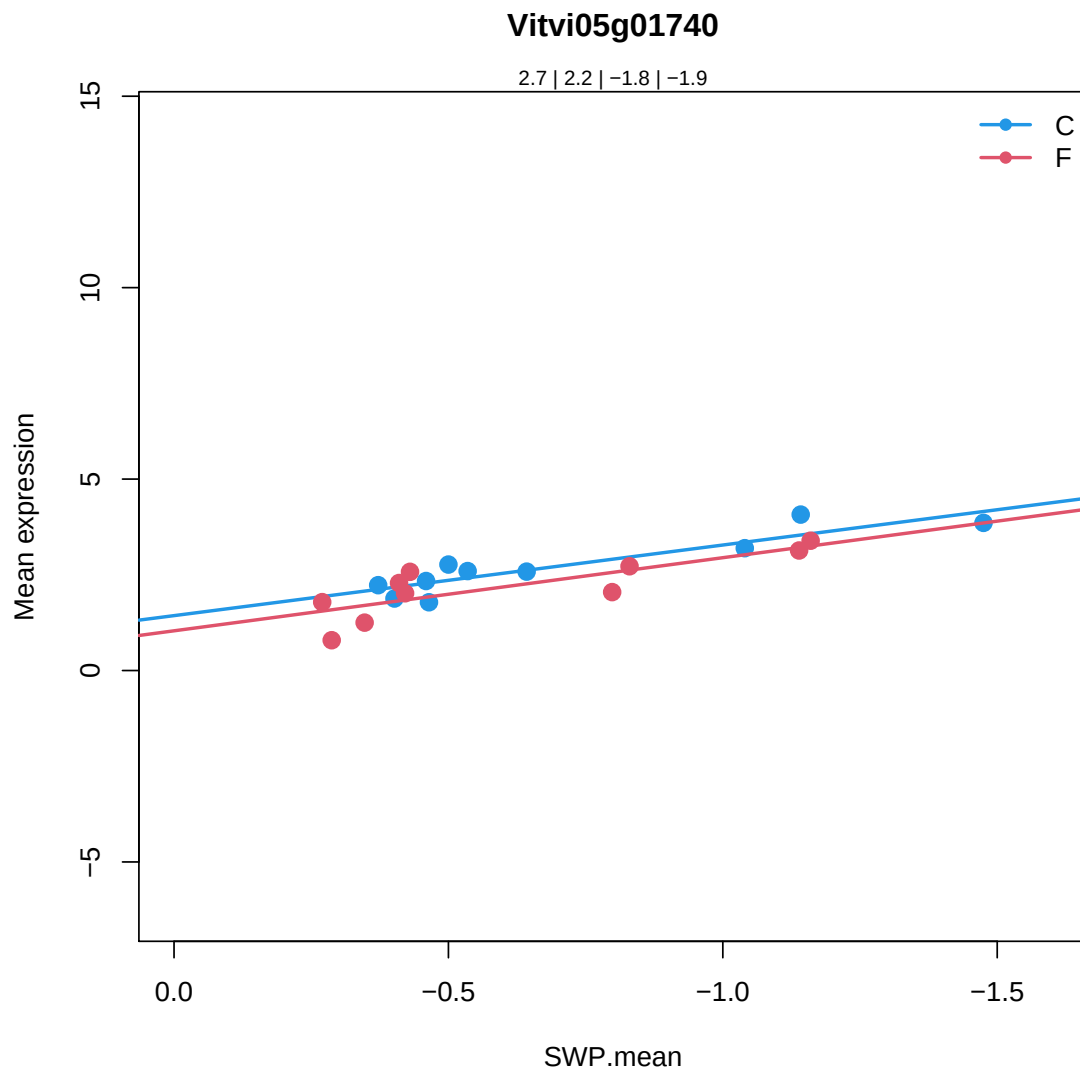
NAD(P)-linked oxidoreductase superfamily protein |

Chr1:22071410-22073067 REVERSE LENGTH=326 |

201606

Coefficients for Vitvi05g01740.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.730013	4.118221e-15	***	7.20665e-15	***
SlopeC	-1.844095	0.0001091579	***	0.07644173	.
MeanF-MeanC	-0.5296411	0.01417235	*	0.09792158	.
SlopeF-SlopeC	-0.06541604	0.9113725		0.9999488	



8.1.463 Vitvi01g00825: Type1.0 *

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

Vitvi01g00825

35.2

not assigned.unknown

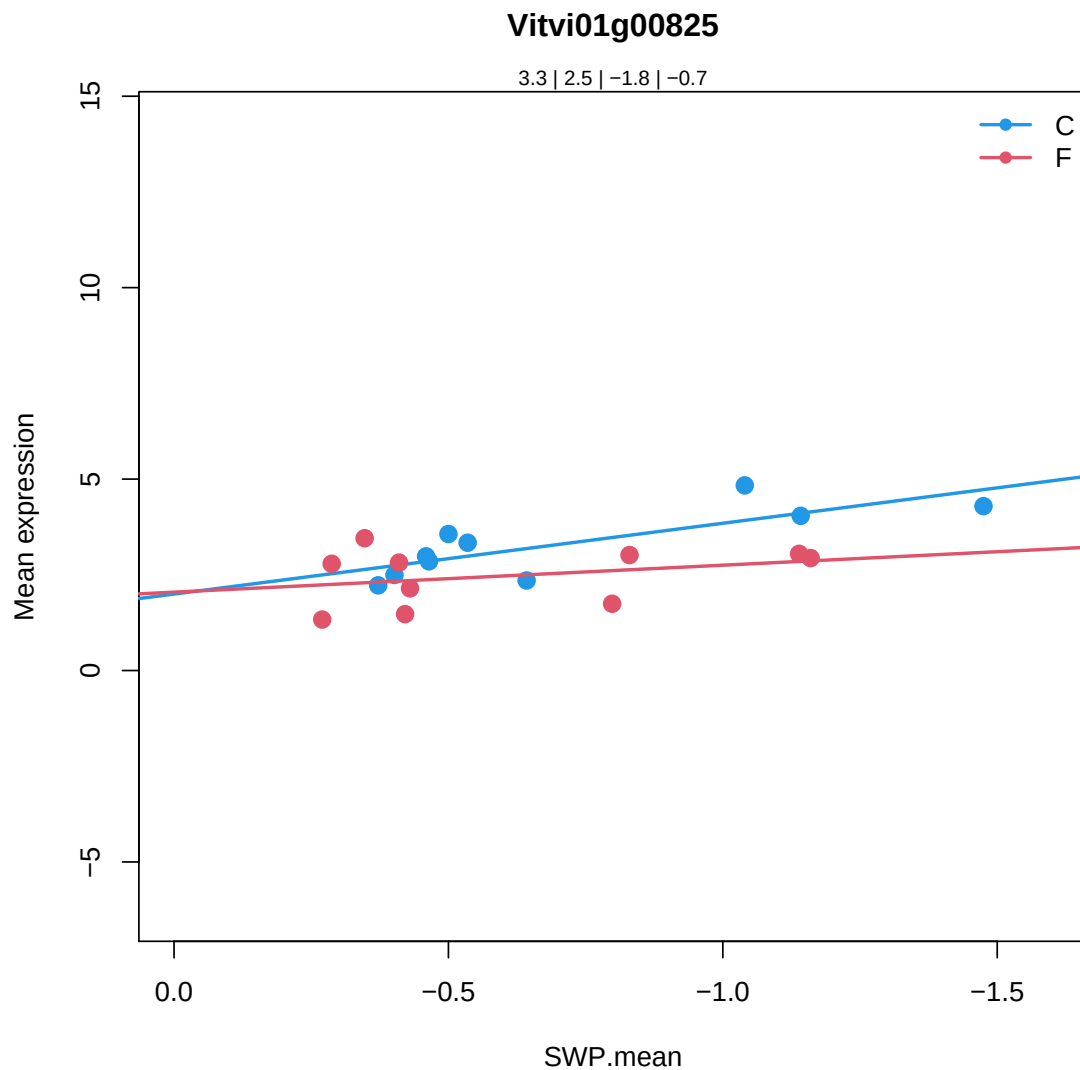
Serine/Threonine-kinase |

Chr1:3470009-3471291 FORWARD LENGTH=179 |

201606

Coefficients for Vitvi01g00825.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.297525	8.377227e-14	***	1.293937e-13	***
SlopeC	-1.849164	0.00277545	**	0.2030621	
MeanF-MeanC	-0.8220092	0.007452071	**	0.06123152	.
SlopeF-SlopeC	1.145135	0.1740949		0.9999488	



8.1.464 Vitvi02g01409: Type1.0 *

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

Vitvi02g01409

20.1.7.5

stress.biotic.PR-proteins.PR5 (thaumatin-like proteins)

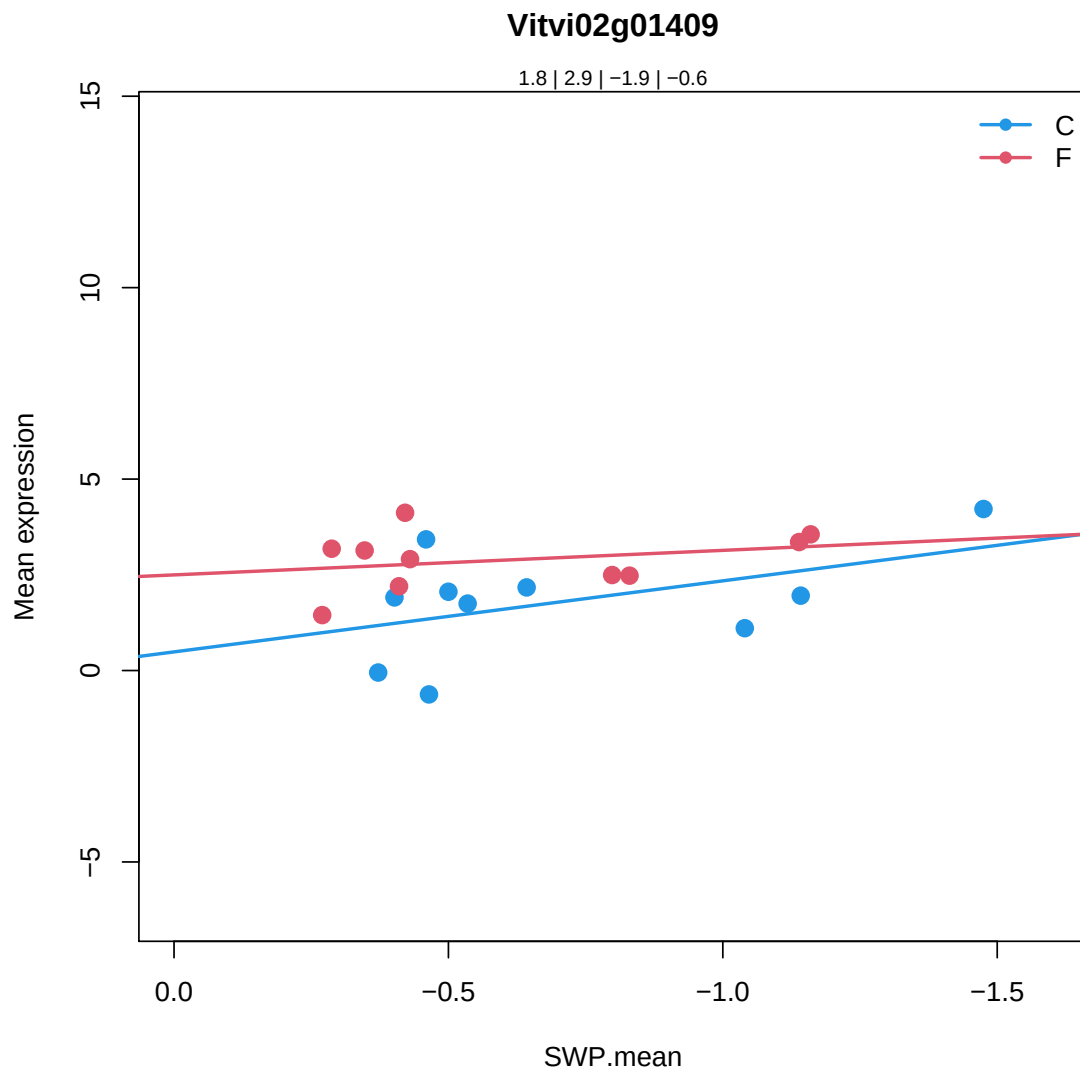
osmotin 34 |

Chr4:7025127-7026113 REVERSE LENGTH=244 |

201606

Coefficients for Vitvi02g01409.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.791083	7.780268e-06	***	8.809661e-06	***
SlopeC	-1.855416	0.04090008	*	0.477587	
MeanF-MeanC	1.09652	0.01931327	*	0.1230958	
SlopeF-SlopeC	1.214481	0.3493272		0.9999488	



8.1.465 Vitvi13g01556: Type1.0 *

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

Vitvi13g01556

33.99

development.unspecified

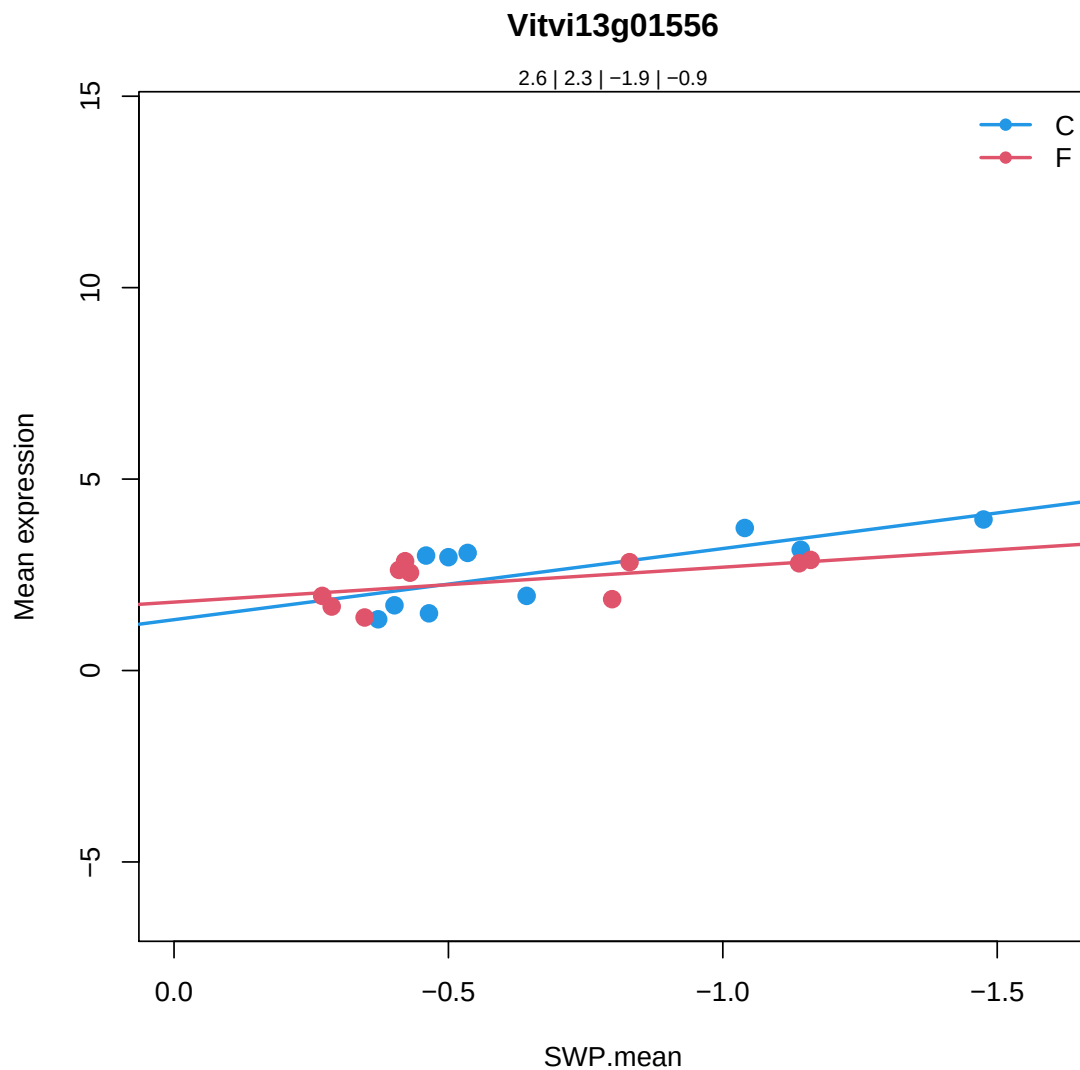
scarecrow-like 3 |

Chr1:18678177-18679625 REVERSE LENGTH=482 |

201606

Coefficients for Vitvi13g01556.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.63391	9.616332e-13	***	1.381843e-12	***
SlopeC	-1.858215	0.001124368	**	0.1338876	
MeanF-MeanC	-0.2915686	0.2587852		0.6203666	
SlopeF-SlopeC	0.9463156	0.2122042		0.9999488	



8.1.466 Vitvi11g00720: Type1.0 *

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

Vitvi11g00720

16.2.1.4

secondary metabolism.phenylpropanoids.lignin biosynthesis.HCT

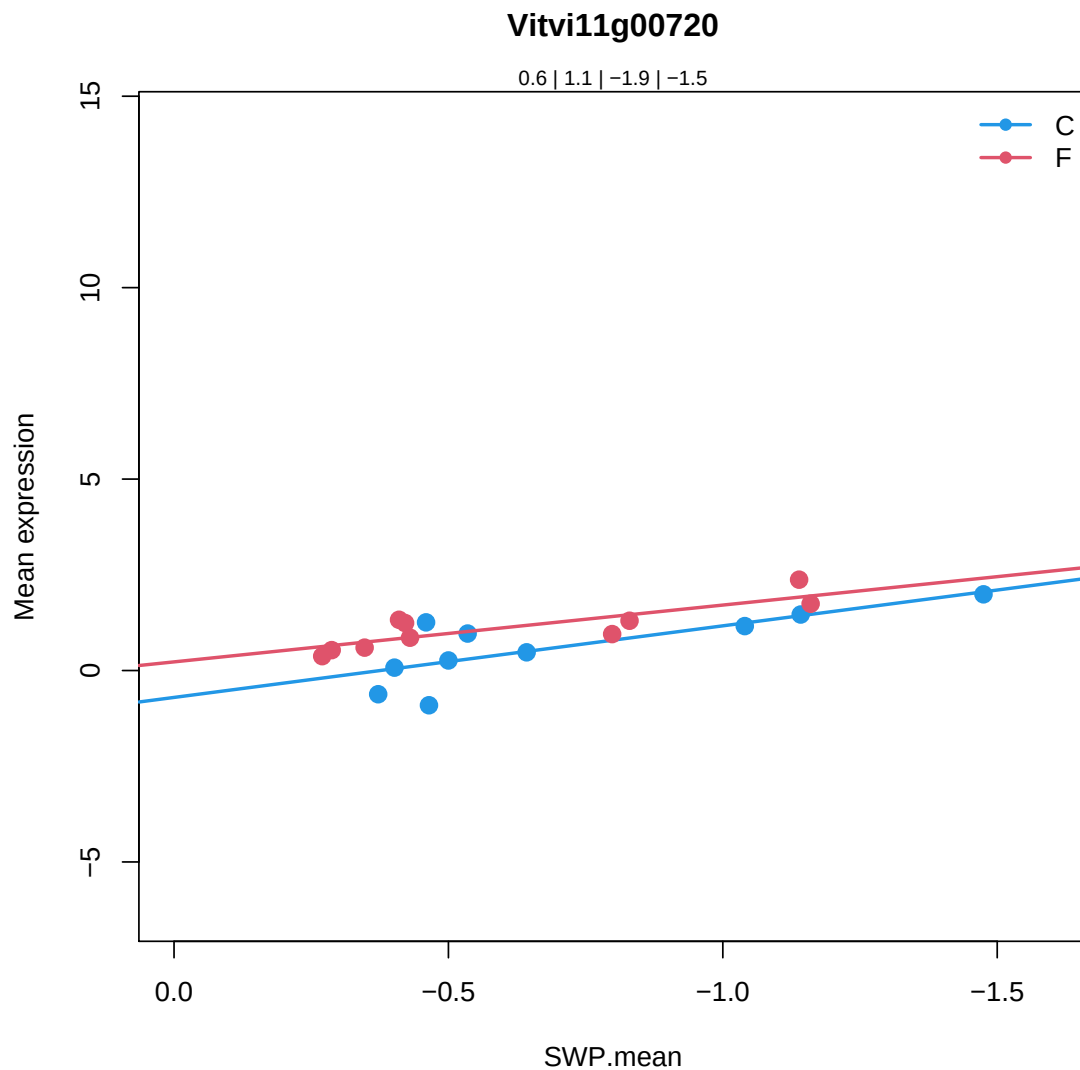
hydroxycinnamoyl-CoA shikimate/quinic acid hydroxycinnamoyl transferase |

Chr5:19836654-19838092 REVERSE LENGTH=433 |

201606

Coefficients for Vitvi11g00720.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6120572	0.0009528719	***	0.001032317	**
SlopeC	-1.869816	0.0003856001	***	0.09467692	.
MeanF-MeanC	0.5173539	0.03242582	*	0.1784782	
SlopeF-SlopeC	0.3861115	0.5659556		0.9999488	



8.1.467 Vitvi05g00681: Type1.0 *

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

Vitvi05g00681

10.2.1

cell wall.cellulose synthesis.cellulose synthase

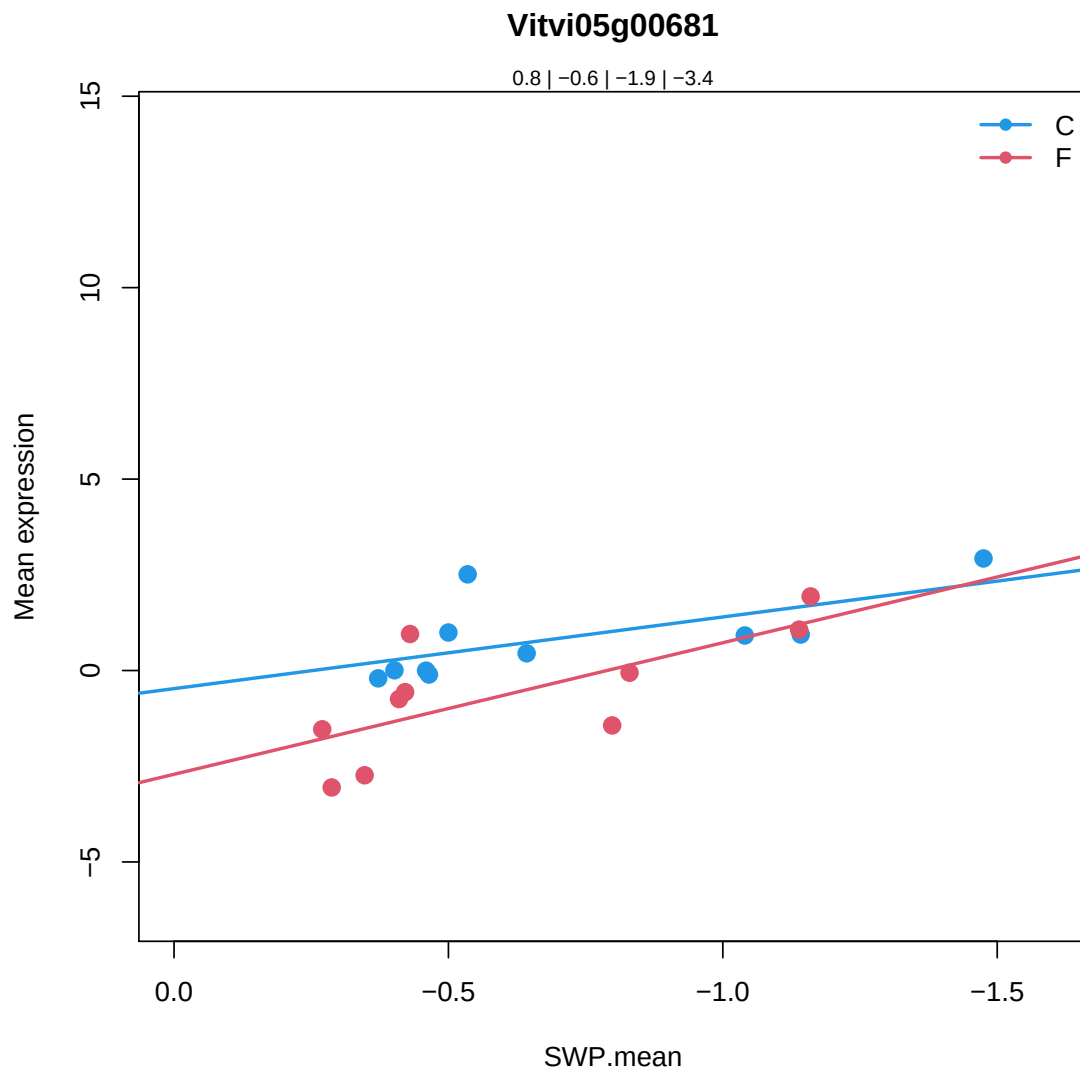
cysteine-rich RECEPTOR-like kinase |

Chr4:12129485-12133157 FORWARD LENGTH=1043 |

201606

Coefficients for Vitvi05g00681.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8430558	0.009925451	**	0.01051311	*
SlopeC	-1.872315	0.03446689	*	0.444078	
MeanF-MeanC	-1.460116	0.002266089	**	0.02434089	*
SlopeF-SlopeC	-1.563097	0.218861		0.9999488	



8.1.468 Vitvi04g00092: Type1.0

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

Vitvi04g00092

20.2.1

stress.abiotic.heat

heat shock transcription factor A2 |

Chr2:11136052-11137217 FORWARD LENGTH=290 |

201606

Vitvi04g00092

27.3.23

RNA.regulation of transcription.heat-shock transcription factor family

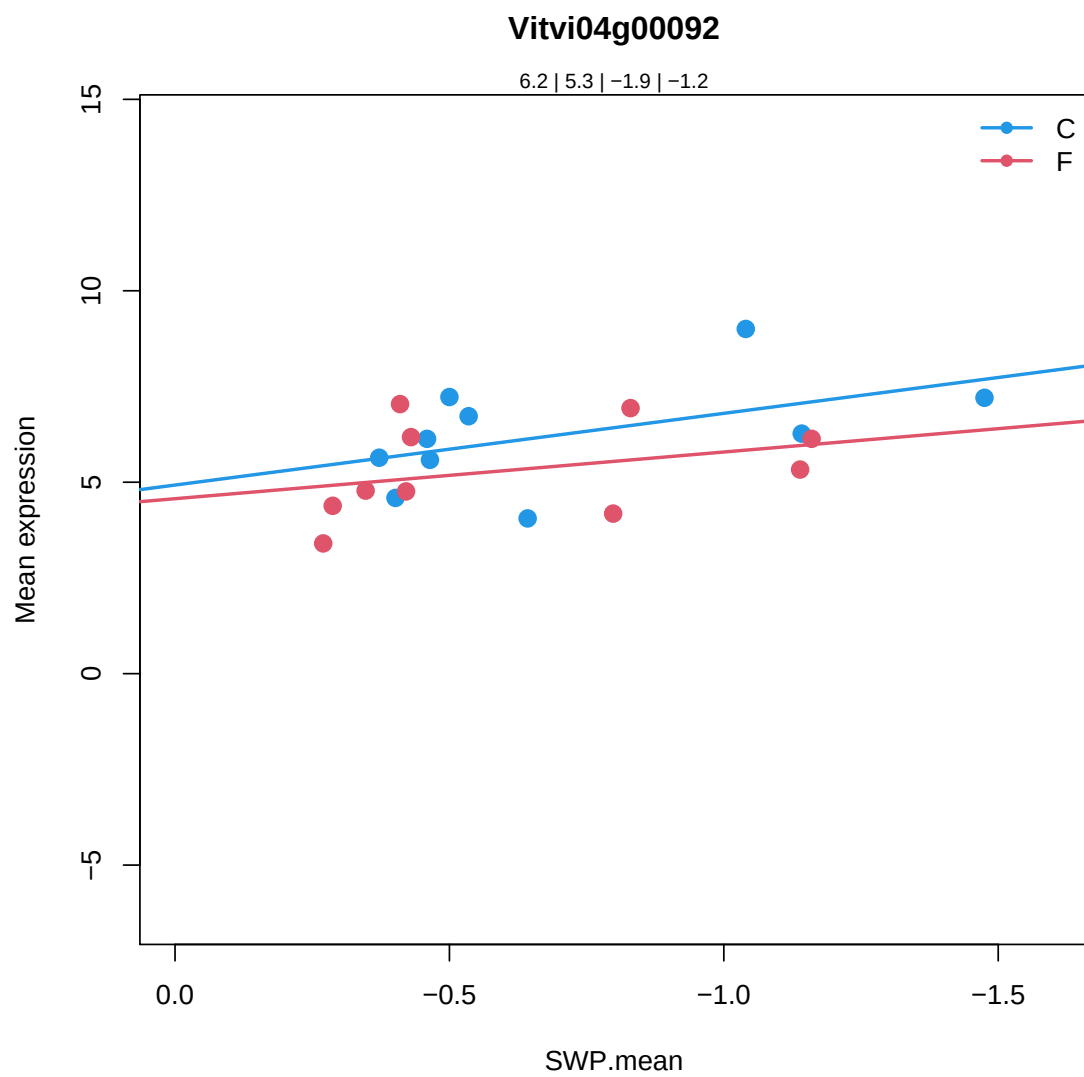
heat shock transcription factor A2 |

Chr2:11136052-11137217 FORWARD LENGTH=290 |

201606

Coefficients for Vitvi04g00092.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.242485	2.837109e-14	***	4.552876e-14	***
SlopeC	-1.872491	0.06992559	.	0.5594697	
MeanF-MeanC	-0.9304304	0.07596648	.	0.3103407	
SlopeF-SlopeC	0.6528582	0.6594544		0.9999488	



8.1.469 Vitvi18g00596: Type1.0 *

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

Vitvi18g00596

35.2

not assigned.unknown

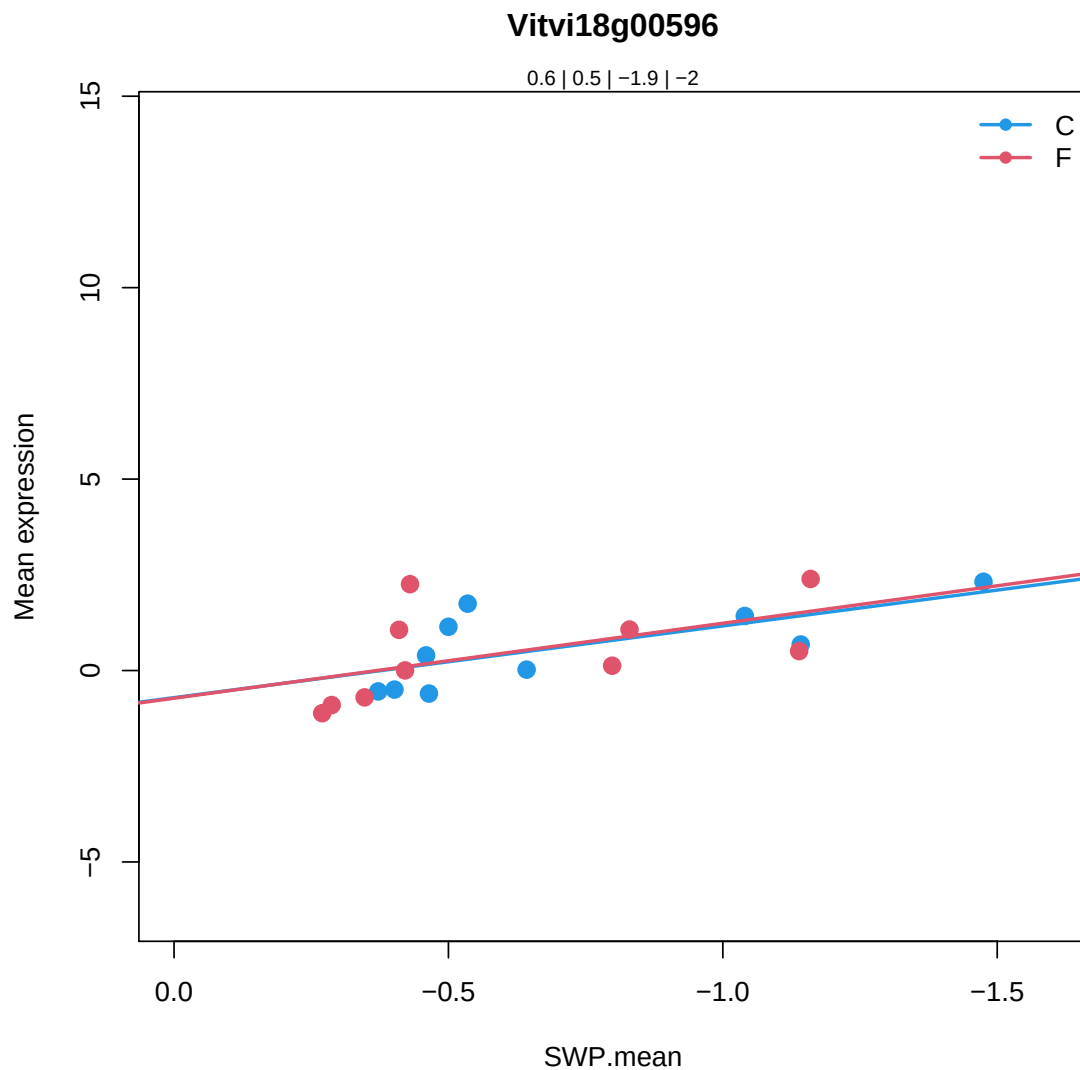
tubulin alpha-6 chain |

Chr1:18520144-18521600 REVERSE LENGTH=209 |

201606

Coefficients for Vitvi18g00596.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6083869	0.03667248	*	0.03830343	*
SlopeC	-1.872526	0.02219784	*	0.3929231	
MeanF-MeanC	-0.1388005	0.7227382		0.9149482	
SlopeF-SlopeC	-0.08545914	0.9404426		0.9999488	



8.1.470 Vitvi08g00763: Type1.0 *

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

Vitvi08g00763

15.2

metal handling.binding, chelation and storage

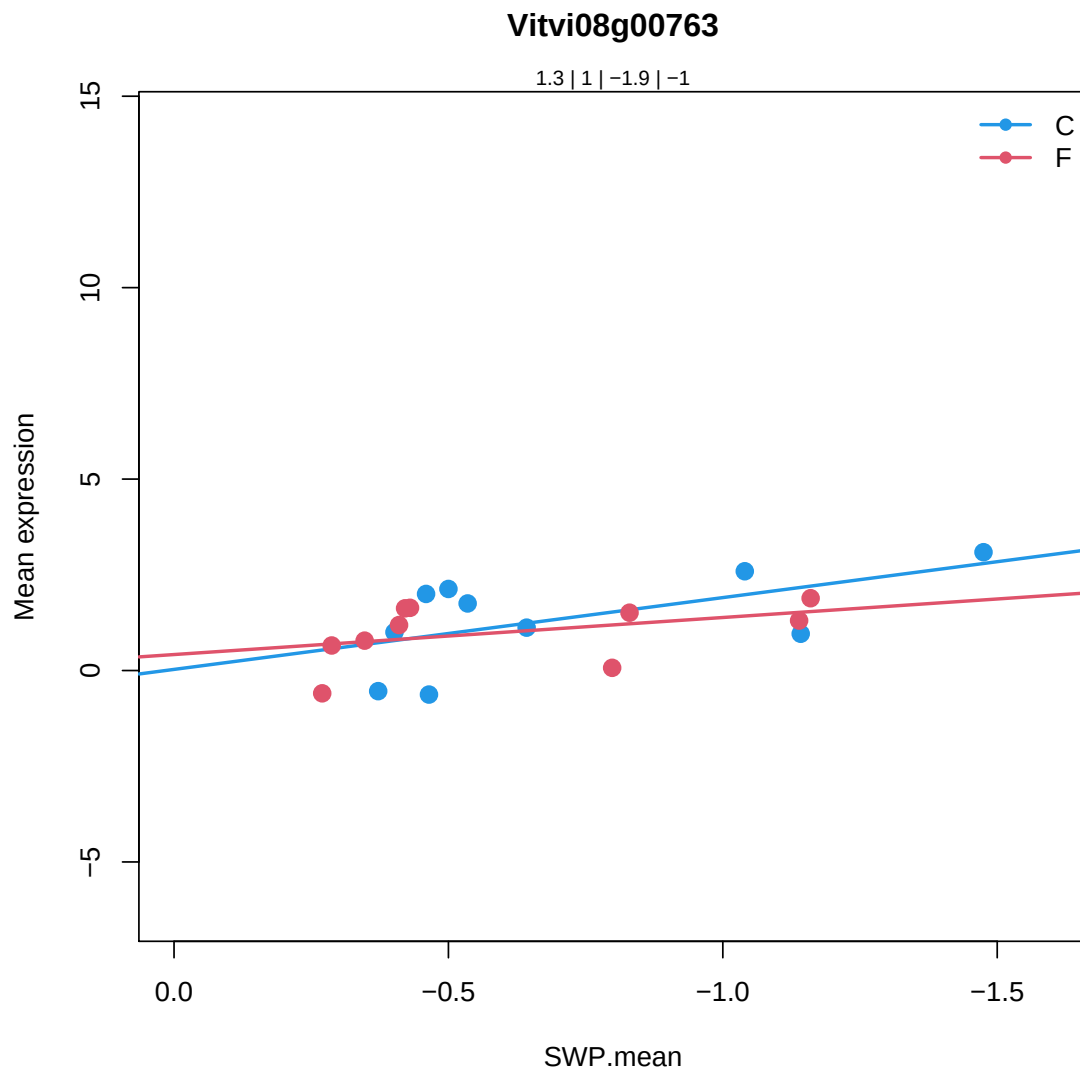
ferritin 4 |

Chr2:16831501-16833214 REVERSE LENGTH=259 |

201606

Coefficients for Vitvi08g00763.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.347744	4.308416e-05	***	4.7923e-05	***
SlopeC	-1.875249	0.01815808	*	0.3617849	
MeanF-MeanC	-0.3415562	0.3696187		0.7242177	
SlopeF-SlopeC	0.9078116	0.4146335		0.9999488	



8.1.471 Vitvi19g01902: Type1.0 *

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

Vitvi19g01902

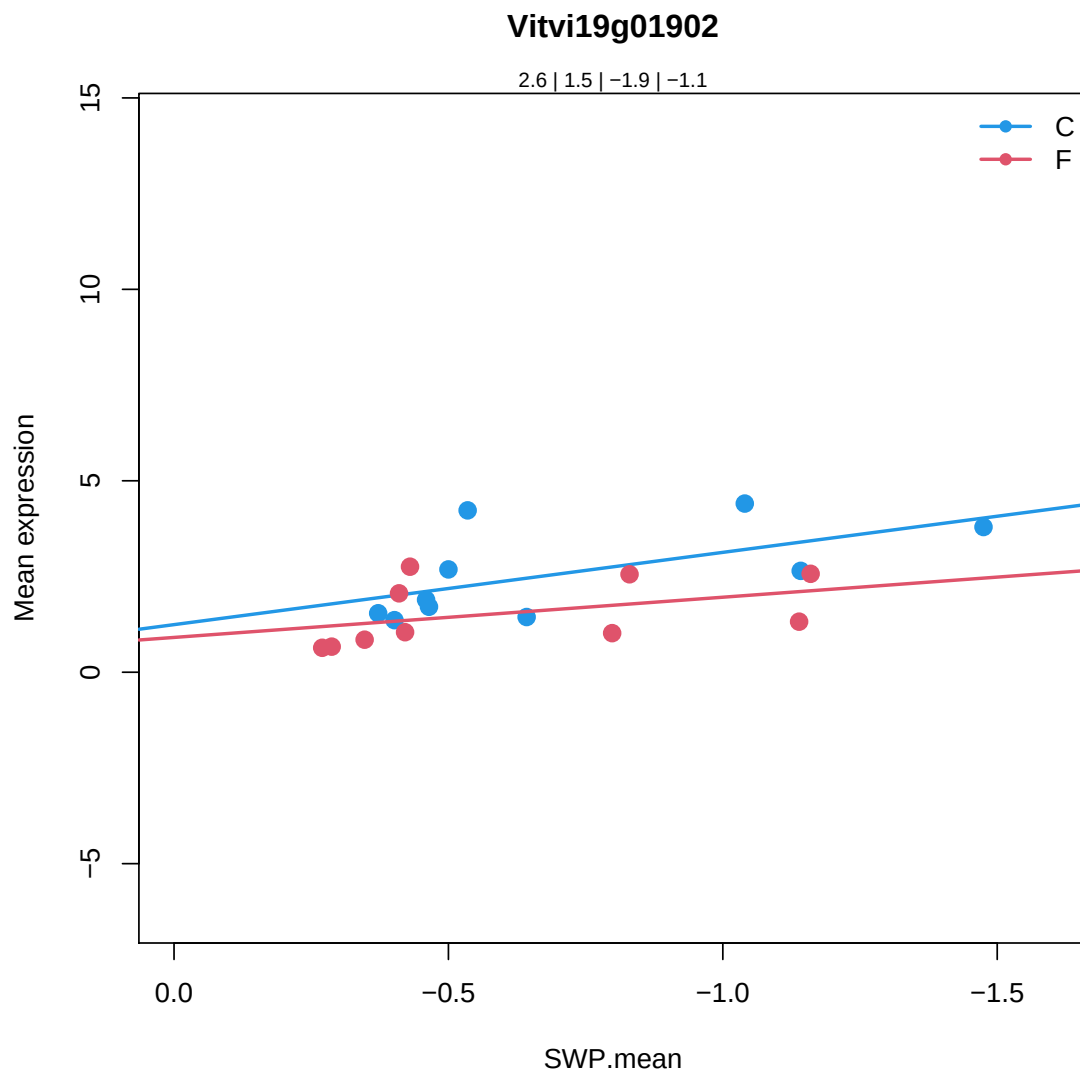
35.2

not assigned.unknown

NA

Coefficients for Vitvi19g01902.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.570038	2.075515e-09	***	2.589637e-09	***
SlopeC	-1.887609	0.01659698	*	0.3523917	
MeanF-MeanC	-1.021476	0.0114264	*	0.08373137	.
SlopeF-SlopeC	0.8372391	0.4471427		0.9999488	



8.1.472 Vitvi08g02189: Type1.0

```
> 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

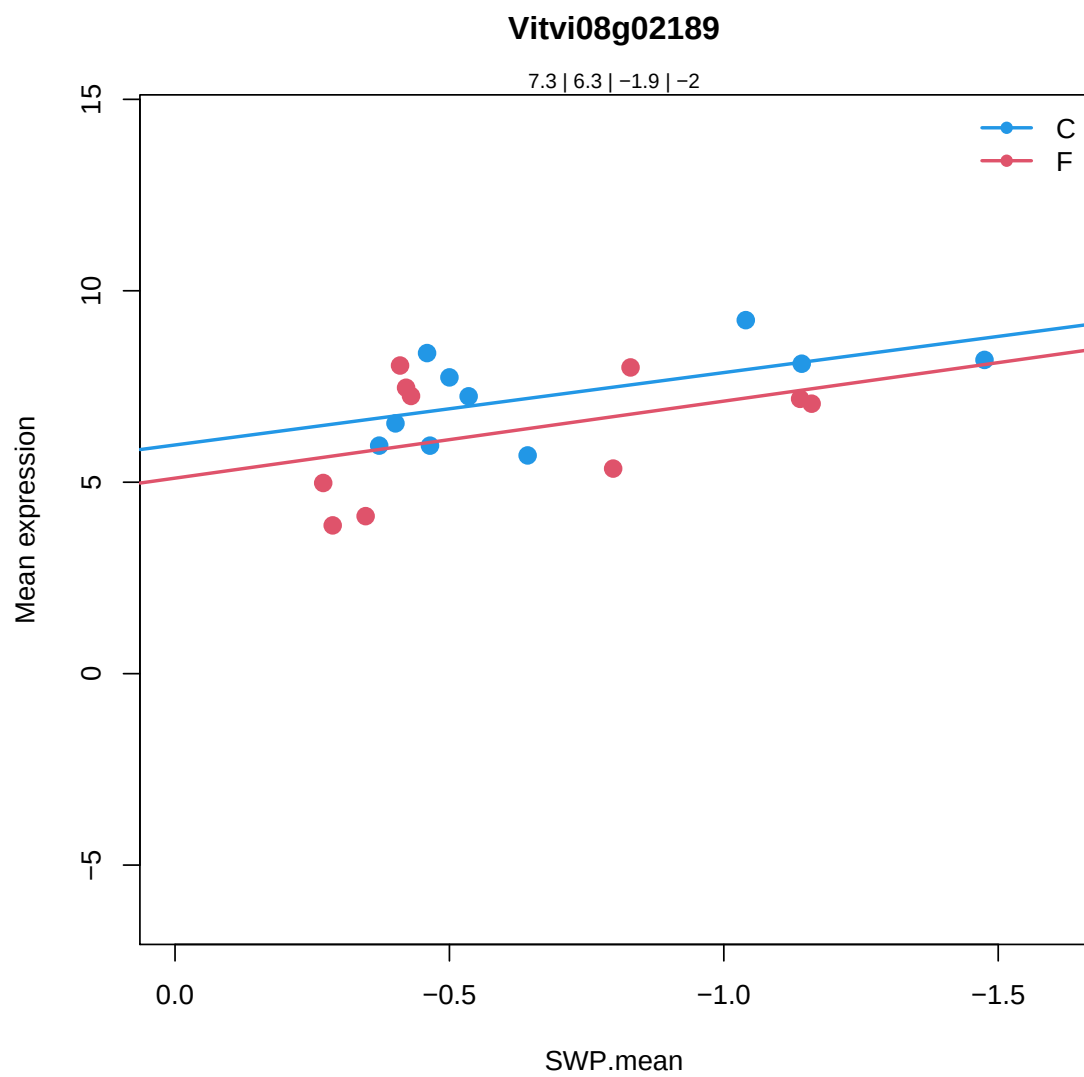
heat shock cognate protein 70-1 |

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	



8.1.473 Vitvi06g00659: Type1.0 *

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

Vitvi06g00659

17.5.1

hormone metabolism.ethylene.synthesis-degradation

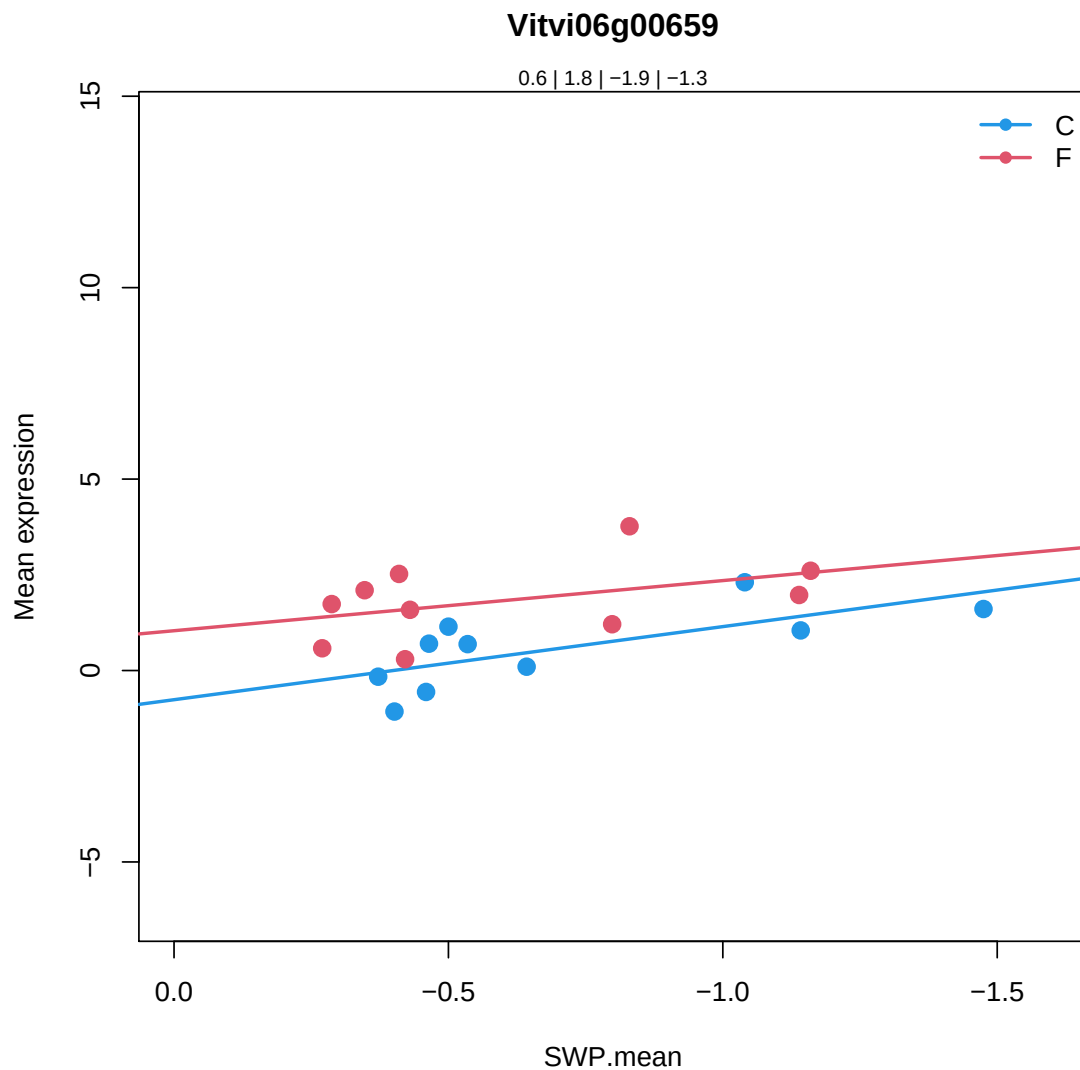
2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein

Chr5:23701509-23703802 FORWARD LENGTH=352 |

201606

Coefficients for Vitvi06g00659.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.5799659	0.03068614	*	0.03211027	*
SlopeC	-1.909444	0.01218283	*	0.3229093	
MeanF-MeanC	1.257125	0.001866494	**	0.02088511	*
SlopeF-SlopeC	0.6000533	0.5692331		0.9999488	



8.1.474 Vitvi07g01297: Type1.0

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

Vitvi07g01297

26.28

misc.GDSL-motif lipase

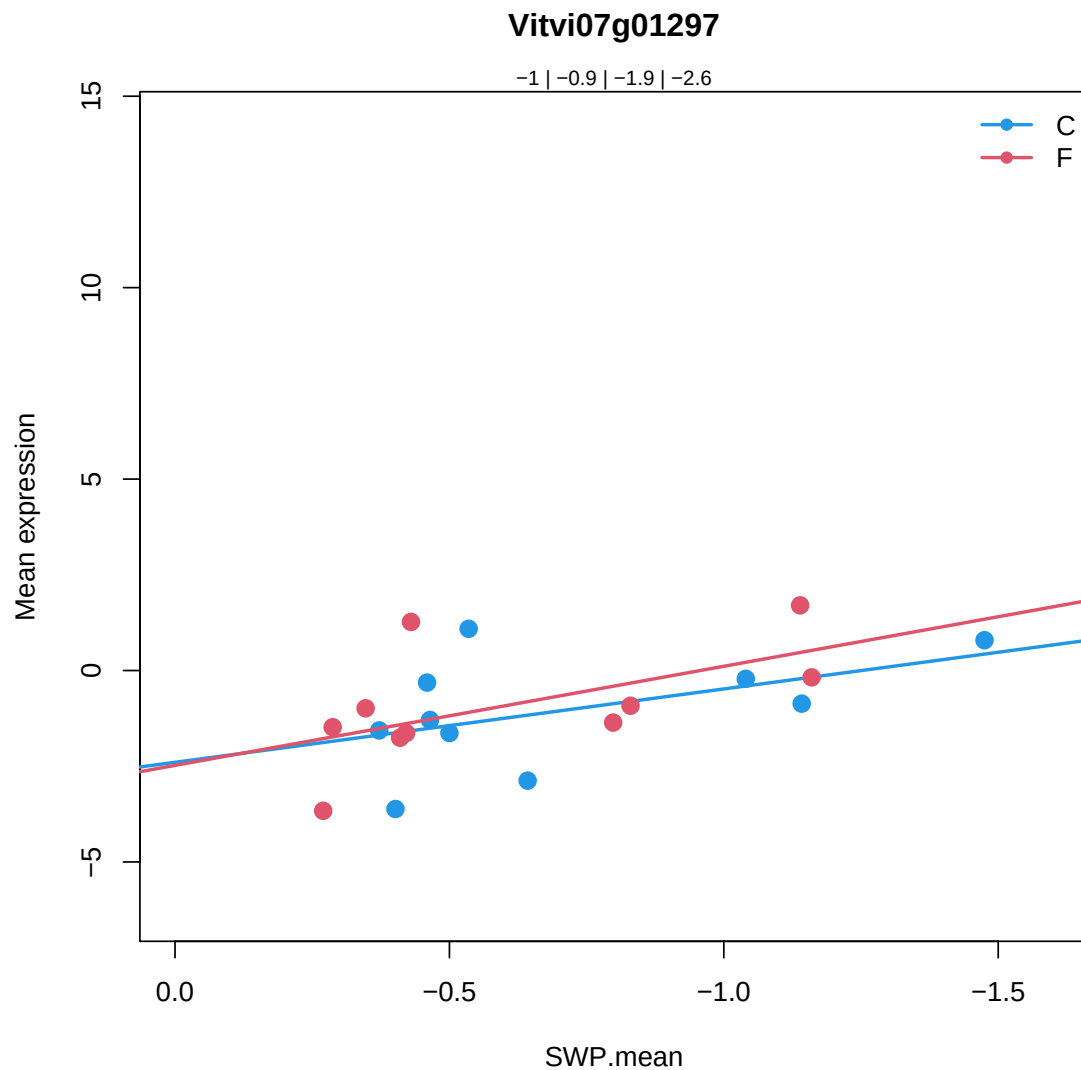
GDSL-like Lipase/Acylhydrolase superfamily protein |

Chr2:10024366-10026058 FORWARD LENGTH=387 |

201606

Coefficients for Vitvi07g01297.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.049876	0.01124818	*	0.0119034	*
SlopeC	-1.916124	0.08284178	.	0.5803324	
MeanF-MeanC	0.149202	0.7831418		0.9384607	
SlopeF-SlopeC	-0.6721018	0.6723638		0.9999488	



8.1.475 Vitvi13g00143: Type1.0

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

Vitvi13g00143

26.12

misc.peroxidases

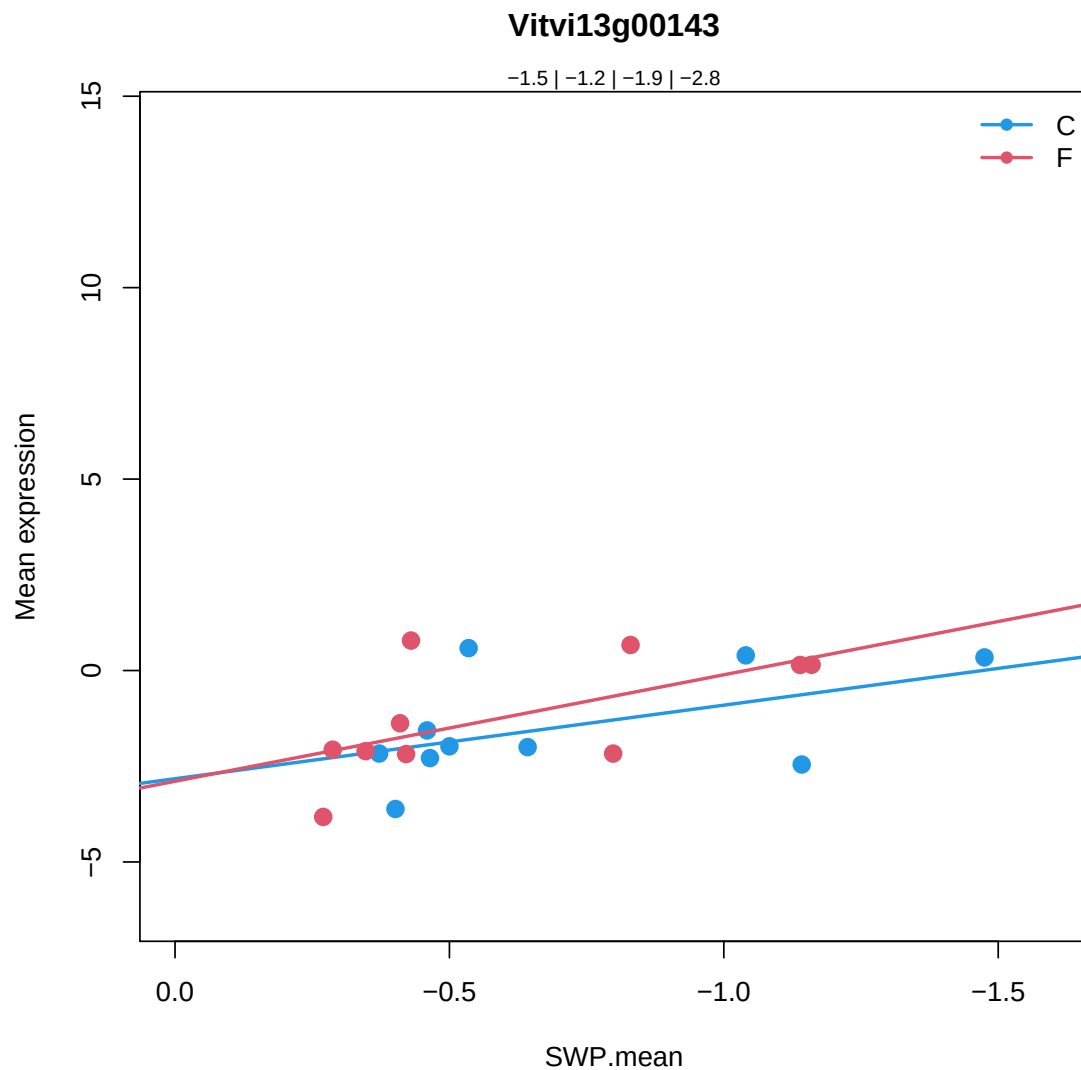
Peroxidase superfamily protein |

Chr5:1579142-1580819 REVERSE LENGTH=324 |

201606

Coefficients for Vitvi13g00143.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.475082	0.0005180539	***	0.0005638918	***
SlopeC	-1.920675	0.06966826	.	0.5587992	
MeanF-MeanC	0.2768745	0.5937343		0.8577063	
SlopeF-SlopeC	-0.8605815	0.5713833		0.9999488	



8.1.476 Vitvi08g01234: Type1.0 *

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

Vitvi08g01234

35.1.3

not assigned.no ontology.armadillo/beta-catenin repeat family protein

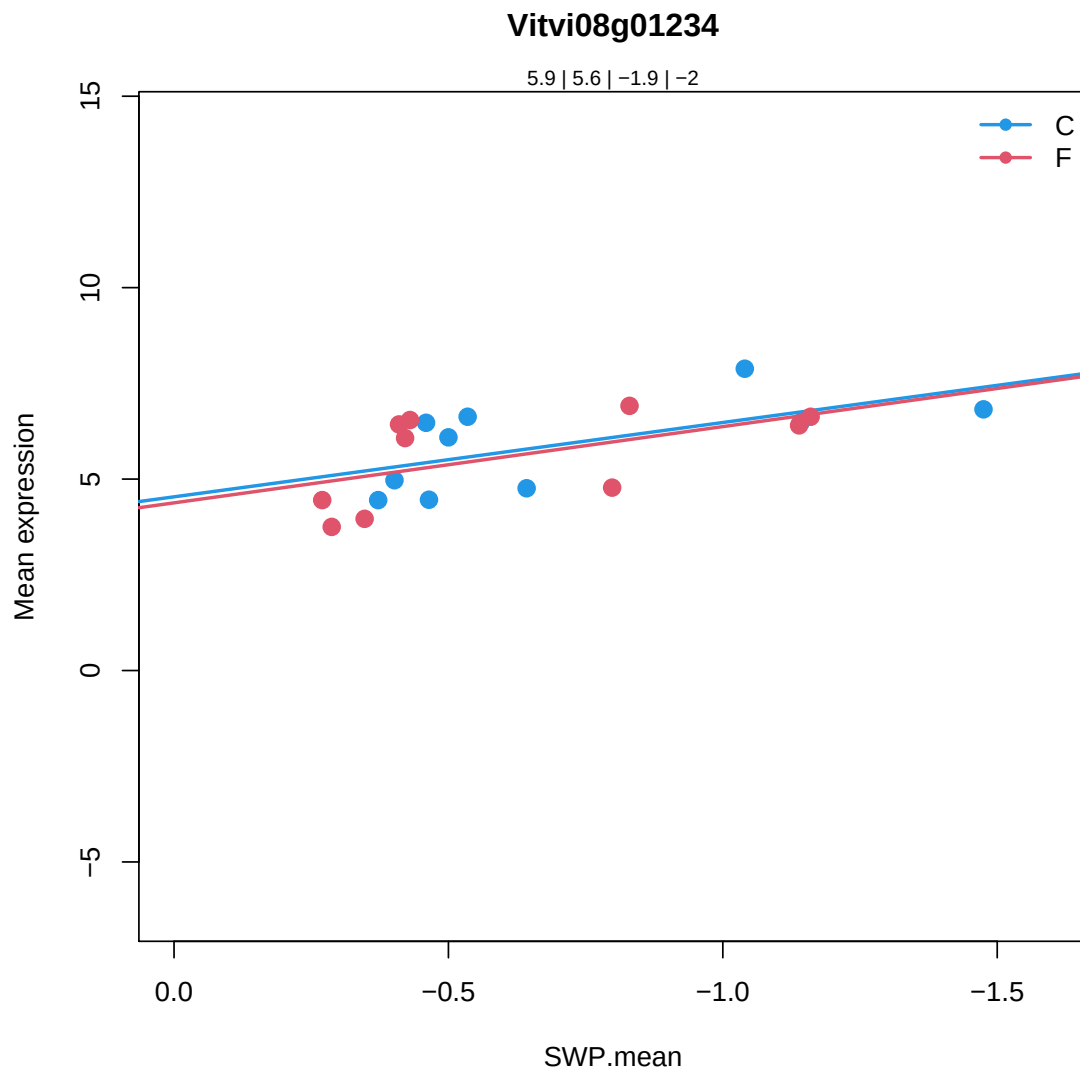
Fes1A |

Chr3:2871710-2873109 FORWARD LENGTH=327 |

201606

Coefficients for Vitvi08g01234.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.90145	1.529707e-15	***	2.79868e-15	***
SlopeC	-1.940814	0.02472301	*	0.4060648	
MeanF-MeanC	-0.3092112	0.4572898		0.7825787	
SlopeF-SlopeC	-0.05059603	0.9666479		0.9999488	



8.1.477 Vitvi01g02009: Type1.0 *

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

Vitvi01g02009

16.8.2

secondary metabolism.flavonoids.chalcones

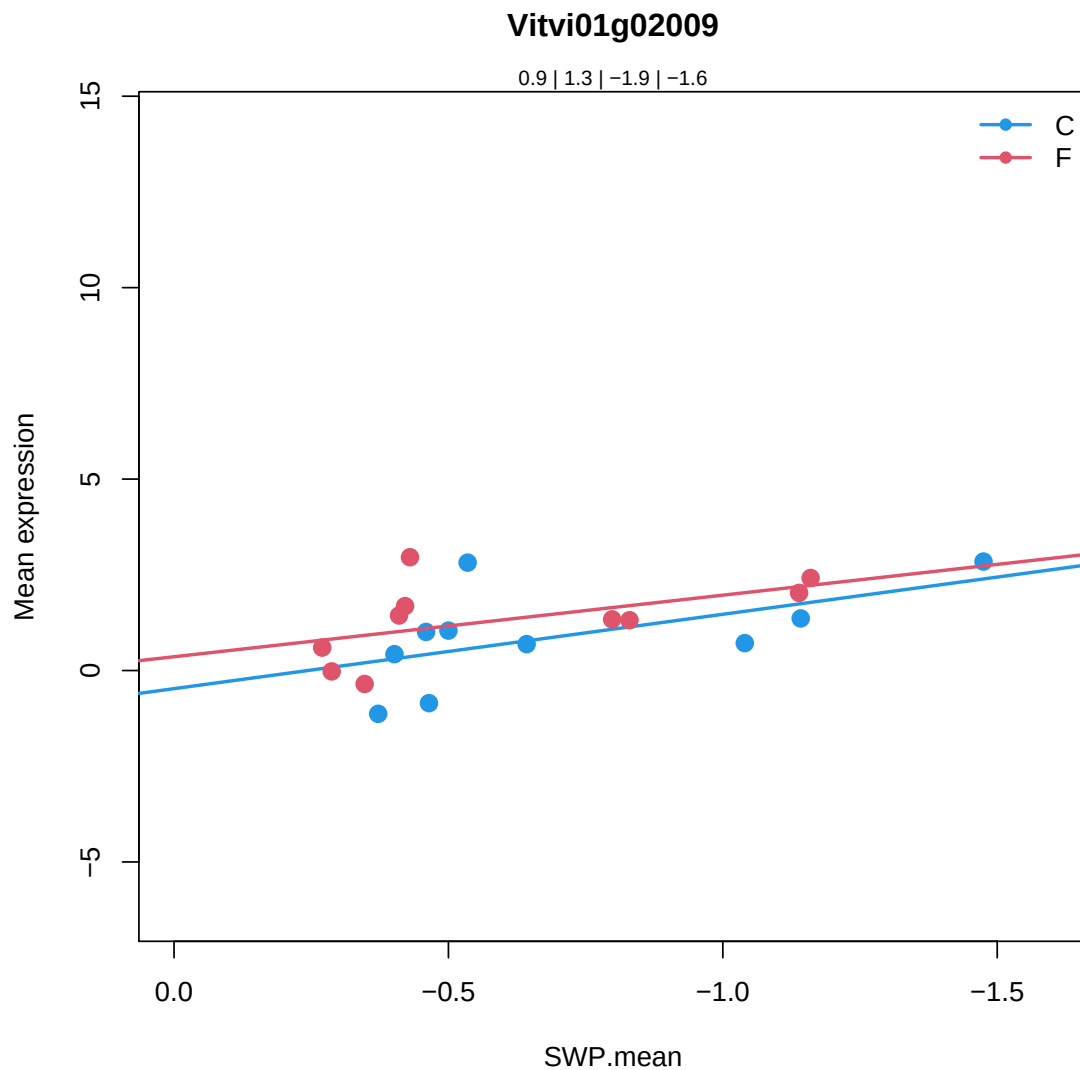
NAD(P)-linked oxidoreductase superfamily protein |

Chr1:22071410-22073067 REVERSE LENGTH=326 |

201606

Coefficients for Vitvi01g02009.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8920748	0.006206541	**	0.006605229	**
SlopeC	-1.942709	0.02693091	*	0.4184311	
MeanF-MeanC	0.4474214	0.2938199		0.6604339	
SlopeF-SlopeC	0.3343367	0.7862208		0.9999488	



8.1.478 Vitvi07g00087: Type1.0 *

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

Vitvi07g00087

35.1

not assigned.no ontology

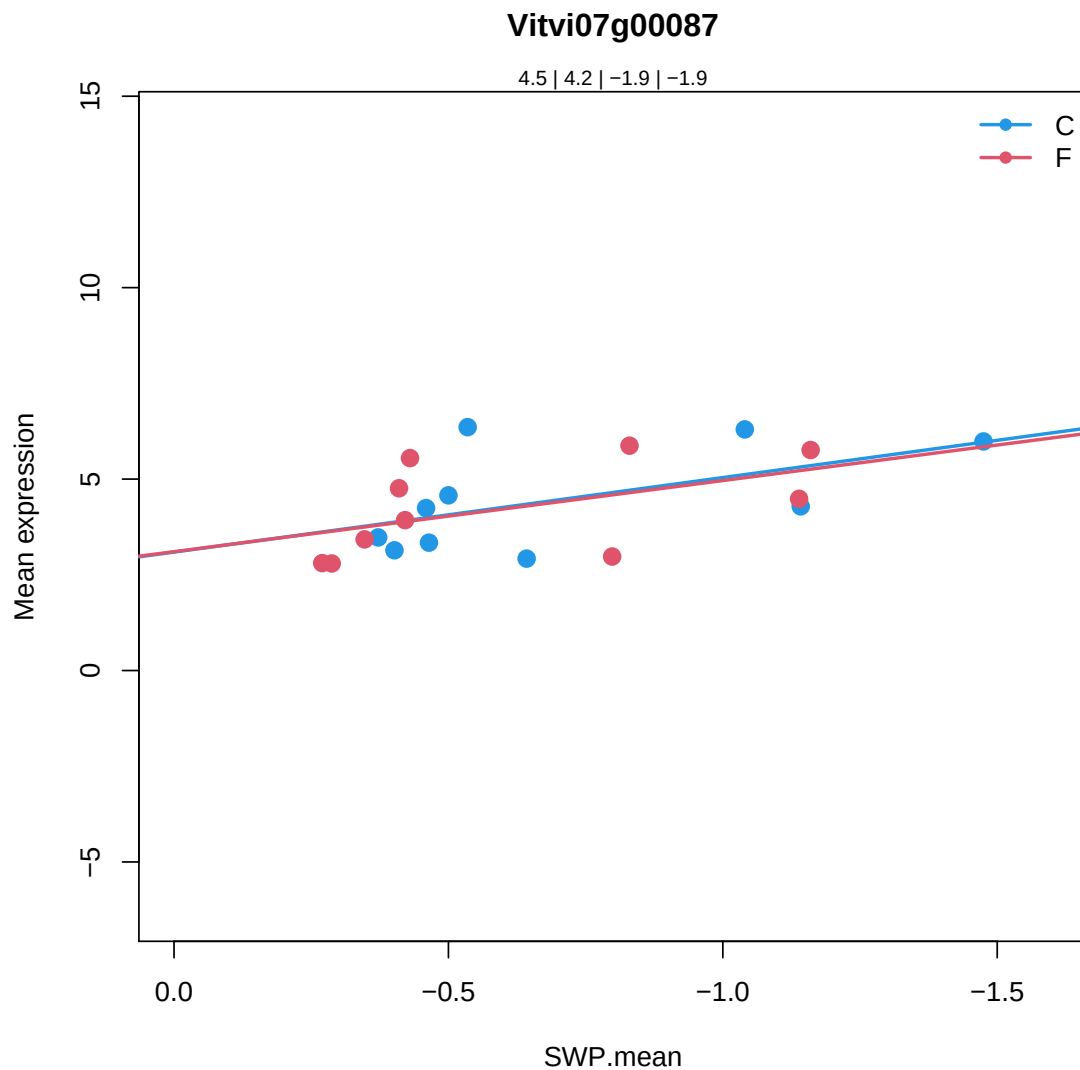
Bax inhibitor-1 family protein |

Chr1:730148-731379 FORWARD LENGTH=247 |

201606

Coefficients for Vitvi07g00087.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.461907	3.187147e-12	***	4.45021e-12	***
SlopeC	-1.946211	0.04011329	*	0.472859	
MeanF-MeanC	-0.2263095	0.6222682		0.8698761	
SlopeF-SlopeC	0.08953531	0.9467777		0.9999488	



8.1.479 Vitvi09g01273: Type1.0 *

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

Vitvi09g01273

35.2

not assigned.unknown

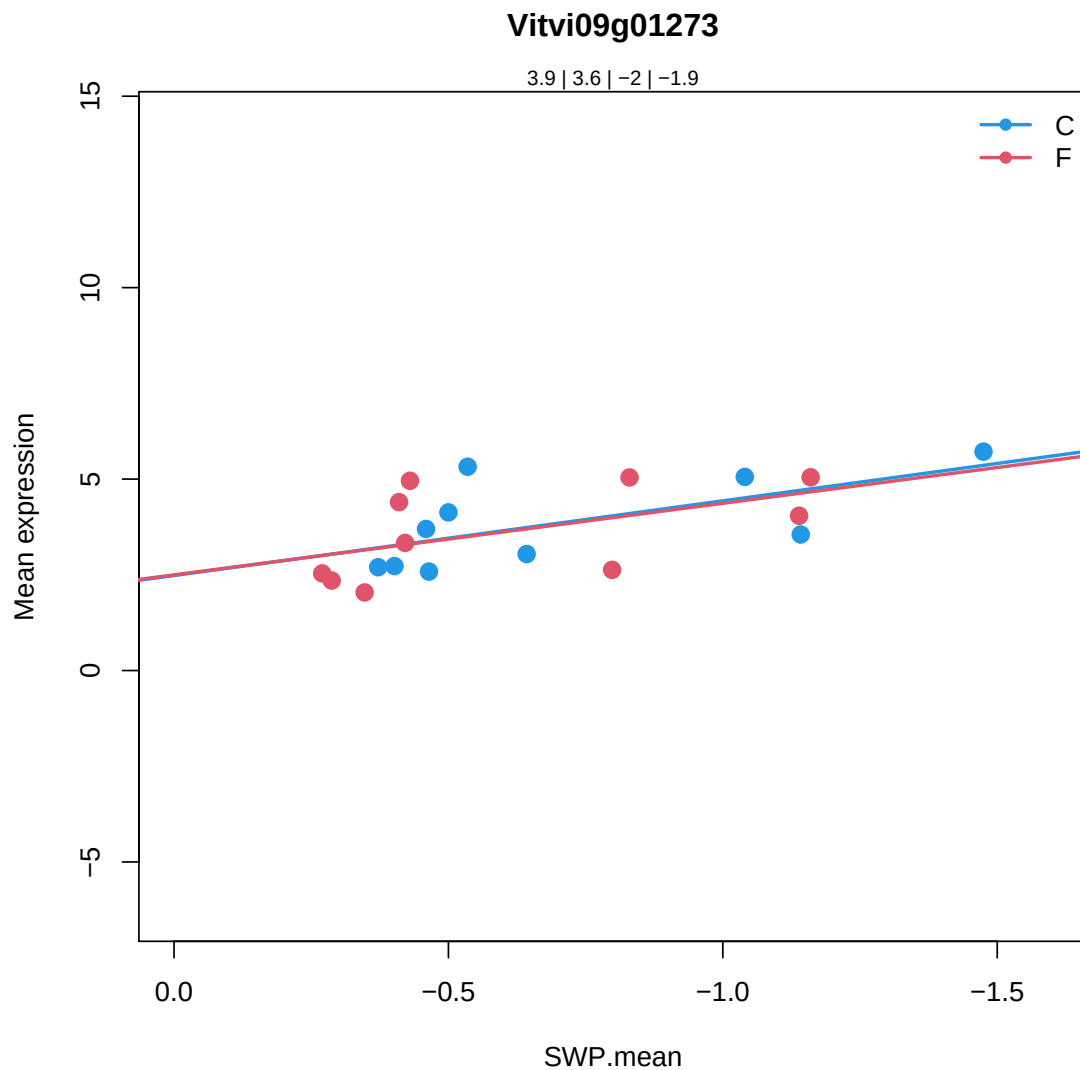
ATP-dependent DNA helicase |

Chr4:14990523-14992855 FORWARD LENGTH=589 |

201606

Coefficients for Vitvi09g01273.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.852927	7.081238e-12	***	9.740297e-12	***
SlopeC	-1.951126	0.02373849	*	0.3983963	
MeanF-MeanC	-0.2157831	0.6018321		0.8611337	
SlopeF-SlopeC	0.08240906	0.9455691		0.9999488	



8.1.480 Vitvi13g00255: Type1.0 *

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

Vitvi13g00255

34.19.2

transport.major intrinsic proteins.TIP

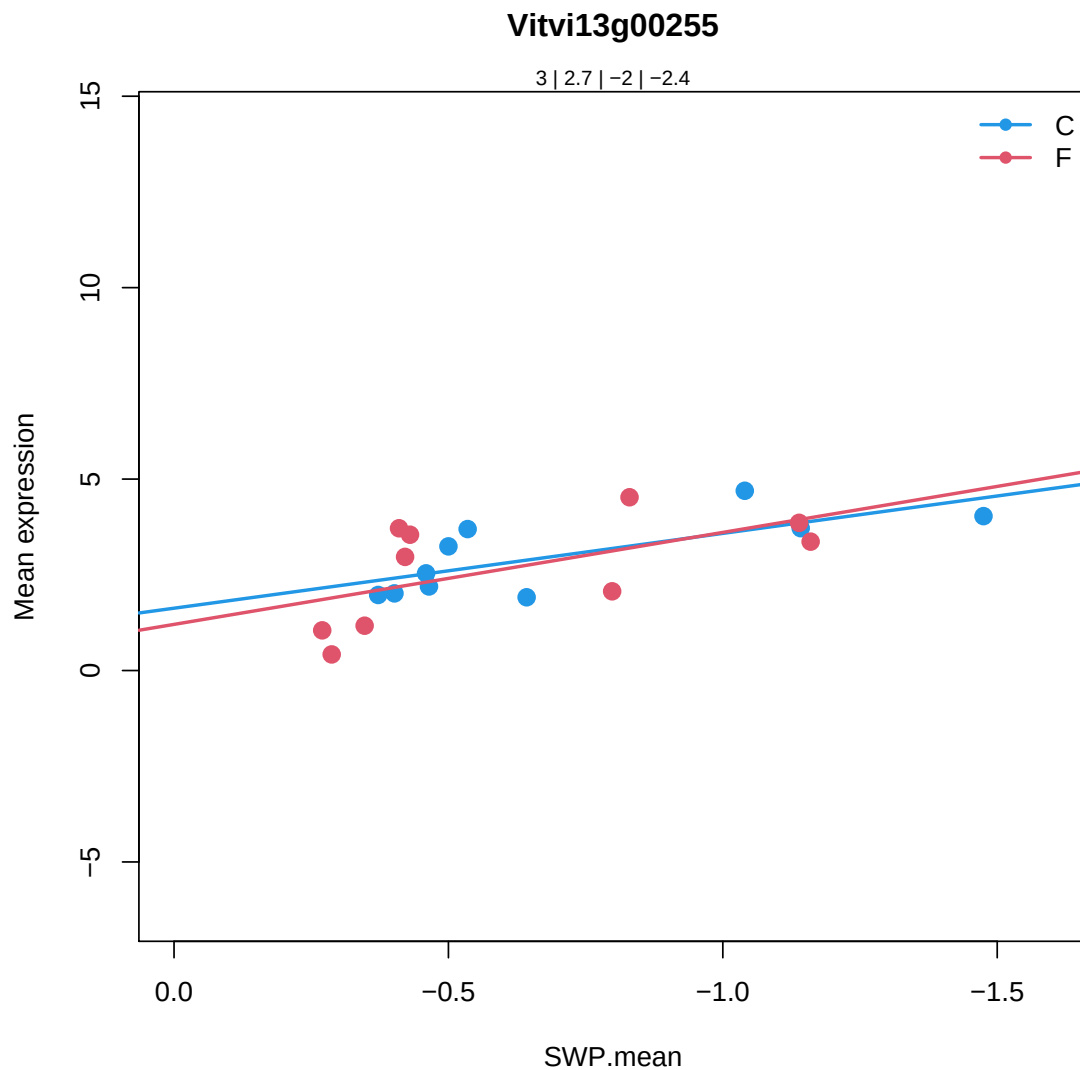
tonoplast intrinsic protein 1%3B3 |

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	



8.1.481 Vitvi17g00078: Type1.0

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

Vitvi17g00078

35.1

not assigned.no ontology

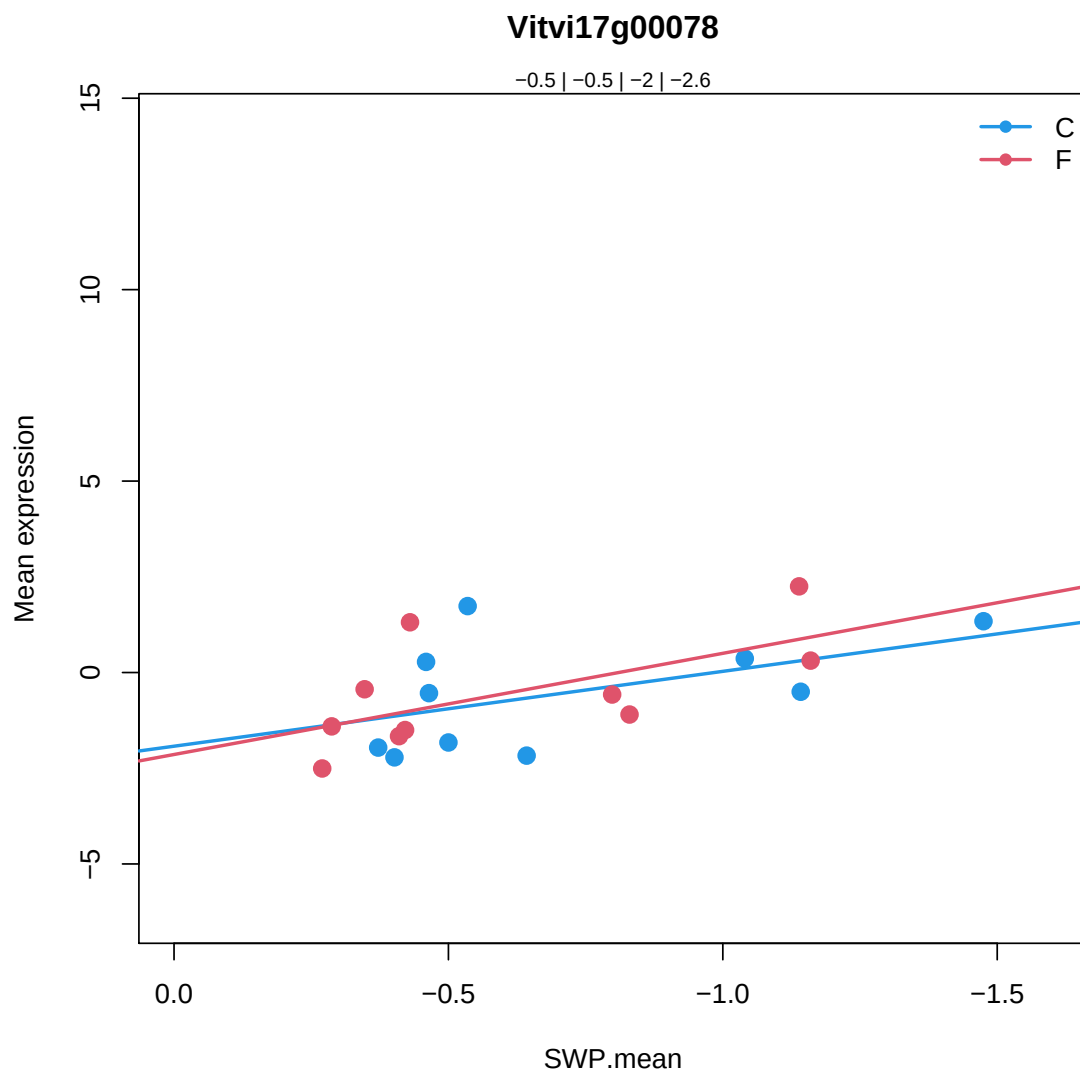
HXXXD-type acyl-transferase family protein |

Chr5:16431448-16433086 FORWARD LENGTH=457 |

201606

Coefficients for Vitvi17g00078.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.5499436	0.1382099		0.142376	
SlopeC	-1.955218	0.06215032	.	0.5453628	
MeanF-MeanC	0.01843645	0.9712182		0.9933672	
SlopeF-SlopeC	-0.6870146	0.6469197		0.9999488	



8.1.482 Vitvi17g00084: Type1.0 *

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

Vitvi17g00084

26.22

misc.short chain dehydrogenase/reductase (SDR)

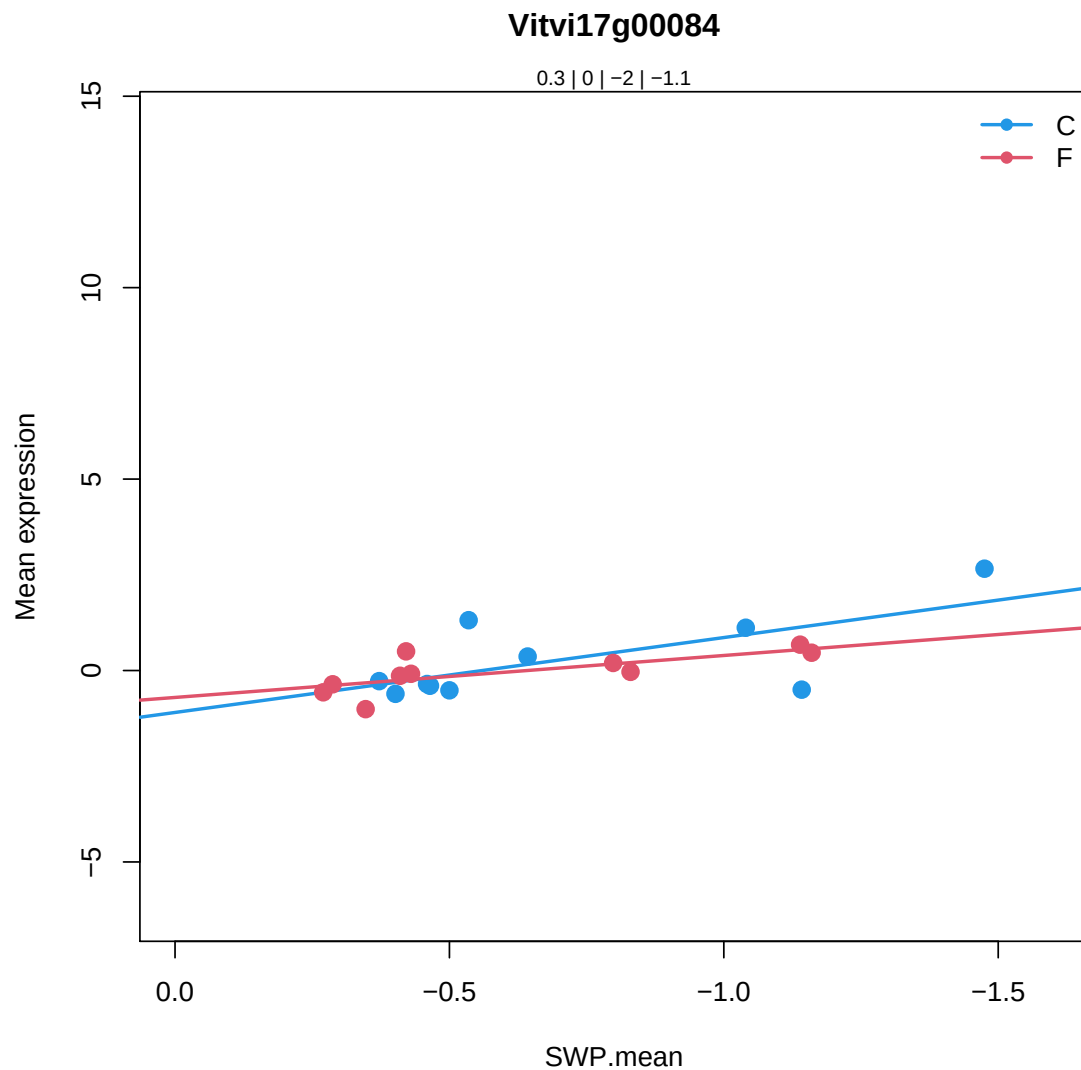
hydroxysteroid dehydrogenase 1 |

Chr5:20623259-20624995 REVERSE LENGTH=349 |

201606

Coefficients for Vitvi17g00084.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.2802448	0.1656568		0.170282	
SlopeC	-1.95649	0.0016358	**	0.1556102	
MeanF-MeanC	-0.3162144	0.2647904		0.6271416	
SlopeF-SlopeC	0.8604446	0.2990925		0.9999488	



8.1.483 Vitvi06g01762: Type1.0 *

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

Vitvi06g01762

26.2

misc.UDP glucosyl and glucoronyl transferases

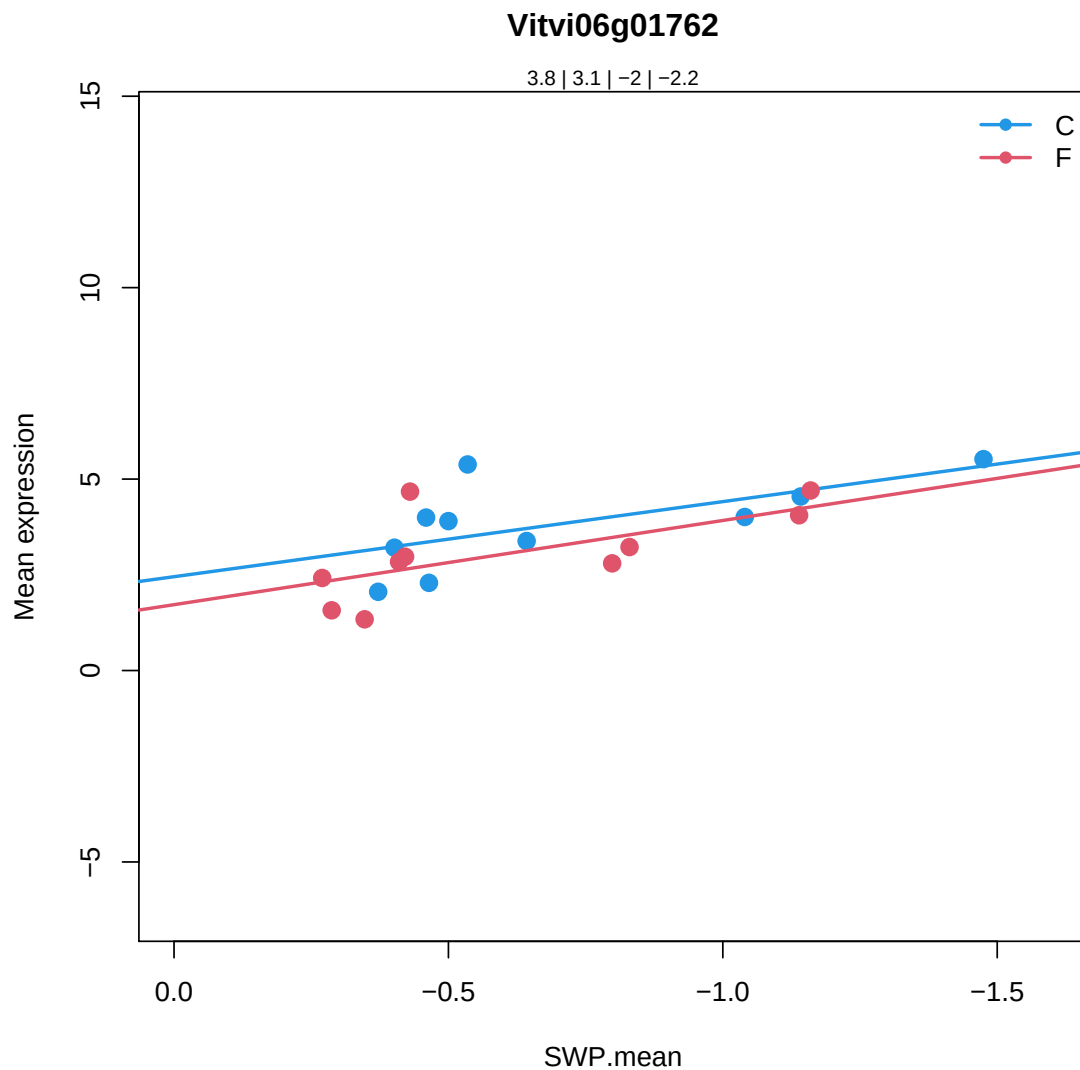
UDP-Glycosyltransferase superfamily protein |

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	



8.1.484 Vitvi05g00430: Type1.0 *

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

Vitvi05g00430

29.5.4

protein.degradation.aspartate protease

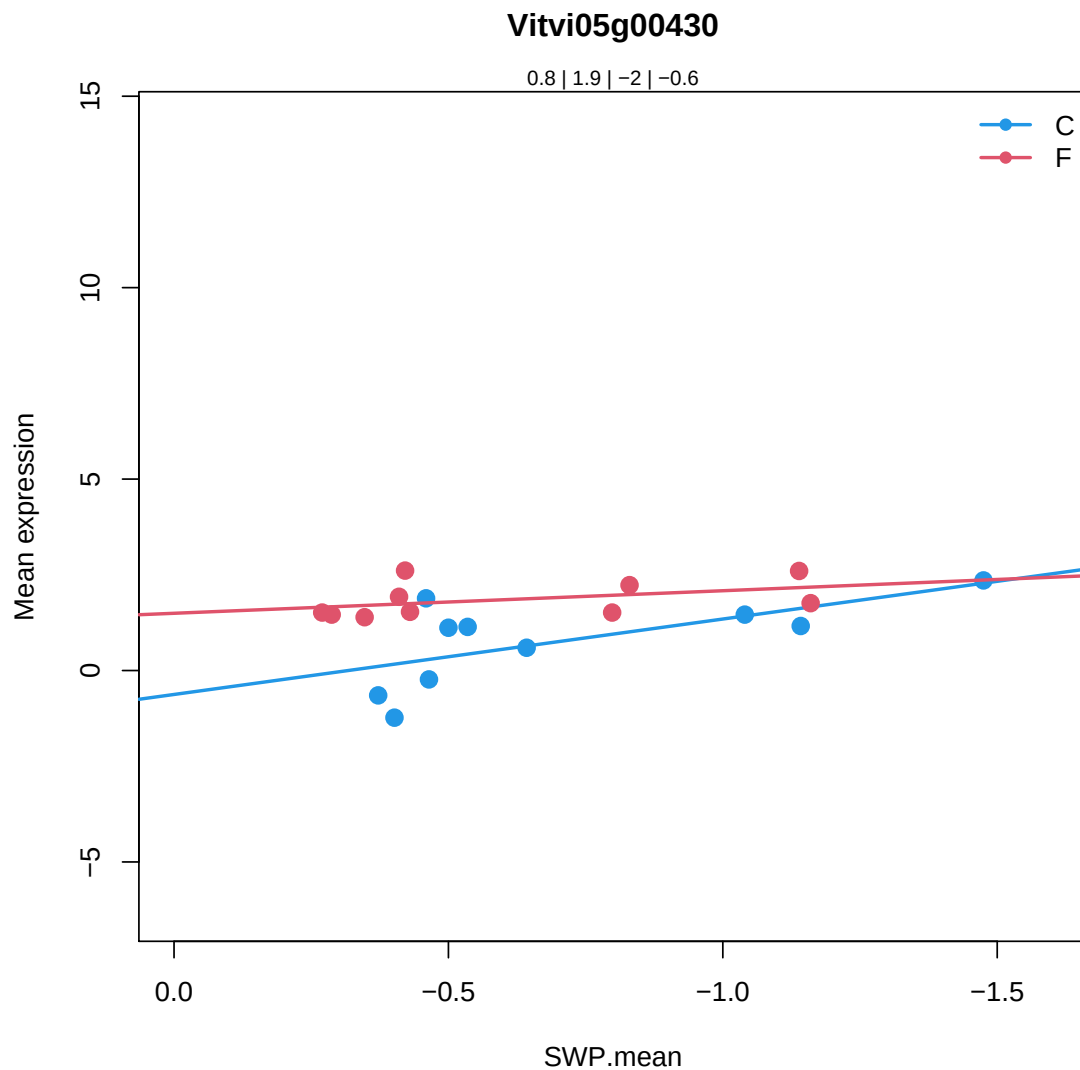
Eukaryotic aspartyl protease family protein |

Chr1:787143-788444 FORWARD LENGTH=433 |

201606

Coefficients for Vitvi05g00430.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.7598059	0.001680489	**	0.001811201	**
SlopeC	-1.970155	0.002998943	**	0.2077722	
MeanF-MeanC	1.093867	0.001440148	**	0.01687681	*
SlopeF-SlopeC	1.381185	0.1296544		0.9999488	



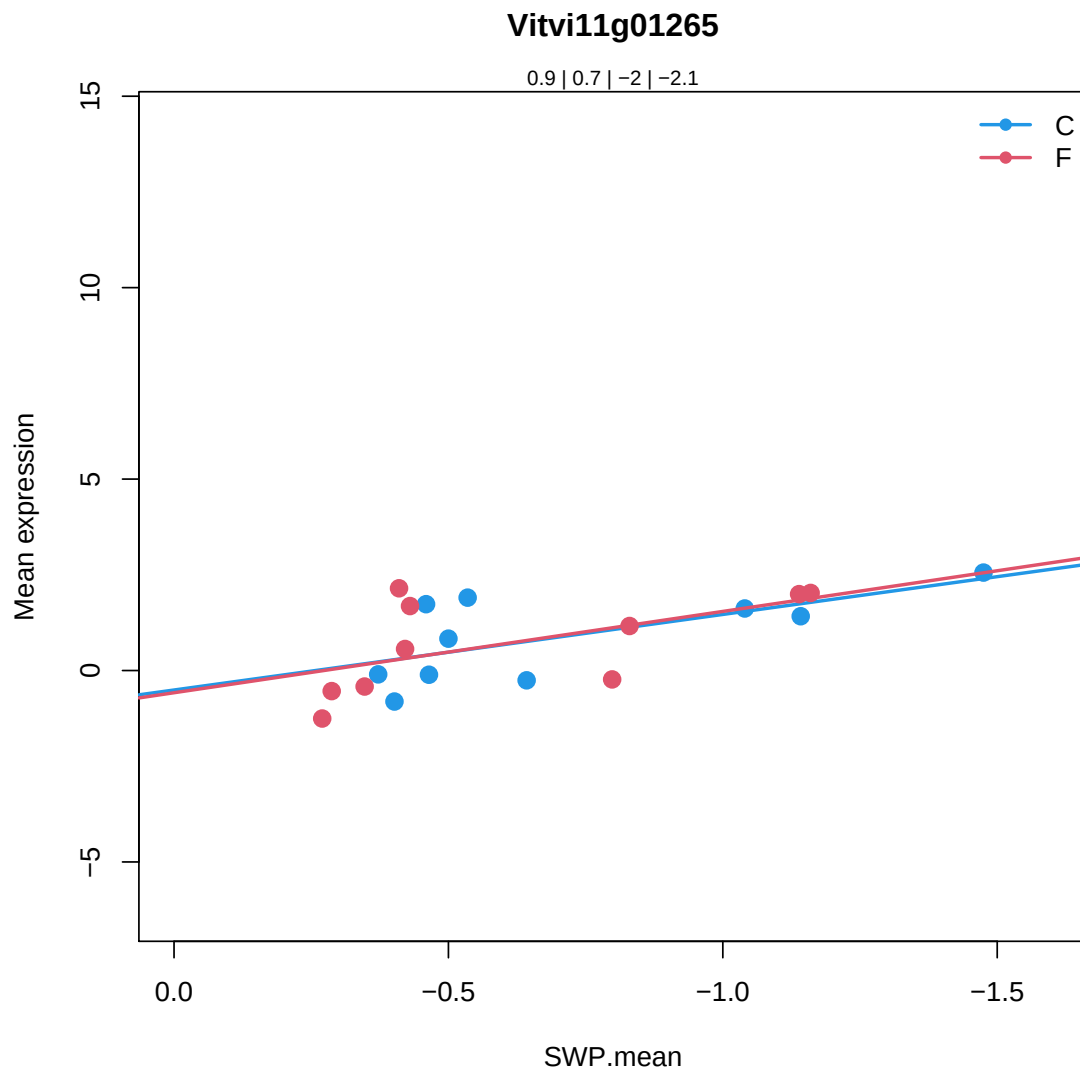
8.1.485 Vitvi11g01265: Type1.0 *

```
> 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	



8.1.486 Vitvi11g00044: Type1.0 *

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

Vitvi11g00044

29.6

protein.folding

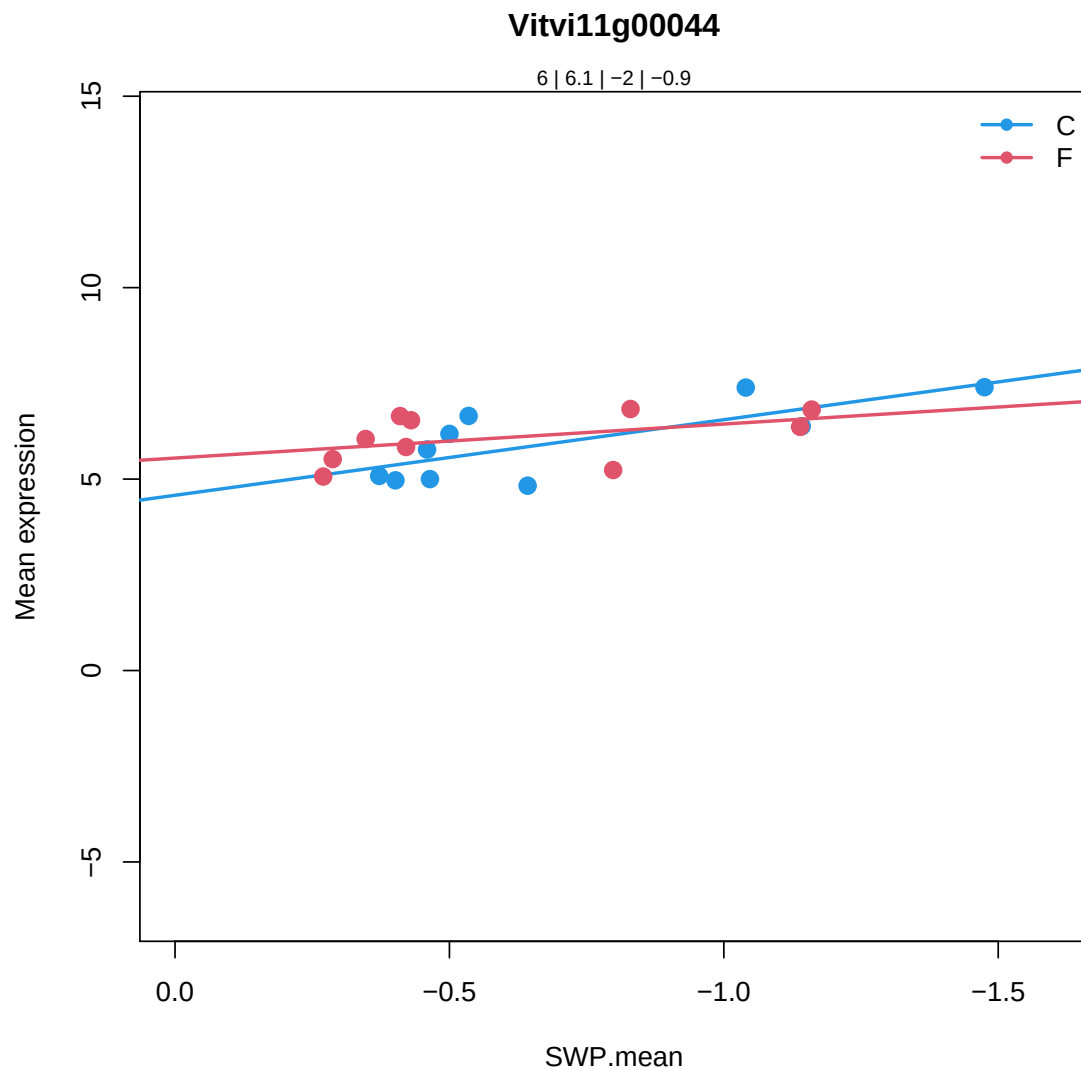
chaperonin 20 |

Chr5:7015015-7016354 FORWARD LENGTH=253 |

201606

Coefficients for Vitvi11g00044.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.964647	3.184481e-19	***	1.282374e-18	***
SlopeC	-1.973579	0.001434563	**	0.1479249	
MeanF-MeanC	0.1254325	0.6521532		0.8832598	
SlopeF-SlopeC	1.084541	0.1910992		0.9999488	



8.1.487 Vitvi03g01897: Type1.0 *

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

Vitvi03g01897

16.7

secondary metabolism.wax

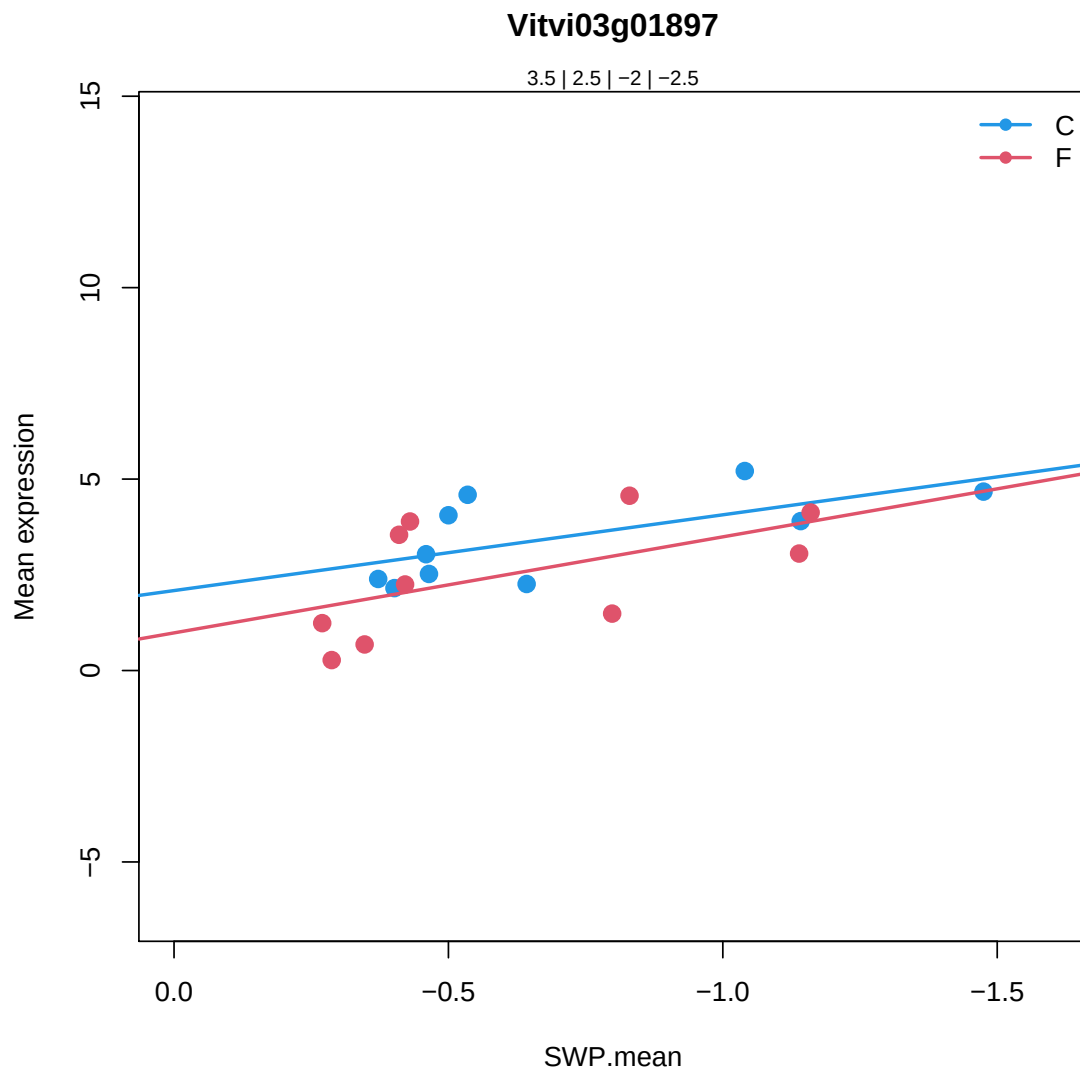
acyl-CoA sterol acyl transferase 1 |

Chr3:19284420-19285457 FORWARD LENGTH=345 |

201606

Coefficients for Vitvi03g01897.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.479295	4.278583e-10	***	5.465485e-10	***
SlopeC	-1.979028	0.03911802	*	0.4699262	
MeanF-MeanC	-0.9685201	0.04625647	*	0.2277492	
SlopeF-SlopeC	-0.5292467	0.6968904		0.9999488	



8.1.488 Vitvi06g00032: Type1.0 *

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

Vitvi06g00032

29.6

protein.folding

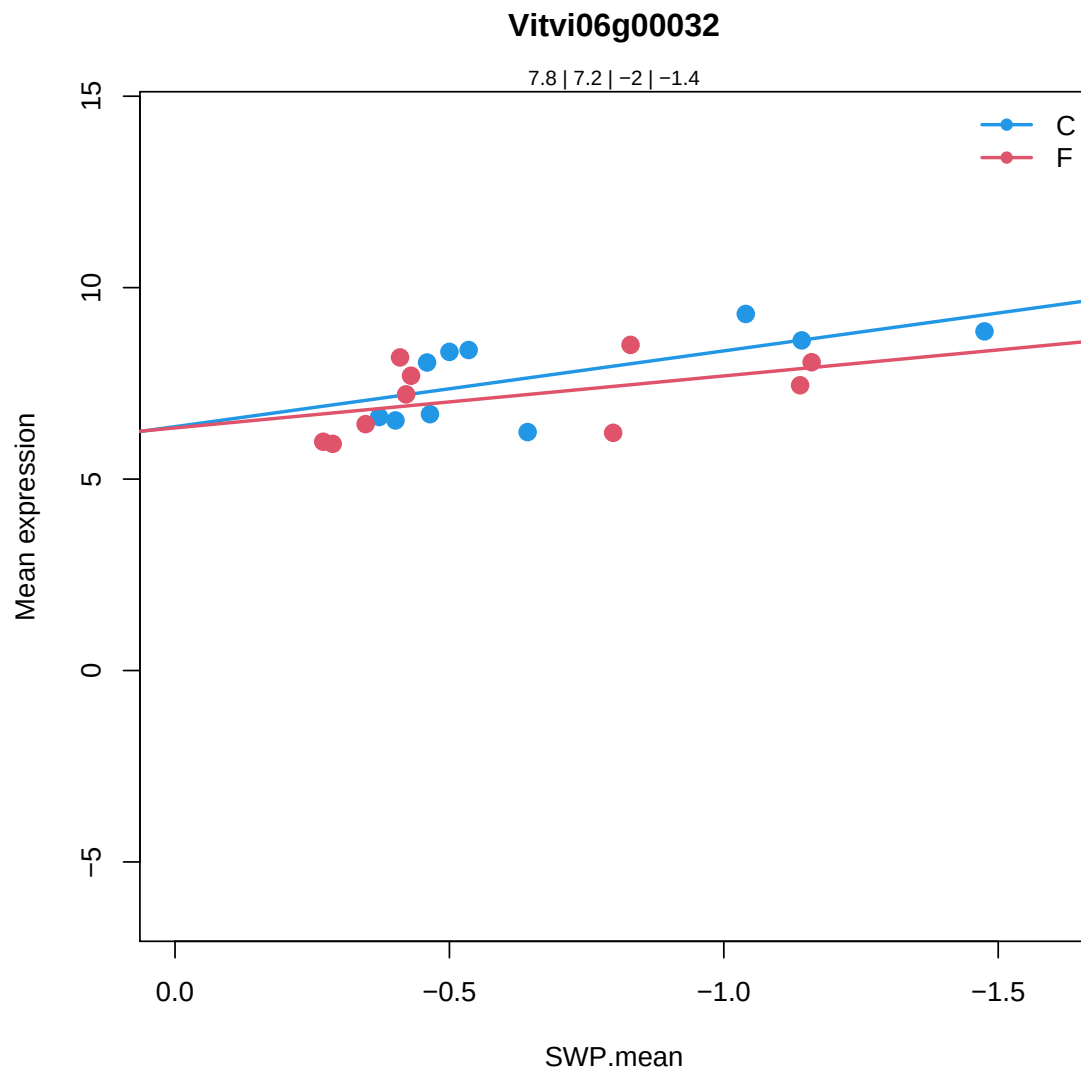
TCP-1/cpn60 chaperonin family protein |

Chr3:4389685-4392624 FORWARD LENGTH=596 |

201606

Coefficients for Vitvi06g00032.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.760565	4.422548e-19	***	1.705249e-18	***
SlopeC	-1.979112	0.01122606	*	0.3145361	
MeanF-MeanC	-0.597057	0.1142354		0.3954469	
SlopeF-SlopeC	0.6210973	0.5646707		0.9999488	



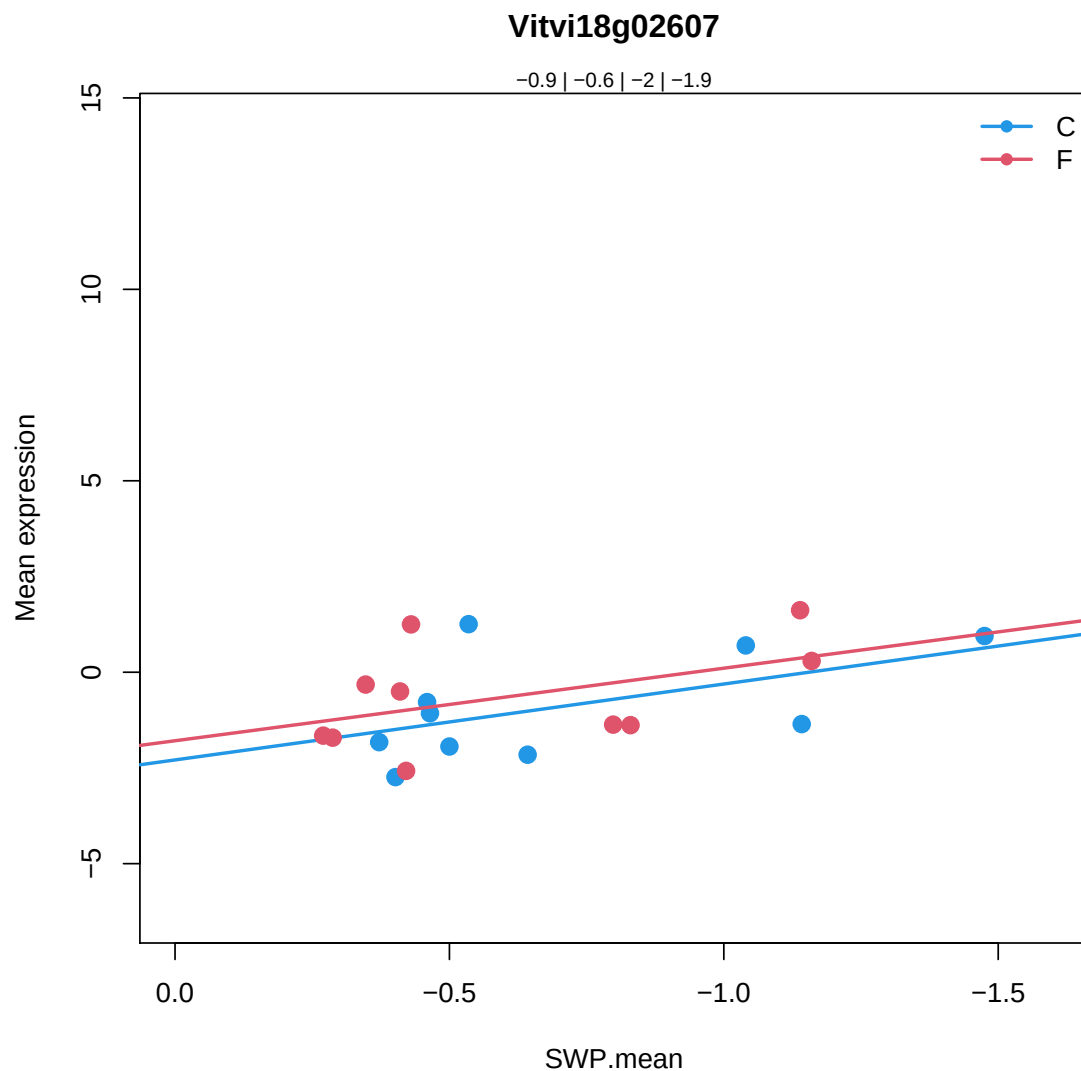
8.1.489 Vitvi18g02607: Type1.0

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

```
Vitvi18g02607
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi18g02607.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.8967429	0.01911297	*	0.02010211	*
SlopeC	-1.98267	0.0567301	.	0.5329089	
MeanF-MeanC	0.2611649	0.6070969		0.8620618	
SlopeF-SlopeC	0.08735273	0.9530133		0.9999488	



8.1.490 Vitvi05g00539: Type1.0 *

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

Vitvi05g00539

13.1.3.4.12

amino acid metabolism.synthesis.aspartate family.methionine.homocysteine

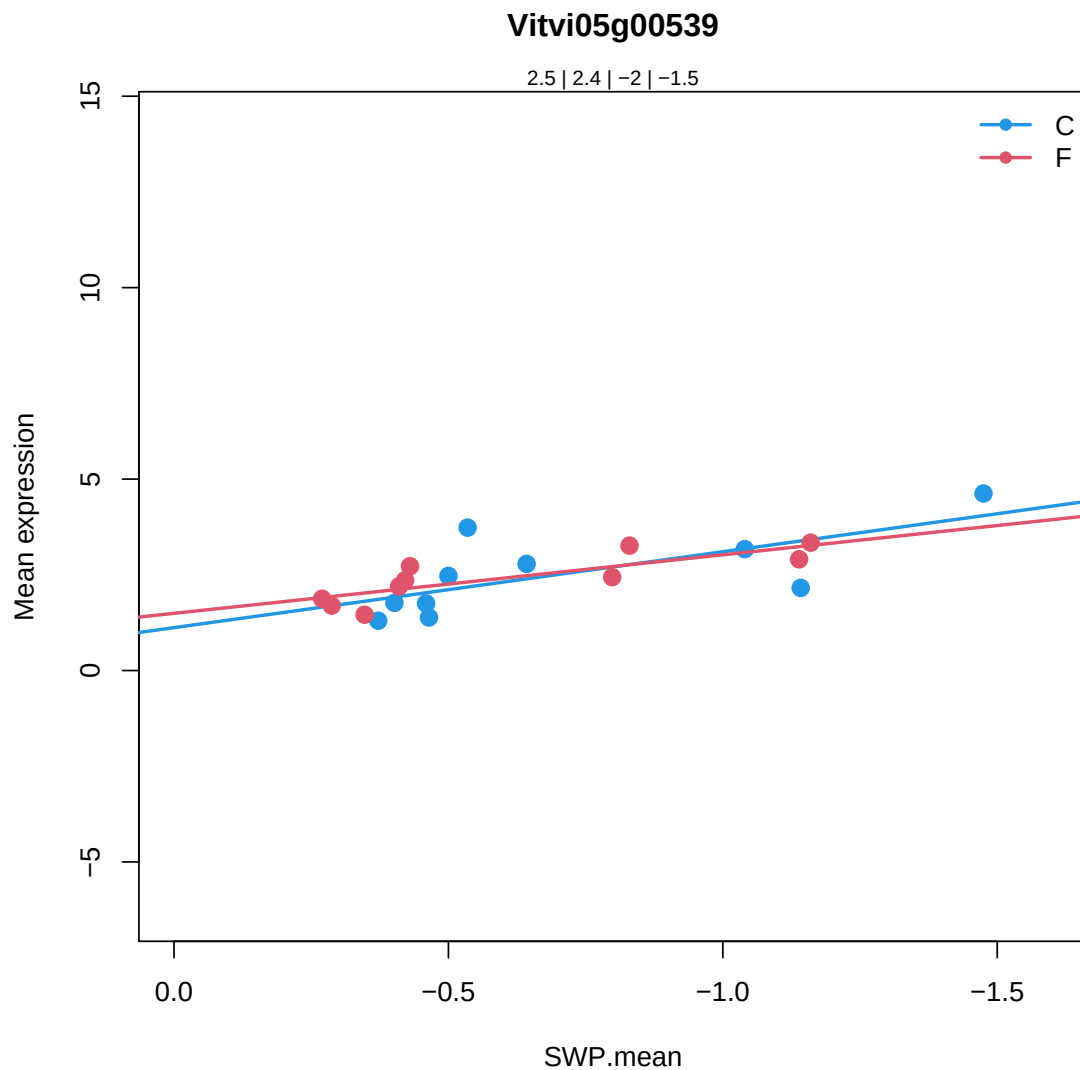
homocysteine methyltransferase 2 |

Chr3:23370575-23371974 REVERSE LENGTH=293 |

201606

Coefficients for Vitvi05g00539.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.514555	1.026531e-11	***	1.399873e-11	***
SlopeC	-1.983181	0.001236499	**	0.1365704	
MeanF-MeanC	-0.08927246	0.7451312		0.9250114	
SlopeF-SlopeC	0.4546535	0.57277		0.9999488	



8.1.491 Vitvi10g02382: Type1.0 *

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

Vitvi10g02382

20.2.1

stress.abiotic.heat

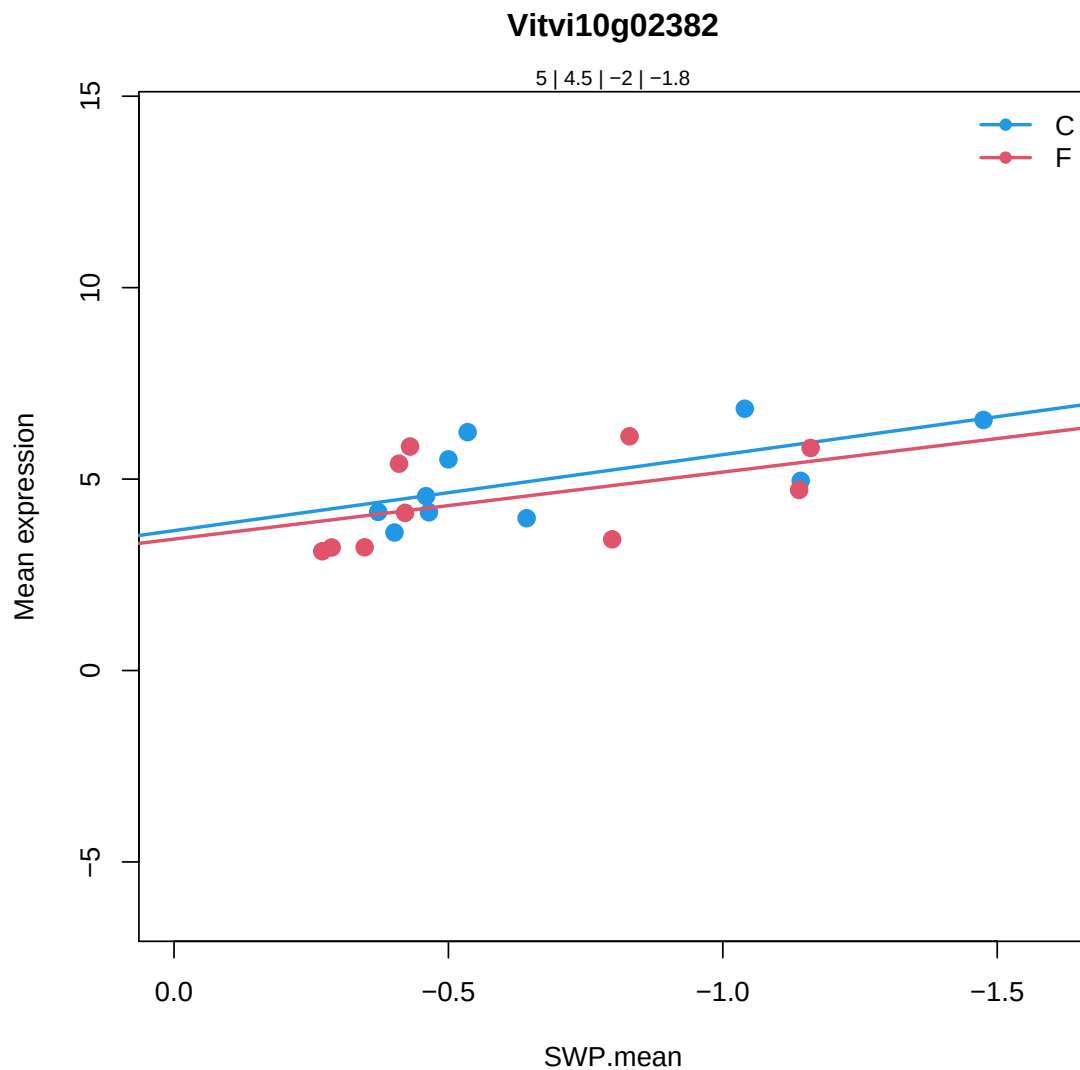
Aldolase-type TIM barrel family protein |

Chr4:11340492-11341732 FORWARD LENGTH=286 |

201606

Coefficients for Vitvi10g02382.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.048511	5.62629e-14	***	8.804509e-14	***
SlopeC	-1.983972	0.02471352	*	0.4060648	
MeanF-MeanC	-0.5497127	0.2018712		0.5452933	
SlopeF-SlopeC	0.2334417	0.8503601		0.9999488	



8.1.492 Vitvi03g01371: Type1.0 *

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

Vitvi03g01371

35.2

not assigned.unknown

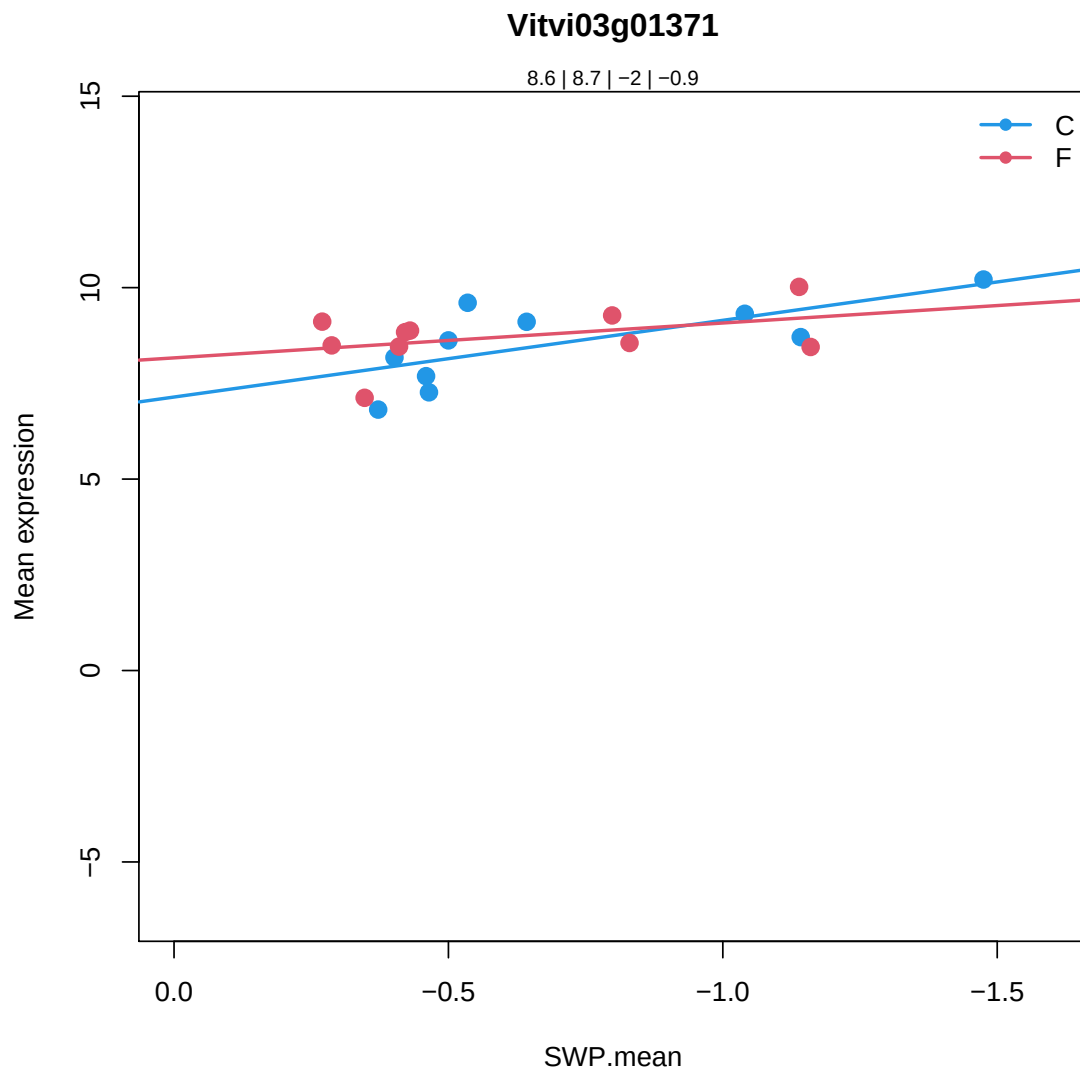
transmembrane protein |

Chr2:9074956-9075351 REVERSE LENGTH=131 |

201606

Coefficients for Vitvi03g01371.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	8.551588	2.693649e-21	***	2.468827e-20	***
SlopeC	-2.00386	0.003780575	**	0.2269459	
MeanF-MeanC	0.1686089	0.5964153		0.8589778	
SlopeF-SlopeC	1.092802	0.2470903		0.9999488	



8.1.493 Vitvi06g01295: Type1.0 *

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

Vitvi06g01295

29.6

protein.folding

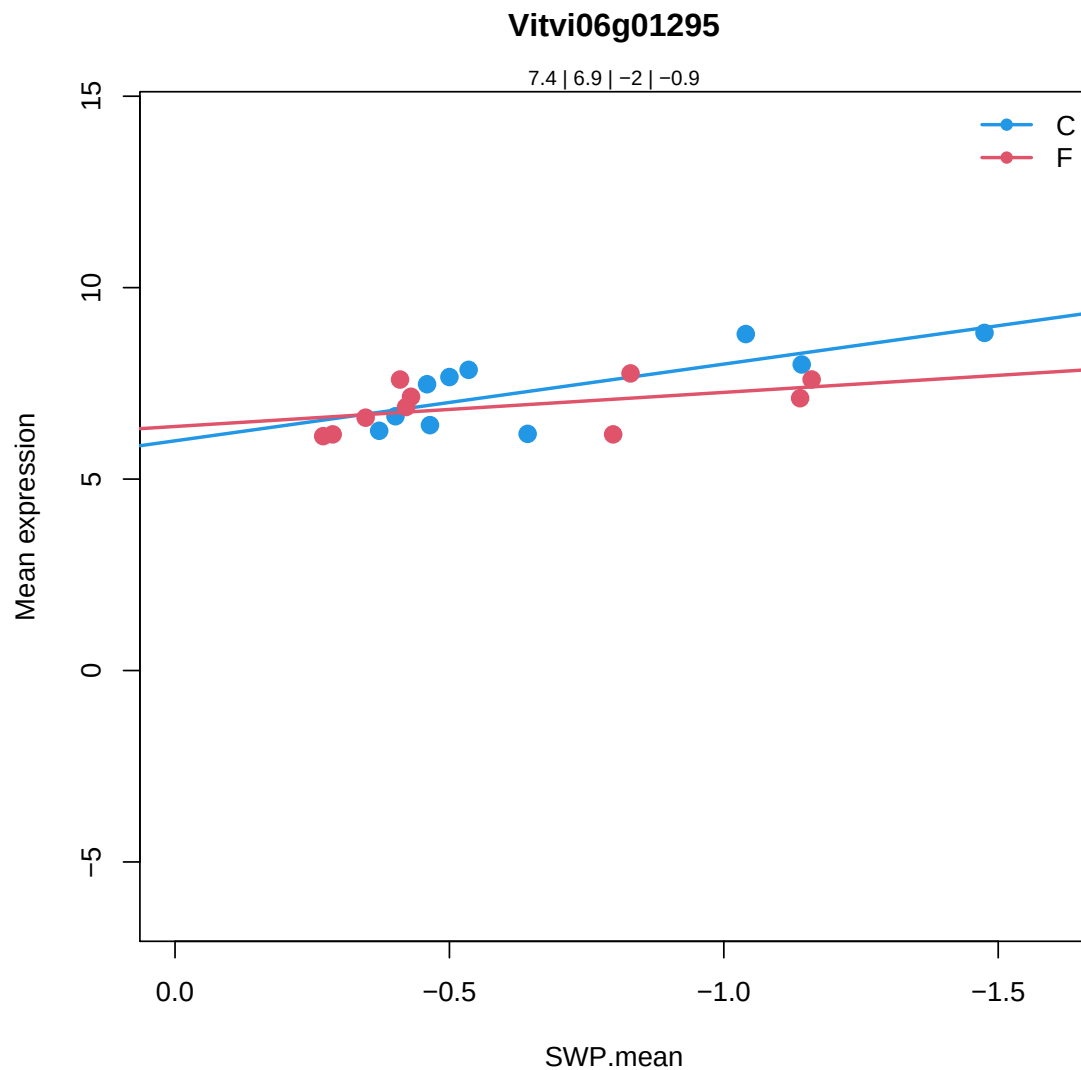
chaperonin-60alpha |

Chr2:11926603-11929184 FORWARD LENGTH=586 |

201606

Coefficients for Vitvi06g01295.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.408536	2.238596e-21	***	2.143258e-20	***
SlopeC	-2.004524	0.001059706	**	0.1285051	
MeanF-MeanC	-0.4920488	0.08169882	.	0.3239473	
SlopeF-SlopeC	1.113483	0.1723597		0.9999488	



8.1.494 Vitvi14g01824: Type1.0 *

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

Vitvi14g01824

27.3.11

RNA.regulation of transcription.C2H2 zinc finger family

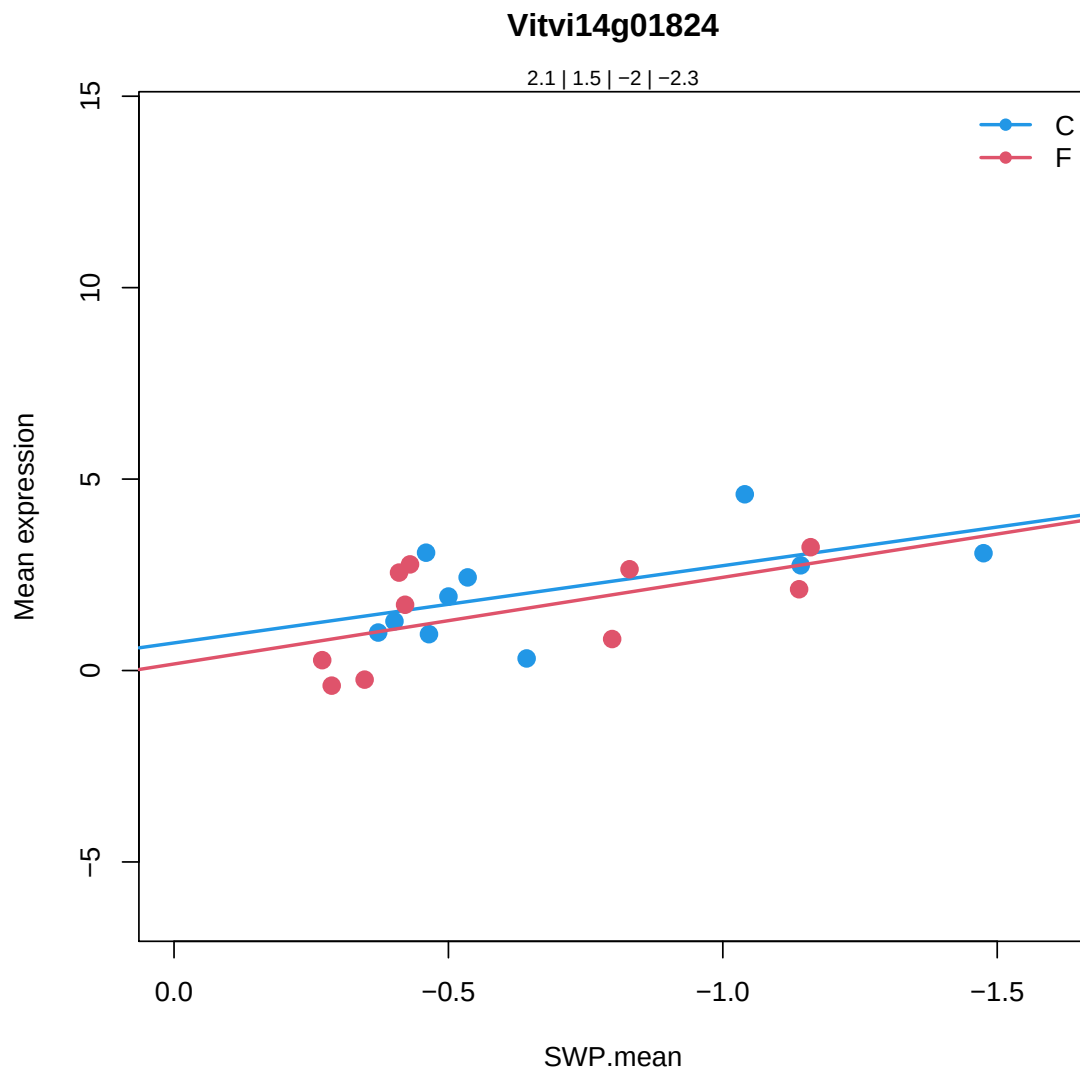
zinc finger (AN1-like) family protein |

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	



8.1.495 Vitvi11g00351: Type1.0 *

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

Vitvi11g00351

35.2

not assigned.unknown

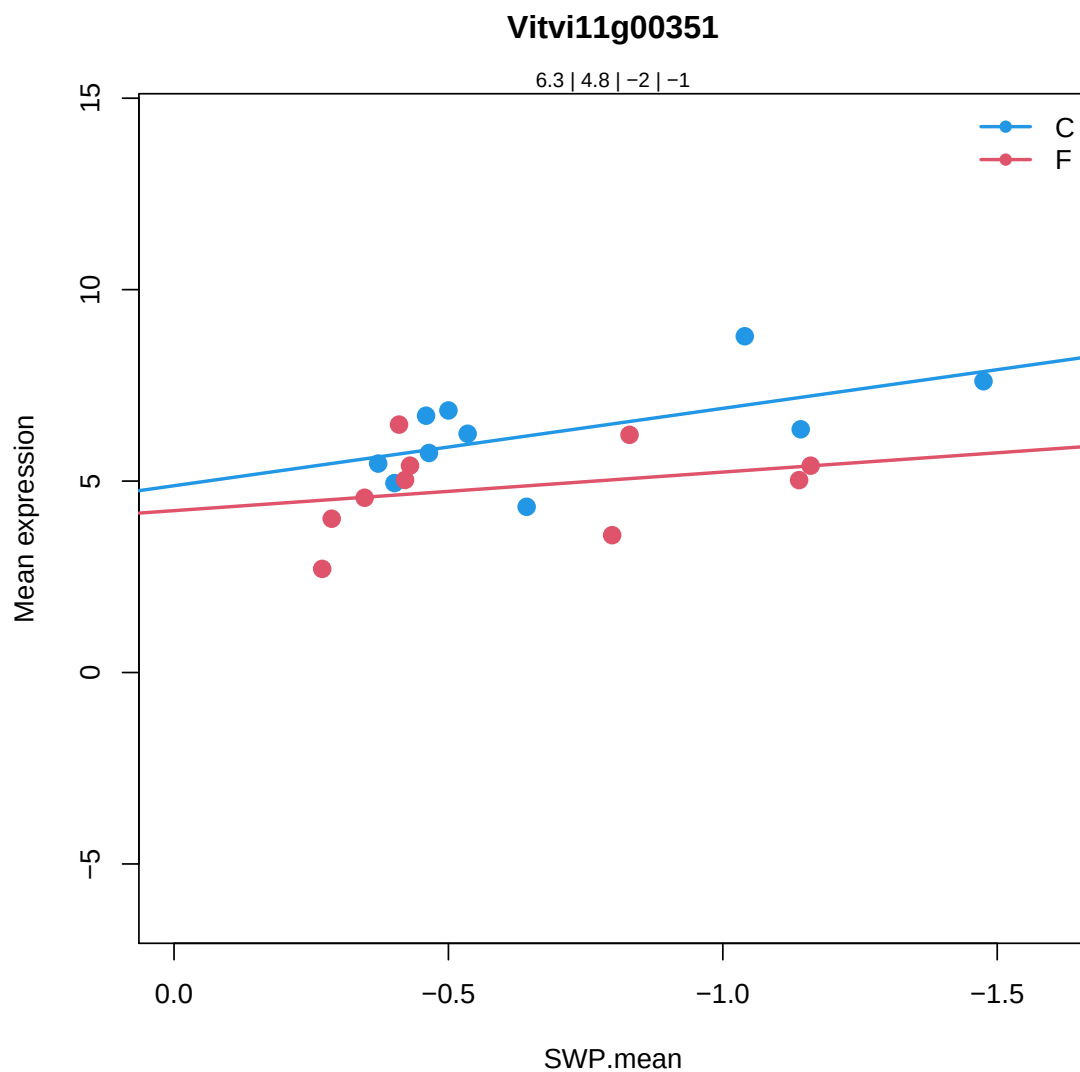
multiprotein bridging factor 1C |

Chr3:8918755-8919201 FORWARD LENGTH=148 |

201606

Coefficients for Vitvi11g00351.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.299756	3.596579e-15	***	6.331242e-15	***
SlopeC	-2.0209	0.03439724	*	0.4439311	
MeanF-MeanC	-1.458163	0.004158195	**	0.03936597	*
SlopeF-SlopeC	1.01326	0.4549109		0.9999488	



8.1.496 Vitvi11g00251: Type1.0 *

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

Vitvi11g00251

35.1

not assigned.no ontology

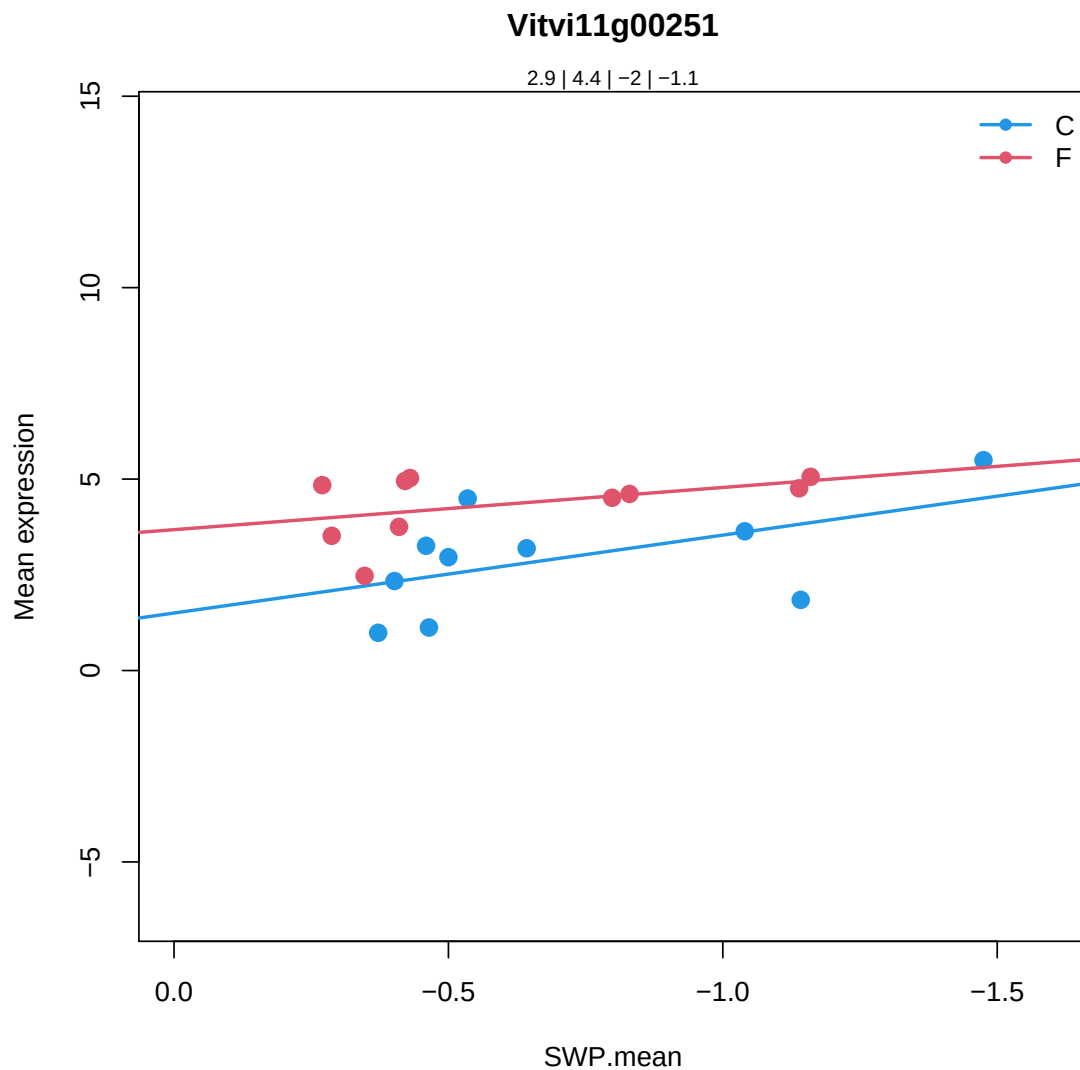
oxidative stress 3 |

Chr5:22895847-22896502 REVERSE LENGTH=172 |

201606

Coefficients for Vitvi11g00251.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.932105	2.382277e-09	***	2.967285e-09	***
SlopeC	-2.034749	0.02363228	*	0.3983963	
MeanF-MeanC	1.418241	0.003037626	**	0.03103183	*
SlopeF-SlopeC	0.9321709	0.4614726		0.9999488	



8.1.497 Vitvi07g02753: Type1.0 *

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

Vitvi07g02753

35.2

not assigned.unknown

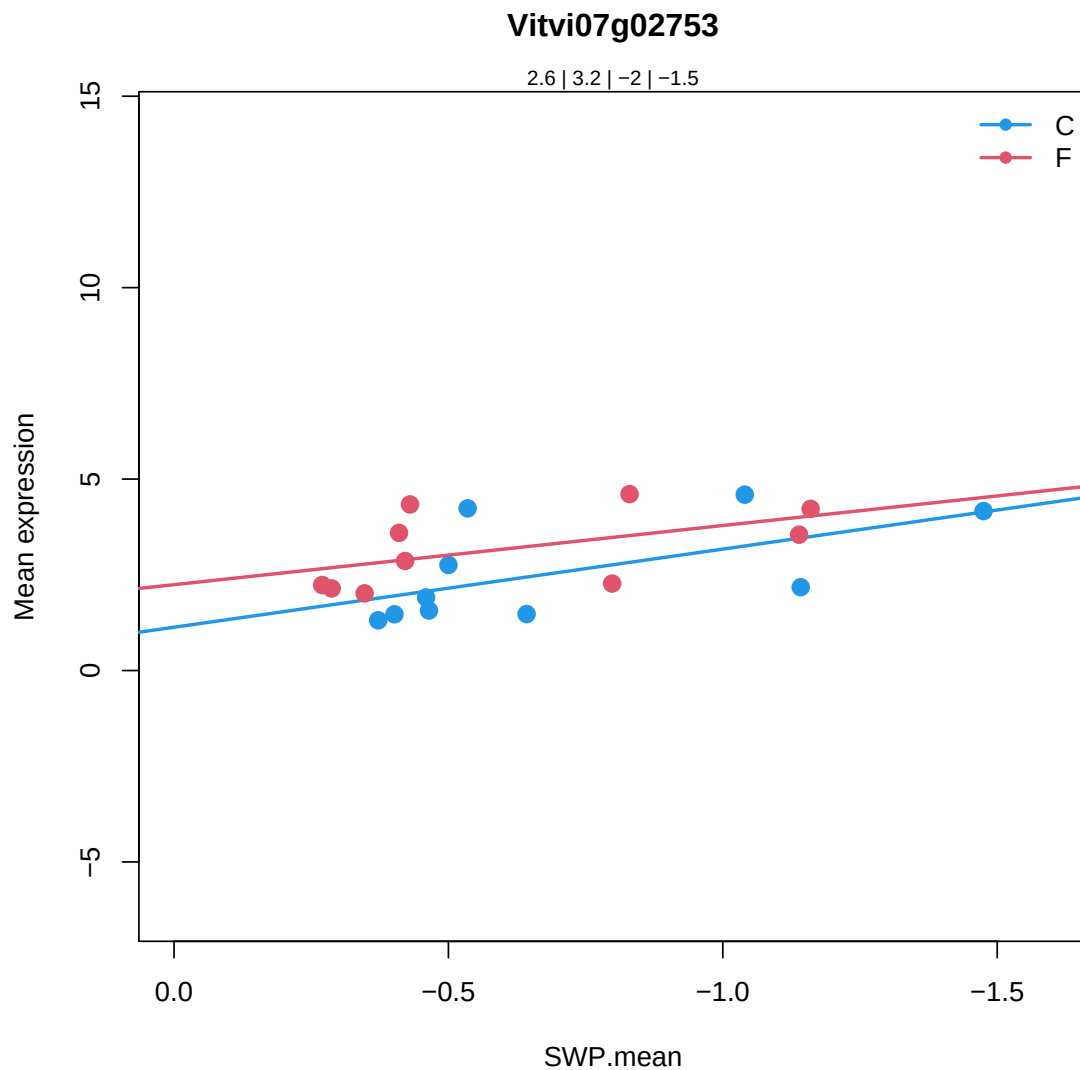
amino acid-ligase |

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	



8.1.498 Vitvi13g00491: Type1.0 *

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

Vitvi13g00491

20.2.1

stress.abiotic.heat

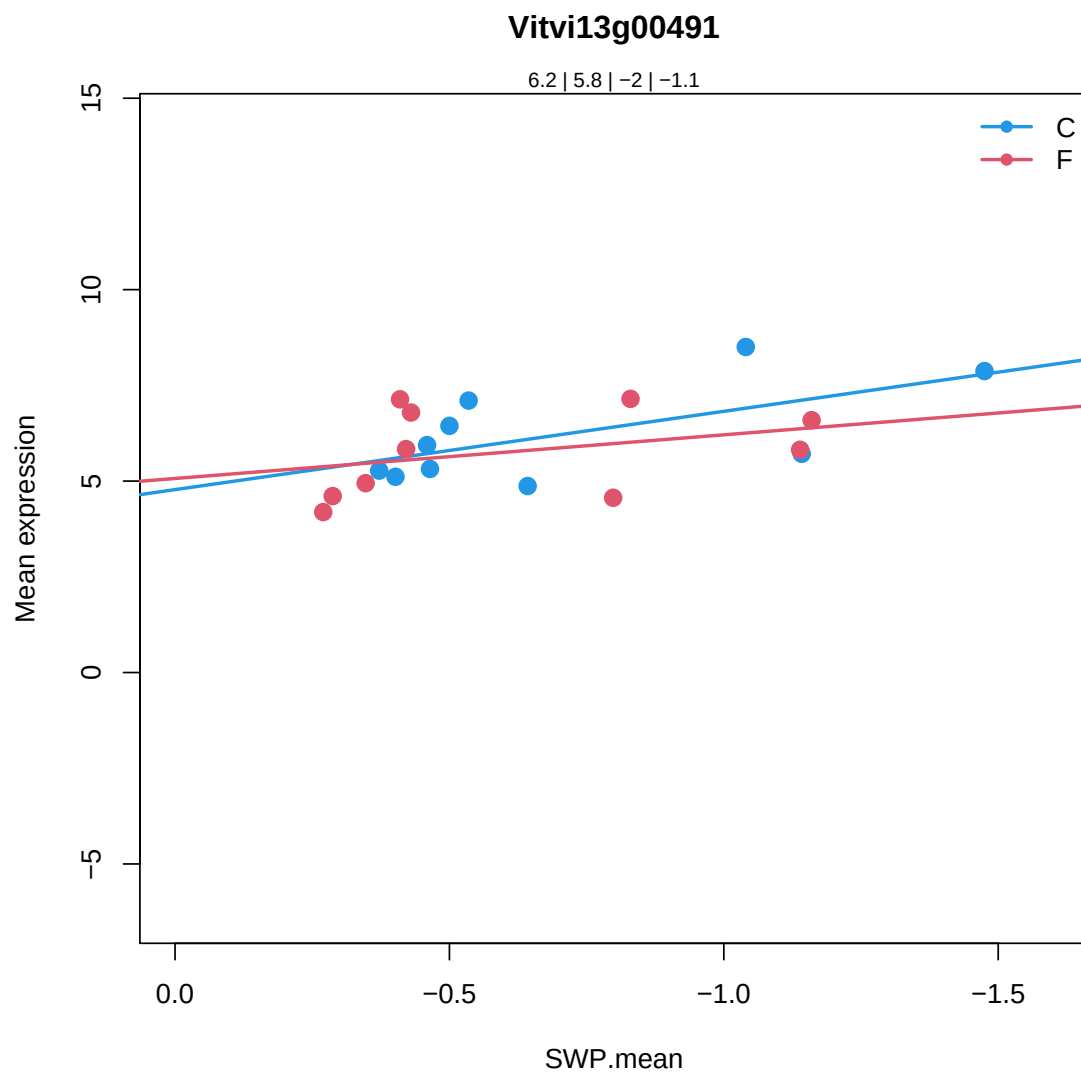
heat shock protein 17.4 |

Chr3:16984263-16984733 REVERSE LENGTH=156 |

201606

Coefficients for Vitvi13g00491.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.214606	1.541119e-15	***	2.818881e-15	***
SlopeC	-2.044997	0.02469476	*	0.4060648	
MeanF-MeanC	-0.4521316	0.3050813		0.6685796	
SlopeF-SlopeC	0.9046063	0.4805214		0.9999488	



8.1.499 Vitvi12g00683: Type1.0 *

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

Vitvi12g00683

20.2.1

stress.abiotic.heat

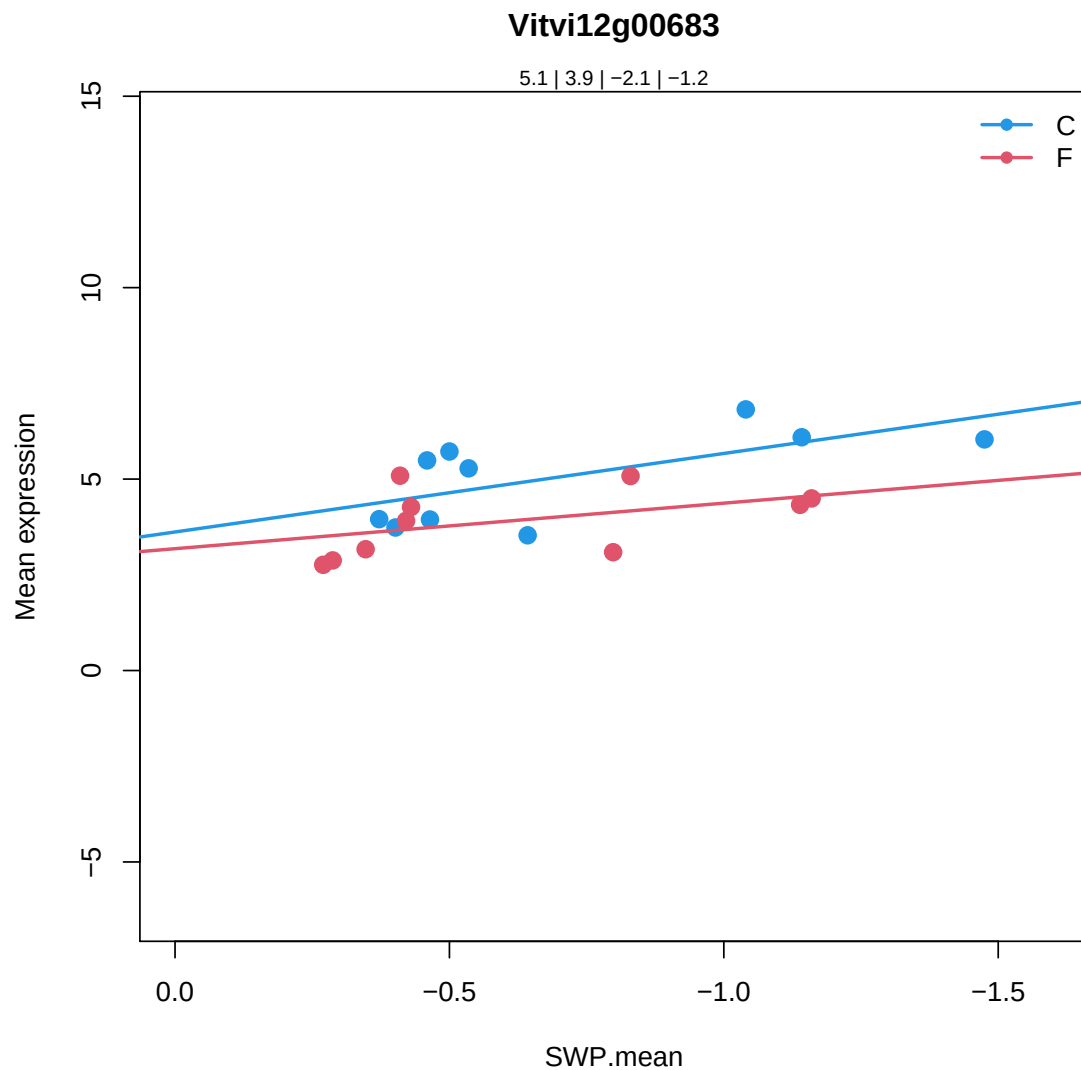
HEAT SHOCK PROTEIN 89.1 |

Chr3:2479611-2483970 FORWARD LENGTH=799 |

201606

Coefficients for Vitvi12g00683.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.060146	2.370268e-15	***	4.259328e-15	***
SlopeC	-2.050629	0.008199425	**	0.2854824	
MeanF-MeanC	-1.153796	0.003990952	**	0.03818587	*
SlopeF-SlopeC	0.8613412	0.4200726		0.9999488	



8.1.500 Vitvi13g00343: Type1.0 *

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

Vitvi13g00343

35.2

not assigned.unknown

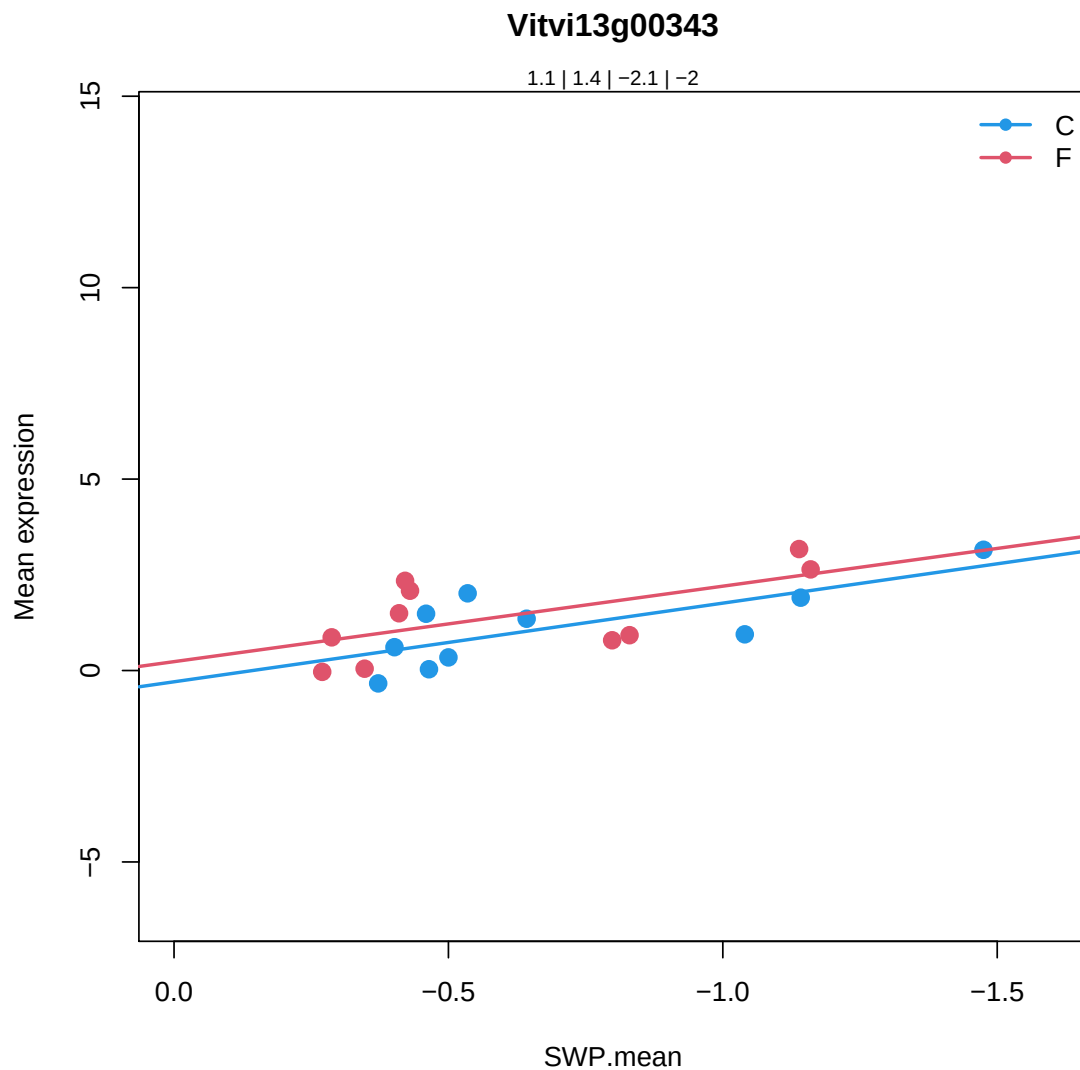
NAD(P)-binding Rossmann-fold superfamily protein |

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	



8.1.501 Vitvi05g00924: Type1.0 *

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

Vitvi05g00924

29.6

protein.folding

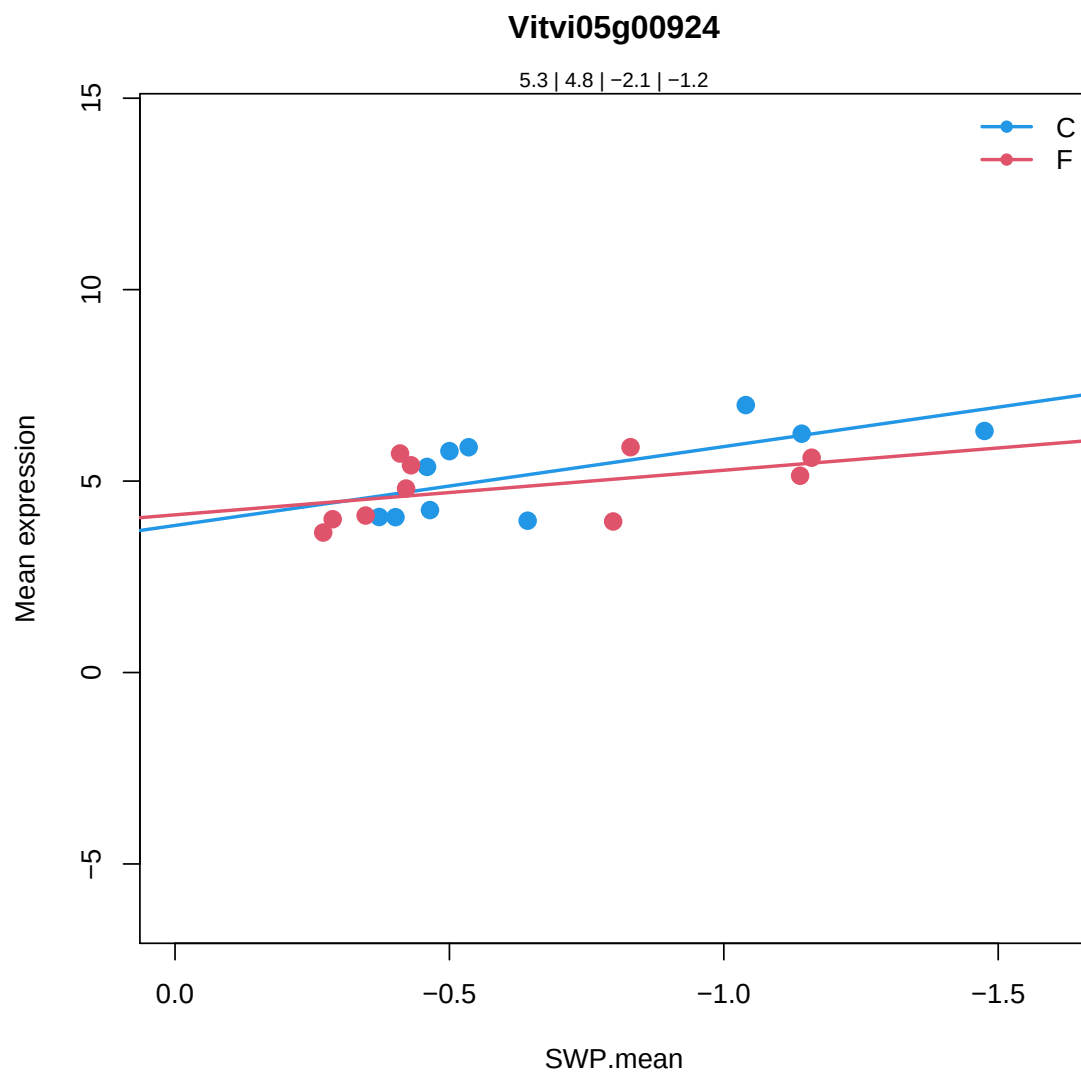
heat shock protein 60 |

Chr3:8669013-8672278 FORWARD LENGTH=577 |

201606

Coefficients for Vitvi05g00924.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.289438	2.406433e-16	***	4.915419e-16	***
SlopeC	-2.060375	0.004968161	**	0.2519339	
MeanF-MeanC	-0.4617451	0.1817553		0.5173321	
SlopeF-SlopeC	0.8957972	0.3706438		0.9999488	



8.1.502 Vitvi08g01890: Type1.0 *

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

Vitvi08g01890

3.1.2.2

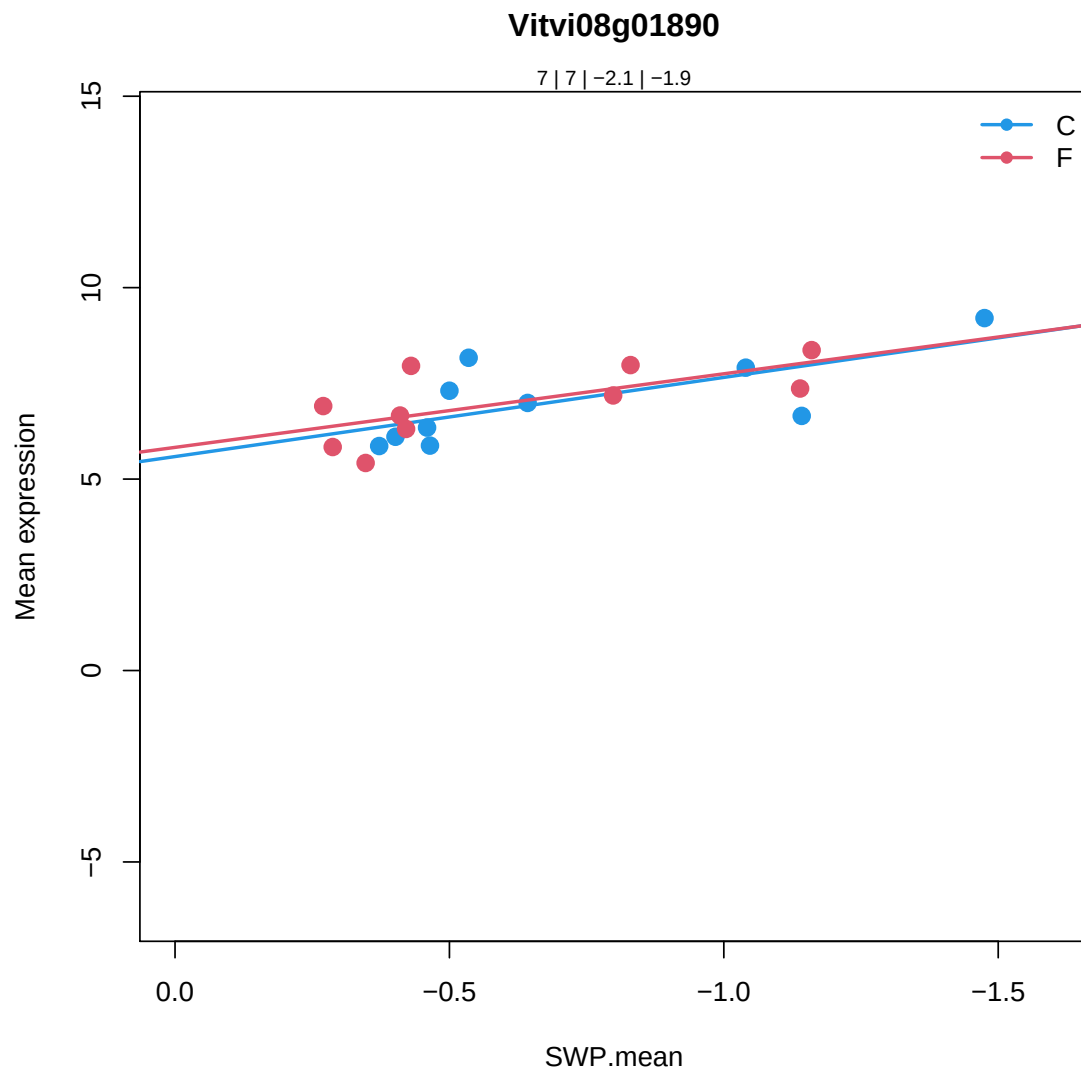
minor CHO metabolism.raffinose family.raffinose synthases.putative
seed imbibition 2 |

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	



8.1.503 Vitvi08g01757: Type1.0 *

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

Vitvi08g01757

35.1

not assigned.no ontology

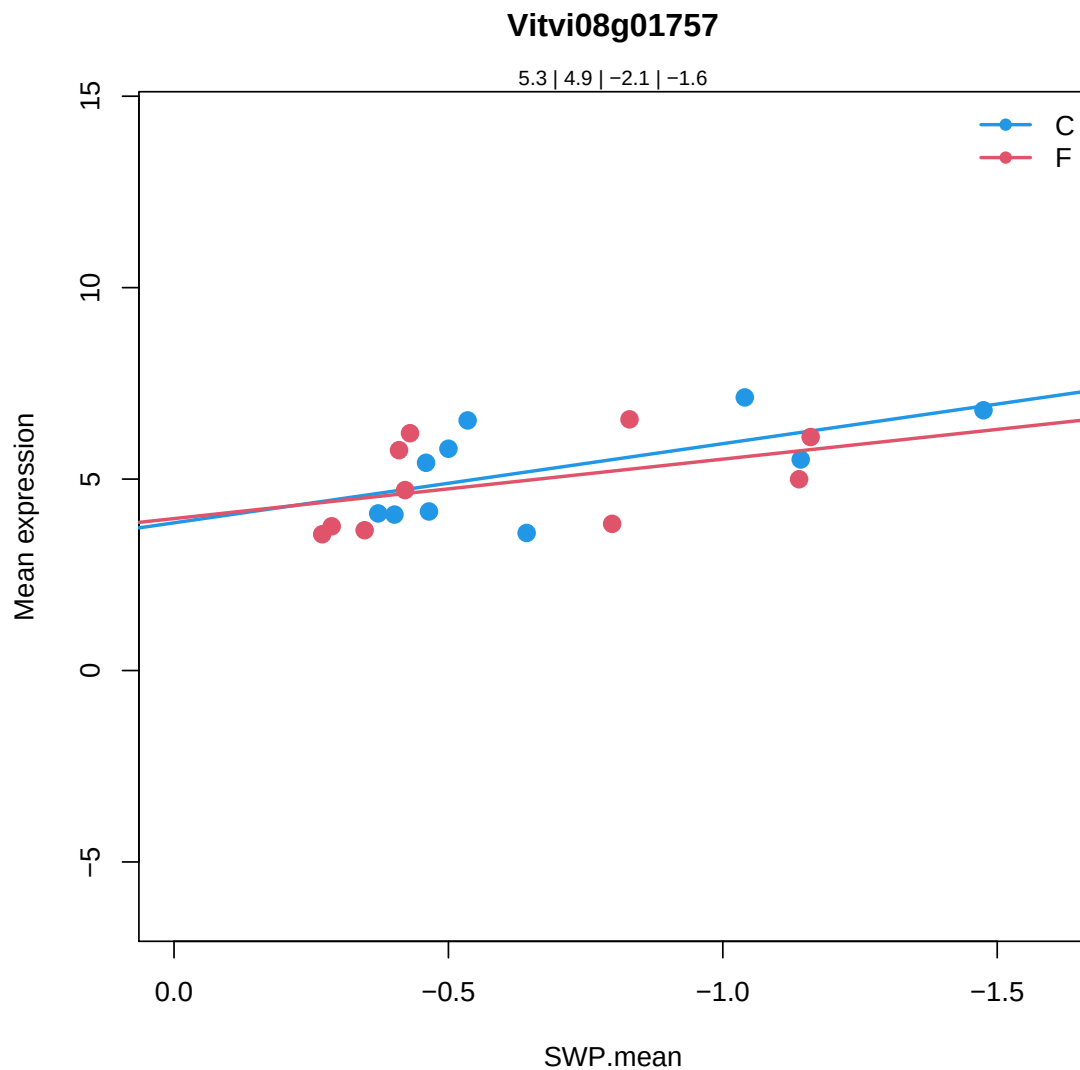
Ahal domain-containing protein |

Chr3:3839289-3841303 FORWARD LENGTH=360 |

201606

Coefficients for Vitvi08g01757.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.311265	4.460549e-14	***	7.040978e-14	***
SlopeC	-2.068001	0.0244177	*	0.4039715	
MeanF-MeanC	-0.397333	0.3703171		0.7247527	
SlopeF-SlopeC	0.5152747	0.6892723		0.9999488	



8.1.504 Vitvi04g01576: Type1.0 *

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

Vitvi04g01576

33.99

development.unspecified

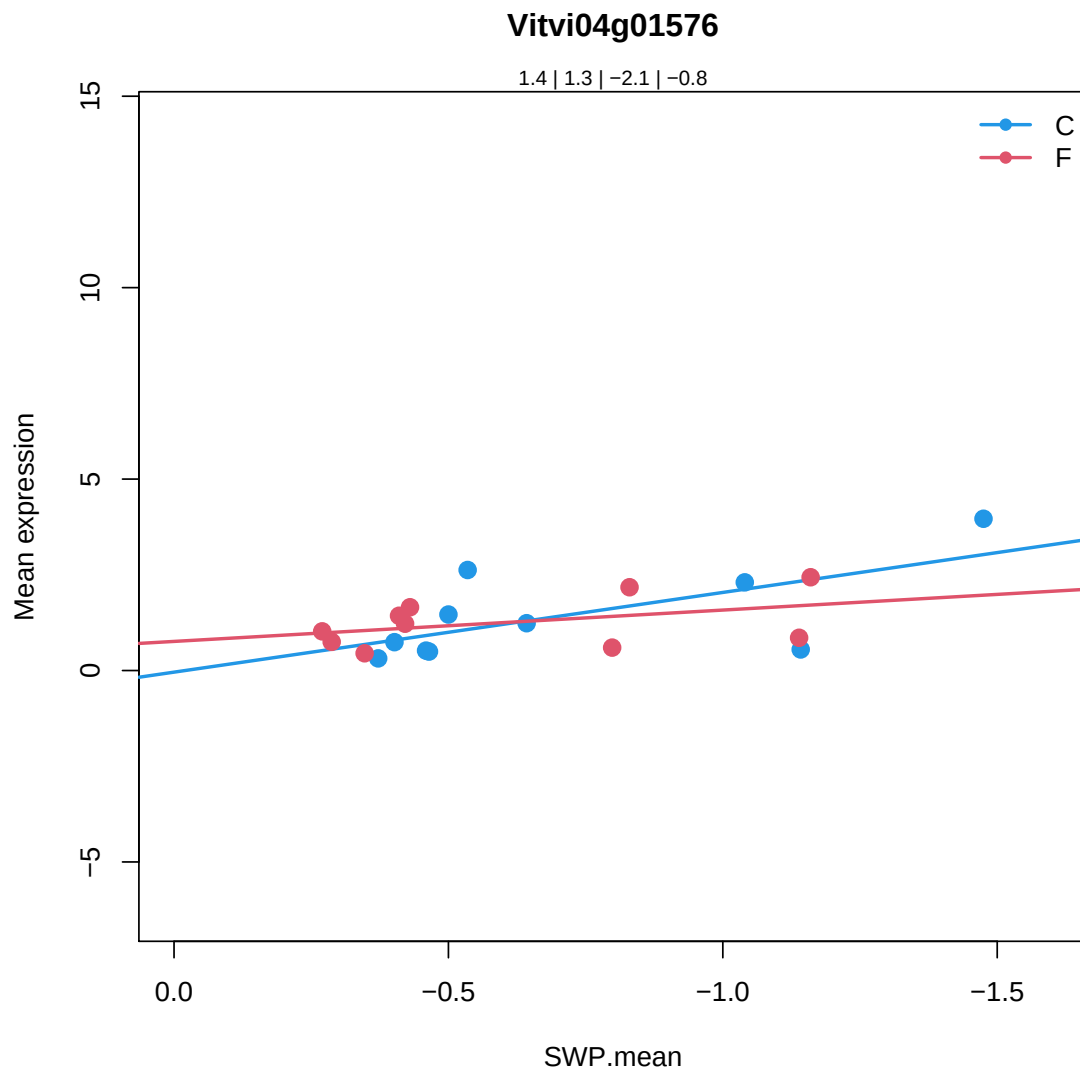
Transducin/WD40 repeat-like superfamily protein |

Chr4:16881562-16886878 FORWARD LENGTH=1049 |

201606

Coefficients for Vitvi04g01576.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.42106	4.804798e-06	***	5.46161e-06	***
SlopeC	-2.081762	0.004355422	**	0.2399107	
MeanF-MeanC	-0.1621285	0.6303034		0.8739274	
SlopeF-SlopeC	1.262886	0.2077446		0.9999488	



8.1.505 Vitvi13g02046: Type1.0

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

Vitvi13g02046

35.2

not assigned.unknown

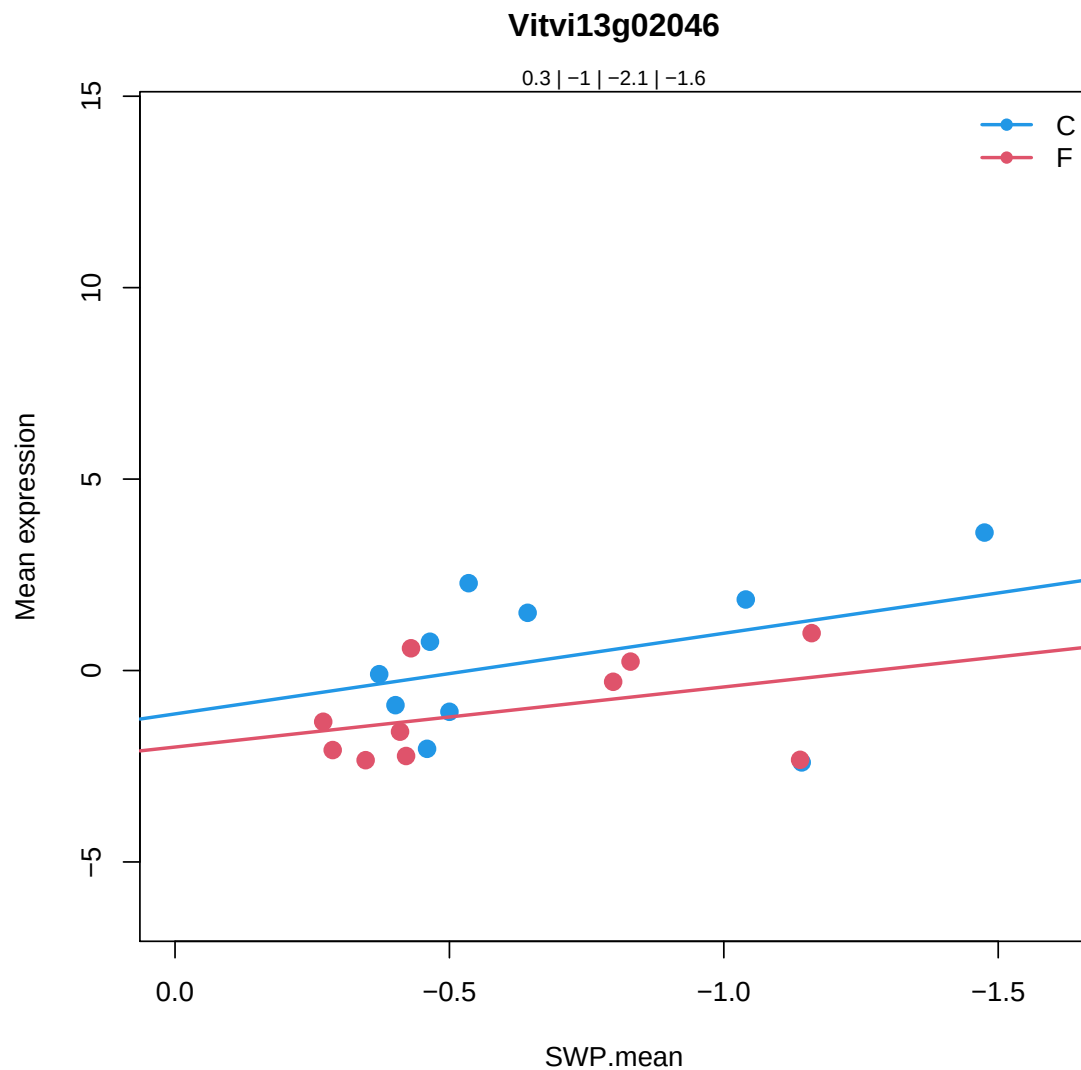
Low temperature and salt responsive protein family |

Chr3:1756195-1756494 REVERSE LENGTH=54 |

201606

Coefficients for Vitvi13g02046.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3474452	0.4477327		0.4538367	
SlopeC	-2.106085	0.10648		0.6211132	
MeanF-MeanC	-1.389891	0.039901	*	0.2059503	
SlopeF-SlopeC	0.5362332	0.7759191		0.9999488	



8.1.506 Vitvi00g01011: Type1.0 *

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

Vitvi00g01011

31.3.1

cell.cycle.peptidylprolyl isomerase

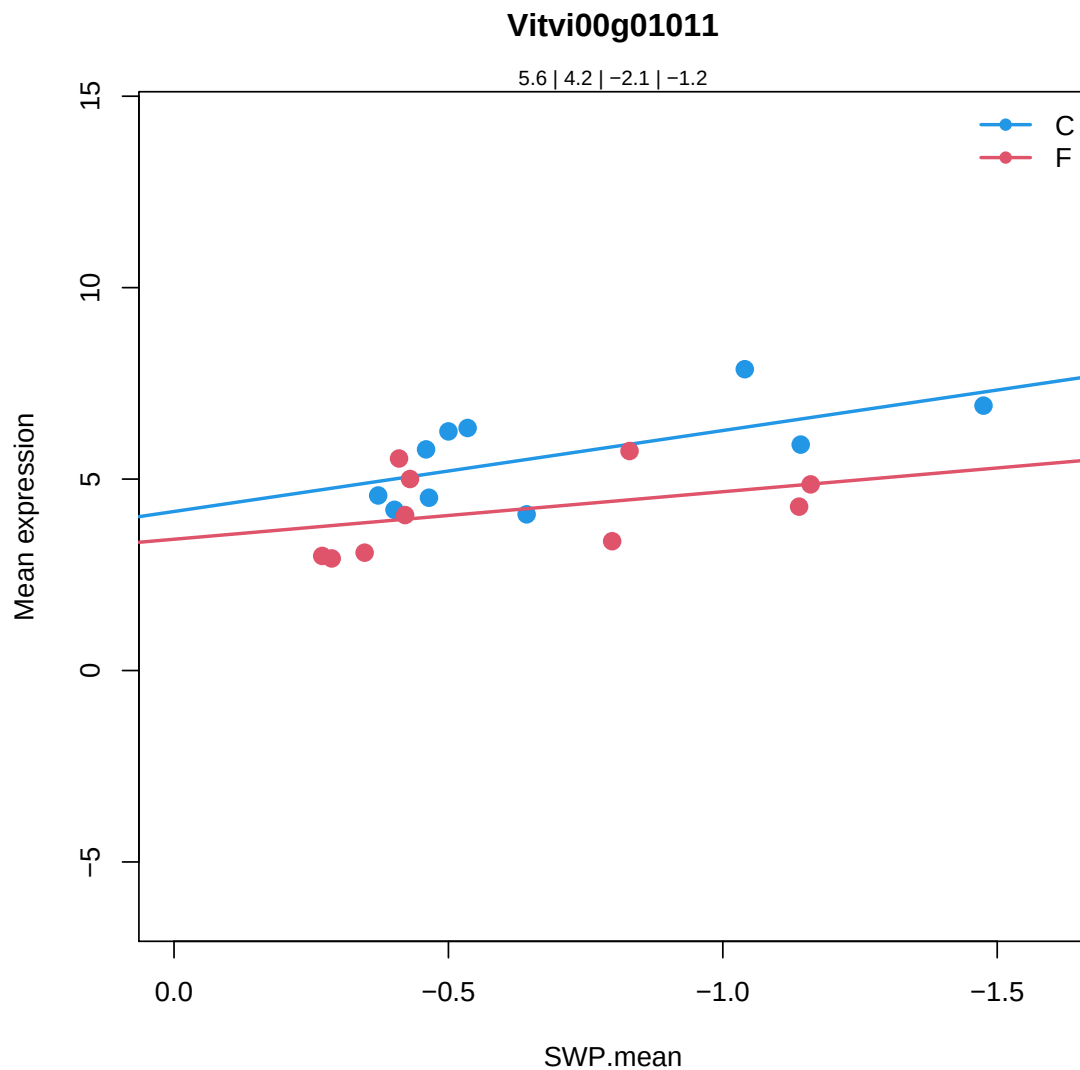
rotamase FKBP 1 |

Chr3:9188257-9191137 FORWARD LENGTH=551 |

201606

Coefficients for Vitvi00g01011.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.640187	5.802743e-15	***	9.947746e-15	***
SlopeC	-2.114463	0.01733592	*	0.3551322	
MeanF-MeanC	-1.455428	0.002122754	**	0.02304059	*
SlopeF-SlopeC	0.8734687	0.4818723		0.9999488	



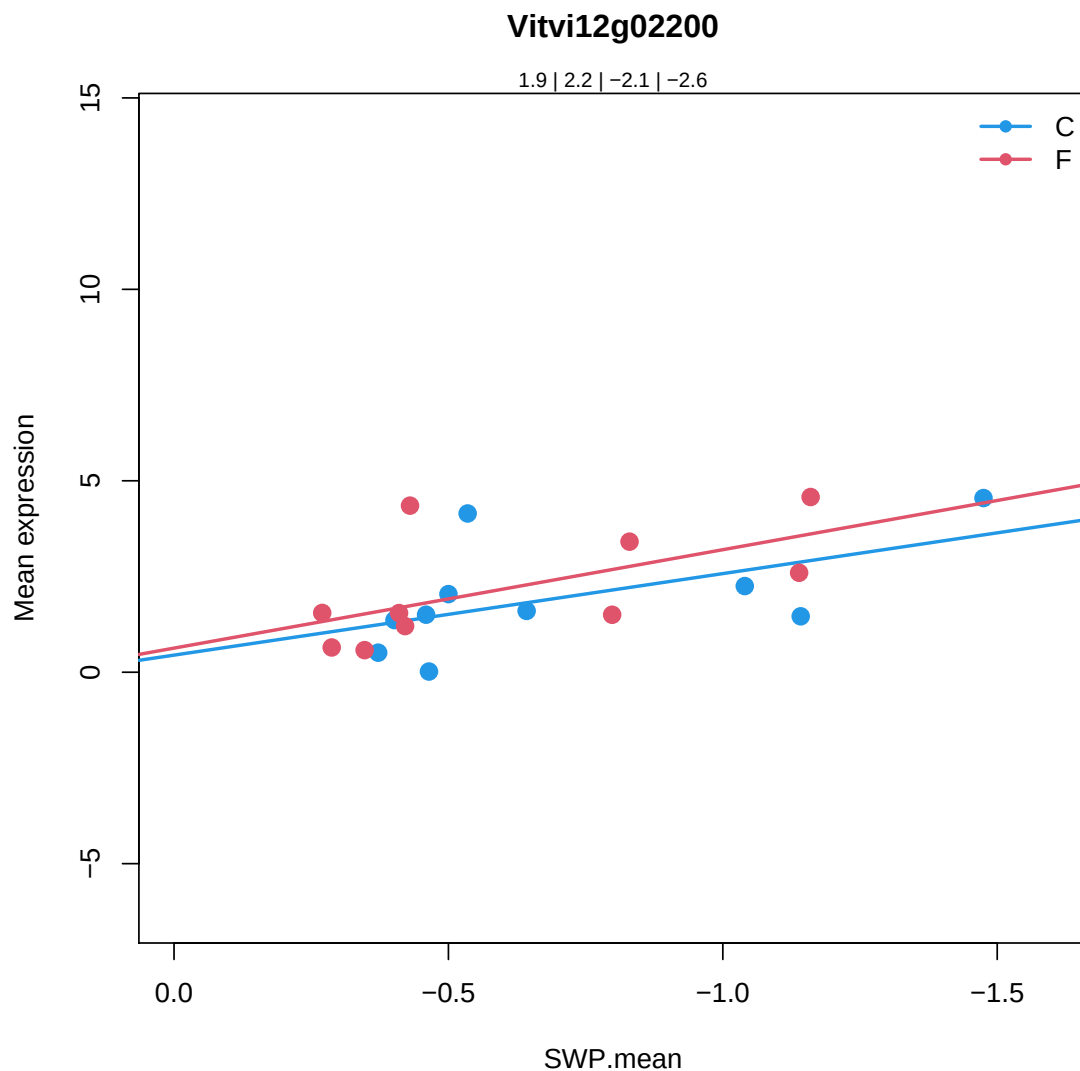
8.1.507 Vitvi12g02200: Type1.0 *

```
> 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	



8.1.508 Vitvi05g00736: Type1.0 *

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

Vitvi05g00736

4.1.16

glycolysis.cytosolic branch.phosphoenolpyruvate carboxykinase (PEPCK)

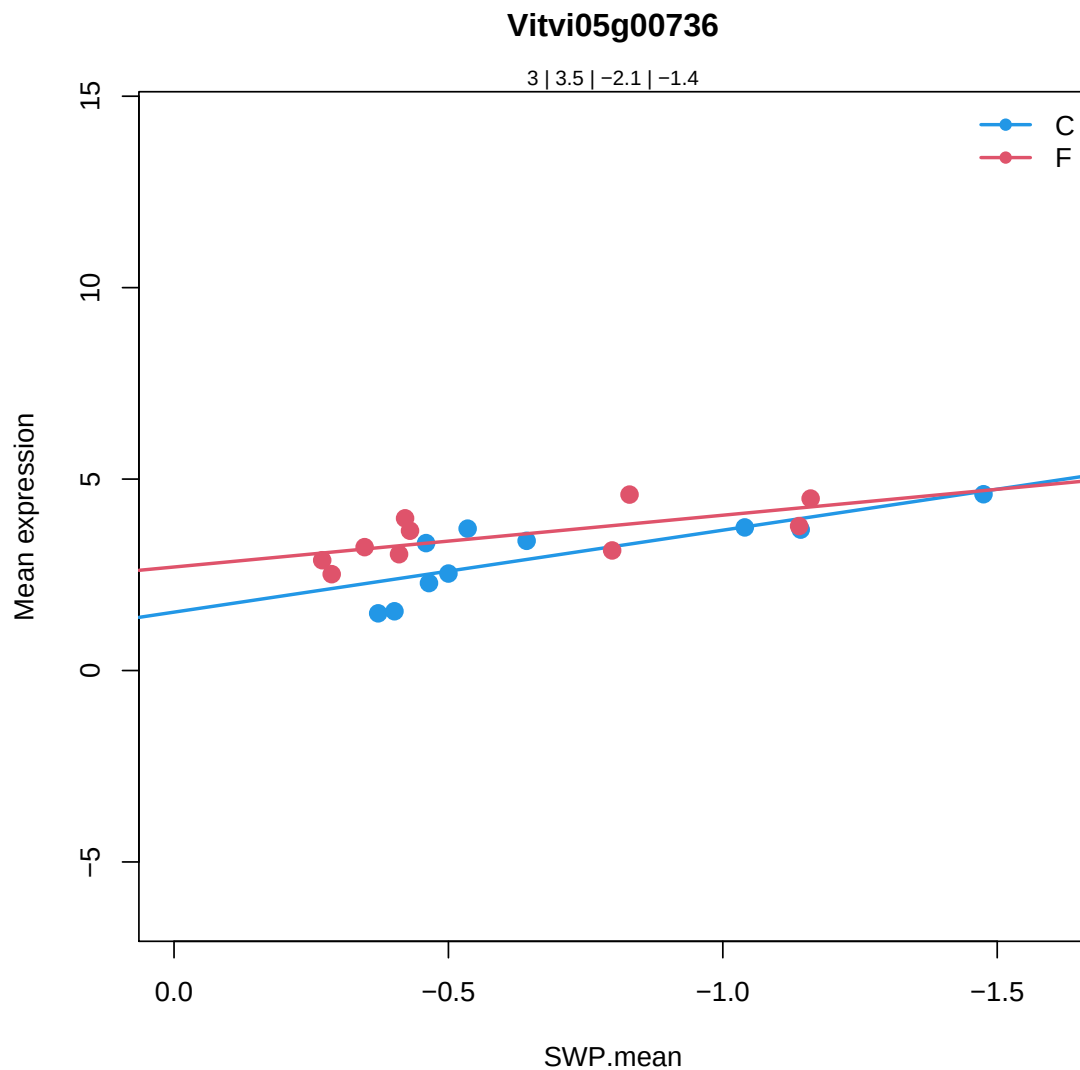
phosphoenolpyruvate carboxylase kinase 1 |

Chr1:2752206-2753150 FORWARD LENGTH=276 |

201606

Coefficients for Vitvi05g00736.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.029799	1.029617e-13	***	1.579769e-13	***
SlopeC	-2.140659	0.0003754351	***	0.09467692	.
MeanF-MeanC	0.4978685	0.06723014	.	0.2884103	
SlopeF-SlopeC	0.7876065	0.3092221		0.9999488	



8.1.509 Vitvi04g01296: Type1.0 *

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

Vitvi04g01296

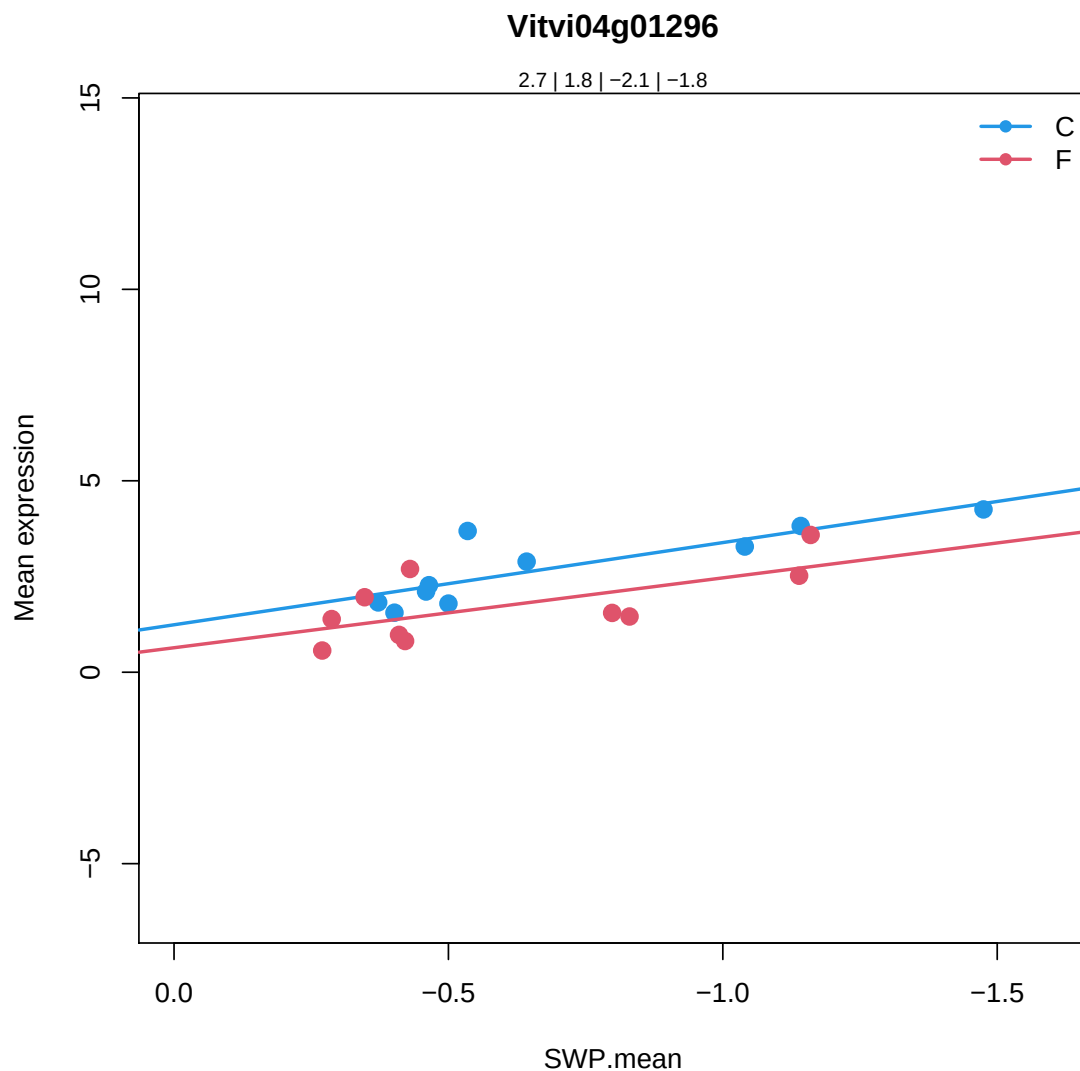
35.1

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	



8.1.510 Vitvi19g00270: Type1.0 *

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

Vitvi19g00270

27.3.27

RNA.regulation of transcription.NAC domain transcription factor family

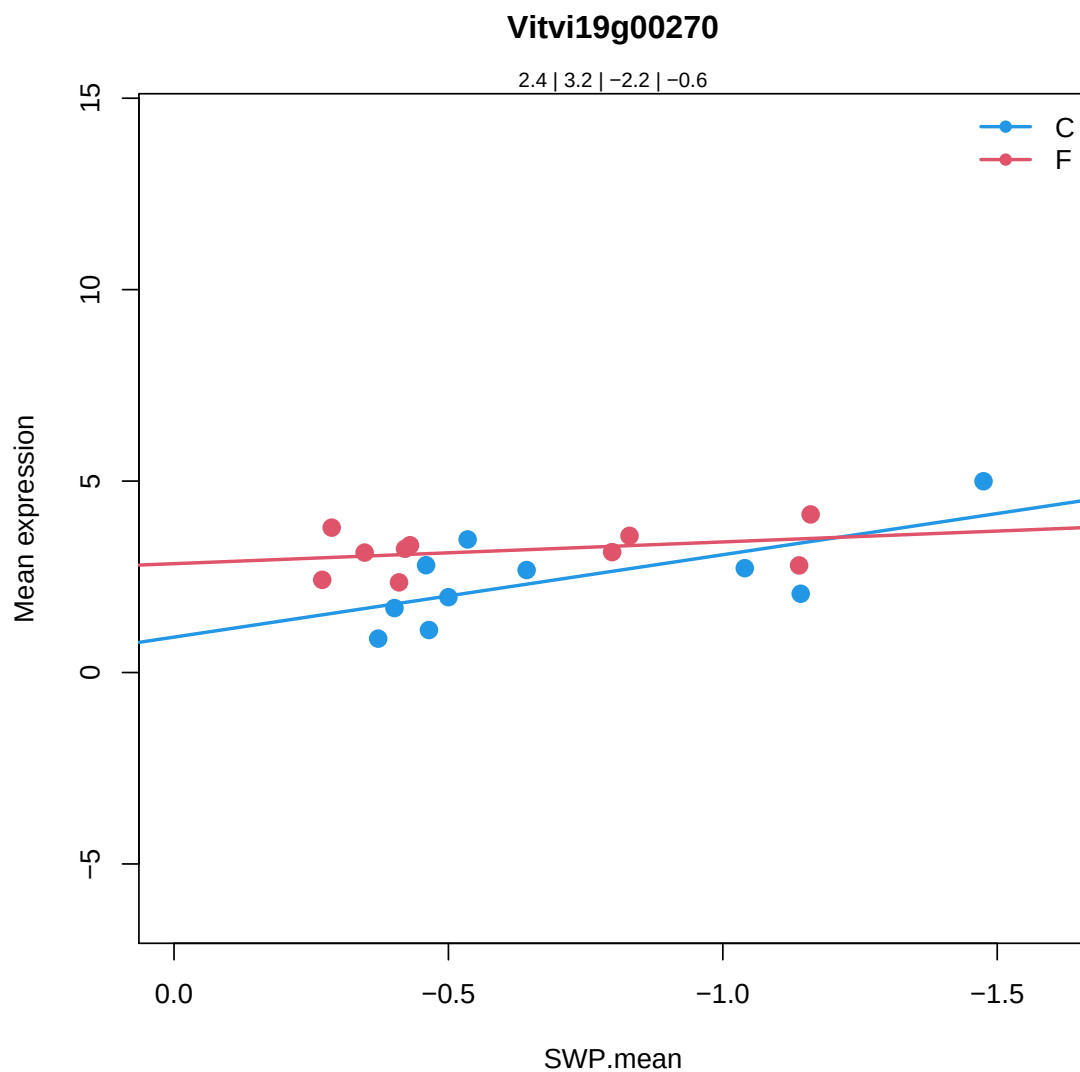
NAC (No Apical Meristem) domain transcriptional regulator superfamily

Chr4:13707928-13709013 REVERSE LENGTH=314 |

201606

Coefficients for Vitvi19g00270.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.437826	3.614564e-10	***	4.629679e-10	***
SlopeC	-2.15214	0.002390578	**	0.185904	
MeanF-MeanC	0.7509303	0.02766146	*	0.1599928	
SlopeF-SlopeC	1.584289	0.1031405		0.9999488	



8.1.511 Vitvi03g01517: Type1.0 *

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

Vitvi03g01517

21.3

redox.heme

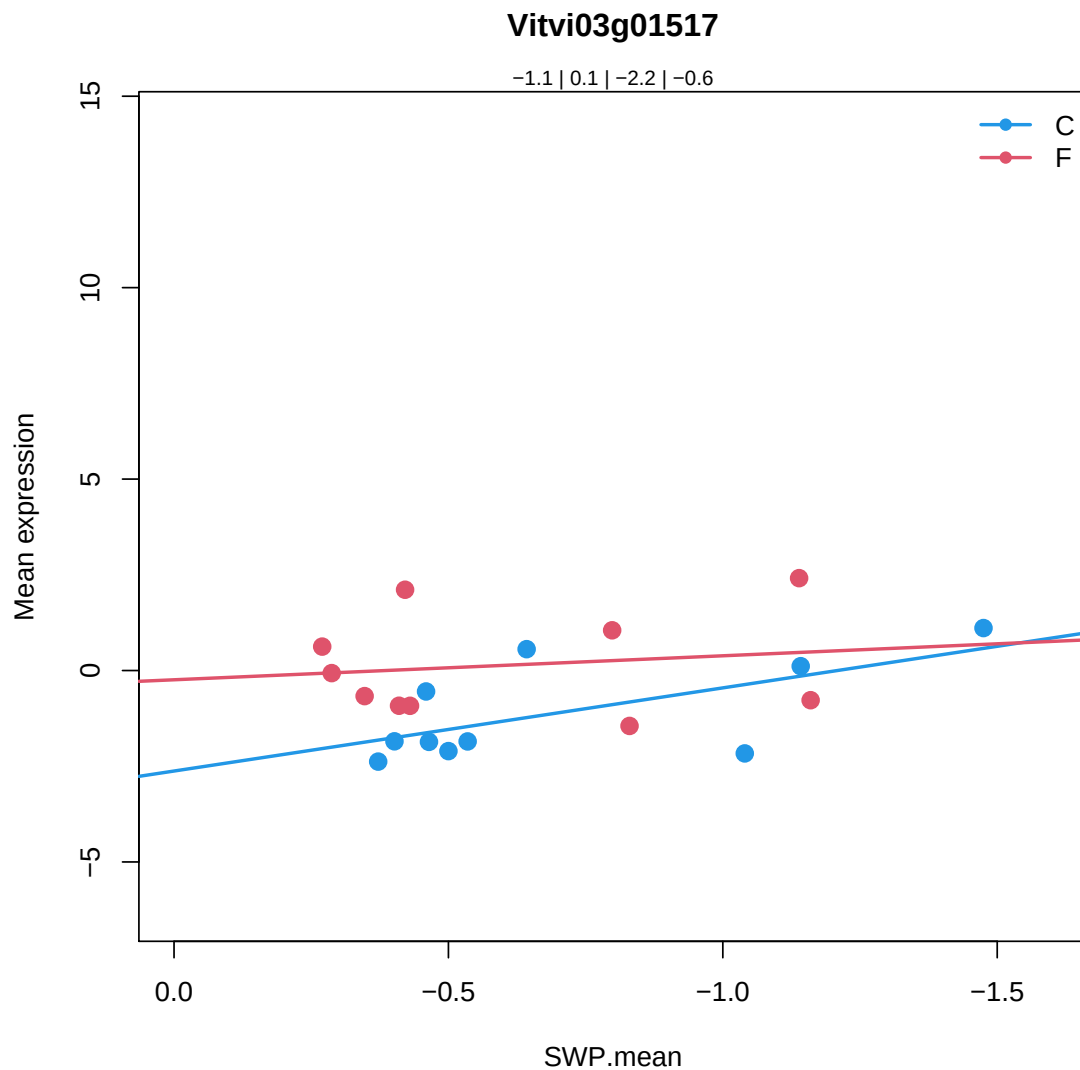
hemoglobin 1 |

Chr2:6982782-6983522 REVERSE LENGTH=160 |

201606

Coefficients for Vitvi03g01517.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.098241	0.004776593	**	0.00509695	**
SlopeC	-2.171324	0.03605059	*	0.455247	
MeanF-MeanC	1.237886	0.02021284	*	0.1273075	
SlopeF-SlopeC	1.54451	0.2969801		0.9999488	



8.1.512 Vitvi05g01350: Type1.0 *

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

Vitvi05g01350

34.3

transport.amino acids

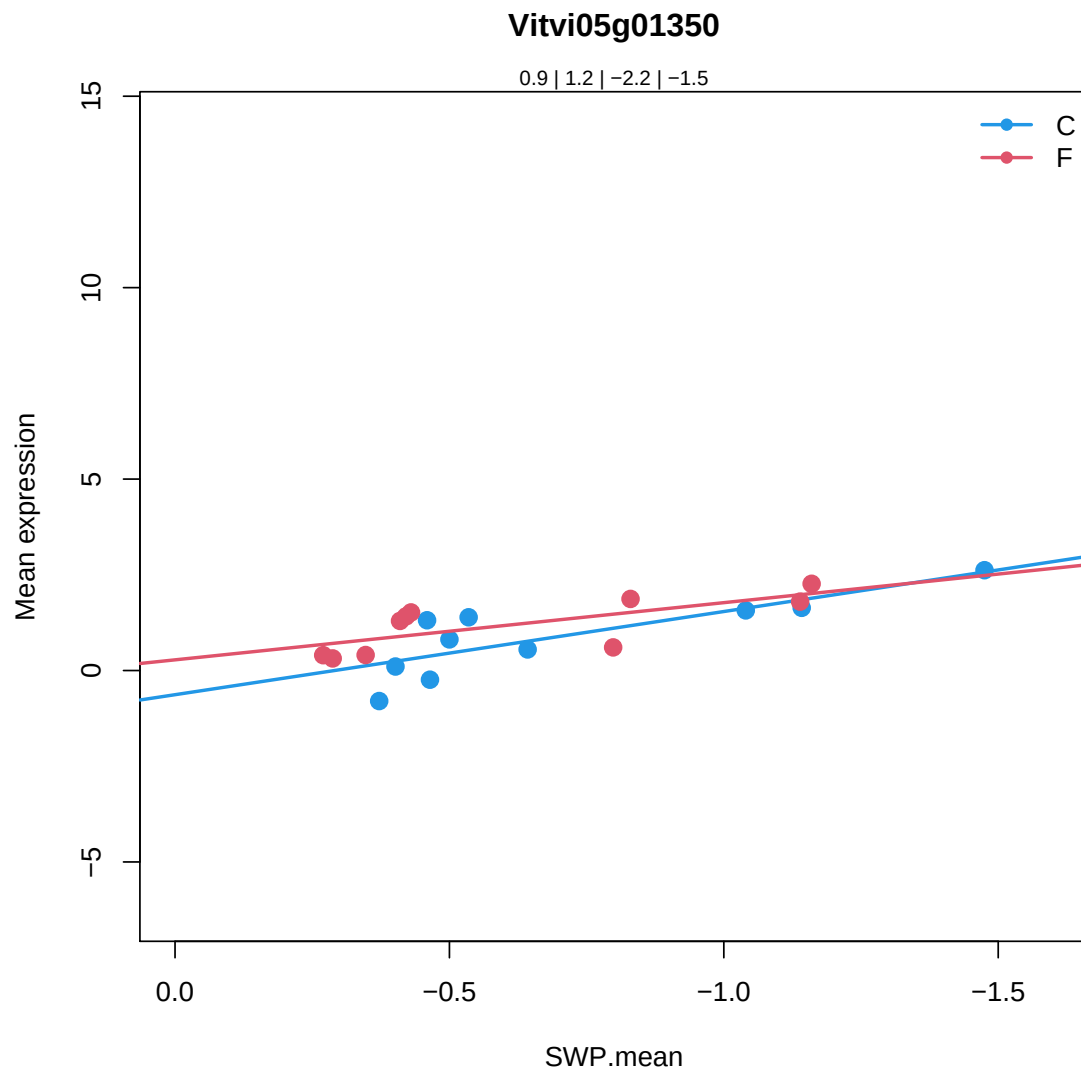
aromatic and neutral transporter 1 |

Chr3:3758523-3760103 FORWARD LENGTH=432 |

201606

Coefficients for Vitvi05g01350.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8959904	4.594444e-05	***	5.107097e-05	***
SlopeC	-2.172338	0.0002207955	***	0.08109226	.
MeanF-MeanC	0.2926224	0.2529561		0.6127712	
SlopeF-SlopeC	0.6785423	0.362533		0.9999488	



8.1.513 Vitvi07g02029: Type1.0 *

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

Vitvi07g02029

26.12

misc.peroxidases

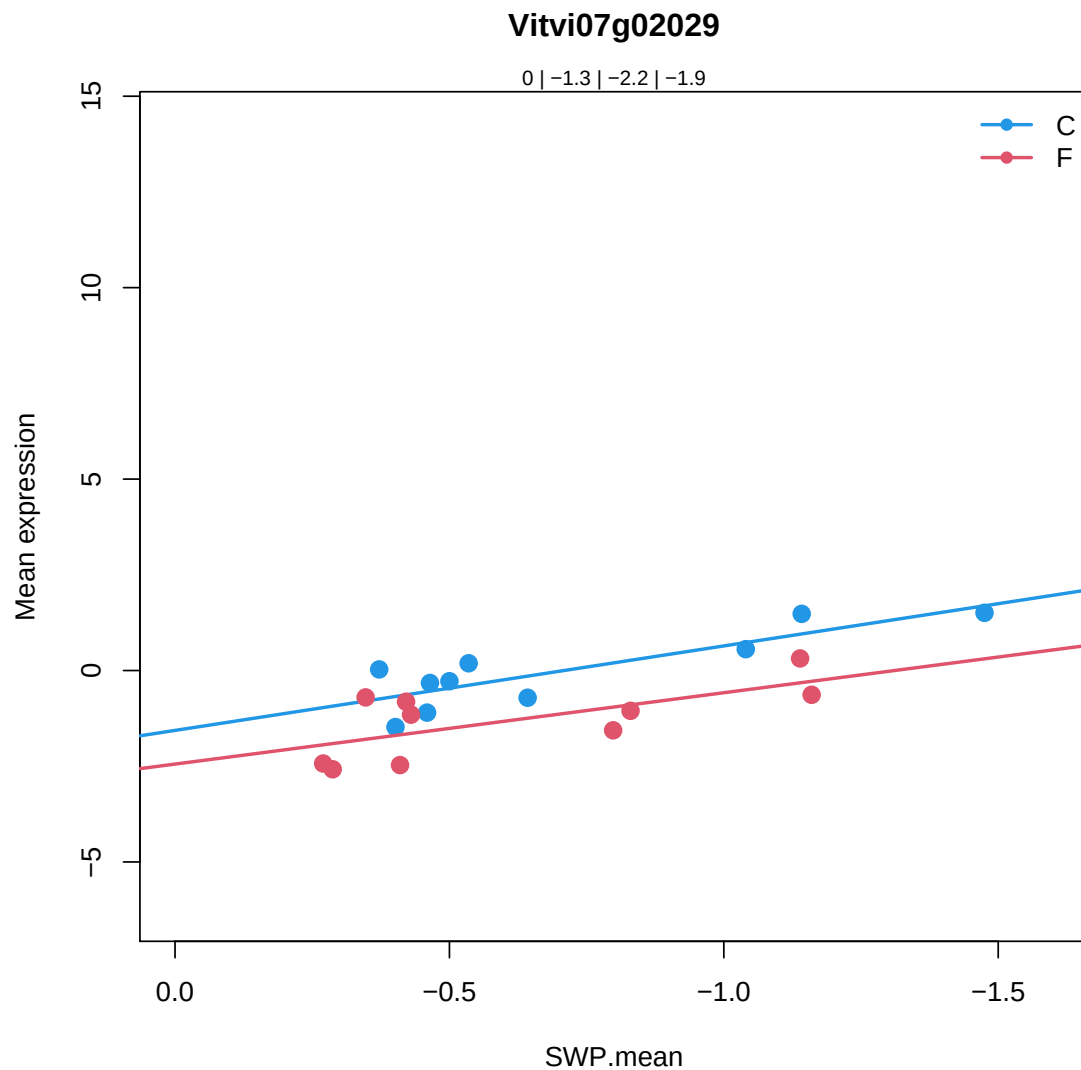
Peroxidase superfamily protein |

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	



8.1.514 Vitvi08g01143: Type1.0

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

Vitvi08g01143

21.2.1

redox.ascorbate and glutathione.ascorbate

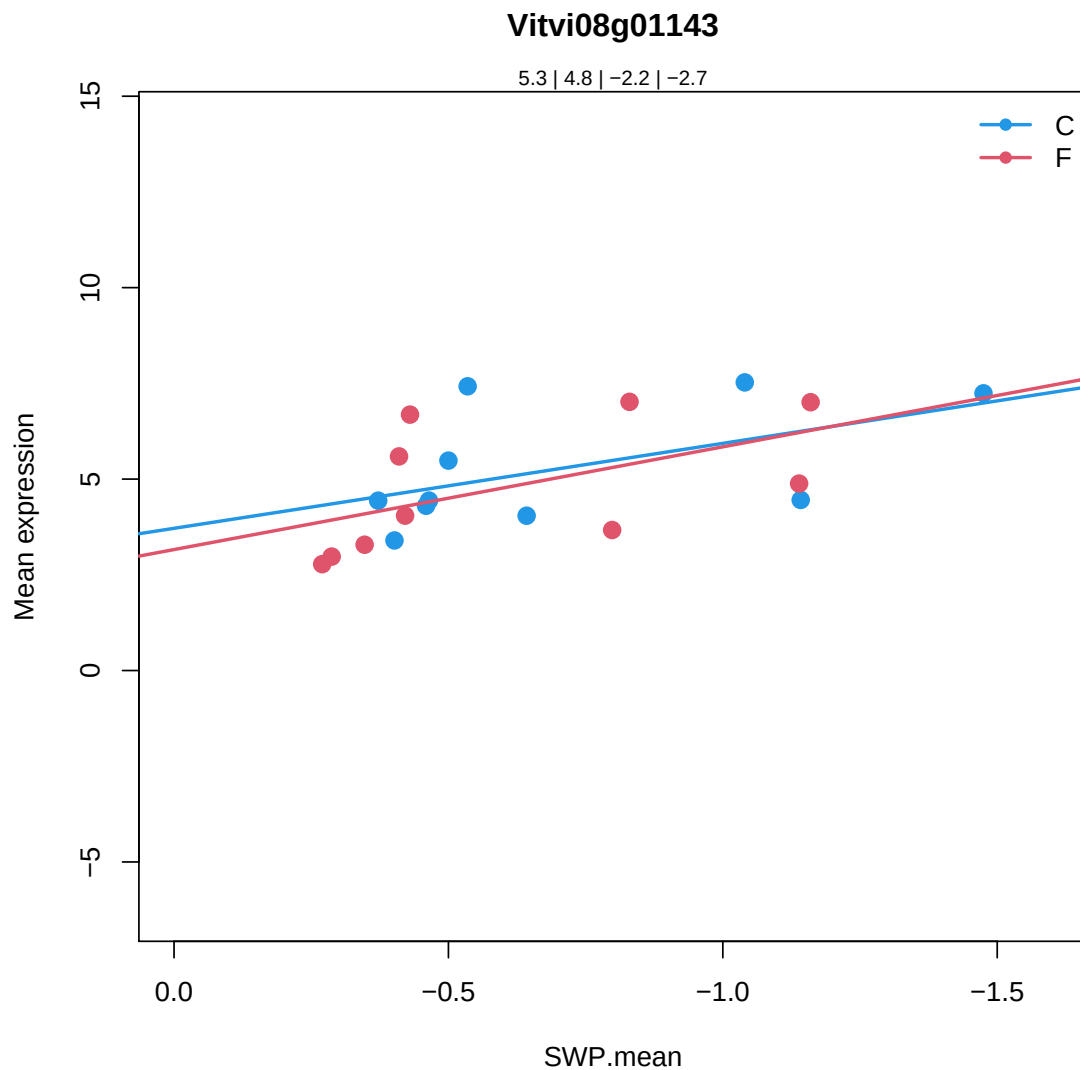
ascorbate peroxidase 2 |

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	



8.1.515 Vitvi06g00292: Type1.0 *

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

Vitvi06g00292

35.2

not assigned.unknown

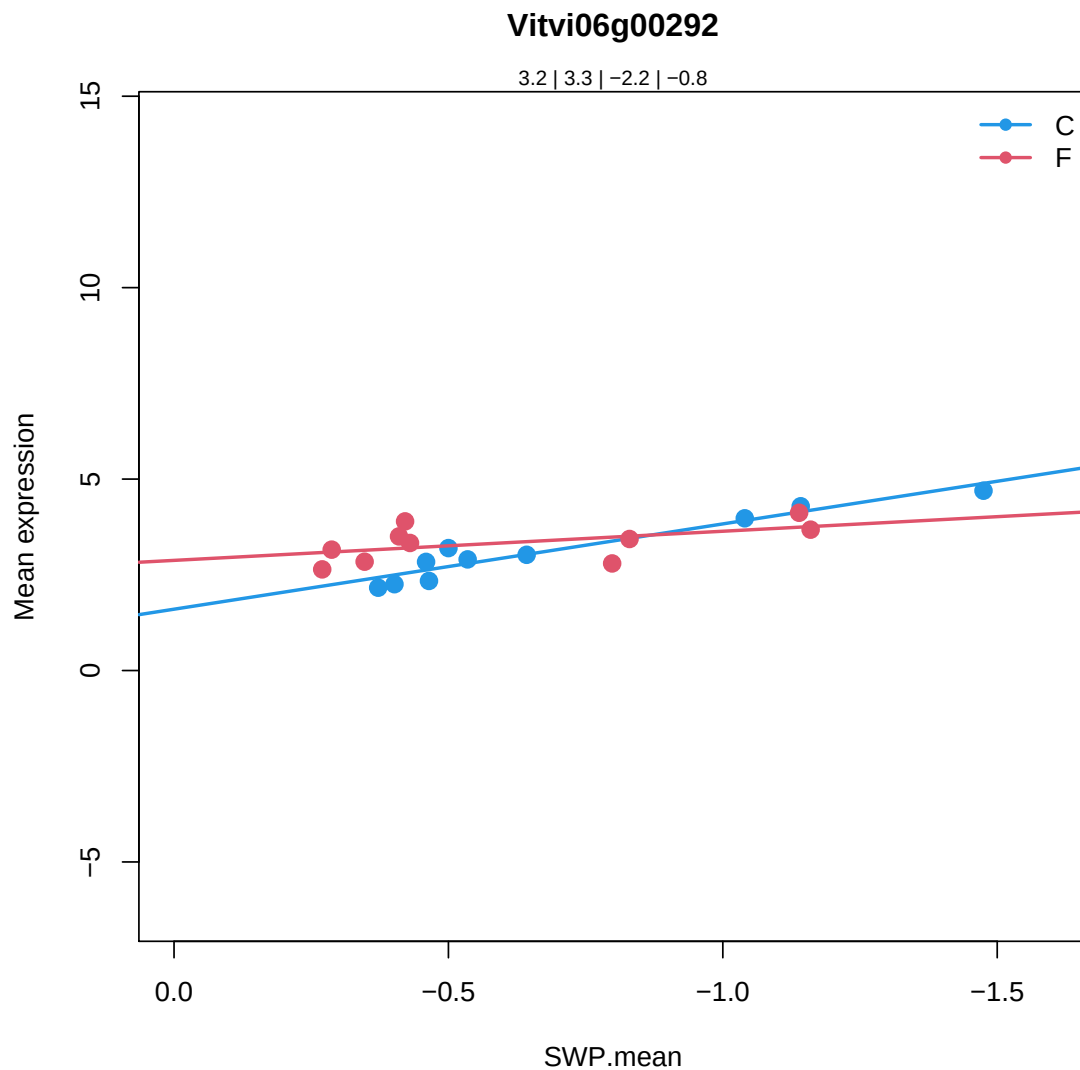
peptide upstream protein |

Chr5:758793-760148 FORWARD LENGTH=451 |

201606

Coefficients for Vitvi06g00292.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.167777	2.045401e-17	***	5.064329e-17	***
SlopeC	-2.227432	2.358344e-06	***	0.01365018	*
MeanF-MeanC	0.1722643	0.3435587		0.7033826	
SlopeF-SlopeC	1.46633	0.01022597	*	0.9999488	



8.1.516 Vitvi15g01058: Type1.0 *

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

Vitvi15g01058

34.99

transport.misc

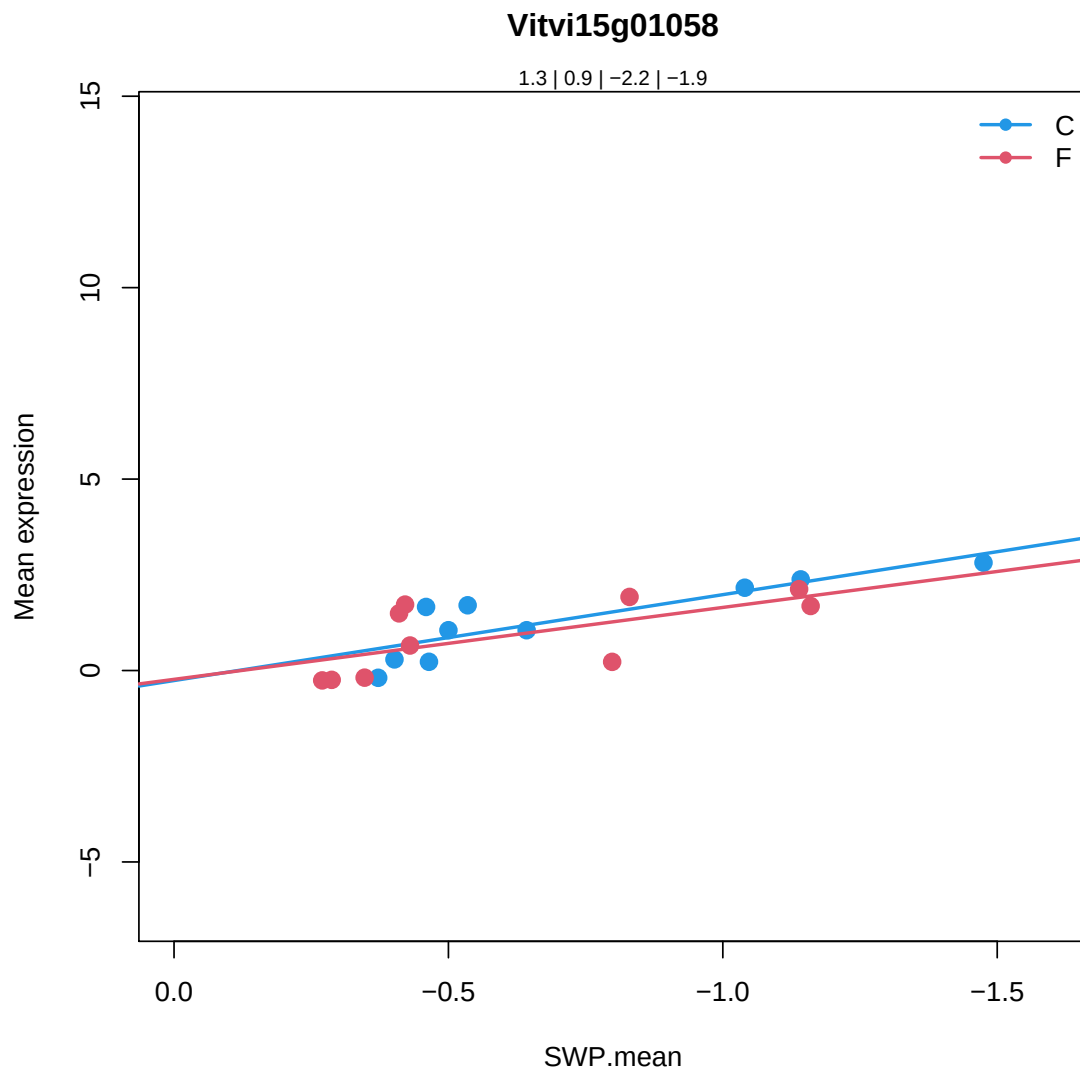
receptor-like protein kinase 4 |

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	



8.1.517 Vitvi14g02430: Type1.0 *

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

Vitvi14g02430

27.3.25

RNA.regulation of transcription.MYB domain transcription factor family

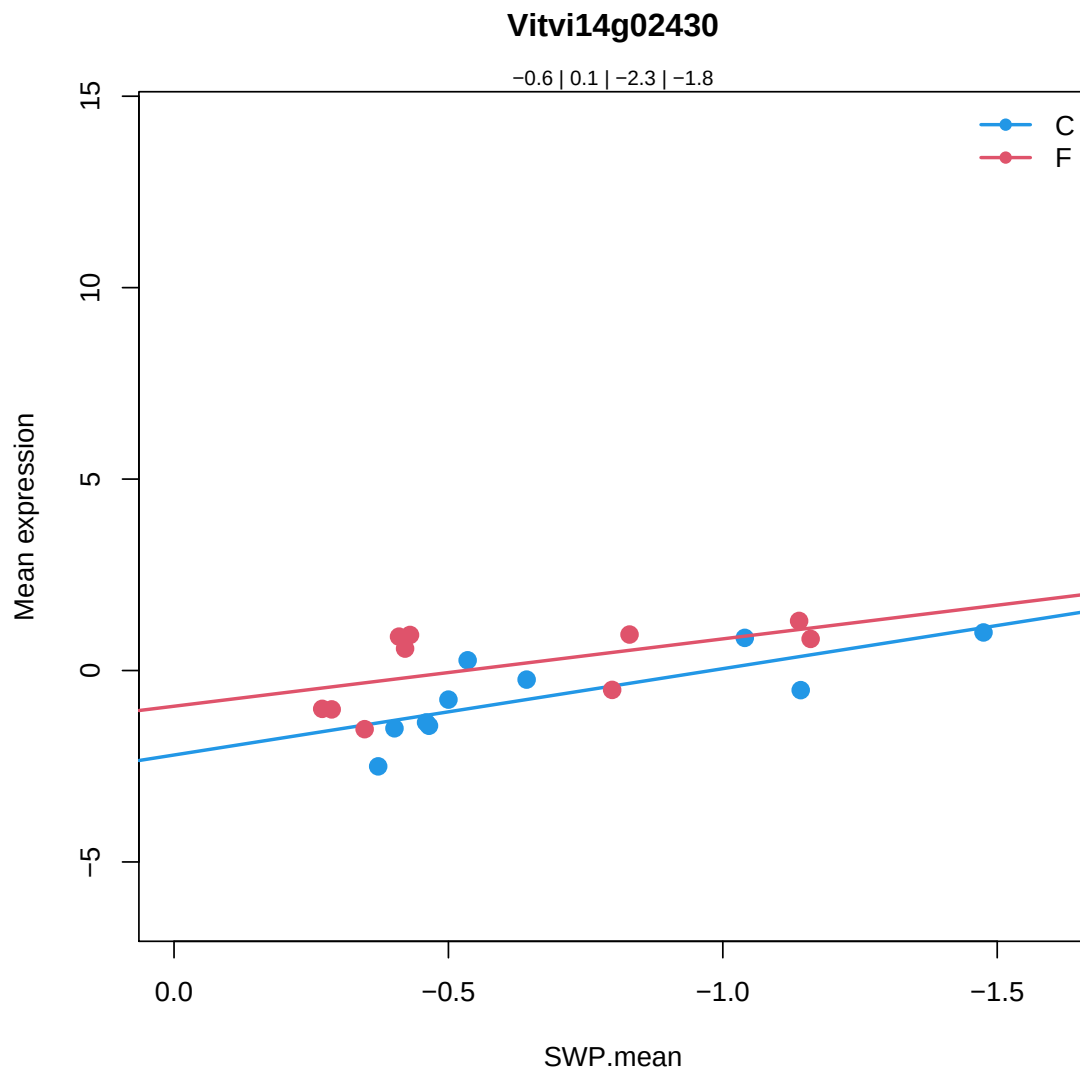
myb domain protein 43 |

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	



8.1.518 Vitvi16g01167: Type1.0 *

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

Vitvi16g01167

30.2.24

signalling.receptor kinases.S-locus glycoprotein like

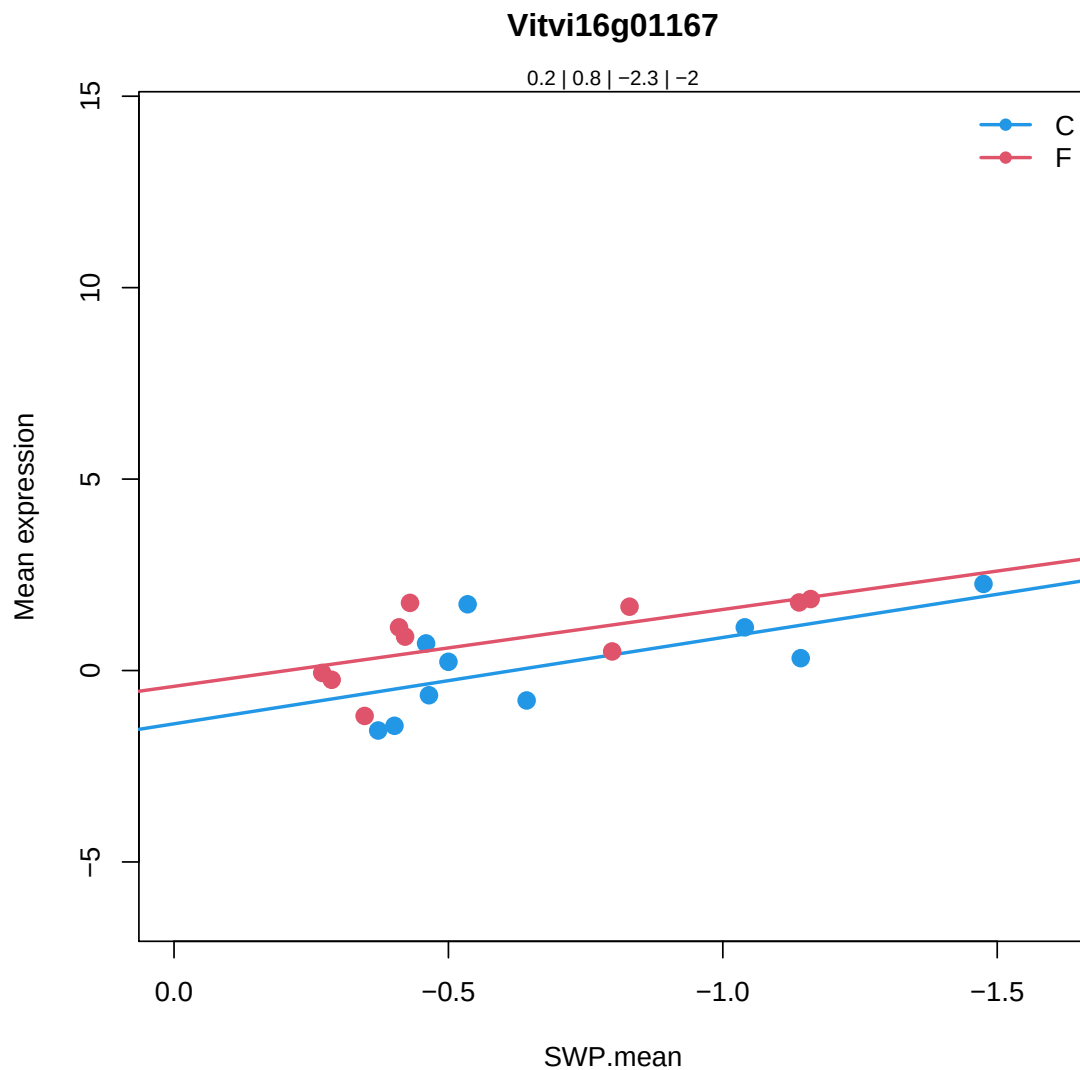
Protein kinase superfamily protein |

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	



8.1.519 Vitvi19g01356: Type1.0 *

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

Vitvi19g01356

17.1.1.1.10

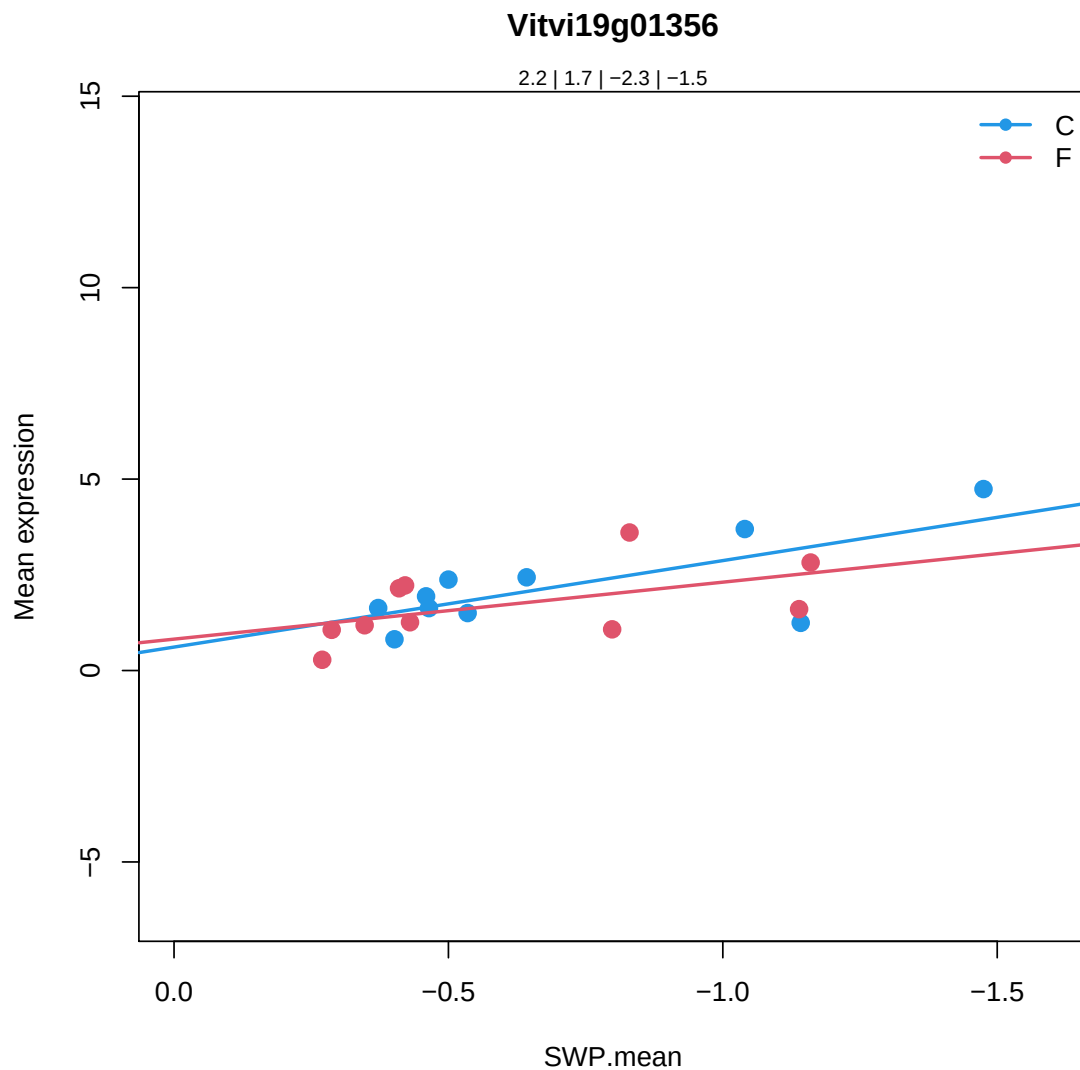
hormone metabolism.abscisic acid.synthesis-degradation.synthesis.9-cis-
nine-cis-epoxycarotenoid dioxygenase 3 |

Chr3:4831678-4833477 REVERSE LENGTH=599 |

201606

Coefficients for Vitvi19g01356.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.200314	1.857715e-08	***	2.249387e-08	***
SlopeC	-2.258629	0.004224881	**	0.2376222	
MeanF-MeanC	-0.474426	0.1999889		0.5427762	
SlopeF-SlopeC	0.7705475	0.4712003		0.9999488	



8.1.520 Vitvi18g01131: Type1.0 *

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

Vitvi18g01131

20.1.7.5

stress.biotic.PR-proteins.PR5 (thaumatin-like proteins)

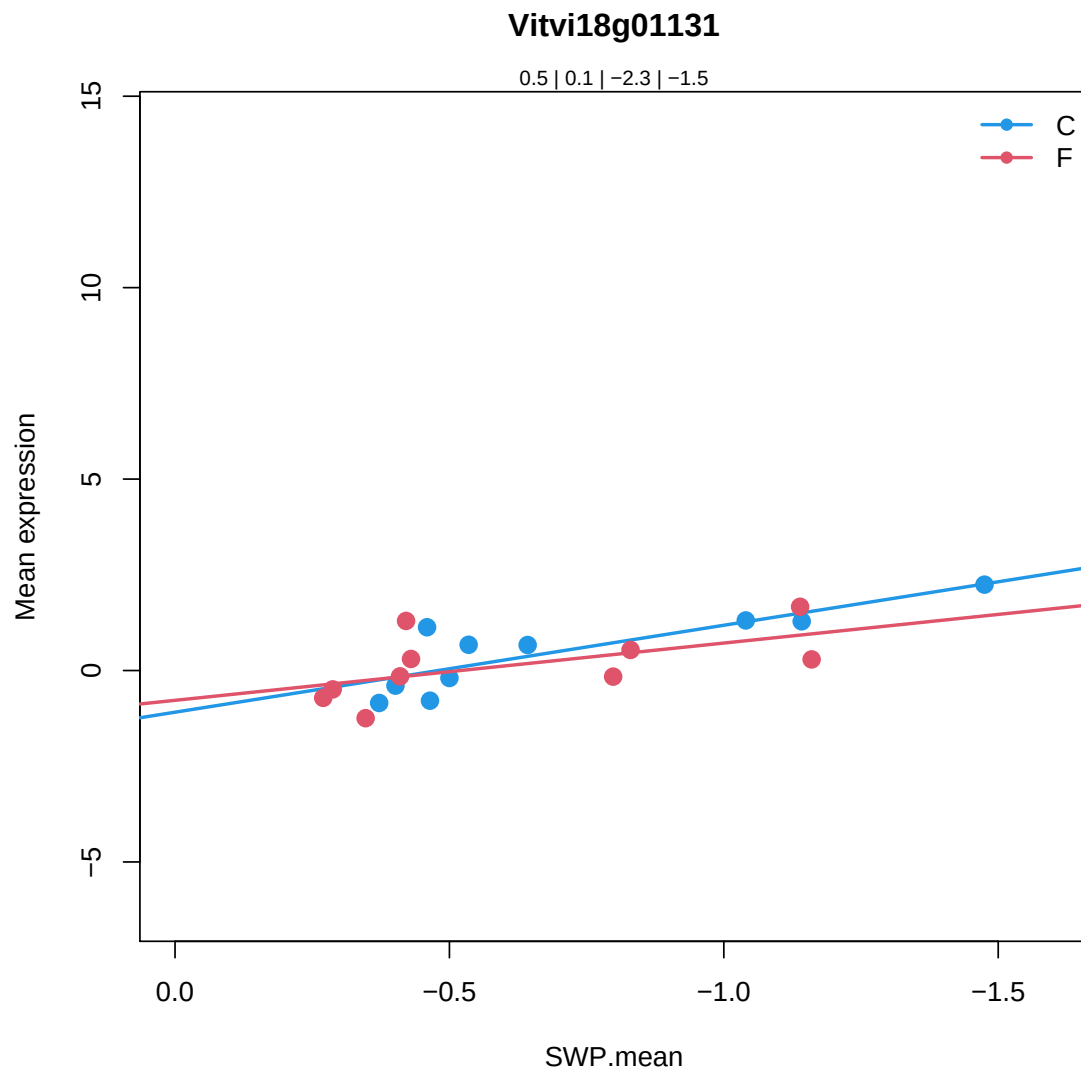
Pathogenesis-related thaumatin superfamily protein |

Chr1:6945725-6947017 FORWARD LENGTH=316 |

201606

Coefficients for Vitvi18g01131.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.5077668	0.02079132	*	0.02185225	*
SlopeC	-2.270921	0.0006108673	***	0.1005065	
MeanF-MeanC	-0.3753939	0.2058622		0.550148	
SlopeF-SlopeC	0.7751361	0.3678058		0.9999488	



8.1.521 Vitvi00g00922: Type1.0 *

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

Vitvi00g00922

31.3.1

cell.cycle.peptidylprolyl isomerase

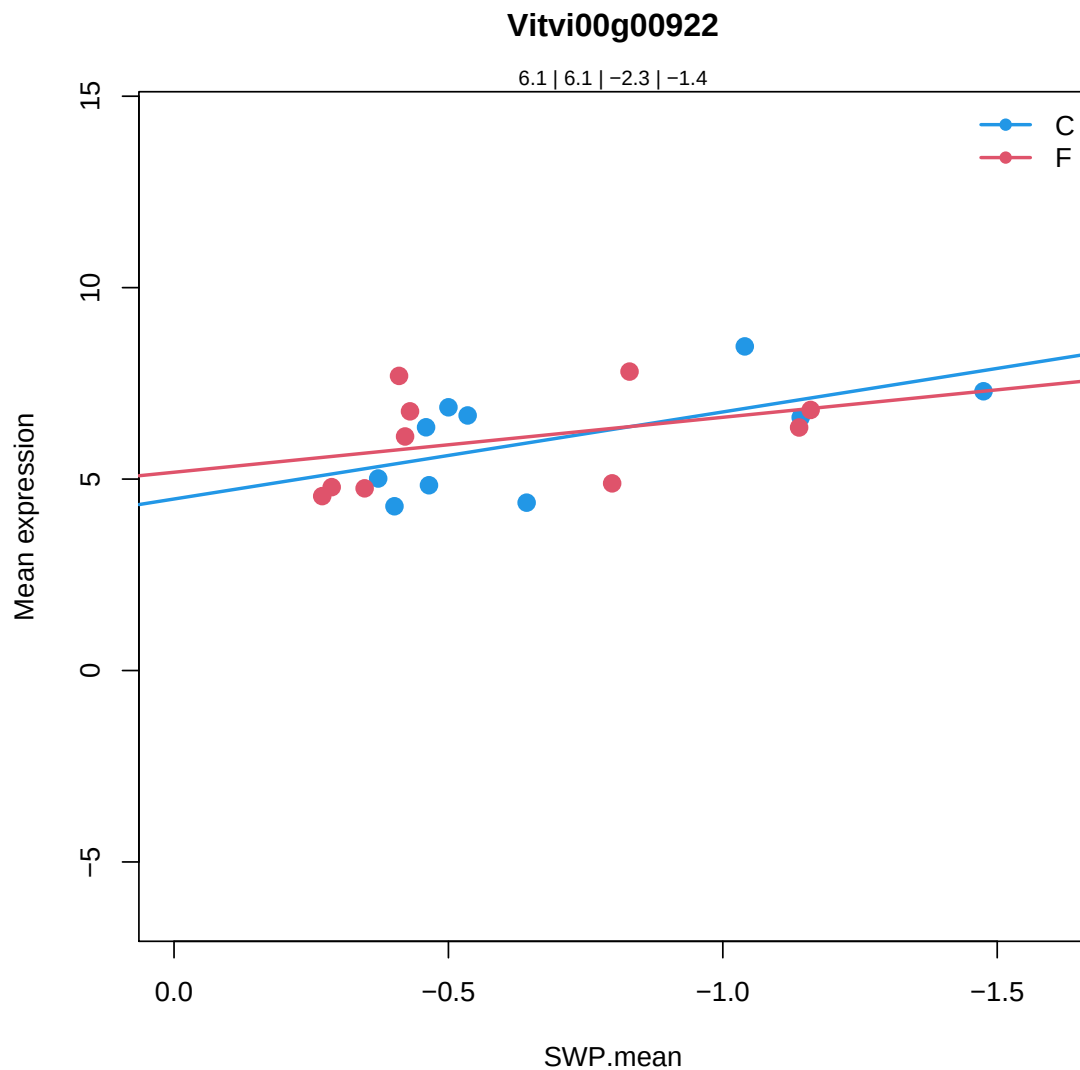
rotamase FKBP 1 |

Chr3:9188257-9191137 FORWARD LENGTH=551 |

201606

Coefficients for Vitvi00g00922.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.078473	1.342143e-14	***	2.215153e-14	***
SlopeC	-2.274125	0.0220105	*	0.3914352	
MeanF-MeanC	-0.02563539	0.956838		0.9900967	
SlopeF-SlopeC	0.8392667	0.5468048		0.9999488	



8.1.522 Vitvi07g01325: Type1.0 *

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

Vitvi07g01325

27.3.20

RNA.regulation of transcription.G2-like transcription factor family (G

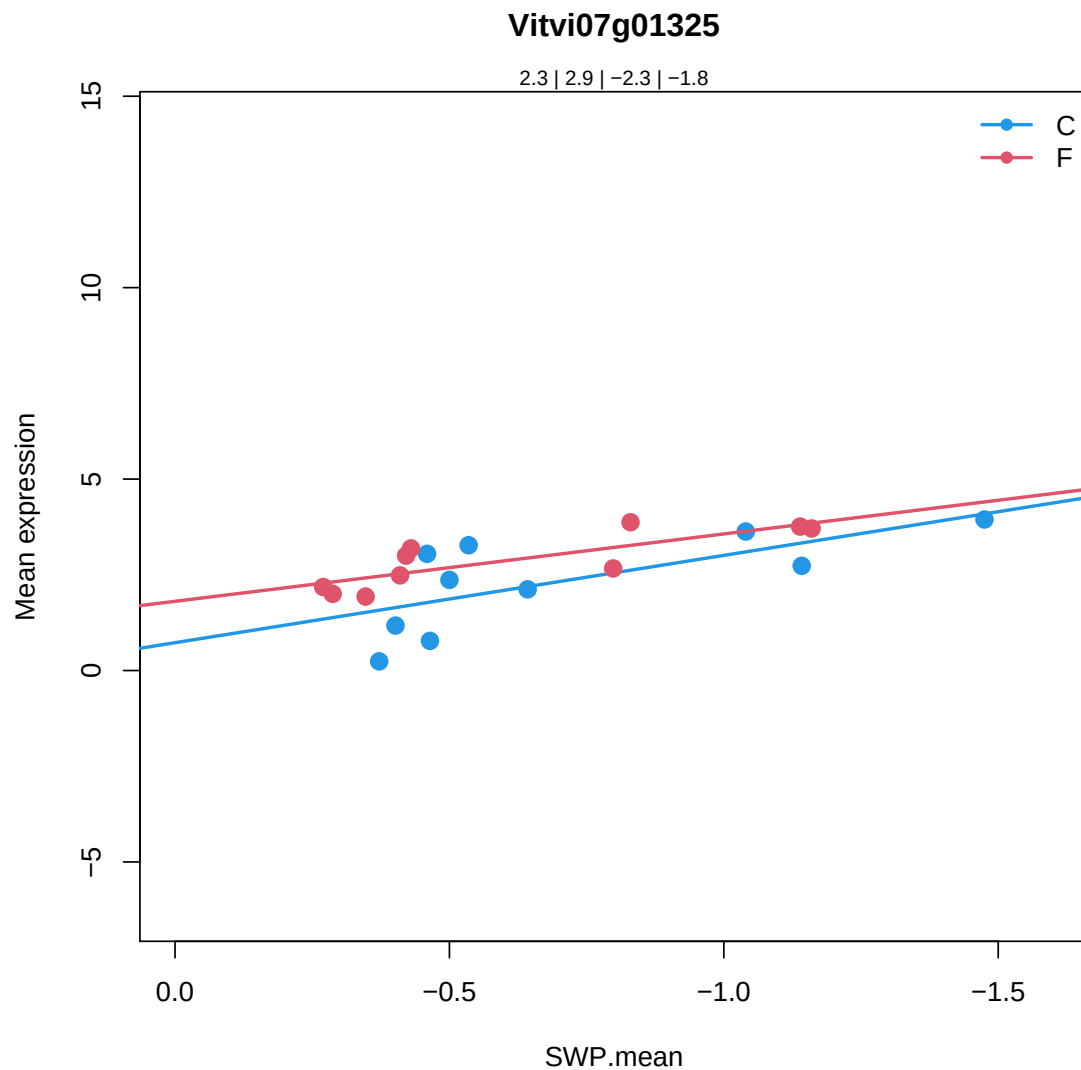
Homeodomain-like superfamily protein |

Chr1:18342725-18344101 FORWARD LENGTH=333 |

201606

Coefficients for Vitvi07g01325.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.330298	5.001066e-10	***	6.373432e-10	***
SlopeC	-2.2804	0.001151921	**	0.1350583	
MeanF-MeanC	0.5493694	0.08987748	.	0.3425335	
SlopeF-SlopeC	0.5207088	0.5712735		0.9999488	



8.1.523 Vitvi17g00609: Type1.0 *

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

Vitvi17g00609

26.28

misc.GDSL-motif lipase

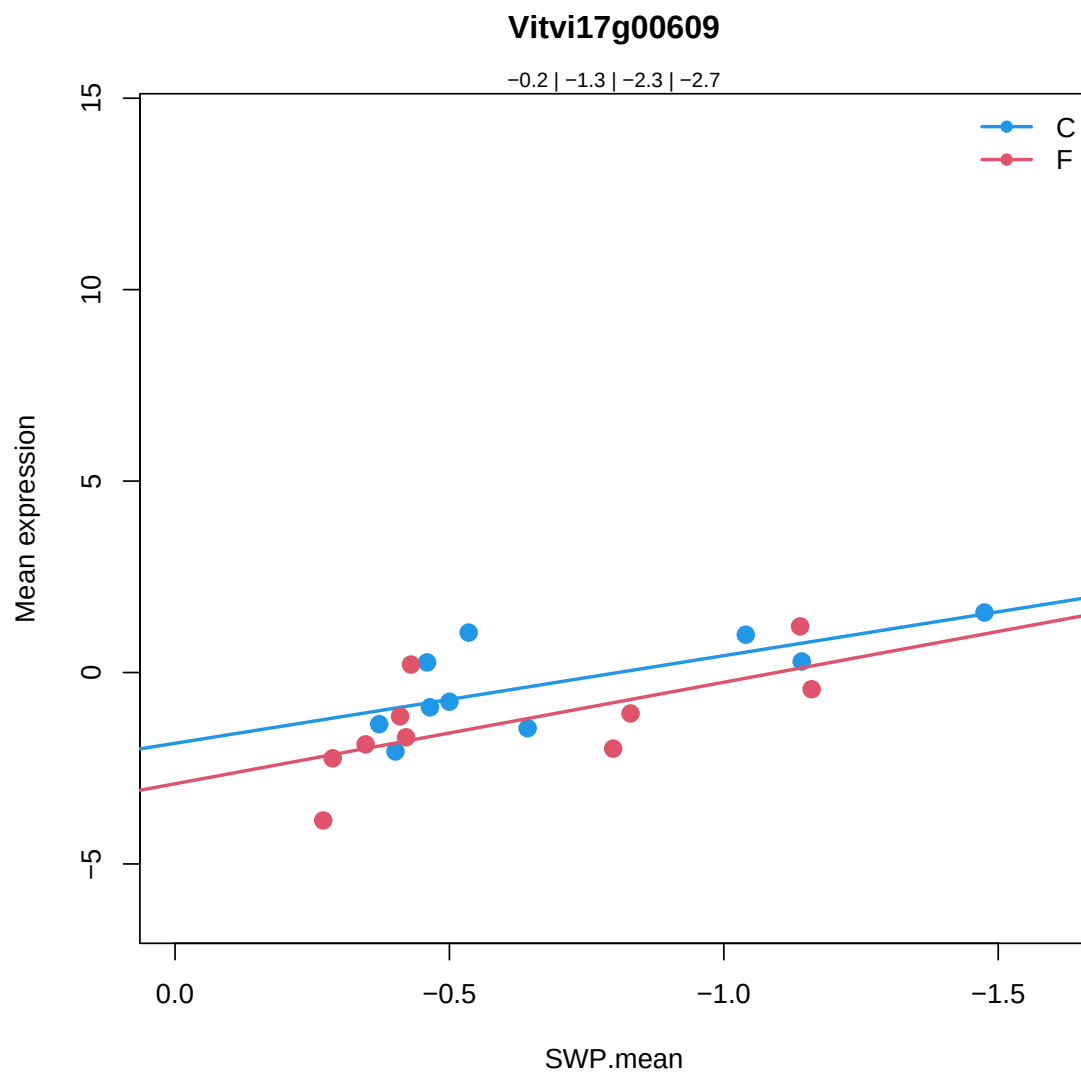
GDSL-like Lipase/Acylhydrolase superfamily protein |

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	



8.1.524 Vitvi01g01038: Type1.0 *

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

Vitvi01g01038

27.3.27

RNA.regulation of transcription.NAC domain transcription factor family

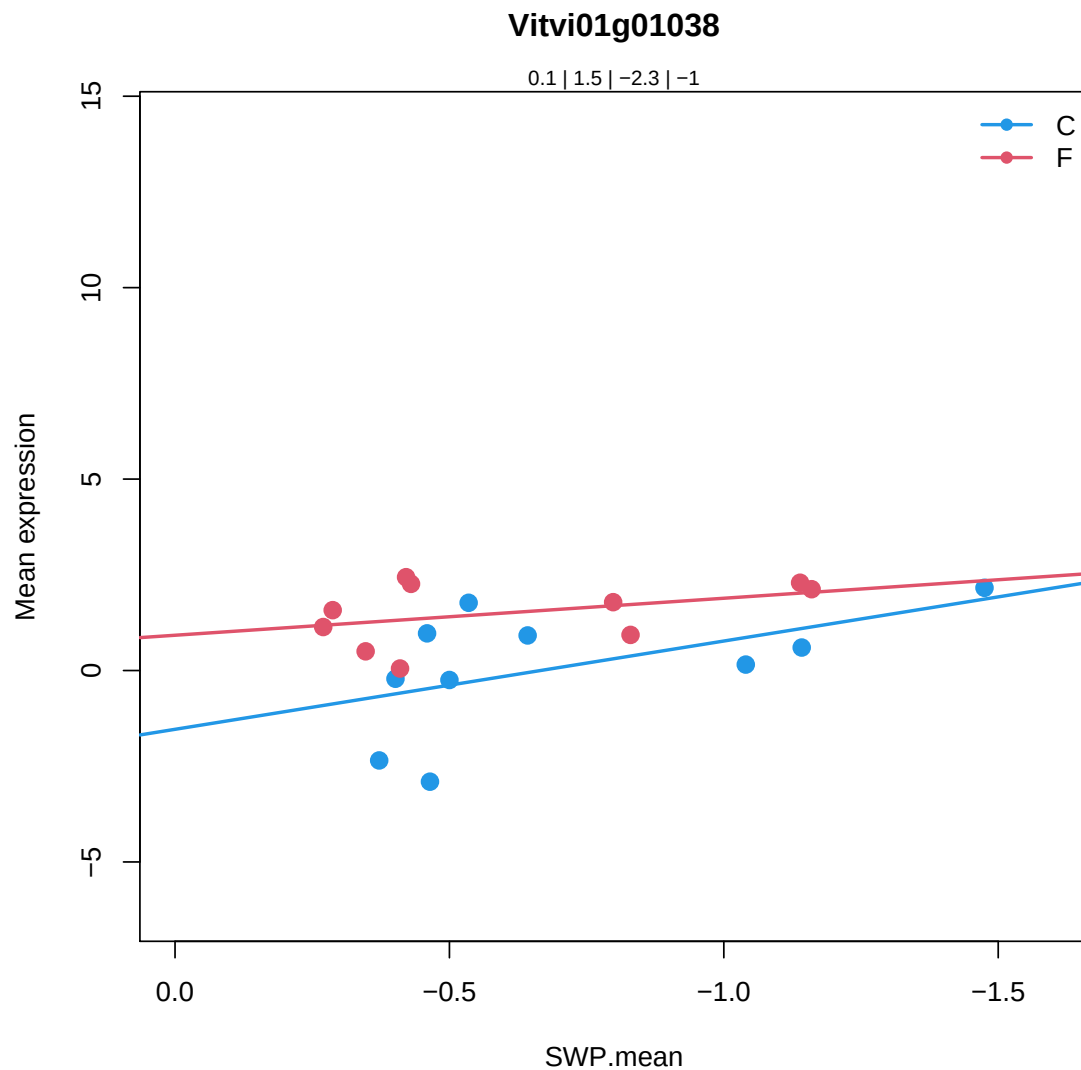
NAC-like%2C activated by AP3/PI |

Chr1:26122233-26123222 FORWARD LENGTH=268 |

201606

Coefficients for Vitvi01g01038.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.08551086	0.7986369		0.8025861	
SlopeC	-2.305732	0.02043799	*	0.3769674	
MeanF-MeanC	1.424204	0.00609815	**	0.05275142	.
SlopeF-SlopeC	1.33945	0.3394109		0.9999488	



8.1.525 Vitvi15g00763: Type1.0 *

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

Vitvi15g00763

29.5.1

protein.degradation.subtilases

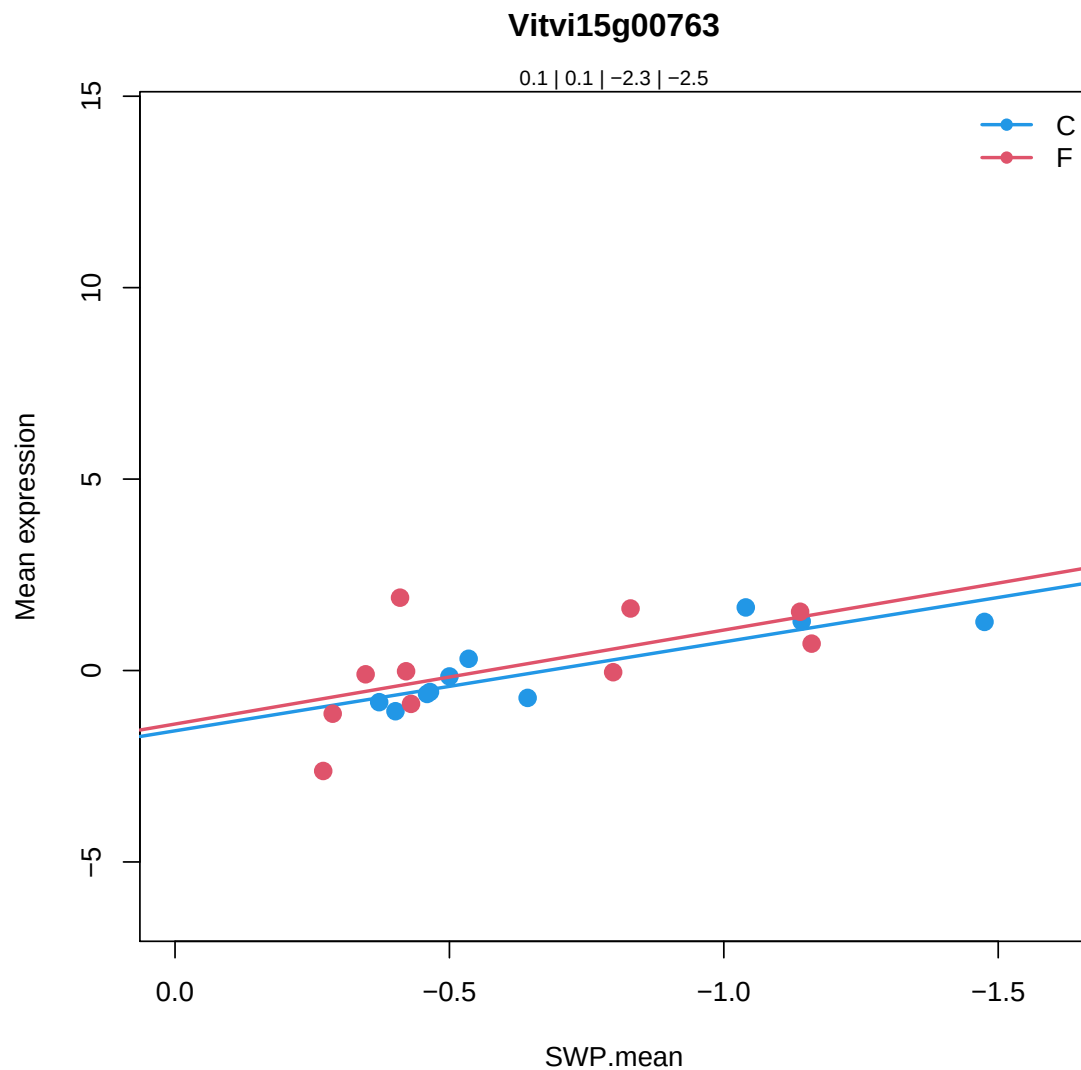
subtilase family protein |

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	



8.1.526 Vitvi08g01112: Type1.0 *

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

Vitvi08g01112

34.16

transport.ABC transporters and multidrug resistance systems

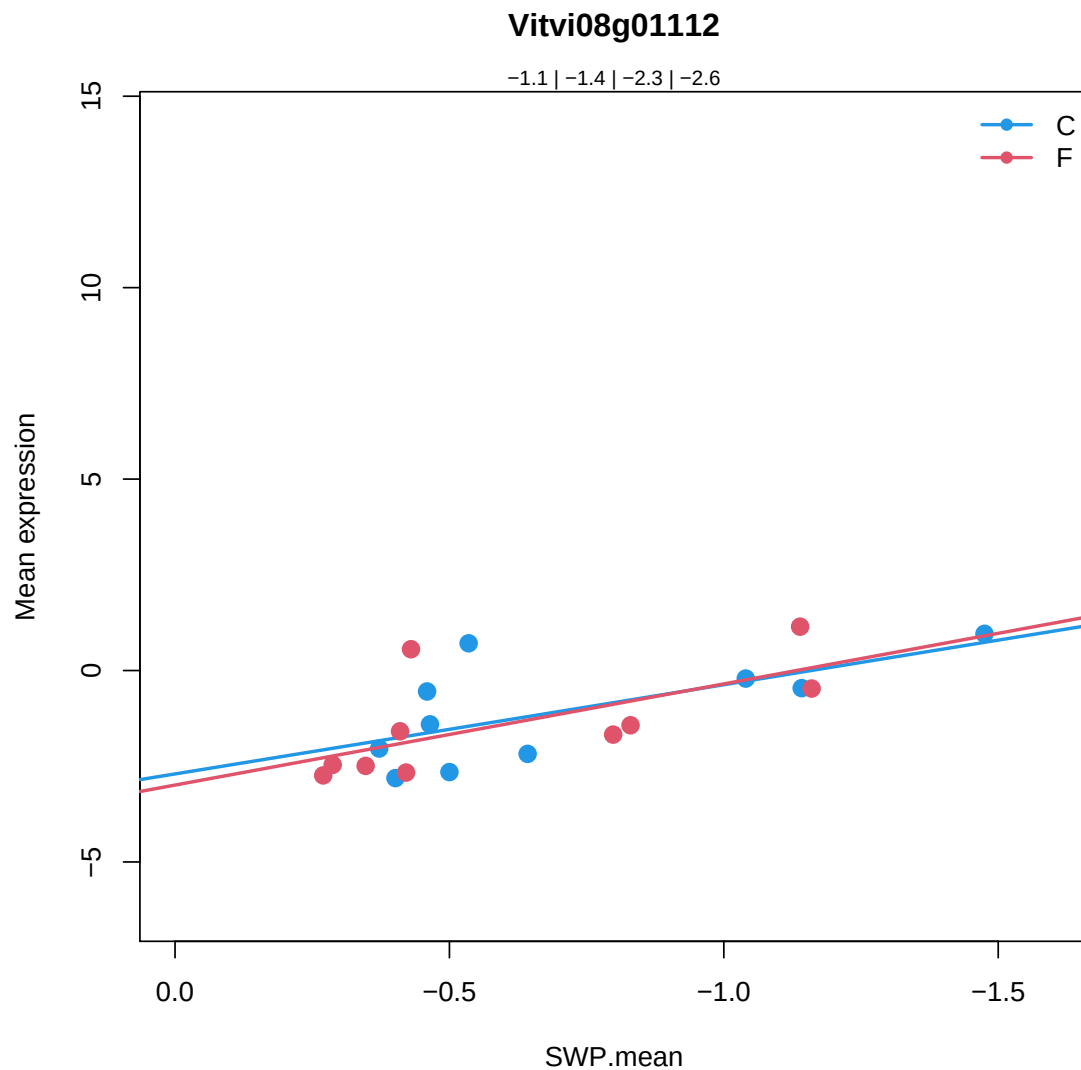
ABC-2 type transporter family protein |

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	



8.1.527 Vitvi18g01966: Type1.0 *

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

Vitvi18g01966

35.1

not assigned.no ontology

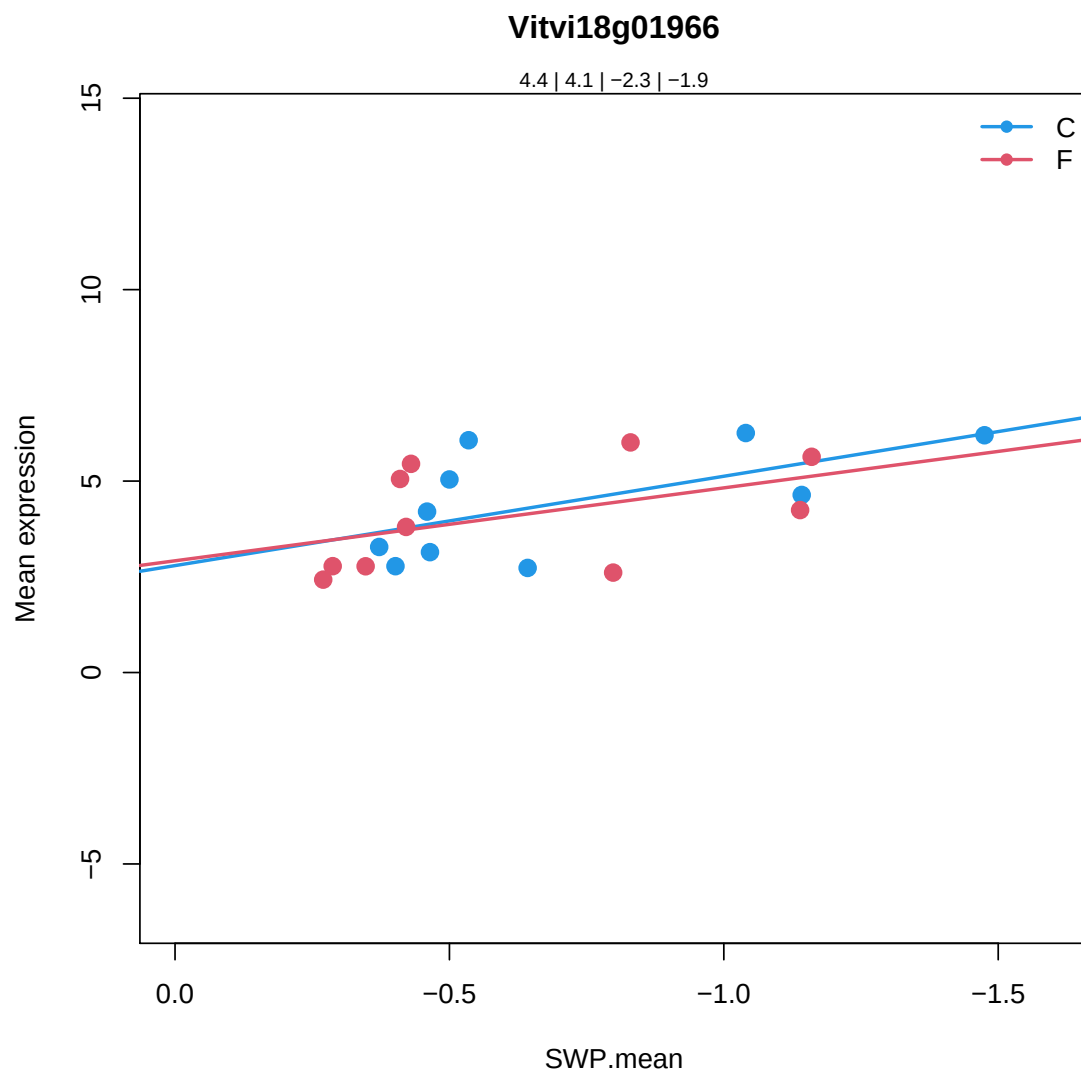
T-complex protein 11 |

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	



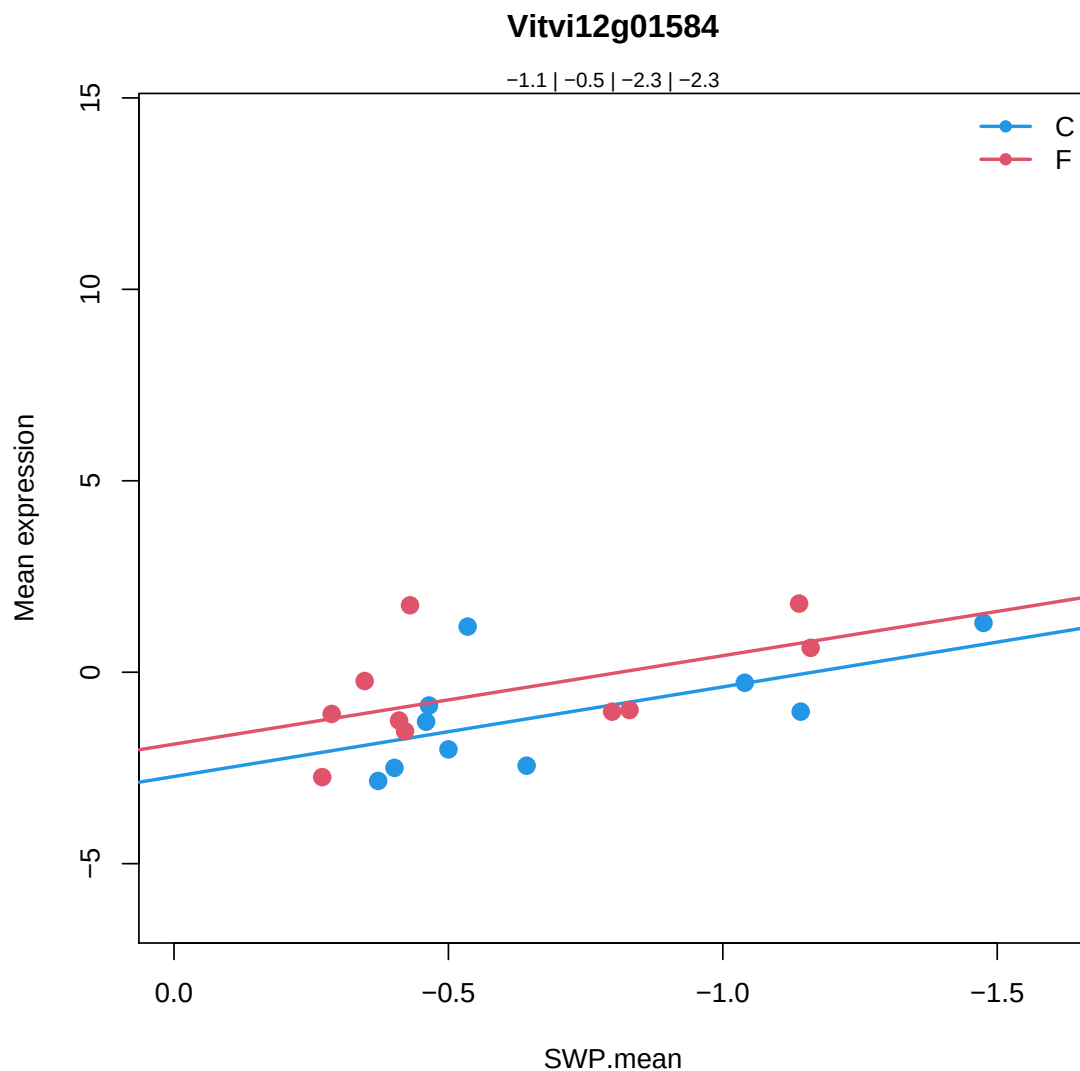
8.1.528 Vitvi12g01584: Type1.0 *

```
> 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	



8.1.529 Vitvi03g00717: Type1.0

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

Vitvi03g00717

29.5.7

protein.degradation.metalloprotease

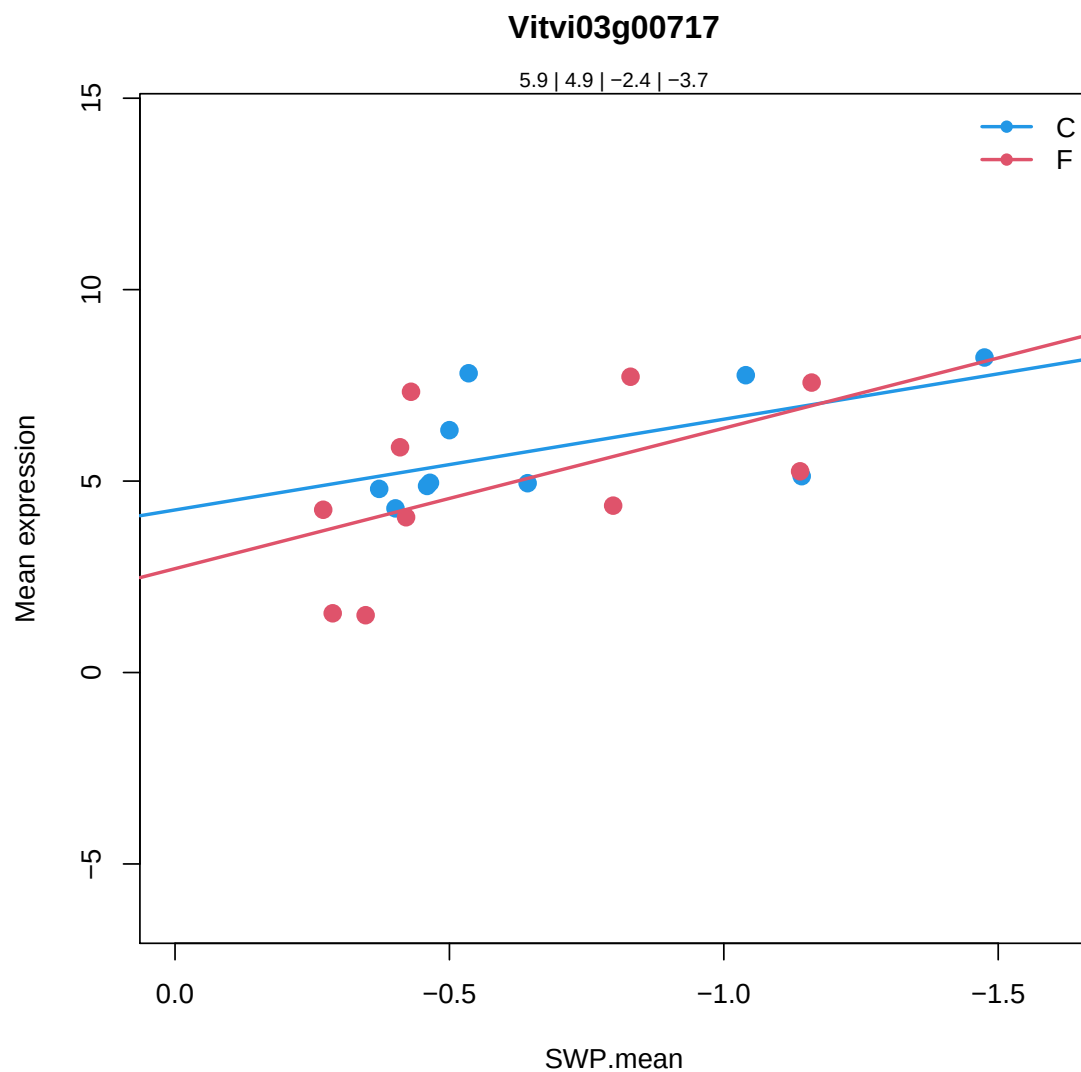
ethylene-dependent gravitropism-deficient and yellow-green-like 3 |

Chr1:6150036-6152185 REVERSE LENGTH=573 |

201606

Coefficients for Vitvi03g00717.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.912186	1.778151e-11	***	2.401221e-11	***
SlopeC	-2.370121	0.08018507	.	0.5749981	
MeanF-MeanC	-0.964544	0.156		0.4765989	
SlopeF-SlopeC	-1.298612	0.5062236		0.9999488	



8.1.530 Vitvi10g00496: Type1.0 *

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

Vitvi10g00496

20.2.1

stress.abiotic.heat

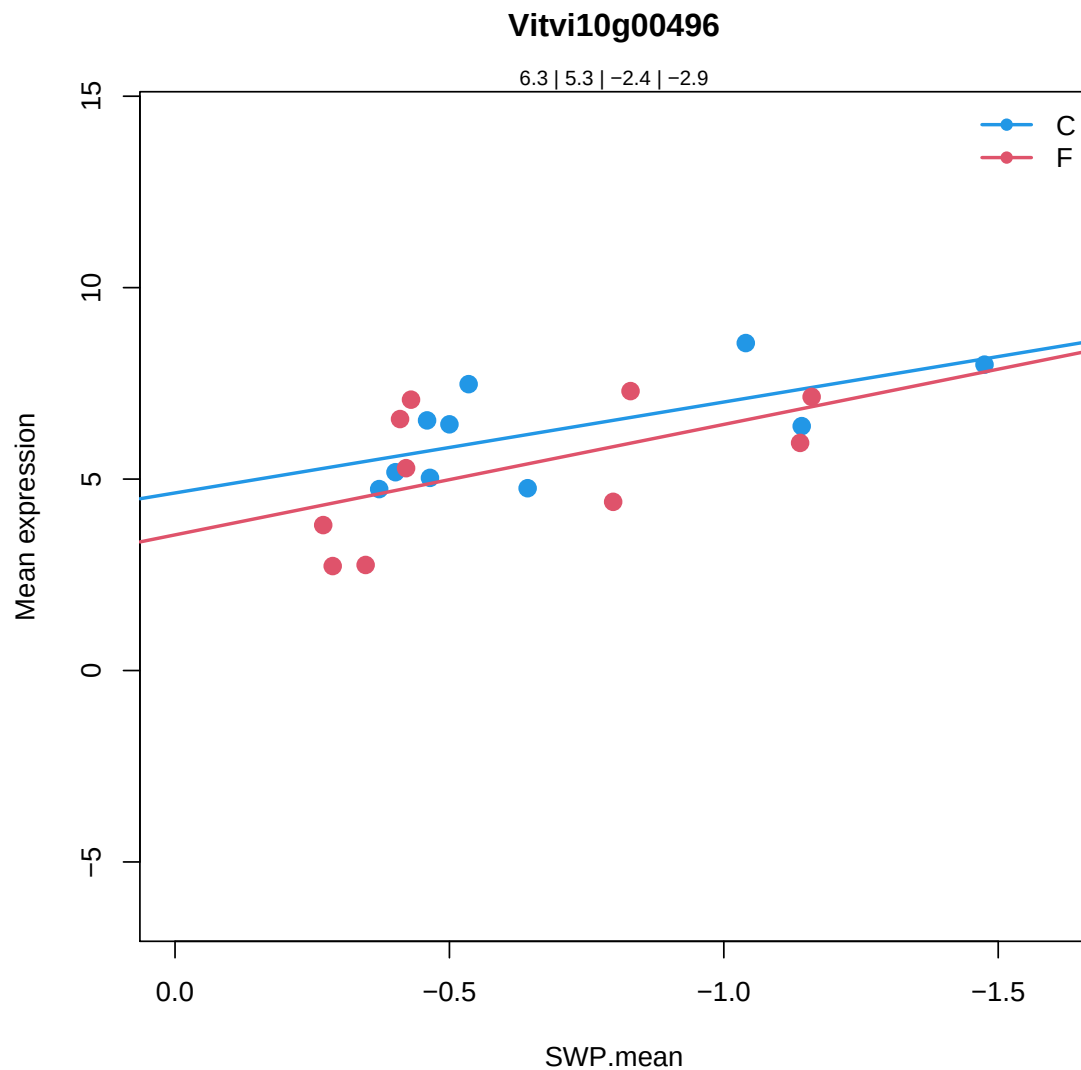
DNAJ heat shock family protein |

Chr2:8848353-8849815 REVERSE LENGTH=337 |

201606

Coefficients for Vitvi10g00496.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.307557	1.015293e-13	***	1.558732e-13	***
SlopeC	-2.37507	0.03527843	*	0.449641	
MeanF-MeanC	-1.007003	0.07458251	.	0.3074175	
SlopeF-SlopeC	-0.5100529	0.7489109		0.9999488	



8.1.531 Vitvi05g00218: Type1.0 *

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

Vitvi05g00218

34.9

transport.metabolite transporters at the mitochondrial membrane

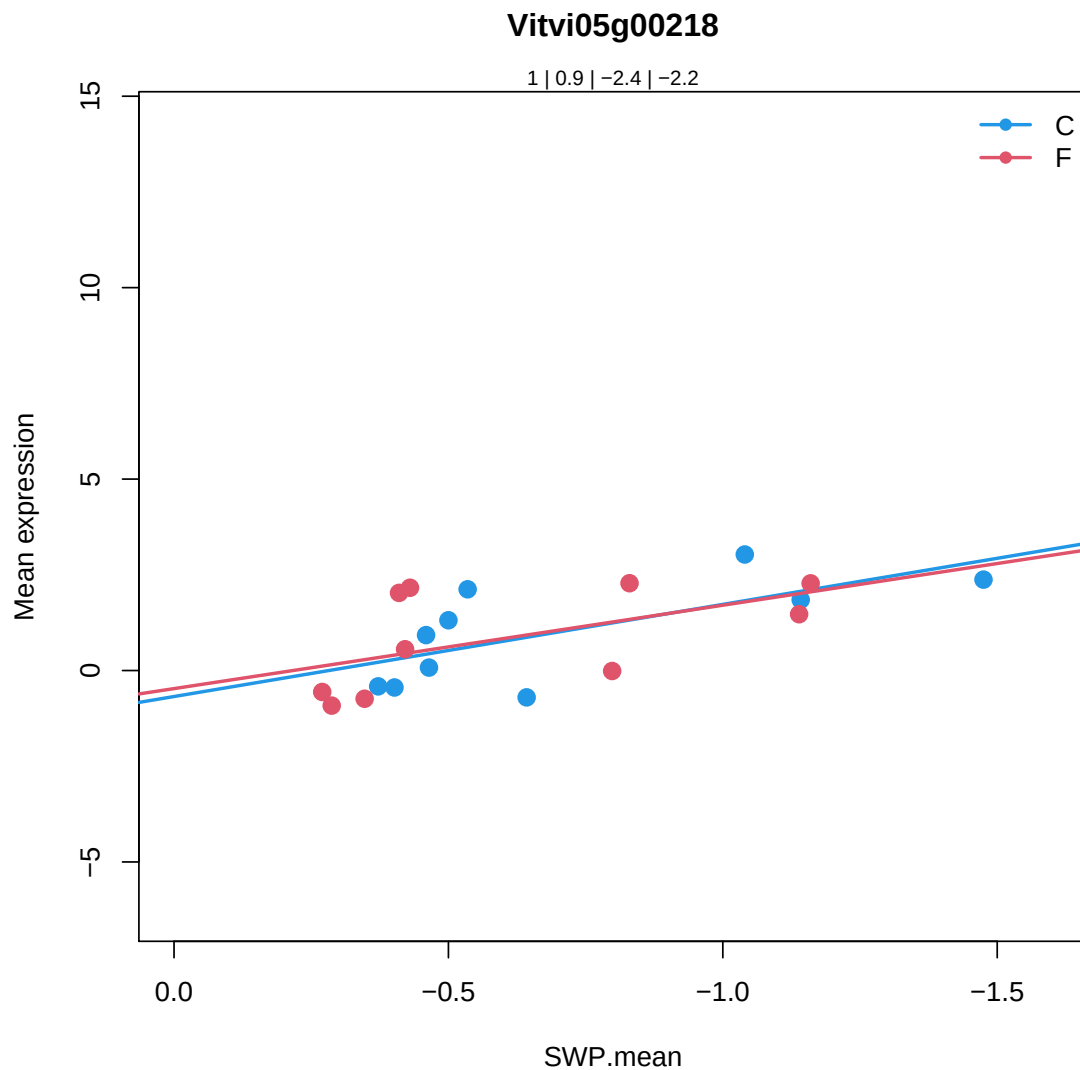
Mitochondrial substrate carrier family protein |

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	



8.1.532 Vitvi06g00443: Type1.0 *

```
> 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

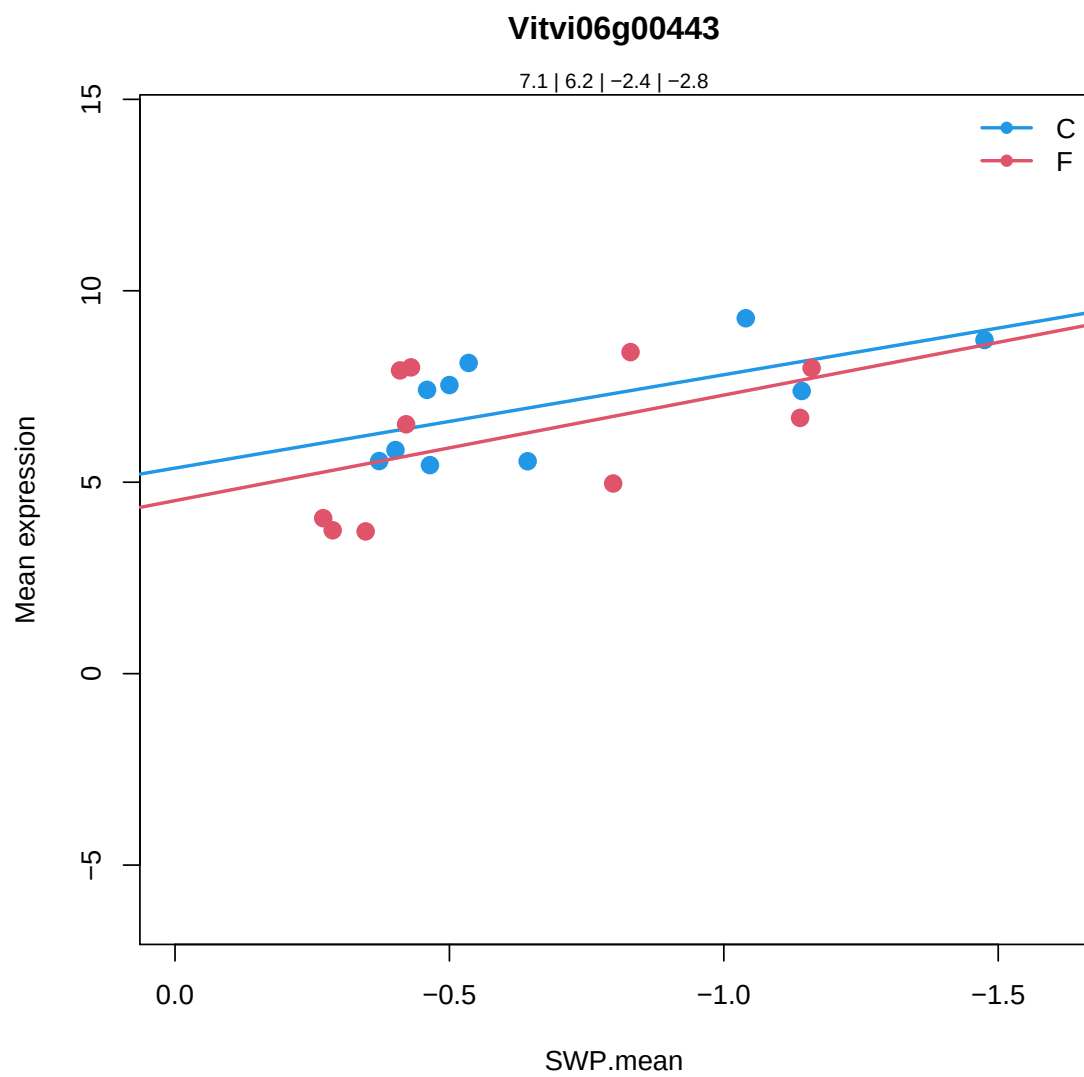
heat shock cognate protein 70-1 |

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	



8.1.533 Vitvi11g00513: Type1.0 *

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

Vitvi11g00513

3.1.2.2

minor CHO metabolism.raffinose family.raffinose synthases.putative

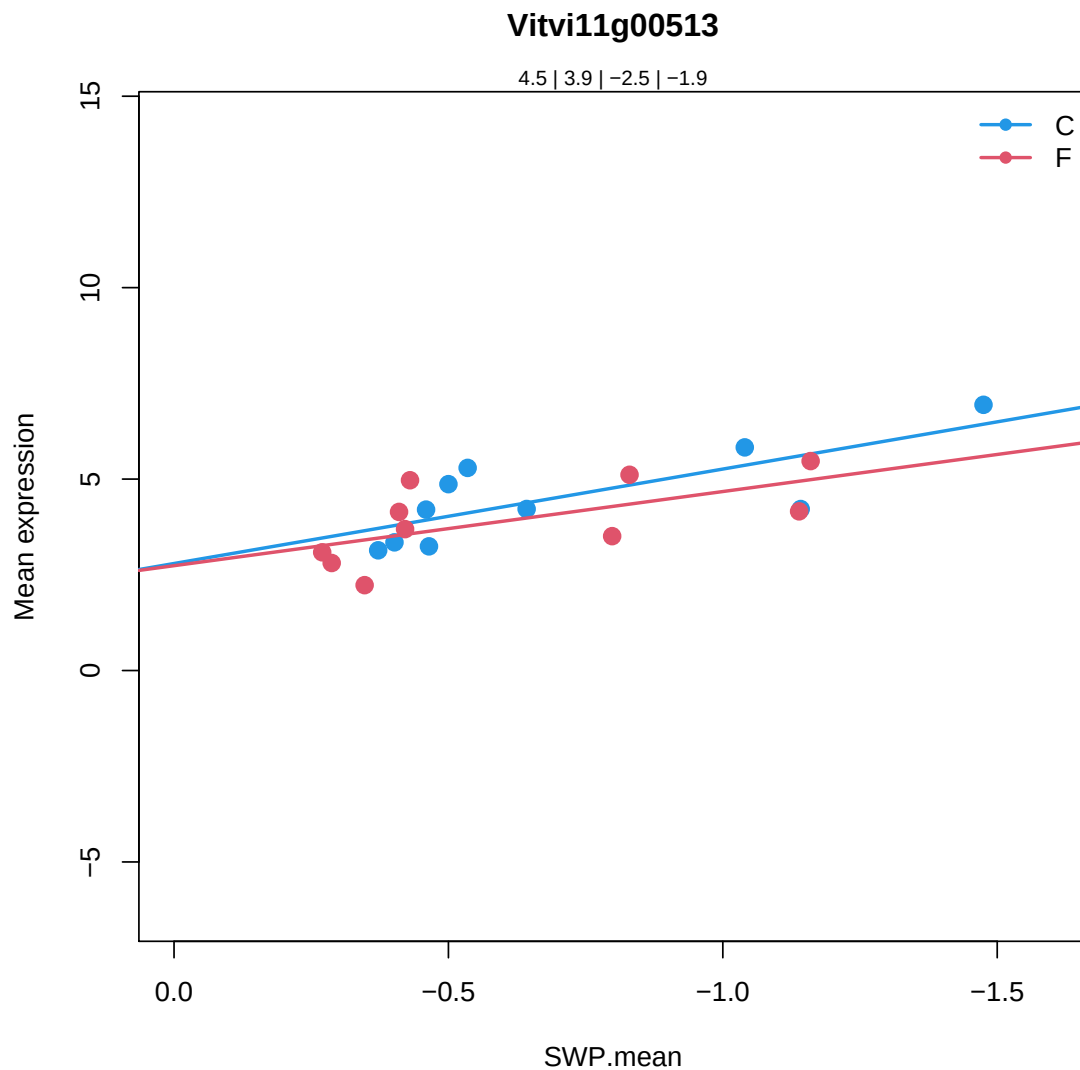
Raffinose synthase family protein |

Chr5:6833730-6836635 FORWARD LENGTH=844 |

201606

Coefficients for Vitvi11g00513.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.529491	1.273499e-14	***	2.106421e-14	***
SlopeC	-2.466365	0.001629253	**	0.1556102	
MeanF-MeanC	-0.6117002	0.09301346	.	0.3495771	
SlopeF-SlopeC	0.5296637	0.6084689		0.9999488	



8.1.534 Vitvi06g00440: Type1.0 *

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

Vitvi06g00440

35.2

not assigned.unknown

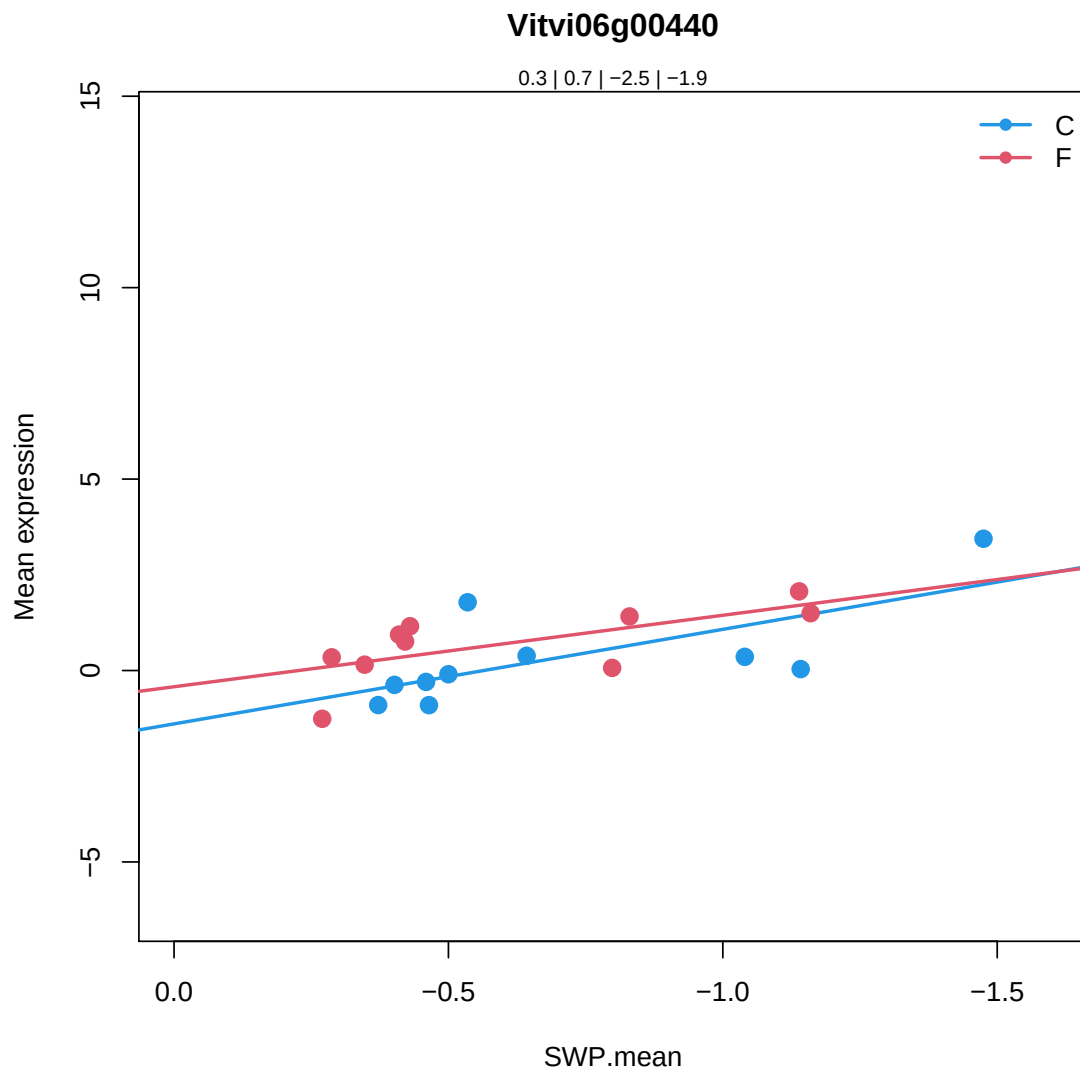
Pathogenesis-related thaumatin superfamily protein |

Chr2:12354664-12355488 REVERSE LENGTH=274 |

201606

Coefficients for Vitvi06g00440.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3426808	0.1888425		0.1937231	
SlopeC	-2.469205	0.002009926	**	0.1692557	
MeanF-MeanC	0.3706863	0.3107926		0.6747237	
SlopeF-SlopeC	0.6023688	0.570529		0.9999488	



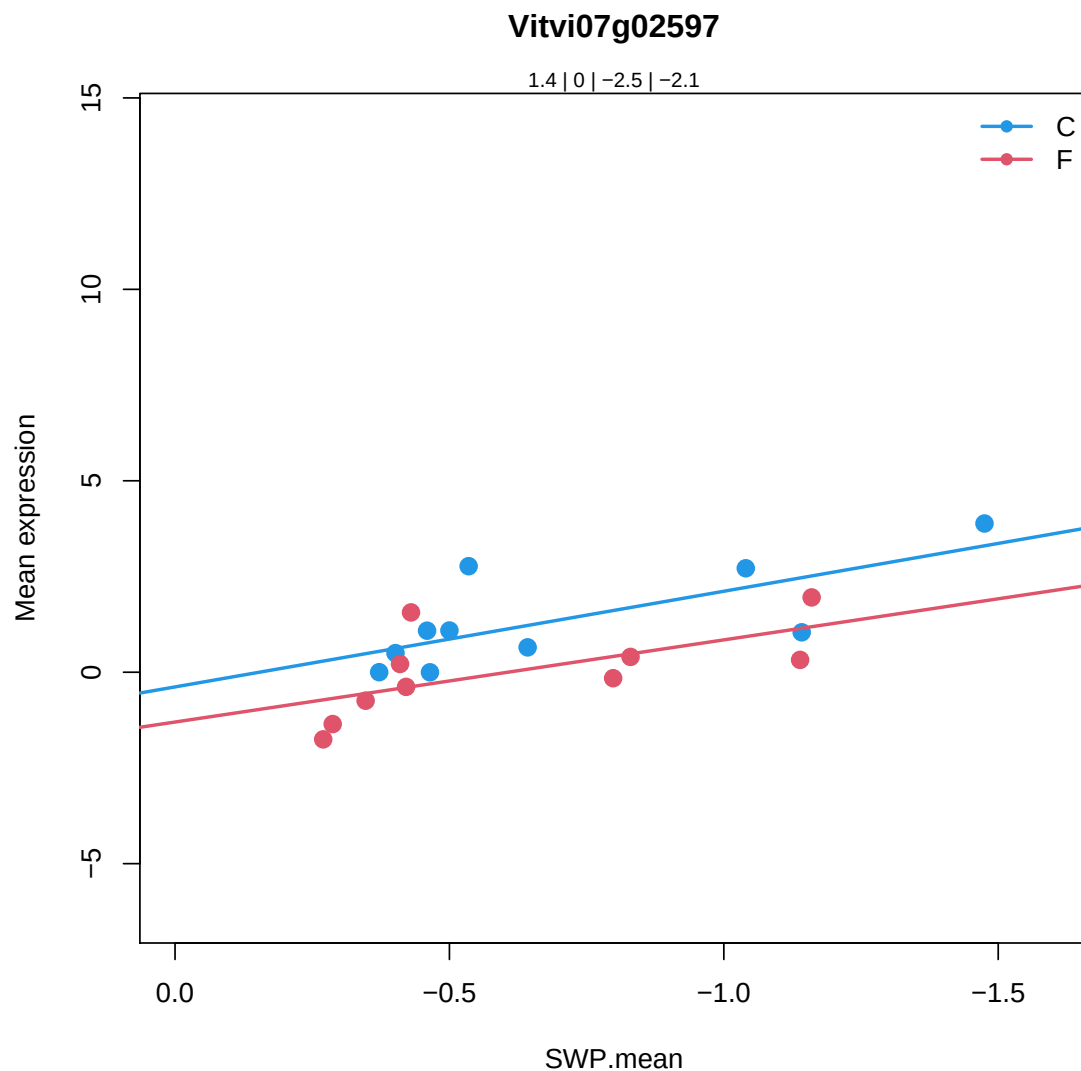
8.1.535 Vitvi07g02597: Type1.0 *

```
> 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	



8.1.536 Vitvi06g00605: Type1.0 *

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

Vitvi06g00605

26.10

misc.cytochrome P450

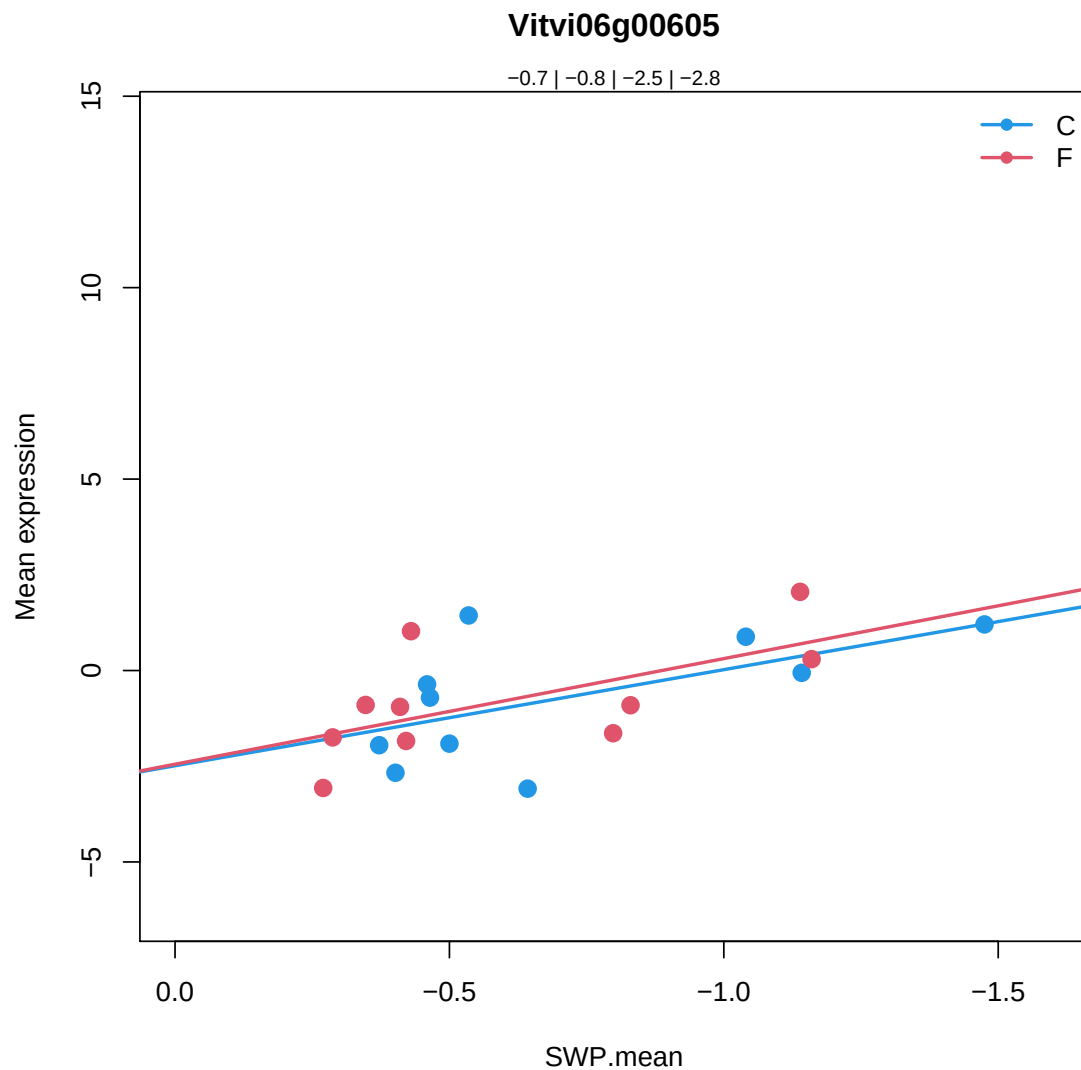
cytochrome P450%2C family 86%2C subfamily A%2C polypeptide 1 |

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	



8.1.537 Vitvi03g00119: Type1.0 *

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

Vitvi03g00119

20.2.1

stress.abiotic.heat

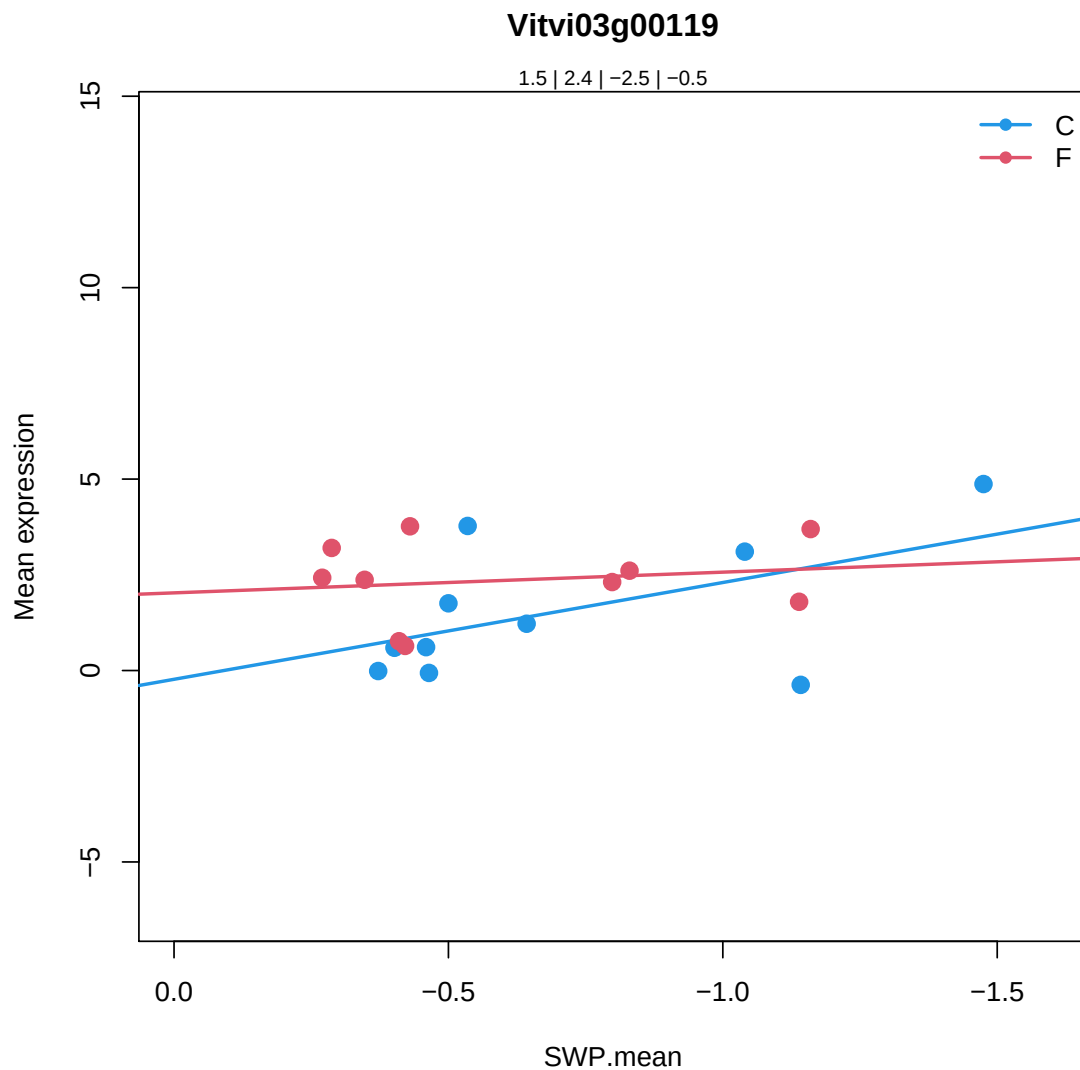
Chaperone DnaJ-domain superfamily protein |

Chr2:7767176-7767658 REVERSE LENGTH=160 |

201606

Coefficients for Vitvi03g00119.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.548045	0.0006344094	***	0.0006897053	***
SlopeC	-2.528126	0.02867679	*	0.4275443	
MeanF-MeanC	0.8094178	0.1541063		0.4733753	
SlopeF-SlopeC	1.987041	0.2288548		0.9999488	



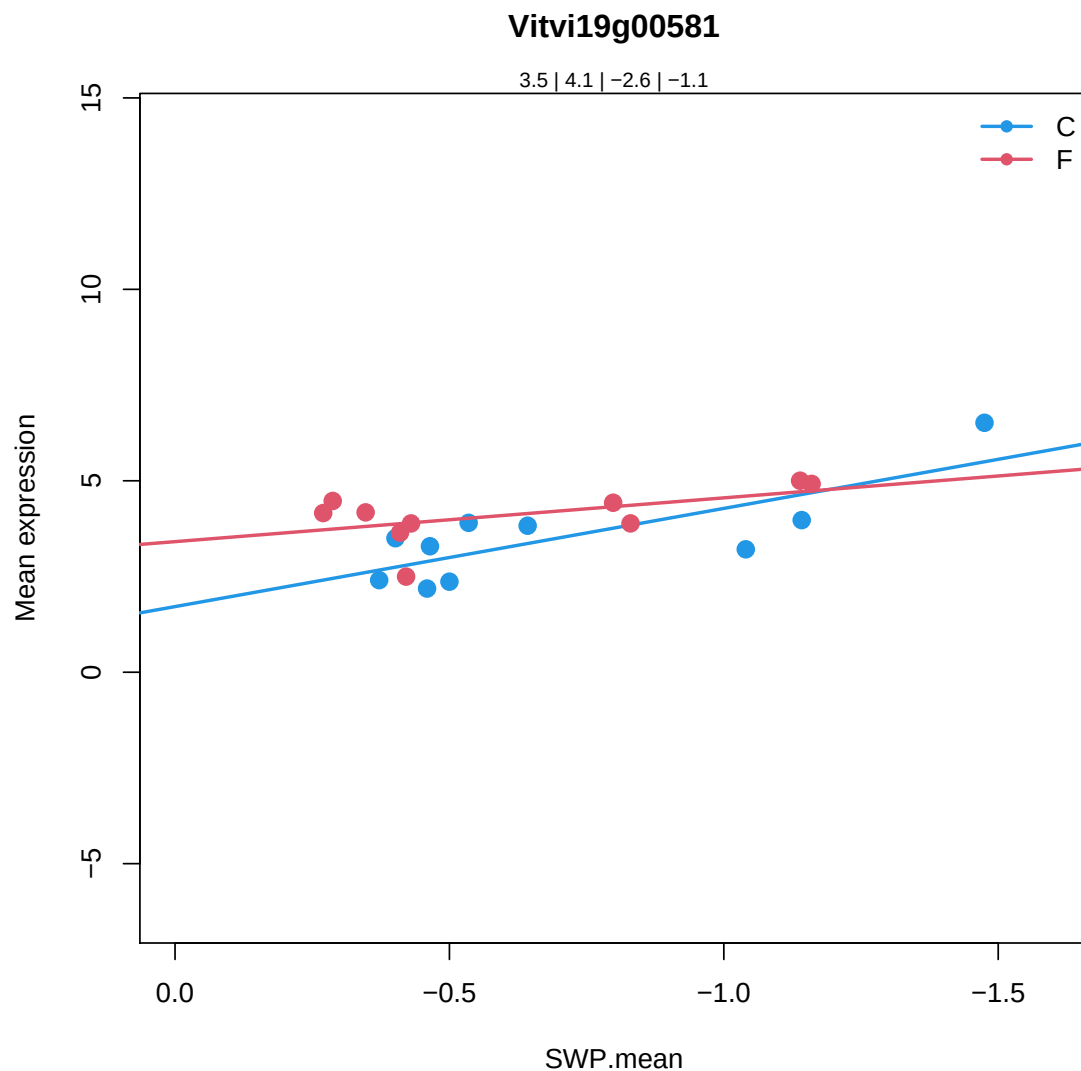
8.1.538 Vitvi19g00581: Type1.0 *

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

```
Vitvi19g00581
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi19g00581.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.517037	1.413724e-13	***	2.145145e-13	***
SlopeC	-2.564452	0.0003199145	***	0.09068993	.
MeanF-MeanC	0.5898893	0.06607941	.	0.2851592	
SlopeF-SlopeC	1.420828	0.1257732		0.9999488	



8.1.539 Vitvi17g00885: Type1.0 *

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

Vitvi17g00885

3.1.2.2

minor CHO metabolism.raffinose family.raffinose synthases.putative

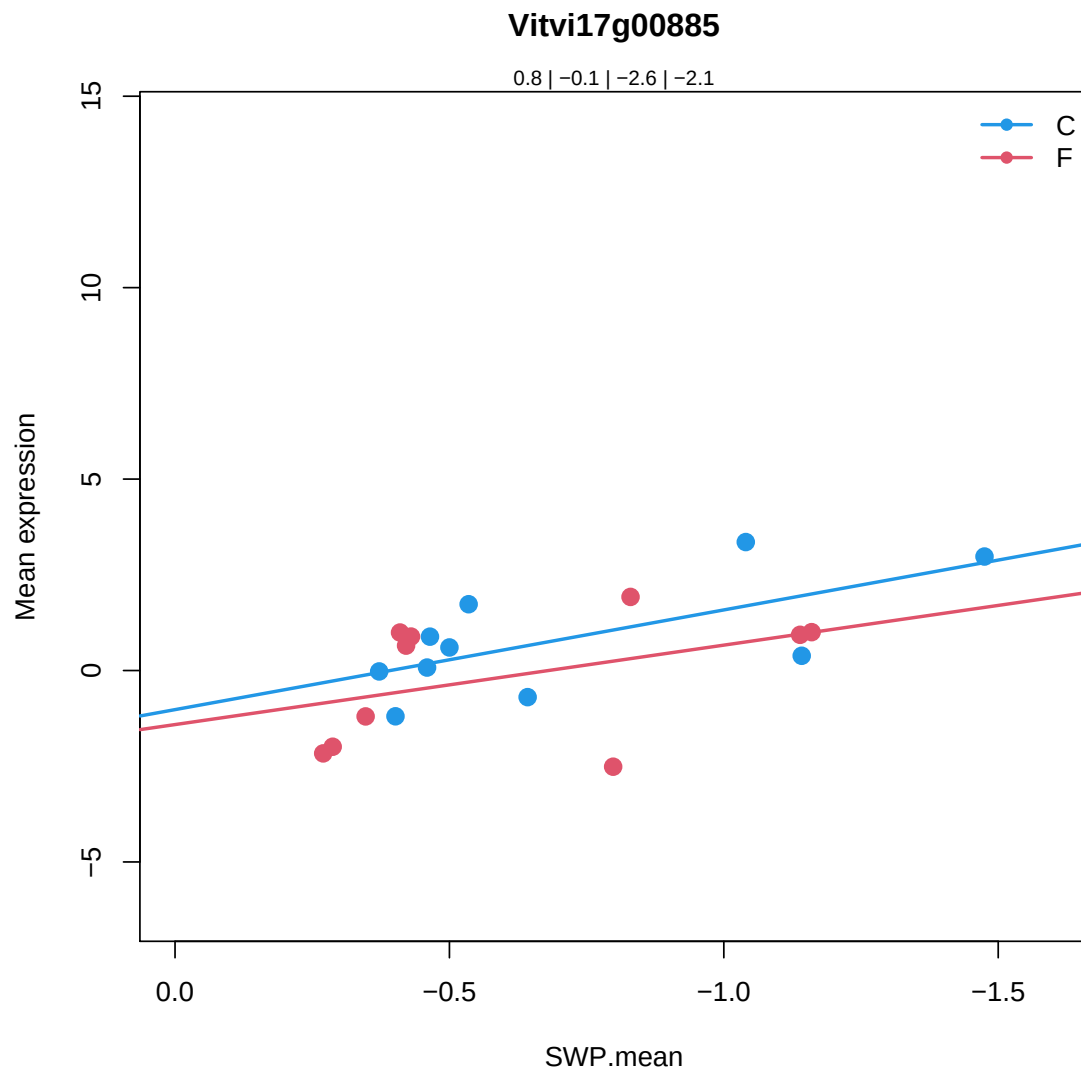
Raffinose synthase family protein |

Chr5:16161720-16165085 FORWARD LENGTH=783 |

201606

Coefficients for Vitvi17g00885.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8096866	0.04713077	*	0.04911912	*
SlopeC	-2.603953	0.02371204	*	0.3983963	
MeanF-MeanC	-0.9577296	0.09238472	.	0.3485586	
SlopeF-SlopeC	0.5290704	0.7428431		0.9999488	



8.1.540 Vitvi04g00522: Type1.0 *

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

Vitvi04g00522

20.2.1

stress.abiotic.heat

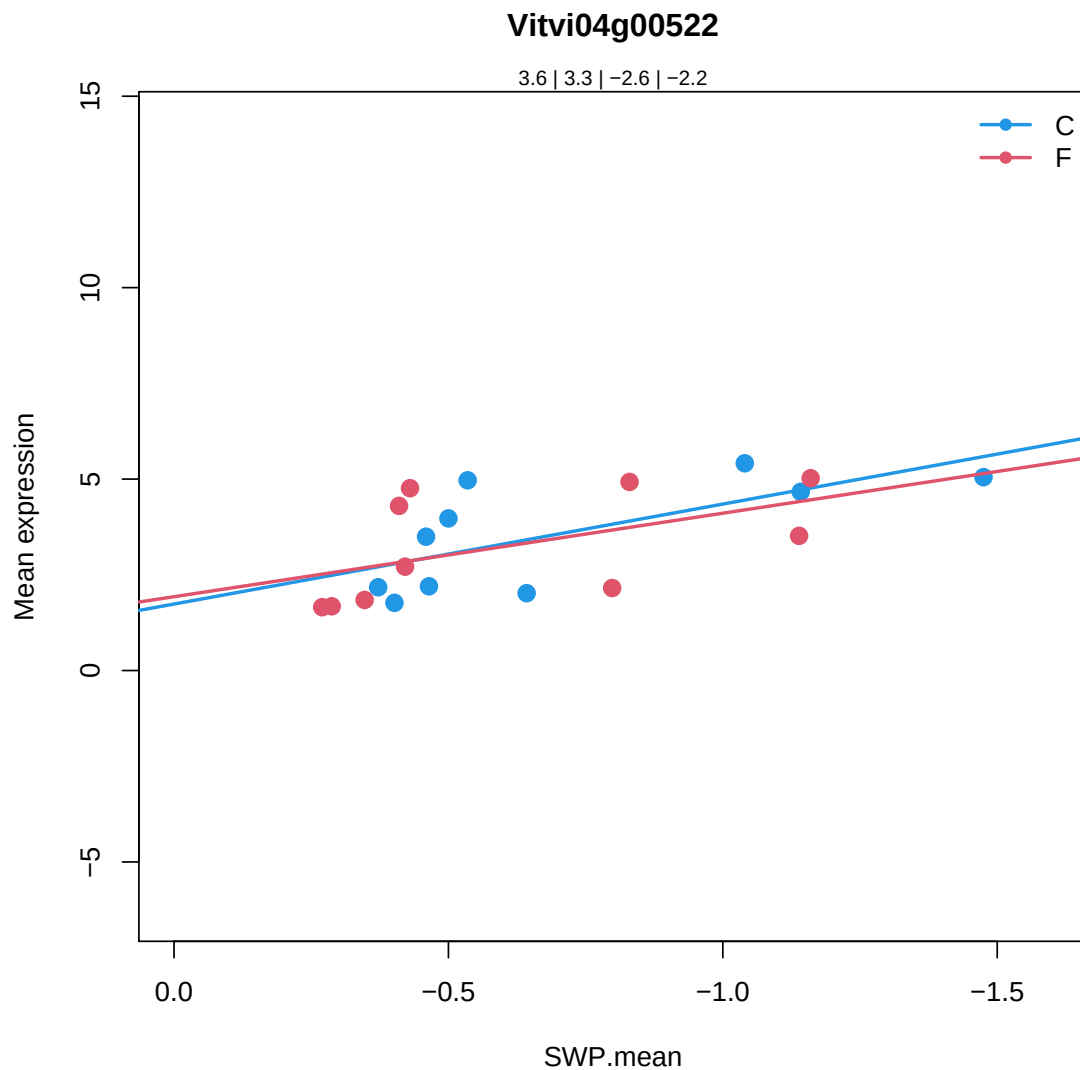
casein lytic proteinase B4 |

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	



8.1.541 Vitvi01g01459: Type1.0 *

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

Vitvi01g01459

17.1.3

hormone metabolism.abscisic acid.induced-regulated-responsive-activate

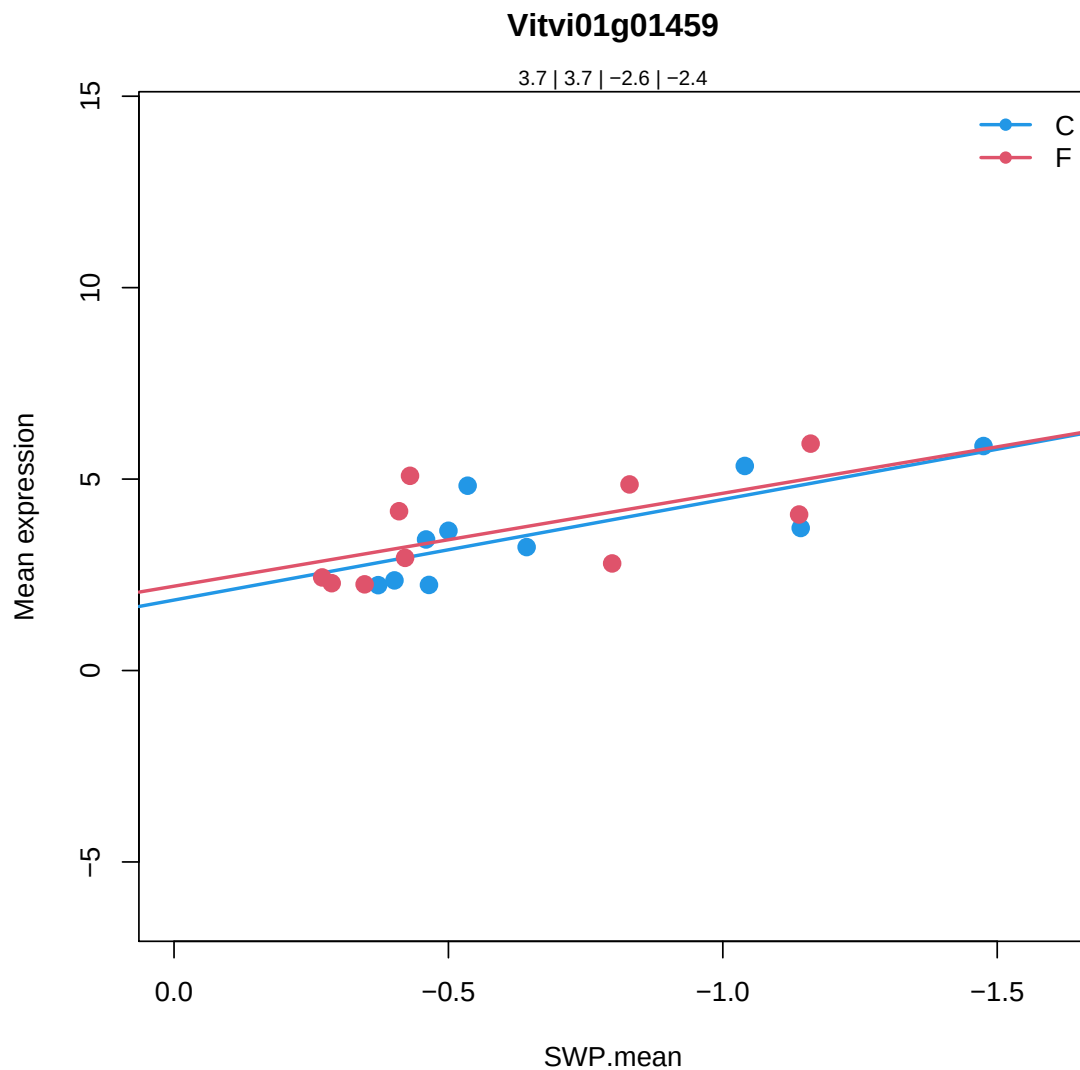
GRAM domain family protein |

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	



8.1.542 Vitvi14g02026: Type1.0 *

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

Vitvi14g02026

20.2.1

stress.abiotic.heat

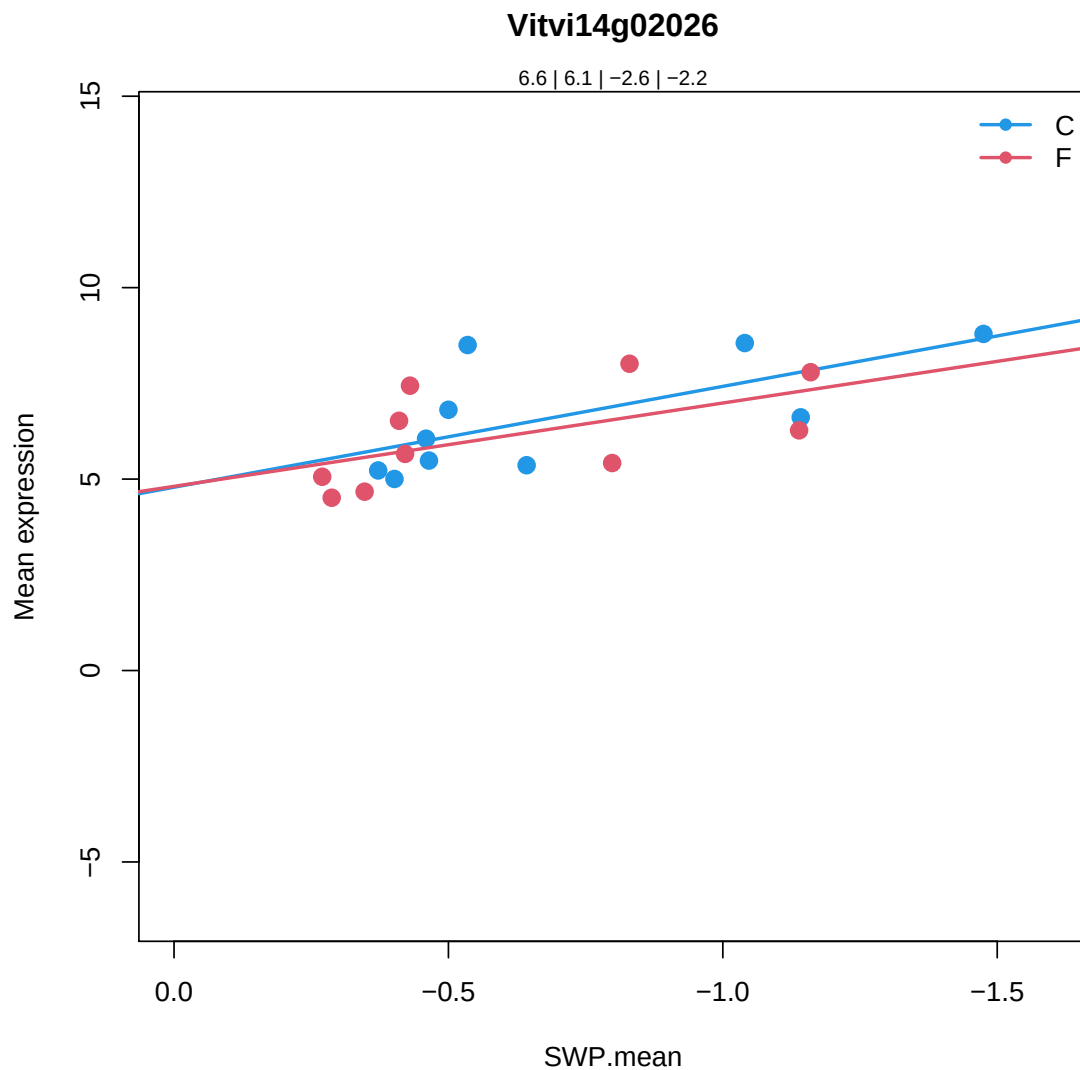
casein lytic proteinase B3 |

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	



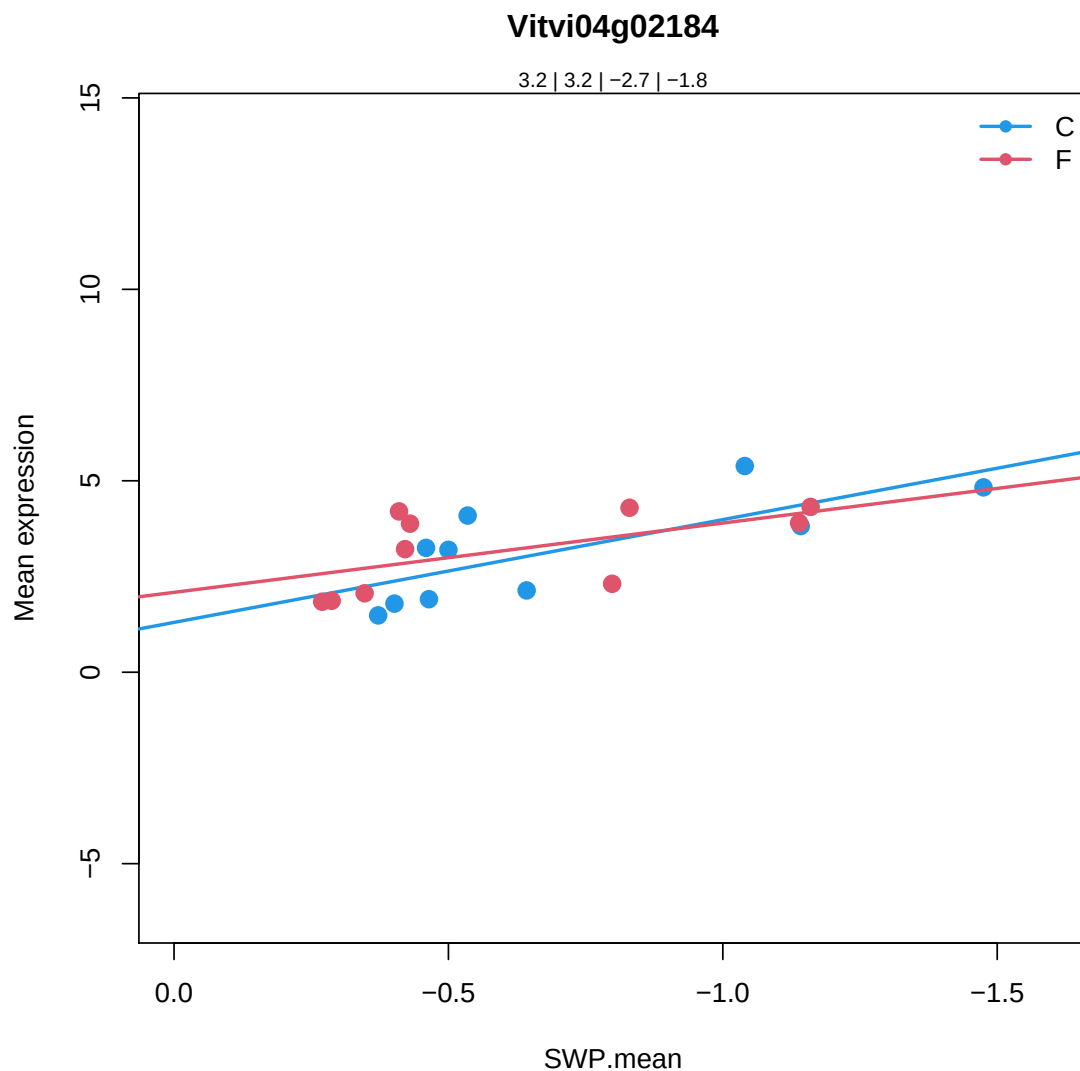
8.1.543 Vitvi04g02184: Type1.0 *

```
> 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	



8.1.544 Vitvi01g00424: Type1.0 *

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

Vitvi01g00424

29

protein

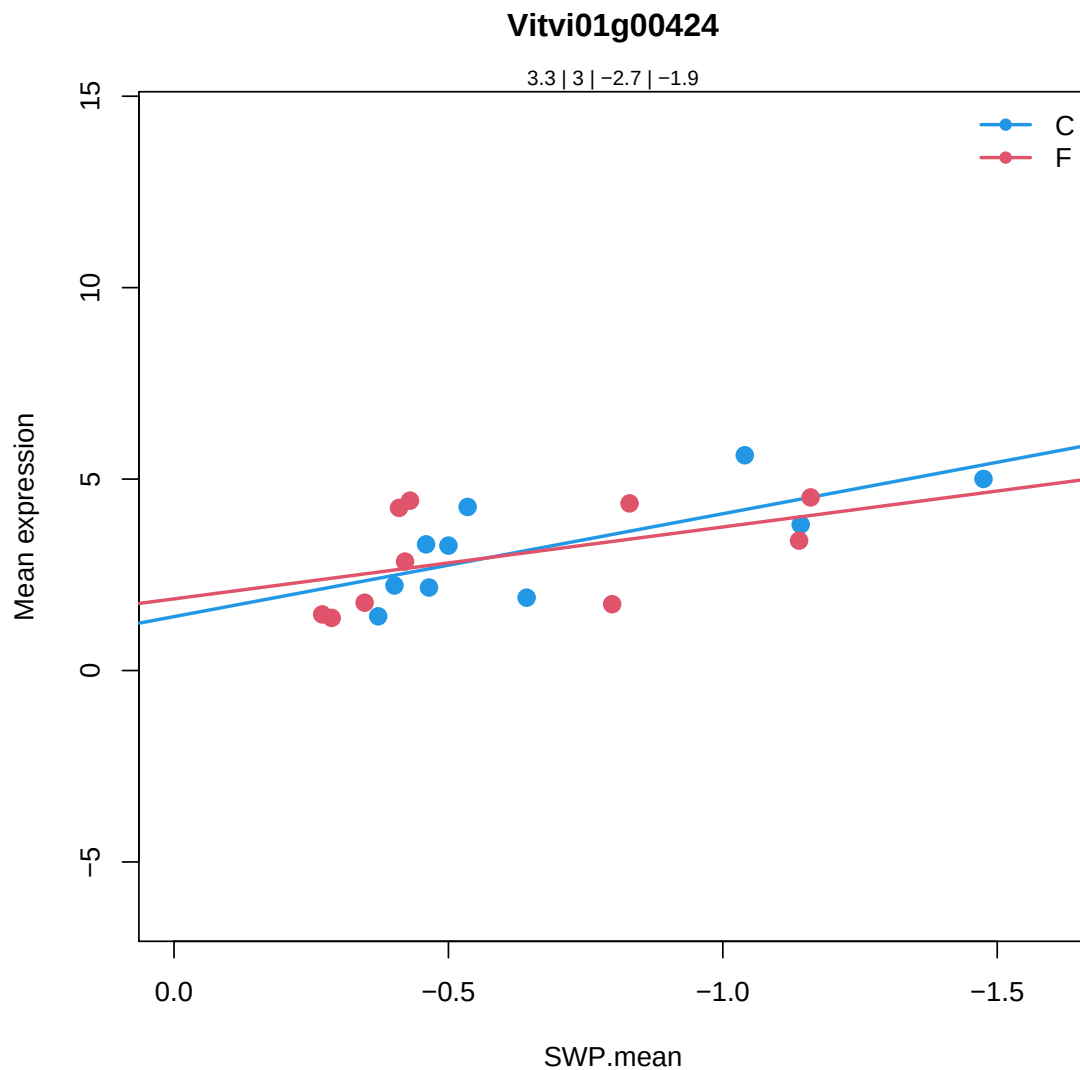
GroES-like family protein |

Chr1:8195867-8196336 FORWARD LENGTH=97 |

201606

Coefficients for Vitvi01g00424.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.297455	8.49922e-10	***	1.073905e-09	***
SlopeC	-2.687409	0.006251116	**	0.2647742	
MeanF-MeanC	-0.2822733	0.5376877		0.8284076	
SlopeF-SlopeC	0.8097099	0.5459104		0.9999488	



8.1.545 Vitvi18g02066: Type1.0 *

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

Vitvi18g02066

20.2.1

stress.abiotic.heat

chloroplast heat shock protein 70-1 |

Chr4:12590094-12593437 FORWARD LENGTH=718 |

201606

Vitvi18g02066

29.6

protein.folding

chloroplast heat shock protein 70-1 |

Chr4:12590094-12593437 FORWARD LENGTH=718 |

201606

Coefficients for Vitvi18g02066.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.868774	7.069221e-14	***	1.098359e-13	***
SlopeC	-2.767941	0.009125501	**	0.2903326	
MeanF-MeanC	-0.6997018	0.1684742		0.4974592	
SlopeF-SlopeC	0.8329396	0.5683183		0.9999488	

8.1.546 Vitvi12g00755: Type1.0 *

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

Vitvi12g00755

29.5.11.4.2

protein.degradation.ubiquitin.E3.RING

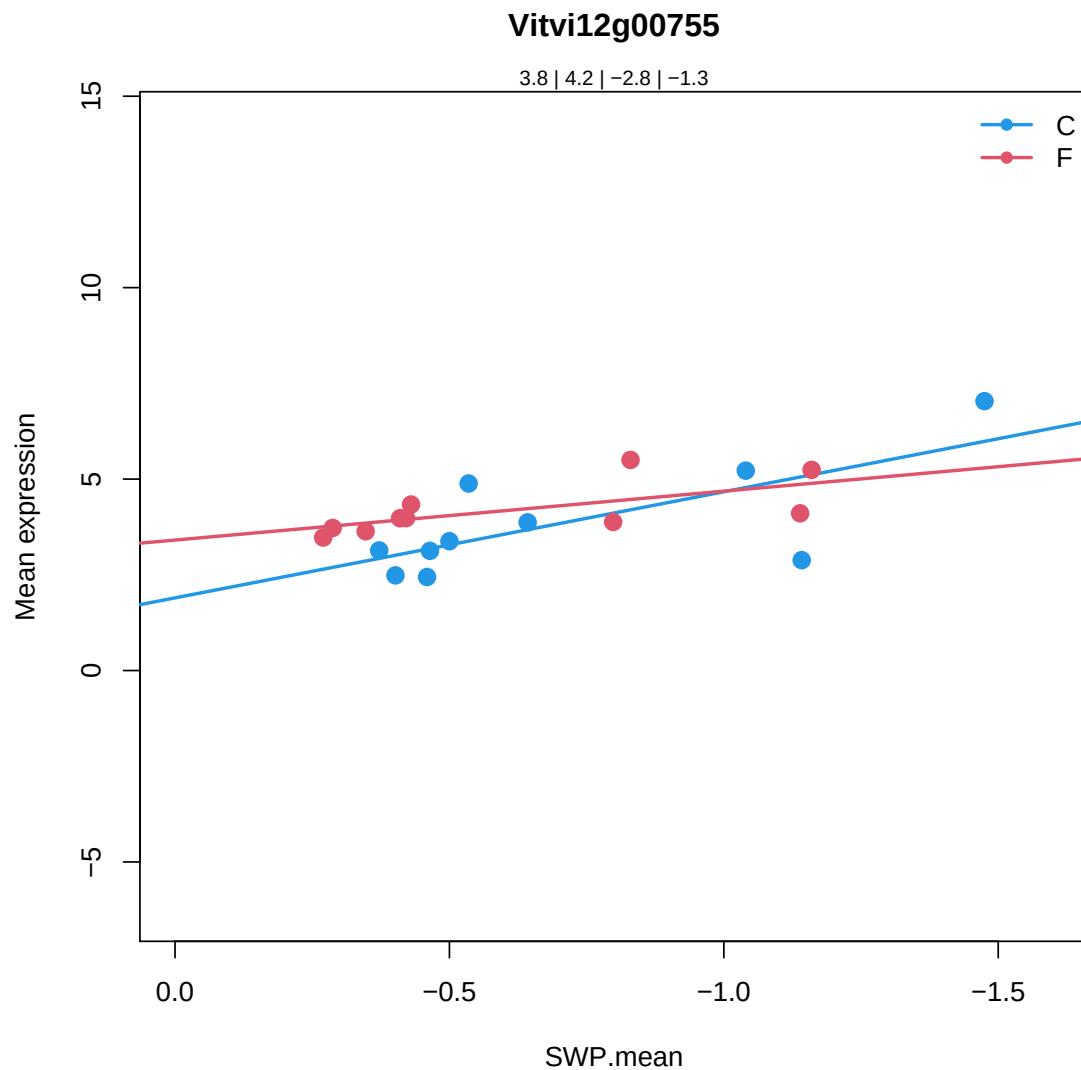
RING/U-box superfamily protein |

Chr2:1461816-1462304 REVERSE LENGTH=162 |

201606

Coefficients for Vitvi12g00755.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.84584	3.048646e-13	***	4.530316e-13	***
SlopeC	-2.771443	0.00053185	***	0.1005065	
MeanF-MeanC	0.3393377	0.3379475		0.6977592	
SlopeF-SlopeC	1.493998	0.1550729		0.9999488	



8.1.547 Vitvi03g00206: Type1.0 *

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

Vitvi03g00206

35.2

not assigned.unknown

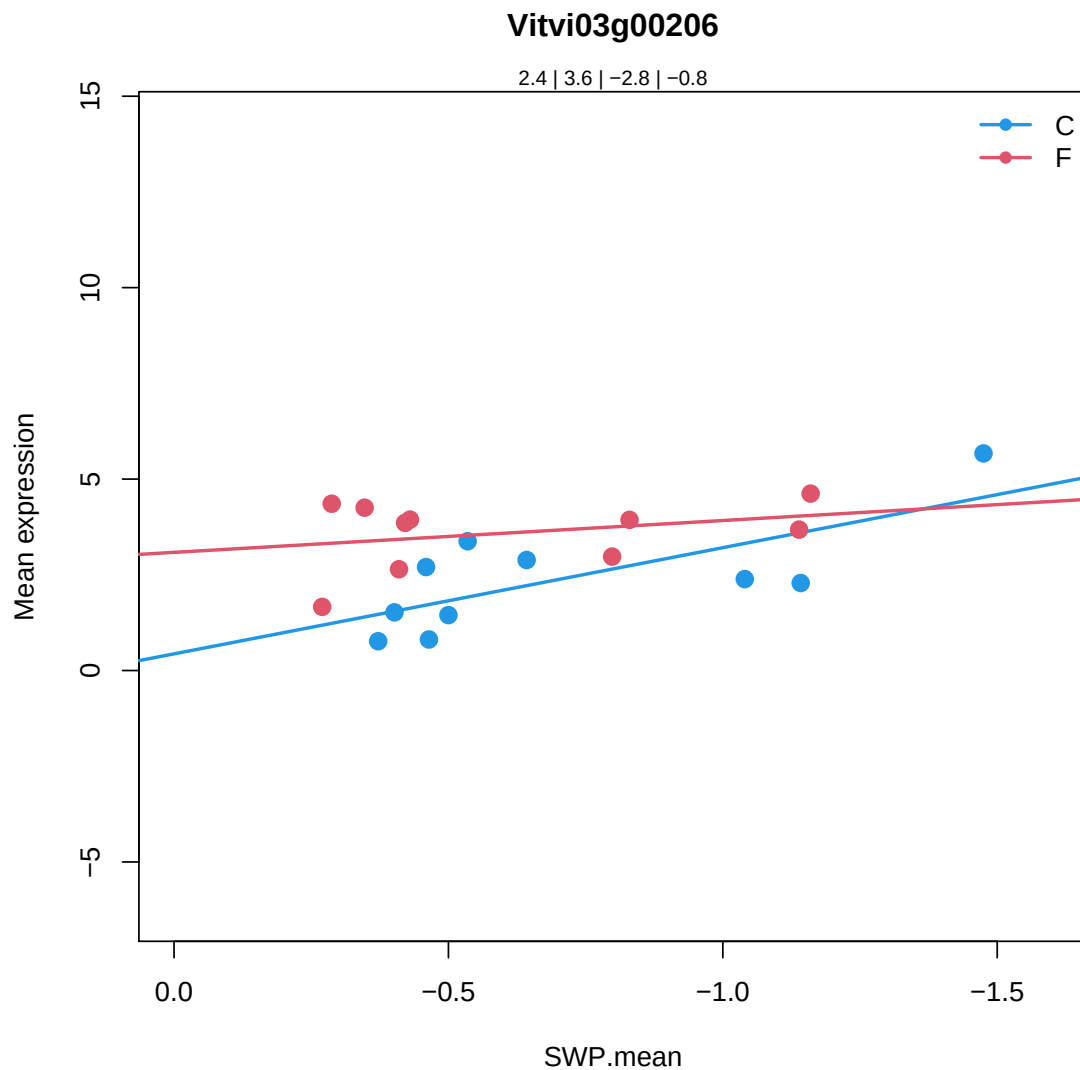
basic chitinase |

Chr3:3962501-3963984 REVERSE LENGTH=335 |

201606

Coefficients for Vitvi03g00206.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.384948	2.642346e-08	***	3.185025e-08	***
SlopeC	-2.772892	0.00185216	**	0.160246	
MeanF-MeanC	1.207401	0.006121461	**	0.05286307	.
SlopeF-SlopeC	1.941377	0.1095353		0.9999488	



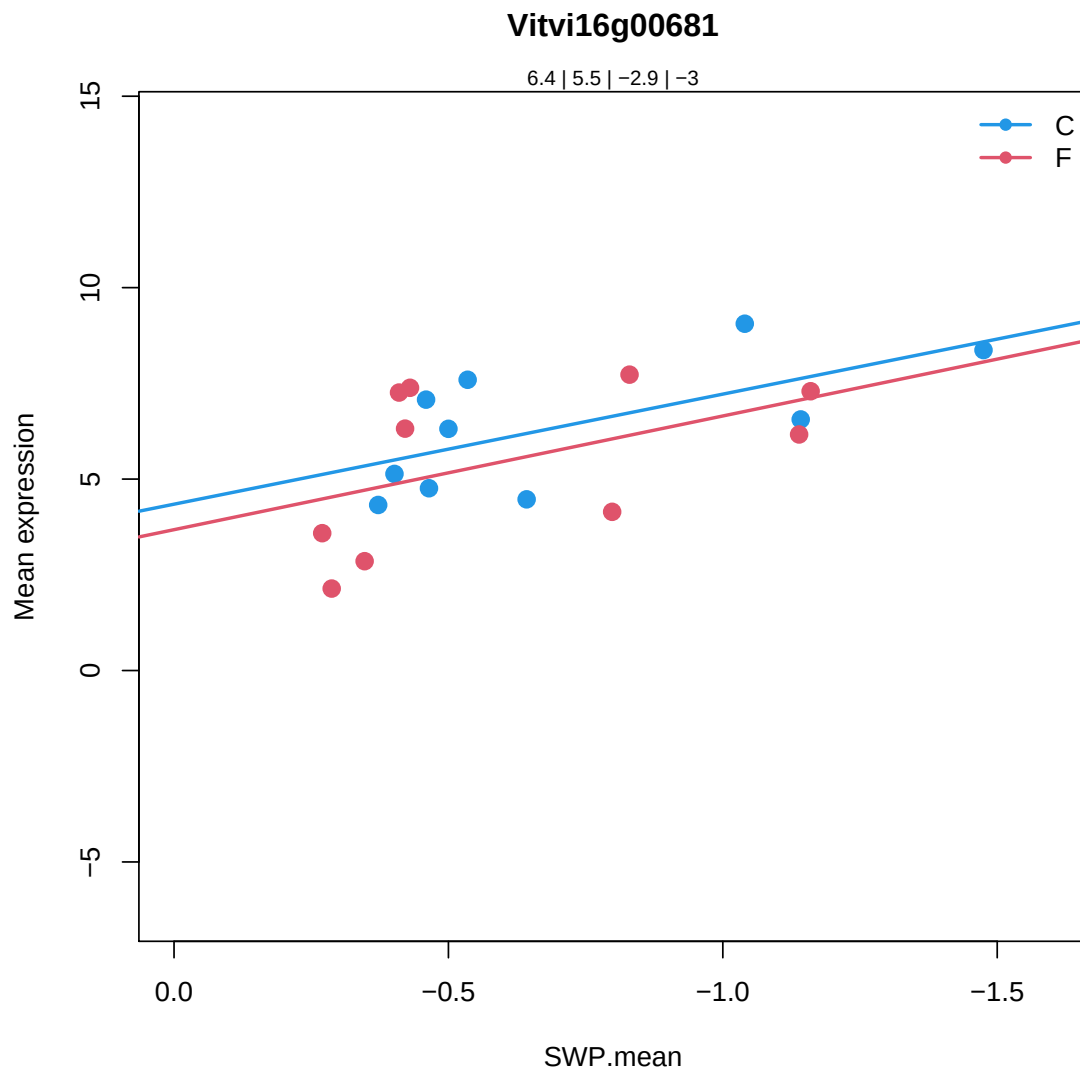
8.1.548 Vitvi16g00681: Type1.0 *

```
> 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	



8.1.549 Vitvi08g00689: Type1.0 *

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

Vitvi08g00689

20.2.1

stress.abiotic.heat

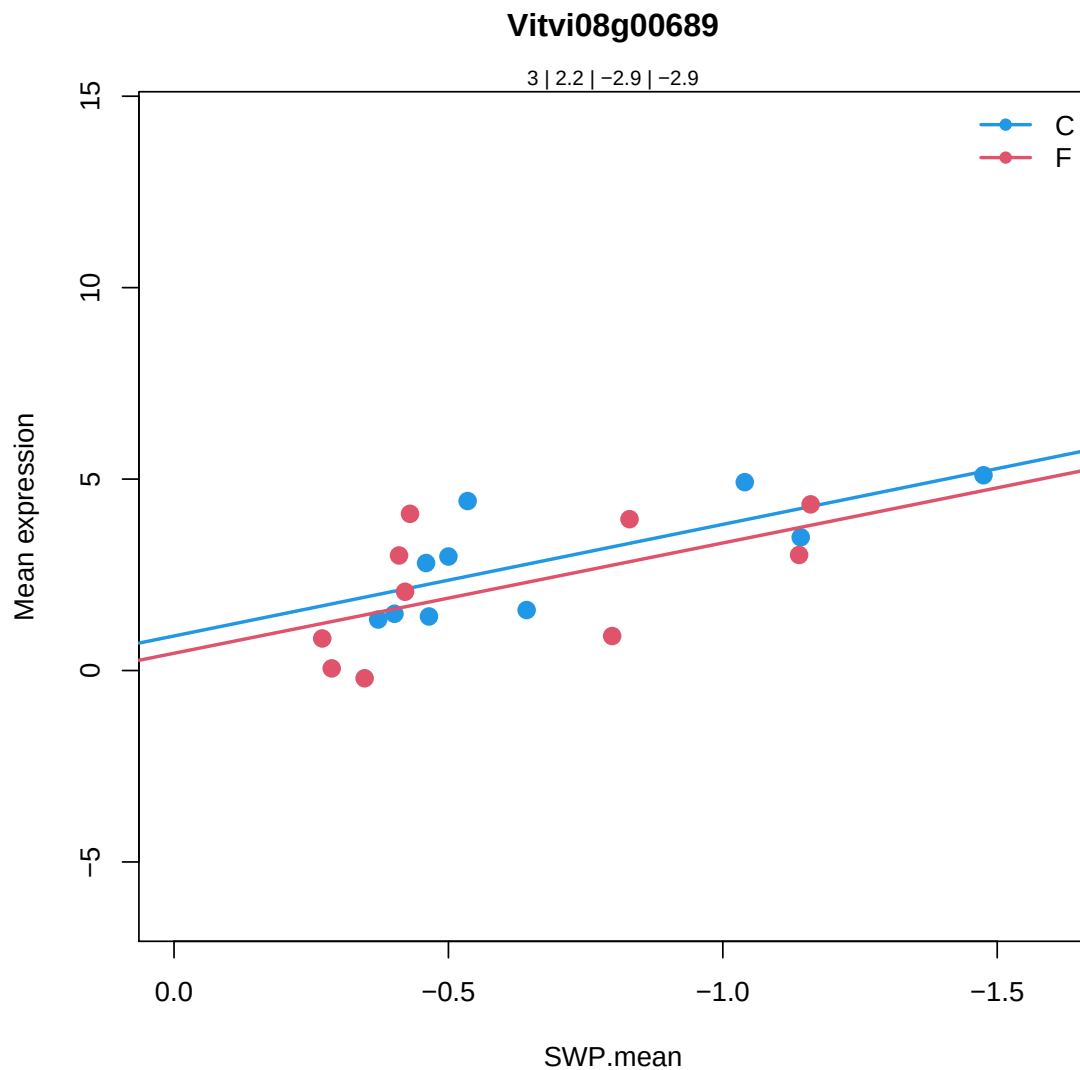
DNAJ heat shock N-terminal domain-containing protein |

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	



8.1.550 Vitvi14g01394: Type1.0 *

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

Vitvi14g01394

29.3.1

protein.targeting.nucleus

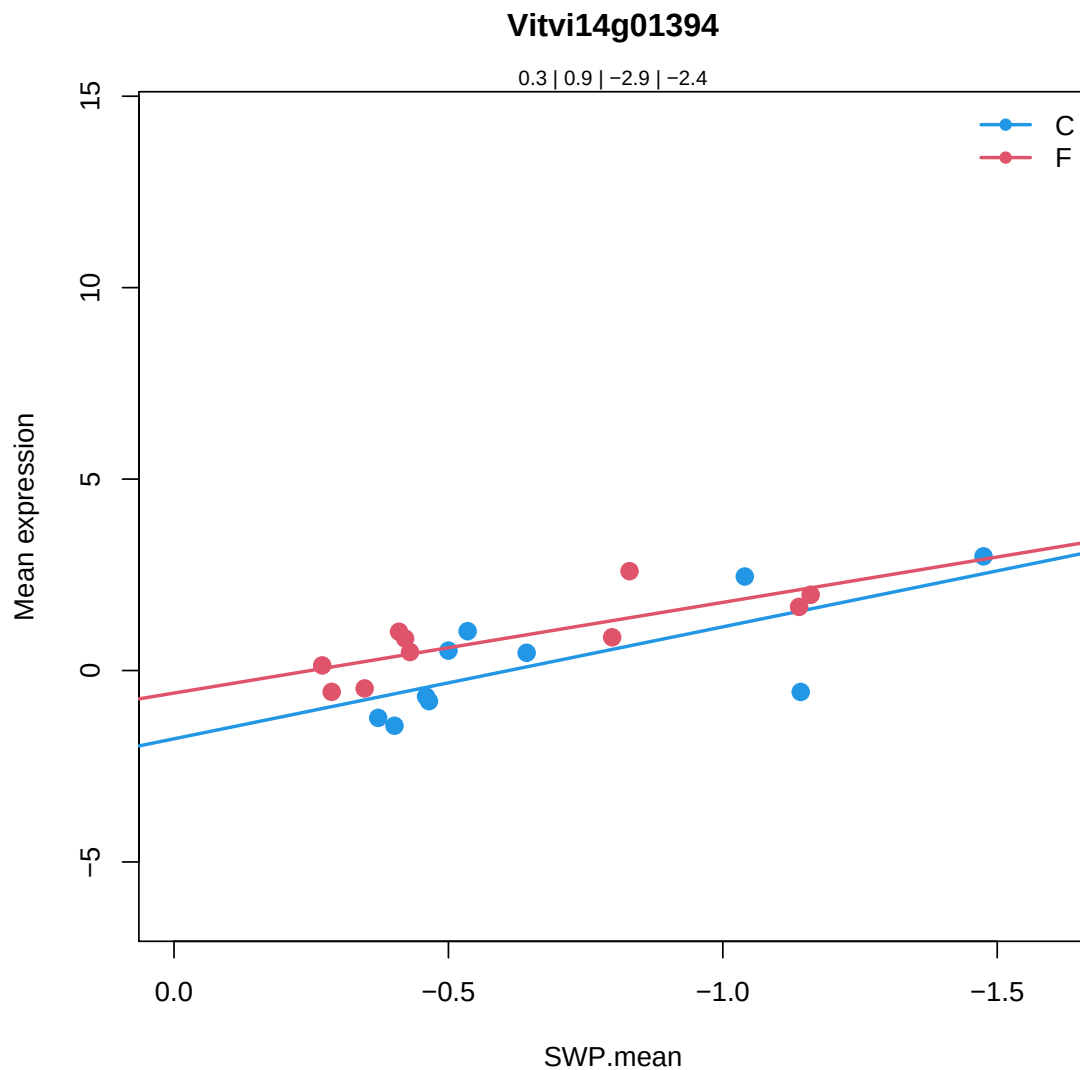
ABI five binding protein 3 |

Chr3:11382416-11383657 REVERSE LENGTH=231 |

201606

Coefficients for Vitvi14g01394.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.2727581	0.3044646		0.3102038	
SlopeC	-2.923734	0.0005521162	***	0.1005065	
MeanF-MeanC	0.5813079	0.1274861		0.4236563	
SlopeF-SlopeC	0.5545693	0.6107287		0.9999488	



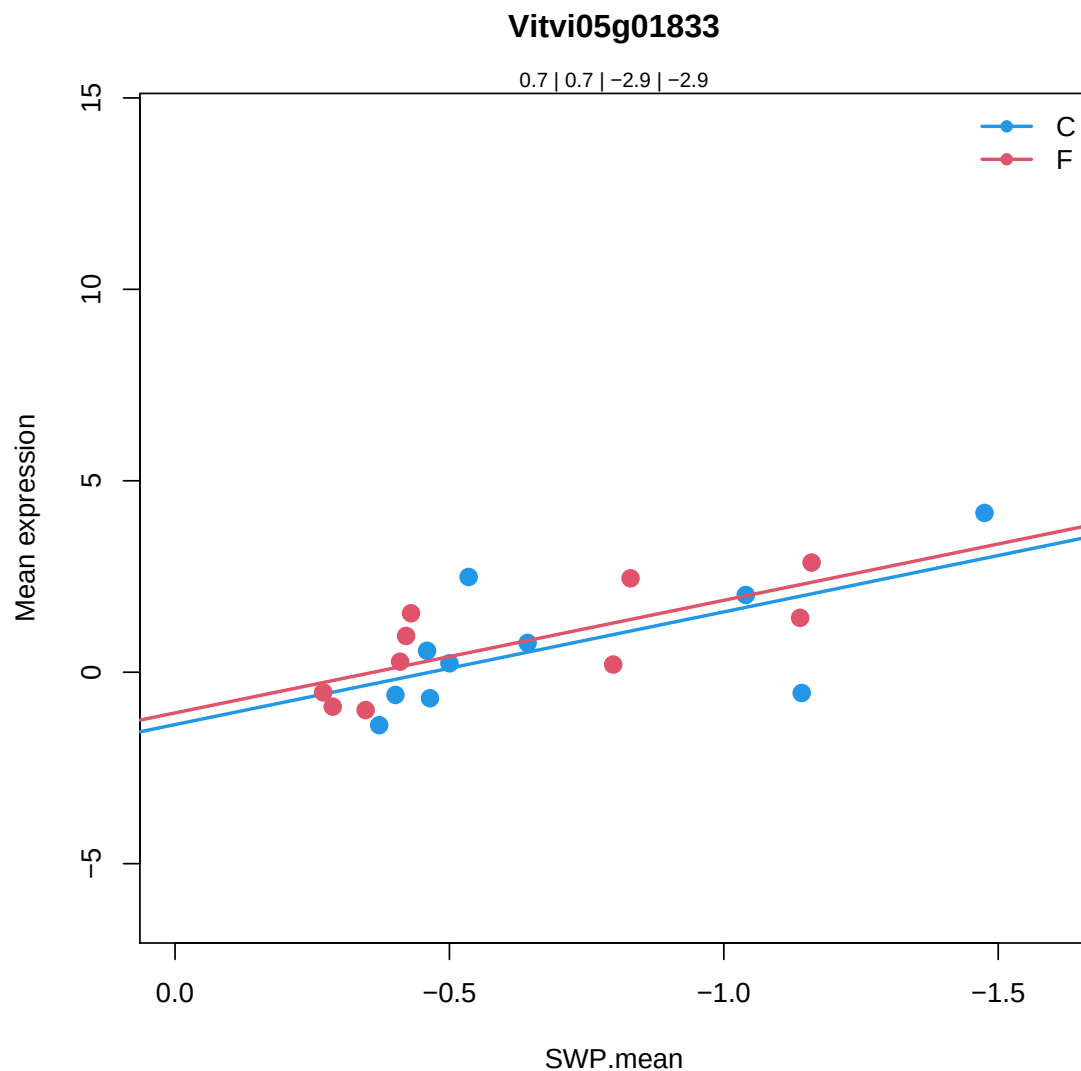
8.1.551 Vitvi05g01833: Type1.0 *

```
> 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	



8.1.552 Vitvi17g00085: Type1.0 *

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

Vitvi17g00085

17.1.3

hormone metabolism.abscisic acid.induced-regulated-responsive-activate

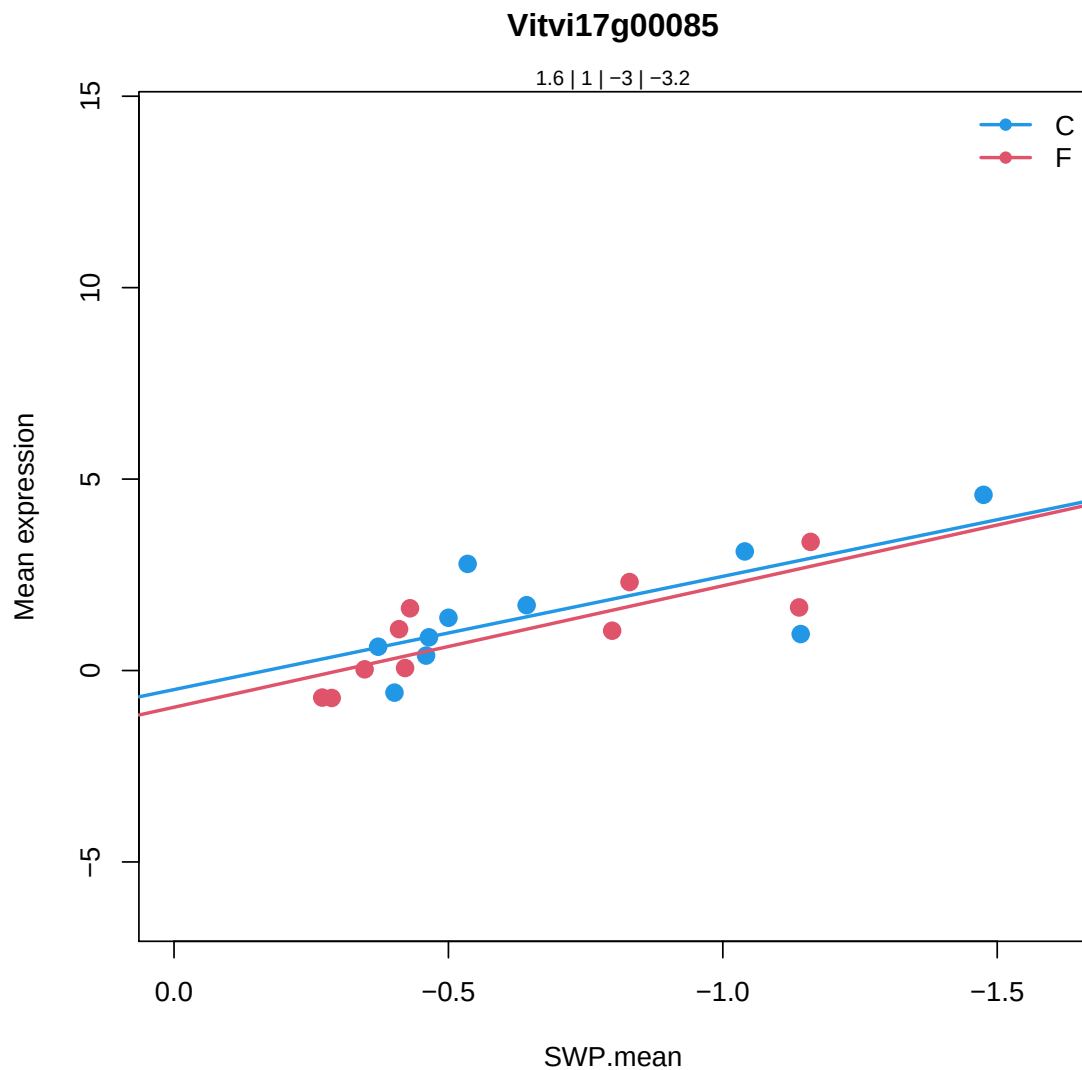
HVA22 homologue D |

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	



8.1.553 Vitvi13g01107: Type1.0

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

Vitvi13g01107

35.2

not assigned.unknown

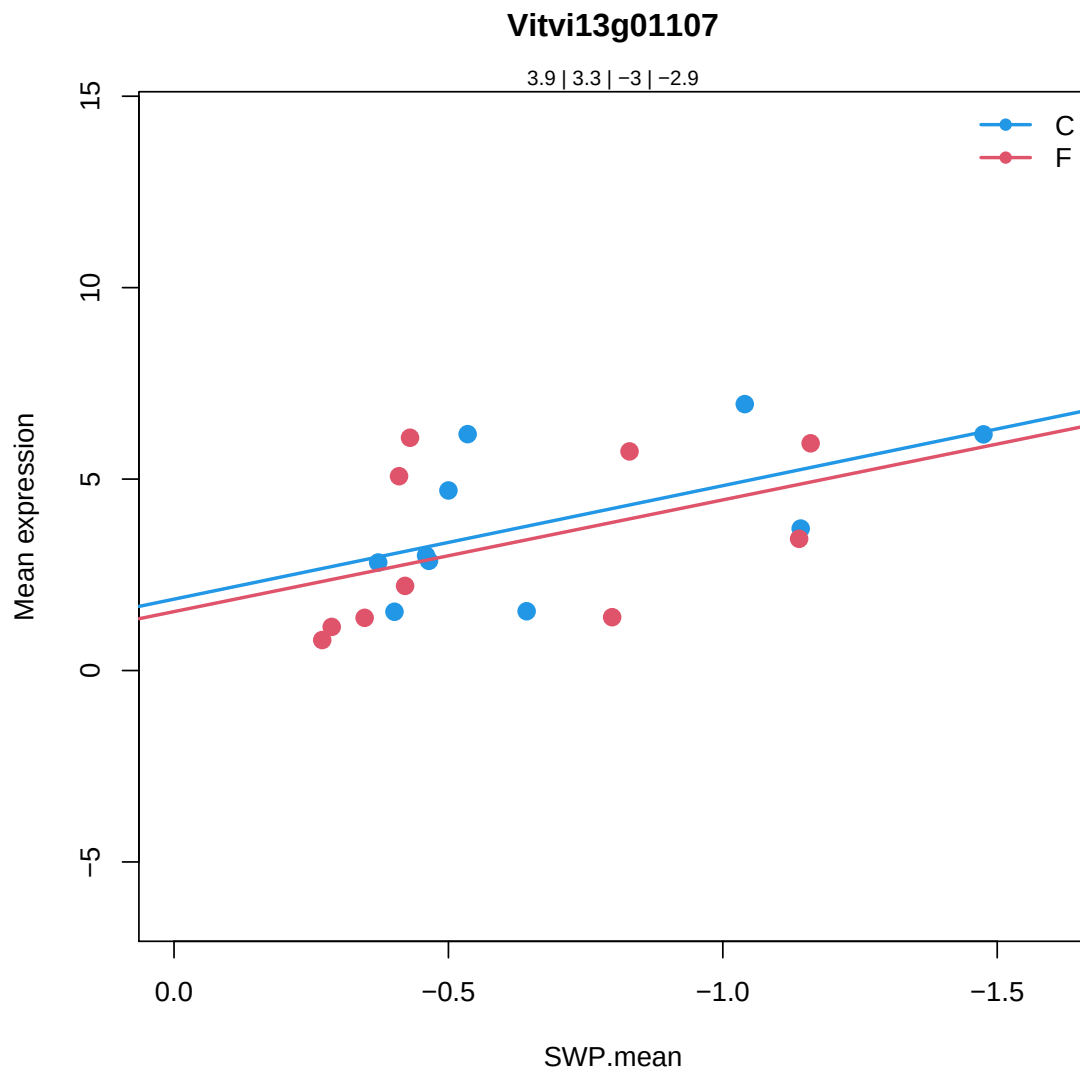
HSP20-like chaperones superfamily protein |

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	



8.1.554 Vitvi07g02433: Type1.0 *

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

Vitvi07g02433

35.1

not assigned.no ontology

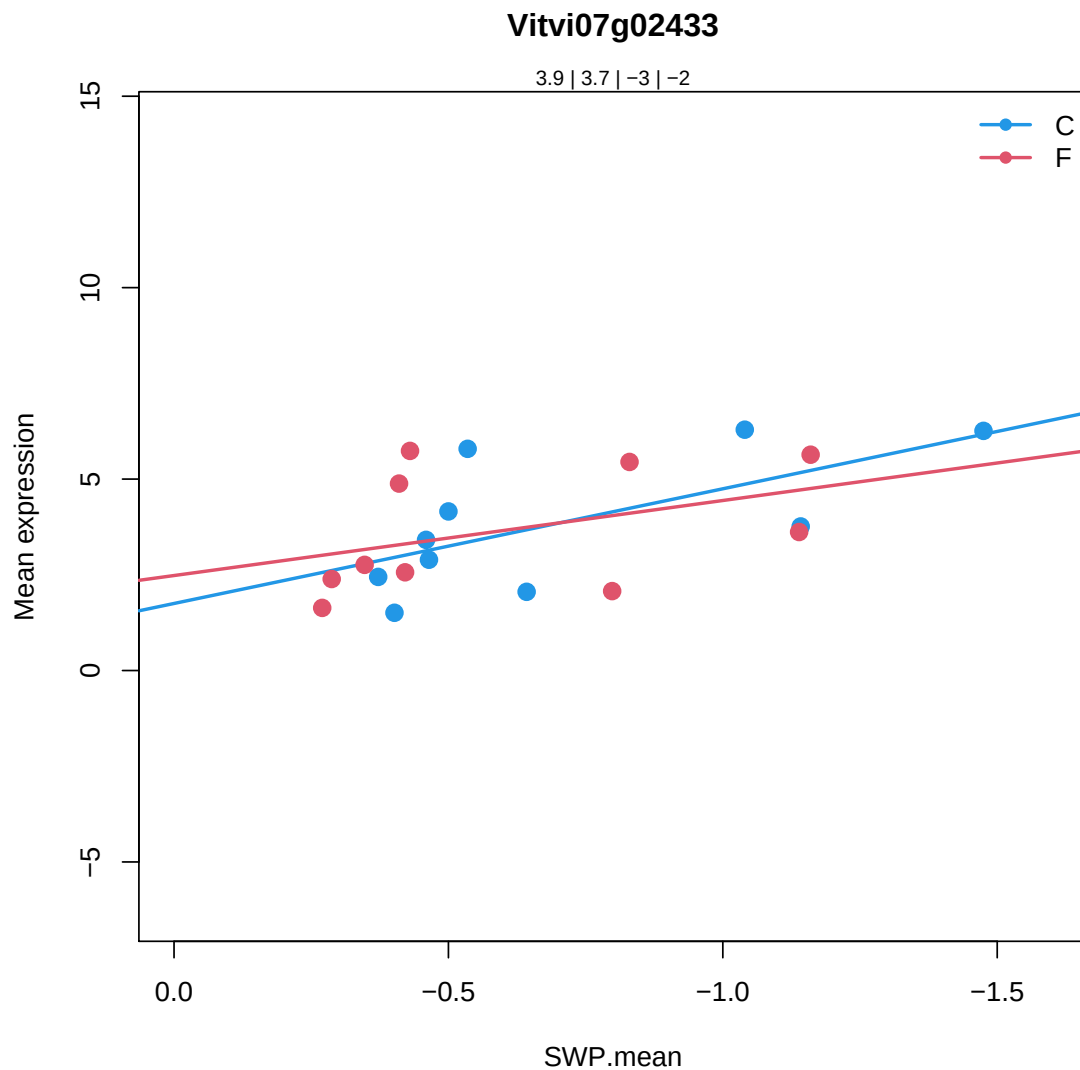
cysteine-rich RECEPTOR-like kinase |

Chr4:12129485-12133157 FORWARD LENGTH=1043 |

201606

Coefficients for Vitvi07g02433.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.85703	4.761988e-09	***	5.8752e-09	***
SlopeC	-2.995349	0.01580358	*	0.3462543	
MeanF-MeanC	-0.1825736	0.7563557		0.928831	
SlopeF-SlopeC	1.036141	0.5488434		0.9999488	



8.1.555 Vitvi11g01243: Type1.0 *

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

Vitvi11g01243

29.5.9

protein.degradation.AAA type

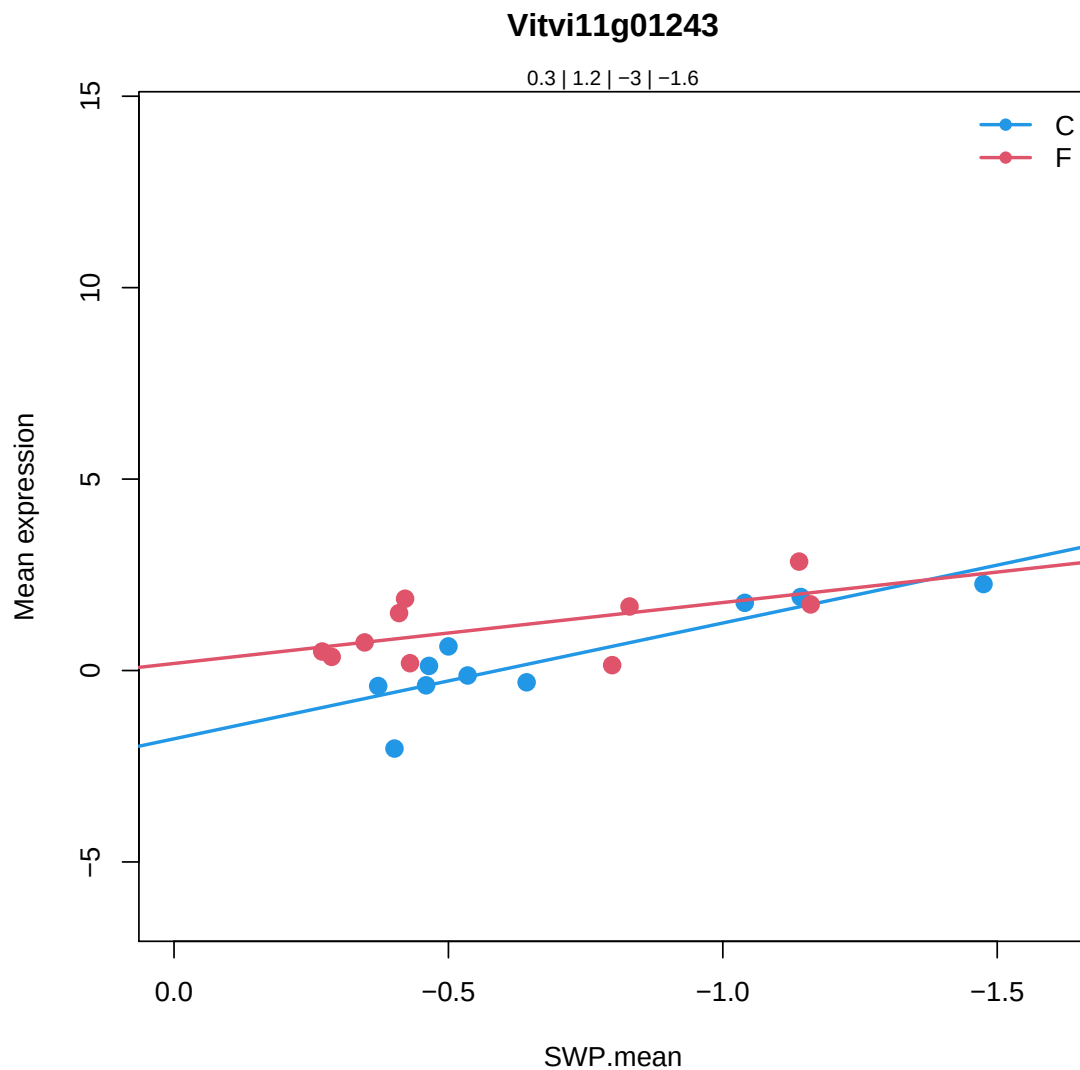
P-loop containing nucleoside triphosphate hydrolases superfamily prote

Chr5:23279406-23280968 REVERSE LENGTH=520 |

201606

Coefficients for Vitvi11g01243.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3426219	0.12401		0.1279557	
SlopeC	-3.024751	4.670611e-05	***	0.06471768	.
MeanF-MeanC	0.810949	0.01387862	*	0.0967243	.
SlopeF-SlopeC	1.433289	0.1204094		0.9999488	



8.1.556 Vitvi01g02030: Type1.0 *

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

Vitvi01g02030

29.5.11.4.2

protein.degradation.ubiquitin.E3.RING

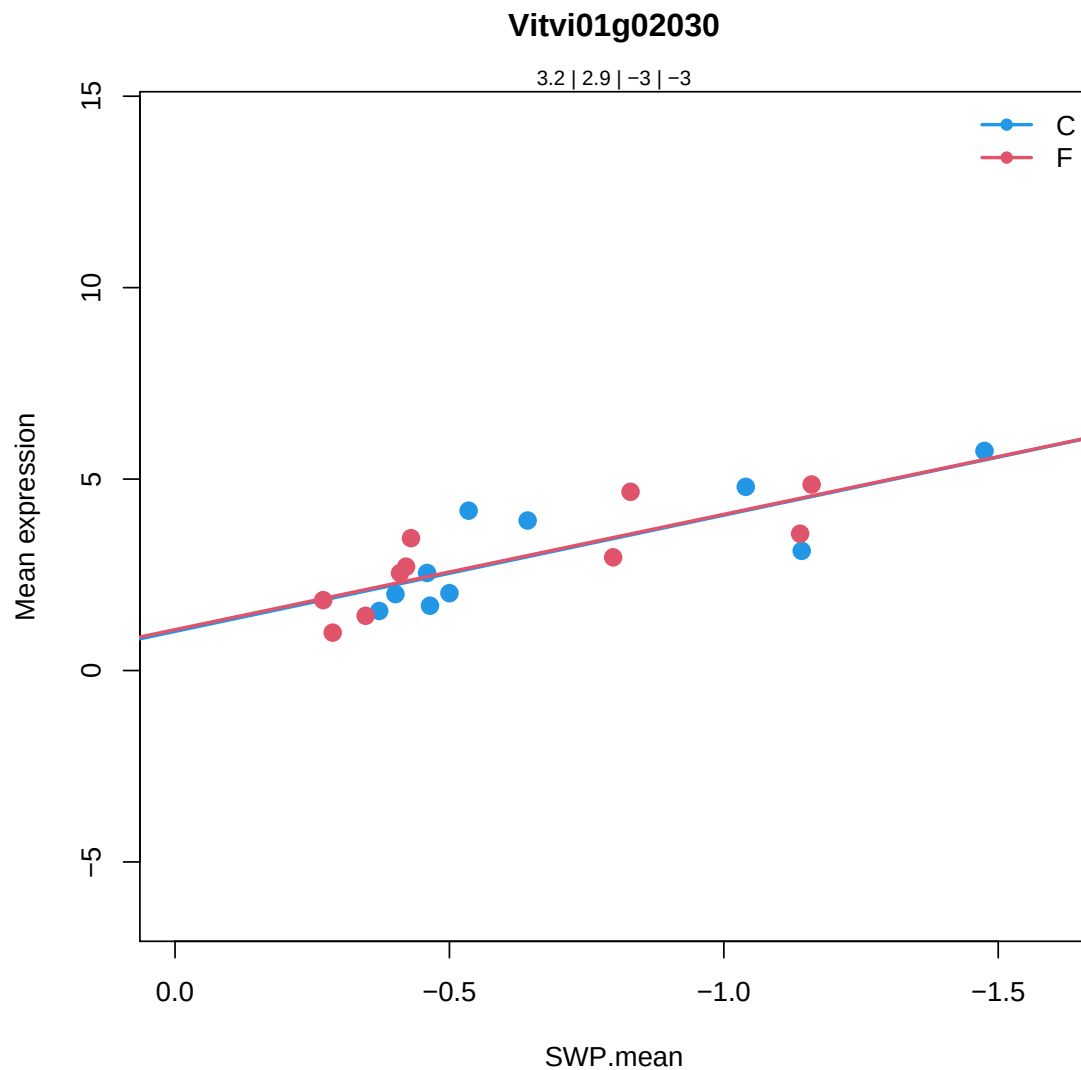
RING/U-box superfamily protein |

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	



8.1.557 Vitvi13g01839: Type1.0 *

```
> 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

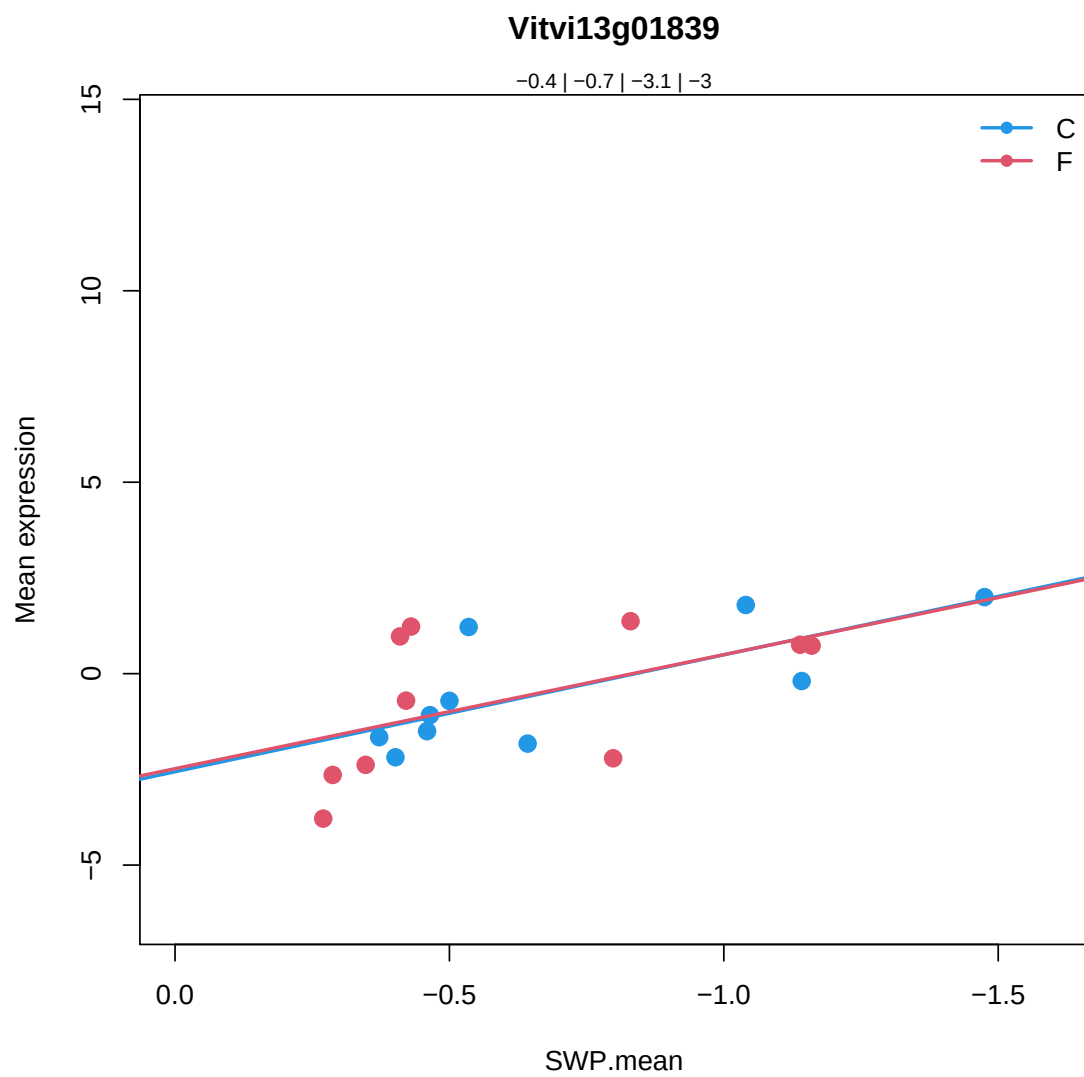
Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin

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	



8.1.558 Vitvi06g00533: Type1.0 *

```
> 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

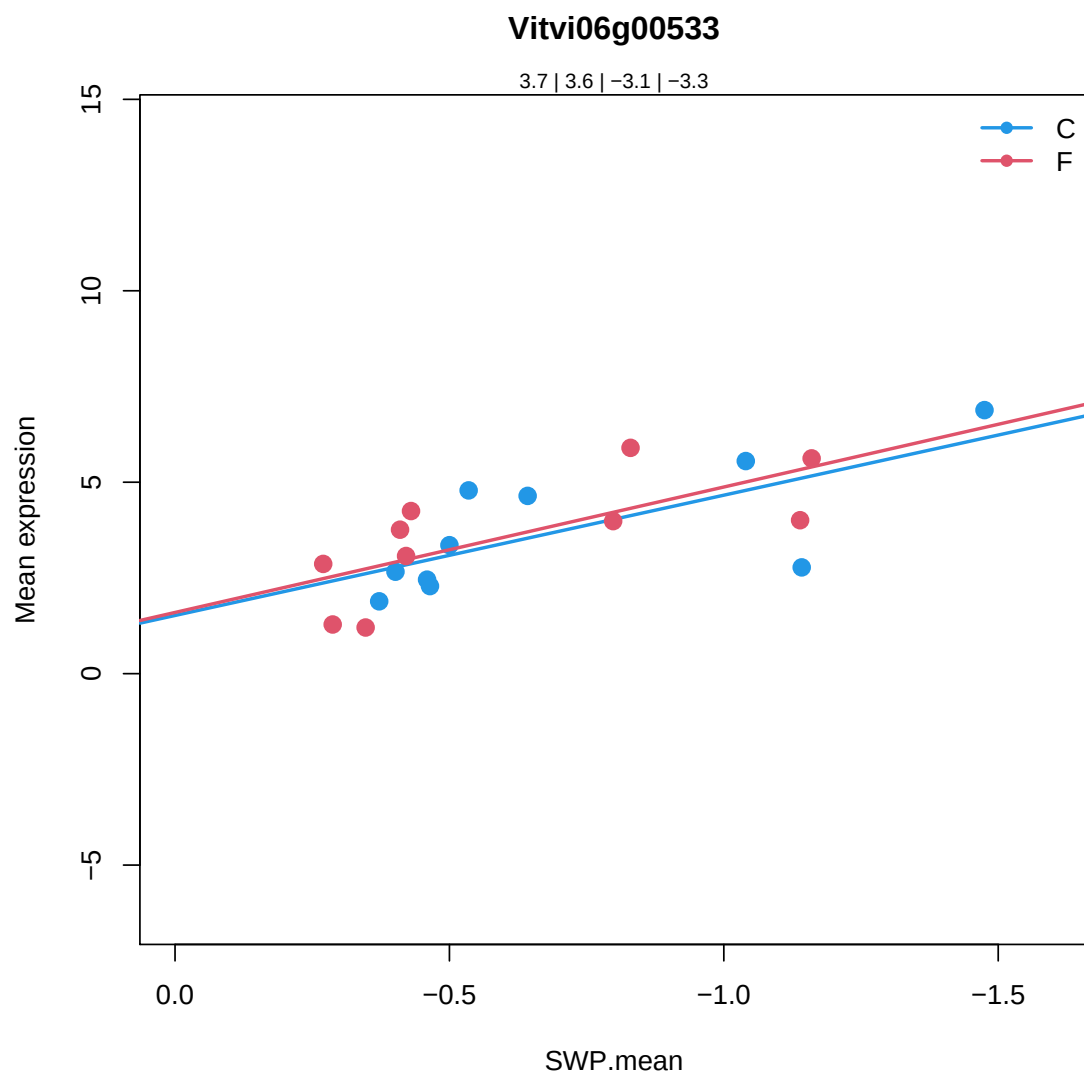
highly ABA-induced PP2C protein 3 |

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	



8.1.559 Vitvi07g00259: Type1.0 *

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

Vitvi07g00259

35.2

not assigned.unknown

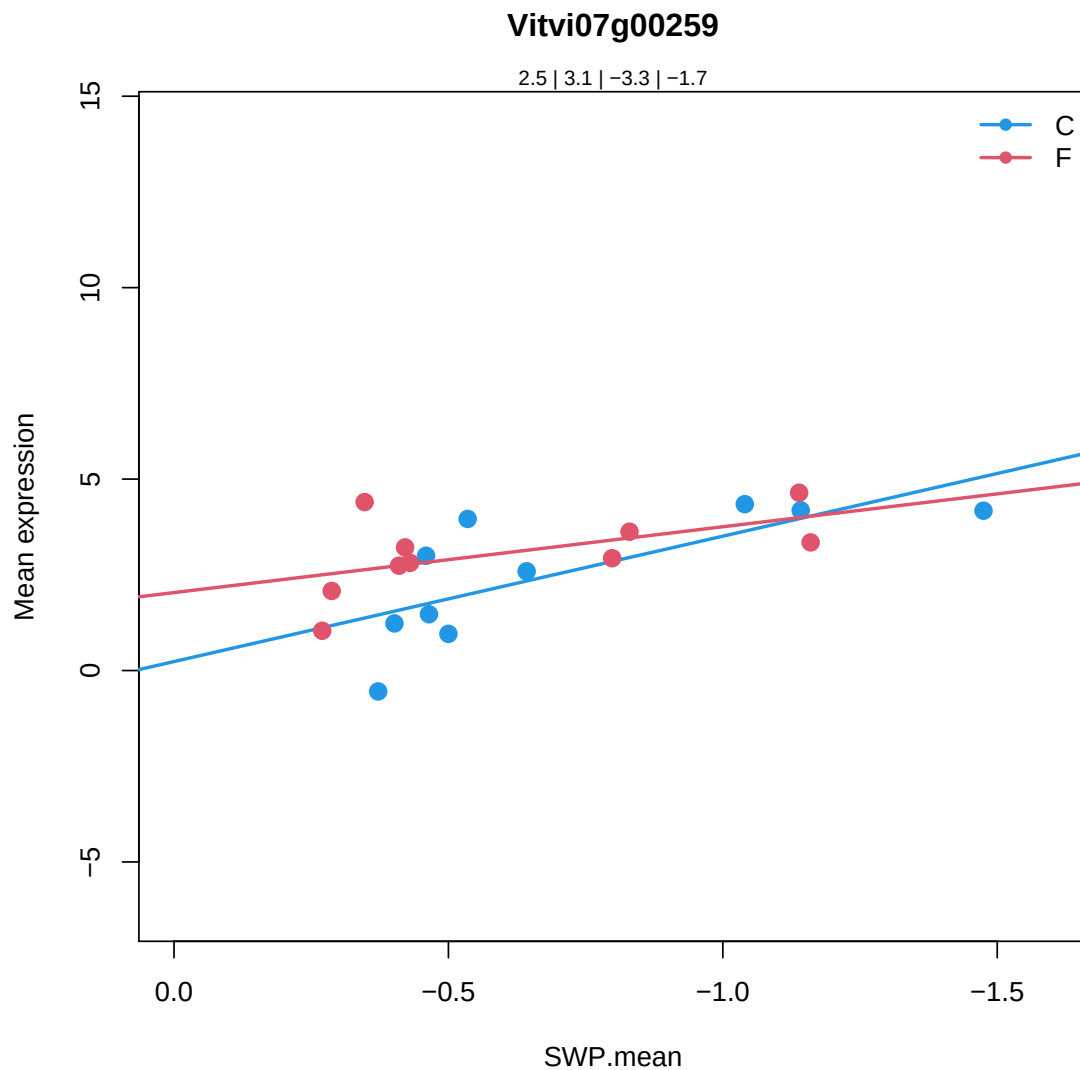
Thioredoxin superfamily protein |

Chr1:698207-698515 REVERSE LENGTH=102 |

201606

Coefficients for Vitvi07g00259.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.536237	3.855964e-08	***	4.624851e-08	***
SlopeC	-3.274596	0.0008950917	***	0.1188465	
MeanF-MeanC	0.5467021	0.2192751		0.5690773	
SlopeF-SlopeC	1.555472	0.2321364		0.9999488	



8.1.560 Vitvi13g02014: Type1.0 *

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

Vitvi13g02014

20.2.1

stress.abiotic.heat

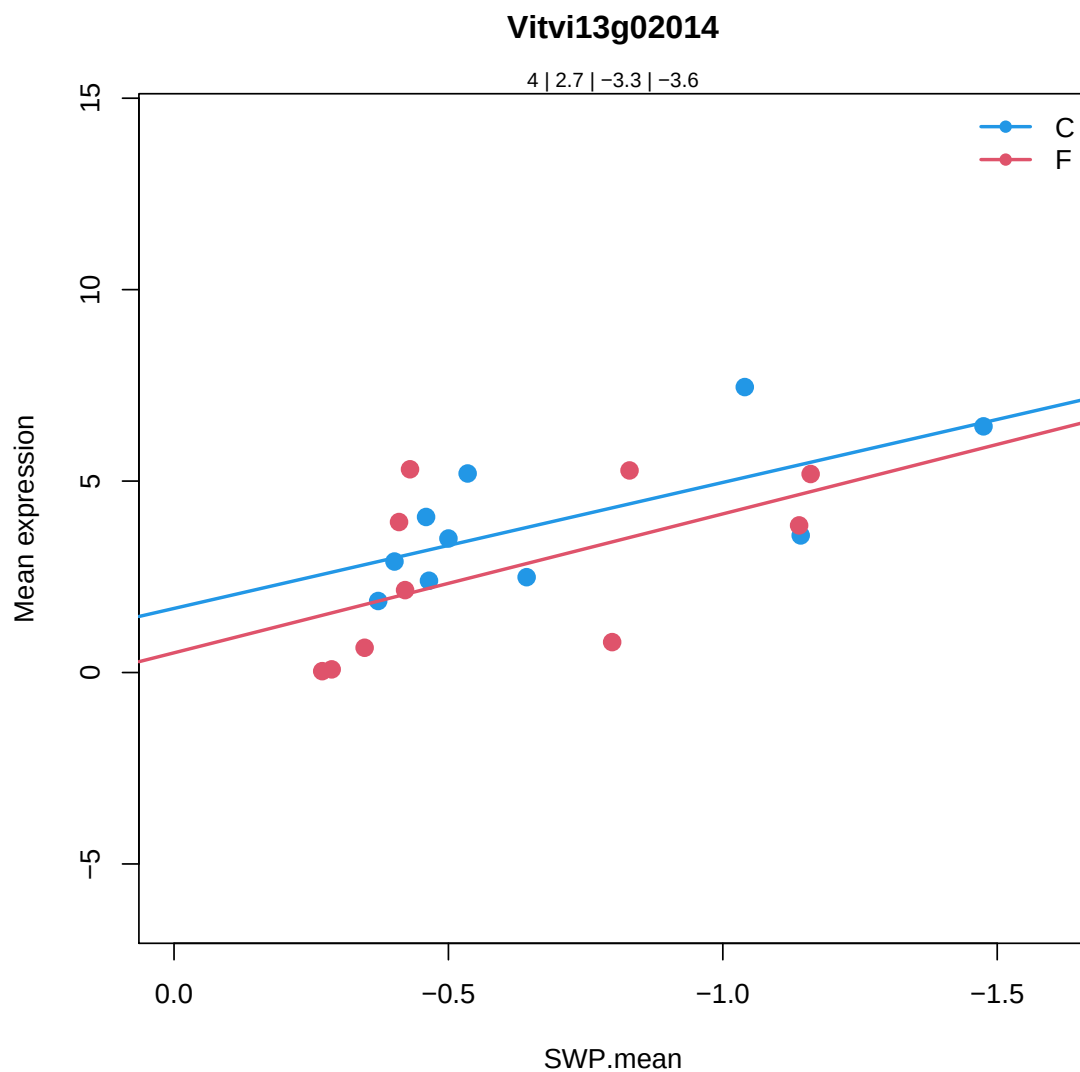
heat shock protein 18.2 |

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	



8.1.561 Vitvi18g02468: Type1.0 *

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

Vitvi18g02468

30.3

signalling.calcium

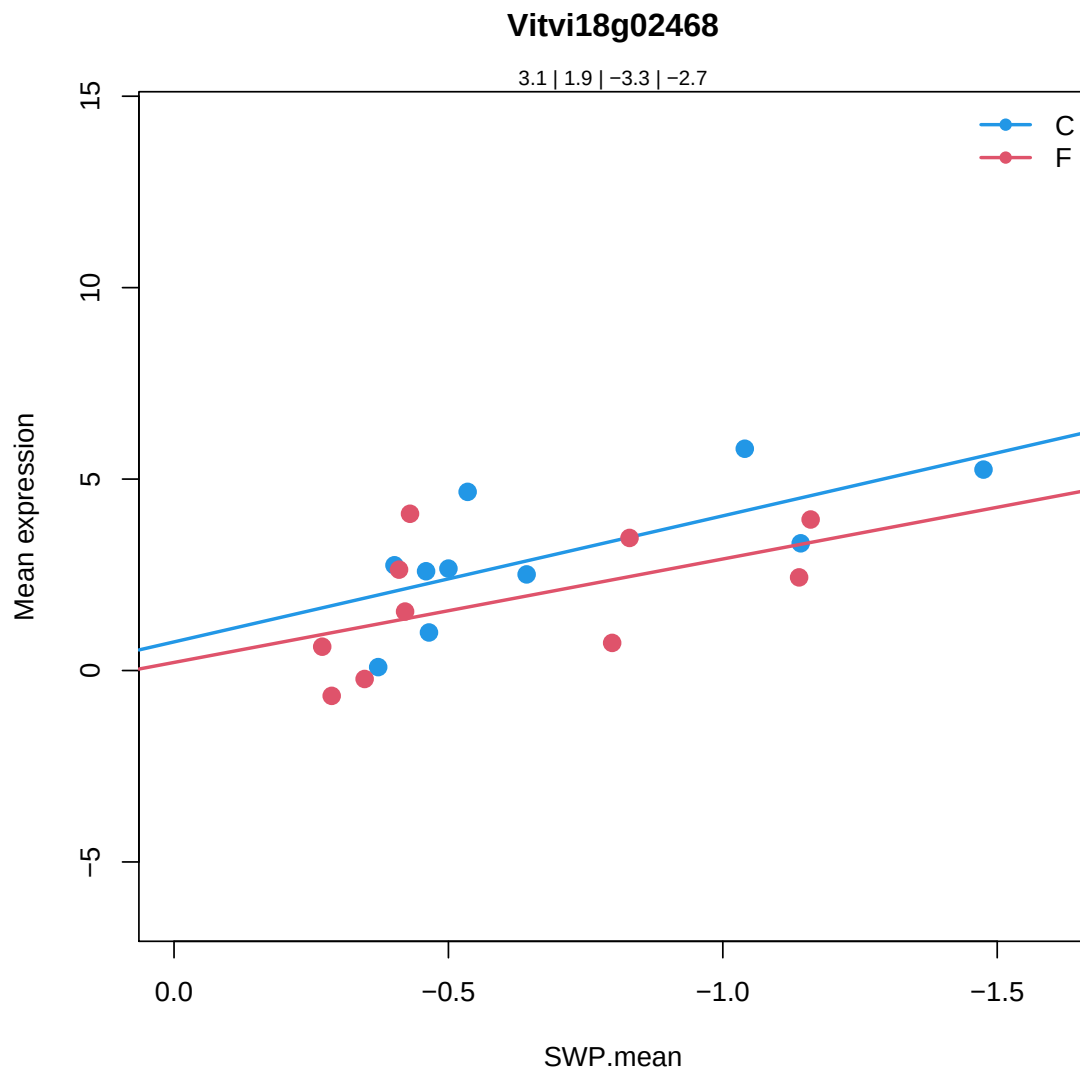
calmodulin like 37 |

Chr5:16942758-16943315 REVERSE LENGTH=185 |

201606

Coefficients for Vitvi18g02468.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.062446	1.604581e-07	***	1.892812e-07	***
SlopeC	-3.292034	0.007741766	**	0.280858	
MeanF-MeanC	-1.205656	0.04612069	*	0.2274849	
SlopeF-SlopeC	0.5903653	0.7267852		0.9999488	



8.1.562 Vitvi04g01792: Type1.0 *

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

Vitvi04g01792

29.2.2.3.3

protein.synthesis.ribosome biogenesis.pre-rRNA processing and modifica

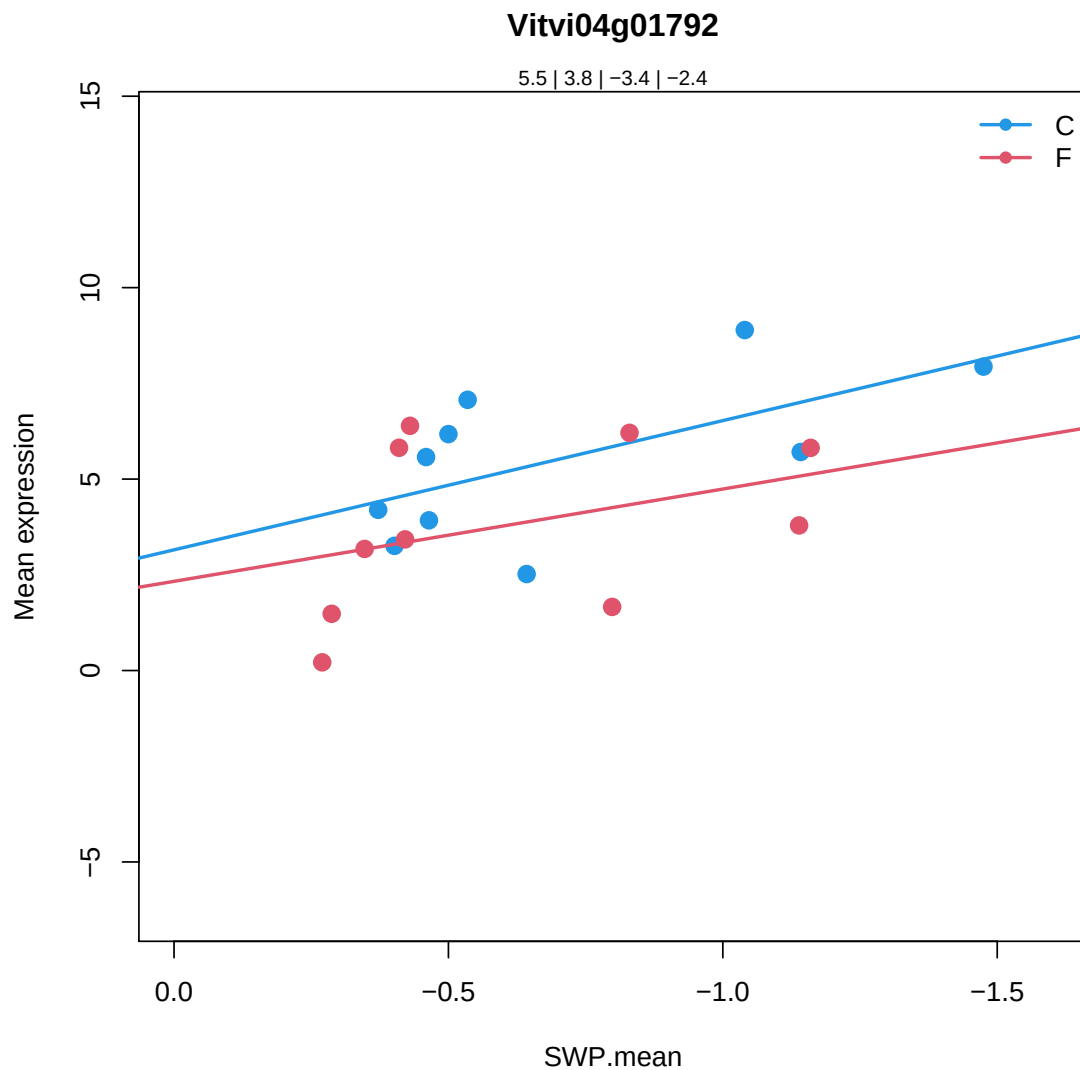
17.6 kDa class II heat shock protein |

Chr5:3882409-3882876 REVERSE LENGTH=155 |

201606

Coefficients for Vitvi04g01792.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.525374	1.099806e-09	***	1.385049e-09	***
SlopeC	-3.37508	0.03583257	*	0.4530652	
MeanF-MeanC	-1.727532	0.03469007	*	0.1865724	
SlopeF-SlopeC	0.9644771	0.6714896		0.9999488	



8.1.563 Vitvi02g00436: Type1.0 *

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

Vitvi02g00436

1.2.6

PS.photorespiration.hydroxypyruvate reductase

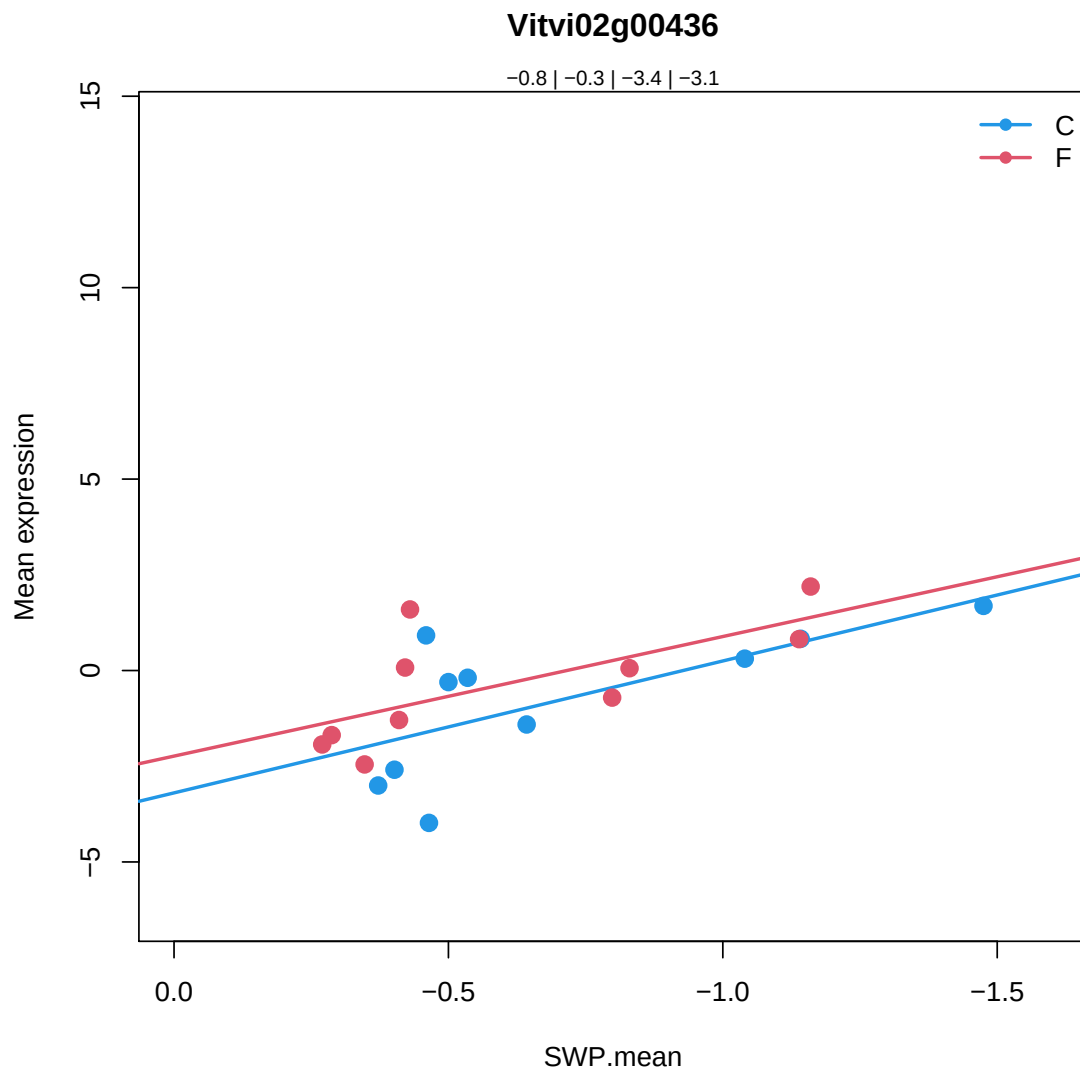
D-isomer specific 2-hydroxyacid dehydrogenase family protein |

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	



8.1.564 Vitvi01g00408: Type1.0 *

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

Vitvi01g00408

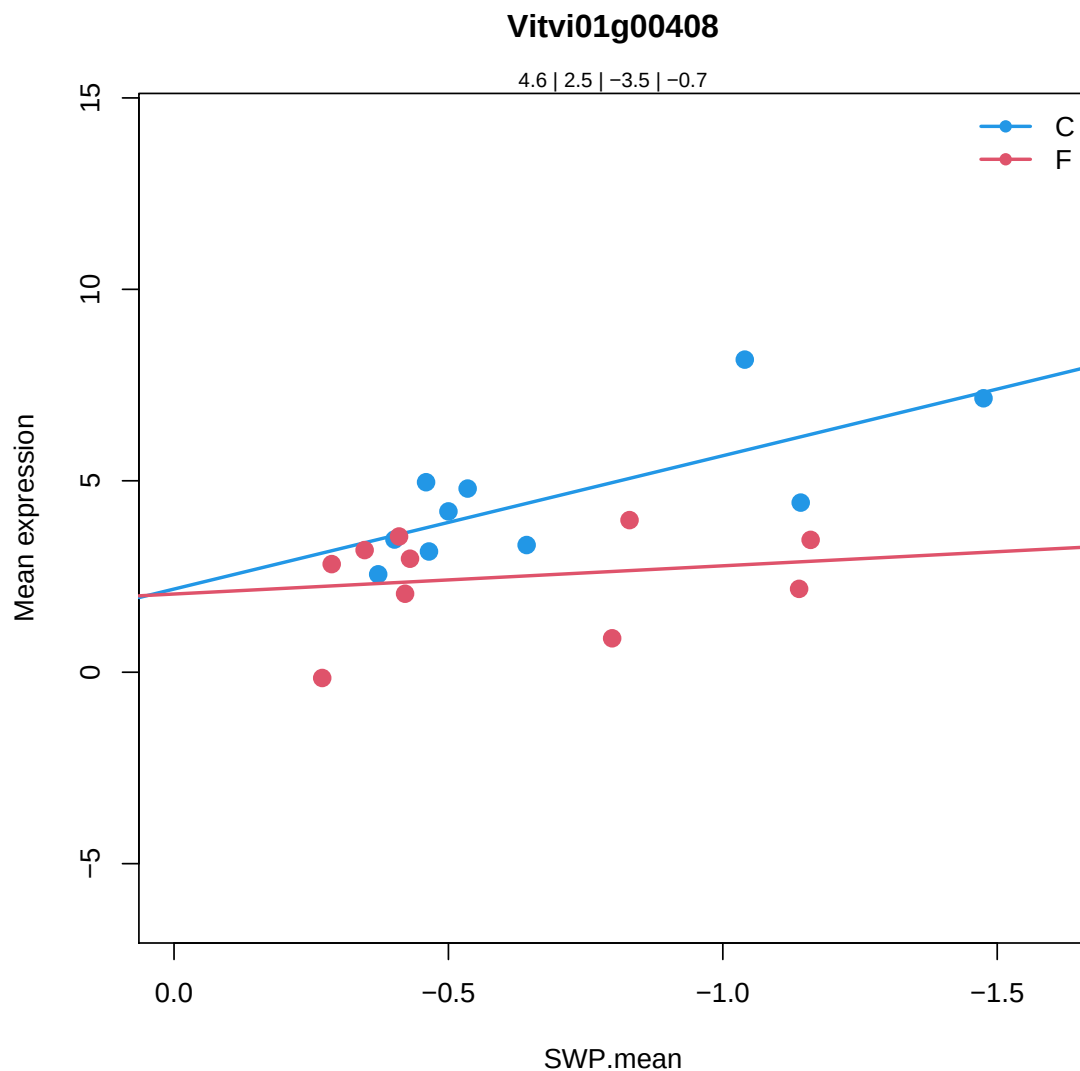
20.2.1

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	



8.1.565 Vitvi08g00853: Type1.0 *

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

Vitvi08g00853

11.6

lipid metabolism.lipid transfer proteins etc

lipid transfer protein 1 |

Chr2:16130418-16130893 FORWARD LENGTH=118 |

201606

Vitvi08g00853

26.21

misc.protease inhibitor/seed storage/lipid transfer protein (LTP) fami

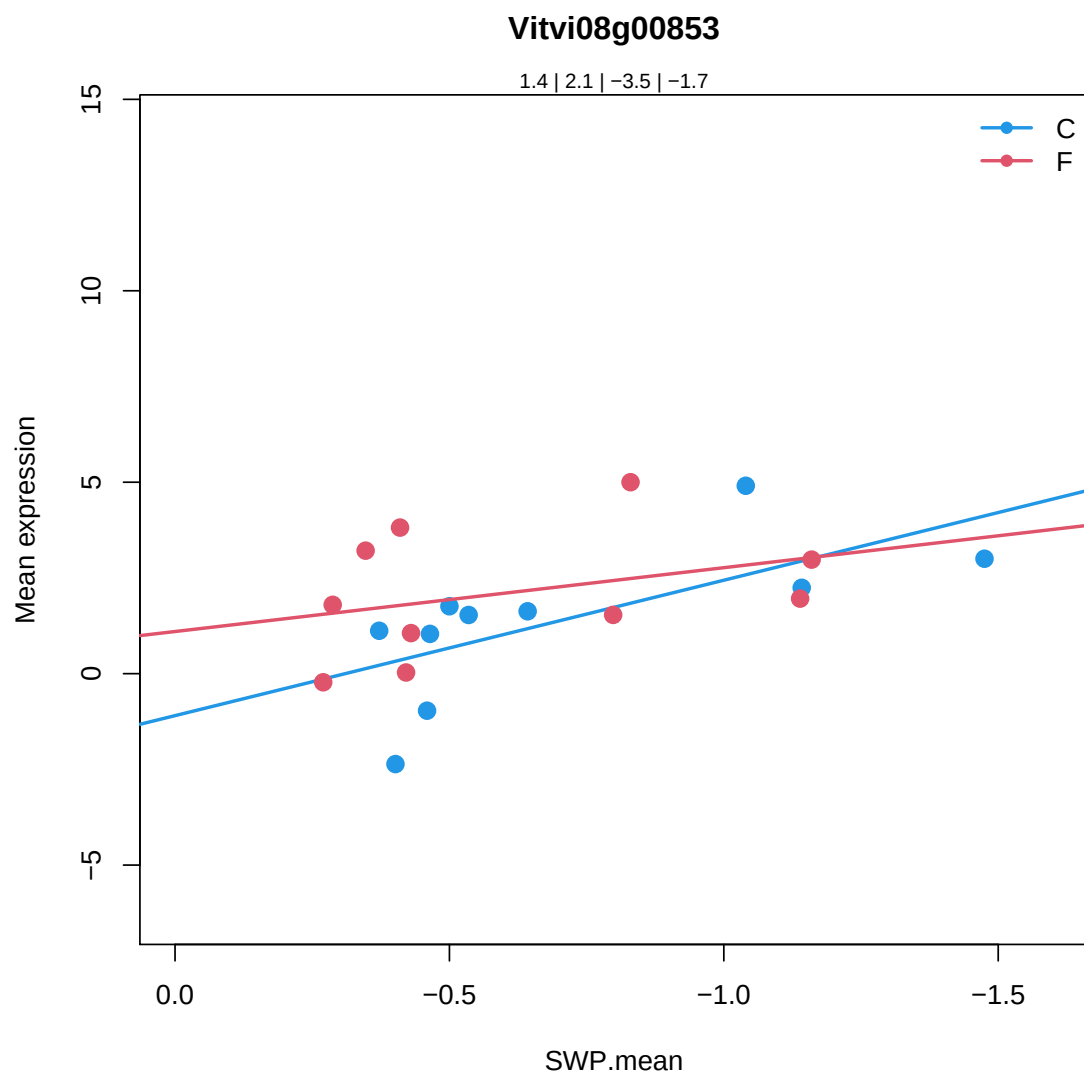
lipid transfer protein 1 |

Chr2:16130418-16130893 FORWARD LENGTH=118 |

201606

Coefficients for Vitvi08g00853.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.390161	0.005062809	**	0.005399337	**
SlopeC	-3.536433	0.009356115	**	0.2940328	
MeanF-MeanC	0.725995	0.2615915		0.6235803	
SlopeF-SlopeC	1.869482	0.3218733		0.9999488	



8.1.566 Vitvi13g00451: Type1.0 *

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

Vitvi13g00451

20.2.1

stress.abiotic.heat

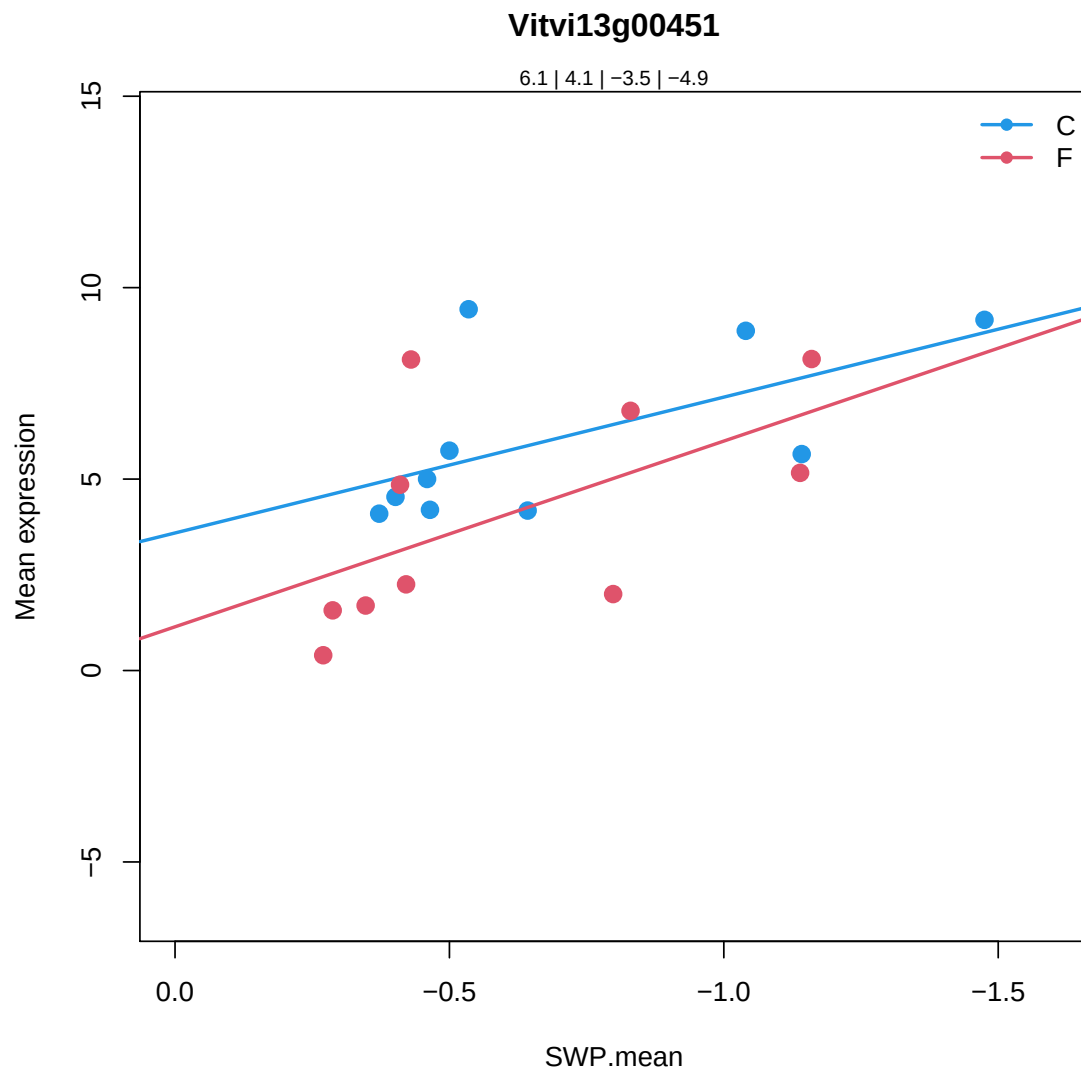
heat shock protein 18.2 |

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	



8.1.567 Vitvi17g00695: Type1.0 *

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

Vitvi17g00695

20.2.1

stress.abiotic.heat

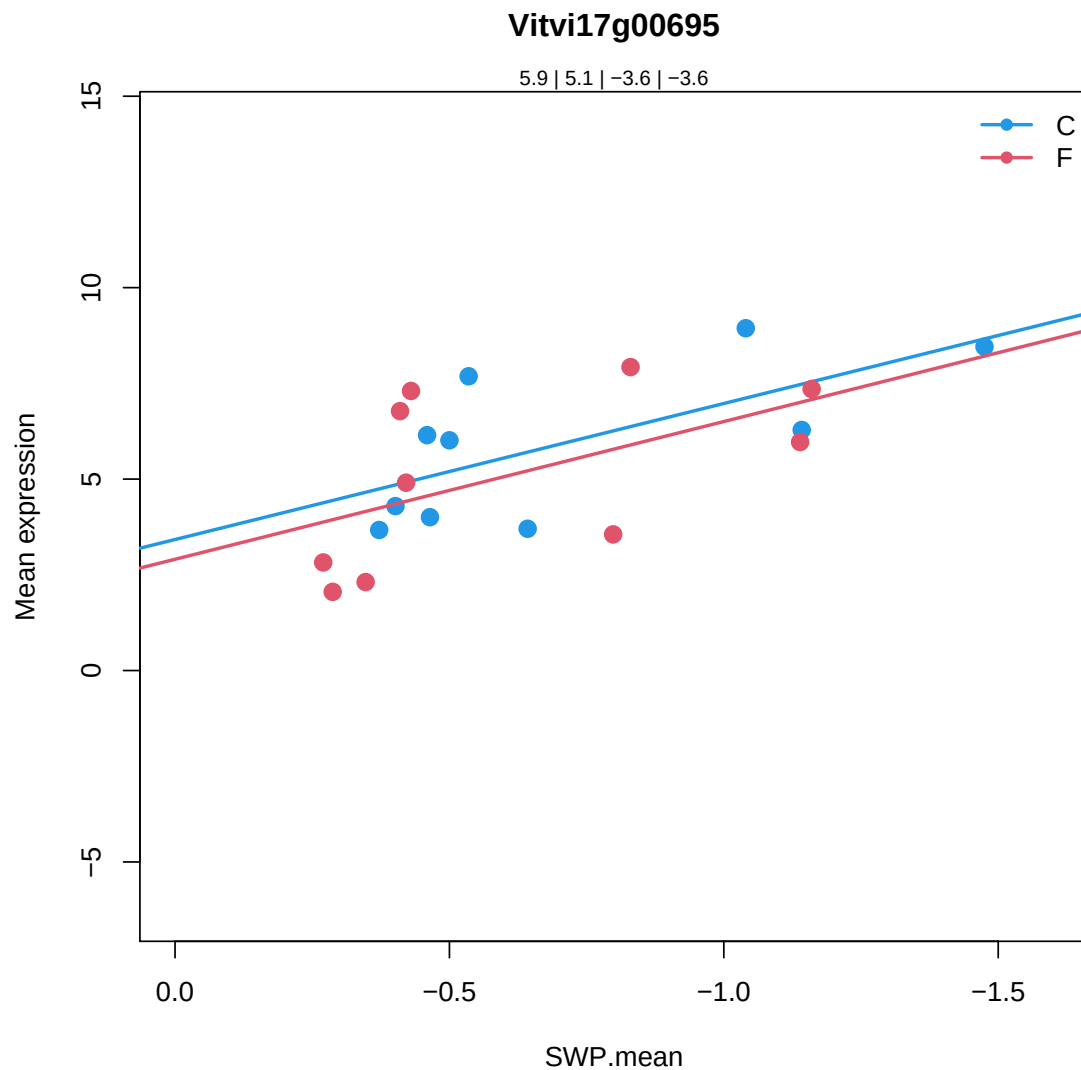
heat shock protein 101 |

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	



8.1.568 Vitvi18g00268: Type1.0 *

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

Vitvi18g00268

35.2

not assigned.unknown

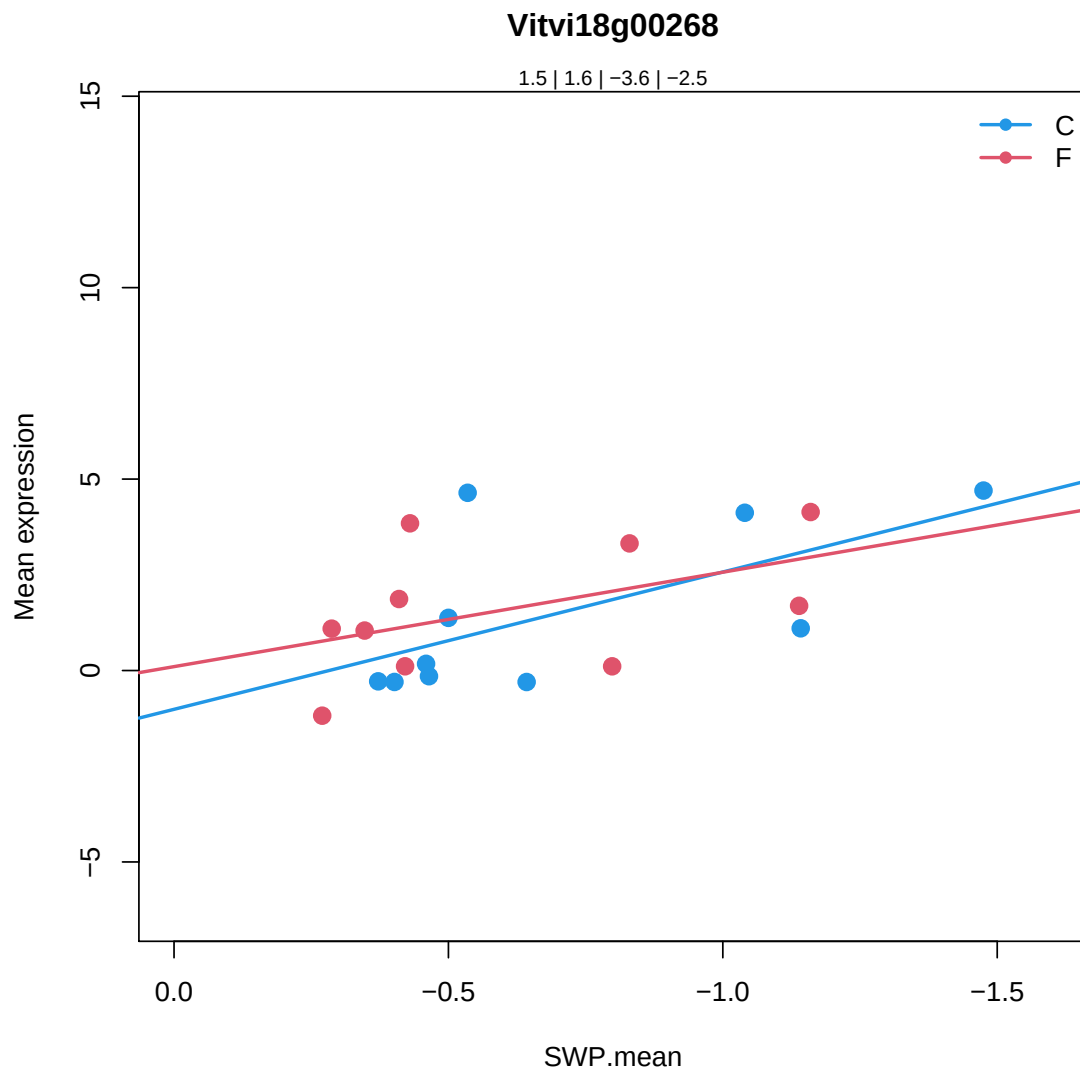
zinc-ribbon domain protein |

Chr1:16847781-16848086 FORWARD LENGTH=101 |

201606

Coefficients for Vitvi18g00268.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.508355	0.003939077	**	0.004211814	**
SlopeC	-3.586619	0.01157776	*	0.318473	
MeanF-MeanC	0.09544746	0.8864347		0.9704088	
SlopeF-SlopeC	1.121175	0.5680897		0.9999488	



8.1.569 Vitvi19g00514: Type1.0 *

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

Vitvi19g00514

26.28

misc.GDSL-motif lipase

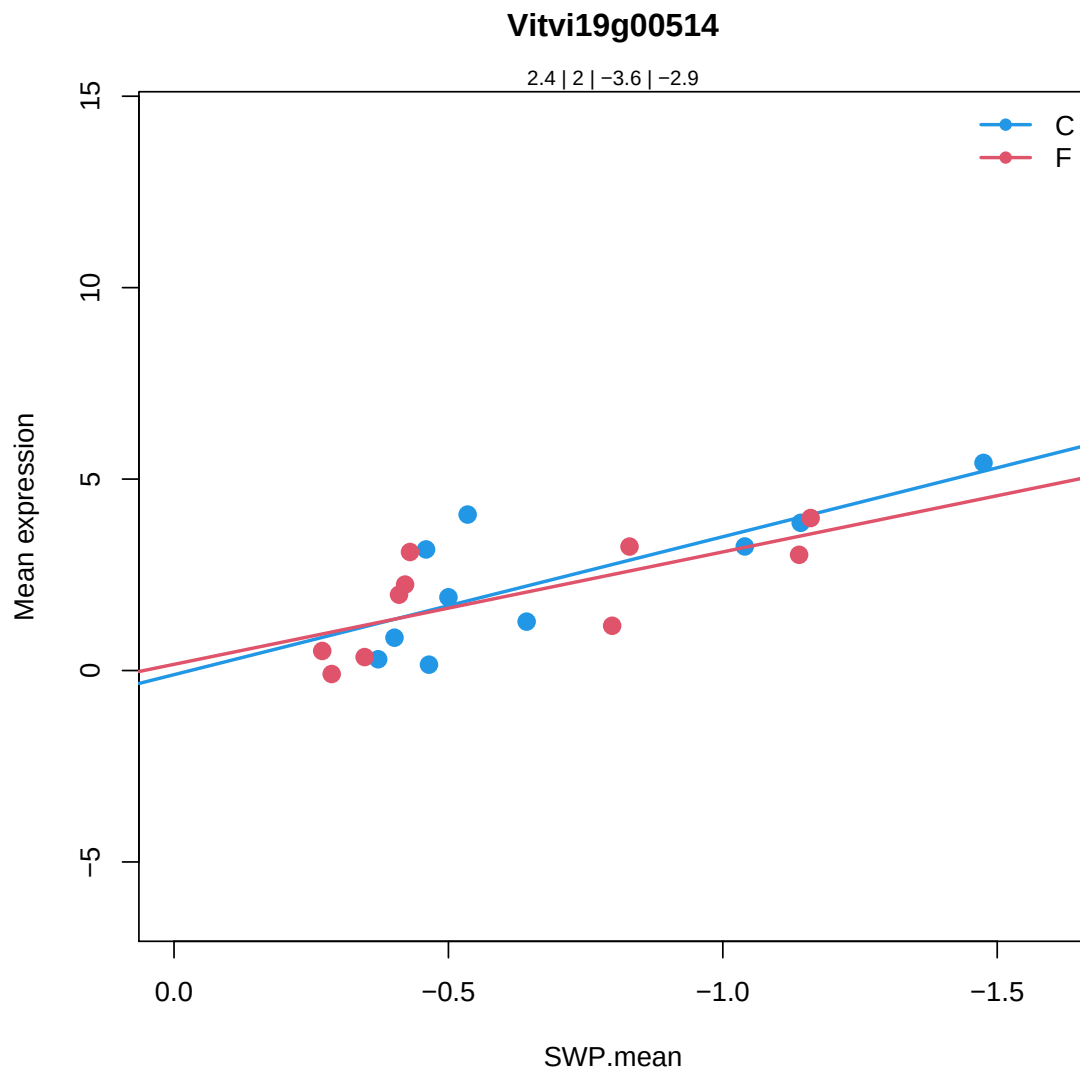
GDSL-like Lipase/Acylhydrolase superfamily protein |

Chr5:22337745-22339741 FORWARD LENGTH=376 |

201606

Coefficients for Vitvi19g00514.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.424878	1.617823e-07	***	1.90799e-07	***
SlopeC	-3.602676	0.0005453082	***	0.1005065	
MeanF-MeanC	-0.4746797	0.3044957		0.6685796	
SlopeF-SlopeC	0.6663077	0.619161		0.9999488	



8.1.570 Vitvi02g00374: Type1.0 *

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

Vitvi02g00374

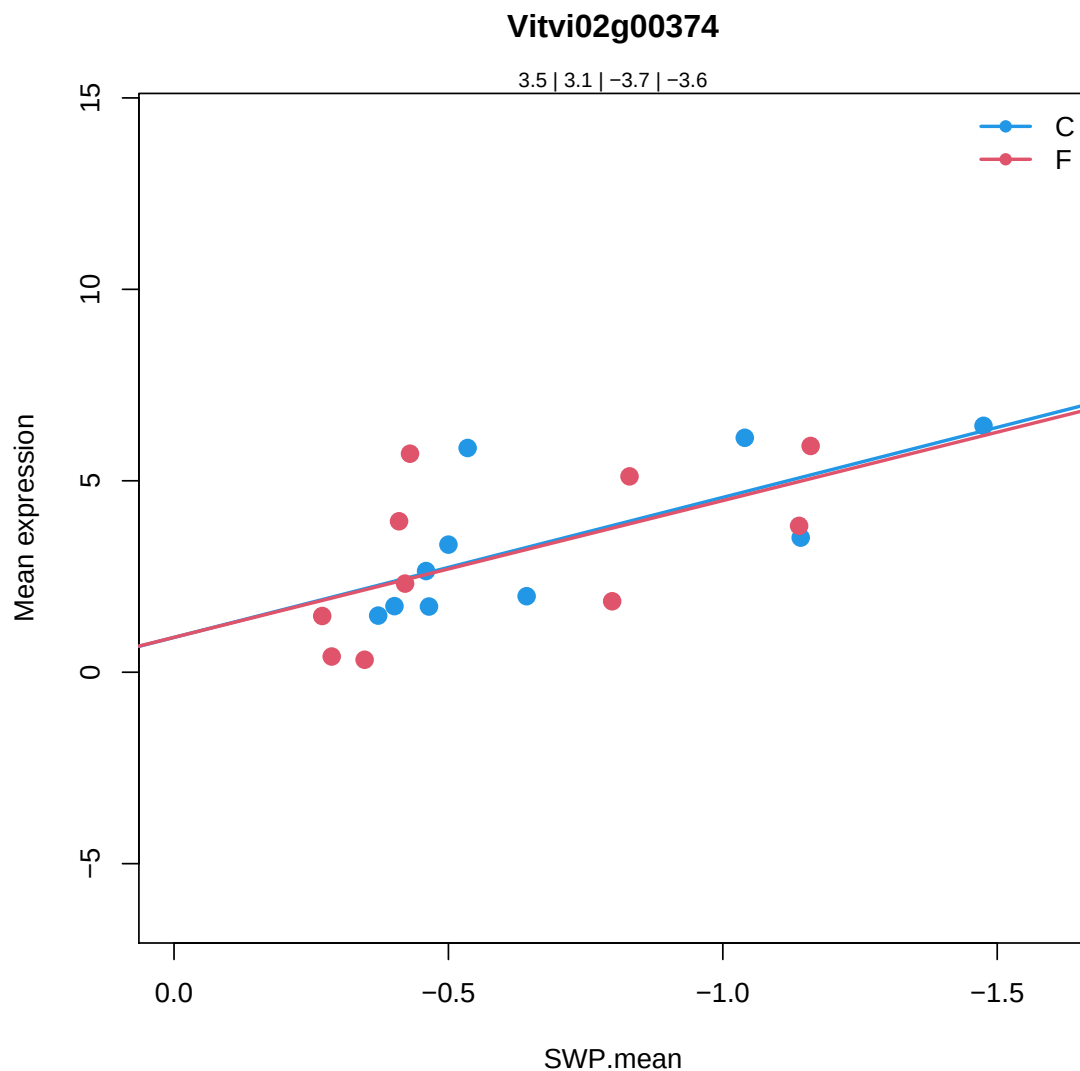
29.5.11

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	



8.1.571 Vitvi18g01510: Type1.0 *

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

Vitvi18g01510

20.2.1

stress.abiotic.heat

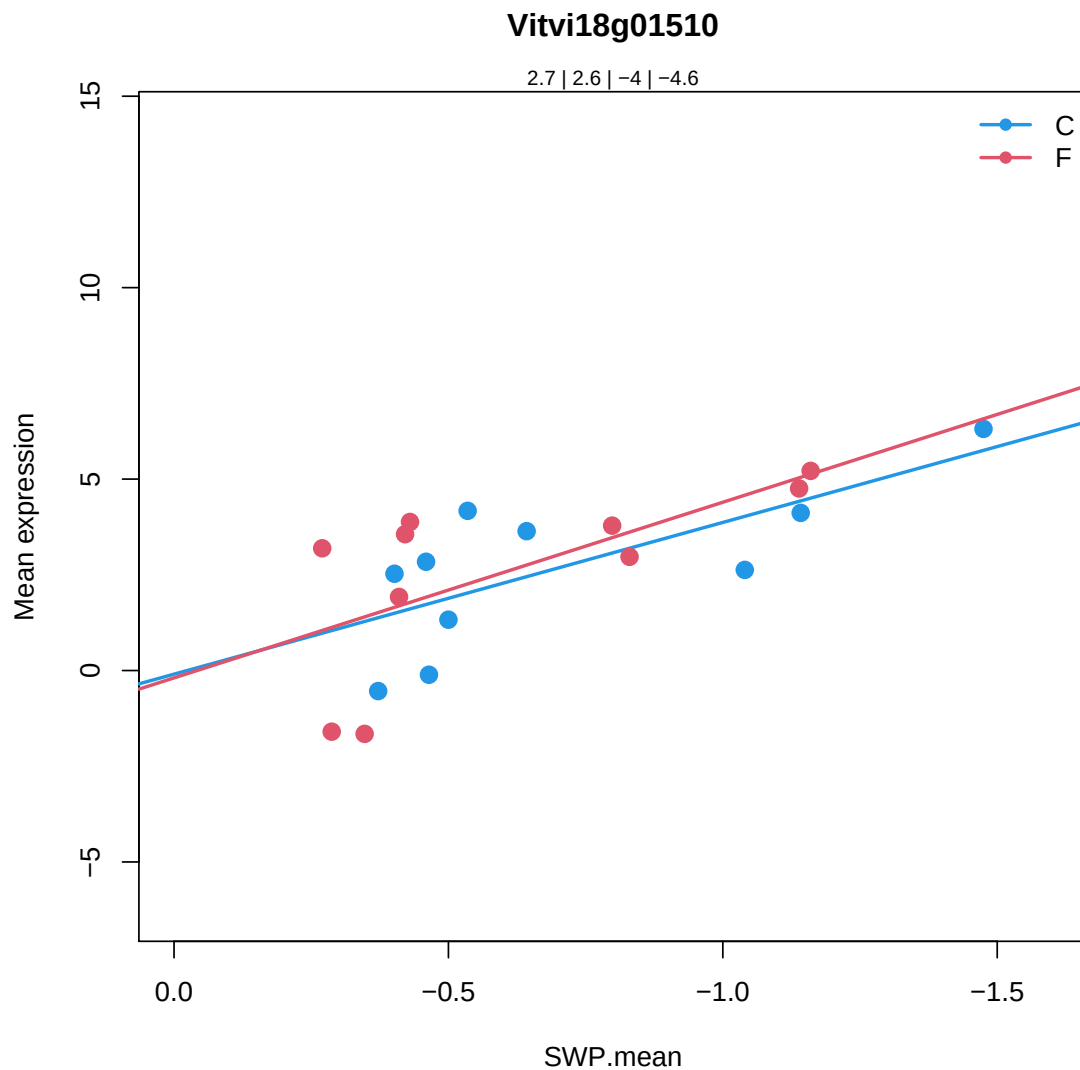
HSP20-like chaperones superfamily protein |

Chr1:19980510-19980983 FORWARD LENGTH=157 |

201606

Coefficients for Vitvi18g01510.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.691284	1.303921e-05	***	1.468259e-05	***
SlopeC	-3.963027	0.007114891	**	0.2775469	
MeanF-MeanC	-0.0887675	0.8969235		0.9730614	
SlopeF-SlopeC	-0.6245041	0.755819		0.9999488	



8.1.572 Vitvi13g00278: Type1.0 *

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

Vitvi13g00278

20.2.1

stress.abiotic.heat

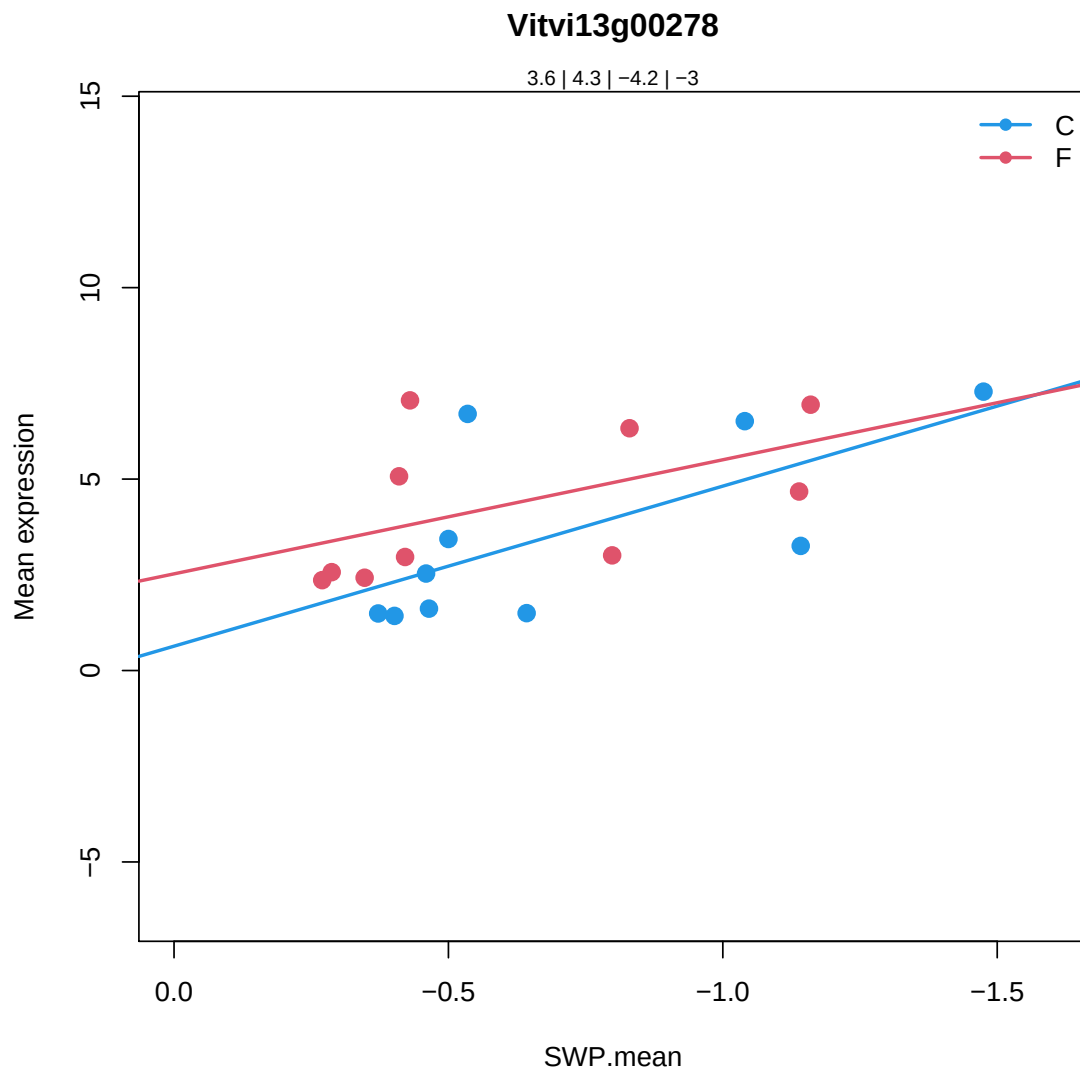
HSP20-like chaperones superfamily protein |

Chr5:14969035-14969448 FORWARD LENGTH=137 |

201606

Coefficients for Vitvi13g00278.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.575152	3.806346e-07	***	4.441951e-07	***
SlopeC	-4.180072	0.006354519	**	0.2661465	
MeanF-MeanC	0.7647119	0.2885058		0.6536088	
SlopeF-SlopeC	1.200427	0.565639		0.9999488	



8.1.573 Vitvi17g01318: Type1.0 *

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

Vitvi17g01318

35.2

not assigned.unknown

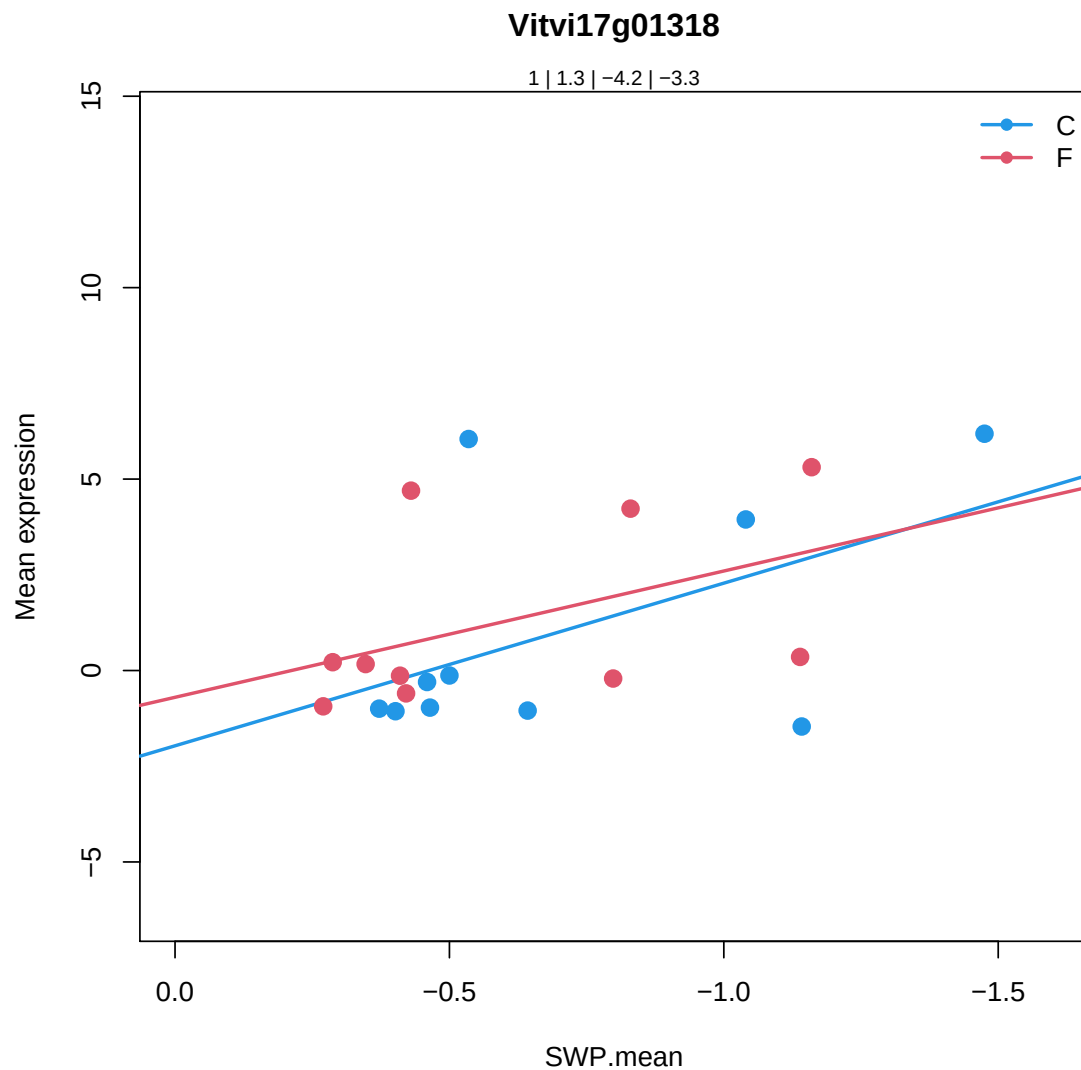
NFU1 iron-sulfur cluster protein |

Chr5:2316064-2316641 FORWARD LENGTH=165 |

201606

Coefficients for Vitvi17g01318.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.020774	0.1596257		0.16416	
SlopeC	-4.248039	0.04059302	*	0.4757357	
MeanF-MeanC	0.2890332	0.773317		0.9351329	
SlopeF-SlopeC	0.9494518	0.7466455		0.9999488	



8.1.574 Vitvi14g00063: Type1.0 *

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

Vitvi14g00063

3.1.1.1

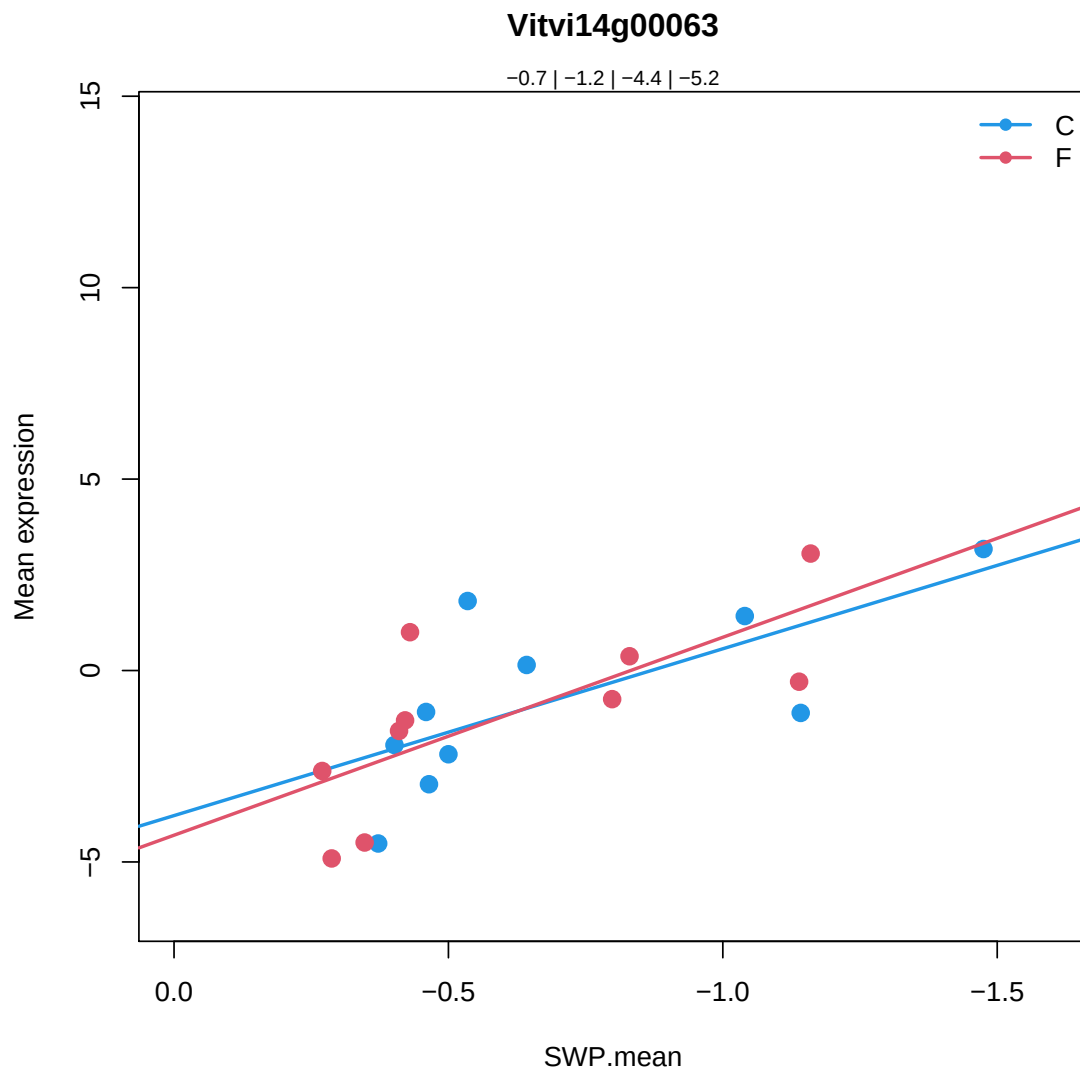
minor CHO metabolism.raffinose family.galactinol synthases.known
galactinol synthase 1 |

Chr2:19369049-19370372 REVERSE LENGTH=344 |

201606

Coefficients for Vitvi14g00063.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.7256696	0.1547876		0.1592704	
SlopeC	-4.356928	0.004398415	**	0.2399107	
MeanF-MeanC	-0.42607	0.5467705		0.8315272	
SlopeF-SlopeC	-0.8128272	0.6938776		0.9999488	



8.1.575 Vitvi17g00152: Type1.0 *

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

Vitvi17g00152

35.2

not assigned.unknown

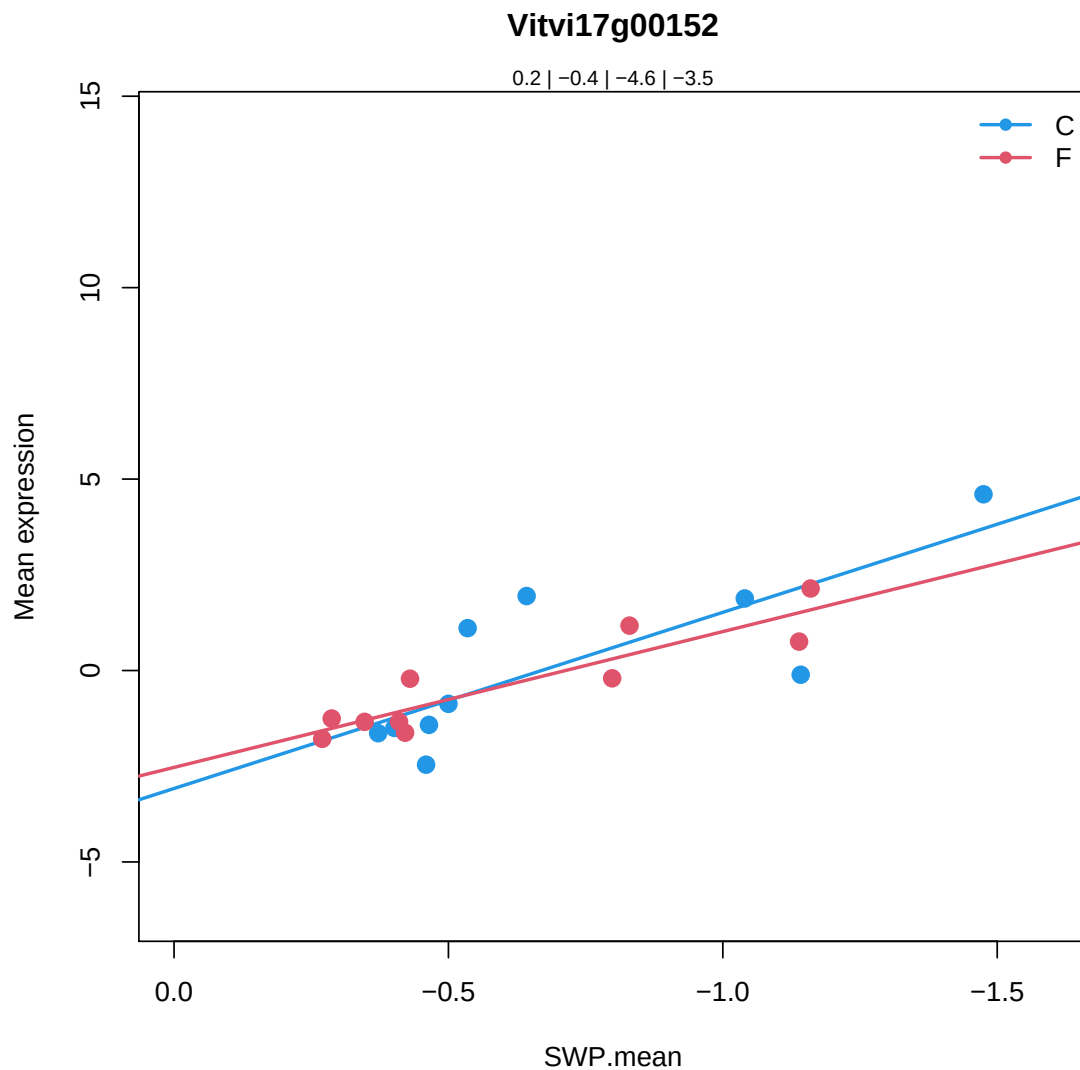
von willebrand factor A domain protein |

Chr5:20505433-20506308 REVERSE LENGTH=291 |

201606

Coefficients for Vitvi17g00152.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1540381	0.6199114		0.6250787	
SlopeC	-4.601115	2.172688e-05	***	0.04768143	*
MeanF-MeanC	-0.5230649	0.2400567		0.5976418	
SlopeF-SlopeC	1.053678	0.4149388		0.9999488	



8.1.576 Vitvi13g00471: Type1.0 *

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

Vitvi13g00471

20.2.1

stress.abiotic.heat

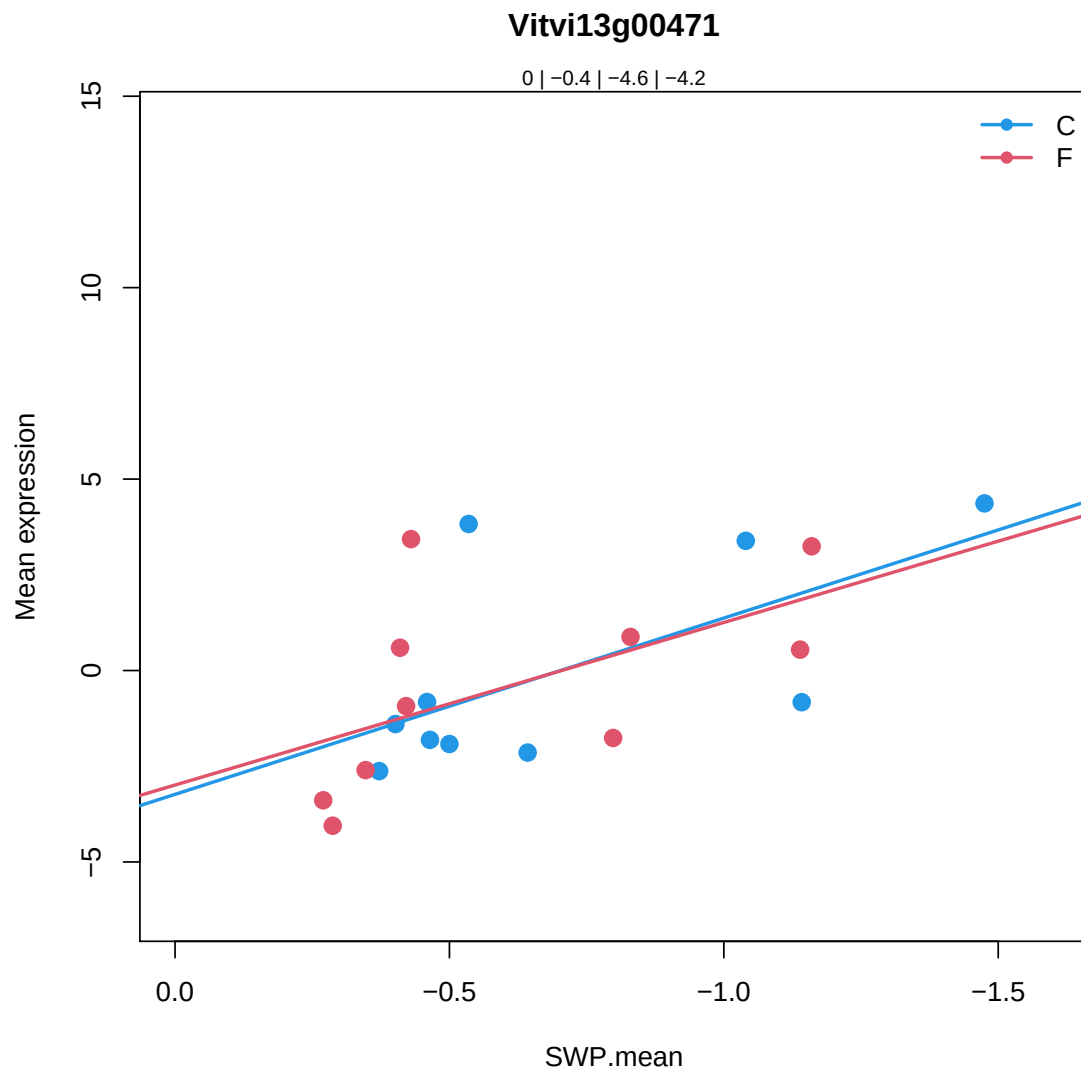
heat shock protein 18.2 |

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	



8.1.577 Vitvi05g00486: Type1.0 *

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

Vitvi05g00486

20.2.1

stress.abiotic.heat

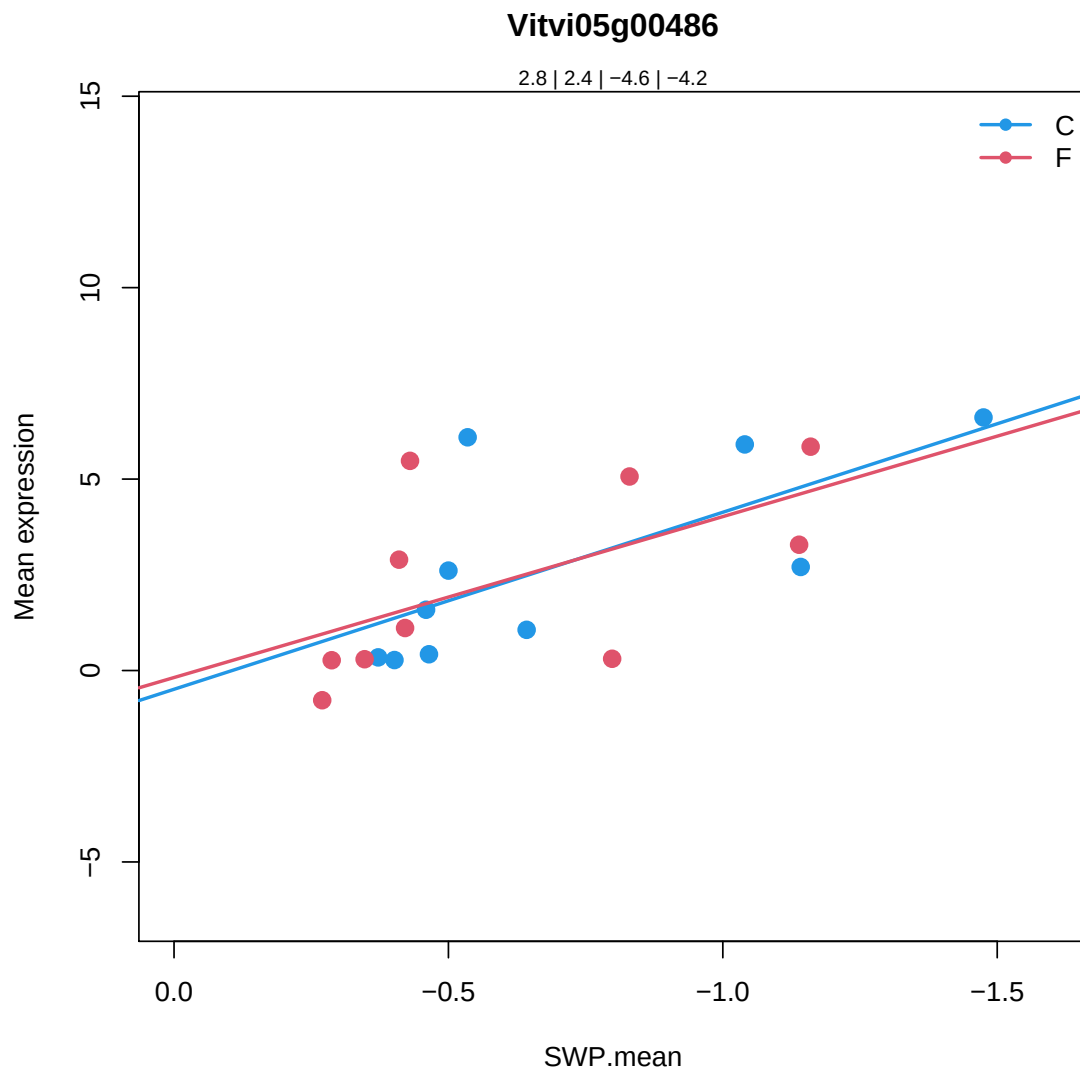
heat-shock protein 70T-2 |

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	



8.1.578 Vitvi13g00490: Type1.0 *

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

Vitvi13g00490

20.2.1

stress.abiotic.heat

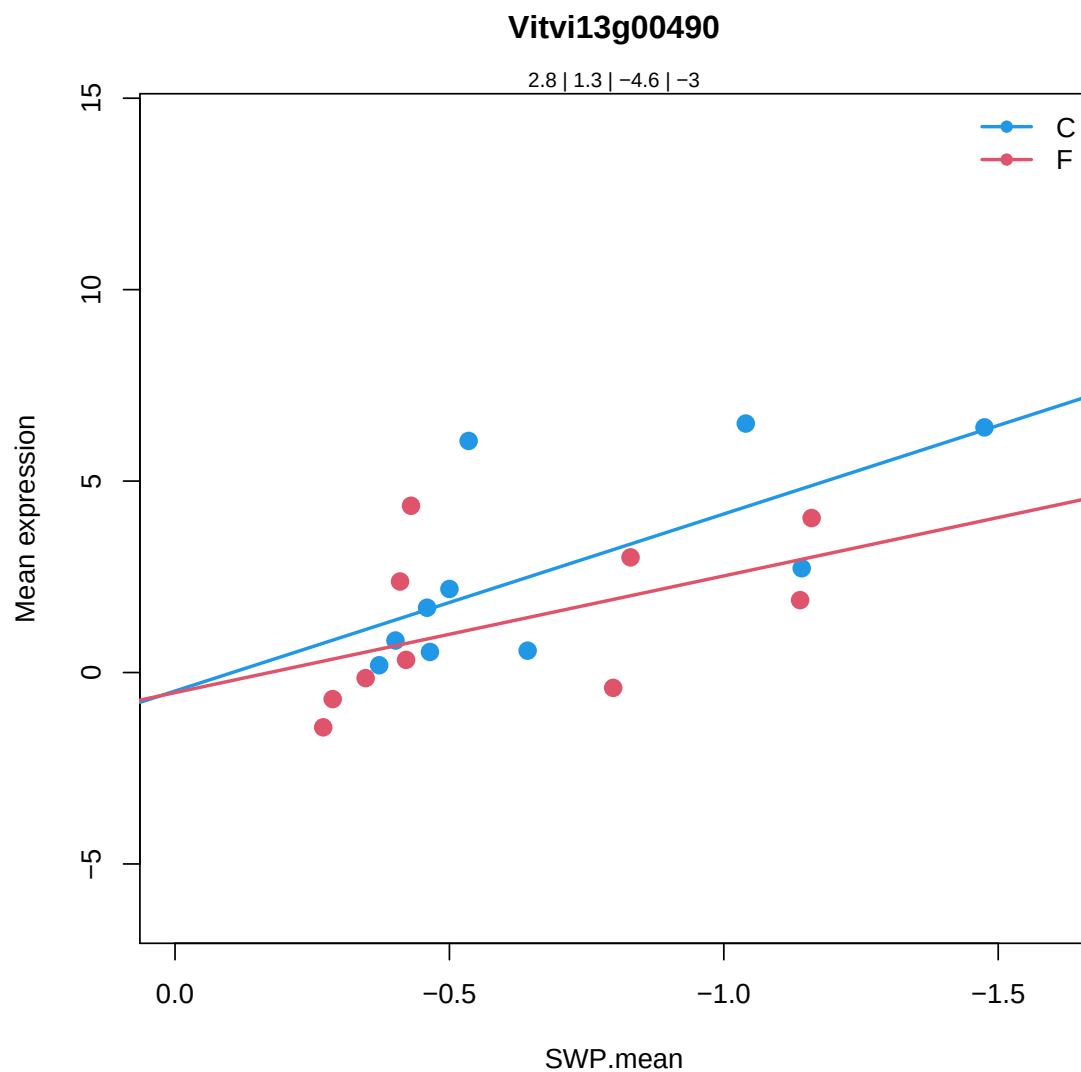
heat shock protein 18.2 |

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	



8.1.579 Vitvi07g00457: Type1.0 *

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

Vitvi07g00457

3.1.1.1

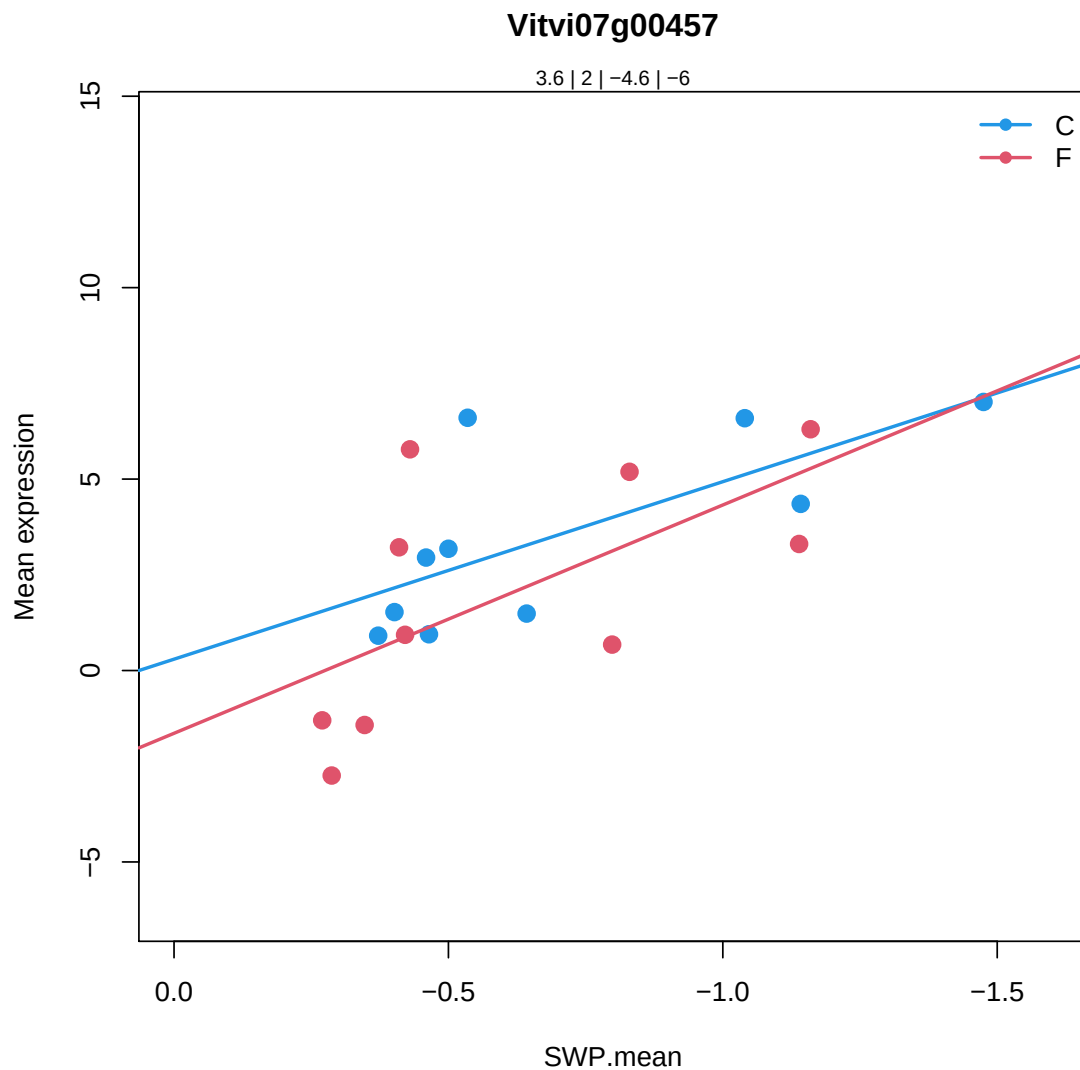
minor CHO metabolism.raffinose family.galactinol synthases.known
galactinol synthase 1 |

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	



8.1.580 Vitvi13g00410: Type1.0 *

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

Vitvi13g00410

35.2

not assigned.unknown

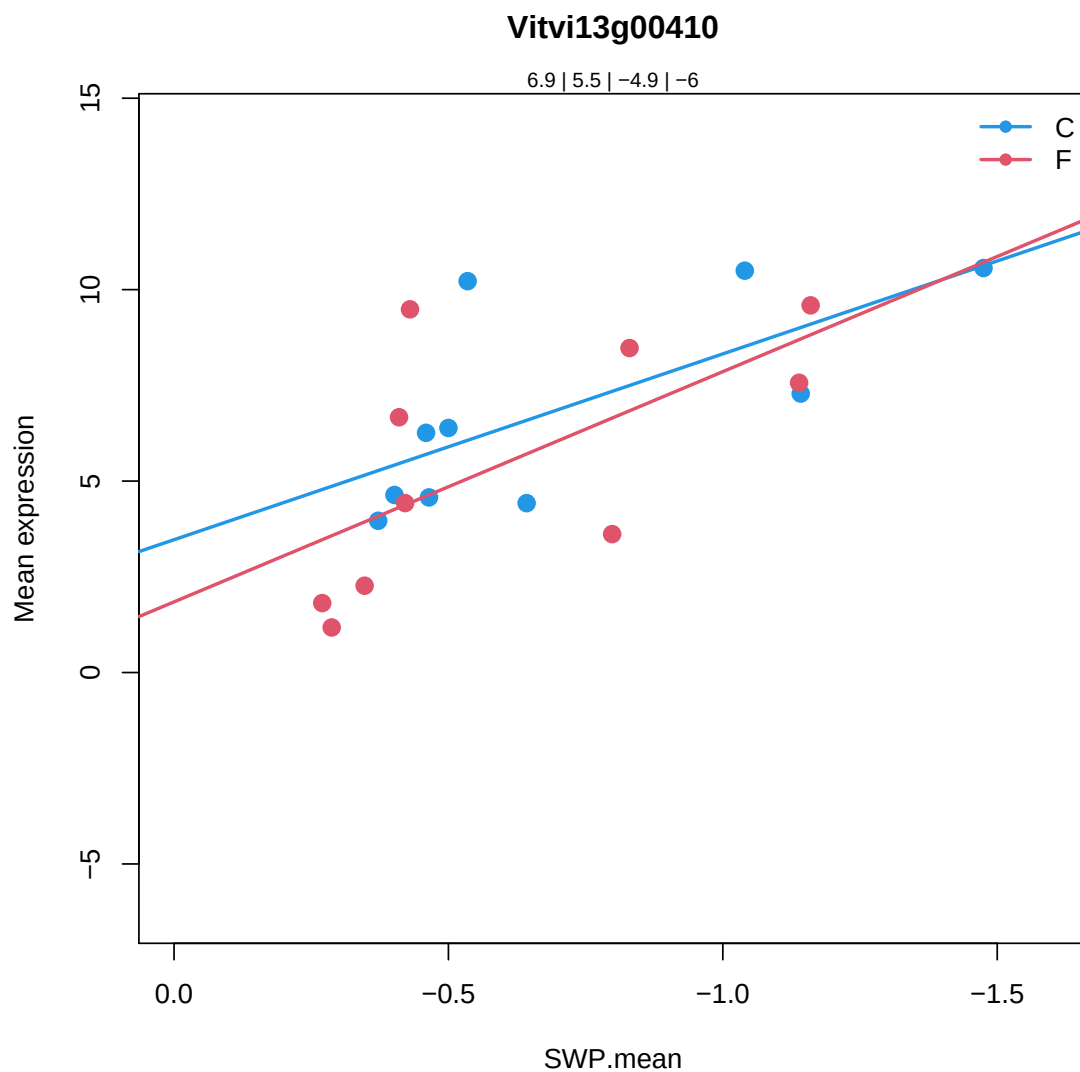
heat shock protein 18.2 |

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	



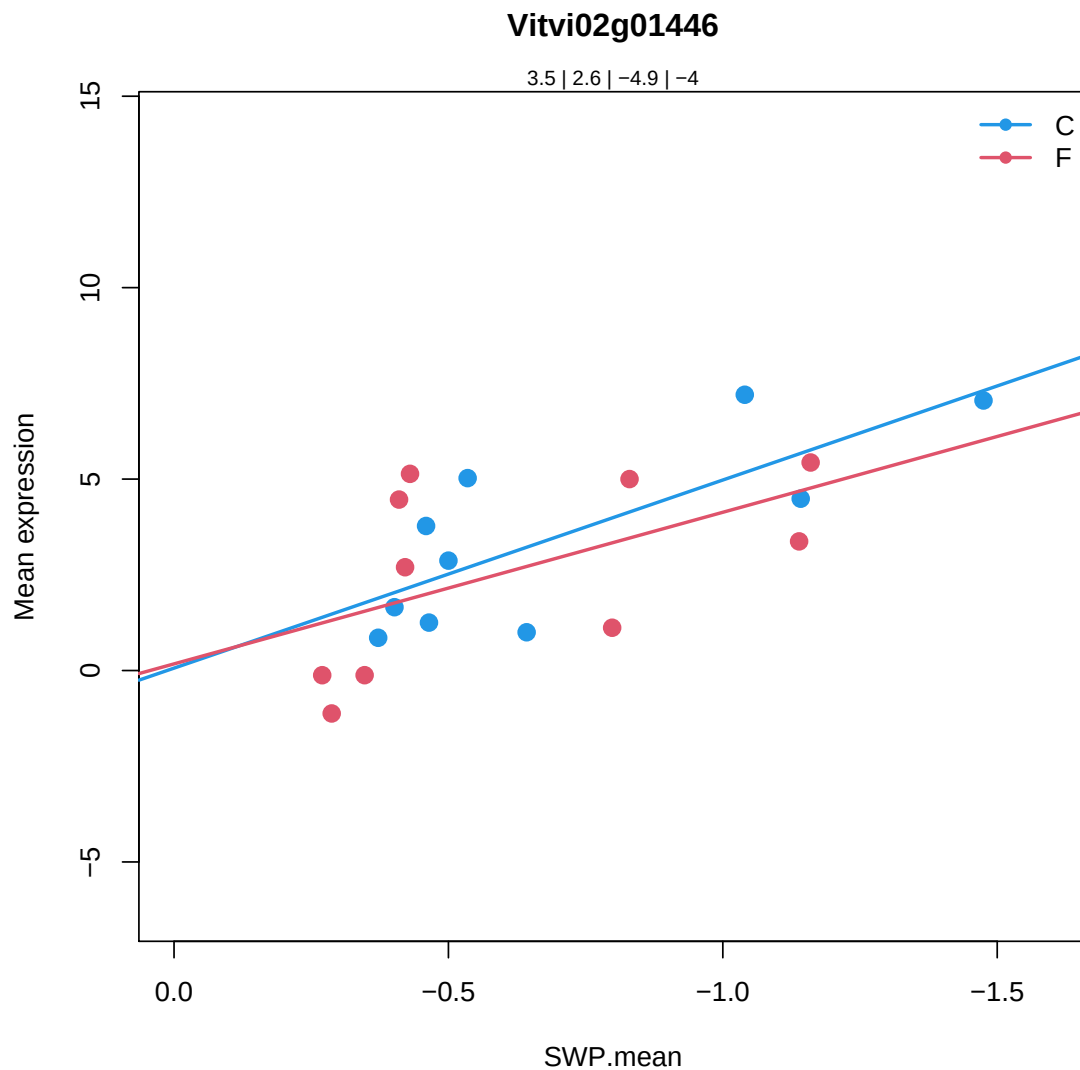
8.1.581 Vitvi02g01446: Type1.0 *

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

```
Vitvi02g01446
20.2.1
stress.abiotic.heat
mitochondrion-localized small heat shock protein 23.6 |
Chr4:12917089-12917858 FORWARD LENGTH=210 |
201606
```

Coefficients for Vitvi02g01446.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.517074	1.324835e-06	***	1.525277e-06	***
SlopeC	-4.913356	0.003142125	**	0.2103859	
MeanF-MeanC	-0.9315877	0.2281248		0.5810625	
SlopeF-SlopeC	0.953823	0.6687367		0.9999488	



8.1.582 Vitvi04g01802: Type1.0 *

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

Vitvi04g01802

20.2.1

stress.abiotic.heat

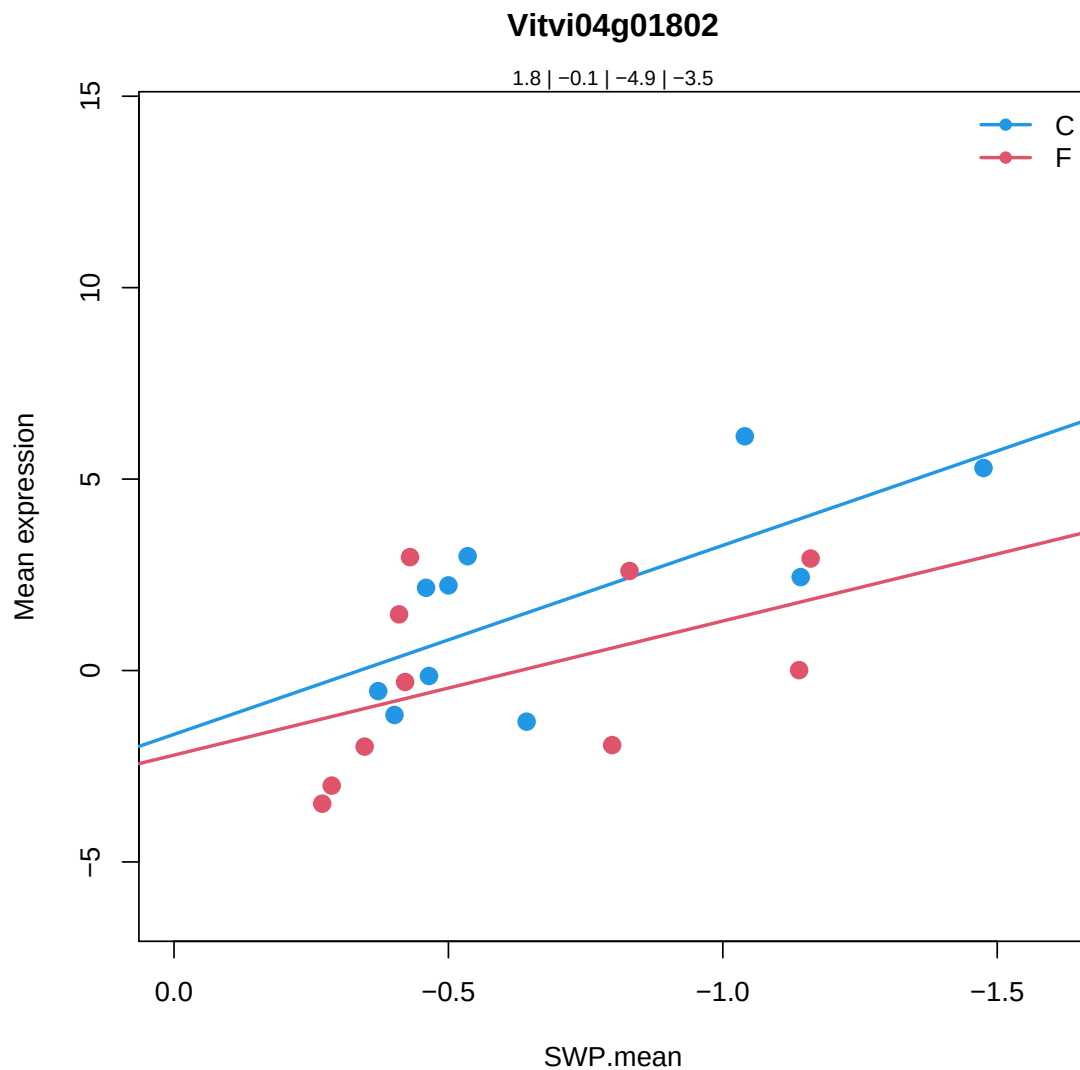
17.6 kDa class II heat shock protein |

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	



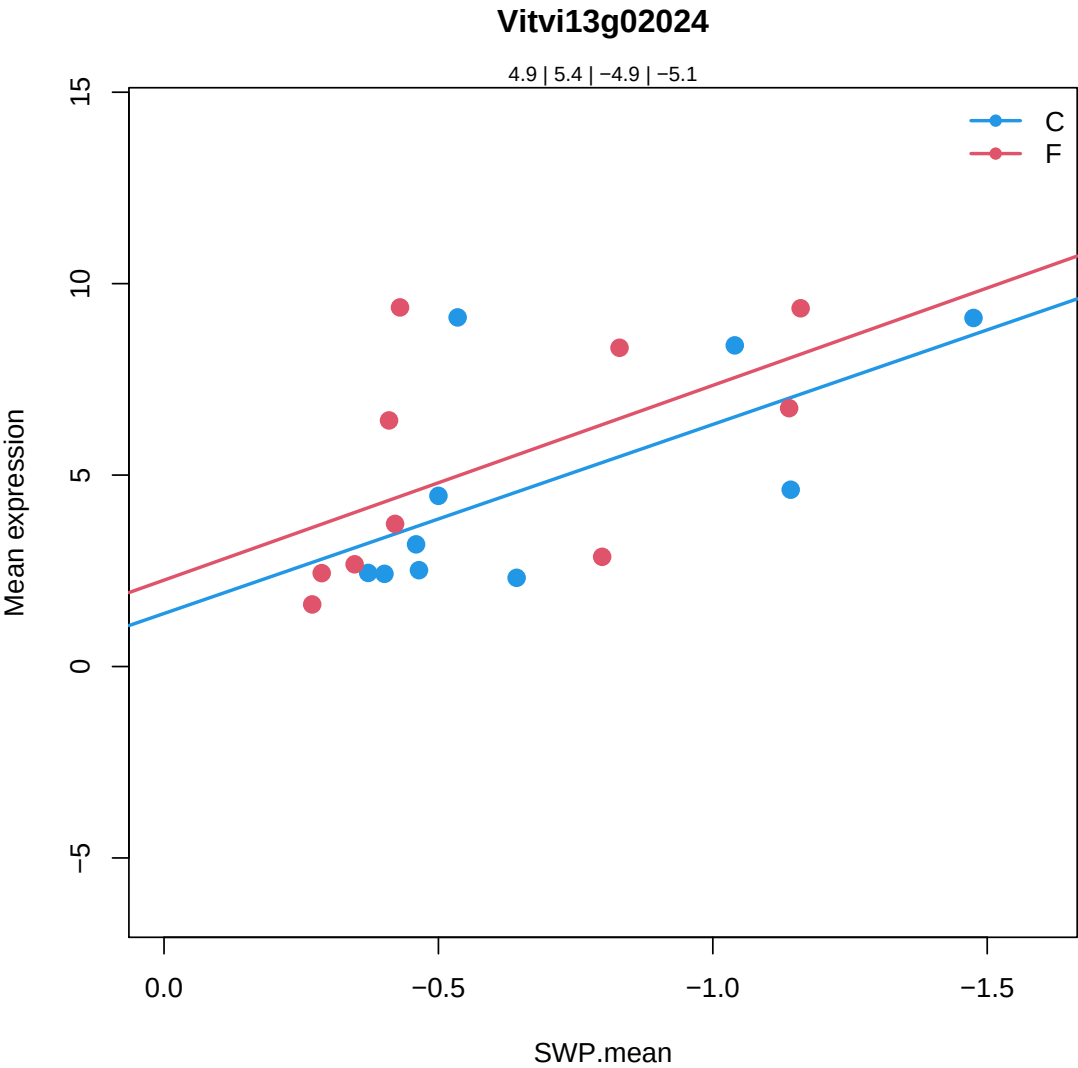
8.1.583 Vitvi13g02024: Type1.0 *

```
> 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	



8.1.584 Vitvi08g00731: Type1.0 *

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

Vitvi08g00731

20.2.1

stress.abiotic.heat

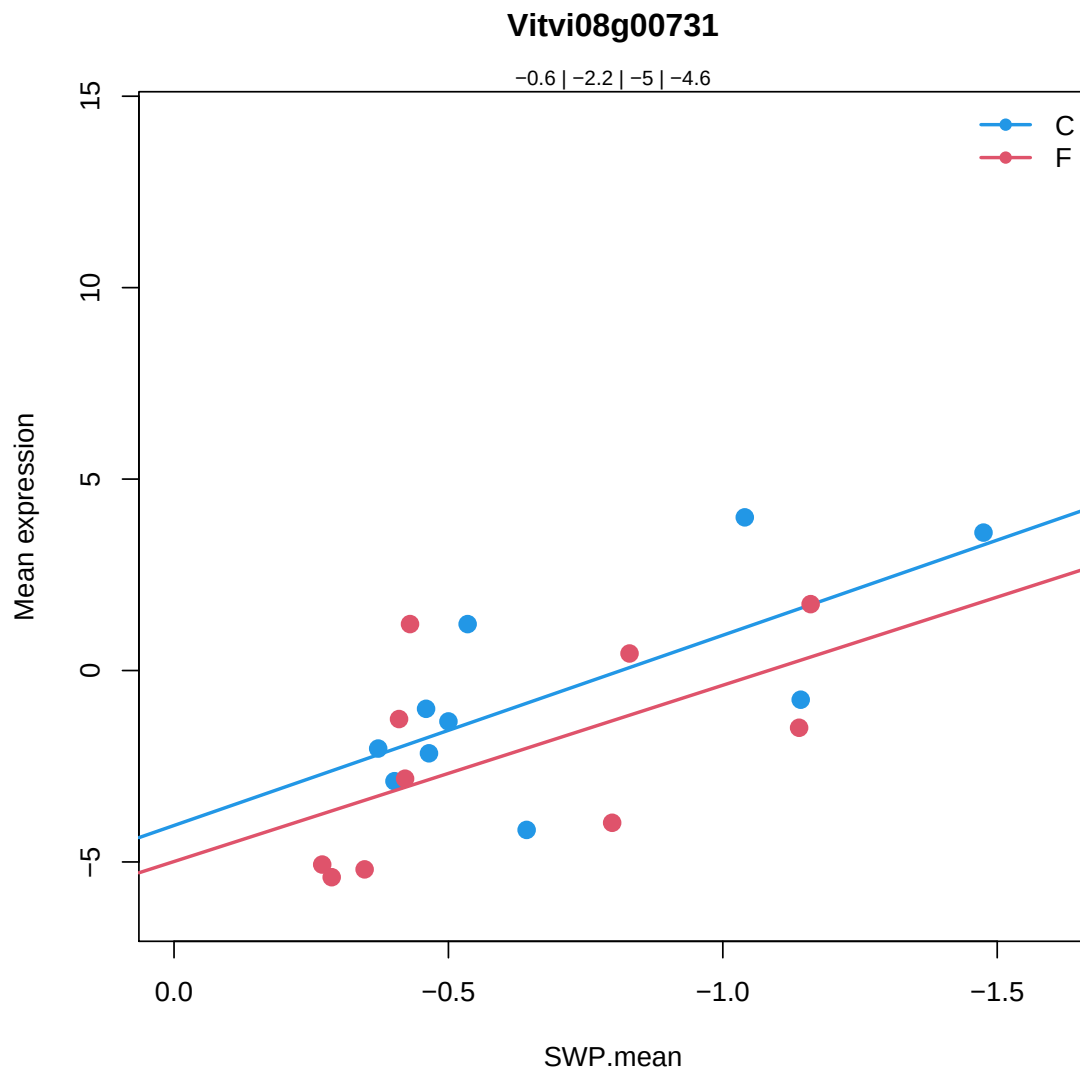
HSP20-like chaperones superfamily protein |

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	



8.1.585 Vitvi01g01512: Type1.0 *

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

Vitvi01g01512

20.2.1

stress.abiotic.heat

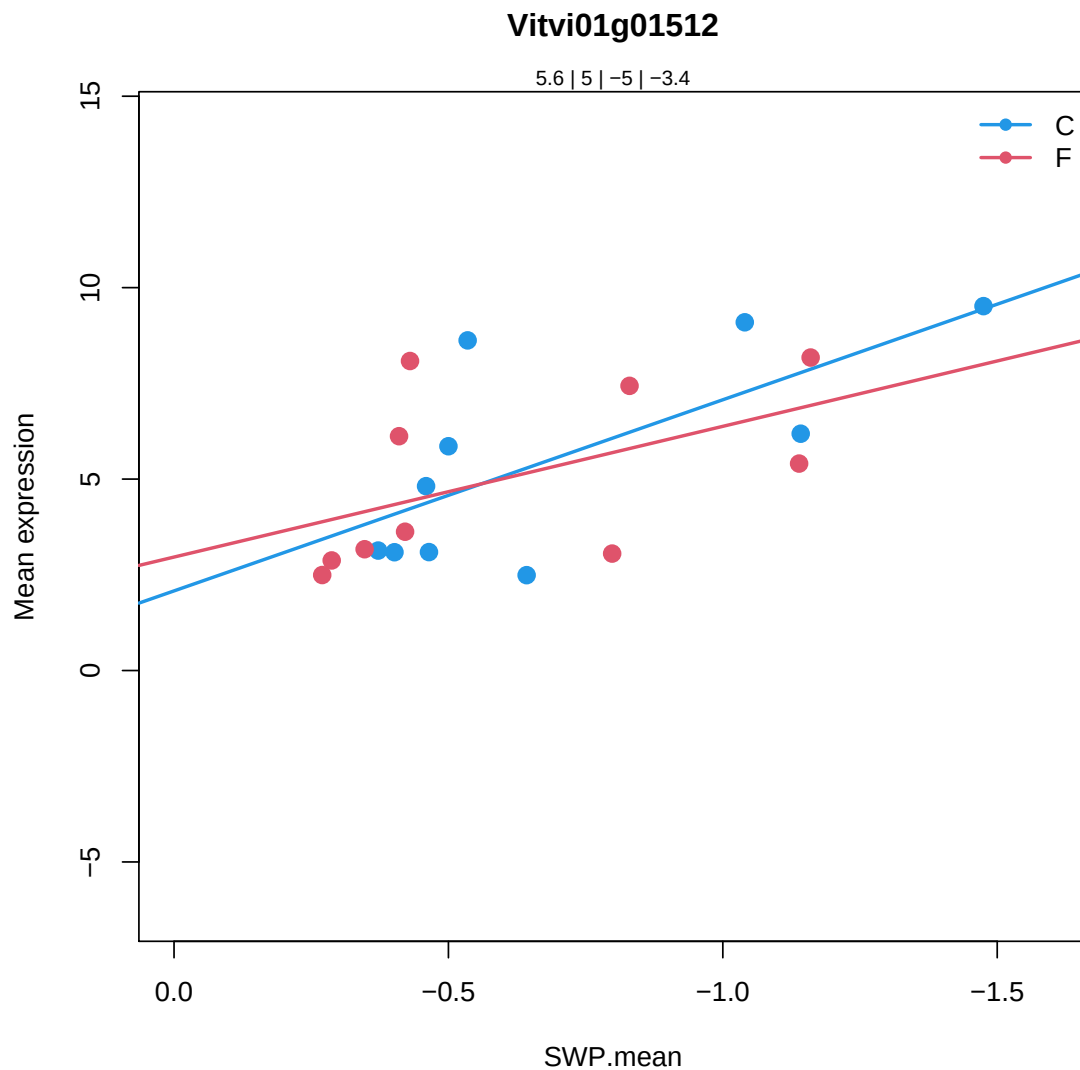
heat shock protein 21 |

Chr4:13819048-13819895 REVERSE LENGTH=227 |

201606

Coefficients for Vitvi01g01512.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.589732	2.181097e-09	***	2.719814e-09	***
SlopeC	-4.991872	0.004738281	**	0.2456492	
MeanF-MeanC	-0.5463244	0.5047801		0.808688	
SlopeF-SlopeC	1.577612	0.5106073		0.9999488	



8.1.586 Vitvi14g02990: Type1.0 *

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

Vitvi14g02990

35.2

not assigned.unknown

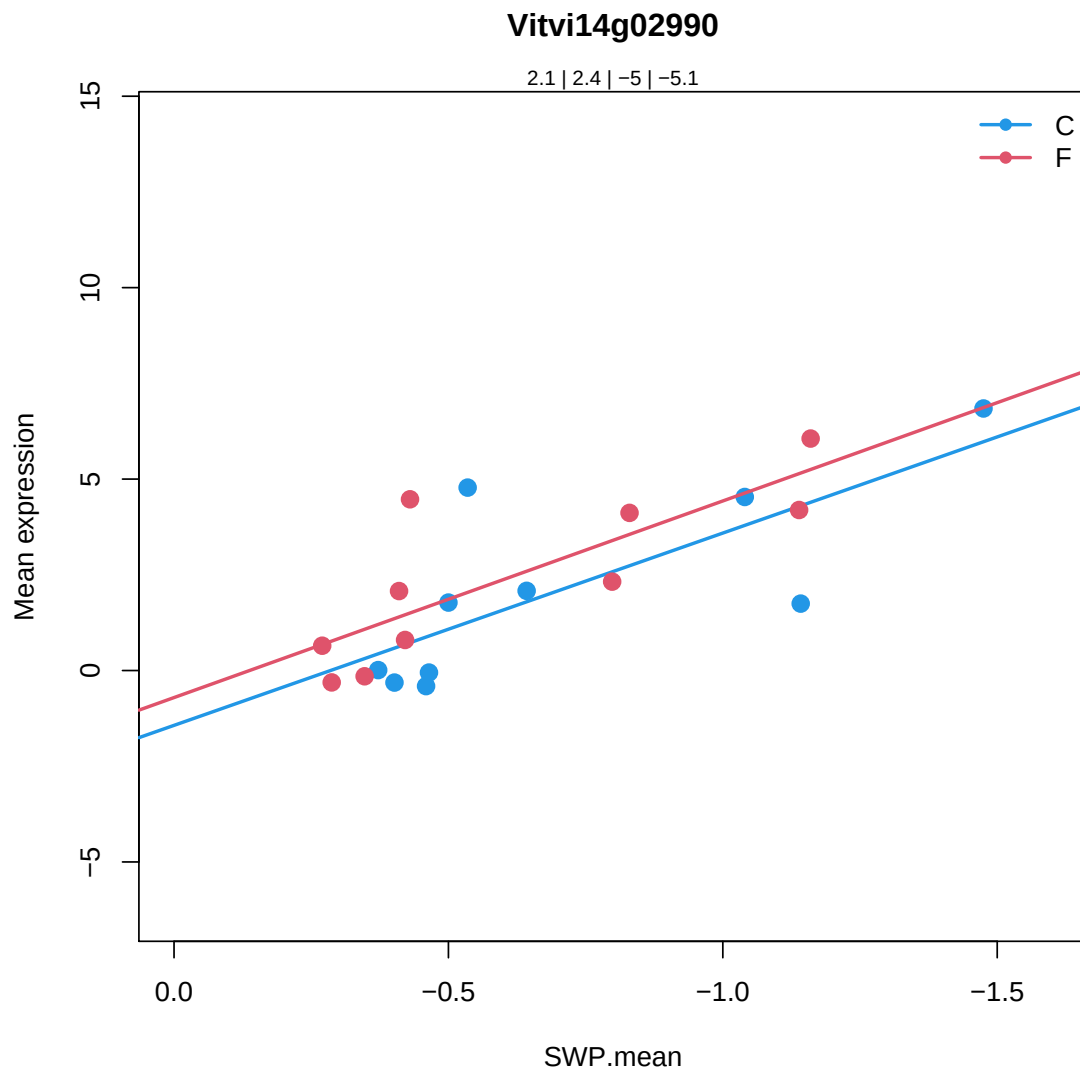
hypothetical protein |

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	



8.1.587 Vitvi11g00724: Type1.0 *

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

Vitvi11g00724

20.2.1

stress.abiotic.heat

heat shock protein 70B |

Chr1:5502386-5504326 REVERSE LENGTH=646 |

201606

Vitvi11g00724

29.6

protein.folding

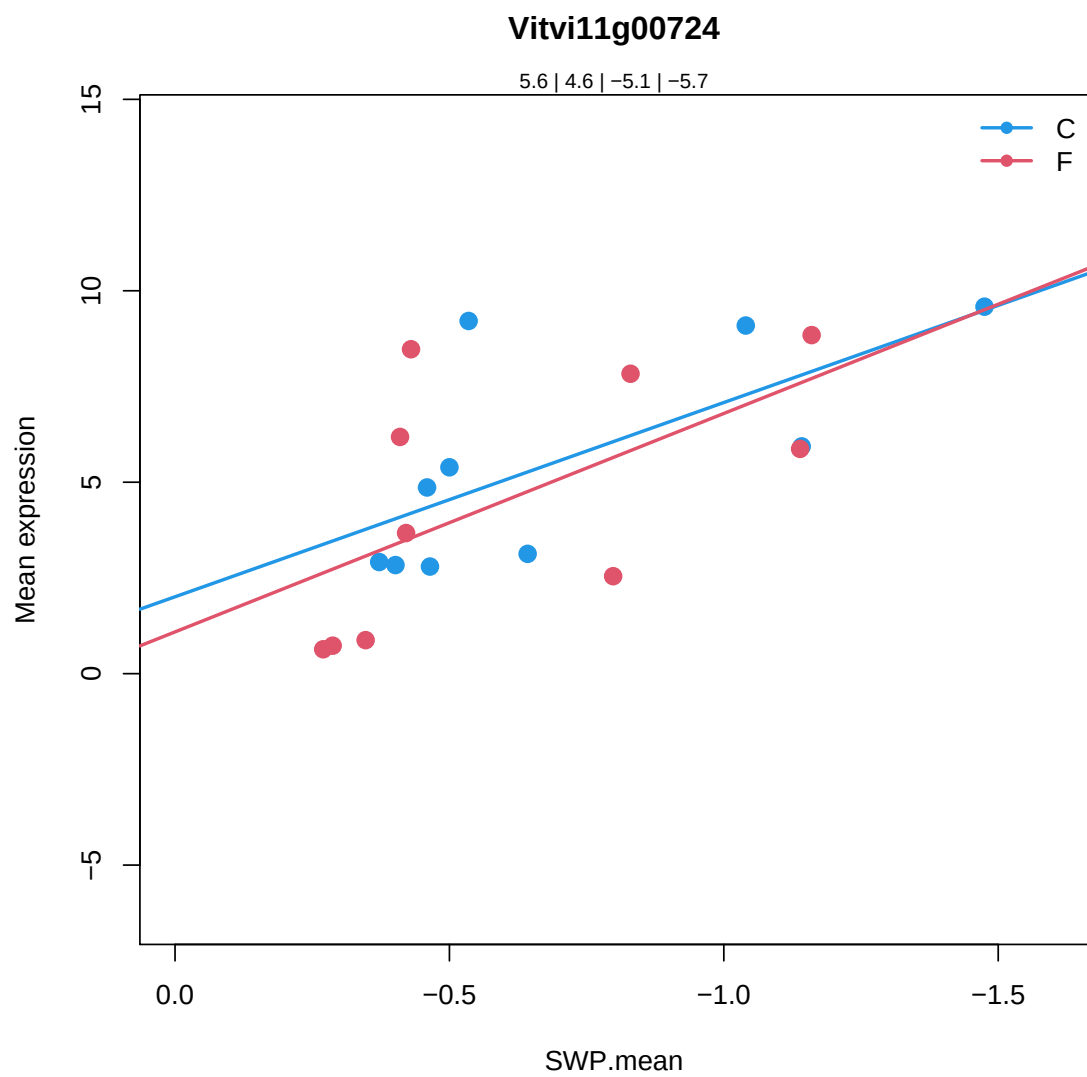
heat shock protein 70B |

Chr1:5502386-5504326 REVERSE LENGTH=646 |

201606

Coefficients for Vitvi11g00724.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.57538	5.63319e-08	***	6.726816e-08	***
SlopeC	-5.073527	0.01469064	*	0.3359386	
MeanF-MeanC	-1.009405	0.3105058		0.6744662	
SlopeF-SlopeC	-0.6317686	0.8263893		0.9999488	



8.1.588 Vitvi04g01801: Type1.0 *

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

Vitvi04g01801

20.2.1

stress.abiotic.heat

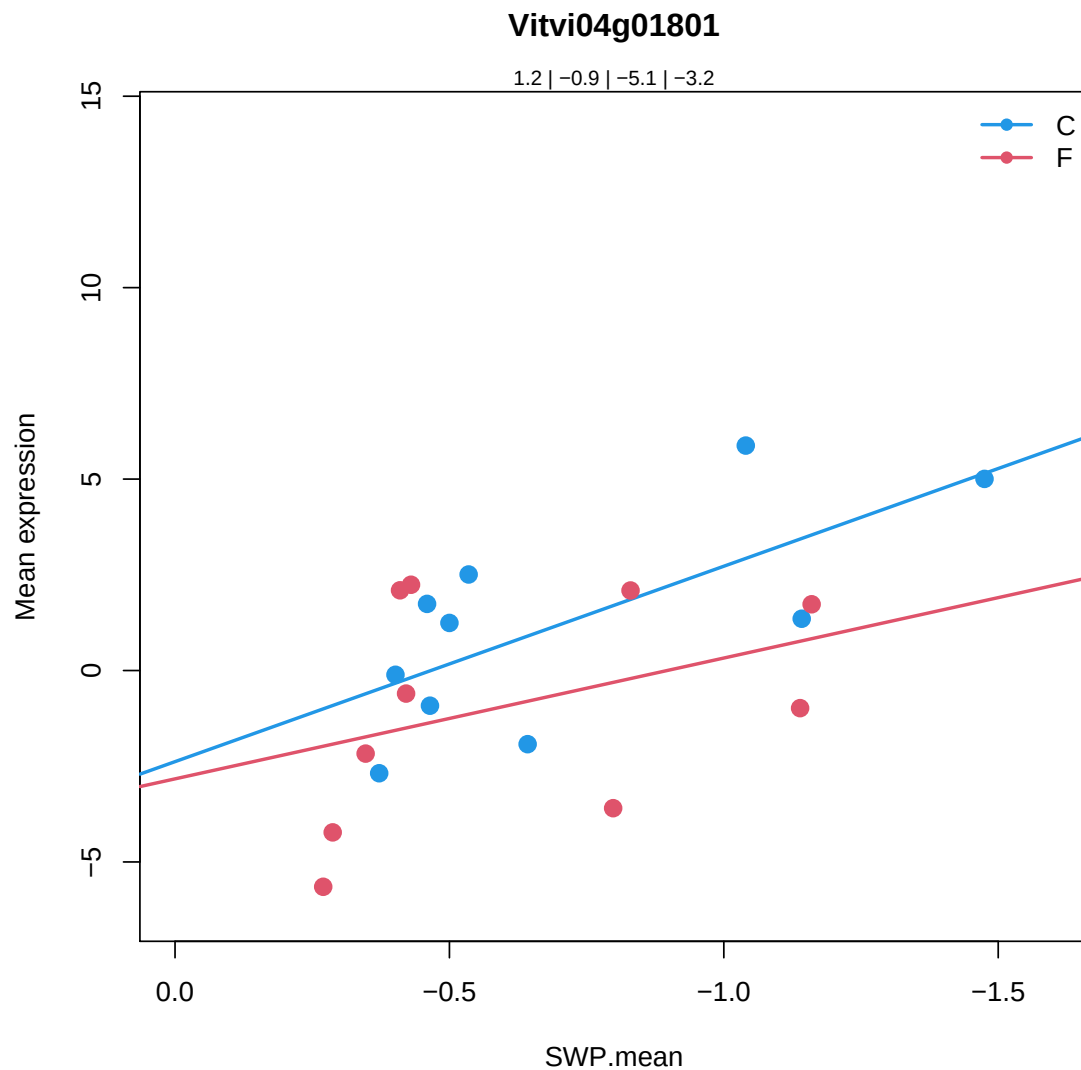
17.6 kDa class II heat shock protein |

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	



8.1.589 Vitvi05g00170: Type1.0 *

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

Vitvi05g00170

3.1.1.1

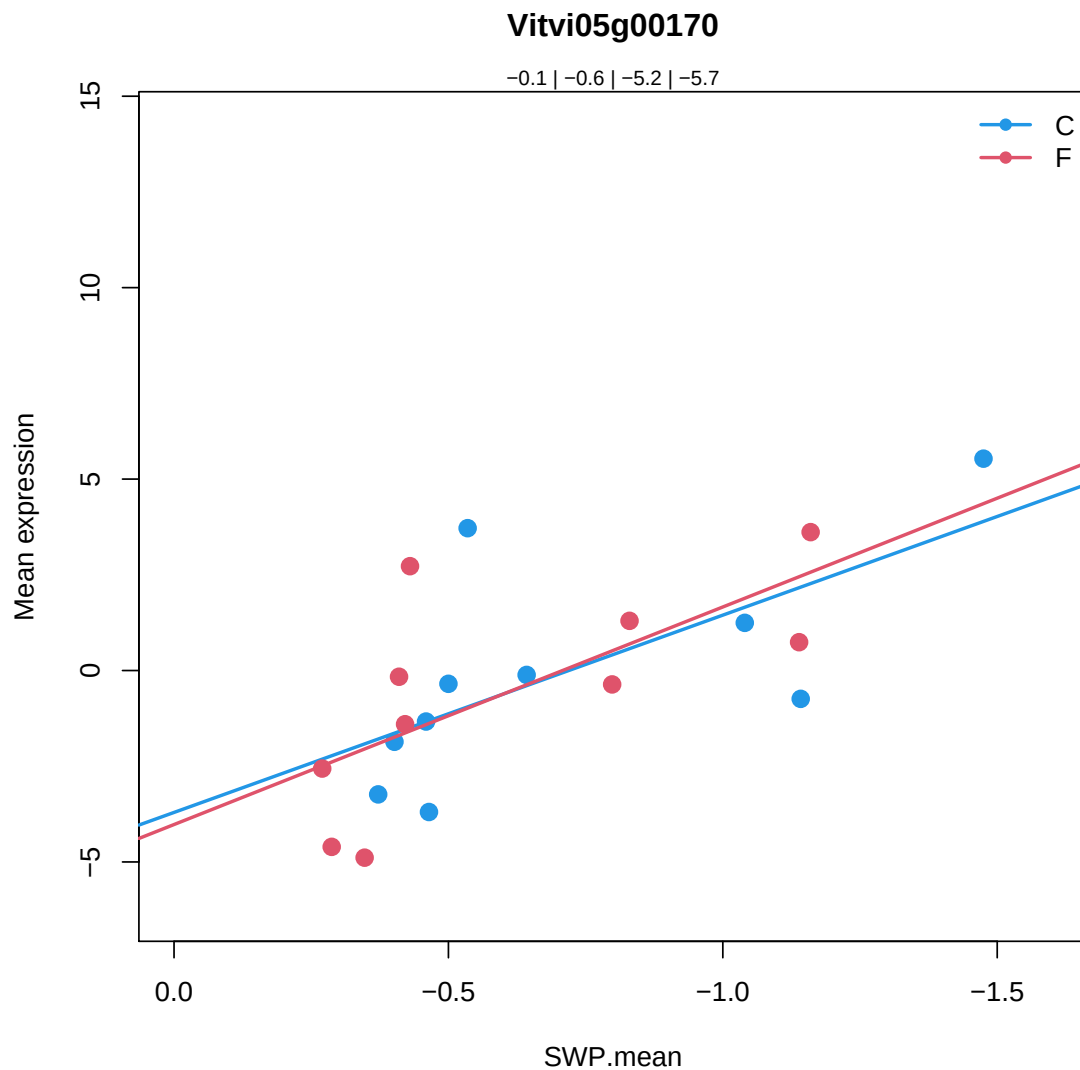
minor CHO metabolism.raffinose family.galactinol synthases.known
galactinol synthase 3 |

Chr1:3019888-3021214 FORWARD LENGTH=334 |

201606

Coefficients for Vitvi05g00170.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.08316482	0.8942845		0.8967556	
SlopeC	-5.15293	0.006799412	**	0.2748982	
MeanF-MeanC	-0.4774518	0.5907784		0.8569322	
SlopeF-SlopeC	-0.5293673	0.8381889		0.9999488	



8.1.590 Vitvi07g00380: Type1.0 *

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

Vitvi07g00380

35.2

not assigned.unknown

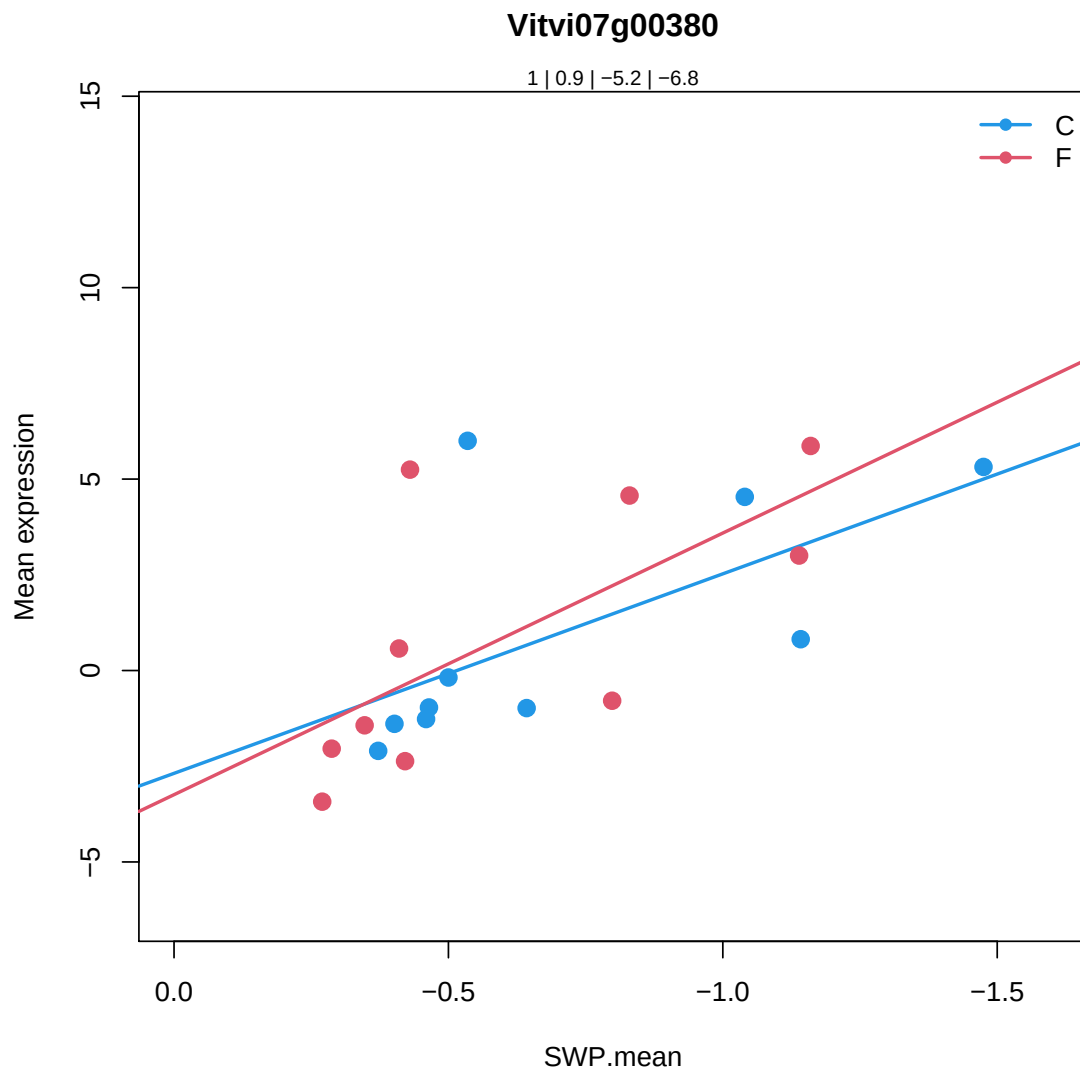
GATA transcription factor-like protein |

Chr1:588367-589232 FORWARD LENGTH=247 |

201606

Coefficients for Vitvi07g00380.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.9780221	0.1867379		0.1916028	
SlopeC	-5.210794	0.01611674	*	0.3486596	
MeanF-MeanC	-0.05760366	0.9552275		0.9897068	
SlopeF-SlopeC	-1.622591	0.5903886		0.9999488	



8.1.591 Vitvi08g02274: Type1.0 *

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

Vitvi08g02274

35.2

not assigned.unknown

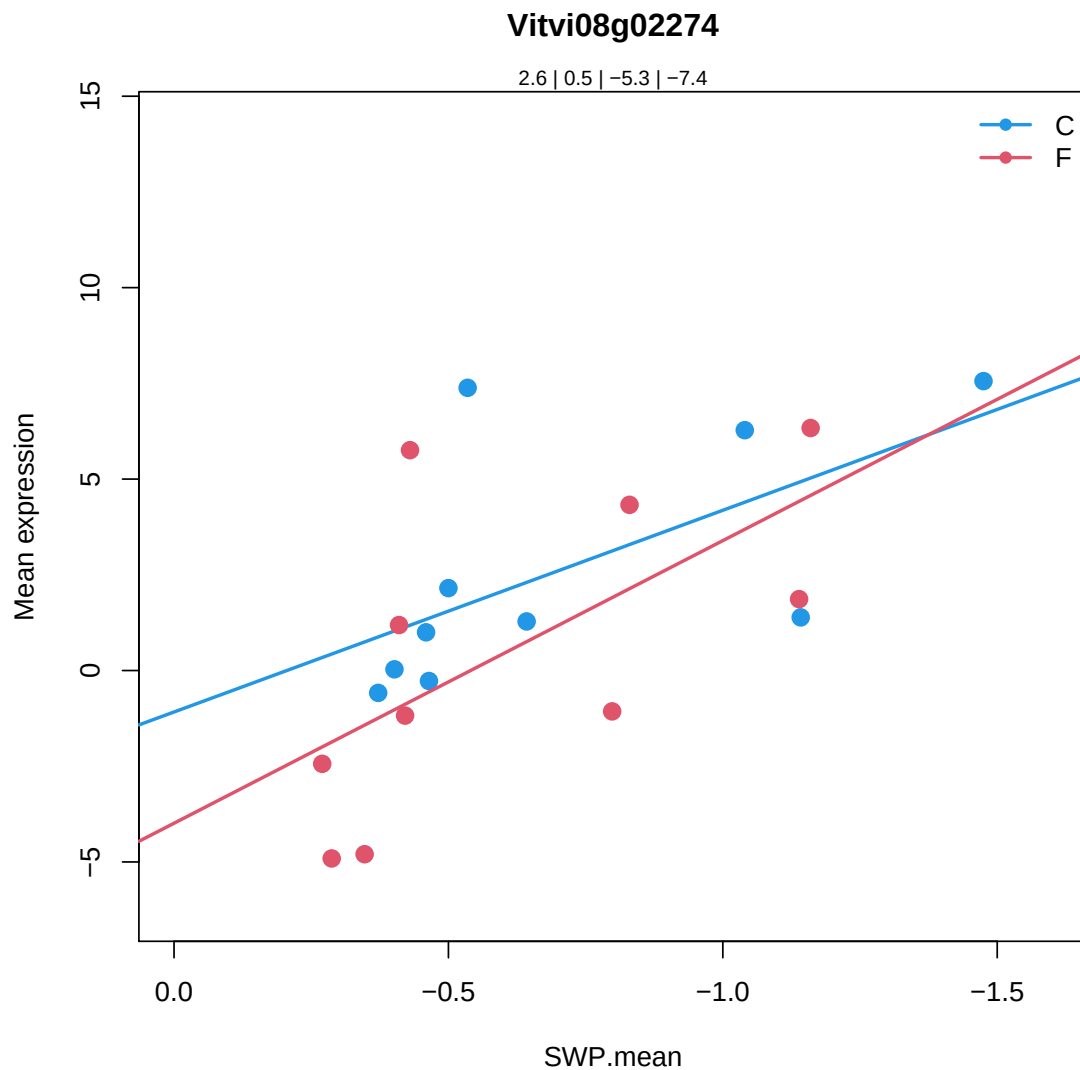
plant/protein |

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	



8.1.592 Vitvi02g00025: Type1.0 *

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

Vitvi02g00025

20.2.1

stress.abiotic.heat

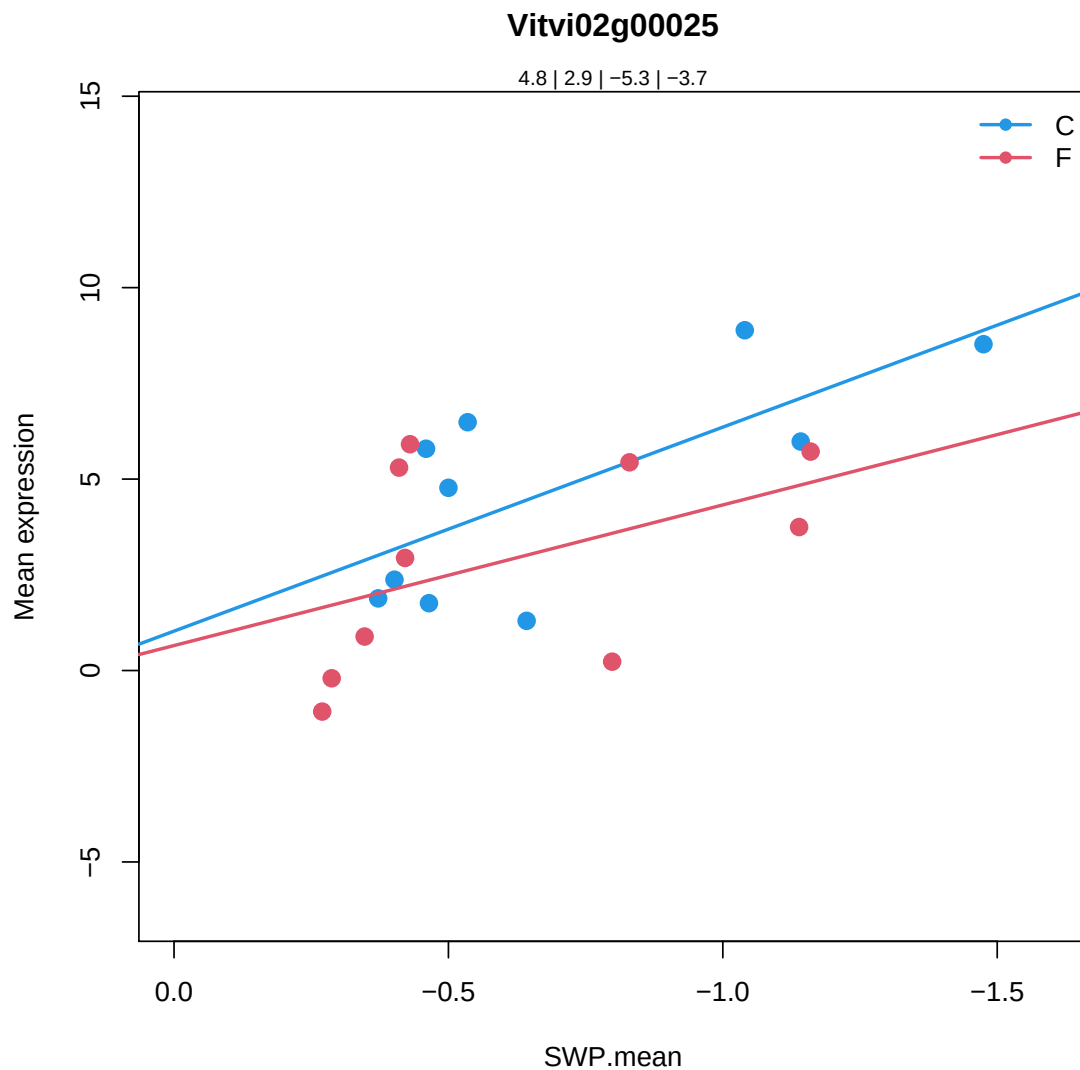
heat shock-like protein |

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	



8.1.593 Vitvi15g01034: Type1.0 *

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

Vitvi15g01034

20.2.1

stress.abiotic.heat

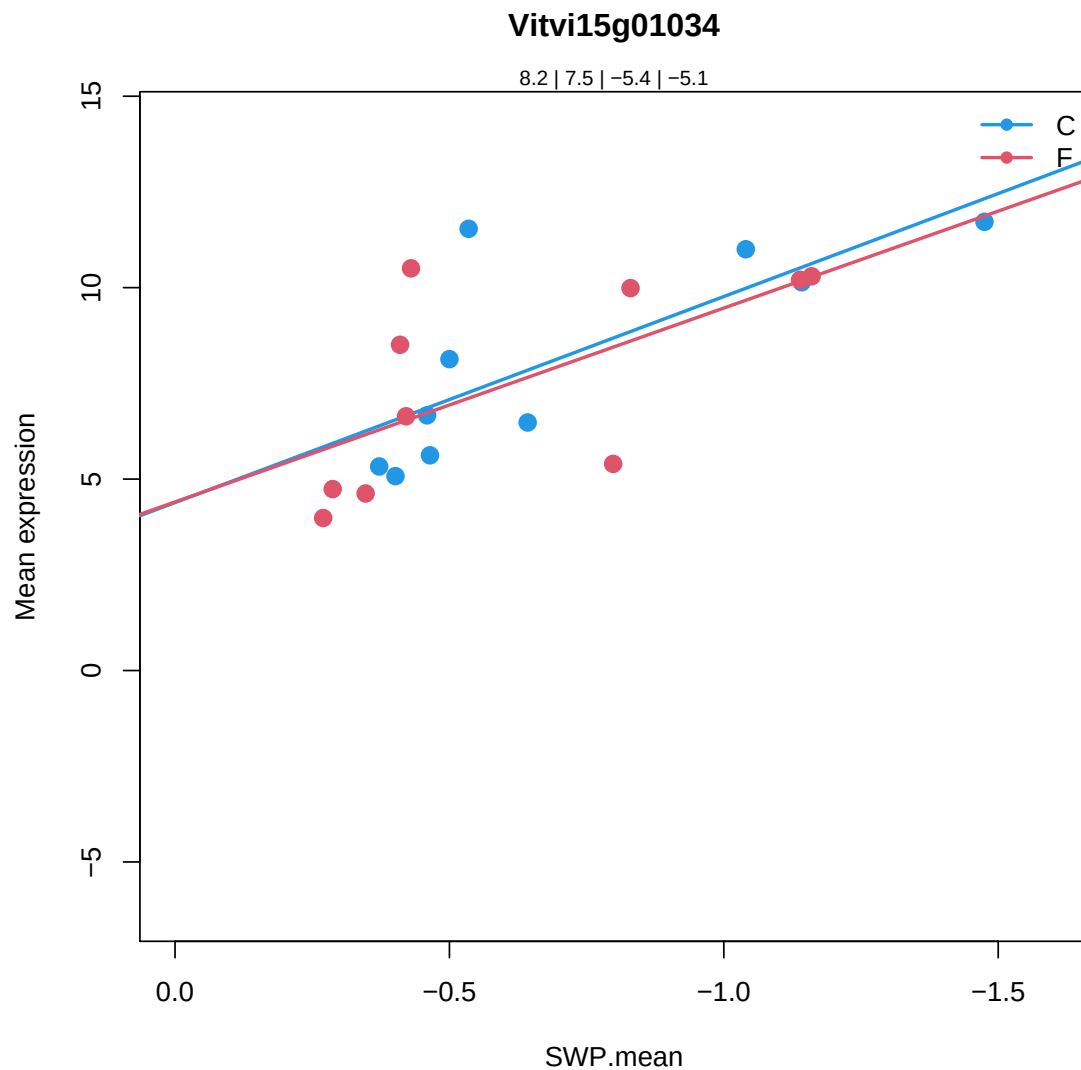
BCL-2-associated athanogene 6 |

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	



8.1.594 Vitvi04g01799: Type1.0 *

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

Vitvi04g01799

20.2.1

stress.abiotic.heat

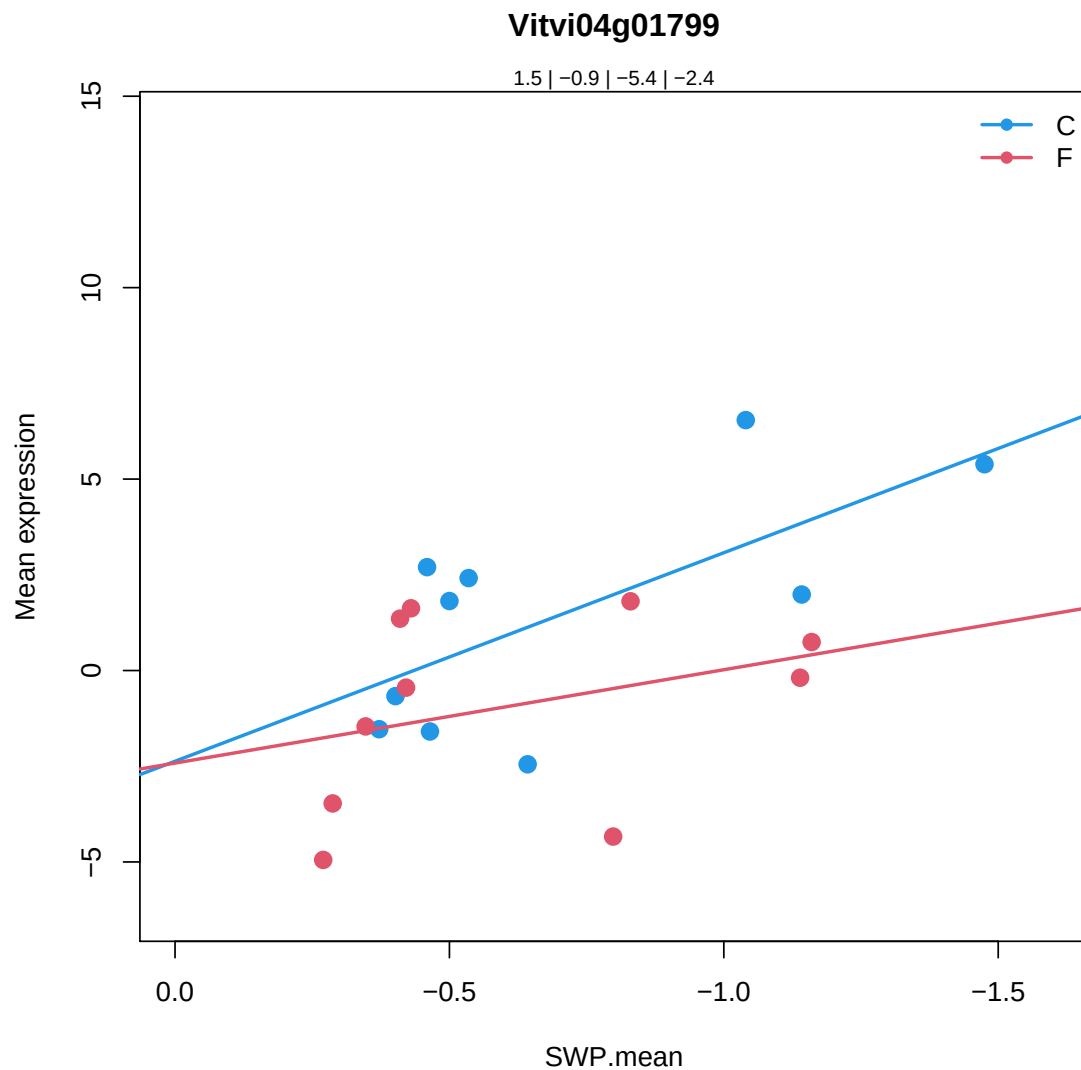
17.6 kDa class II heat shock protein |

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	



8.1.595 Vitvi04g01794: Type1.0 *

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

Vitvi04g01794

20.2.1

stress.abiotic.heat

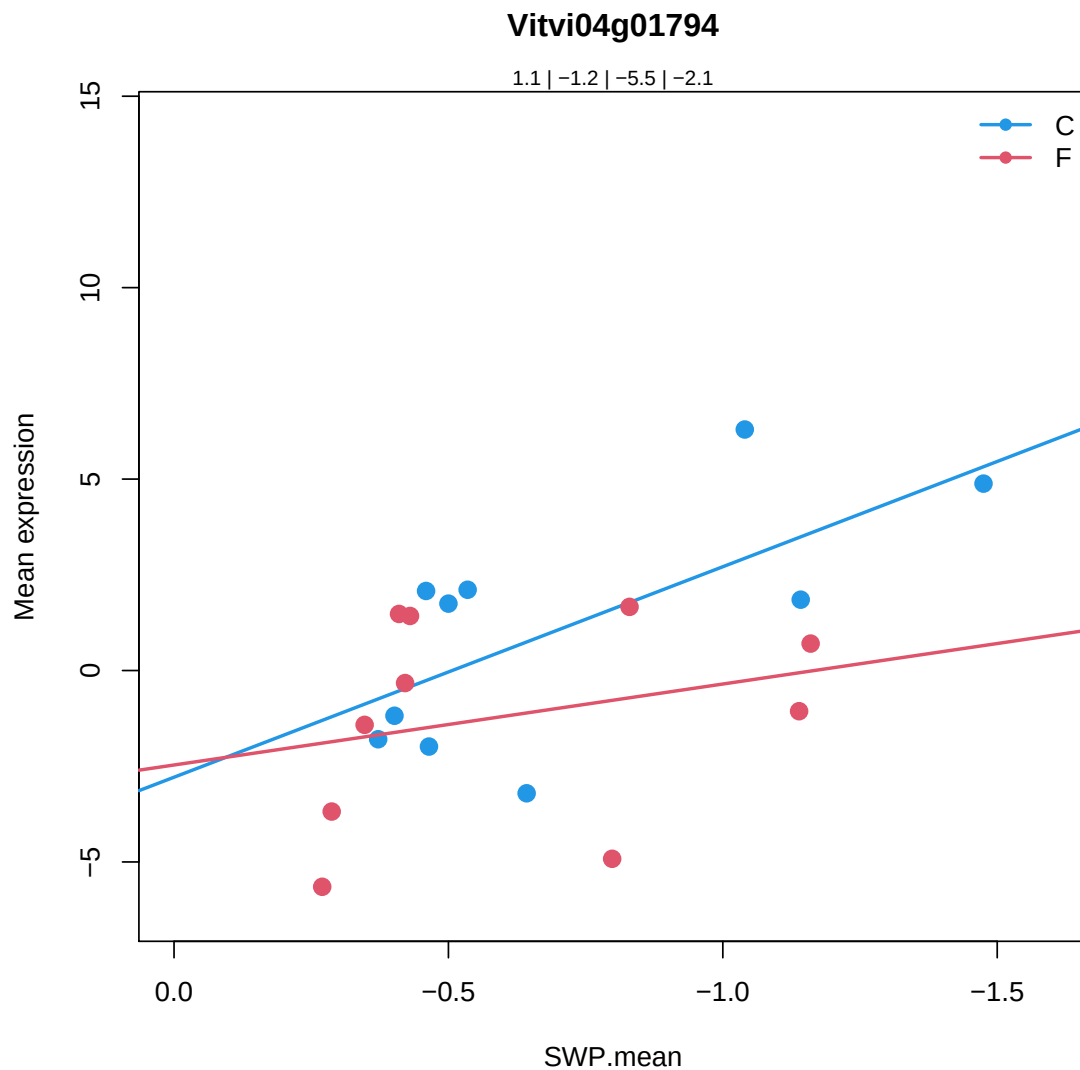
17.6 kDa class II heat shock protein |

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	



8.1.596 Vitvi13g00409: Type1.0 *

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

Vitvi13g00409

35.2

not assigned.unknown

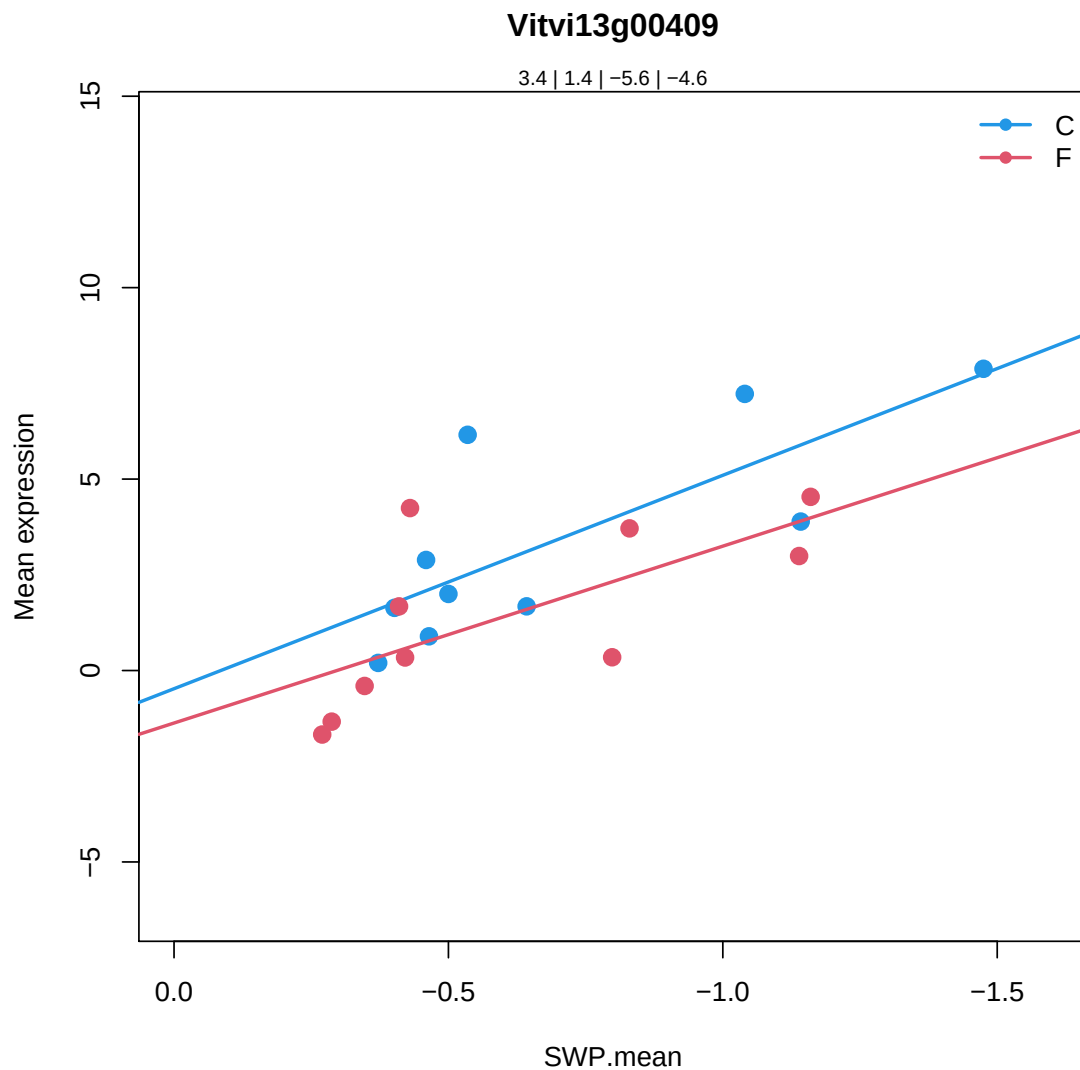
heat shock protein 18.2 |

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	



8.1.597 Vitvi13g02017: Type1.0 *

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

Vitvi13g02017

20.2.1

stress.abiotic.heat

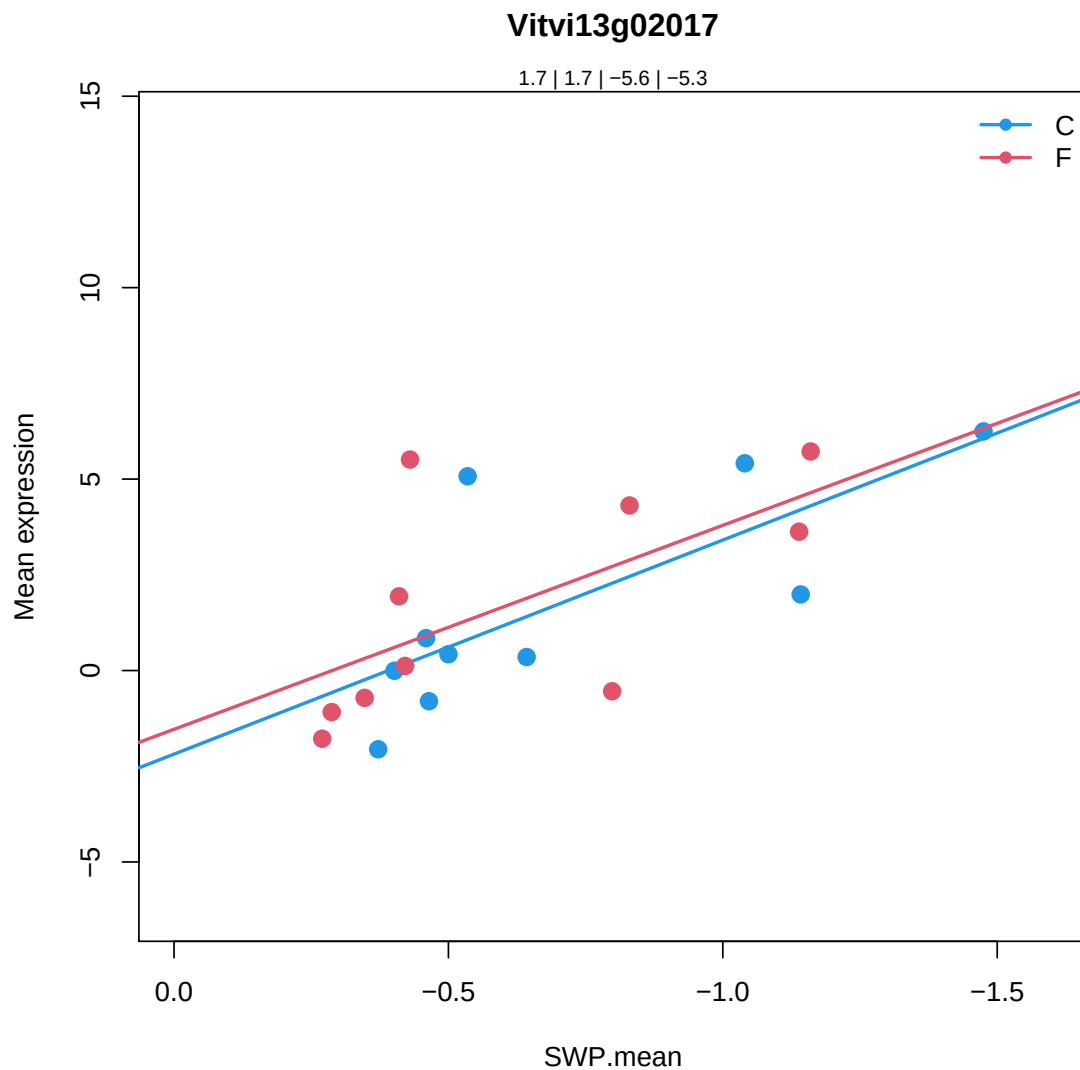
heat shock protein 18.2 |

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	



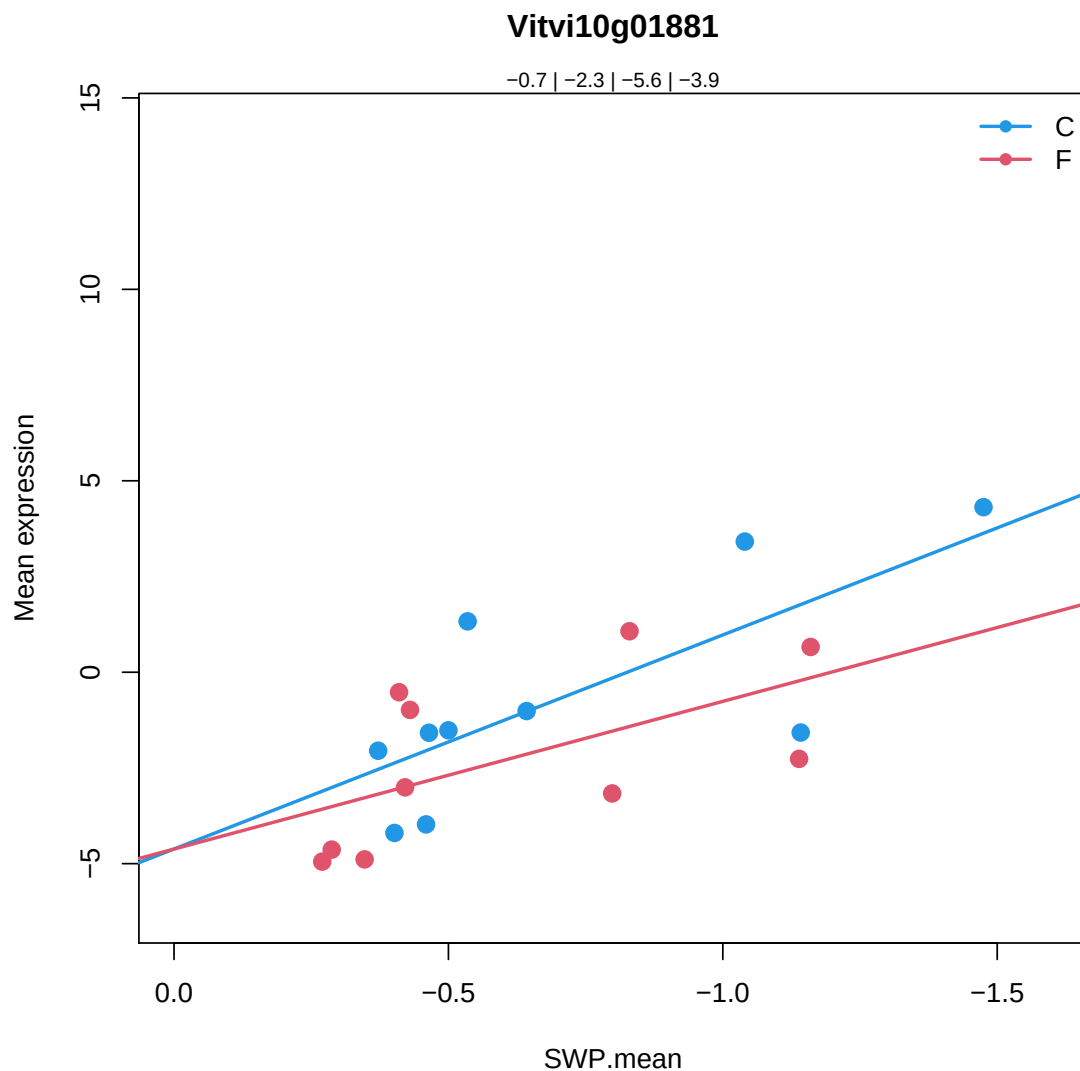
8.1.598 Vitvi10g01881: Type1.0 *

```
> 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	



8.1.599 Vitvi13g02016: Type1.0 *

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

Vitvi13g02016

20.2.1

stress.abiotic.heat

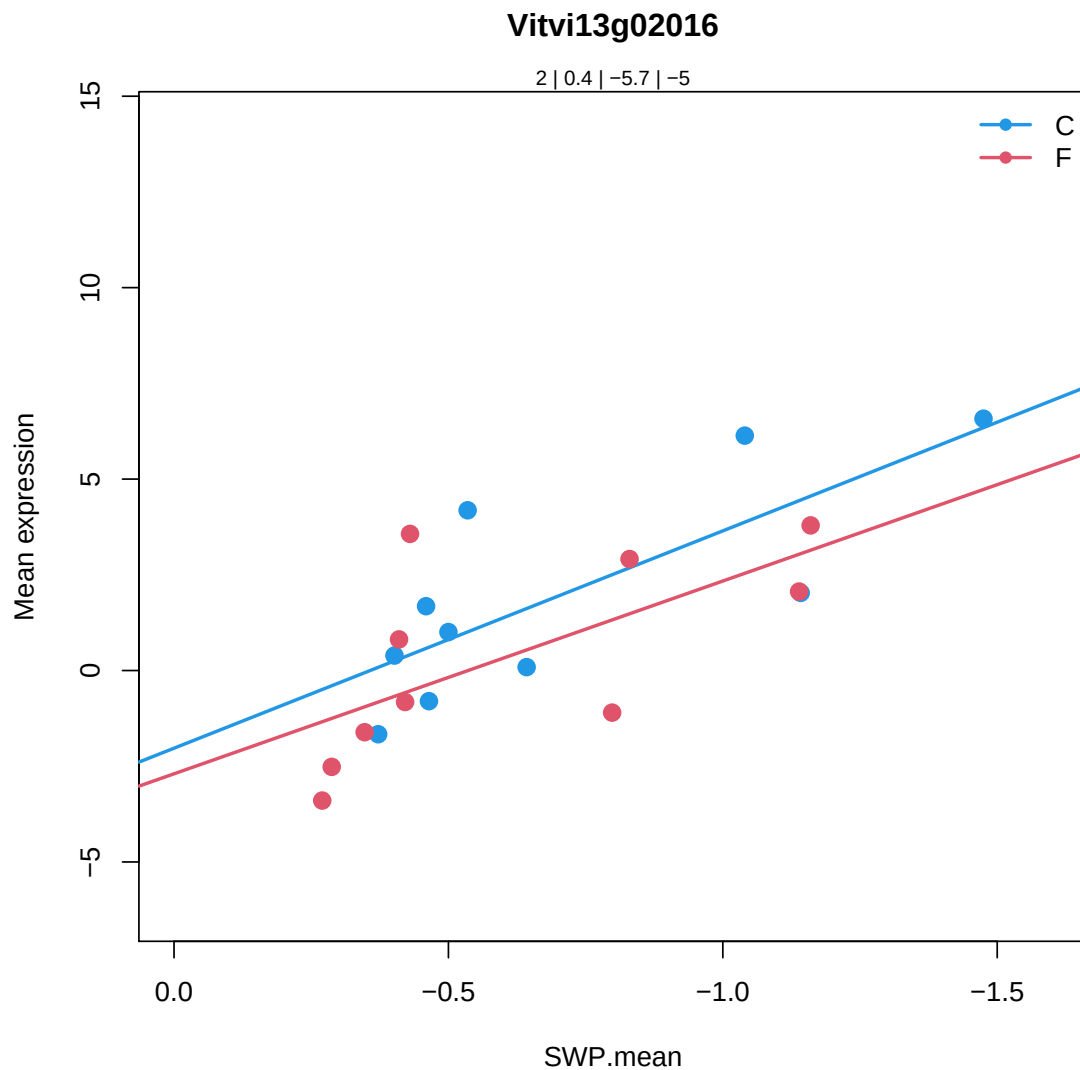
HSP20-like chaperones superfamily protein |

Chr1:19980510-19980983 FORWARD LENGTH=157 |

201606

Coefficients for Vitvi13g02016.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.962441	0.001860074	**	0.002001642	**
SlopeC	-5.676271	0.001329333	**	0.1432275	
MeanF-MeanC	-1.5925	0.05433262	.	0.2525382	
SlopeF-SlopeC	0.6414647	0.7821337		0.9999488	



8.1.600 Vitvi05g01933: Type1.0 *

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

Vitvi05g01933

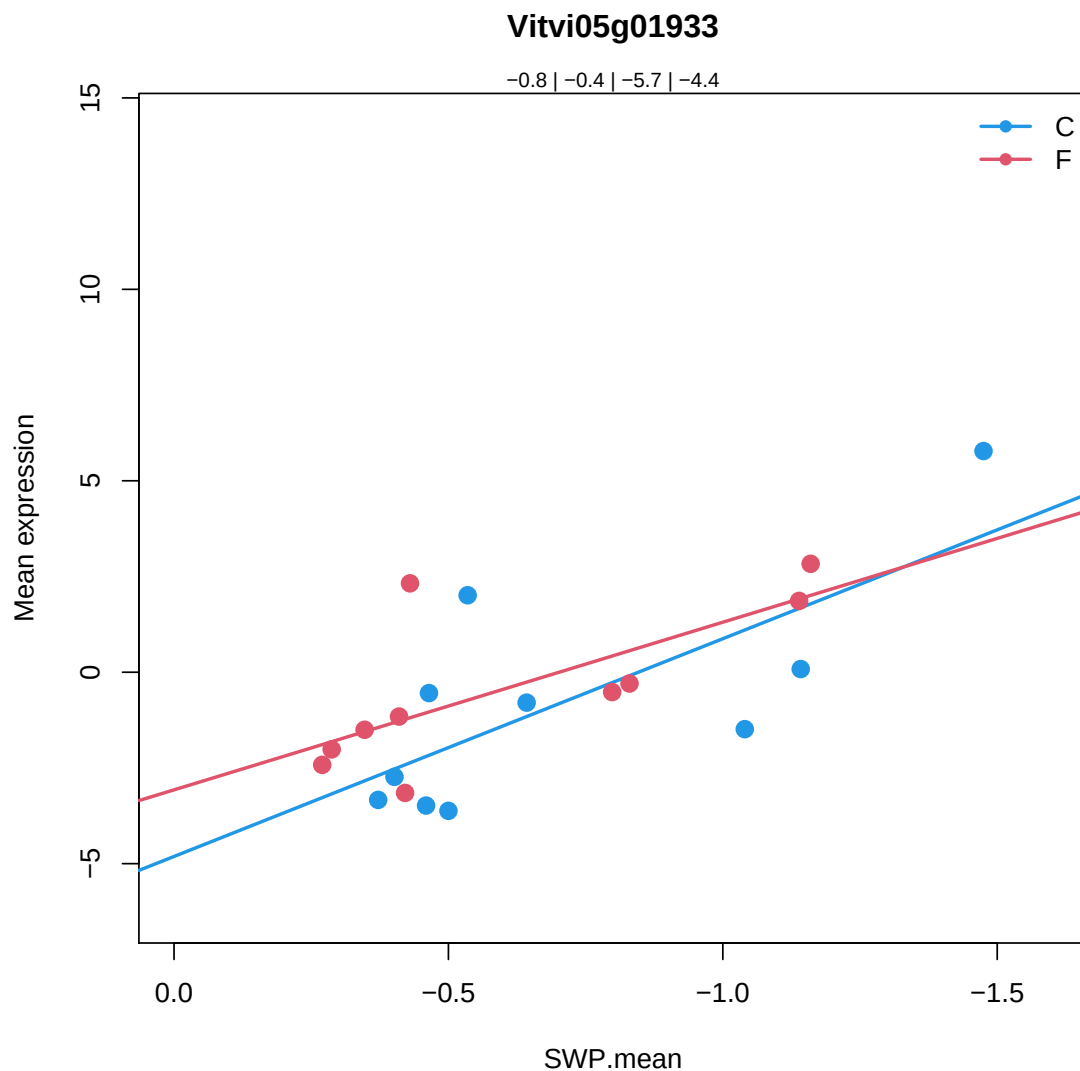
35.2

not assigned.unknown

NA

Coefficients for Vitvi05g01933.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.8128464	0.1262312		0.1302211	
SlopeC	-5.687122	0.0006264347	***	0.1005065	
MeanF-MeanC	0.4081079	0.5780324		0.8510697	
SlopeF-SlopeC	1.308549	0.542724		0.9999488	



8.1.601 Vitvi16g01985: Type1.0 *

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

Vitvi16g01985

35.2

not assigned.unknown

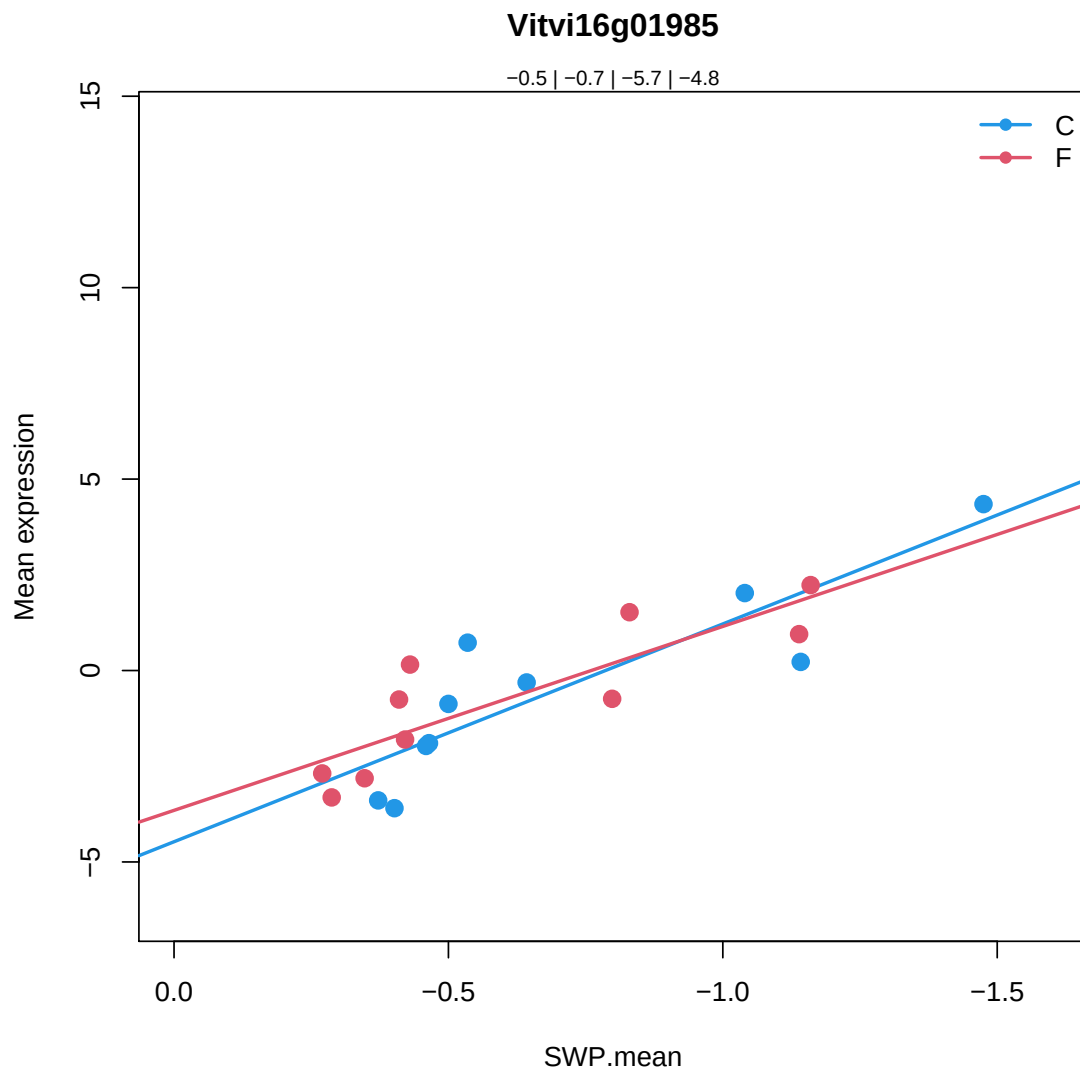
highly ABA-induced PP2C protein 3 |

Chr2:12608855-12610124 FORWARD LENGTH=362 |

201606

Coefficients for Vitvi16g01985.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.4719704	0.159837		0.1643662	
SlopeC	-5.688522	2.68669e-06	***	0.01365018	*
MeanF-MeanC	-0.2536551	0.5857293		0.8542535	
SlopeF-SlopeC	0.8843373	0.5169724		0.9999488	



8.1.602 Vitvi14g01942: Type1.0 *

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

Vitvi14g01942

29.5.7

protein.degradation.metalloprotease

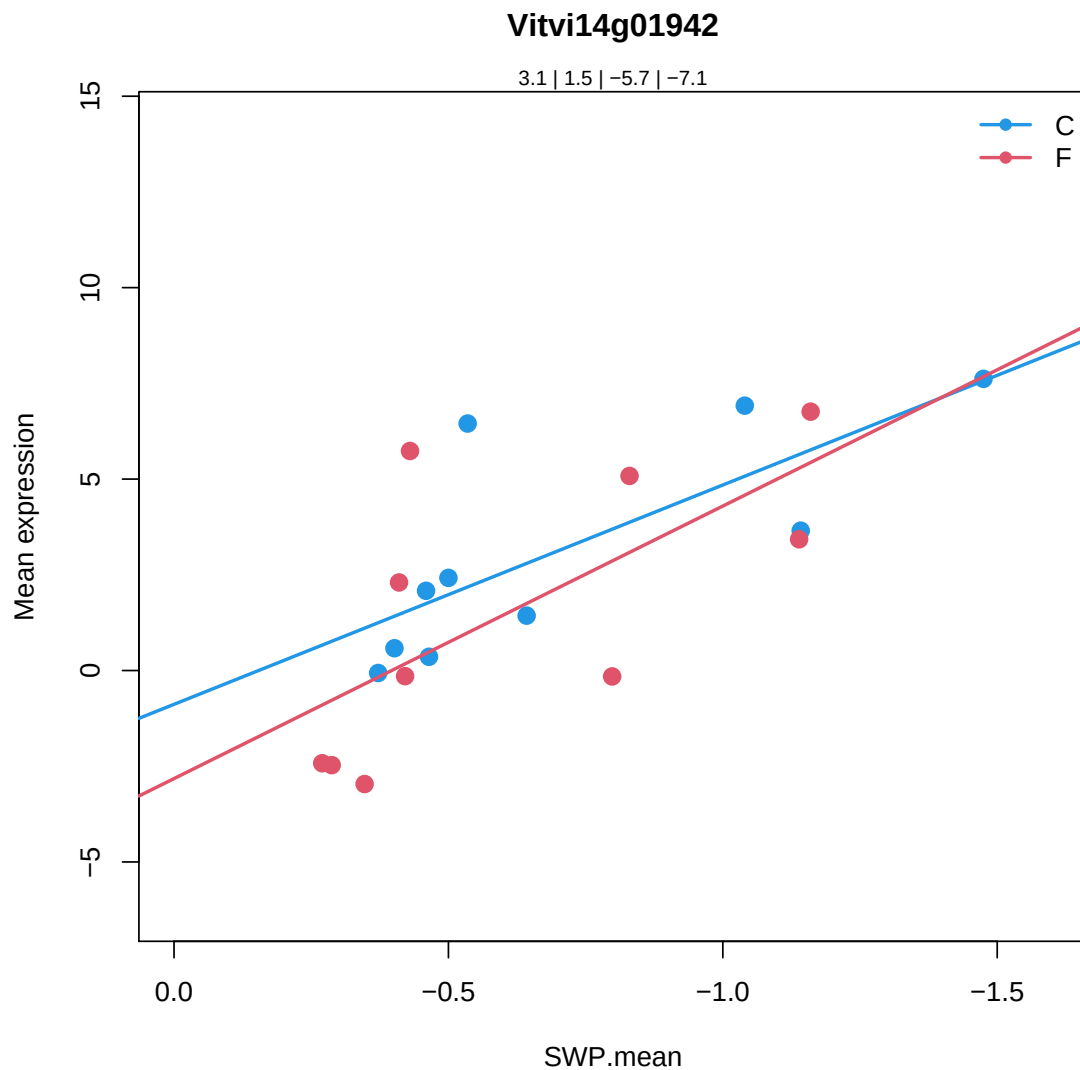
FTSH protease 6 |

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	



8.1.603 Vitvi06g00561: Type1.0 *

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

Vitvi06g00561

35.2

not assigned.unknown

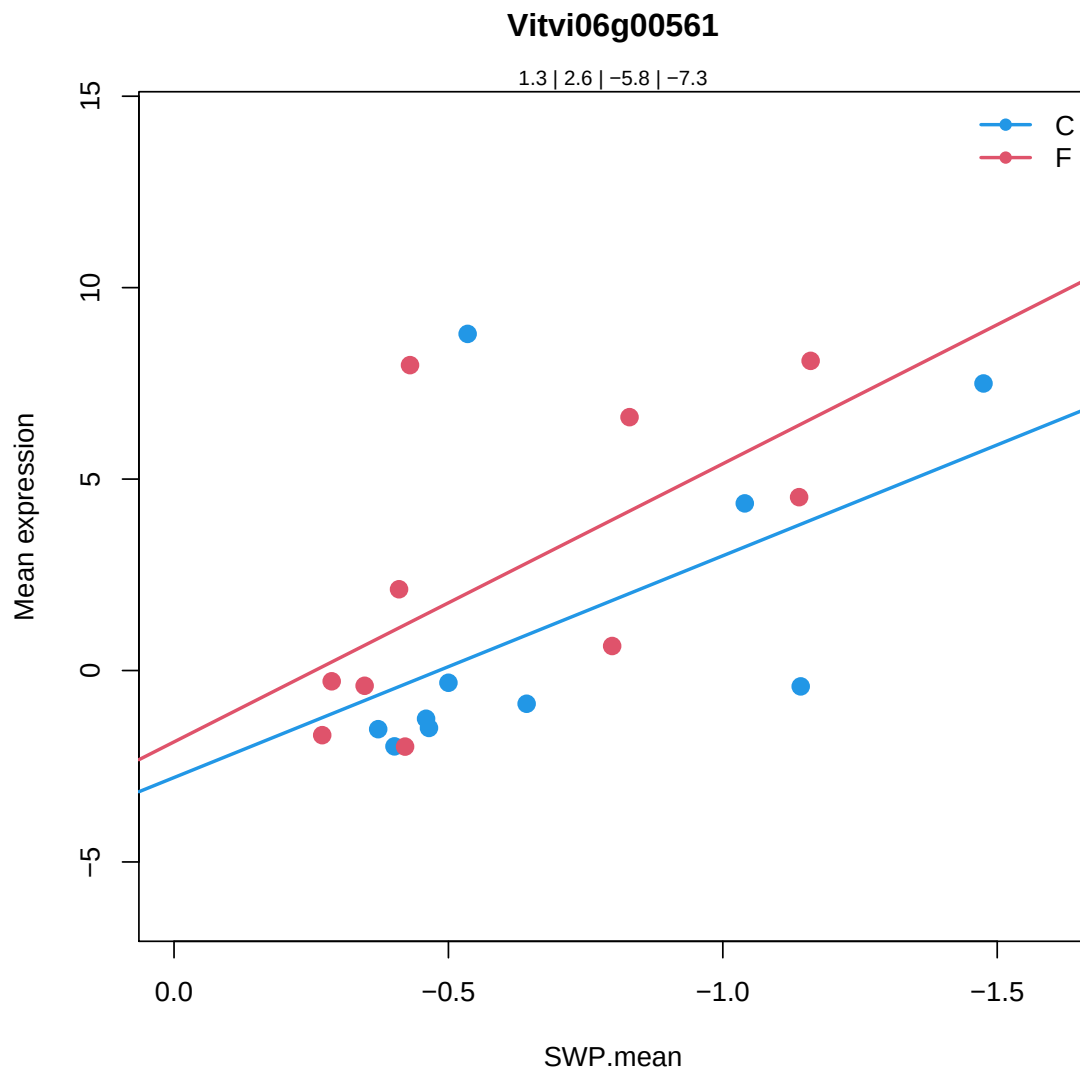
HSP20-like chaperones superfamily protein |

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	



8.1.604 Vitvi13g00405: Type1.0 *

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

Vitvi13g00405

35.2

not assigned.unknown

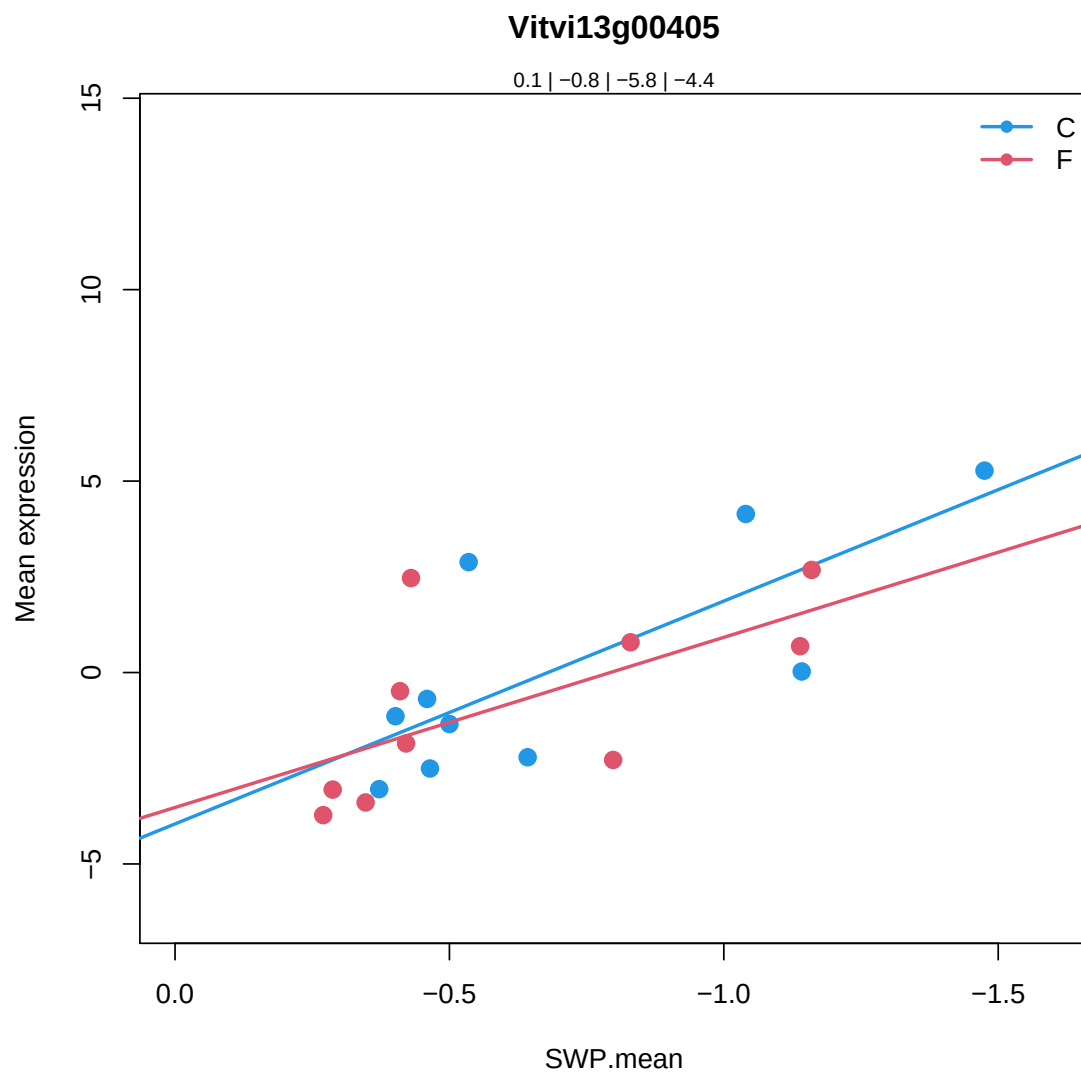
heat shock protein 18.2 |

Chr5:24062632-24063117 FORWARD LENGTH=161 |

201606

Coefficients for Vitvi13g00405.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1379442	0.8045375		0.8083561	
SlopeC	-5.819808	0.001017611	**	0.1271346	
MeanF-MeanC	-0.955591	0.2329947		0.5880329	
SlopeF-SlopeC	1.375953	0.5524628		0.9999488	



8.1.605 Vitvi02g01447: Type1.0 *

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

Vitvi02g01447

20.2.1

stress.abiotic.heat

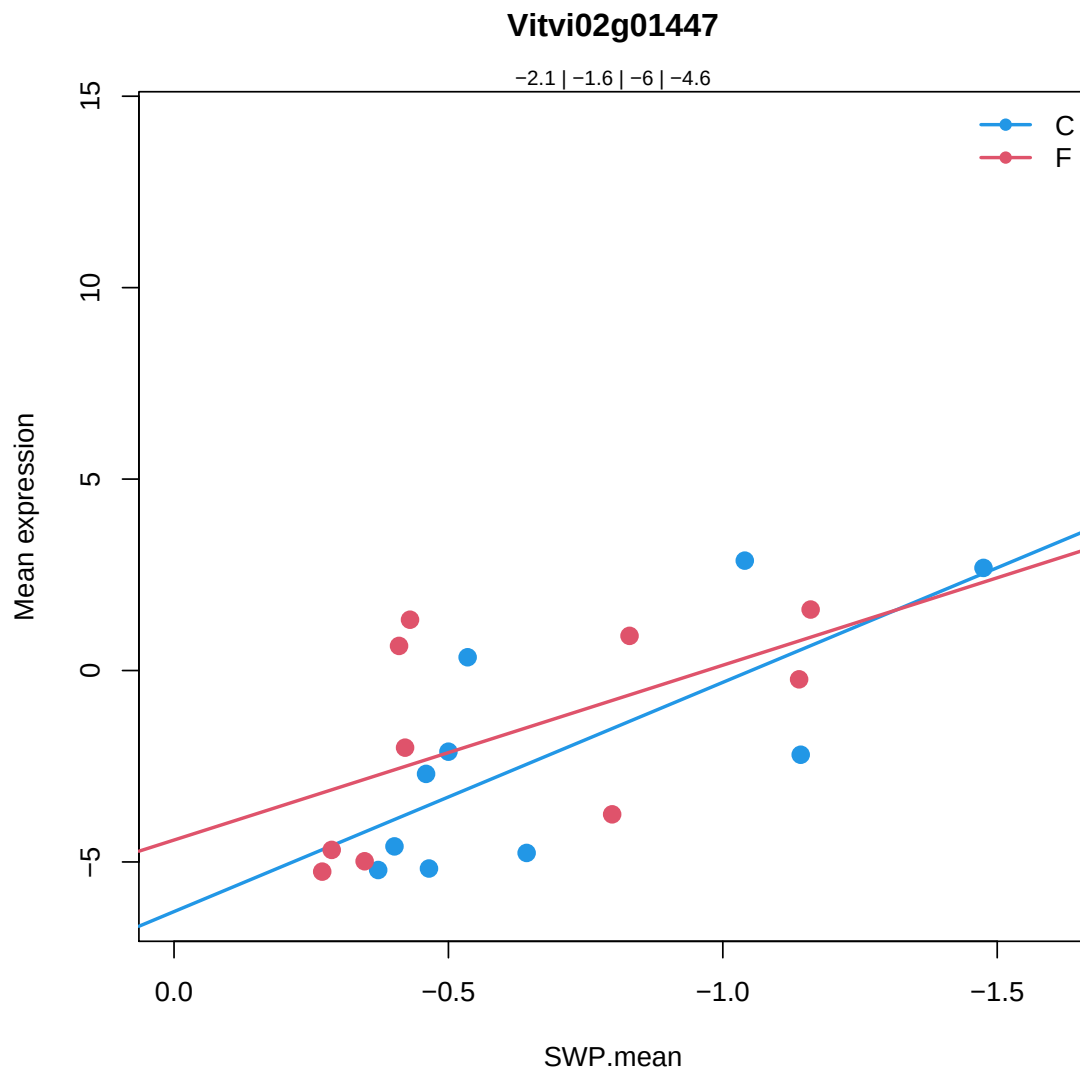
mitochondrion-localized small heat shock protein 23.6 |

Chr4:12917089-12917858 FORWARD LENGTH=210 |

201606

Coefficients for Vitvi02g01447.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-2.086395	0.004061142	**	0.004340809	**
SlopeC	-5.987309	0.003202305	**	0.2103859	
MeanF-MeanC	0.44105	0.6354848		0.8759034	
SlopeF-SlopeC	1.42107	0.6021419		0.9999488	



8.1.606 Vitvi19g01760: Type1.0 *

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

Vitvi19g01760

35.2

not assigned.unknown

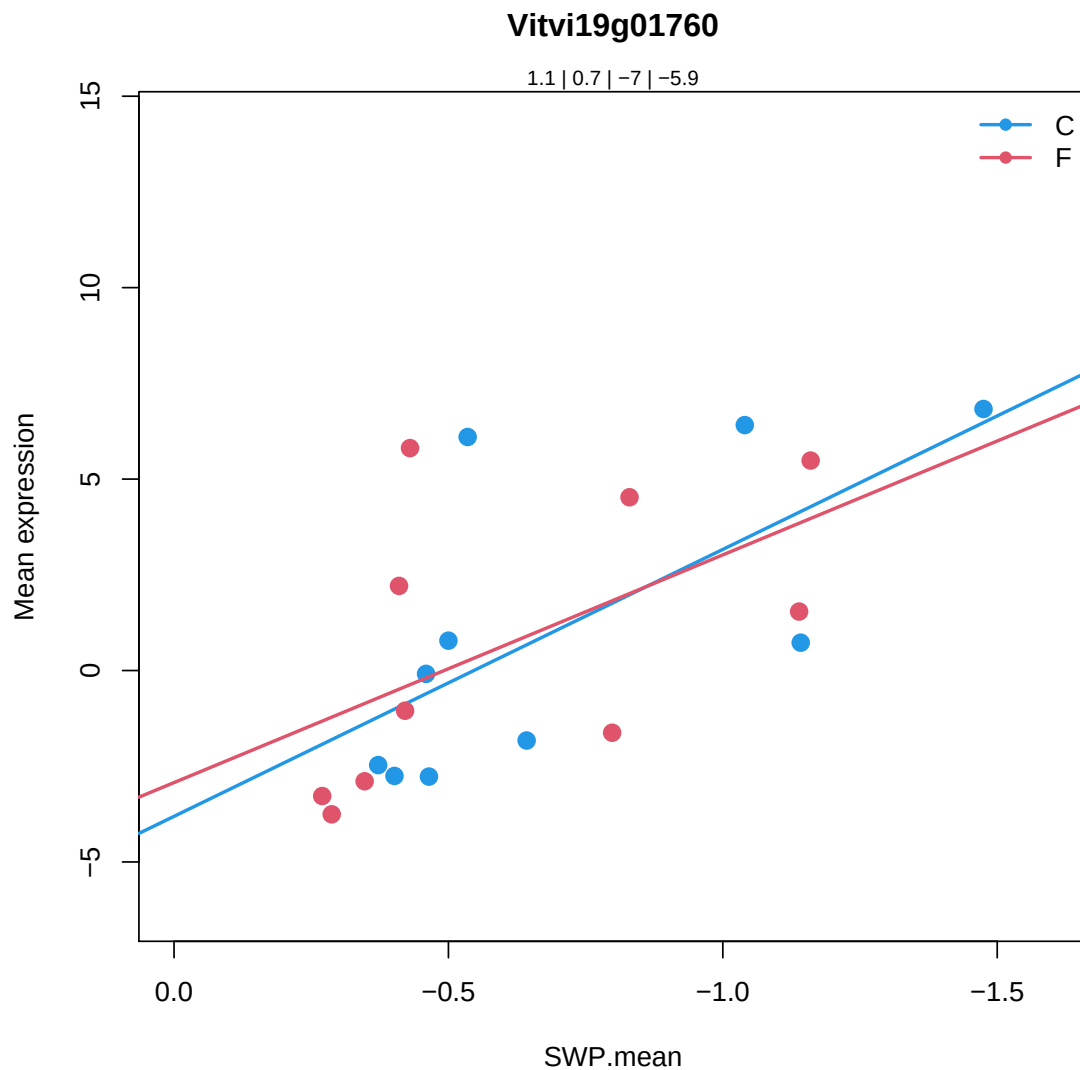
HSP20-like chaperones superfamily protein |

Chr1:19980510-19980983 FORWARD LENGTH=157 |

201606

Coefficients for Vitvi19g01760.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.093868	0.2236535		0.2290176	
SlopeC	-6.972297	0.009023451	**	0.2903326	
MeanF-MeanC	-0.3972341	0.7507341		0.9269839	
SlopeF-SlopeC	1.024981	0.7794621		0.9999488	



8.1.607 Vitvi12g02138: Type1.0 *

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

Vitvi12g02138

20.2.1

stress.abiotic.heat

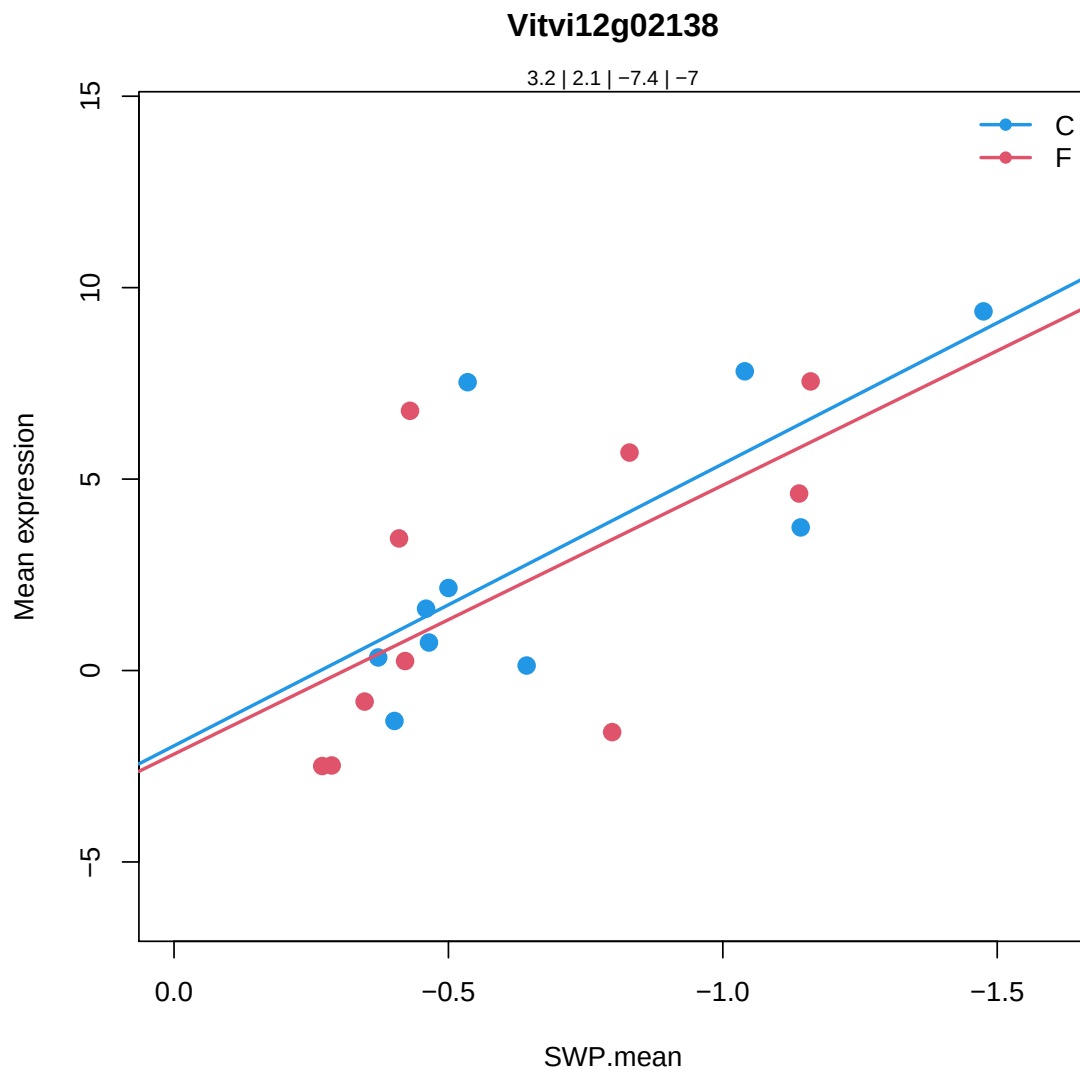
HSP20-like chaperones superfamily protein |

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	



8.1.608 Vitvi16g01352: Type1.0 *

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

Vitvi16g01352

20.2.1

stress.abiotic.heat

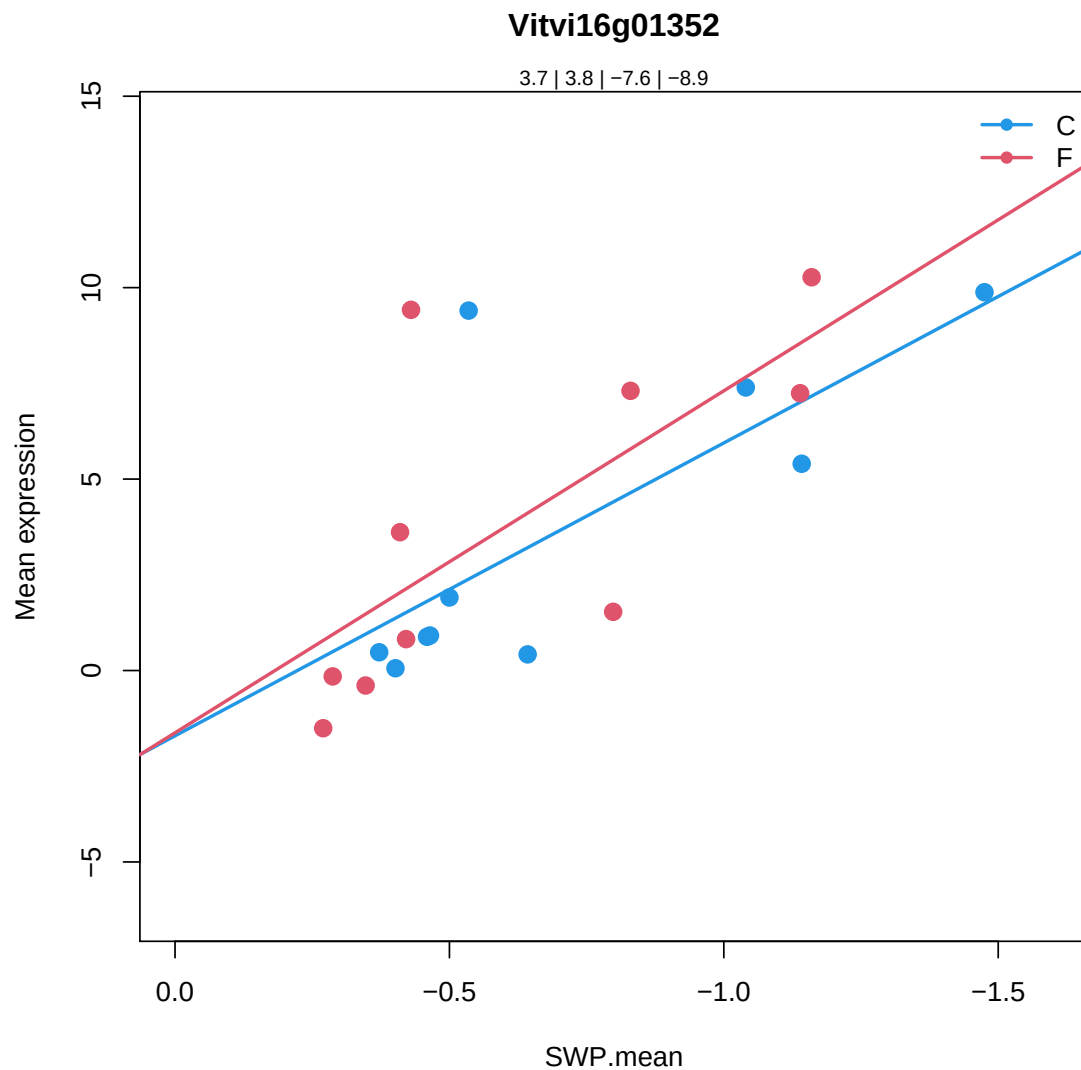
heat shock protein 21 |

Chr4:13819048-13819895 REVERSE LENGTH=227 |

201606

Coefficients for Vitvi16g01352.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.673182	0.0002848136	***	0.0003116389	***
SlopeC	-7.649088	0.00385391	**	0.2269459	
MeanF-MeanC	0.1420623	0.9068882		0.9757034	
SlopeF-SlopeC	-1.282333	0.7187855		0.9999488	



8.1.609 Vitvi04g00135: Type1.0 *

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

Vitvi04g00135

20.2.1

stress.abiotic.heat

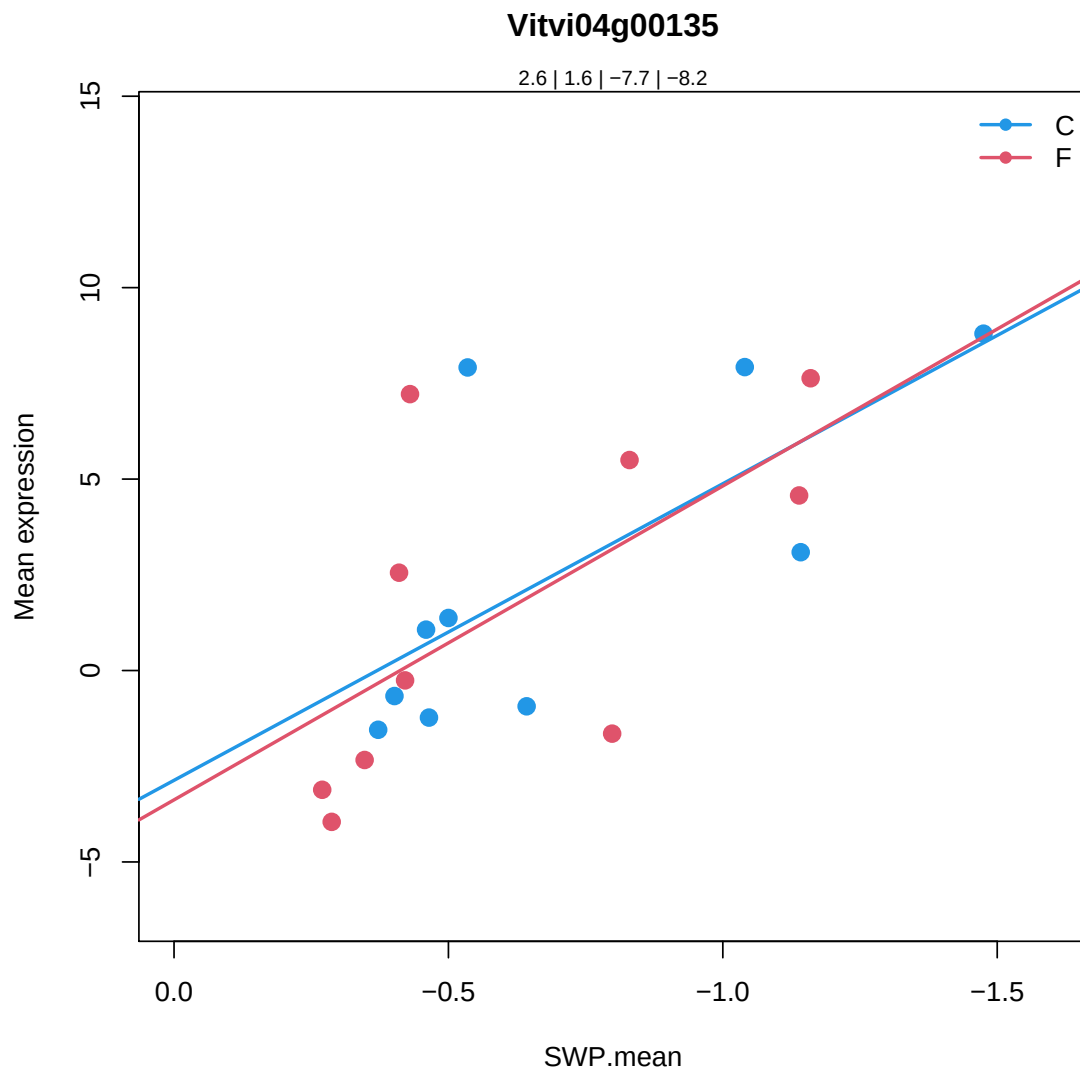
17.6 kDa class II heat shock protein |

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	



8.1.610 Vitvi18g02423: Type1.0 *

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

Vitvi18g02423

35.2

not assigned.unknown

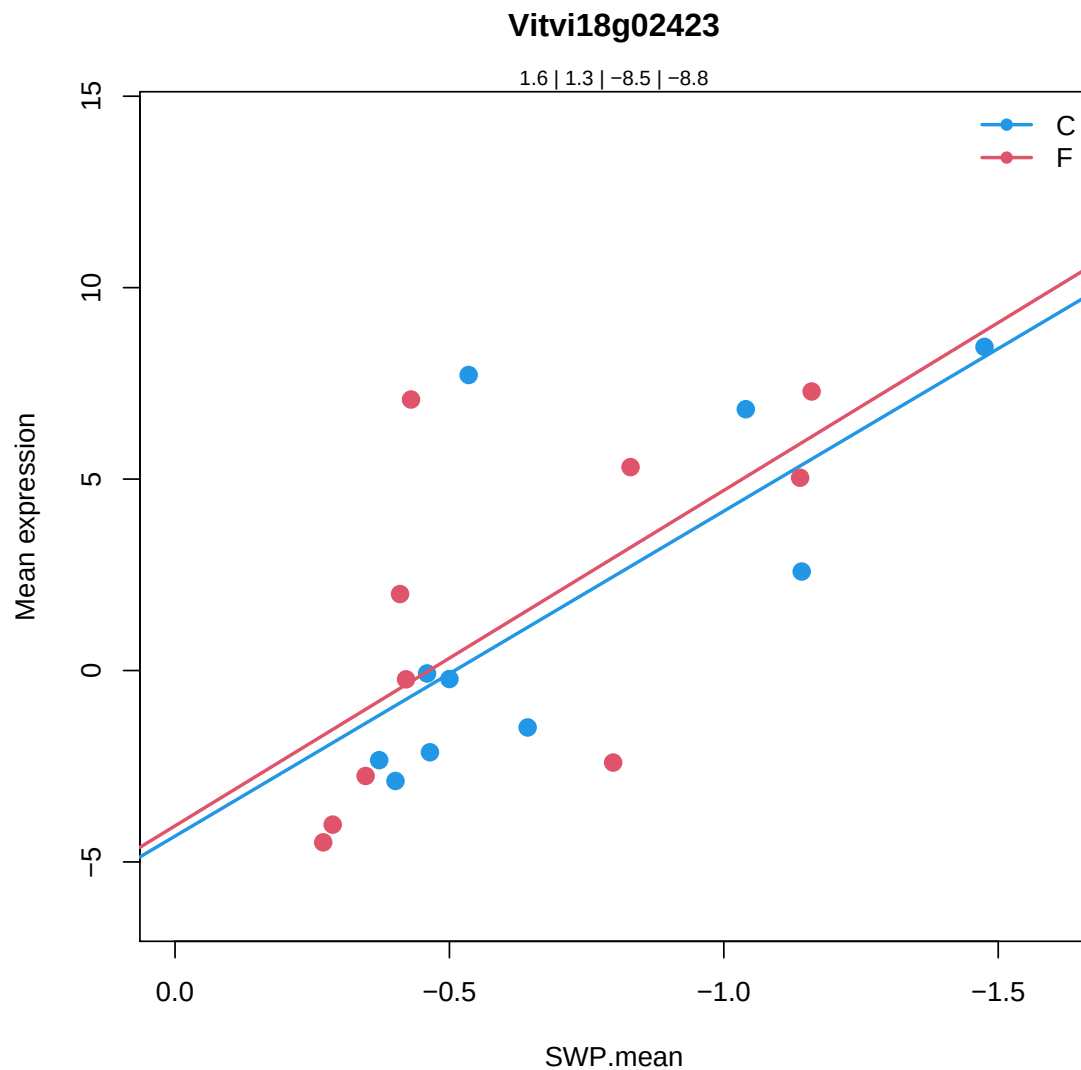
HSP20-like chaperones superfamily protein |

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	



8.2 Type3.C

8.2.1 Vitvi09g01874: Type3.C *

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

Vitvi09g01874

35.2

not assigned.unknown

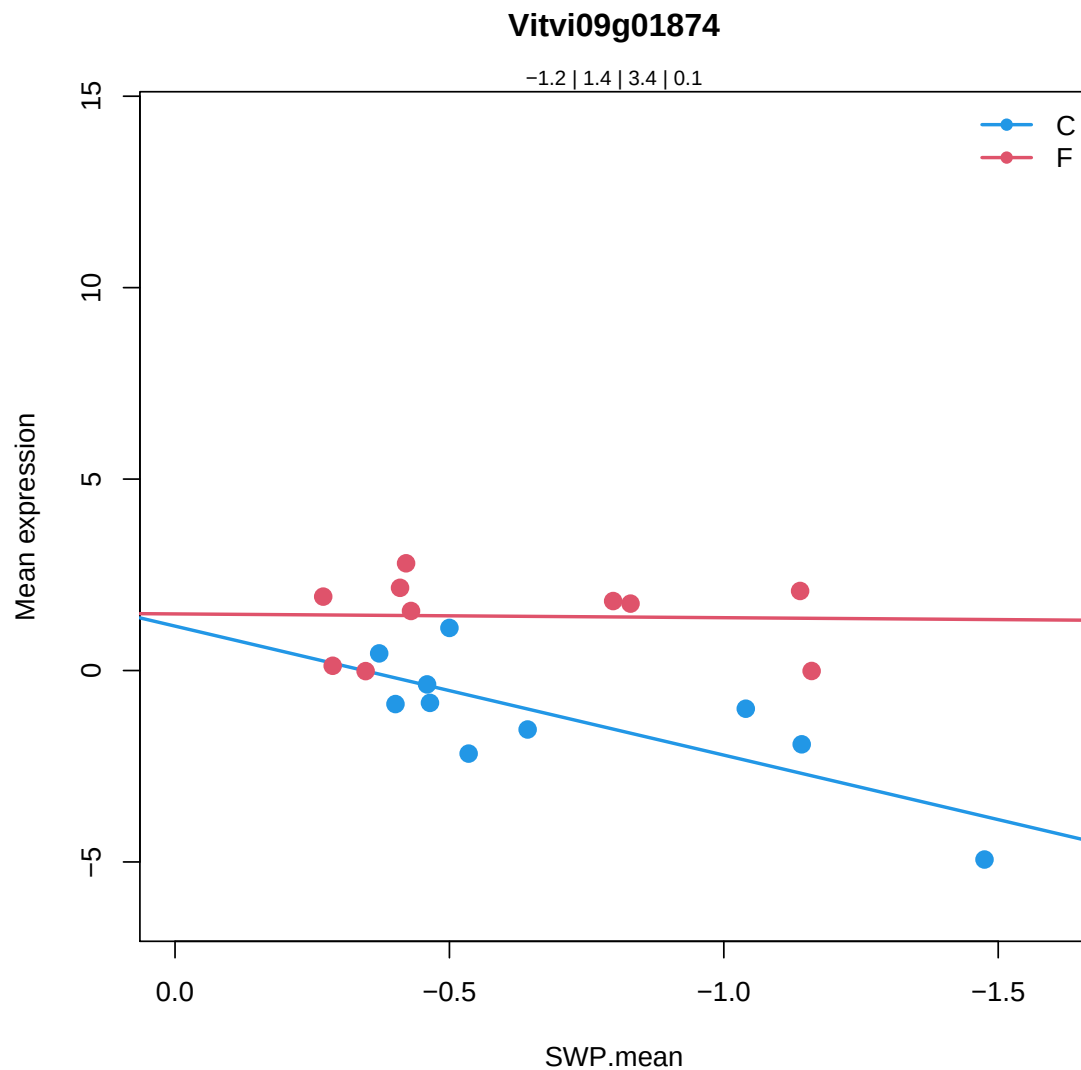
disease resistance family protein / LRR family protein |

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	



8.2.2 Vitvi10g00663: Type3.C *

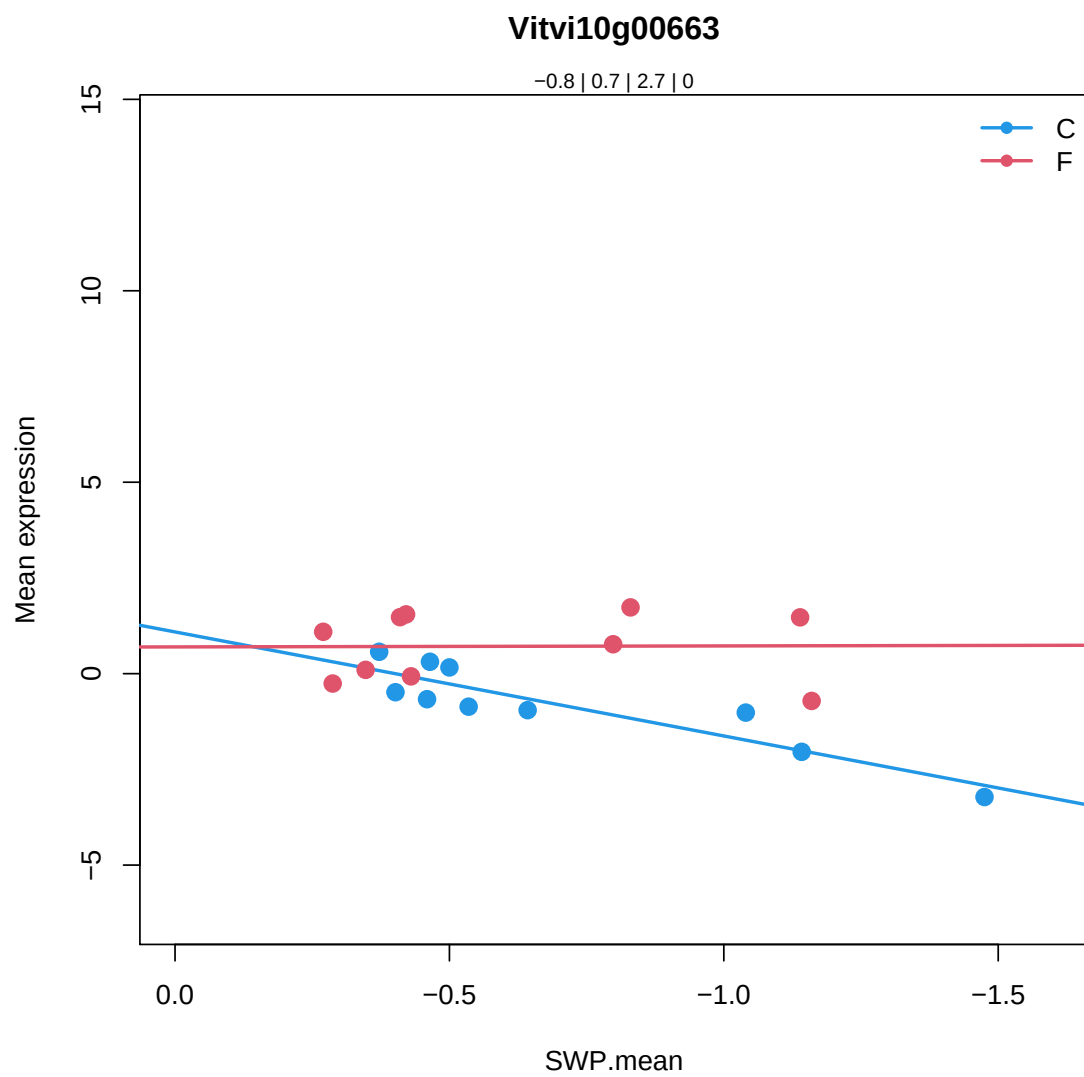
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
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	

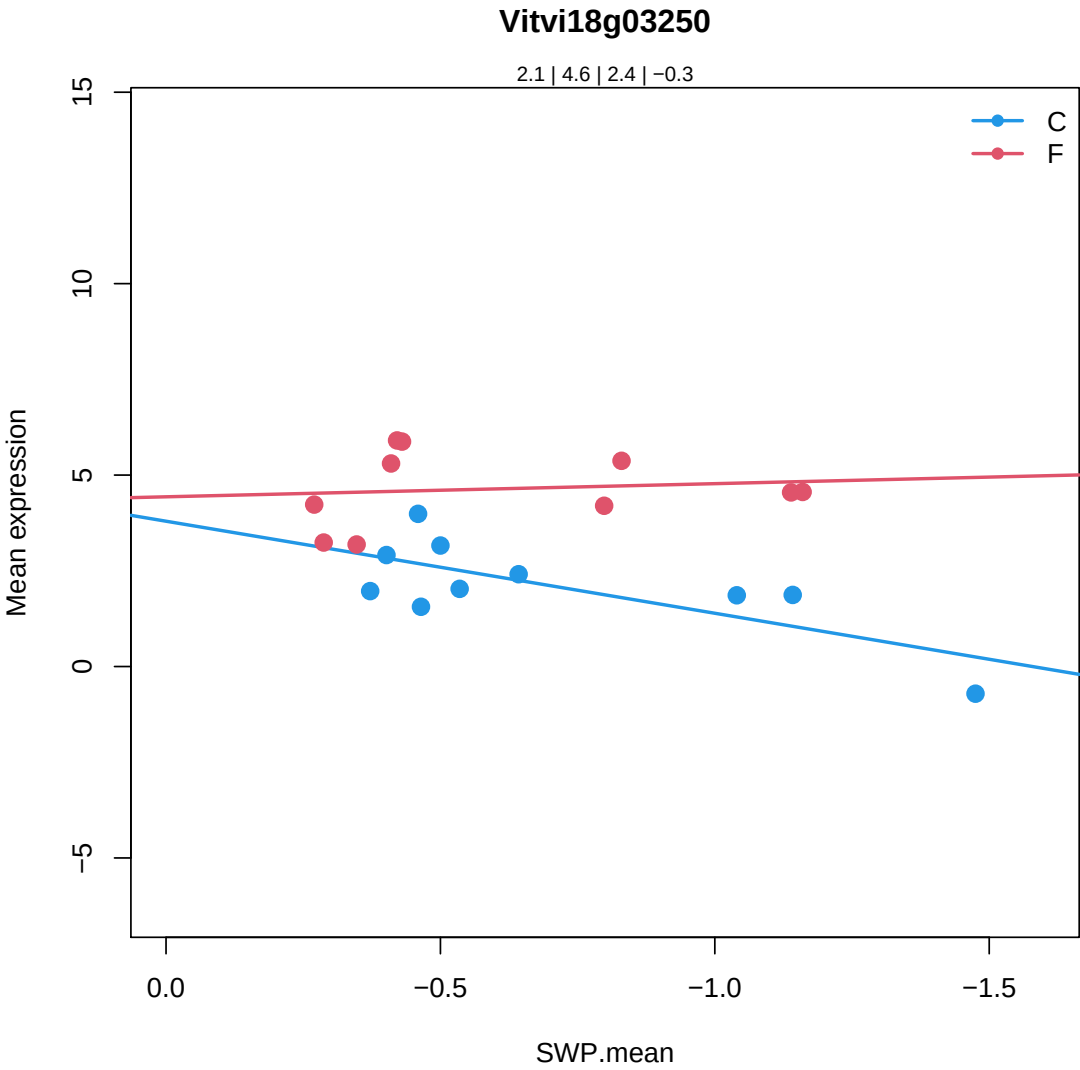


8.2.3 Vitvi18g03250: Type3.C *

```
> 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	



8.2.4 Vitvi05g01758: Type3.C

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

Vitvi05g01758

35.2

not assigned.unknown

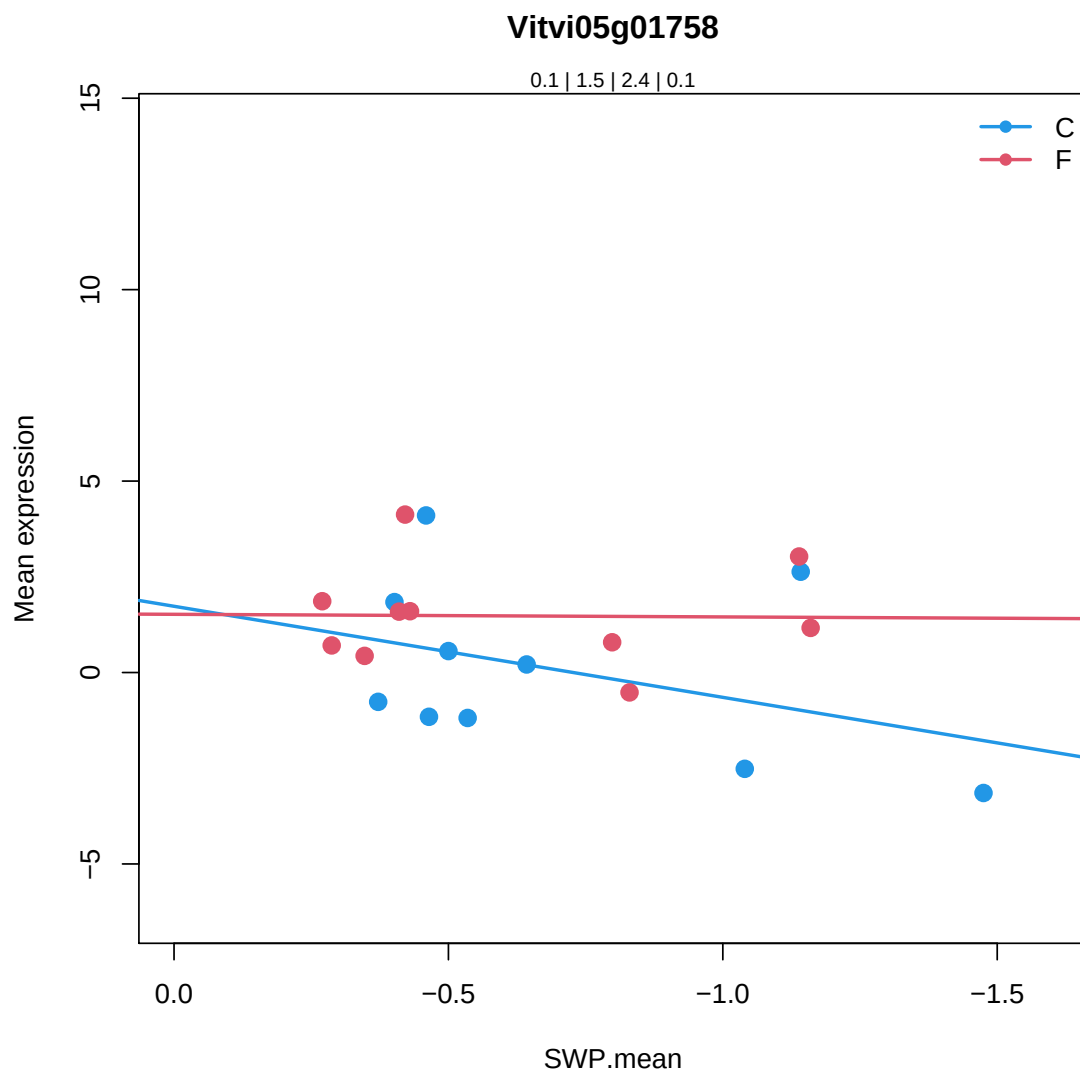
MLP-like protein 423 |

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	



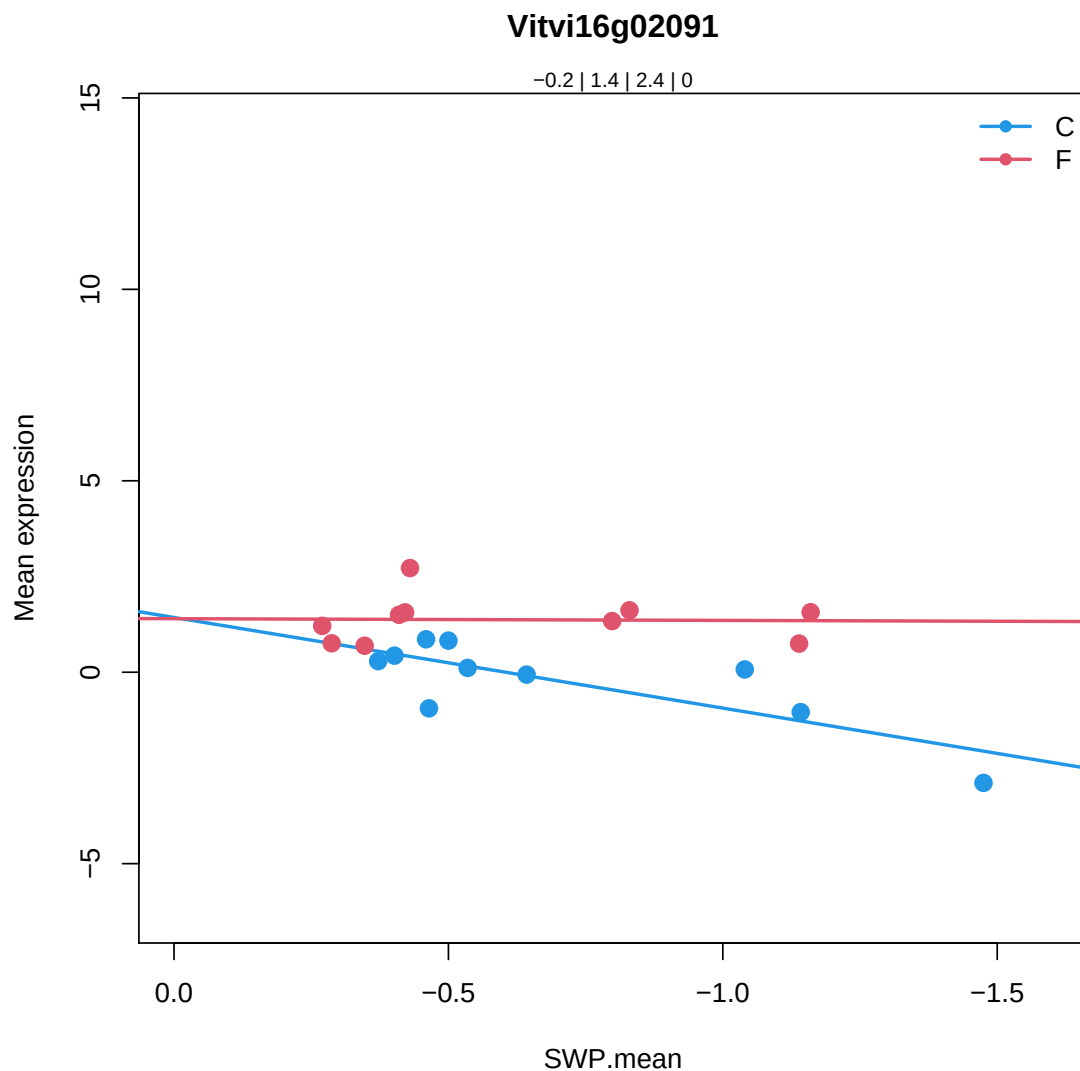
8.2.5 Vitvi16g02091: Type3.C *

```
> 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	



8.2.6 Vitvi16g02098: Type3.C *

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

Vitvi16g02098

35.2

not assigned.unknown

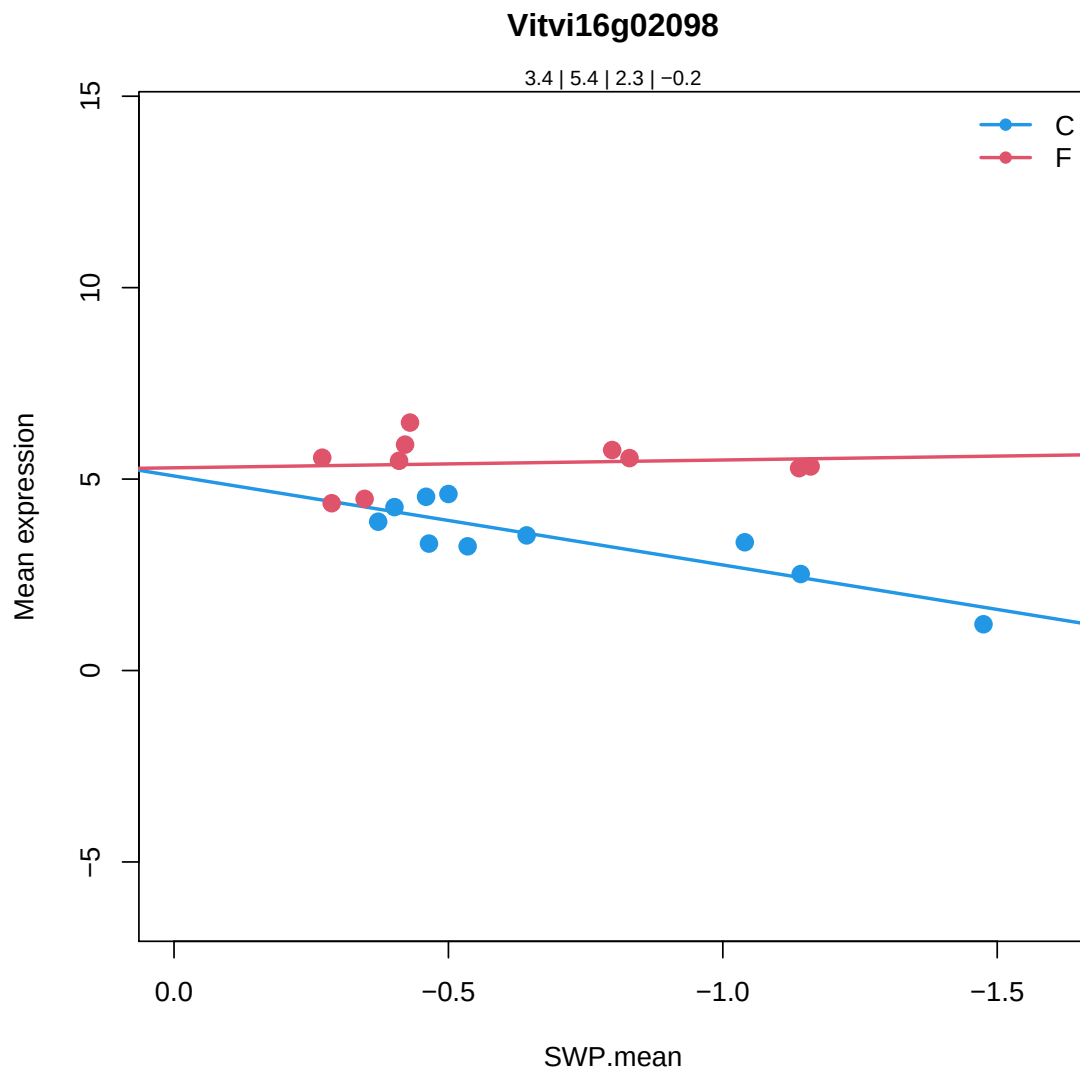
PR5-like receptor kinase |

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	



8.2.7 Vitvi00g02226: Type3.C *

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

Vitvi00g02226

35.2

not assigned.unknown

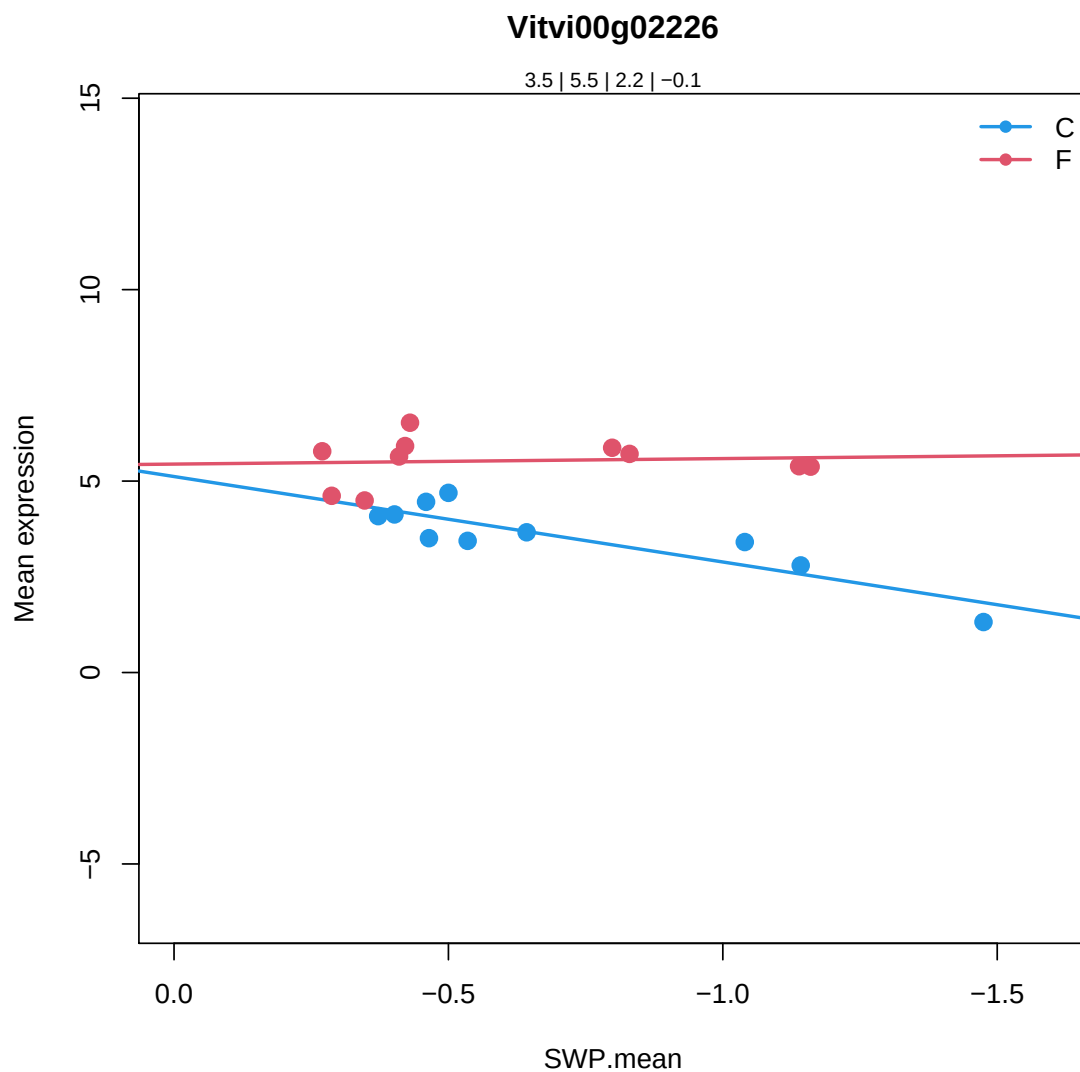
PR5-like receptor kinase |

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	



8.2.8 Vitvi09g01948: Type3.C *

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

```
Vitvi09g01948
```

```
35.2
```

```
not assigned.unknown
```

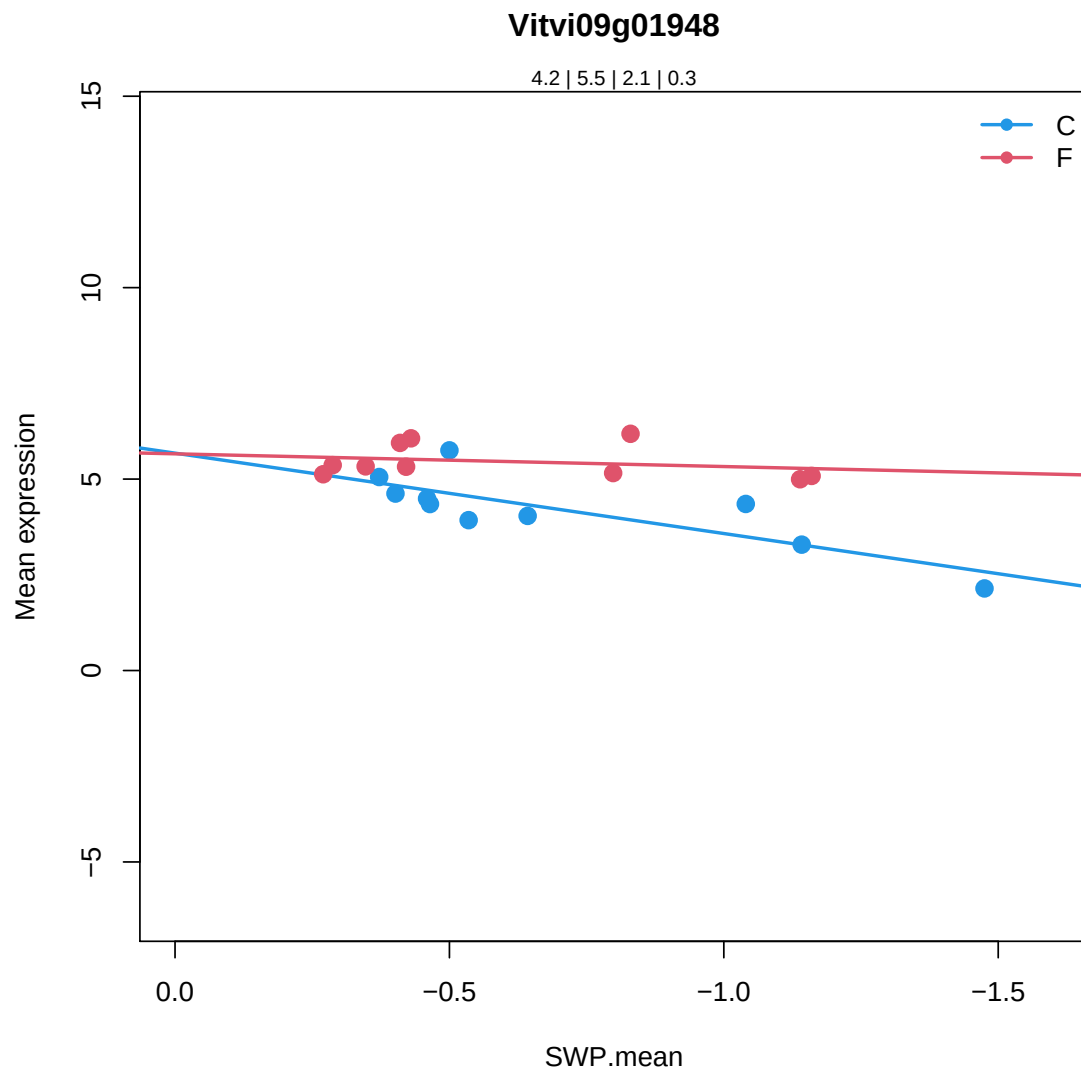
```
disease resistance family protein / LRR family protein |
```

```
Chr2:14737169-14739886 REVERSE LENGTH=905 |
```

```
201606
```

Coefficients for Vitvi09g01948.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.200998	1.598364e-17	***	4.037499e-17	***
SlopeC	2.099137	0.0001557553	***	0.07644173	.
MeanF-MeanC	1.256068	2.246776e-05	***	0.0005036082	***
SlopeF-SlopeC	-1.766936	0.01695143	*	0.9999488	



8.2.9 Vitvi09g01335: Type3.C *

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

Vitvi09g01335

35.2

not assigned.unknown

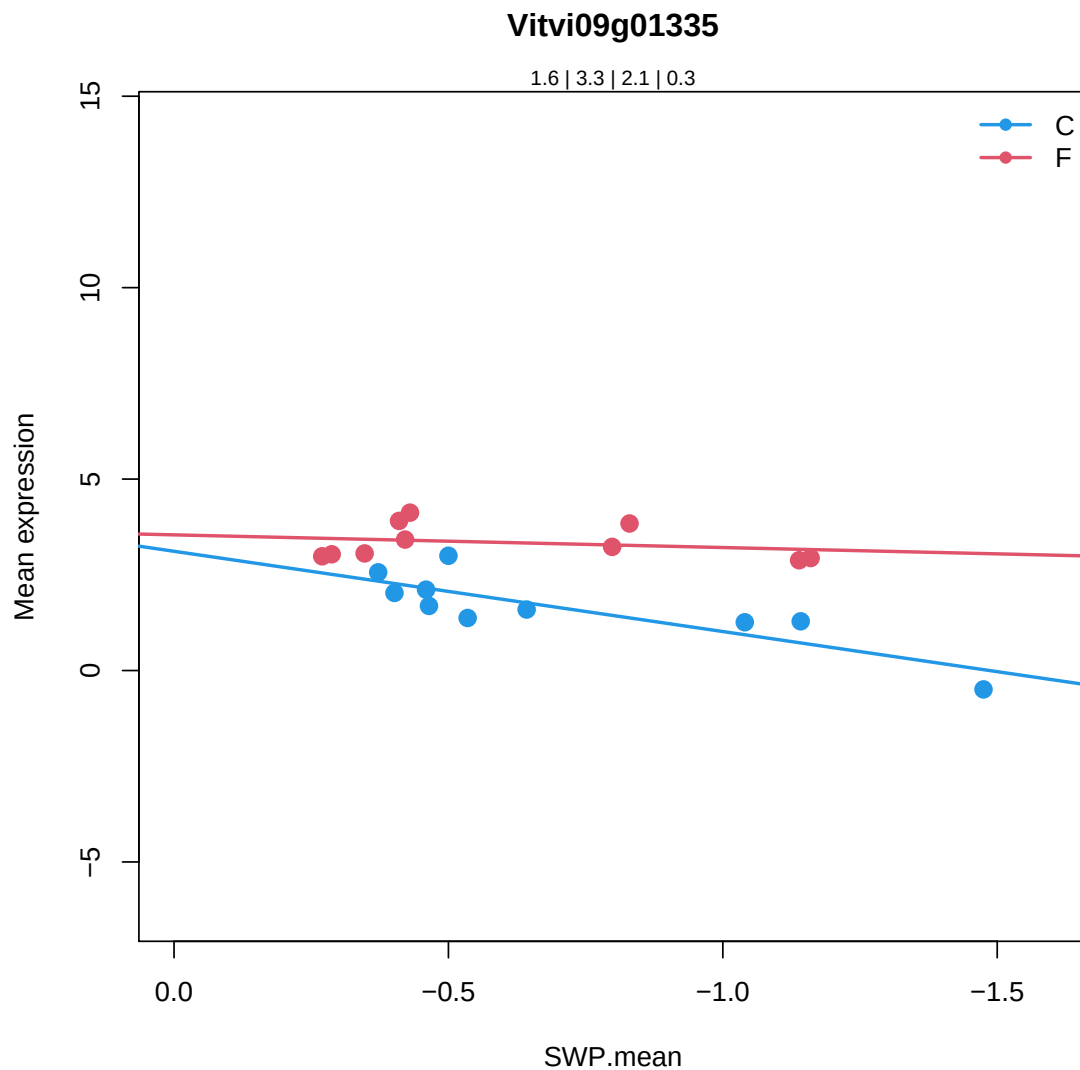
disease resistance family protein / LRR family protein |

Chr2:14737169-14739886 REVERSE LENGTH=905 |

201606

Coefficients for Vitvi09g01335.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.640402	8.137972e-10	***	1.029284e-09	***
SlopeC	2.095882	9.96398e-05	***	0.07644173	.
MeanF-MeanC	1.701105	1.598465e-07	***	6.152474e-06	***
SlopeF-SlopeC	-1.765299	0.01338604	*	0.9999488	



8.2.10 Vitvi16g01549: Type3.C *

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

Vitvi16g01549

35.2

not assigned.unknown

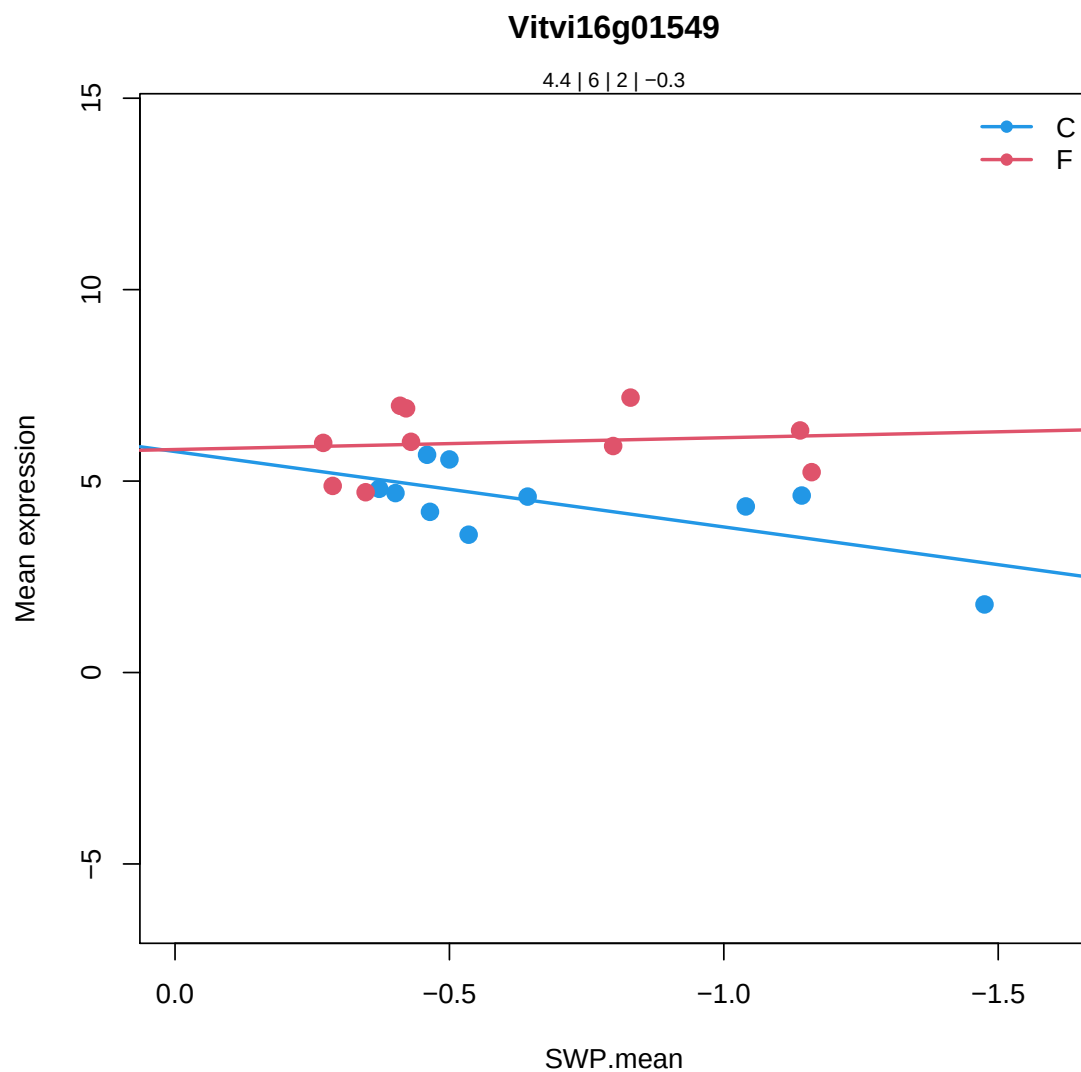
receptor like protein 34 |

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	



8.2.11 Vitvi16g01995: Type3.C *

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

Vitvi16g01995

35.2

not assigned.unknown

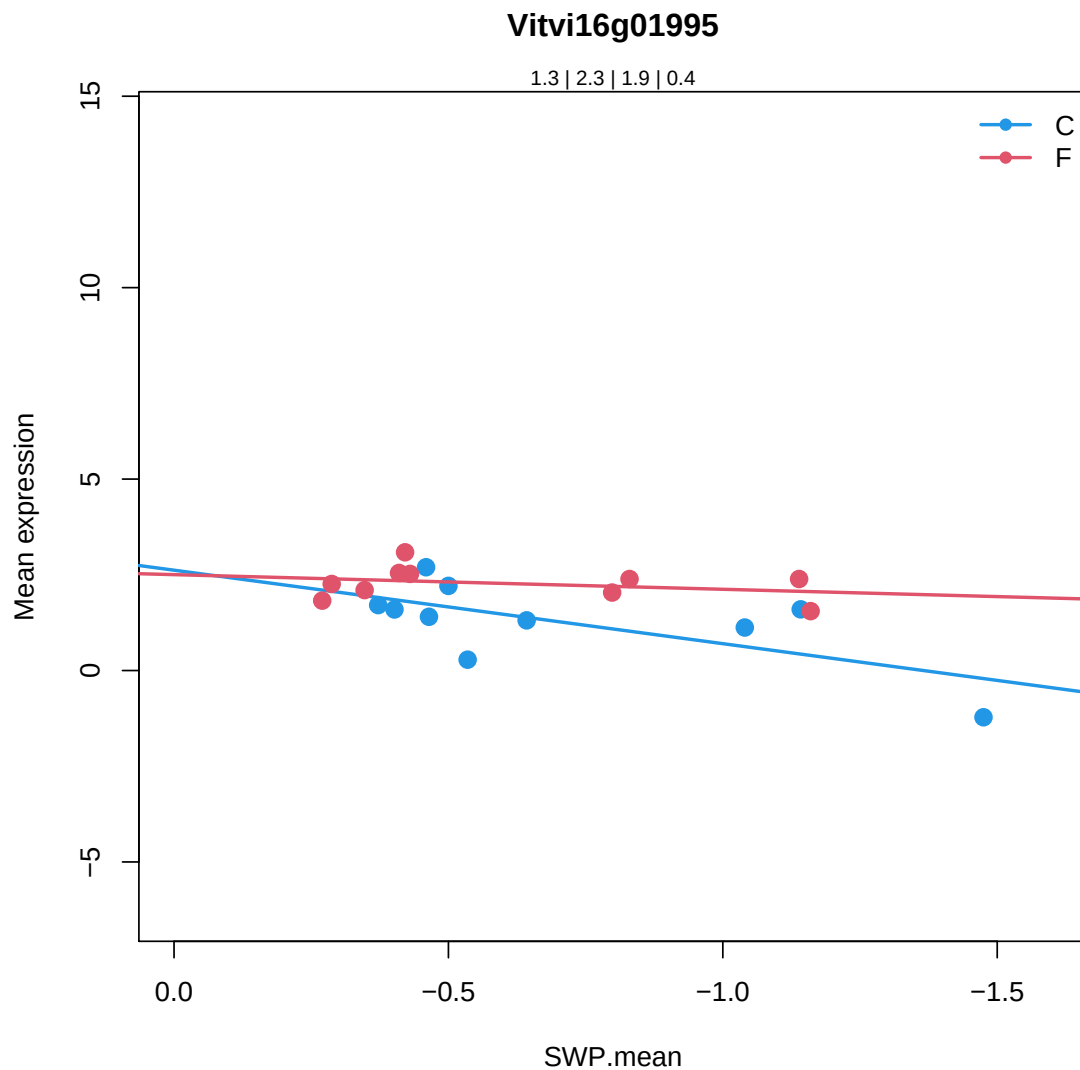
PR5-like receptor kinase |

Chr5:15293325-15295838 REVERSE LENGTH=665 |

201606

Coefficients for Vitvi16g01995.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.270518	2.436594e-06	***	2.787971e-06	***
SlopeC	1.918908	0.002355775	**	0.1841371	
MeanF-MeanC	1.000552	0.001907489	**	0.02124687	*
SlopeF-SlopeC	-1.536769	0.07734706	.	0.9999488	



8.2.12 Vitvi14g03032: Type3.C *

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

Vitvi14g03032

35.2

not assigned.unknown

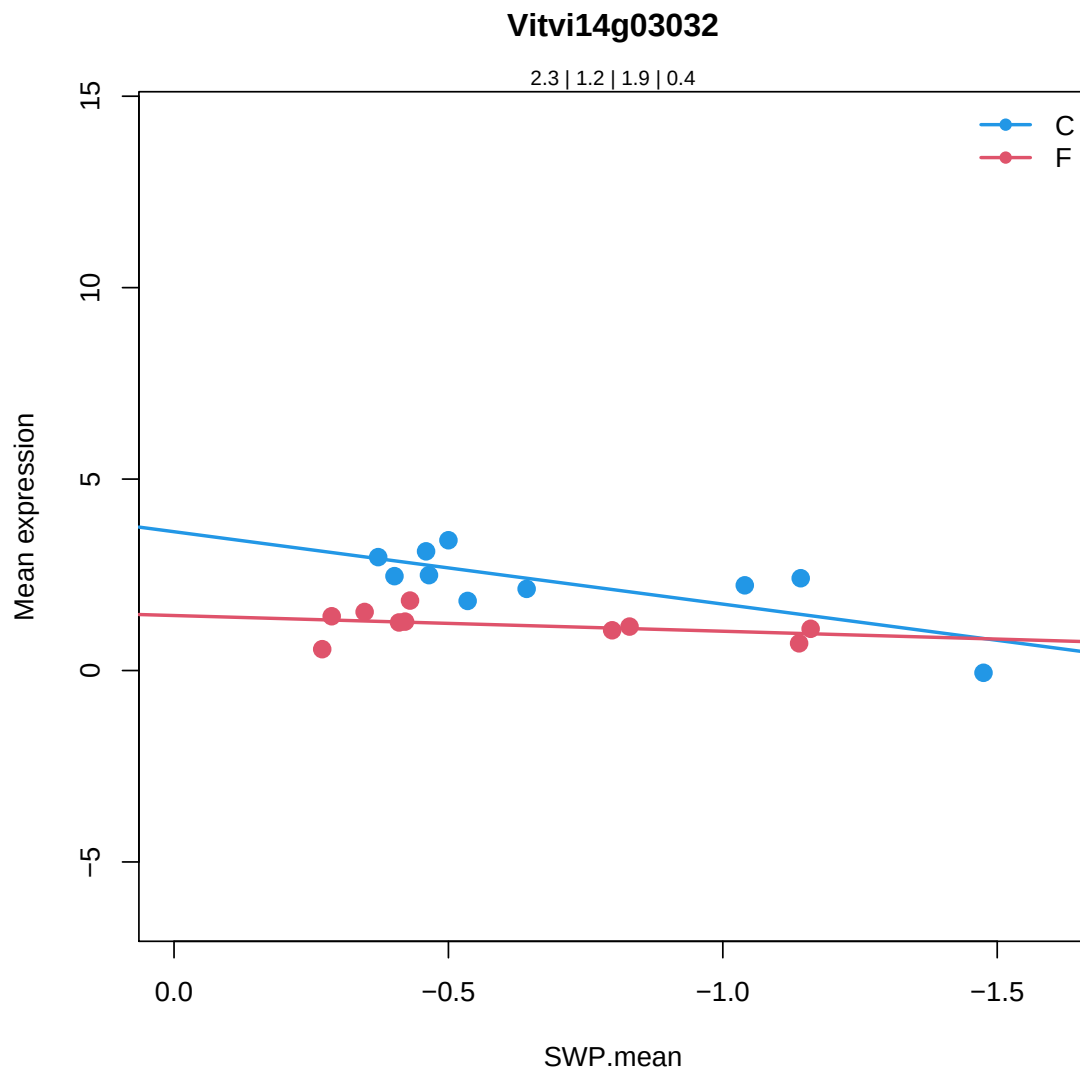
senescence-associated gene 101 |

Chr5:4828754-4830769 FORWARD LENGTH=537 |

201606

Coefficients for Vitvi14g03032.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.295758	4.137197e-12	***	5.741001e-12	***
SlopeC	1.890992	0.0005292593	***	0.1005065	
MeanF-MeanC	-1.109618	0.00011621	***	0.002052459	**
SlopeF-SlopeC	-1.481025	0.04379561	*	0.9999488	



8.2.13 Vitvi05g01285: Type3.C *

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

Vitvi05g01285

35.2

not assigned.unknown

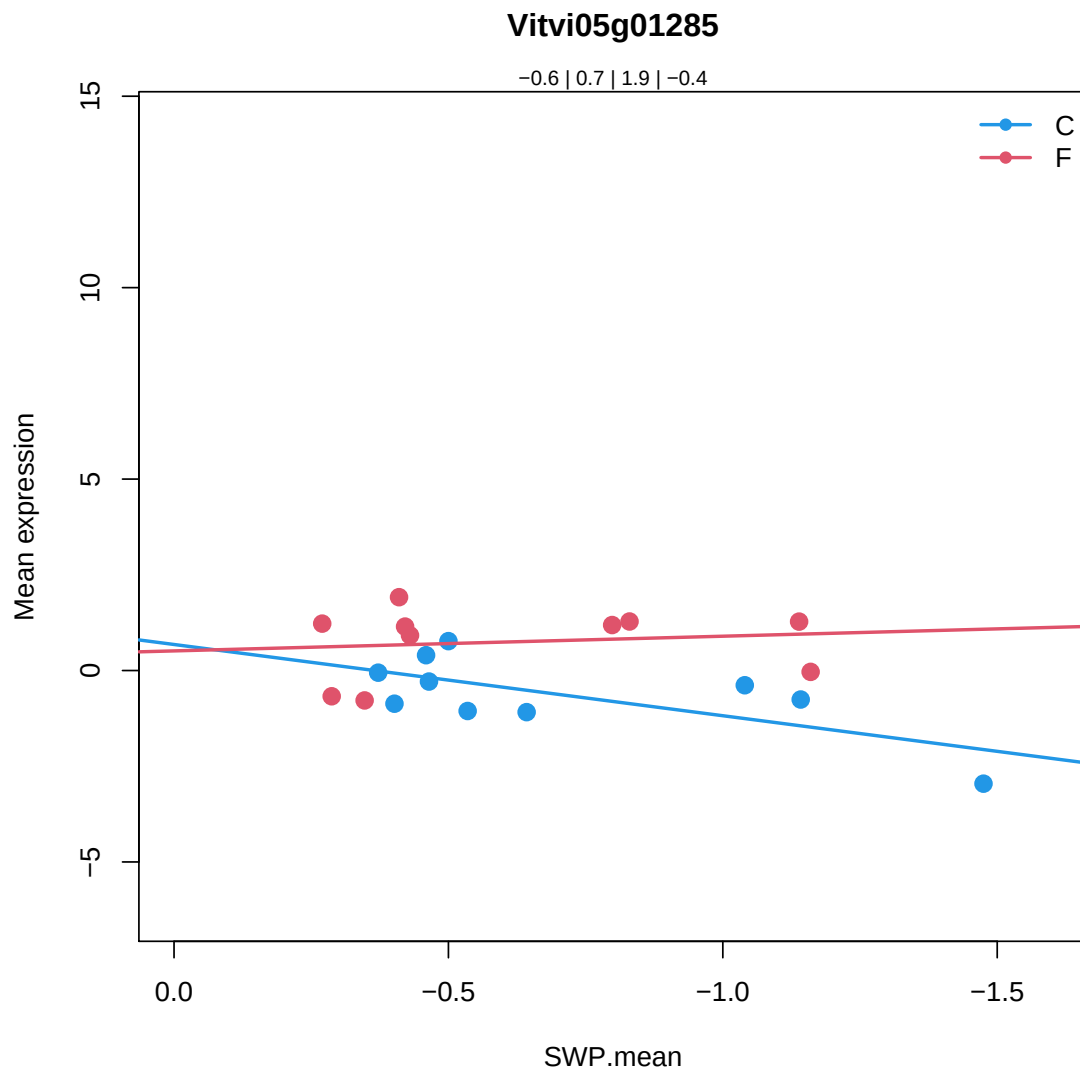
indole-3-acetate beta-D-glucosyltransferase |

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	



8.2.14 Vitvi14g03057: Type3.C *

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

Vitvi14g03057

35.2

not assigned.unknown

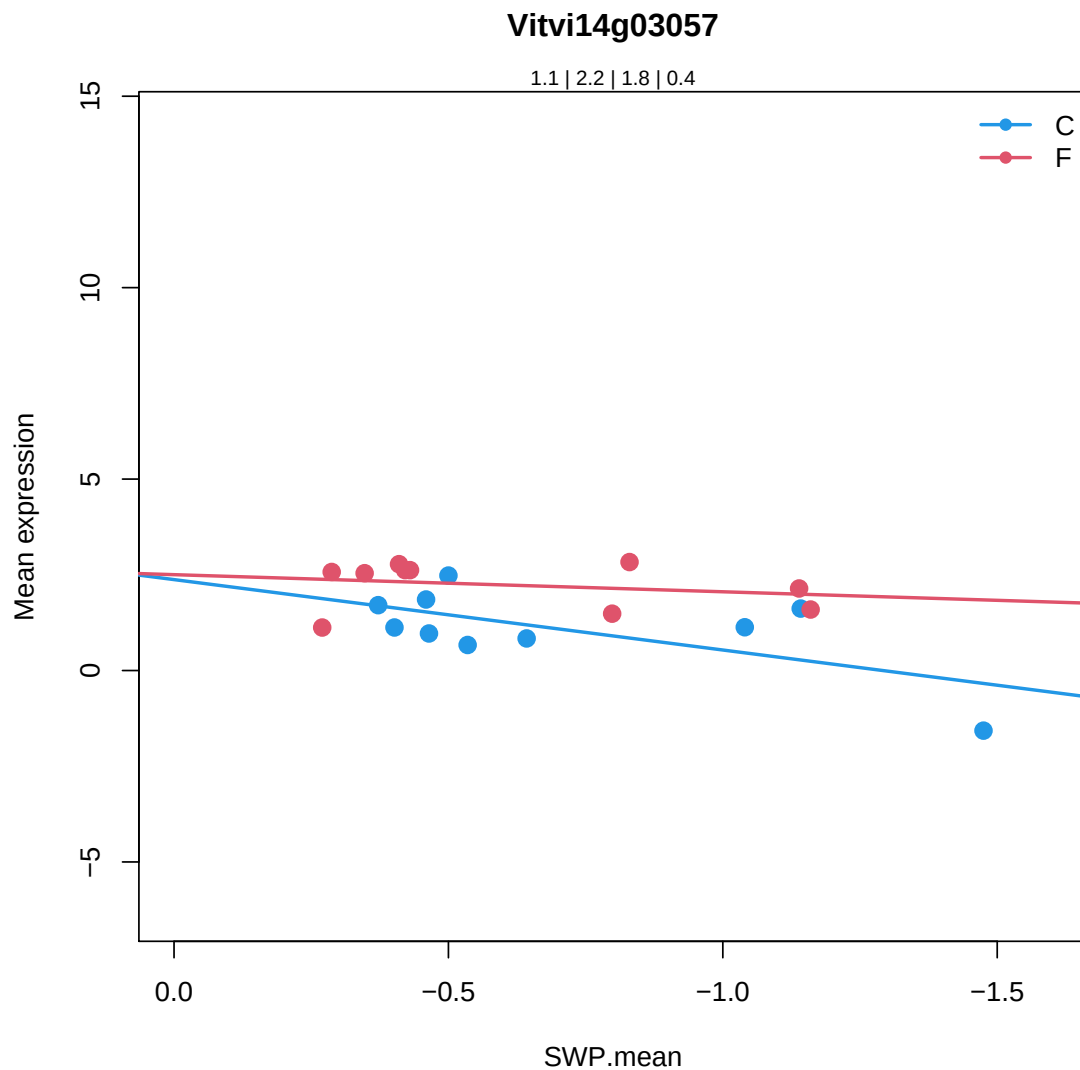
Leucine-rich repeat receptor-like protein kinase family protein |

Chr4:5637467-5640496 REVERSE LENGTH=1009 |

201606

Coefficients for Vitvi14g03057.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.081444	7.919614e-05	***	8.76176e-05	***
SlopeC	1.839061	0.007193766	**	0.2775469	
MeanF-MeanC	1.149688	0.001446577	**	0.01693451	*
SlopeF-SlopeC	-1.391957	0.1455251		0.9999488	



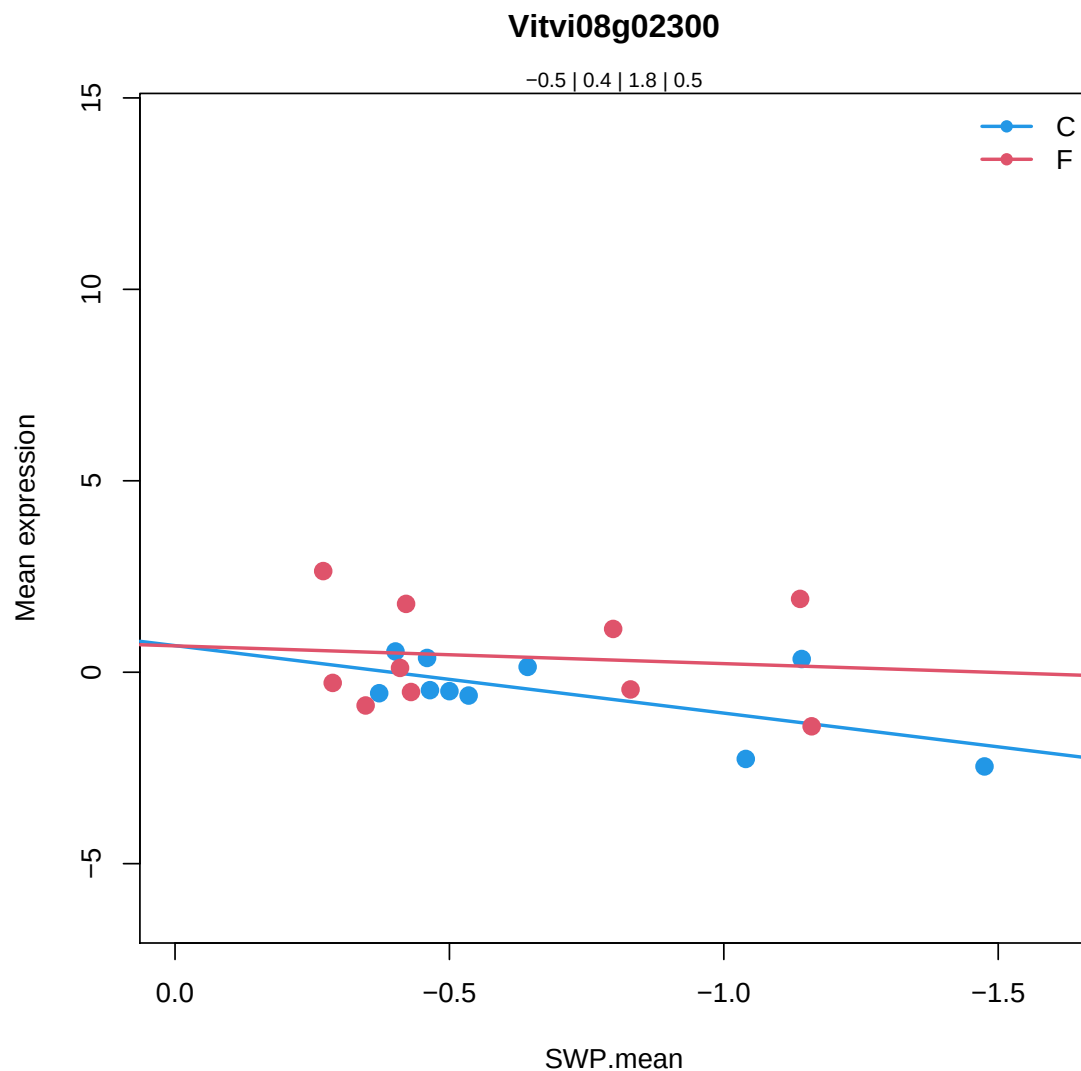
8.2.15 Vitvi08g02300: Type3.C

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

```
Vitvi08g02300
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi08g02300.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.5448287	0.1162978		0.1200712	
SlopeC	1.762531	0.07054354	.	0.5607758	
MeanF-MeanC	0.9504926	0.05616735	.	0.25794	
SlopeF-SlopeC	-1.298304	0.3567596		0.9999488	



8.2.16 Vitvi18g00973: Type3.C *

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

Vitvi18g00973

27.3.25

RNA.regulation of transcription.MYB domain transcription factor family

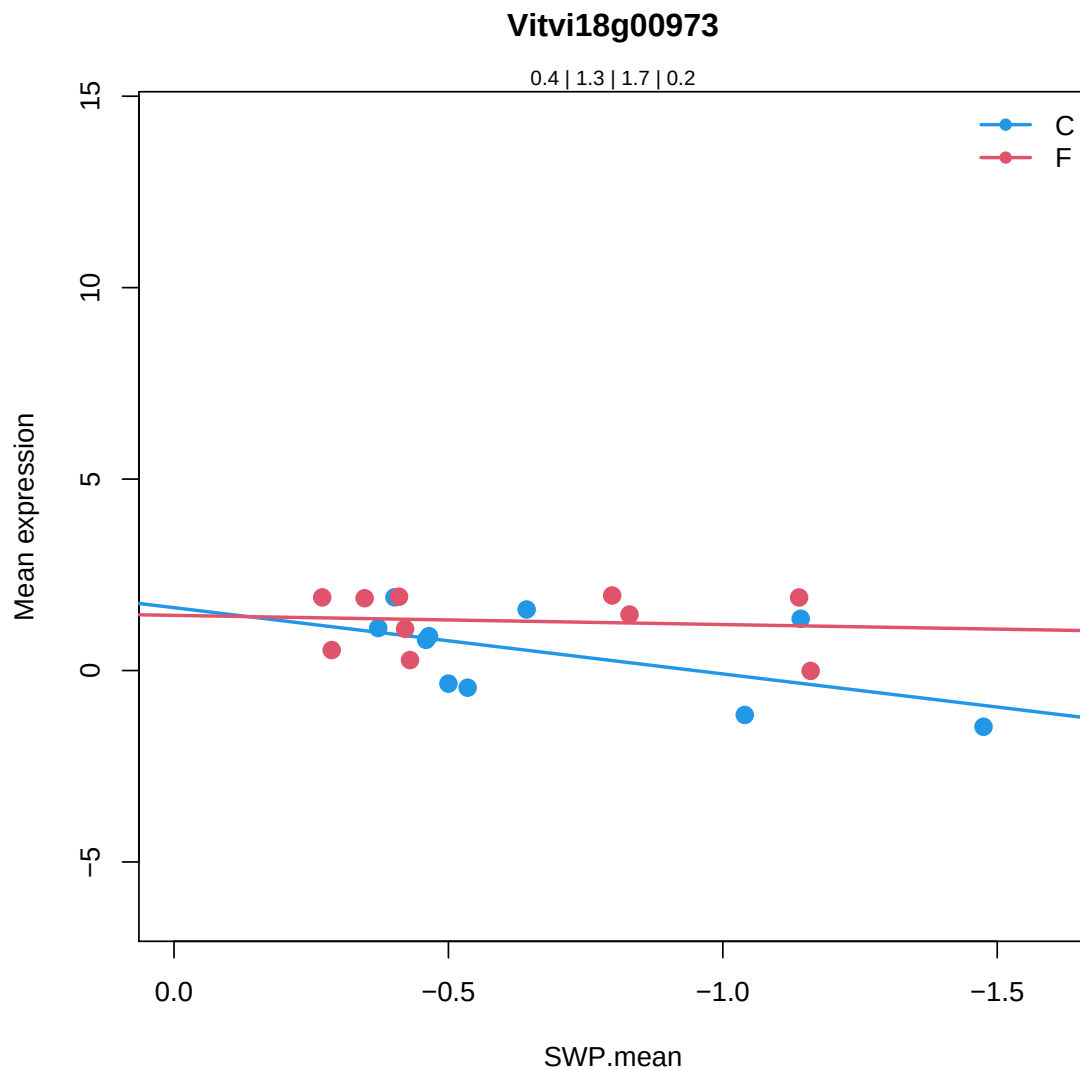
RAD-like 1 |

Chr4:18271457-18271857 REVERSE LENGTH=100 |

201606

Coefficients for Vitvi18g00973.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4243761	0.1283994		0.1324309	
SlopeC	1.730751	0.03038041	*	0.4320841	
MeanF-MeanC	0.8696495	0.03213576	*	0.1776605	
SlopeF-SlopeC	-1.491567	0.1935135		0.9999488	



8.2.17 Vitvi16g01960: Type3.C *

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

Vitvi16g01960

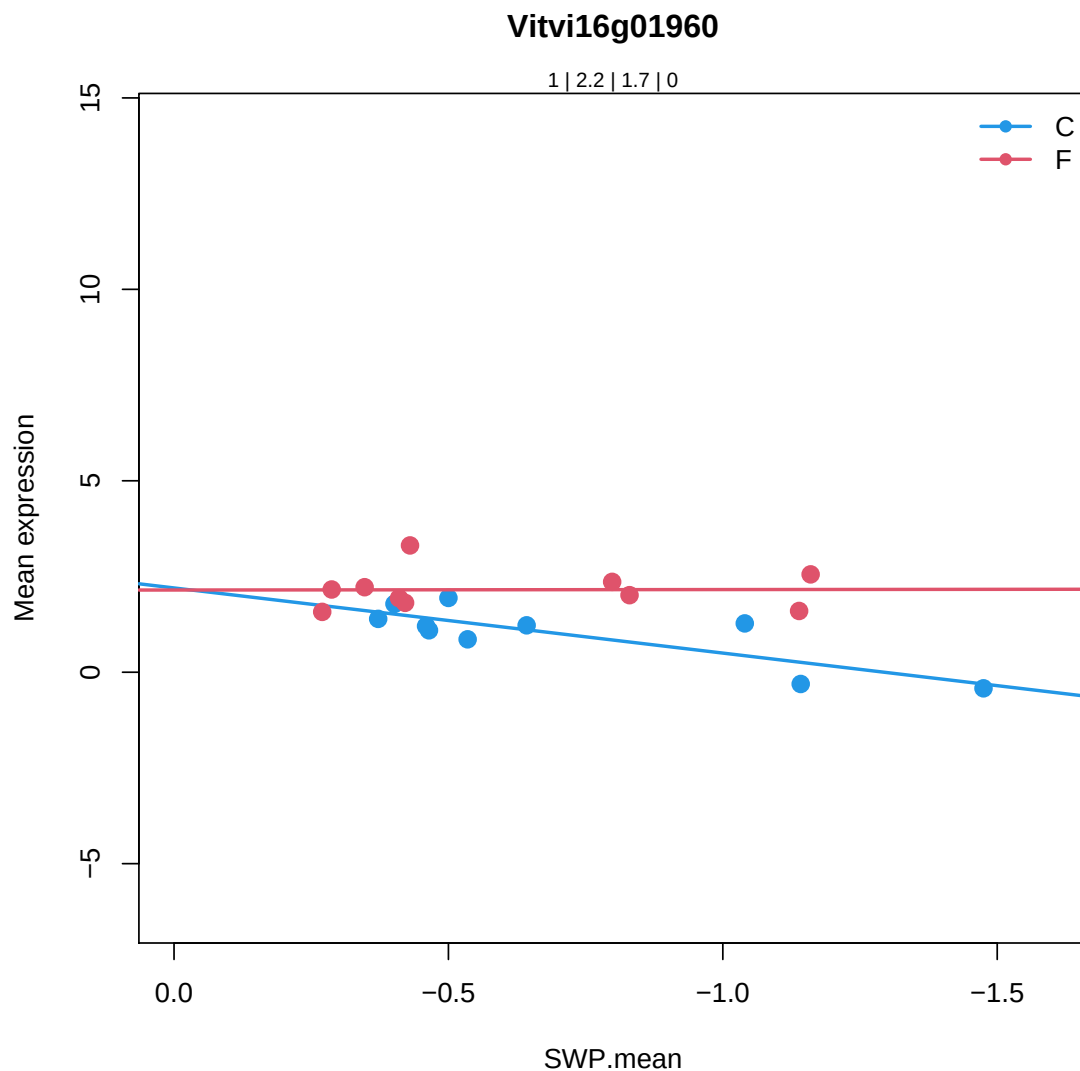
30.2.24

signalling.receptor kinases.S-locus glycoprotein like

NA

Coefficients for Vitvi16g01960.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.004778	2.984788e-06	***	3.408056e-06	***
SlopeC	1.701228	0.0009907854	***	0.1271346	
MeanF-MeanC	1.149623	4.831542e-05	***	0.0009563943	***
SlopeF-SlopeC	-1.713058	0.0173612	*	0.9999488	



8.2.18 Vitvi18g01262: Type3.C *

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

Vitvi18g01262

30.2.12

signalling.receptor kinases.leucine rich repeat XII

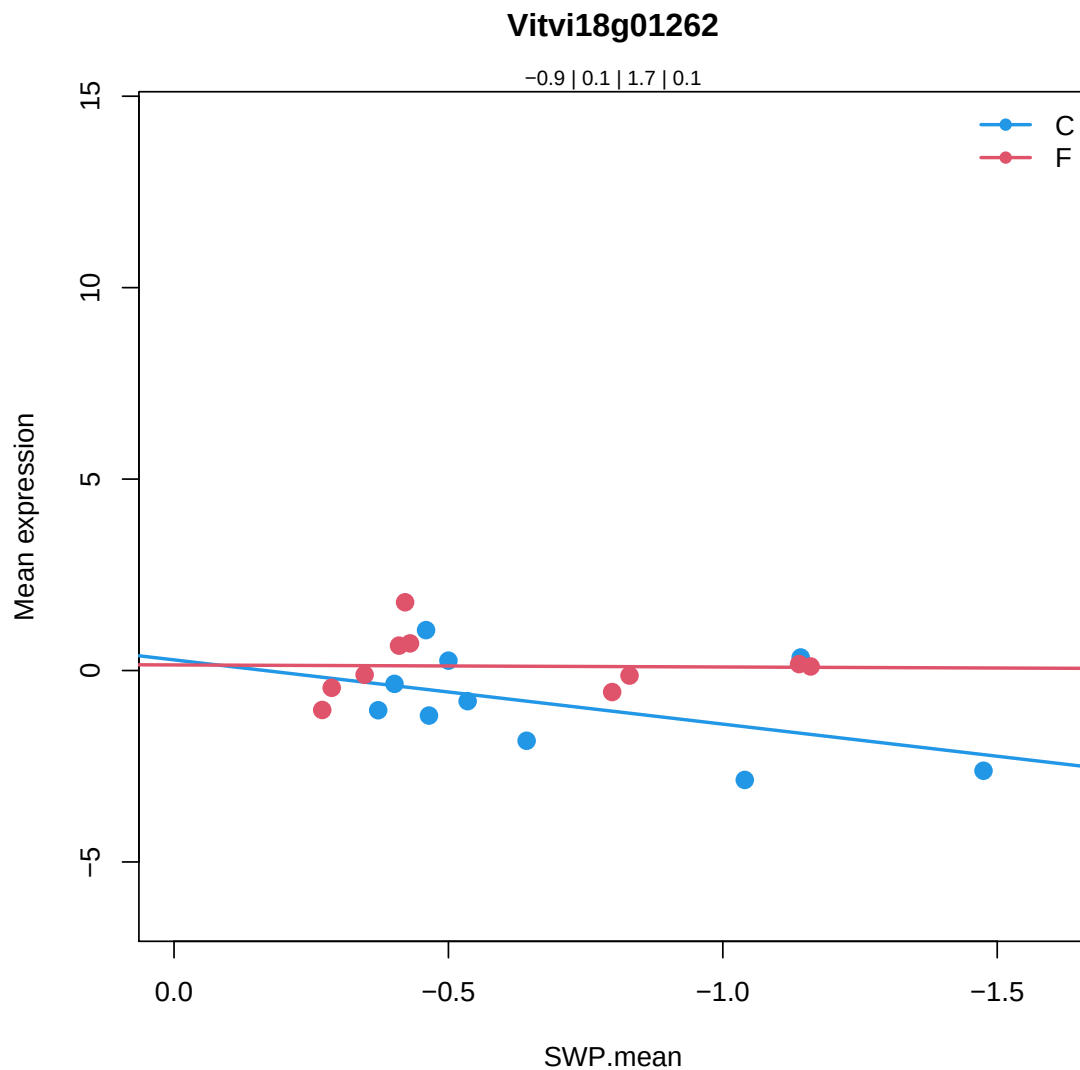
Leucine-rich repeat protein kinase family protein |

Chr3:17527611-17530748 FORWARD LENGTH=1010 |

201606

Coefficients for Vitvi18g01262.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.902123	0.005227458	**	0.005572202	**
SlopeC	1.678005	0.04986674	*	0.5091026	
MeanF-MeanC	1.014862	0.02184095	*	0.1343421	
SlopeF-SlopeC	-1.624447	0.1905261		0.9999488	



8.2.19 Vitvi11g00766: Type3.C *

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

Vitvi11g00766

30.2.12

signalling.receptor kinases.leucine rich repeat XII

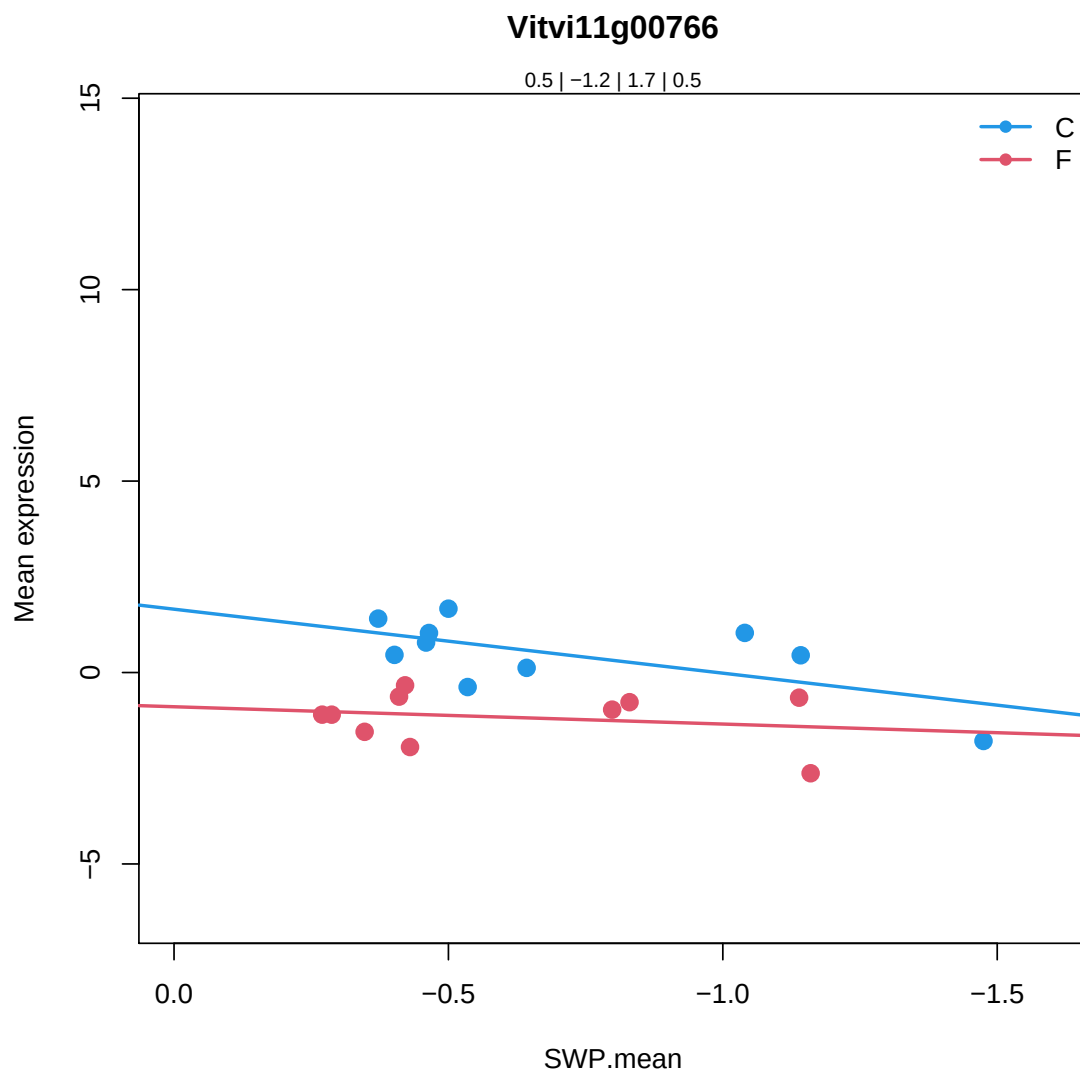
kinase family with leucine-rich repeat domain-containing protein |

Chr1:13220940-13224386 FORWARD LENGTH=1120 |

201606

Coefficients for Vitvi11g00766.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.479062	0.04456731	*	0.04647612	*
SlopeC	1.67106	0.01401099	*	0.3359386	
MeanF-MeanC	-1.648529	3.581314e-05	***	0.000745199	***
SlopeF-SlopeC	-1.219236	0.2035843		0.9999488	



8.2.20 Vitvi08g00630: Type3.C *

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

Vitvi08g00630

35.2

not assigned.unknown

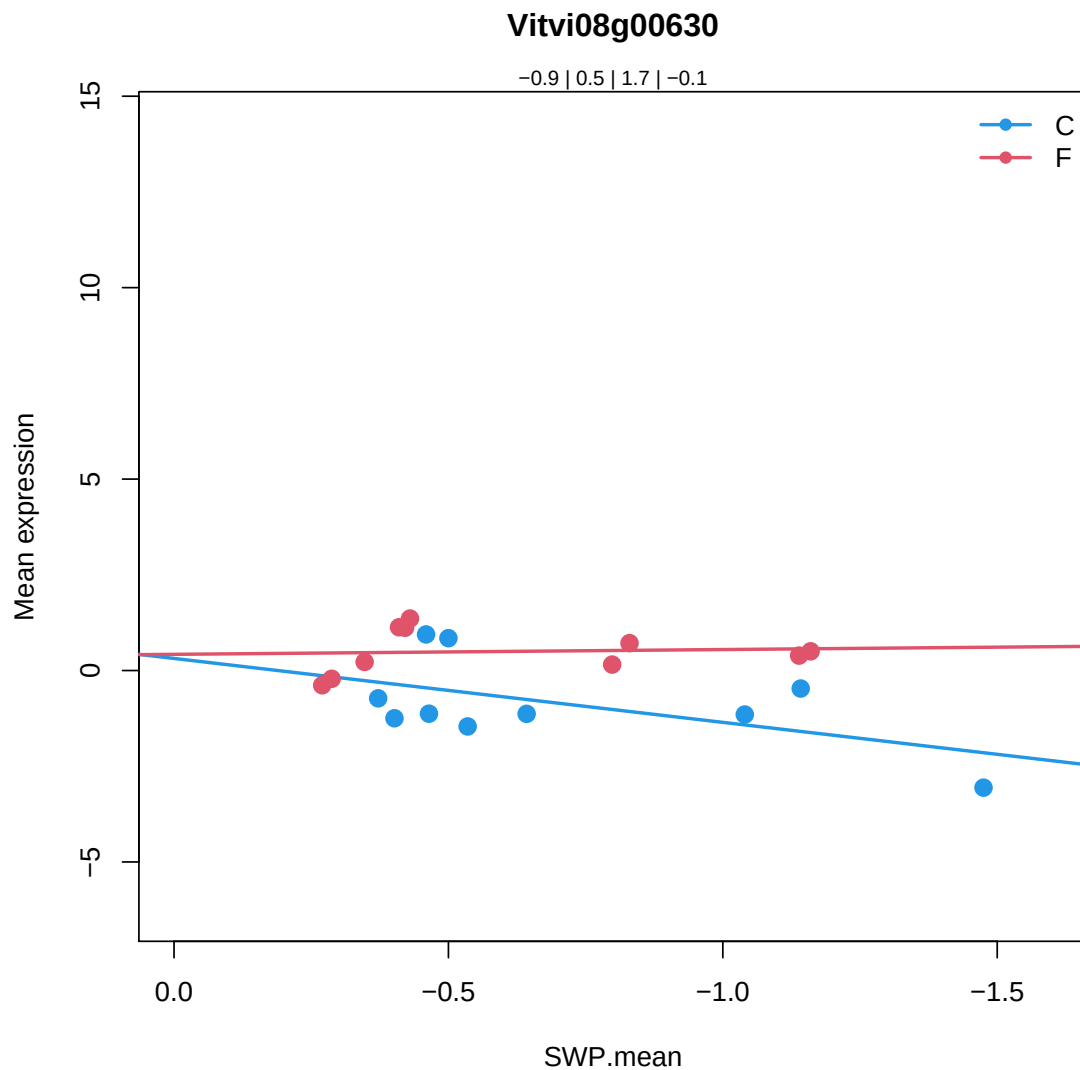
E3 ubiquitin-protein ligase PUB24-like protein |

Chr3:3736578-3738208 REVERSE LENGTH=456 |

201606

Coefficients for Vitvi08g00630.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.8585846	0.001922776	**	0.002068677	**
SlopeC	1.668838	0.0220346	*	0.3914352	
MeanF-MeanC	1.357437	0.0007080838	***	0.009384875	**
SlopeF-SlopeC	-1.793805	0.08877097	.	0.9999488	



8.2.21 Vitvi16g02010: Type3.C *

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

Vitvi16g02010

29.5.11.4.2

protein.degradation.ubiquitin.E3.RING

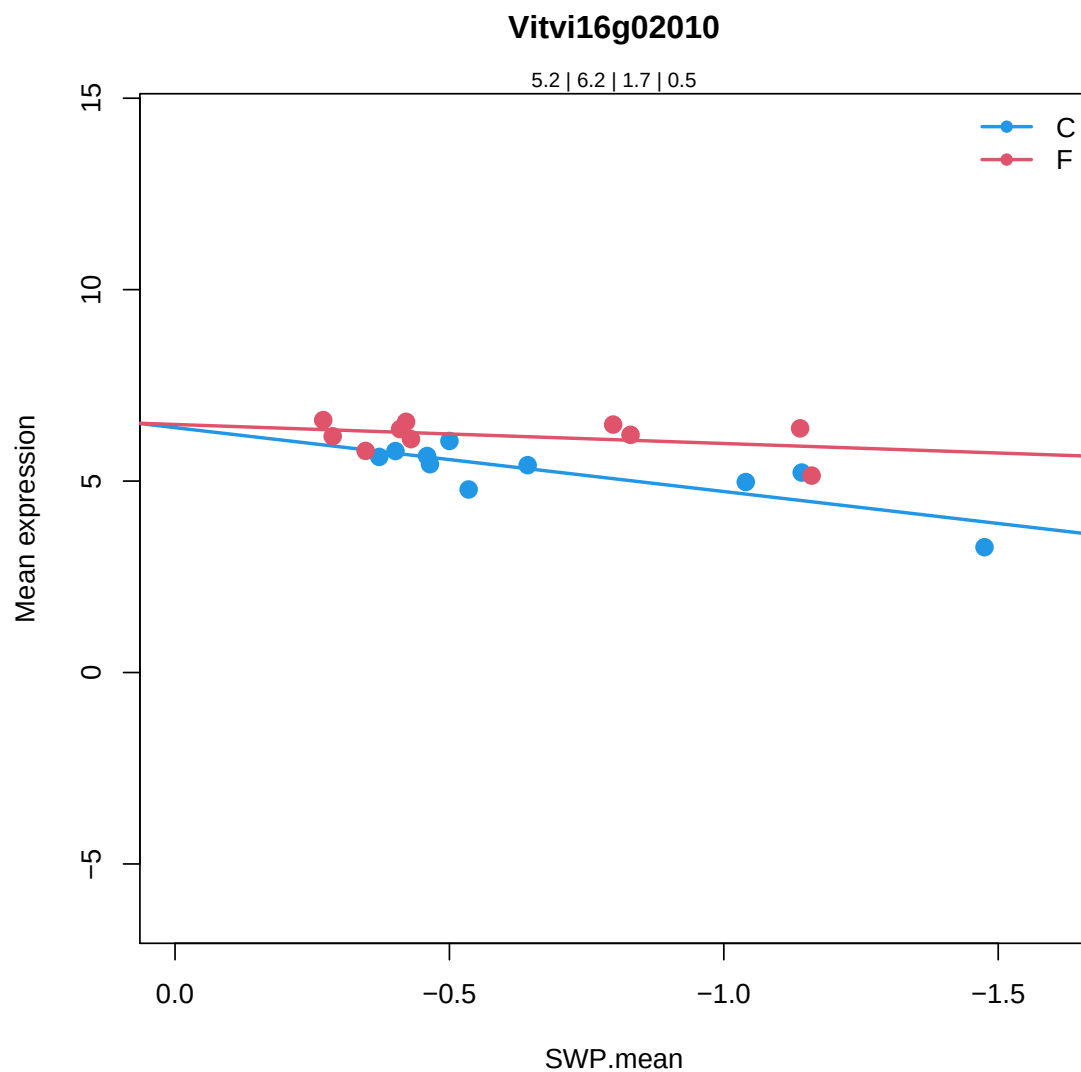
Protein kinase superfamily protein |

Chr1:24965410-24967432 REVERSE LENGTH=609 |

201606

Coefficients for Vitvi16g02010.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.222345	1.552625e-20	***	1.013495e-19	***
SlopeC	1.668473	0.0005237736	***	0.1005065	
MeanF-MeanC	0.9532332	0.0001547785	***	0.002583936	**
SlopeF-SlopeC	-1.171397	0.06793874	.	0.9999488	



8.2.22 Vitvi01g02251: Type3.C *

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

```
Vitvi01g02251
```

```
35.2
```

```
not assigned.unknown
```

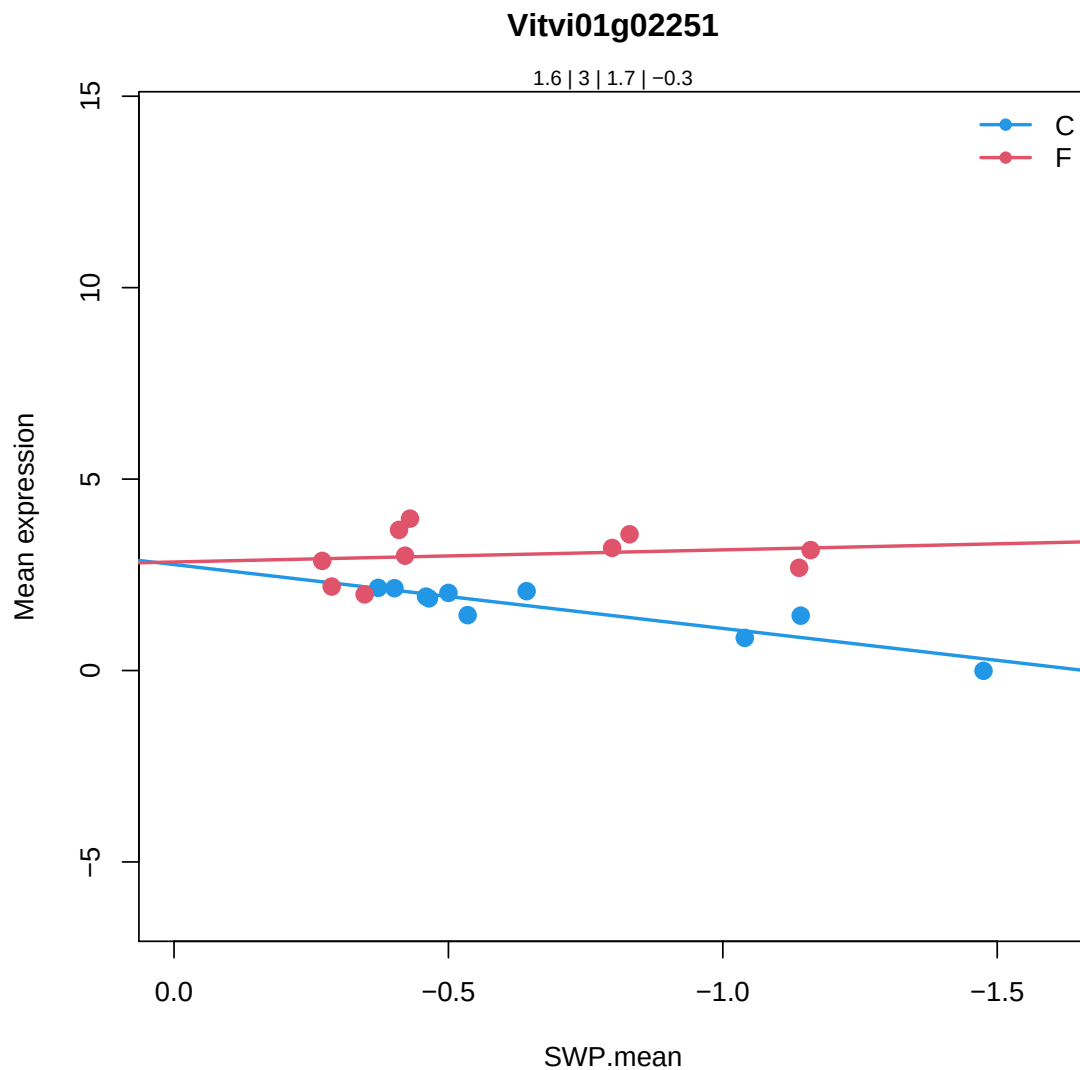
```
disease resistance family protein / LRR family protein |
```

```
Chr2:14737169-14739886 REVERSE LENGTH=905 |
```

```
201606
```

Coefficients for Vitvi01g02251.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.594571	1.864711e-09	***	2.33043e-09	***
SlopeC	1.66785	0.001222641	**	0.1365704	
MeanF-MeanC	1.432543	2.793651e-06	***	8.079855e-05	***
SlopeF-SlopeC	-1.98467	0.007088398	**	0.9999488	



8.2.23 Vitvi18g01321: Type3.C *

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

Vitvi18g01321

33.99

development.unspecified

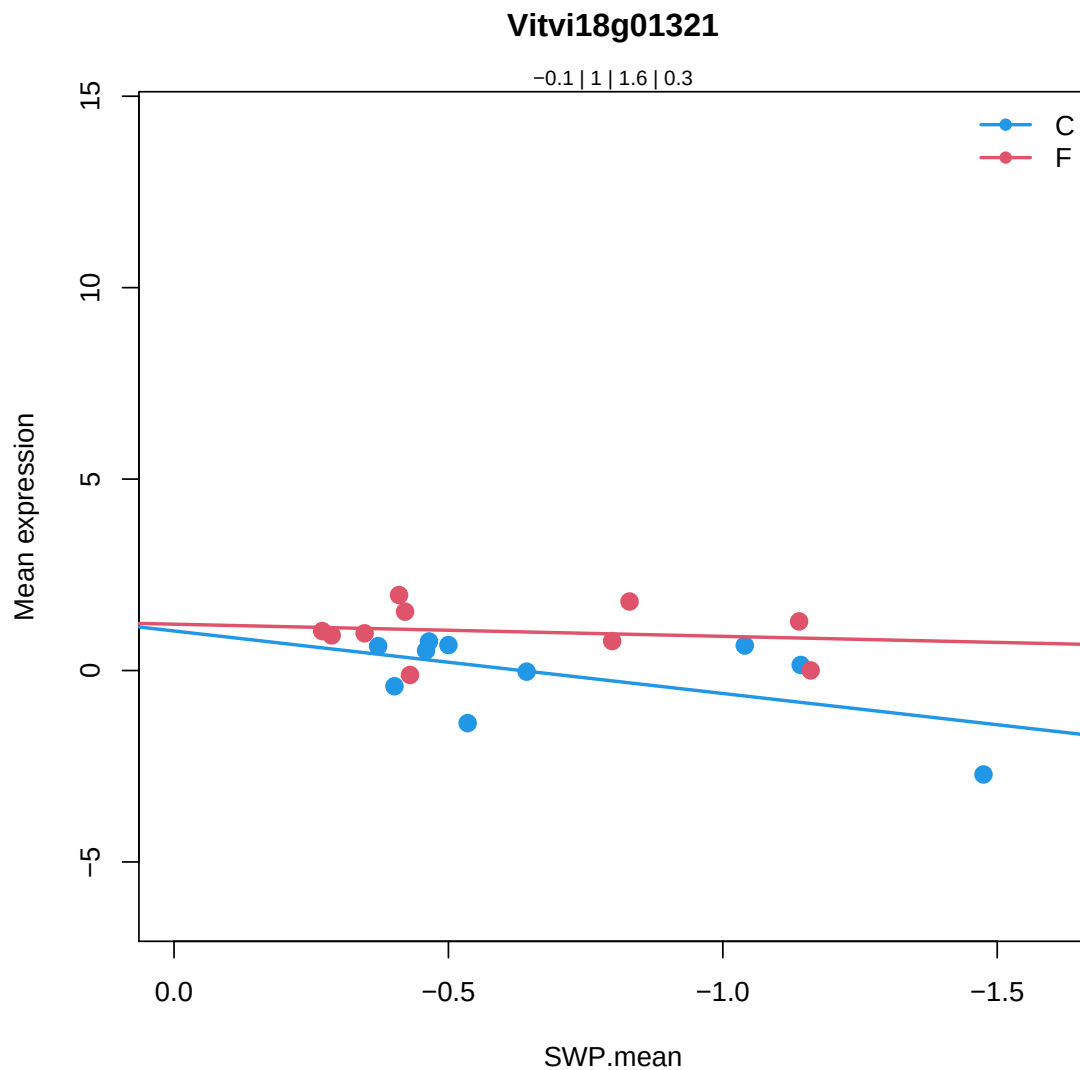
cysteine-rich RECEPTOR-like kinase |

Chr4:12129485-12133157 FORWARD LENGTH=1043 |

201606

Coefficients for Vitvi18g01321.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.1149328	0.650885		0.6558333	
SlopeC	1.632696	0.02881099	*	0.4275443	
MeanF-MeanC	1.131846	0.004265536	**	0.04015769	*
SlopeF-SlopeC	-1.315766	0.2180917		0.9999488	



8.2.24 Vitvi01g01520: Type3.C *

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

Vitvi01g01520

35.2

not assigned.unknown

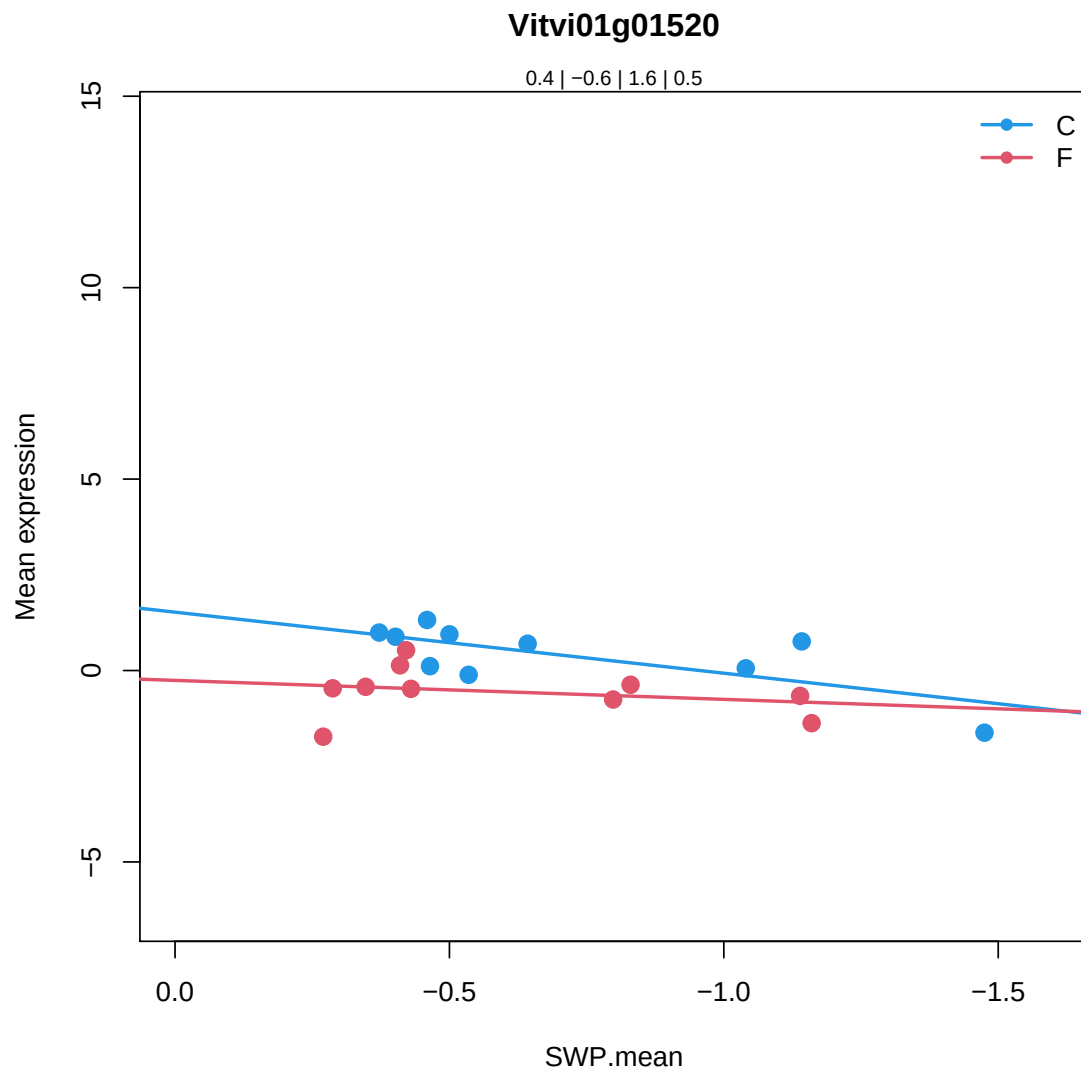
HXXXD-type acyl-transferase family protein |

Chr3:9519741-9521069 FORWARD LENGTH=442 |

201606

Coefficients for Vitvi01g01520.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4033867	0.04994232	*	0.05200662	.
SlopeC	1.5941	0.007517301	**	0.2777732	
MeanF-MeanC	-0.9633581	0.002041678	**	0.02237186	*
SlopeF-SlopeC	-1.09904	0.1857964		0.9999488	



8.2.25 Vitvi14g01615: Type3.C *

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

Vitvi14g01615

27.3.25

RNA.regulation of transcription.MYB domain transcription factor family

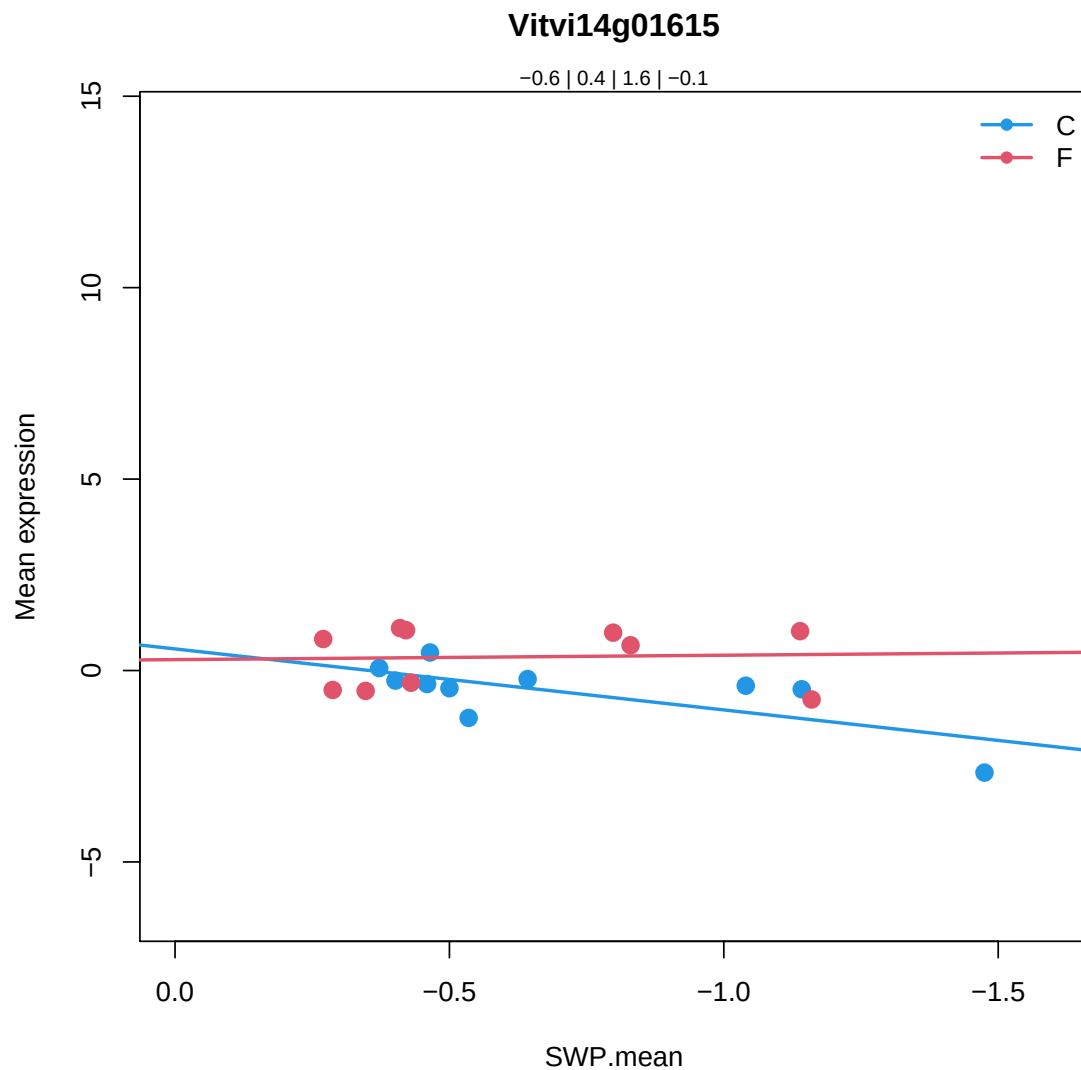
myb domain protein 63 |

Chr1:29786509-29787589 FORWARD LENGTH=327 |

201606

Coefficients for Vitvi14g01615.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.5559626	0.01792939	*	0.01887161	*
SlopeC	1.593458	0.01512027	*	0.3384188	
MeanF-MeanC	0.9101389	0.007240515	**	0.0599131	.
SlopeF-SlopeC	-1.708661	0.07060673	.	0.9999488	



8.2.26 Vitvi02g00514: Type3.C *

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

Vitvi02g00514

3.2.2

minor CHO metabolism.trehalose.TPP

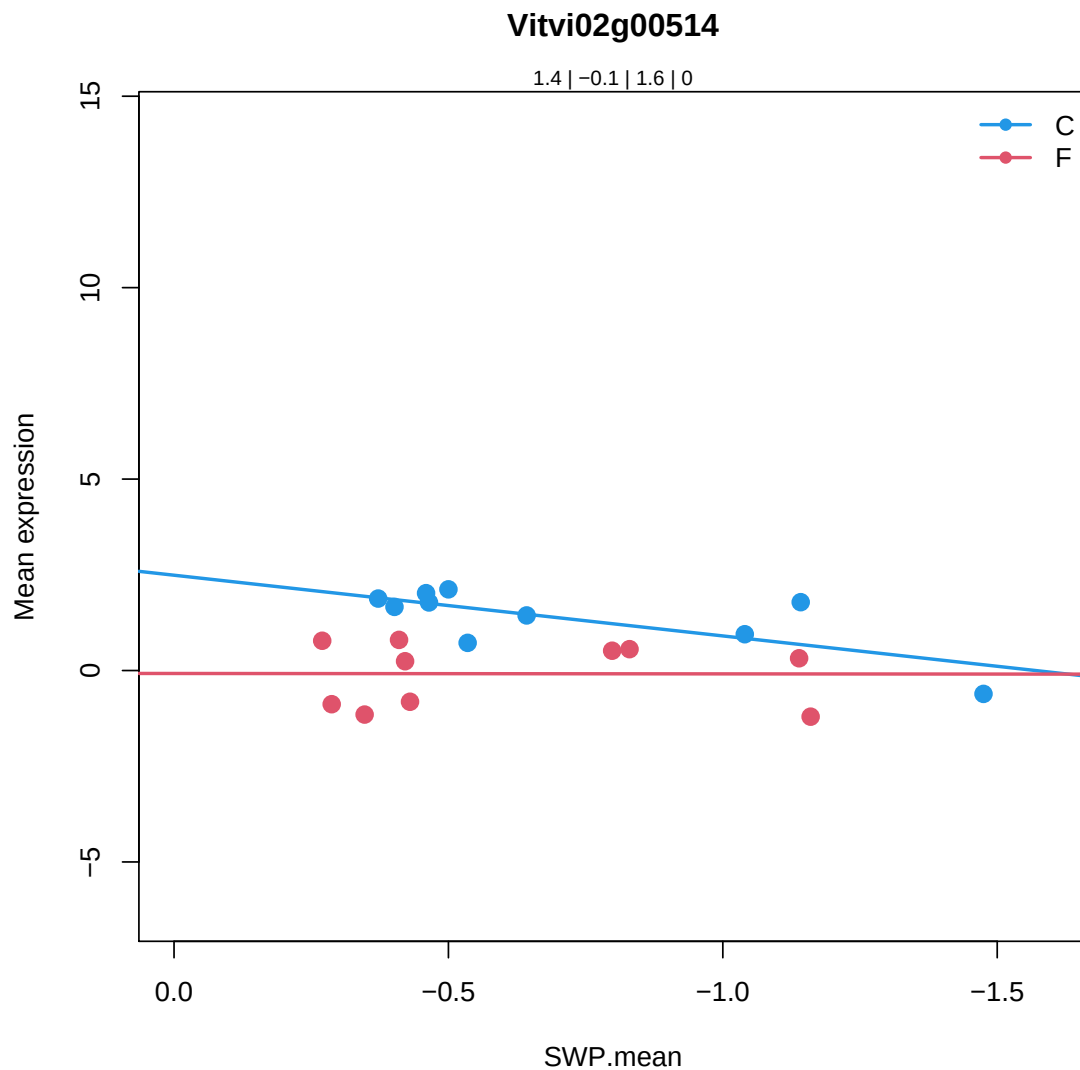
Haloacid dehalogenase-like hydrolase (HAD) superfamily protein |

Chr4:7365480-7367346 REVERSE LENGTH=368 |

201606

Coefficients for Vitvi02g00514.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.374201	3.098048e-06	***	3.536053e-06	***
SlopeC	1.585843	0.01689594	*	0.3532619	
MeanF-MeanC	-1.458001	0.0001202433	***	0.002114546	**
SlopeF-SlopeC	-1.575343	0.0981852	.	0.9999488	



8.2.27 Vitvi18g03246: Type3.C *

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

Vitvi18g03246

30.2.12

signalling.receptor kinases.leucine rich repeat XII

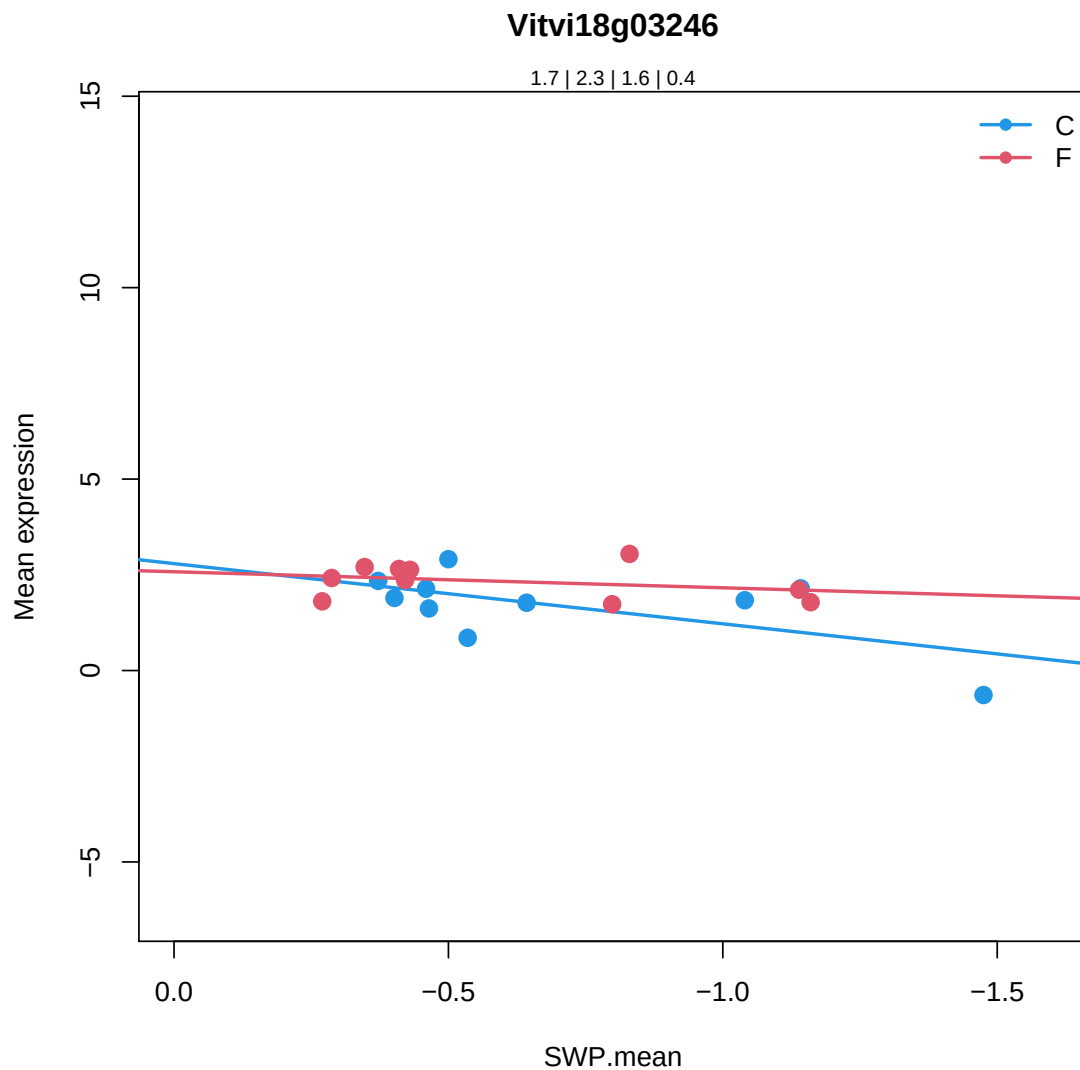
receptor like protein 6 |

Chr1:17183550-17186534 REVERSE LENGTH=994 |

201606

Coefficients for Vitvi18g03246.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.686416	2.199991e-08	***	2.657283e-08	***
SlopeC	1.572368	0.008889031	**	0.2903326	
MeanF-MeanC	0.6376899	0.03185468	*	0.176556	
SlopeF-SlopeC	-1.153825	0.1703506		0.9999488	



8.2.28 Vitvi13g00085: Type3.C

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

Vitvi13g00085

27.3.37

RNA.regulation of transcription.lateral organ boundaries gene family (

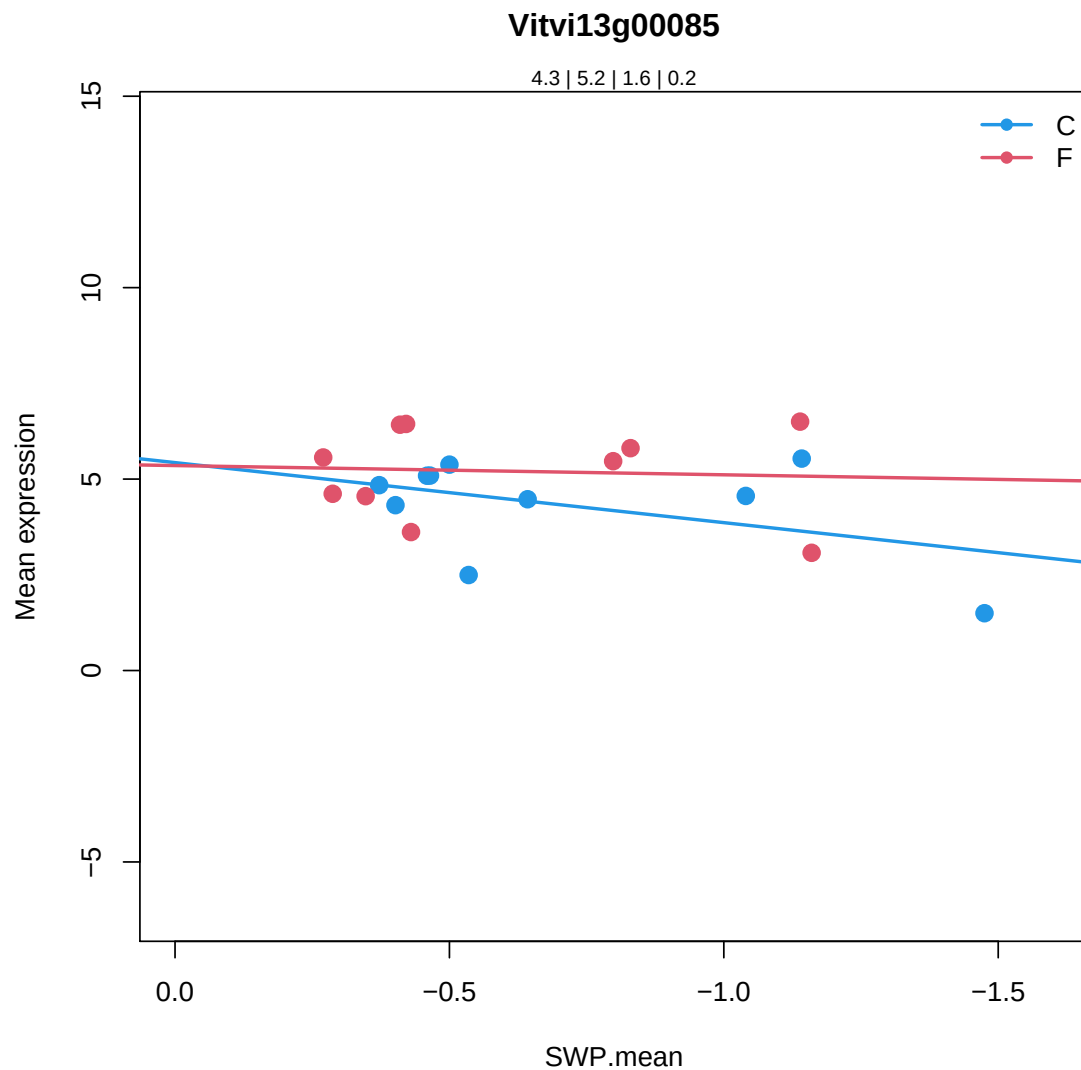
LOB domain-containing protein 21 |

Chr3:3475036-3475533 FORWARD LENGTH=165 |

201606

Coefficients for Vitvi13g00085.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.327386	3.542528e-11	***	4.720273e-11	***
SlopeC	1.567726	0.1241348		0.6455347	
MeanF-MeanC	0.8784706	0.09193566	.	0.3472821	
SlopeF-SlopeC	-1.32646	0.3730393		0.9999488	



8.2.29 Vitvi16g02015: Type3.C *

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

Vitvi16g02015

35.2

not assigned.unknown

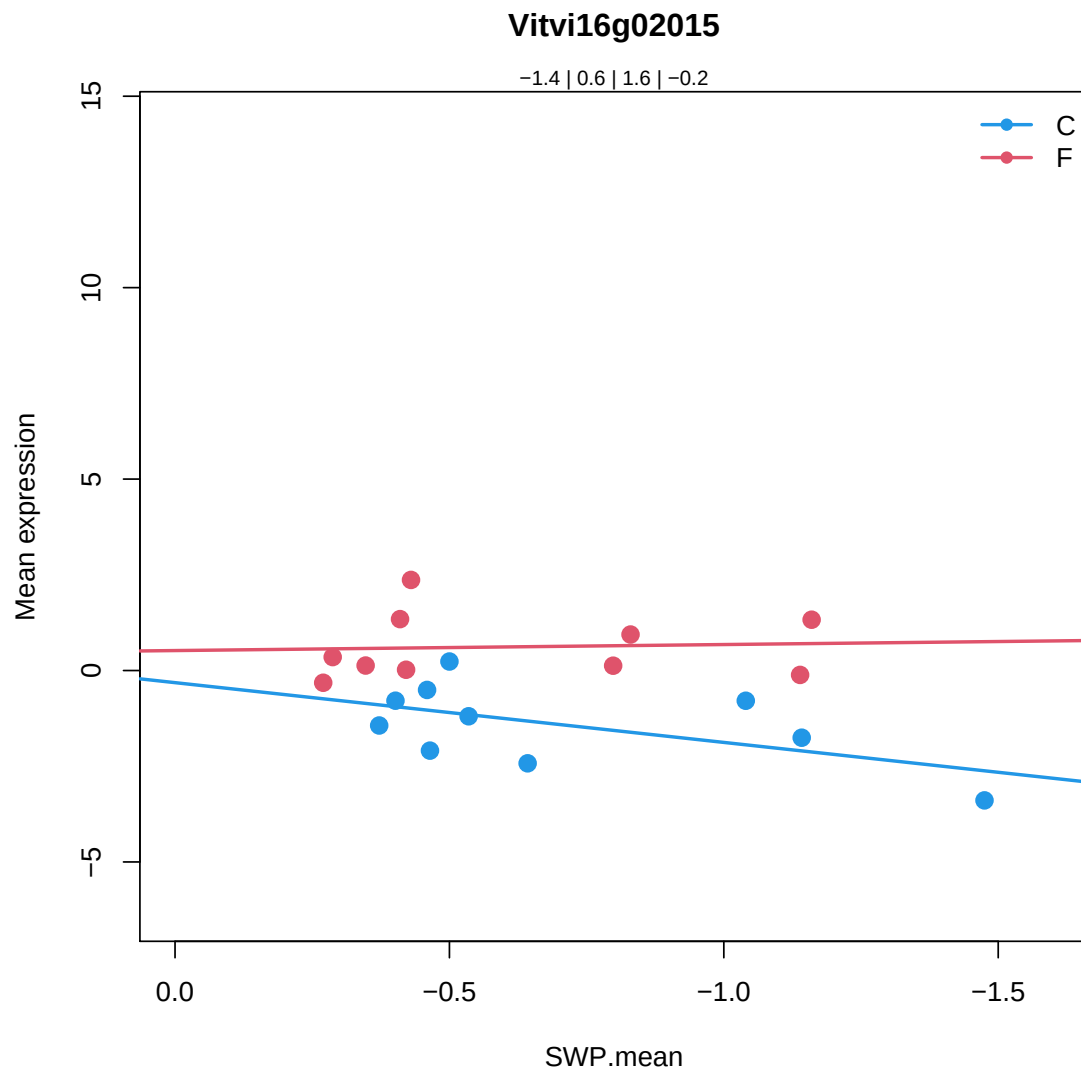
PR5-like receptor kinase |

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	



8.2.30 Vitvi16g02019: Type3.C *

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

Vitvi16g02019

35.2

not assigned.unknown

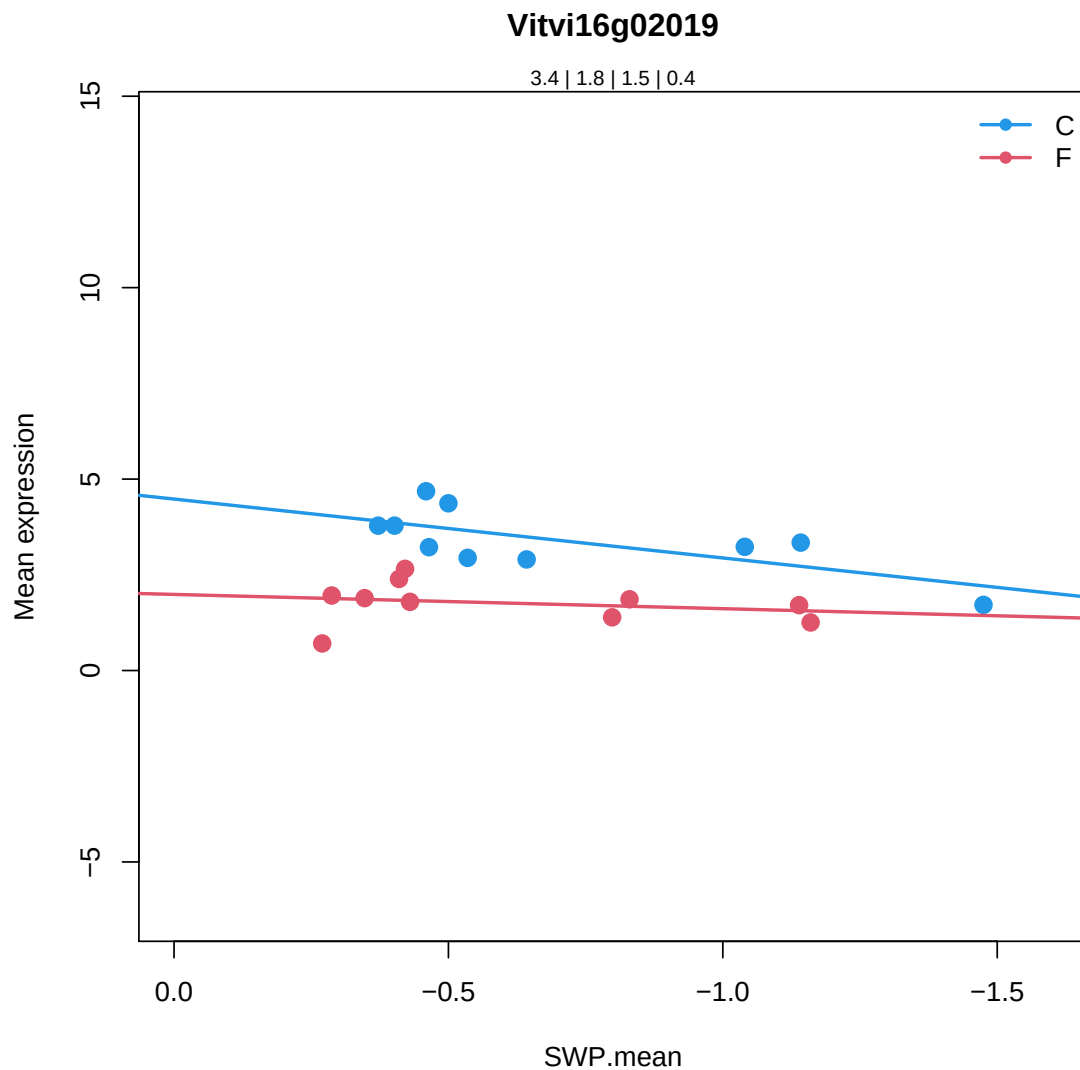
PR5-like receptor kinase |

Chr5:15293325-15295838 REVERSE LENGTH=665 |

201606

Coefficients for Vitvi16g02019.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.39667	9.859704e-15	***	1.649633e-14	***
SlopeC	1.537975	0.006208008	**	0.2647742	
MeanF-MeanC	-1.635778	2.45203e-06	***	7.201126e-05	***
SlopeF-SlopeC	-1.165723	0.1369239		0.9999488	



8.2.31 Vitvi17g00400: Type3.C *

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

Vitvi17g00400

30.2.25

signalling.receptor kinases.wall associated kinase

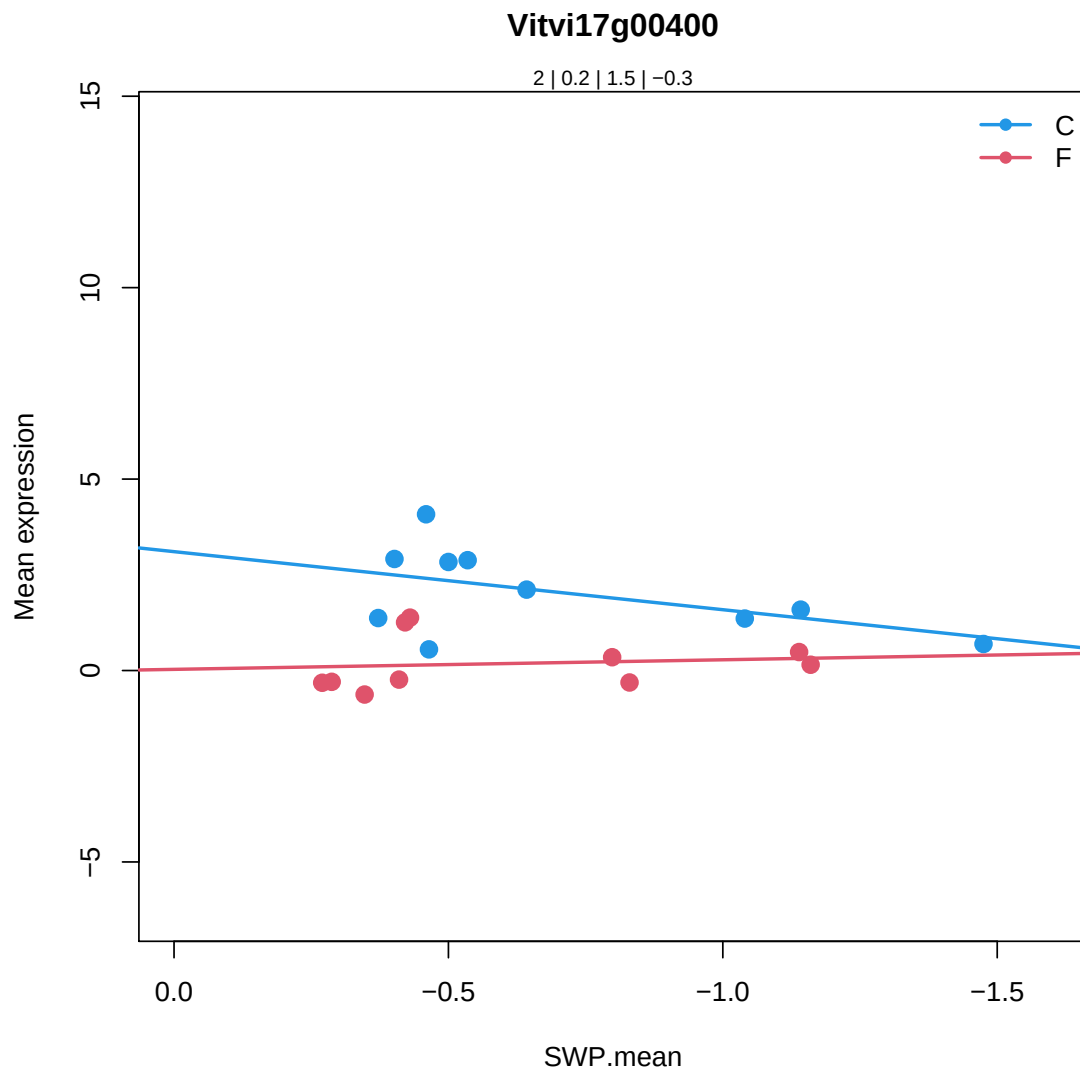
Wall-associated kinase family protein |

Chr1:26228703-26231339 REVERSE LENGTH=792 |

201606

Coefficients for Vitvi17g00400.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.038537	7.219069e-08	***	8.594317e-08	***
SlopeC	1.516381	0.04429824	*	0.4885628	
MeanF-MeanC	-1.855852	4.008841e-05	***	0.000815791	***
SlopeF-SlopeC	-1.766717	0.108939		0.9999488	



8.2.32 Vitvi13g02359: Type3.C *

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

Vitvi13g02359

27.2

RNA.transcription

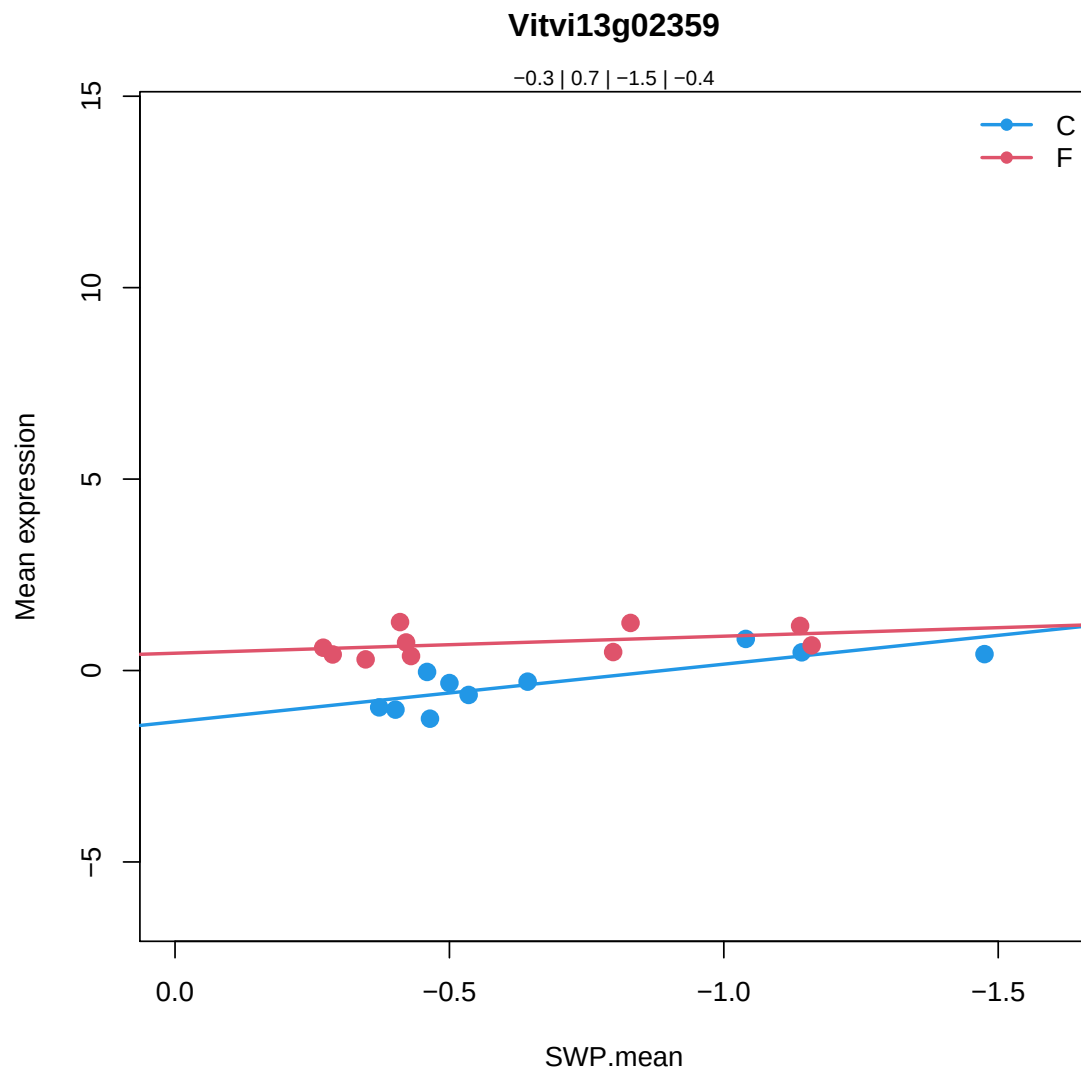
RNA polymerase II fifth largest subunit%2C E |

Chr3:20173673-20175297 FORWARD LENGTH=233 |

201606

Coefficients for Vitvi13g02359.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.28085	0.04842468	*	0.05043659	.
SlopeC	-1.504967	0.0005830364	***	0.1005065	
MeanF-MeanC	1.003501	2.853815e-05	***	0.0006213979	***
SlopeF-SlopeC	1.060049	0.06991798	.	0.9999488	



8.2.33 Vitvi07g01329: Type3.C *

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

Vitvi07g01329

29.2.1.1.3.2

protein.synthesis.ribosomal protein.prokaryotic.unknown organellar.50S

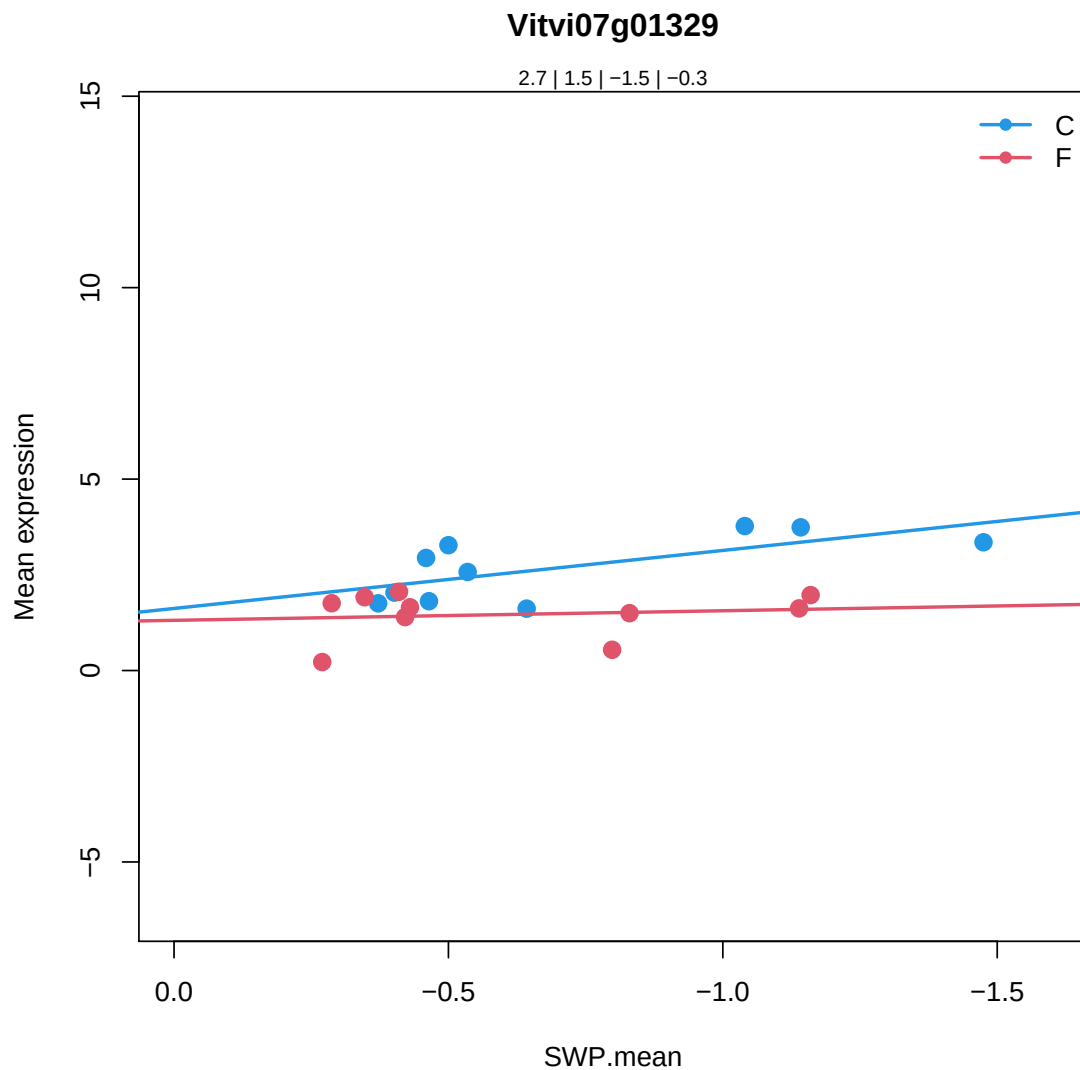
Ribosomal protein L25/Gln-tRNA synthetase%2C anti-codon-binding domain

Chr5:26701233-26702531 REVERSE LENGTH=249 |

201606

Coefficients for Vitvi07g01329.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.686338	3.285794e-12	***	4.584172e-12	***
SlopeC	-1.5151	0.01010604	*	0.3042563	
MeanF-MeanC	-1.22352	0.0001964968	***	0.00321008	**
SlopeF-SlopeC	1.26484	0.1282284		0.9999488	



8.2.34 Vitvi06g00668: Type3.C

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

```
Vitvi06g00668
```

```
30.6
```

```
signalling.MAP kinases
```

```
mitogen-activated protein kinase kinase kinase 13 |
```

```
Chr1:2194279-2195778 REVERSE LENGTH=499 |
```

```
201606
```

```
Vitvi06g00668
```

```
29.4
```

```
protein.postranslational modification
```

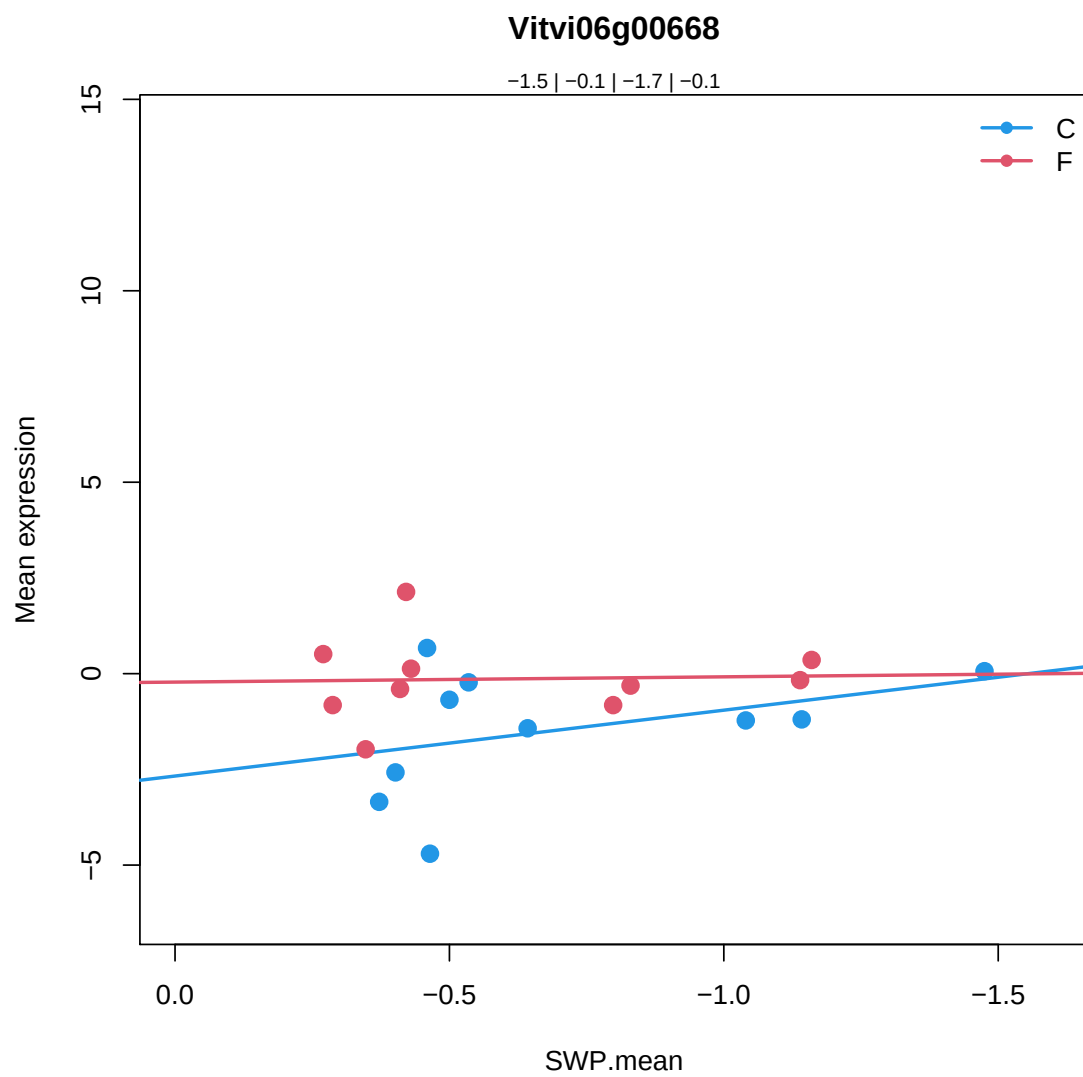
```
mitogen-activated protein kinase kinase kinase 13 |
```

```
Chr1:2194279-2195778 REVERSE LENGTH=499 |
```

```
201606
```

Coefficients for Vitvi06g00668.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.464965	0.001070088	**	0.001158071	**
SlopeC	-1.720059	0.1254121		0.6460361	
MeanF-MeanC	1.328022	0.02435779	*	0.1456157	
SlopeF-SlopeC	1.582692	0.3351886		0.9999488	



8.2.35 Vitvi14g01560: Type3.C *

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

Vitvi14g01560

34.18

transport.unspecified anions

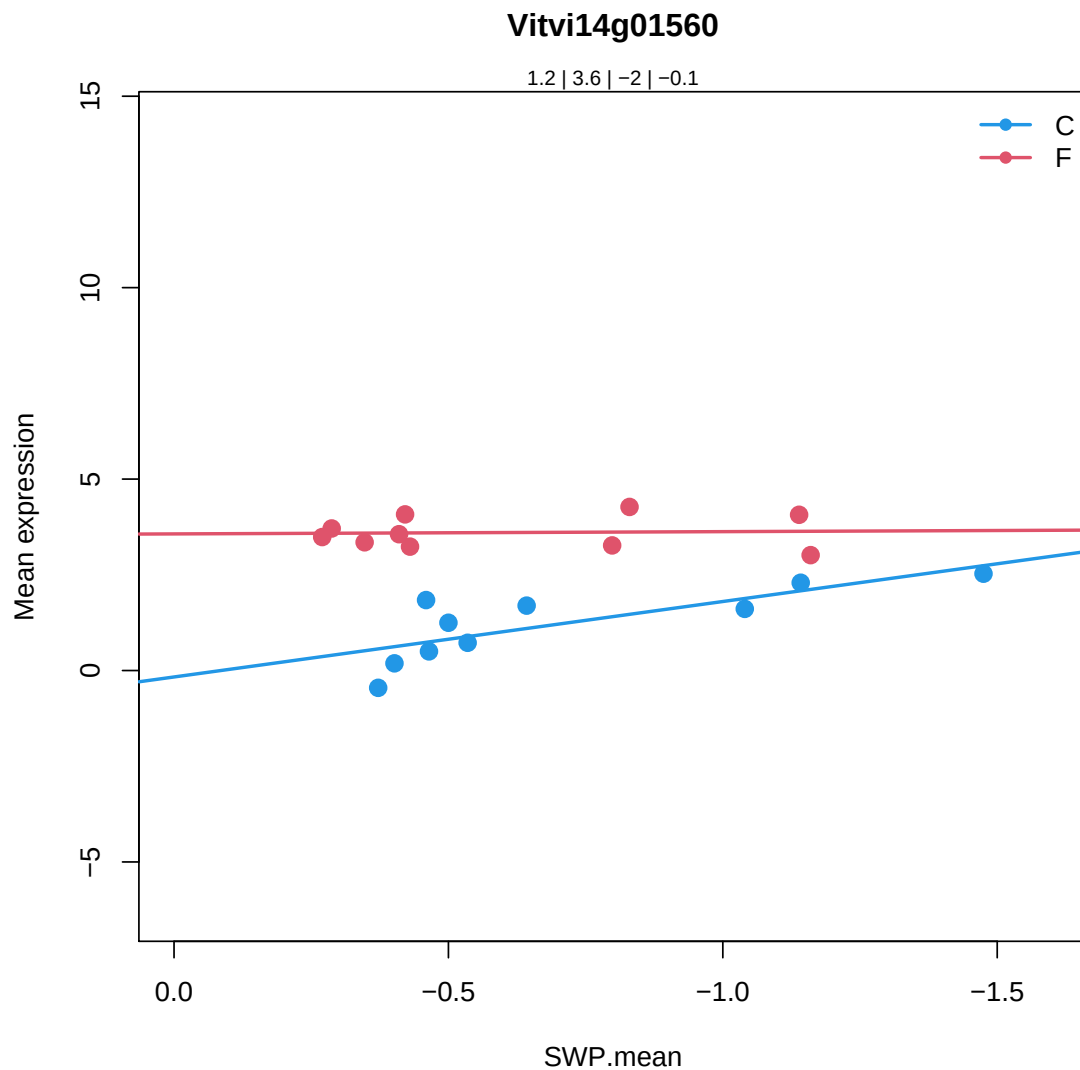
chloride channel B |

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	



8.2.36 Vitvi05g01789: Type3.C *

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

Vitvi05g01789

35.2

not assigned.unknown

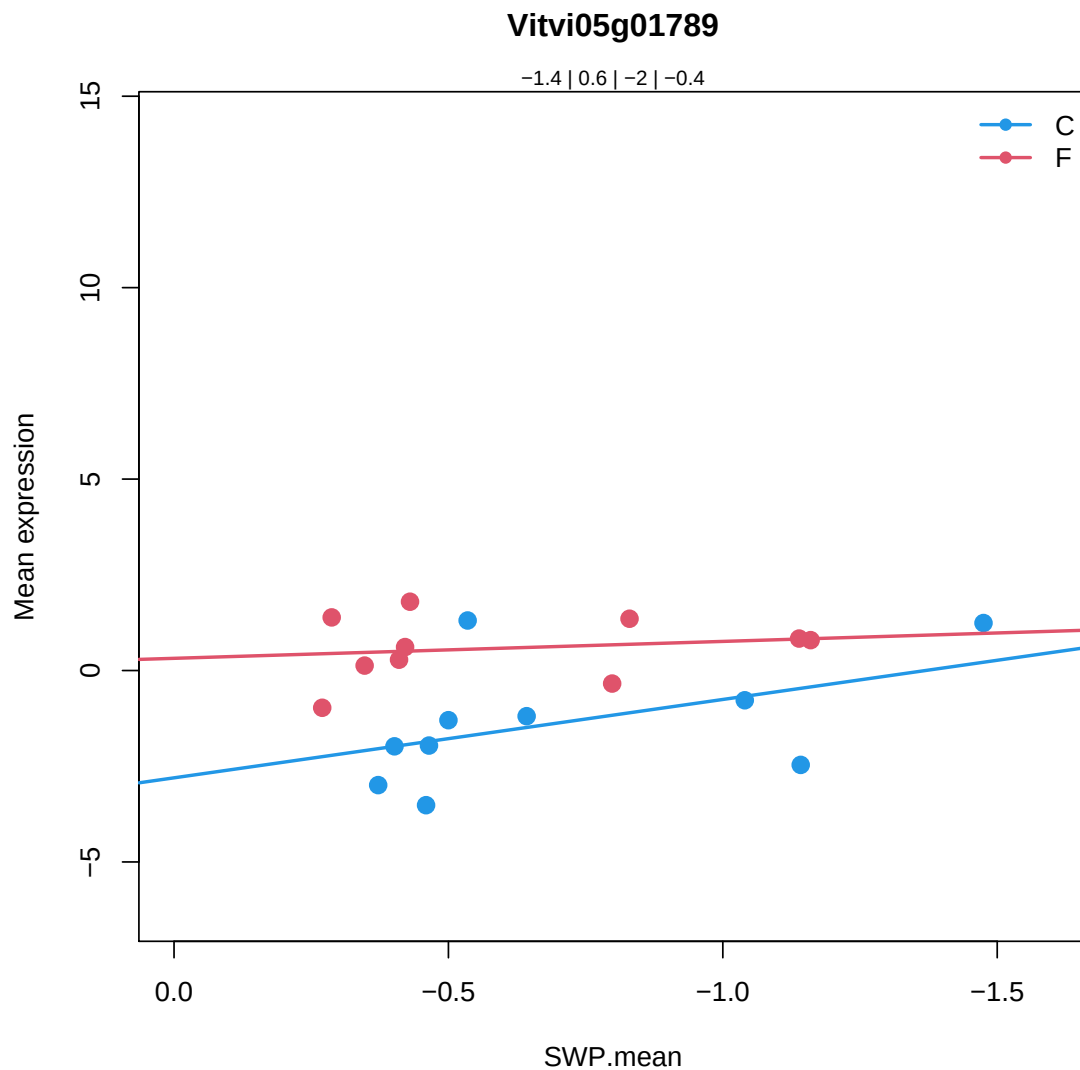
hAT dimerization domain-containing protein |

Chr3:5972793-5975684 REVERSE LENGTH=877 |

201606

Coefficients for Vitvi05g01789.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.363668	0.0007159484	***	0.0007777411	***
SlopeC	-2.046809	0.04501978	*	0.4904752	
MeanF-MeanC	1.951171	0.0006402893	***	0.008670318	**
SlopeF-SlopeC	1.605349	0.2743618		0.9999488	



8.3 Type3.F

8.3.1 Vitvi06g01743: Type3.F

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

Vitvi06g01743

35.2

not assigned.unknown

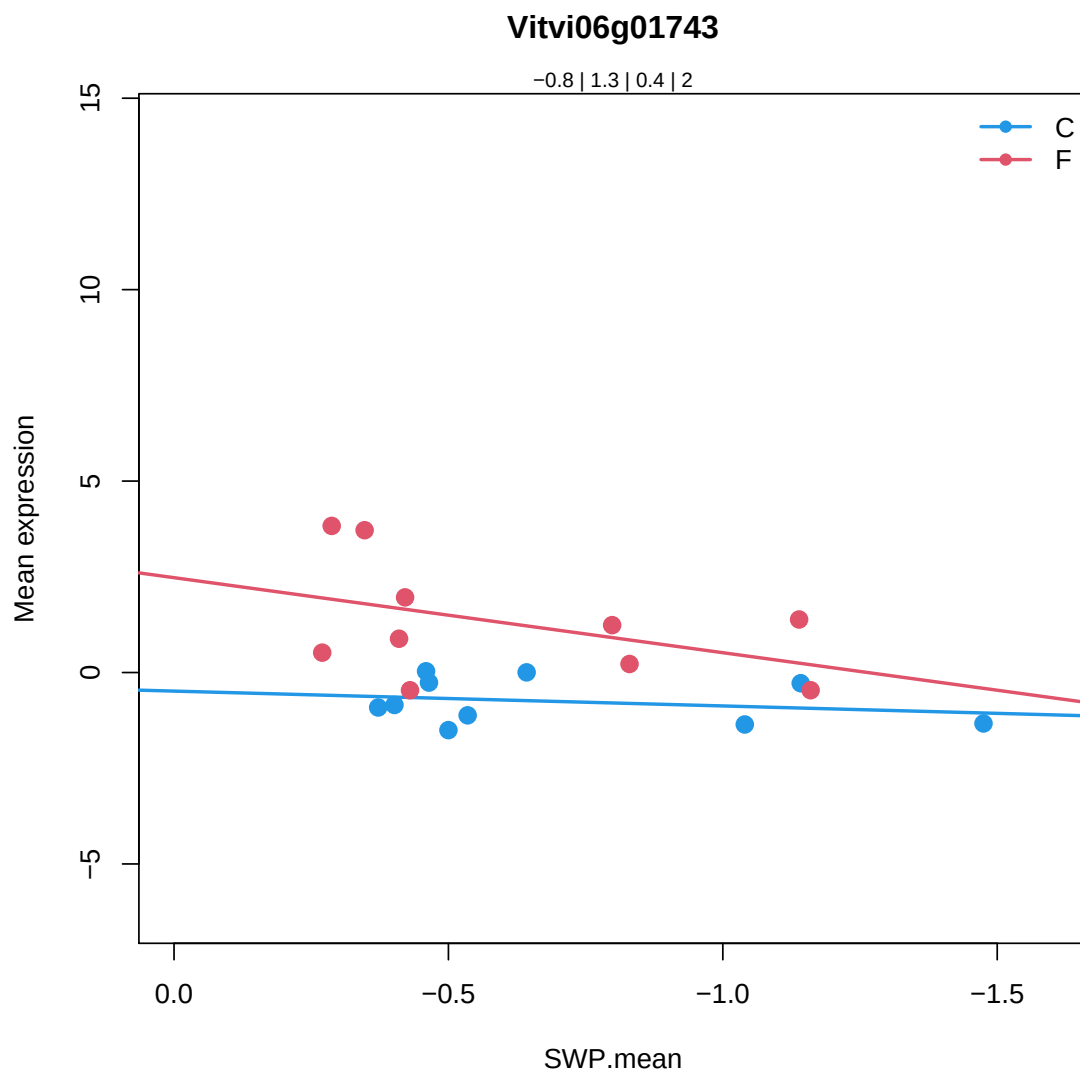
UDP-glucosyl transferase 71C4 |

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	



8.3.2 Vitvi19g01966: Type3.F

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

```
Vitvi19g01966
```

```
30.2.24
```

```
signalling.receptor kinases.S-locus glycoprotein like
```

```
S-locus lectin protein kinase family protein |
```

```
Chr4:13666281-13669202 FORWARD LENGTH=783 |
```

```
201606
```

```
Vitvi19g01966
```

```
29.4
```

```
protein.postranslational modification
```

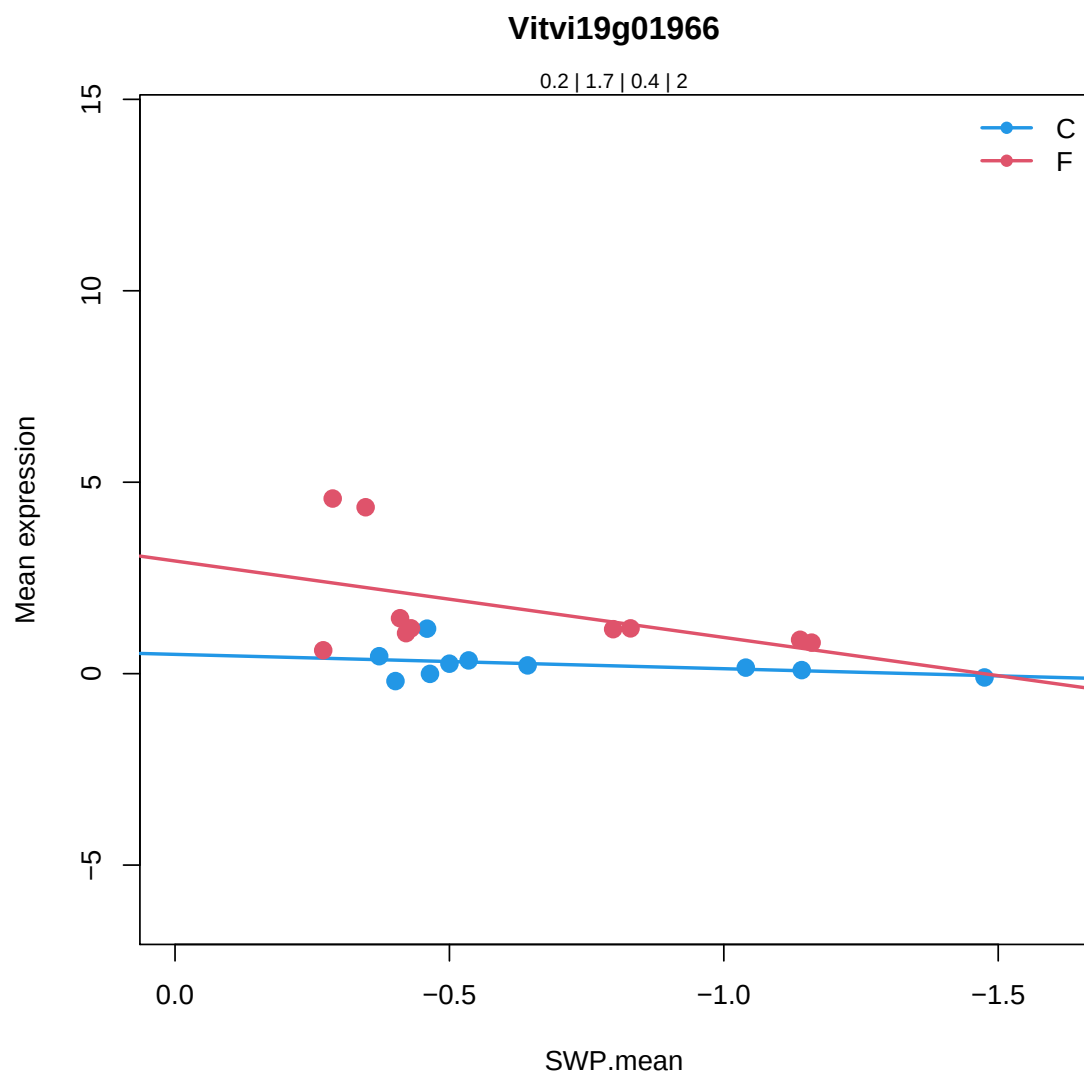
```
S-locus lectin protein kinase family protein |
```

```
Chr4:13666281-13669202 FORWARD LENGTH=783 |
```

```
201606
```

Coefficients for Vitvi19g01966.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.2401875	0.4085668		0.4146608	
SlopeC	0.3750725	0.6408989		0.9150039	
MeanF-MeanC	1.485613	0.001334182	**	0.01587478	*
SlopeF-SlopeC	1.621511	0.183549		0.9999488	



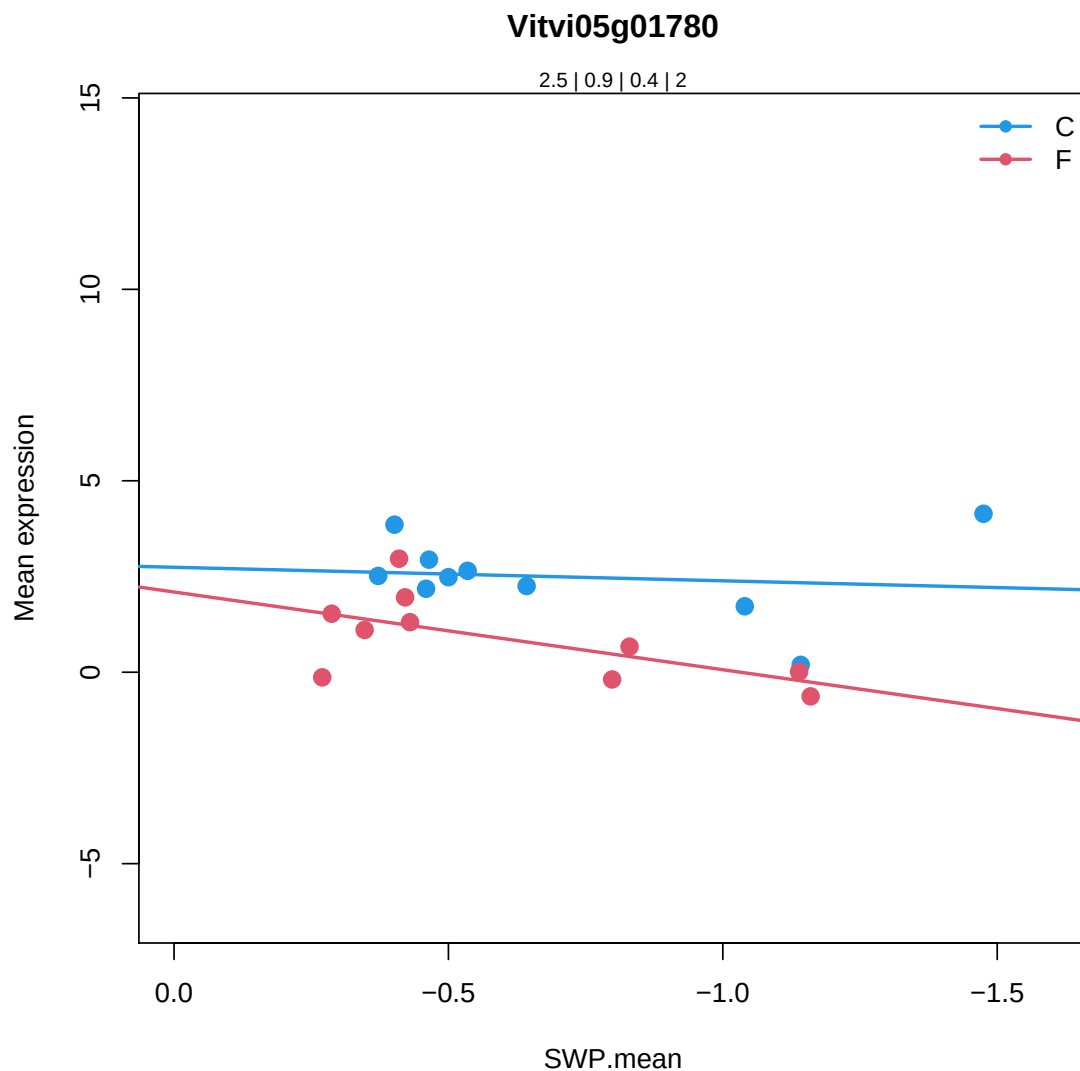
8.3.3 Vitvi05g01780: Type3.F

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

```
Vitvi05g01780
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi05g01780.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.492285	3.342069e-08	***	4.017336e-08	***
SlopeC	0.3531567	0.6739755		0.9246326	
MeanF-MeanC	-1.633824	0.0008349926	***	0.01076731	*
SlopeF-SlopeC	1.677069	0.1876866		0.9999488	



8.3.4 Vitvi19g00391: Type3.F

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

Vitvi19g00391

16.1.5

secondary metabolism.isoprenoids.terpenoids

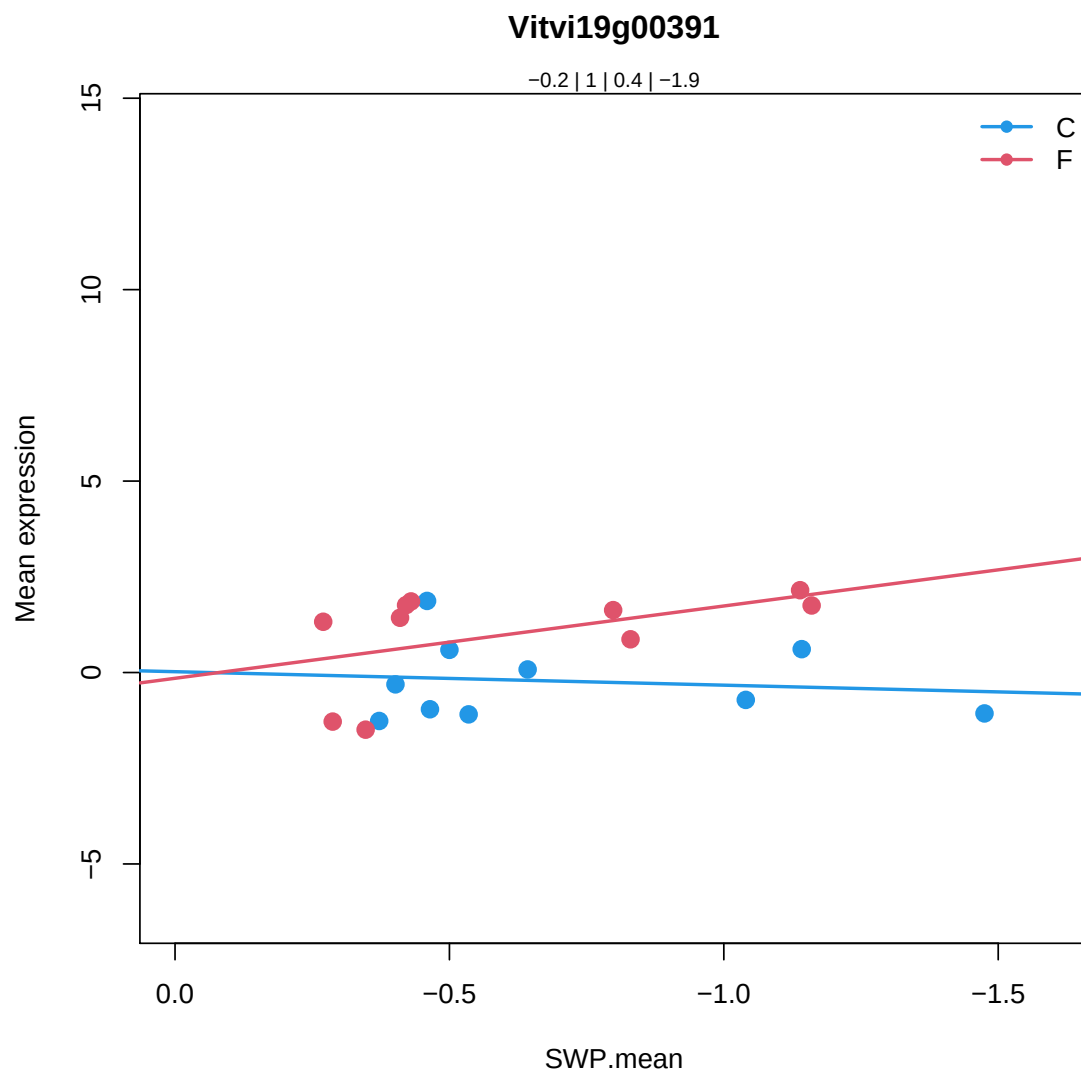
terpene synthase 21 |

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	



8.3.5 Vitvi05g01675: Type3.F +

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

Vitvi05g01675

26.11.1

misc.alcohol dehydrogenases.cinnamyl alcohol dehydrogenase

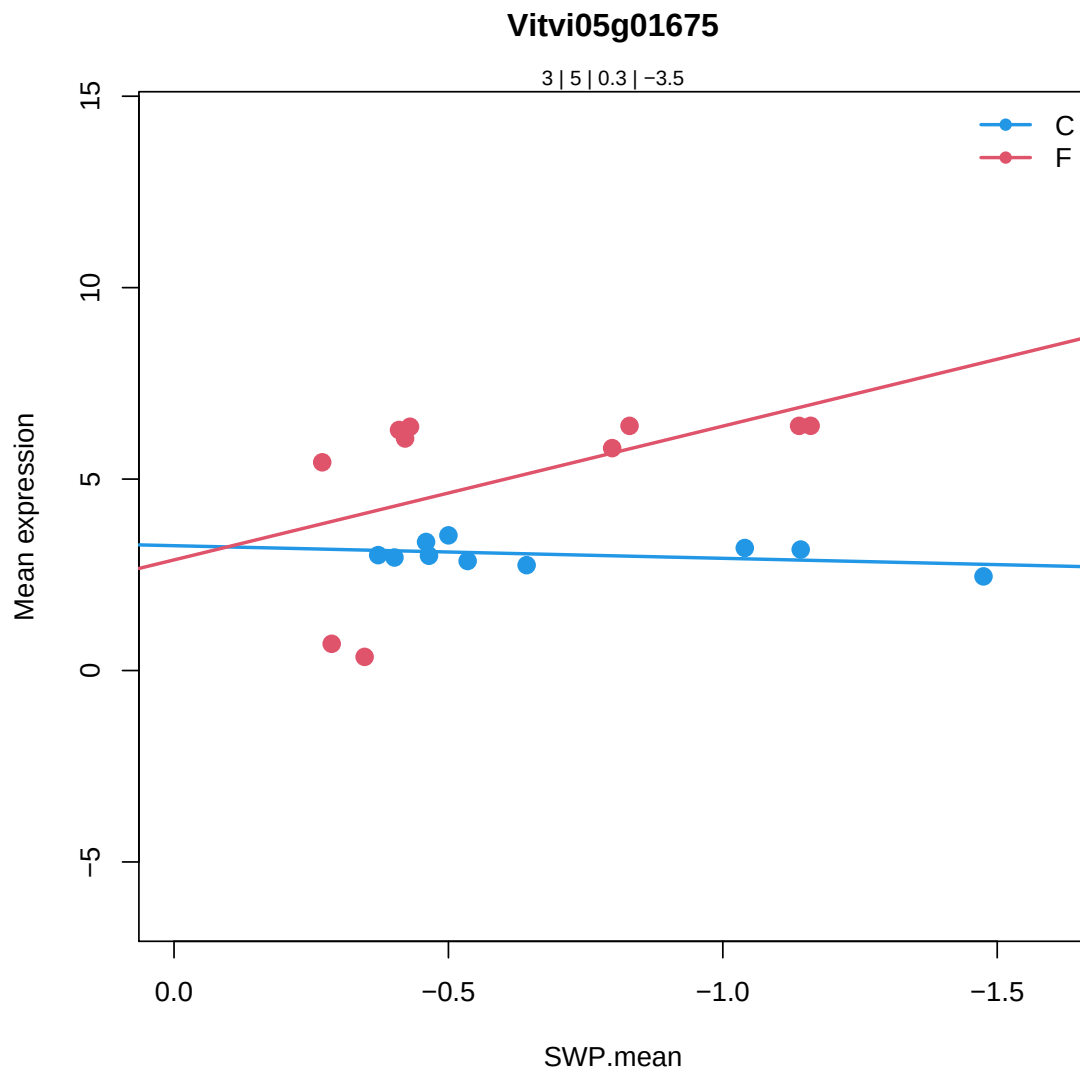
Zinc-binding dehydrogenase family protein |

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	



8.3.6 Vitvi14g03071: Type3.F +

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

Vitvi14g03071

35.2

not assigned.unknown

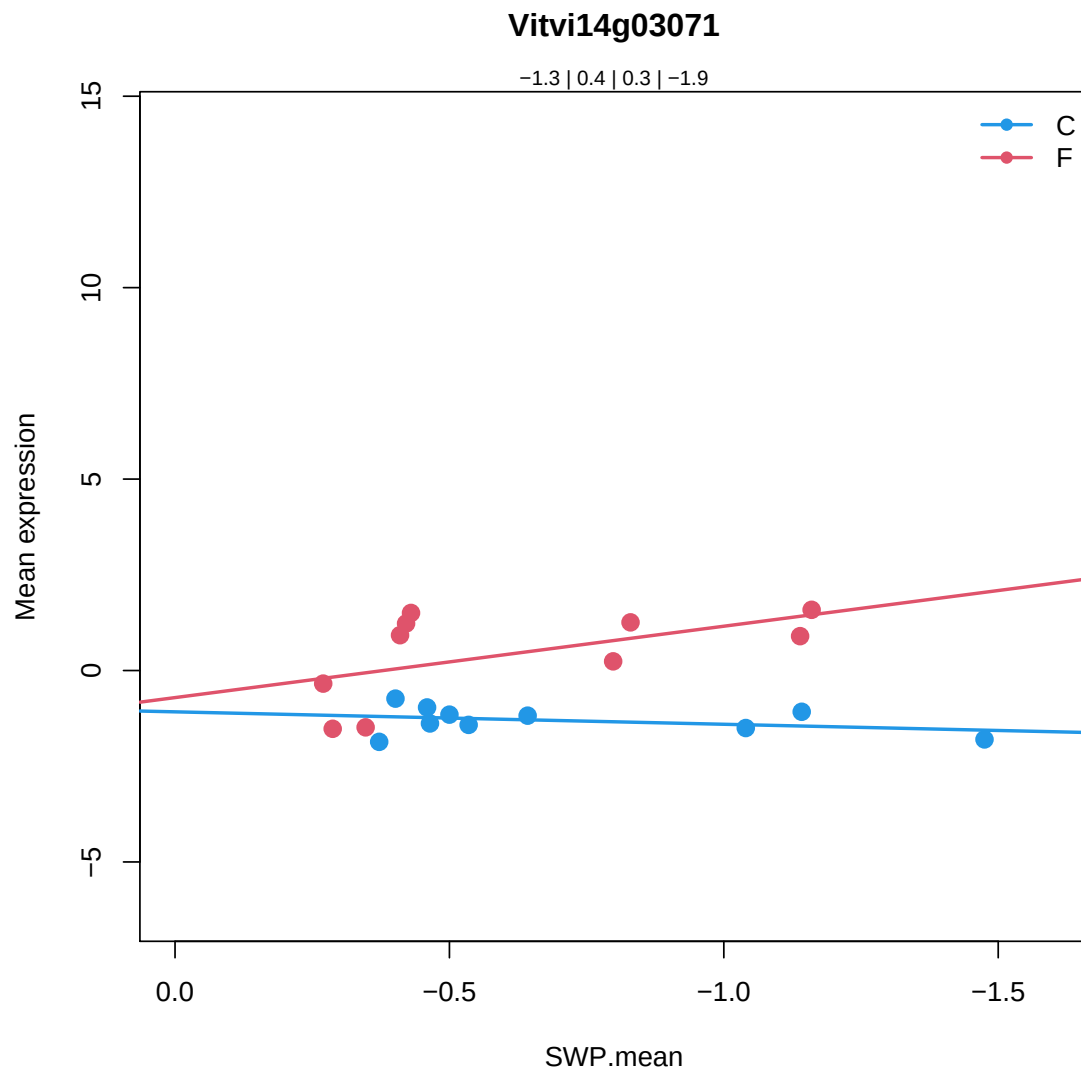
kinase family with leucine-rich repeat domain-containing protein |

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	



8.3.7 Vitvi01g02299: Type3.F

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

Vitvi01g02299

35.2

not assigned.unknown

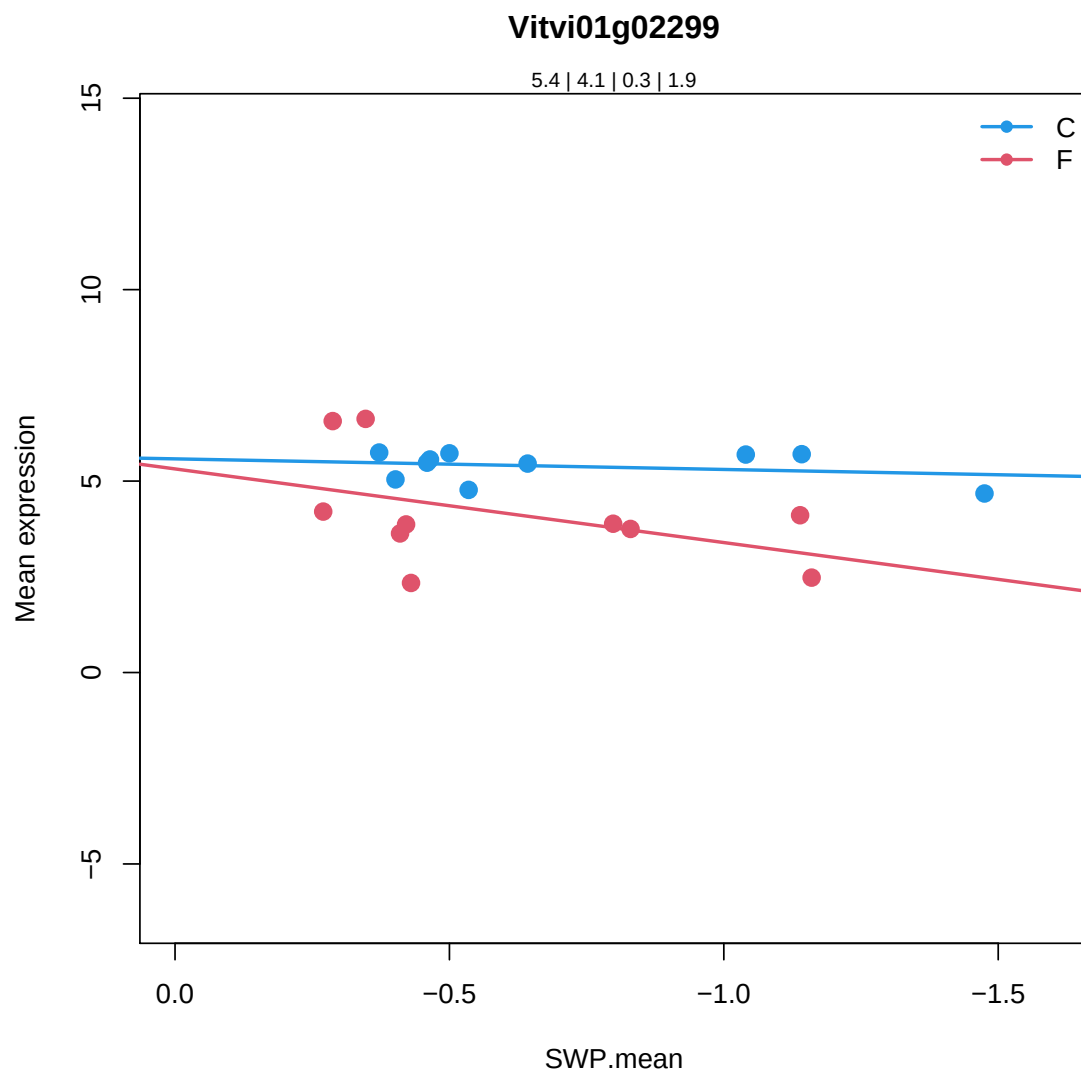
Major facilitator superfamily protein |

Chr5:4296854-4299079 REVERSE LENGTH=624 |

201606

Coefficients for Vitvi01g02299.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.38558	7.345511e-15	***	1.245248e-14	***
SlopeC	0.2763339	0.7305845		0.9406676	
MeanF-MeanC	-1.240036	0.005587167	**	0.04964575	*
SlopeF-SlopeC	1.64721	0.1766302		0.9999488	



8.3.8 Vitvi13g00600: Type3.F

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

Vitvi13g00600

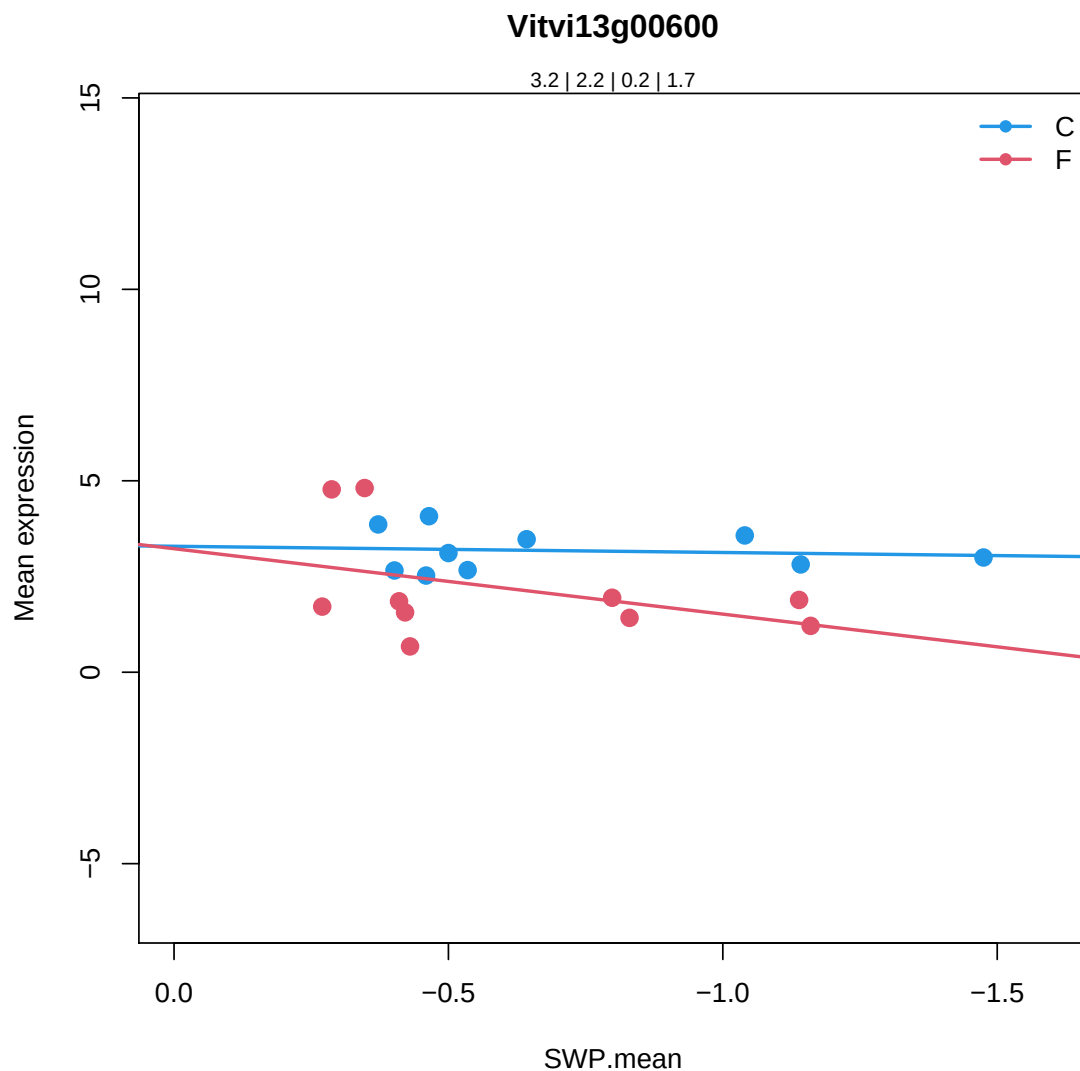
34.3

transport.amino acids

Tyrosine-specific transport protein IPR018227 Tryptophan_tyrosine perm

Coefficients for Vitvi13g00600.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.175325	5.143251e-10	***	6.550253e-10	***
SlopeC	0.1619251	0.8472215		0.9711946	
MeanF-MeanC	-0.990095	0.02867047	*	0.1640545	
SlopeF-SlopeC	1.546758	0.2242124		0.9999488	



8.3.9 Vitvi07g01779: Type3.F

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

Vitvi07g01779

34.6

transport.sulphate

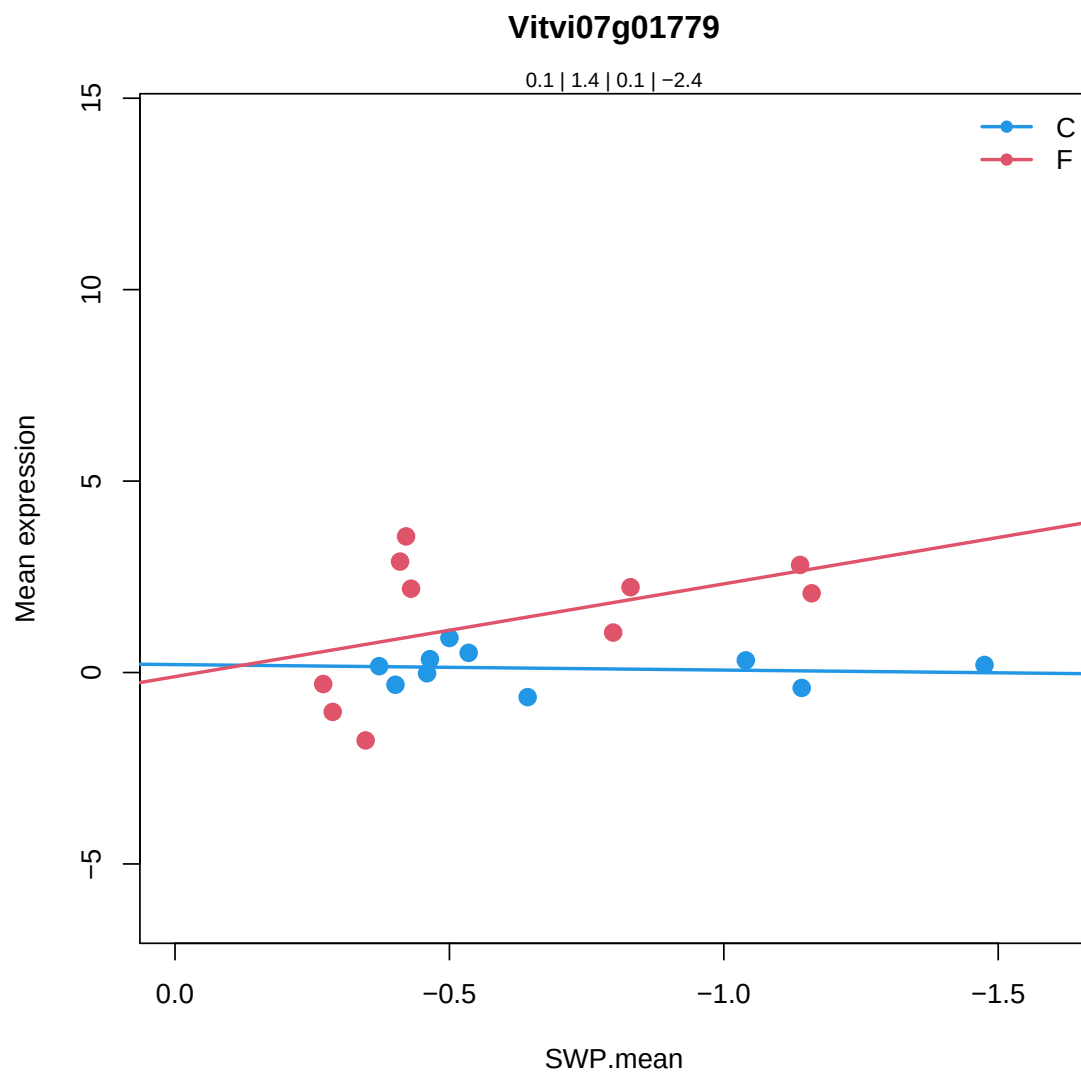
STAS domain / Sulfate transporter family |

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	



8.3.10 Vitvi15g00727: Type3.F

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

Vitvi15g00727

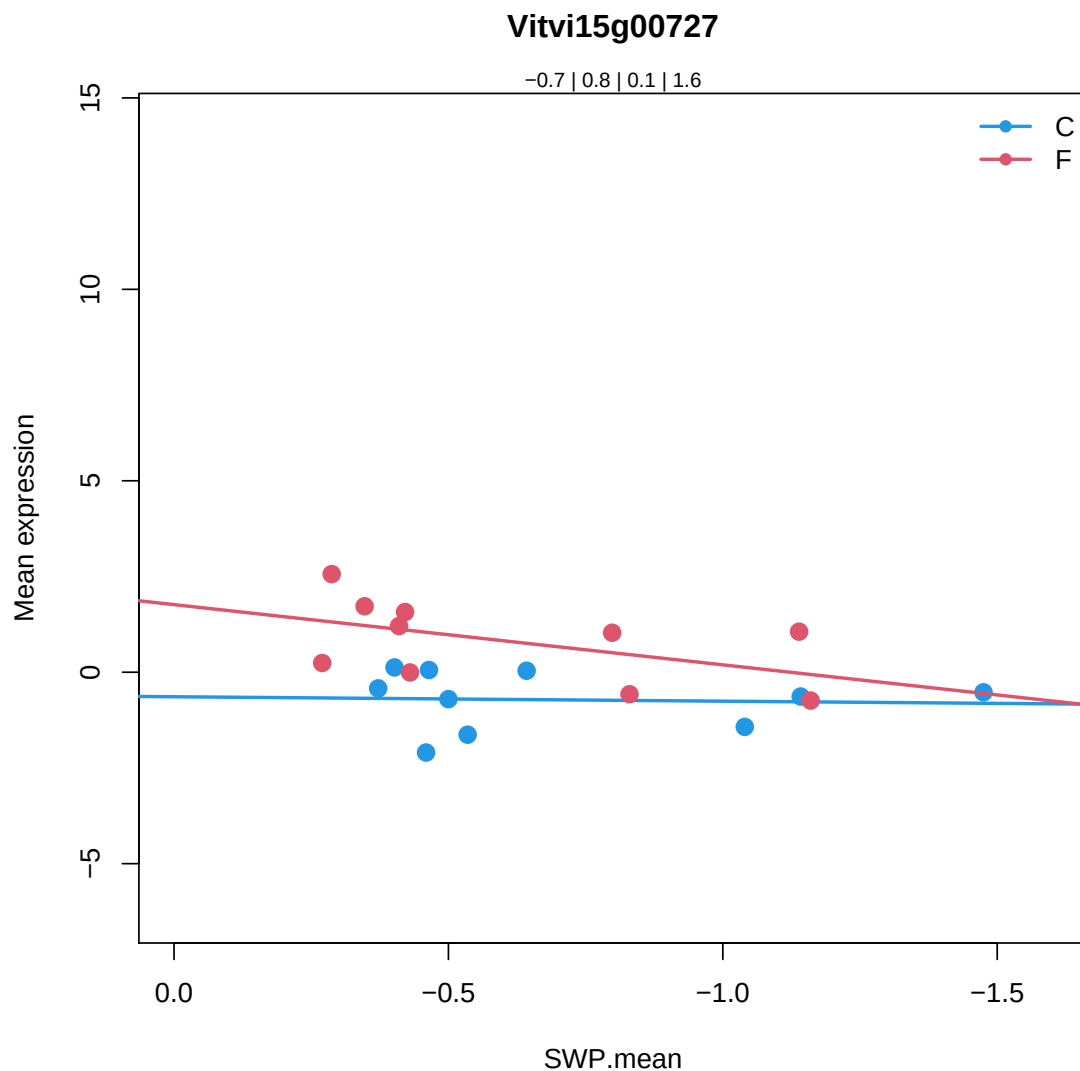
35.2

not assigned.unknown

Unknown Protein

Coefficients for Vitvi15g00727.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.7217807	0.009994891	**	0.01058593	*
SlopeC	0.1155023	0.8724035		0.9762394	
MeanF-MeanC	1.529218	0.0003576357	***	0.005333741	**
SlopeF-SlopeC	1.457204	0.1824867		0.9999488	



8.3.11 Vitvi15g01075: Type3.F

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

Vitvi15g01075

16.8.1.12

secondary metabolism.flavonoids.anthocyanins.anthocyanidin 3-O-glucosyl

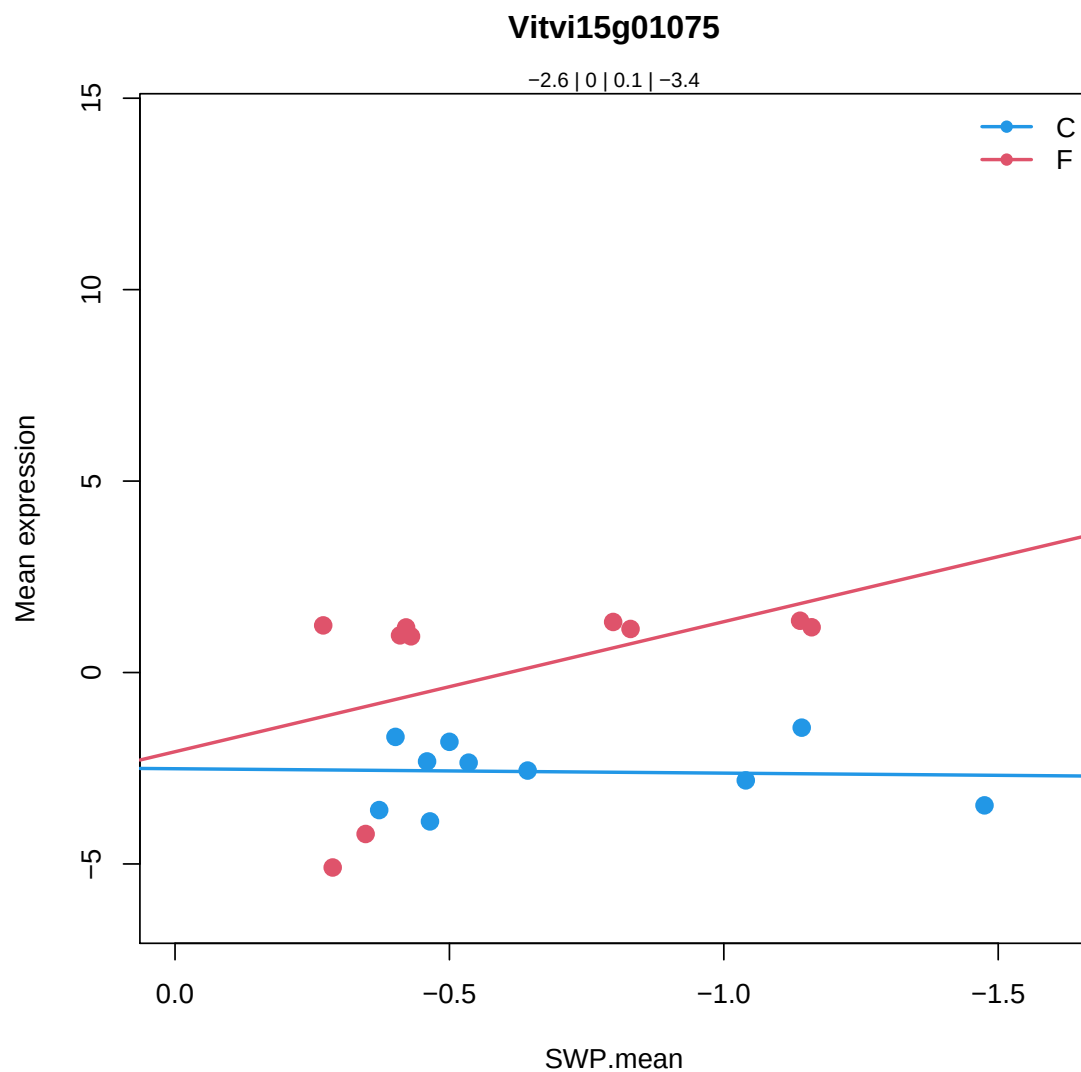
UDP-Glycosyltransferase superfamily protein |

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	



8.3.12 Vitvi18g02012: Type3.F

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

Vitvi18g02012

26.2

misc.UDP glucosyl and glucoronyl transferases

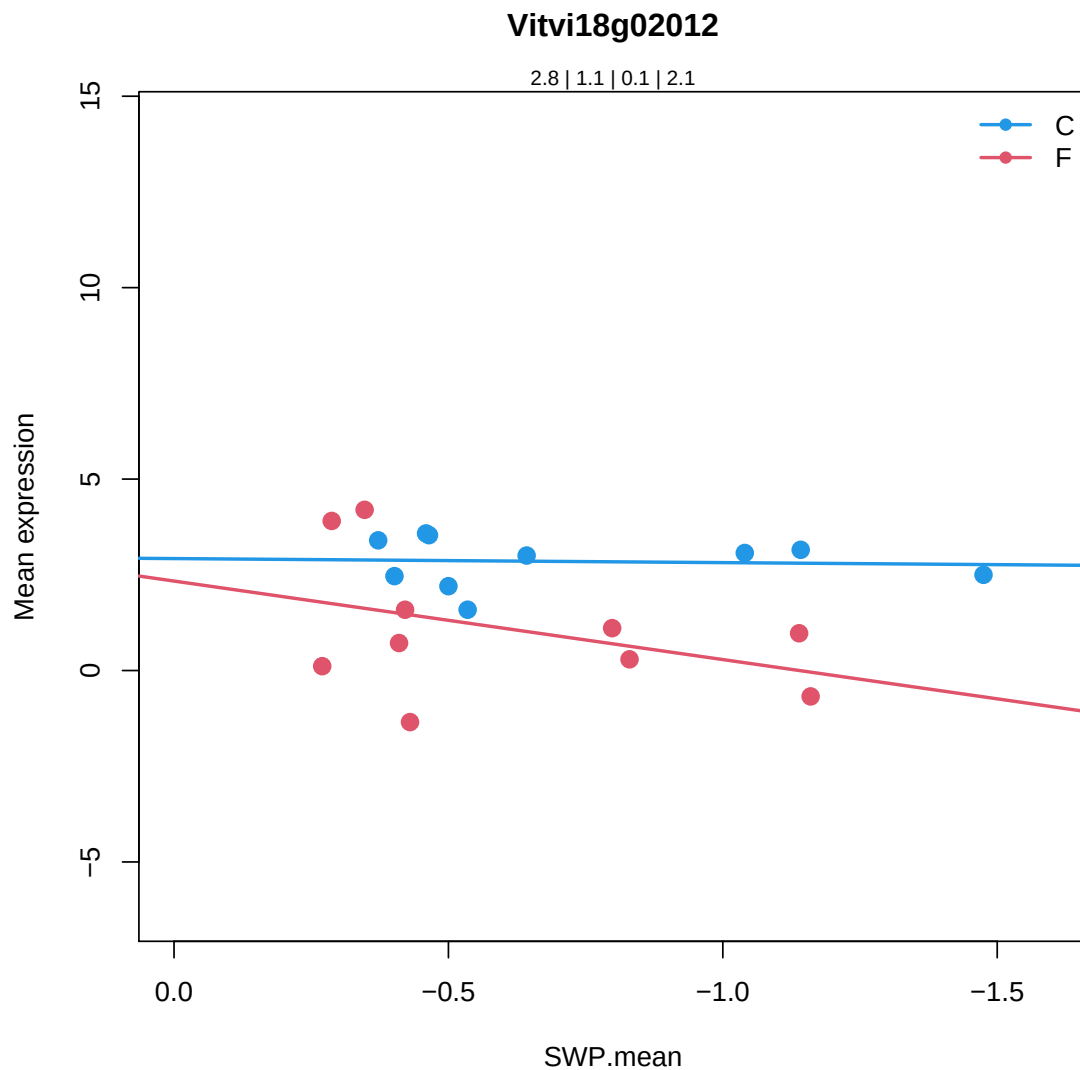
UDP-glucosyl transferase 88A1 |

Chr3:5618847-5620833 REVERSE LENGTH=446 |

201606

Coefficients for Vitvi18g02012.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.849471	1.2602e-07	***	1.491301e-07	***
SlopeC	0.1057251	0.9189502		0.9851716	
MeanF-MeanC	-1.76252	0.002789493	**	0.02898258	*
SlopeF-SlopeC	1.945201	0.2167274		0.9999488	



8.3.13 Vitvi04g01421: Type3.F

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

Vitvi04g01421

1.3.6

PS.calvin cycle.aldolase

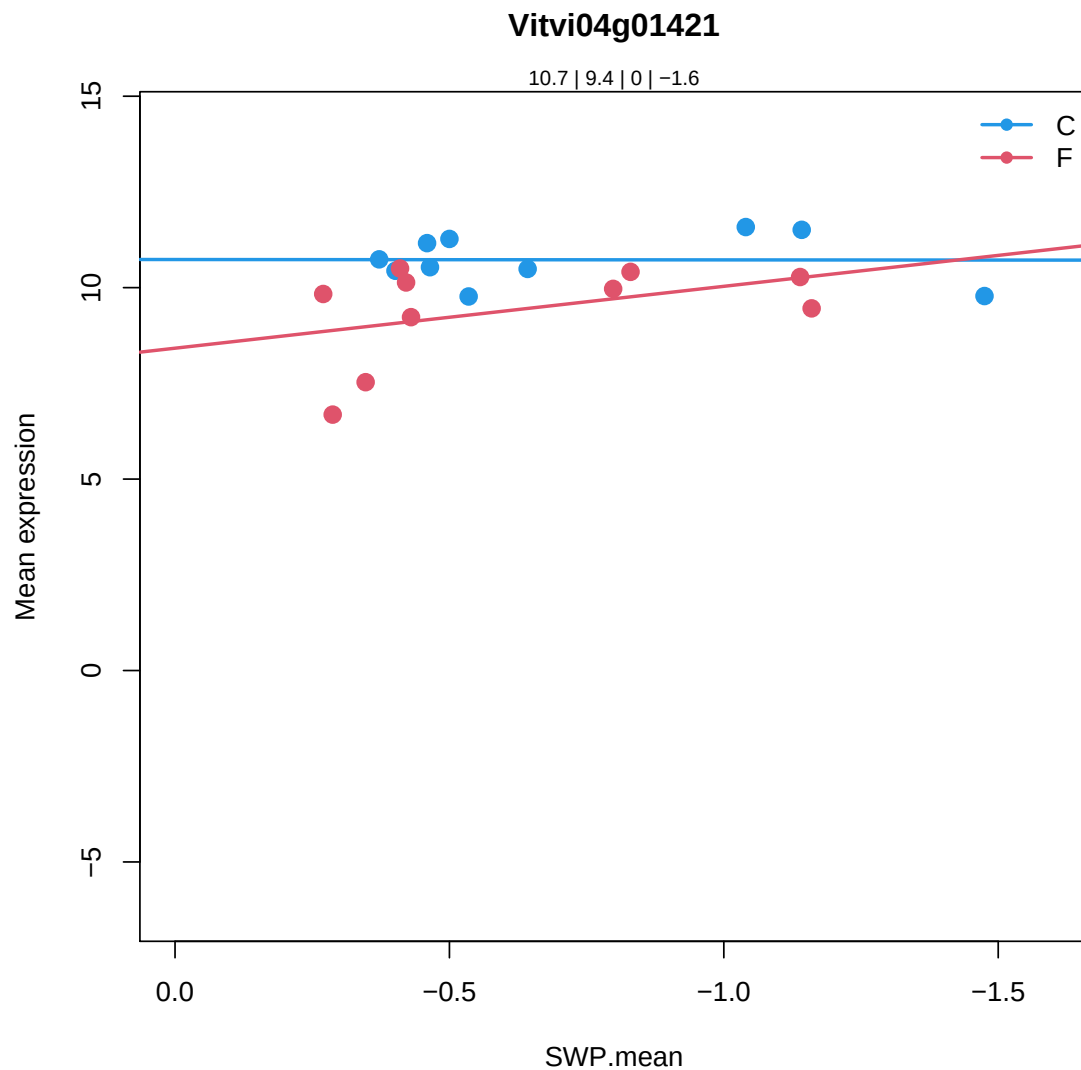
fructose-bisphosphate aldolase 1 |

Chr2:9128416-9130152 REVERSE LENGTH=399 |

201606

Coefficients for Vitvi04g01421.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	10.72777	4.215446e-21	***	3.550678e-20	***
SlopeC	0.009195738	0.9908277		0.9983274	
MeanF-MeanC	-1.324901	0.003368974	**	0.03362796	*
SlopeF-SlopeC	-1.625479	0.1814085		0.9999488	



8.3.14 Vitvi01g00064: Type3.F

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

Vitvi01g00064

2.2.2.2

major CHO metabolism.degradation.starch.starch phosphorylase

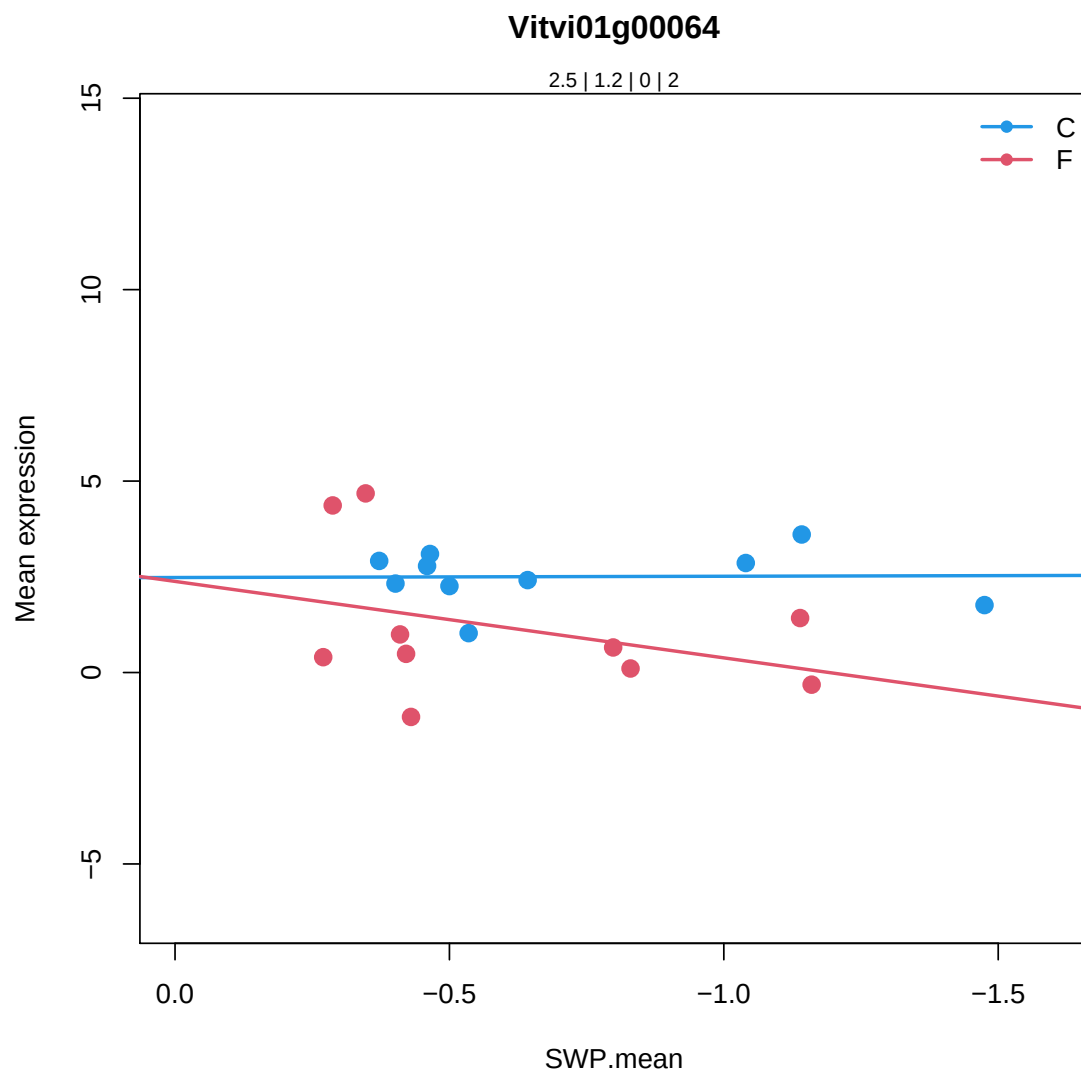
Glycosyl transferase%2C family 35 |

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	



8.3.15 Vitvi18g00154: Type3.F

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

Vitvi18g00154

29.4

protein.postranslational modification

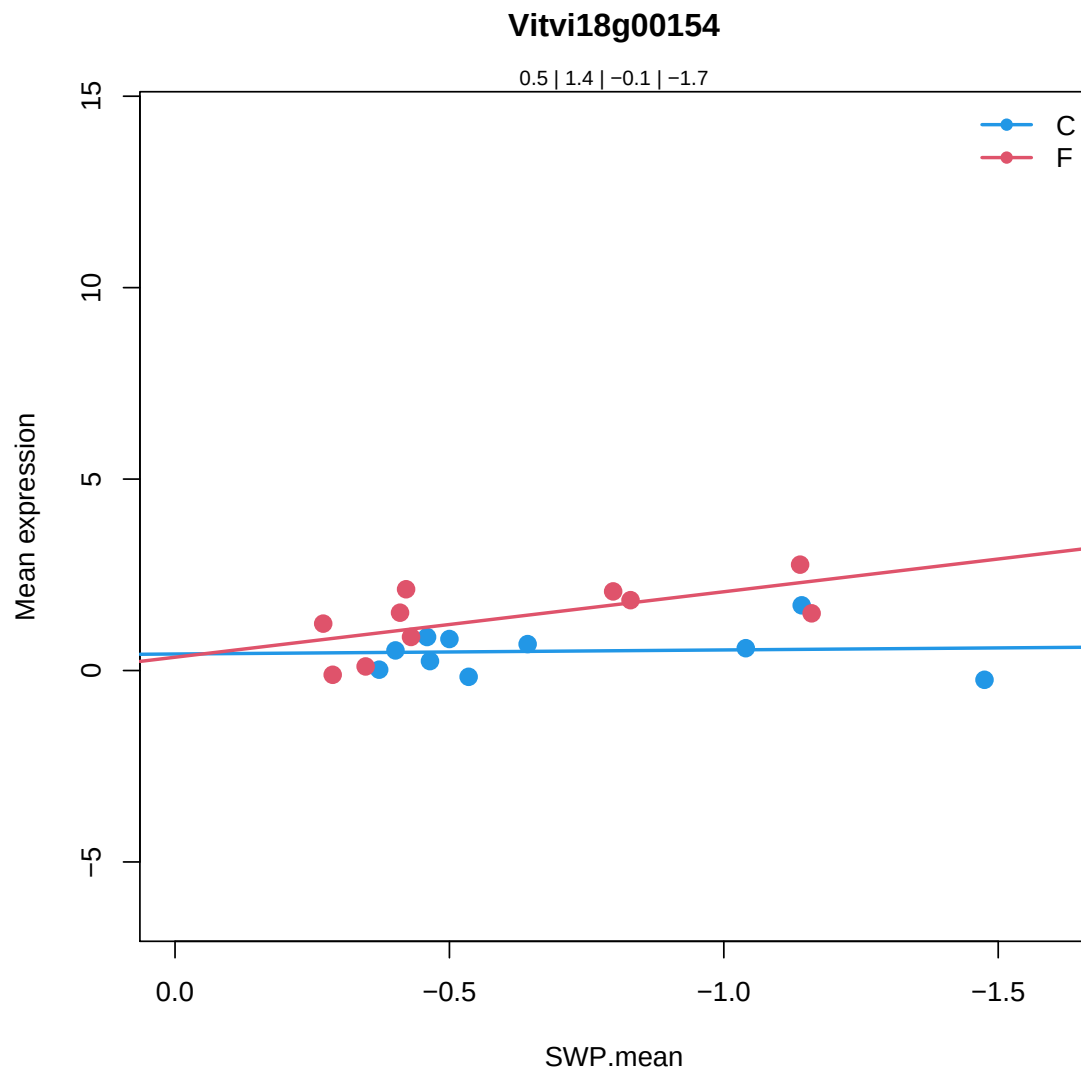
ACT-like protein tyrosine kinase family protein |

Chr4:17999432-18003193 FORWARD LENGTH=508 |

201606

Coefficients for Vitvi18g00154.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.5058717	0.01887407	*	0.01985496	*
SlopeC	-0.1060377	0.8500358		0.9719233	
MeanF-MeanC	0.8832002	0.004908278	**	0.04506746	*
SlopeF-SlopeC	-1.604135	0.06499196	.	0.9999488	



8.3.16 Vitvi08g00662: Type3.F

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

Vitvi08g00662

11.2.3

lipid metabolism.FA desaturation.omega 3 desaturase

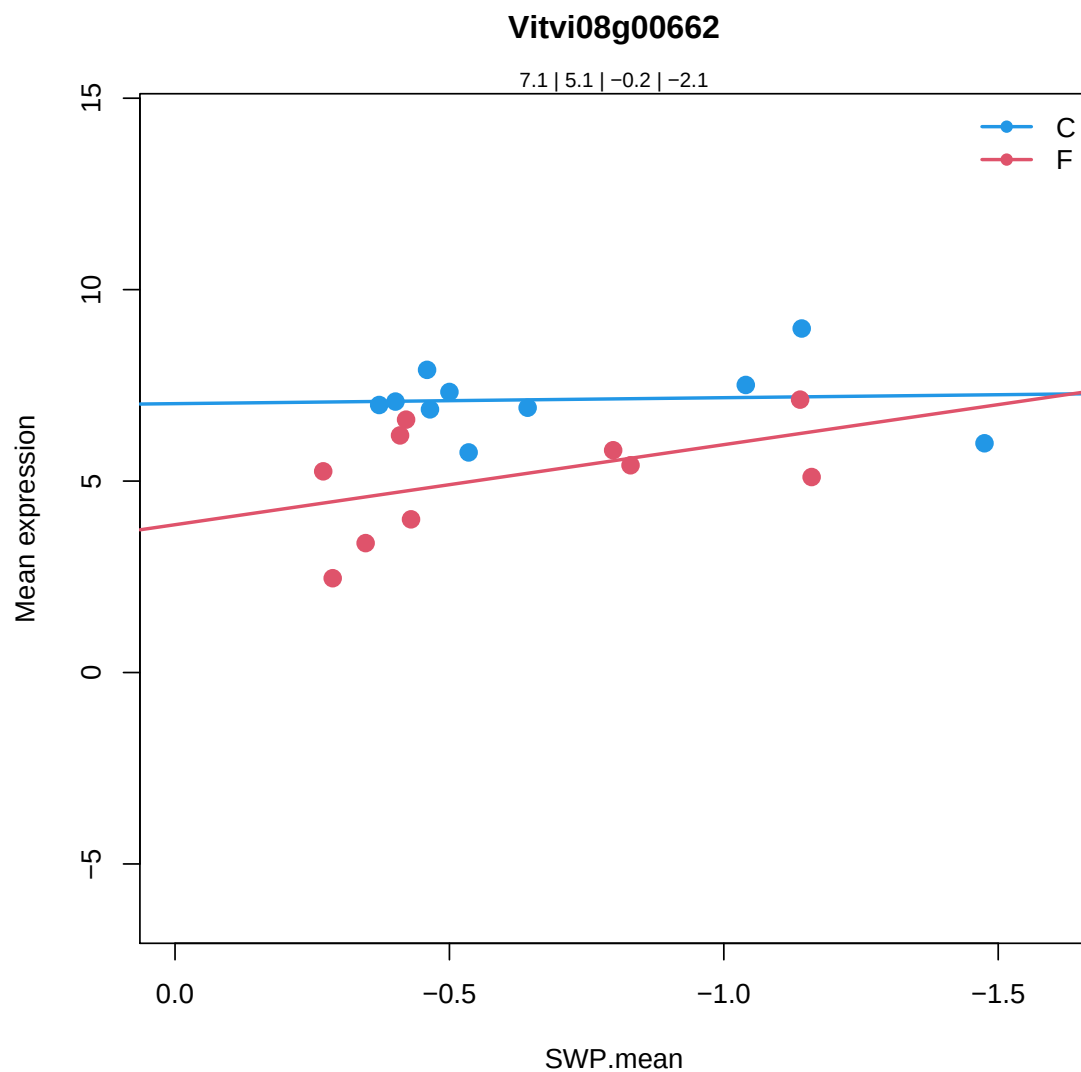
fatty acid desaturase 7 |

Chr3:3499959-3502126 FORWARD LENGTH=446 |

201606

Coefficients for Vitvi08g00662.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.131549	5.18266e-16	***	1.007321e-15	***
SlopeC	-0.1554342	0.867576		0.975839	
MeanF-MeanC	-1.997009	0.0003312959	***	0.005009536	**
SlopeF-SlopeC	-1.935515	0.1723518		0.9999488	



8.3.17 Vitvi15g00795: Type3.F

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

Vitvi15g00795

26.10

misc.cytochrome P450

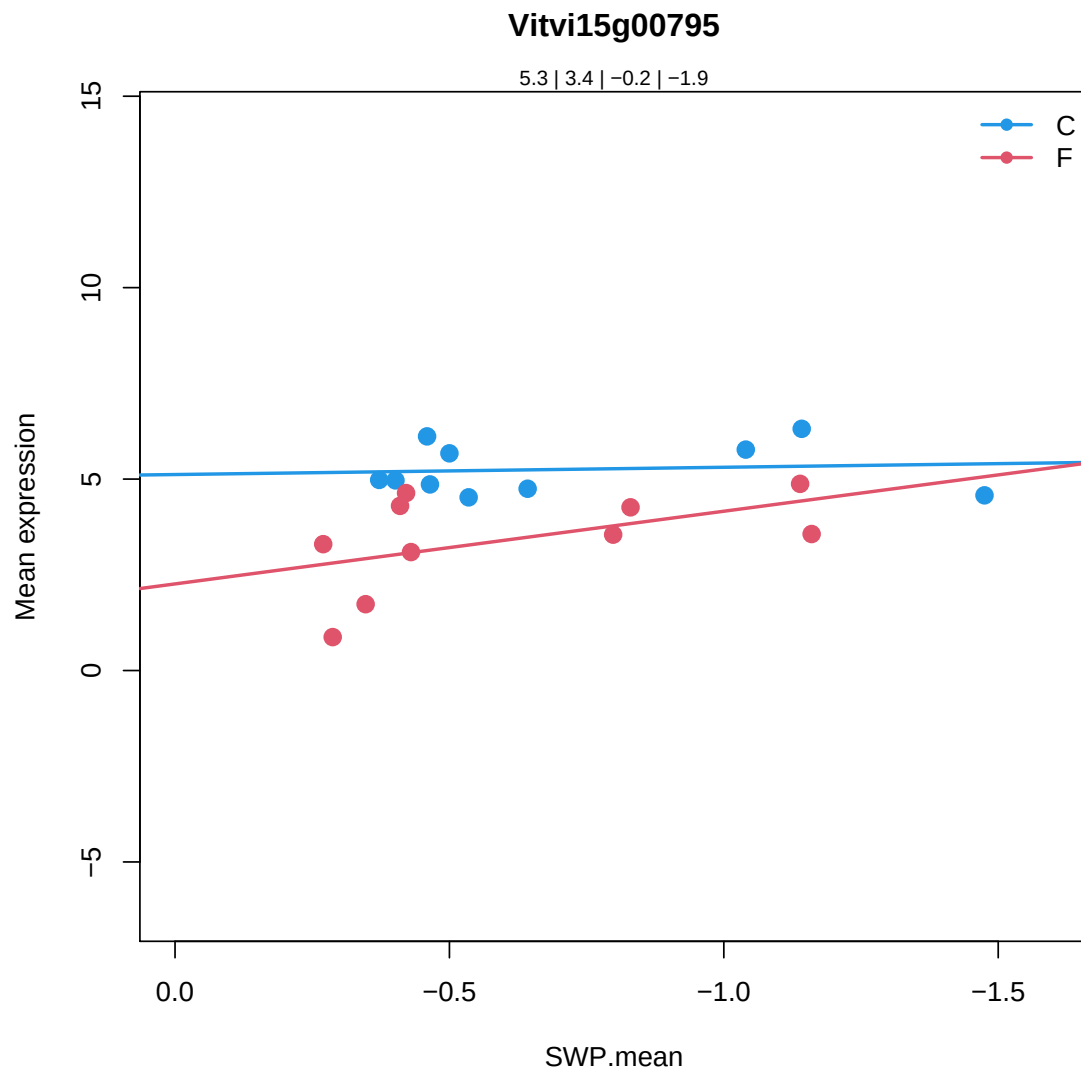
cytochrome P450%2C family 76%2C subfamily C%2C polypeptide 6 |

Chr1:12220957-12222171 REVERSE LENGTH=404 |

201606

Coefficients for Vitvi15g00795.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.252041	4.859016e-15	***	8.432326e-15	***
SlopeC	-0.1898245	0.8043535		0.9573096	
MeanF-MeanC	-1.833566	9.910431e-05	***	0.001796133	**
SlopeF-SlopeC	-1.708449	0.1439725		0.9999488	



8.3.18 Vitvi00g01320: Type3.F

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

```
Vitvi00g01320
```

```
29.5.11.4.2
```

```
protein.degradation.ubiquitin.E3.RING
```

```
plant U-box 8 |
```

```
Chr4:11356143-11357267 REVERSE LENGTH=374 |  
201606
```

```
Vitvi00g01320
```

```
35.2
```

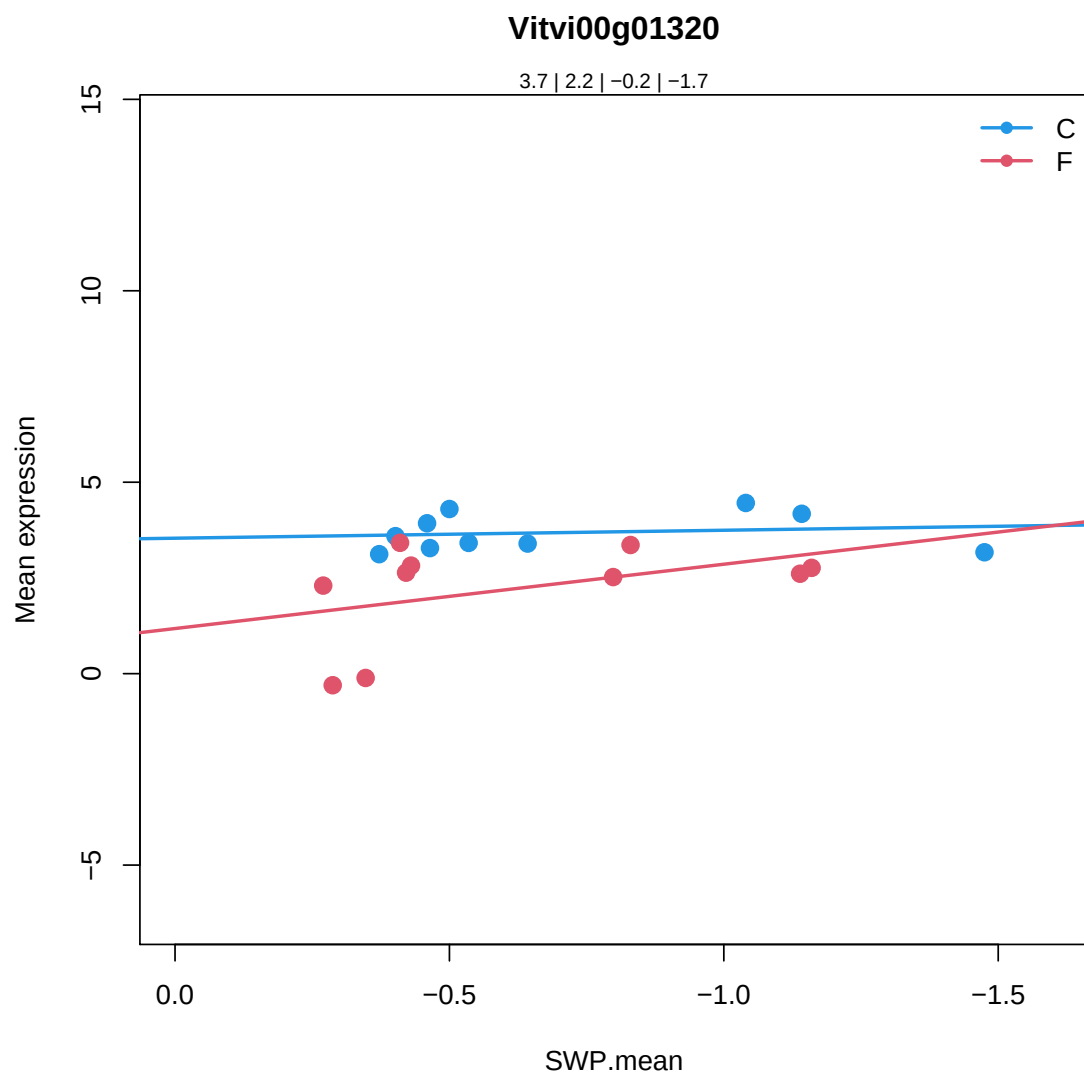
```
not assigned.unknown
```

```
plant U-box 8 |
```

```
Chr4:11356143-11357267 REVERSE LENGTH=374 |  
201606
```

Coefficients for Vitvi00g01320.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.683425	6.235563e-12	***	8.592574e-12	***
SlopeC	-0.2077702	0.7875161		0.9533712	
MeanF-MeanC	-1.481705	0.0009480829	***	0.01196248	*
SlopeF-SlopeC	-1.472132	0.2076405		0.9999488	



8.3.19 Vitvi19g01715: Type3.F

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

Vitvi19g01715

34.12

transport.metal

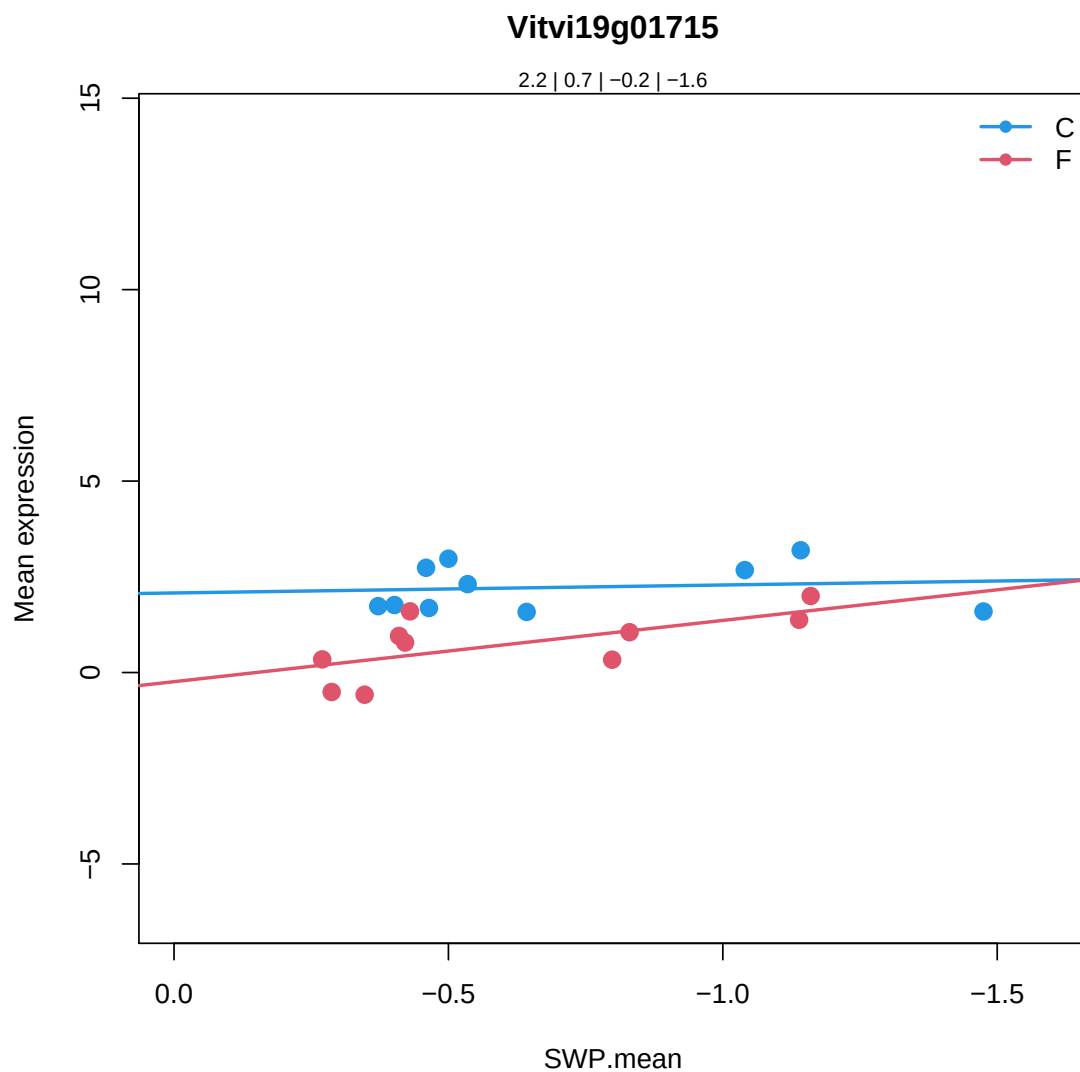
Cation efflux family protein |

Chr1:5579300-5580585 FORWARD LENGTH=315 |

201606

Coefficients for Vitvi19g01715.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.224069	2.212116e-10	***	2.855685e-10	***
SlopeC	-0.2082918	0.7113119		0.9350571	
MeanF-MeanC	-1.488937	2.947183e-05	***	0.0006389896	***
SlopeF-SlopeC	-1.391626	0.1067773		0.9999488	



8.3.20 Vitvi12g00574: Type3.F +

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

Vitvi12g00574

16.1.5

secondary metabolism.isoprenoids.terpenoids

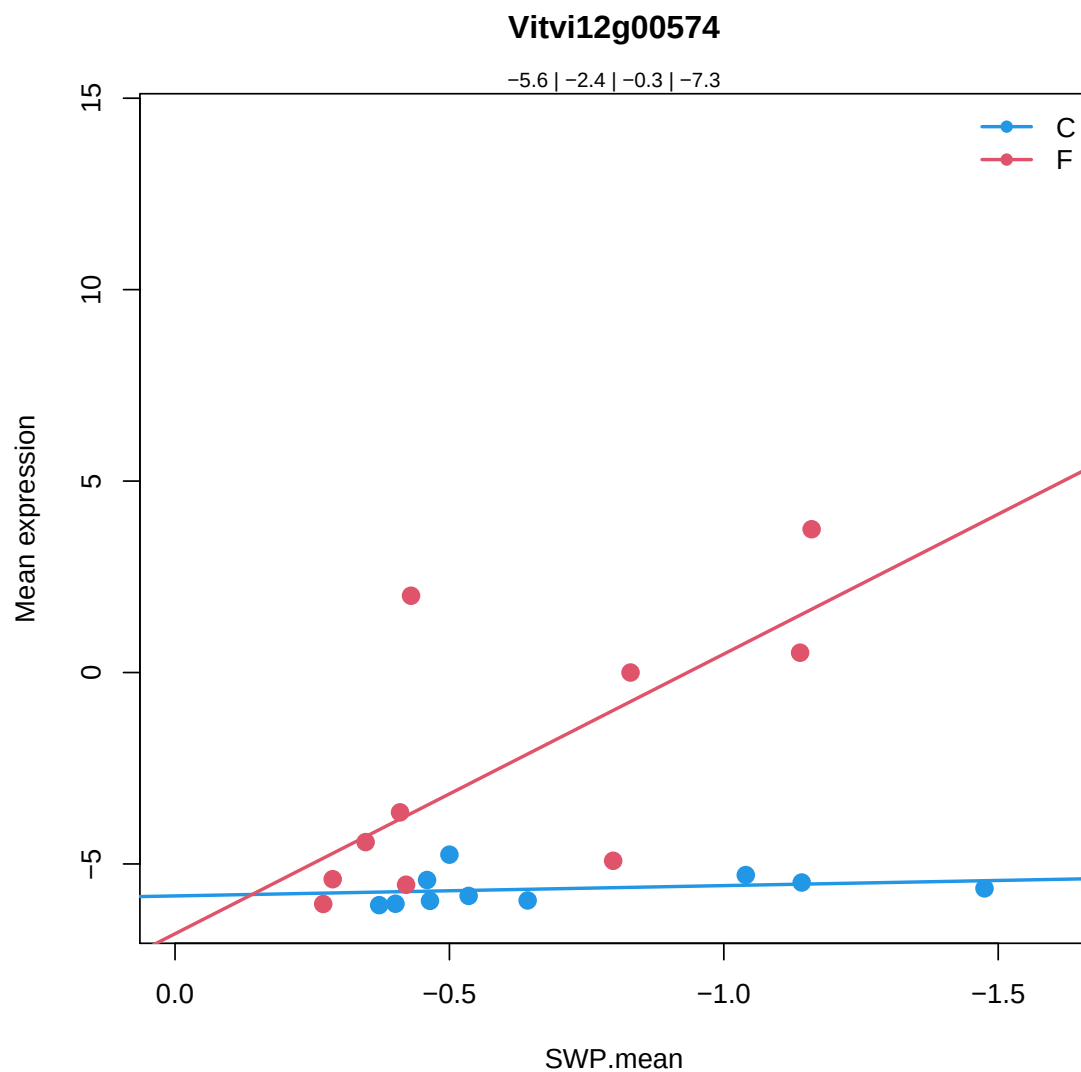
terpene synthase-like sequence-1%2C8-cineole |

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	



8.3.21 Vitvi01g01284: Type3.F

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

Vitvi01g01284

26.2

misc.UDP glucosyl and glucoronyl transferases

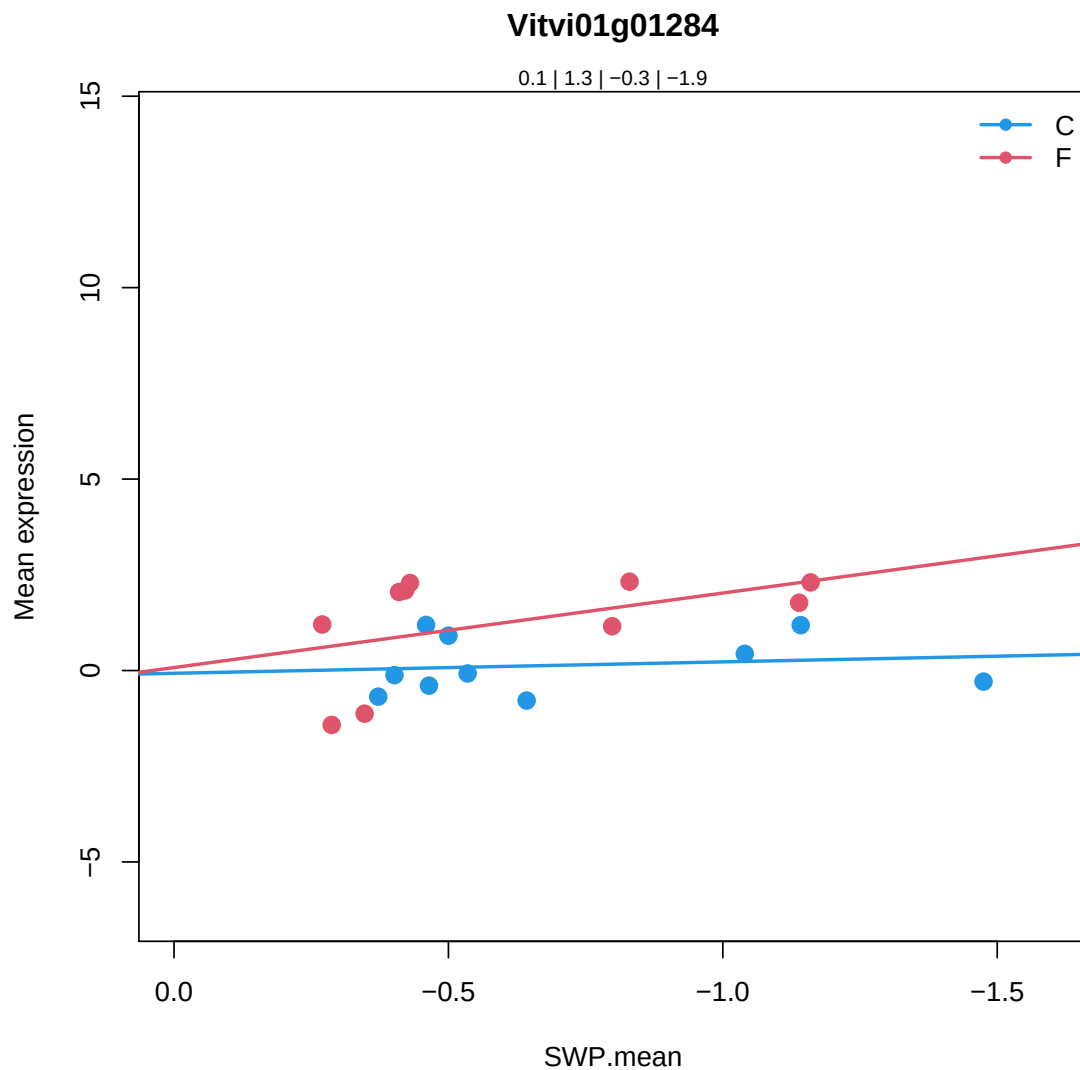
UDP-Glycosyltransferase superfamily protein |

Chr3:7867806-7870053 FORWARD LENGTH=461 |

201606

Coefficients for Vitvi01g01284.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1370866	0.6571859		0.6620507	
SlopeC	-0.297883	0.7286342		0.9401373	
MeanF-MeanC	1.125667	0.01607415	*	0.1069411	
SlopeF-SlopeC	-1.648302	0.2051119		0.9999488	



8.3.22 Vitvi19g02155: Type3.F

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

Vitvi19g02155

26.10

misc.cytochrome P450

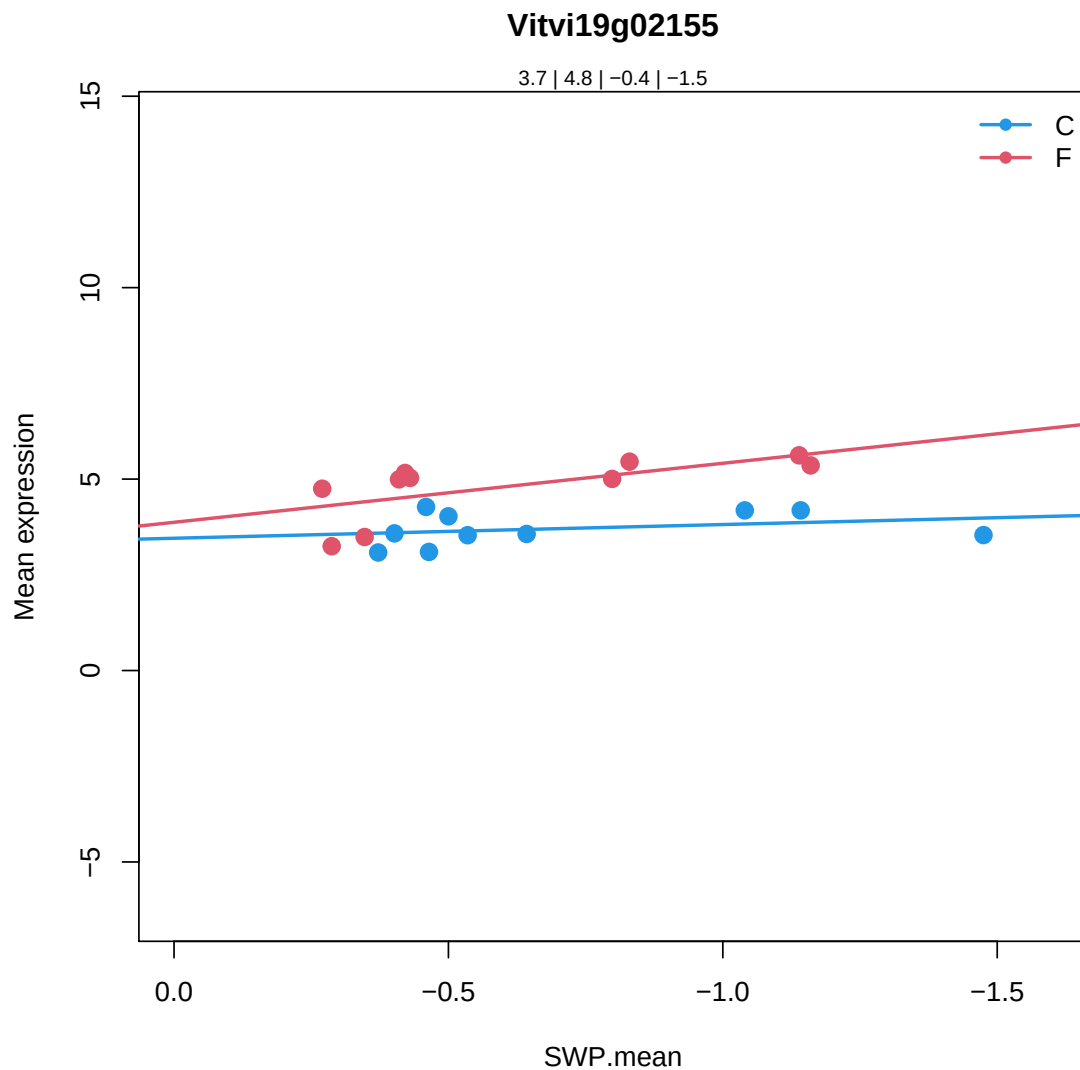
cytochrome P450%2C family 72%2C subfamily A%2C polypeptide 15 |

Chr3:4937410-4939310 FORWARD LENGTH=512 |

201606

Coefficients for Vitvi19g02155.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.70633	3.792541e-16	***	7.527791e-16	***
SlopeC	-0.3578616	0.4561085		0.8579805	
MeanF-MeanC	1.103896	0.0001455722	***	0.002468088	**
SlopeF-SlopeC	-1.183277	0.1062559		0.9999488	



8.3.23 Vitvi18g02446: Type3.F

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

Vitvi18g02446

16.1.5

secondary metabolism.isoprenoids.terpenoids

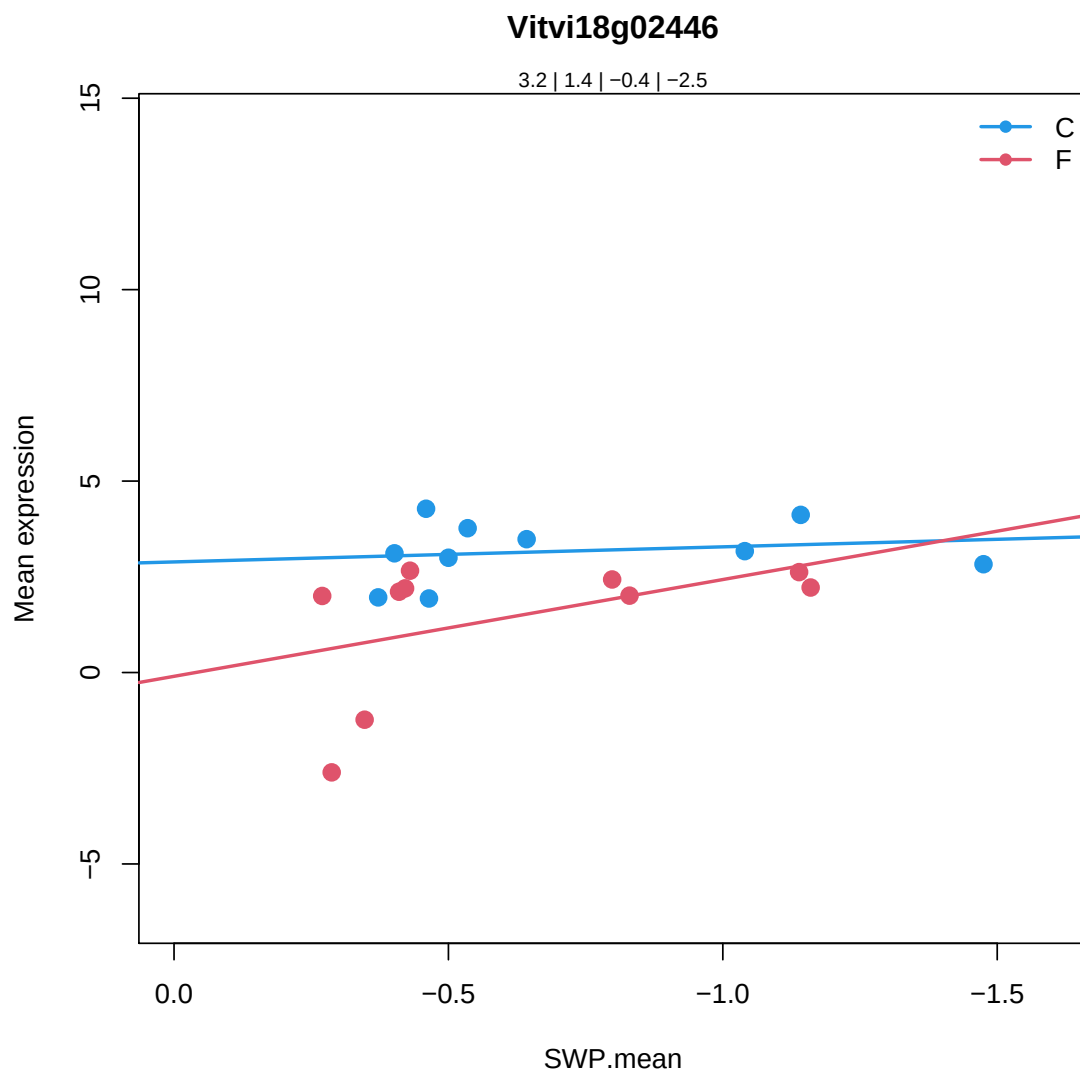
terpene synthase 21 |

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	



8.3.24 Vitvi09g00303: Type3.F

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

Vitvi09g00303

34.16

transport.ABC transporters and multidrug resistance systems

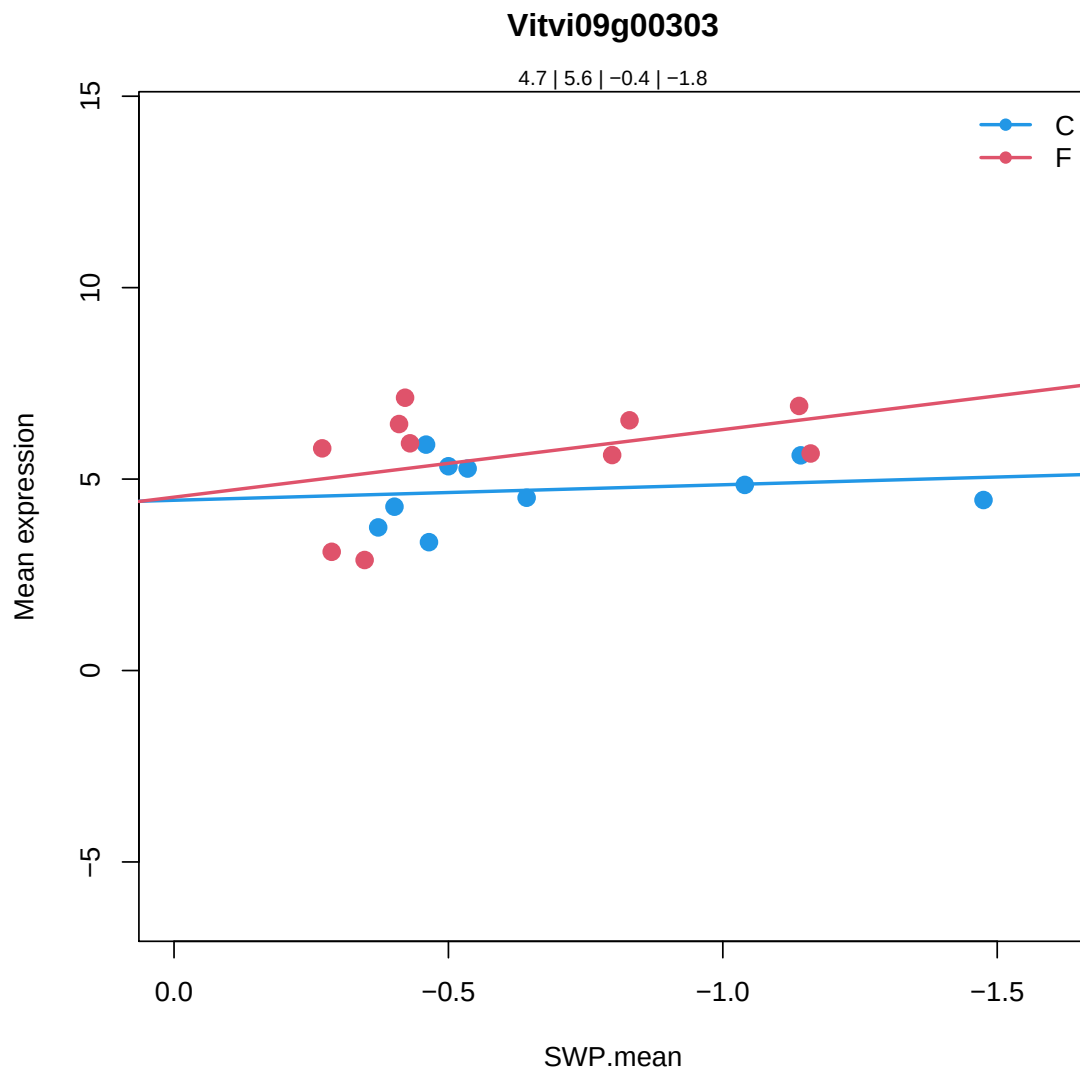
pleiotropic drug resistance 1 |

Chr3:5539897-5546263 FORWARD LENGTH=1411 |

201606

Coefficients for Vitvi09g00303.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.73112	1.740727e-12	***	2.463068e-12	***
SlopeC	-0.4047651	0.6628311		0.9225525	
MeanF-MeanC	0.8715695	0.07479004	.	0.3078422	
SlopeF-SlopeC	-1.360039	0.3293618		0.9999488	



8.3.25 Vitvi01g01021: Type3.F

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

Vitvi01g01021

27.1.19

RNA.processing.ribonucleases

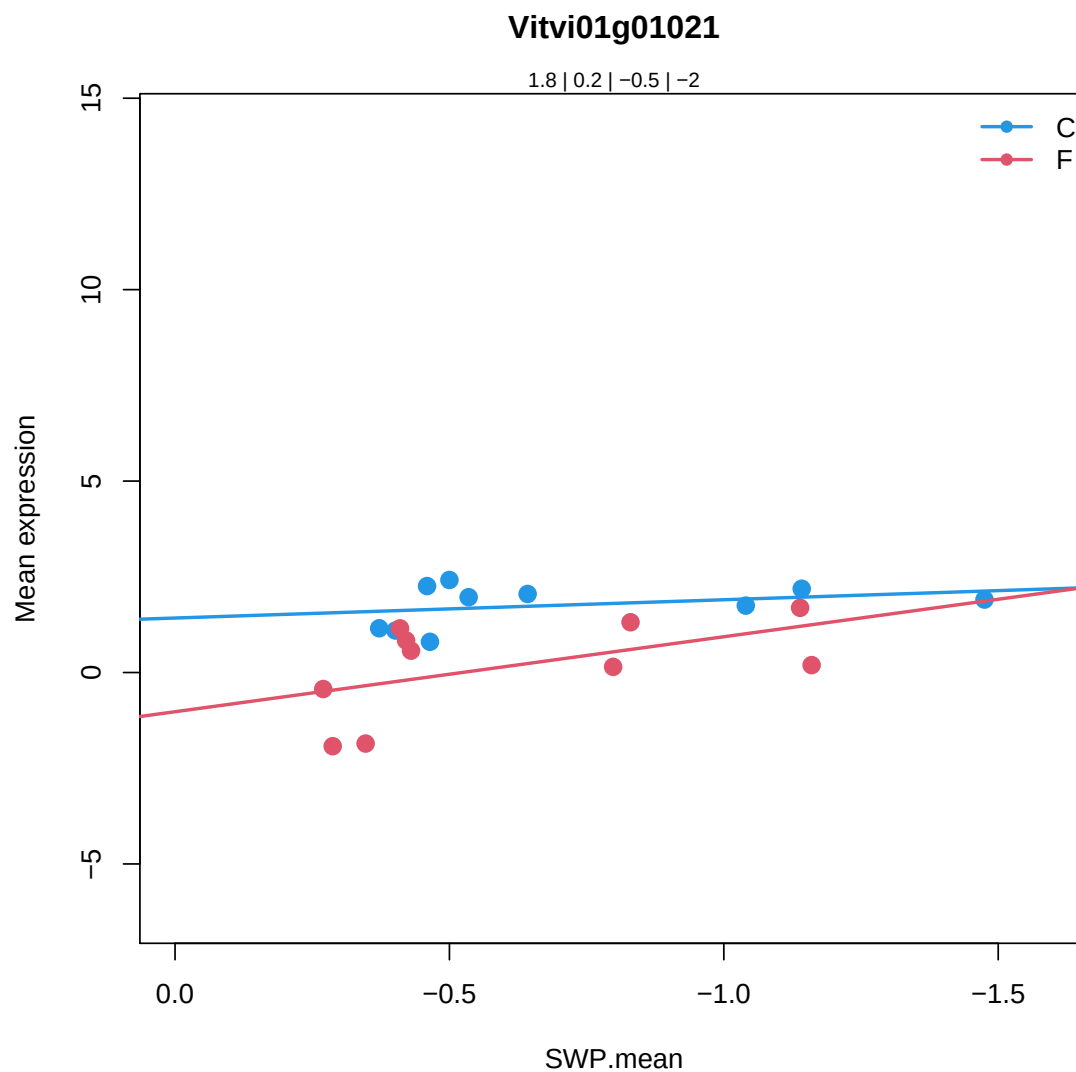
ribonuclease 1 |

Chr2:873714-874667 FORWARD LENGTH=230 |

201606

Coefficients for Vitvi01g01021.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.758743	6.402902e-07	***	7.427737e-07	***
SlopeC	-0.477187	0.5048389		0.8706312	
MeanF-MeanC	-1.589466	0.0002147614	***	0.003456592	**
SlopeF-SlopeC	-1.48126	0.1715283		0.9999488	



8.4 Type5.0

8.4.1 Vitvi03g00325: Type5.0 *

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

Vitvi03g00325

27.3.25

RNA.regulation of transcription.MYB domain transcription factor family

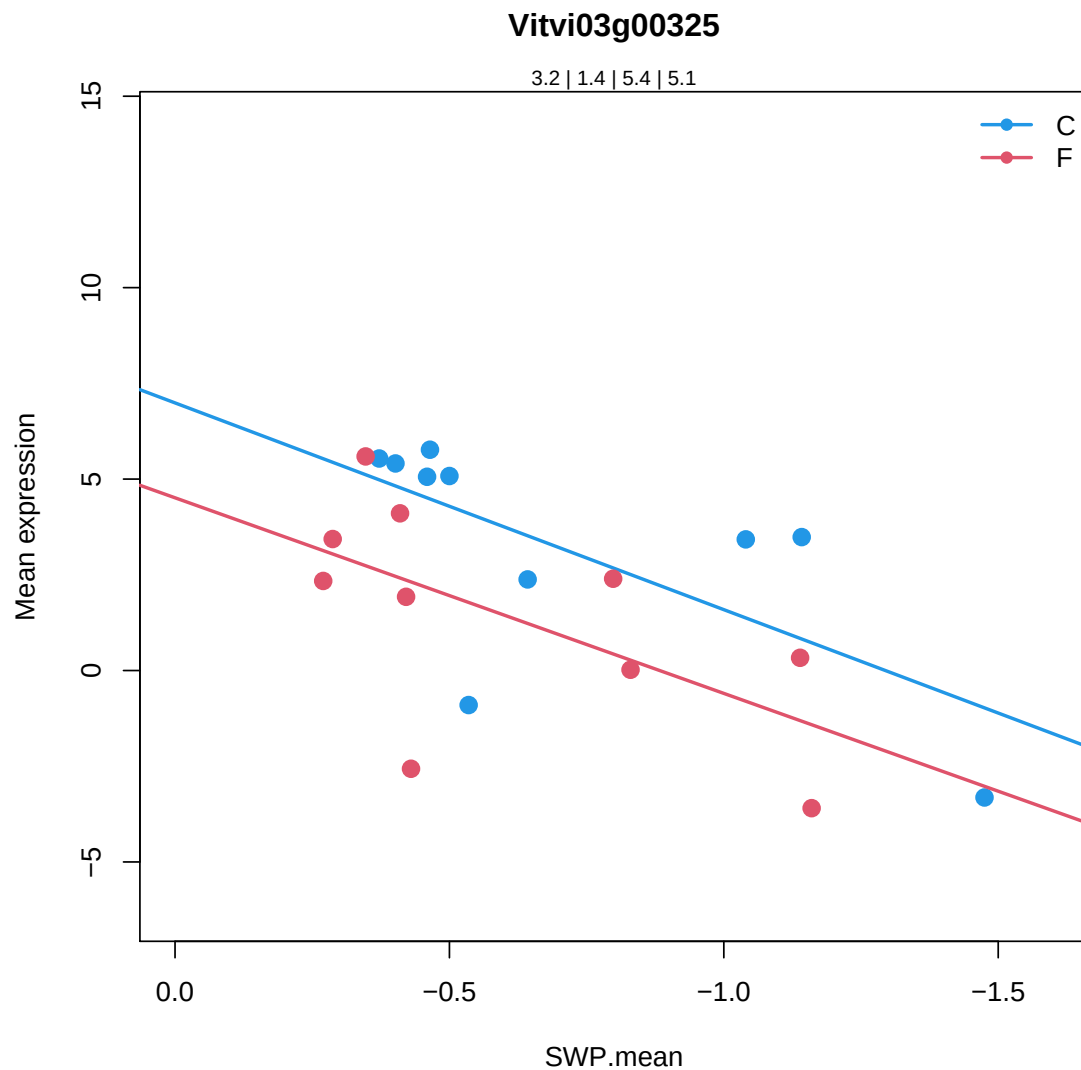
RAD-like 1 |

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	



8.4.2 Vitvi17g00601: Type5.0 *

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

Vitvi17g00601

17.6.3

hormone metabolism.gibberelin.induced-regulated-responsive-activated

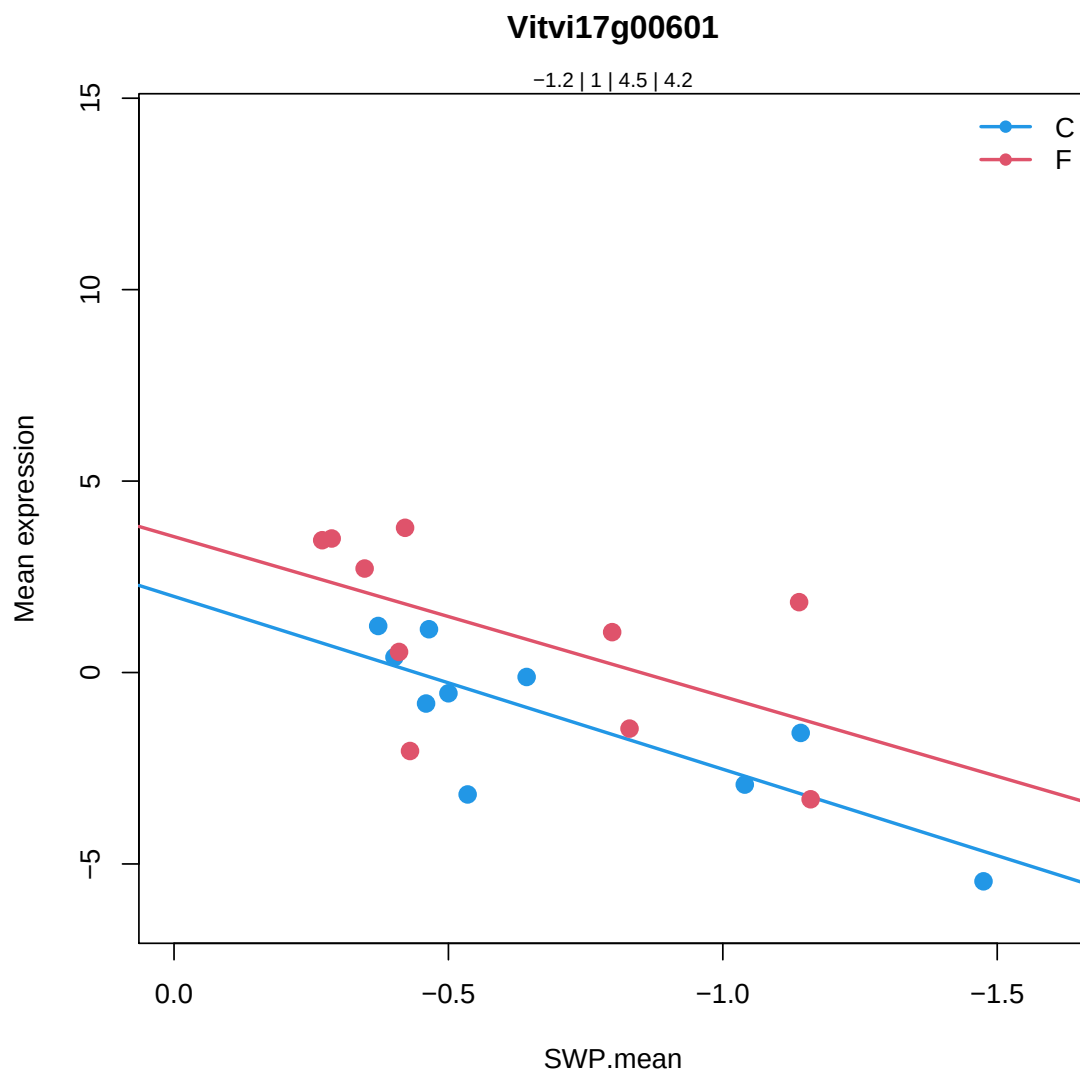
Gibberellin-regulated family protein |

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	



8.4.3 Vitvi05g01577: Type5.0 *

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

Vitvi05g01577

20.1.7.3

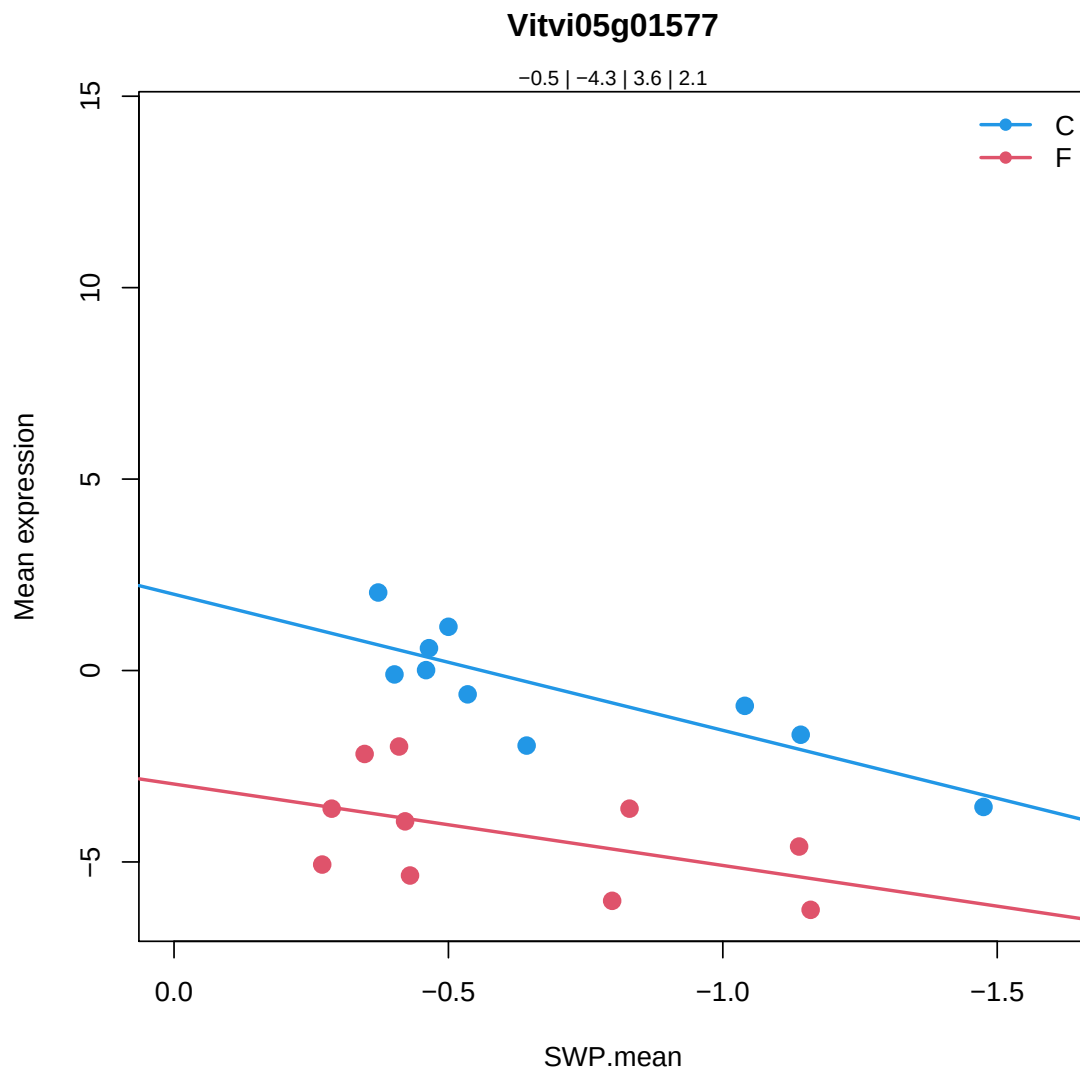
stress.biotic.PR-proteins.PR3/4/8/11 (chitinases and chitin binding pr
homolog of carrot EP3-3 chitinase |

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	



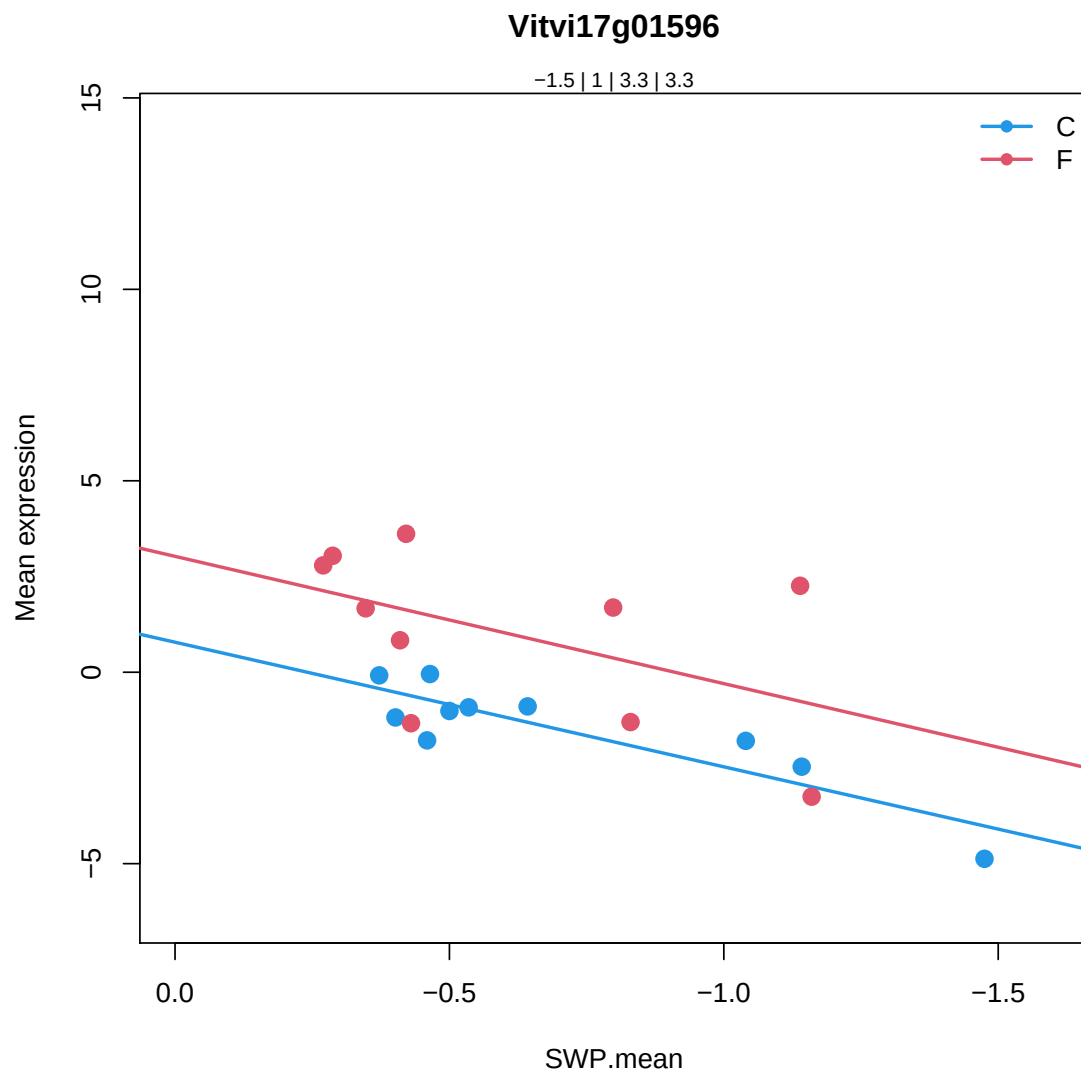
8.4.4 Vitvi17g01596: Type5.0 *

```
> 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	



8.4.5 Vitvi07g00445: Type5.0

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

Vitvi07g00445

11.1.9

lipid metabolism.FA synthesis and FA elongation.long chain fatty acid

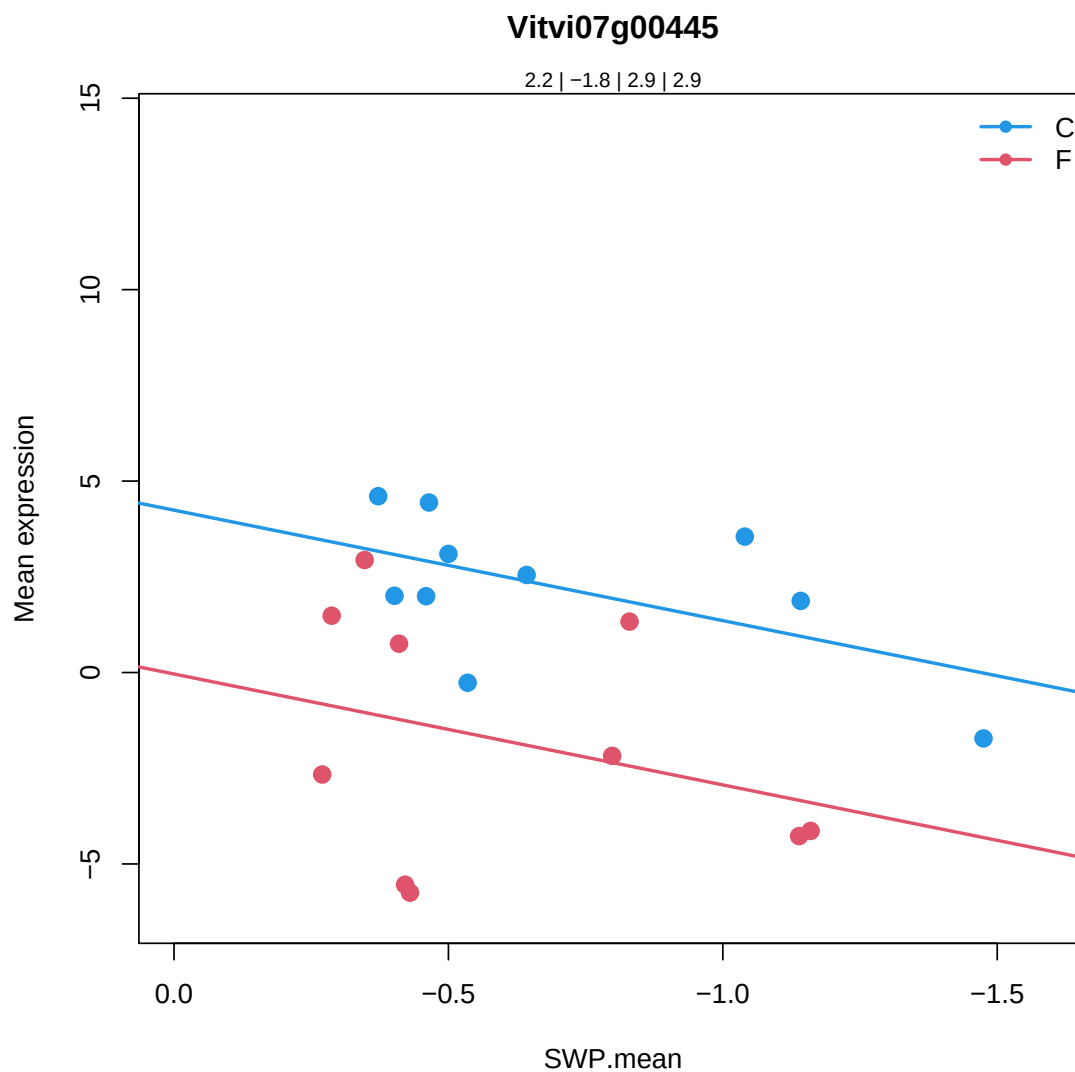
AMP-dependent synthetase and ligase family protein |

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	



8.4.6 Vitvi18g01938: Type5.0 *

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

Vitvi18g01938

30.2.25

signalling.receptor kinases.wall associated kinase

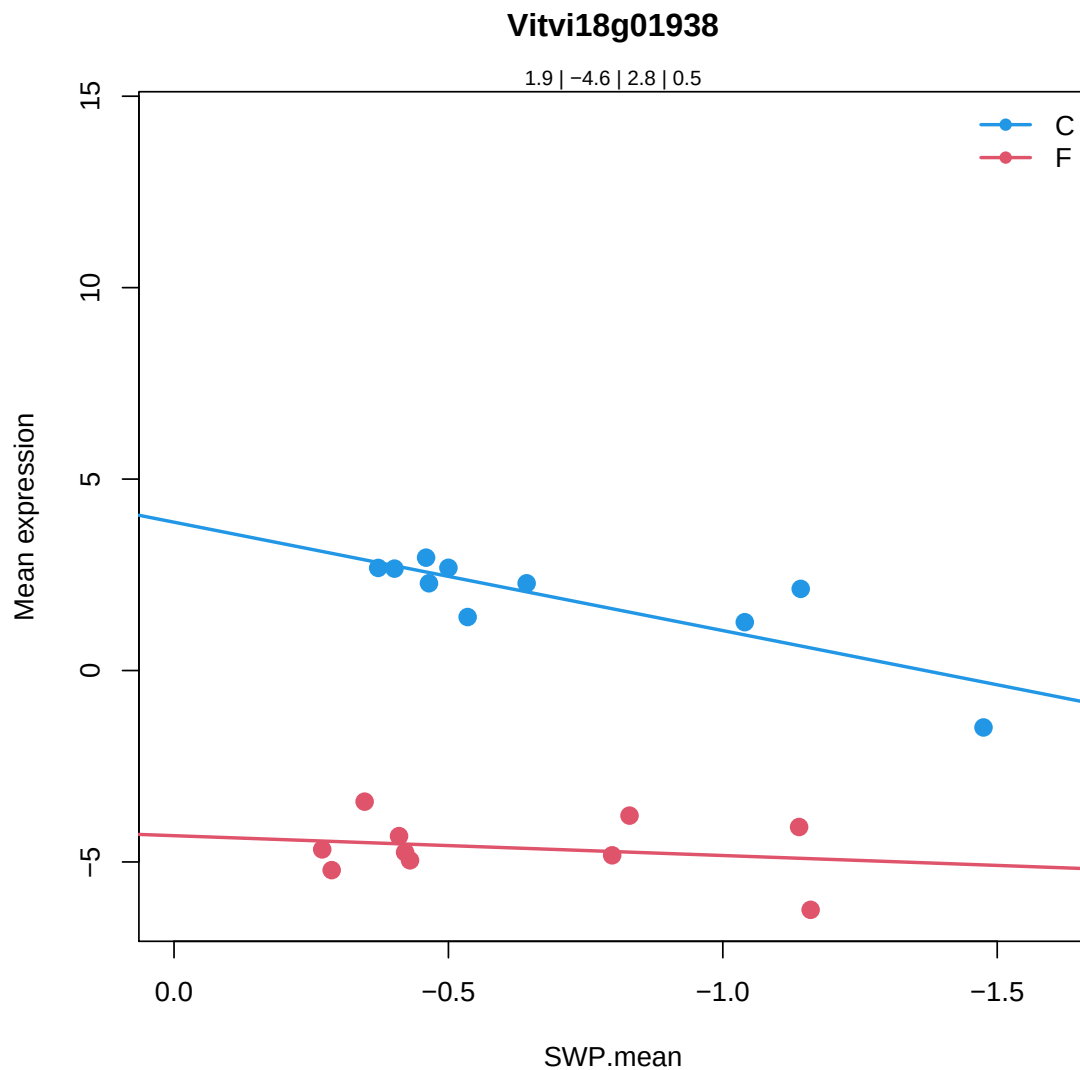
wall associated kinase 3 |

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	



8.4.7 Vitvi07g00586: Type5.0 *

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

Vitvi07g00586

29.5.4

protein.degradation.aspartate protease

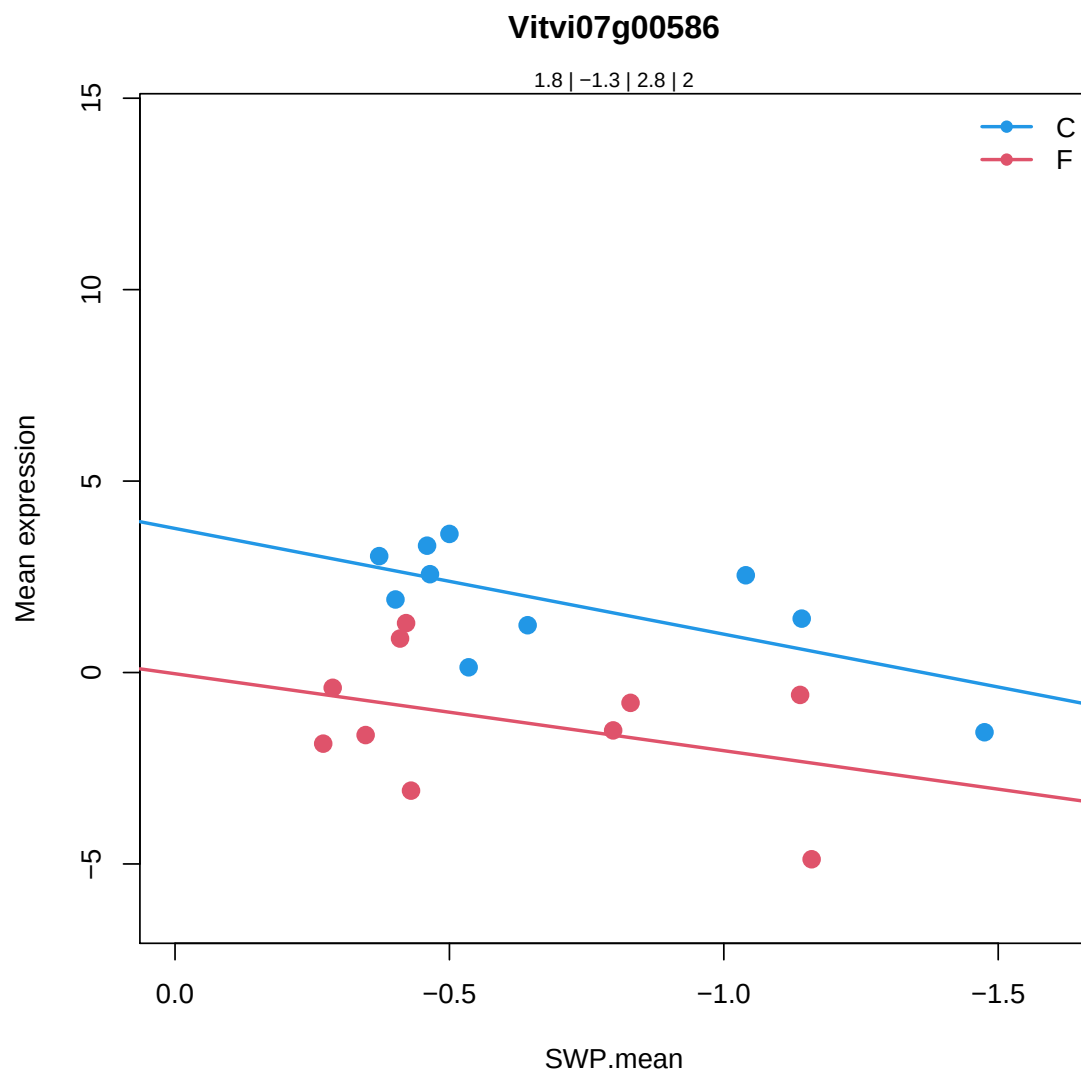
Eukaryotic aspartyl protease family protein |

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	



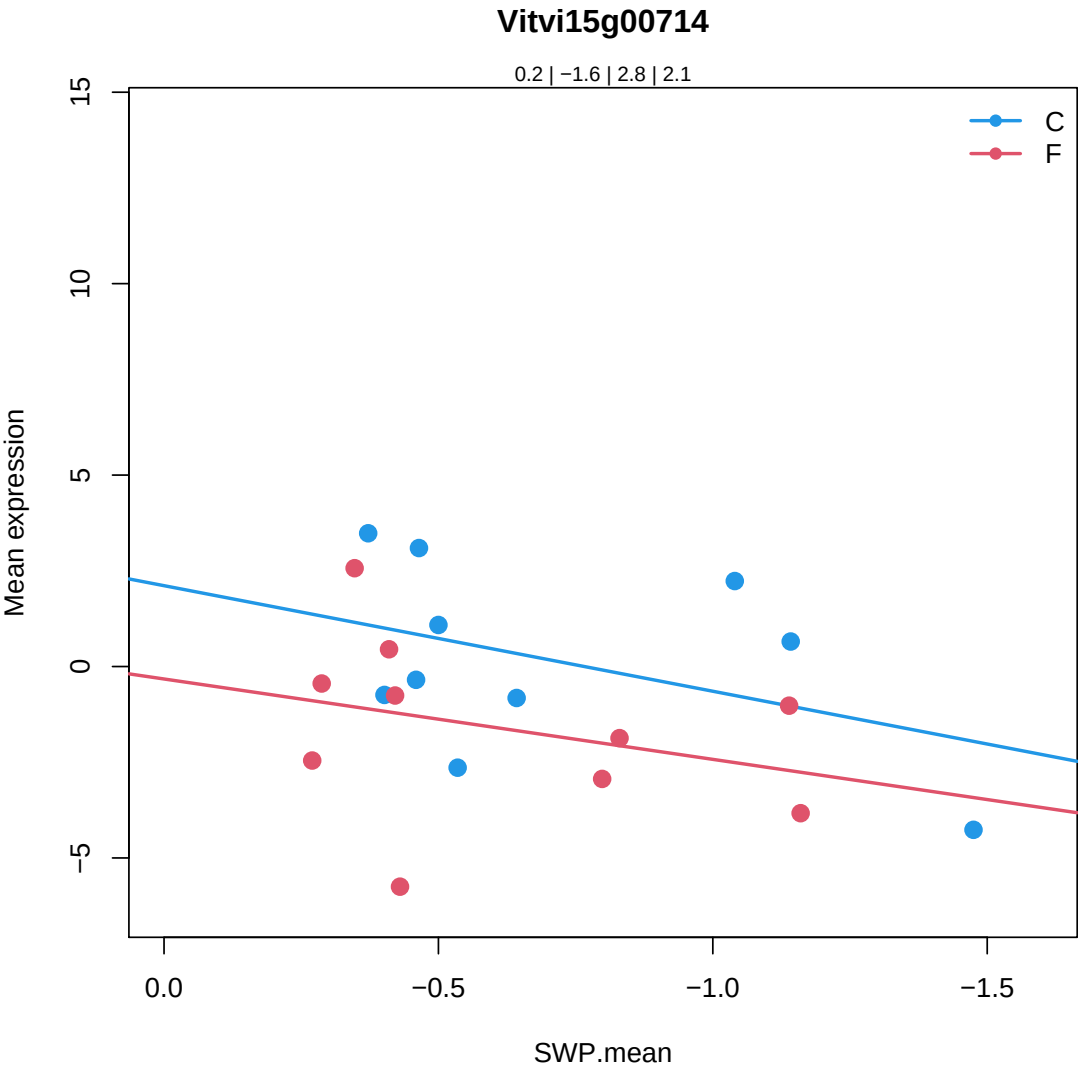
8.4.8 Vitvi15g00714: Type5.0

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

```
Vitvi15g00714
26.21
misc.protease inhibitor/seed storage/lipid transfer protein (LTP) fami
Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin
Chr4:69433-69819 REVERSE LENGTH=128 |
201606
```

Coefficients for Vitvi15g00714.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1724214	0.7927213		0.7967463	
SlopeC	2.757195	0.1407973		0.6676582	
MeanF-MeanC	-1.777328	0.06572122	.	0.2846357	
SlopeF-SlopeC	-0.6577505	0.8086901		0.9999488	



8.4.9 Vitvi01g00593: Type5.0 *

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

Vitvi01g00593

10.6.3

cell wall.degradation.pectate lyases and polygalacturonases

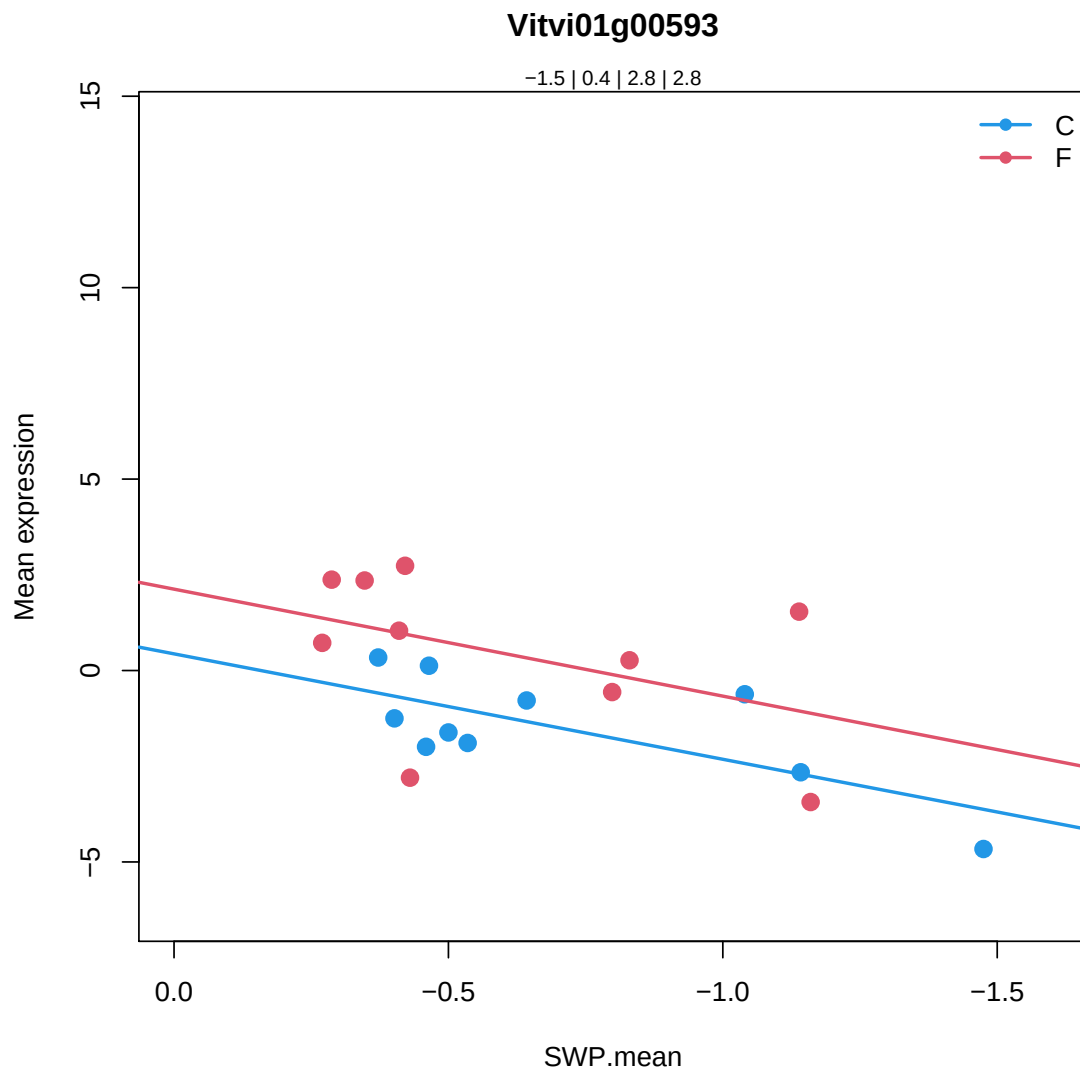
Pectate lyase family protein |

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	



8.4.10 Vitvi18g02709: Type5.0 *

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

Vitvi18g02709

35.1.40

not assigned.no ontology.glycine rich proteins

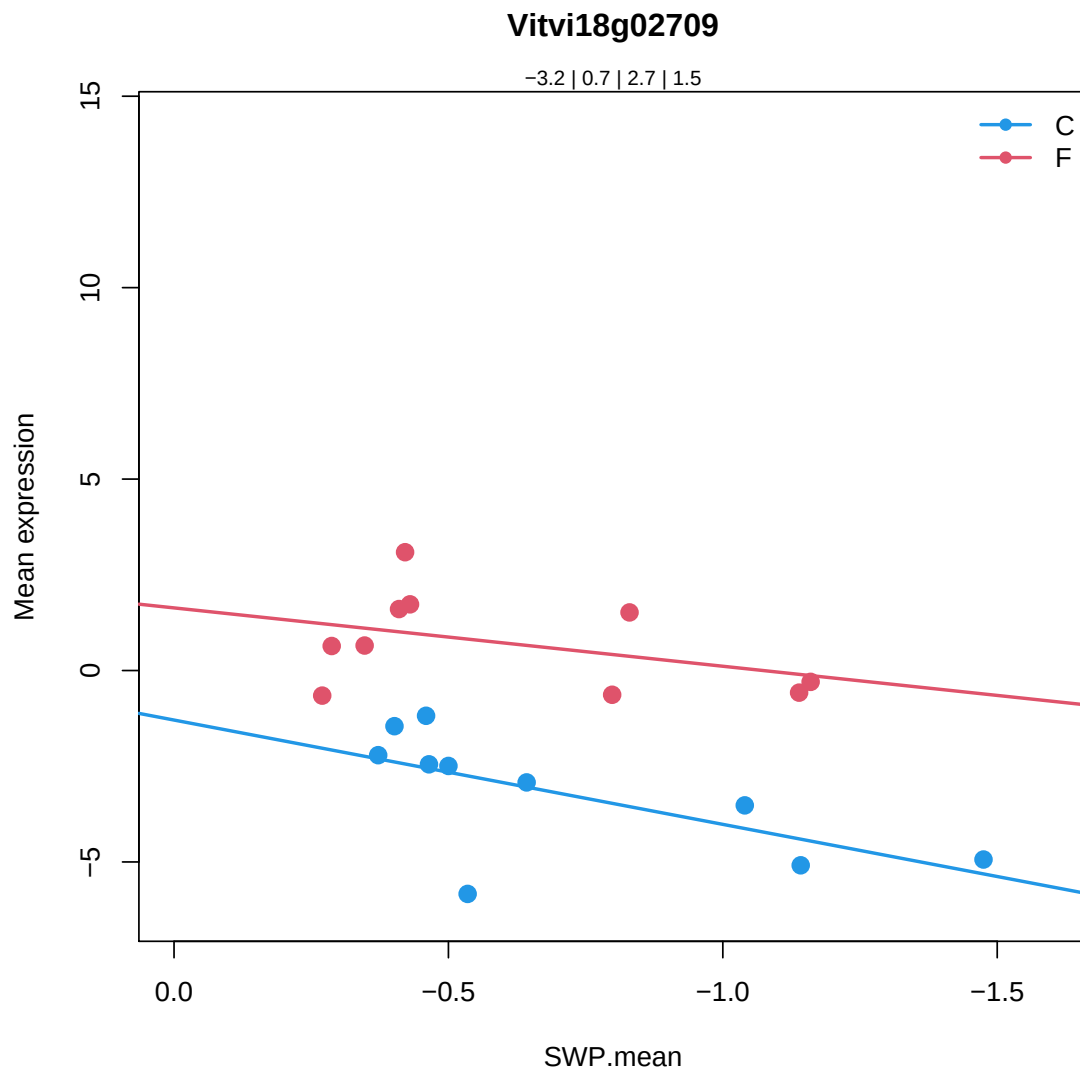
Cupredoxin superfamily protein |

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	



8.4.11 Vitvi09g00258: Type5.0 *

```
> 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
```

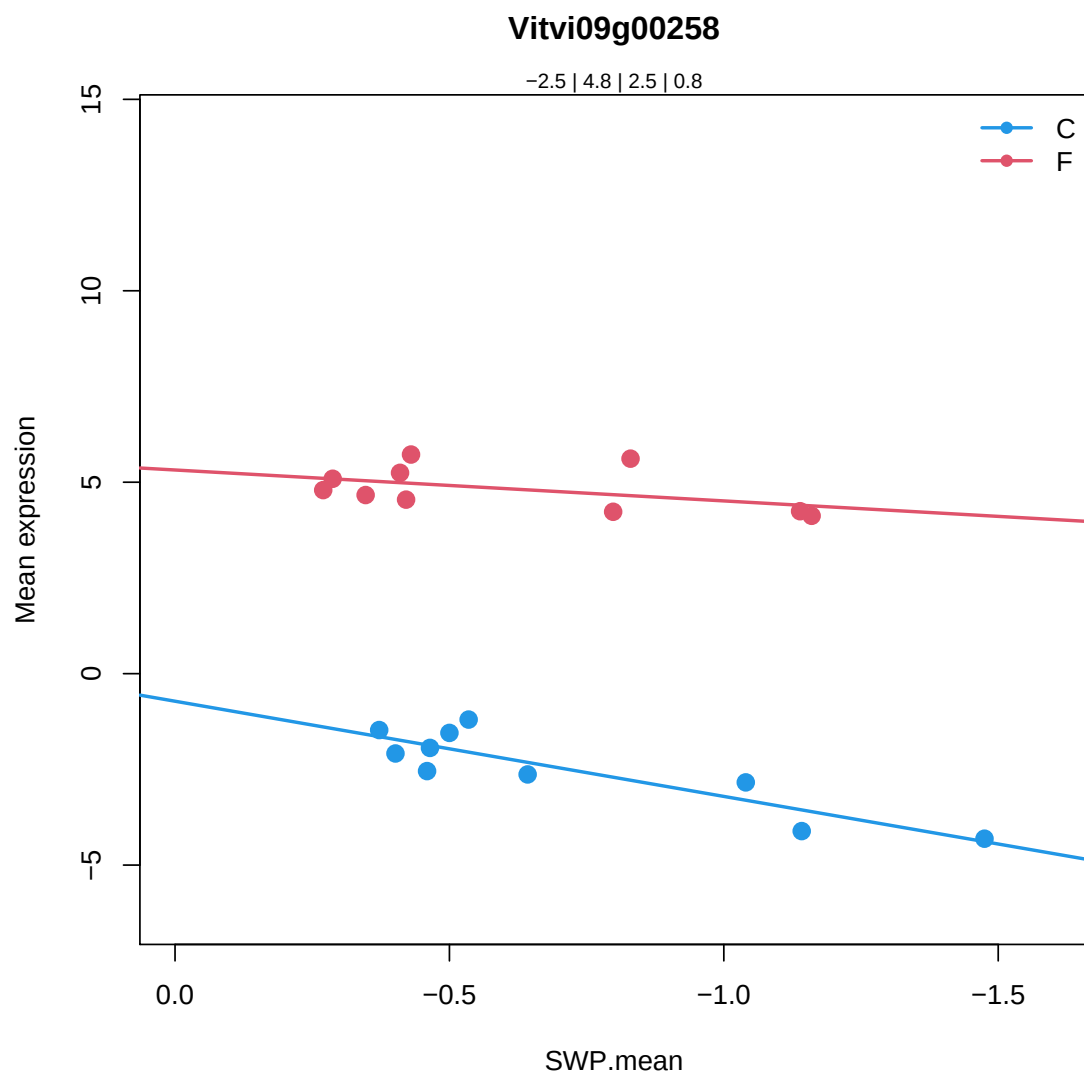
```
root hair specific 6 |
```

```
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	



8.4.12 Vitvi09g01932: Type5.0 *

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

Vitvi09g01932

20.1.2

stress.biotic.receptors

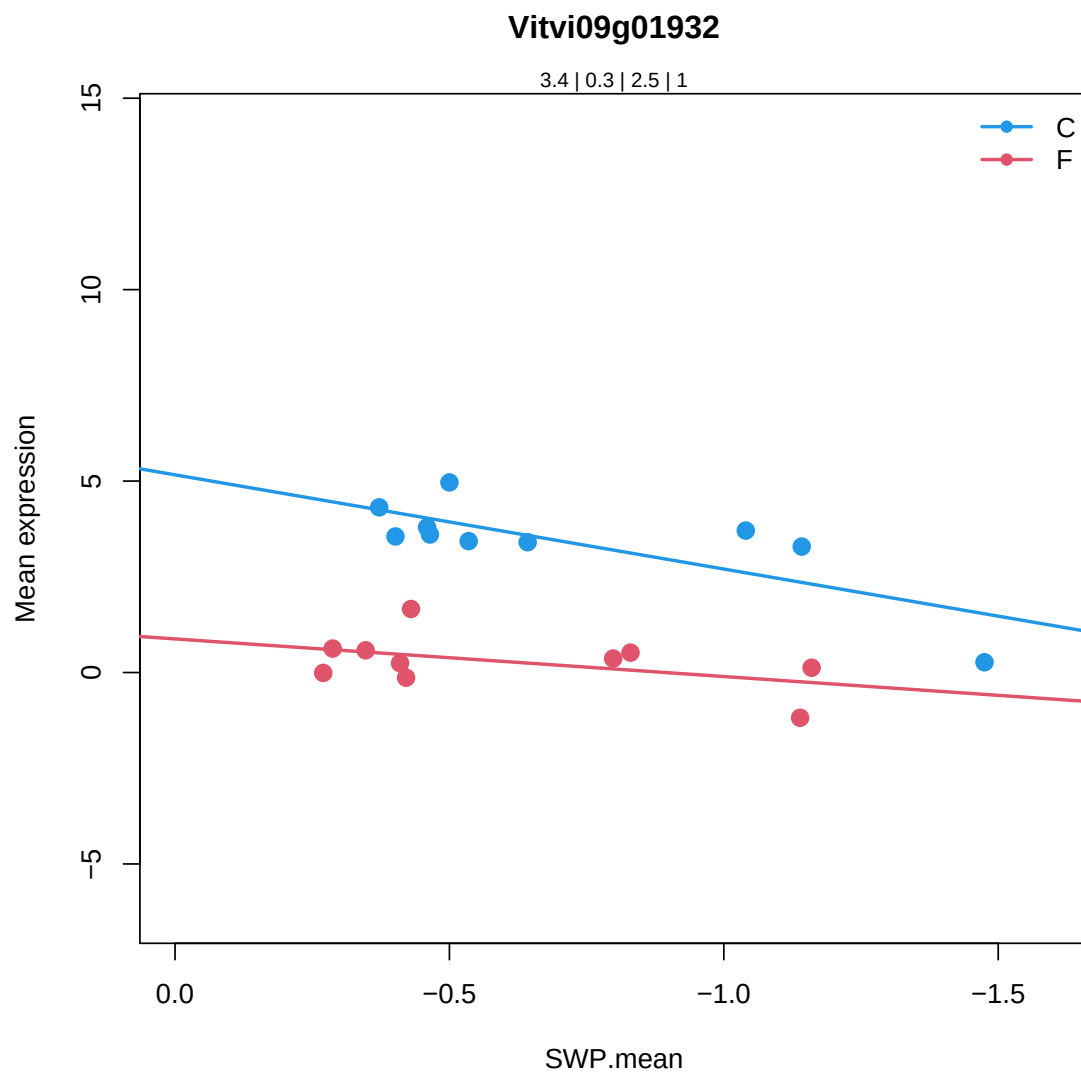
disease resistance family protein / LRR family protein |

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	



8.4.13 Vitvi03g00318: Type5.0 *

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

Vitvi03g00318

27.3.25

RNA.regulation of transcription.MYB domain transcription factor family

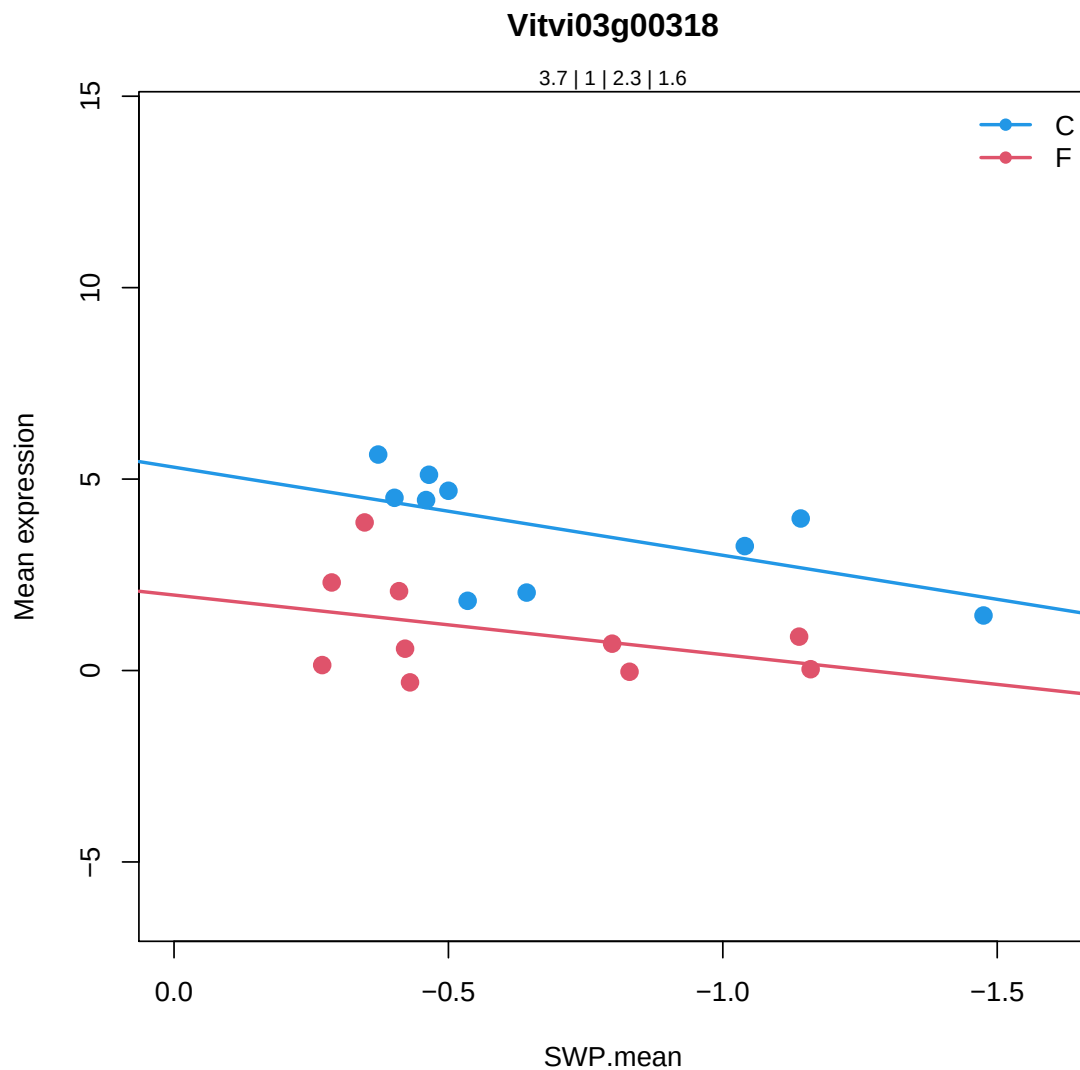
RAD-like 6 |

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	

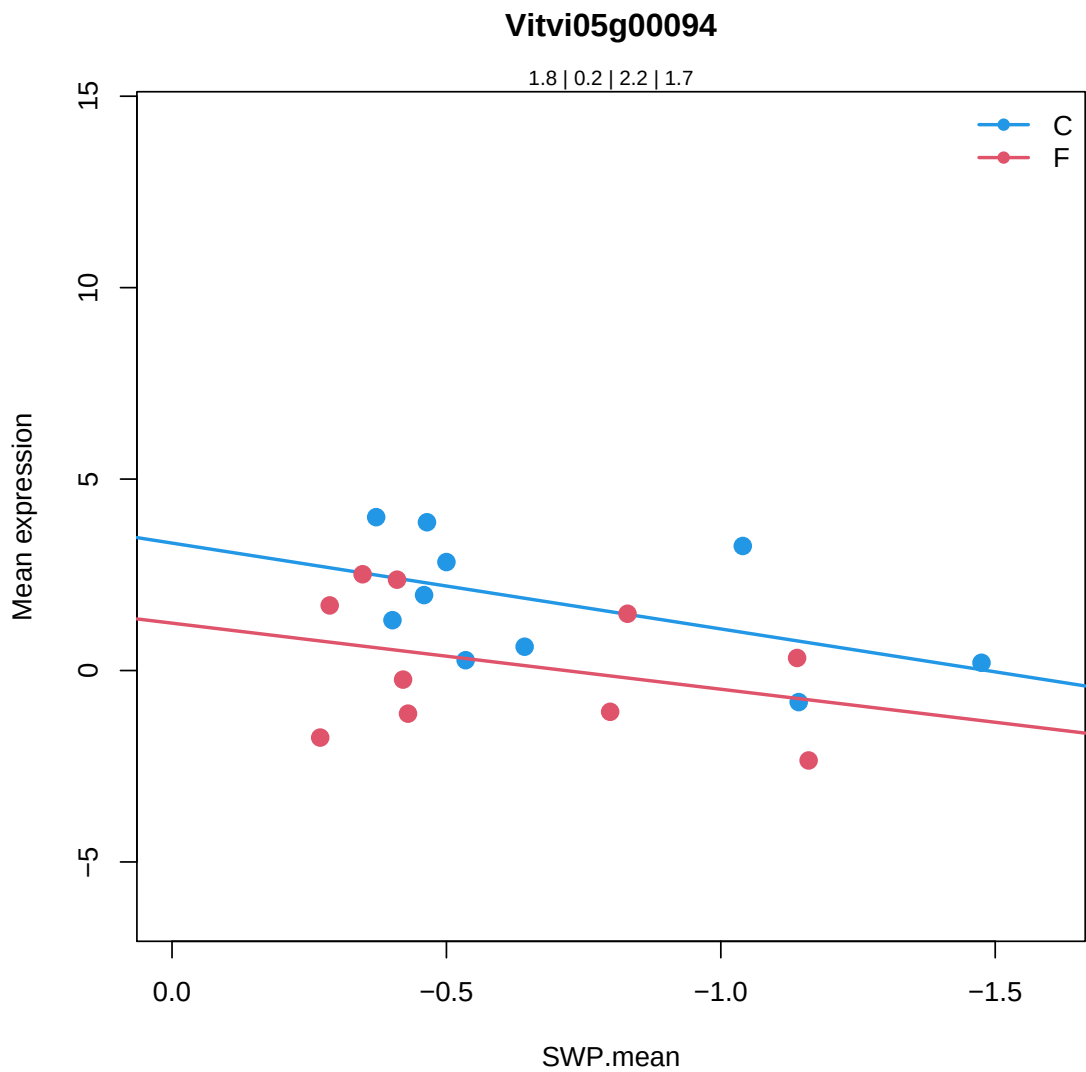


8.4.14 Vitvi05g00094: Type5.0

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
Vitvi05g00094
20.1.7.3
stress.biotic.PR-proteins.PR3/4/8/11 (chitinases and chitin binding pr
Chitinase family protein |
Chr1:1766833-1768117 REVERSE LENGTH=321 |
201606
```

Coefficients for Vitvi05g00094.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.75152	0.0009882148	***	0.001070151	**
SlopeC	2.242017	0.09374752	.	0.6028633	
MeanF-MeanC	-1.566073	0.02500179	*	0.1486222	
SlopeF-SlopeC	-0.5159695	0.7888473		0.9999488	



8.4.15 Vitvi07g00665: Type5.0

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

Vitvi07g00665

10.2.1

cell wall.cellulose synthesis.cellulose synthase

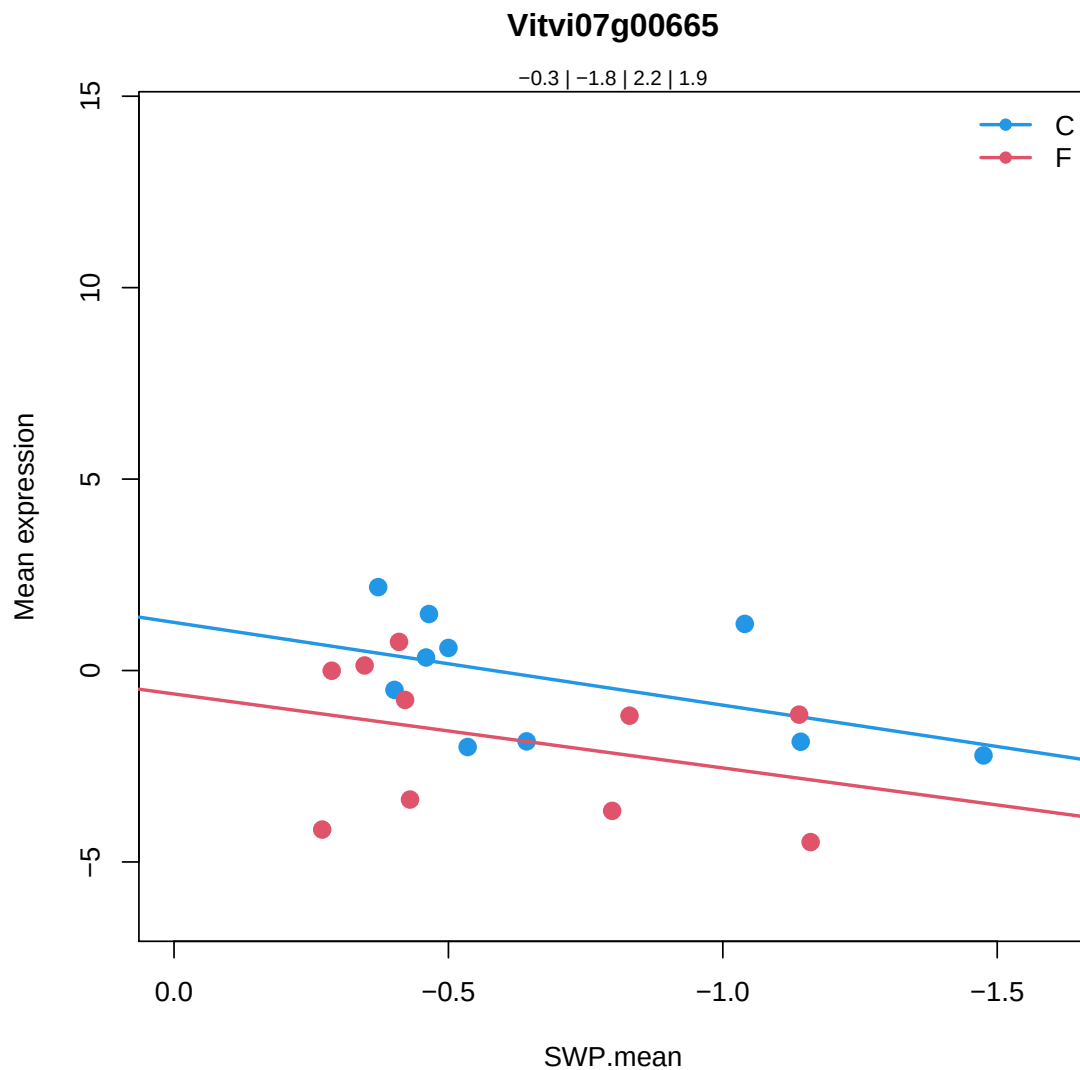
cellulose synthase A4 |

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	



8.4.16 Vitvi16g02137: Type5.0 *

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

Vitvi16g02137

35.2

not assigned.unknown

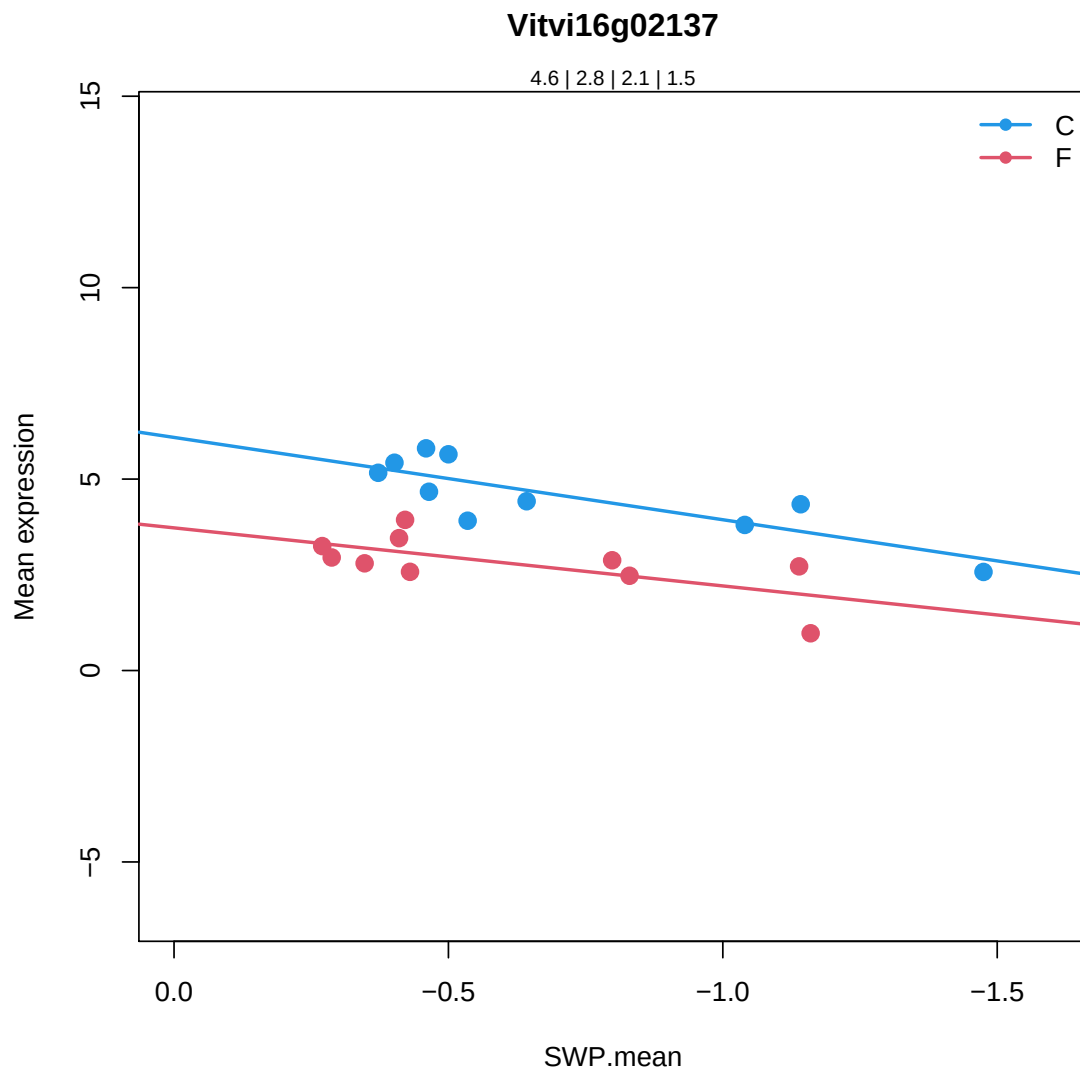
PR5-like receptor kinase |

Chr5:15293325-15295838 REVERSE LENGTH=665 |

201606

Coefficients for Vitvi16g02137.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.576307	2.446722e-17	***	5.954484e-17	***
SlopeC	2.149758	0.0003725907	***	0.09467692	.
MeanF-MeanC	-1.774357	8.117334e-07	***	2.701199e-05	***
SlopeF-SlopeC	-0.6336356	0.4129181		0.9999488	



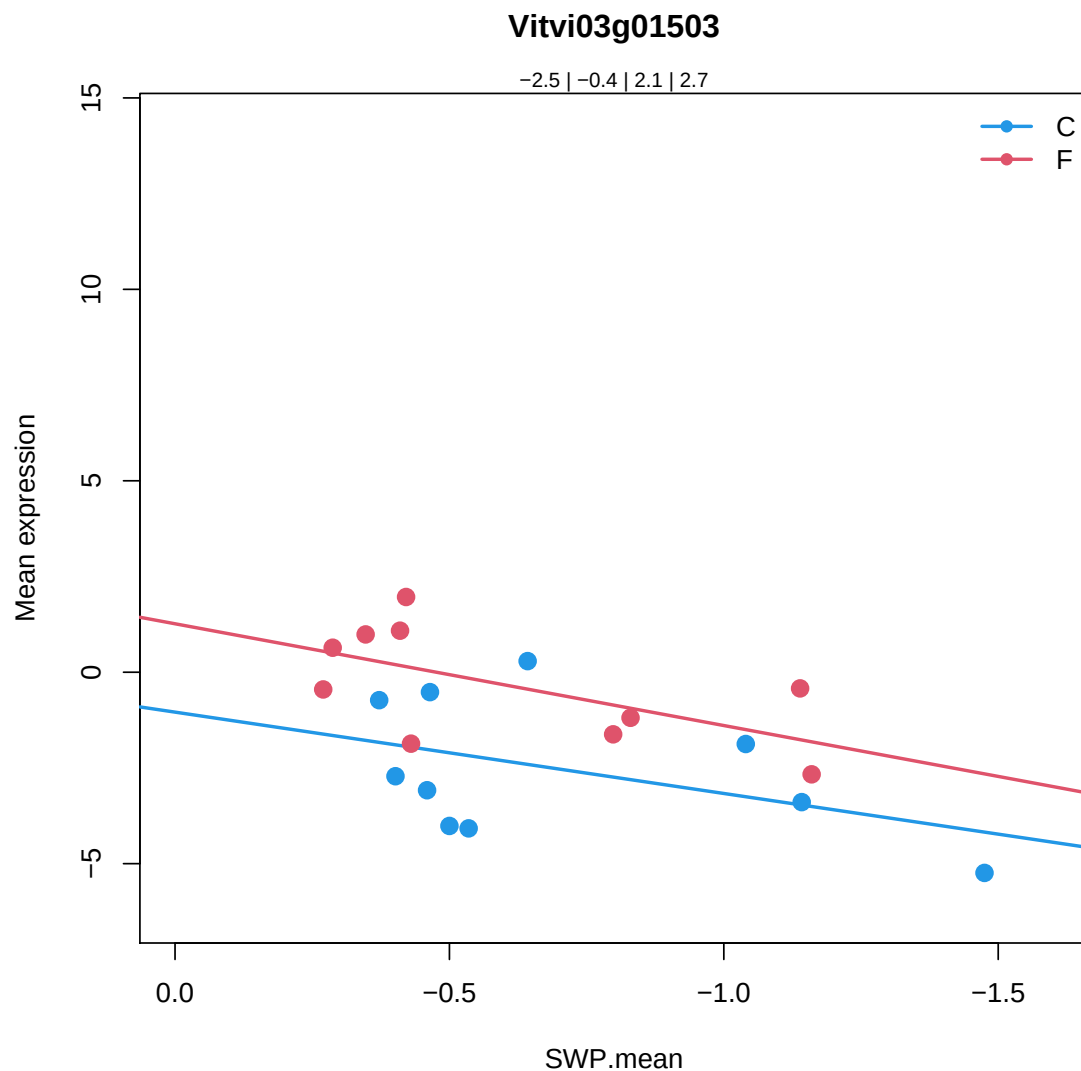
8.4.17 Vitvi03g01503: Type5.0

```
> 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	



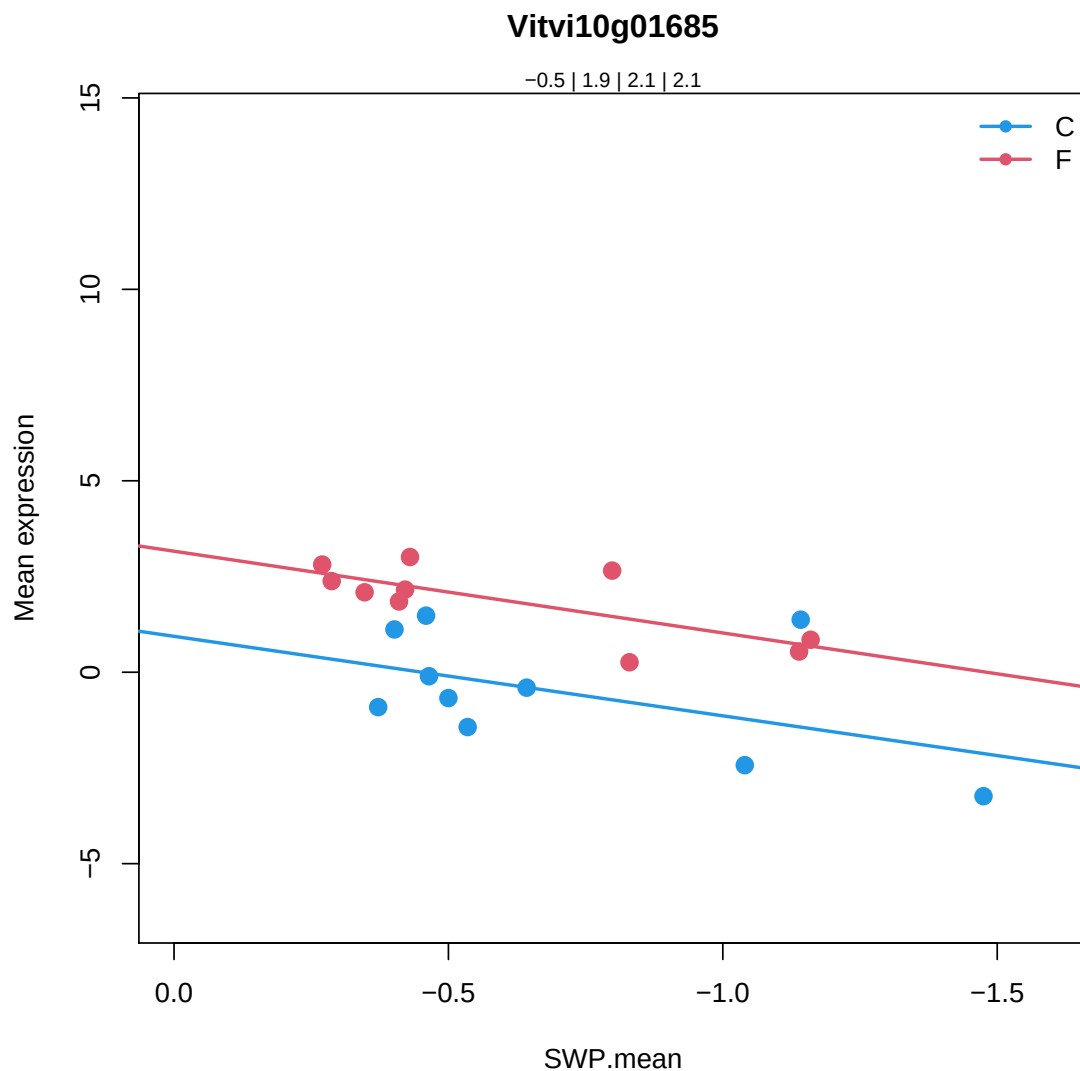
8.4.18 Vitvi10g01685: Type5.0 *

```
> 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	



8.4.19 Vitvi16g01251: Type5.0 *

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

Vitvi16g01251

35.2

not assigned.unknown

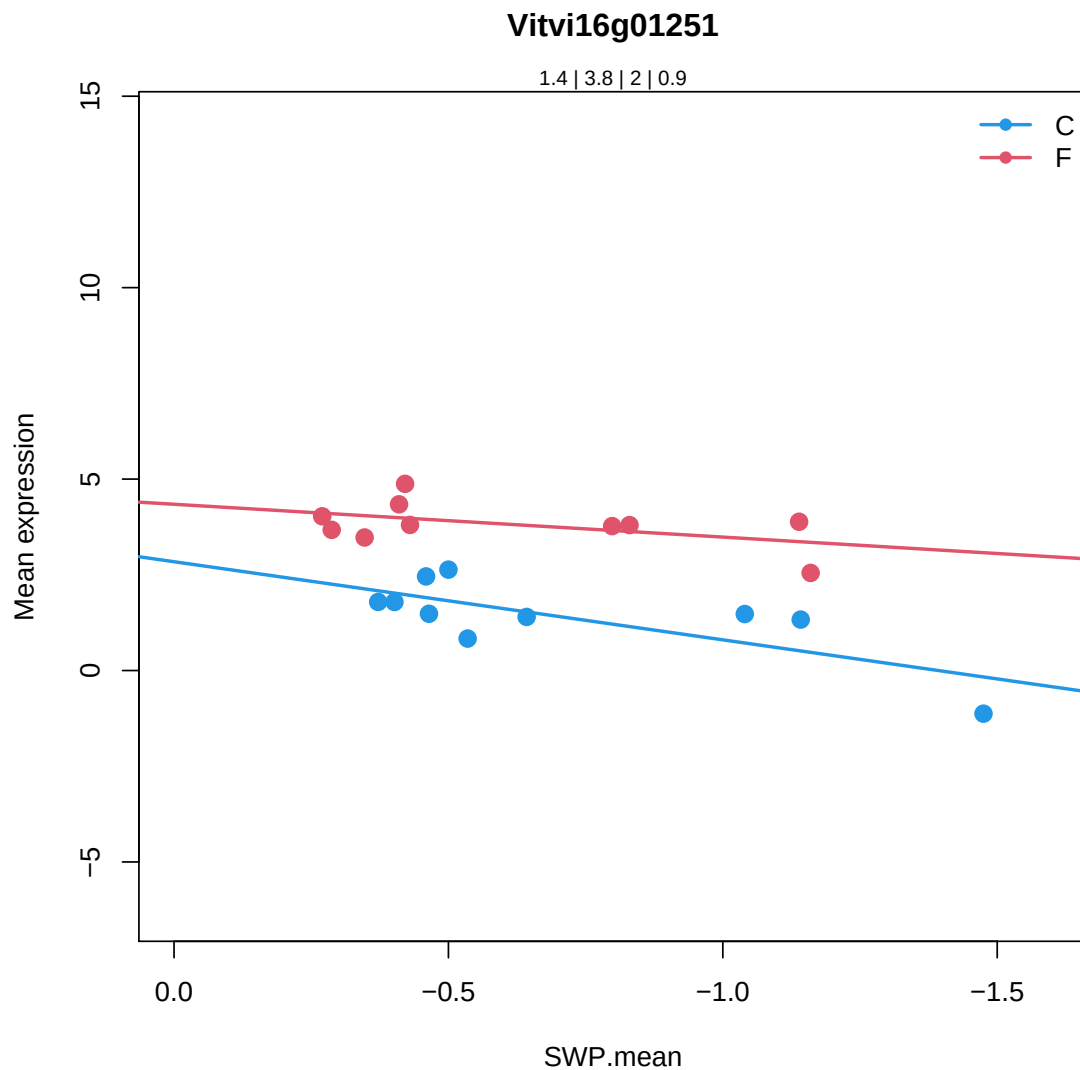
PR5-like receptor kinase |

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	



8.4.20 Vitvi11g00726: Type5.0

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

Vitvi11g00726

10.2.1

cell wall.cellulose synthesis.cellulose synthase

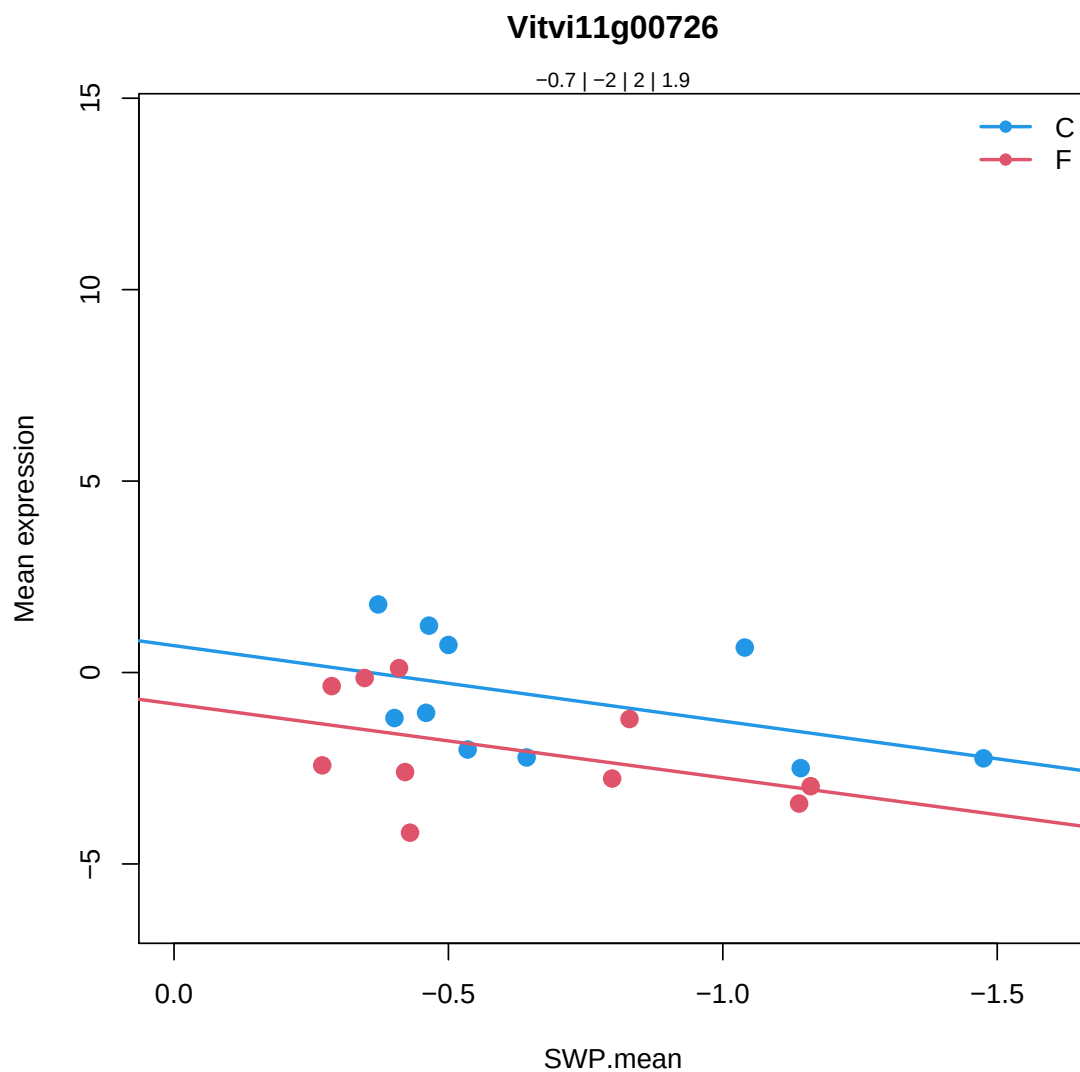
Cellulose synthase family protein |

Chr5:5736859-5741407 REVERSE LENGTH=1026 |

201606

Coefficients for Vitvi11g00726.

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



8.4.21 Vitvi14g02893: Type5.0

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

Vitvi14g02893

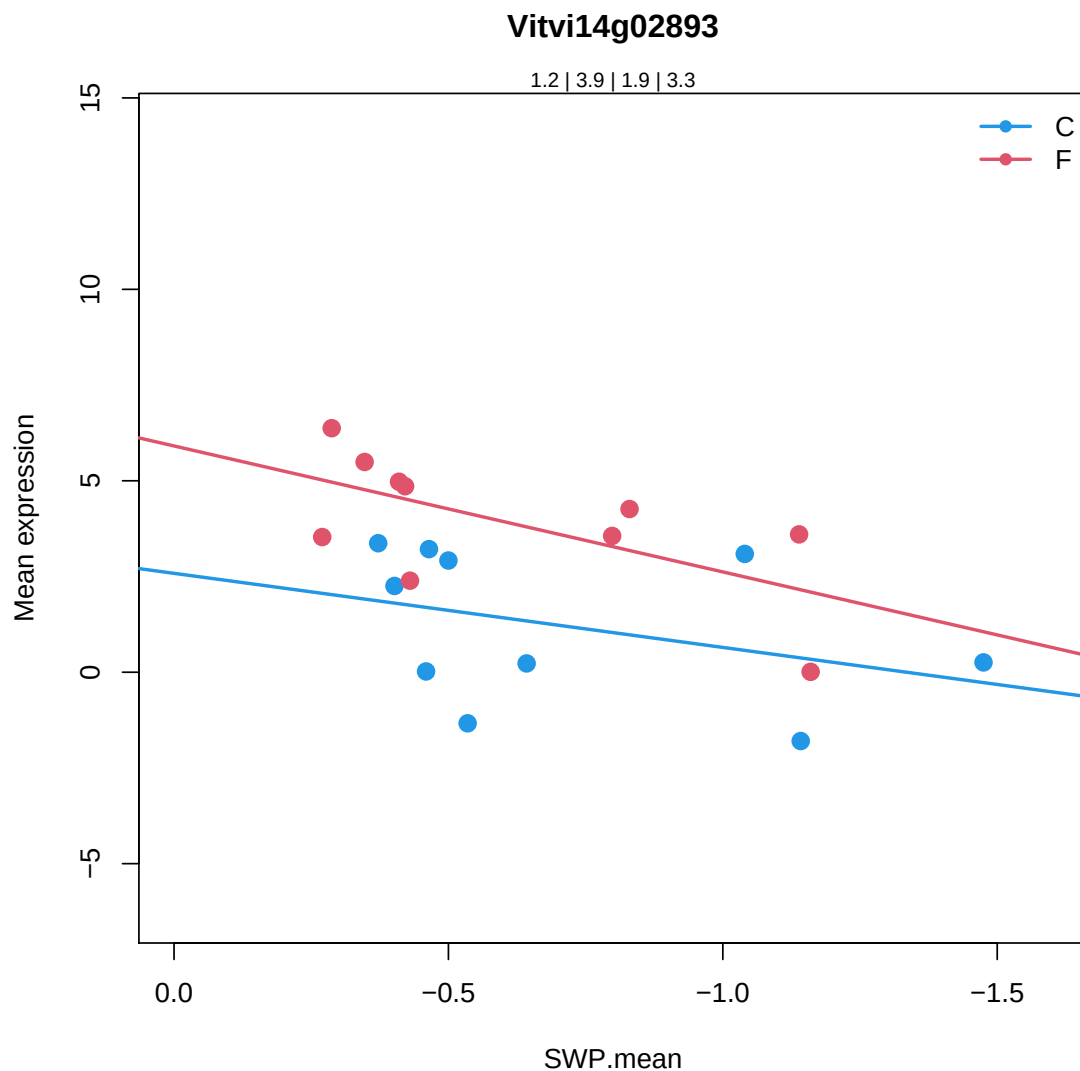
35.2

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	



8.4.22 Vitvi16g02004: Type5.0 *

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

Vitvi16g02004

35.2

not assigned.unknown

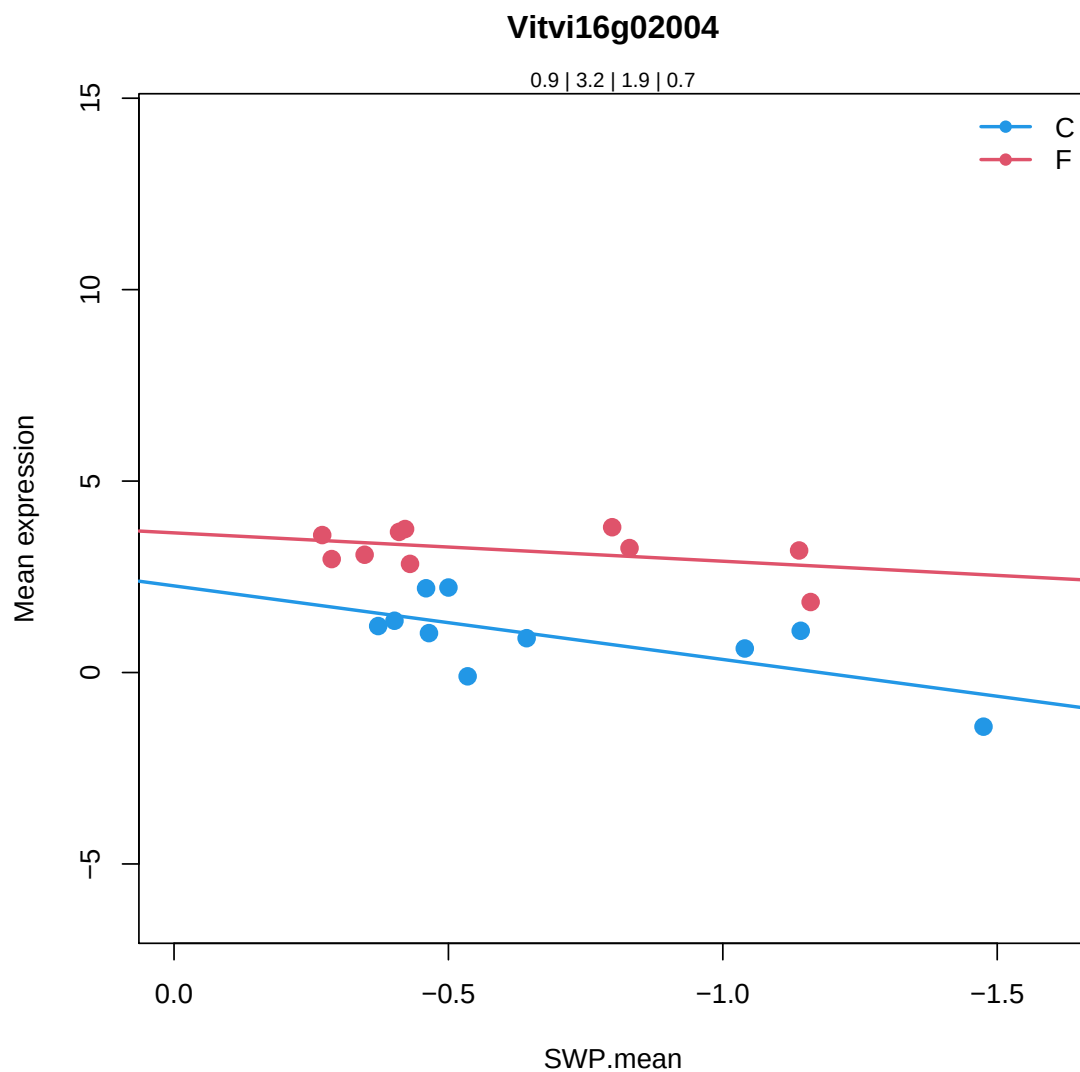
Protein kinase superfamily protein |

Chr1:24961634-24963941 REVERSE LENGTH=663 |

201606

Coefficients for Vitvi16g02004.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.9113851	0.0002464427	***	0.0002700417	***
SlopeC	1.921524	0.003150659	**	0.2103859	
MeanF-MeanC	2.284602	1.120093e-07	***	4.480959e-06	***
SlopeF-SlopeC	-1.180849	0.1839705		0.9999488	



8.4.23 Vitvi13g01997: Type5.0 *

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

Vitvi13g01997

26.8

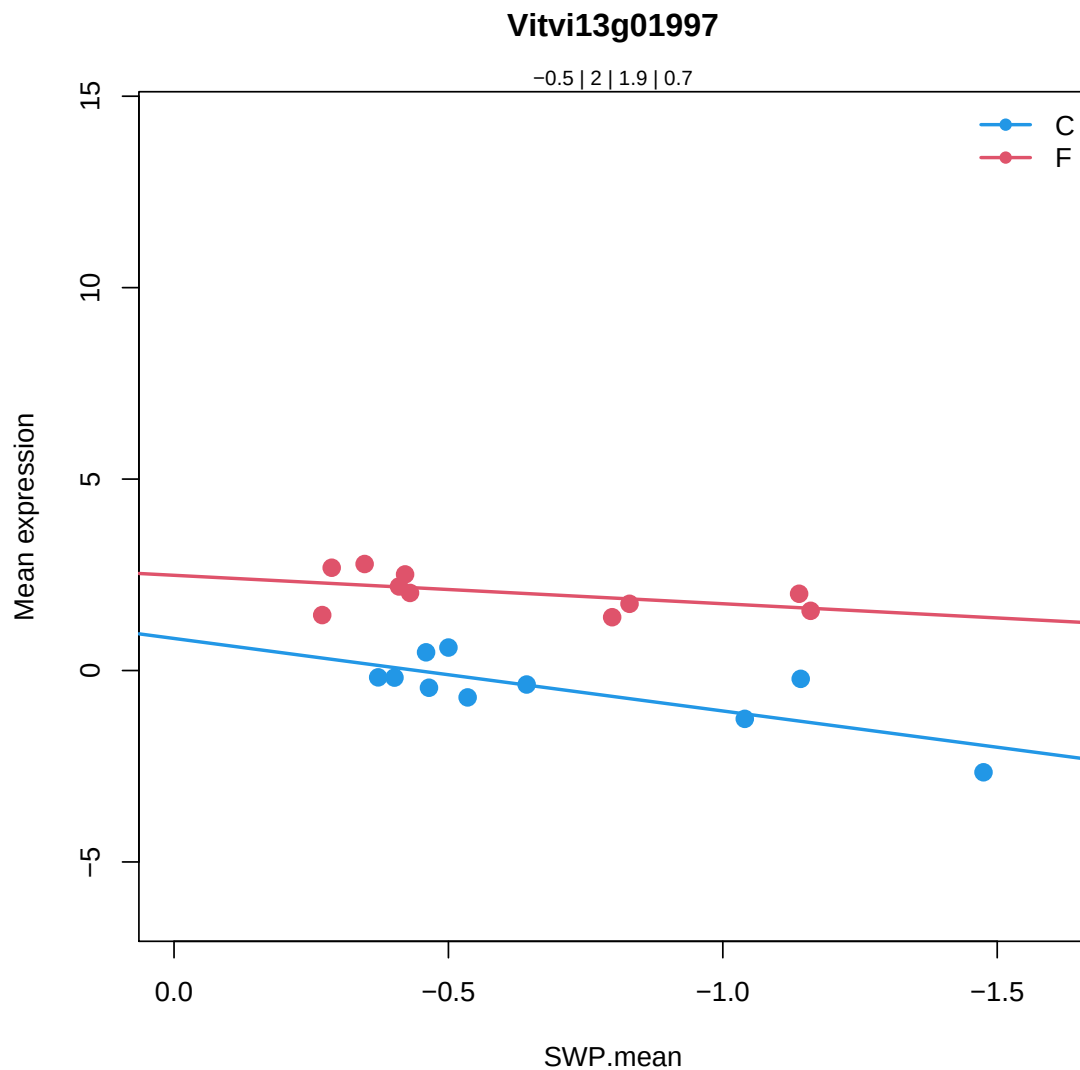
misc.nitrilases, nitrile lyases, berberine bridge enzymes, reticuline
NAD(P)-binding Rossmann-fold superfamily protein |

Chr2:12586509-12587684 FORWARD LENGTH=245 |

201606

Coefficients for Vitvi13g01997.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.4945913	0.007974908	**	0.008466501	**
SlopeC	1.894216	0.000588995	***	0.1005065	
MeanF-MeanC	2.528975	5.726677e-10	***	3.562694e-08	***
SlopeF-SlopeC	-1.151737	0.1145477		0.9999488	



8.4.24 Vitvi01g00784: Type5.0

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

Vitvi01g00784

10.7

cell wall.modification

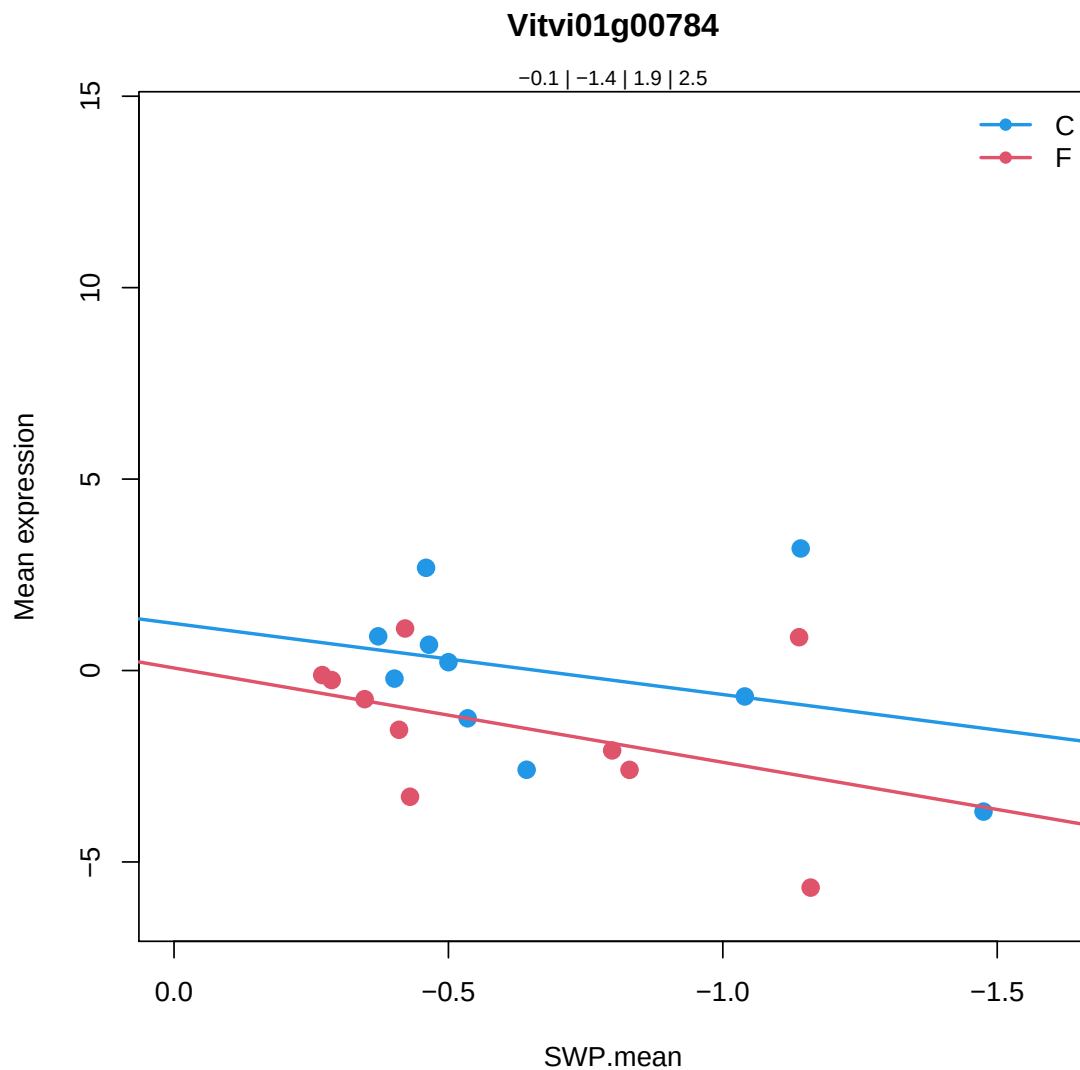
xyloglucan:xyloglucosyl transferase 33 |

Chr1:3479257-3480957 REVERSE LENGTH=310 |

201606

Coefficients for Vitvi01g00784.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.07603549	0.8952843		0.89764	
SlopeC	1.85592	0.2554205		0.7656086	
MeanF-MeanC	-1.358668	0.1069009		0.3801643	
SlopeF-SlopeC	0.6076206	0.7995979		0.9999488	



8.4.25 Vitvi18g01019: Type5.0

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

```
Vitvi18g01019
```

```
17.4.1
```

```
hormone metabolism.cytokinin.synthesis-degradation
```

```
cytokinin oxidase 5 |
```

```
Chr1:28315248-28318064 REVERSE LENGTH=540 |
```

```
201606
```

```
Vitvi18g01019
```

```
35.2
```

```
not assigned.unknown
```

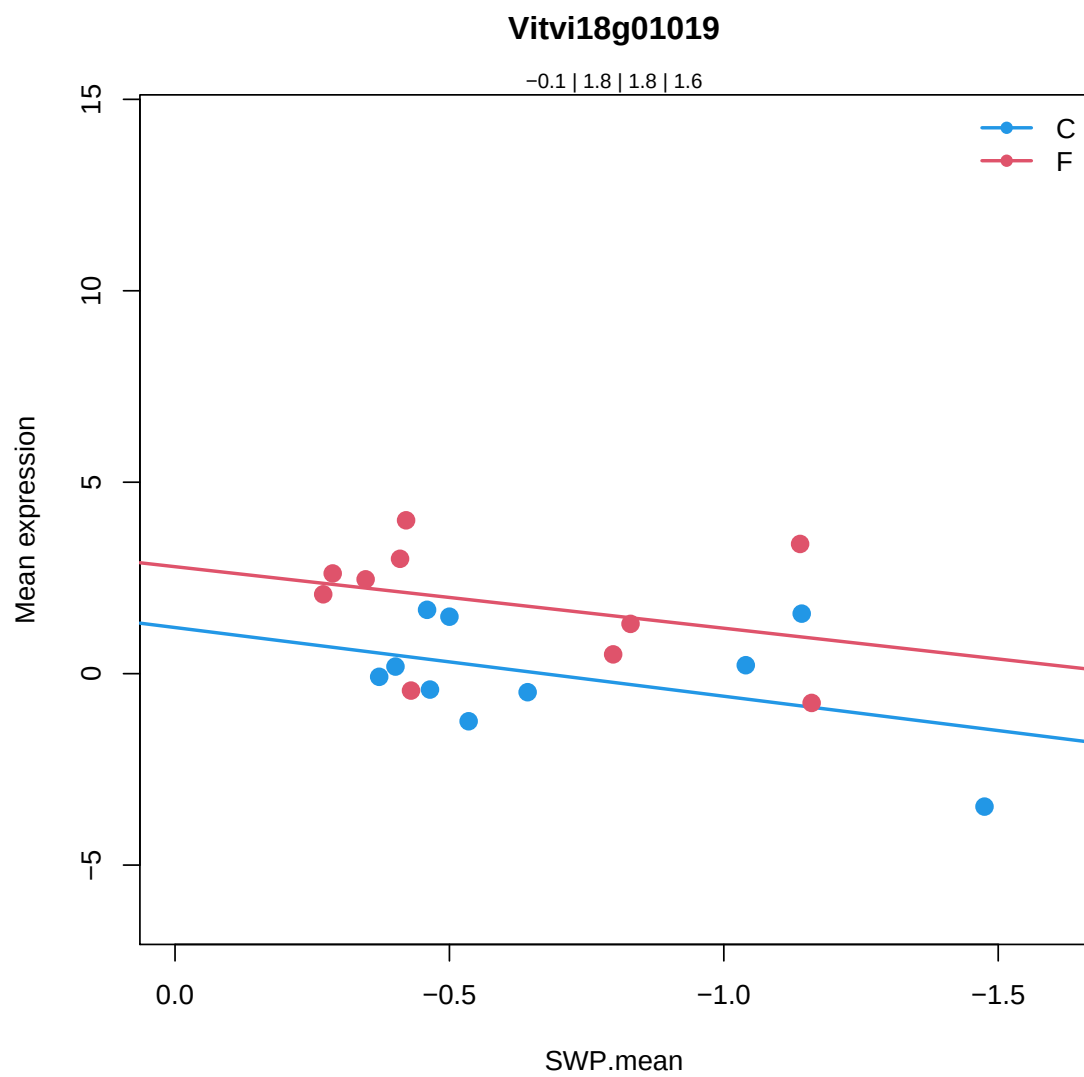
```
cytokinin oxidase 5 |
```

```
Chr1:28315248-28318064 REVERSE LENGTH=540 |
```

```
201606
```

Coefficients for Vitvi18g01019.

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



8.4.26 Vitvi04g00644: Type5.0 *

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

Vitvi04g00644

27.3.99

RNA.regulation of transcription.unclassified

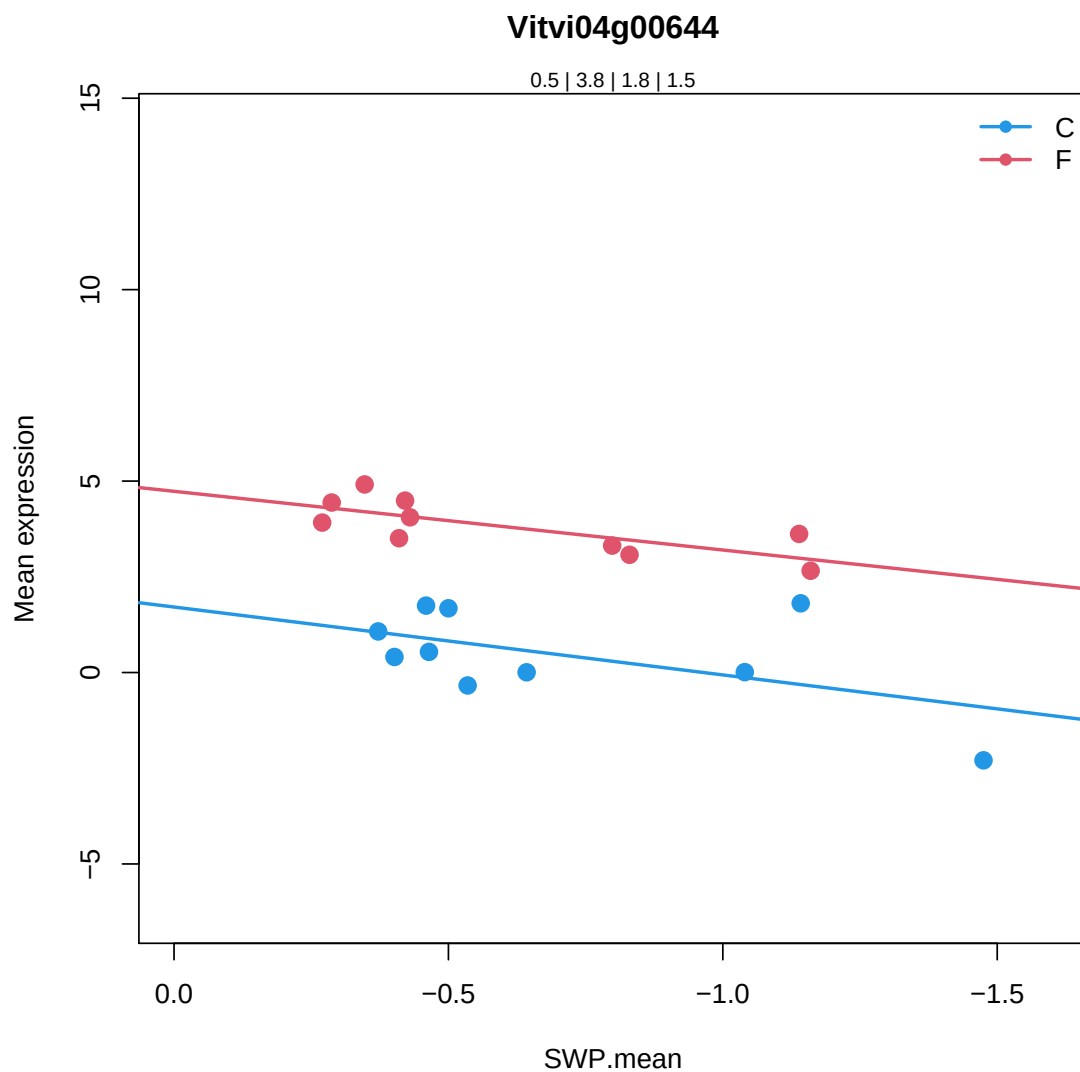
Eukaryotic aspartyl protease family protein |

Chr5:3403331-3405331 REVERSE LENGTH=474 |

201606

Coefficients for Vitvi04g00644.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4634607	0.07445566	.	0.07723768	.
SlopeC	1.773287	0.01733481	*	0.3551322	
MeanF-MeanC	3.335309	3.590415e-09	***	1.887073e-07	***
SlopeF-SlopeC	-0.240009	0.8168131		0.9999488	



8.4.27 Vitvi16g01994: Type5.0 *

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

Vitvi16g01994

35.2

not assigned.unknown

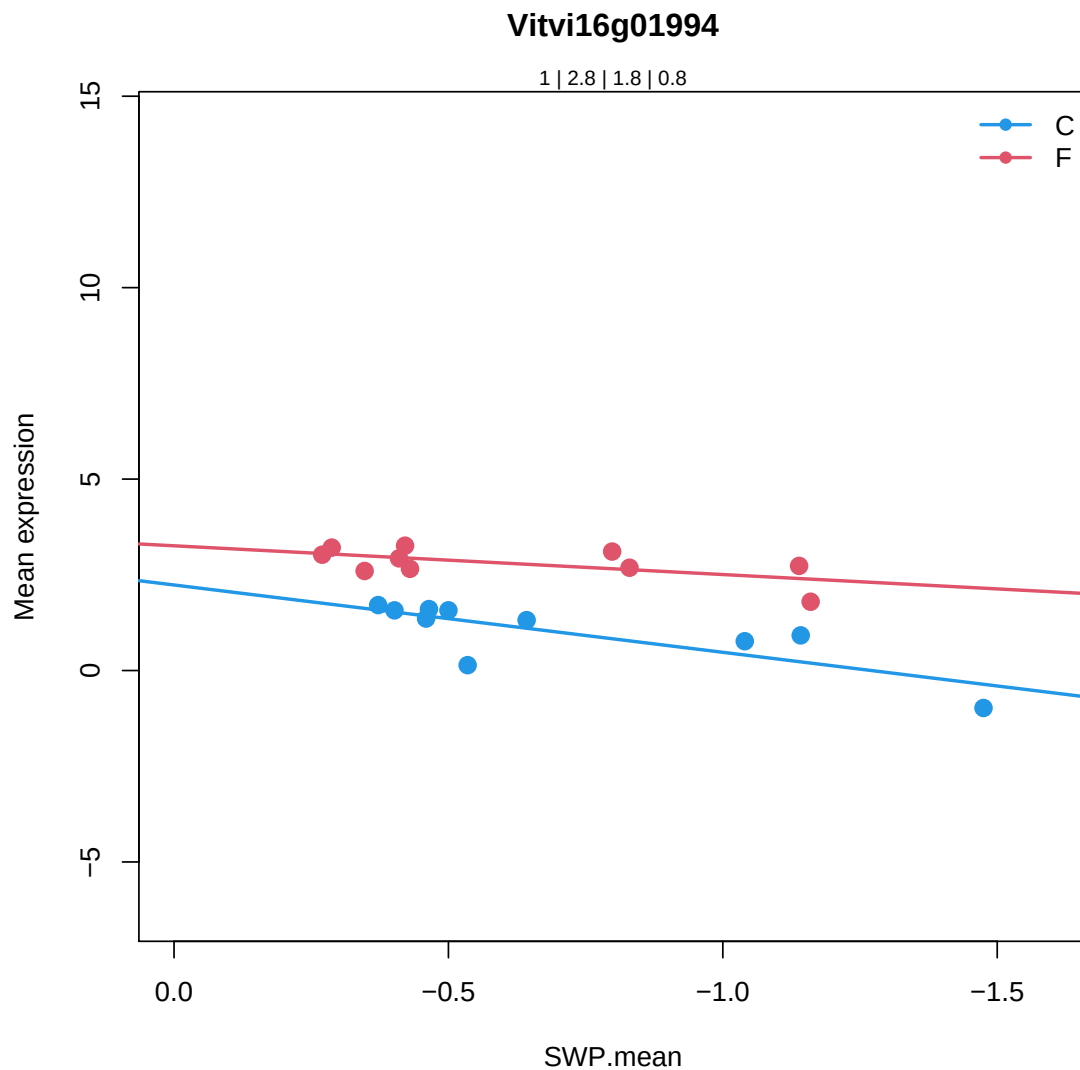
Protein kinase superfamily protein |

Chr1:24961634-24963941 REVERSE LENGTH=666 |

201606

Coefficients for Vitvi16g01994.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.9974805	1.216897e-06	***	1.401855e-06	***
SlopeC	1.758243	0.0003683803	***	0.09467692	.
MeanF-MeanC	1.802633	2.536484e-08	***	1.175109e-06	***
SlopeF-SlopeC	-1.007525	0.1187312		0.9999488	



8.4.28 Vitvi16g01118: Type5.0 *

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

Vitvi16g01118

31.1

cell.organisation

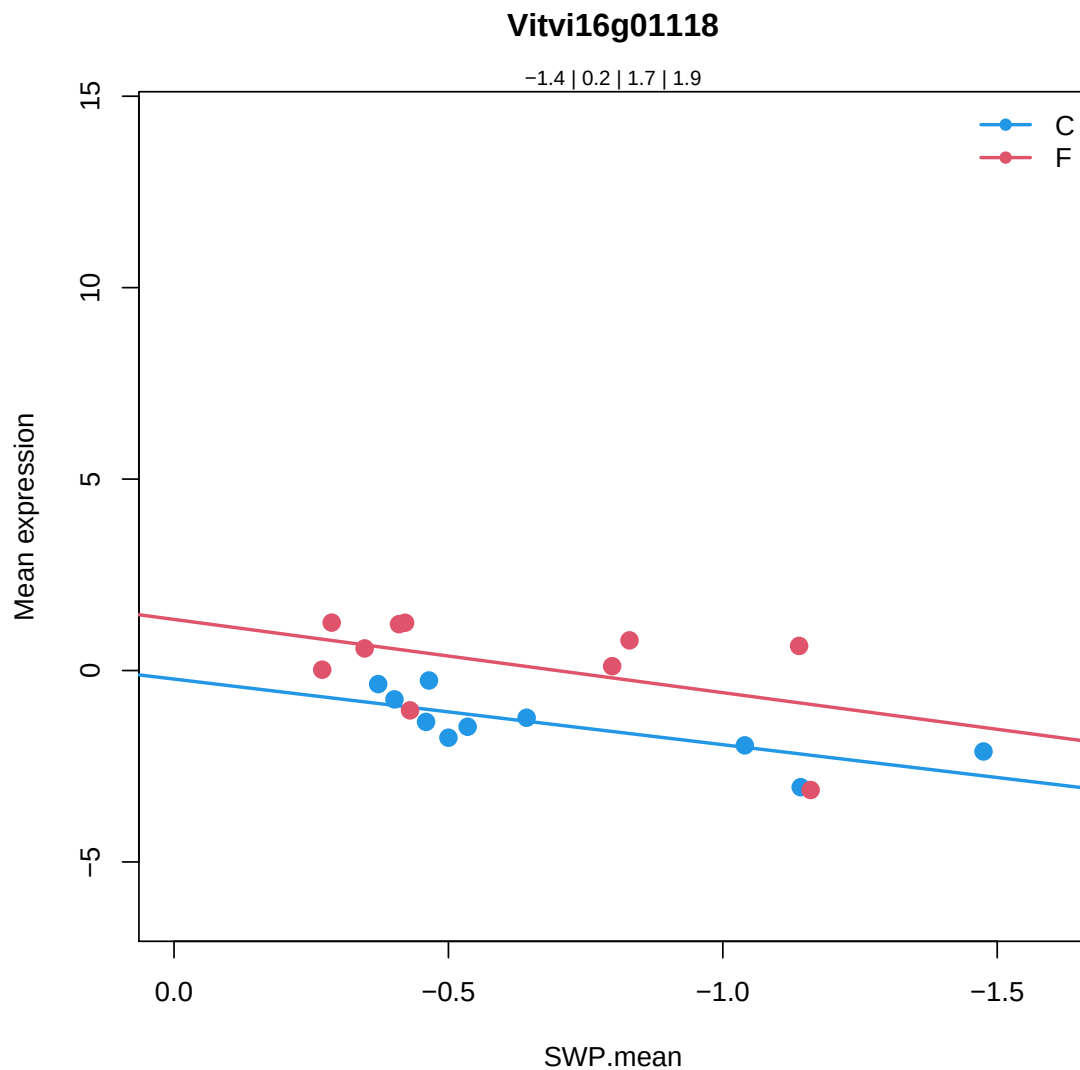
cysteine-rich RECEPTOR-like kinase |

Chr4:12129485-12133157 FORWARD LENGTH=1043 |

201606

Coefficients for Vitvi16g01118.

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



8.4.29 Vitvi16g02033: Type5.0 *

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

Vitvi16g02033

35.2

not assigned.unknown

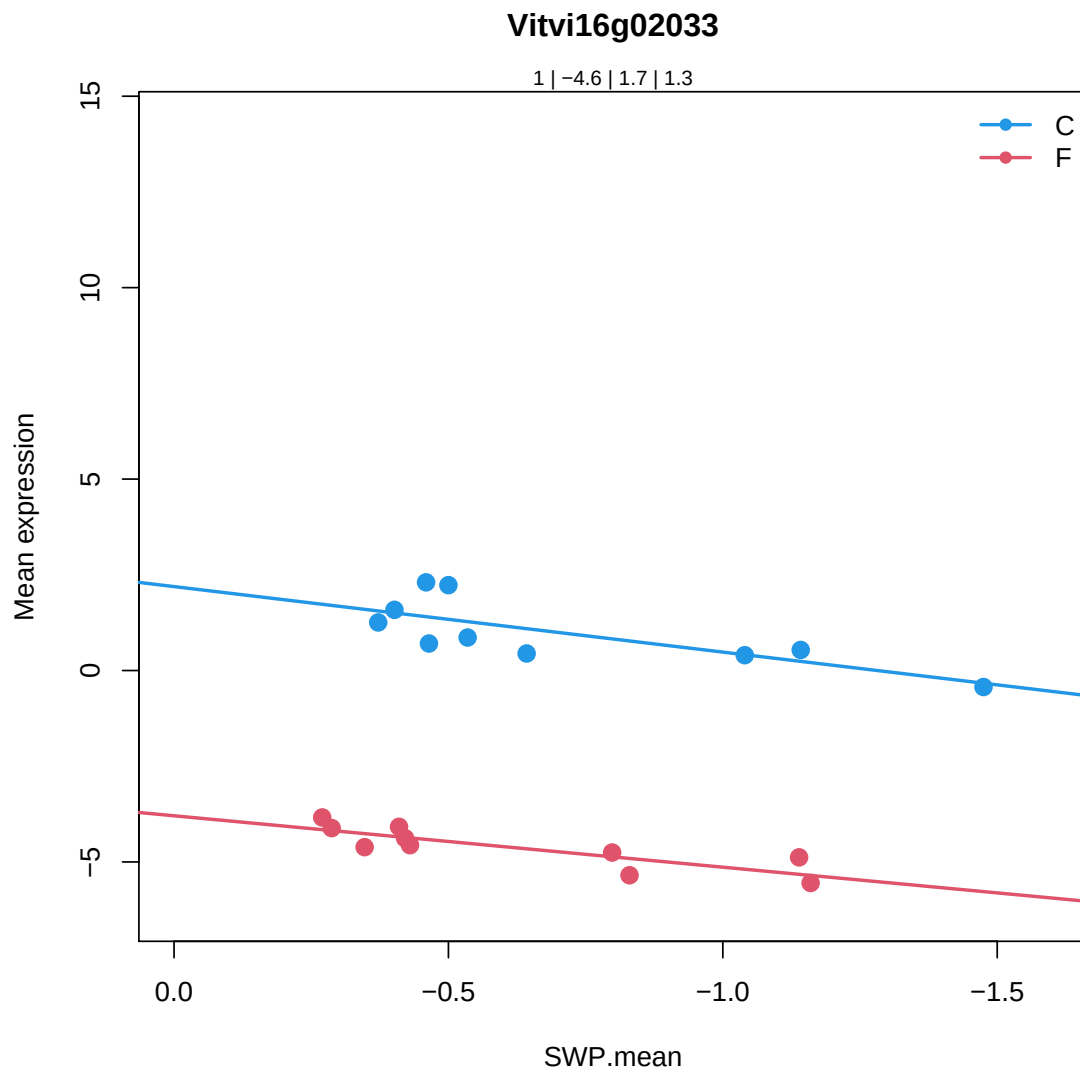
PR5-like receptor kinase |

Chr5:15293325-15295838 REVERSE LENGTH=665 |

201606

Coefficients for Vitvi16g02033.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.9889555	1.720114e-06	***	1.975137e-06	***
SlopeC	1.710997	0.0005617774	***	0.1005065	
MeanF-MeanC	-5.601053	1.00955e-17	***	2.167263e-15	***
SlopeF-SlopeC	-0.3682916	0.564525		0.9999488	



8.4.30 Vitvi13g01760: Type5.0

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

Vitvi13g01760

35.2

not assigned.unknown

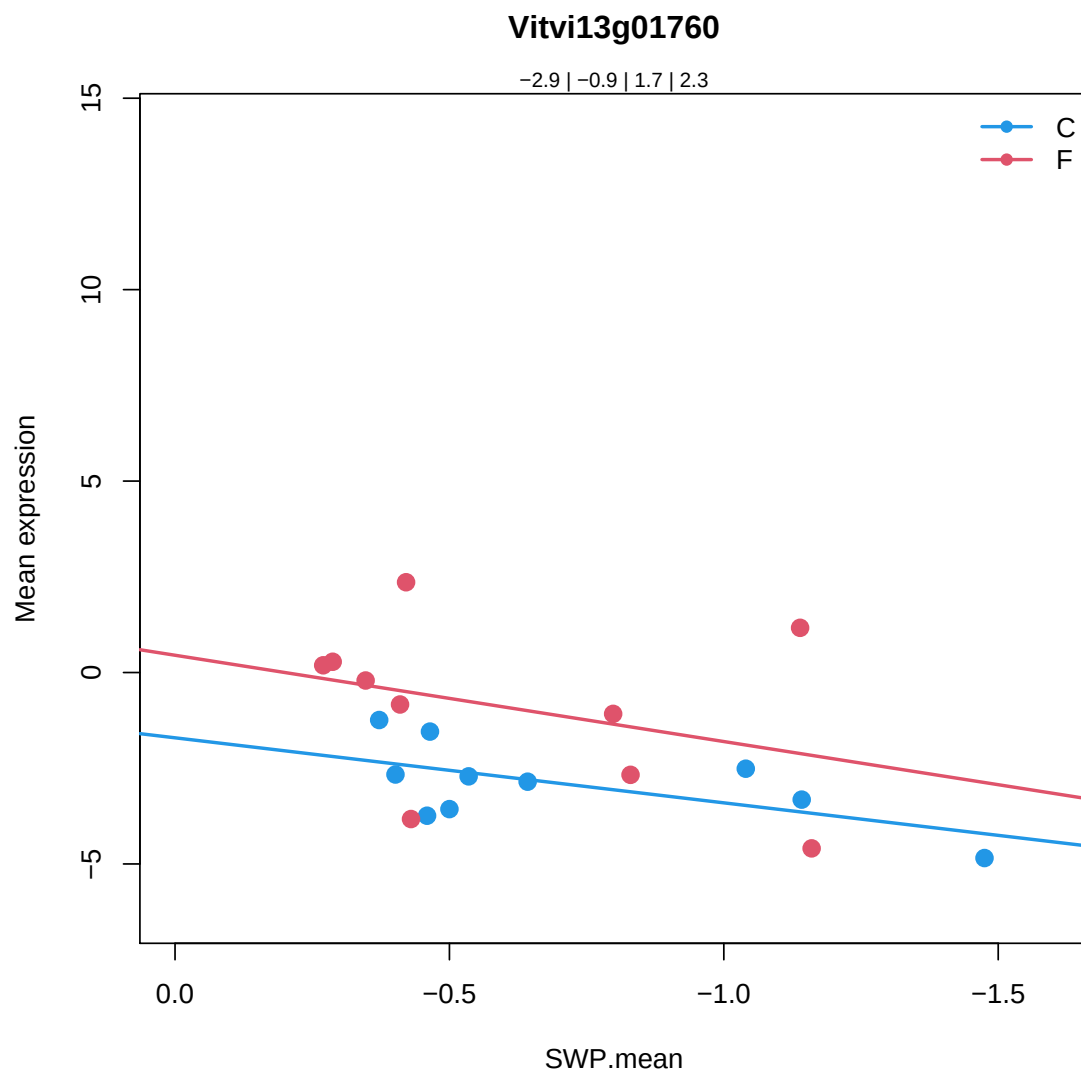
Leucine-rich repeat (LRR) family protein |

Chr3:7280930-7282027 FORWARD LENGTH=365 |

201606

Coefficients for Vitvi13g01760.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-2.899762	2.749233e-06	***	3.140979e-06	***
SlopeC	1.698164	0.1988836		0.7265417	
MeanF-MeanC	1.977597	0.00616659	**	0.05307237	.
SlopeF-SlopeC	0.5558194	0.7734422		0.9999488	

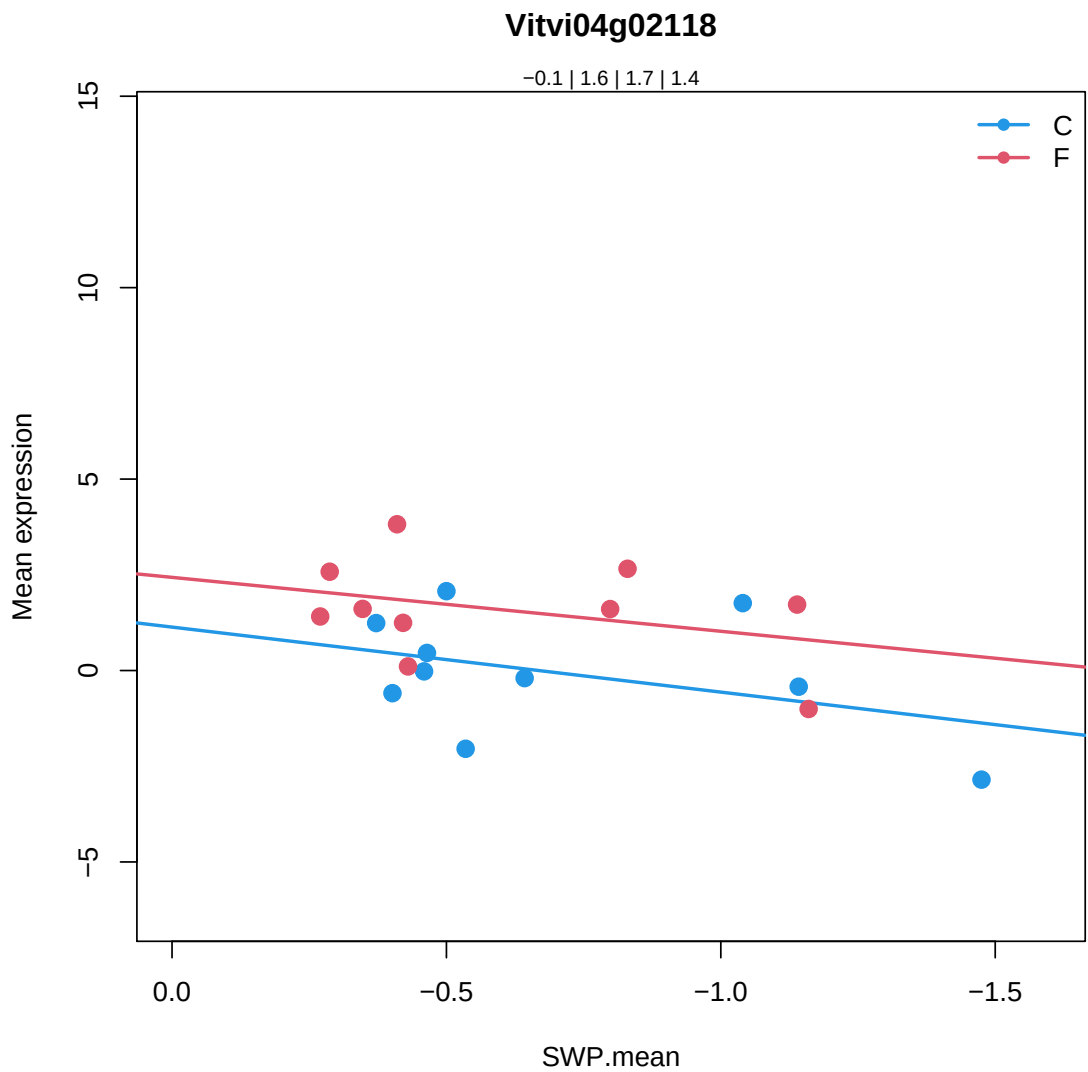


8.4.31 Vitvi04g02118: Type5.0

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
Vitvi04g02118
17.8.1.1.7
hormone metabolism.salicylic acid.synthesis-degradation.synthesis.meth
S-adenosyl-L-methionine-dependent methyltransferases superfamily prote
Chr3:3614544-3617137 FORWARD LENGTH=379 |
201606
```

Coefficients for Vitvi04g02118.

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



8.4.32 Vitvi16g02116: Type5.0 *

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

Vitvi16g02116

35.2

not assigned.unknown

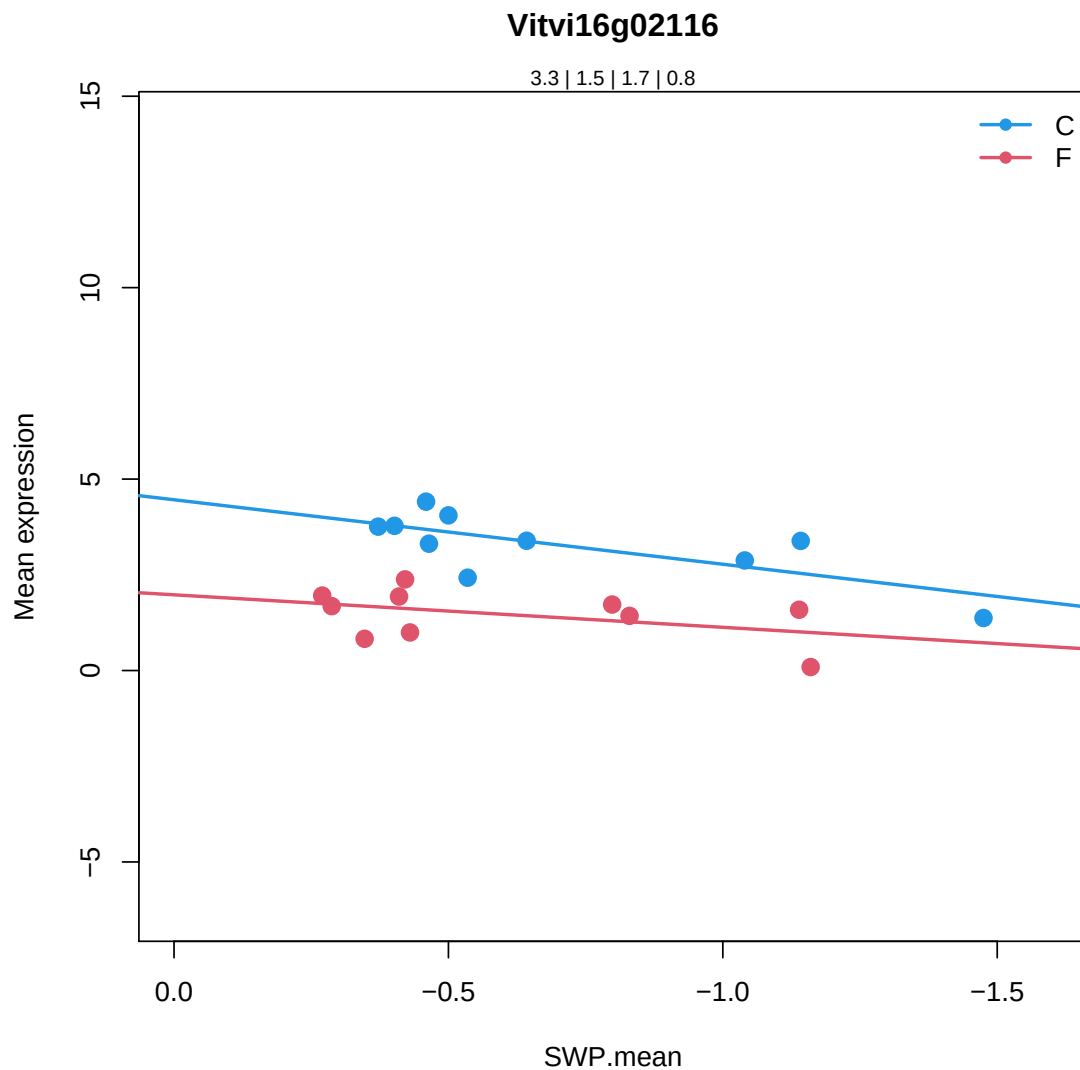
RING/U-box superfamily protein |

Chr5:21529022-21533008 FORWARD LENGTH=382 |

201606

Coefficients for Vitvi16g02116.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.275639	4.757624e-14	***	7.494389e-14	***
SlopeC	1.684163	0.004358604	**	0.2399107	
MeanF-MeanC	-1.815409	9.866378e-07	***	3.23405e-05	***
SlopeF-SlopeC	-0.8352023	0.3001471		0.9999488	



8.4.33 Vitvi09g00112: Type5.0

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

Vitvi09g00112

27.3.25

RNA.regulation of transcription.MYB domain transcription factor family

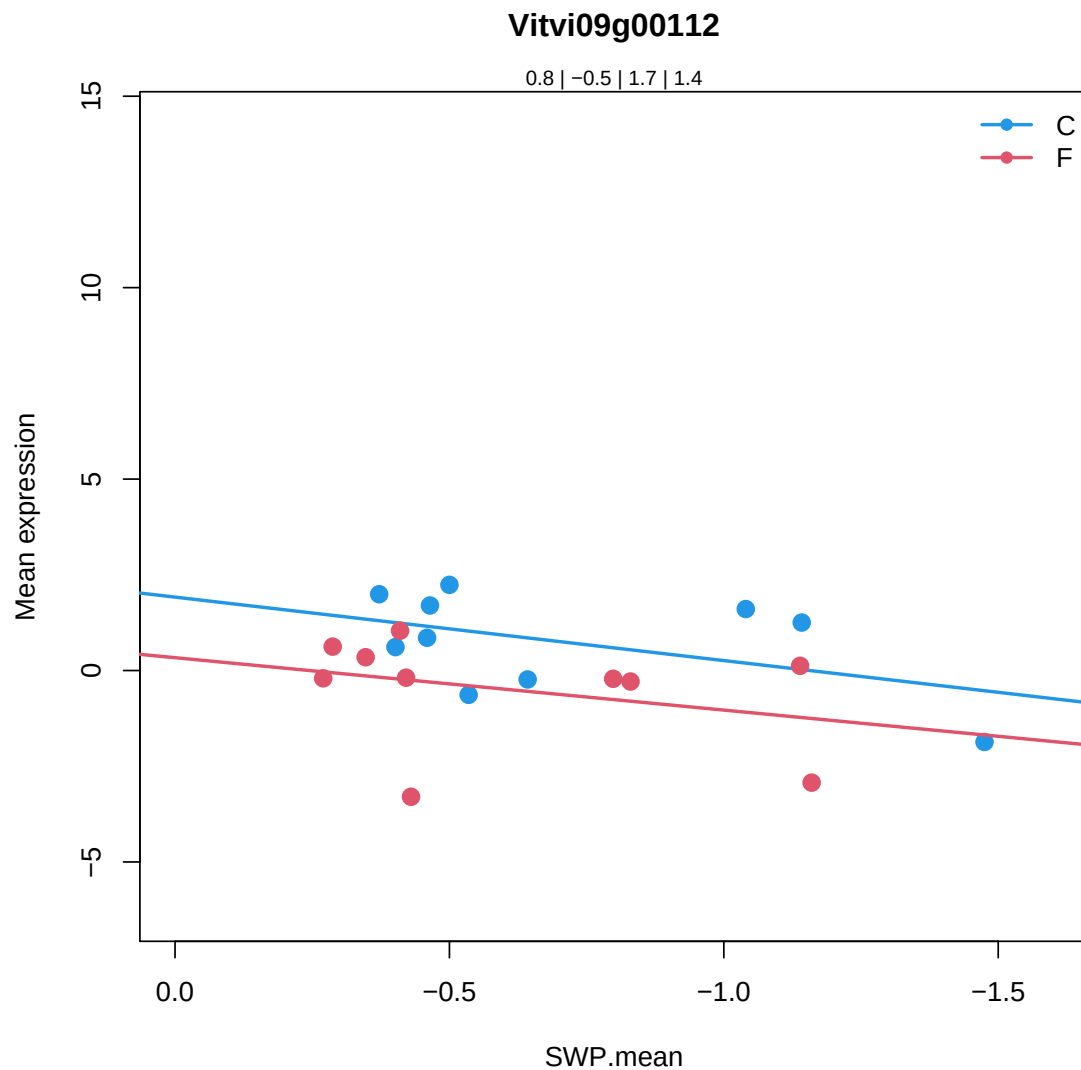
myb domain protein 7 |

Chr2:7255669-7256550 REVERSE LENGTH=269 |

201606

Coefficients for Vitvi09g00112.

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



8.4.34 Vitvi10g00650: Type5.0 *

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

Vitvi10g00650

30.2.8.2

signalling.receptor kinases.leucine rich repeat VIII.type 2

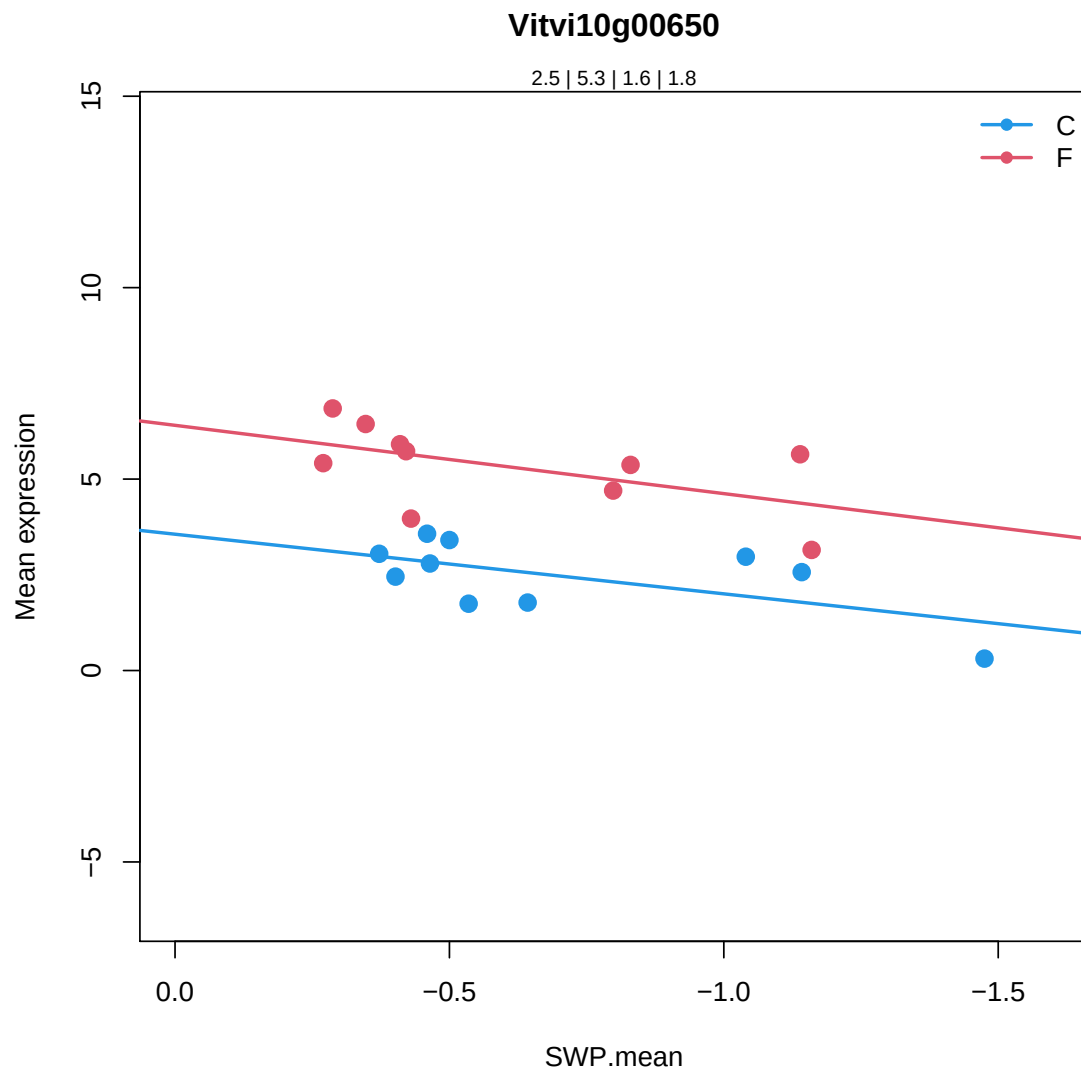
Leucine-rich repeat transmembrane protein kinase |

Chr1:2359817-2363859 REVERSE LENGTH=801 |

201606

Coefficients for Vitvi10g00650.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.464913	3.775848e-09	***	4.66987e-09	***
SlopeC	1.557723	0.04212555	*	0.4812642	
MeanF-MeanC	2.852172	1.1026e-07	***	4.434256e-06	***
SlopeF-SlopeC	0.2259447	0.835169		0.9999488	



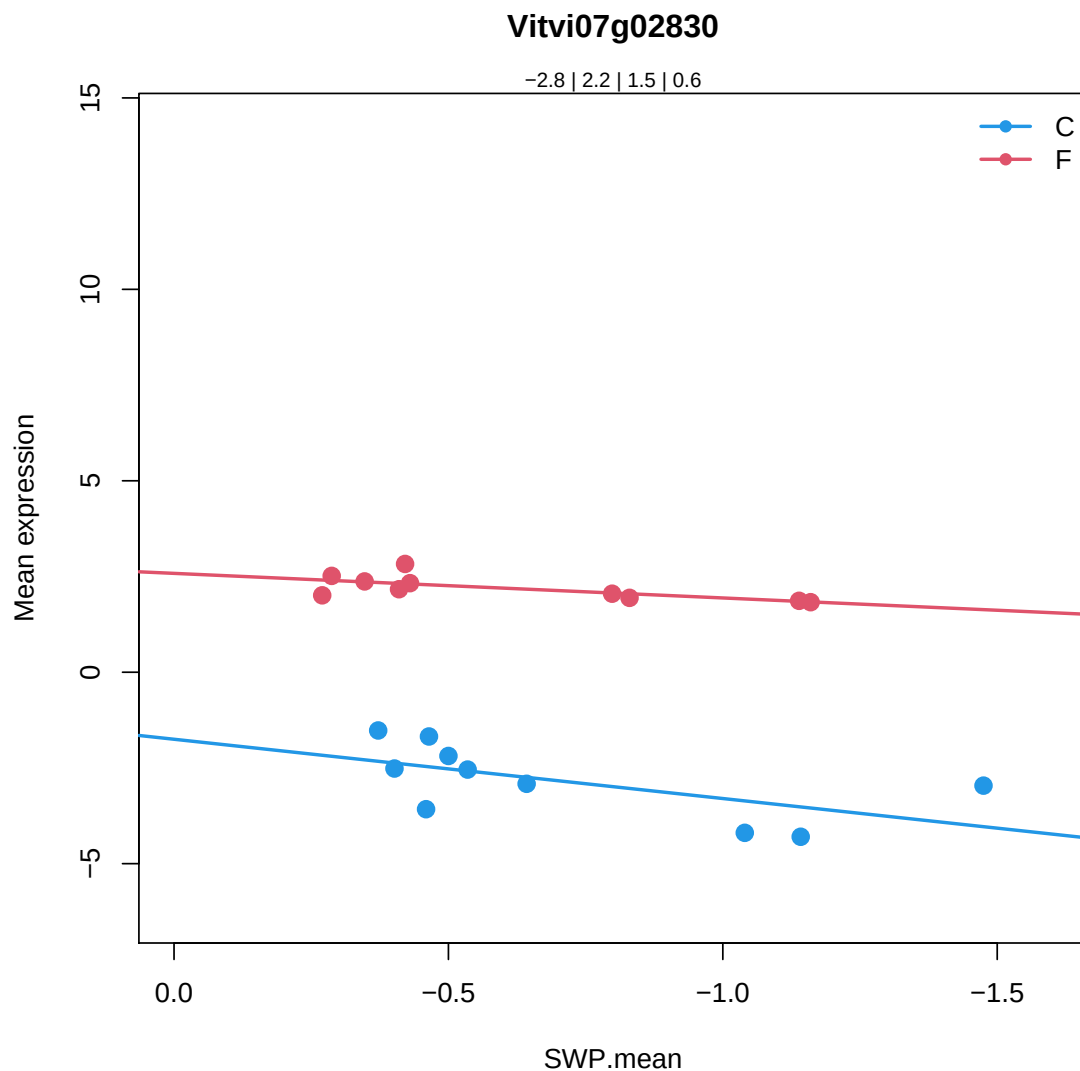
8.4.35 Vitvi07g02830: Type5.0 *

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

```
Vitvi07g02830
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi07g02830.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-2.839209	2.699108e-13	***	4.025816e-13	***
SlopeC	1.548037	0.005361432	**	0.2577627	
MeanF-MeanC	5.029586	2.906795e-15	***	3.955836e-13	***
SlopeF-SlopeC	-0.9060718	0.2363952		0.9999488	



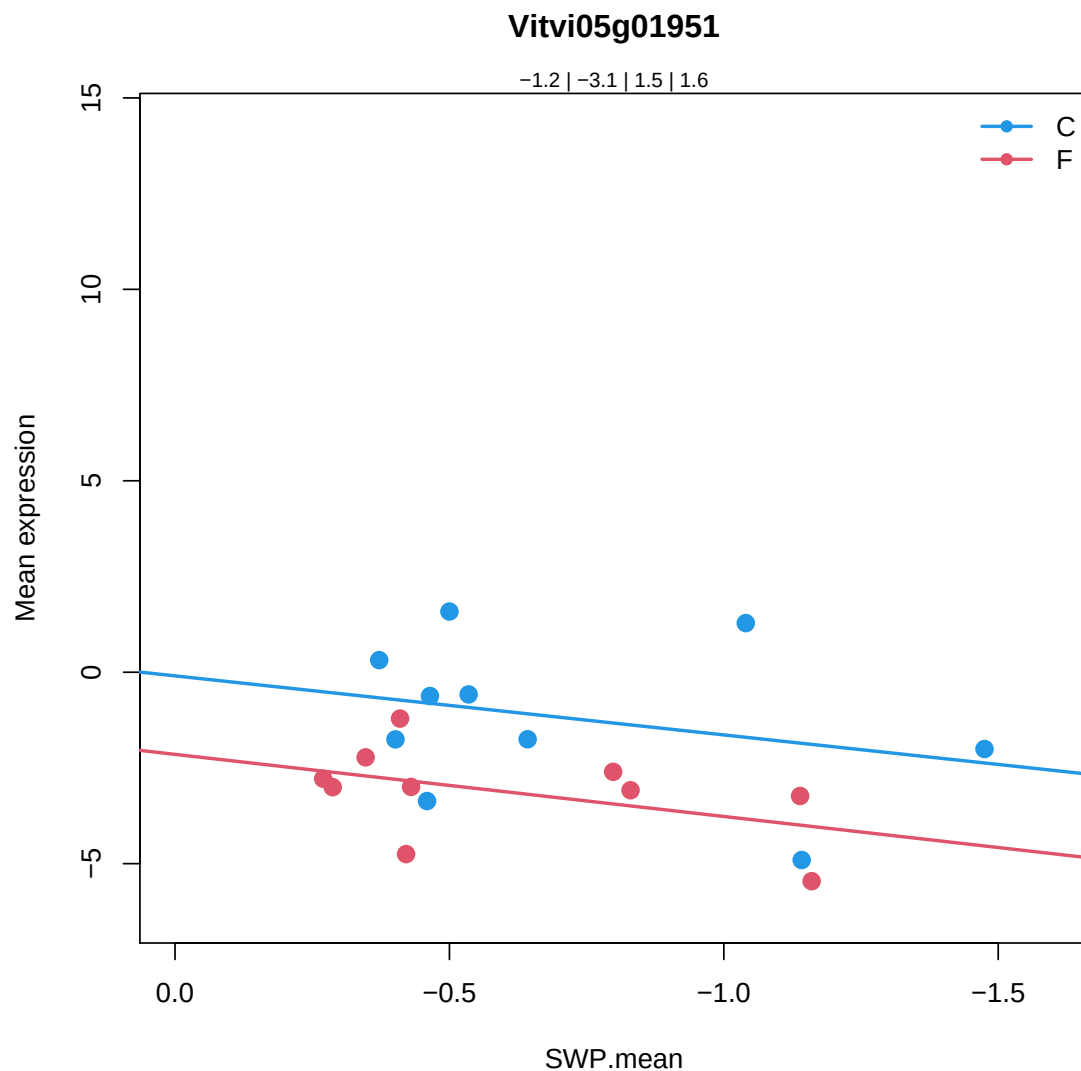
8.4.36 Vitvi05g01951: Type5.0

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

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

Coefficients for Vitvi05g01951.

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



8.4.37 Vitvi12g00036: Type5.0

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

Vitvi12g00036

11.3

lipid metabolism.phospholipid synthesis

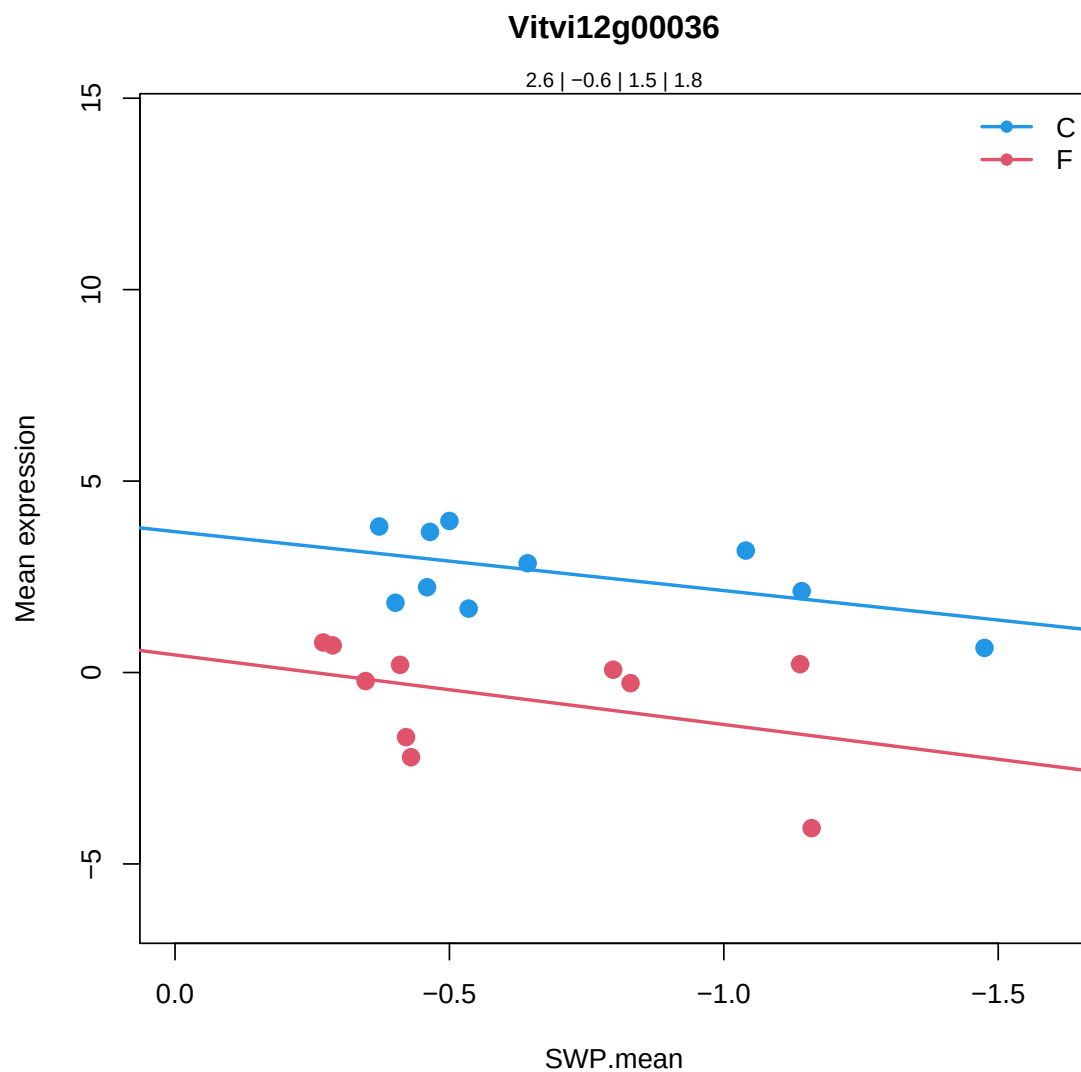
glycerol-3-phosphate acyltransferase 1 |

Chr1:1994170-1996067 REVERSE LENGTH=585 |

201606

Coefficients for Vitvi12g00036.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.596959	2.662307e-07	***	3.119533e-07	***
SlopeC	1.53938	0.1313064		0.6540431	
MeanF-MeanC	-3.245096	1.721806e-06	***	5.291083e-05	***
SlopeF-SlopeC	0.2776615	0.8509929		0.9999488	



8.4.38 Vitvi12g02245: Type5.0

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

Vitvi12g02245

26.6

misc.O-methyl transferases

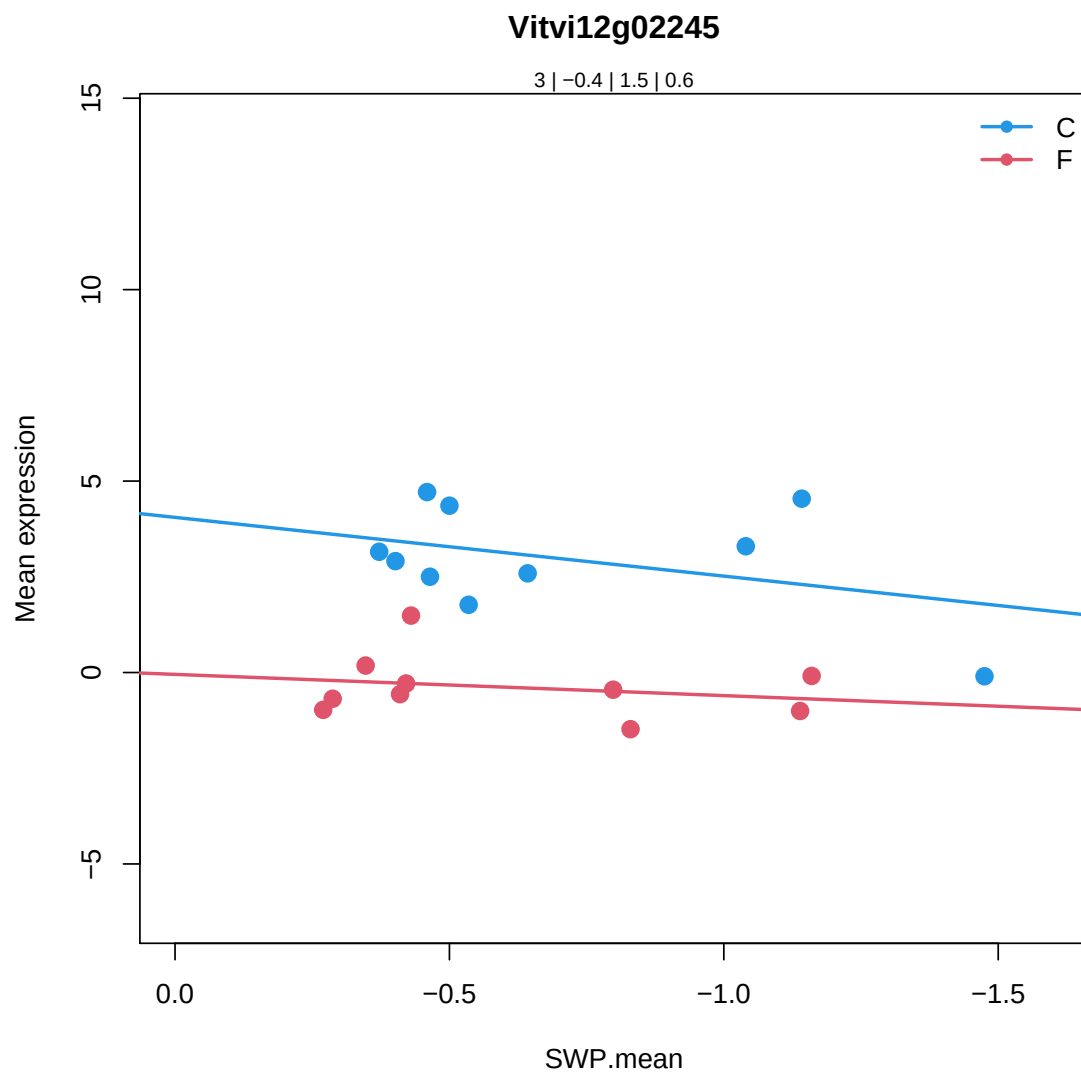
O-methyltransferase family protein |

Chr4:16730989-16732808 REVERSE LENGTH=382 |

201606

Coefficients for Vitvi12g02245.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.973277	7.660899e-09	***	9.382677e-09	***
SlopeC	1.534084	0.1047146		0.6180159	
MeanF-MeanC	-3.359933	3.051465e-07	***	1.12344e-05	***
SlopeF-SlopeC	-0.9798485	0.4750741		0.9999488	



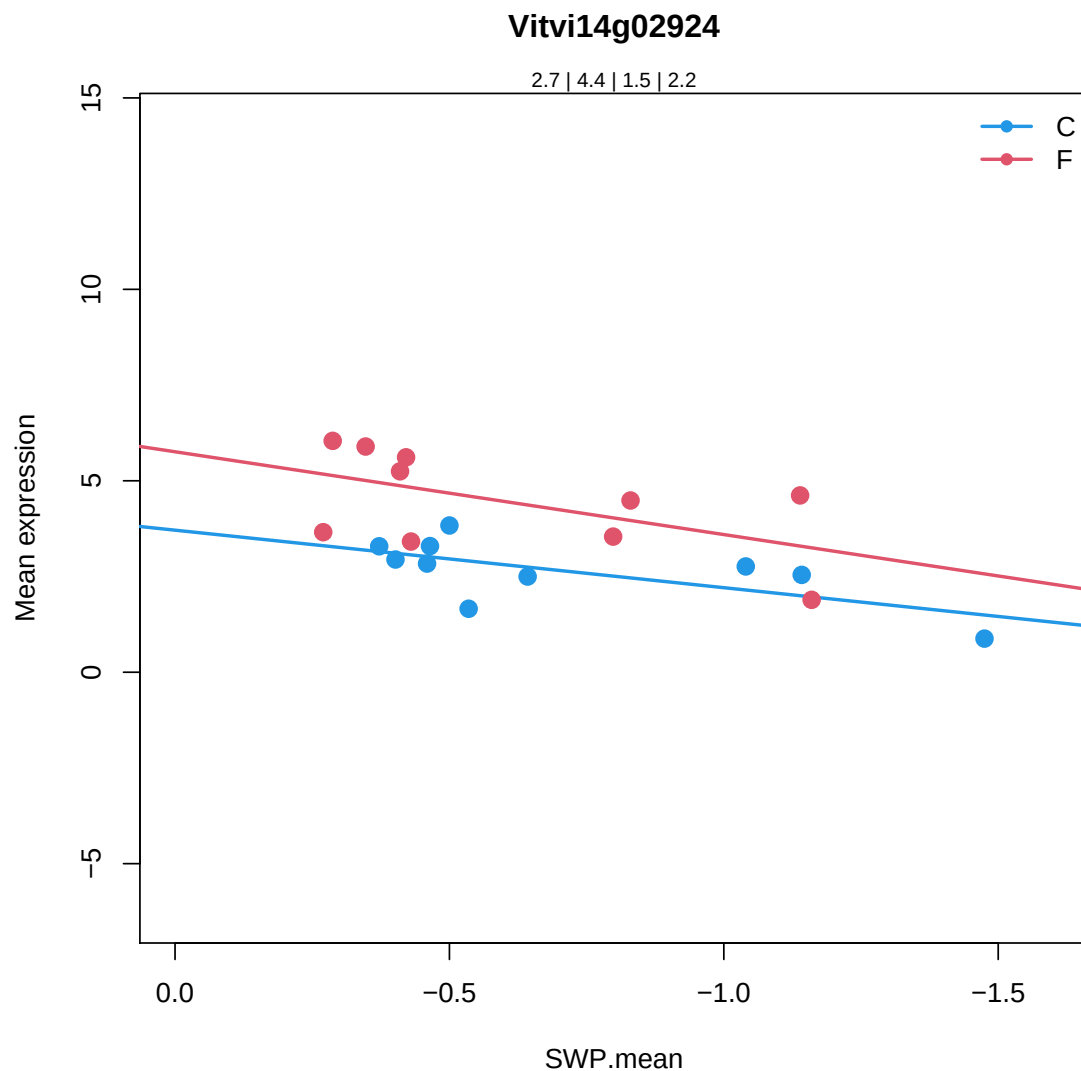
8.4.39 Vitvi14g02924: Type5.0

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

```
Vitvi14g02924
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi14g02924.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.65358	2.158855e-09	***	2.692518e-09	***
SlopeC	1.502144	0.05850777	.	0.5384614	
MeanF-MeanC	1.786688	0.0001229555	***	0.002154124	**
SlopeF-SlopeC	0.660274	0.5612348		0.9999488	



8.4.40 Vitvi14g01809: Type5.0

```
> 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	

8.4.41 Vitvi04g01937: Type5.0

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

Vitvi04g01937

27.3.99

RNA.regulation of transcription.unclassified

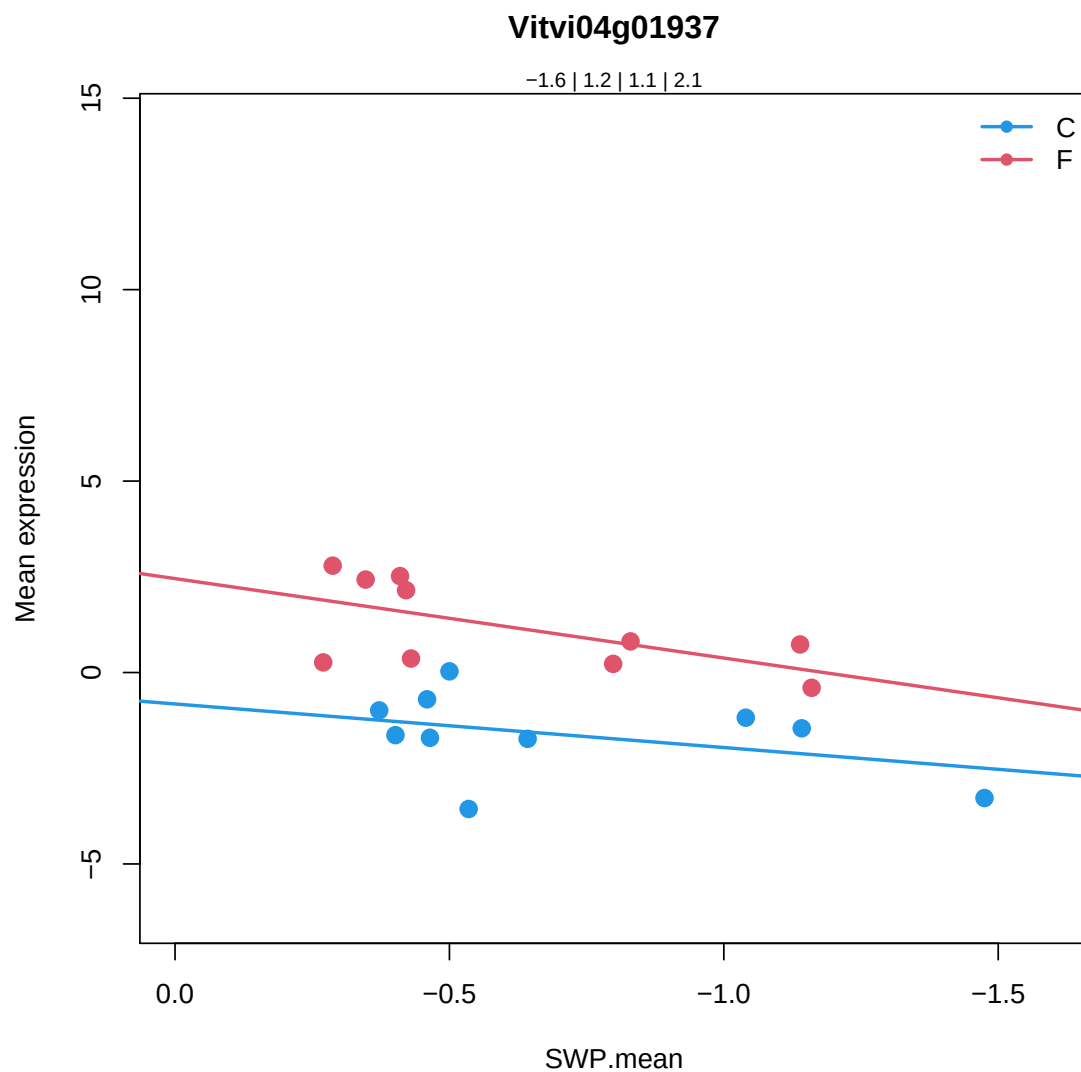
Eukaryotic aspartyl protease family protein |

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	



8.4.42 Vitvi11g00097: Type5.0

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

Vitvi11g00097

27.3.25

RNA.regulation of transcription.MYB domain transcription factor family

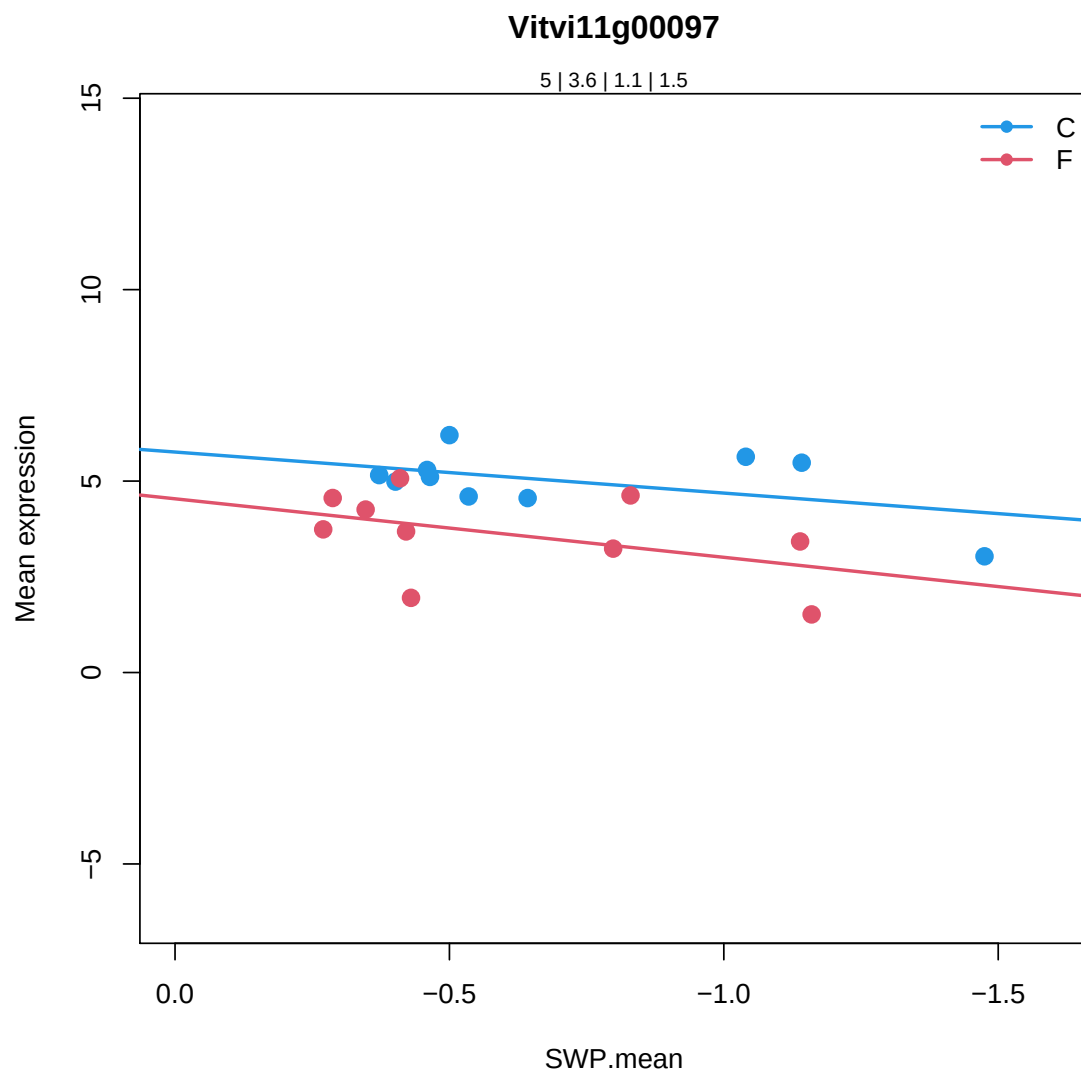
Duplicated homeodomain-like superfamily protein |

Chr5:13726807-13727729 FORWARD LENGTH=258 |

201606

Coefficients for Vitvi11g00097.

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



8.4.43 Vitvi07g00283: Type5.0

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

Vitvi07g00283

26.9

misc.glutathione S transferases

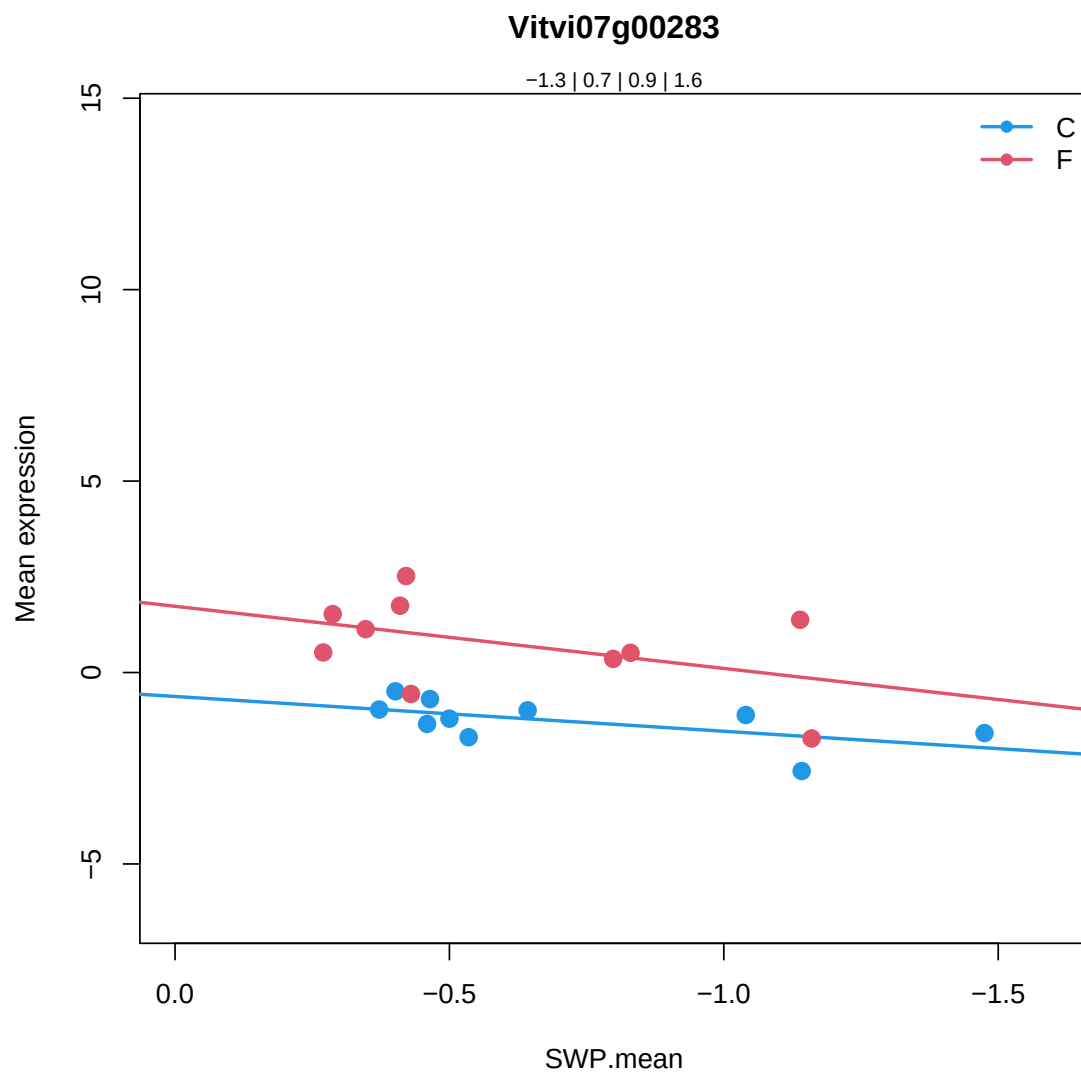
glutathione S-transferase phi 8 |

Chr2:19558213-19559266 FORWARD LENGTH=263 |

201606

Coefficients for Vitvi07g00283.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.264137	6.185009e-05	***	6.858133e-05	***
SlopeC	0.9084089	0.2136027		0.7371282	
MeanF-MeanC	2.005367	1.480113e-05	***	0.0003552736	***
SlopeF-SlopeC	0.7148398	0.5052139		0.9999488	



8.4.44 Vitvi13g00807: Type5.0

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

Vitvi13g00807

35.2

not assigned.unknown

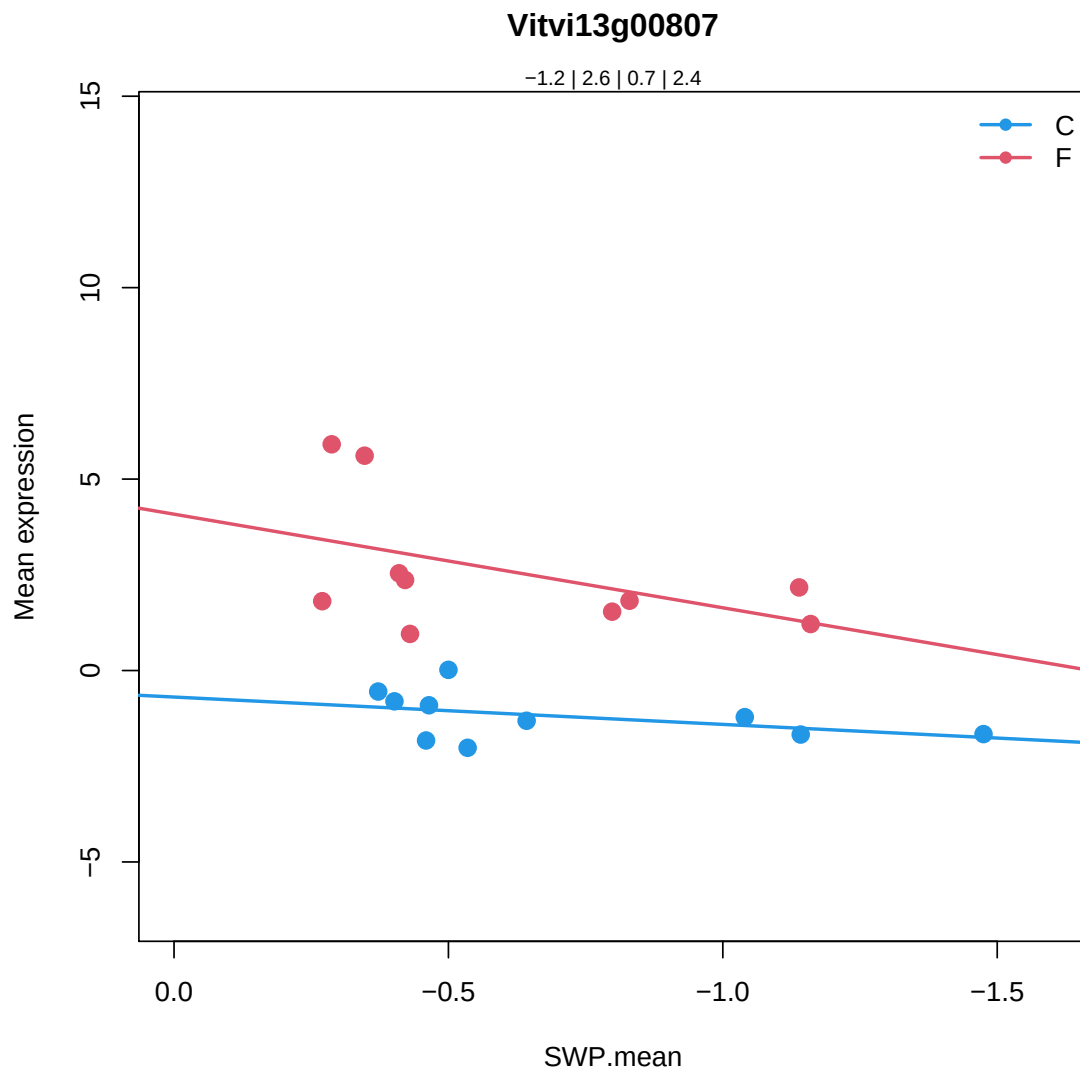
Ankyrin repeat family protein |

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	



8.4.45 Vitvi05g00847: Type5.0 +

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

Vitvi05g00847

30.3

signalling.calcium

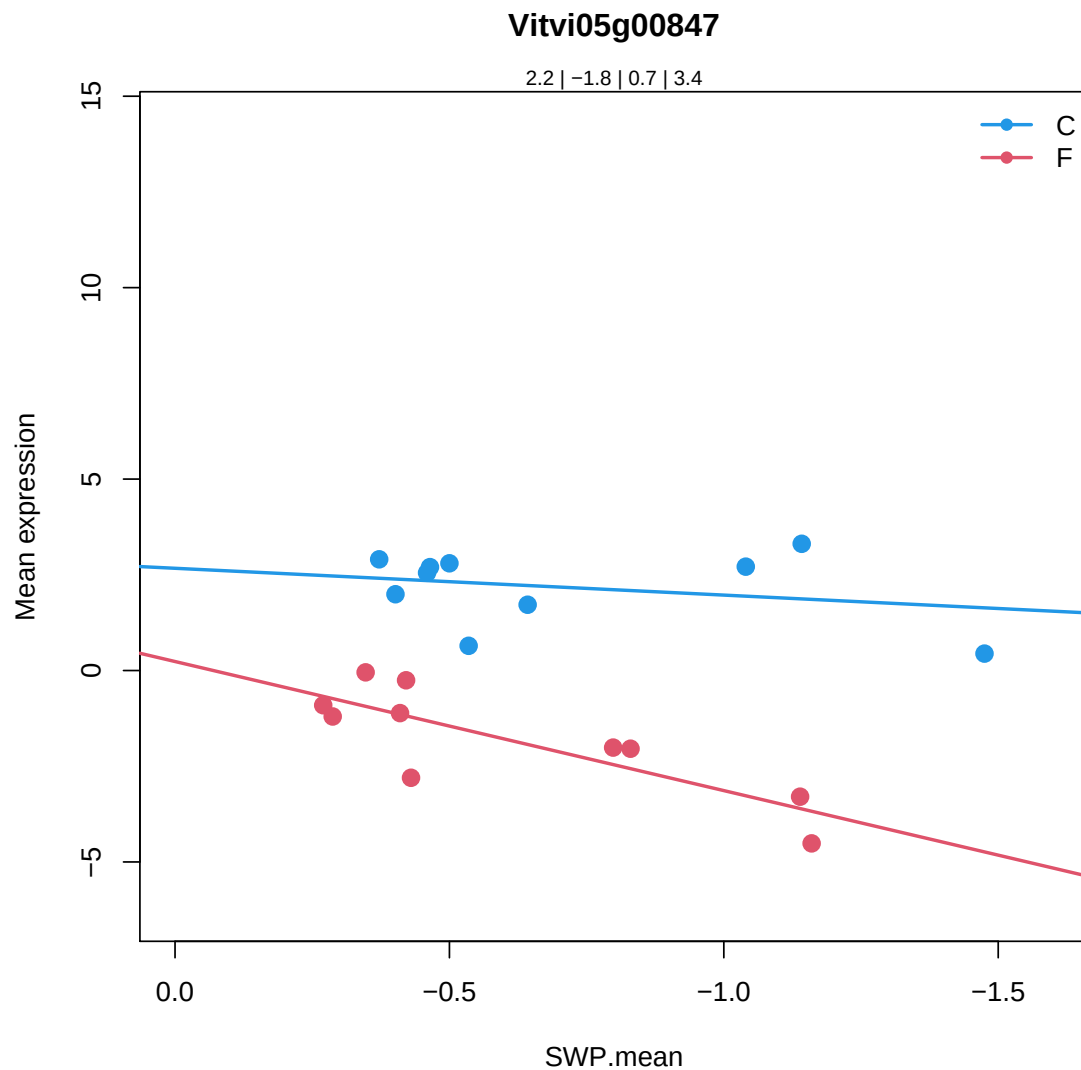
Calcium-binding EF-hand family protein |

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	



8.4.46 Vitvi15g00804: Type5.0

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

Vitvi15g00804

26.10

misc.cytochrome P450

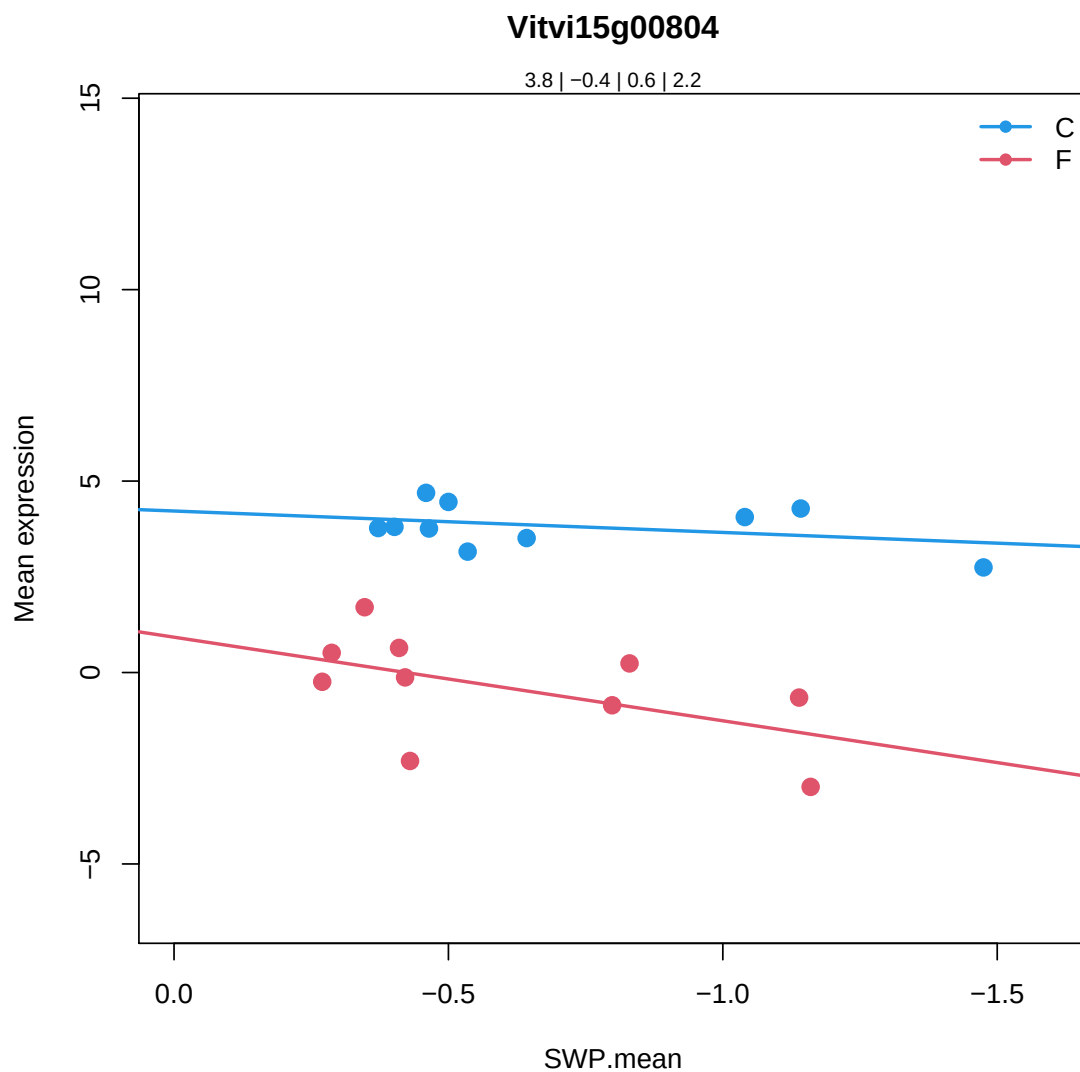
cytochrome P450%2C family 76%2C subfamily C%2C polypeptide 2 |

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	



8.4.47 Vitvi13g01724: Type5.0

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

Vitvi13g01724

17.1.1.1.10

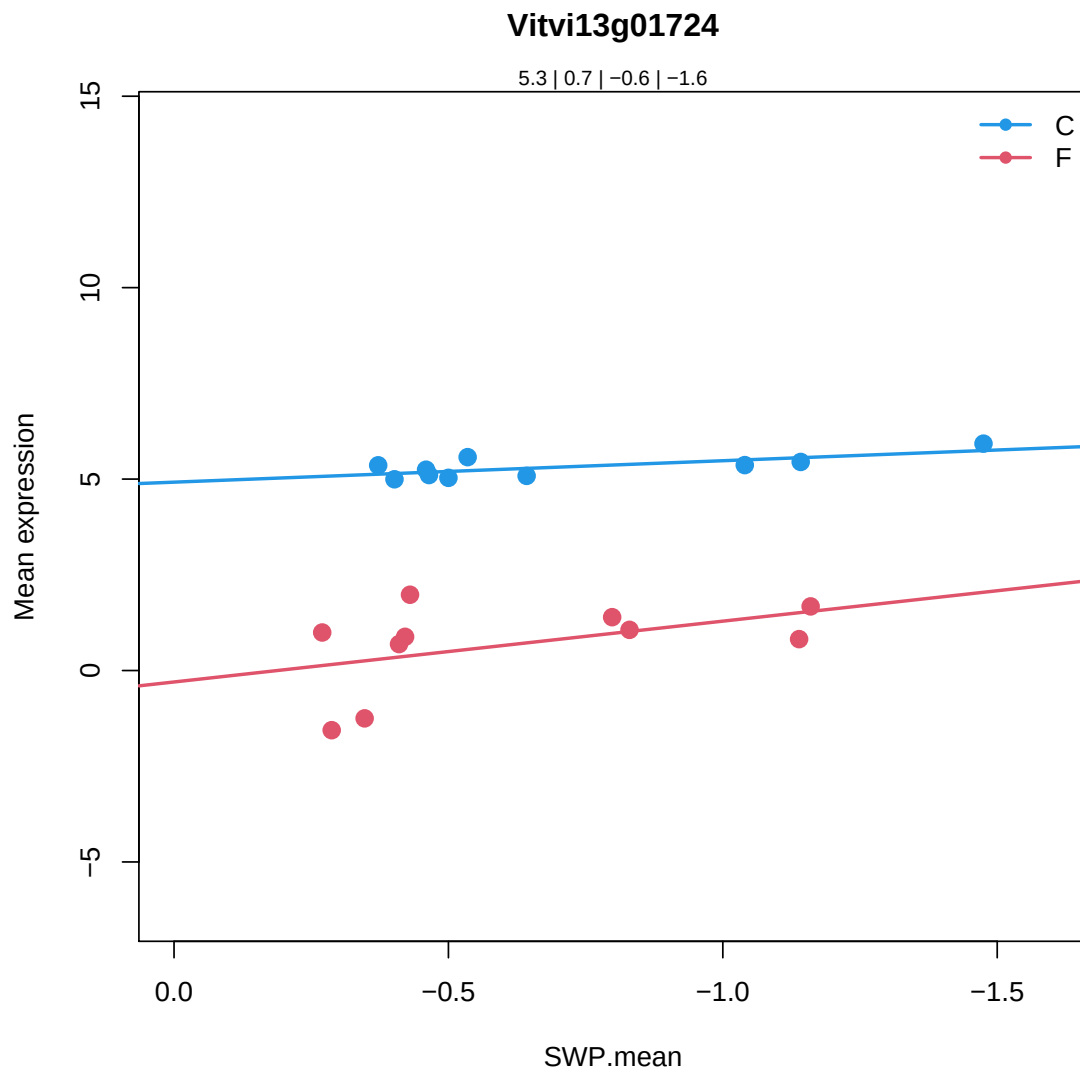
hormone metabolism.abscisic acid.synthesis-degradation.synthesis.9-cis
carotenoid cleavage dioxygenase 1 |

Chr3:23452940-23455896 FORWARD LENGTH=538 |

201606

Coefficients for Vitvi13g01724.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.313104	1.065947e-16	***	2.305544e-16	***
SlopeC	-0.560095	0.3879137		0.8295407	
MeanF-MeanC	-4.644629	1.740046e-12	***	1.506919e-10	***
SlopeF-SlopeC	-1.02838	0.2890149		0.9999488	



8.4.48 Vitvi03g01524: Type5.0

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

Vitvi03g01524

26.10

misc.cytochrome P450

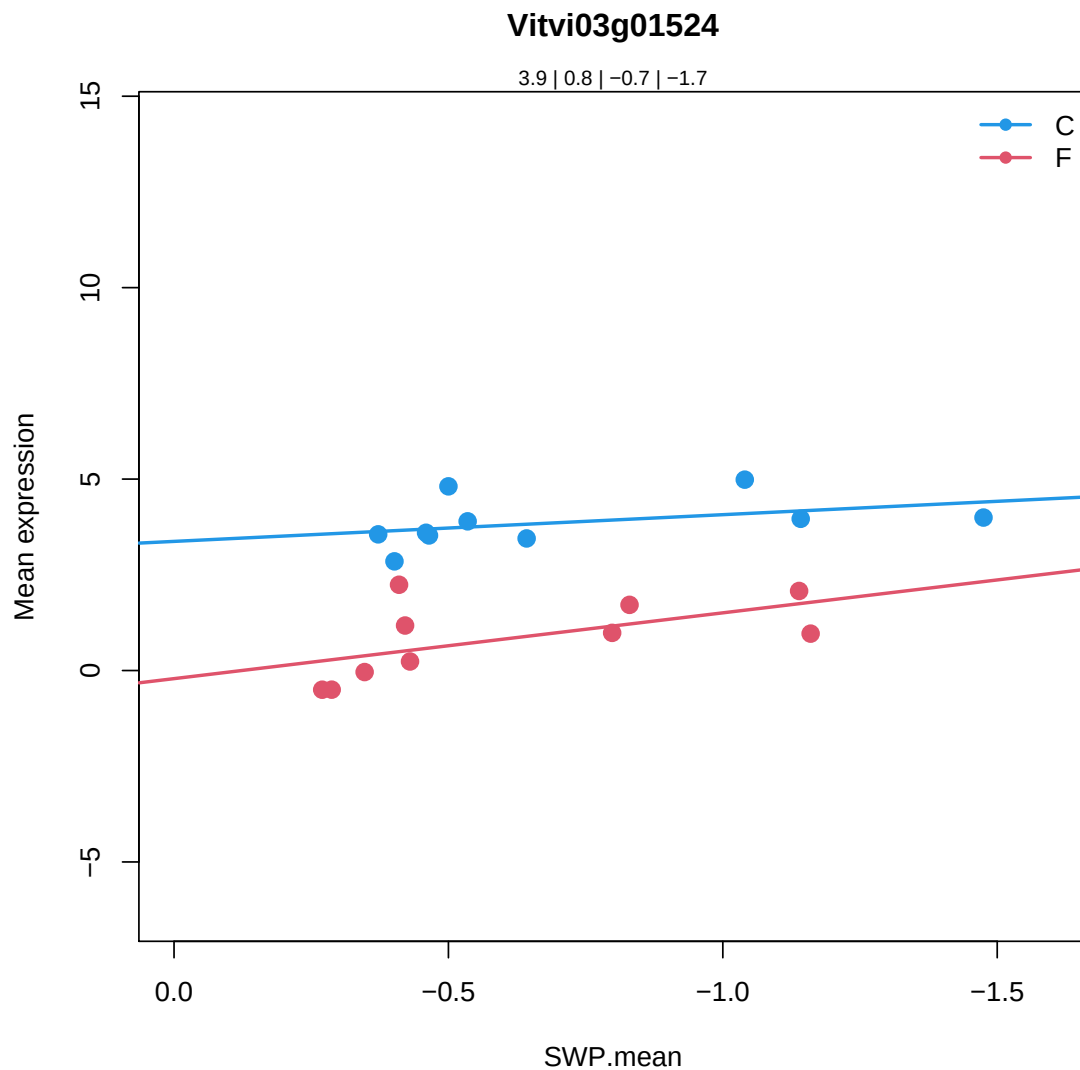
cytochrome P450%2C family 82%2C subfamily C%2C polypeptide 2 |

Chr4:15462408-15464358 FORWARD LENGTH=523 |

201606

Coefficients for Vitvi03g01524.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.863115	3.164956e-14	***	5.057161e-14	***
SlopeC	-0.6979398	0.2657481		0.7701943	
MeanF-MeanC	-3.028344	2.438519e-09	***	1.308729e-07	***
SlopeF-SlopeC	-1.020488	0.2740226		0.9999488	



8.4.49 Vitvi13g00829: Type5.0

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

Vitvi13g00829

26.28

misc.GDSL-motif lipase

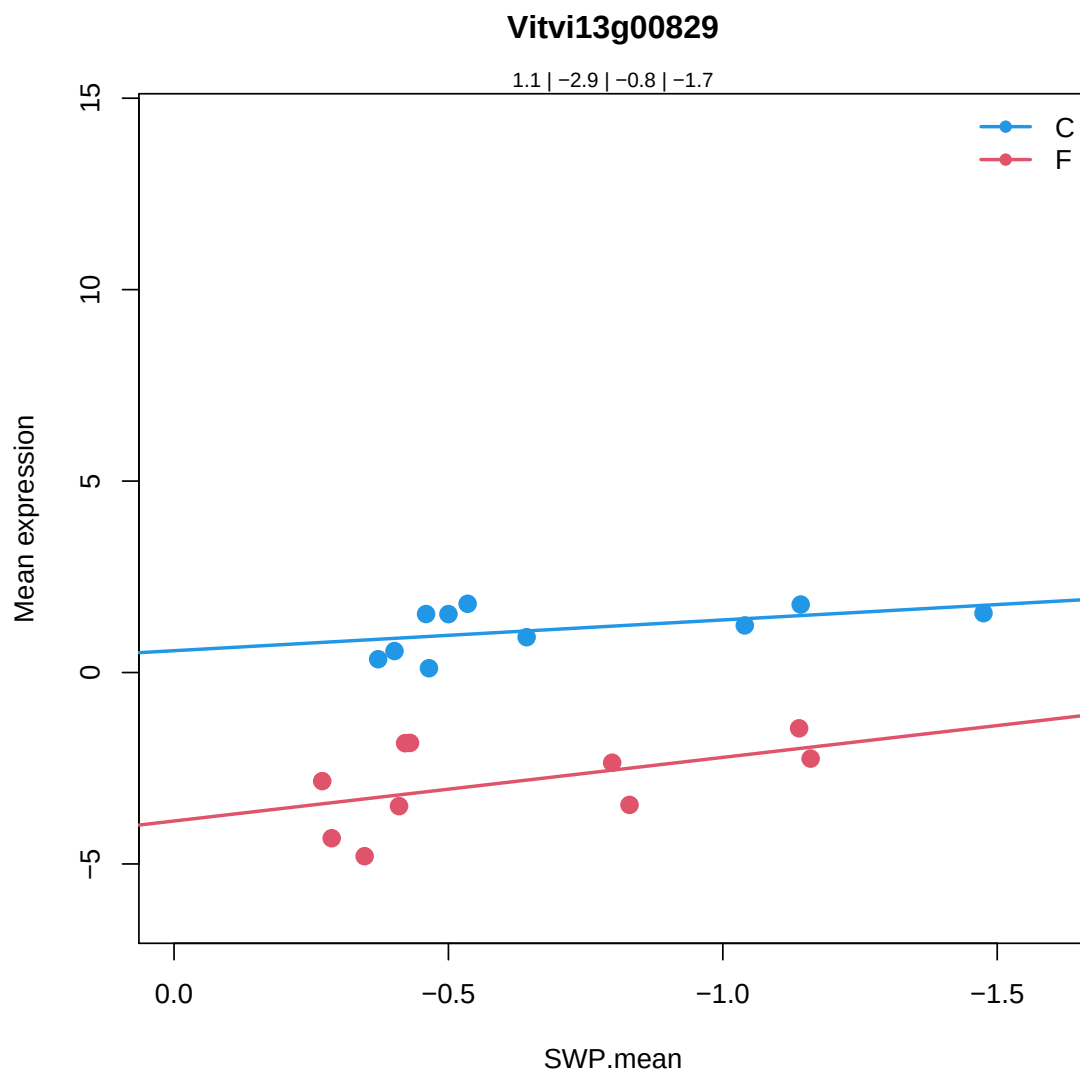
GDSL-like Lipase/Acylhydrolase superfamily protein |

Chr5:915650-918326 FORWARD LENGTH=359 |

201606

Coefficients for Vitvi13g00829.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.134556	0.0001034462	***	0.0001141728	***
SlopeC	-0.8037133	0.2398442		0.7540013	
MeanF-MeanC	-4.000103	7.183617e-11	***	5.140502e-09	***
SlopeF-SlopeC	-0.8582677	0.3953278		0.9999488	



8.4.50 Vitvi04g01100: Type5.0

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

Vitvi04g01100

31.1

cell.organisation

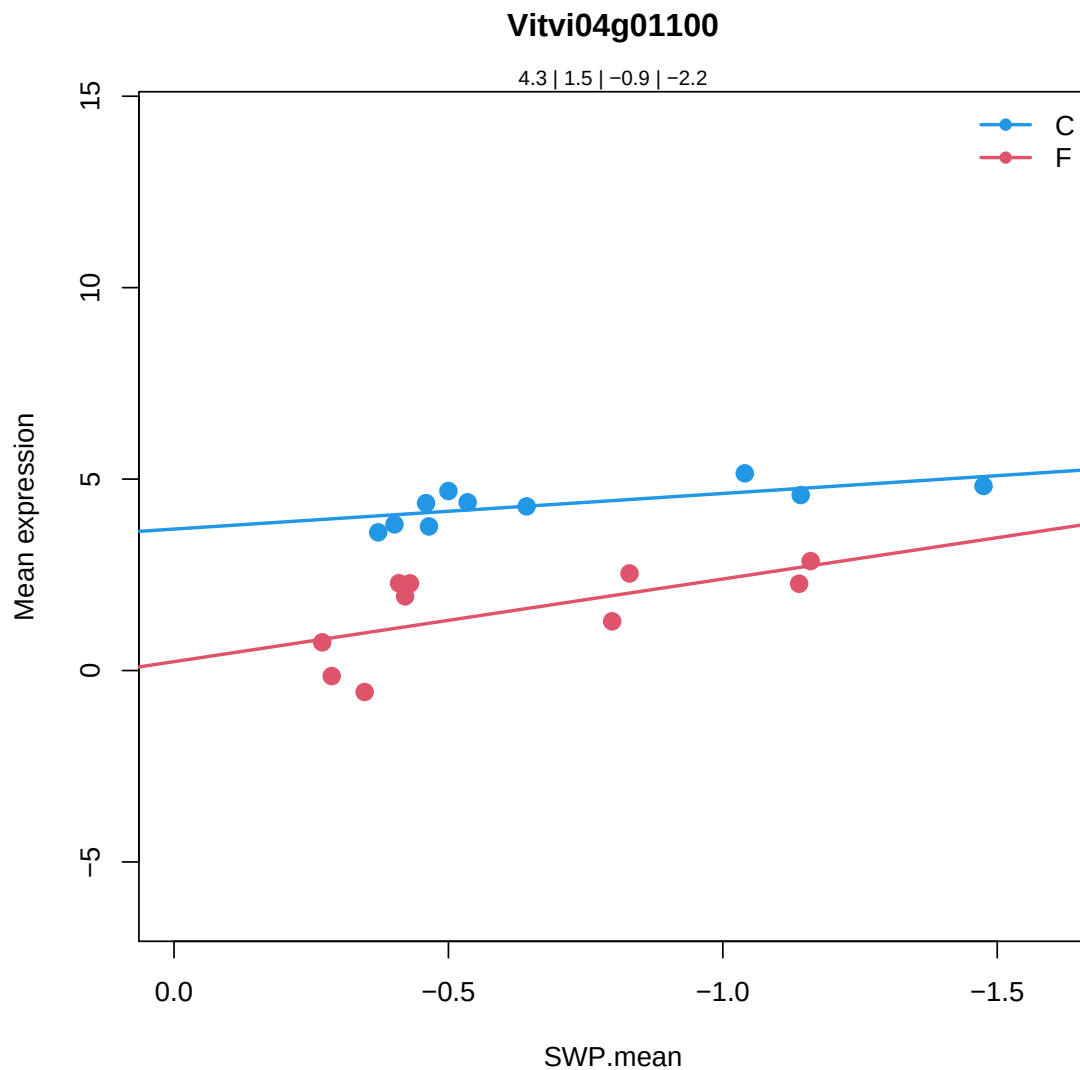
phloem protein 2-B1 |

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	



8.4.51 Vitvi07g01150: Type5.0

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

Vitvi07g01150

35.2

not assigned.unknown

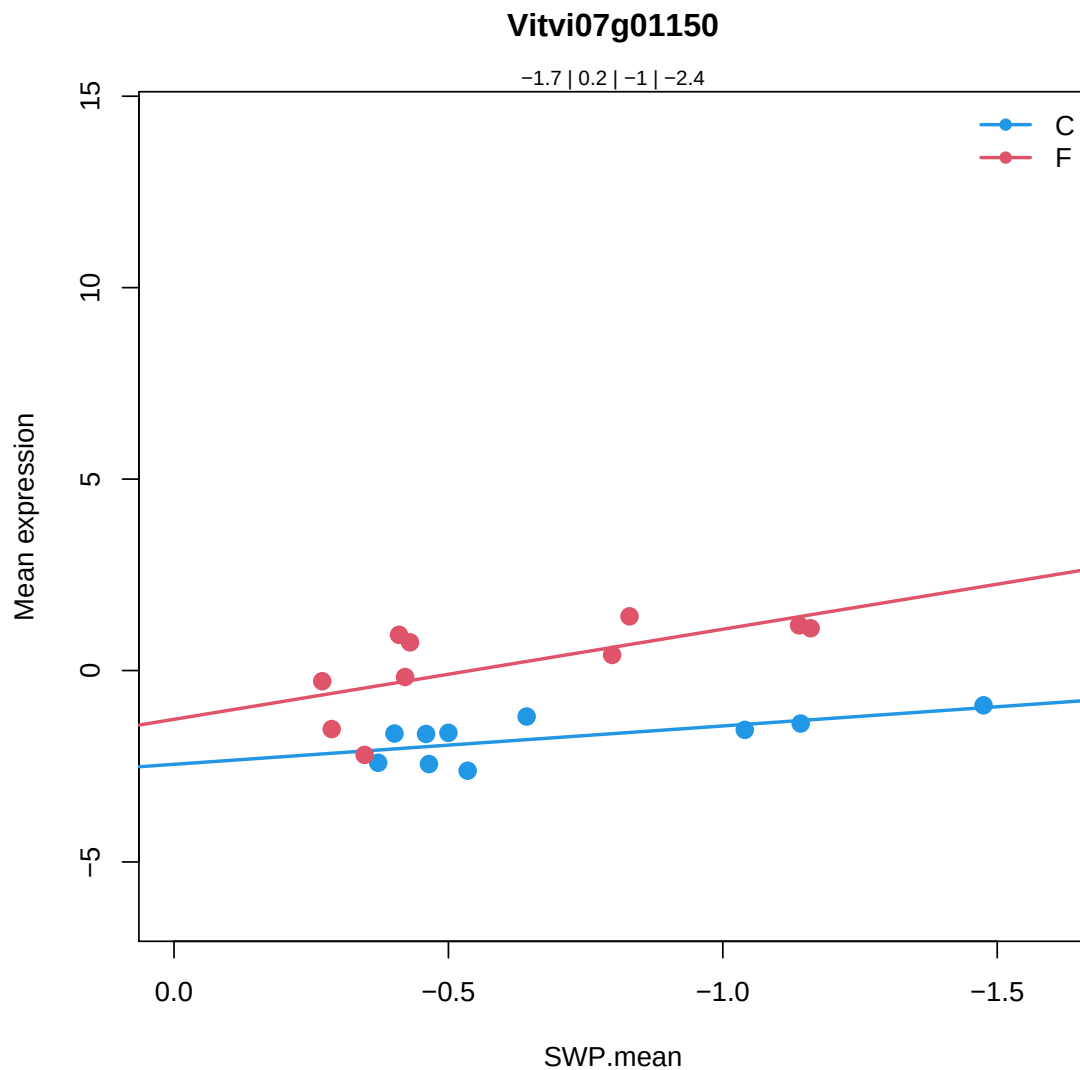
ARF-GAP domain 11 |

Chr3:2391189-2391650 FORWARD LENGTH=153 |

201606

Coefficients for Vitvi07g01150.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.745033	7.366304e-08	***	8.767547e-08	***
SlopeC	-1.002056	0.1140523		0.6311525	
MeanF-MeanC	1.904152	3.773537e-06	***	0.0001049567	***
SlopeF-SlopeC	-1.350546	0.1503227		0.9999488	



8.4.52 Vitvi14g01128: Type5.0

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

```
Vitvi14g01128
```

```
26.21
```

```
misc.protease inhibitor/seed storage/lipid transfer protein (LTP) fami
```

```
Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin
```

```
Chr3:6267102-6267392 FORWARD LENGTH=96 |
```

```
201606
```

```
Vitvi14g01128
```

```
11.6
```

```
lipid metabolism.lipid transfer proteins etc
```

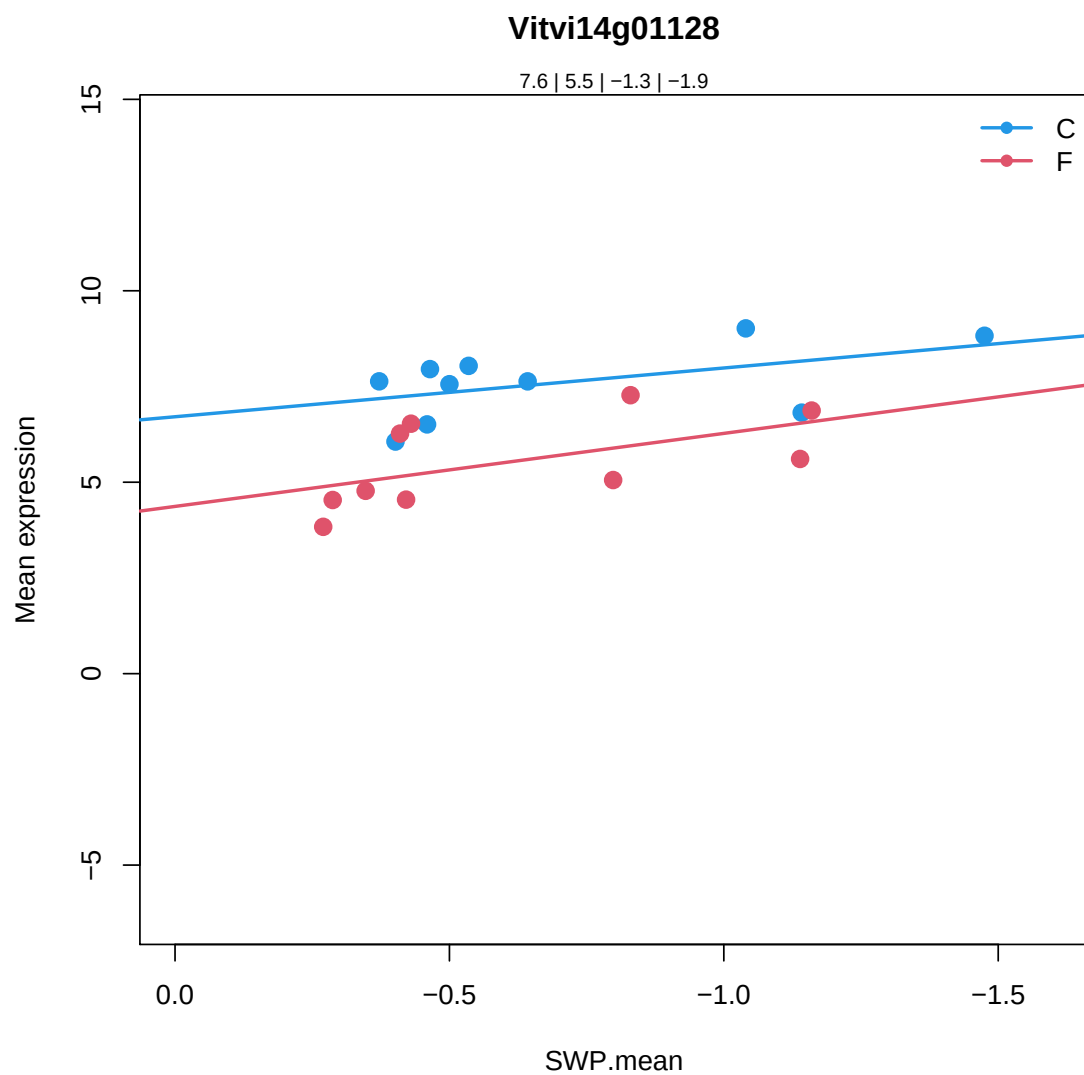
```
Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin
```

```
Chr3:6267102-6267392 FORWARD LENGTH=96 |
```

```
201606
```

Coefficients for Vitvi14g01128.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.605298	1.655195e-18	***	5.34955e-18	***
SlopeC	-1.2737	0.1015743		0.6135572	
MeanF-MeanC	-2.075585	1.796388e-05	***	0.0004222686	***
SlopeF-SlopeC	-0.6333015	0.5736211		0.9999488	



8.4.53 Vitvi15g01073: Type5.0

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

Vitvi15g01073

16.8.1.12

secondary metabolism.flavonoids.anthocyanins.anthocyanidin 3-O-glucosyl

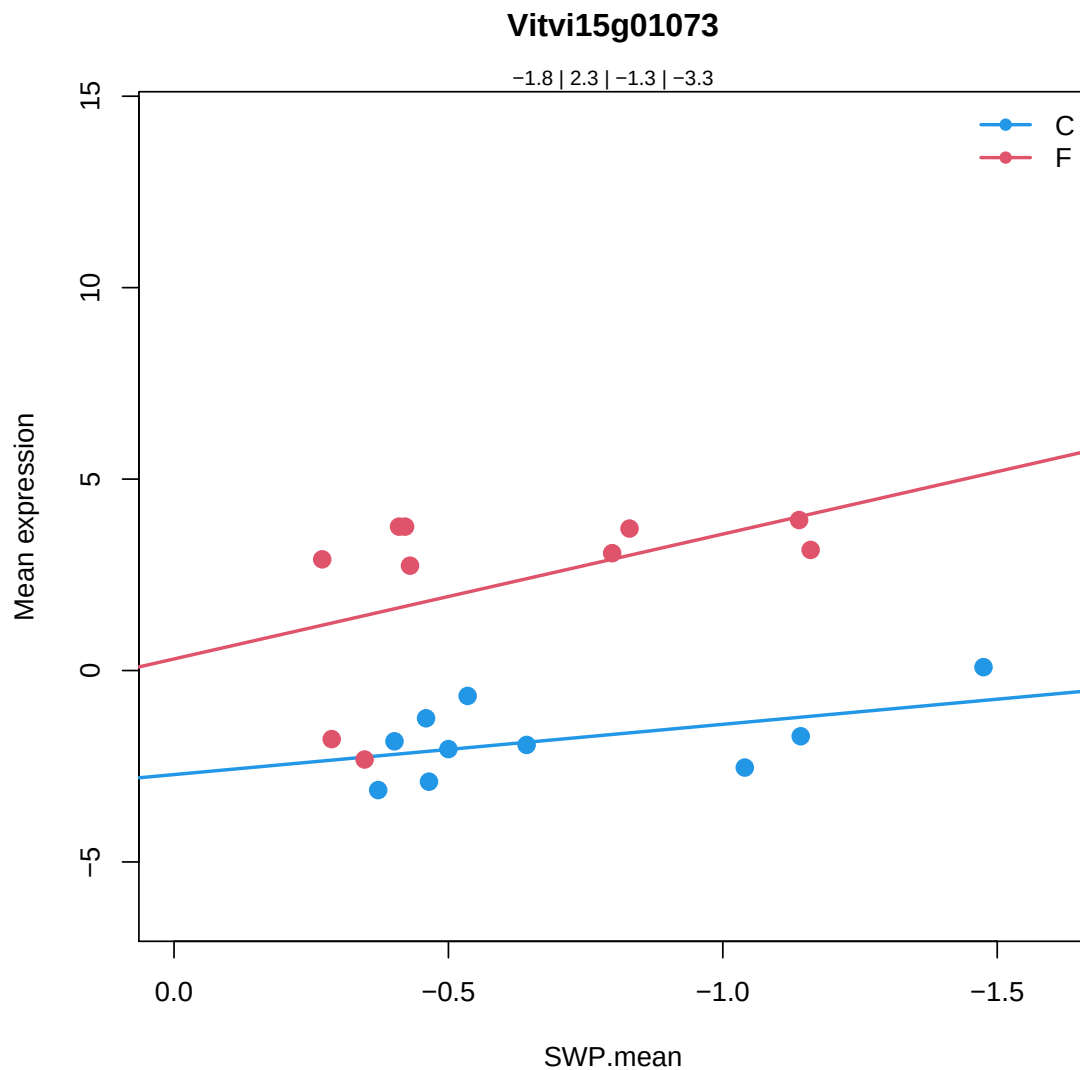
UDP-Glycosyltransferase superfamily protein |

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	



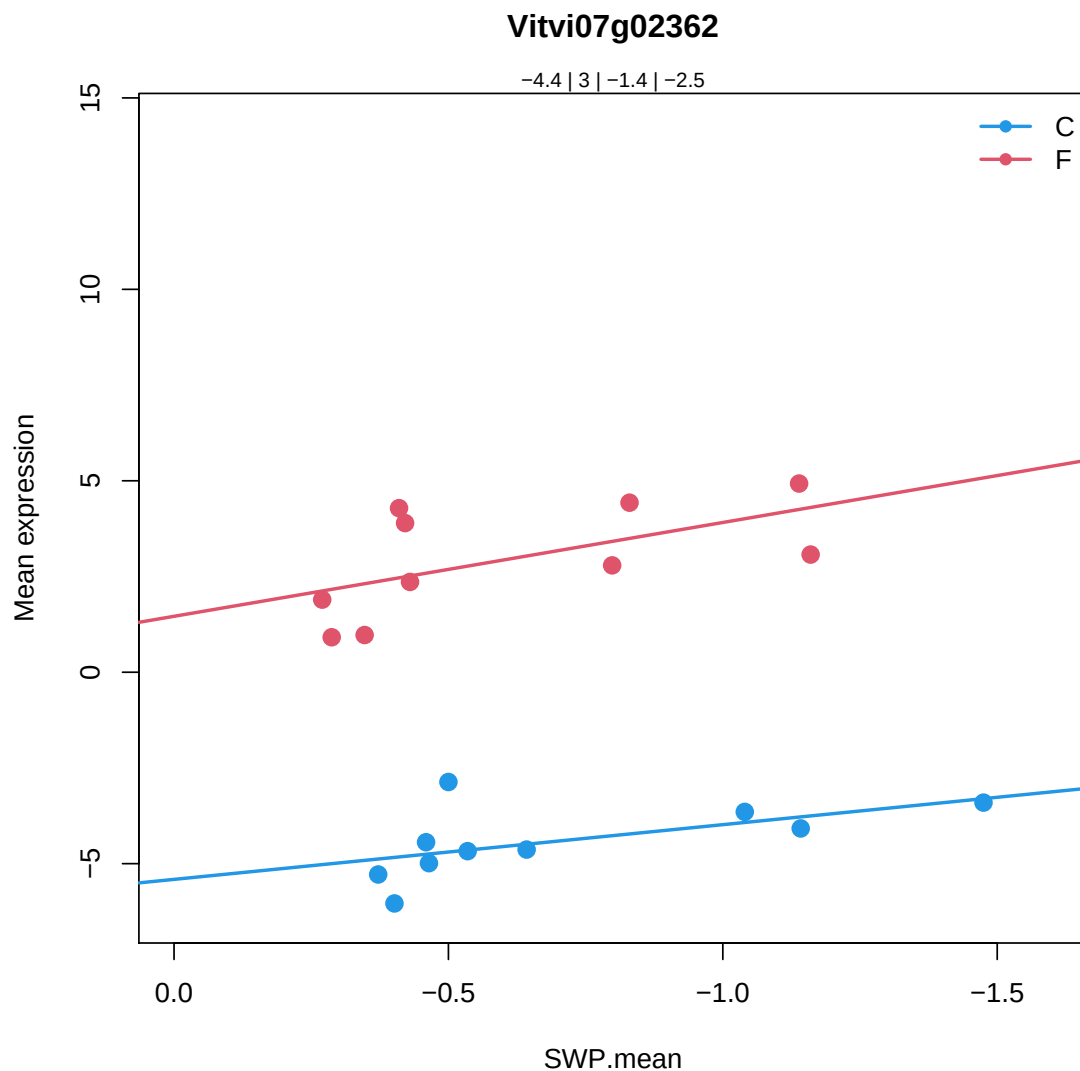
8.4.54 Vitvi07g02362: Type5.0

```
> 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	



8.4.55 Vitvi03g00432: Type5.0 *

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

Vitvi03g00432

21.2

redox.ascorbate and glutathione

2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protei

Chr3:6554004-6554987 REVERSE LENGTH=278 |

201606

Vitvi03g00432

26.8

misc.nitrilases, nitrile lyases, berberine bridge enzymes, reticuline

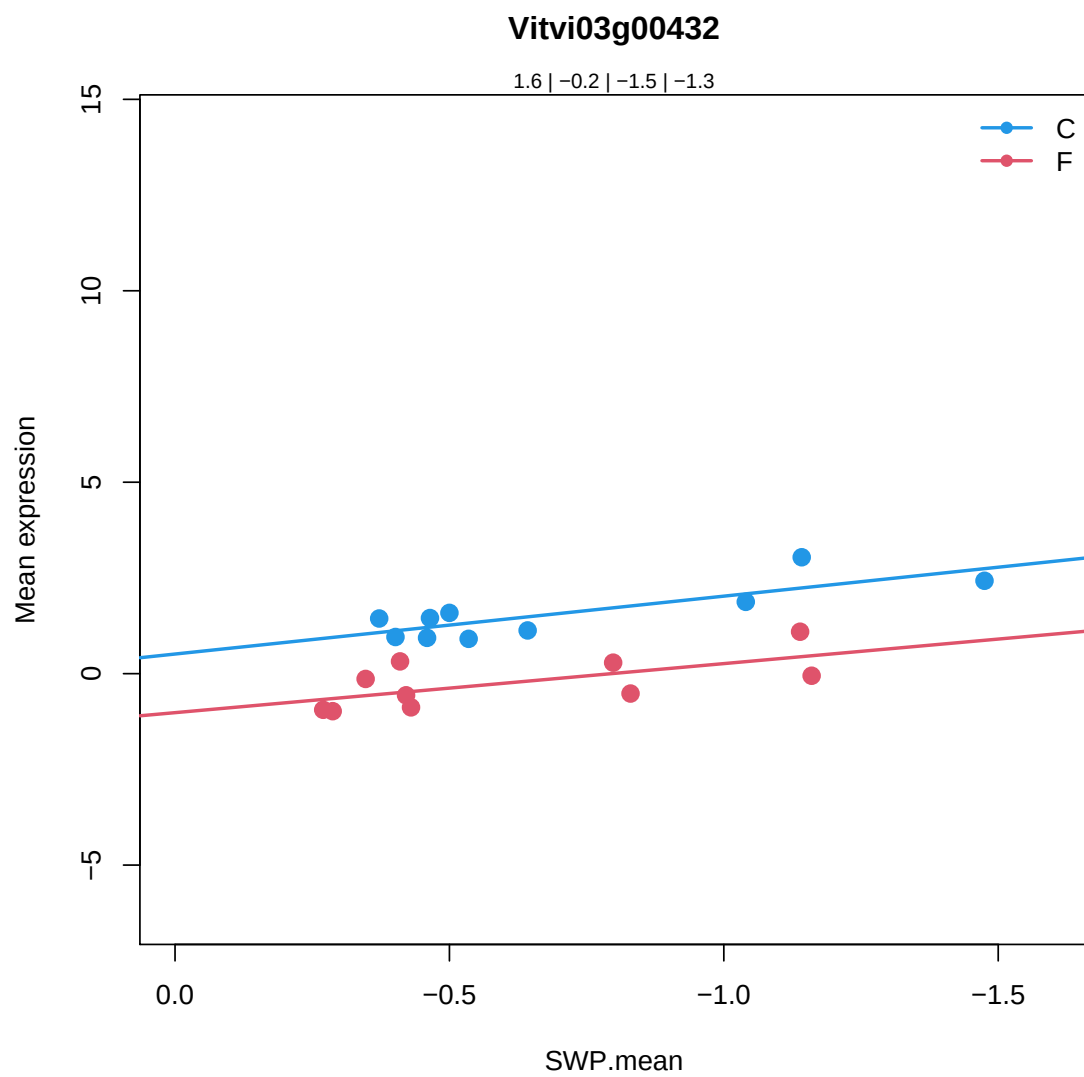
2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protei

Chr3:6554004-6554987 REVERSE LENGTH=278 |

201606

Coefficients for Vitvi03g00432.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.575091	1.062316e-09	***	1.338499e-09	***
SlopeC	-1.511848	0.001957741	**	0.1673186	
MeanF-MeanC	-1.813218	3.728598e-08	***	1.681399e-06	***
SlopeF-SlopeC	0.230625	0.7213458		0.9999488	



8.4.56 Vitvi12g00101: Type5.0 *

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

```
Vitvi12g00101
```

```
34.16
```

```
transport.ABC transporters and multidrug resistance systems
```

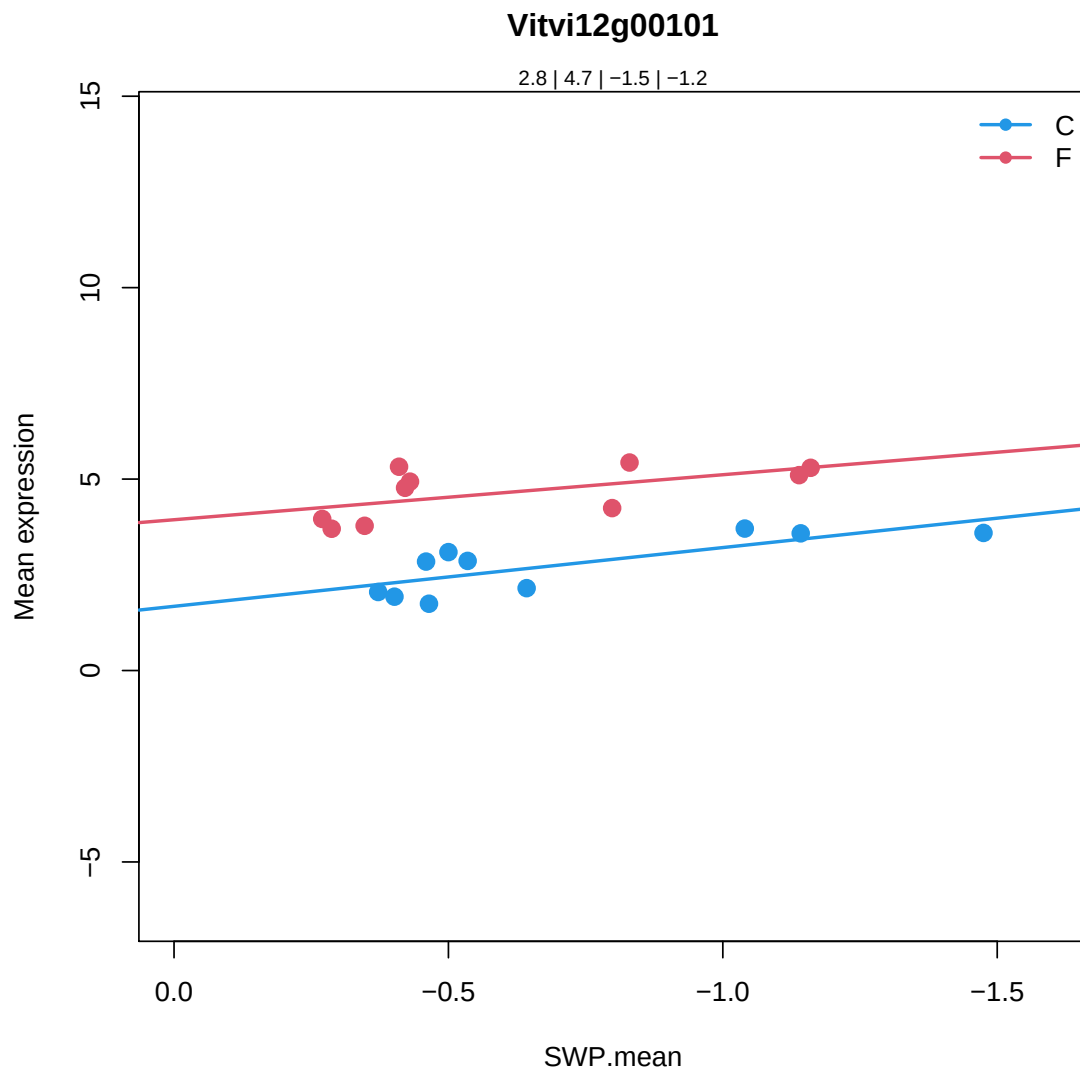
```
MATE efflux family protein |
```

```
Chr3:21819124-21821288 FORWARD LENGTH=507 |
```

```
201606
```

Coefficients for Vitvi12g00101.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.755737	9.506814e-14	***	1.462779e-13	***
SlopeC	-1.534671	0.003082809	**	0.2103859	
MeanF-MeanC	1.898405	5.628455e-08	***	2.451112e-06	***
SlopeF-SlopeC	0.359012	0.6056038		0.9999488	



8.4.57 Vitvi01g02061: Type5.0 *

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

Vitvi01g02061

35.1.26

not assigned.no ontology.DC1 domain containing protein

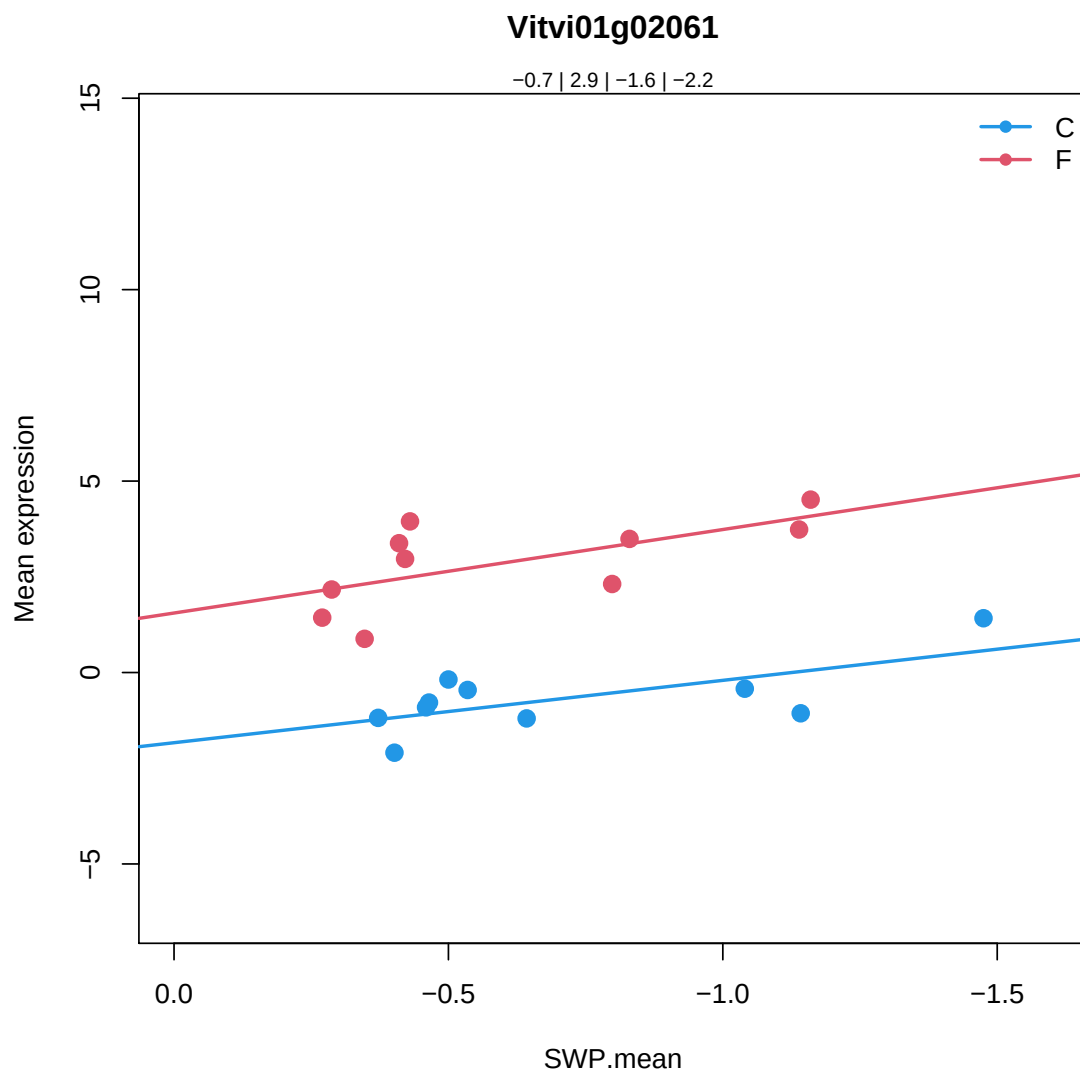
DC1 domain-containing protein |

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	



8.4.58 Vitvi05g01116: Type5.0 *

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

Vitvi05g01116

11.1.11

lipid metabolism.FA synthesis and FA elongation.fatty acid elongase

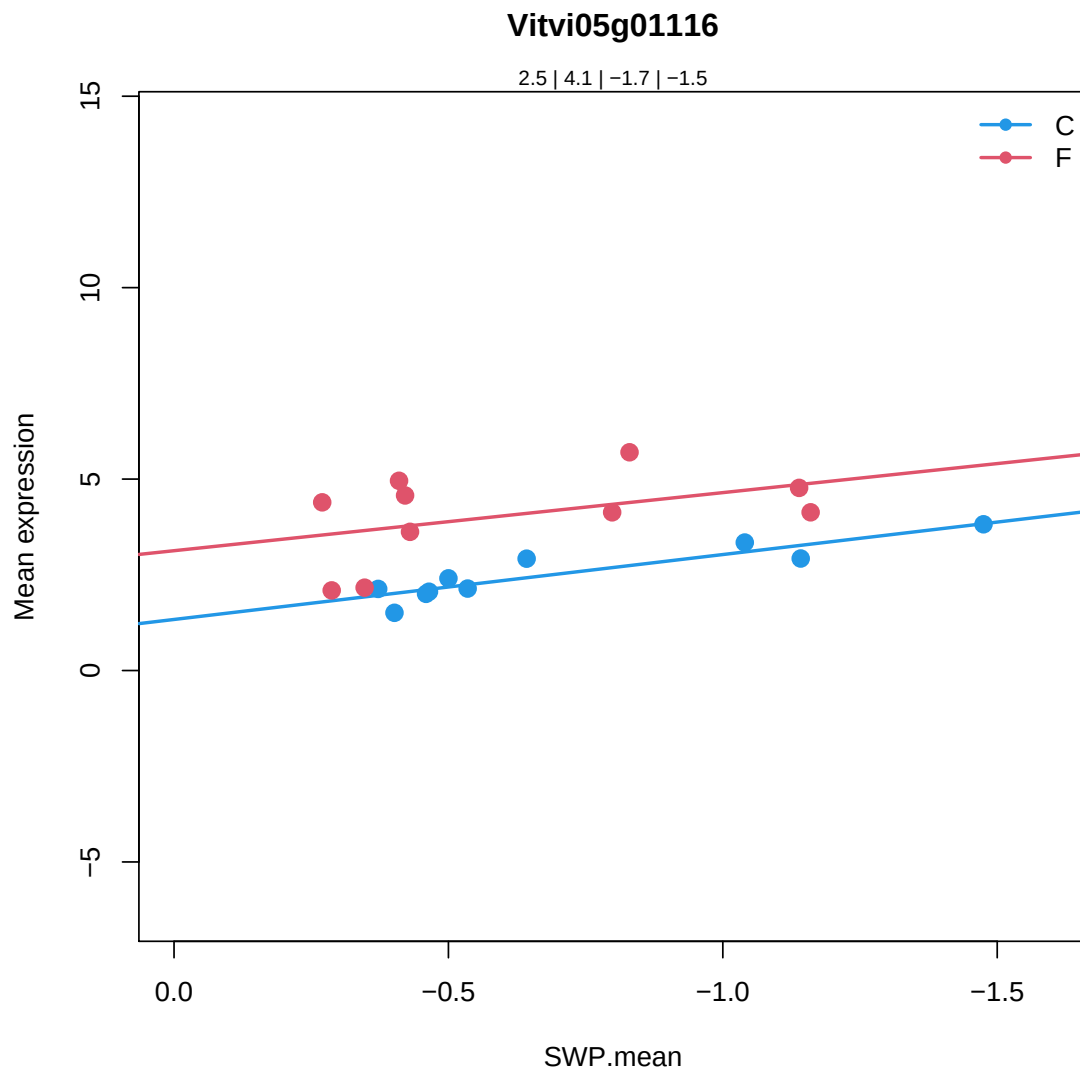
HXXXD-type acyl-transferase family protein |

Chr4:12660929-12662537 FORWARD LENGTH=421 |

201606

Coefficients for Vitvi05g01116.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.52539	3.801912e-10	***	4.865962e-10	***
SlopeC	-1.695659	0.01616485	*	0.3486596	
MeanF-MeanC	1.527811	0.0001382594	***	0.002365151	**
SlopeF-SlopeC	0.1786811	0.8550996		0.9999488	



8.4.59 Vitvi14g01919: Type5.0 *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi14g01919

35.2

not assigned.unknown

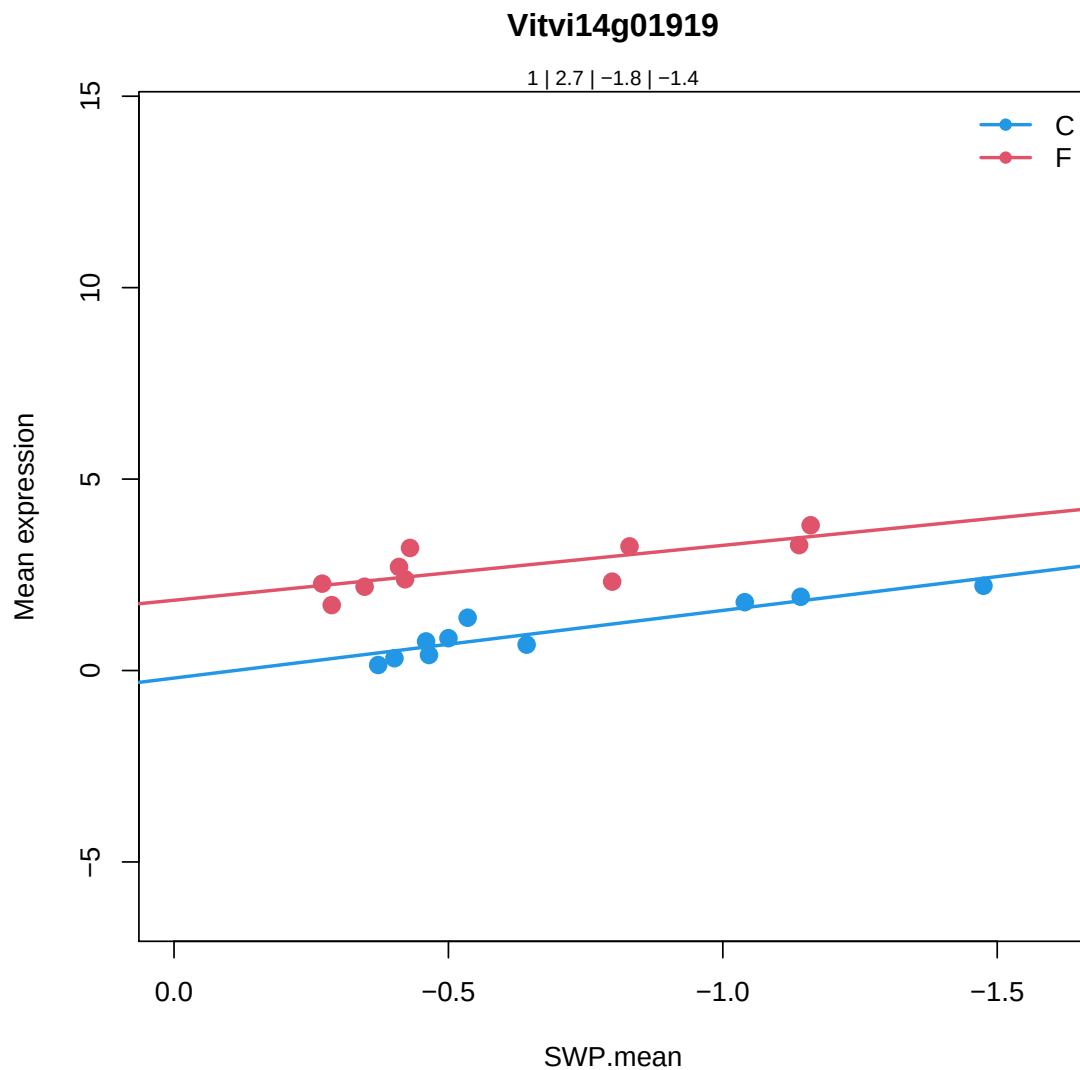
3-dehydroquinate synthase |

Chr3:10793126-10795304 REVERSE LENGTH=422 |

201606

Coefficients for Vitvi14g01919.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.045312	6.751507e-08	***	8.041452e-08	***
SlopeC	-1.767111	7.61116e-05	***	0.07644173	.
MeanF-MeanC	1.663539	9.349791e-09	***	4.687813e-07	***
SlopeF-SlopeC	0.333937	0.5423894		0.9999488	



8.4.60 Vitvi18g00508: Type5.0 *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi18g00508

9.8

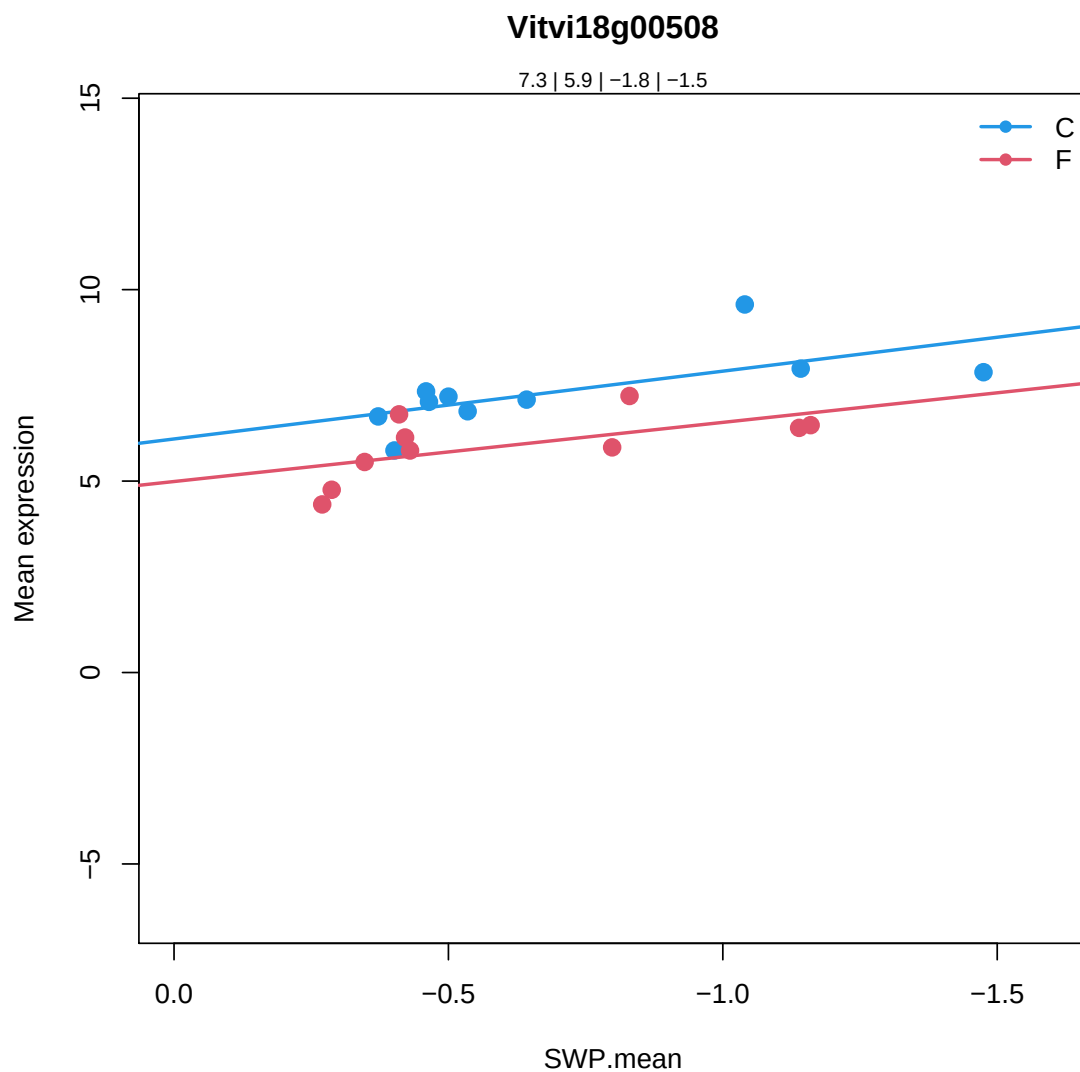
mitochondrial electron transport / ATP synthesis.uncoupling protein
uncoupling protein 5 |

Chr2:9563531-9564472 REVERSE LENGTH=313 |

201606

Coefficients for Vitvi18g00508.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.344885	6.22014e-20	***	3.185732e-19	***
SlopeC	-1.770808	0.008851147	**	0.2903326	
MeanF-MeanC	-1.415514	0.0001756439	***	0.002897364	**
SlopeF-SlopeC	0.2259134	0.8074009		0.9999488	



8.4.61 Vitvi07g02448: Type5.0 *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi07g02448

26.2

misc.UDP glucosyl and glucoronyl transferases

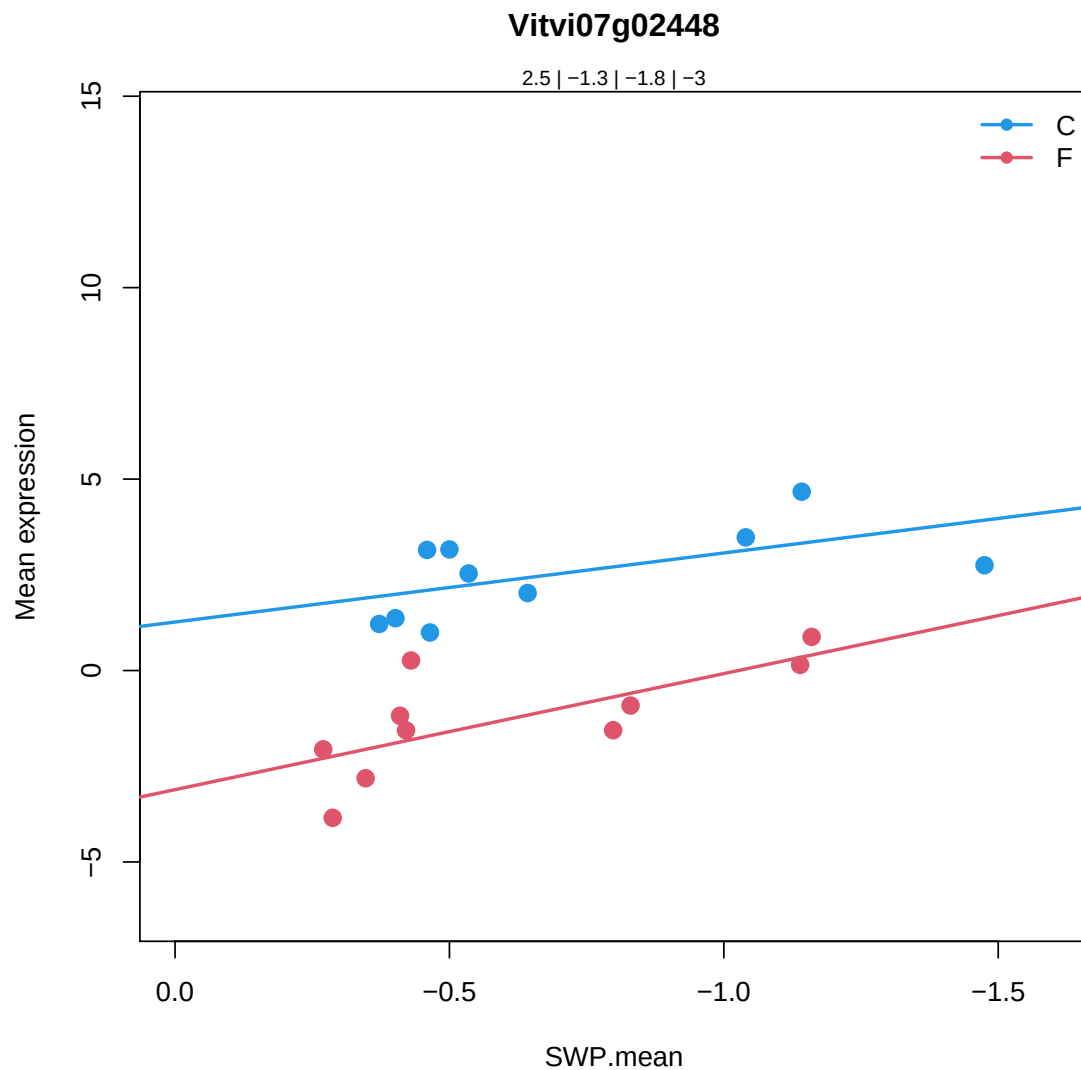
Uridine diphosphate glycosyltransferase 74E2 |

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	



8.4.62 Vitvi15g01396: Type5.0

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi15g01396

35.2

not assigned.unknown

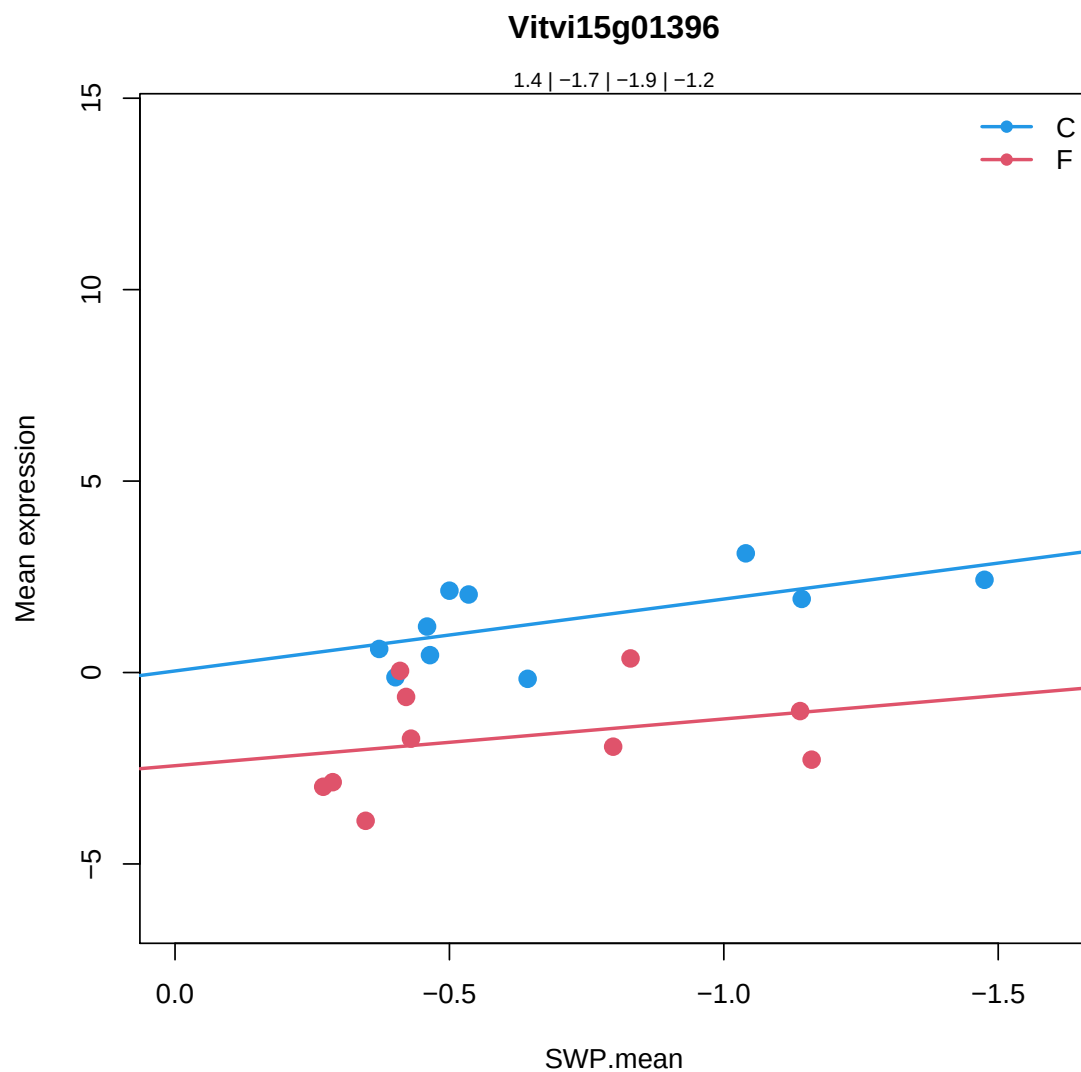
cation exchanger 9 |

Chr3:4661143-4663074 REVERSE LENGTH=643 |

201606

Coefficients for Vitvi15g01396.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.361299	0.000500317	***	0.0005447801	***
SlopeC	-1.878113	0.0549002	.	0.5230463	
MeanF-MeanC	-3.051023	1.790801e-06	***	5.449958e-05	***
SlopeF-SlopeC	0.6565928	0.638243		0.9999488	



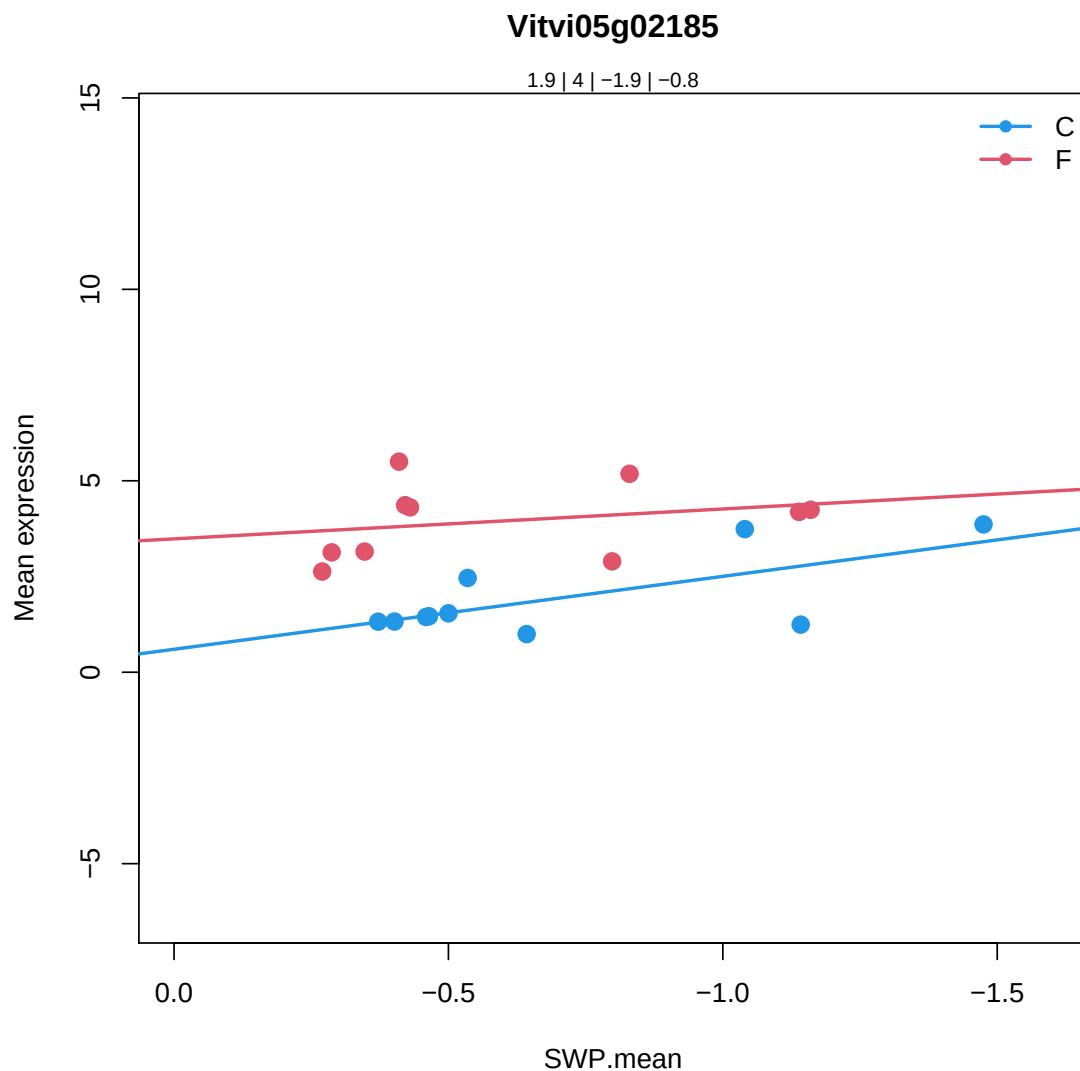
8.4.63 Vitvi05g02185: Type5.0 *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi05g02185
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi05g02185.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.938307	2.171468e-07	***	2.552245e-07	***
SlopeC	-1.903955	0.0153545	*	0.3393703	
MeanF-MeanC	2.020325	1.737192e-05	***	0.000409247	***
SlopeF-SlopeC	1.123199	0.3081246		0.9999488	



8.4.64 Vitvi19g01048: Type5.0

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi19g01048

26.9

misc.glutathione S transferases

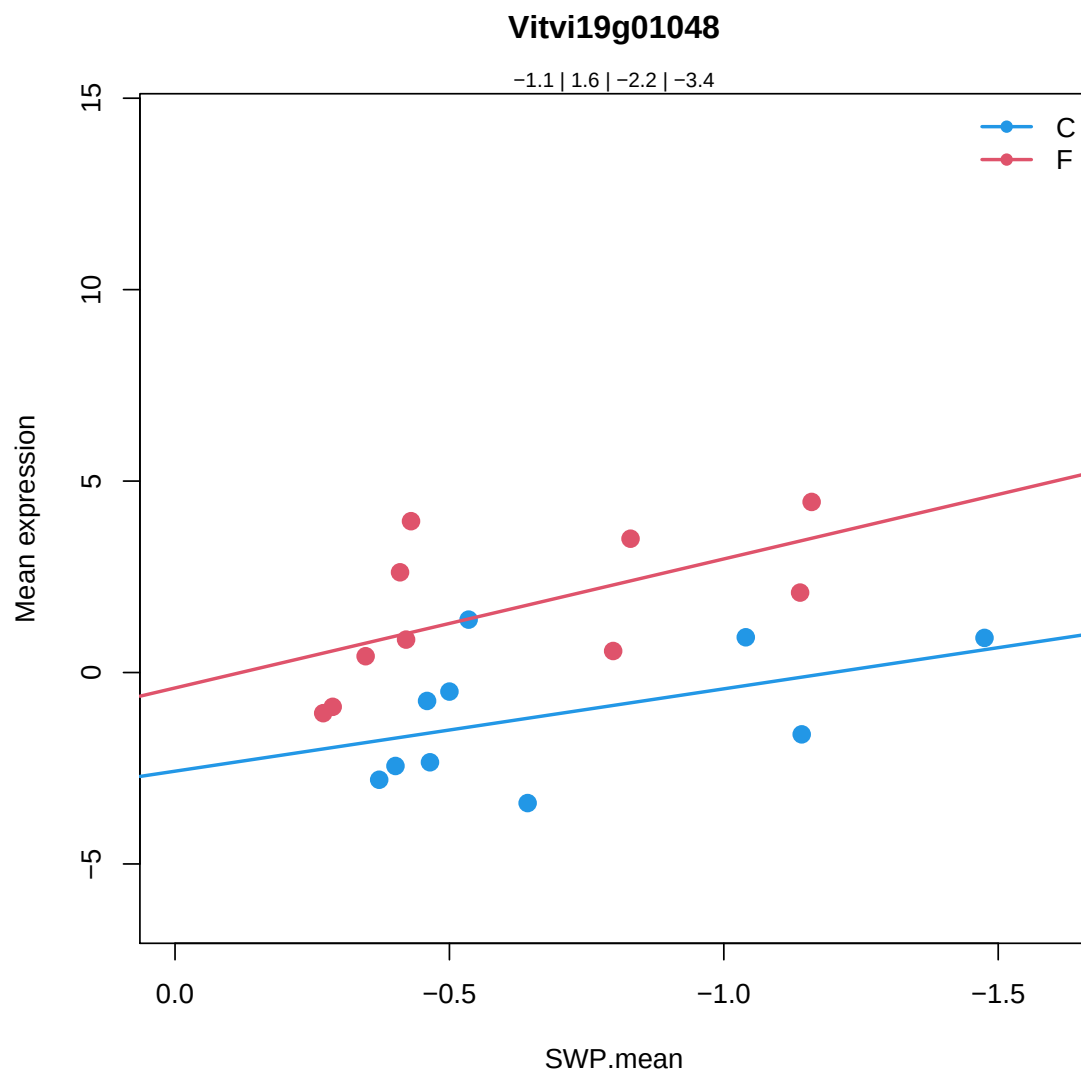
glutathione S-transferase TAU 25 |

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	



8.4.65 Vitvi03g00443: Type5.0 *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi03g00443

26.8

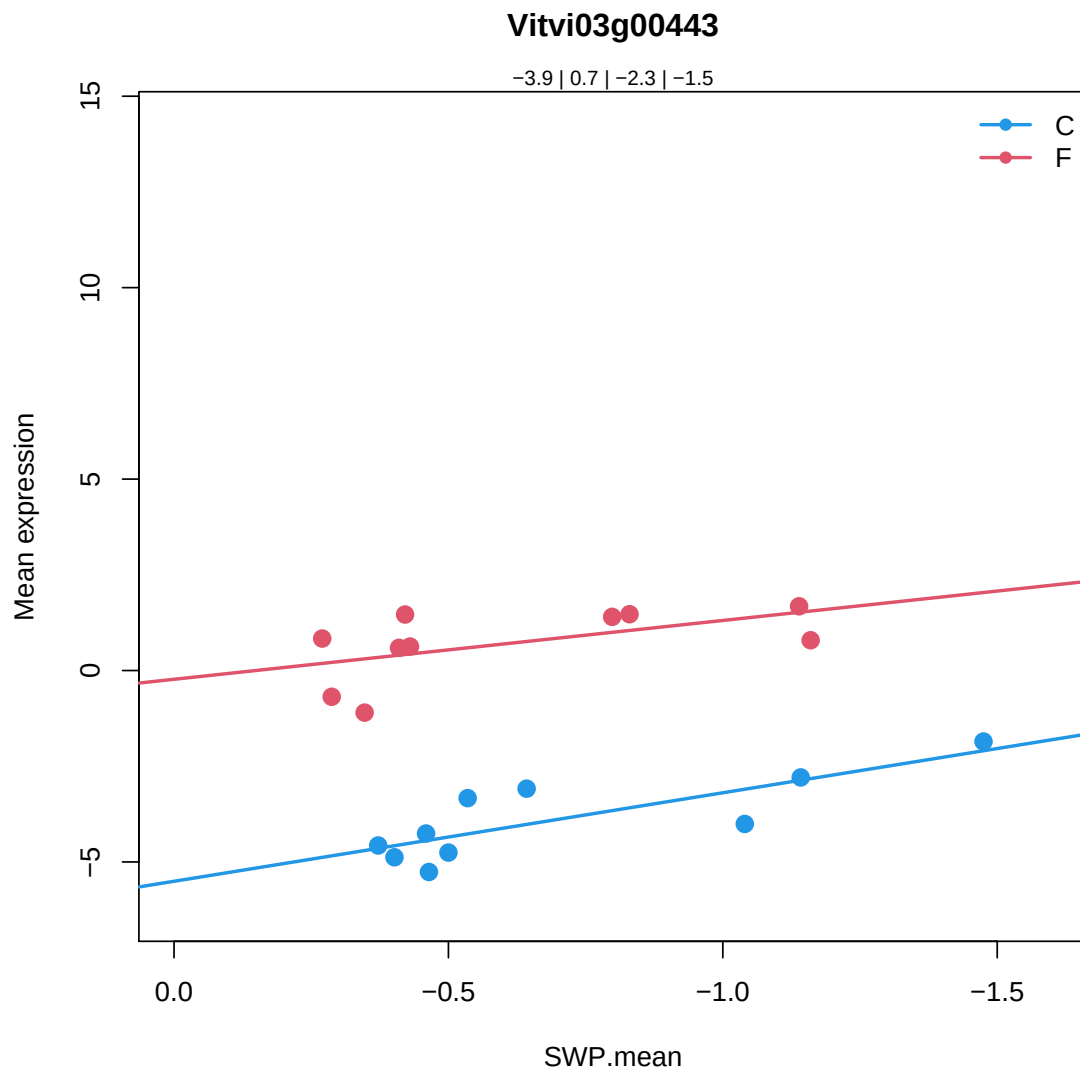
misc.nitrilases, nitrile lyases, berberine bridge enzymes, reticuline
acetone-cyanohydrin lyase |

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	



8.4.66 Vitvi02g00263: Type5.0

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi02g00263

26.6

misc.O-methyl transferases

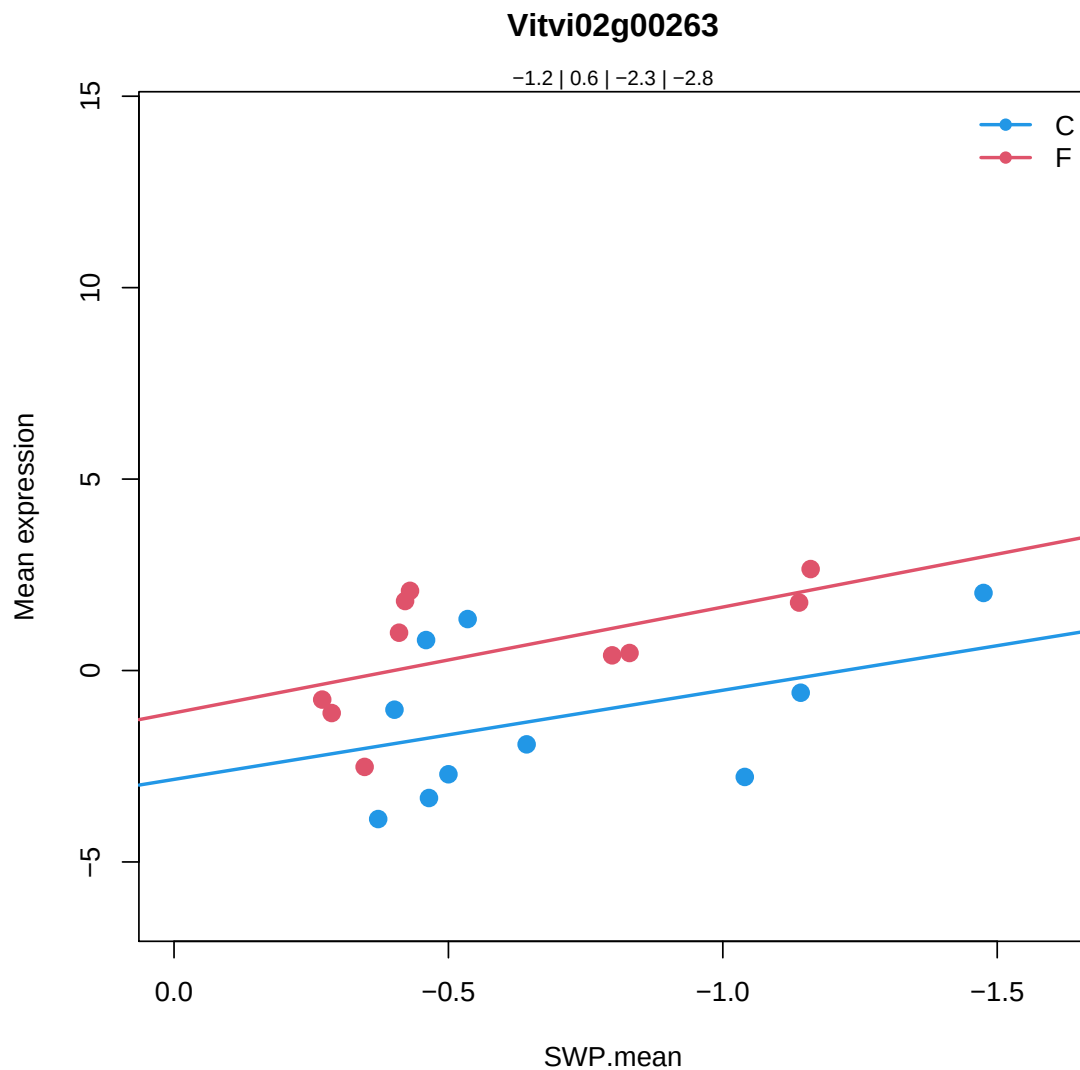
O-methyltransferase 1 |

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	



8.4.67 Vitvi09g01282: Type5.0

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi09g01282

26.13

misc.acid and other phosphatases

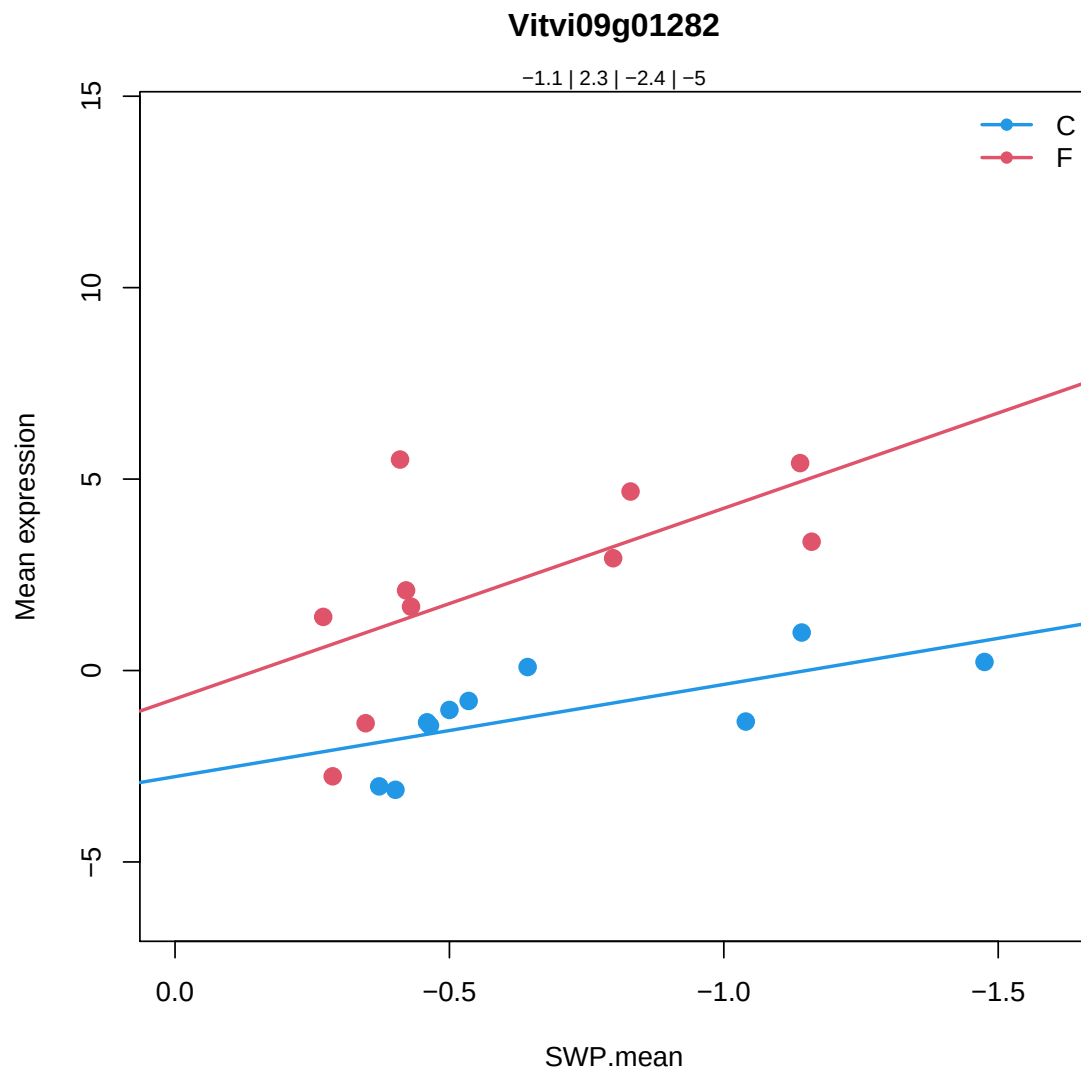
HAD superfamily%2C subfamily IIIB acid phosphatase |

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	



8.4.68 Vitvi07g01552: Type5.0 *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi07g01552

35.2

not assigned.unknown

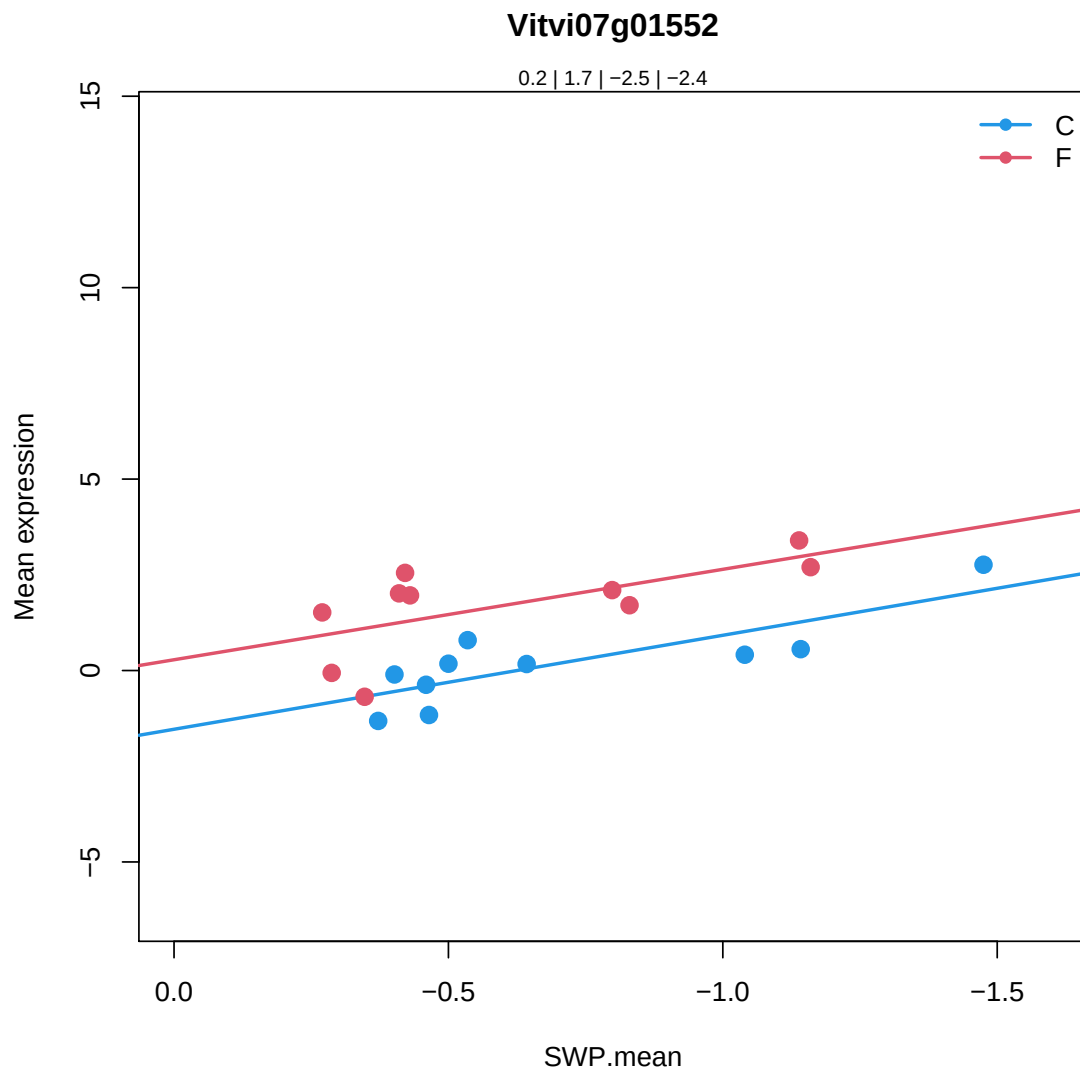
basic leucine-zipper 6 |

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	



8.4.69 Vitvi07g01120: Type5.0

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi07g01120

35.2

not assigned.unknown

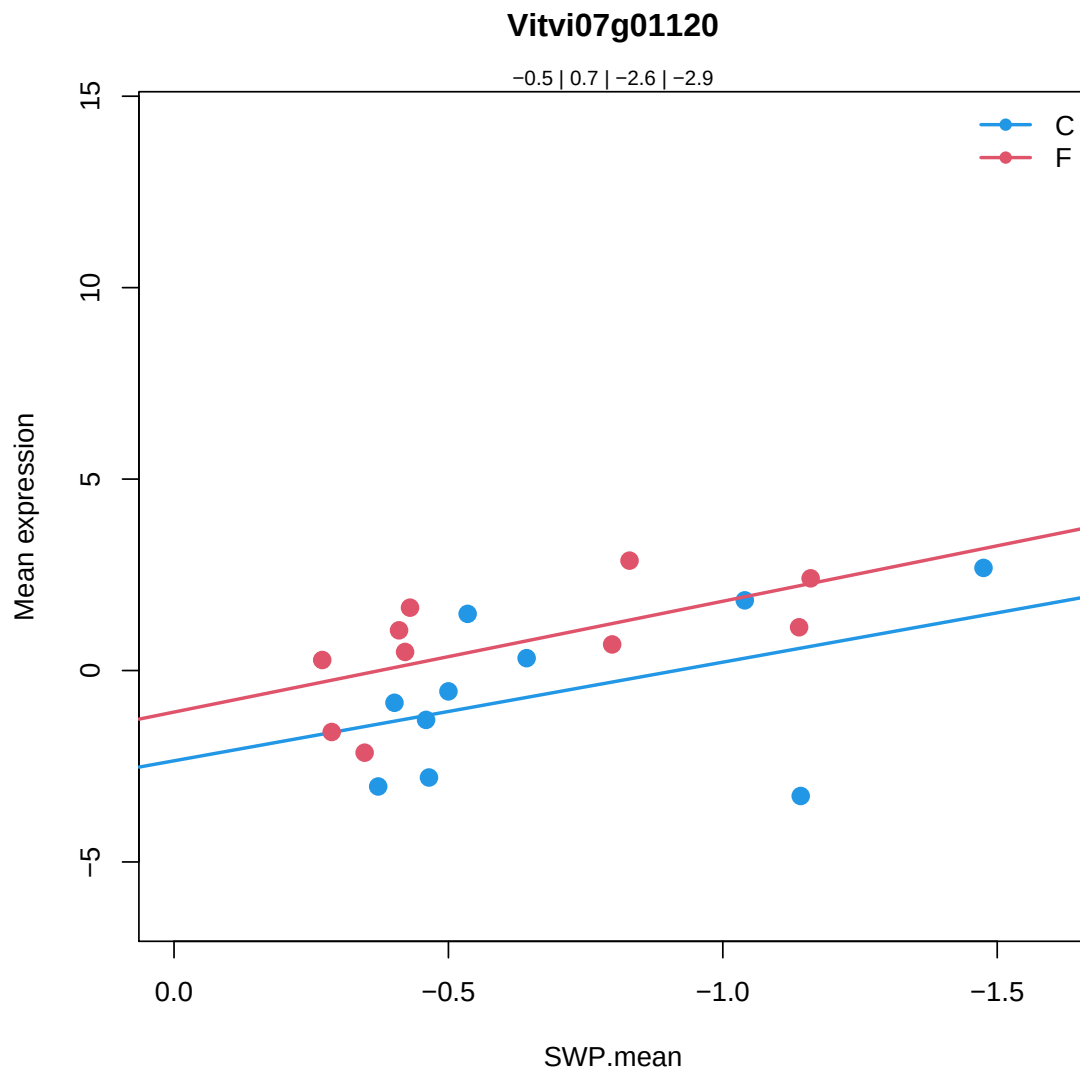
nuclear transport factor 2/RNA recognition motif protein |

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	



8.4.70 Vitvi05g00421: Type5.0 *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi05g00421

17.4.1

hormone metabolism.cytokinin.synthesis-degradation

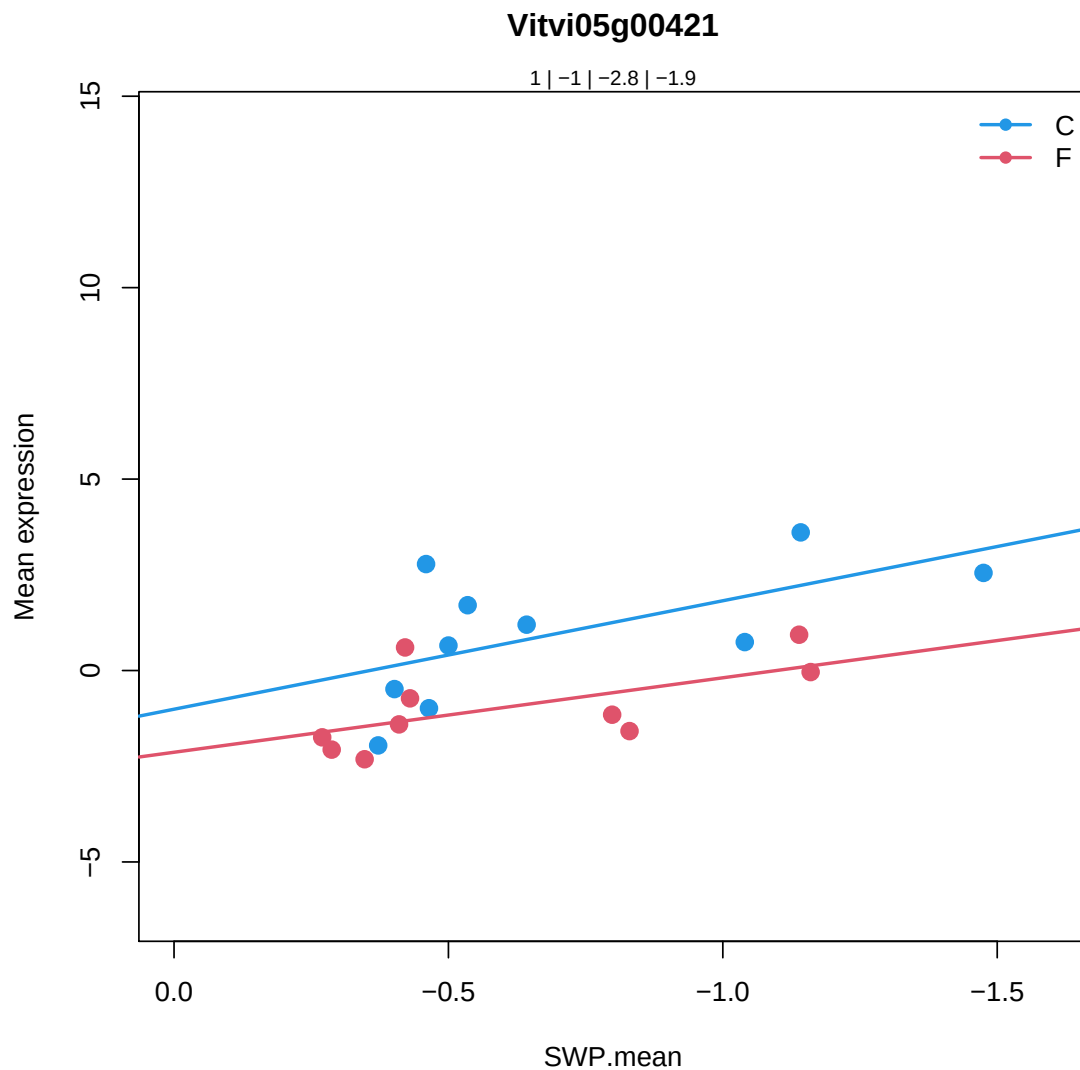
isopentenyltransferase 5 |

Chr5:6362389-6363381 REVERSE LENGTH=330 |

201606

Coefficients for Vitvi05g00421.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.9809172	0.01036541	*	0.01097607	*
SlopeC	-2.832505	0.008139059	**	0.2851324	
MeanF-MeanC	-1.931301	0.0007771899	***	0.01010745	*
SlopeF-SlopeC	0.8876307	0.5456677		0.9999488	



8.4.71 Vitvi01g01708: Type5.0 *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi01g01708

20.2.1

stress.abiotic.heat

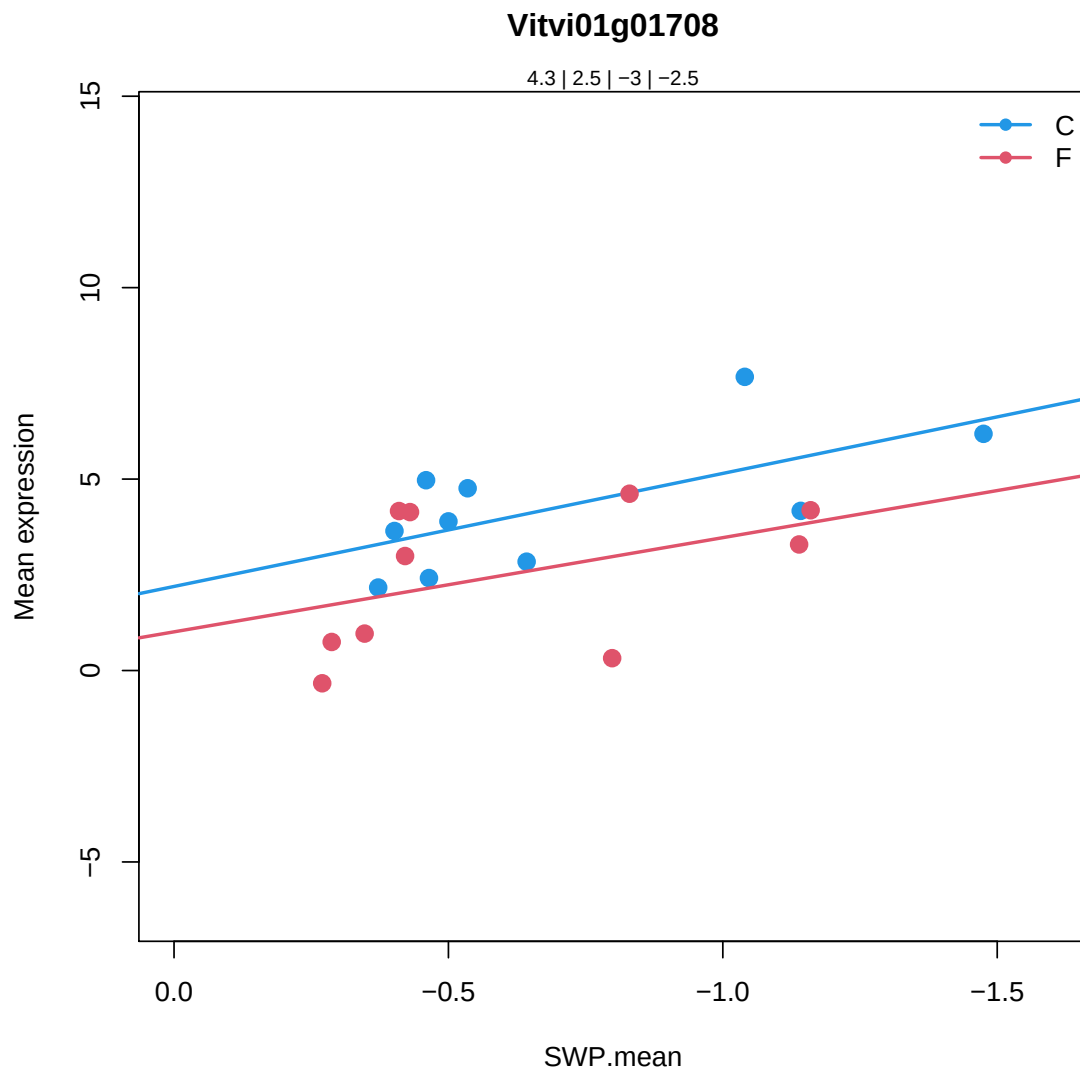
BCL-2-associated athanogene 5 |

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	



8.4.72 Vitvi09g00045: Type5.0 *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi09g00045

20.2.1

stress.abiotic.heat

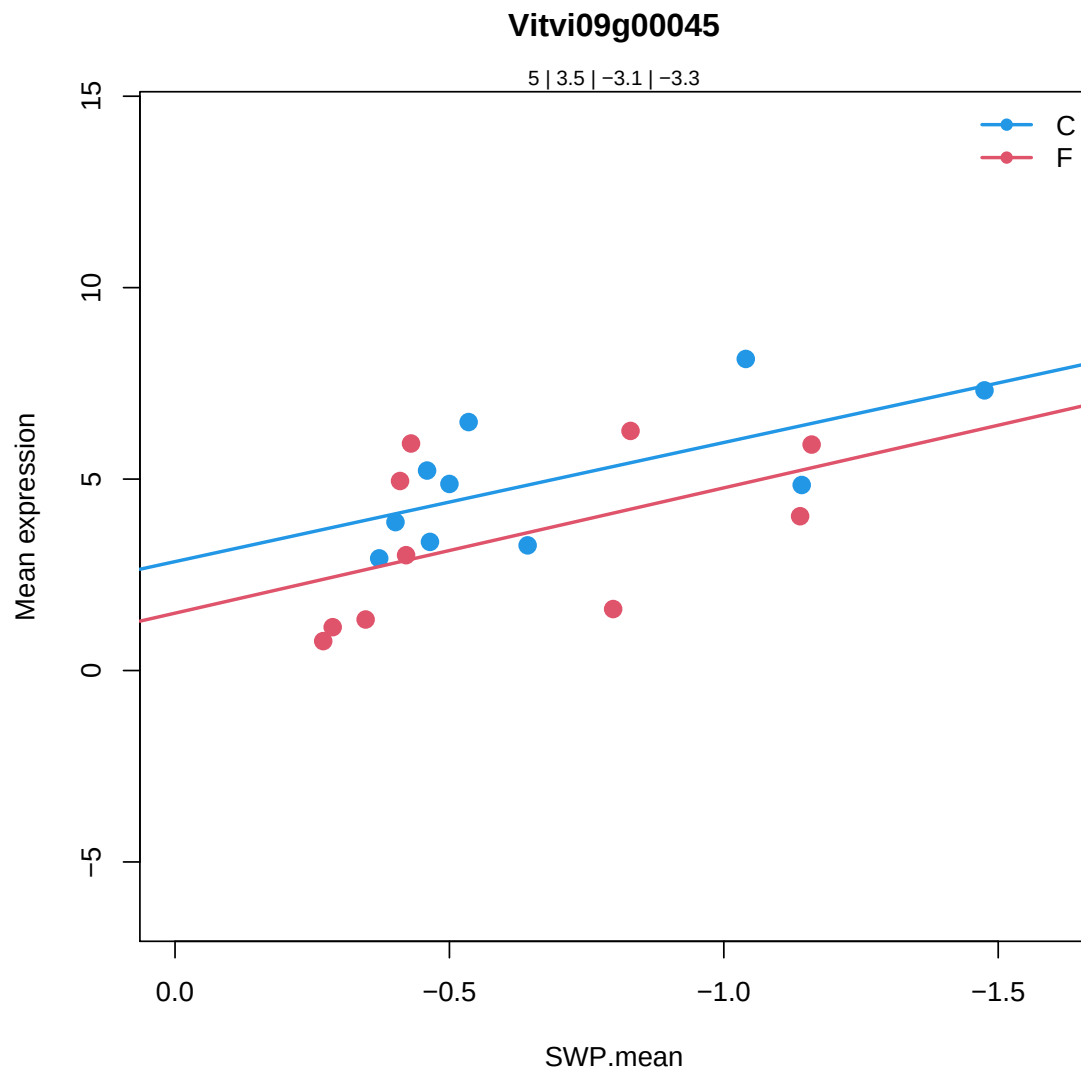
HSP20-like chaperones superfamily protein |

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	



8.4.73 Vitvi19g02145: Type5.0 *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi19g02145

26.9

misc.glutathione S transferases

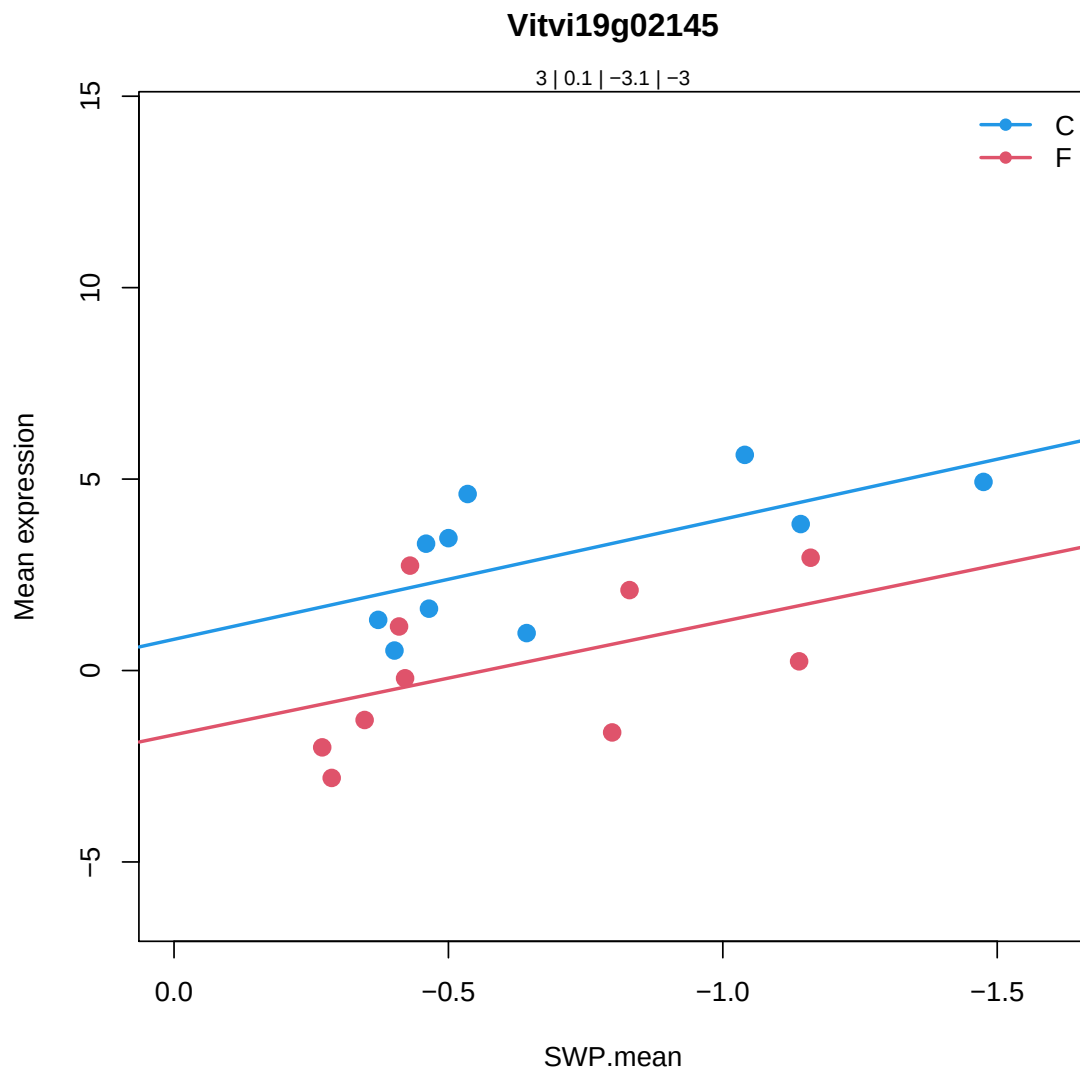
glutathione S-transferase TAU 25 |

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	



8.4.74 Vitvi11g01516: Type5.0 *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi11g01516

29.5.5

protein.degradation.serine protease

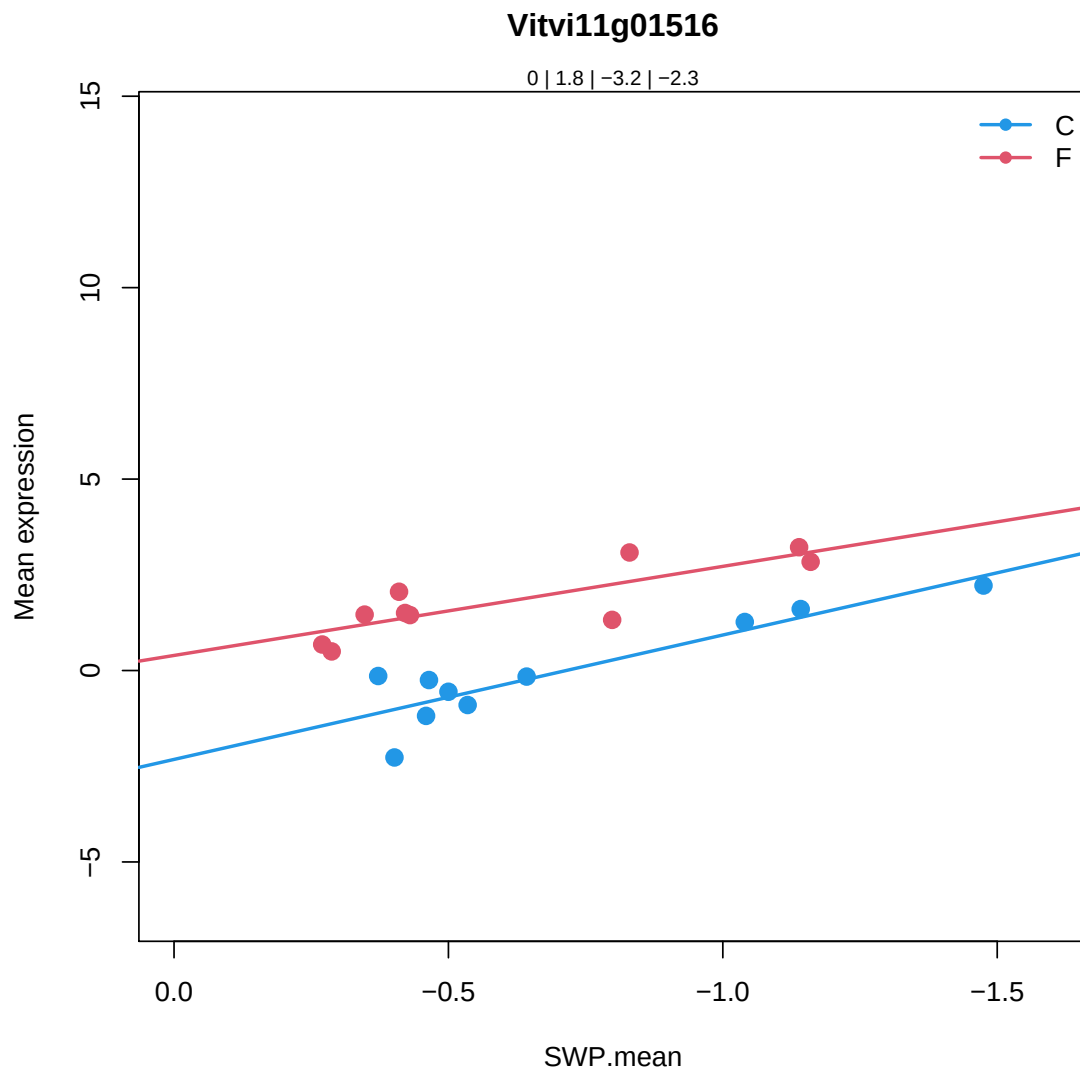
serine carboxypeptidase-like 29 |

Chr4:15003474-15006017 FORWARD LENGTH=479 |

201606

Coefficients for Vitvi11g01516.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.03709564	0.840428		0.8435271	
SlopeC	-3.24962	2.102715e-06	***	0.01365018	*
MeanF-MeanC	1.848123	3.942282e-07	***	1.417176e-05	***
SlopeF-SlopeC	0.9230391	0.2339817		0.9999488	



8.4.75 Vitvi05g00857: Type5.0 *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi05g00857

34.99

transport.misc

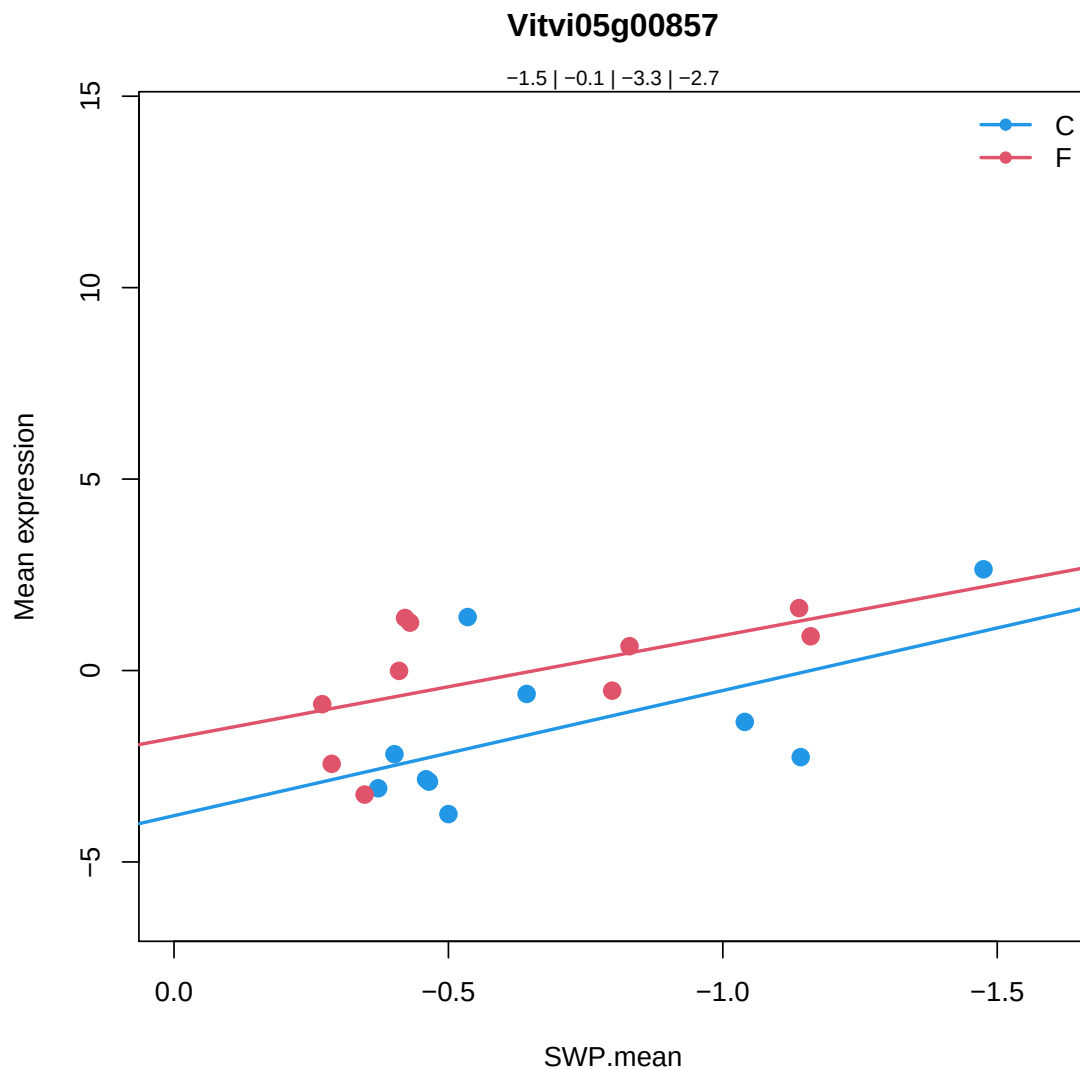
AWPM-19-like family protein |

Chr1:1245070-1245888 FORWARD LENGTH=186 |

201606

Coefficients for Vitvi05g00857.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.493231	0.003146049	**	0.003369788	**
SlopeC	-3.268603	0.01595194	*	0.3483374	
MeanF-MeanC	1.361971	0.04355944	*	0.2186479	
SlopeF-SlopeC	0.5892431	0.754362		0.9999488	



8.4.76 Vitvi13g02018: Type5.0 *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi13g02018

20.2.1

stress.abiotic.heat

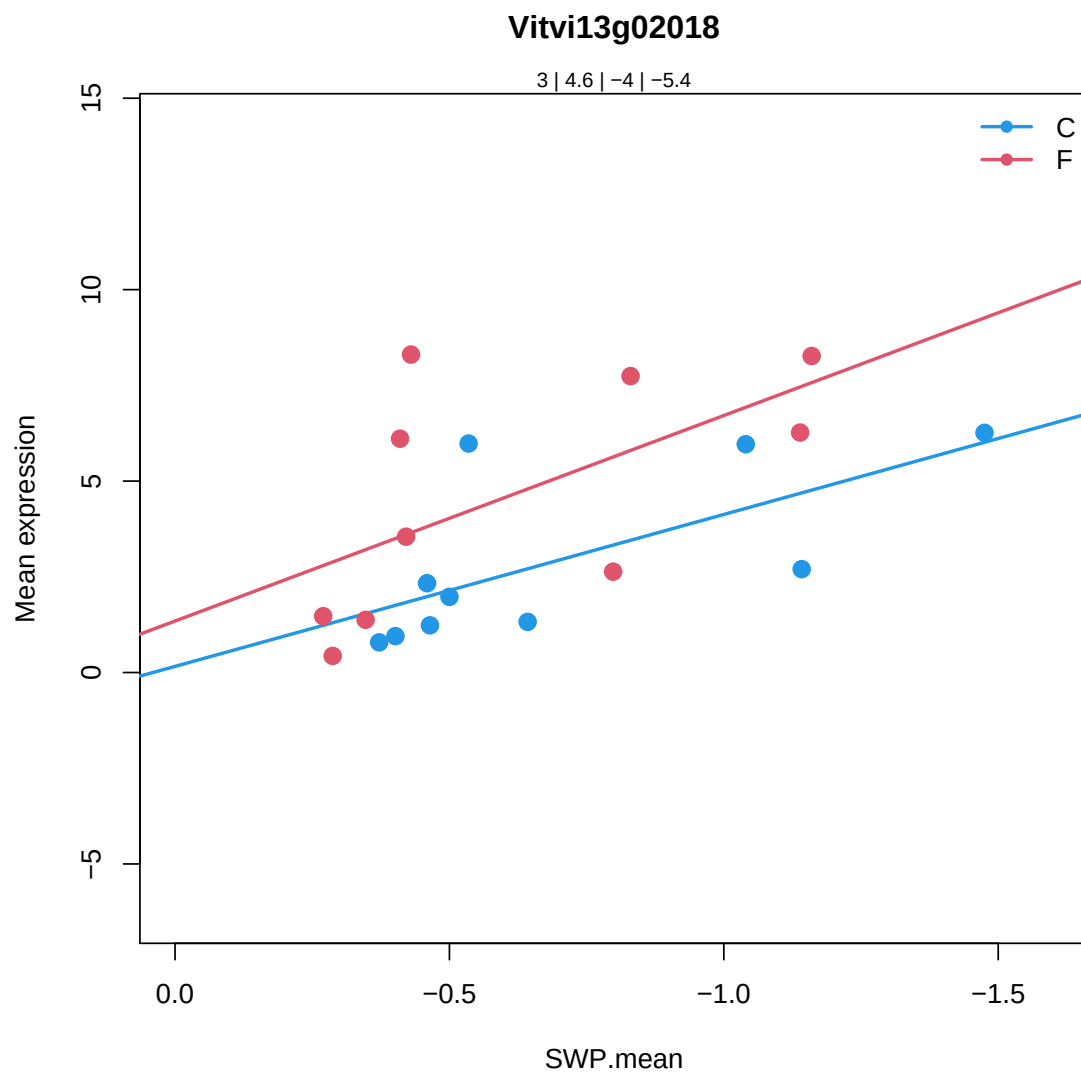
heat shock protein 18.2 |

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	



8.4.77 Vitvi07g02242: Type5.0 *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi07g02242

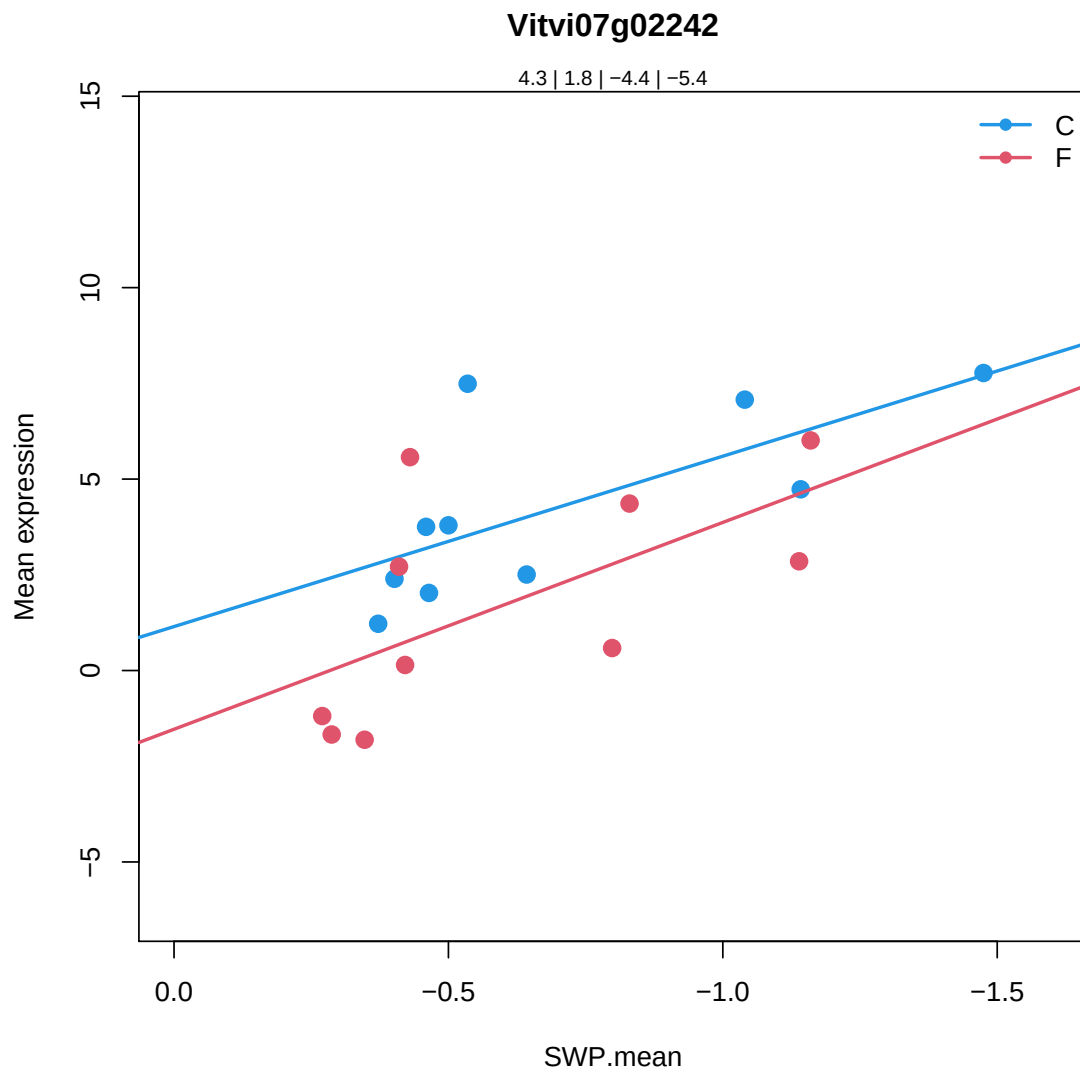
3.1.1.1

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	



8.4.78 Vitvi09g00599: Type5.0 *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi09g00599

20.2.1

stress.abiotic.heat

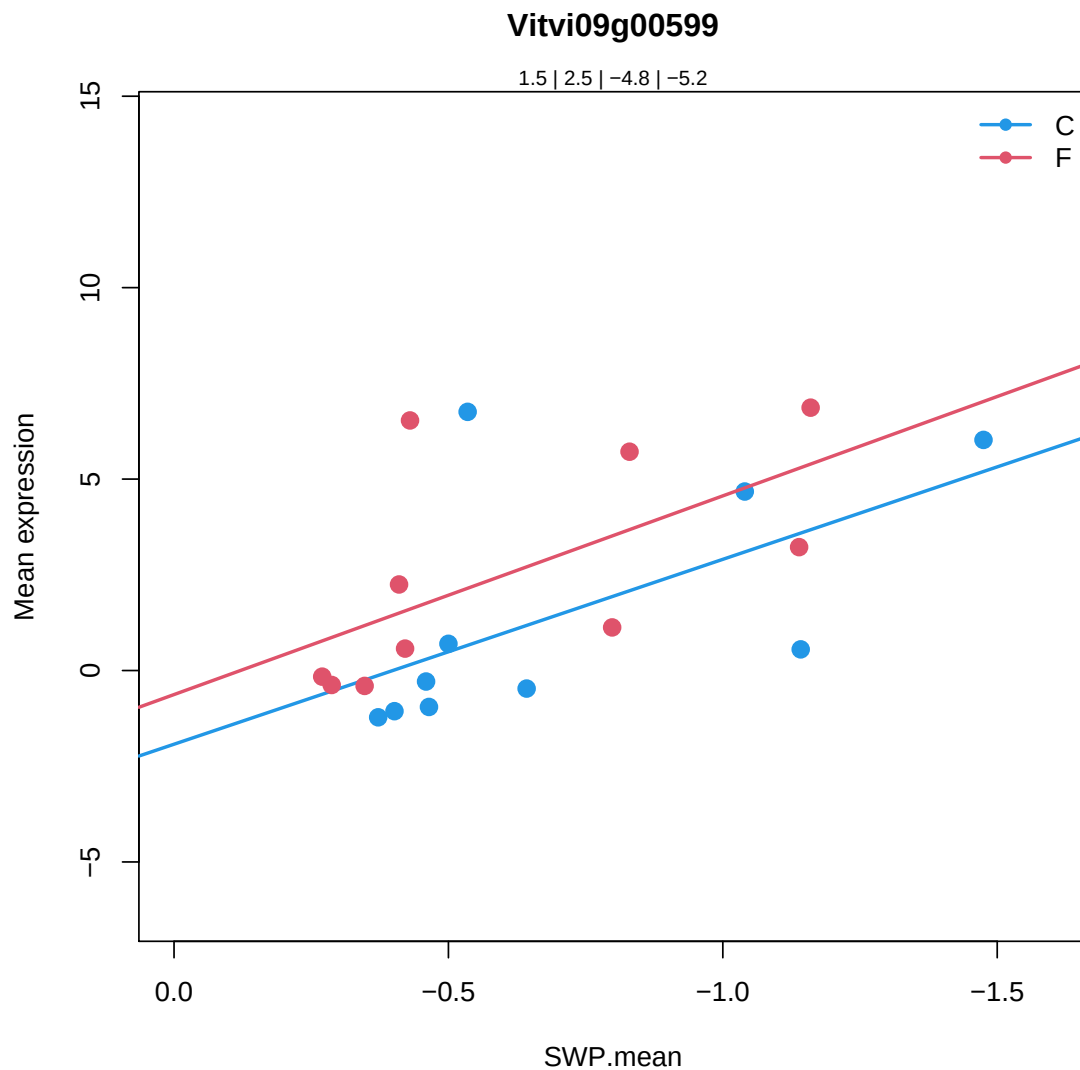
HSP20-like chaperones superfamily protein |

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	



8.4.79 Vitvi16g01103: Type5.0 *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi16g01103

20.2.1

stress.abiotic.heat

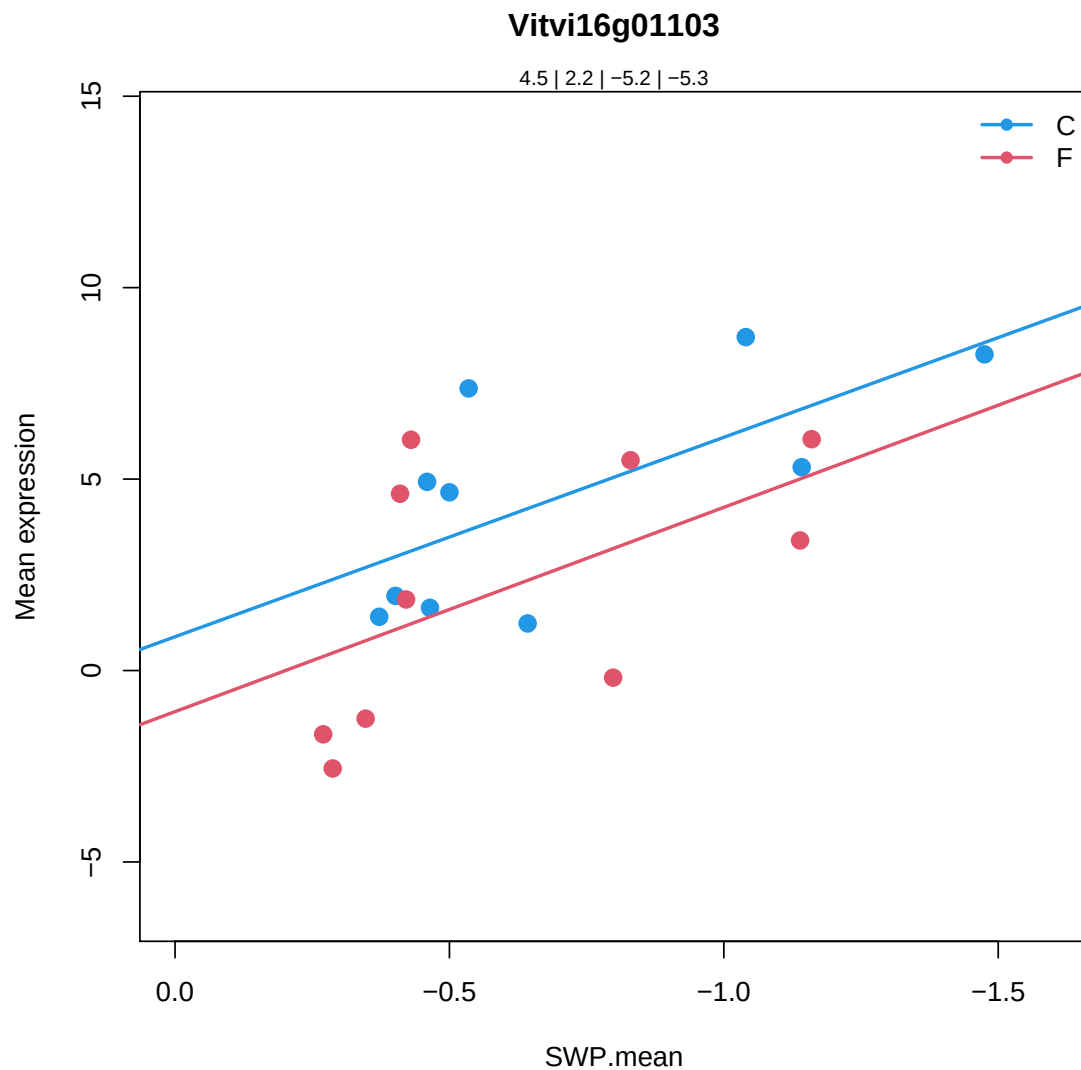
heat shock-like protein |

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	



8.5 Type6.C

8.5.1 Vitvi18g03084: Type6.C *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi18g03084

30.2.25

signalling.receptor kinases.wall associated kinase

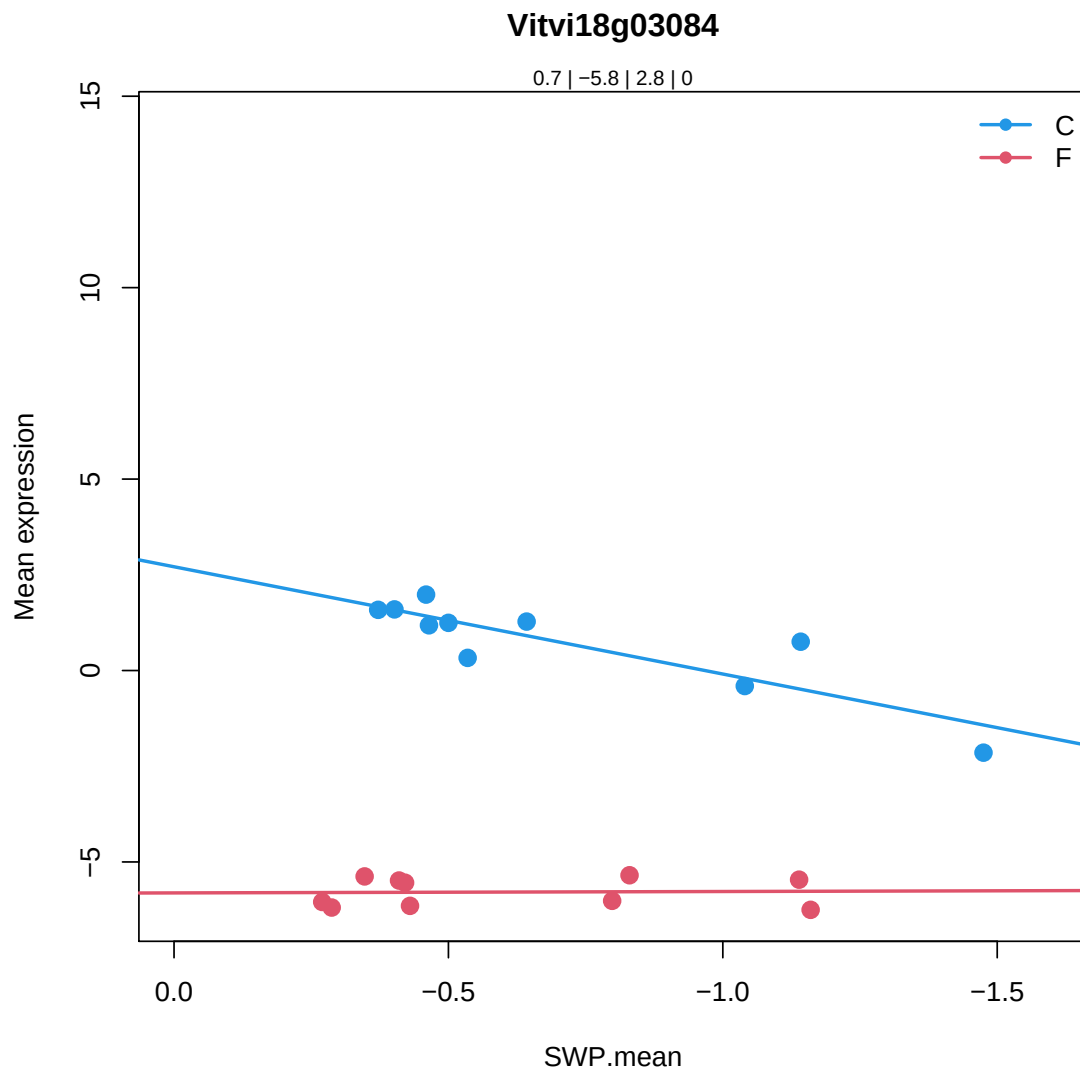
Protein kinase family protein |

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	



8.5.2 Vitvi16g02090: Type6.C *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi16g02090

35.2

not assigned.unknown

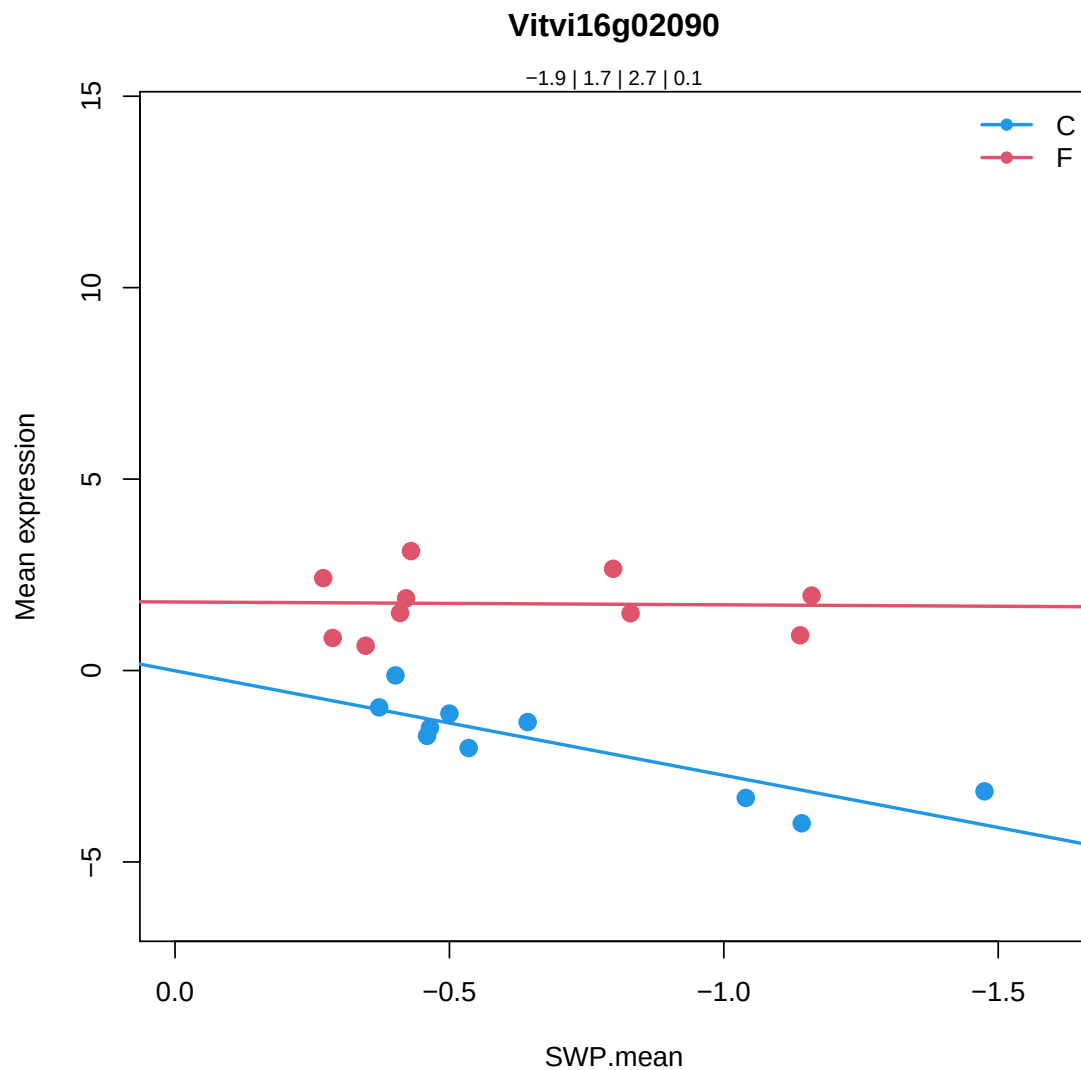
PR5-like receptor kinase |

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	



8.5.3 Vitvi16g02003: Type6.C *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi16g02003

35.2

not assigned.unknown

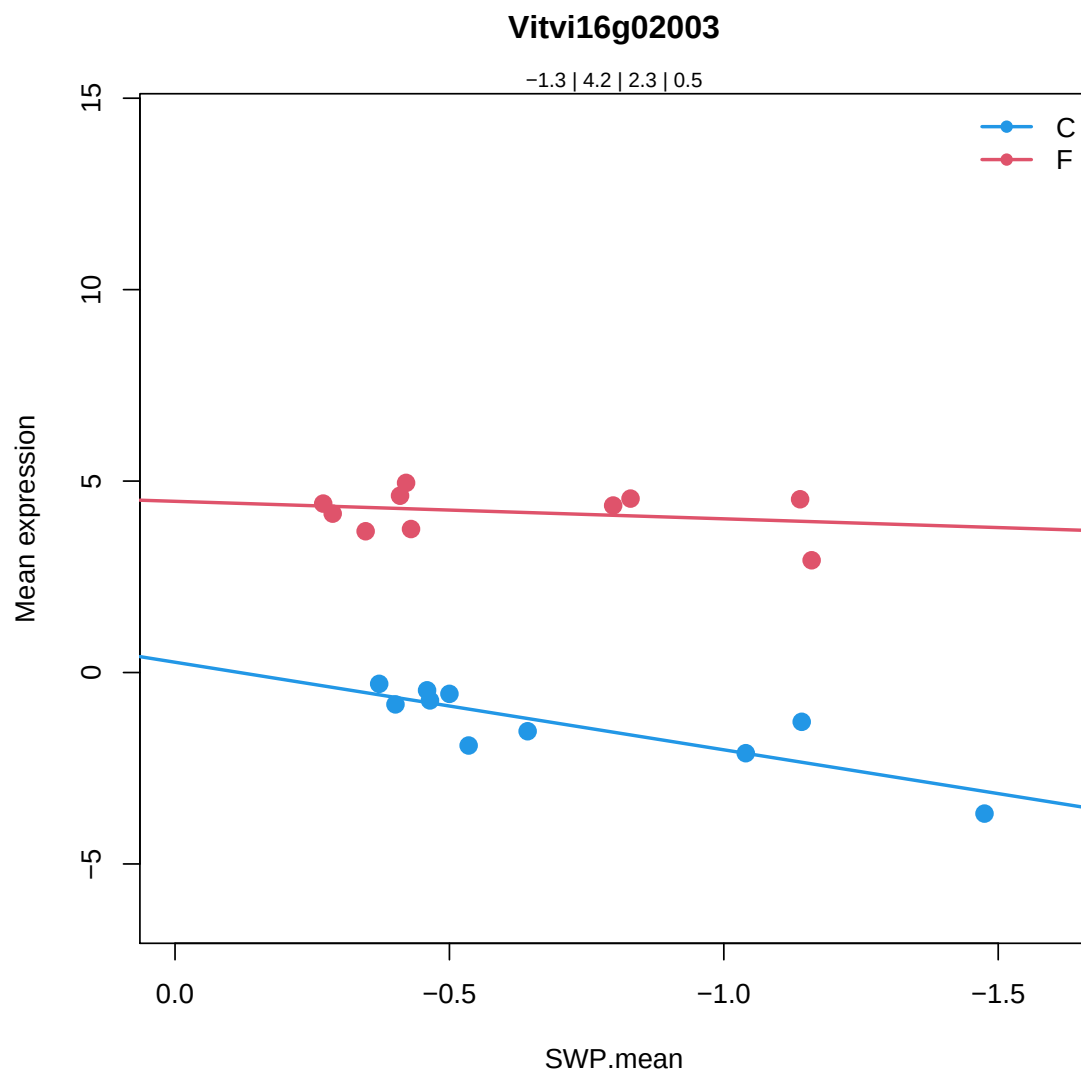
PR5-like receptor kinase |

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	



8.5.4 Vitvi16g01548: Type6.C *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi16g01548

35.2

not assigned.unknown

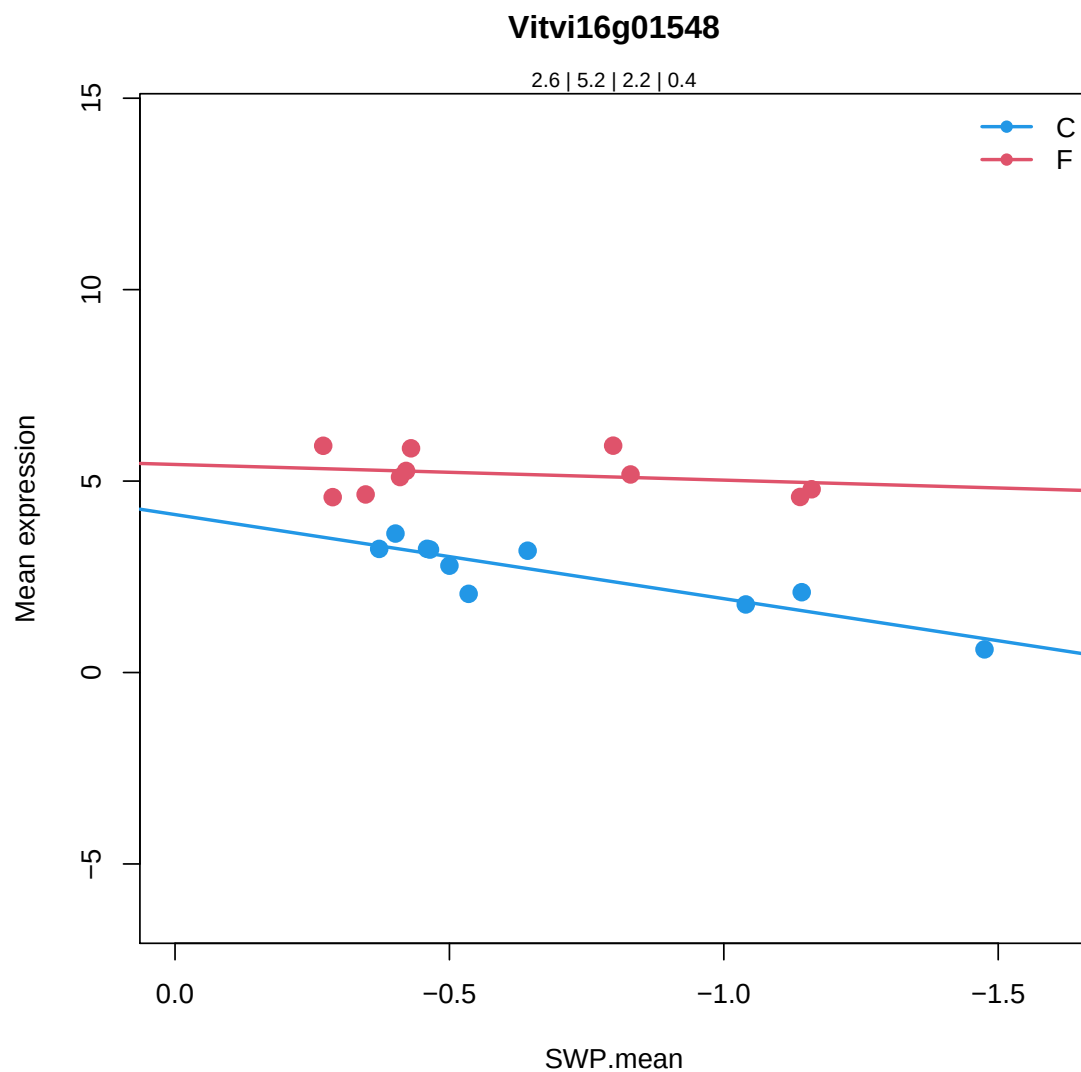
dihydroflavonol 4-reductase |

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	



8.5.5 Vitvi09g00681: Type6.C *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi09g00681

20.1.2

stress.biotic.receptors

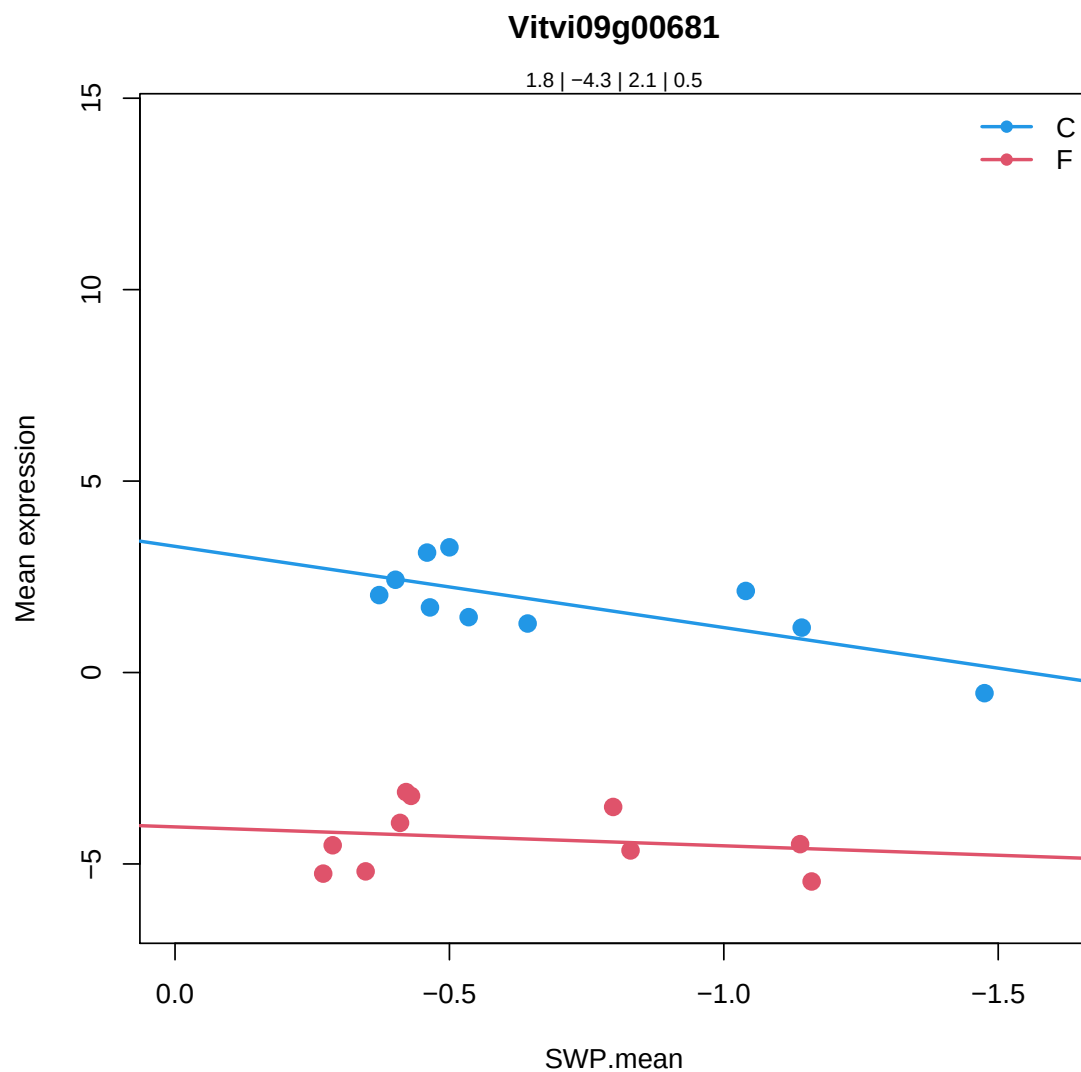
receptor like protein 1 |

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	



8.5.6 Vitvi12g00606: Type6.C *

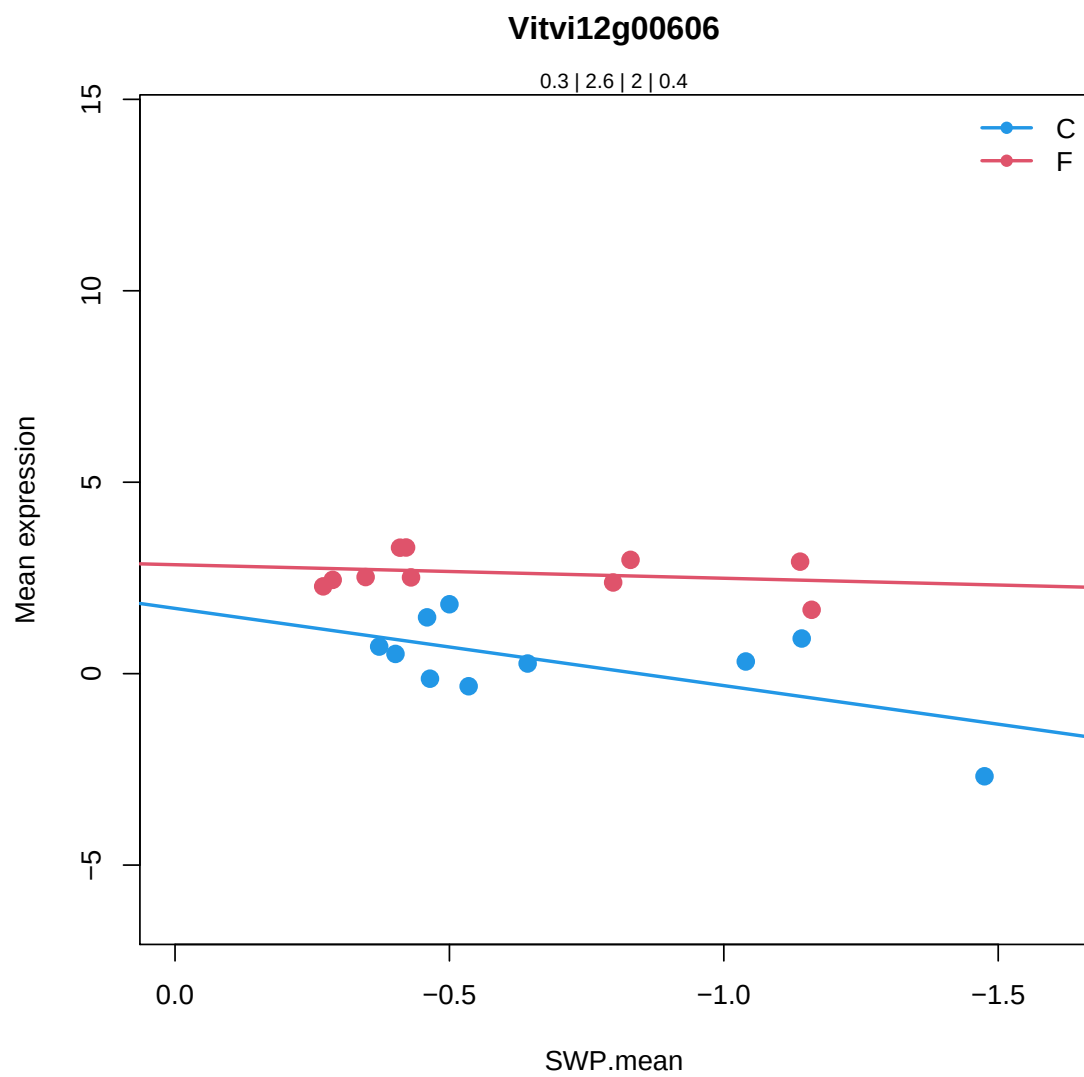
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
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	



8.5.7 Vitvi07g02459: Type6.C *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi07g02459

35.2

not assigned.unknown

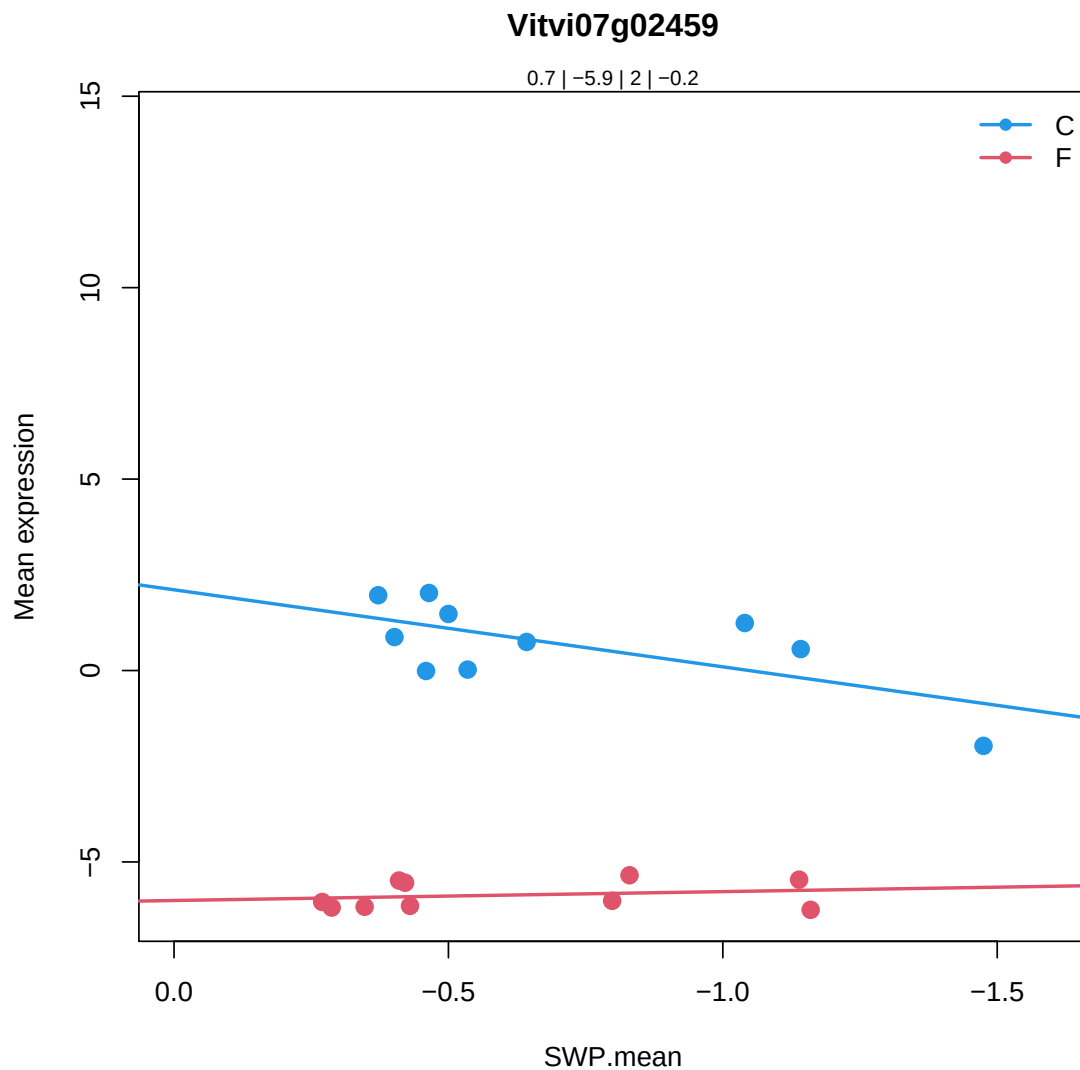
Ankyrin repeat family protein |

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	



8.5.8 Vitvi08g00723: Type6.C *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi08g00723

34.5

transport.ammonium

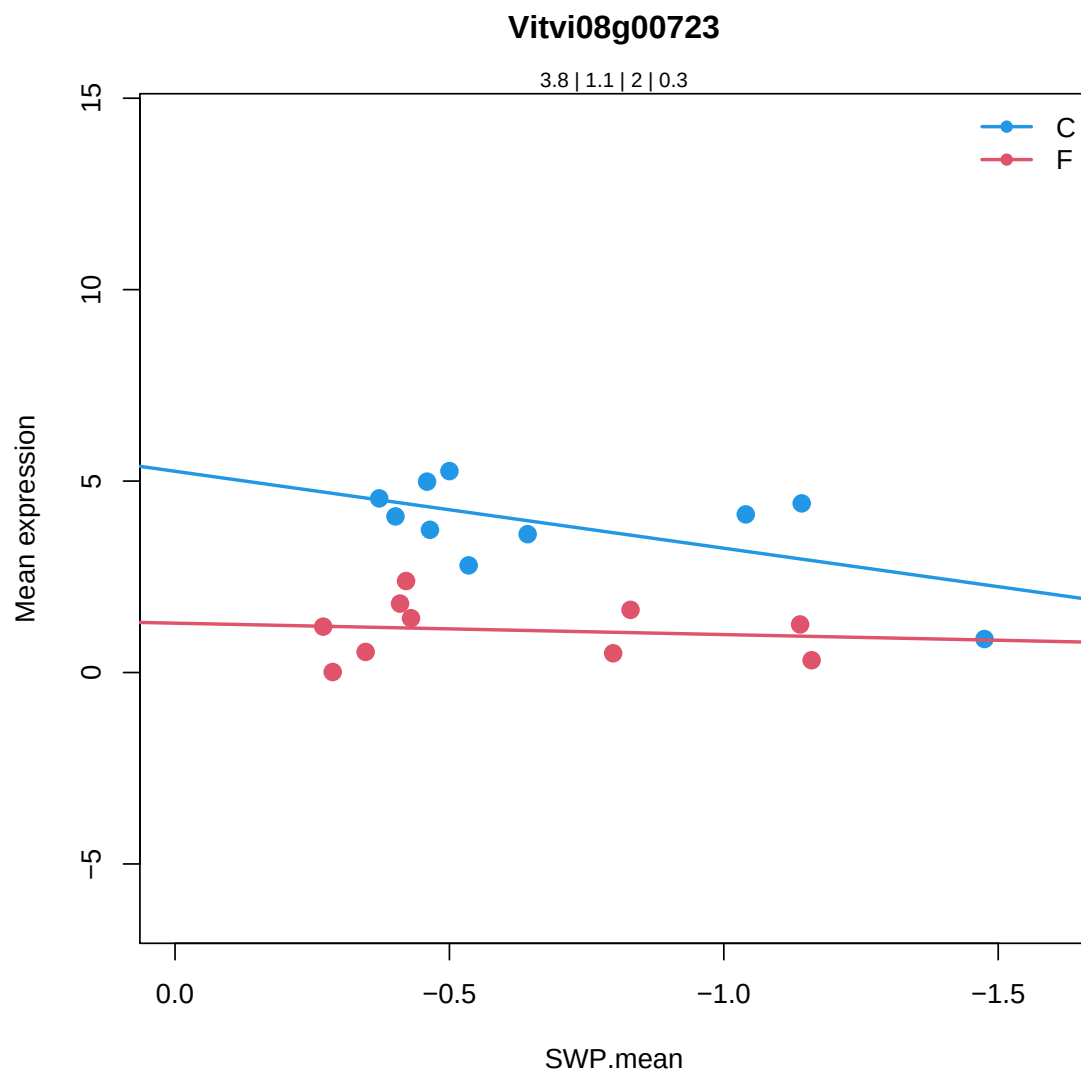
ammonium transporter 2 |

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	



8.5.9 Vitvi16g01010: Type6.C *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi16g01010

35.2

not assigned.unknown

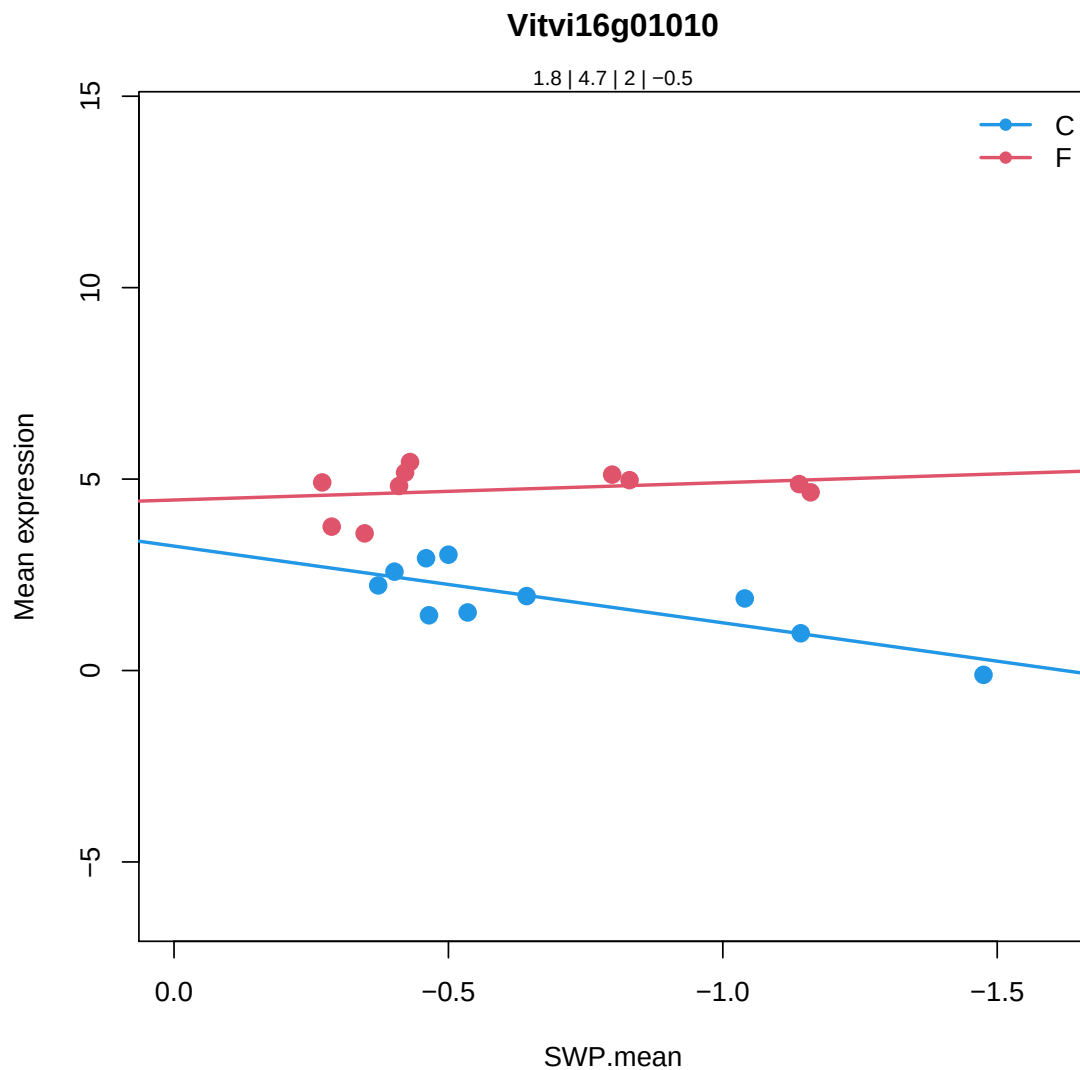
suppressor of npr1-1 constitutive 4 |

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	



8.5.10 Vitvi14g03027: Type6.C *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi14g03027

35.2

not assigned.unknown

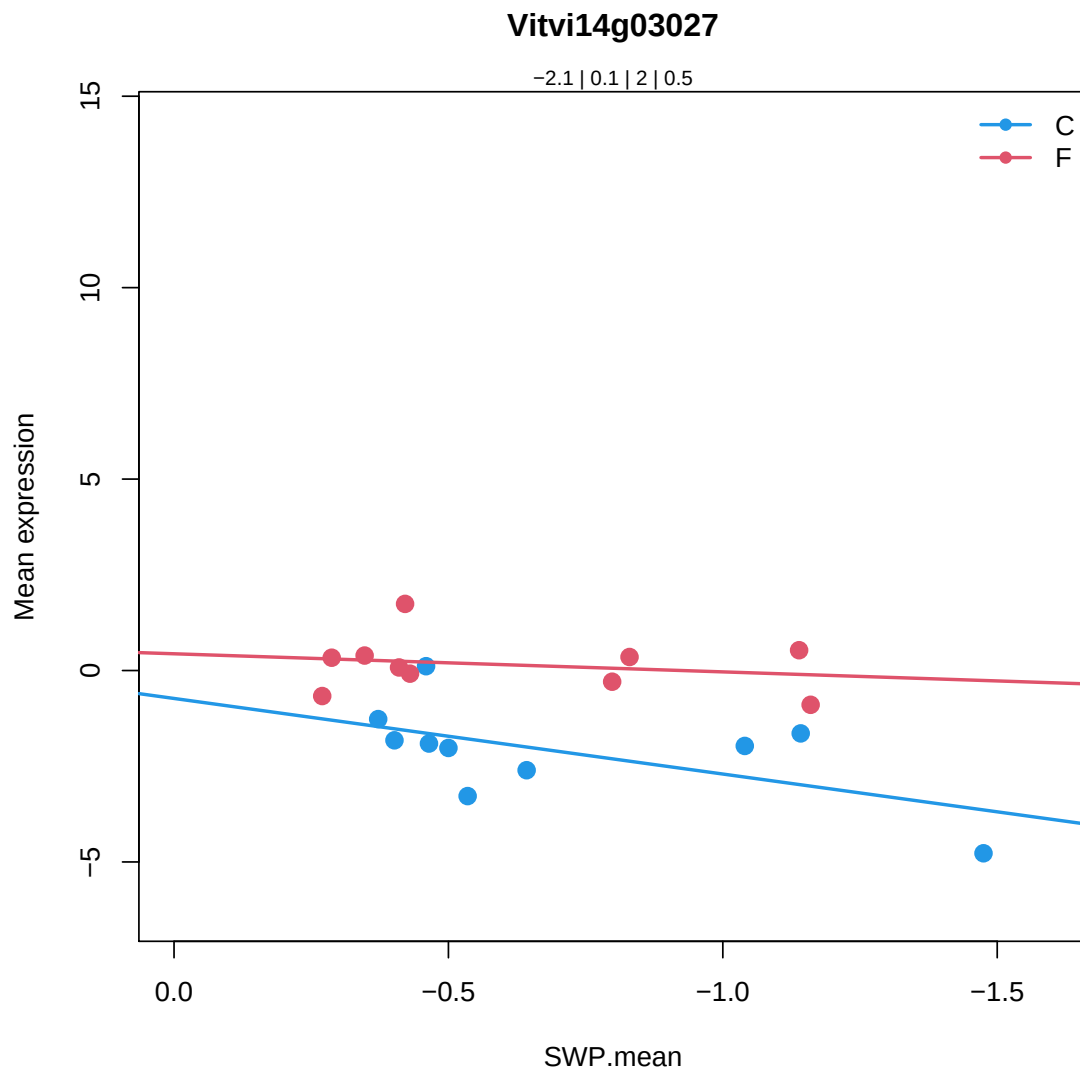
transmembrane protein |

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	



8.5.11 Vitvi12g02241: Type6.C *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi12g02241

26.6

misc.O-methyl transferases

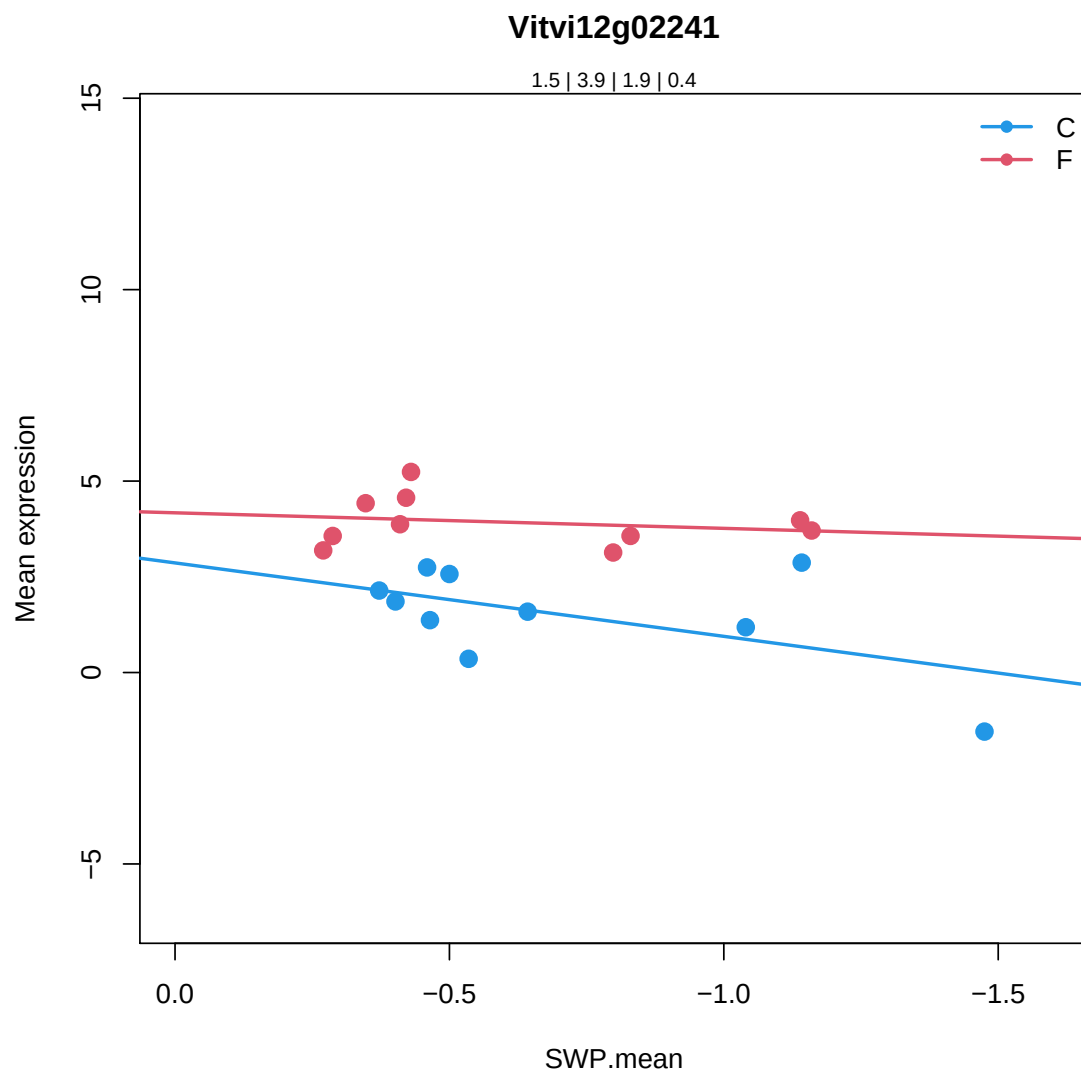
O-methyltransferase family protein |

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	



8.5.12 Vitvi16g01695: Type6.C *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi16g01695

35.2

not assigned.unknown

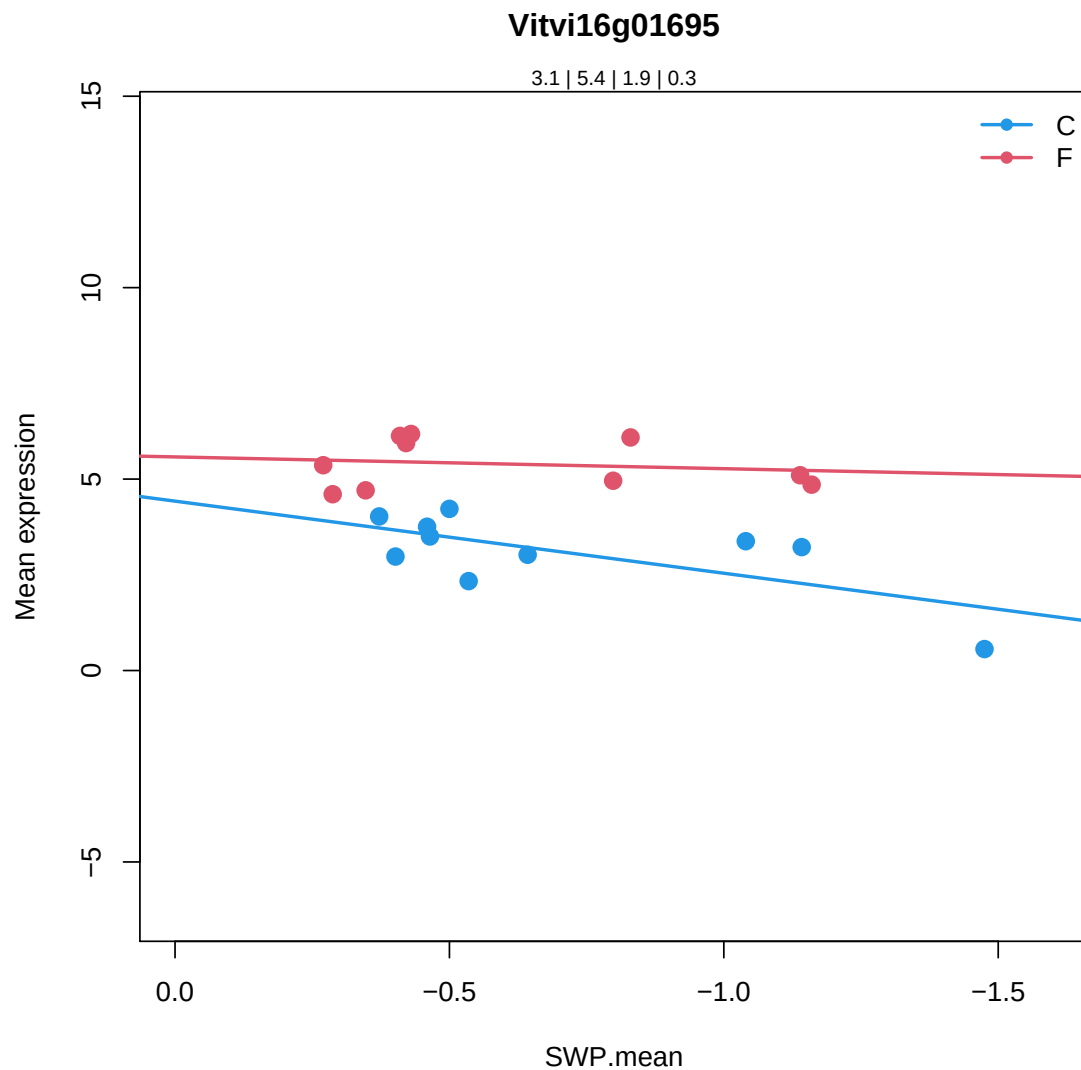
receptor like protein 6 |

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	

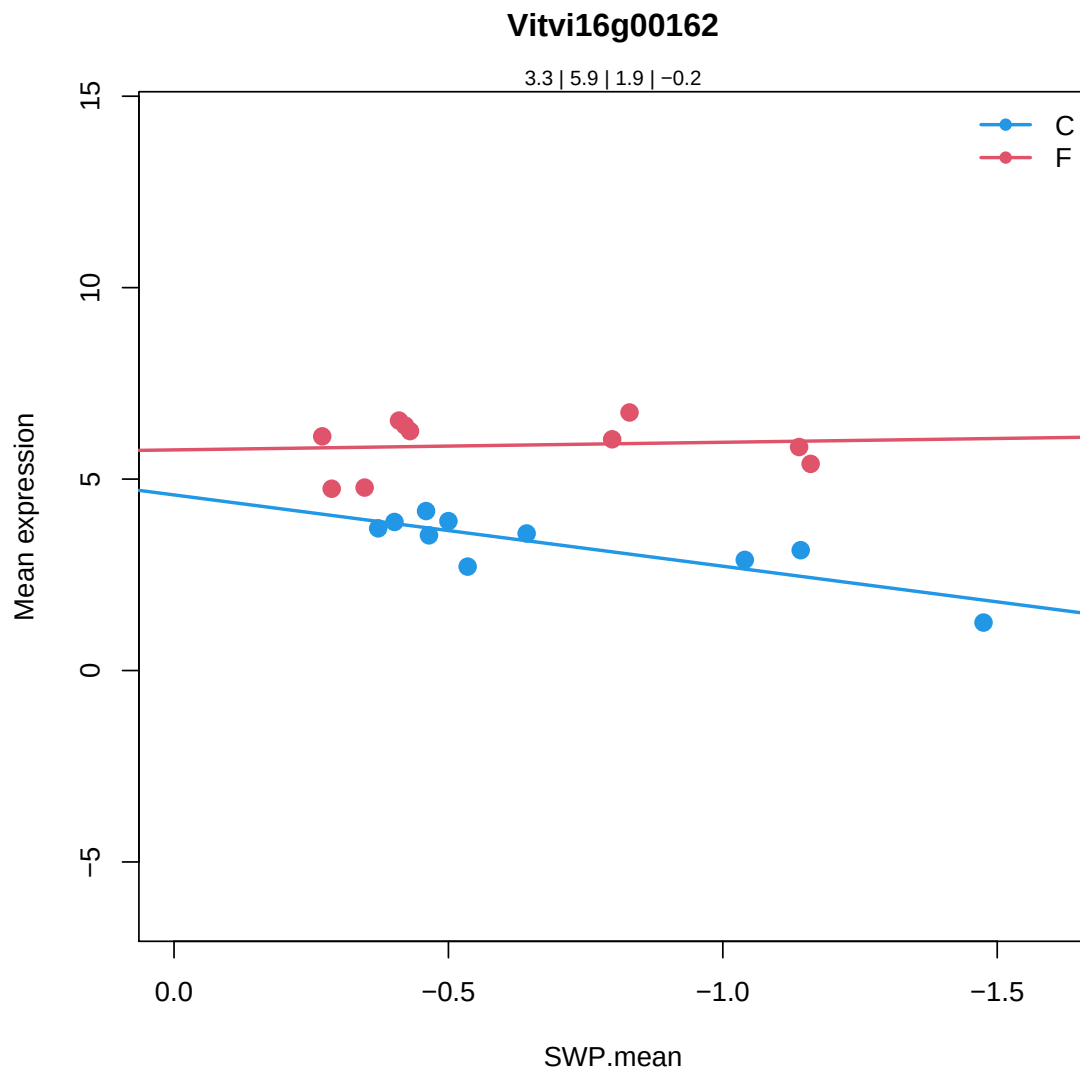


8.5.13 Vitvi16g00162: Type6.C *

```
> 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	



8.5.14 Vitvi07g01975: Type6.C *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi07g01975
```

```
35.2
```

```
not assigned.unknown
```

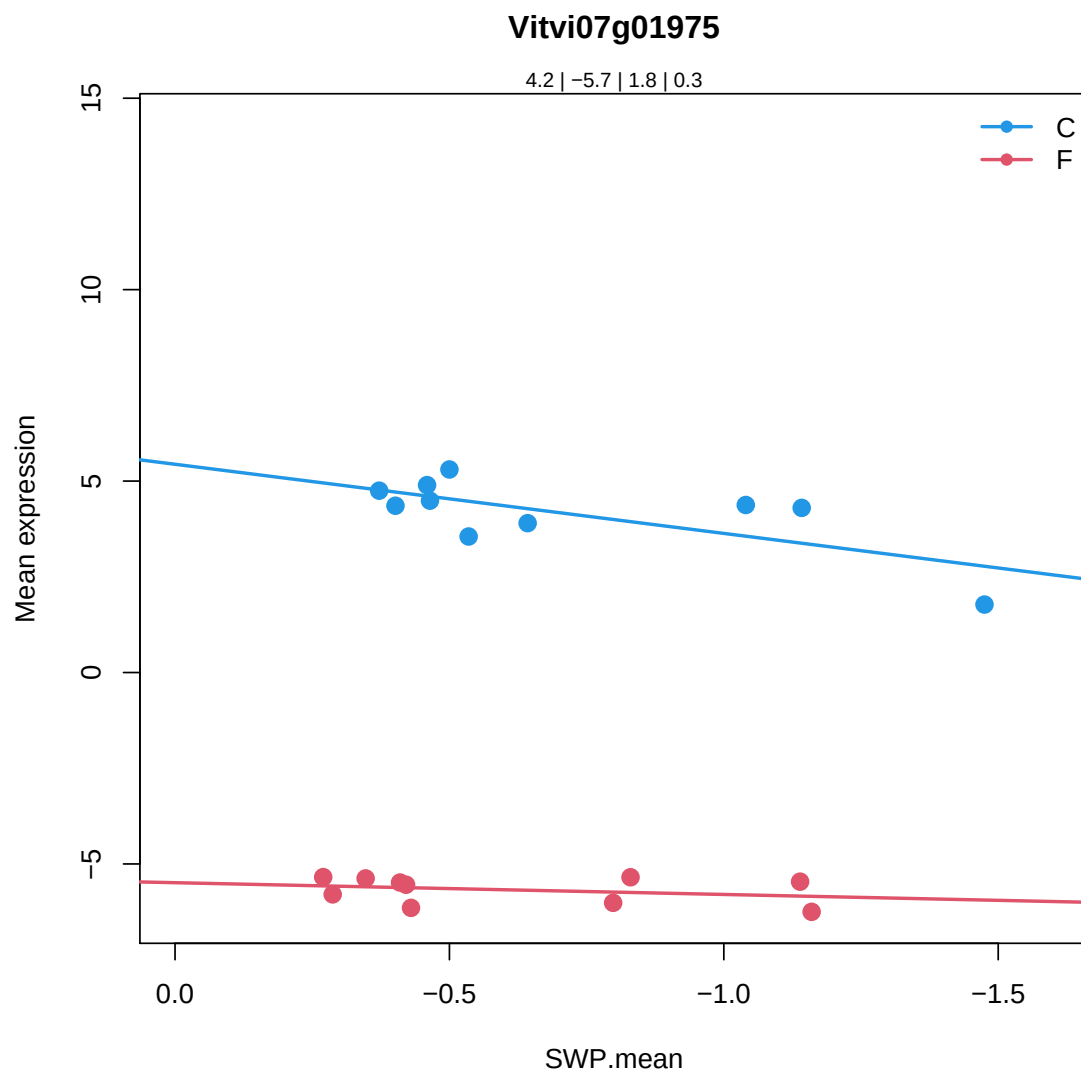
```
ammonium transporter 2 |
```

```
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	



8.5.15 Vitvi12g02434: Type6.C *

```
> 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

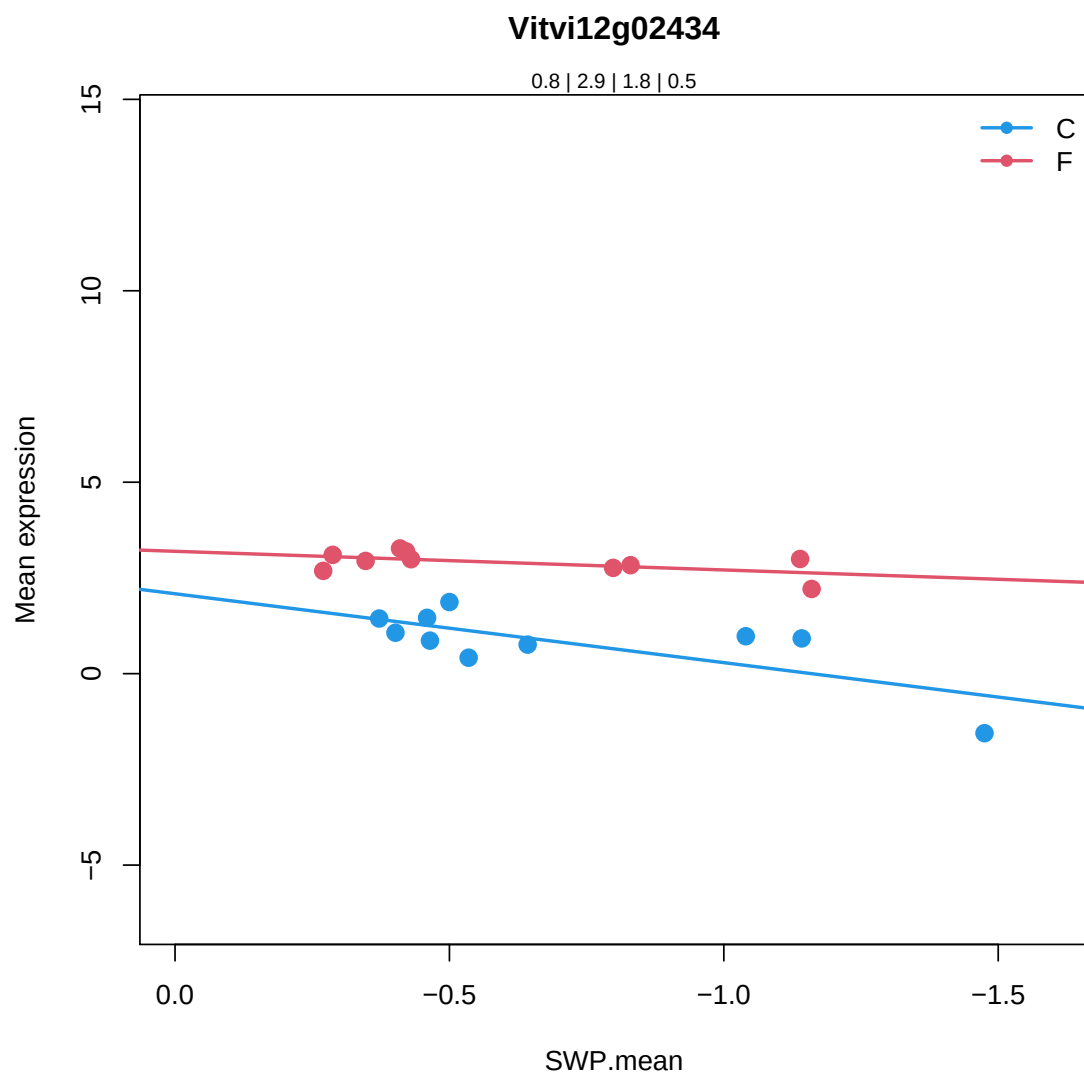
G-type lectin S-receptor-like Serine/Threonine-kinase |

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	



8.5.16 Vitvi17g01499: Type6.C *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi17g01499

26.2

misc.UDP glucosyl and glucoronyl transferases

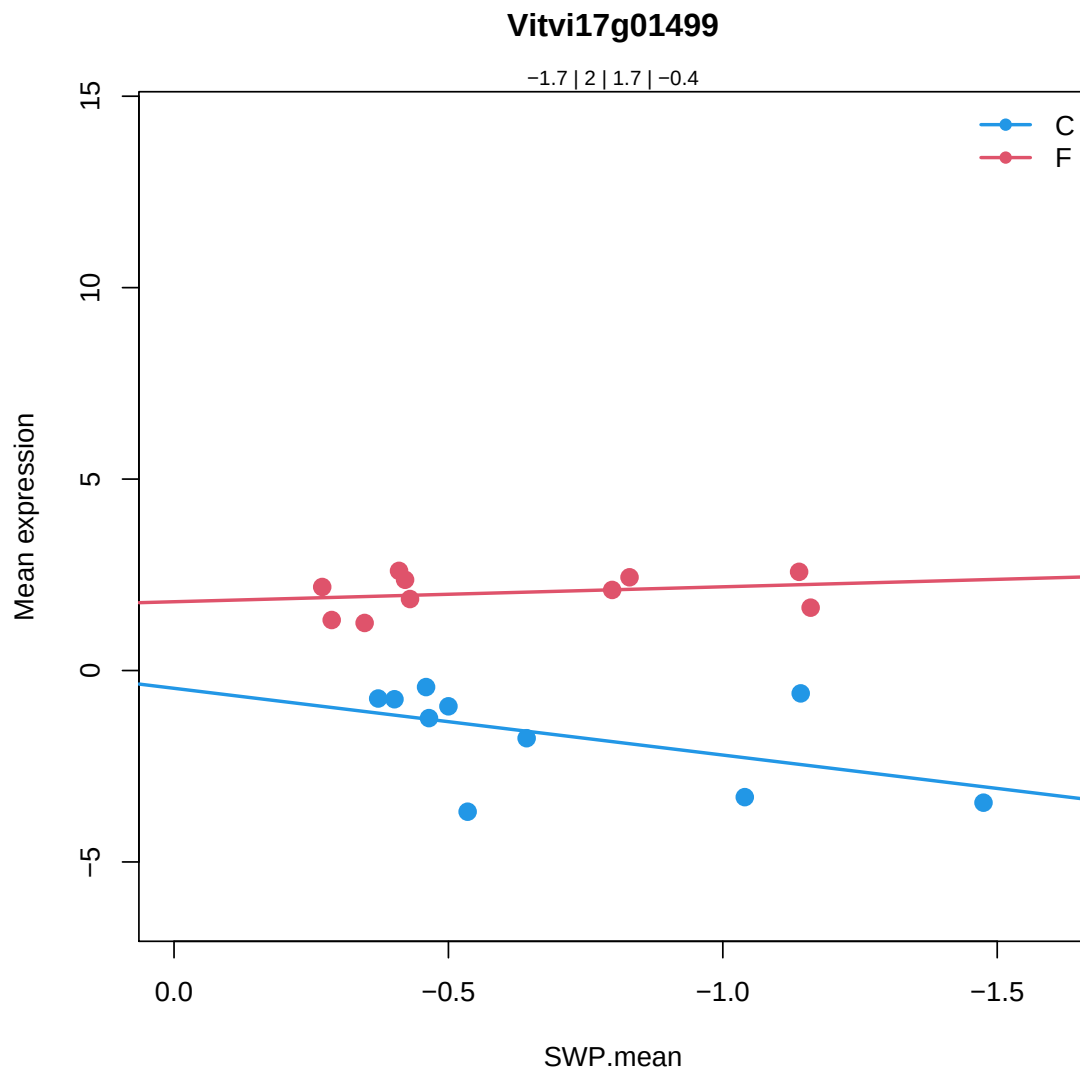
UDP-Glycosyltransferase superfamily protein |

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	



8.5.17 Vitvi09g00253: Type6.C *

```
> 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

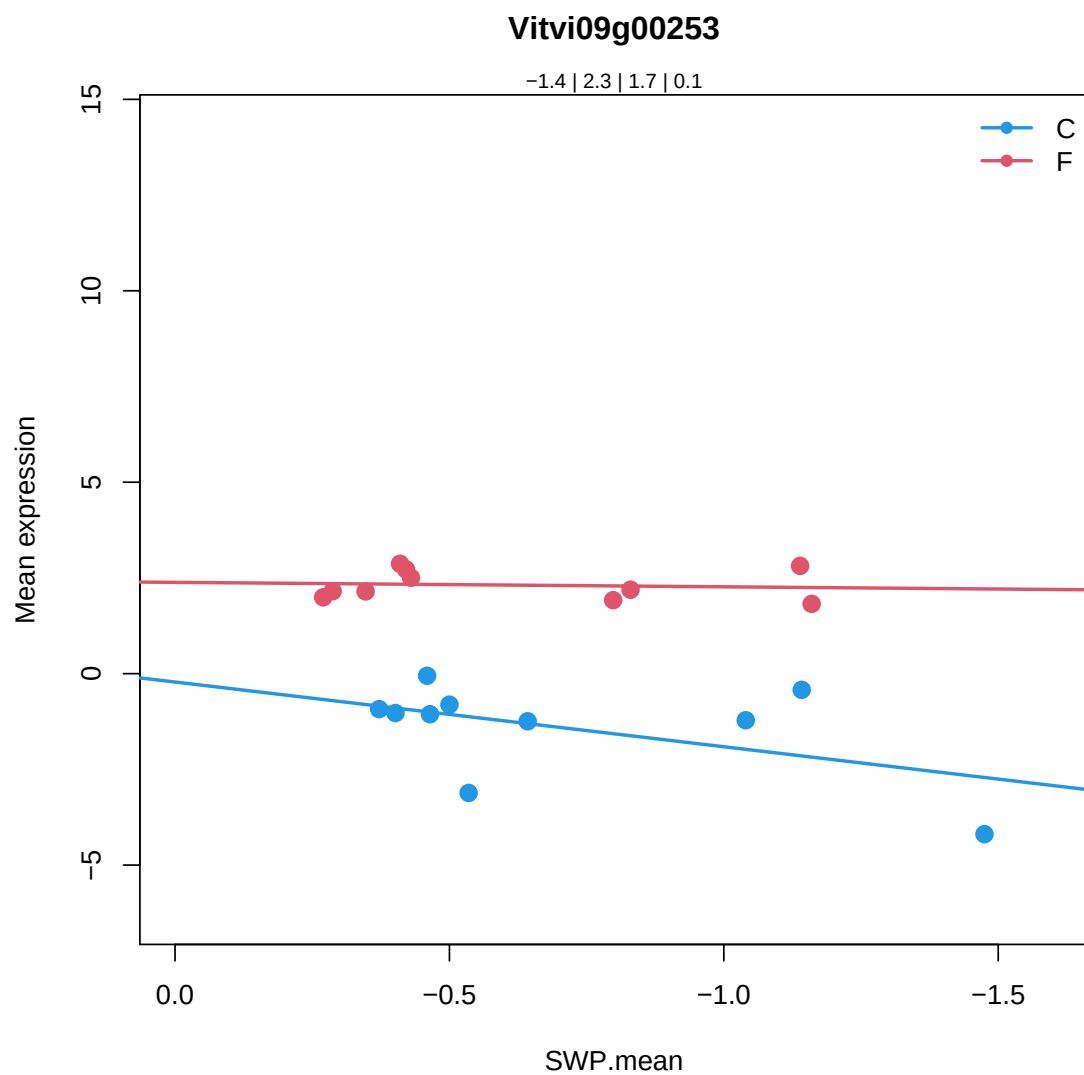
Leucine-rich repeat transmembrane protein kinase protein |

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	



8.5.18 Vitvi07g02479: Type6.C *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi07g02479

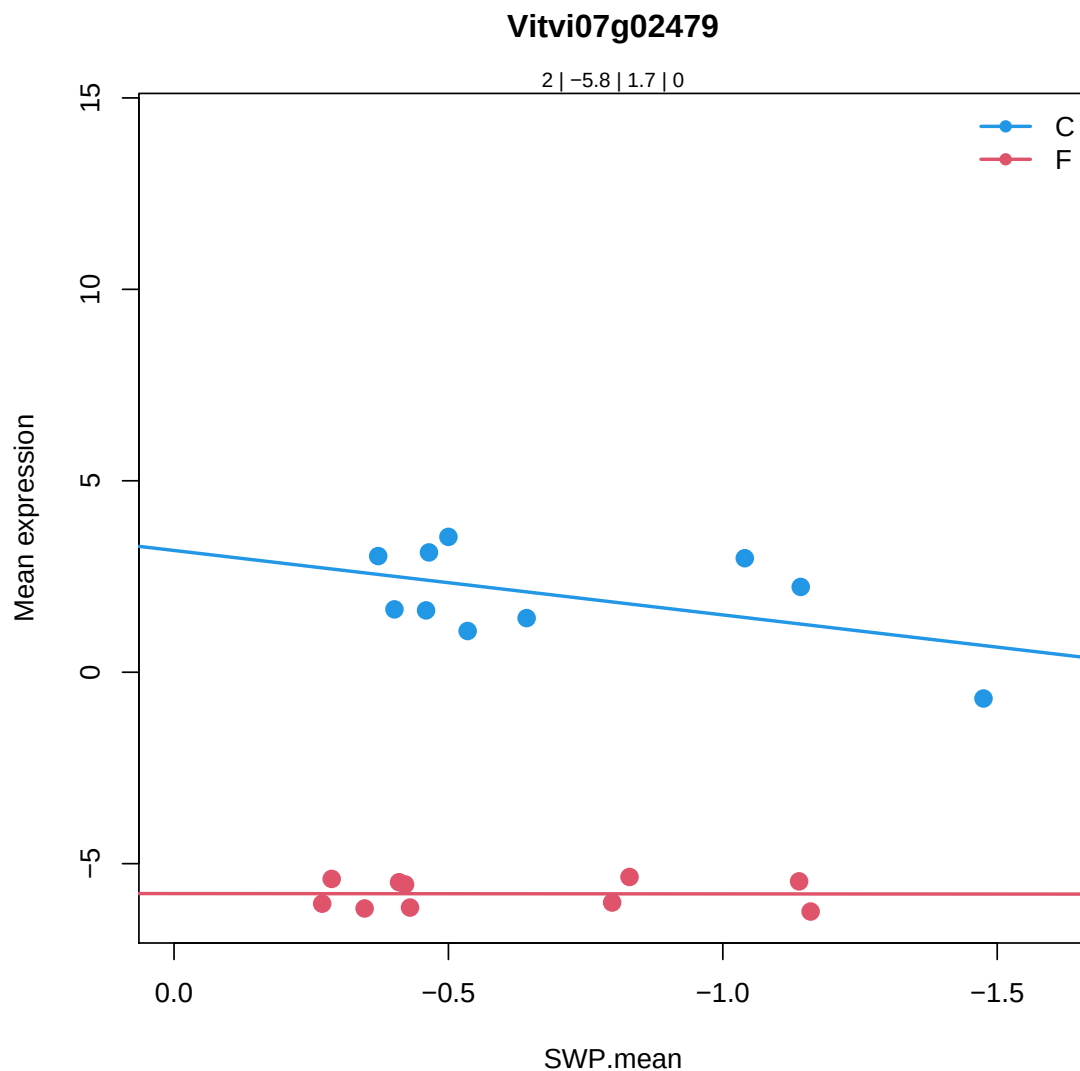
35.2

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	



8.5.19 Vitvi07g03003: Type6.C *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi07g03003

31.1

cell.organisation

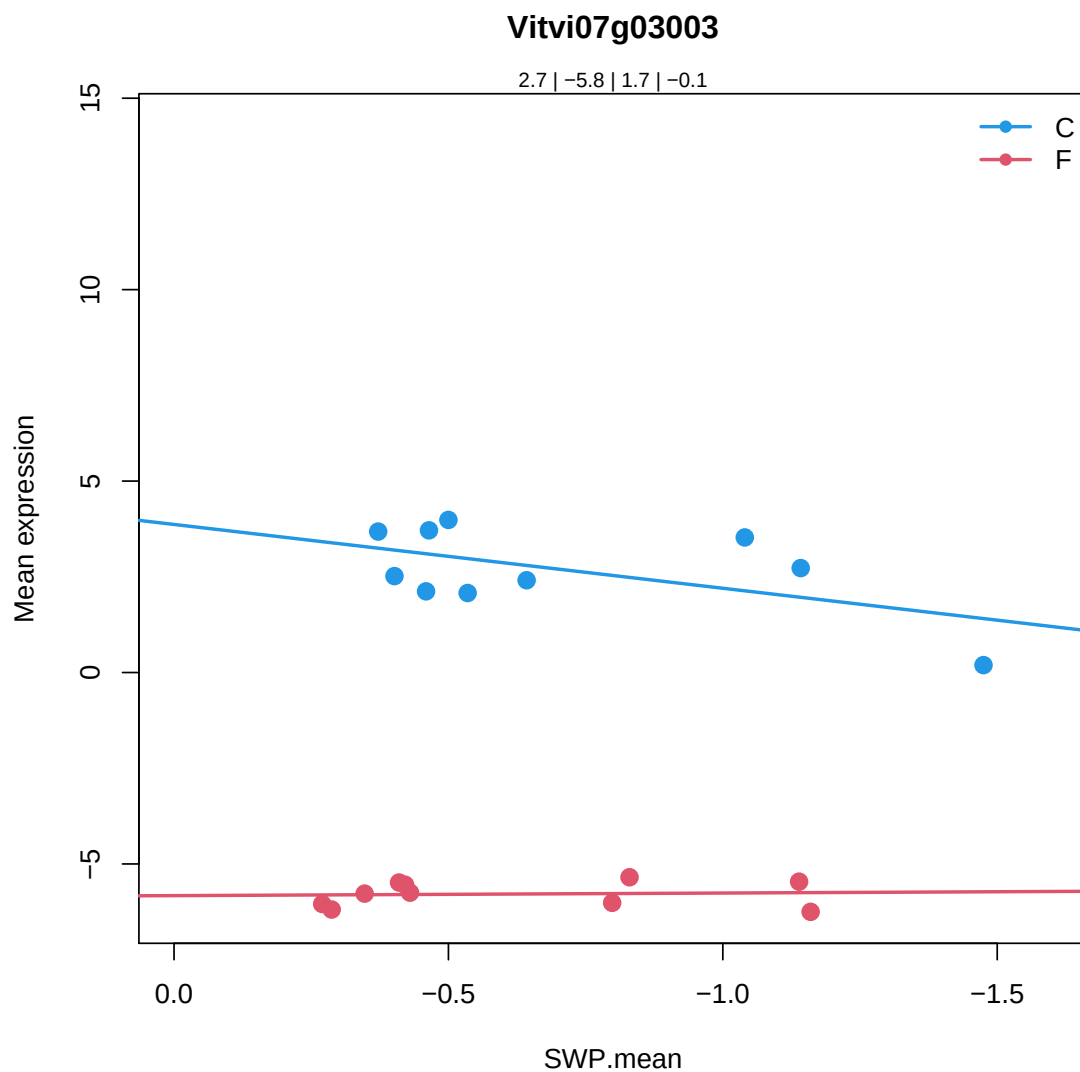
Ankyrin repeat family protein |

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	



8.5.20 Vitvi11g00749: Type6.C

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi11g00749

30.2.12

signalling.receptor kinases.leucine rich repeat XII

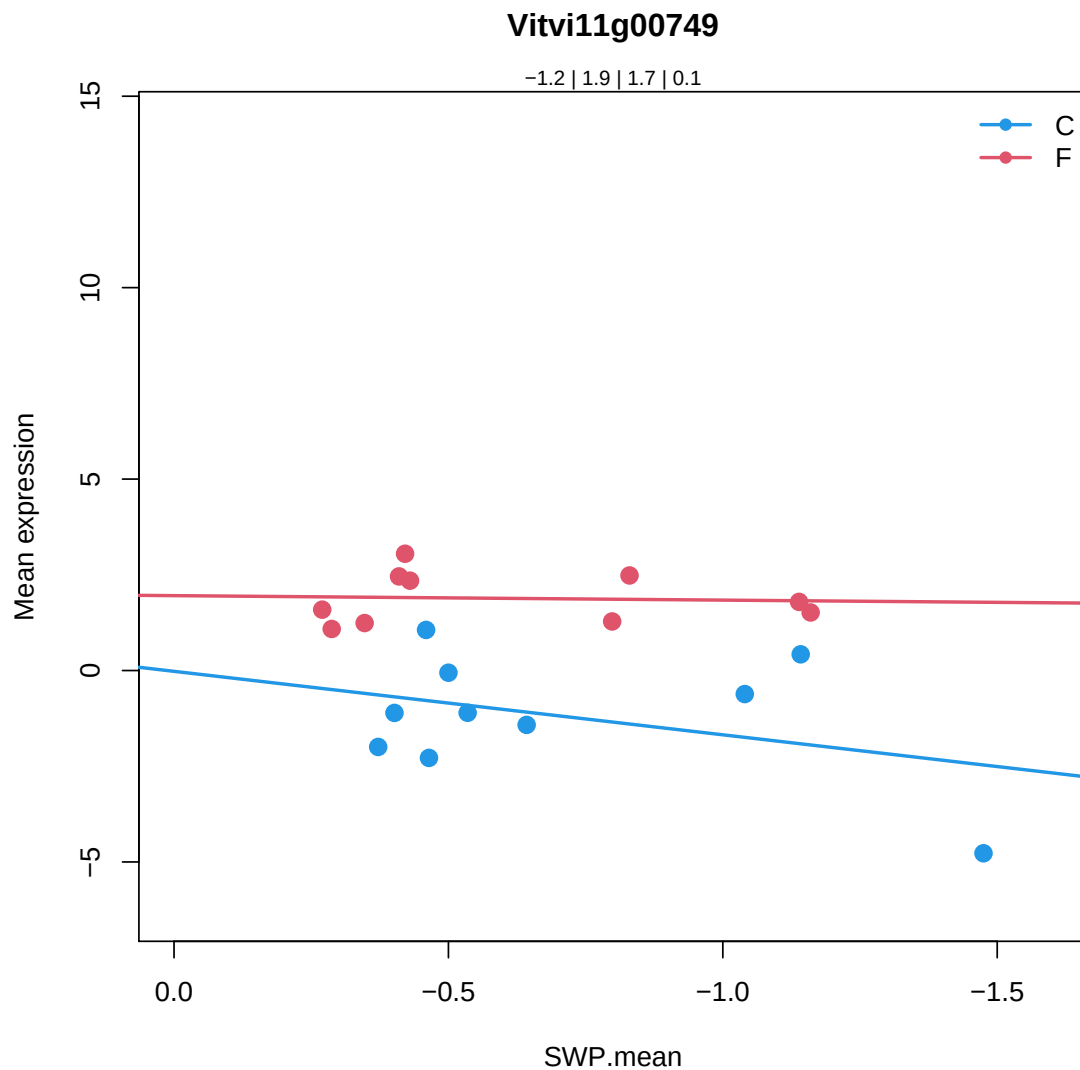
kinase family with leucine-rich repeat domain-containing protein |

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	



8.5.21 Vitvi16g02128: Type6.C *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi16g02128
```

```
35.2
```

```
not assigned.unknown
```

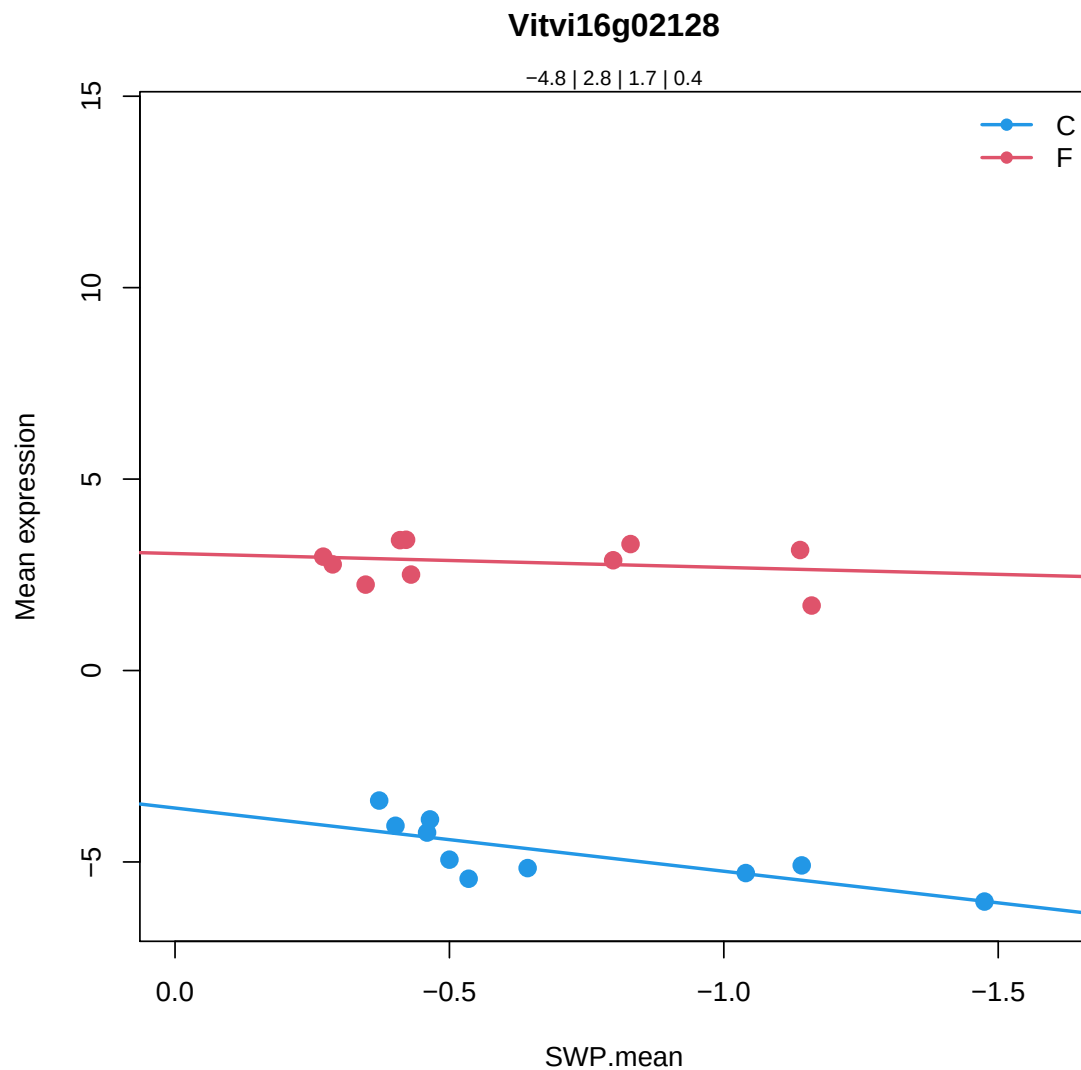
```
PR5-like receptor kinase |
```

```
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	



8.5.22 Vitvi12g02492: Type6.C *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi12g02492

30.2.12

signalling.receptor kinases.leucine rich repeat XII

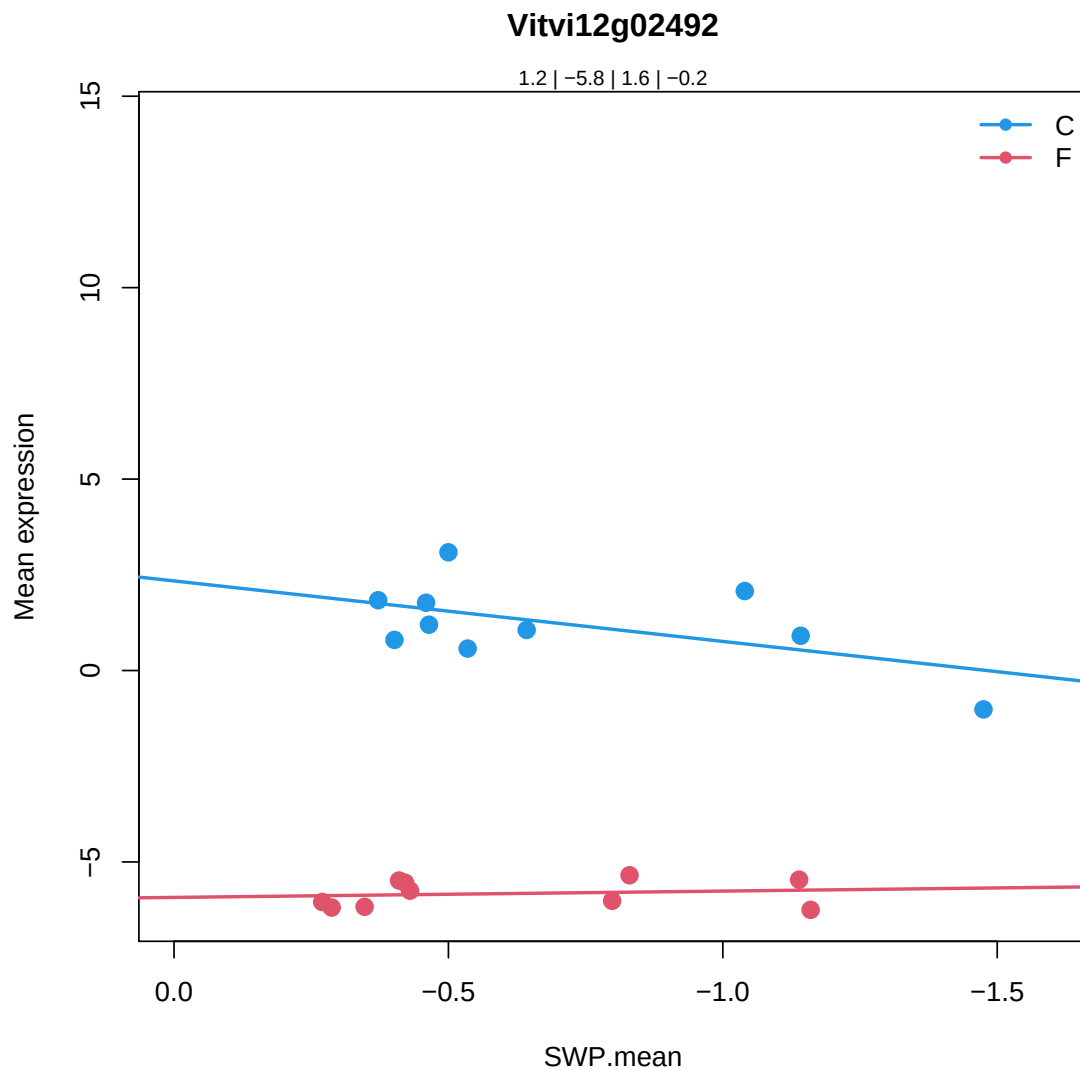
receptor like protein 22 |

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	



8.5.23 Vitvi07g01880: Type6.C *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi07g01880

29.2.1.2.2.3

protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L3

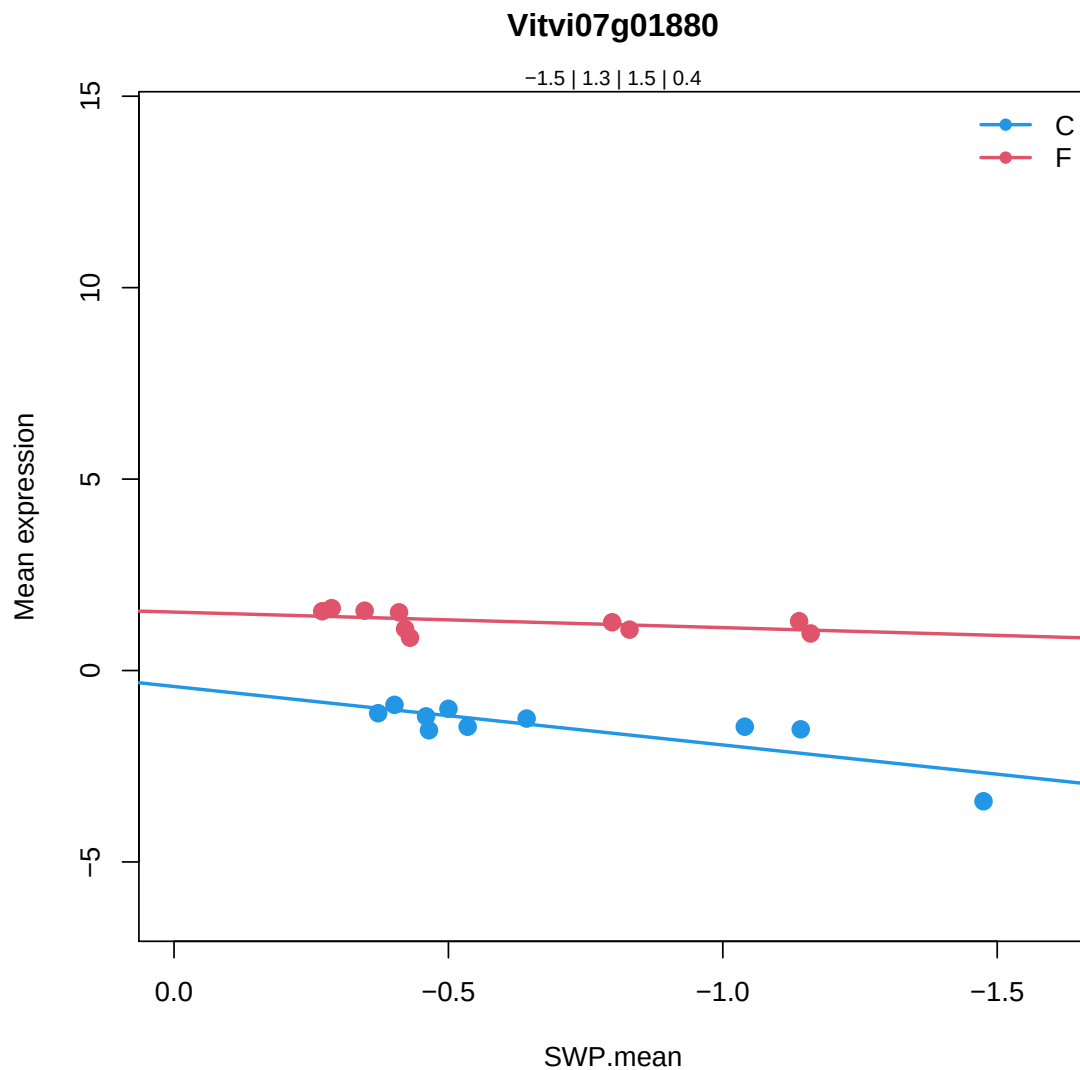
cysteine-rich RECEPTOR-like kinase |

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	



8.5.24 Vitvi09g00038: Type6.C

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi09g00038

26.28

misc.GDSL-motif lipase

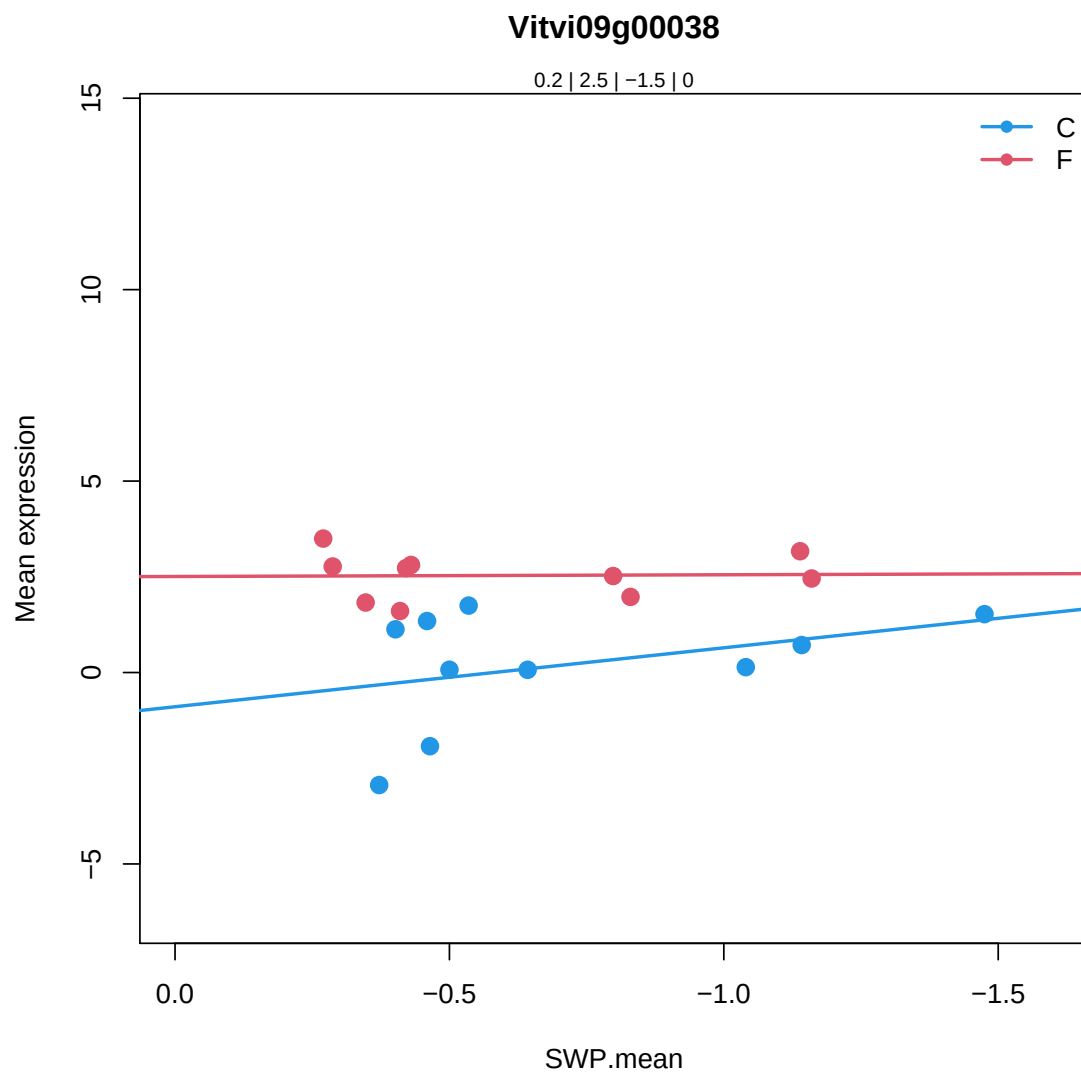
GDSL lipase 1 |

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	



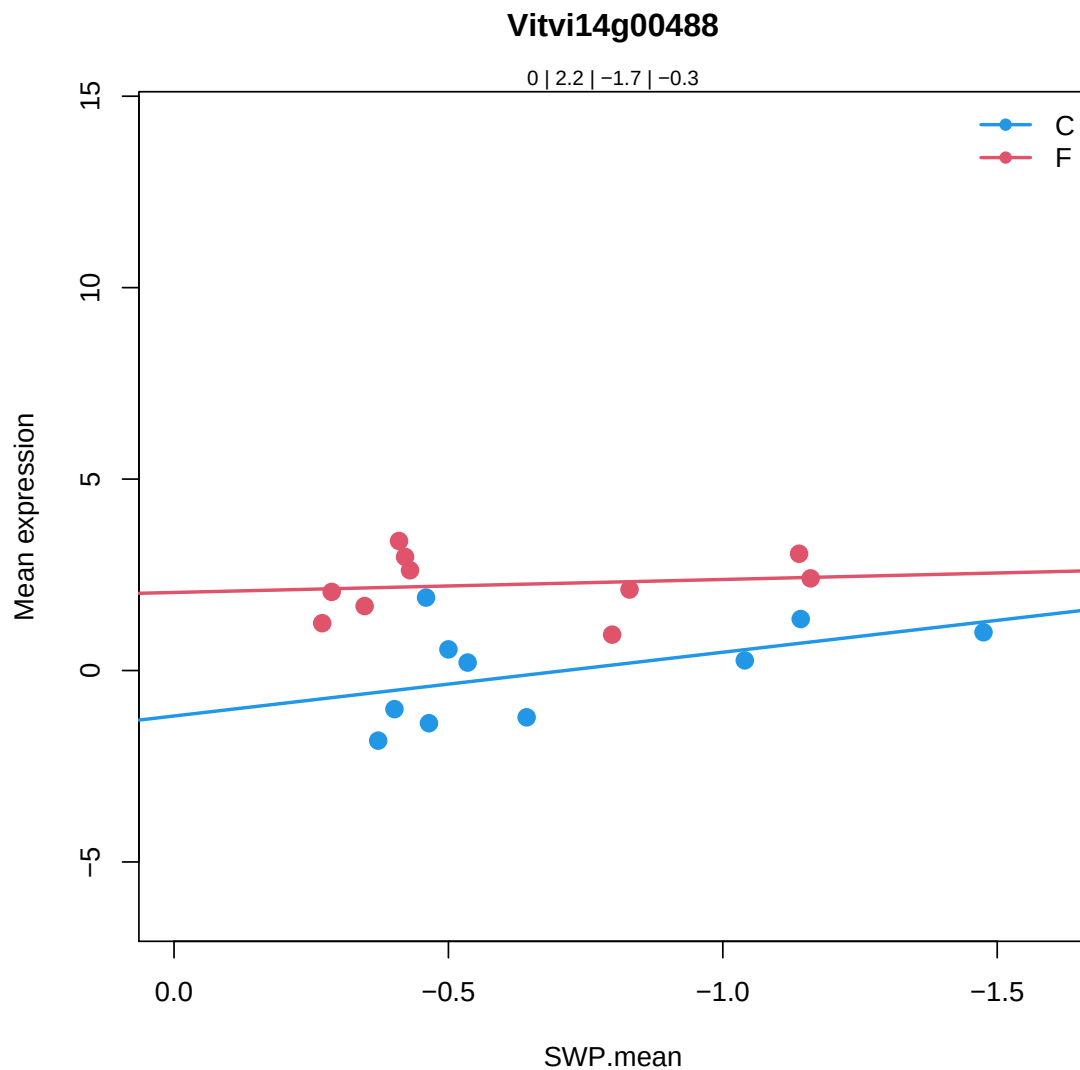
8.5.25 Vitvi14g00488: Type6.C

```
> 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	



8.5.26 Vitvi01g01977: Type6.C *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi01g01977

20.1

stress.biotic

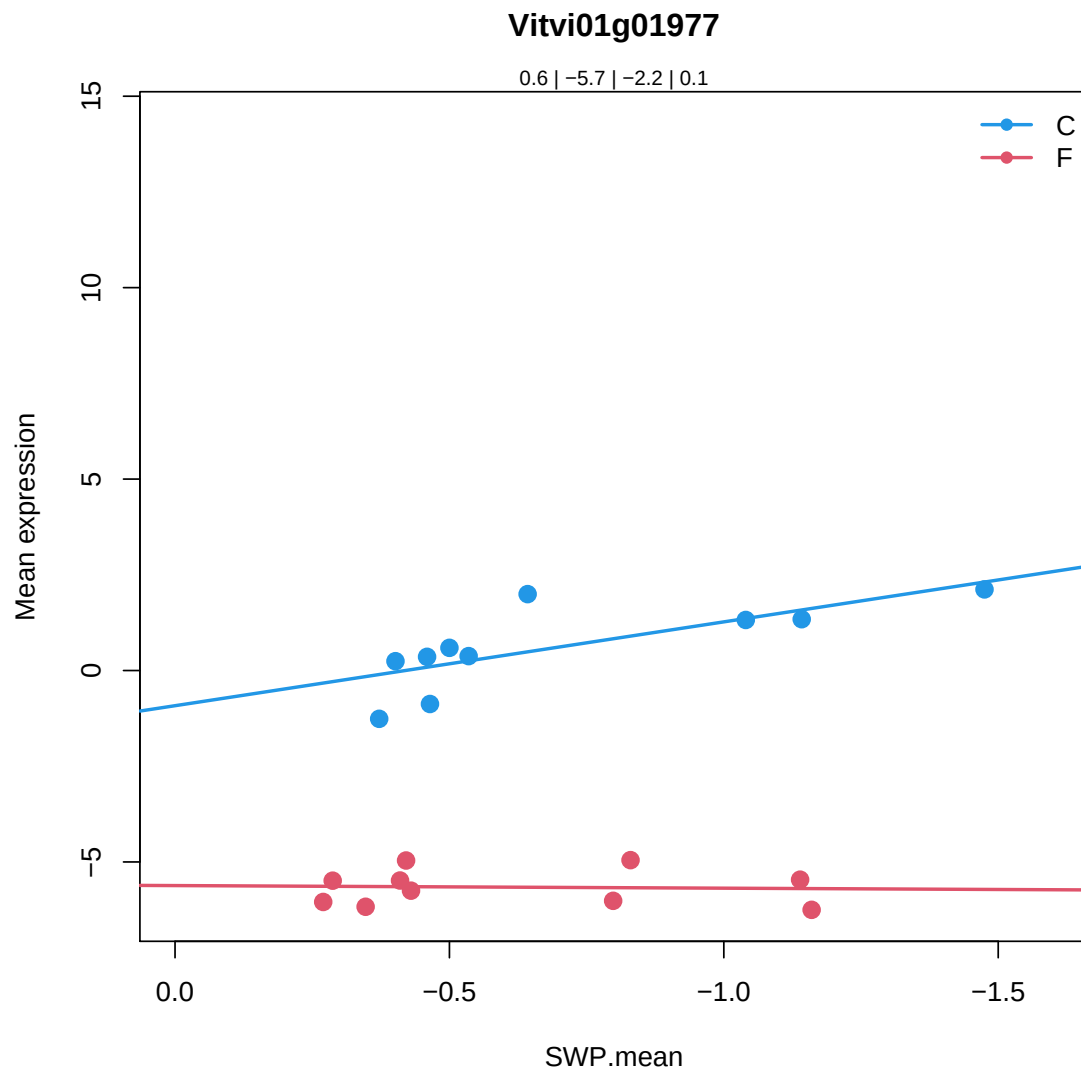
Polyketide cyclase/dehydrase and lipid transport superfamily protein |

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	



8.5.27 Vitvi03g01431: Type6.C *

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi03g01431

26.7

misc.oxidases - copper, flavone etc

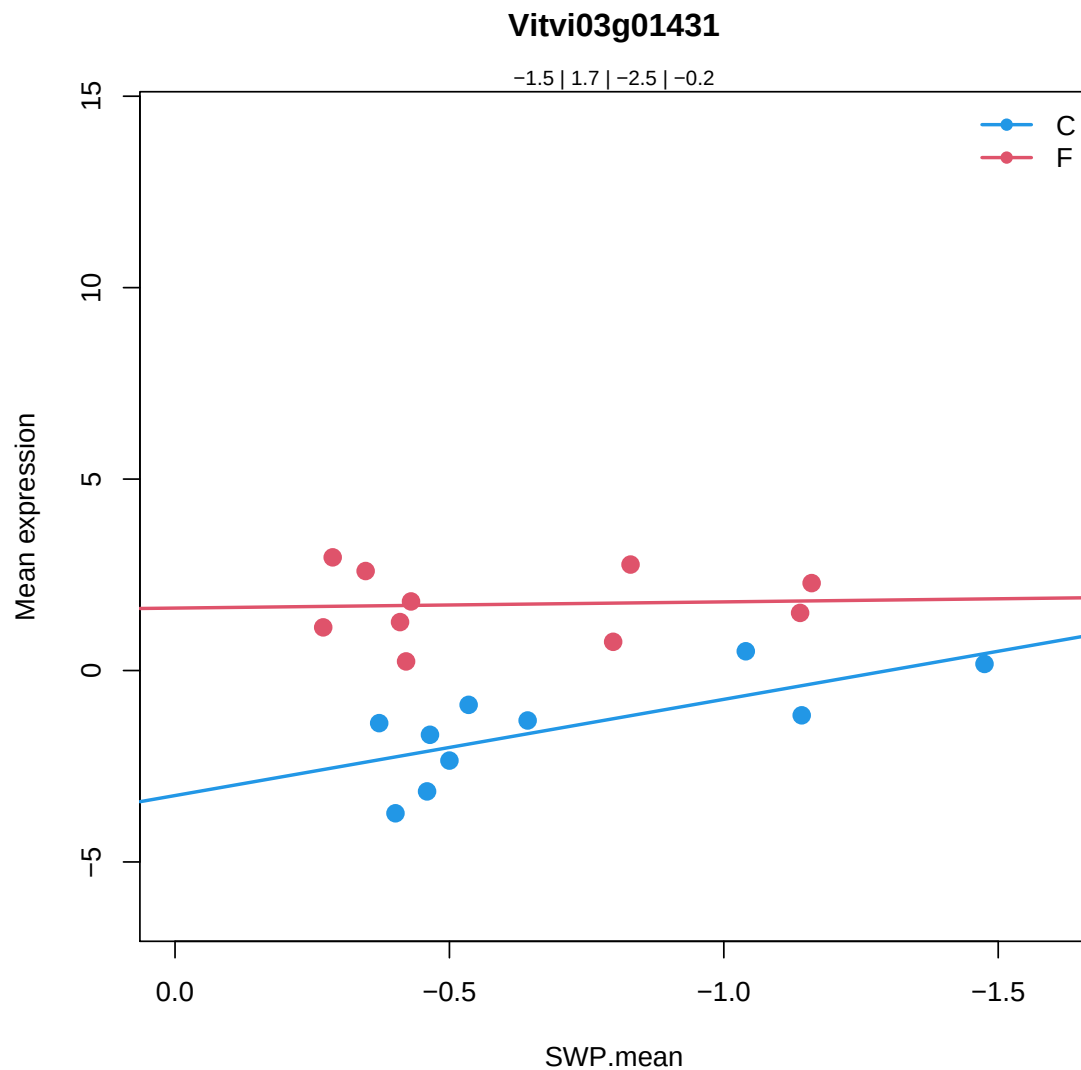
flavin-dependent monooxygenase 1 |

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	



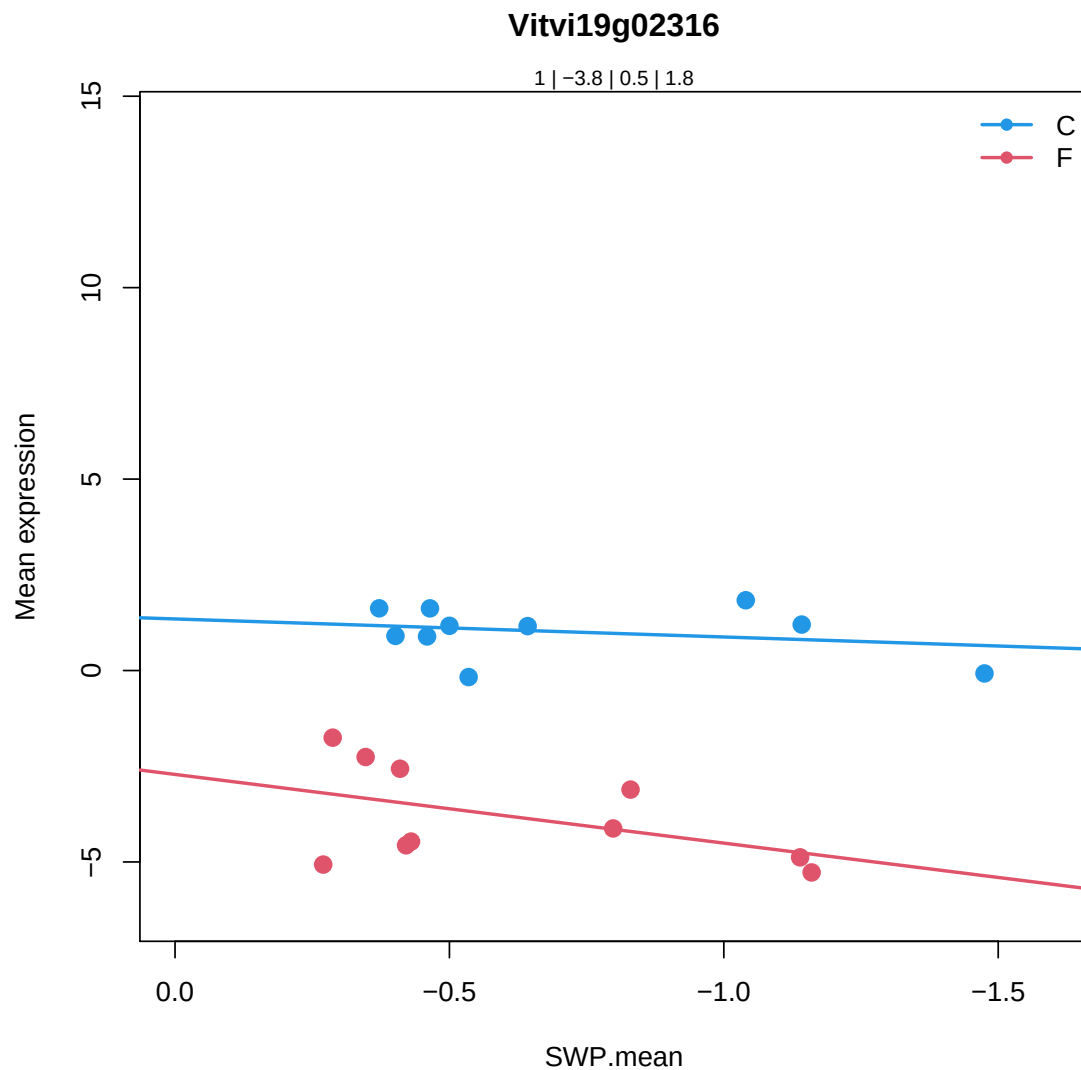
8.6 Type6.F

8.6.1 Vitvi19g02316: Type6.F

```
> 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	



8.6.2 Vitvi17g00175: Type6.F

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi17g00175

30.2.25

signalling.receptor kinases.wall associated kinase

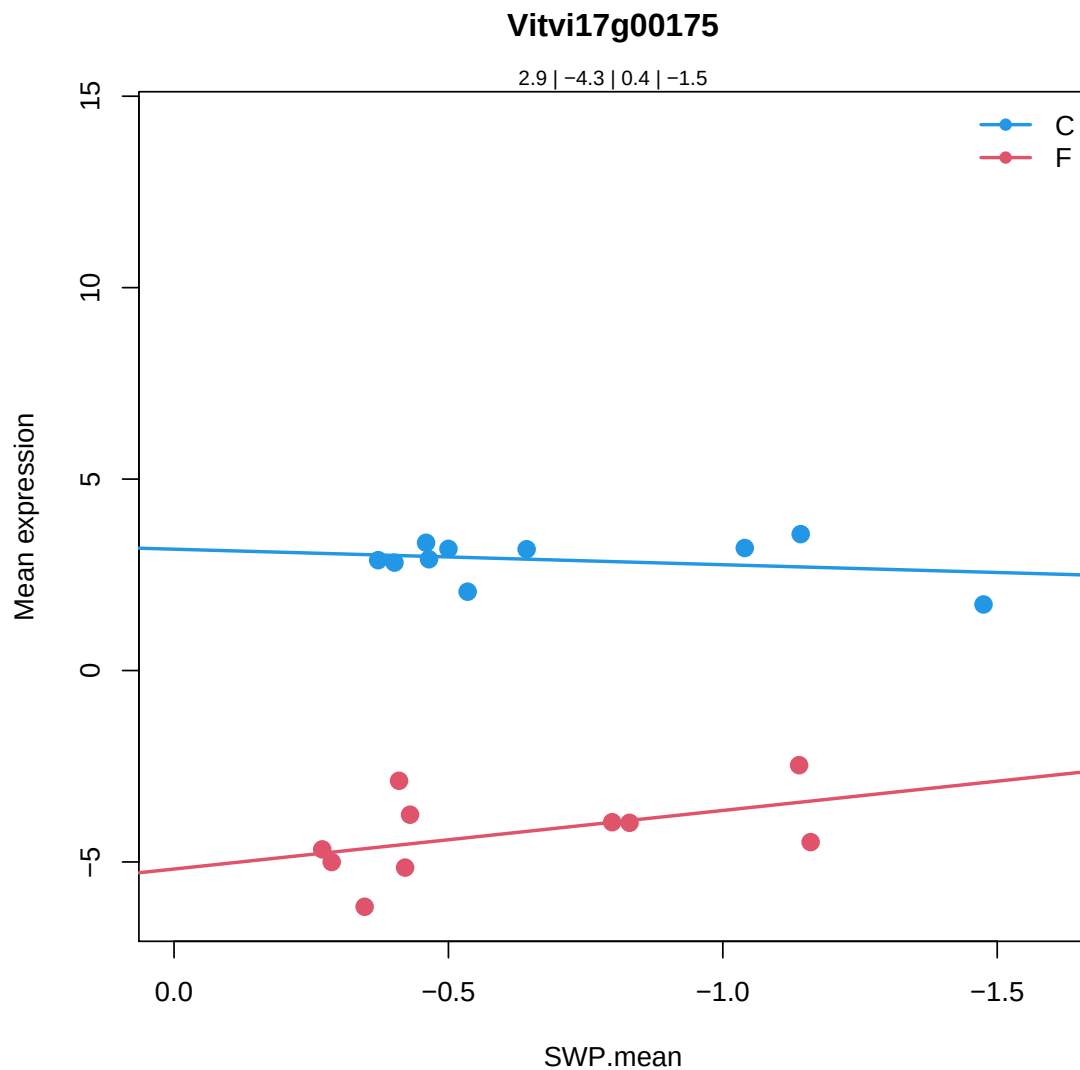
wall associated kinase 5 |

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	



8.6.3 Vitvi05g00038: Type6.F

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi05g00038

26.3.5

misc.gluco-, galacto- and mannosidases.glycosyl hydrolase family 5

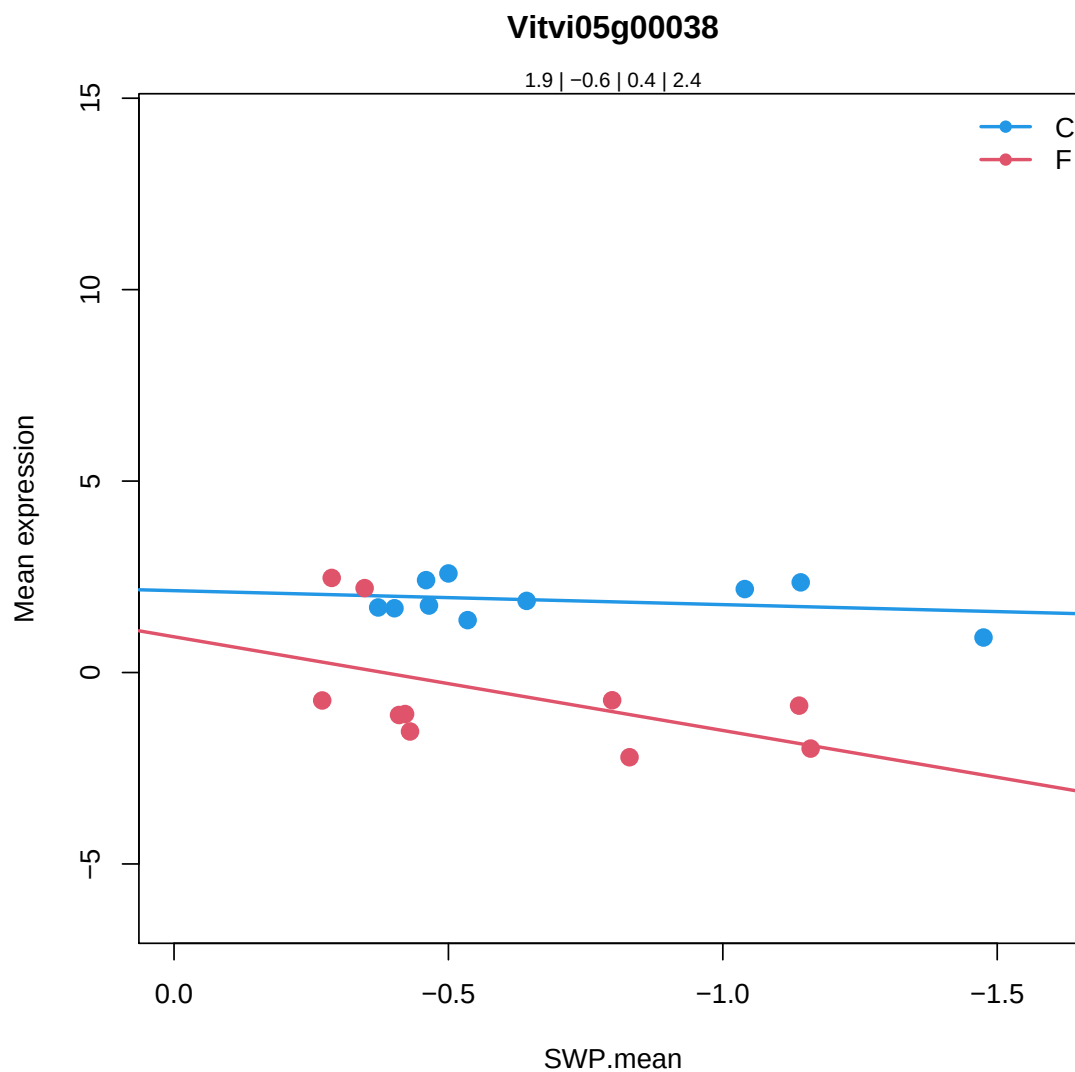
alpha/beta-Hydrolases superfamily protein |

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	



8.6.4 Vitvi15g01643: Type6.F

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi15g01643

16.8.1.12

secondary metabolism.flavonoids.anthocyanins.anthocyanidin 3-O-glucosyl

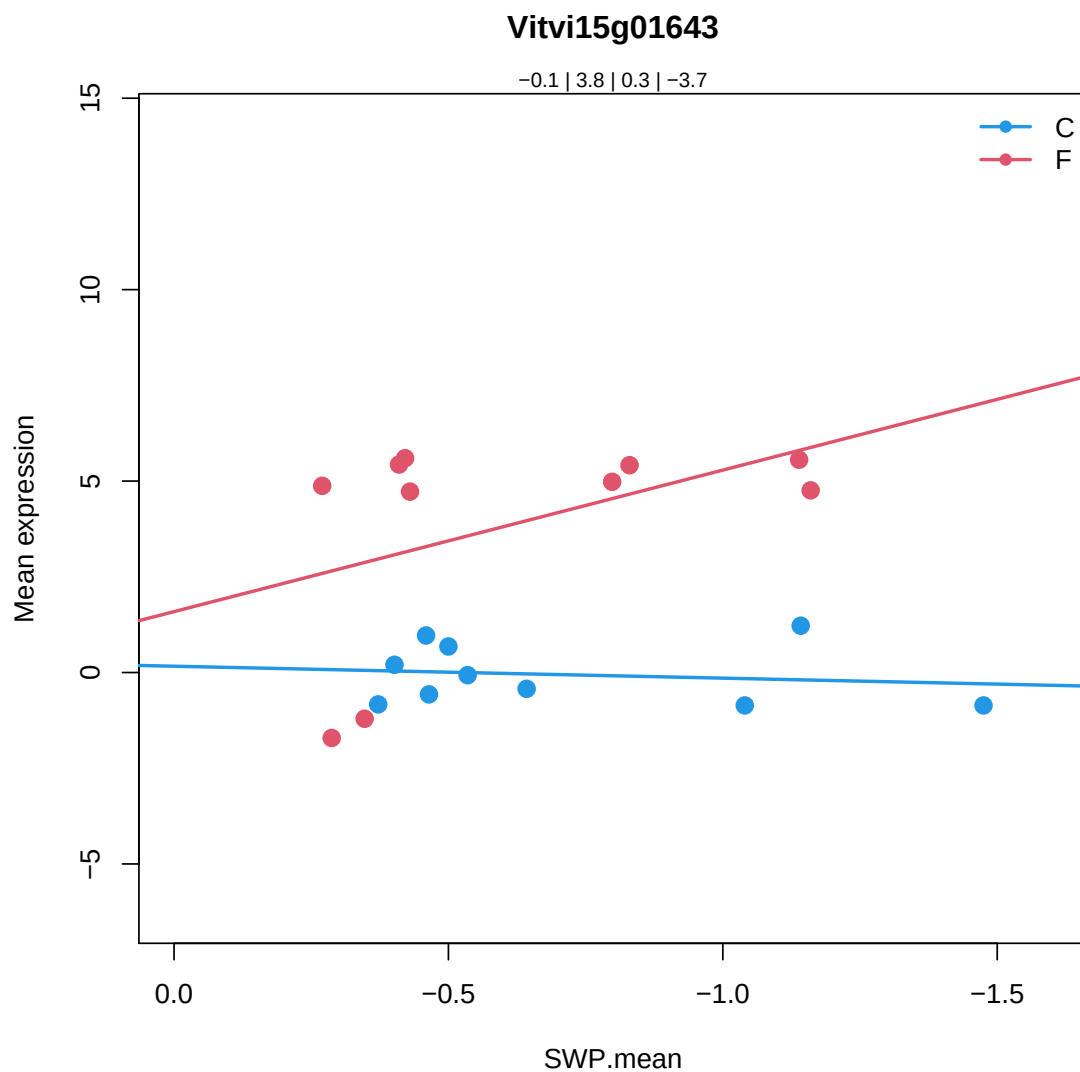
UDP-Glycosyltransferase superfamily protein |

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	



8.6.5 Vitvi05g01578: Type6.F

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi05g01578

35.2

not assigned.unknown

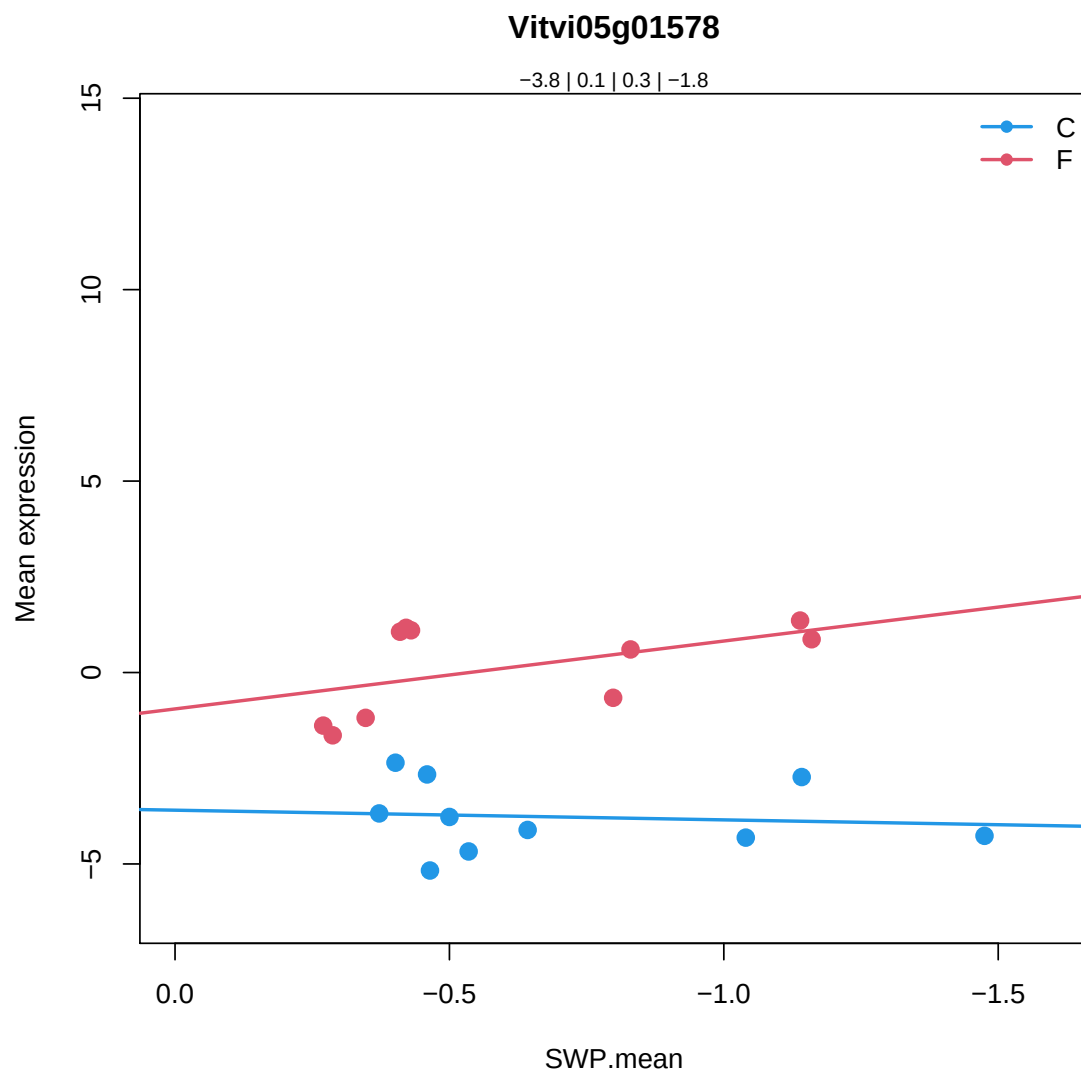
homolog of carrot EP3-3 chitinase |

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	



8.6.6 Vitvi11g00865: Type6.F

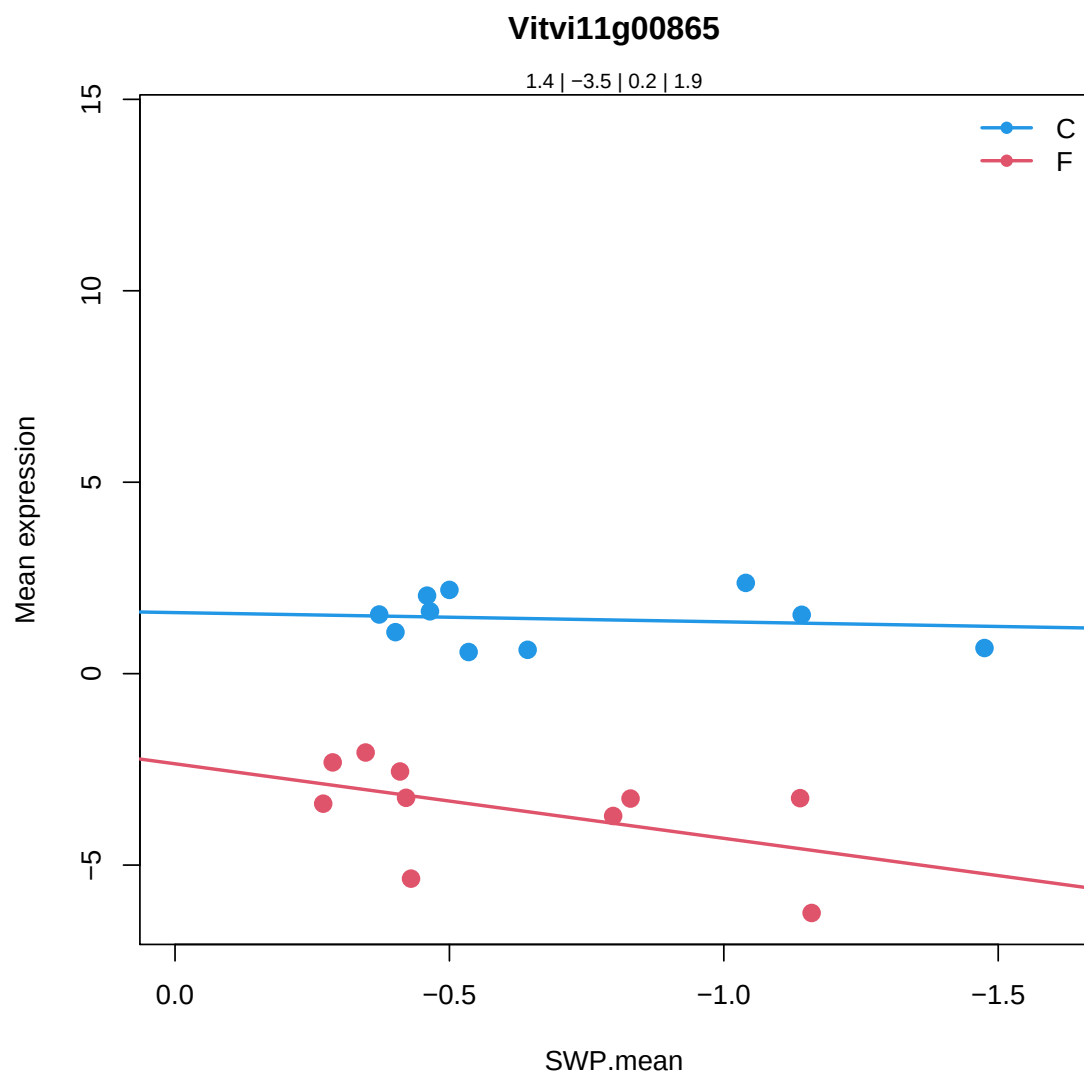
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
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	



8.6.7 Vitvi10g00313: Type6.F

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi10g00313

29.5.11.4.2

protein.degradation.ubiquitin.E3.RING

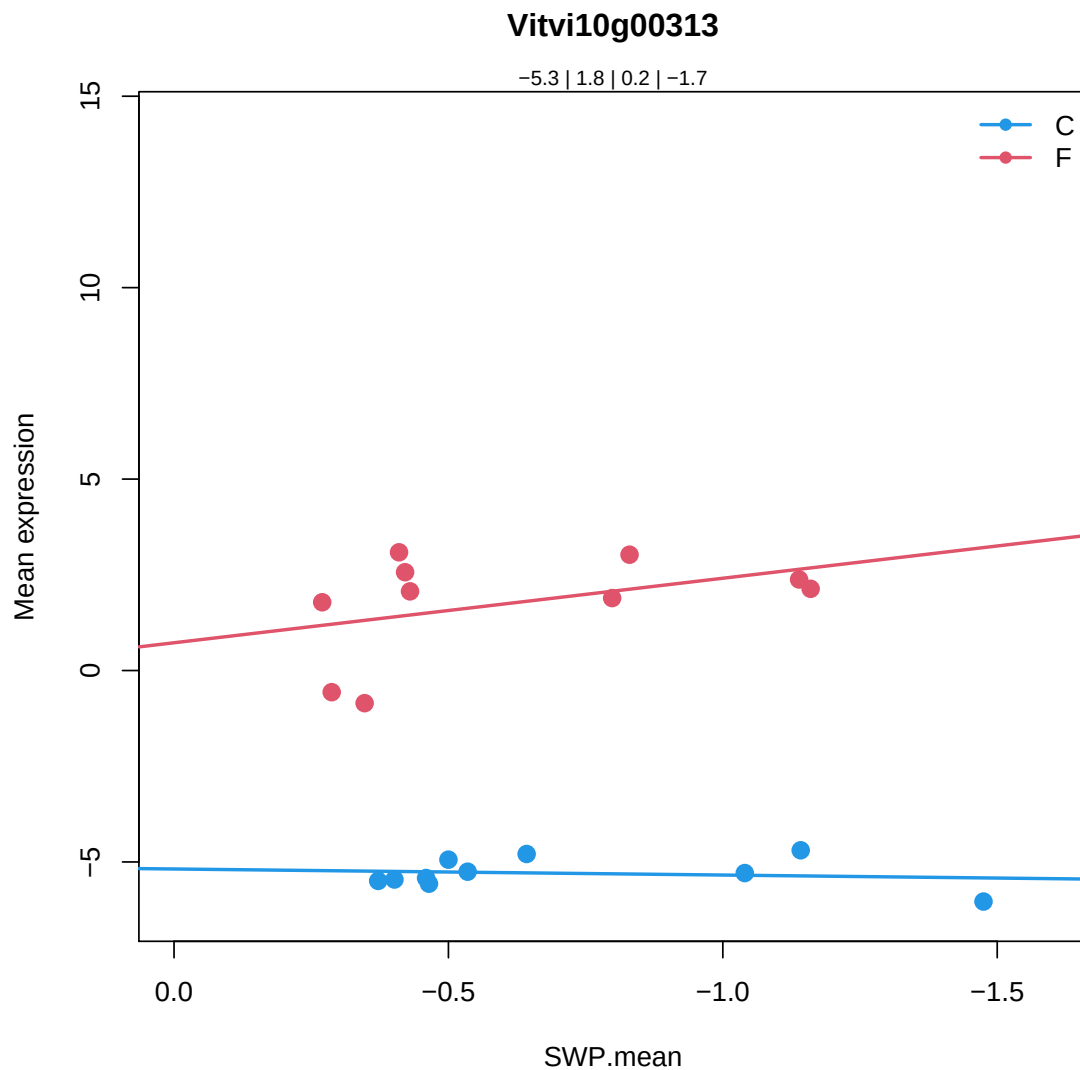
plant U-box 8 |

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	



8.6.8 Vitvi12g02177: Type6.F

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi12g02177

16.1.5

secondary metabolism.isoprenoids.terpenoids

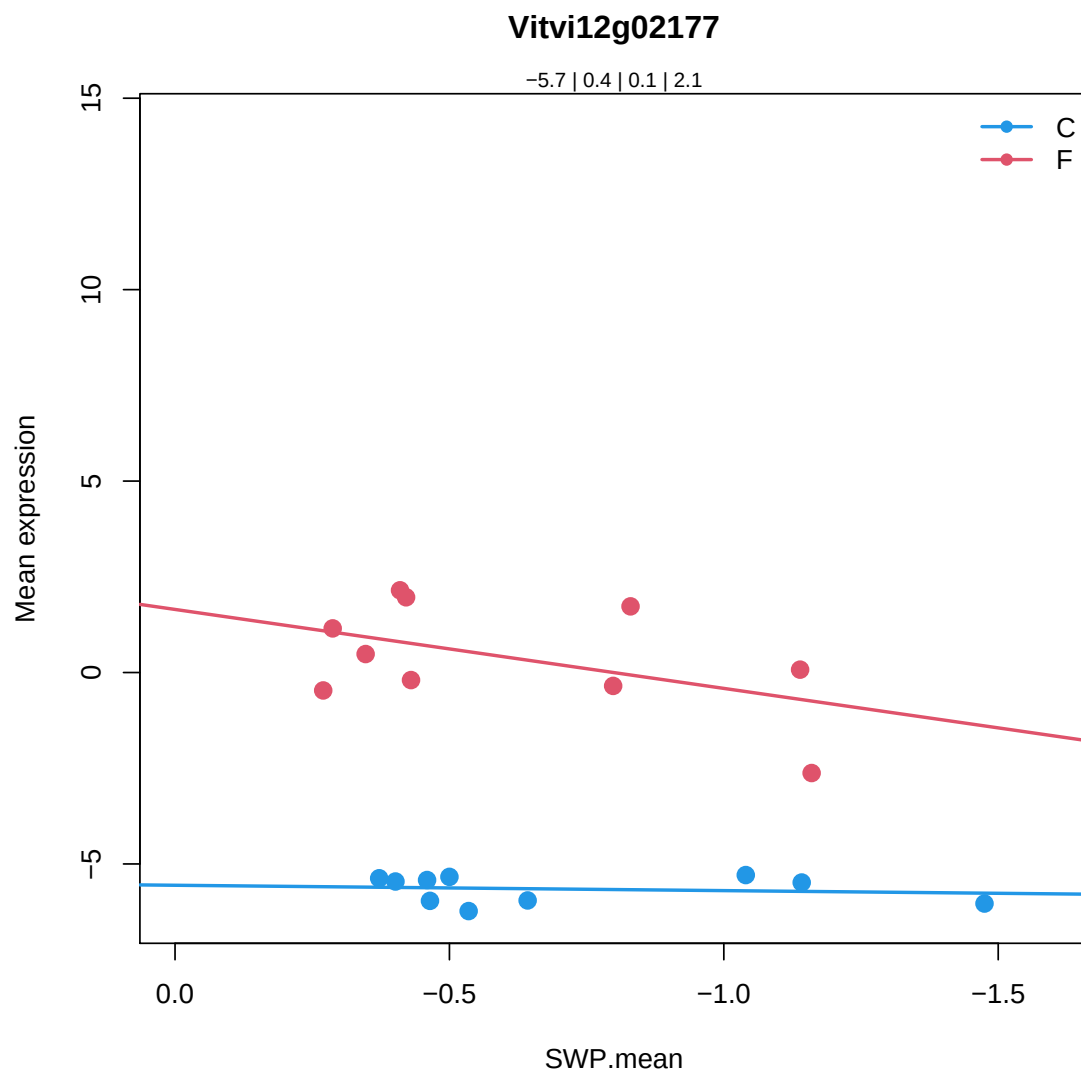
terpene synthase 21 |

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	



8.6.9 Vitvi07g03123: Type6.F

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi07g03123

31.1

cell.organisation

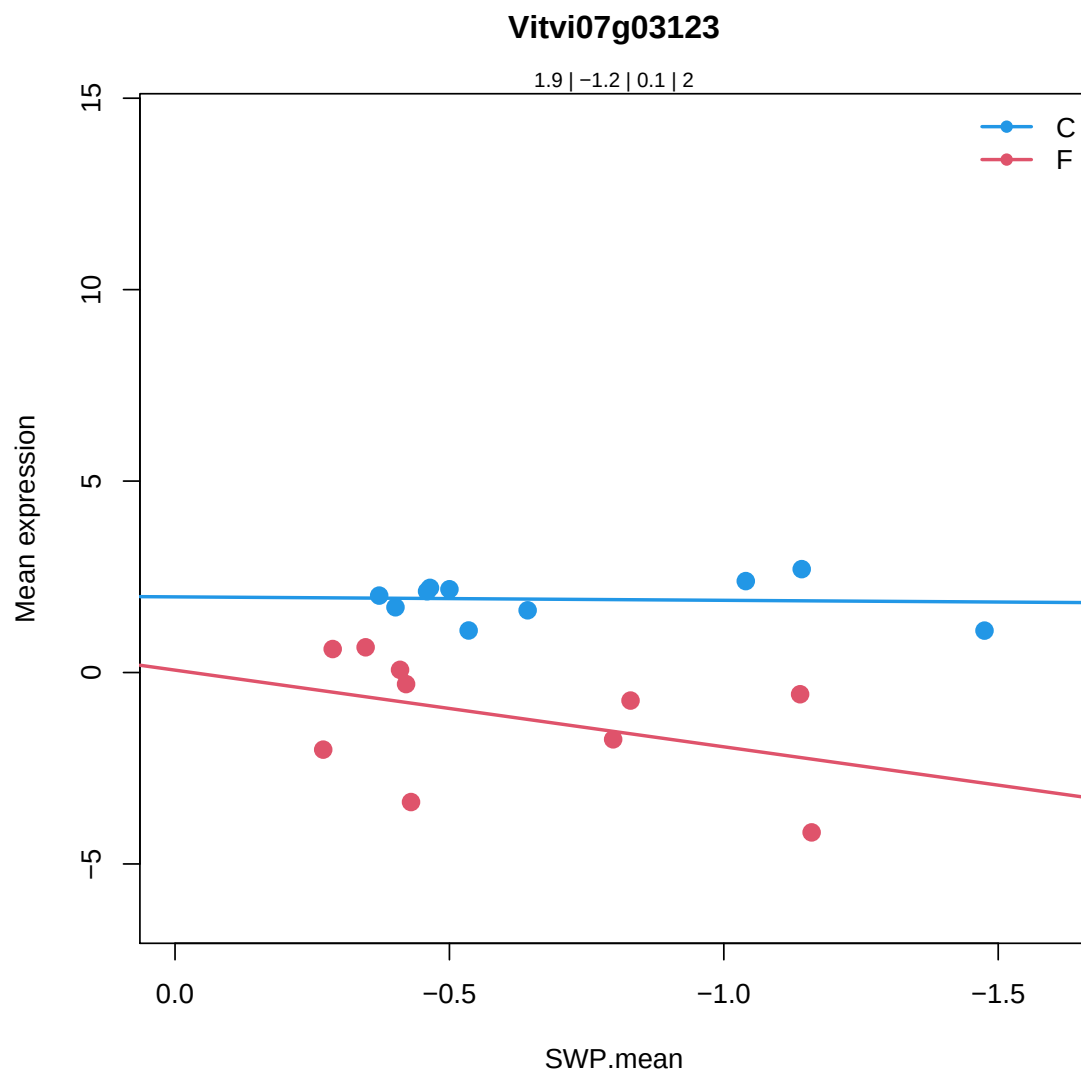
tubulin alpha-5 |

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	



8.6.10 Vitvi10g02396: Type6.F

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi10g02396

14.2

S-assimilation.APR

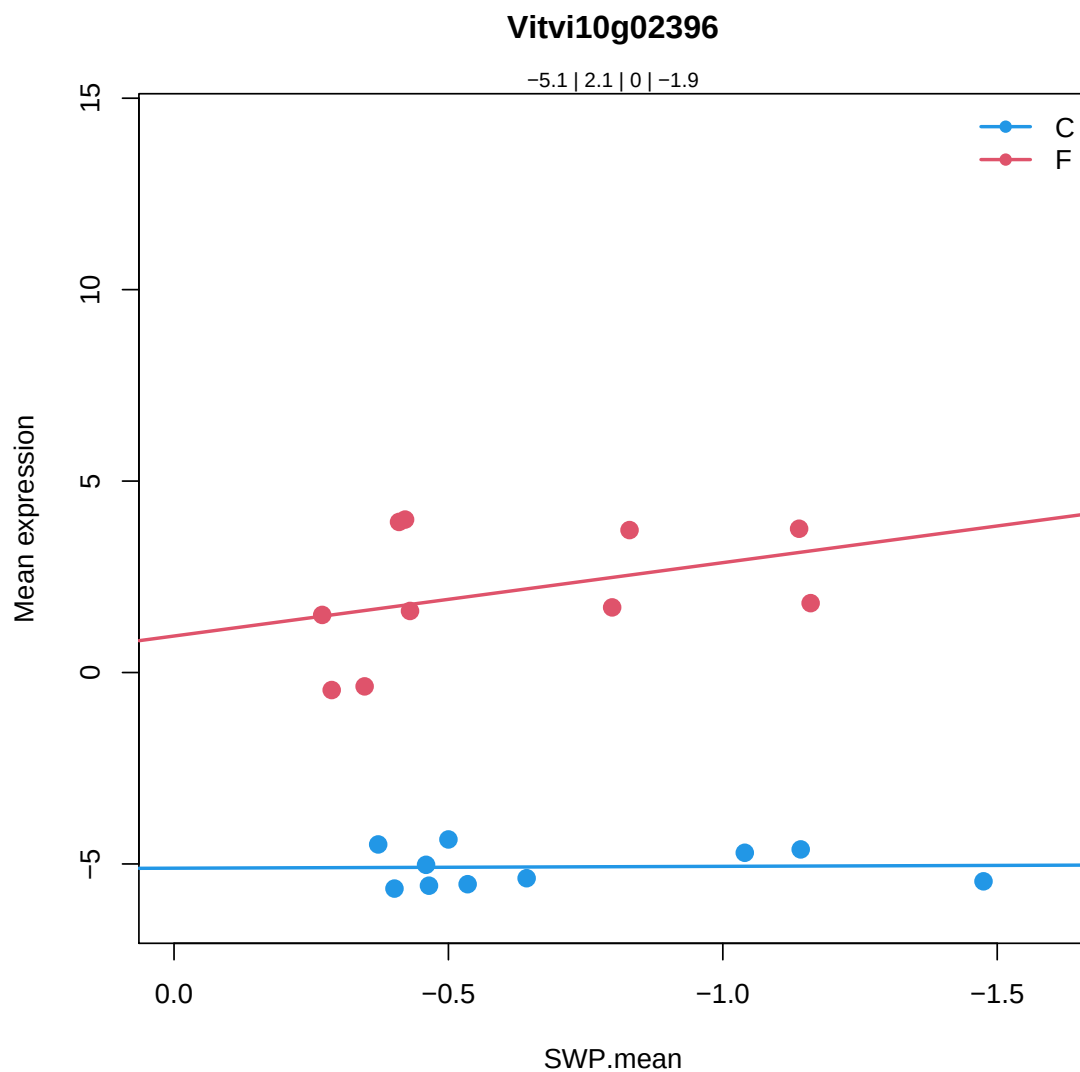
APS reductase 1 |

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	



8.6.11 Vitvi07g03066: Type6.F

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi07g03066

35.2

not assigned.unknown

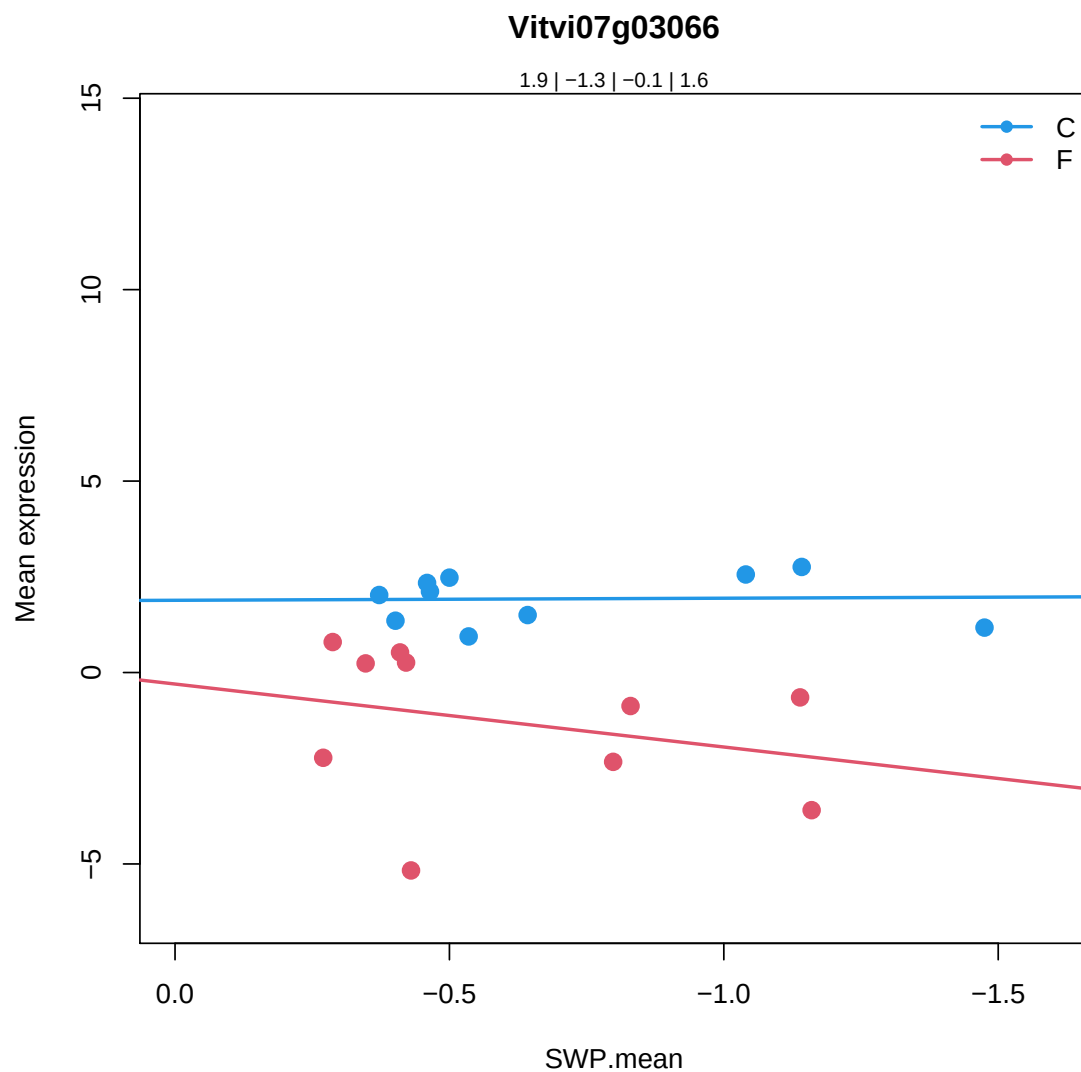
tubulin alpha-5 |

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	



8.6.12 Vitvi18g01877: Type6.F

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi18g01877

20.1.2.2

stress.biotic.receptors.TIR-NBS-LRR

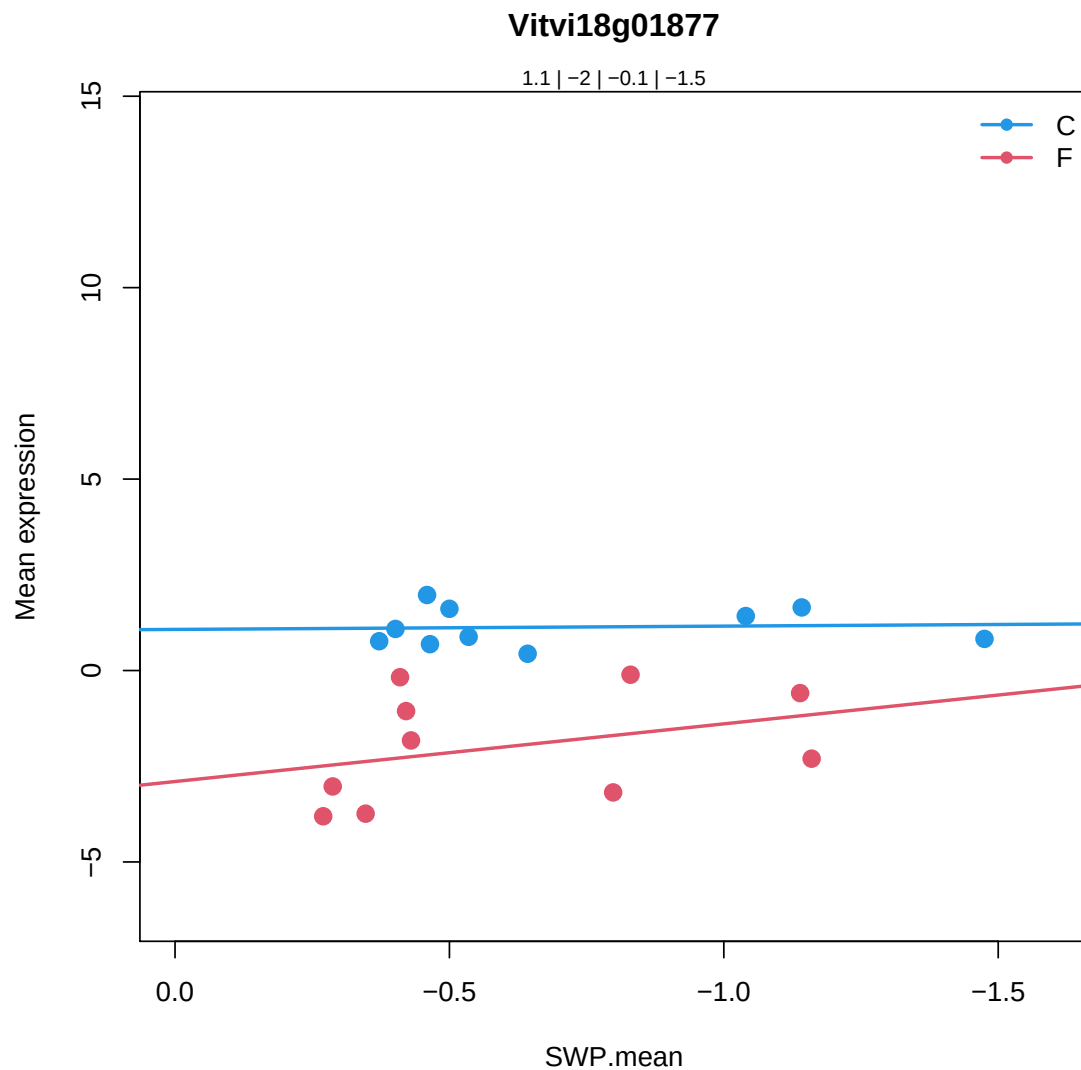
Disease resistance protein (TIR-NBS-LRR class) family |

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	



8.6.13 Vitvi08g02249: Type6.F

```
> 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
```

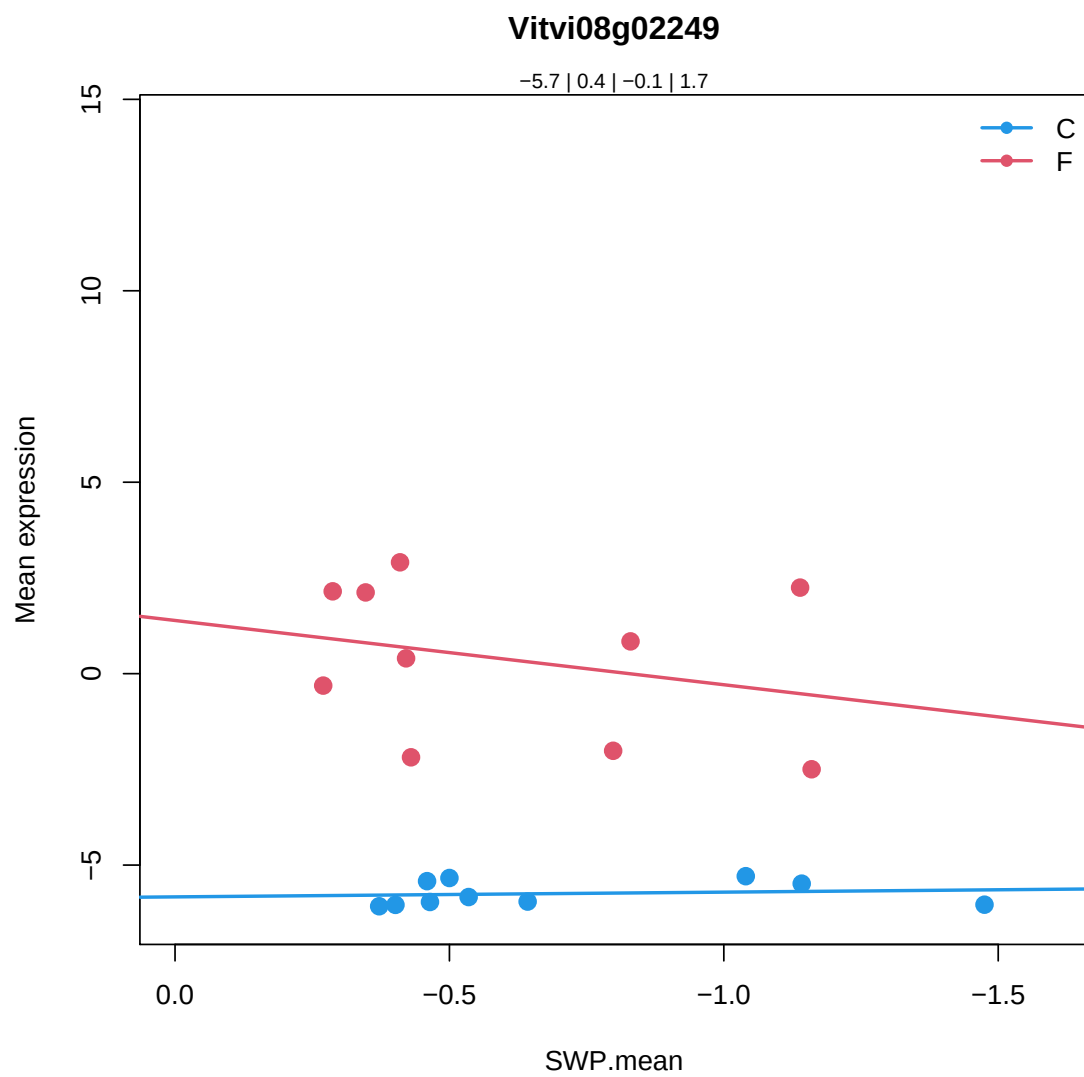
```
Eukaryotic aspartyl protease family protein |
```

```
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	



8.6.14 Vitvi13g00261: Type6.F +

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi13g00261

35.2

not assigned.unknown

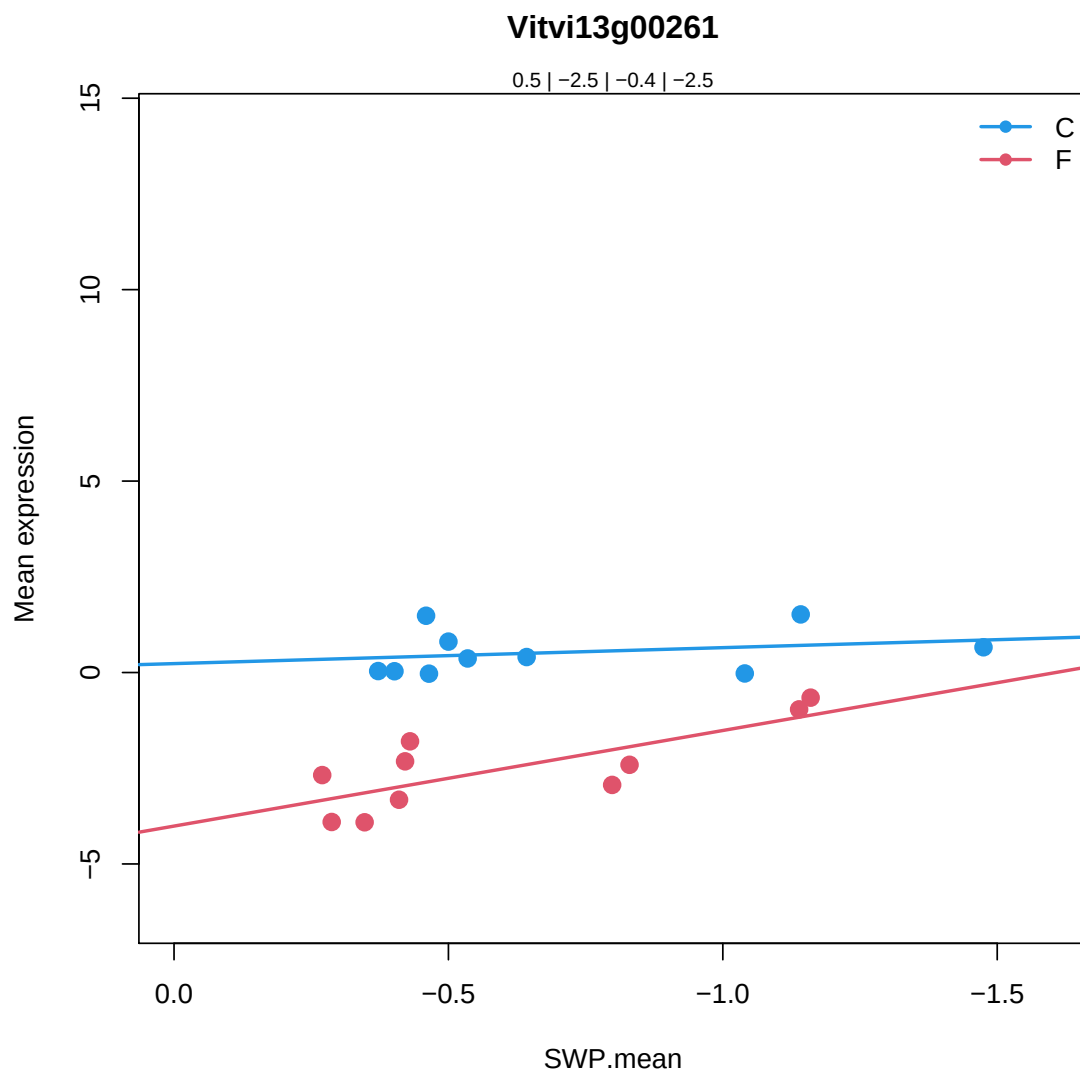
PIF / Ping-Pong family of plant transposase |

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	



8.6.15 Vitvi00g02022: Type6.F

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi00g02022

17.1.2

hormone metabolism.abscisic acid.signal transduction

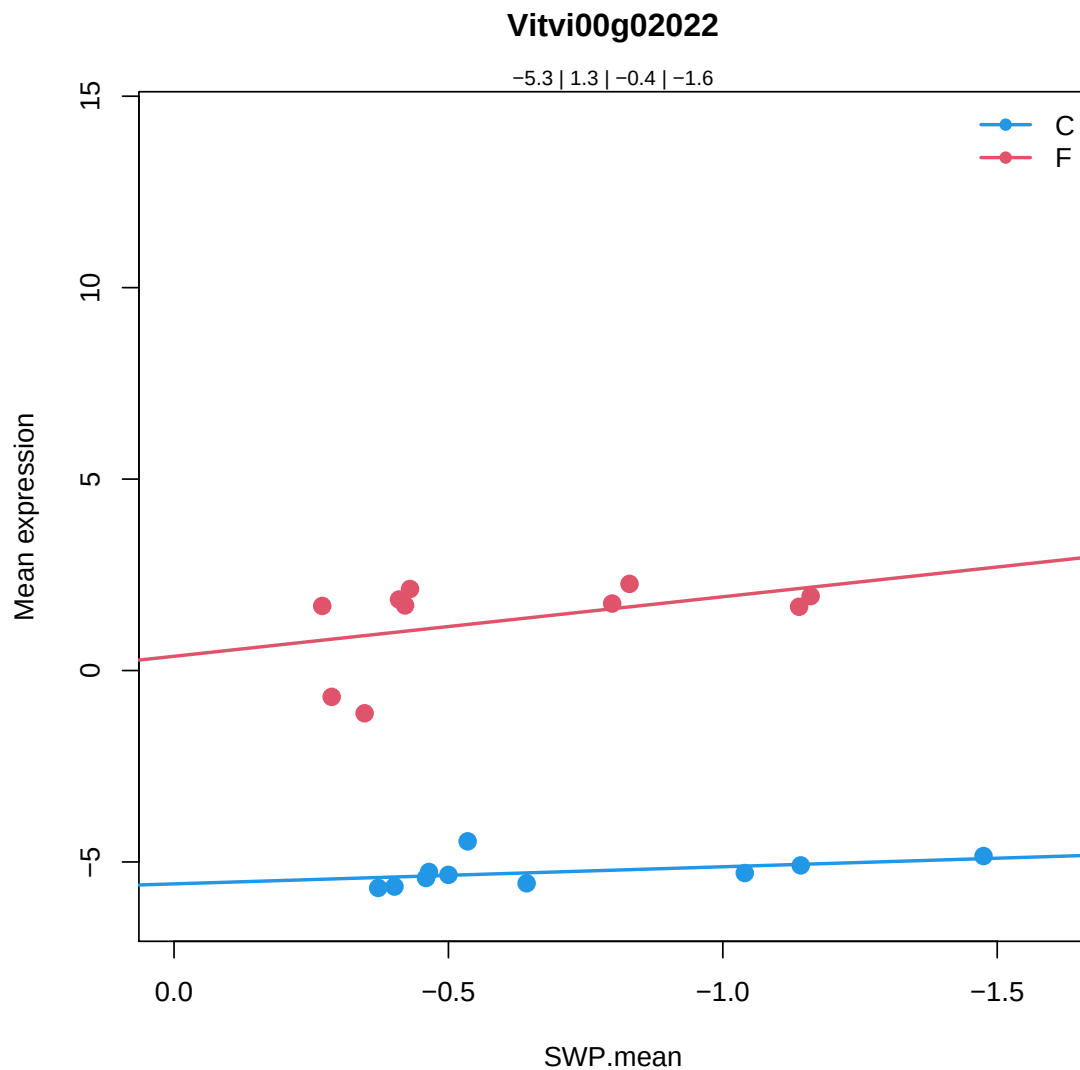
GCR2-like 1 |

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	



8.6.16 Vitvi17g01497: Type6.F

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi17g01497

26.2

misc.UDP glucosyl and glucoronyl transferases

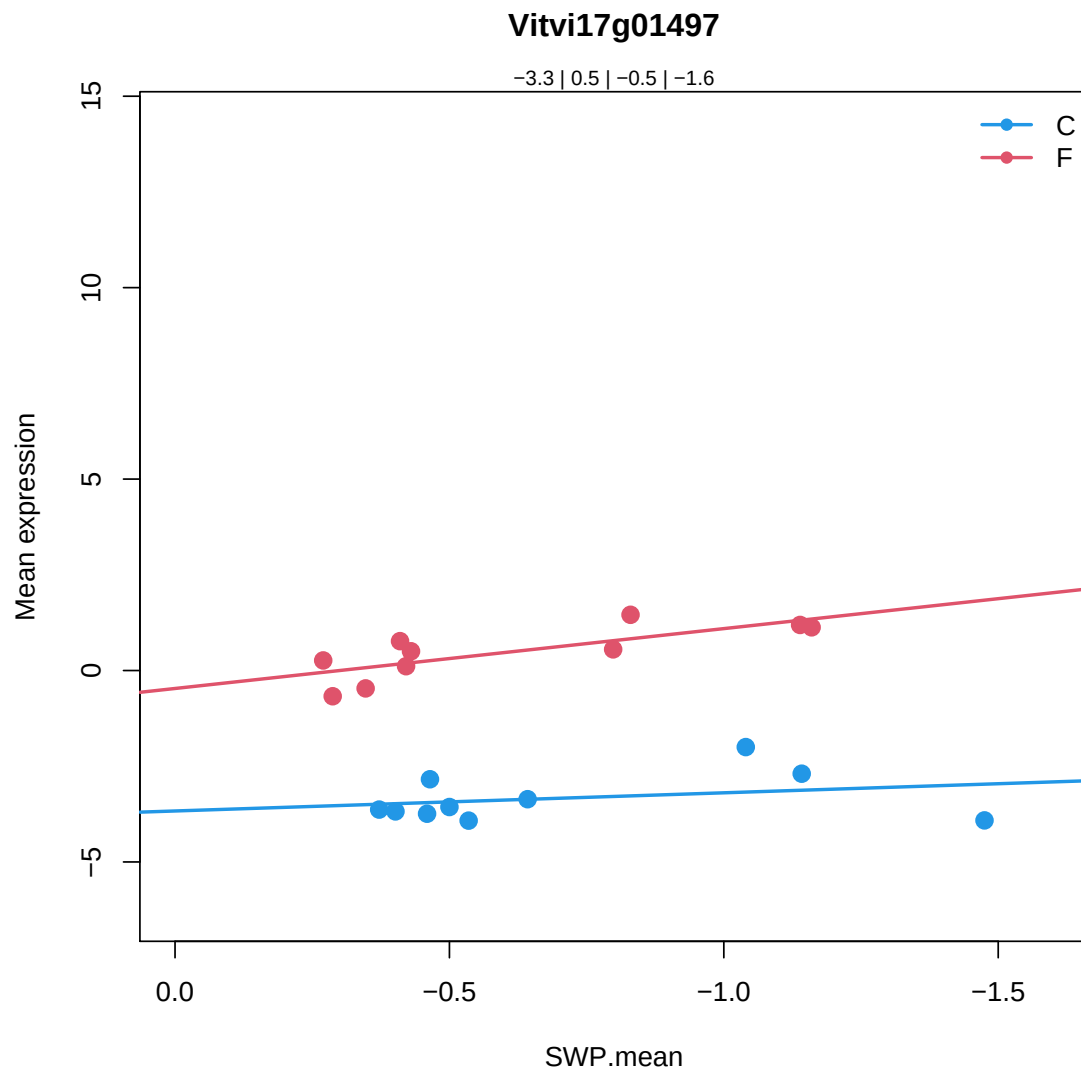
UDP-Glycosyltransferase superfamily protein |

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	



```

> #
> 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 perform 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
Transcript stats:	/output/50_Expression-water-stress-0.05-1.5-0.5-1-1/lm-fit-means-swpXvariety-statistics.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_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 0.4.10, 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 0.3.6, withr 2.3.0, xfun 0.19

Analysis project path: [\[link\]](#)

Local

D:

DEJAVNOSTI

OMIKE

pISA-projects

_p_VinskaTrta

_I_EnViRoS

_S_01_Integ

_A_01_Desc-R

other

Network

O:

DEJAVNOSTI

OMIKE

pISA-projects

_p_VinskaTrta

_I_EnViRoS

_S_01_Integ

_A_01_Desc-R

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=".")))
```