Expression analysis - water potential .alpha=0.05 .r=r

A. Blejec

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Contents

1 Task

Final document in folder /reports:

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

2 Information from pISA

Data directory

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

Results directory

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

```
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))
```

List of data objects:

```
> my.objects
       name                   description      class lenght ncol
1       t18          Transcripts for 2018 data.frame  15242   48
2       t19          Transcripts for 2019 data.frame  15242   32
3     t1819 Transcripts for 2018 and 2019 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 and 2019 data.frame     80   21
```

Factor for days within the year

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

3.1 Water potential

On Dec 12 we decided to include water stress as a prediction factor.

In addition to expression data, we need water stress data.

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

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

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

```
> X <- wpdata
> X$treat <- factor(X$treatment,levels=c("WW","WS"))
> X$variety <- factor(X$variey)
> # Date of sampling might be useful as well
> require(lubridate)
> X$date <- as_date(X$date, format="%d.%m.%Y")
> X$year <- year(X$date)
> table(data.frame(X$date,"Count"=1))
```

```
            Count
X.date       1
  2018-06-04 4
  2018-06-15 4
  2018-06-21 4
  2018-06-29 4
  2018-07-04 4
  2018-07-10 4
  2018-07-16 4
  2018-07-23 4
  2018-07-31 4
  2018-08-07 4
  2019-06-18 4
  2019-06-26 4
  2019-07-08 4
  2019-07-12 4
  2019-07-17 4
  2019-07-22 2
  2019-07-30 4
  2019-08-06 4
  2019-08-12 4
  2019-08-19 4
```

```
> str(X)
```

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

Order by date

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

```
> wpdata <- X
```

Tidy dates ...

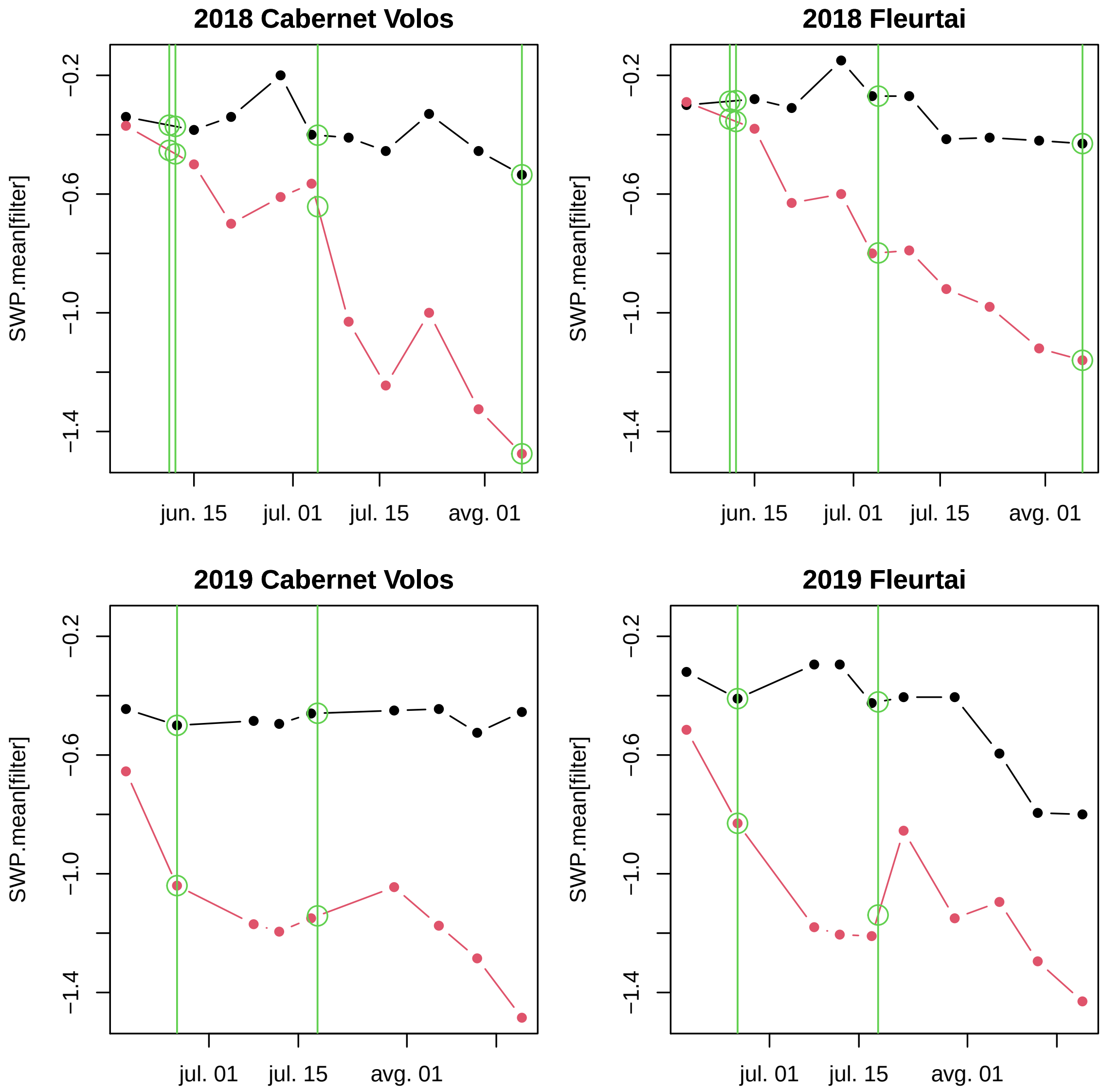
```
> table(wpdata$date,wpdata$variety)
```

```
             Cabernet Volos Fleurtai
  2018-06-04              2        2
  2018-06-15              2        2
  2018-06-21              2        2
  2018-06-29              2        2
  2018-07-04              2        2
  2018-07-10              2        2
  2018-07-16              2        2
  2018-07-23              2        2
  2018-07-31              2        2
  2018-08-07              2        2
  2019-06-18              2        2
  2019-06-26              2        2
  2019-07-08              2        2
  2019-07-12              2        2
  2019-07-17              2        2
  2019-07-22              0        2
  2019-07-30              2        2
  2019-08-06              2        2
  2019-08-12              2        2
  2019-08-19              2        2
> table(pdata1819$date)

< table of extent 0 >

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


2018-06-11 2018-06-12 2018-07-05 2018-08-07 2019-06-26 2019-07-18 
         8          8         16         16         16         16 

> pdata1819$Year <- factor(paste0("20",pdata1819$year))
```

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

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

```
+     treat=tr))
+     points(wpa,col=3,cex=2)
+     }
+     })
+   }
+ }
```



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

@

Order water potential data by date

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

```
Time differences in days
 [1]  23  33 -57   1  23  33 -57   1  23  33 -57   1  23  33 -57 380
[17]  22 -22  22 -22  22 -22  22
```

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

```
Time differences in days
 [1]   0   0   0   1   0   0   0  23   0   0   0  33   0   0   0 323
[17]   0   0   0  22   0   0   0
```

Convert treatment and variety into factors

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

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

Check date consistency

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

Add interpolated WP values to measured date to phenodata.

```
> mapdate <- match(pdata1819$date,wpas$date)
> pdata1819w <- pdata1819
> pdata1819w$swp <- wpas[mapdate,c("swp")]
> dim(pdata1819w)
[1] 80 24
> head(pdata1819w)
                     ID        Variety       Date variety year day
C18_11d_WS1 C18_11d_WS1 Cabernet Volos 12.06.2018       C   18  11
C18_11d_WS2 C18_11d_WS2 Cabernet Volos 12.06.2018       C   18  11
C18_11d_WS3 C18_11d_WS3 Cabernet Volos 12.06.2018       C   18  11
C18_11d_WS4 C18_11d_WS4 Cabernet Volos 12.06.2018       C   18  11
C18_11d_WW1 C18_11d_WW1 Cabernet Volos 12.06.2018       C   18  11
C18_11d_WW2 C18_11d_WW2 Cabernet Volos 12.06.2018       C   18  11
            treat rep project.name        species plant.name tissue
C18_11d_WS1    WS   1      EnViros Vitis vinifera  grapevine   leaf
C18_11d_WS2    WS   2      EnViros Vitis vinifera  grapevine   leaf
C18_11d_WS3    WS   3      EnViros Vitis vinifera  grapevine   leaf
C18_11d_WS4    WS   4      EnViros Vitis vinifera  grapevine   leaf
C18_11d_WW1    WW   1      EnViros Vitis vinifera  grapevine   leaf
C18_11d_WW2    WW   2      EnViros Vitis vinifera  grapevine   leaf
```

```
            health.status plant.number growth.location
C18_11d_WS1  water stress           R1           Udine
C18_11d_WS2  water stress           R2           Udine
C18_11d_WS3  water stress           R3           Udine
C18_11d_WS4  water stress           R4           Udine
C18_11d_WW1  well watered           R1           Udine
C18_11d_WW2  well watered           R2           Udine
            growth.conditions
C18_11d_WS1           outside
C18_11d_WS2           outside
C18_11d_WS3           outside
C18_11d_WS4           outside
C18_11d_WW1           outside
C18_11d_WW2           outside

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

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

One plot:

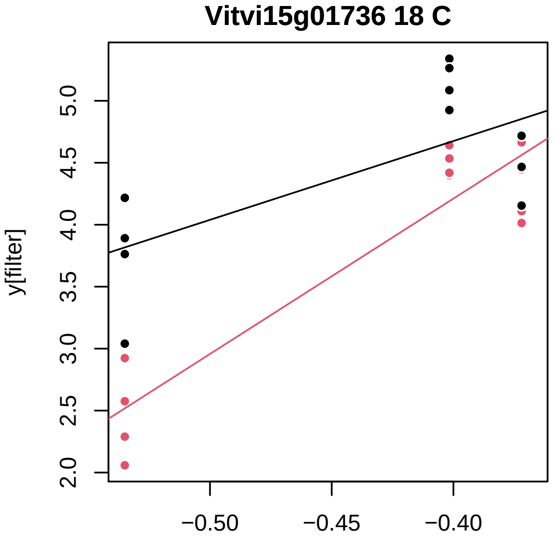
```
> t1819[1,]
```

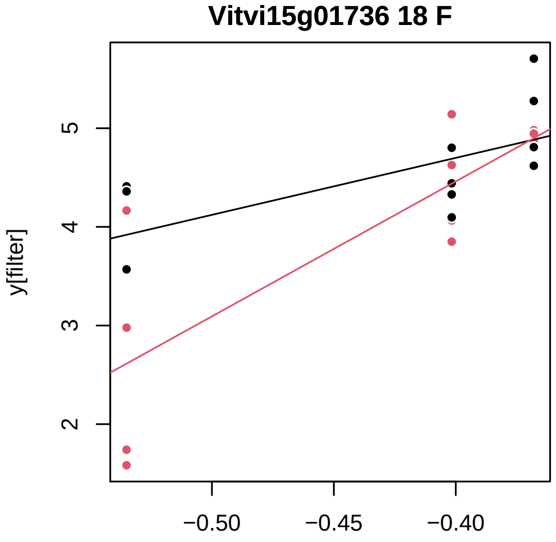
```
              C18_11d_WS1 C18_11d_WS2 C18_11d_WS3 C18_11d_WS4
Vitvi15g01736    4.664602    4.109897     4.44822    4.013955
              C18_11d_WW1 C18_11d_WW2 C18_11d_WW3 C18_11d_WW4
Vitvi15g01736    4.717536    4.154237    4.475261    4.466465
              C18_34d_WS1 C18_34d_WS2 C18_34d_WS3 C18_34d_WS4
Vitvi15g01736    4.400333    4.641164    4.419123    4.534438
              C18_34d_WW1 C18_34d_WW2 C18_34d_WW3 C18_34d_WW4
Vitvi15g01736    4.924801     5.08569    5.339735    5.263629
              C18_67d_WS1 C18_67d_WS2 C18_67d_WS3 C18_67d_WS4
Vitvi15g01736    2.058717    2.289503    2.923483    2.575657
              C18_67d_WW1 C18_67d_WW2 C18_67d_WW3 C18_67d_WW4
Vitvi15g01736    3.891121    3.040087    4.216897    3.763086
              F18_10d_WS1 F18_10d_WS2 F18_10d_WS3 F18_10d_WS4
Vitvi15g01736    4.859141    4.866943     4.98059    4.945395
              F18_10d_WW1 F18_10d_WW2 F18_10d_WW3 F18_10d_WW4
Vitvi15g01736    5.705006    4.619238    4.808548    5.276124
              F18_34d_WS1 F18_34d_WS2 F18_34d_WS3 F18_34d_WS4
Vitvi15g01736    4.064718    3.850458    5.141832    4.626909
              F18_34d_WW1 F18_34d_WW2 F18_34d_WW3 F18_34d_WW4
Vitvi15g01736    4.096173    4.802221    4.329152    4.441903
              F18_67d_WS1 F18_67d_WS2 F18_67d_WS3 F18_67d_WS4
Vitvi15g01736    1.583128    1.740858    2.978406    4.166406
              F18_67d_WW1 F18_67d_WW2 F18_67d_WW3 F18_67d_WW4
Vitvi15g01736    3.558043    3.569471    4.411209    4.359744
              C19_22d_WS1 C19_22d_WS2 C19_22d_WS3 C19_22d_WS4
Vitvi15g01736        3.18         3.5        3.19        3.61
              C19_22d_WW1 C19_22d_WW2 C19_22d_WW3 C19_22d_WW4
Vitvi15g01736        5.42        5.35        4.68        4.92
              C19_44d_WS1 C19_44d_WS2 C19_44d_WS3 C19_44d_WS4
Vitvi15g01736        5.13        5.19        5.71        5.29
              C19_44d_WW1 C19_44d_WW2 C19_44d_WW3 C19_44d_WW4
Vitvi15g01736        6.19        5.62        5.62        6.19
              F19_22d_WS1 F19_22d_WS2 F19_22d_WS3 F19_22d_WS4
Vitvi15g01736        3.03        3.93        4.24        2.85
              F19_22d_WW1 F19_22d_WW2 F19_22d_WW3 F19_22d_WW4
Vitvi15g01736           5        4.97        4.47        5.51
              F19_44d_WS1 F19_44d_WS2 F19_44d_WS3 F19_44d_WS4
Vitvi15g01736        5.84        5.83        4.56        5.23
              F19_44d_WW1 F19_44d_WW2 F19_44d_WW3 F19_44d_WW4
Vitvi15g01736        5.44        6.13        5.96        6.16
> (varname <- rownames(t1819)[1])
[1] "Vitvi15g01736"

> .testing <- !TRUE
> pd <- pdata1819w
> par(mfrow=c(2,2),mar=c(3,4,2,1))
> (varname <- rownames(t1819)[1])
[1] "Vitvi15g01736"
> (yr <- unique(pd$year)[1])
[1] 18
Levels: 18 19
```

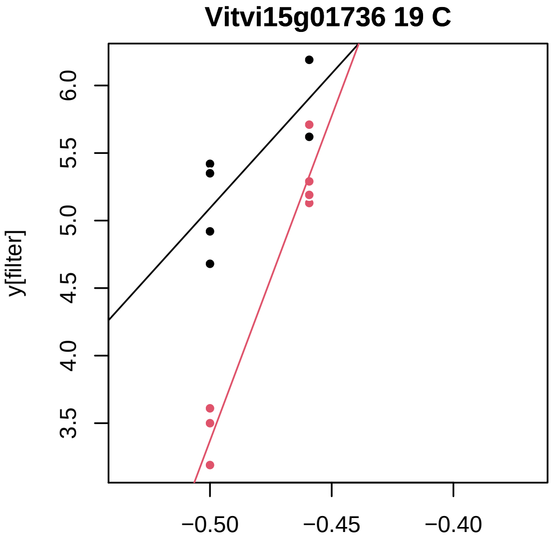
```
> (vari  <-  levels(pd$variety)[1])
[1] "C"
> for( yr in unique(pd$year)){
+ for (vari in levels(pd$variety)) {
+     filter <- (pd$year %in% yr) & (pd$variety %in% vari)
+     print(filter)
+     print(pd$date[filter])
+ (    y <- unlist(t1819[varname,]))
+   with(pd, {
+     plot(pd$swp[filter], y[filter],
+        type="p",
+        bg=pd$treat[filter],
+        pch=21,
+        cex=1,
+        col="white",
+        xlim=range(pd$swp)
+        )
+     for(i in 1:length(levels(treat))){
+     tr <- levels(pd$treat)[i]
+     select <- filter & (pd$treat %in% tr)
+     fit <- lm(y[select]~pd$swp[select])
+     print(fit)
+     abline(fit,col=i)
+ #    lines(date[select],swp[select],type="b",pch=16,col=treat[select])
+     title(paste(varname, yr, vari))
+     }
+     })
+   }
+ }
 [1]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
[12]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
[23]  TRUE  TRUE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[34] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[45] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[56] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[67] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[78] FALSE FALSE FALSE
 [1] "2018-06-12" "2018-06-12" "2018-06-12" "2018-06-12" "2018-06-12"
 [6] "2018-06-12" "2018-06-12" "2018-06-12" "2018-07-05" "2018-07-05"
[11] "2018-07-05" "2018-07-05" "2018-07-05" "2018-07-05" "2018-07-05"
[16] "2018-07-05" "2018-08-07" "2018-08-07" "2018-08-07" "2018-08-07"
[21] "2018-08-07" "2018-08-07" "2018-08-07" "2018-08-07"

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

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


Call:
```

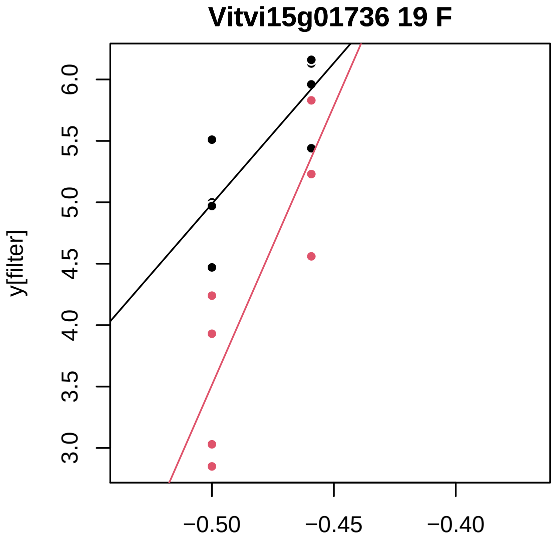
```
lm(formula = y[select] ~ pd$swp[select])

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

 [1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[12] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[23] FALSE FALSE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
[34]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
[45]  TRUE  TRUE  TRUE  TRUE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[56] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[67] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[78] FALSE FALSE FALSE
 [1] "2018-06-11" "2018-06-11" "2018-06-11" "2018-06-11" "2018-06-11"
 [6] "2018-06-11" "2018-06-11" "2018-06-11" "2018-07-05" "2018-07-05"
[11] "2018-07-05" "2018-07-05" "2018-07-05" "2018-07-05" "2018-07-05"
[16] "2018-07-05" "2018-08-07" "2018-08-07" "2018-08-07" "2018-08-07"
[21] "2018-08-07" "2018-08-07" "2018-08-07" "2018-08-07"

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

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


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

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

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

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

Coefficients:
   (Intercept)  pd$swp[select]
```

```
         15.06            19.93


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

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

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


Vitvi15g01736 18 C


Vitvi15g01736 18 F


Vitvi15g01736 19 C


Vitvi15g01736 19 F

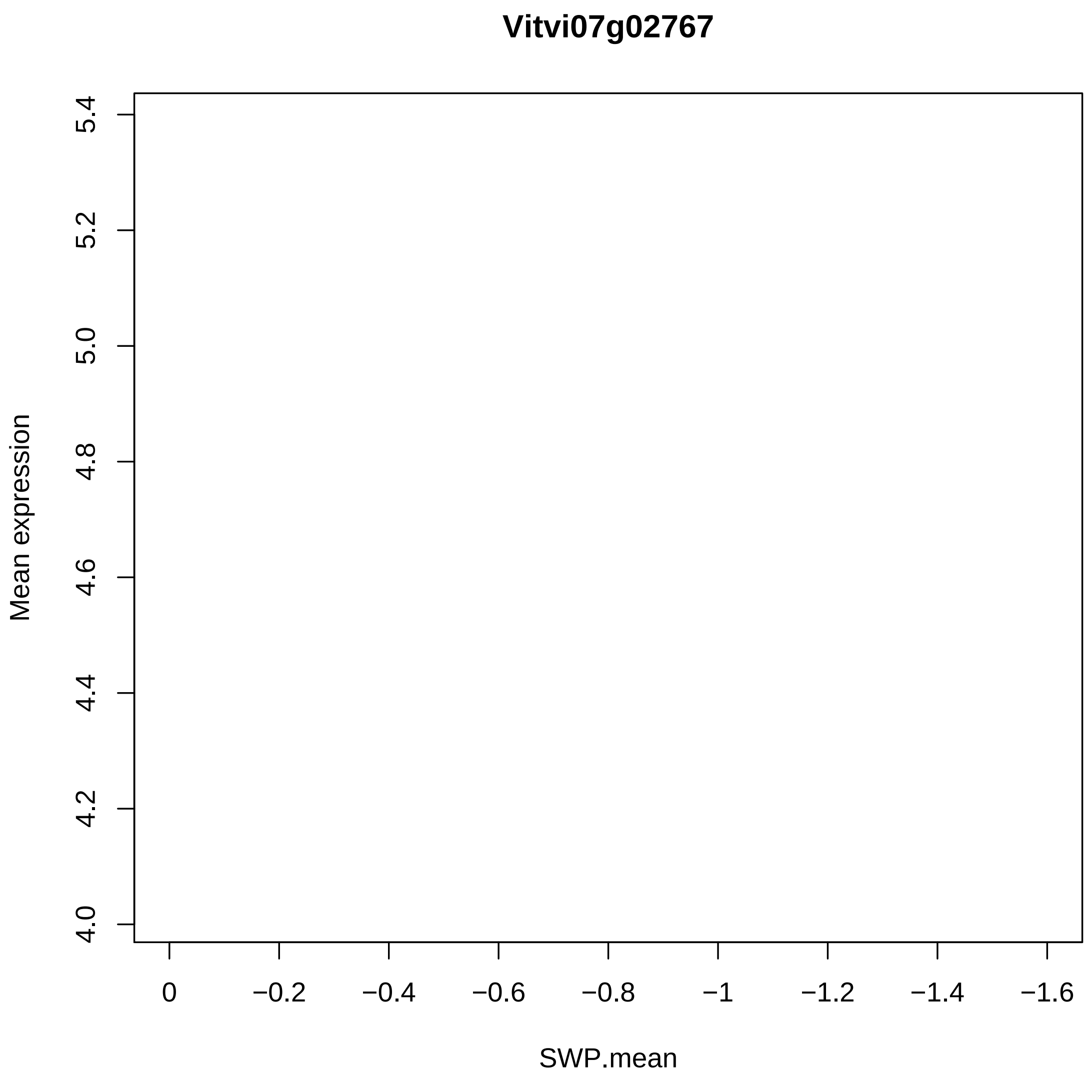
```
Call:
lm(formula = y[select] ~ pd$swp[select])

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


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

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

4 Expression and water poential analysis

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

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

, , variety = F

            treat
date               WW       WS
```

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

> varname <- rownames(t1819)[10]
> #varname <- rownames(t1819)[runif(1,1,10000)]
> (y <- unlist(t1819[varname,]))
C18_11d_WS1 C18_11d_WS2 C18_11d_WS3 C18_11d_WS4 C18_11d_WW1
   4.088427    3.961216    4.127170    3.916955    4.472212
C18_11d_WW2 C18_11d_WW3 C18_11d_WW4 C18_34d_WS1 C18_34d_WS2
   4.309540    4.212060    4.154032    4.086692    3.914995
C18_34d_WS3 C18_34d_WS4 C18_34d_WW1 C18_34d_WW2 C18_34d_WW3
   4.065776    4.081348    4.313965    4.041339    4.318997
C18_34d_WW4 C18_67d_WS1 C18_67d_WS2 C18_67d_WS3 C18_67d_WS4
   4.238240    4.441597    4.248104    4.242540    3.969094
C18_67d_WW1 C18_67d_WW2 C18_67d_WW3 C18_67d_WW4 F18_10d_WS1
   4.160356    4.676748    4.467201    4.359372    4.102511
F18_10d_WS2 F18_10d_WS3 F18_10d_WS4 F18_10d_WW1 F18_10d_WW2
   4.307786    4.261419    4.248699    4.239323    4.289799
F18_10d_WW3 F18_10d_WW4 F18_34d_WS1 F18_34d_WS2 F18_34d_WS3
   4.620659    4.532309    4.114948    4.149386    4.350818
F18_34d_WS4 F18_34d_WW1 F18_34d_WW2 F18_34d_WW3 F18_34d_WW4
   4.075166    4.239367    4.109161    4.460006    4.507653
F18_67d_WS1 F18_67d_WS2 F18_67d_WS3 F18_67d_WS4 F18_67d_WW1
   4.443768    4.392282    4.258226    4.311732    4.659167
F18_67d_WW2 F18_67d_WW3 F18_67d_WW4 C19_22d_WS1 C19_22d_WS2
   4.584738    4.404701    4.488189    5.160000    5.040000
C19_22d_WS3 C19_22d_WS4 C19_22d_WW1 C19_22d_WW2 C19_22d_WW3
   4.950000    4.920000    5.060000    4.710000    5.410000
C19_22d_WW4 C19_44d_WS1 C19_44d_WS2 C19_44d_WS3 C19_44d_WS4
   5.070000    4.420000    4.480000    4.490000    4.570000
C19_44d_WW1 C19_44d_WW2 C19_44d_WW3 C19_44d_WW4 F19_22d_WS1
   4.930000    5.000000    4.820000    4.770000    5.560000
F19_22d_WS2 F19_22d_WS3 F19_22d_WS4 F19_22d_WW1 F19_22d_WW2
   5.150000    5.130000    5.690000    5.060000    5.160000
F19_22d_WW3 F19_22d_WW4 F19_44d_WS1 F19_44d_WS2 F19_44d_WS3
   5.250000    4.940000    4.710000    4.320000    4.910000
F19_44d_WS4 F19_44d_WW1 F19_44d_WW2 F19_44d_WW3 F19_44d_WW4
   4.540000    5.030000    4.700000    4.820000    4.720000
> means <- tapply(y,pd[,c("date","treat","variety")],mean,na.rm=TRUE)
> swps <- tapply(pd$swp,pd[,c("date","treat","variety")],unique)
```

```
Error in tapply(pd$swp, pd[, c("date", "treat", "variety")], unique): argument
> means
, , variety = C

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

, , variety = F

            treat
date               WW       WS
  2018-06-11 4.420523 4.230104
  2018-06-12       NA       NA
  2018-07-05 4.329047 4.172579
  2018-08-07 4.534199 4.351502
  2019-06-26 5.102500 5.382500
  2019-07-18 4.817500 4.620000

> ylim <- range(means, na.rm=TRUE)
> xlim <- c(min(wpas$swp,-1.6,na.rm=TRUE), max(wpas$swp,0, na.rm=TRUE))
> vlvls <- unique(wpas$variety)
> tlvls <- rev(unique(wpas$treat))
> cols <- c(4,2)
> pchs <- c(16,16)
> plot(1,1, #wpas$swp[tfilter & vfilter], means[,"WS",vlvls[i]],
+       ylim=ylim,
+       xlim=-rev(xlim),
+       xlab = "SWP.mean",
+       ylab = "Mean expression",
+       type="n",
+       axes=FALSE
+       )
> axis(2)
> box()
> axis(1,at=seq(0,2,0.2),labels=-(seq(0,2,0.2)))
> title(varname)
```



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

4.1 Expression vs water potential

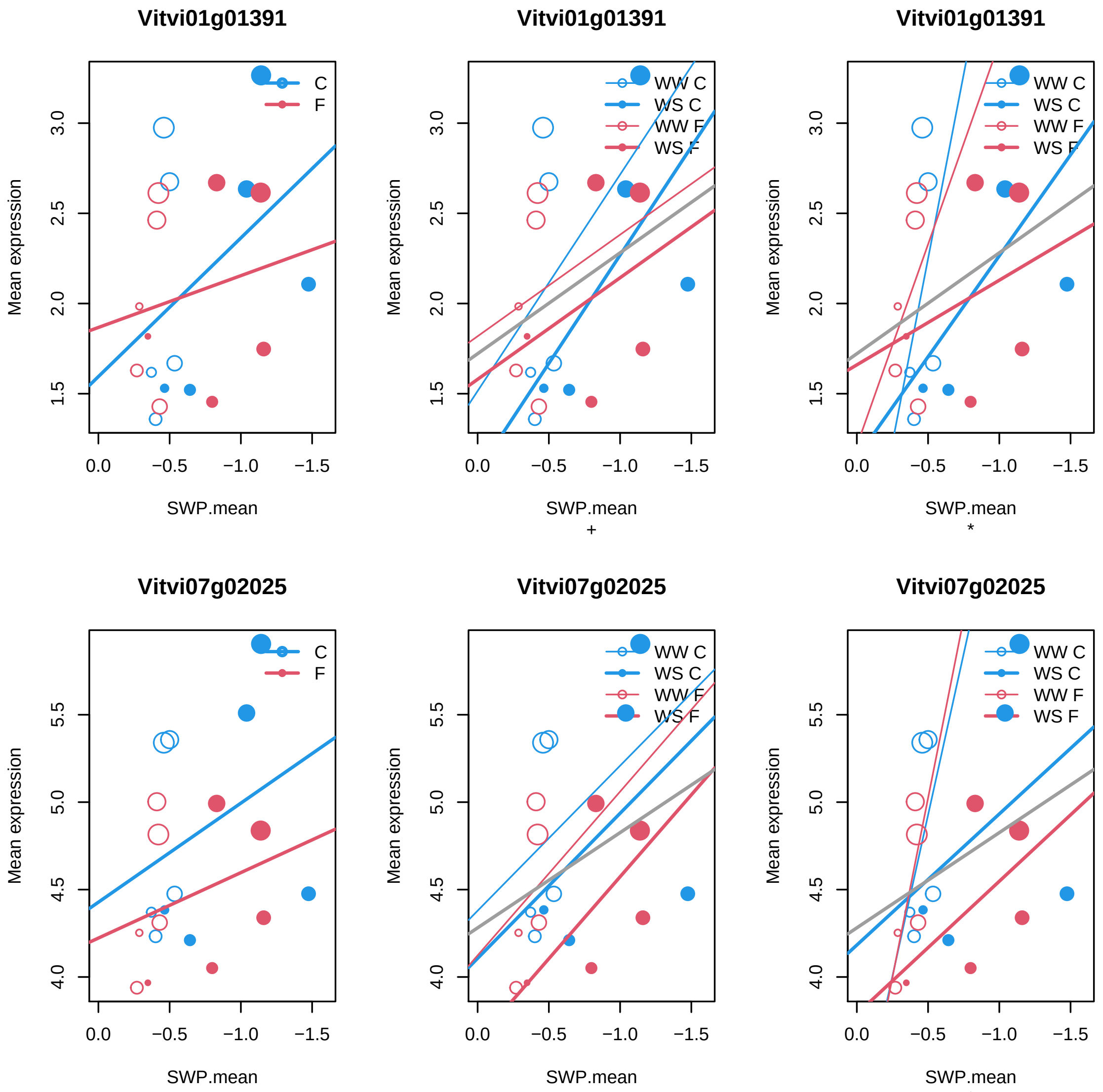
```
> plot.ewp <- function(varname,cols=c(4,2),pchs=c(1,16),lwd=c(1,2,1,2)
+       ,model=c("*"), verbose=FALSE, exprs=t1819, pd=pdata1819,ylim=NULL, cex=
+ if(verbose) print(varname)
+ (y <- unlist(exprs[varname,]))
+ means <- tapply(y,pd[,c("date","treat","variety")],mean,na.rm=TRUE)
+ #print(means)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

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

```
> par(mfrow=c(2,3))
> #
> varname <- rownames(t1819)[10]
> varname
```

```
[1] "Vitvi07g02767"
```

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



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

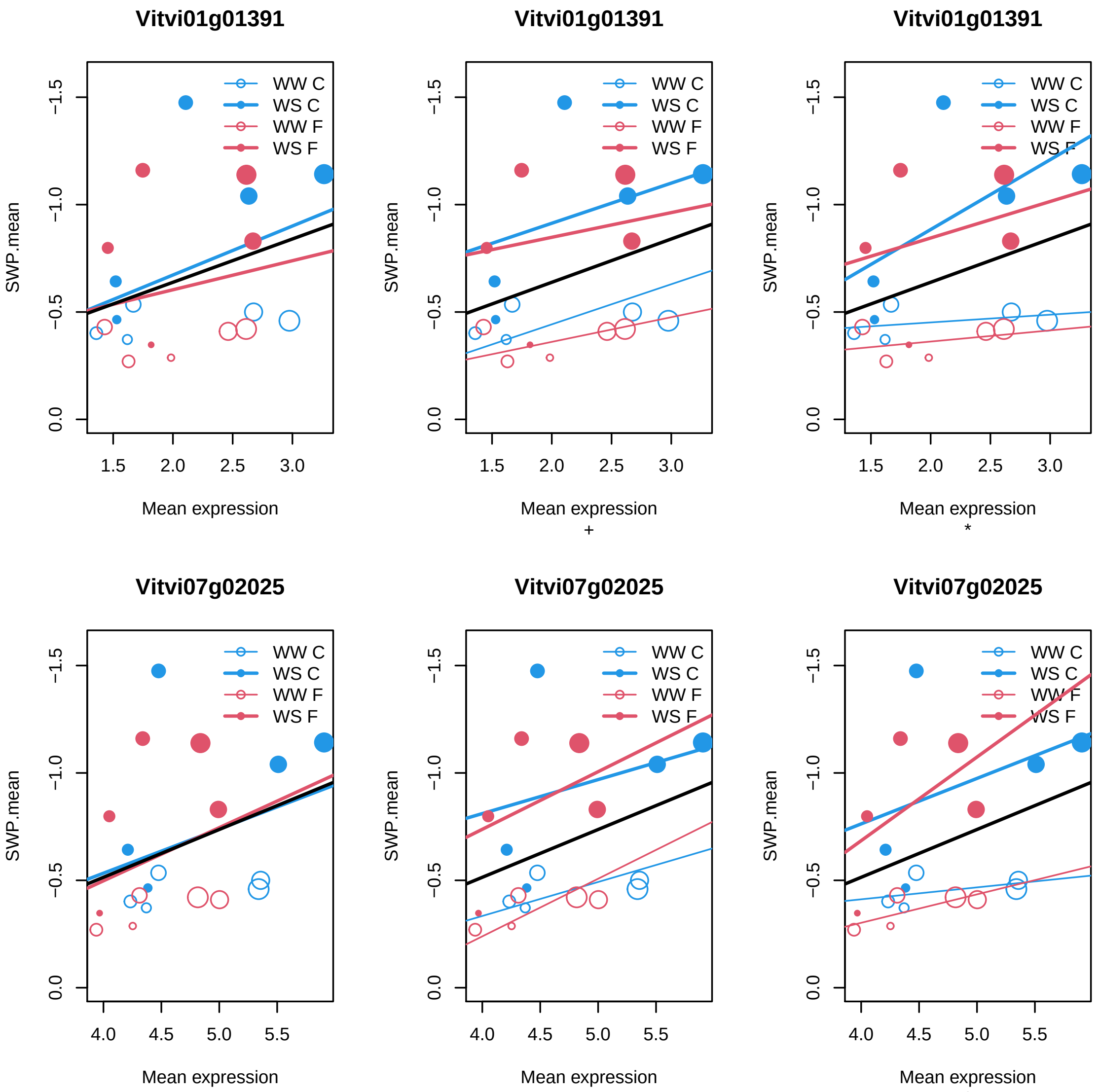
4.2 Water potential vs Expression

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

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

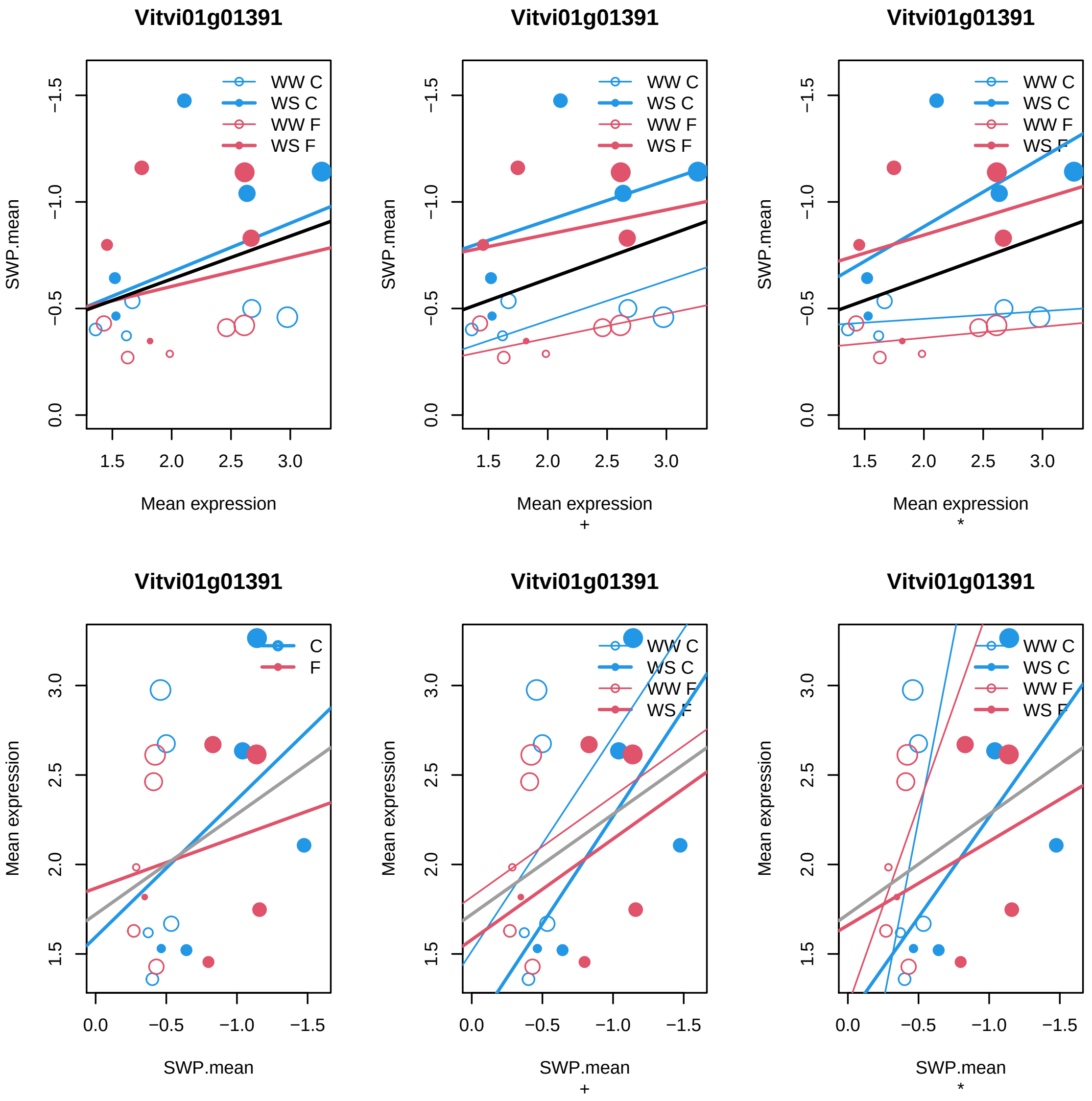
```
+ fits[["r"]] <- cor(ally,allx,use="complete")
+ if (verbose) print(summary(fit))
+ abline(fit$coefficients,lwd=2)
+ #points(-swps,means,cex=1.5)
+ invisible(fits)
+ }
```

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



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

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

> testvar <- "Vitvi01g01391"

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

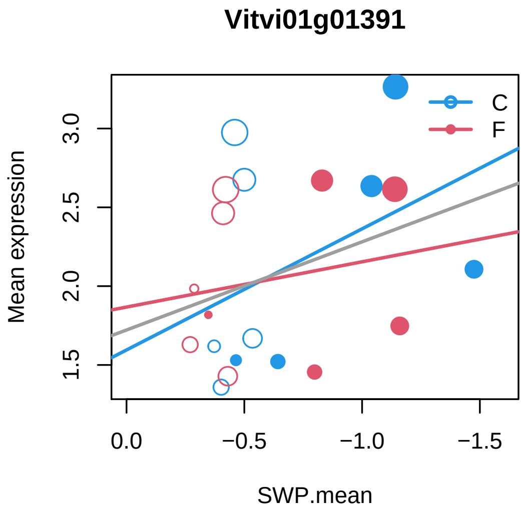


```
> fits
```

```
$name
[1] "Vitvi01g01391"

$C

Call:
lm(formula = yy ~ xx)

Coefficients:
(Intercept)           xx
     1.5950      -0.7686


$F

Call:
lm(formula = yy ~ xx)

Coefficients:
(Intercept)           xx
     1.8673      -0.2872


$all

Call:
lm(formula = ally ~ allx)

Coefficients:
(Intercept)         allx
     1.7218      -0.5594


$r
[1] -0.3359093

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

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

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

, , variety = F

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

> par(mfrow=c(2,2))
> plot.ewp(varname,model="")
> usr <- par("usr")
> for(i in 1:2){
+   par(usr=usr)
+   wpa$swp
+   ( yy <- as.vector( ( means[as.character(wpa$date), ,vlvls[i]]) ) )
+   xx <- -rep(wpa$swp, length(tlvls))[!is.na(yy)]
+   yy <- yy[!is.na(yy)]
```

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



5 Linear models for water potential

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

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

    plotMA
```

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

We will use models on average expressions across replicates.

```
> varname <- testvar
> (y <- unlist(t1819[varname,]))
C18_11d_WS1 C18_11d_WS2 C18_11d_WS3 C18_11d_WS4 C18_11d_WW1
  1.5776032   1.4525081   1.5639675   1.5265365   1.5687083
C18_11d_WW2 C18_11d_WW3 C18_11d_WW4 C18_34d_WS1 C18_34d_WS2
  1.5729410   1.3865447   1.9464369   1.7347063   1.2654132
C18_34d_WS3 C18_34d_WS4 C18_34d_WW1 C18_34d_WW2 C18_34d_WW3
  1.4874714   1.5978309   1.4698219   0.8040958   1.3141315
C18_34d_WW4 C18_67d_WS1 C18_67d_WS2 C18_67d_WS3 C18_67d_WS4
  1.8480061   2.4172910   2.2355638   2.1438253   1.6317226
C18_67d_WW1 C18_67d_WW2 C18_67d_WW3 C18_67d_WW4 F18_10d_WS1
  1.6332742   1.9178152   1.4992723   1.6246928   1.7805825
F18_10d_WS2 F18_10d_WS3 F18_10d_WS4 F18_10d_WW1 F18_10d_WW2
  1.8735295   1.9142822   1.7035168   2.0980960   2.1052765
F18_10d_WW3 F18_10d_WW4 F18_34d_WS1 F18_34d_WS2 F18_34d_WS3
  1.9447357   1.7887485   1.5892246   1.3699329   1.4469174
F18_34d_WS4 F18_34d_WW1 F18_34d_WW2 F18_34d_WW3 F18_34d_WW4
  1.4139991   1.5153857   1.4749029   1.9144891   1.6107161
F18_67d_WS1 F18_67d_WS2 F18_67d_WS3 F18_67d_WS4 F18_67d_WW1
  1.9483340   1.6580581   1.9058175   1.4784712   1.4242818
F18_67d_WW2 F18_67d_WW3 F18_67d_WW4 C19_22d_WS1 C19_22d_WS2
  1.3742853   1.4653761   1.4504864   2.8000000   2.6400000
C19_22d_WS3 C19_22d_WS4 C19_22d_WW1 C19_22d_WW2 C19_22d_WW3
  2.2900000   2.8100000   2.5900000   2.7900000   2.7500000
C19_22d_WW4 C19_44d_WS1 C19_44d_WS2 C19_44d_WS3 C19_44d_WS4
  2.5700000   2.9400000   3.3900000   3.3900000   3.3400000
C19_44d_WW1 C19_44d_WW2 C19_44d_WW3 C19_44d_WW4 F19_22d_WS1
  2.6900000   3.1600000   3.1200000   2.9300000   2.5900000
F19_22d_WS2 F19_22d_WS3 F19_22d_WS4 F19_22d_WW1 F19_22d_WW2
  2.9200000   2.8600000   2.3100000   2.4100000   2.1600000
F19_22d_WW3 F19_22d_WW4 F19_44d_WS1 F19_44d_WS2 F19_44d_WS3
  2.7200000   2.5600000   2.4800000   2.6400000   2.8200000
F19_44d_WS4 F19_44d_WW1 F19_44d_WW2 F19_44d_WW3 F19_44d_WW4
  2.5200000   2.6300000   2.5300000   2.6400000   2.6500000
> means <- tapply(y,pd[,c("date","treat","variety")],mean,na.rm=TRUE)
> means
, , variety = C

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

, , variety = F
```

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

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

```
, , variety = C

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

, , variety = F

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

Small phenodata

```
> exp <- unlist(as.data.frame(means))
> swp <- unlist(as.data.frame(swps))
> treat <- factor(substr(names(swp),1,2),levels=levels(wpas$treat))
> variety <- factor(substr(names(swp),4,4))
> sday <- as.numeric(substr(names(swp),5,5))
> pd1 <- data.frame(swp,treat,variety,sday=sday,date=dimnames(swps)[[1]],
+      row.names=names(swp))
> 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
```

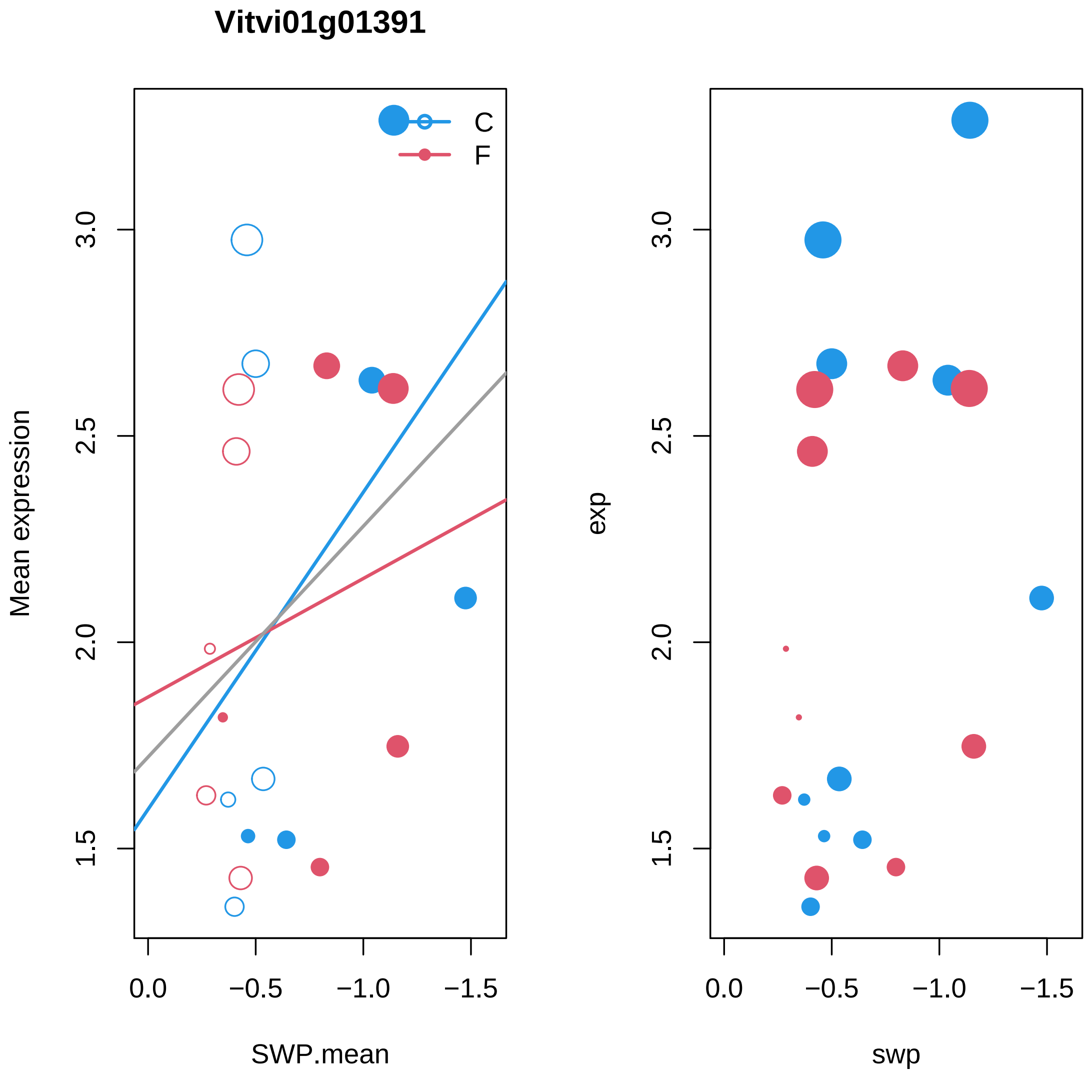
```
WS.C4 -1.4750000    WS       C    4 2018-08-07
WS.C5 -1.0400000    WS       C    5 2019-06-26
WS.C6 -1.1419231    WS       C    6 2019-07-18
WW.F1 -0.2872727    WW       F    1 2018-06-11
WW.F2 -0.2854545    WW       F    2 2018-06-12
WW.F3 -0.2700000    WW       F    3 2018-07-05
WW.F4 -0.4300000    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
```

```
> 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" ...
```

Graphical test, check the points positions :(

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



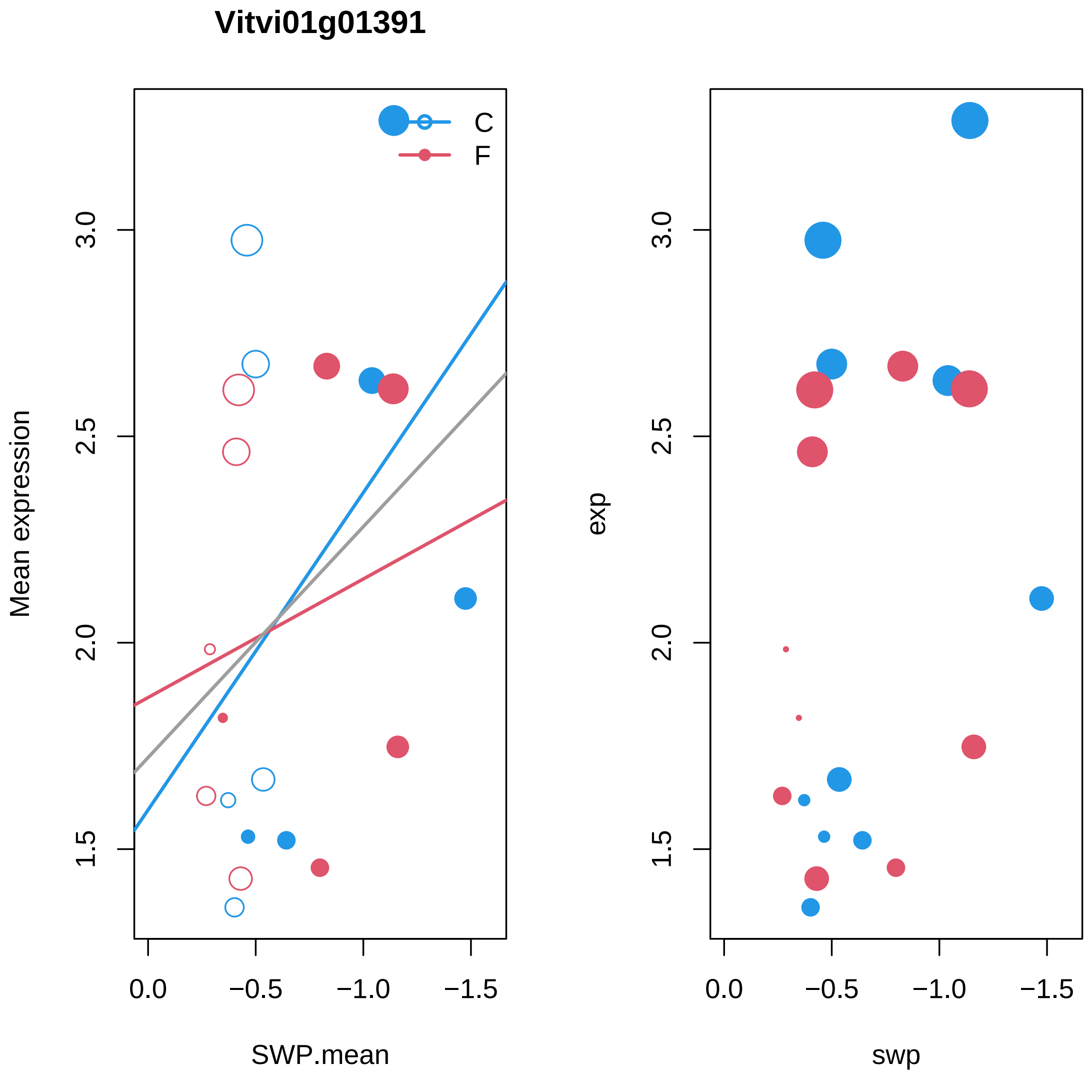
Aggregated expressions

```
> FUN <- function(x) unlist(as.data.frame(tapply(unlist(x),pd[,c("date","treat
> FUN(exprs[1,])
   WW.C1    WW.C2    WW.C3    WW.C4    WW.C5    WW.C6    WS.C1
      NA 4.453375 5.153464 3.727798 5.092500 5.905000       NA
   WS.C2    WS.C3    WS.C4    WS.C5    WS.C6    WW.F1    WW.F2
4.309168 4.498764 2.461840 3.370000 5.330000 5.102229       NA
   WW.F3    WW.F4    WW.F5    WW.F6    WS.F1    WS.F2    WS.F3
4.417362 3.974617 4.987500 5.922500 4.913018       NA 4.420979
   WS.F4    WS.F5    WS.F6
2.617199 3.512500 5.365000
> expr <- t(apply(exprs,1, FUN=FUN))
> dim(expr)
[1] 15242    24
> str(expr)
 num [1:15242, 1:24] NA NA NA NA NA NA NA NA NA NA ...
 - attr(*, "dimnames")=List of 2
  ..$ : chr [1:15242] "Vitvi15g01736" "Vitvi07g02832" "Vitvi07g02830" "Vitvi07
  ..$ : chr [1:24] "WW.C1" "WW.C2" "WW.C3" "WW.C4" ...
```

```
> filter <- apply(expr,2,function(x) !all(is.na(x)))
> expr <- expr[,filter]
> pd1 <- pd1[filter,]
> dim(expr)
[1] 15242    20
> dim(pd1)
[1] 20  5
> str(expr)
 num [1:15242, 1:20] 4.453 -2.47 -1.522 -0.894 2.059 ...
 - attr(*, "dimnames")=List of 2
  ..$ : chr [1:15242] "Vitvi15g01736" "Vitvi07g02832" "Vitvi07g02830" "Vitvi07
  ..$ : chr [1:20] "WW.C2" "WW.C3" "WW.C4" "WW.C5" ...
> str(pd1)
'data.frame':	20 obs. of  5 variables:
 $ swp    : num  -0.372 -0.402 -0.535 -0.5 -0.459 ...
 $ treat  : Factor w/ 2 levels "WW","WS": 1 1 1 1 1 2 2 2 2 2 ...
 $ variety: Factor w/ 2 levels "C","F": 1 1 1 1 1 1 1 1 1 1 ...
 $ sday   : num  2 3 4 5 6 2 3 4 5 6 ...
 $ date   : chr  "2018-06-12" "2018-07-05" "2018-08-07" "2019-06-26" ...
```

Check regressions

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



```
> lapply(fits[2:4],function(x) x$coefficients)
```

```
$C
(Intercept)          xx
  1.5950412  -0.7685916

$F
(Intercept)          xx
  1.8672599  -0.2871816

$all
(Intercept)        allx
  1.7217725  -0.5593981
```

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

```
(Intercept)     pd1$swp
  1.5950412  -0.7685916
```

```
> fitf <- c(fitc[1]+fitc[3],fitc[2]+fitc[4])
> fitf
```

```
(Intercept)     pd1$swp
  1.8672599  -0.2871816
```

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

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

Looks ok.

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

```
[1] TRUE
```

Replace expressions and phenodata with the reduced ones.

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


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

```
[1] TRUE
```

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


> testvar <- "Vitvi01g01391"
```

5.1 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)
```

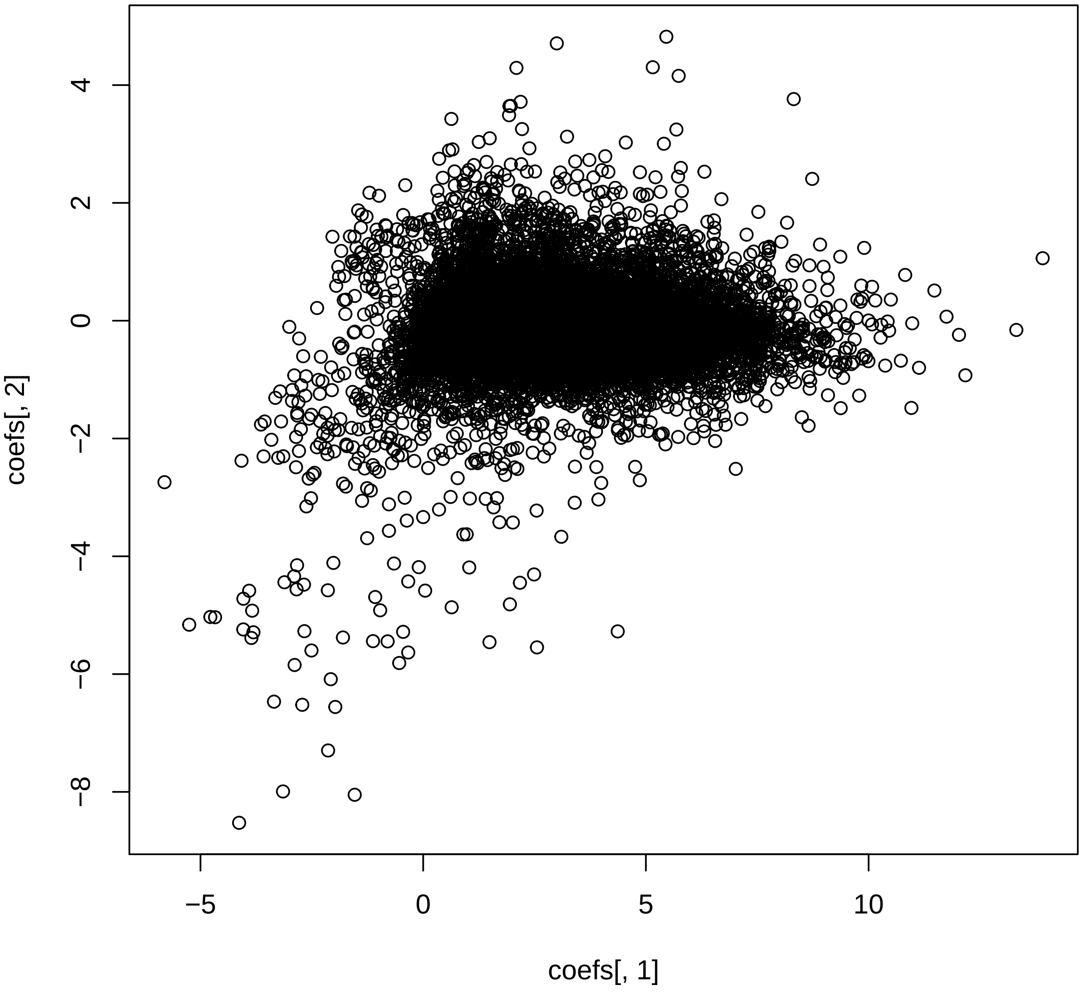
```
             (Intercept)       swp
Vitvi15g01736  5.42287213 1.4417521
Vitvi07g02832  0.79297631 1.4868377
Vitvi07g02830  1.05522190 2.1023461
Vitvi07g02812  0.02875199 0.5715781
Vitvi07g02811  3.02521622 0.8198777
Vitvi09g02033 -0.13442101 0.9949253
```

```
> 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
```

5.2 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
```

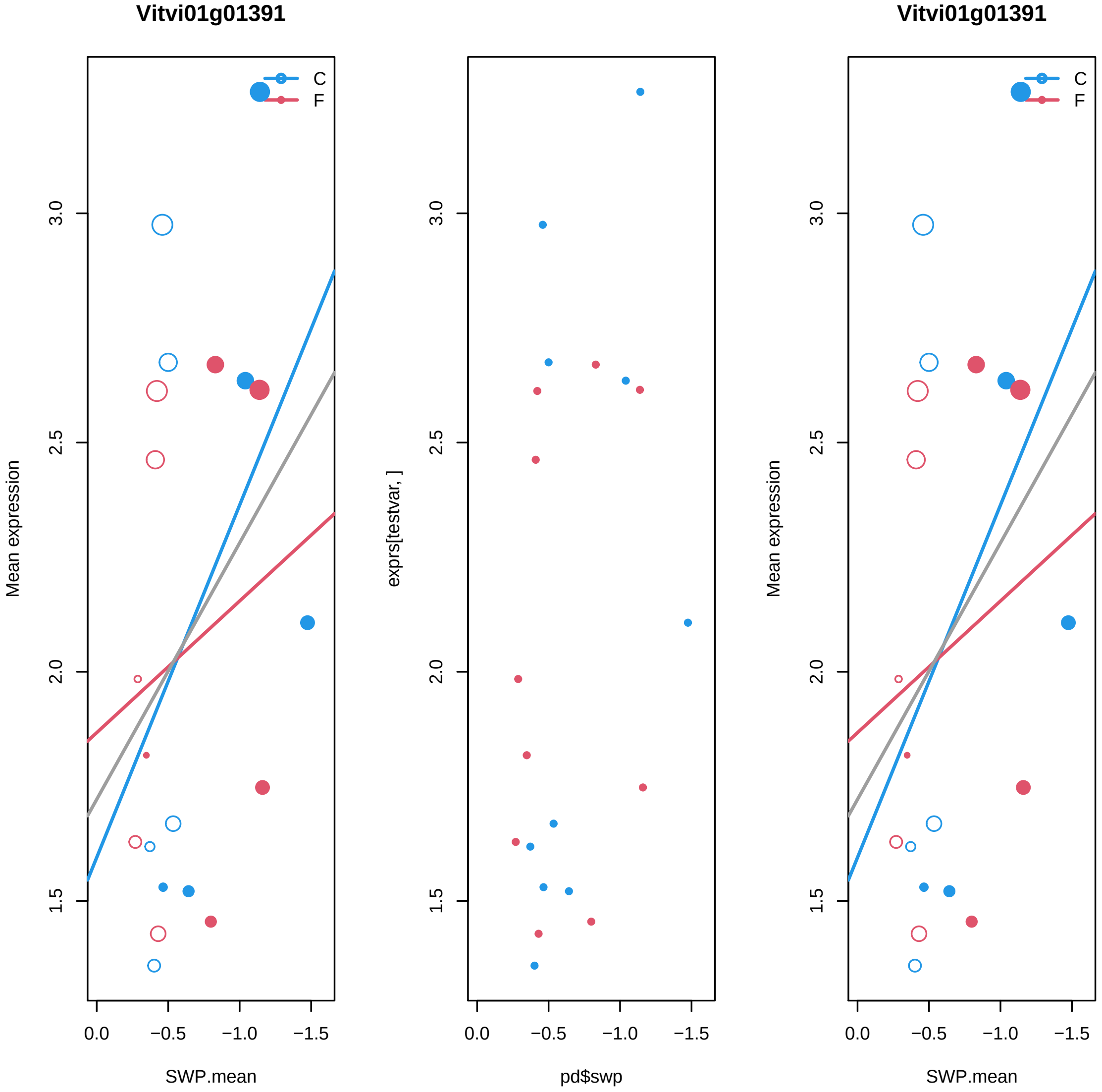
```
> varname <- testvar
> par(mfrow=c(1,3))
> p <- plot.ewp(varname,model="")
> plot(pd$swp,exprs[testvar,],  xlim=c(0,-1.6),
+    ,pch=16, col=6-as.numeric(pd$variety)*2,cex=pd$day/2)
> c(p$C$coef[2],p$F$coef[2])
```

```
        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
```

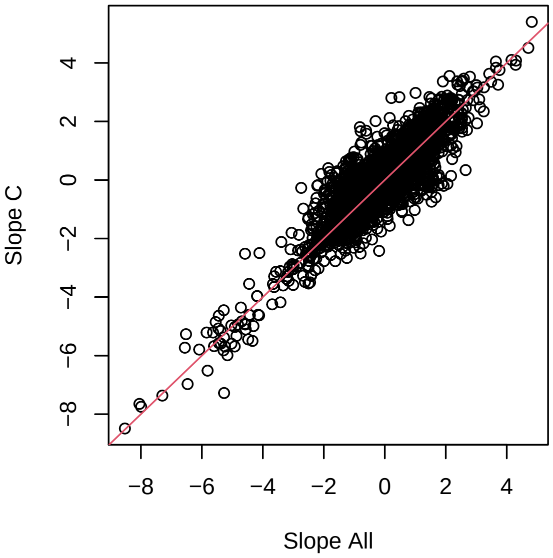
For comparison, here is the beginning of coefficients for overall model.

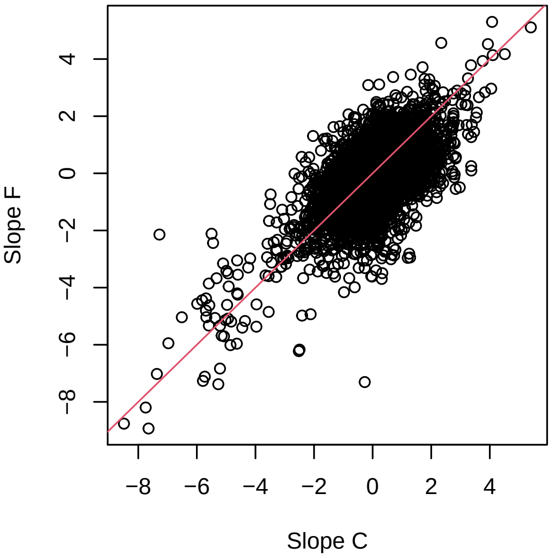
```
> head(fit1[1:6,]$coefficients)
              (Intercept)       swp
Vitvi15g01736  5.42287213 1.4417521
Vitvi07g02832  0.79297631 1.4868377
Vitvi07g02830  1.05522190 2.1023461
Vitvi07g02812  0.02875199 0.5715781
Vitvi07g02811  3.02521622 0.8198777
Vitvi09g02033 -0.13442101 0.9949253
```

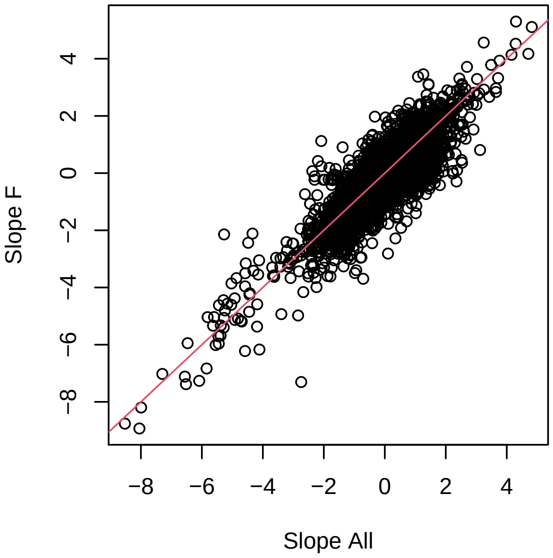
```
> fita[2]
   pd1$swp
-0.5593981
> fit1[testvar,]$coefficients[2]
[1] -0.5593981
> fitc[2]
   pd1$swp
-0.7685916
> fit2[testvar,]$coefficients[2]
[1] -0.7685916
> fitf[2]
   pd1$swp
-0.2871816
> fit2[testvar,]$coefficients[2]+fit2[testvar,]$coefficients[4]
[1] -0.2871816
```

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)
```

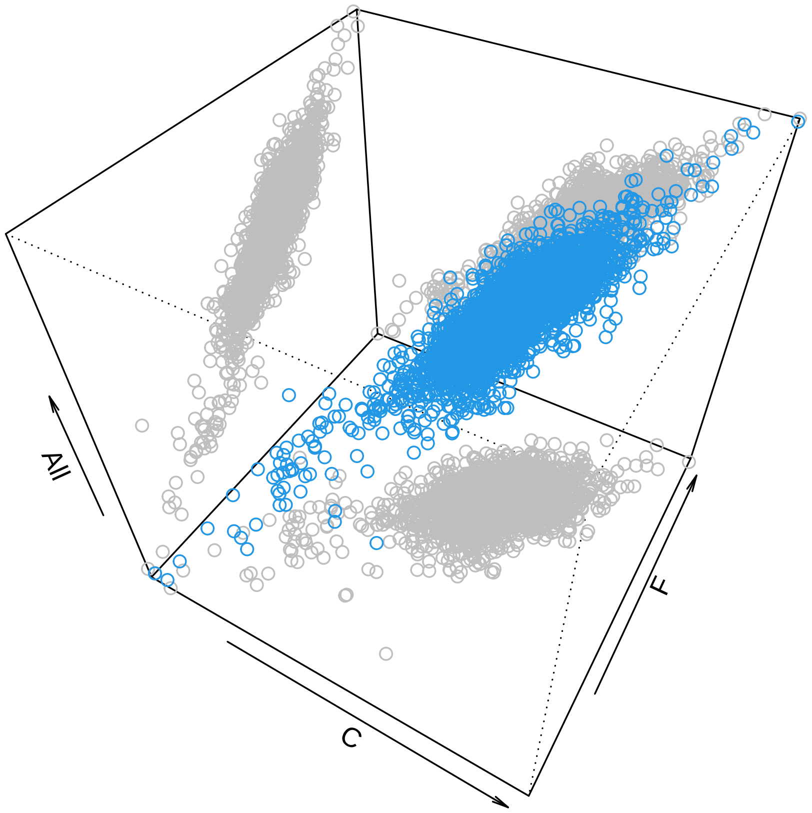






```
Warning: package 'fields' was built under R version 4.0.3
Loading required package: spam
Warning: package 'spam' was built under R version 4.0.3
Loading required package: dotCall64
Warning: package 'dotCall64' was built under R version 4.0.3
Loading required package: grid
Spam version 2.6-0 (2020-12-14) is loaded.
Type 'help( Spam)' or 'demo( spam)' for a short introduction
and overview of this package.
Help for individual functions is also obtained by adding the
suffix '.spam' to the function name, e.g. 'help( chol.spam)'.

Attaching package: 'spam'
The following object is masked from 'package:xtable':

    display
```

```
The following objects are masked from 'package:base':

    backsolve, forwardsolve
See https://github.com/NCAR/Fields for
 an extensive vignette, other supplements and source code

Attaching package: 'fields'
The following object is masked from 'package:Hmisc':

    describe
2222222222
```



5.3 Mean expressions

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

```
                (Intercept)       swp   varietyF swp:varietyF
Vitvi15g01736    5.550751 1.5935452 -0.2500355   -0.3175892
Vitvi07g02832   -2.634115 0.5081557  5.4166972   -0.2510959
> my.predict(fit2)[1:2,]
                     mc       mf
Vitvi15g01736  7.144296 6.576671
Vitvi07g02832 -2.125959 3.039642
> my.predict(fit2)[testvar,]
                     mc       mf
Vitvi01g01391 0.8264496 1.580078
> ma <- fit1$coefficients%*%c(1,mean(swp))
> macf <- data.frame(ma=ma,my.predict(fit2, x=mean(swp)))
> head(macf)
                      ma        mc        mf
Vitvi15g01736  4.4767407  4.505007 4.4633851
Vitvi07g02832 -0.1827419 -2.967585 2.6138903
Vitvi07g02830 -0.3244159 -2.766529 2.1602371
Vitvi07g02812 -0.3463388 -1.374935 0.6633139
Vitvi07g02811  2.4871819  1.864570 3.1087423
Vitvi09g02033 -0.7873280 -3.118171 1.5792098

> macf[testvar,]
                   ma      mc       mf
Vitvi01g01391 2.08887 2.09942 2.055719
```

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

```
> design3 <- with(pd, model.matrix(~ 0+variety))
> head(design3)
  varietyC varietyF
1        1        0
2        1        0
3        1        0
4        1        0
5        1        0
6        1        0
> tail(design3)
   varietyC varietyF
15        0        1
16        0        1
17        0        1
18        0        1
19        0        1
20        0        1
> fit3 <- lmFit(exprs, design3)
> fit3[testvar,]$coefficients
              varietyC varietyF
Vitvi01g01391 2.135505 2.042236
> mswps <- with(pd, aggregate(swp, list(variety), mean) )$x
> my.predict(fit2, mswps[1])[testvar,1]
[1] 2.135505
> my.predict(fit2, mswps[2])[testvar,2]
[1] 2.042236
```

Object `fit3` holds mean expressins for varieties.

5.3.1 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

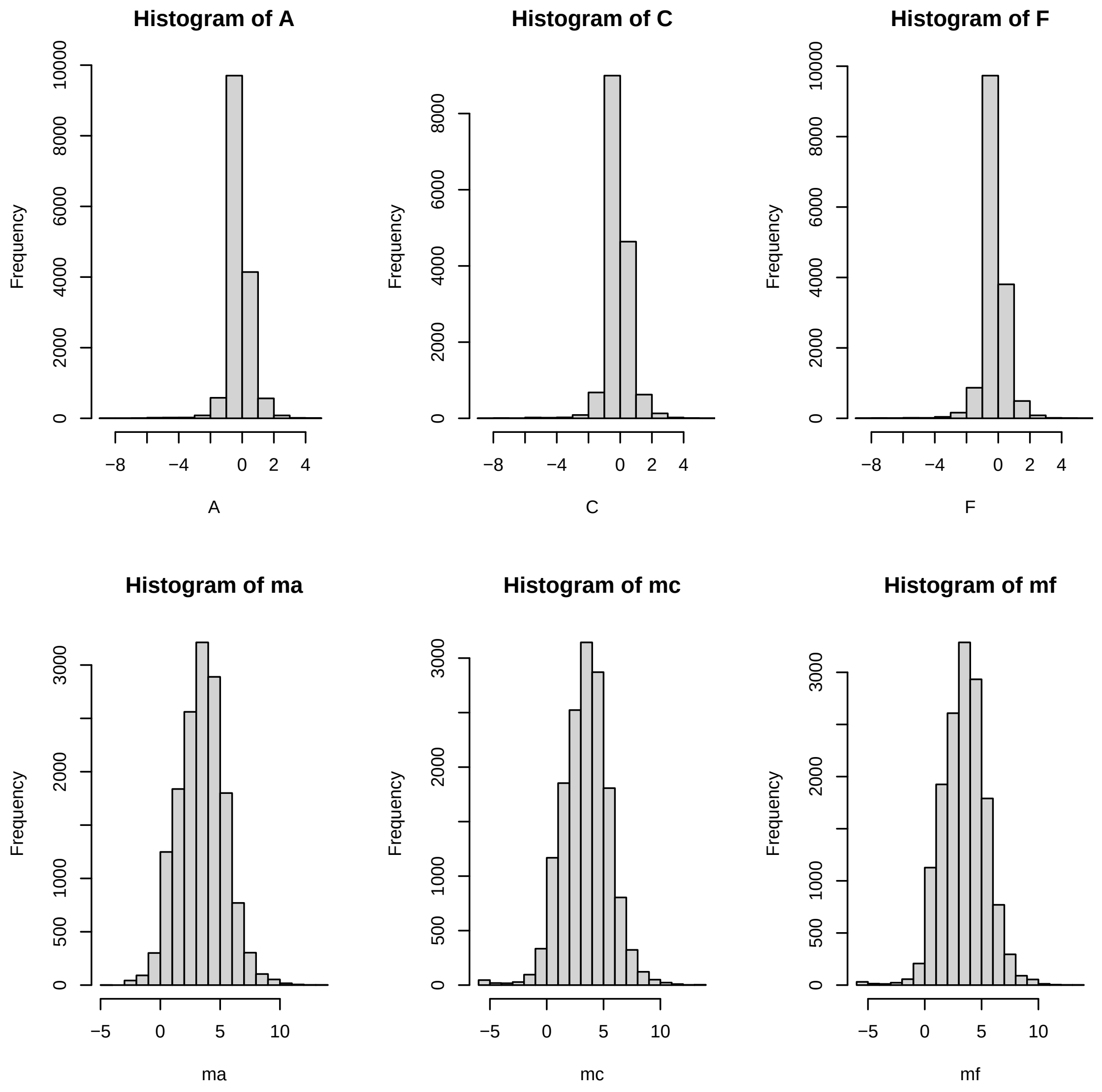
```
> A <- fit1$coefficients[,2]
> C <- fit2$coefficients[,2]
> F <- fit2$coefficients[,2]+fit2$coefficients[,4]
> ma <- macf[,"ma"]
> mc <- fit3$coefficients[,1]
> mf <- fit3$coefficients[,2]
> coefs <- data.frame(A,C,F,ma,mc,mf)
> head(coefs)
```

```
                      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
```

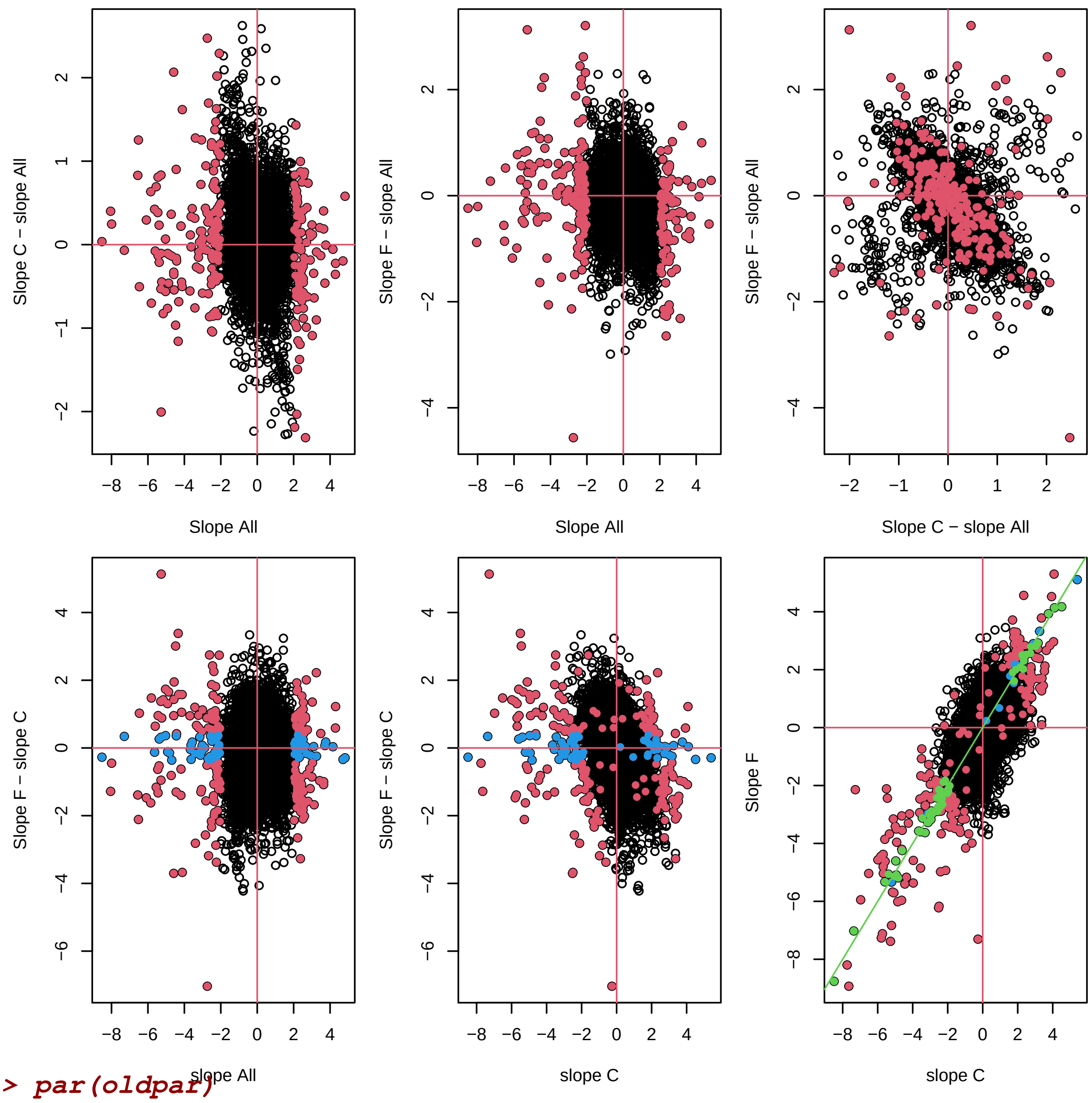
```
> par(mfrow=c(2,3))
> hist(A,xlim=range(c(A,C,F)))
> hist(C,xlim=range(c(A,C,F)))
> hist(F,xlim=range(c(A,C,F)))
> hist(ma)
> hist(mc)
> hist(mf)
```



5.3.2 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)
```

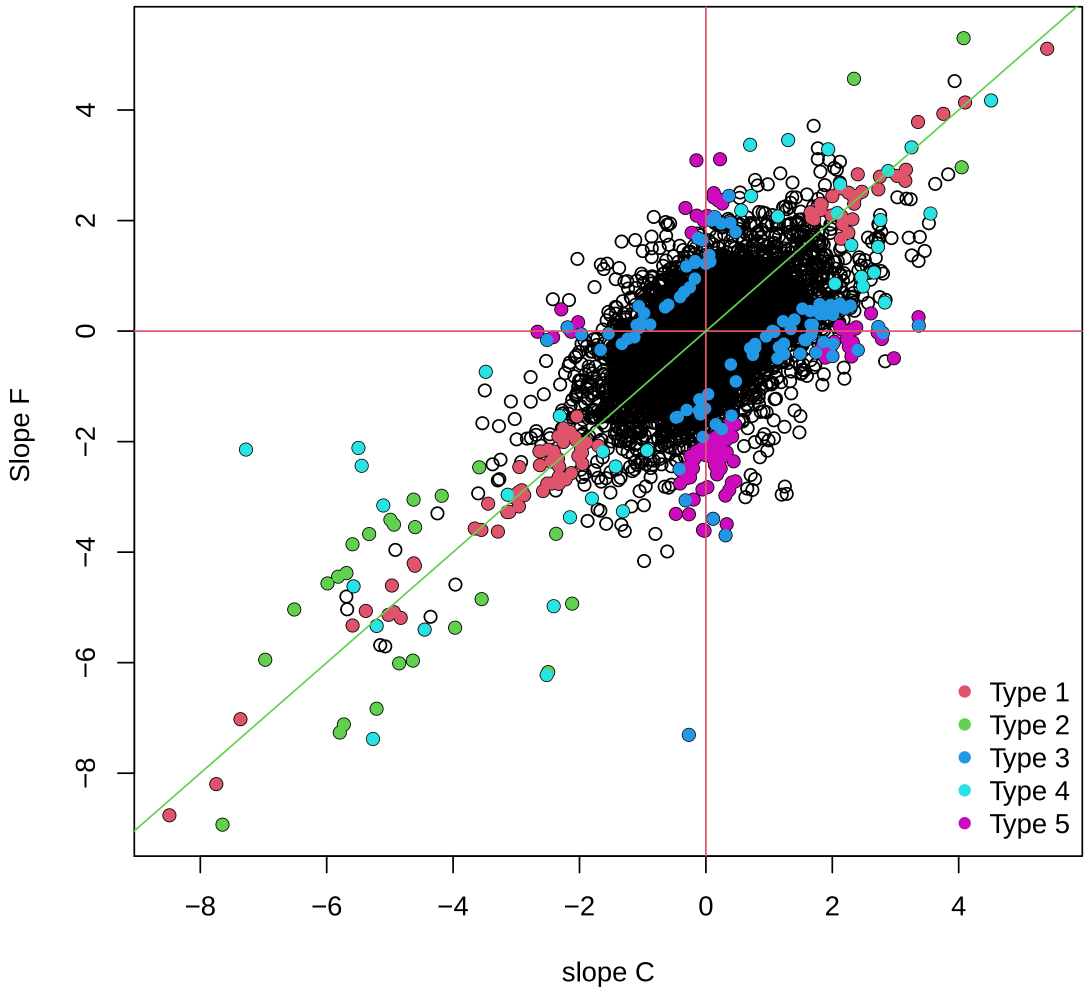
6 Situation types and Type selection criteria

Boundaries:
min for at least ... (>)
max for at most ... (<)
delta difference at most ... (<)

```
> #
> delta <- 2
> #
> deltam <- 2
> minA <- 2        # slope A larger
> maxC <- 0.5      # slope C smaller
> maxF <- maxC     # slope F smaller
> maxfc <- 0.5     # difference F - C smaller
> minfc <- 1       # differende F - C larger
> minC <- minA     # slope C larger
> minF <- minA     # slope F larger
```

```
> maxca <- maxfc  # difference C - A smaller
> maxfa <- maxfc  # difference F - A smaller
> #
> large_abs_A <- abs(A)> minA
> large_abs_C <- abs(C)> minC
> large_abs_F <- abs(F)> minF
> #
> small_fc <- abs(fc) < maxfc
> small_ca <- abs(ca) < maxca
> small_fa <- abs(fa) < maxfa
> plot(C,F, xlab="slope C",ylab="Slope F ")
> #points(C[large_abs_A],F[large_abs_A],col=2,pch=16)
> #
>
> type10 <- large_abs_A & small_fc & small_ca
> type1 <- (large_abs_C|large_abs_F) & small_fc & (abs(mc-mf)<deltam)
> table(type10,type1)
       type1
type10  FALSE  TRUE
  FALSE 15149    13
  TRUE      8    72
> points(
+    C[type1],
+    F[type1],
+    col=2, pch=16)
> #
> type2 <- (large_abs_C & large_abs_F) & (abs(fc) > minfc)
> type2 <- type2 & ( (C*F >0) )
> points(
+    C[type2],
+    F[type2],
+    col=3,pch=16)
> #
> type30 <- ((abs(C)<maxC)|(abs(F)<maxF)) & (abs(fc)> minfc)
> type3 <- ((abs(C)<maxC)|(abs(F)<maxF)) & (abs(fc)> minfc)&(abs(mc-mf)>deltam
> table(type3,type30)
       type30
type3   FALSE  TRUE
  FALSE 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)<maxC)|(abs(F)<maxF)) & (abs(fc)> minfc*2)&(abs(mc-mf)<delt
```

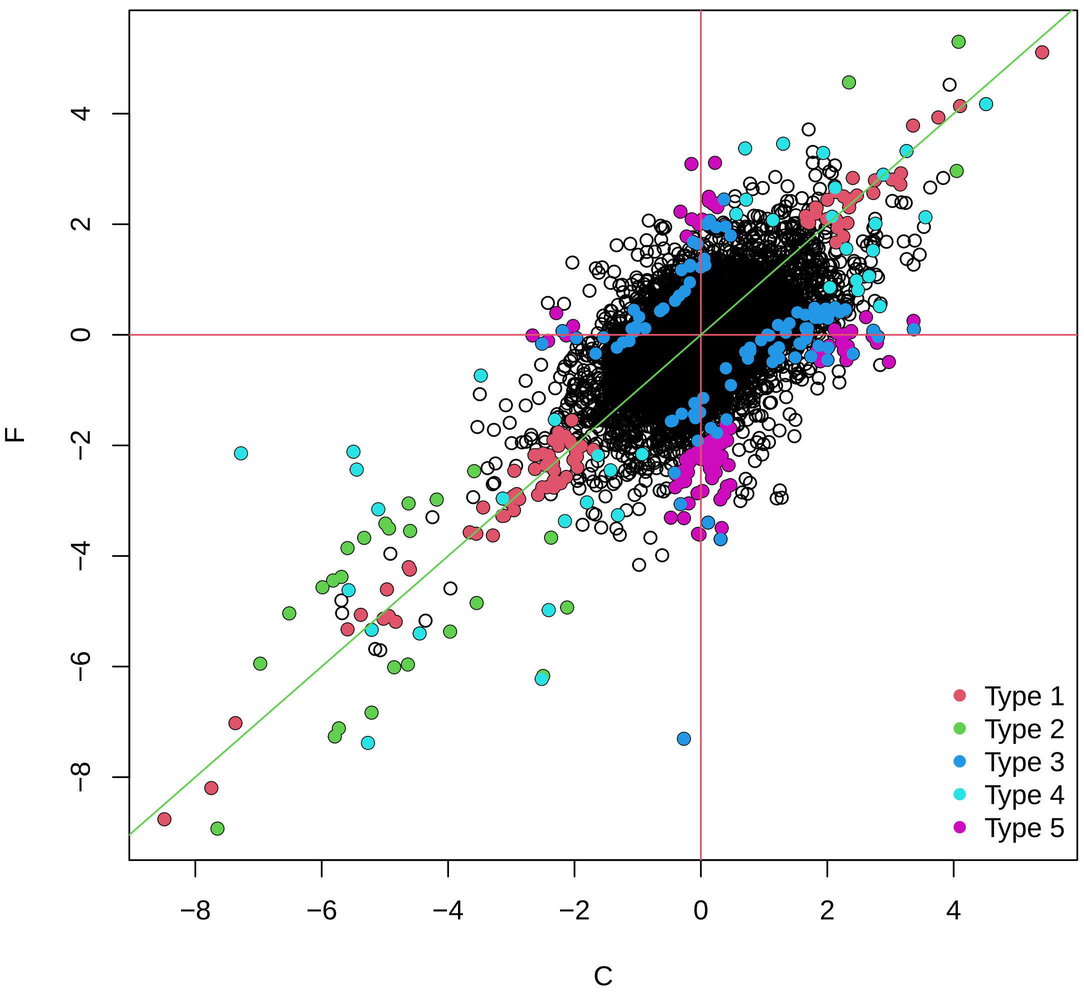
```
> points(
+     C[type5],
+     F[type5],
+     col=6,pch=16)
>
> table(type3,type5)
       type5
type3   FALSE  TRUE
  FALSE 15055    93
  TRUE     94     0
> points(
+     C[type3],
+     F[type3],
+     col=4,pch=16)
> # type 3 is a subset of type5, type3 & large mean difference
>
> #
> abline(h=0,v=0,col=2)
> abline(c(0,1),col=3)
> legend("bottomright",pch=rep(16,5),col=2:6,legend=paste("Type",1:5),bty="n")
```



```
> types <- data.frame(type1,type2,type3,type4,type5)
```

```
> head(types)
              type1 type2 type3 type4 type5
Vitvi15g01736 FALSE FALSE FALSE FALSE FALSE
Vitvi07g02832 FALSE FALSE FALSE FALSE FALSE
Vitvi07g02830 FALSE FALSE FALSE FALSE FALSE
Vitvi07g02812 FALSE FALSE FALSE FALSE FALSE
Vitvi07g02811 FALSE FALSE FALSE FALSE FALSE
Vitvi09g02033 FALSE FALSE FALSE FALSE FALSE
```

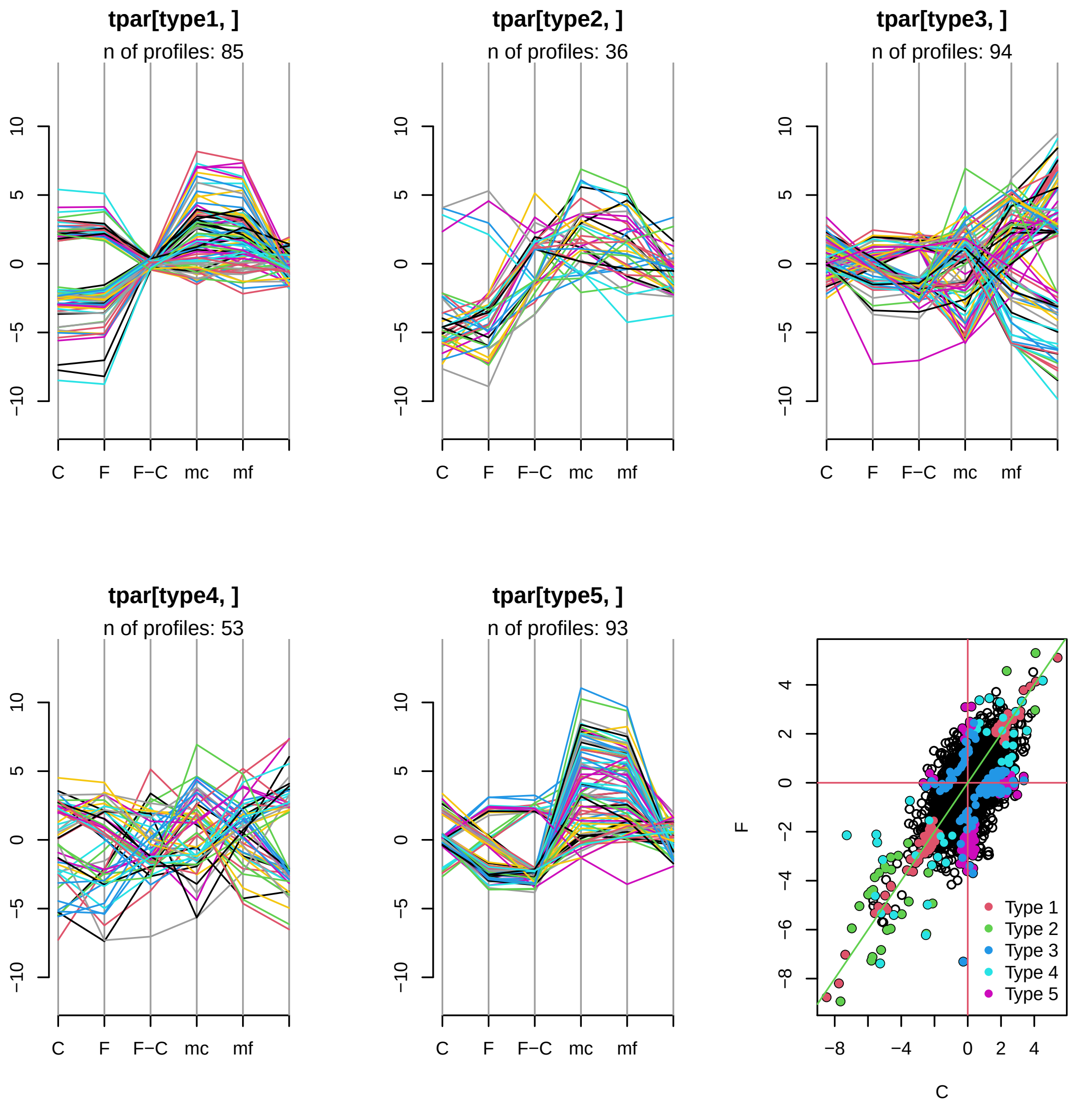
```
> plot.types <- function(x=C, y=F, type=types,title,...){
+ xlab <- deparse(substitute(x))
+ ylab <- deparse(substitute(y))
+
+ plot(x,y, xlab=xlab,ylab=ylab)
+ m <- ncol(type)
+ sek <- c(1,2,4,5,3)
+ for( i in sek){
+ points(
+    x[types[,i]],
+    y[types[,i]],
+    col=i+1,pch=16)
+    }
+    abline(h=0,v=0,col=2)
+ abline(c(0,1),col=3)
+ if(!missing(title)) title(title)
+ legend("bottomright",pch=rep(16,m),col=1+(1:m),legend=paste("Type",1:m),bty=
+ }
> plot.types()
```



```
> x <- coefs[type1,]
> ylim <- range(x)
> my.parallelplot <- function(x, ylim = range(x), title,  ...){
+ if(missing(title)) title <- deparse(substitute(x))
+ m <- ncol(x)
+ plot(0,0, type = "n"
+      , xlim = c(1,m)
+      , ylim = ylim
+      , axes = FALSE
+      , ann=FALSE
+      )
+ title(title)
+ mtext(paste("n of profiles:", nrow(x)),cex=0.75)
+ axis(2)
+ axis(1, at=1:m,labels=gsub("\\.\\.\\.","-",colnames(x)),cex=0.9,xpd=TRUE)
+ abline(v=1:m,col=8)
+ x$col <- 1:nrow(x)
+ apply(x,1,function(y) lines(1:m,y[-(m+1)],col=y[m+1]))
+ invisible(nrow(x))
```

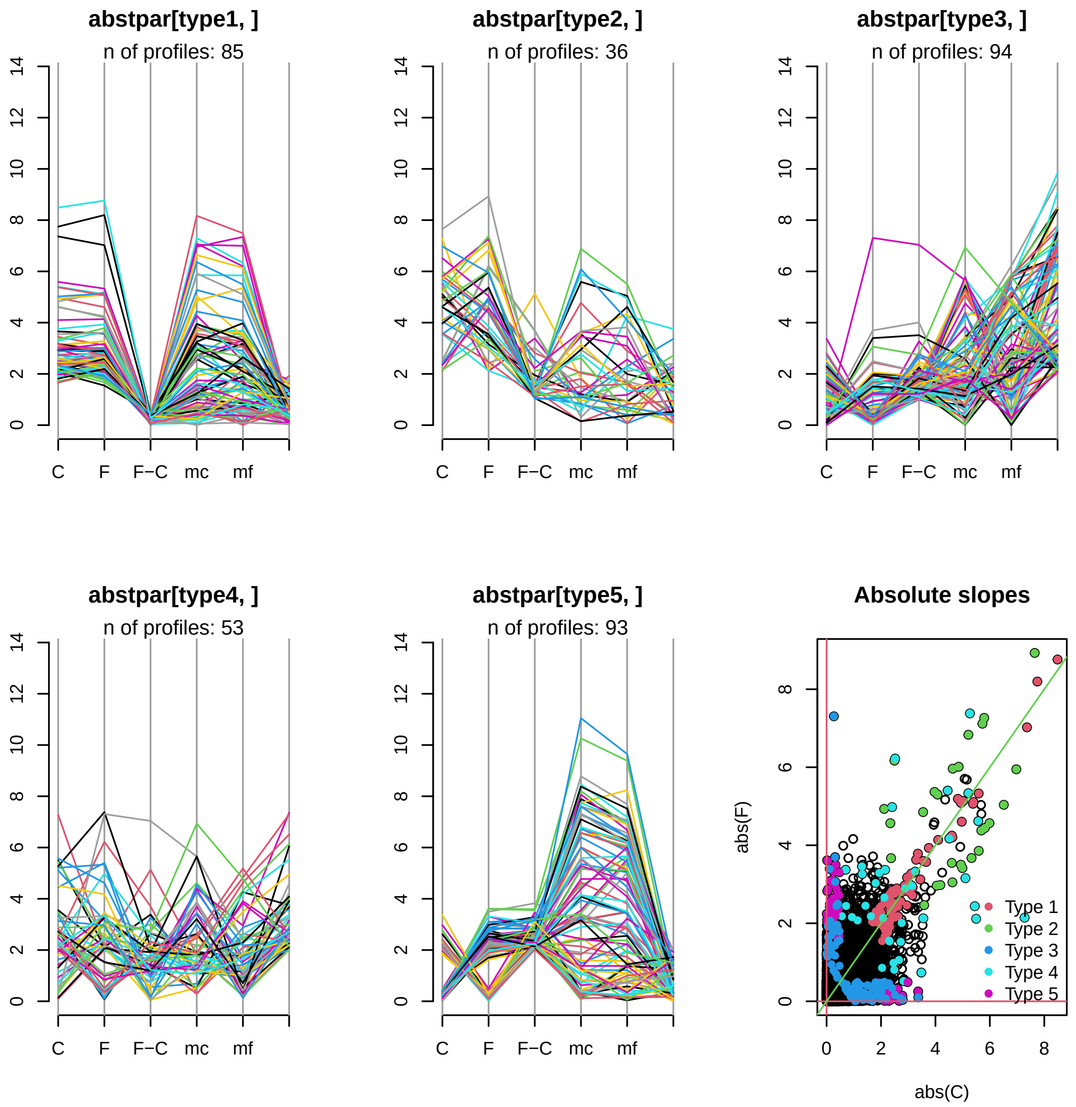
```
+ }
> if(interactive()) my.parallelplot(coefs[type1,])
```

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

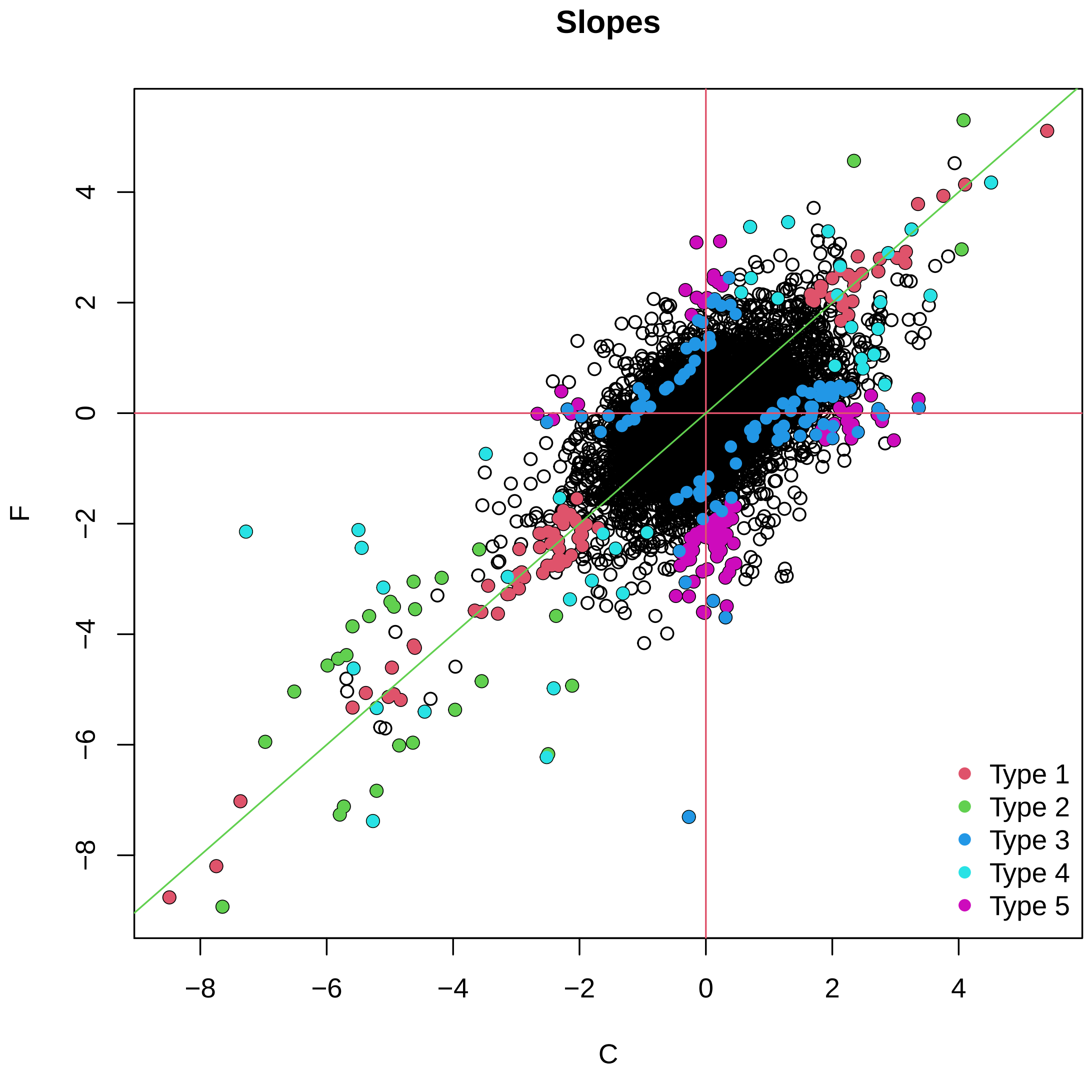


```
> par(mfrow=c(2,3))
> tpar <- data.frame(C,F,F-C,mc,mf,mf-mc)
> abstpar <- abs(tpar)
> ylim <- range(abstpar)
> my.parallelplot(abstpar[type1,], ylim=ylim)
> my.parallelplot(abstpar[type2,], ylim=ylim)
```

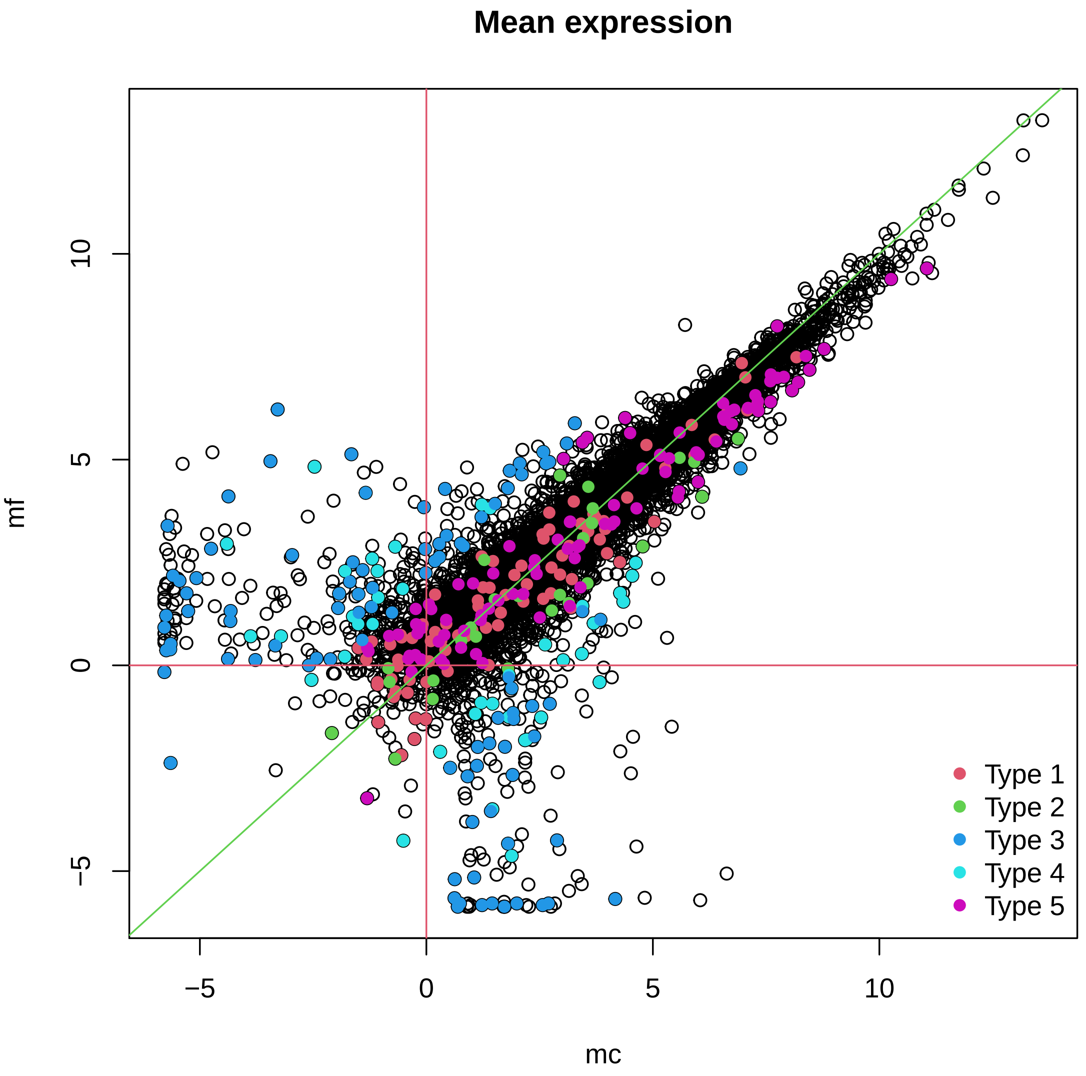
```
> my.parallelplot(abstpar[type3,], ylim=ylim)
> my.parallelplot(abstpar[type4,], ylim=ylim)
> my.parallelplot(abstpar[type5,], ylim=ylim)
> plot.types(abs(C),abs(F),title="Absolute slopes")
```



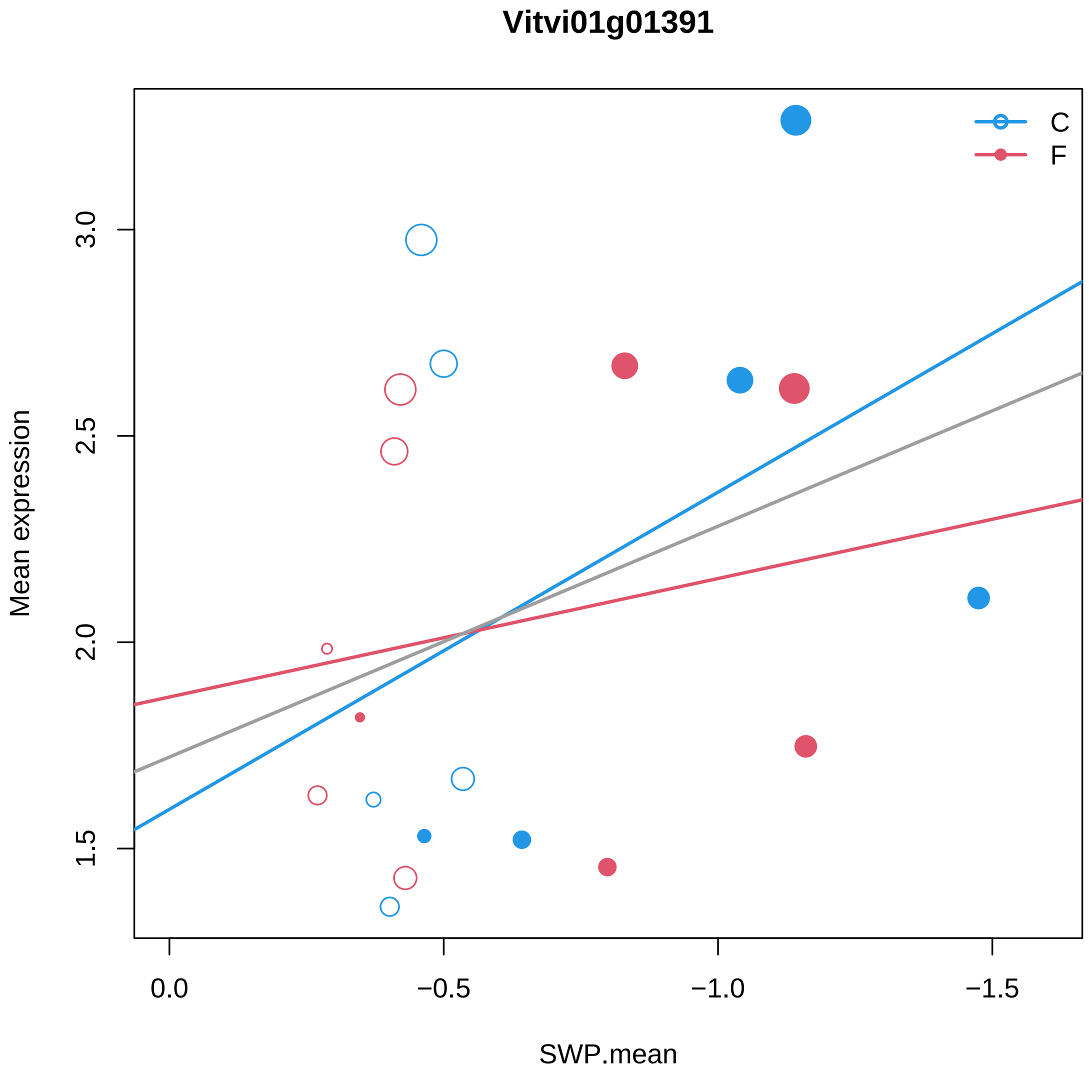
```
> plot.types(C,F,title="Slopes")
```



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

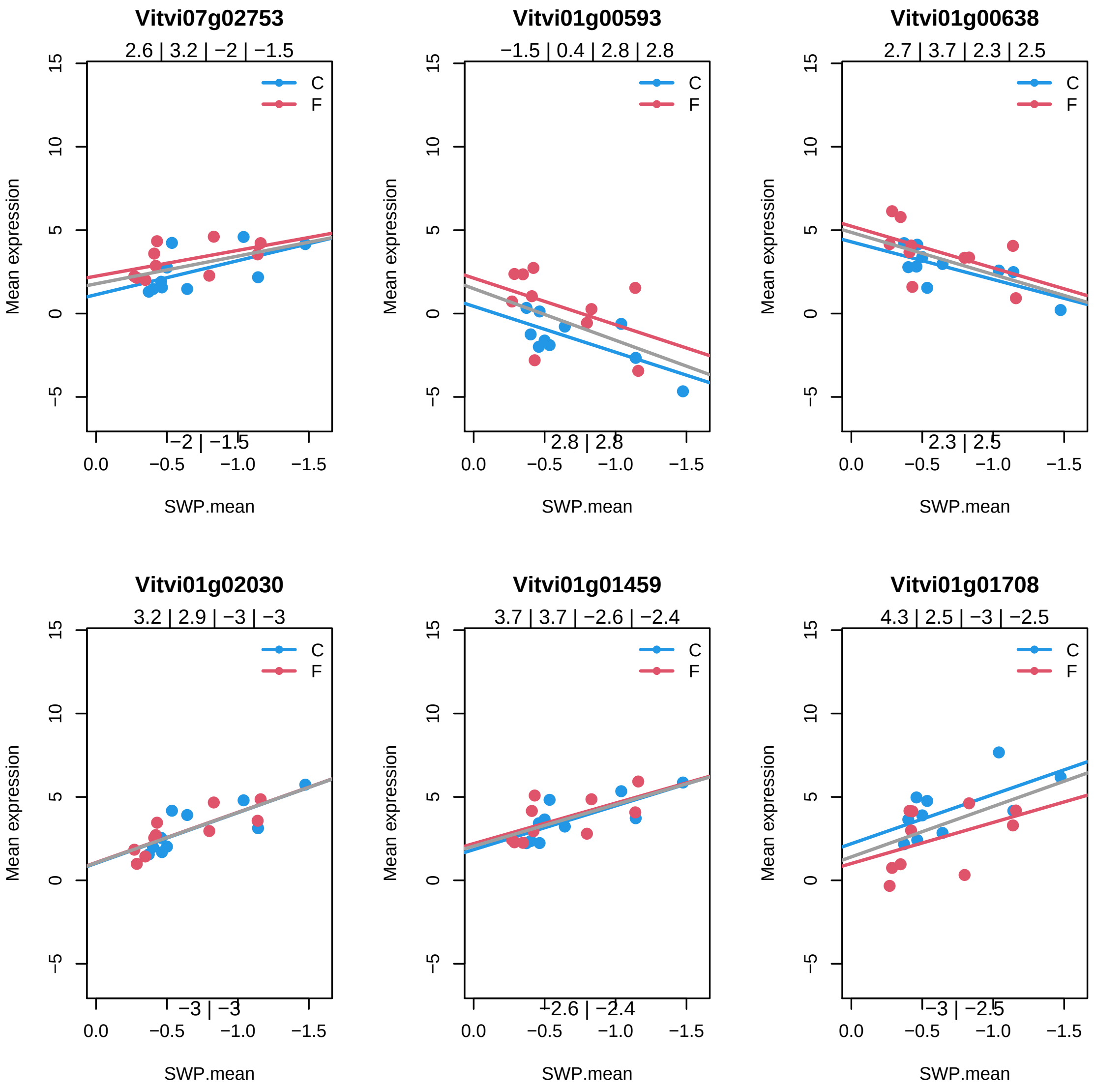


```
> varname <- testvar
> plot.ewp(varname,model="", exprs=exprs, pd=pd)
```

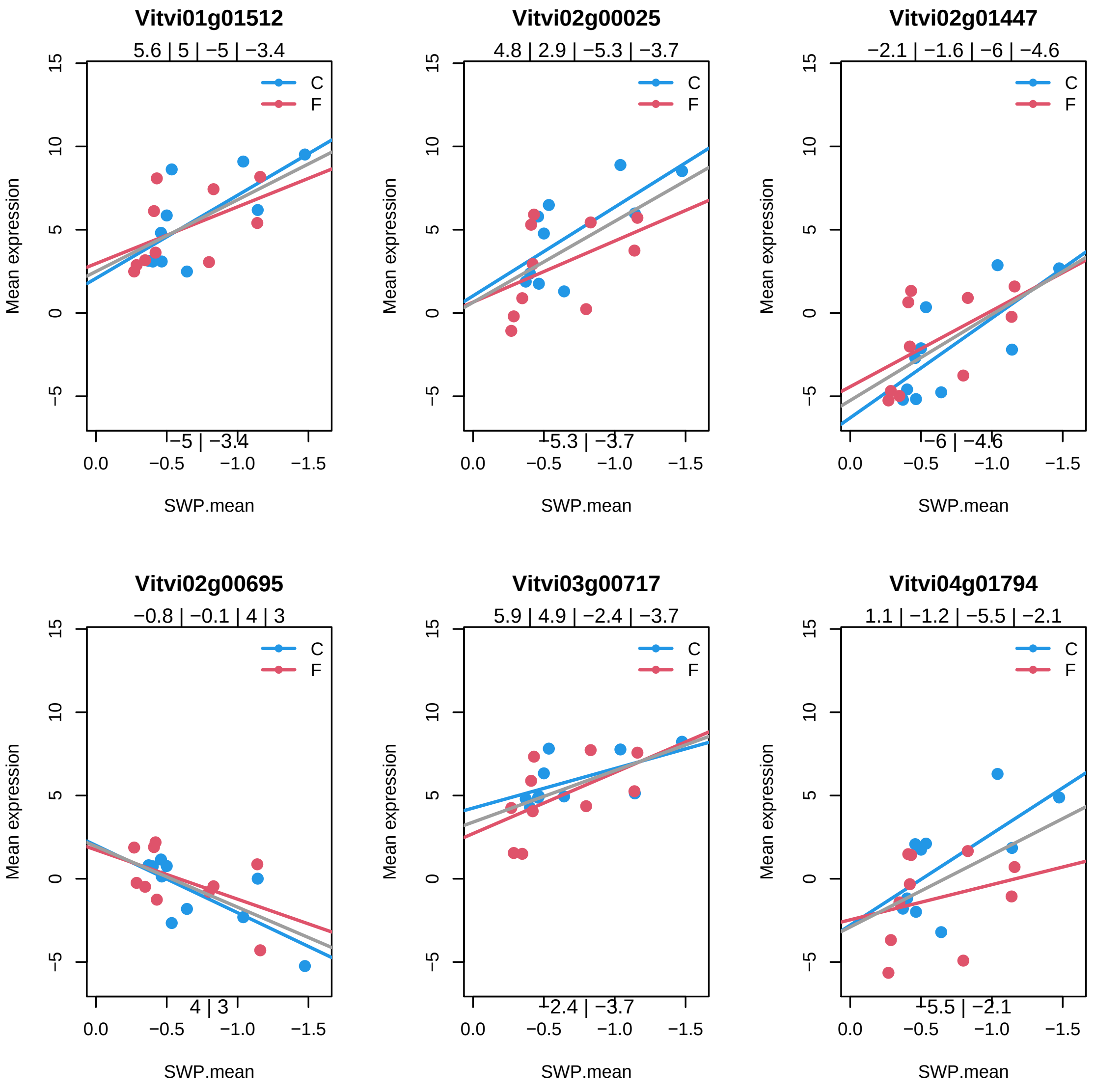


```
> apply(data.frame(type1,type2,type3,type4, type5),2,sum)
type1 type2 type3 type4 type5
   85    36    94    53    93
```

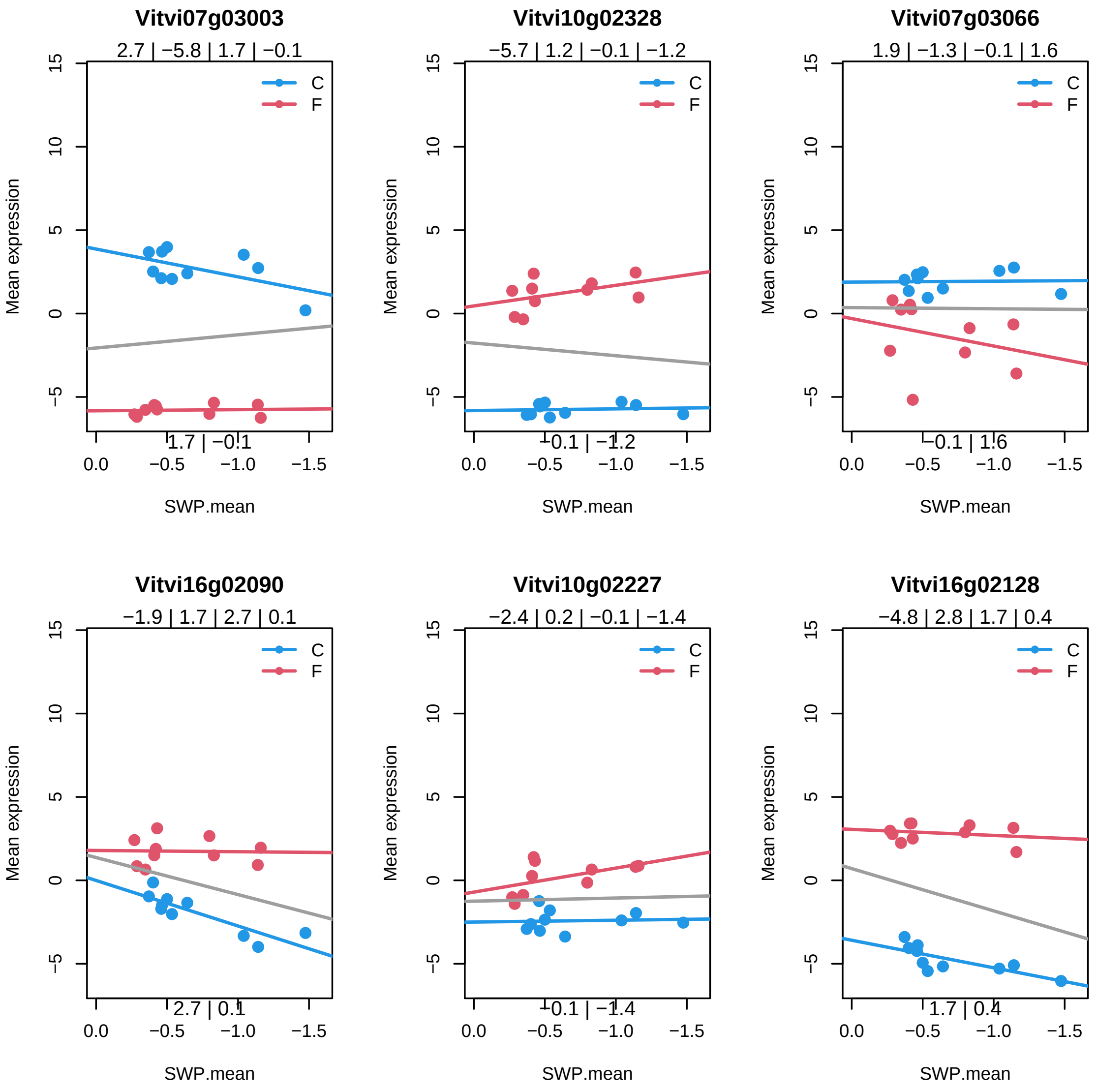
```
> par(mfrow=c(2,3))
> filt <- type1
> print(sum(filt))
[1] 85
> for(i in 1:min(sum(filt),6)){
+ varname <- rownames(exprs)[filt][i]
+ p <- plot.ewp(varname,model="", exprs=exprs, pd=pd, ylim=range(exprs)
+       , cex= 1.5
+       , pch = c(16,16)
+       )
+ mtext(paste(round(coefs[varname,],1),collapse=" | "),cex=0.75)
+ mtext(paste(round(c(p$C$coefficients[2],p$F$coefficients[2]),1)
+ ,collapse=" | "),1,cex=0.75)
+ }
```



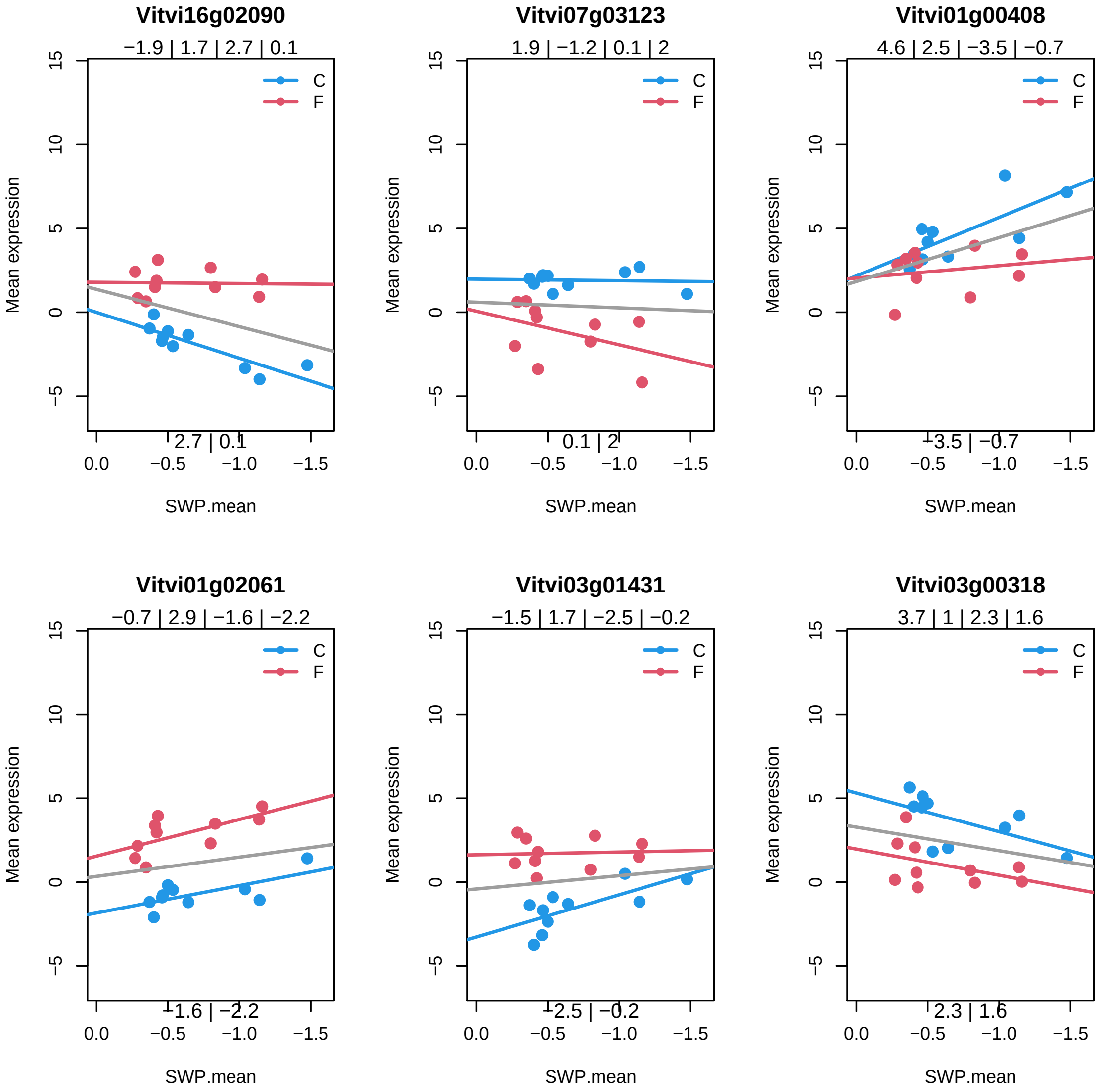
```
> par(mfrow=c(2,3))
> filt <- type2
> print(sum(filt))
[1] 36
> for(i in 1:min(sum(filt),6)){
+ varname <- rownames(exprs)[filt][i]
+ p <- plot.ewp(varname,model="", exprs=exprs, pd=pd, ylim=range(exprs)
+       , cex= 1.5
+       , pch = c(16,16)
+       )
+ mtext(paste(round(coefs[varname,],1),collapse=" | "),cex=0.75)
+ mtext(paste(round(c(p$C$coefficients[2],p$F$coefficients[2]),1)
+ ,collapse=" | "),1,cex=0.75)
+ }
```



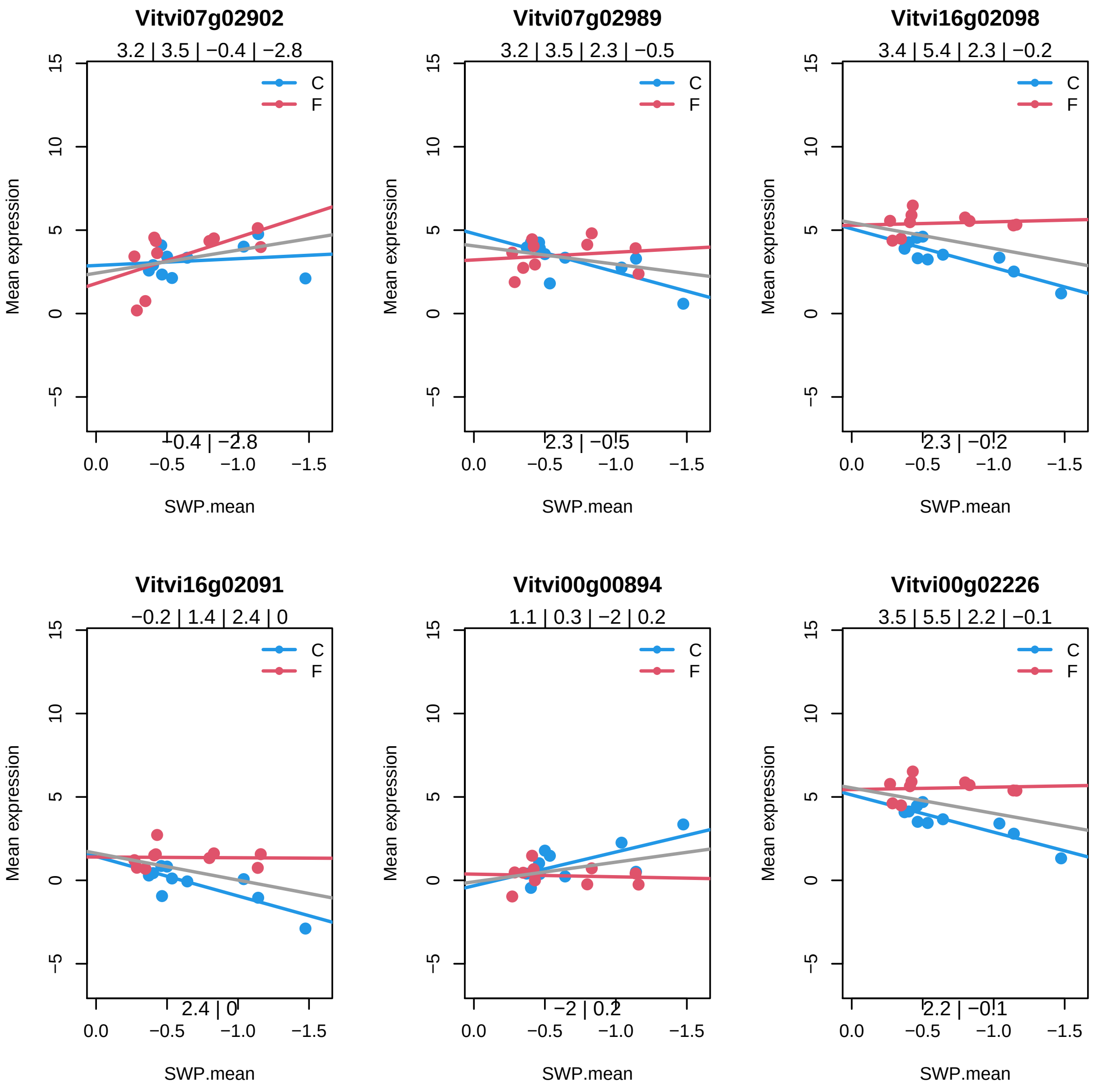
```
> par(mfrow=c(2,3))
> filt <- type3
> print(sum(filt))

[1] 94

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



```
> par(mfrow=c(2,3))
> filt <- type4
> print(sum(filt))
[1] 53
> for(i in 1:min(sum(filt),6)){
+ varname <- rownames(exprs)[filt][i]
+ p <- plot.ewp(varname,model="", exprs=exprs, pd=pd, ylim=range(exprs)
+       , cex= 1.5
+       , pch = c(16,16)
+       )
+ mtext(paste(round(coefs[varname,],1),collapse=" | "),cex=0.75)
+ mtext(paste(round(c(p$C$coefficients[2],p$F$coefficients[2]),1)
+ ,collapse=" | "),1,cex=0.75)
+ }
```



```
> par(mfrow=c(2,3))
> filt <- type5
> print(sum(filt))
[1] 93
> for(i in 1:min(sum(filt),6)){
+ varname <- rownames(exprs)[filt][i]
+ p <- plot.ewp(varname,model="", exprs=exprs, pd=pd, ylim=range(exprs)
+       , cex= 1.5
+       , pch = c(16,16)
+       )
+ mtext(paste(round(coefs[varname,],1),collapse=" | "),cex=0.75)
+ mtext(paste(round(c(p$C$coefficients[2],p$F$coefficients[2]),1)
+ ,collapse=" | "),1,cex=0.75)
+ }
```



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

6.0.1 Export output files

Export fit in a form:

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

```
        A        Coef.(Intercept)        Coef.swp        Coef.varietyF
Vitvi15g01736        4.47674068175        5.55075053709523        1.5935451902
Vitvi07g02832        -0.1827419310625        -2.63411470430457        0.508155
Vitvi07g02830        -0.3244159185        -1.75065019963238        1.548036561
Vitvi07g02812        -0.3463388427625        -1.38136290124246        -0.00979
Vitvi07g02811        2.4871819448375        2.23617701208318        0.56626956
Vitvi09g02033        -0.78732802375        -2.84283707706586        0.41956448
```

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

Export top table

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

Removing intercept from test coefficients

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

[1] TRUE

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

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

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

```
Error in eval(expr, envir, enclos): object '.topn' not found
```

6.1 Genes in types

Plots of situation for genes in determined types

Figures caption:

Mean expression (E) and mean water potential (WP). Upper panels show WP vs E and regression lines for three models. Left: all C (blue) and all F (blue). Middle: separate models for combinations of treatment and variety, same slope (+). Right: separate for combinations, different slopes (interaction, *). Black line is regression of all data, regardles of treatment and variety. Lower panels have swaped variables: E vs WP. Symbol sizes are related to time, large is later.

Order tt by swp

```
> ordr <- rev(order(tt$swp))
> tt <- tt[ordr,]
> types <- types[rownames(tt),]
> all(rownames(tt)==rownames(types))
```

```
[1] TRUE
```

```
> out <- ""
> (cname <- "")
```

```
[1] ""
```

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

6.2 type1

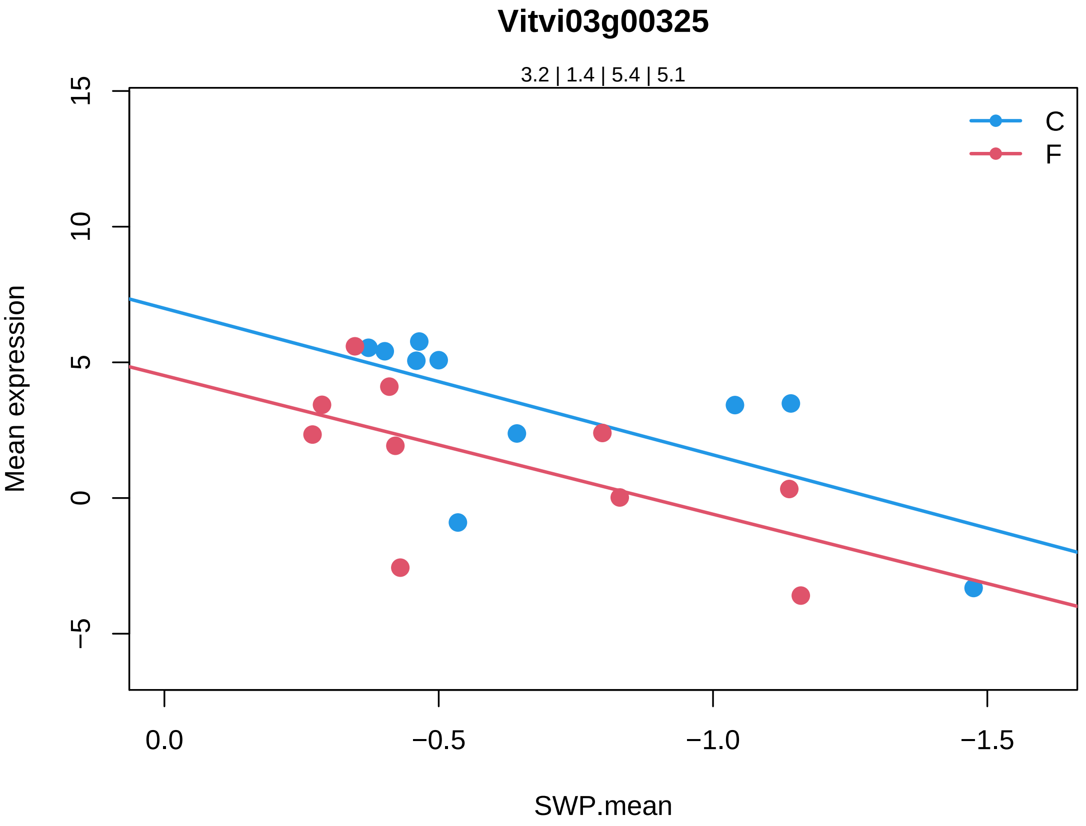
6.2.1 Vitvi03g00325

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

```
Vitvi03g00325
        27.03.2025
        RNA.regulation of transcription.MYB domain transcription factor family
        RAD-like 1 |
        Chr4:18271457-18271857 REVERSE LENGTH=100 |
        201606
```

Coefficients for Vitvi03g00325.

```
                   swp   varietyF swp.varietyF  AveExpr        F
Vitvi03g00325 5.400429 -2.478825   -0.2916254 2.295297 6.146473
                  P.Value  adj.P.Val  type
Vitvi03g00325 0.003512429 0.03910624 type1
```



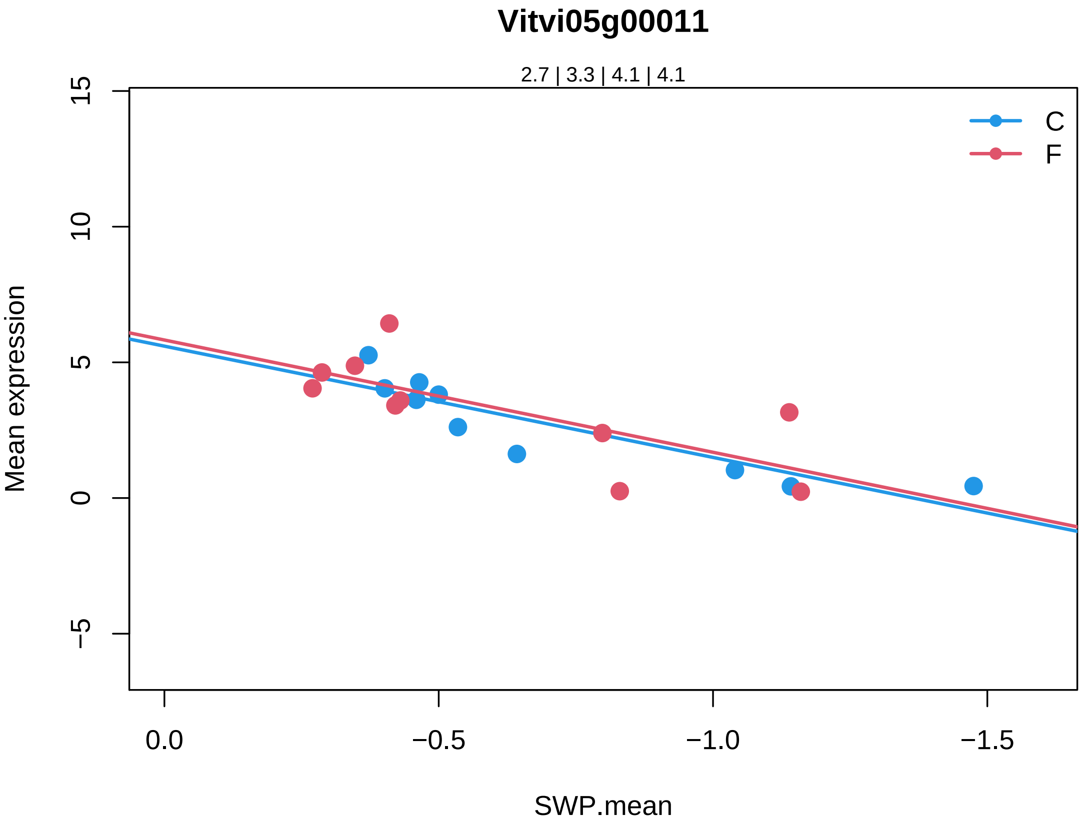
6.2.2 Vitvi05g00011

```
> 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.

```
                   swp  varietyF swp.varietyF  AveExpr        F
Vitvi05g00011 4.101024 0.2253048   0.03610049 3.007825 13.10389
                   P.Value   adj.P.Val  type
Vitvi05g00011 4.450019e-05 0.001153524 type1
```



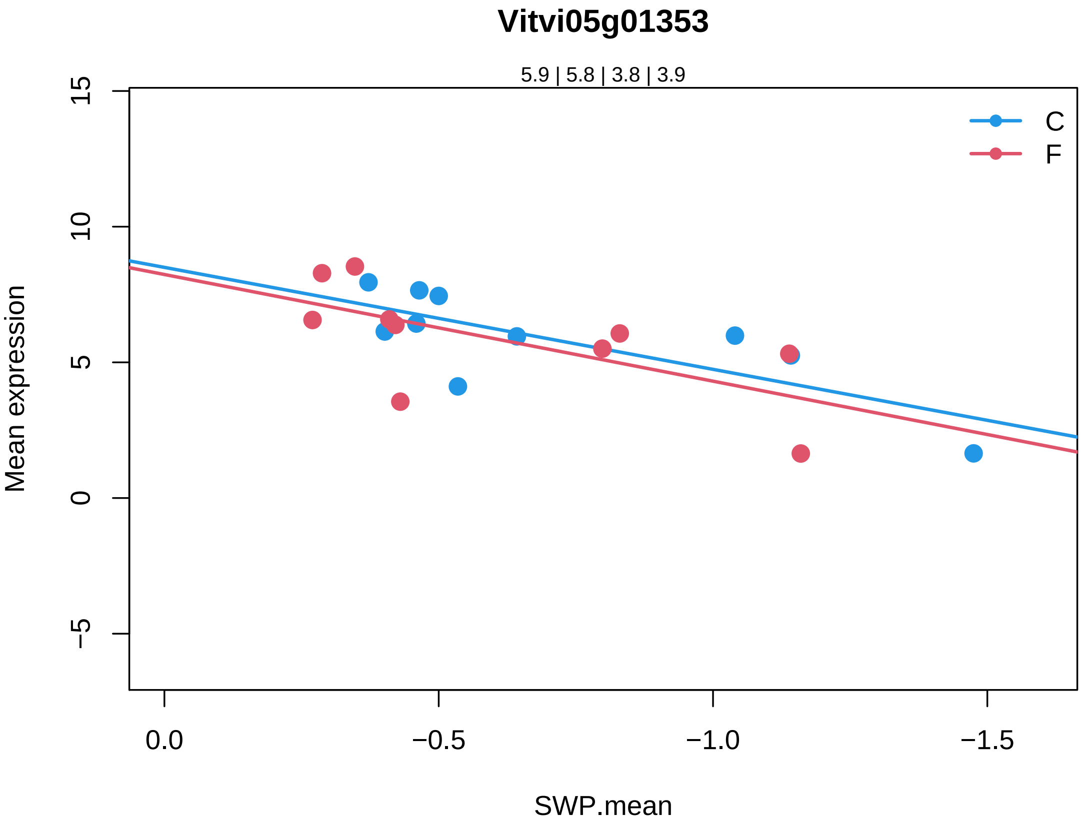
6.2.3 Vitvi05g01353

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

```
Vitvi05g01353
        10.08.2001
        cell wall.pectinesterases.PME
        pectin methylesterase 61 |
        Chr3:21803015-21805098 REVERSE LENGTH=529 |
        201606
```

Coefficients for Vitvi05g01353.

```
                   swp  varietyF swp.varietyF  AveExpr        F
Vitvi05g01353 3.757248 -0.261732    0.1744137 5.849725 6.835749
                  P.Value  adj.P.Val  type
Vitvi05g01353 0.002091322 0.02647503 type1
```



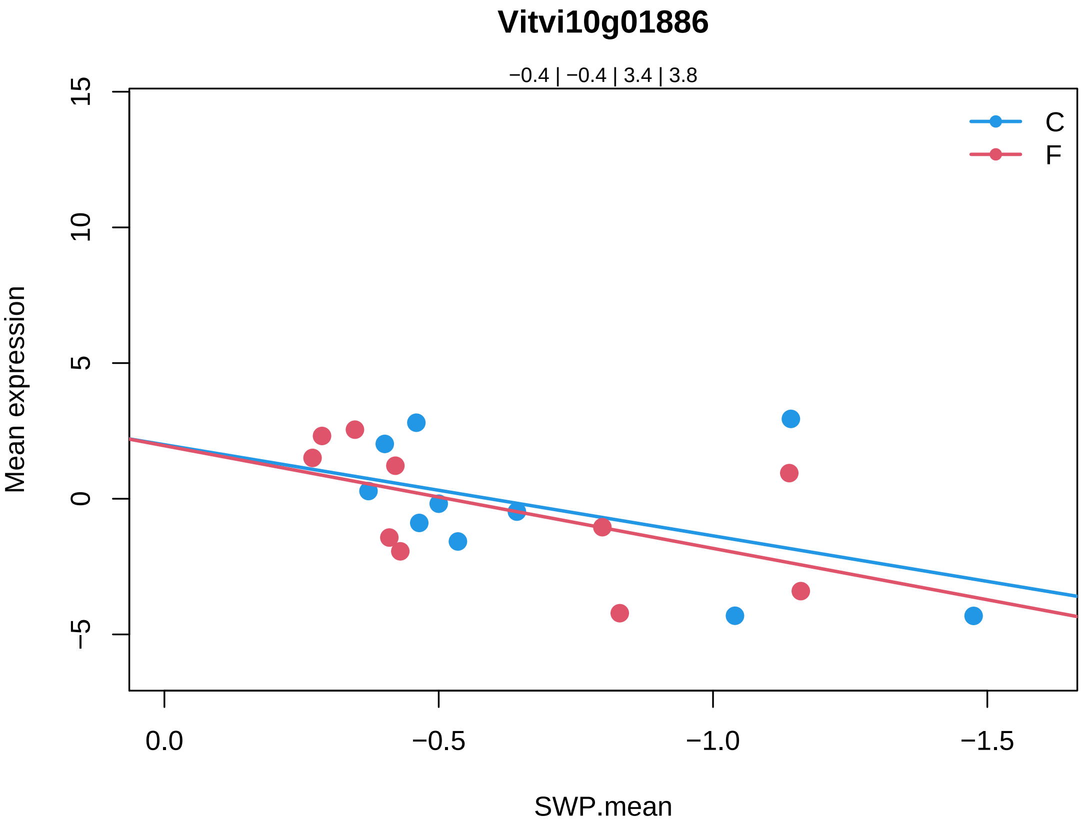
6.2.4 Vitvi10g01886

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

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

Coefficients for Vitvi10g01886.

```
                    swp    varietyF swp.varietyF    AveExpr        F
Vitvi10g01886 3.356612 -0.03526013    0.4277199 -0.3606944 2.561078
                 P.Value adj.P.Val  type
Vitvi10g01886 0.08162976 0.3287188 type1
```



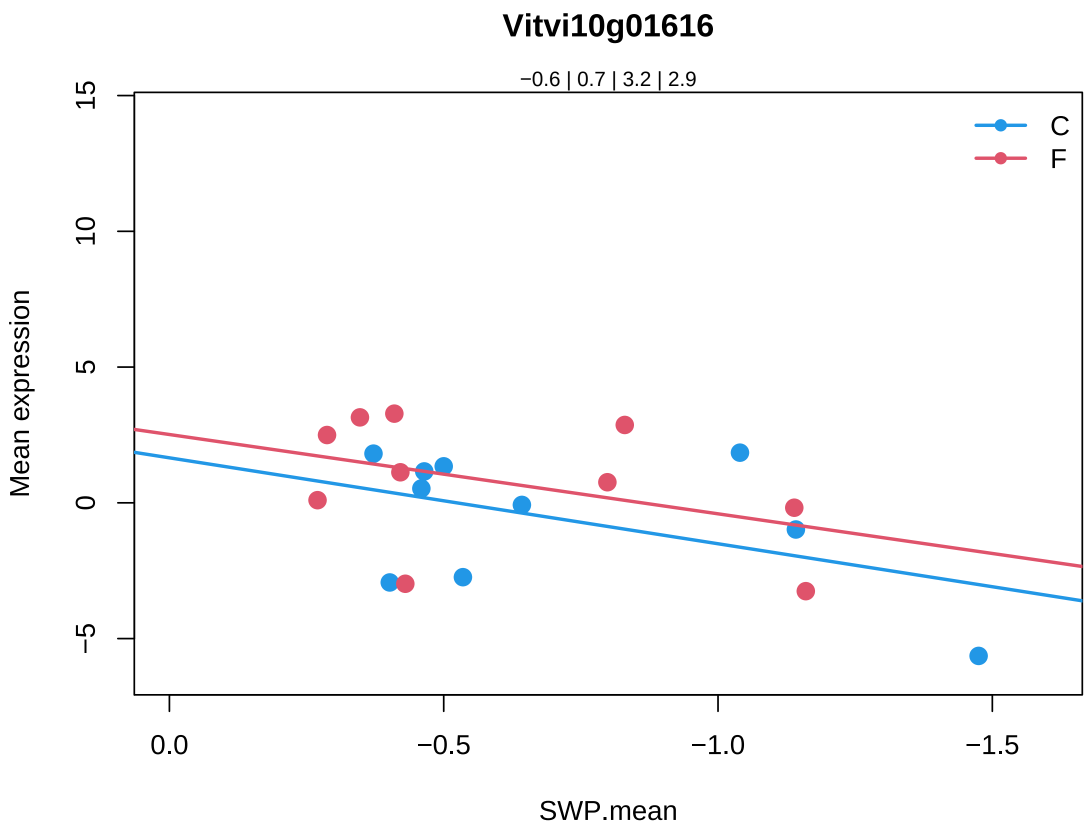
6.2.5 Vitvi10g01616

```
> 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.

```
                   swp varietyF swp.varietyF    AveExpr        F
Vitvi10g01616 3.165031 0.857917   -0.2446635 0.08410838 2.531608
                 P.Value adj.P.Val  type
Vitvi10g01616 0.08406367 0.3341936 type1
```



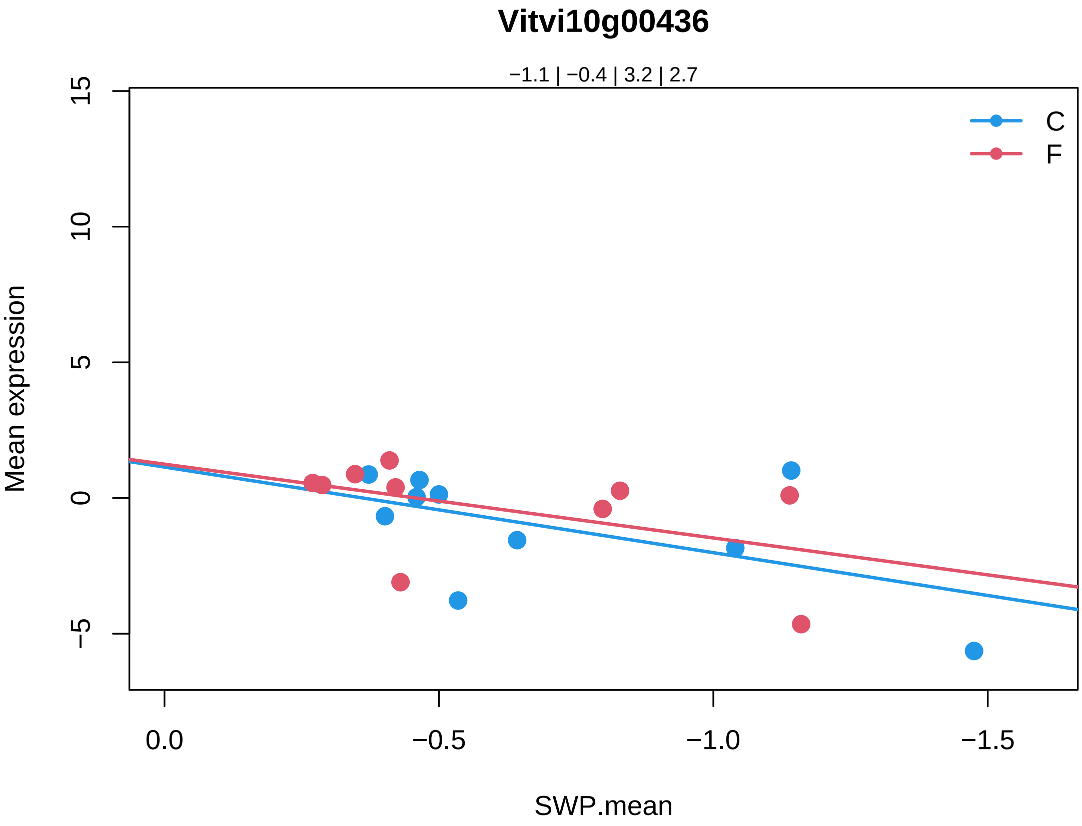
6.2.6 Vitvi10g00436

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

```
Vitvi10g00436
        3.08.2002
        minor CHO metabolism.galactose.alpha-galactosidases
        Melibiase family protein |
        Chr3:20882886-20885745 FORWARD LENGTH=437 |
        201606
```

Coefficients for Vitvi10g00436.

```
                   swp  varietyF swp.varietyF    AveExpr        F
Vitvi10g00436 3.15566 0.1051938   -0.4366108 -0.7434155 2.894105
                 P.Value adj.P.Val  type
Vitvi10g00436 0.05880868 0.2685326 type1
```



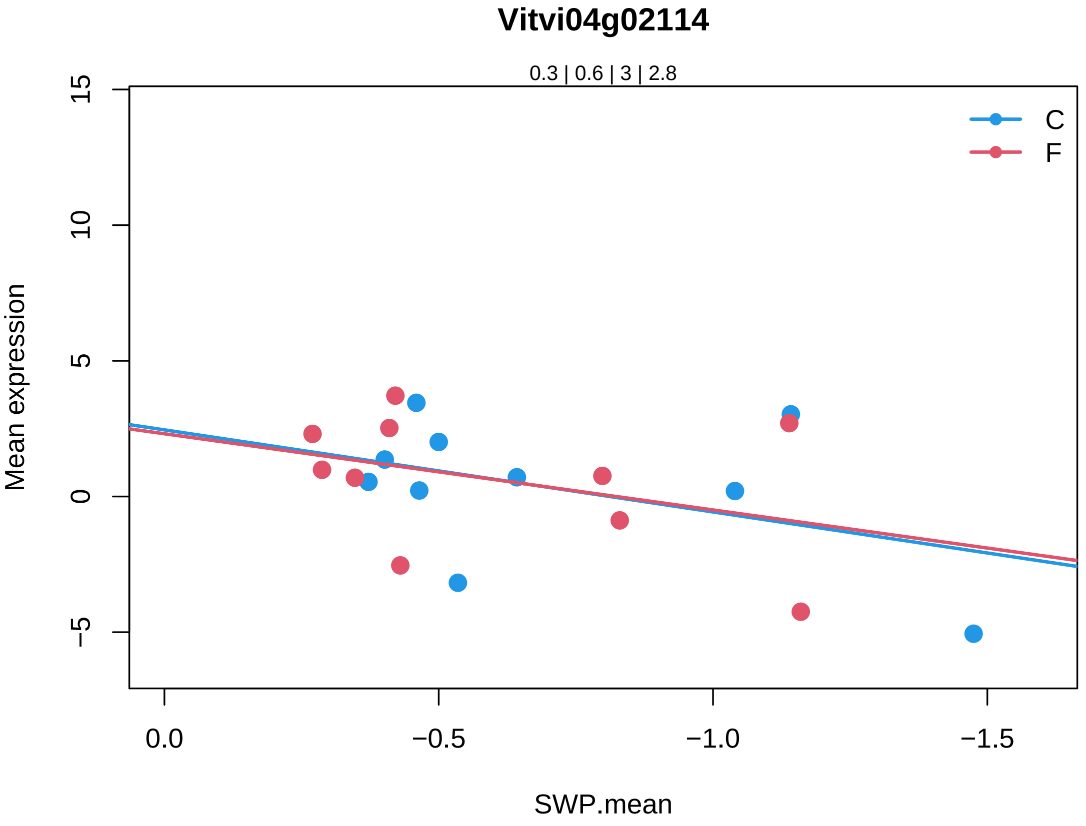
6.2.7 Vitvi04g02114

```
> 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.

```
                    swp    varietyF swp.varietyF   AveExpr       F
Vitvi04g02114 3.024528 -0.1427578   -0.2163602 0.4649671 1.47011
                 P.Value adj.P.Val  type
Vitvi04g02114 0.2507619  0.601718 type1
```



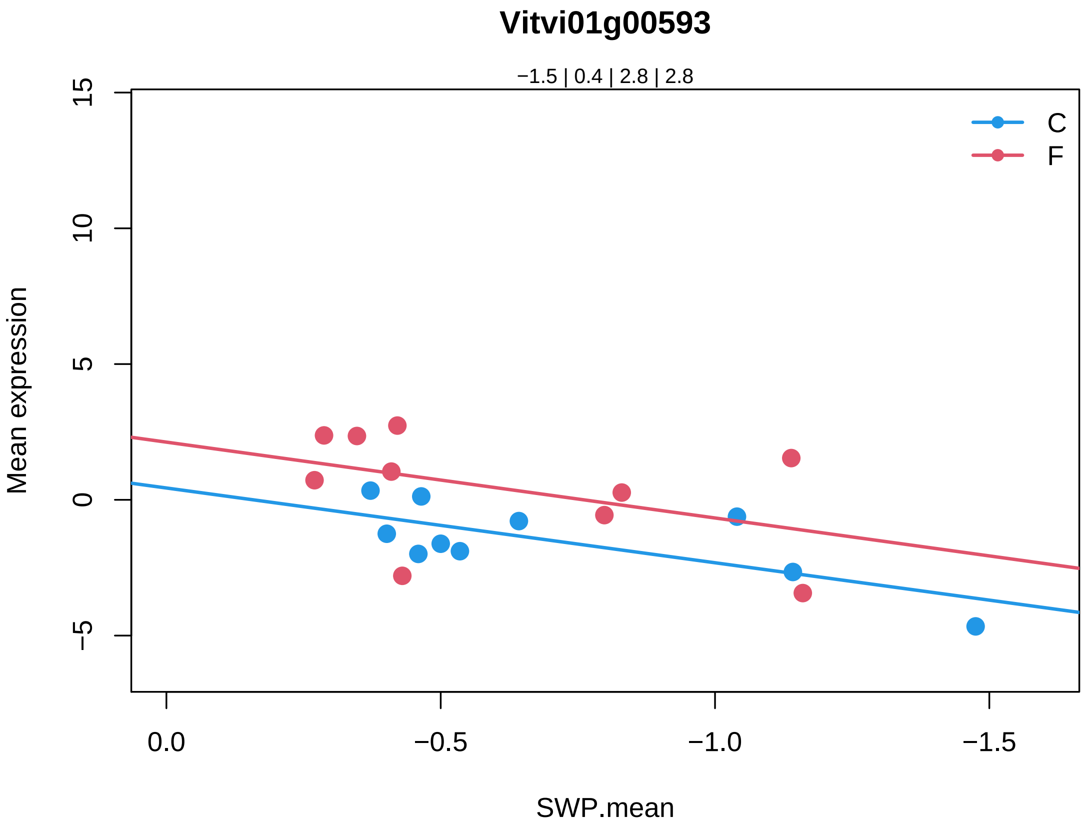
6.2.8 Vitvi01g00593

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

```
Vitvi01g00593
        10.06.2003
        cell wall.degradation.pectate lyases and polygalacturonases
        Pectate lyase family protein |
        Chr1:25401660-25403165 FORWARD LENGTH=408 |
        201606
```

Coefficients for Vitvi01g00593.

```
                   swp varietyF swp.varietyF    AveExpr        F
Vitvi01g00593 2.753643 1.689857   0.04027117 -0.5389909 6.059348
                  P.Value  adj.P.Val  type
Vitvi01g00593 0.003756847 0.04104793 type1
```



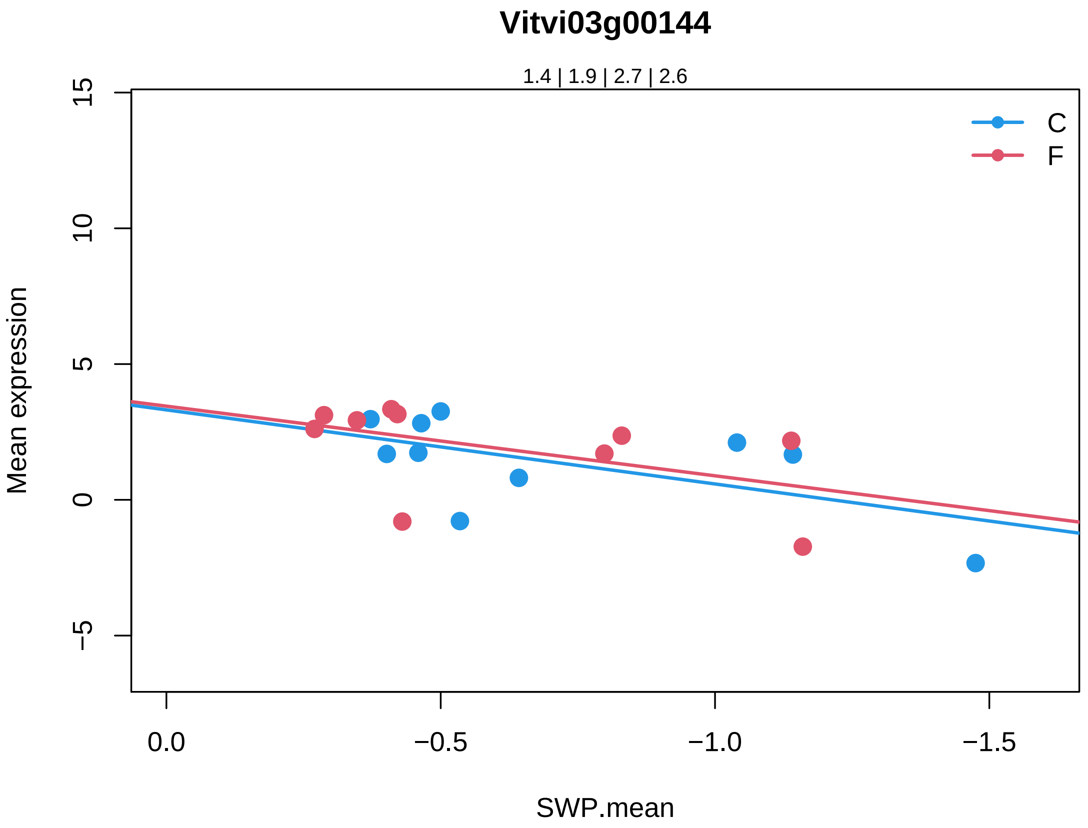
6.2.9 Vitvi03g00144

```
> 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.

```
                   swp  varietyF swp.varietyF  AveExpr        F
Vitvi03g00144 2.728777 0.1364519   -0.1638066 1.640435 3.196893
                P.Value adj.P.Val  type
Vitvi03g00144 0.0439392 0.2257494 type1
```



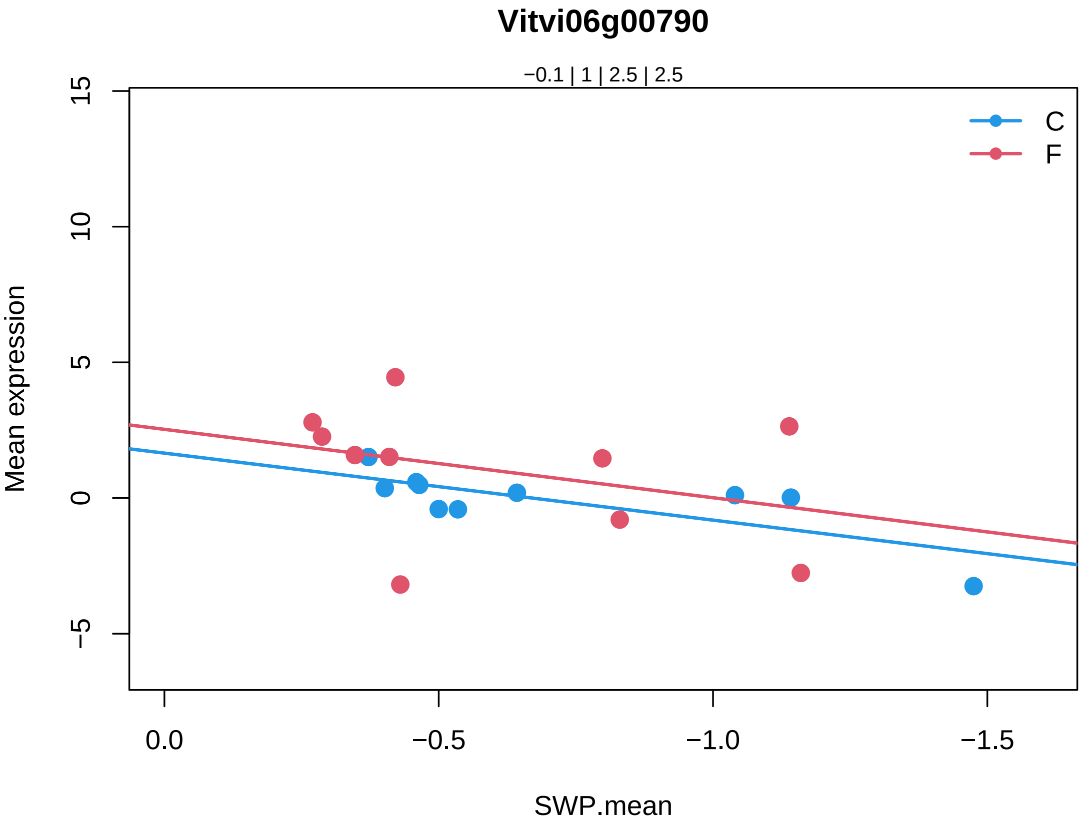
6.2.10 Vitvi06g00790

```
> 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.

```
                   swp  varietyF swp.varietyF   AveExpr       F
Vitvi06g00790 2.469095 0.8770364   0.05143393 0.4571057 2.62482
                 P.Value adj.P.Val  type
Vitvi06g00790 0.07661914 0.3146939 type1
```



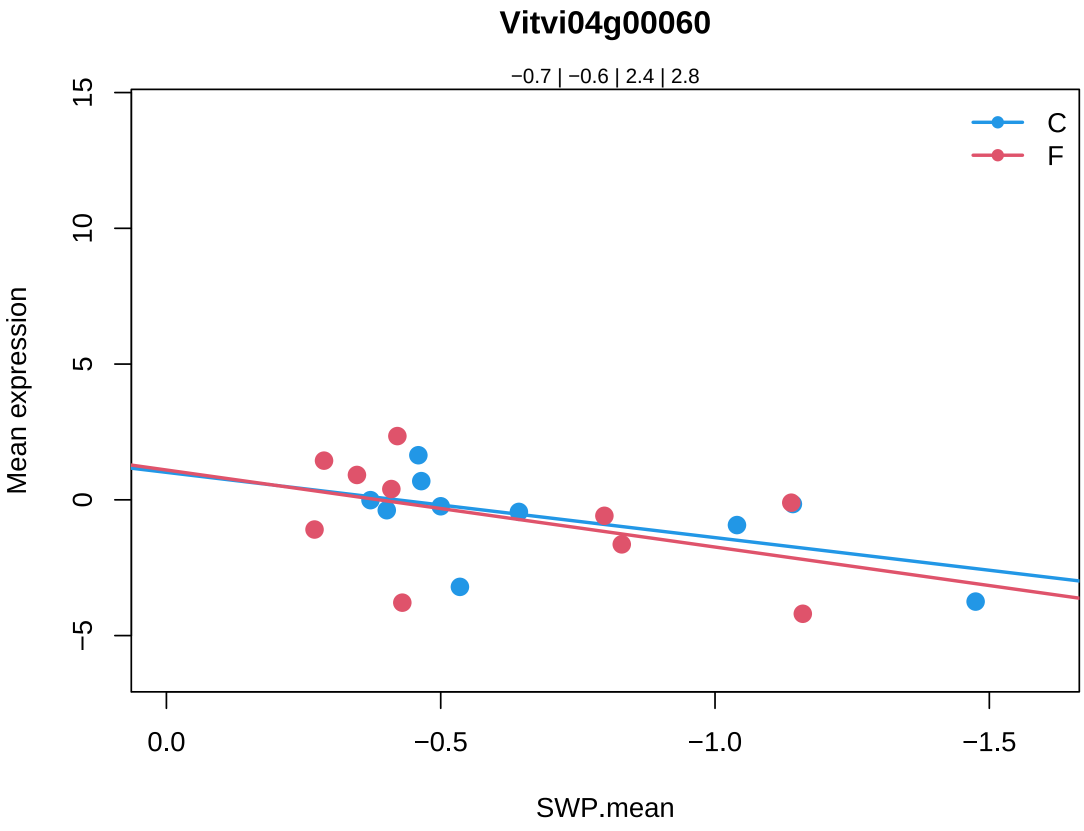
6.2.11 Vitvi04g00060

```
> 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.

```
                   swp   varietyF swp.varietyF    AveExpr        F
Vitvi04g00060 2.403369 0.08622858    0.4336031 -0.6545995 2.278491
                P.Value adj.P.Val  type
Vitvi04g00060 0.1084498 0.3898566 type1
```



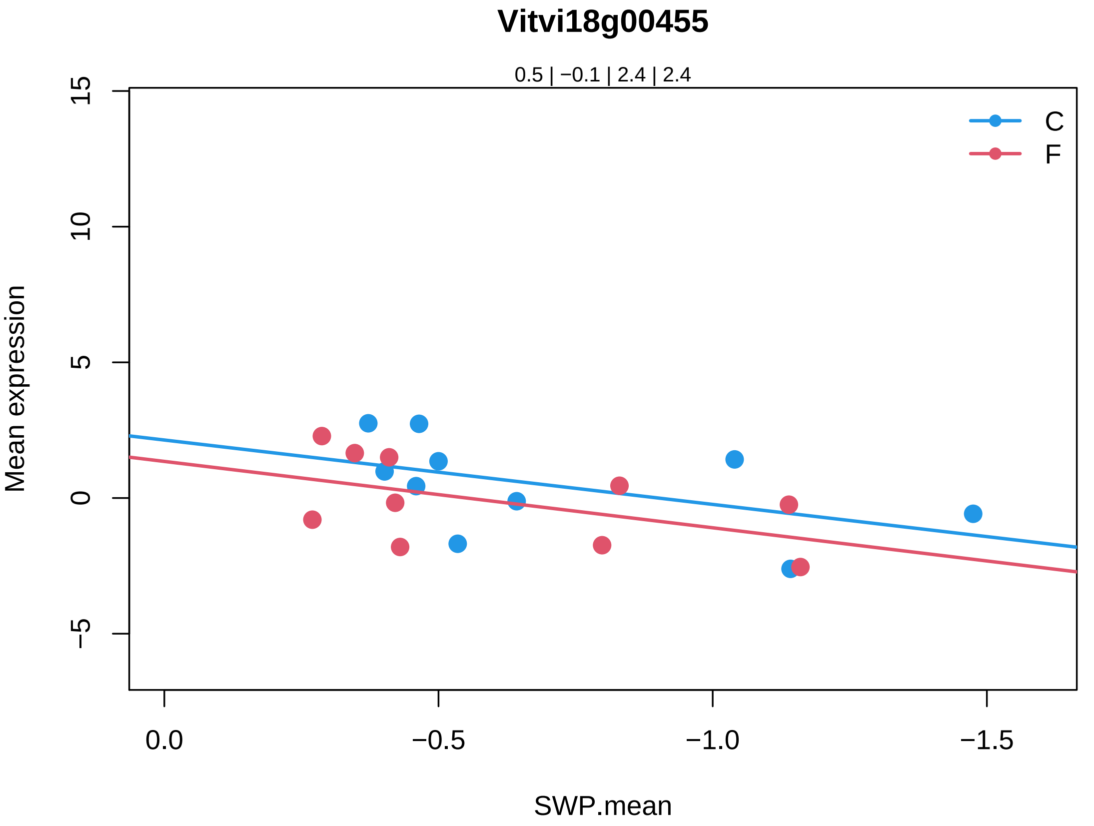
6.2.12 Vitvi18g00455

```
> 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.

```
                   swp  varietyF swp.varietyF   AveExpr        F
Vitvi18g00455 2.373306 -0.789135   0.07233783 0.1637595 2.823053
                P.Value adj.P.Val  type
Vitvi18g00455 0.0630299 0.2794362 type1
```



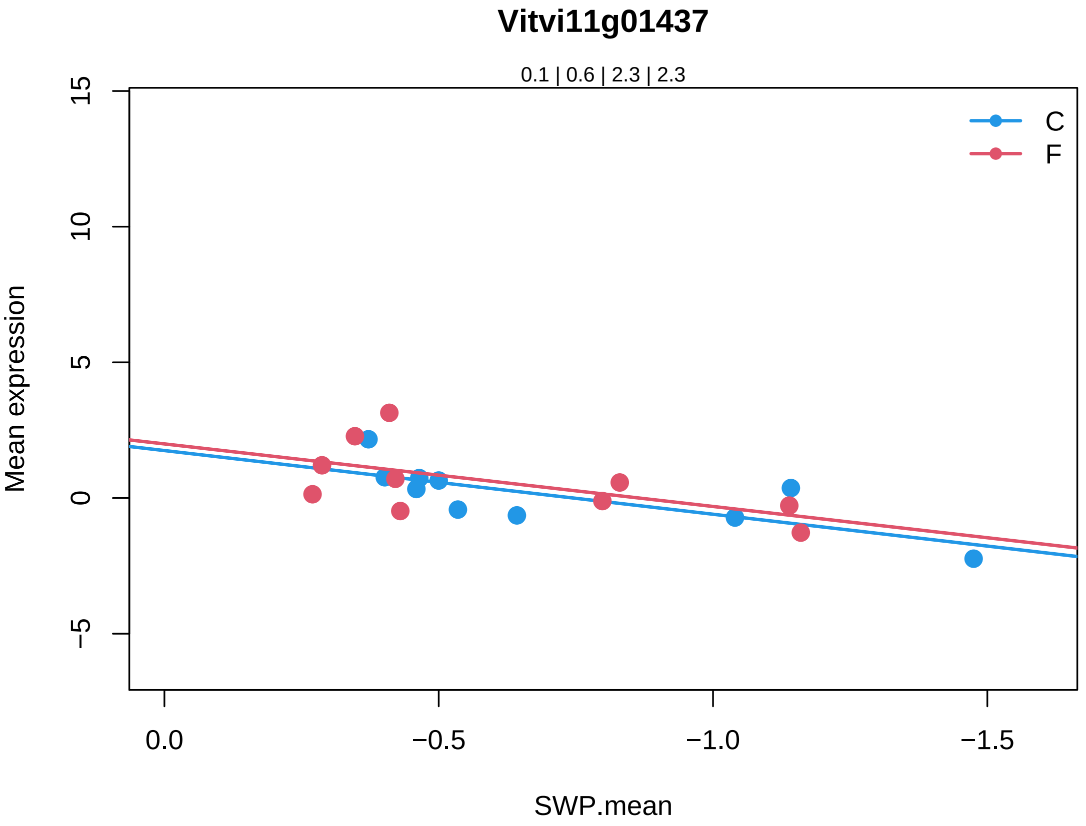
6.2.13 Vitvi11g01437

```
> 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.

```
                   swp  varietyF swp.varietyF   AveExpr        F
Vitvi11g01437 2.346685 0.2454462  -0.04140832 0.3442818 5.926509
                  P.Value  adj.P.Val  type
Vitvi11g01437 0.004165869 0.04427906 type1
```



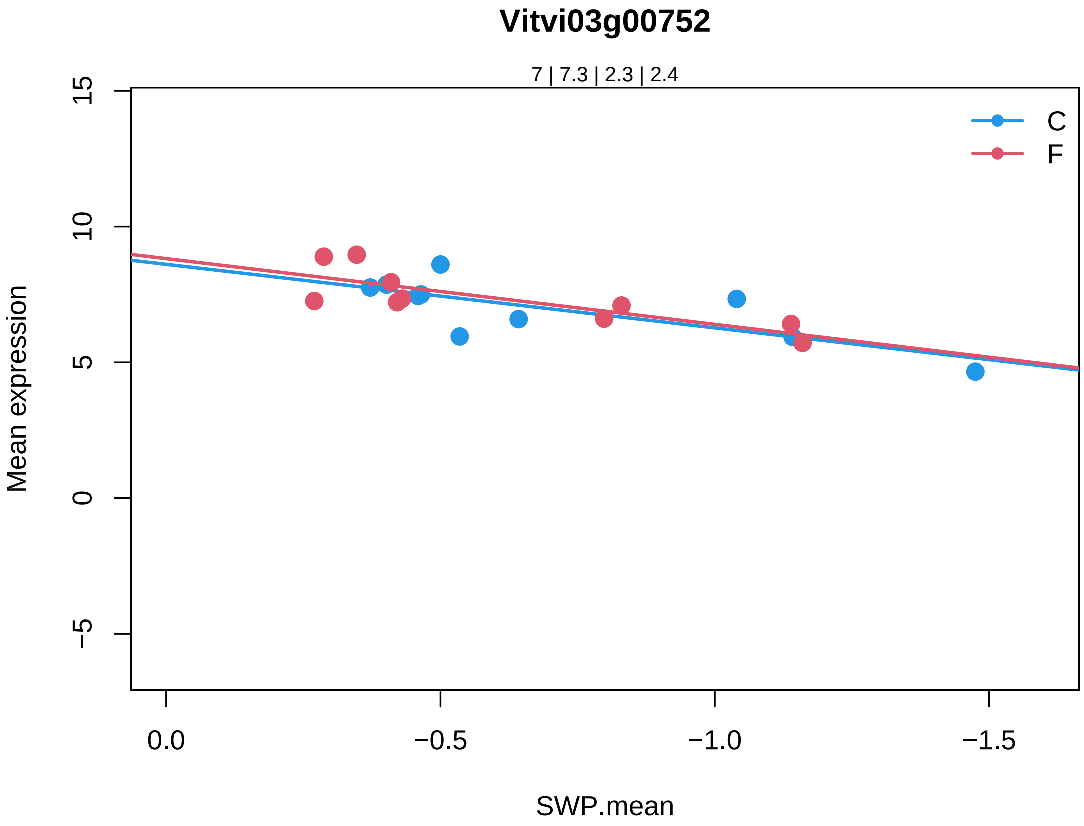
6.2.14 Vitvi03g00752

```
> 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.

```
                   swp  varietyF swp.varietyF  AveExpr        F
Vitvi03g00752 2.340669 0.2104346   0.07947066 7.153861 10.19027
                   P.Value   adj.P.Val  type
Vitvi03g00752 0.0002256549 0.004420863 type1
```



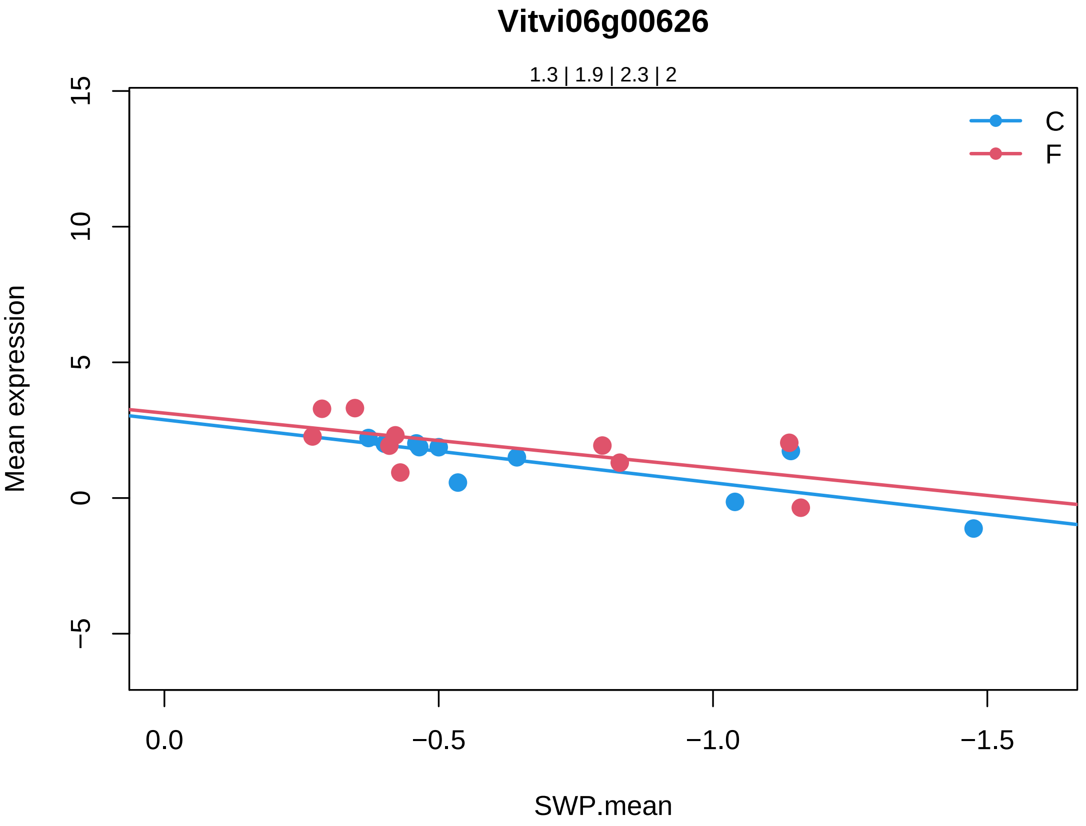
6.2.15 Vitvi06g00626

```
> 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.

```
                   swp varietyF swp.varietyF  AveExpr        F
Vitvi06g00626 2.319803 0.246751    -0.297086 1.573643 8.100371
                   P.Value adj.P.Val  type
Vitvi06g00626 0.0008563151 0.0130259 type1
```



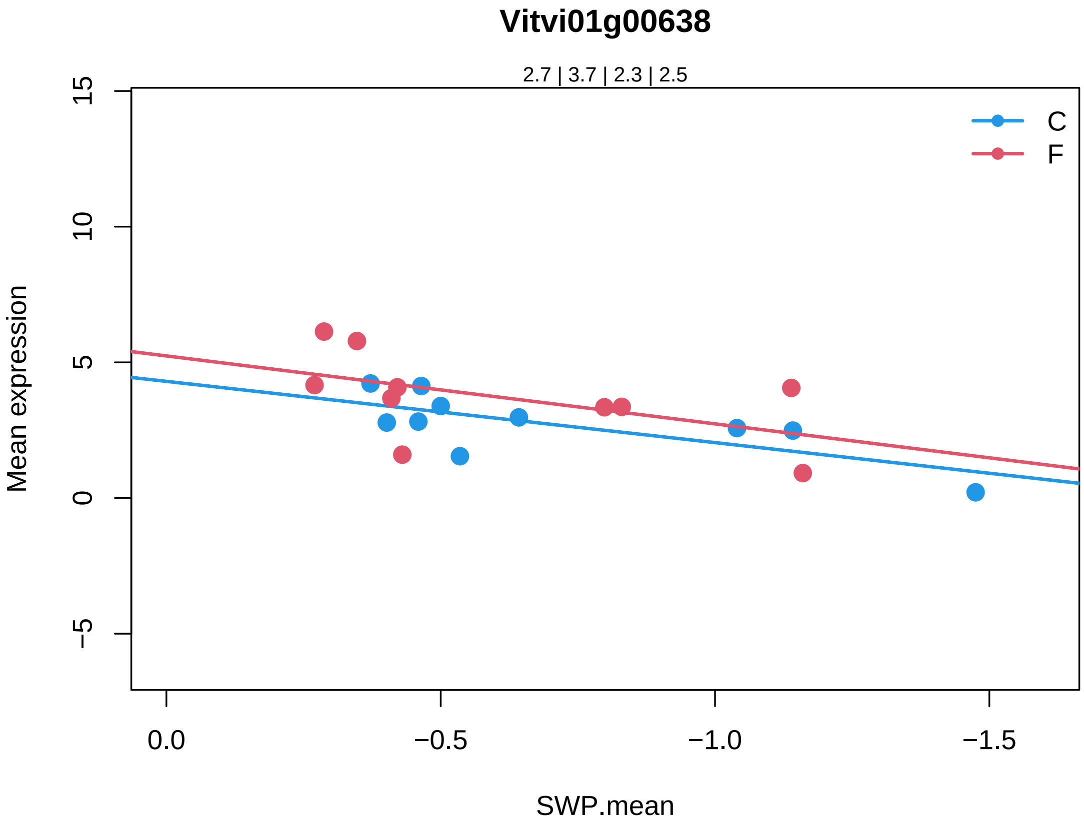
6.2.16 Vitvi01g00638

```
> 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.

```
                   swp varietyF swp.varietyF  AveExpr        F
Vitvi01g00638 2.257332 0.937572    0.2461278 3.212291 5.493411
                  P.Value  adj.P.Val  type
Vitvi01g00638 0.005874018 0.05761415 type1
```



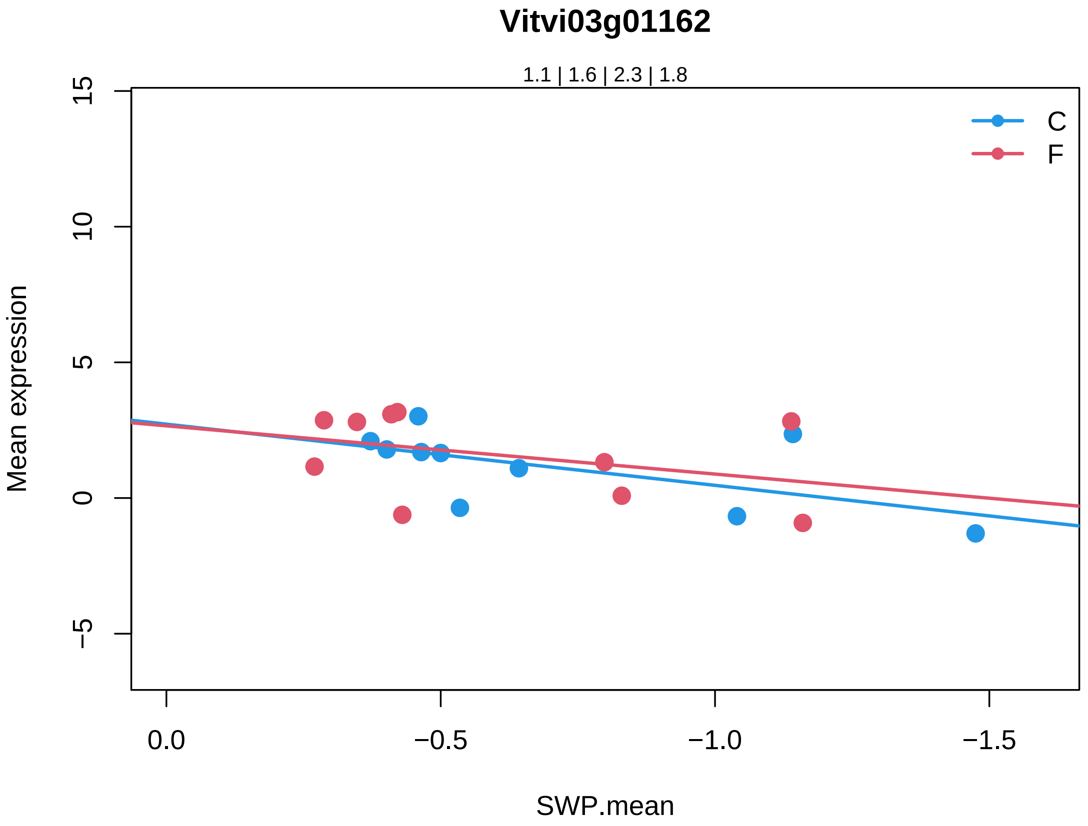
6.2.17 Vitvi03g01162

```
> 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.

```
                   swp   varietyF swp.varietyF  AveExpr        F
Vitvi03g01162 2.254074 -0.0609989   -0.4754753 1.357255 2.372616
                 P.Value adj.P.Val  type
Vitvi03g01162 0.09860085 0.3679488 type1
```



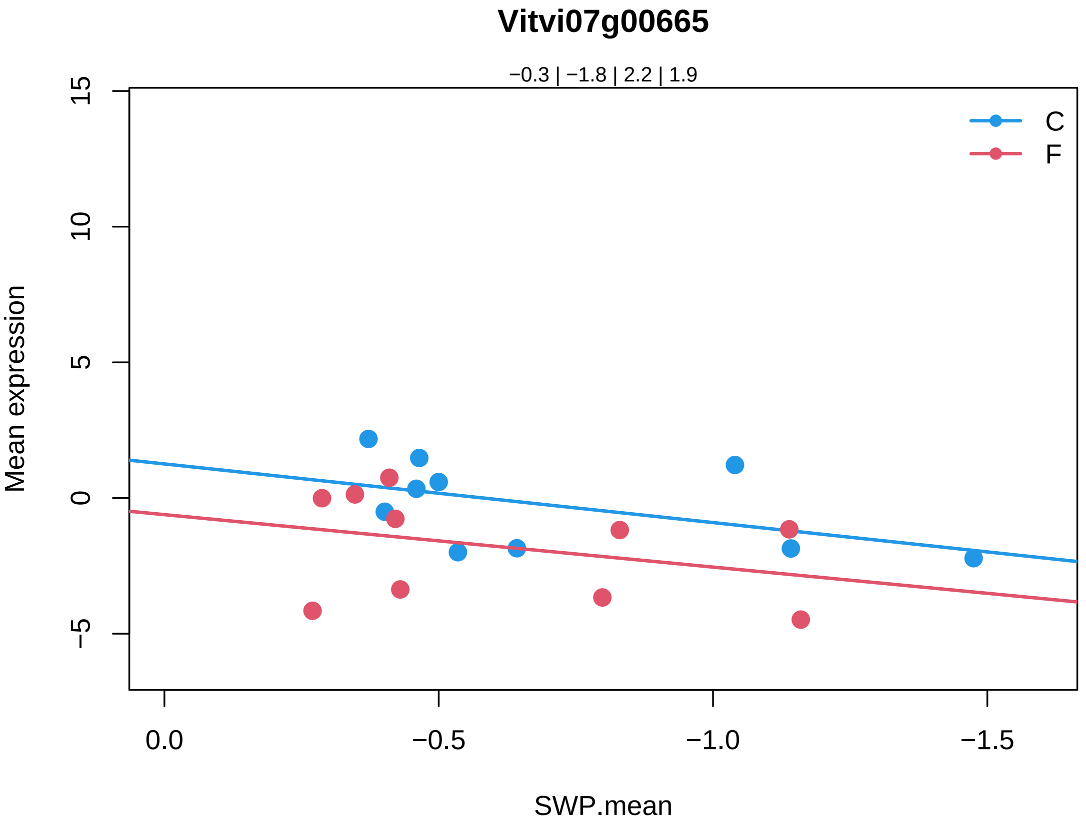
6.2.18 Vitvi07g00665

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

```
Vitvi07g00665
        10.02.2001
        cell wall.cellulose synthesis.cellulose synthase
        cellulose synthase A4 |
        Chr5:17714713-17719564 FORWARD LENGTH=1078 |
        201606
```

Coefficients for Vitvi07g00665.

```
                   swp varietyF swp.varietyF   AveExpr       F
Vitvi07g00665 2.161511 -1.86872    -0.228278 -1.026405 3.12748
                 P.Value adj.P.Val  type
Vitvi07g00665 0.04694916 0.2346996 type1
```



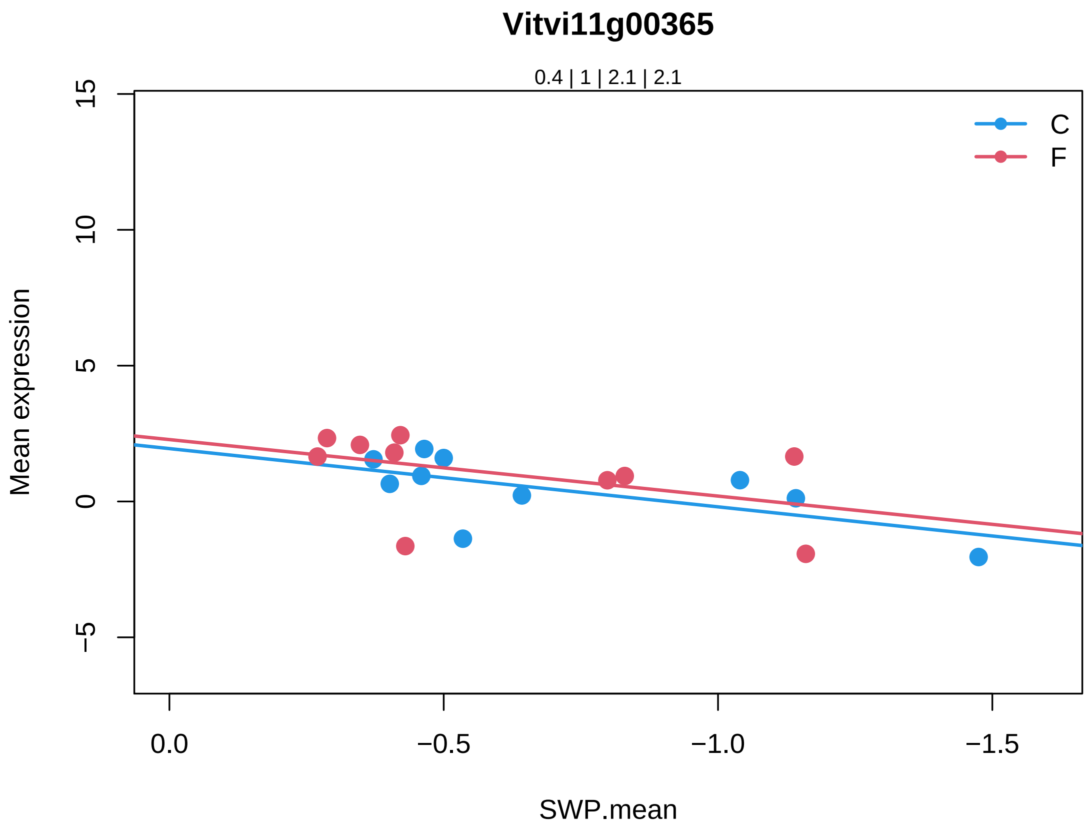
6.2.19 Vitvi11g00365

```
> 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.

```
                   swp  varietyF swp.varietyF   AveExpr        F
Vitvi11g00365 2.144061 0.3321869  -0.06396351 0.7250174 3.142283
                 P.Value adj.P.Val  type
Vitvi11g00365 0.04628912 0.2330049 type1
```



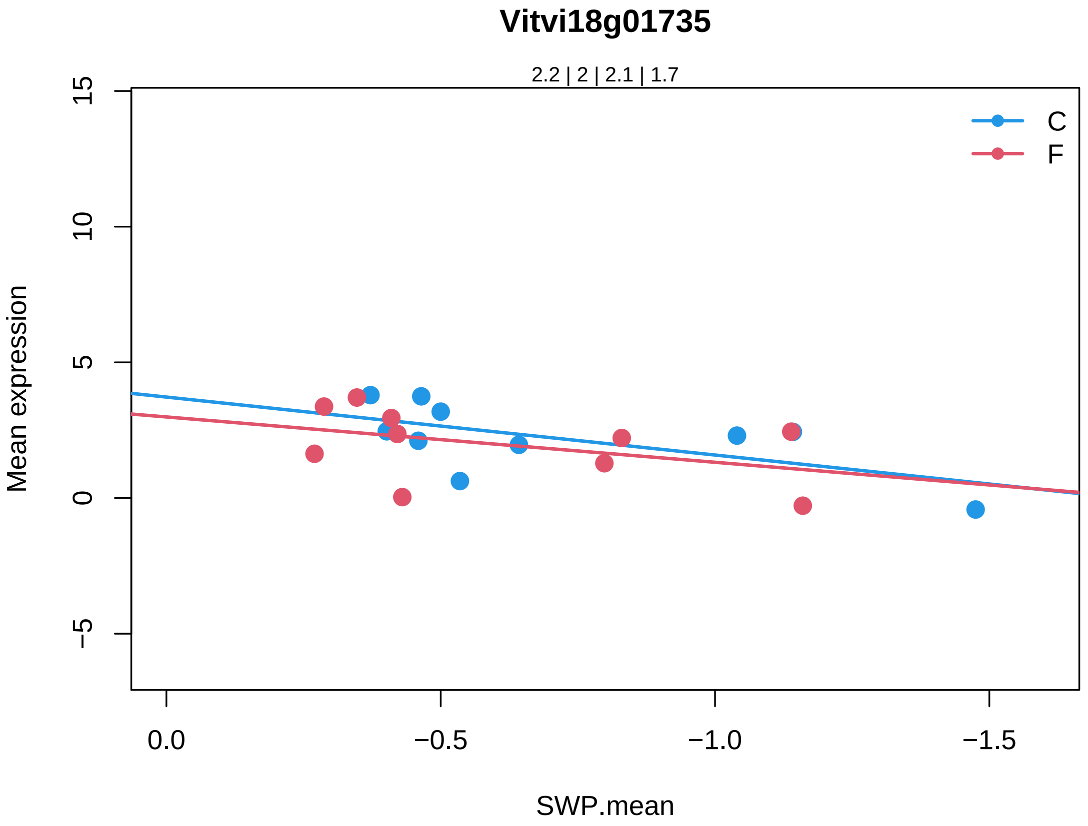
6.2.20 Vitvi18g01735

```
> 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.

```
                   swp   varietyF swp.varietyF  AveExpr        F
Vitvi18g01735 2.136215 -0.7323873   -0.4651096 2.094547 2.770429
                 P.Value adj.P.Val  type
Vitvi18g01735 0.06636535 0.2873989 type1
```



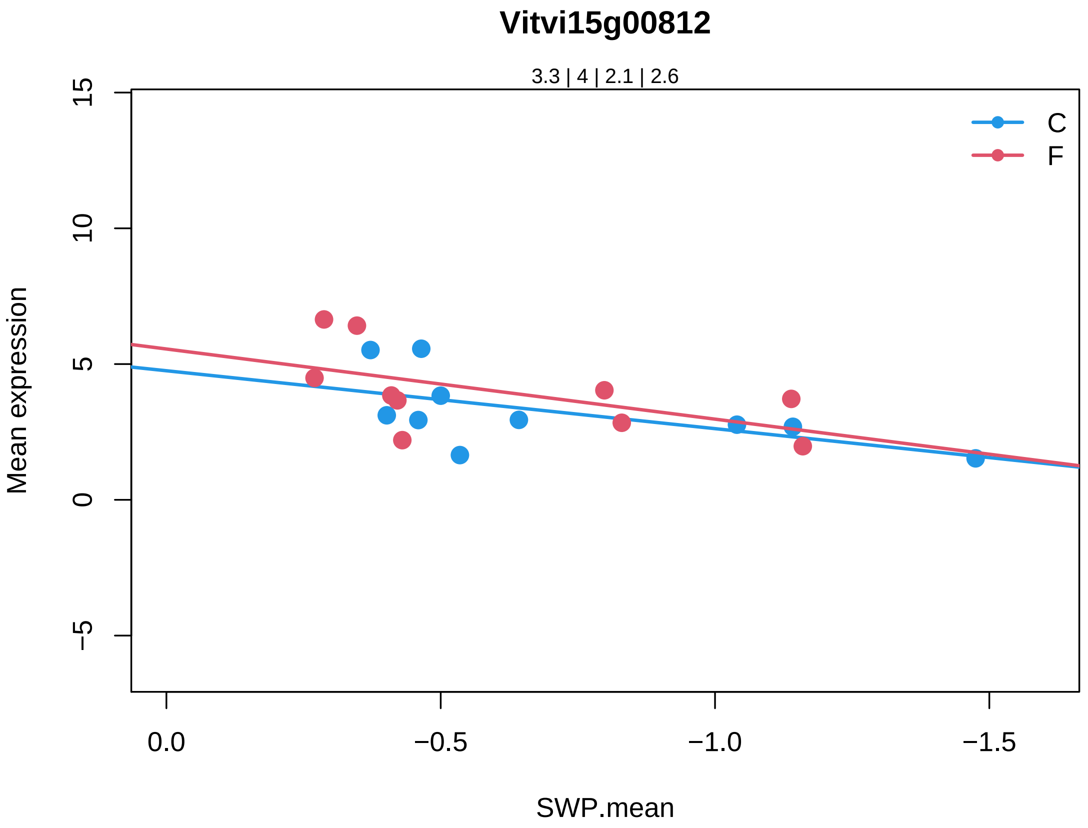
6.2.21 Vitvi15g00812

```
> 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.

```
                   swp  varietyF swp.varietyF  AveExpr        F
Vitvi15g00812 2.132014 0.8019037    0.4515342 3.617839 4.065342
                 P.Value adj.P.Val  type
Vitvi15g00812 0.01972272 0.1339011 type1
```



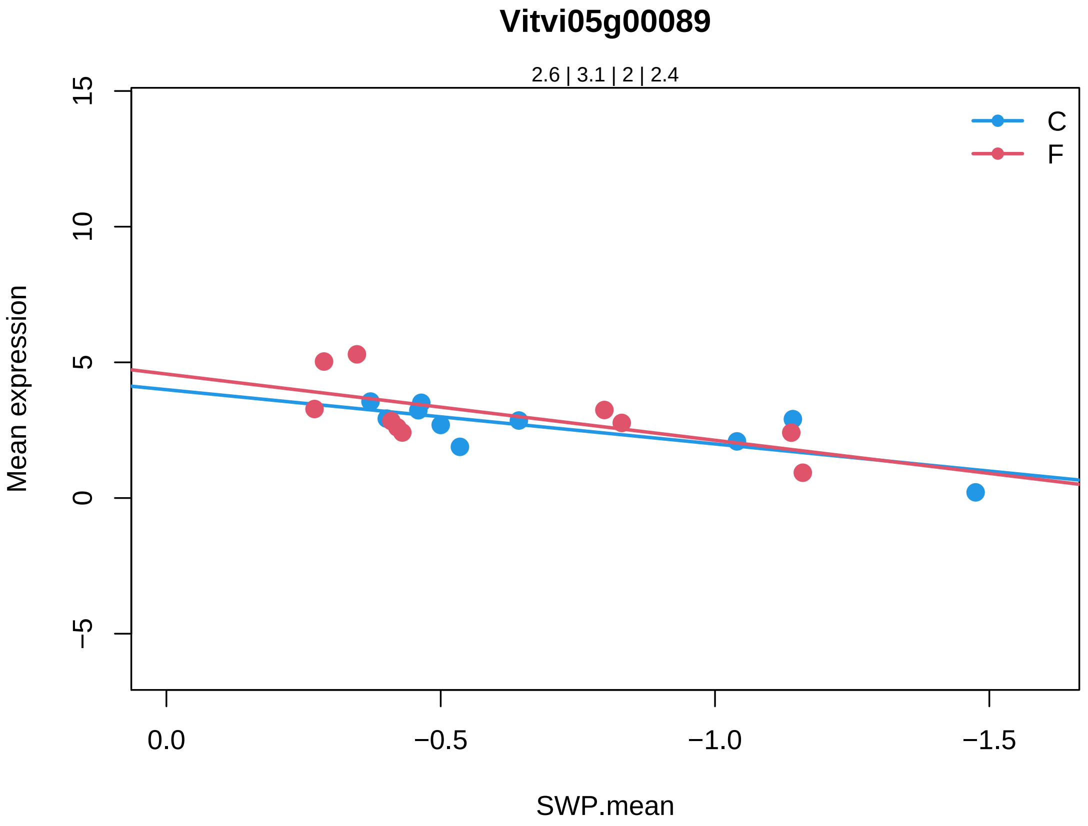
6.2.22 Vitvi05g00089

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

```
Vitvi05g00089
        10.06.2002
        cell wall.degradation.mannan-xylose-arabinose-fucose
        beta-xylosidase 1 |
        Chr5:20012179-20016659 REVERSE LENGTH=774 |
        201606
```

Coefficients for Vitvi05g00089.

```
                   swp  varietyF swp.varietyF  AveExpr        F
Vitvi05g00089 2.000394 0.5756574    0.4406078 2.833928 6.798116
                  P.Value  adj.P.Val  type
Vitvi05g00089 0.002150061 0.02699443 type1
```



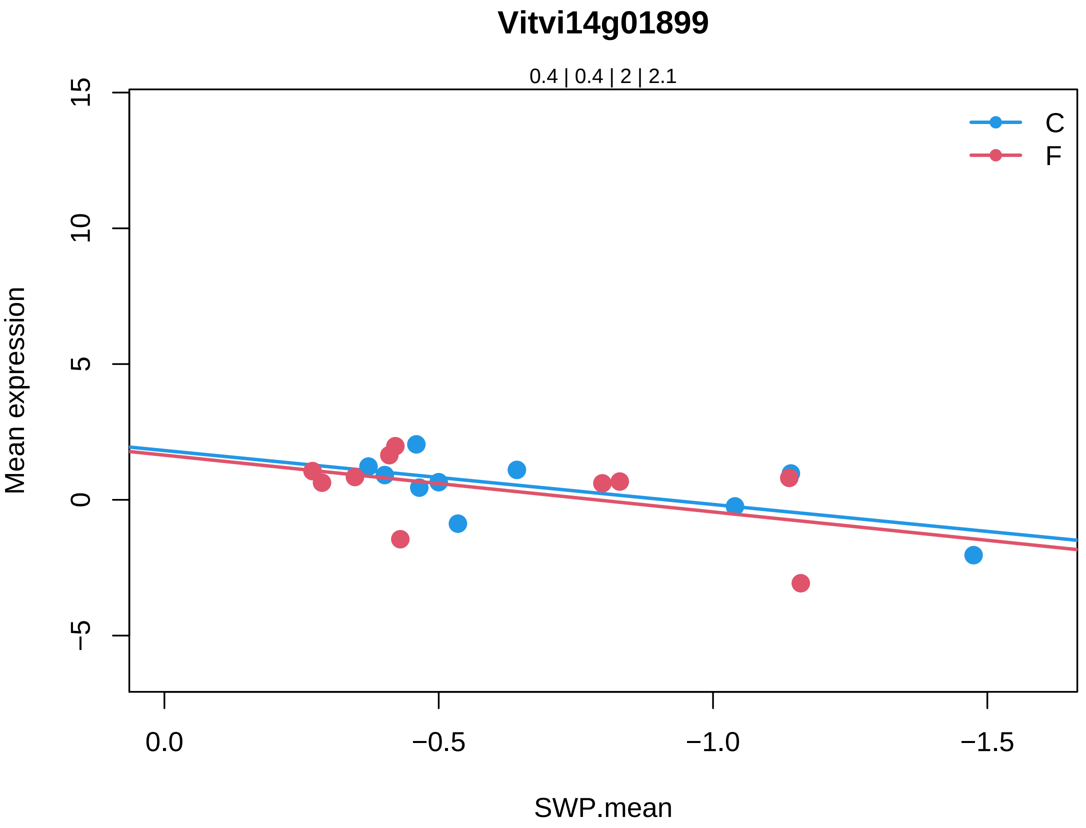
6.2.23 Vitvi14g01899

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

```
Vitvi14g01899
        17.02.2002
        hormone metabolism.auxin.signal transduction
        Auxin efflux carrier family protein |
        Chr5:4892159-4893937 REVERSE LENGTH=367 |
        201606
```

Coefficients for Vitvi14g01899.

```
                   swp   varietyF swp.varietyF   AveExpr       F
Vitvi14g01899 1.986801 -0.1708037    0.1041887 0.3953405 2.84337
                 P.Value adj.P.Val  type
Vitvi14g01899 0.06179068  0.276516 type1
```



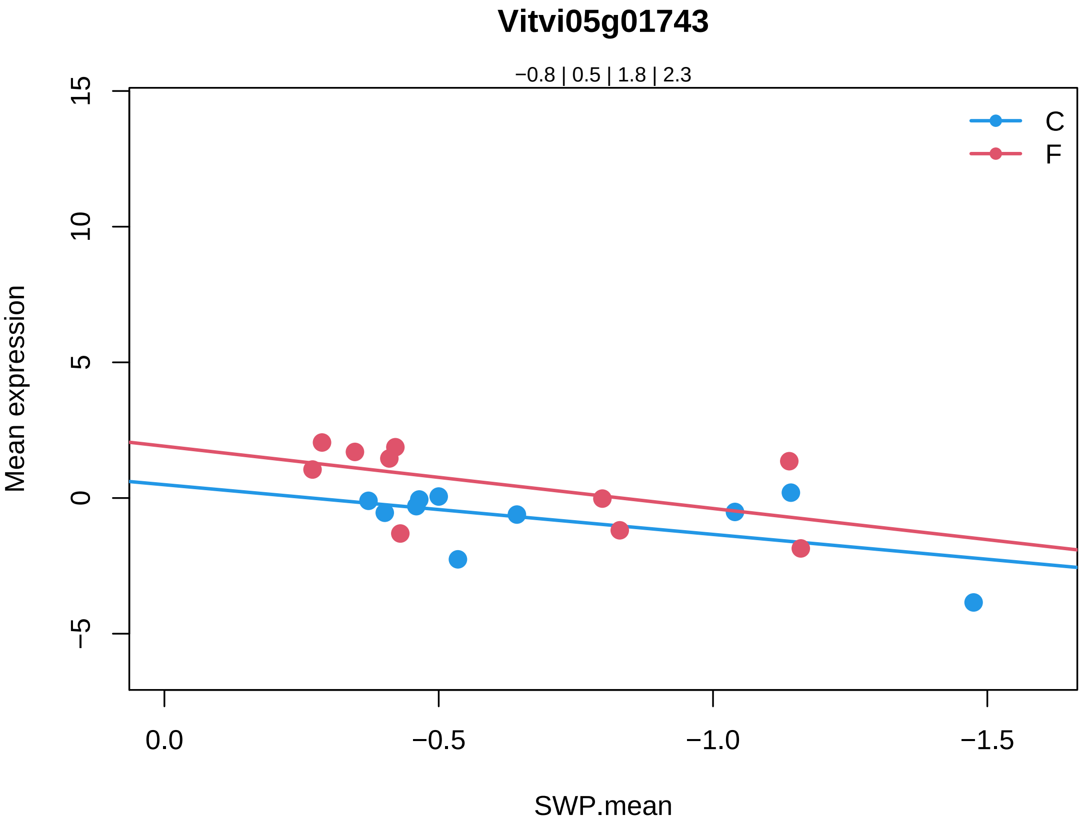
6.2.24 Vitvi05g01743

```
> 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.

```
                   swp varietyF swp.varietyF    AveExpr        F
Vitvi05g01743 1.831631 1.418614    0.4631932 -0.1436041 5.158489
                  P.Value  adj.P.Val  type
Vitvi05g01743 0.007717733 0.06952345 type1
```



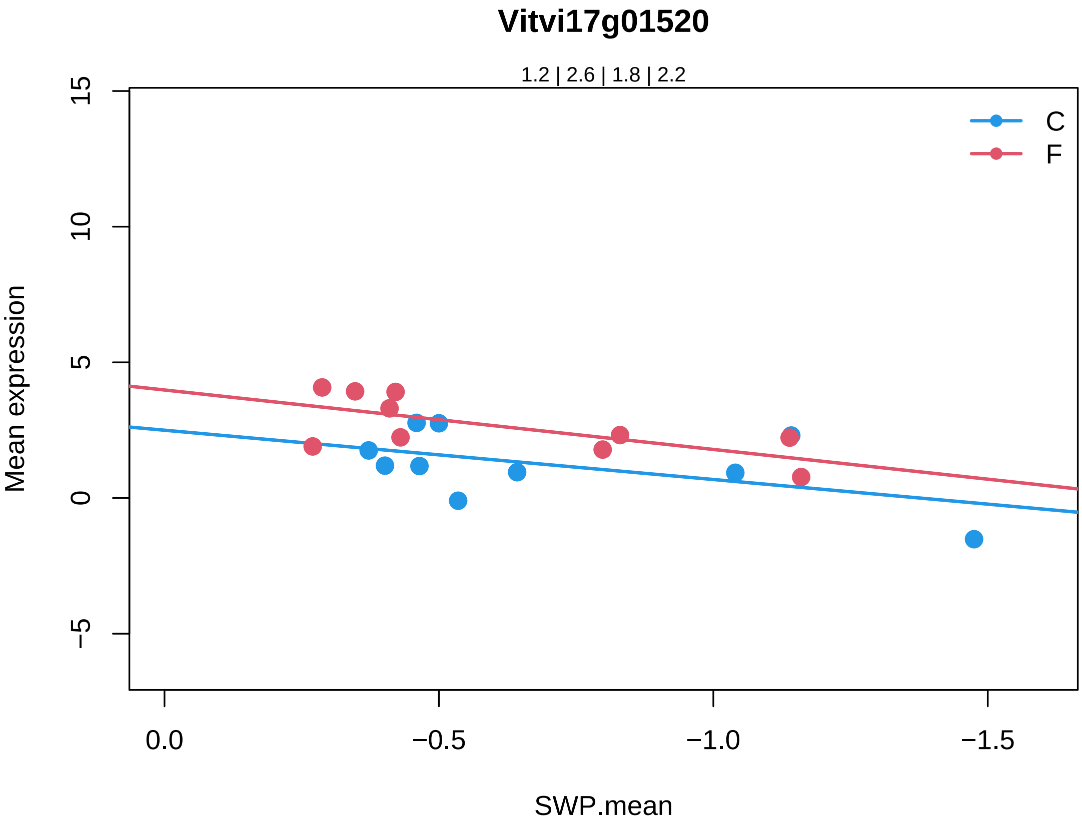
6.2.25 Vitvi17g01520

```
> 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.

```
                   swp varietyF swp.varietyF  AveExpr        F
Vitvi17g01520 1.815974 1.482473    0.3752235 1.933961 7.522588
                  P.Value  adj.P.Val  type
Vitvi17g01520 0.001276294 0.01781001 type1
```



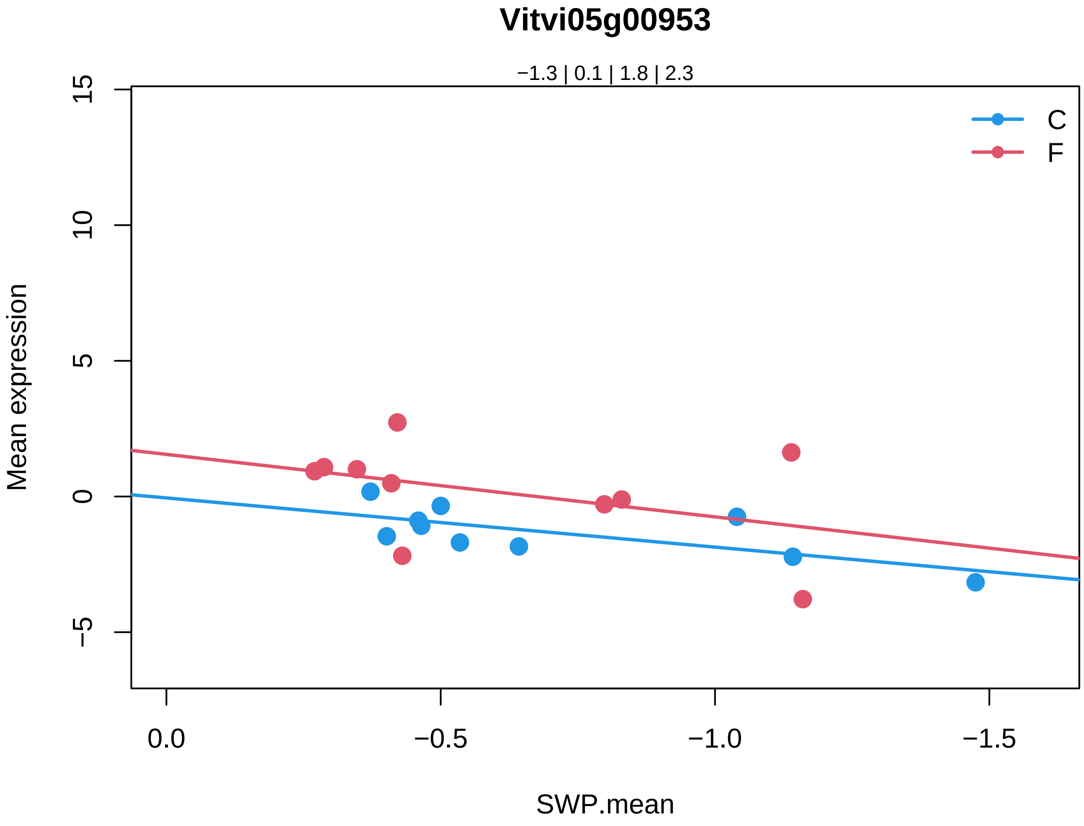
6.2.26 Vitvi05g00953

```
> 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
        10.06.2003
        cell wall.degradation.pectate lyases and polygalacturonases
        Pectin lyase-like superfamily protein |
        Chr3:2212973-2214614 REVERSE LENGTH=383 |
        201606
```

Coefficients for Vitvi05g00953.

```
                  swp varietyF swp.varietyF    AveExpr       F
Vitvi05g00953 1.81224 1.605018    0.4911137 -0.5890888 4.61853
                 P.Value  adj.P.Val  type
Vitvi05g00953 0.01215372 0.09578439 type1
```



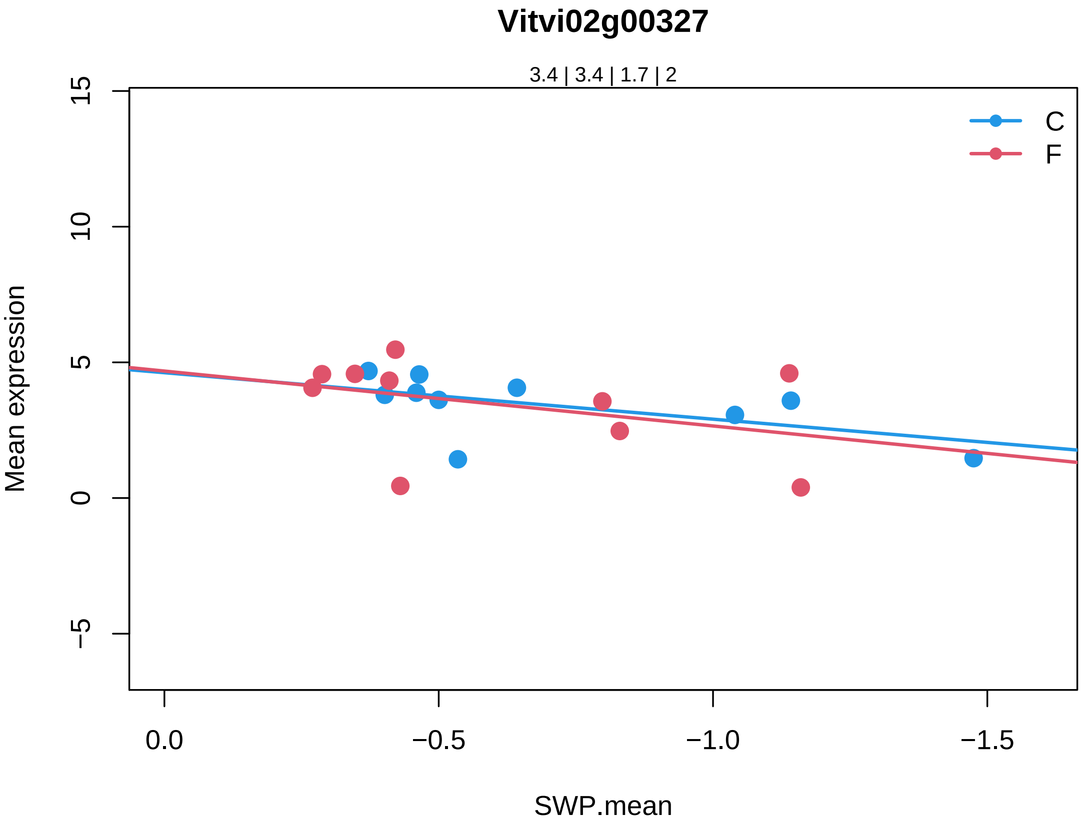
6.2.27 Vitvi02g00327

```
> 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.

```
                   swp   varietyF swp.varietyF  AveExpr        F
Vitvi02g00327 1.713415 0.05891086    0.3093124 3.430217 1.755144
                P.Value adj.P.Val  type
Vitvi02g00327 0.1859218 0.5162772 type1
```



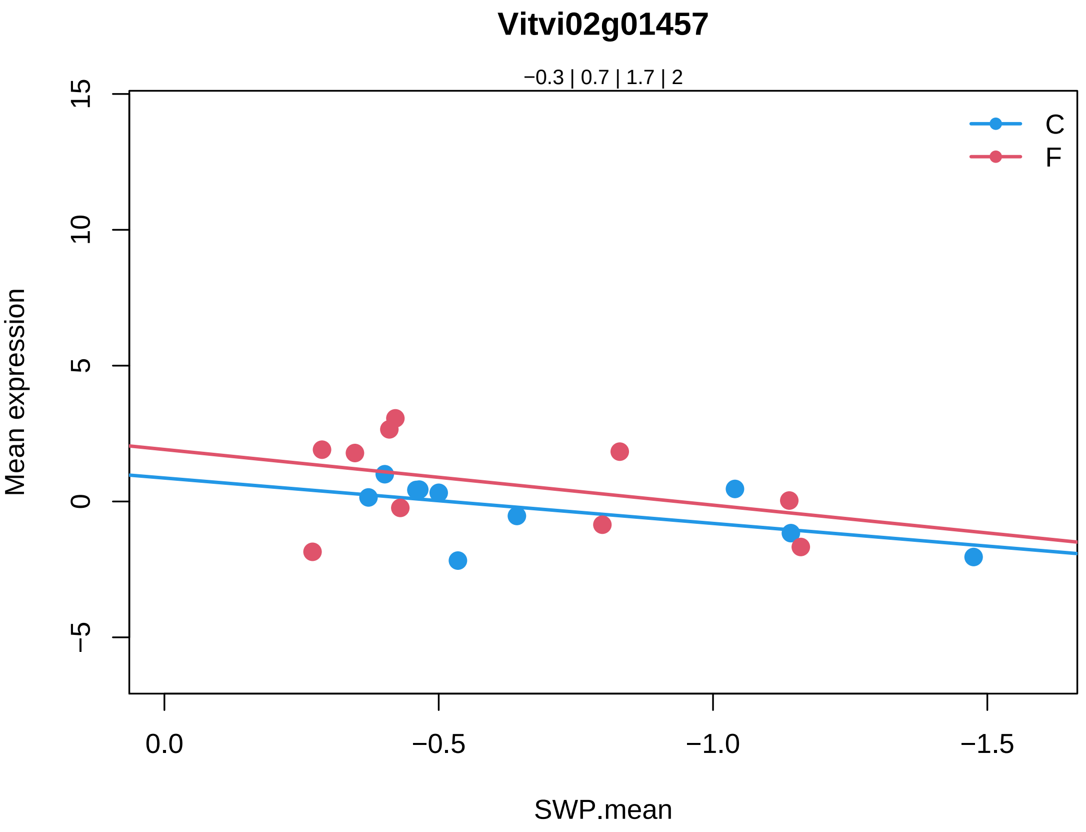
6.2.28 Vitvi02g01457

```
> 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.

```
                   swp varietyF swp.varietyF   AveExpr        F
Vitvi02g01457 1.671346 1.049884    0.3760593 0.1770082 2.722271
                 P.Value adj.P.Val  type
Vitvi02g01457 0.06958385 0.2965046 type1
```



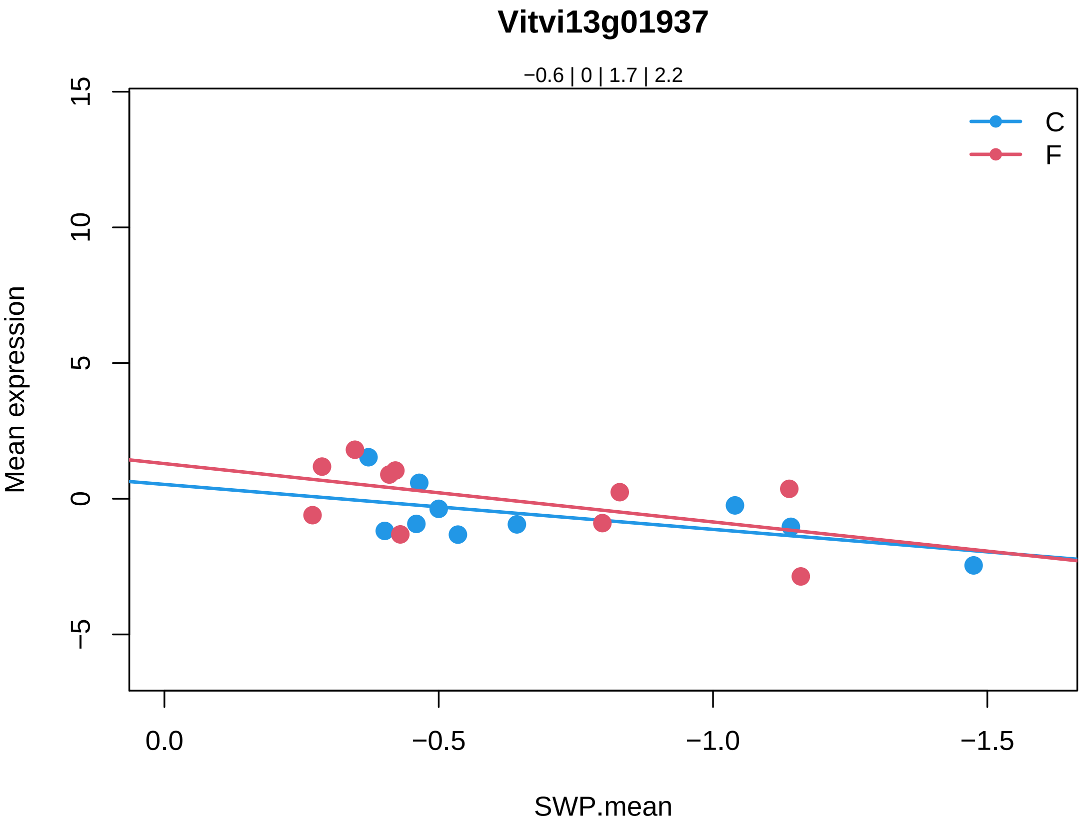
6.2.29 Vitvi13g01937

```
> 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.

```
                   swp varietyF swp.varietyF   AveExpr        F
Vitvi13g01937 1.656786 0.767675    0.4941654 -0.325932 3.455755
                 P.Value adj.P.Val  type
Vitvi13g01937 0.03442042 0.1929518 type1
```



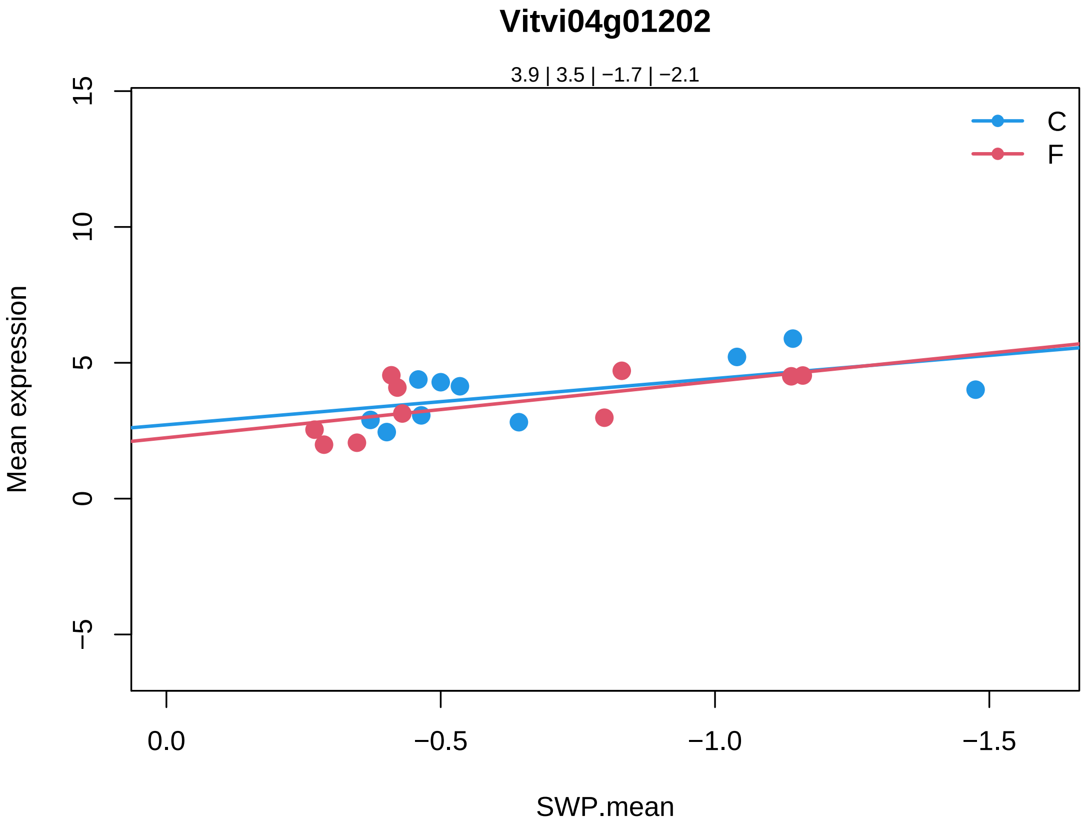
6.2.30 Vitvi04g01202

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

```
Vitvi04g01202
        27.01.2020
        RNA.processing.degradation dicer
        dicer-like 2 |
        Chr3:768020-774525 REVERSE LENGTH=1374 |
        201606
```

Coefficients for Vitvi04g01202.

```
                    swp   varietyF swp.varietyF  AveExpr        F
Vitvi04g01202 -1.702794 -0.4759554   -0.3731589 3.710224 4.435462
                 P.Value adj.P.Val  type
Vitvi04g01202 0.01423468 0.1068793 type1
```



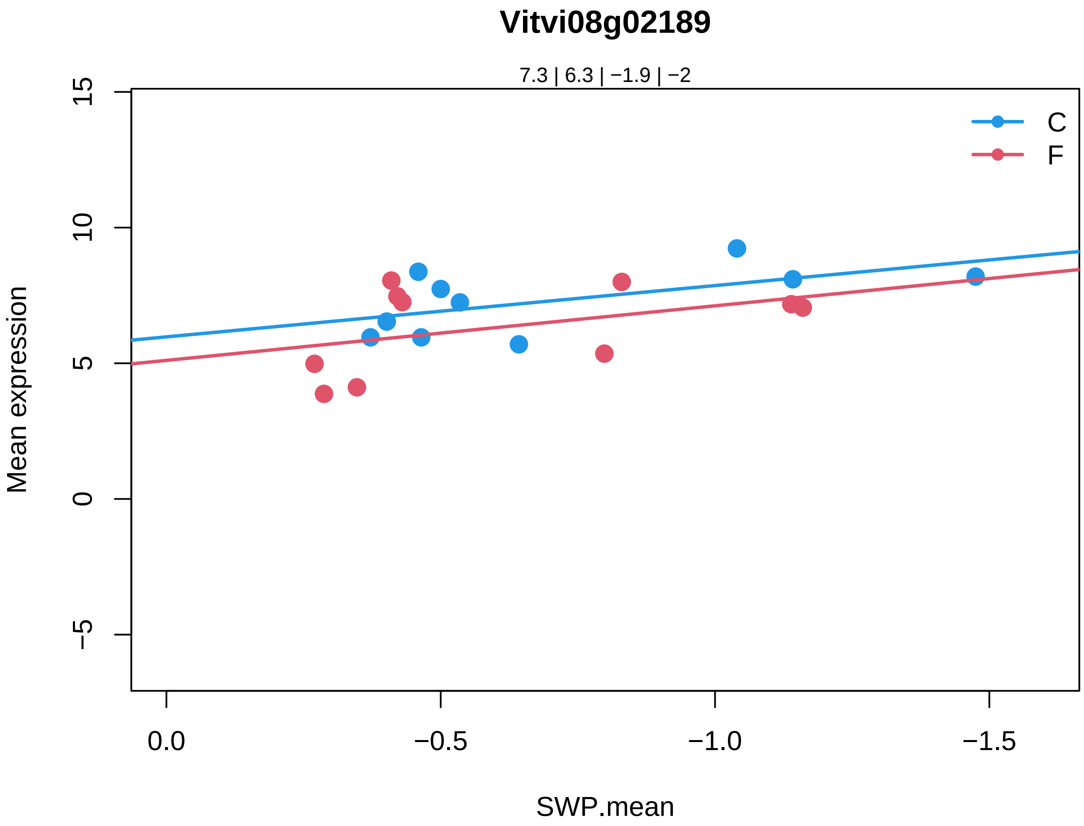
6.2.31 Vitvi08g02189

```
> 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
        20.02.2001
        stress.abiotic.heat
        heat shock cognate protein 70-1 |
        Chr5:554055-556334 REVERSE LENGTH=651 |
        201606
```

Coefficients for Vitvi08g02189.

```
                    swp   varietyF swp.varietyF  AveExpr       F
Vitvi08g02189 -1.890543 -0.8668898   -0.1210553 6.816799 3.41836
                 P.Value adj.P.Val  type
Vitvi08g02189 0.03564593  0.197929 type1
```


Vitvi08g02189
7.3 | 6.3 | −1.9 | −2
C
F
Mean expression
15
10
5
0
−5
0.0
−0.5
−1.0
−1.5
SWP.mean

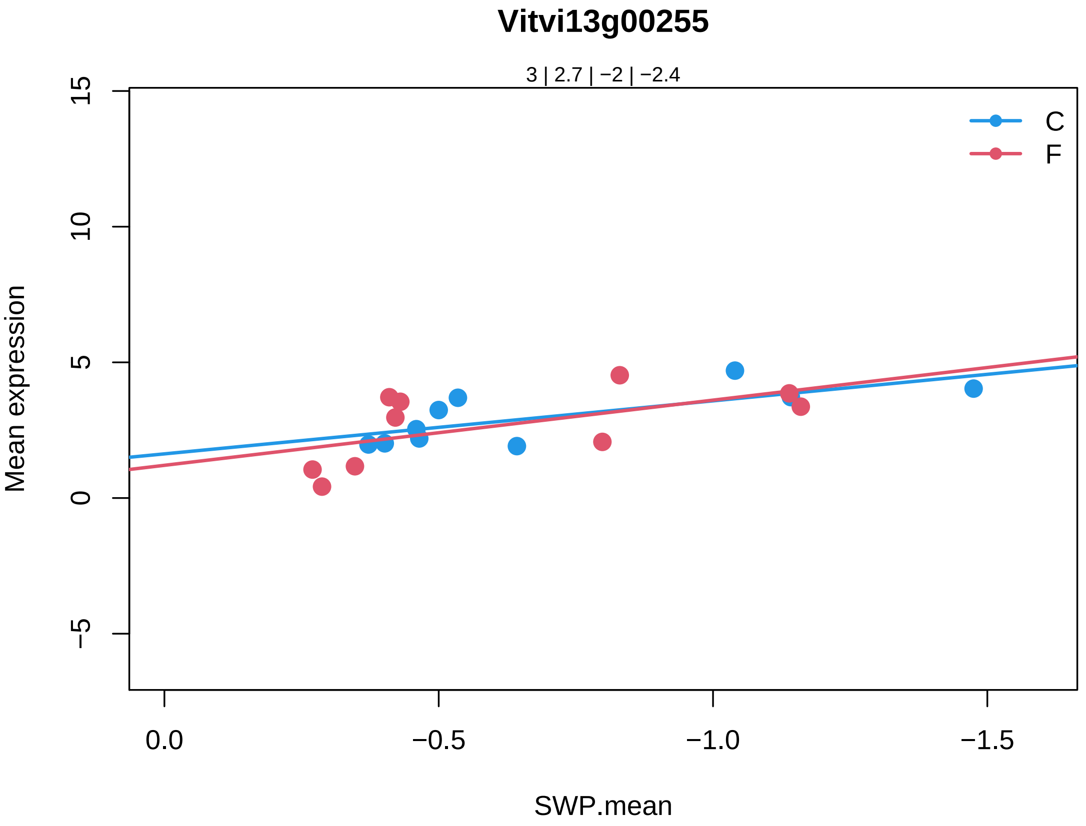
6.2.32 Vitvi13g00255

```
> 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.

```
                    swp   varietyF swp.varietyF  AveExpr        F
Vitvi13g00255 -1.953979 -0.4224872   -0.4483182 2.835045 4.918424
                  P.Value  adj.P.Val  type
Vitvi13g00255 0.009423785 0.07993174 type1
```



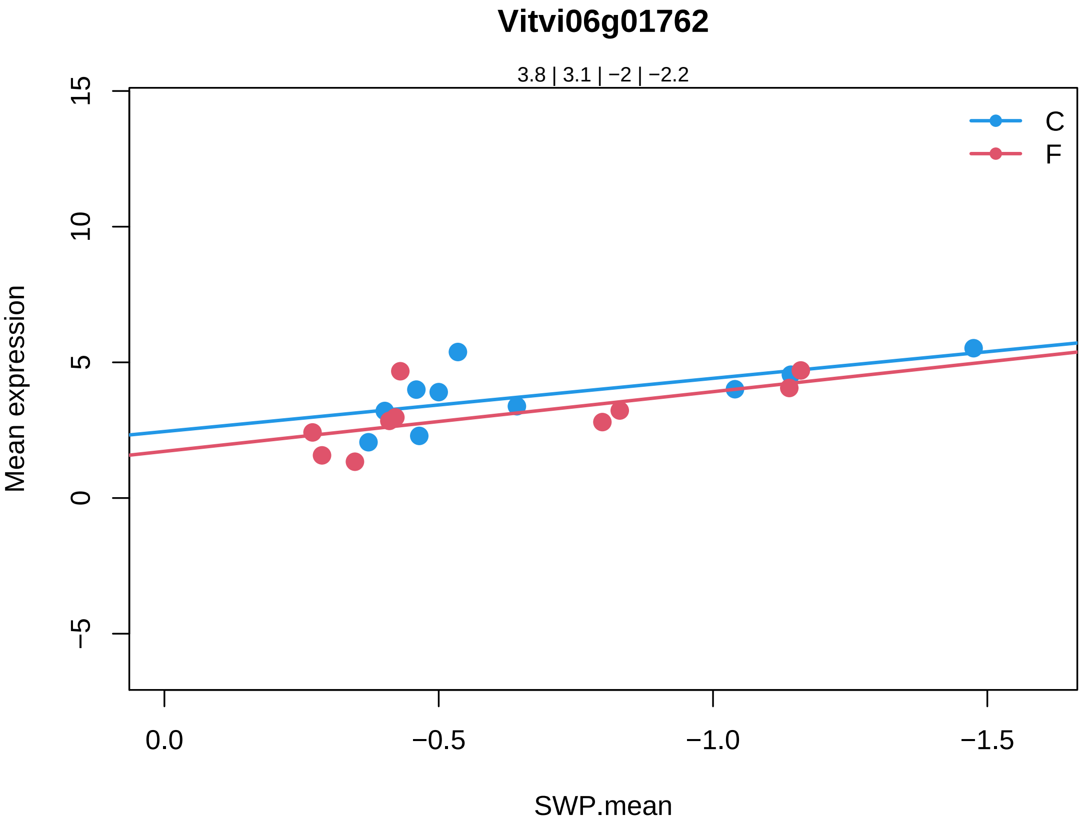
6.2.33 Vitvi06g01762

```
> 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.

```
                   swp   varietyF swp.varietyF  AveExpr        F
Vitvi06g01762 -1.96081 -0.7304003   -0.2379683 3.444288 6.153219
                  P.Value  adj.P.Val  type
Vitvi06g01762 0.003494239 0.03901023 type1
```



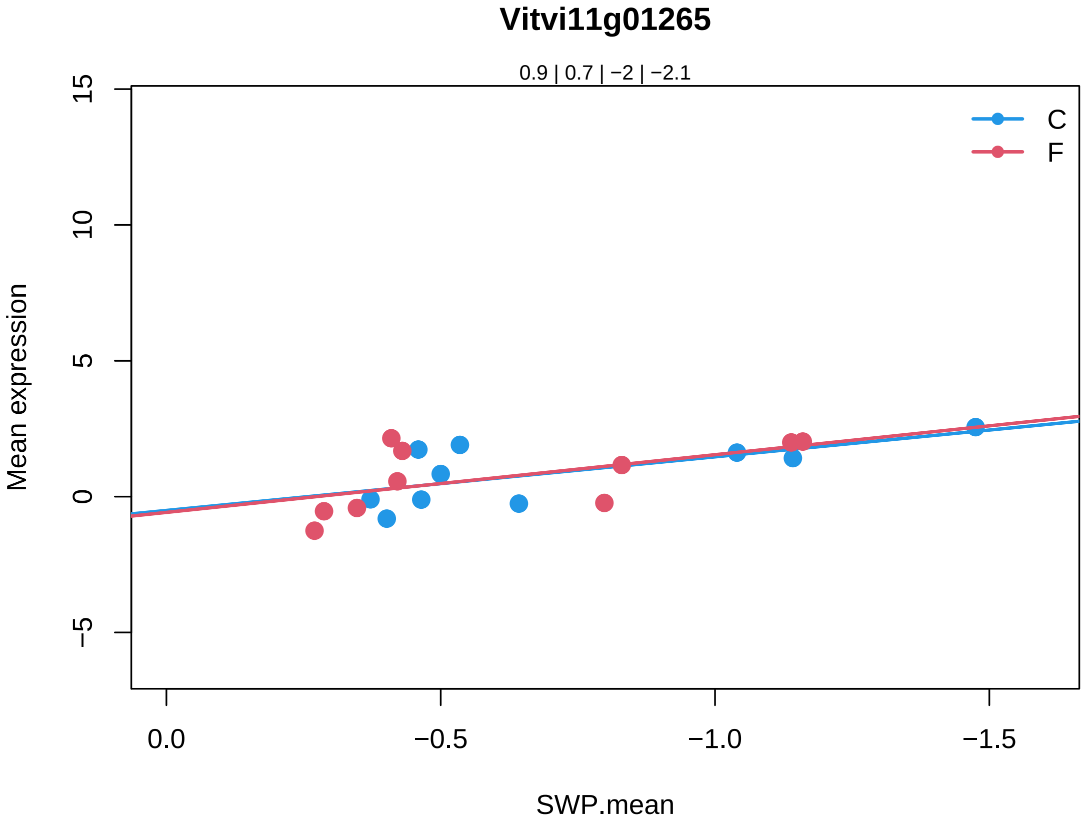
6.2.34 Vitvi11g01265

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

```
Vitvi11g01265
        10.06.2002
        cell wall.degradation.mannan-xylose-arabinose-fucose
        xyloglucan endotransglycosylase 6 |
        Chr4:13128694-13129715 FORWARD LENGTH=286 |
        201606
```

Coefficients for Vitvi11g01265.

```
                    swp    varietyF swp.varietyF   AveExpr        F
Vitvi11g01265 -1.973338 -0.07155404   -0.1505334 0.7960607 4.139653
                 P.Value adj.P.Val  type
Vitvi11g01265 0.01845962 0.1281246 type1
```



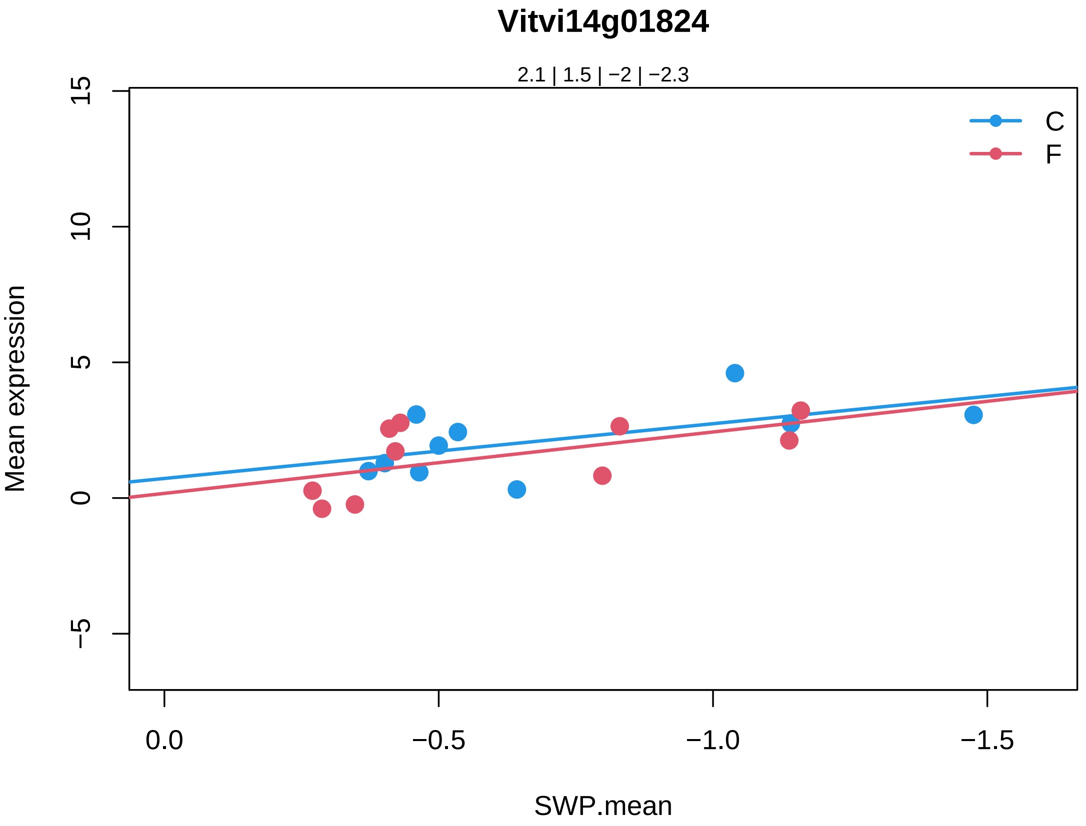
6.2.35 Vitvi14g01824

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

```
Vitvi14g01824
        27.03.2011
        RNA.regulation of transcription.C2H2 zinc finger family
        zinc finger (AN1-like) family protein |
        Chr3:10520585-10521223 FORWARD LENGTH=186 |
        201606
```

Coefficients for Vitvi14g01824.

```
                    swp   varietyF swp.varietyF  AveExpr        F
Vitvi14g01824 -2.017435 -0.5500801   -0.2450116 1.844538 4.097626
                 P.Value adj.P.Val  type
Vitvi14g01824 0.01916283 0.1312129 type1
```



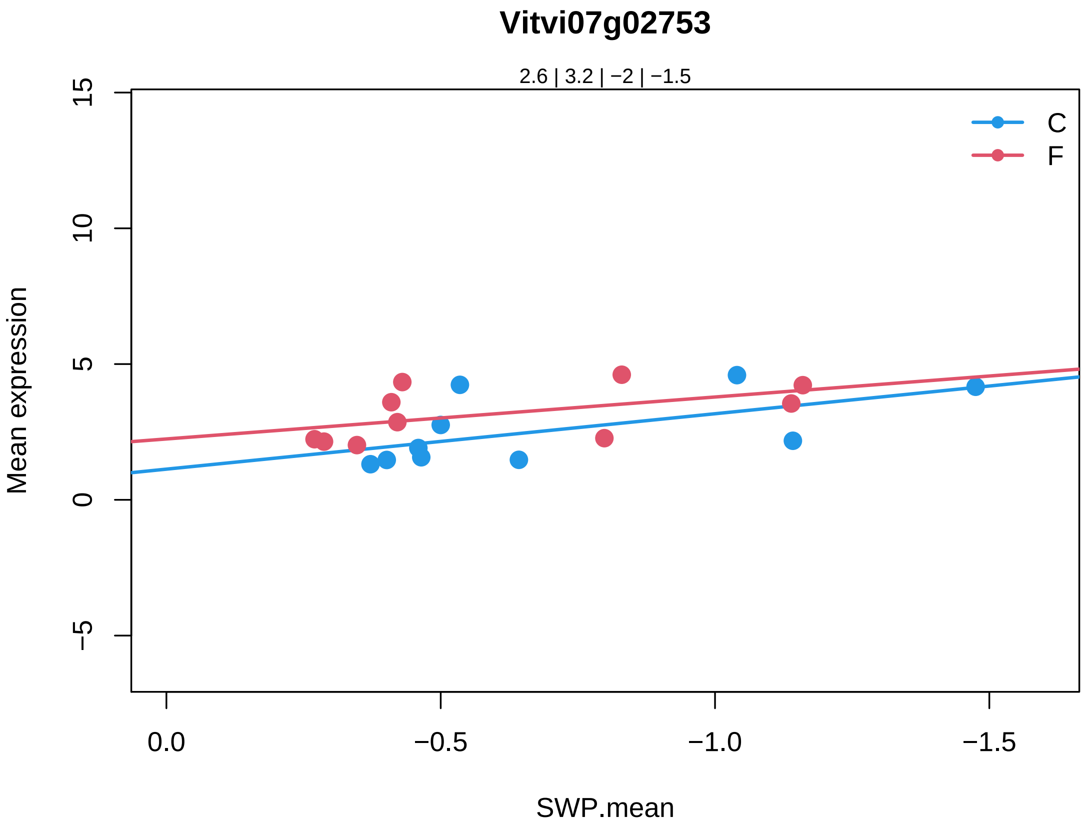
6.2.36 Vitvi07g02753

```
> 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.

```
                    swp varietyF swp.varietyF  AveExpr        F
Vitvi07g02753 -2.040545 1.111666    0.4955967 2.874241 4.023405
                 P.Value adj.P.Val  type
Vitvi07g02753 0.02047663 0.1375517 type1
```



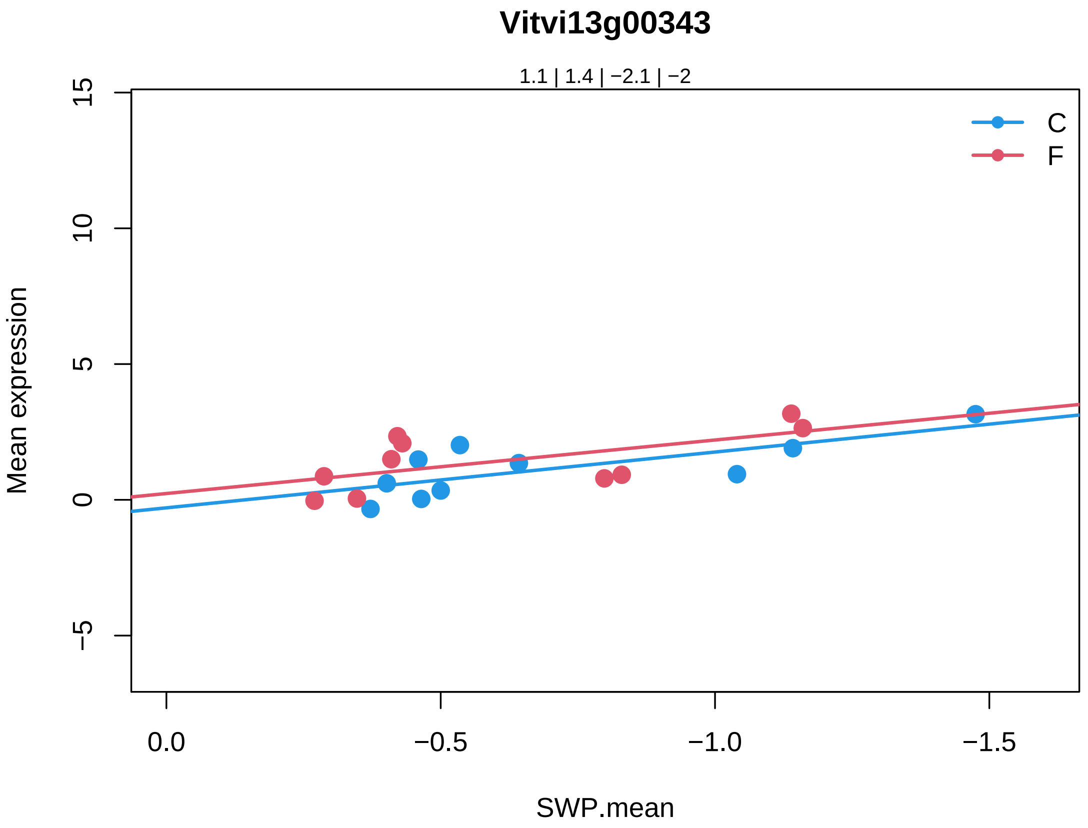
6.2.37 Vitvi13g00343

```
> 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.

```
                    swp varietyF swp.varietyF  AveExpr        F
Vitvi13g00343 -2.05435 0.526508   0.08342333 1.291319 5.727022
                  P.Value adj.P.Val  type
Vitvi13g00343 0.004873973 0.0500938 type1
```



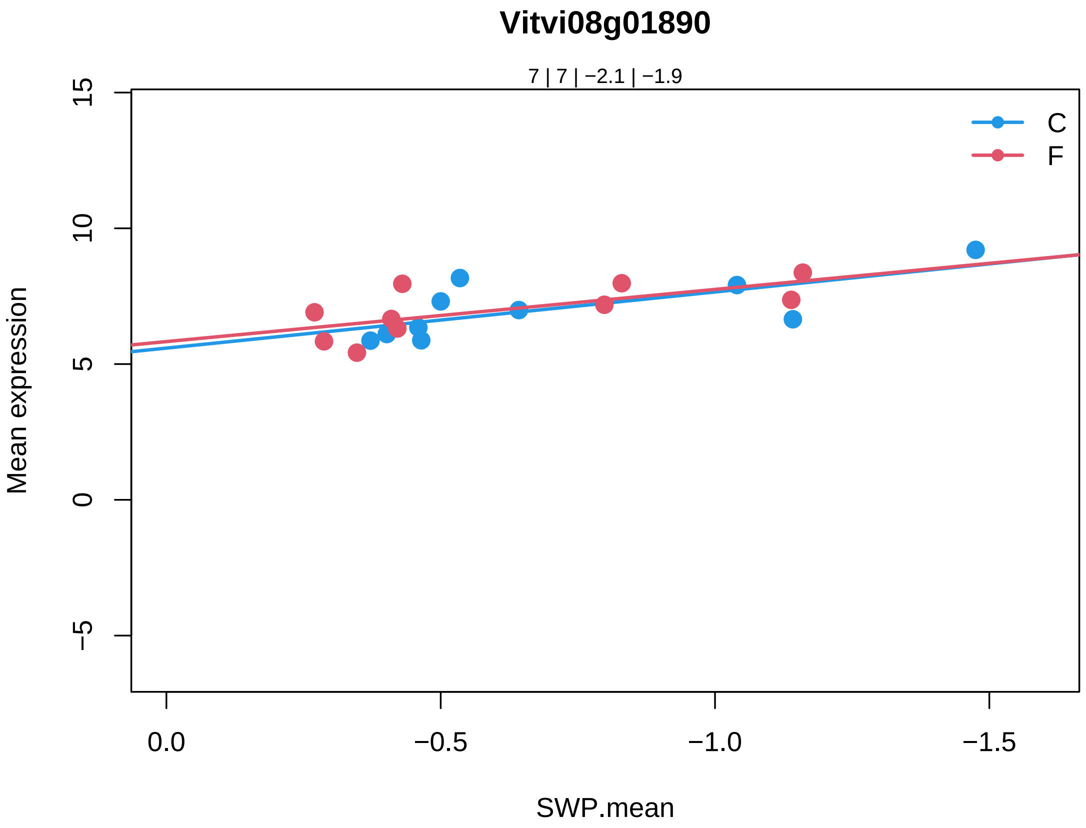
6.2.38 Vitvi08g01890

```
> 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.

```
                    swp  varietyF swp.varietyF AveExpr        F
Vitvi08g01890 -2.067362 0.2395076    0.1452297 7.02013 6.005619
                  P.Value  adj.P.Val  type
Vitvi08g01890 0.003916766 0.04227999 type1
```



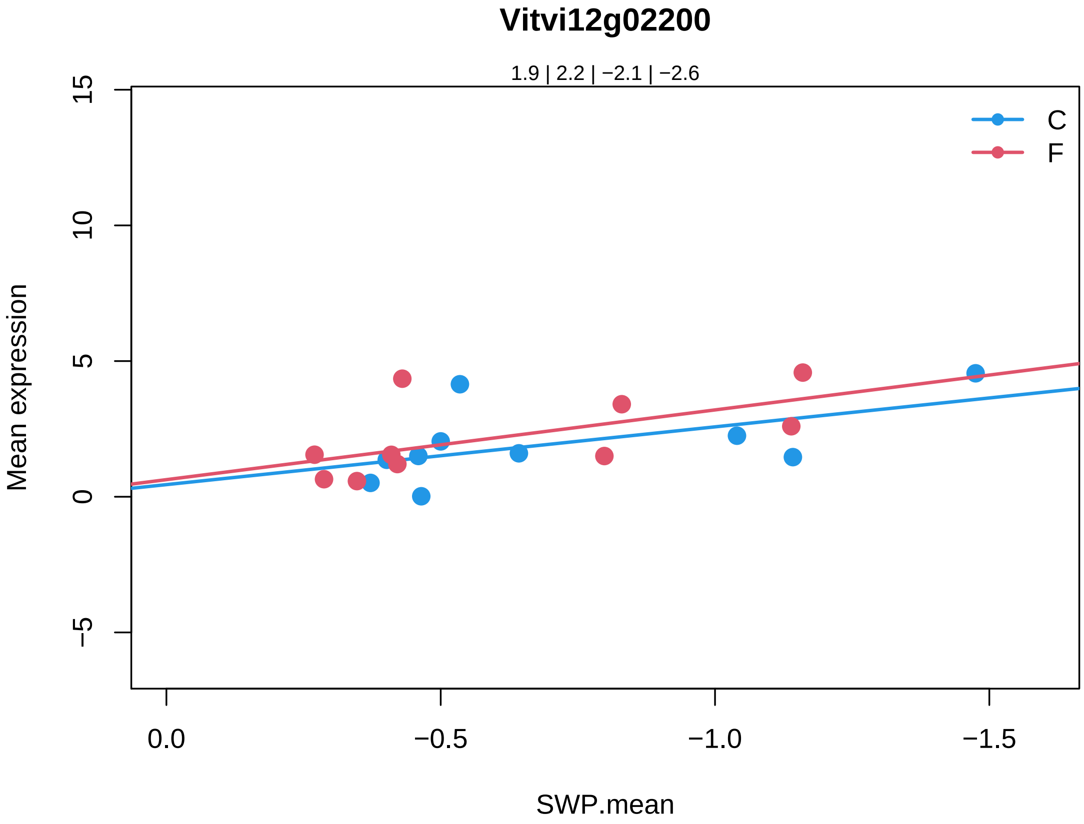
6.2.39 Vitvi12g02200

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

```
Vitvi12g02200
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi12g02200.

```
                    swp  varietyF swp.varietyF  AveExpr        F
Vitvi12g02200 -2.128876 0.1828088   -0.4414103 2.069744 3.614367
                 P.Value adj.P.Val  type
Vitvi12g02200 0.02970542 0.1755822 type1
```



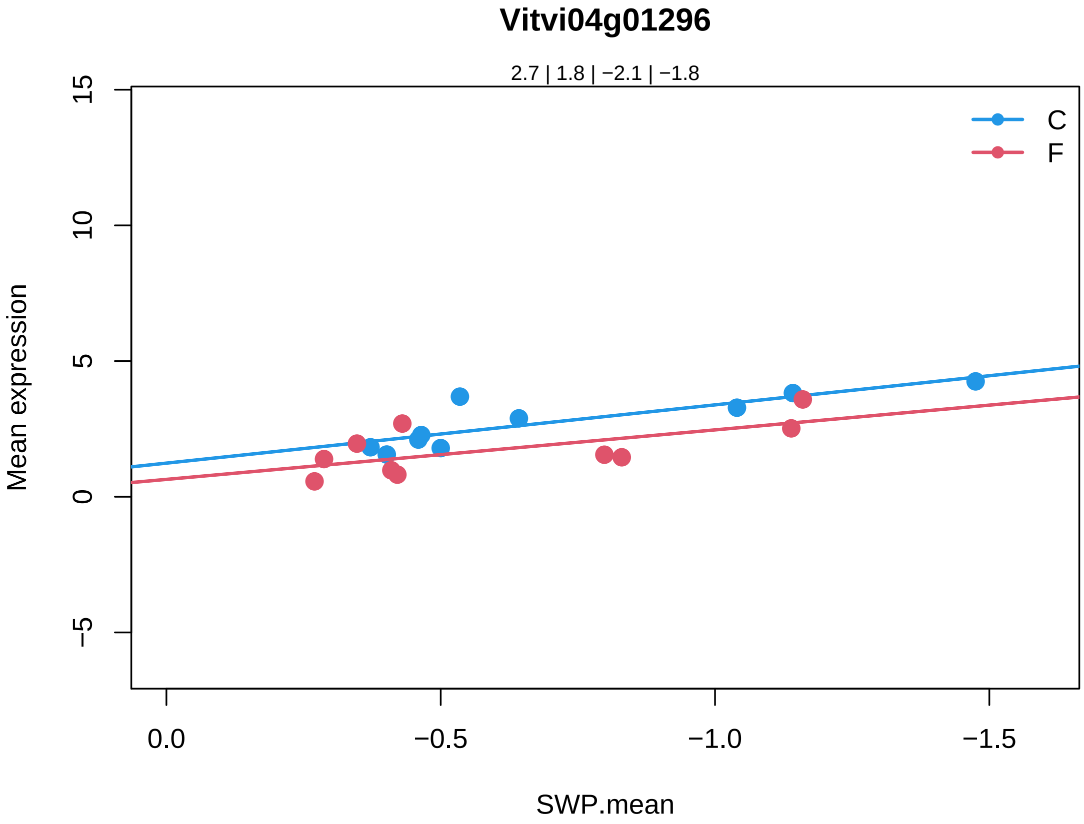
6.2.40 Vitvi04g01296

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

```
Vitvi04g01296
        35.1
        not assigned.no ontology
        NA
```

Coefficients for Vitvi04g01296.

```
                    swp   varietyF swp.varietyF  AveExpr        F
Vitvi04g01296 -2.146713 -0.5995979    0.3222407 2.249635 12.49437
                   P.Value   adj.P.Val  type
Vitvi04g01296 6.129263e-05 0.001489988 type1
```



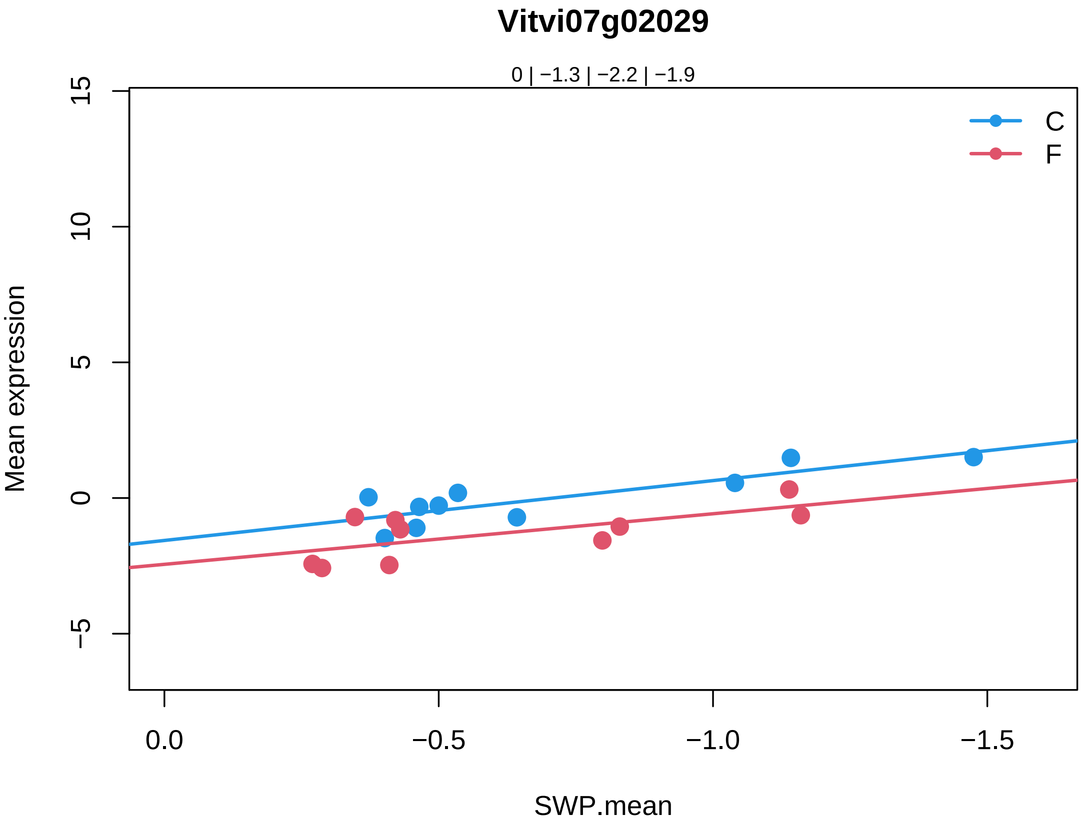
6.2.41 Vitvi07g02029

```
> 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.

```
                    swp   varietyF swp.varietyF    AveExpr        F
Vitvi07g02029 -2.206244 -0.879284    0.3426853 -0.6606395 15.84203
                   P.Value    adj.P.Val  type
Vitvi07g02029 1.174653e-05 0.0003595193 type1
```



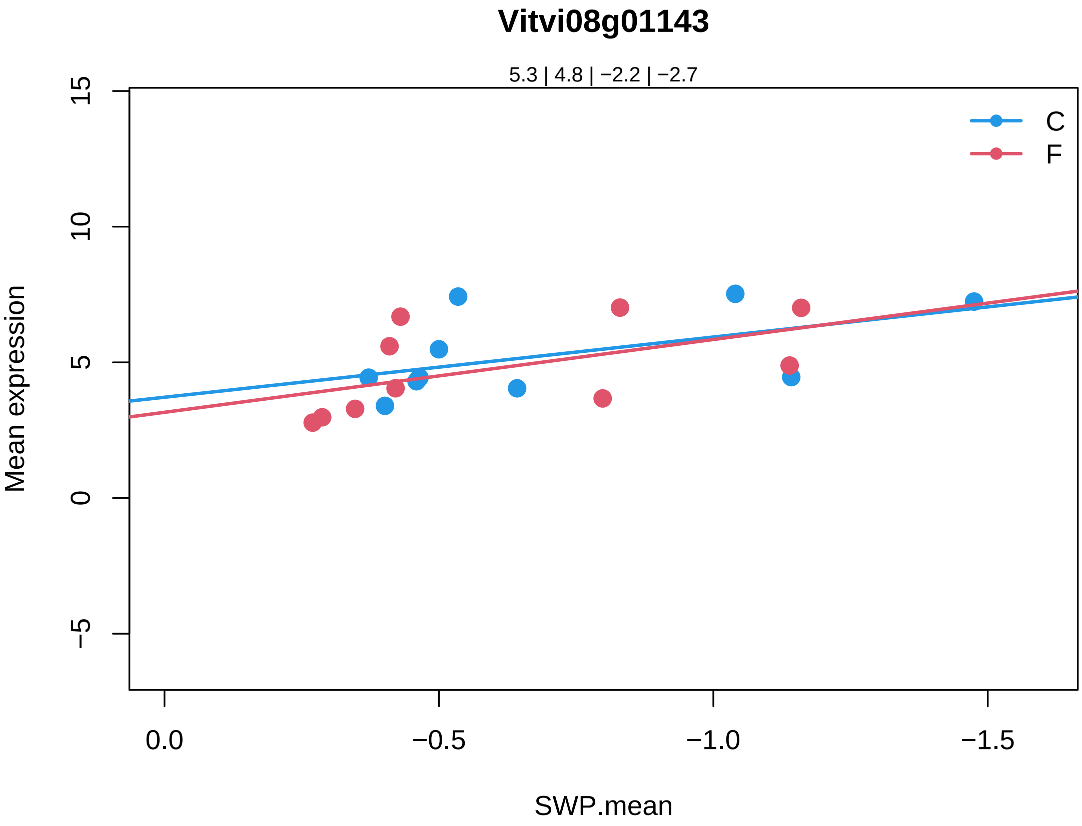
6.2.42 Vitvi08g01143

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

```
Vitvi08g01143
        21.02.2001
        redox.ascorbate and glutathione.ascorbate
        ascorbate peroxidase 2 |
        Chr3:2956301-2958163 FORWARD LENGTH=251 |
        201606
```

Coefficients for Vitvi08g01143.

```
                    swp  varietyF swp.varietyF  AveExpr        F
Vitvi08g01143 -2.218766 -0.555083   -0.4643908 5.033964 3.145005
                 P.Value adj.P.Val  type
Vitvi08g01143 0.04616882 0.2327067 type1
```



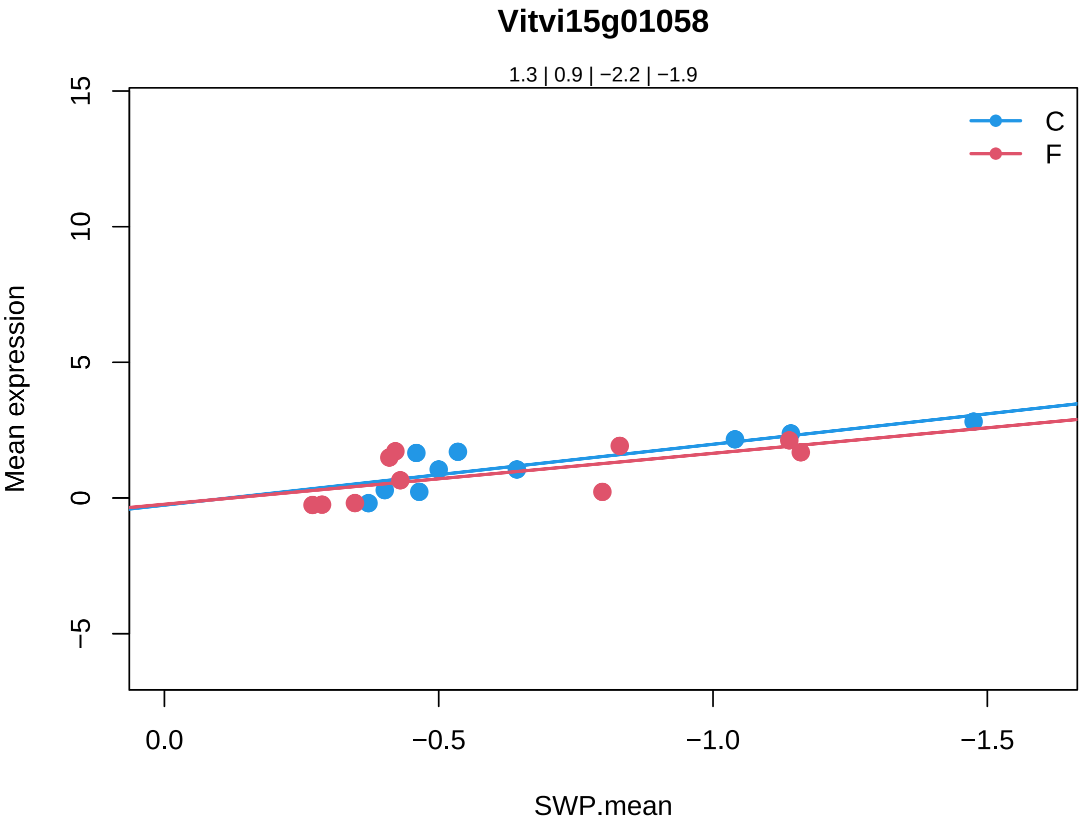
6.2.43 Vitvi15g01058

```
> 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.

```
                    swp   varietyF swp.varietyF  AveExpr        F
Vitvi15g01058 -2.243262 0.03139967    0.3650419 1.114629 9.187782
                   P.Value   adj.P.Val  type
Vitvi15g01058 0.0004192903 0.007254055 type1
```



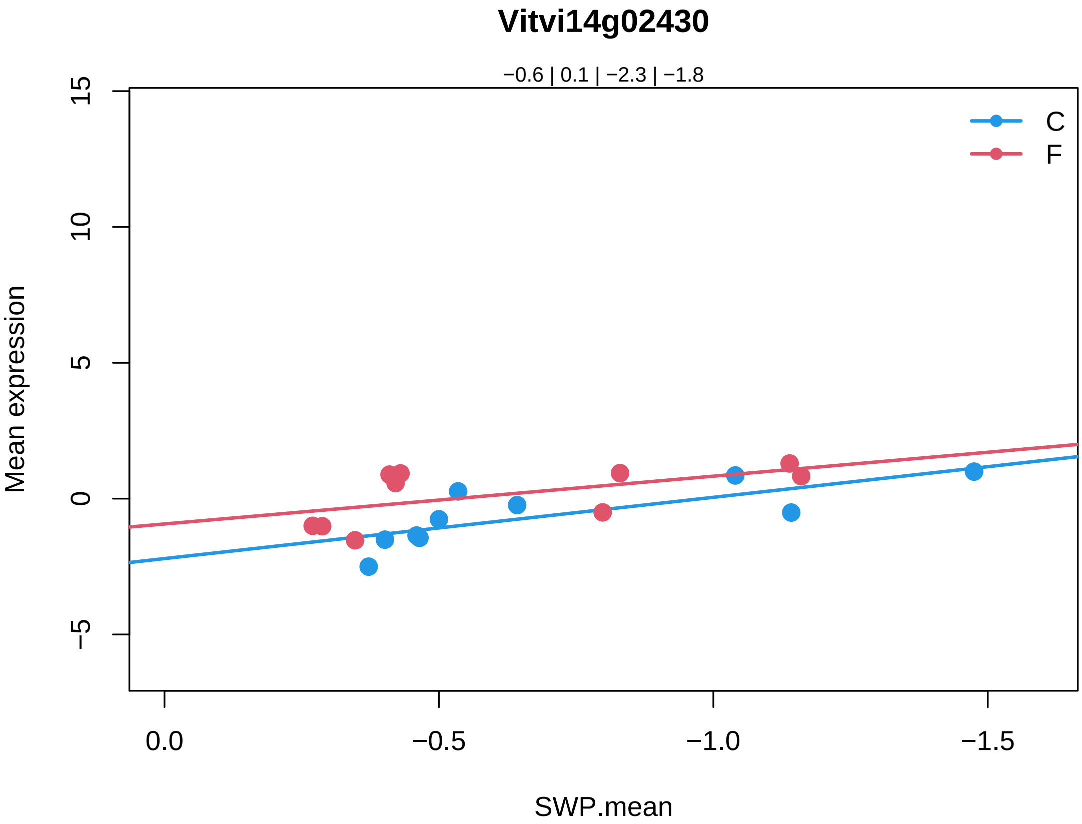
6.2.44 Vitvi14g02430

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

```
Vitvi14g02430
        27.03.2025
        RNA.regulation of transcription.MYB domain transcription factor family
        myb domain protein 43 |
        Chr5:5438291-5440214 FORWARD LENGTH=327 |
        201606
```

Coefficients for Vitvi14g02430.

```
                    swp varietyF swp.varietyF    AveExpr        F
Vitvi14g02430 -2.254746 1.273756    0.4955903 -0.2409231 7.344667
                  P.Value adj.P.Val  type
Vitvi14g02430 0.001447444 0.0197334 type1
```



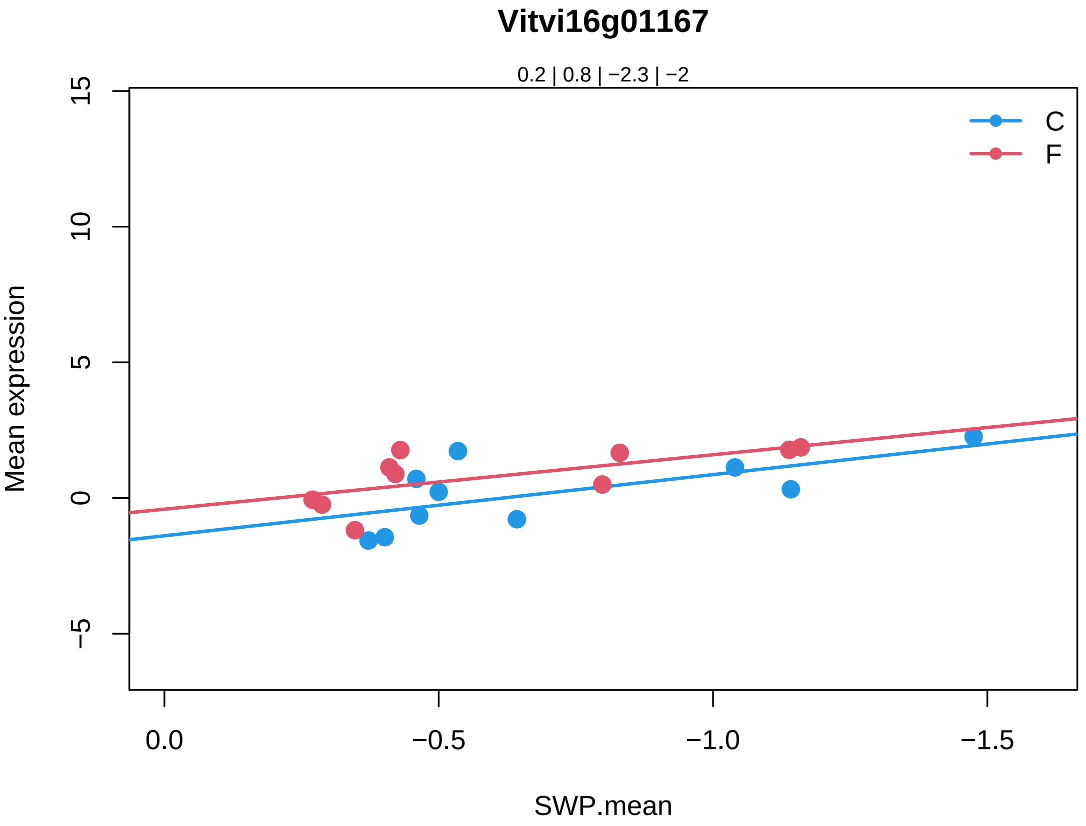
6.2.45 Vitvi16g01167

```
> 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.

```
                    swp  varietyF swp.varietyF  AveExpr        F
Vitvi16g01167 -2.254897 0.9785199    0.2474672 0.501756 5.900198
                  P.Value  adj.P.Val  type
Vitvi16g01167 0.004252498 0.04494908 type1
```



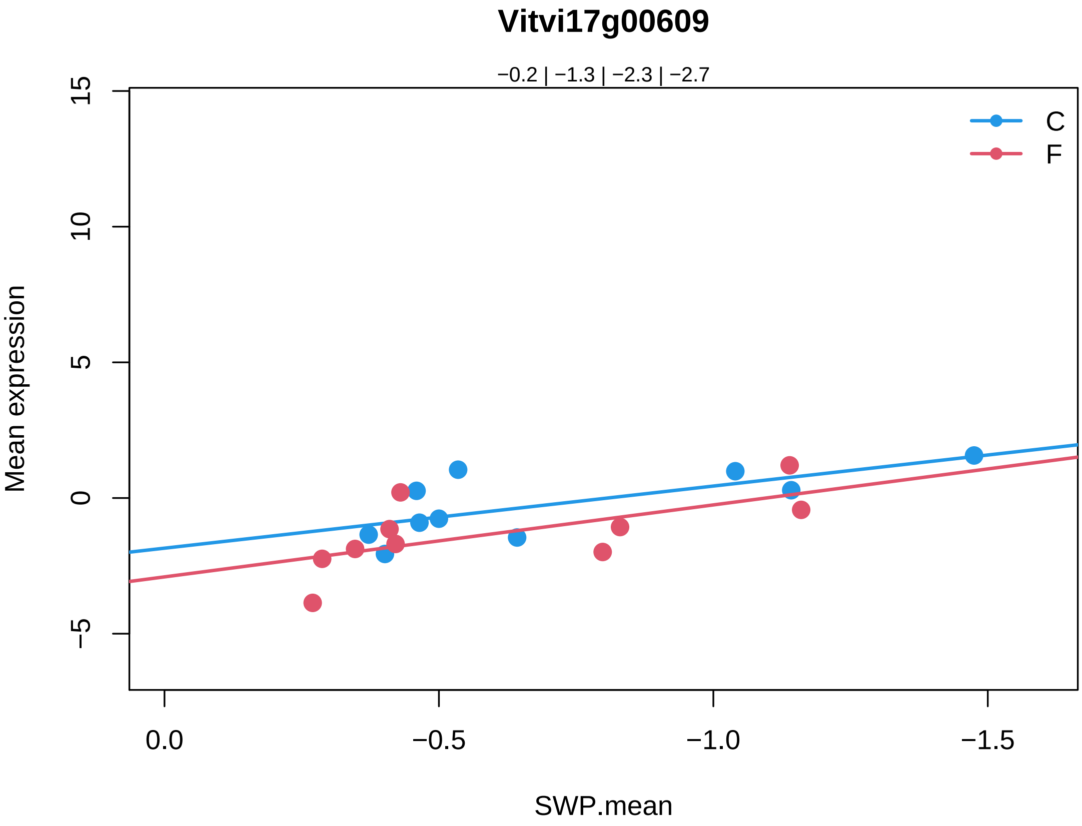
6.2.46 Vitvi17g00609

```
> 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.

```
                    swp  varietyF swp.varietyF    AveExpr        F
Vitvi17g00609 -2.289082 -1.057806   -0.3631281 -0.7644044 7.618508
                  P.Value  adj.P.Val  type
Vitvi17g00609 0.001193279 0.01693479 type1
```



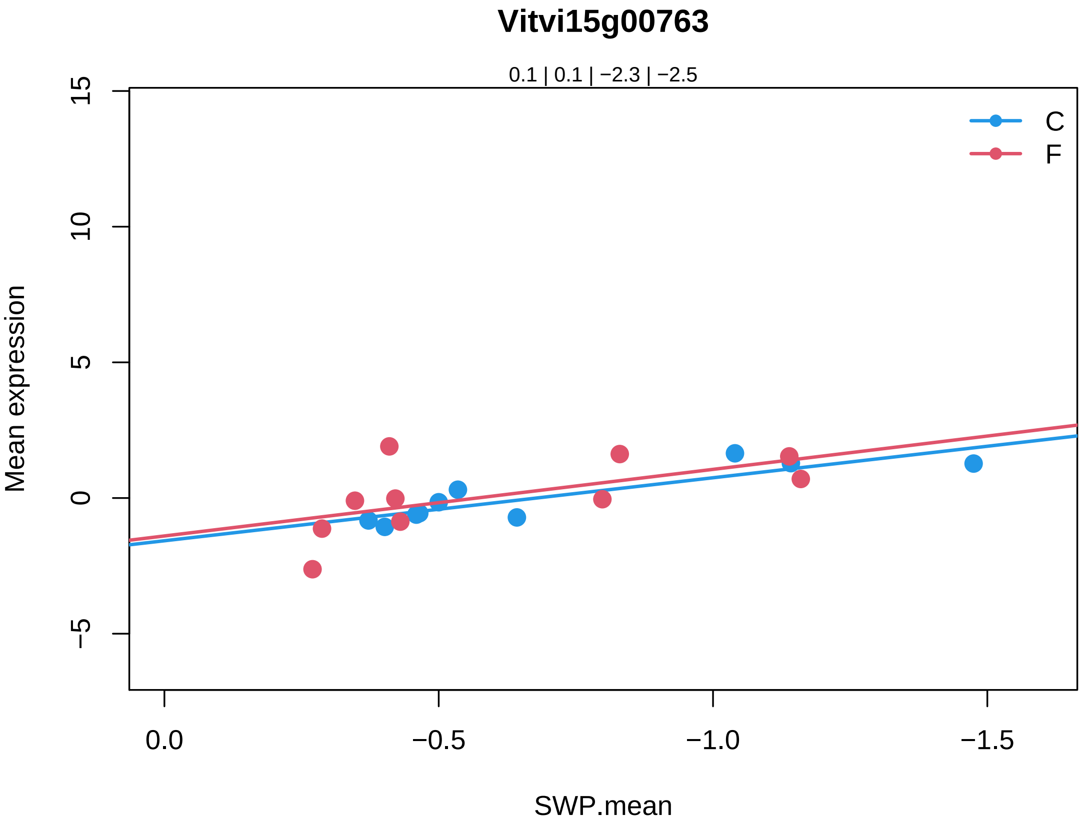
6.2.47 Vitvi15g00763

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

```
Vitvi15g00763
        29.05.2001
        protein.degradation.subtilases
        subtilase family protein |
        Chr1:310332-313011 FORWARD LENGTH=774 |
        201606
```

Coefficients for Vitvi15g00763.

```
                    swp  varietyF swp.varietyF    AveExpr        F
Vitvi15g00763 -2.321806 0.1772842   -0.1323801 0.07748381 6.397761
                  P.Value  adj.P.Val  type
Vitvi15g00763 0.002899374 0.03397453 type1
```



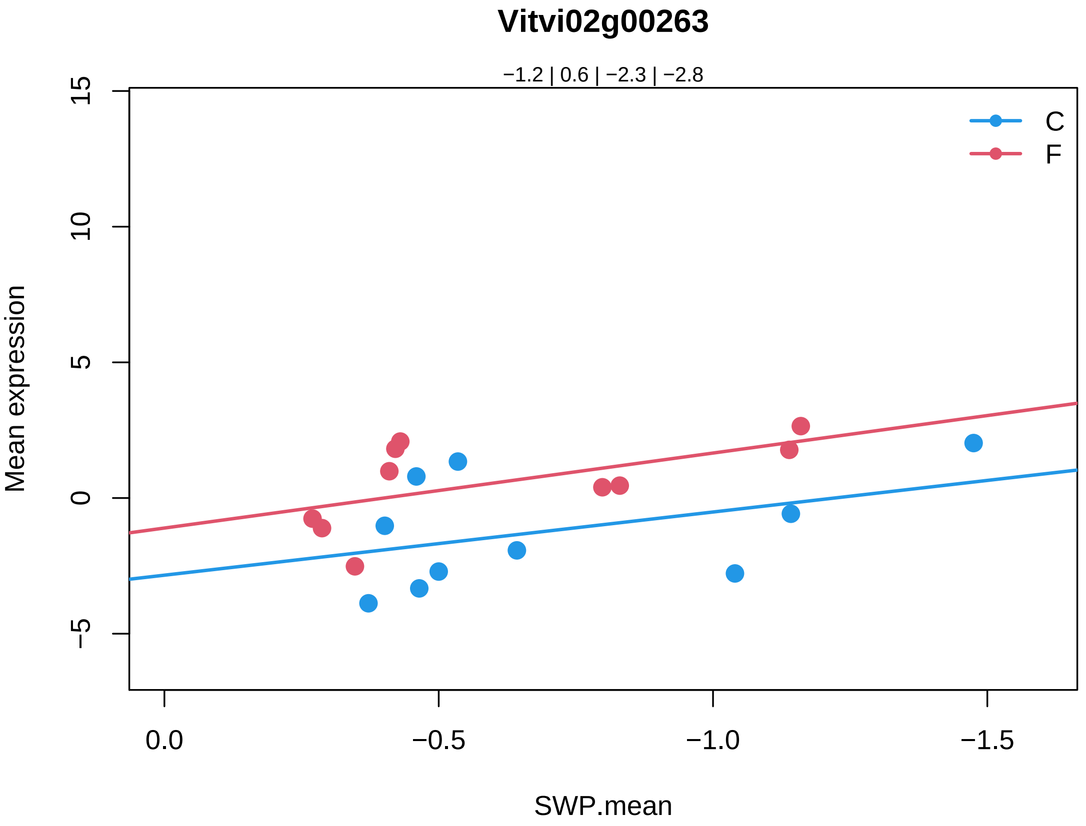
6.2.48 Vitvi02g00263

```
> 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.

```
                    swp varietyF swp.varietyF    AveExpr       F
Vitvi02g00263 -2.328381  1.73727   -0.4357503 -0.3145931 4.58147
                 P.Value  adj.P.Val  type
Vitvi02g00263 0.01254673 0.09736901 type1
```



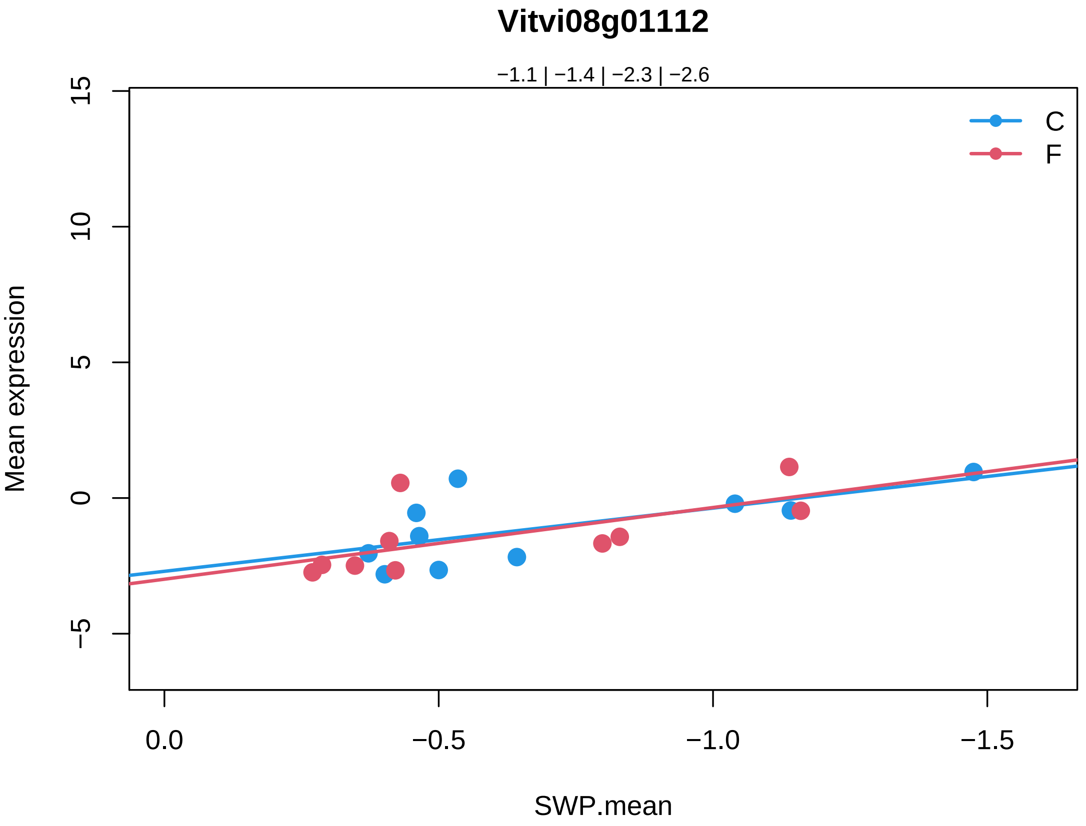
6.2.49 Vitvi08g01112

```
> 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.

```
                    swp   varietyF swp.varietyF   AveExpr        F
Vitvi08g01112 -2.329875 -0.2903136   -0.3120123 -1.222446 5.249798
                P.Value  adj.P.Val  type
Vitvi08g01112 0.0071596 0.06601732 type1
```



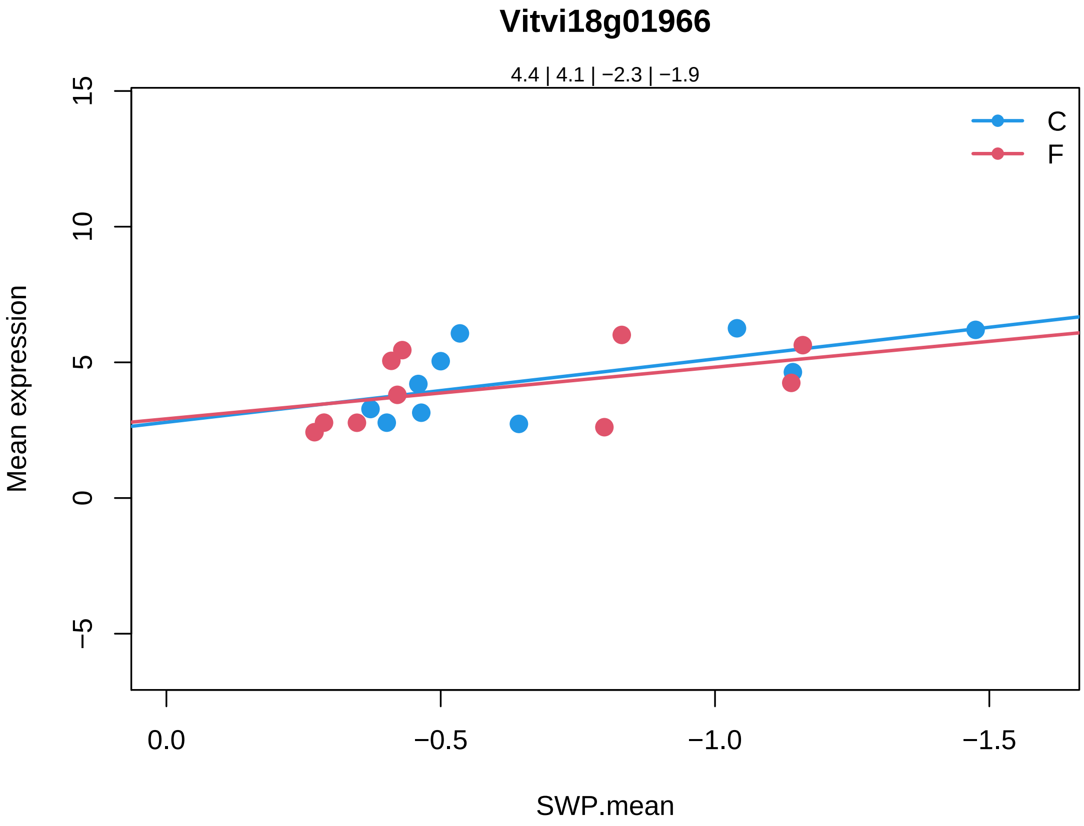
6.2.50 Vitvi18g01966

```
> 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.

```
                    swp varietyF swp.varietyF  AveExpr        F
Vitvi18g01966 -2.333415 0.125324    0.4288107 4.255793 3.169546
                 P.Value adj.P.Val  type
Vitvi18g01966 0.04509948 0.2293185 type1
```



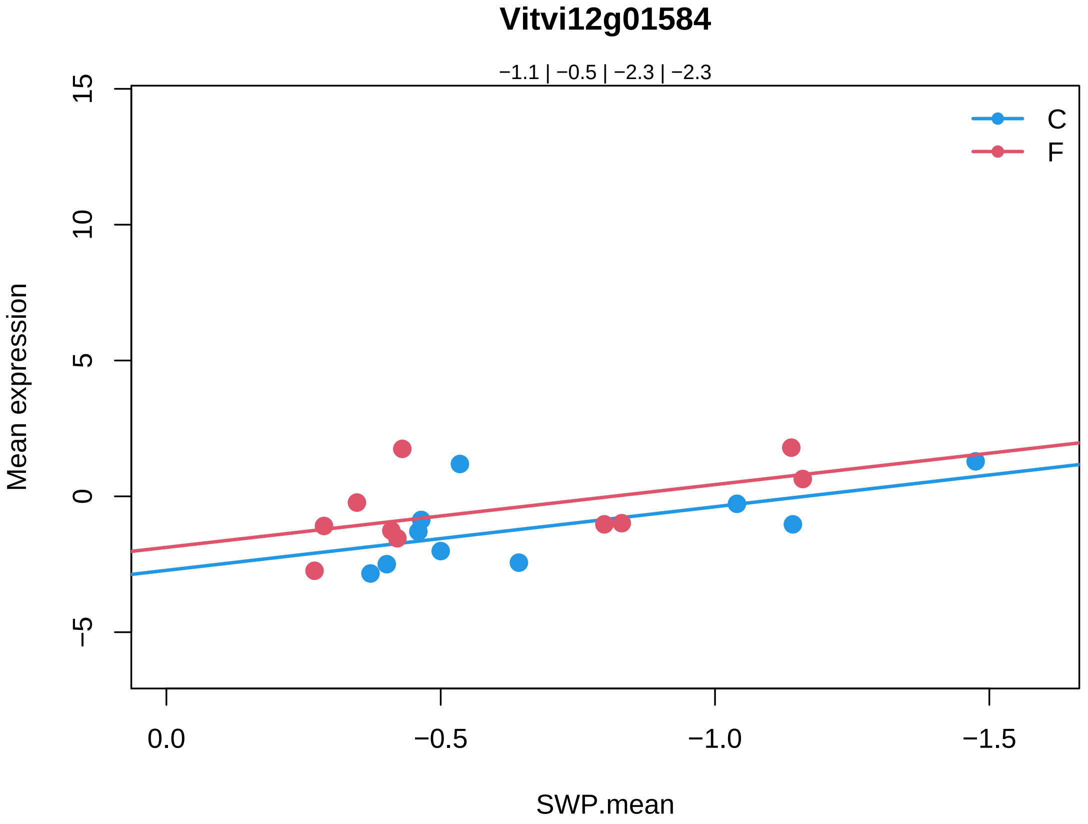
6.2.51 Vitvi12g01584

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

```
Vitvi12g01584
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi12g01584.

```
                    swp varietyF swp.varietyF    AveExpr        F
Vitvi12g01584 -2.340025 0.845044   0.02913283 -0.7741958 3.848185
                 P.Value adj.P.Val  type
Vitvi12g01584 0.02398145 0.1533887 type1
```



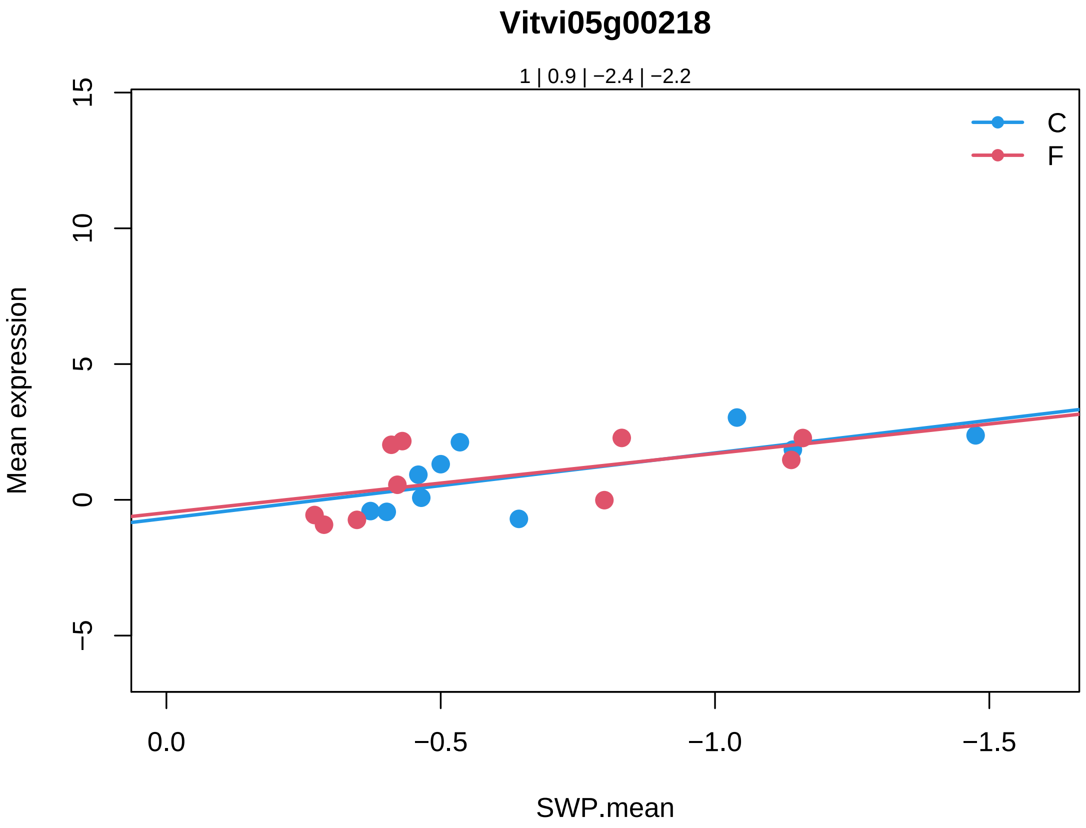
6.2.52 Vitvi05g00218

```
> 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.

```
                    swp  varietyF swp.varietyF  AveExpr        F
Vitvi05g00218 -2.406759 0.2069042    0.2287034 0.933593 4.362156
                P.Value adj.P.Val  type
Vitvi05g00218 0.0151737 0.1122537 type1
```



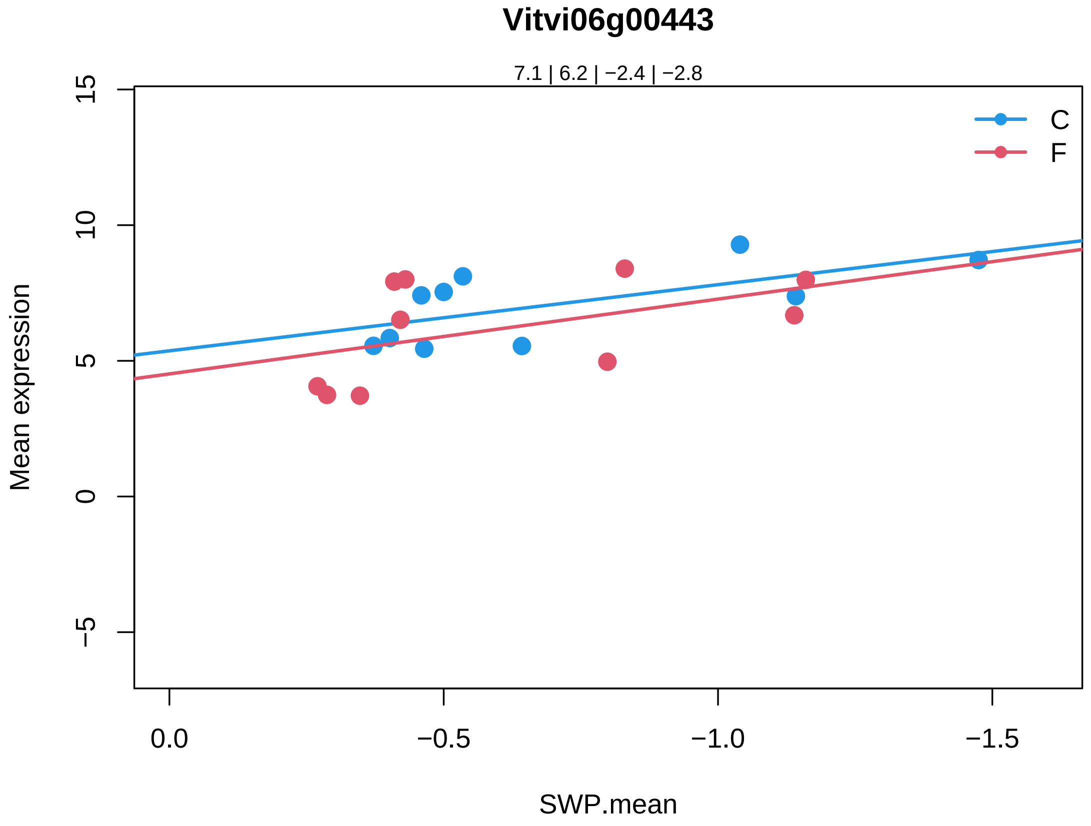
6.2.53 Vitvi06g00443

```
> 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
        20.02.2001
        stress.abiotic.heat
        heat shock cognate protein 70-1 |
        Chr5:554055-556334 REVERSE LENGTH=651 |
        201606
```

Coefficients for Vitvi06g00443.

```
                    swp   varietyF swp.varietyF  AveExpr        F
Vitvi06g00443 -2.438983 -0.8499639   -0.3183393 6.640504 3.879227
                 P.Value adj.P.Val  type
Vitvi06g00443 0.02331601 0.1509237 type1
```



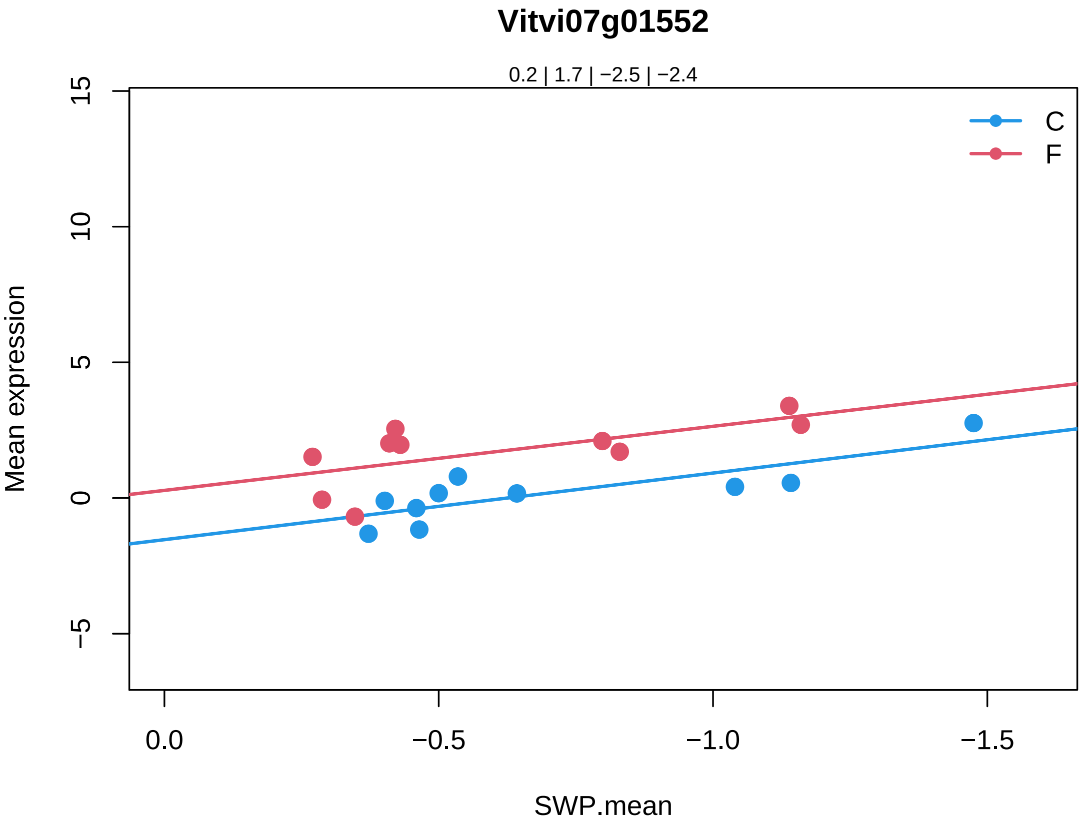
6.2.54 Vitvi07g01552

```
> 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.

```
                    swp varietyF swp.varietyF   AveExpr        F
Vitvi07g01552 -2.454713 1.815182   0.09286943 0.9558154 13.94291
                  P.Value   adj.P.Val  type
Vitvi07g01552 2.90693e-05 0.000791204 type1
```



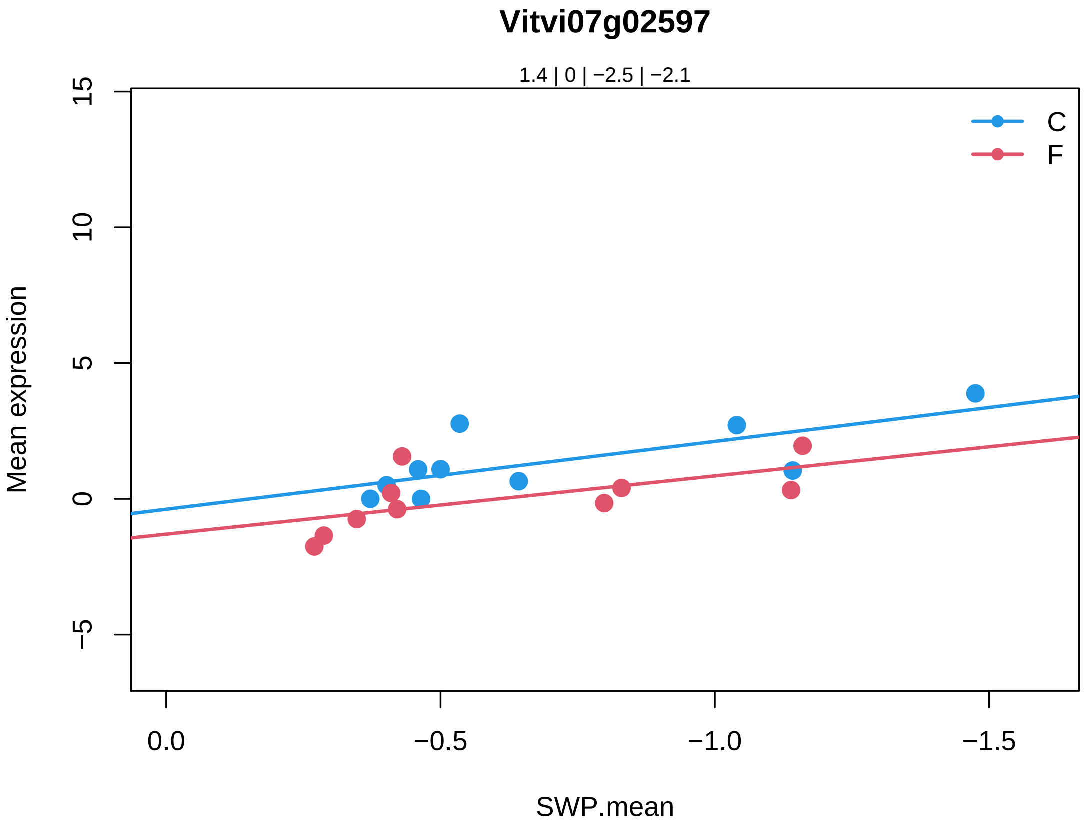
6.2.55 Vitvi07g02597

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

```
Vitvi07g02597
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi07g02597.

```
                    swp   varietyF swp.varietyF   AveExpr        F
Vitvi07g02597 -2.498658 -0.9171895    0.3531685 0.6898084 9.999766
                   P.Value   adj.P.Val  type
Vitvi07g02597 0.0002531733 0.004825462 type1
```



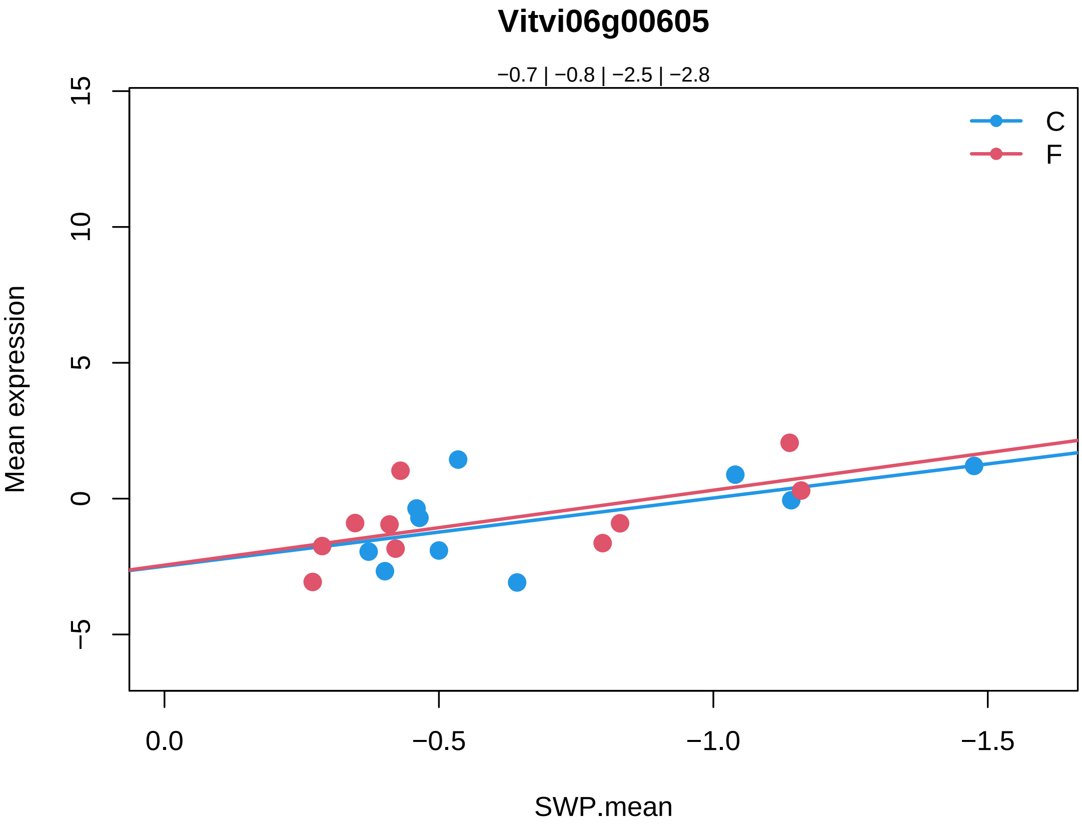
6.2.56 Vitvi06g00605

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

```
Vitvi06g00605
        26.1
        misc.cytochrome P450
        cytochrome P450%2C family 86%2C subfamily A%2C polypeptide 1 |
        Chr5:23765999-23767997 REVERSE LENGTH=513 |
        201606
```

Coefficients for Vitvi06g00605.

```
                    swp   varietyF swp.varietyF    AveExpr        F
Vitvi06g00605 -2.509662 0.03913772   -0.2491978 -0.7447302 3.941348
                 P.Value adj.P.Val  type
Vitvi06g00605 0.02204356 0.1450099 type1
```



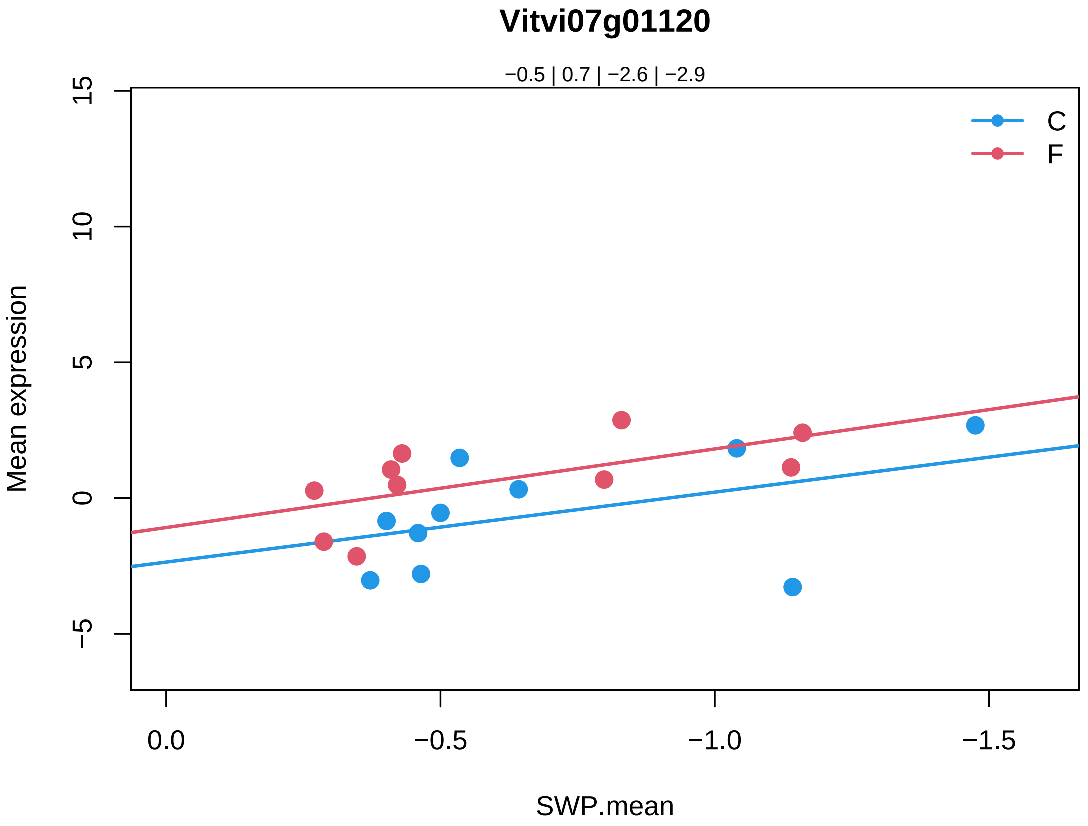
6.2.57 Vitvi07g01120

```
> 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.

```
                    swp varietyF swp.varietyF    AveExpr        F
Vitvi07g01120 -2.576419 1.273004    -0.318679 0.06615197 3.839372
                 P.Value adj.P.Val  type
Vitvi07g01120 0.02417408 0.1541679 type1
```



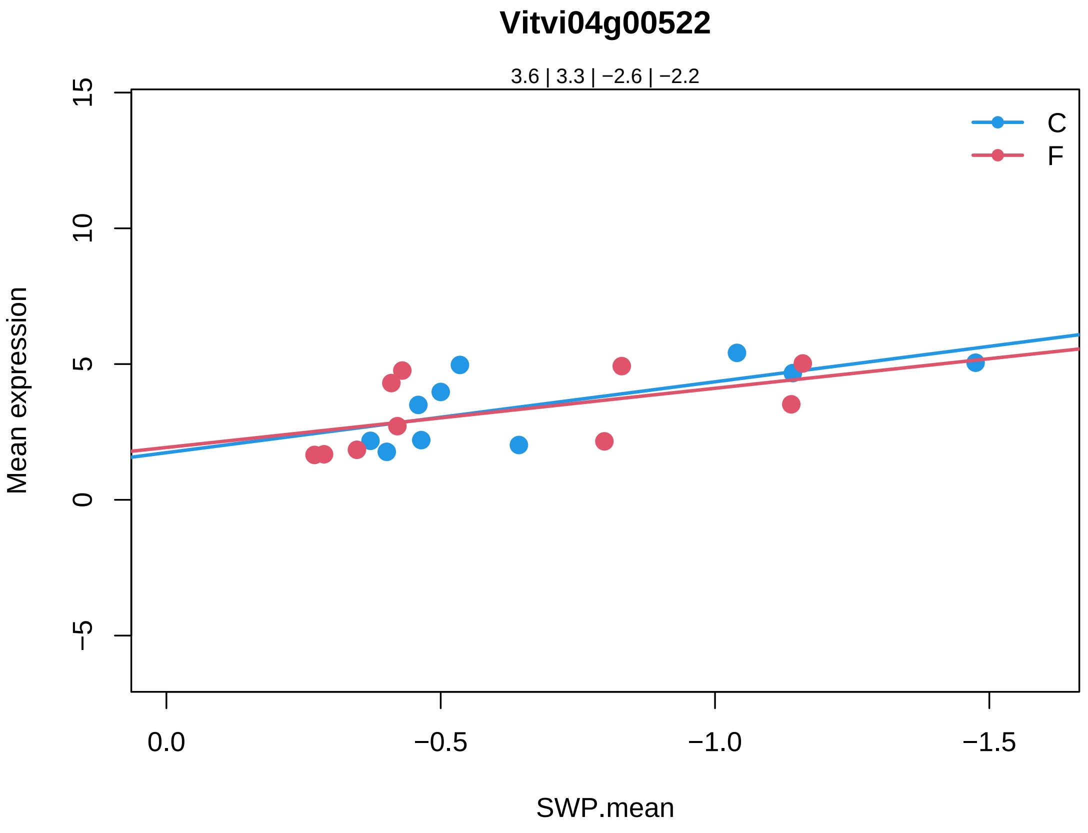
6.2.58 Vitvi04g00522

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

```
Vitvi04g00522
        20.02.2001
        stress.abiotic.heat
        casein lytic proteinase B4 |
        Chr2:10697877-10701998 REVERSE LENGTH=964 |
        201606
```

Coefficients for Vitvi04g00522.

```
                    swp  varietyF swp.varietyF  AveExpr        F
Vitvi04g00522 -2.610525 0.1915148    0.4302342 3.414499 4.322581
                 P.Value adj.P.Val  type
Vitvi04g00522 0.01570838   0.11522 type1
```



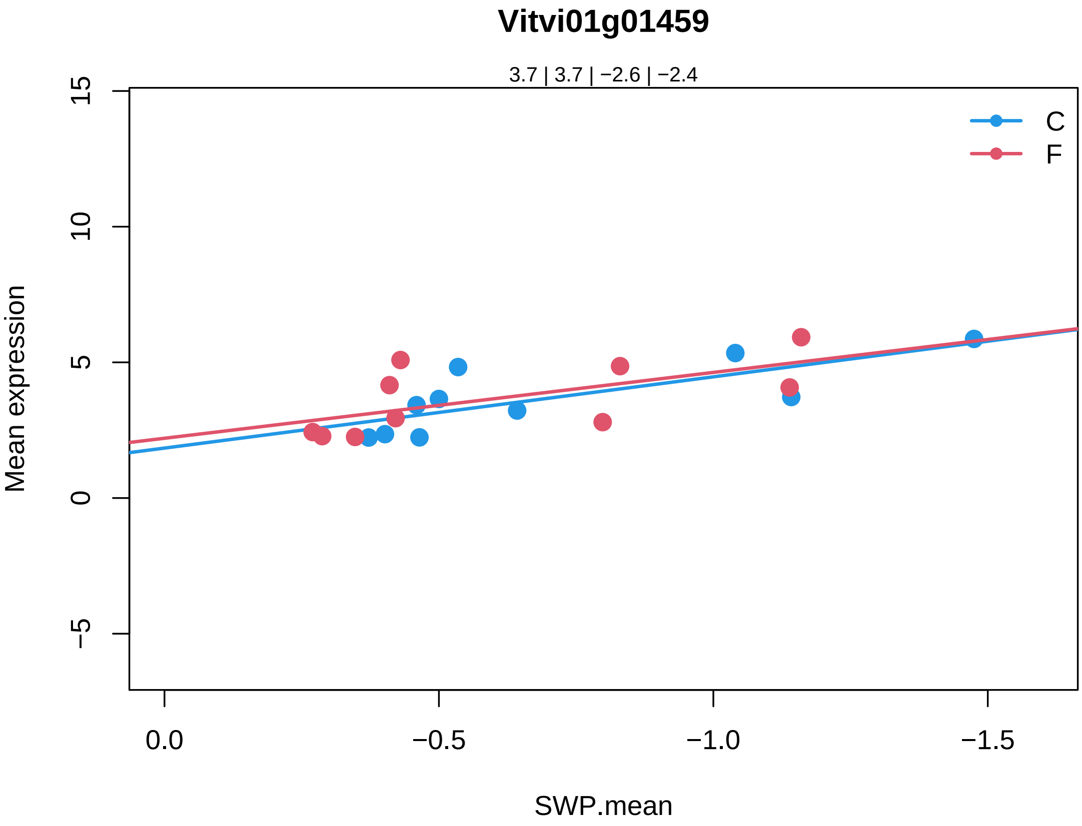
6.2.59 Vitvi01g01459

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

```
Vitvi01g01459
        17.01.2003
        hormone metabolism.abscisic acid.induced-regulated-responsive-activate
        GRAM domain family protein |
        Chr5:4207081-4207812 FORWARD LENGTH=213 |
        201606
```

Coefficients for Vitvi01g01459.

```
                    swp  varietyF swp.varietyF  AveExpr        F
Vitvi01g01459 -2.625931 0.3621058    0.1996119 3.683872 6.416037
                 P.Value  adj.P.Val  type
Vitvi01g01459 0.00285957 0.03365681 type1
```



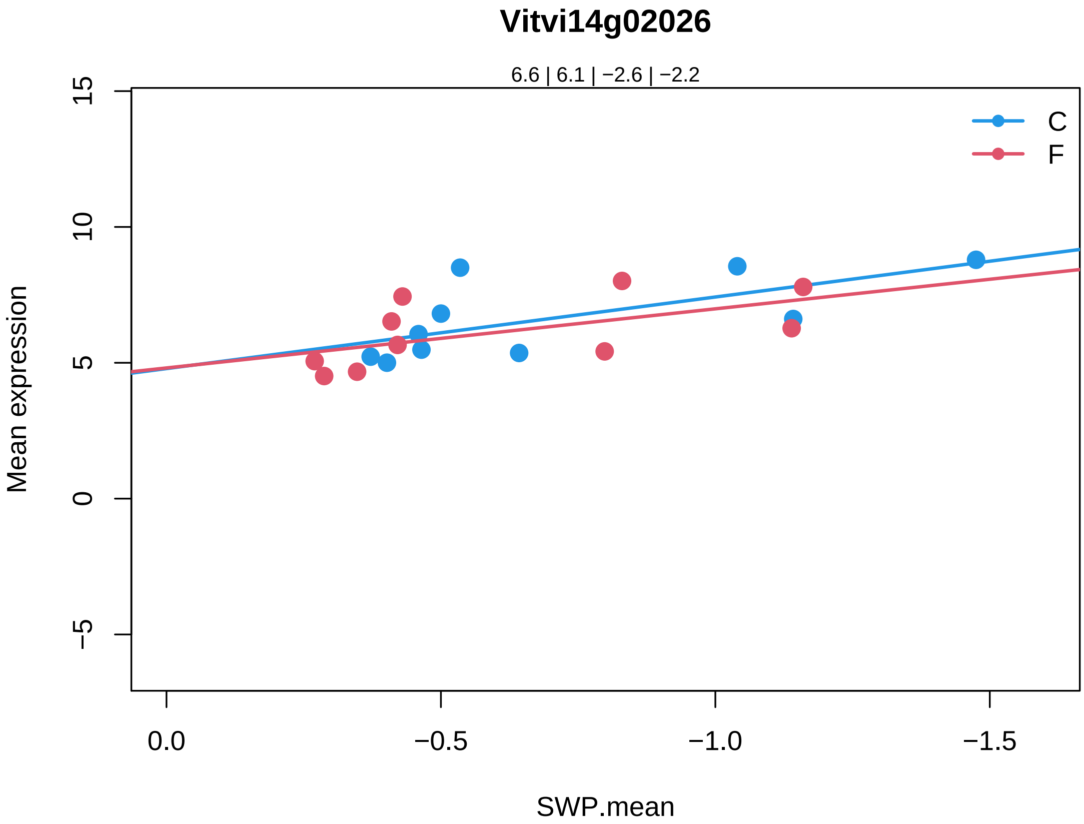
6.2.60 Vitvi14g02026

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

```
Vitvi14g02026
        20.02.2001
        stress.abiotic.heat
        casein lytic proteinase B3 |
        Chr5:5014399-5018255 REVERSE LENGTH=968 |
        201606
```

Coefficients for Vitvi14g02026.

```
                    swp   varietyF swp.varietyF  AveExpr        F
Vitvi14g02026 -2.634207 0.02286267    0.4582077 6.387659 4.985062
                  P.Value  adj.P.Val  type
Vitvi14g02026 0.008912492 0.07681021 type1
```



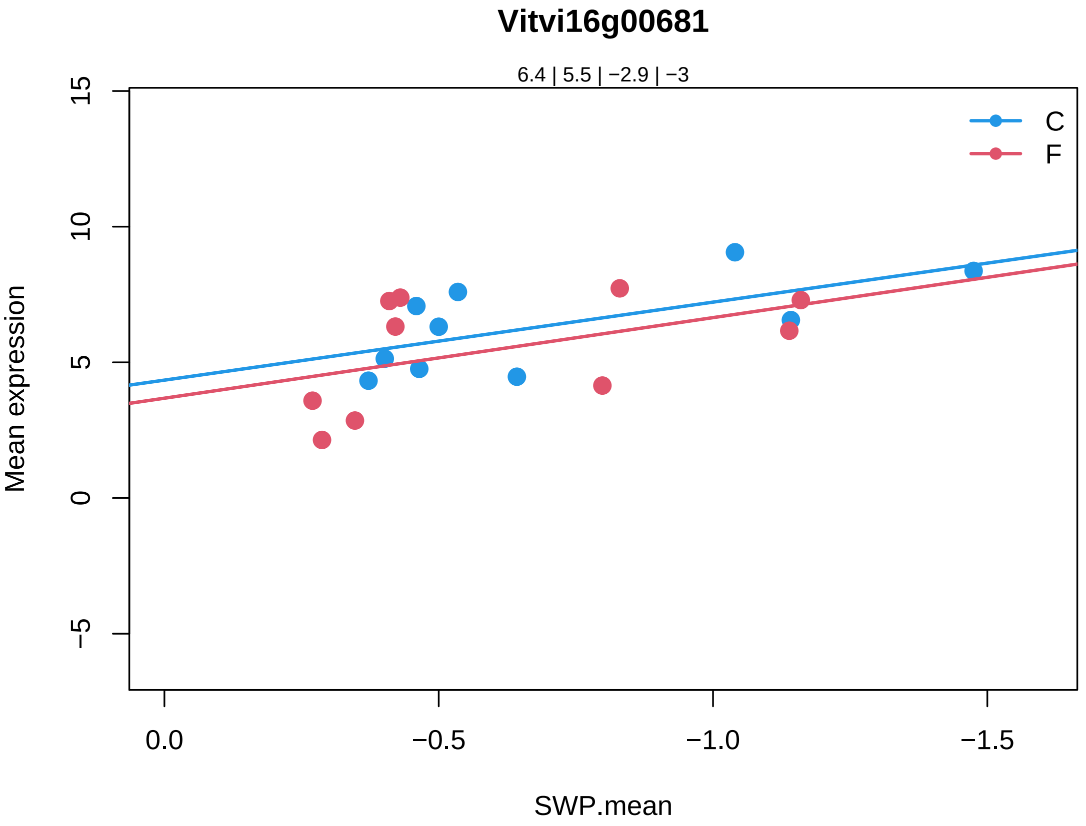
6.2.61 Vitvi16g00681

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

```
Vitvi16g00681
        20.02.2001
        stress.abiotic.heat
        mitochondrion-localized small heat shock protein 23.6 |
        Chr4:12917089-12917858 FORWARD LENGTH=210 |
        201606
```

Coefficients for Vitvi16g00681.

```
                    swp   varietyF swp.varietyF  AveExpr        F
Vitvi16g00681 -2.874618 -0.6660445  -0.09509428 5.926522 3.703495
                 P.Value adj.P.Val  type
Vitvi16g00681 0.02736596 0.1671792 type1
```



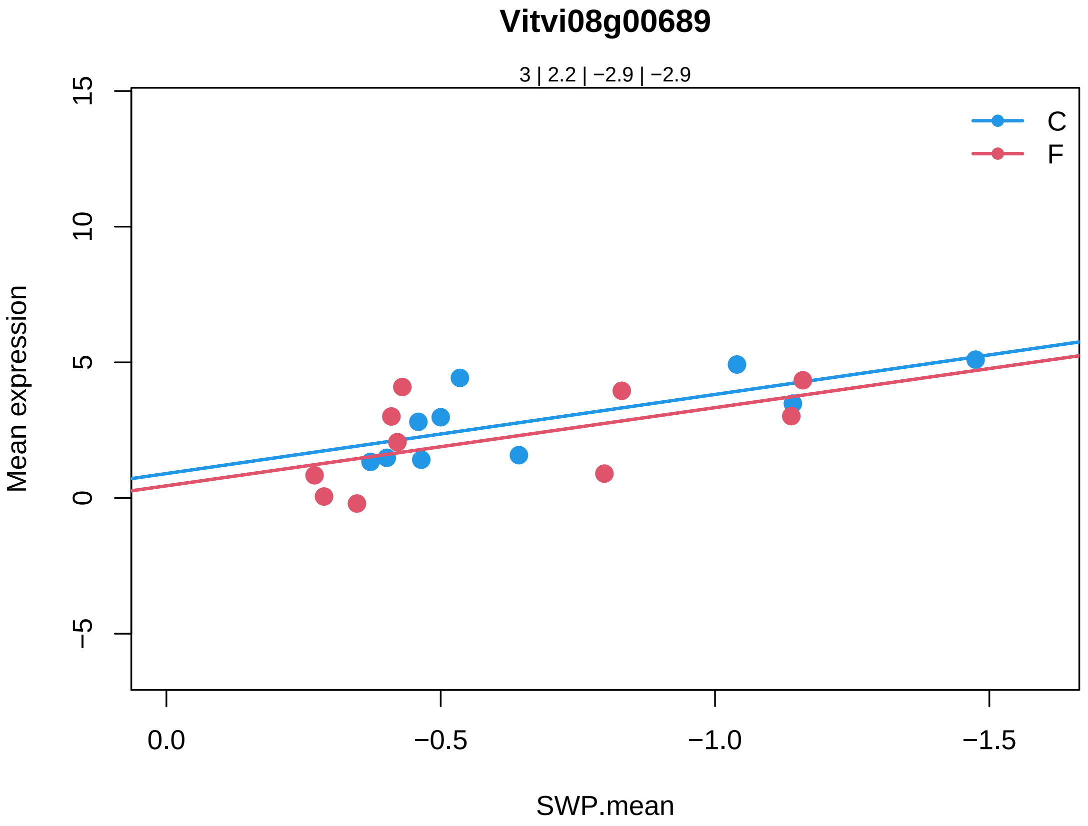
6.2.62 Vitvi08g00689

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

```
Vitvi08g00689
        20.02.2001
        stress.abiotic.heat
        DNAJ heat shock N-terminal domain-containing protein |
        Chr3:2737589-2740265 FORWARD LENGTH=572 |
        201606
```

Coefficients for Vitvi08g00689.

```
                    swp   varietyF swp.varietyF  AveExpr        F
Vitvi08g00689 -2.914322 -0.4517708   0.03394978 2.578551 5.761494
                  P.Value  adj.P.Val  type
Vitvi08g00689 0.004742796 0.04904321 type1
```



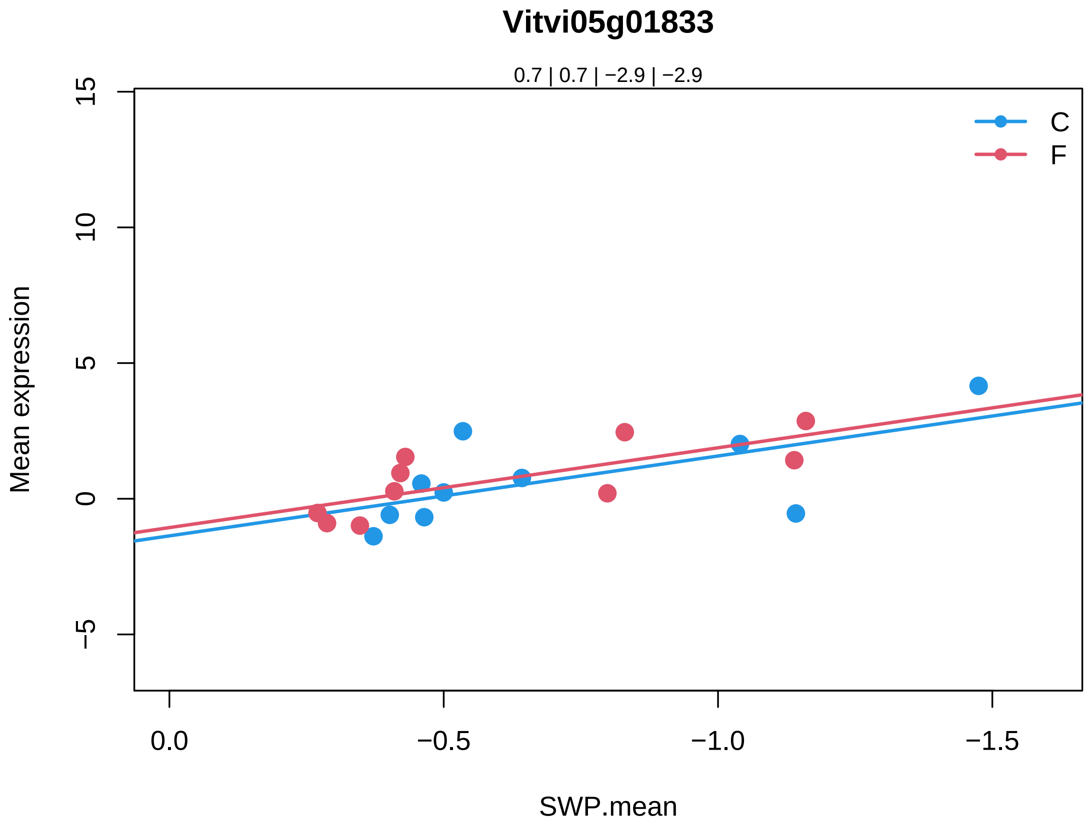
6.2.63 Vitvi05g01833

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

```
Vitvi05g01833
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi05g01833.

```
                    swp  varietyF swp.varietyF  AveExpr        F
Vitvi05g01833 -2.943432 0.3039696  0.002075687 0.715509 6.099971
                  P.Value  adj.P.Val  type
Vitvi05g01833 0.003640656 0.04018166 type1
```



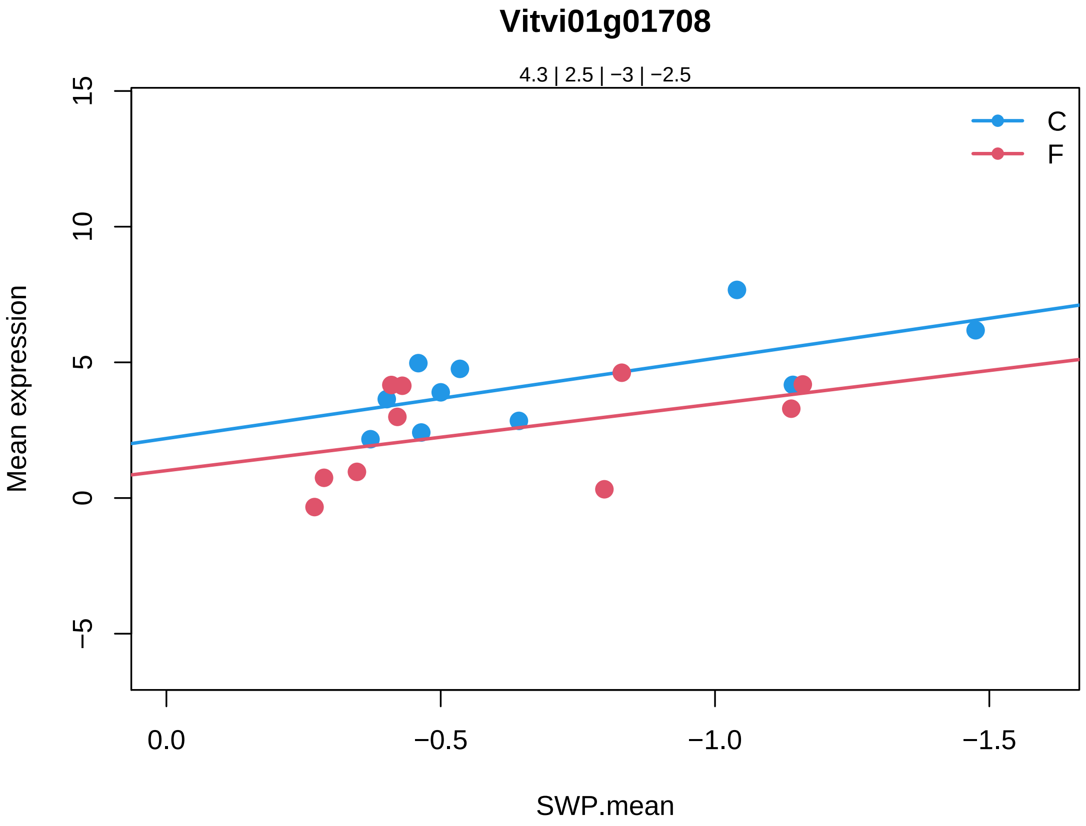
6.2.64 Vitvi01g01708

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

```
Vitvi01g01708
        20.02.2001
        stress.abiotic.heat
        BCL-2-associated athanogene 5 |
        Chr1:4076334-4076981 FORWARD LENGTH=215 |
        201606
```

Coefficients for Vitvi01g01708.

```
                    swp  varietyF swp.varietyF  AveExpr        F
Vitvi01g01708 -2.952446 -1.185501    0.4926336 3.390157 5.674894
                  P.Value  adj.P.Val  type
Vitvi01g01708 0.005079894 0.05152009 type1
```



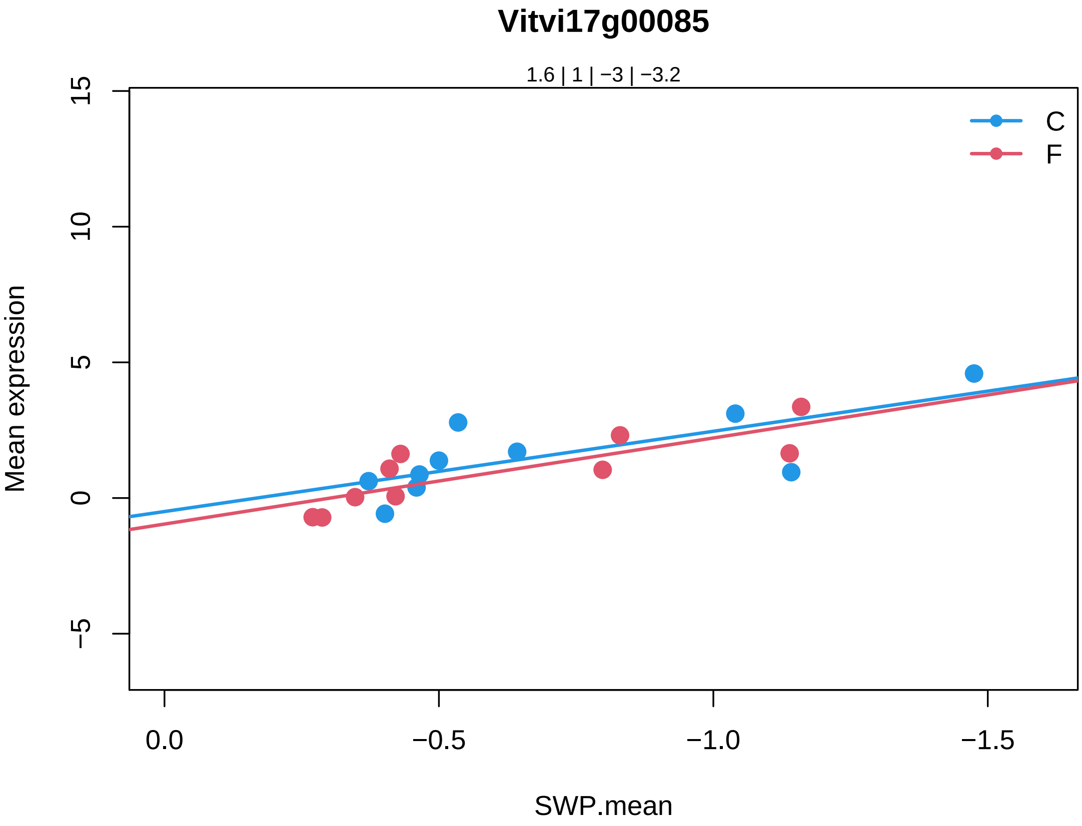
6.2.65 Vitvi17g00085

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

```
Vitvi17g00085
        17.01.2003
        hormone metabolism.abscisic acid.induced-regulated-responsive-activate
        HVA22 homologue D |
        Chr4:12828237-12829019 FORWARD LENGTH=135 |
        201606
```

Coefficients for Vitvi17g00085.

```
                    swp   varietyF swp.varietyF  AveExpr       F
Vitvi17g00085 -2.957952 -0.4614312   -0.2145244 1.277598 10.7473
                   P.Value   adj.P.Val  type
Vitvi17g00085 0.0001622821 0.003383727 type1
```



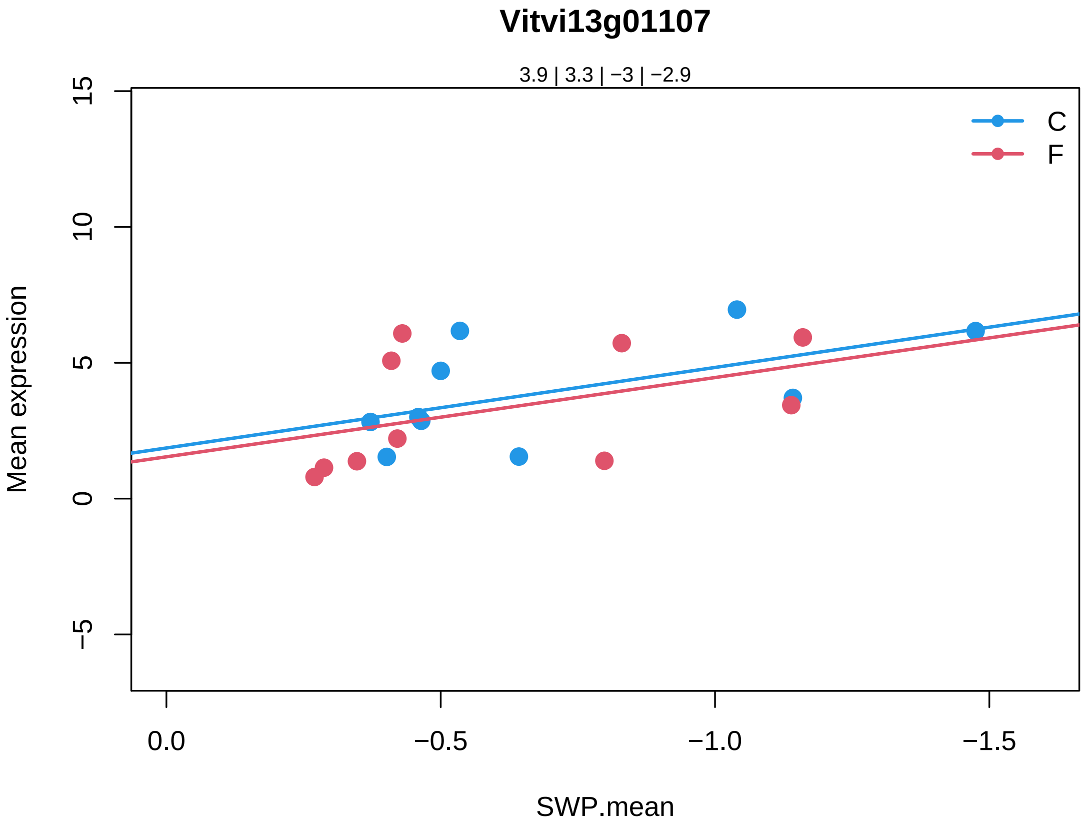
6.2.66 Vitvi13g01107

```
> 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.

```
                    swp   varietyF swp.varietyF  AveExpr        F
Vitvi13g01107 -2.964306 -0.3246467   0.04693335 3.632156 2.733214
                 P.Value adj.P.Val  type
Vitvi13g01107 0.06883806 0.2943141 type1
```



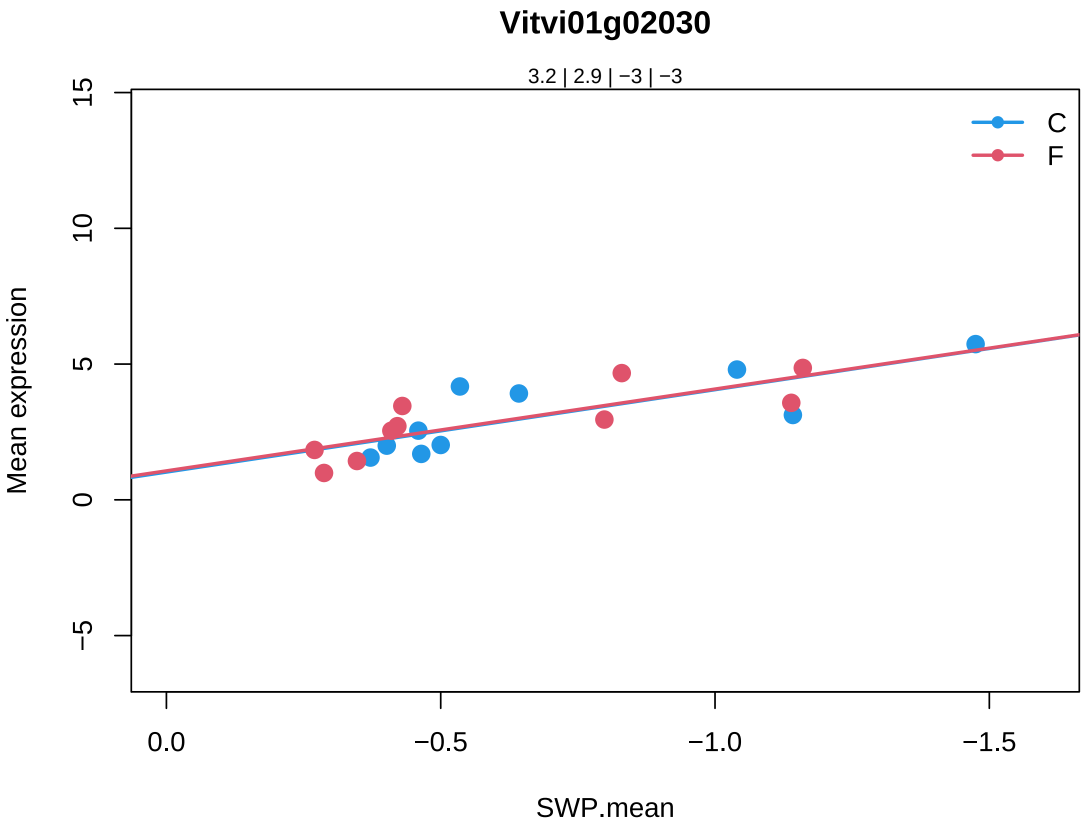
6.2.67 Vitvi01g02030

```
> 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.

```
                    swp   varietyF swp.varietyF  AveExpr        F
Vitvi01g02030 -3.035038 0.04517591   0.02234586 3.029255 11.78708
                   P.Value   adj.P.Val  type
Vitvi01g02030 8.996448e-05 0.002073435 type1
```



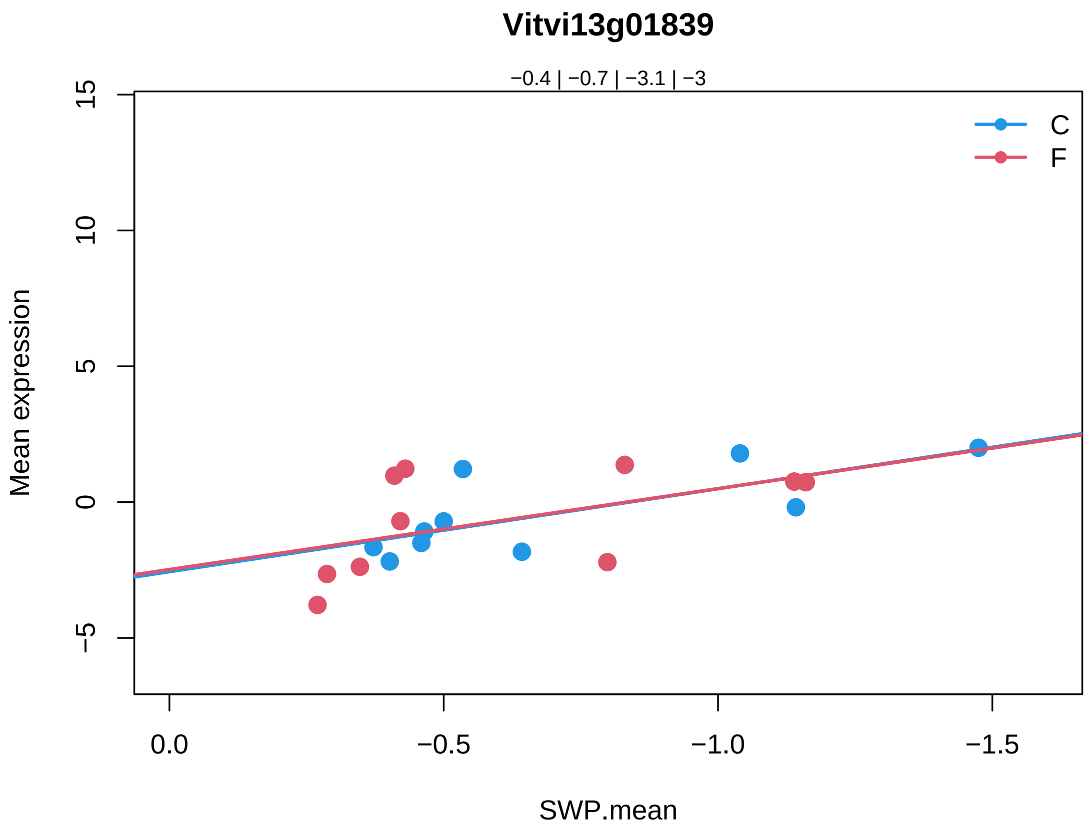
6.2.68 Vitvi13g01839

```
> 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.

```
                    swp   varietyF swp.varietyF    AveExpr        F
Vitvi13g01839 -3.054071 0.08078933   0.07550815 -0.5411129 4.449996
                P.Value adj.P.Val  type
Vitvi13g01839 0.0140561 0.1057801 type1
```



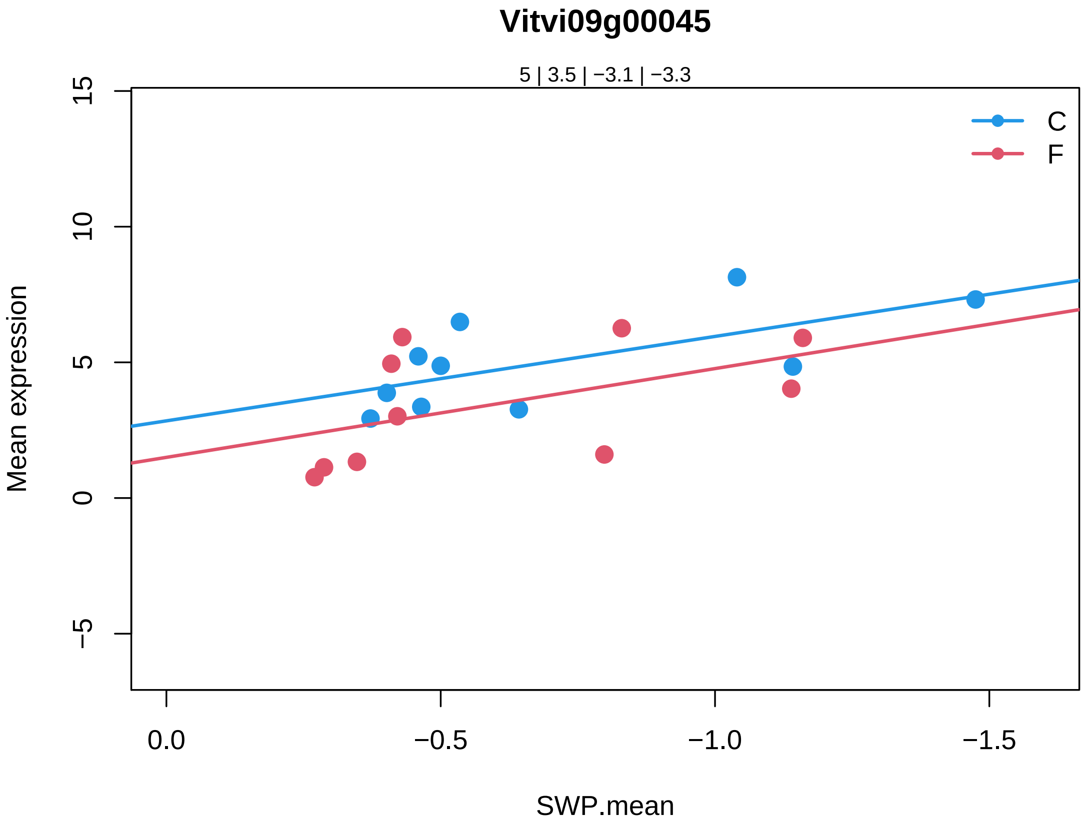
6.2.69 Vitvi09g00045

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

```
Vitvi09g00045
        20.02.2001
        stress.abiotic.heat
        HSP20-like chaperones superfamily protein |
        Chr1:20179558-20180122 REVERSE LENGTH=155 |
        201606
```

Coefficients for Vitvi09g00045.

```
                    swp  varietyF swp.varietyF  AveExpr        F
Vitvi09g00045 -3.111025 -1.345777   -0.1609299 4.261683 5.168299
                  P.Value  adj.P.Val  type
Vitvi09g00045 0.007655557 0.06920878 type1
```



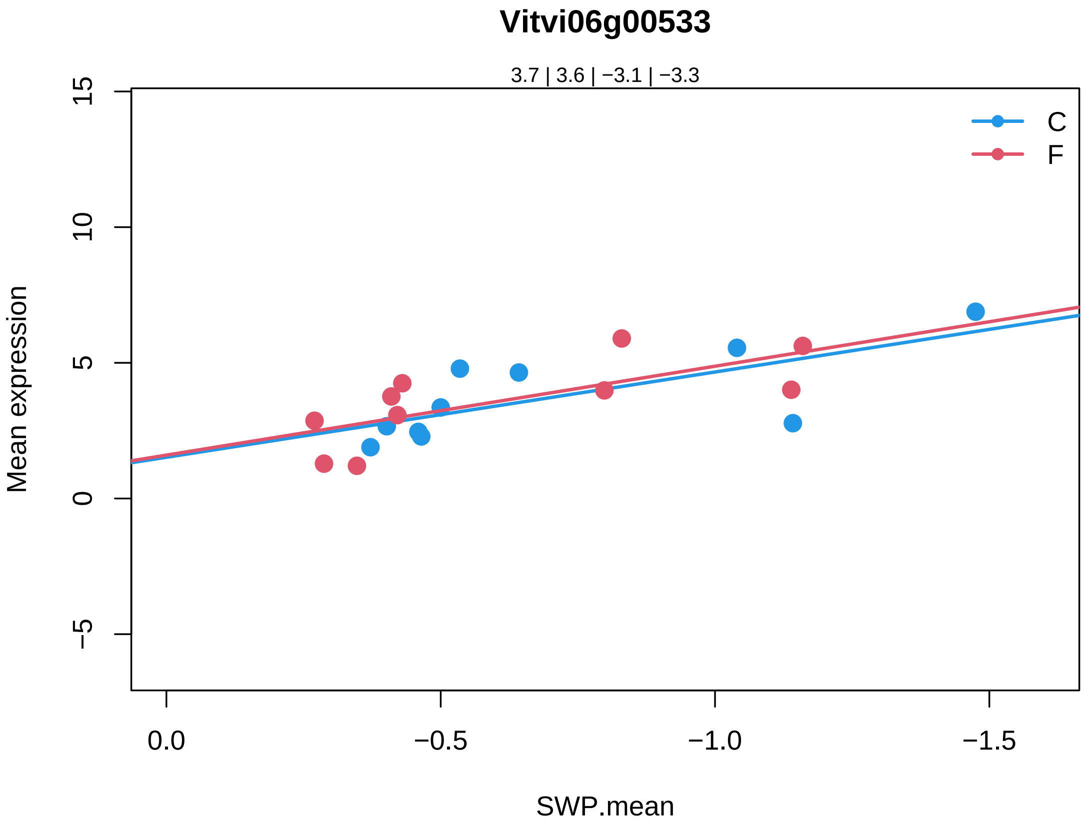
6.2.70 Vitvi06g00533

```
> 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
        17.01.2002
        hormone metabolism.abscisic acid.signal transduction
        highly ABA-induced PP2C protein 3 |
        Chr2:12608855-12610124 FORWARD LENGTH=362 |
        201606
```

Coefficients for Vitvi06g00533.

```
                    swp   varietyF swp.varietyF  AveExpr        F
Vitvi06g00533 -3.141484 0.07860975   -0.1347465 3.661599 7.317093
                  P.Value  adj.P.Val  type
Vitvi06g00533 0.001476139 0.02005286 type1
```



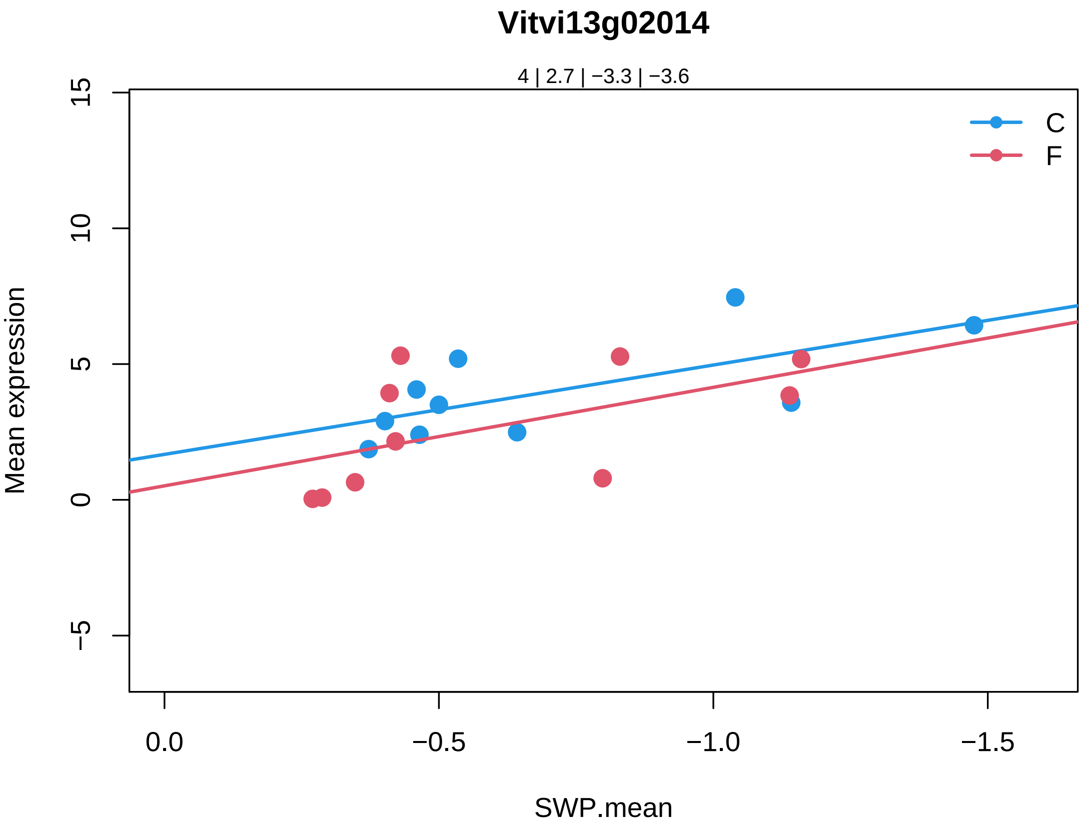
6.2.71 Vitvi13g02014

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

```
Vitvi13g02014
        20.02.2001
        stress.abiotic.heat
        heat shock protein 18.2 |
        Chr5:24062632-24063117 FORWARD LENGTH=161 |
        201606
```

Coefficients for Vitvi13g02014.

```
                    swp   varietyF swp.varietyF  AveExpr        F
Vitvi13g02014 -3.29079 -1.159109   -0.3375916 3.356592 5.335668
                   P.Value   adj.P.Val  type
Vitvi13g02014 0.006674552 0.06283726 type1
```



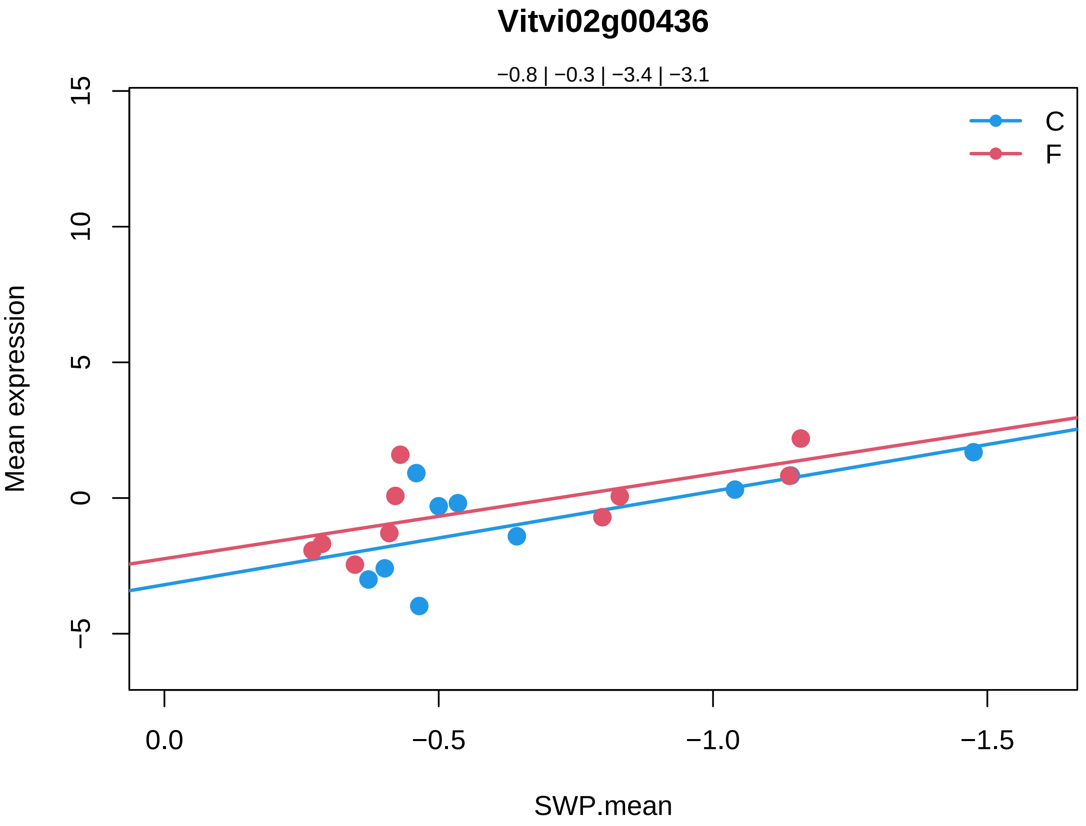
6.2.72 Vitvi02g00436

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

```
Vitvi02g00436
        1.02.2006
        PS.photorespiration.hydroxypyruvate reductase
        D-isomer specific 2-hydroxyacid dehydrogenase family protein |
        Chr1:4274649-4275831 FORWARD LENGTH=323 |
        201606
```

Coefficients for Vitvi02g00436.

```
                    swp varietyF swp.varietyF    AveExpr        F
Vitvi02g00436 -3.44536 0.960575    0.3224828 -0.5529786 6.467344
                  P.Value  adj.P.Val  type
Vitvi02g00436 0.002750969 0.03268142 type1
```



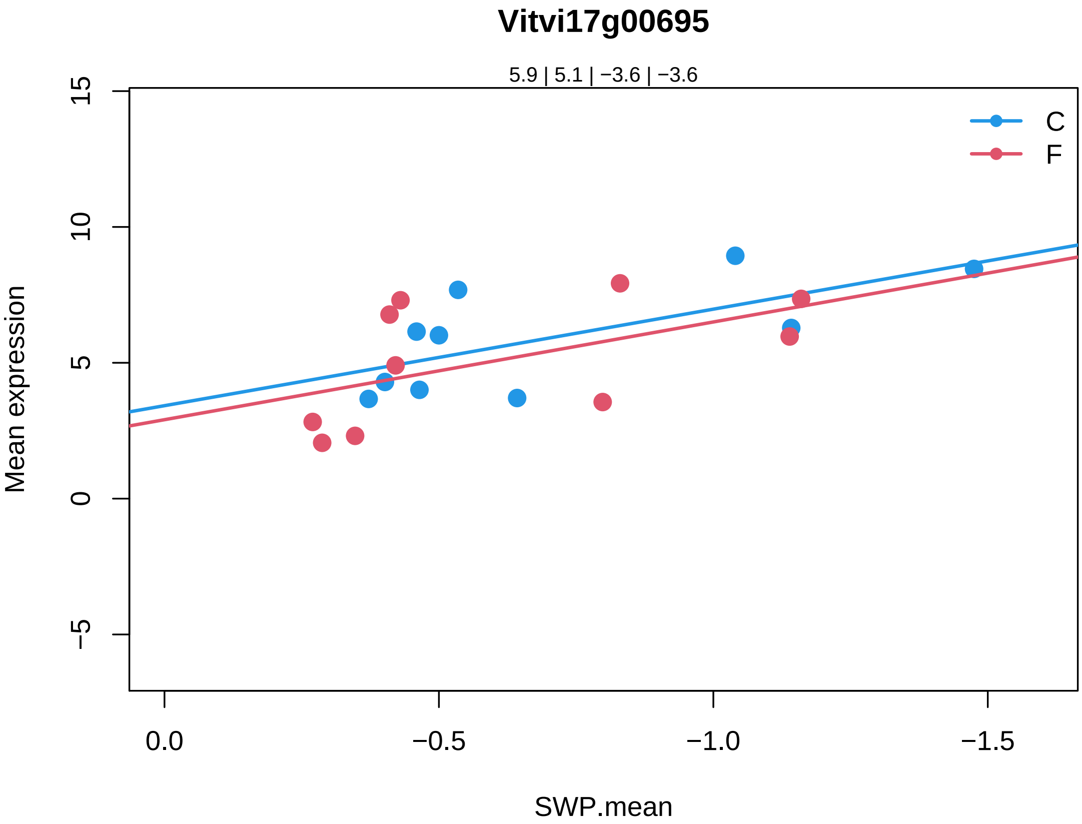
6.2.73 Vitvi17g00695

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

```
Vitvi17g00695
        20.02.2001
        stress.abiotic.heat
        heat shock protein 101 |
        Chr1:27936715-27939862 REVERSE LENGTH=911 |
        201606
```

Coefficients for Vitvi17g00695.

```
                    swp   varietyF swp.varietyF  AveExpr        F
Vitvi17g00695 -3.552929 -0.5159036  -0.04441921 5.508229 4.551577
                 P.Value  adj.P.Val  type
Vitvi17g00695 0.01287377 0.09935316 type1
```



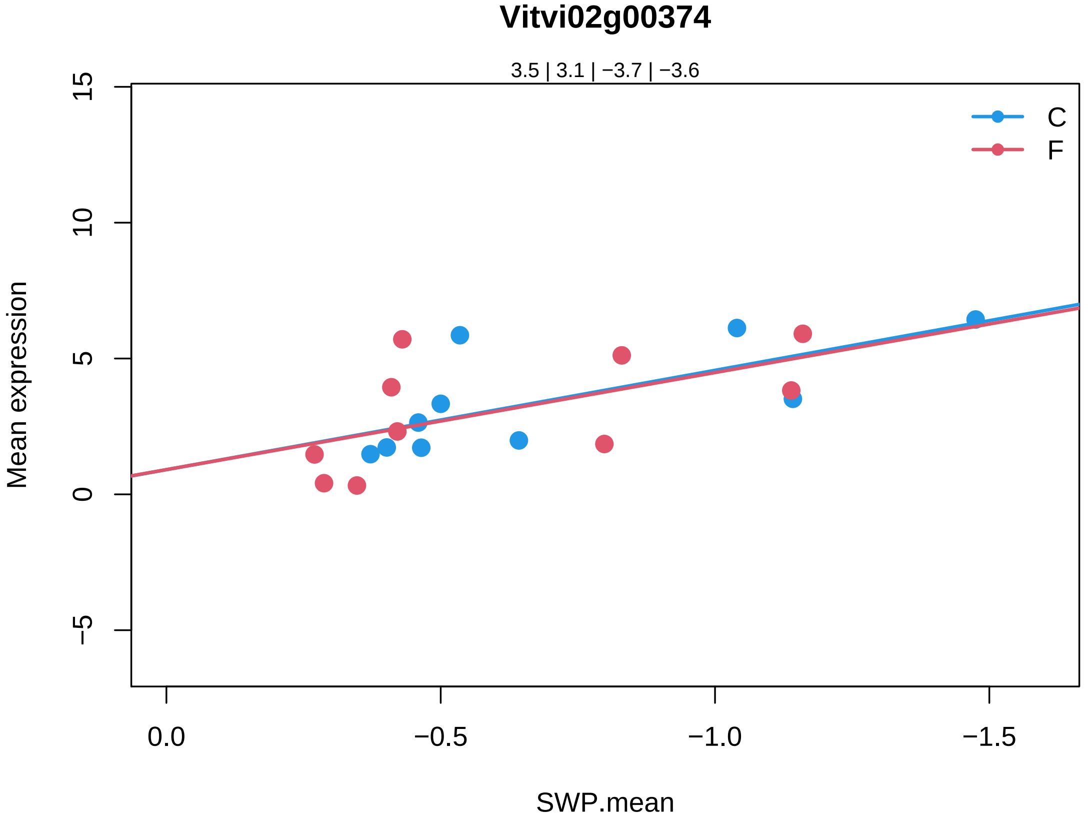
6.2.74 Vitvi02g00374

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

```
Vitvi02g00374
        29.05.2011
        protein.degradation.ubiquitin
        UBX domain-containing protein IPR001012 UBX
```

Coefficients for Vitvi02g00374.

```
                    swp     varietyF swp.varietyF AveExpr        F
Vitvi02g00374 -3.65719 0.0007157822   0.08429943 3.28388 5.053809
                  P.Value   adj.P.Val  type
Vitvi02g00374 0.008416413 0.07375416 type1
```



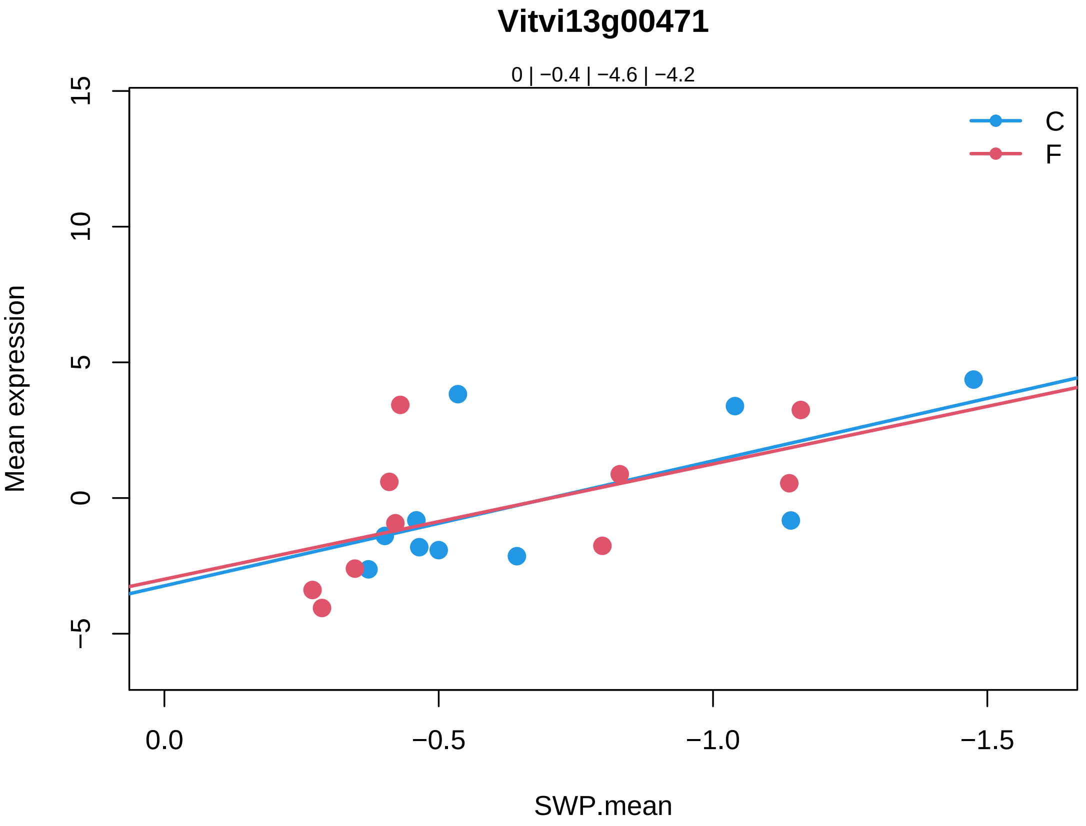
6.2.75 Vitvi13g00471

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

```
Vitvi13g00471
        20.02.2001
        stress.abiotic.heat
        heat shock protein 18.2 |
        Chr5:24062632-24063117 FORWARD LENGTH=161 |
        201606
```

Coefficients for Vitvi13g00471.

```
                    swp  varietyF swp.varietyF    AveExpr        F
Vitvi13g00471 -4.604229 0.2433888    0.3580492 -0.2006487 4.107523
                 P.Value adj.P.Val  type
Vitvi13g00471 0.01899467  0.130693 type1
```



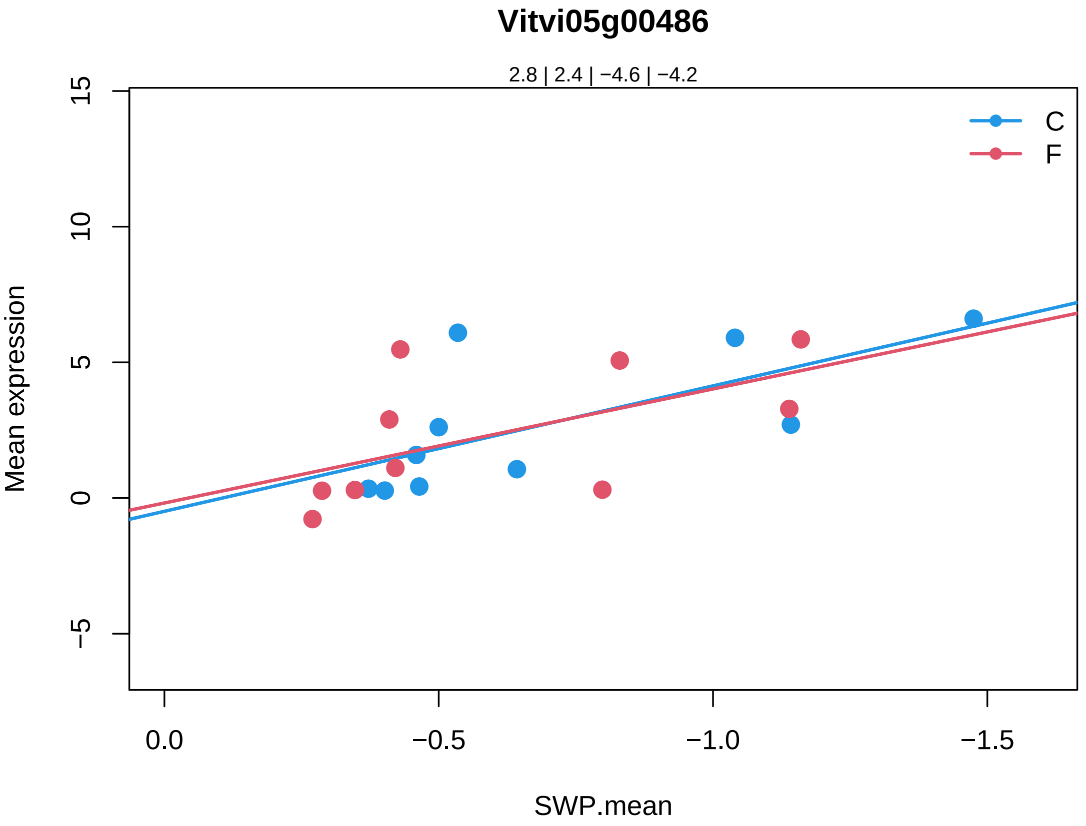
6.2.76 Vitvi05g00486

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

```
Vitvi05g00486
        20.02.2001
        stress.abiotic.heat
        heat-shock protein 70T-2 |
        Chr2:13651720-13653411 REVERSE LENGTH=563 |
        201606
```

Coefficients for Vitvi05g00486.

```
                    swp  varietyF swp.varietyF  AveExpr        F
Vitvi05g00486 -4.622837 0.3062449    0.4200715 2.569209 5.022231
                 P.Value   adj.P.Val  type
Vitvi05g00486 0.00864045 0.07516994 type1
```



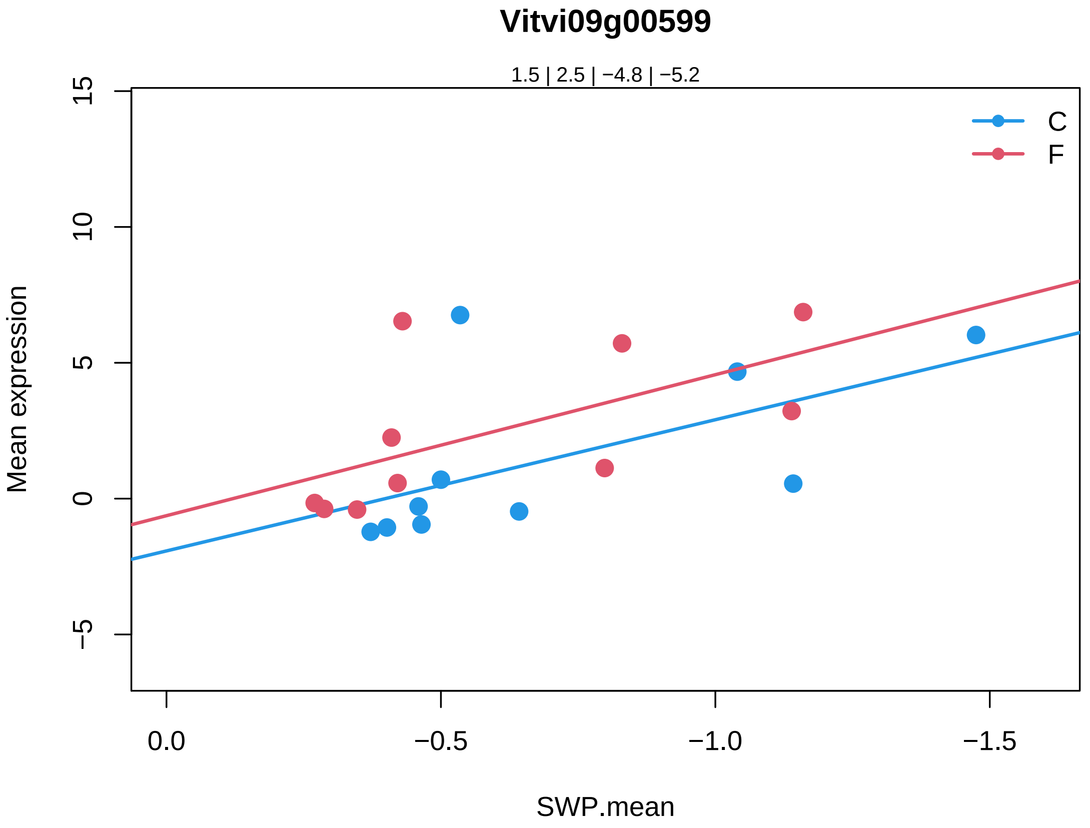
6.2.77 Vitvi09g00599

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

```
Vitvi09g00599
        20.02.2001
        stress.abiotic.heat
        HSP20-like chaperones superfamily protein |
        Chr1:19574783-19575766 REVERSE LENGTH=232 |
        201606
```

Coefficients for Vitvi09g00599.

```
                    swp varietyF swp.varietyF  AveExpr        F
Vitvi09g00599 -4.828826 1.296853   -0.3605426 2.002367 4.387194
                 P.Value adj.P.Val  type
Vitvi09g00599 0.01484563 0.1103253 type1
```



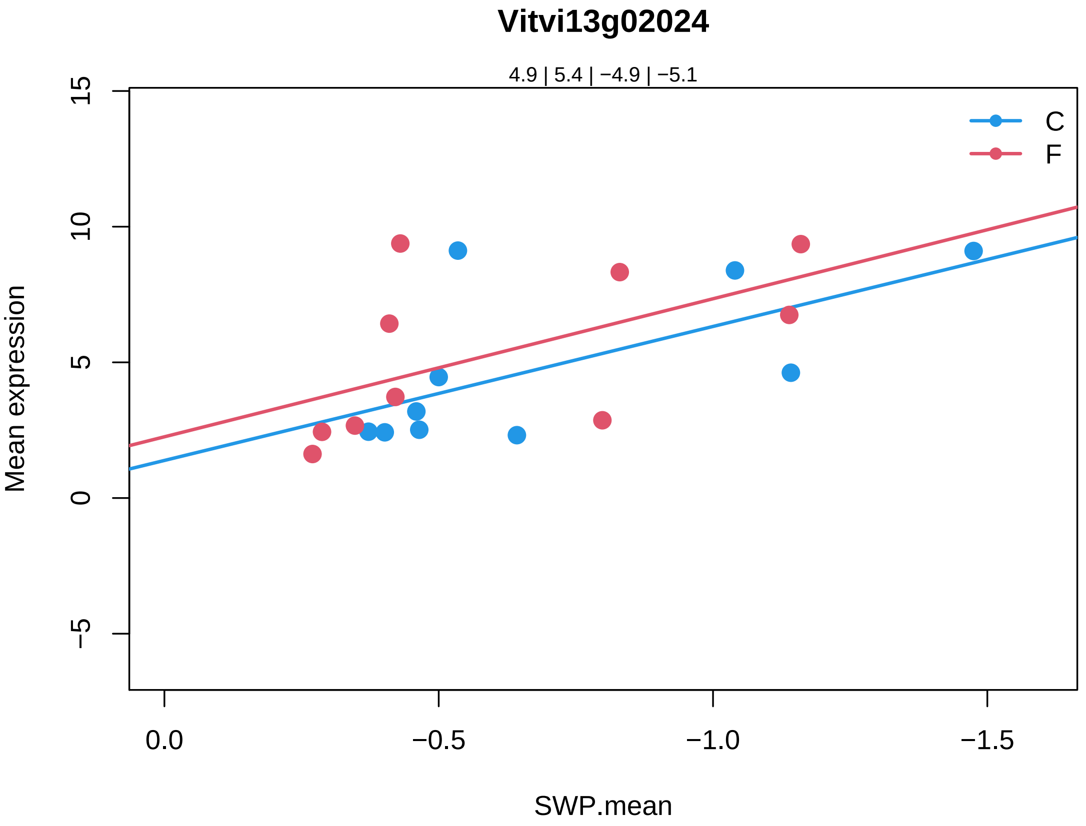
6.2.78 Vitvi13g02024

```
> 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.

```
                    swp  varietyF swp.varietyF  AveExpr        F
Vitvi13g02024 -4.938026 0.8716546   -0.1483944 5.106388 4.294635
                 P.Value adj.P.Val  type
Vitvi13g02024 0.01609824 0.1170137 type1
```



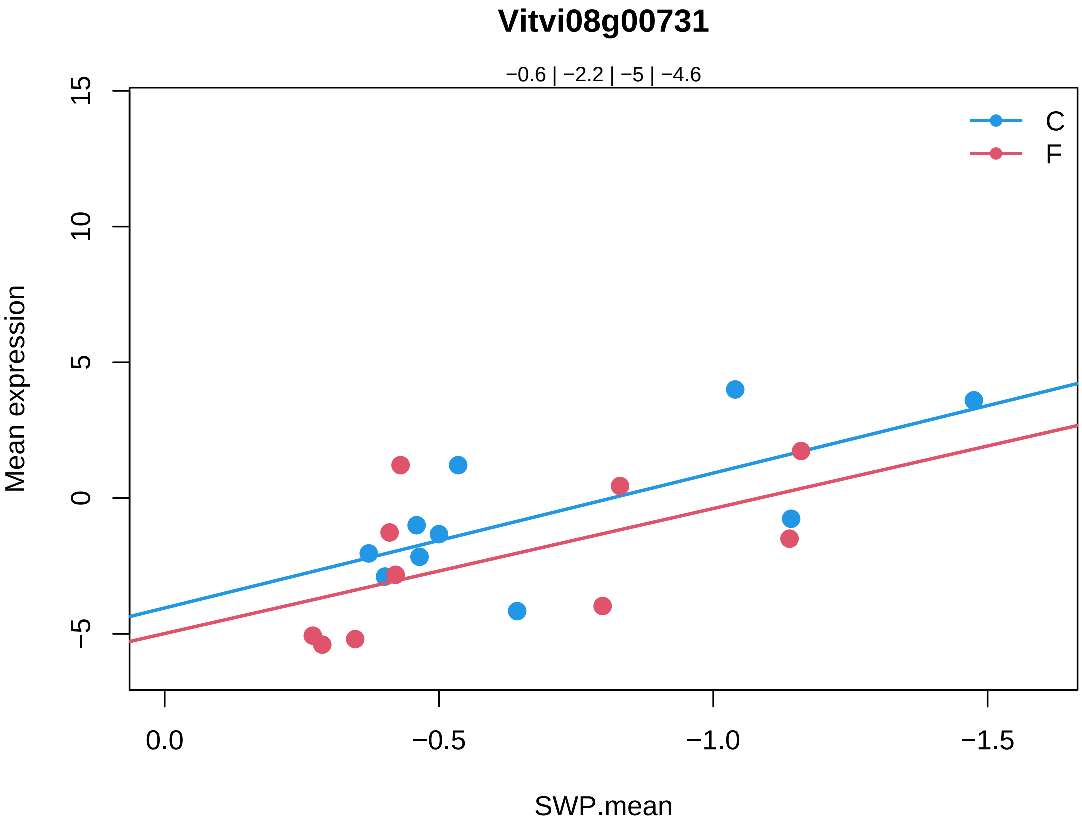
6.2.79 Vitvi08g00731

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

```
Vitvi08g00731
        20.02.2001
        stress.abiotic.heat
        HSP20-like chaperones superfamily protein |
        Chr1:19980510-19980983 FORWARD LENGTH=157 |
        201606
```

Coefficients for Vitvi08g00731.

```
                    swp   varietyF swp.varietyF   AveExpr        F
Vitvi08g00731 -4.968213 -0.941974    0.3636611 -1.368275 6.159246
                  P.Value  adj.P.Val  type
Vitvi08g00731 0.003478074 0.03890496 type1
```



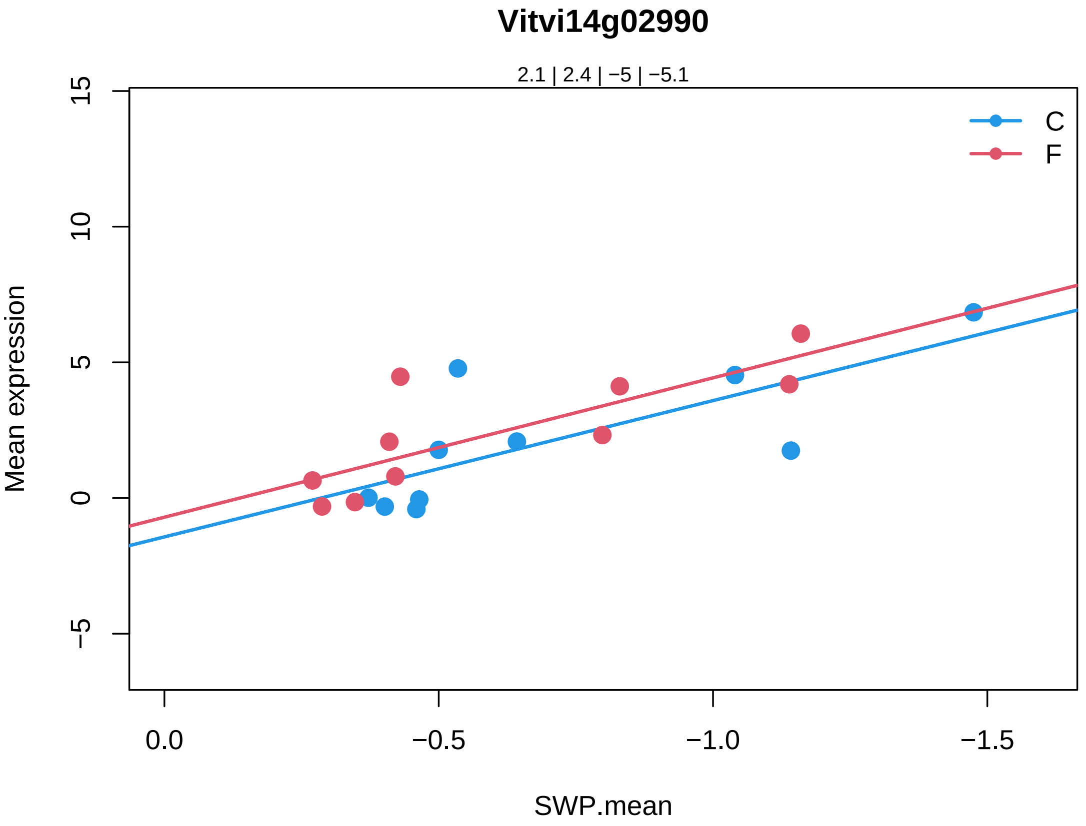
6.2.80 Vitvi14g02990

```
> 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.

```
                    swp  varietyF swp.varietyF  AveExpr       F
Vitvi14g02990 -5.022153 0.7255139   -0.1129527 2.260604 10.6418
                   P.Value   adj.P.Val  type
Vitvi14g02990 0.0001726067 0.003548162 type1
```



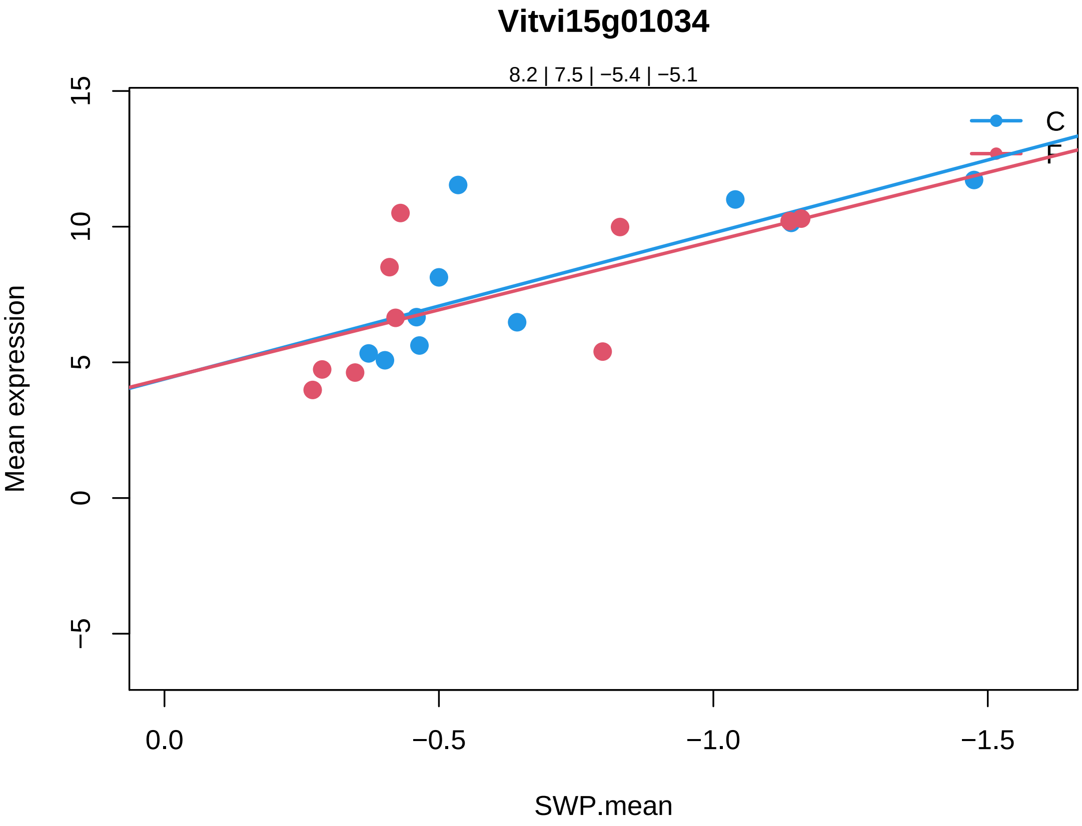
6.2.81 Vitvi15g01034

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

```
Vitvi15g01034
        20.02.2001
        stress.abiotic.heat
        BCL-2-associated athanogene 6 |
        Chr2:18986586-18989827 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi15g01034.

```
                    swp   varietyF swp.varietyF  AveExpr        F
Vitvi15g01034 -5.38071 0.01638255     0.316925 7.829037 7.194461
                  P.Value  adj.P.Val  type
Vitvi15g01034 0.001611484 0.02151327 type1
```



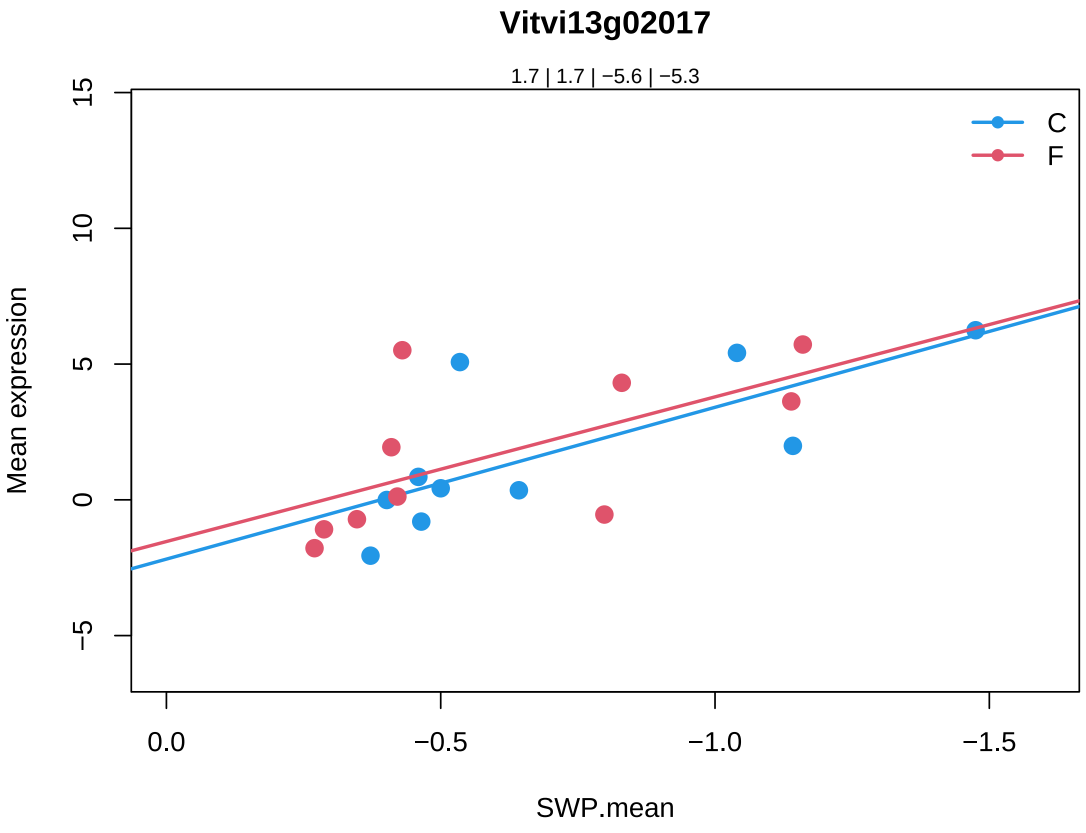
6.2.82 Vitvi13g02017

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

```
Vitvi13g02017
        20.02.2001
        stress.abiotic.heat
        heat shock protein 18.2 |
        Chr5:24062632-24063117 FORWARD LENGTH=161 |
        201606
```

Coefficients for Vitvi13g02017.

```
                    swp  varietyF swp.varietyF  AveExpr        F
Vitvi13g02017 -5.59067 0.6476173    0.2632103 1.728743 6.418066
                  P.Value  adj.P.Val  type
Vitvi13g02017 0.002855187 0.03363119 type1
```



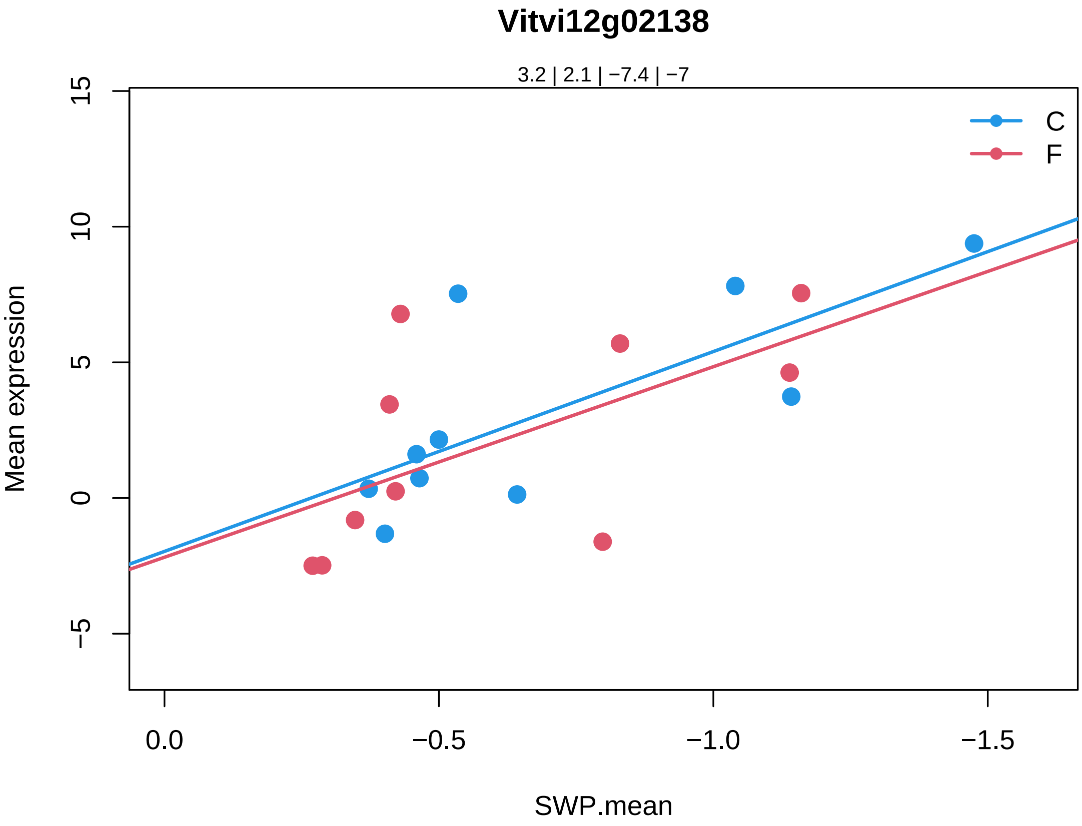
6.2.83 Vitvi12g02138

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

```
Vitvi12g02138
        20.02.2001
        stress.abiotic.heat
        HSP20-like chaperones superfamily protein |
        Chr4:6370537-6371124 FORWARD LENGTH=195 |
        201606
```

Coefficients for Vitvi12g02138.

```
                    swp    varietyF swp.varietyF  AveExpr        F
Vitvi12g02138 -7.364735 -0.2170548    0.3417037 2.653465 6.323957
                  P.Value  adj.P.Val  type
Vitvi12g02138 0.003066367 0.03562315 type1
```



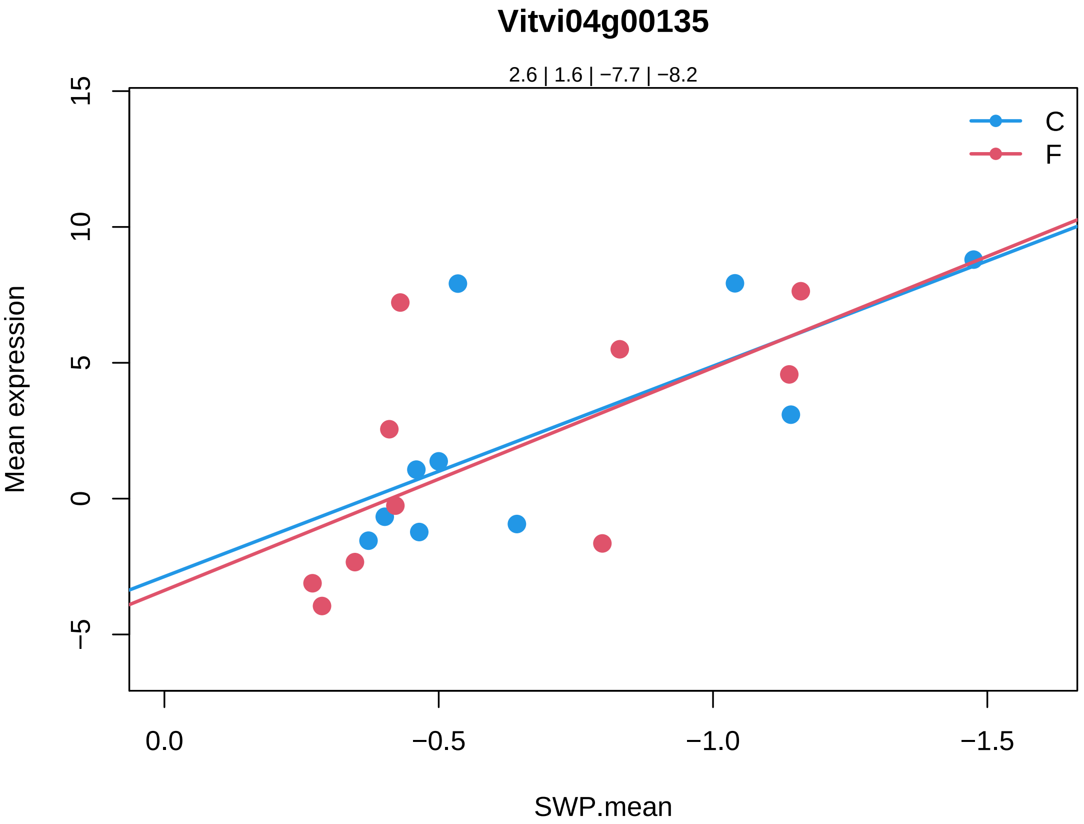
6.2.84 Vitvi04g00135

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

```
Vitvi04g00135
        20.02.2001
        stress.abiotic.heat
        17.6 kDa class II heat shock protein |
        Chr5:3882409-3882876 REVERSE LENGTH=155 |
        201606
```

Coefficients for Vitvi04g00135.

```
                    swp   varietyF swp.varietyF AveExpr        F
Vitvi04g00135 -7.746727 -0.5095023   -0.4507473 2.09779 6.033692
                  P.Value  adj.P.Val  type
Vitvi04g00135 0.003832305 0.04145634 type1
```



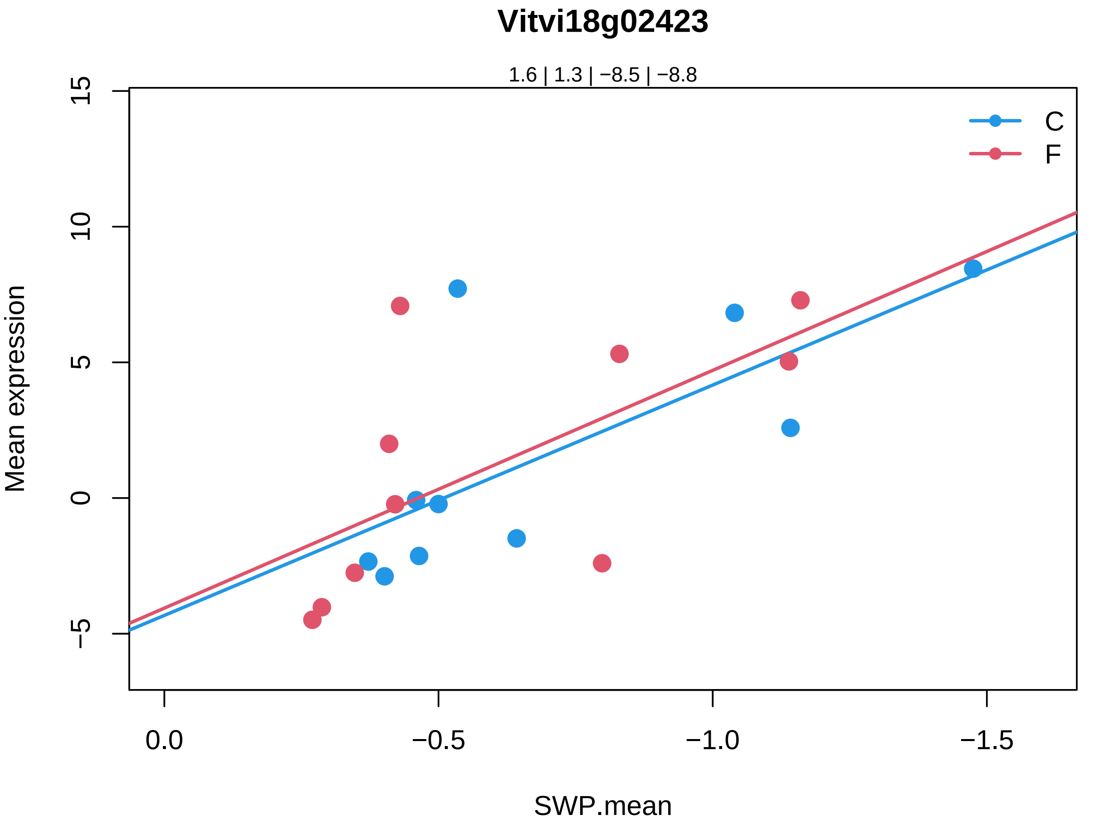
6.2.85 Vitvi18g02423

```
> 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.

```
                    swp  varietyF swp.varietyF  AveExpr        F
Vitvi18g02423 -8.488894 0.2684968   -0.2732159 1.462056 6.310886
                 P.Value  adj.P.Val  type
Vitvi18g02423 0.00309702 0.03589717 type1
```



6.3 type2

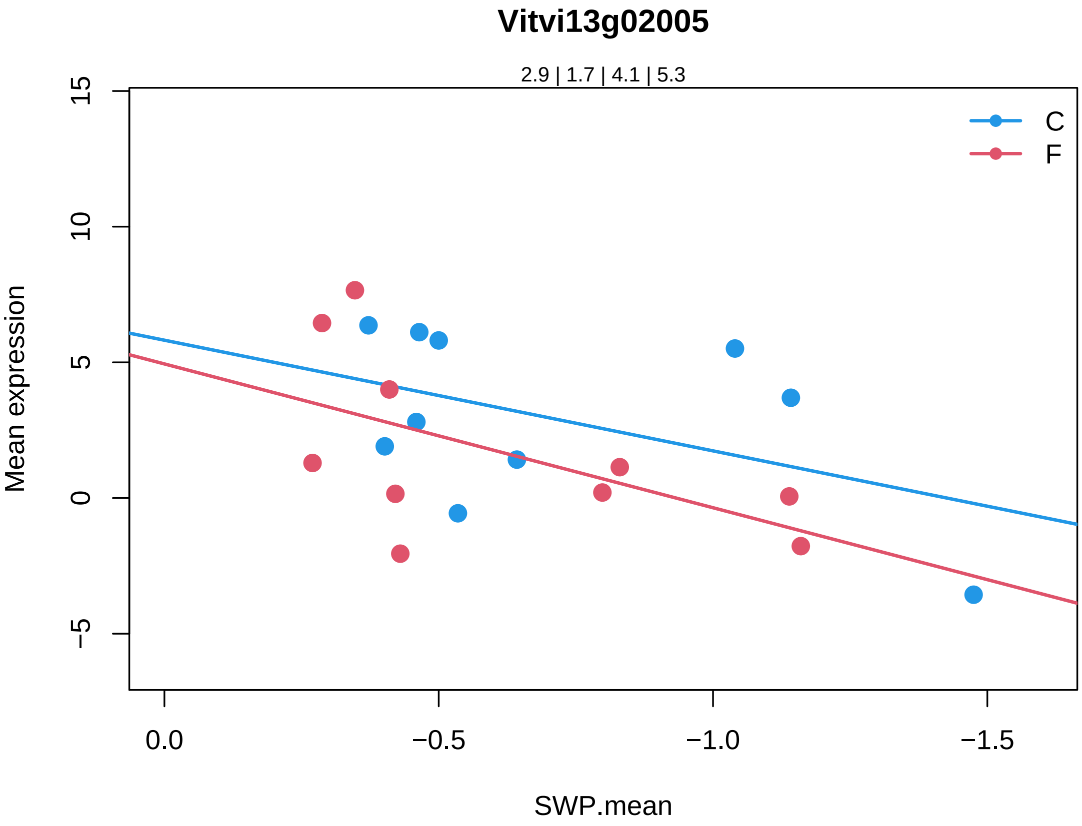
6.3.1 Vitvi13g02005

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

```
Vitvi13g02005
        29.05.2001
        protein.degradation.subtilases
        Subtilisin-like serine endopeptidase family protein |
        Chr5:23755787-23758600 FORWARD LENGTH=710 |
        201606
```

Coefficients for Vitvi13g02005.

```
                  swp  varietyF swp.varietyF  AveExpr        F
Vitvi13g02005 4.07808 -0.874001     1.221977 2.330616 2.961028
                 P.Value adj.P.Val  type
Vitvi13g02005 0.05510925 0.2582156 type2
```



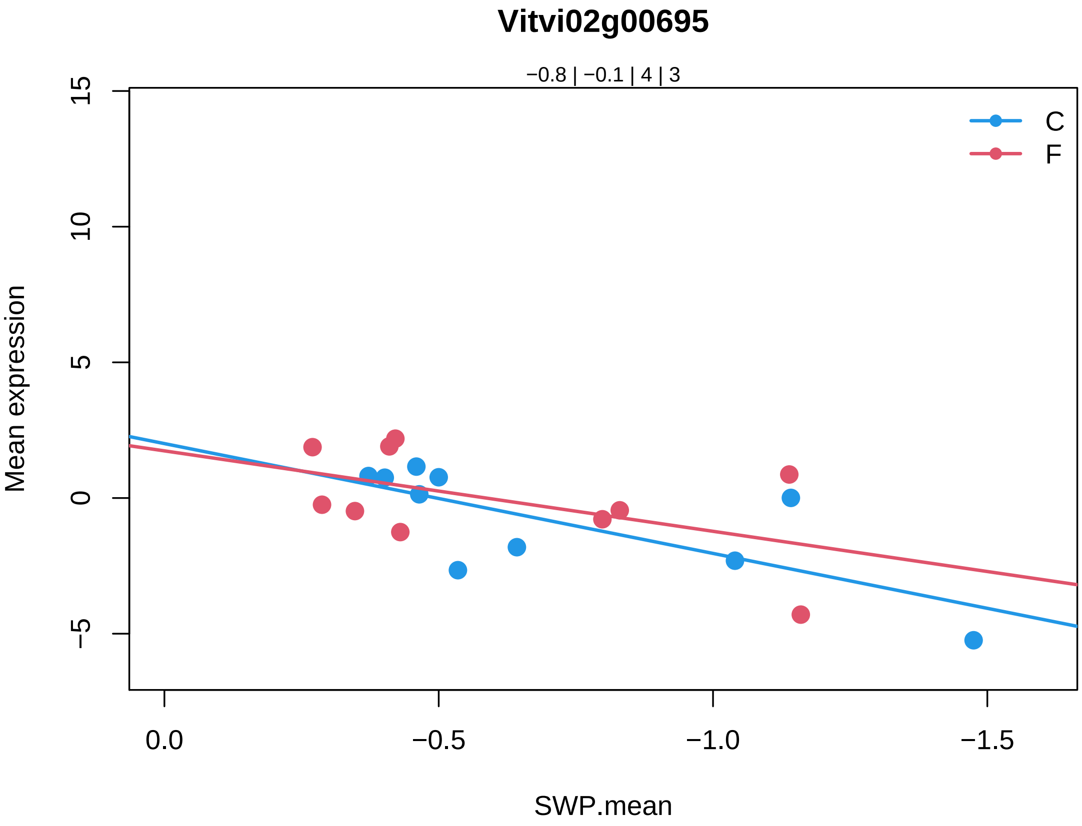
6.3.2 Vitvi02g00695

```
> 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.

```
                   swp   varietyF swp.varietyF    AveExpr        F
Vitvi02g00695 4.04752 -0.2688544    -1.083729 -0.4542073 5.456573
                  P.Value  adj.P.Val  type
Vitvi02g00695 0.006051153 0.05871028 type2
```



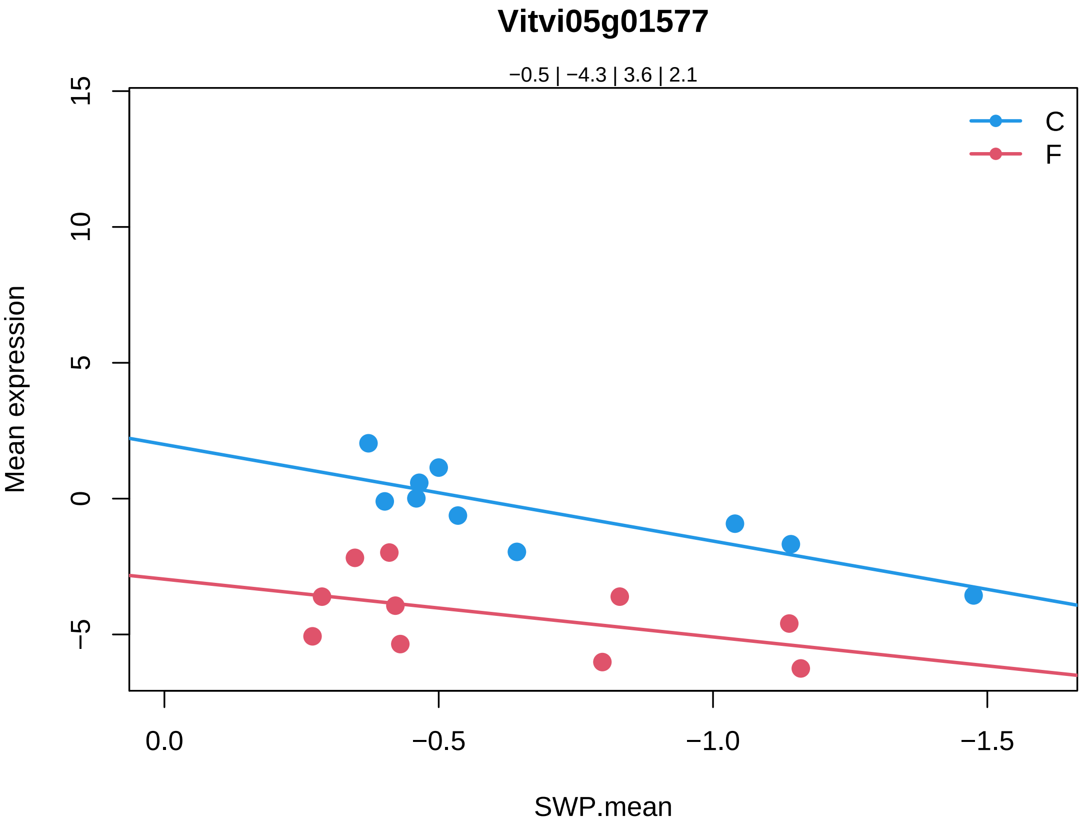
6.3.3 Vitvi05g01577

```
> 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.

```
                   swp  varietyF swp.varietyF   AveExpr        F
Vitvi05g01577 3.553568 -4.955944     -1.42671 -2.384056 27.87609
                   P.Value    adj.P.Val  type
Vitvi05g01577 1.372726e-07 6.621229e-06 type4
```



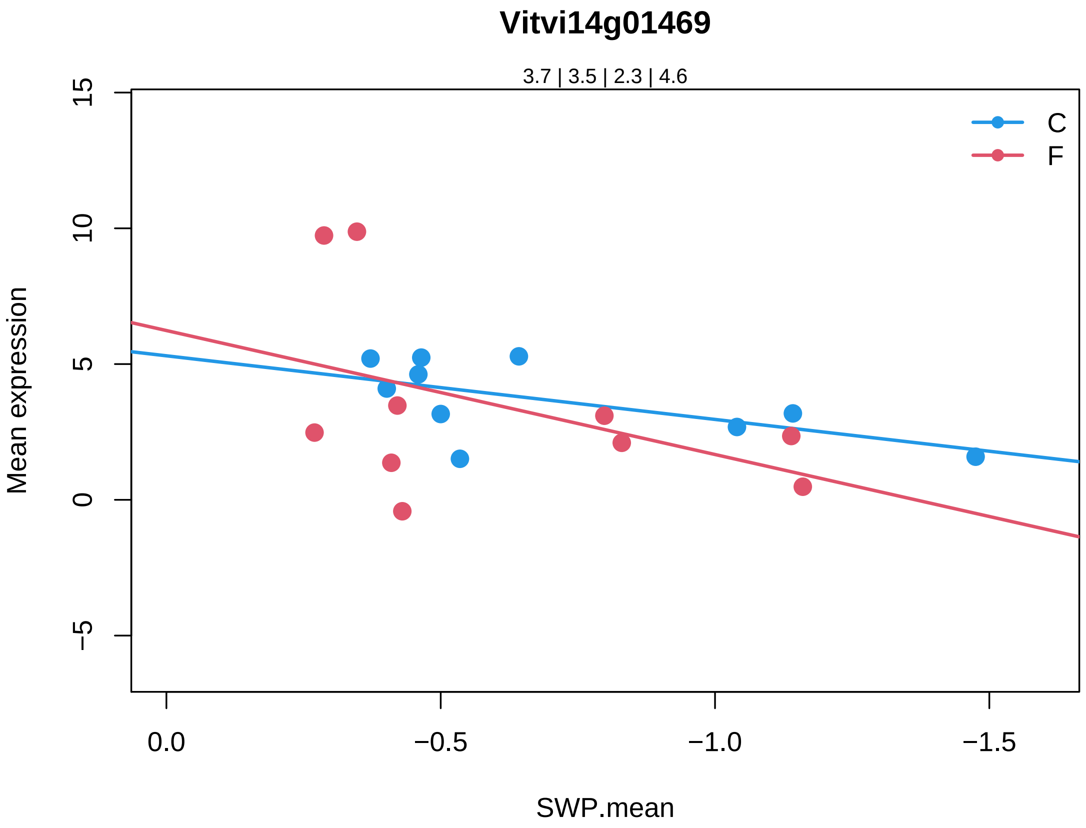
6.3.4 Vitvi14g01469

```
> 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.

```
                   swp varietyF swp.varietyF  AveExpr        F
Vitvi14g01469 2.343466  0.93044     2.222219 3.555123 2.023495
                P.Value adj.P.Val  type
Vitvi14g01469 0.1407507 0.4488962 type2
```



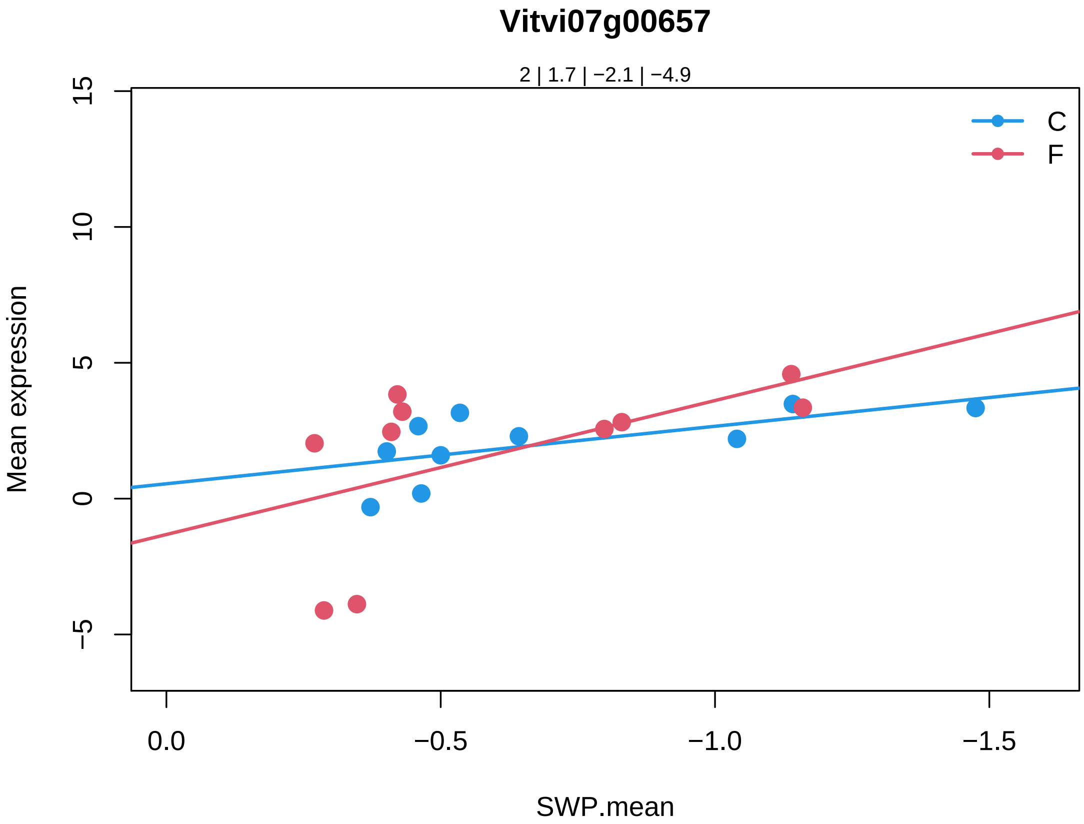
6.3.5 Vitvi07g00657

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

```
Vitvi07g00657
        34.13
        transport.peptides and oligopeptides
        peptide transporter 3 |
        Chr5:18675062-18676657 REVERSE LENGTH=470 |
        201606
```

Coefficients for Vitvi07g00657.

```
                    swp   varietyF swp.varietyF  AveExpr      F
Vitvi07g00657 -2.116357 -1.867228    -2.815318 1.859156 3.2972
                 P.Value adj.P.Val  type
Vitvi07g00657 0.03995076  0.212388 type2
```



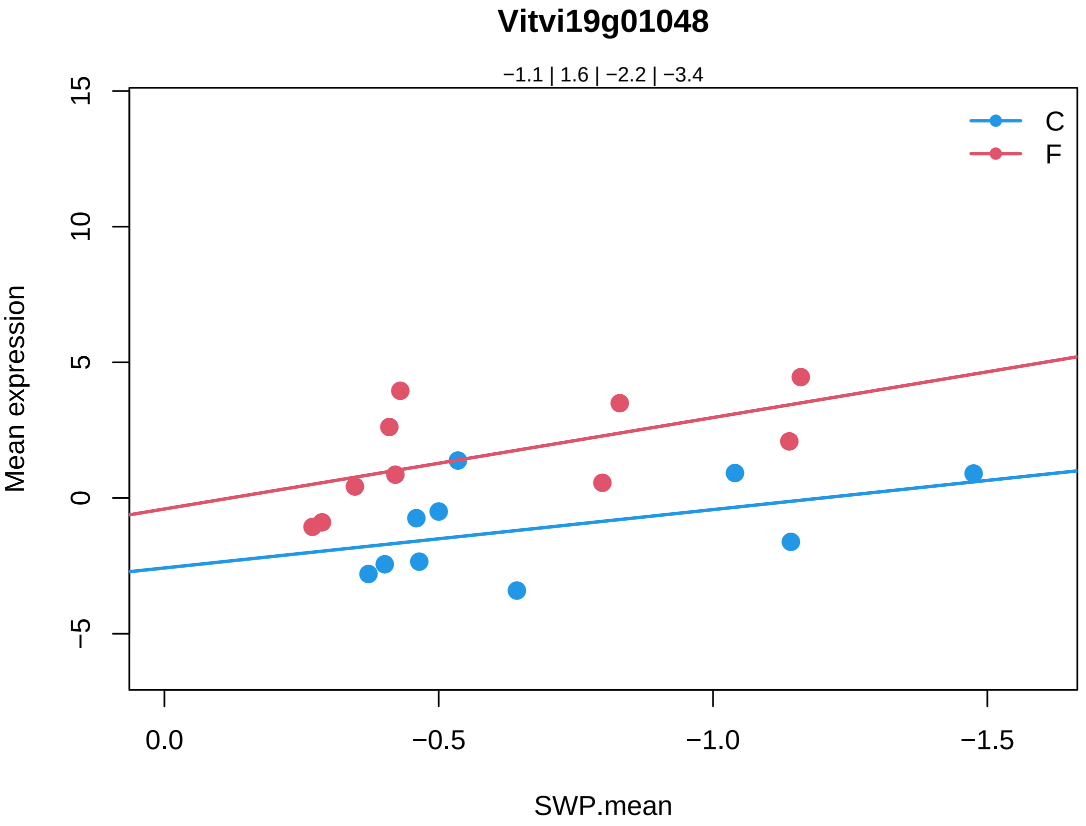
6.3.6 Vitvi19g01048

```
> 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.

```
                    swp varietyF swp.varietyF   AveExpr        F
Vitvi19g01048 -2.150775  2.17355    -1.218795 0.2925552 8.779439
                   P.Value   adj.P.Val  type
Vitvi19g01048 0.0005452867 0.008975443 type4
```



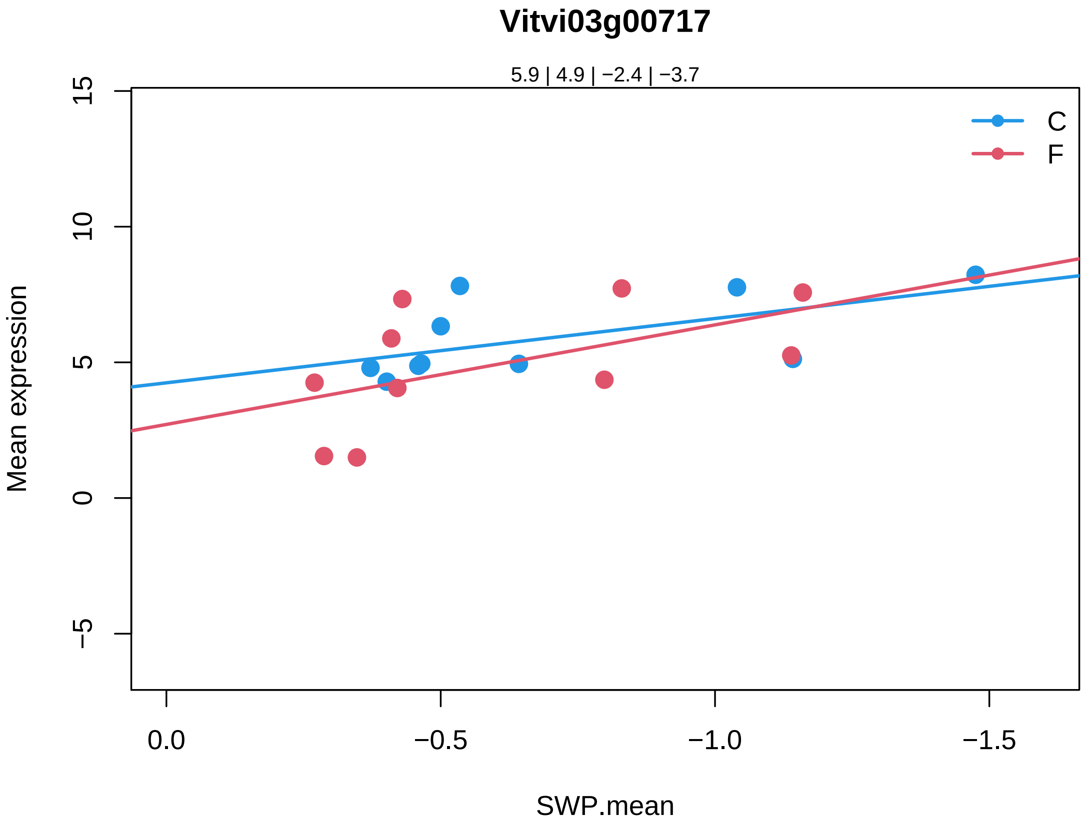
6.3.7 Vitvi03g00717

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

```
Vitvi03g00717
        29.05.2007
        protein.degradation.metalloprotease
        ethylene-dependent gravitropism-deficient and yellow-green-like 3 |
        Chr1:6150036-6152185 REVERSE LENGTH=573 |
        201606
```

Coefficients for Vitvi03g00717.

```
                    swp  varietyF swp.varietyF  AveExpr        F
Vitvi03g00717 -2.370121 -1.533221    -1.298612 5.429914 4.061491
                 P.Value adj.P.Val  type
Vitvi03g00717 0.01979069 0.1341261 type2
```



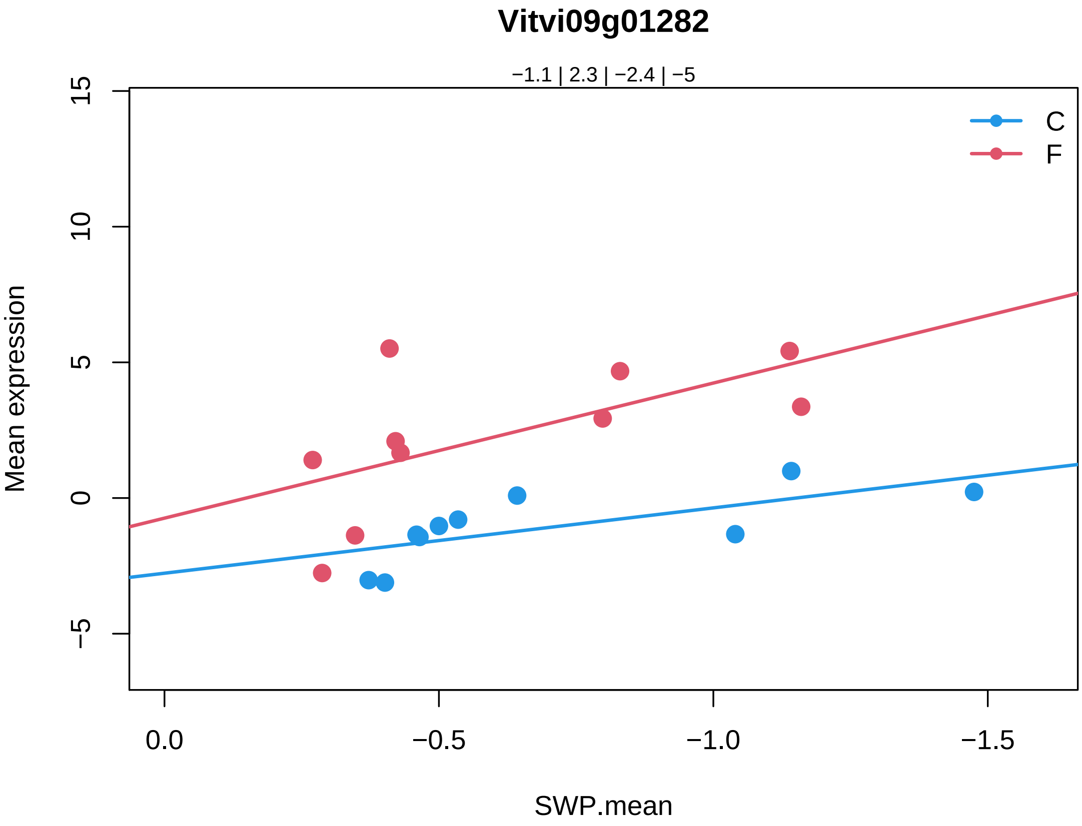
6.3.8 Vitvi09g01282

```
> 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.

```
                    swp varietyF swp.varietyF   AveExpr        F
Vitvi09g01282 -2.408129 2.029899    -2.570707 0.6068136 12.77438
                   P.Value   adj.P.Val   type
Vitvi09g01282 5.284715e-05 0.00131617 type4
```



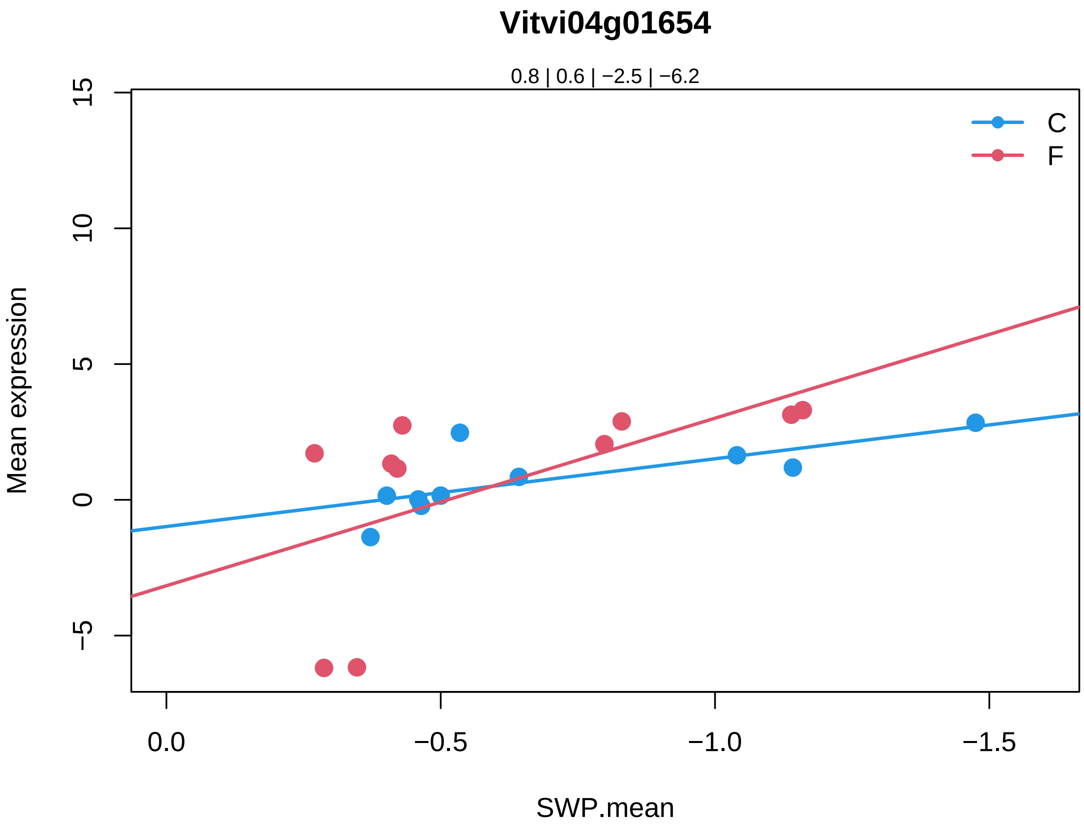
6.3.9 Vitvi04g01654

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

```
Vitvi04g01654
        35.2
        not assigned.unknown
        hypothetical protein (DUF506) |
        Chr4:8389246-8390448 REVERSE LENGTH=341 |
        201606
```

Coefficients for Vitvi04g01654.

```
                    swp  varietyF swp.varietyF   AveExpr        F
Vitvi04g01654 -2.495151 -2.180846    -3.675405 0.6828582 3.977525
                P.Value adj.P.Val  type
Vitvi04g01654 0.0213373 0.1417094 type2
```



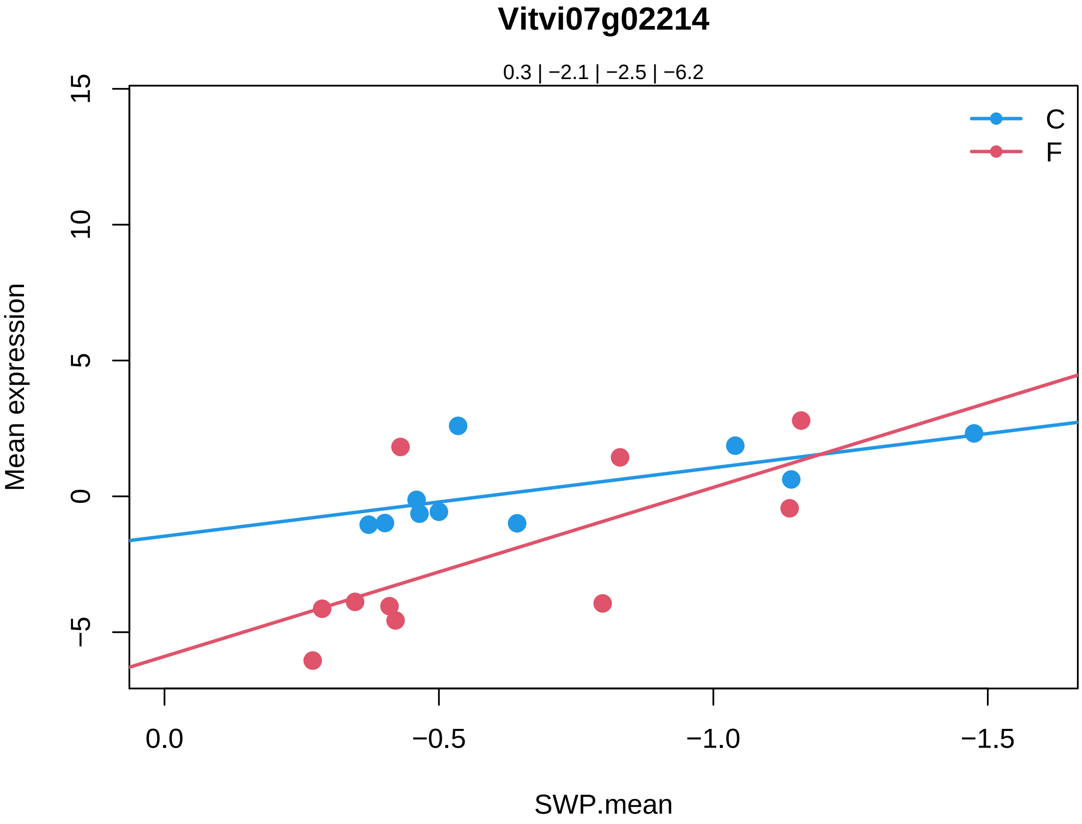
6.3.10 Vitvi07g02214

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

```
Vitvi07g02214
        35.2
        not assigned.unknown
        GATA transcription factor 22 IPR000679 Zinc finger, GATA-type
```

Coefficients for Vitvi07g02214.

```
                    swp  varietyF swp.varietyF    AveExpr        F
Vitvi07g02214 -2.518808 -4.426367     -3.70436 -0.8983373 9.111532
                  P.Value   adj.P.Val  type
Vitvi07g02214 0.000440166 0.007521313 type4
```



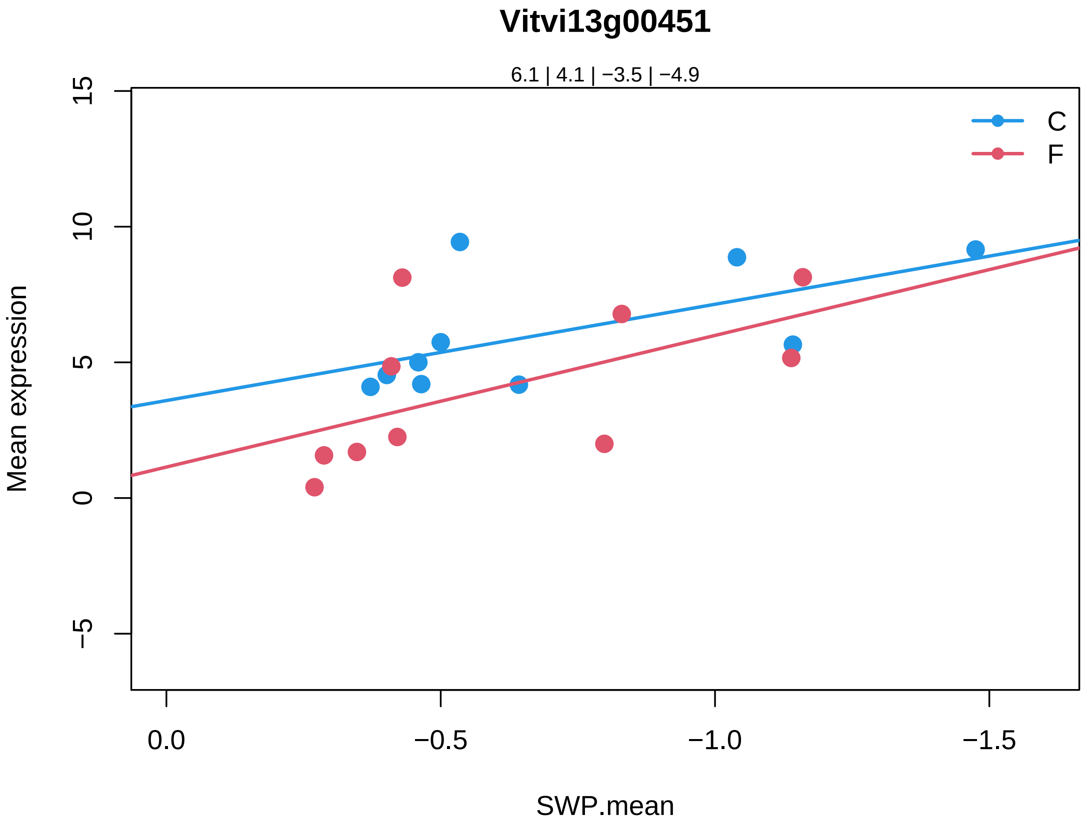
6.3.11 Vitvi13g00451

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

```
Vitvi13g00451
        20.02.2001
        stress.abiotic.heat
        heat shock protein 18.2 |
        Chr5:24062632-24063117 FORWARD LENGTH=161 |
        201606
```

Coefficients for Vitvi13g00451.

```
                    swp  varietyF swp.varietyF  AveExpr        F
Vitvi13g00451 -3.548031 -2.450561    -1.302419 5.091936 5.554609
                  P.Value  adj.P.Val  type
Vitvi13g00451 0.005592089 0.05567252 type2
```



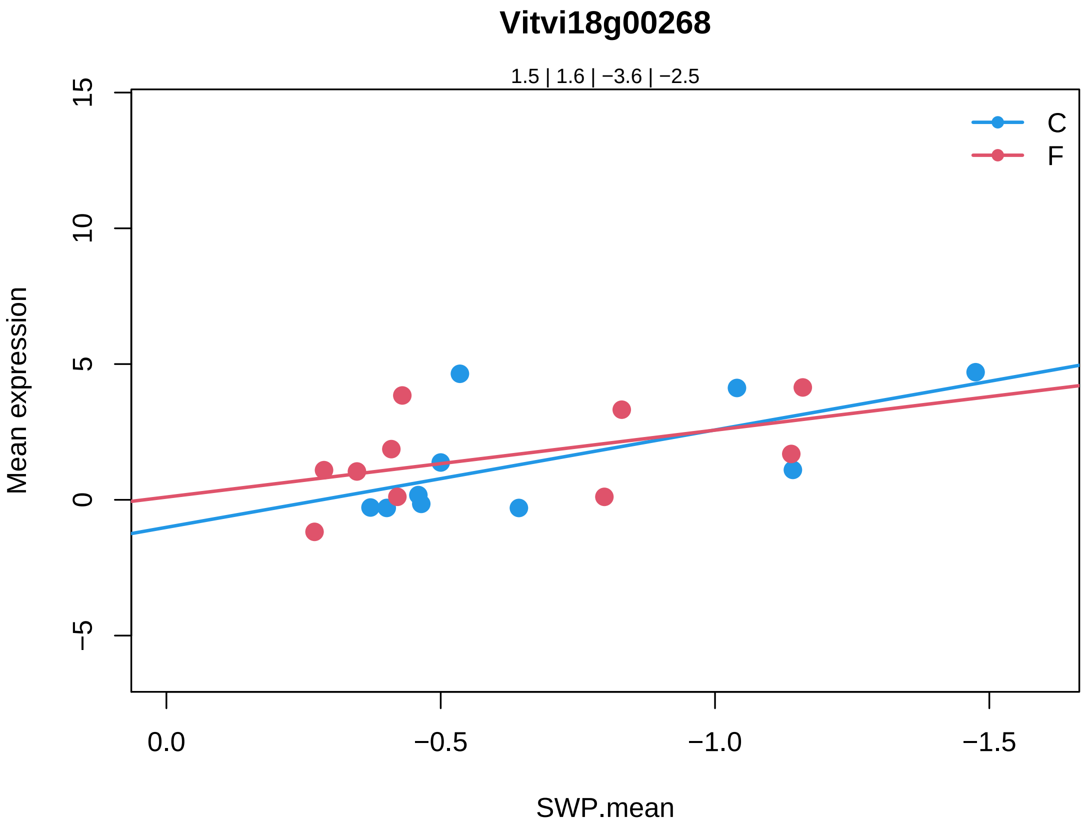
6.3.12 Vitvi18g00268

```
> 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.

```
                    swp varietyF swp.varietyF  AveExpr       F
Vitvi18g00268 -3.586619 1.115345     1.121175 1.556079 3.53502
                 P.Value adj.P.Val  type
Vitvi18g00268 0.03197044 0.1837456 type2
```



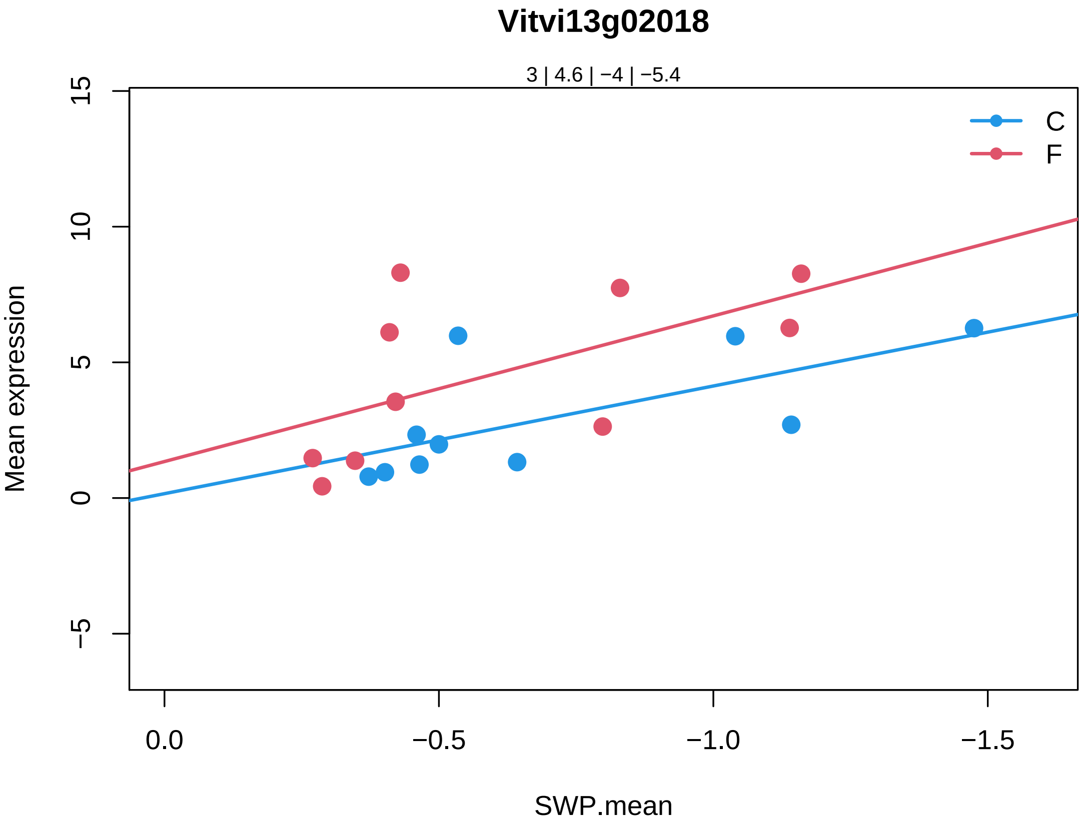
6.3.13 Vitvi13g02018

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

```
Vitvi13g02018
        20.02.2001
        stress.abiotic.heat
        heat shock protein 18.2 |
        Chr5:24062632-24063117 FORWARD LENGTH=161 |
        201606
```

Coefficients for Vitvi13g02018.

```
                    swp varietyF swp.varietyF  AveExpr       F
Vitvi13g02018 -3.968203 1.184325    -1.399499 3.782728 5.80364
                  P.Value  adj.P.Val  type
Vitvi13g02018 0.004587608 0.04770972 type2
```



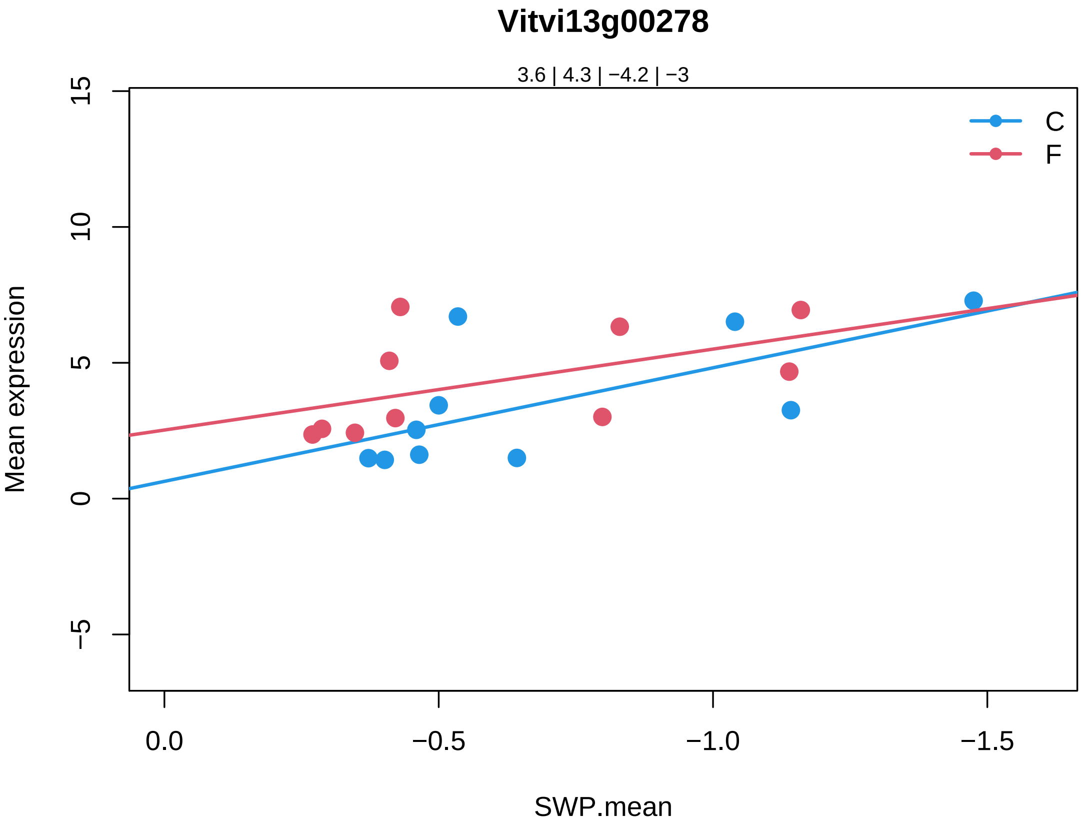
6.3.14 Vitvi13g00278

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

```
Vitvi13g00278
        20.02.2001
        stress.abiotic.heat
        HSP20-like chaperones superfamily protein |
        Chr5:14969035-14969448 FORWARD LENGTH=137 |
        201606
```

Coefficients for Vitvi13g00278.

```
                    swp varietyF swp.varietyF  AveExpr        F
Vitvi13g00278 -4.180072 1.888621     1.200427 3.957508 4.718054
                 P.Value  adj.P.Val  type
Vitvi13g00278 0.01116289 0.09011909 type2
```



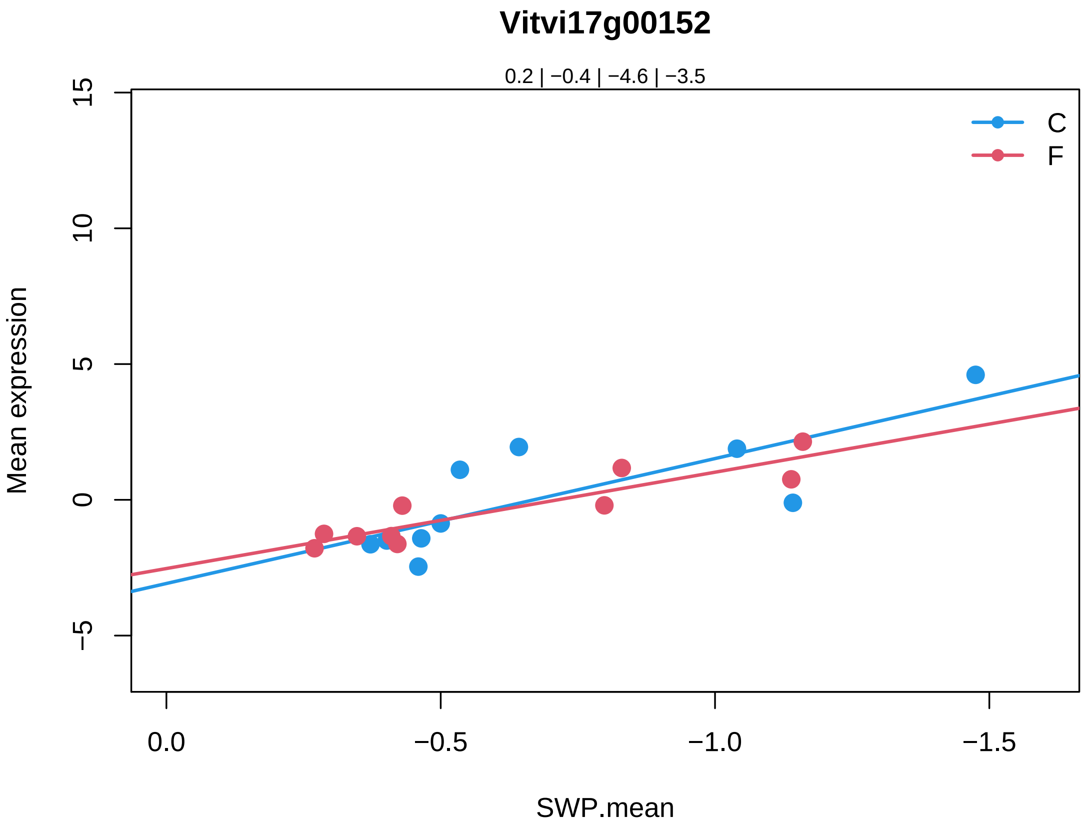
6.3.15 Vitvi17g00152

```
> 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.

```
                    swp varietyF swp.varietyF    AveExpr        F
Vitvi17g00152 -4.601115 0.550967     1.053678 -0.1074944 14.97833
                   P.Value    adj.P.Val  type
Vitvi17g00152 1.757141e-05 0.0005082038 type2
```



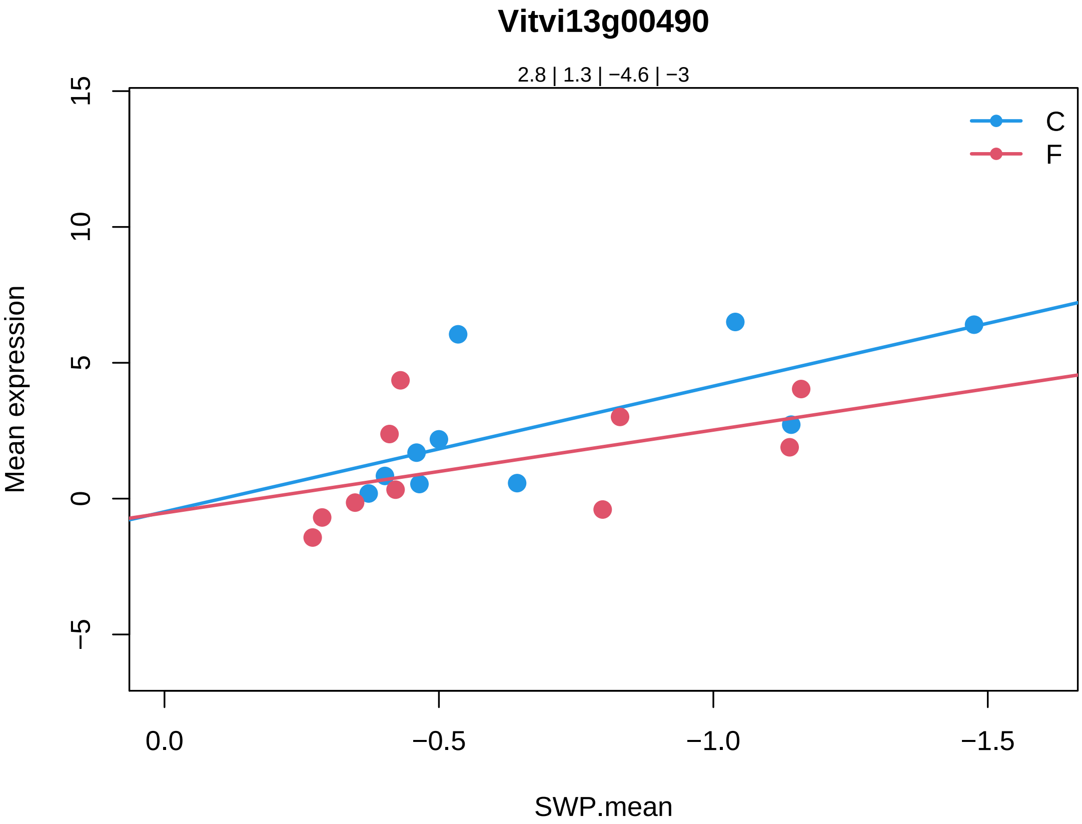
6.3.16 Vitvi13g00490

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

```
Vitvi13g00490
        20.02.2001
        stress.abiotic.heat
        heat shock protein 18.2 |
        Chr5:24062632-24063117 FORWARD LENGTH=161 |
        201606
```

Coefficients for Vitvi13g00490.

```
                    swp    varietyF swp.varietyF  AveExpr        F
Vitvi13g00490 -4.624813 -0.04217964     1.575339 2.050225 5.515874
                  P.Value  adj.P.Val  type
Vitvi13g00490 0.005768781 0.05691117 type2
```



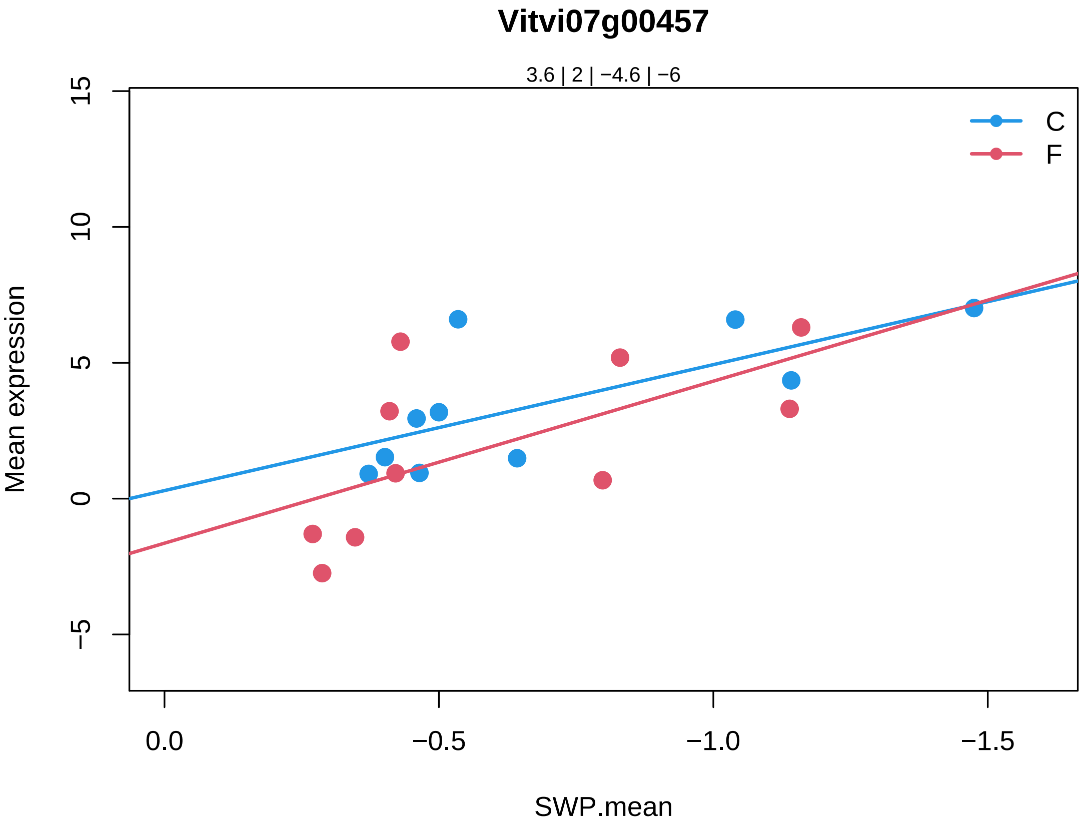
6.3.17 Vitvi07g00457

```
> 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.

```
                    swp   varietyF swp.varietyF  AveExpr        F
Vitvi07g00457 -4.635979 -1.935658    -1.327112 2.774566 6.644803
                  P.Value  adj.P.Val  type
Vitvi07g00457 0.002408627 0.02936983 type2
```



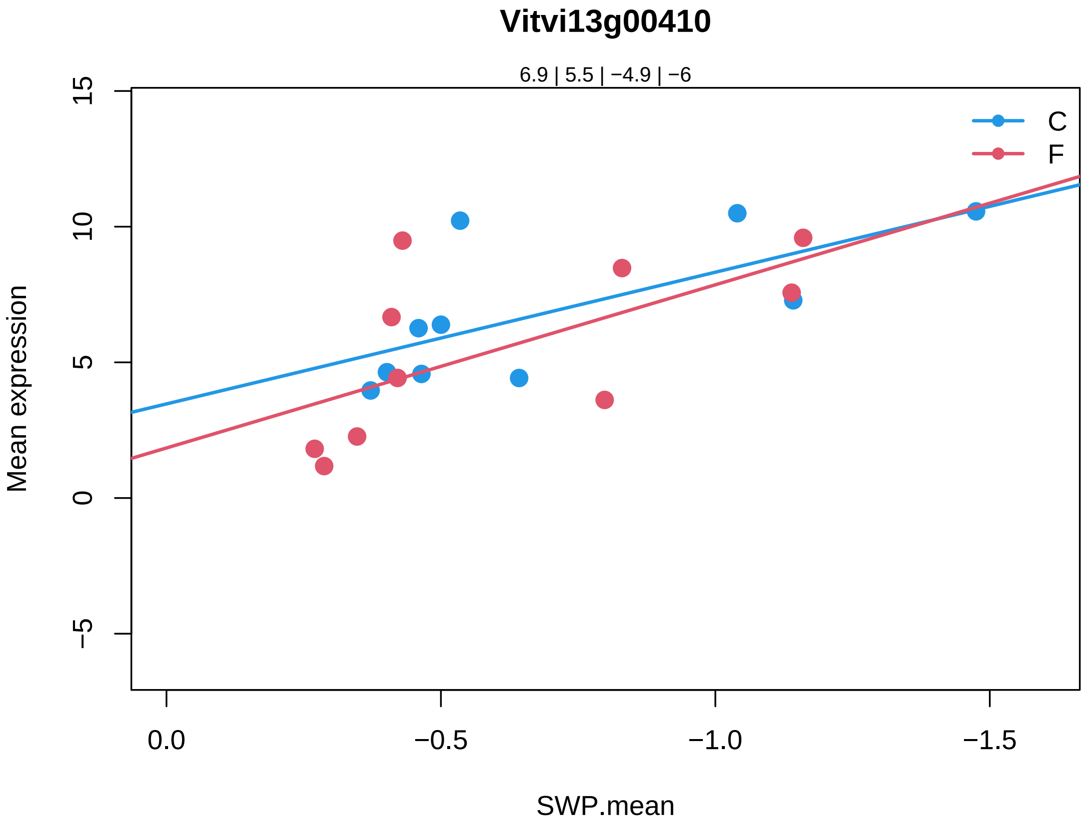
6.3.18 Vitvi13g00410

```
> 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.

```
                    swp  varietyF swp.varietyF AveExpr        F
Vitvi13g00410 -4.853089 -1.623752    -1.160051 6.19465 6.185204
                  P.Value  adj.P.Val  type
Vitvi13g00410 0.003409379 0.03849315 type2
```



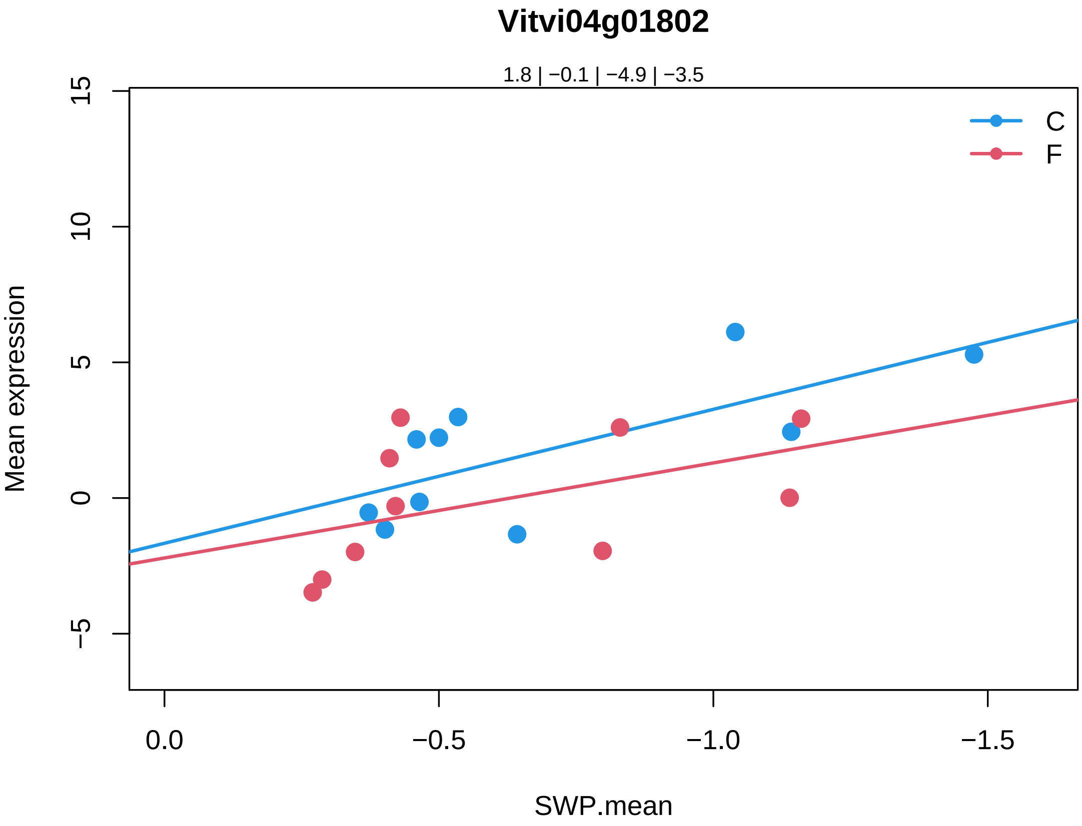
6.3.19 Vitvi04g01802

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

```
Vitvi04g01802
        20.02.2001
        stress.abiotic.heat
        17.6 kDa class II heat shock protein |
        Chr5:3882409-3882876 REVERSE LENGTH=155 |
        201606
```

Coefficients for Vitvi04g01802.

```
                    swp   varietyF swp.varietyF   AveExpr        F
Vitvi04g01802 -4.935441 -0.5423861     1.433256 0.8639588 6.109152
                  P.Value  adj.P.Val  type
Vitvi04g01802 0.003614942 0.03995573 type2
```



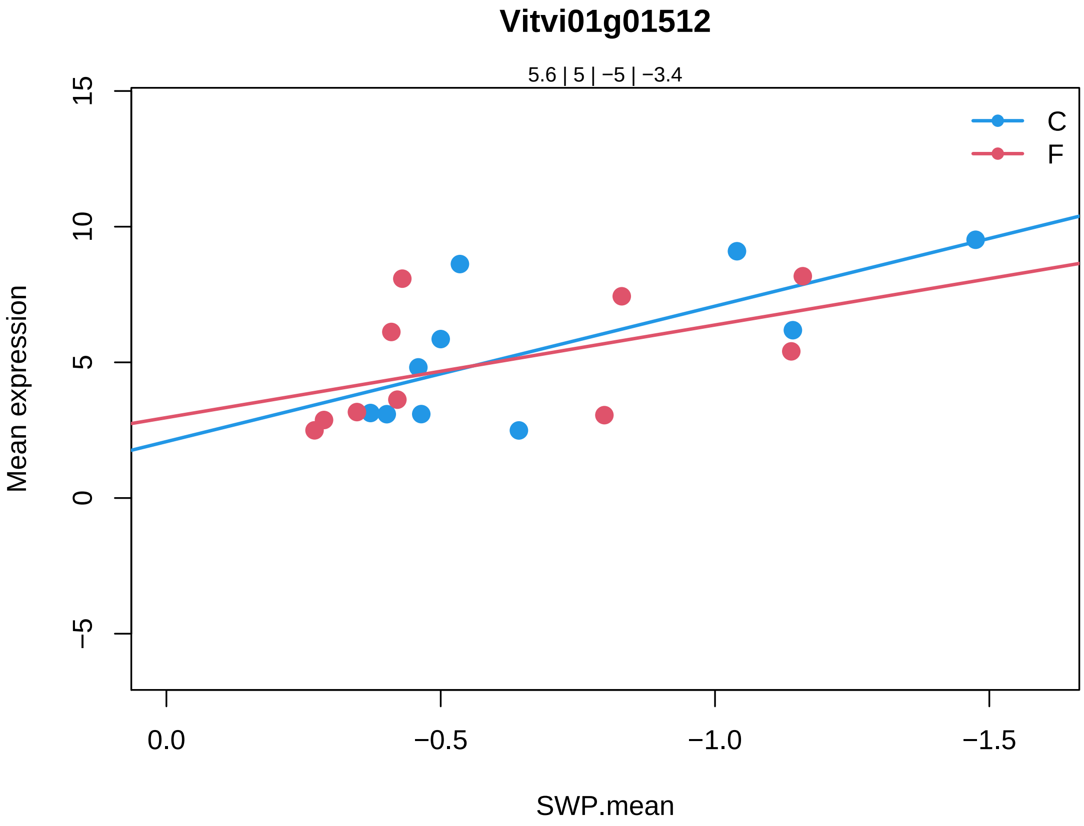
6.3.20 Vitvi01g01512

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

```
Vitvi01g01512
        20.02.2001
        stress.abiotic.heat
        heat shock protein 21 |
        Chr4:13819048-13819895 REVERSE LENGTH=227 |
        201606
```

Coefficients for Vitvi01g01512.

```
                    swp  varietyF swp.varietyF AveExpr       F
Vitvi01g01512 -4.991872 0.8836259     1.577612 5.31657 4.73663
                 P.Value  adj.P.Val  type
Vitvi01g01512 0.01098786 0.08910762 type2
```



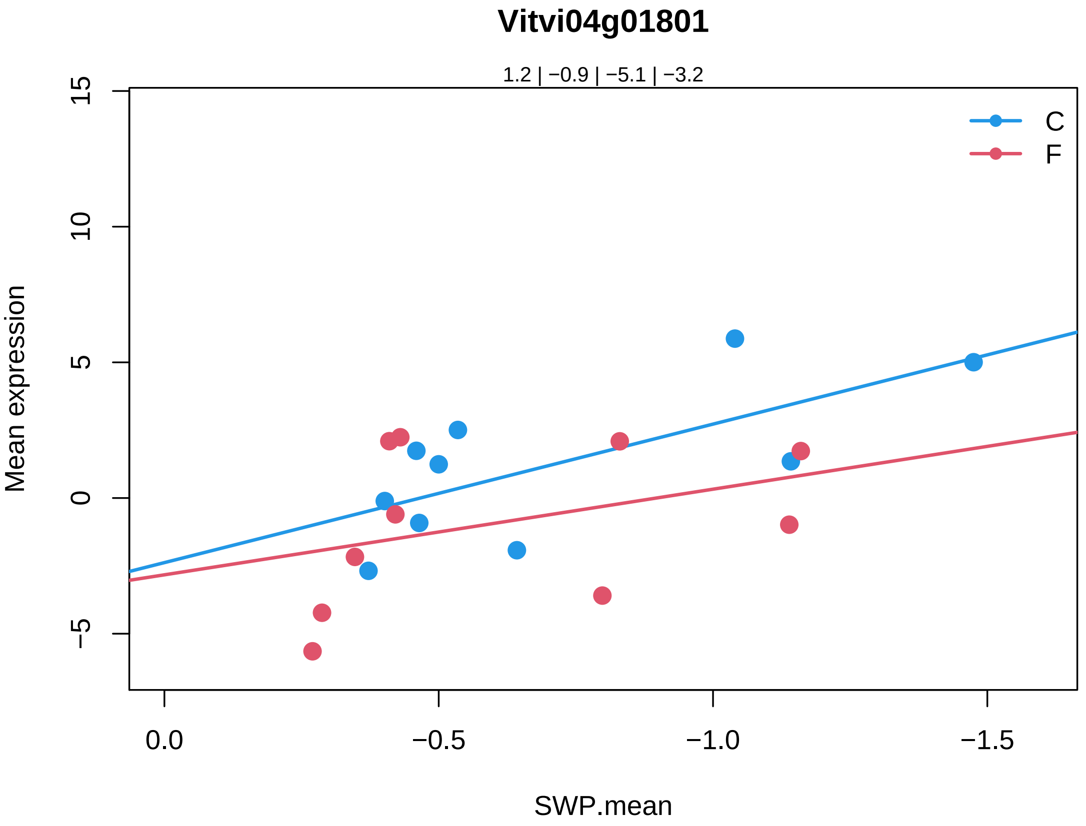
6.3.21 Vitvi04g01801

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

```
Vitvi04g01801
        20.02.2001
        stress.abiotic.heat
        17.6 kDa class II heat shock protein |
        Chr5:3882409-3882876 REVERSE LENGTH=155 |
        201606
```

Coefficients for Vitvi04g01801.

```
                    swp   varietyF swp.varietyF   AveExpr        F
Vitvi04g01801 -5.104125 -0.4493229     1.948595 0.1506614 4.590001
                 P.Value   adj.P.Val  type
Vitvi04g01801 0.01245505 0.09712467 type4
```



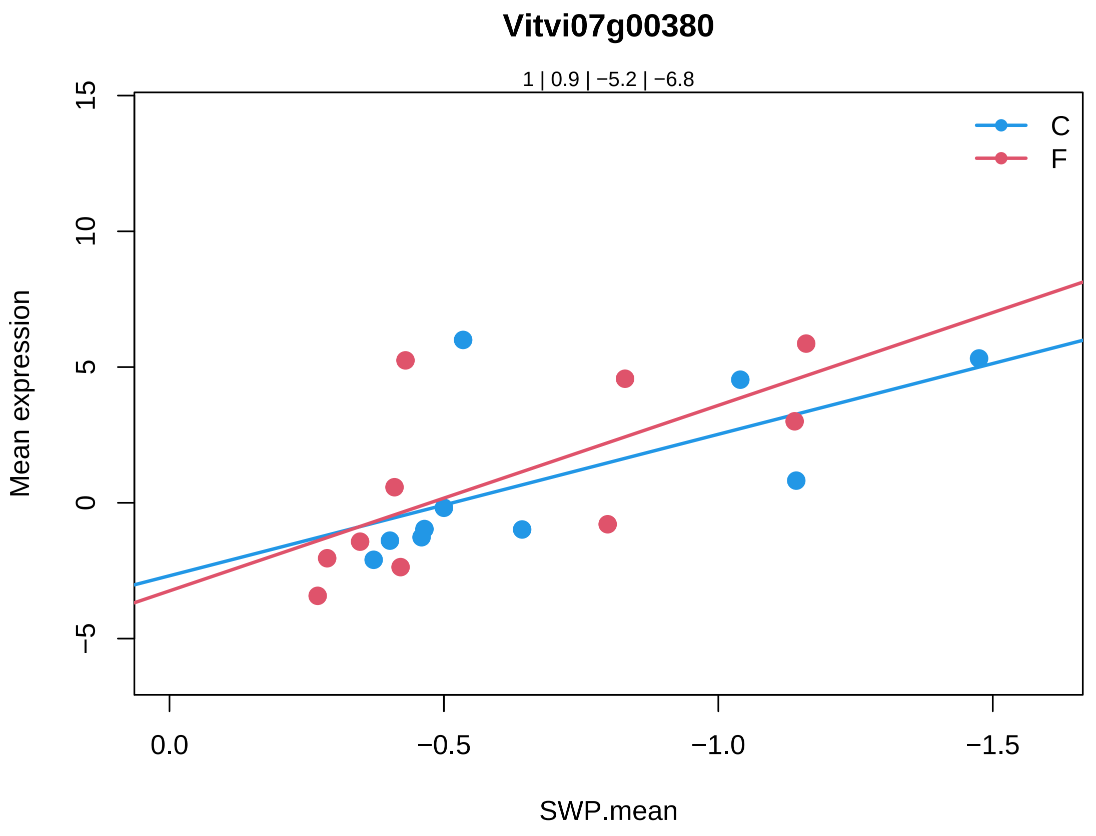
6.3.22 Vitvi07g00380

```
> 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.

```
                    swp   varietyF swp.varietyF   AveExpr        F
Vitvi07g00380 -5.210794 -0.5569416    -1.622591 0.9492202 5.493403
                  P.Value  adj.P.Val  type
Vitvi07g00380 0.005874058 0.05761415 type2
```



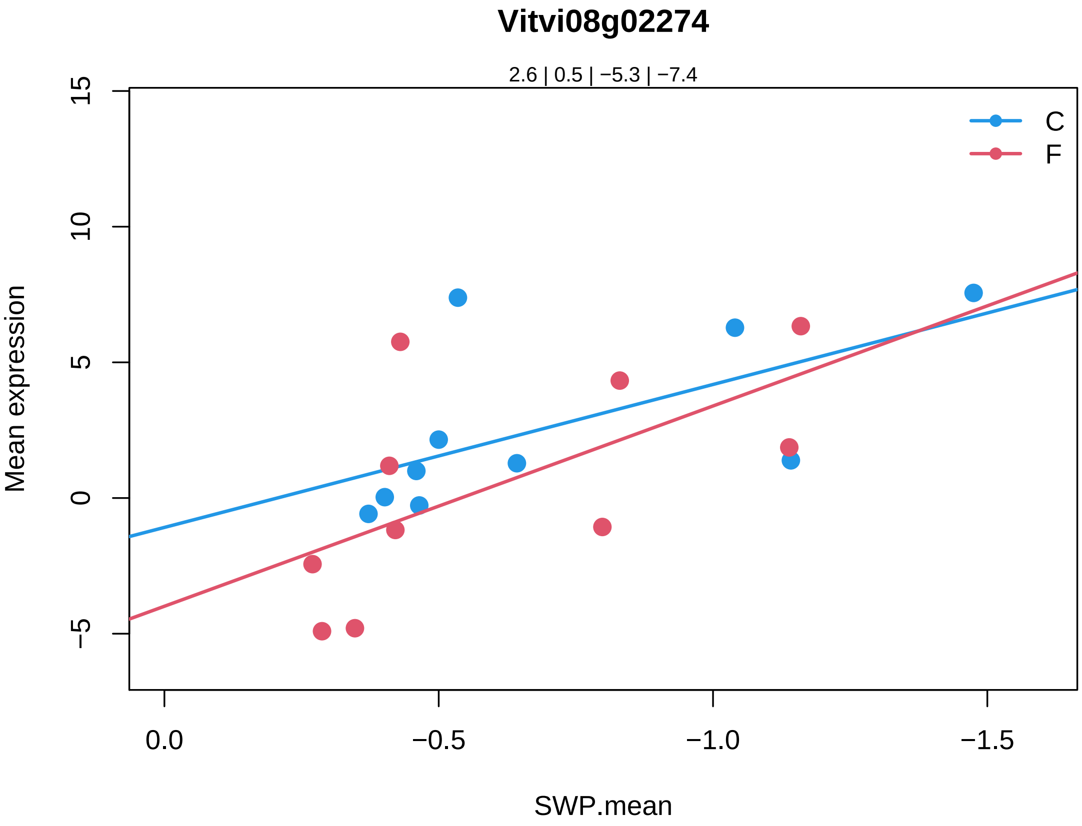
6.3.23 Vitvi08g02274

```
> 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.

```
                    swp   varietyF swp.varietyF  AveExpr        F
Vitvi08g02274 -5.267913 -2.905845    -2.113051 1.564665 5.555981
                  P.Value  adj.P.Val  type
Vitvi08g02274 0.005585942 0.05564767 type4
```



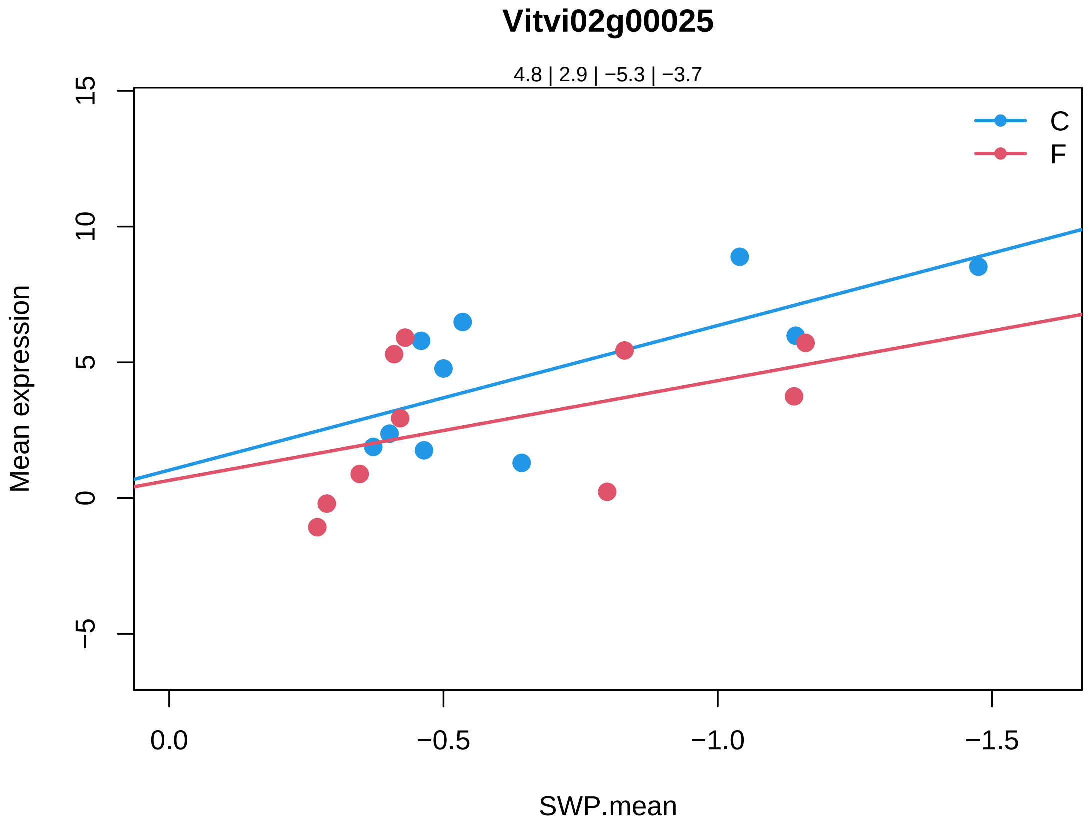
6.3.24 Vitvi02g00025

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

```
Vitvi02g00025
        20.02.2001
        stress.abiotic.heat
        heat shock-like protein |
        Chr5:21352557-21355147 FORWARD LENGTH=700 |
        201606
```

Coefficients for Vitvi02g00025.

```
                    swp    varietyF swp.varietyF  AveExpr        F
Vitvi02g00025 -5.328021 -0.3770194     1.655038 3.832428 5.557562
                  P.Value  adj.P.Val  type
Vitvi02g00025 0.005578862 0.05561349 type2
```



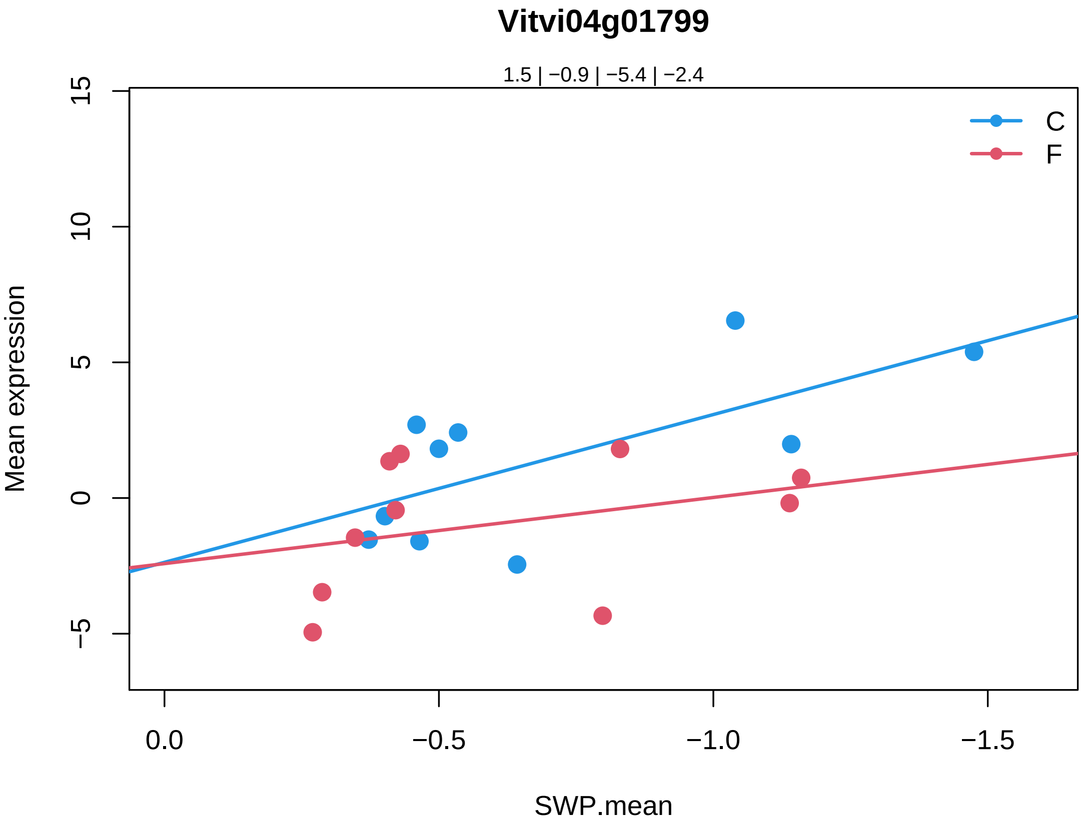
6.3.25 Vitvi04g01799

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

```
Vitvi04g01799
        20.02.2001
        stress.abiotic.heat
        17.6 kDa class II heat shock protein |
        Chr5:3882409-3882876 REVERSE LENGTH=155 |
        201606
```

Coefficients for Vitvi04g01799.

```
                    swp    varietyF swp.varietyF   AveExpr         F
Vitvi04g01799 -5.446372 -0.04695522     3.008905 0.2639579 5.443978
                  P.Value   adj.P.Val  type
Vitvi04g01799 0.006113039 0.05915869 type4
```



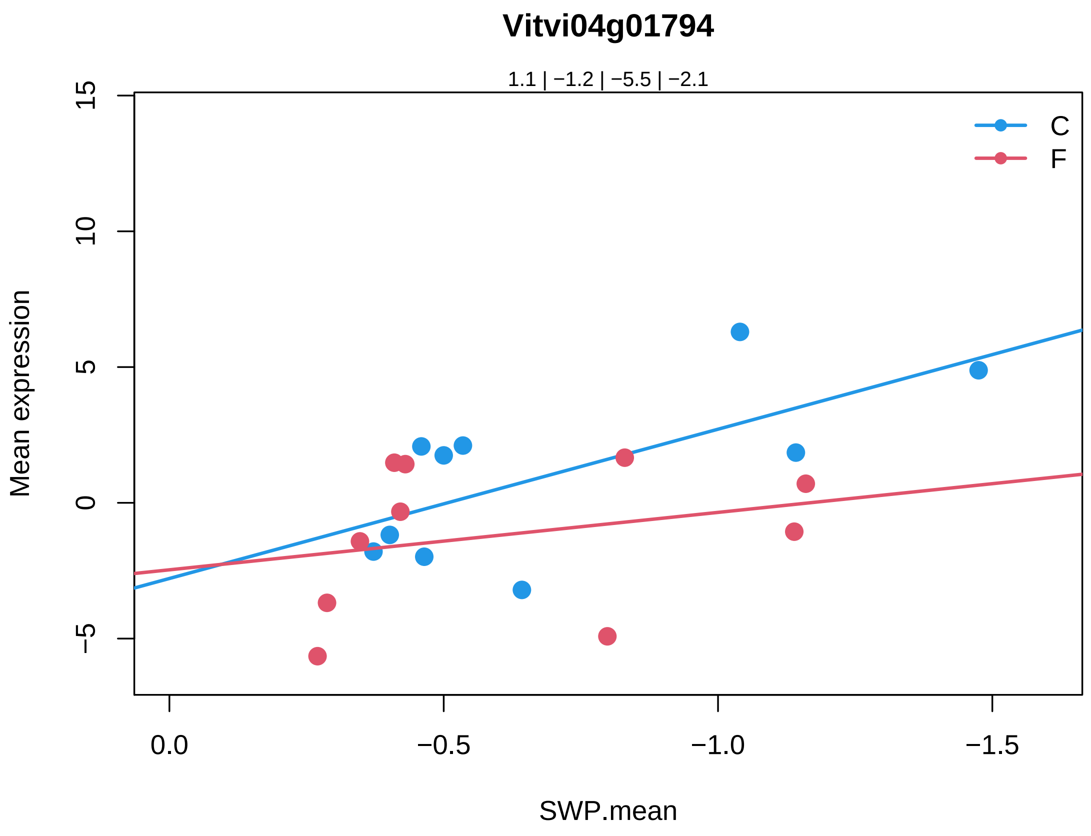
6.3.26 Vitvi04g01794

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

```
Vitvi04g01794
        20.02.2001
        stress.abiotic.heat
        17.6 kDa class II heat shock protein |
        Chr5:3882409-3882876 REVERSE LENGTH=155 |
        201606
```

Coefficients for Vitvi04g01794.

```
                    swp  varietyF swp.varietyF     AveExpr        F
Vitvi04g01794 -5.497568 0.3190796     3.382727 -0.04996061 4.507491
               P.Value adj.P.Val  type
Vitvi04g01794 0.0133731 0.1020184 type4
```



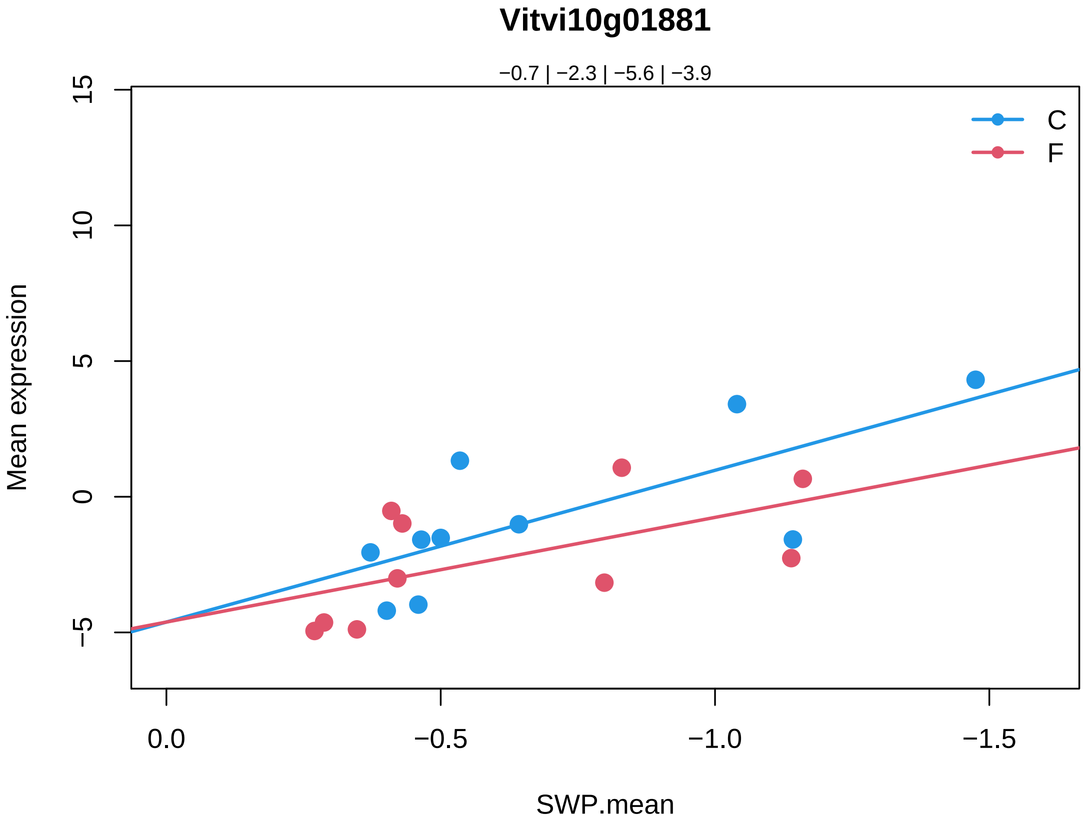
6.3.27 Vitvi10g01881

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

```
Vitvi10g01881
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi10g01881.

```
                    swp      varietyF swp.varietyF   AveExpr      F
Vitvi10g01881 -5.591522 -0.0006302969     1.734231 -1.477062 7.7086
                  P.Value  adj.P.Val  type
Vitvi10g01881 0.001120647 0.01620937 type2
```



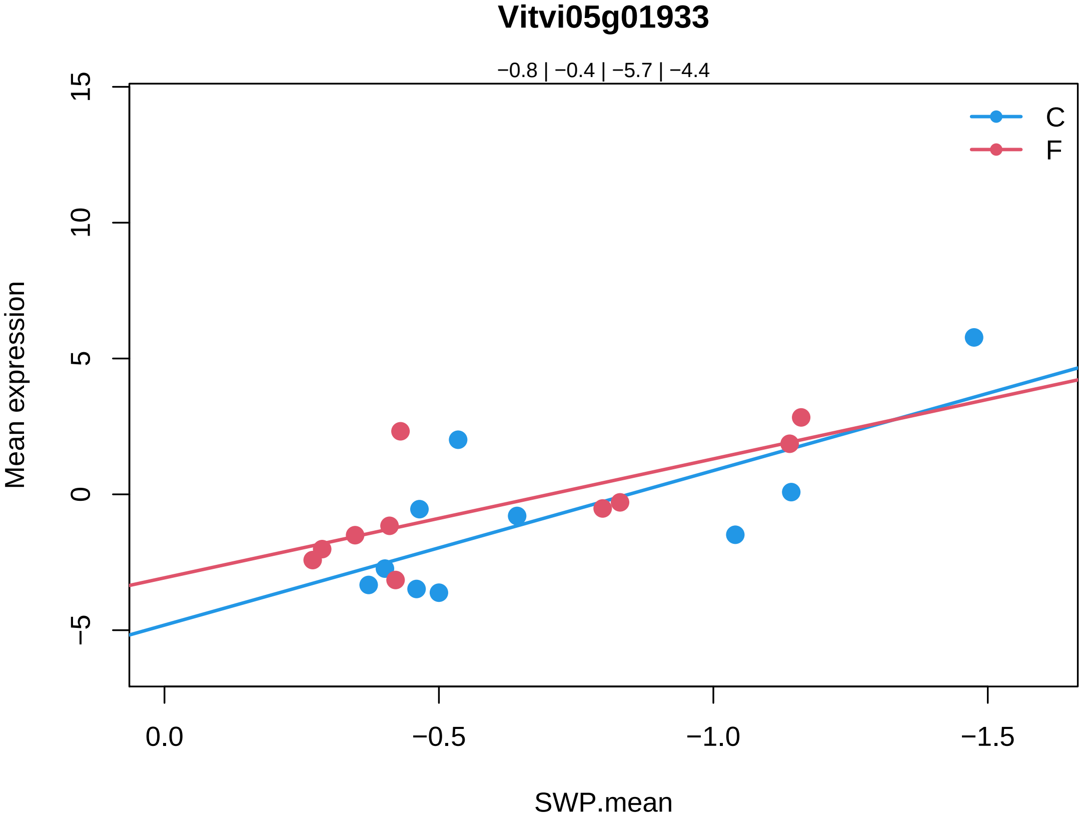
6.3.28 Vitvi05g01933

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

```
Vitvi05g01933
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi05g01933.

```
                    swp varietyF swp.varietyF    AveExpr       F
Vitvi05g01933 -5.687122 1.739405     1.308549 -0.6087925 8.04602
                   P.Value   adj.P.Val  type
Vitvi05g01933 0.0008885332 0.01346225 type2
```



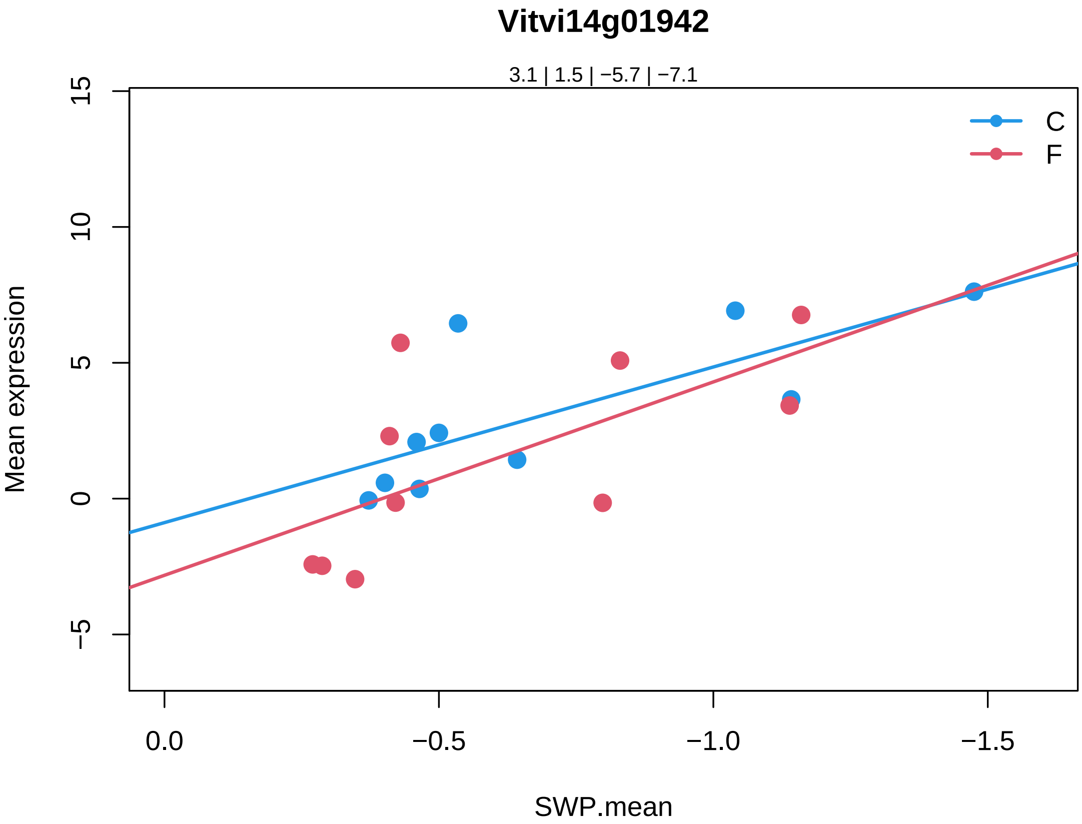
6.3.29 Vitvi14g01942

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

```
Vitvi14g01942
        29.05.2007
        protein.degradation.metalloprotease
        FTSH protease 6 |
        Chr5:4951071-4952777 REVERSE LENGTH=514 |
        201606
```

Coefficients for Vitvi14g01942.

```
                    swp  varietyF swp.varietyF  AveExpr        F
Vitvi14g01942 -5.728533 -1.938914    -1.388999 2.329706 7.906843
                  P.Value  adj.P.Val  type
Vitvi14g01942 0.000977222 0.01457419 type2
```



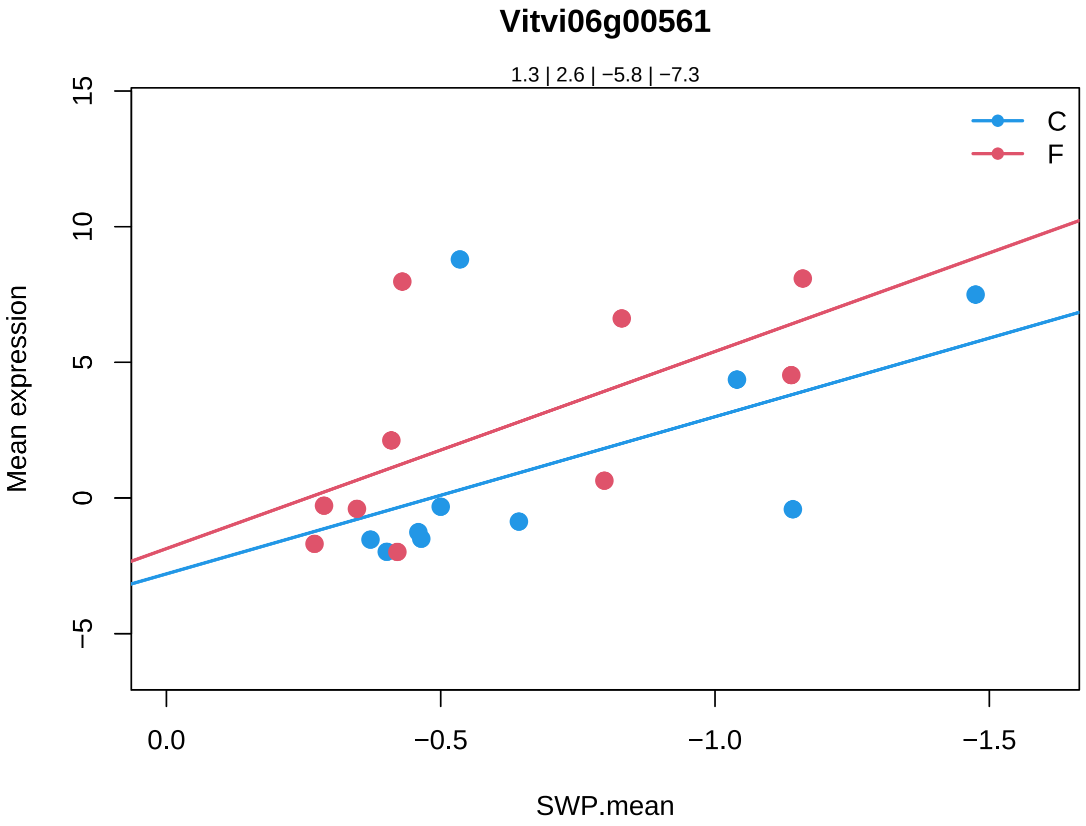
6.3.30 Vitvi06g00561

```
> 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.

```
                    swp  varietyF swp.varietyF AveExpr        F
Vitvi06g00561 -5.792331 0.9305757     -1.47236 1.91967 4.075053
                 P.Value adj.P.Val  type
Vitvi06g00561 0.01955248 0.1331036 type2
```



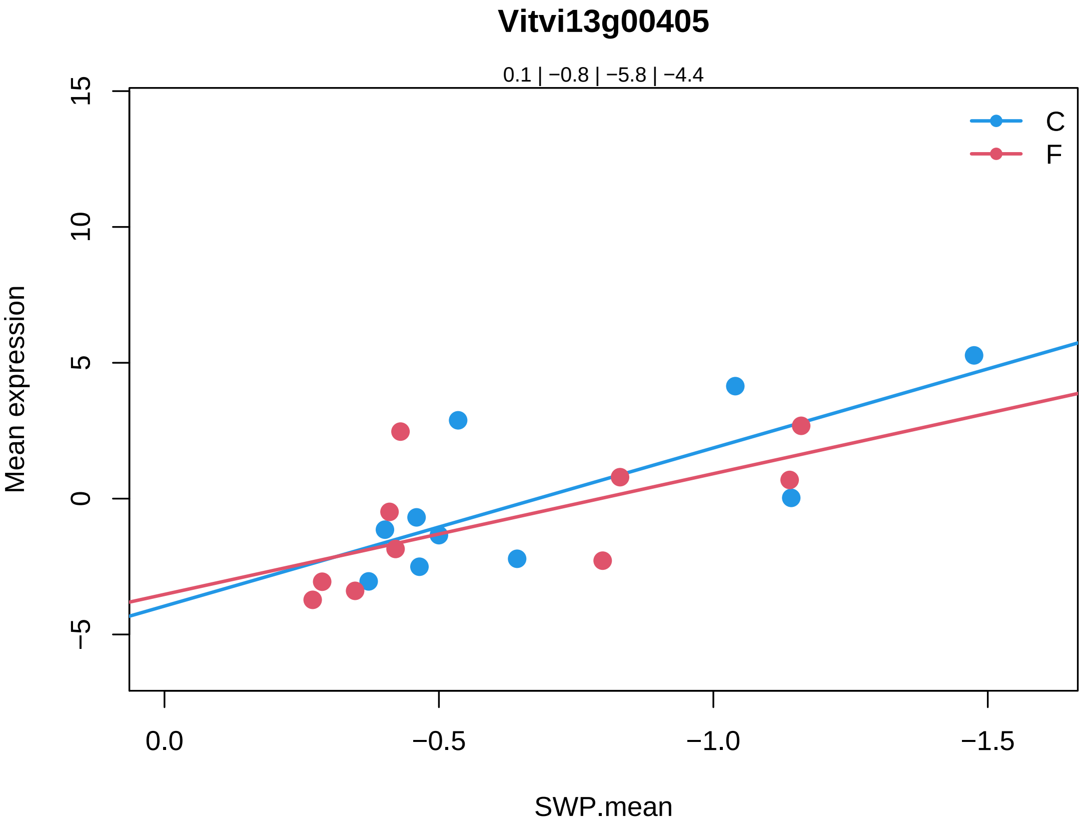
6.3.31 Vitvi13g00405

```
> 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.

```
                    swp  varietyF swp.varietyF    AveExpr        F
Vitvi13g00405 -5.819808 0.4292331     1.375953 -0.3398512 7.623451
                  P.Value  adj.P.Val  type
Vitvi13g00405 0.001189165 0.01689212 type2
```



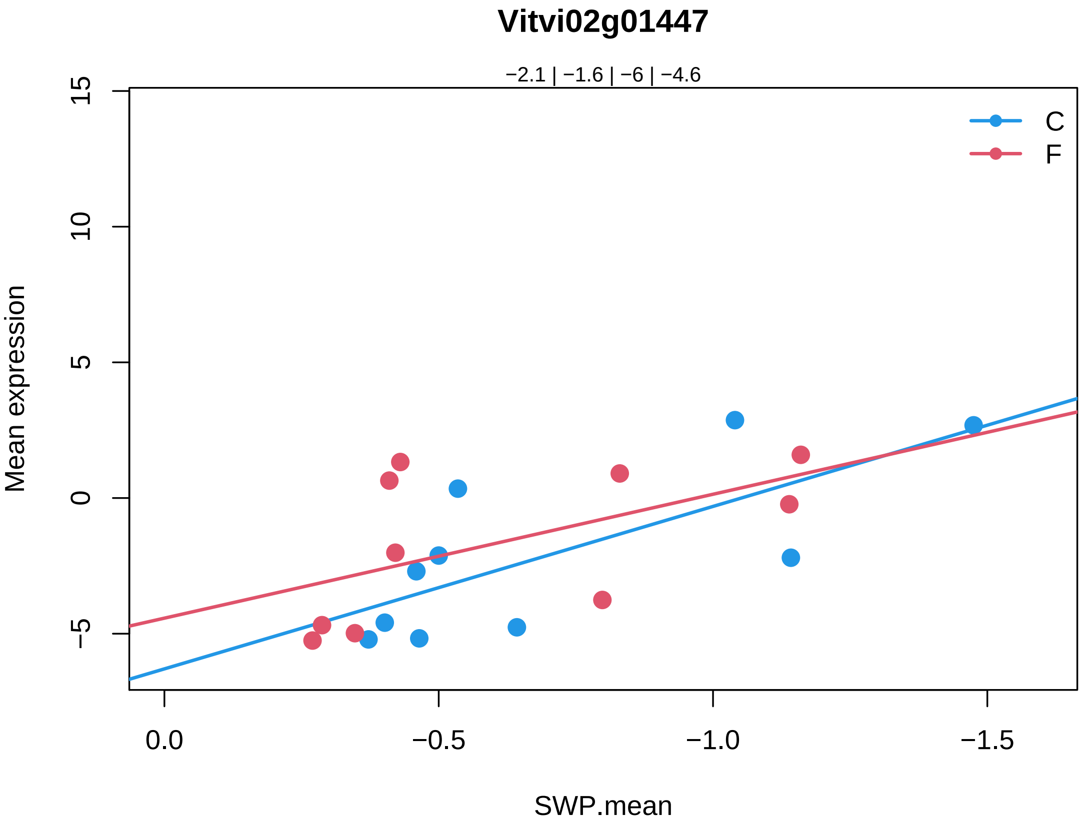
6.3.32 Vitvi02g01447

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

```
Vitvi02g01447
        20.02.2001
        stress.abiotic.heat
        mitochondrion-localized small heat shock protein 23.6 |
        Chr4:12917089-12917858 FORWARD LENGTH=210 |
        201606
```

Coefficients for Vitvi02g01447.

```
                    swp varietyF swp.varietyF  AveExpr        F
Vitvi02g01447 -5.987309 1.869091      1.42107 -1.86587 5.503785
                  P.Value  adj.P.Val  type
Vitvi02g01447 0.005825159 0.05727263 type2
```



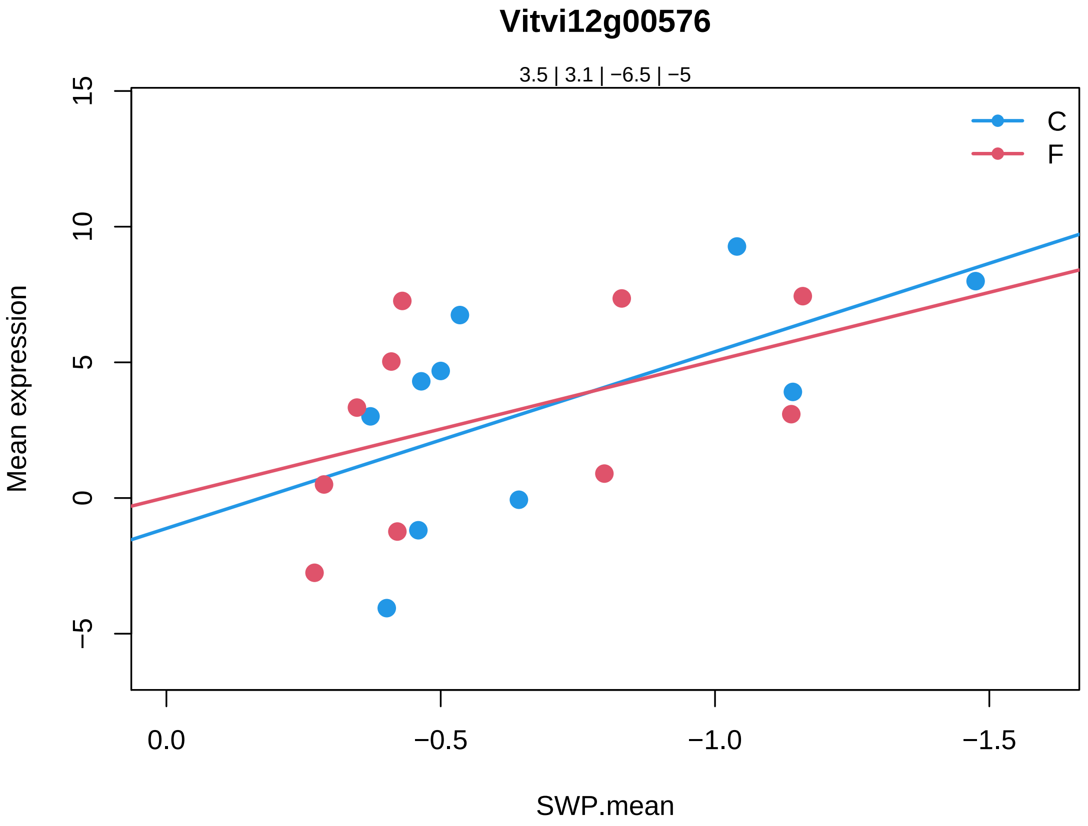
6.3.33 Vitvi12g00576

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

```
Vitvi12g00576
        35.2
        not assigned.unknown
        Terpenoid cyclases/Protein prenyltransferases superfamily protein |
        Chr3:9430805-9433844 FORWARD LENGTH=598 |
        201606
```

Coefficients for Vitvi12g00576.

```
                    swp varietyF swp.varietyF  AveExpr        F
Vitvi12g00576 -6.513191 1.142324     1.475287 3.275887 2.940355
                P.Value adj.P.Val  type
Vitvi12g00576 0.0562246 0.2607959 type2
```



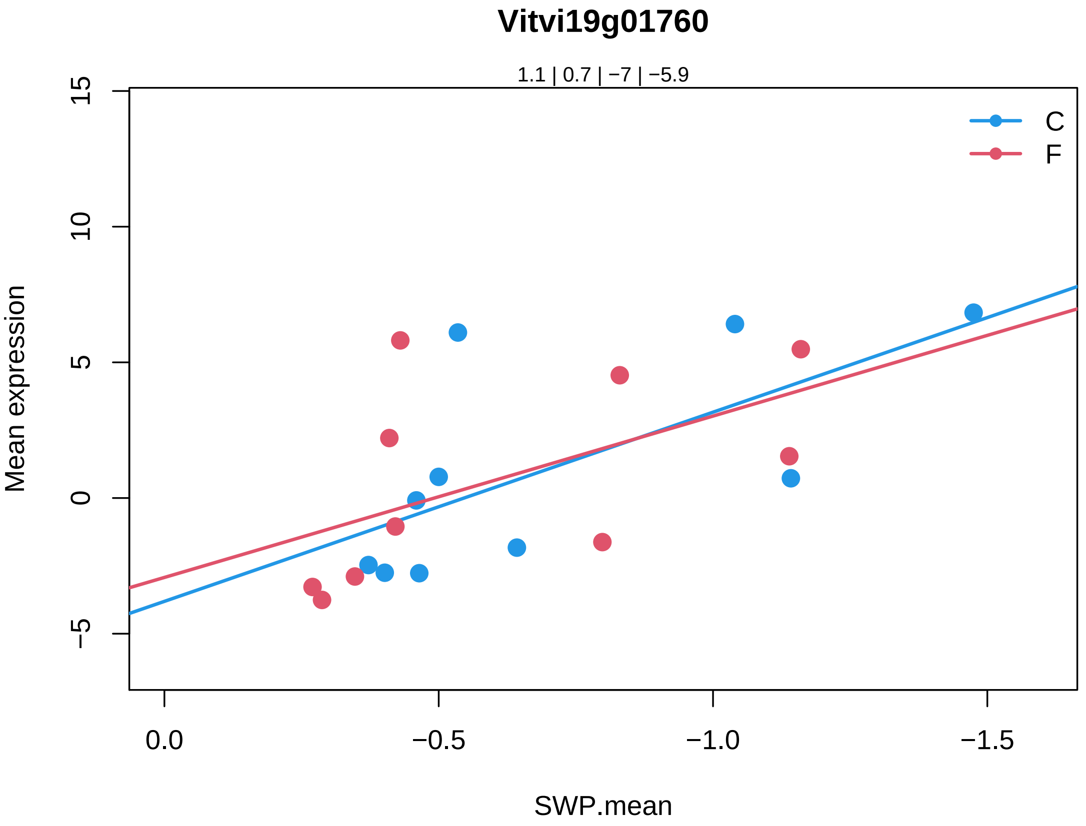
6.3.34 Vitvi19g01760

```
> 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.

```
                    swp  varietyF swp.varietyF   AveExpr        F
Vitvi19g01760 -6.972297 0.8819644     1.024981 0.8952506 4.426955
                 P.Value adj.P.Val  type
Vitvi19g01760 0.01434035 0.1074082 type2
```



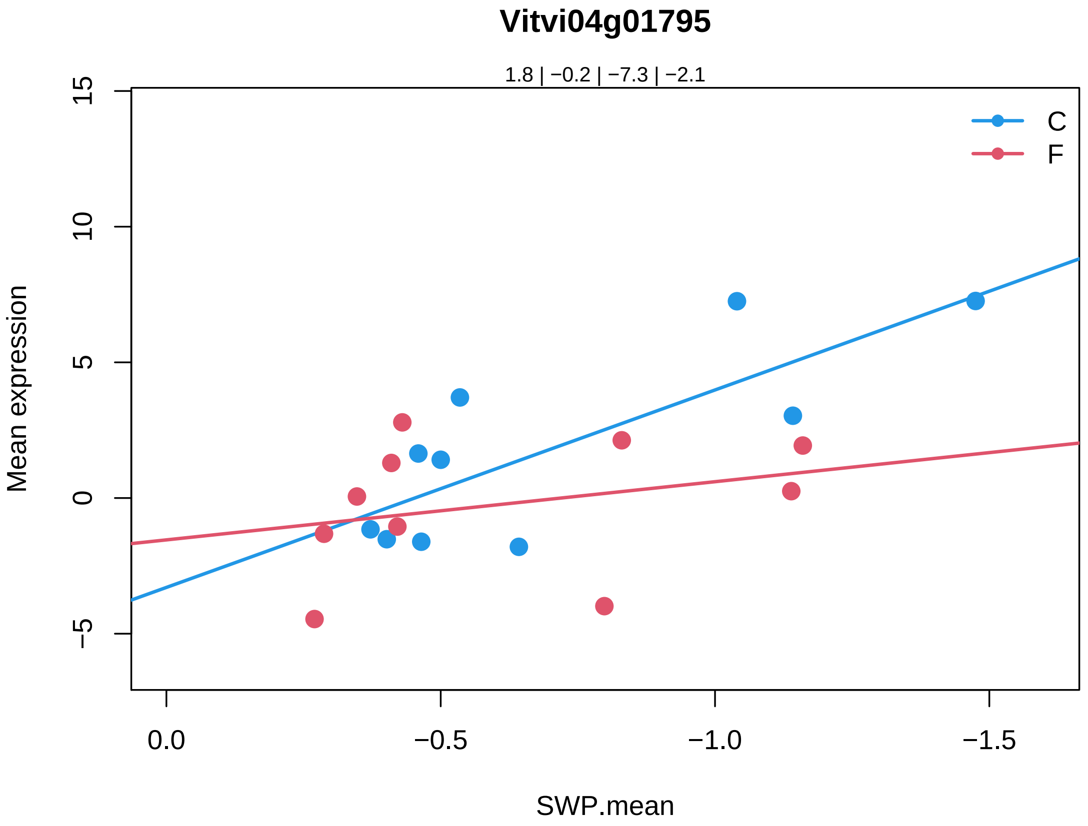
6.3.35 Vitvi04g01795

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

```
Vitvi04g01795
        35.2
        not assigned.unknown
        17.6 kDa class II heat shock protein |
        Chr5:3882409-3882876 REVERSE LENGTH=155 |
        201606
```

Coefficients for Vitvi04g01795.

```
                    swp varietyF swp.varietyF   AveExpr        F
Vitvi04g01795 -7.277261 1.752825     5.133591 0.7928205 7.258489
                  P.Value  adj.P.Val  type
Vitvi04g01795 0.001539206 0.02077996 type4
```



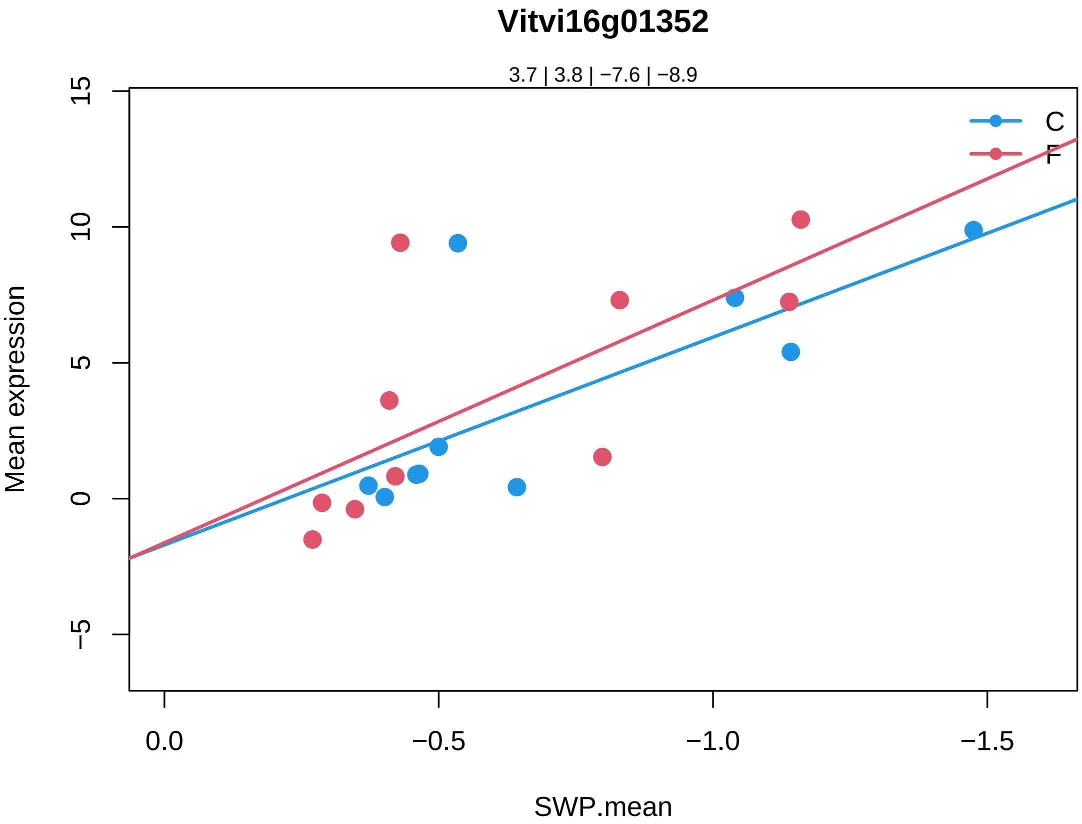
6.3.36 Vitvi16g01352

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

```
Vitvi16g01352
        20.02.2001
        stress.abiotic.heat
        heat shock protein 21 |
        Chr4:13819048-13819895 REVERSE LENGTH=227 |
        201606
```

Coefficients for Vitvi16g01352.

```
                    swp   varietyF swp.varietyF  AveExpr        F
Vitvi16g01352 -7.649088 0.07899212    -1.282333 3.744213 7.426517
                  P.Value adj.P.Val  type
Vitvi16g01352 0.001365788 0.0188222 type2
```



6.4 type3

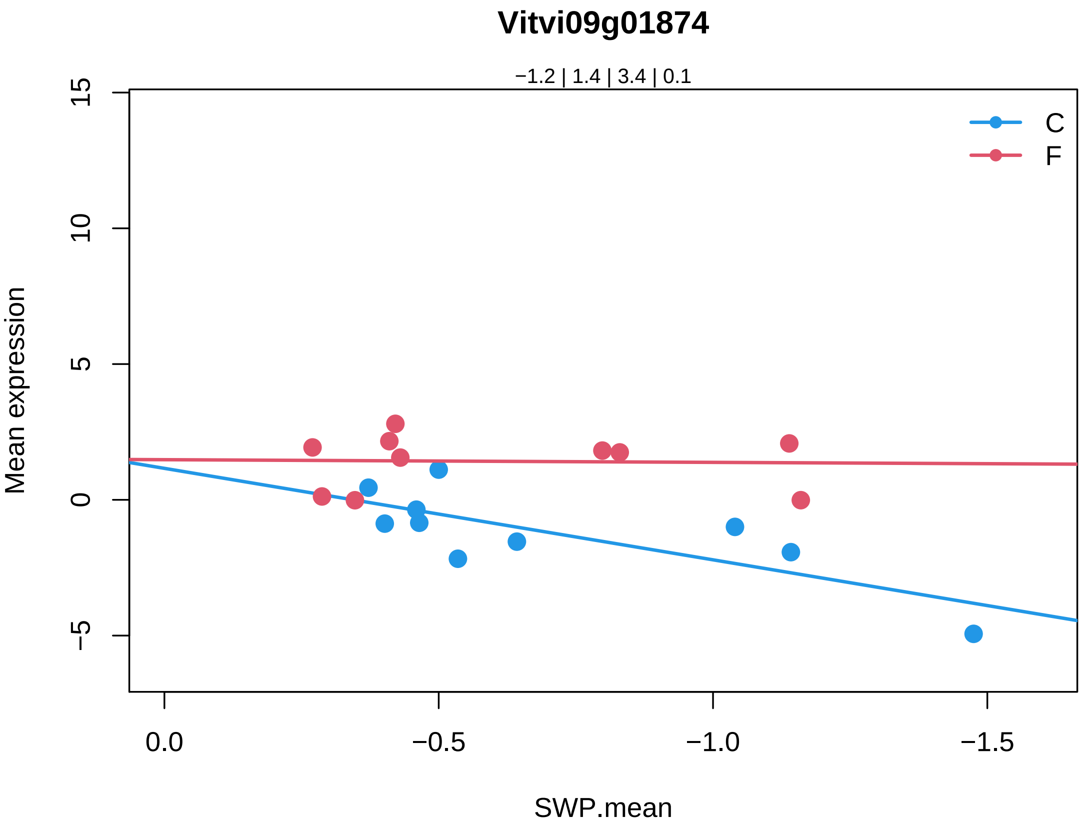
6.4.1 Vitvi09g01874

```
> 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.

```
                   swp  varietyF swp.varietyF   AveExpr        F
Vitvi09g01874 3.369133 0.3187773    -3.270373 0.1041741 17.21374
                   P.Value    adj.P.Val  type
Vitvi09g01874 6.380859e-06 0.0002114284 type4
```



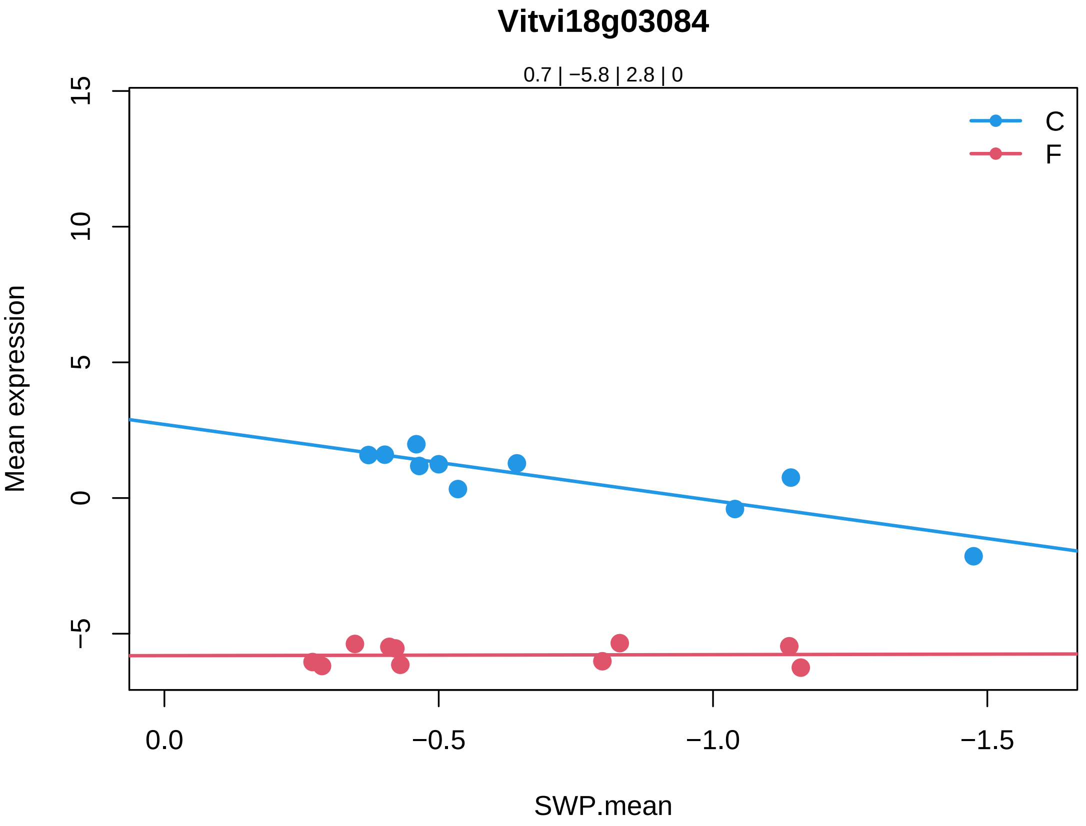
6.4.2 Vitvi18g03084

```
> 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.

```
                   swp  varietyF swp.varietyF   AveExpr        F
Vitvi18g03084 2.801771 -8.518865    -2.838533 -2.523183 268.4567
                   P.Value    adj.P.Val  type
Vitvi18g03084 3.731676e-17 9.443009e-15 type3
```



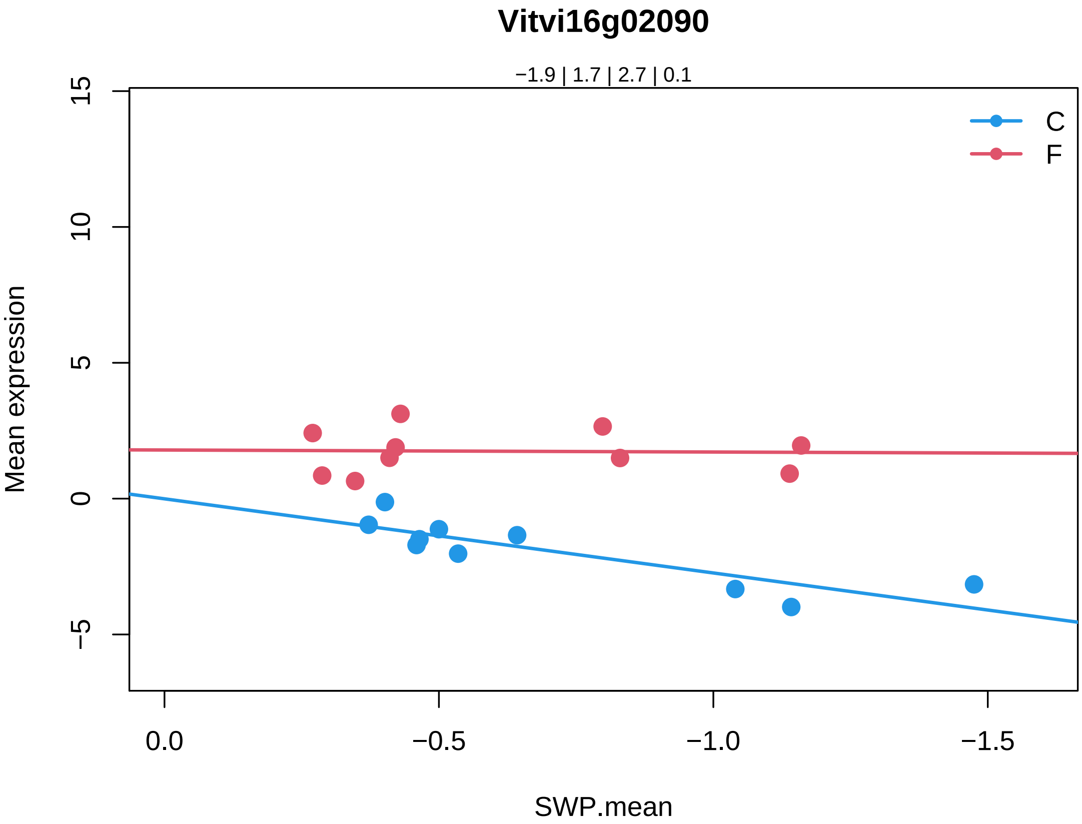
6.4.3 Vitvi16g02090

```
> 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.

```
                   swp varietyF swp.varietyF    AveExpr        F
Vitvi16g02090 2.729033 1.796787    -2.654757 -0.0909231 50.77959
                   P.Value    adj.P.Val  type
Vitvi16g02090 6.511182e-10 4.725878e-08 type4
```



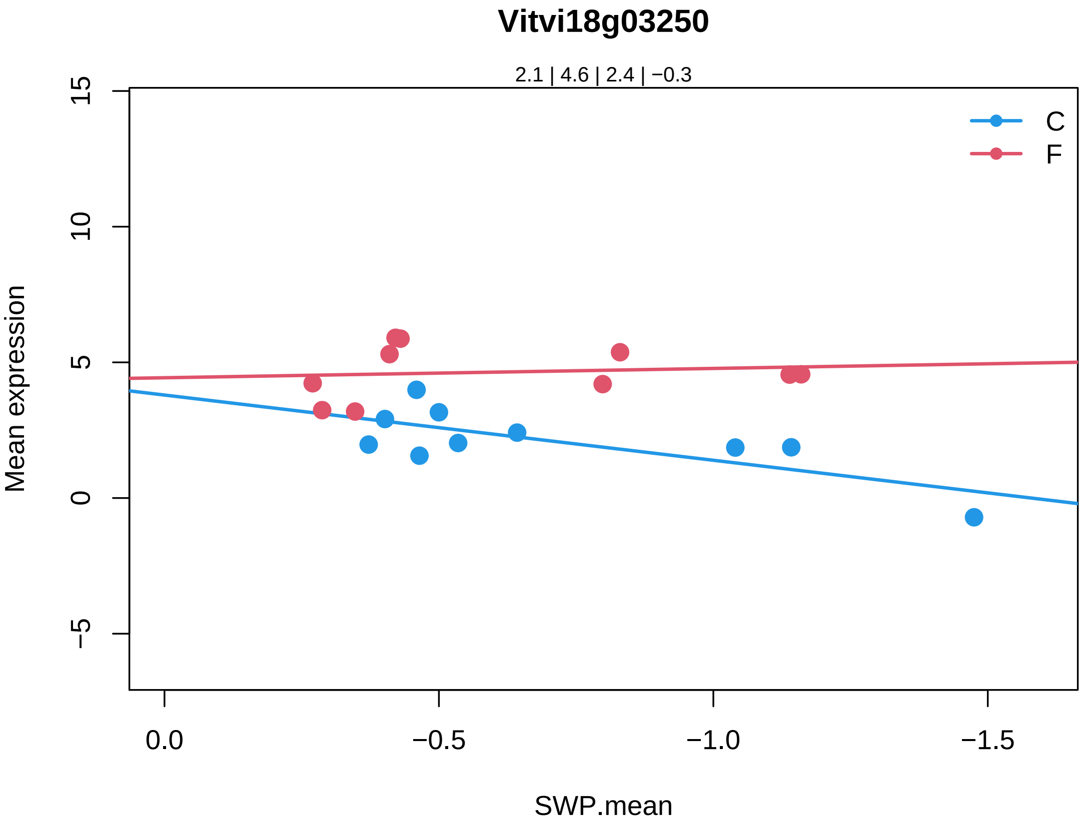
6.4.4 Vitvi18g03250

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

```
Vitvi18g03250
        26.1
        misc.cytochrome P450
        cytochrome P450%2C family 714%2C subfamily A%2C polypeptide 1 |
        Chr5:8567674-8570260 REVERSE LENGTH=532 |
        201606
```

Coefficients for Vitvi18g03250.

```
                   swp  varietyF swp.varietyF AveExpr        F
Vitvi18g03250 2.403889 0.6372638    -2.746937  3.3731 17.73114
                   P.Value    adj.P.Val  type
Vitvi18g03250 5.113021e-06 0.0001735694 type3
```



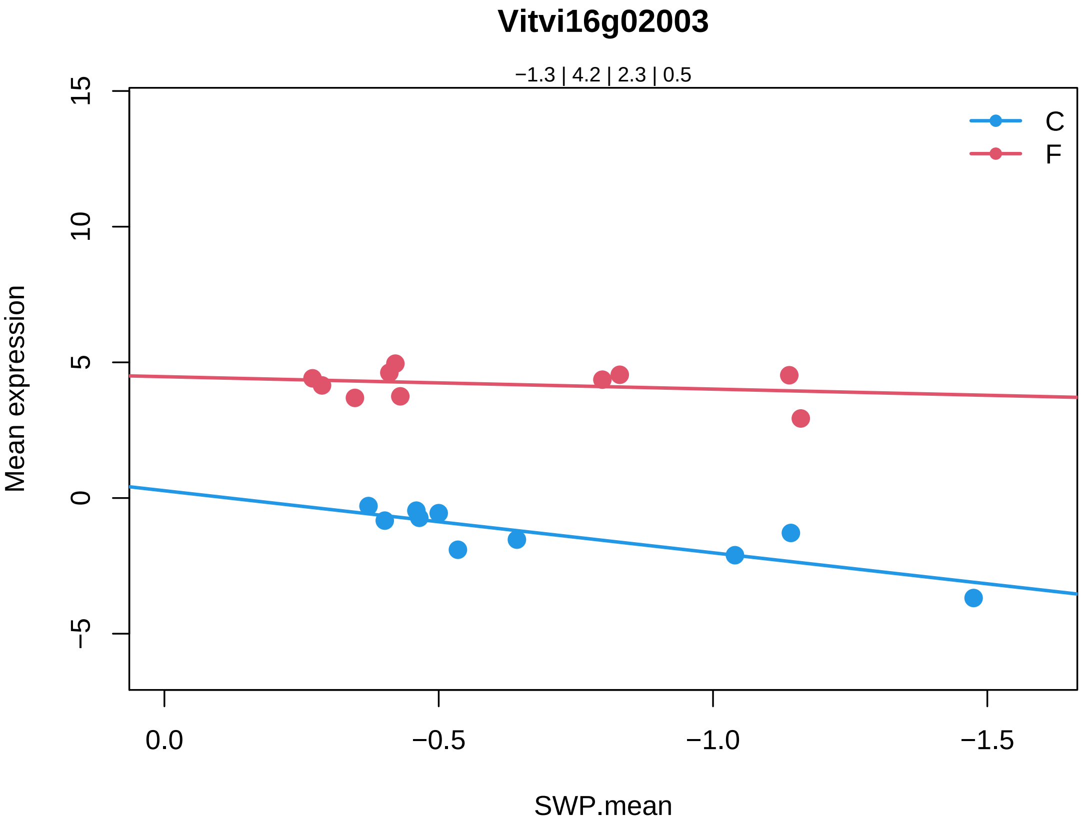
6.4.5 Vitvi16g02003

```
> 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.

```
                 swp varietyF swp.varietyF  AveExpr        F
Vitvi16g02003 2.2875 4.203023    -1.830222 1.426501 163.8027
                   P.Value    adj.P.Val  type
Vitvi16g02003 6.199962e-15 1.016127e-12 type4
```



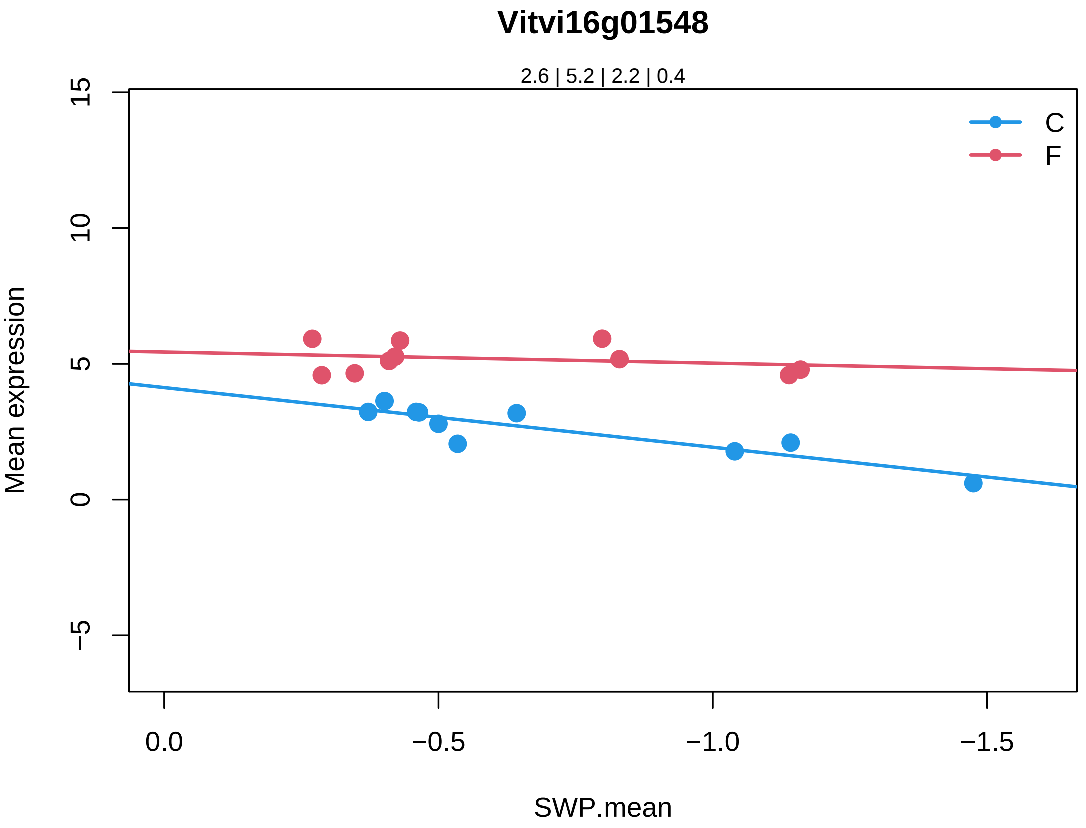
6.4.6 Vitvi16g01548

```
> 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.

```
                   swp varietyF swp.varietyF  AveExpr        F
Vitvi16g01548 2.196869 1.308994    -1.787469 3.882578 53.13999
                   P.Value    adj.P.Val  type
Vitvi16g01548 4.253783e-10 3.147386e-08 type4
```



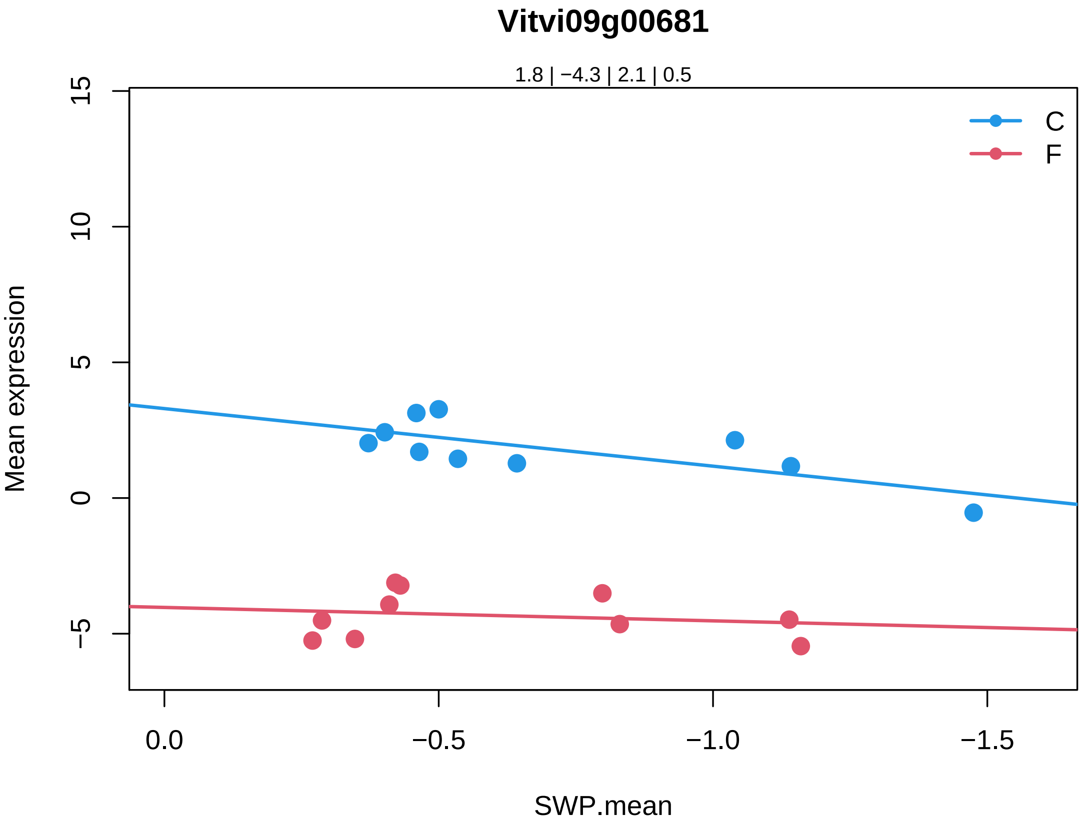
6.4.7 Vitvi09g00681

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

```
Vitvi09g00681
        20.01.2002
        stress.biotic.receptors
        receptor like protein 1 |
        Chr1:2270633-2274654 FORWARD LENGTH=913 |
        201606
```

Coefficients for Vitvi09g00681.

```
                   swp  varietyF swp.varietyF   AveExpr        F
Vitvi09g00681 2.121009 -7.326997    -1.626761 -1.264715 110.8171
                  P.Value    adj.P.Val  type
Vitvi09g00681 3.27978e-13 4.031484e-11 type4
```



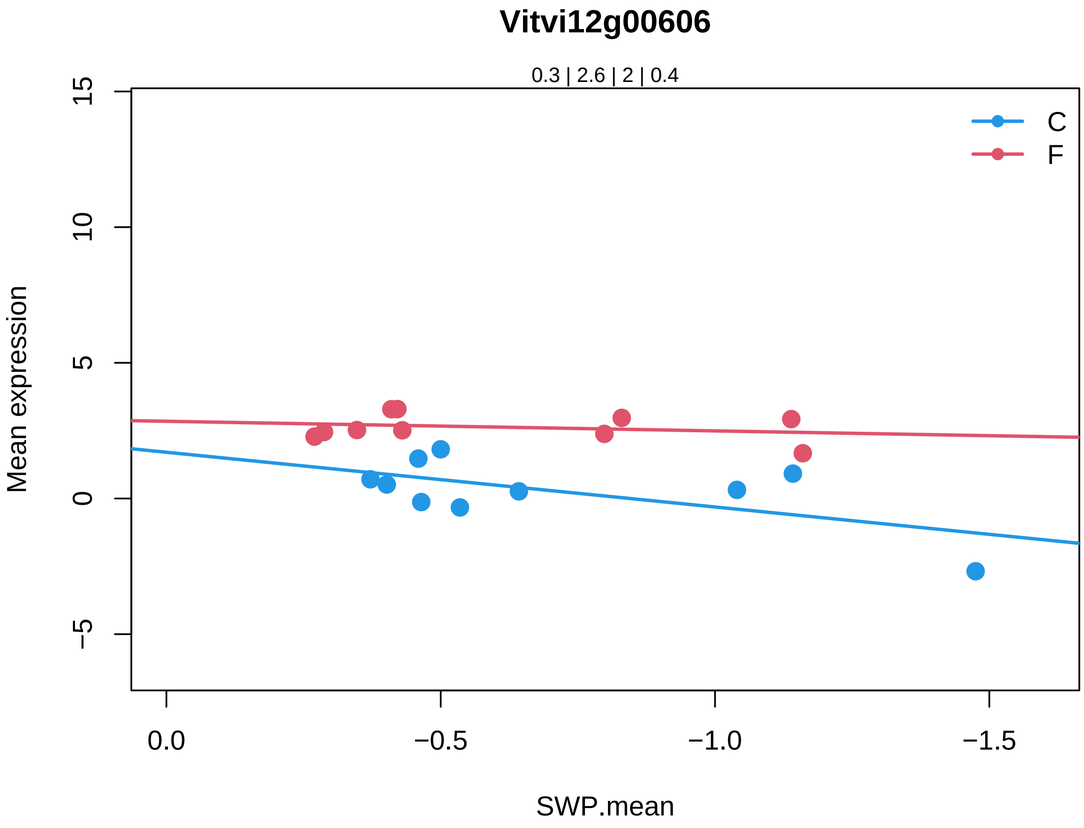
6.4.8 Vitvi12g00606

```
> 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.

```
                   swp varietyF swp.varietyF  AveExpr        F
Vitvi12g00606 2.016467 1.140932    -1.662881 1.457987 19.74785
                   P.Value    adj.P.Val  type
Vitvi12g00606 2.246443e-06 8.290625e-05 type4
```



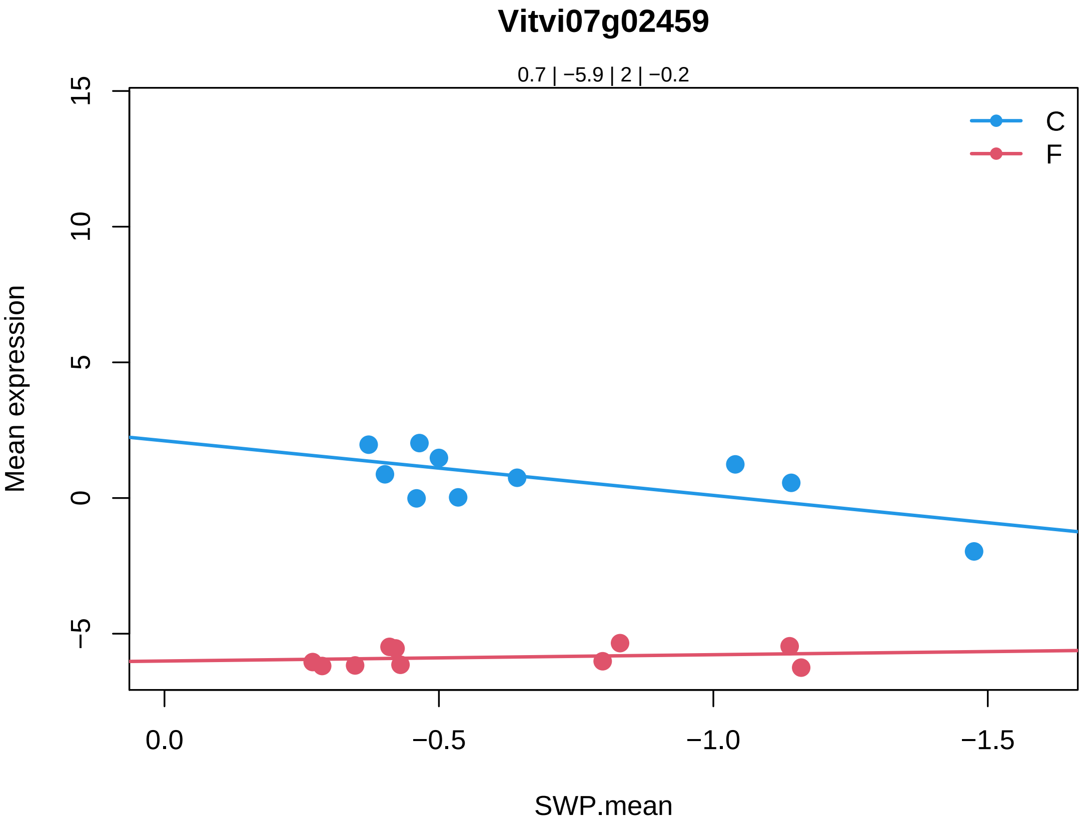
6.4.9 Vitvi07g02459

```
> 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.

```
                   swp  varietyF swp.varietyF   AveExpr      F
Vitvi07g02459 2.012497 -8.115418    -2.244575 -2.586153 164.65
                   P.Value    adj.P.Val  type
Vitvi07g02459 5.880473e-15 9.742409e-13 type3
```



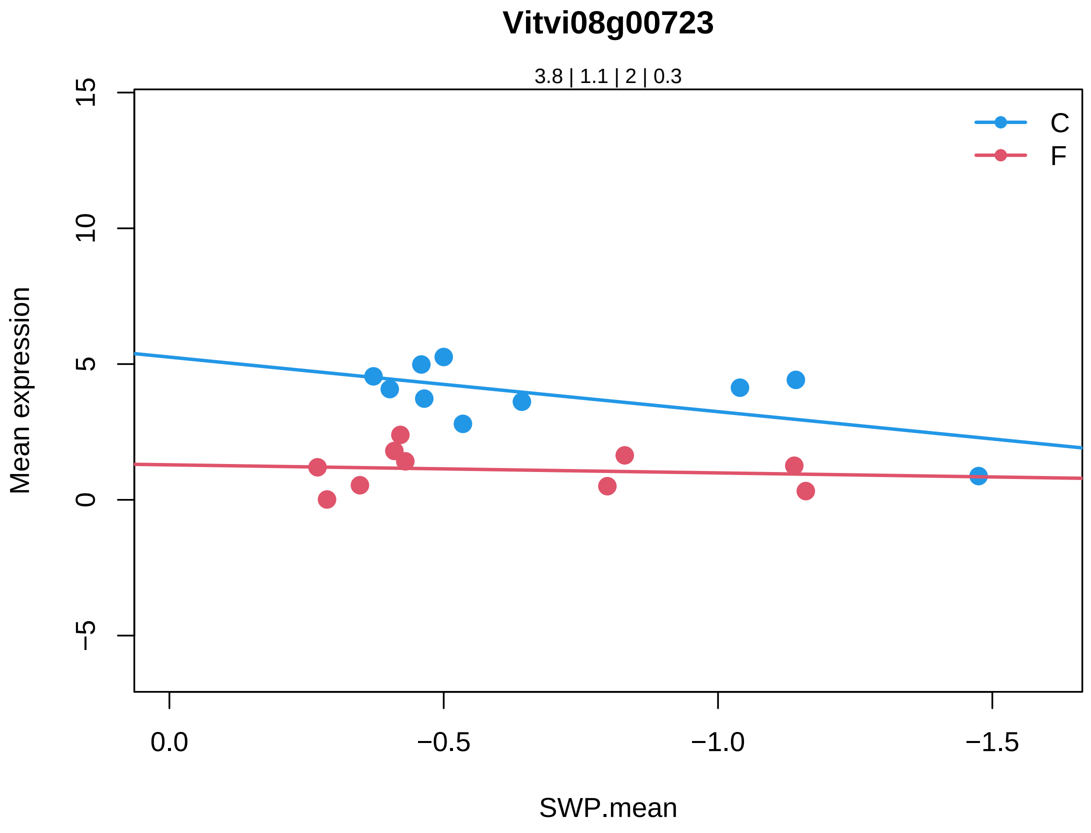
6.4.10 Vitvi08g00723

```
> 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.

```
                   swp   varietyF swp.varietyF AveExpr        F
Vitvi08g00723 2.009066 -3.967297    -1.711553 2.47519 19.98487
                   P.Value    adj.P.Val  type
Vitvi08g00723 2.047632e-06 7.63081e-05 type4
```



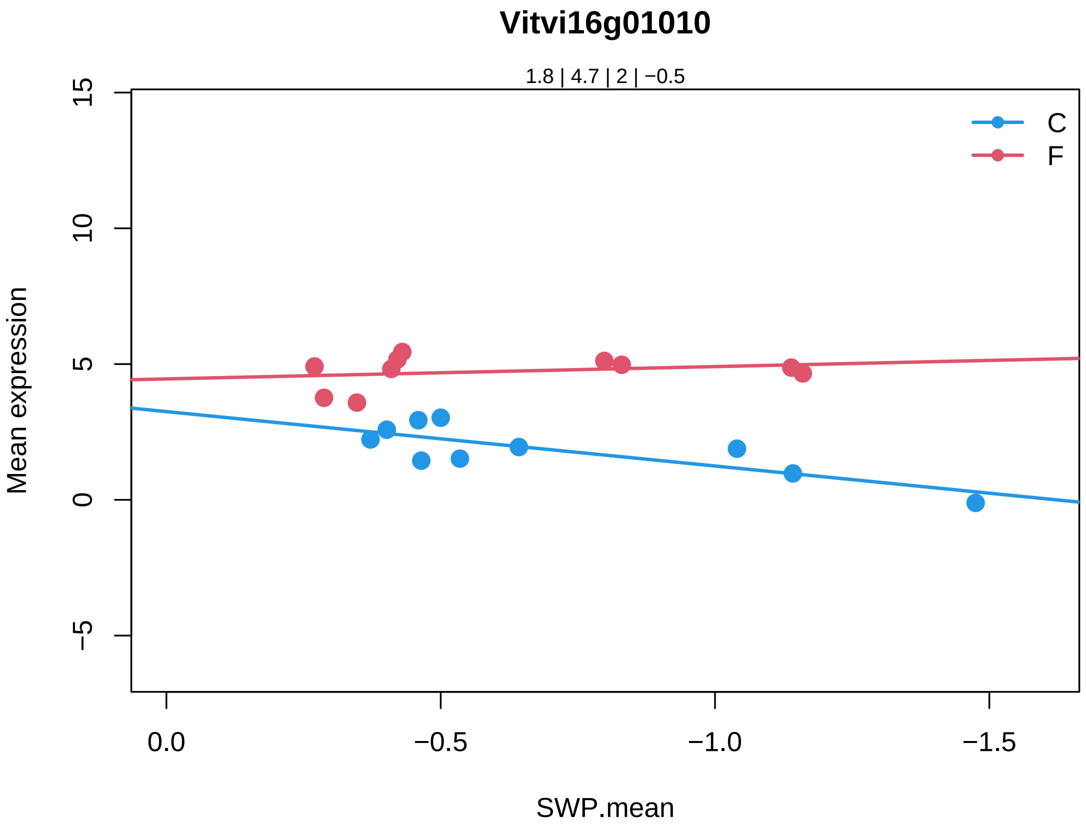
6.4.11 Vitvi16g01010

```
> 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.

```
                   swp varietyF swp.varietyF  AveExpr        F
Vitvi16g01010 2.003371 1.203708    -2.457307 3.285178 46.27152
                   P.Value    adj.P.Val  type
Vitvi16g01010 1.543643e-09 1.069464e-07 type3
```



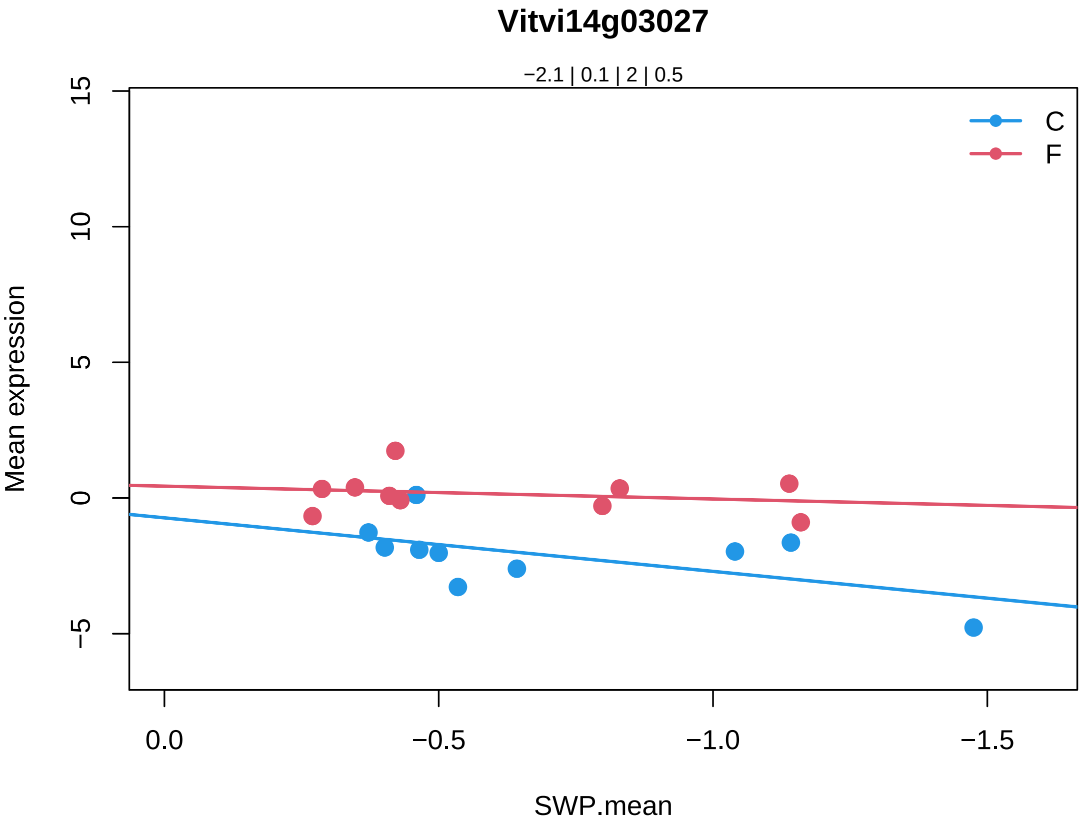
6.4.12 Vitvi14g03027

```
> 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.

```
                   swp varietyF swp.varietyF    AveExpr        F
Vitvi14g03027 1.973808 1.167041    -1.501193 -0.9844131 14.20717
                   P.Value    adj.P.Val  type
Vitvi14g03027 2.550724e-05 0.0007068752 type3
```



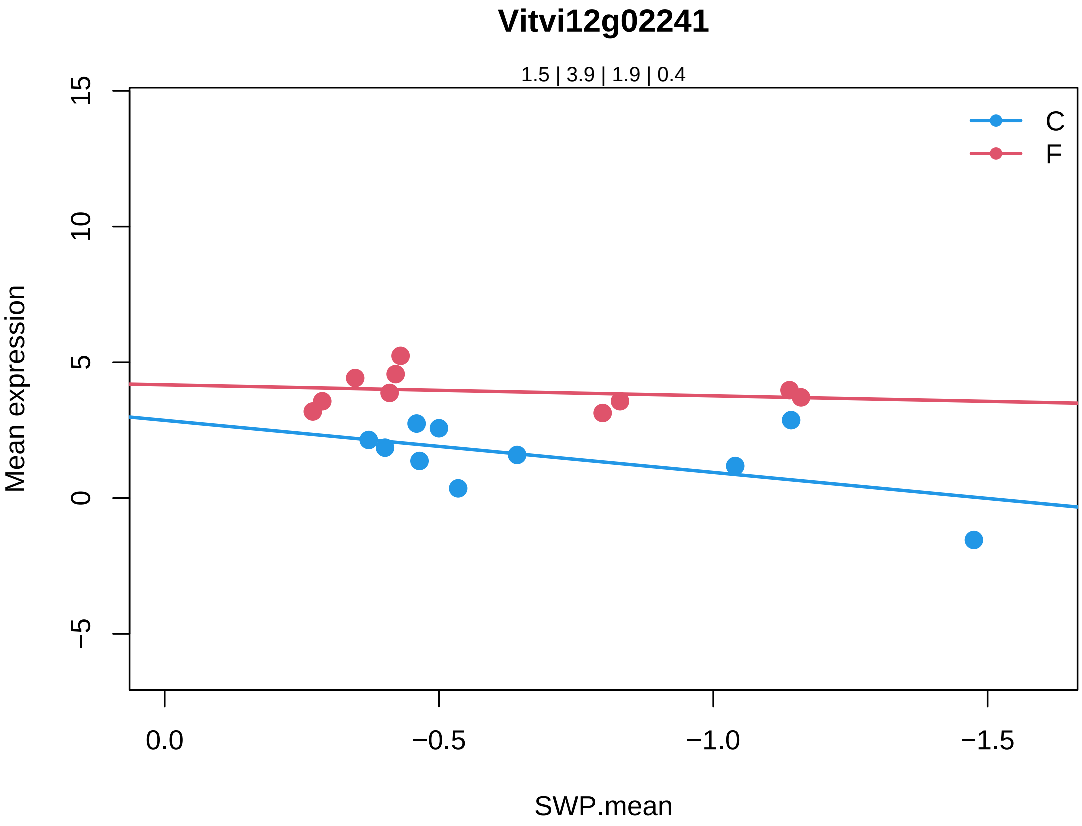
6.4.13 Vitvi12g02241

```
> 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.

```
                   swp varietyF swp.varietyF  AveExpr        F
Vitvi12g02241 1.917744 1.308867    -1.511665 2.718899 15.13494
                   P.Value    adj.P.Val  type
Vitvi12g02241 1.631568e-05 0.0004792522 type3
```



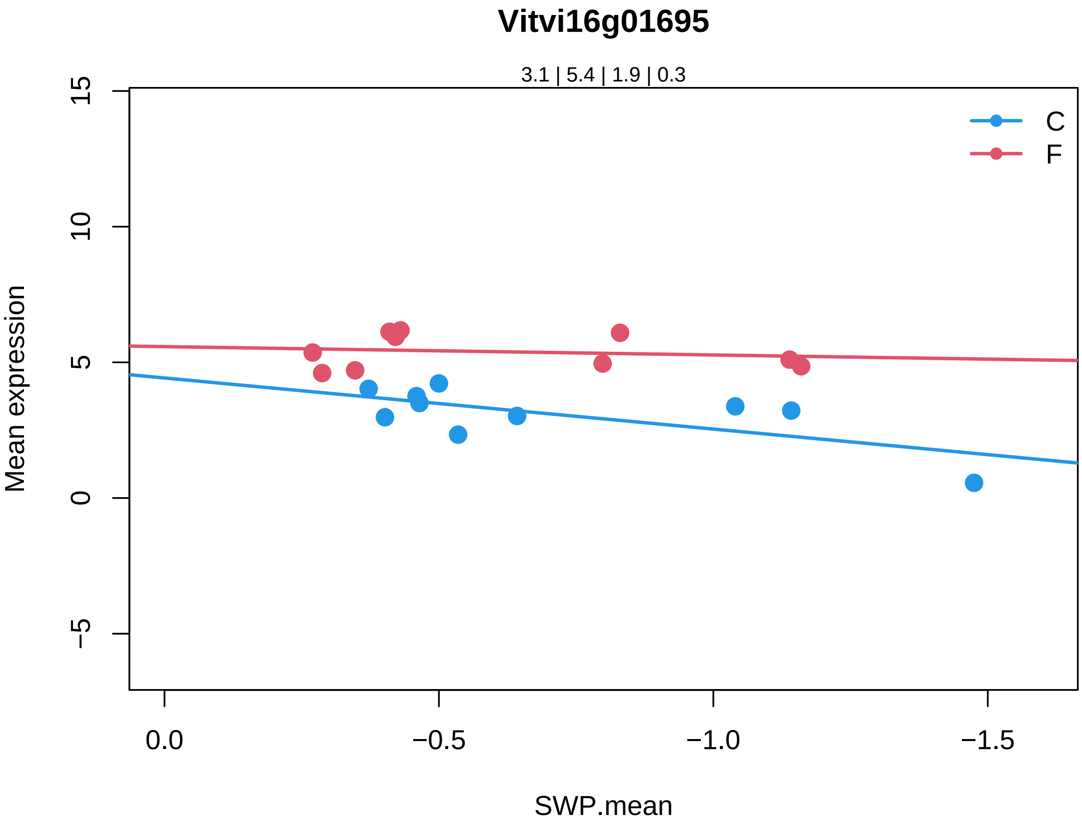
6.4.14 Vitvi16g01695

```
> 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.

```
                  swp varietyF swp.varietyF  AveExpr        F
Vitvi16g01695 1.88261 1.155416    -1.575394 4.245718 21.94197
                  P.Value    adj.P.Val  type
Vitvi16g01695 9.80737e-07 3.965091e-05 type3
```



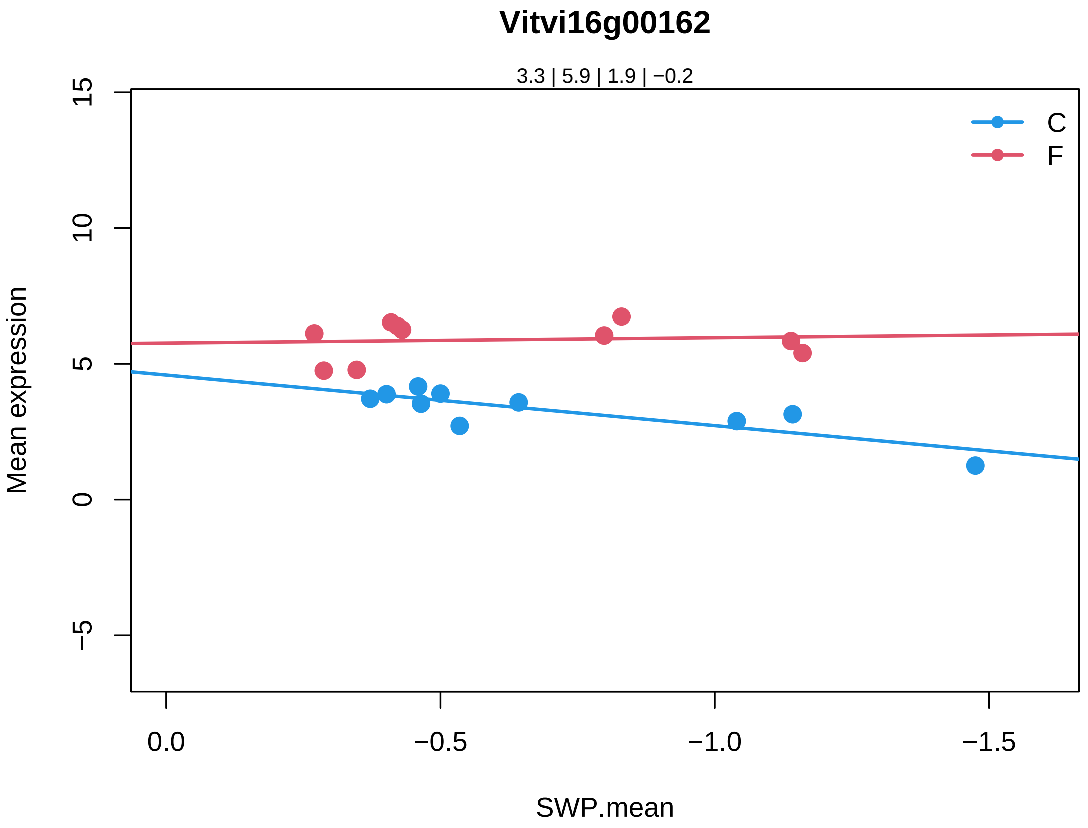
6.4.15 Vitvi16g00162

```
> 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.

```
                   swp varietyF swp.varietyF  AveExpr        F
Vitvi16g00162 1.862536 1.175659     -2.06133 4.580106 36.02592
                   P.Value    adj.P.Val  type
Vitvi16g00162 1.488406e-08 8.496733e-07 type3
```



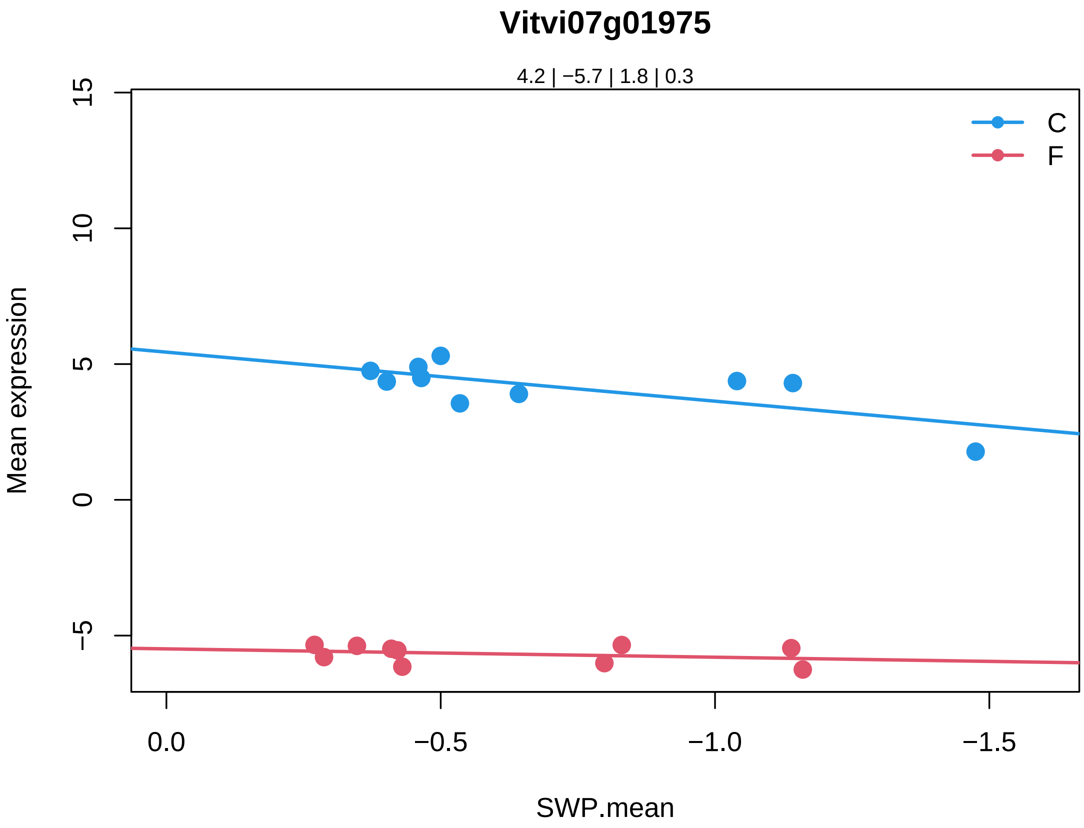
6.4.16 Vitvi07g01975

```
> 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.

```
                   swp  varietyF swp.varietyF    AveExpr        F
Vitvi07g01975 1.805957 -10.92862    -1.498707 -0.7535728 528.7142
                   P.Value    adj.P.Val  type
Vitvi07g01975 3.009809e-20 1.994588e-17 type3
```



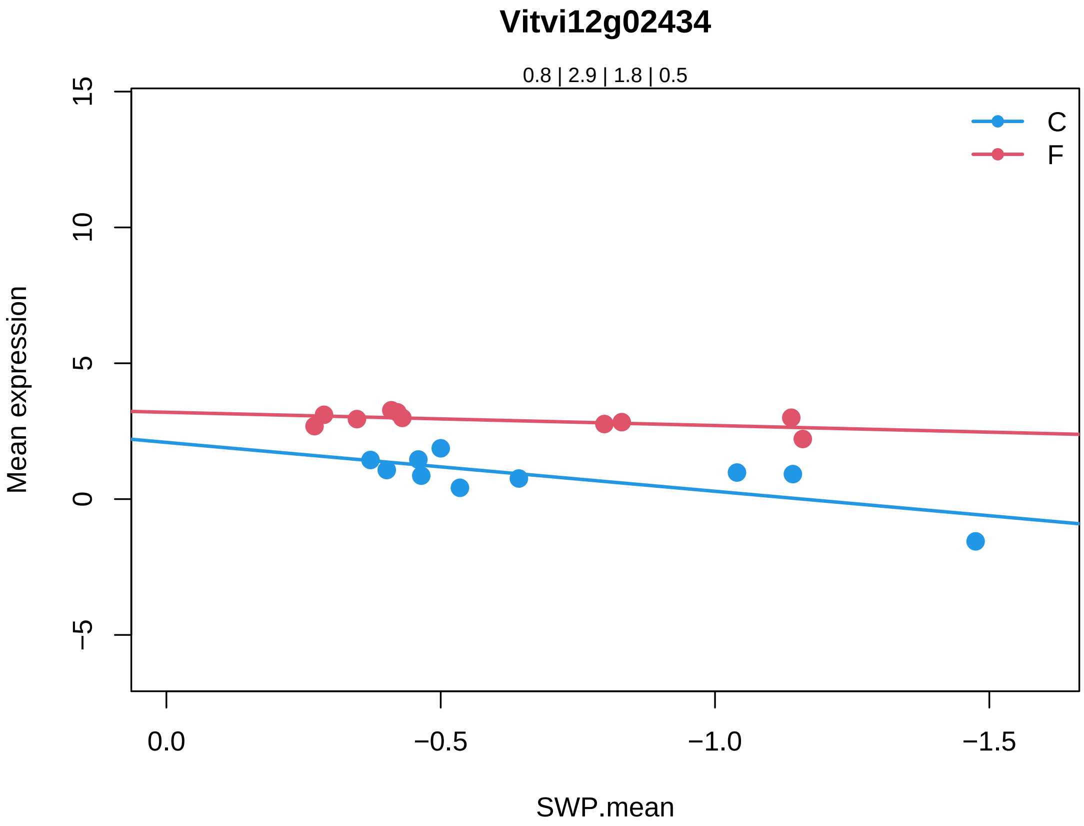
6.4.17 Vitvi12g02434

```
> 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.

```
                   swp varietyF swp.varietyF  AveExpr       F
Vitvi12g02434 1.798958 1.109027    -1.311562 1.859977 33.7848
                   P.Value    adj.P.Val  type
Vitvi12g02434 2.622927e-08 1.407699e-06 type3
```



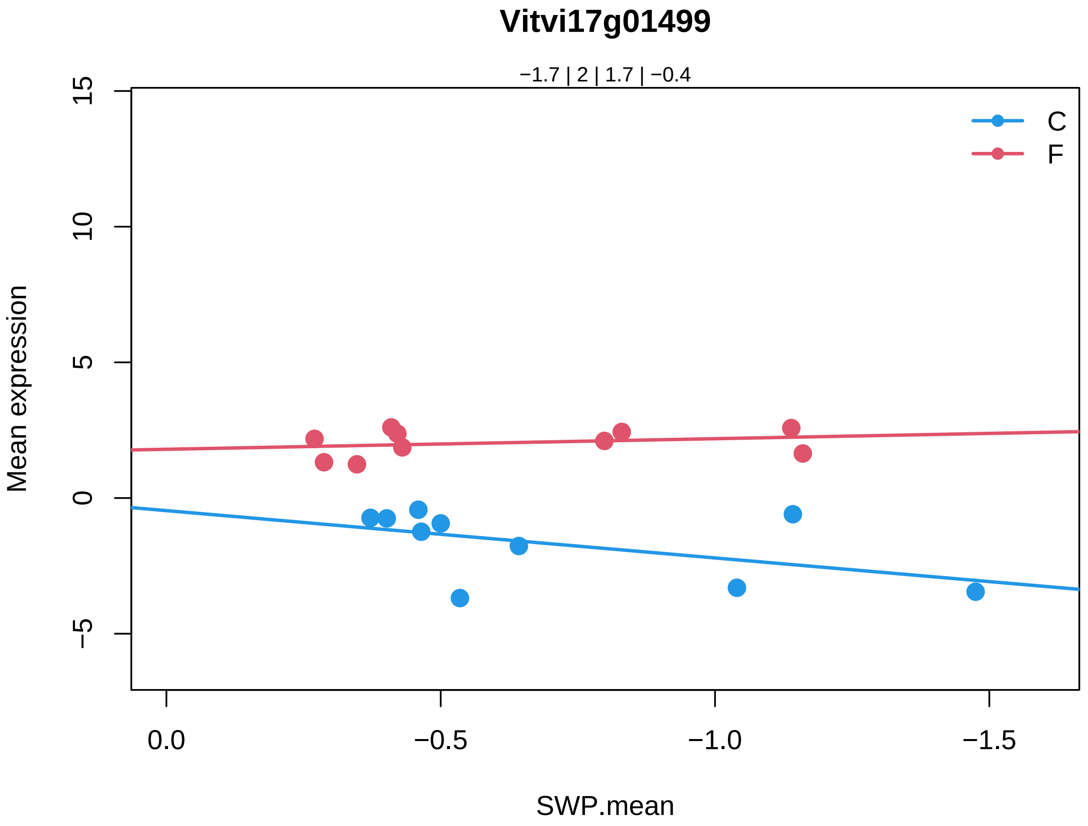
6.4.18 Vitvi17g01499

```
> 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.

```
                   swp varietyF swp.varietyF   AveExpr        F
Vitvi17g01499 1.743445 2.260813    -2.133583 0.1717443 36.14726
                  P.Value   adj.P.Val  type
Vitvi17g01499 1.44465e-08 8.30919e-07 type3
```



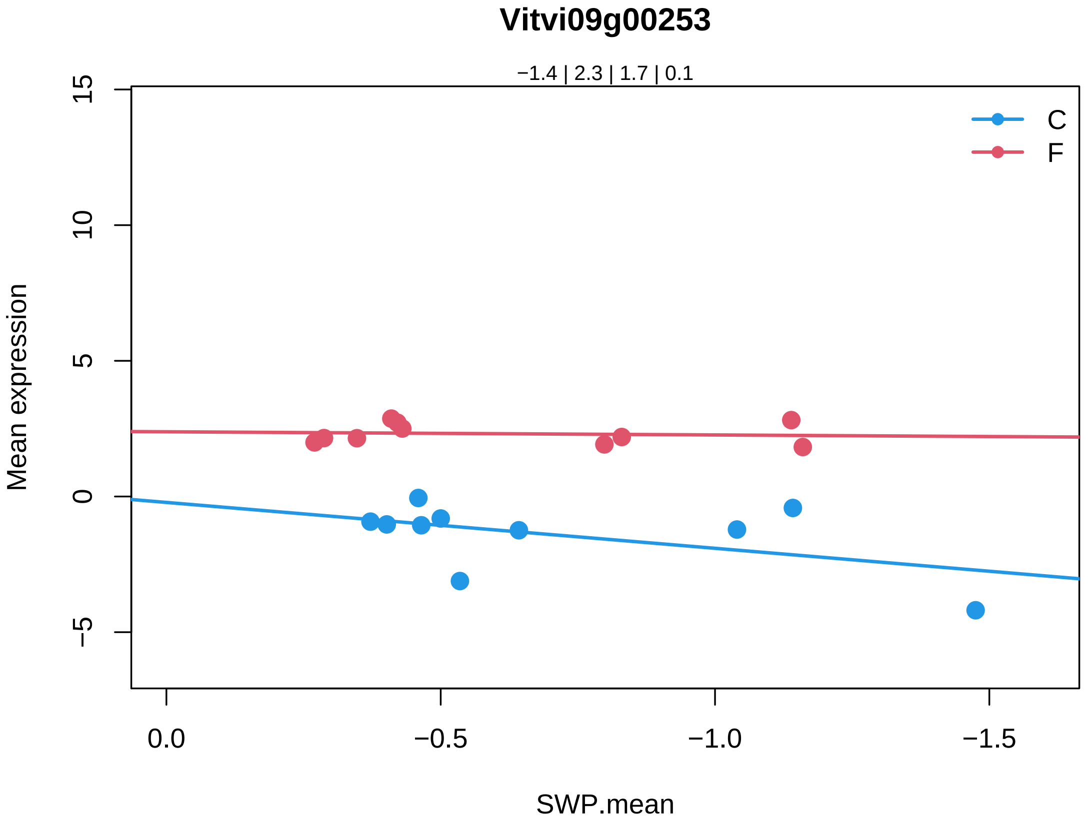
6.4.19 Vitvi09g00253

```
> 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.

```
                   swp varietyF swp.varietyF   AveExpr        F
Vitvi09g00253 1.690283 2.603352    -1.574086 0.4531853 39.13731
                   P.Value    adj.P.Val  type
Vitvi09g00253 7.100646e-09 4.329122e-07 type3
```



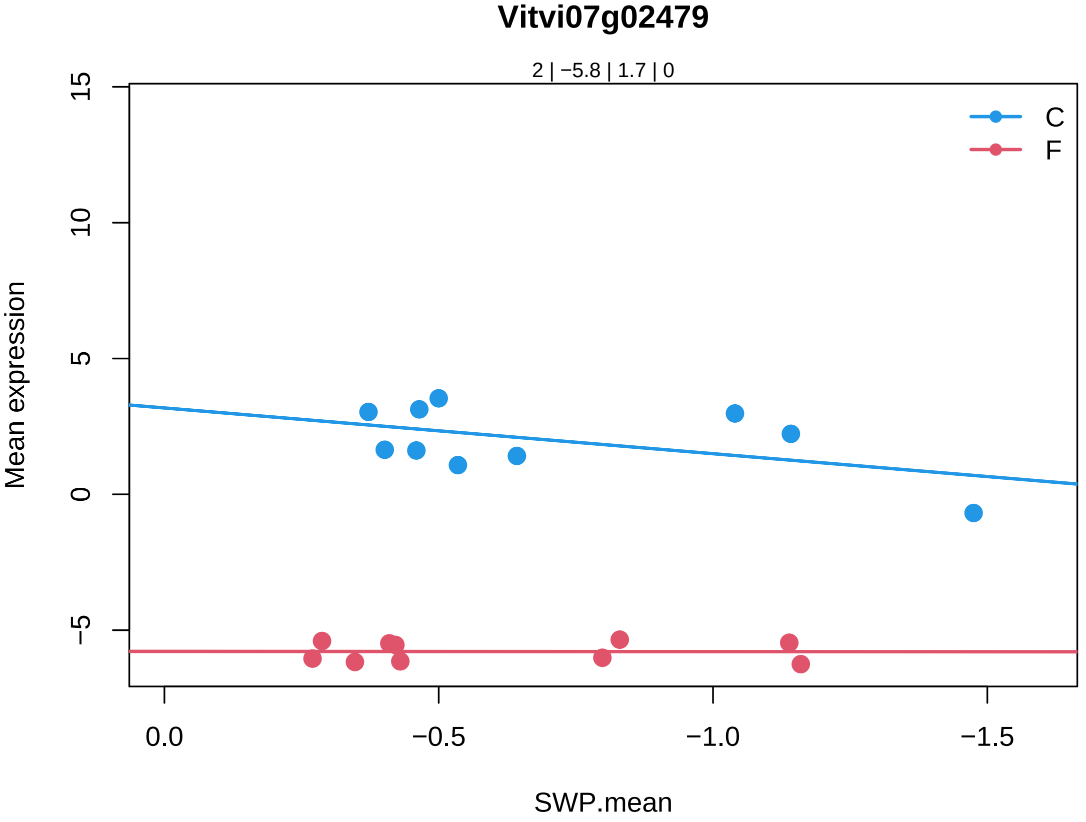
6.4.20 Vitvi07g02479

```
> 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.

```
                   swp   varietyF swp.varietyF   AveExpr        F
Vitvi07g02479 1.683394 -8.961387     -1.67543 -1.895083 165.2893
                   P.Value    adj.P.Val  type
Vitvi07g02479 5.651294e-15 9.465608e-13 type3
```



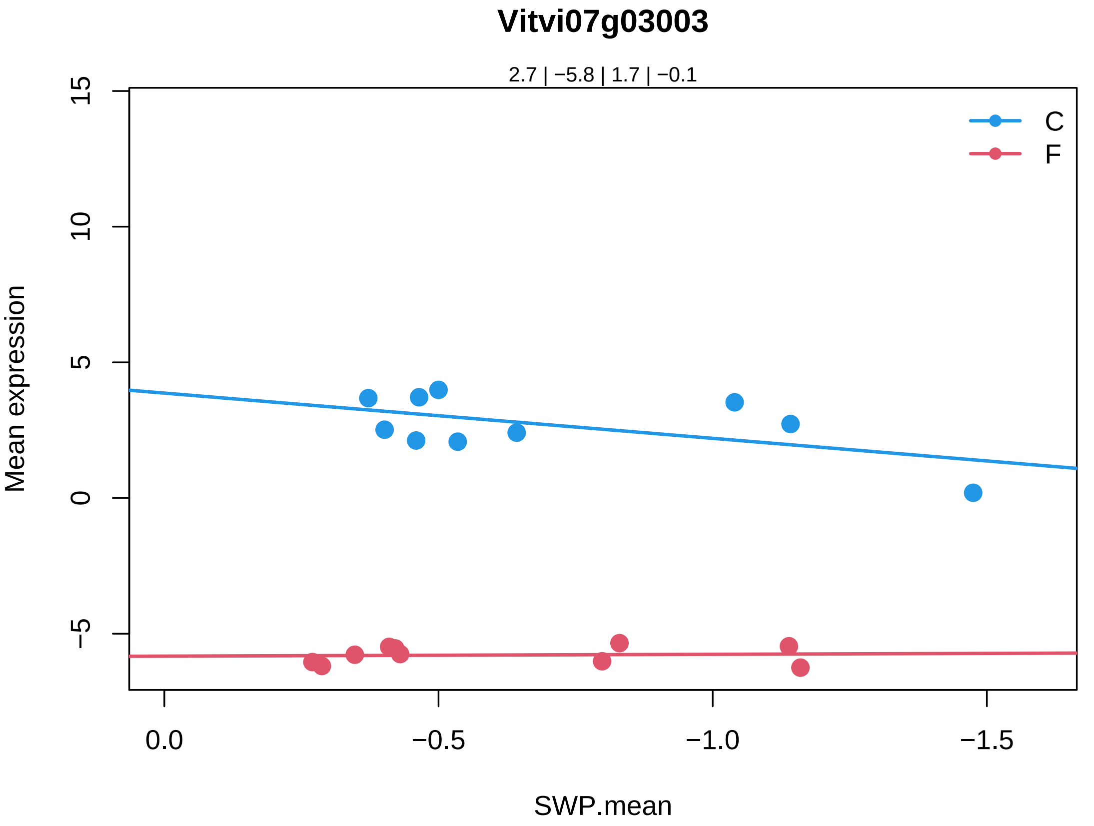
6.4.21 Vitvi07g03003

```
> 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.

```
                     swp   varietyF swp.varietyF   AveExpr        F
Vitvi07g03003 1.666543 -9.694668    -1.734139 -1.545537 256.7179
                   P.Value    adj.P.Val  type
Vitvi07g03003 5.947509e-17 1.462128e-14 type3
```



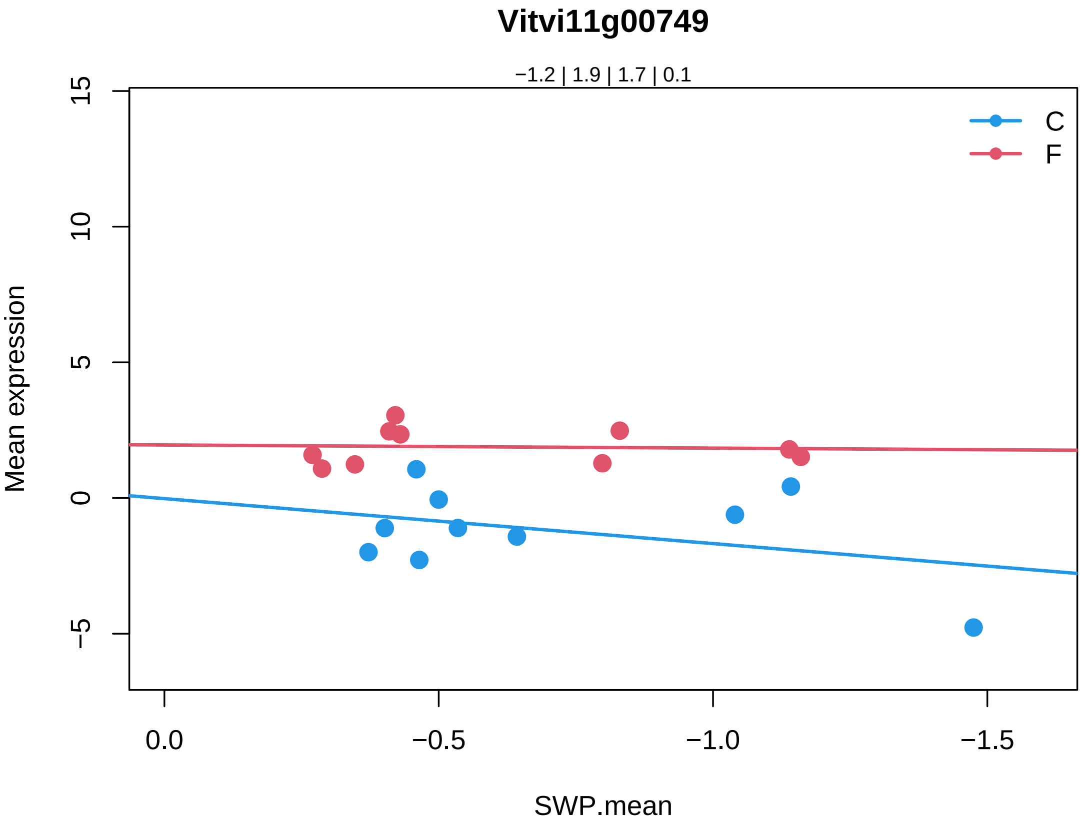
6.4.22 Vitvi11g00749

```
> 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.

```
                   swp varietyF swp.varietyF  AveExpr        F
Vitvi11g00749 1.657462 1.977015    -1.540859 0.348429 14.12192
                   P.Value    adj.P.Val  type
Vitvi11g00749 2.660129e-05 0.0007318716 type3
```



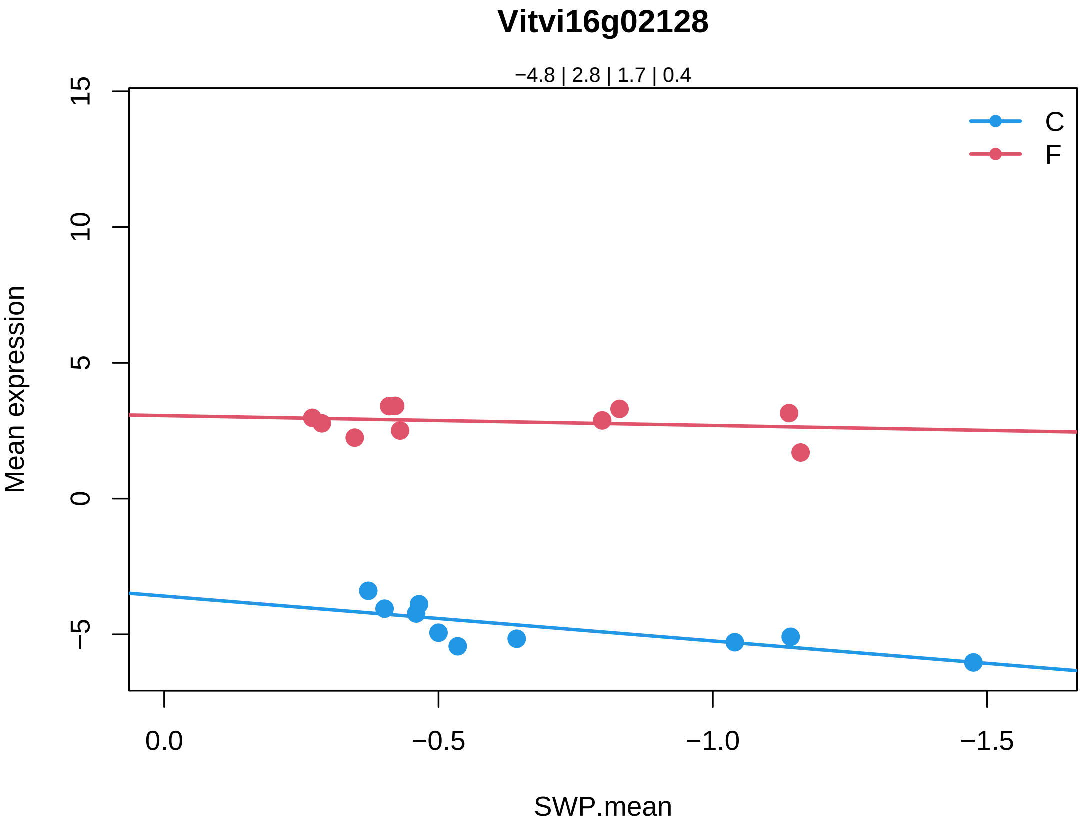
6.4.23 Vitvi16g02128

```
> 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.

```
                   swp varietyF swp.varietyF    AveExpr        F
Vitvi16g02128 1.650819 6.646728    -1.288502 -0.9592224 322.2722
                   P.Value    adj.P.Val  type
Vitvi16g02128 5.524125e-18 1.619206e-15 type3
```



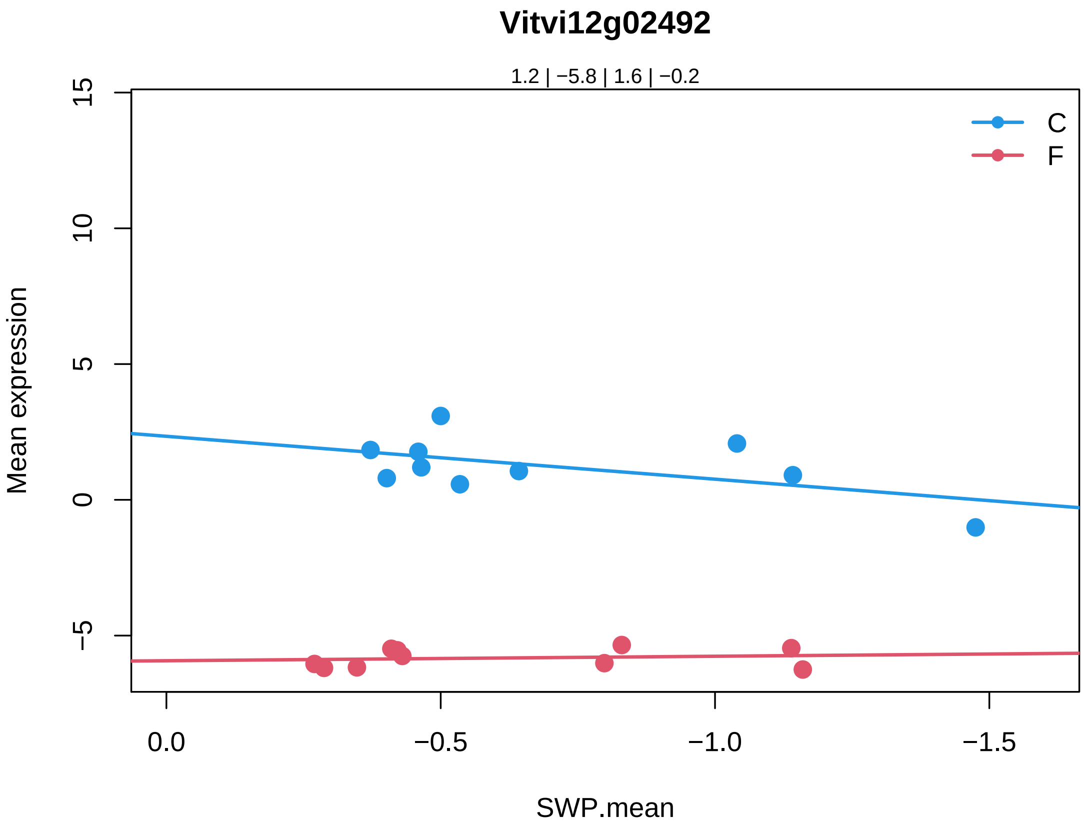
6.4.24 Vitvi12g02492

```
> 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.

```
                   swp  varietyF swp.varietyF   AveExpr        F
Vitvi12g02492 1.579994 -8.266505    -1.745248 -2.298563 184.8223
                   P.Value    adj.P.Val  type
Vitvi12g02492 1.792171e-15 3.291117e-13 type3
```



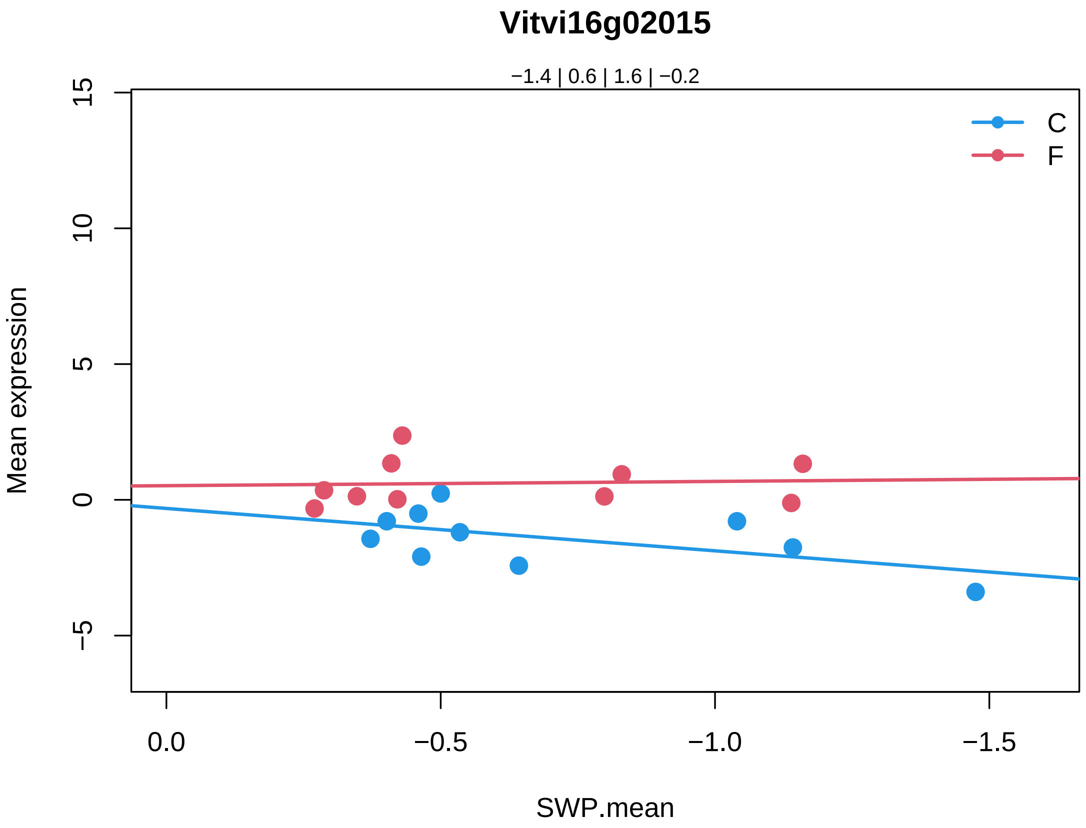
6.4.25 Vitvi16g02015

```
> 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.

```
                   swp   varietyF swp.varietyF    AveExpr        F
Vitvi16g02015 1.561065 0.8379566     -1.71816 -0.3989139 11.71652
                   P.Value    adj.P.Val  type
Vitvi16g02015 9.354598e-05 0.002137673 type3
```



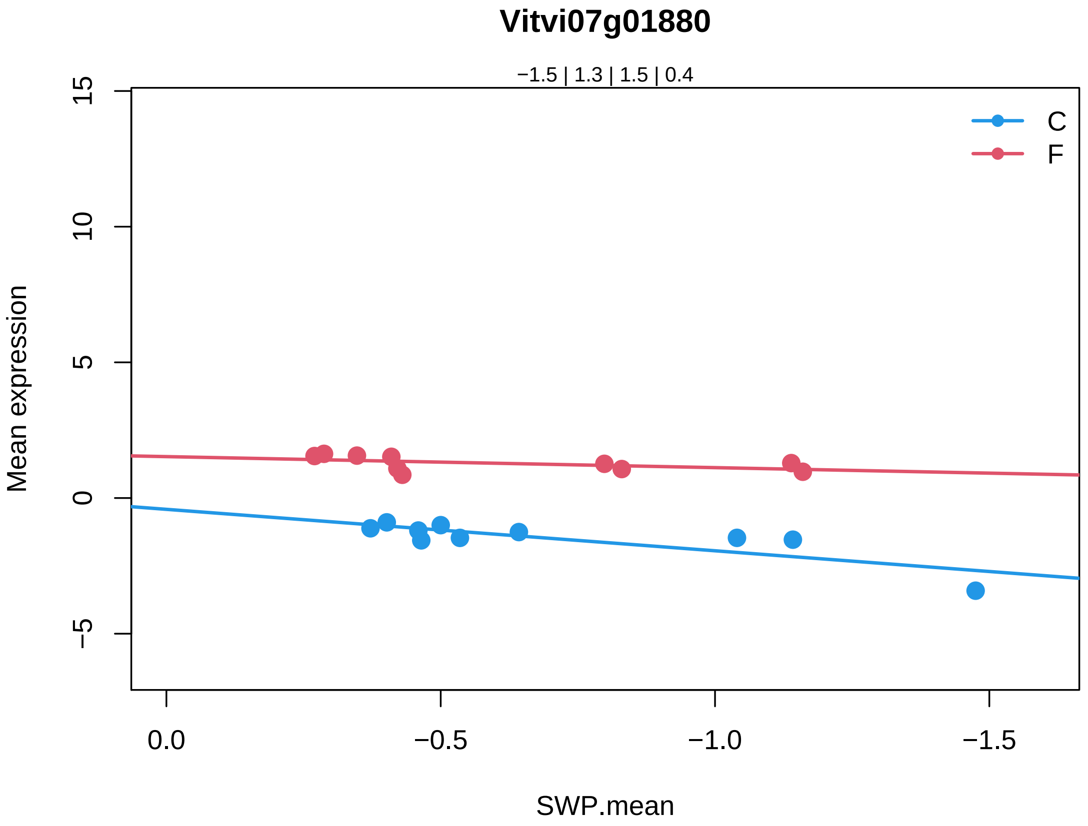
6.4.26 Vitvi07g01880

```
> 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.

```
                   swp varietyF swp.varietyF    AveExpr        F
Vitvi07g01880 1.527266 1.942915    -1.121594 -0.1062362 87.40072
                   P.Value    adj.P.Val  type
Vitvi07g01880 3.491005e-12 3.547326e-10 type3
```



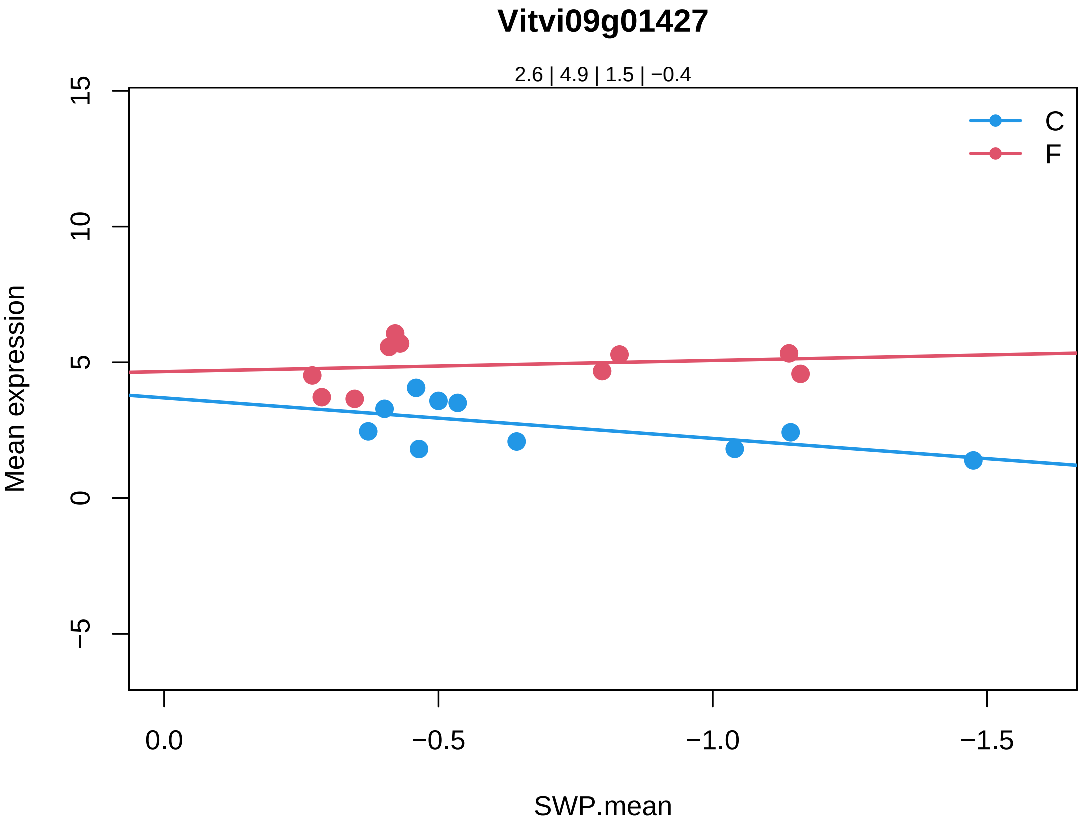
6.4.27 Vitvi09g01427

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

```
Vitvi09g01427
        16.01.2005
        secondary metabolism.isoprenoids.terpenoids
        lupeol synthase 2 |
        Chr1:29696722-29701024 FORWARD LENGTH=763 |
        201606
```

Coefficients for Vitvi09g01427.

```
                  swp  varietyF swp.varietyF  AveExpr        F
Vitvi09g01427 1.49161 0.9696872     -1.90059 3.774254 17.59975
                   P.Value    adj.P.Val  type
Vitvi09g01427 5.406556e-06 0.0001815126 type3
```



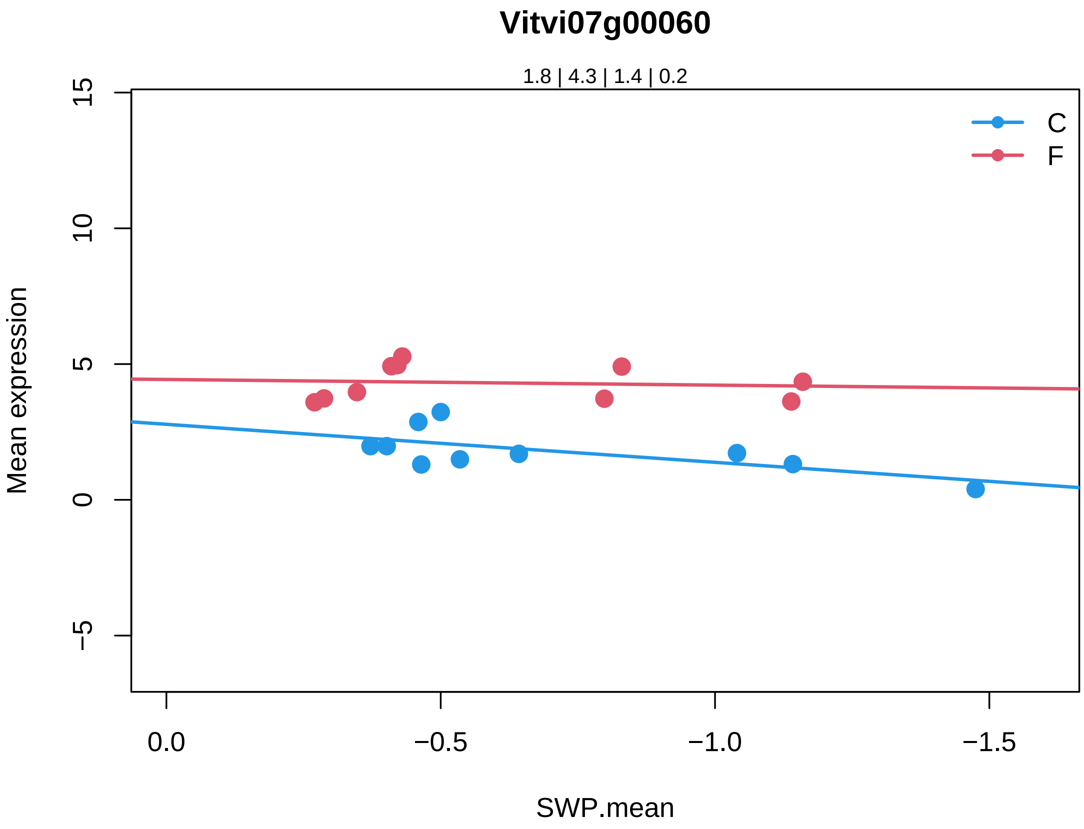
6.4.28 Vitvi07g00060

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

```
Vitvi07g00060
        35.2
        not assigned.unknown
        Ubiquitin-conjugating enzyme/RWD-like protein |
        Chr2:16225777-16226772 FORWARD LENGTH=331 |
        201606
```

Coefficients for Vitvi07g00060.

```
                   swp varietyF swp.varietyF  AveExpr        F
Vitvi07g00060 1.400516  1.65096    -1.192193 3.051484 28.90883
                   P.Value   adj.P.Val  type
Vitvi07g00060 1.008551e-07 4.95882e-06 type3
```



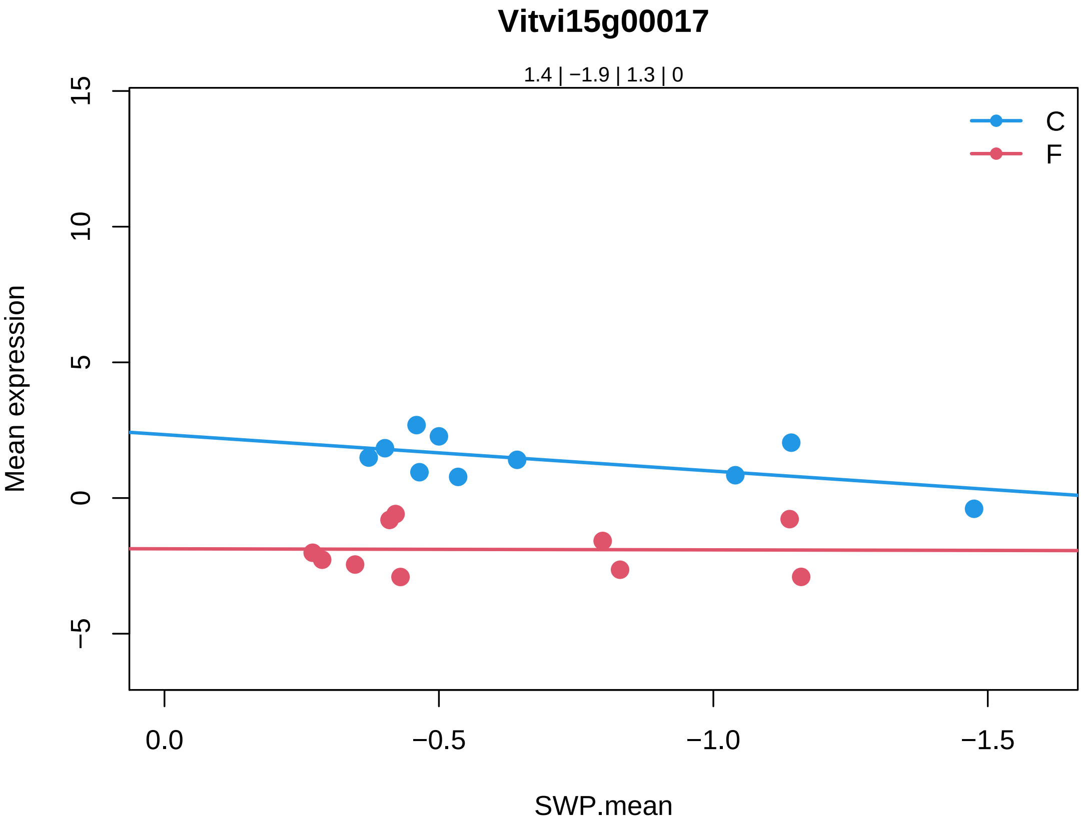
6.4.29 Vitvi15g00017

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

```
Vitvi15g00017
        35.2
        not assigned.unknown
        NB-ARC domain-containing disease resistance protein |
        Chr3:4857940-4861104 FORWARD LENGTH=1054 |
        201606
```

Coefficients for Vitvi15g00017.

```
                   swp  varietyF swp.varietyF    AveExpr        F
Vitvi15g00017 1.343637 -4.207471    -1.304475 -0.2524733 29.96158
                   P.Value    adj.P.Val  type
Vitvi15g00017 7.431202e-08 3.701516e-06 type3
```



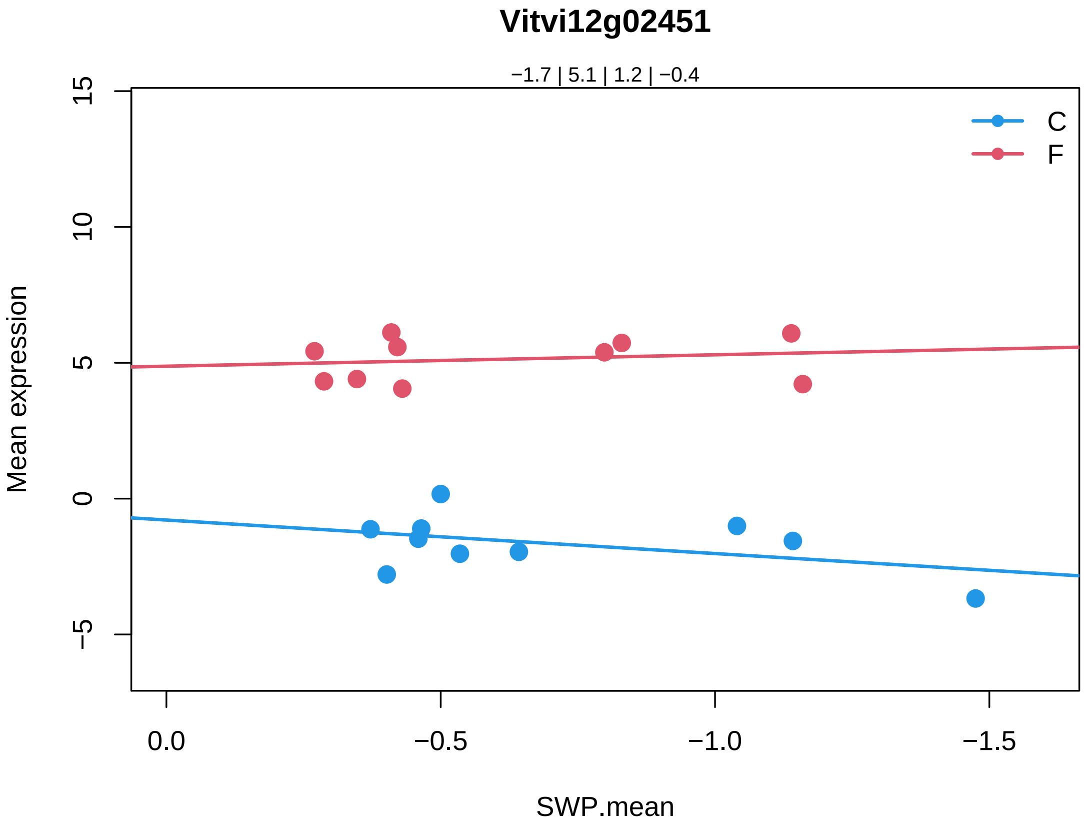
6.4.30 Vitvi12g02451

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

```
Vitvi12g02451
        16.8.1.21
        secondary metabolism.flavonoids.anthocyanins.anthocyanin 5-aromatic ac
        HXXXD-type acyl-transferase family protein |
        Chr1:1009542-1010951 REVERSE LENGTH=469 |
        201606
```

Coefficients for Vitvi12g02451.

```
                   swp varietyF swp.varietyF  AveExpr        F
Vitvi12g02451 1.234009 5.661412    -1.654182 1.737127 111.3461
                   P.Value    adj.P.Val  type
Vitvi12g02451 3.126561e-13 3.906152e-11 type3
```



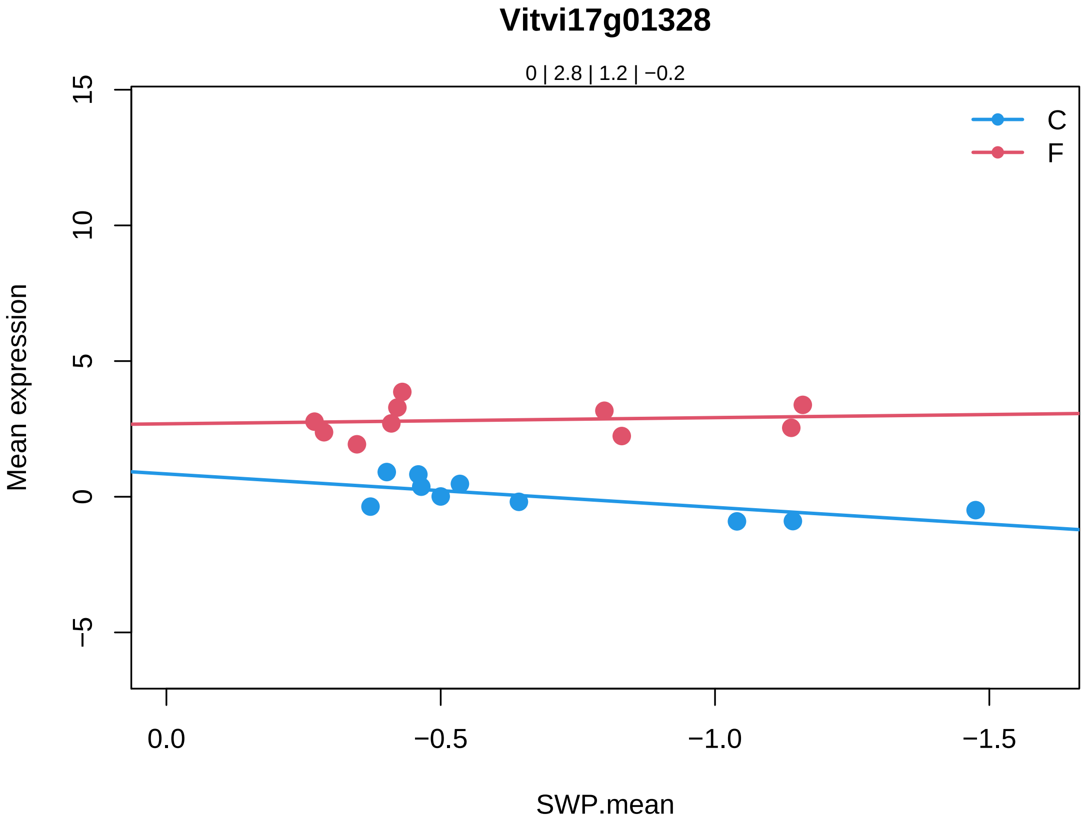
6.4.31 Vitvi17g01328

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

```
Vitvi17g01328
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi17g01328.

```
                   swp varietyF swp.varietyF  AveExpr        F
Vitvi17g01328 1.233294 1.846943    -1.460876 1.399914 48.07206
                   P.Value    adj.P.Val  type
Vitvi17g01328 1.084375e-09 7.723384e-08 type3
```



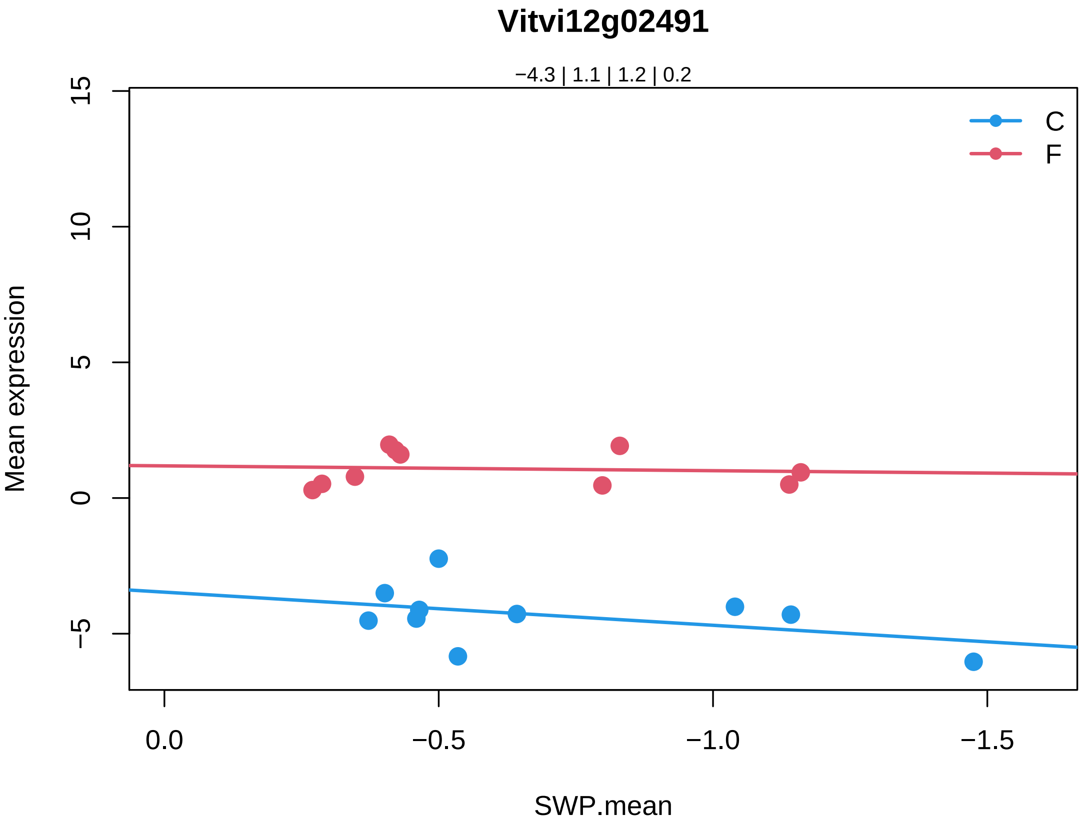
6.4.32 Vitvi12g02491

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

```
Vitvi12g02491
        30.2.12
        signalling.receptor kinases.leucine rich repeat XII
        receptor like protein 6 |
        Chr1:17183550-17186534 REVERSE LENGTH=994 |
        201606
```

Coefficients for Vitvi12g02491.

```
                   swp varietyF swp.varietyF   AveExpr        F
Vitvi12g02491 1.220752 4.654194    -1.042901 -1.625063 76.77944
                   P.Value    adj.P.Val  type
Vitvi12g02491 1.246636e-11 1.144652e-09 type3
```



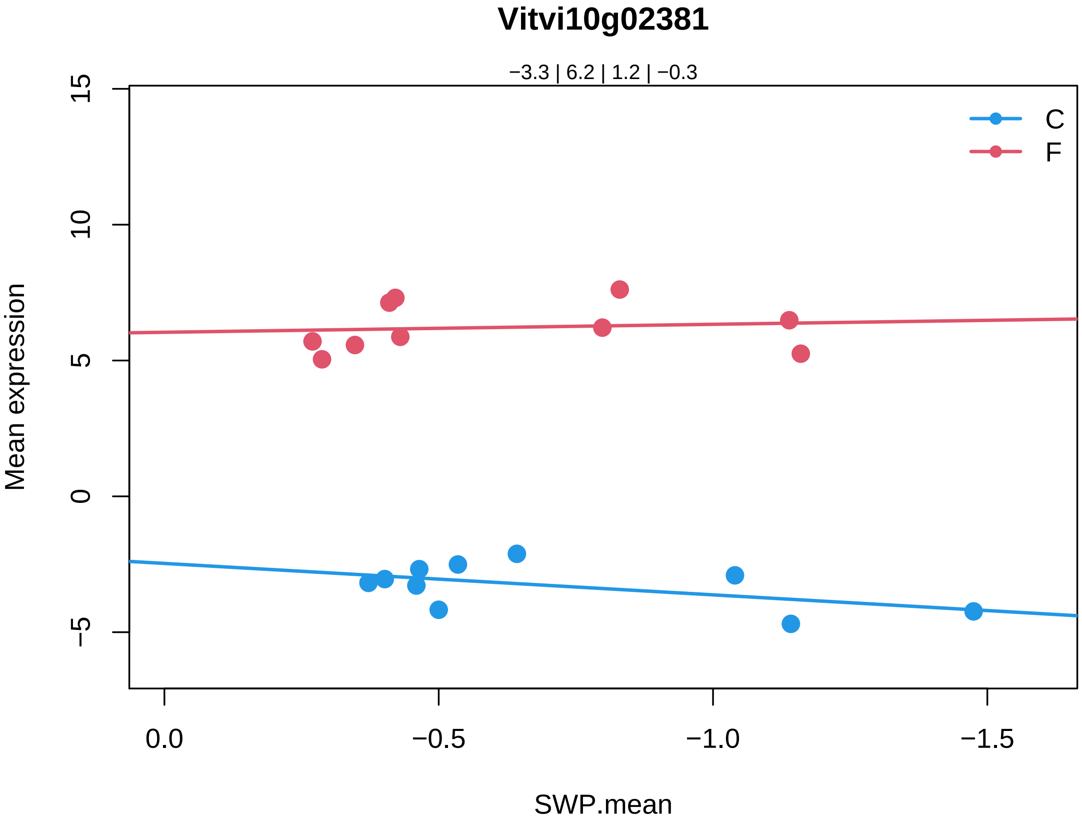
6.4.33 Vitvi10g02381

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

```
Vitvi10g02381
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi10g02381.

```
                   swp varietyF swp.varietyF  AveExpr        F
Vitvi10g02381 1.156847 8.508498     -1.44987 1.467694 251.9189
                   P.Value    adj.P.Val  type
Vitvi10g02381 7.239286e-17 1.724081e-14 type3
```



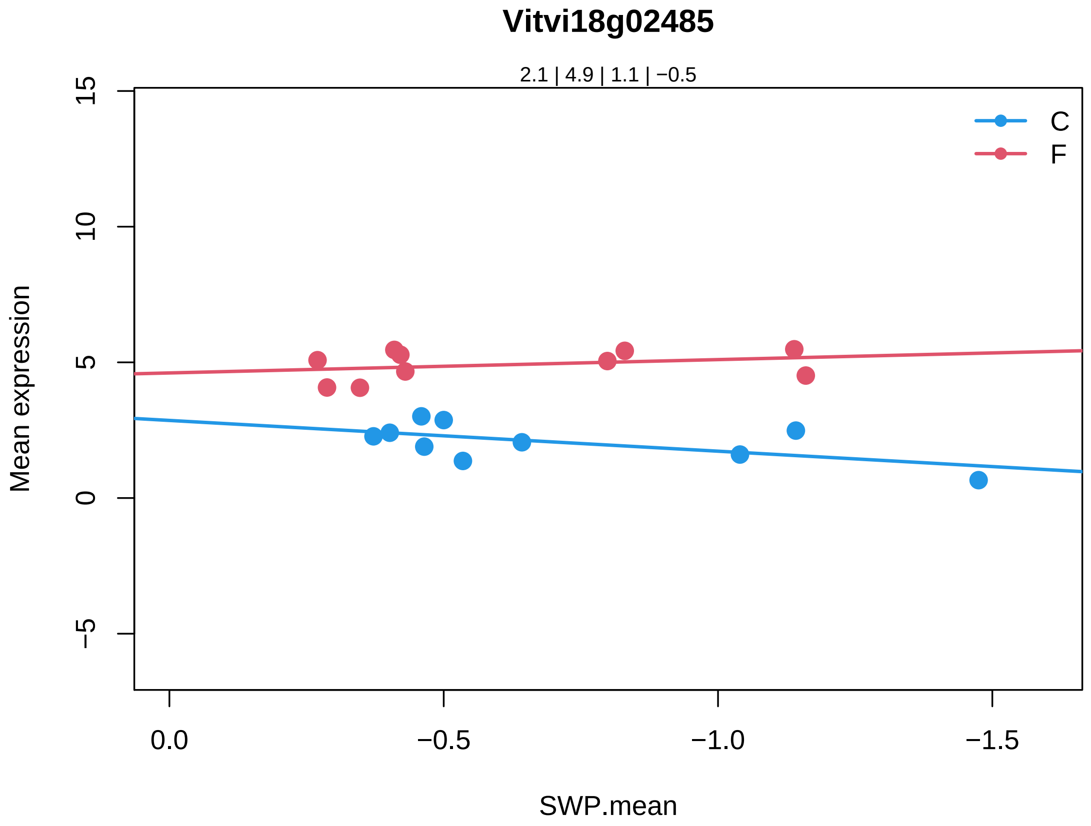
6.4.34 Vitvi18g02485

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

```
Vitvi18g02485
        17.7.1.5
        hormone metabolism.jasmonate.synthesis-degradation.12-oxophytodienoate
        12-oxophytodienoate reductase 2 |
        Chr1:28778976-28780355 FORWARD LENGTH=374 |
        201606
```

Coefficients for Vitvi18g02485.

```
                  swp varietyF swp.varietyF  AveExpr        F
Vitvi18g02485 1.13339 1.750197    -1.625173 3.485423 45.29278
                   P.Value    adj.P.Val  type
Vitvi18g02485 1.879667e-09 1.273328e-07 type3
```



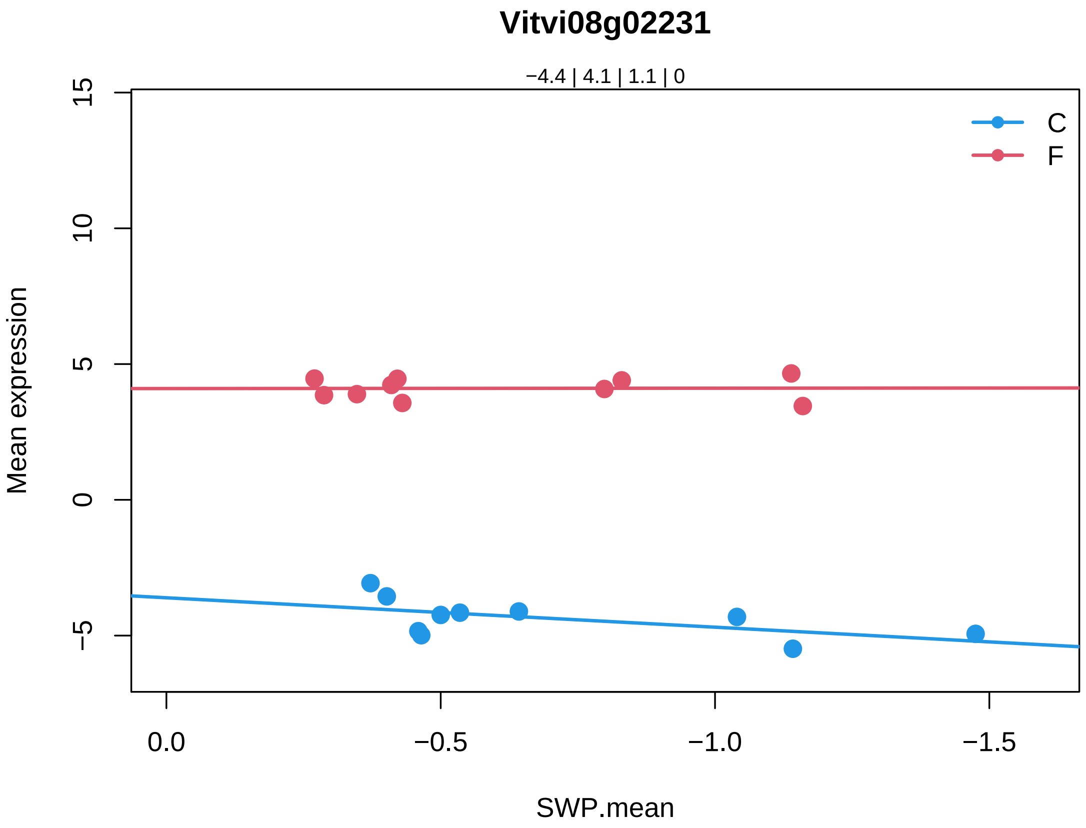
6.4.35 Vitvi08g02231

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

```
Vitvi08g02231
        1.03.2007
        PS.calvin cycle.FBPase
        high cyclic electron flow 1 |
        Chr3:20016951-20018527 FORWARD LENGTH=417 |
        201606
```

Coefficients for Vitvi08g02231.

```
                   swp varietyF swp.varietyF    AveExpr        F
Vitvi08g02231 1.083398  7.70538    -1.096231 -0.1317216 435.4744
                  P.Value    adj.P.Val  type
Vitvi08g02231 2.33368e-19 1.147418e-16 type3
```



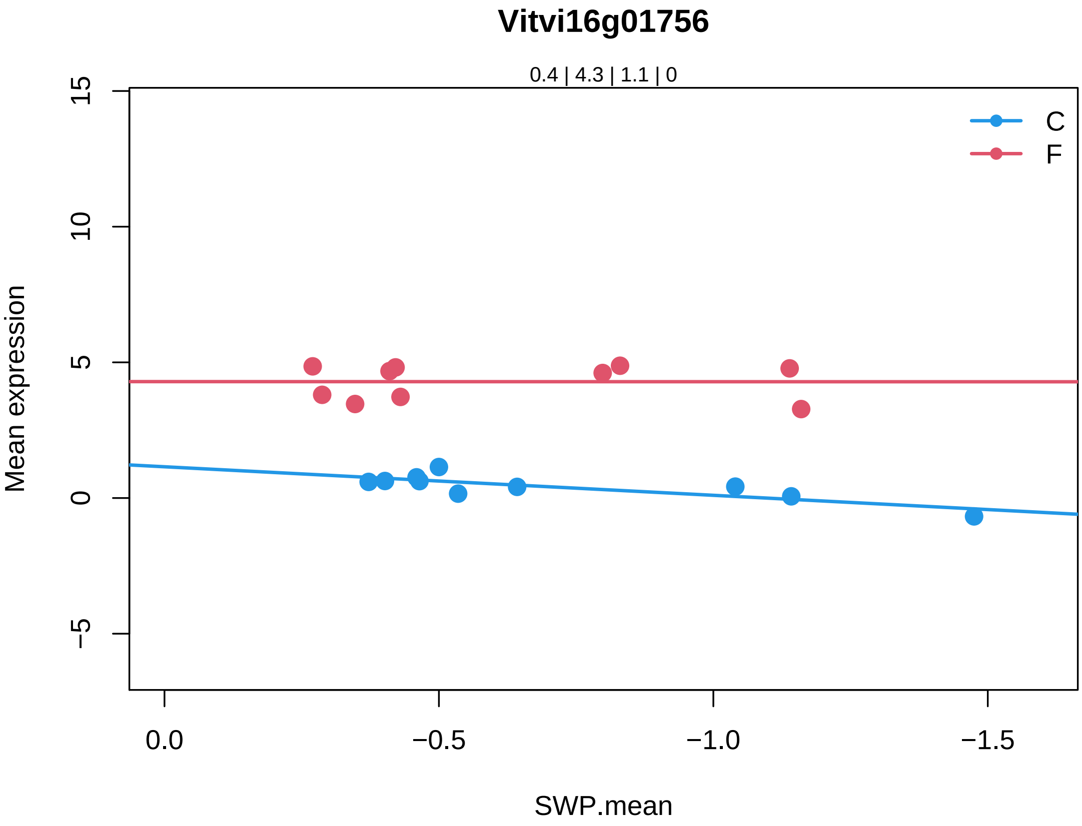
6.4.36 Vitvi16g01756

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

```
Vitvi16g01756
        20.1.2.1
        stress.biotic.receptors.CC-NBS-LRR
        NB-ARC domain-containing disease resistance protein |
        Chr3:4857940-4861104 FORWARD LENGTH=1054 |
        201606
```

Coefficients for Vitvi16g01756.

```
                   swp varietyF swp.varietyF  AveExpr        F
Vitvi16g01756 1.051572 3.137489    -1.048555 2.350159 95.69663
                   P.Value    adj.P.Val  type
Vitvi16g01756 1.421168e-12 1.536273e-10 type3
```



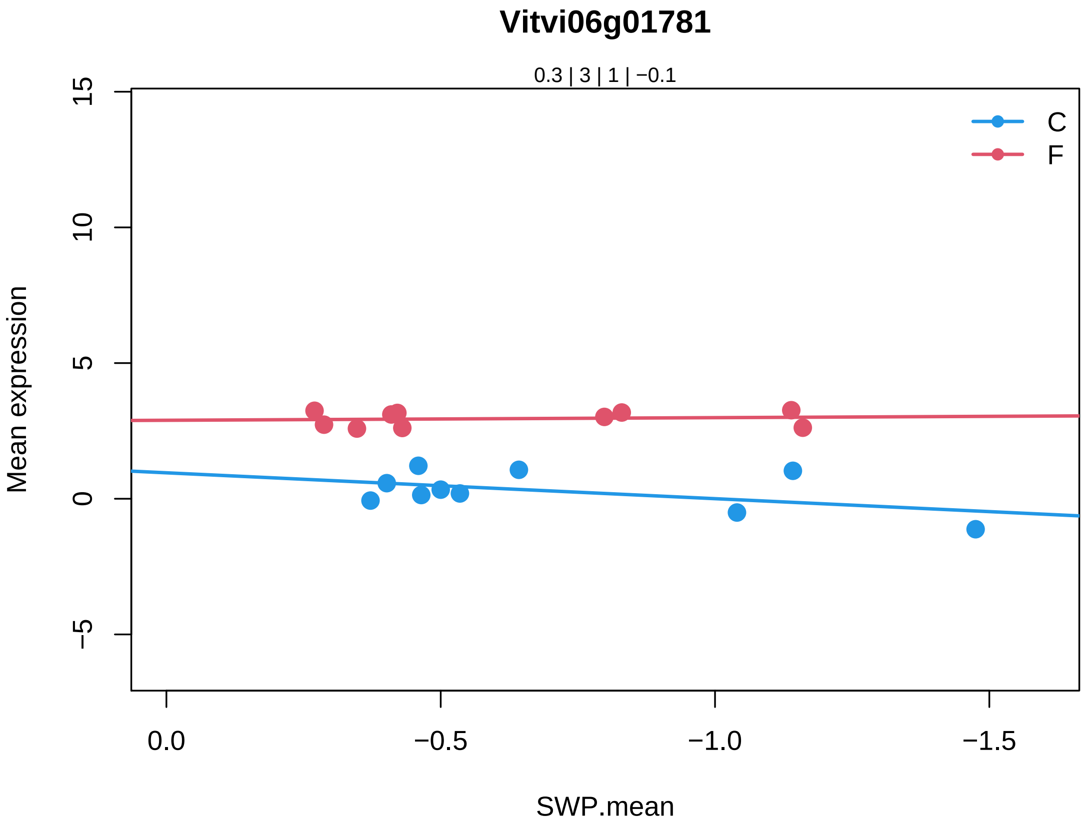
6.4.37 Vitvi06g01781

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

```
Vitvi06g01781
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi06g01781.

```
                    swp varietyF swp.varietyF  AveExpr        F
Vitvi06g01781 0.9534047 1.936245    -1.049892 1.618129 45.84969
                   P.Value    adj.P.Val  type
Vitvi06g01781 1.679652e-09 1.144244e-07 type3
```



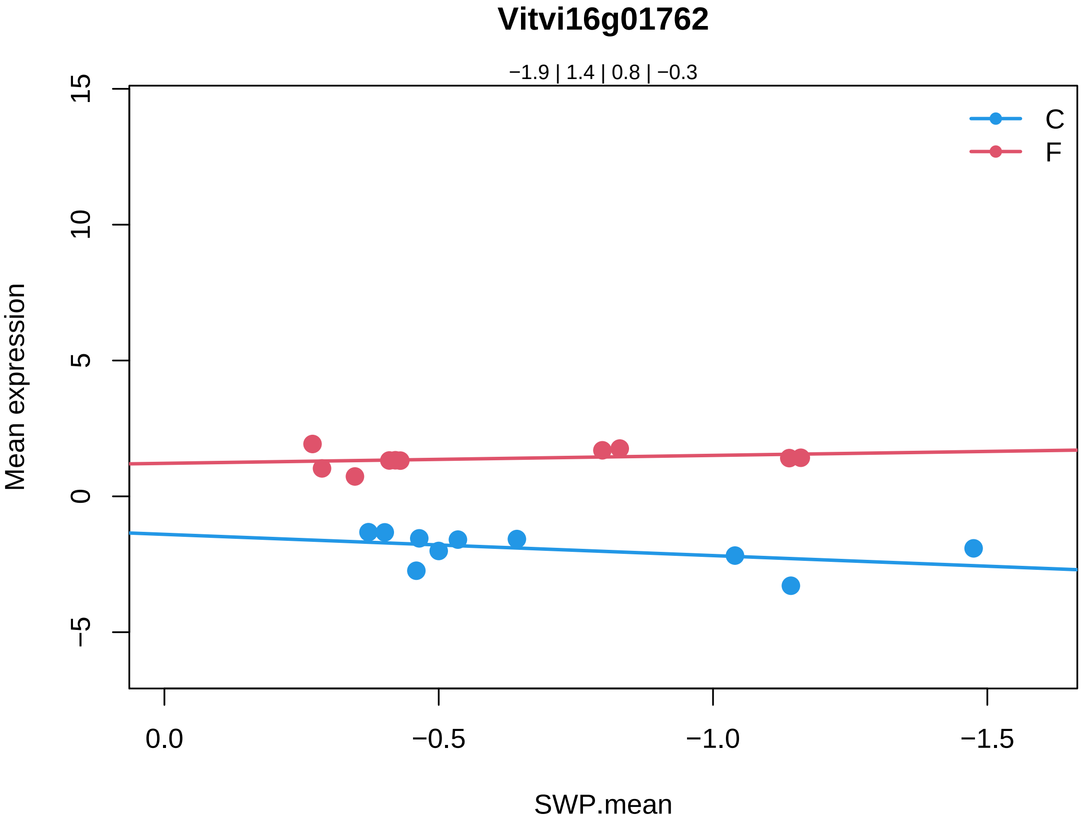
6.4.38 Vitvi16g01762

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

```
Vitvi16g01762
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi16g01762.

```
                    swp varietyF swp.varietyF    AveExpr        F
Vitvi16g01762 0.7816522  2.61383    -1.074305 -0.2776802 77.63237
                   P.Value   adj.P.Val  type
Vitvi16g01762 1.119035e-11 1.04002e-09 type3
```



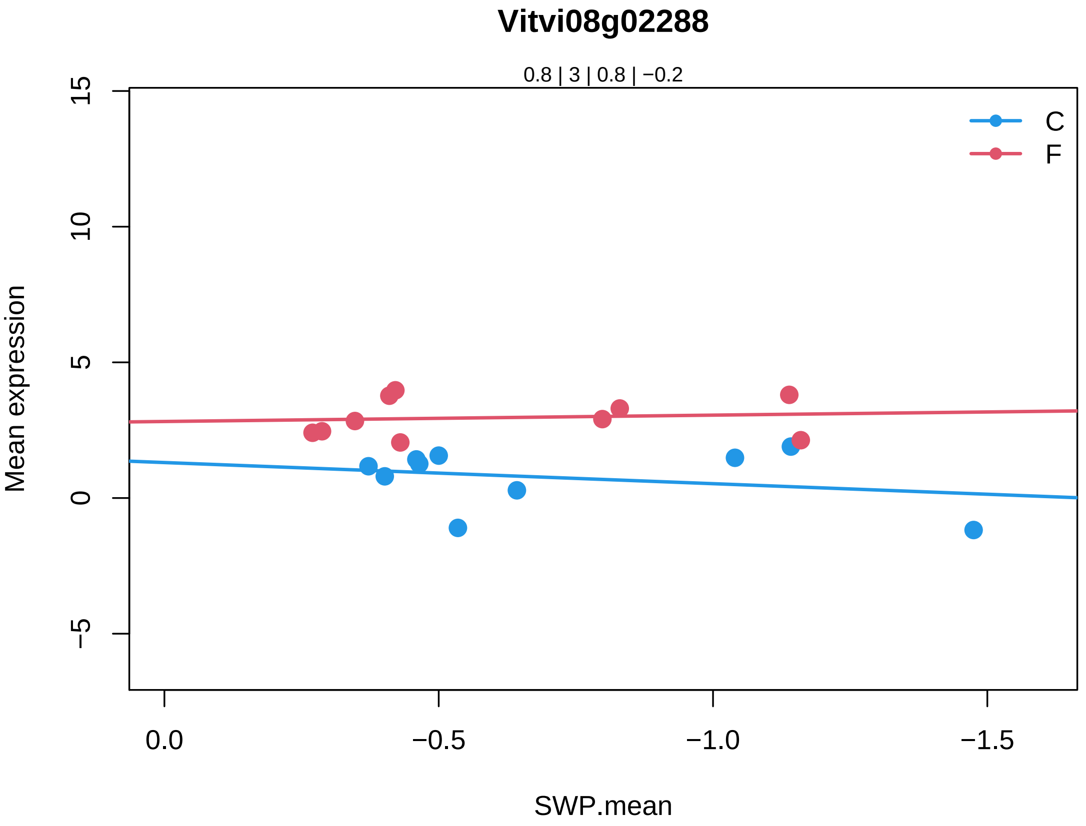
6.4.39 Vitvi08g02288

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

```
Vitvi08g02288
        26.2
        misc.UDP glucosyl and glucoronyl transferases
        UDP-Glycosyltransferase superfamily protein |
        Chr2:15415227-15416717 REVERSE LENGTH=496 |
        201606
```

Coefficients for Vitvi08g02288.

```
                    swp varietyF swp.varietyF  AveExpr        F
Vitvi08g02288 0.7784241 1.513625    -1.012031 1.861445 11.34185
                   P.Value   adj.P.Val  type
Vitvi08g02288 0.0001153665 0.002544742 type3
```



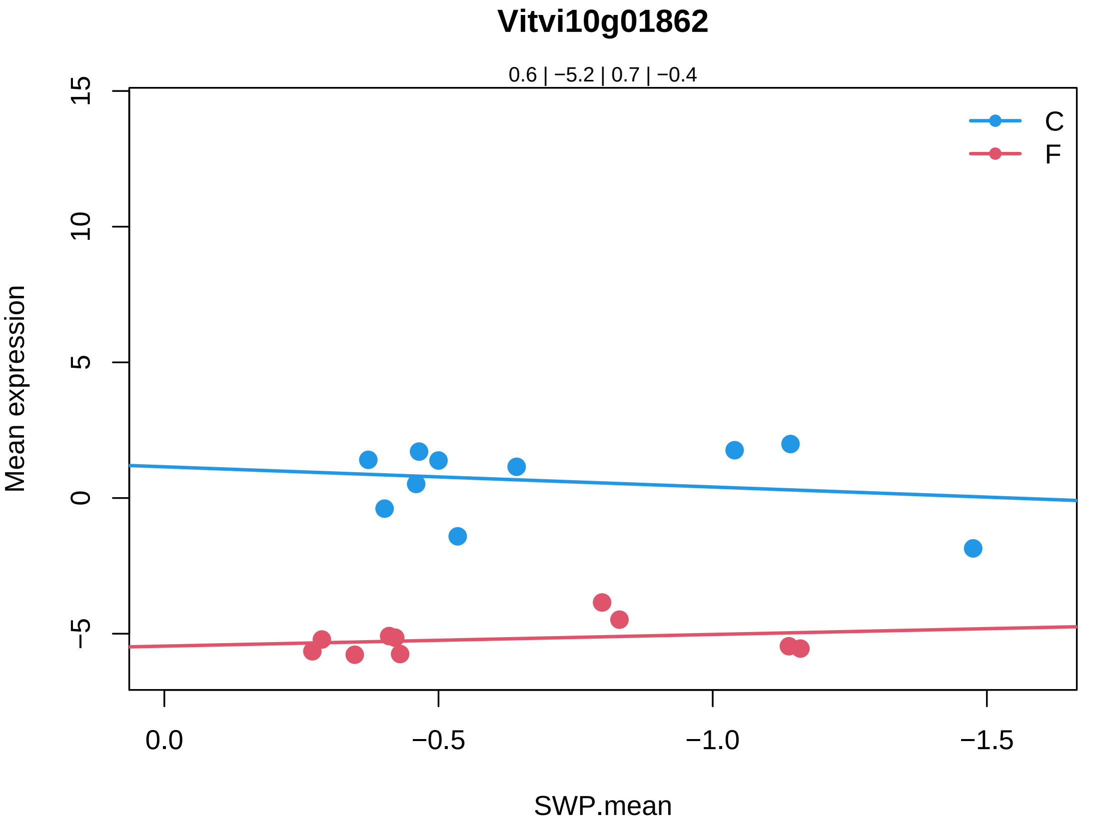
6.4.40 Vitvi10g01862

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

```
Vitvi10g01862
        16.01.2005
        secondary metabolism.isoprenoids.terpenoids
        Terpenoid cyclases family protein |
        Chr1:29684558-29688673 REVERSE LENGTH=759 |
        201606
```

Coefficients for Vitvi10g01862.

```
                    swp  varietyF swp.varietyF  AveExpr        F
Vitvi10g01862 0.7447214 -6.607979    -1.173754 -2.28511 58.23862
                   P.Value    adj.P.Val  type
Vitvi10g01862 1.789845e-10 1.443429e-08 type3
```



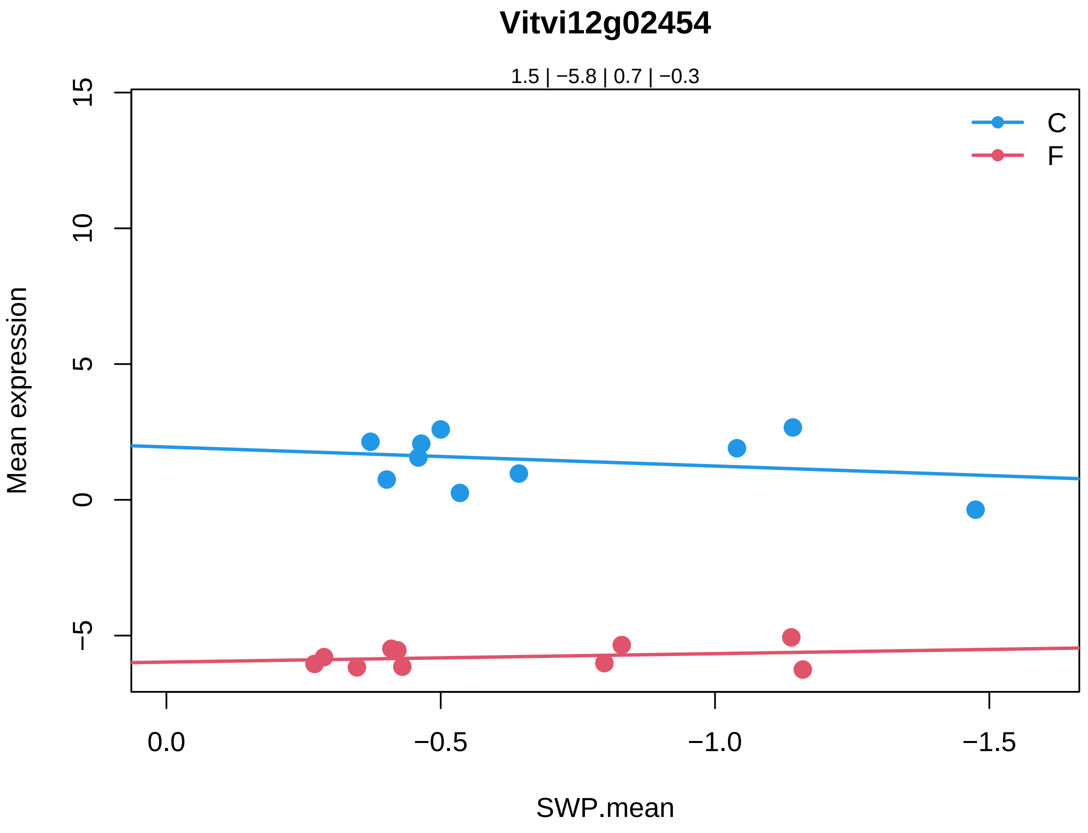
6.4.41 Vitvi12g02454

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

```
Vitvi12g02454
        16.8.1.21
        secondary metabolism.flavonoids.anthocyanins.anthocyanin 5-aromatic ac
        HXXXD-type acyl-transferase family protein |
        Chr1:1009542-1010951 REVERSE LENGTH=469 |
        201606
```

Coefficients for Vitvi12g02454.

```
                    swp  varietyF swp.varietyF   AveExpr        F
Vitvi12g02454 0.7013162 -7.920645    -1.011435 -2.166938 165.5169
                   P.Value    adj.P.Val  type
Vitvi12g02454 5.572091e-15 9.436645e-13 type3
```



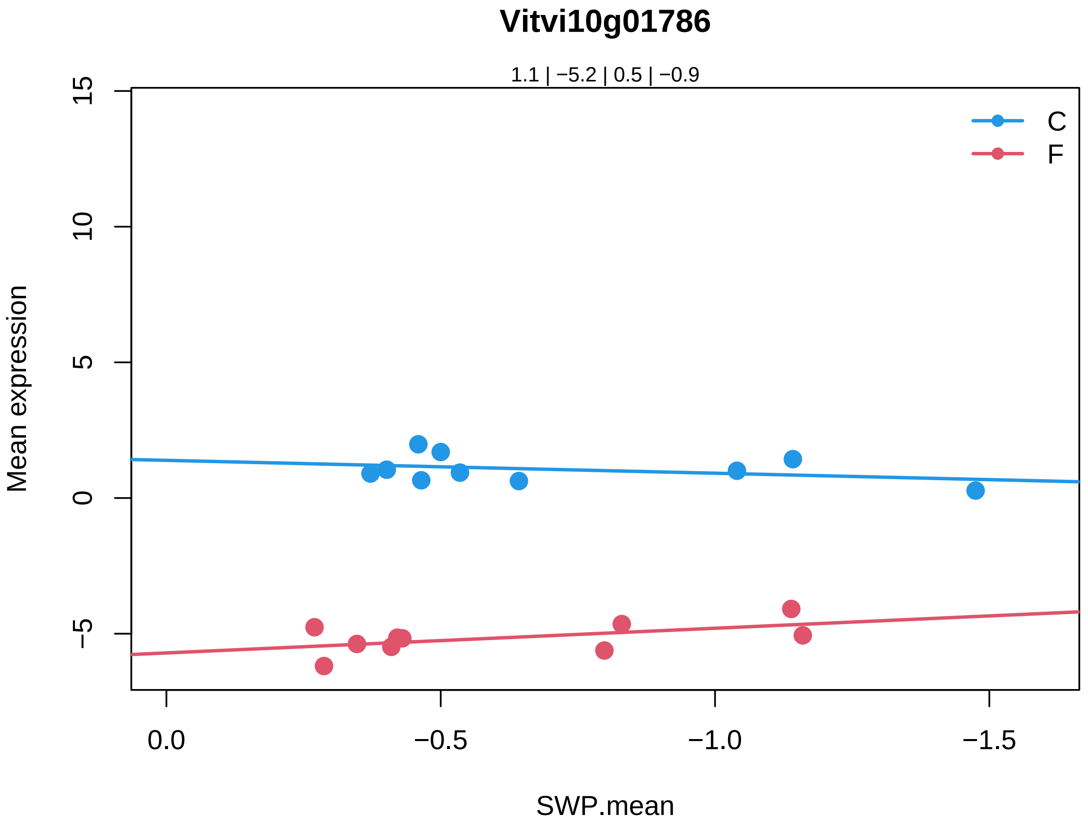
6.4.42 Vitvi10g01786

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

```
Vitvi10g01786
        35.2
        not assigned.unknown
        glutamate receptor 2.9 |
        Chr2:12501092-12504912 REVERSE LENGTH=940 |
        201606
```

Coefficients for Vitvi10g01786.

```
                    swp  varietyF swp.varietyF  AveExpr       F
Vitvi10g01786 0.4742976 -7.097644    -1.384343 -2.04986 249.985
                   P.Value    adj.P.Val  type
Vitvi10g01786 7.844063e-17 1.839373e-14 type3
```



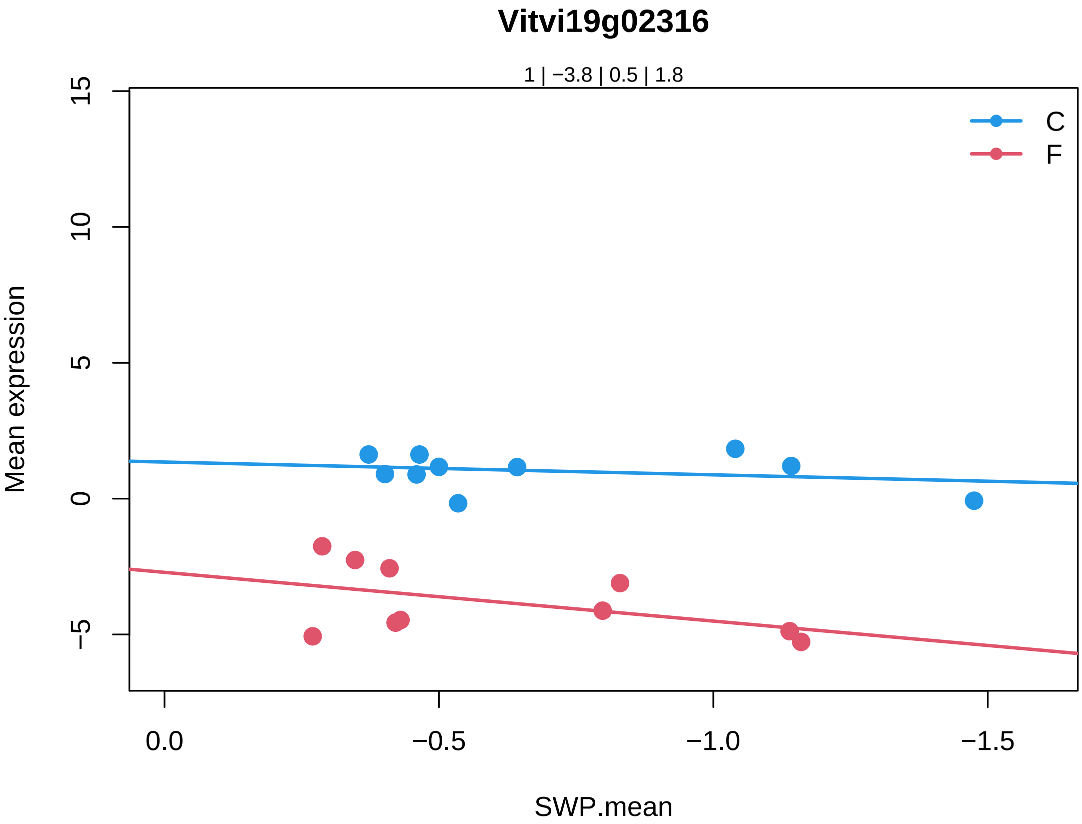
6.4.43 Vitvi19g02316

```
> 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.

```
                    swp  varietyF swp.varietyF   AveExpr        F
Vitvi19g02316 0.4709163 -4.060383     1.323198 -1.395607 52.41762
                   P.Value    adj.P.Val  type
Vitvi19g02316 4.837067e-10 3.544547e-08 type3
```



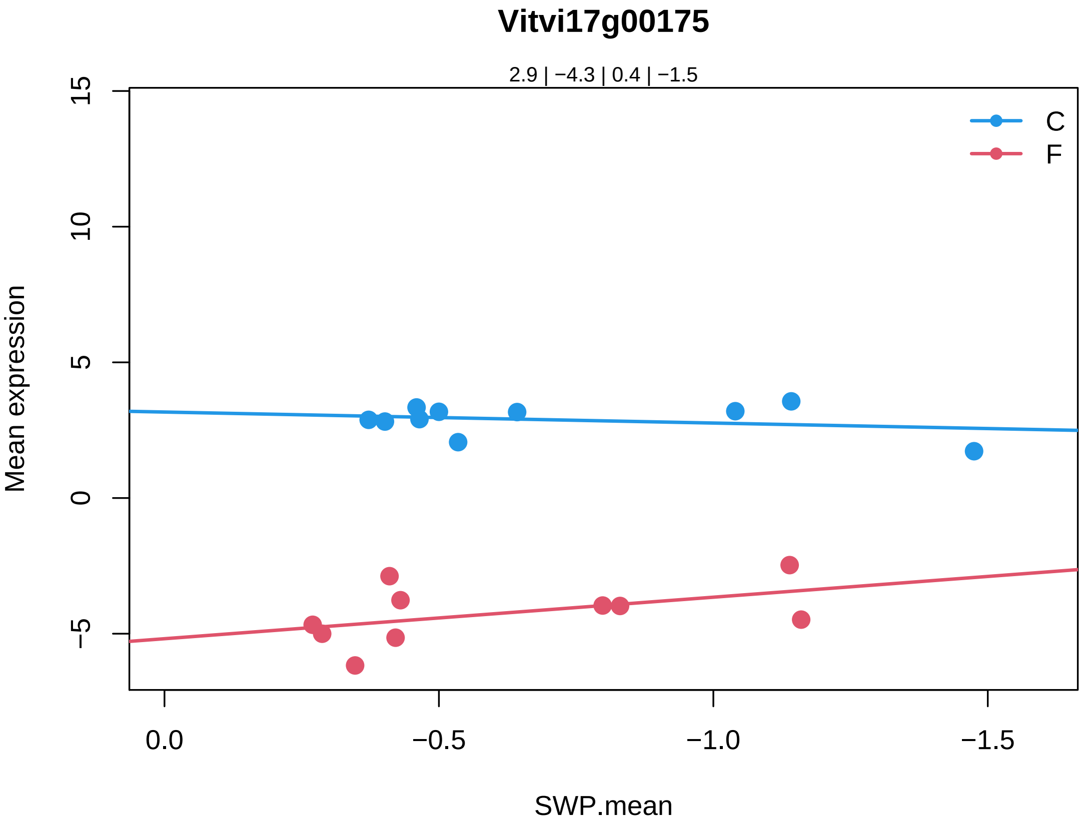
6.4.44 Vitvi17g00175

```
> 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.

```
                    swp  varietyF swp.varietyF    AveExpr        F
Vitvi17g00175 0.4052957 -8.353905    -1.935313 -0.6847511 149.7081
                   P.Value    adj.P.Val  type
Vitvi17g00175 1.556884e-14 2.303886e-12 type3
```



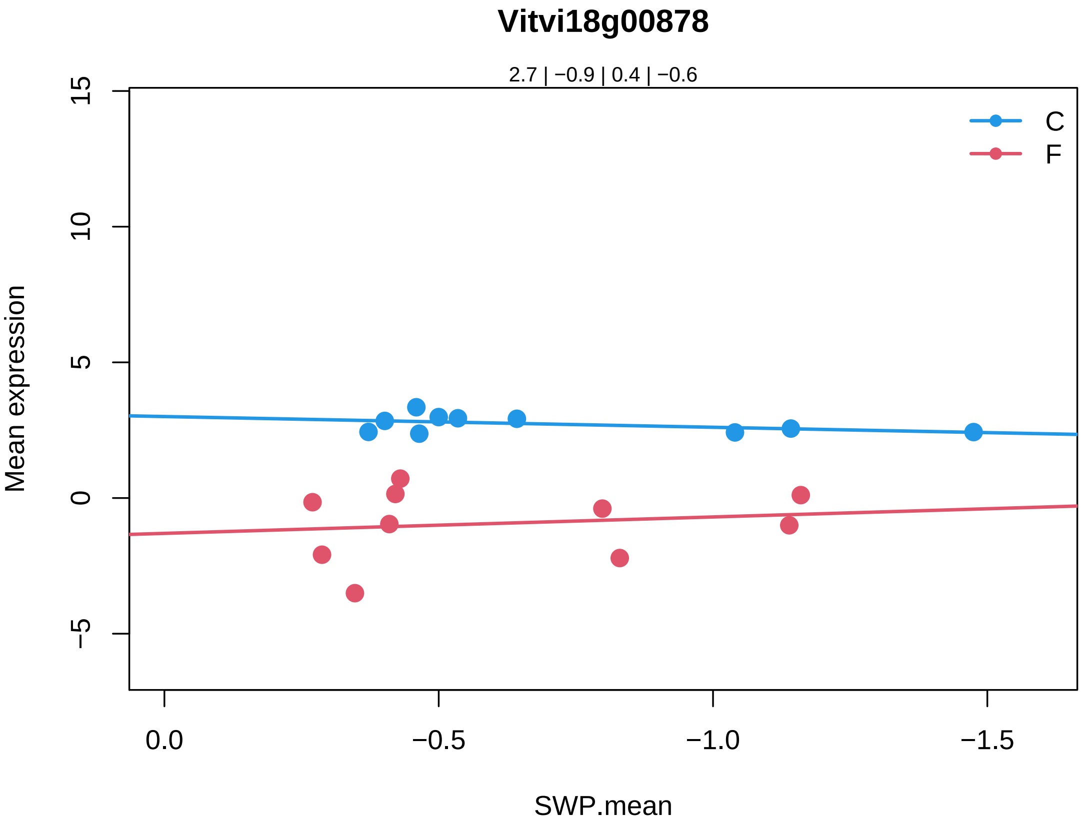
6.4.45 Vitvi18g00878

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

```
Vitvi18g00878
        26.1
        misc.cytochrome P450
        cytochrome P450%2C family 82%2C subfamily C%2C polypeptide 4 |
        Chr4:15452040-15453966 FORWARD LENGTH=524 |
        201606
```

Coefficients for Vitvi18g00878.

```
                    swp  varietyF swp.varietyF   AveExpr        F
Vitvi18g00878 0.3950882 -4.305351    -1.000008 0.8948832 28.13418
                   P.Value    adj.P.Val  type
Vitvi18g00878 1.269882e-07 6.183881e-06 type3
```



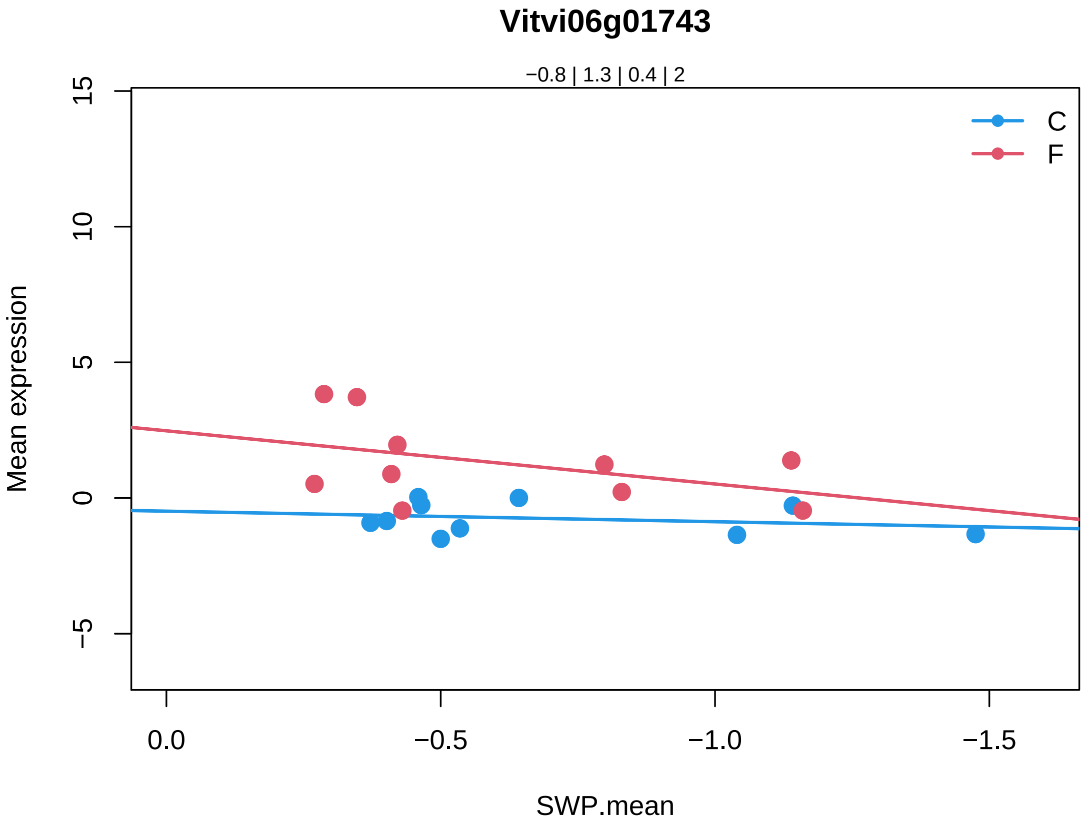
6.4.46 Vitvi06g01743

```
> 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.

```
                    swp varietyF swp.varietyF   AveExpr        F
Vitvi06g01743 0.3874884 2.962541     1.572361 0.2625299 8.560269
                   P.Value  adj.P.Val  type
Vitvi06g01743 0.0006295268 0.01010026 type3
```



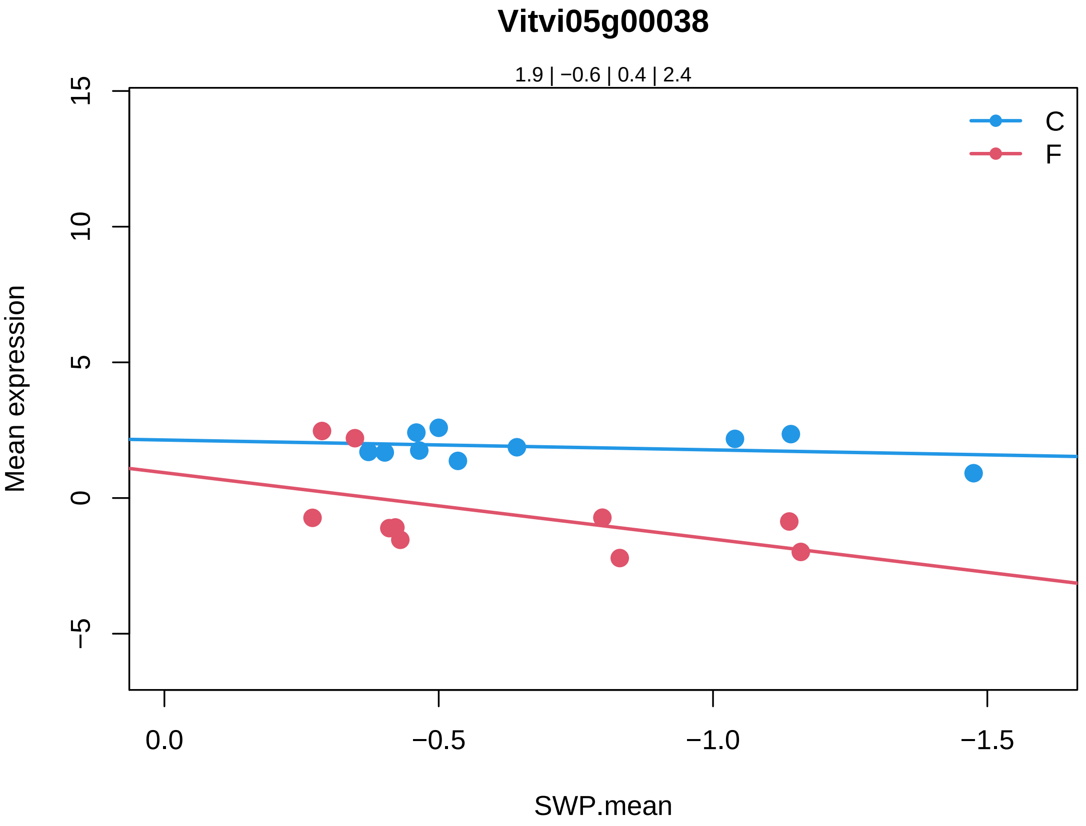
6.4.47 Vitvi05g00038

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

```
Vitvi05g00038
        26.03.2005
        misc.gluco-, galacto- and mannosidases.glycosyl hydrolase family 5
        alpha/beta-Hydrolases superfamily protein |
        Chr4:1035722-1037403 FORWARD LENGTH=324 |
        201606
```

Coefficients for Vitvi05g00038.

```
                    swp   varietyF swp.varietyF   AveExpr        F
Vitvi05g00038 0.3647677 -1.204967     2.082283 0.6618194 12.69346
                   P.Value   adj.P.Val  type
Vitvi05g00038 5.514927e-05 0.00136017 type4
```



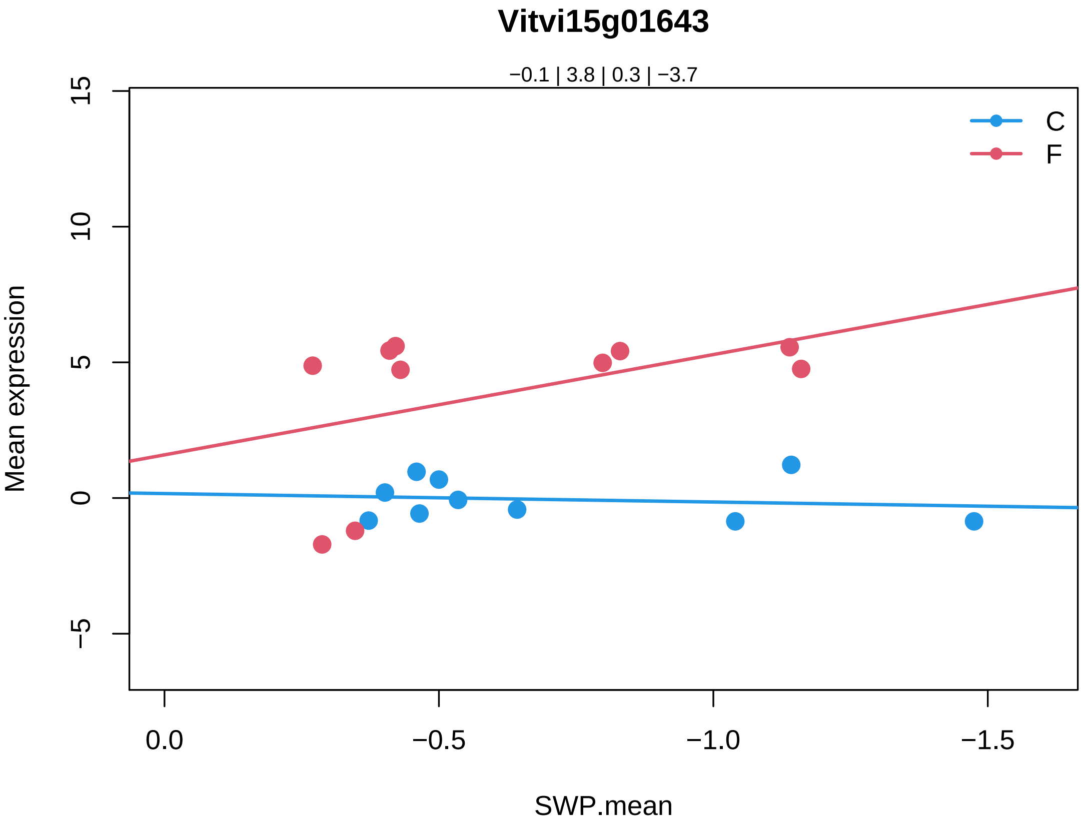
6.4.48 Vitvi15g01643

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

```
Vitvi15g01643
        16.8.1.12
        secondary metabolism.flavonoids.anthocyanins.anthocyanidin 3-O-glucosy
        UDP-Glycosyltransferase superfamily protein |
        Chr2:9593012-9594424 FORWARD LENGTH=470 |
        201606
```

Coefficients for Vitvi15g01643.

```
                    swp varietyF swp.varietyF  AveExpr        F
Vitvi15g01643 0.3115766 1.425993    -4.007713 1.893933 10.18312
                   P.Value   adj.P.Val  type
Vitvi15g01643 0.0002266261 0.004434191 type3
```



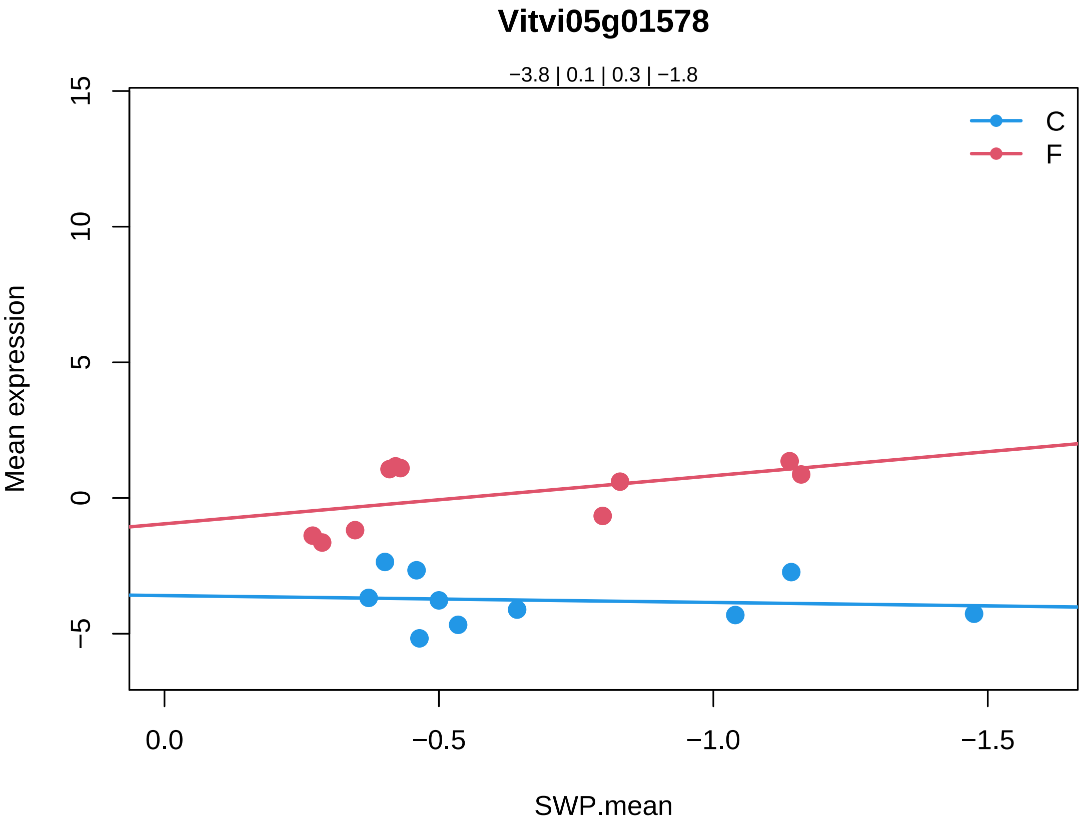
6.4.49 Vitvi05g01578

```
> 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.

```
                    swp varietyF swp.varietyF   AveExpr        F
Vitvi05g01578 0.2532287 2.644563    -2.026263 -1.822154 30.59555
                   P.Value    adj.P.Val  type
Vitvi05g01578 6.208185e-08 3.133283e-06 type3
```



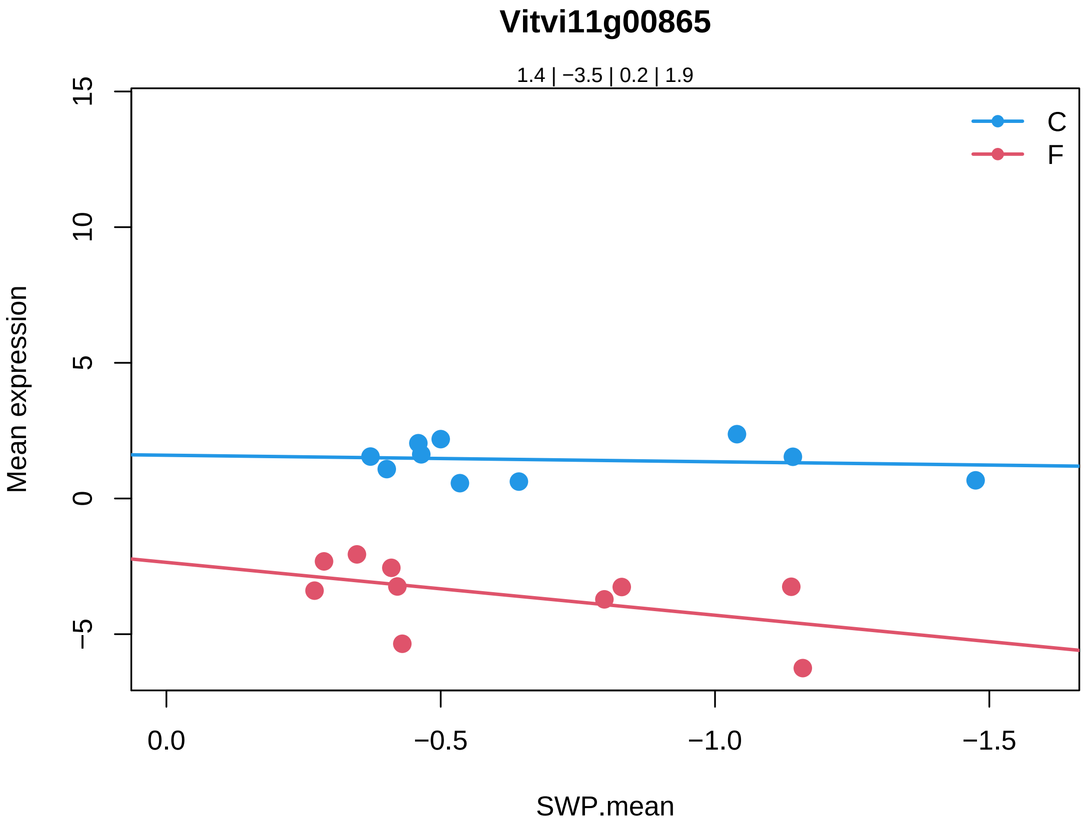
6.4.50 Vitvi11g00865

```
> 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.

```
                    swp  varietyF swp.varietyF  AveExpr        F
Vitvi11g00865 0.241433 -3.948727     1.705682 -1.05811 54.24604
                  P.Value    adj.P.Val  type
Vitvi11g00865 3.50431e-10 2.670634e-08 type3
```



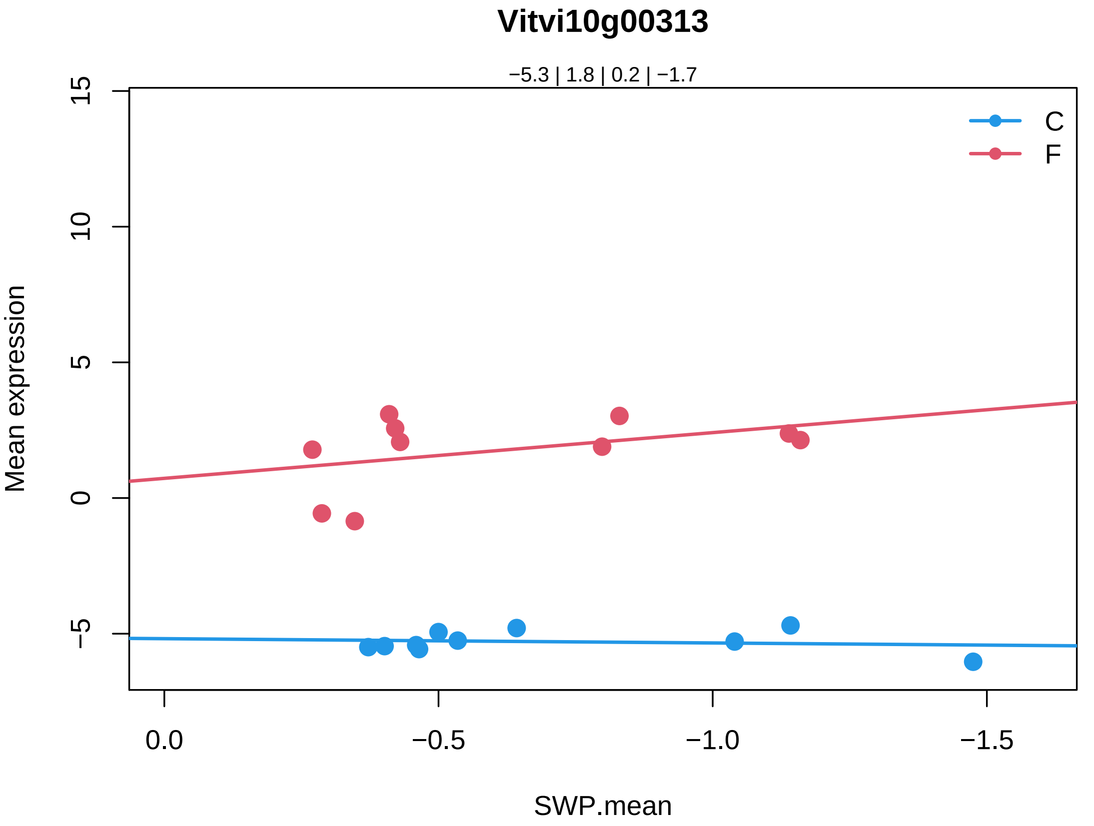
6.4.51 Vitvi10g00313

```
> 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.

```
                    swp varietyF swp.varietyF   AveExpr        F
Vitvi10g00313 0.1580878 5.908168    -1.843471 -1.771591 108.3066
                   P.Value    adj.P.Val  type
Vitvi10g00313 4.127875e-13 4.877292e-11 type3
```



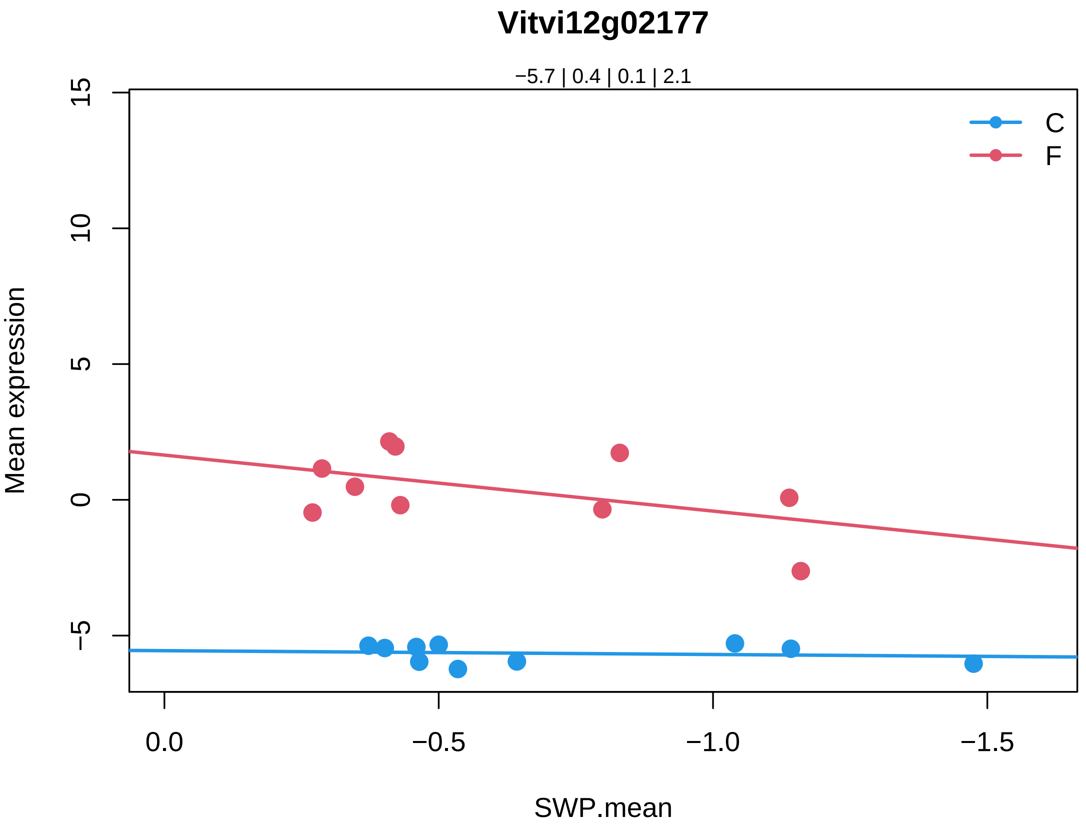
6.4.52 Vitvi12g02177

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

```
Vitvi12g02177
        16.01.2005
        secondary metabolism.isoprenoids.terpenoids
        terpene synthase 21 |
        Chr5:8092969-8095128 FORWARD LENGTH=545 |
        201606
```

Coefficients for Vitvi12g02177.

```
                    swp varietyF swp.varietyF   AveExpr       F
Vitvi12g02177 0.1400847 7.203545     1.922026 -2.631891 80.5119
                   P.Value    adj.P.Val  type
Vitvi12g02177 7.832868e-12 7.604368e-10 type4
```



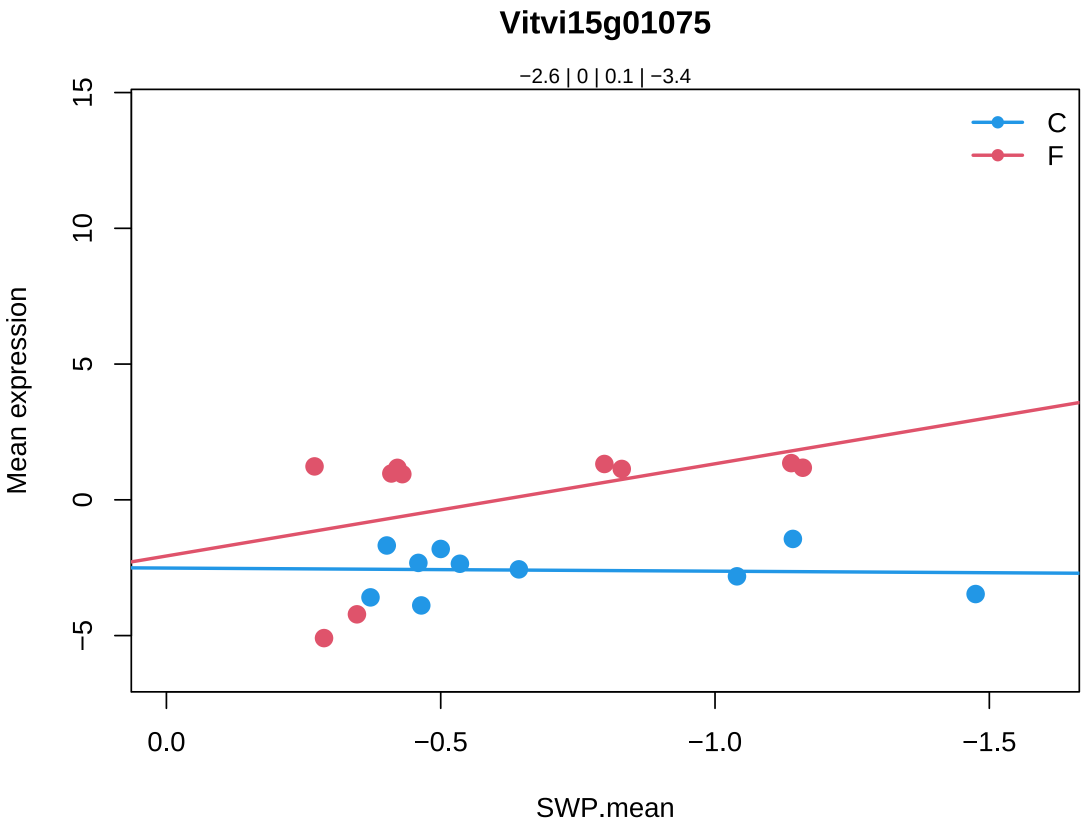
6.4.53 Vitvi15g01075

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

```
Vitvi15g01075
        16.8.1.12
        secondary metabolism.flavonoids.anthocyanins.anthocyanidin 3-O-glucosy
        UDP-Glycosyltransferase superfamily protein |
        Chr2:9593012-9594424 FORWARD LENGTH=470 |
        201606
```

Coefficients for Vitvi15g01075.

```
                    swp  varietyF swp.varietyF   AveExpr        F
Vitvi15g01075 0.1146464 0.4444895    -3.510991 -1.296593 6.546786
                  P.Value  adj.P.Val  type
Vitvi15g01075 0.002591574 0.03110297 type3
```



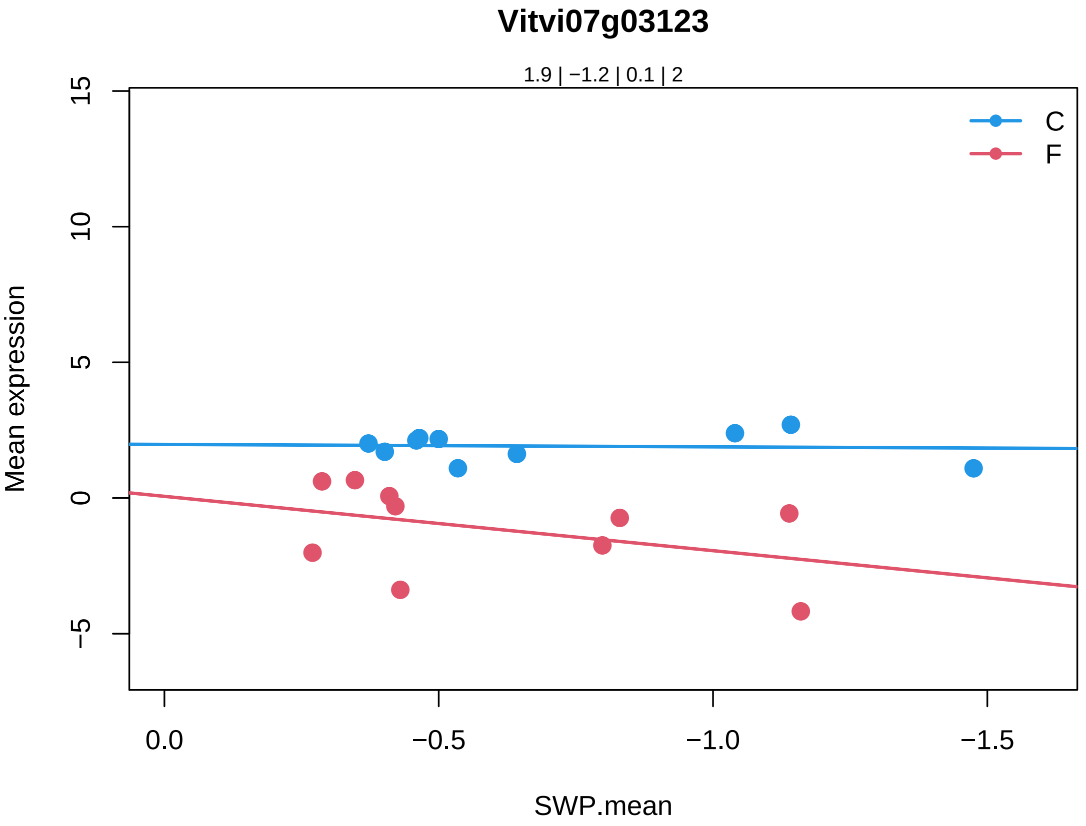
6.4.54 Vitvi07g03123

```
> 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.

```
                    swp   varietyF swp.varietyF   AveExpr        F
Vitvi07g03123 0.0898298 -1.913572     1.912759 0.3773528 15.38188
                   P.Value   adj.P.Val  type
Vitvi07g03123 1.453035e-05 0.000434258 type4
```



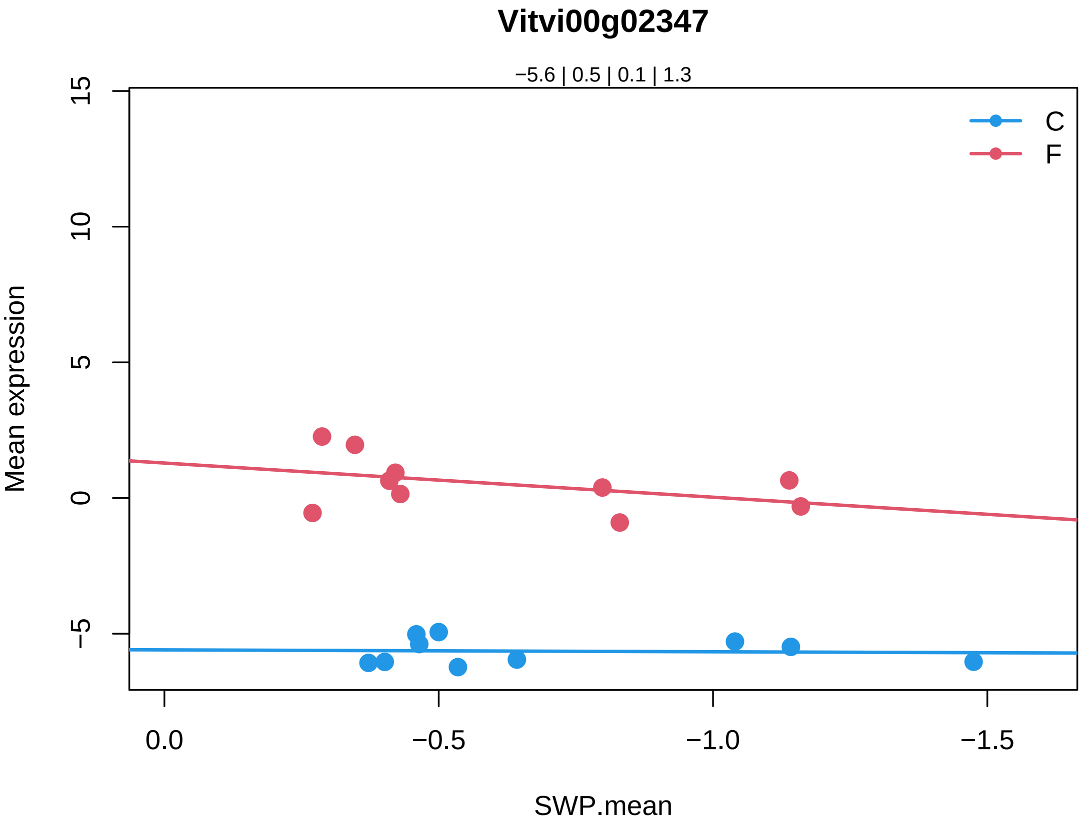
6.4.55 Vitvi00g02347

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

```
Vitvi00g02347
        35.2
        not assigned.unknown
        S-locus lectin protein kinase family protein |
        Chr1:3810372-3813053 FORWARD LENGTH=748 |
        201606
```

Coefficients for Vitvi00g02347.

```
                     swp varietyF swp.varietyF   AveExpr        F
Vitvi00g02347 0.06949314 6.885558     1.189664 -2.561773 124.7856
                   P.Value    adj.P.Val  type
Vitvi00g02347 9.911054e-14 1.291148e-11 type3
```



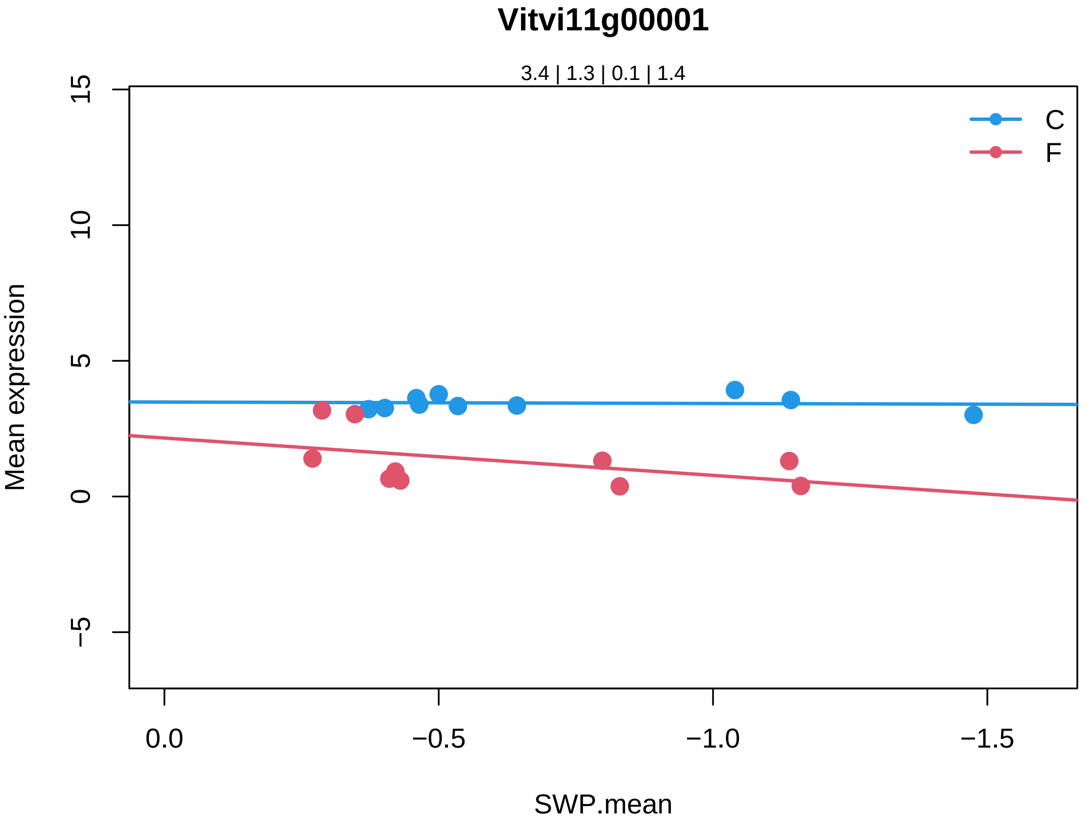
6.4.56 Vitvi11g00001

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

```
Vitvi11g00001
        11.10.2002
        lipid metabolism.glycolipid synthesis.DGDG synthase
        digalactosyl diacylglycerol deficient 2 |
        Chr4:238154-240019 REVERSE LENGTH=473 |
        201606

Vitvi11g00001
        35.2
        not assigned.unknown
        digalactosyl diacylglycerol deficient 2 |
        Chr4:238154-240019 REVERSE LENGTH=473 |
        201606
```

Coefficients for Vitvi11g00001.

```
                     swp   varietyF swp.varietyF  AveExpr        F
Vitvi11g00001 0.05303929 -1.325372     1.323482 2.379576 19.05761
                   P.Value    adj.P.Val  type
Vitvi11g00001 2.955991e-06 0.0001059376 type3
```



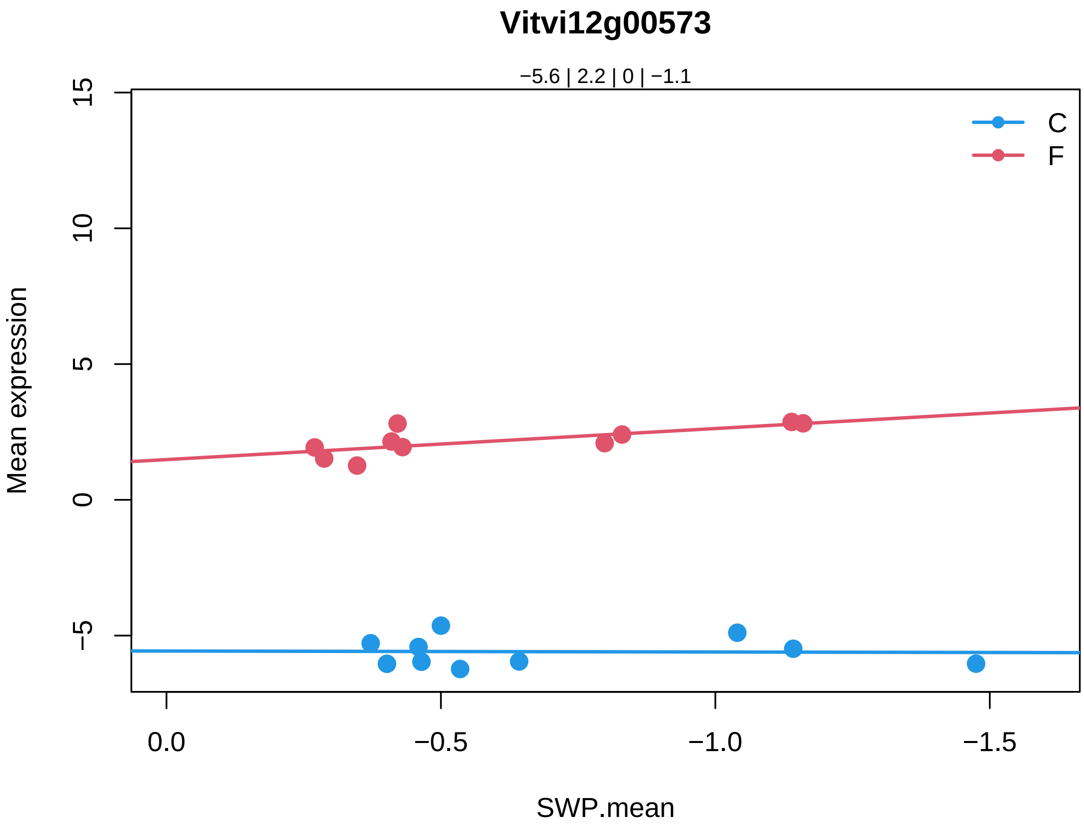
6.4.57 Vitvi12g00573

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

```
Vitvi12g00573
        16.01.2005
        secondary metabolism.isoprenoids.terpenoids
        Terpenoid cyclases/Protein prenyltransferases superfamily protein |
        Chr3:9430805-9433844 FORWARD LENGTH=598 |
        201606
```

Coefficients for Vitvi12g00573.

```
                    swp varietyF swp.varietyF   AveExpr        F
Vitvi12g00573 0.0353512 7.051062    -1.179046 -1.707561 412.4164
                   P.Value    adj.P.Val  type
Vitvi12g00573 4.139672e-19 1.705321e-16 type3
```



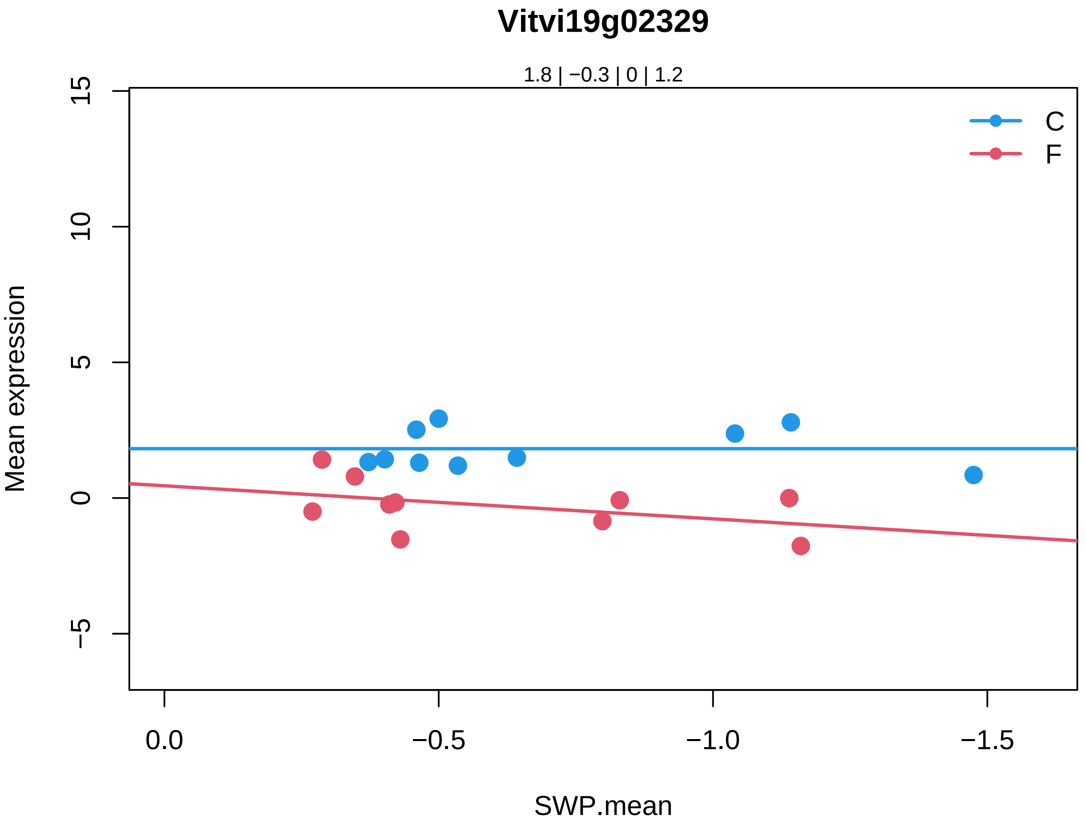
6.4.58 Vitvi19g02329

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

```
Vitvi19g02329
        26.03.2005
        misc.gluco-, galacto- and mannosidases.glycosyl hydrolase family 5
        NB-ARC domain-containing disease resistance protein |
        Chr3:4857940-4861104 FORWARD LENGTH=1054 |
        201606
```

Coefficients for Vitvi19g02329.

```
                       swp  varietyF swp.varietyF   AveExpr        F
Vitvi19g02329 0.0001976475 -1.368327      1.21853 0.7635371 13.01569
                   P.Value   adj.P.Val  type
Vitvi19g02329 4.658331e-05 0.001189318 type3
```



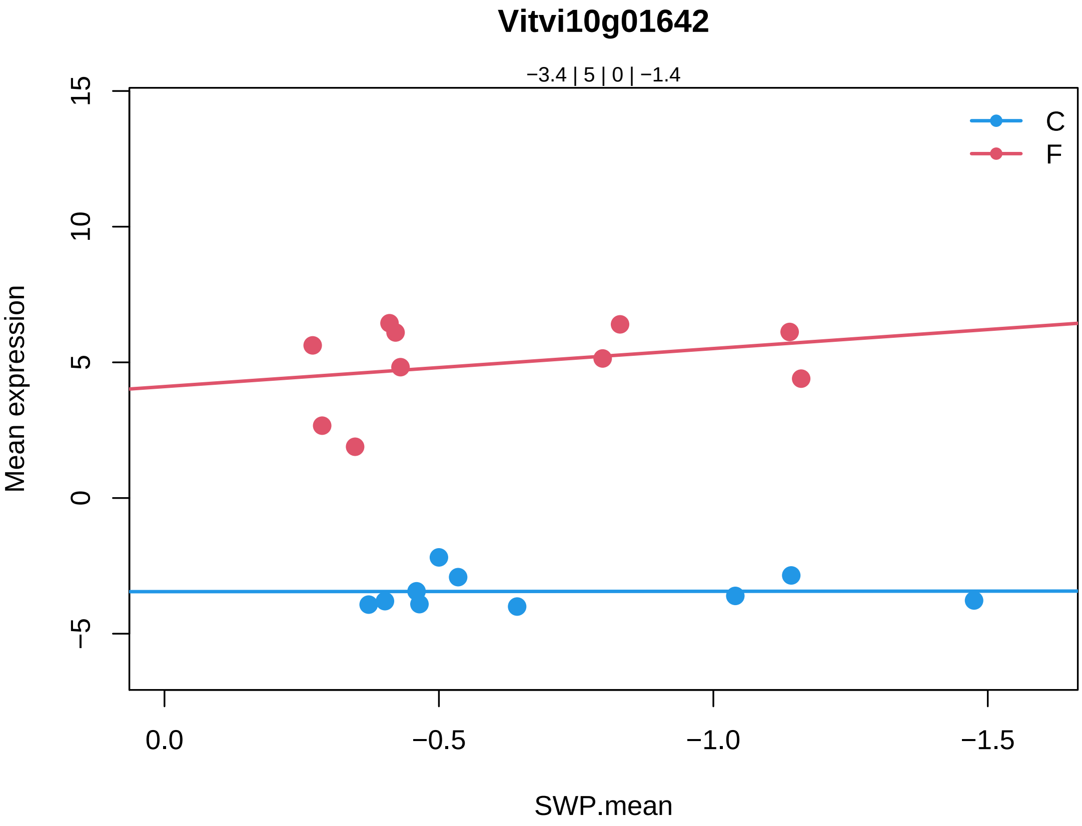
6.4.59 Vitvi10g01642

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

```
Vitvi10g01642
        35.2
        not assigned.unknown
        senescence regulator (Protein of unknown function%2C DUF584) |
        Chr1:3945852-3946457 FORWARD LENGTH=201 |
        201606
```

Coefficients for Vitvi10g01642.

```
                      swp varietyF swp.varietyF   AveExpr        F
Vitvi10g01642 -0.01243179 7.557195    -1.389259 0.7596291 102.0764
                   P.Value    adj.P.Val  type
Vitvi10g01642 7.469185e-13 8.370979e-11 type3
```



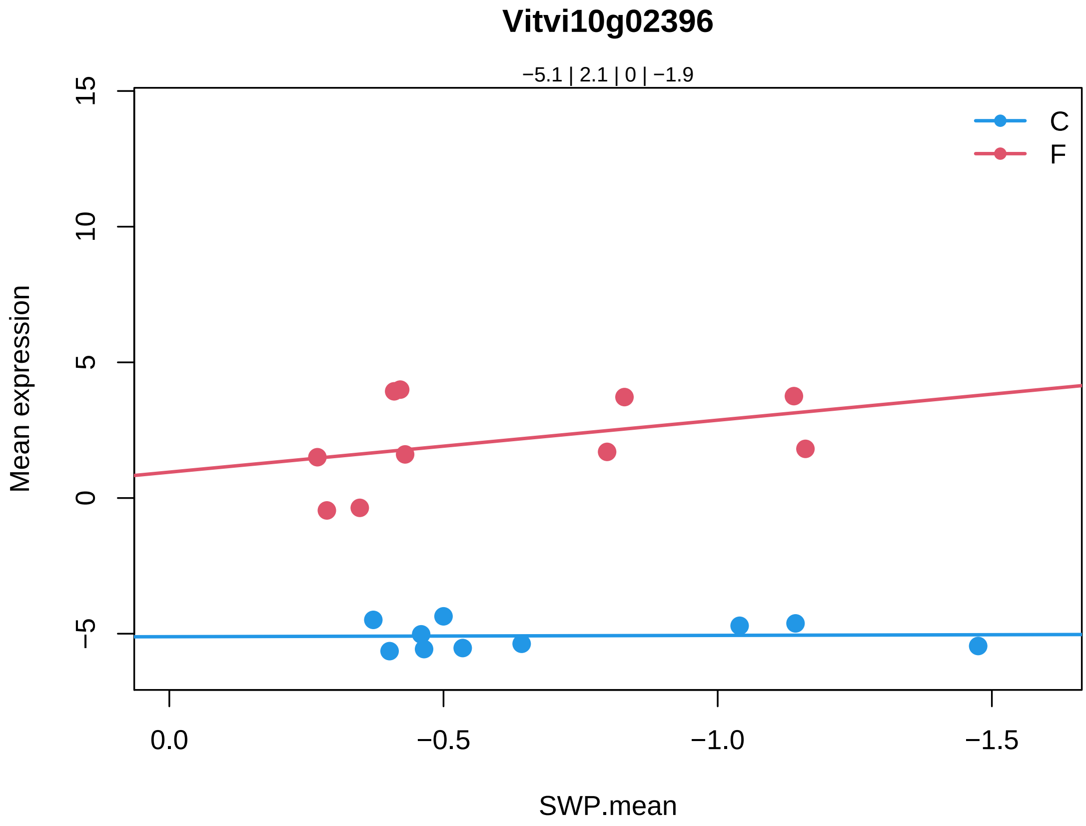
6.4.60 Vitvi10g02396

```
> 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.

```
                      swp varietyF swp.varietyF AveExpr        F
Vitvi10g02396 -0.04830116 6.063859    -1.867763  -1.478 74.11585
                   P.Value    adj.P.Val  type
Vitvi10g02396 1.759159e-11 1.558901e-09 type3
```



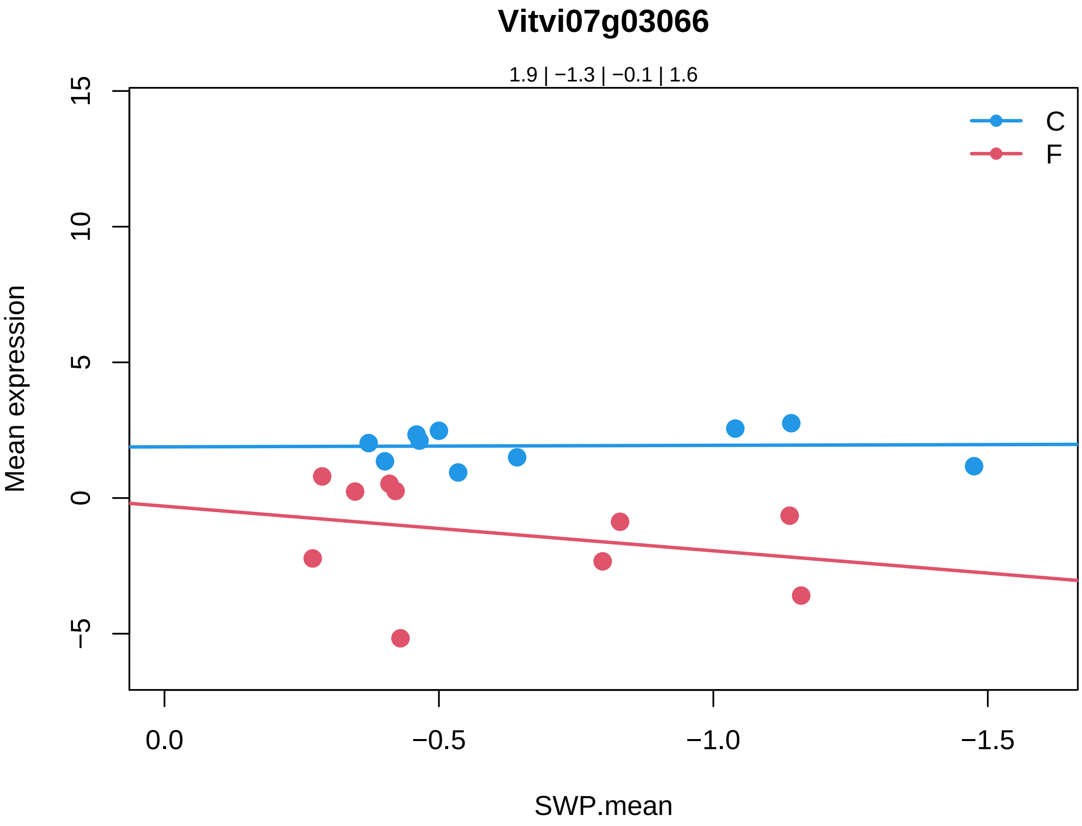
6.4.61 Vitvi07g03066

```
> 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.

```
                     swp varietyF swp.varietyF   AveExpr        F
Vitvi07g03066 -0.0543839 -2.18726     1.698955 0.3106513 10.50913
                  P.Value   adj.P.Val  type
Vitvi07g03066 0.000186621 0.003775739 type3
```



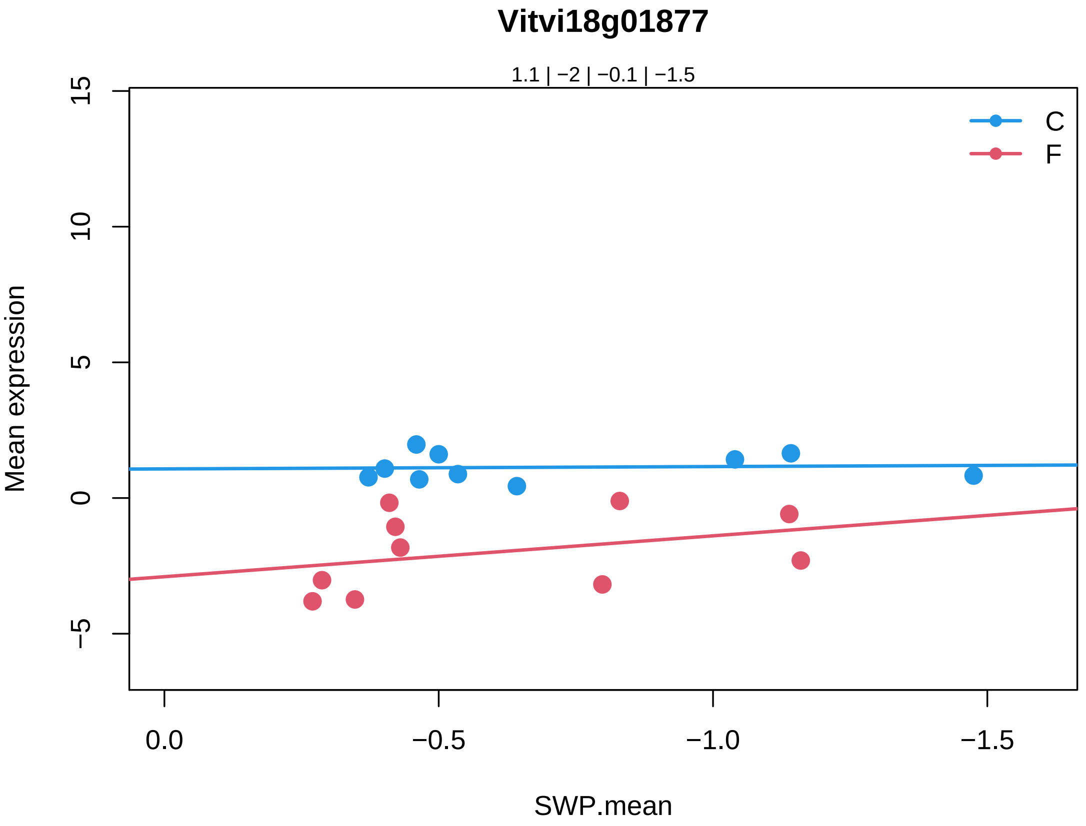
6.4.62 Vitvi18g01877

```
> 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.

```
                      swp  varietyF swp.varietyF    AveExpr        F
Vitvi18g01877 -0.08588147 -3.973192    -1.420387 -0.4242541 18.40735
                  P.Value    adj.P.Val  type
Vitvi18g01877 3.85348e-06 0.0001350224 type3
```



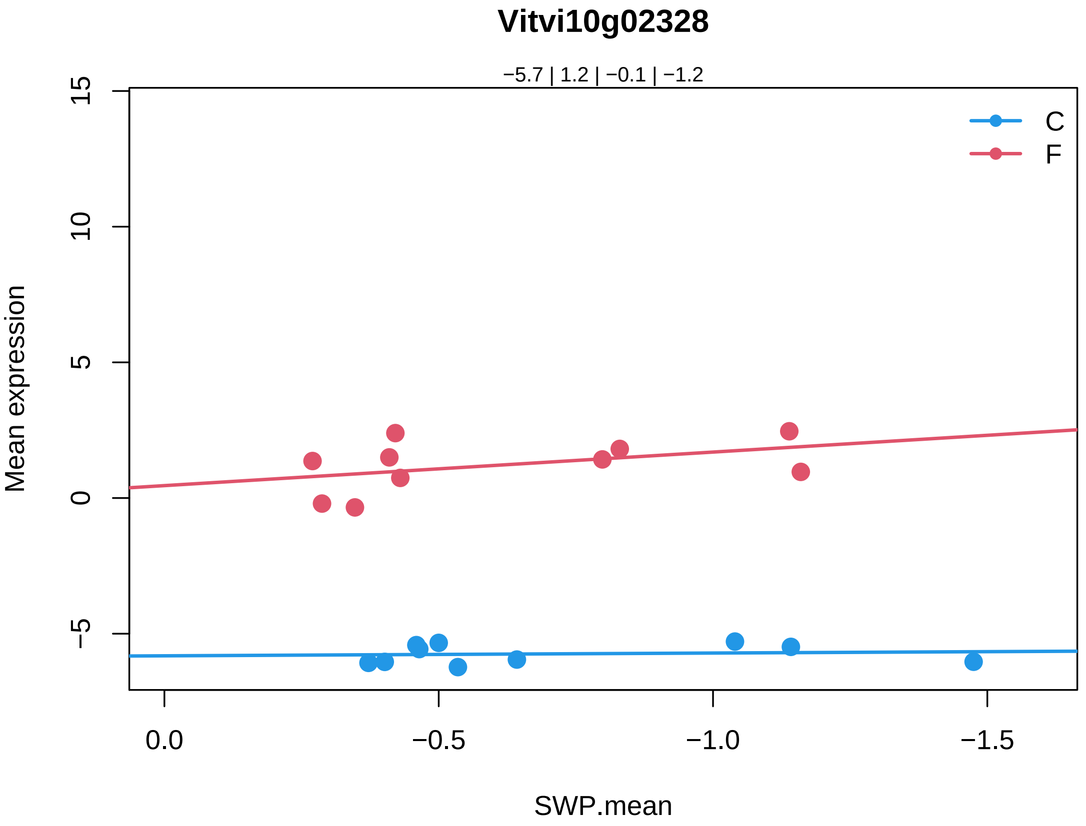
6.4.63 Vitvi10g02328

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

```
Vitvi10g02328
        35.2
        not assigned.unknown
        B-box type zinc finger family protein |
        Chr4:13675853-13676616 FORWARD LENGTH=223 |
        201606
```

Coefficients for Vitvi10g02328.

```
                     swp varietyF swp.varietyF   AveExpr        F
Vitvi10g02328 -0.1021136 6.271869    -1.134082 -2.266683 193.6768
                   P.Value    adj.P.Val  type
Vitvi10g02328 1.106018e-15 2.133914e-13 type3
```



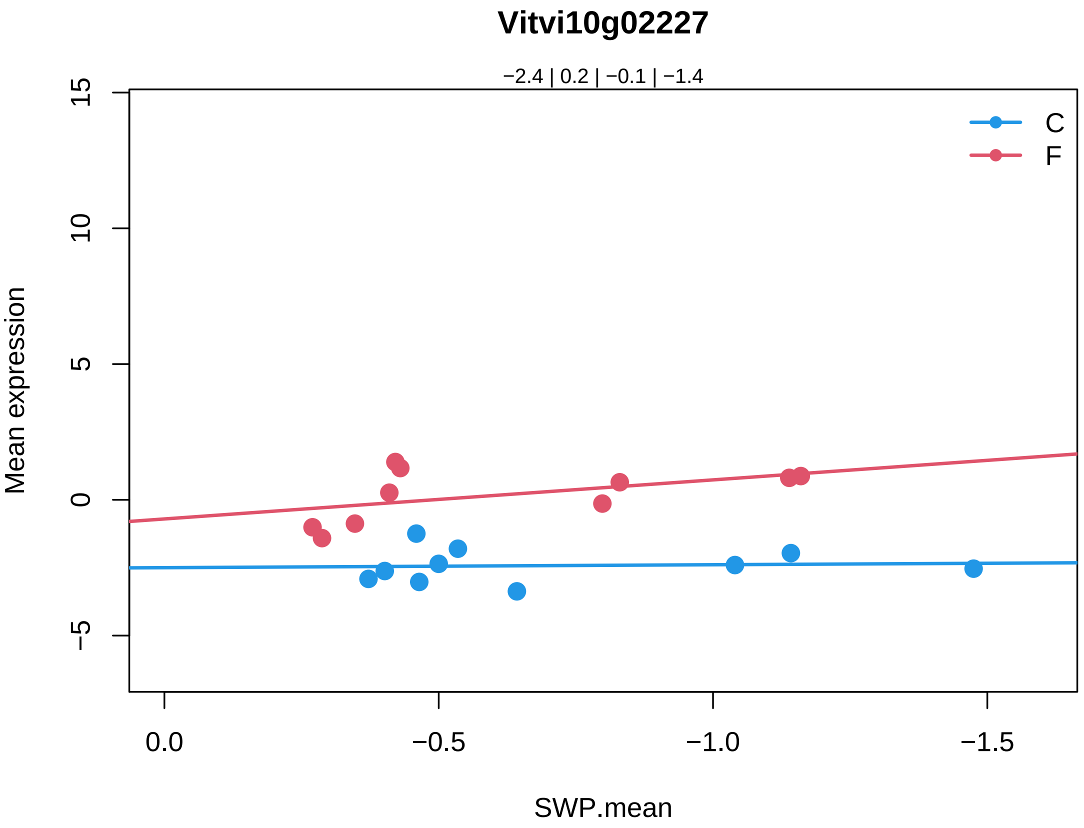
6.4.64 Vitvi10g02227

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

```
Vitvi10g02227
        30.2.17
        signalling.receptor kinases.DUF 26
        Receptor-like protein kinase-related family protein |
        Chr3:7771065-7772137 FORWARD LENGTH=252 |
        201606
```

Coefficients for Vitvi10g02227.

```
                     swp varietyF swp.varietyF   AveExpr        F
Vitvi10g02227 -0.1082359 1.794623    -1.330957 -1.125606 22.60515
                   P.Value    adj.P.Val  type
Vitvi10g02227 7.726698e-07 3.217769e-05 type3
```



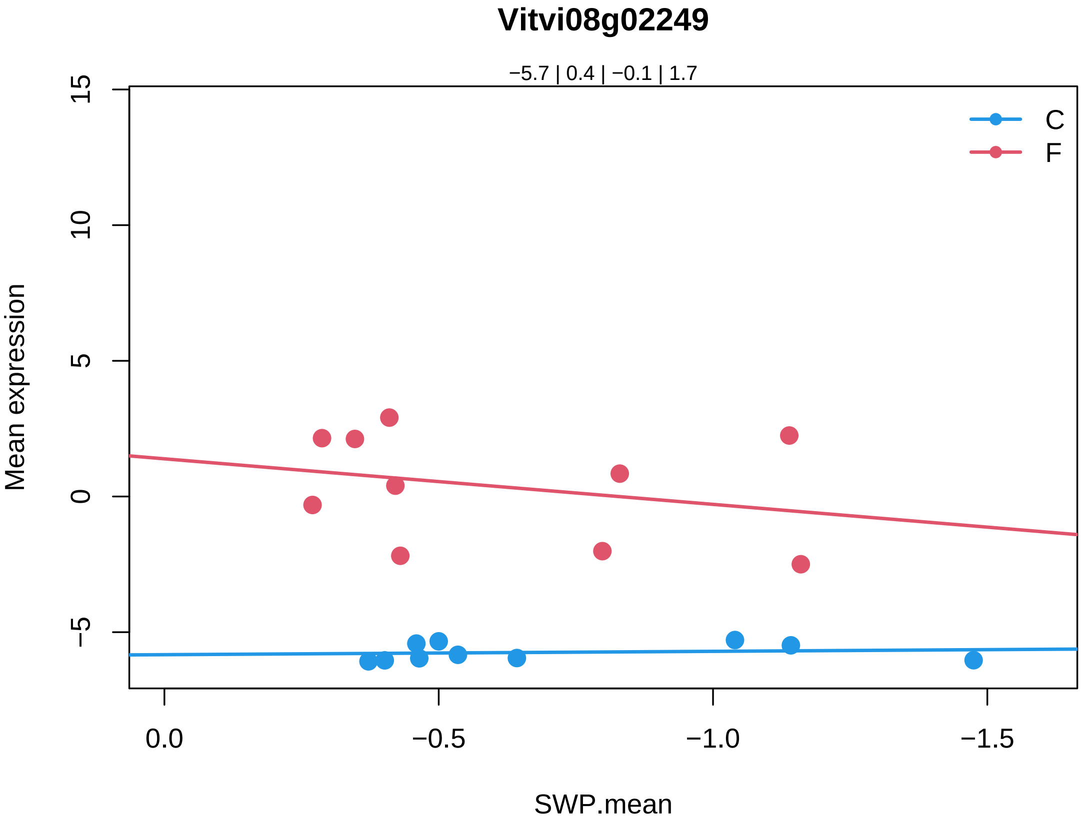
6.4.65 Vitvi08g02249

```
> 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.

```
                     swp varietyF swp.varietyF   AveExpr        F
Vitvi08g02249 -0.1237221 7.219131     1.802499 -2.688678 37.09491
                   P.Value    adj.P.Val  type
Vitvi08g02249 1.147554e-08 6.727313e-07 type3
```



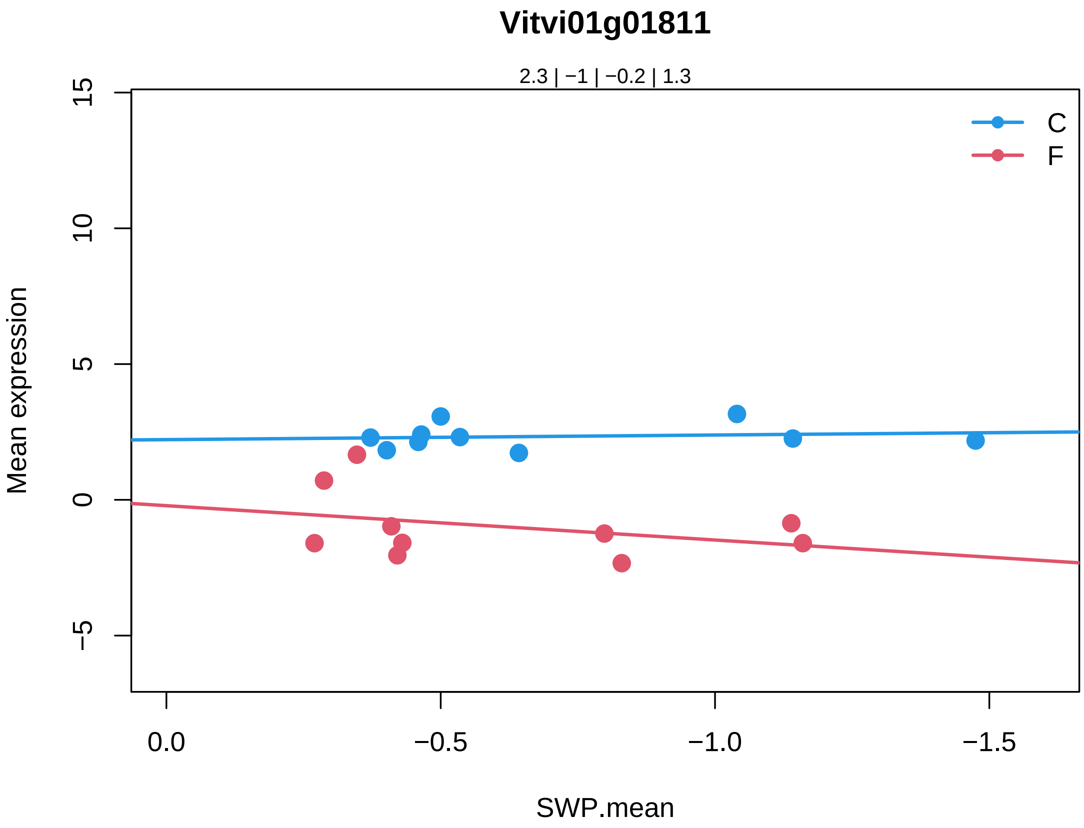
6.4.66 Vitvi01g01811

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

```
Vitvi01g01811
        35.2
        not assigned.unknown
        heparan-alpha-glucosaminide N-acetyltransferase-like protein (DUF1624)
        Chr5:19392408-19394689 FORWARD LENGTH=403 |
        201606
```

Coefficients for Vitvi01g01811.

```
                     swp   varietyF swp.varietyF   AveExpr        F
Vitvi01g01811 -0.1698524 -2.433275     1.433989 0.6751097 26.26739
                   P.Value    adj.P.Val  type
Vitvi01g01811 2.259963e-07 1.050194e-05 type3
```



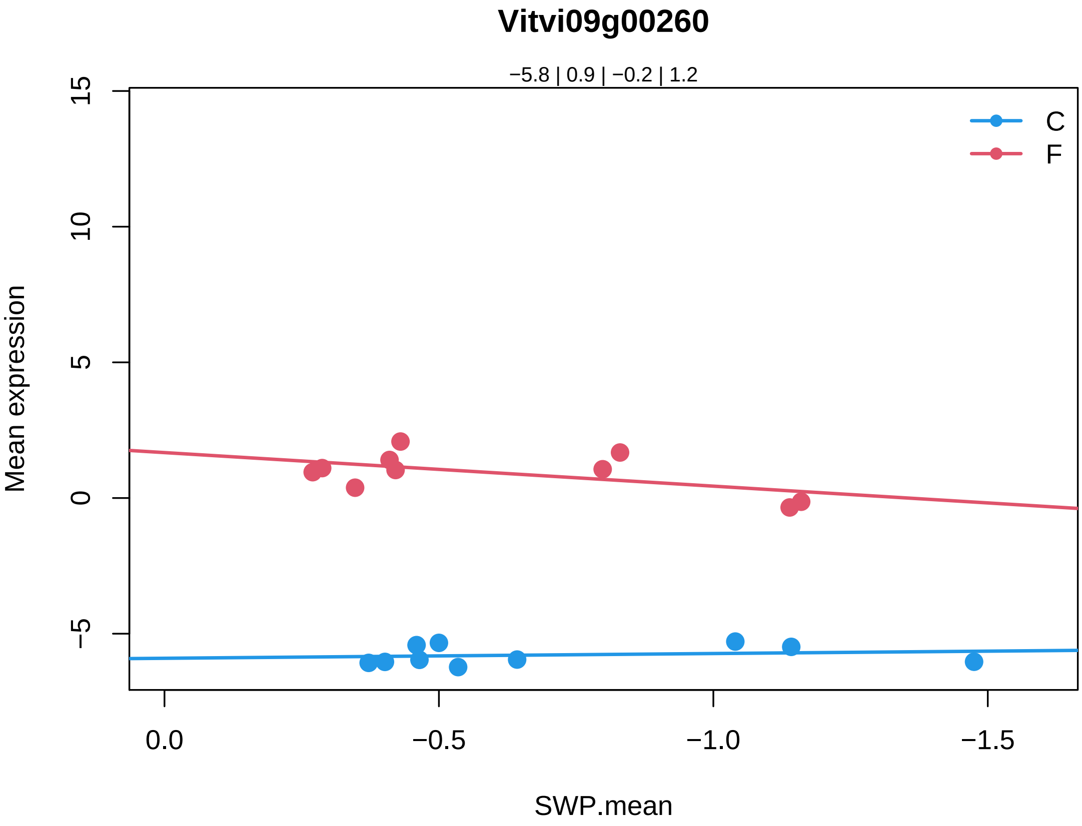
6.4.67 Vitvi09g00260

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

```
Vitvi09g00260
        35.2
        not assigned.unknown
        root hair specific 16 |
        Chr4:14385631-14389524 FORWARD LENGTH=911 |
        201606
```

Coefficients for Vitvi09g00260.

```
                    swp varietyF swp.varietyF   AveExpr        F
Vitvi09g00260 -0.175305 7.579752     1.411262 -2.431225 268.7274
                   P.Value    adj.P.Val  type
Vitvi09g00260 3.692654e-17 9.443009e-15 type3
```



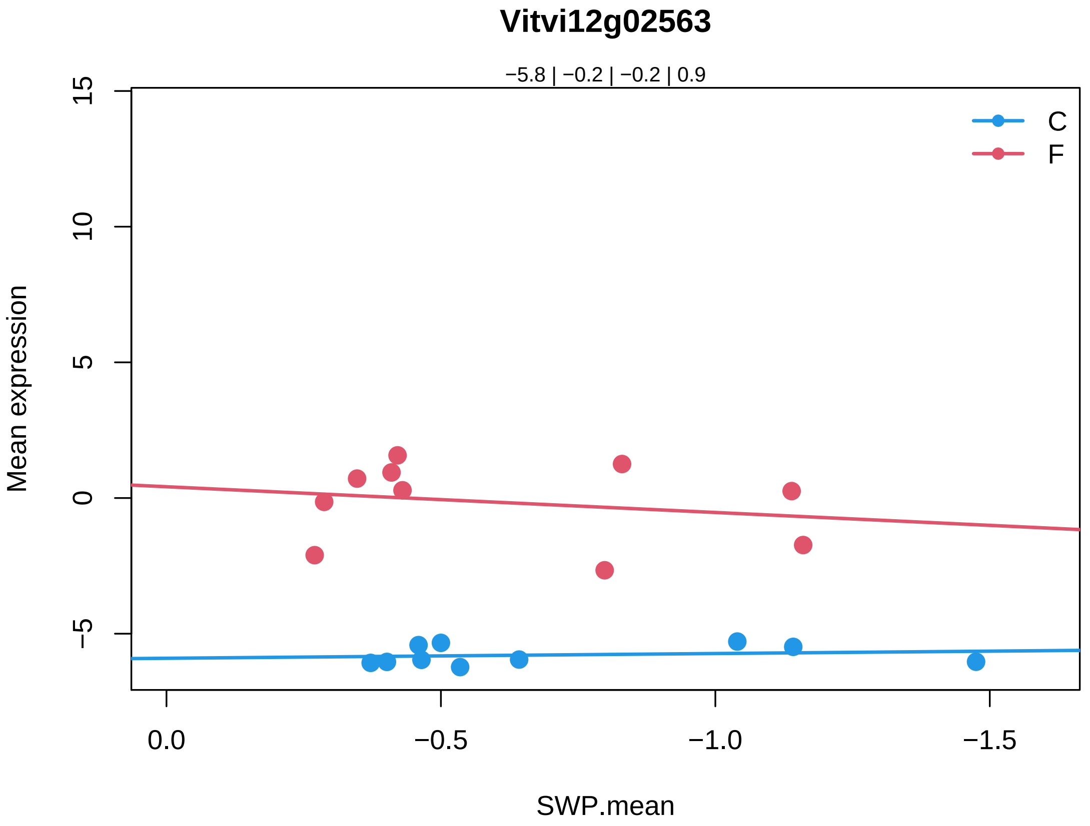
6.4.68 Vitvi12g02563

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

```
Vitvi12g02563
        35.2
        not assigned.unknown
        Peroxidase superfamily protein |
        Chr5:25659551-25660946 REVERSE LENGTH=328 |
        201606
```

Coefficients for Vitvi12g02563.

```
                    swp varietyF swp.varietyF  AveExpr        F
Vitvi12g02563 -0.175305 6.322029     1.123919 -2.97255 53.27693
                   P.Value    adj.P.Val  type
Vitvi12g02563 4.152129e-10 3.087158e-08 type3
```



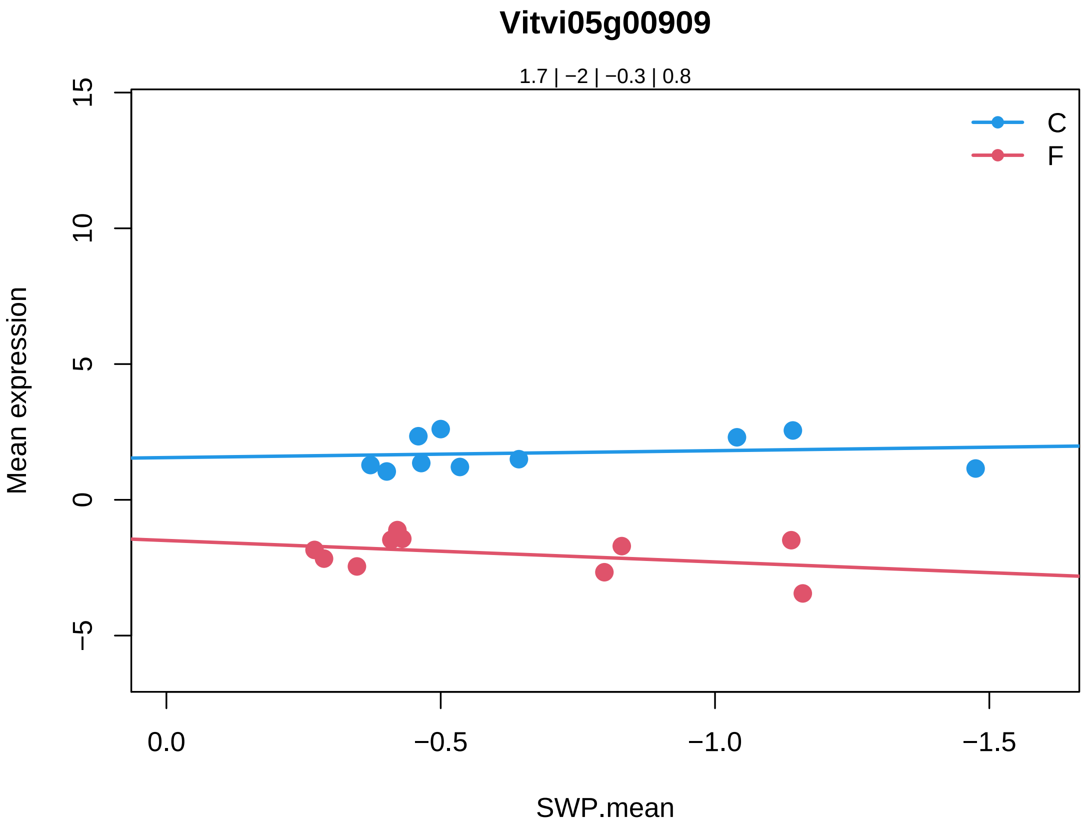
6.4.69 Vitvi05g00909

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

```
Vitvi05g00909
        20.1.2.2
        stress.biotic.receptors.TIR-NBS-LRR
        disease resistance protein (TIR-NBS-LRR class) |
        Chr5:5822999-5827153 FORWARD LENGTH=1295 |
        201606
```

Coefficients for Vitvi05g00909.

```
                     swp  varietyF swp.varietyF    AveExpr        F
Vitvi05g00909 -0.2554092 -3.052617     1.045479 -0.1223915 57.25393
                  P.Value    adj.P.Val  type
Vitvi05g00909 2.10426e-10 1.679342e-08 type3
```



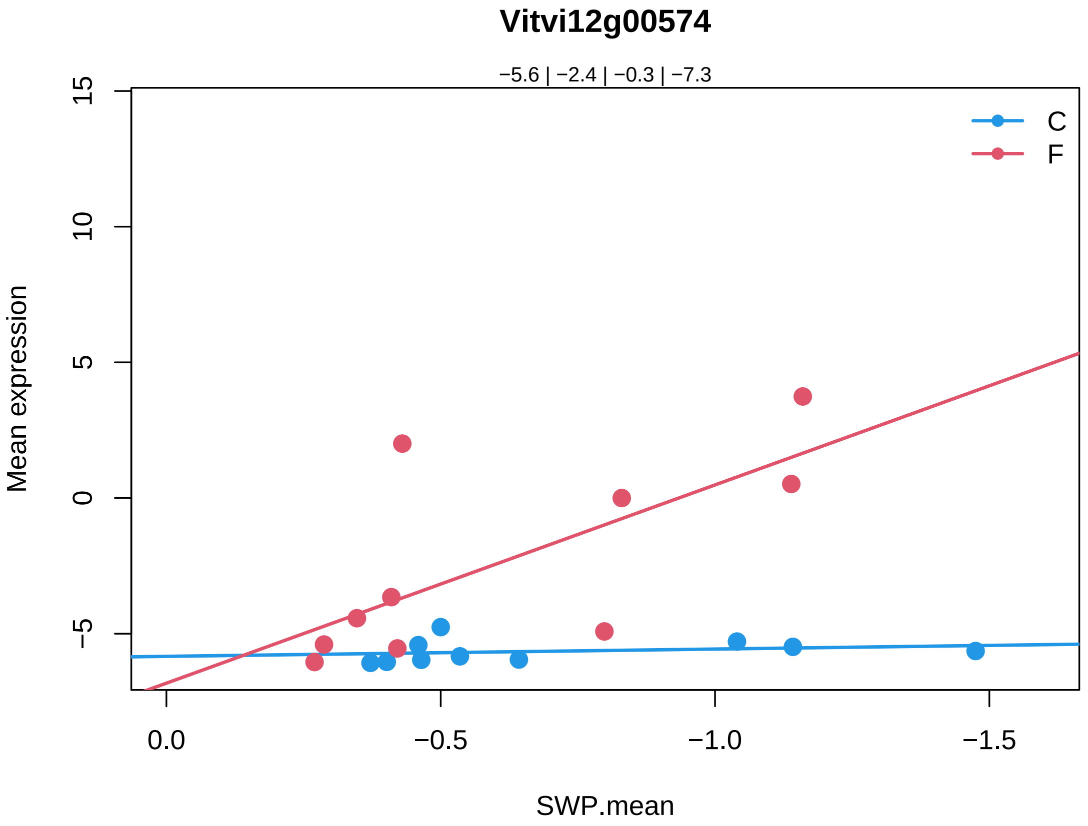
6.4.70 Vitvi12g00574

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

```
Vitvi12g00574
        16.01.2005
        secondary metabolism.isoprenoids.terpenoids
        terpene synthase-like sequence-1%2C8-cineole |
        Chr3:9447545-9450316 FORWARD LENGTH=600 |
        201606
```

Coefficients for Vitvi12g00574.

```
                     swp   varietyF swp.varietyF   AveExpr        F
Vitvi12g00574 -0.2692201 -0.9884648    -7.036961 -4.008795 12.81278
                   P.Value  adj.P.Val  type
Vitvi12g00574 5.179173e-05 0.00130051 type4
```



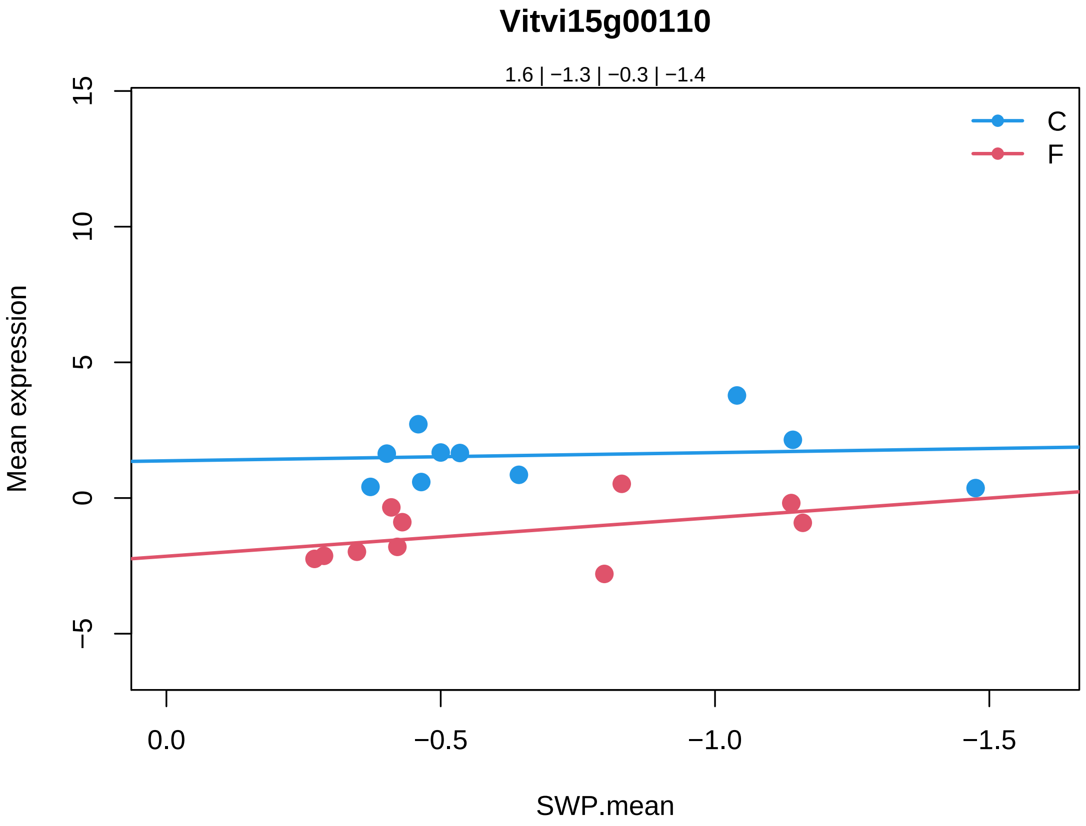
6.4.71 Vitvi15g00110

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

```
Vitvi15g00110
        35.2
        not assigned.unknown
        Pentatricopeptide repeat (PPR) superfamily protein |
        Chr4:14962617-14964995 REVERSE LENGTH=792 |
        201606
```

Coefficients for Vitvi15g00110.

```
                     swp  varietyF swp.varietyF   AveExpr        F
Vitvi15g00110 -0.3035374 -3.516339    -1.124079 0.1537531 15.30332
                   P.Value    adj.P.Val  type
Vitvi15g00110 1.507404e-05 0.0004487472 type3
```



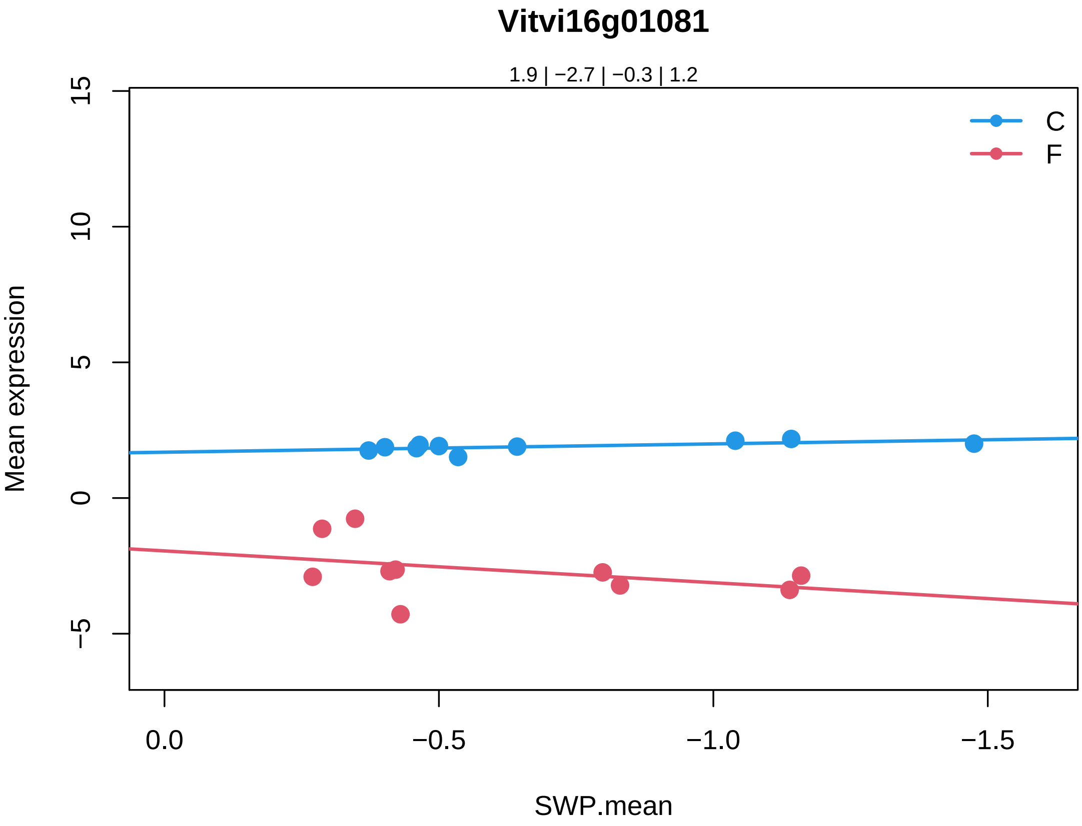
6.4.72 Vitvi16g01081

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

```
Vitvi16g01081
        35.1
        not assigned.no ontology
        Ribosomal protein L31 |
        Chr1:28272163-28272687 FORWARD LENGTH=144 |
        201606
```

Coefficients for Vitvi16g01081.

```
                     swp varietyF swp.varietyF    AveExpr        F
Vitvi16g01081 -0.3059787 -3.63805     1.476801 -0.3797921 79.21062
                   P.Value    adj.P.Val  type
Vitvi16g01081 9.189545e-12 8.809248e-10 type3
```



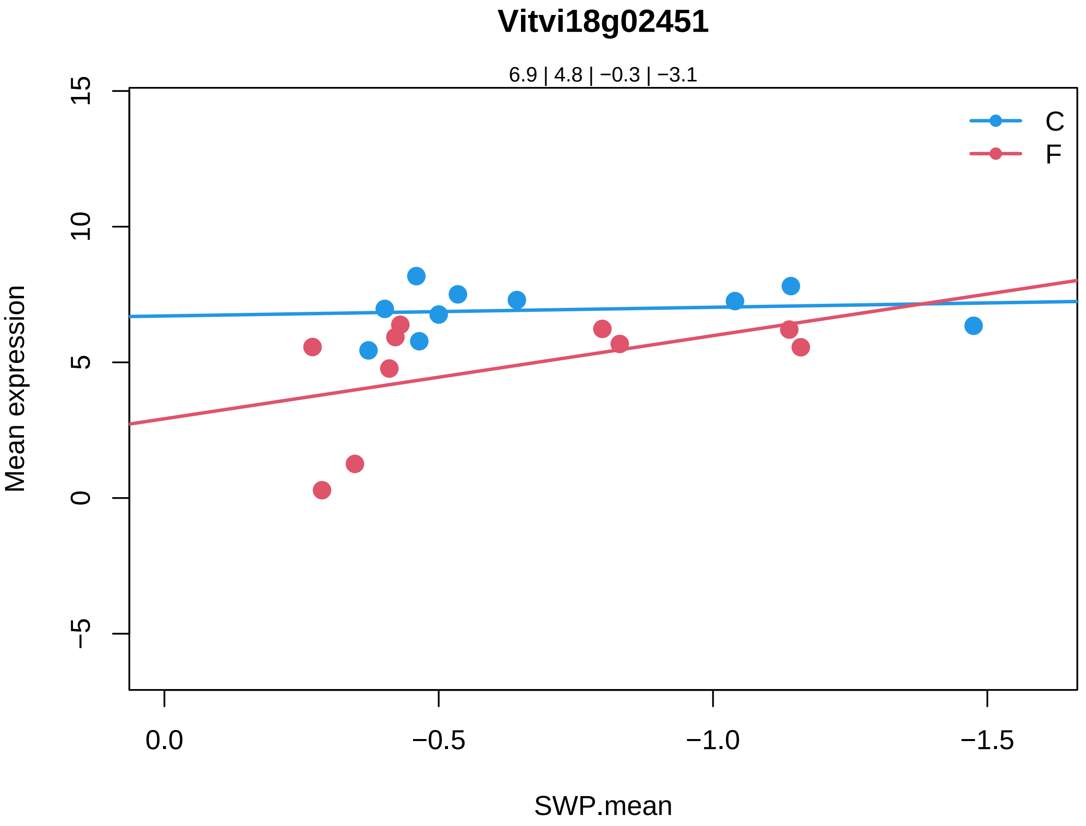
6.4.73 Vitvi18g02451

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

```
Vitvi18g02451
        16.01.2005
        secondary metabolism.isoprenoids.terpenoids
        terpene synthase 21 |
        Chr5:8092969-8095128 FORWARD LENGTH=545 |
        201606
```

Coefficients for Vitvi18g02451.

```
                     swp  varietyF swp.varietyF AveExpr        F
Vitvi18g02451 -0.3205063 -3.788492    -2.742855 5.86091 5.829124
                  P.Value  adj.P.Val  type
Vitvi18g02451 0.004496459 0.04697397 type4
```



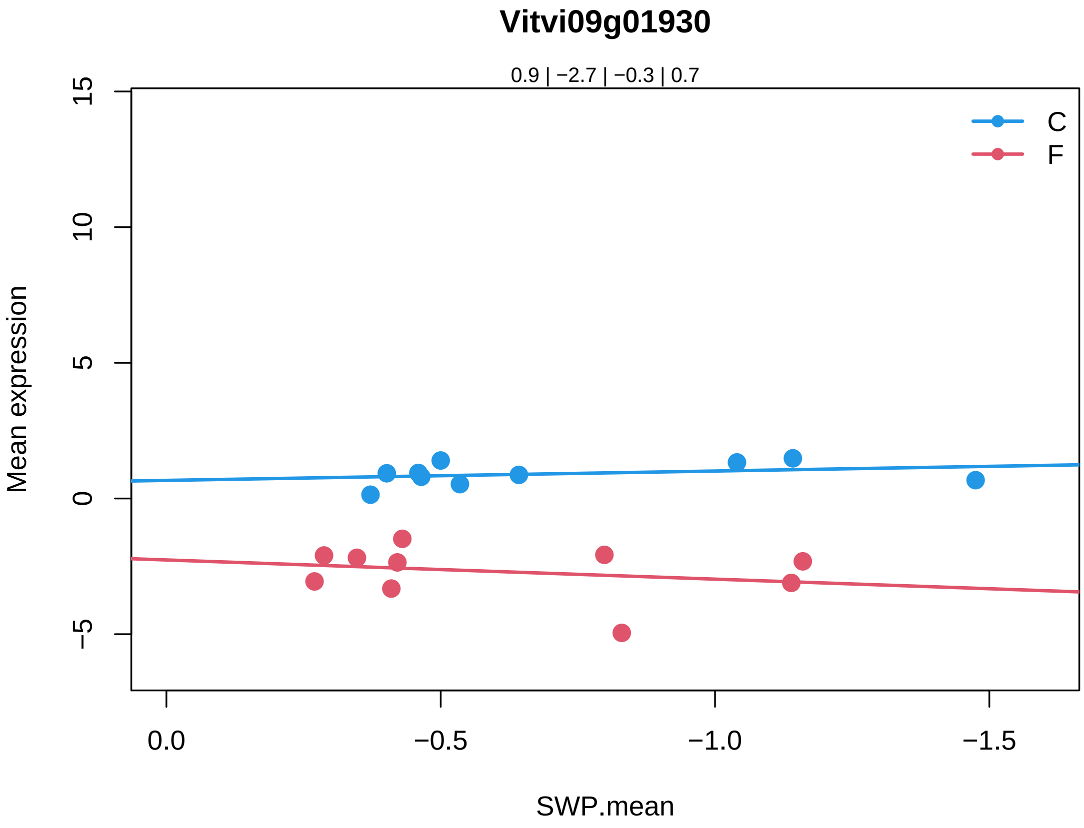
6.4.74 Vitvi09g01930

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

```
Vitvi09g01930
        29.2.1.2.2.7
        protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L7
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606

Vitvi09g01930
        20.01.2002
        stress.biotic.receptors
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606
```

Coefficients for Vitvi09g01930.

```
                     swp   varietyF swp.varietyF    AveExpr        F
Vitvi09g01930 -0.3447382 -2.932197     1.051695 -0.8931816 43.96049
                   P.Value    adj.P.Val  type
Vitvi09g01930 2.472265e-09 1.645513e-07 type3
```



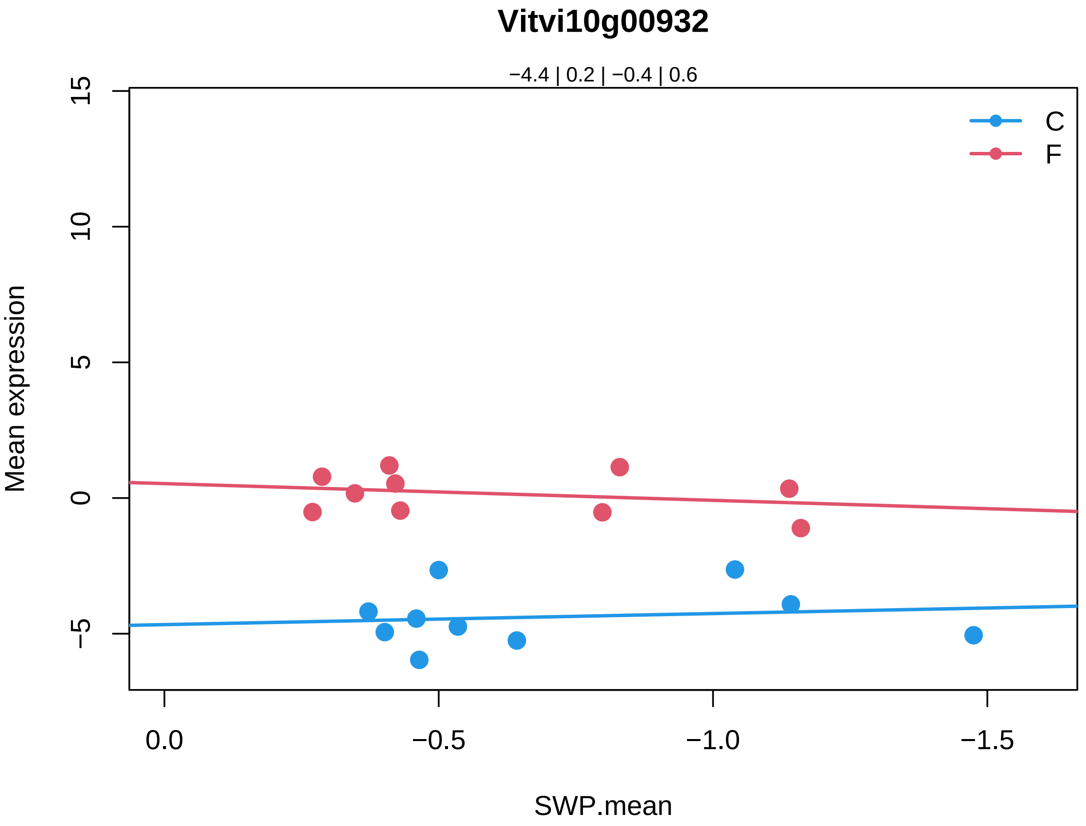
6.4.75 Vitvi10g00932

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

```
Vitvi10g00932
        30.2.12
        signalling.receptor kinases.leucine rich repeat XII
        Leucine-rich receptor-like protein kinase family protein |
        Chr2:11208367-11213895 REVERSE LENGTH=976 |
        201606
```

Coefficients for Vitvi10g00932.

```
                     swp varietyF swp.varietyF   AveExpr        F
Vitvi10g00932 -0.4084059 5.197119     1.024973 -2.111403 44.36035
                   P.Value    adj.P.Val  type
Vitvi10g00932 2.275386e-09 1.527816e-07 type3
```



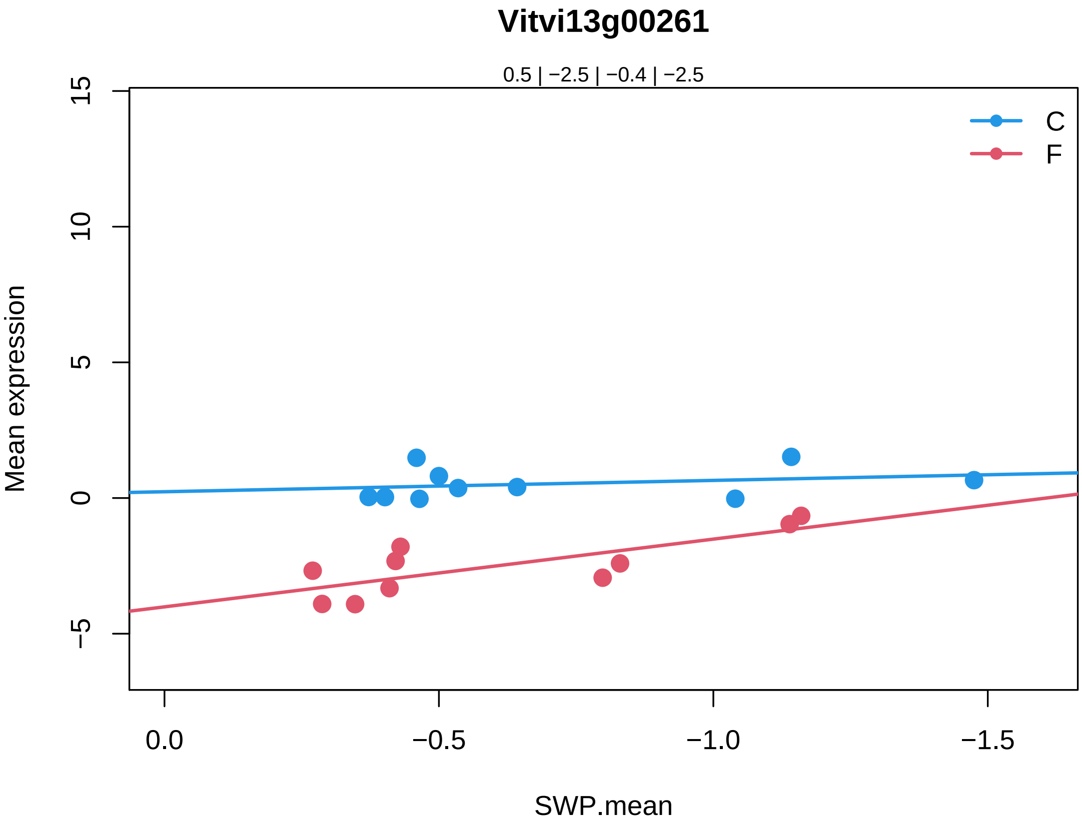
6.4.76 Vitvi13g00261

```
> 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.

```
                     swp   varietyF swp.varietyF    AveExpr        F
Vitvi13g00261 -0.4169403 -4.243055    -2.079326 -0.9822559 42.75431
                   P.Value    adj.P.Val  type
Vitvi13g00261 3.188076e-09 2.076609e-07 type4
```



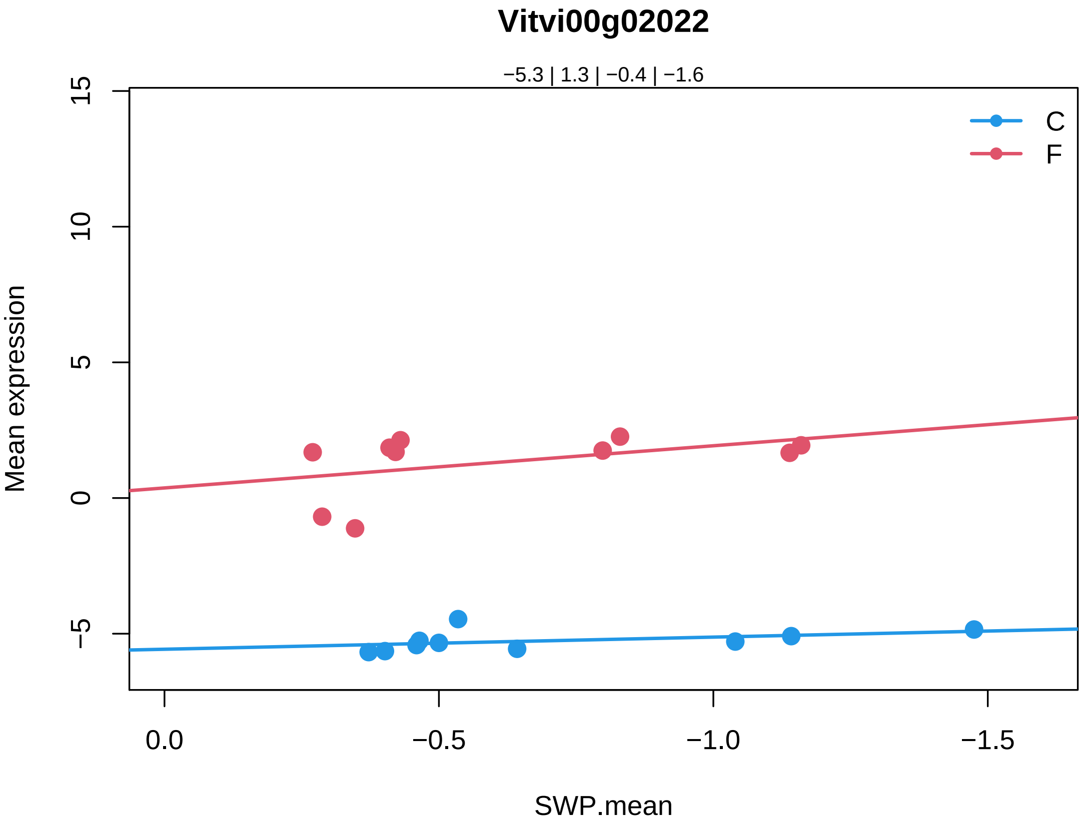
6.4.77 Vitvi00g02022

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

```
Vitvi00g02022
        17.01.2002
        hormone metabolism.abscisic acid.signal transduction
        GCR2-like 1 |
        Chr5:26086129-26087304 REVERSE LENGTH=311 |
        201606
```

Coefficients for Vitvi00g02022.

```
                    swp varietyF swp.varietyF   AveExpr        F
Vitvi00g02022 -0.446971 5.944277    -1.107401 -1.970074 124.9439
                   P.Value    adj.P.Val  type
Vitvi00g02022 9.784716e-14 1.285678e-11 type3
```



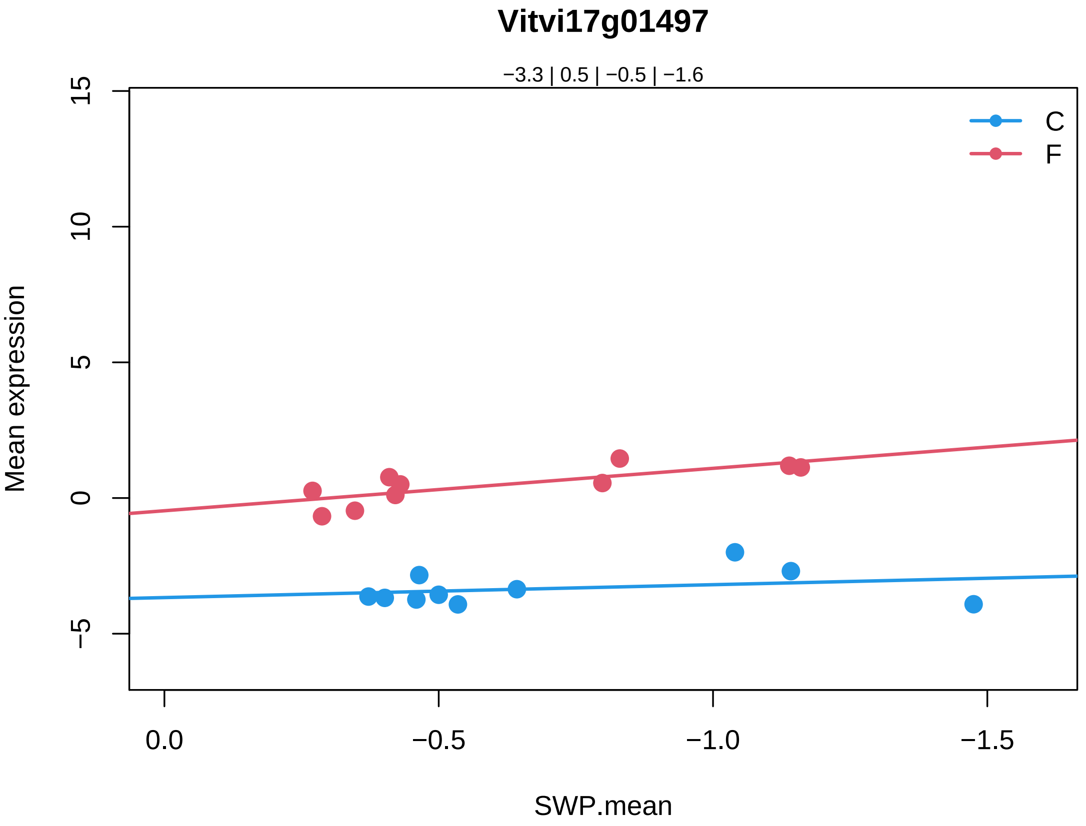
6.4.78 Vitvi17g01497

```
> 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.

```
                     swp varietyF swp.varietyF   AveExpr        F
Vitvi17g01497 -0.4744792  3.19887    -1.089142 -1.425839 85.59192
                   P.Value    adj.P.Val  type
Vitvi17g01497 4.291165e-12 4.303022e-10 type3
```



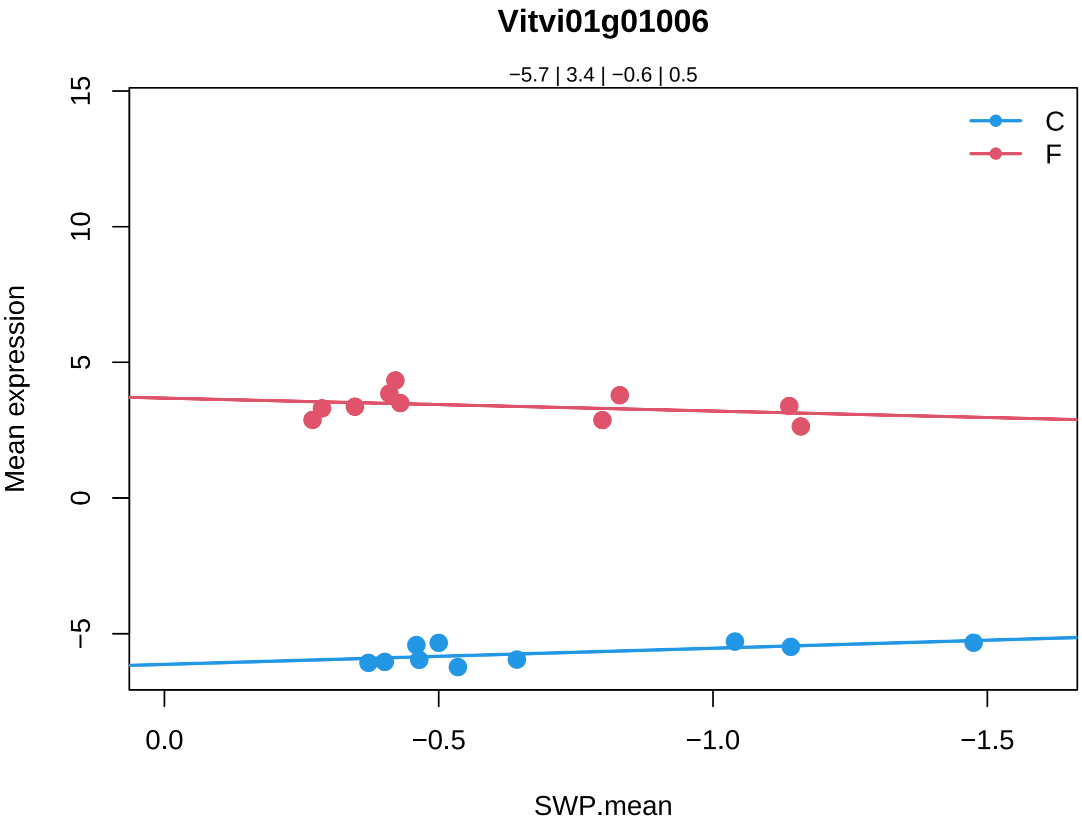
6.4.79 Vitvi01g01006

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

```
Vitvi01g01006
        35.2
        not assigned.unknown
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606
```

Coefficients for Vitvi01g01006.

```
                    swp varietyF swp.varietyF   AveExpr        F
Vitvi01g01006 -0.594586  9.81187     1.070103 -1.160735 704.7199
                   P.Value   adj.P.Val  type
Vitvi01g01006 1.434785e-21 1.68223e-18 type3
```



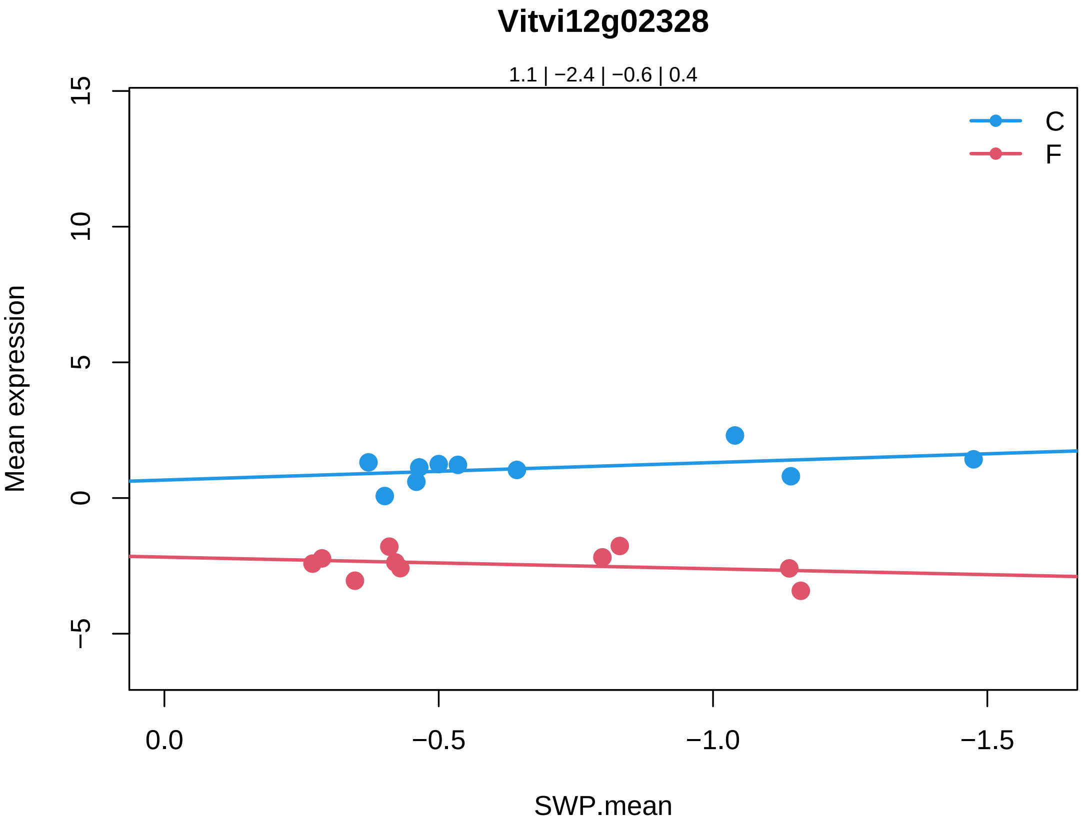
6.4.80 Vitvi12g02328

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

```
Vitvi12g02328
        35.2
        not assigned.unknown
        Ankyrin repeat family protein |
        Chr4:1524199-1527133 REVERSE LENGTH=751 |
        201606
```

Coefficients for Vitvi12g02328.

```
                    swp  varietyF swp.varietyF    AveExpr       F
Vitvi12g02328 -0.645458 -2.840399     1.075452 -0.6624452 76.6071
                   P.Value    adj.P.Val  type
Vitvi12g02328 1.274304e-11 1.163051e-09 type3
```



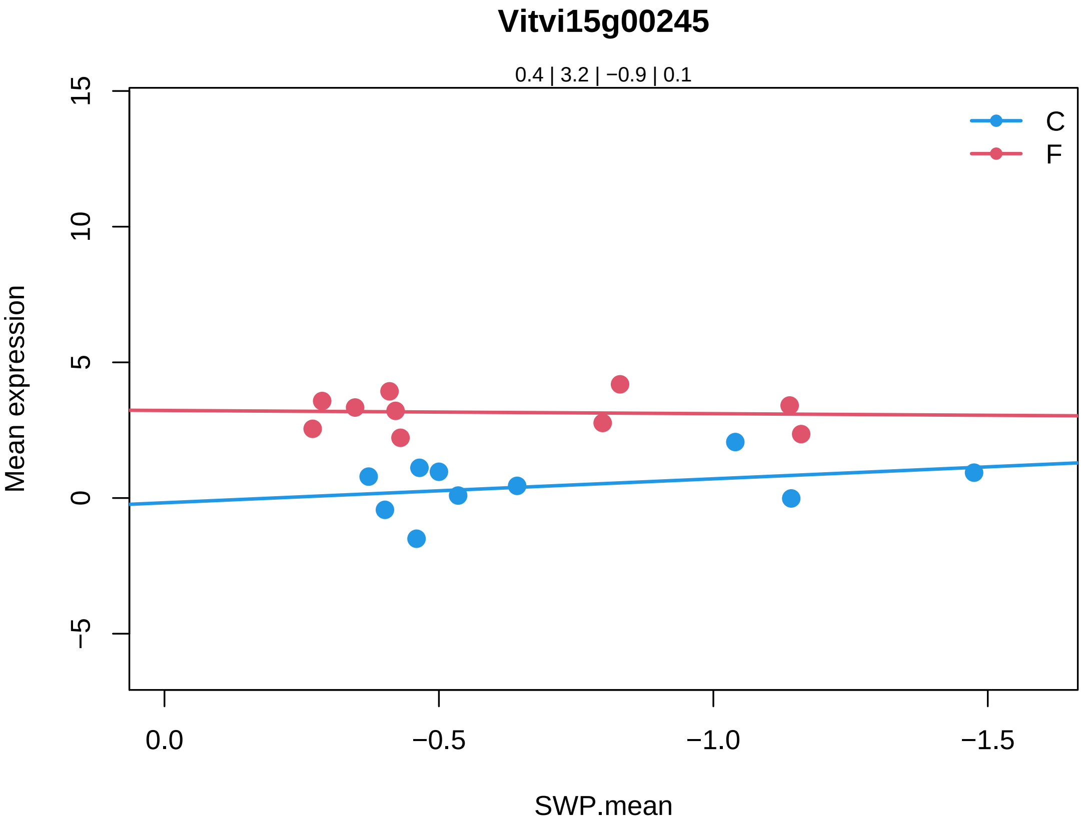
6.4.81 Vitvi15g00245

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

```
Vitvi15g00245
        20.1.2.2
        stress.biotic.receptors.TIR-NBS-LRR
        disease resistance protein (TIR-NBS-LRR class) |
        Chr5:5822999-5827153 FORWARD LENGTH=1295 |
        201606
```

Coefficients for Vitvi15g00245.

```
                     swp varietyF swp.varietyF AveExpr        F
Vitvi15g00245 -0.8828349 3.401885     1.000898 1.80022 20.96904
                   P.Value   adj.P.Val  type
Vitvi15g00245 1.405252e-06 5.4088e-05 type3
```



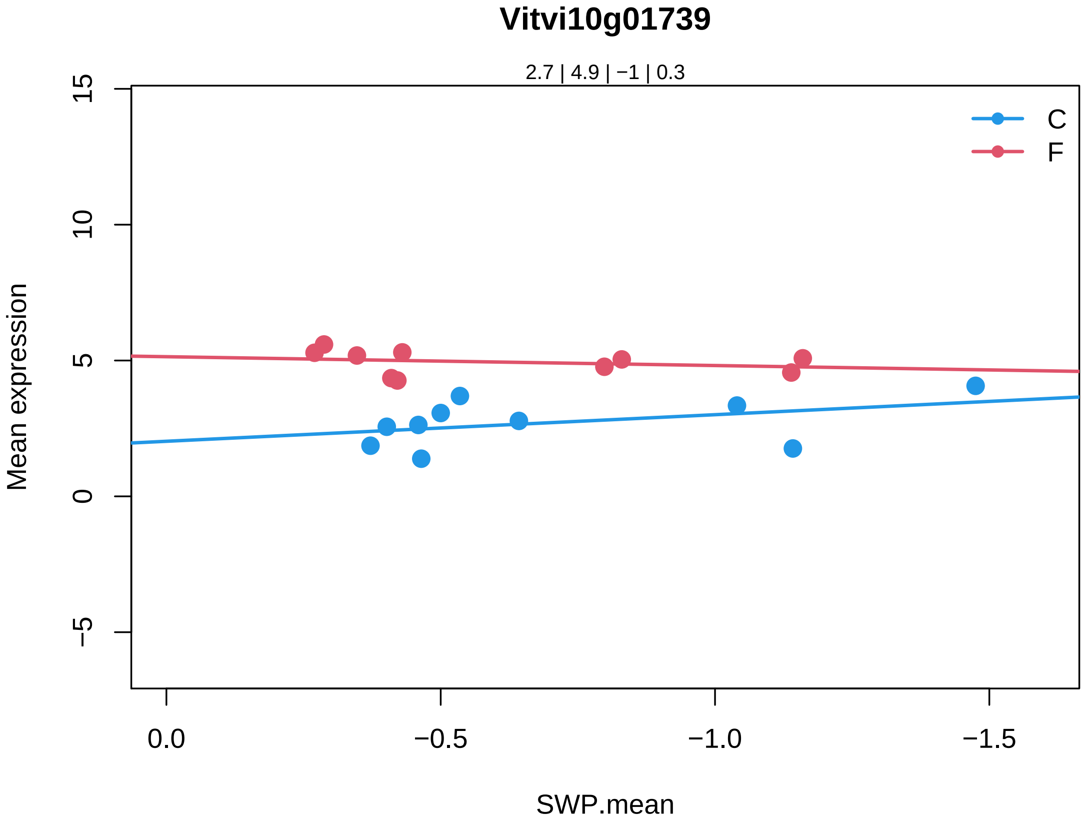
6.4.82 Vitvi10g01739

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

```
Vitvi10g01739
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi10g01739.

```
                     swp varietyF swp.varietyF  AveExpr        F
Vitvi10g01739 -0.9783917 3.113392     1.302982 3.828674 22.17922
                  P.Value    adj.P.Val  type
Vitvi10g01739 8.99996e-07 3.677678e-05 type3
```



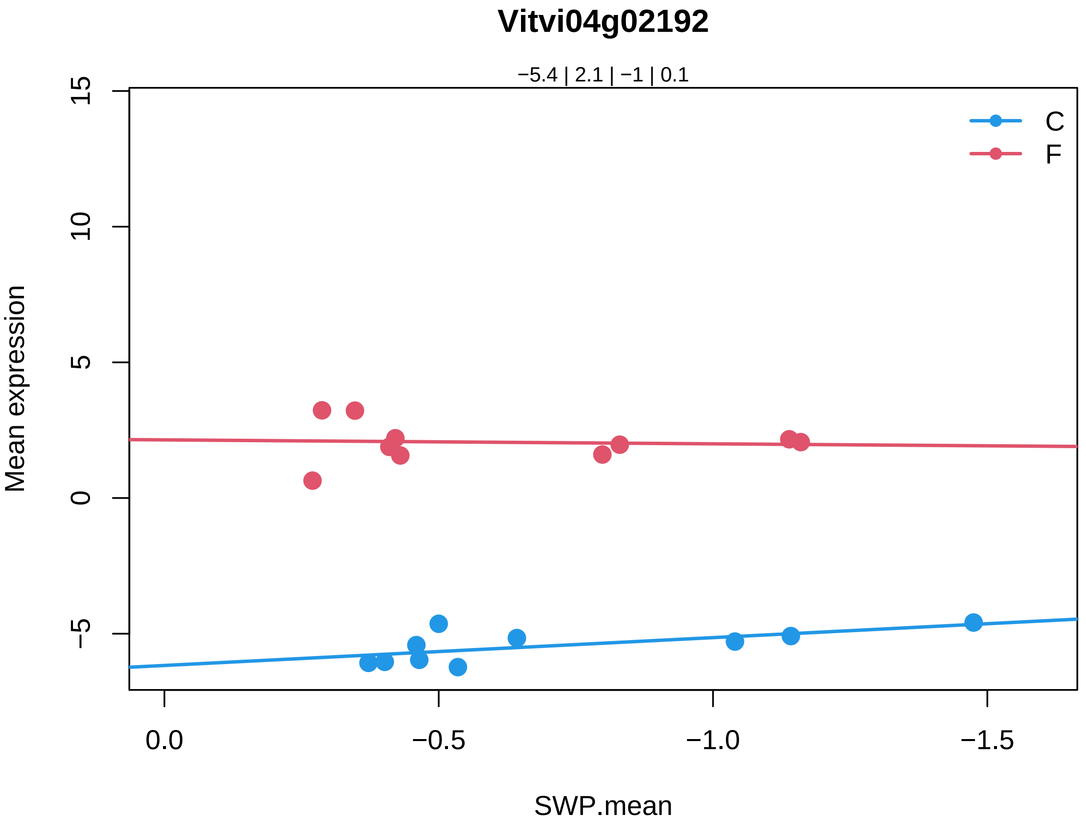
6.4.83 Vitvi04g02192

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

```
Vitvi04g02192
        16.04.2001
        secondary metabolism.N misc.alkaloid-like
        Calcium-dependent phosphotriesterase superfamily protein |
        Chr3:19086548-19087909 FORWARD LENGTH=371 |
        201606
```

Coefficients for Vitvi04g02192.

```
                    swp varietyF swp.varietyF  AveExpr        F
Vitvi04g02192 -1.026036 8.313572     1.171818 -1.69753 239.5537
                   P.Value    adj.P.Val  type
Vitvi04g02192 1.222161e-16 2.699736e-14 type3
```



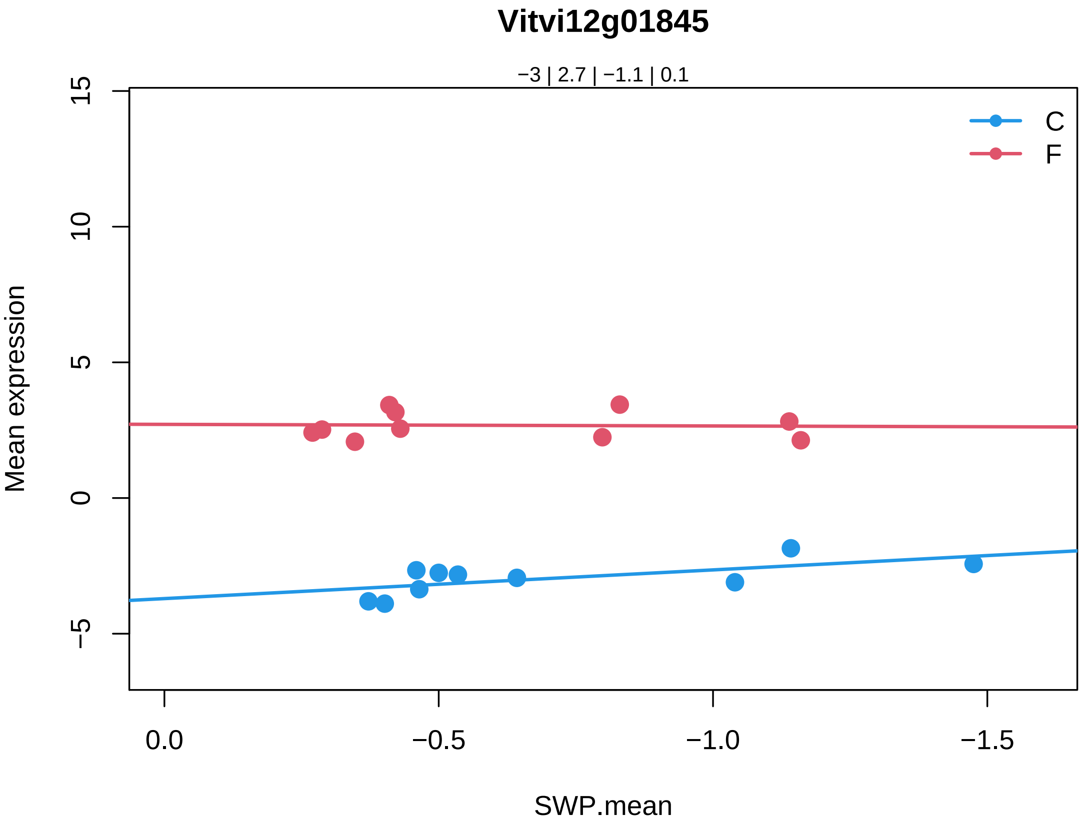
6.4.84 Vitvi12g01845

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

```
Vitvi12g01845
        20.1.2.1
        stress.biotic.receptors.CC-NBS-LRR
        NB-ARC domain-containing disease resistance protein |
        Chr3:4857940-4861104 FORWARD LENGTH=1054 |
        201606
```

Coefficients for Vitvi12g01845.

```
                    swp varietyF swp.varietyF    AveExpr        F
Vitvi12g01845 -1.057327  6.42091     1.115801 -0.1422073 203.1583
                   P.Value    adj.P.Val  type
Vitvi12g01845 6.749824e-16 1.353695e-13 type3
```



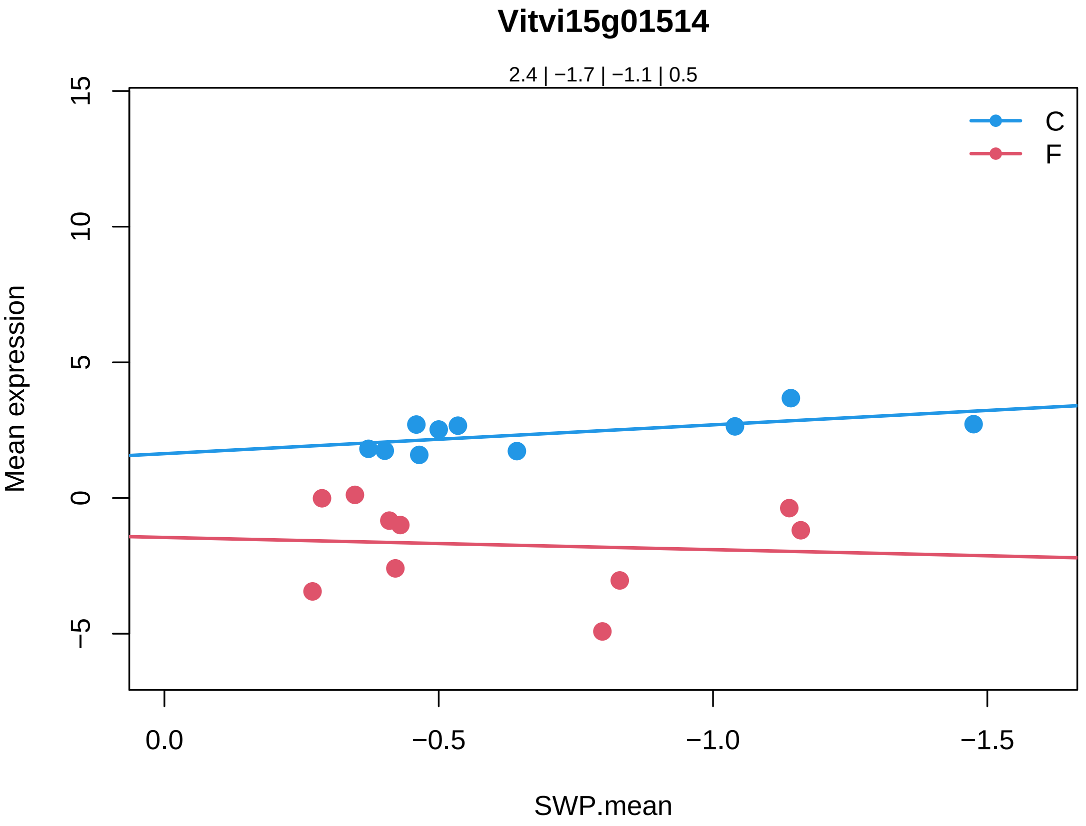
6.4.85 Vitvi15g01514

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

```
Vitvi15g01514
        35.2
        not assigned.unknown
        cytochrome P450%2C family 76%2C subfamily C%2C polypeptide 1 |
        Chr2:18776391-18778354 REVERSE LENGTH=512 |
        201606
```

Coefficients for Vitvi15g01514.

```
                    swp   varietyF swp.varietyF   AveExpr        F
Vitvi15g01514 -1.06173 -3.087574     1.512169 0.3272667 21.29969
                   P.Value    adj.P.Val  type
Vitvi15g01514 1.241886e-06 4.853544e-05 type3
```



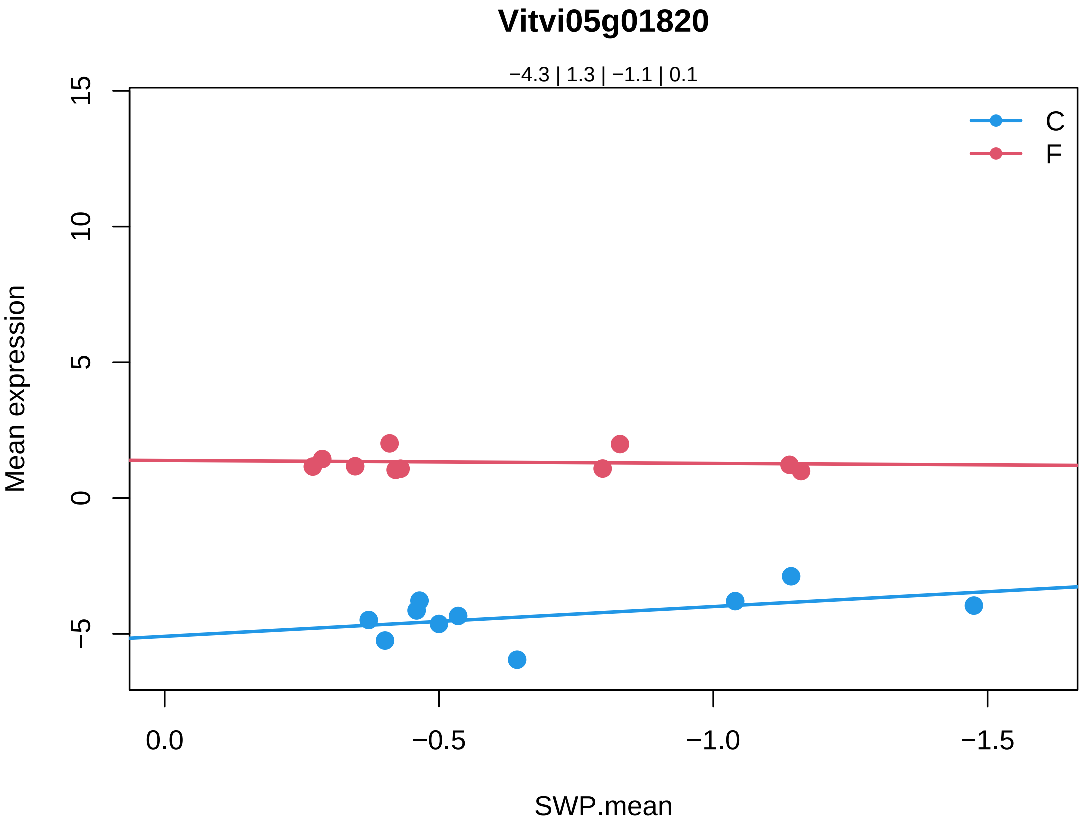
6.4.86 Vitvi05g01820

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

```
Vitvi05g01820
        35.2
        not assigned.unknown
        RNA-directed DNA polymerase (reverse transcriptase)-related family pro
        Chr3:8789309-8790907 FORWARD LENGTH=532 |
        201606
```

Coefficients for Vitvi05g01820.

```
                    swp varietyF swp.varietyF   AveExpr        F
Vitvi05g01820 -1.095343 6.477777     1.203532 -1.500723 153.1409
                   P.Value    adj.P.Val  type
Vitvi05g01820 1.234978e-14 1.863716e-12 type3
```



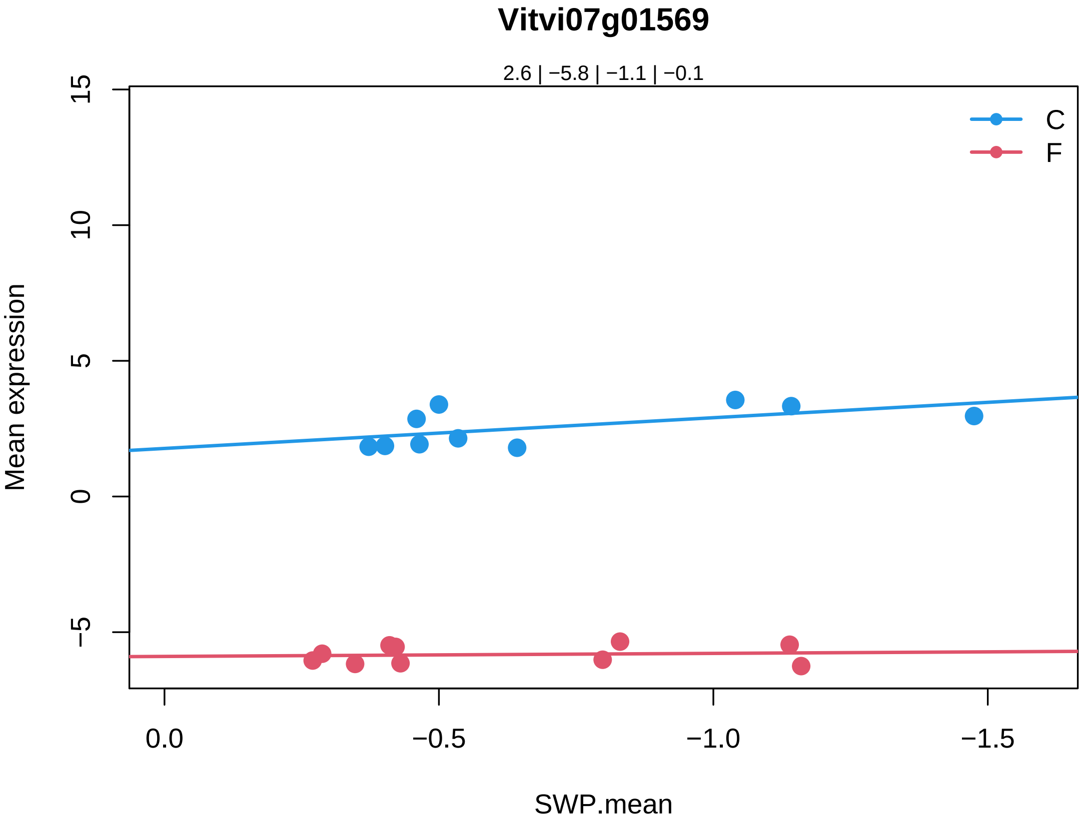
6.4.87 Vitvi07g01569

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

```
Vitvi07g01569
        26.24
        misc.GCN5-related N-acetyltransferase
        N-acetyl-l-glutamate synthase 1 |
        Chr2:9749988-9752737 FORWARD LENGTH=609 |
        201606

Vitvi07g01569
        35.2
        not assigned.unknown
        N-acetyl-l-glutamate synthase 1 |
        Chr2:9749988-9752737 FORWARD LENGTH=609 |
        201606
```

Coefficients for Vitvi07g01569.

```
                    swp varietyF swp.varietyF   AveExpr        F
Vitvi07g01569 -1.132495 -7.66461     1.020438 -1.629612 469.9552
                   P.Value    adj.P.Val  type
Vitvi07g01569 1.044703e-19 5.897541e-17 type3
```



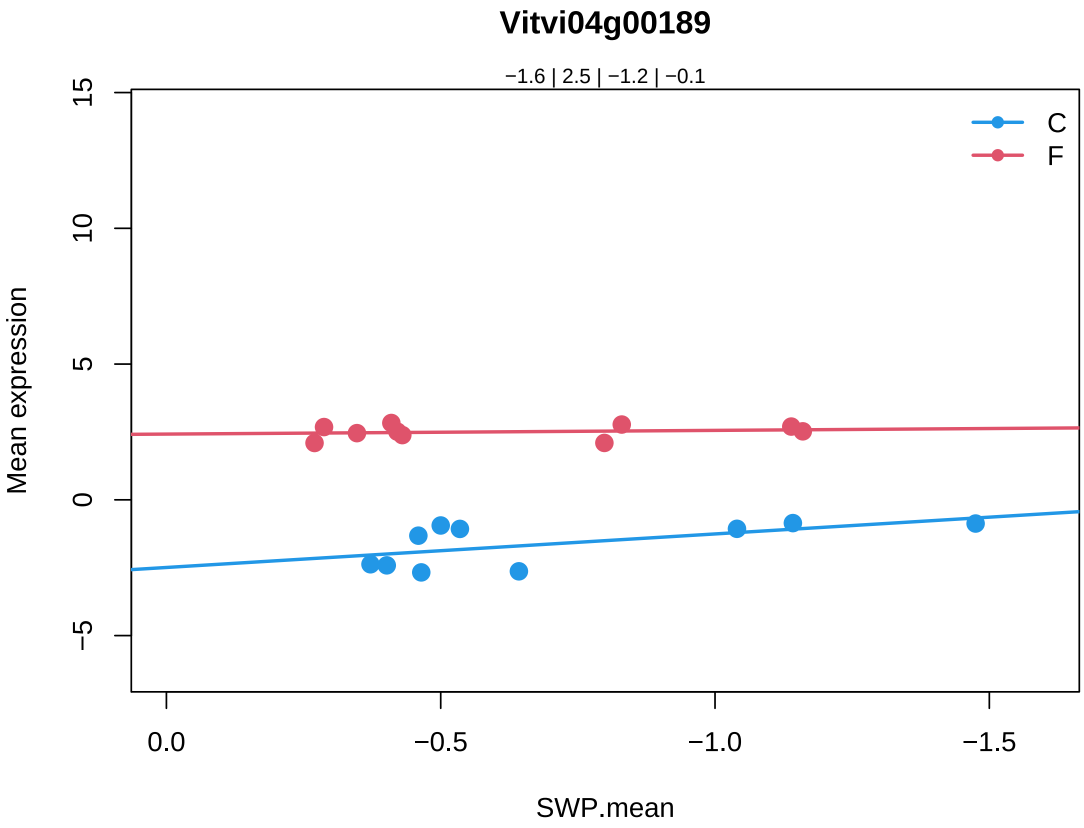
6.4.88 Vitvi04g00189

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

```
Vitvi04g00189
        28.2
        DNA.repair
        sterile alpha motif (SAM) domain-containing protein |
        Chr2:18827761-18830505 REVERSE LENGTH=631 |
        201606
```

Coefficients for Vitvi04g00189.

```
                    swp varietyF swp.varietyF   AveExpr       F
Vitvi04g00189 -1.235233 4.912217     1.098512 0.4406836 112.445
                   P.Value    adj.P.Val  type
Vitvi04g00189 2.832728e-13 3.568301e-11 type3
```



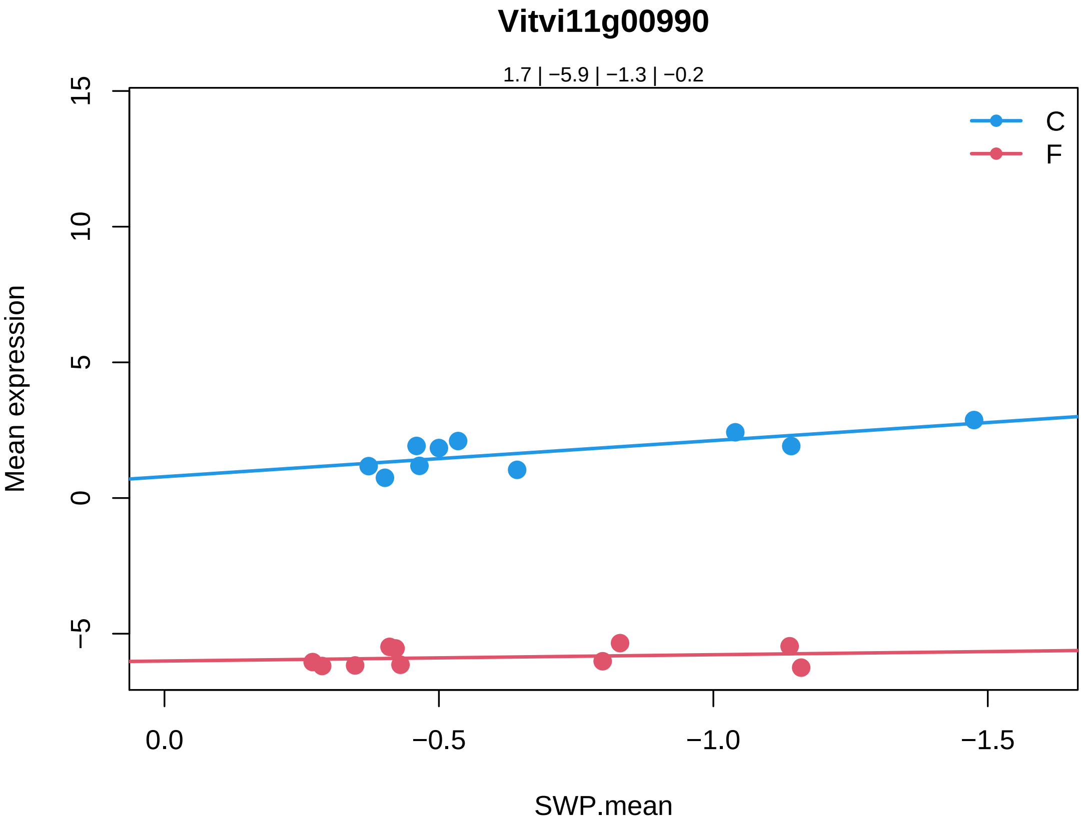
6.4.89 Vitvi11g00990

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

```
Vitvi11g00990
        35.2
        not assigned.unknown
        RING/U-box superfamily protein |
        Chr2:8093469-8094452 FORWARD LENGTH=181 |
        201606
```

Coefficients for Vitvi11g00990.

```
                    swp  varietyF swp.varietyF   AveExpr        F
Vitvi11g00990 -1.330176 -6.793417     1.098097 -2.071893 495.7336
                   P.Value    adj.P.Val  type
Vitvi11g00990 5.944721e-20 3.484979e-17 type3
```



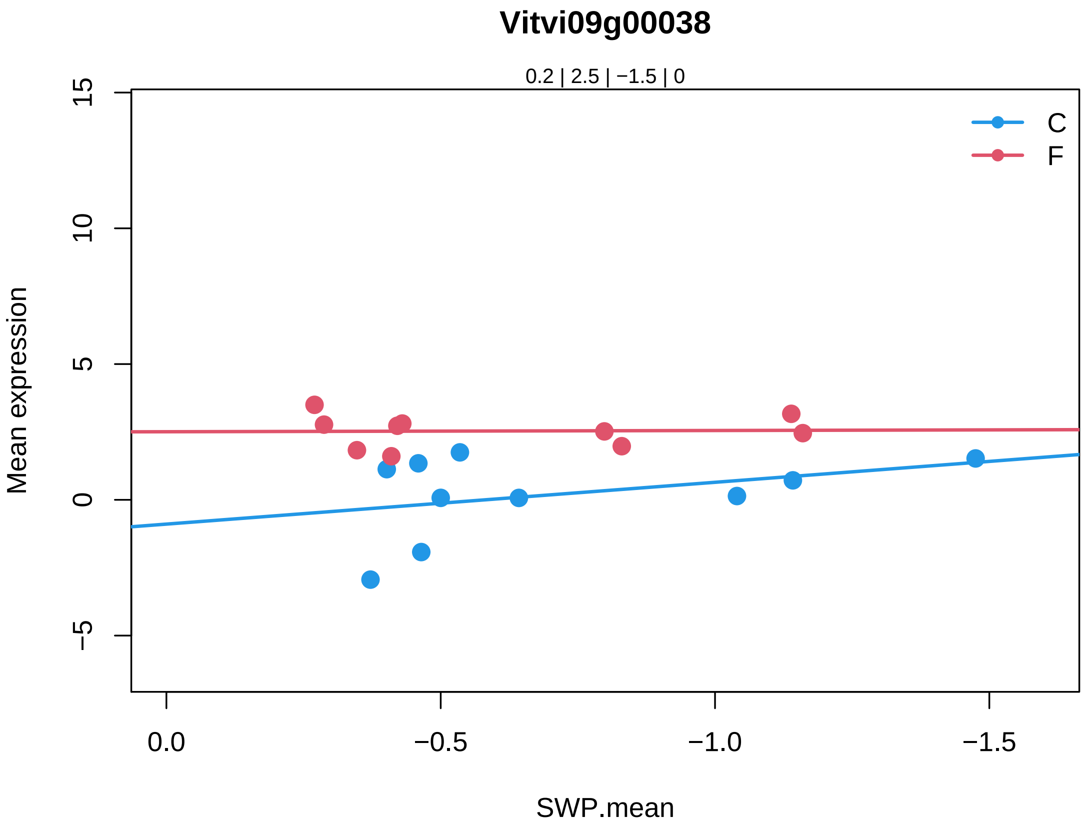
6.4.90 Vitvi09g00038

```
> 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.

```
                    swp varietyF swp.varietyF  AveExpr        F
Vitvi09g00038 -1.539814 3.402522     1.494714 1.361973 9.762087
                   P.Value   adj.P.Val  type
Vitvi09g00038 0.0002927607 0.005395719 type3
```



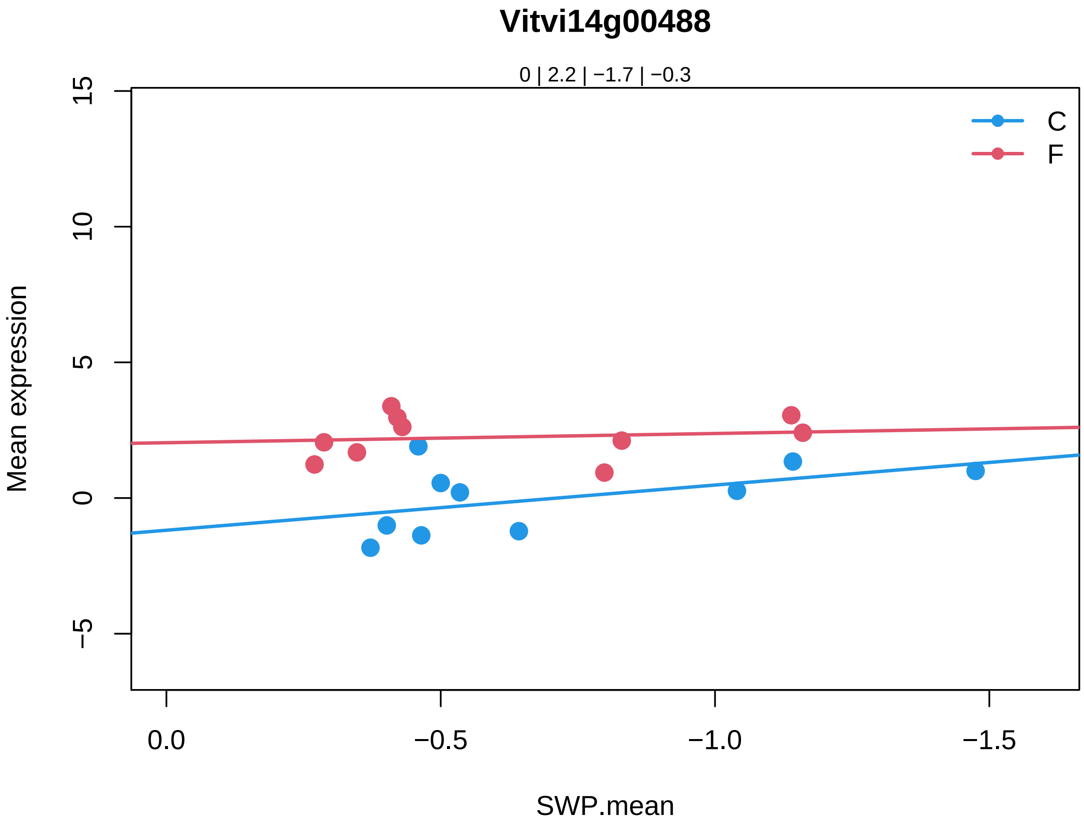
6.4.91 Vitvi14g00488

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

```
Vitvi14g00488
        20.01.2007
        stress.biotic.PR-proteins
        pathogenesis-related 4 |
        Chr3:1285691-1286531 REVERSE LENGTH=212 |
        201606
```

Coefficients for Vitvi14g00488.

```
                    swp varietyF swp.varietyF  AveExpr        F
Vitvi14g00488 -1.665567 3.225945     1.326057 1.114212 11.66374
                   P.Value   adj.P.Val  type
Vitvi14g00488 9.632629e-05 0.002191351 type3
```



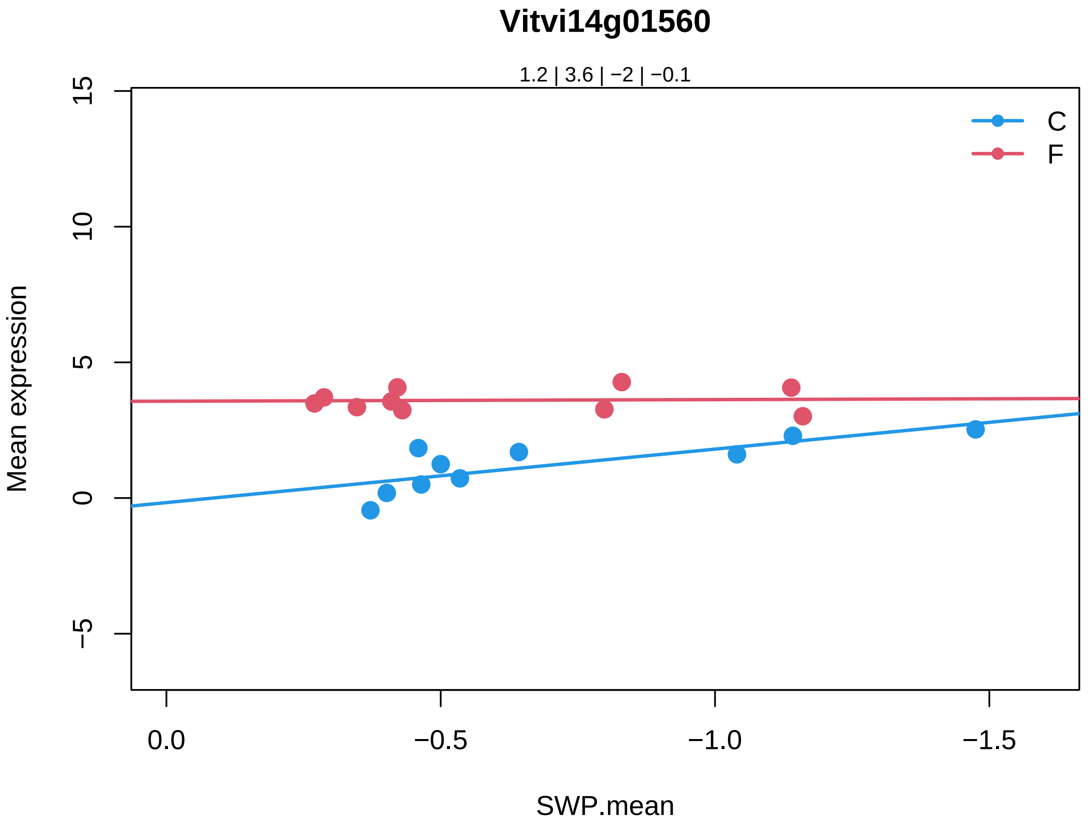
6.4.92 Vitvi14g01560

```
> 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.

```
                    swp varietyF swp.varietyF  AveExpr        F
Vitvi14g01560 -1.971048 3.736567     1.911944 2.410521 39.17574
                   P.Value    adj.P.Val  type
Vitvi14g01560 7.038224e-09 4.308298e-07 type3
```



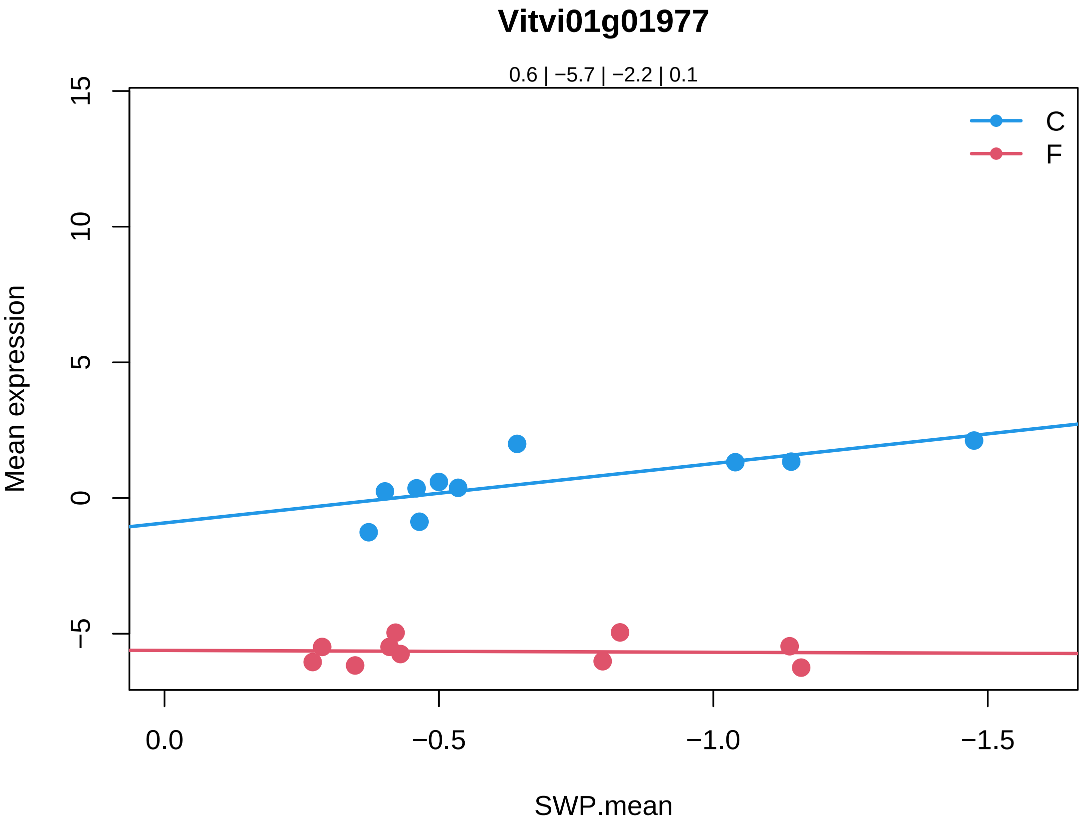
6.4.93 Vitvi01g01977

```
> 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.

```
                    swp   varietyF swp.varietyF   AveExpr       F
Vitvi01g01977 -2.189318 -4.698008     2.257369 -2.518788 175.595
                   P.Value    adj.P.Val  type
Vitvi01g01977 3.036373e-15 5.301925e-13 type3
```



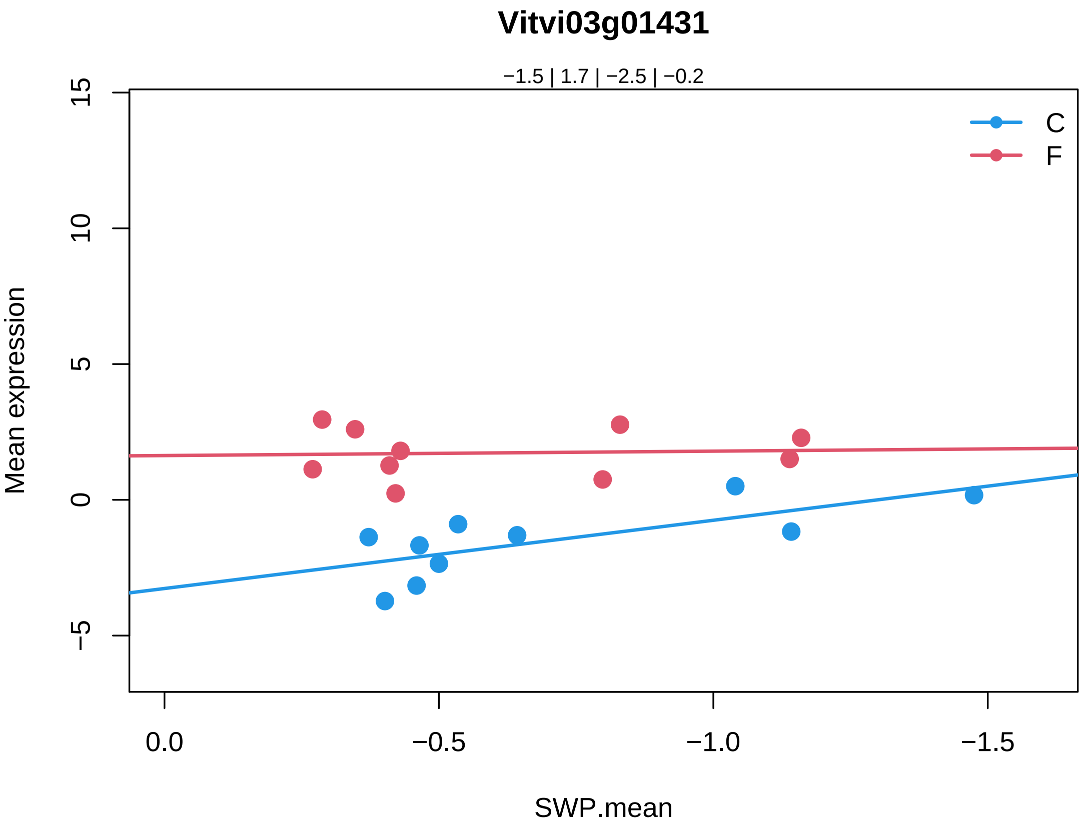
6.4.94 Vitvi03g01431

```
> 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.

```
                    swp varietyF swp.varietyF   AveExpr        F
Vitvi03g01431 -2.513015  4.89664     2.351136 0.1151543 26.29632
                   P.Value    adj.P.Val  type
Vitvi03g01431 2.239329e-07 1.043788e-05 type4
```



6.5 type4

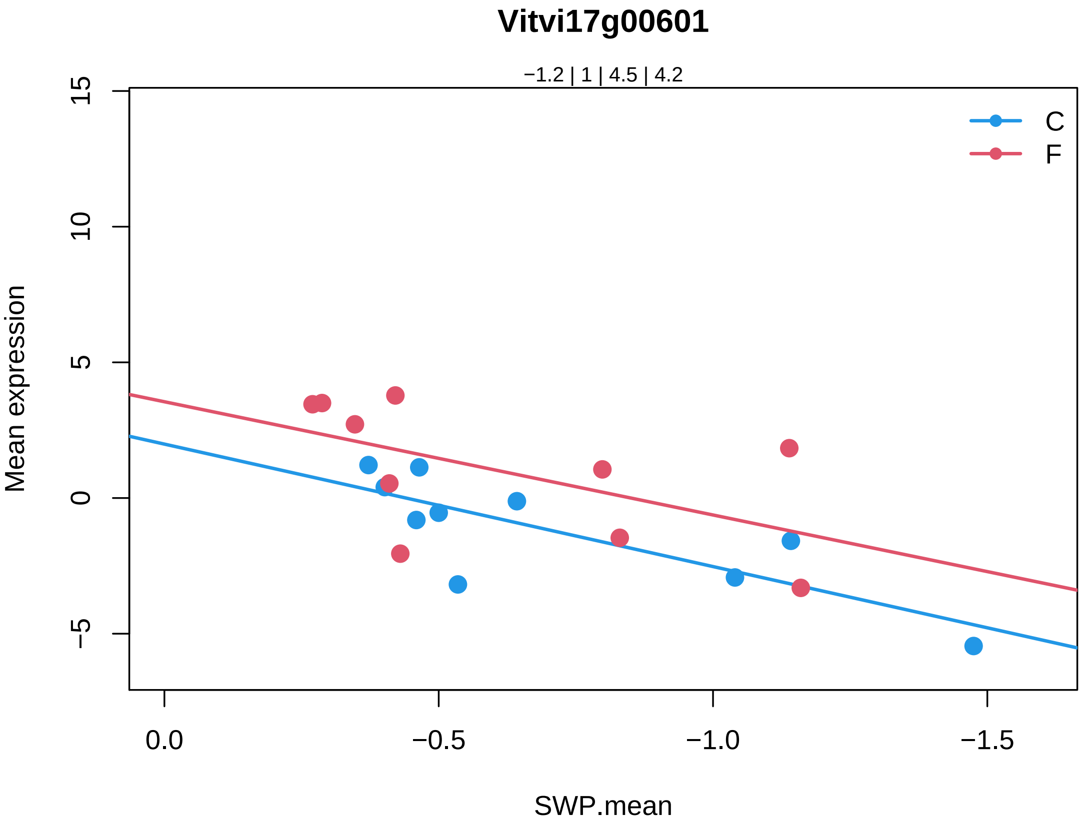
6.5.1 Vitvi17g00601

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

```
Vitvi17g00601
        17.06.2003
        hormone metabolism.gibberelin.induced-regulated-responsive-activated
        Gibberellin-regulated family protein |
        Chr1:28053378-28053893 FORWARD LENGTH=101 |
        201606
```

Coefficients for Vitvi17g00601.

```
                   swp varietyF swp.varietyF     AveExpr        F
Vitvi17g00601 4.512791 1.561406   -0.3397197 -0.09054575 8.936692
                   P.Value   adj.P.Val  type
Vitvi17g00601 0.0004924448 0.008239125 type4
```



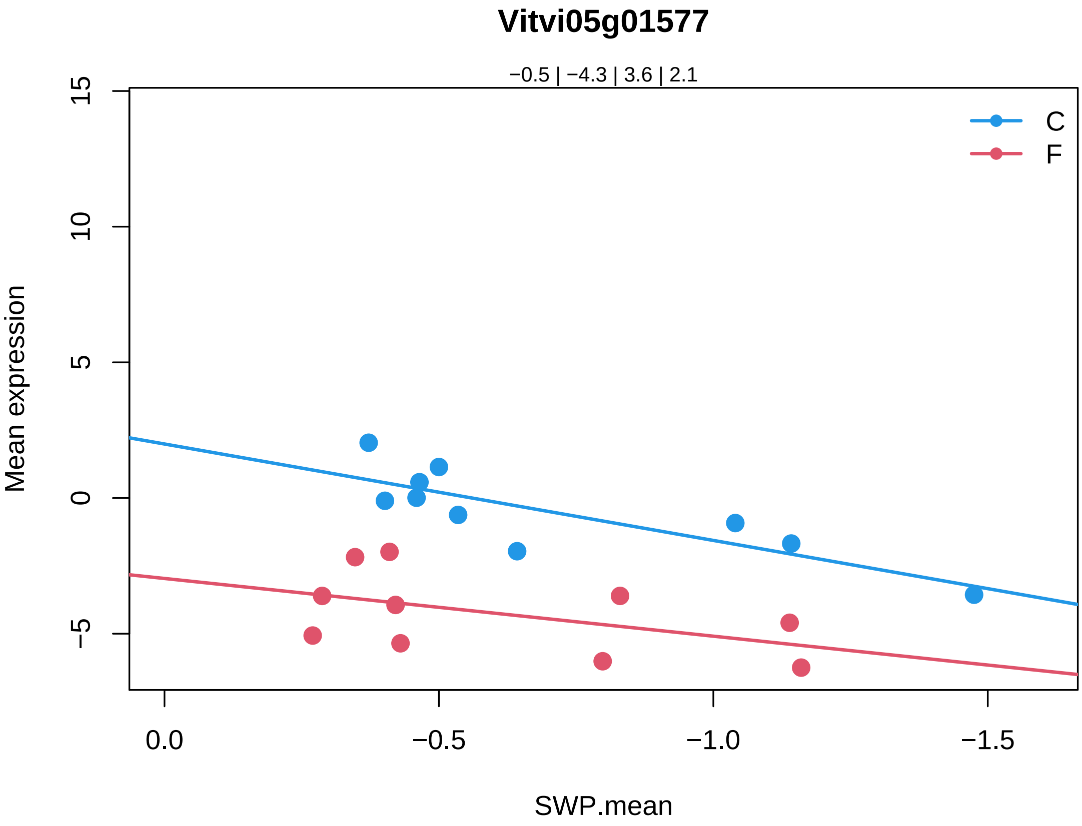
6.5.2 Vitvi05g01577

```
> 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.

```
                   swp  varietyF swp.varietyF   AveExpr        F
Vitvi05g01577 3.553568 -4.955944     -1.42671 -2.384056 27.87609
                   P.Value    adj.P.Val  type
Vitvi05g01577 1.372726e-07 6.621229e-06 type4
```



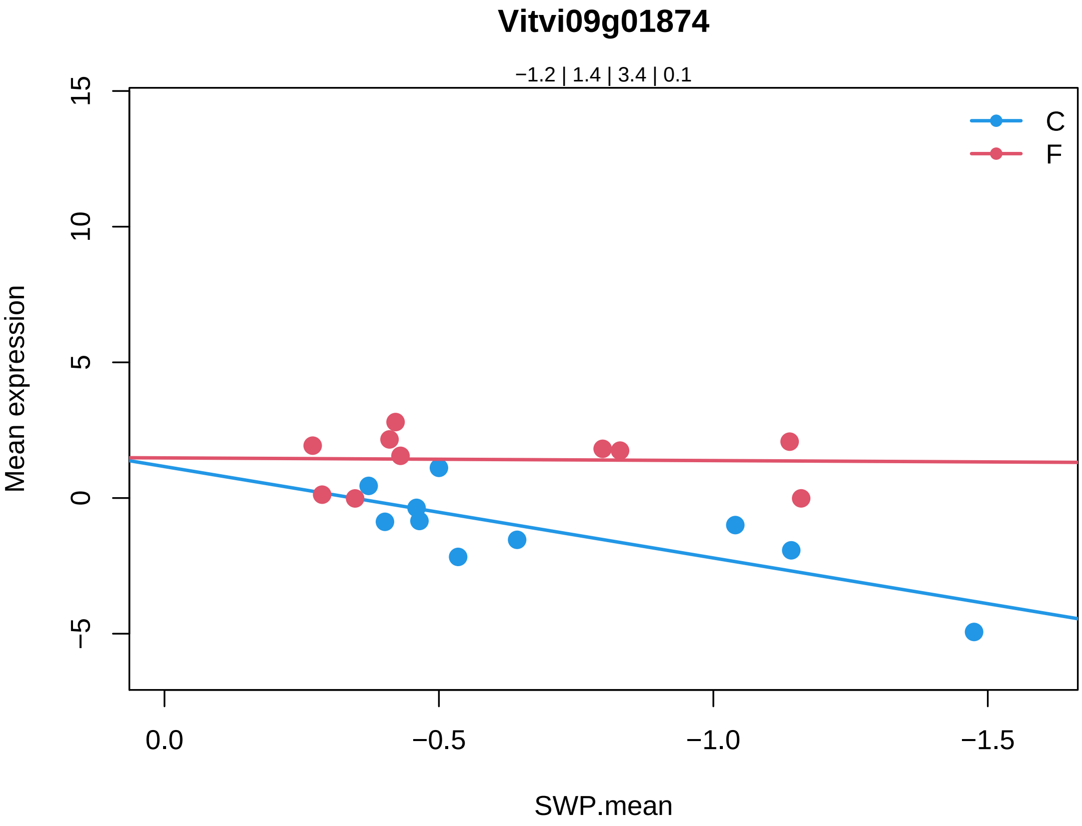
6.5.3 Vitvi09g01874

```
> 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.

```
                   swp  varietyF swp.varietyF   AveExpr        F
Vitvi09g01874 3.369133 0.3187773    -3.270373 0.1041741 17.21374
                   P.Value    adj.P.Val  type
Vitvi09g01874 6.380859e-06 0.0002114284 type4
```



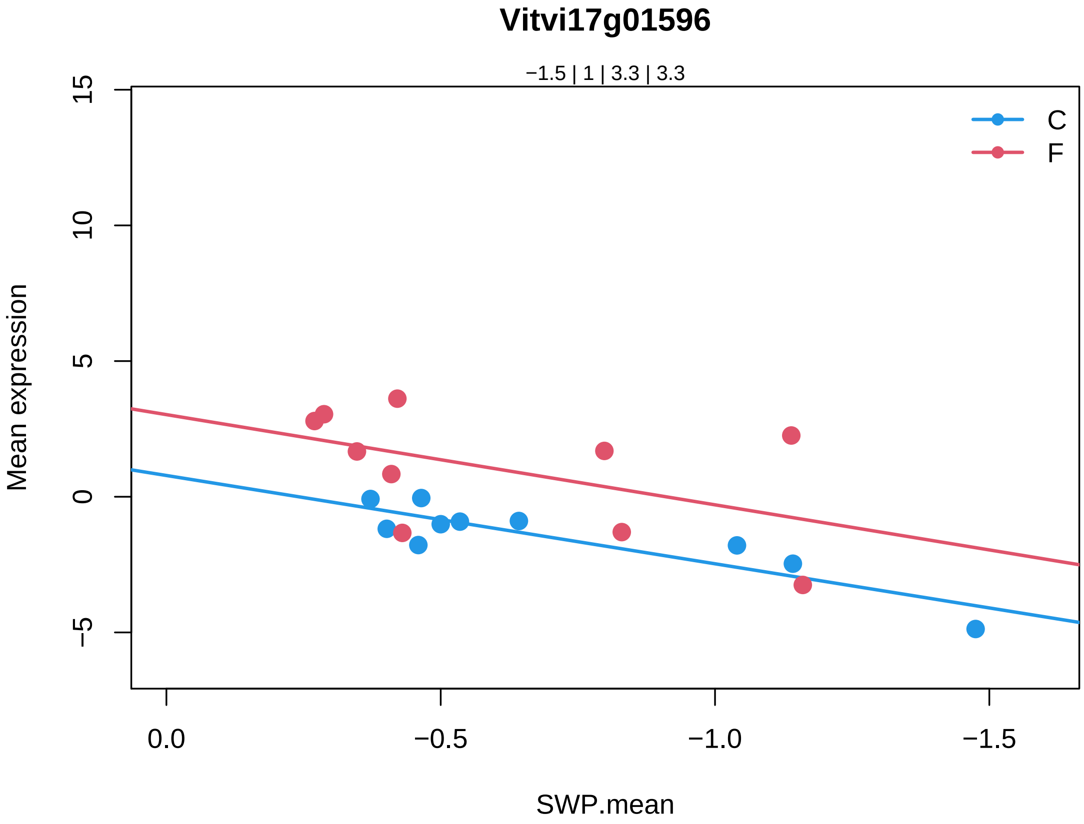
6.5.4 Vitvi17g01596

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

```
Vitvi17g01596
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi17g01596.

```
                   swp varietyF swp.varietyF    AveExpr       F
Vitvi17g01596 3.254213 2.243246   0.07011039 -0.2518399 10.3963
                   P.Value    adj.P.Val  type
Vitvi17g01596 0.0001995185 0.004006669 type4
```



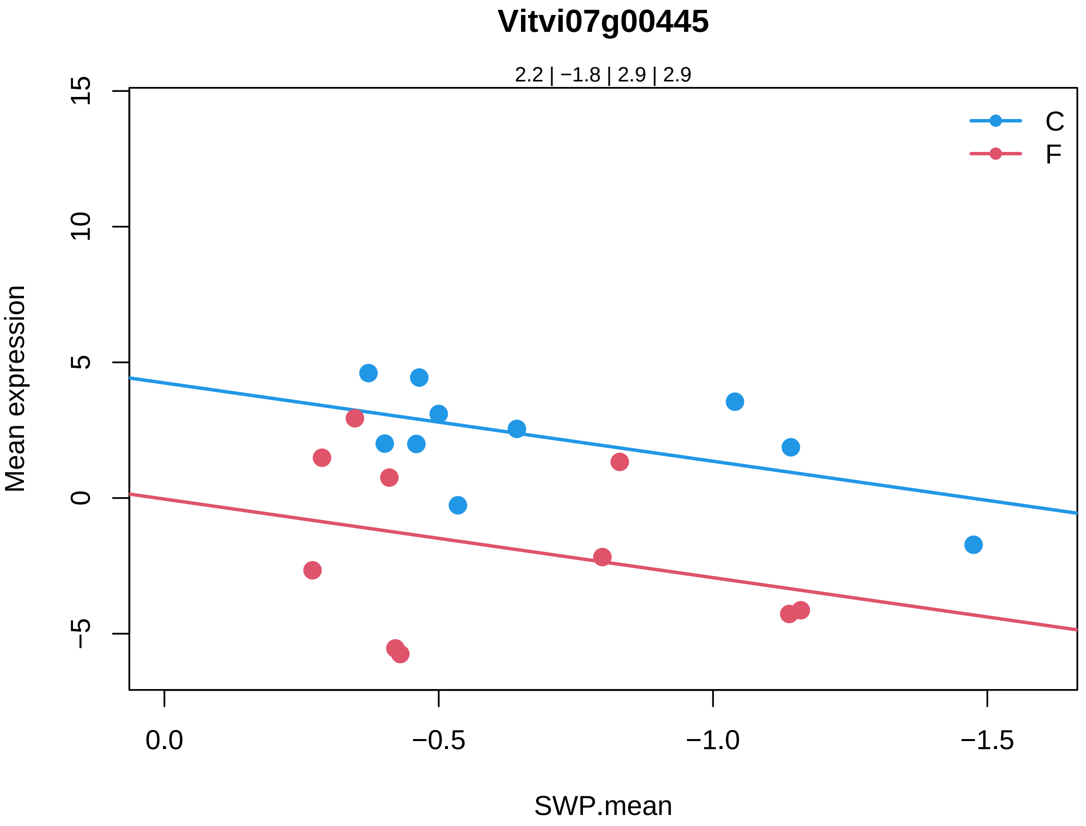
6.5.5 Vitvi07g00445

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

```
Vitvi07g00445
        11.01.2009
        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.

```
                   swp  varietyF swp.varietyF   AveExpr        F
Vitvi07g00445 2.884577 -4.279105   0.01163635 0.2040772 6.608034
                  P.Value  adj.P.Val  type
Vitvi07g00445 0.002475552 0.02999393 type4
```



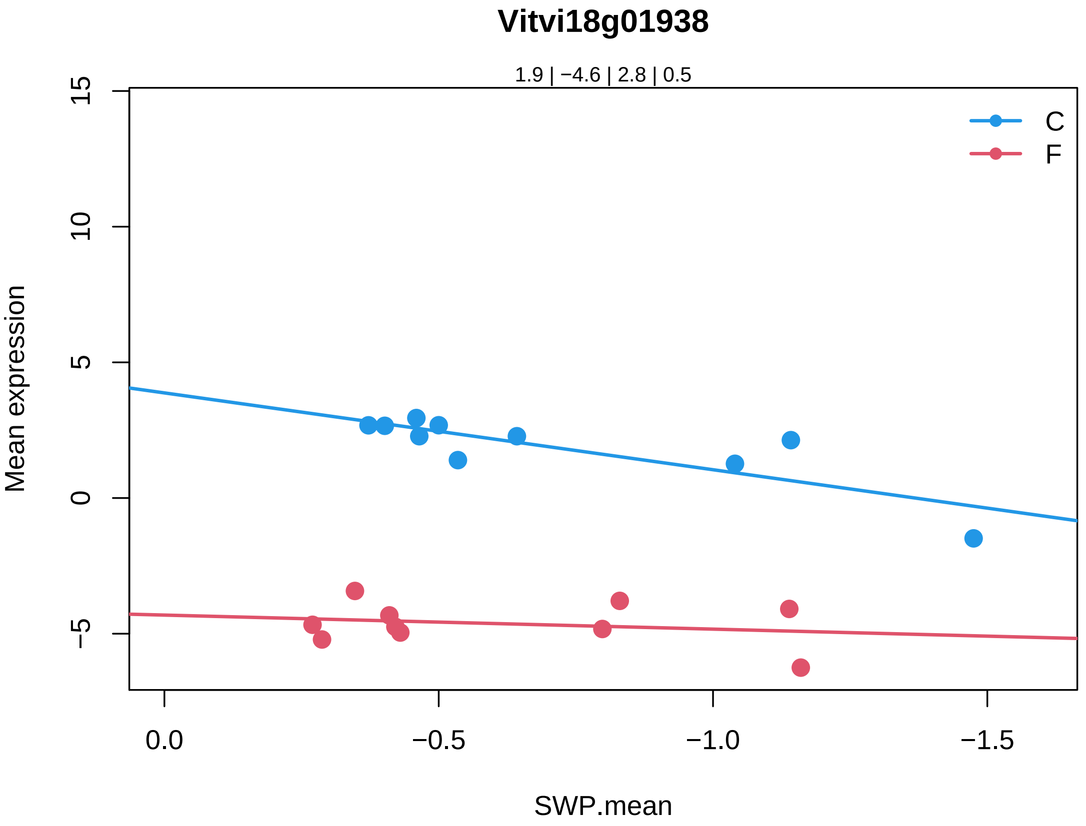
6.5.6 Vitvi18g01938

```
> 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.

```
                   swp  varietyF swp.varietyF   AveExpr        F
Vitvi18g01938 2.831106 -8.188031    -2.313519 -1.373227 135.9605
                   P.Value   adj.P.Val  type
Vitvi18g01938 4.153722e-14 5.65277e-12 type4
```



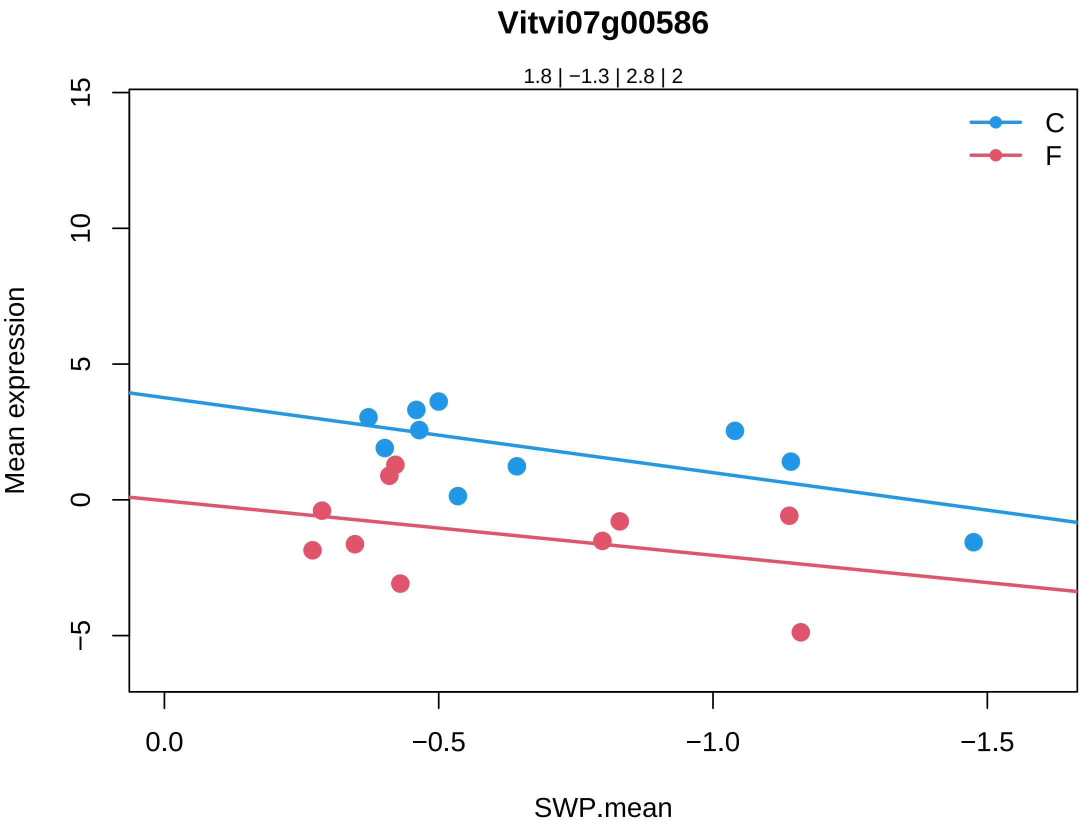
6.5.7 Vitvi07g00586

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

```
Vitvi07g00586
        29.05.2004
        protein.degradation.aspartate protease
        Eukaryotic aspartyl protease family protein |
        Chr2:966506-967891 REVERSE LENGTH=461 |
        201606
```

Coefficients for Vitvi07g00586.

```
                   swp  varietyF swp.varietyF   AveExpr        F
Vitvi07g00586 2.761208 -3.794189   -0.7514262 0.2820346 11.12961
                   P.Value   adj.P.Val  type
Vitvi07g00586 0.0001301517 0.002807383 type4
```



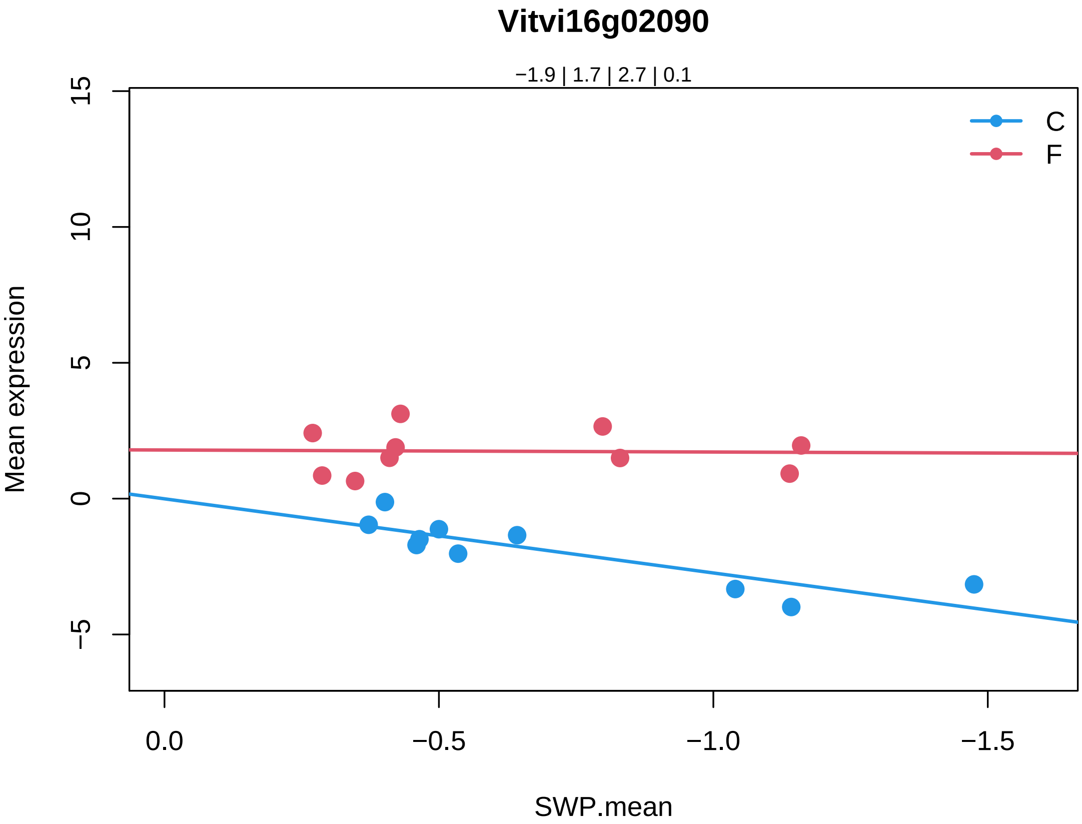
6.5.8 Vitvi16g02090

```
> 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.

```
                   swp varietyF swp.varietyF    AveExpr        F
Vitvi16g02090 2.729033 1.796787    -2.654757 -0.0909231 50.77959
                   P.Value    adj.P.Val  type
Vitvi16g02090 6.511182e-10 4.725878e-08 type4
```



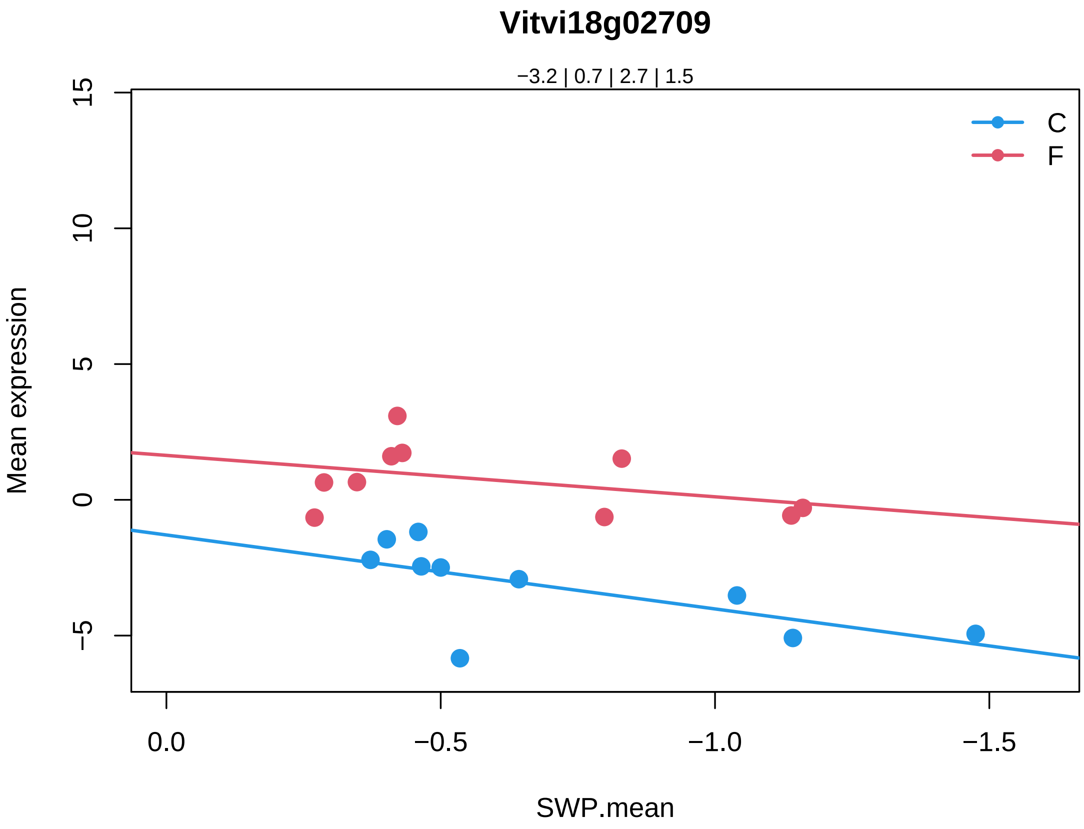
6.5.9 Vitvi18g02709

```
> 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.

```
                   swp varietyF swp.varietyF   AveExpr        F
Vitvi18g02709 2.724042 2.929642    -1.199916 -1.251207 23.83792
                   P.Value   adj.P.Val  type
Vitvi18g02709 5.027859e-07 2.17712e-05 type4
```



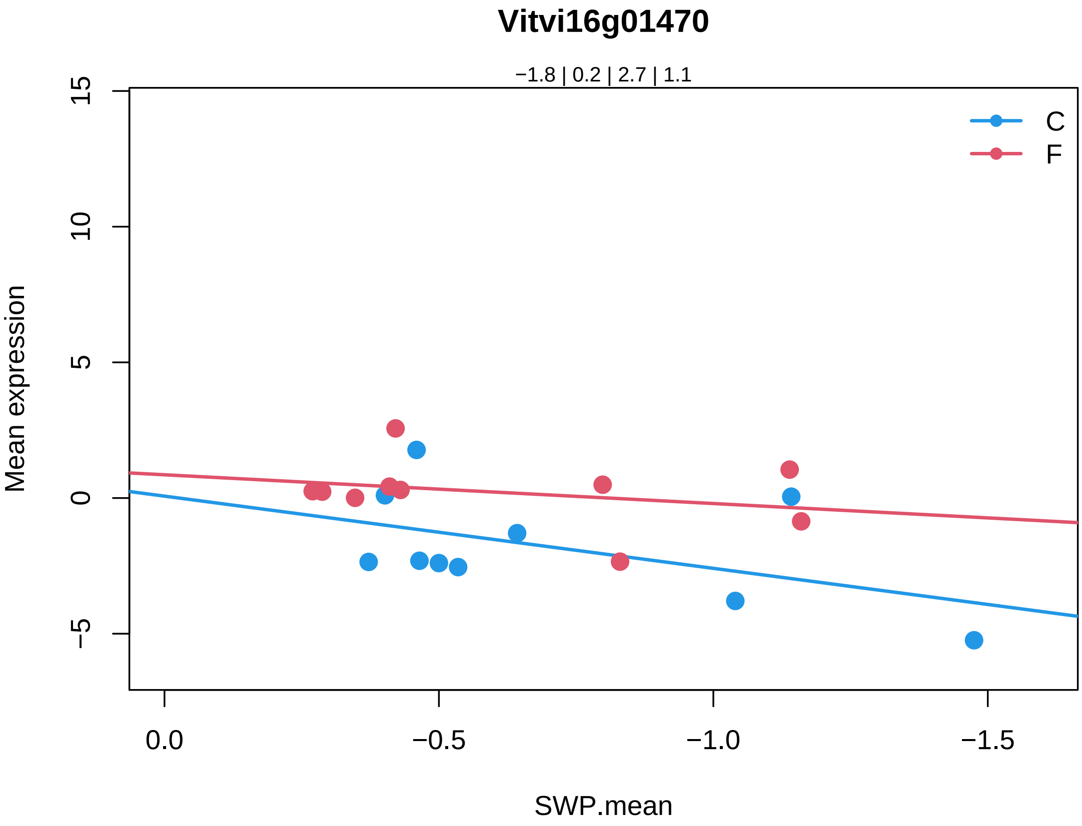
6.5.10 Vitvi16g01470

```
> 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.

```
                   swp  varietyF swp.varietyF    AveExpr        F
Vitvi16g01470 2.661094 0.7870727    -1.601562 -0.7953825 5.157004
                 P.Value  adj.P.Val  type
Vitvi16g01470 0.00772719 0.06956753 type4
```



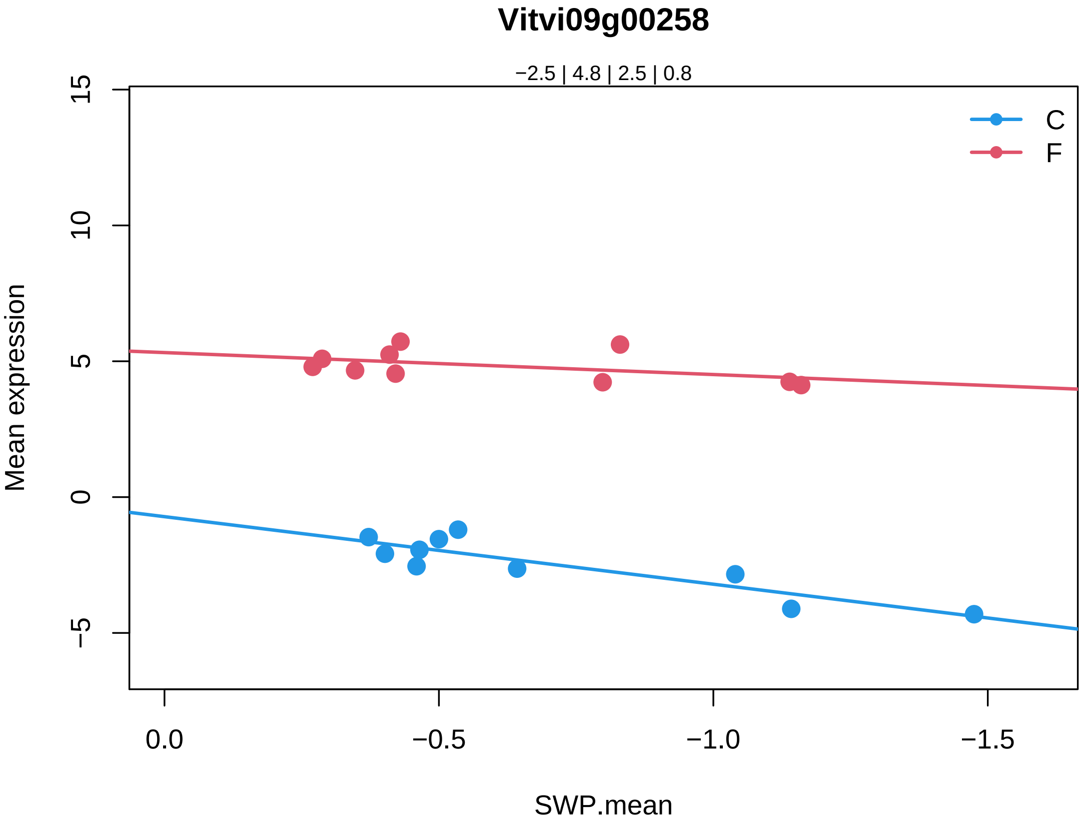
6.5.11 Vitvi09g00258

```
> 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.

```
                   swp varietyF swp.varietyF  AveExpr        F
Vitvi09g00258 2.485974 6.039525    -1.678231 1.179217 341.9488
                   P.Value    adj.P.Val  type
Vitvi09g00258 2.967466e-18 9.230637e-16 type4
```



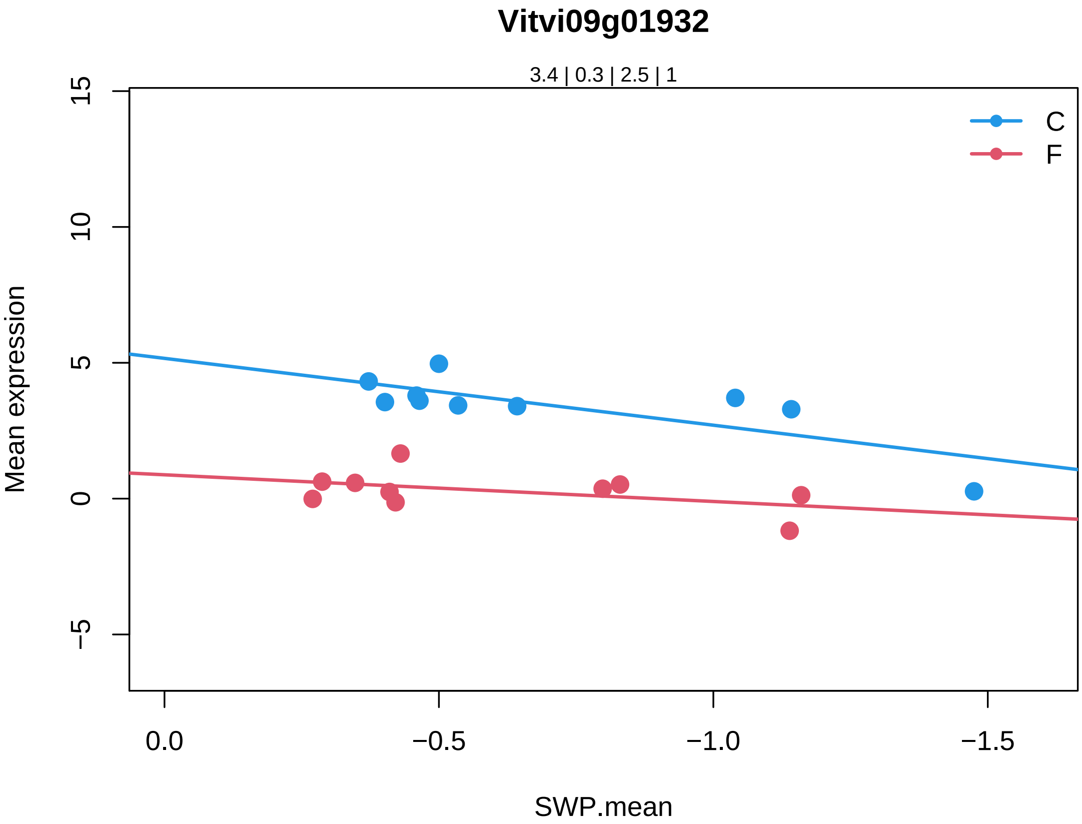
6.5.12 Vitvi09g01932

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

```
Vitvi09g01932
        20.01.2002
        stress.biotic.receptors
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606
```

Coefficients for Vitvi09g01932.

```
                   swp   varietyF swp.varietyF  AveExpr        F
Vitvi09g01932 2.460612 -4.285472    -1.478196 1.856141 40.00595
                   P.Value    adj.P.Val  type
Vitvi09g01932 5.826144e-09 3.639771e-07 type4
```



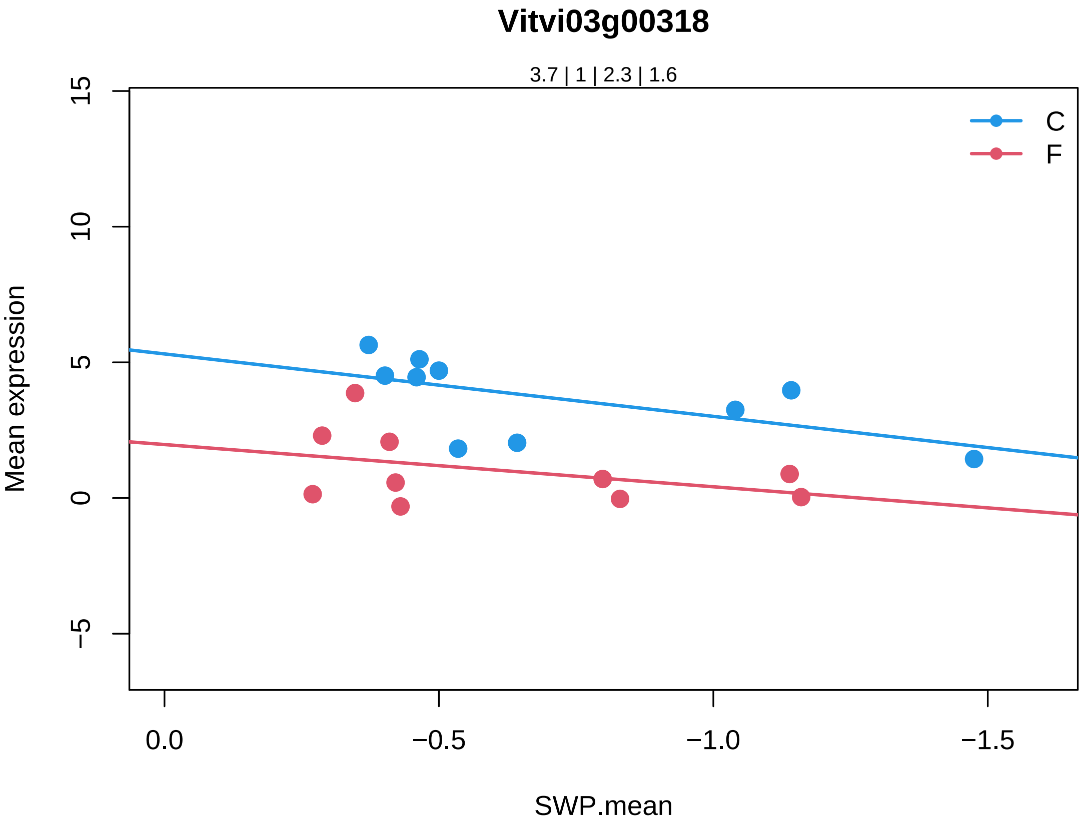
6.5.13 Vitvi03g00318

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

```
Vitvi03g00318
        27.03.2025
        RNA.regulation of transcription.MYB domain transcription factor family
        RAD-like 6 |
        Chr1:28245073-28245453 REVERSE LENGTH=126 |
        201606
```

Coefficients for Vitvi03g00318.

```
                   swp  varietyF swp.varietyF  AveExpr        F
Vitvi03g00318 2.300824 -3.339604   -0.7449947 2.357736 11.76716
                   P.Value   adj.P.Val  type
Vitvi03g00318 9.096021e-05 0.002087975 type4
```



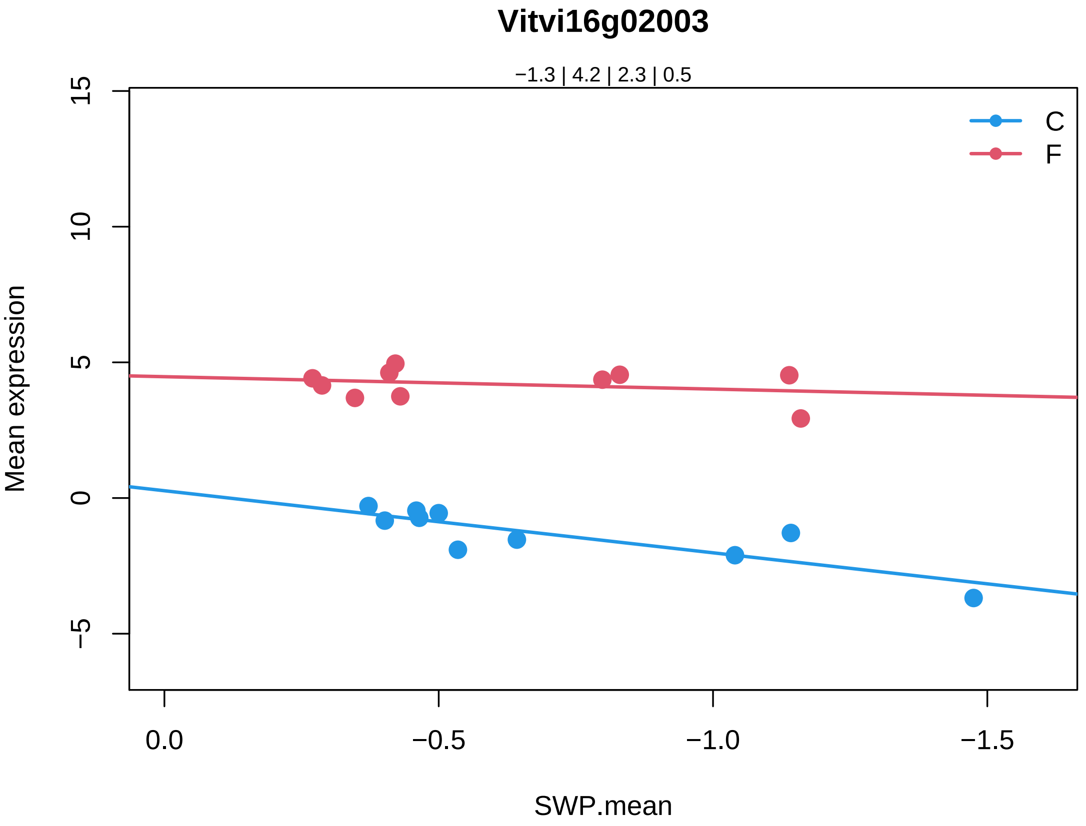
6.5.14 Vitvi16g02003

```
> 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.

```
                 swp varietyF swp.varietyF  AveExpr        F
Vitvi16g02003 2.2875 4.203023    -1.830222 1.426501 163.8027
                   P.Value    adj.P.Val  type
Vitvi16g02003 6.199962e-15 1.016127e-12 type4
```



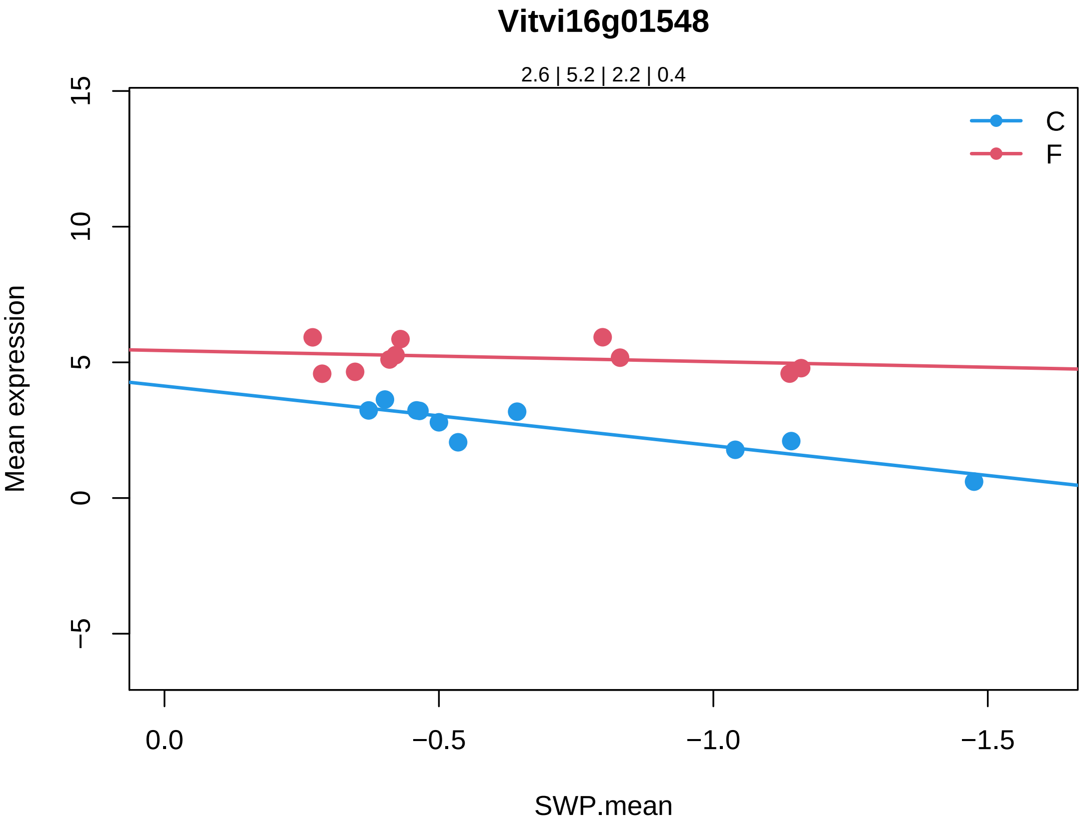
6.5.15 Vitvi16g01548

```
> 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.

```
                   swp varietyF swp.varietyF  AveExpr        F
Vitvi16g01548 2.196869 1.308994    -1.787469 3.882578 53.13999
                   P.Value    adj.P.Val  type
Vitvi16g01548 4.253783e-10 3.147386e-08 type4
```



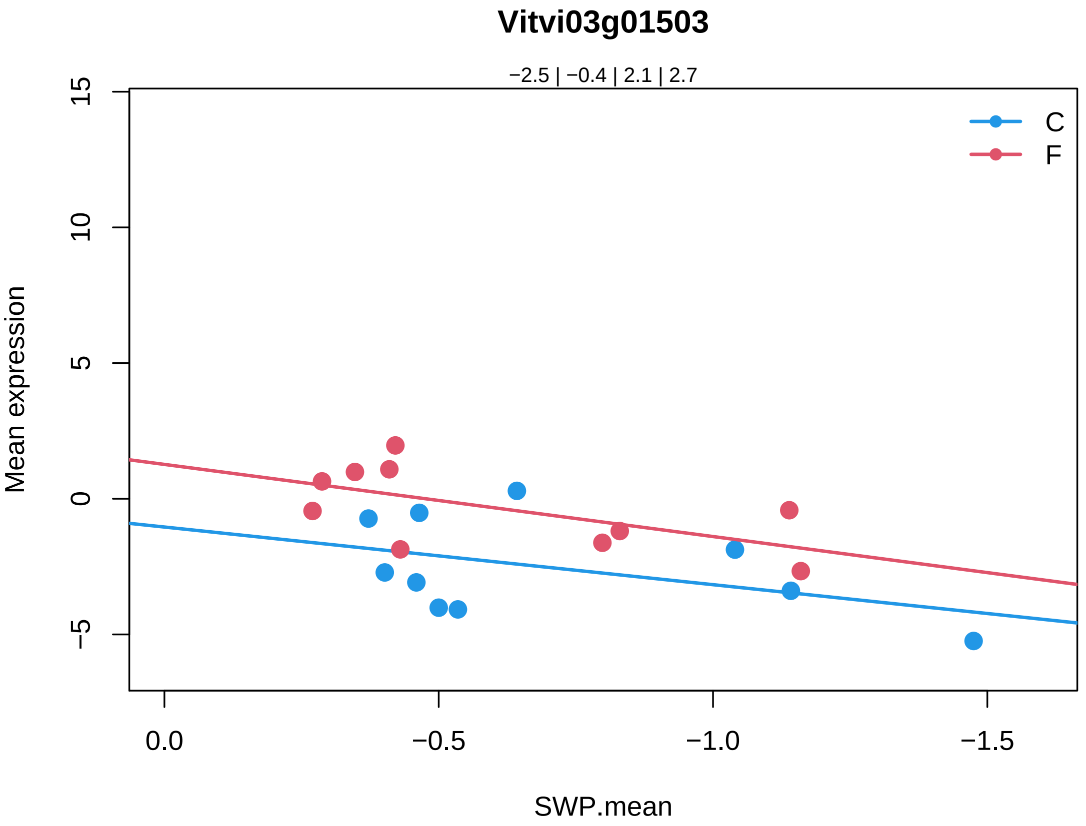
6.5.16 Vitvi03g01503

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

```
Vitvi03g01503
        35.2
        not assigned.unknown
        Organ-specific protein S2
```

Coefficients for Vitvi03g01503.

```
                   swp varietyF swp.varietyF   AveExpr        F
Vitvi03g01503 2.124611 2.307339    0.5331686 -1.445128 7.202361
                  P.Value  adj.P.Val  type
Vitvi03g01503 0.001602369 0.02142396 type4
```



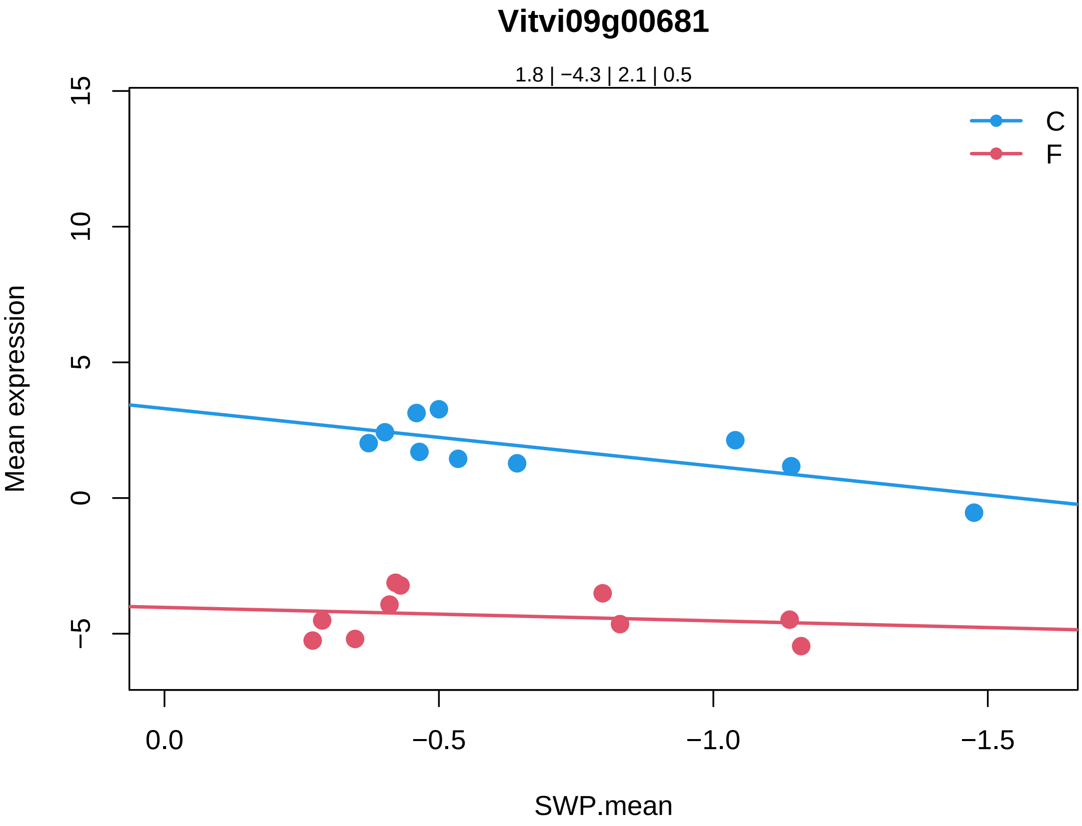
6.5.17 Vitvi09g00681

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

```
Vitvi09g00681
        20.01.2002
        stress.biotic.receptors
        receptor like protein 1 |
        Chr1:2270633-2274654 FORWARD LENGTH=913 |
        201606
```

Coefficients for Vitvi09g00681.

```
                   swp  varietyF swp.varietyF   AveExpr        F
Vitvi09g00681 2.121009 -7.326997    -1.626761 -1.264715 110.8171
                  P.Value    adj.P.Val  type
Vitvi09g00681 3.27978e-13 4.031484e-11 type4
```

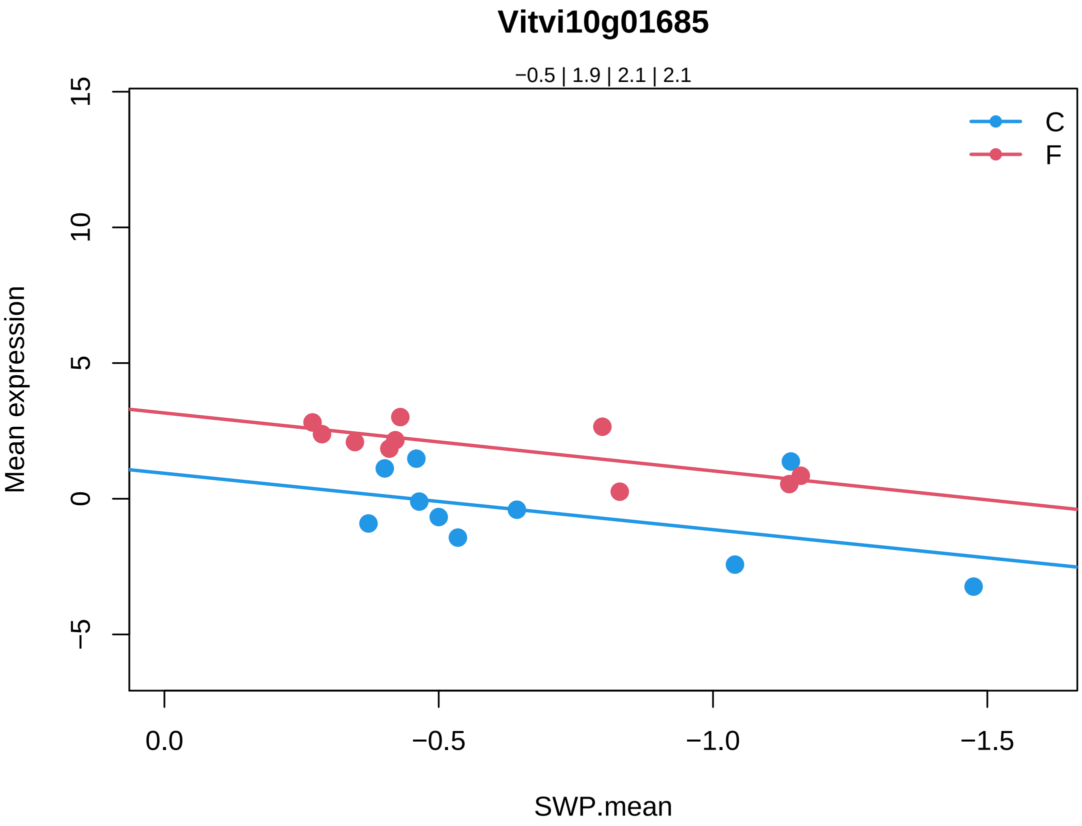


6.5.18 Vitvi10g01685

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
Vitvi10g01685
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi10g01685.

```
                   swp varietyF swp.varietyF   AveExpr        F
Vitvi10g01685 2.076279 2.222847   0.05856843 0.6685785 12.62397
                   P.Value   adj.P.Val  type
Vitvi10g01685 5.721339e-05 0.001402004 type4
```



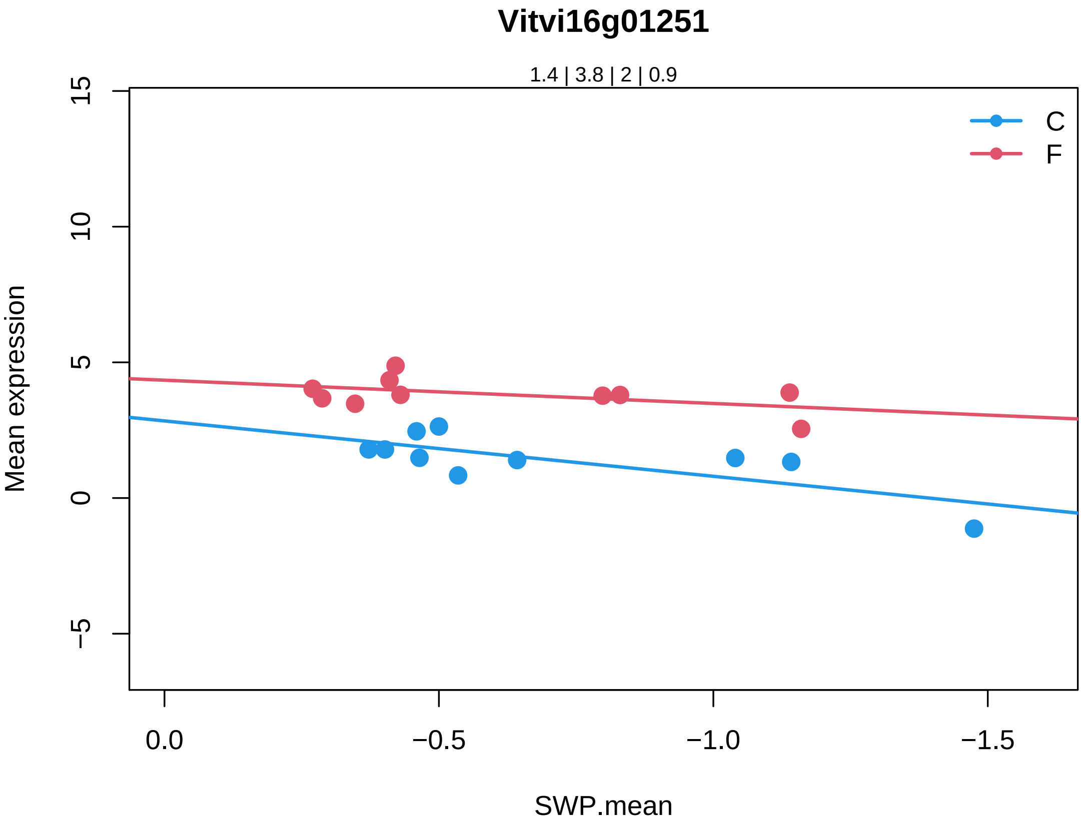
6.5.19 Vitvi16g01251

```
> 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.

```
                   swp varietyF swp.varietyF  AveExpr        F
Vitvi16g01251 2.040488 1.500827    -1.182968 2.613151 31.48459
                  P.Value    adj.P.Val  type
Vitvi16g01251 4.84848e-08 2.505103e-06 type4
```



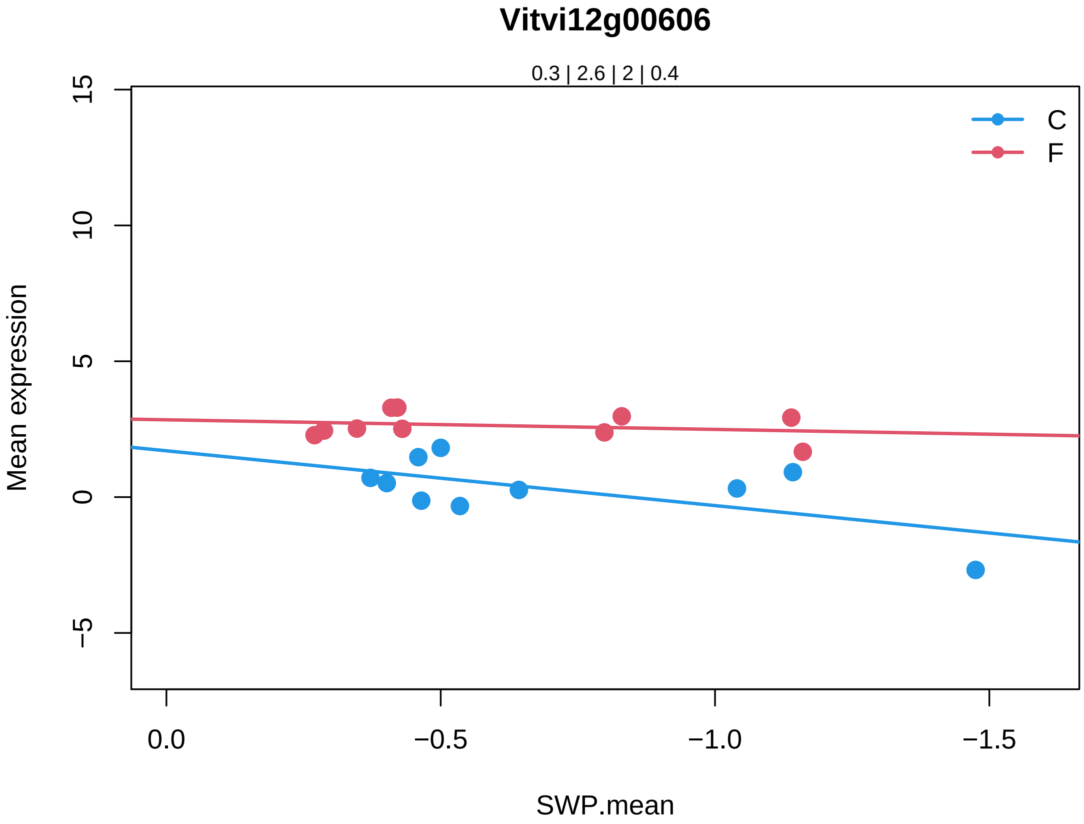
6.5.20 Vitvi12g00606

```
> 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.

```
                   swp varietyF swp.varietyF  AveExpr        F
Vitvi12g00606 2.016467 1.140932    -1.662881 1.457987 19.74785
                   P.Value    adj.P.Val  type
Vitvi12g00606 2.246443e-06 8.290625e-05 type4
```



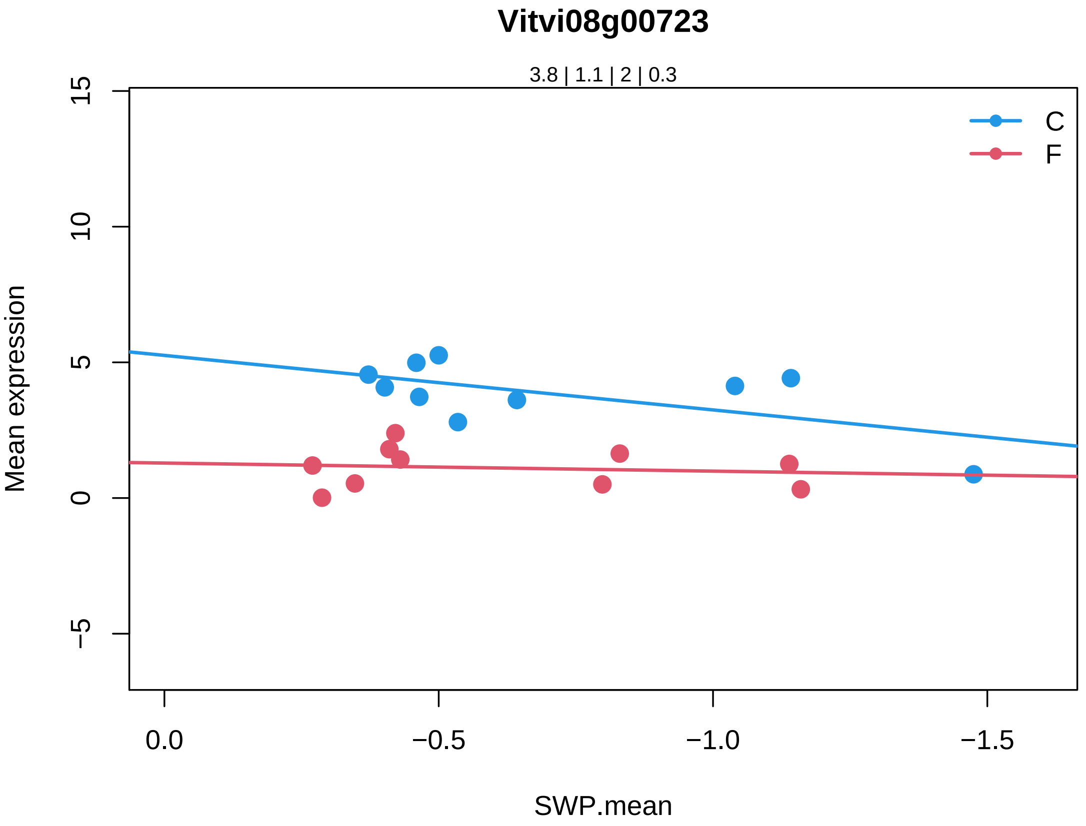
6.5.21 Vitvi08g00723

```
> 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.

```
                   swp  varietyF swp.varietyF AveExpr        F
Vitvi08g00723 2.009066 -3.967297    -1.711553 2.47519 19.98487
                   P.Value   adj.P.Val  type
Vitvi08g00723 2.047632e-06 7.63081e-05 type4
```



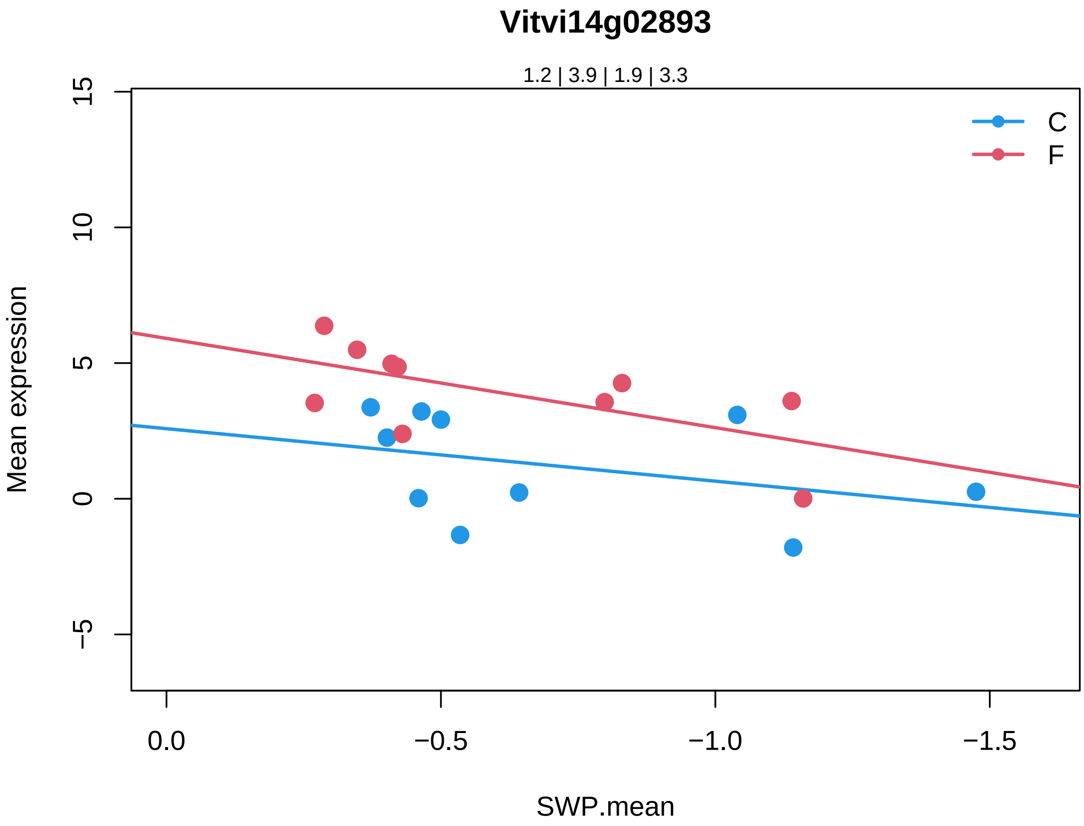
6.5.22 Vitvi14g02893

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

```
Vitvi14g02893
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi14g02893.

```
                   swp varietyF swp.varietyF AveExpr        F
Vitvi14g02893 1.934911 3.327107     1.355003 2.56359 7.698762
                  P.Value  adj.P.Val  type
Vitvi14g02893 0.001128339 0.01630156 type4
```



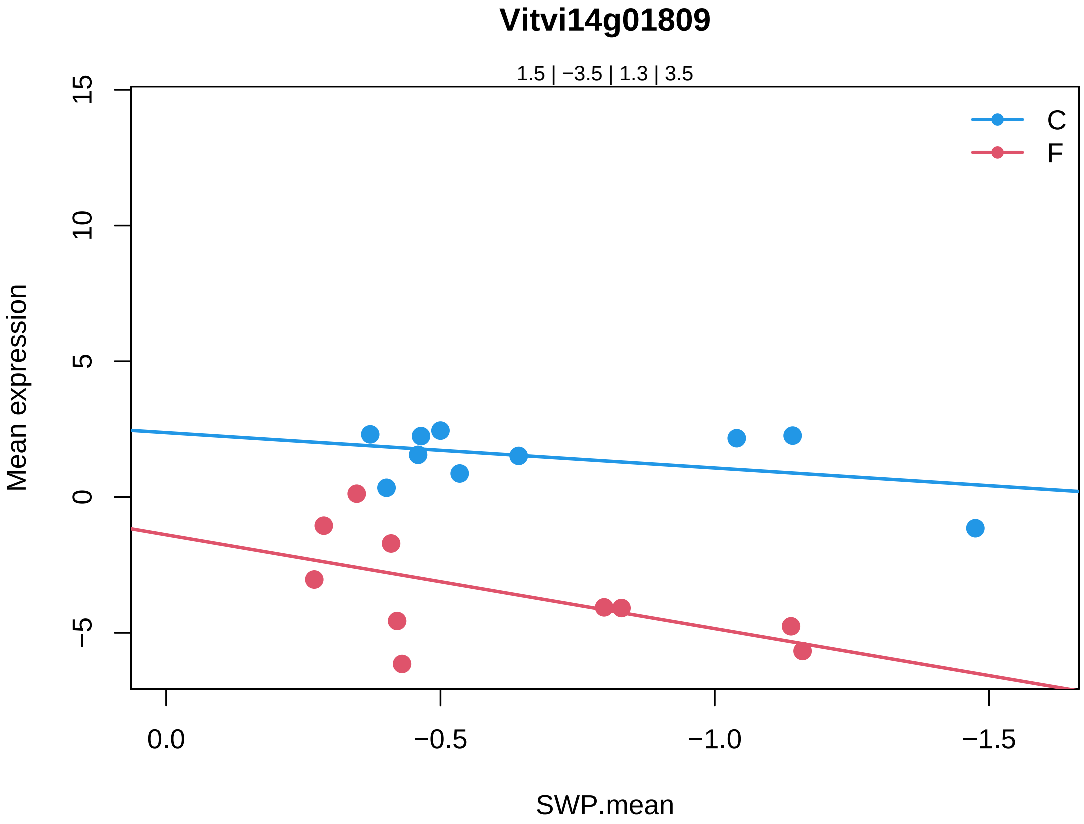
6.5.23 Vitvi14g01809

```
> 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.

```
                   swp  varietyF swp.varietyF   AveExpr        F
Vitvi14g01809 1.301701 -3.762681     2.154381 -1.020287 27.37223
                   P.Value    adj.P.Val  type
Vitvi14g01809 1.600759e-07 7.648517e-06 type4
```



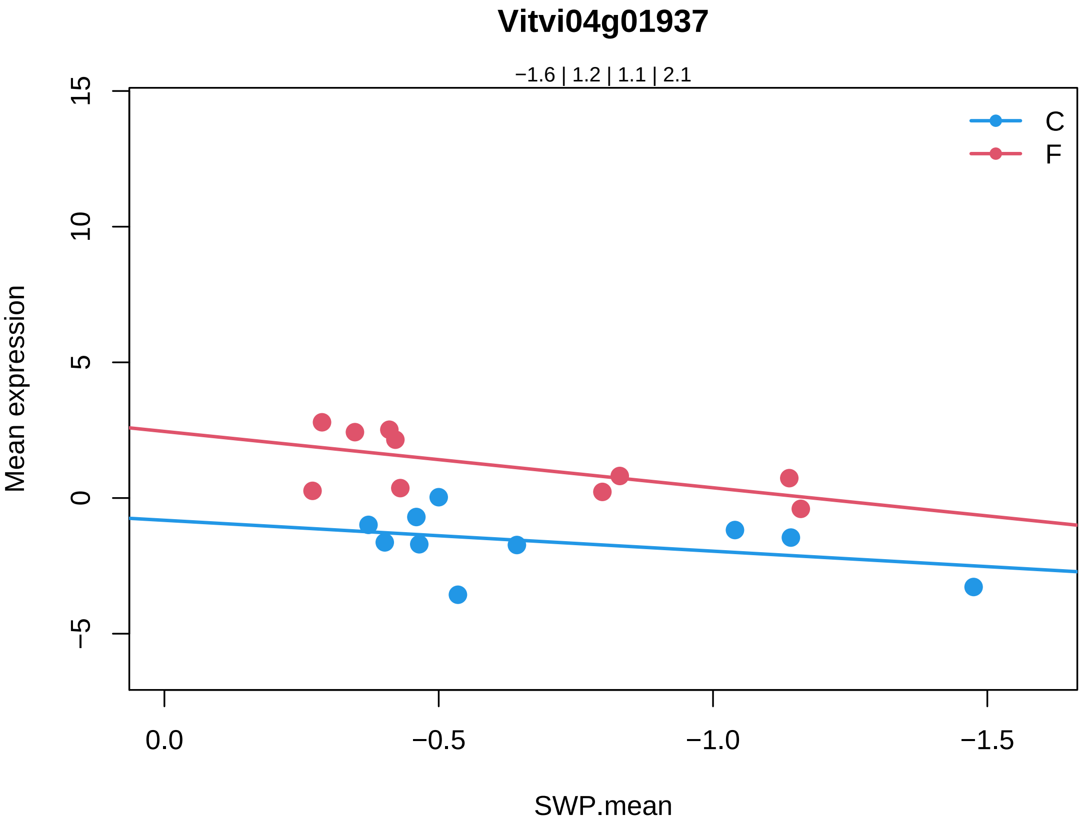
6.5.24 Vitvi04g01937

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

```
Vitvi04g01937
        27.03.1999
        RNA.regulation of transcription.unclassified
        Eukaryotic aspartyl protease family protein |
        Chr5:3403331-3405331 REVERSE LENGTH=474 |
        201606
```

Coefficients for Vitvi04g01937.

```
                  swp varietyF swp.varietyF    AveExpr        F
Vitvi04g01937 1.13847 3.273734    0.9367621 -0.2162805 18.24259
                   P.Value    adj.P.Val  type
Vitvi04g01937 4.125569e-06 0.0001429135 type4
```



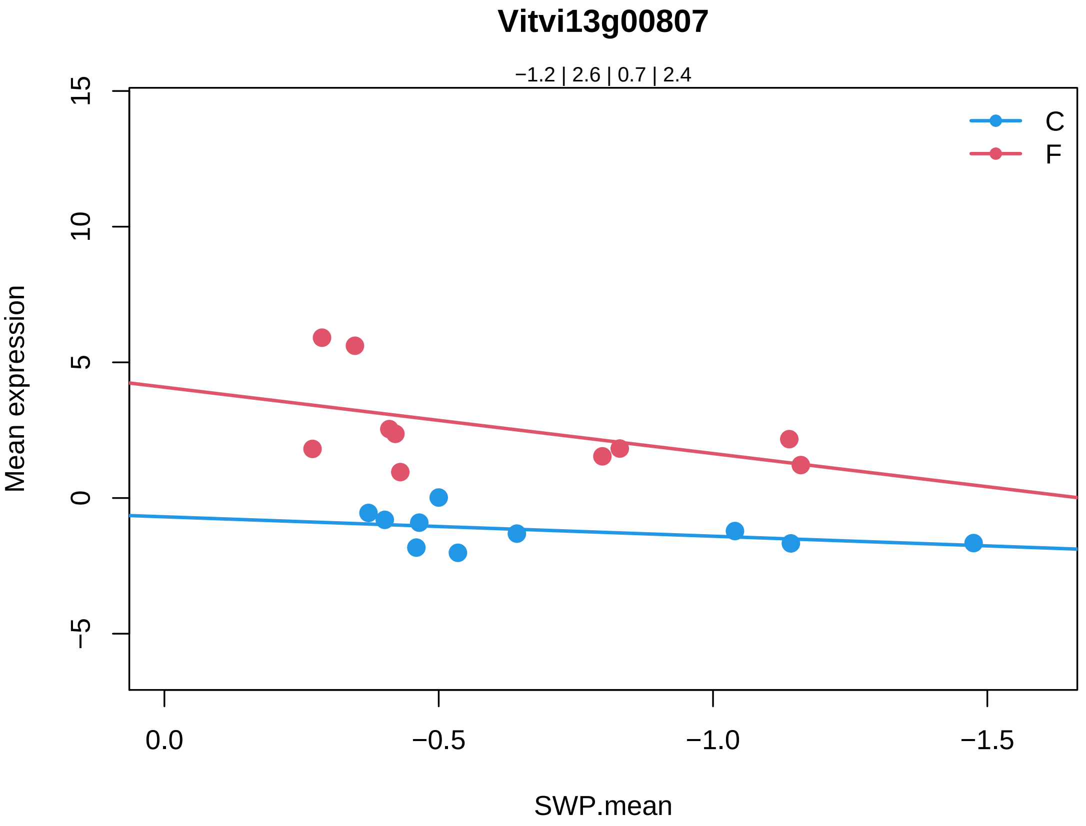
6.5.25 Vitvi13g00807

```
> 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.

```
                    swp varietyF swp.varietyF  AveExpr       F
Vitvi13g00807 0.7145515 4.775852     1.730151 0.699065 22.3554
                   P.Value    adj.P.Val  type
Vitvi13g00807 8.447419e-07 3.498793e-05 type4
```



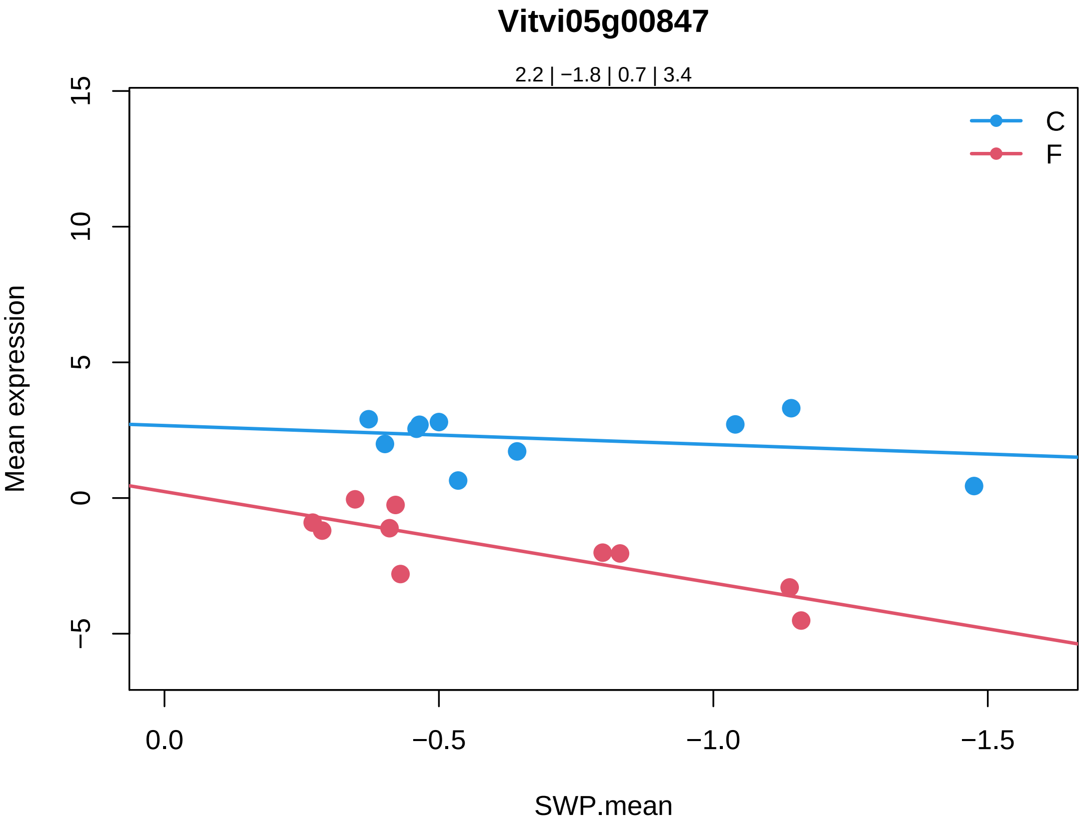
6.5.26 Vitvi05g00847

```
> 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.

```
                    swp   varietyF swp.varietyF  AveExpr        F
Vitvi05g00847 0.7001947 -2.435001     2.671128 0.179306 44.44483
                   P.Value   adj.P.Val  type
Vitvi05g00847 2.236024e-09 1.50803e-07 type4
```



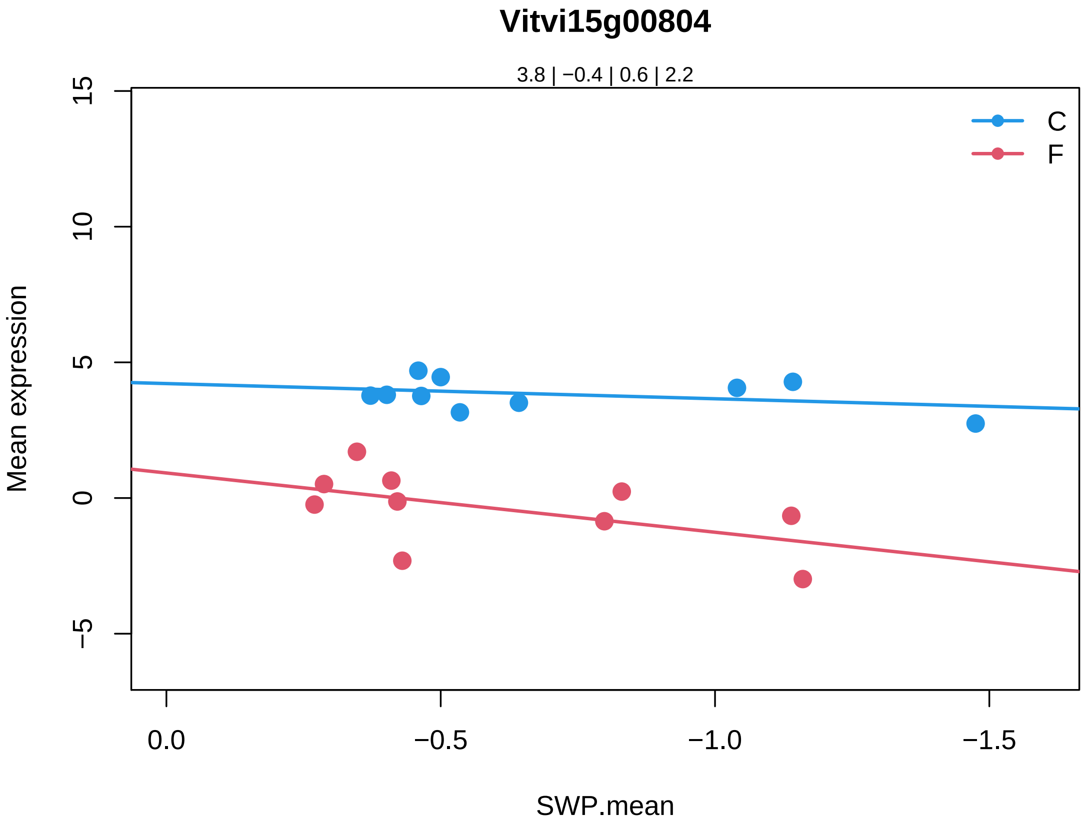
6.5.27 Vitvi15g00804

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

```
Vitvi15g00804
        26.1
        misc.cytochrome P450
        cytochrome P450%2C family 76%2C subfamily C%2C polypeptide 2 |
        Chr2:18779935-18781922 REVERSE LENGTH=512 |
        201606
```

Coefficients for Vitvi15g00804.

```
                    swp  varietyF swp.varietyF  AveExpr        F
Vitvi15g00804 0.5598445 -3.295391     1.623612 1.708167 41.31328
                   P.Value    adj.P.Val  type
Vitvi15g00804 4.355005e-09 2.777363e-07 type4
```



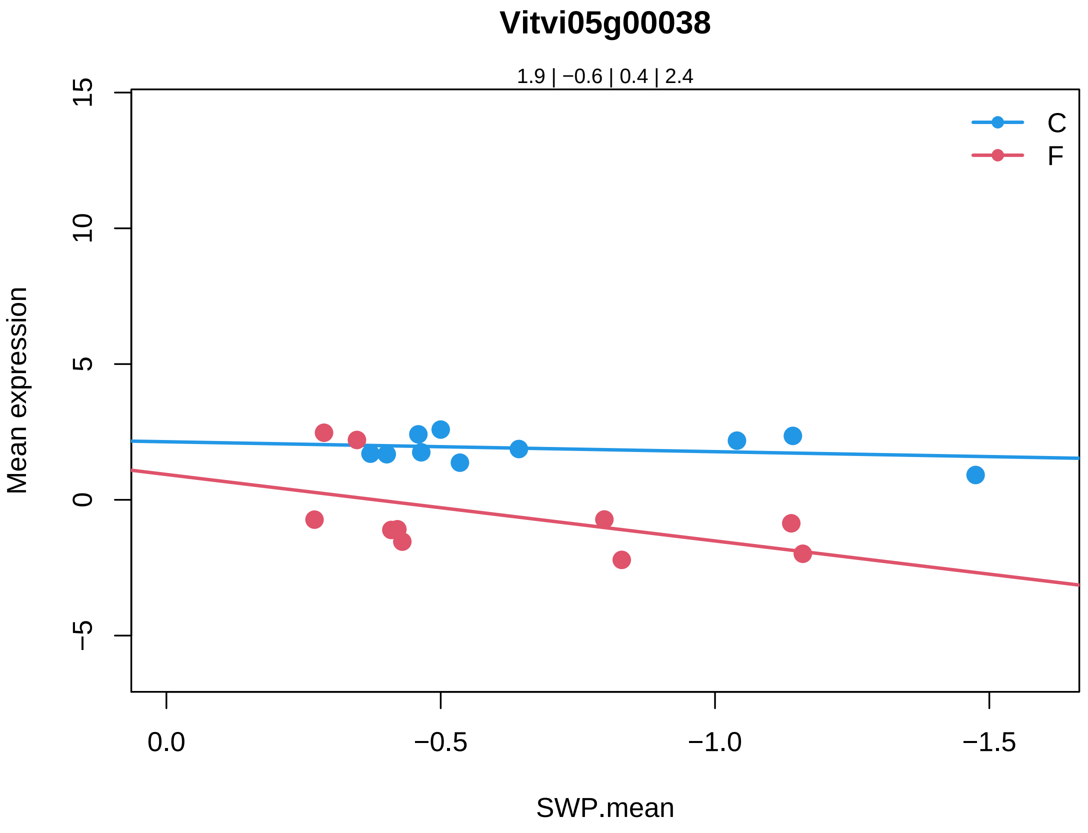
6.5.28 Vitvi05g00038

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

```
Vitvi05g00038
        26.03.2005
        misc.gluco-, galacto- and mannosidases.glycosyl hydrolase family 5
        alpha/beta-Hydrolases superfamily protein |
        Chr4:1035722-1037403 FORWARD LENGTH=324 |
        201606
```

Coefficients for Vitvi05g00038.

```
                    swp   varietyF swp.varietyF   AveExpr        F
Vitvi05g00038 0.3647677 -1.204967     2.082283 0.6618194 12.69346
                   P.Value   adj.P.Val  type
Vitvi05g00038 5.514927e-05 0.00136017 type4
```



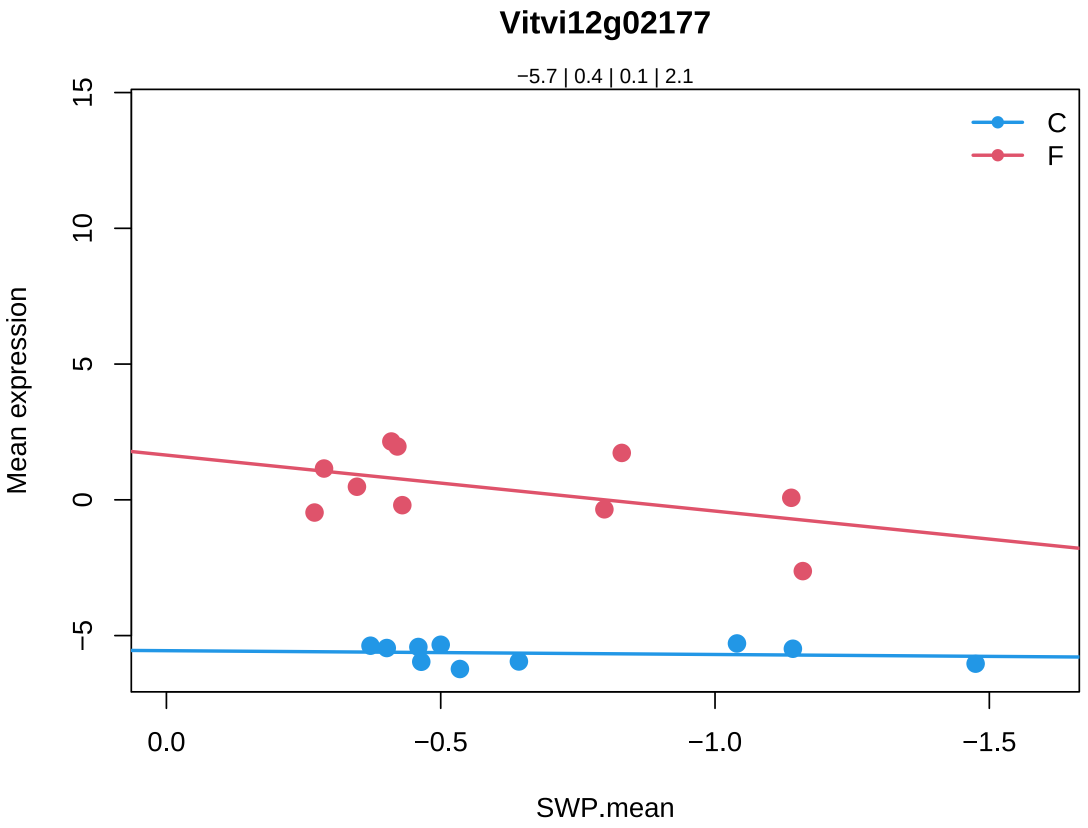
6.5.29 Vitvi12g02177

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

```
Vitvi12g02177
        16.01.2005
        secondary metabolism.isoprenoids.terpenoids
        terpene synthase 21 |
        Chr5:8092969-8095128 FORWARD LENGTH=545 |
        201606
```

Coefficients for Vitvi12g02177.

```
                    swp varietyF swp.varietyF   AveExpr       F
Vitvi12g02177 0.1400847 7.203545     1.922026 -2.631891 80.5119
                   P.Value    adj.P.Val  type
Vitvi12g02177 7.832868e-12 7.604368e-10 type4
```



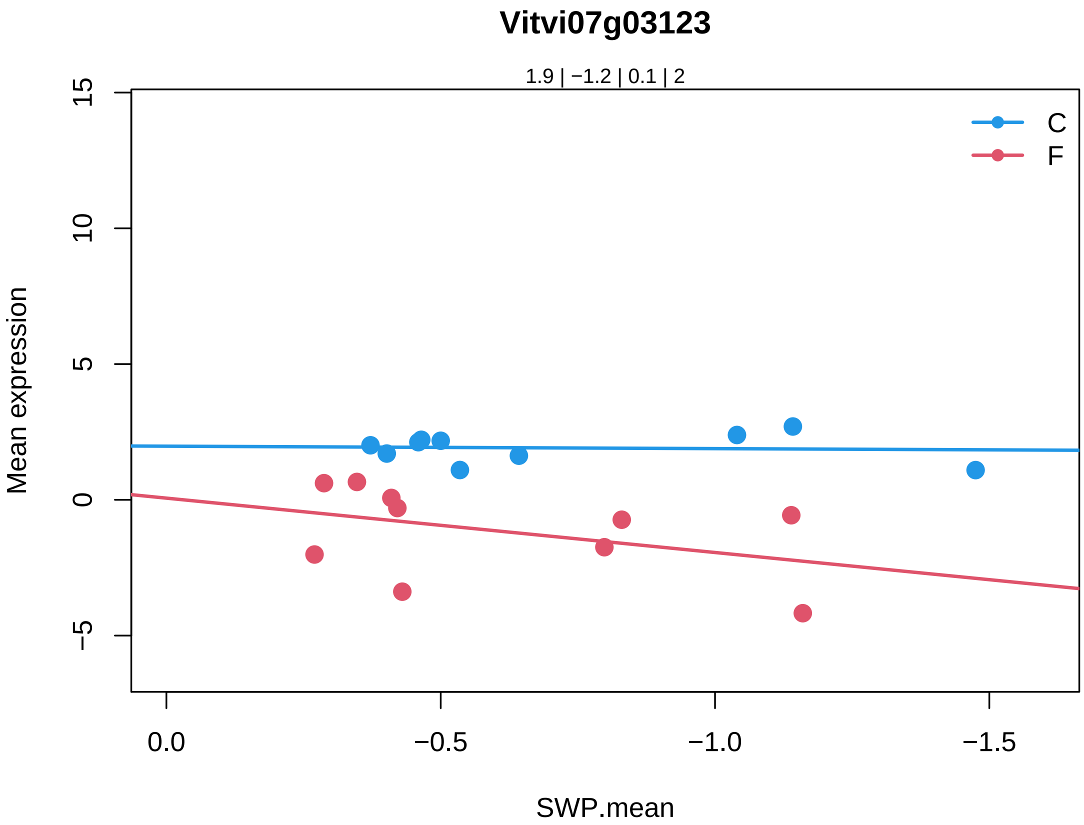
6.5.30 Vitvi07g03123

```
> 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.

```
                    swp   varietyF swp.varietyF   AveExpr        F
Vitvi07g03123 0.0898298 -1.913572     1.912759 0.3773528 15.38188
                   P.Value   adj.P.Val  type
Vitvi07g03123 1.453035e-05 0.000434258 type4
```



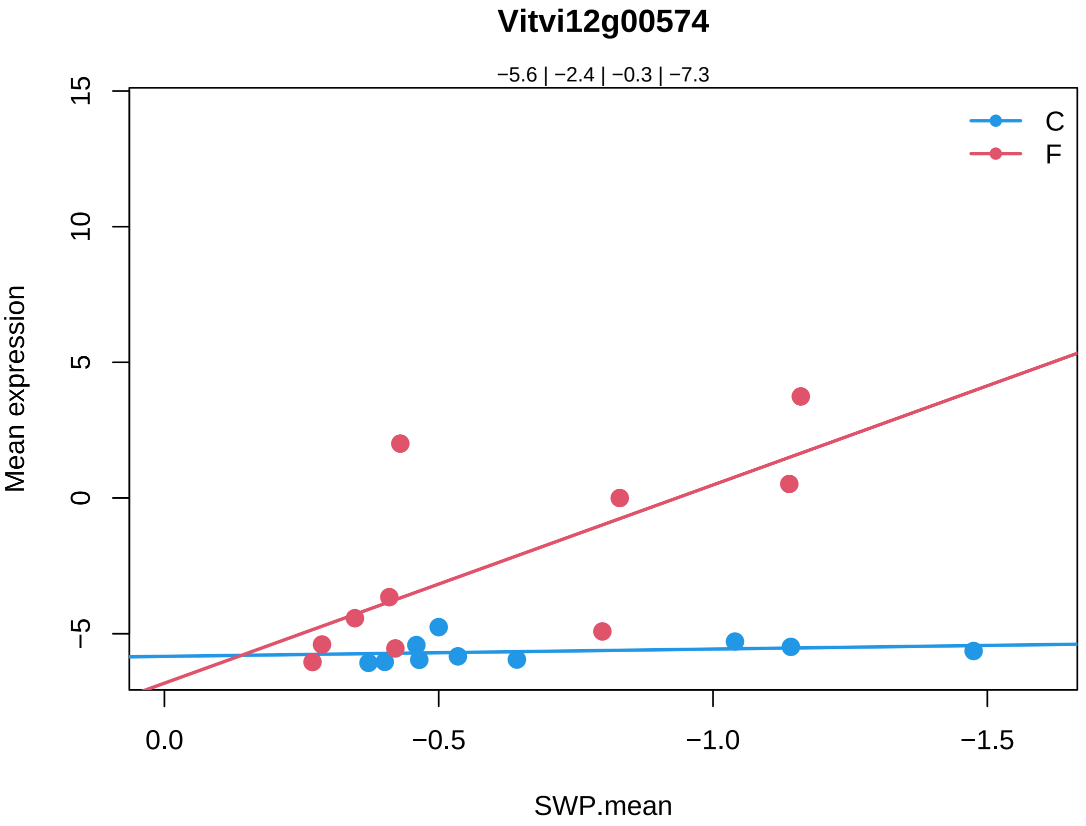
6.5.31 Vitvi12g00574

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

```
Vitvi12g00574
        16.01.2005
        secondary metabolism.isoprenoids.terpenoids
        terpene synthase-like sequence-1%2C8-cineole |
        Chr3:9447545-9450316 FORWARD LENGTH=600 |
        201606
```

Coefficients for Vitvi12g00574.

```
                     swp   varietyF swp.varietyF   AveExpr        F
Vitvi12g00574 -0.2692201 -0.9884648    -7.036961 -4.008795 12.81278
                   P.Value   adj.P.Val  type
Vitvi12g00574 5.179173e-05 0.00130051 type4
```



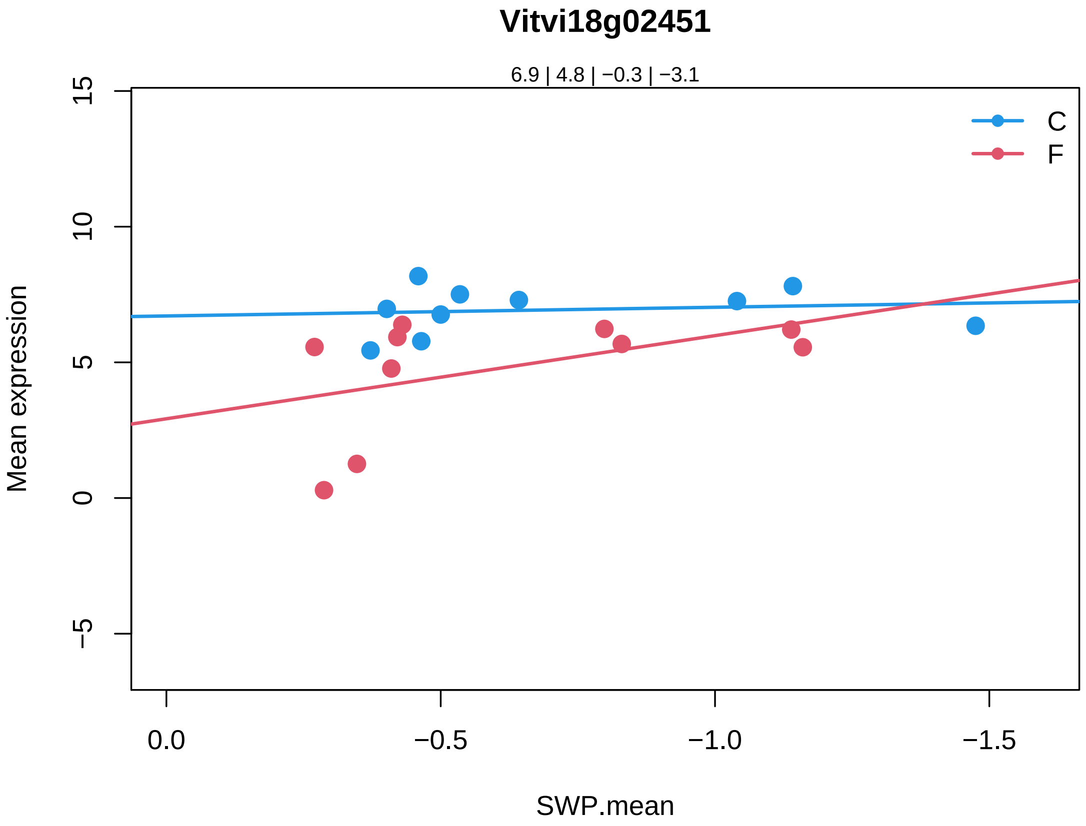
6.5.32 Vitvi18g02451

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

```
Vitvi18g02451
        16.01.2005
        secondary metabolism.isoprenoids.terpenoids
        terpene synthase 21 |
        Chr5:8092969-8095128 FORWARD LENGTH=545 |
        201606
```

Coefficients for Vitvi18g02451.

```
                     swp   varietyF swp.varietyF AveExpr        F
Vitvi18g02451 -0.3205063 -3.788492    -2.742855 5.86091 5.829124
                  P.Value  adj.P.Val  type
Vitvi18g02451 0.004496459 0.04697397 type4
```



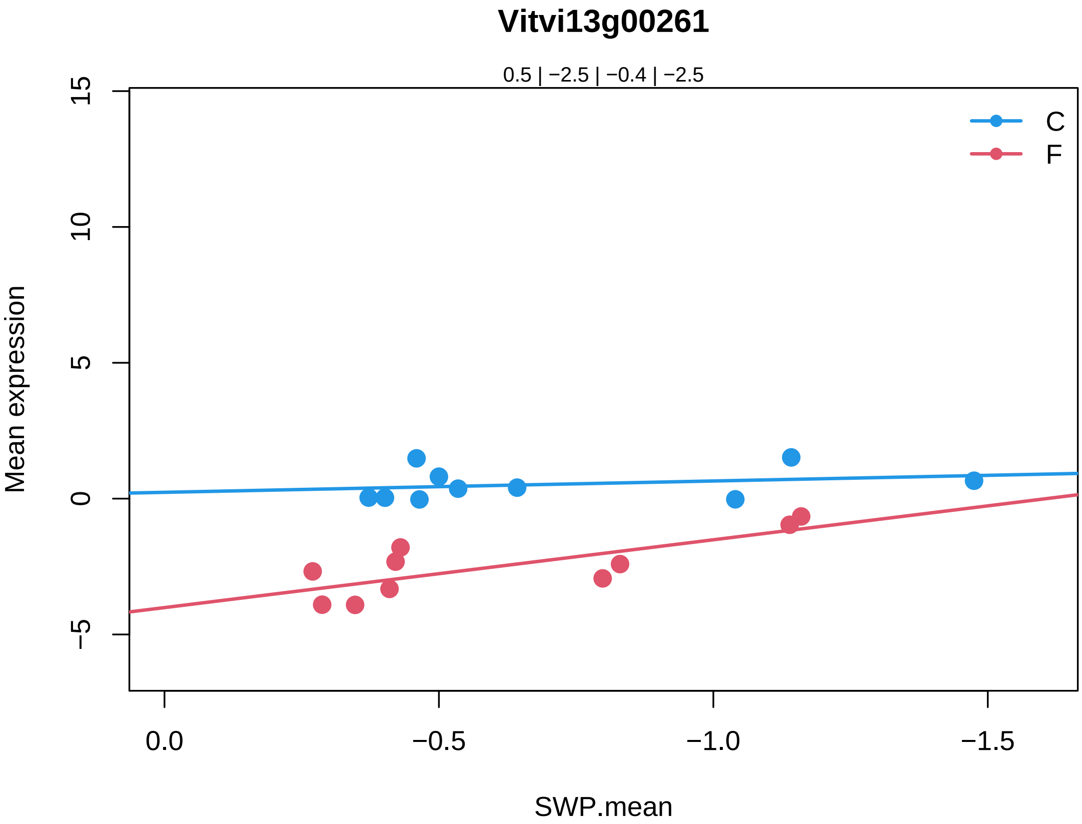
6.5.33 Vitvi13g00261

```
> 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.

```
                     swp  varietyF swp.varietyF    AveExpr        F
Vitvi13g00261 -0.4169403 -4.243055    -2.079326 -0.9822559 42.75431
                   P.Value    adj.P.Val  type
Vitvi13g00261 3.188076e-09 2.076609e-07 type4
```



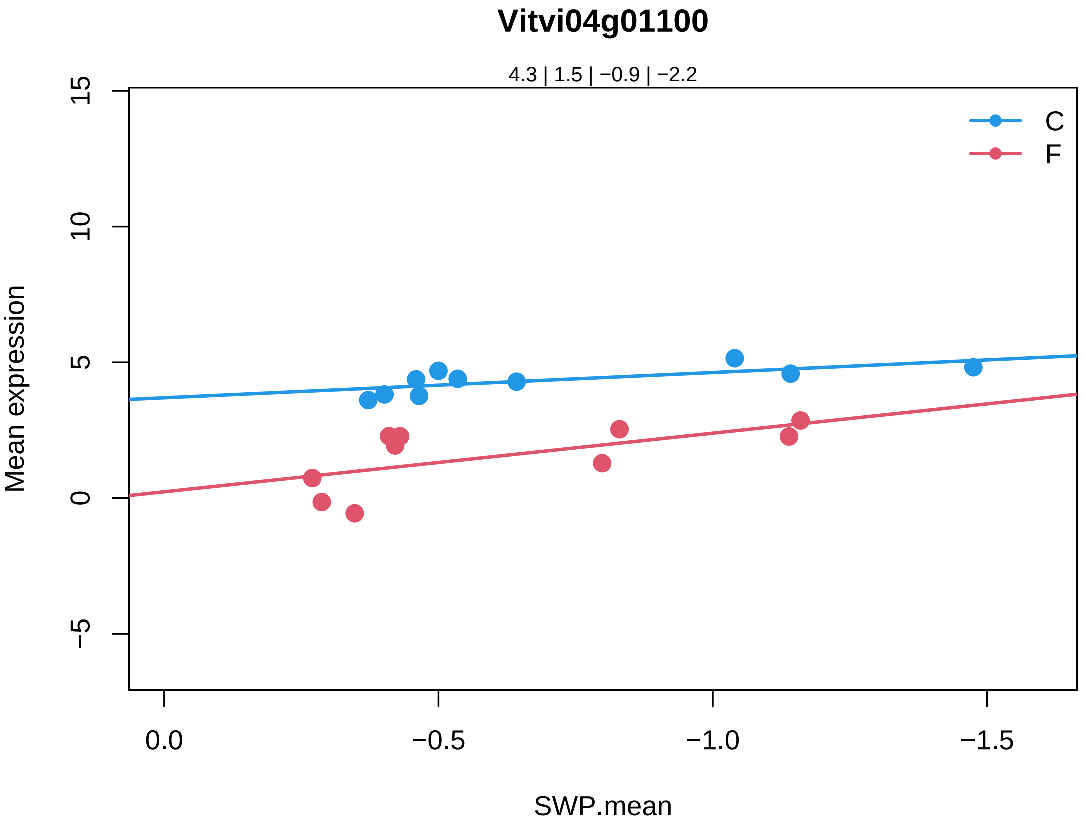
6.5.34 Vitvi04g01100

```
> 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.

```
                     swp   varietyF swp.varietyF AveExpr        F
Vitvi04g01100 -0.9302426 -3.462217    -1.228185 2.94742 32.63831
                   P.Value    adj.P.Val  type
Vitvi04g01100 3.547063e-08 1.870738e-06 type4
```



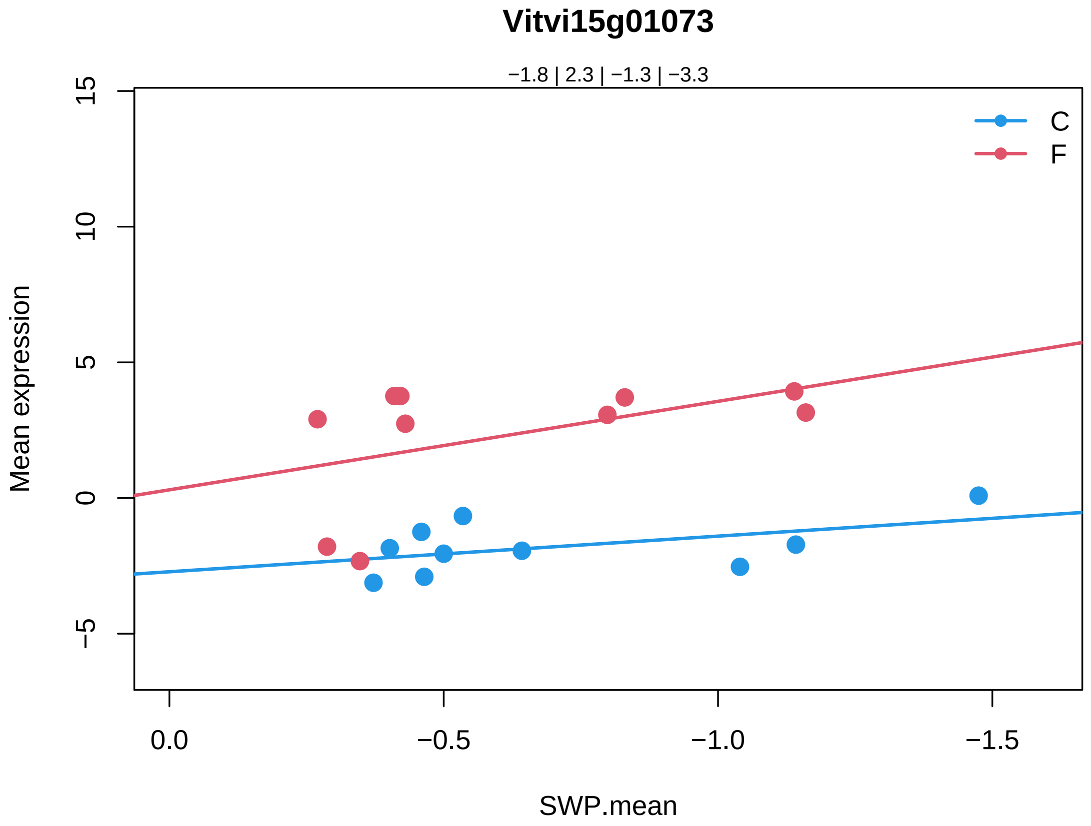
6.5.35 Vitvi15g01073

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

```
Vitvi15g01073
        16.8.1.12
        secondary metabolism.flavonoids.anthocyanins.anthocyanidin 3-O-glucosy
        UDP-Glycosyltransferase superfamily protein |
        Chr2:9593012-9594424 FORWARD LENGTH=470 |
        201606
```

Coefficients for Vitvi15g01073.

```
                    swp varietyF swp.varietyF   AveExpr        F
Vitvi15g01073 -1.312703  3.01979    -1.948958 0.2472983 15.25673
                  P.Value    adj.P.Val  type
Vitvi15g01073 1.54069e-05 0.0004561373 type4
```



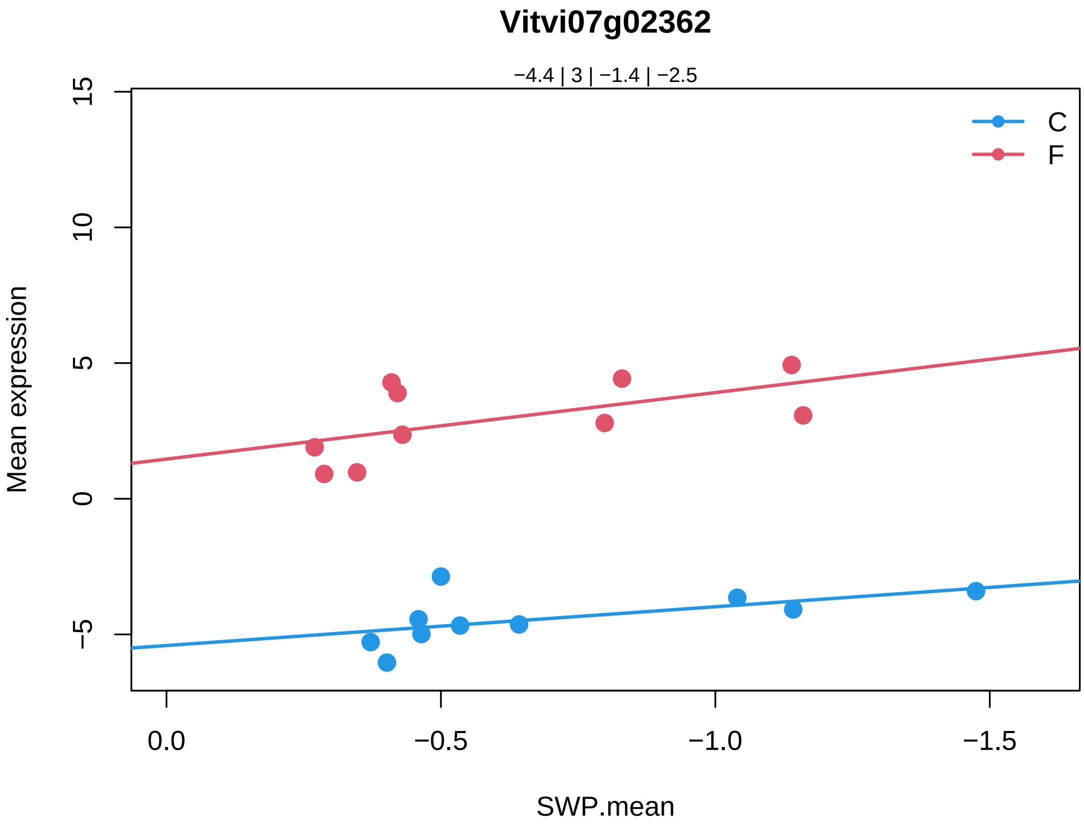
6.5.36 Vitvi07g02362

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

```
Vitvi07g02362
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi07g02362.

```
                    swp varietyF swp.varietyF    AveExpr        F
Vitvi07g02362 -1.429156 6.871178    -1.021377 -0.7258975 107.7366
                   P.Value    adj.P.Val  type
Vitvi07g02362 4.352195e-13 5.102781e-11 type4
```



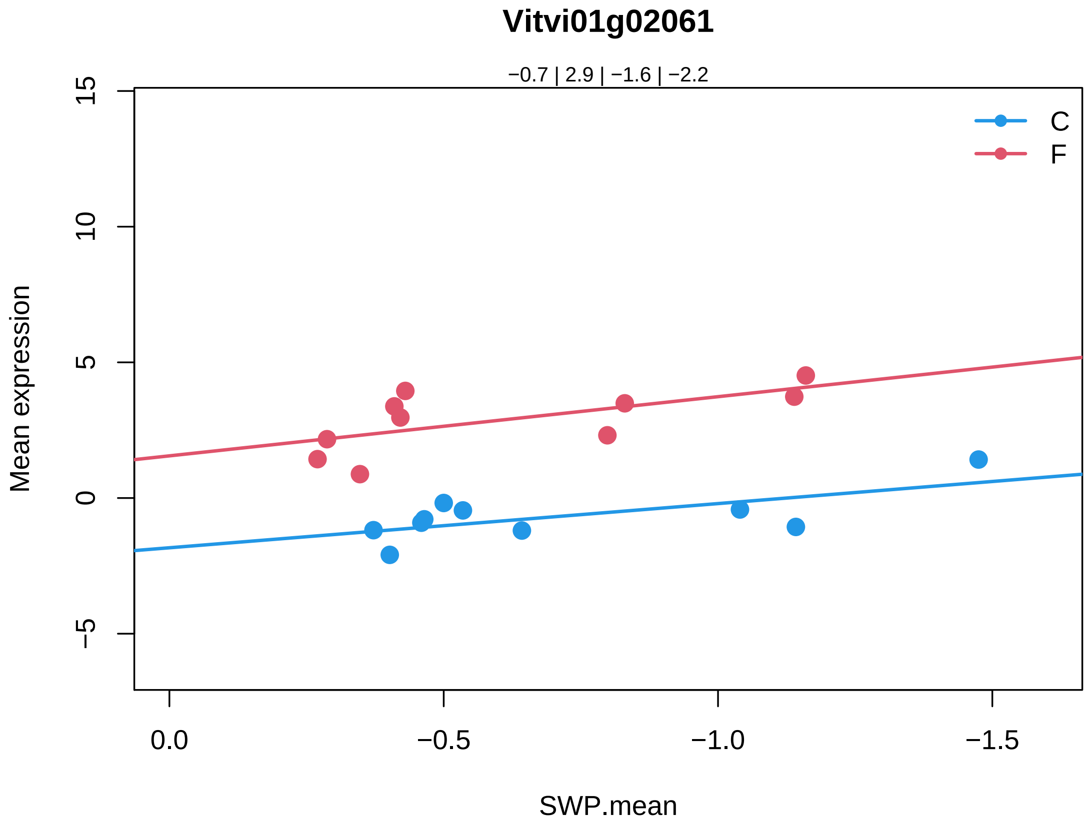
6.5.37 Vitvi01g02061

```
> 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.

```
                    swp varietyF swp.varietyF  AveExpr        F
Vitvi01g02061 -1.628569 3.387101   -0.5520575 1.097244 41.56221
                   P.Value    adj.P.Val  type
Vitvi01g02061 4.123874e-09 2.652155e-07 type4
```



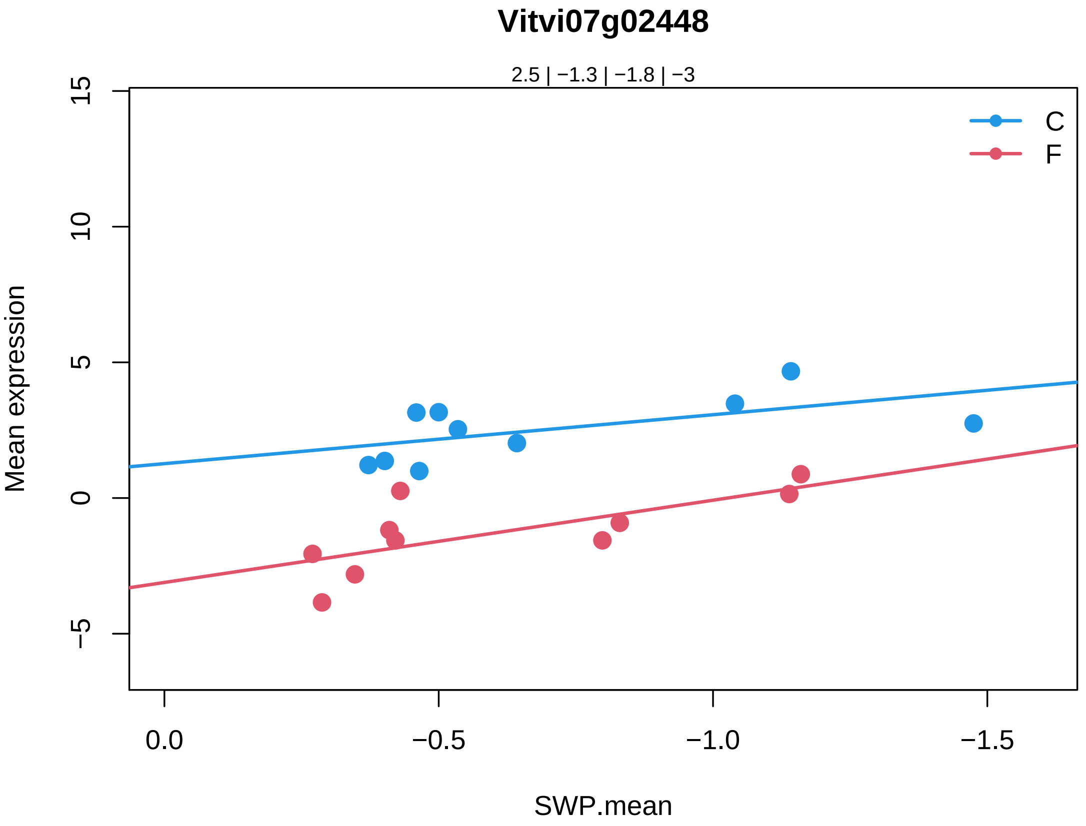
6.5.38 Vitvi07g02448

```
> 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.

```
                    swp  varietyF swp.varietyF   AveExpr        F
Vitvi07g02448 -1.803435 -4.378368    -1.227884 0.6345322 33.70819
                   P.Value    adj.P.Val  type
Vitvi07g02448 2.675661e-08 1.430962e-06 type4
```



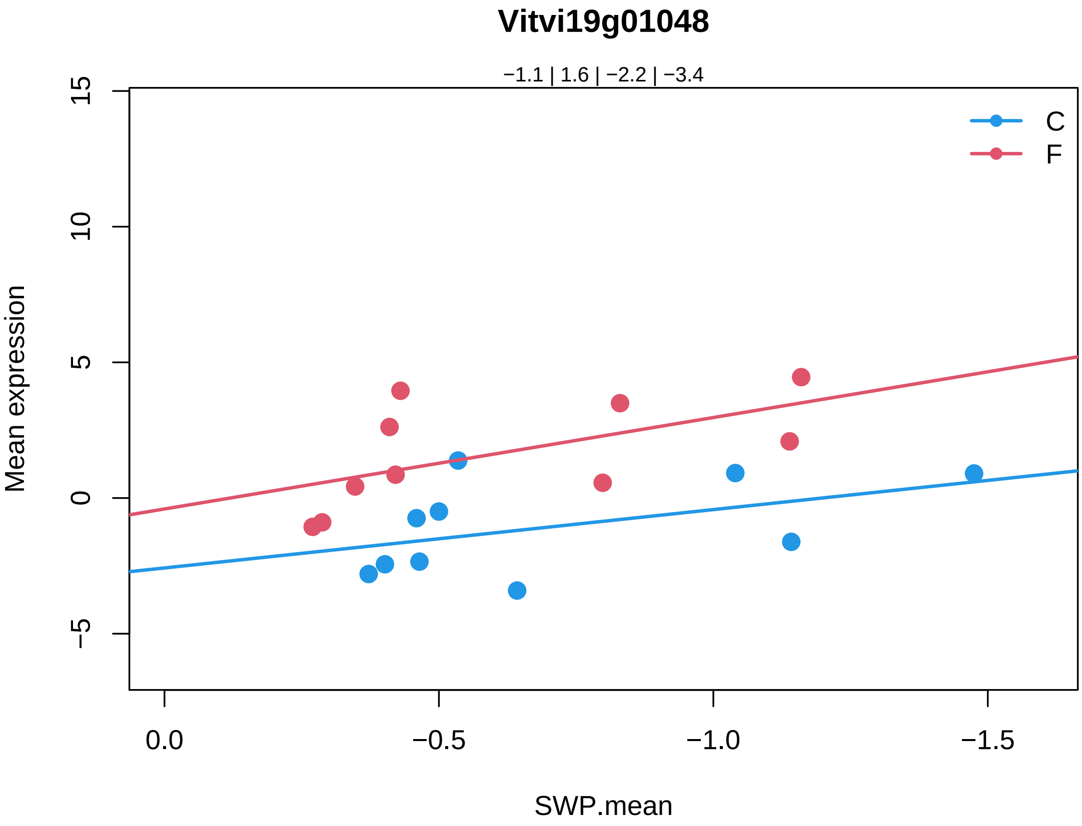
6.5.39 Vitvi19g01048

```
> 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.

```
                    swp varietyF swp.varietyF   AveExpr        F
Vitvi19g01048 -2.150775  2.17355    -1.218795 0.2925552 8.779439
                   P.Value   adj.P.Val  type
Vitvi19g01048 0.0005452867 0.008975443 type4
```



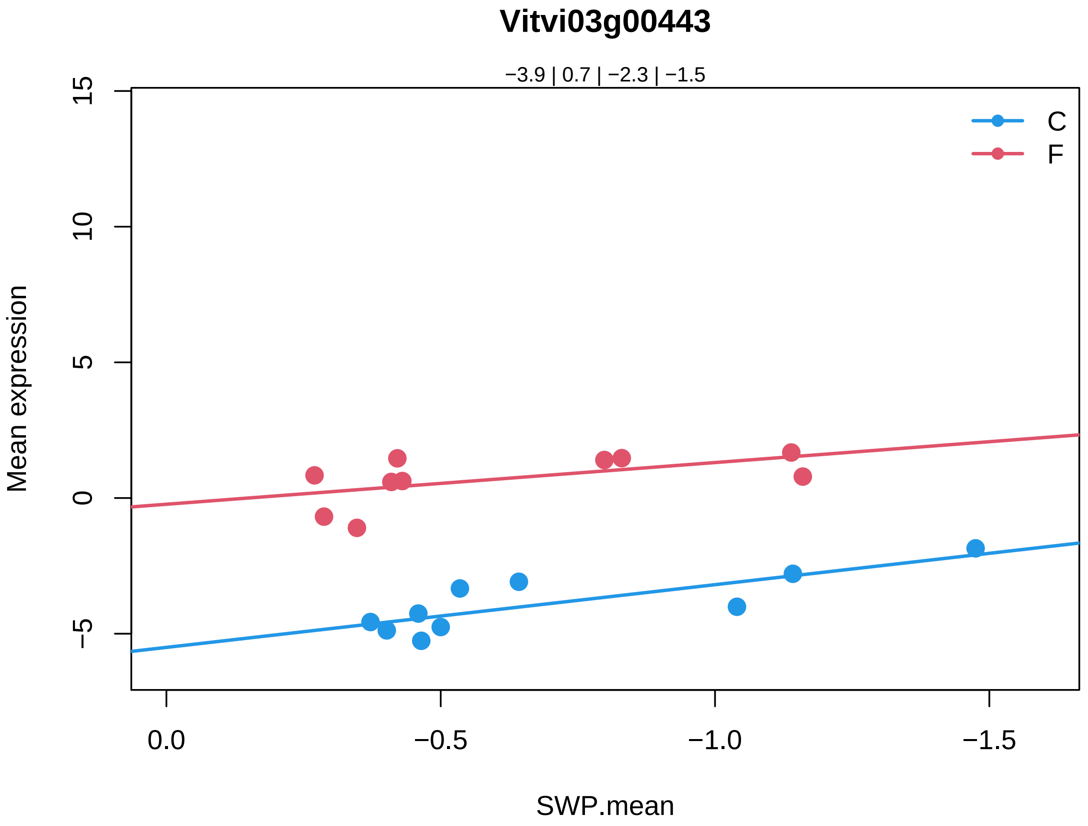
6.5.40 Vitvi03g00443

```
> 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.

```
                    swp varietyF swp.varietyF AveExpr        F
Vitvi03g00443 -2.311521 5.275856    0.7750986 -1.5863 79.96619
                   P.Value    adj.P.Val  type
Vitvi03g00443 8.373128e-12 8.077419e-10 type4
```



6.5.41 Vitvi09g01282

```
> 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.

```
                    swp varietyF swp.varietyF   AveExpr        F
Vitvi09g01282 -2.408129 2.029899    -2.570707 0.6068136 12.77438
                   P.Value  adj.P.Val  type
Vitvi09g01282 5.284715e-05 0.00131617 type4
```

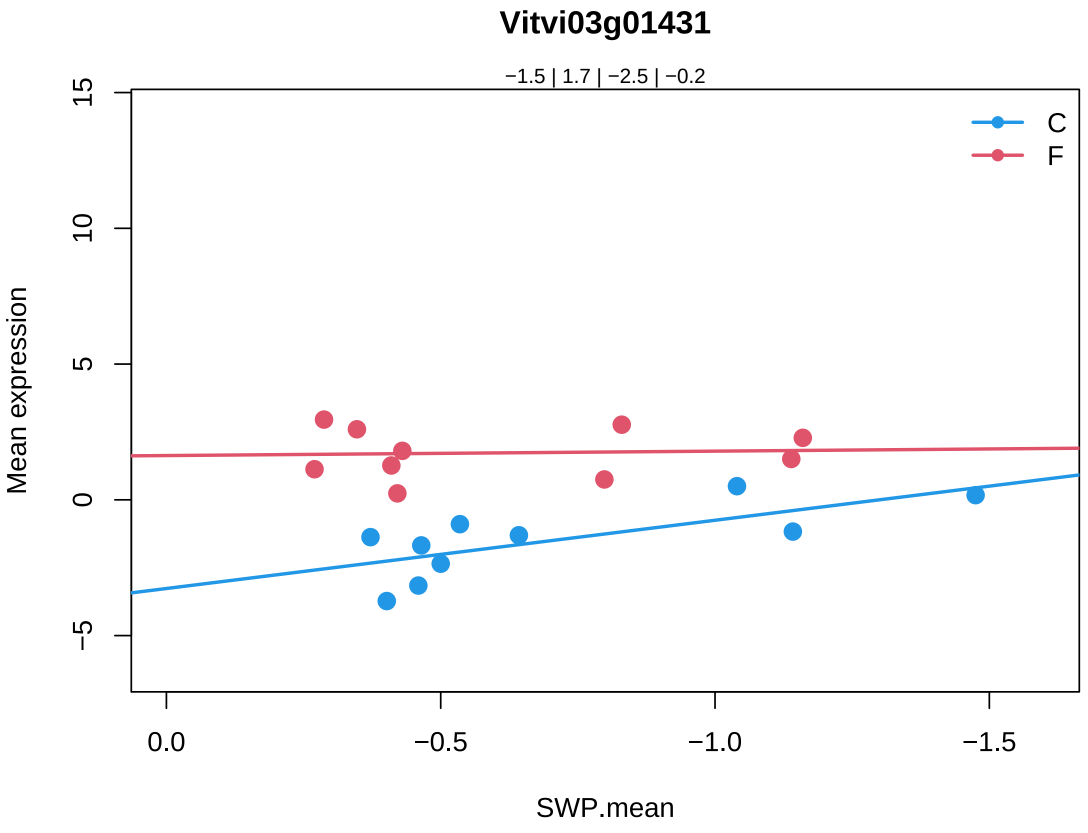
6.5.42 Vitvi03g01431

```
> 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.

```
                    swp varietyF swp.varietyF   AveExpr        F
Vitvi03g01431 -2.513015  4.89664     2.351136 0.1151543 26.29632
                   P.Value    adj.P.Val  type
Vitvi03g01431 2.239329e-07 1.043788e-05 type4
```



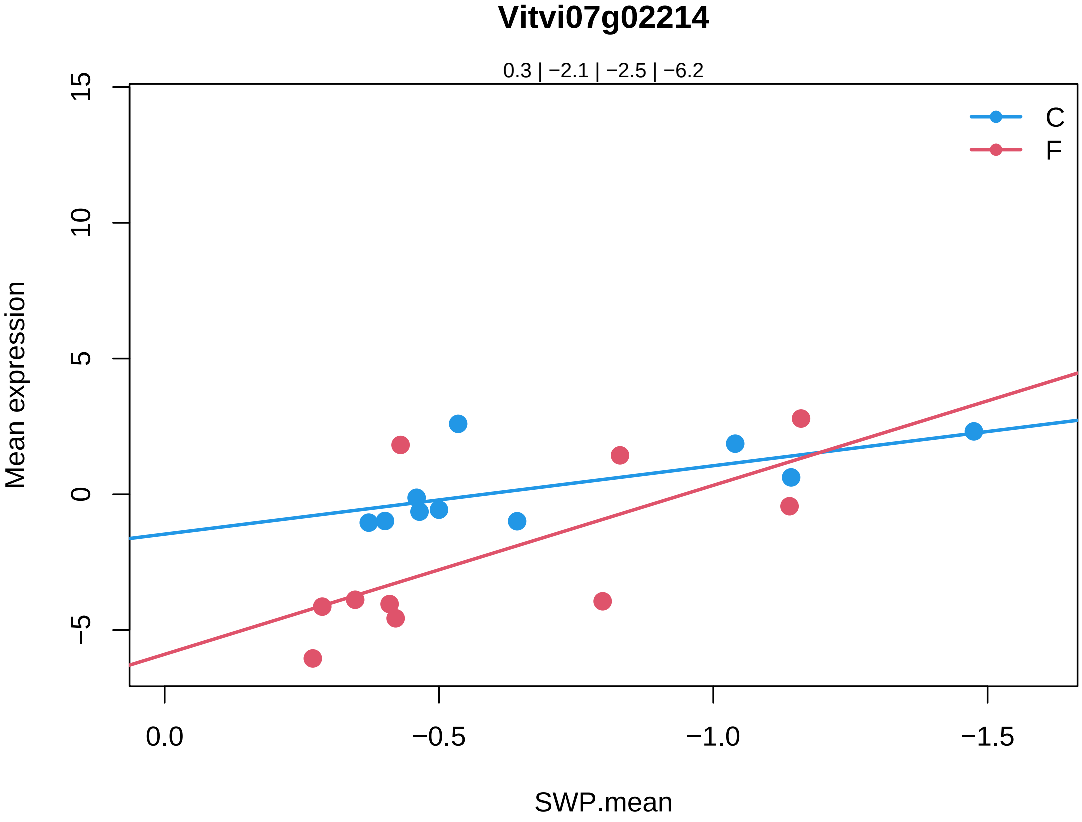
6.5.43 Vitvi07g02214

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

```
Vitvi07g02214
        35.2
        not assigned.unknown
        GATA transcription factor 22 IPR000679 Zinc finger, GATA-type
```

Coefficients for Vitvi07g02214.

```
                    swp  varietyF swp.varietyF    AveExpr        F
Vitvi07g02214 -2.518808 -4.426367     -3.70436 -0.8983373 9.111532
                  P.Value   adj.P.Val  type
Vitvi07g02214 0.000440166 0.007521313 type4
```



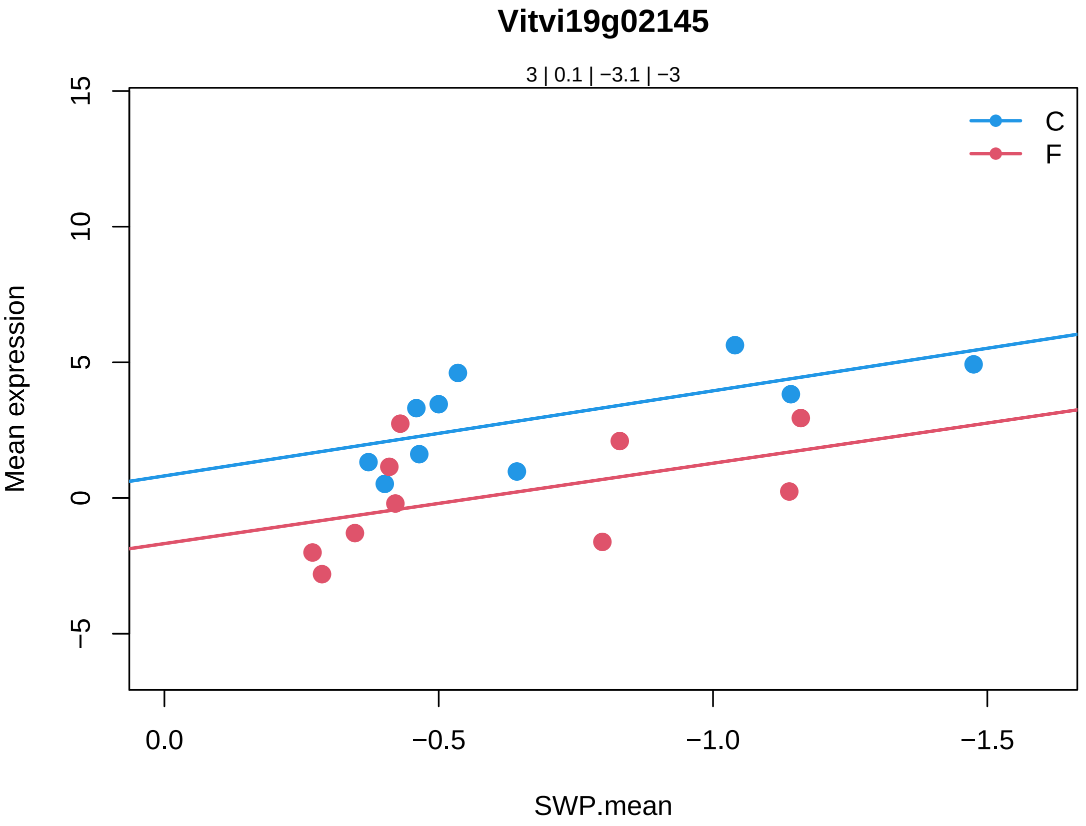
6.5.44 Vitvi19g02145

```
> 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.

```
                    swp varietyF swp.varietyF  AveExpr        F
Vitvi19g02145 -3.135408 -2.49434    0.1742035 1.572573 9.824082
                   P.Value   adj.P.Val  type
Vitvi19g02145 0.0002818218 0.005238448 type4
```



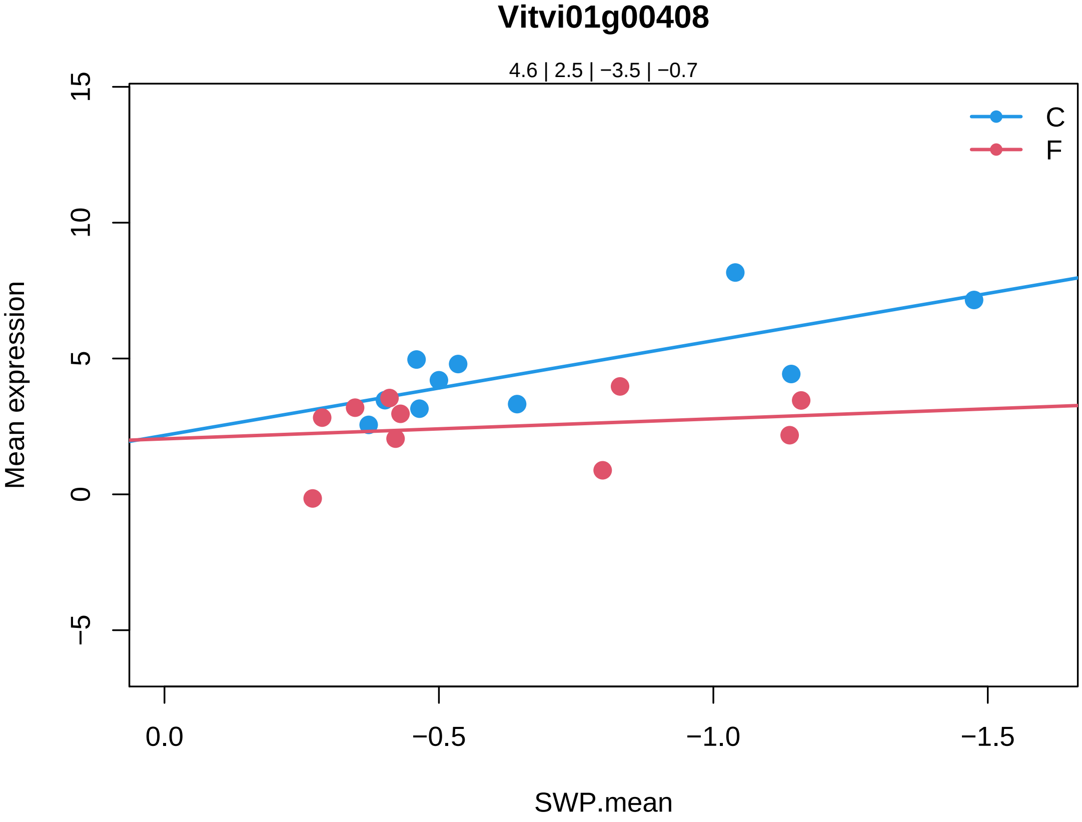
6.5.45 Vitvi01g00408

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

```
Vitvi01g00408
        20.02.2001
        stress.abiotic.heat
        Chaperone protein dnaJ IPR001623 Heat shock protein DnaJ, N-terminal
```

Coefficients for Vitvi01g00408.

```
                    swp   varietyF swp.varietyF  AveExpr        F
Vitvi01g00408 -3.482485 -0.1293856     2.745564 3.556127 9.674596
                   P.Value   adj.P.Val  type
Vitvi01g00408 0.0003089947 0.005667505 type4
```



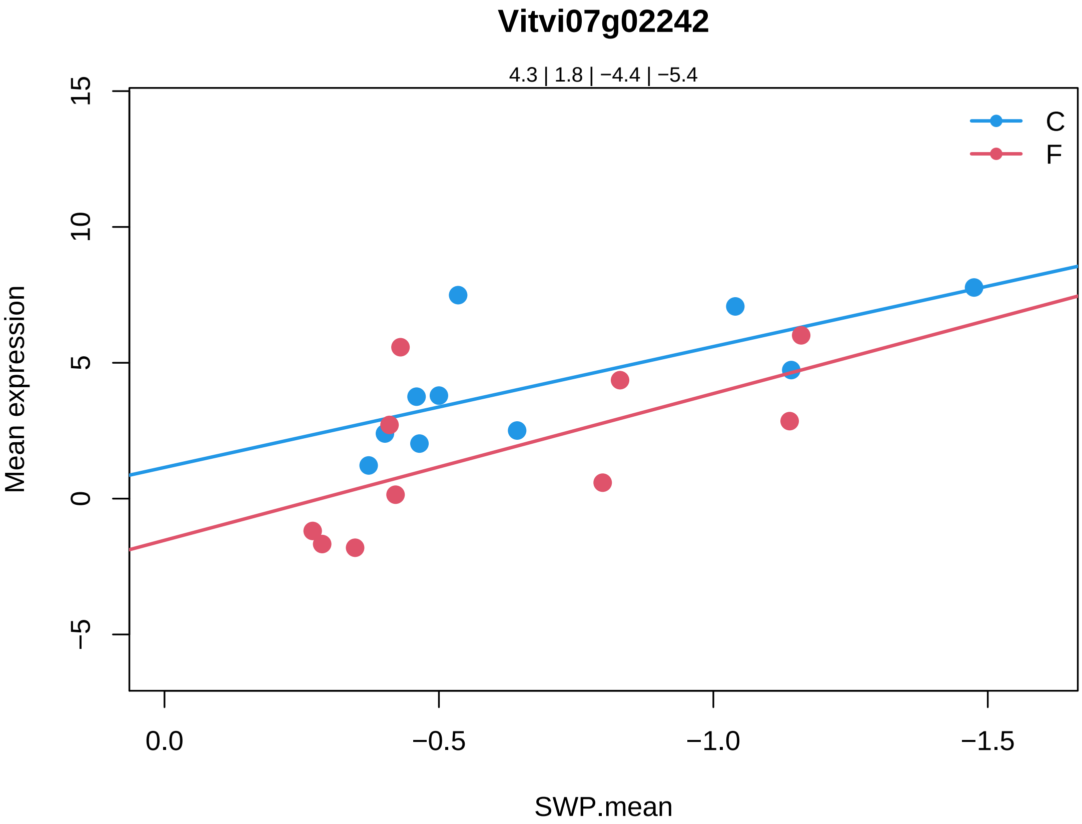
6.5.46 Vitvi07g02242

```
> 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.

```
                    swp   varietyF swp.varietyF  AveExpr        F
Vitvi07g02242 -4.449677 -2.681454   -0.9519606 3.016669 8.361039
                   P.Value   adj.P.Val  type
Vitvi07g02242 0.0007185253 0.01125567 type4
```



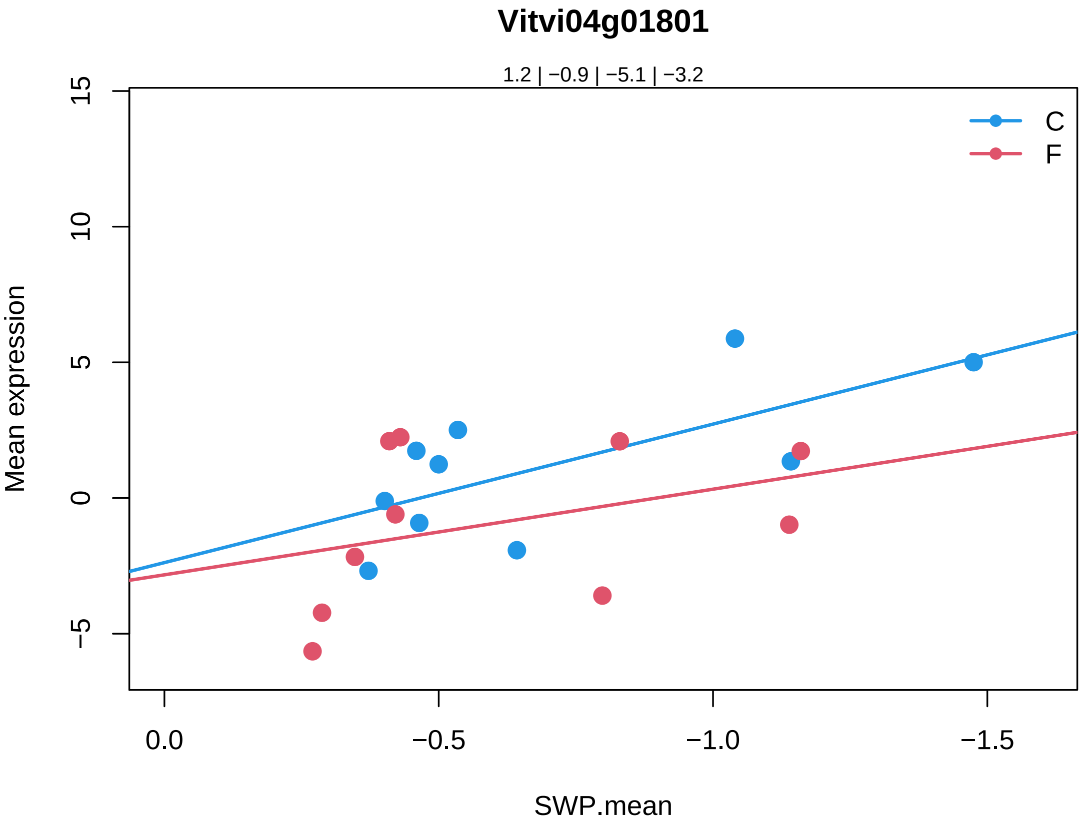
6.5.47 Vitvi04g01801

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

```
Vitvi04g01801
        20.02.2001
        stress.abiotic.heat
        17.6 kDa class II heat shock protein |
        Chr5:3882409-3882876 REVERSE LENGTH=155 |
        201606
```

Coefficients for Vitvi04g01801.

```
                    swp   varietyF swp.varietyF   AveExpr        F
Vitvi04g01801 -5.104125 -0.4493229     1.948595 0.1506614 4.590001
                 P.Value  adj.P.Val  type
Vitvi04g01801 0.01245505 0.09712467 type4
```



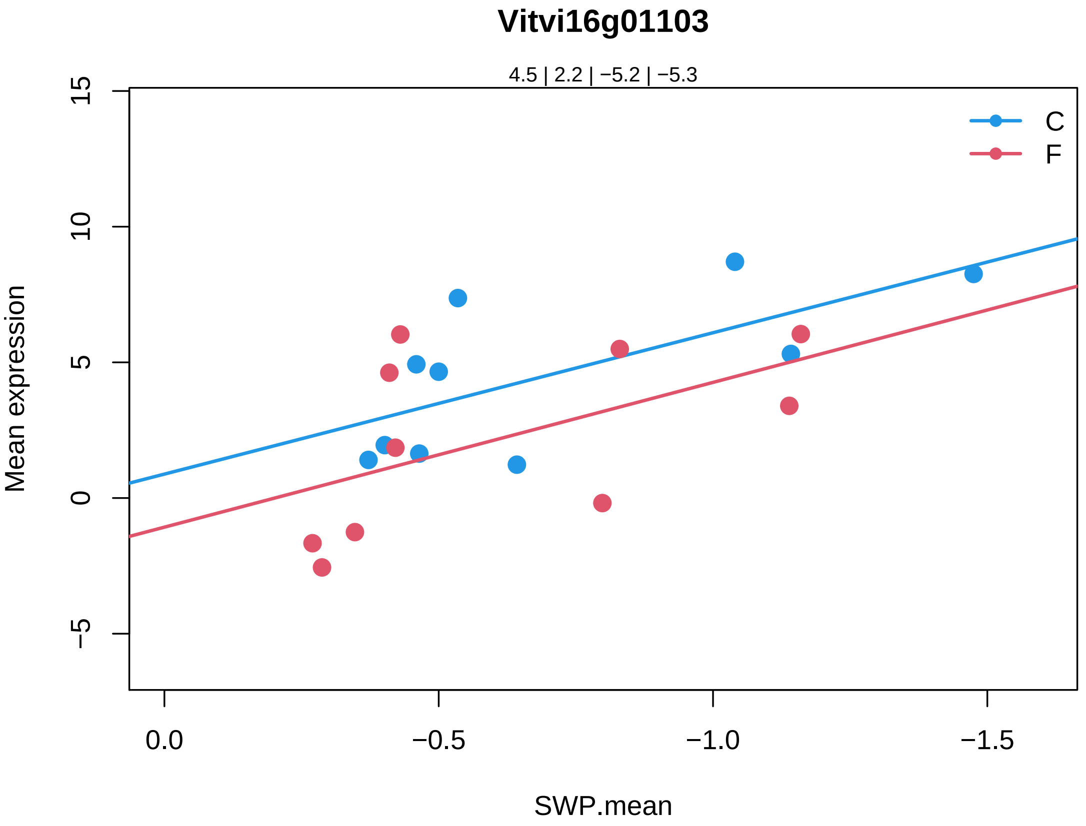
6.5.48 Vitvi16g01103

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

```
Vitvi16g01103
        20.02.2001
        stress.abiotic.heat
        heat shock-like protein |
        Chr5:21352557-21355147 FORWARD LENGTH=700 |
        201606
```

Coefficients for Vitvi16g01103.

```
                    swp  varietyF swp.varietyF  AveExpr        F
Vitvi16g01103 -5.209495 -1.955856   -0.1260899 3.360583 5.817065
                  P.Value  adj.P.Val  type
Vitvi16g01103 0.004539344 0.04732468 type4
```



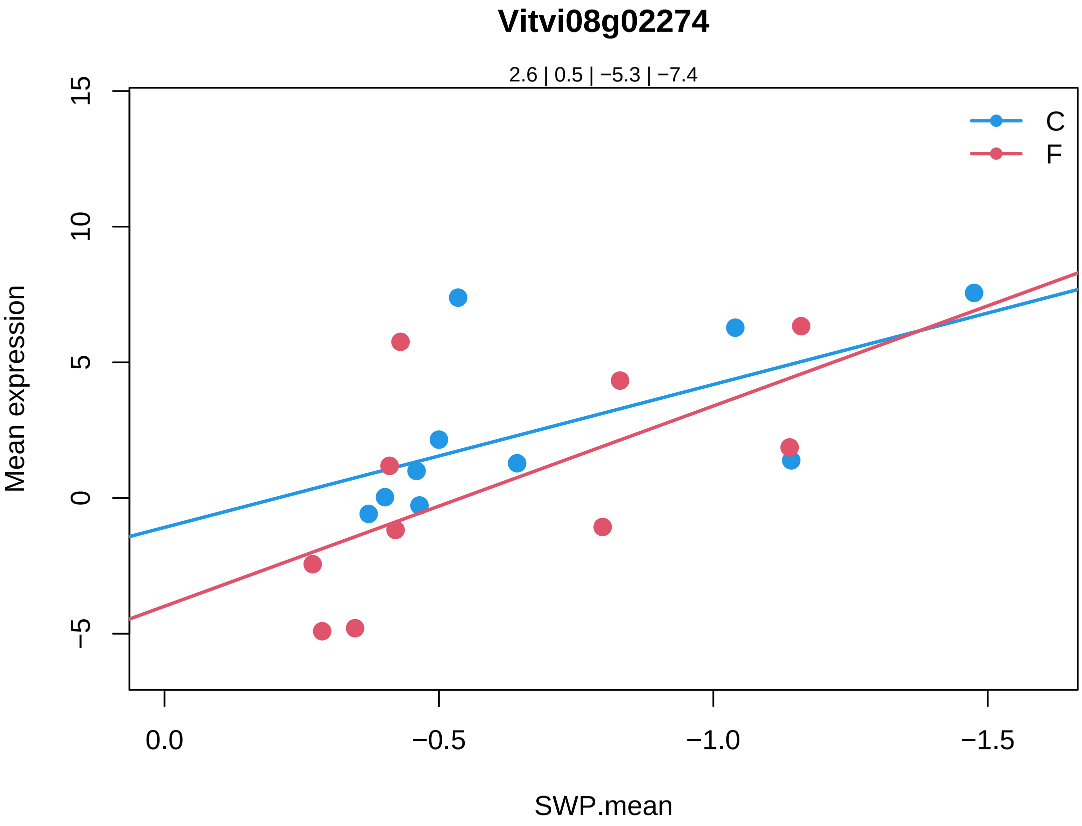
6.5.49 Vitvi08g02274

```
> 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.

```
                    swp   varietyF swp.varietyF  AveExpr        F
Vitvi08g02274 -5.267913 -2.905845    -2.113051 1.564665 5.555981
                  P.Value  adj.P.Val  type
Vitvi08g02274 0.005585942 0.05564767 type4
```



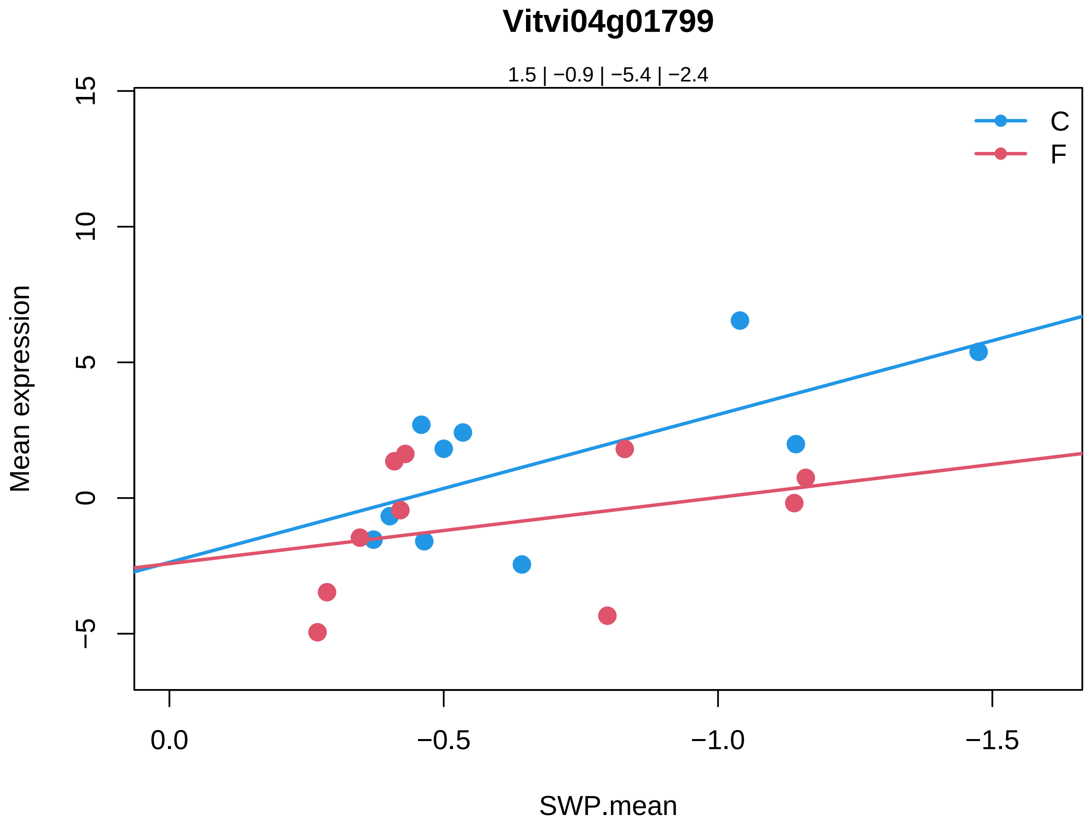
6.5.50 Vitvi04g01799

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

```
Vitvi04g01799
        20.02.2001
        stress.abiotic.heat
        17.6 kDa class II heat shock protein |
        Chr5:3882409-3882876 REVERSE LENGTH=155 |
        201606
```

Coefficients for Vitvi04g01799.

```
                    swp    varietyF swp.varietyF   AveExpr        F
Vitvi04g01799 -5.446372 -0.04695522     3.008905 0.2639579 5.443978
                  P.Value  adj.P.Val  type
Vitvi04g01799 0.006113039 0.05915869 type4
```



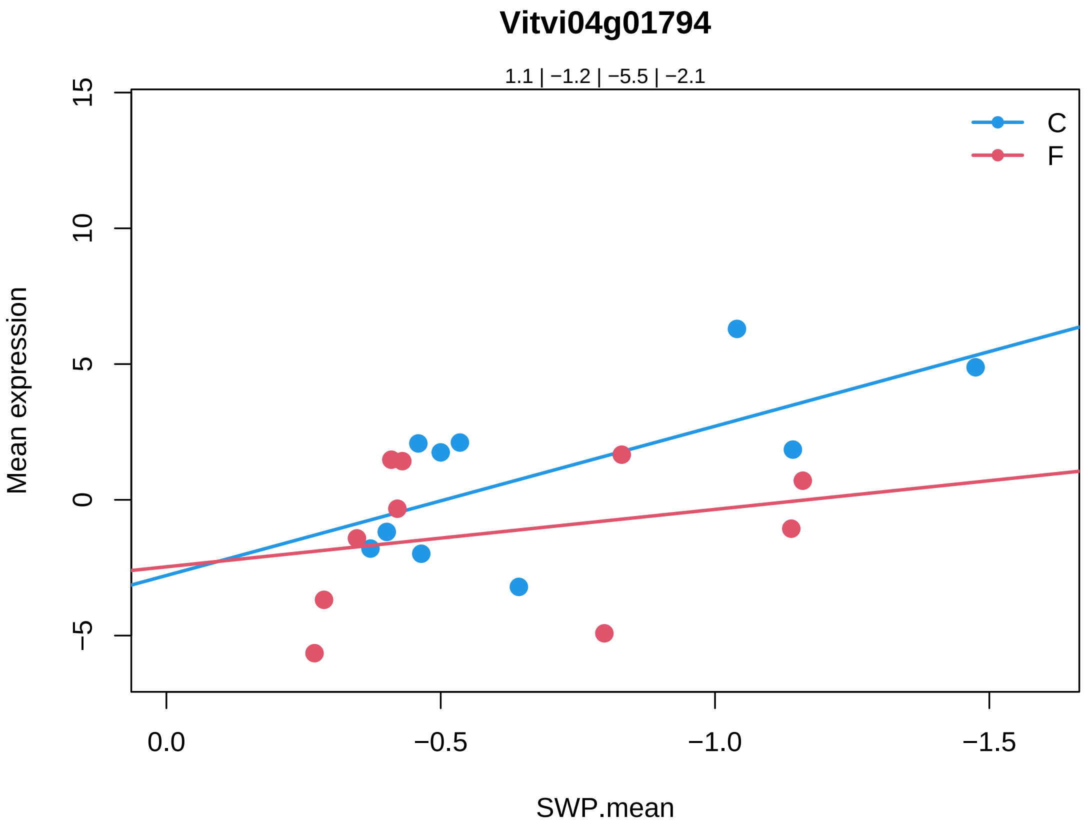
6.5.51 Vitvi04g01794

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

```
Vitvi04g01794
        20.02.2001
        stress.abiotic.heat
        17.6 kDa class II heat shock protein |
        Chr5:3882409-3882876 REVERSE LENGTH=155 |
        201606
```

Coefficients for Vitvi04g01794.

```
                    swp  varietyF swp.varietyF     AveExpr        F
Vitvi04g01794 -5.497568 0.3190796     3.382727 -0.04996061 4.507491
                P.Value adj.P.Val  type
Vitvi04g01794 0.0133731 0.1020184 type4
```



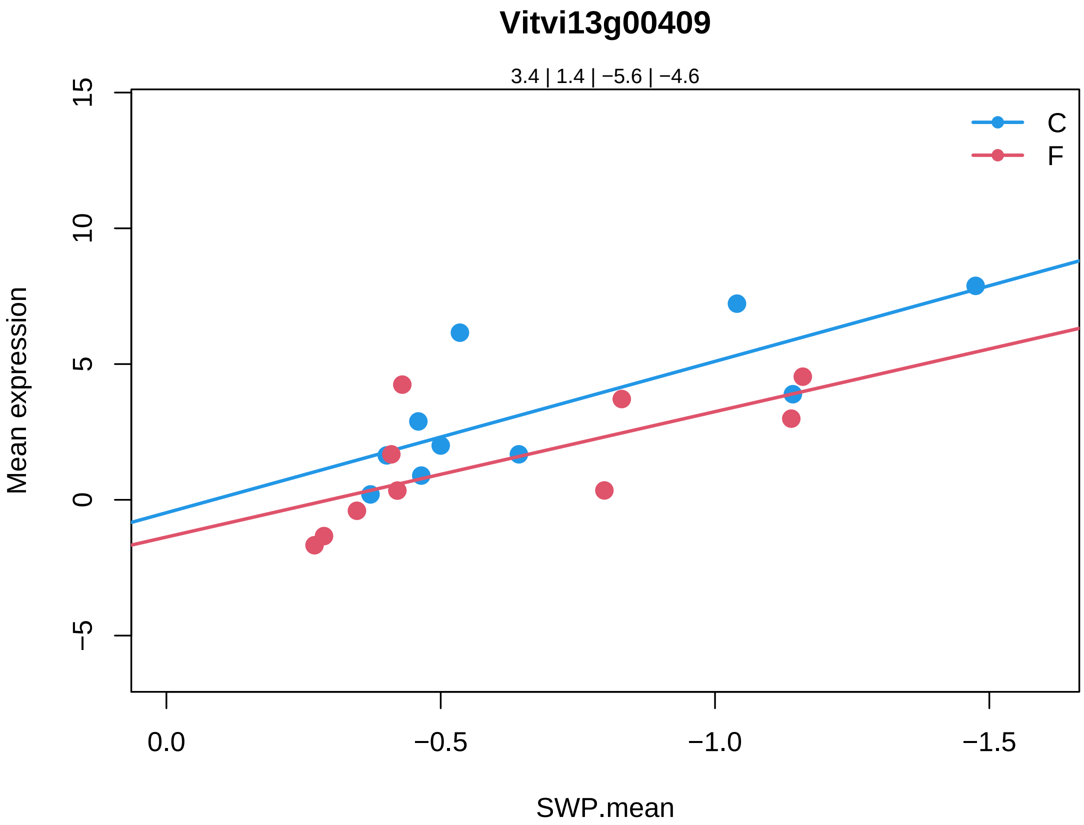
6.5.52 Vitvi13g00409

```
> 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.

```
                    swp   varietyF swp.varietyF  AveExpr        F
Vitvi13g00409 -5.574561 -0.8958015    0.9551048 2.443698 10.95039
                   P.Value   adj.P.Val  type
Vitvi13g00409 0.0001442541 0.003049545 type4
```



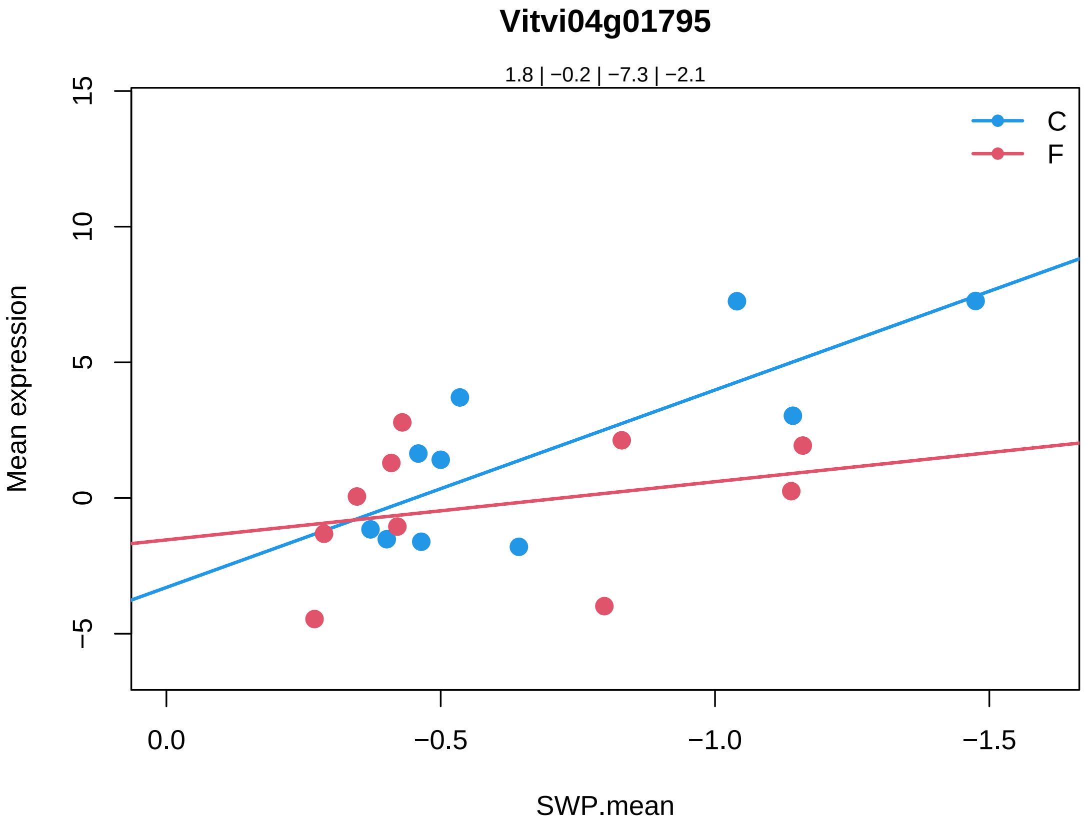
6.5.53 Vitvi04g01795

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

```
Vitvi04g01795
        35.2
        not assigned.unknown
        17.6 kDa class II heat shock protein |
        Chr5:3882409-3882876 REVERSE LENGTH=155 |
        201606
```

Coefficients for Vitvi04g01795.

```
                    swp varietyF swp.varietyF   AveExpr        F
Vitvi04g01795 -7.277261 1.752825     5.133591 0.7928205 7.258489
                  P.Value  adj.P.Val  type
Vitvi04g01795 0.001539206 0.02077996 type4
```



6.6 type5

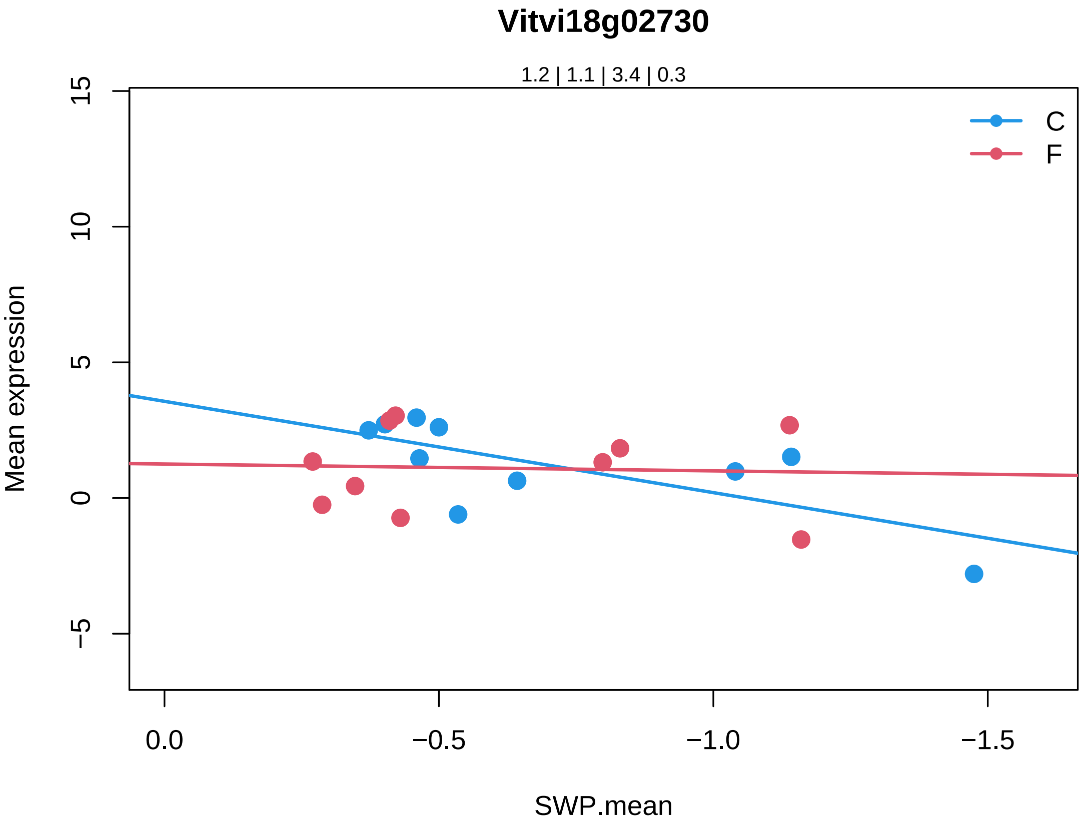
6.6.1 Vitvi18g02730

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

```
Vitvi18g02730
        35.2
        not assigned.unknown
        calcium uniporter (DUF607) |
        Chr5:17062507-17063934 FORWARD LENGTH=293 |
        201606
```

Coefficients for Vitvi18g02730.

```
                   swp  varietyF swp.varietyF  AveExpr       F
Vitvi18g02730 3.364707 -2.310702    -3.112693 1.148592 2.77706
                 P.Value adj.P.Val  type
Vitvi18g02730 0.06593486 0.2869194 type5
```



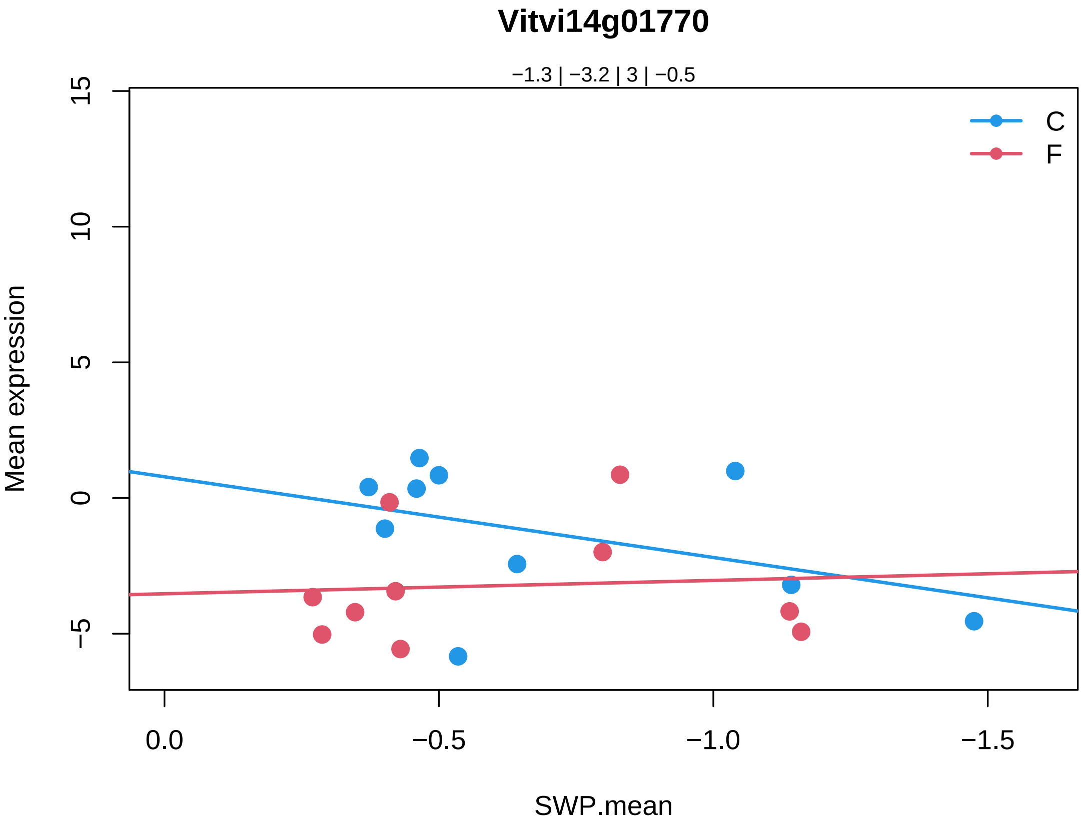
6.6.2 Vitvi14g01770

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

```
Vitvi14g01770
        28.99
        DNA.unspecified
        Exonuclease family protein |
        Chr3:10389609-10391544 FORWARD LENGTH=357 |
        201606
```

Coefficients for Vitvi14g01770.

```
                    swp   varietyF swp.varietyF   AveExpr       F
Vitvi14g01770 2.974912 -4.312405    -3.466655 -2.268585 2.39169
                  P.Value adj.P.Val  type
Vitvi14g01770 0.09672358 0.3637881 type5
```



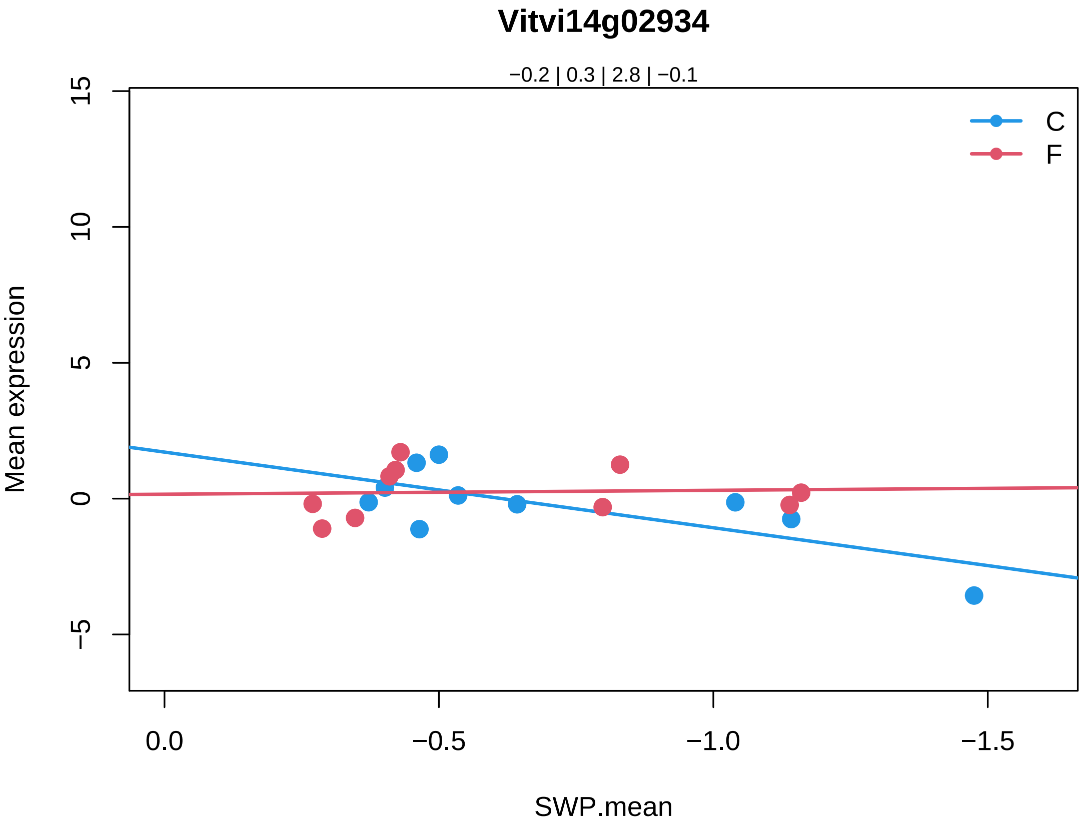
6.6.3 Vitvi14g02934

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

```
Vitvi14g02934
        34.16
        transport.ABC transporters and multidrug resistance systems
        transporter associated with antigen processing protein 2 |
        Chr5:15625660-15629621 FORWARD LENGTH=644 |
        201606
```

Coefficients for Vitvi14g02934.

```
                   swp varietyF swp.varietyF     AveExpr        F
Vitvi14g02934 2.784639 -1.54975    -2.928269 0.002286418 4.620679
                 P.Value   adj.P.Val  type
Vitvi14g02934 0.01213134 0.09570701 type5
```



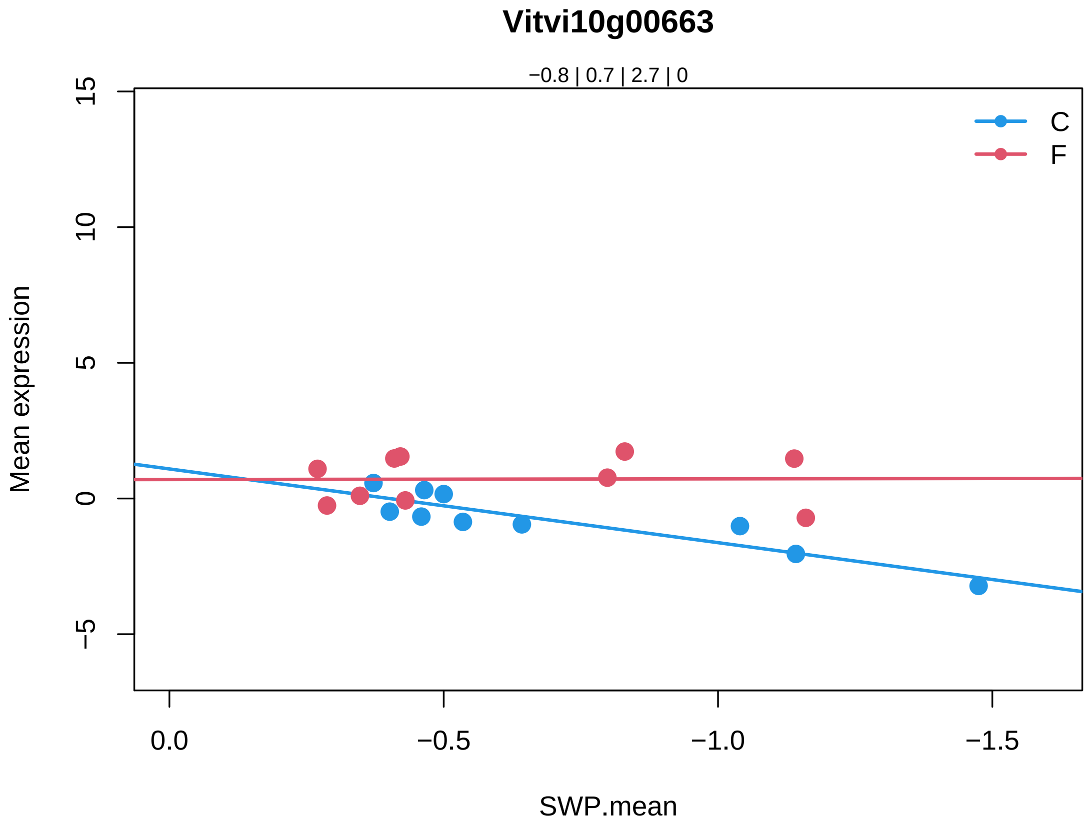
6.6.4 Vitvi10g00663

```
> 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
        27.03.2024
        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.

```
                   swp  varietyF swp.varietyF     AveExpr        F
Vitvi10g00663 2.716708 -0.390792    -2.742007 -0.05342949 14.64066
                   P.Value    adj.P.Val  type
Vitvi10g00663 2.065354e-05 0.0005884135 type5
```



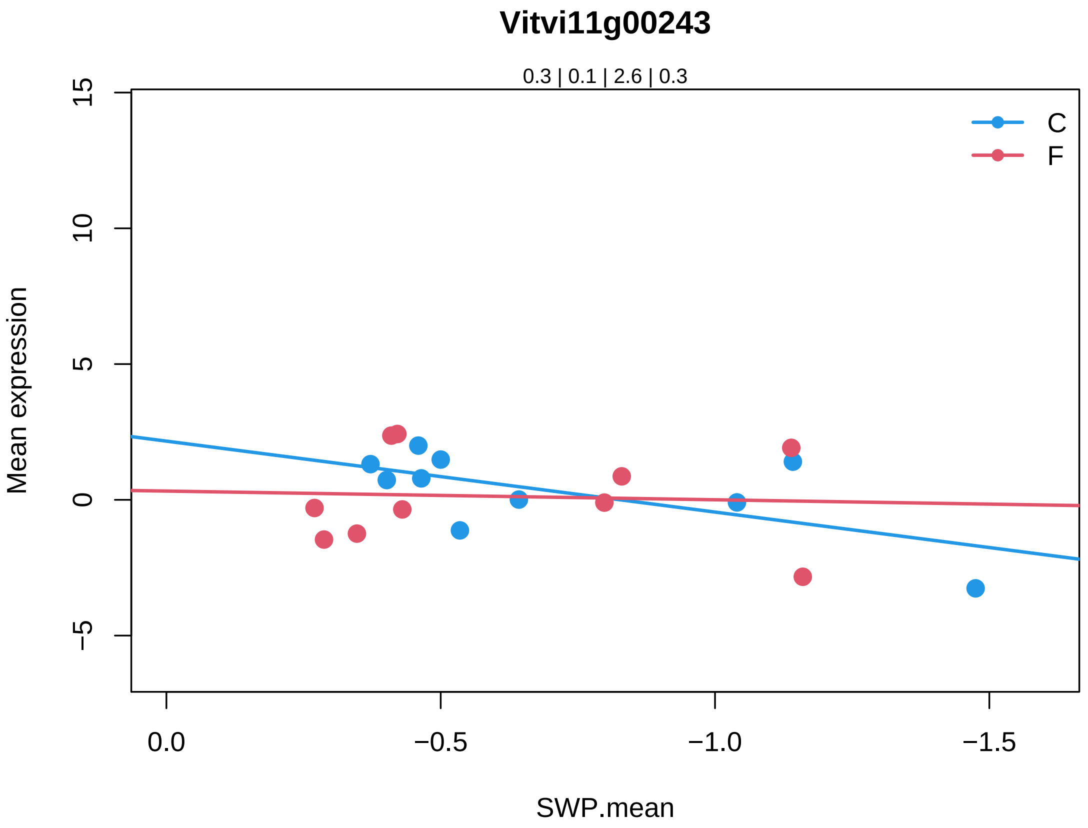
6.6.5 Vitvi11g00243

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

```
Vitvi11g00243
        10.05.2003
        cell wall.cell wall proteins.LRR
        Leucine-rich repeat (LRR) family protein |
        Chr4:14418826-14420073 FORWARD LENGTH=415 |
        201606
```

Coefficients for Vitvi11g00243.

```
                   swp  varietyF swp.varietyF   AveExpr        F
Vitvi11g00243 2.612418 -1.839593    -2.292601 0.2257056 1.553668
                P.Value adj.P.Val  type
Vitvi11g00243 0.2296378 0.5790138 type5
```



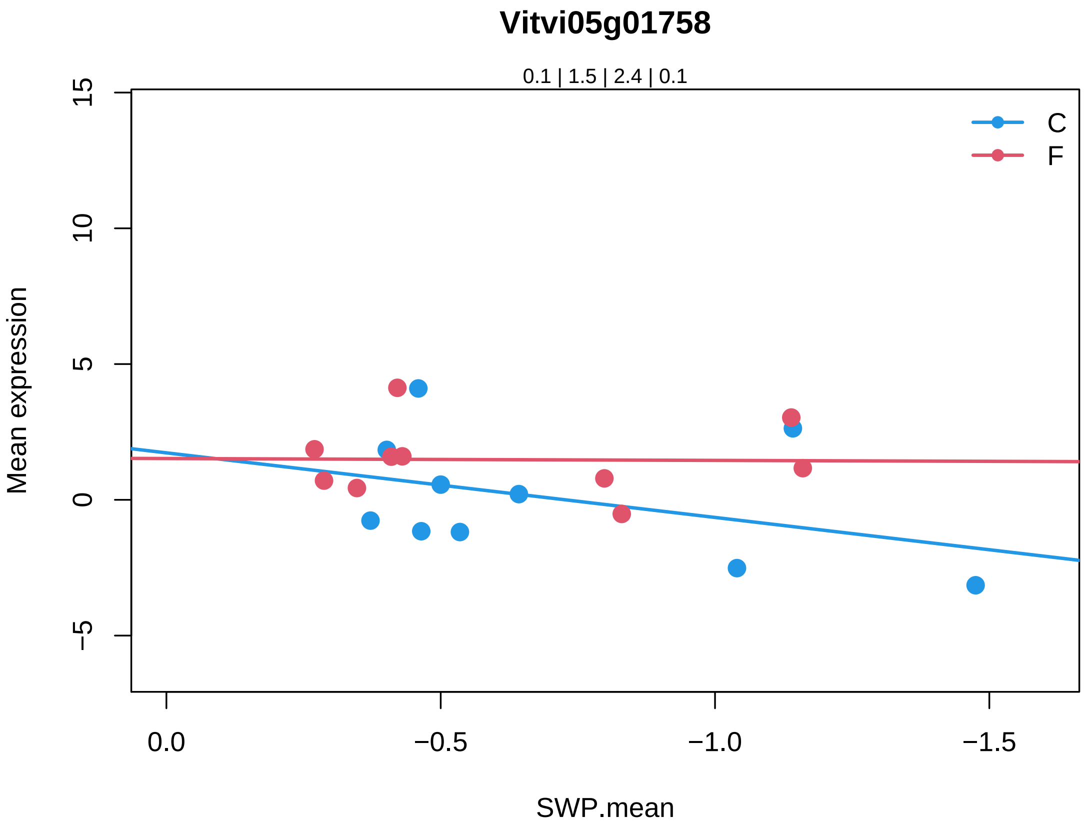
6.6.6 Vitvi05g01758

```
> 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.

```
                   swp   varietyF swp.varietyF   AveExpr       F
Vitvi05g01758 2.378762 -0.2099583    -2.310635 0.7679721 2.18935
                P.Value adj.P.Val  type
Vitvi05g01758 0.1187443 0.4080949 type5
```



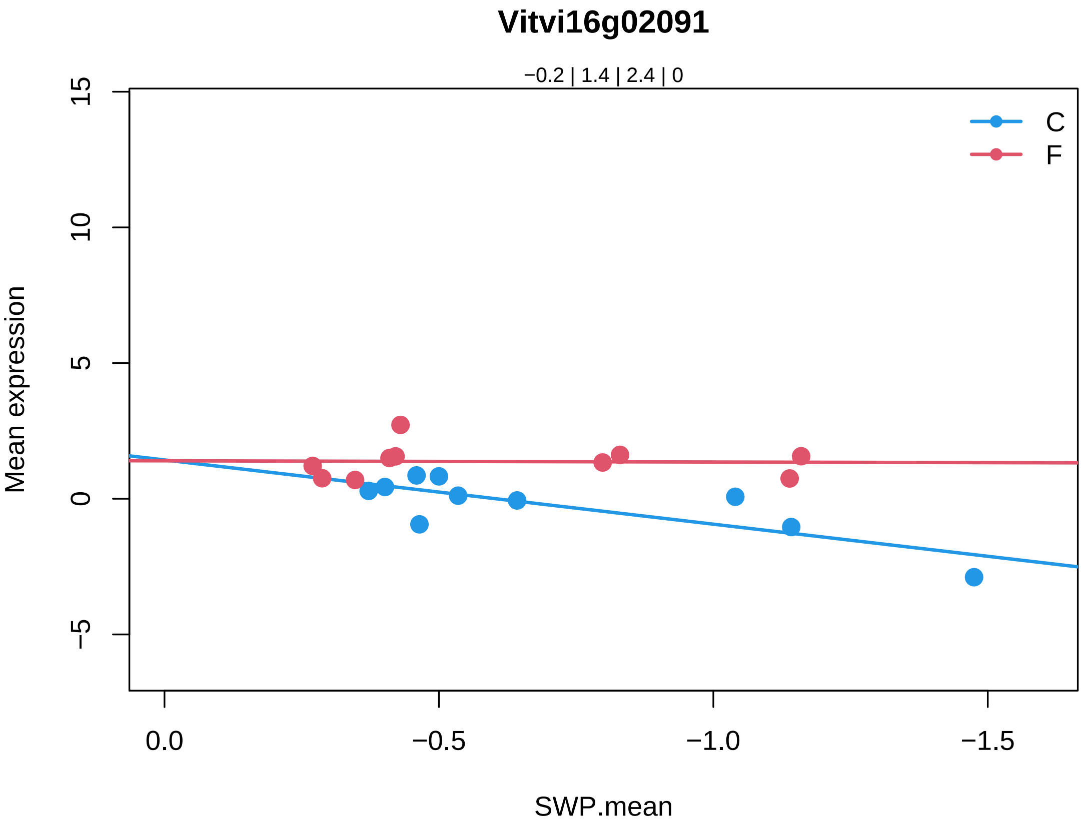
6.6.7 Vitvi16g02091

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

```
Vitvi16g02091
        35.2
        not assigned.unknown
        Receptor-like protein kinase
```

Coefficients for Vitvi16g02091.

```
                   swp    varietyF swp.varietyF   AveExpr        F
Vitvi16g02091 2.366765 -0.0312854    -2.321945 0.5681804 16.36561
                   P.Value     adj.P.Val  type
Vitvi16g02091 9.267725e-06 0.0002955202 type5
```



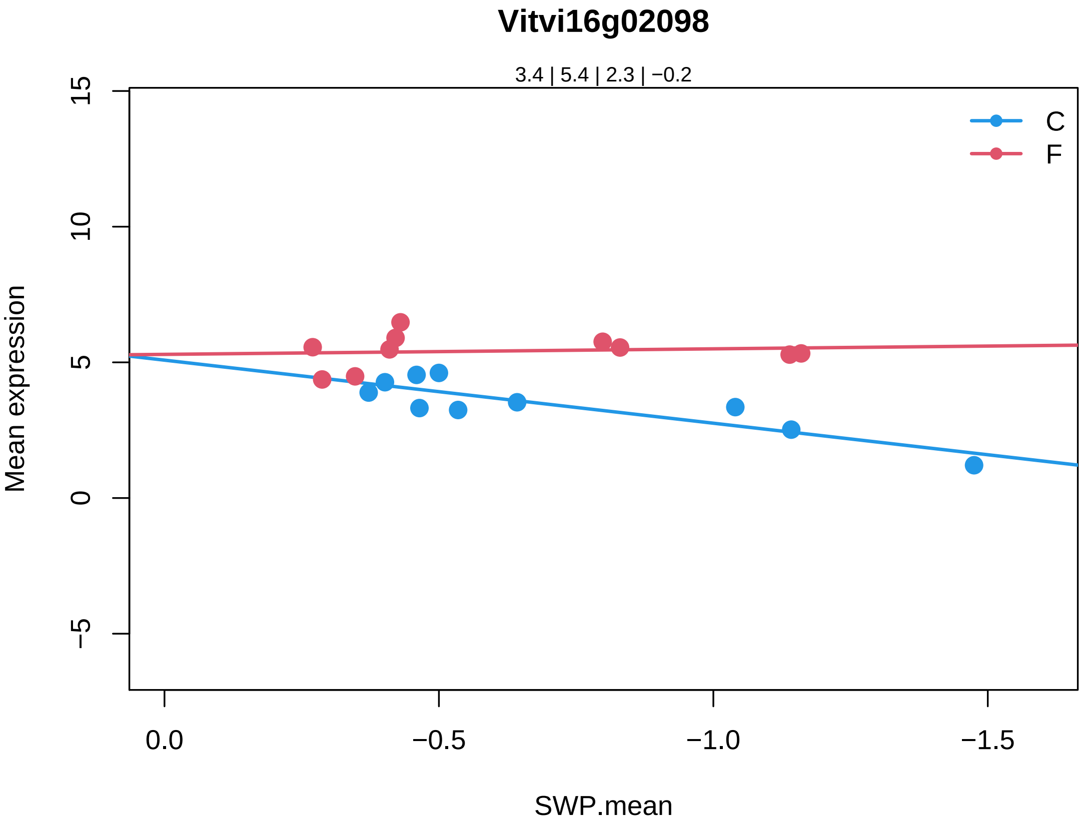
6.6.8 Vitvi16g02098

```
> 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.

```
                  swp  varietyF swp.varietyF  AveExpr        F
Vitvi16g02098 2.32385 0.2134255    -2.527587 4.432661 26.45487
                   P.Value    adj.P.Val  type
Vitvi16g02098 2.129829e-07 9.988572e-06 type5
```



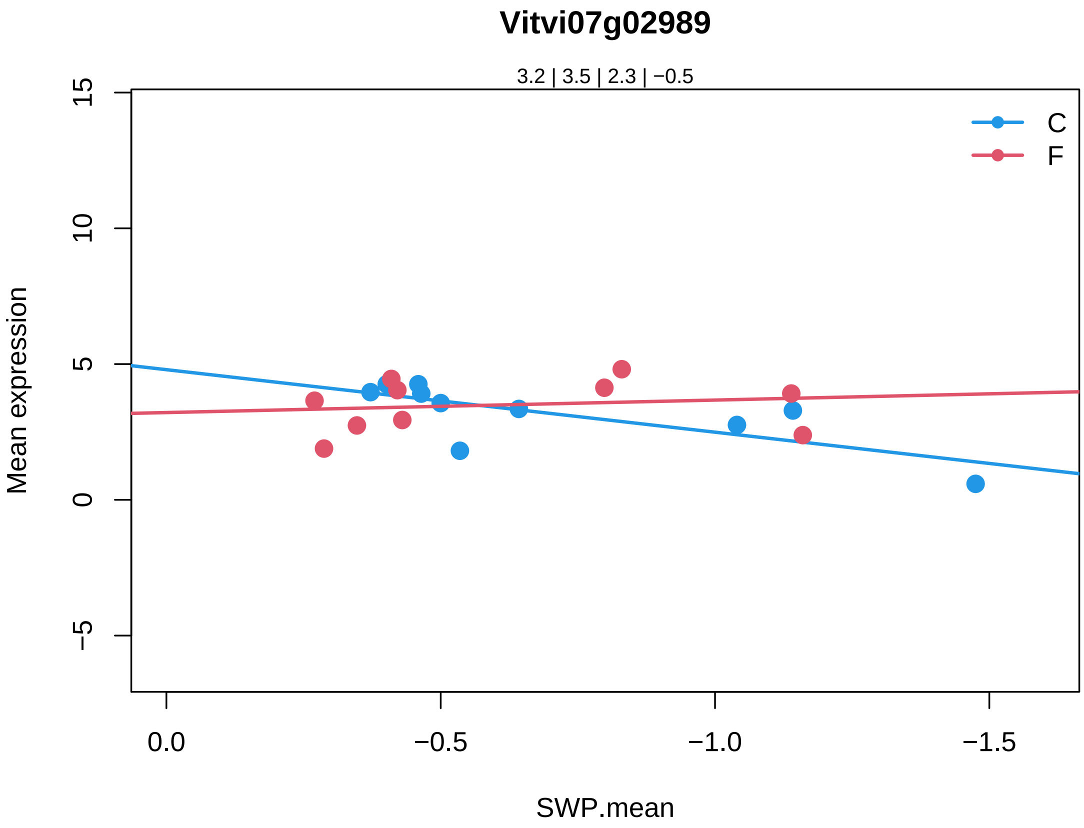
6.6.9 Vitvi07g02989

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

```
Vitvi07g02989
        29.7
        protein.glycosylation
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi07g02989.

```
                   swp  varietyF swp.varietyF  AveExpr        F
Vitvi07g02989 2.302397 -1.579855    -2.762497 3.334613 3.630787
                 P.Value adj.P.Val  type
Vitvi07g02989 0.02925868 0.1742438 type5
```



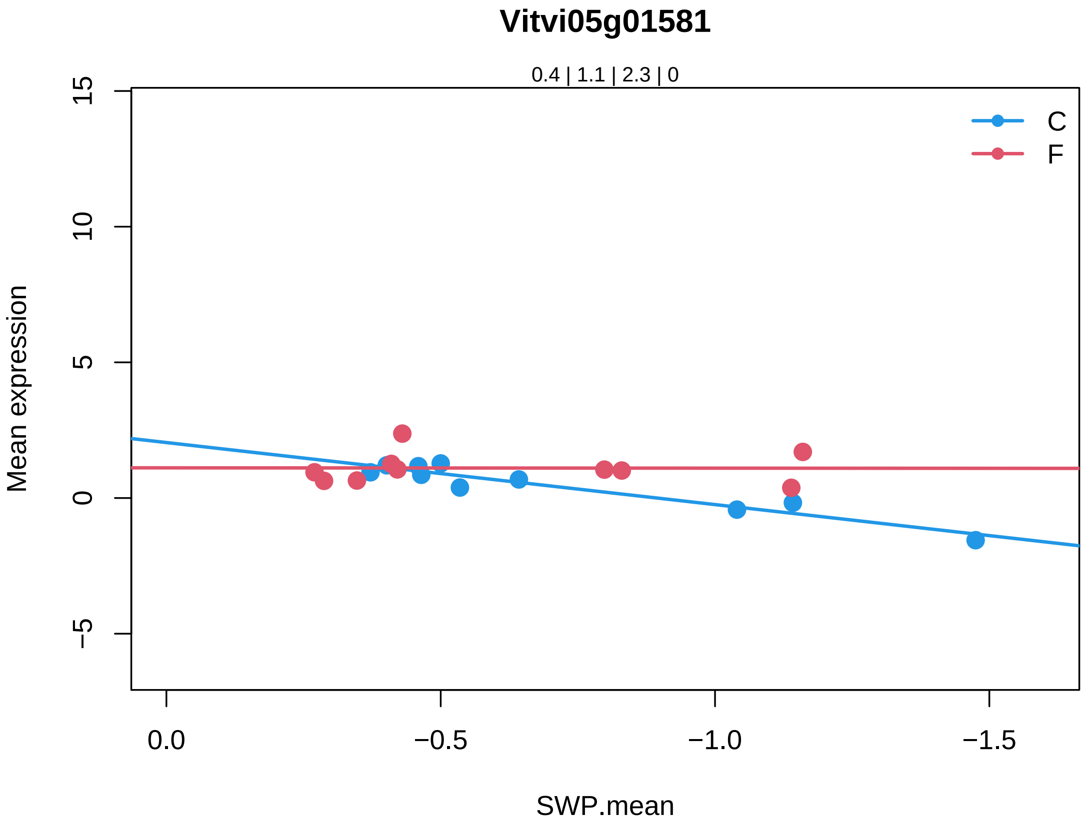
6.6.10 Vitvi05g01581

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

```
Vitvi05g01581
        20.1.7.3
        stress.biotic.PR-proteins.PR3/4/8/11 (chitinases and chitin binding pr
        homolog of carrot EP3-3 chitinase |
        Chr3:20145935-20147034 FORWARD LENGTH=273 |
        201606
```

Coefficients for Vitvi05g01581.

```
                 swp   varietyF swp.varietyF   AveExpr        F
Vitvi05g01581 2.2861 -0.9325242    -2.274535 0.7708642 12.93125
                   P.Value   adj.P.Val  type
Vitvi05g01581 4.867779e-05 0.001230426 type5
```



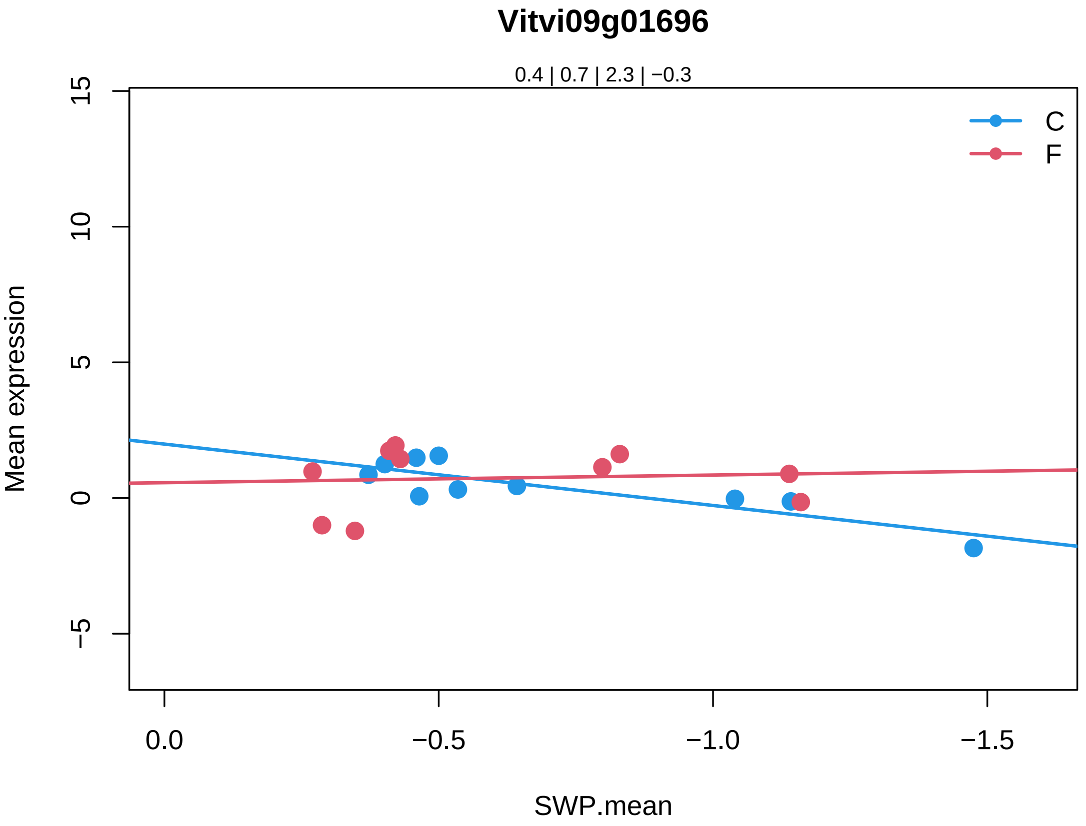
6.6.11 Vitvi09g01696

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

```
Vitvi09g01696
        20.01.2002
        stress.biotic.receptors
        receptor like protein 1 |
        Chr1:2270633-2274654 FORWARD LENGTH=913 |
        201606
```

Coefficients for Vitvi09g01696.

```
                   swp  varietyF swp.varietyF   AveExpr        F
Vitvi09g01696 2.261964 -1.422698    -2.543567 0.5674302 3.410662
                 P.Value adj.P.Val  type
Vitvi09g01696 0.03590399 0.1987105 type5
```



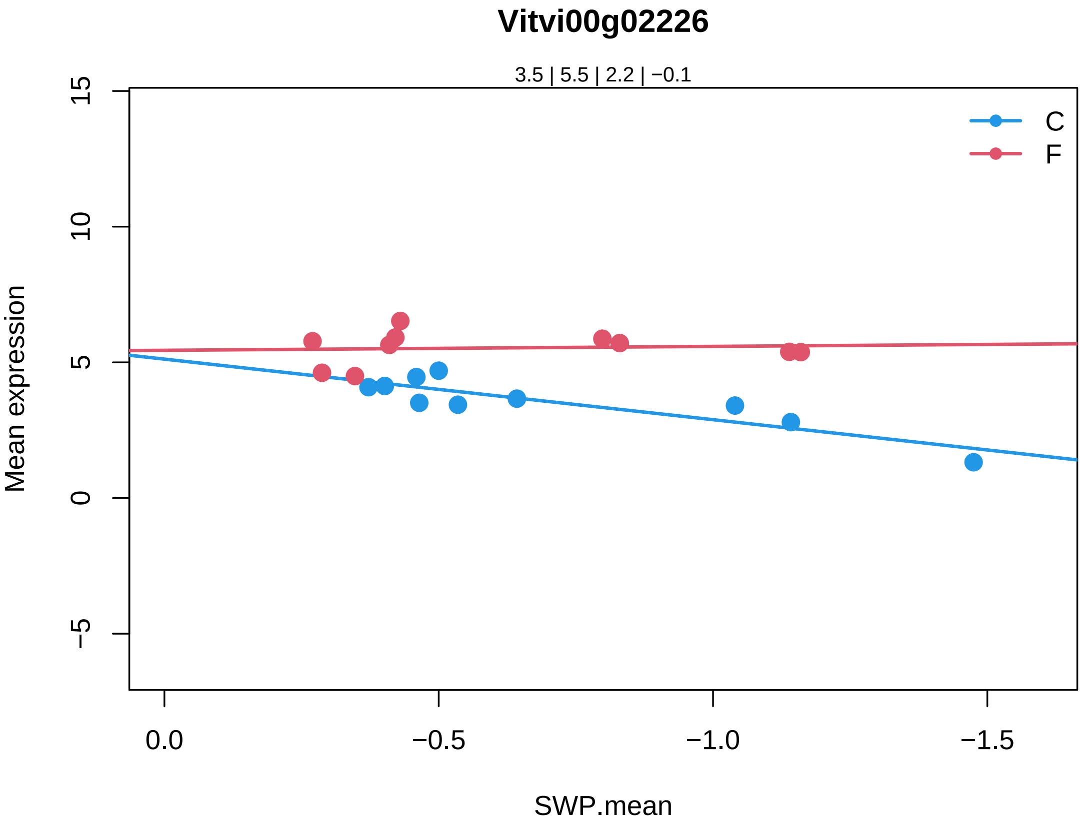
6.6.12 Vitvi00g02226

```
> 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.

```
                   swp  varietyF swp.varietyF  AveExpr        F
Vitvi00g02226 2.231859 0.3245653    -2.375927 4.540463 28.67024
                   P.Value    adj.P.Val  type
Vitvi00g02226 1.082155e-07 5.303603e-06 type5
```



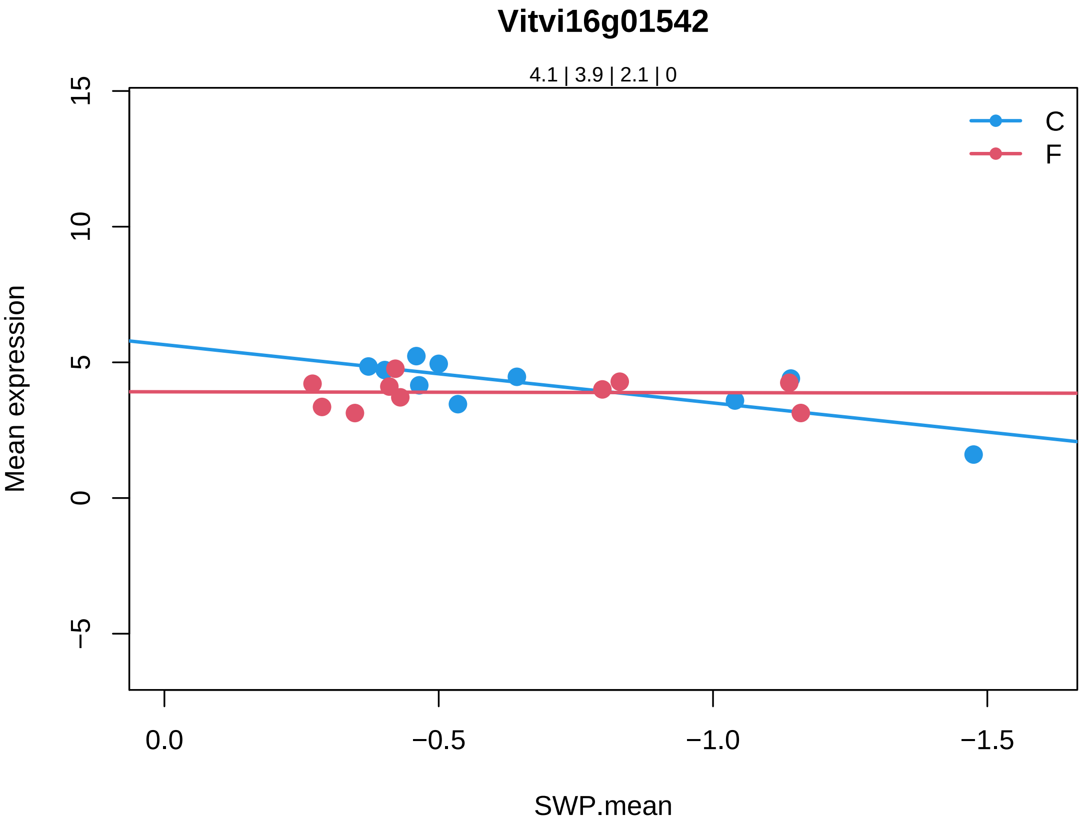
6.6.13 Vitvi16g01542

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

```
Vitvi16g01542
        35.2
        not assigned.unknown
        disease resistance family protein / LRR family protein |
        Chr2:14737169-14739886 REVERSE LENGTH=905 |
        201606
```

Coefficients for Vitvi16g01542.

```
                   swp  varietyF swp.varietyF  AveExpr        F
Vitvi16g01542 2.146633 -1.736602    -2.115503 4.018409 5.535344
                  P.Value adj.P.Val  type
Vitvi16g01542 0.005679219 0.0563559 type5
```



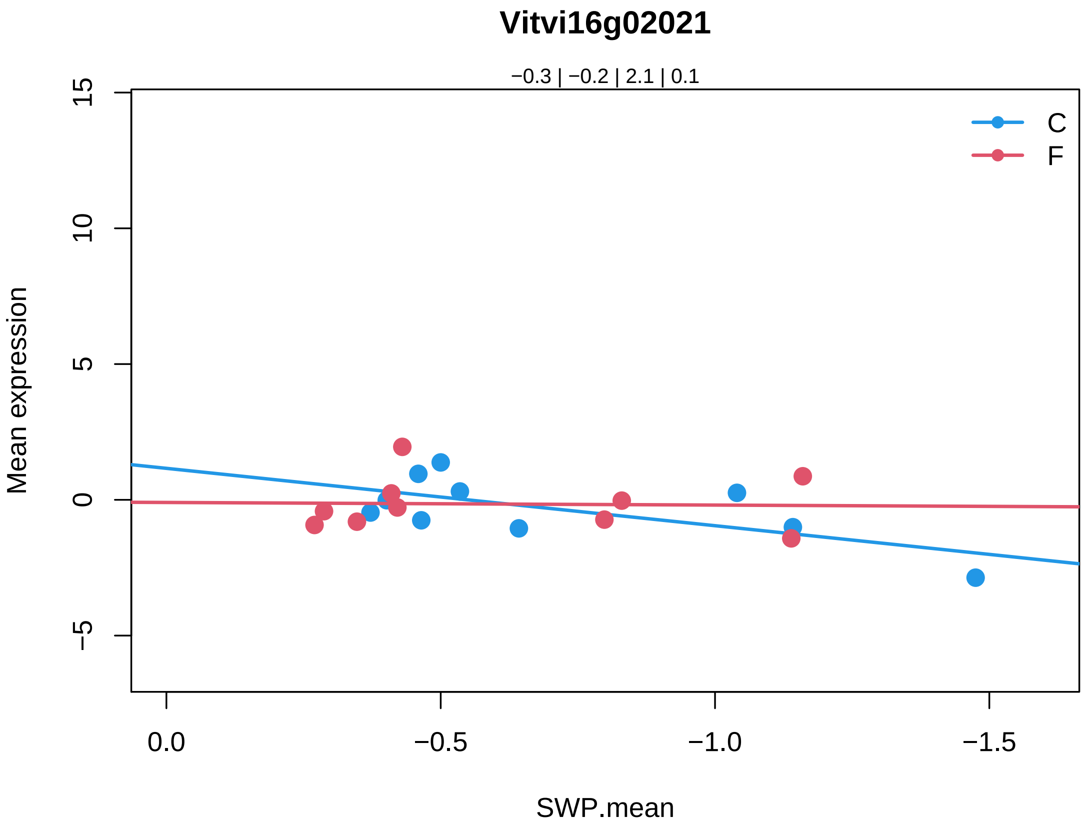
6.6.14 Vitvi16g02021

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

```
Vitvi16g02021
        35.2
        not assigned.unknown
        PR5-like receptor kinase |
        Chr5:15293325-15295838 REVERSE LENGTH=665 |
        201606
```

Coefficients for Vitvi16g02021.

```
                   swp varietyF swp.varietyF    AveExpr        F
Vitvi16g02021 2.113053 -1.25667    -2.016905 -0.2409573 2.453978
                 P.Value adj.P.Val  type
Vitvi16g02021 0.09085335 0.3493151 type5
```



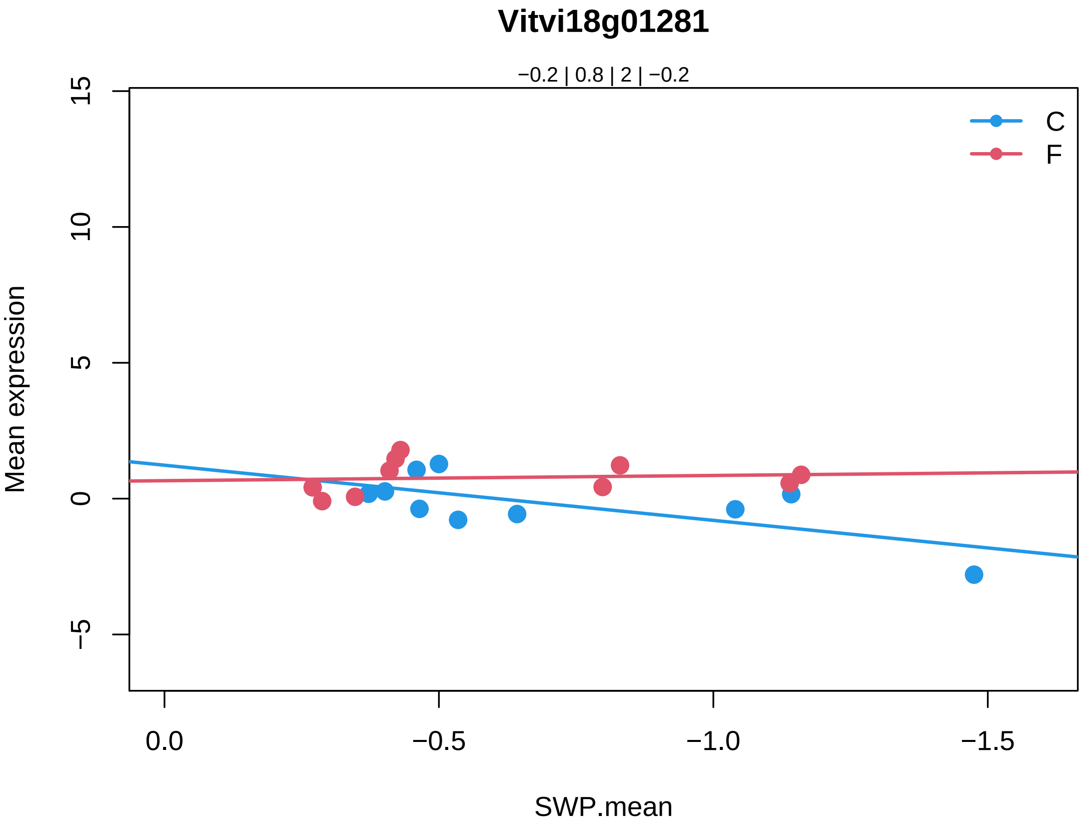
6.6.15 Vitvi18g01281

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

```
Vitvi18g01281
        29.4
        protein.postranslational modification
        receptor-like protein kinase 1 |
        Chr5:24498467-24501494 REVERSE LENGTH=832 |
        201606
```

Coefficients for Vitvi18g01281.

```
                   swp   varietyF swp.varietyF   AveExpr      F
Vitvi18g01281 2.029457 -0.5697098    -2.221749 0.2896596 6.6764
                  P.Value   adj.P.Val  type
Vitvi18g01281 0.002352688 0.02895021 type5
```



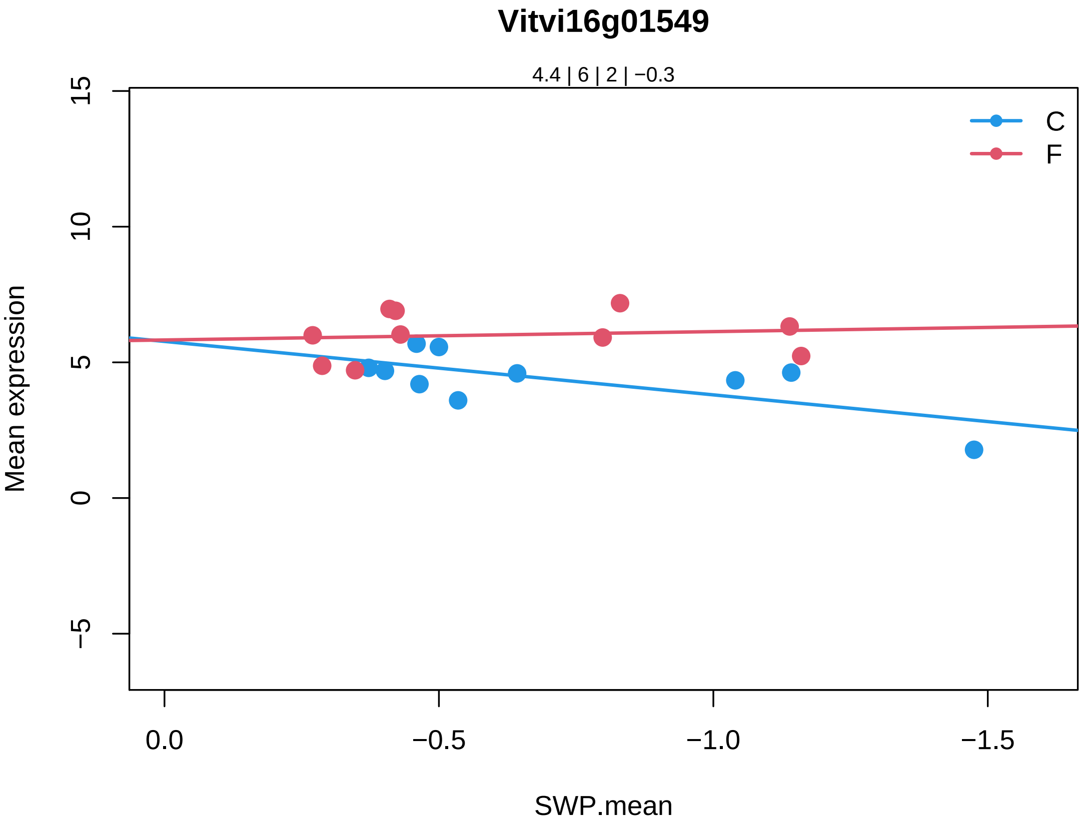
6.6.16 Vitvi16g01549

```
> 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.

```
                   swp   varietyF swp.varietyF  AveExpr        F
Vitvi16g01549 1.969869 0.05268409    -2.278492 5.199432 9.447054
                  P.Value   adj.P.Val  type
Vitvi16g01549 0.000356003 0.006391281 type5
```



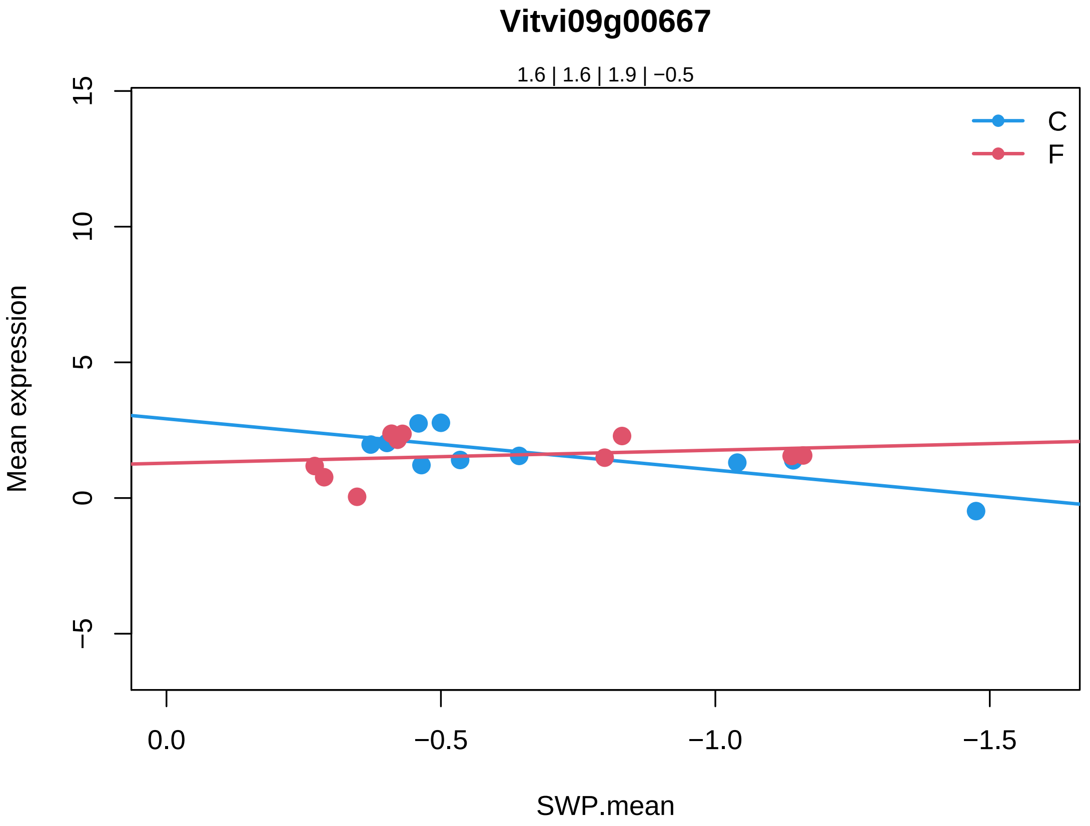
6.6.17 Vitvi09g00667

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

```
Vitvi09g00667
        20.01.2002
        stress.biotic.receptors
        receptor like protein 1 |
        Chr1:2270633-2274654 FORWARD LENGTH=913 |
        201606
```

Coefficients for Vitvi09g00667.

```
                   swp  varietyF swp.varietyF  AveExpr        F
Vitvi09g00667 1.889958 -1.635525    -2.370296 1.583119 3.707458
                 P.Value adj.P.Val  type
Vitvi09g00667 0.02726667 0.1667951 type5
```



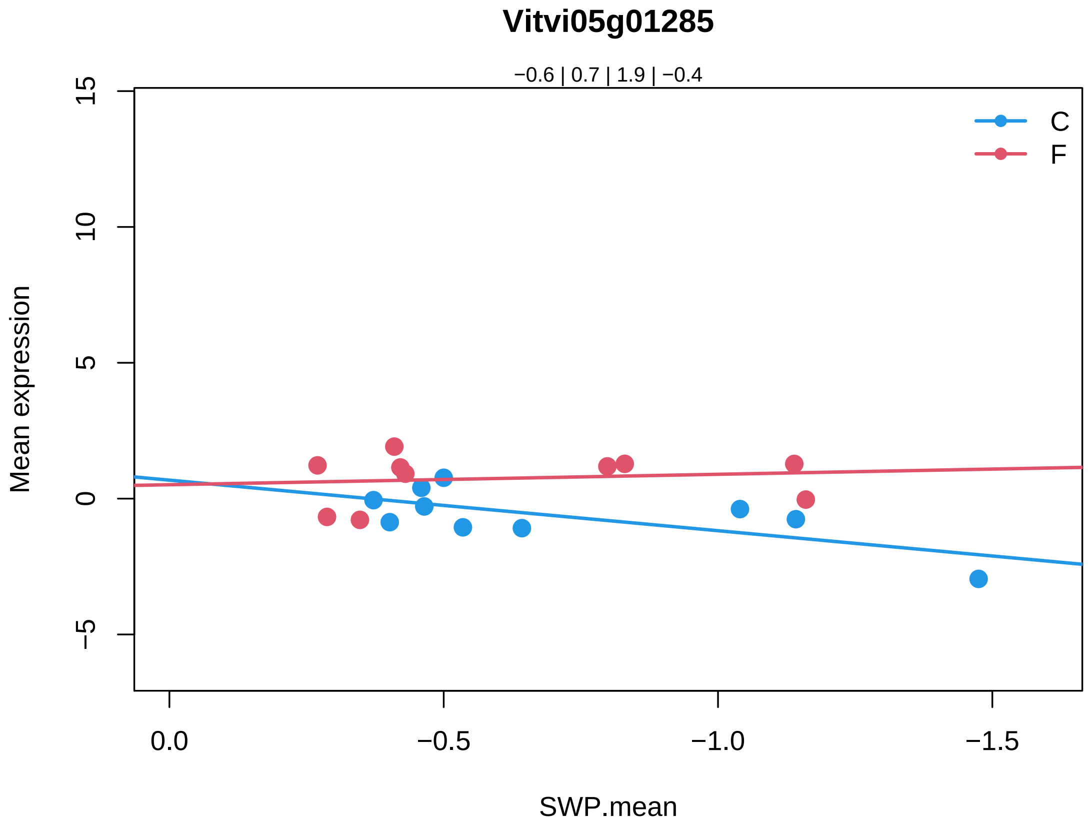
6.6.18 Vitvi05g01285

```
> 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.

```
                   swp   varietyF swp.varietyF    AveExpr        F
Vitvi05g01285 1.860691 -0.1675265    -2.244205 0.05873131 7.411829
                  P.Value  adj.P.Val  type
Vitvi05g01285 0.001380064 0.01896748 type5
```



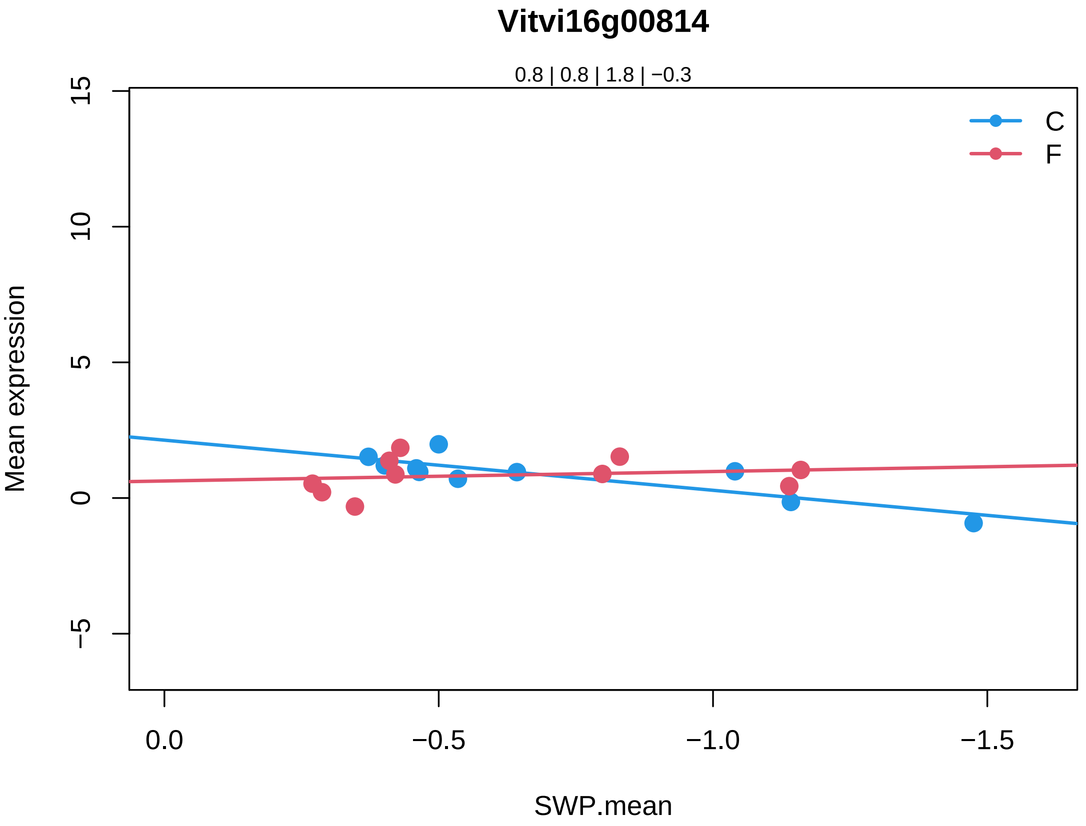
6.6.19 Vitvi16g00814

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

```
Vitvi16g00814
        35.2
        not assigned.unknown
        Protein kinase superfamily protein |
        Chr1:24961634-24963941 REVERSE LENGTH=666 |
        201606
```

Coefficients for Vitvi16g00814.

```
                   swp  varietyF swp.varietyF   AveExpr       F
Vitvi16g00814 1.847189 -1.504357    -2.195694 0.8369013 4.86124
                  P.Value  adj.P.Val  type
Vitvi16g00814 0.009887985 0.08276368 type5
```



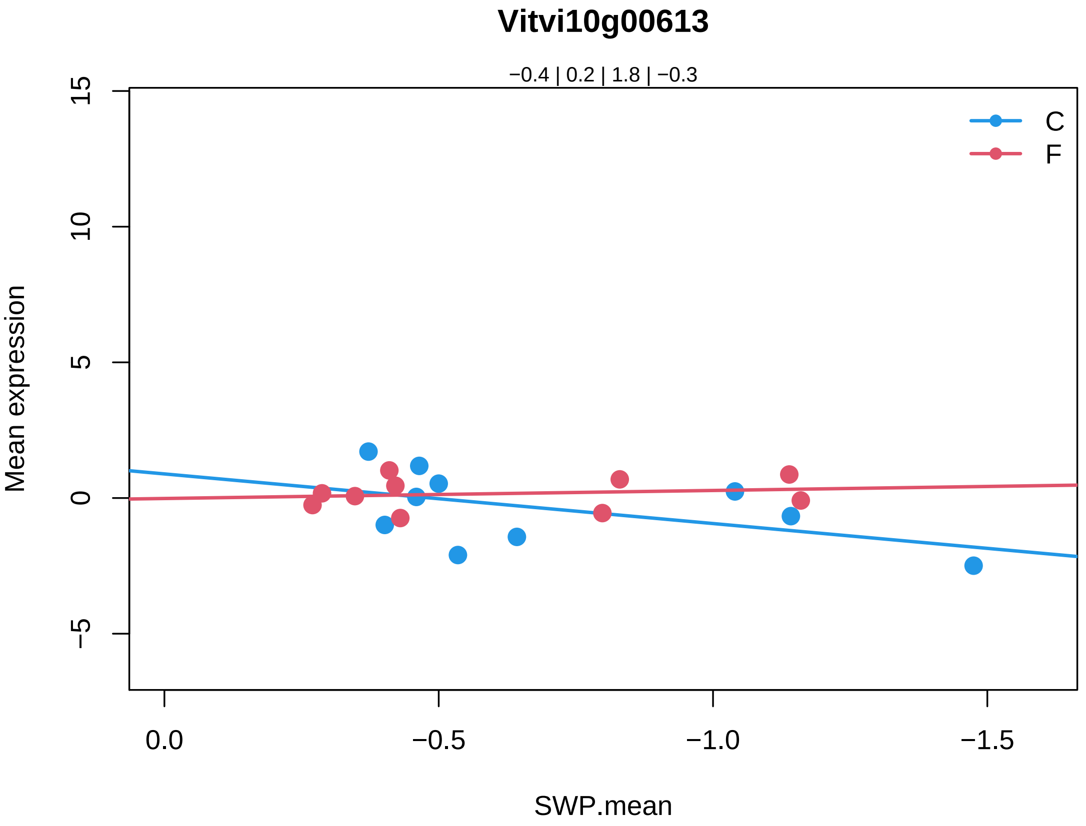
6.6.20 Vitvi10g00613

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

```
Vitvi10g00613
        10.02.2001
        cell wall.cellulose synthesis.cellulose synthase
        cellulose synthase family protein |
        Chr4:10312846-10316719 REVERSE LENGTH=985 |
        201606
```

Coefficients for Vitvi10g00613.

```
                   swp   varietyF swp.varietyF    AveExpr        F
Vitvi10g00613 1.828719 -0.9057469    -2.124476 -0.1176839 2.478109
                 P.Value adj.P.Val  type
Vitvi10g00613 0.08868226 0.3451724 type5
```



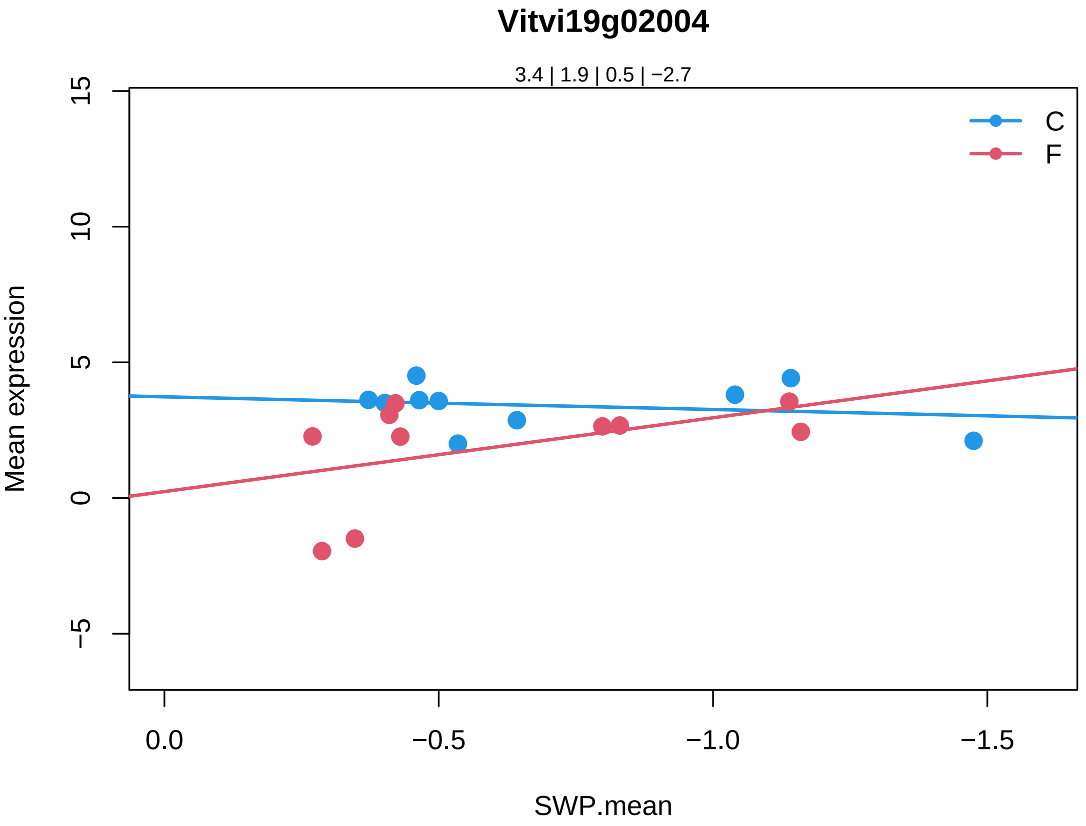
6.6.21 Vitvi19g02004

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

```
Vitvi19g02004
        35.2
        not assigned.unknown
        fatty acid desaturase A |
        Chr4:13571951-13572922 FORWARD LENGTH=323 |
        201606
```

Coefficients for Vitvi19g02004.

```
                    swp   varietyF swp.varietyF AveExpr        F
Vitvi19g02004 0.4667448 -3.492017    -3.186127 2.64793 4.059835
                 P.Value adj.P.Val  type
Vitvi19g02004 0.01981999 0.1342054 type5
```



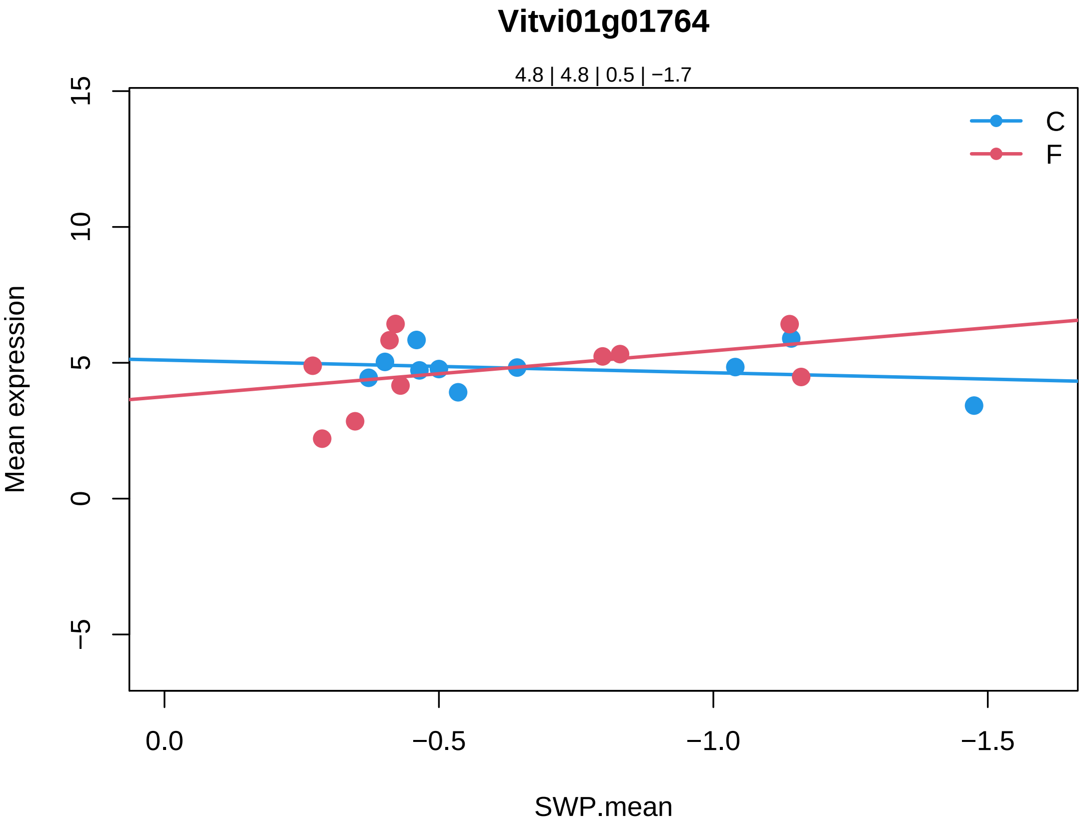
6.6.22 Vitvi01g01764

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

```
Vitvi01g01764
        19.99
        tetrapyrrole synthesis.unspecified
        SOUL heme-binding family protein |
        Chr1:5844766-5845539 FORWARD LENGTH=232 |
        201606
```

Coefficients for Vitvi01g01764.

```
                    swp  varietyF swp.varietyF  AveExpr        F
Vitvi01g01764 0.4655929 -1.346499    -2.156261 4.776619 1.130663
               P.Value adj.P.Val  type
Vitvi01g01764 0.358912 0.7047845 type5
```



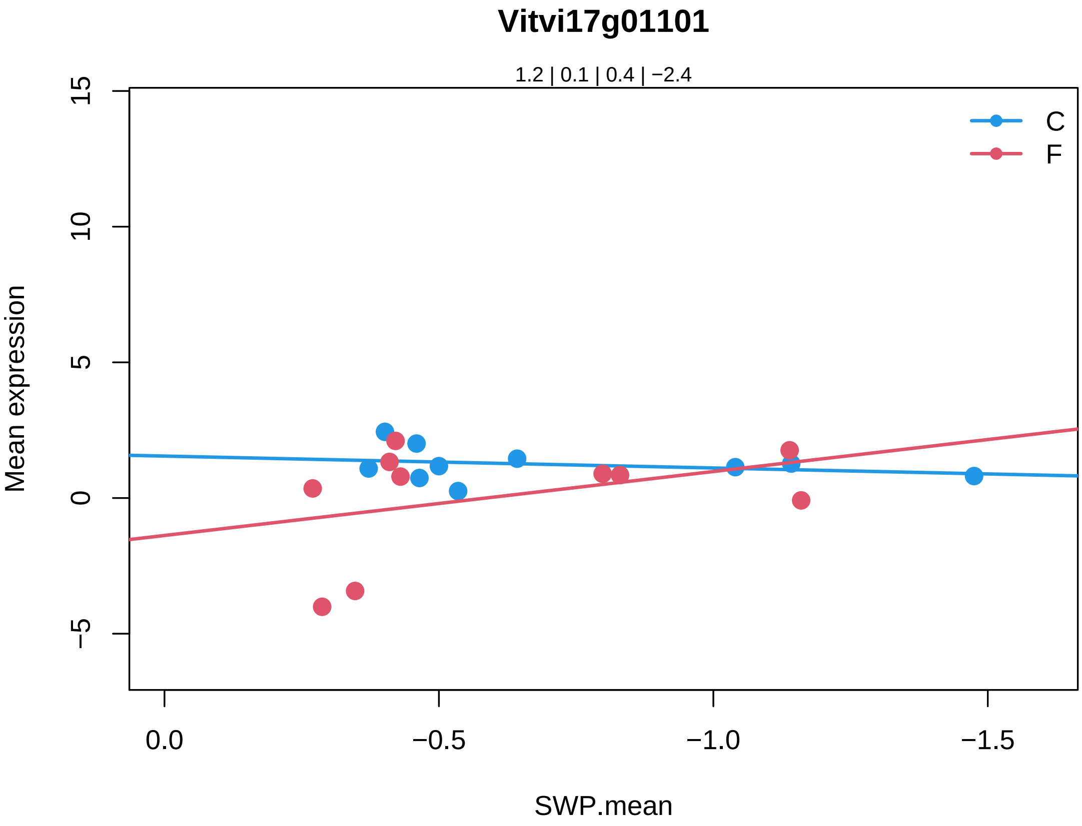
6.6.23 Vitvi17g01101

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

```
Vitvi17g01101
        34.14
        transport.unspecified cations
        organic cation/carnitine transporter1 |
        Chr1:27538387-27540109 FORWARD LENGTH=539 |
        201606
```

Coefficients for Vitvi17g01101.

```
                    swp  varietyF swp.varietyF  AveExpr        F
Vitvi17g01101 0.4385322 -2.925461     -2.79515 0.646452 2.469662
                 P.Value adj.P.Val  type
Vitvi17g01101 0.08943585 0.3469786 type5
```



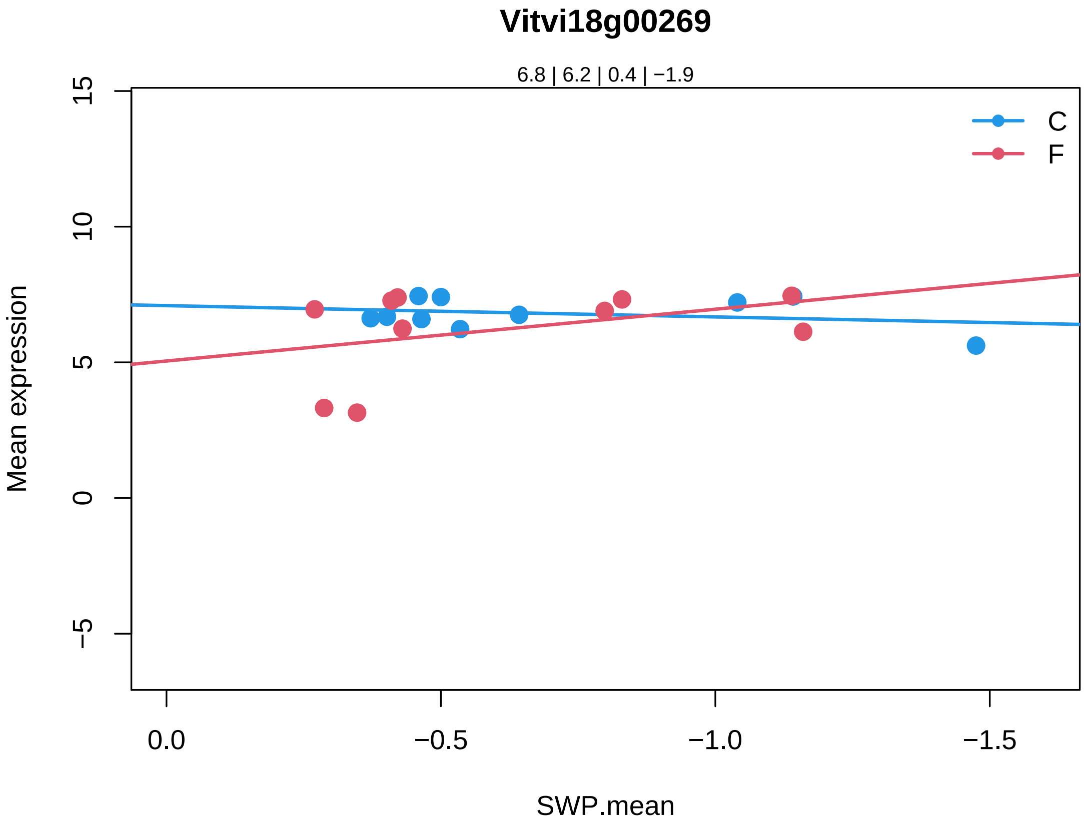
6.6.24 Vitvi18g00269

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

```
Vitvi18g00269
        19.16
        tetrapyrrole synthesis.chlorophyll b synthase
        Pheophorbide a oxygenase family protein with Rieske 2Fe-2S domain-cont
        Chr1:16848664-16850718 REVERSE LENGTH=434 |
        201606
```

Coefficients for Vitvi18g00269.

```
                    swp  varietyF swp.varietyF  AveExpr        F
Vitvi18g00269 0.4156576 -2.040581    -2.324171 6.505018 1.698496
                P.Value adj.P.Val  type
Vitvi18g00269 0.1972624 0.5349002 type5
```



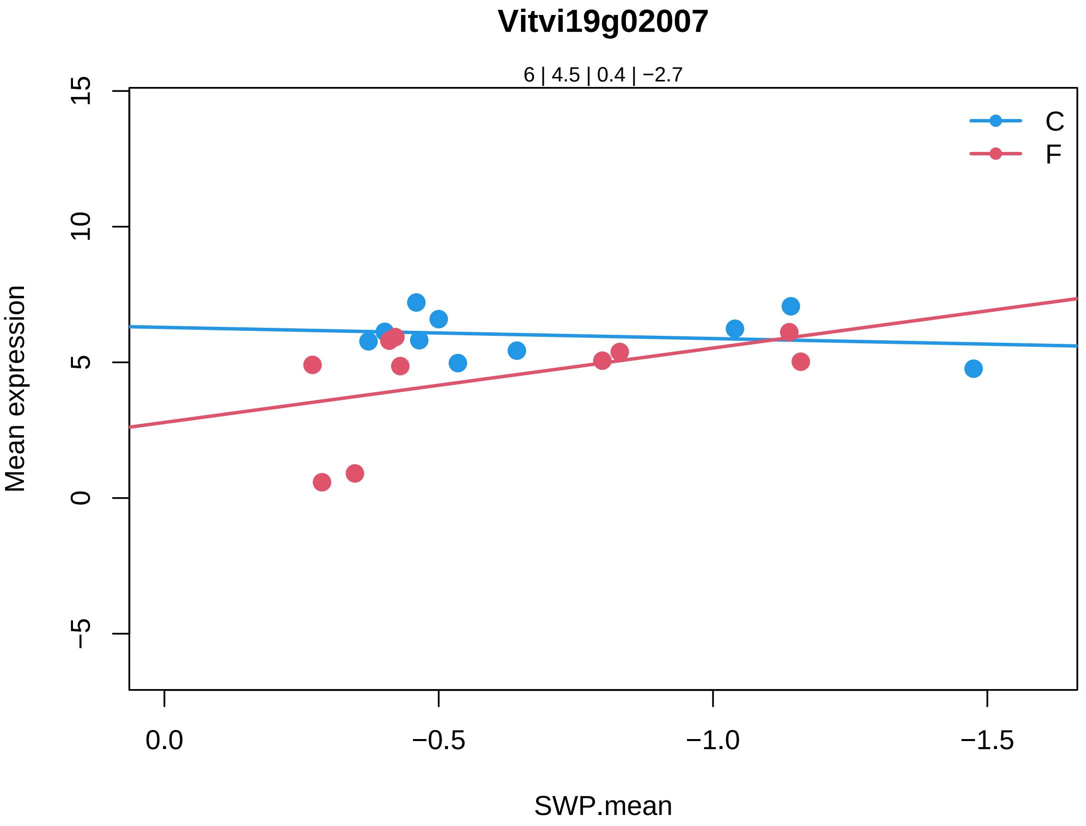
6.6.25 Vitvi19g02007

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

```
Vitvi19g02007
        35.2
        not assigned.unknown
        fatty acid desaturase A |
        Chr4:13571951-13572922 FORWARD LENGTH=323 |
        201606
```

Coefficients for Vitvi19g02007.

```
                    swp   varietyF swp.varietyF  AveExpr        F
Vitvi19g02007 0.4107341 -3.500847     -3.15221 5.227172 4.062874
                 P.Value adj.P.Val  type
Vitvi19g02007 0.01976625 0.1340201 type5
```



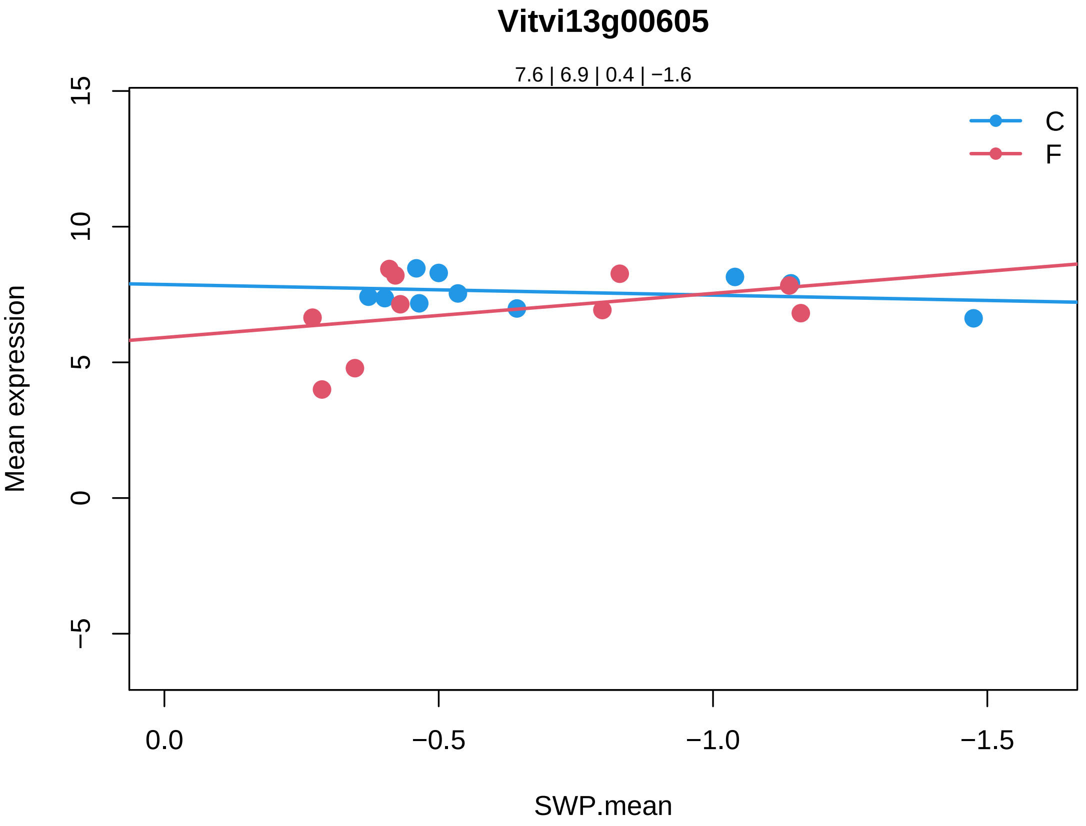
6.6.26 Vitvi13g00605

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

```
Vitvi13g00605
        34.19.1
        transport.major intrinsic proteins.PIP
        plasma membrane intrinsic protein 2 |
        Chr2:15613624-15614791 REVERSE LENGTH=285 |
        201606
```

Coefficients for Vitvi13g00605.

```
                    swp  varietyF swp.varietyF  AveExpr        F
Vitvi13g00605 0.3913983 -1.954209    -2.019107 7.249083 1.799733
                P.Value adj.P.Val  type
Vitvi13g00605 0.1774739 0.5051309 type5
```



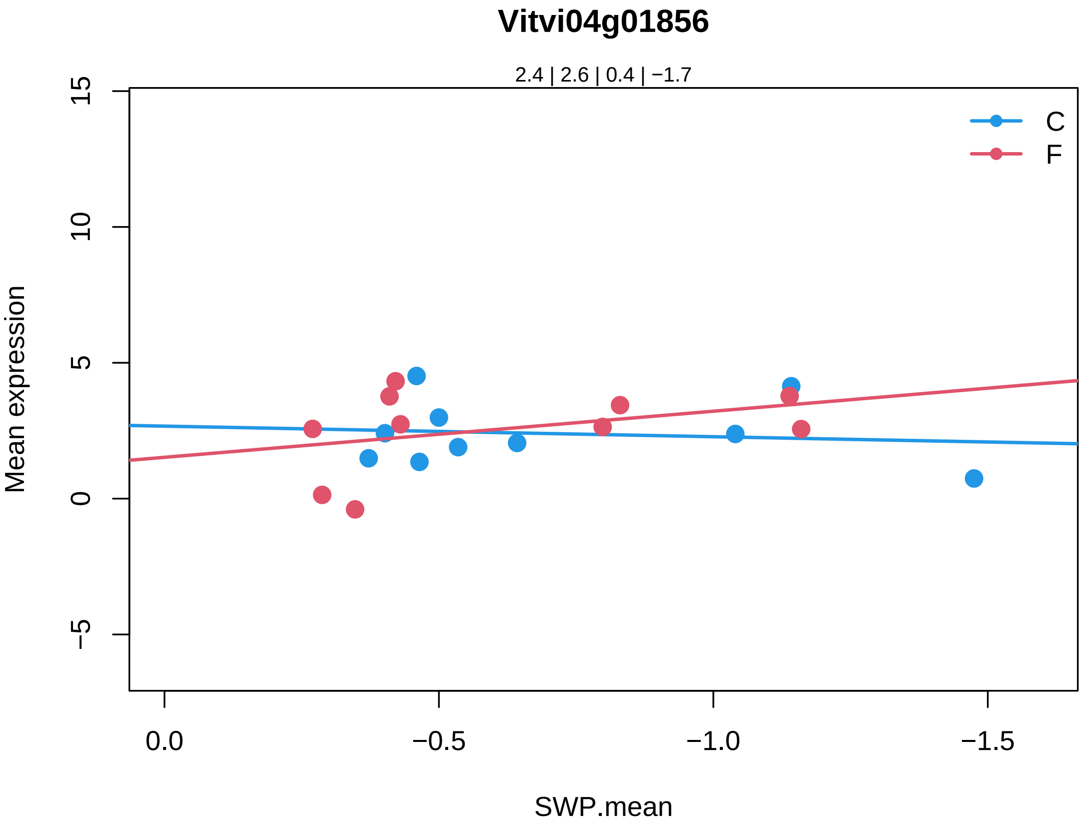
6.6.27 Vitvi04g01856

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

```
Vitvi04g01856
        31.1
        cell.organisation
        Ankyrin repeat family protein |
        Chr1:3390475-3392481 REVERSE LENGTH=578 |
        201606
```

Coefficients for Vitvi04g01856.

```
                    swp  varietyF swp.varietyF  AveExpr         F
Vitvi04g01856 0.3888641 -1.147908    -2.085775 2.474487 0.7465881
                P.Value adj.P.Val  type
Vitvi04g01856 0.5361628 0.8218871 type5
```



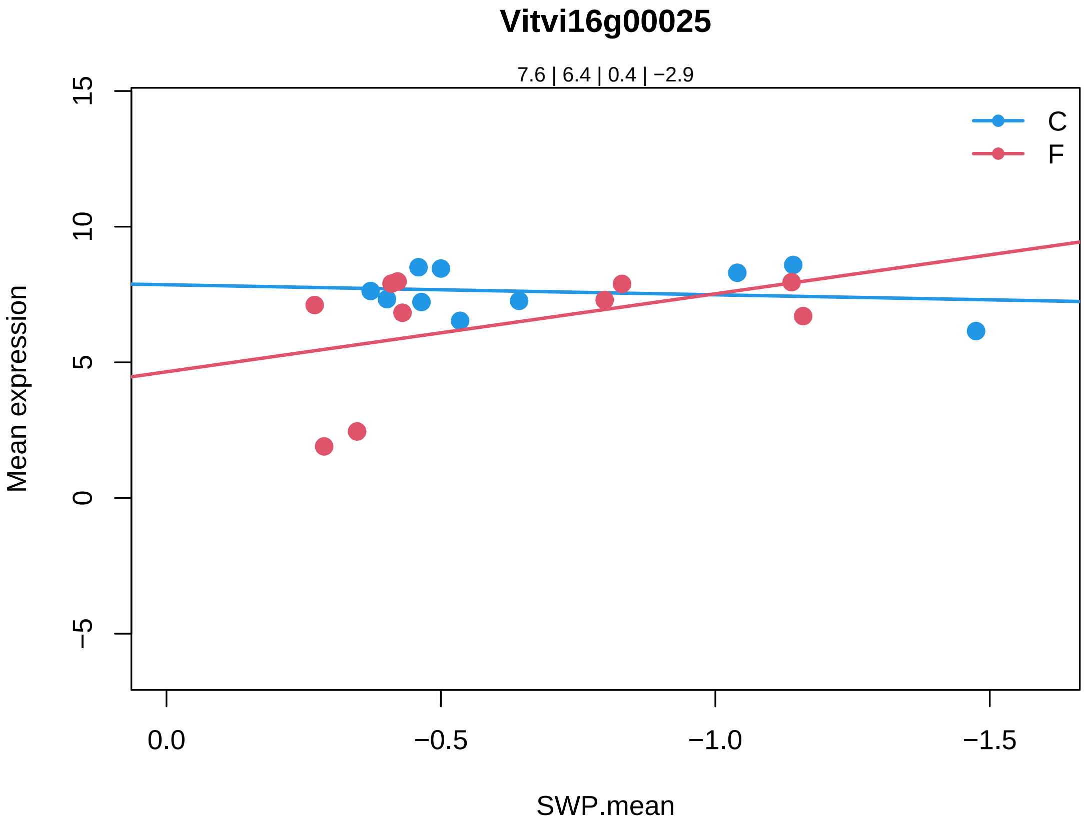
6.6.28 Vitvi16g00025

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

```
Vitvi16g00025
        28.99
        DNA.unspecified
        P-loop containing nucleoside triphosphate hydrolases superfamily prote
        Chr5:14119060-14123078 REVERSE LENGTH=961 |
        201606
```

Coefficients for Vitvi16g00025.

```
                  swp  varietyF swp.varietyF  AveExpr        F
Vitvi16g00025 0.36987 -3.207582    -3.244807 7.000897 2.518667
                 P.Value adj.P.Val  type
Vitvi16g00025 0.08515683 0.3366949 type5
```



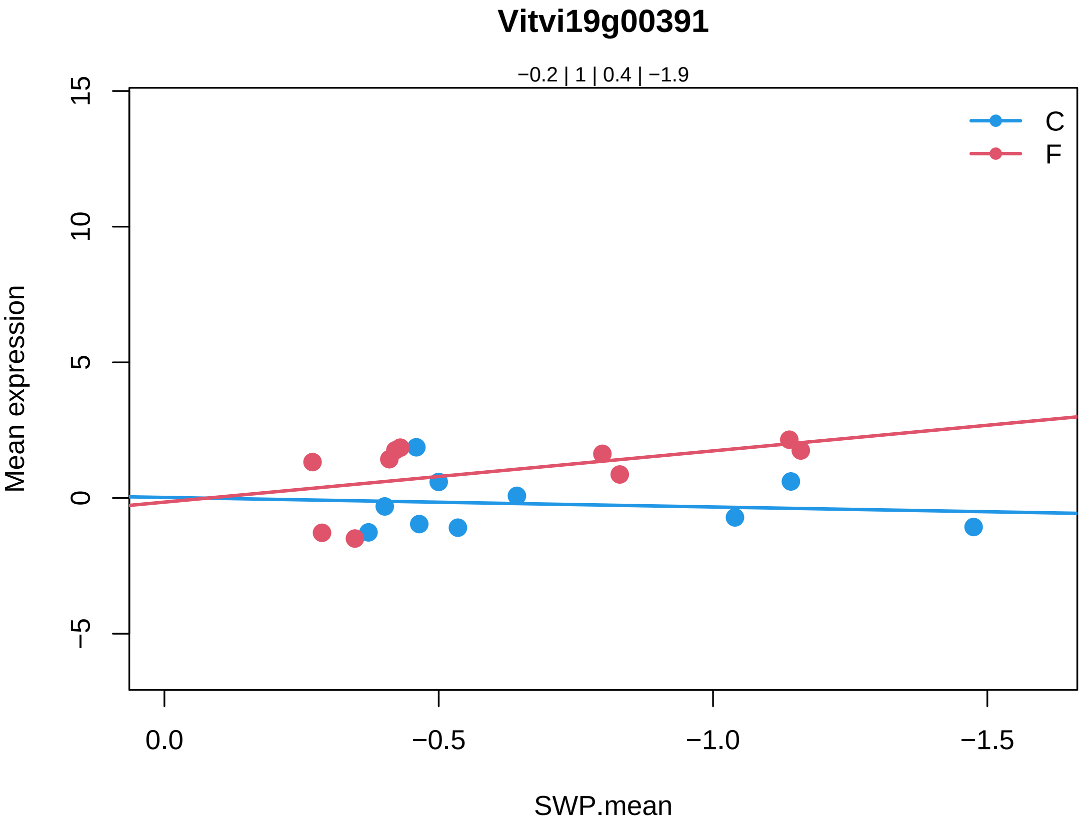
6.6.29 Vitvi19g00391

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

```
Vitvi19g00391
        16.01.2005
        secondary metabolism.isoprenoids.terpenoids
        terpene synthase 21 |
        Chr5:8092969-8095128 FORWARD LENGTH=545 |
        201606
```

Coefficients for Vitvi19g00391.

```
                    swp   varietyF swp.varietyF   AveExpr       F
Vitvi19g00391 0.3515541 -0.1723642    -2.240139 0.3867802 3.74656
                 P.Value adj.P.Val  type
Vitvi19g00391 0.02630762 0.1628018 type5
```



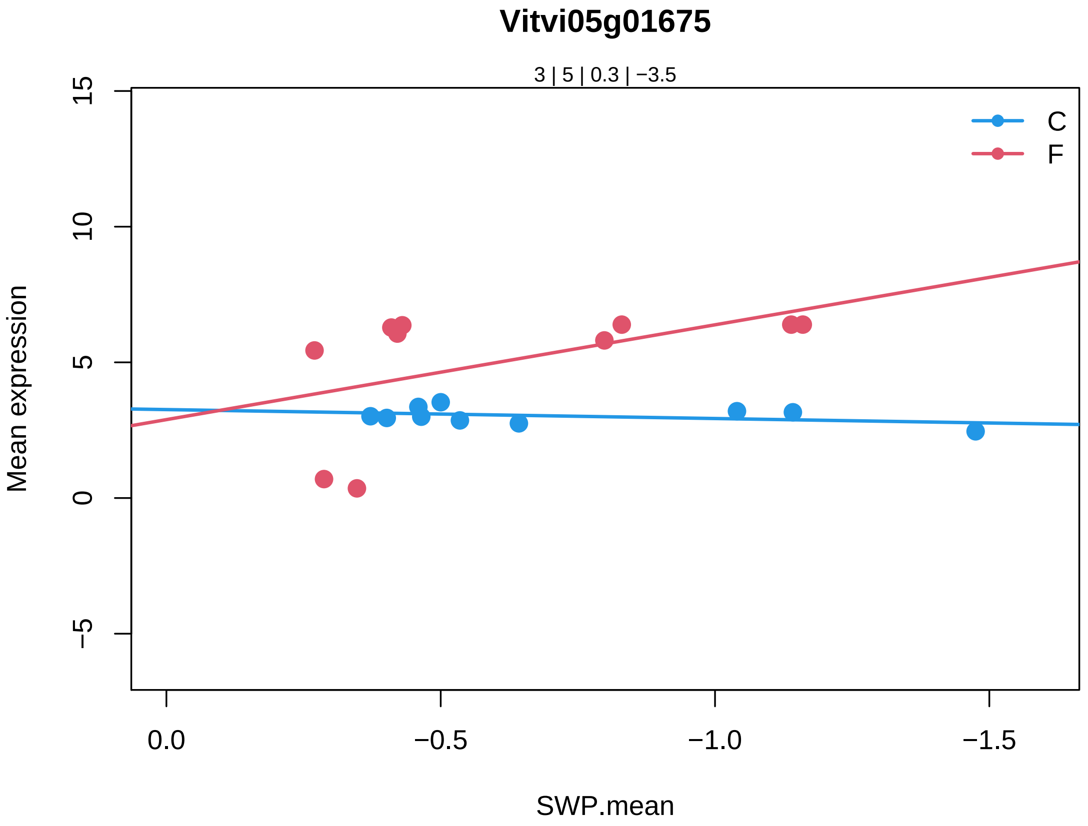
6.6.30 Vitvi05g01675

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

```
Vitvi05g01675
        26.11.2001
        misc.alcohol dehydrogenases.cinnamyl alcohol dehydrogenase
        Zinc-binding dehydrogenase family protein |
        Chr5:5584983-5586991 REVERSE LENGTH=345 |
        201606
```

Coefficients for Vitvi05g01675.

```
                    swp   varietyF swp.varietyF  AveExpr       F
Vitvi05g01675 0.3297008 -0.3707486    -3.824121 4.023001 5.82822
                 P.Value  adj.P.Val  type
Vitvi05g01675 0.00449966 0.04697522 type5
```



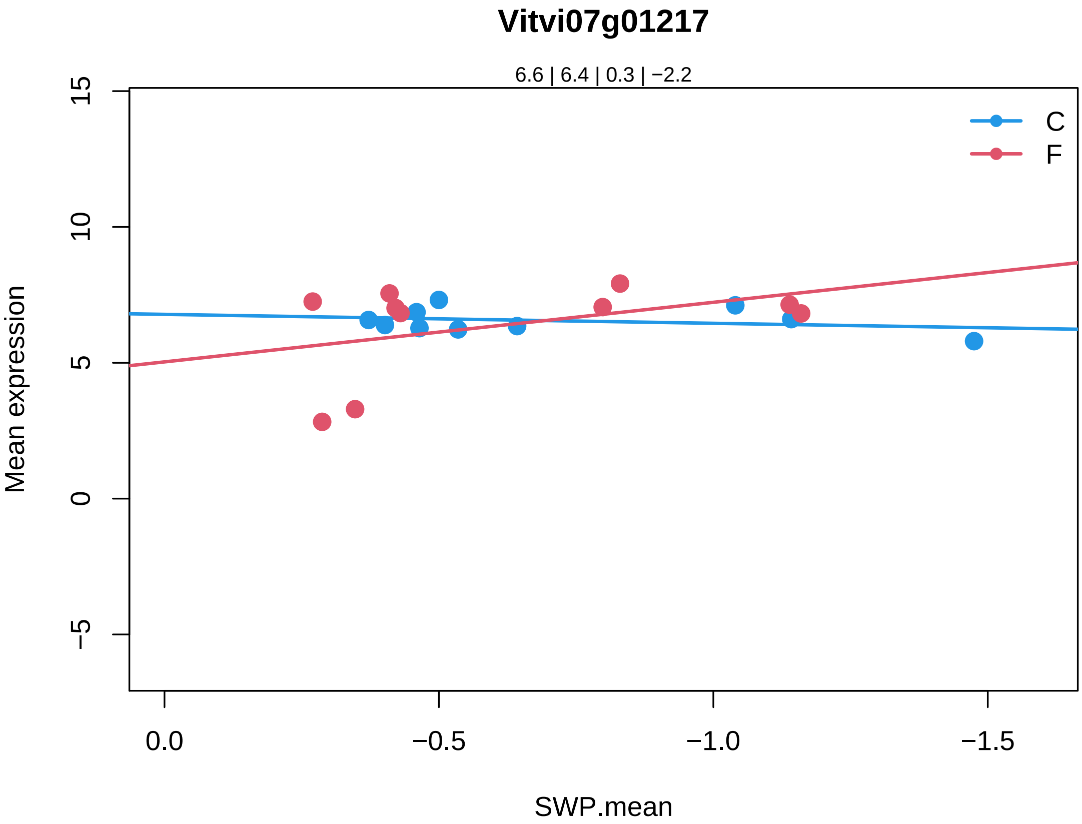
6.6.31 Vitvi07g01217

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

```
Vitvi07g01217
        20.1.3.1
        stress.biotic.signalling.MLO-like
        Seven transmembrane MLO family protein |
        Chr4:1144141-1147156 FORWARD LENGTH=526 |
        201606
```

Coefficients for Vitvi07g01217.

```
                    swp  varietyF swp.varietyF  AveExpr        F
Vitvi07g01217 0.3290549 -1.749802    -2.522145 6.460186 1.470295
                P.Value adj.P.Val  type
Vitvi07g01217 0.2507132 0.6016958 type5
```



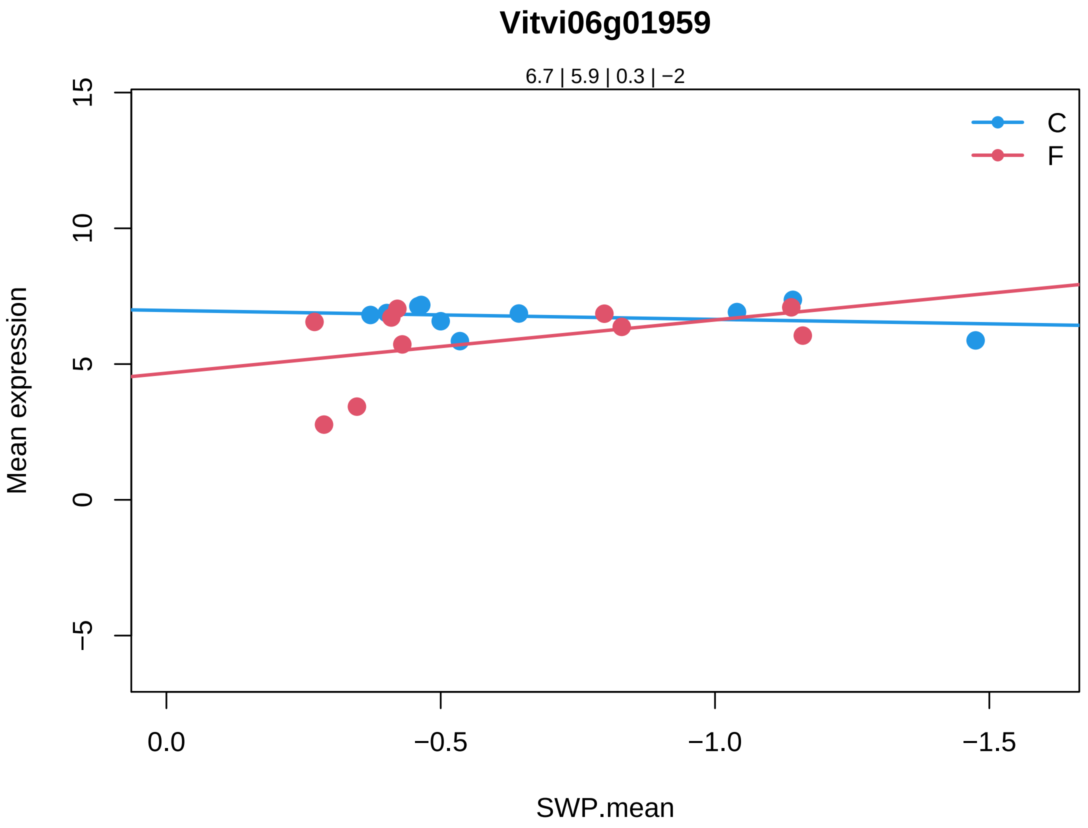
6.6.32 Vitvi06g01959

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

```
Vitvi06g01959
        35.2
        not assigned.unknown
        hypothetical protein |
        Chr3:19546446-19546868 REVERSE LENGTH=140 |
        201606
```

Coefficients for Vitvi06g01959.

```
                    swp  varietyF swp.varietyF  AveExpr        F
Vitvi06g01959 0.3287882 -2.309543    -2.289575 6.301046 2.861129
                 P.Value adj.P.Val  type
Vitvi06g01959 0.06072881 0.2741791 type5
```



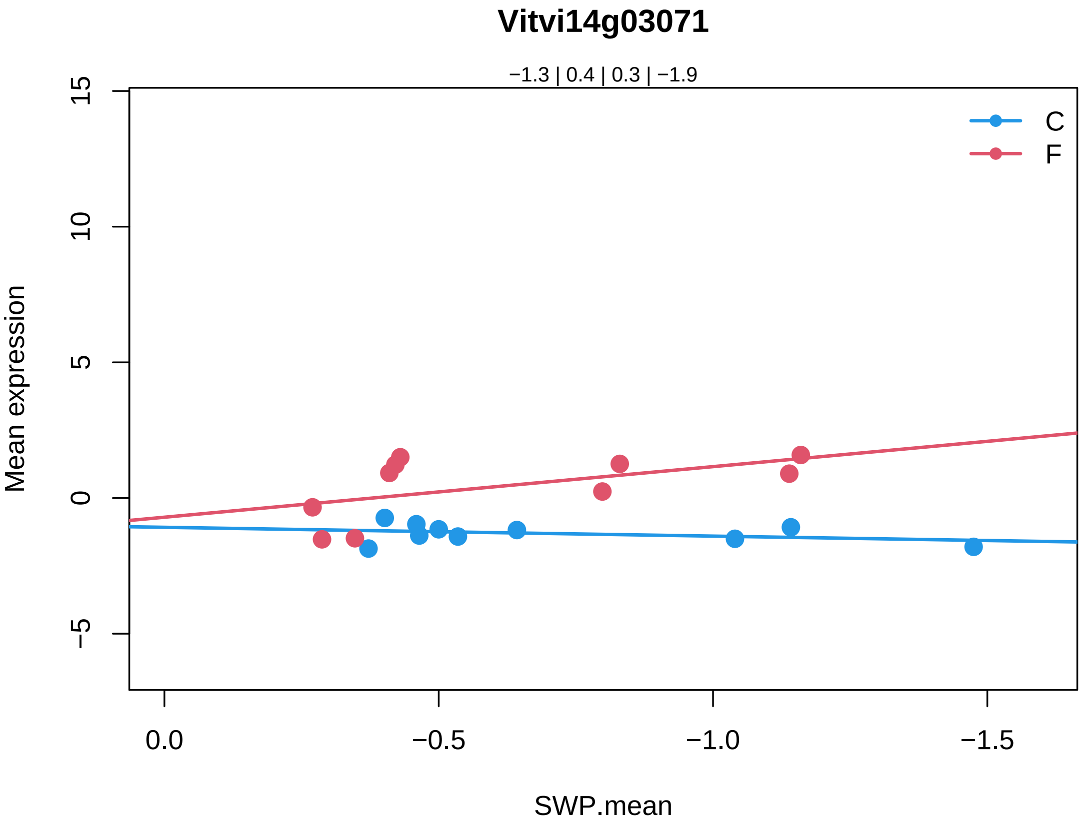
6.6.33 Vitvi14g03071

```
> 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.

```
                    swp varietyF swp.varietyF    AveExpr        F
Vitvi14g03071 0.3246997 0.372033    -2.188816 -0.4395587 12.28072
                   P.Value   adj.P.Val  type
Vitvi14g03071 6.872806e-05 0.001652292 type5
```



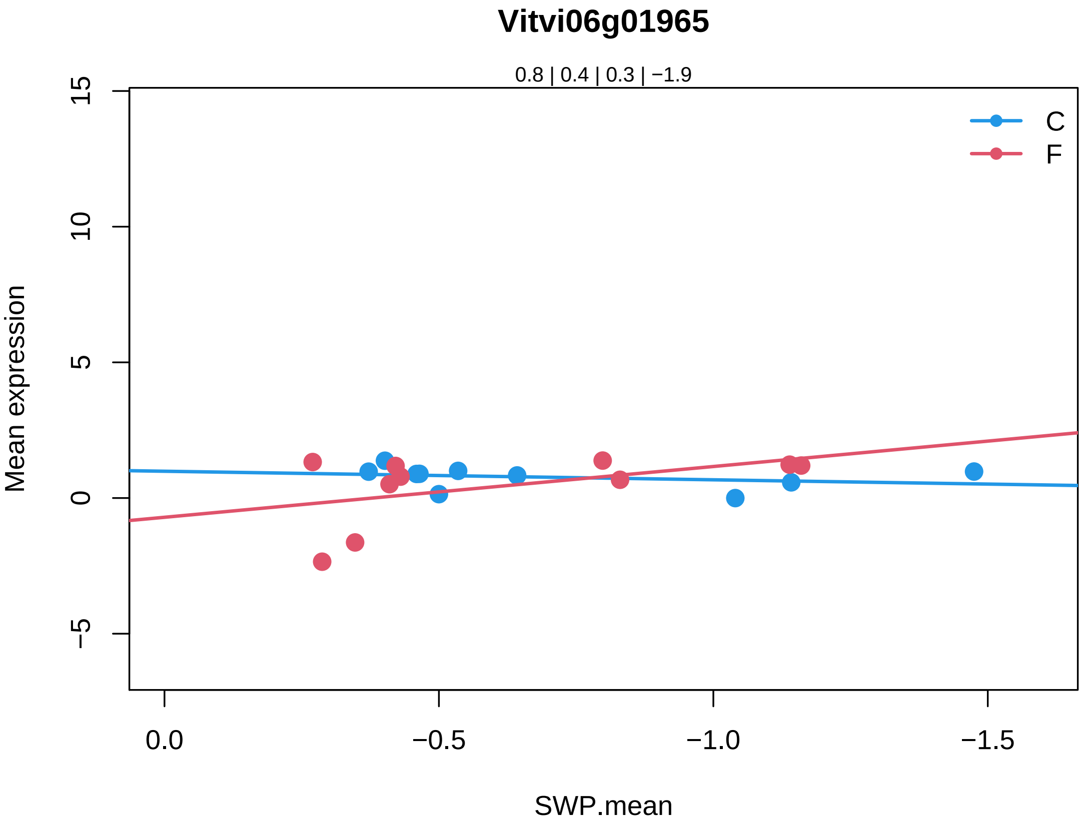
6.6.34 Vitvi06g01965

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

```
Vitvi06g01965
        35.2
        not assigned.unknown
        BED zinc finger and hAT dimerization domain-containing protein DAYSLEE
        Chr3:14321838-14323928 FORWARD LENGTH=696 |
        201606
```

Coefficients for Vitvi06g01965.

```
                    swp  varietyF swp.varietyF   AveExpr       F
Vitvi06g01965 0.3157152 -1.697272    -2.186908 0.5975635 2.14613
                P.Value adj.P.Val  type
Vitvi06g01965 0.1241038 0.4191403 type5
```



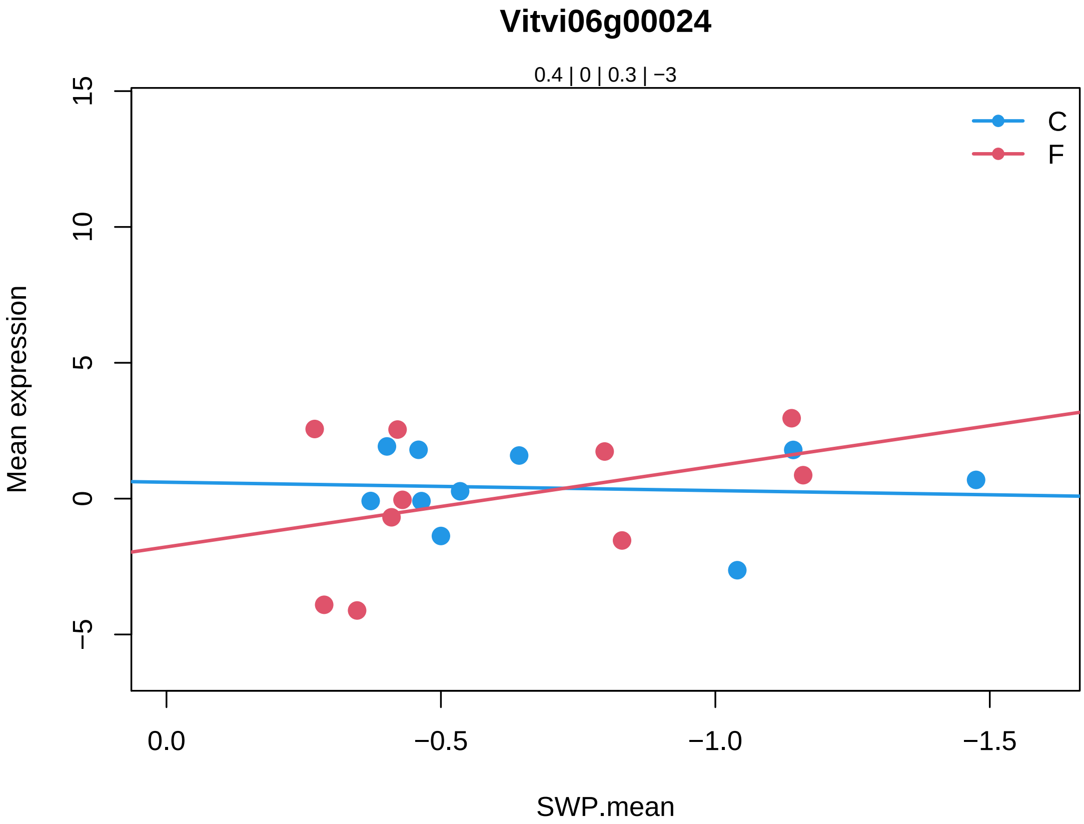
6.6.35 Vitvi06g00024

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

```
Vitvi06g00024
        27.03.2025
        RNA.regulation of transcription.MYB domain transcription factor family
        Homeodomain-like superfamily protein |
        Chr3:1042920-1044574 REVERSE LENGTH=388 |
        201606
```

Coefficients for Vitvi06g00024.

```
                    swp  varietyF swp.varietyF  AveExpr        F
Vitvi06g00024 0.3085189 -2.381052    -3.285553 0.211744 0.995669
                P.Value adj.P.Val  type
Vitvi06g00024 0.4137626 0.7484654 type5
```



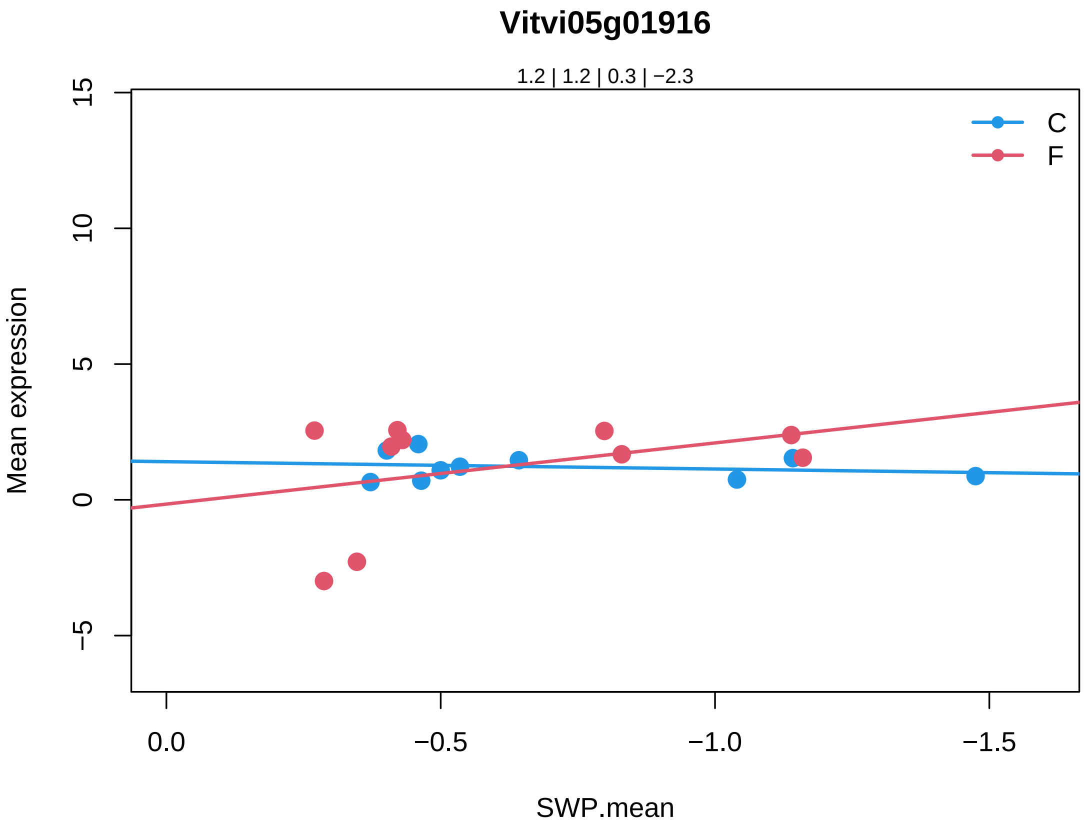
6.6.36 Vitvi05g01916

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

```
Vitvi05g01916
        35.2
        not assigned.unknown
        AT-hook motif nuclear-localized protein 20 |
        Chr4:8320972-8321817 FORWARD LENGTH=281 |
        201606
```

Coefficients for Vitvi05g01916.

```
                    swp varietyF swp.varietyF  AveExpr        F
Vitvi05g01916 0.2702258 -1.56207    -2.523015 1.215171 1.076087
                P.Value adj.P.Val  type
Vitvi05g01916 0.3801831 0.7206407 type5
```



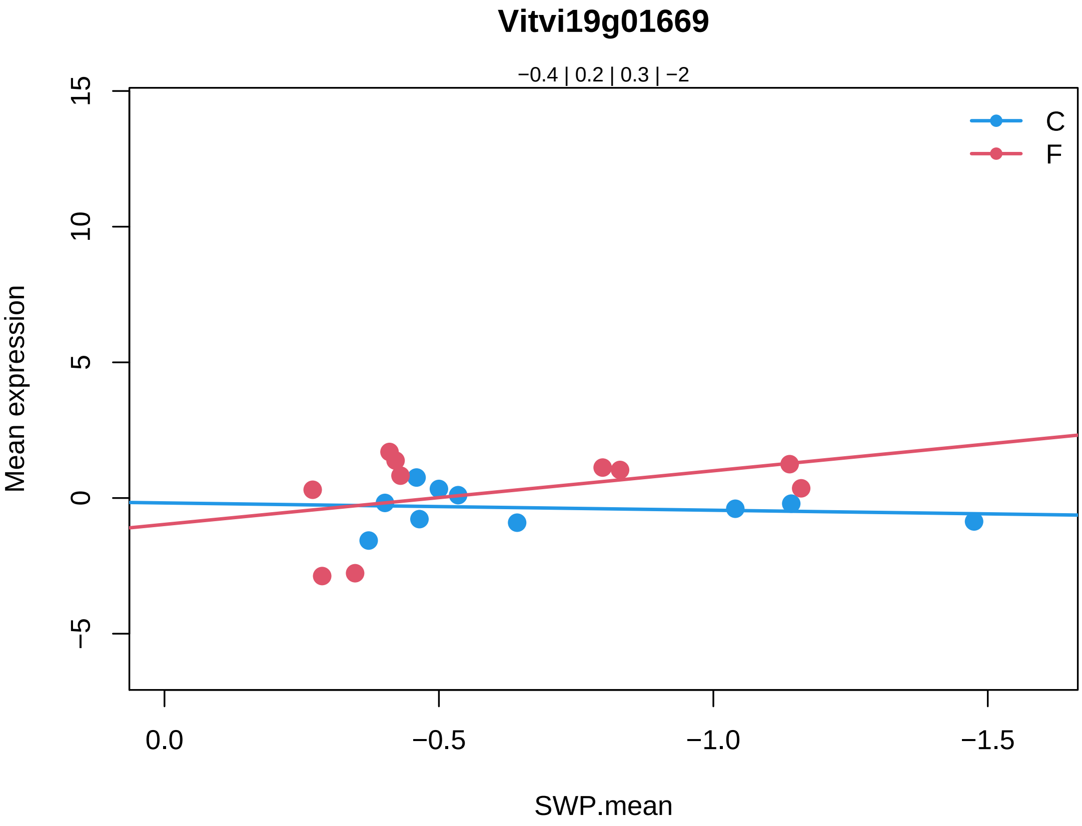
6.6.37 Vitvi19g01669

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

```
Vitvi19g01669
        27.03.2025
        RNA.regulation of transcription.MYB domain transcription factor family
        myb domain protein 58 |
        Chr1:5629859-5630844 REVERSE LENGTH=274 |
        201606
```

Coefficients for Vitvi19g01669.

```
                    swp   varietyF swp.varietyF     AveExpr       F
Vitvi19g01669 0.2686673 -0.7906223    -2.245104 -0.06913811 1.65156
                P.Value adj.P.Val  type
Vitvi19g01669 0.2072026 0.5488673 type5
```



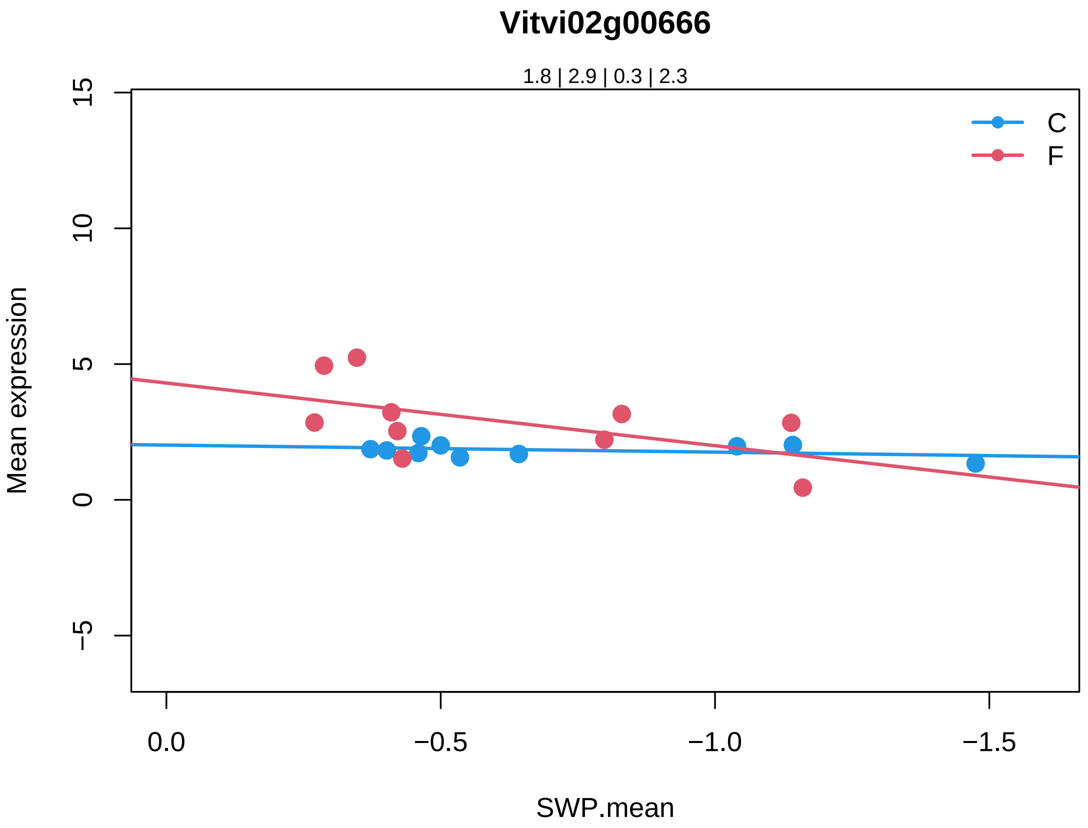
6.6.38 Vitvi02g00666

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

```
Vitvi02g00666
        27.03.1999
        RNA.regulation of transcription.unclassified
        lsd one like 1 |
        Chr1:11768253-11769591 FORWARD LENGTH=187 |
        201606
```

Coefficients for Vitvi02g00666.

```
                    swp varietyF swp.varietyF  AveExpr        F
Vitvi02g00666 0.2596456 2.285948     2.048877 2.364745 5.590674
                  P.Value  adj.P.Val  type
Vitvi02g00666 0.005432858 0.05444289 type5
```



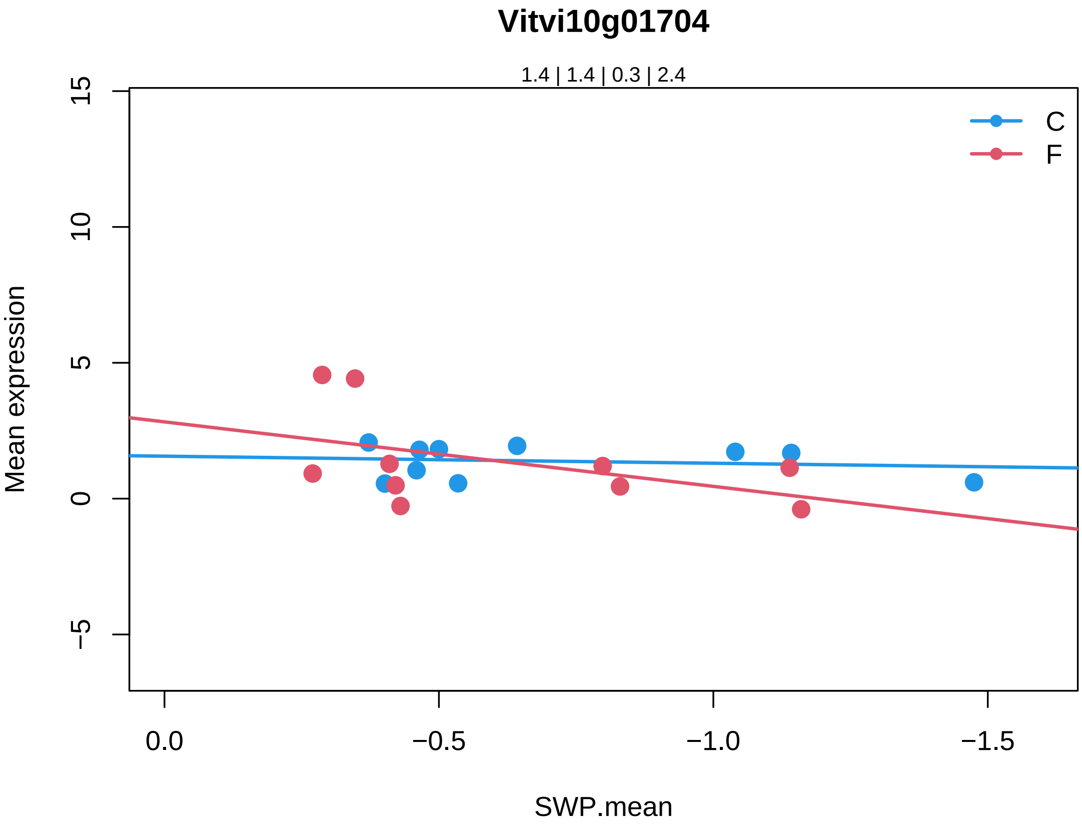
6.6.39 Vitvi10g01704

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

```
Vitvi10g01704
        35.2
        not assigned.unknown
        Heavy metal transport/detoxification superfamily protein |
        Chr4:9255062-9255955 FORWARD LENGTH=261 |
        201606
```

Coefficients for Vitvi10g01704.

```
                    swp varietyF swp.varietyF  AveExpr        F
Vitvi10g01704 0.2596266 1.263227      2.11457 1.379016 1.684316
                P.Value adj.P.Val  type
Vitvi10g01704 0.2002121 0.5395387 type5
```



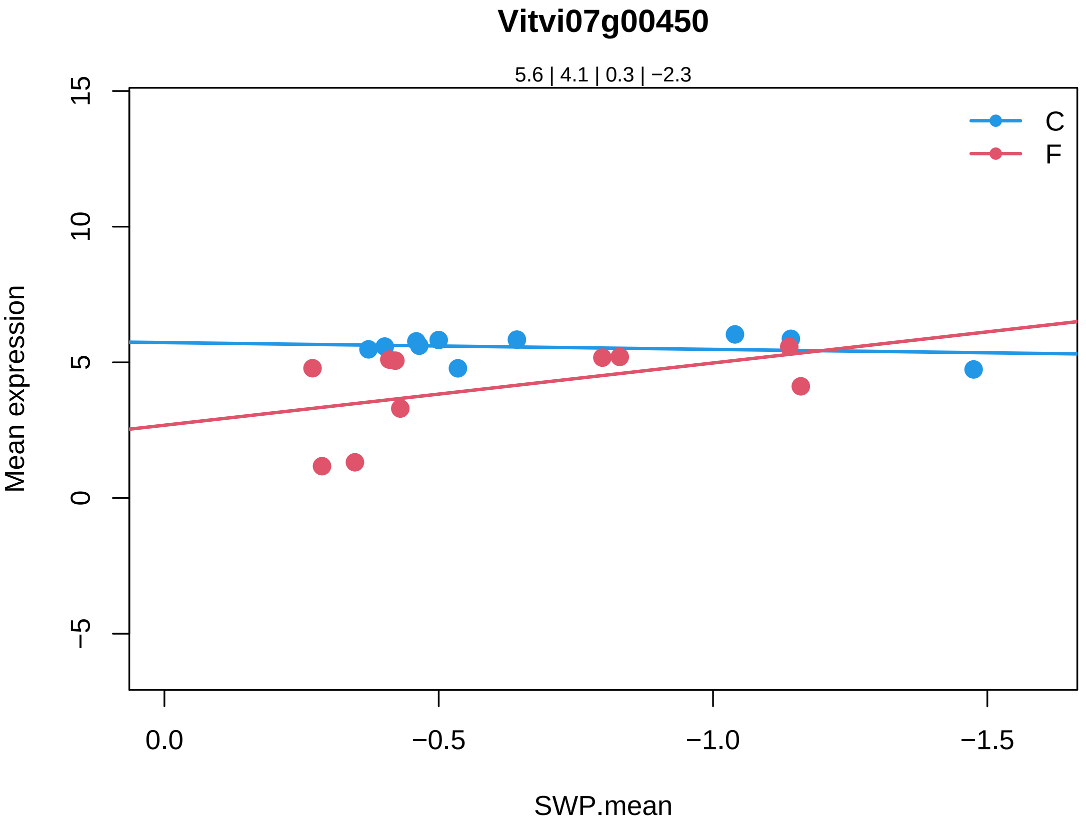
6.6.40 Vitvi07g00450

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

```
Vitvi07g00450
        35.2
        not assigned.unknown
        insulin-induced protein |
        Chr4:841102-842228 FORWARD LENGTH=256 |
        201606
```

Coefficients for Vitvi07g00450.

```
                    swp  varietyF swp.varietyF  AveExpr        F
Vitvi07g00450 0.2505644 -3.045759    -2.544415 4.816298 5.535411
                  P.Value adj.P.Val  type
Vitvi07g00450 0.005678914 0.0563559 type5
```



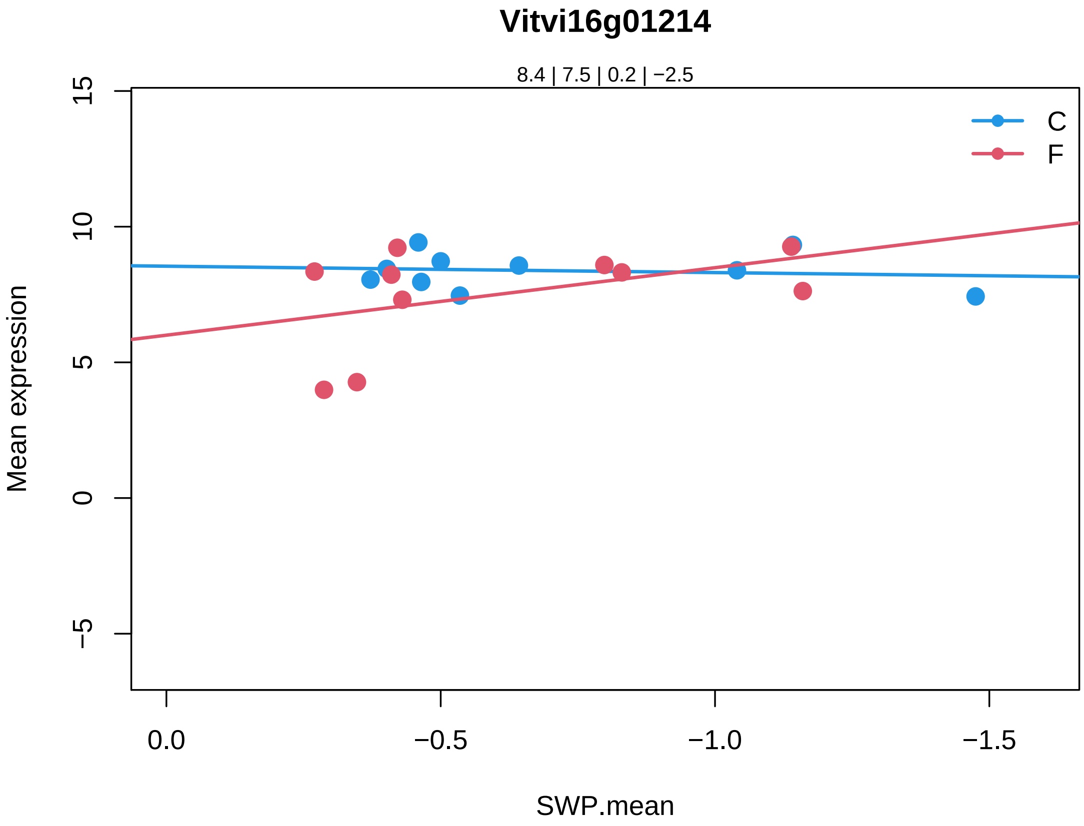
6.6.41 Vitvi16g01214

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

```
Vitvi16g01214
        27.03.1985
        RNA.regulation of transcription.sigma like plant
        sigma factor E |
        Chr5:8157794-8159746 REVERSE LENGTH=517 |
        201606
```

Coefficients for Vitvi16g01214.

```
                    swp  varietyF swp.varietyF  AveExpr        F
Vitvi16g01214 0.2347942 -2.542071    -2.721939 7.946922 2.402494
                 P.Value adj.P.Val  type
Vitvi16g01214 0.09567705   0.36132 type5
```



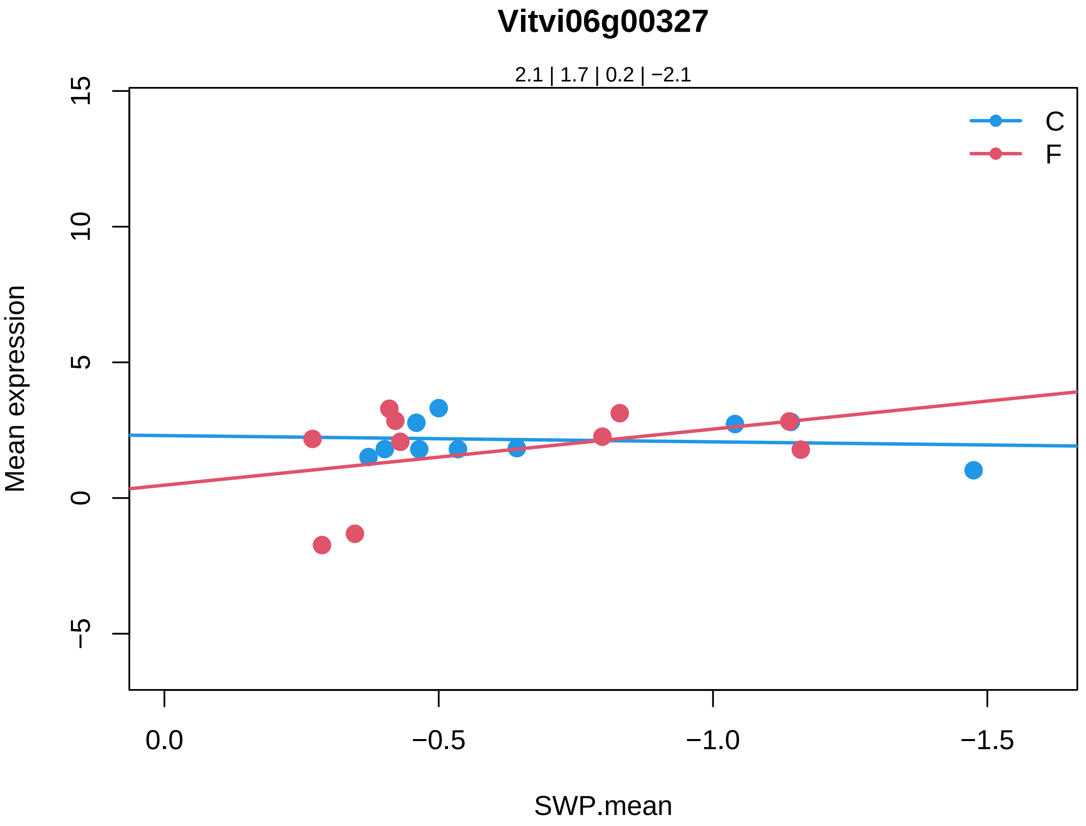
6.6.42 Vitvi06g00327

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

```
Vitvi06g00327
        35.2
        not assigned.unknown
        lectin protein kinase family protein |
        Chr1:12503450-12505939 FORWARD LENGTH=829 |
        201606
```

Coefficients for Vitvi06g00327.

```
                   swp   varietyF swp.varietyF  AveExpr        F
Vitvi06g00327 0.230431 -1.826747    -2.296154 1.935905 1.290722
                P.Value adj.P.Val  type
Vitvi06g00327 0.3030622 0.6553091 type5
```



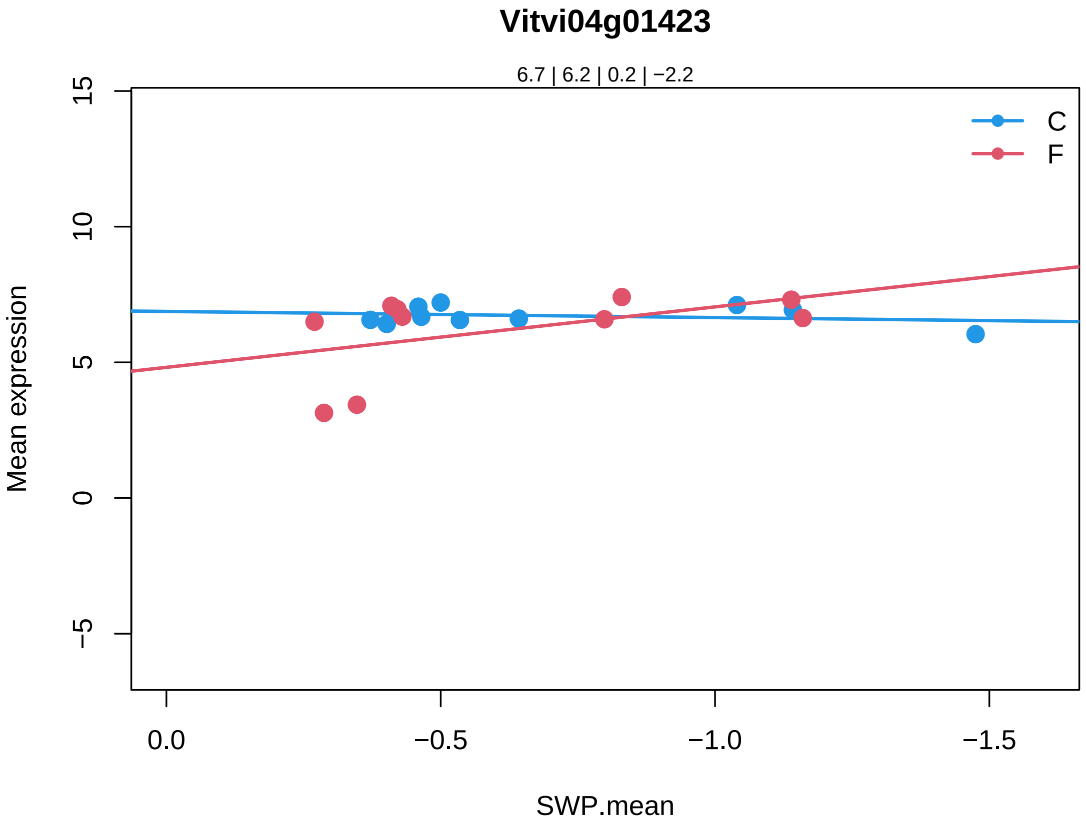
6.6.43 Vitvi04g01423

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

```
Vitvi04g01423
        27.03.2007
        RNA.regulation of transcription.C2C2(Zn) Constans-like zinc finger fam
        B-box type zinc finger family protein |
        Chr4:18161576-18163045 FORWARD LENGTH=183 |
        201606
```

Coefficients for Vitvi04g01423.

```
                    swp   varietyF swp.varietyF  AveExpr        F
Vitvi04g01423 0.2254381 -2.059676    -2.453074 6.445043 2.588908
                 P.Value adj.P.Val  type
Vitvi04g01423 0.07940036 0.3228115 type5
```



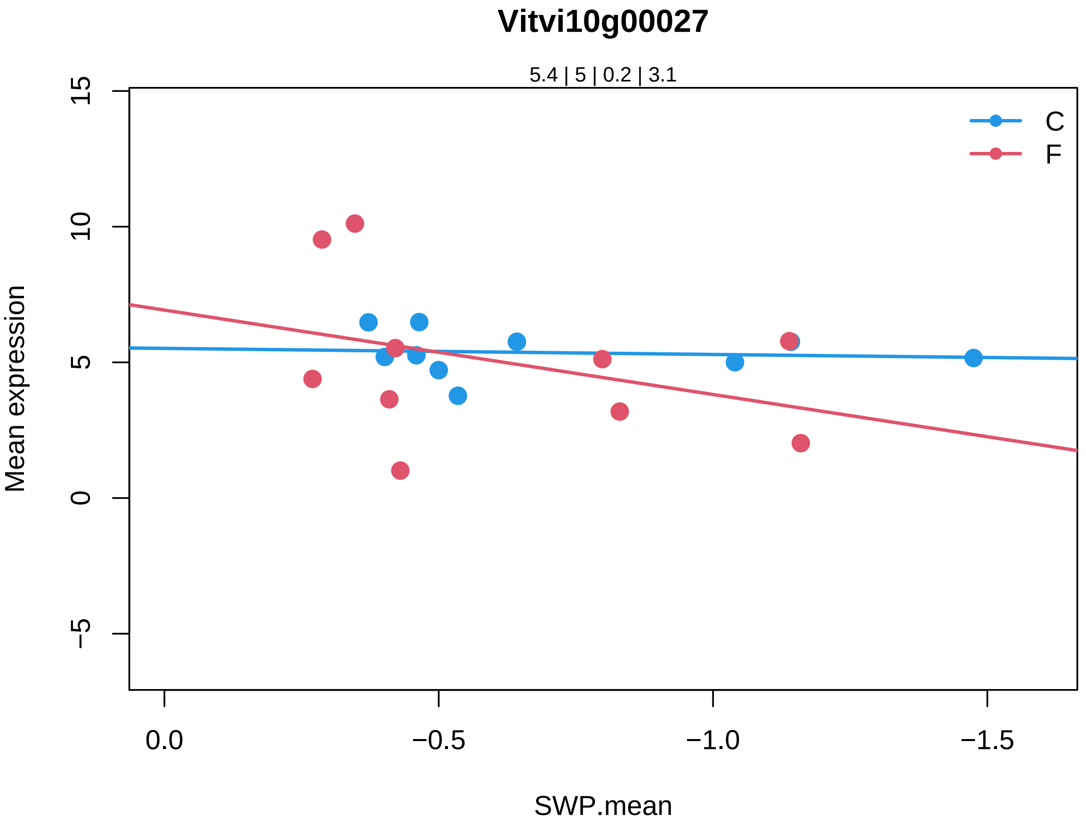
6.6.44 Vitvi10g00027

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

```
Vitvi10g00027
        18.2
        Co-factor and vitamine metabolism.thiamine
        thiazole biosynthetic enzyme%2C chloroplast (ARA6) (THI1) (THI4) |
        Chr5:22246634-22247891 FORWARD LENGTH=349 |
        201606
```

Coefficients for Vitvi10g00027.

```
                    swp varietyF swp.varietyF  AveExpr        F
Vitvi10g00027 0.2236902 1.411303     2.886813 5.193977 1.040322
                P.Value adj.P.Val  type
Vitvi10g00027 0.3947805 0.7326487 type5
```



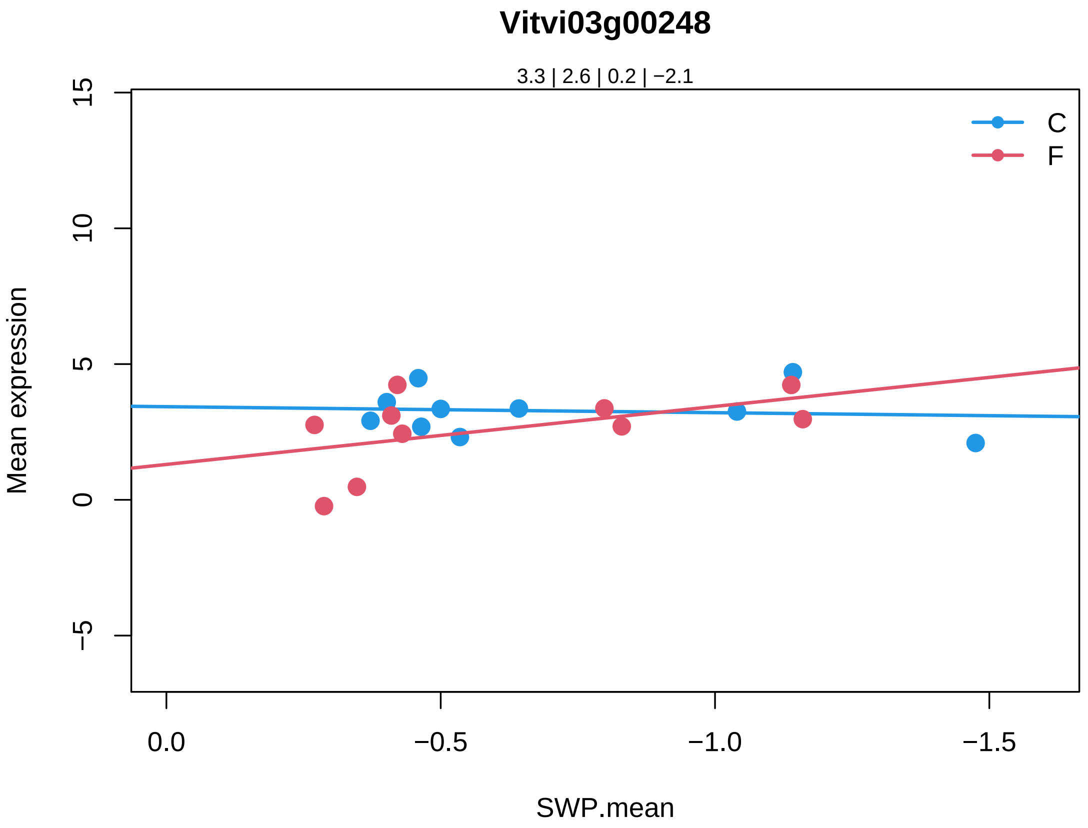
6.6.45 Vitvi03g00248

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

```
Vitvi03g00248
        34.9
        transport.metabolite transporters at the mitochondrial membrane
        phosphate transporter 3%3B3 |
        Chr2:7510456-7512118 FORWARD LENGTH=309 |
        201606
```

Coefficients for Vitvi03g00248.

```
                    swp  varietyF swp.varietyF  AveExpr        F
Vitvi03g00248 0.2201906 -2.127068    -2.357623 2.939794 2.361324
                 P.Value adj.P.Val  type
Vitvi03g00248 0.09973057 0.3706641 type5
```



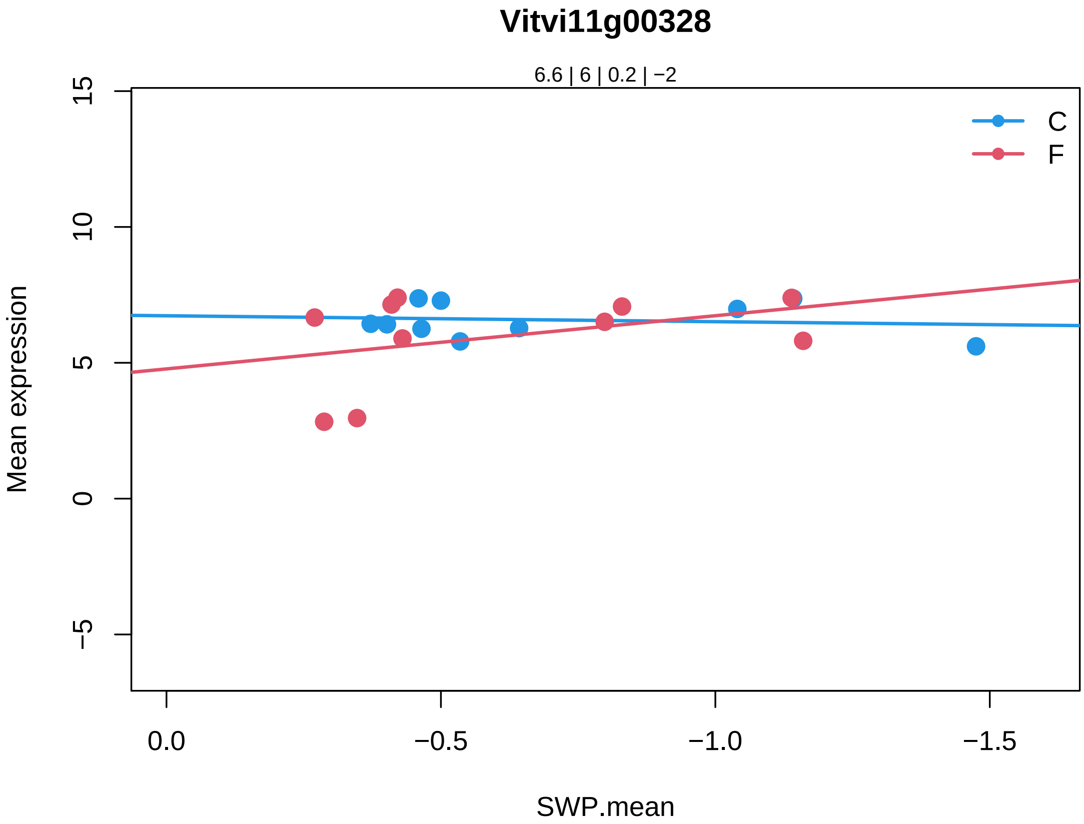
6.6.46 Vitvi11g00328

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

```
Vitvi11g00328
        29.4
        protein.postranslational modification
        protein kinase family protein |
        Chr5:7209422-7213700 FORWARD LENGTH=831 |
        201606
```

Coefficients for Vitvi11g00328.

```
                    swp varietyF swp.varietyF  AveExpr        F
Vitvi11g00328 0.2169187 -1.95565    -2.174644 6.272609 1.573834
                P.Value adj.P.Val  type
Vitvi11g00328 0.2248194 0.5723563 type5
```



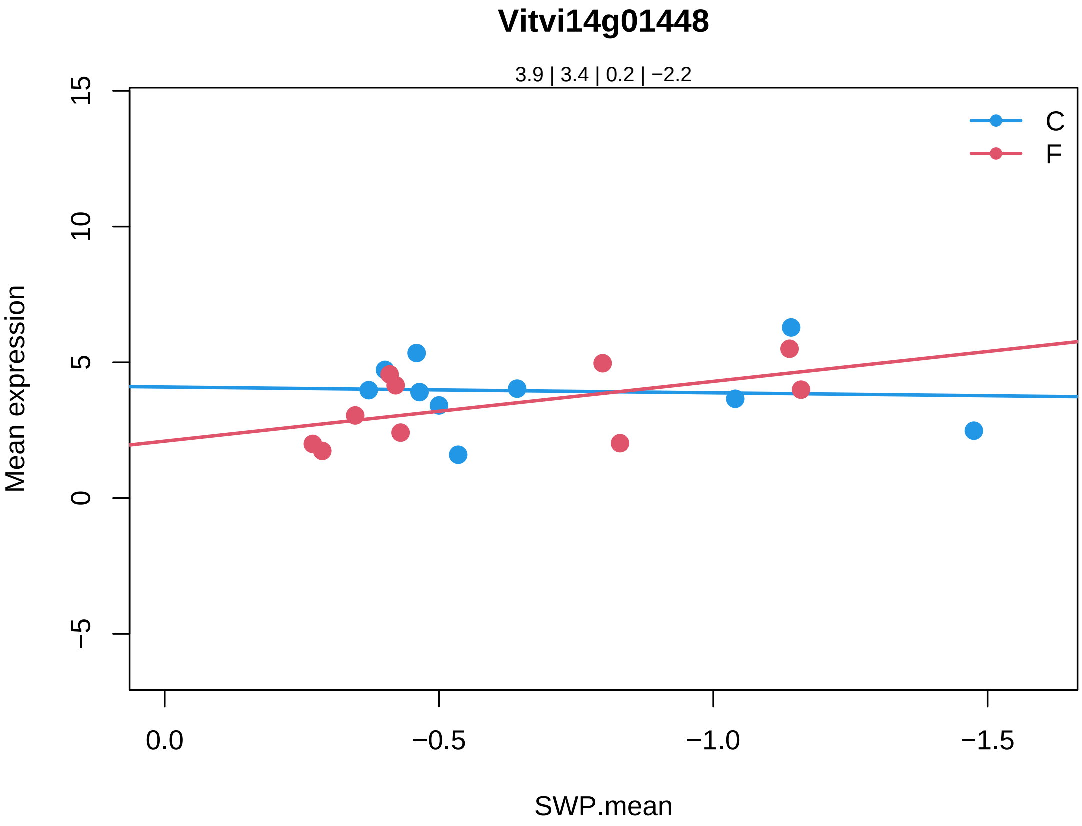
6.6.47 Vitvi14g01448

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

```
Vitvi14g01448
        16.8.2.1
        secondary metabolism.flavonoids.chalcones.naringenin-chalcone synthase
        Chalcone and stilbene synthase family protein |
        Chr5:4488762-4490035 FORWARD LENGTH=395 |
        201606
```

Coefficients for Vitvi14g01448.

```
                   swp  varietyF swp.varietyF AveExpr        F
Vitvi14g01448 0.214132 -1.994422    -2.415744 3.68948 1.595084
                P.Value adj.P.Val  type
Vitvi14g01448 0.2198545 0.5658599 type5
```



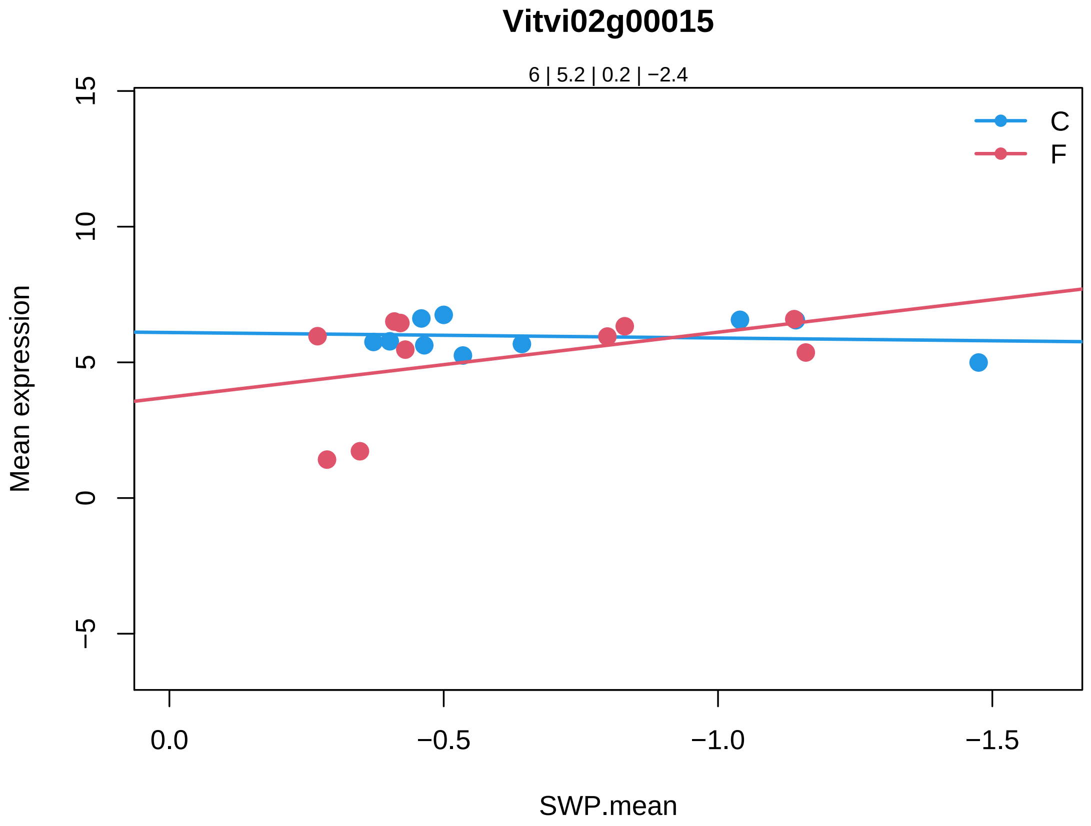
6.6.48 Vitvi02g00015

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

```
Vitvi02g00015
        4.01.2012
        glycolysis.cytosolic branch.phosphoglycerate mutase
        Phosphoglycerate mutase family protein |
        Chr3:1466738-1468219 FORWARD LENGTH=316 |
        201606
```

Coefficients for Vitvi02g00015.

```
                    swp  varietyF swp.varietyF  AveExpr        F
Vitvi02g00015 0.2023908 -2.381064    -2.596304 5.566505 2.004431
                P.Value adj.P.Val  type
Vitvi02g00015 0.1435432 0.4536359 type5
```



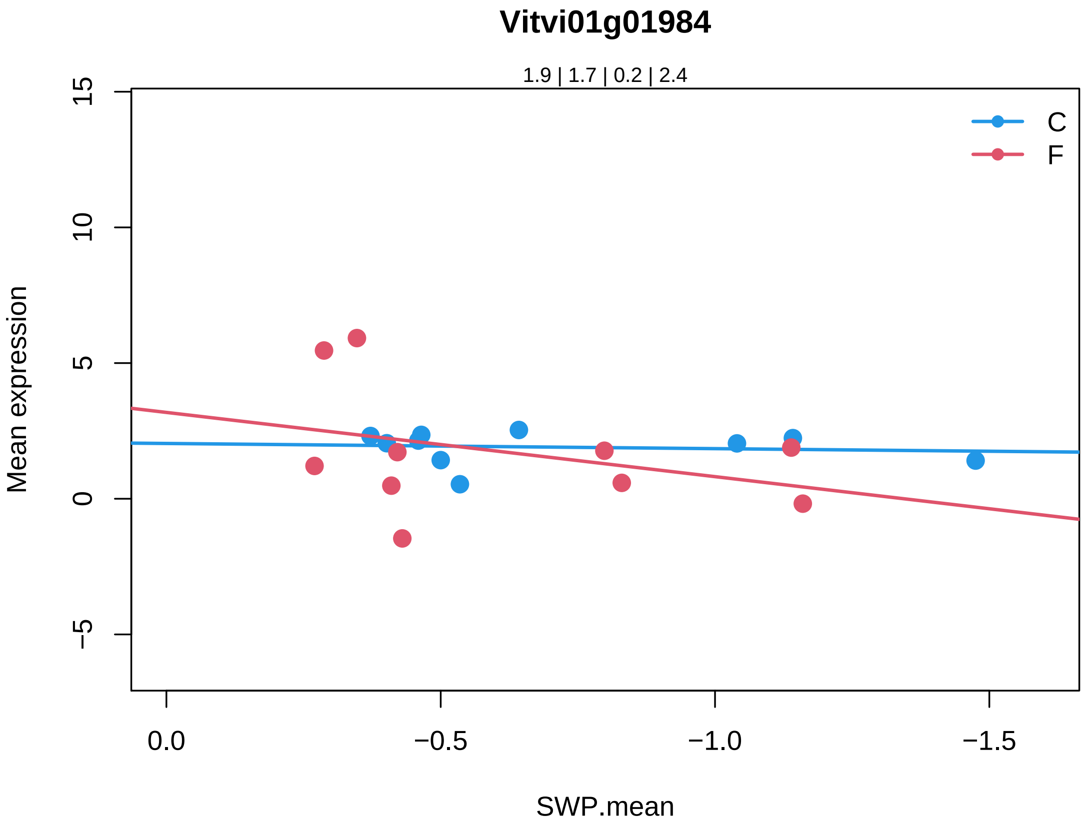
6.6.49 Vitvi01g01984

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

```
Vitvi01g01984
        1.01.2006
        PS.lightreaction.NADH DH
        Unknown Protein
```

Coefficients for Vitvi01g01984.

```
                      swp varietyF swp.varietyF  AveExpr         F
Vitvi01g01984 0.1912234 1.143816     2.175521 1.820929 0.9304102
                  P.Value adj.P.Val  type
Vitvi01g01984 0.4430676 0.7691448 type5
```



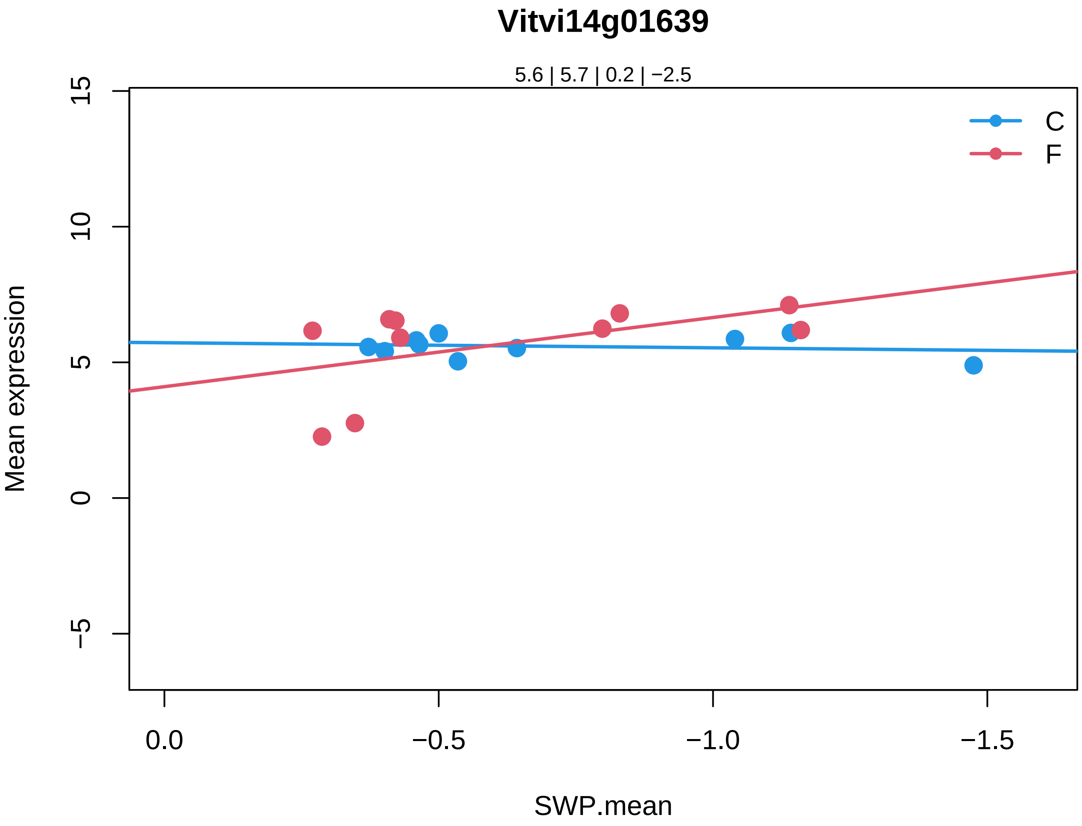
6.6.50 Vitvi14g01639

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

```
Vitvi14g01639
        11.05.2002
        lipid metabolism.glycerol metabolism.glycerol-3-phosphate dehydrogenas
        NAD-dependent glycerol-3-phosphate dehydrogenase family protein |
        Chr5:16265071-16267258 REVERSE LENGTH=400 |
        201606
```

Coefficients for Vitvi14g01639.

```
                    swp   varietyF swp.varietyF  AveExpr        F
Vitvi14g01639 0.1867008 -1.618738    -2.735318 5.624012 2.295516
                P.Value adj.P.Val  type
Vitvi14g01639 0.1065937 0.3860065 type5
```



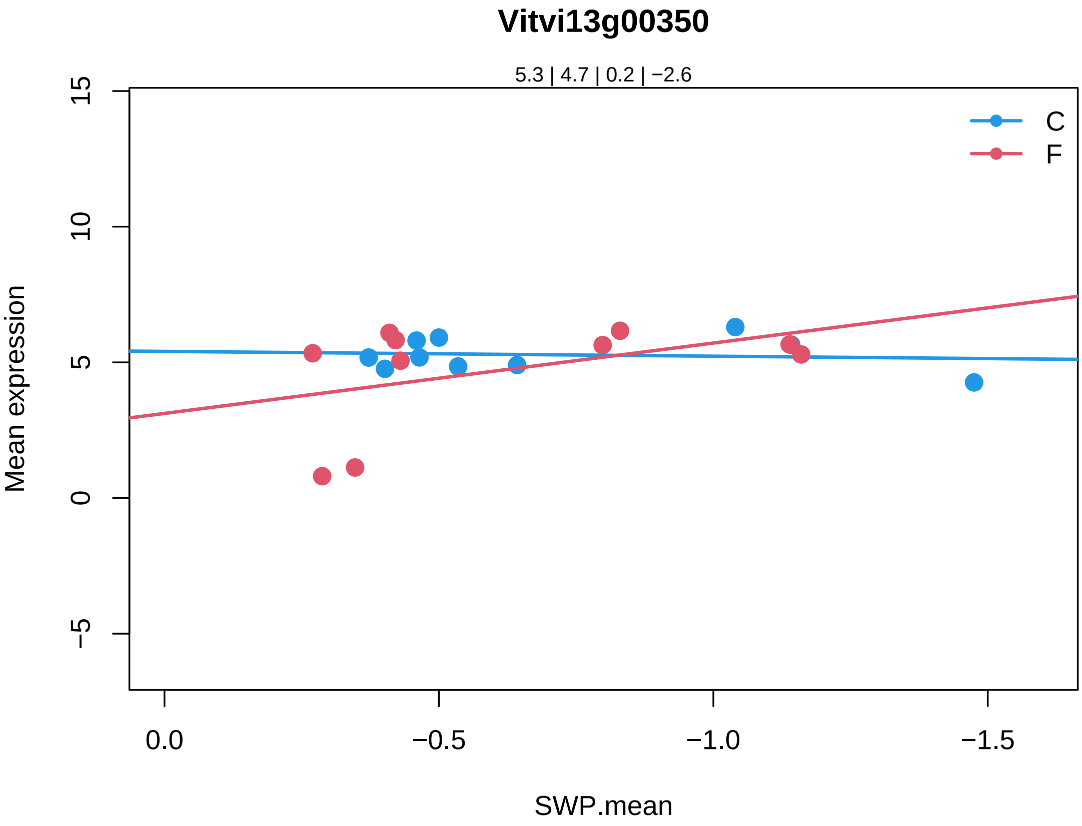
6.6.51 Vitvi13g00350

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

```
Vitvi13g00350
        31.2
        cell.division
        Regulator of chromosome condensation (RCC1) family protein |
        Chr3:20612766-20615730 FORWARD LENGTH=488 |
        201606
```

Coefficients for Vitvi13g00350.

```
                    swp  varietyF swp.varietyF  AveExpr       F
Vitvi13g00350 0.1761415 -2.285294    -2.769591 4.989153 1.89066
                P.Value adj.P.Val  type
Vitvi13g00350 0.1614666 0.4811483 type5
```



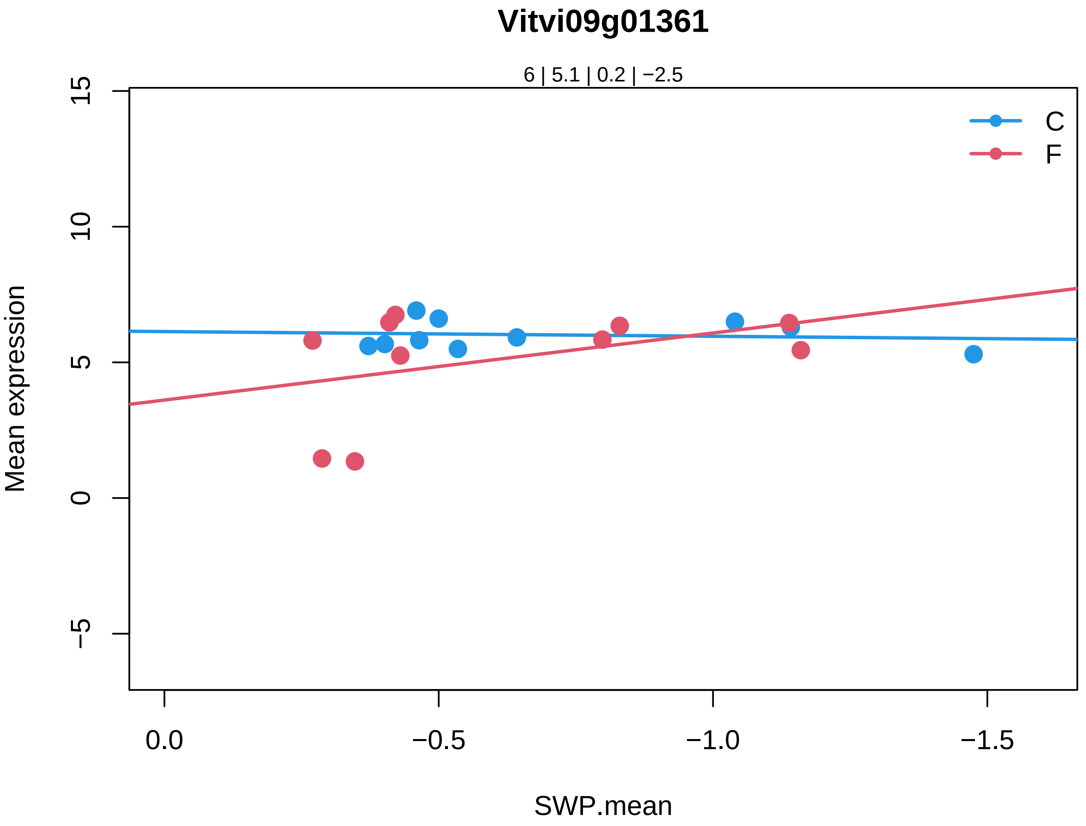
6.6.52 Vitvi09g01361

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

```
Vitvi09g01361
        35.2
        not assigned.unknown
        B-box 32 |
        Chr3:7412713-7413390 REVERSE LENGTH=225 |
        201606
```

Coefficients for Vitvi09g01361.

```
                   swp  varietyF swp.varietyF  AveExpr        F
Vitvi09g01361 0.172968 -2.523182    -2.644642 5.564115 2.226797
                P.Value adj.P.Val  type
Vitvi09g01361 0.1142989 0.3997577 type5
```



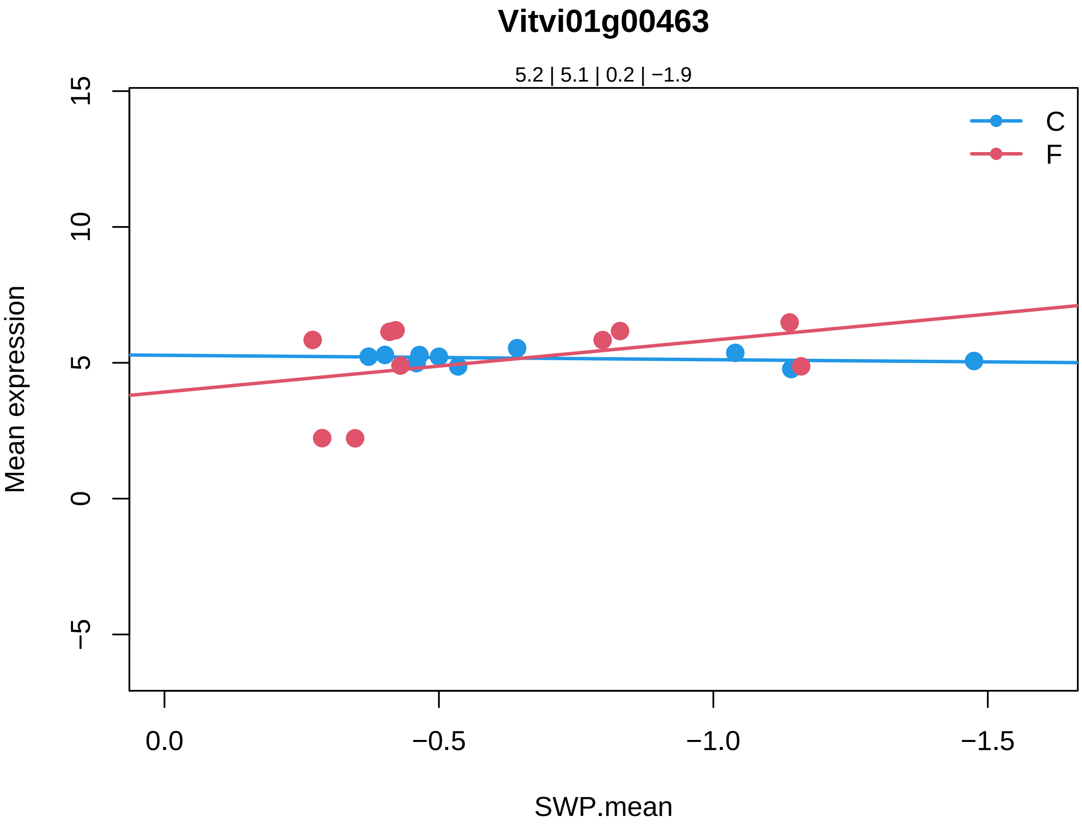
6.6.53 Vitvi01g00463

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

```
Vitvi01g00463
        35.1
        not assigned.no ontology
        PLANT CADMIUM RESISTANCE 2 |
        Chr1:5128591-5129458 REVERSE LENGTH=152 |
        201606
```

Coefficients for Vitvi01g00463.

```
                    swp   varietyF swp.varietyF  AveExpr        F
Vitvi01g00463 0.1617388 -1.351285    -2.072604 5.125111 1.344337
               P.Value adj.P.Val  type
Vitvi01g00463 0.286367  0.638851 type5
```



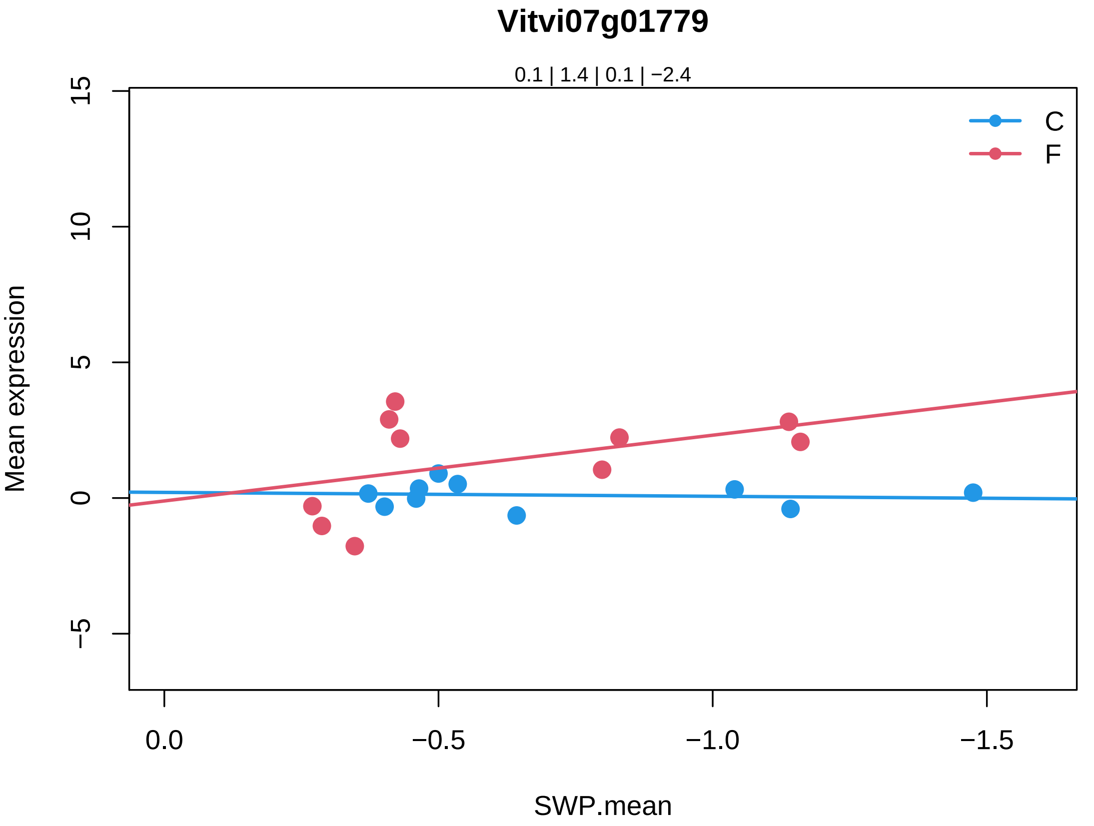
6.6.54 Vitvi07g01779

```
> 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.

```
                    swp   varietyF swp.varietyF   AveExpr        F
Vitvi07g01779 0.1430805 -0.3142242    -2.565898 0.7374675 3.827365
                 P.Value adj.P.Val  type
Vitvi07g01779 0.02443924 0.1549513 type5
```



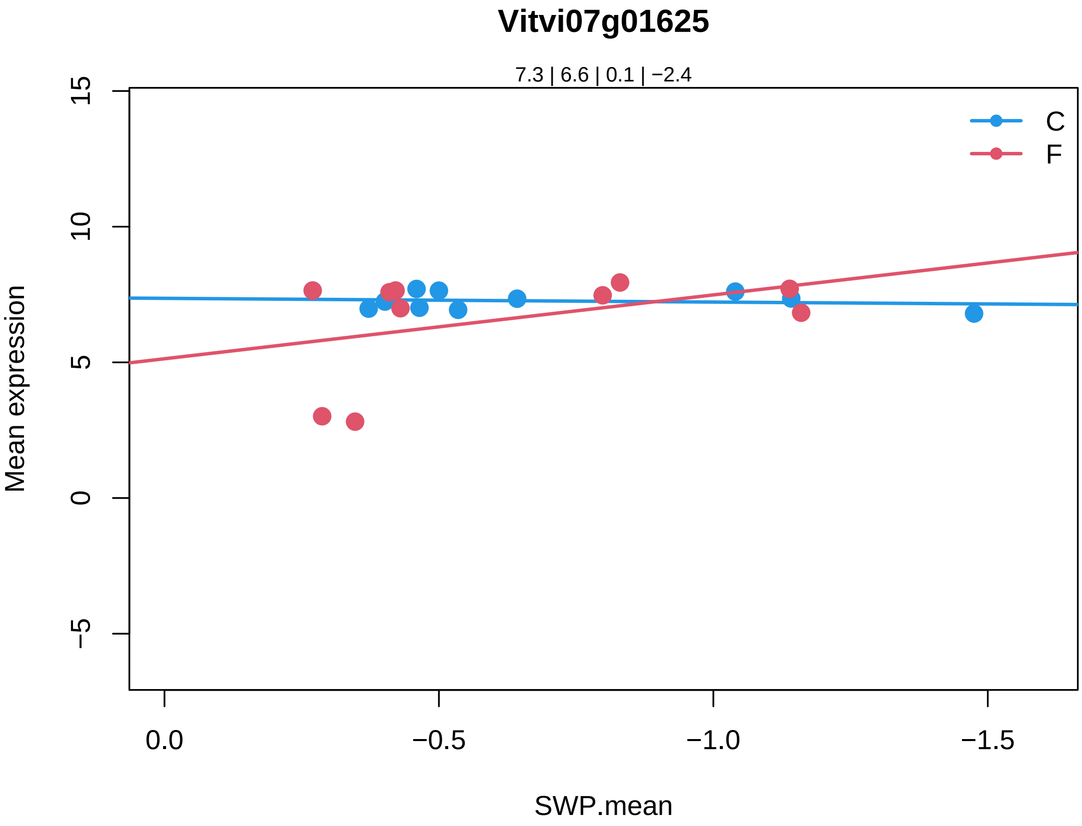
6.6.55 Vitvi07g01625

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

```
Vitvi07g01625
        35.2
        not assigned.unknown
        DUF1230 family protein (DUF1230) |
        Chr5:26877667-26879465 REVERSE LENGTH=327 |
        201606
```

Coefficients for Vitvi07g01625.

```
                    swp  varietyF swp.varietyF  AveExpr        F
Vitvi07g01625 0.1377329 -2.227412    -2.491219 6.913792 1.942646
                P.Value adj.P.Val  type
Vitvi07g01625 0.1530013 0.4682644 type5
```



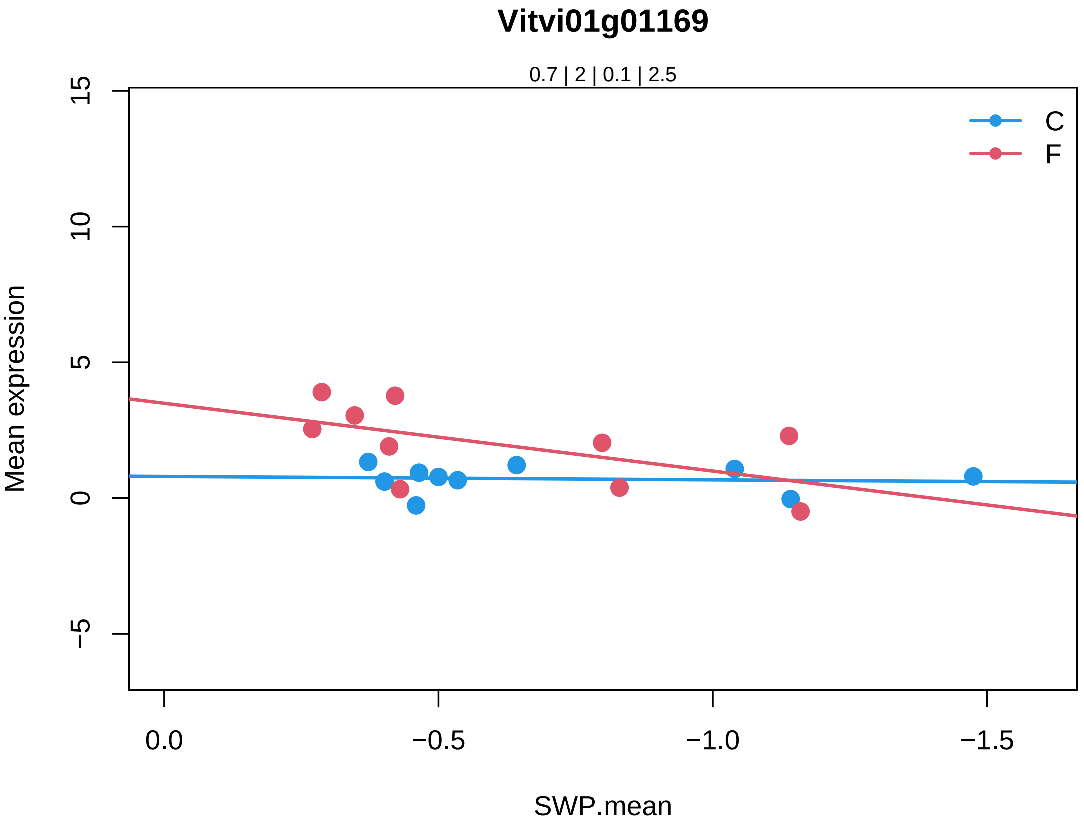
6.6.56 Vitvi01g01169

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

```
Vitvi01g01169
        28.2
        DNA.repair
        DNA glycosylase superfamily protein |
        Chr5:18024461-18025893 REVERSE LENGTH=353 |
        201606
```

Coefficients for Vitvi01g01169.

```
                    swp varietyF swp.varietyF AveExpr        F
Vitvi01g01169 0.1261609 2.694352     2.370177 1.33957 6.187421
                  P.Value  adj.P.Val  type
Vitvi01g01169 0.003403582 0.03845618 type5
```



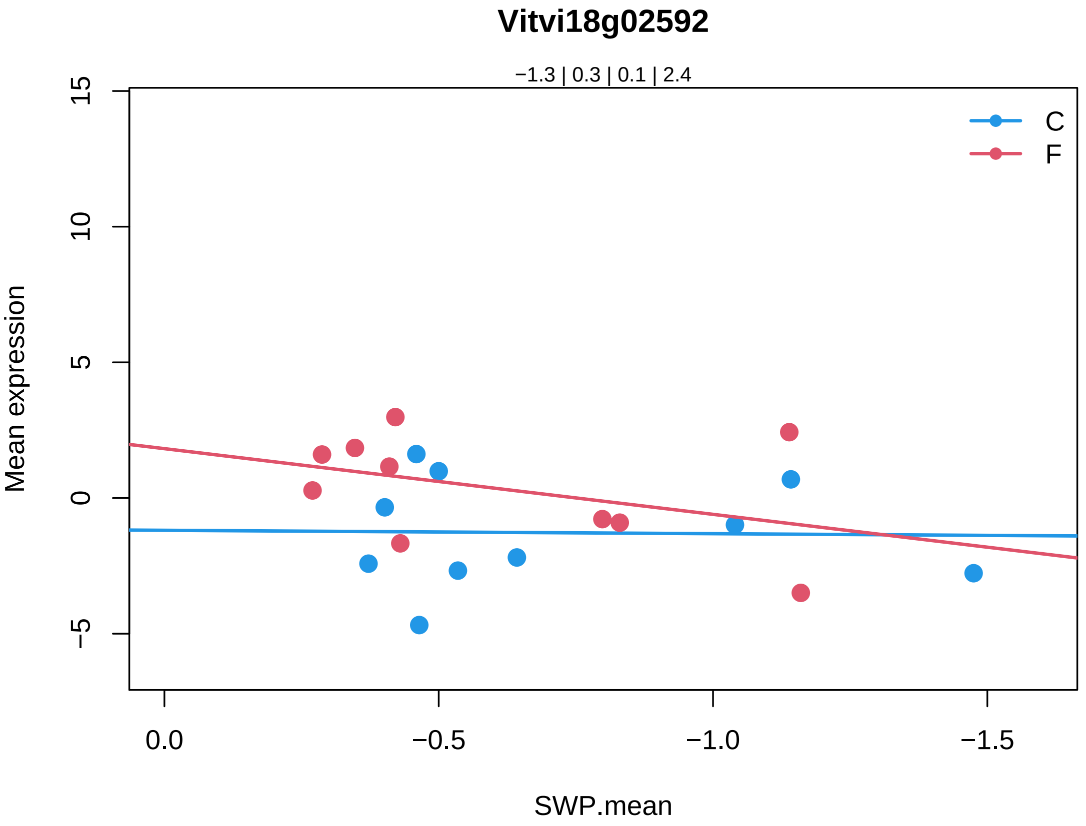
6.6.57 Vitvi18g02592

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

```
Vitvi18g02592
        26.12
        misc.peroxidases
        Peroxidase superfamily protein |
        Chr5:1579142-1580819 REVERSE LENGTH=324 |
        201606
```

Coefficients for Vitvi18g02592.

```
                    swp varietyF swp.varietyF    AveExpr        F
Vitvi18g02592 0.1244362 3.009008     2.296027 -0.4664369 2.016866
                P.Value adj.P.Val  type
Vitvi18g02592 0.1417152 0.4508597 type5
```



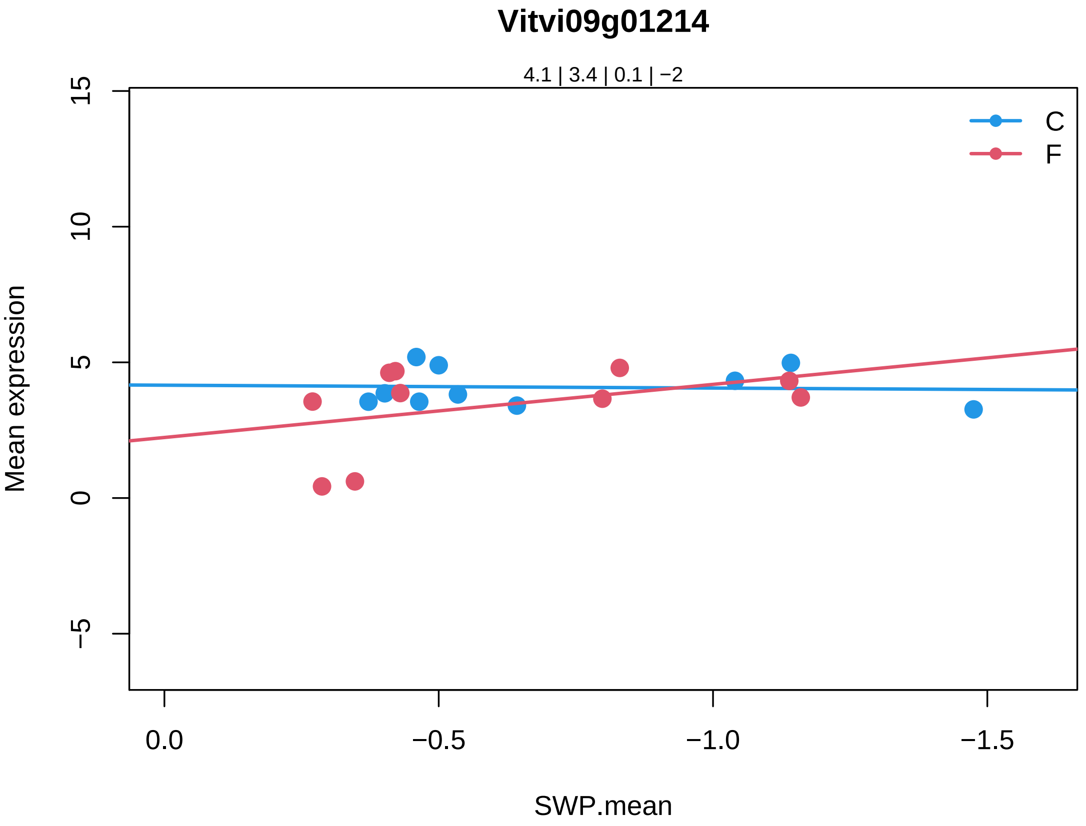
6.6.58 Vitvi09g01214

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

```
Vitvi09g01214
        30.2.12
        signalling.receptor kinases.leucine rich repeat XII
        Leucine-rich repeat protein kinase family protein |
        Chr3:17527611-17530748 FORWARD LENGTH=1010 |
        201606
```

Coefficients for Vitvi09g01214.

```
                   swp  varietyF swp.varietyF  AveExpr        F
Vitvi09g01214 0.105182 -1.926902    -2.062439 3.753418 1.815774
                P.Value adj.P.Val  type
Vitvi09g01214 0.1745338 0.5009039 type5
```



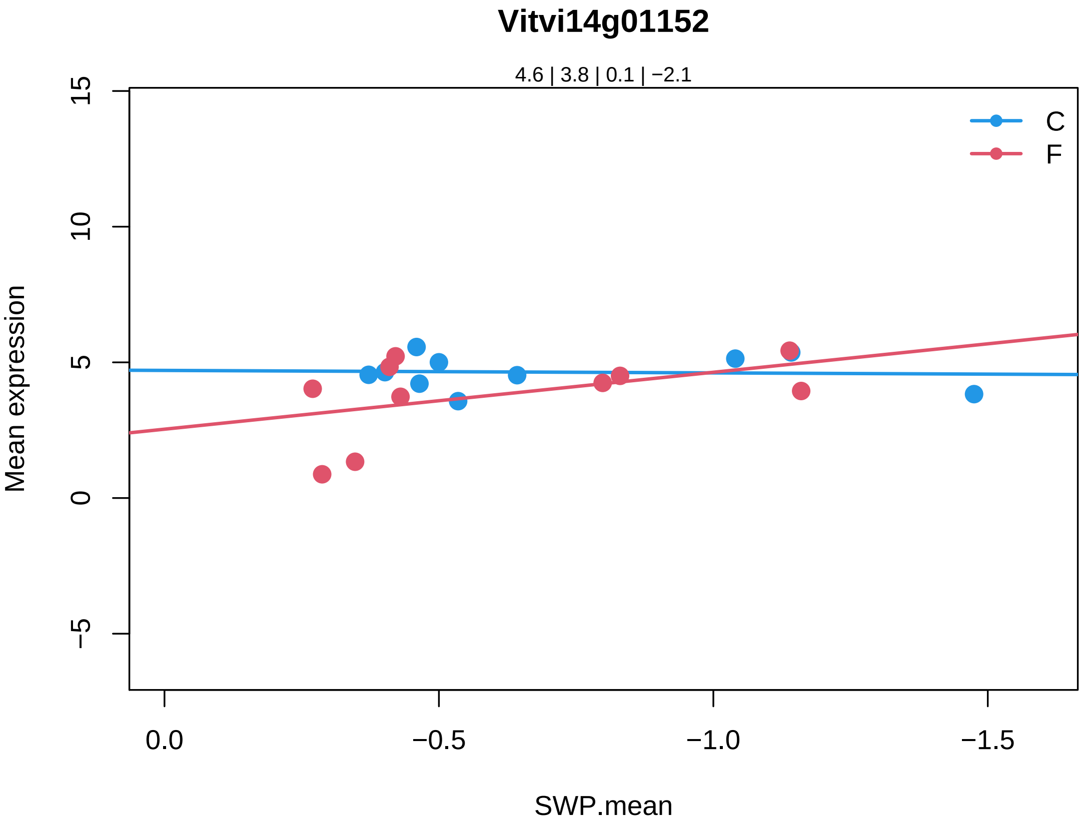
6.6.59 Vitvi14g01152

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

```
Vitvi14g01152
        17.3.1.2.6
        hormone metabolism.brassinosteroid.synthesis-degradation.sterols.DWF7
        sterol 1 |
        Chr3:547048-548615 FORWARD LENGTH=281 |
        201606
```

Coefficients for Vitvi14g01152.

```
                     swp  varietyF swp.varietyF  AveExpr        F
Vitvi14g01152 0.09131105 -2.166459    -2.189018 4.226734 2.684395
                 P.Value adj.P.Val  type
Vitvi14g01152 0.07223245 0.3034639 type5
```



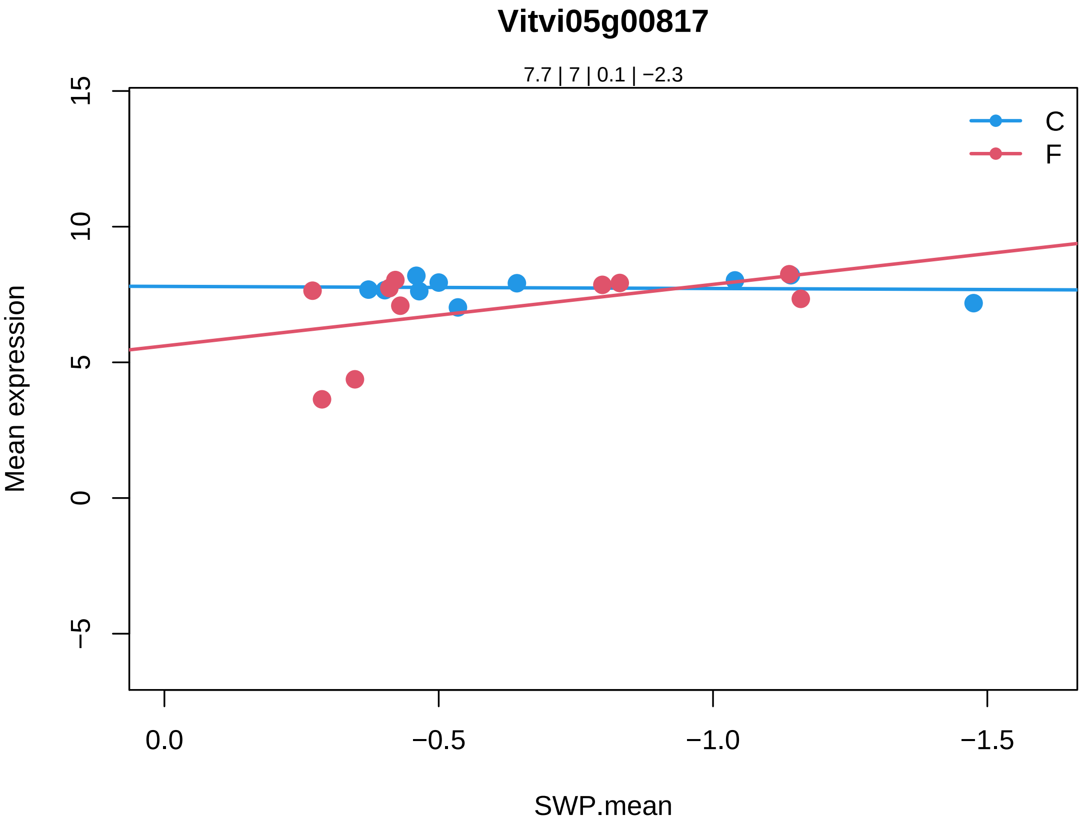
6.6.60 Vitvi05g00817

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

```
Vitvi05g00817
        1.01.1940
        PS.lightreaction.cyclic electron flow-chlororespiration
        proton gradient regulation 5 |
        Chr2:2081204-2081687 REVERSE LENGTH=133 |
        201606
```

Coefficients for Vitvi05g00817.

```
                     swp   varietyF swp.varietyF  AveExpr        F
Vitvi05g00817 0.07654634 -2.192199    -2.344279 7.365966 2.874032
                 P.Value adj.P.Val  type
Vitvi05g00817 0.05996961  0.272023 type5
```



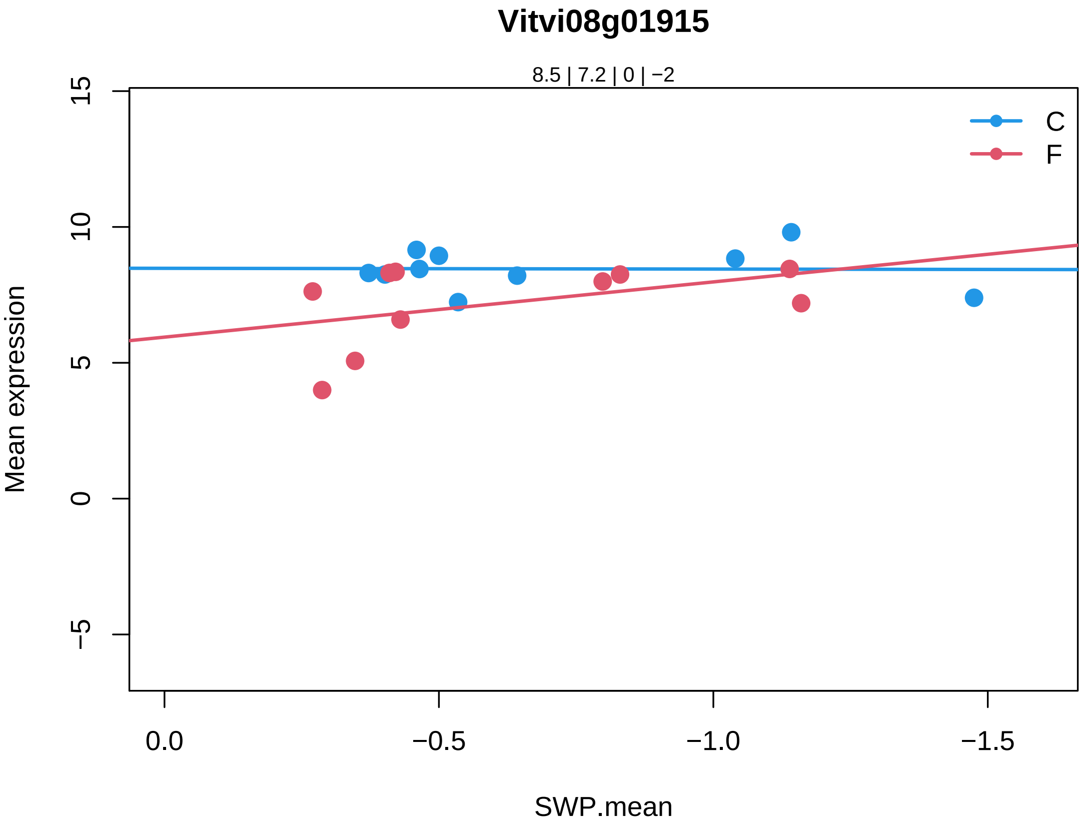
6.6.61 Vitvi08g01915

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

```
Vitvi08g01915
        19.1
        tetrapyrrole synthesis.magnesium chelatase
        magnesium-chelatase subunit chlH%2C chloroplast%2C putative / Mg-proto
        Chr5:4387567-4392082 REVERSE LENGTH=1381 |
        201606
```

Coefficients for Vitvi08g01915.

```
                     swp varietyF swp.varietyF  AveExpr        F
Vitvi08g01915 0.02775976  -2.5328    -2.060202 7.820197 3.799162
                 P.Value adj.P.Val  type
Vitvi08g01915 0.02507453 0.1578434 type5
```



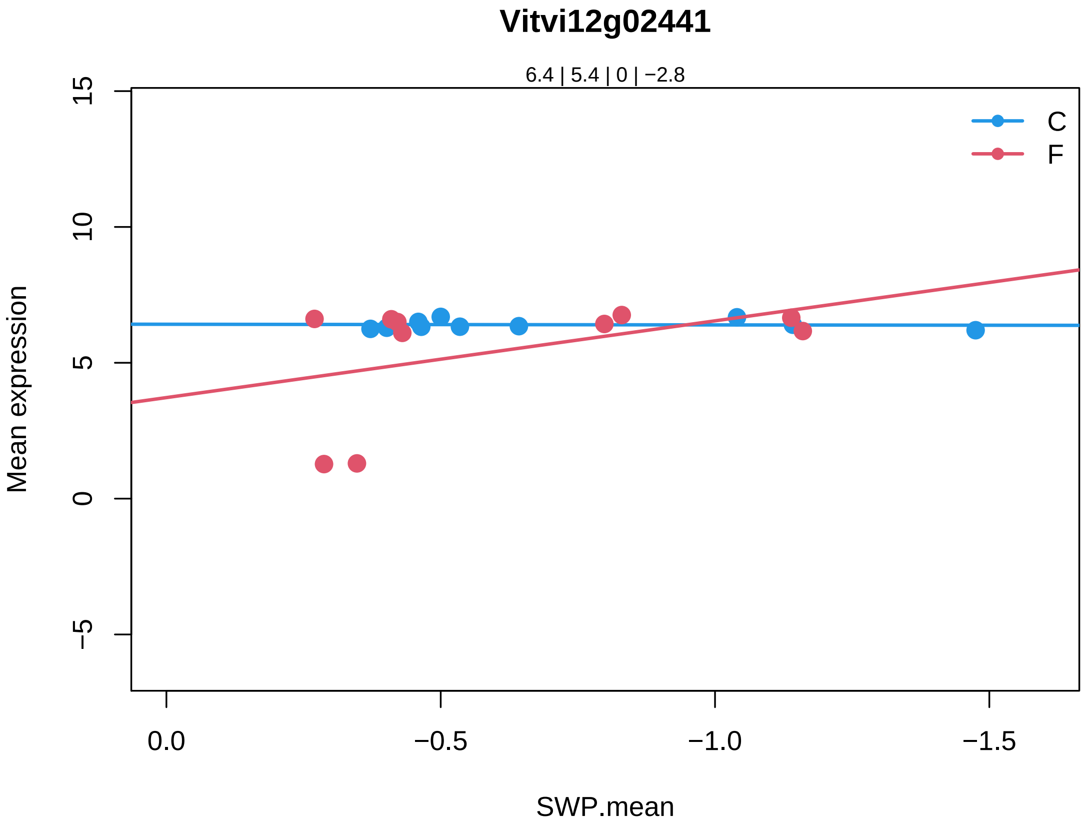
6.6.62 Vitvi12g02441

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

```
Vitvi12g02441
        27.03.2007
        RNA.regulation of transcription.C2C2(Zn) Constans-like zinc finger fam
        B-box type zinc finger family protein |
        Chr4:13675853-13676616 FORWARD LENGTH=223 |
        201606
```

Coefficients for Vitvi12g02441.

```
                     swp  varietyF swp.varietyF AveExpr        F
Vitvi12g02441 0.02401503 -2.699338    -2.848841 5.92039 2.555567
                 P.Value adj.P.Val  type
Vitvi12g02441 0.08207919 0.3295709 type5
```



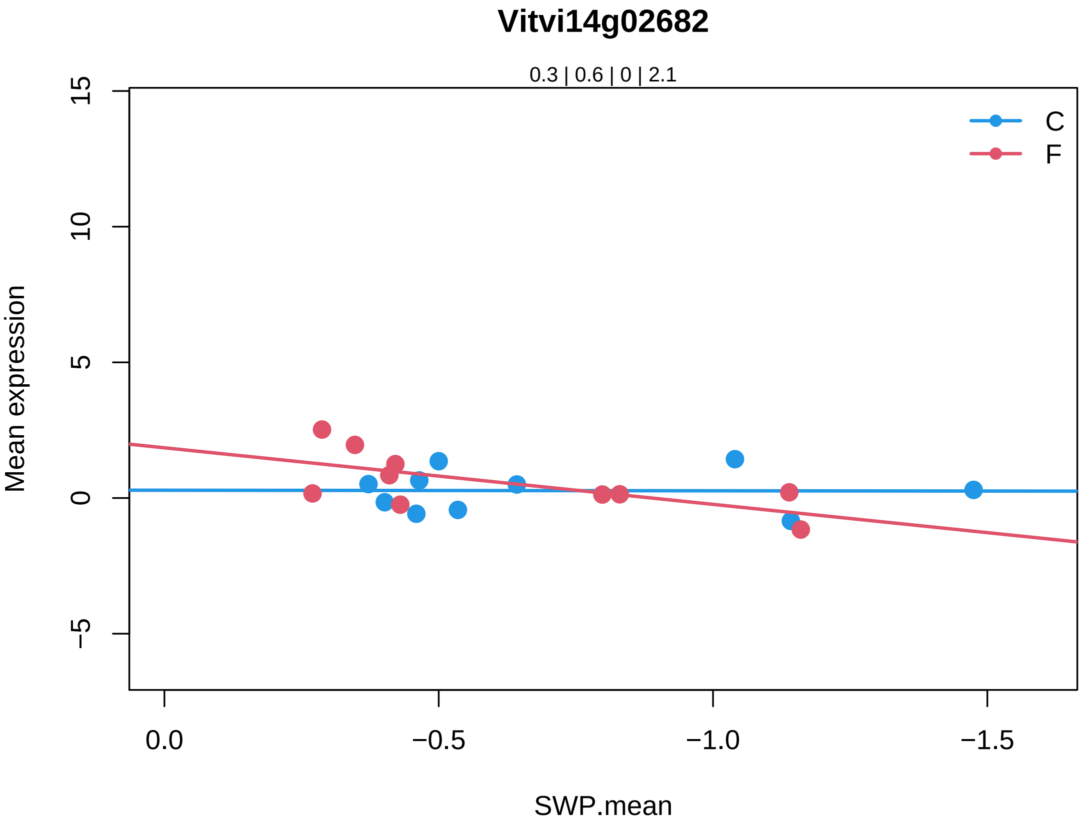
6.6.63 Vitvi14g02682

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

```
Vitvi14g02682
        31.1
        cell.organisation
        Ankyrin repeat family protein |
        Chr4:1554420-1556571 FORWARD LENGTH=629 |
        201606
```

Coefficients for Vitvi14g02682.

```
                     swp varietyF swp.varietyF   AveExpr        F
Vitvi14g02682 0.01968125  1.56393     2.064588 0.4270078 2.857357
                P.Value adj.P.Val  type
Vitvi14g02682 0.0609527 0.2749456 type5
```



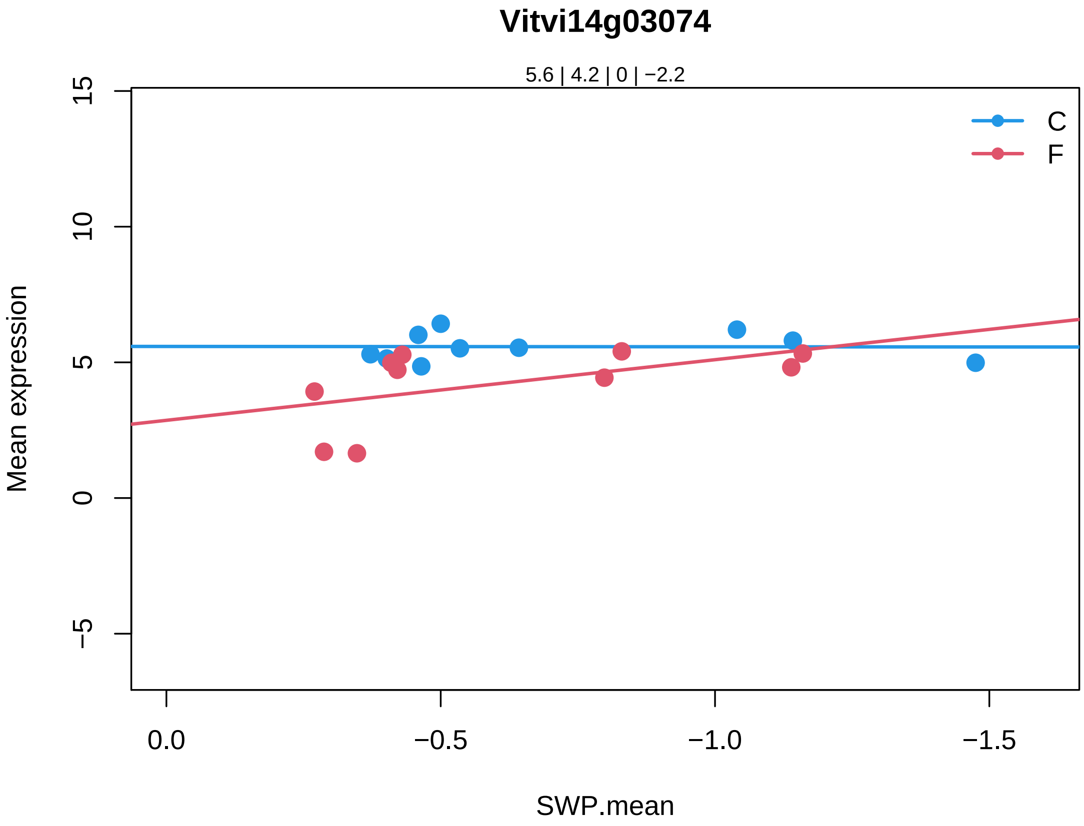
6.6.64 Vitvi14g03074

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

```
Vitvi14g03074
        35.2
        not assigned.unknown
        Leucine-rich repeat receptor-like protein kinase family protein |
        Chr4:5637467-5640496 REVERSE LENGTH=1009 |
        201606
```

Coefficients for Vitvi14g03074.

```
                     swp   varietyF swp.varietyF  AveExpr        F
Vitvi14g03074 0.01214811 -2.722047    -2.246425 4.901117 6.250515
                  P.Value  adj.P.Val  type
Vitvi14g03074 0.003242987 0.03719308 type5
```



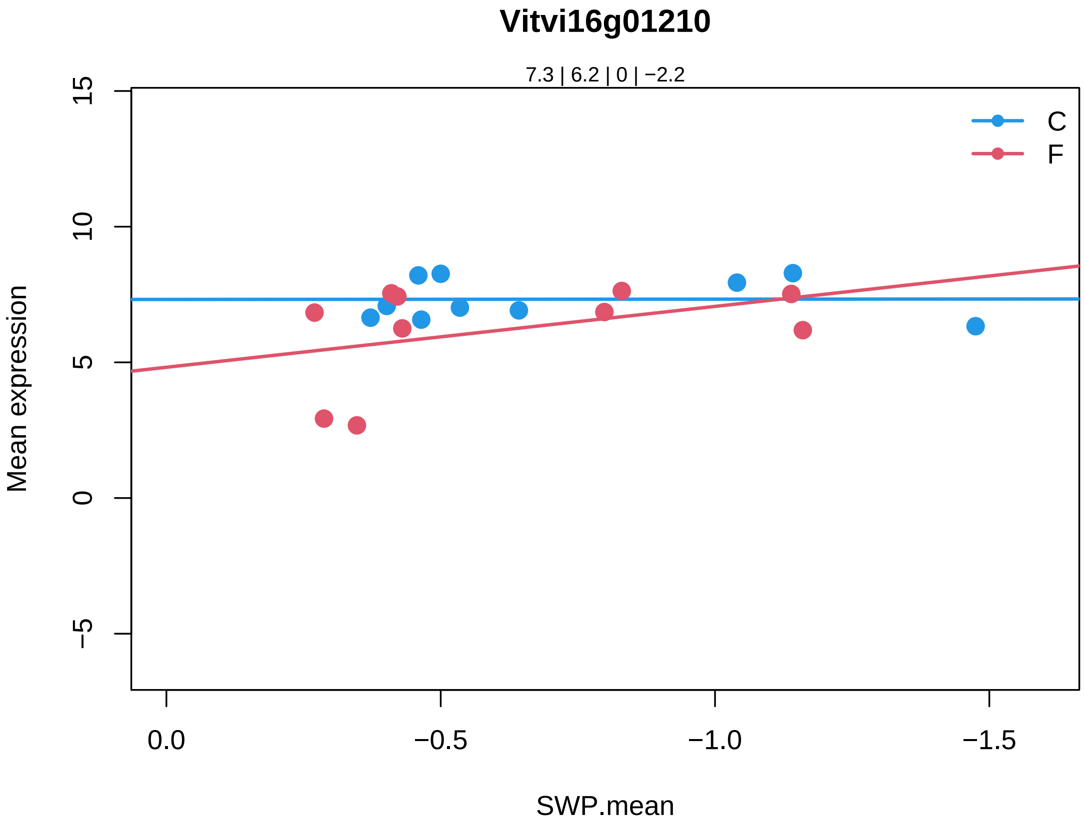
6.6.65 Vitvi16g01210

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

```
Vitvi16g01210
        34.16
        transport.ABC transporters and multidrug resistance systems
        multidrug resistance-associated protein 14 |
        Chr3:21863519-21868701 REVERSE LENGTH=1453 |
        201606
```

Coefficients for Vitvi16g01210.

```
                       swp  varietyF swp.varietyF  AveExpr        F
Vitvi16g01210 -0.009695296 -2.500408    -2.233358 6.755368 2.622358
                 P.Value adj.P.Val  type
Vitvi16g01210 0.07680642 0.3150821 type5
```



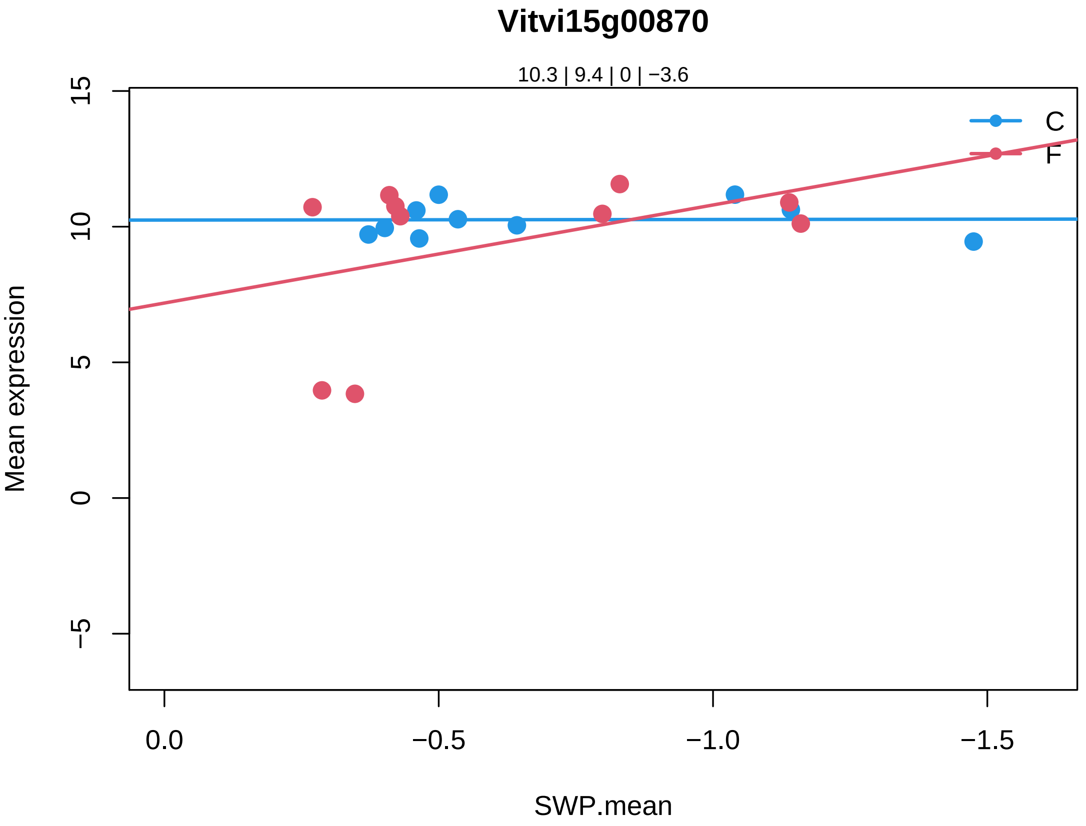
6.6.66 Vitvi15g00870

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

```
Vitvi15g00870
        35.2
        not assigned.unknown
        Homeodomain-like superfamily protein |
        Chr1:33992-37061 REVERSE LENGTH=645 |
        201606
```

Coefficients for Vitvi15g00870.

```
                      swp  varietyF swp.varietyF  AveExpr        F
Vitvi15g00870 -0.02089706 -3.058805    -3.592952 9.822828 1.870387
                P.Value adj.P.Val  type
Vitvi15g00870 0.1648997 0.4869045 type5
```



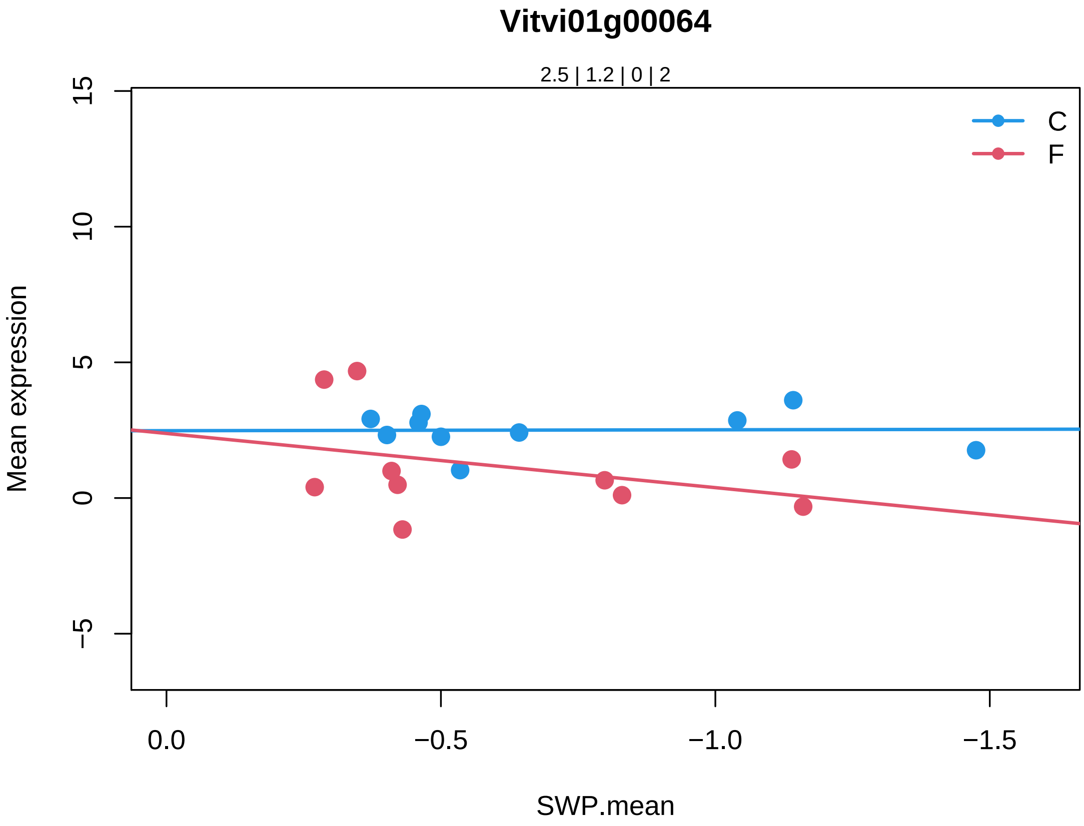
6.6.67 Vitvi01g00064

```
> 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.

```
                      swp   varietyF swp.varietyF  AveExpr        F
Vitvi01g00064 -0.03291293 -0.1013047     2.030061 1.833567 2.739461
                 P.Value adj.P.Val  type
Vitvi01g00064 0.06841623 0.2929214 type5
```



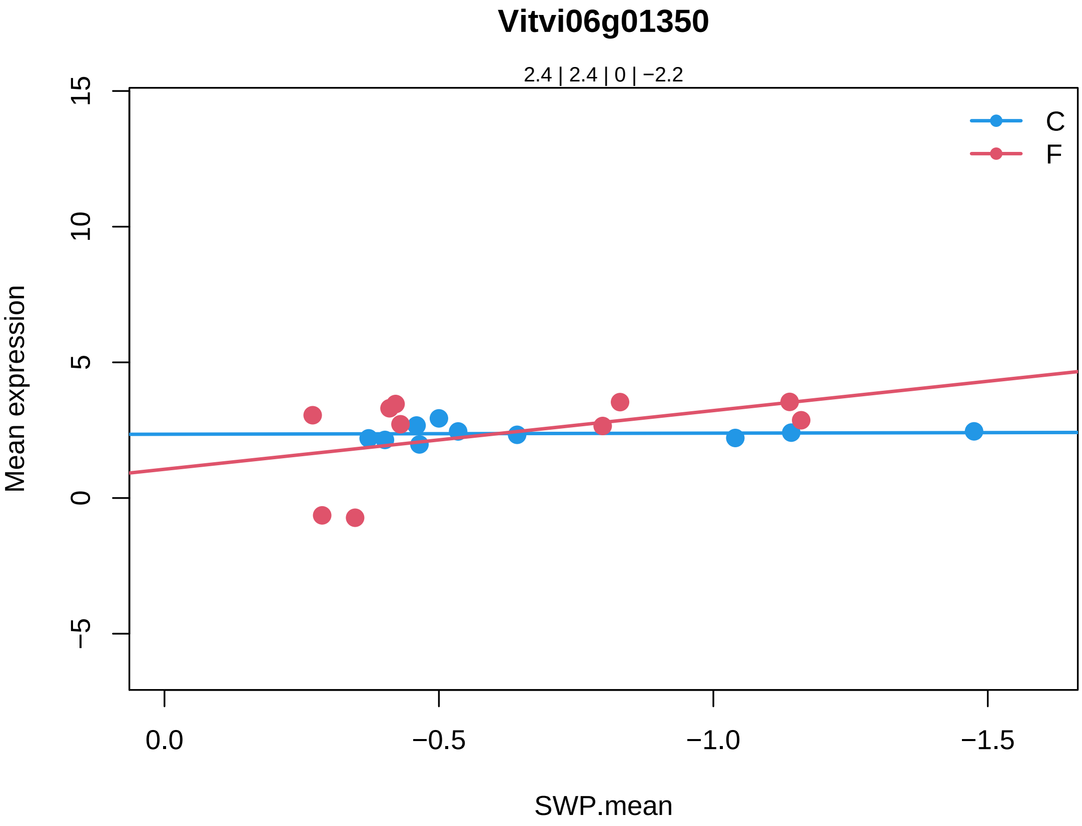
6.6.68 Vitvi06g01350

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

```
Vitvi06g01350
        27.03.2011
        RNA.regulation of transcription.C2H2 zinc finger family
        C2H2-type zinc finger family protein |
        Chr2:12024321-12025181 FORWARD LENGTH=286 |
        201606
```

Coefficients for Vitvi06g01350.

```
                      swp  varietyF swp.varietyF  AveExpr        F
Vitvi06g01350 -0.03982735 -1.290587    -2.122684 2.377978 1.661965
                P.Value adj.P.Val  type
Vitvi06g01350 0.2049551 0.5451877 type5
```



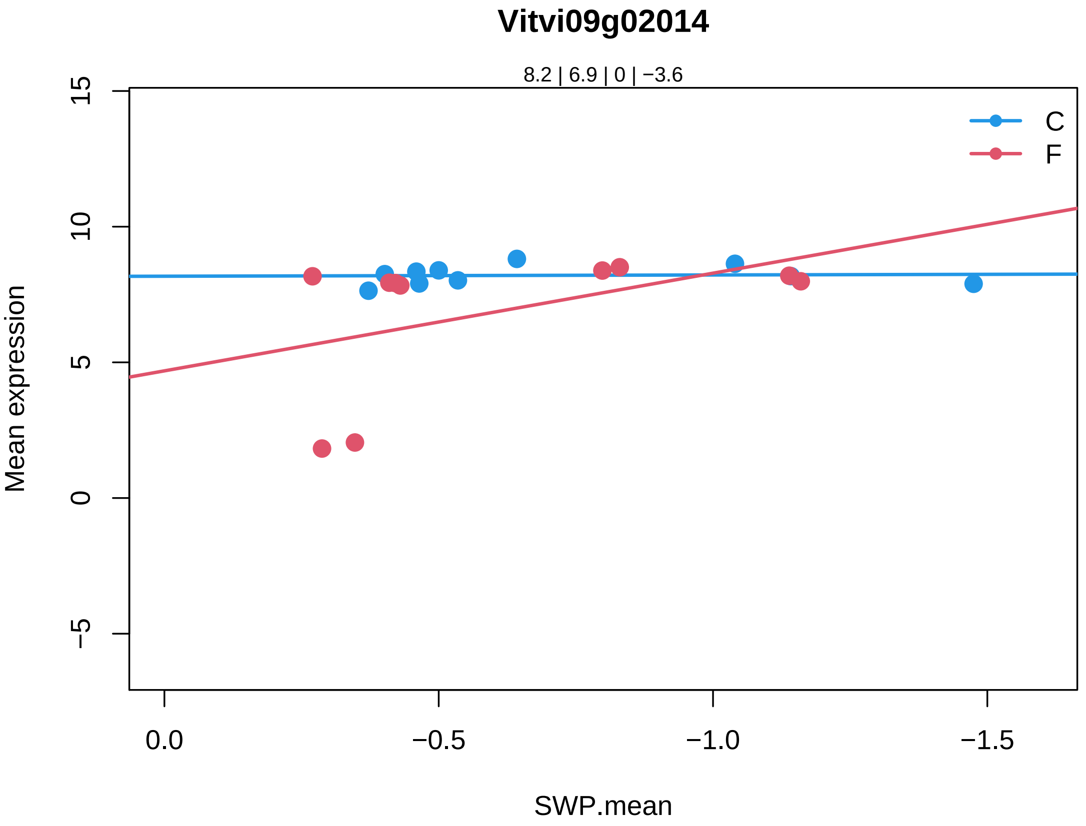
6.6.69 Vitvi09g02014

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

```
Vitvi09g02014
        35.2
        not assigned.unknown
        hypothetical protein |
        Chr1:5726617-5727312 REVERSE LENGTH=202 |
        201606
```

Coefficients for Vitvi09g02014.

```
                      swp  varietyF swp.varietyF  AveExpr        F
Vitvi09g02014 -0.04628244 -3.487672    -3.553714 7.543452 3.213061
                 P.Value adj.P.Val  type
Vitvi09g02014 0.04326834 0.2240136 type5
```



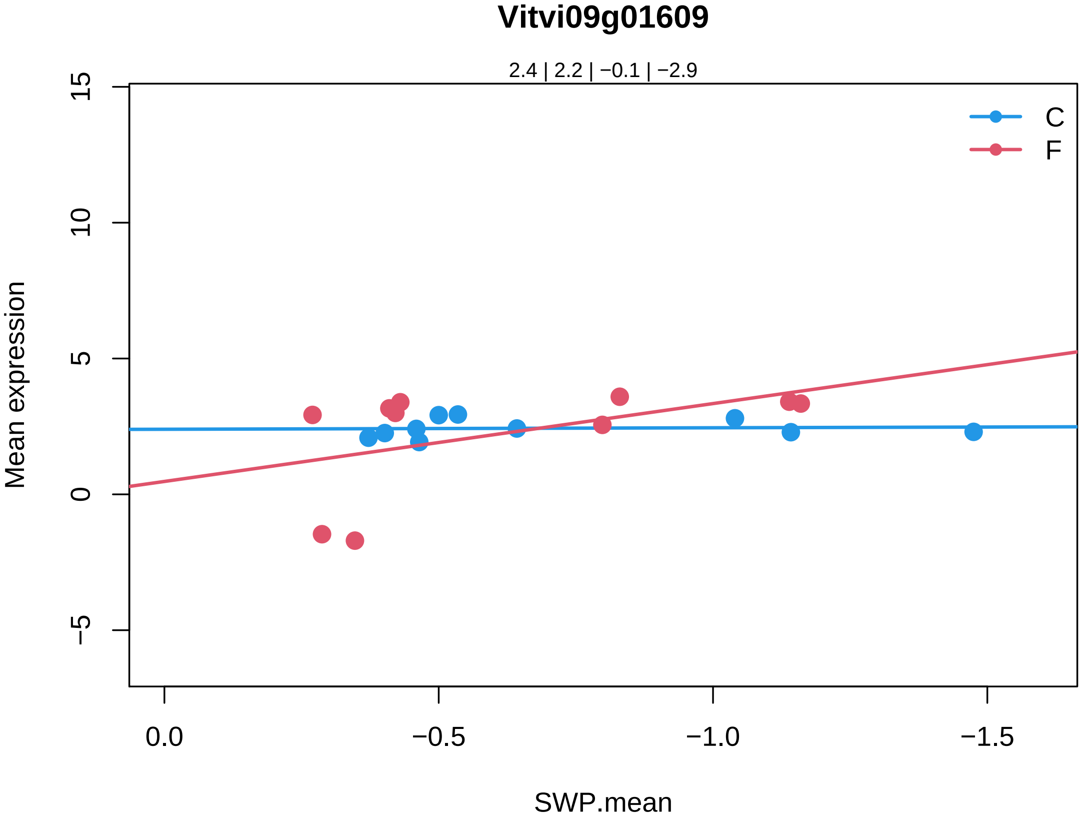
6.6.70 Vitvi09g01609

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

```
Vitvi09g01609
        35.2
        not assigned.unknown
        Unknown Protein
```

Coefficients for Vitvi09g01609.

```
                      swp  varietyF swp.varietyF  AveExpr        F
Vitvi09g01609 -0.05467525 -1.921055    -2.811312 2.327486 2.089076
                P.Value adj.P.Val  type
Vitvi09g01609 0.1315738 0.4324881 type5
```



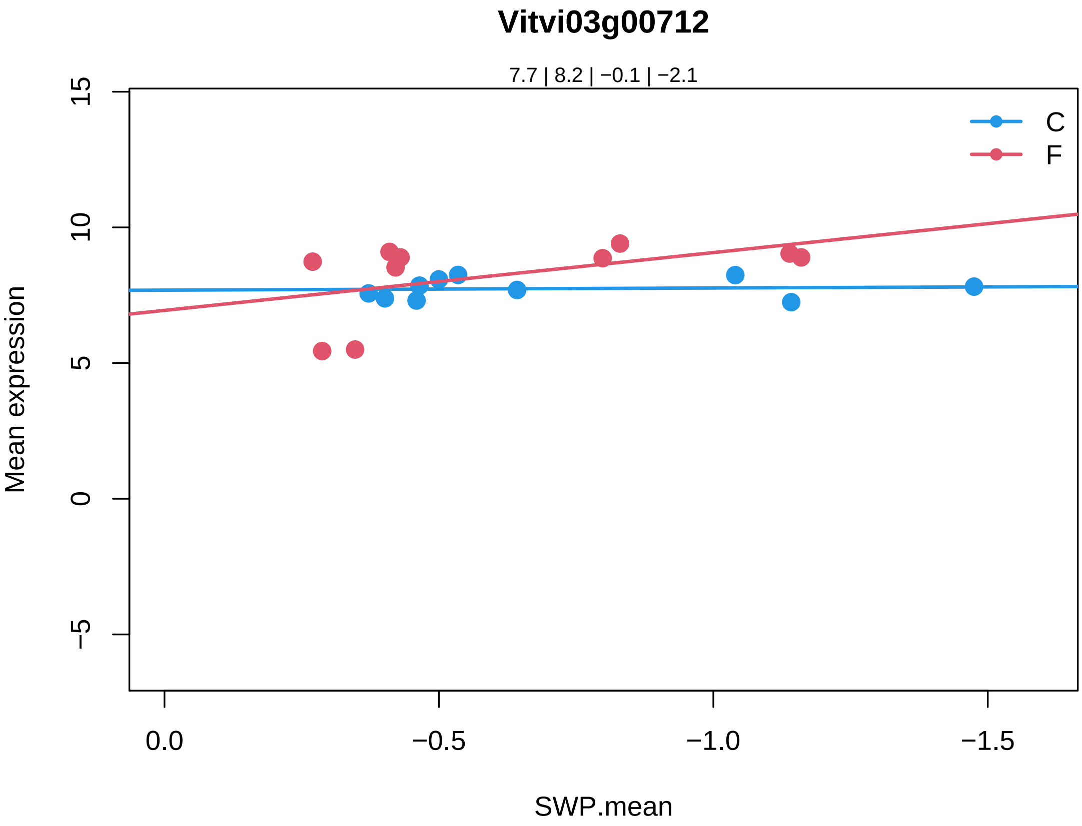
6.6.71 Vitvi03g00712

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

```
Vitvi03g00712
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi03g00712.

```
                      swp   varietyF swp.varietyF  AveExpr       F
Vitvi03g00712 -0.07900518 -0.7471964    -2.052156 7.992135 2.49924
                 P.Value adj.P.Val  type
Vitvi03g00712 0.08682643 0.3412045 type5
```



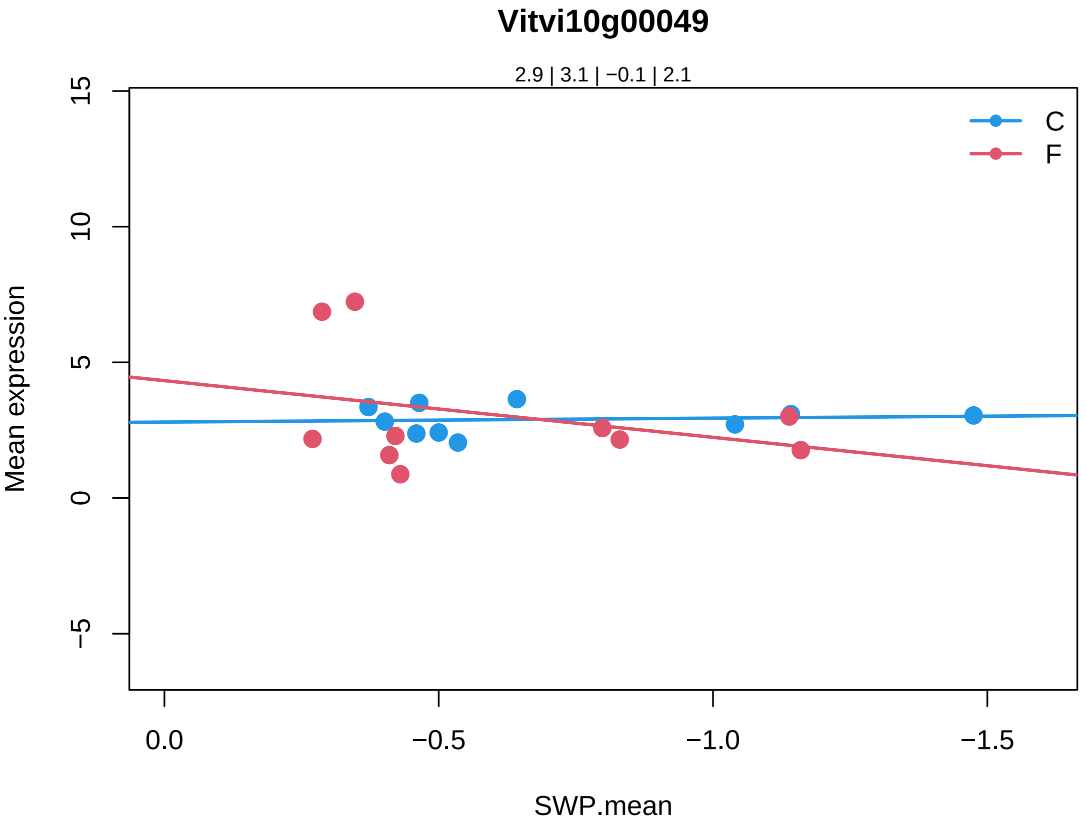
6.6.72 Vitvi10g00049

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

```
Vitvi10g00049
        35.2
        not assigned.unknown
        Chaperonin-like RbcX protein |
        Chr4:2116700-2118563 REVERSE LENGTH=174 |
        201606
```

Coefficients for Vitvi10g00049.

```
                     swp varietyF swp.varietyF  AveExpr         F
Vitvi10g00049 -0.1446943 1.526603     2.234213 2.976414 0.8126884
                P.Value adj.P.Val  type
Vitvi10g00049 0.5008449 0.8031629 type5
```



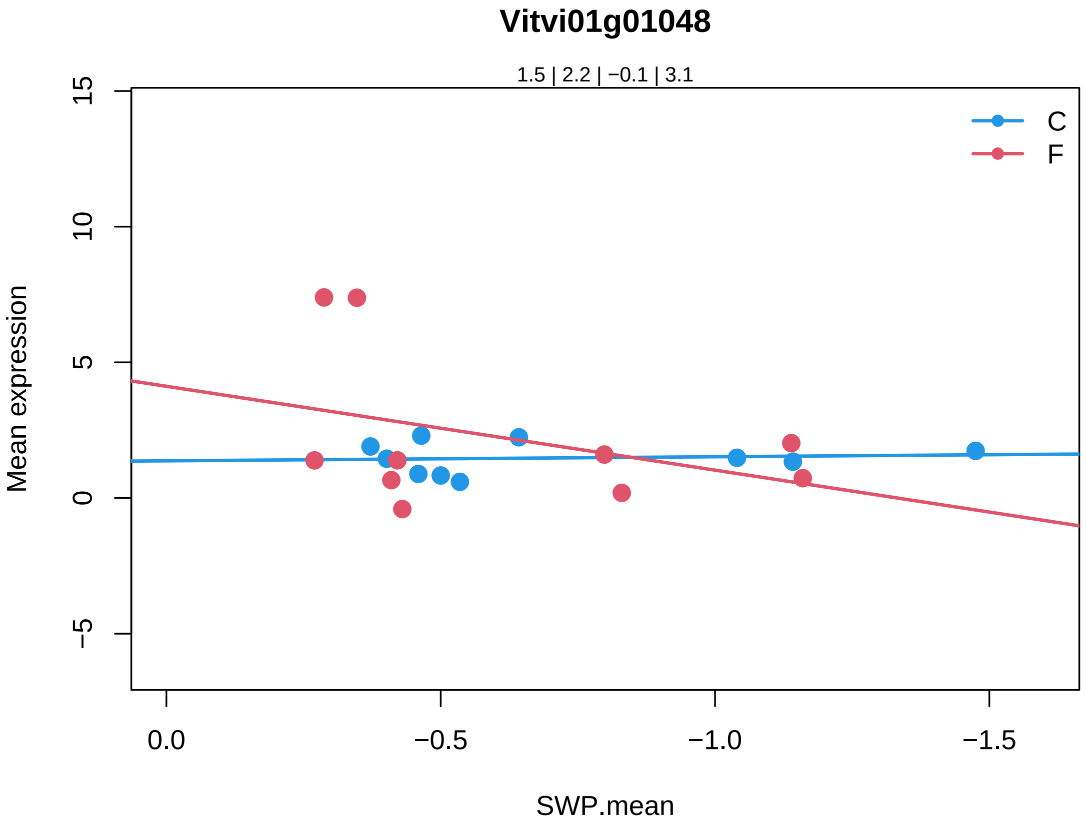
6.6.73 Vitvi01g01048

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

```
Vitvi01g01048
        35.2
        not assigned.unknown
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi01g01048.

```
                     swp varietyF swp.varietyF  AveExpr        F
Vitvi01g01048 -0.1494626 2.746796     3.239226 1.855502 1.435024
                P.Value adj.P.Val  type
Vitvi01g01048 0.2602156 0.6116913 type5
```



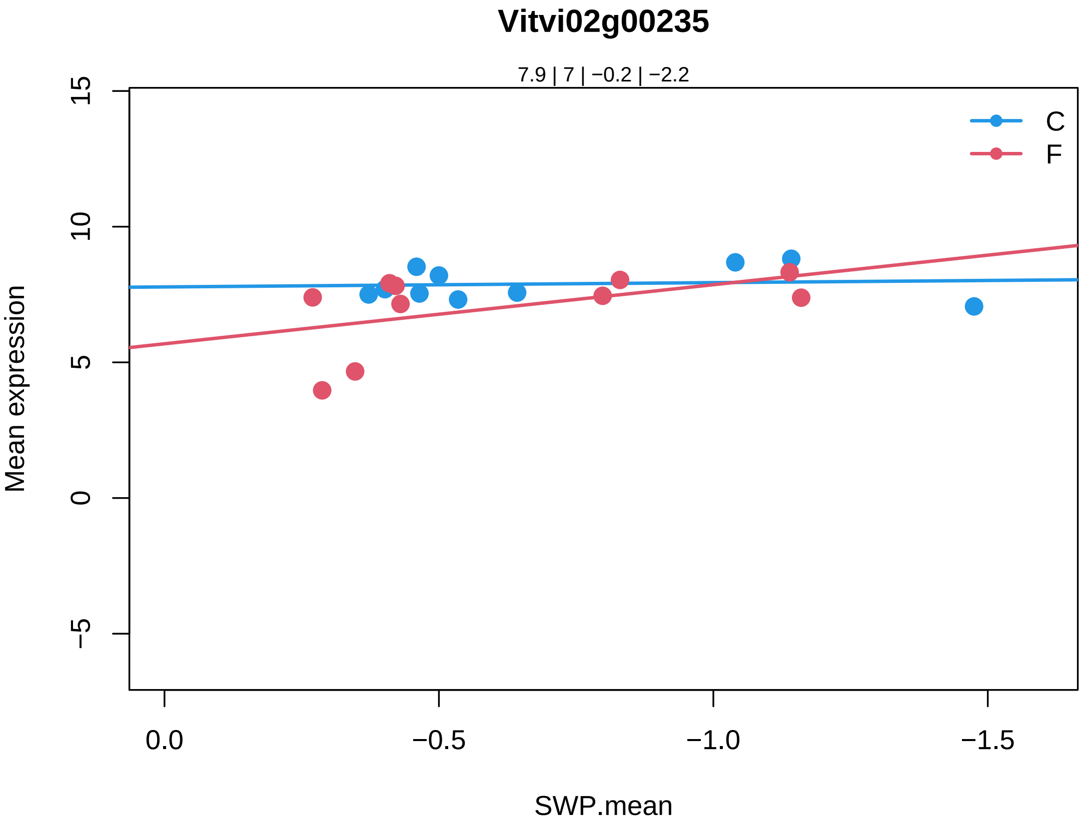
6.6.74 Vitvi02g00235

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

```
Vitvi02g00235
        35.2
        not assigned.unknown
        beta-carotene isomerase D27 |
        Chr1:24036071-24036768 FORWARD LENGTH=204 |
        201606
```

Coefficients for Vitvi02g00235.

```
                     swp  varietyF swp.varietyF  AveExpr        F
Vitvi02g00235 -0.1585789 -2.095305    -2.019059 7.450659 3.338132
                 P.Value adj.P.Val  type
Vitvi02g00235 0.03843683 0.2078971 type5
```



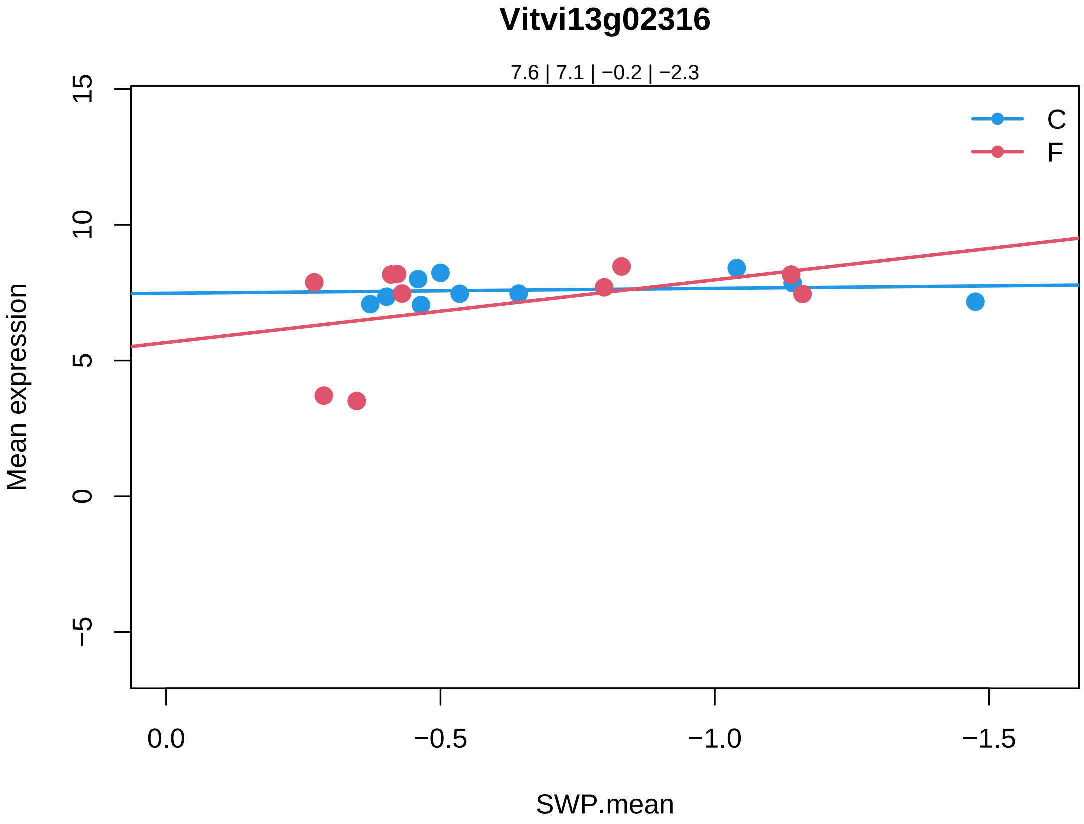
6.6.75 Vitvi13g02316

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

```
Vitvi13g02316
        35.2
        not assigned.unknown
        NA
```

Coefficients for Vitvi13g02316.

```
                      swp   varietyF swp.varietyF  AveExpr        F
Vitvi13g02316 -0.1815475 -1.815586    -2.128751 7.337323 1.784303
                P.Value adj.P.Val  type
Vitvi13g02316 0.1803511 0.5090576 type5
```



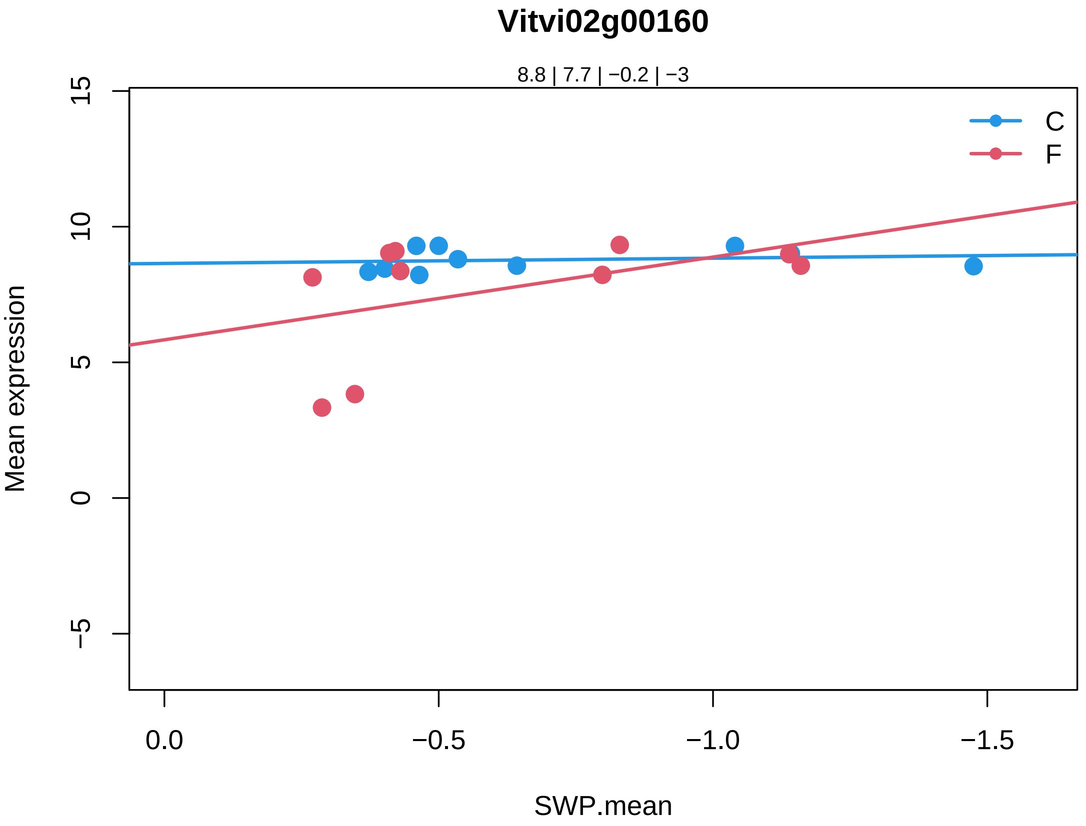
6.6.76 Vitvi02g00160

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

```
Vitvi02g00160
        21.4
        redox.glutaredoxins
        Glutaredoxin family protein |
        Chr1:23953270-23954376 FORWARD LENGTH=368 |
        201606
```

Coefficients for Vitvi02g00160.

```
                     swp  varietyF swp.varietyF  AveExpr        F
Vitvi02g00160 -0.1937055 -2.813748    -2.854744 8.234496 3.100127
                 P.Value adj.P.Val  type
Vitvi02g00160 0.04819558 0.2378345 type5
```



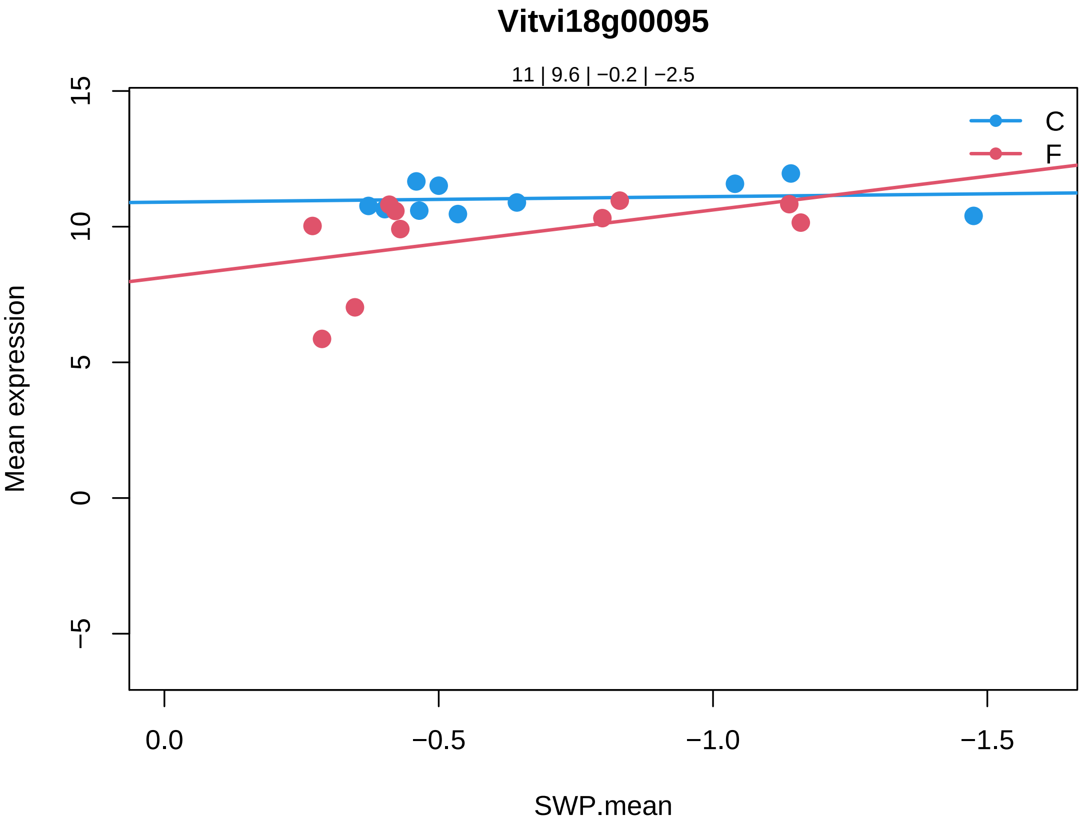
6.6.77 Vitvi18g00095

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

```
Vitvi18g00095
        21.6
        redox.dismutases and catalases
        catalase 2 |
        Chr4:16700937-16702955 REVERSE LENGTH=492 |
        201606
```

Coefficients for Vitvi18g00095.

```
                     swp  varietyF swp.varietyF  AveExpr        F
Vitvi18g00095 -0.2041556 -2.769709    -2.279565 10.34728 4.677199
                 P.Value  adj.P.Val  type
Vitvi18g00095 0.01155861 0.09229037 type5
```



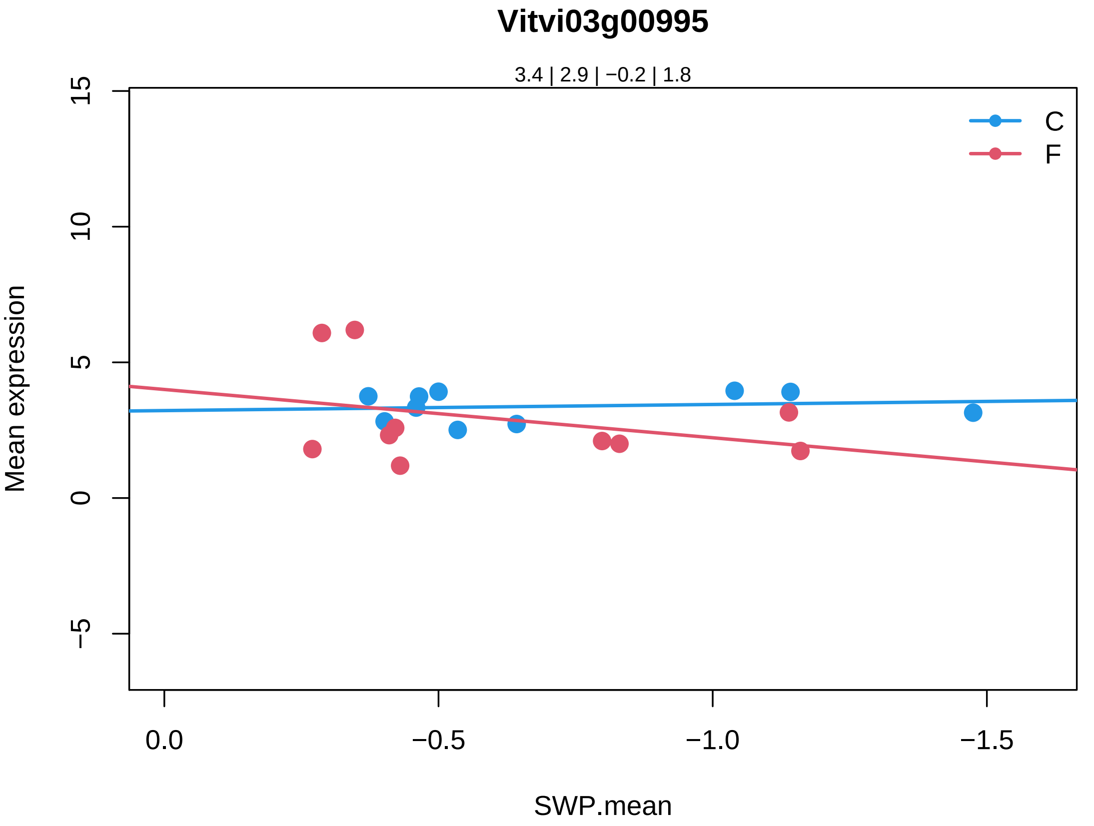
6.6.78 Vitvi03g00995

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

```
Vitvi03g00995
        35.2
        not assigned.unknown
        nicotinamidase 1 |
        Chr2:9589604-9590846 REVERSE LENGTH=244 |
        201606
```

Coefficients for Vitvi03g00995.

```
                     swp  varietyF swp.varietyF  AveExpr        F
Vitvi03g00995 -0.2252086 0.7777521      2.00419 3.148647 1.111318
                P.Value adj.P.Val  type
Vitvi03g00995 0.3663157 0.7105349 type5
```



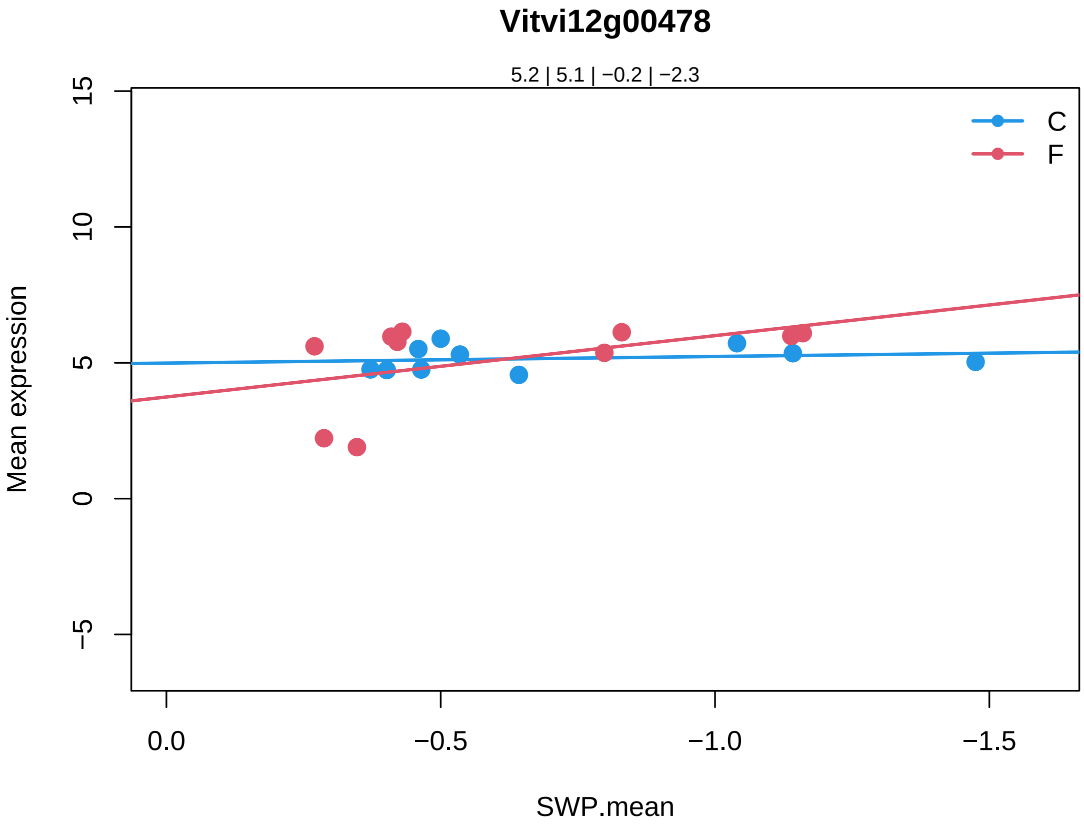
6.6.79 Vitvi12g00478

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

```
Vitvi12g00478
        35.1
        not assigned.no ontology
        Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein |
        Chr4:1501907-1503503 FORWARD LENGTH=361 |
        201606
```

Coefficients for Vitvi12g00478.

```
                     swp  varietyF swp.varietyF  AveExpr        F
Vitvi12g00478 -0.2434733 -1.247249    -2.014384 5.138625 1.813236
                P.Value adj.P.Val  type
Vitvi12g00478 0.1749956 0.5015576 type5
```



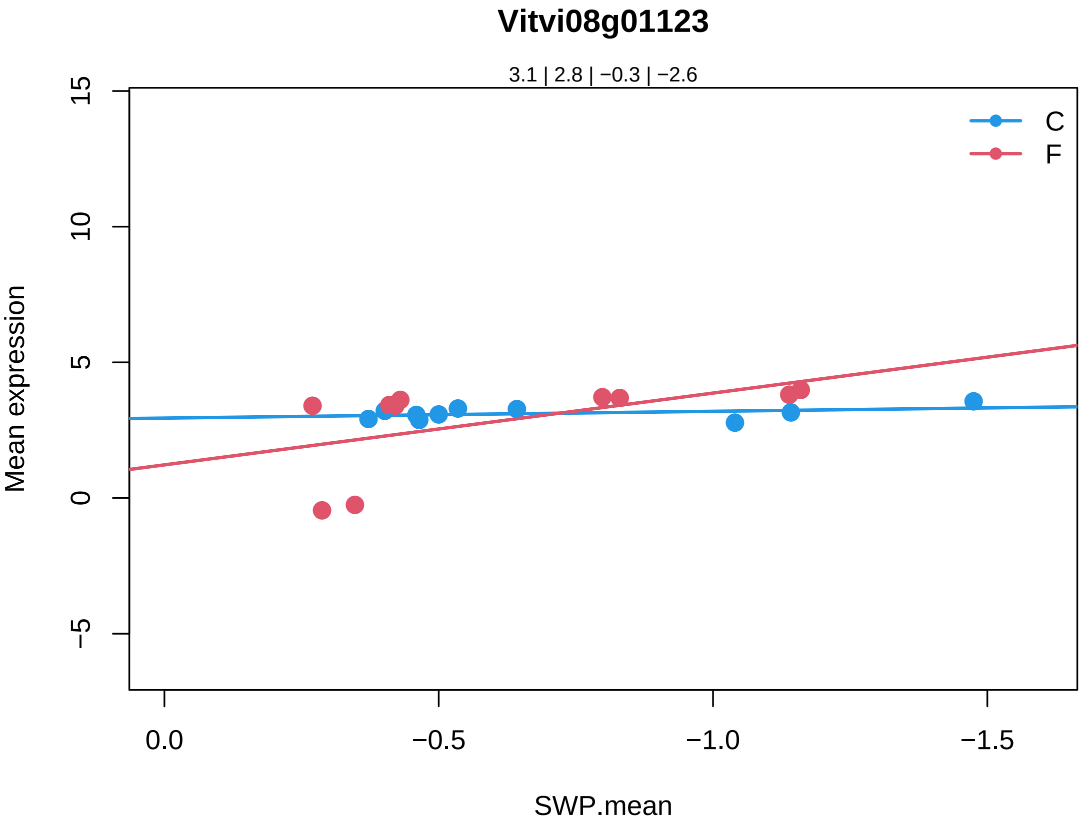
6.6.80 Vitvi08g01123

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

```
Vitvi08g01123
        35.1.5
        not assigned.no ontology.pentatricopeptide (PPR) repeat-containing pro
        RING/U-box superfamily protein |
        Chr5:620101-620952 FORWARD LENGTH=283 |
        201606
```

Coefficients for Vitvi08g01123.

```
                     swp   varietyF swp.varietyF  AveExpr        F
Vitvi08g01123 -0.2506405 -1.723866    -2.395258 2.977528 2.836692
                 P.Value adj.P.Val  type
Vitvi08g01123 0.06219509 0.2775922 type5
```



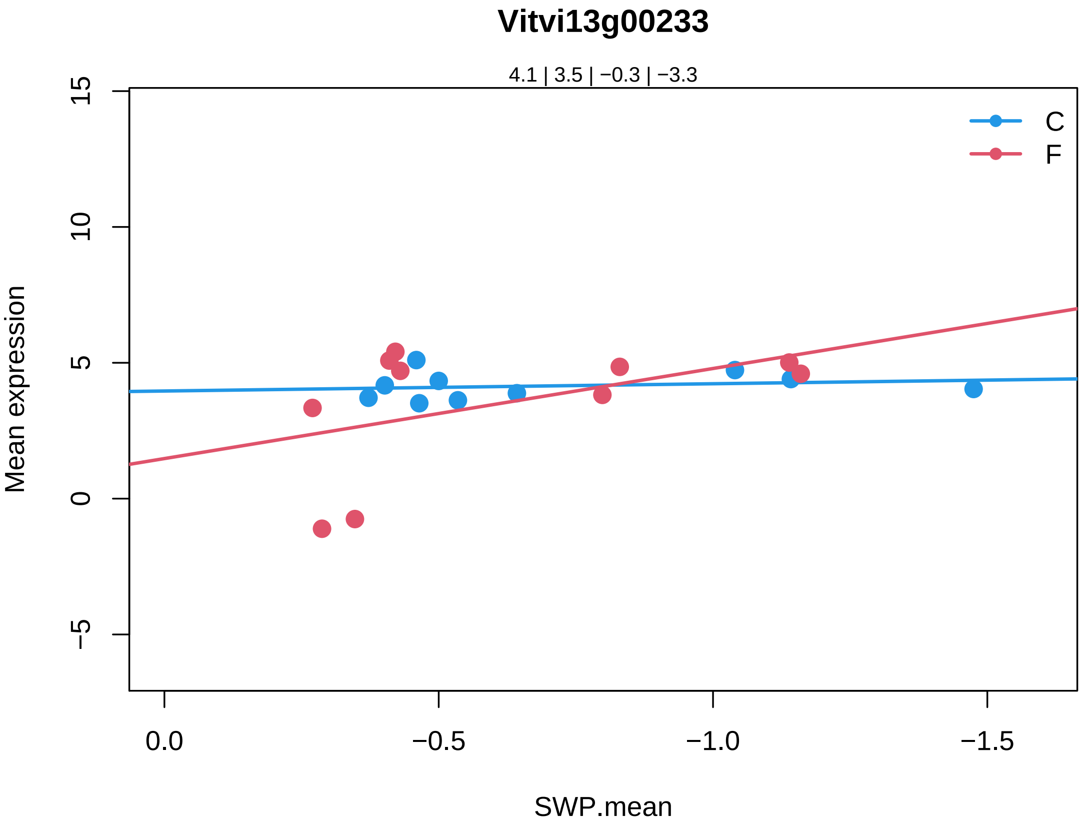
6.6.81 Vitvi13g00233

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

```
Vitvi13g00233
        35.2
        not assigned.unknown
        exocyst subunit exo70 family protein H2 |
        Chr2:16447096-16449009 REVERSE LENGTH=637 |
        201606
```

Coefficients for Vitvi13g00233.

```
                     swp varietyF swp.varietyF  AveExpr        F
Vitvi13g00233 -0.2676308 -2.48726    -3.048163 3.821838 2.253904
                P.Value adj.P.Val  type
Vitvi13g00233 0.1111911 0.3944461 type5
```



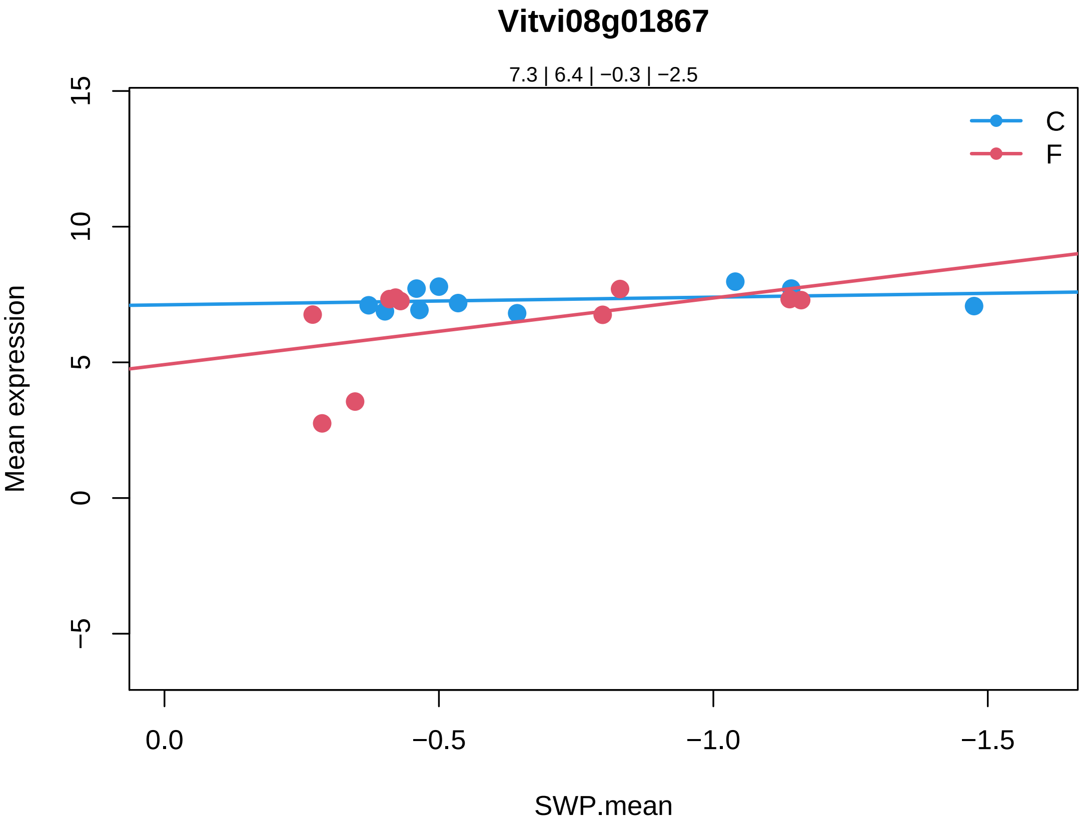
6.6.82 Vitvi08g01867

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

```
Vitvi08g01867
        29.5
        protein.degradation
        Peptidase S41 family protein |
        Chr3:21381664-21383629 FORWARD LENGTH=370 |
        201606
```

Coefficients for Vitvi08g01867.

```
                     swp  varietyF swp.varietyF  AveExpr        F
Vitvi08g01867 -0.2826572 -2.204034    -2.173633 6.865112 3.152423
                 P.Value adj.P.Val  type
Vitvi08g01867 0.04584275 0.2315994 type5
```



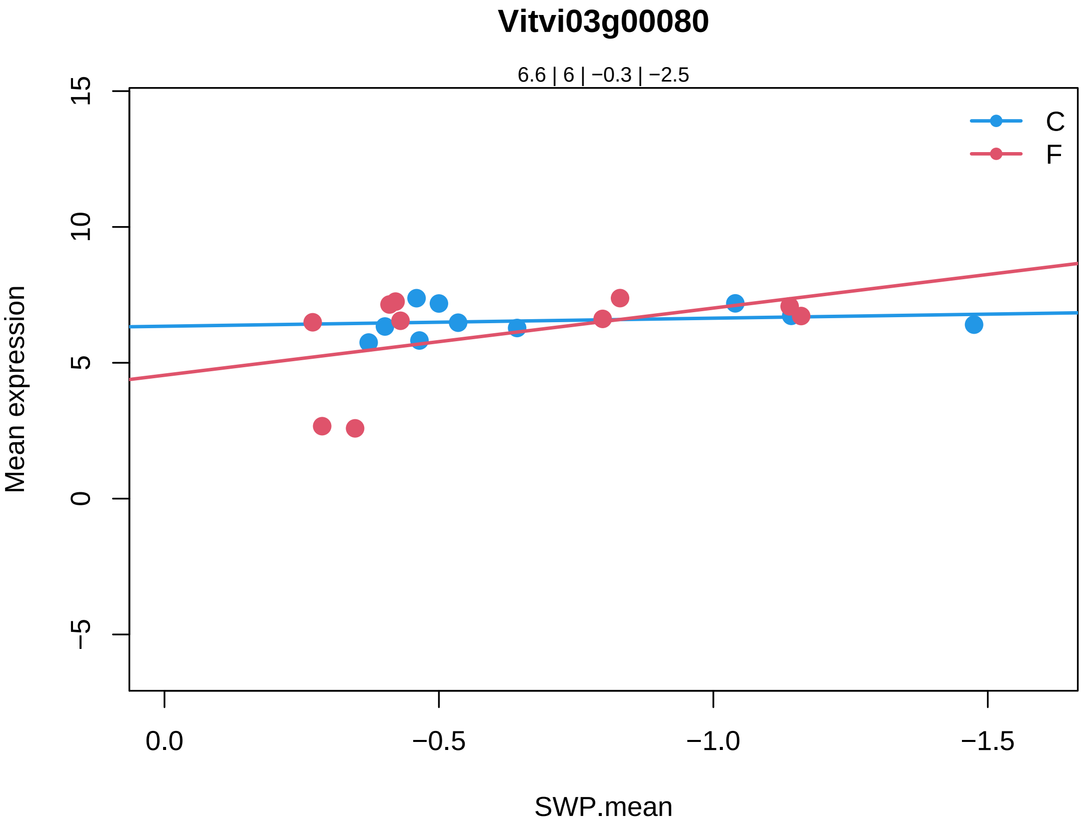
6.6.83 Vitvi03g00080

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

```
Vitvi03g00080
        30.3
        signalling.calcium
        Calcium-binding EF-hand family protein |
        Chr4:18115607-18118860 REVERSE LENGTH=375 |
        201606
```

Coefficients for Vitvi03g00080.

```
                     swp  varietyF swp.varietyF  AveExpr        F
Vitvi03g00080 -0.2966889 -1.802738      -2.1751 6.300933 2.037102
                P.Value adj.P.Val  type
Vitvi03g00080 0.1387926 0.4452925 type5
```



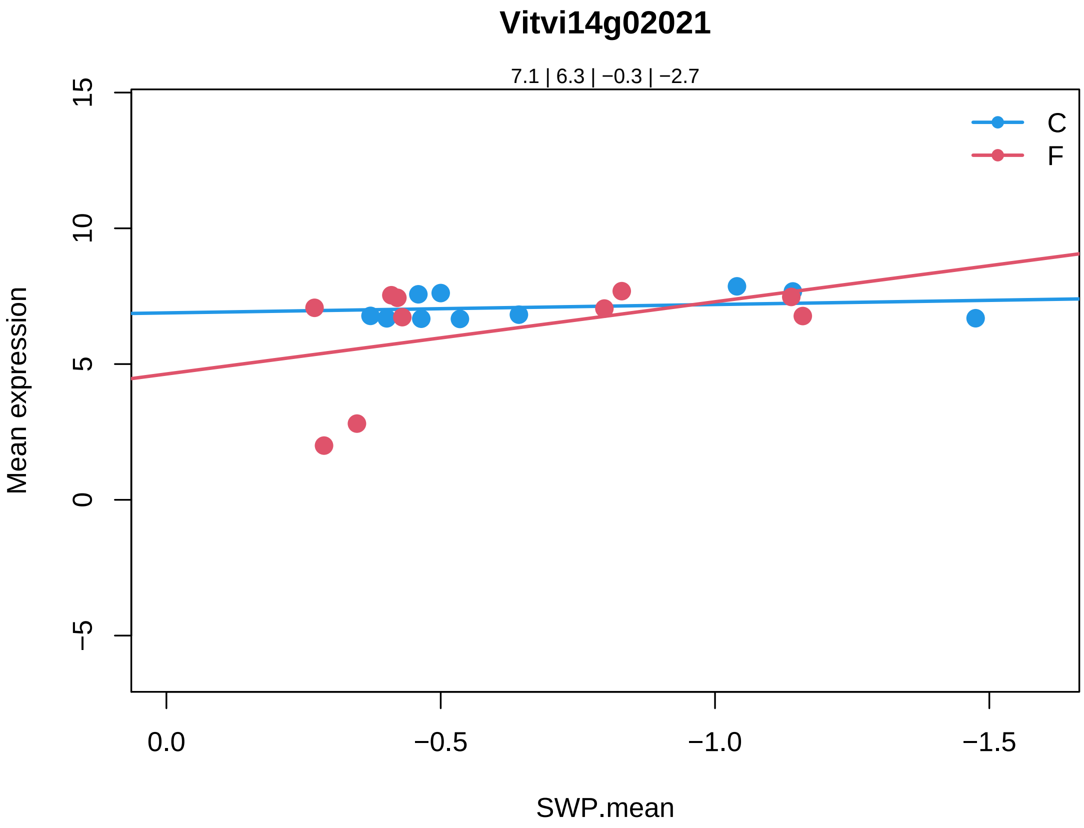
6.6.84 Vitvi14g02021

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

```
Vitvi14g02021
        35.2
        not assigned.unknown
        lysine-tRNA ligase |
        Chr3:17055-18782 REVERSE LENGTH=372 |
        201606
```

Coefficients for Vitvi14g02021.

```
                     swp  varietyF swp.varietyF AveExpr        F
Vitvi14g02021 -0.3086503 -2.250423    -2.350934 6.67856 2.337866
                P.Value adj.P.Val  type
Vitvi14g02021 0.1021215 0.3752497 type5
```



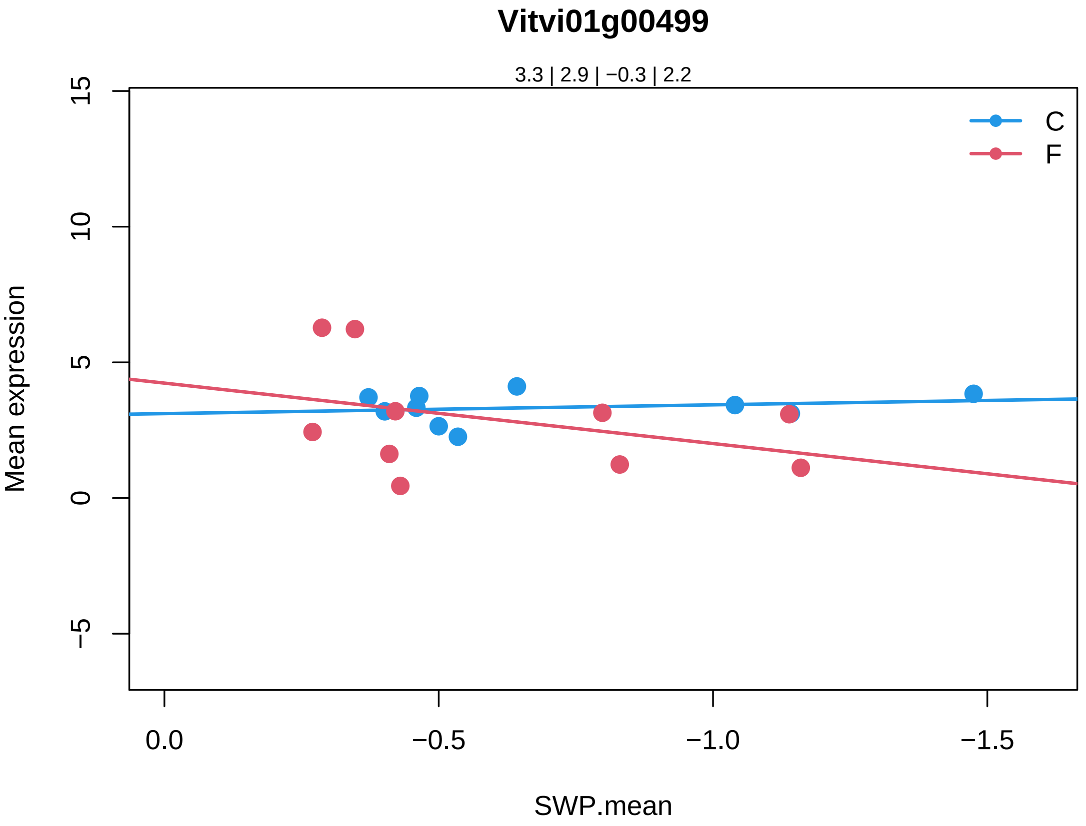
6.6.85 Vitvi01g00499

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

```
Vitvi01g00499
        29.5.11.4.3.2
        protein.degradation.ubiquitin.E3.SCF.FBOX
        flavin-binding%2C kelch repeat%2C f box 1 |
        Chr1:25508737-25510697 FORWARD LENGTH=619 |
        201606
```

Coefficients for Vitvi01g00499.

```
                    swp varietyF swp.varietyF  AveExpr        F
Vitvi01g00499 -0.323465 1.124167     2.551102 3.108341 1.312487
                P.Value adj.P.Val  type
Vitvi01g00499 0.2961696 0.6480358 type5
```



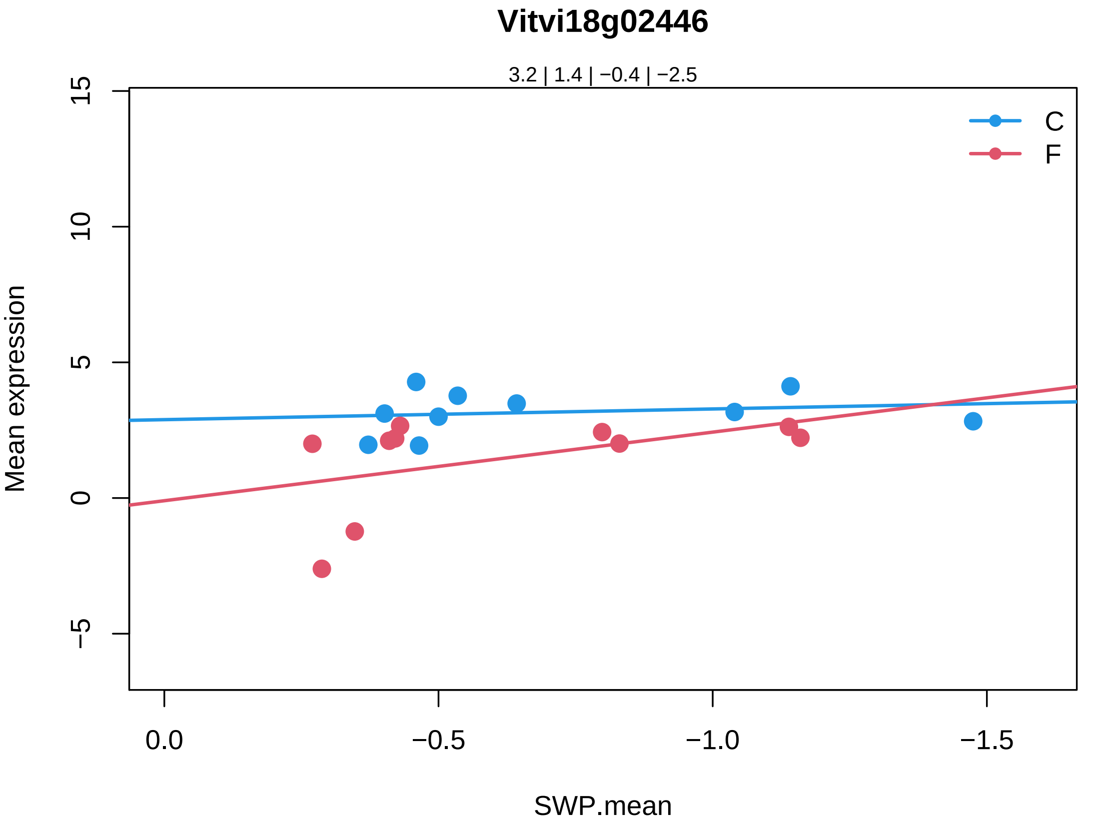
6.6.86 Vitvi18g02446

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

```
Vitvi18g02446
        16.01.2005
        secondary metabolism.isoprenoids.terpenoids
        terpene synthase 21 |
        Chr5:8092969-8095128 FORWARD LENGTH=547 |
        201606
```

Coefficients for Vitvi18g02446.

```
                     swp  varietyF swp.varietyF  AveExpr        F
Vitvi18g02446 -0.3940815 -2.987407     -2.13365 2.302884 5.263006
                  P.Value  adj.P.Val  type
Vitvi18g02446 0.007082561 0.06560794 type5
```



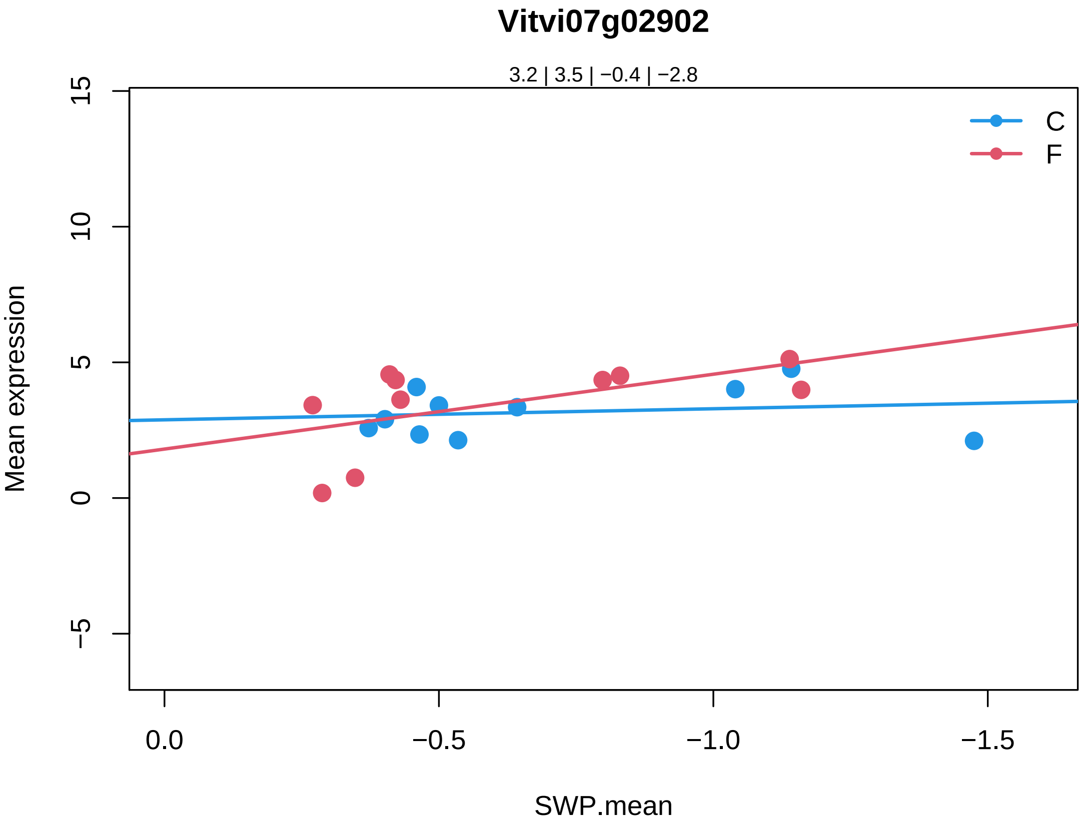
6.6.87 Vitvi07g02902

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

```
Vitvi07g02902
        35.2
        not assigned.unknown
        cysteine-rich RECEPTOR-like kinase |
        Chr4:12129485-12133157 FORWARD LENGTH=1043 |
        201606
```

Coefficients for Vitvi07g02902.

```
                     swp   varietyF swp.varietyF  AveExpr        F
Vitvi07g02902 -0.4080718 -1.077532    -2.349575 3.326616 2.463025
                 P.Value adj.P.Val  type
Vitvi07g02902 0.09003276 0.3475885 type5
```



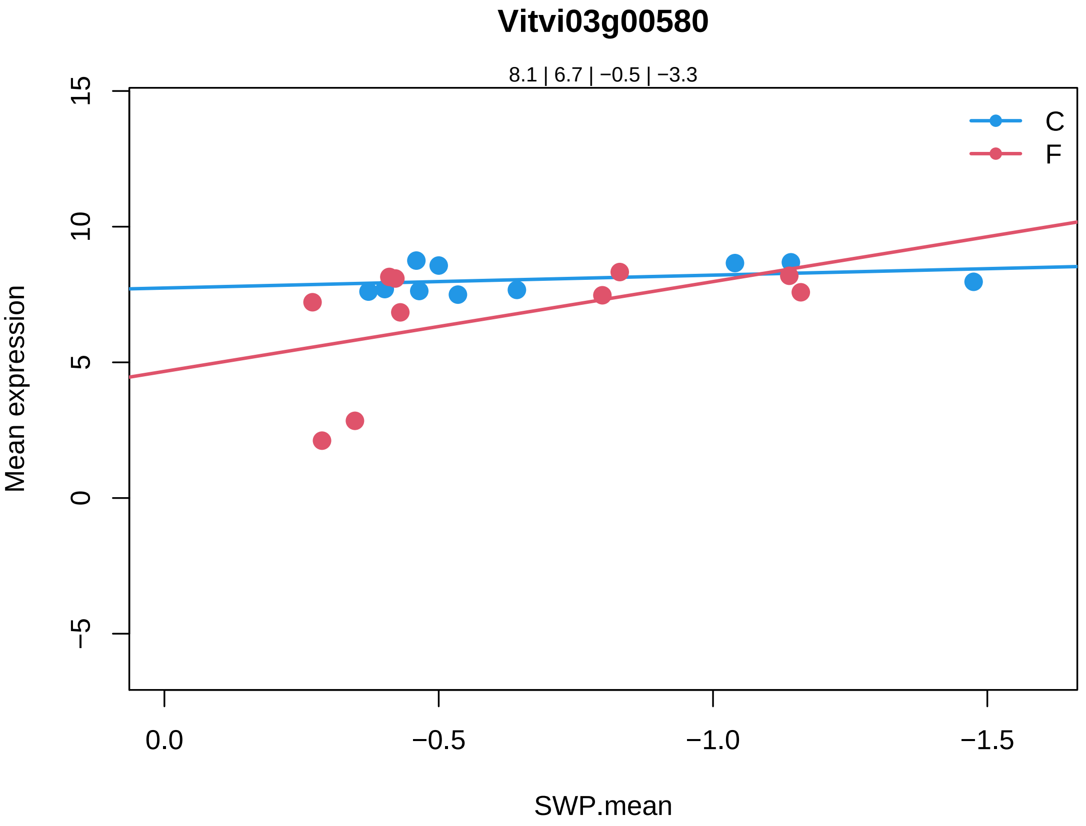
6.6.88 Vitvi03g00580

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

```
Vitvi03g00580
        35.2
        not assigned.unknown
        hypothetical protein |
        Chr2:6491706-6493286 REVERSE LENGTH=526 |
        201606
```

Coefficients for Vitvi03g00580.

```
                    swp   varietyF swp.varietyF AveExpr        F
Vitvi03g00580 -0.475253 -3.072056    -2.832606 7.37799 4.028906
                 P.Value adj.P.Val  type
Vitvi03g00580 0.02037598 0.1369963 type5
```



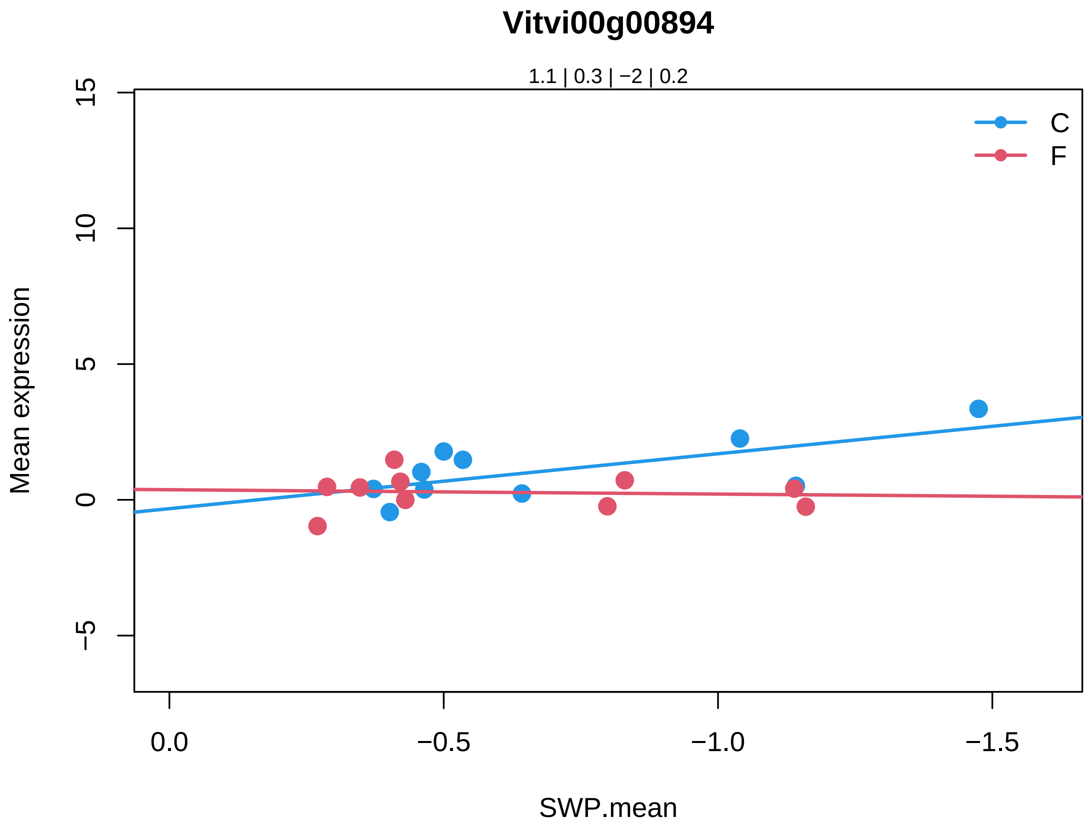
6.6.89 Vitvi00g00894

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

```
Vitvi00g00894
        26.1
        misc.cytochrome P450
        cytochrome P450%2C family 81%2C subfamily D%2C polypeptide 3 |
        Chr4:17564953-17566706 REVERSE LENGTH=500 |
        201606
```

Coefficients for Vitvi00g00894.

```
                    swp  varietyF swp.varietyF   AveExpr        F
Vitvi00g00894 -2.021627 0.6968549     2.181716 0.6853082 5.368034
                P.Value  adj.P.Val  type
Vitvi00g00894 0.0065011 0.06174462 type5
```



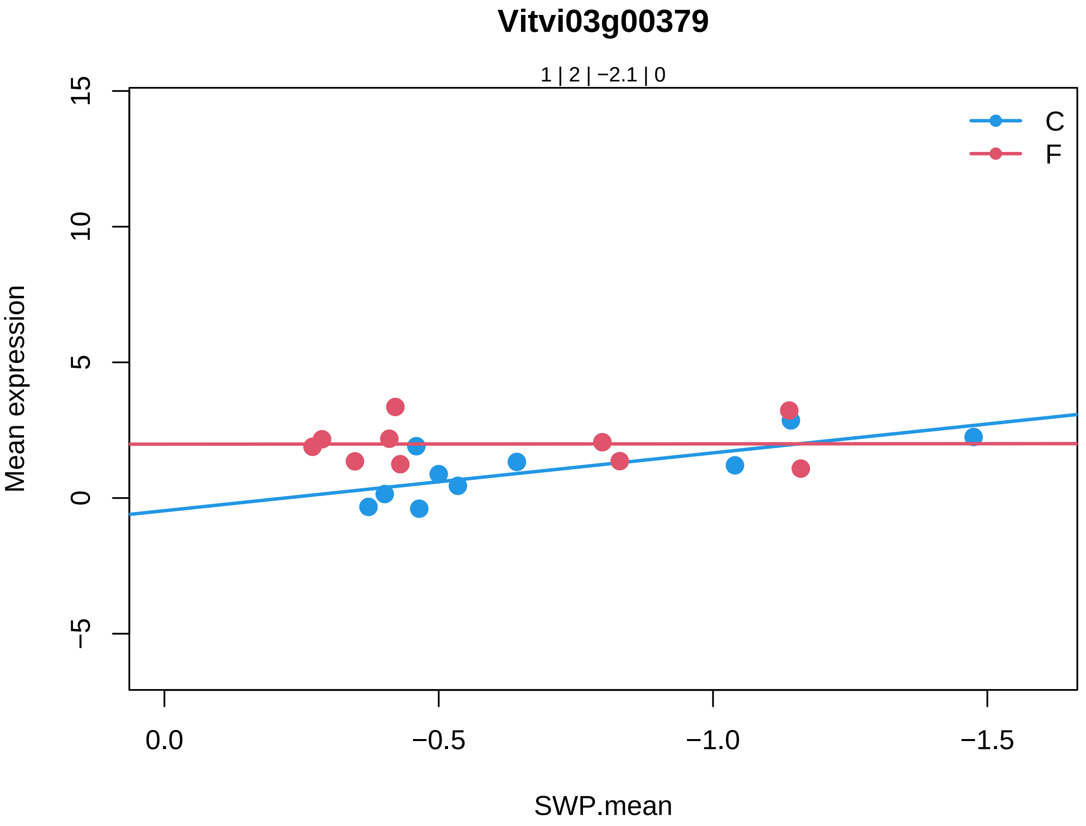
6.6.90 Vitvi03g00379

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

```
Vitvi03g00379
        21.3
        redox.heme
        hemoglobin 1 |
        Chr2:6982782-6983522 REVERSE LENGTH=160 |
        201606
```

Coefficients for Vitvi03g00379.

```
                    swp varietyF swp.varietyF  AveExpr       F
Vitvi03g00379 -2.130936 2.452085     2.119206 1.511264 6.33464
                 P.Value adj.P.Val  type
Vitvi03g00379 0.00304156 0.0353619 type5
```



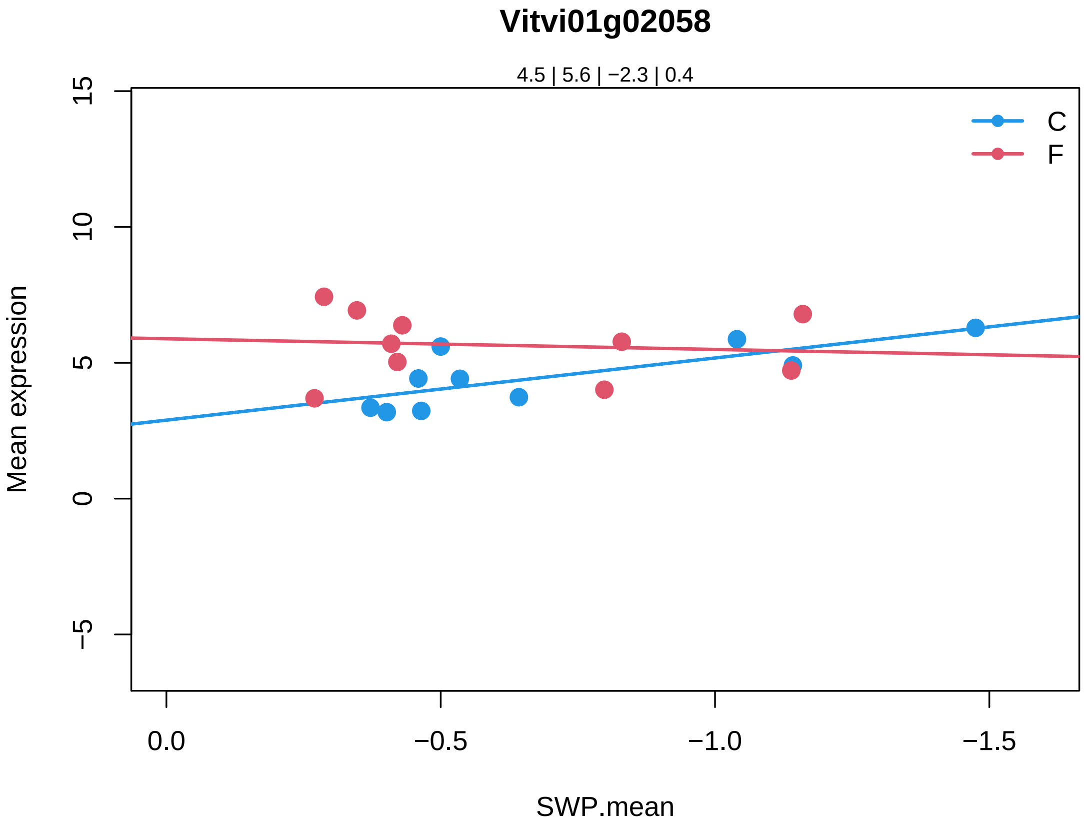
6.6.91 Vitvi01g02058

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

```
Vitvi01g02058
        35.1.26
        not assigned.no ontology.DC1 domain containing protein
        DC1 domain-containing protein |
        Chr1:22261978-22264243 FORWARD LENGTH=578 |
        201606
```

Coefficients for Vitvi01g02058.

```
                    swp varietyF swp.varietyF  AveExpr        F
Vitvi01g02058 -2.287997 2.995656     2.681258 5.071657 4.702769
                P.Value  adj.P.Val  type
Vitvi01g02058 0.0113092 0.09091497 type5
```



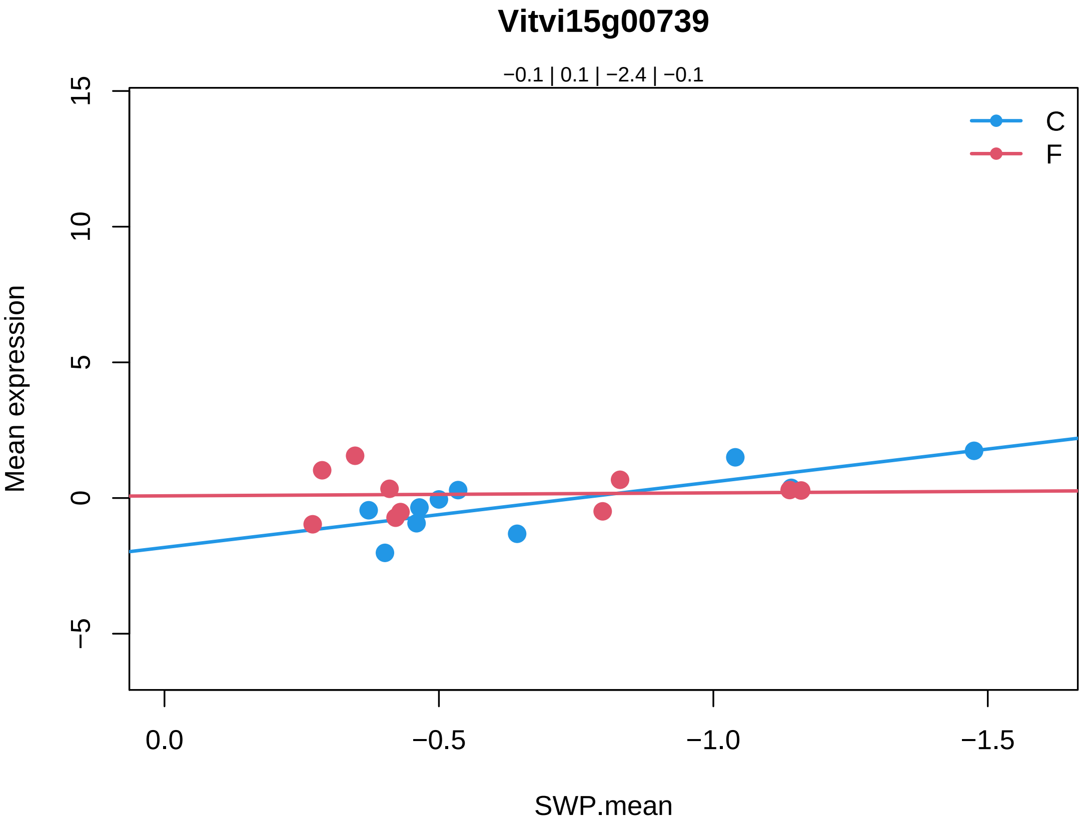
6.6.92 Vitvi15g00739

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

```
Vitvi15g00739
        31.1
        cell.organisation
        microtubule-associated protein 65-9 |
        Chr5:25005756-25008096 FORWARD LENGTH=549 |
        201606
```

Coefficients for Vitvi15g00739.

```
                    swp varietyF swp.varietyF    AveExpr        F
Vitvi15g00739 -2.417377 1.900468     2.306901 0.01245226 4.689195
                 P.Value  adj.P.Val  type
Vitvi15g00739 0.01144086 0.09177981 type5
```



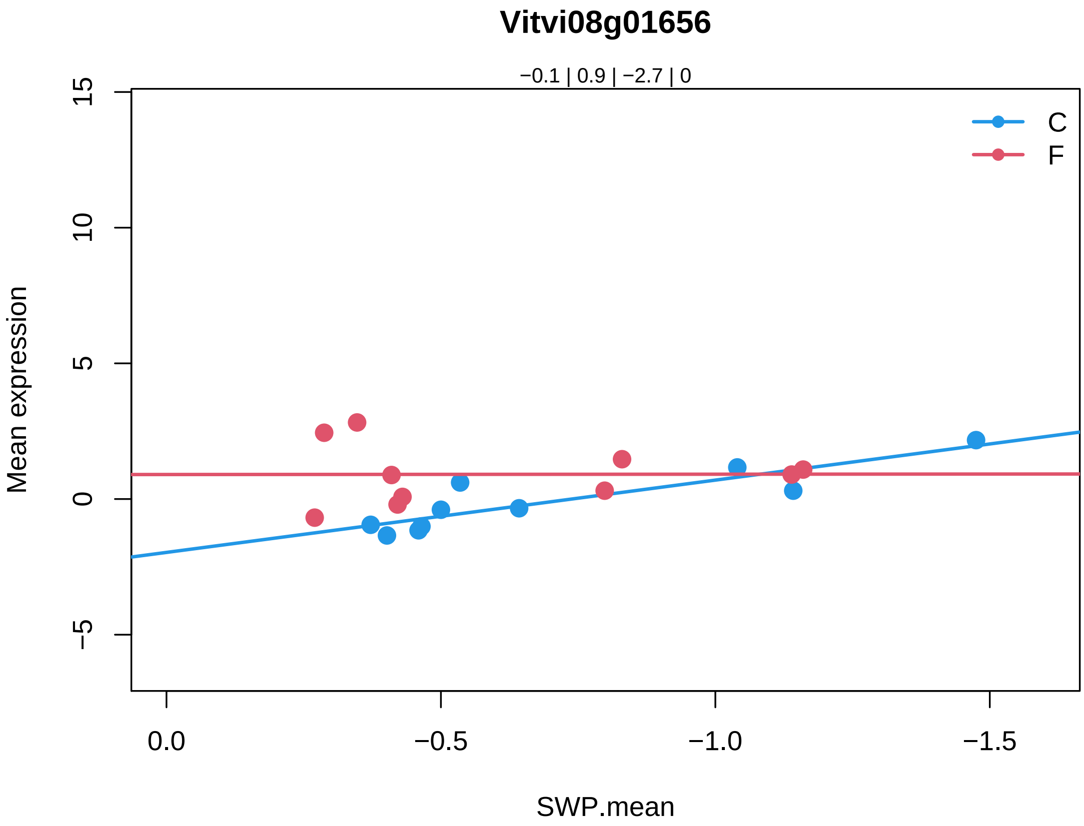
6.6.93 Vitvi08g01656

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

```
Vitvi08g01656
        16.04.2001
        secondary metabolism.N misc.alkaloid-like
        strictosidine synthase-like 2 |
        Chr2:17210599-17212904 REVERSE LENGTH=376 |
        201606
```

Coefficients for Vitvi08g01656.

```
                    swp varietyF swp.varietyF   AveExpr        F
Vitvi08g01656 -2.664662 2.870711     2.653252 0.4082147 6.733144
                  P.Value  adj.P.Val  type
Vitvi08g01656 0.002255747 0.02807212 type5
```



7 Types by significance of contrasts

Starting point is fit2

Model with water potential by variety.

```
> design2 <- with(pd, model.matrix(~ swp*variety))
> head(design2)
```

```
  (Intercept)        swp varietyF swp:varietyF
1           1 -0.3720000        0            0
2           1 -0.4016667        0            0
3           1 -0.5350000        0            0
4           1 -0.5000000        0            0
5           1 -0.4592308        0            0
6           1 -0.4645455        0            0
```

```
> tail(design2)
```

```
   (Intercept)        swp varietyF swp:varietyF
15           1 -0.4210000        1   -0.4210000
16           1 -0.3472727        1   -0.3472727
17           1 -0.7983333        1   -0.7983333
18           1 -1.1600000        1   -1.1600000
19           1 -0.8300000        1   -0.8300000
20           1 -1.1390000        1   -1.1390000
```

Linear model

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


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

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

```
> tail(design3)
```

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

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

```
              varietyC varietyF
Vitvi01g01391 2.135505 2.042236
```

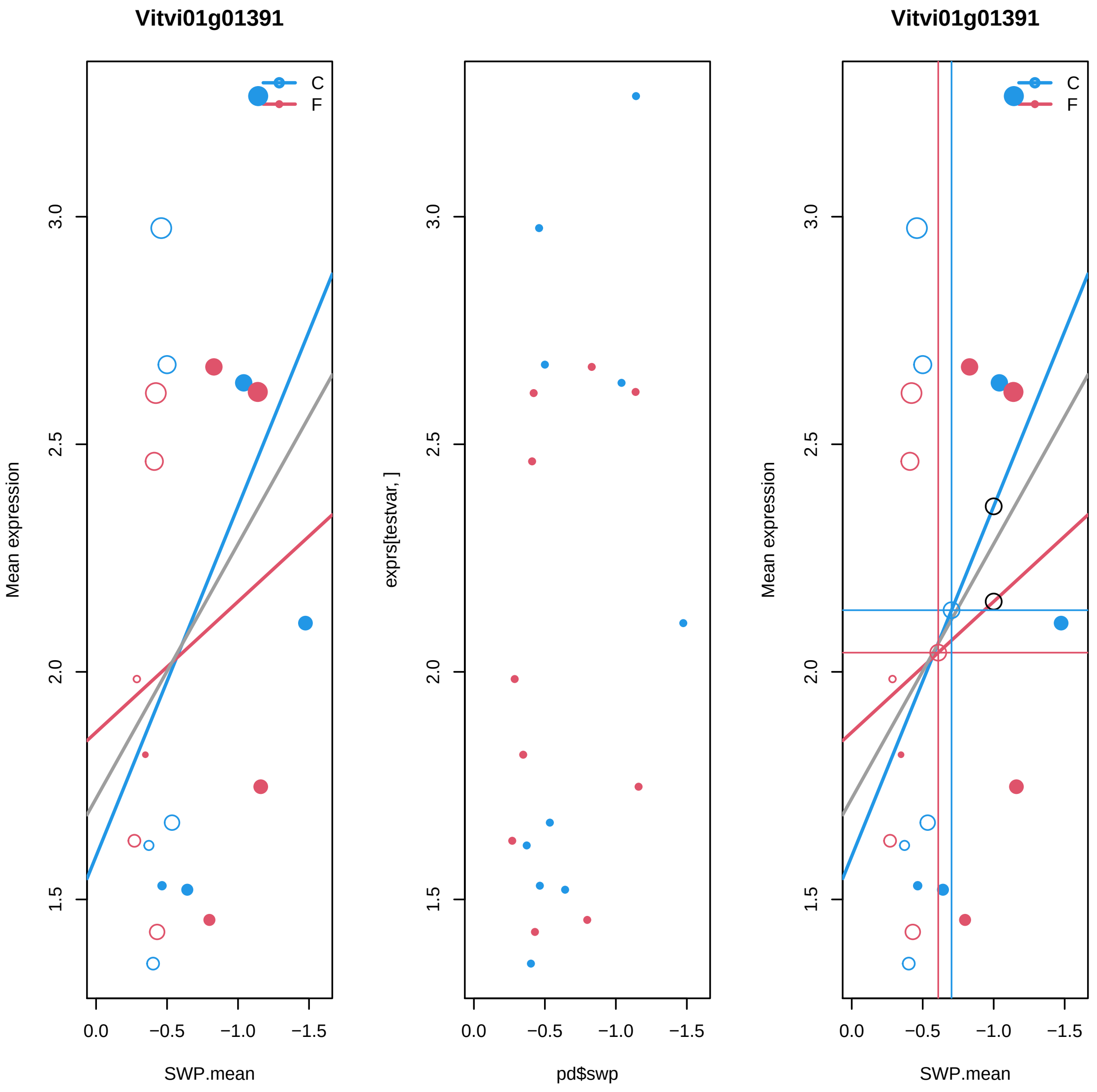
```
> my.predict(fit2, mean(swp))[testvar,]
```

```
                   mc       mf
Vitvi01g01391 2.09942 2.055719
```

Contrasts

```
> #contrasts <- makeContrasts(fit2)
```

```
> 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)
> #
> isC <- regexpr("C",colnames(exprs))>0
> (mswpC <- mean(swp[isC]))

[1] -0.7031866

> (mswpF <- mean(swp[!isC]))

[1] -0.6092879

> (msC <- my.predict(fit2, mswpC)[testvar,][1])

                   mc
Vitvi01g01391 2.135505

> (msF <- my.predict(fit2, mswpF)[testvar,][2])

                   mf
Vitvi01g01391 2.042236

> points(mswpC, msC, cex=2, col=4)
> points(mswpF, msF, cex=2,col=2)
> ms2 <- my.predict(fit2,-1)[testvar,]
> ms2

                   mc       mf
Vitvi01g01391 2.363633 2.154441

> points(rep(-1,2), ms2, cex=2)
> ms3 <- fit3[testvar,]$coefficients
> ms3

              varietyC varietyF
Vitvi01g01391 2.135505 2.042236

> abline(h=ms3,col=c(4,2))
> abline(v=c(mswpC,mswpF), col=c(4,2))
```



```
> #
> 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 1: 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 2: 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 3: 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 4: Assay metadata

Item	Value
Assay:	_A_01_Desc-R
Short Name:	01_Desc-R
Assay Class:	DRY
Assay Type:	R
Title:	Data overview and descriptive statistical presentation
Description:	First we will organize the data and perfom preliminary data analyses to overview what we have.
pISA Assay creation date:	2020-11-13
pISA Assay creator:	Andrej Blejec
Analyst:	Andrej Blejec
Phenodata:	Phenodata_20201109.txt
Featuredata:	Transcripts1819-unique.txt
Transcript data 18:	/input/Transcripts 2018.txt
Transcript data 19:	/input/Transcripts 2019.txt
Water potential data:	/input/Stem water potential 2018 2019.txt

B SessionInfo

Windows 10 x64 (build 19041)

- R version 4.0.2 (2020-06-22), x86_64-w64-mingw32
- Locale: LC_COLLATE=Slovenian_Slovenia.1250, LC_CTYPE=Slovenian_Slovenia.1250, LC_MONETARY=Slovenian_Slovenia.1250, LC_NUMERIC=C, LC_TIME=Slovenian_Slovenia.1250
- Running under: Windows 10 x64 (build 19041)
- Matrix products: default
- Base packages: base, datasets, graphics, grDevices, grid, methods, parallel, stats, utils
- Other packages: amisc 0.1.0, Biobase 2.50.0, BiocGenerics 0.36.0, dotCall64 1.0-0, fields 11.6, Formula 1.2-4, ggplot2 3.3.2, Hmisc 4.4-1, knitr 1.30, lattice 0.20-41, limma 3.46.0, lubridate 1.7.9.2, 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 1.5.2, jpeg 0.1-8.1, latticeExtra 0.6-29, lifecycle 0.2.0, magrittr 1.5, maps 3.3.0, Matrix 1.2-18, munsell 0.5.0, nnet 7.3-14, pillar 1.4.6, pkgconfig 2.0.3, plyr 1.8.6, png 0.1-7, purrr 0.3.4, R6 2.5.0, RColorBrewer 1.1-2, Rcpp 1.0.5, rlang 0.4.8, rpart 4.1-15, rstudioapi 0.12, scales 1.1.1, splines 4.0.2, stringi 1.5.3, stringr 1.4.0, tibble 3.0.4, tidyselect 1.1.0, tools 4.0.2, vctrs 0.3.4, withr 2.3.0, xfun 0.19

Analysis project path: [link]

Local	Network
D:	O:
DEJAVNOSTI	DEJAVNOSTI
OMIKE	OMIKE
pISA-projects	pISA-projects
_p_VinskaTrta	_p_VinskaTrta
_I_EnViRoS	_I_EnViRoS
_S_01_Integ	_S_01_Integ
_A_01_Desc-R	_A_01_Desc-R
other	other

Main file : ../doc/50_Expression-water-stress.Rnw
Main file : ../scripts/50_Expression-water-stress.Rnw
Project file: [link]

View as vignette

Source files can be viewed by pasting this code to R console:

```
projectName <-"other"
mainFile <-"50_Expression-water-stress"
commandArgs()
library(tkWidgets)
openPDF(file.path(dirname(getwd()),"doc",
paste(mainFile,"PDF",sep=".")))
viewVignette("viewVignette", projectName,
file.path("../doc",paste(mainFile,"Rnw",sep=".")))
```