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

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Contents

1 Task

Final document in folder /reports:

```
> fileName(outputFile)
[1] "40_Expression-water-stress_0.05-r"
```

2 Information from pISA

Data directory

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

Results directory

```
> .oroot
[1] "../../output/40_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 ...

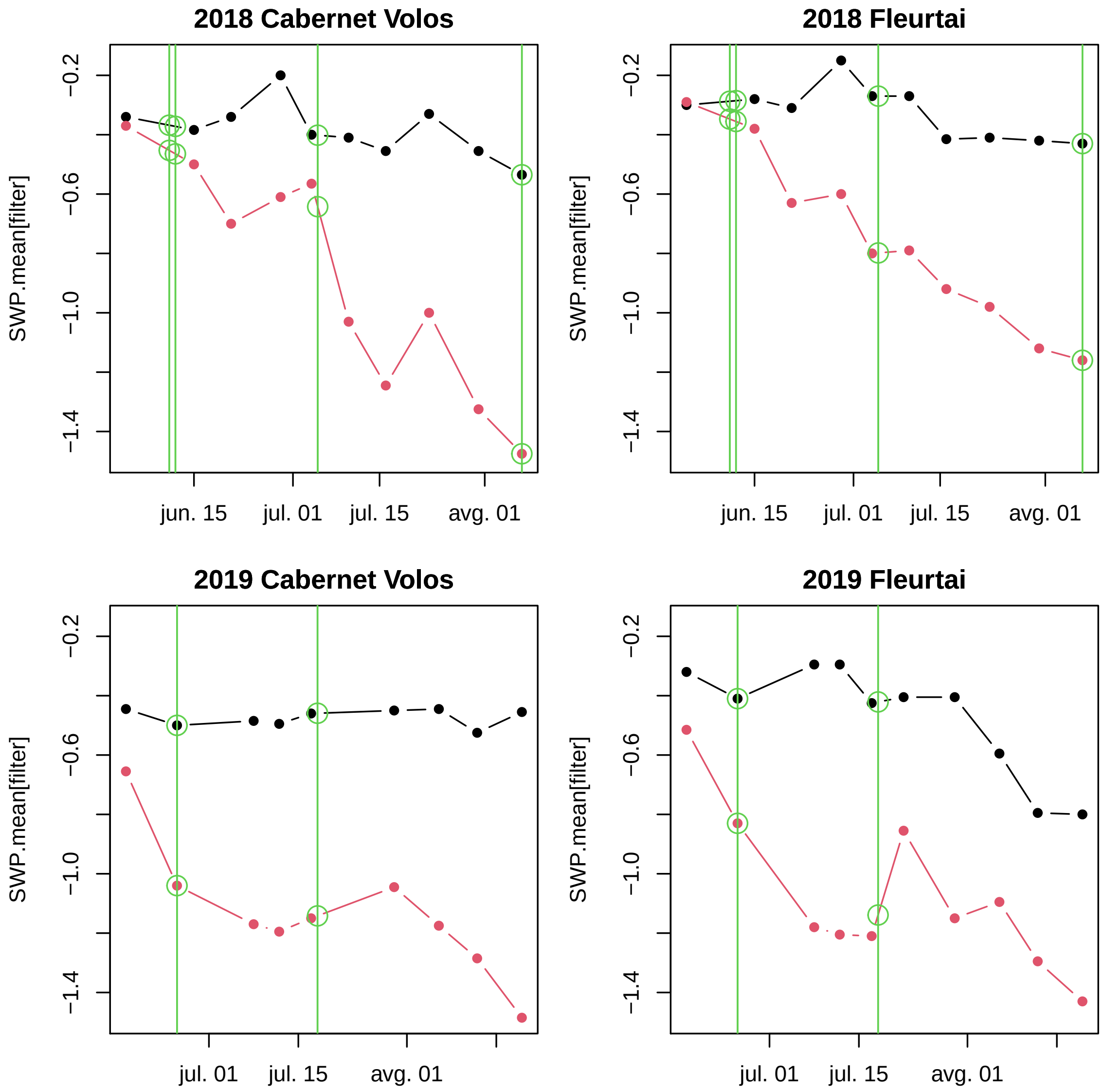
```
> table(wpdata$date,wpdata$variety)
```

```
             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,]
```

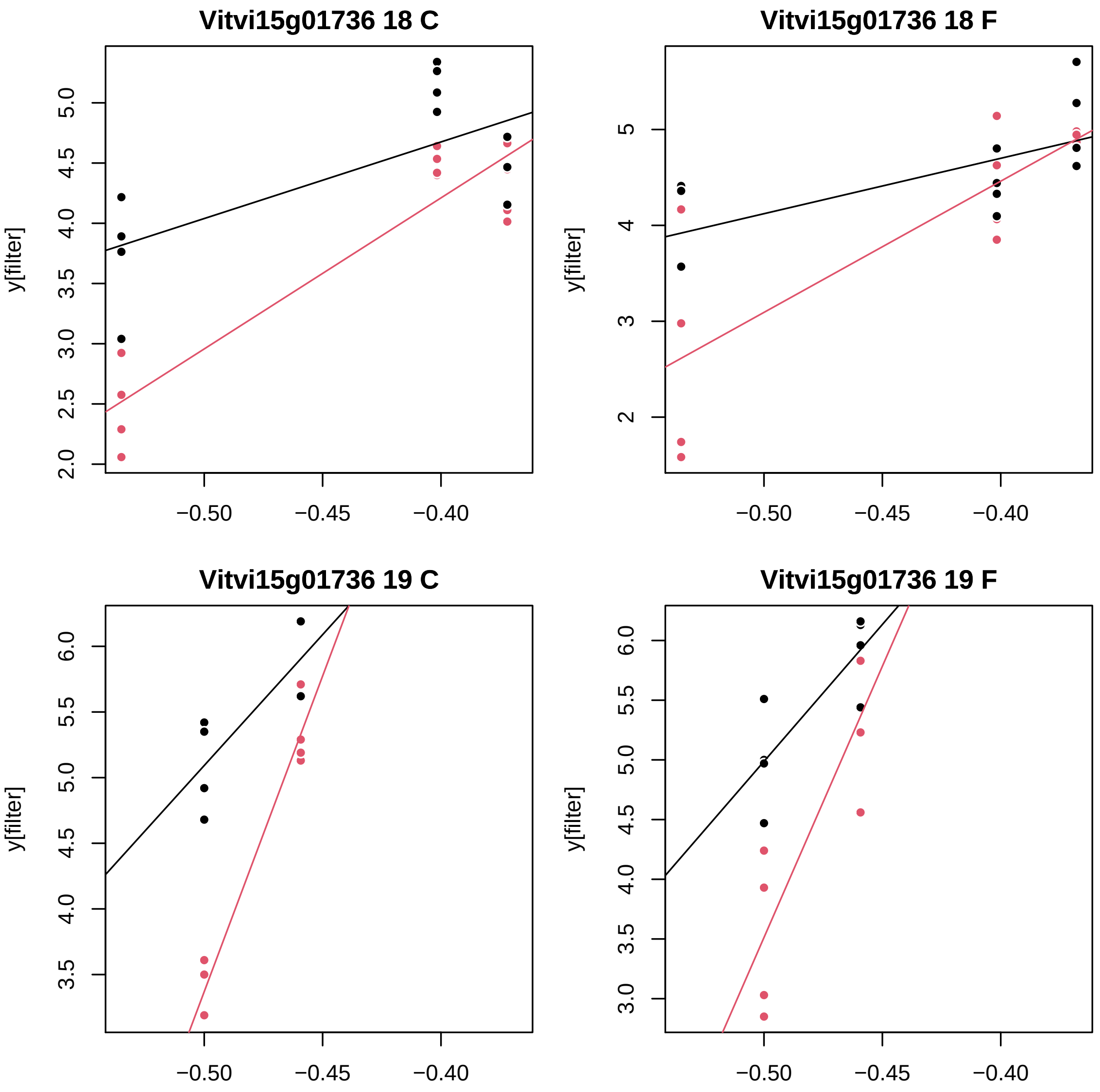
```
              C18_11d_WS1 C18_11d_WS2 C18_11d_WS3 C18_11d_WS4
Vitvi15g01736    4.664602    4.109897     4.44822    4.013955
              C18_11d_WW1 C18_11d_WW2 C18_11d_WW3 C18_11d_WW4
Vitvi15g01736    4.717536    4.154237    4.475261    4.466465
              C18_34d_WS1 C18_34d_WS2 C18_34d_WS3 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"
```



```
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
```

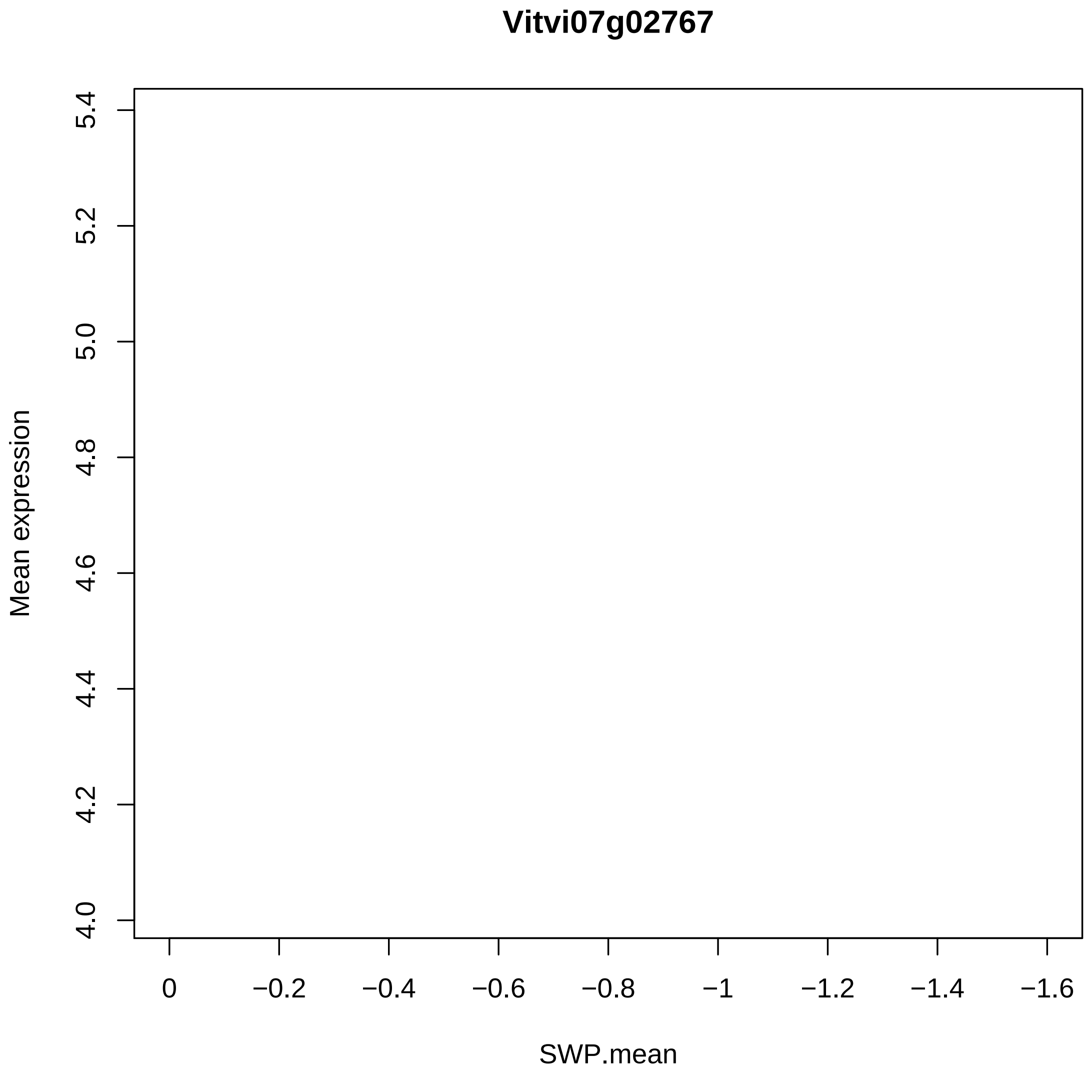
4 Expression and water poential analysis

```
> 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)
```



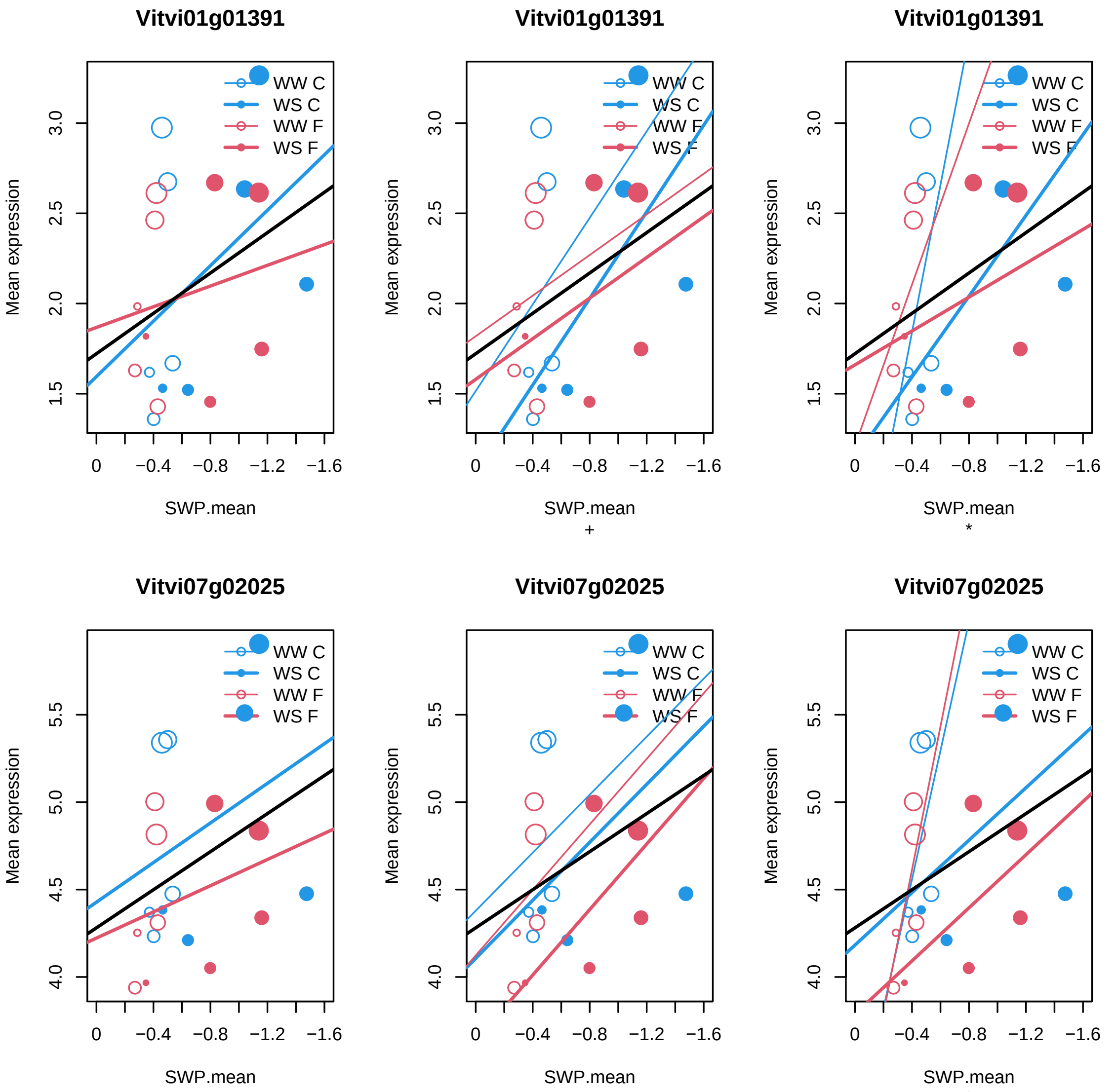
```
> legend("topright", bty="n", pch=pchs, col=cols,legend <- vlvls)
Error in as.graphicsAnnot(legend): argument "legend" is missing, with no defau
> #
> for(i in 1:length(vlvls)){
+ for( j in 1:length(tlvls)){
+ tfilter <- wpas$treat %in% tlvls[j]
+ vfilter <- wpas$variety %in% vlvls[i]
+ yy <- means[as.character(wpa$date),tlvls[j],vlvls[i]]
+ wpa <- wpas[tfilter & vfilter,]
+ all(wpa$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){
+ if(verbose) print(varname)
+ (y <- unlist(t1819[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]],
+       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,model)
+ legend("topright", bty="n", pch=pchs, col=rep(cols,each=2),lwd=lwd,
+        legend= outer(tlvls,vlvls,paste))
+ #
+ allx <- NULL
+ ally <- NULL
+ fits <- NULL
+ fits <- list()
+ 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"]
+ points(-xx , yy,
+       col = cols[i],
+       pch = pchs[as.numeric(mns$treat)]
+      , cex=0.5+as.numeric(mns$date)/3
+       )
```

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

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



```
> length(fits)
[1] 4
> names(fits)
[1] "C"   "F"   "all" "r"
```

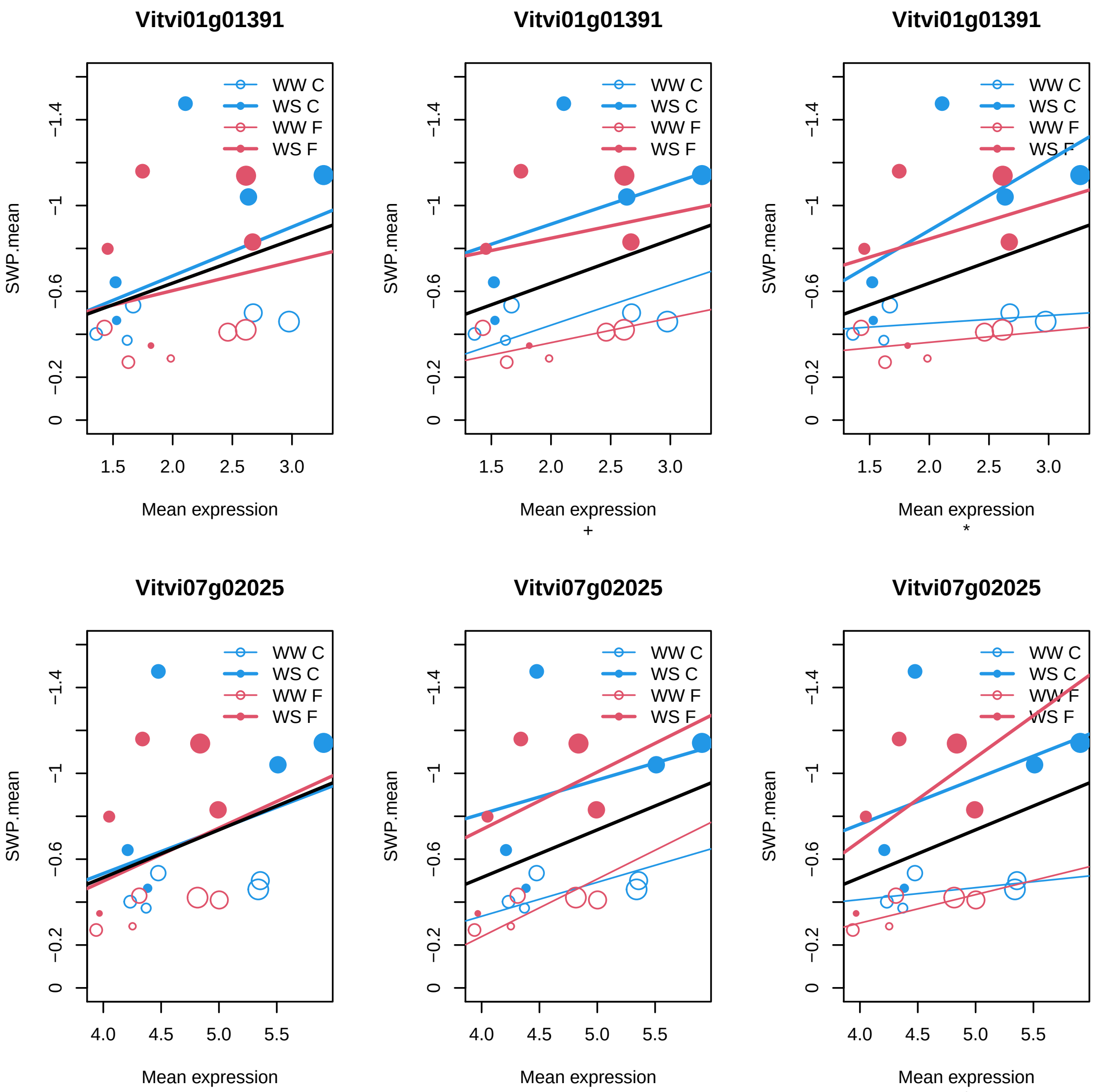
4.2 Water potential vs Expression

```
> plot.wpe <- function(varname,cols=c(4,2),pchs=c(1,16),lwd=c(1,2,1,2)
+       ,model=c("*"), verbose=FALSE){
+ if(verbose) print(varname)
+ (y <- unlist(t1819[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$swp[tfilter & vfilter], means[,"WS",vlvls[i]],
+       xlim=ylim,
+       ylim=-rev(xlim),
+       ylab = "SWP.mean",
+       xlab = "Mean expression",
+       type="n",
+       axes=FALSE
+       )
+ axis(1)
+ box()
+ axis(2,at=seq(0,2,0.2),labels=-(seq(0,2,0.2)))
+ title(varname, model)
+ legend("topright", bty="n", pch=pchs, col=rep(cols,each=2),lwd=lwd,
+        legend= outer(tlvls,vlvls,paste))
+ #
+ ally <- NULL
+ allx <- NULL
+ fits <- NULL
+ for(i in 1:length(vlvls)){
+ #for( j in 1:length(tlvls)){
+ #tfilter <- wpas$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)$date)
+ yy <- mns[,"value"]
+ xx <- wp[,"value"]
+ points(yy, -xx,
+       col = cols[i],
+       pch = pchs[as.numeric(mns$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
+ }
```

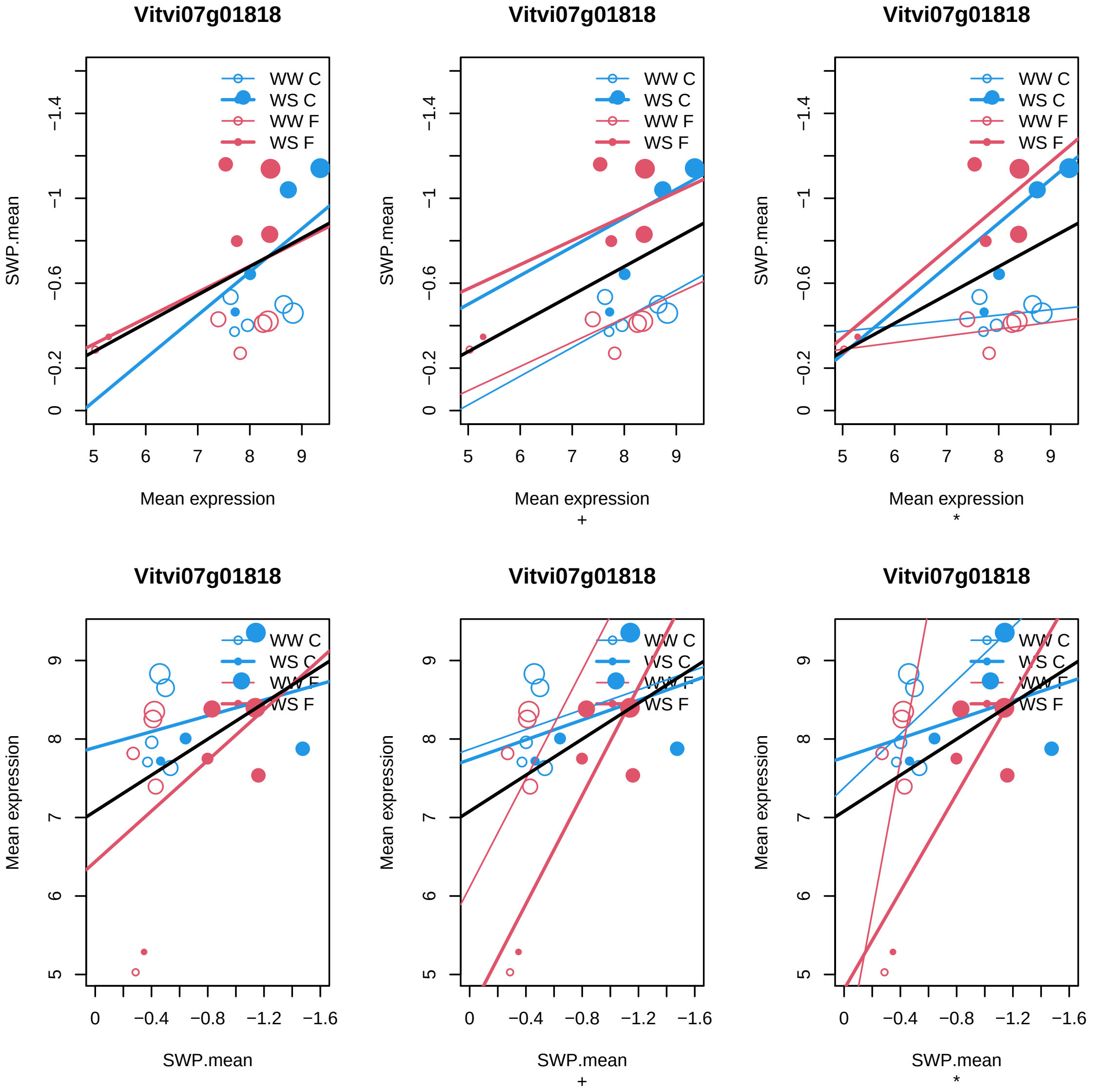
```
+ fit <- lm(allx~ally)
+ fits[["all"]] <- fit
+ if (verbose) print(summary(fit))
+ abline(fit$coefficients,lwd=2)
+ #points(-swps,means,cex=1.5)
+ invisible(fits)
+ }
```

```
> 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] 3
> names(fits)
[1] "C"   "F"   "all"

> 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="*")
> plot.ewp(varname,model="")
> plot.ewp(varname,model="+")
> plot.ewp(varname,model="*")
```



```
> for(i in 1:2){
+   ( 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 as.vector((means[as.character(wpa$date), , vlvls[i]])): object 'wpa'
```

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
```

```
> cat(knit_child(file.path("../doc/","40a_limma-fit-swp.Rnw"),quiet=TRUE))
```

5.1 Model design

Simple model with water potential for all data:

```
> design <- with(pd, model.matrix(~ swp))
> design[,2] <- (-design[,2])
> head(design)
```

```
  (Intercept)   swp
1           1 0.372
2           1 0.372
3           1 0.372
4           1 0.372
5           1 0.372
6           1 0.372
```

```
> tail(design)
```

```
   (Intercept)       swp
75           1 0.4592308
76           1 0.4592308
77           1 0.4592308
78           1 0.4592308
79           1 0.4592308
80           1 0.4592308
```

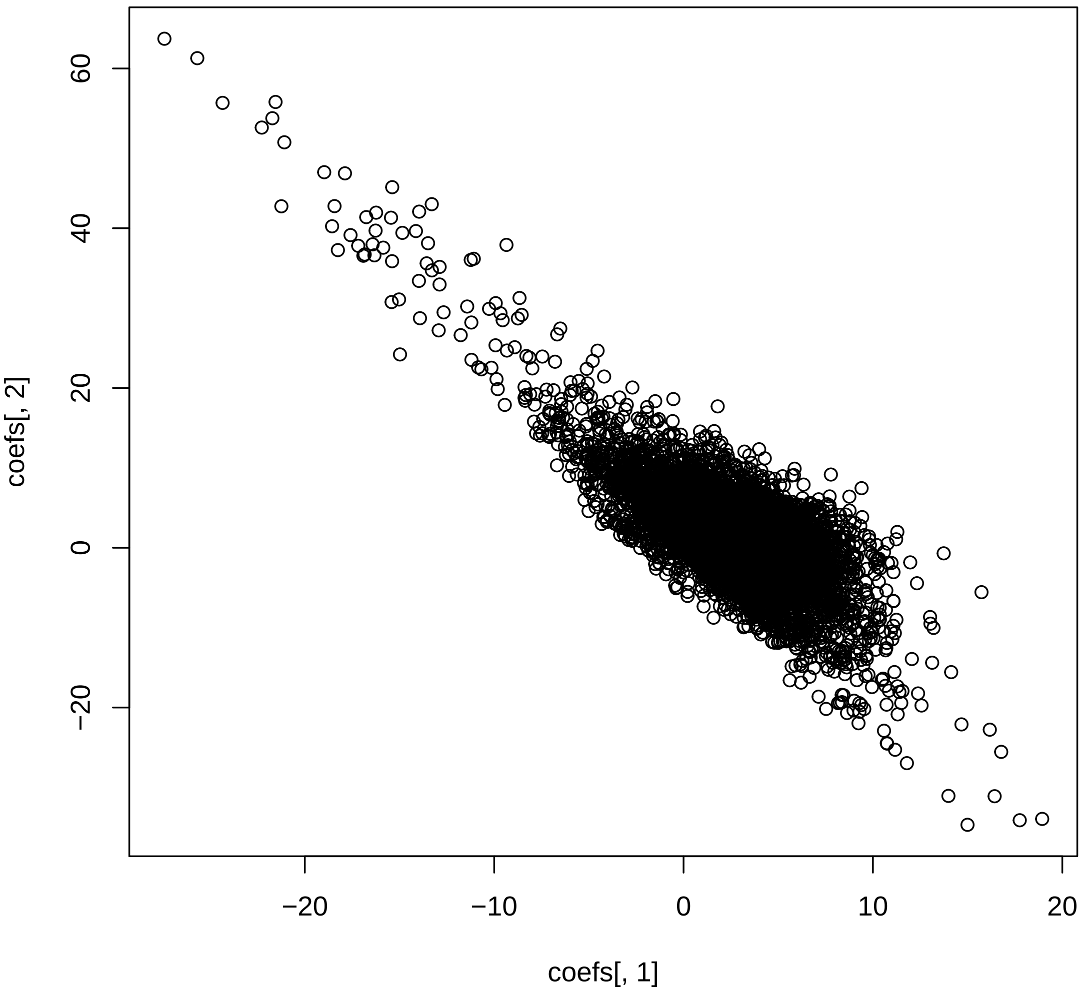
Linear models

```
> fit1 <- lmFit(exprs, design)
> fit1 <- eBayes(fit1)
> head(fit1[1:6,]$coefficients)
```

```
            (Intercept)        swp
Vitvi15g01736   7.7878435 -7.3063828
Vitvi07g02832   0.3638262 -1.2060744
Vitvi07g02830   1.6475442 -4.3513888
Vitvi07g02812  -0.1783863 -0.3706094
Vitvi07g02811   2.9235068 -0.9628080
Vitvi09g02033  -0.1698934 -1.3624505
```

```
> fit <- fit1
```

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



```
> coefs[abs(coefs[,2])>20,]
              (Intercept)       swp
Vitvi01g01048   11.306956 -20.85587
Vitvi01g01512  -11.078026  36.17683
Vitvi01g01708   -7.456518  23.93461
Vitvi01g02286    7.528961 -20.17774
Vitvi02g00025  -14.133401  39.64396
Vitvi02g00220    9.289836 -20.53148
Vitvi02g00263   -9.877397  21.10158
Vitvi02g00374  -10.270324  29.90913
Vitvi02g00436  -10.674876  22.33529
Vitvi02g01446  -12.881222  35.15716
Vitvi02g01447  -21.237525  42.74610
Vitvi02g01121   -5.533024  20.87824
Vitvi03g00325   17.753139 -34.10975
Vitvi03g00717   -6.673047  26.70677
Vitvi04g01792   -8.549161  29.15129
Vitvi04g01794  -17.179458  37.79848
Vitvi04g01795  -16.420240  37.98288
```

Vitvi04g01799	-16.324341	36.60426
Vitvi04g01801	-17.586092	39.13847
Vitvi04g01802	-15.392201	35.87135
Vitvi04g00135	-25.677235	61.28924
Vitvi04g00501	10.734803	-24.45325
Vitvi04g00522	-5.970696	20.70966
Vitvi04g01654	-12.671731	29.46865
Vitvi05g00170	-18.560034	40.24486
Vitvi05g01833	-8.396689	20.10726
Vitvi05g00486	-13.565366	35.60306
Vitvi05g01933	-10.842490	22.58200
Vitvi05g01353	16.171054	-22.77537
Vitvi06g00443	-4.540227	24.67175
Vitvi06g00561	-21.081489	50.75508
Vitvi07g02123	11.170024	-25.28741
Vitvi07g00380	-18.432074	42.76737
Vitvi07g02214	-13.919915	28.73382
Vitvi07g00445	10.585392	-22.90773
Vitvi07g00457	-16.236313	41.95000
Vitvi07g02242	-14.847715	39.42011
Vitvi07g00657	-9.328816	24.68773
Vitvi07g02433	-6.787508	23.28713
Vitvi07g01120	-10.145850	22.53412
Vitvi08g00689	-8.300061	24.00508
Vitvi08g00731	-18.253897	37.26034
Vitvi08g01143	-5.114917	22.39484
Vitvi08g02274	-22.273550	52.60215
Vitvi09g00045	-8.748078	28.70774
Vitvi09g00599	-16.755009	41.39061
Vitvi10g00027	16.773920	-25.55267
Vitvi10g00436	8.632955	-20.69019
Vitvi10g00496	-4.796882	23.39236
Vitvi10g01881	-15.416105	30.75833
Vitvi10g01886	10.748013	-24.51282
Vitvi11g00724	-15.384832	45.13777
Vitvi11g01645	11.792997	-26.96392
Vitvi12g00574	-14.974719	24.19775
Vitvi12g00576	-15.448071	41.31687
Vitvi12g02138	-21.714093	53.77021
Vitvi13g00278	-9.919179	30.62073
Vitvi13g02005	16.426164	-31.10367
Vitvi13g02014	-9.551786	28.48403
Vitvi13g02016	-15.857617	37.56527
Vitvi13g02017	-16.263225	39.70164
Vitvi13g02018	-13.493238	38.12168
Vitvi13g00405	-16.906999	36.55759
Vitvi13g00409	-13.290217	34.71895
Vitvi13g00410	-13.296353	43.00946
Vitvi13g02024	-13.962153	42.07724
Vitvi13g00451	-11.236659	36.03119
Vitvi13g00471	-16.839013	36.71473
Vitvi13g00490	-12.884408	32.95523
Vitvi13g01107	-9.667692	29.34786

```
Vitvi13g01839  -11.200693  23.52176
Vitvi14g00063  -15.023680  31.08035
Vitvi14g01381   14.994303 -34.68278
Vitvi14g01469   18.938154 -33.94468
Vitvi14g02990  -11.425592  30.20039
Vitvi14g01942  -18.975683  47.01313
Vitvi14g02026   -2.702445  20.05851
Vitvi15g00714    9.238437 -21.96631
Vitvi15g01034   -9.352648  37.91364
Vitvi16g00681   -6.508296  27.43906
Vitvi16g00890    9.542375 -20.18448
Vitvi16g01103  -17.880477  46.87118
Vitvi16g01985  -12.930117  27.21067
Vitvi16g01352  -21.545840  55.80582
Vitvi17g01318  -13.974271  33.40743
Vitvi17g00601   13.987170 -31.06433
Vitvi17g00695   -8.661915  31.26828
Vitvi17g01596    8.975235 -20.36075
Vitvi18g02468   -8.914837  25.09923
Vitvi18g00268   -9.928831  25.34296
Vitvi18g01510   -8.136715  23.79546
Vitvi18g01966   -5.065014  20.56758
Vitvi18g02066   -4.194130  21.43313
Vitvi18g02423  -27.414763  63.72049
Vitvi19g00041   14.675960 -22.11331
Vitvi19g00514   -7.985757  22.44871
Vitvi19g02145  -11.206279  28.19821
Vitvi19g01048  -11.768042  26.61329
Vitvi19g01760  -24.342365  55.69011
```

Top table

```
> which <- 2
>   tt <- topTable(fit,coef=which, number=Inf)
>   head(tt)
                 logFC  AveExpr        t      P.Value    adj.P.Val
Vitvi02g00374 29.90913 3.283880 18.79698 2.300407e-31 3.506281e-27
Vitvi04g00522 20.70966 3.414499 17.94327 4.900852e-30 3.734939e-26
Vitvi09g01273 17.79031 3.745035 17.75236 9.830851e-30 3.831175e-26
Vitvi11g00724 45.13777 5.070678 17.74622 1.005426e-29 3.831175e-26
Vitvi01g01943 12.14569 4.556800 17.51369 2.361916e-29 6.767539e-26
Vitvi08g00689 24.00508 2.578551 17.48107 2.664036e-29 6.767539e-26
                     B
Vitvi02g00374 55.20282
Vitvi04g00522 52.74622
Vitvi09g01273 52.18207
Vitvi11g00724 52.16383
Vitvi01g01943 51.46908
Vitvi08g00689 51.37095
```

5.1.1 Export output files

Export fit in a form:

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

```
        A         Coef.(Intercept)       Coef.swp        t.(Intercept)
Vitvi15g01736       4.47674068175       7.78784348921542         -7.306382793
Vitvi07g02832       -0.1827419310625       0.363826241712366         -1.20607
Vitvi07g02830       -0.3244159185       1.64754420617268         -4.351388755
Vitvi07g02812       -0.3463388427625       -0.178386273275306         -0.3706
Vitvi07g02811       2.4871819448375       2.92350680207491        -0.9628080
Vitvi09g02033       -0.78732802375       -0.169893388093836         -1.362450
```

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

Export top table

```
> ttfn <- "TopTable.txt"
> my.write.table(tt,file=file.path(.oroot,ttfn))
```

Warning in write.table(x, file = file, col.names = col.names, sep = sep, : appending column names to file Object: tt
Label:
File :
../../output/40_Expression-water-stress-0.05-r/TopTable.txt

```
> par(mfrow=c(2,3))
> cf <- 10
> ns <- c(500,300,200,100,50,25)
> for(i in 1:length(ns)){
+ plot(coefs[,1],coefs[,2],xlab="Intercept",ylab="Slope")
+ filter <- rownames(tt)[1:ns[i]]
+ points(coefs[filter,1],coefs[filter,2], col=i+1,pch=16)
+ abline(h=c(-cf,cf), col="white")
+ title(paste("Top ",ns[i]))
+ }
```

Many significant genes:

```
> .alpha <- 0.05
> sum(tt$adj.P.Val < .alpha)
```

```
[1] 9004
```

```
> sum((tt$adj.P.Val < .alpha) & (abs(tt$logFC)>cf))
```

```
[1] 607
```

```
> sum((tt$adj.P.Val < .alpha) & (abs(tt$logFC)>2*cf))
```

```
[1] 99
```

We should consider to set a treshold for effect (slope), e.g. absolute slope larger than certain treshold. In the figure a cutoff 10 is used.

Z apregled je boljše pogledati prvih nekaj in zadnjih nekaj.

```
> topn <- 20
```

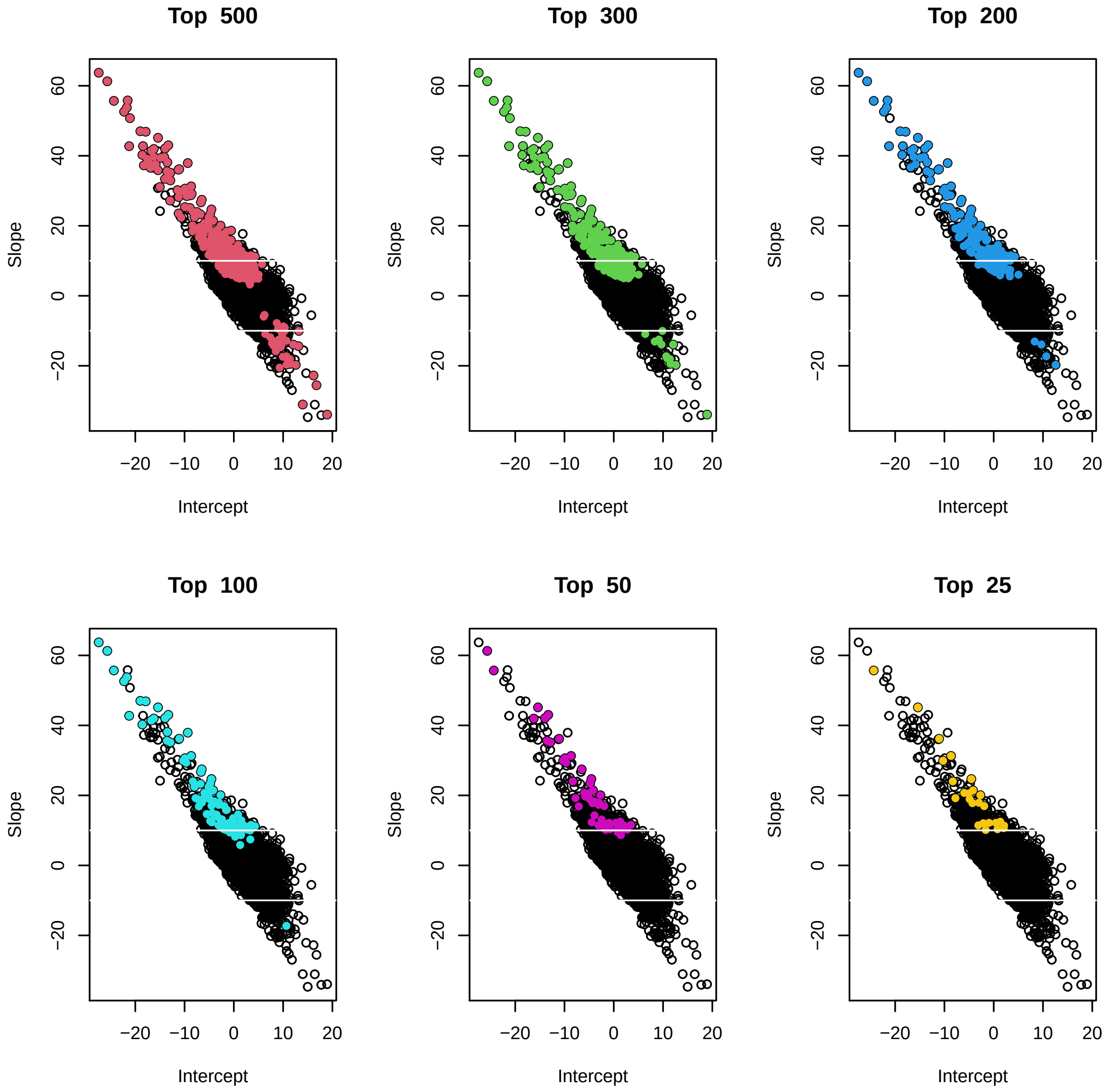


Figure 1: Coefficients for labeled number of top significant genes are indicated by colors. White line is a proposed treshold.

5.2 Top 20 genes

Plots of situation for top 20 genes.

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.

```
> out <- ""
> (cname <- colnames(coefs)[2])
```

```
[1] "swp"
```

```
> varnames <- rownames(head(tt,topn))
> varname <- varnames[1]
> for(varname in varnames)
+  out <- paste(out,knit_child(file.path("../doc/","40aa_one-gene-plots.Rnw"),
```

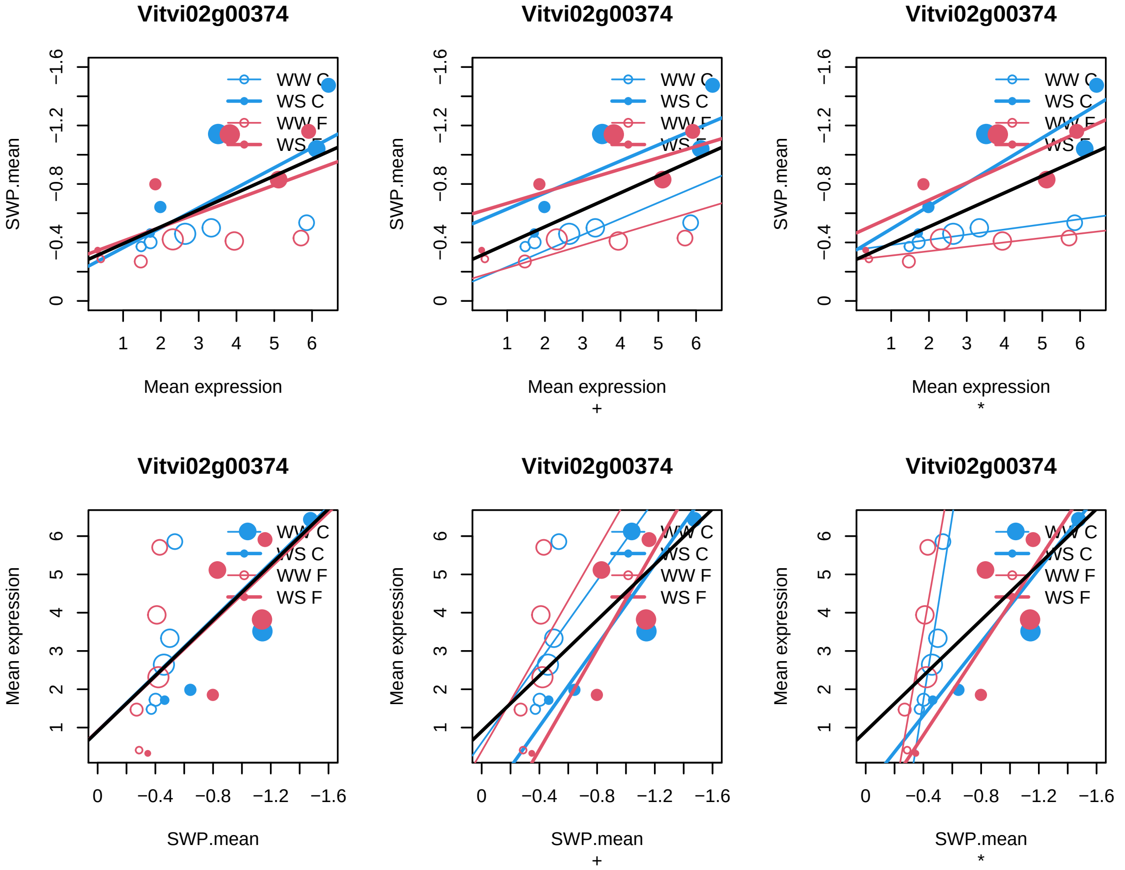
5.2.1 Vitvi02g00374

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

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

Coefficient swp for Vitvi02g00374.

```
                 logFC  AveExpr         t      P.Value     adj.P.Val
Vitvi02g00374 29.90913 3.28388 18.79698 2.300407e-31 3.506281e-27
                     B
Vitvi02g00374 55.20282
```



Correlation of all measurements (not just means): $r = 0.9026$, $r^2 = 0.8147$
Correlation of mean values (plots): $r_2 = 0.6490$

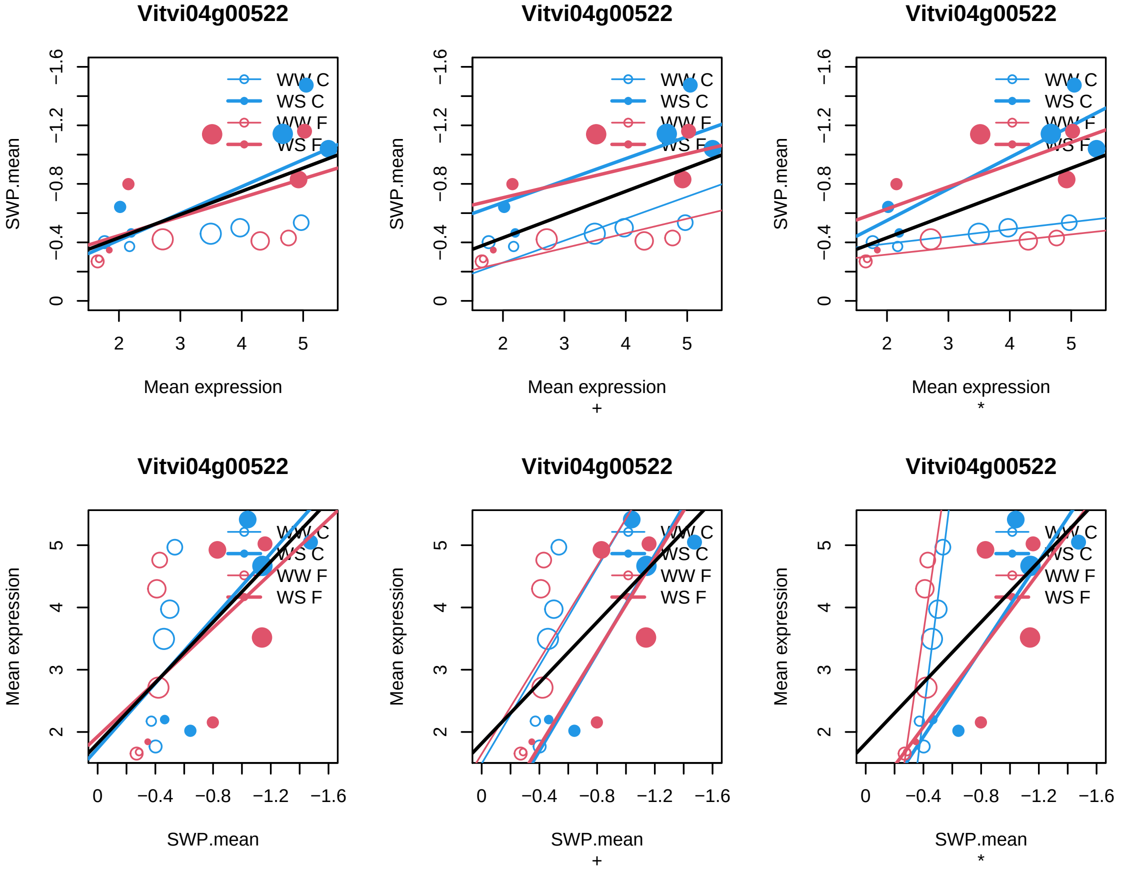
5.2.2 Vitvi04g00522

```
> 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
```

Coefficient swp for Vitvi04g00522.

```
                 logFC  AveExpr        t      P.Value    adj.P.Val
Vitvi04g00522 20.70966 3.414499 17.94327 4.900852e-30 3.734939e-26
                     B
Vitvi04g00522 52.74622
```



Correlation of all measurements (not just means): $r = 0.8957$, $r^2 = 0.8022$
Correlation of mean values (plots): $r_2 = 0.6215$

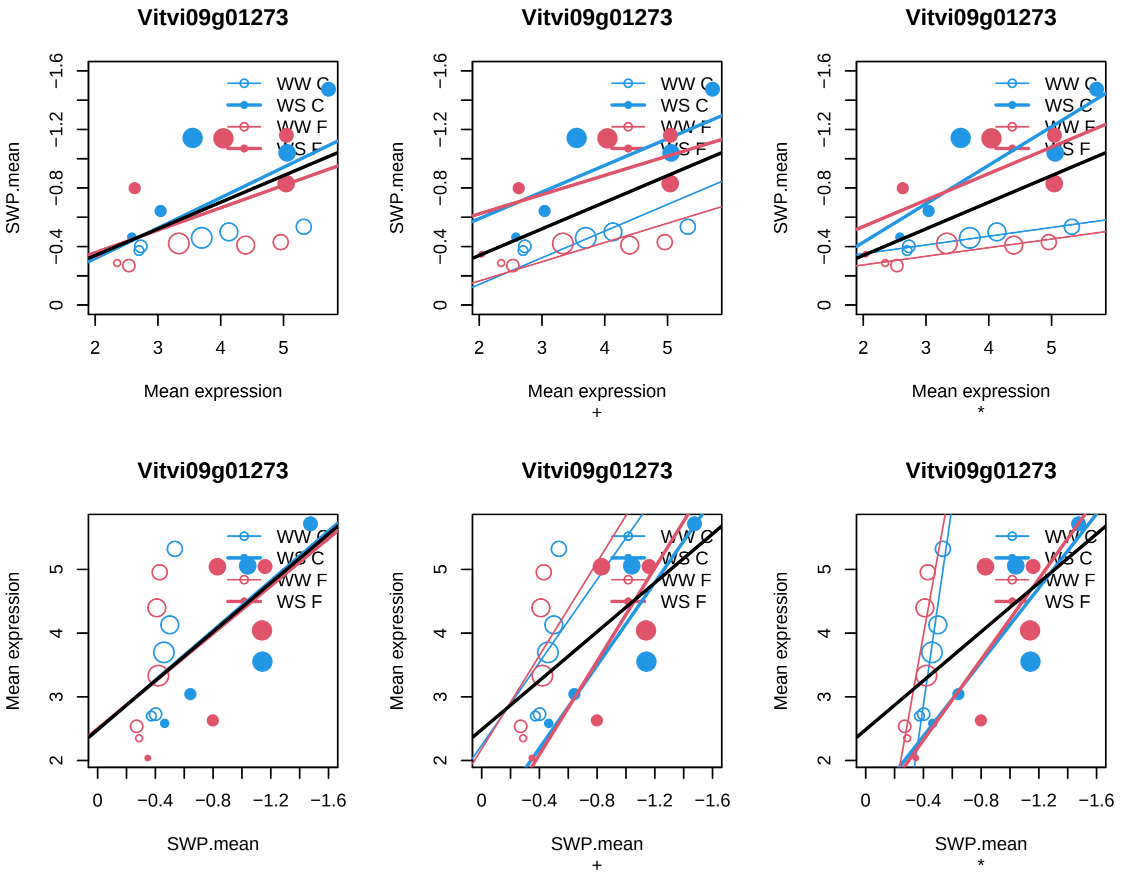
5.2.3 Vitvi09g01273

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

```
Vitvi09g01273
        35.2
        not assigned.unknown
        ATP-dependent DNA helicase |
        Chr4:14990523-14992855 FORWARD LENGTH=589 |
        201606
```

Coefficient swp for Vitvi09g01273.

```
                 logFC  AveExpr         t      P.Value    adj.P.Val
Vitvi09g01273 17.79031 3.745035 17.75236 9.830851e-30 3.831175e-26
                     B
Vitvi09g01273 52.18207
```



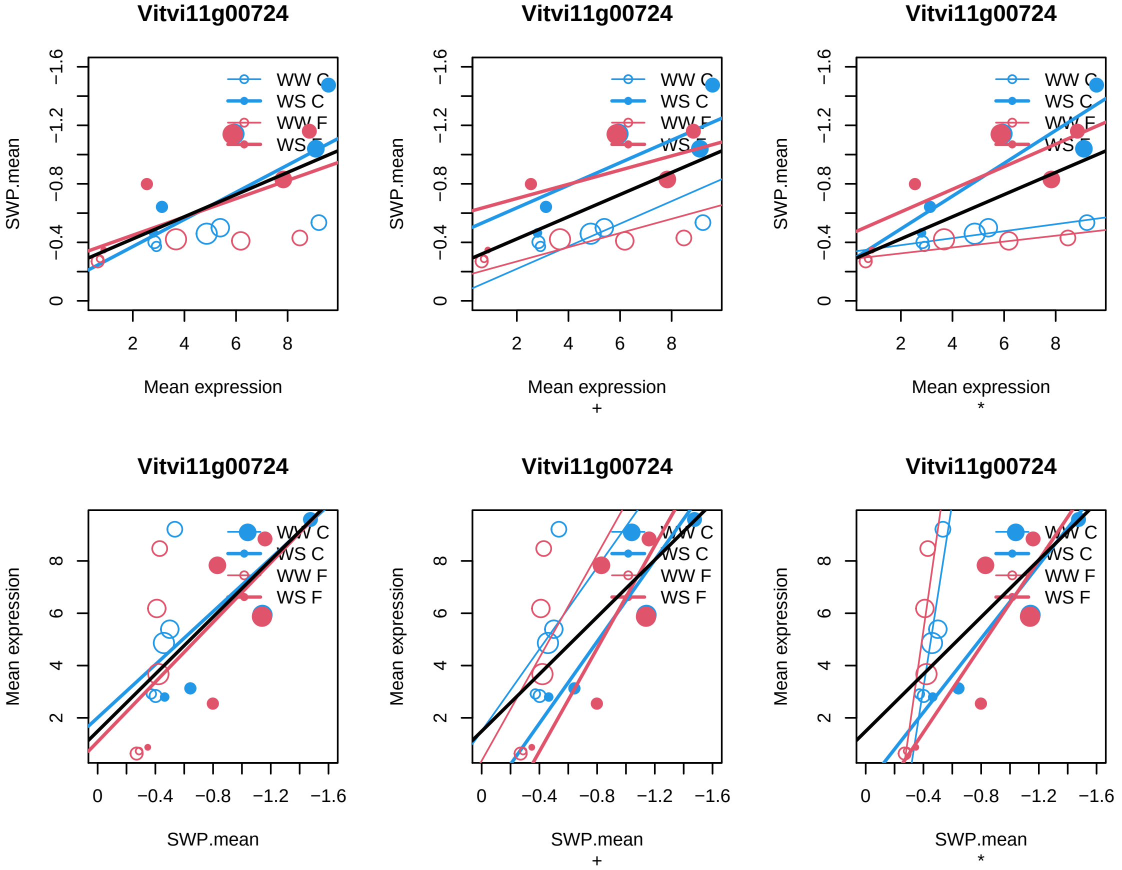
Correlation of all measurements (not just means): $r = 0.8945$, $r^2 = 0.8002$
Correlation of mean values (plots): $r_2 = 0.5909$

5.2.4 Vitvi11g00724

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
Vitvi11g00724
        20.02.2001
        stress.abiotic.heat
        heat shock protein 70B |
        Chr1:5502386-5504326 REVERSE LENGTH=646 |
        201606

Vitvi11g00724
        29.6
        protein.folding
        heat shock protein 70B |
        Chr1:5502386-5504326 REVERSE LENGTH=646 |
        201606
```

Coefficient swp for Vitvi11g00724.

```
                 logFC  AveExpr        t      P.Value    adj.P.Val
Vitvi11g00724 45.13777 5.070678 17.74622 1.005426e-29 3.831175e-26
                     B
Vitvi11g00724 52.16383
```



Correlation of all measurements (not just means): $r = 0.8918$, $r^2 = 0.7953$
Correlation of mean values (plots): $r_2 = 0.6429$

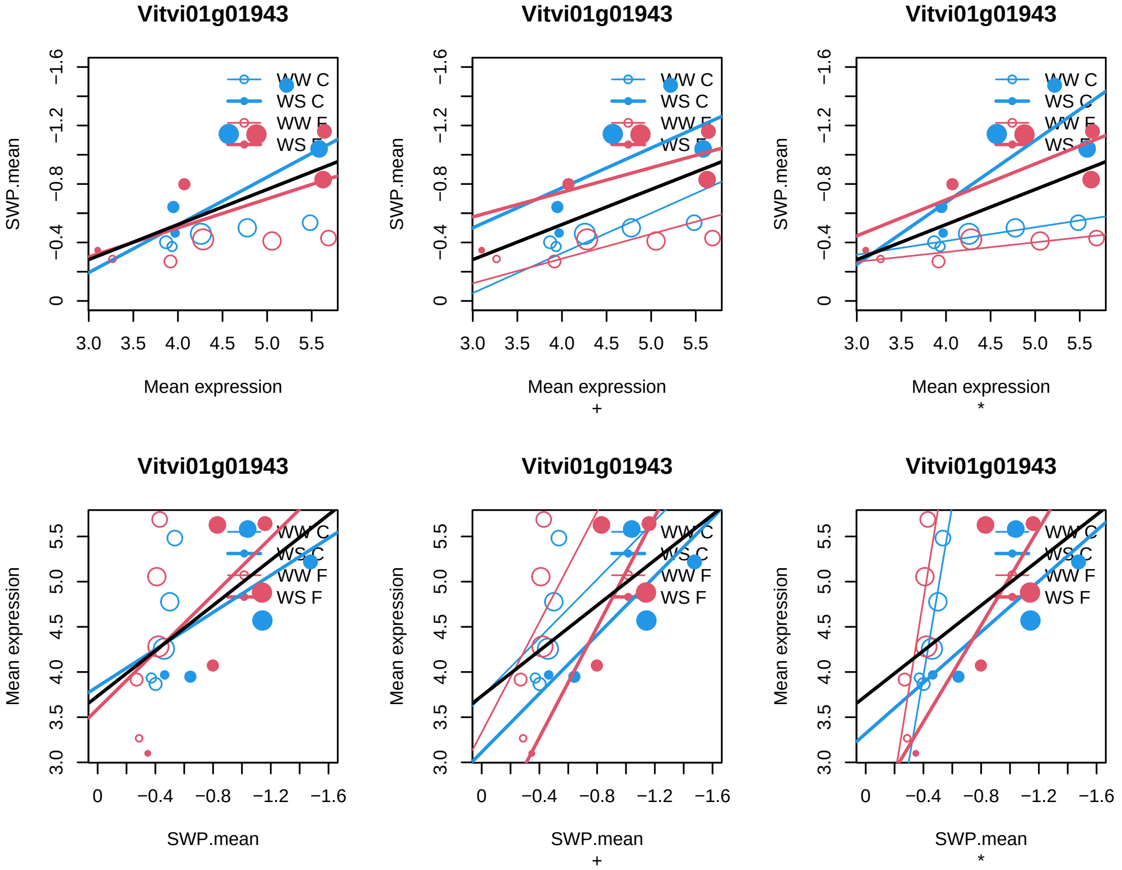
5.2.5 Vitvi01g01943

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

```
Vitvi01g01943
        20
        stress
        NA
```

Coefficient swp for Vitvi01g01943.

```
                 logFC AveExpr        t      P.Value    adj.P.Val
Vitvi01g01943 12.14569  4.5568 17.51369 2.361916e-29 6.767539e-26
                     B
Vitvi01g01943 51.46908
```



Correlation of all measurements (not just means): $r = 0.8956$, $r^2 = 0.8021$
Correlation of mean values (plots): $r_2 = 0.5485$

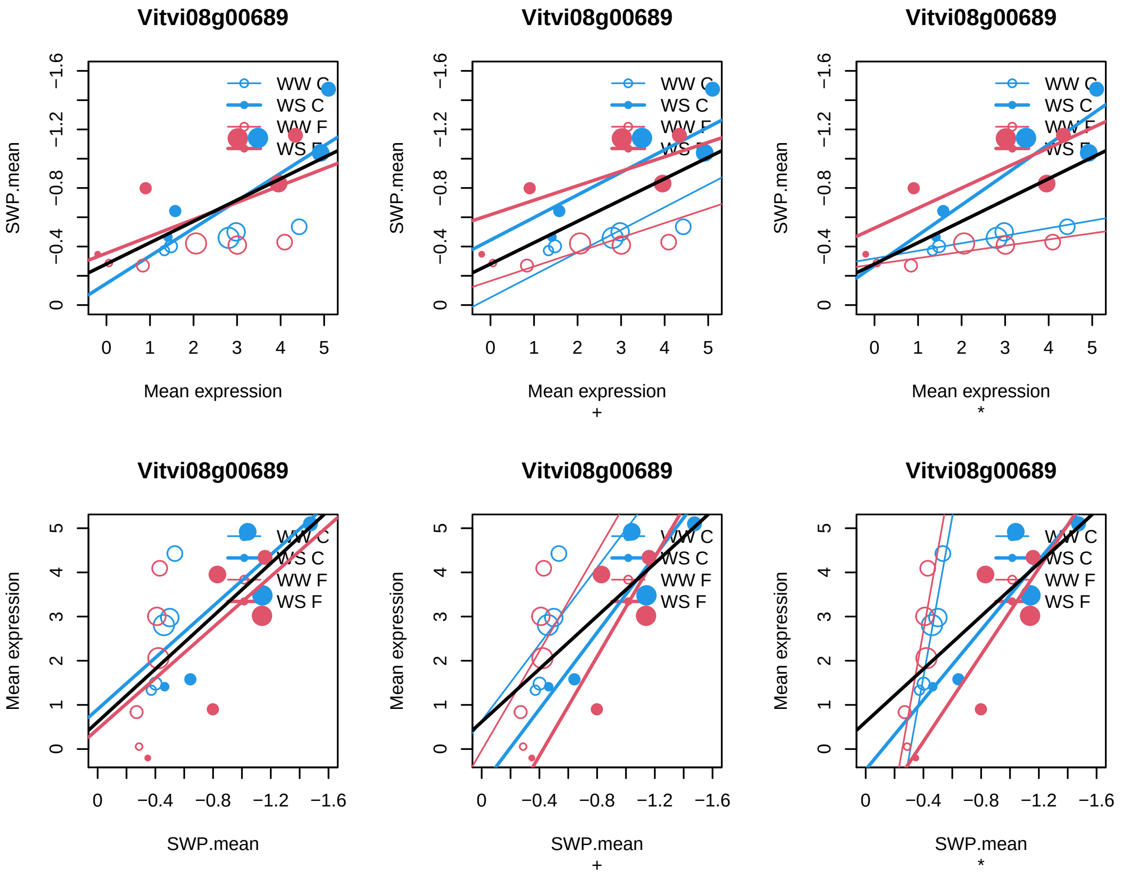
5.2.6 Vitvi08g00689

```
> 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
```

Coefficient swp for Vitvi08g00689.

```
                 logFC  AveExpr        t      P.Value    adj.P.Val
Vitvi08g00689 24.00508 2.578551 17.48107 2.664036e-29 6.767539e-26
                     B
Vitvi08g00689 51.37095
```



Correlation of all measurements (not just means): $r = 0.8902$, $r^2 = 0.7925$
Correlation of mean values (plots): $r_2 = 0.6601$

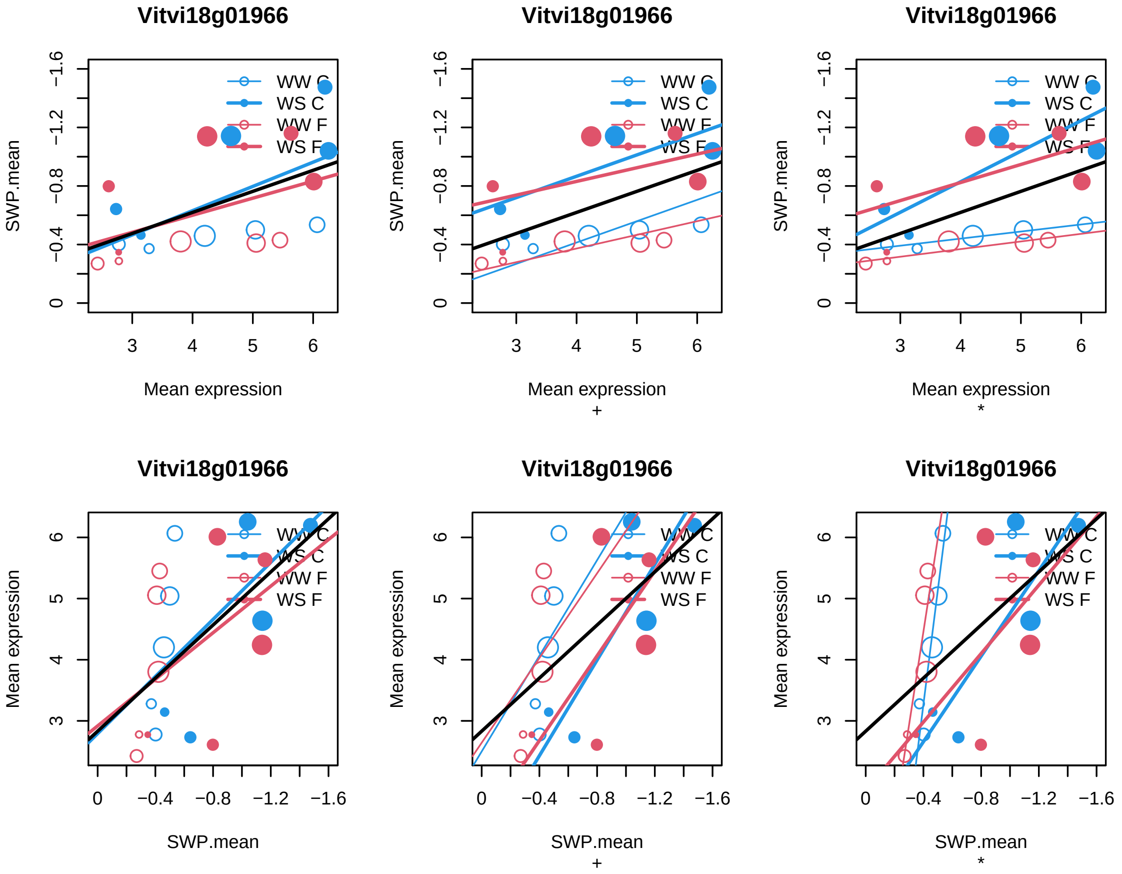
5.2.7 Vitvi18g01966

```
> 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
```

Coefficient swp for Vitvi18g01966.

```
                 logFC  AveExpr        t      P.Value    adj.P.Val
Vitvi18g01966 20.56758 4.255793 17.39113 3.714865e-29 8.088852e-26
                     B
Vitvi18g01966 51.09958
```



Correlation of all measurements (not just means): $r = 0.8899$, $r^2 = 0.7919$
Correlation of mean values (plots): $r_2 = 0.5587$

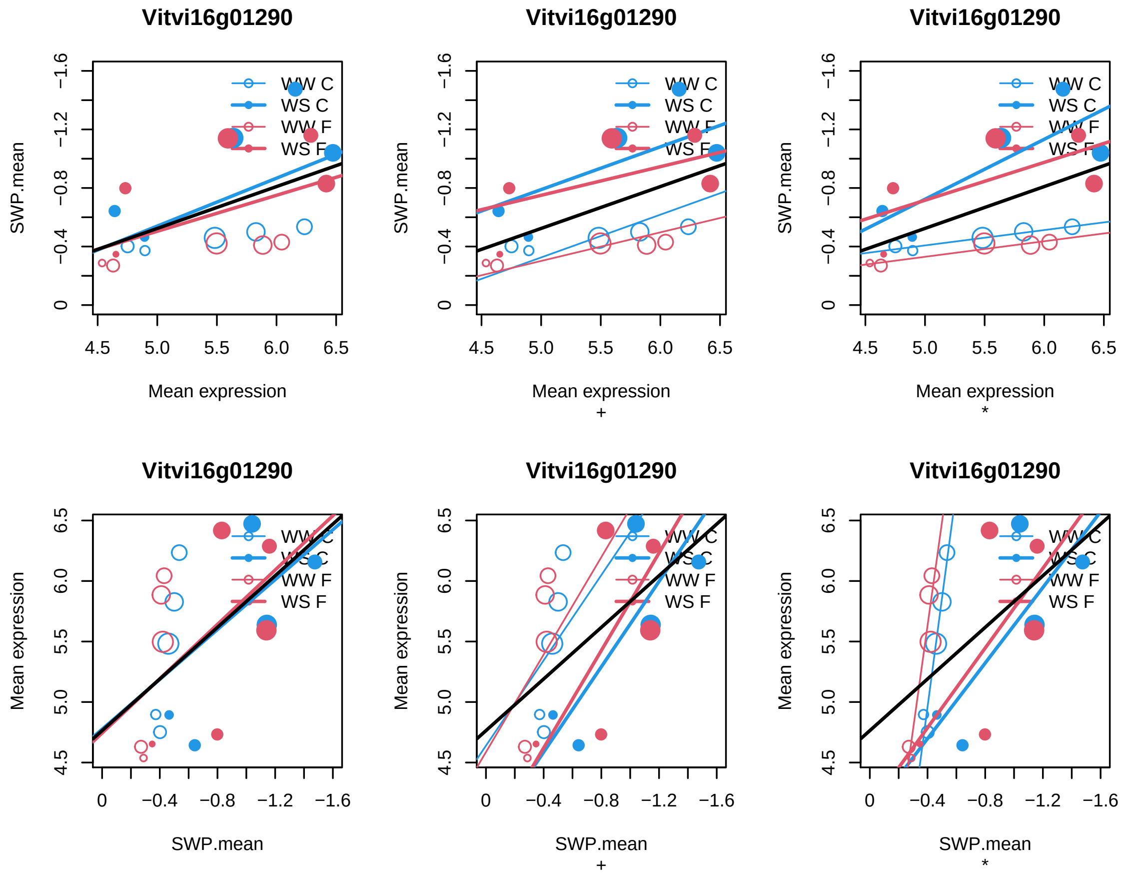
5.2.8 Vitvi16g01290

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

```
Vitvi16g01290
        20.02.2001
        stress.abiotic.heat
        HSP20-like chaperones superfamily protein |
        Chr5:21661588-21663383 FORWARD LENGTH=304 |
        201606
```

Coefficient swp for Vitvi16g01290.

```
                 logFC  AveExpr        t      P.Value    adj.P.Val
Vitvi16g01290 10.34352 5.463575 17.27953 5.619824e-29 1.070717e-25
                     B
Vitvi16g01290 50.76115
```



Correlation of all measurements (not just means): $r = 0.8955$, $r^2 = 0.8020$
Correlation of mean values (plots): $r_2 = 0.5522$

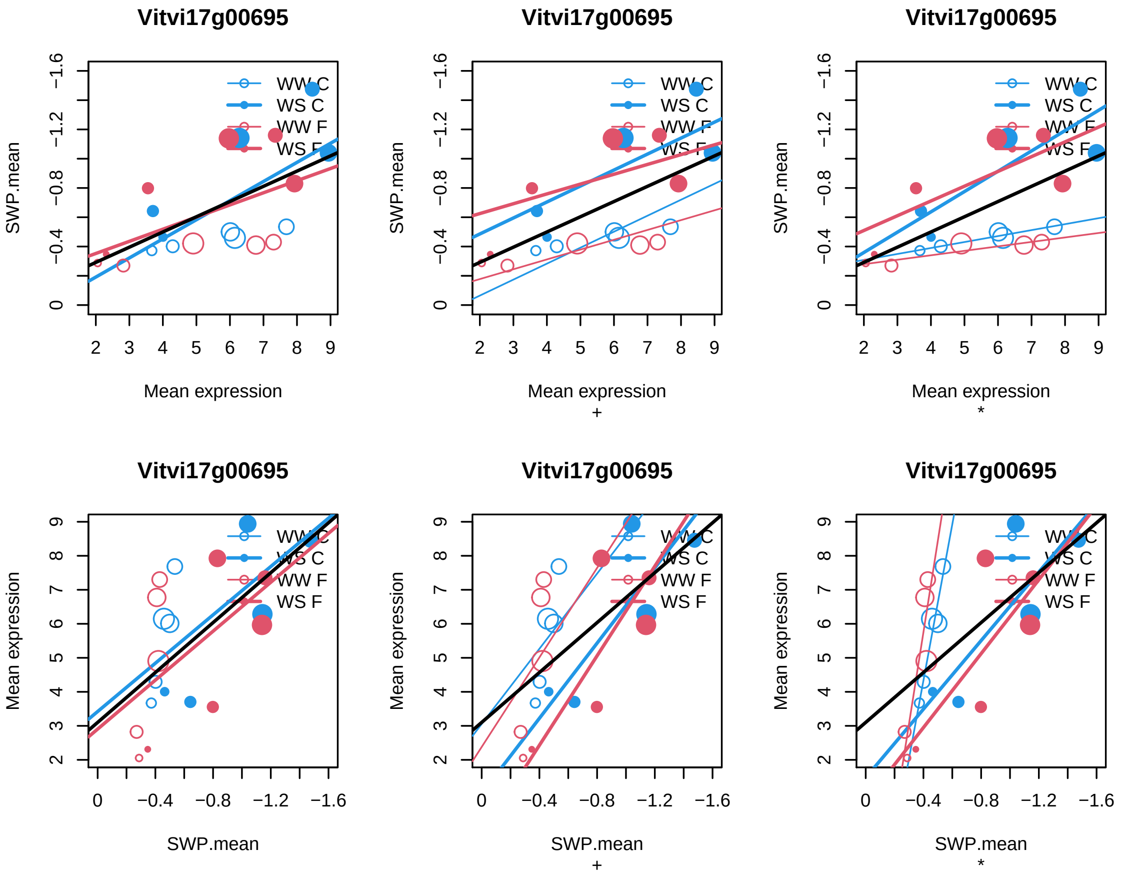
5.2.9 Vitvi17g00695

```
> 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
```

Coefficient swp for Vitvi17g00695.

```
                 logFC  AveExpr        t      P.Value    adj.P.Val
Vitvi17g00695 31.26828 5.508229 17.18961 7.853662e-29 1.330061e-25
                     B
Vitvi17g00695 50.48708
```



Correlation of all measurements (not just means): $r = 0.8863$, $r^2 = 0.7856$
Correlation of mean values (plots): $r_2 = 0.6175$

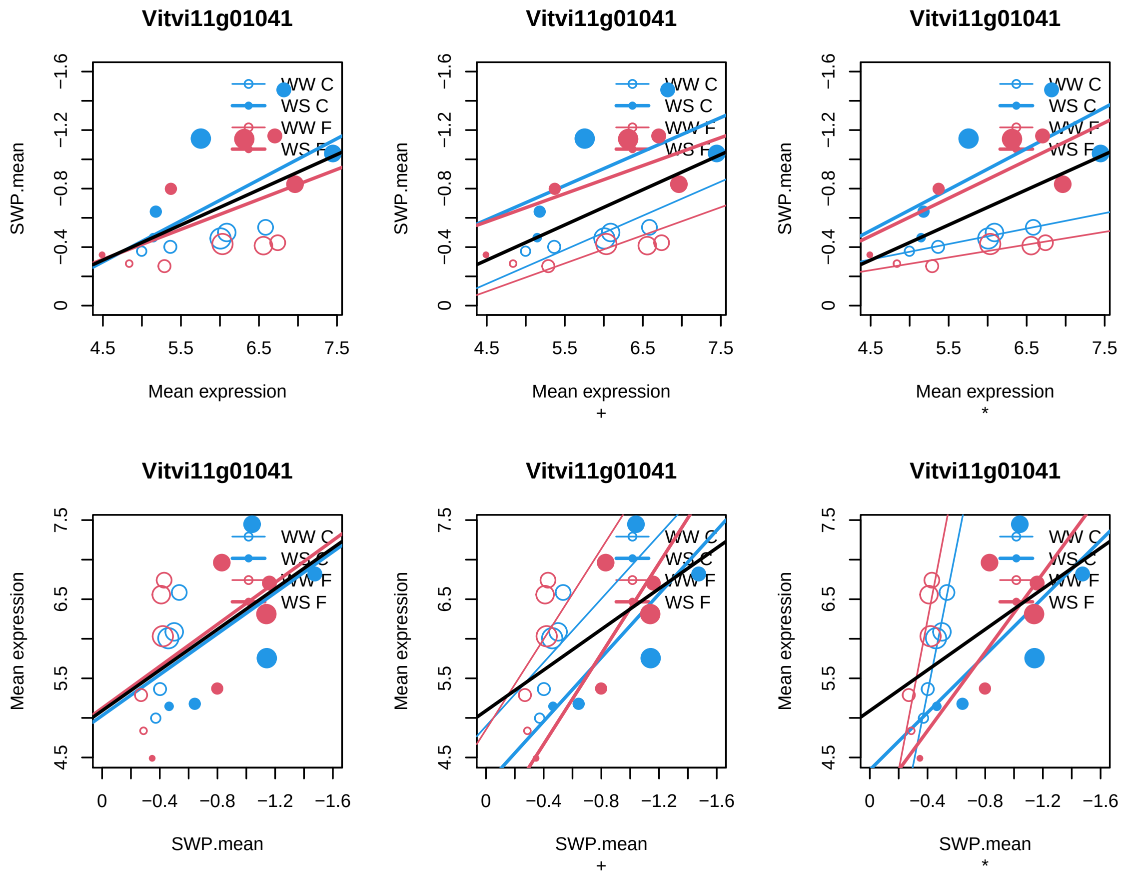
5.2.10 Vitvi11g01041

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

```
Vitvi11g01041
        35.2
        not assigned.unknown
        Genomic DNA chromosome 5 P1 clone MVP2
```

Coefficient swp for Vitvi11g01041.

```
                 logFC  AveExpr       t      P.Value    adj.P.Val
Vitvi11g01041 12.15265 5.934203 17.0483 1.331594e-28 2.017785e-25
                     B
Vitvi11g01041 50.05386
```



Correlation of all measurements (not just means): $r = 0.8903$, $r^2 = 0.7927$
Correlation of mean values (plots): $r_2 = 0.5562$

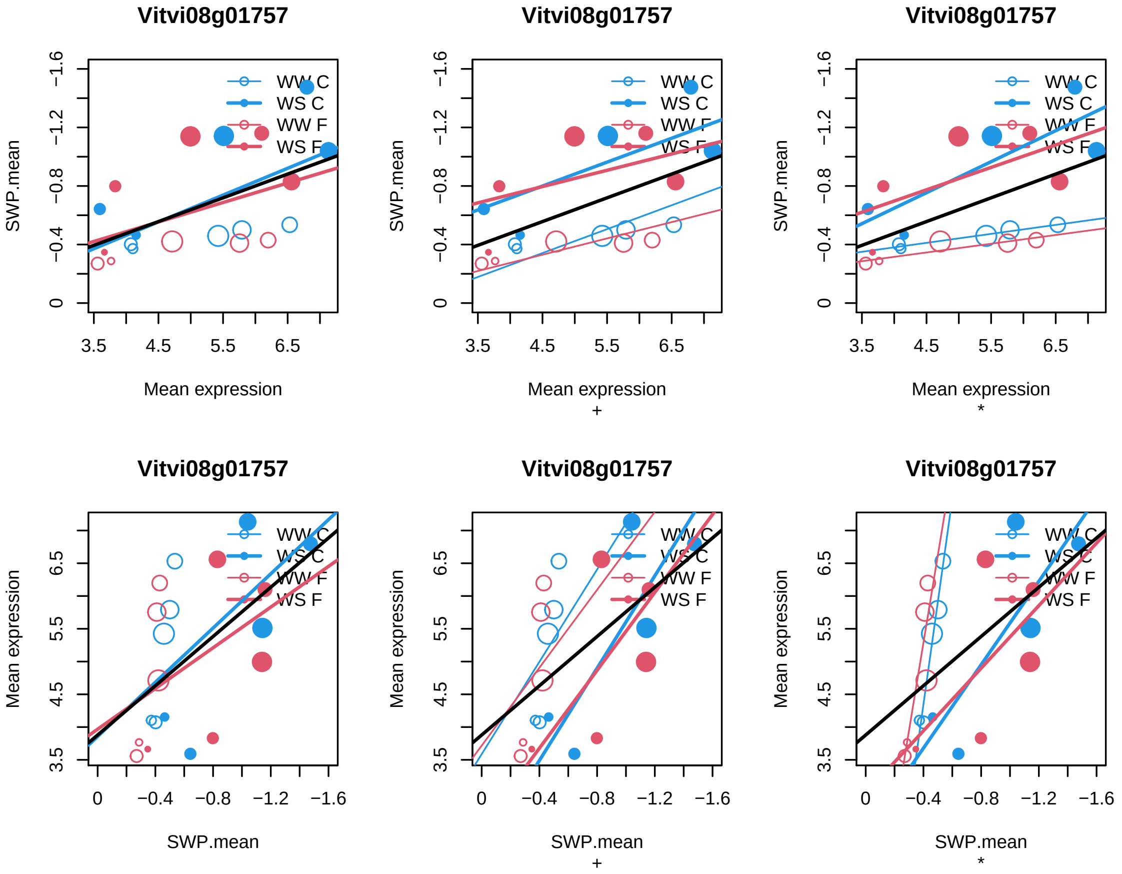
5.2.11 Vitvi08g01757

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

```
Vitvi08g01757
        35.1
        not assigned.no ontology
        Aha1 domain-containing protein |
        Chr3:3839289-3841303 FORWARD LENGTH=360 |
        201606
```

Coefficient swp for Vitvi08g01757.

```
                 logFC  AveExpr        t      P.Value    adj.P.Val
Vitvi08g01757 17.90111 5.112598 17.02443 1.456216e-28 2.017785e-25
                     B
Vitvi08g01757 49.98036
```



Correlation of all measurements (not just means): $r = 0.8865$, $r^2 = 0.7859$
Correlation of mean values (plots): $r_2 = 0.5523$

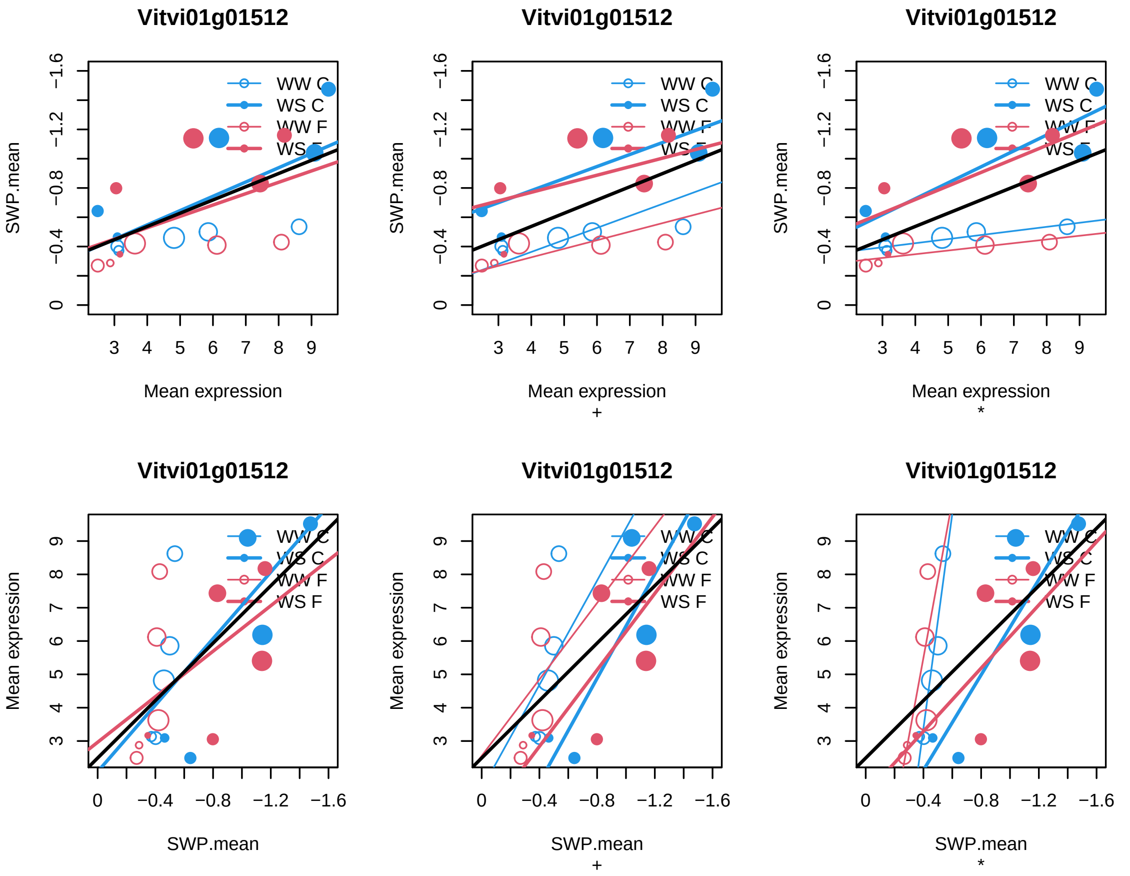
5.2.12 Vitvi01g01512

```
> 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
```

Coefficient swp for Vitvi01g01512.

```
                  logFC AveExpr        t      P.Value    adj.P.Val
Vitvi01g01512 36.17683 5.31657 16.82069 3.133275e-28 3.979781e-25
                     B
Vitvi01g01512 49.3496
```



Correlation of all measurements (not just means): $r = 0.8819$, $r^2 = 0.7777$
Correlation of mean values (plots): $r_2 = 0.6241$

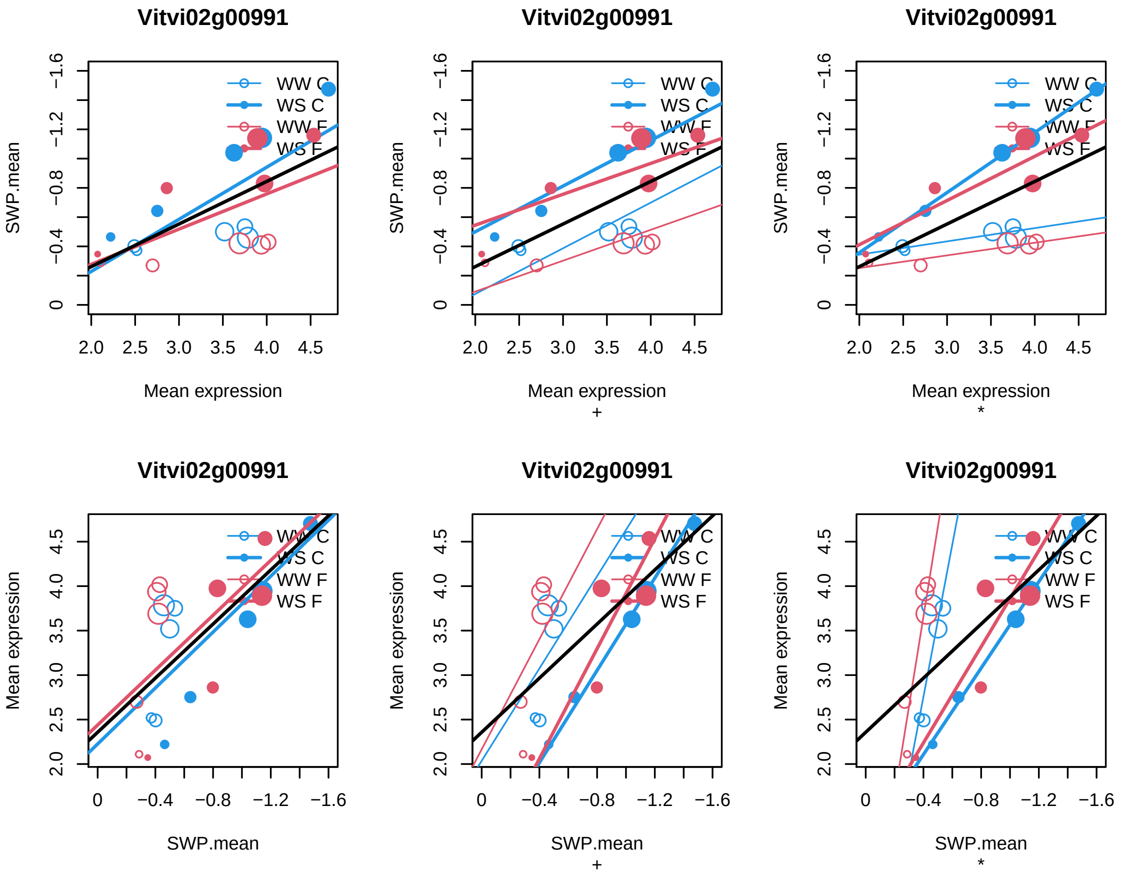
5.2.13 Vitvi02g00991

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

```
Vitvi02g00991
        35.2
        not assigned.unknown
        UDP-Glycosyltransferase superfamily protein |
        Chr2:15417618-15419108 REVERSE LENGTH=496 |
        201606
```

Coefficient swp for Vitvi02g00991.

```
                 logFC AveExpr        t      P.Value    adj.P.Val
Vitvi02g00991 12.05033 3.35527 16.64172 6.168548e-28 7.232385e-25
                     B
Vitvi02g00991 48.79022
```



Correlation of all measurements (not just means): $r = 0.8856$, $r^2 = 0.7843$
Correlation of mean values (plots): $r_2 = 0.6655$

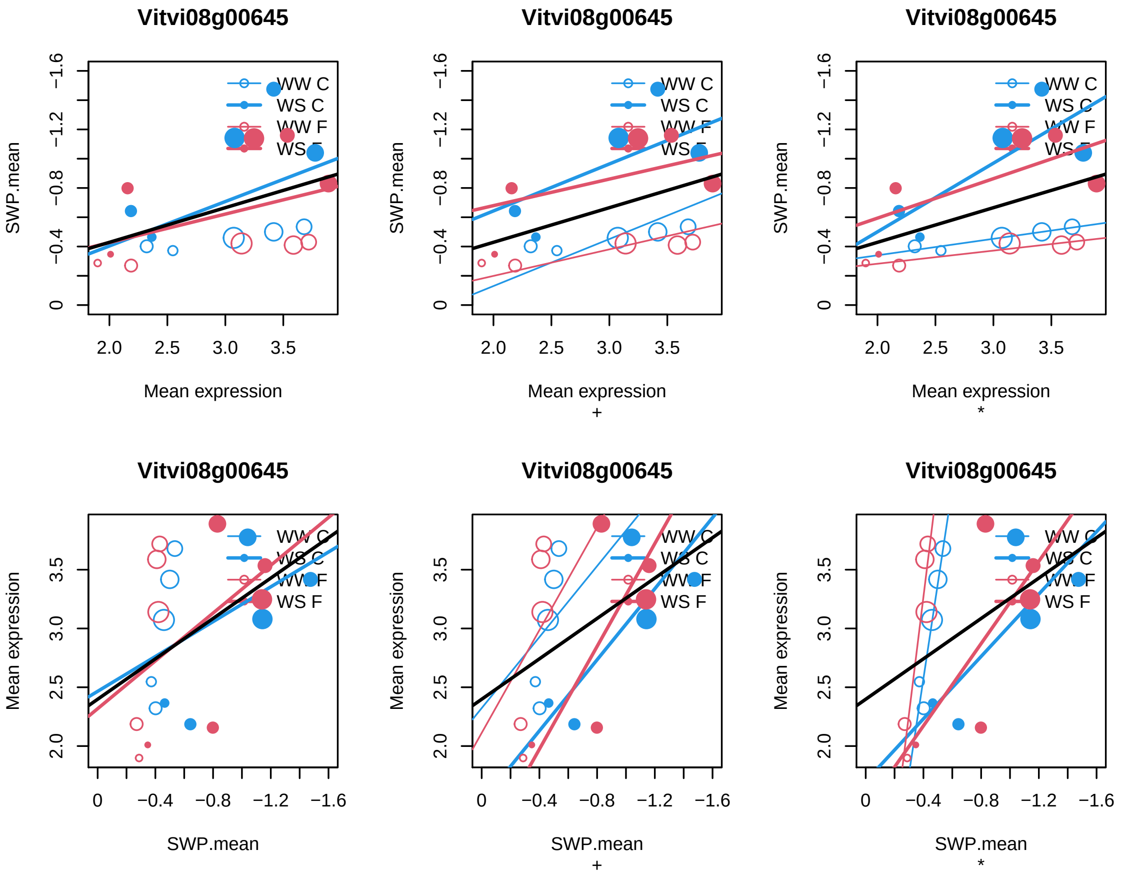
5.2.14 Vitvi08g00645

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

```
Vitvi08g00645
        29.03.1999
        protein.targeting.unknown
        Haloacid dehalogenase-like hydrolase (HAD) superfamily protein |
        Chr3:20760797-20762892 REVERSE LENGTH=305 |
        201606
```

Coefficient swp for Vitvi08g00645.

```
                  logFC  AveExpr        t      P.Value    adj.P.Val
Vitvi08g00645 10.12433 2.961665 16.61784 6.754009e-28 7.353186e-25
                     B
Vitvi08g00645 48.71522
```



Correlation of all measurements (not just means): $r = 0.8881$, $r^2 = 0.7887$
Correlation of mean values (plots): $r_2 = 0.4506$

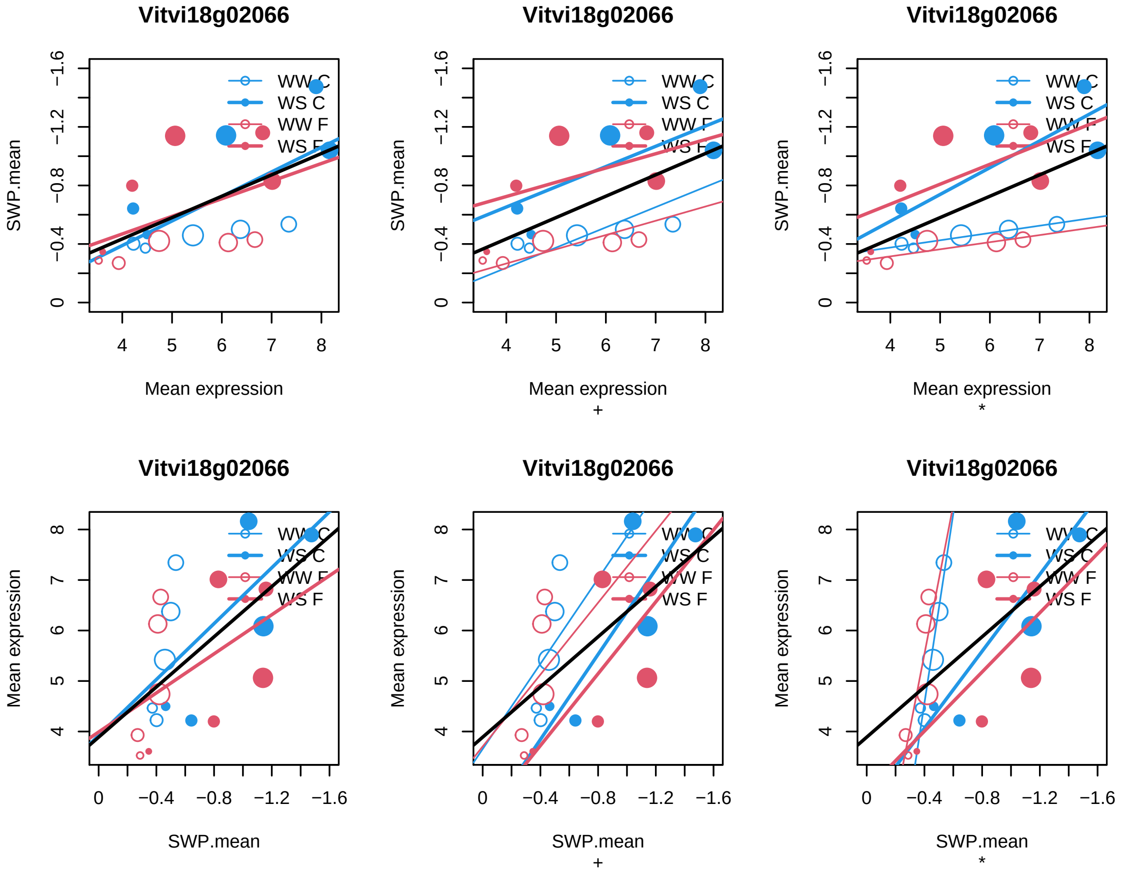
5.2.15 Vitvi18g02066

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

```
Vitvi18g02066
        20.02.2001
        stress.abiotic.heat
        chloroplast heat shock protein 70-1 |
        Chr4:12590094-12593437 FORWARD LENGTH=718 |
        201606

Vitvi18g02066
        29.6
        protein.folding
        chloroplast heat shock protein 70-1 |
        Chr4:12590094-12593437 FORWARD LENGTH=718 |
        201606
```

Coefficient swp for Vitvi18g02066.

```
                  logFC  AveExpr        t      P.Value    adj.P.Val
Vitvi18g02066 21.43313 5.518923 16.41996 1.435959e-27 1.459126e-24
                      B
Vitvi18g02066 48.09019
```



Correlation of all measurements (not just means): $r = 0.8784$, $r^2 = 0.7715$
Correlation of mean values (plots): $r_2 = 0.6021$

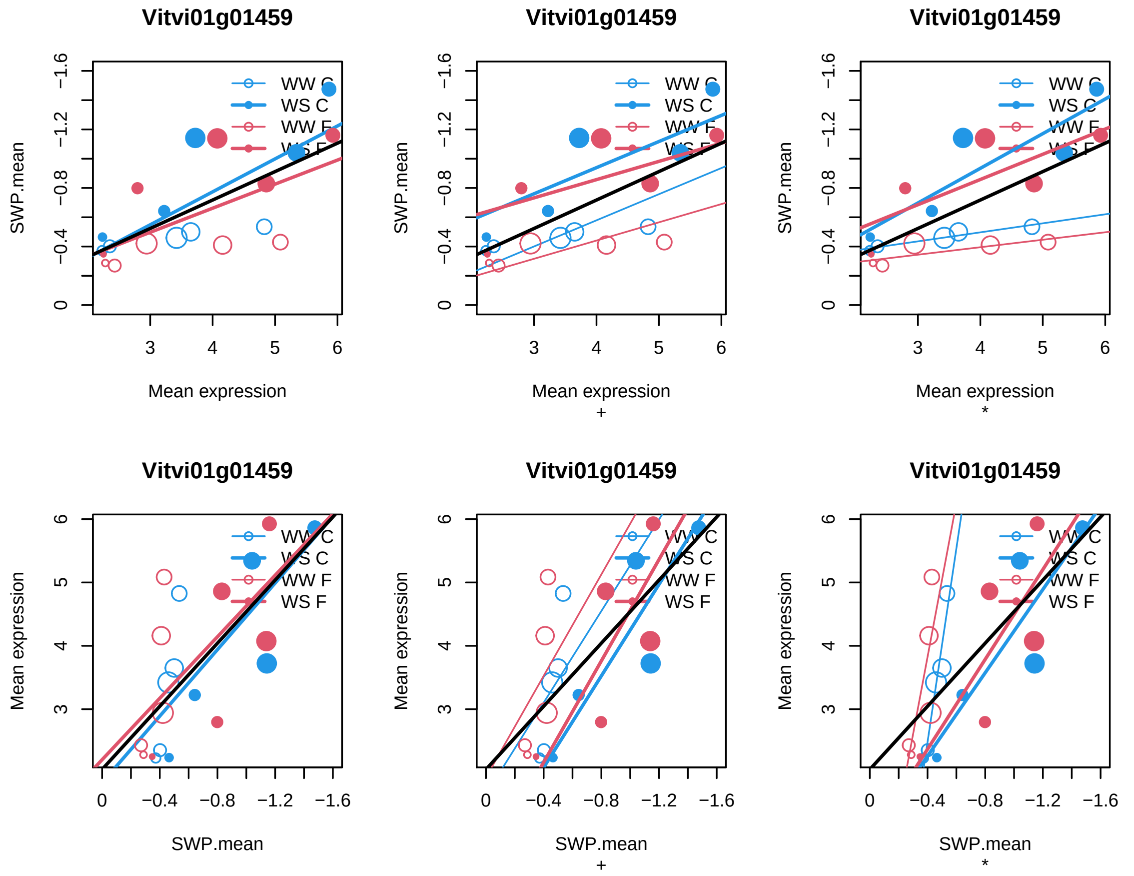
5.2.16 Vitvi01g01459

```
> 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
```

Coefficient swp for Vitvi01g01459.

```
                 logFC  AveExpr        t      P.Value    adj.P.Val
Vitvi01g01459 18.91439 3.683872 16.32173 2.091898e-27 1.992795e-24
                     B
Vitvi01g01459 47.77767
```



Correlation of all measurements (not just means): $r = 0.8777$, $r^2 = 0.7704$
Correlation of mean values (plots): $r_2 = 0.6956$

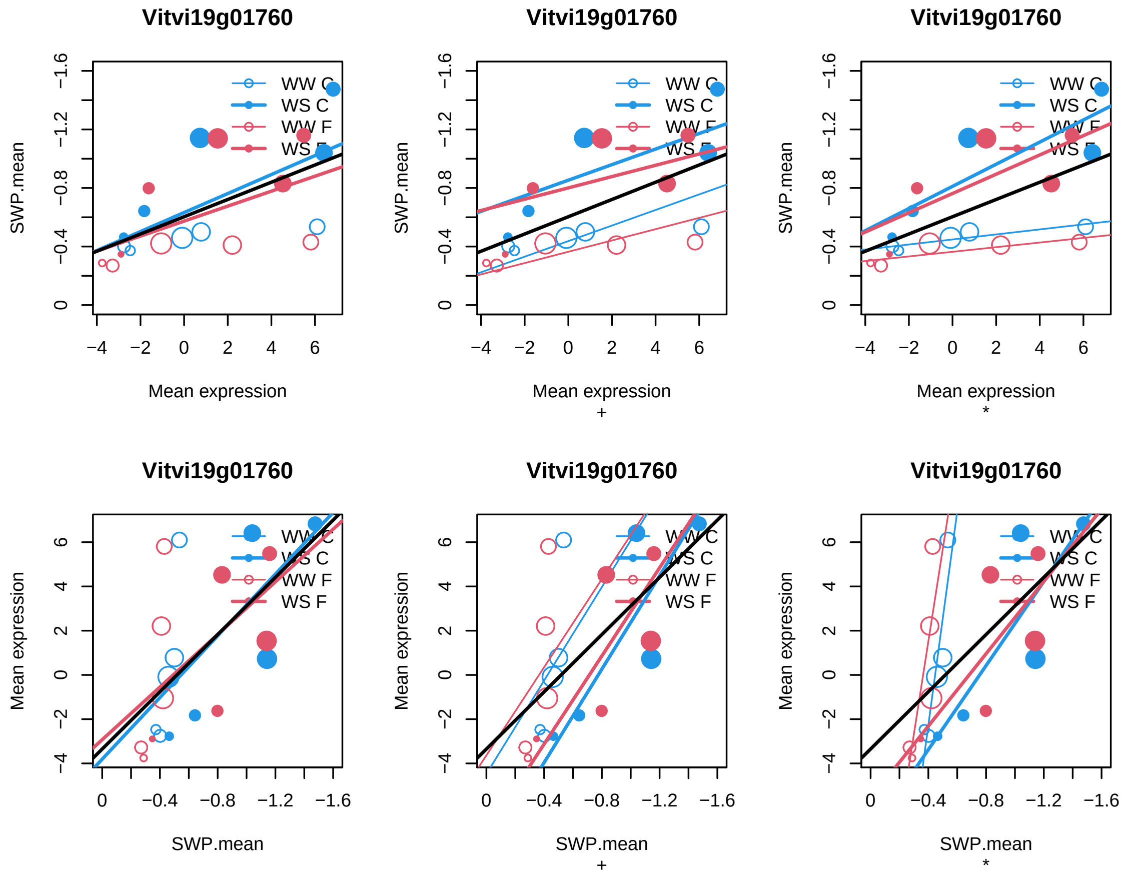
5.2.17 Vitvi19g01760

```
> 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
```

Coefficient swp for Vitvi19g01760.

```
                 logFC   AveExpr        t      P.Value    adj.P.Val
Vitvi19g01760 55.69011 0.8952506 16.20667 3.255542e-27 2.918881e-24
                     B
Vitvi19g01760 47.40966
```



Correlation of all measurements (not just means): $r = 0.8739$, $r^2 = 0.7638$
Correlation of mean values (plots): $r_2 = 0.6174$

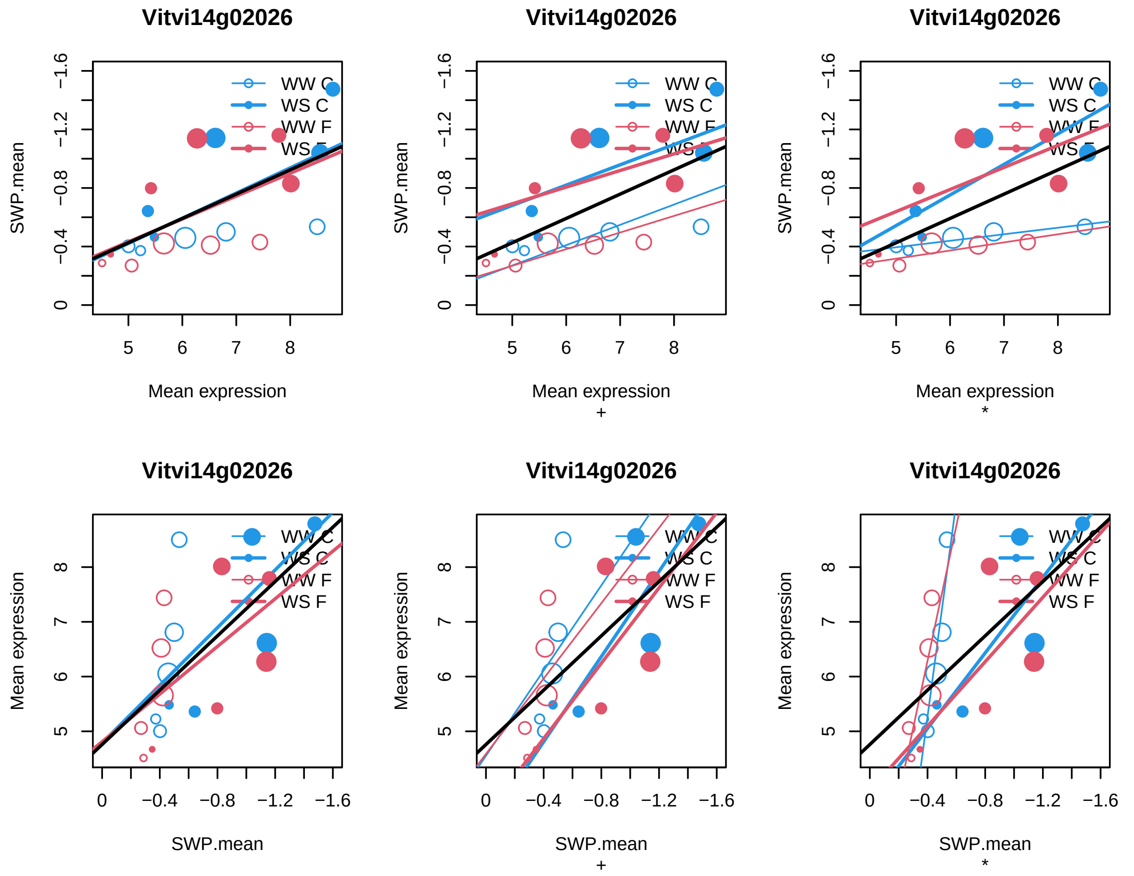
5.2.18 Vitvi14g02026

```
> 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
```

Coefficient swp for Vitvi14g02026.

```
                 logFC  AveExpr        t      P.Value    adj.P.Val
Vitvi14g02026 20.05851 6.387659 16.17746 3.643339e-27 3.044873e-24
                     B
Vitvi14g02026 47.31591
```



Correlation of all measurements (not just means): $r = 0.8756$, $r^2 = 0.7666$
Correlation of mean values (plots): $r_2 = 0.6419$

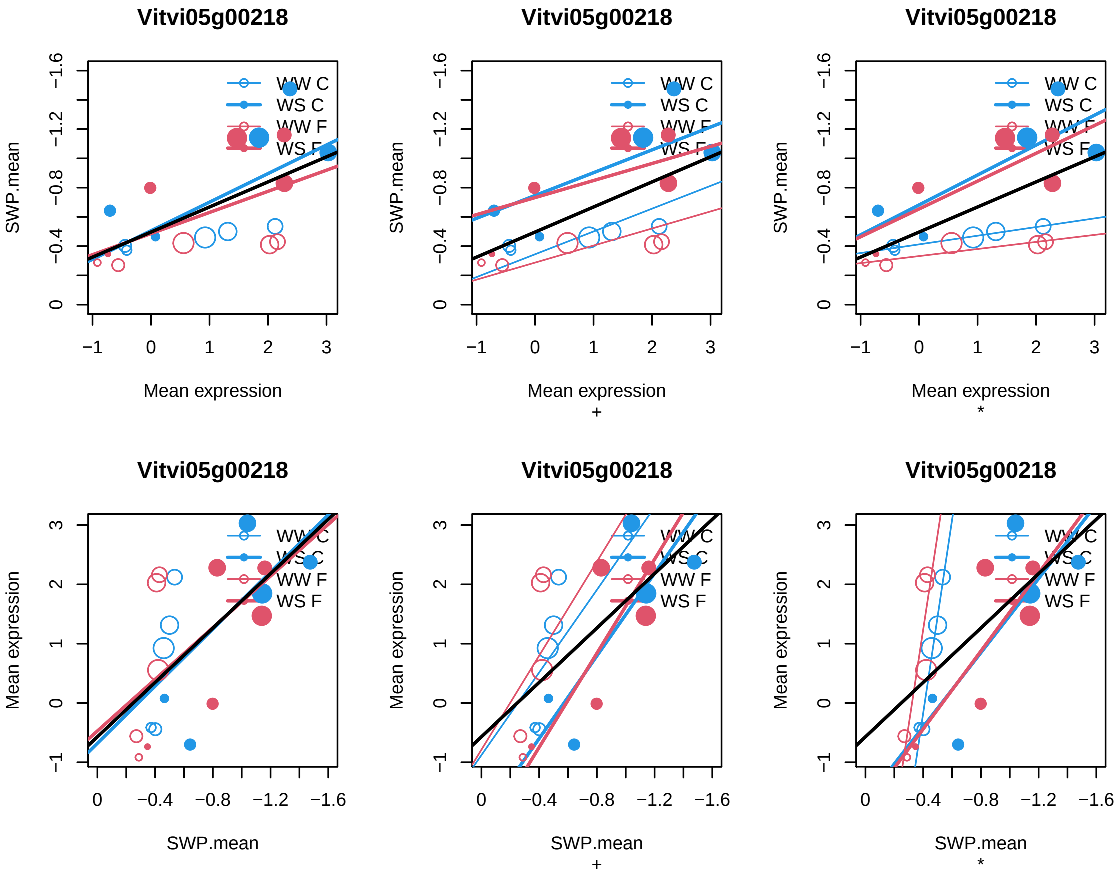
5.2.19 Vitvi05g00218

```
> 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
```

Coefficient swp for Vitvi05g00218.

```
                 logFC  AveExpr        t      P.Value    adj.P.Val
Vitvi05g00218 19.21392 0.933593 16.16684 3.795603e-27 3.044873e-24
                    B
Vitvi05g00218 47.2818
```



Correlation of all measurements (not just means): $r = 0.8756$, $r^2 = 0.7668$
Correlation of mean values (plots): $r_2 = 0.6269$

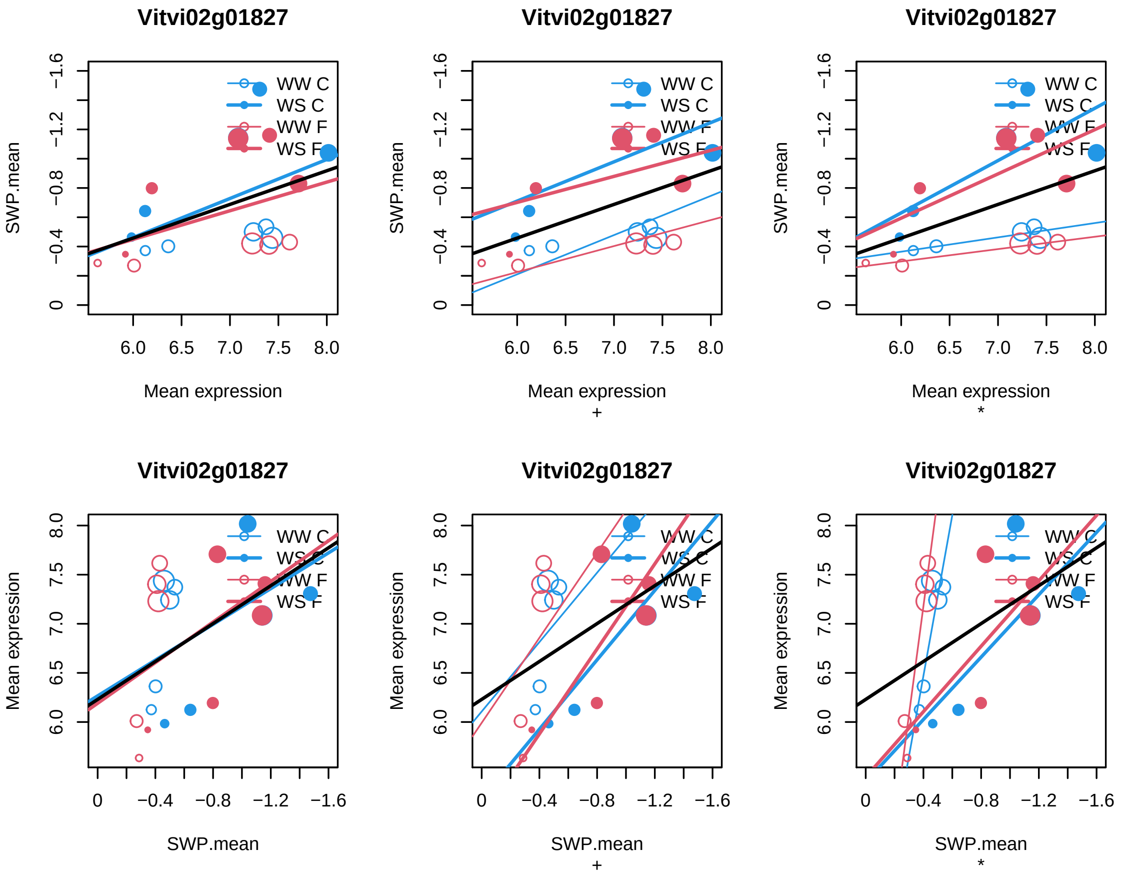
5.2.20 Vitvi02g01827

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

```
Vitvi02g01827
        31.05.2002
        cell.cell death.apoptosis
        BAX inhibitor 1 |
        Chr5:19136071-19137585 FORWARD LENGTH=247 |
        201606
```

Coefficient swp for Vitvi02g01827.

```
                 logFC  AveExpr        t      P.Value    adj.P.Val
Vitvi02g01827 10.64761 6.863265 16.12778 4.413194e-27 3.363295e-24
                     B
Vitvi02g01827 47.15613
```



Correlation of all measurements (not just means): $r = 0.8809$, $r^2 = 0.7760$
Correlation of mean values (plots): $r_2 = 0.4711$

5.3 Bottom 20 genes

Plots of situation for top 20 genes

```
> out <- ""
> (cname <- colnames(coefs)[2])
```

```
[1] "swp"
```

```
> varnames <- rownames(tail(tt,topn))
> varname <- varnames[1]
> for(varname in varnames)
+  out <- paste(out,knit_child(file.path("../doc/","40aa_one-gene-plots.Rnw"),
```

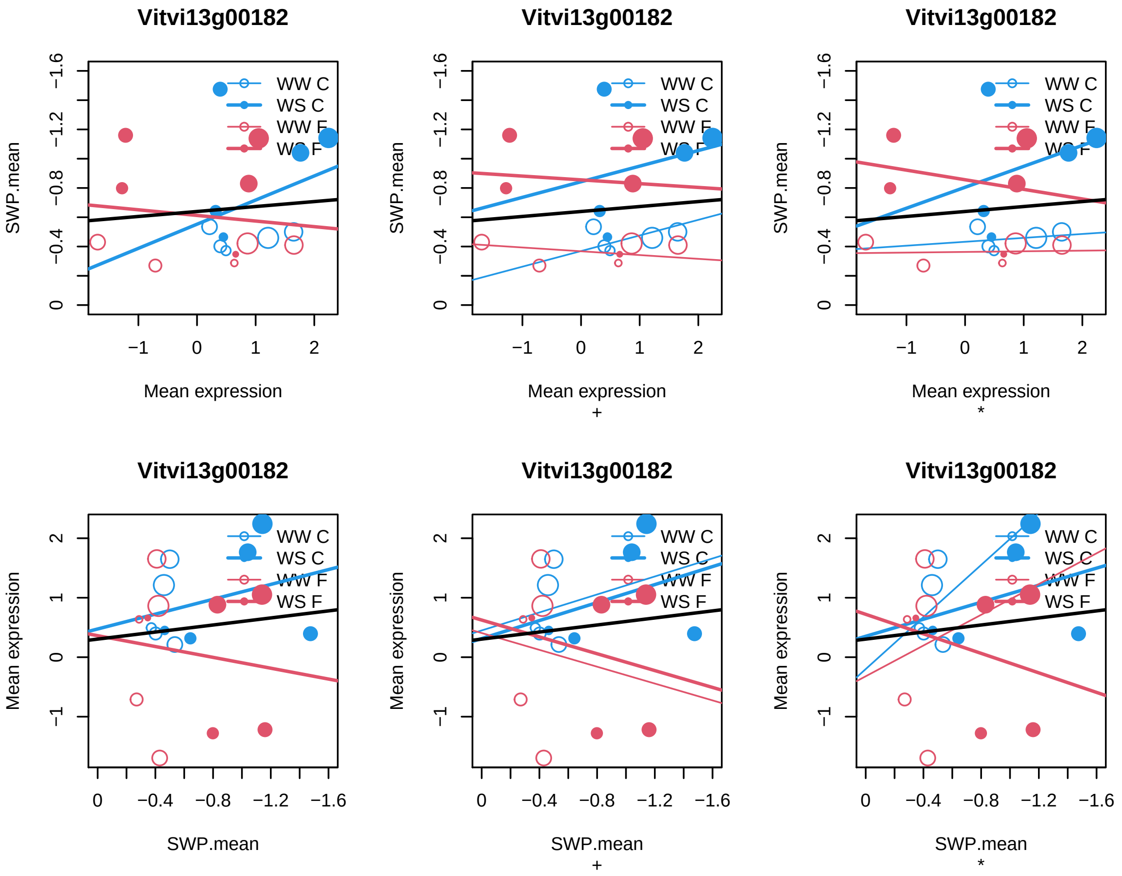
5.3.1 Vitvi13g00182

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

```
Vitvi13g00182
        30.2.7
        signalling.receptor kinases.leucine rich repeat VII
        Leucine-rich repeat protein kinase family protein |
        Chr3:20899403-20902390 REVERSE LENGTH=964 |
        201606
```

Coefficient swp for Vitvi13g00182.

```
                   logFC   AveExpr           t   P.Value adj.P.Val
Vitvi13g00182 0.01401526 0.4989287 0.006841771 0.9945578 0.9957991
                        B
Vitvi13g00182 -6.117765
```



Correlation of all measurements (not just means): $r = 8e - 04$, $r^2 = 6e - 07$
Correlation of mean values (plots): $r_2 = 0.1003$

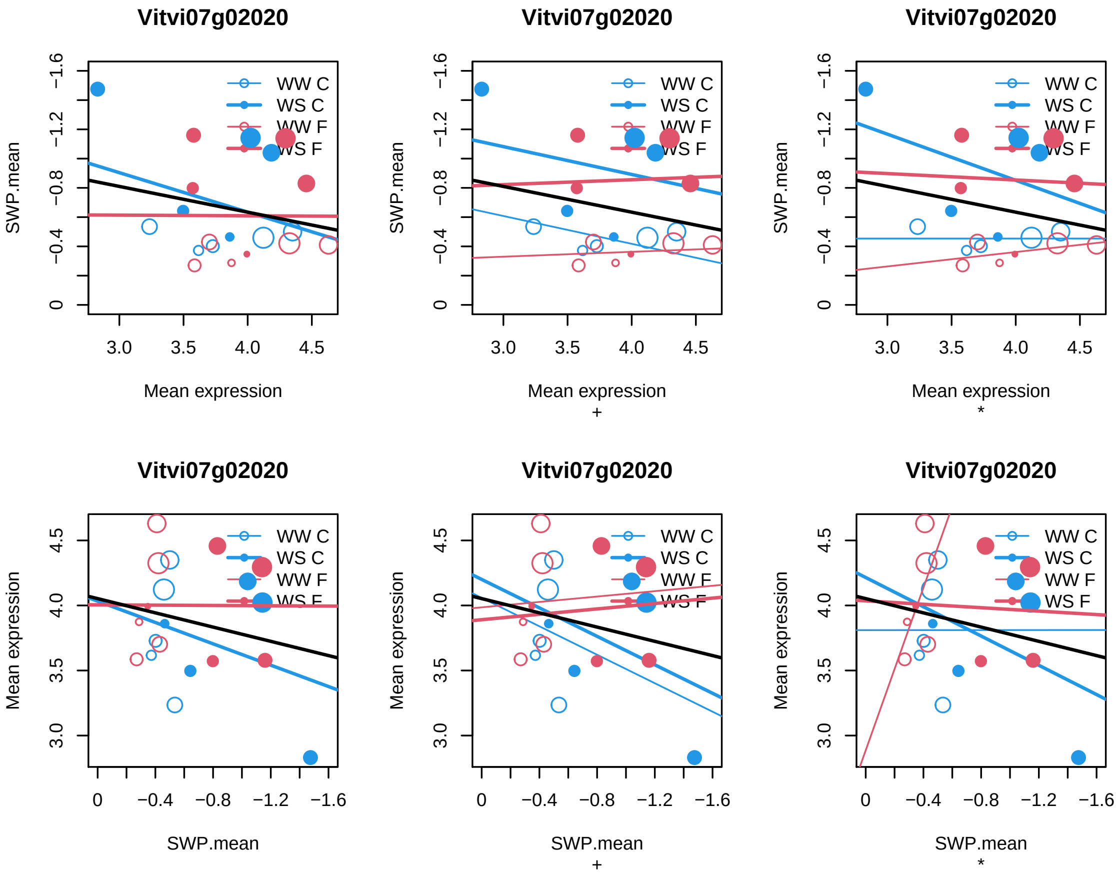
5.3.2 Vitvi07g02020

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

```
Vitvi07g02020
        11.9.4.5
        lipid metabolism.lipid degradation.beta-oxidation.acyl-CoA thioesteras
        Thioesterase superfamily protein |
        Chr1:1147888-1148352 REVERSE LENGTH=127 |
        201606
```

Coefficient swp for Vitvi07g02020.

```
                    logFC  AveExpr           t   P.Value adj.P.Val
Vitvi07g02020 0.005691716 3.873045 0.006632351 0.9947244 0.9959005
                      B
Vitvi07g02020 -6.117766
```



Correlation of all measurements (not just means): $r = 8e-04$, $r^2 = 6e-07$
Correlation of mean values (plots): $r_2 = -0.2195$

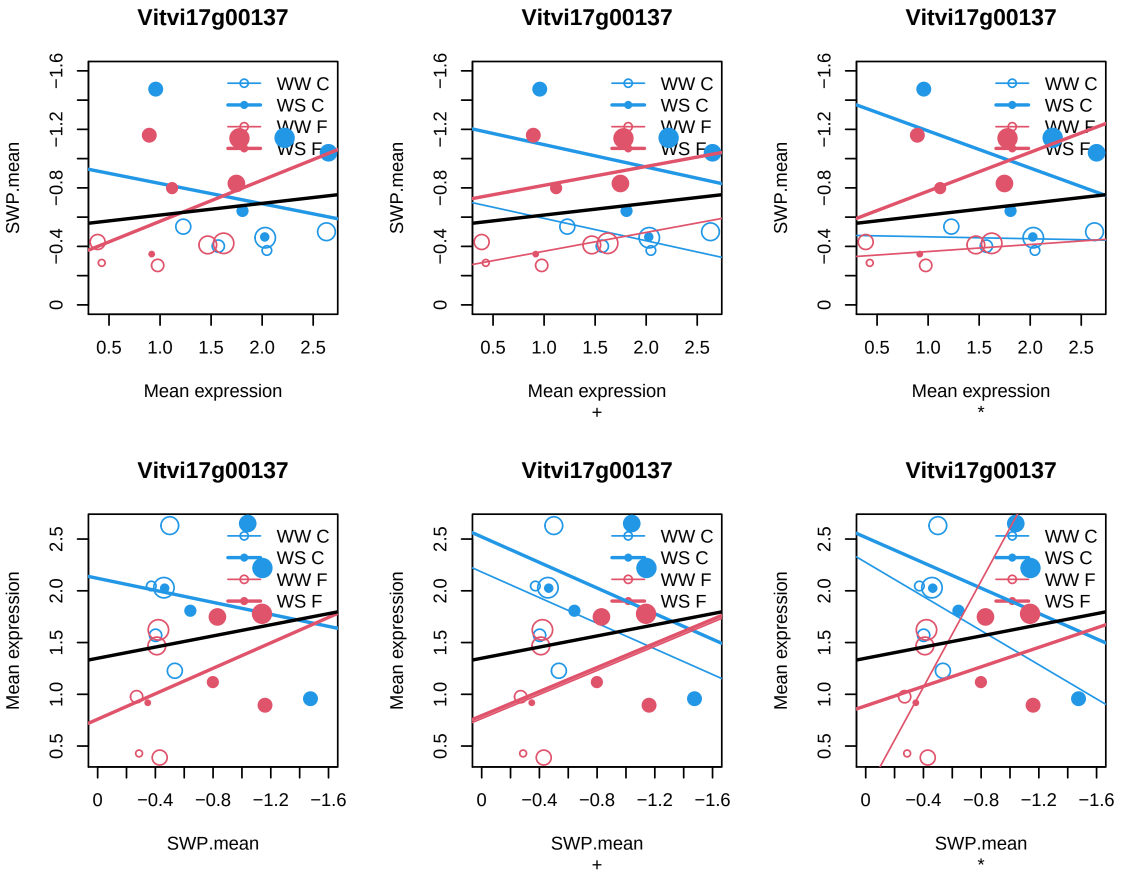
5.3.3 Vitvi17g00137

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

```
Vitvi17g00137
        23.04.2001
        nucleotide metabolism.phosphotransfer and pyrophosphatases.adenylate k
        P-loop containing nucleoside triphosphate hydrolases superfamily prote
        Chr3:293981-295357 REVERSE LENGTH=263 |
        201606
```

Coefficient swp for Vitvi17g00137.

```
                    logFC  AveExpr           t   P.Value adj.P.Val
Vitvi17g00137 0.008198947 1.525163 0.006493677 0.9948347 0.9959455
                      B
Vitvi17g00137 -6.117767
```



Correlation of all measurements (not just means): $r = 7e - 04, r^2 = 5e - 07$
Correlation of mean values (plots): $r_2 = 0.1466$

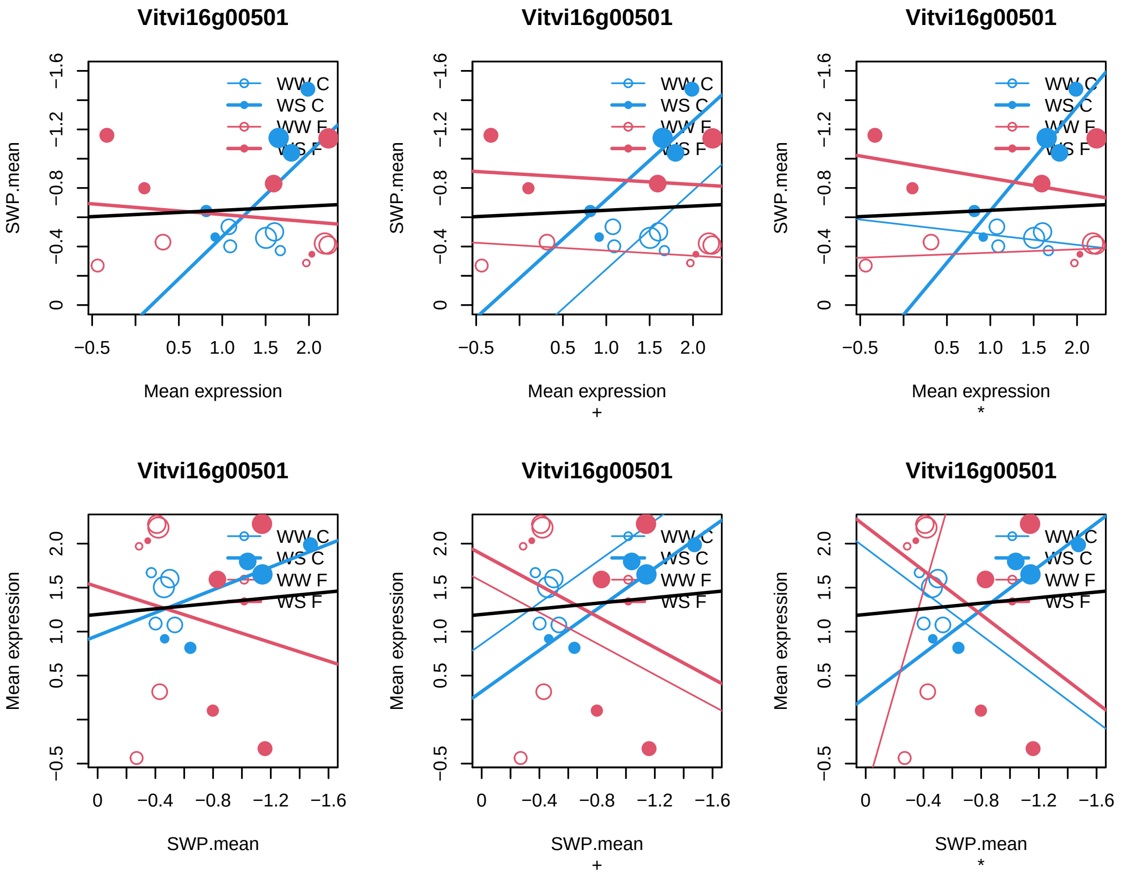
5.3.4 Vitvi16g00501

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

```
Vitvi16g00501
        30.2.11
        signalling.receptor kinases.leucine rich repeat XI
        Leucine-rich repeat protein kinase family protein |
        Chr5:24724541-24727842 REVERSE LENGTH=1041 |
        201606
```

Coefficient swp for Vitvi16g00501.

```
                   logFC  AveExpr           t   P.Value adj.P.Val
Vitvi16g00501 0.01244711 1.299418 0.006334405 0.9949614 0.9960069
                      B
Vitvi16g00501 -6.117768
```



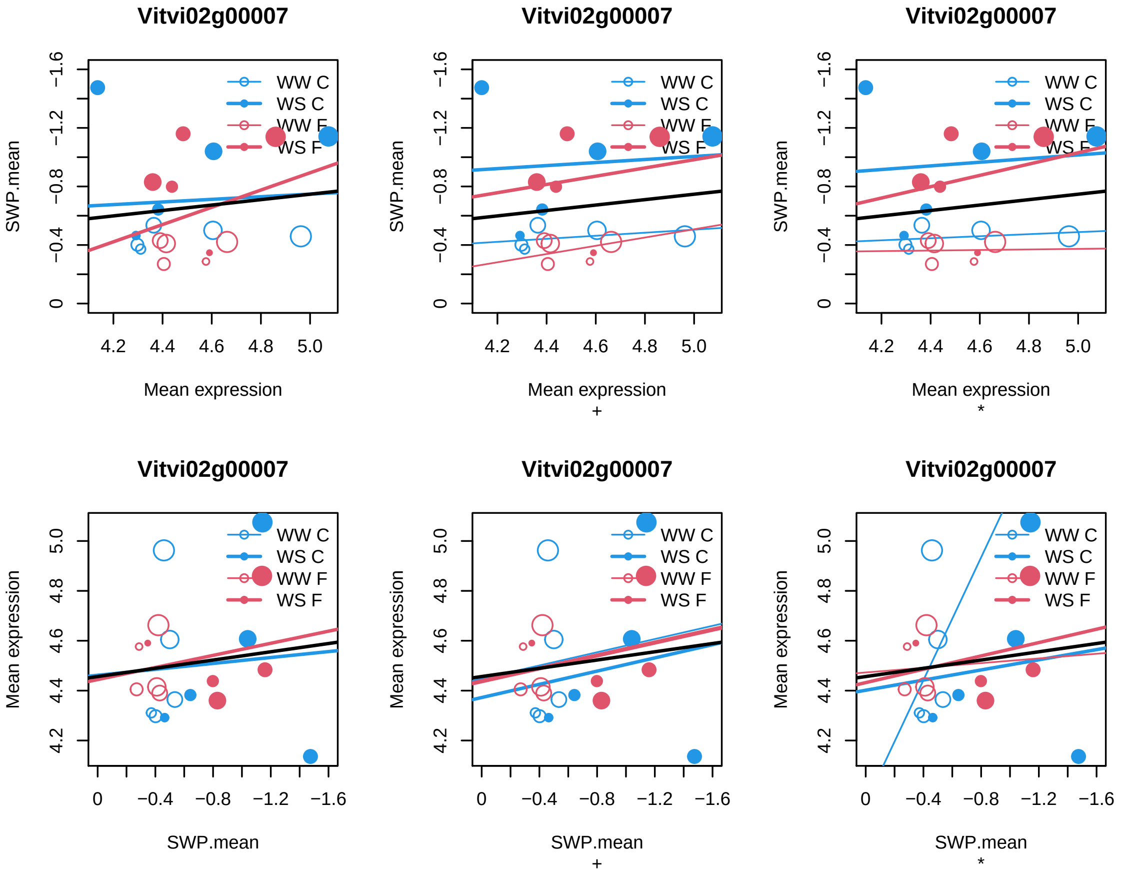
Correlation of all measurements (not just means): $r = 7e - 04$, $r^2 = 5e - 07$
Correlation of mean values (plots): $r_2 = 0.0679$

5.3.5 Vitvi02g00007

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
Vitvi02g00007
        35.2
        not assigned.unknown
        RNA-binding (RRM/RBD/RNP motifs) family protein |
        Chr4:16953404-16955127 REVERSE LENGTH=187 |
        201606

Vitvi02g00007
        27.4
        RNA.RNA binding
        RNA-binding (RRM/RBD/RNP motifs) family protein |
        Chr4:16953404-16955127 REVERSE LENGTH=187 |
        201606
```

Coefficient swp for Vitvi02g00007.

```
                    logFC  AveExpr           t   P.Value adj.P.Val
Vitvi02g00007 0.003011828 4.510734 0.006025826 0.9952068 0.9961872
                     B
Vitvi02g00007 -6.11777
```



Correlation of all measurements (not just means): $r = 7e-04$, $r^2 = 5e-07$
Correlation of mean values (plots): $r_2 = 0.1238$

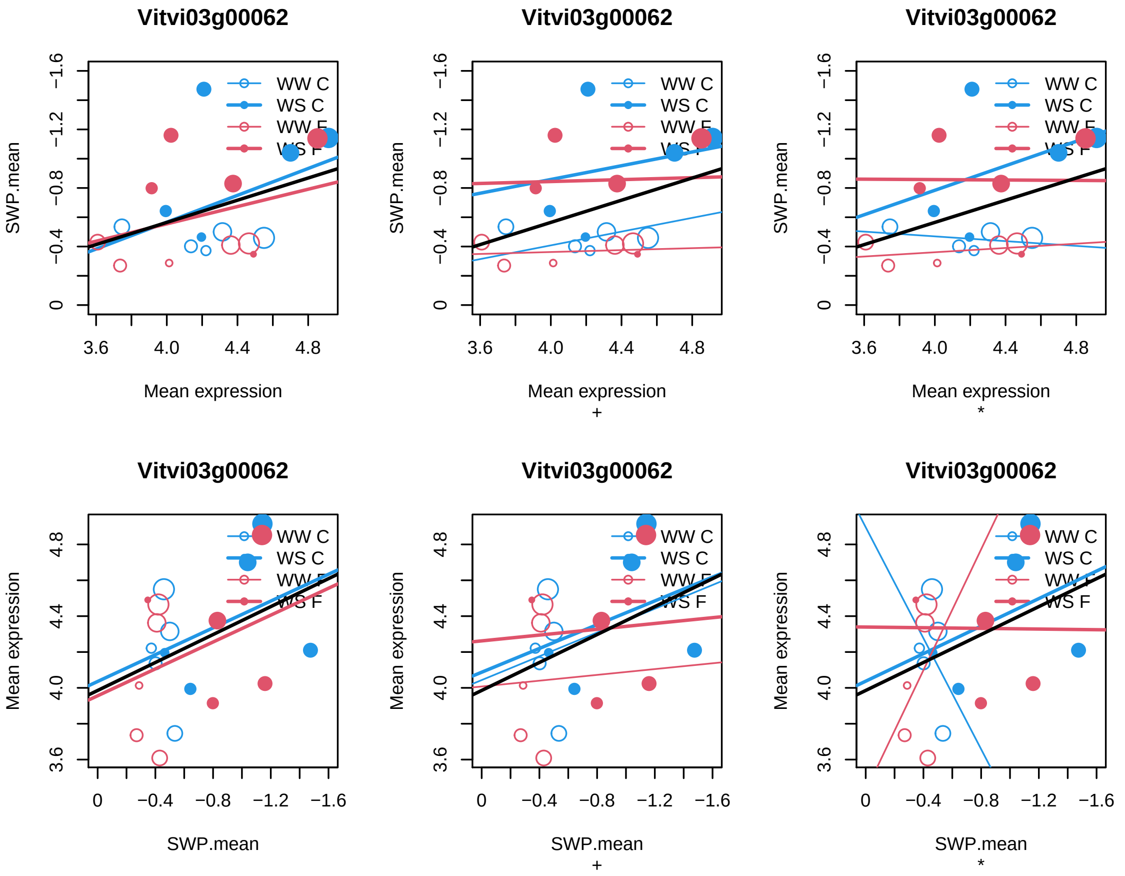
5.3.6 Vitvi03g00062

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

```
Vitvi03g00062
        27.1
        RNA.processing
        ribosome-binding factor A family protein |
        Chr4:16570019-16571274 REVERSE LENGTH=215 |
        201606
```

Coefficient swp for Vitvi03g00062.

```
                    logFC  AveExpr            t  P.Value adj.P.Val
Vitvi03g00062 -0.004168606 4.241324 -0.005574307 0.995566 0.9964813
                        B
Vitvi03g00062 -6.117772
```



Correlation of all measurements (not just means): $r = -6e - 04$, $r^2 = 4e - 07$
Correlation of mean values (plots): $r_2 = 0.3844$

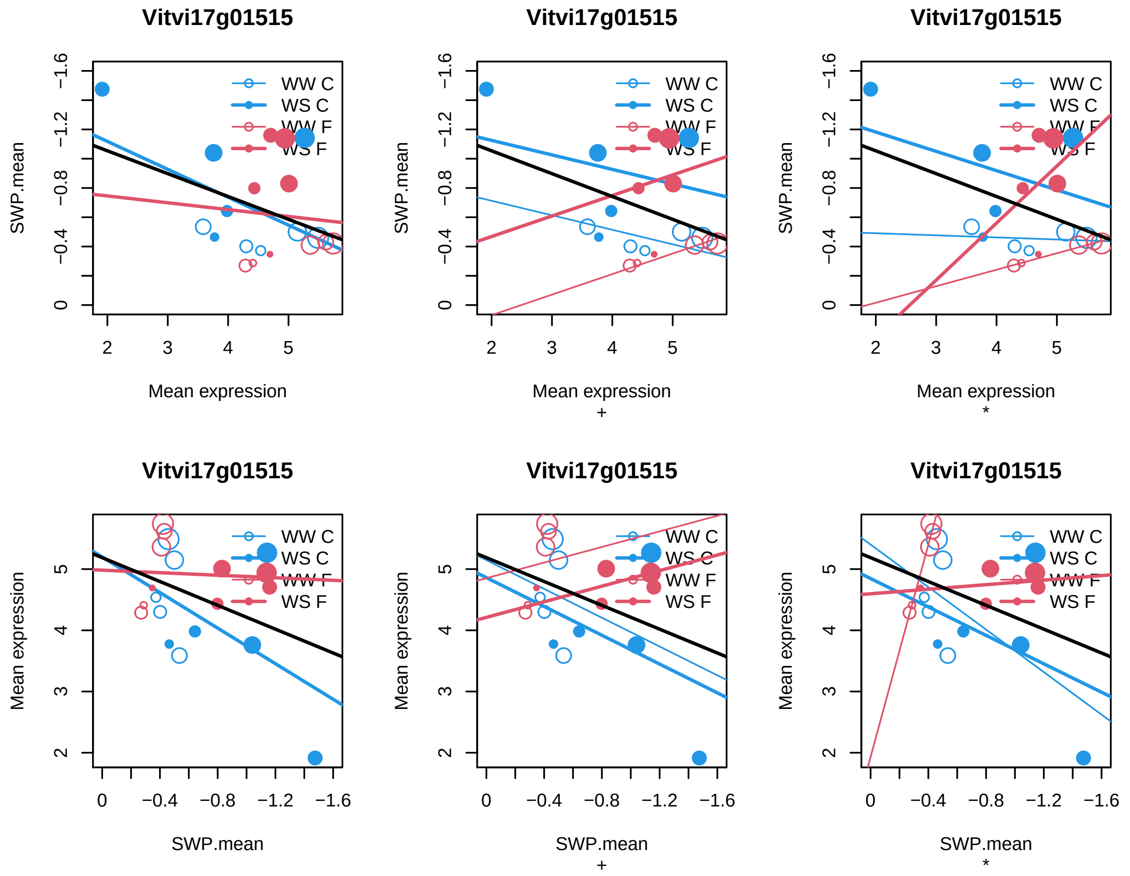
5.3.7 Vitvi17g01515

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

```
Vitvi17g01515
        35.2
        not assigned.unknown
        alpha/beta-Hydrolases superfamily protein |
        Chr3:17755553-17757692 REVERSE LENGTH=623 |
        201606
```

Coefficient swp for Vitvi17g01515.

```
                    logFC  AveExpr           t   P.Value adj.P.Val
Vitvi17g01515 0.008828815 4.548098 0.005108763 0.9959363 0.9967865
                      B
Vitvi17g01515 -6.117775
```



Correlation of all measurements (not just means): $r = 6e - 04$, $r^2 = 3e - 07$
Correlation of mean values (plots): $r_2 = -0.3898$

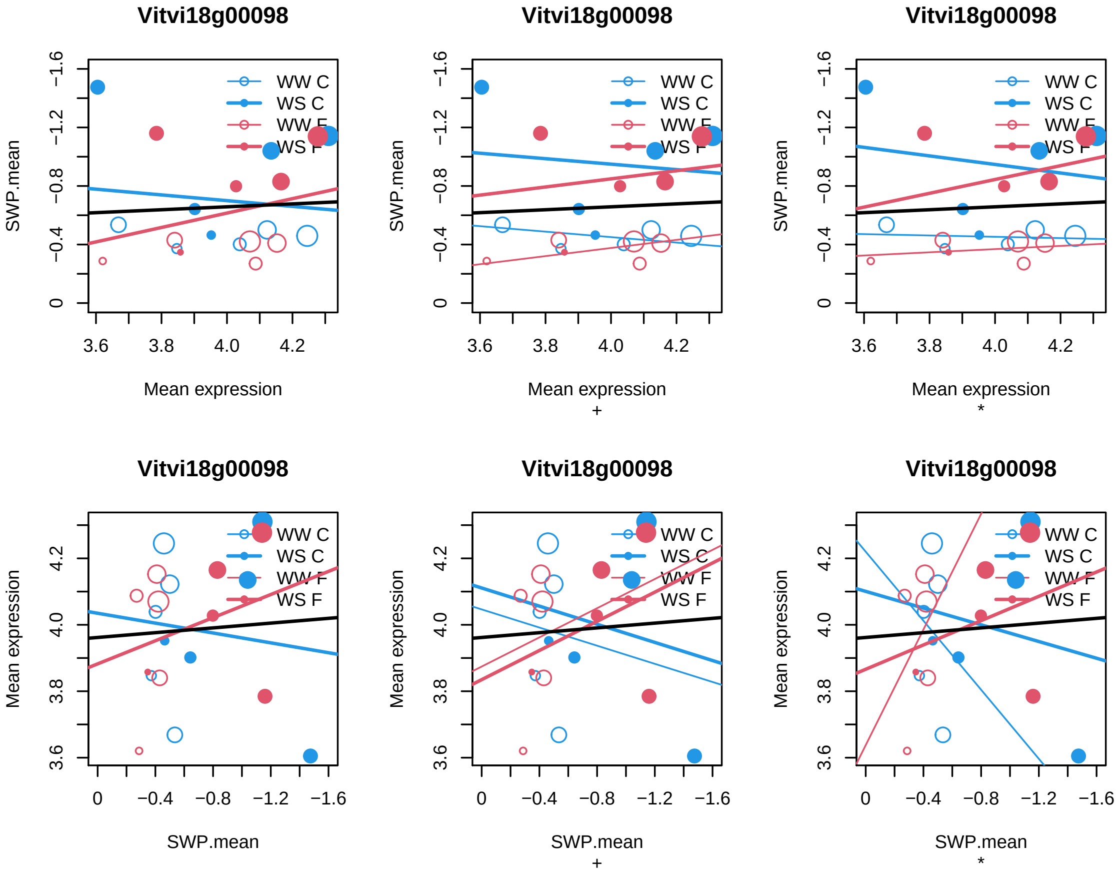
5.3.8 Vitvi18g00098

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

```
Vitvi18g00098
       27.1
       RNA.processing
       Small nuclear ribonucleoprotein family protein |
       Chr1:7128979-7130371 FORWARD LENGTH=131 |
       201606
```

Coefficient swp for Vitvi18g00098.

```
                  logFC  AveExpr           t   P.Value adj.P.Val
Vitvi18g00098 0.002265333 3.985465 0.004627403 0.9963192 0.9971042
                      B
Vitvi18g00098 -6.117777
```



Correlation of all measurements (not just means): $r = 6e - 04$, $r^2 = 3e - 07$
Correlation of mean values (plots): $r_2 = 0.0599$

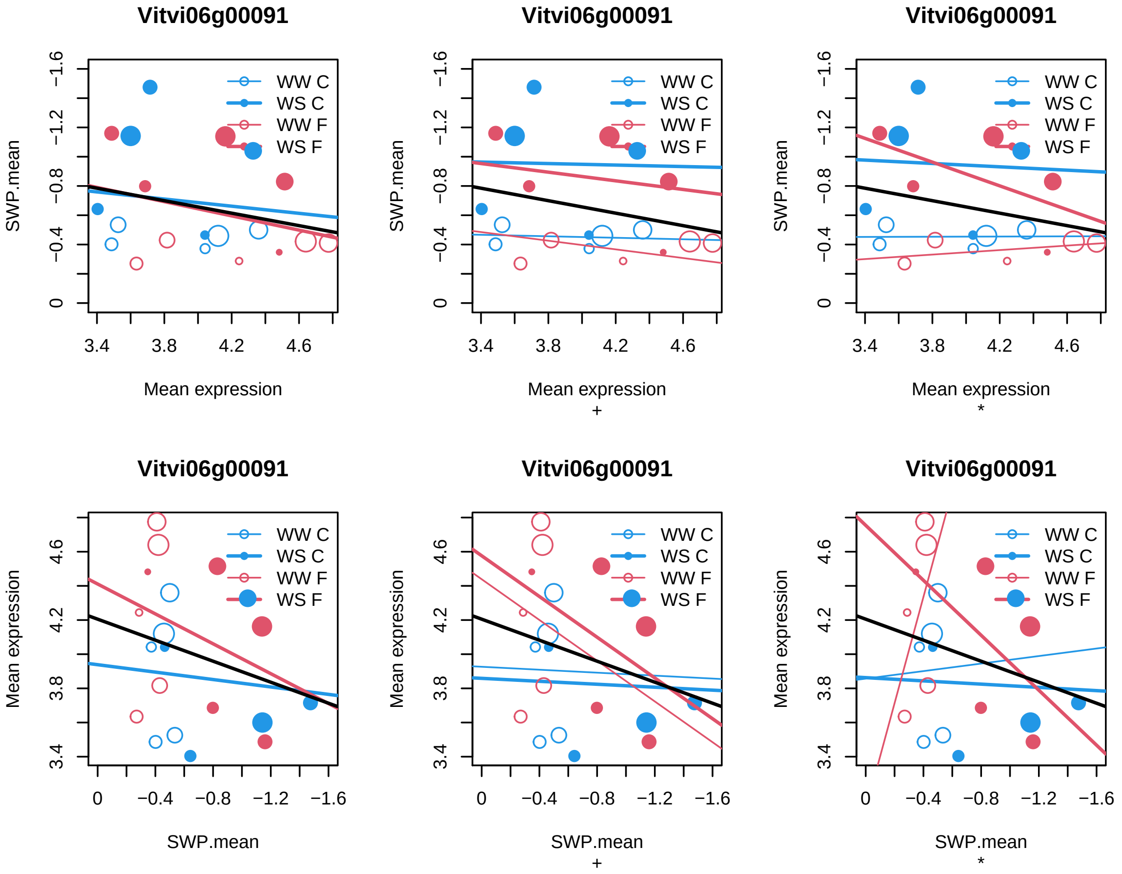
5.3.9 Vitvi06g00091

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

```
Vitvi06g00091
        35.2
        not assigned.unknown
        transmembrane protein%2C putative (Protein of unknown function%2C DUF5
        Chr5:6714533-6715837 REVERSE LENGTH=181 |
        201606
```

Coefficient swp for Vitvi06g00091.

```
                    logFC  AveExpr           t   P.Value adj.P.Val
Vitvi06g00091 0.003007602 4.003266 0.003585786 0.9971477 0.9978679
                      B
Vitvi06g00091 -6.117781
```



Correlation of all measurements (not just means): $r = 4e - 04$, $r^2 = 2e - 07$
Correlation of mean values (plots): $r_2 = -0.2560$

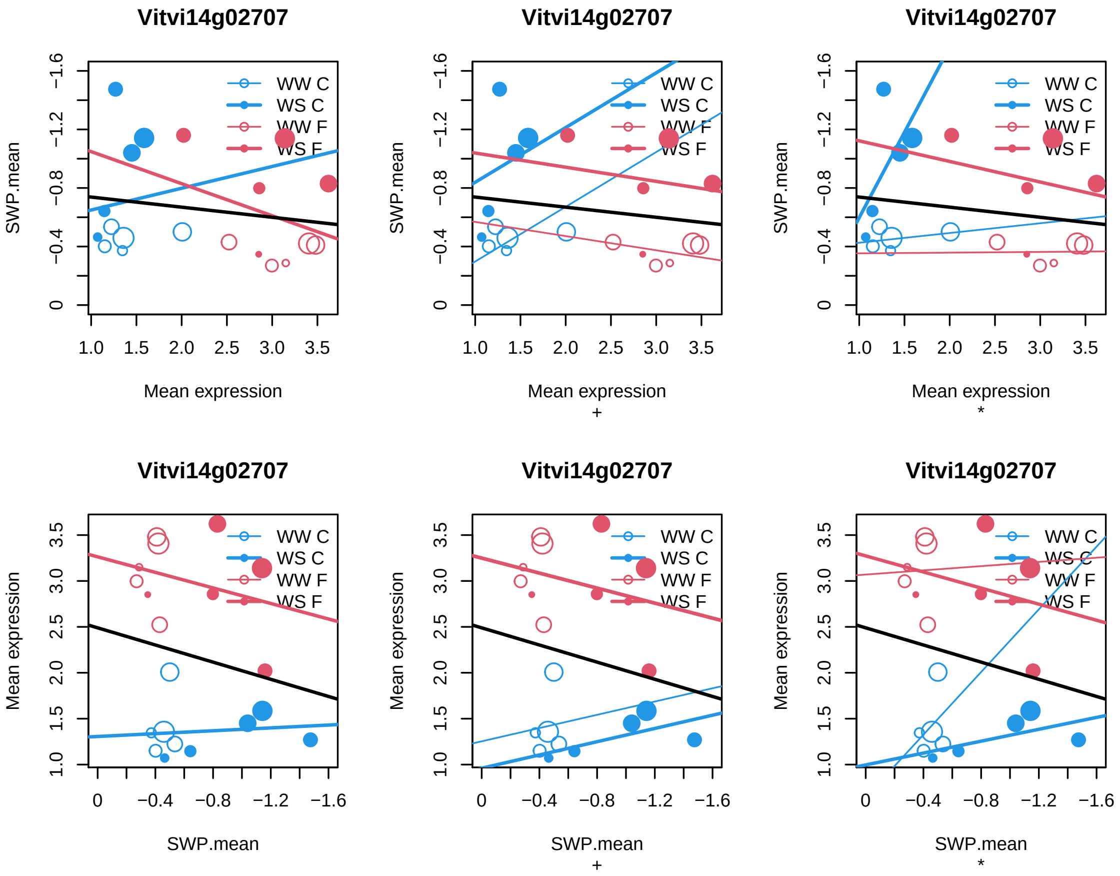
5.3.10 Vitvi14g02707

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

```
Vitvi14g02707
        20.1.2.1
        stress.biotic.receptors.CC-NBS-LRR
        NB-ARC domain-containing disease resistance protein |
        Chr4:13633953-13636712 REVERSE LENGTH=919 |
        201606
```

Coefficient swp for Vitvi14g02707.

```
                    logFC  AveExpr           t   P.Value adj.P.Val
Vitvi14g02707 0.005784772 2.182838 0.003387544 0.9973054 0.9978996
                      B
Vitvi14g02707 -6.117782
```



Correlation of all measurements (not just means): $r = 4e - 04$, $r^2 = 1e - 07$
Correlation of mean values (plots): $r_2 = -0.1795$

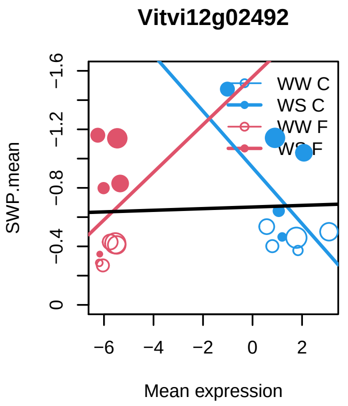
5.3.11 Vitvi12g02492

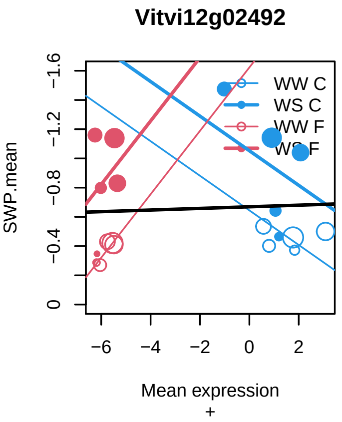
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

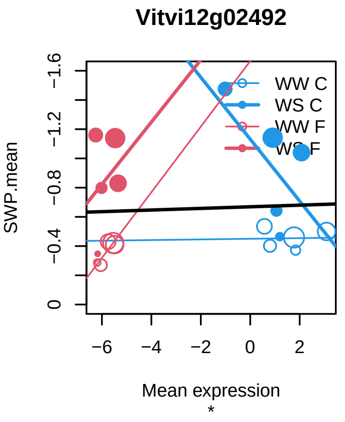
```
Vitvi12g02492
        30.2.12
        signalling.receptor kinases.leucine rich repeat XII
        receptor like protein 22 |
        Chr2:13853897-13855666 REVERSE LENGTH=589 |
        201606
```

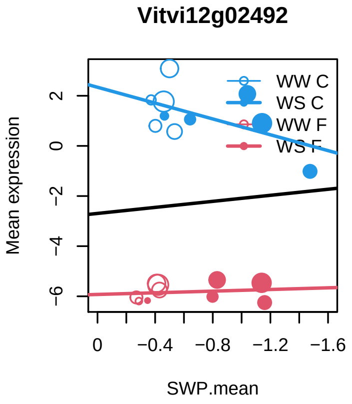
Coefficient swp for Vitvi12g02492.

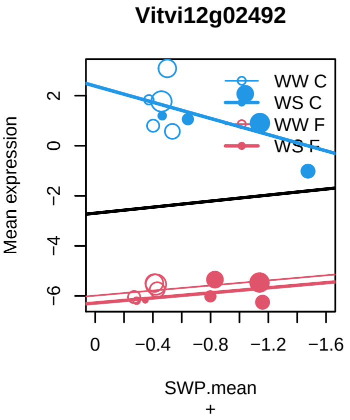
```
                    logFC   AveExpr            t   P.Value adj.P.Val
Vitvi12g02492 -0.02233725 -2.298563 -0.003381299 0.9973104 0.9978996
                      B
Vitvi12g02492 -6.117782
```

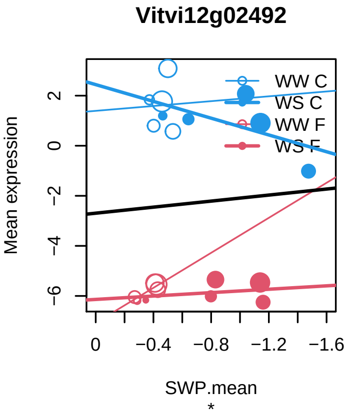












Correlation of all measurements (not just means): $r = -4e-04$, $r^2 = 1e-07$
Correlation of mean values (plots): $r_2 = 0.0579$

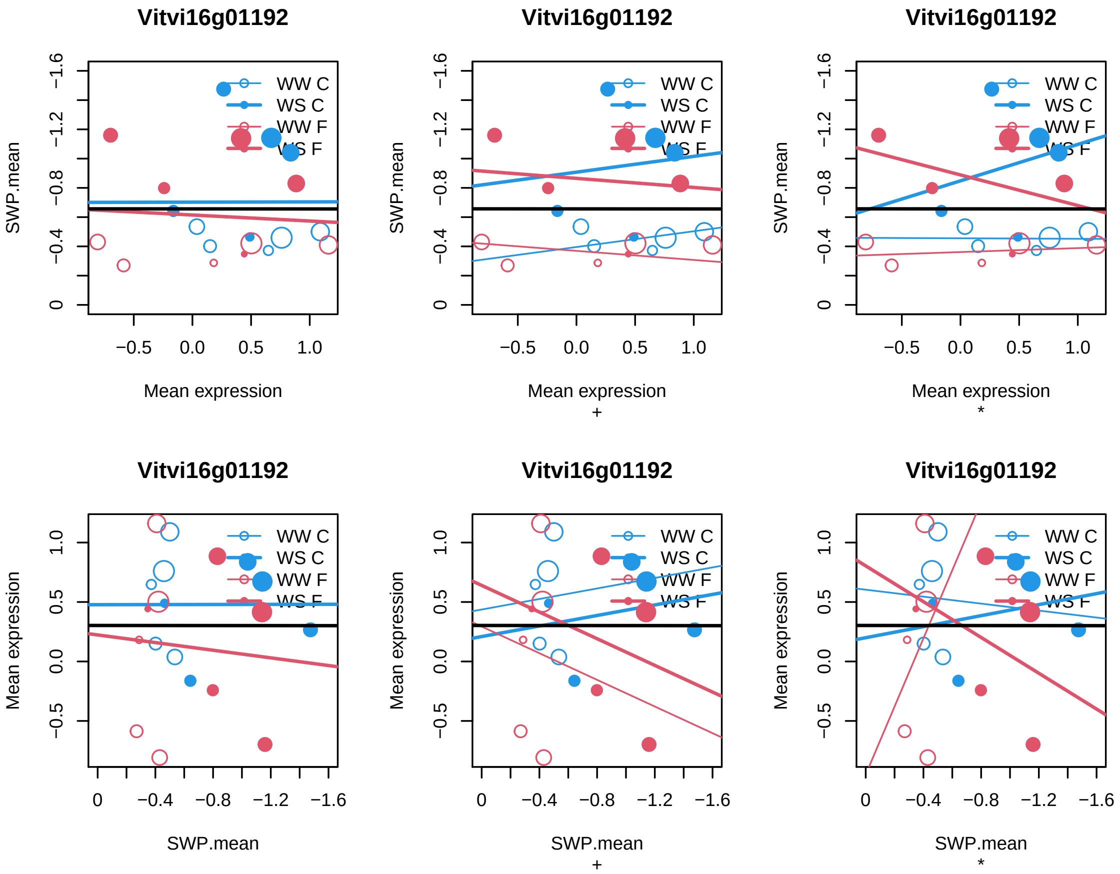
5.3.12 Vitvi16g01192

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

```
Vitvi16g01192
        28.1
        DNA.synthesis/chromatin structure
        P-loop containing nucleoside triphosphate hydrolases superfamily prote
        Chr1:24477043-24480728 REVERSE LENGTH=1050 |
        201606
```

Coefficient swp for Vitvi16g01192.

```
                     logFC   AveExpr            t   P.Value adj.P.Val
Vitvi16g01192 -0.003194491 0.3020401 -0.002557562 0.9979656 0.9984897
                         B
Vitvi16g01192 -6.117784
```



Correlation of all measurements (not just means): $r = -3e - 04$, $r^2 = 8e - 08$
Correlation of mean values (plots): $r_2 = -6e - 04$

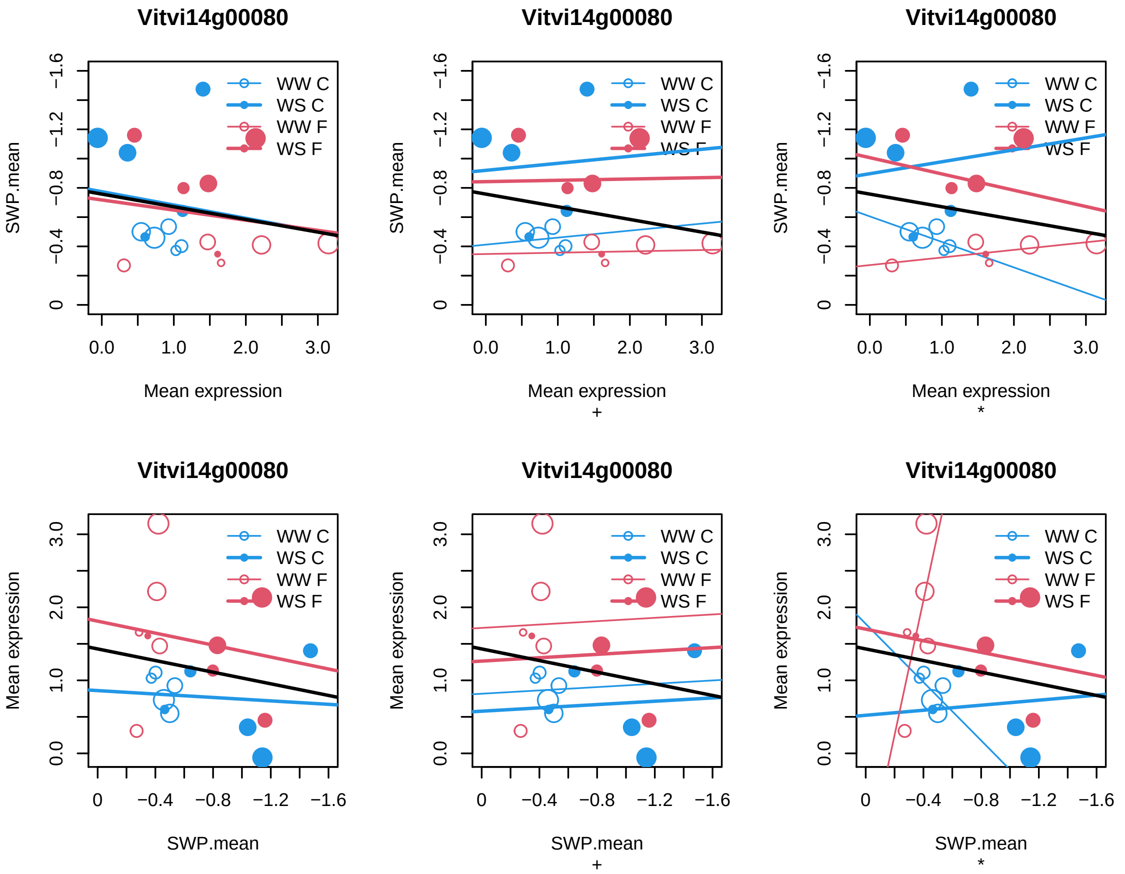
5.3.13 Vitvi14g00080

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

```
Vitvi14g00080
        35.2
        not assigned.unknown
        Polynucleotidyl transferase%2C ribonuclease H-like superfamily protei
        Chr3:3946267-3946959 REVERSE LENGTH=230 |
        201606
```

Coefficient swp for Vitvi14g00080.

```
                    logFC  AveExpr          t   P.Value adj.P.Val
Vitvi14g00080 0.005137988 1.169004 0.002383192 0.9981043 0.9985629
                      B
Vitvi14g00080 -6.117785
```



Correlation of all measurements (not just means): $r = 3e-04$, $r^2 = 7e-08$
Correlation of mean values (plots): $r_2 = -0.1857$

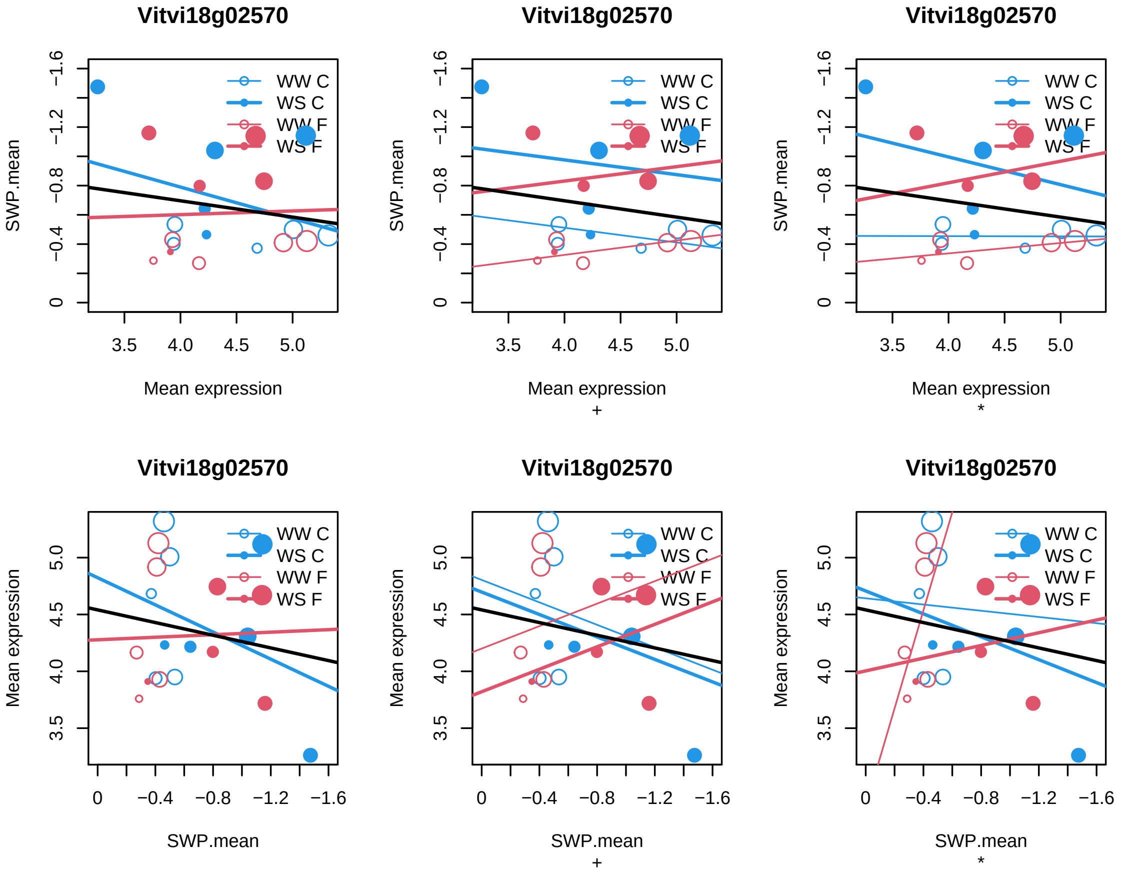
5.3.14 Vitvi18g02570

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

```
Vitvi18g02570
        35.2
        not assigned.unknown
        Glucan 1 3-beta-glucosidase IPR001547 Glycoside hydrolase, family 5
```

Coefficient swp for Vitvi18g02570.

```
                    logFC AveExpr           t   P.Value adj.P.Val
Vitvi18g02570 0.002364193 4.35735 0.002093285 0.9983349 0.9987281
                      B
Vitvi18g02570 -6.117785
```



Correlation of all measurements (not just means): $r = 2e - 04$, $r^2 = 6e - 08$
Correlation of mean values (plots): $r_2 = -0.1764$

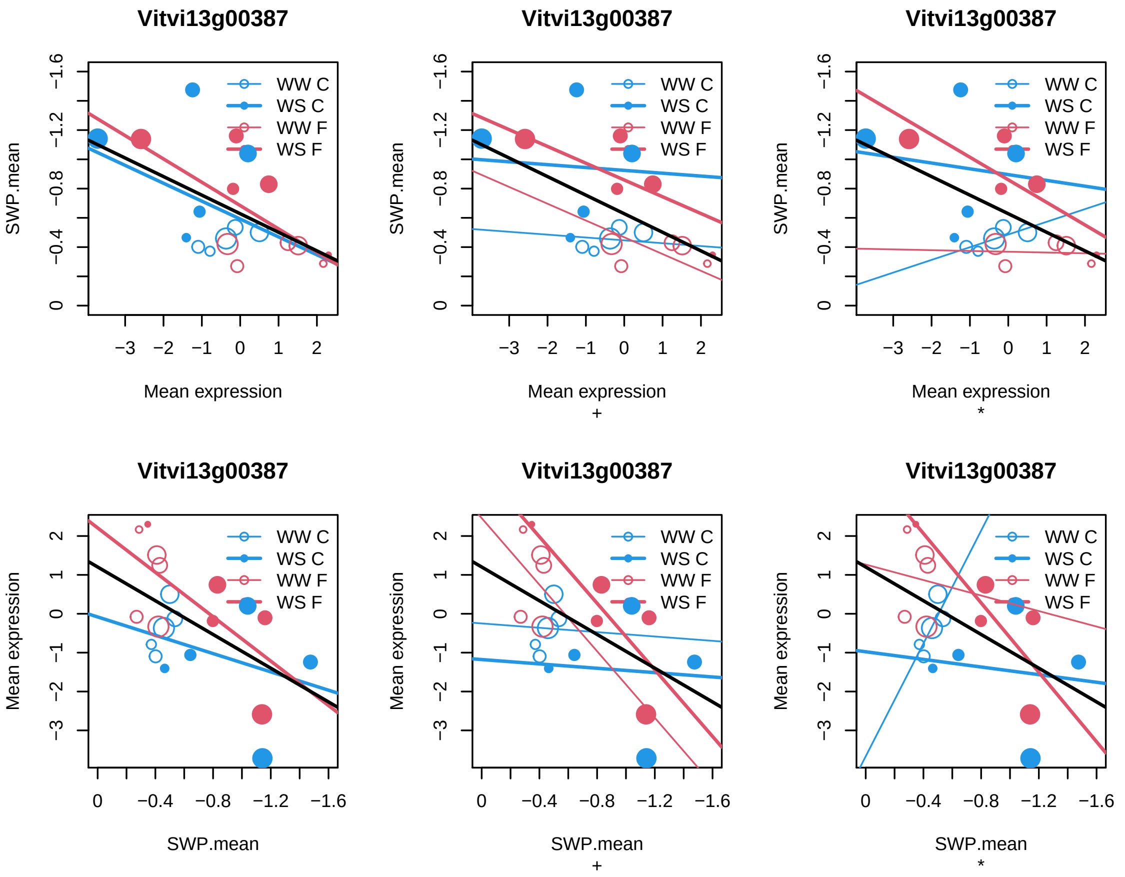
5.3.15 Vitvi13g00387

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

```
Vitvi13g00387
        35.2
        not assigned.unknown
        NA
```

Coefficient swp for Vitvi13g00387.

```
                    logFC    AveExpr            t   P.Value adj.P.Val
Vitvi13g00387 -0.00537456 -0.2205684 -0.001790019 0.9985761 0.9988888
                      B
Vitvi13g00387 -6.117786
```



Correlation of all measurements (not just means): $r = -2e - 04$, $r^2 = 4e - 08$
Correlation of mean values (plots): $r_2 = -0.5247$

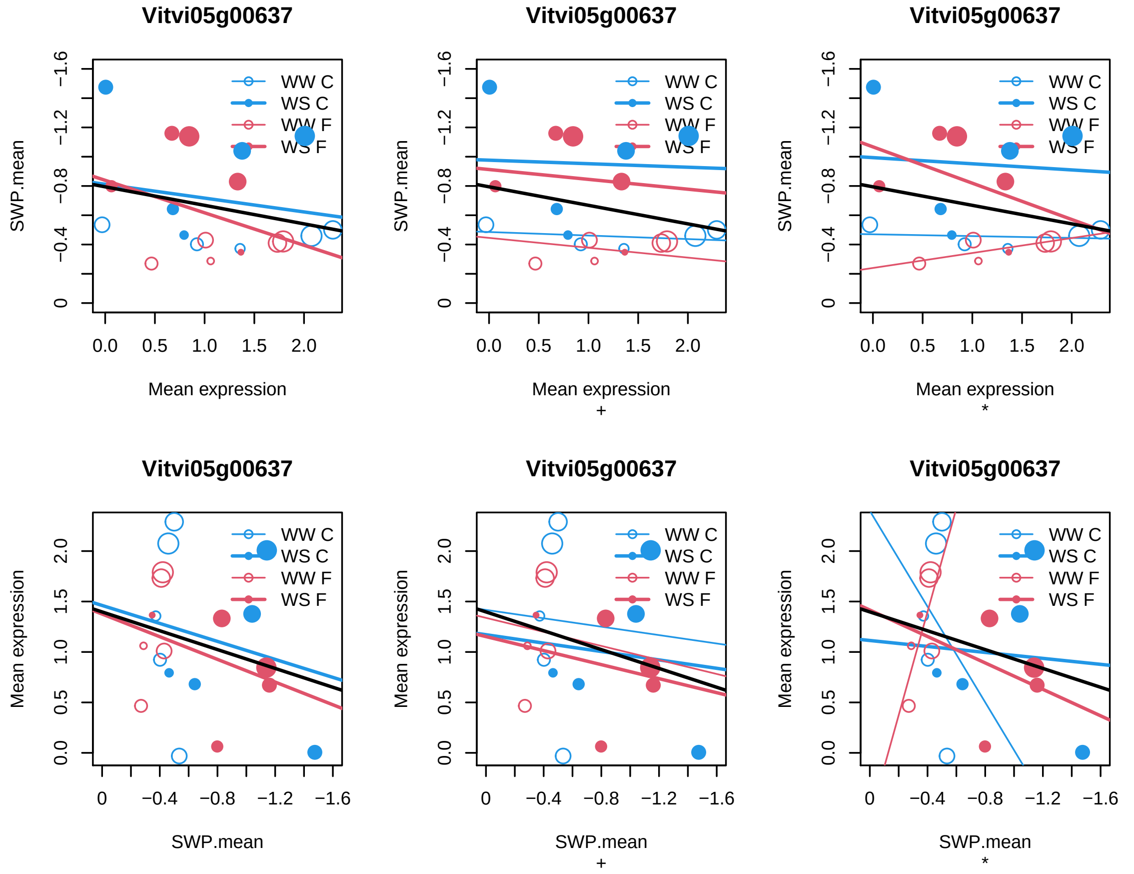
5.3.16 Vitvi05g00637

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

```
Vitvi05g00637
        31.1
        cell.organisation
        Ankyrin repeat family protein |
        Chr4:1554420-1556571 FORWARD LENGTH=629 |
        201606
```

Coefficient swp for Vitvi05g00637.

```
                    logFC  AveExpr           t   P.Value adj.P.Val
Vitvi05g00637 0.002396486 1.090674 0.001721486 0.9986307 0.9988888
                      B
Vitvi05g00637 -6.117786
```



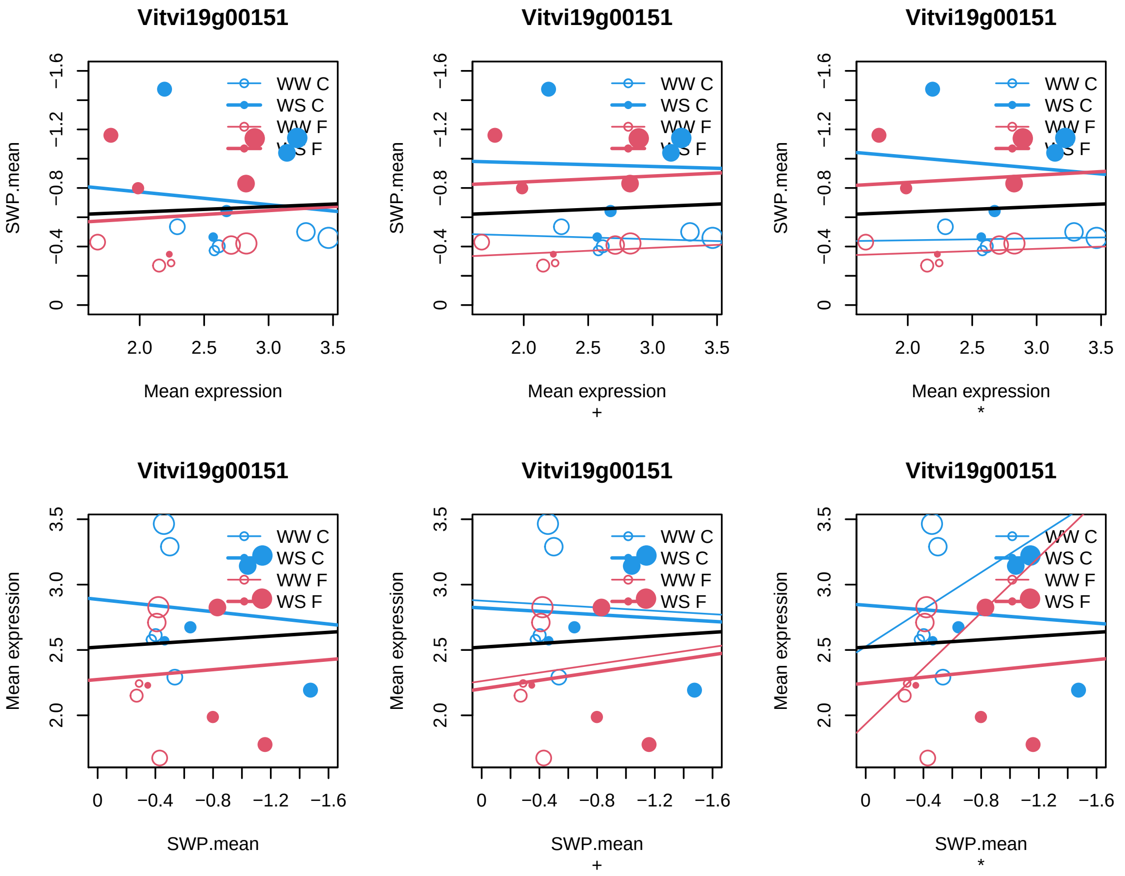
Correlation of all measurements (not just means): $r = 2e - 04$, $r^2 = 4e - 08$
Correlation of mean values (plots): $r_2 = -0.2430$

5.3.17 Vitvi19g00151

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
Vitvi19g00151
        35.2
        not assigned.unknown
        TAF RNA polymerase I subunit A |
        Chr1:19840486-19842692 REVERSE LENGTH=474 |
        201606
```

Coefficient swp for Vitvi19g00151.

```
                    logFC  AveExpr           t   P.Value adj.P.Val
Vitvi19g00151 0.001547361 2.567847 0.001644123 0.9986922 0.9988888
                      B
Vitvi19g00151 -6.117786
```



Correlation of all measurements (not just means): $r = 2e - 04$, $r^2 = 3e - 08$
Correlation of mean values (plots): $r_2 = 0.0506$

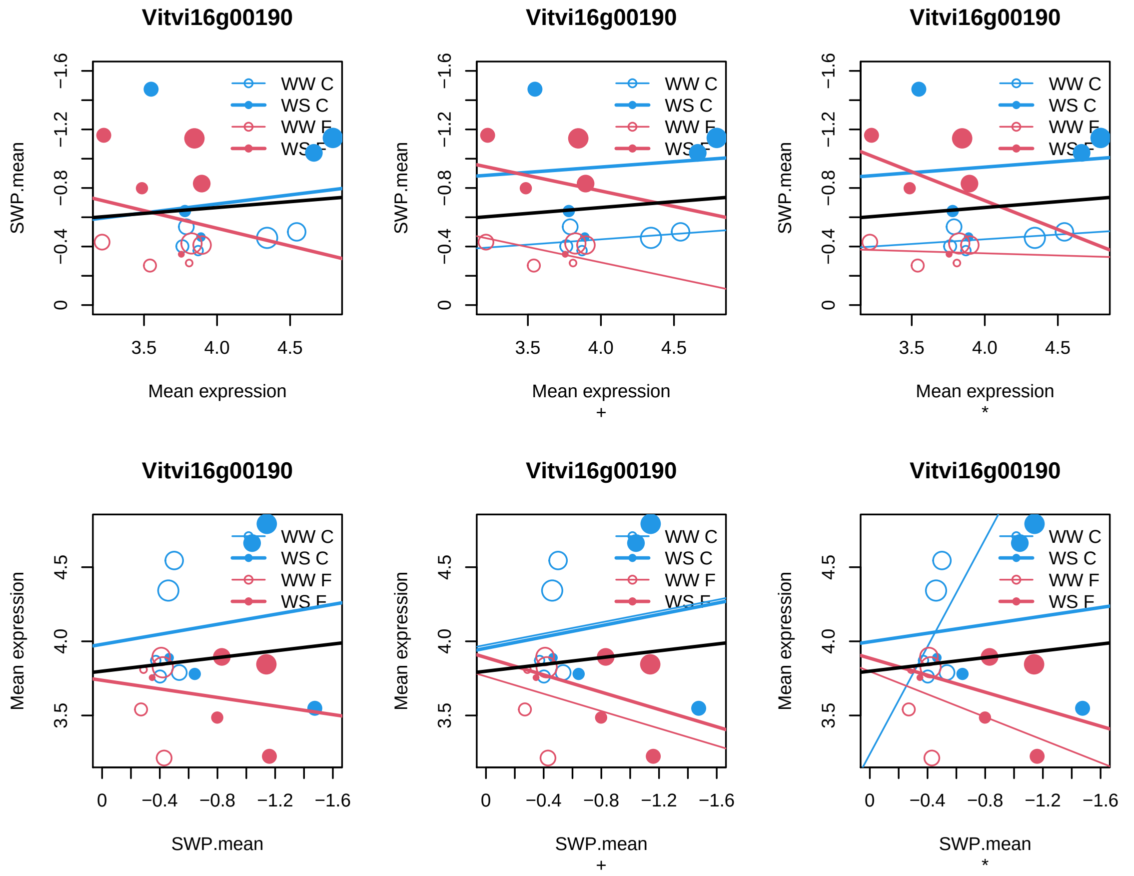
5.3.18 Vitvi16g00190

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

```
Vitvi16g00190
        27.01.2019
        RNA.processing.ribonucleases
        exoribonuclease 4 |
        Chr1:20350697-20356650 FORWARD LENGTH=889 |
        201606
```

Coefficient swp for Vitvi16g00190.

```
                    logFC  AveExpr             t   P.Value adj.P.Val
Vitvi16g00190 -0.000811887 3.873747 -0.0009974645 0.9992066 0.9993377
                        B
Vitvi16g00190 -6.117787
```



Correlation of all measurements (not just means): $r = -1e - 04$, $r^2 = 1e - 08$
Correlation of mean values (plots): $r_2 = 0.0960$

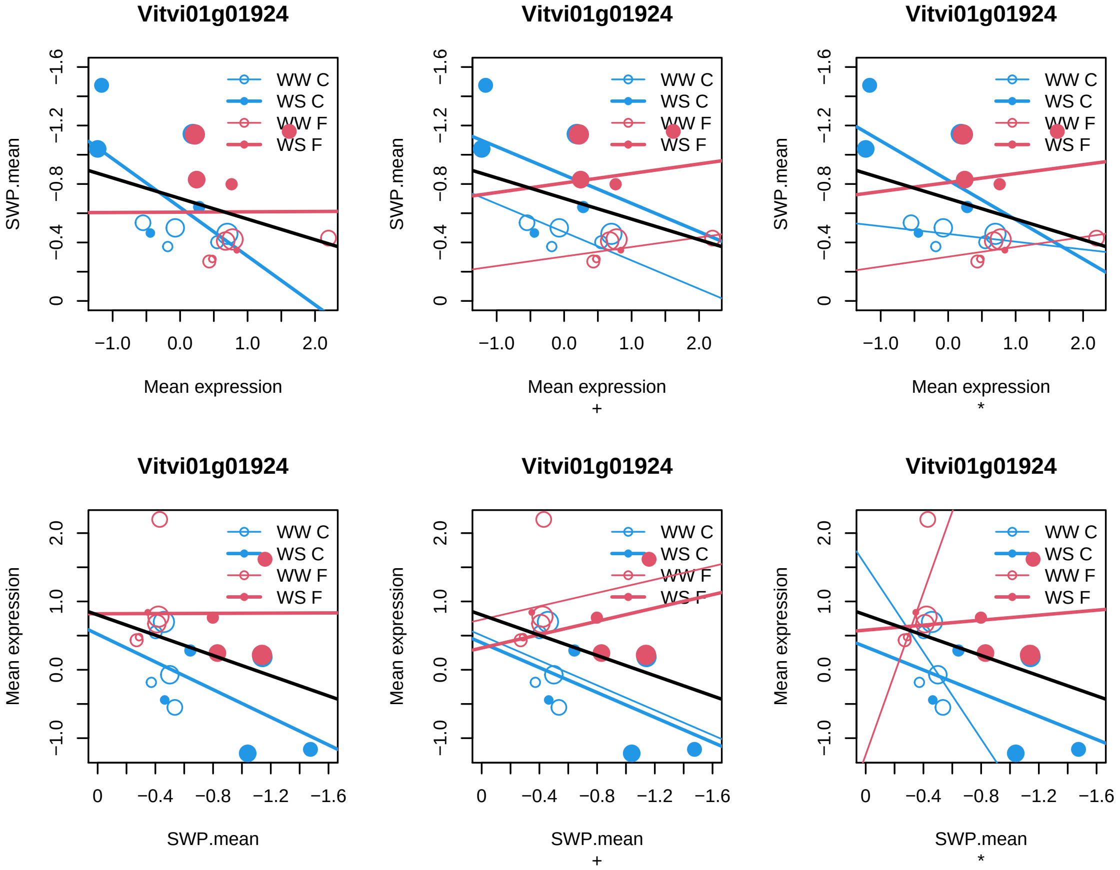
5.3.19 Vitvi01g01924

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

```
Vitvi01g01924
        35.2
        not assigned.unknown
        Protein IDA
```

Coefficient swp for Vitvi01g01924.

```
                      logFC   AveExpr             t   P.Value
Vitvi01g01924 -0.001325135 0.3165117 -0.0007298412 0.9994195
              adj.P.Val         B
Vitvi01g01924  0.999485 -6.117787
```



Correlation of all measurements (not just means): $r = -8e-05, r^2 = 7e-09$
Correlation of mean values (plots): $r_2 = -0.3230$

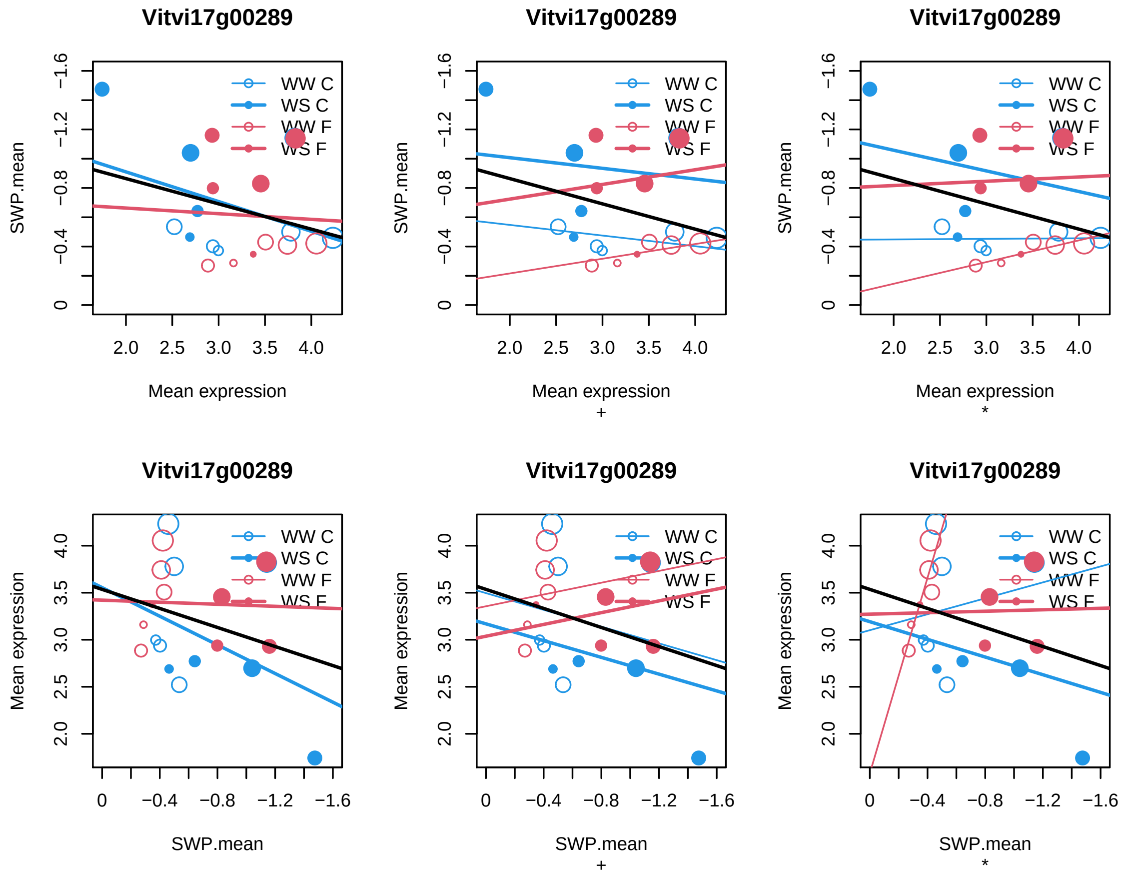
5.3.20 Vitvi17g00289

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

```
Vitvi17g00289
        30.2.20
        signalling.receptor kinases.wheat LRK10 like
        Serine/Threonine kinase family catalytic domain protein |
        Chr1:6327463-6329935 FORWARD LENGTH=654 |
        201606
```

Coefficient swp for Vitvi17g00289.

```
                    logFC  AveExpr            t   P.Value adj.P.Val
Vitvi17g00289 -0.0004491722 3.203332 -0.000382496 0.9996957 0.9996957
                        B
Vitvi17g00289 -6.117787
```



Correlation of all measurements (not just means): $r = -4e - 05, r^2 = 2e - 09$
Correlation of mean values (plots): $r_2 = -0.2958$

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, methods, parallel, stats, utils
- Other packages: amisc 0.1.0, Biobase 2.50.0, BiocGenerics 0.36.0, 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, 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, grid 4.0.2, 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, 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/40_Expression-water-stress.Rnw
Main file : ../scripts/40_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 <-"40_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=".")))
```