

Expression analysis - water potential

.alpha=0.05 .r=r .topn=100

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January 7, 2021

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5.2.39	Vitvi10g00496	77
5.2.40	Vitvi16g00681	78
5.2.41	Vitvi13g00410	79
5.2.42	Vitvi05g00277	80
5.2.43	Vitvi13g02053	81
5.2.44	Vitvi03g00335	82
5.2.45	Vitvi07g00457	83
5.2.46	Vitvi04g00135	84
5.2.47	Vitvi13g01107	85
5.2.48	Vitvi02g00983	86
5.2.49	Vitvi12g01613	87
5.2.50	Vitvi13g02054	88
5.2.51	Vitvi04g00962	89
5.2.52	Vitvi10g00798	90
5.2.53	Vitvi02g00310	91
5.2.54	Vitvi15g01034	92
5.2.55	Vitvi16g01103	93
5.2.56	Vitvi06g01562	94
5.2.57	Vitvi04g02184	95
5.2.58	Vitvi06g00582	96
5.2.59	Vitvi13g00241	97
5.2.60	Vitvi07g02433	98
5.2.61	Vitvi04g00548	99
5.2.62	Vitvi18g02423	100
5.2.63	Vitvi03g01897	101
5.2.64	Vitvi05g01924	102
5.2.65	Vitvi02g01447	103
5.2.66	Vitvi18g00748	104
5.2.67	Vitvi14g01942	105
5.2.68	Vitvi12g02138	106
5.2.69	Vitvi01g00037	107
5.2.70	Vitvi03g00717	108
5.2.71	Vitvi04g00039	109
5.2.72	Vitvi08g01143	110
5.2.73	Vitvi13g00062	111
5.2.74	Vitvi09g00375	112
5.2.75	Vitvi11g00657	113
5.2.76	Vitvi15g00653	114
5.2.77	Vitvi09g00772	115
5.2.78	Vitvi08g02274	116
5.2.79	Vitvi14g01896	117
5.2.80	Vitvi06g01354	118
5.2.81	Vitvi01g00921	119
5.2.82	Vitvi12g00905	120
5.2.83	Vitvi08g01095	121

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5.2.87	Vitvi19g00514	125
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5.2.92	Vitvi03g00322	130
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5.2.95	Vitvi07g01566	133
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5.3.9	Vitvi07g00563	148
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5.3.11	Vitvi01g00959	150
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5.3.13	Vitvi18g02613	152
5.3.14	Vitvi16g00072	153
5.3.15	Vitvi18g01050	154
5.3.16	Vitvi14g01444	155
5.3.17	Vitvi02g01540	156
5.3.18	Vitvi07g02860	157
5.3.19	Vitvi07g00939	158
5.3.20	Vitvi18g01148	159
5.3.21	Vitvi15g00245	160
5.3.22	Vitvi06g00502	161
5.3.23	Vitvi06g01487	162
5.3.24	Vitvi18g02965	163
5.3.25	Vitvi02g01110	164
5.3.26	Vitvi09g01029	165
5.3.27	Vitvi18g02777	166
5.3.28	Vitvi12g00288	167
5.3.29	Vitvi08g01768	168
5.3.30	Vitvi05g00077	169
5.3.31	Vitvi01g01023	170
5.3.32	Vitvi06g00110	171

5.3.33	Vitvi10g00516	172
5.3.34	Vitvi14g02885	173
5.3.35	Vitvi15g00247	174
5.3.36	Vitvi16g01941	175
5.3.37	Vitvi13g02500	176
5.3.38	Vitvi12g02311	177
5.3.39	Vitvi16g00189	178
5.3.40	Vitvi11g01151	179
5.3.41	Vitvi09g01961	180
5.3.42	Vitvi14g02007	181
5.3.43	Vitvi06g00693	182
5.3.44	Vitvi11g00980	183
5.3.45	Vitvi15g00900	184
5.3.46	Vitvi04g01131	185
5.3.47	Vitvi13g01340	186
5.3.48	Vitvi08g02296	187
5.3.49	Vitvi08g01332	188
5.3.50	Vitvi09g00069	189
5.3.51	Vitvi08g01926	190
5.3.52	Vitvi13g00052	191
5.3.53	Vitvi06g00121	192
5.3.54	Vitvi15g00410	193
5.3.55	Vitvi09g00161	194
5.3.56	Vitvi13g02109	195
5.3.57	Vitvi12g02299	196
5.3.58	Vitvi12g00032	197
5.3.59	Vitvi18g01254	198
5.3.60	Vitvi04g01274	199
5.3.61	Vitvi10g00270	200
5.3.62	Vitvi07g00361	201
5.3.63	Vitvi17g01348	202
5.3.64	Vitvi05g00459	203
5.3.65	Vitvi15g00936	204
5.3.66	Vitvi18g00410	205
5.3.67	Vitvi19g00271	206
5.3.68	Vitvi02g00828	207
5.3.69	Vitvi11g00053	208
5.3.70	Vitvi12g00562	209
5.3.71	Vitvi10g00022	210
5.3.72	Vitvi19g00154	211
5.3.73	Vitvi07g02286	212
5.3.74	Vitvi09g00373	213
5.3.75	Vitvi08g00642	214
5.3.76	Vitvi19g01988	215
5.3.77	Vitvi12g01812	216
5.3.78	Vitvi14g03090	217
5.3.79	Vitvi05g00906	218
5.3.80	Vitvi02g00473	219
5.3.81	Vitvi13g00182	220
5.3.82	Vitvi07g02020	221

5.3.83	Vitvi17g00137	222
5.3.84	Vitvi16g00501	223
5.3.85	Vitvi02g00007	224
5.3.86	Vitvi03g00062	225
5.3.87	Vitvi17g01515	226
5.3.88	Vitvi18g00098	227
5.3.89	Vitvi06g00091	228
5.3.90	Vitvi14g02707	229
5.3.91	Vitvi12g02492	230
5.3.92	Vitvi16g01192	231
5.3.93	Vitvi14g00080	232
5.3.94	Vitvi18g02570	233
5.3.95	Vitvi13g00387	234
5.3.96	Vitvi05g00637	235
5.3.97	Vitvi19g00151	236
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1 Task

Final document in folder /reports:

```
> fileName(outputFile)
```

```
[1] "40_Expression-water-stress_0.05-r-100"
```

2 Information from pISA

Data directory

```
> .inroot
```

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

Results directory

```
> .oroot
```

```
[1] "../..output/40_Expression-water-stress-0.05-r-100"
```

```
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	length	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	Fleurtaï
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))

```

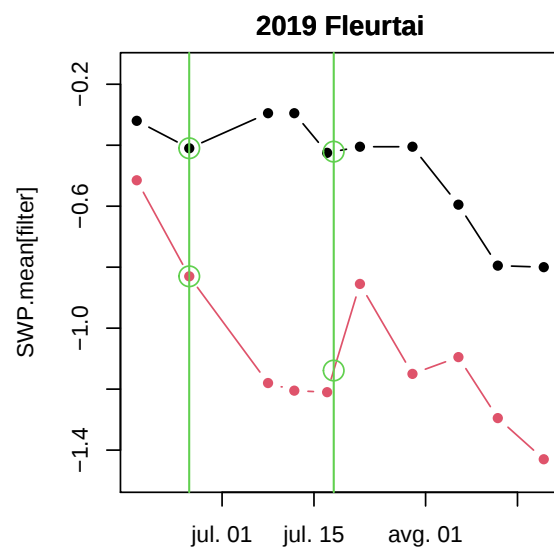
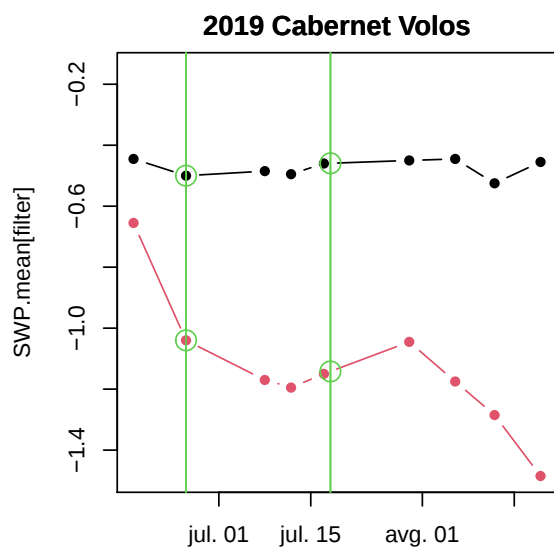
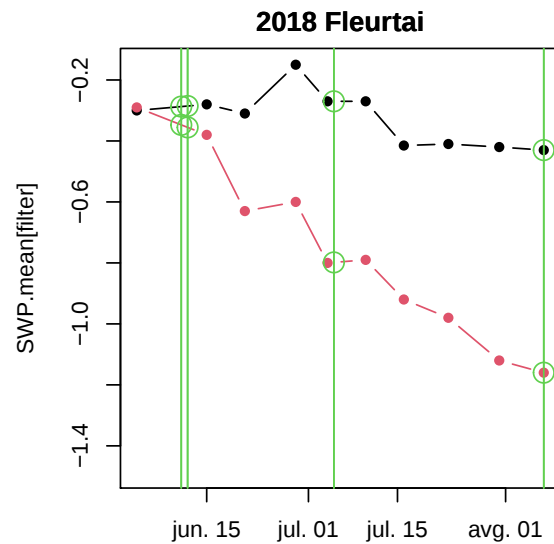
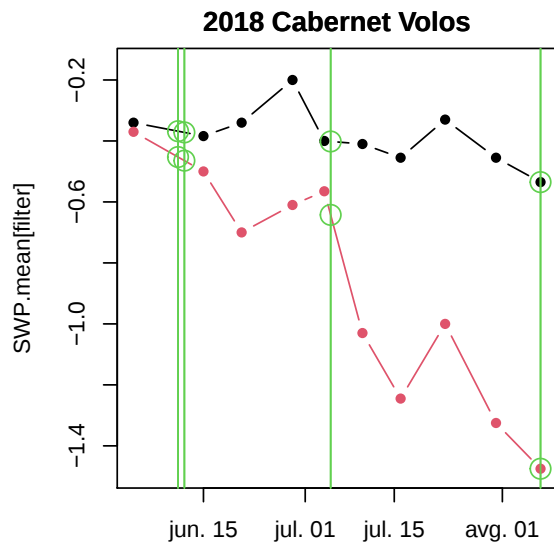
Water potential and transcriptomics are not measured at the same dates. We will interpolate the water potential to matching dates.

```

> 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
[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  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

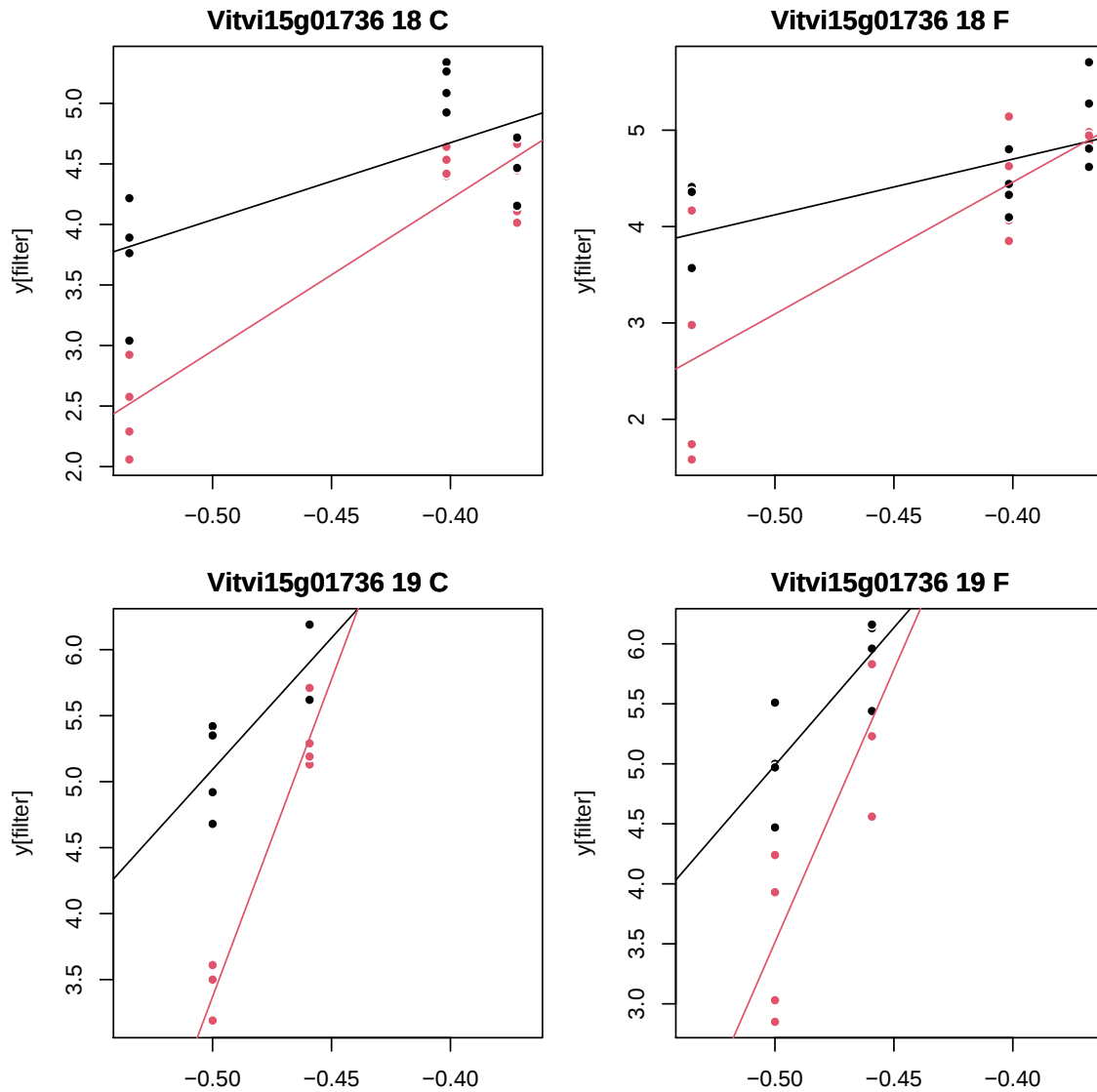
Call:

```
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 FALSE 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)

```

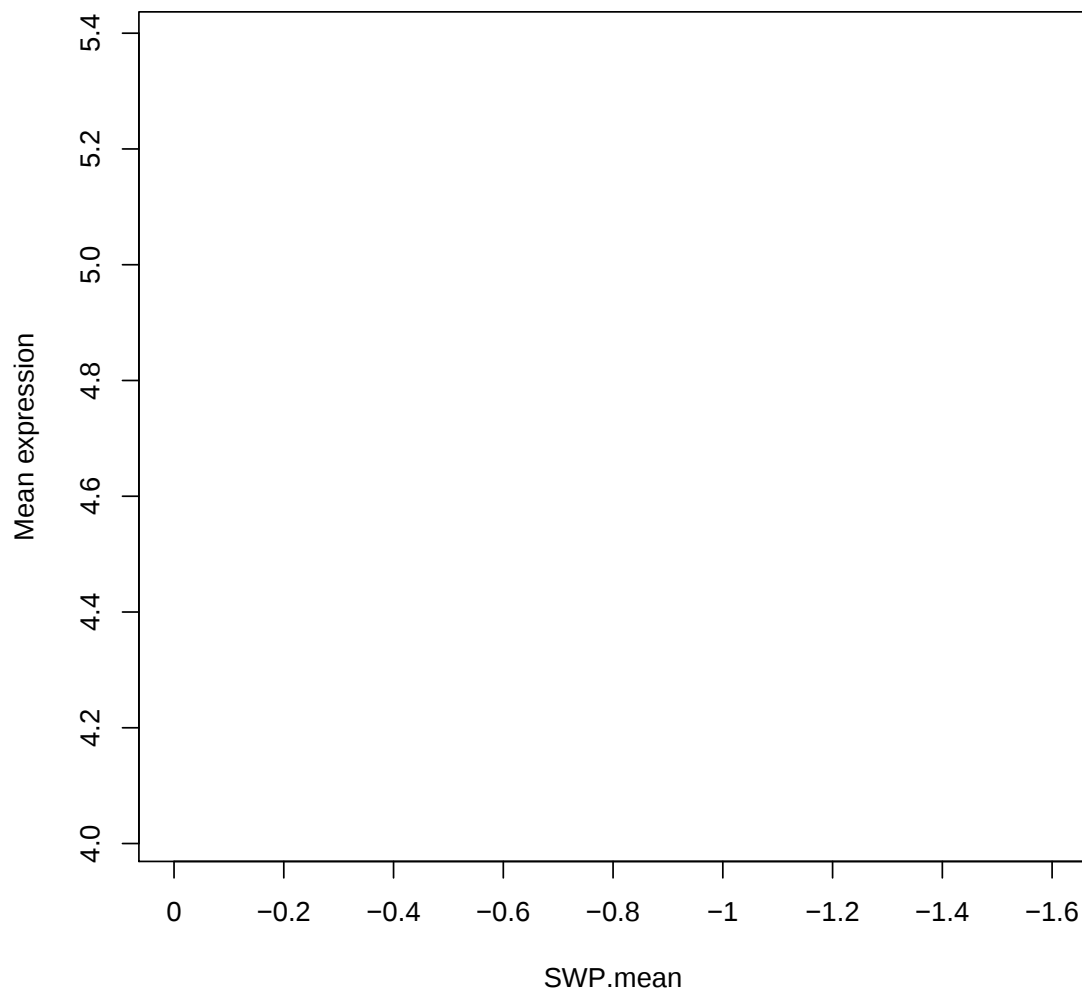
```
Error in tapply(pd$swp, pd[, c("date", "treat", "variety")], unique): argument
> means
, , variety = C

      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))
> vlvl <- unique(wpas$variety)
> tlvl <- rev(unique(wpas$treat))
> cols <- c(4, 2)
> pchs <- c(16, 16)
> plot(1, 1, #wpas$swp[tfilter & vfilter], means[, "WS", vlvl[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 default
```

```
> #
```

```
> for(i in 1:length(vlvls)){
```

```
+ for( j in 1:length(tlvls)){
```

```
+ tfilter <- wpa$treat %in% tlvls[j]
```

```
+ vfilter <- wpa$variety %in% vlvls[i]
```

```
+ yy <- means[as.character(wpa$date), tlvls[j], vlvls[i]]
```

```
+ wpa <- wpa[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

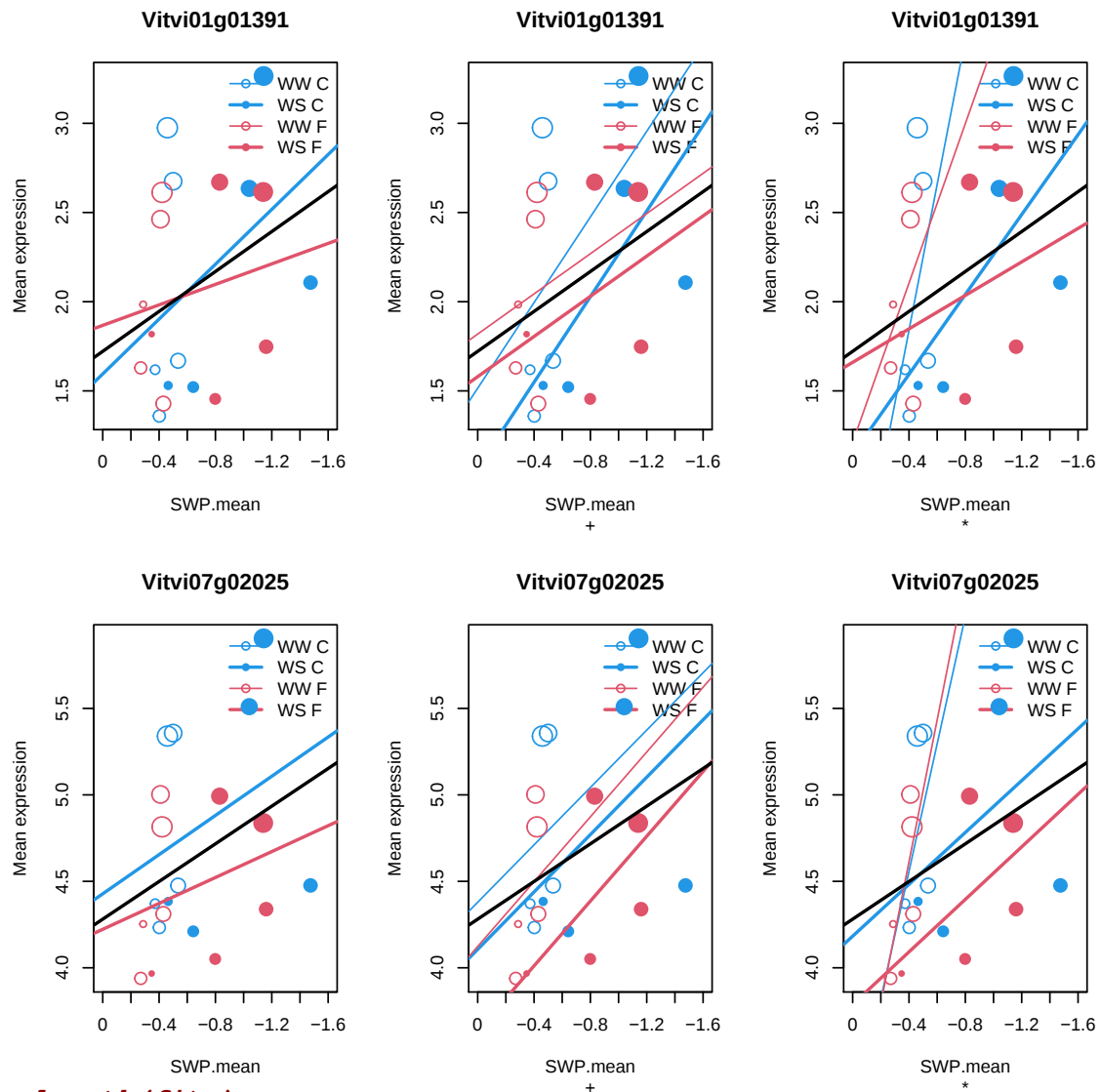
```
> plot.ewp <- function(varname, cols=c(4,2), pchs=c(1,16), lwd=c(1,2,1,2)
+       , model=c("*"), verbose=FALSE) {
+   if(verbose) print(varname)
+   (y <- unlist(t1819[varname,]))
+   means <- tapply(y, pd[,c("date", "treat", "variety")], mean, na.rm=TRUE)
+   means
+   swps <- tapply(wpas$swp, wpas[,c("date", "treat", "variety")], function(x) x[1])
+   swps
+   ylim <- range(means, na.rm=TRUE)
+   xlim <- c(min(wpas$swp, -1.6, na.rm=TRUE), max(wpas$swp, 0, na.rm=TRUE))
+   vlvs <- levels(wpas$variety)
+   tlvs <- levels(wpas$treat)
+   #cols <- c(4,2)
+   #pchs <- c(1,16)
+   plot(1,1, #wpas$swp[tfilter & vfilter], means[, "WS", vlvs[i]],
+        ylim=ylim,
+        xlim=-rev(xlim),
+        xlab = "SWP.mean",
+        ylab = "Mean expression",
+        type="n",
+        axes=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(tlvs, vlvs, paste))
+   #
+   allx <- NULL
+   ally <- NULL
+   fits <- NULL
+   fits <- list()
+   for(i in 1:length(vlvs)) {
+     #for( j in 1:length(tlvs)) {
+     #tfilter <- wpas$treat %in% tlvs[j]
+     vfilter <- wpas$variety %in% vlvs[i]
+     wpa <- wpas[vfilter,]
+     means[, vlvs[i]]
+     mns <- melt(means[, vlvs[i]])
+     mns
+     wp <- melt(swps[, vlvs[i]])
+     wp
+     all(wpa$date==dimnames(mns)$date)
+     yy <- mns[, "value"]
+     xx <- wp[, "value"]
+     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$swp, 0, na.rm=TRUE))
+   vlvs <- levels(wpas$variety)
+   tlvs <- levels(wpas$treat)
+   #cols <- c(4,2)
```

```

+ #pchs <- c(1,16)
+ plot(1,1, #wpas$swp[tfilter & vfilter], means[, "WS", vlvls[i]],
+      xlim=ylim,
+      ylim=-rev(xlim),
+      ylab = "SWP.mean",
+      xlab = "Mean expression",
+      type="n",
+      axes=FALSE
+      )
+ axis(1)
+ box()
+ axis(2, at=seq(0, 2, 0.2), labels=-(seq(0, 2, 0.2)))
+ title(varname, model)
+ legend("topright", bty="n", pch=pchs, col=rep(cols, each=2), lwd=lwd,
+       legend= outer(tlvls, vlvls, paste))
+ #
+ ally <- NULL
+ allx <- NULL
+ fits <- NULL
+ for(i in 1:length(vlvls)){
+   #for( j in 1:length(tlvls)){
+   #tfilter <- wpas$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
+ }

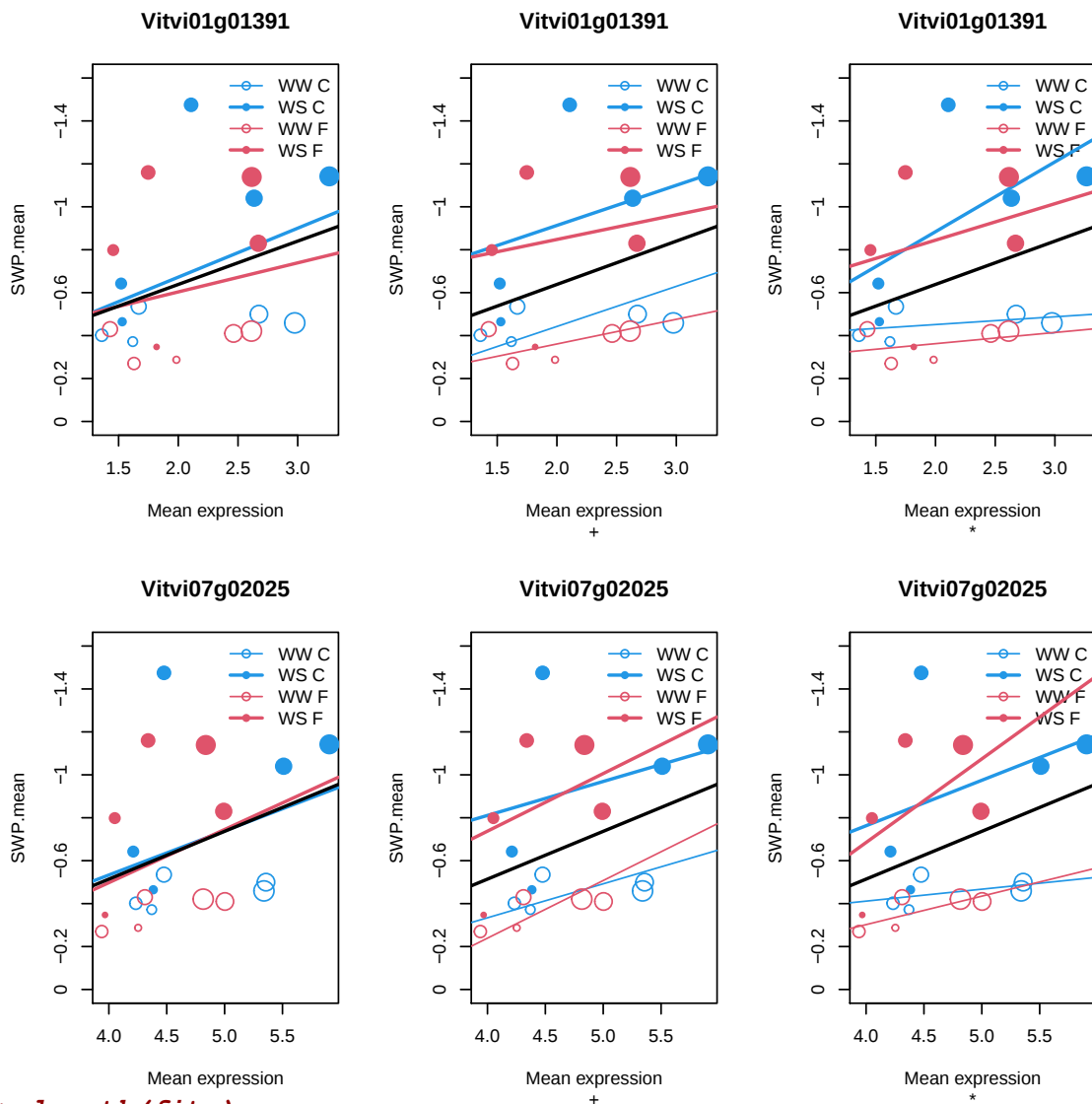
```

```

+ 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)

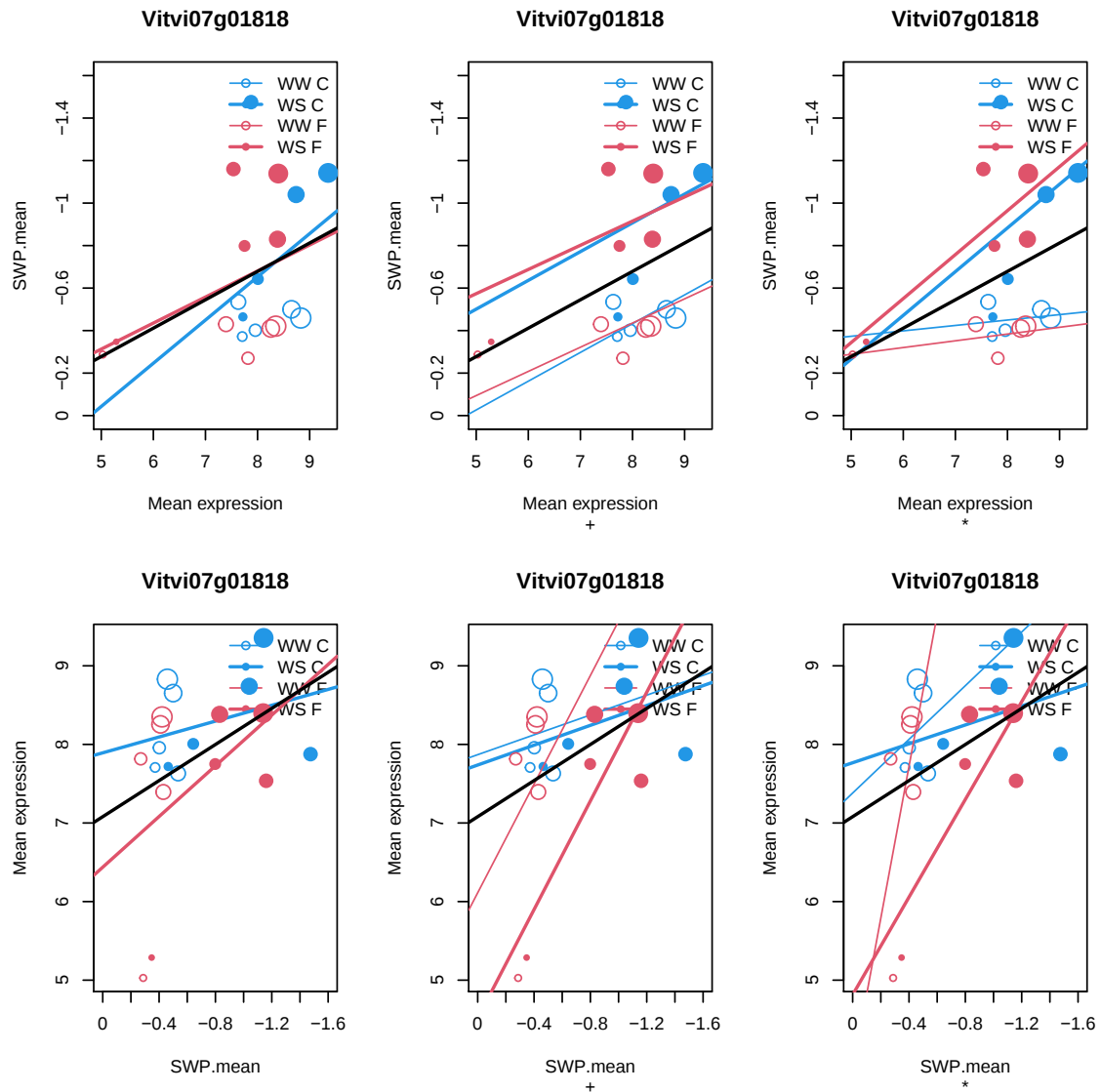
```

```

[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

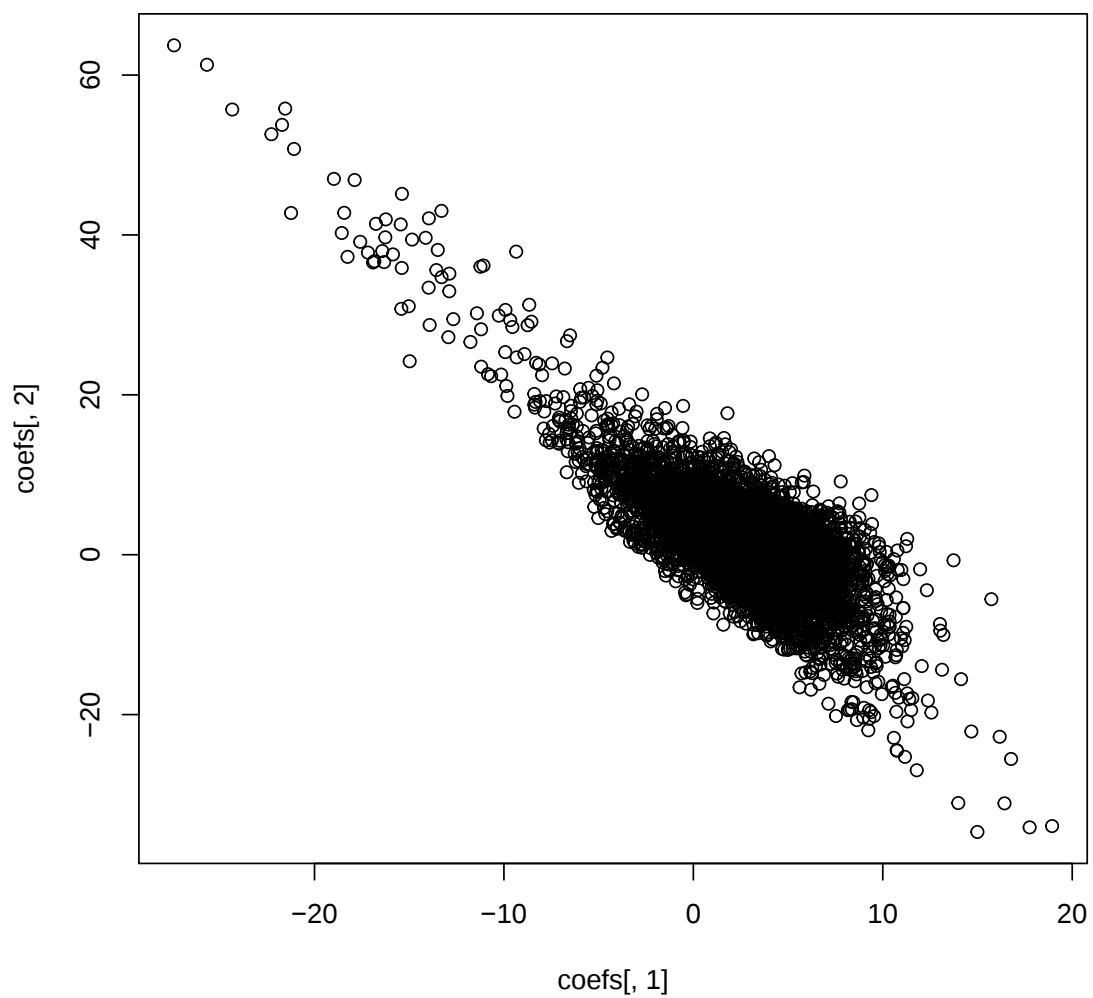
> tail(design)
      (Intercept)      swp
75              1 0.4592308
76              1 0.4592308
77              1 0.4592308
78              1 0.4592308
79              1 0.4592308
80              1 0.4592308
```

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
Vitvi02g00374	29.90913	3.283880	18.79698	2.300407e-31
Vitvi04g00522	20.70966	3.414499	17.94327	4.900852e-30
Vitvi09g01273	17.79031	3.745035	17.75236	9.830851e-30
Vitvi11g00724	45.13777	5.070678	17.74622	1.005426e-29
Vitvi01g01943	12.14569	4.556800	17.51369	2.361916e-29
Vitvi08g00689	24.00508	2.578551	17.48107	2.664036e-29
	adj.P.Val	B		
Vitvi02g00374	3.506281e-27	55.20282		
Vitvi04g00522	3.734939e-26	52.74622		
Vitvi09g01273	3.831175e-26	52.18207		
Vitvi11g00724	3.831175e-26	52.16383		
Vitvi01g01943	6.767539e-26	51.46908		
Vitvi08g00689	6.767539e-26	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"
> 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/40_Expression-water-stress-0.05-r-100/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 threshold for effect (slope), e.g. absolute slope larger than certain threshold. In the figure a cutoff 10 is used.

Za pregled je boljše pogledati prvih nekaj in zadnjih nekaj.

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

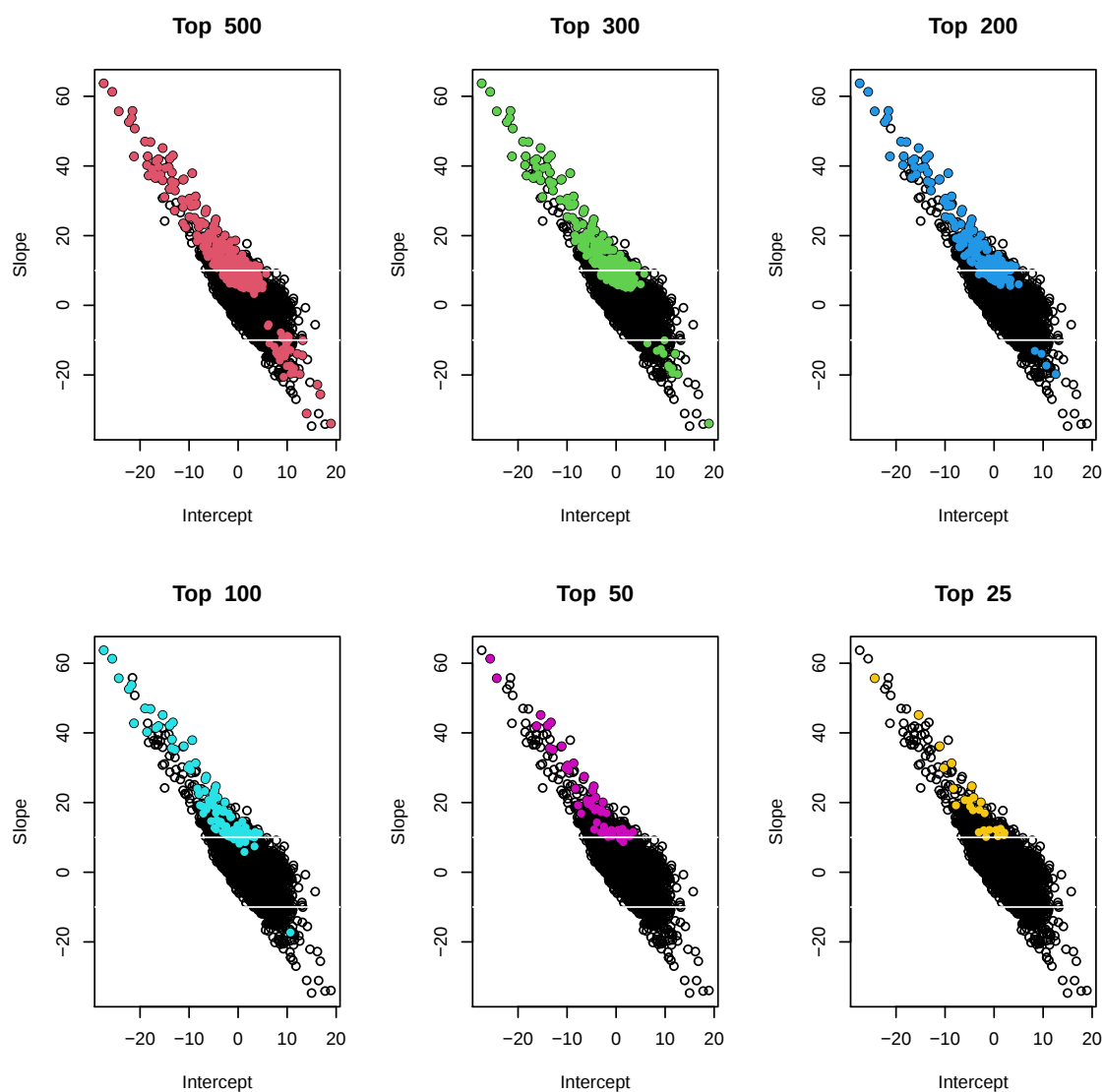


Figure 1: Coefficients for labeled number of top significant genes are indicated by colors. White line is a proposed threshold.

5.2 Top 100 genes

Plots of situation for top 100 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, regardless of treatment and variety. Lower panels have swapped 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

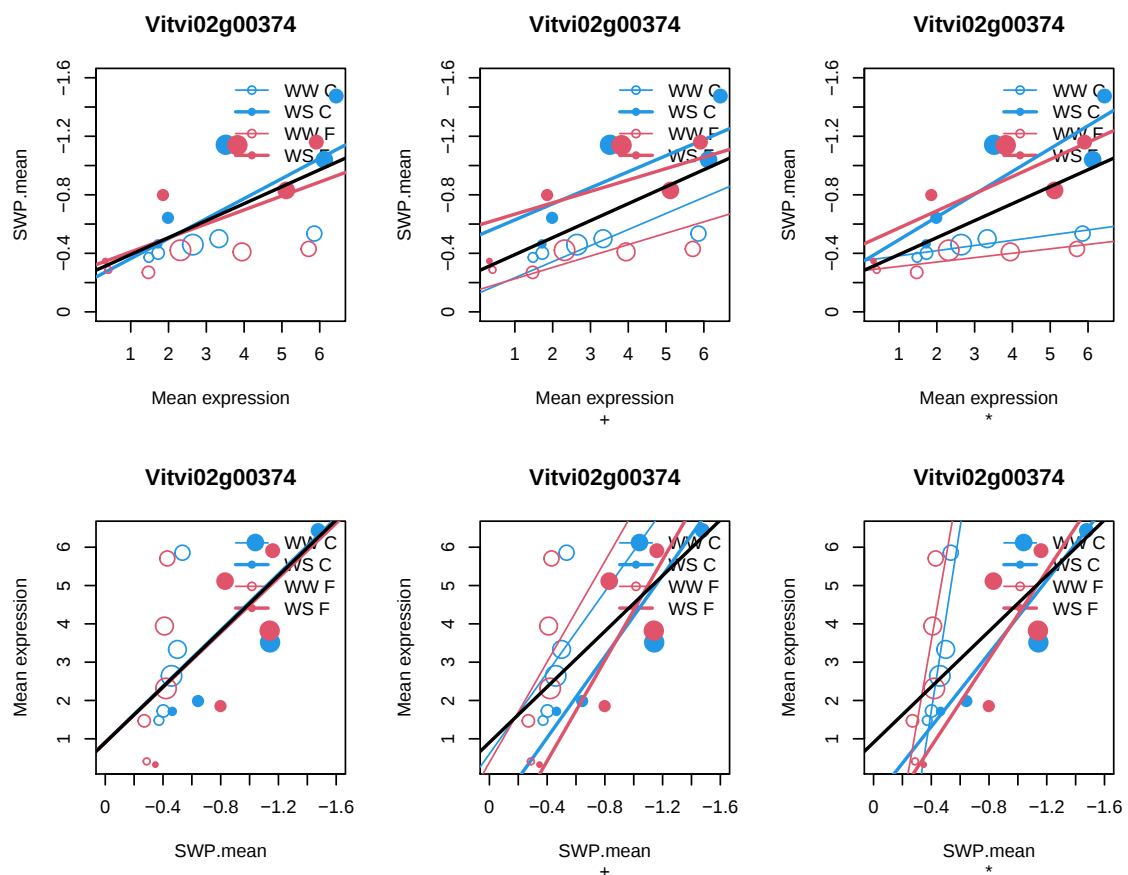
UBX domain-containing protein IPR001012 UBX

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 |

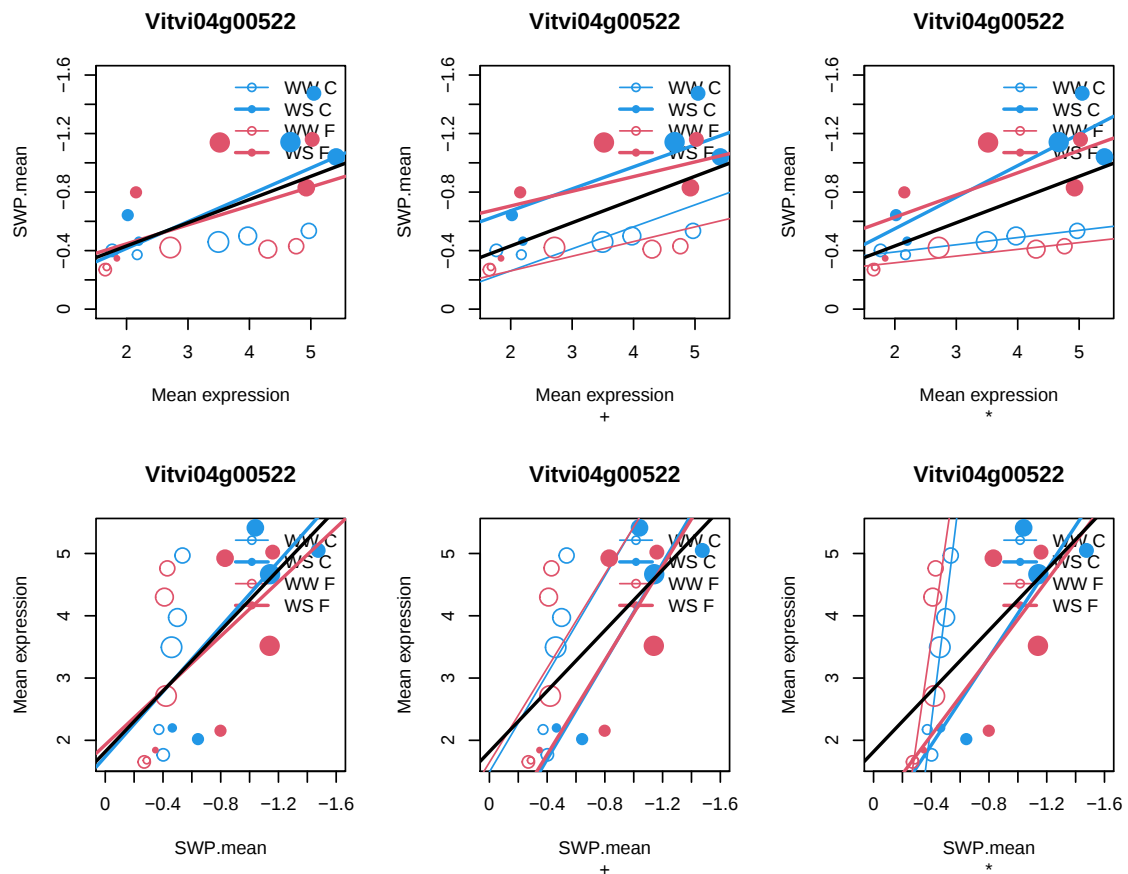
201606

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 |

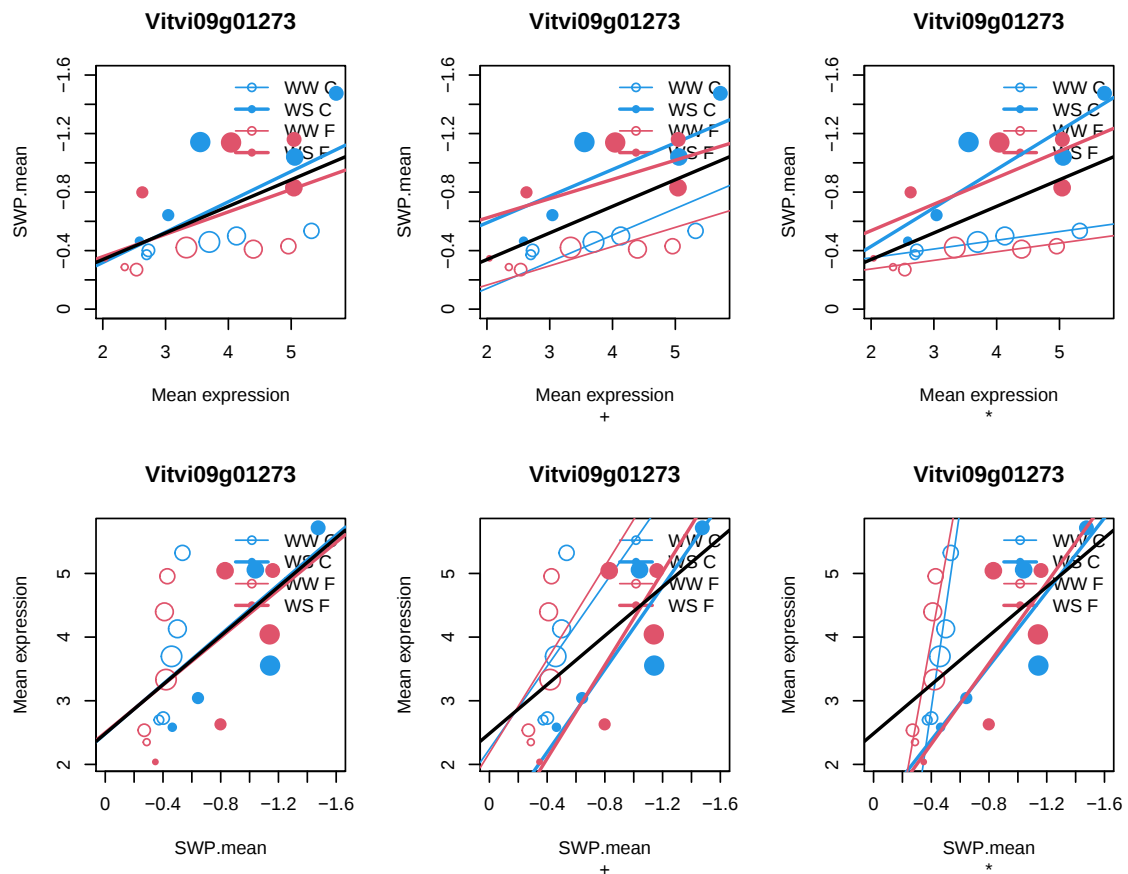
201606

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

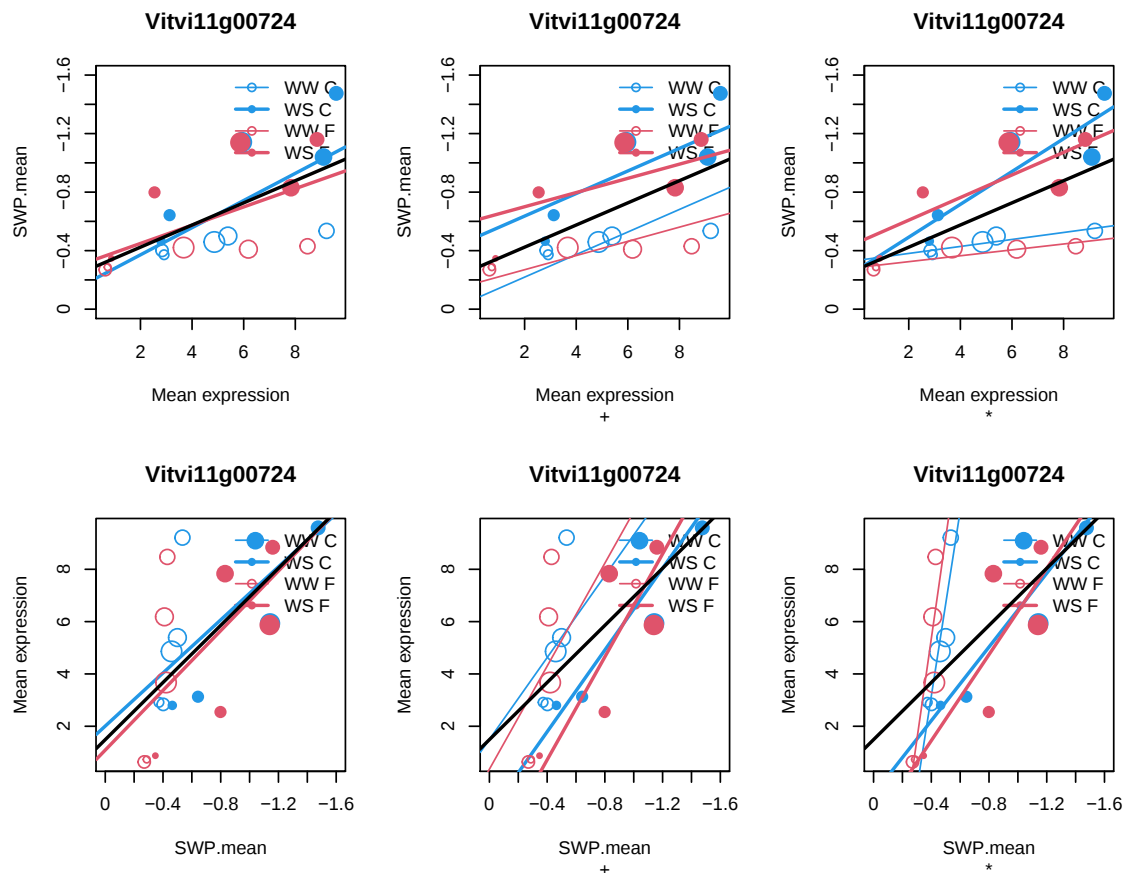
heat shock protein 70B |

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])
```

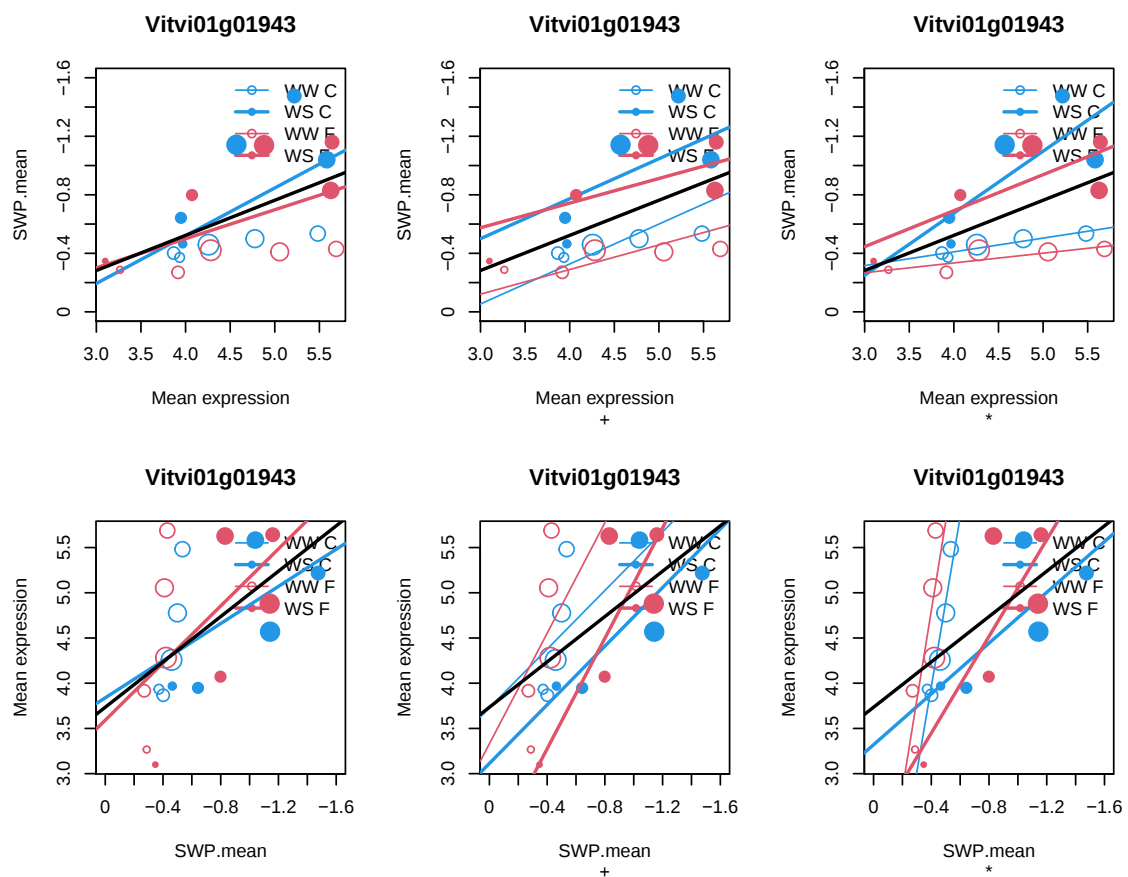
```
Vitvi01g01943
20
stress
NA
```

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 |

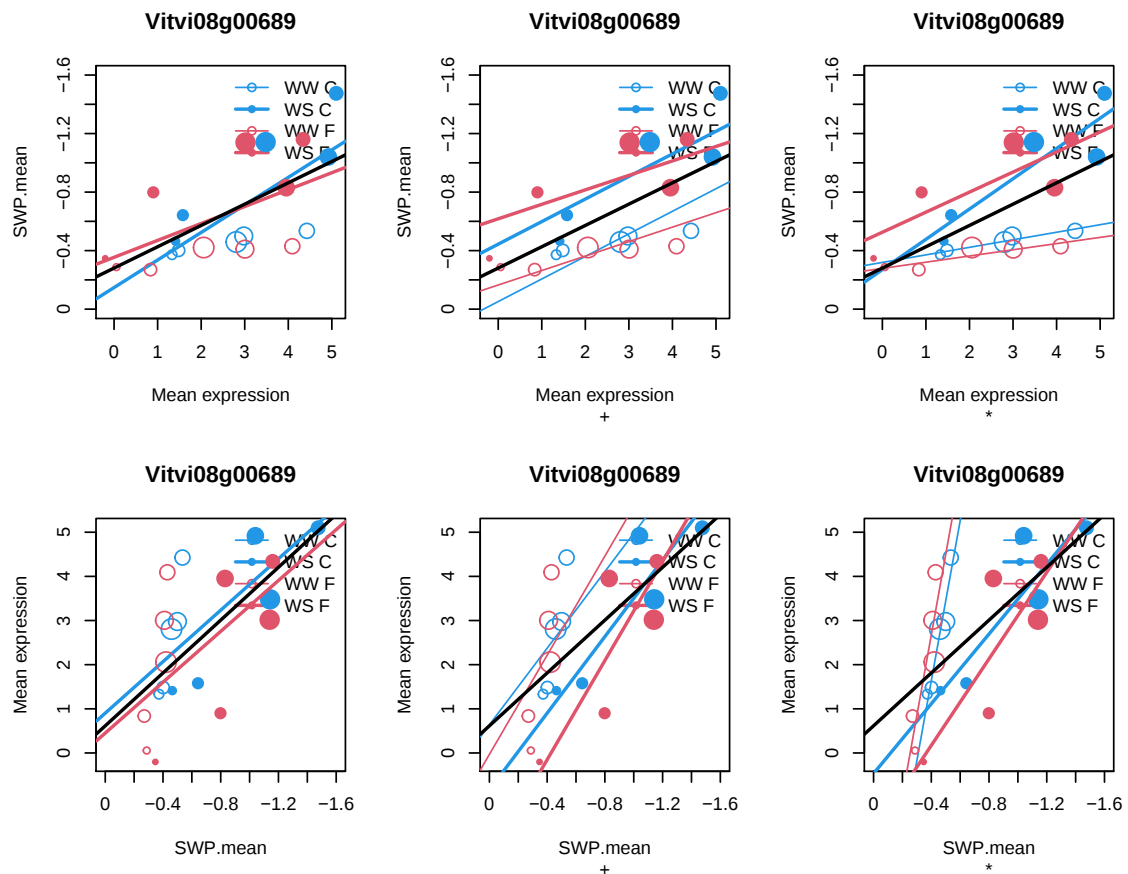
201606

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 |

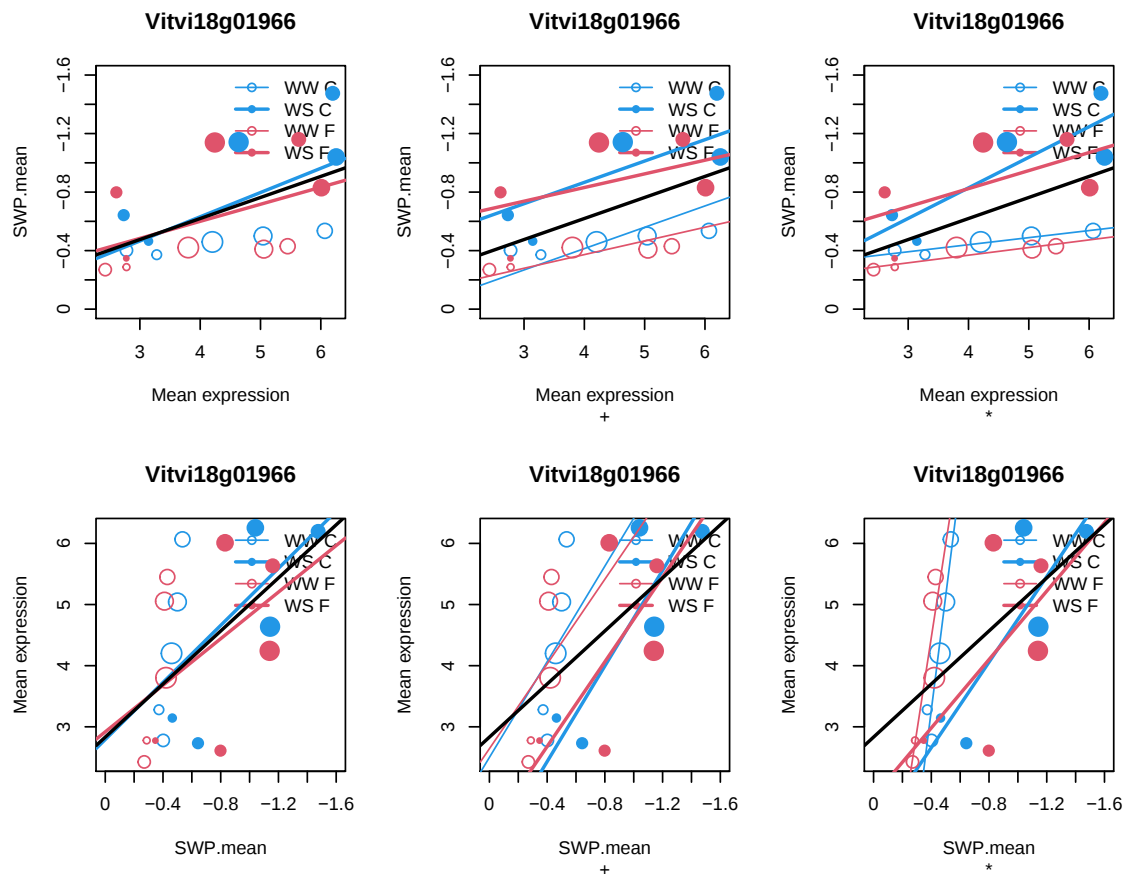
201606

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 |

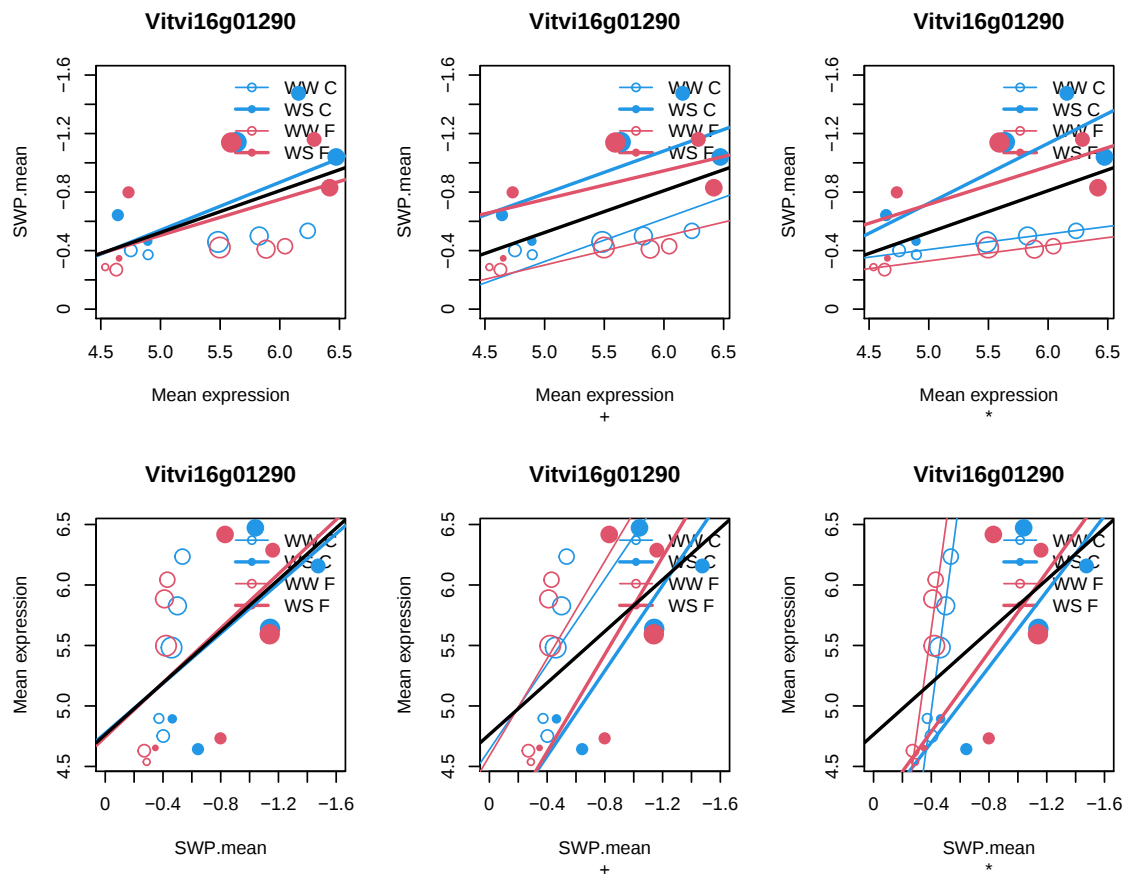
201606

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 |

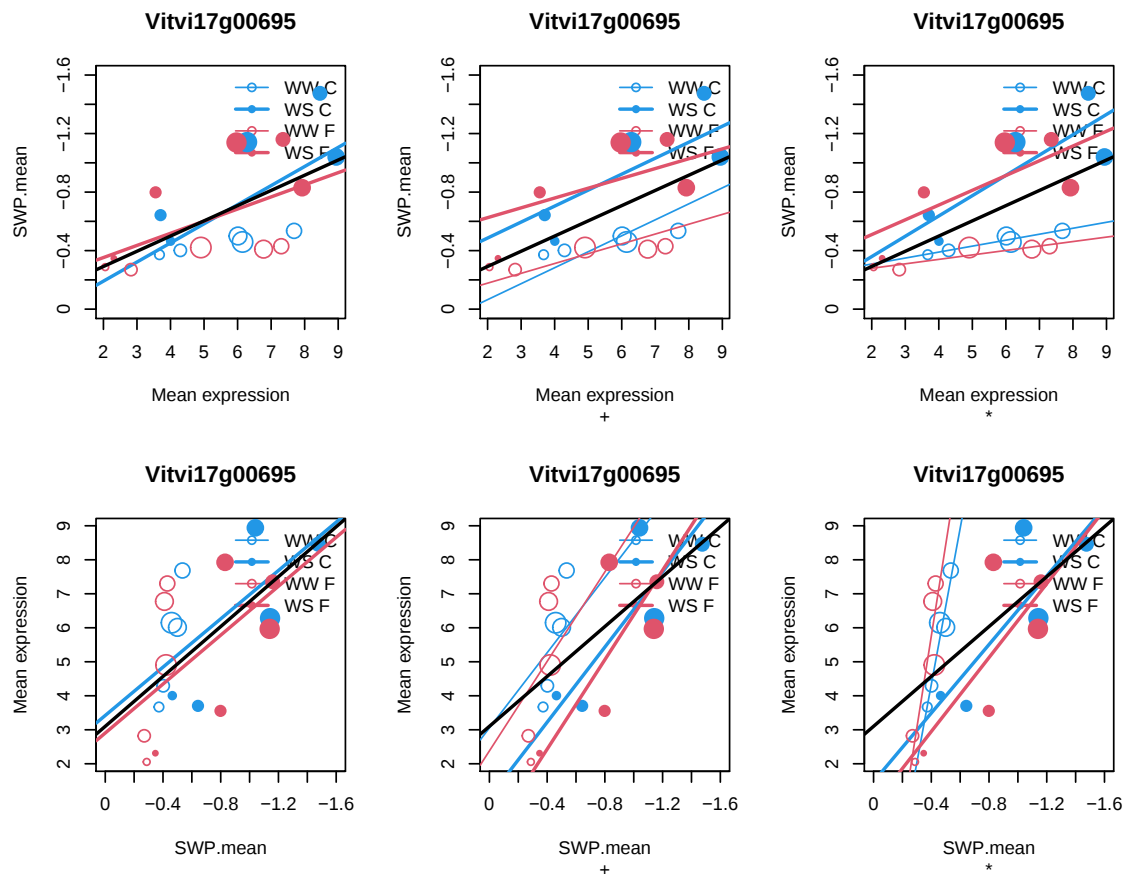
201606

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

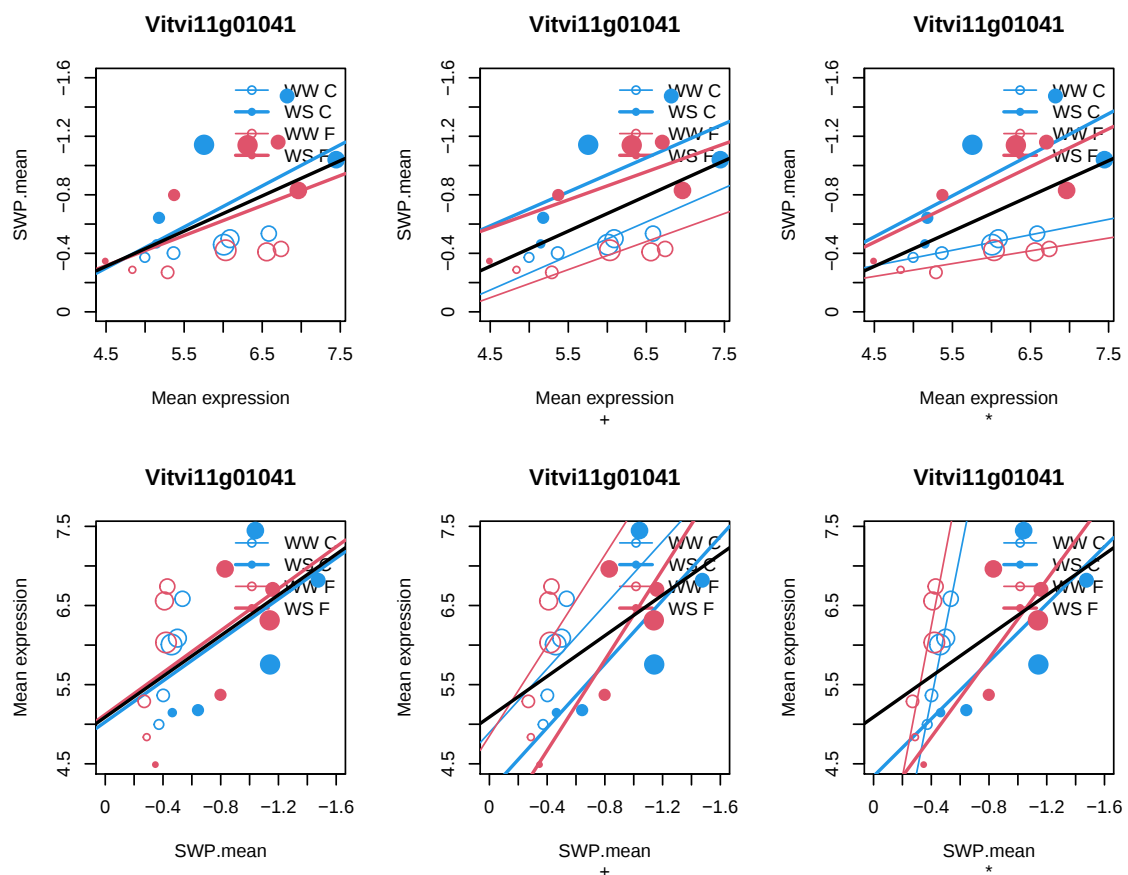
35.2

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

Ahal domain-containing protein |

Chr3:3839289-3841303 FORWARD LENGTH=360 |

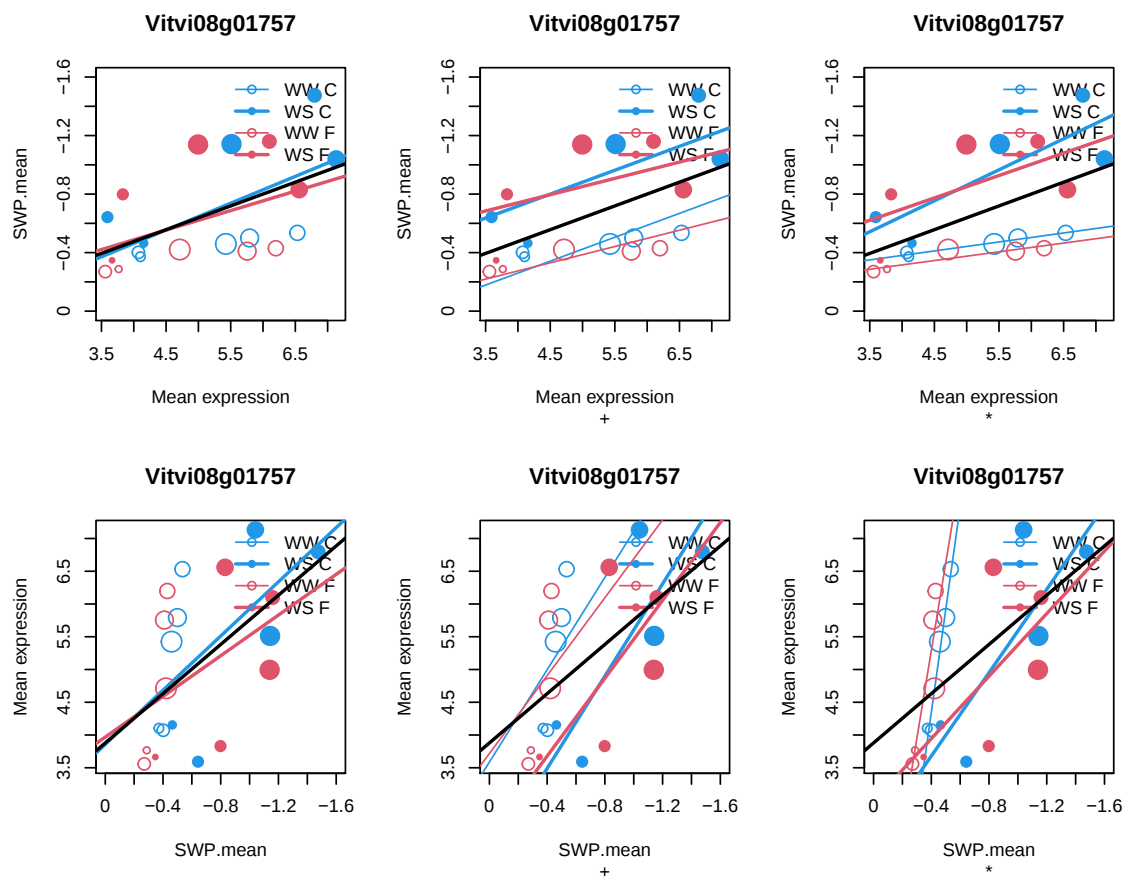
201606

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 |

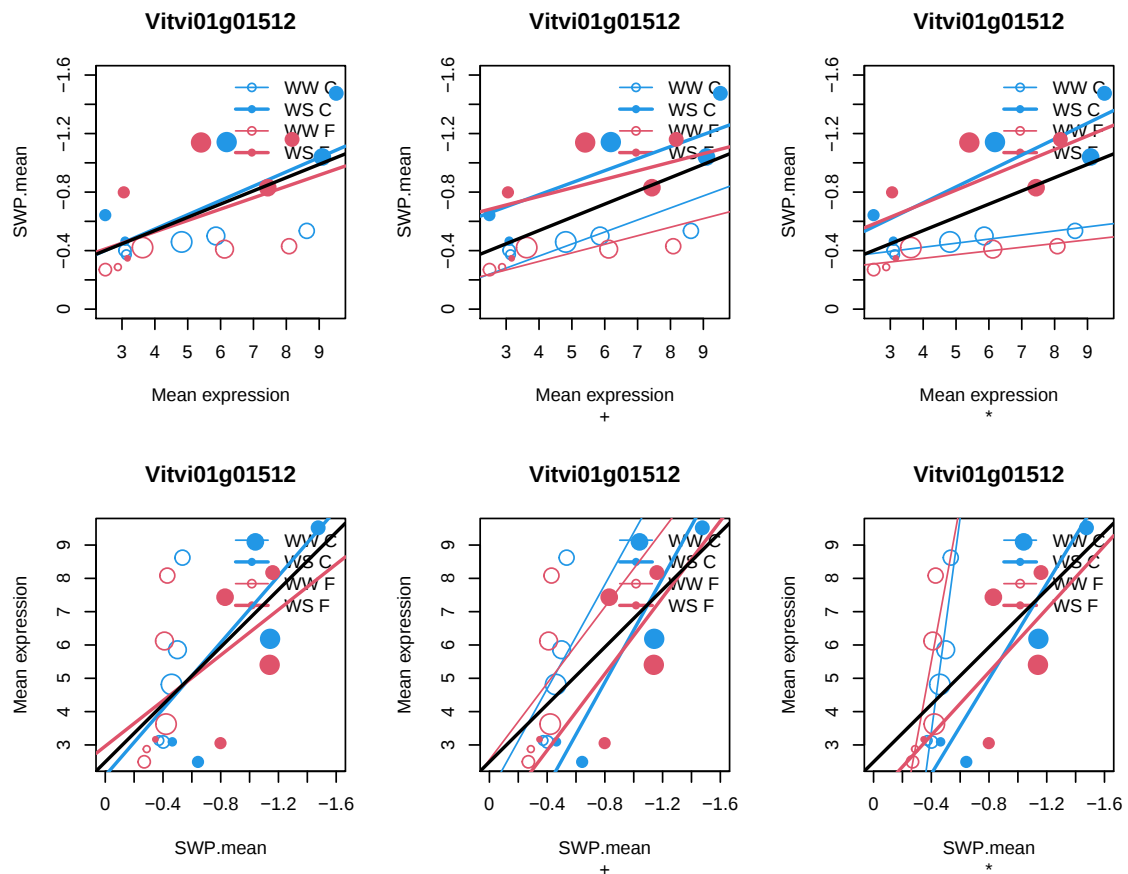
201606

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 |

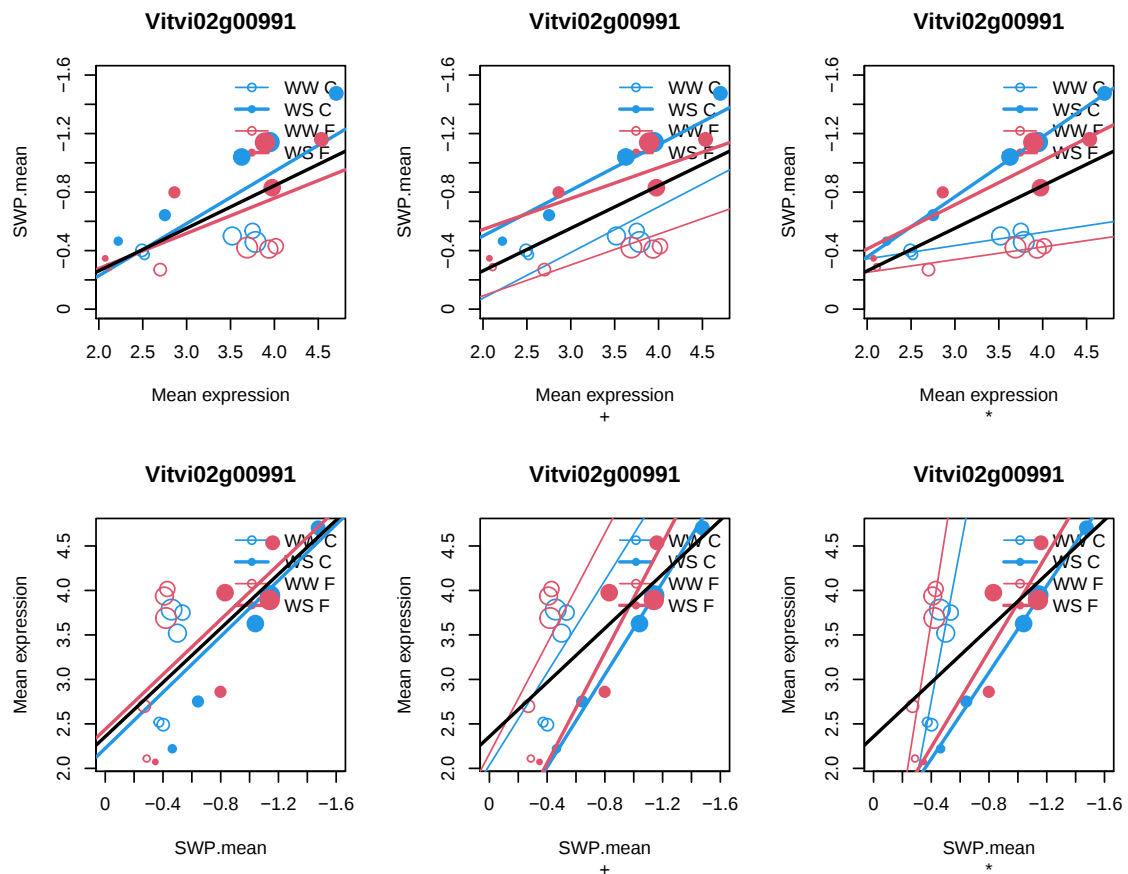
201606

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 |

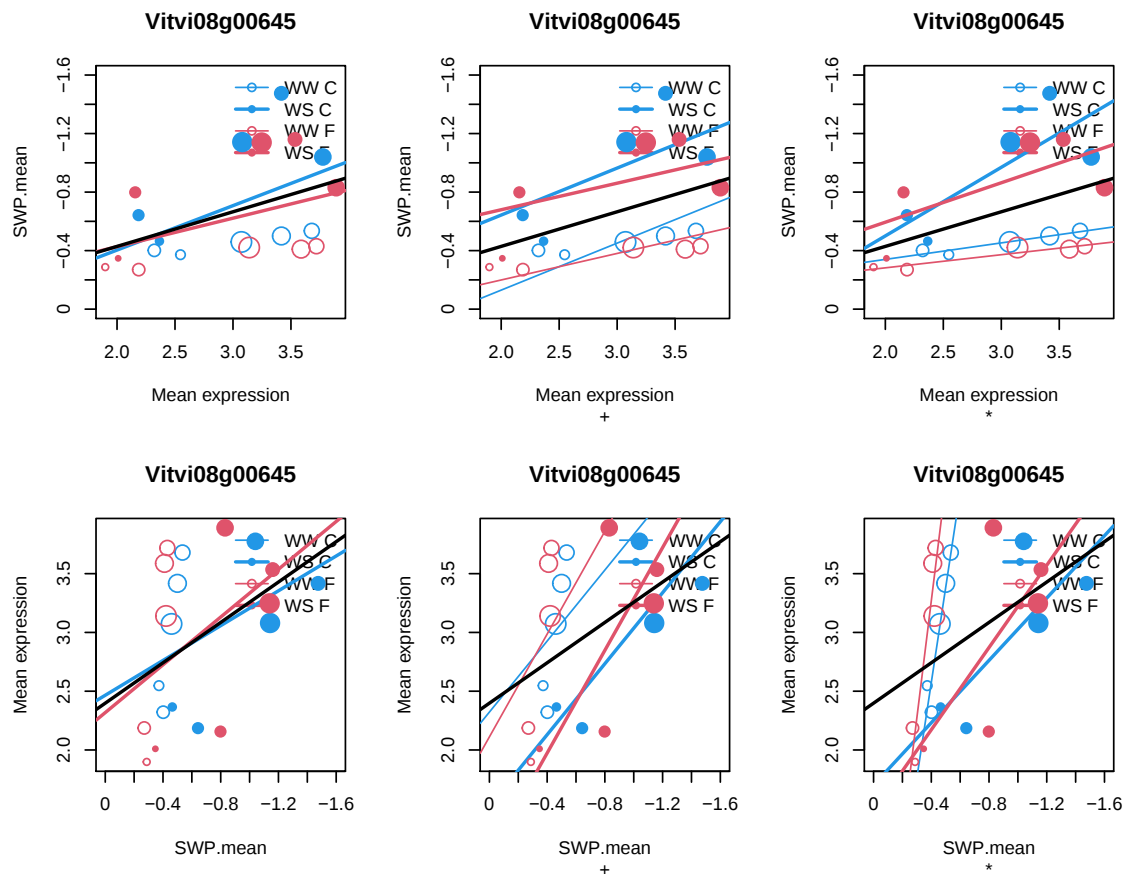
201606

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

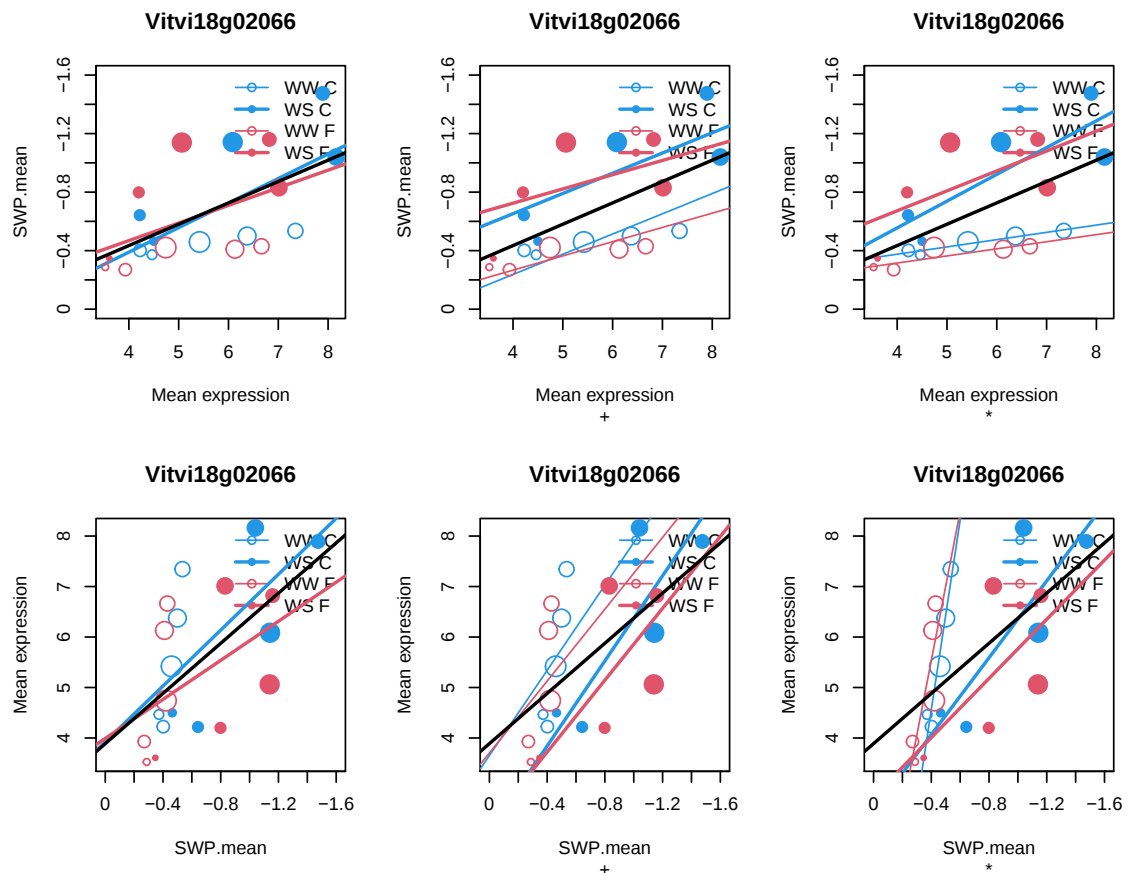
chloroplast heat shock protein 70-1 |

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 |

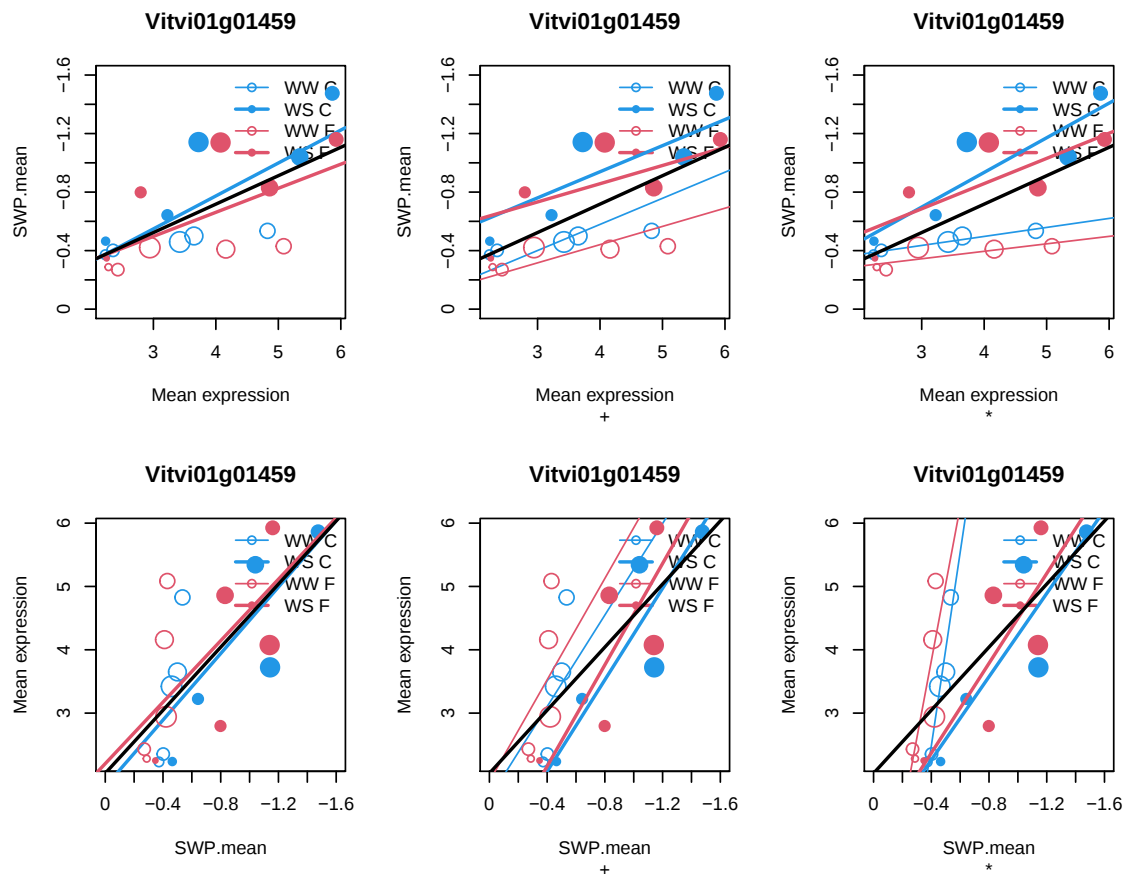
201606

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 |

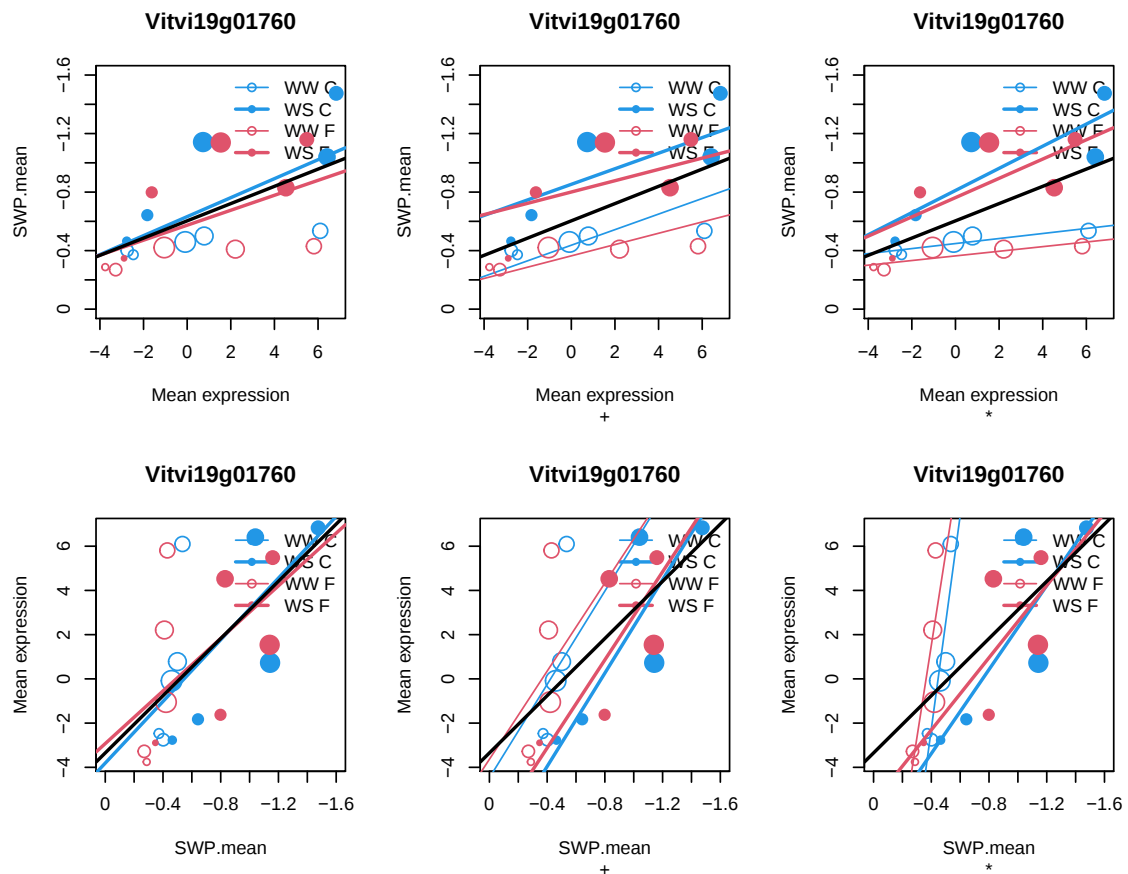
201606

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 |

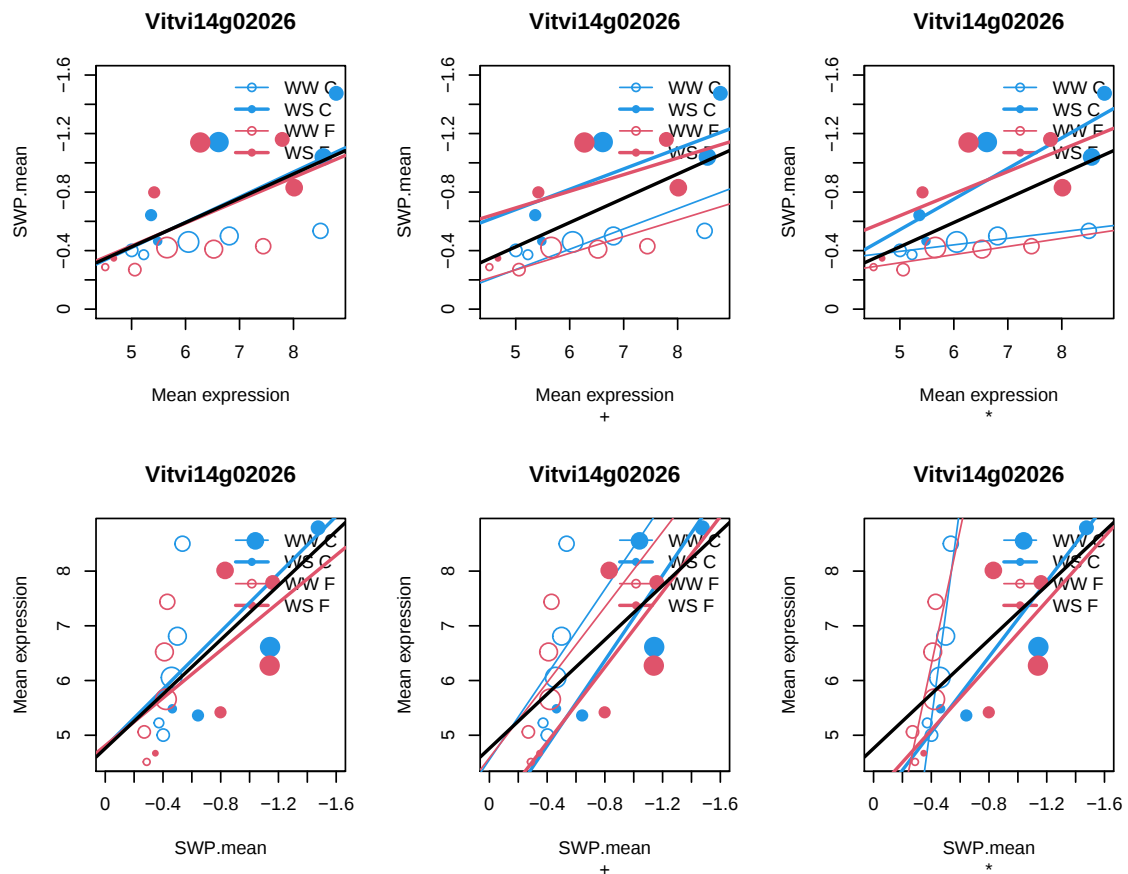
201606

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 |

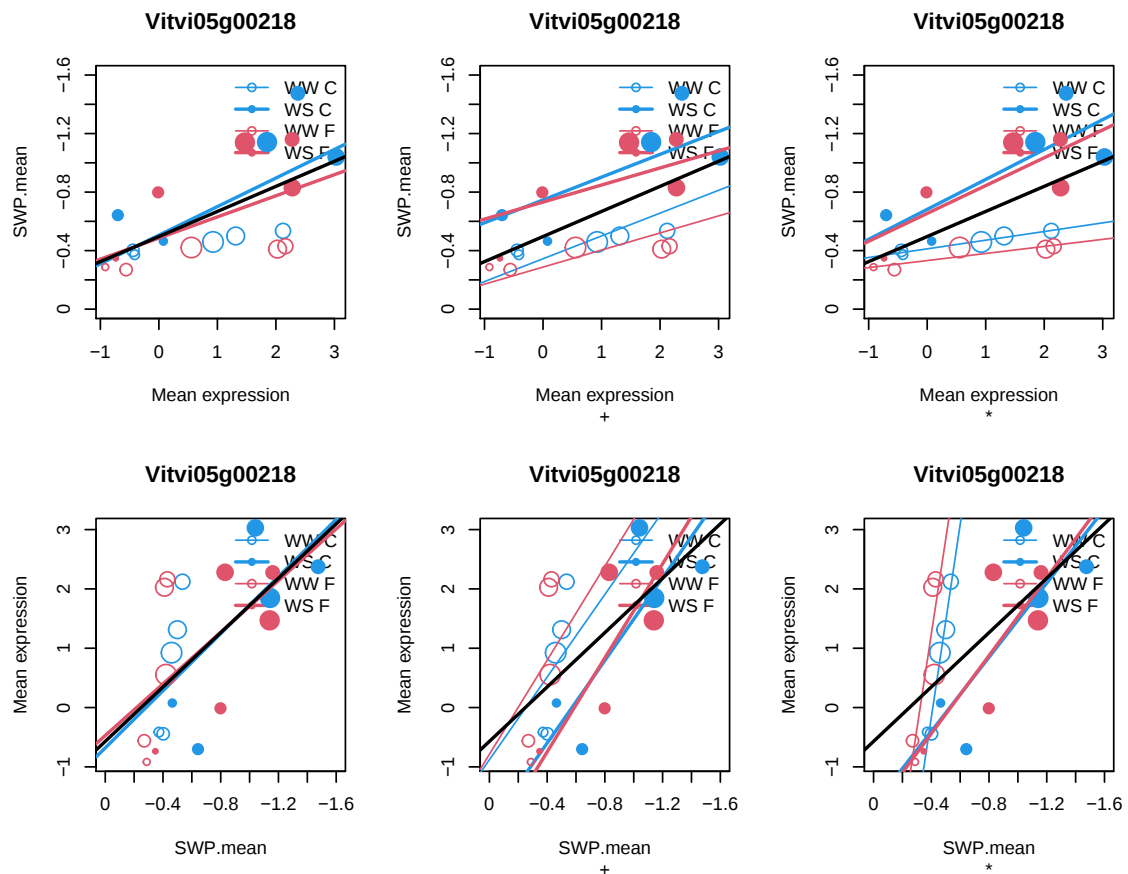
201606

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

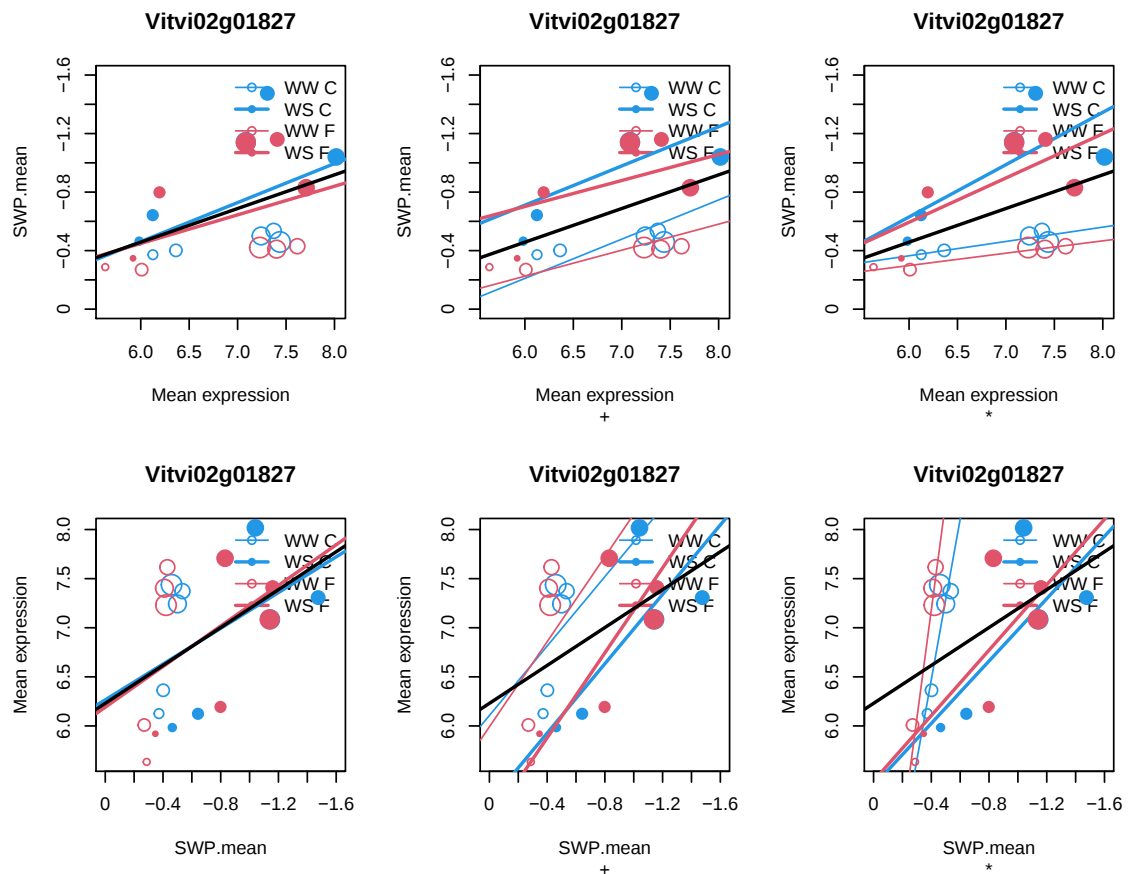
BAX inhibitor 1 |

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): $r_2 = 0.4711$

5.2.21 Vitvi08g01234

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

Vitvi08g01234

35.1.3

not assigned.no ontology.armadillo/beta-catenin repeat family protein

Fes1A |

Chr3:2871710-2873109 FORWARD LENGTH=327 |

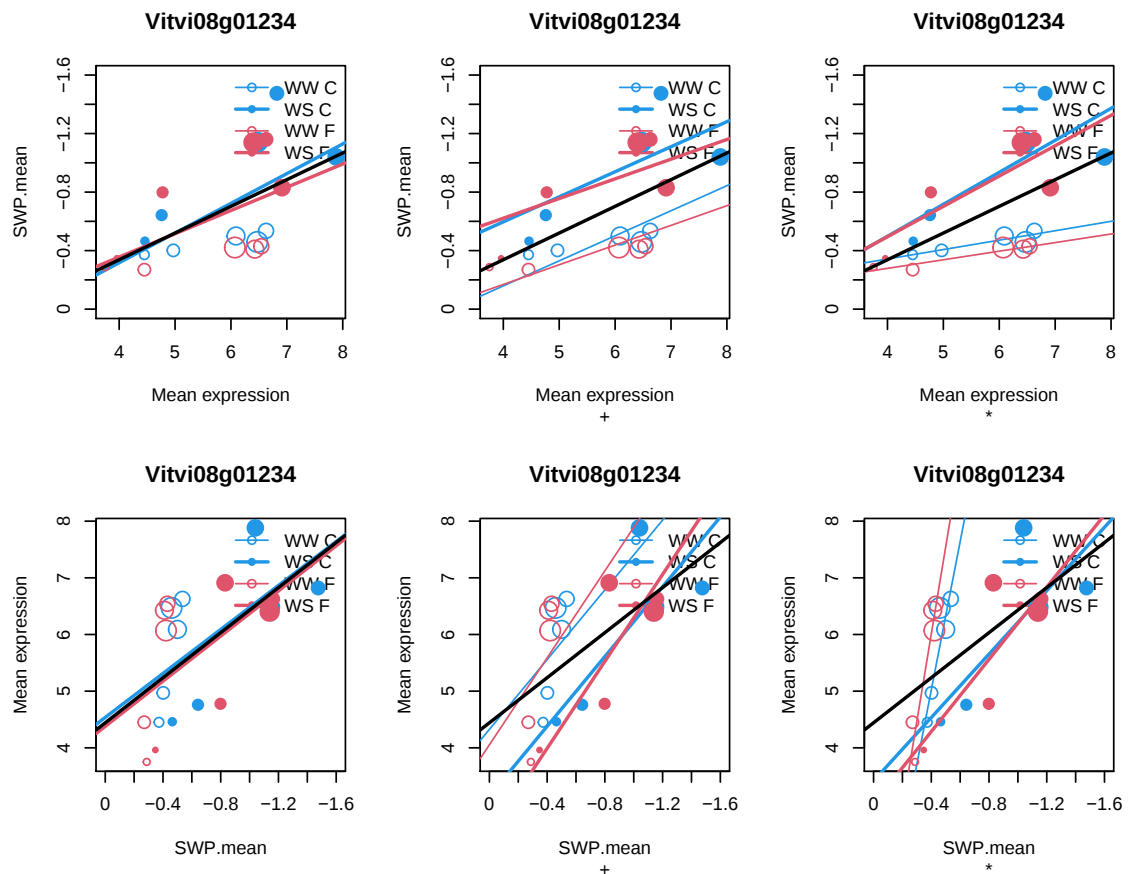
201606

Coefficient swp for Vitvi08g01234.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi08g01234	16.94196	5.746844	16.08566	5.193177e-27	3.769257e-24

B

Vitvi08g01234 47.02037



Correlation of all measurements (not just means): $r = 0.8753$, $r^2 = 0.7662$

Correlation of mean values (plots): $r_2 = 0.6023$

5.2.22 Vitvi06g01417

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

Vitvi06g01417

35.2

not assigned.unknown

UDP-Glycosyltransferase superfamily protein |

Chr5:26198410-26199810 REVERSE LENGTH=466 |

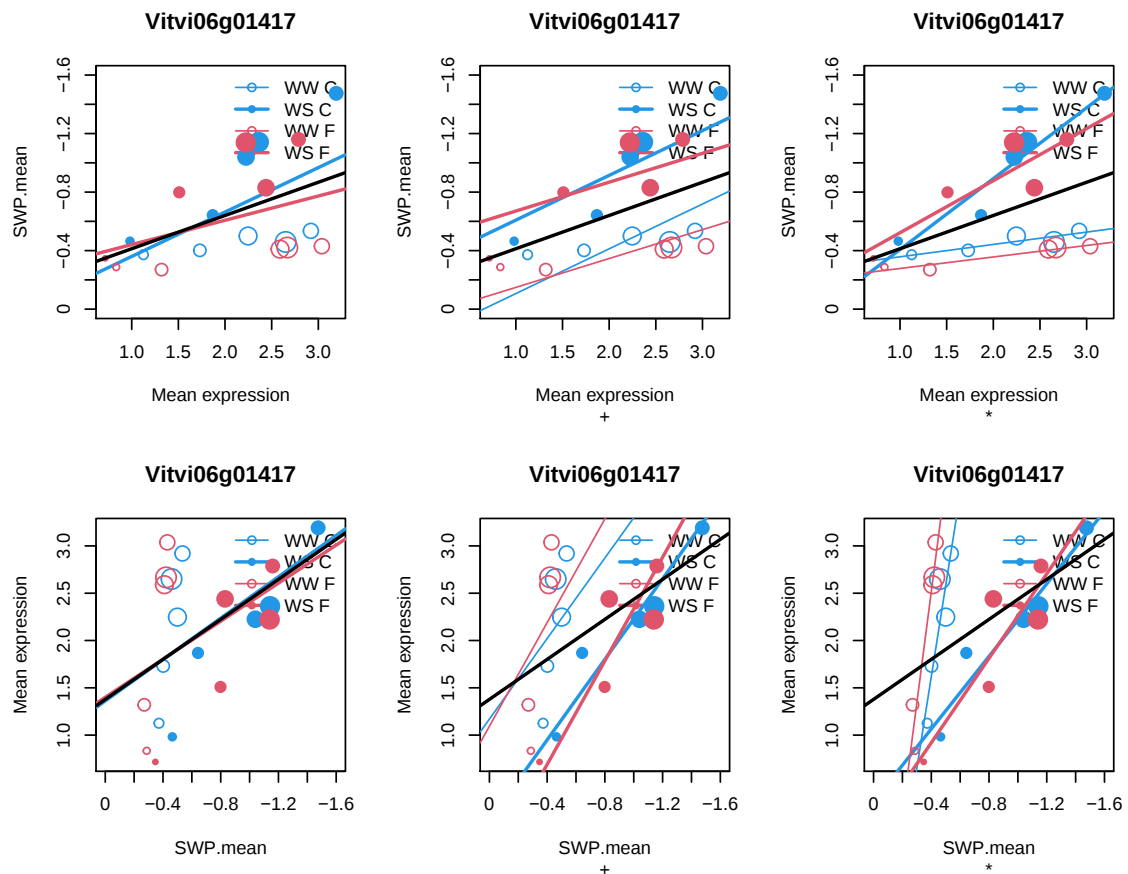
201606

Coefficient swp for Vitvi06g01417.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi06g01417	11.44977	2.071407	16.0265	6.529179e-27	4.523534e-24

B

Vitvi06g01417 46.82925



Correlation of all measurements (not just means): $r = 0.8784$, $r^2 = 0.7716$

Correlation of mean values (plots): $r_2 = 0.4902$

5.2.23 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

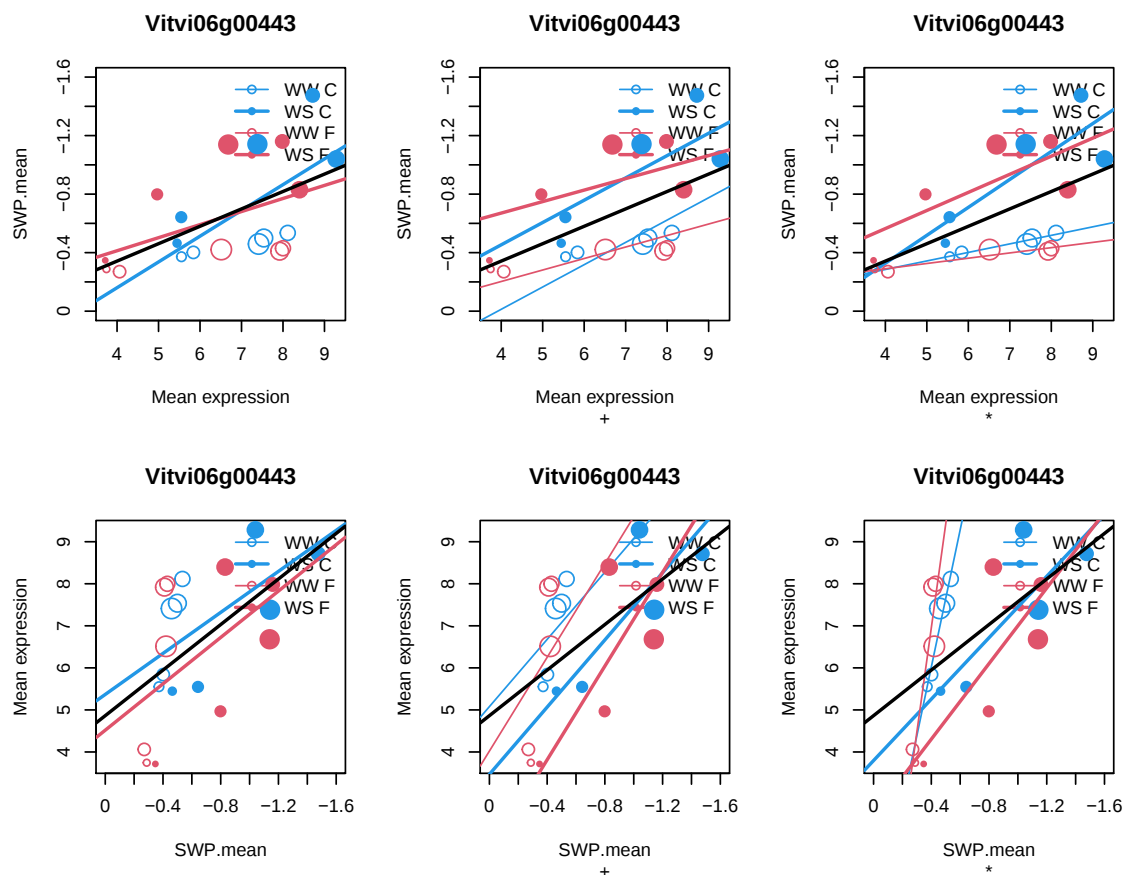
heat shock cognate protein 70-1 |

Chr5:554055-556334 REVERSE LENGTH=651 |

201606

Coefficient swp for Vitvi06g00443.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi06g00443	24.67175	6.640504	15.6815	2.503914e-26	1.659333e-23
B					
Vitvi06g00443	45.70355				



Correlation of all measurements (not just means): $r = 0.8682$, $r^2 = 0.7537$

Correlation of mean values (plots): $r_2 = 0.5675$

5.2.24 Vitvi11g00658

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

Vitvi11g00658

34.99

transport.misc

temperature-induced lipocalin |

Chr5:23500512-23501156 REVERSE LENGTH=186 |

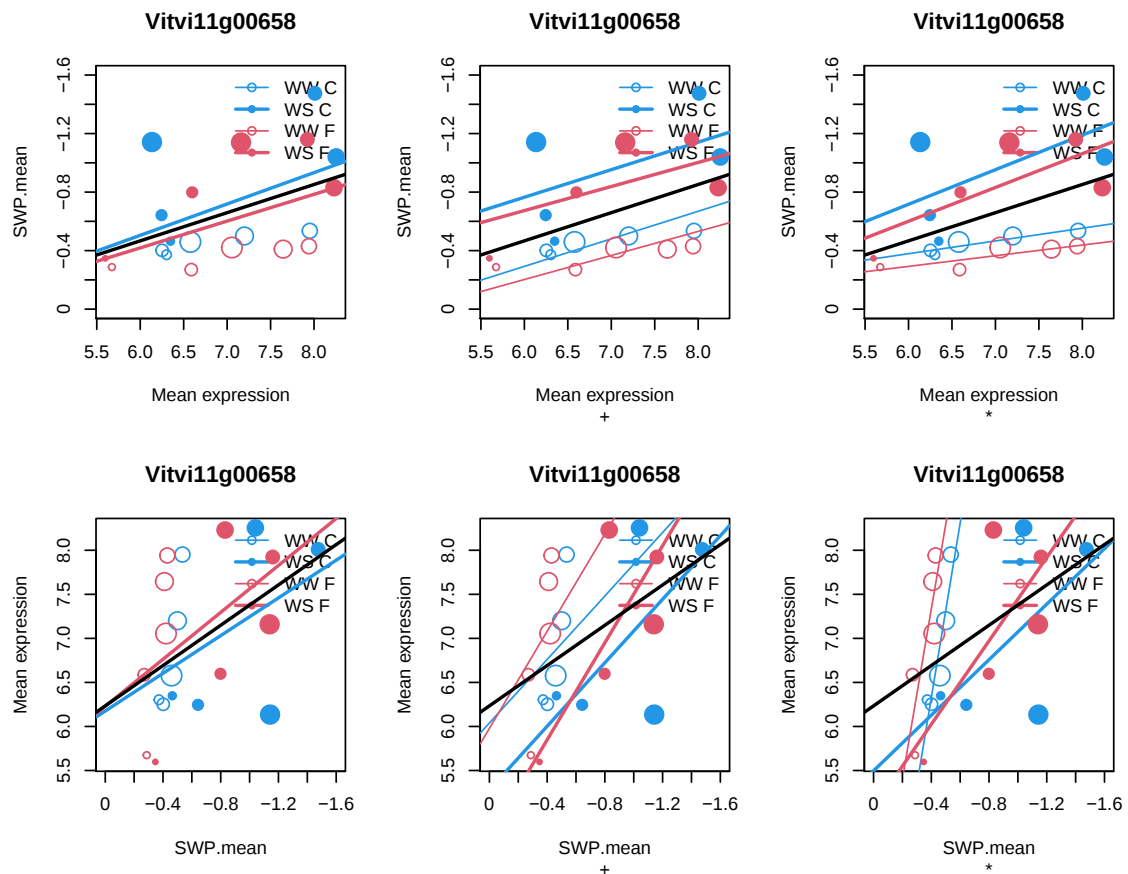
201606

Coefficient swp for Vitvi11g00658.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi11g00658	12.48308	6.984476	15.58819	3.611063e-26	2.293326e-23

B

Vitvi11g00658 45.39586



Correlation of all measurements (not just means): $r = 0.8712$, $r^2 = 0.7590$

Correlation of mean values (plots): $r_2 = 0.4694$

5.2.25 Vitvi02g00479

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

Vitvi02g00479

35.1.40

not assigned.no ontology.glycine rich proteins

glycine-rich protein |

Chr4:11944050-11945565 REVERSE LENGTH=356 |

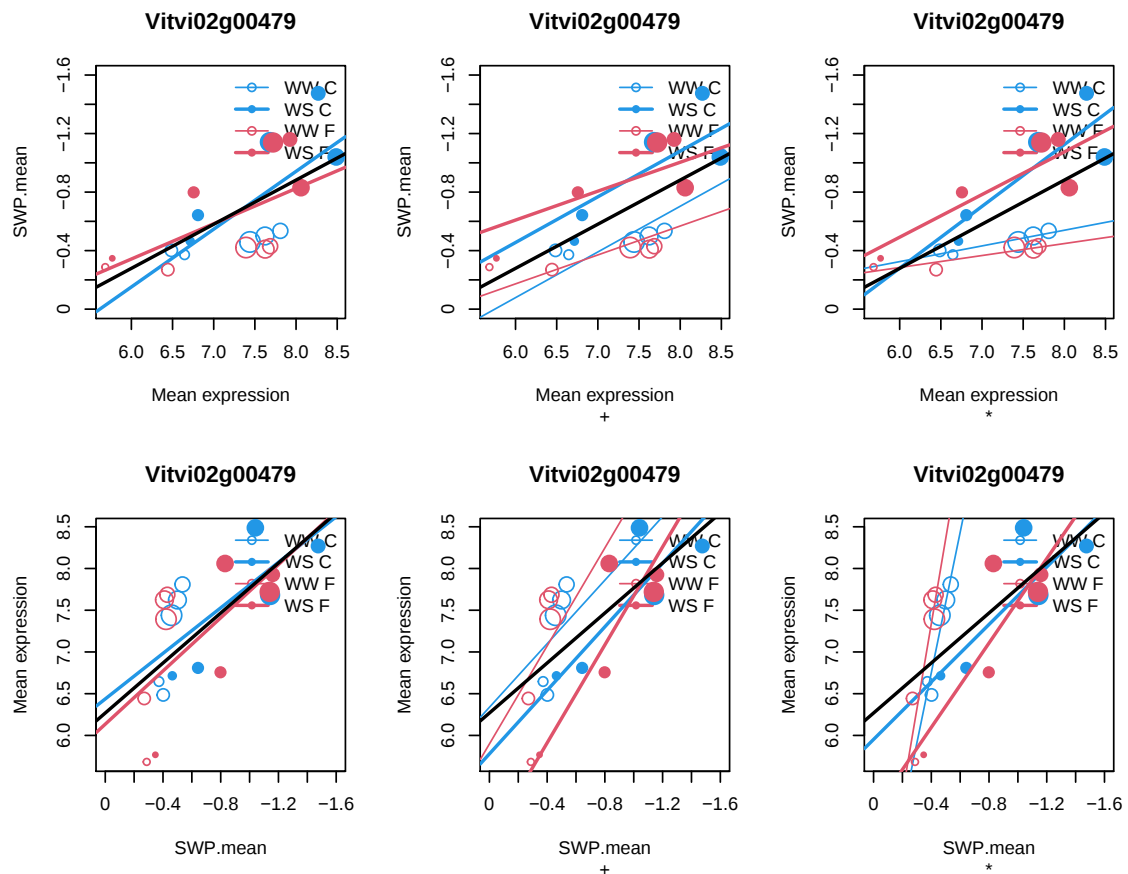
201606

Coefficient swp for Vitvi02g00479.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi02g00479	11.34914	7.251234	15.54722	4.242243e-26	2.586411e-23

B

Vitvi02g00479 45.26035



Correlation of all measurements (not just means): $r = 0.8719$, $r^2 = 0.7602$

Correlation of mean values (plots): $r_2 = 0.6722$

5.2.26 Vitvi10g02382

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

Vitvi10g02382

20.02.2001

stress.abiotic.heat

Aldolase-type TIM barrel family protein |

Chr4:11340492-11341732 FORWARD LENGTH=286 |

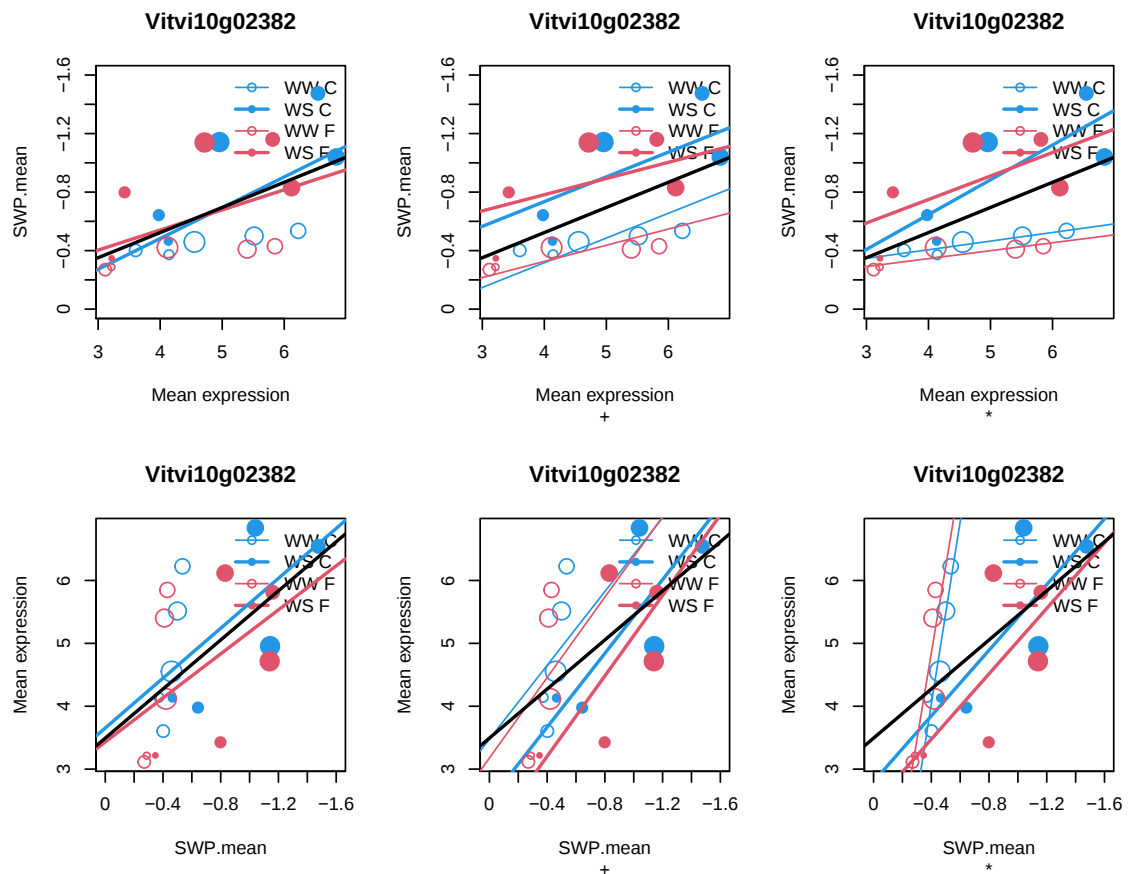
201606

Coefficient swp for Vitvi10g02382.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi10g02382	17.30654	4.773655	15.52275	4.671329e-26	2.644348e-23

B

Vitvi10g02382 45.17925



Correlation of all measurements (not just means): $r = 0.8675$, $r^2 = 0.7525$

Correlation of mean values (plots): $r_2 = 0.5792$

5.2.27 Vitvi16g01007

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

Vitvi16g01007

28.1

DNA.synthesis/chromatin structure

single-stranded DNA endonuclease family protein |

Chr3:18131854-18136239 FORWARD LENGTH=600 |

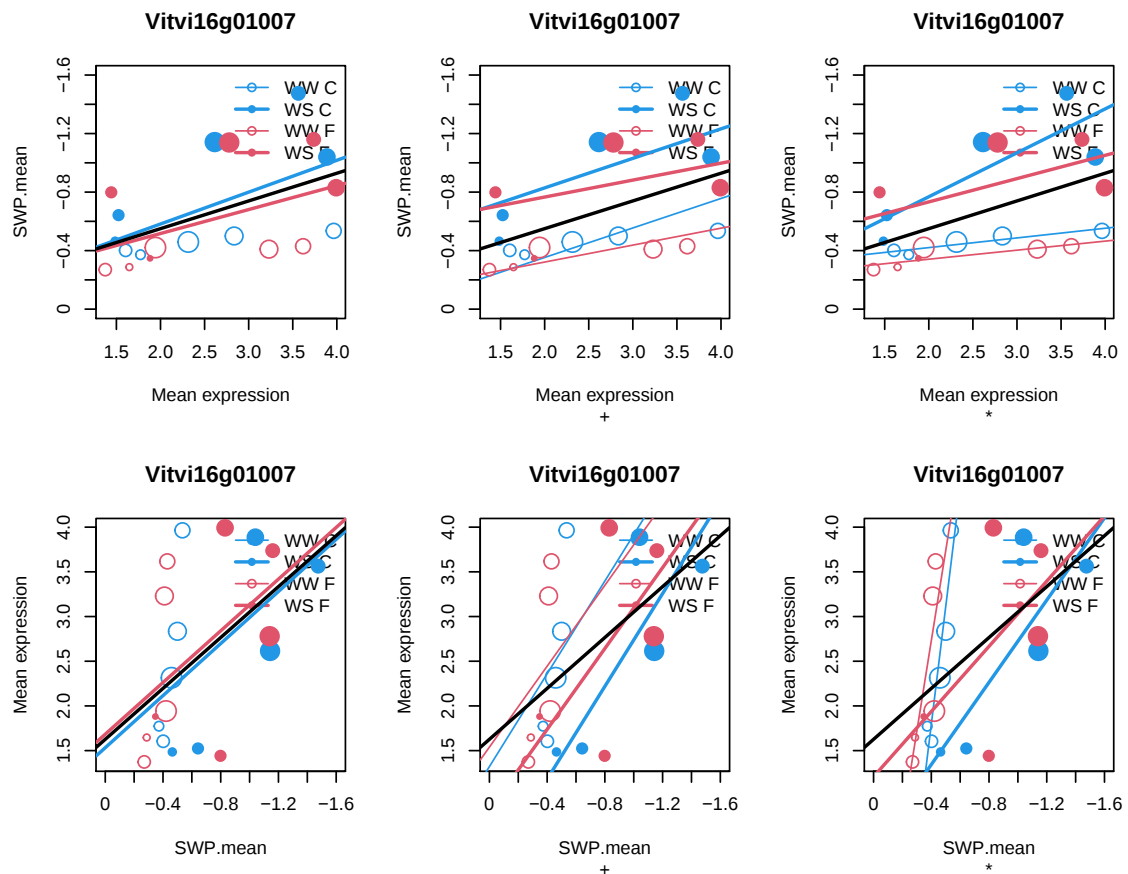
201606

Coefficient swp for Vitvi16g01007.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi16g01007	14.2946	2.560492	15.52205	4.684253e-26	2.644348e-23

B

Vitvi16g01007 45.17693



Correlation of all measurements (not just means): $r = 0.8689$, $r^2 = 0.7550$

Correlation of mean values (plots): $r_2 = 0.5193$

5.2.28 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 |

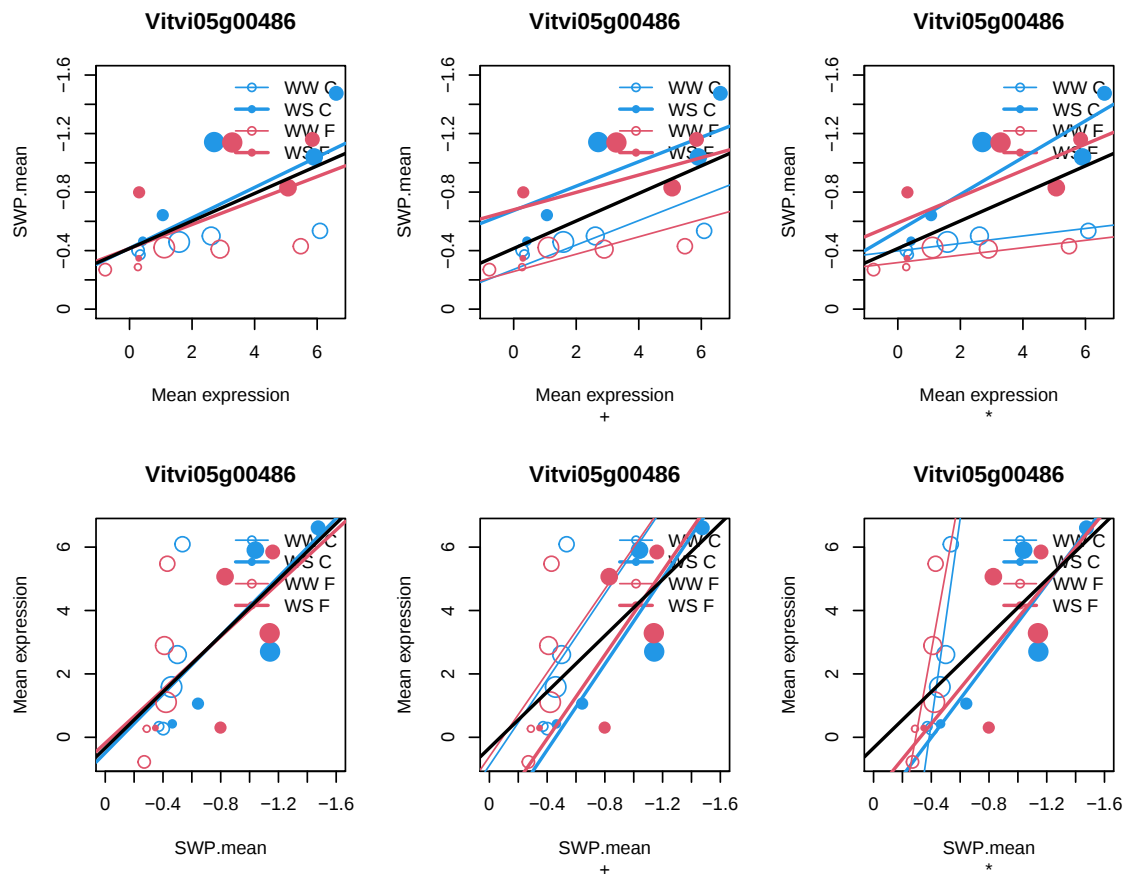
201606

Coefficient swp for Vitvi05g00486.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi05g00486	35.60306	2.569209	15.48479	5.424916e-26	2.953092e-23

B

Vitvi05g00486 45.05332



Correlation of all measurements (not just means): $r = 0.8646$, $r^2 = 0.7476$

Correlation of mean values (plots): $r_2 = 0.6454$

5.2.29 Vitvi09g01808

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

Vitvi09g01808

35.2

not assigned.unknown

DNAse I-like superfamily protein |

Chr1:16528880-16531065 REVERSE LENGTH=626 |

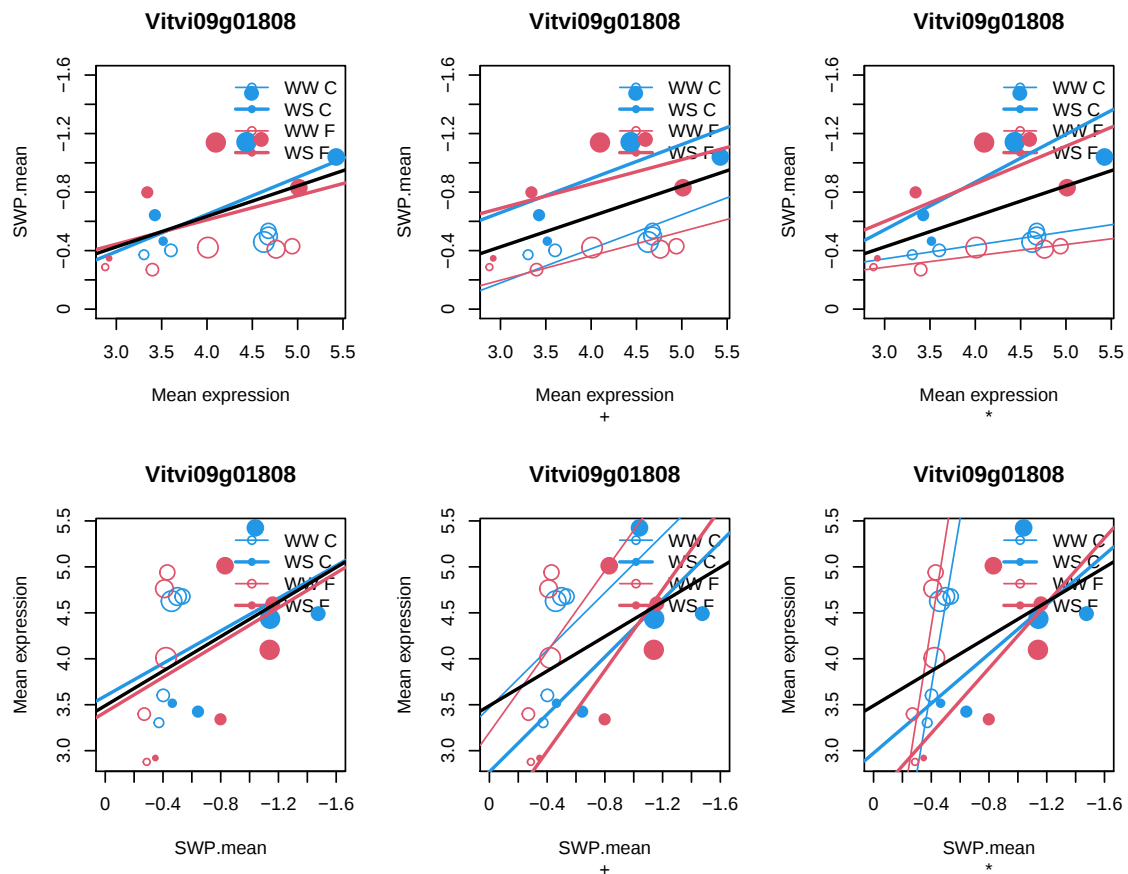
201606

Coefficient swp for Vitvi09g01808.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi09g01808	10.92559	4.106985	15.34492	9.42885e-26	4.955673e-23

B

Vitvi09g01808 44.58723



Correlation of all measurements (not just means): $r = 0.8695$, $r^2 = 0.7560$

Correlation of mean values (plots): $r_2 = 0.4427$

5.2.30 Vitvi02g00161

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

Vitvi02g00161

31.5

cell.cell death

DCD (Development and Cell Death) domain protein |

Chr3:9990020-9991407 FORWARD LENGTH=296 |

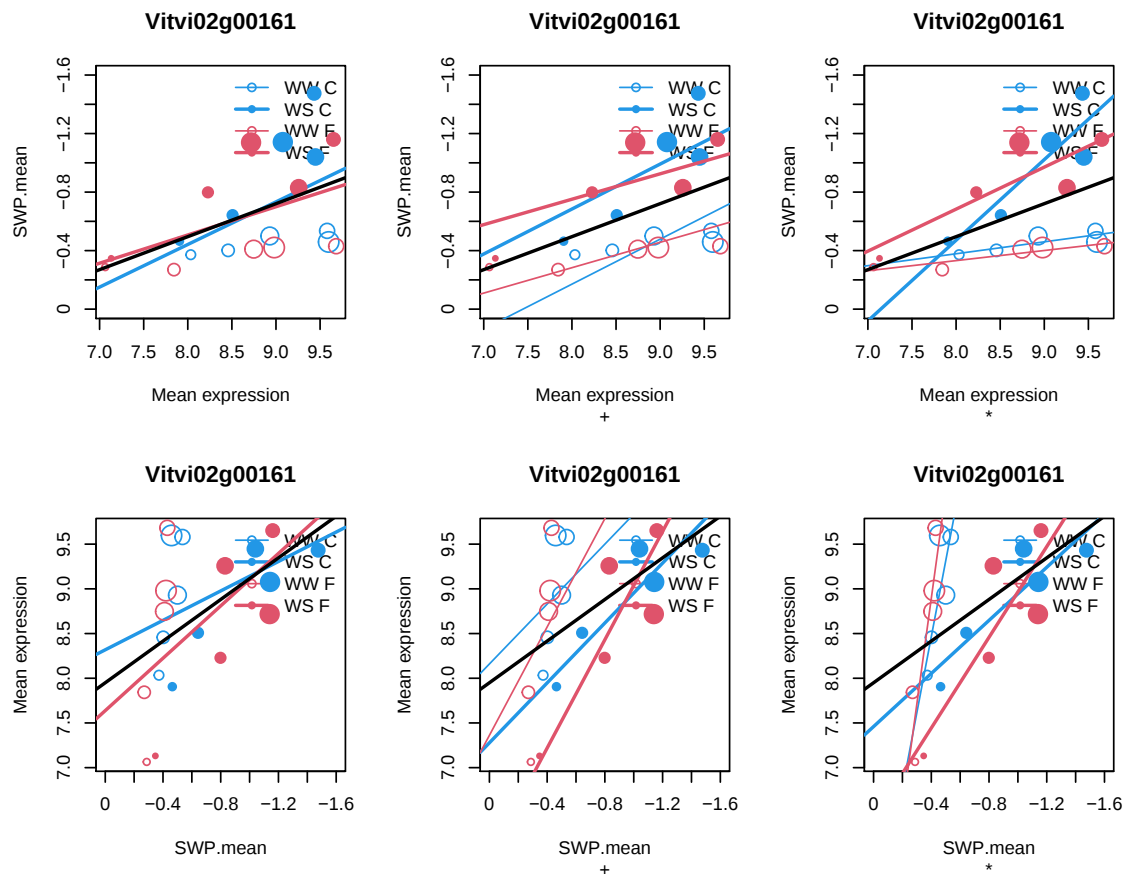
201606

Coefficient swp for Vitvi02g00161.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi02g00161	11.56936	8.7137	15.29201	1.162934e-25	5.908479e-23

B

Vitvi02g00161 44.4101



Correlation of all measurements (not just means): $r = 0.8679$, $r^2 = 0.7532$

Correlation of mean values (plots): $r_2 = 0.5123$

5.2.31 Vitvi07g00087

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

Vitvi07g00087

35.1

not assigned.no ontology

Bax inhibitor-1 family protein |

Chr1:730148-731379 FORWARD LENGTH=247 |

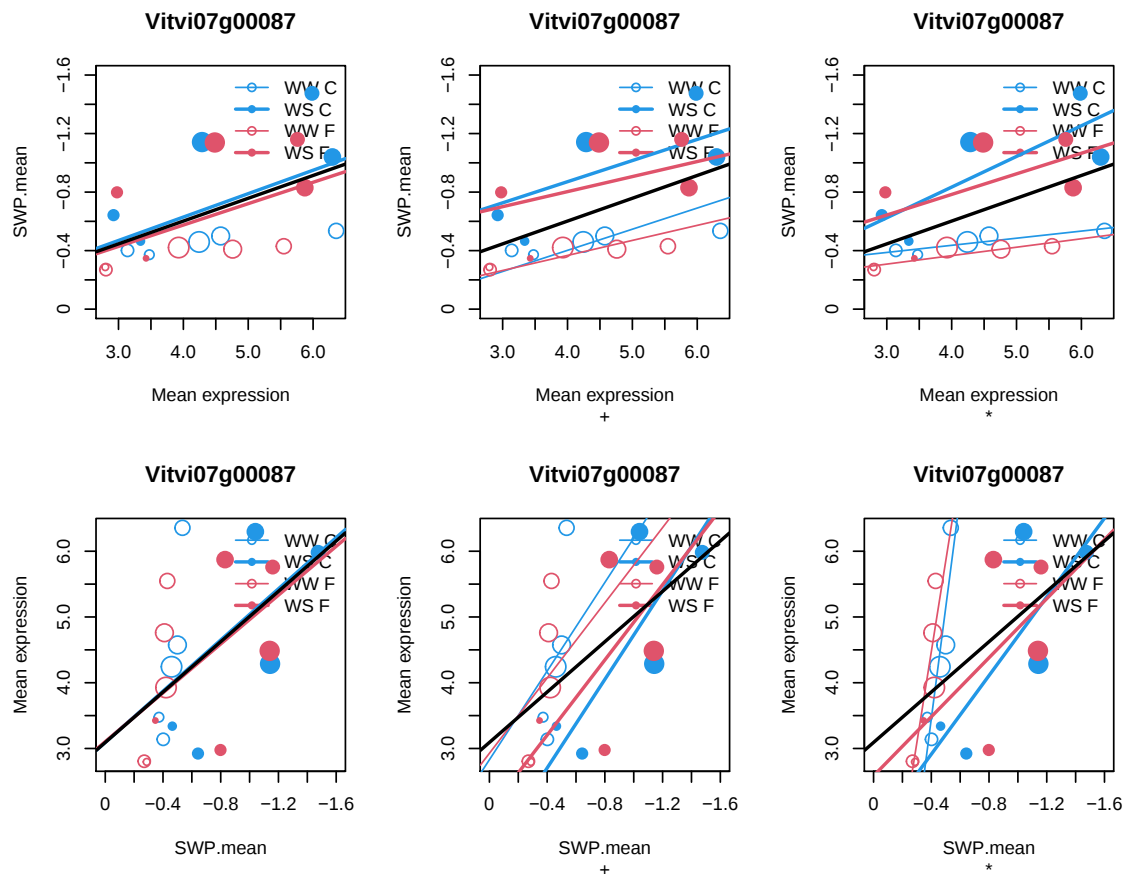
201606

Coefficient swp for Vitvi07g00087.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi07g00087	18.25528	4.348752	15.26939	1.272159e-25	6.254919e-23

B

Vitvi07g00087 44.33425



Correlation of all measurements (not just means): $r = 0.8635$, $r^2 = 0.7456$

Correlation of mean values (plots): $r_2 = 0.5463$

5.2.32 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 |

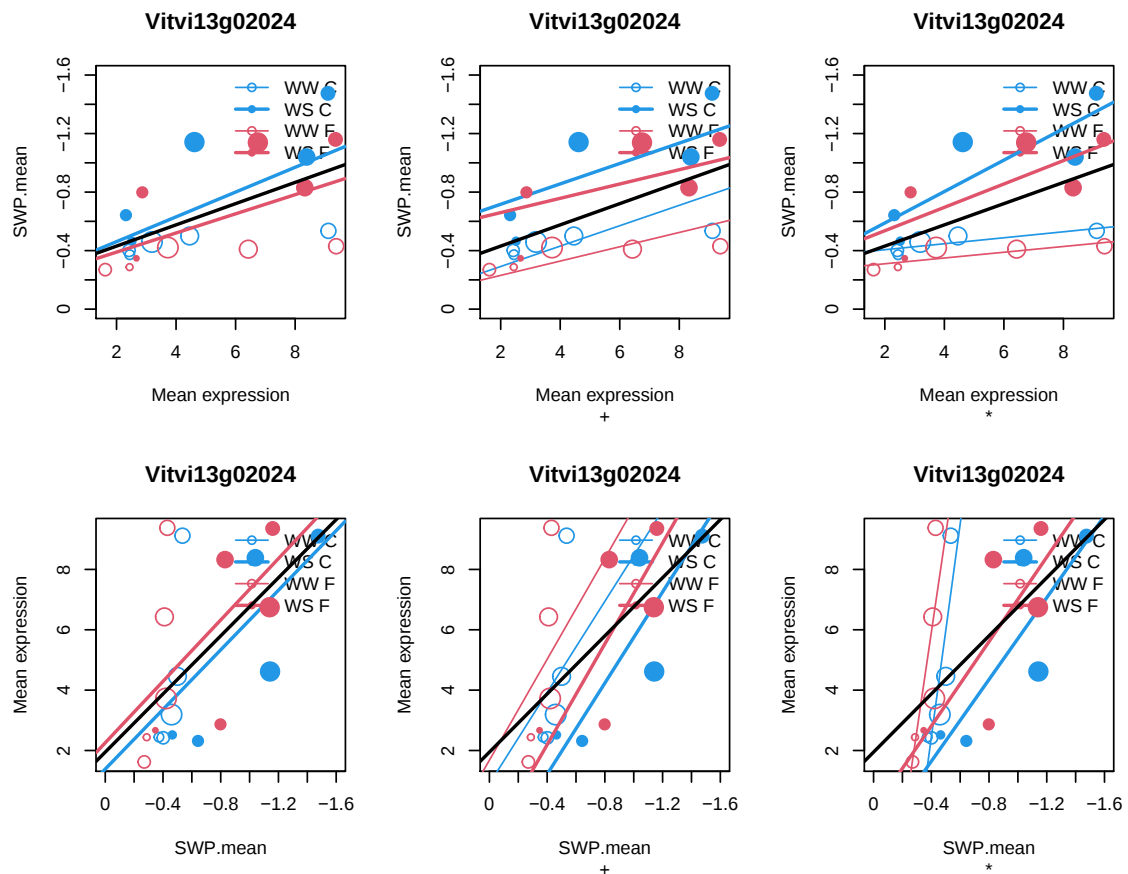
201606

Coefficient swp for Vitvi13g02024.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi13g02024	42.07724	5.106388	15.23682	1.4479e-25	6.896527e-23

B

Vitvi13g02024 44.22488



Correlation of all measurements (not just means): $r = 0.8609$, $r^2 = 0.7411$

Correlation of mean values (plots): $r_2 = 0.5911$

5.2.33 Vitvi19g00043

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

Vitvi19g00043

31.4

cell.vesicle transport

Target of Myb protein 1 |

Chr5:5549658-5551021 FORWARD LENGTH=297 |

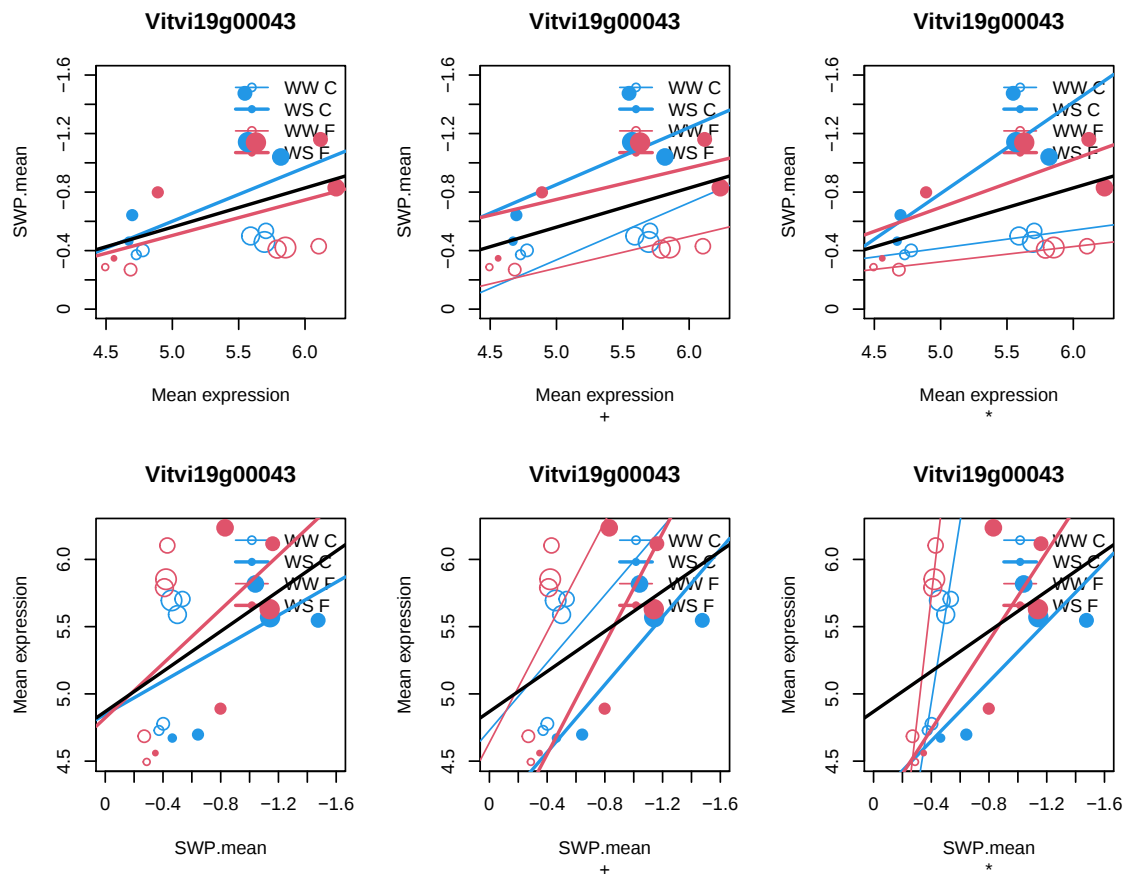
201606

Coefficient swp for Vitvi19g00043.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi19g00043	8.644668	5.357847	15.16403	1.934392e-25	8.934549e-23

B

Vitvi19g00043 43.97982



Correlation of all measurements (not just means): $r = 0.8713$, $r^2 = 0.7592$

Correlation of mean values (plots): $r_2 = 0.4471$

5.2.34 Vitvi01g01824

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

Vitvi01g01824

35.2

not assigned.unknown

cysteine-rich RECEPTOR-like kinase |

Chr4:12129485-12133157 FORWARD LENGTH=1043 |

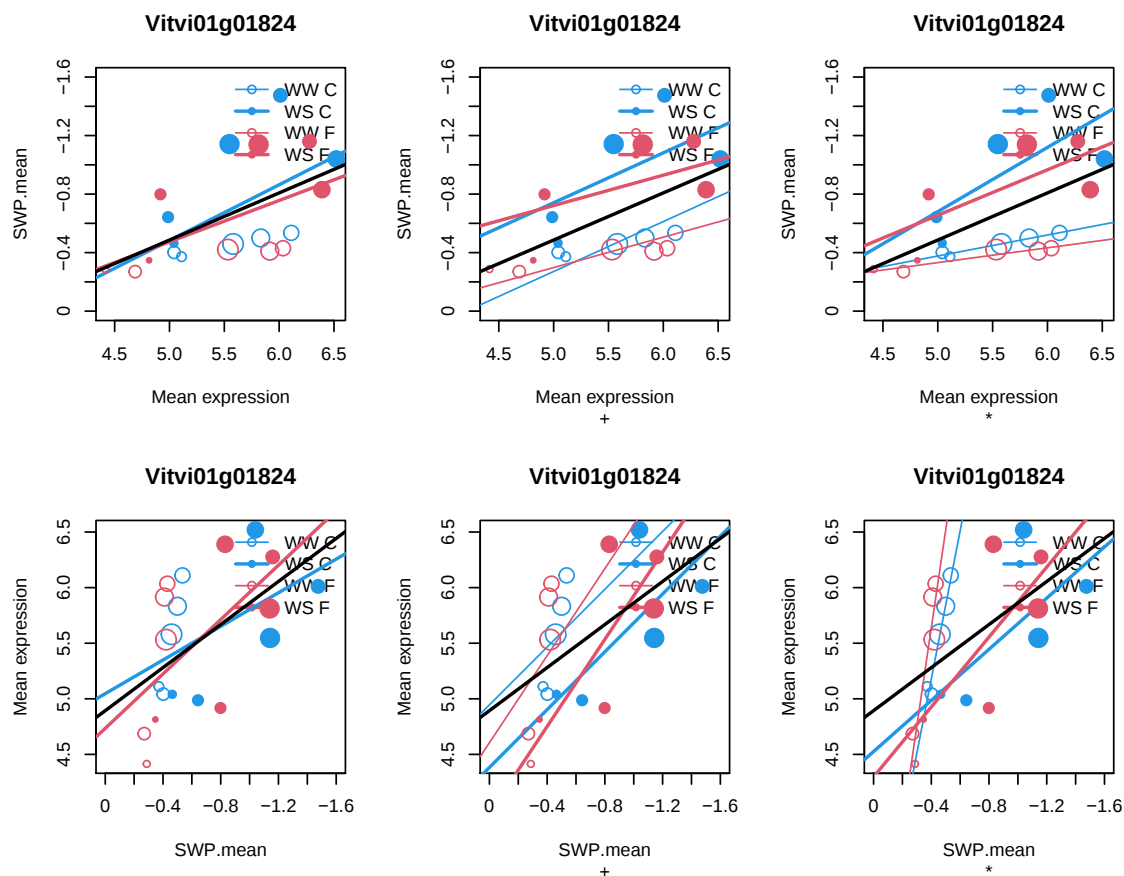
201606

Coefficient swp for Vitvi01g01824.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi01g01824	9.028991	5.528773	15.14836	2.059012e-25	9.23043e-23

B

Vitvi01g01824 43.92697



Correlation of all measurements (not just means): $r = 0.8701$, $r^2 = 0.7570$

Correlation of mean values (plots): $r_2 = 0.5584$

5.2.35 Vitvi01g00424

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

Vitvi01g00424

29

protein

GroES-like family protein |

Chr1:8195867-8196336 FORWARD LENGTH=97 |

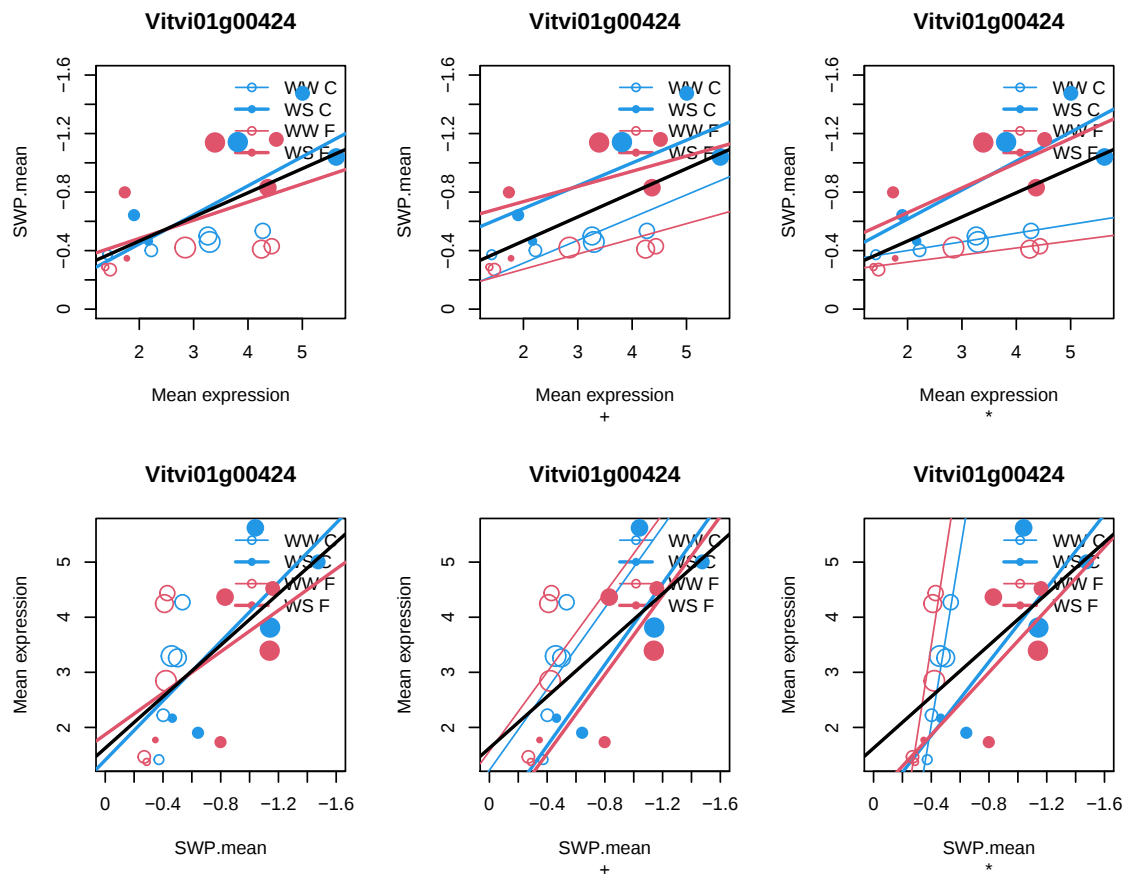
201606

Coefficient swp for Vitvi01g00424.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi01g00424	19.67503	3.156319	15.14069	2.122938e-25	9.245091e-23

B

Vitvi01g00424	43.90109
---------------	----------



Correlation of all measurements (not just means): $r = 0.8612$, $r^2 = 0.7417$

Correlation of mean values (plots): $r_2 = 0.6206$

5.2.36 Vitvi02g01446

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

Vitvi02g01446

20.02.2001

stress.abiotic.heat

mitochondrion-localized small heat shock protein 23.6 |

Chr4:12917089-12917858 FORWARD LENGTH=210 |

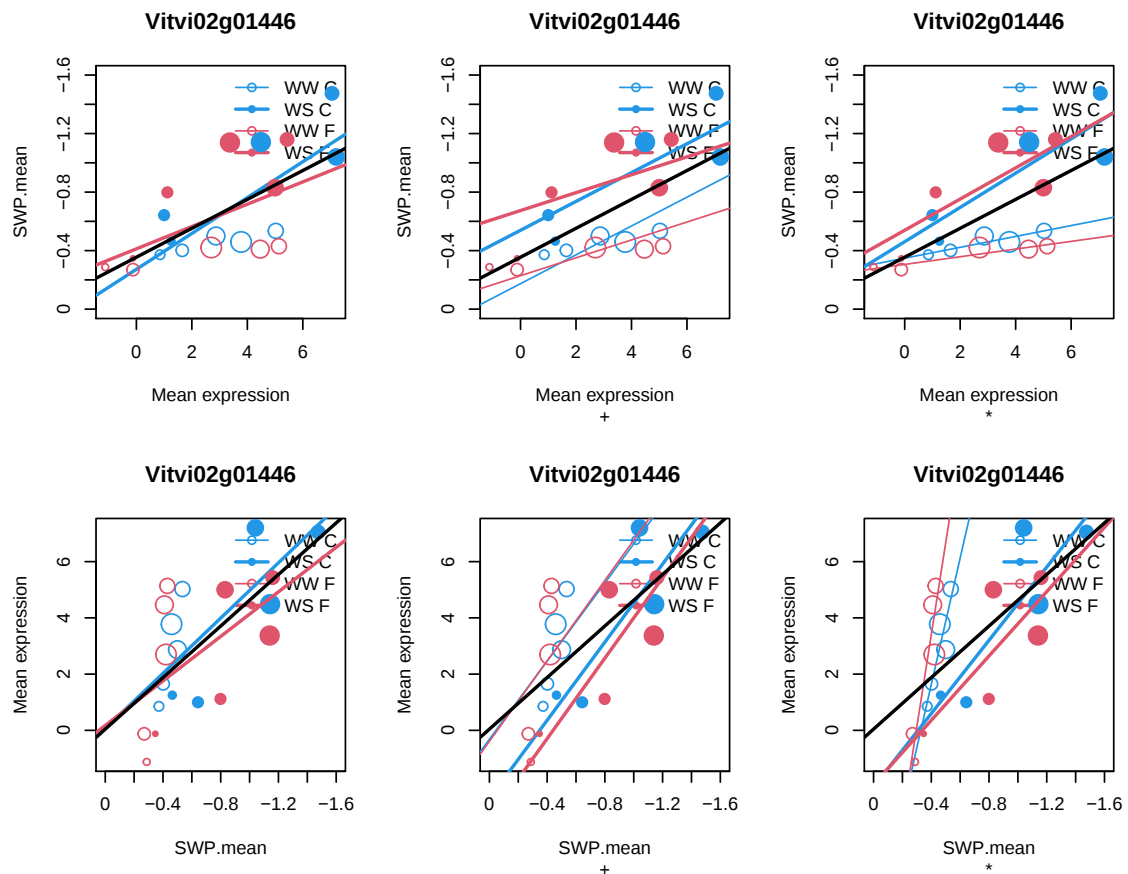
201606

Coefficient swp for Vitvi02g01446.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi02g01446	35.15716	3.05128	15.08728	2.627201e-25	1.112328e-22

B

Vitvi02g01446 43.72057



Correlation of all measurements (not just means): $r = 0.8589$, $r^2 = 0.7376$

Correlation of mean values (plots): $r_2 = 0.6727$

5.2.37 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 |

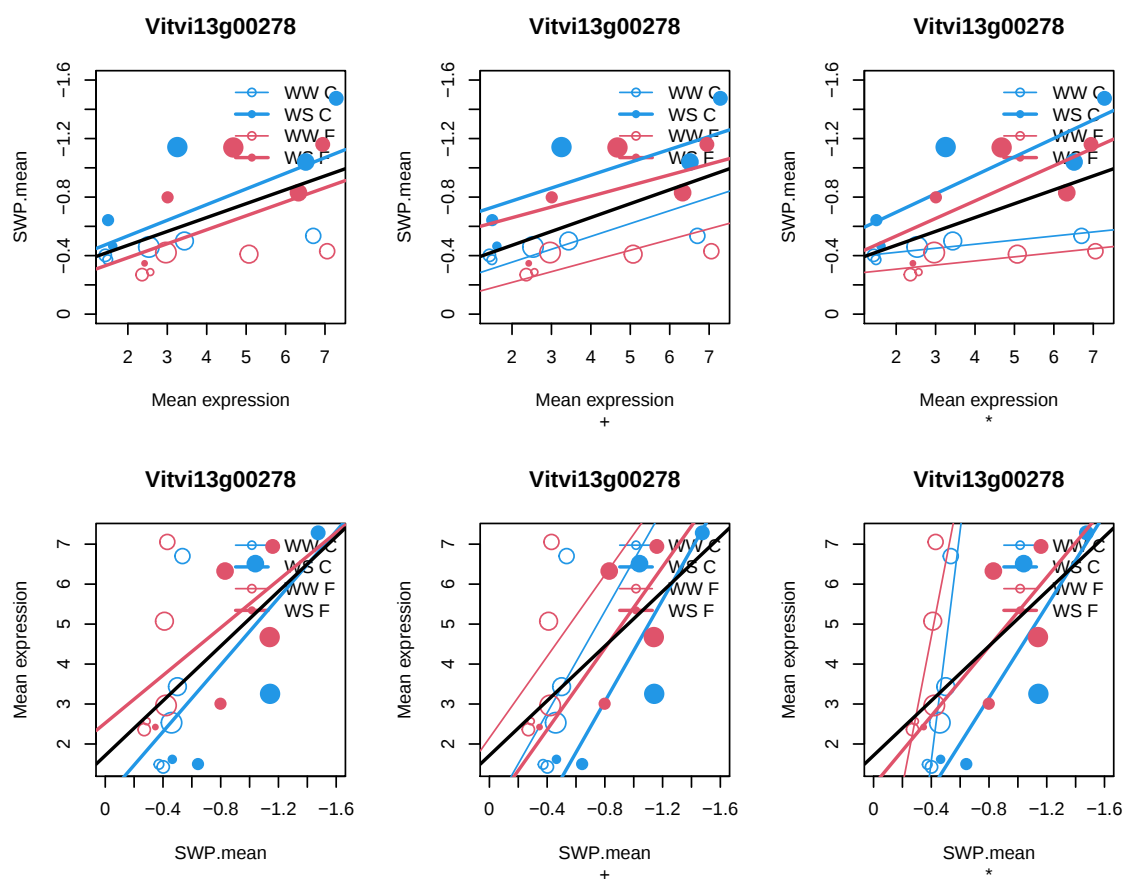
201606

Coefficient swp for Vitvi13g00278.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi13g00278	30.62073	3.957508	15.07971	2.707846e-25	1.115486e-22

B

Vitvi13g00278	43.69495
---------------	----------



Correlation of all measurements (not just means): $r = 0.8590$, $r^2 = 0.7378$

Correlation of mean values (plots): $r_2 = 0.5697$

5.2.38 Vitvi18g00596

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

Vitvi18g00596

35.2

not assigned.unknown

tubulin alpha-6 chain |

Chr1:18520144-18521600 REVERSE LENGTH=209 |

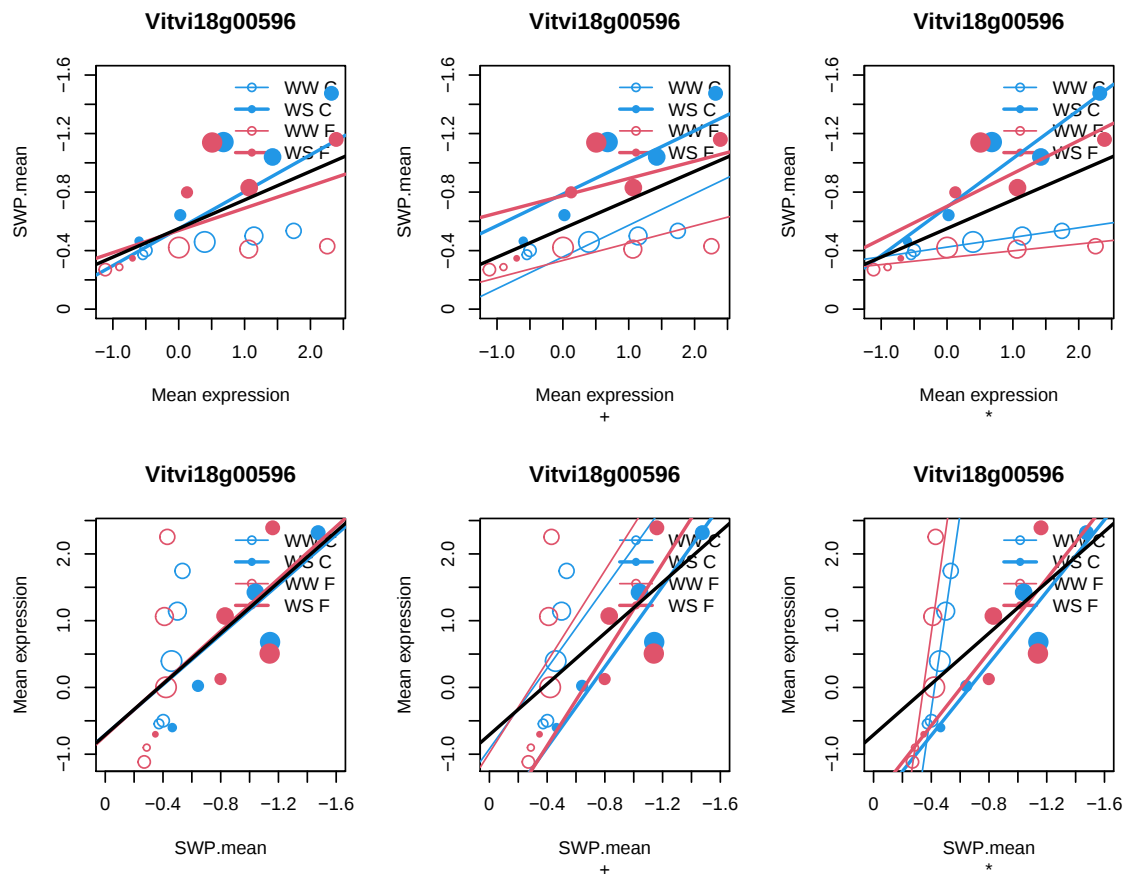
201606

Coefficient swp for Vitvi18g00596.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi18g00596	16.85873	0.5389867	15.02462	3.375075e-25	1.35376e-22

B

Vitvi18g00596 43.5082



Correlation of all measurements (not just means): $r = 0.8603$, $r^2 = 0.7401$

Correlation of mean values (plots): $r_2 = 0.6097$

5.2.39 Vitvi10g00496

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

Vitvi10g00496

20.02.2001

stress.abiotic.heat

DNAJ heat shock family protein |

Chr2:8848353-8849815 REVERSE LENGTH=337 |

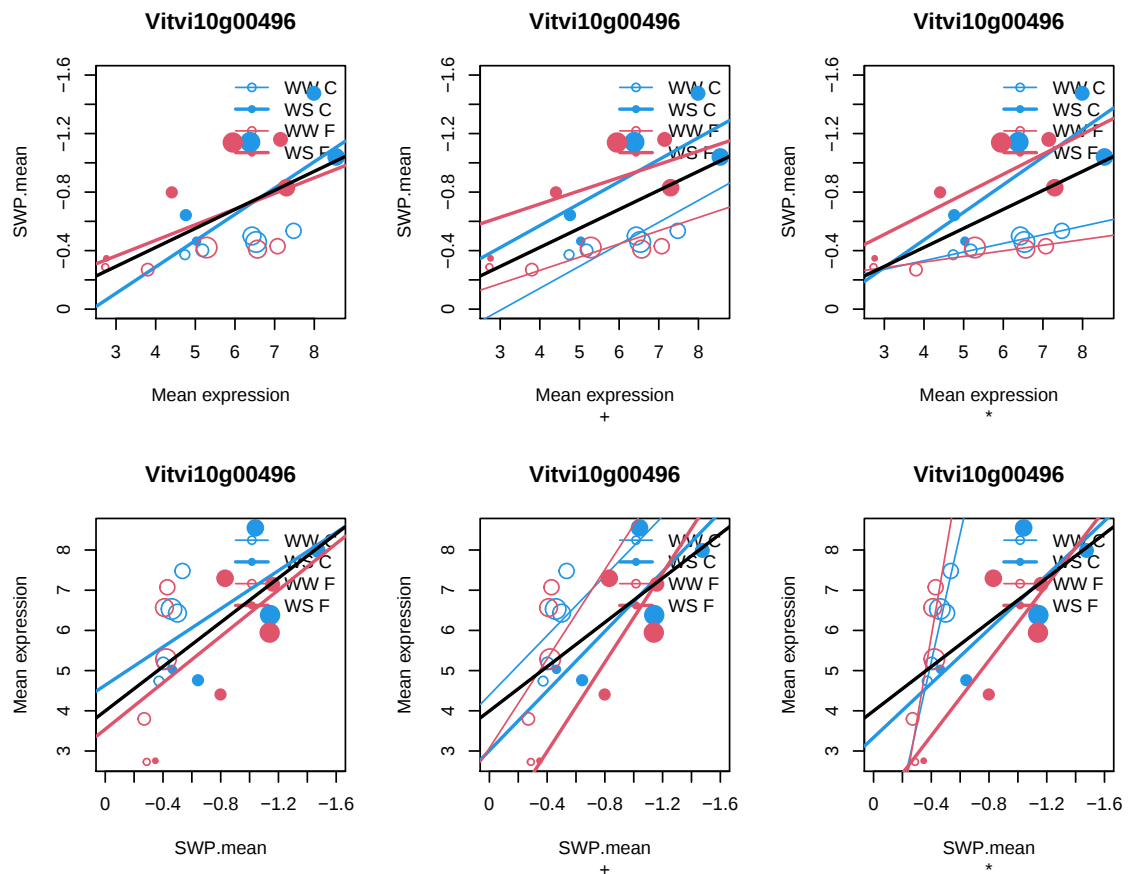
201606

Coefficient swp for Vitvi10g00496.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi10g00496	23.39236	5.804056	15.0042	3.662524e-25	1.43139e-22

B

Vitvi10g00496 43.43886



Correlation of all measurements (not just means): $r = 0.8585$, $r^2 = 0.7370$

Correlation of mean values (plots): $r_2 = 0.5983$

5.2.40 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 |

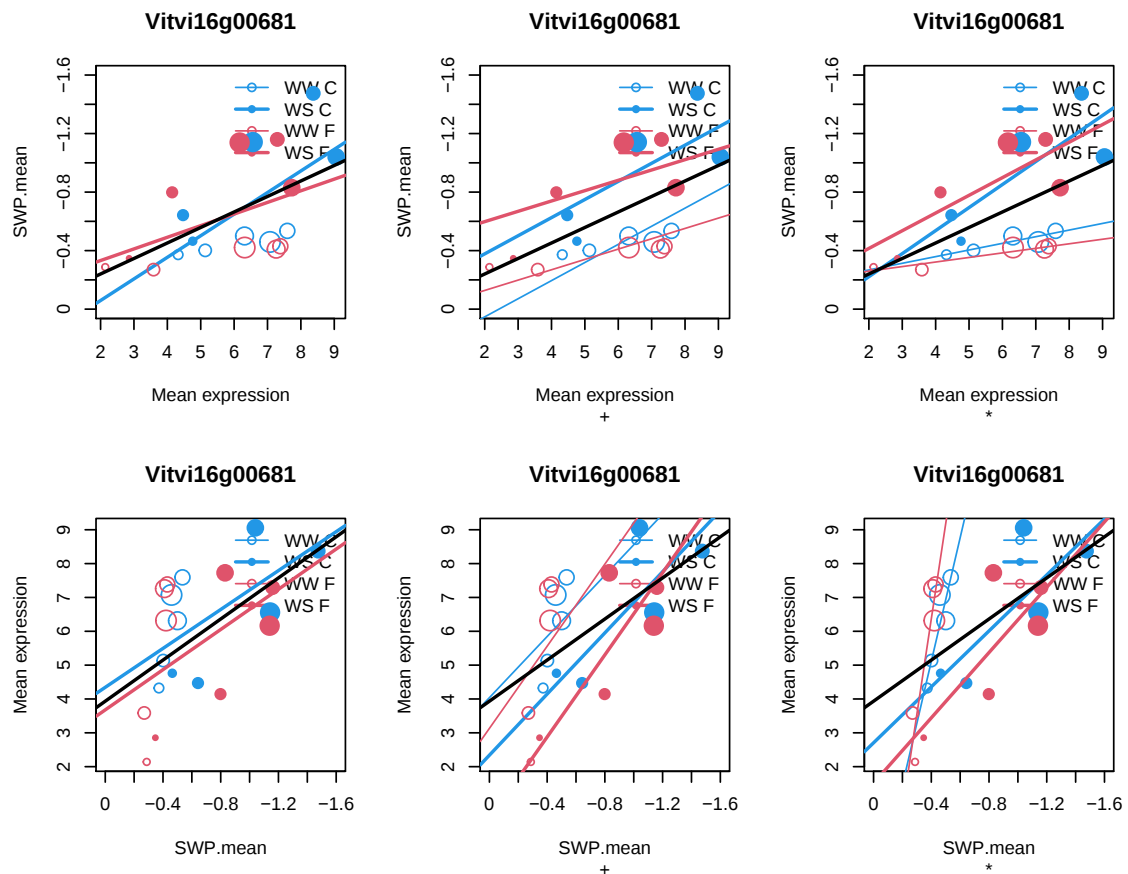
201606

Coefficient swp for Vitvi16g00681.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi16g00681	27.43906	5.926522	14.93093	4.913059e-25	1.872121e-22

B

Vitvi16g00681 43.1895



Correlation of all measurements (not just means): $r = 0.8569$, $r^2 = 0.7343$

Correlation of mean values (plots): $r_2 = 0.5672$

5.2.41 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 |

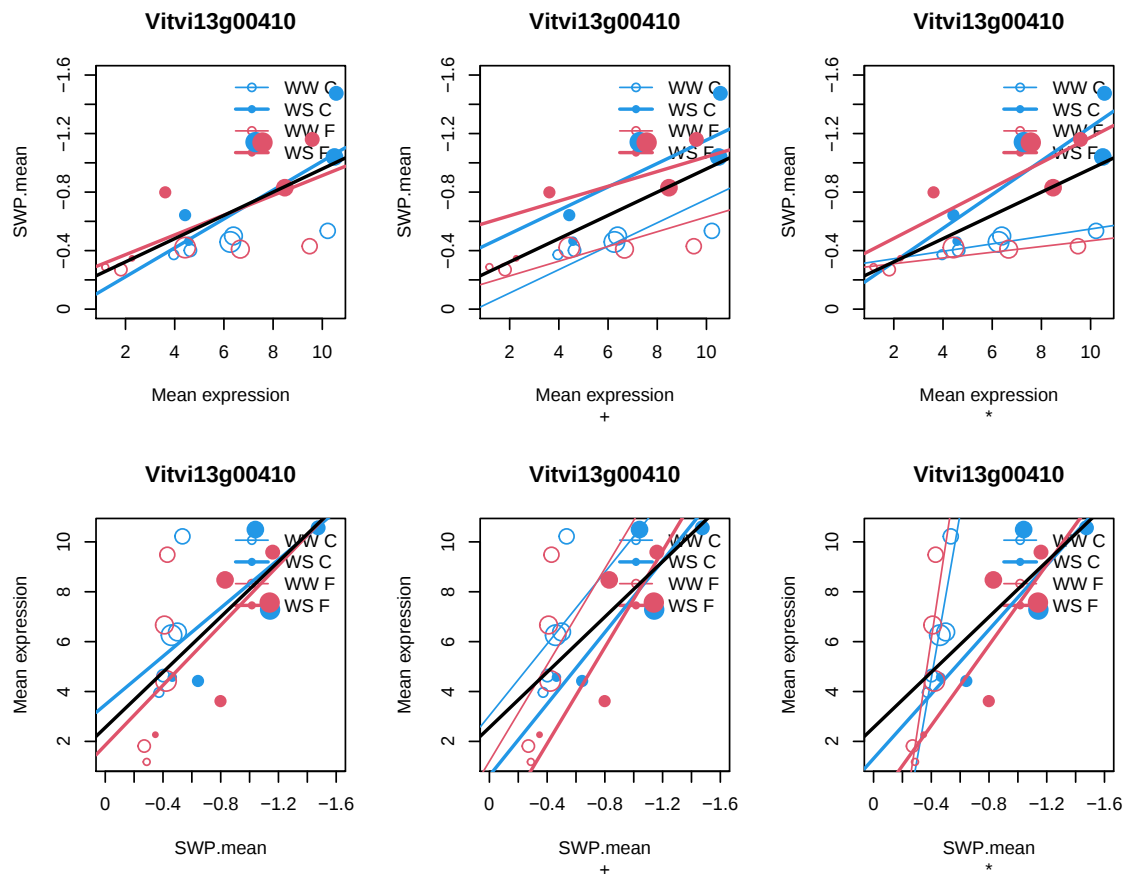
201606

Coefficient swp for Vitvi13g00410.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi13g00410	43.00946	6.19465	14.84743	6.872202e-25	2.554783e-22

B

Vitvi13g00410 42.90429



Correlation of all measurements (not just means): $r = 0.8550$, $r^2 = 0.7309$

Correlation of mean values (plots): $r_2 = 0.6639$

5.2.42 Vitvi05g00277

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

Vitvi05g00277

27.03.1999

RNA.regulation of transcription.unclassified

RHOMBOID-like protein 14 |

Chr3:6024946-6026173 FORWARD LENGTH=334 |

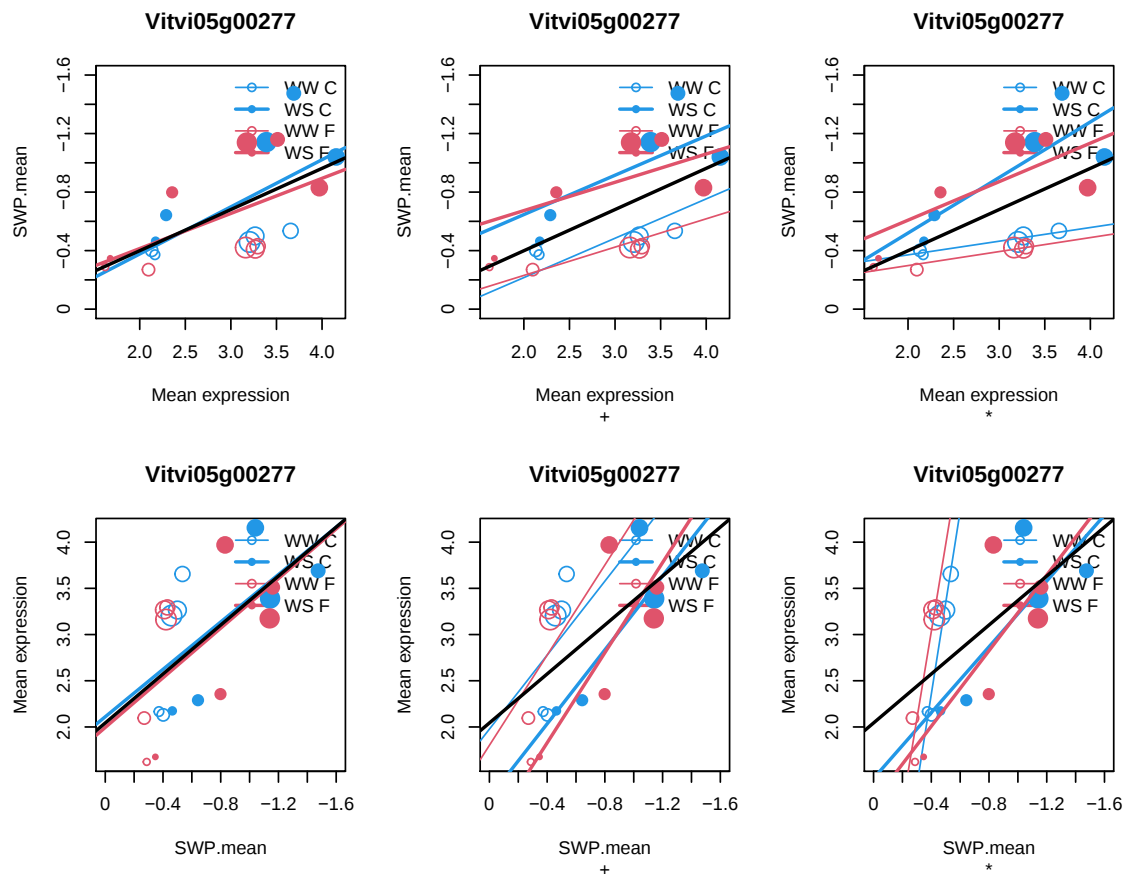
201606

Coefficient swp for Vitvi05g00277.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi05g00277	11.24373	2.912583	14.83251	7.297643e-25	2.648349e-22

B

Vitvi05g00277 42.8532



Correlation of all measurements (not just means): $r = 0.8612$, $r^2 = 0.7416$

Correlation of mean values (plots): $r_2 = 0.6106$

5.2.43 Vitvi13g02053

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

Vitvi13g02053

29.02.2004

protein.synthesis.elongation

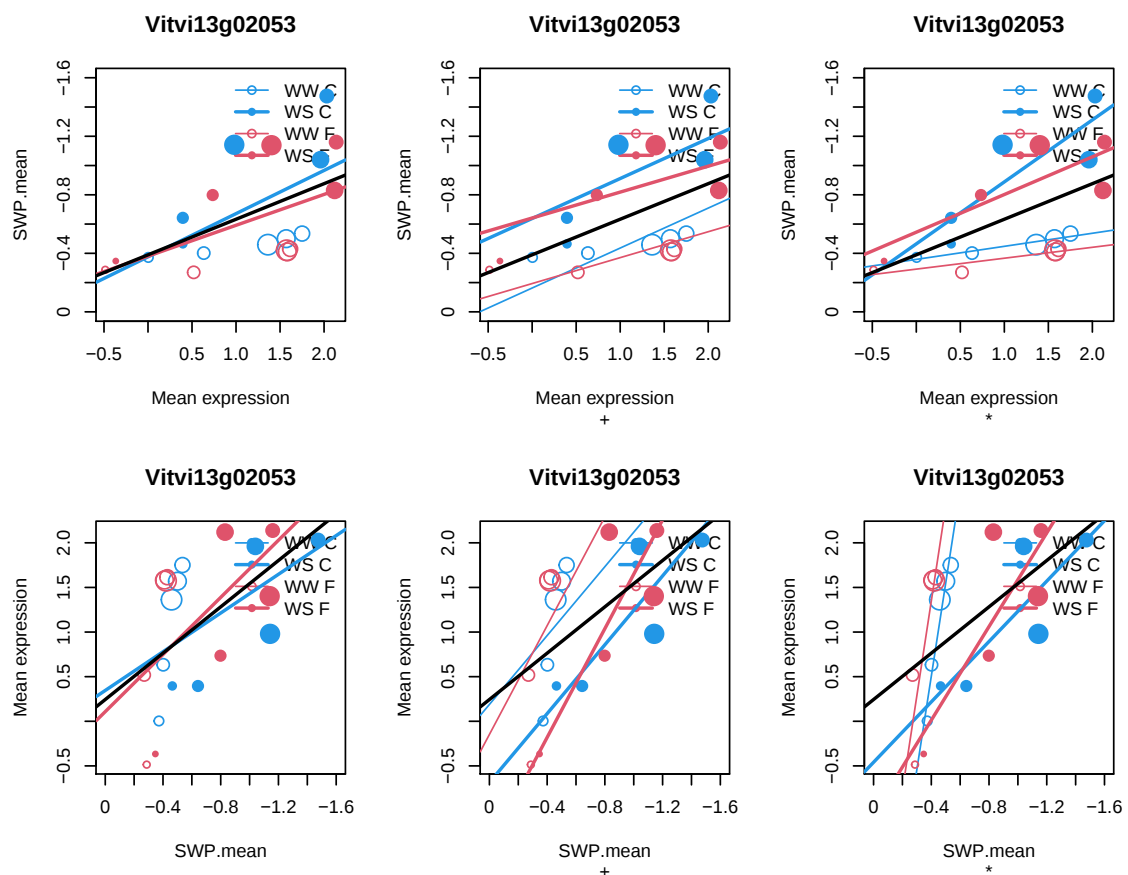
NA

Coefficient swp for Vitvi13g02053.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi13g02053	12.2951	1.095843	14.82025	7.666807e-25	2.717616e-22

B

Vitvi13g02053	42.81122
---------------	----------



Correlation of all measurements (not just means): $r = 0.8598$, $r^2 = 0.7393$

Correlation of mean values (plots): $r_2 = 0.5618$

5.2.44 Vitvi03g00335

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

Vitvi03g00335

35.2

not assigned.unknown

BTB/POZ domain-containing protein |

Chr1:23696962-23698708 FORWARD LENGTH=548 |

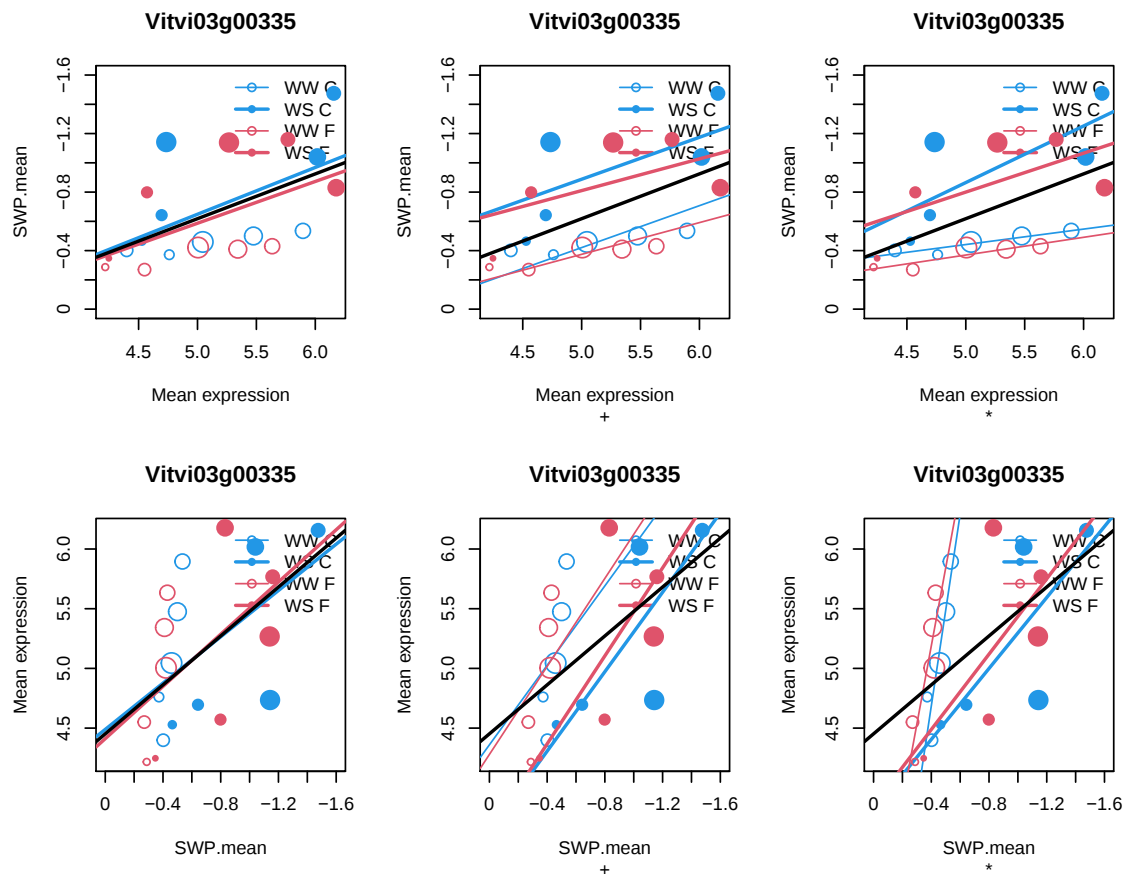
201606

Coefficient swp for Vitvi03g00335.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi03g00335	9.518701	5.12439	14.78607	8.798997e-25	3.048052e-22

B

Vitvi03g00335 42.69401



Correlation of all measurements (not just means): $r = 0.8632$, $r^2 = 0.7452$

Correlation of mean values (plots): $r_2 = 0.5601$

5.2.45 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 |

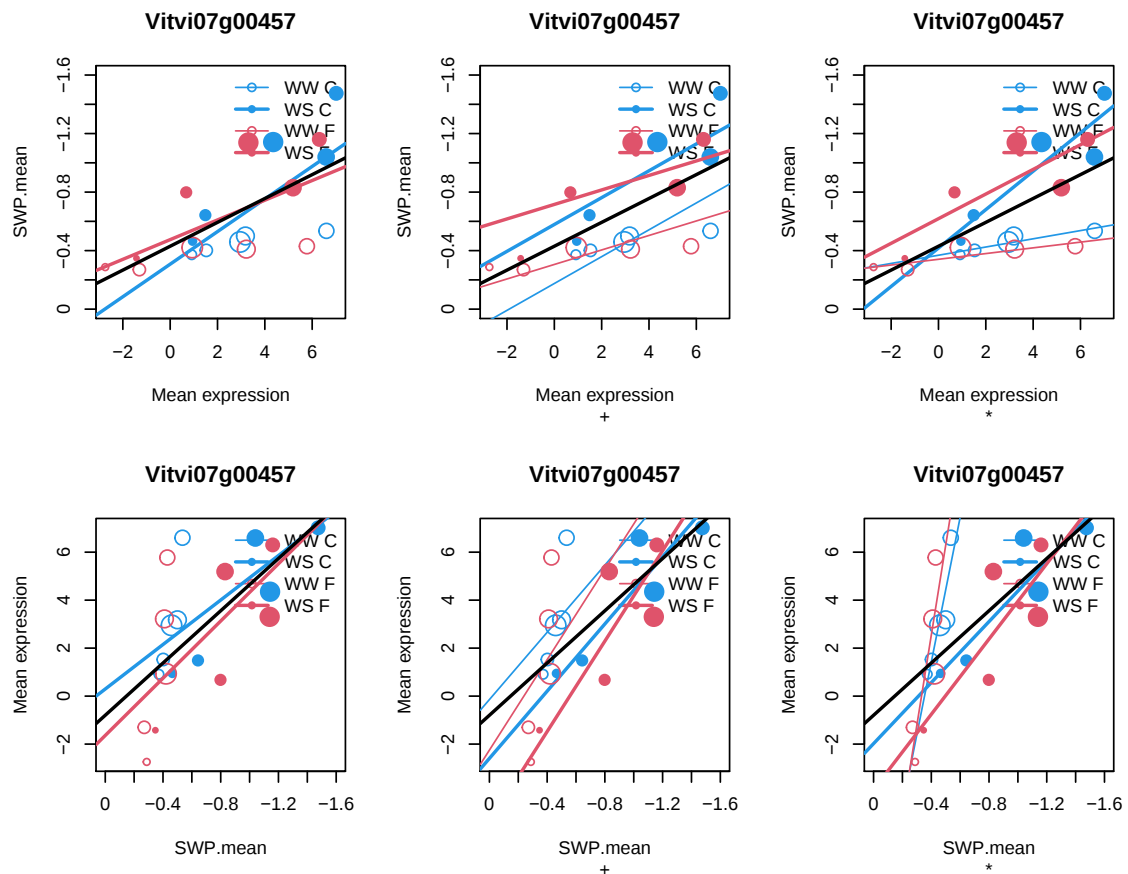
201606

Coefficient swp for Vitvi07g00457.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi07g00457	41.95	2.774566	14.77192	9.315767e-25	3.155354e-22

B

Vitvi07g00457 42.64543



Correlation of all measurements (not just means): $r = 0.8538$, $r^2 = 0.7290$

Correlation of mean values (plots): $r_2 = 0.6664$

5.2.46 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 |

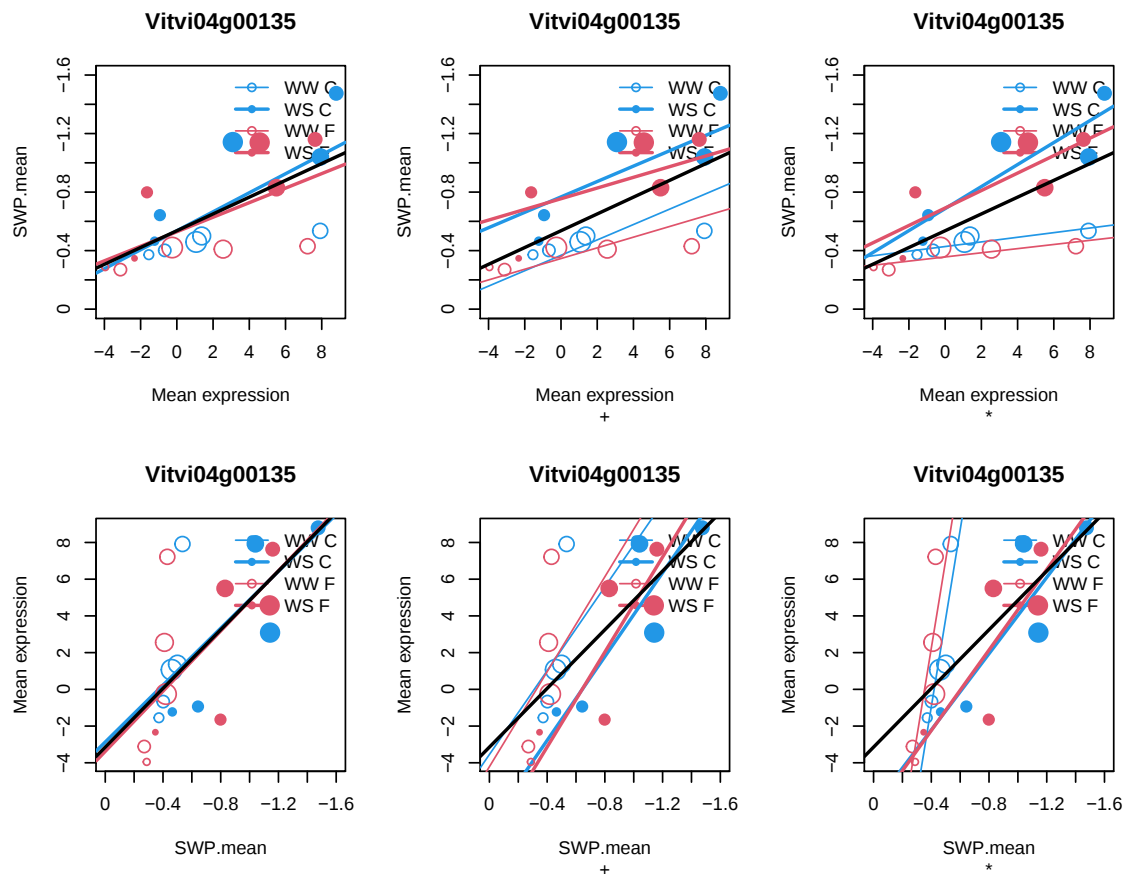
201606

Coefficient swp for Vitvi04g00135.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi04g00135	61.28924	2.09779	14.70429	1.224128e-24	4.056122e-22

B

Vitvi04g00135 42.4128



Correlation of all measurements (not just means): $r = 0.8525$, $r^2 = 0.7267$

Correlation of mean values (plots): $r_2 = 0.6771$

5.2.47 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 |

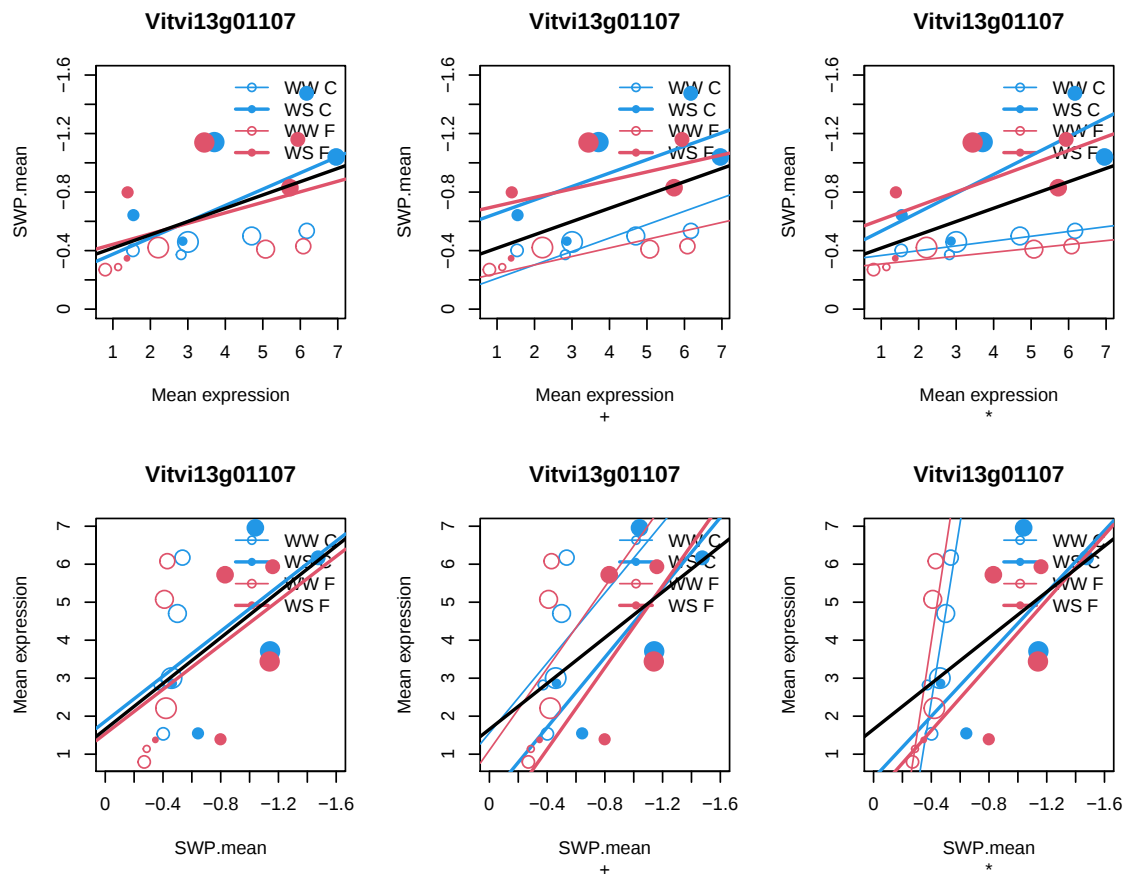
201606

Coefficient swp for Vitvi13g01107.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi13g01107	29.34786	3.632156	14.69854	1.25293e-24	4.063225e-22

B

Vitvi13g01107 42.39298



Correlation of all measurements (not just means): $r = 0.8531$, $r^2 = 0.7279$

Correlation of mean values (plots): $r_2 = 0.5228$

5.2.48 Vitvi02g00983

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

Vitvi02g00983

35.2

not assigned.unknown

UDP-Glycosyltransferase superfamily protein |

Chr2:15417618-15419108 REVERSE LENGTH=496 |

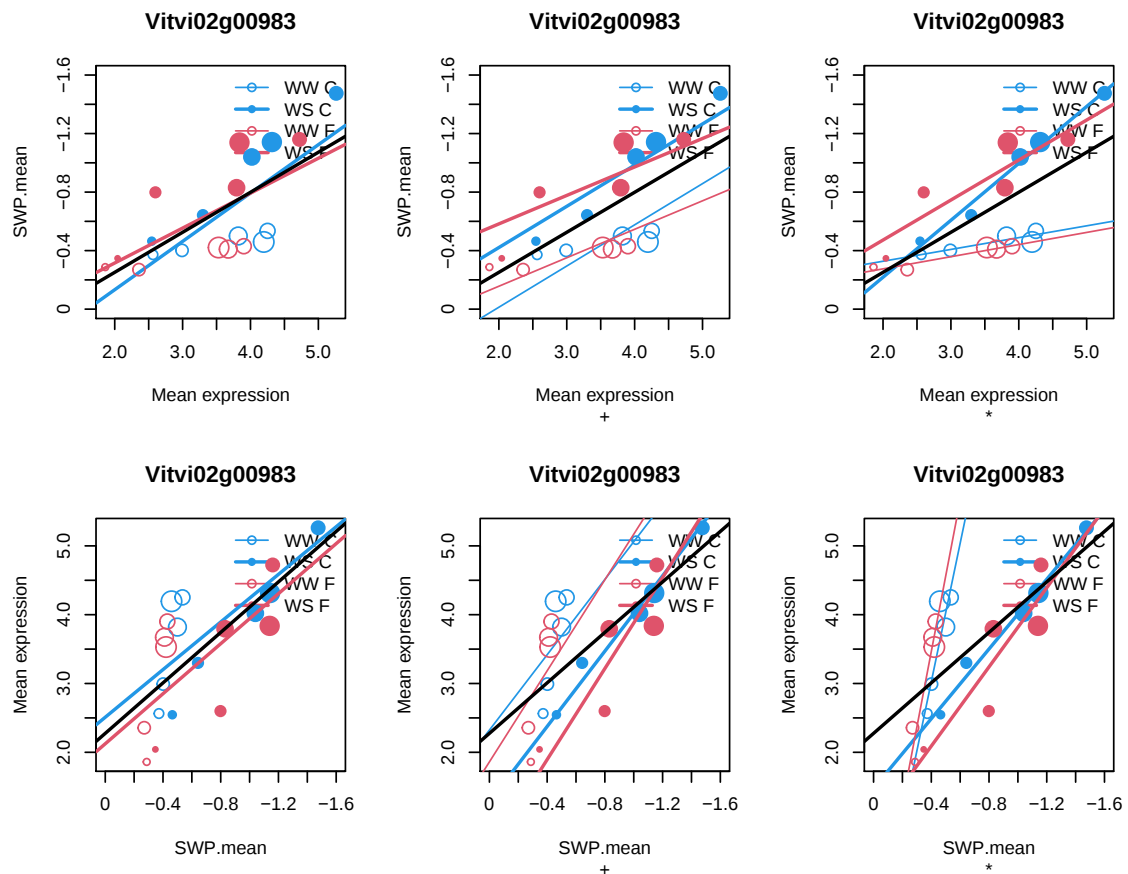
201606

Coefficient swp for Vitvi02g00983.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi02g00983	13.11216	3.479019	14.66224	1.451128e-24	4.607935e-22

B

Vitvi02g00983 42.26779



Correlation of all measurements (not just means): $r = 0.8566$, $r^2 = 0.7338$

Correlation of mean values (plots): $r_2 = 0.7083$

5.2.49 Vitvi12g01613

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

Vitvi12g01613

35.1

not assigned.no ontology

cysteine-rich RECEPTOR-like kinase |

Chr4:12129485-12133157 FORWARD LENGTH=1043 |

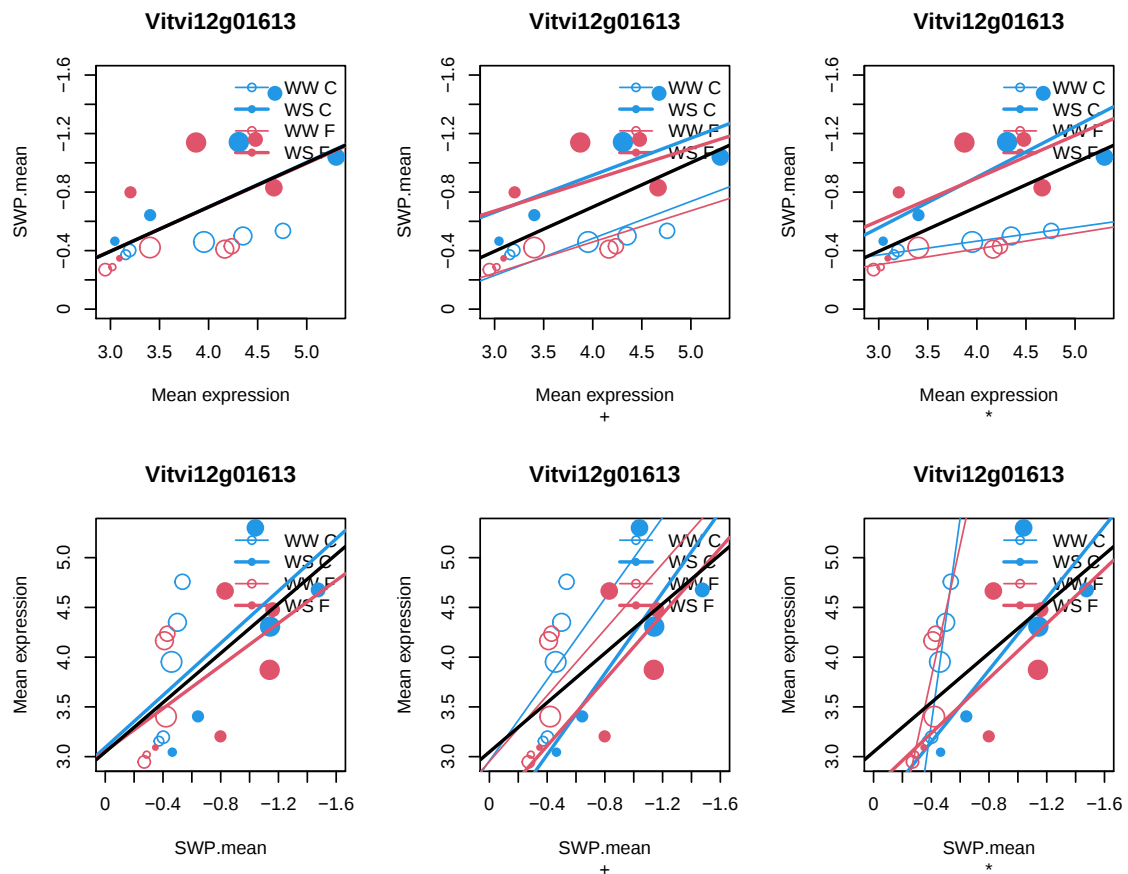
201606

Coefficient swp for Vitvi12g01613.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi12g01613	10.31476	3.861246	14.5667	2.137475e-24	6.627425e-22

B

Vitvi12g01613 41.93731



Correlation of all measurements (not just means): $r = 0.8582$, $r^2 = 0.7365$

Correlation of mean values (plots): $r_2 = 0.6129$

5.2.50 Vitvi13g02054

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

Vitvi13g02054

29.02.2004

protein.synthesis.elongation

GTP binding Elongation factor Tu family protein |

Chr5:24289226-24290675 FORWARD LENGTH=449 |

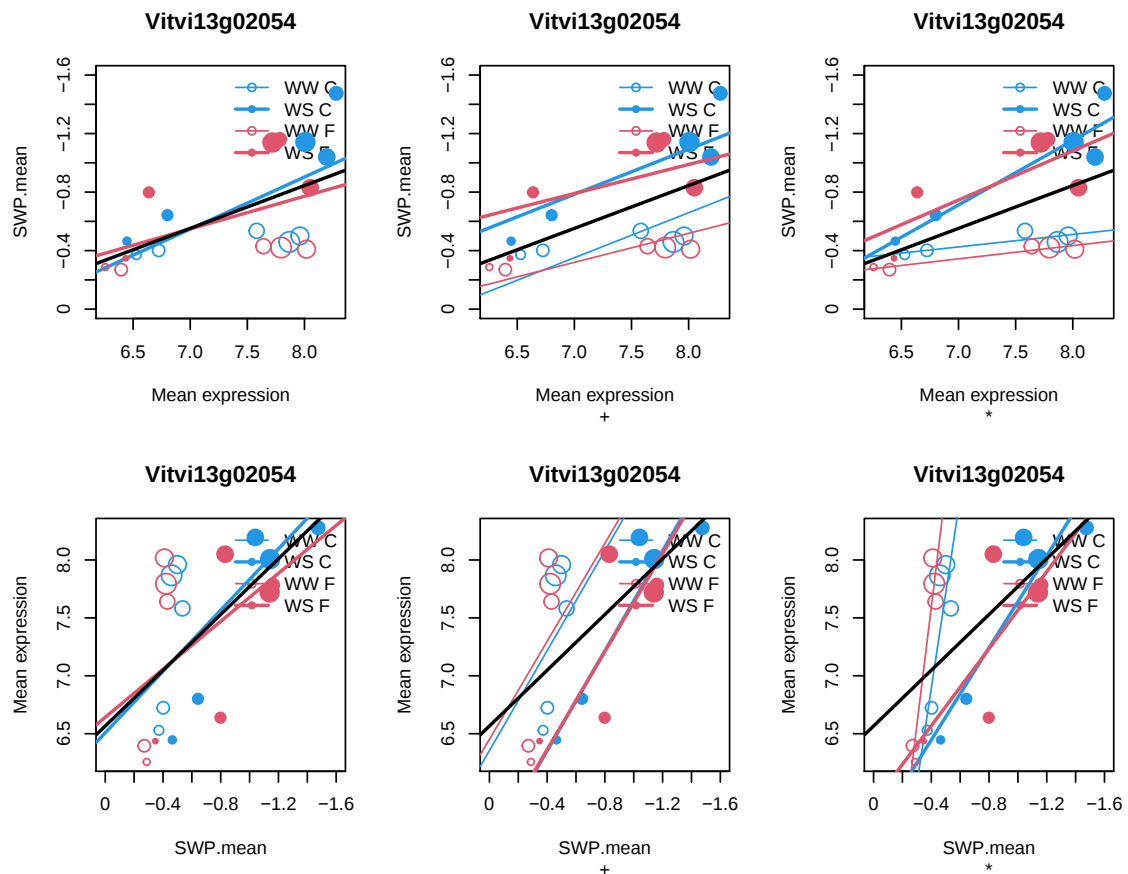
201606

Coefficient swp for Vitvi13g02054.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi13g02054	10.21059	7.356143	14.56252	2.174067e-24	6.627425e-22

B

Vitvi13g02054 41.92281



Correlation of all measurements (not just means): $r = 0.8583$, $r^2 = 0.7366$

Correlation of mean values (plots): $r_2 = 0.5934$

5.2.51 Vitvi04g00962

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

Vitvi04g00962

35.2

not assigned.unknown

hikeshi-like protein |

Chr1:24600356-24601027 REVERSE LENGTH=190 |

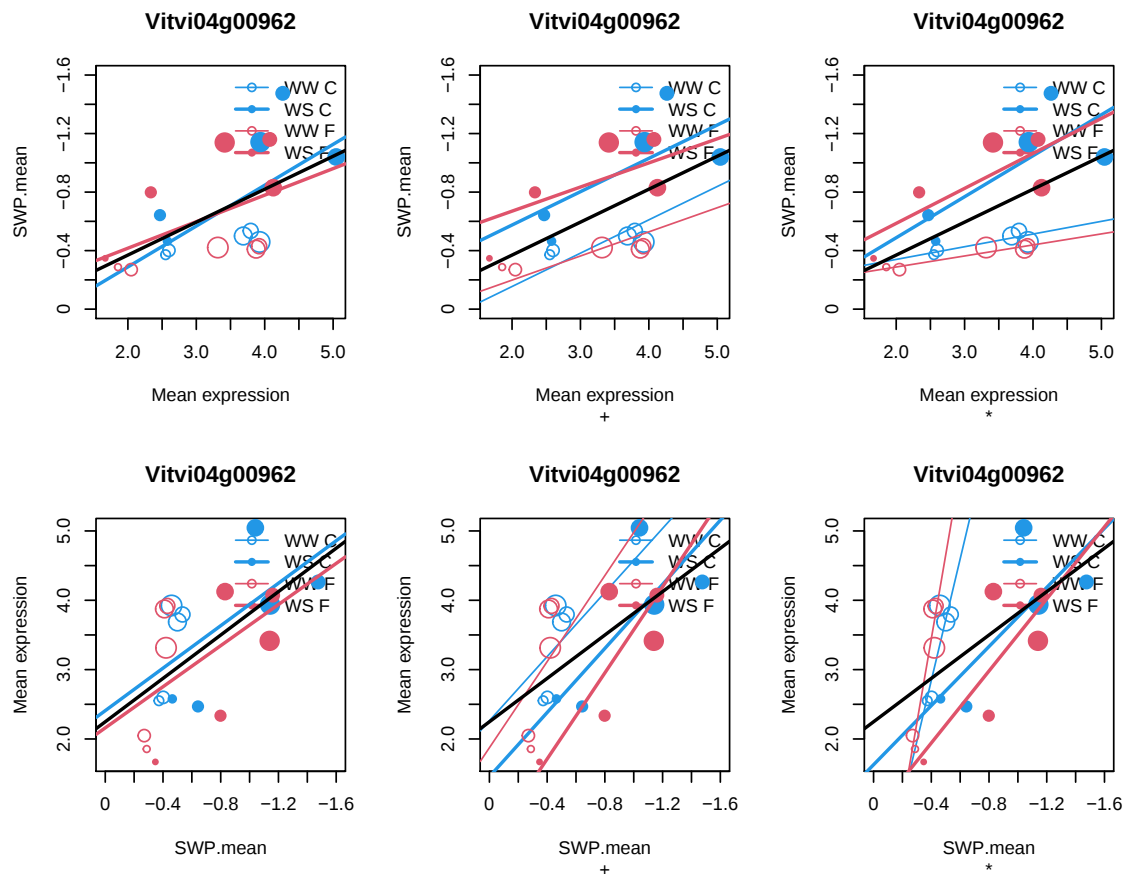
201606

Coefficient swp for Vitvi04g00962.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi04g00962	13.2652	3.274122	14.52392	2.543254e-24	7.600839e-22

B

Vitvi04g00962 41.78883



Correlation of all measurements (not just means): $r = 0.8542$, $r^2 = 0.7297$

Correlation of mean values (plots): $r_2 = 0.5934$

5.2.52 Vitvi10g00798

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

Vitvi10g00798

29.5.11.4.3.3

protein.degradation.ubiquitin.E3.SCF.cullin

SGS domain-containing protein |

Chr1:10546794-10548072 REVERSE LENGTH=229 |

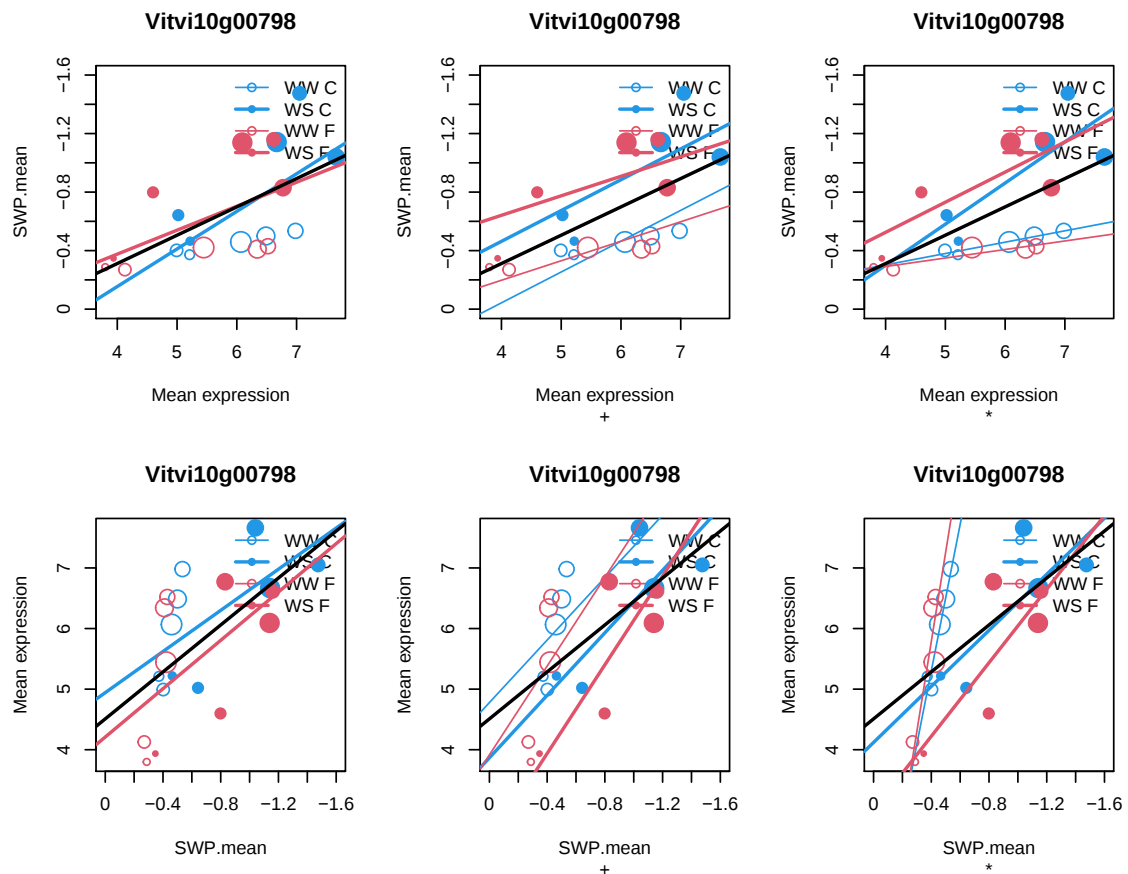
201606

Coefficient swp for Vitvi10g00798.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi10g00798	15.88523	5.780401	14.50996	2.691739e-24	7.889901e-22

B

Vitvi10g00798 41.74034



Correlation of all measurements (not just means): $r = 0.8525$, $r^2 = 0.7268$

Correlation of mean values (plots): $r_2 = 0.6124$

5.2.53 Vitvi02g00310

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

Vitvi02g00310

34.19.1

transport.major intrinsic proteins.PIP

plasma membrane intrinsic protein 1B |

Chr2:18910450-18911579 FORWARD LENGTH=274 |

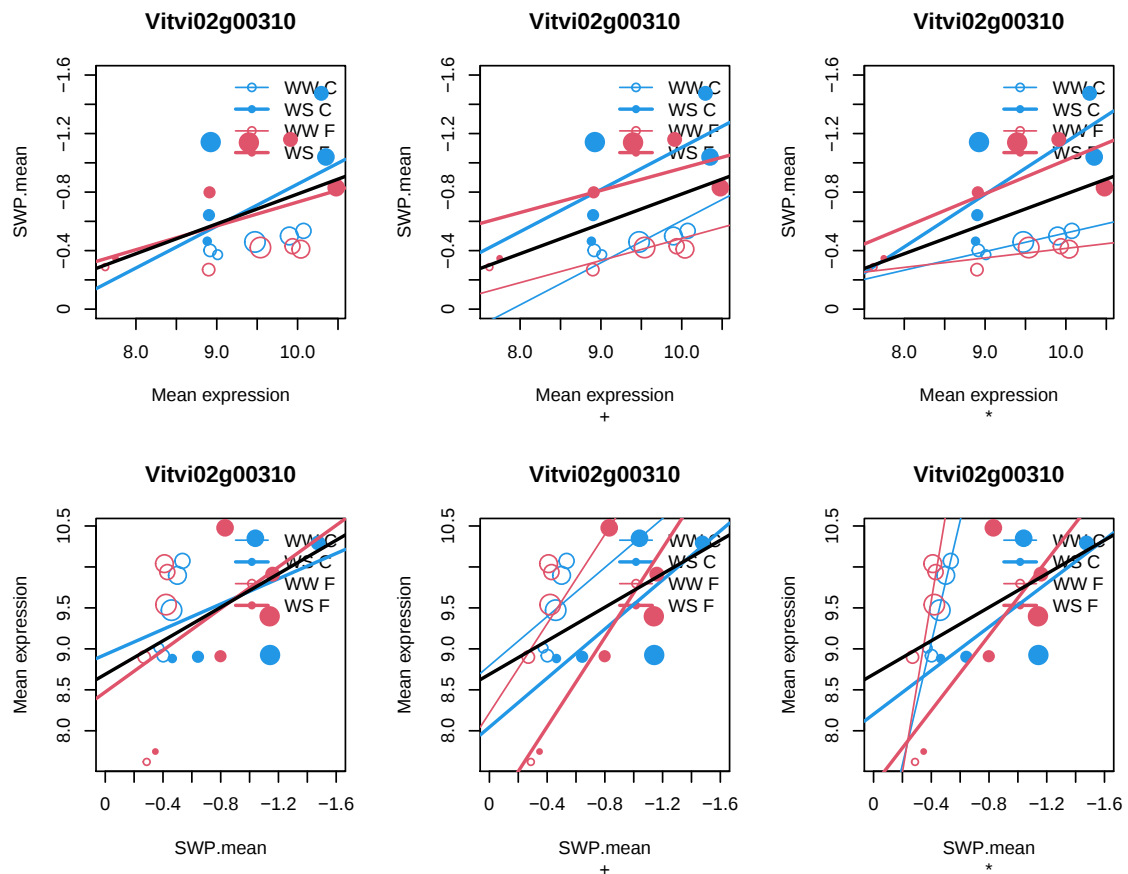
201606

Coefficient swp for Vitvi02g00310.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi02g00310	11.19132	9.360302	14.50237	2.776167e-24	7.983838e-22

B

Vitvi02g00310 41.71395



Correlation of all measurements (not just means): $r = 0.8559$, $r^2 = 0.7325$

Correlation of mean values (plots): $r_2 = 0.4567$

5.2.54 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 |

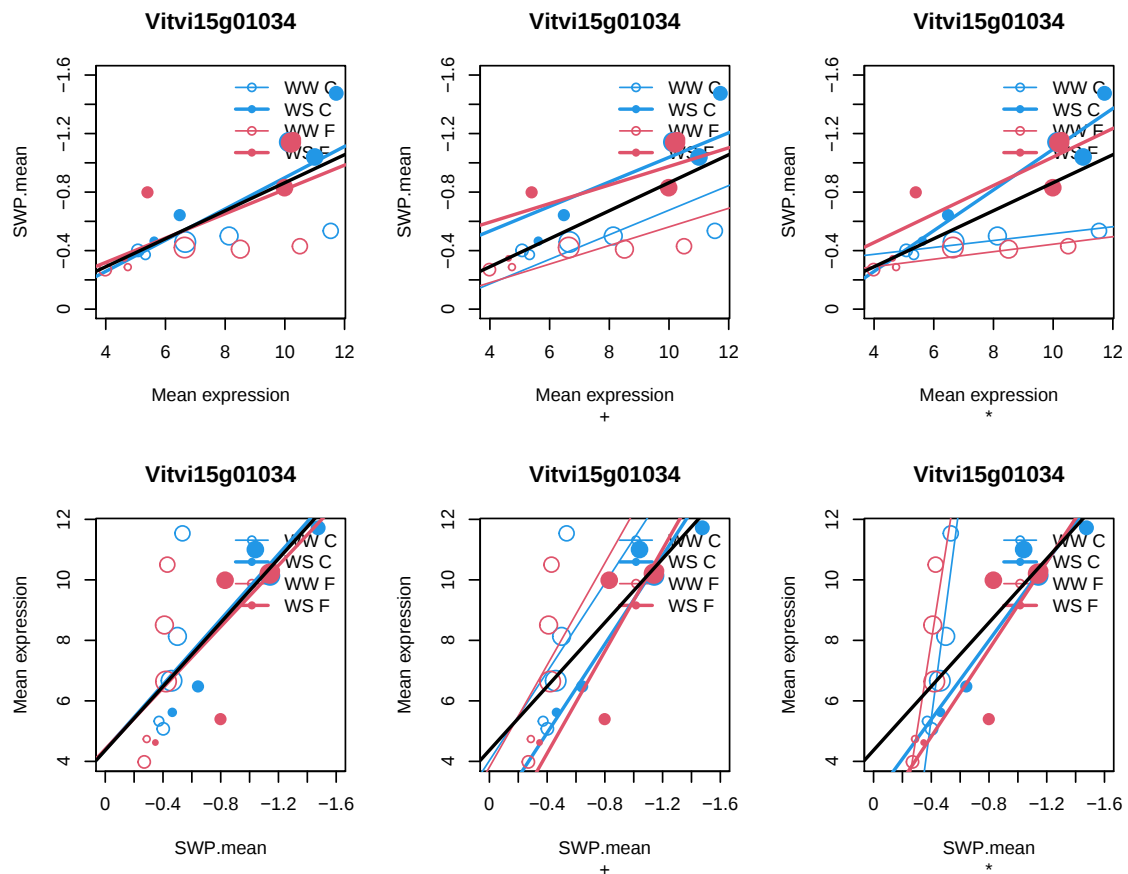
201606

Coefficient swp for Vitvi15g01034.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi15g01034	37.91364	7.829037	14.4788	3.055685e-24	8.624954e-22

B

Vitvi15g01034	41.63194
---------------	----------



Correlation of all measurements (not just means): $r = 0.8492$, $r^2 = 0.7211$

Correlation of mean values (plots): $r_2 = 0.7105$

5.2.55 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 |

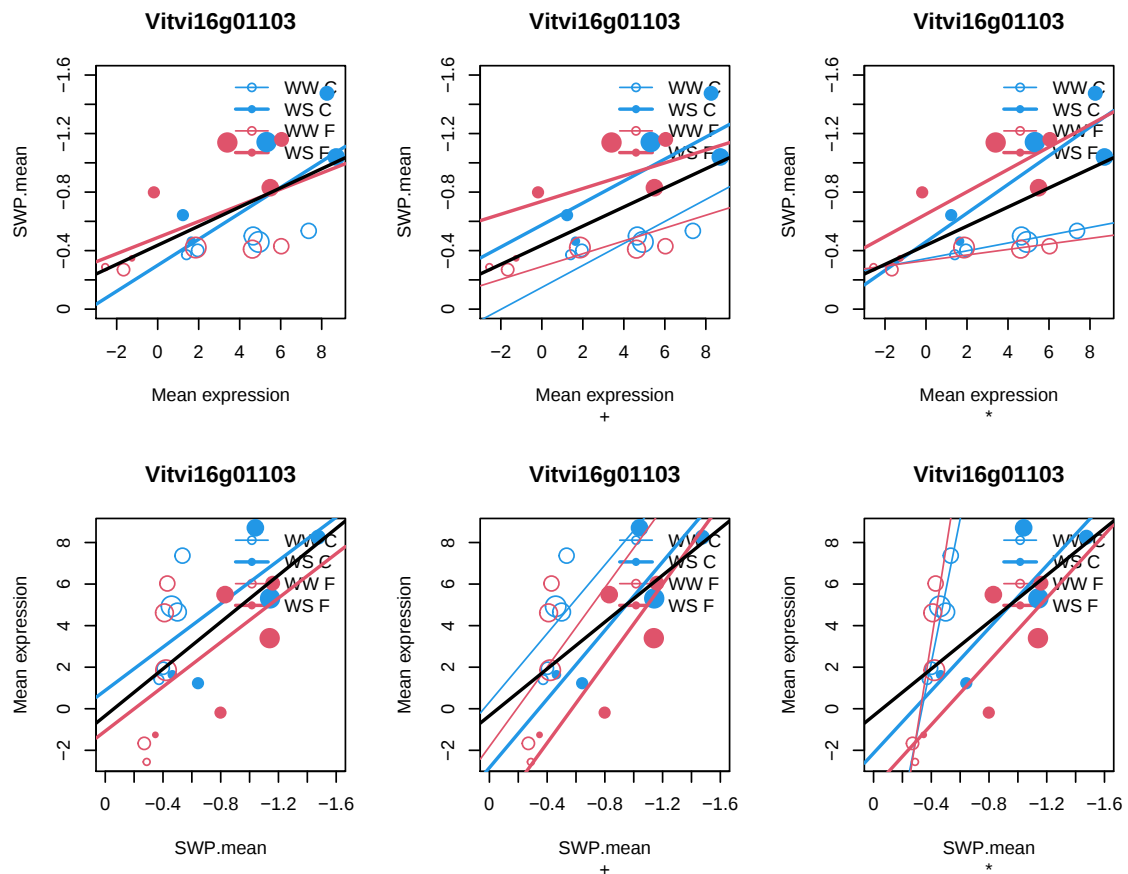
201606

Coefficient swp for Vitvi16g01103.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi16g01103	46.87118	3.360583	14.43845	3.601545e-24	9.980863e-22

B

Vitvi16g01103 41.49137



Correlation of all measurements (not just means): $r = 0.8483$, $r^2 = 0.7196$

Correlation of mean values (plots): $r_2 = 0.6068$

5.2.56 Vitvi06g01562

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

Vitvi06g01562

20.02.2001

stress.abiotic.heat

DNAJ homologue 3 |

Chr3:15869115-15871059 REVERSE LENGTH=420 |

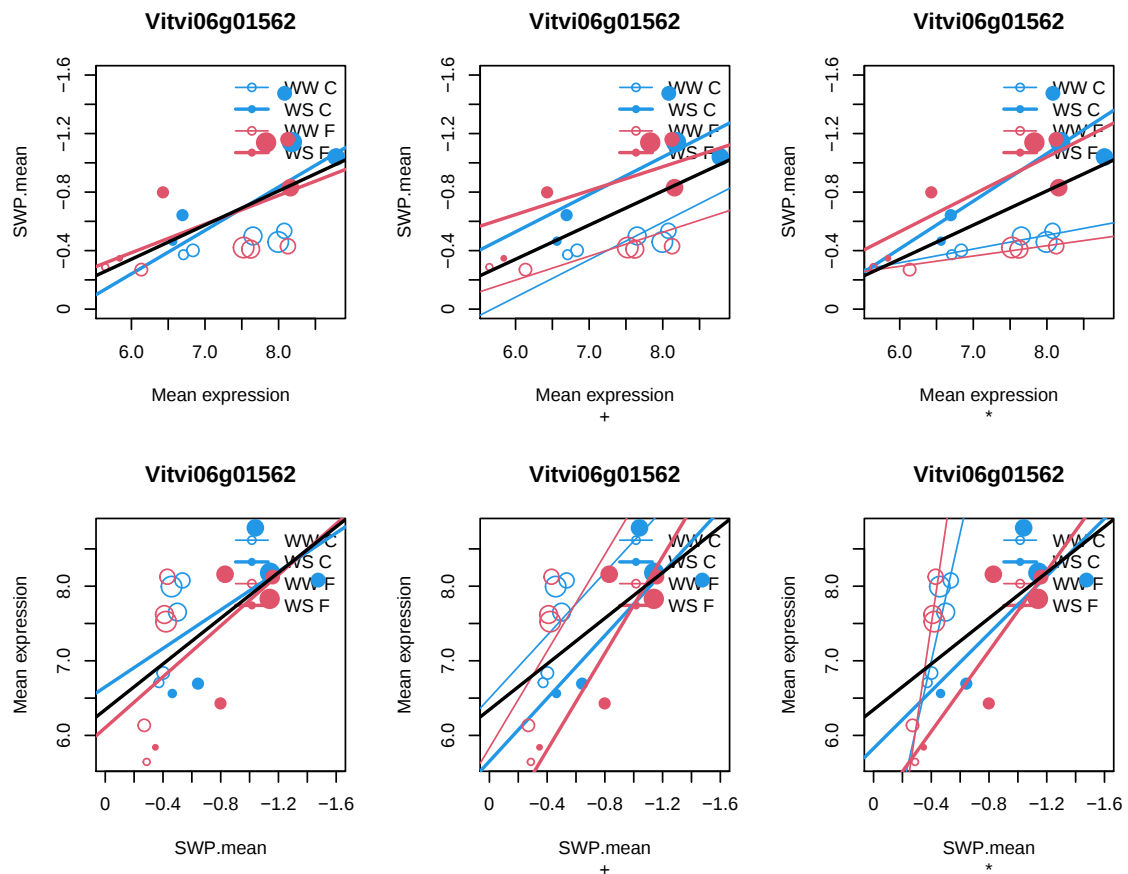
201606

Coefficient swp for Vitvi06g01562.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi06g01562	12.8551	7.350008	14.36782	4.804513e-24	1.307685e-21

B

Vitvi06g01562 41.24469



Correlation of all measurements (not just means): $r = 0.8519$, $r^2 = 0.7258$

Correlation of mean values (plots): $r_2 = 0.5981$

5.2.57 Vitvi04g02184

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

Vitvi04g02184

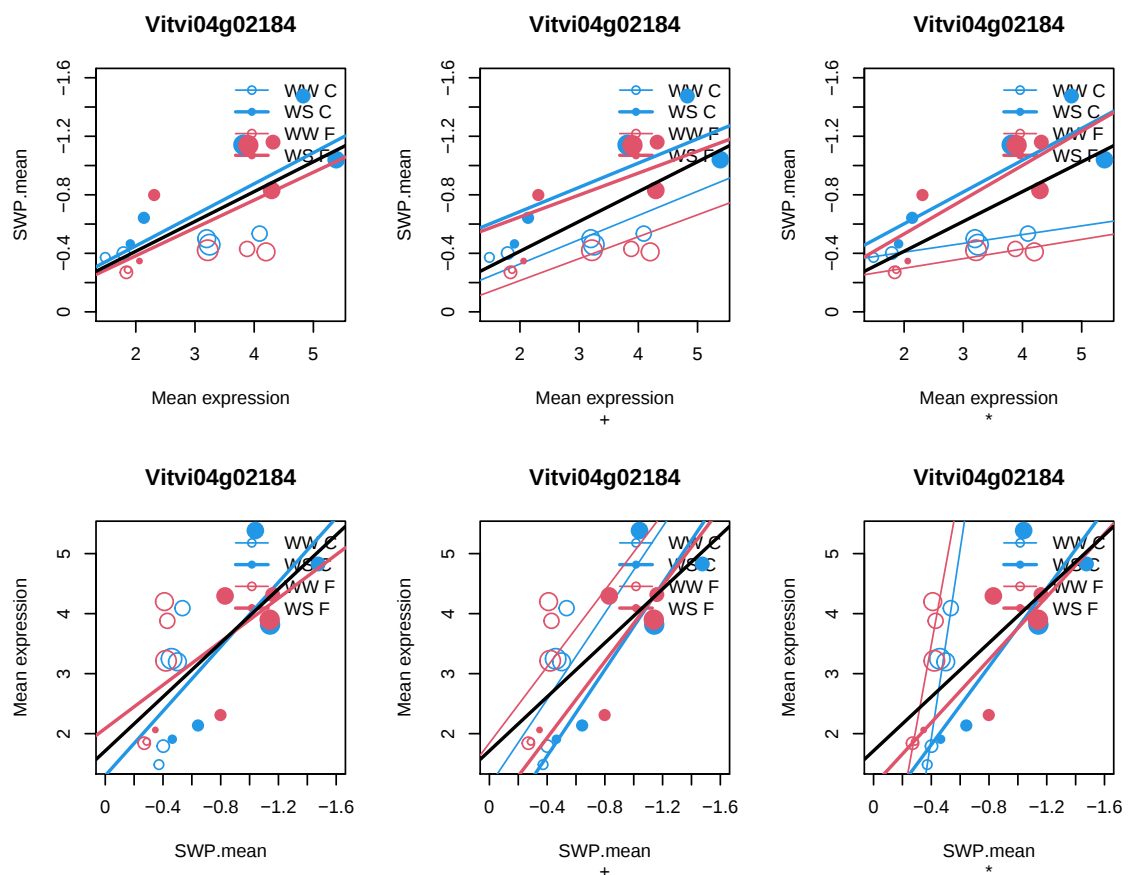
35.2

not assigned.unknown

NA

Coefficient swp for Vitvi04g02184.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi04g02184	17.02469	3.18867	14.35028	5.161446e-24	1.380189e-21
	B				
Vitvi04g02184	41.18332				



Correlation of all measurements (not just means): $r = 0.8494$, $r^2 = 0.7215$
 Correlation of mean values (plots): $r_2 = 0.6770$

5.2.58 Vitvi06g00582

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

Vitvi06g00582

27.4

RNA.RNA binding

RNA-binding (RRM/RBD/RNP motifs) family protein |

Chr1:2258751-2259586 REVERSE LENGTH=203 |

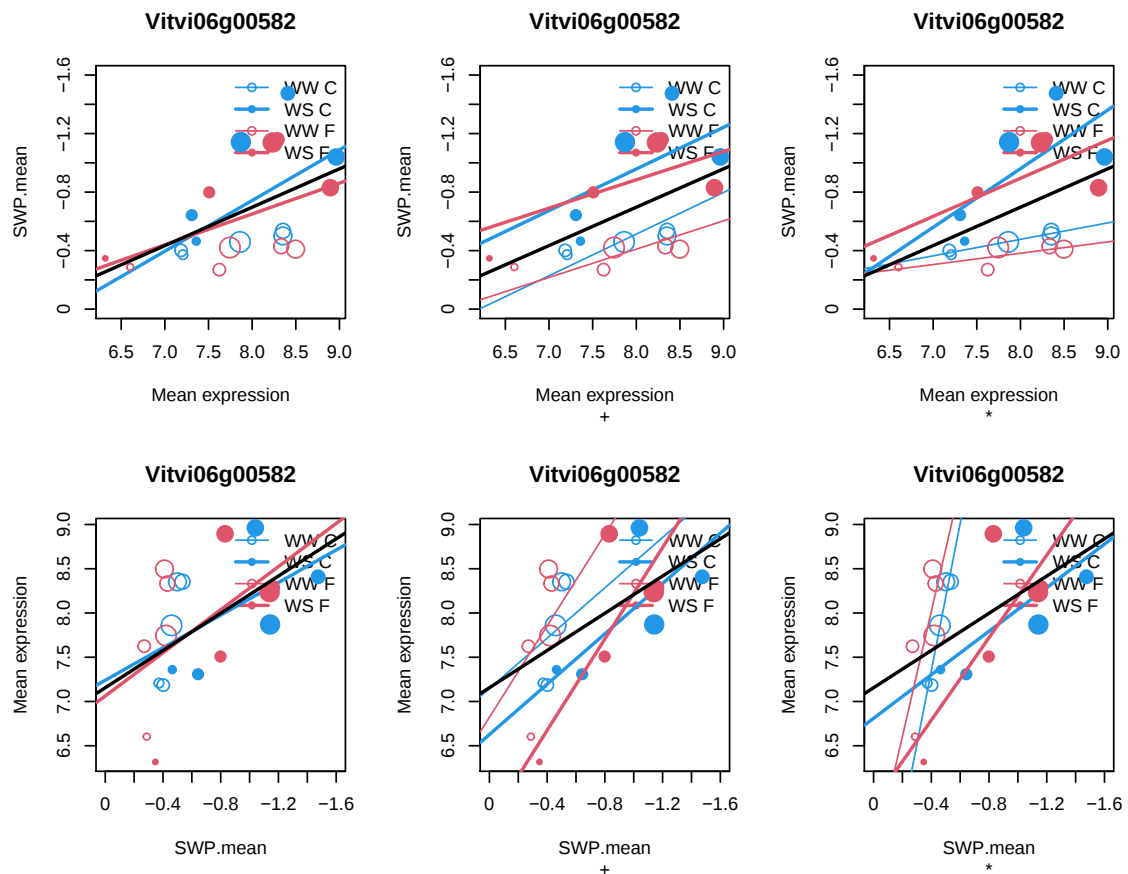
201606

Coefficient swp for Vitvi06g00582.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi06g00582	9.989057	7.845743	14.33779	5.43188e-24	1.42746e-21

B

Vitvi06g00582 41.13957



Correlation of all measurements (not just means): $r = 0.8548$, $r^2 = 0.7307$

Correlation of mean values (plots): $r_2 = 0.5253$

5.2.59 Vitvi13g00241

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

Vitvi13g00241

21.02.2001

redox.ascorbate and glutathione.ascorbate

dehydroascorbate reductase 2 |

Chr1:28250255-28251237 REVERSE LENGTH=213 |

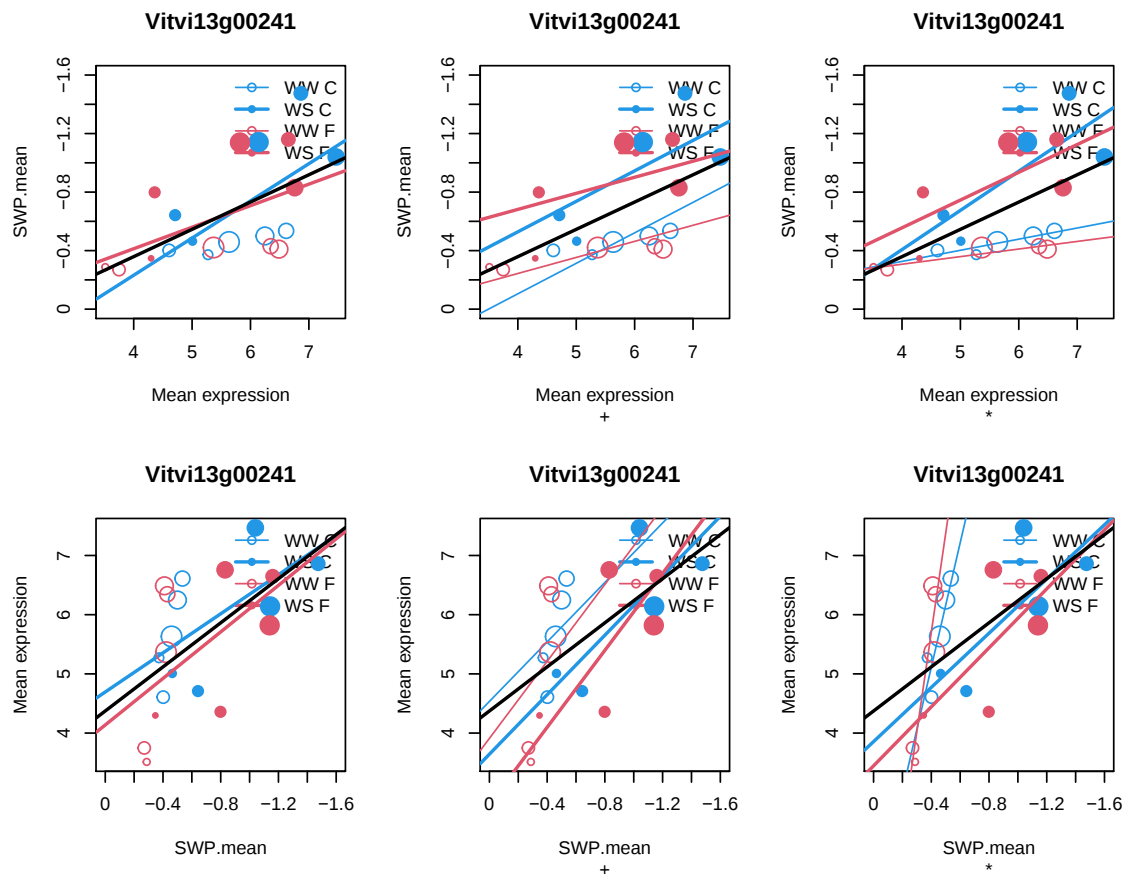
201606

Coefficient swp for Vitvi13g00241.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi13g00241	15.80218	5.595104	14.29358	6.508867e-24	1.681494e-21

B

Vitvi13g00241 40.98455



Correlation of all measurements (not just means): $r = 0.8489$, $r^2 = 0.7206$

Correlation of mean values (plots): $r_2 = 0.5894$

5.2.60 Vitvi07g02433

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

Vitvi07g02433

35.1

not assigned.no ontology

cysteine-rich RECEPTOR-like kinase |

Chr4:12129485-12133157 FORWARD LENGTH=1043 |

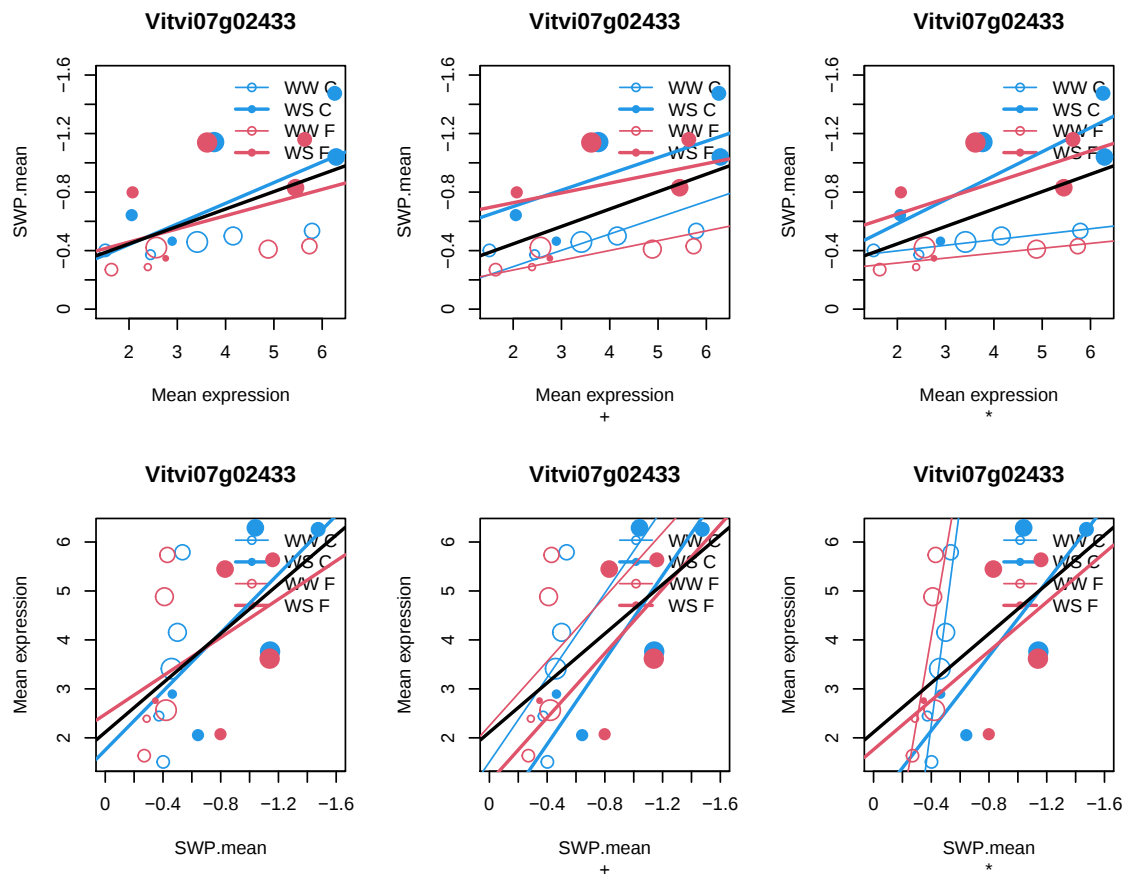
201606

Coefficient swp for Vitvi07g02433.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi07g02433	23.28713	3.765743	14.28306	6.795588e-24	1.726306e-21

B

Vitvi07g02433 40.94759



Correlation of all measurements (not just means): $r = 0.8469$, $r^2 = 0.7172$

Correlation of mean values (plots): $r_2 = 0.5474$

5.2.61 Vitvi04g00548

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

Vitvi04g00548

35.1.3

not assigned.no ontology.armadillo/beta-catenin repeat family protein
cysteine-rich RECEPTOR-like kinase |

Chr4:12129485-12133157 FORWARD LENGTH=1043 |

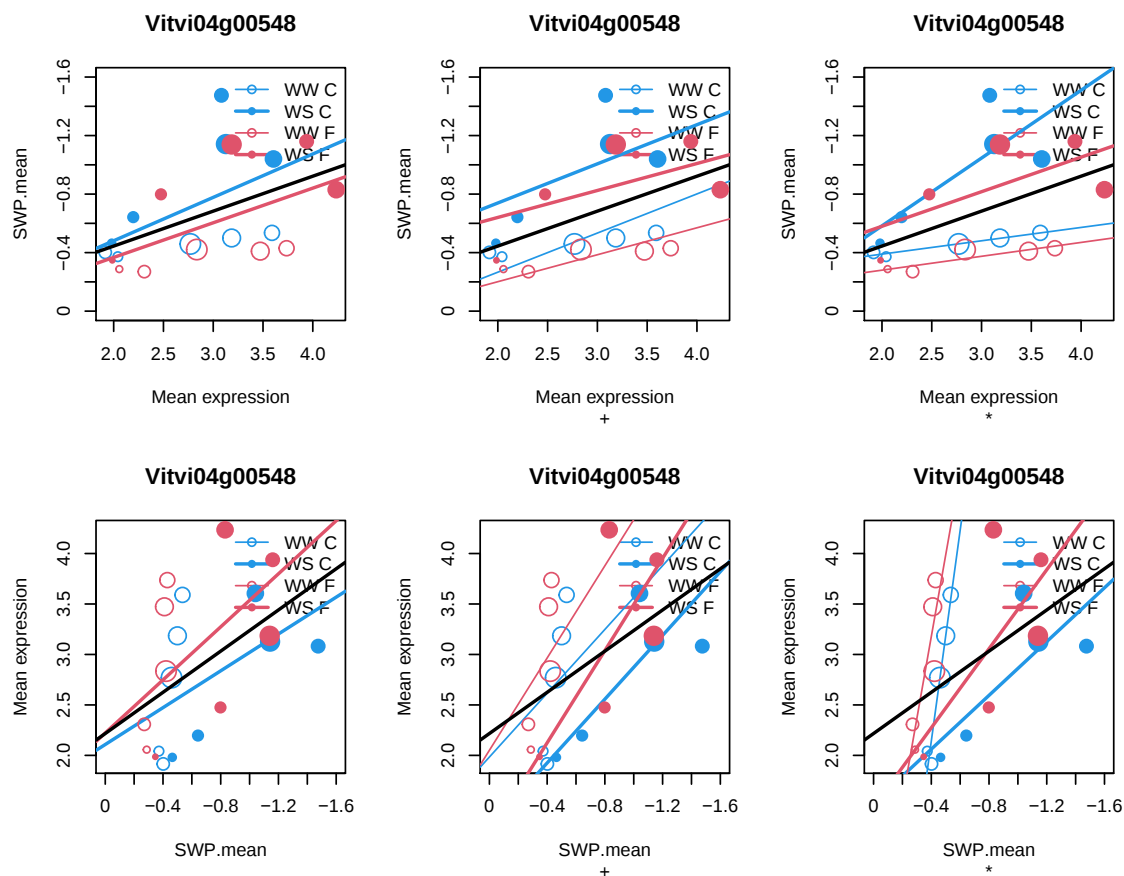
201606

Coefficient swp for Vitvi04g00548.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi04g00548	10.75342	2.886124	14.22848	8.49934e-24	2.12372e-21

B

Vitvi04g00548 40.7557



Correlation of all measurements (not just means): $r = 0.8517$, $r^2 = 0.7255$

Correlation of mean values (plots): $r_2 = 0.4936$

5.2.62 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 |

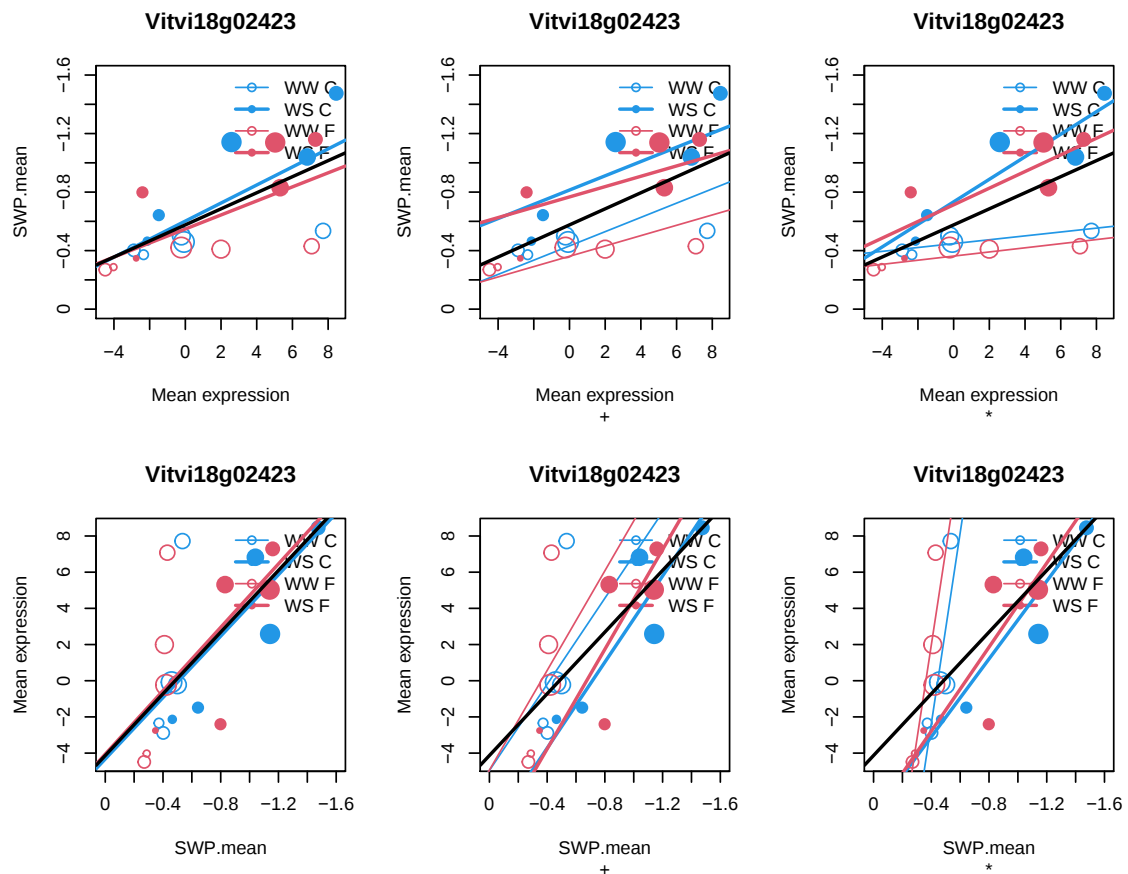
201606

Coefficient swp for Vitvi18g02423.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi18g02423	63.72049	1.462056	14.16194	1.117033e-23	2.746099e-21

B

Vitvi18g02423 40.5211



Correlation of all measurements (not just means): $r = 0.8435$, $r^2 = 0.7115$

Correlation of mean values (plots): $r_2 = 0.6840$

5.2.63 Vitvi03g01897

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

Vitvi03g01897

16.7

secondary metabolism.wax

acyl-CoA sterol acyl transferase 1 |

Chr3:19284420-19285457 FORWARD LENGTH=345 |

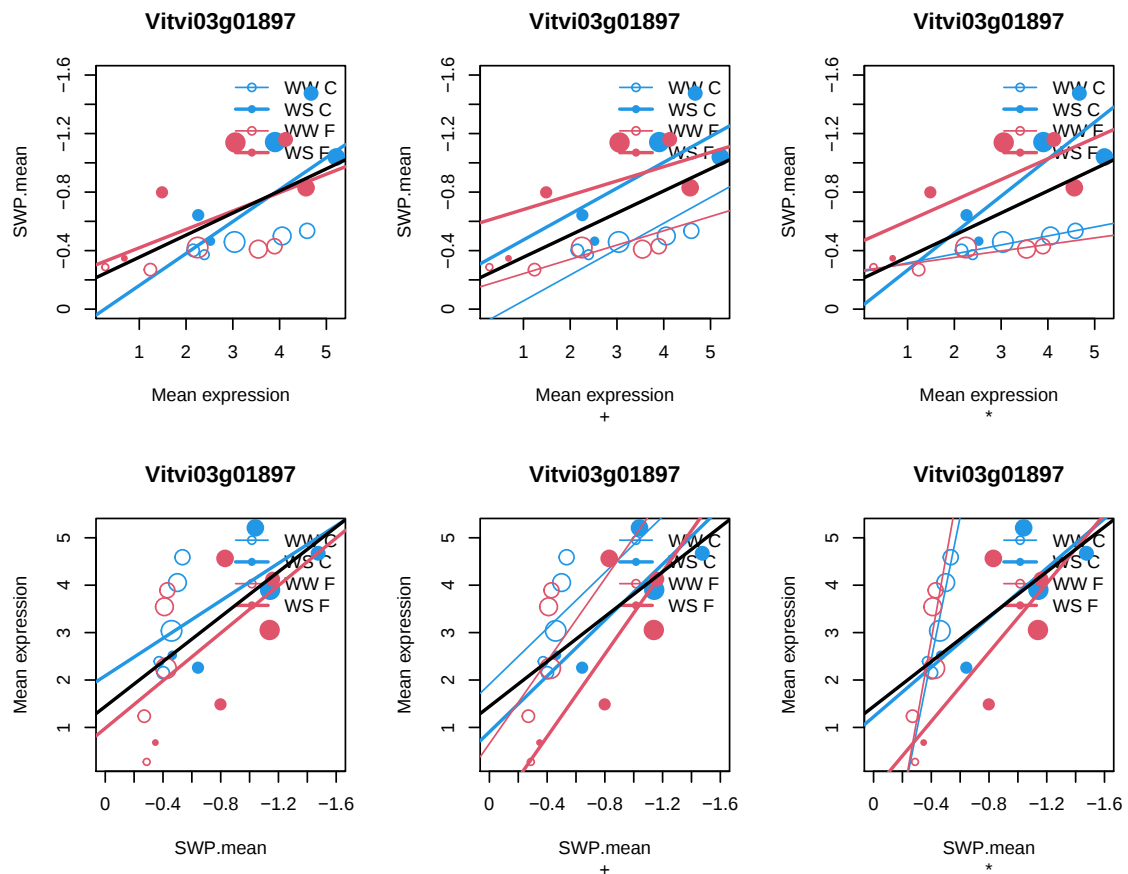
201606

Coefficient swp for Vitvi03g01897.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi03g01897	19.64853	2.995035	14.12832	1.282682e-23	3.103276e-21

B

Vitvi03g01897 40.40231



Correlation of all measurements (not just means): $r = 0.8449$, $r^2 = 0.7138$

Correlation of mean values (plots): $r_2 = 0.5978$

5.2.64 Vitvi05g01924

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

Vitvi05g01924

17.05.2001

hormone metabolism.ethylene.synthesis-degradation

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

Chr1:842895-844158 REVERSE LENGTH=379 |

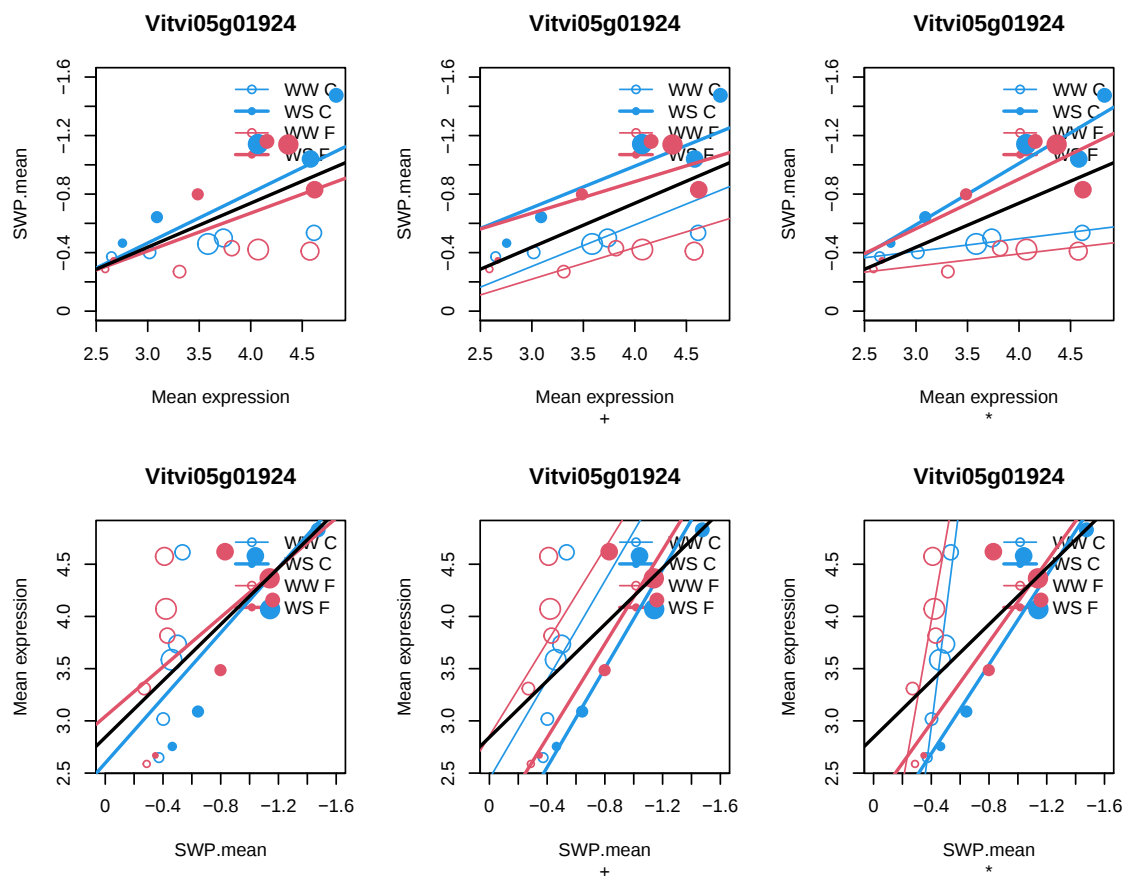
201606

Coefficient swp for Vitvi05g01924.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi05g01924	10.69276	3.729089	14.11137	1.375379e-23	3.275552e-21

B

Vitvi05g01924	40.34235
---------------	----------



Correlation of all measurements (not just means): $r = 0.8498$, $r^2 = 0.7221$

Correlation of mean values (plots): $r_2 = 0.6377$

5.2.65 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 |

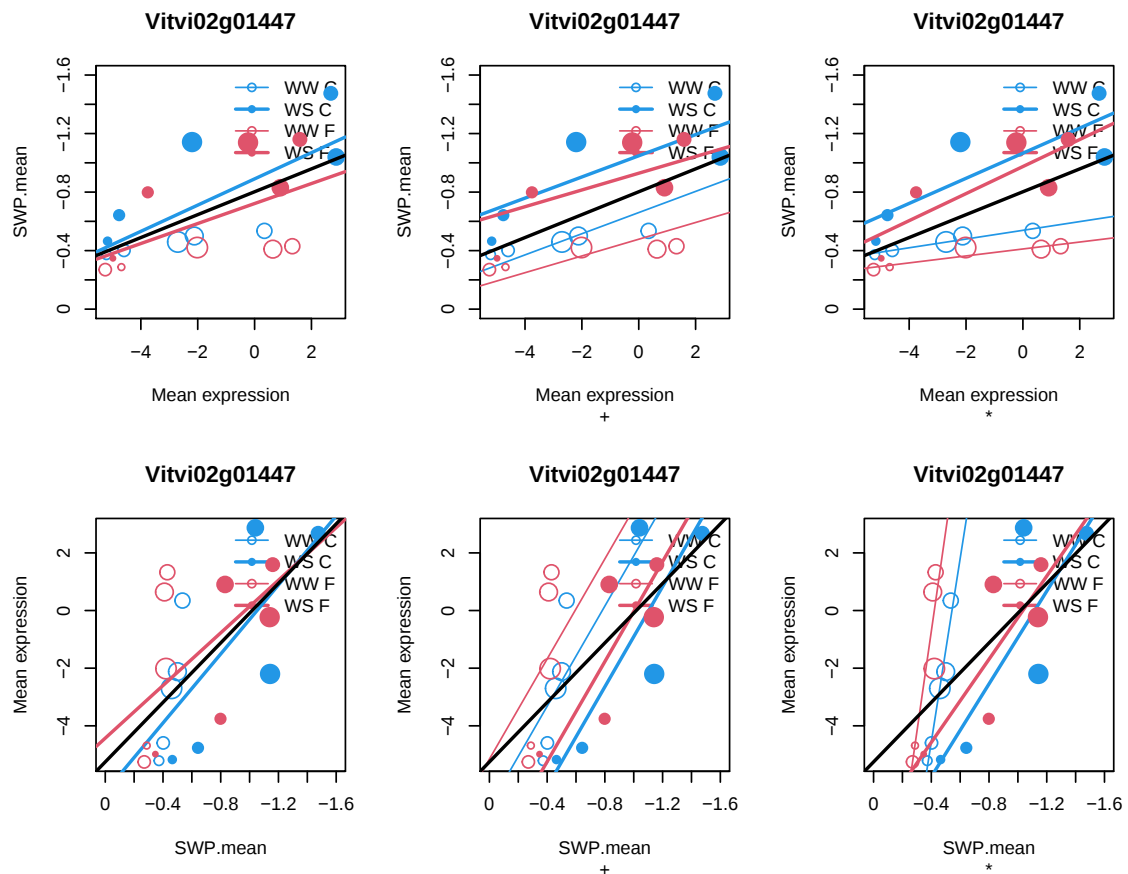
201606

Coefficient swp for Vitvi02g01447.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi02g01447	42.7461	-1.86587	14.10104	1.435145e-23	3.365304e-21

B

Vitvi02g01447 40.30578



Correlation of all measurements (not just means): $r = 0.8427$, $r^2 = 0.7101$

Correlation of mean values (plots): $r_2 = 0.6353$

5.2.66 Vitvi18g00748

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

Vitvi18g00748

35.2

not assigned.unknown

hypothetical protein |

Chr5:19373013-19374312 REVERSE LENGTH=177 |

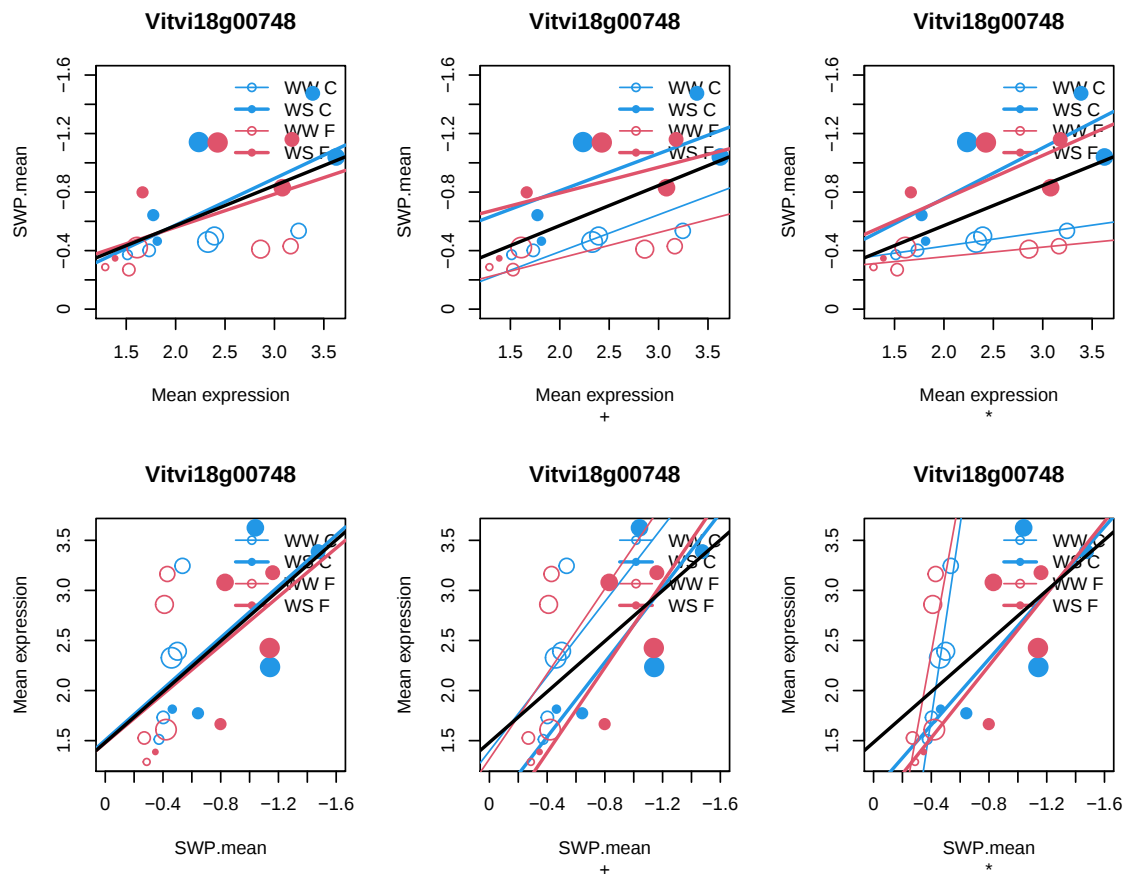
201606

Coefficient swp for Vitvi18g00748.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi18g00748	11.2231	2.311365	14.04118	1.836729e-23	4.24173e-21

B

Vitvi18g00748 40.09361



Correlation of all measurements (not just means): $r = 0.8478$, $r^2 = 0.7188$

Correlation of mean values (plots): $r_2 = 0.5879$

5.2.67 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 |

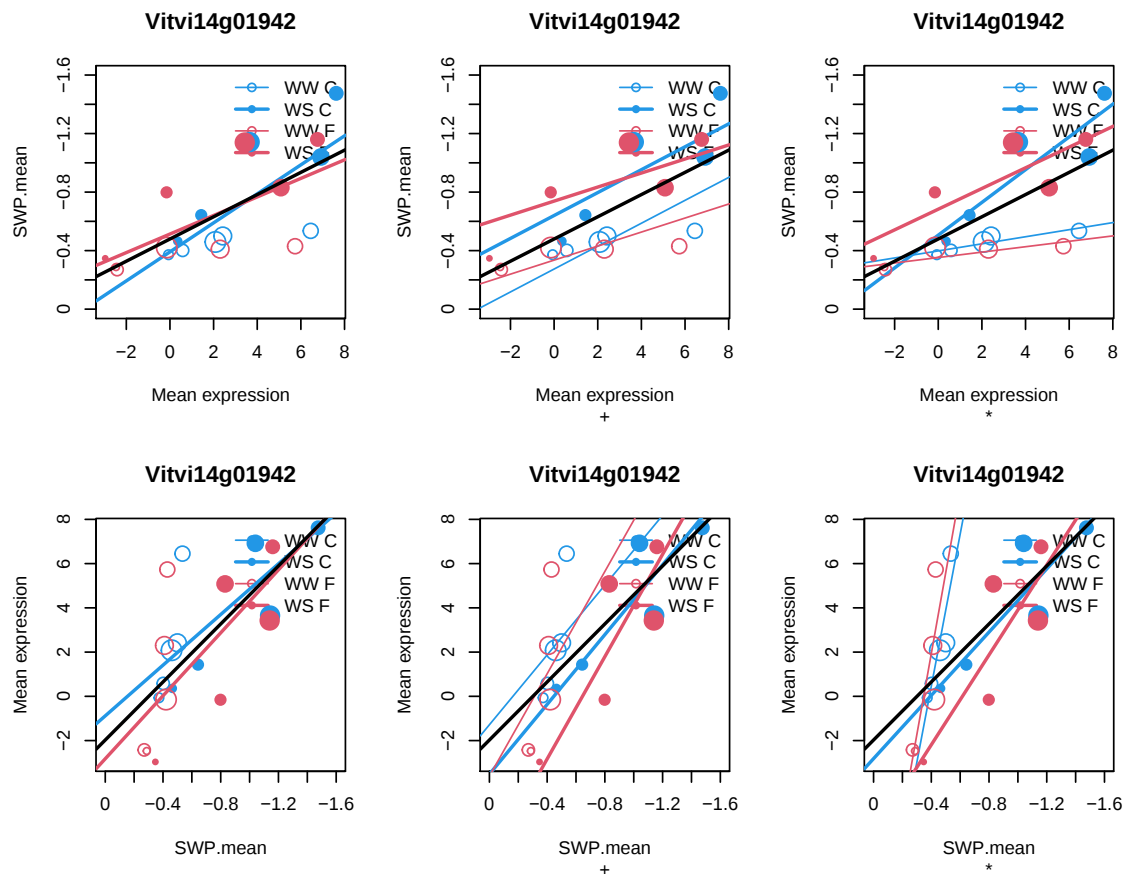
201606

Coefficient swp for Vitvi14g01942.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi14g01942	47.01313	2.329706	14.01033	2.086187e-23	4.74592e-21

B

Vitvi14g01942 39.98402



Correlation of all measurements (not just means): $r = 0.8410$, $r^2 = 0.7073$

Correlation of mean values (plots): $r_2 = 0.7056$

5.2.68 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 |

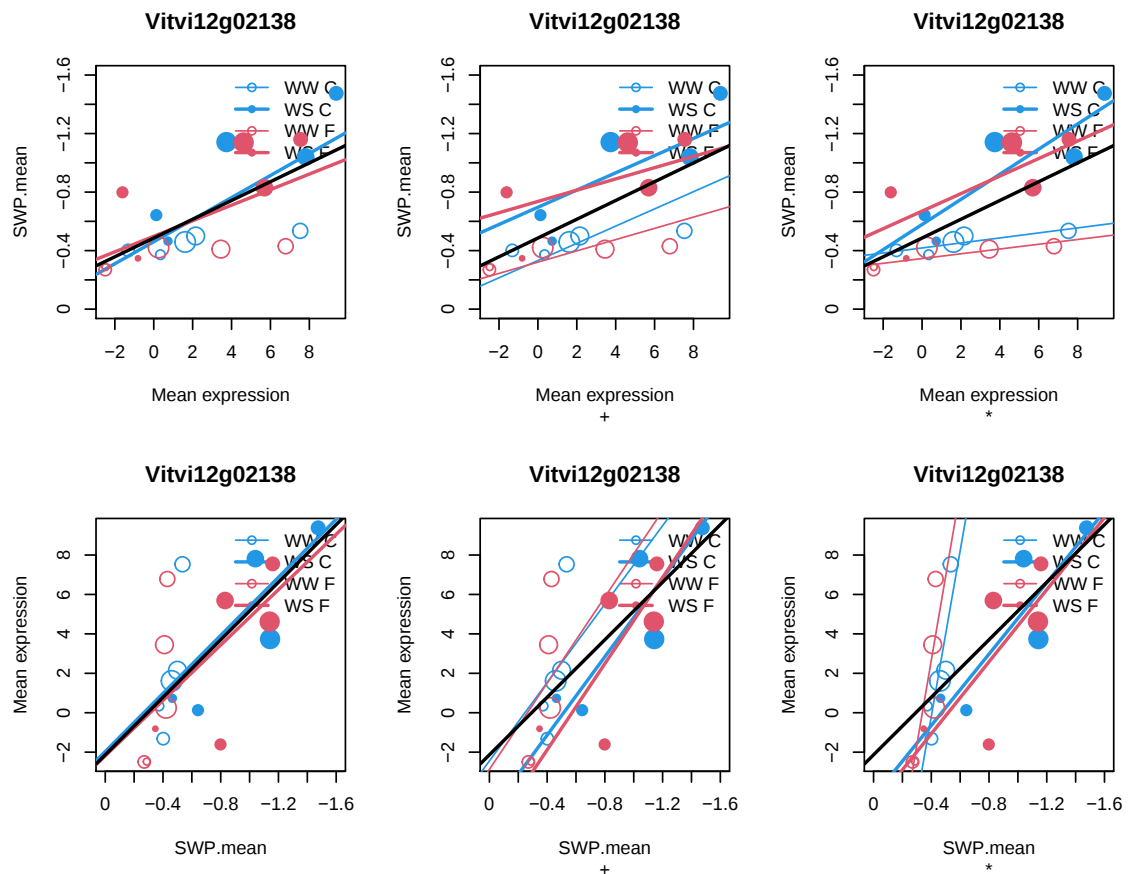
201606

Coefficient swp for Vitvi12g02138.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi12g02138	53.77021	2.653465	13.80705	4.842452e-23	1.085421e-20

B

Vitvi12g02138 39.25819



Correlation of all measurements (not just means): $r = 0.8373$, $r^2 = 0.7011$

Correlation of mean values (plots): $r_2 = 0.6841$

5.2.69 Vitvi01g00037

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

Vitvi01g00037

35.2

not assigned.unknown

ABI five binding protein 2 |

Chr1:4713969-4715158 FORWARD LENGTH=348 |

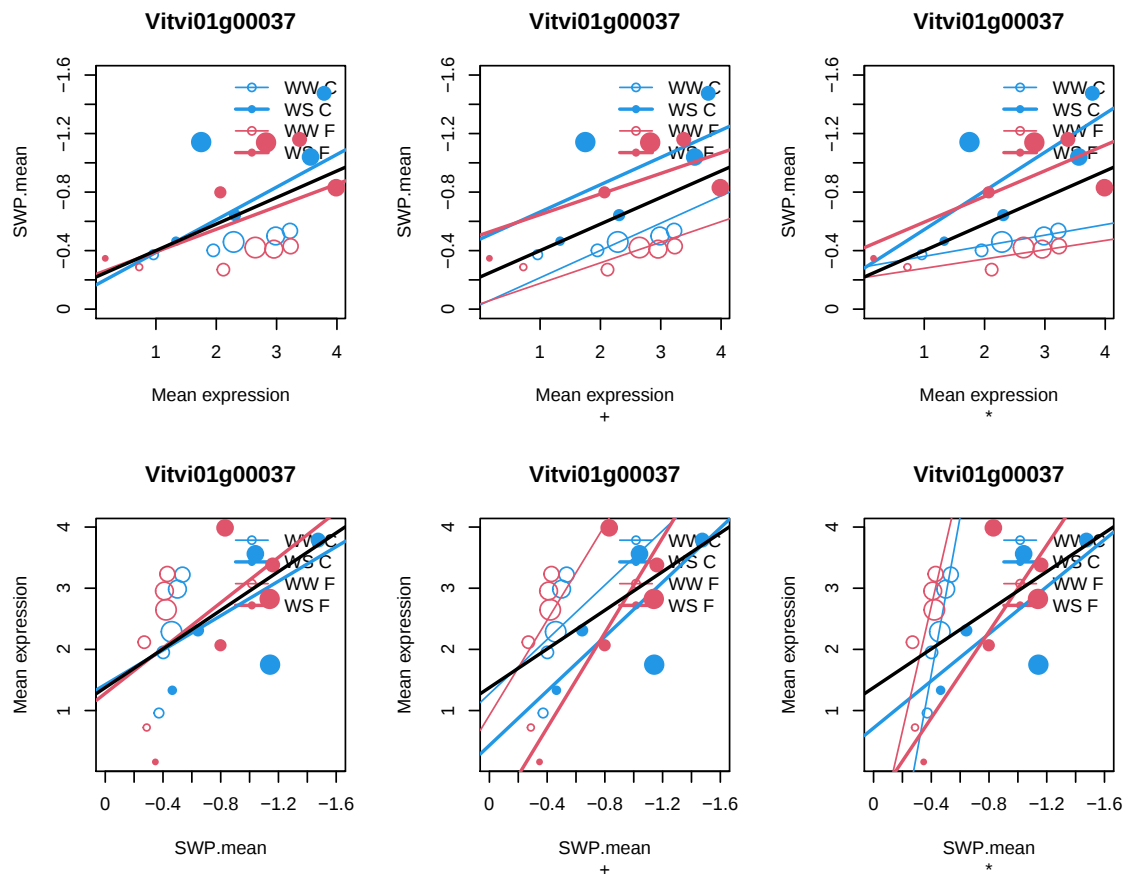
201606

Coefficient swp for Vitvi01g00037.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi01g00037	14.96564	2.412082	13.79788	5.030634e-23	1.11126e-20

B

Vitvi01g00037	39.22528
---------------	----------



Correlation of all measurements (not just means): $r = 0.8405$, $r^2 = 0.7064$

Correlation of mean values (plots): $r_2 = 0.5355$

5.2.70 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 |

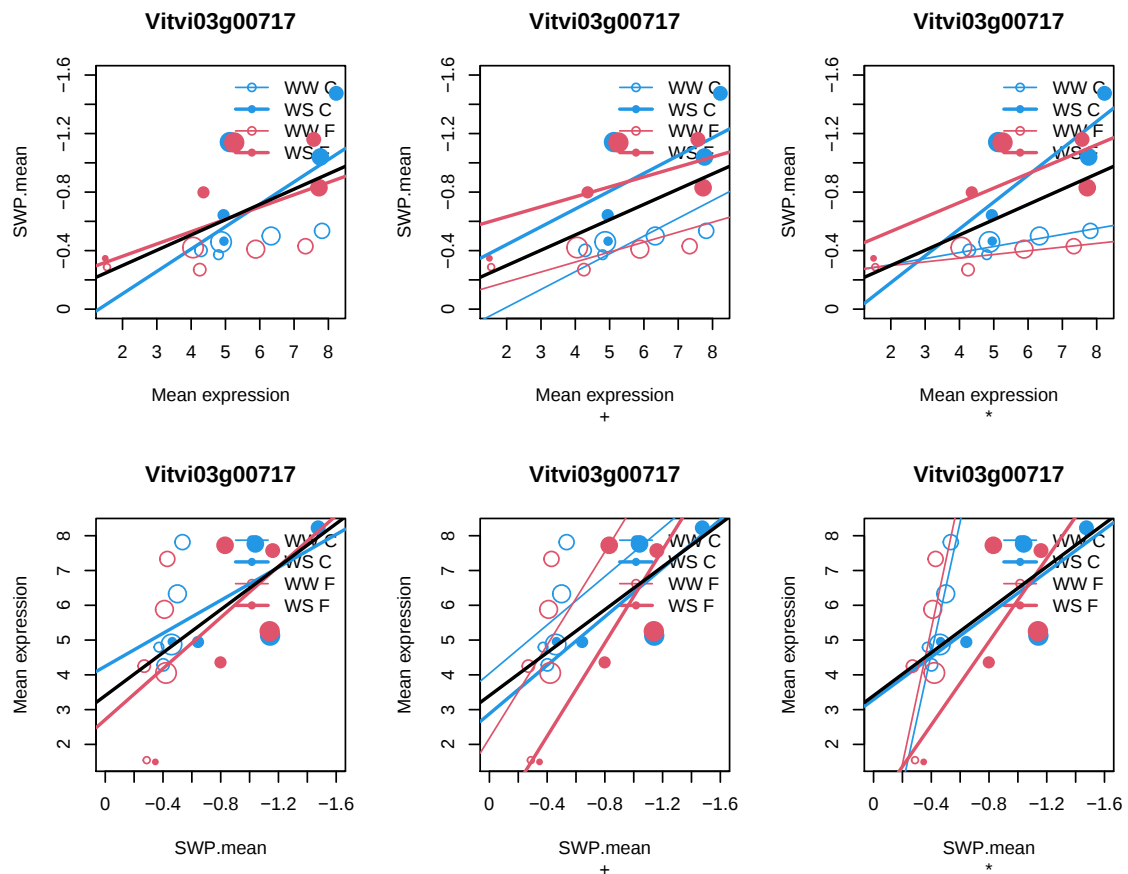
201606

Coefficient swp for Vitvi03g00717.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi03g00717	26.70677	5.429914	13.77934	5.433637e-23	1.183136e-20

B

Vitvi03g00717 39.15875



Correlation of all measurements (not just means): $r = 0.8376$, $r^2 = 0.7016$

Correlation of mean values (plots): $r_2 = 0.5680$

5.2.71 Vitvi04g00039

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

Vitvi04g00039

29.5

protein.degradation

DERLIN-1 |

Chr4:14444937-14446705 FORWARD LENGTH=215 |

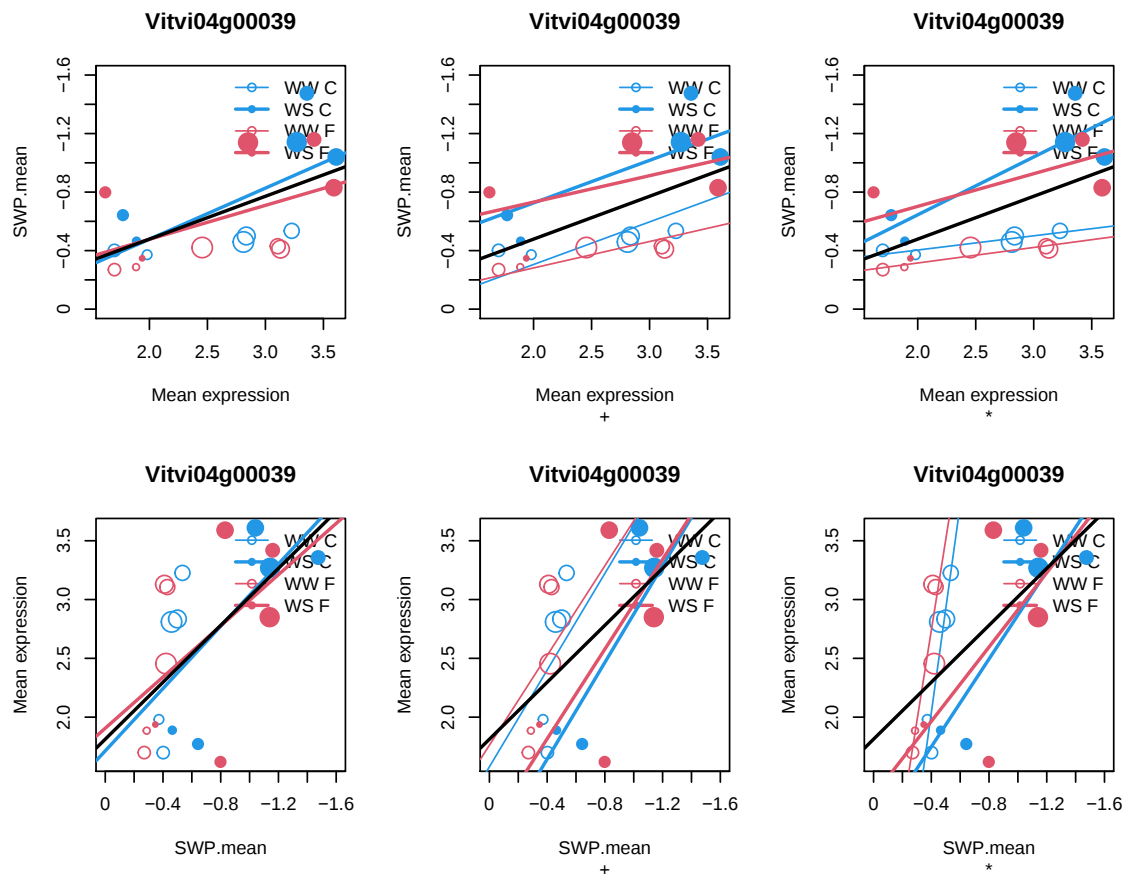
201606

Coefficient swp for Vitvi04g00039.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi04g00039	10.38527	2.606914	13.74644	6.230753e-23	1.337594e-20

B

Vitvi04g00039 39.04052



Correlation of all measurements (not just means): $r = 0.8435$, $r^2 = 0.7115$

Correlation of mean values (plots): $r_2 = 0.5953$

5.2.72 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 |

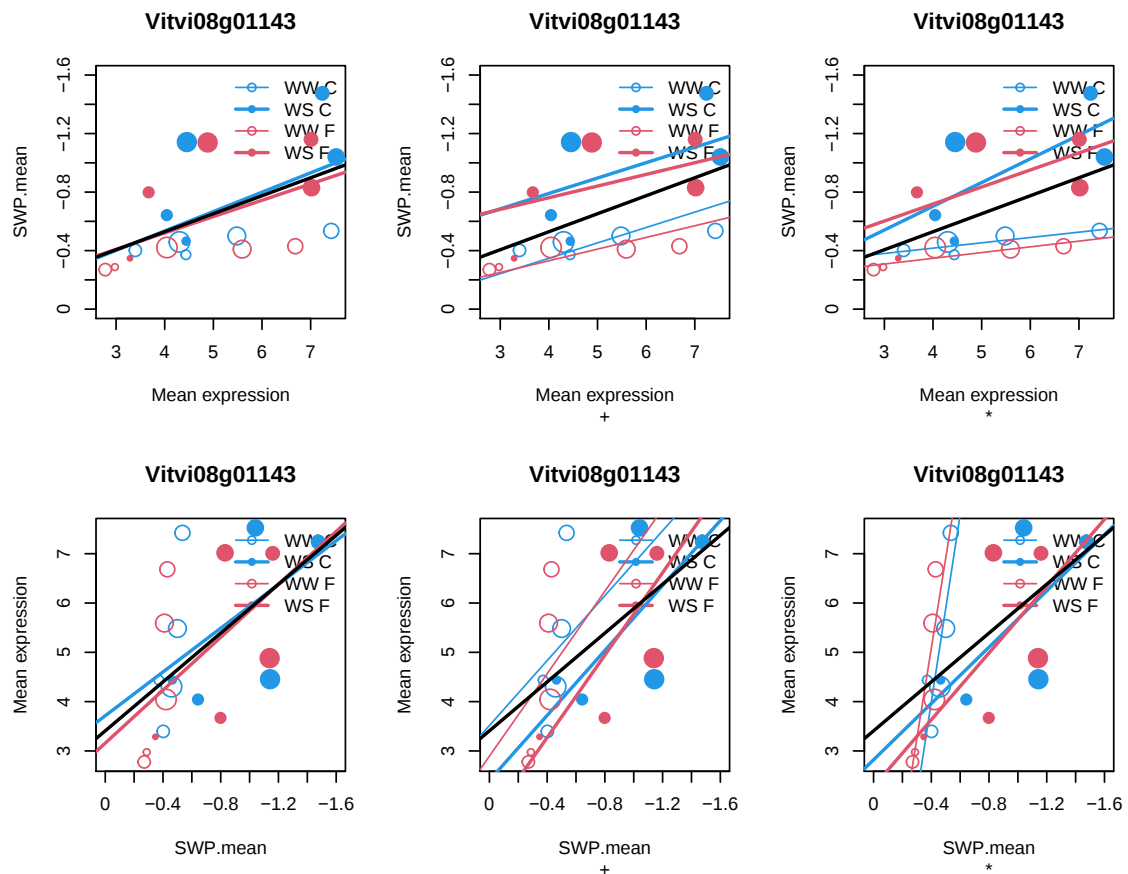
201606

Coefficient swp for Vitvi08g01143.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi08g01143	22.39484	5.033964	13.70861	7.294207e-23	1.544143e-20

B

Vitvi08g01143 38.90435



Correlation of all measurements (not just means): $r = 0.8368$, $r^2 = 0.7003$

Correlation of mean values (plots): $r_2 = 0.5520$

5.2.73 Vitvi13g00062

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

Vitvi13g00062

35.2

not assigned.unknown

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

Chr3:3492986-3494599 REVERSE LENGTH=371 |

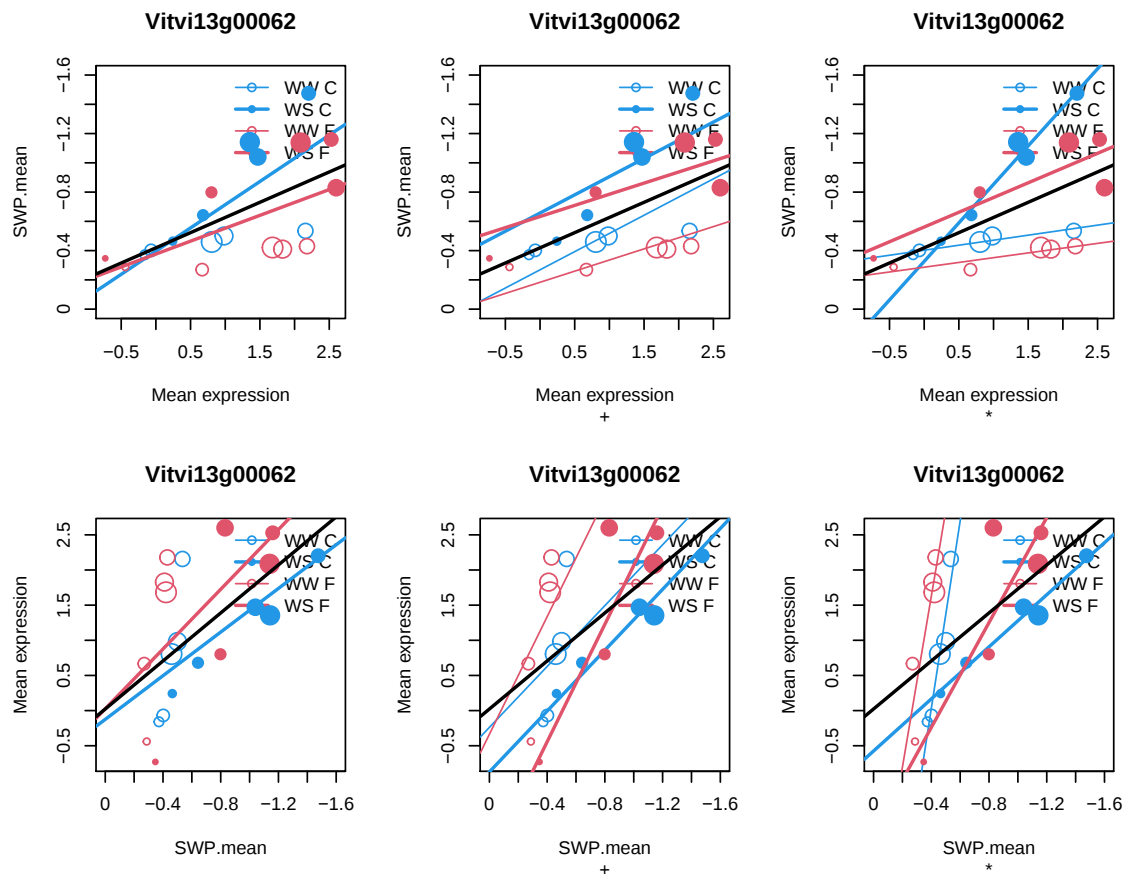
201606

Coefficient swp for Vitvi13g00062.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi13g00062	14.67181	1.143541	13.65791	9.011384e-23	1.881528e-20

B

Vitvi13g00062 38.72157



Correlation of all measurements (not just means): $r = 0.8380$, $r^2 = 0.7023$

Correlation of mean values (plots): $r_2 = 0.5952$

5.2.74 Vitvi09g00375

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

Vitvi09g00375

18

Co-factor and vitamine metabolism

pyridoxine biosynthesis 1.2 |

Chr3:5444121-5445065 REVERSE LENGTH=314 |

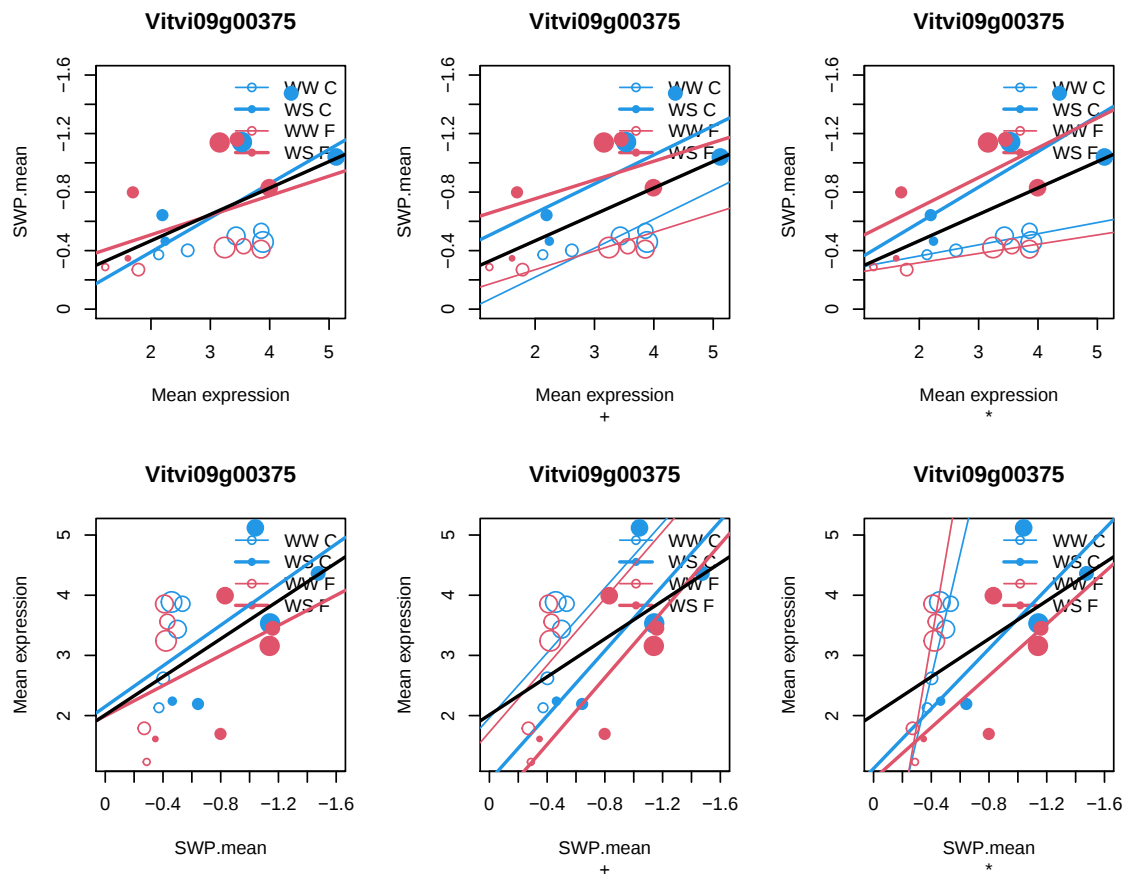
201606

Coefficient swp for Vitvi09g00375.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi09g00375	14.50921	3.048009	13.63598	9.875351e-23	2.034055e-20

B

Vitvi09g00375 38.64237



Correlation of all measurements (not just means): $r = 0.8377$, $r^2 = 0.7018$

Correlation of mean values (plots): $r_2 = 0.5338$

5.2.75 Vitvi11g00657

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

Vitvi11g00657

29.5

protein.degradation

alpha/beta-Hydrolases superfamily protein |

Chr2:10334622-10336579 FORWARD LENGTH=434 |

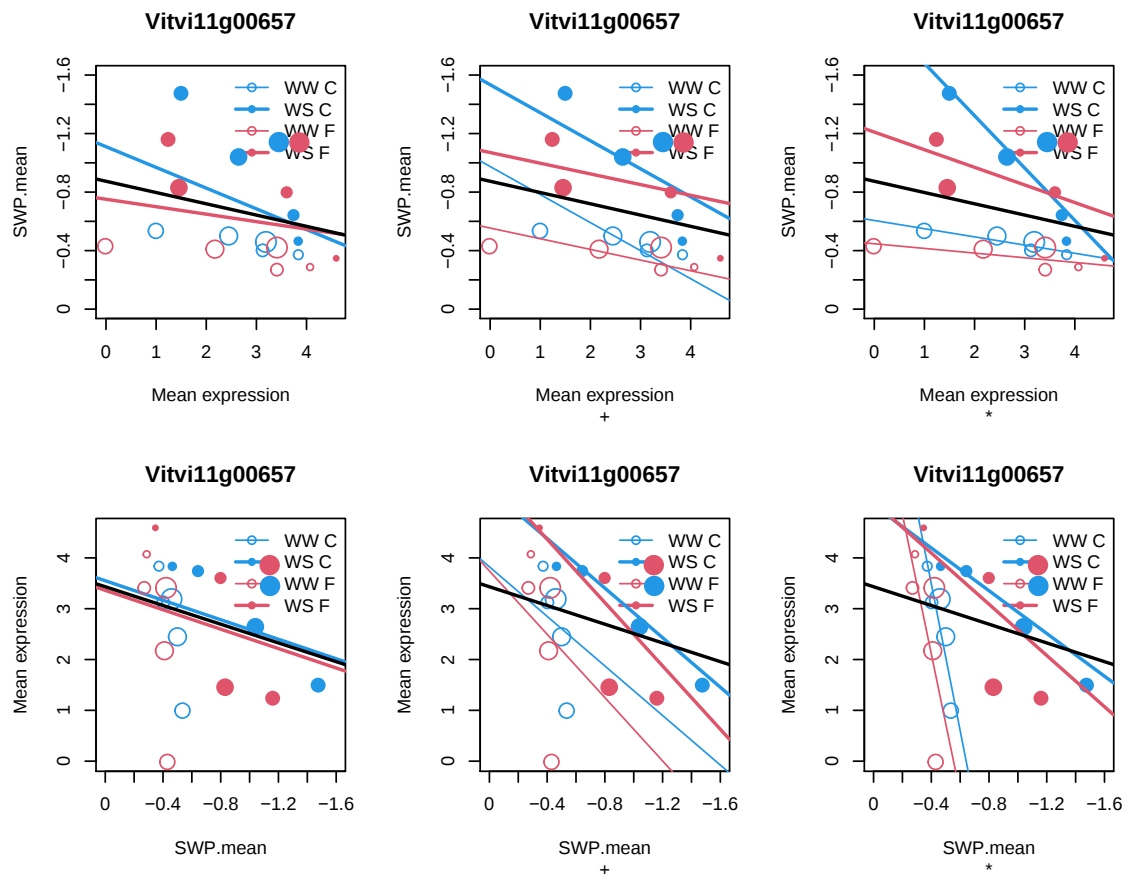
201606

Coefficient swp for Vitvi11g00657.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi11g00657	-17.28468	2.827435	-13.61886	1.06076e-22	2.155747e-20

B

Vitvi11g00657 38.58047



Correlation of all measurements (not just means): $r = -0.8362$, $r^2 = 0.6993$

Correlation of mean values (plots): $r_2 = -0.2663$

5.2.76 Vitvi15g00653

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

Vitvi15g00653

35.1

not assigned.no ontology

ELCH-like protein |

Chr5:4473212-4474318 REVERSE LENGTH=368 |

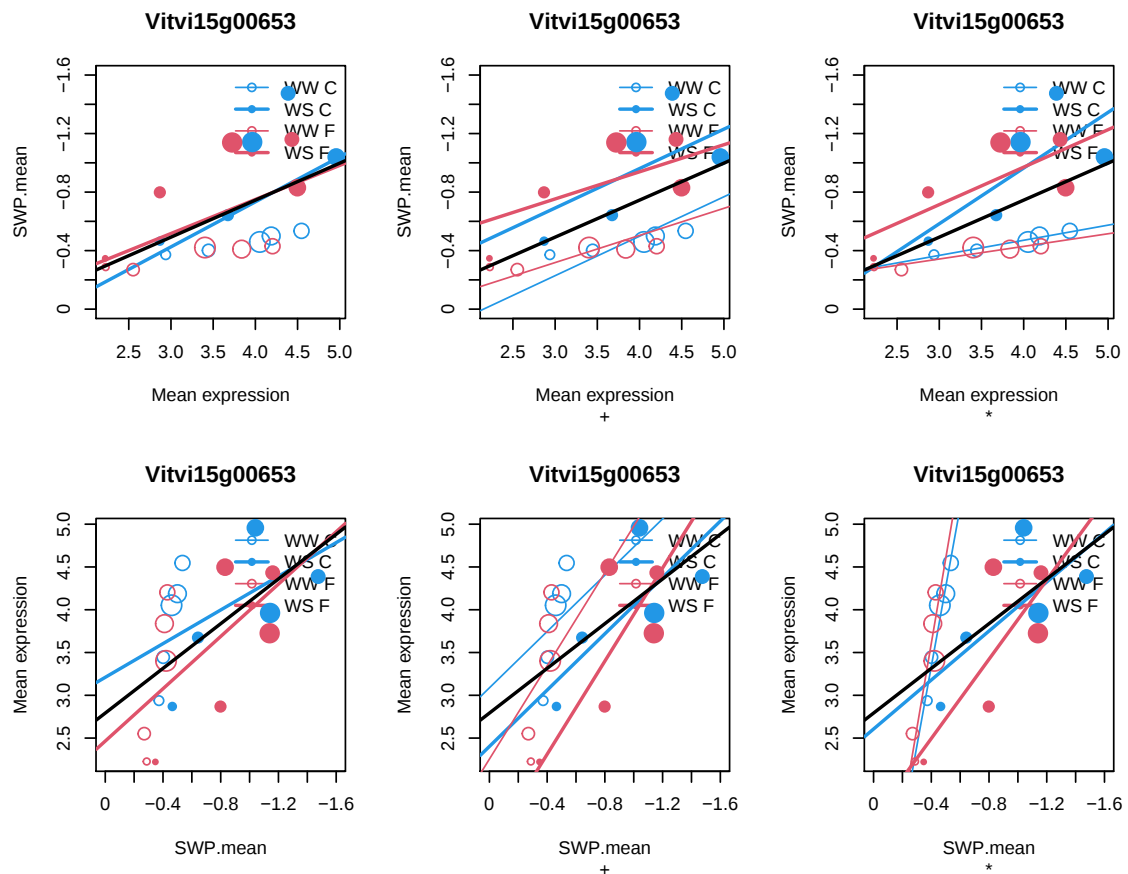
201606

Coefficient swp for Vitvi15g00653.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi15g00653	11.50655	3.649326	13.61349	1.084834e-22	2.175663e-20

B

Vitvi15g00653 38.56105



Correlation of all measurements (not just means): $r = 0.8396$, $r^2 = 0.7049$

Correlation of mean values (plots): $r_2 = 0.5748$

5.2.77 Vitvi09g00772

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

Vitvi09g00772

35.2

not assigned.unknown

serine-rich protein-like protein |

Chr5:8773882-8774544 FORWARD LENGTH=220 |

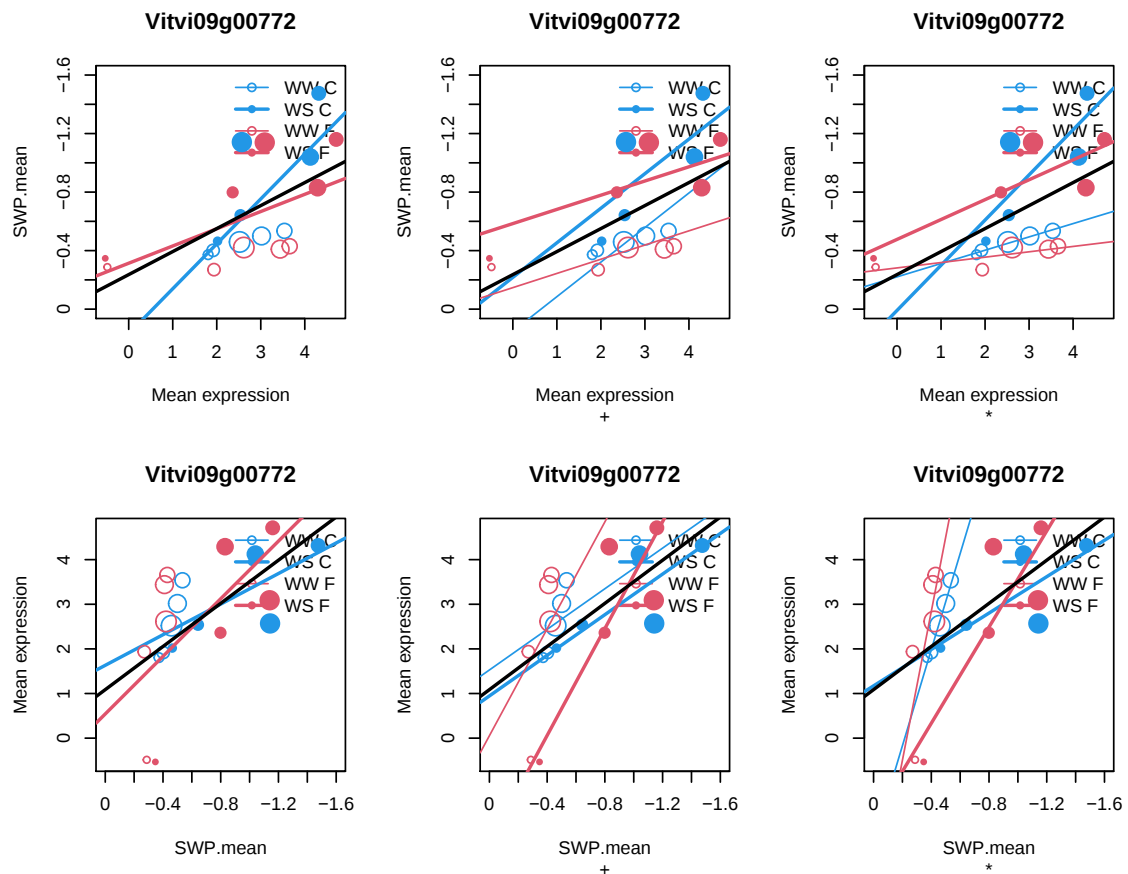
201606

Coefficient swp for Vitvi09g00772.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi09g00772	19.11473	2.672678	13.5803	1.246299e-22	2.467024e-20

B

Vitvi09g00772 38.44095



Correlation of all measurements (not just means): $r = 0.8350$, $r^2 = 0.6973$

Correlation of mean values (plots): $r_2 = 0.6165$

5.2.78 Vitvi08g02274

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

Vitvi08g02274

35.2

not assigned.unknown

plant/protein |

Chr3:3091225-3091674 REVERSE LENGTH=149 |

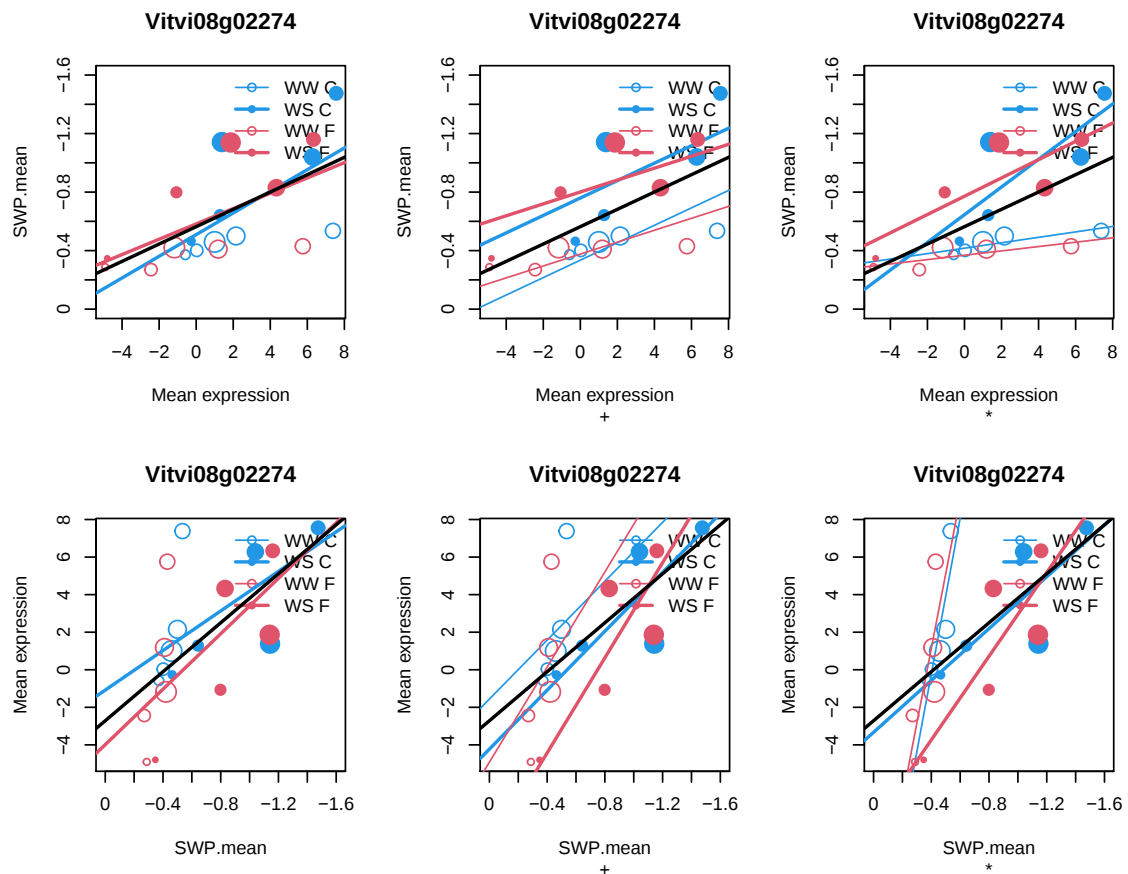
201606

Coefficient swp for Vitvi08g02274.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi08g02274	52.60215	1.564665	13.56517	1.327762e-22	2.568425e-20

B

Vitvi08g02274 38.38612



Correlation of all measurements (not just means): $r = 0.8328$, $r^2 = 0.6936$

Correlation of mean values (plots): $r_2 = 0.6215$

5.2.79 Vitvi14g01896

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

Vitvi14g01896

27.1.3.14

RNA.processing.3' end processing.Clp1

CLP-similar protein 3 |

Chr3:1270053-1272415 REVERSE LENGTH=444 |

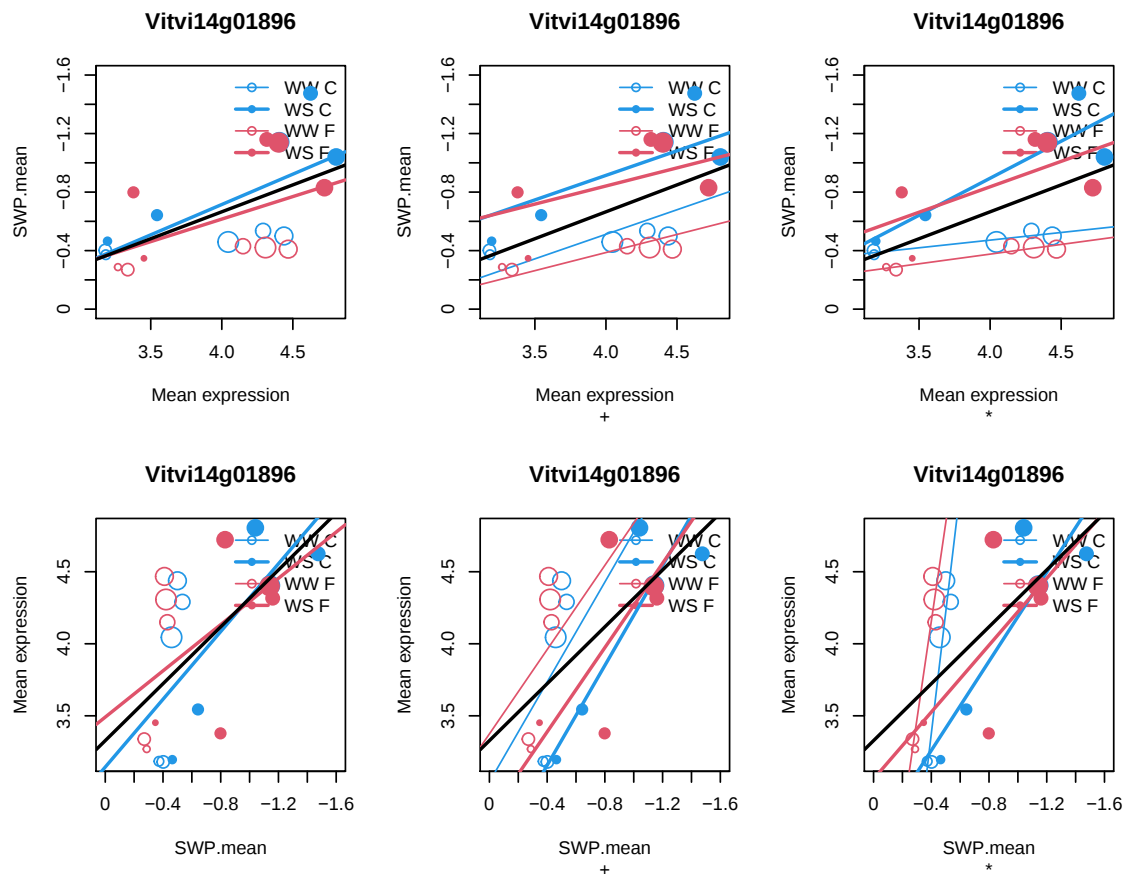
201606

Coefficient swp for Vitvi14g01896.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi14g01896	8.192262	3.975613	13.56455	1.331227e-22	2.568425e-20

B

Vitvi14g01896 38.38386



Correlation of all measurements (not just means): $r = 0.8447$, $r^2 = 0.7136$

Correlation of mean values (plots): $r_2 = 0.6027$

5.2.80 Vitvi06g01354

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

Vitvi06g01354

31.05.2001

cell.cell death.plants

Pheophorbide a oxygenase family protein with Rieske 2Fe-2S domain-cont

Chr3:16383858-16386204 FORWARD LENGTH=537 |

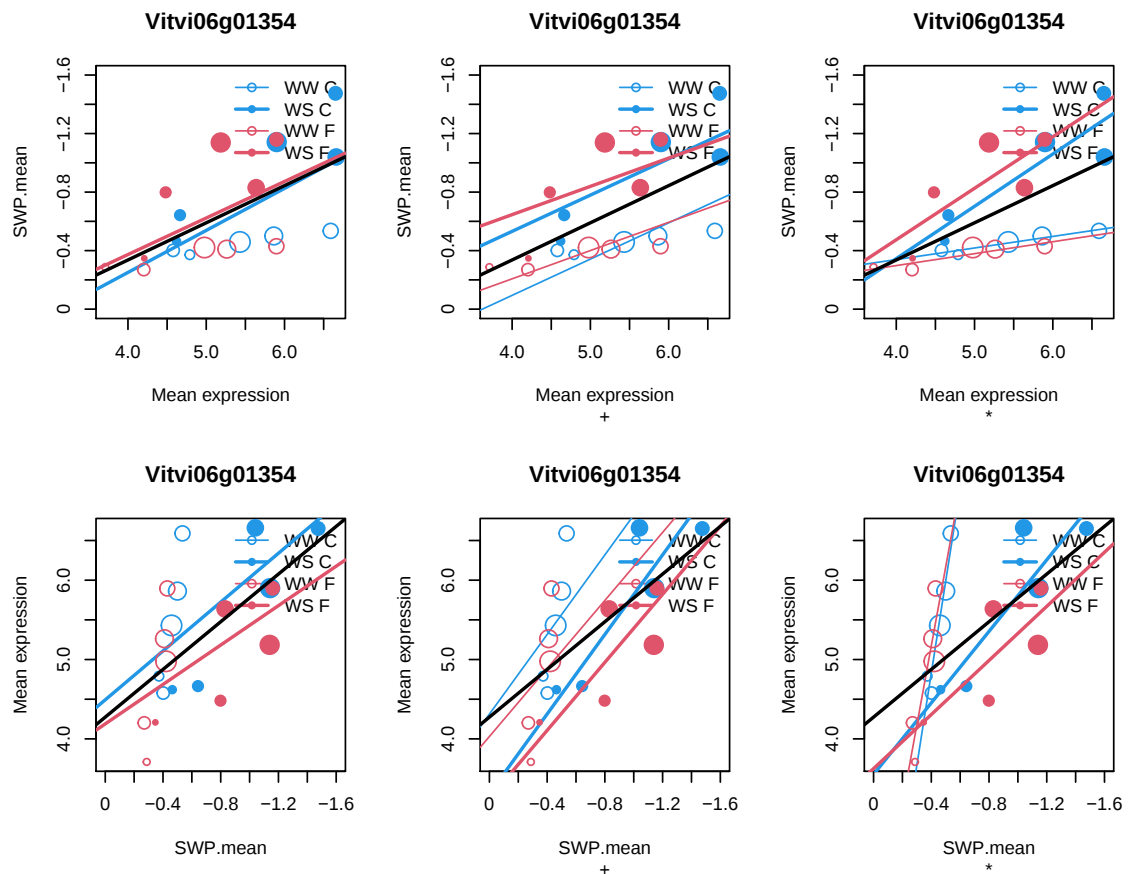
201606

Coefficient swp for Vitvi06g01354.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi06g01354	12.34149	5.260267	13.51415	1.644069e-22	3.132363e-20

B

Vitvi06g01354 38.20101



Correlation of all measurements (not just means): $r = 0.8369$, $r^2 = 0.7003$

Correlation of mean values (plots): $r_2 = 0.6177$

5.2.81 Vitvi01g00921

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

Vitvi01g00921

34.4

transport.nitrate

nitrate transporter 1:2 |

Chr1:26296945-26300407 REVERSE LENGTH=585 |

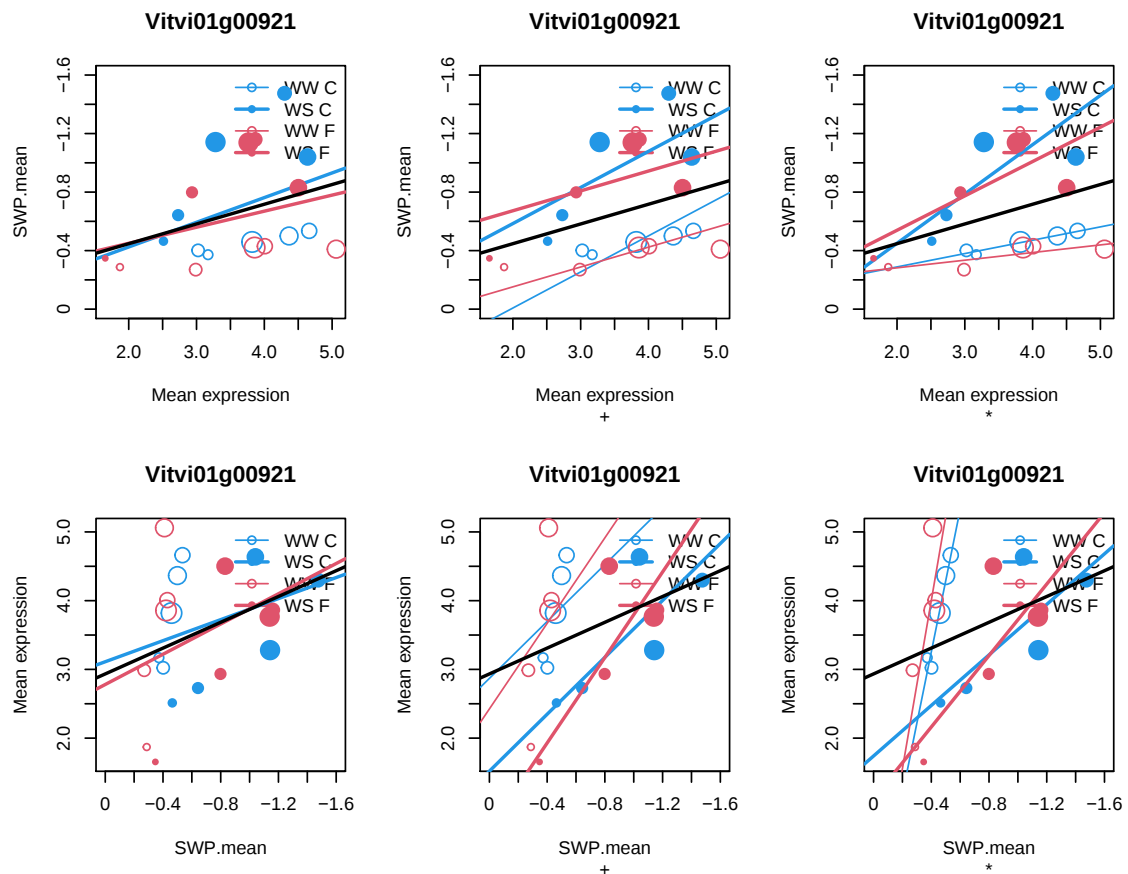
201606

Coefficient swp for Vitvi01g00921.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi01g00921	13.14613	3.550119	13.41595	2.482628e-22	4.671631e-20

B

Vitvi01g00921 37.8436



Correlation of all measurements (not just means): $r = 0.8343$, $r^2 = 0.6961$

Correlation of mean values (plots): $r_2 = 0.3557$

5.2.82 Vitvi12g00905

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

Vitvi12g00905

9.4

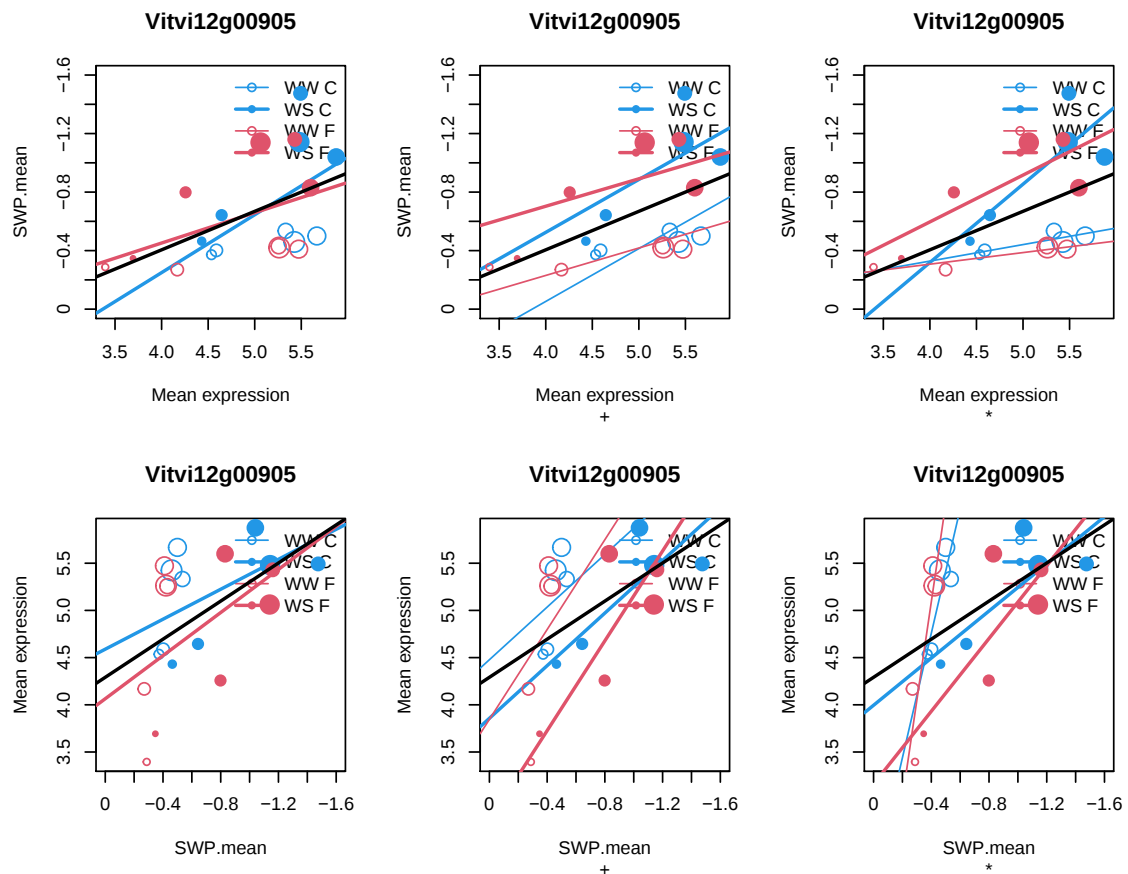
mitochondrial electron transport / ATP synthesis.alternative oxidase
cysteine-rich RECEPTOR-like kinase |
Chr4:12129485-12133157 FORWARD LENGTH=1043 |
201606

Coefficient swp for Vitvi12g00905.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi12g00905	9.541702	4.953541	13.39272	2.73731e-22	5.074001e-20

B

Vitvi12g00905	37.75885
---------------	----------



Correlation of all measurements (not just means): $r = 0.8381$, $r^2 = 0.7024$

Correlation of mean values (plots): $r_2 = 0.5153$

5.2.83 Vitvi08g01095

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

Vitvi08g01095

35.1.27

not assigned.no ontology.tetratricopeptide repeat (TPR)

Tetratricopeptide repeat (TPR)-like superfamily protein |

Chr2:15696365-15697366 REVERSE LENGTH=333 |

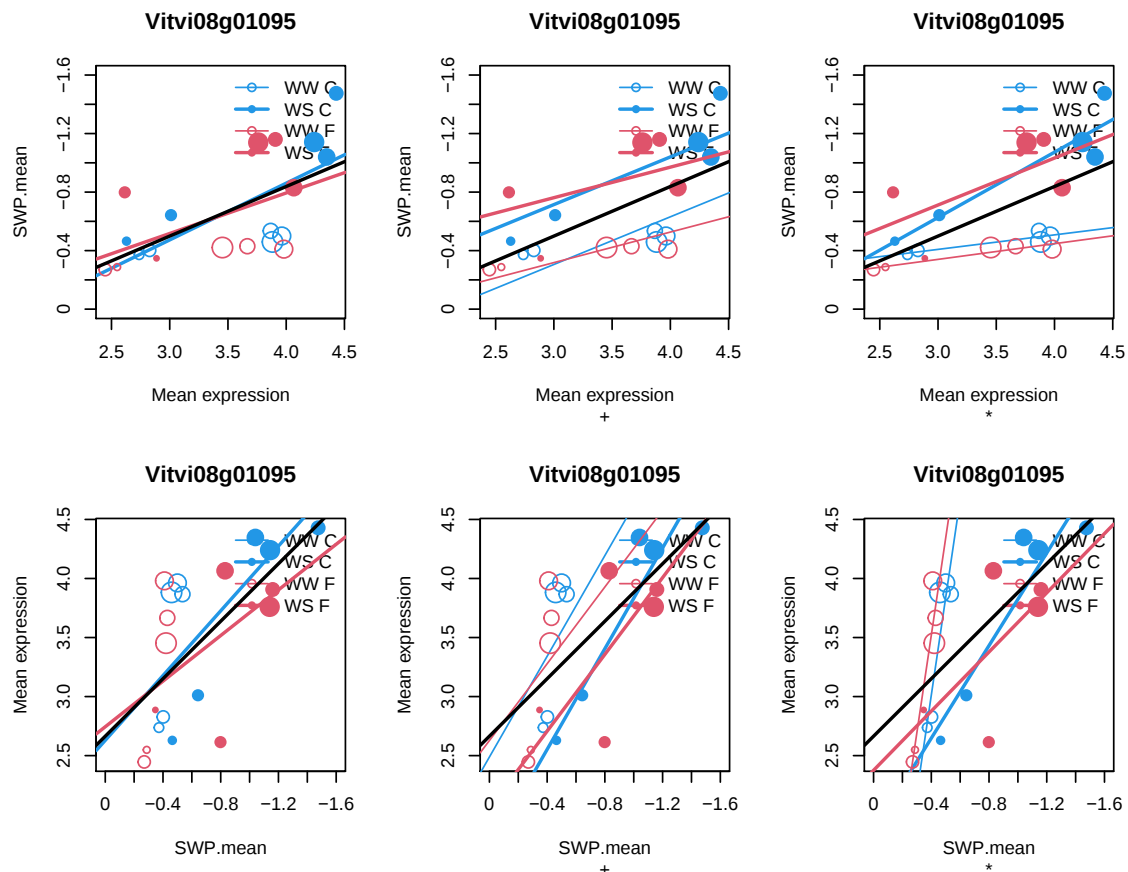
201606

Coefficient swp for Vitvi08g01095.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi08g01095	9.417669	3.463034	13.3905	2.763037e-22	5.074001e-20

B

Vitvi08g01095 37.75073



Correlation of all measurements (not just means): $r = 0.8383$, $r^2 = 0.7027$

Correlation of mean values (plots): $r_2 = 0.6423$

5.2.84 Vitvi16g01232

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

Vitvi16g01232

4.01.2014

glycolysis.cytosolic branch.pyruvate kinase (PK)

pyruvate kinase family protein |

Chr3:18222132-18224415 REVERSE LENGTH=710 |

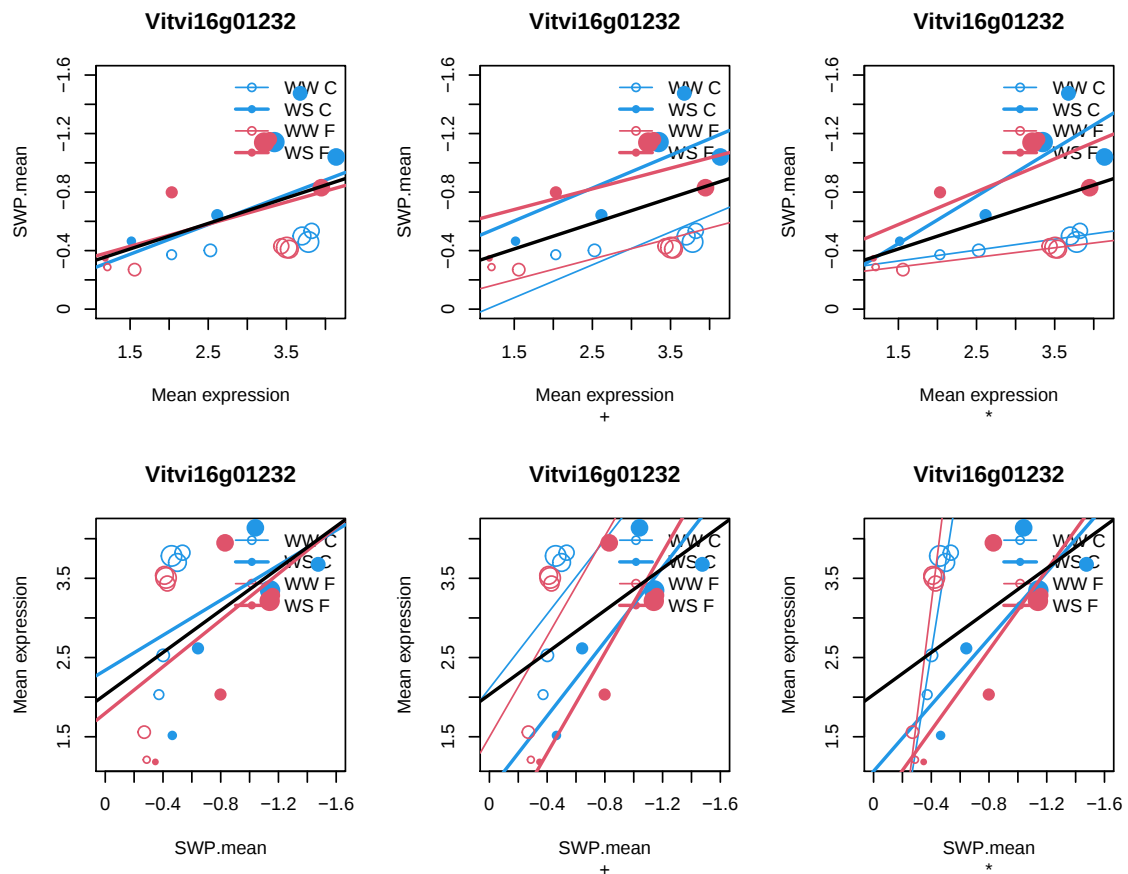
201606

Coefficient swp for Vitvi16g01232.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi16g01232	13.82526	2.903356	13.34277	3.377701e-22	6.128918e-20

B

Vitvi16g01232 37.57631



Correlation of all measurements (not just means): $r = 0.8324$, $r^2 = 0.6929$

Correlation of mean values (plots): $r_2 = 0.4813$

5.2.85 Vitvi12g01692

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

Vitvi12g01692

35.2

not assigned.unknown

UDP-Glycosyltransferase superfamily protein |

Chr3:7667099-7668556 FORWARD LENGTH=485 |

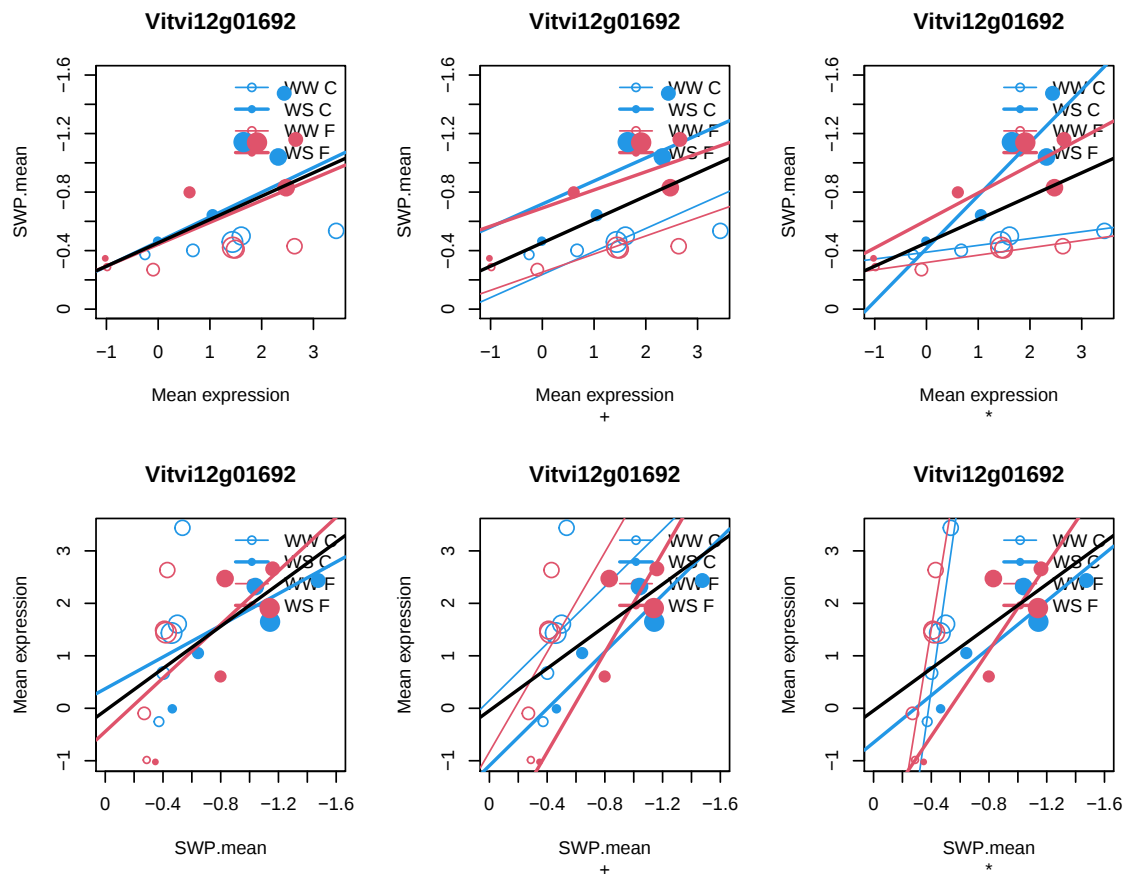
201606

Coefficient swp for Vitvi12g01692.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi12g01692	18.91374	1.272642	13.31795	3.750146e-22	6.724674e-20

B

Vitvi12g01692 37.48544



Correlation of all measurements (not just means): $r = 0.8300$, $r^2 = 0.6889$

Correlation of mean values (plots): $r_2 = 0.5658$

5.2.86 Vitvi01g00299

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

Vitvi01g00299

35.2

not assigned.unknown

transmembrane protein |

Chr1:8911463-8912329 REVERSE LENGTH=288 |

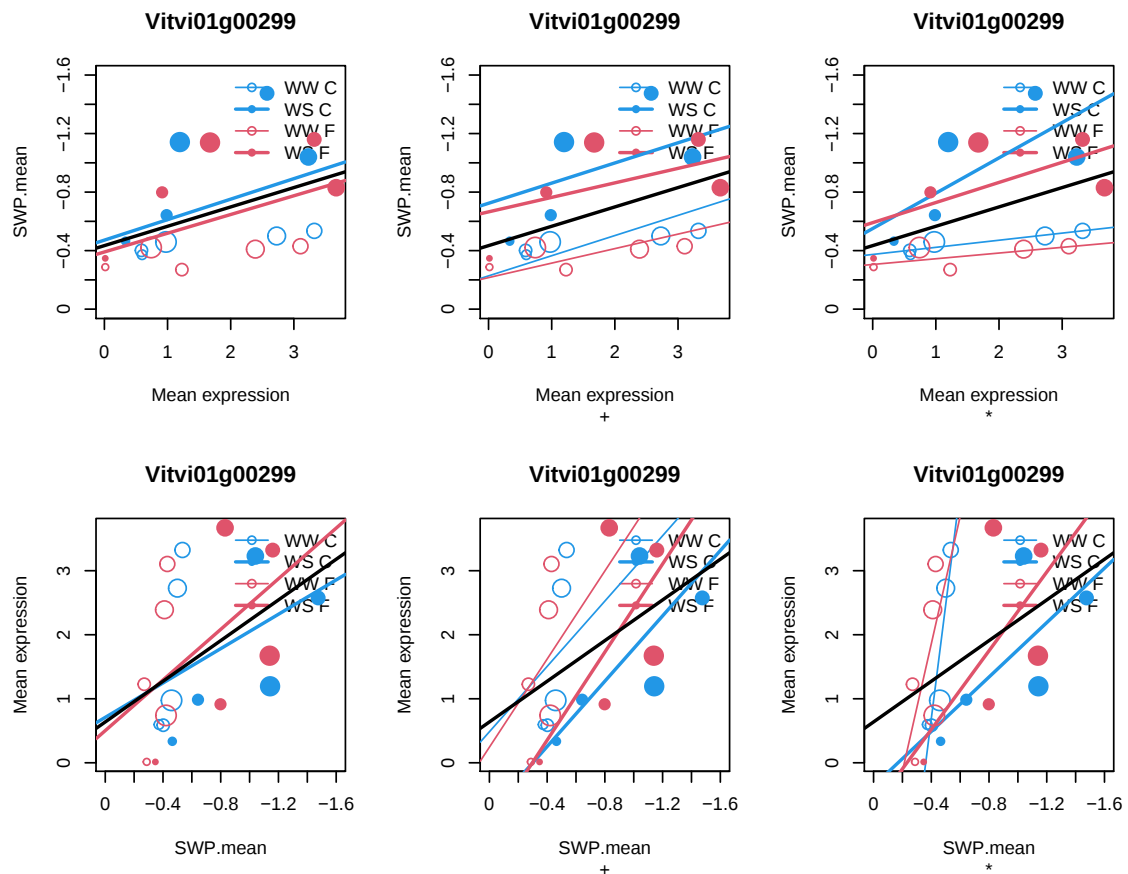
201606

Coefficient swp for Vitvi01g00299.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi01g00299	17.96672	1.679939	13.311	3.861608e-22	6.844026e-20

B

Vitvi01g00299 37.45999



Correlation of all measurements (not just means): $r = 0.8301$, $r^2 = 0.6891$

Correlation of mean values (plots): $r_2 = 0.4583$

5.2.87 Vitvi19g00514

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

Vitvi19g00514

26.28

misc.GDSL-motif lipase

GDSL-like Lipase/Acylhydrolase superfamily protein |

Chr5:22337745-22339741 FORWARD LENGTH=376 |

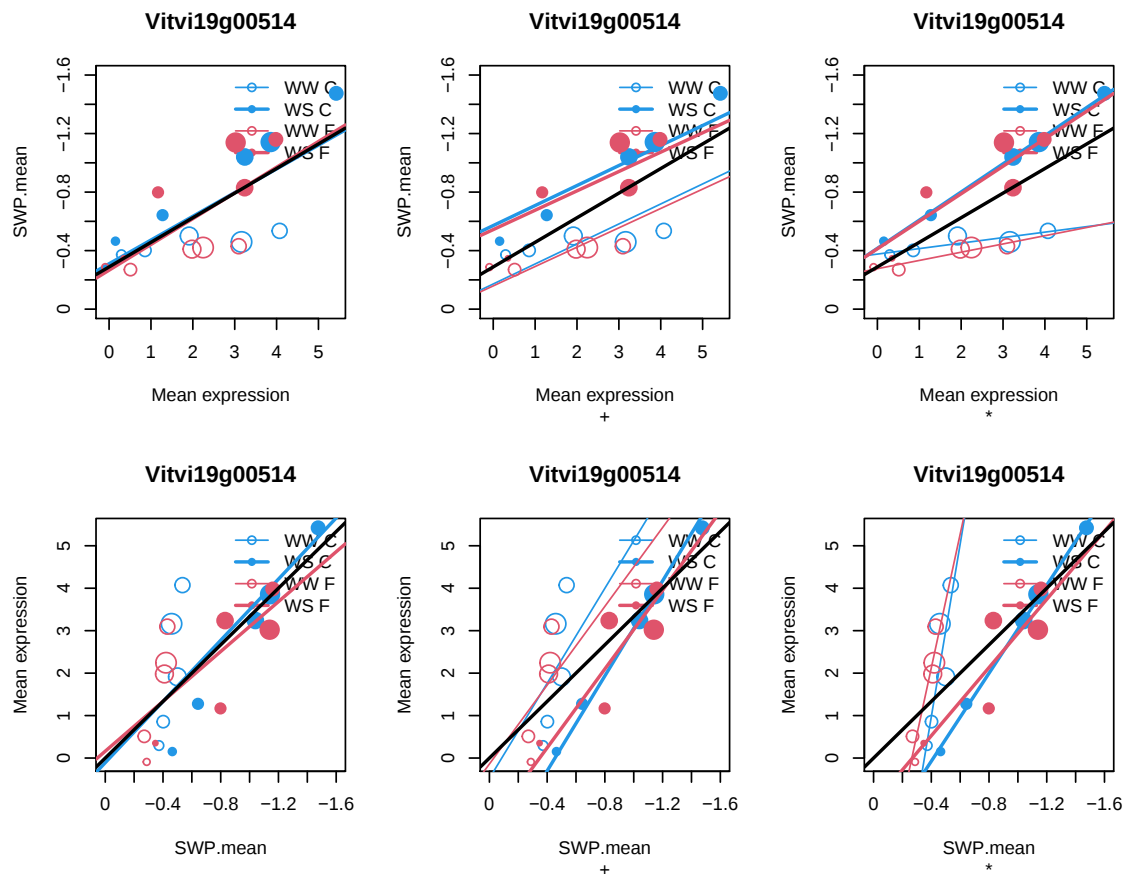
201606

Coefficient swp for Vitvi19g00514.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi19g00514	22.44871	2.187538	13.29585	4.116307e-22	7.21158e-20

B

Vitvi19g00514 37.40448



Correlation of all measurements (not just means): $r = 0.8289$, $r^2 = 0.6871$

Correlation of mean values (plots): $r_2 = 0.7487$

5.2.88 Vitvi02g00387

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

Vitvi02g00387

27.03.2023

RNA.regulation of transcription.heat-shock transcription factor family
winged-helix DNA-binding transcription factor family protein |
Chr4:7043006-7044227 FORWARD LENGTH=377 |
201606

Vitvi02g00387

20.02.2001

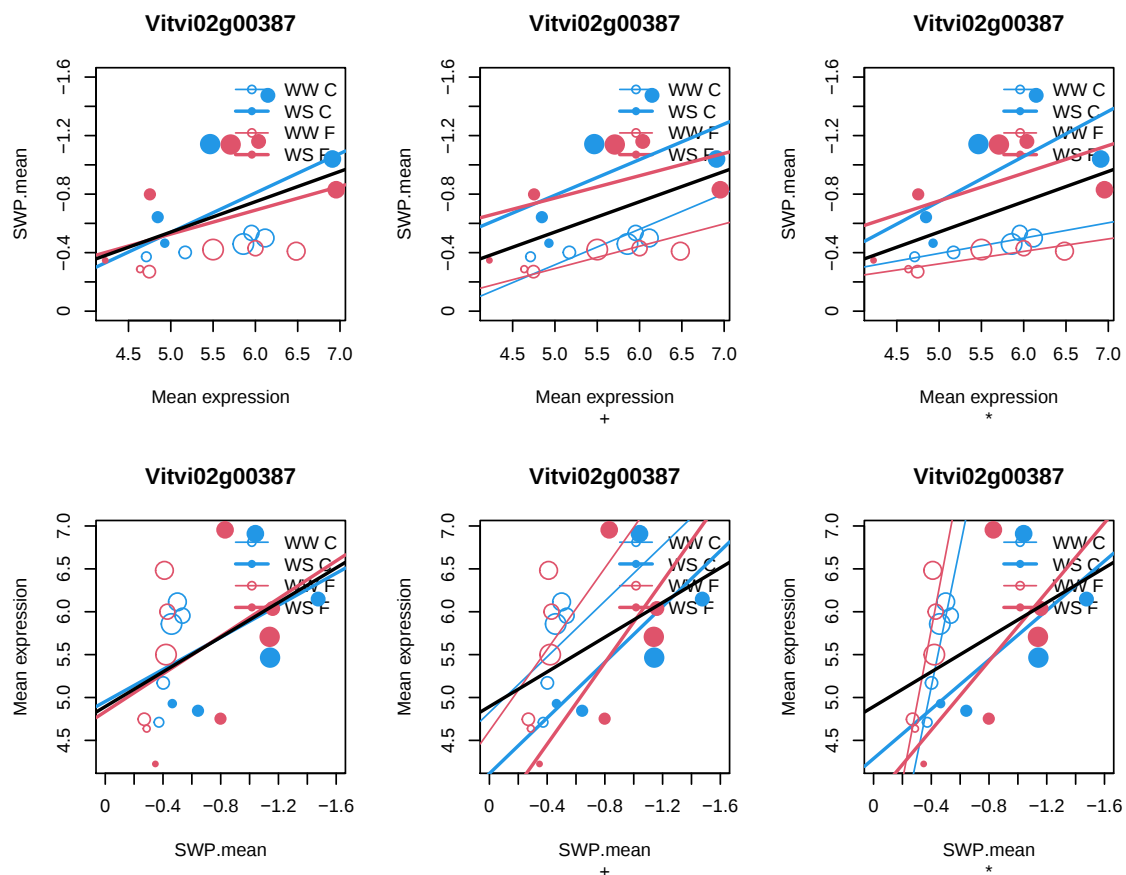
stress.abiotic.heat
winged-helix DNA-binding transcription factor family protein |
Chr4:7043006-7044227 FORWARD LENGTH=377 |
201606

Coefficient swp for Vitvi02g00387.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi02g00387	10.91598	5.55751	13.28519	4.305763e-22	7.457778e-20

B

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi02g00387	37.36537				



Correlation of all measurements (not just means): $r = 0.8338$, $r^2 = 0.6953$
Correlation of mean values (plots): $r_2 = 0.4578$

5.2.89 Vitvi05g00410

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

Vitvi05g00410

26.03.2005

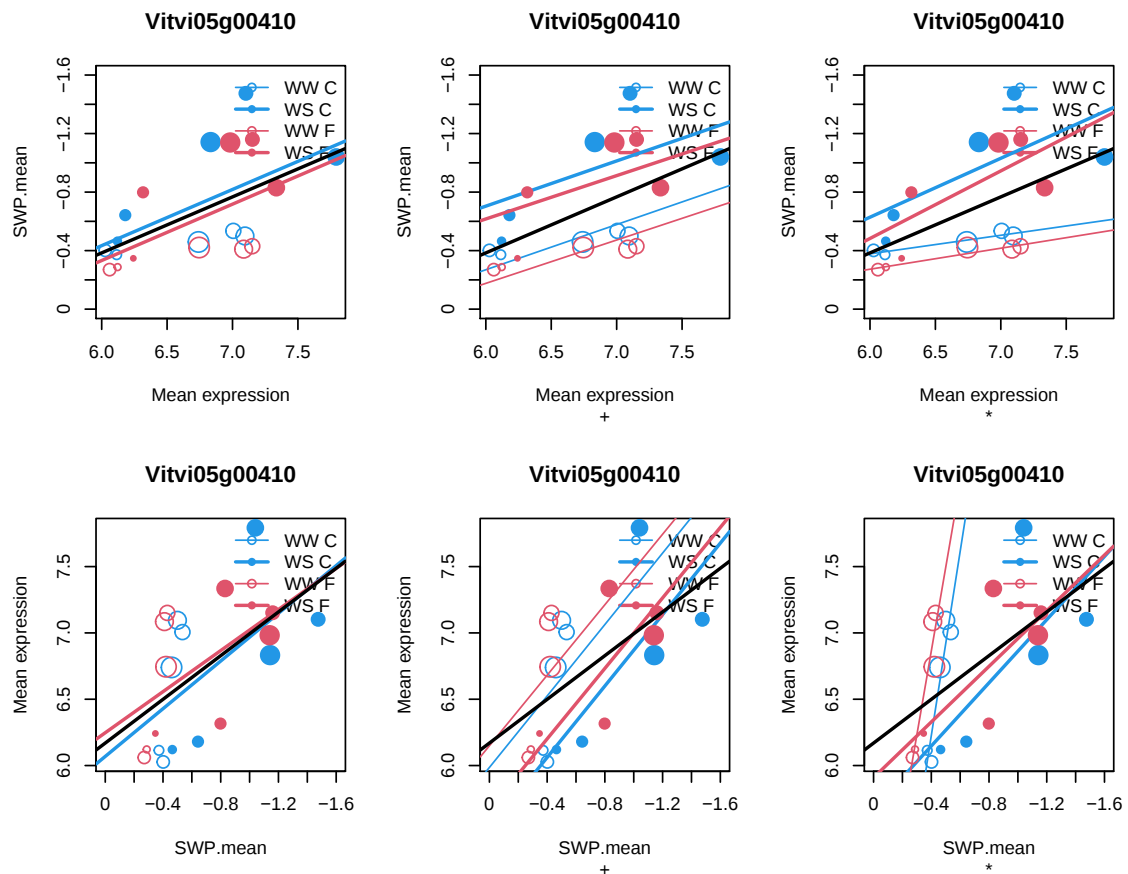
misc.gluco-, galacto- and mannosidases.glycosyl hydrolase family 5
alpha/beta-Hydrolases superfamily protein |
Chr3:8473833-8475655 FORWARD LENGTH=239 |
201606

Coefficient swp for Vitvi05g00410.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi05g00410	7.422891	6.710099	13.26093	4.769928e-22	8.168903e-20

B

Vitvi05g00410 37.27636



Correlation of all measurements (not just means): $r = 0.8413$, $r^2 = 0.7078$

Correlation of mean values (plots): $r_2 = 0.5615$

5.2.90 Vitvi13g02028

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

Vitvi13g02028

35.2

not assigned.unknown

UDP-Glycosyltransferase superfamily protein |

Chr1:7903851-7906607 REVERSE LENGTH=489 |

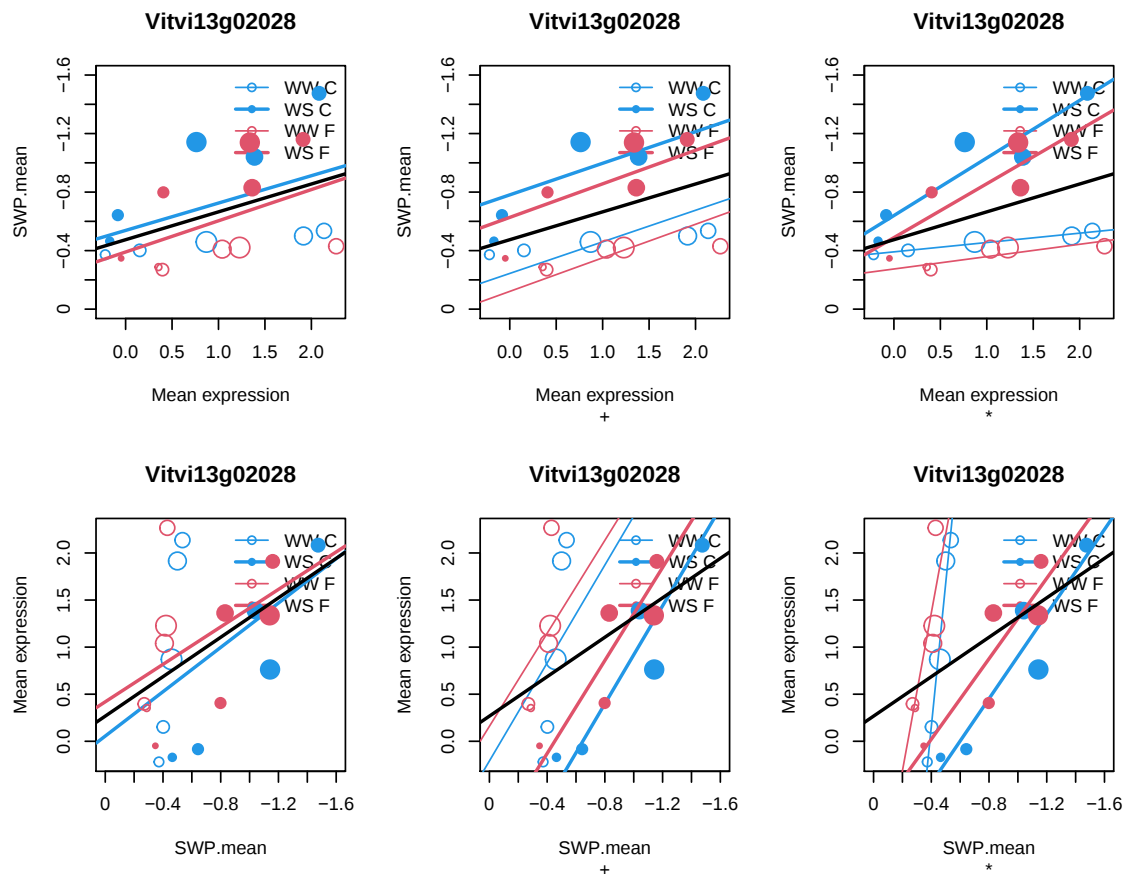
201606

Coefficient swp for Vitvi13g02028.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi13g02028	12.70639	0.9543269	13.24466	5.109203e-22	8.652719e-20

B

Vitvi13g02028	37.21661
---------------	----------



Correlation of all measurements (not just means): $r = 0.8312$, $r^2 = 0.6910$

Correlation of mean values (plots): $r_2 = 0.4464$

5.2.91 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 |

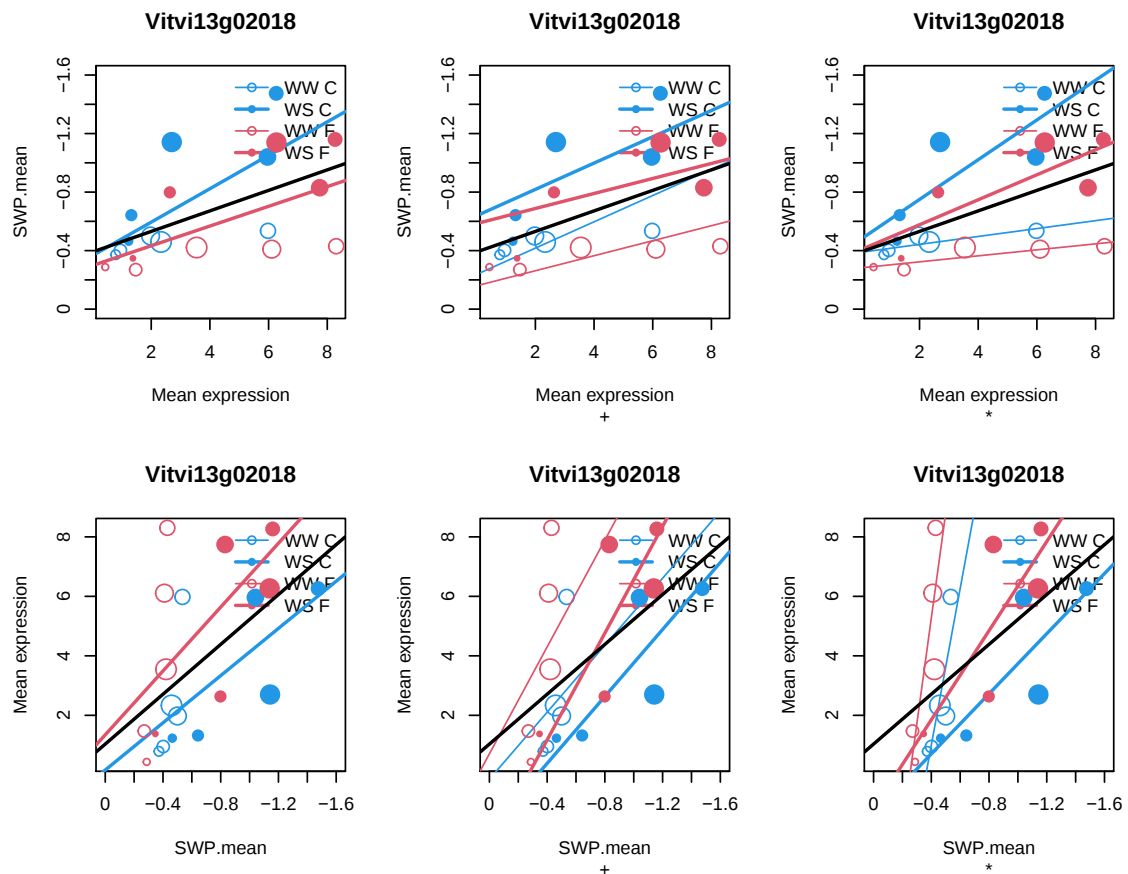
201606

Coefficient swp for Vitvi13g02018.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi13g02018	38.12168	3.782728	13.21065	5.898826e-22	9.88021e-20

B

Vitvi13g02018 37.09159



Correlation of all measurements (not just means): $r = 0.8262$, $r^2 = 0.6826$

Correlation of mean values (plots): $r_2 = 0.5420$

5.2.92 Vitvi03g00322

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

Vitvi03g00322

11.1

lipid metabolism.FA synthesis and FA elongation

3-ketoacyl-CoA synthase 4 |

Chr1:6729119-6730669 FORWARD LENGTH=516 |

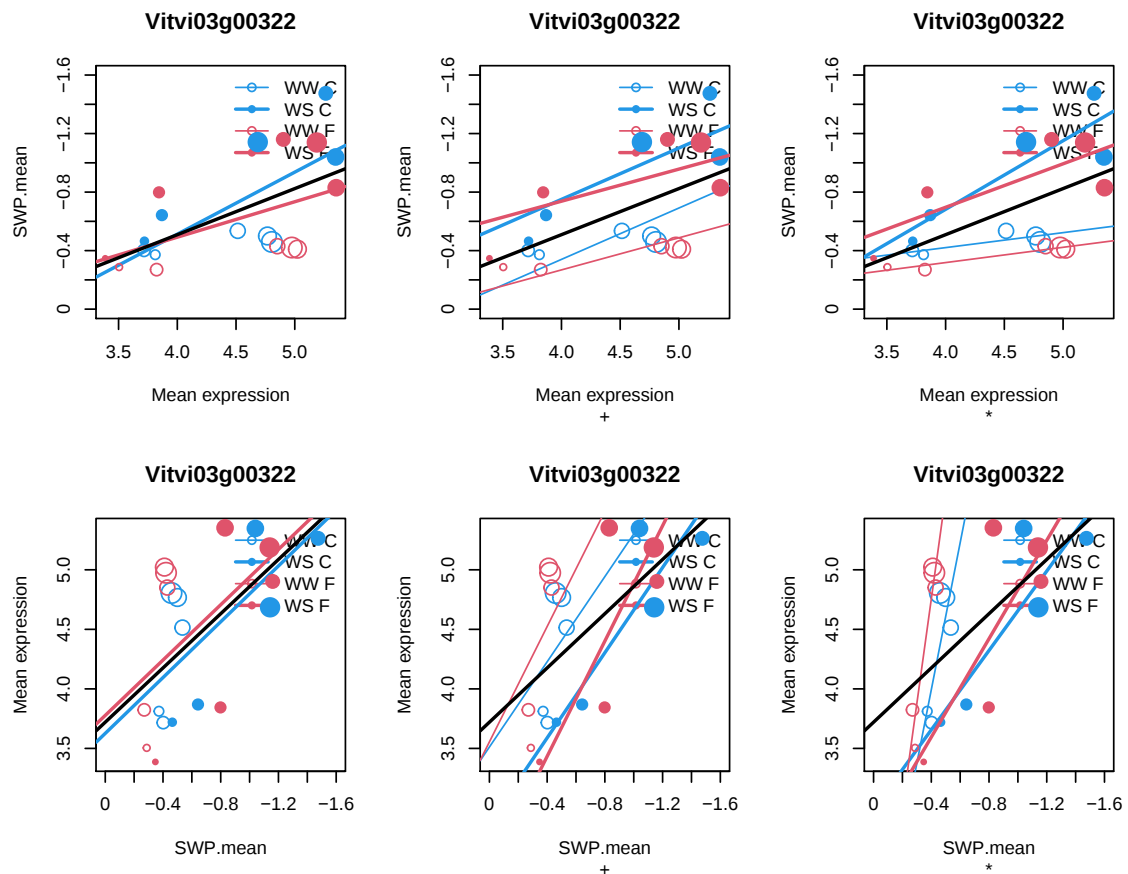
201606

Coefficient swp for Vitvi03g00322.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi03g00322	9.353941	4.467597	13.19577	6.281978e-22	1.04076e-19

B

Vitvi03g00322 37.03683



Correlation of all measurements (not just means): $r = 0.8344$, $r^2 = 0.6963$

Correlation of mean values (plots): $r_2 = 0.5990$

5.2.93 Vitvi06g00234

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

Vitvi06g00234

11.9.2.1

lipid metabolism.lipid degradation.lipases.triacylglycerol lipase

alpha/beta-Hydrolases superfamily protein |

Chr1:19070971-19072554 FORWARD LENGTH=527 |

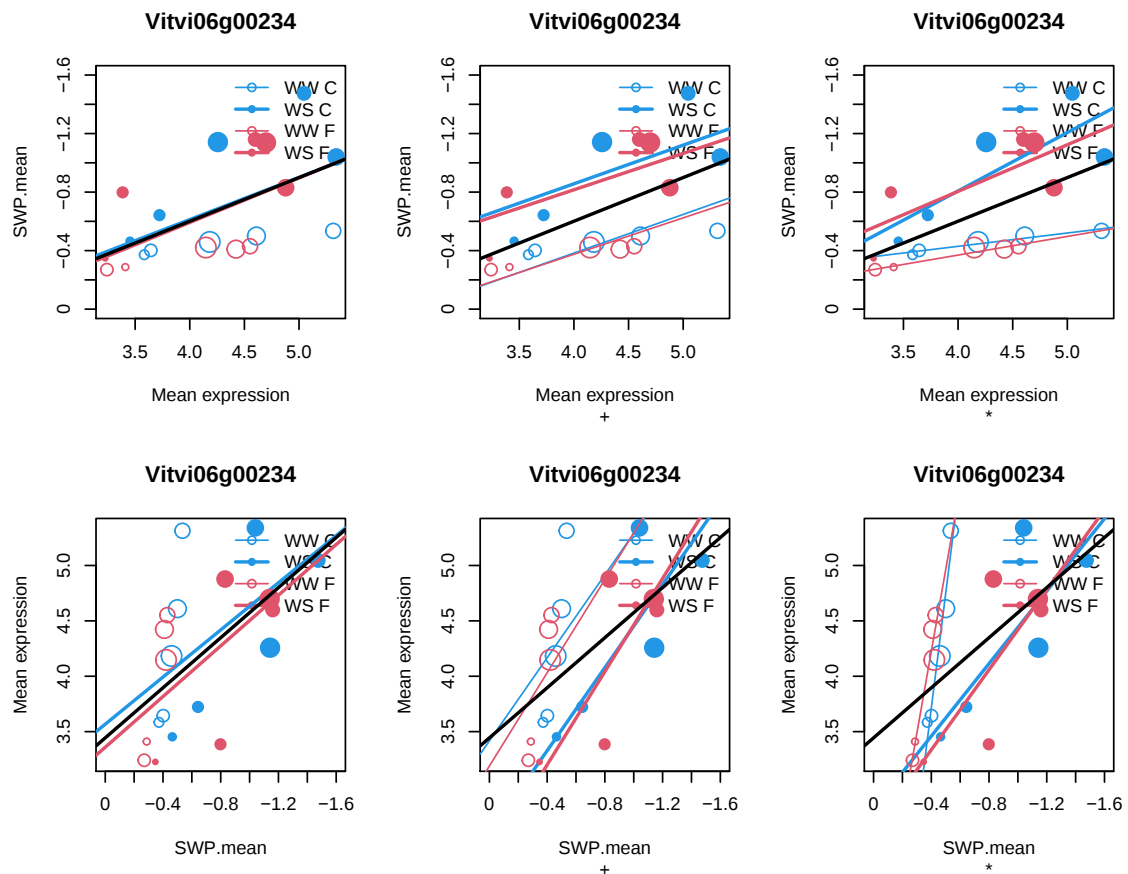
201606

Coefficient swp for Vitvi06g00234.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi06g00234	10.06485	4.185581	13.18889	6.467481e-22	1.059971e-19

B

Vitvi06g00234 37.0115



Correlation of all measurements (not just means): $r = 0.8331$, $r^2 = 0.6940$

Correlation of mean values (plots): $r_2 = 0.5807$

5.2.94 Vitvi06g00032

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

Vitvi06g00032

29.6

protein.folding

TCP-1/cpn60 chaperonin family protein |

Chr3:4389685-4392624 FORWARD LENGTH=596 |

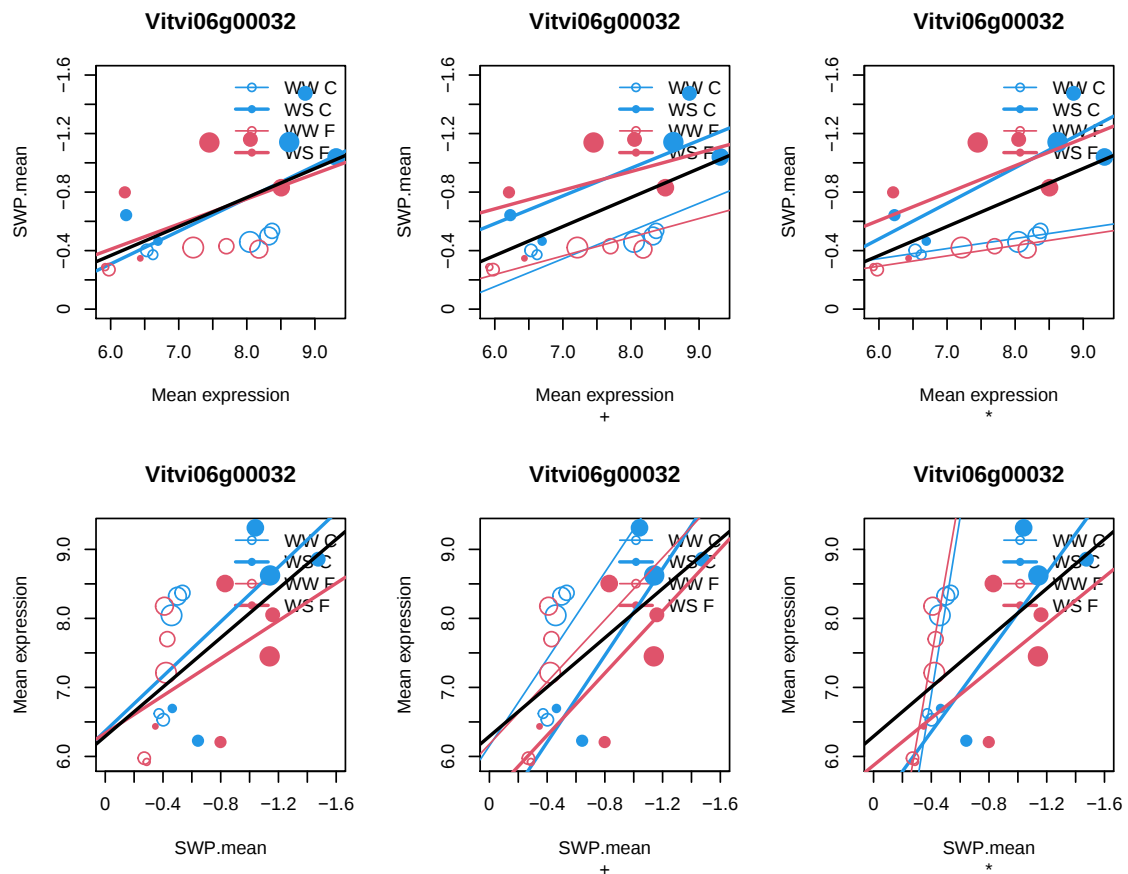
201606

Coefficient swp for Vitvi06g00032.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi06g00032	14.54823	7.462036	13.16656	7.108177e-22	1.152583e-19

B

Vitvi06g00032 36.92927



Correlation of all measurements (not just means): $r = 0.8285$, $r^2 = 0.6864$

Correlation of mean values (plots): $r_2 = 0.5948$

5.2.95 Vitvi07g01566

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

Vitvi07g01566

29.6

protein.folding

TCP-1/cpn60 chaperonin family protein |

Chr3:3732734-3736156 FORWARD LENGTH=557 |

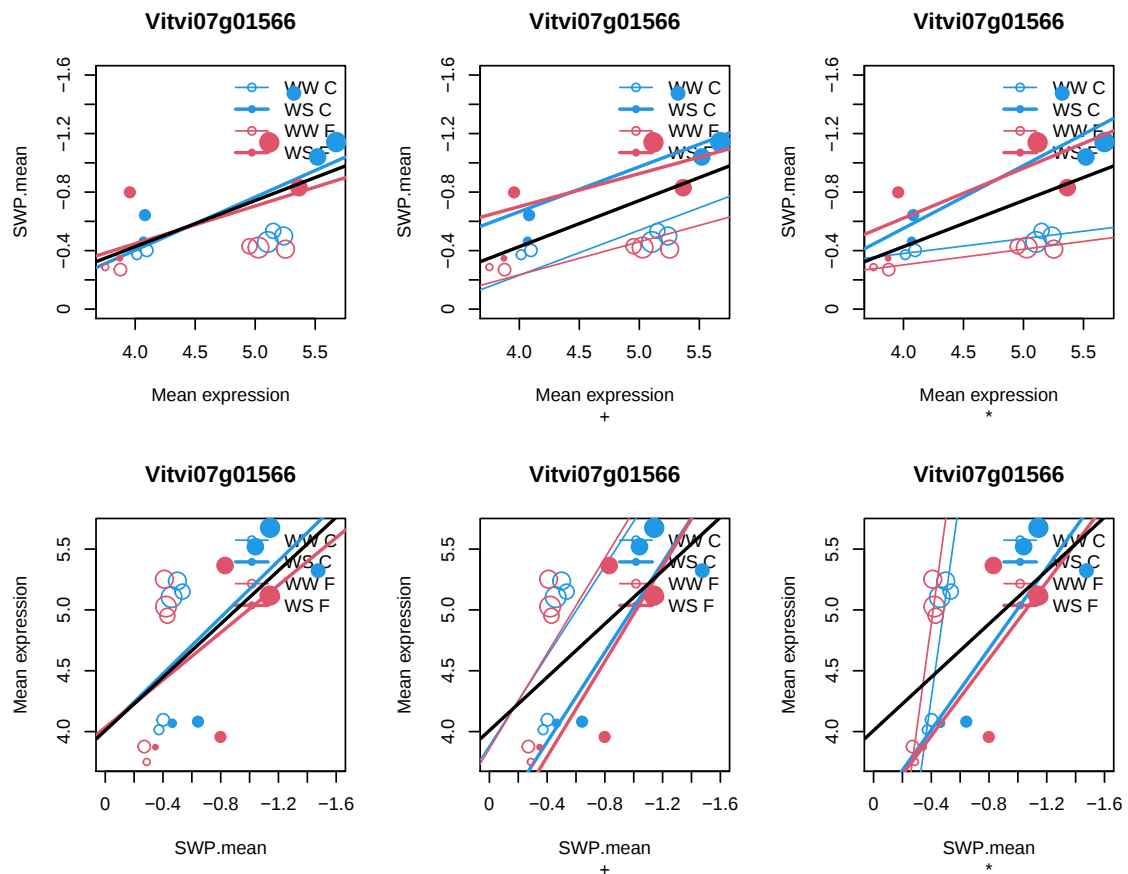
201606

Coefficient swp for Vitvi07g01566.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi07g01566	9.151224	4.727572	13.04688	1.180734e-21	1.881576e-19

B

Vitvi07g01566 36.4871



Correlation of all measurements (not just means): $r = 0.8318$, $r^2 = 0.6918$

Correlation of mean values (plots): $r_2 = 0.5874$

5.2.96 Vitvi04g00871

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

Vitvi04g00871

20

stress

Adenine nucleotide alpha hydrolases-like superfamily protein |

Chr3:762136-763075 REVERSE LENGTH=159 |

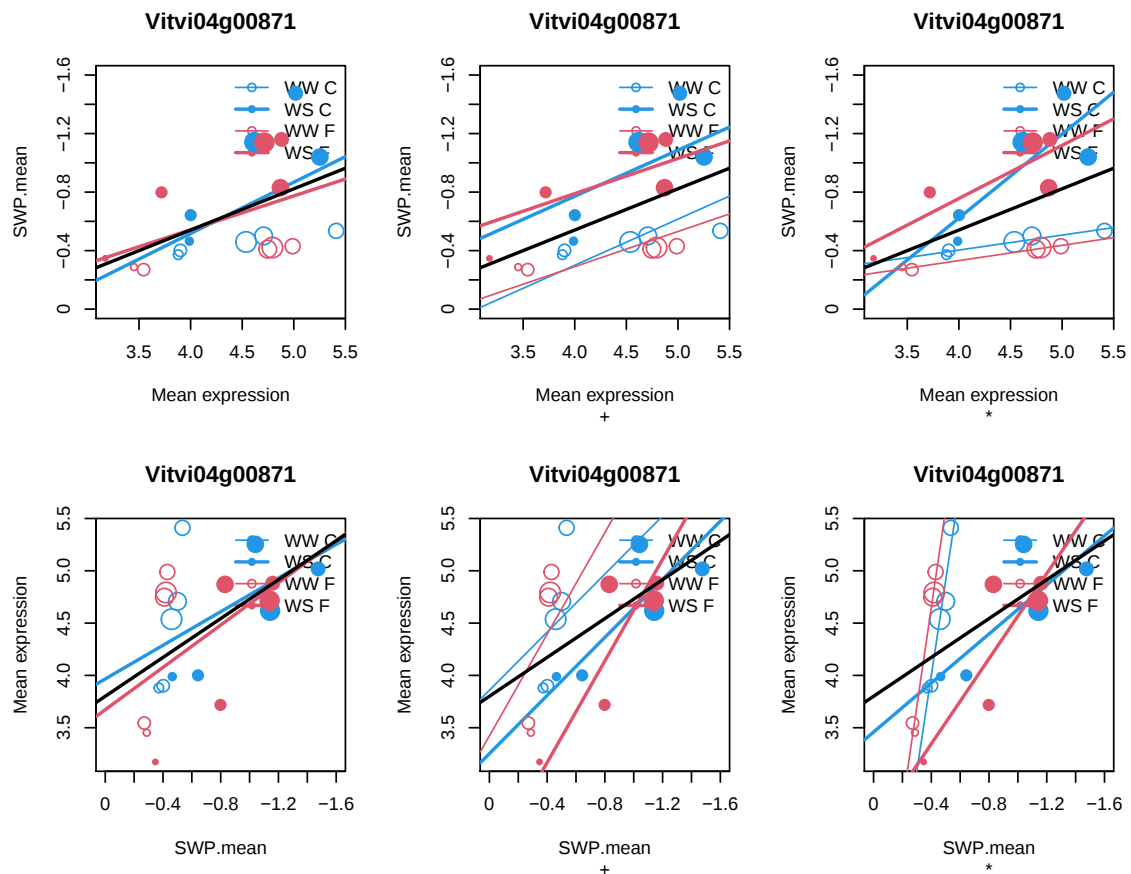
201606

Coefficient swp for Vitvi04g00871.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi04g00871	9.542879	4.409863	13.04511	1.189651e-21	1.881576e-19

B

Vitvi04g00871 36.48054



Correlation of all measurements (not just means): $r = 0.8310$, $r^2 = 0.6905$

Correlation of mean values (plots): $r_2 = 0.5114$

5.2.97 Vitvi08g01887

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

Vitvi08g01887

35.2

not assigned.unknown

Remorin family protein |

Chr2:17471119-17472519 REVERSE LENGTH=274 |

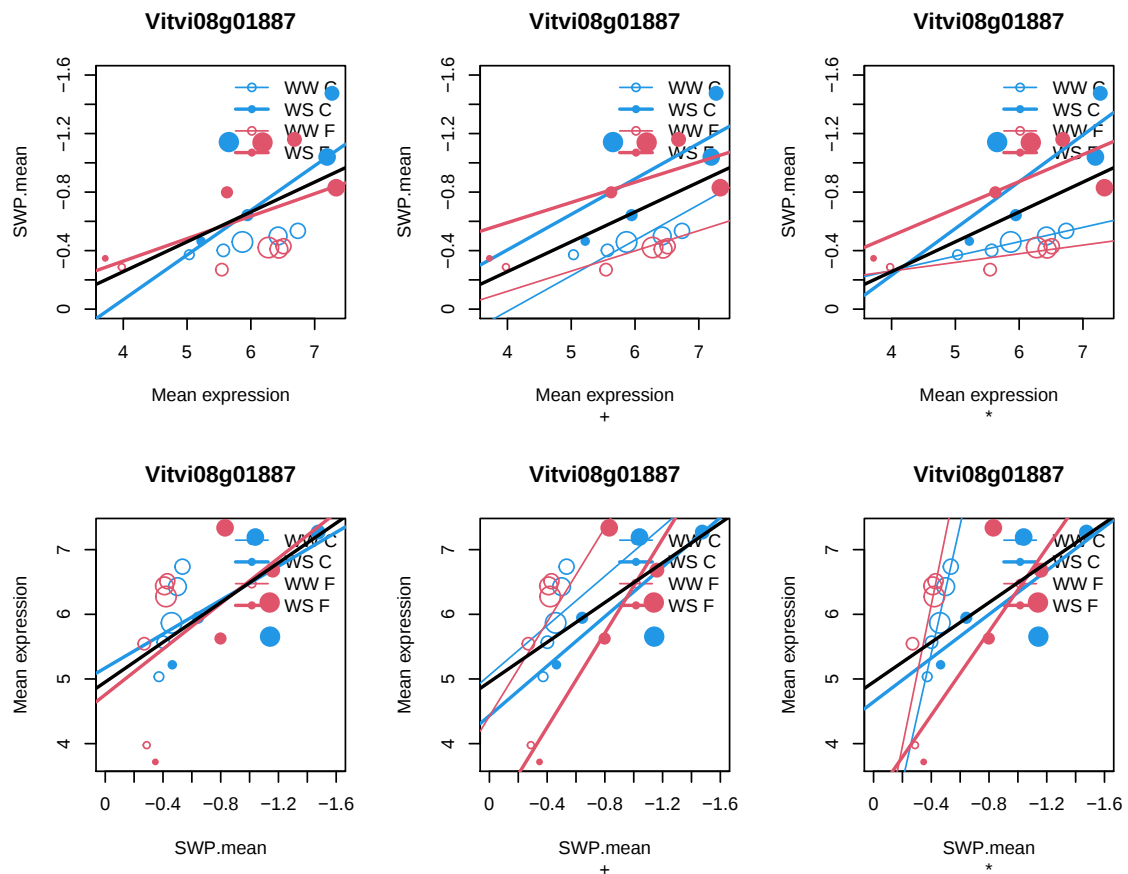
201606

Coefficient swp for Vitvi08g01887.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi08g01887	13.47736	5.960886	13.04358	1.197434e-21	1.881576e-19

B

Vitvi08g01887	36.47486
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Correlation of all measurements (not just means): $r = 0.8266$, $r^2 = 0.6832$

Correlation of mean values (plots): $r_2 = 0.5598$

5.2.98 Vitvi05g00170

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

Vitvi05g00170

3.1.1.1

minor CHO metabolism.raffinose family.galactinol synthases.known
galactinol synthase 3 |

Chr1:3019888-3021214 FORWARD LENGTH=334 |

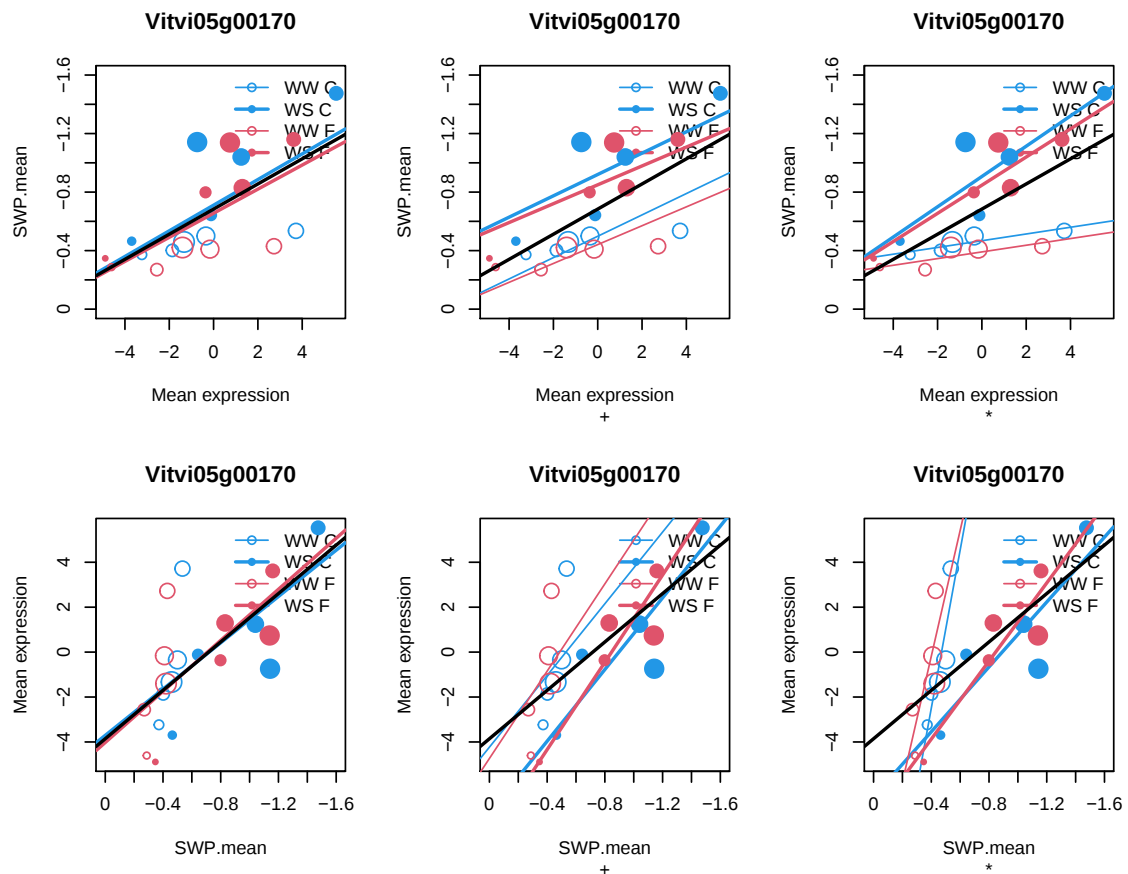
201606

Coefficient swp for Vitvi05g00170.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi05g00170	40.24486	-0.3218907	13.03767	1.227827e-21	1.909647e-19

B

Vitvi05g00170 36.453



Correlation of all measurements (not just means): $r = 0.8227$, $r^2 = 0.6768$

Correlation of mean values (plots): $r_2 = 0.6801$

5.2.99 Vitvi14g01732

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

Vitvi14g01732

8.01.2004

TCA / organic transformation.TCA.IDH

Isocitrate/isopropylmalate dehydrogenase family protein |

Chr5:4703533-4706627 REVERSE LENGTH=485 |

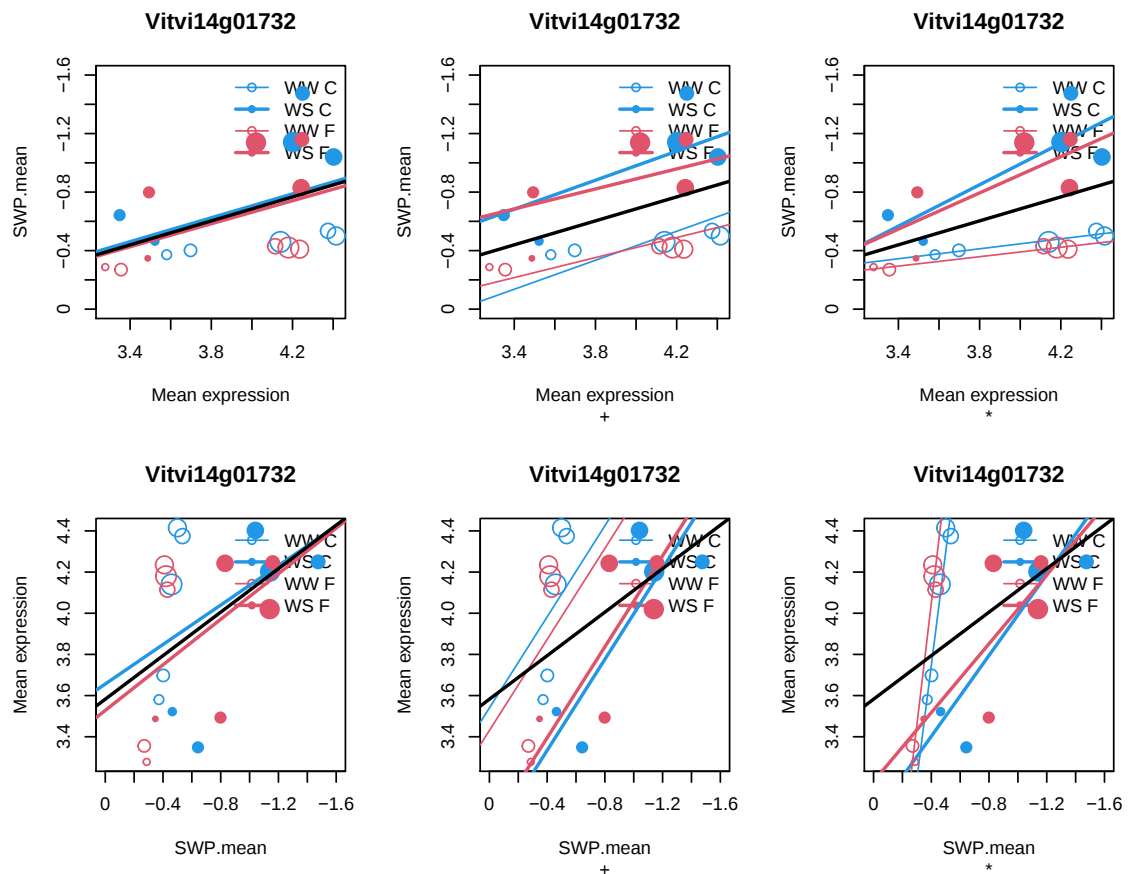
201606

Coefficient swp for Vitvi14g01732.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi14g01732	5.825565	3.929213	12.99162	1.493359e-21	2.299169e-19

B

Vitvi14g01732 36.28221



Correlation of all measurements (not just means): $r = 0.8449$, $r^2 = 0.7138$

Correlation of mean values (plots): $r_2 = 0.4652$

5.2.100 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 |

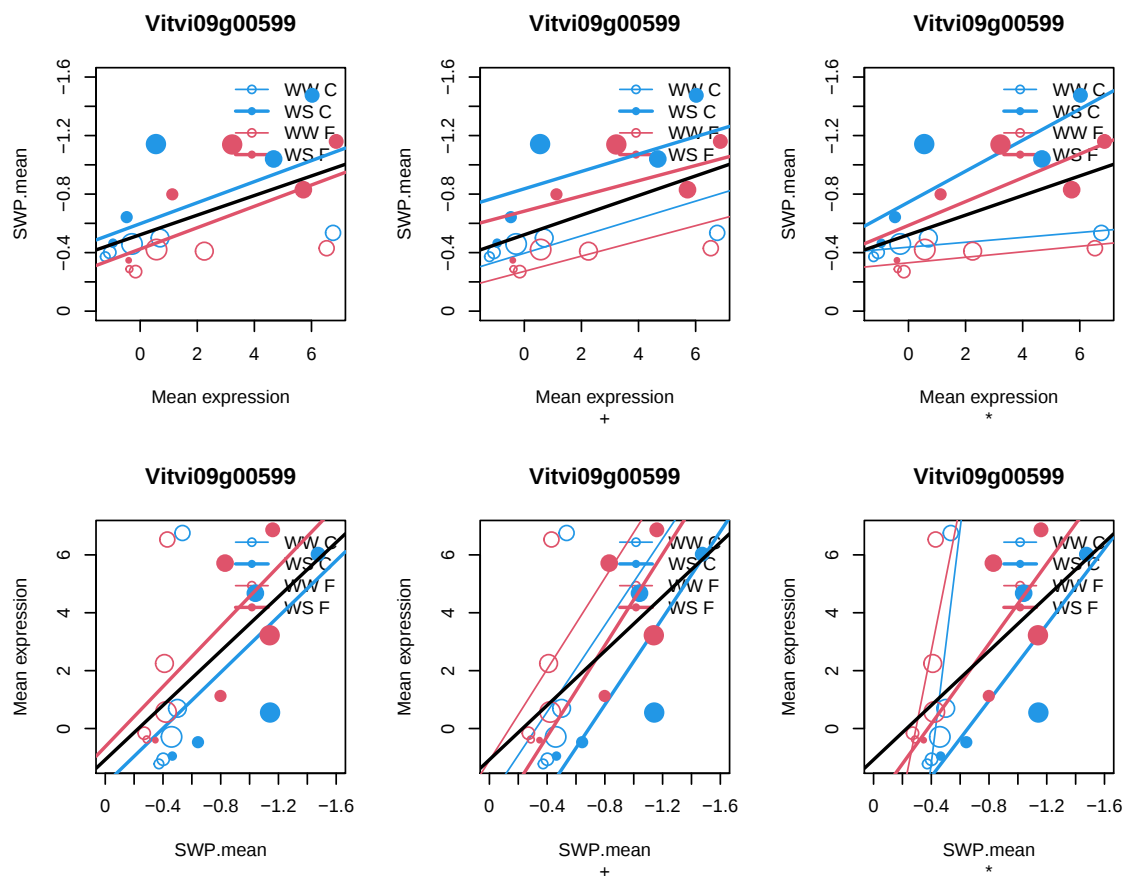
201606

Coefficient swp for Vitvi09g00599.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi09g00599	41.39061	2.002367	12.97348	1.613201e-21	2.458841e-19

B

Vitvi09g00599 36.21484



Correlation of all measurements (not just means): $r = 0.8213$, $r^2 = 0.6746$

Correlation of mean values (plots): $r_2 = 0.5606$

5.3 Bottom 100 genes

Plots of situation for top 100 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 Vitvi16g01964

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

Vitvi16g01964

35.2

not assigned.unknown

disease resistance family protein / LRR family protein |

Chr2:14737169-14739886 REVERSE LENGTH=905 |

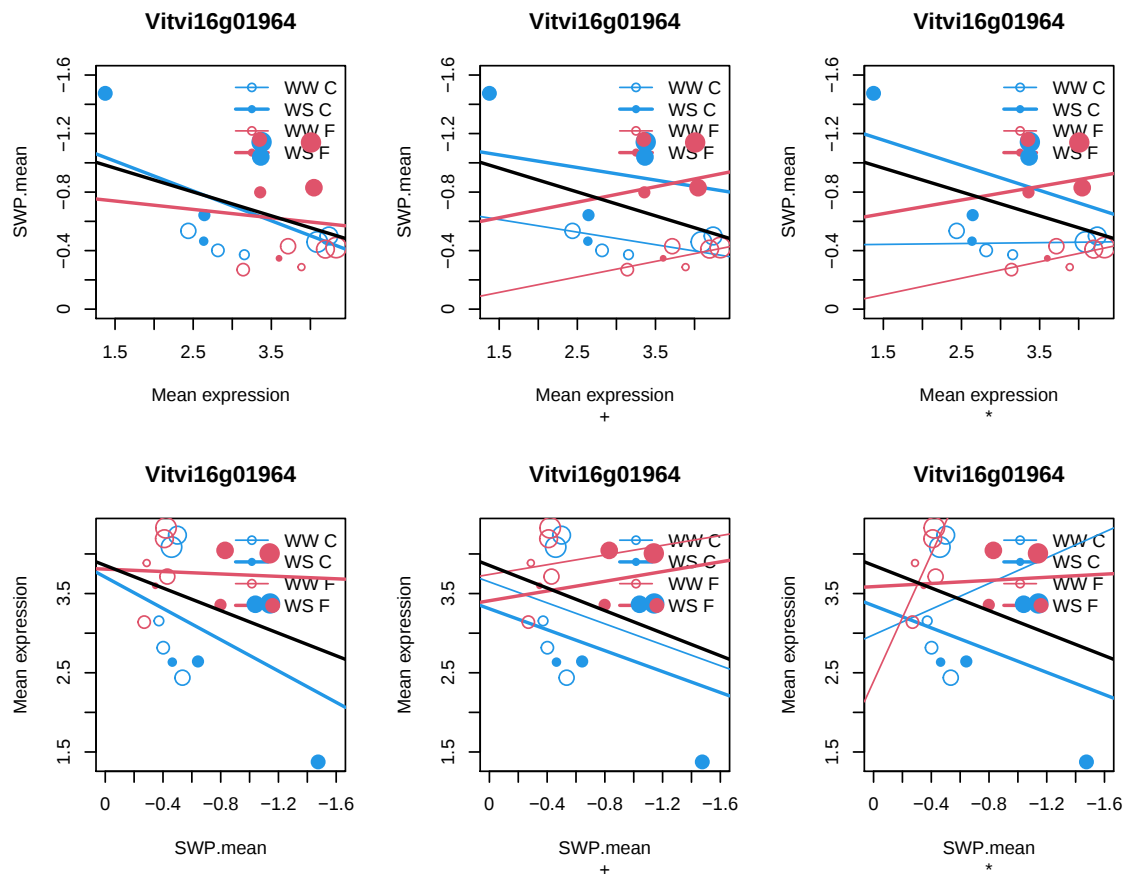
201606

Coefficient swp for Vitvi16g01964.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi16g01964	0.05162801	3.38731	0.03589914	0.9714506	0.9778016

B

Vitvi16g01964 -6.117166



Correlation of all measurements (not just means): $r = 0.0040$, $r^2 = 2e - 05$

Correlation of mean values (plots): $r_2 = -0.3408$

5.3.2 Vitvi10g02400

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

Vitvi10g02400

35.2

not assigned.unknown

transmembrane protein |

Chr4:9262019-9262576 REVERSE LENGTH=185 |

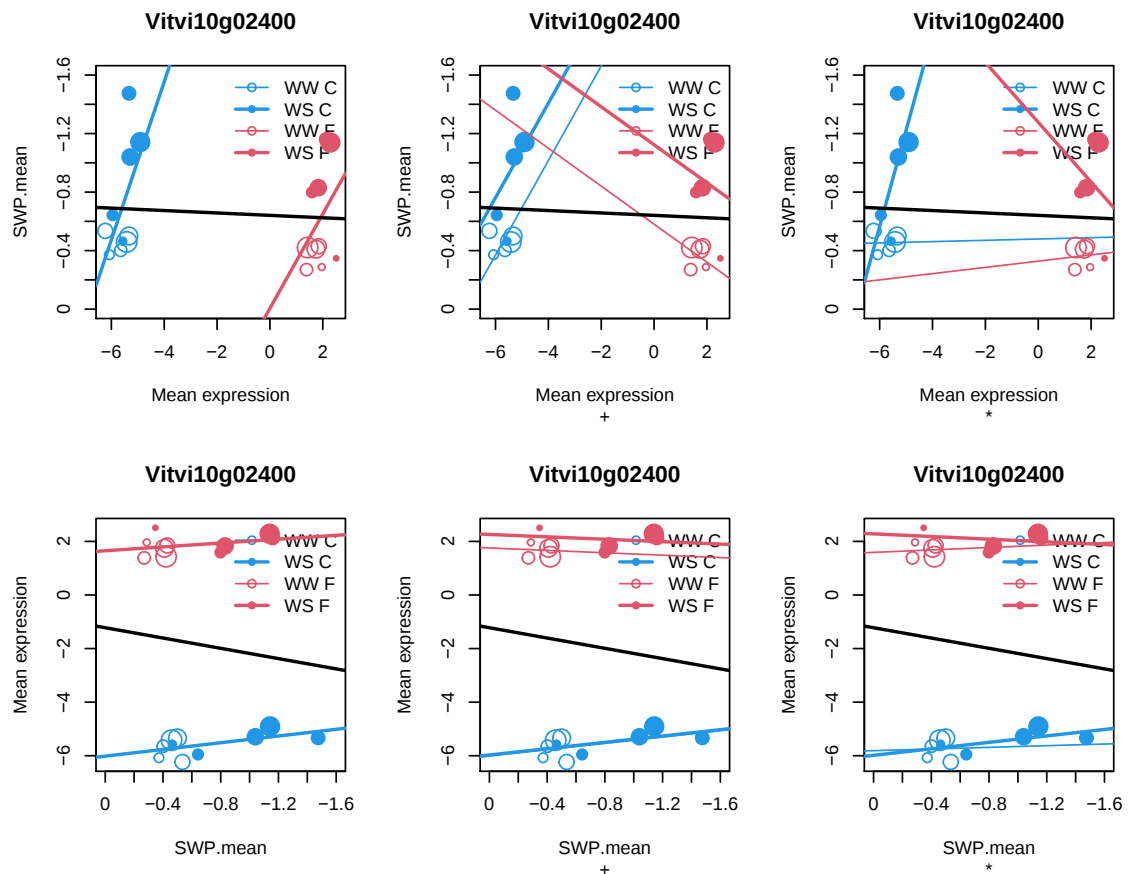
201606

Coefficient swp for Vitvi10g02400.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi10g02400	0.2374713	-1.852567	0.03459238	0.9724894	0.9787451

B

Vitvi10g02400 -6.117211



Correlation of all measurements (not just means): $r = 0.0038, r^2 = 1e - 05$

Correlation of mean values (plots): $r_2 = -0.0889$

5.3.3 Vitvi01g00632

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

Vitvi01g00632

18.7

Co-factor and vitamine metabolism.iron-sulphur clusters
sulfur E2 |

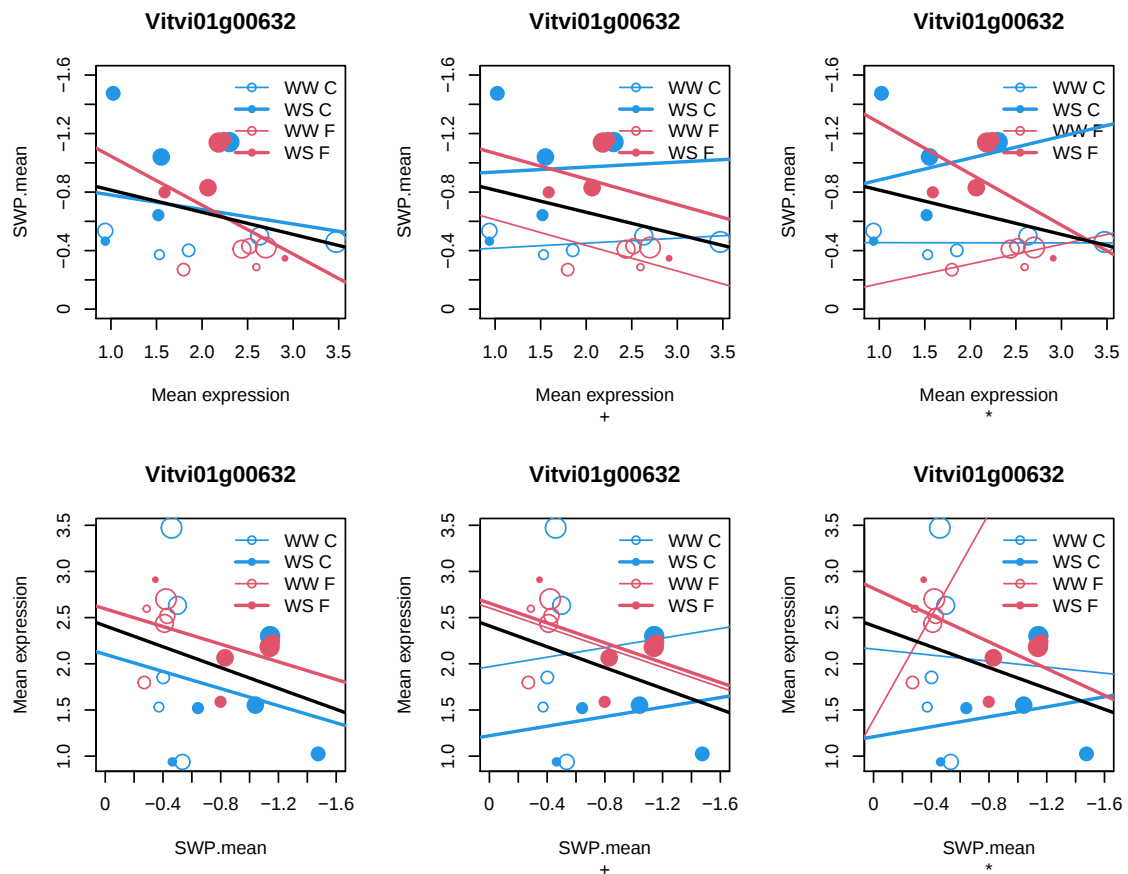
Chr1:25426488-25427264 FORWARD LENGTH=258 |
201606

Coefficient swp for Vitvi01g00632.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi01g00632	0.04787974	2.039923	0.03455841	0.9725164	0.9787451

B

Vitvi01g00632 -6.117212



Correlation of all measurements (not just means): $r = 0.0039, r^2 = 1e - 05$

Correlation of mean values (plots): $r_2 = -0.2924$

5.3.4 Vitvi18g02720

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

Vitvi18g02720

26.1

misc.cytochrome P450

cytochrome P450%2C family 82%2C subfamily C%2C polypeptide 4 |

Chr4:15452040-15453966 FORWARD LENGTH=524 |

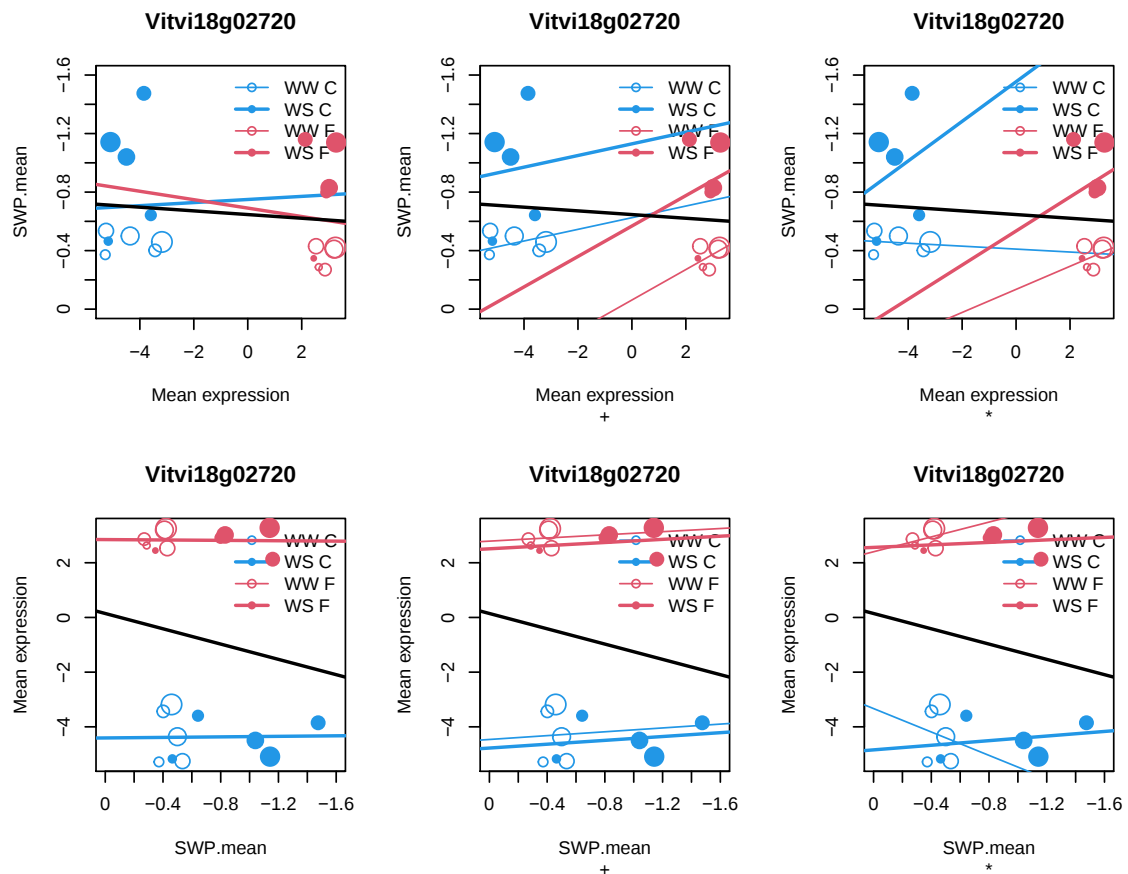
201606

Coefficient swp for Vitvi18g02720.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi18g02720	-0.2330786	-0.7730861	-0.0342779	0.9727394	0.9789049

B

Vitvi18g02720 -6.117221



Correlation of all measurements (not just means): $r = -0.0038$, $r^2 = 1e - 05$

Correlation of mean values (plots): $r_2 = -0.1327$

5.3.5 Vitvi15g00744

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

Vitvi15g00744

30.8

signalling.misc

Ku80 family protein |

Chr1:17723498-17726730 FORWARD LENGTH=663 |

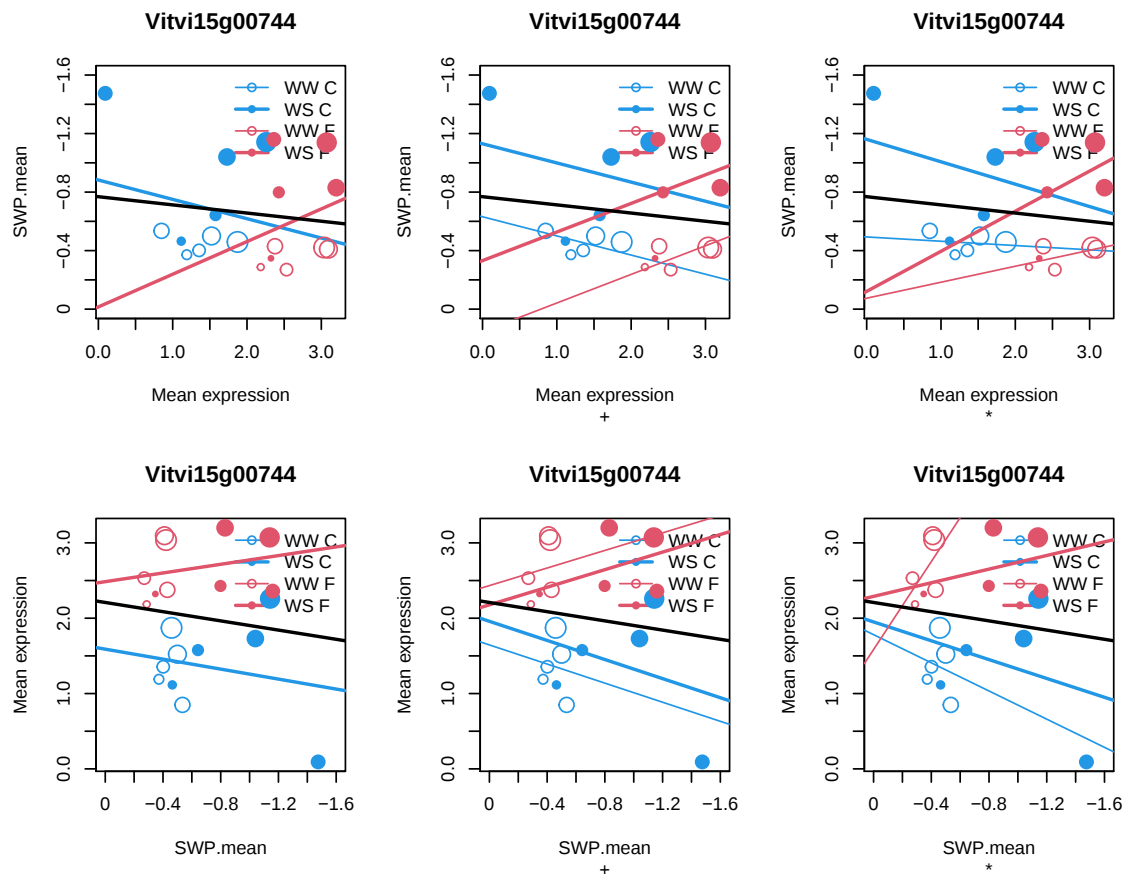
201606

Coefficient swp for Vitvi15g00744.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi15g00744	-0.0523988	2.008607	-0.03399821	0.9729617	0.979064

B

Vitvi15g00744 -6.11723



Correlation of all measurements (not just means): $r = -0.0038$, $r^2 = 1e - 05$

Correlation of mean values (plots): $r_2 = -0.1307$

5.3.6 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 |

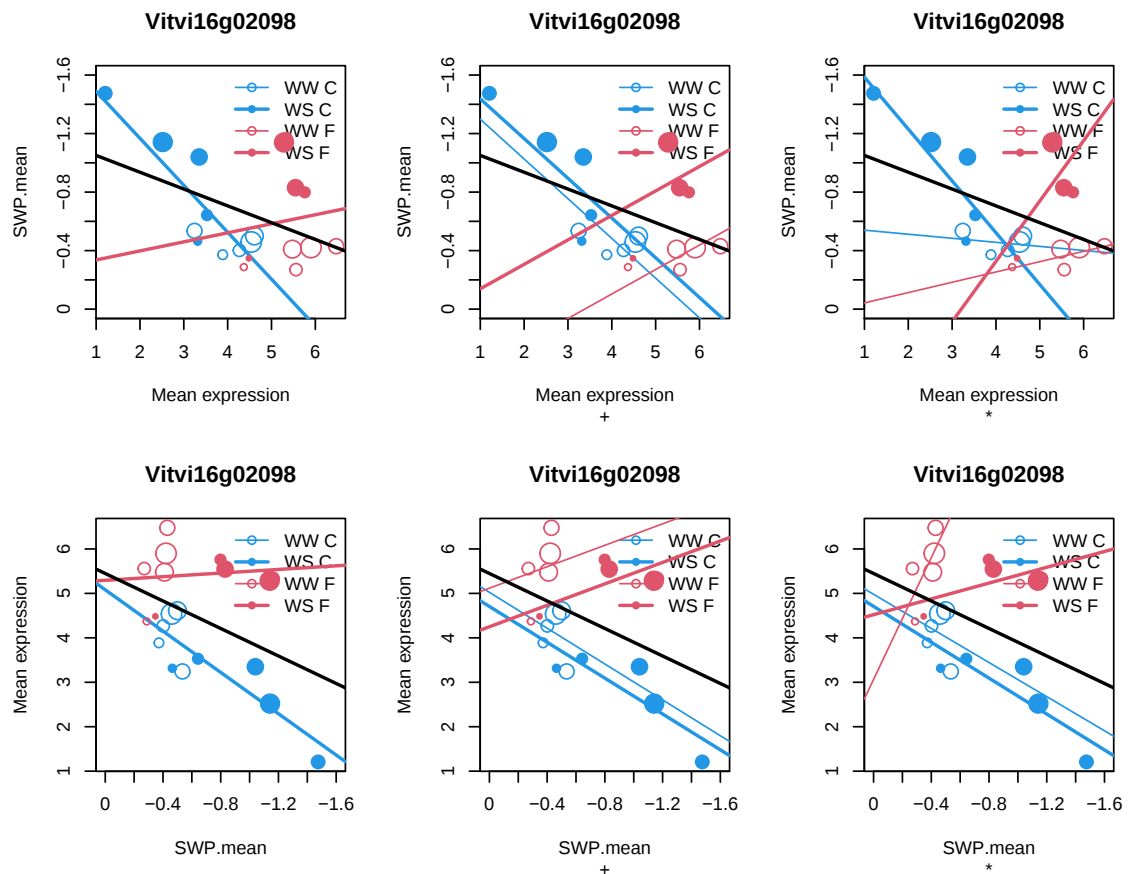
201606

Coefficient swp for Vitvi16g02098.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi16g02098	0.08251854	4.432661	0.03379929	0.9731199	0.9791585

B

Vitvi16g02098 -6.117237



Correlation of all measurements (not just means): $r = 0.0038, r^2 = 1e - 05$

Correlation of mean values (plots): $r_2 = -0.4216$

5.3.7 Vitvi18g02150

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

Vitvi18g02150

27.03.1934

RNA.regulation of transcription.orphan family

LIM domain-containing protein |

Chr4:17358580-17361189 REVERSE LENGTH=553 |

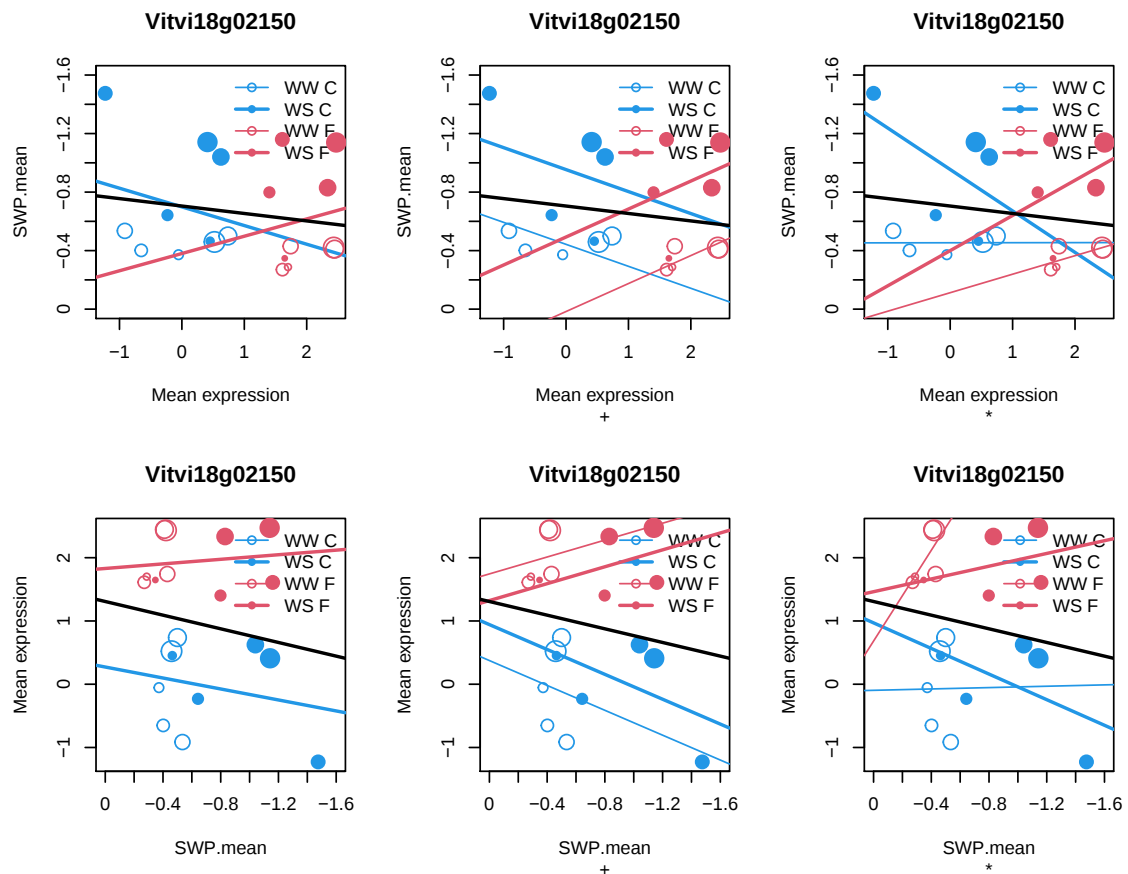
201606

Coefficient swp for Vitvi18g02150.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi18g02150	-0.07217027	0.953493	-0.03368955	0.9732071	0.9791817

B

Vitvi18g02150 -6.11724



Correlation of all measurements (not just means): $r = -0.0037$, $r^2 = 1e - 05$

Correlation of mean values (plots): $r_2 = -0.1656$

5.3.8 Vitvi14g00165

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

Vitvi14g00165

29.2.1.2.1.21

protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S21

RNA-directed DNA polymerase (reverse transcriptase)-related family pro

Chr3:8789471-8790907 FORWARD LENGTH=478 |

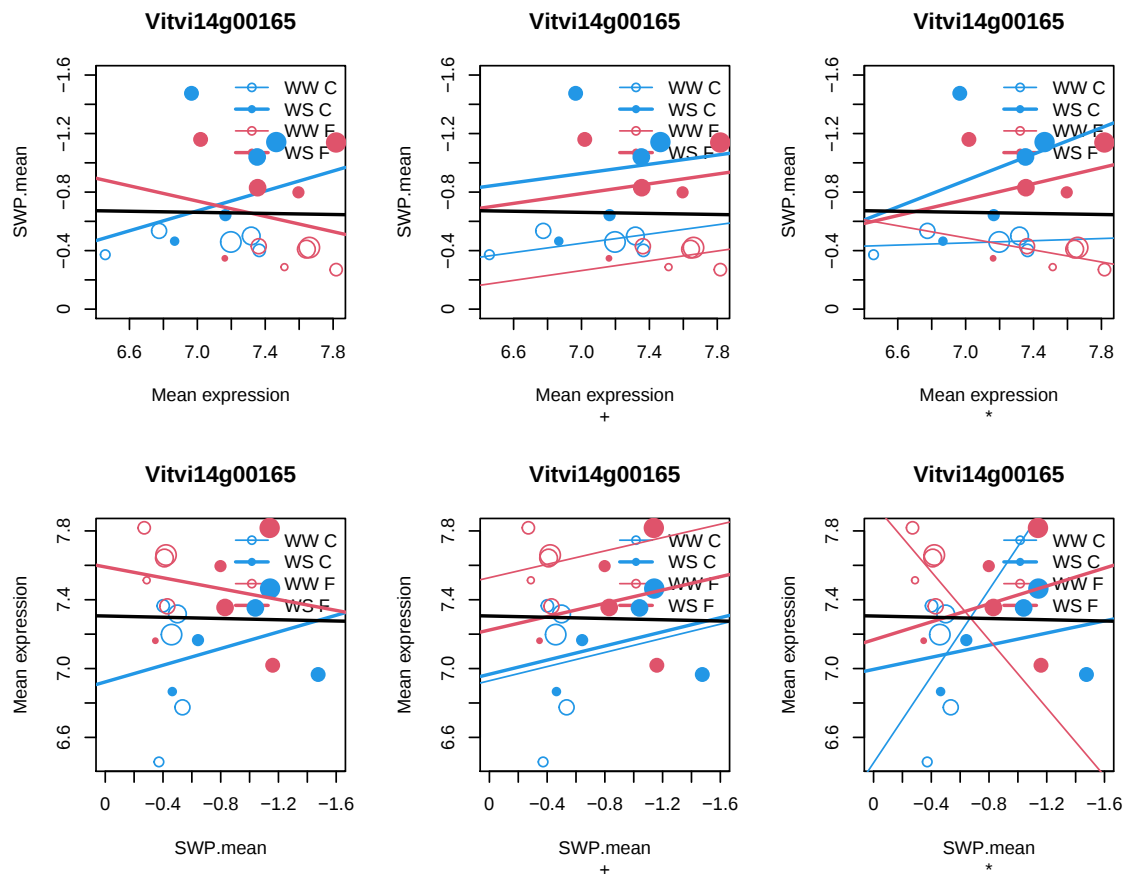
201606

Coefficient swp for Vitvi14g00165.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi14g00165	-0.02429016	7.293553	-0.03342914	0.9734141	0.9793253

B

Vitvi14g00165 -6.117249



Correlation of all measurements (not just means): $r = -0.0038$, $r^2 = 1e - 05$

Correlation of mean values (plots): $r_2 = -0.0183$

5.3.9 Vitvi07g00563

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

Vitvi07g00563

27.03.1950

RNA.regulation of transcription.general transcription

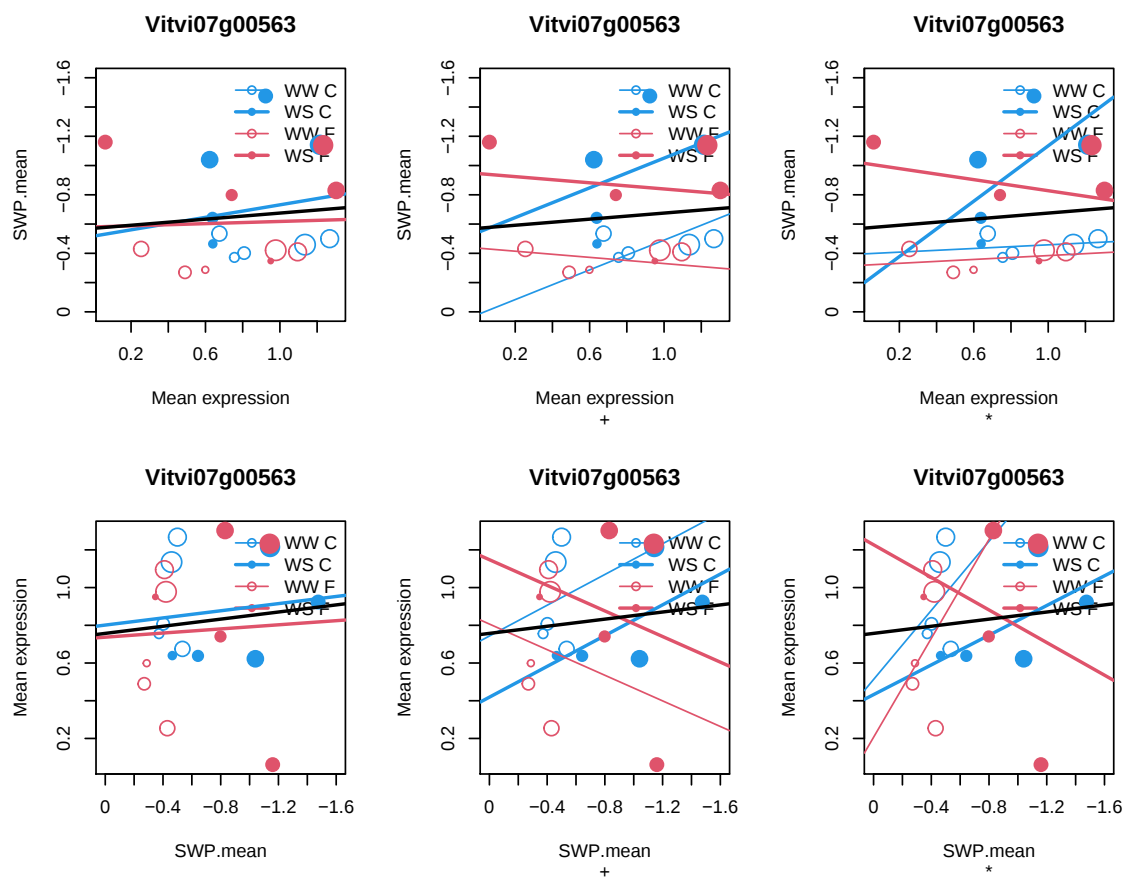
NA

Coefficient swp for Vitvi07g00563.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi07g00563	0.02501472	0.8190884	0.03320985	0.9735885	0.979436

B

Vitvi07g00563	-6.117256
---------------	-----------



Correlation of all measurements (not just means): $r = 0.0038$, $r^2 = 1e - 05$
 Correlation of mean values (plots): $r_2 = 0.0991$

5.3.10 Vitvi16g01289

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

Vitvi16g01289

35.2

not assigned.unknown

CCT motif family protein |

Chr5:21673683-21675080 FORWARD LENGTH=205 |

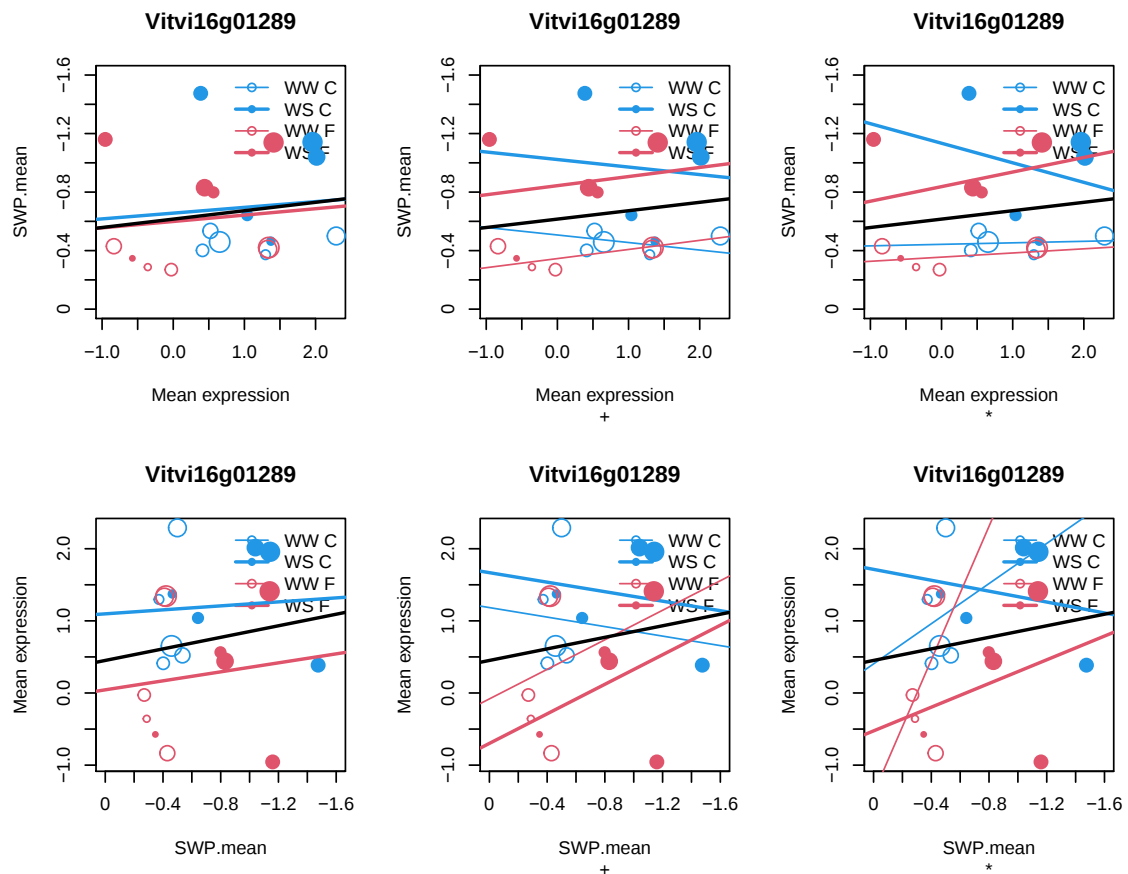
201606

Coefficient swp for Vitvi16g01289.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi16g01289	0.06582562	0.7141025	0.03300433	0.9737519	0.9795358

B

Vitvi16g01289 -6.117262



Correlation of all measurements (not just means): $r = 0.0037, r^2 = 1e - 05$

Correlation of mean values (plots): $r_2 = 0.1516$

5.3.11 Vitvi01g00959

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

Vitvi01g00959

34.2.1

transport.sugars.sucrose

sucrose transporter 2 |

Chr2:828546-831276 REVERSE LENGTH=464 |

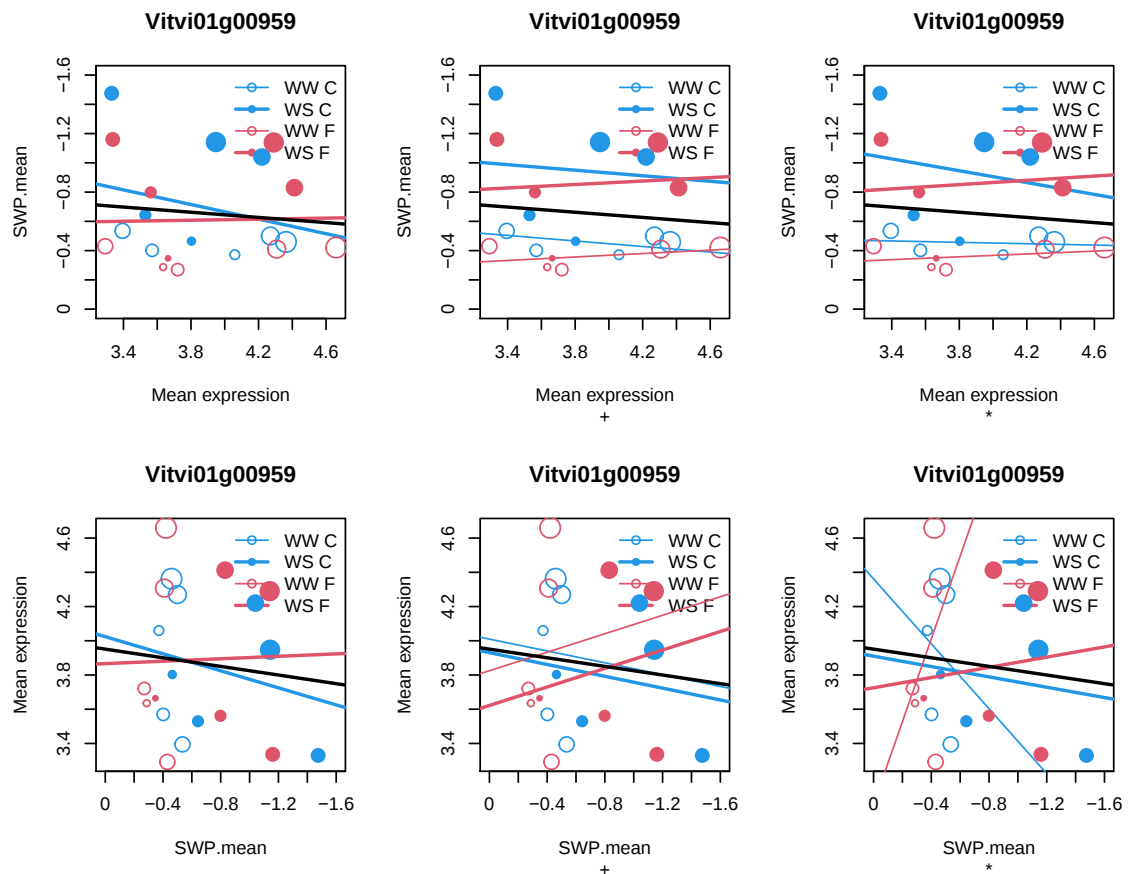
201606

Coefficient swp for Vitvi01g00959.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi01g00959	0.02621161	3.868332	0.03285431	0.9738711	0.9795911

B

Vitvi01g00959 -6.117267



Correlation of all measurements (not just means): $r = 0.0037, r^2 = 1e - 05$

Correlation of mean values (plots): $r_2 = -0.1057$

5.3.12 Vitvi05g00064

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

Vitvi05g00064

35.2

not assigned.unknown

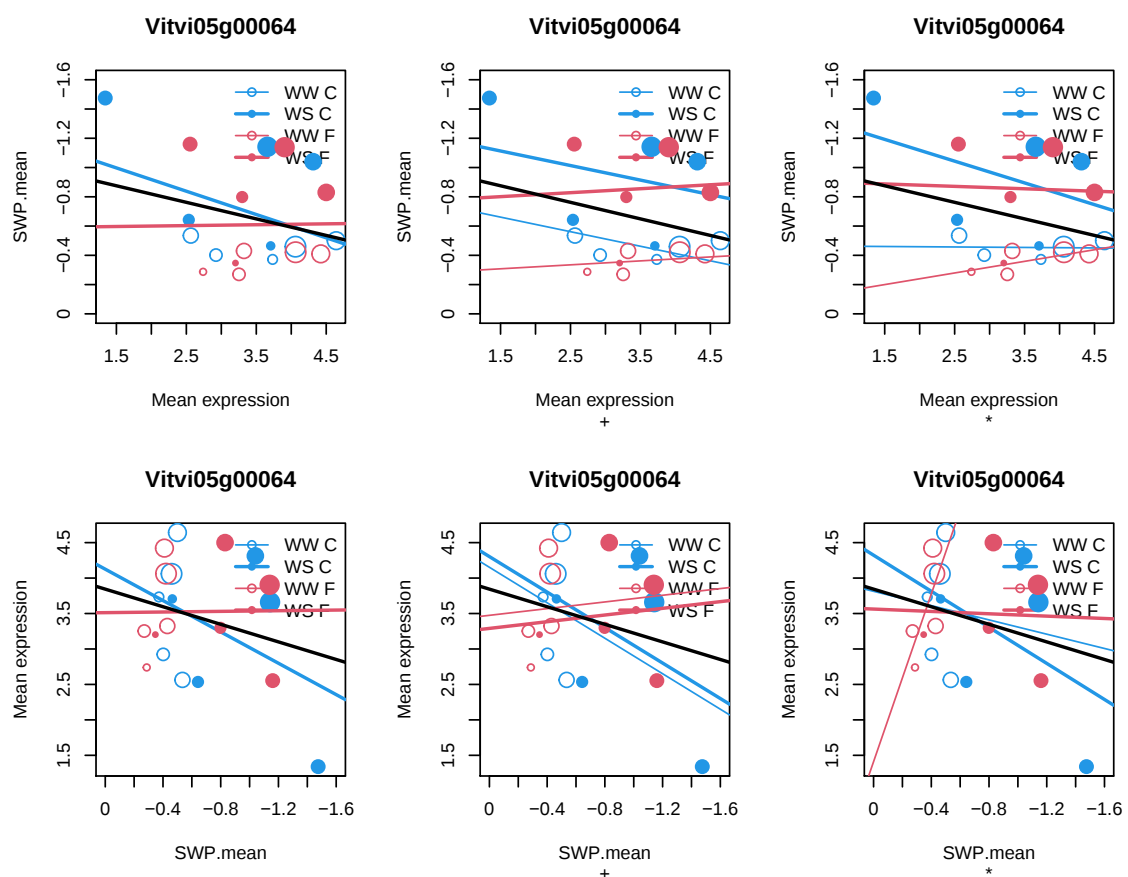
Heavy-metal associated domain protein IPR006121 Heavy metal transport_

Coefficient swp for Vitvi05g00064.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi05g00064	0.04819595	3.436941	0.03095021	0.9753849	0.981049

B

Vitvi05g00064	-6.117326
---------------	-----------



Correlation of all measurements (not just means): $r = 0.0035$, $r^2 = 1e-05$
 Correlation of mean values (plots): $r_2 = -0.2649$

5.3.13 Vitvi18g02613

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

Vitvi18g02613

35.1.41

not assigned.no ontology.hydroxyproline rich proteins

hydroxyproline-rich glycoprotein family protein |

Chr4:12658732-12660211 FORWARD LENGTH=290 |

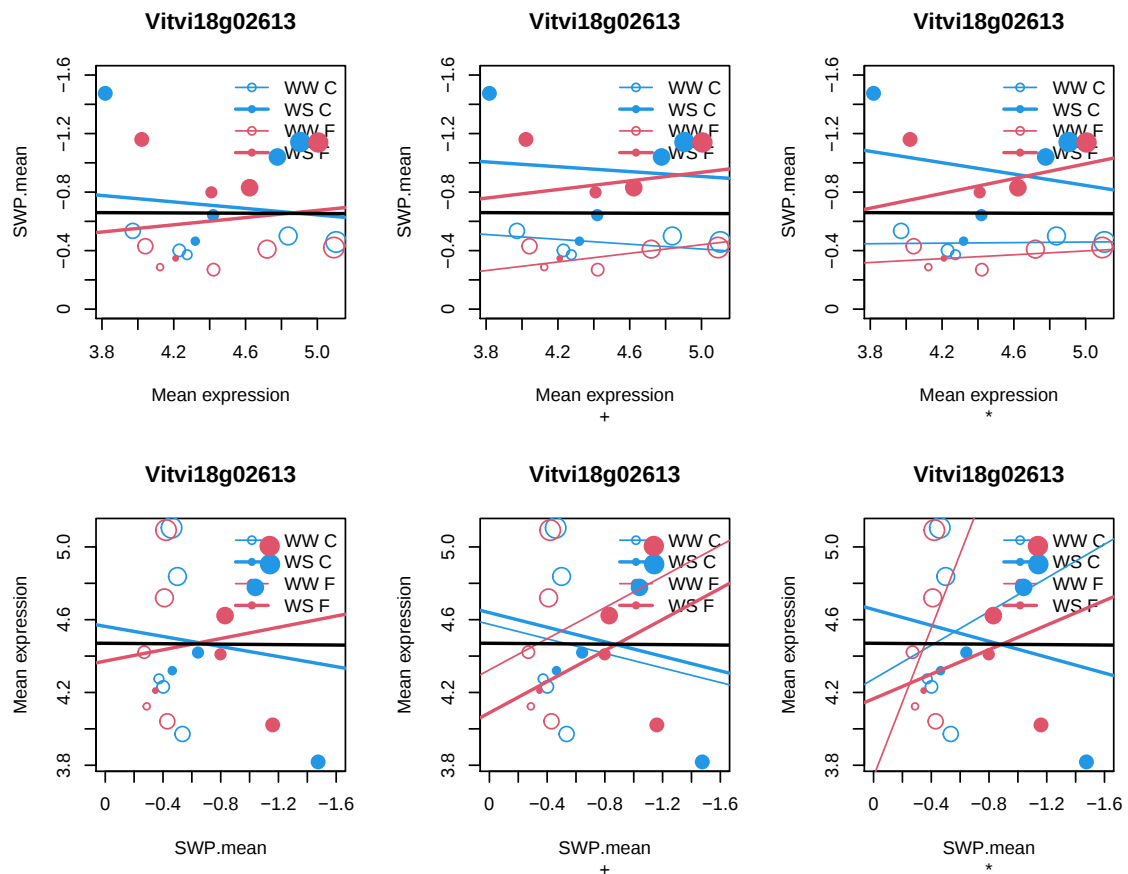
201606

Coefficient swp for Vitvi18g02613.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi18g02613	-0.02311972	4.466398	-0.0308314	0.9754794	0.9810793

B

Vitvi18g02613 -6.117329



Correlation of all measurements (not just means): $r = -0.0035$, $r^2 = 1e - 05$

Correlation of mean values (plots): $r_2 = -0.0055$

5.3.14 Vitvi16g00072

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

Vitvi16g00072

35.2

not assigned.unknown

cysteine-rich RECEPTOR-like kinase |

Chr4:12129485-12133157 FORWARD LENGTH=1043 |

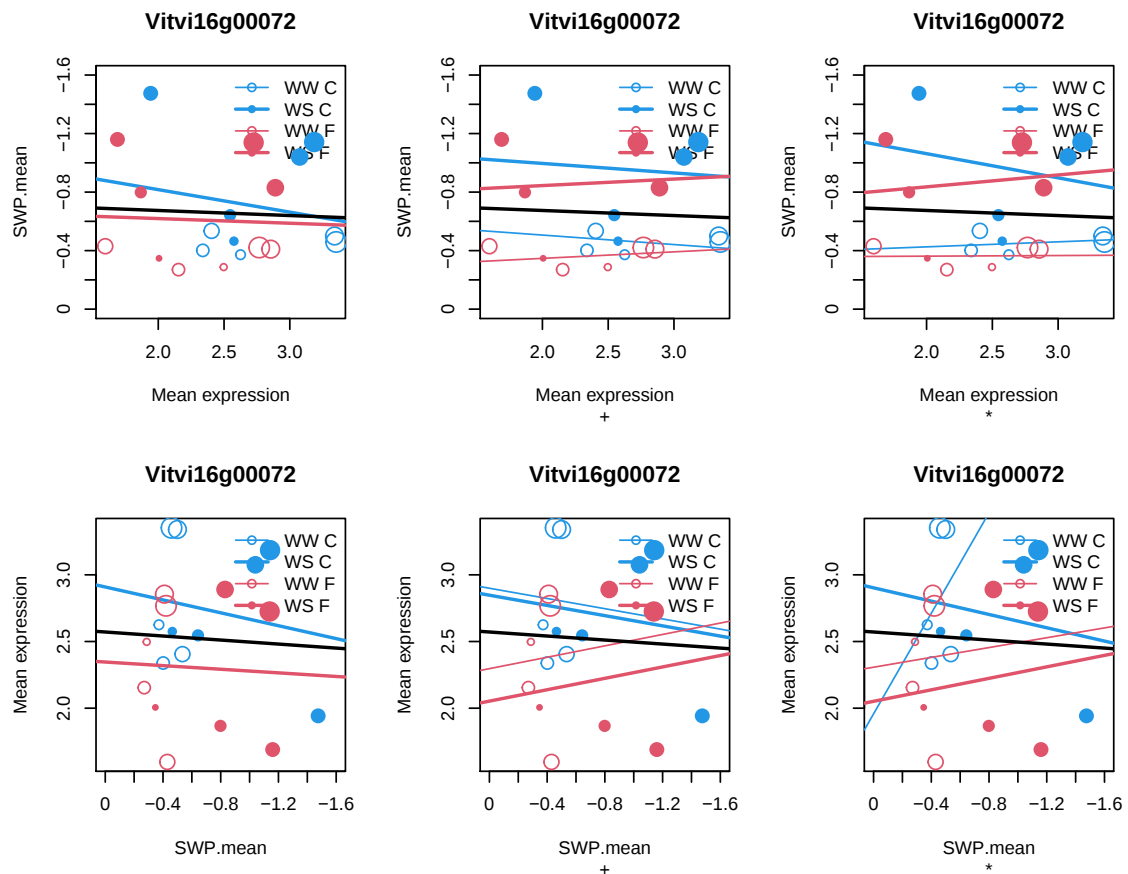
201606

Coefficient swp for Vitvi16g00072.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi16g00072	0.03098897	2.5217	0.03063255	0.9756375	0.9811736

B

Vitvi16g00072 -6.117335



Correlation of all measurements (not just means): $r = 0.0035$, $r^2 = 1e - 05$

Correlation of mean values (plots): $r_2 = -0.0511$

5.3.15 Vitvi18g01050

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

Vitvi18g01050

27.03.1967

RNA.regulation of transcription.putative transcription regulator

zinc knuckle (CCHC-type) family protein |

Chr1:28371420-28372717 REVERSE LENGTH=257 |

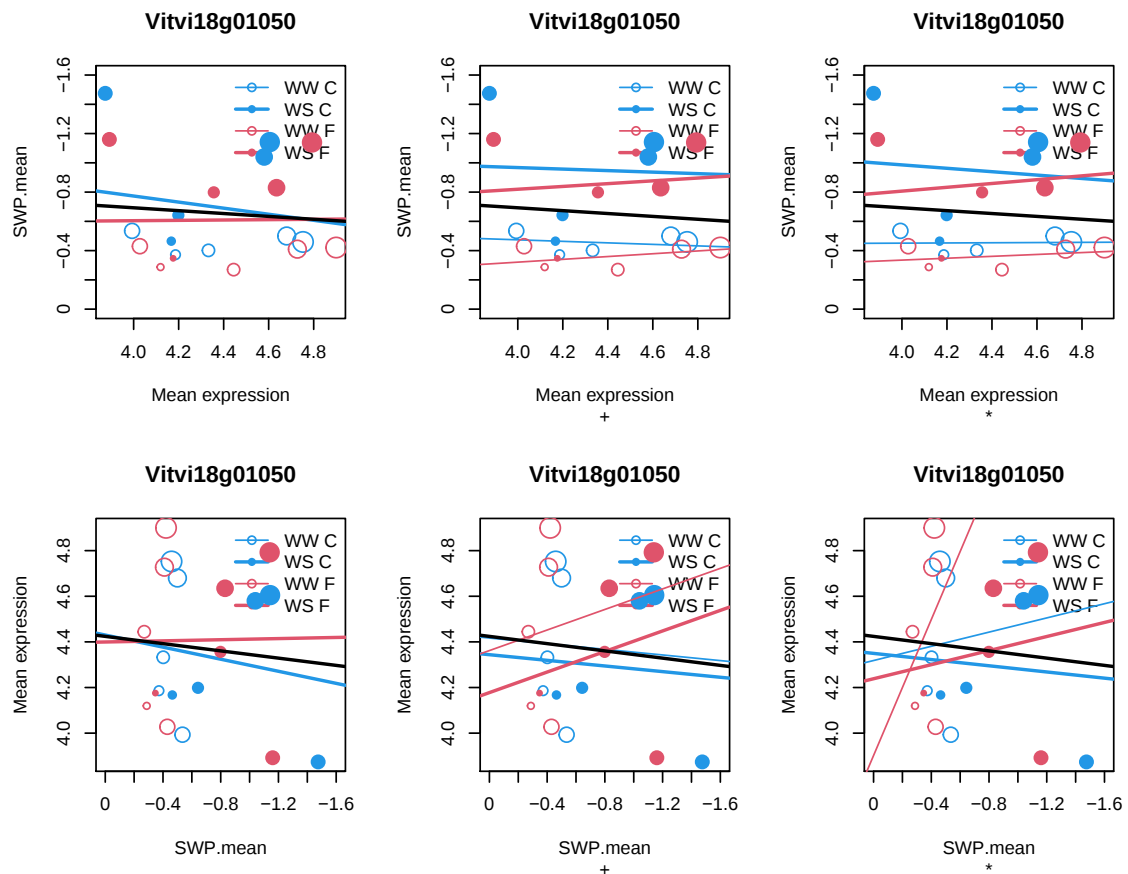
201606

Coefficient swp for Vitvi18g01050.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi18g01050	0.01894357	4.371979	0.0303182	0.9758874	0.9813602

B

Vitvi18g01050 -6.117344



Correlation of all measurements (not just means): $r = 0.0035$, $r^2 = 1e - 05$

Correlation of mean values (plots): $r_2 = -0.0883$

5.3.16 Vitvi14g01444

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

Vitvi14g01444

29.2.1.2.1.27

protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S27

ribosomal protein S27 |

Chr3:22611710-22612632 FORWARD LENGTH=86 |

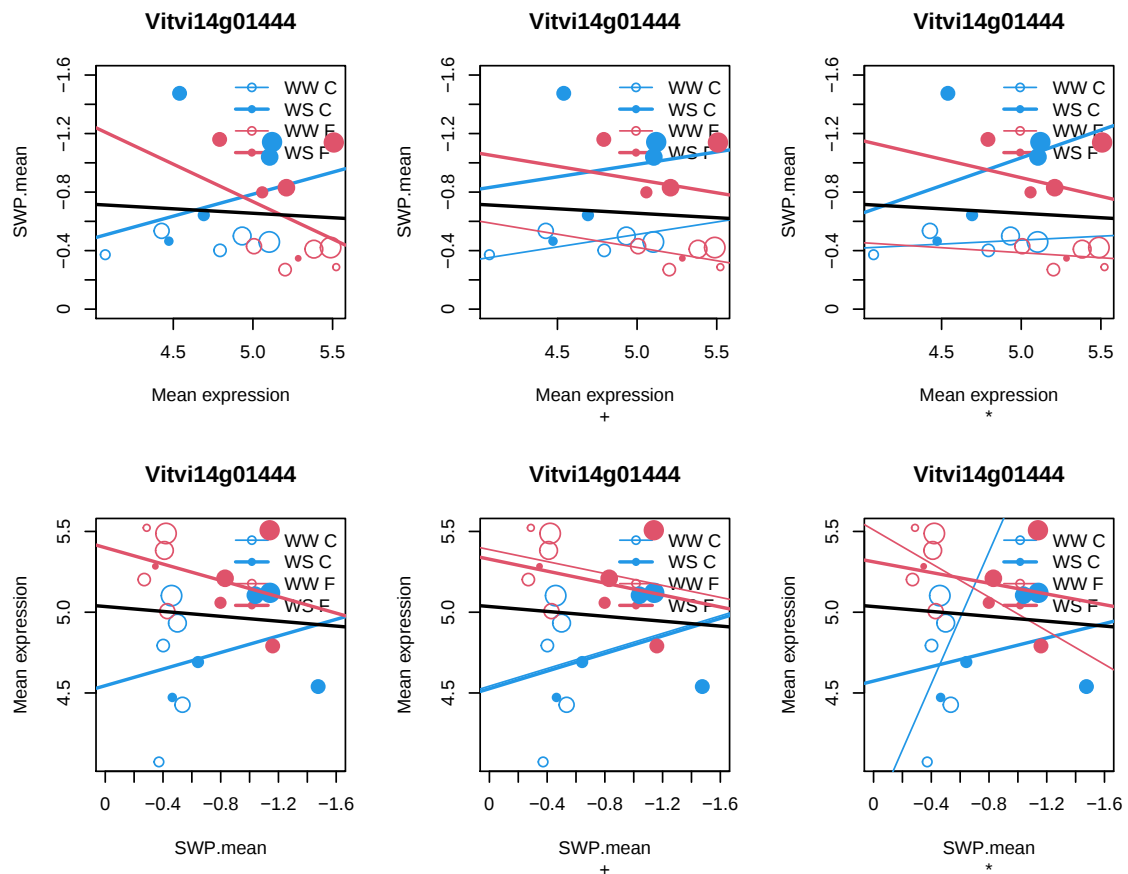
201606

Coefficient swp for Vitvi14g01444.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi14g01444	-0.02375231	4.985432	-0.02999825	0.9761418	0.9815512

B

Vitvi14g01444 -6.117354



Correlation of all measurements (not just means): $r = -0.0034$, $r^2 = 1e - 05$

Correlation of mean values (plots): $r_2 = -0.0679$

5.3.17 Vitvi02g01540

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

Vitvi02g01540

35.2

not assigned.unknown

putative acyl-coenzyme A oxidase |

Chr3:2115589-2116825 REVERSE LENGTH=187 |

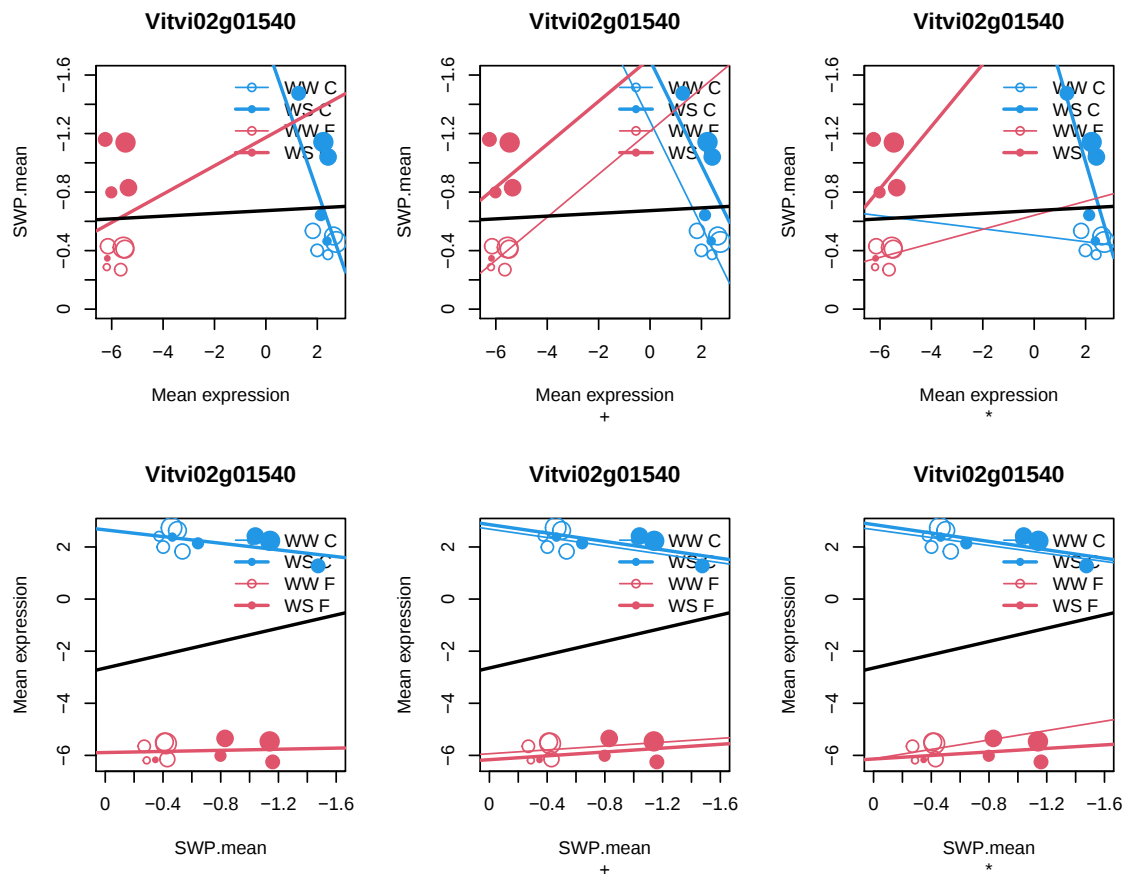
201606

Coefficient swp for Vitvi02g01540.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi02g01540	-0.2137159	-1.810604	-0.02903919	0.9769044	0.9822031

B

Vitvi02g01540 -6.117381



Correlation of all measurements (not just means): $r = -0.0032$, $r^2 = 1e - 05$

Correlation of mean values (plots): $r_2 = 0.1093$

5.3.18 Vitvi07g02860

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

Vitvi07g02860

35.2

not assigned.unknown

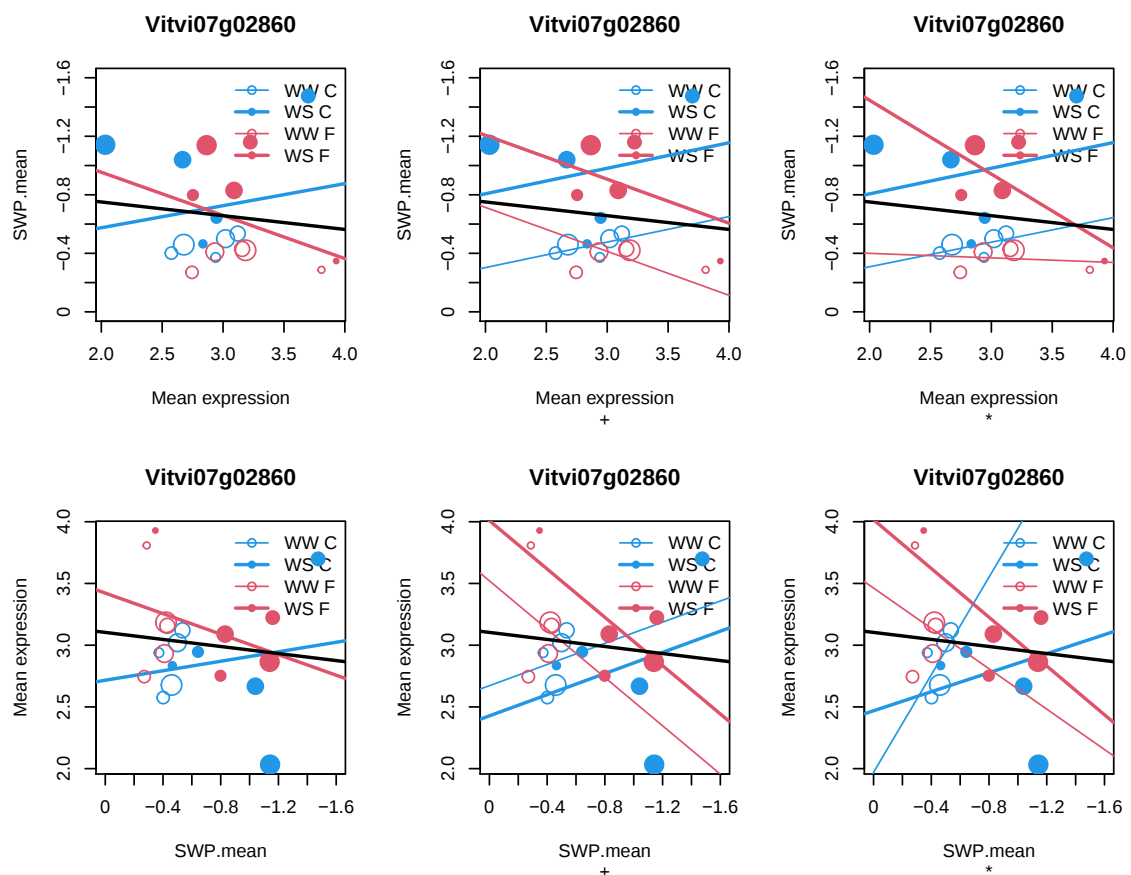
NA

Coefficient swp for Vitvi07g02860.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi07g02860	-0.02654815	3.009993	-0.02899638	0.9769384	0.9822031

B

Vitvi07g02860	-6.117382
---------------	-----------



Correlation of all measurements (not just means): $r = -0.0033$, $r^2 = 1e - 05$
 Correlation of mean values (plots): $r_2 = -0.1158$

5.3.19 Vitvi07g00939

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

Vitvi07g00939

29.3.4.99

protein.targeting.secretory pathway.unspecified

Sec14p-like phosphatidylinositol transfer family protein |

Chr3:9067301-9070256 FORWARD LENGTH=580 |

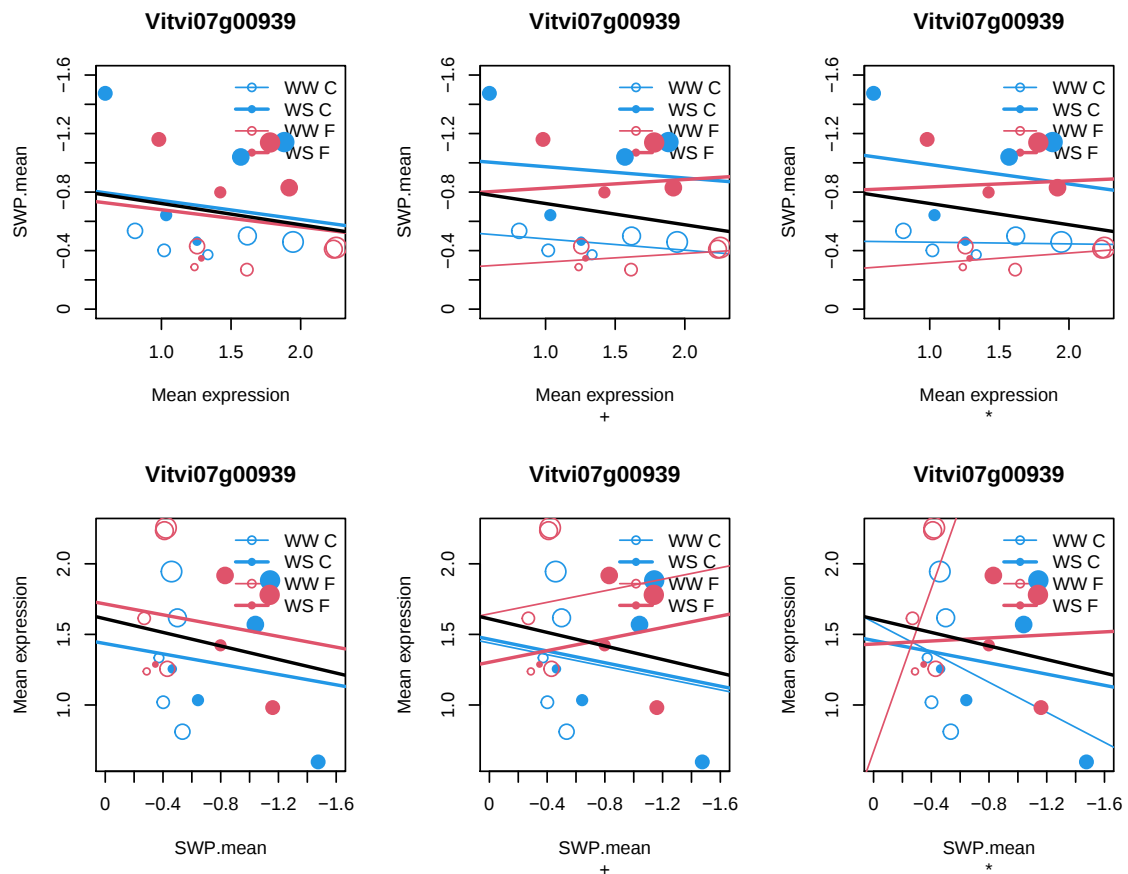
201606

Coefficient swp for Vitvi07g00939.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi07g00939	0.02724043	1.452589	0.0288836	0.9770281	0.9822031

B

Vitvi07g00939 -6.117385



Correlation of all measurements (not just means): $r = 0.0033, r^2 = 1e - 05$

Correlation of mean values (plots): $r_2 = -0.1866$

5.3.20 Vitvi18g01148

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

Vitvi18g01148

34.16

transport.ABC transporters and multidrug resistance systems

P-glycoprotein 13 |

Chr1:9733597-9737211 REVERSE LENGTH=1031 |

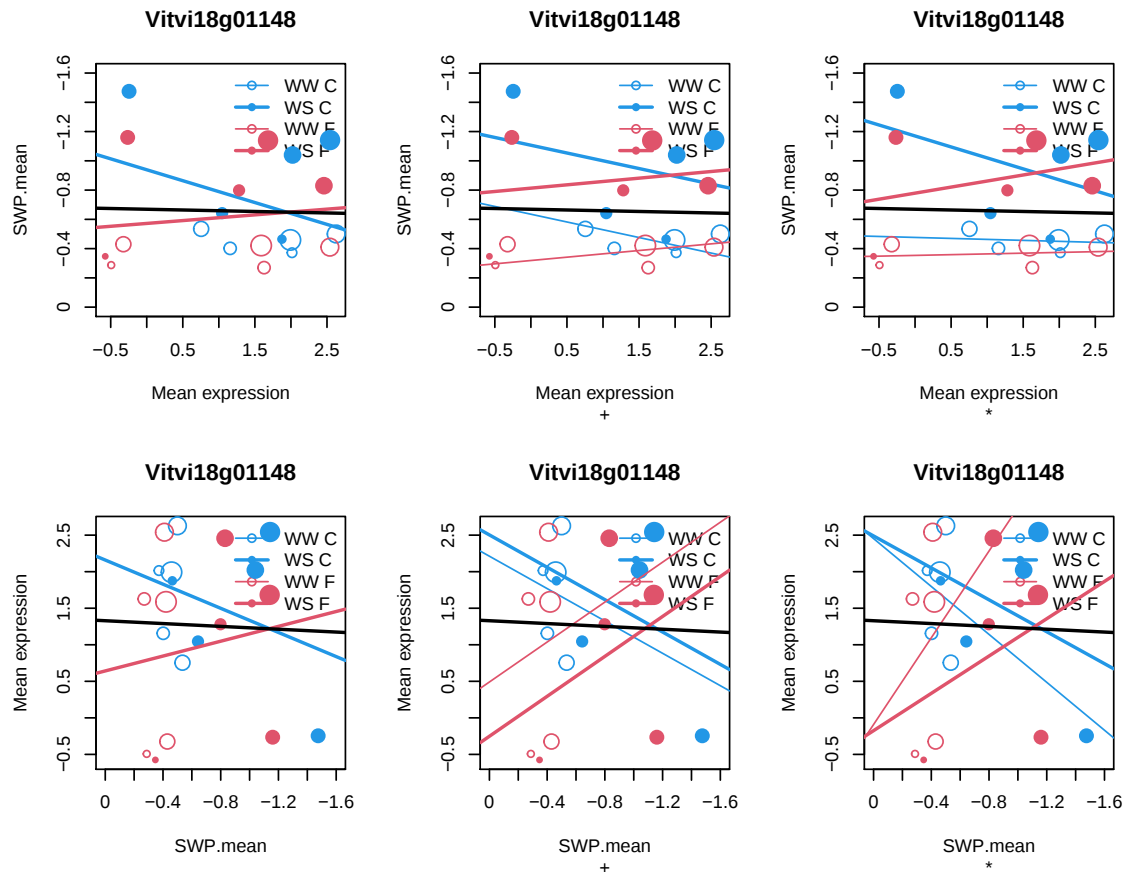
201606

Coefficient swp for Vitvi18g01148.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi18g01148	0.05967232	1.265222	0.02885865	0.9770479	0.9822031

B

Vitvi18g01148 -6.117386



Correlation of all measurements (not just means): $r = 0.0032$, $r^2 = 1e - 05$

Correlation of mean values (plots): $r_2 = -0.0313$

5.3.21 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 |

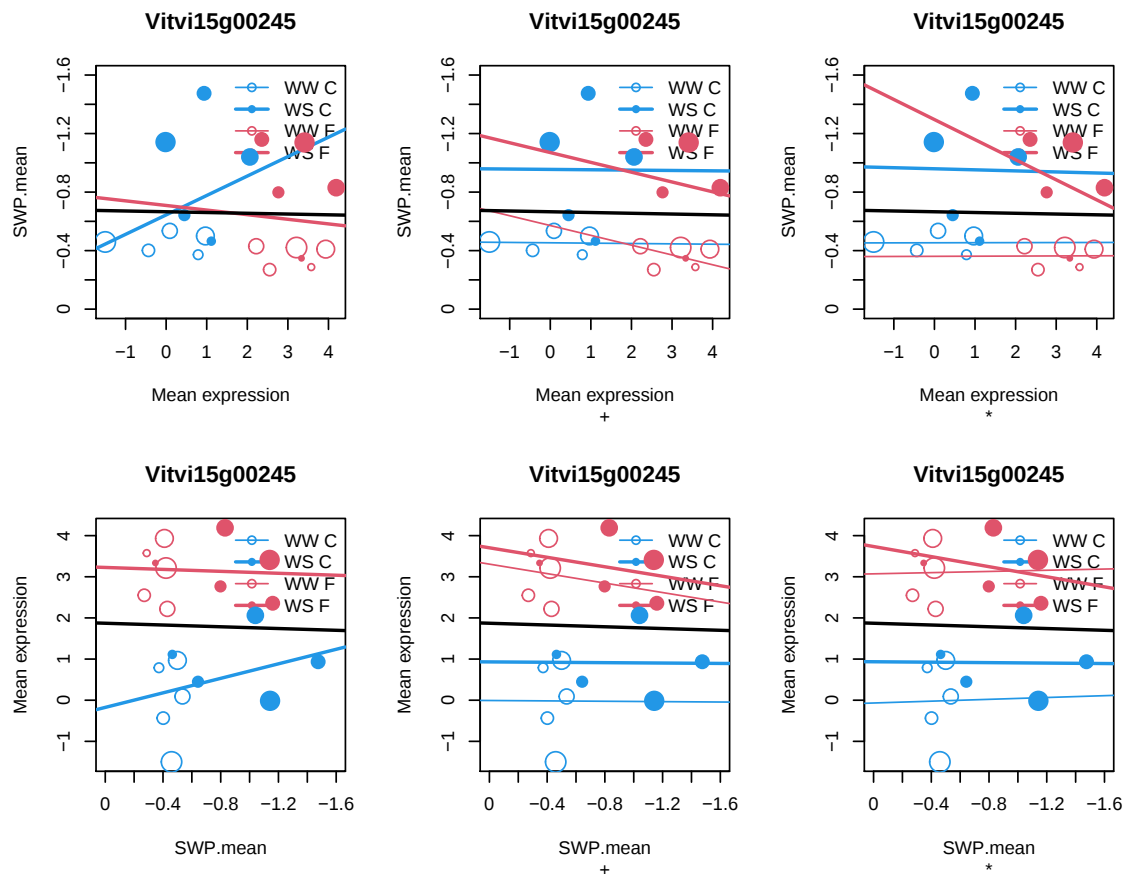
201606

Coefficient swp for Vitvi15g00245.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi15g00245	-0.08476055	1.80022	-0.02822277	0.9775535	0.9826375

B

Vitvi15g00245 -6.117403



Correlation of all measurements (not just means): $r = -0.0031$, $r^2 = 1e - 05$

Correlation of mean values (plots): $r_2 = -0.0236$

5.3.22 Vitvi06g00502

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

Vitvi06g00502

29.5.11.4.2

protein.degradation.ubiquitin.E3.RING

zinc finger (C3HC4-type RING finger) family protein |

Chr3:17178837-17180024 REVERSE LENGTH=395 |

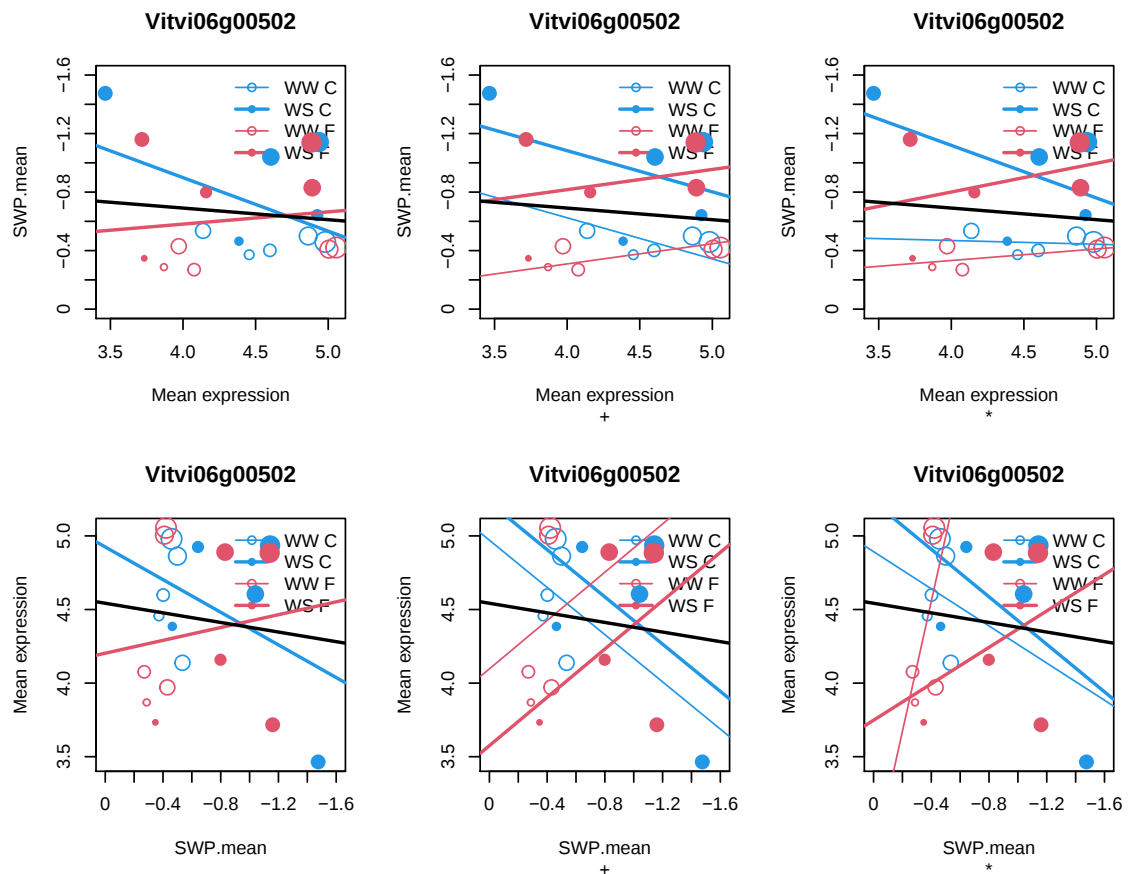
201606

Coefficient swp for Vitvi06g00502.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi06g00502	-0.03048319	4.435491	-0.0281531	0.9776089	0.9826375

B

Vitvi06g00502 -6.117405



Correlation of all measurements (not just means): $r = -0.0032$, $r^2 = 1e - 05$

Correlation of mean values (plots): $r_2 = -0.1138$

5.3.23 Vitvi06g01487

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

Vitvi06g01487

35.2

not assigned.unknown

ferredoxin 3 |

Chr2:11758281-11758748 REVERSE LENGTH=155 |

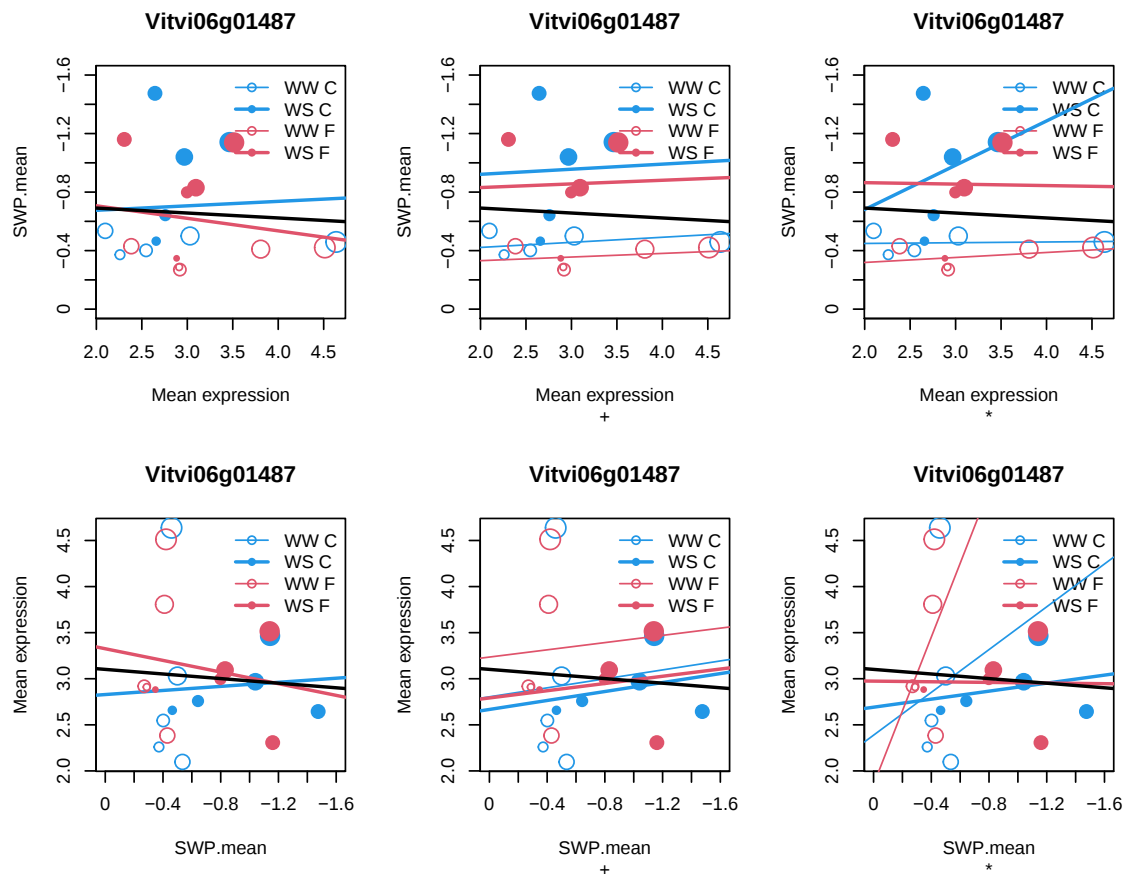
201606

Coefficient swp for Vitvi06g01487.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi06g01487	0.03840085	3.019663	0.02802441	0.9777112	0.9826755

B

Vitvi06g01487 -6.117409



Correlation of all measurements (not just means): $r = 0.0031$, $r^2 = 1e - 05$

Correlation of mean values (plots): $r_2 = -0.0650$

5.3.24 Vitvi18g02965

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

Vitvi18g02965

27.03.1969

RNA.regulation of transcription.SET-domain transcriptional regulator f

SET domain group 26 |

Chr1:28789887-28792371 REVERSE LENGTH=492 |

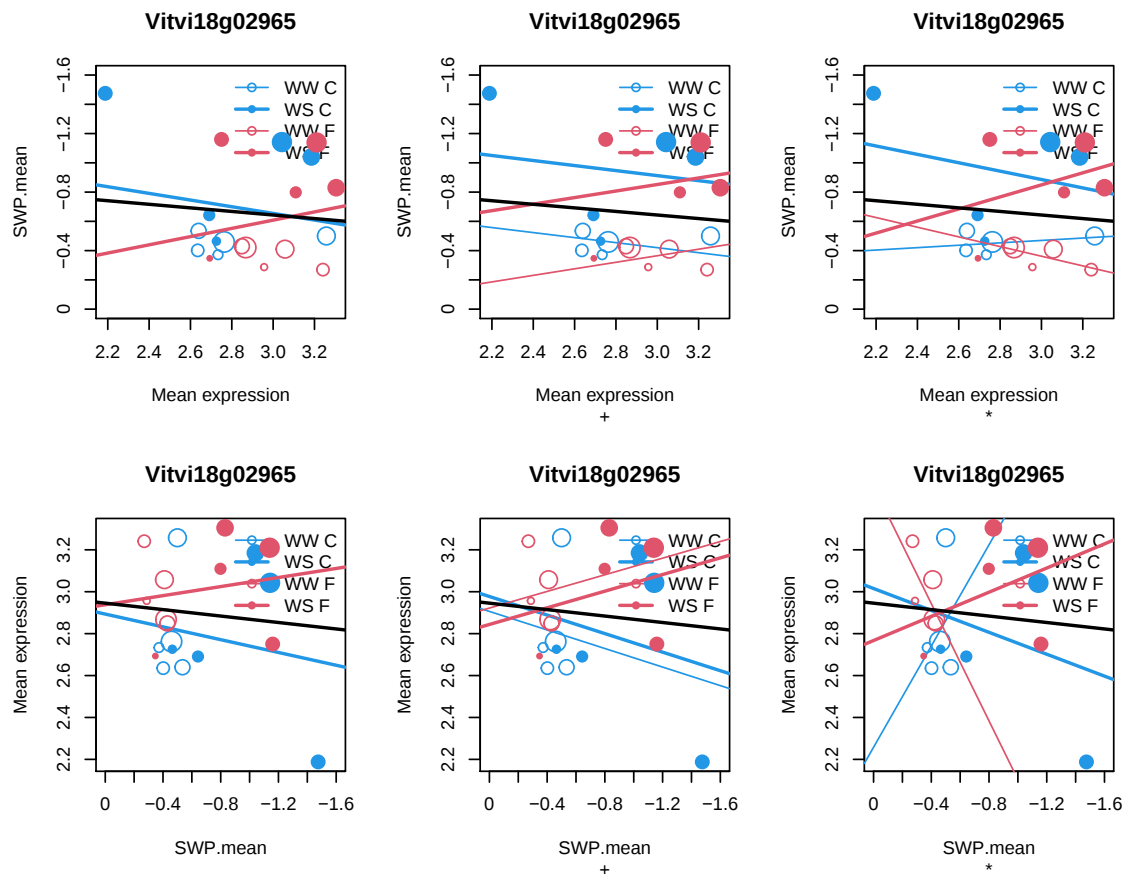
201606

Coefficient swp for Vitvi18g02965.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi18g02965	-0.01800087	2.894948	-0.02678184	0.9786992	0.9836037

B

Vitvi18g02965 -6.117442



Correlation of all measurements (not just means): $r = -0.0031$, $r^2 = 1e - 05$

Correlation of mean values (plots): $r_2 = -0.0968$

5.3.25 Vitvi02g01110

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

Vitvi02g01110

20.1

stress.biotic

HXXXD-type acyl-transferase family protein |

Chr5:5782061-5783682 REVERSE LENGTH=461 |

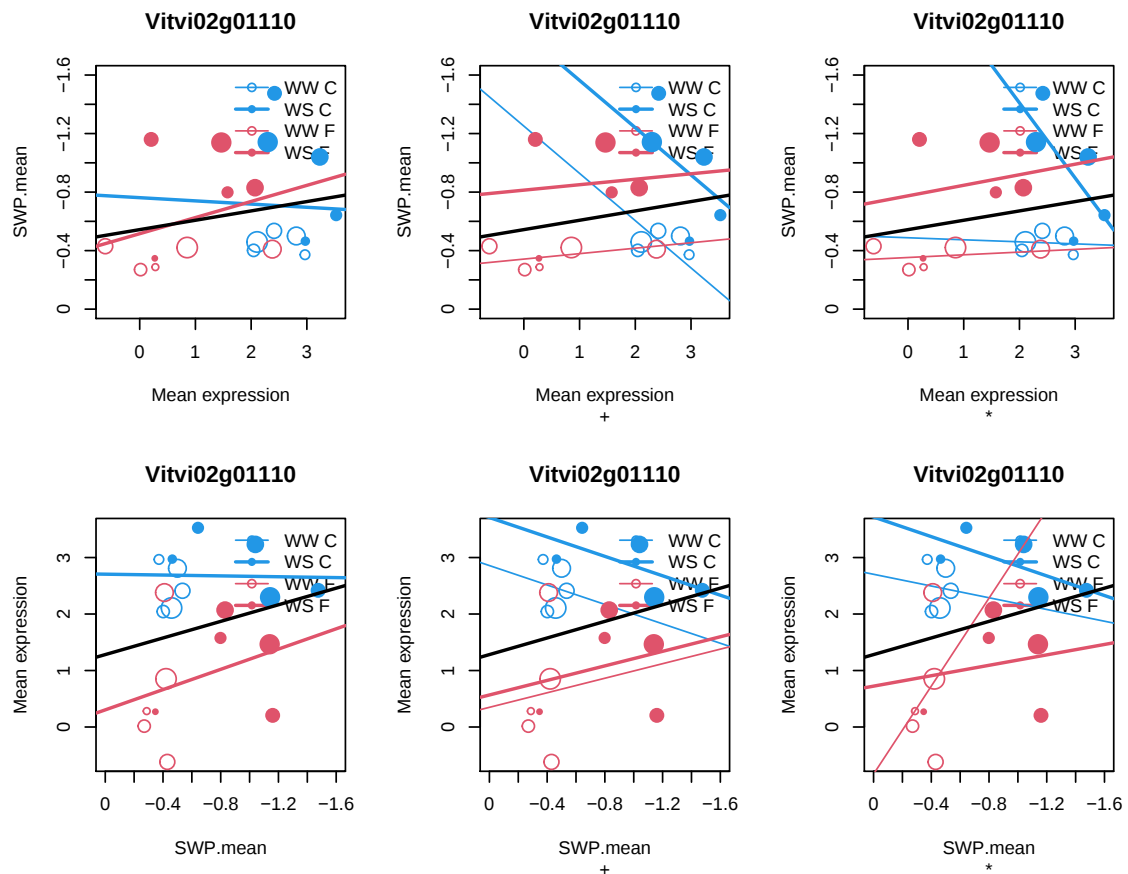
201606

Coefficient swp for Vitvi02g01110.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi02g01110	-0.06252571	1.764422	-0.0262938	0.9790873	0.9839288

B

Vitvi02g01110 -6.117454



Correlation of all measurements (not just means): $r = -0.0029$, $r^2 = 9e - 06$

Correlation of mean values (plots): $r_2 = 0.2167$

5.3.26 Vitvi09g01029

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

Vitvi09g01029

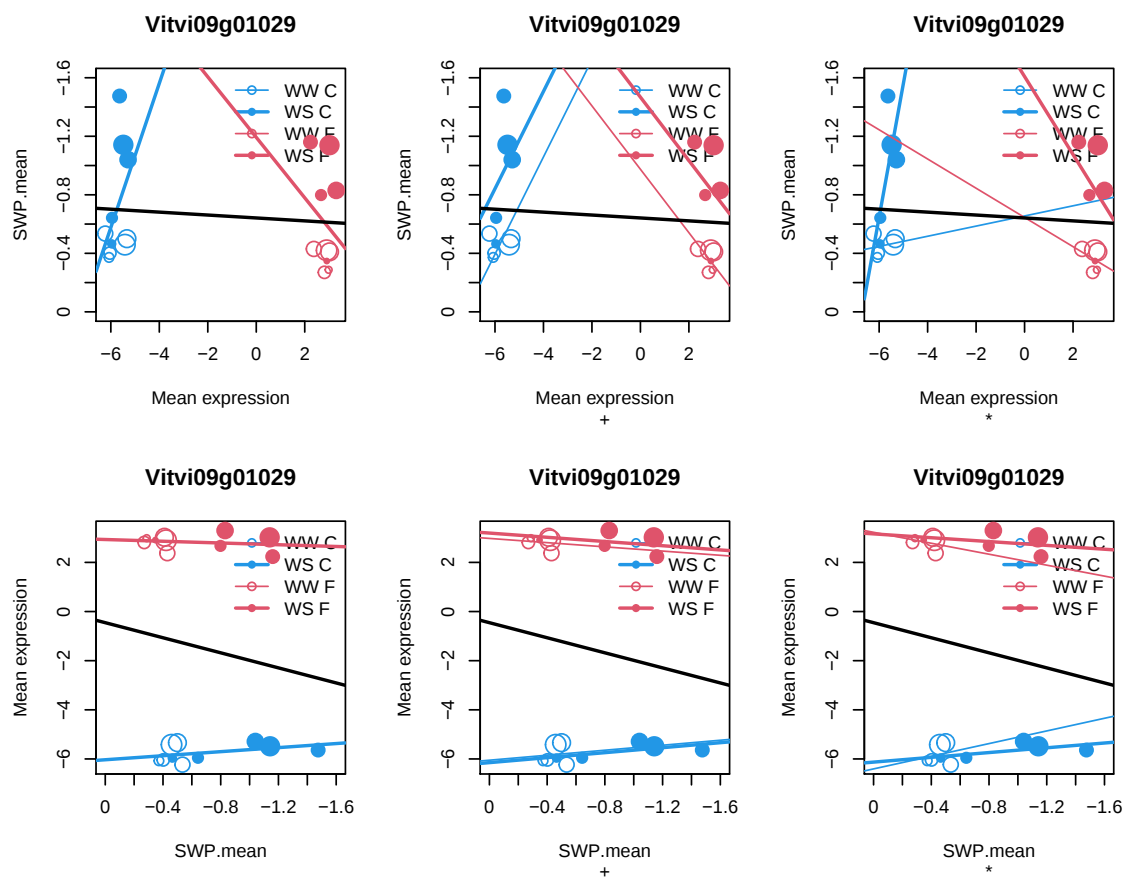
35.2

not assigned.unknown

F-box family protein IPR001810 Cyclin-like F-box

Coefficient swp for Vitvi09g01029.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi09g01029	-0.205356	-1.459981	-0.02620782	0.9791557	0.9839327
	B				
Vitvi09g01029	-6.117456				



Correlation of all measurements (not just means): $r = -0.0029$, $r^2 = 8e - 06$
 Correlation of mean values (plots): $r_2 = -0.1236$

5.3.27 Vitvi18g02777

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

Vitvi18g02777

26.27

misc.calcineurin-like phosphoesterase family protein

purple acid phosphatase 12 |

Chr2:11621400-11623438 REVERSE LENGTH=469 |

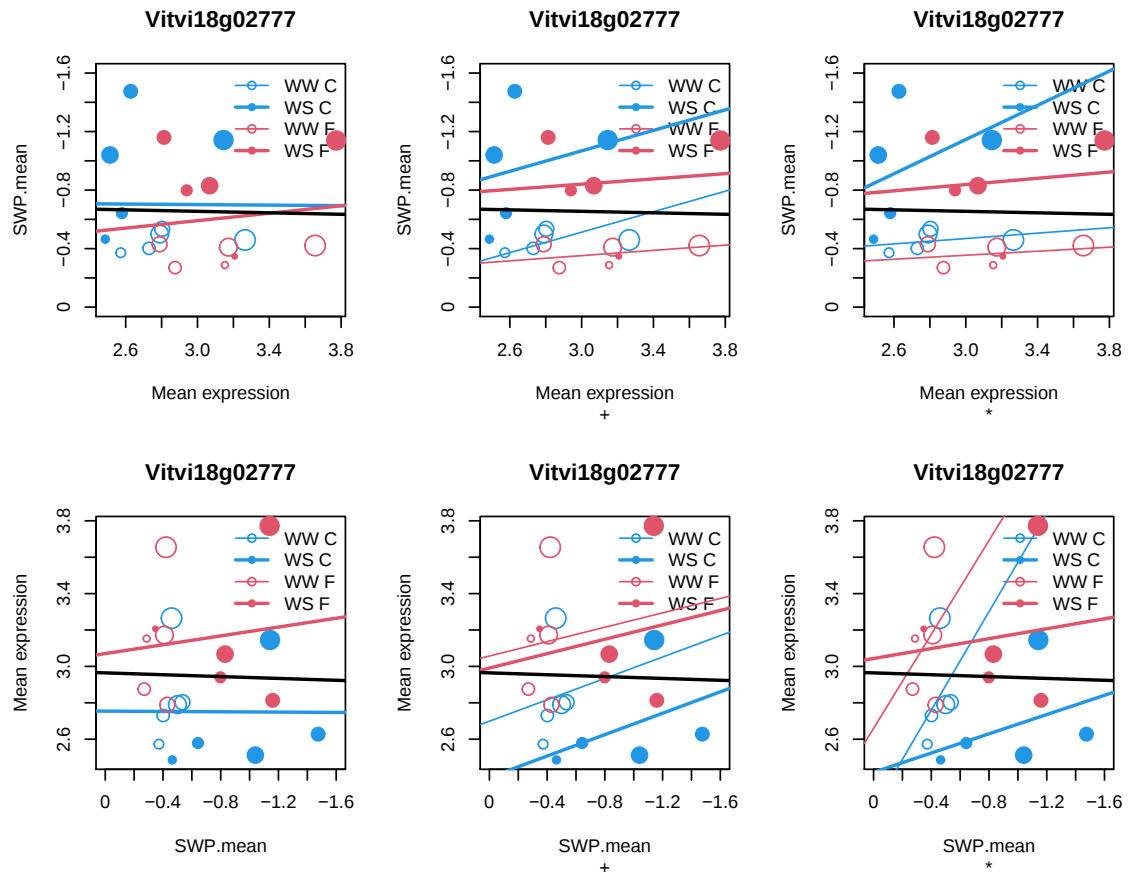
201606

Coefficient swp for Vitvi18g02777.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi18g02777	0.01998467	2.947781	0.02576848	0.979505	0.9842188

B

Vitvi18g02777 -6.117467



Correlation of all measurements (not just means): $r = 0.0029$, $r^2 = 9e - 06$

Correlation of mean values (plots): $r_2 = -0.0254$

5.3.28 Vitvi12g00288

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

Vitvi12g00288

35.1

not assigned.no ontology

Prefoldin chaperone subunit family protein |

Chr1:941211-943320 REVERSE LENGTH=391 |

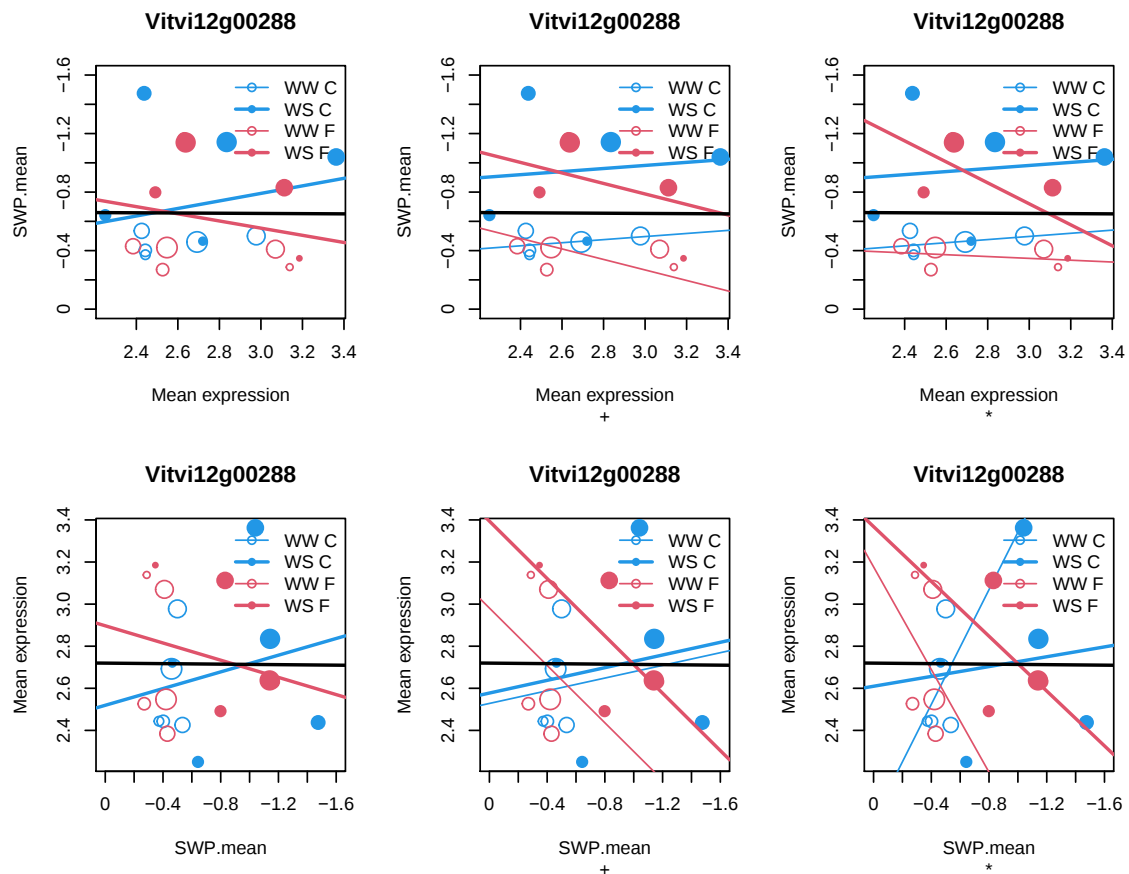
201606

Coefficient swp for Vitvi12g00288.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi12g00288	0.01814224	2.715637	0.02552028	0.9797024	0.9843523

B

Vitvi12g00288 -6.117473



Correlation of all measurements (not just means): $r = 0.0029$, $r^2 = 9e-06$

Correlation of mean values (plots): $r_2 = -0.0067$

5.3.29 Vitvi08g01768

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

Vitvi08g01768

31.1

cell.organisation

P-loop containing nucleoside triphosphate hydrolases superfamily prote

Chr3:3827016-3834146 FORWARD LENGTH=965 |

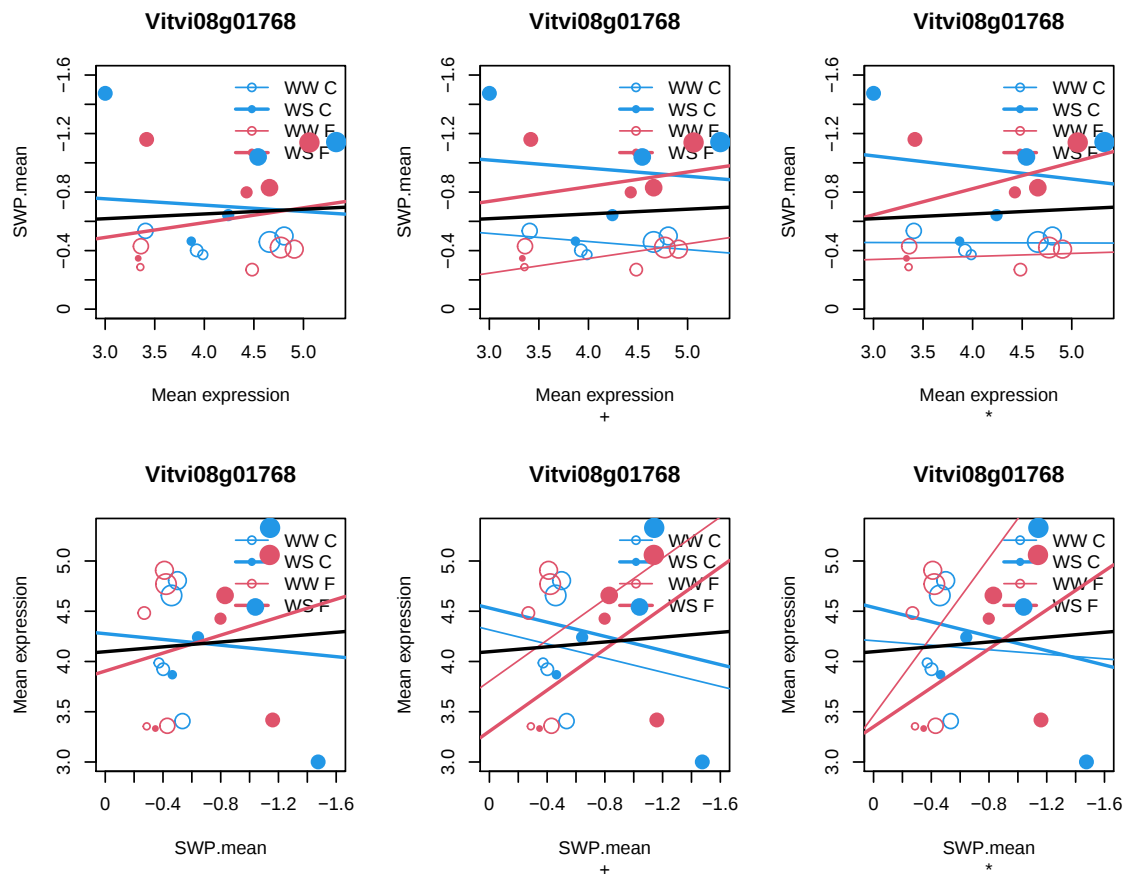
201606

Coefficient swp for Vitvi08g01768.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi08g01768	-0.03238378	4.176565	-0.02538688	0.9798085	0.9843863

B

Vitvi08g01768 -6.117477



Correlation of all measurements (not just means): $r = -0.0028$, $r^2 = 8e - 06$

Correlation of mean values (plots): $r_2 = 0.0625$

5.3.30 Vitvi05g00077

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

Vitvi05g00077

27.03.2009

RNA.regulation of transcription.C2C2(Zn) GATA transcription factor fam

GATA transcription factor 16 |

Chr5:19984849-19985475 REVERSE LENGTH=139 |

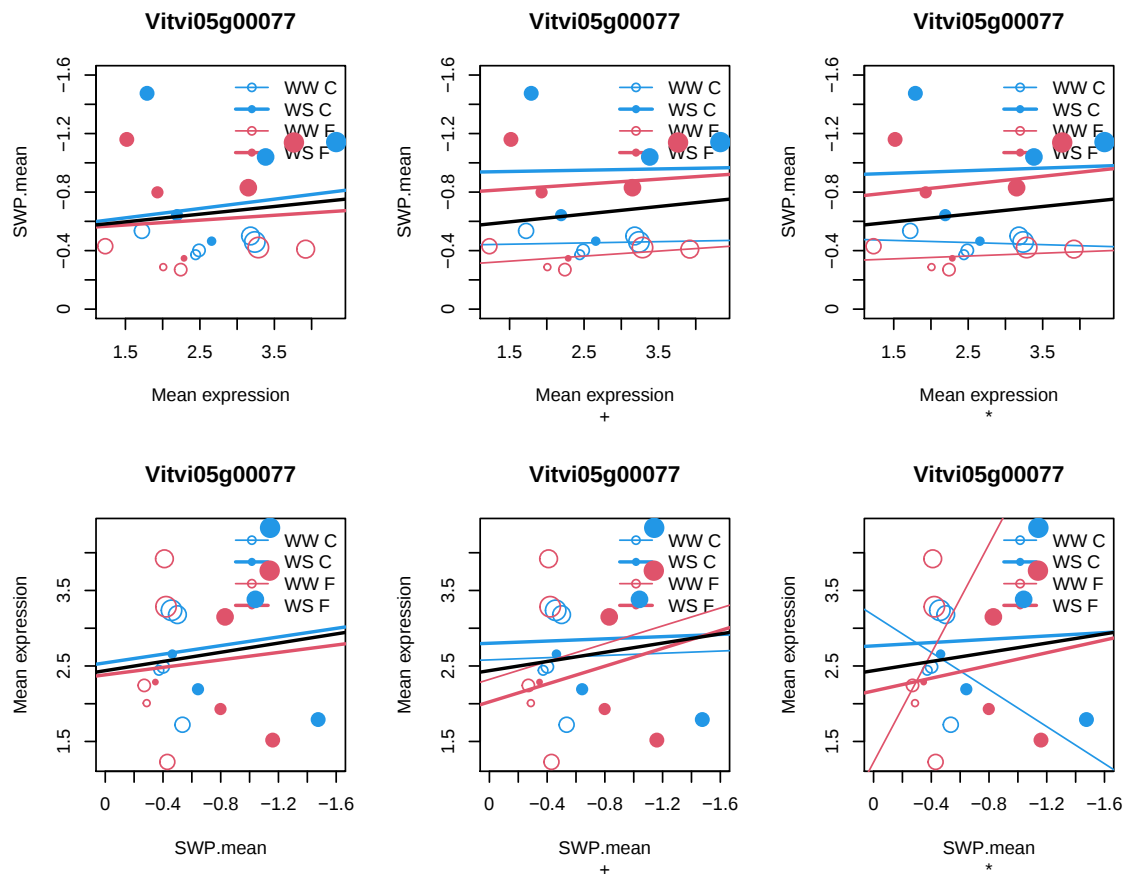
201606

Coefficient swp for Vitvi05g00077.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi05g00077	0.04154244	2.637692	0.02531046	0.9798692	0.9843863

B

Vitvi05g00077 -6.117479



Correlation of all measurements (not just means): $r = 0.0028, r^2 = 8e - 06$

Correlation of mean values (plots): $r_2 = 0.1264$

5.3.31 Vitvi01g01023

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

Vitvi01g01023

29.5.11.4.2

protein.degradation.ubiquitin.E3.RING

RING/U-box superfamily protein |

Chr1:9285576-9286190 REVERSE LENGTH=204 |

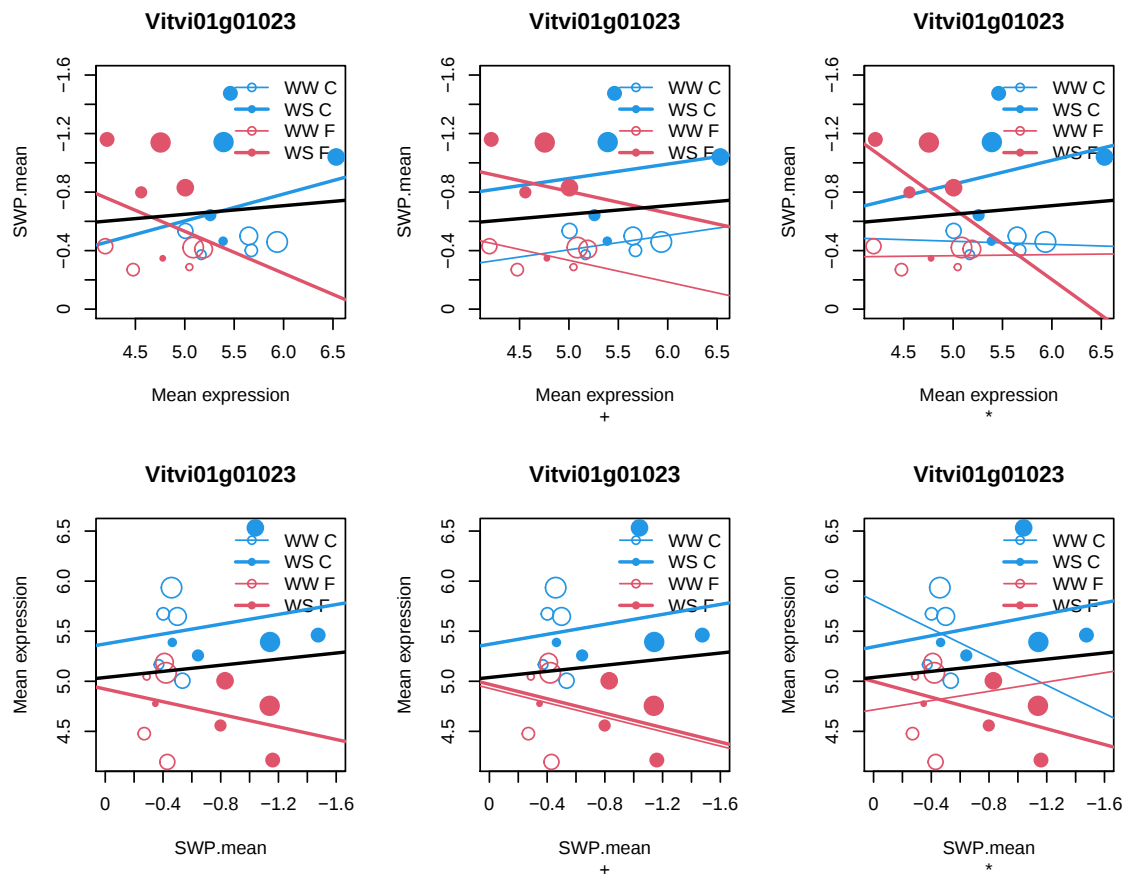
201606

Coefficient swp for Vitvi01g01023.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi01g01023	-0.02835114	5.138171	-0.0251763	0.9799759	0.9843863

B

Vitvi01g01023 -6.117482



Correlation of all measurements (not just means): $r = -0.0028$, $r^2 = 8e - 06$

Correlation of mean values (plots): $r_2 = 0.0948$

5.3.32 Vitvi06g00110

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

Vitvi06g00110

25.2

C1-metabolism.formate-tetrahydrofolate ligase

10-formyltetrahydrofolate synthetase |

Chr1:18702064-18704687 FORWARD LENGTH=634 |

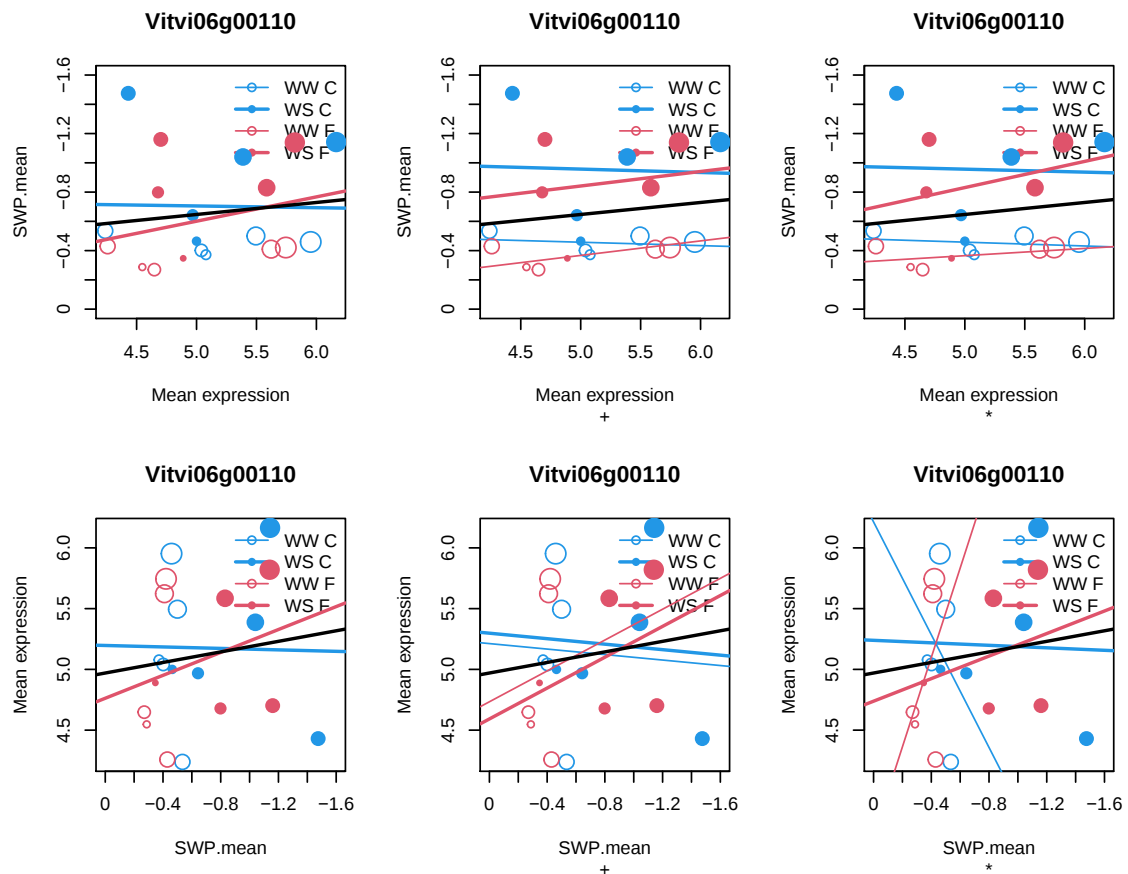
201606

Coefficient swp for Vitvi06g00110.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi06g00110	0.02727214	5.112553	0.02515274	0.9799946	0.9843863

B

Vitvi06g00110 -6.117482



Correlation of all measurements (not just means): $r = 0.0028, r^2 = 8e - 06$

Correlation of mean values (plots): $r_2 = 0.1335$

5.3.33 Vitvi10g00516

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

Vitvi10g00516

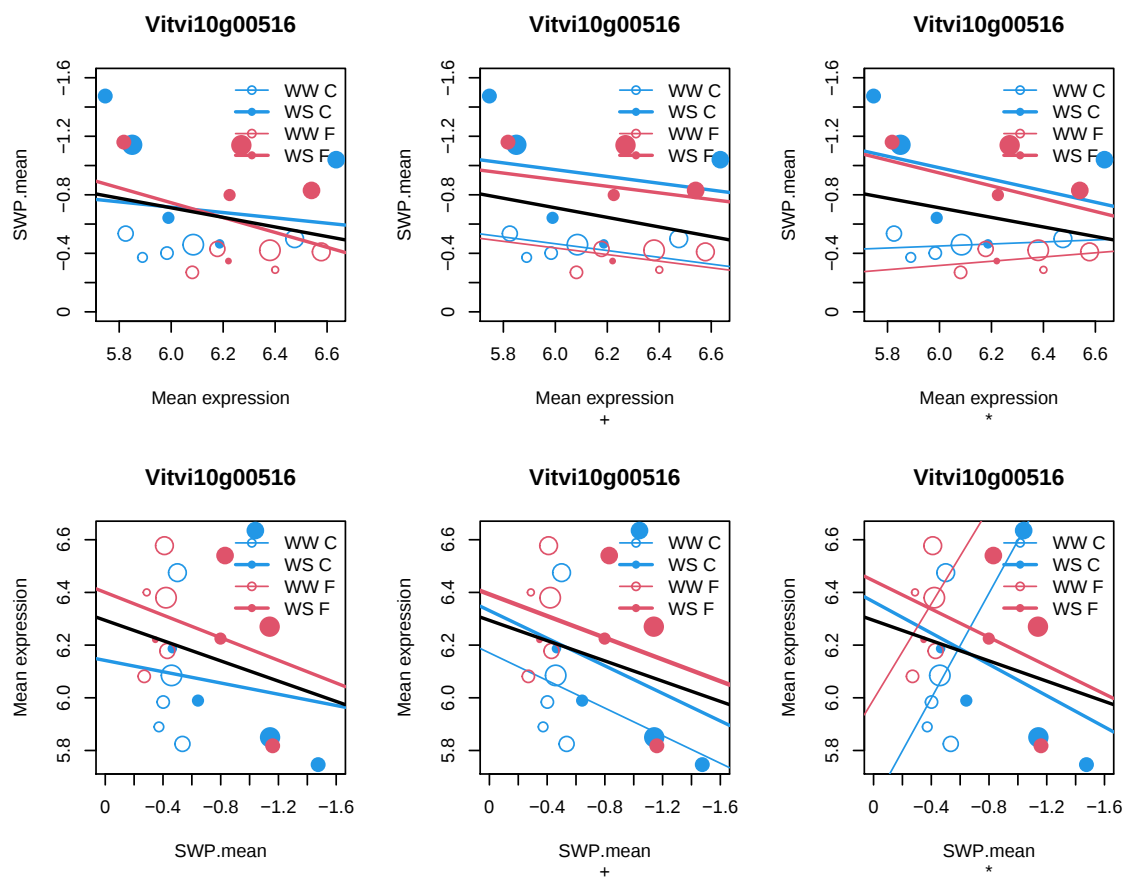
35.2

not assigned.unknown

NA

Coefficient swp for Vitvi10g00516.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi10g00516	-0.01409559	6.167776	-0.02442972	0.9805696	0.9848989
	B				
Vitvi10g00516	-6.1175				



Correlation of all measurements (not just means): $r = -0.0029$, $r^2 = 8e - 06$
 Correlation of mean values (plots): $r_2 = -0.2508$

5.3.34 Vitvi14g02885

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

Vitvi14g02885

35.2

not assigned.unknown

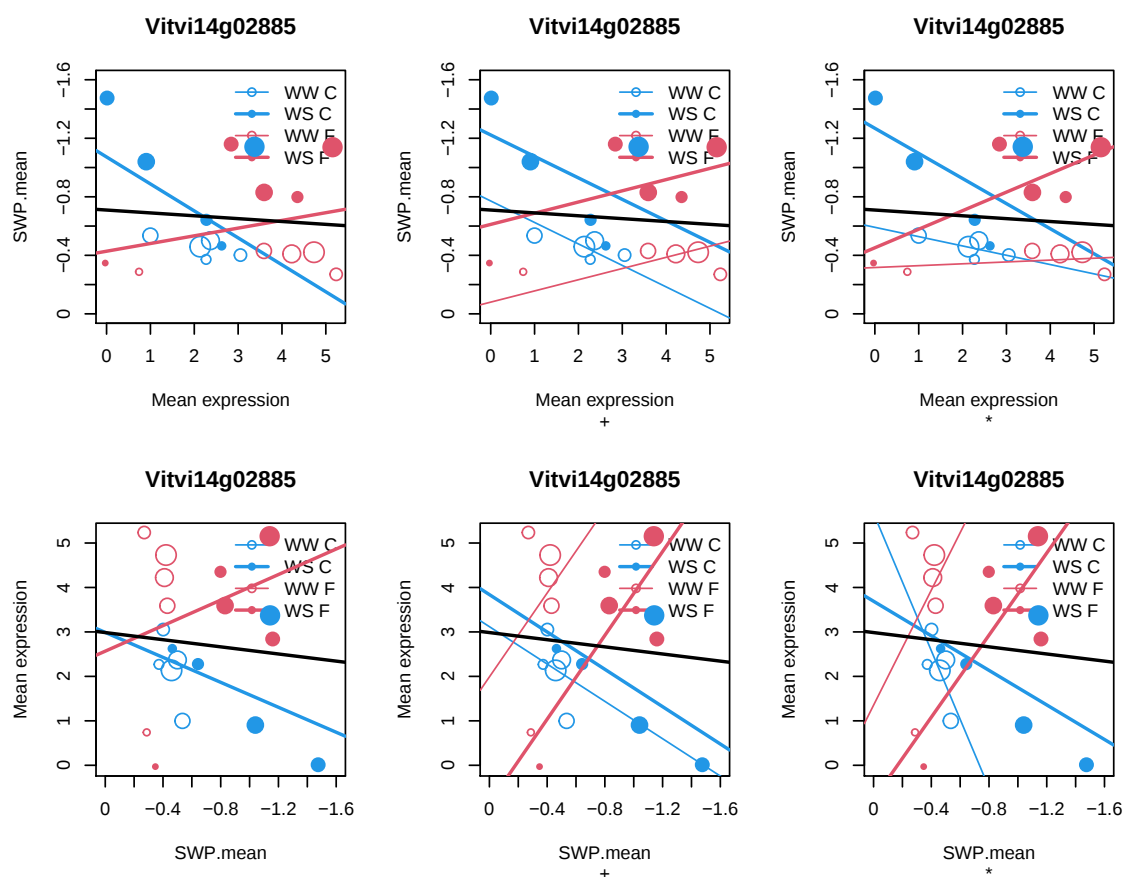
NA

Coefficient swp for Vitvi14g02885.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi14g02885	-0.06985021	2.7222	-0.02375309	0.9811076	0.9853568

B

	logFC
Vitvi14g02885	-6.117515



Correlation of all measurements (not just means): $r = -0.0026$, $r^2 = 7e - 06$
 Correlation of mean values (plots): $r_2 = -0.0886$

5.3.35 Vitvi15g00247

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

Vitvi15g00247

30.3

signalling.calcium

Calcium-binding EF hand family protein |

Chr1:24096548-24097574 REVERSE LENGTH=162 |

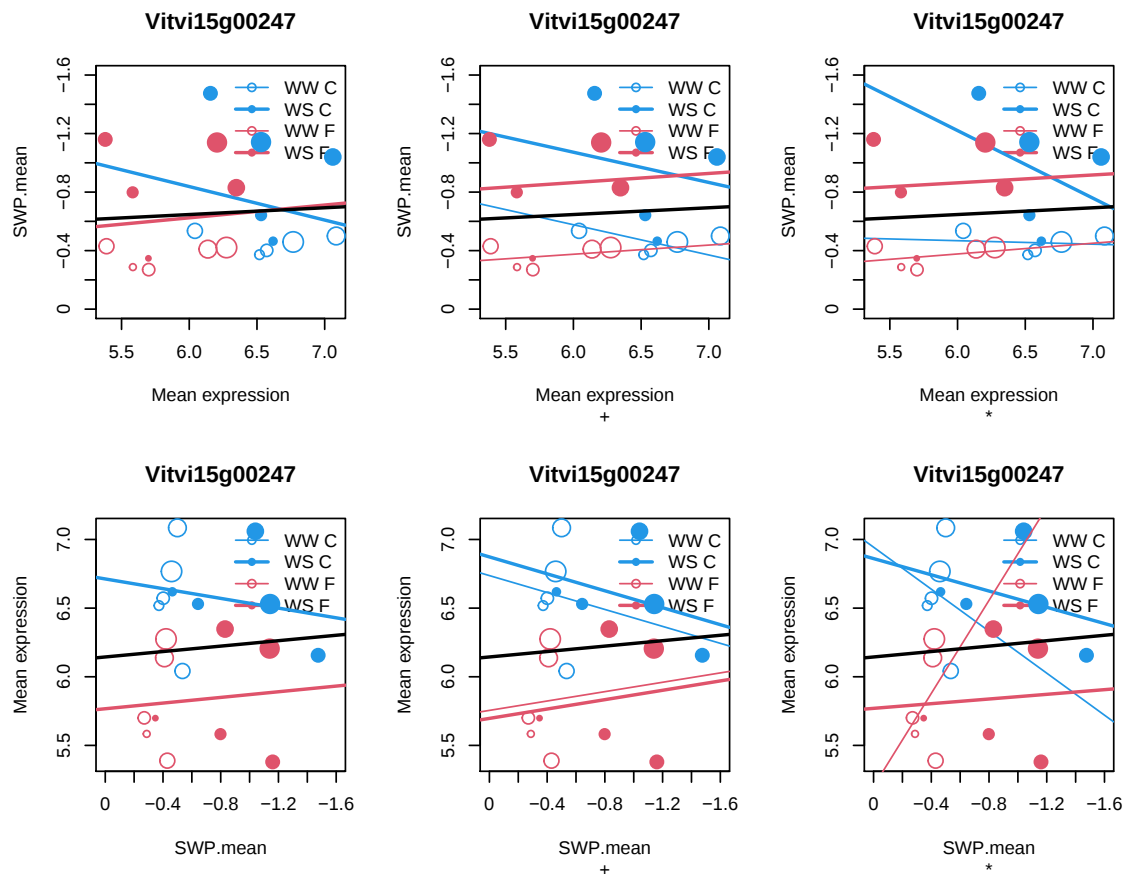
201606

Coefficient swp for Vitvi15g00247.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi15g00247	-0.02283337	6.20896	-0.02369387	0.9811547	0.9853568

B

Vitvi15g00247 -6.117517



Correlation of all measurements (not just means): $r = -0.0027$, $r^2 = 7e - 06$

Correlation of mean values (plots): $r_2 = 0.0676$

5.3.36 Vitvi16g01941

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

Vitvi16g01941

35.2

not assigned.unknown

disease resistance family protein / LRR family protein |

Chr2:14737169-14739886 REVERSE LENGTH=905 |

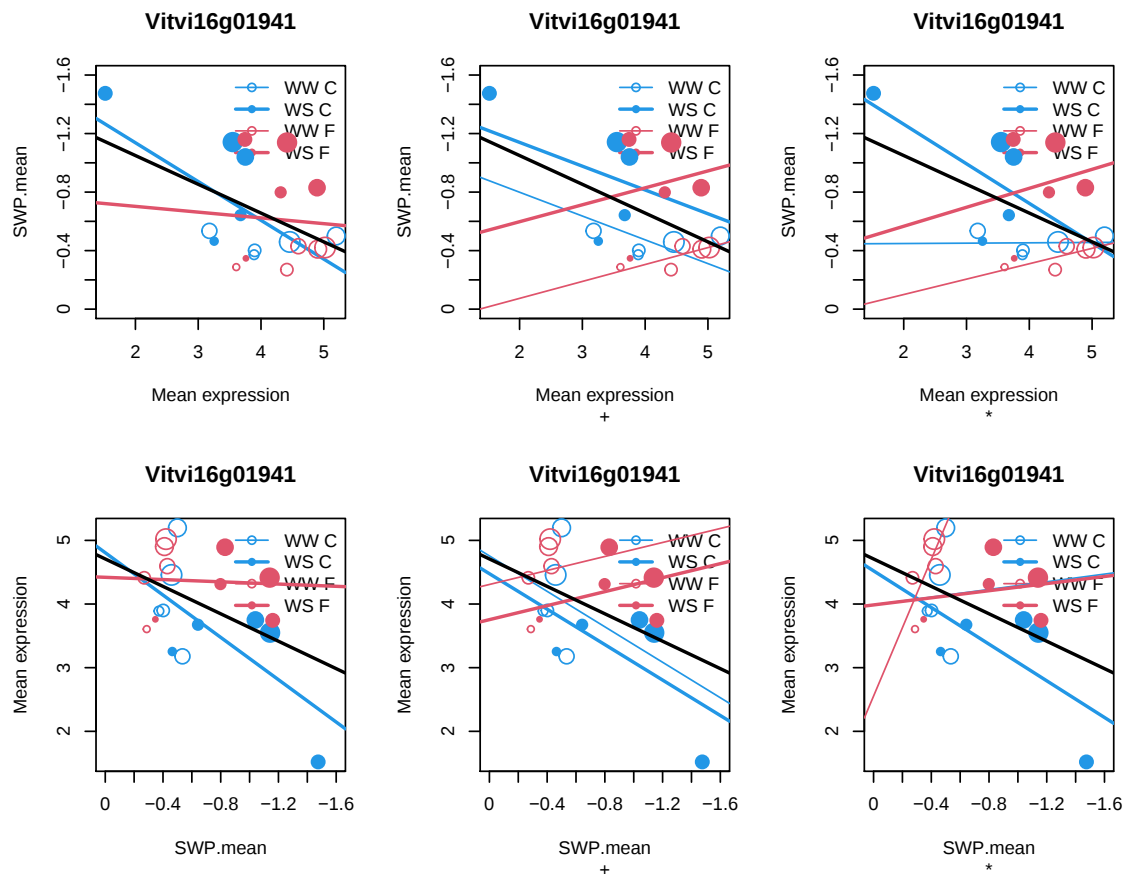
201606

Coefficient swp for Vitvi16g01941.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi16g01941	0.03731173	4.0015	0.02346775	0.9813345	0.9854725

B

Vitvi16g01941 -6.117522



Correlation of all measurements (not just means): $r = 0.0026$, $r^2 = 7e - 06$

Correlation of mean values (plots): $r_2 = -0.4602$

5.3.37 Vitvi13g02500

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

Vitvi13g02500

35.2

not assigned.unknown

NB-ARC domain-containing disease resistance protein |

Chr3:4857940-4861104 FORWARD LENGTH=1054 |

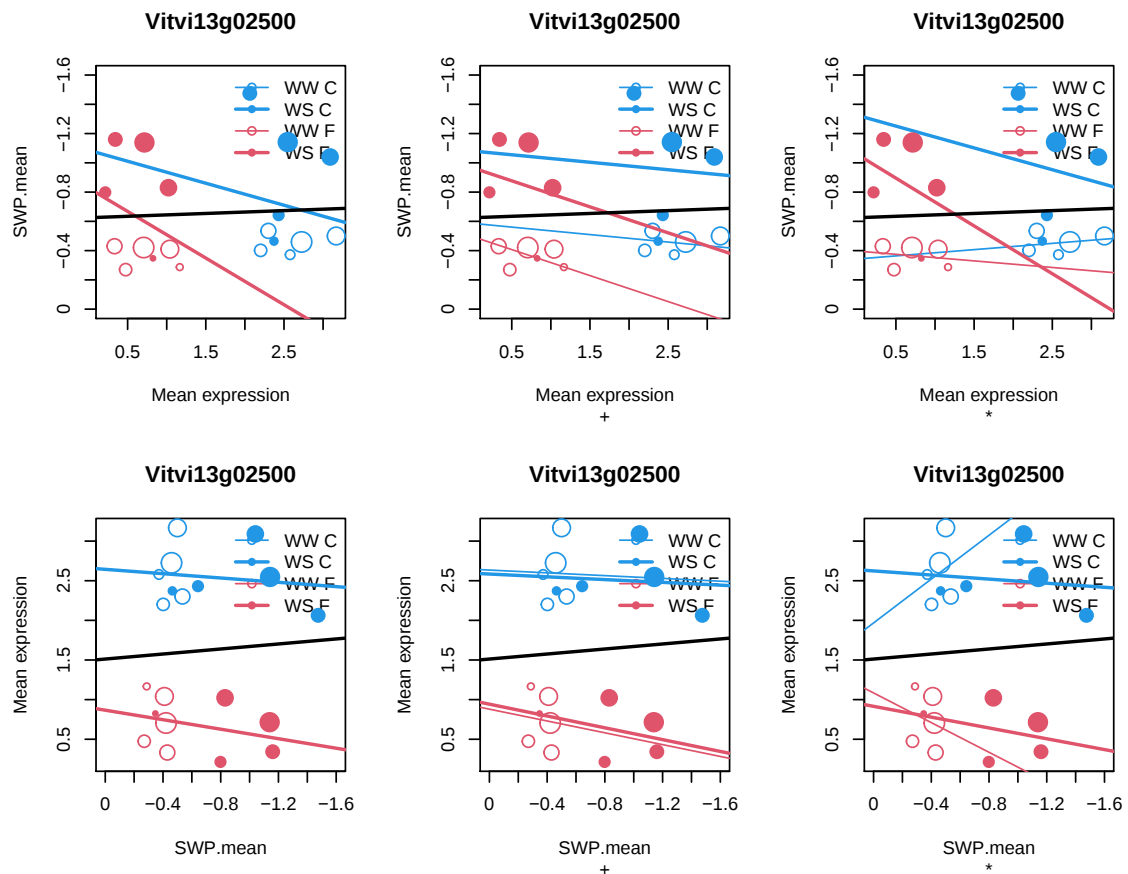
201606

Coefficient swp for Vitvi13g02500.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi13g02500	-0.04409957	1.615715	-0.02297406	0.9817271	0.9858018

B

Vitvi13g02500 -6.117533



Correlation of all measurements (not just means): $r = -0.0026$, $r^2 = 7e-06$

Correlation of mean values (plots): $r_2 = 0.0555$

5.3.38 Vitvi12g02311

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

Vitvi12g02311

29.05.2007

protein.degradation.metalloprotease

[Sotub10g009050.1.1]: Unknown Protein [Sotub10g009050.1.1]: Unknown Protein

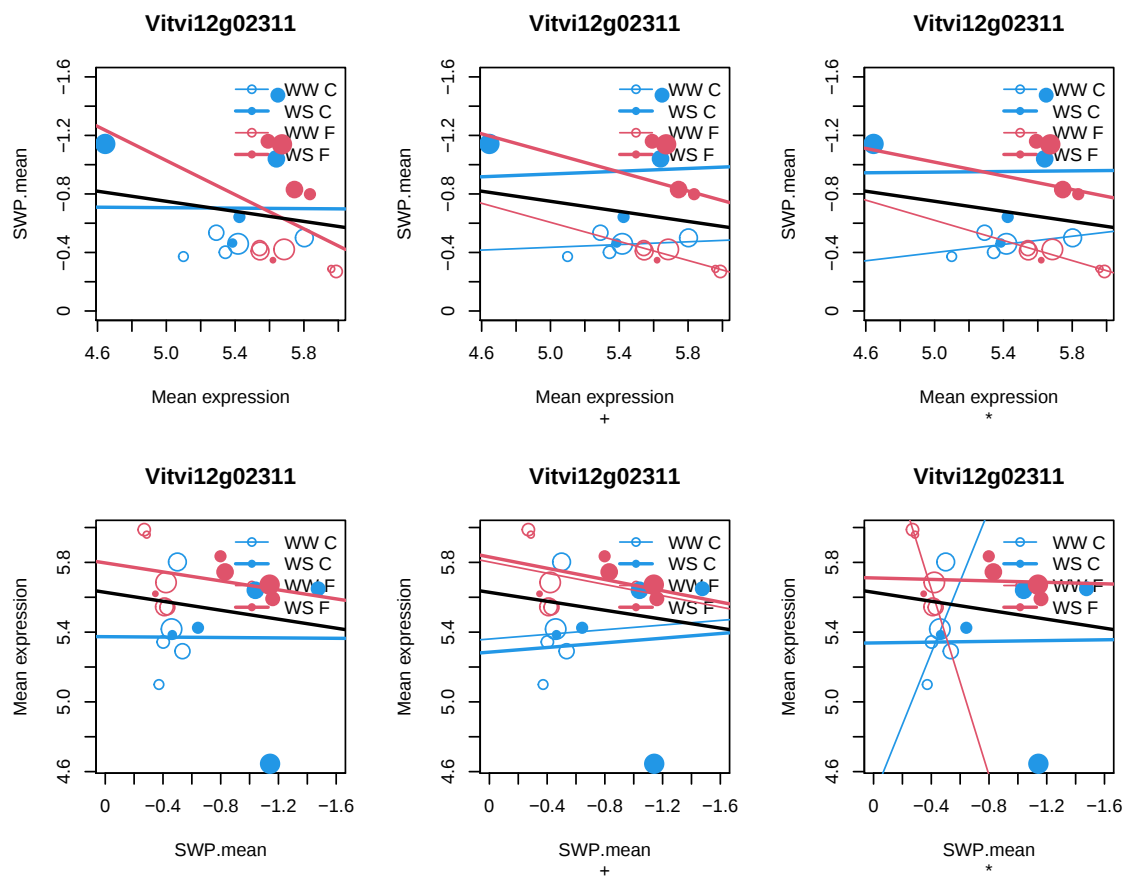
[stNIB-v1_0017431]

Coefficient swp for Vitvi12g02311.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi12g02311	-0.01657514	5.54402	-0.02288825	0.9817954	0.9858053

B

	logFC
Vitvi12g02311	-6.117535



Correlation of all measurements (not just means): $r = -0.0026$, $r^2 = 7e - 06$
 Correlation of mean values (plots): $r_2 = -0.1487$

5.3.39 Vitvi16g00189

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

Vitvi16g00189

35.2

not assigned.unknown

krueppel-like factor |

Chr5:5572640-5572939 FORWARD LENGTH=99 |

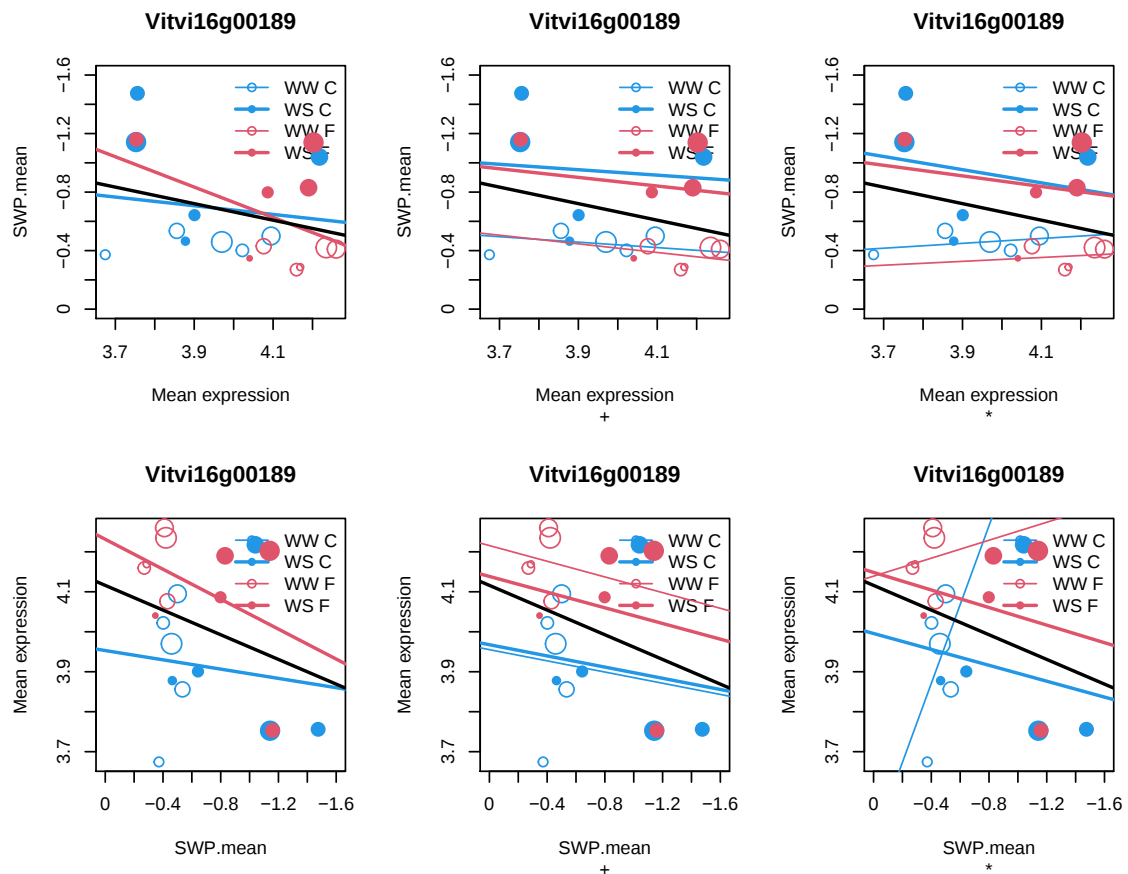
201606

Coefficient swp for Vitvi16g00189.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi16g00189	0.01103498	4.014703	0.02276618	0.9818924	0.9858358

B

Vitvi16g00189 -6.117538



Correlation of all measurements (not just means): $r = 0.0027$, $r^2 = 7e-06$

Correlation of mean values (plots): $r_2 = -0.2954$

5.3.40 Vitvi11g01151

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

Vitvi11g01151

29.8

protein.assembly and cofactor ligation

APO RNA-binding protein (DUF794) |

Chr5:24866230-24867665 REVERSE LENGTH=402 |

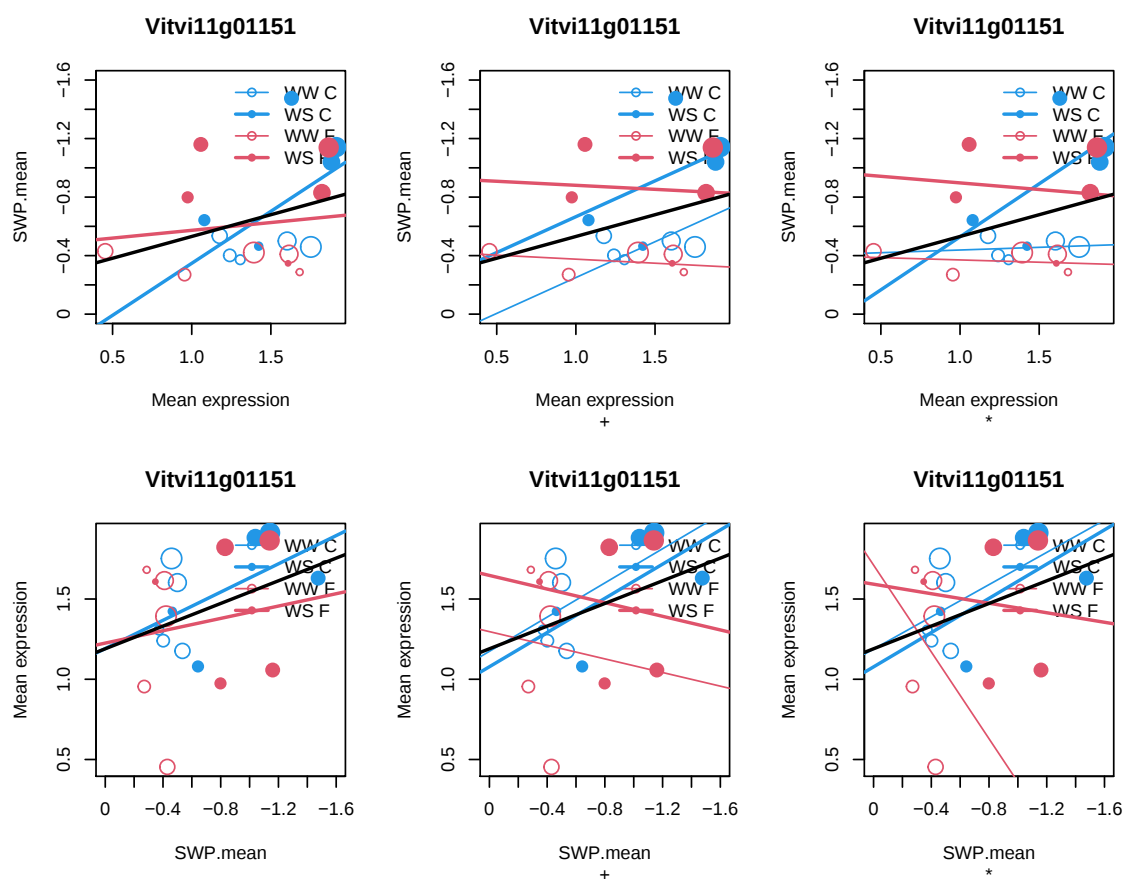
201606

Coefficient swp for Vitvi11g01151.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi11g01151	-0.01907197	1.421583	-0.02268742	0.9819551	0.9858358

B

Vitvi11g01151 -6.117539



Correlation of all measurements (not just means): $r = -0.0026$, $r^2 = 7e - 06$

Correlation of mean values (plots): $r_2 = 0.3241$

5.3.41 Vitvi09g01961

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

Vitvi09g01961

35.2

not assigned.unknown

disease resistance family protein / LRR family protein |

Chr2:14737169-14739886 REVERSE LENGTH=905 |

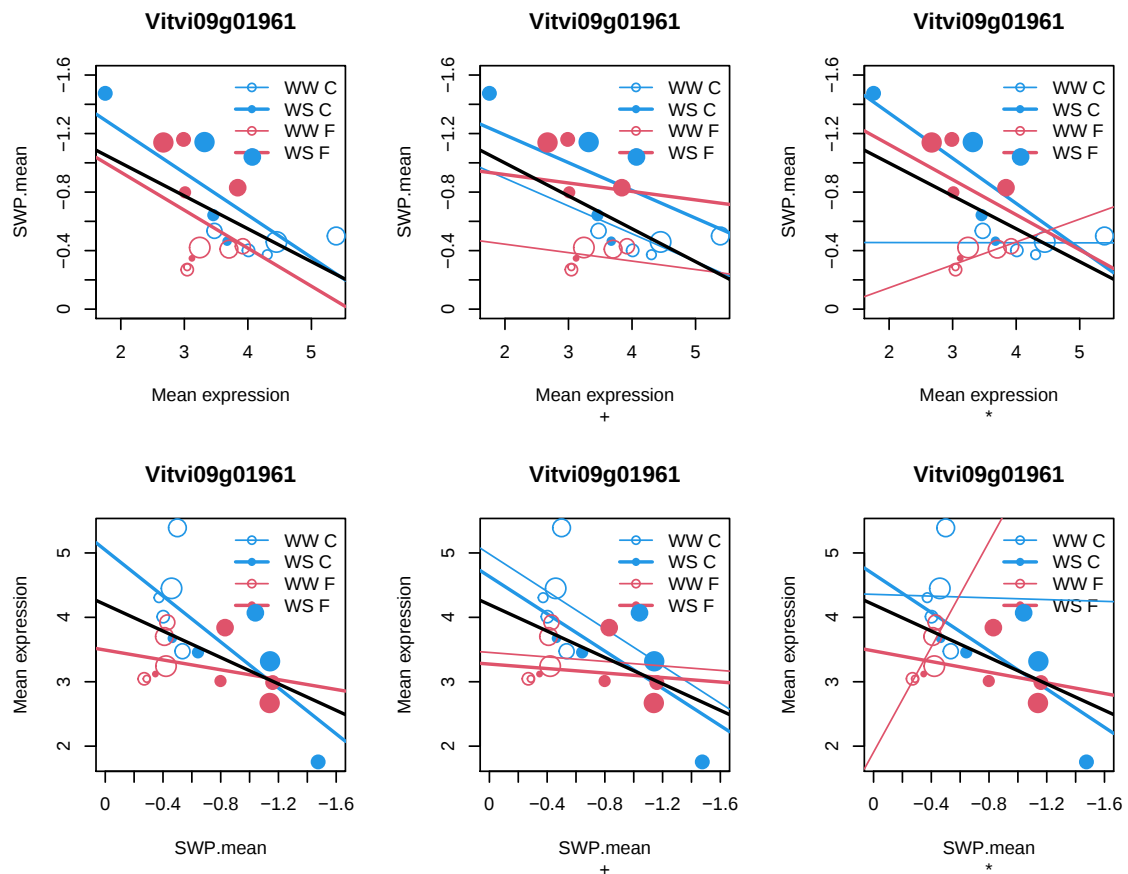
201606

Coefficient swp for Vitvi09g01961.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi09g01961	0.03292069	3.524352	0.02189841	0.9825825	0.9863358

B

Vitvi09g01961 -6.117556



Correlation of all measurements (not just means): $r = 0.0024$, $r^2 = 6e - 06$

Correlation of mean values (plots): $r_2 = -0.4803$

5.3.42 Vitvi14g02007

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

Vitvi14g02007

35.2

not assigned.unknown

WRKY DNA-binding protein 3 |

Chr2:1014724-1016936 REVERSE LENGTH=513 |

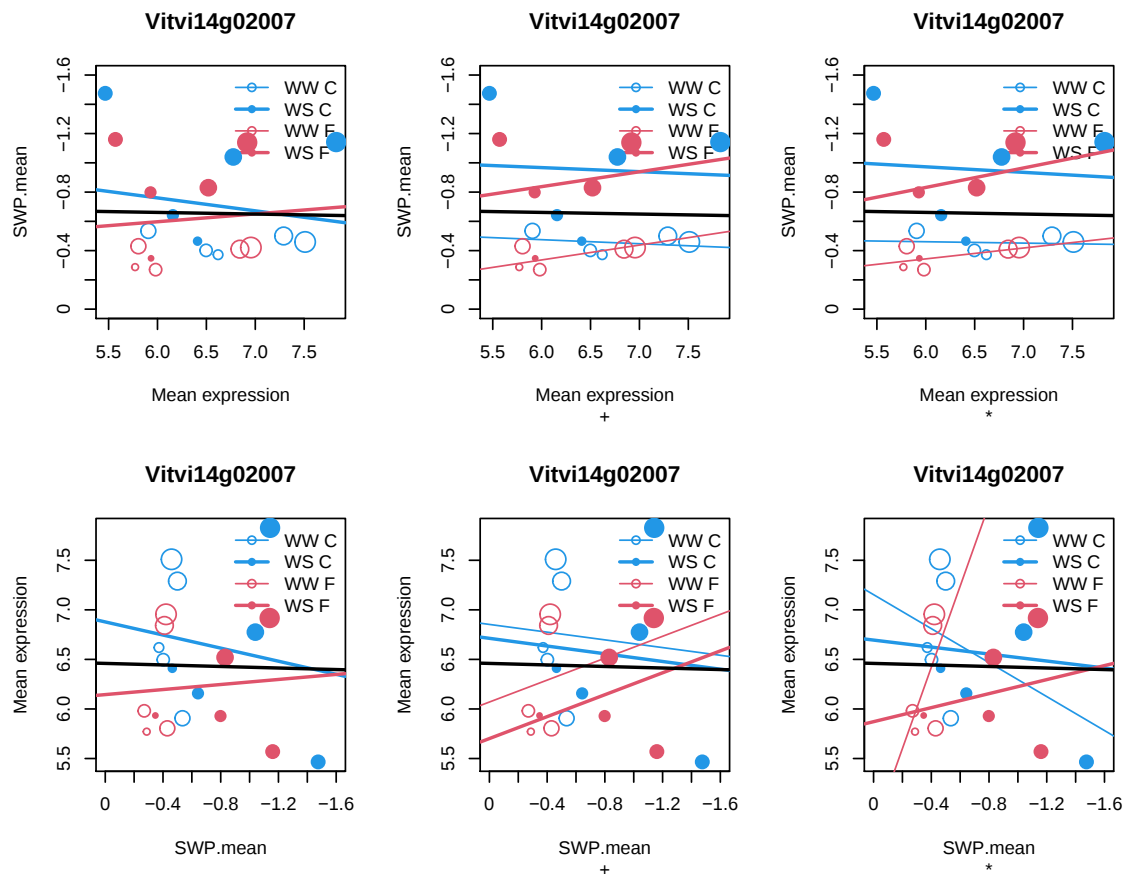
201606

Coefficient swp for Vitvi14g02007.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi14g02007	0.02640272	6.434134	0.02189839	0.9825826	0.9863358

B

Vitvi14g02007 -6.117556



Correlation of all measurements (not just means): $r = 0.0025$, $r^2 = 6e - 06$

Correlation of mean values (plots): $r_2 = -0.0208$

5.3.43 Vitvi06g00693

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

Vitvi06g00693

29.04.2001

protein.postranslational modification.kinase

Protein kinase superfamily protein |

Chr5:23655312-23657943 FORWARD LENGTH=604 |

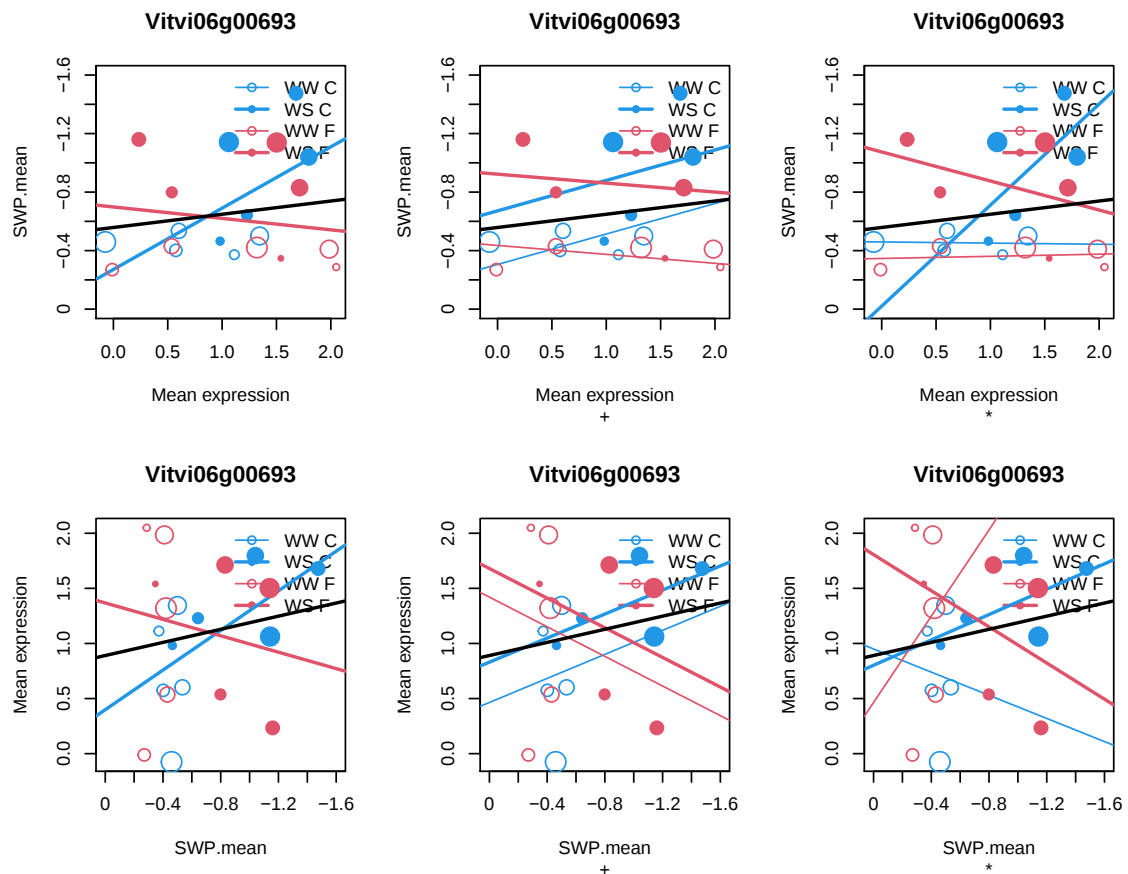
201606

Coefficient swp for Vitvi06g00693.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi06g00693	-0.03613652	1.085786	-0.02131237	0.9830486	0.9867387

B

Vitvi06g00693 -6.117568



Correlation of all measurements (not just means): $r = -0.0024$, $r^2 = 6e - 06$

Correlation of mean values (plots): $r_2 = 0.1641$

5.3.44 Vitvi11g00980

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

Vitvi11g00980

35.1.5

not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein

Pentatricopeptide repeat (PPR-like) superfamily protein |

Chr5:4445461-4447290 FORWARD LENGTH=609 |

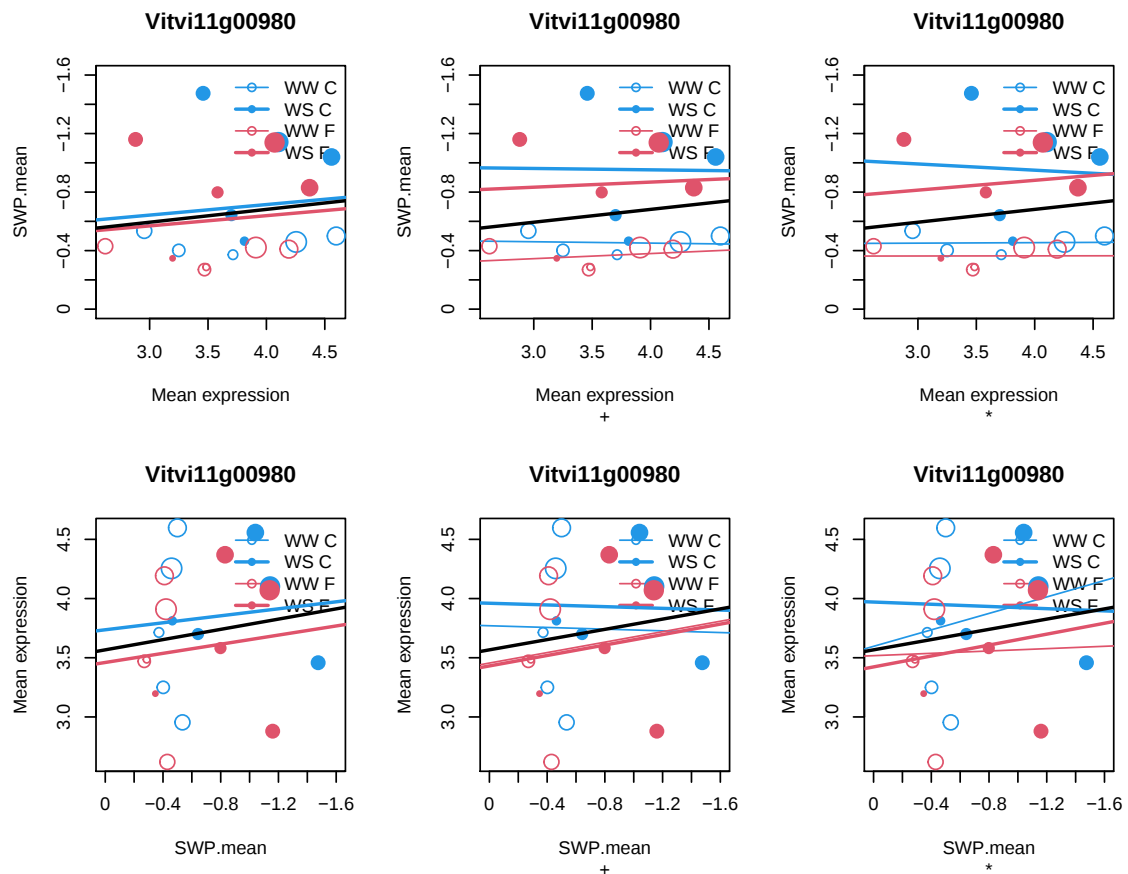
201606

Coefficient swp for Vitvi11g00980.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi11g00980	0.02282708	3.708823	0.02061054	0.9836067	0.9872339

B

Vitvi11g00980 -6.117583



Correlation of all measurements (not just means): $r = 0.0023$, $r^2 = 5e - 06$

Correlation of mean values (plots): $r_2 = 0.1377$

5.3.45 Vitvi15g00900

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

Vitvi15g00900

29.04.2001

protein.postranslational modification.kinase

CBL-interacting protein kinase 9 |

Chr1:64398-67512 REVERSE LENGTH=449 |

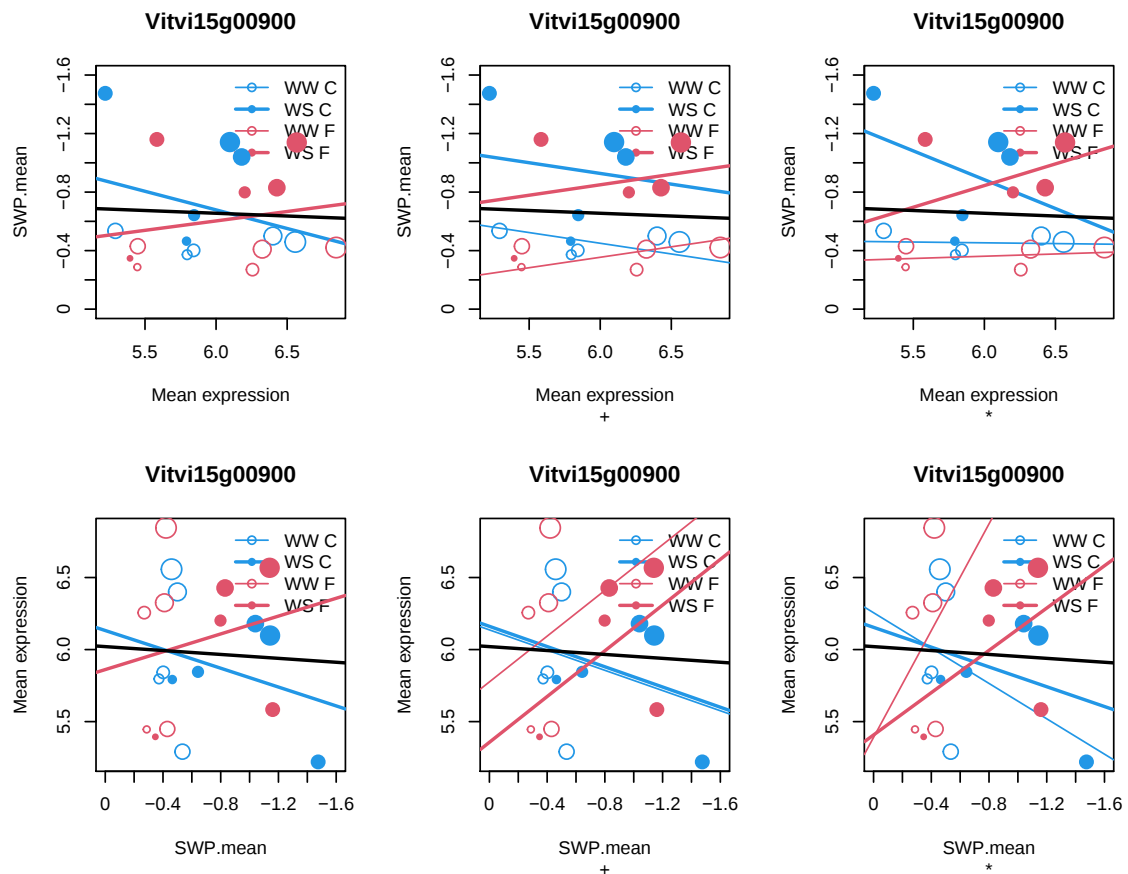
201606

Coefficient swp for Vitvi15g00900.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi15g00900	-0.0176634	5.97592	-0.01990671	0.9841665	0.9876957

B

Vitvi15g00900 -6.117596



Correlation of all measurements (not just means): $r = -0.0023$, $r^2 = 5e - 06$

Correlation of mean values (plots): $r_2 = -0.0505$

5.3.46 Vitvi04g01131

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

Vitvi04g01131

35.2

not assigned.unknown

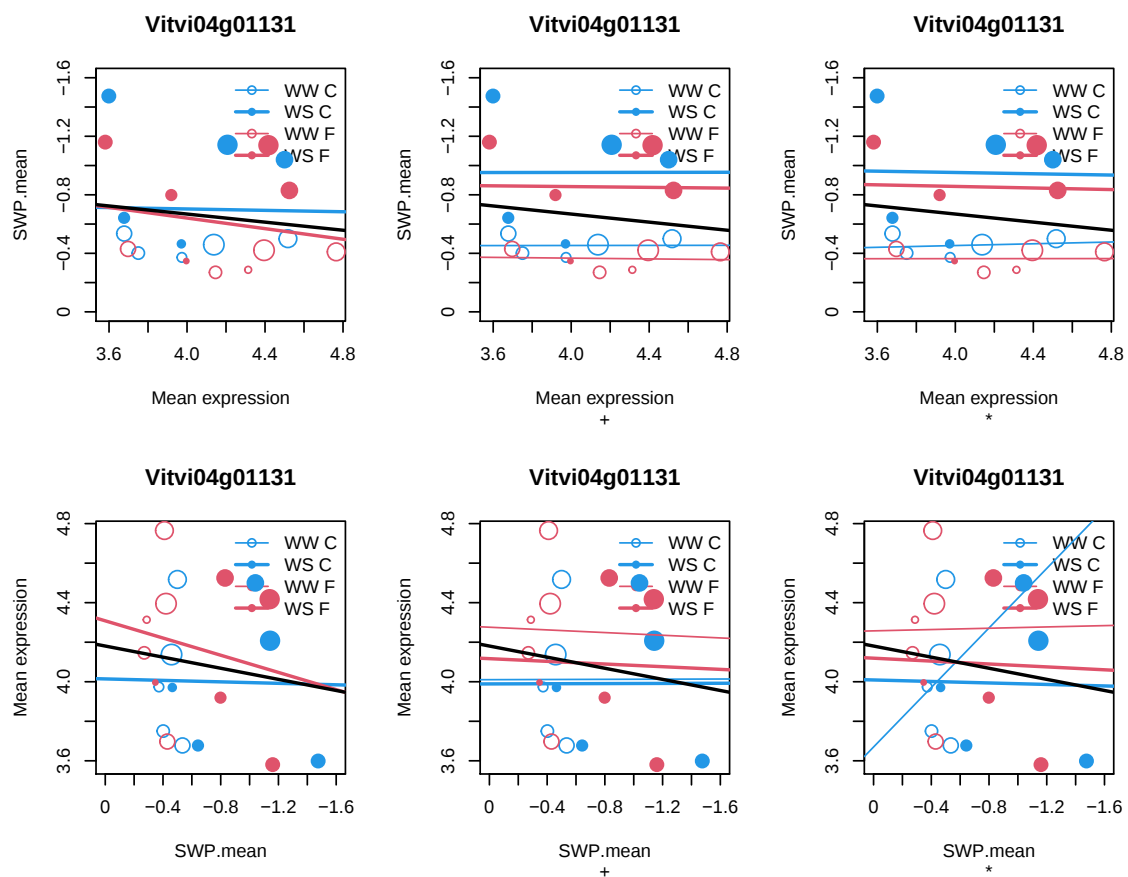
R3H domain-containing protein 2 IPR001374 Single-stranded nucleic acid

Coefficient swp for Vitvi04g01131.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi04g01131	0.01373914	4.088375	0.01986902	0.9841964	0.9876957

B

Vitvi04g01131	-6.117597
---------------	-----------



Correlation of all measurements (not just means): $r = 0.0023$, $r^2 = 5e - 06$
 Correlation of mean values (plots): $r_2 = -0.1394$

5.3.47 Vitvi13g01340

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

Vitvi13g01340

27.03.1930

RNA.regulation of transcription.triple-helix transcription factor fami
sequence-specific DNA binding transcription factor |

Chr3:20137912-20138863 REVERSE LENGTH=296 |

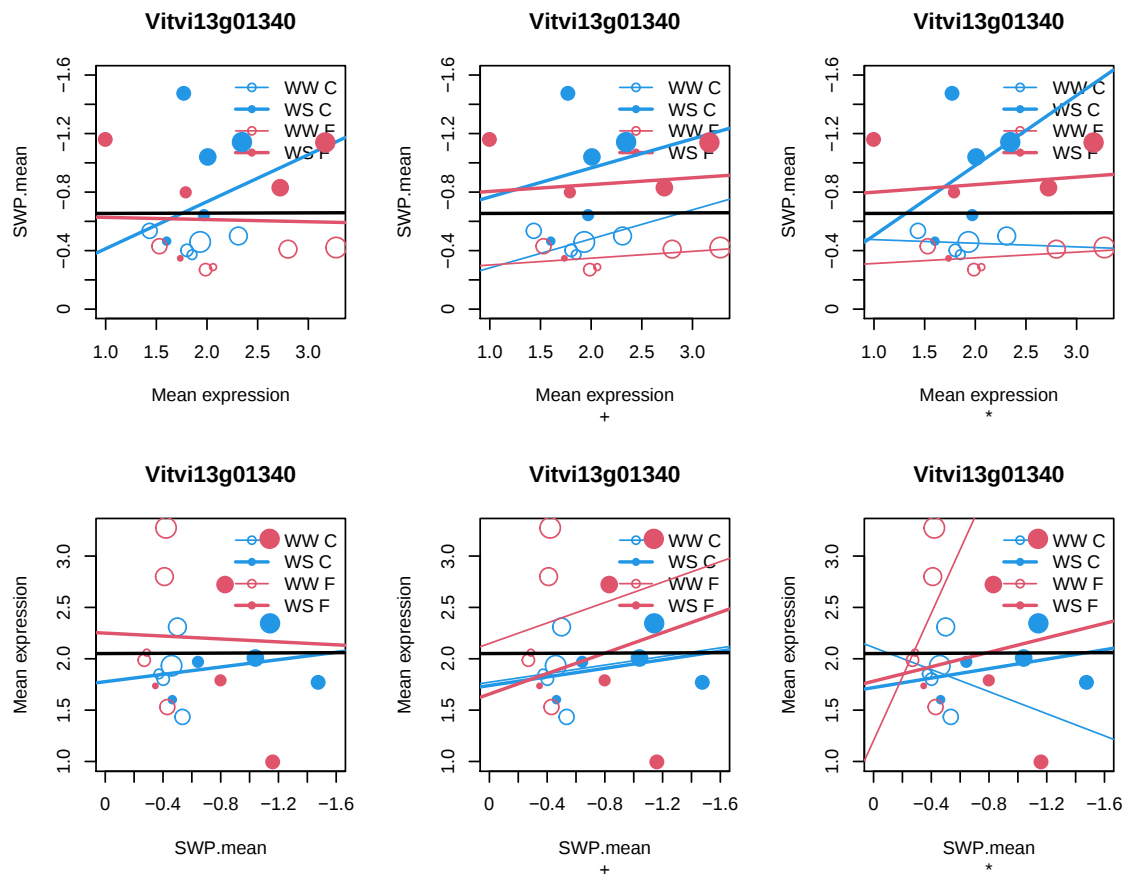
201606

Coefficient swp for Vitvi13g01340.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi13g01340	0.02512764	2.054412	0.01931603	0.9846362	0.988072

B

Vitvi13g01340 -6.117608



Correlation of all measurements (not just means): $r = 0.0022$, $r^2 = 5e - 06$

Correlation of mean values (plots): $r_2 = 0.0033$

5.3.48 Vitvi08g02296

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

Vitvi08g02296

35.2

not assigned.unknown

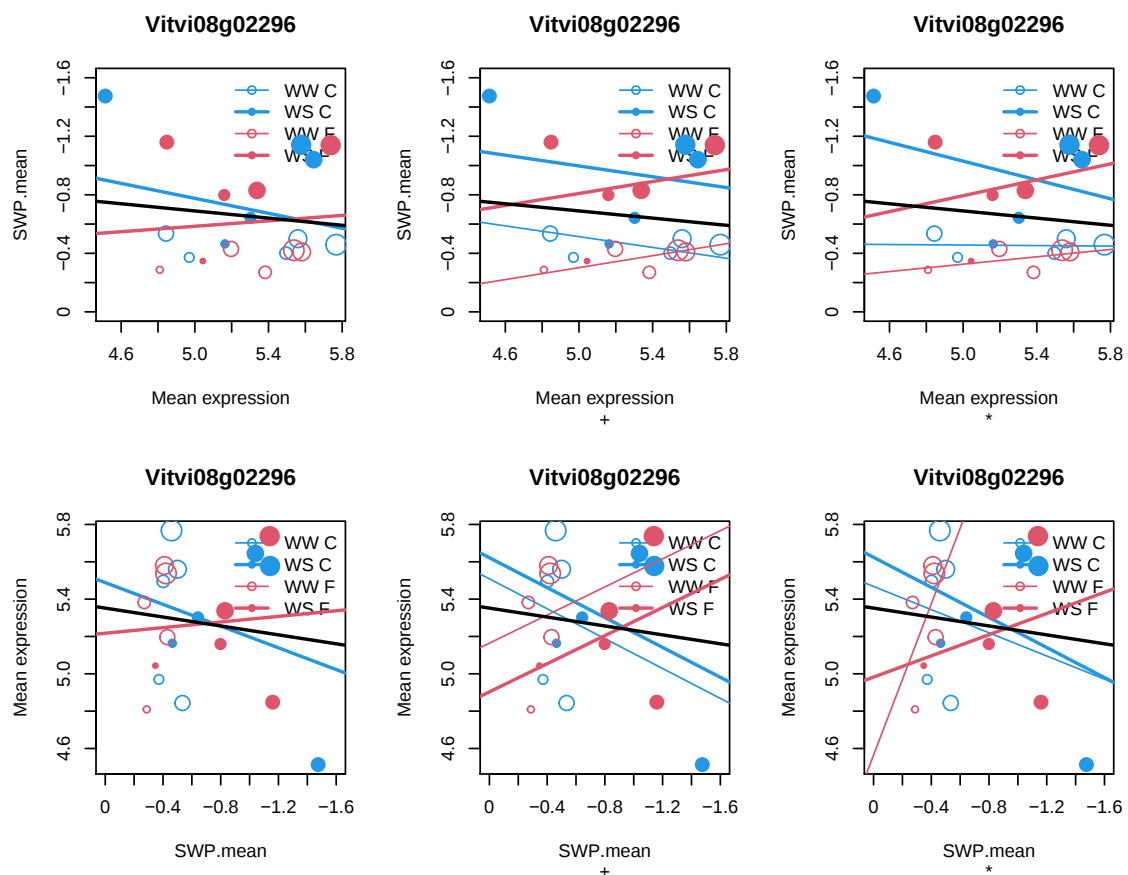
NA

Coefficient swp for Vitvi08g02296.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi08g02296	-0.01336535	5.273452	-0.01913332	0.9847815	0.9881527

B

Vitvi08g02296	-6.117611
---------------	-----------



Correlation of all measurements (not just means): $r = -0.0022$, $r^2 = 5e - 06$
 Correlation of mean values (plots): $r_2 = -0.1210$

5.3.49 Vitvi08g01332

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

Vitvi08g01332

34.13

transport.peptides and oligopeptides

8-amino-7-oxononanoate synthase |

Chr3:2764860-2765907 FORWARD LENGTH=258 |

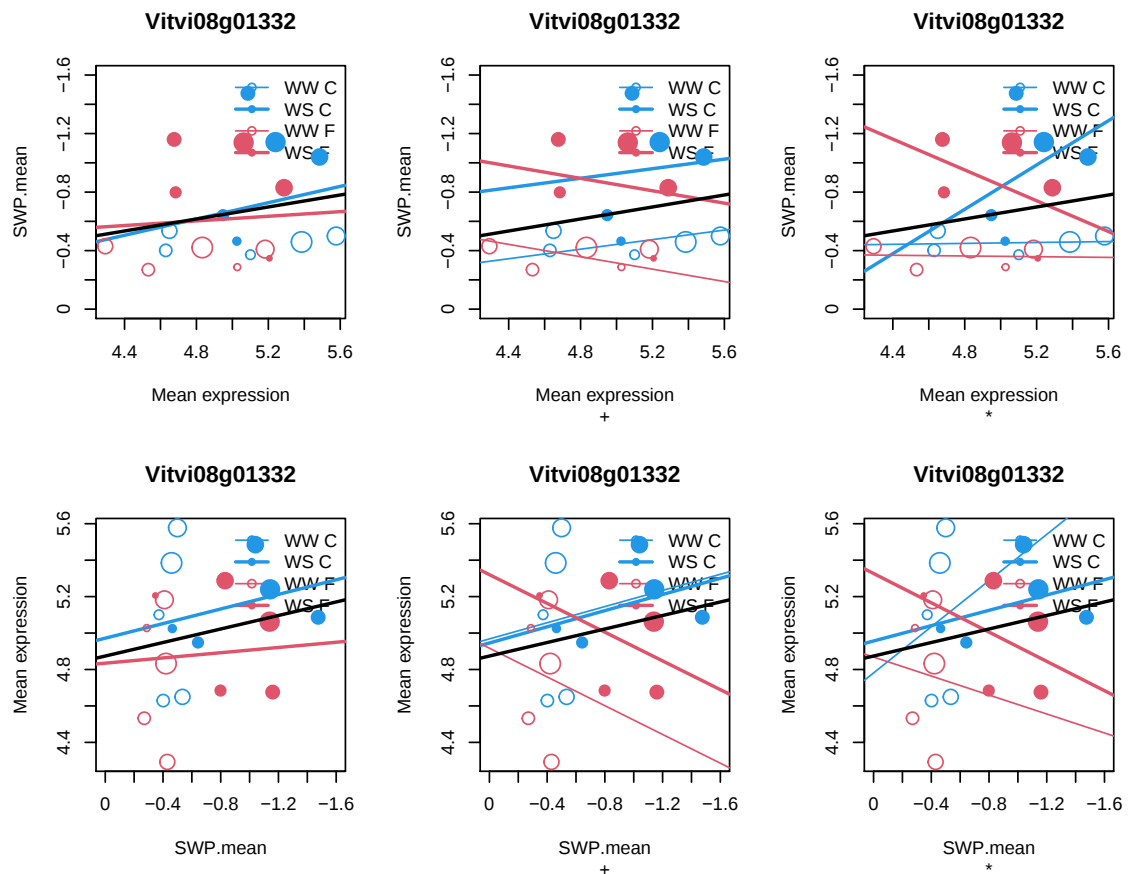
201606

Coefficient swp for Vitvi08g01332.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi08g01332	0.0135843	4.995503	0.01857236	0.9852277	0.9885353

B

Vitvi08g01332 -6.117621



Correlation of all measurements (not just means): $r = 0.0021$, $r^2 = 5e - 06$

Correlation of mean values (plots): $r_2 = 0.1950$

5.3.50 Vitvi09g00069

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

Vitvi09g00069

27.1

RNA.processing

Small nuclear ribonucleoprotein family protein |

Chr3:4668350-4668989 FORWARD LENGTH=118 |

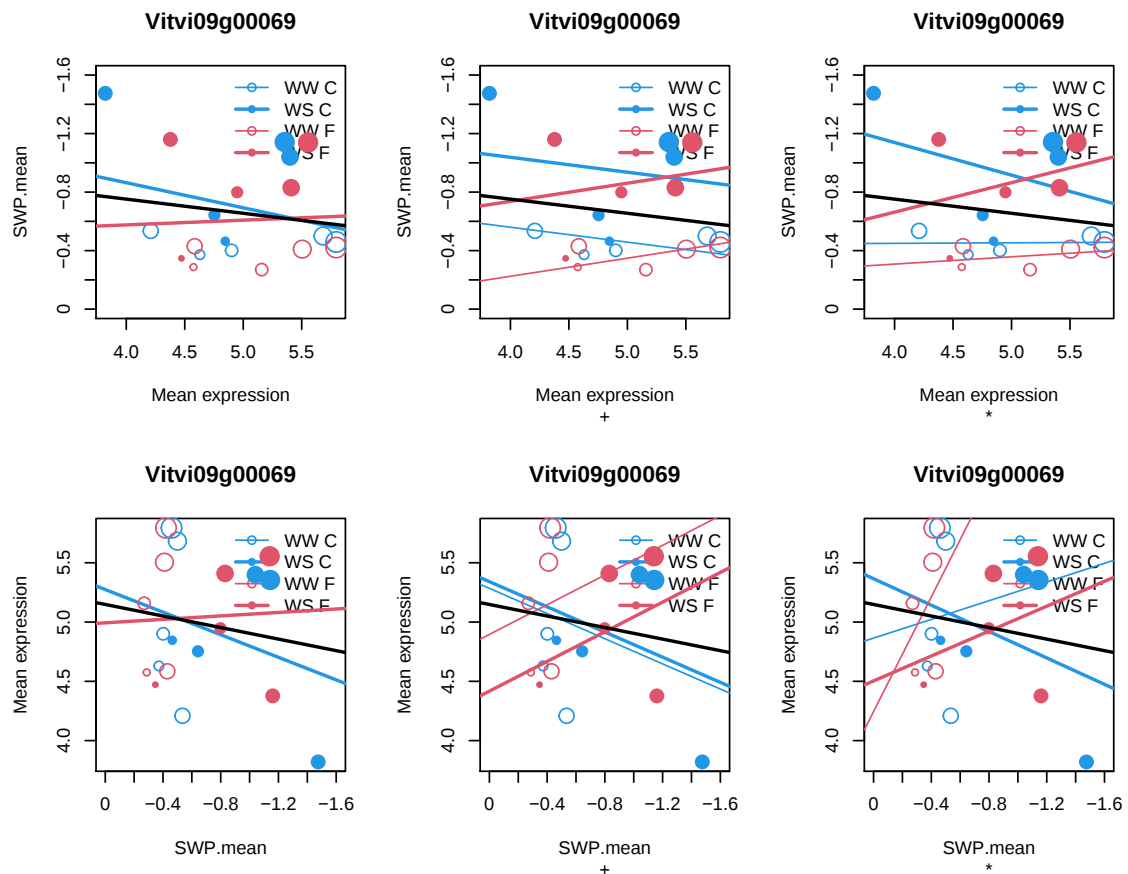
201606

Coefficient swp for Vitvi09g00069.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi09g00069	-0.01896949	4.988576	-0.01805106	0.9856423	0.9888862

B

Vitvi09g00069 -6.11763



Correlation of all measurements (not just means): $r = -0.0020$, $r^2 = 4e - 06$

Correlation of mean values (plots): $r_2 = -0.1535$

5.3.51 Vitvi08g01926

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

Vitvi08g01926

35.2

not assigned.unknown

amino-terminal glutamine amidohydrolase |

Chr2:17422864-17424255 FORWARD LENGTH=221 |

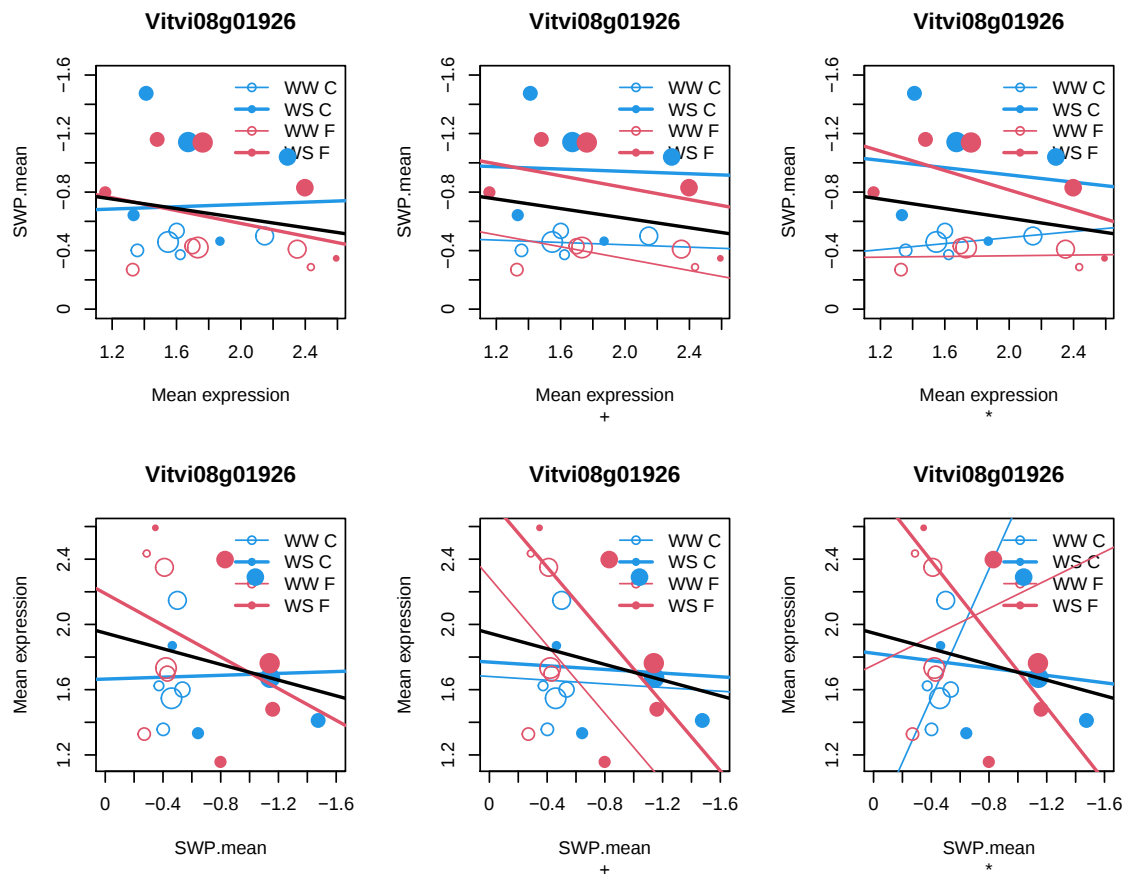
201606

Coefficient swp for Vitvi08g01926.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi08g01926	-0.01607702	1.78932	-0.01779396	0.9858467	0.9890263

B

Vitvi08g01926 -6.117635



Correlation of all measurements (not just means): $r = -0.0020$, $r^2 = 4e - 06$

Correlation of mean values (plots): $r_2 = -0.1983$

5.3.52 Vitvi13g00052

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

Vitvi13g00052

29.04.2001

protein.postranslational modification.kinase

Protein kinase superfamily protein |

Chr2:16755137-16757258 REVERSE LENGTH=570 |

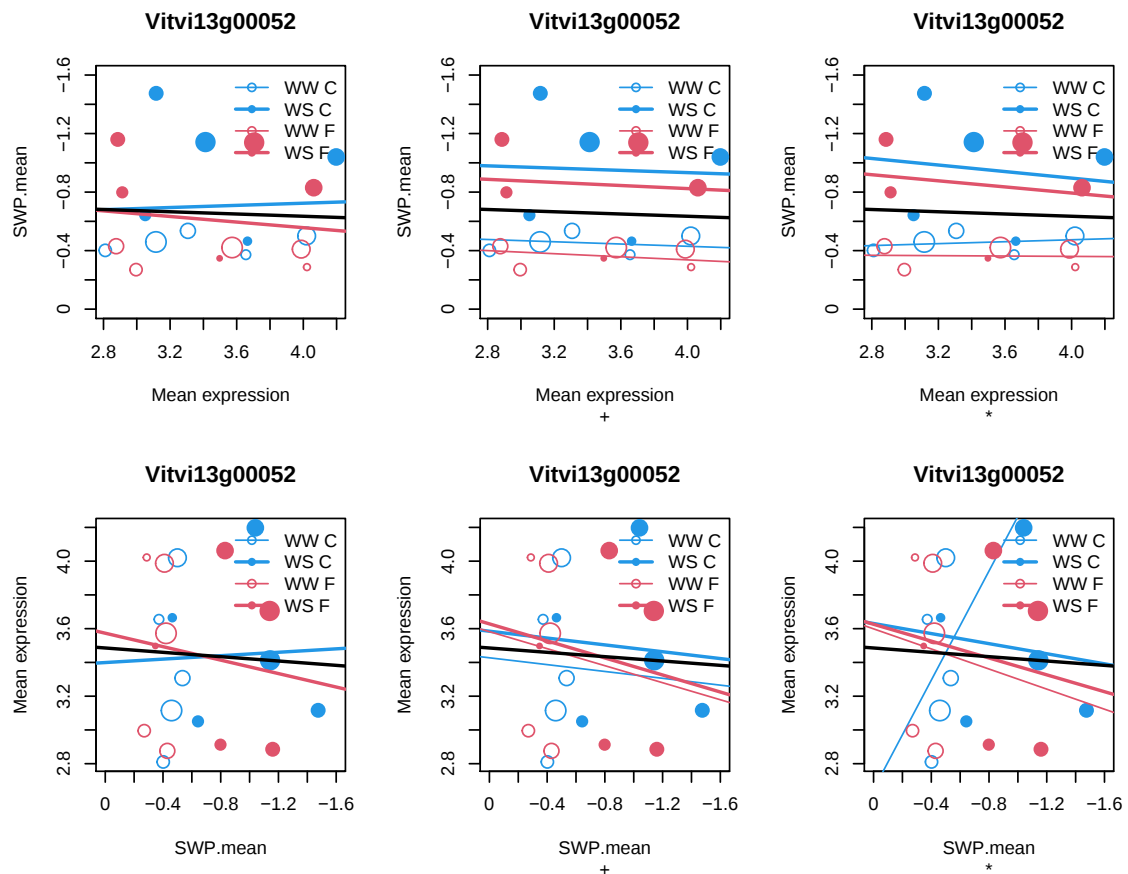
201606

Coefficient swp for Vitvi13g00052.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi13g00052	0.01562152	3.44332	0.017469	0.9861052	0.9892204

B

Vitvi13g00052 -6.11764



Correlation of all measurements (not just means): $r = 0.0020$, $r^2 = 4e - 06$

Correlation of mean values (plots): $r_2 = -0.0497$

5.3.53 Vitvi06g00121

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

Vitvi06g00121

3.6

minor CHO metabolism.callose

glucan synthase-like 12 |

Chr5:4110445-4121202 REVERSE LENGTH=1914 |

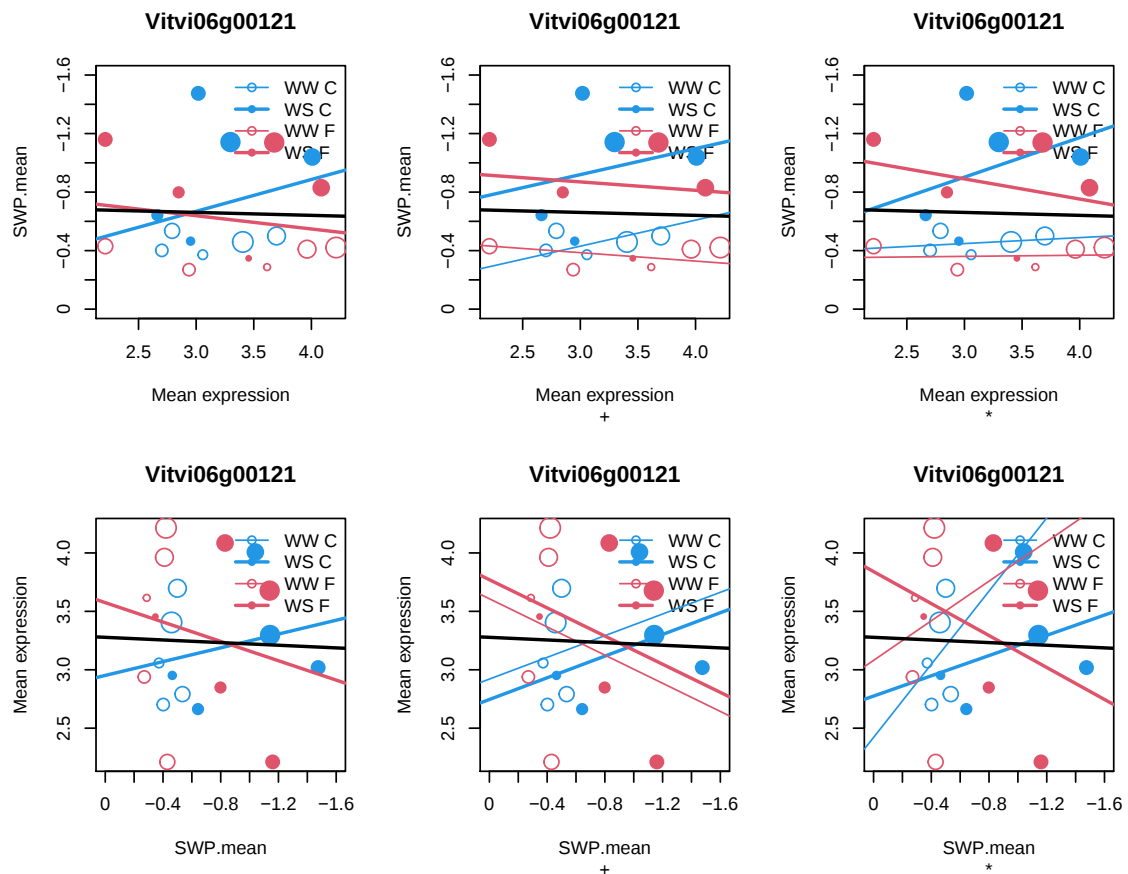
201606

Coefficient swp for Vitvi06g00121.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi06g00121	-0.02016823	3.240657	-0.01718655	0.9863298	0.9893379

B

Vitvi06g00121 -6.117645



Correlation of all measurements (not just means): $r = -0.0019$, $r^2 = 4e - 06$

Correlation of mean values (plots): $r_2 = -0.0337$

5.3.54 Vitvi15g00410

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

Vitvi15g00410

29.5.11.4.2

protein.degradation.ubiquitin.E3.RING

zinc ion binding protein |

Chr2:18402081-18403412 REVERSE LENGTH=386 |

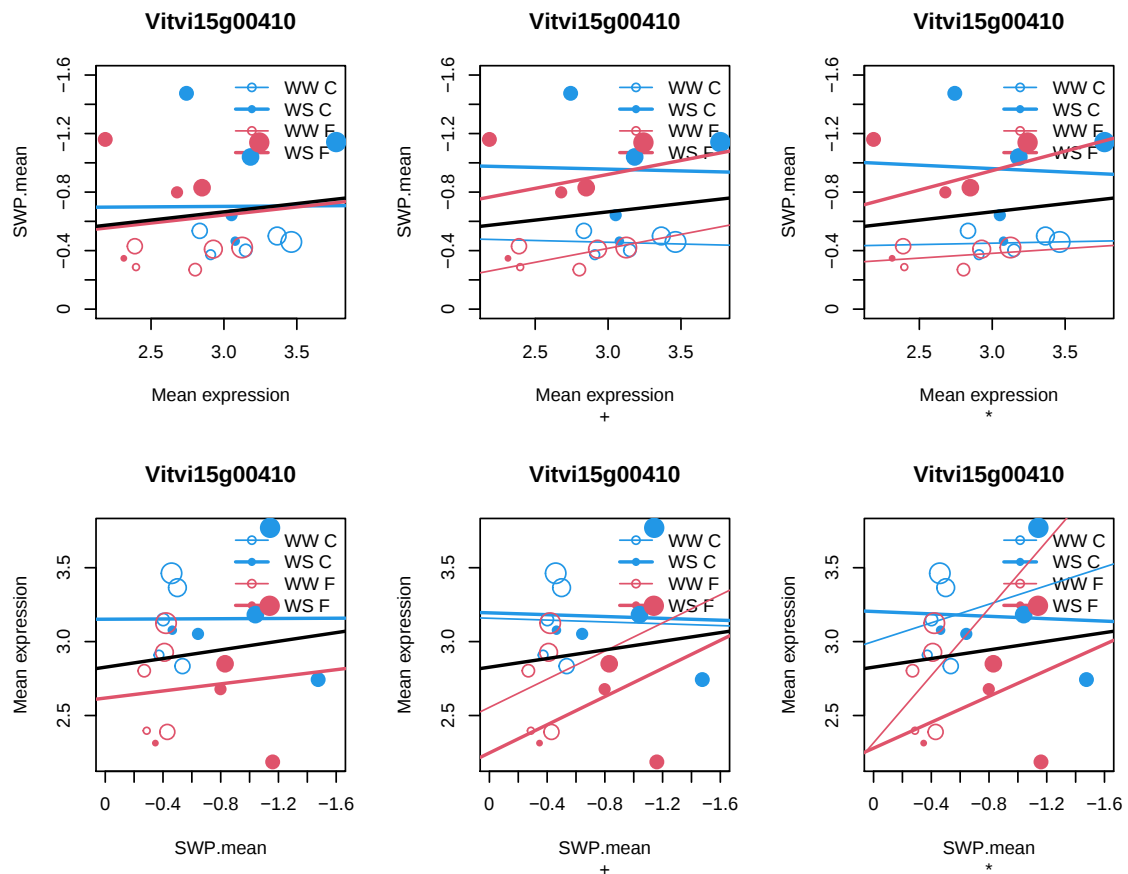
201606

Coefficient swp for Vitvi15g00410.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi15g00410	0.01356891	2.922824	0.0171585	0.9863521	0.9893379

B

Vitvi15g00410 -6.117646



Correlation of all measurements (not just means): $r = 0.0020$, $r^2 = 4e - 06$

Correlation of mean values (plots): $r_2 = 0.1285$

5.3.55 Vitvi09g00161

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

Vitvi09g00161

29.5

protein.degradation

aminopeptidase M1 |

Chr4:15965915-15970418 REVERSE LENGTH=879 |

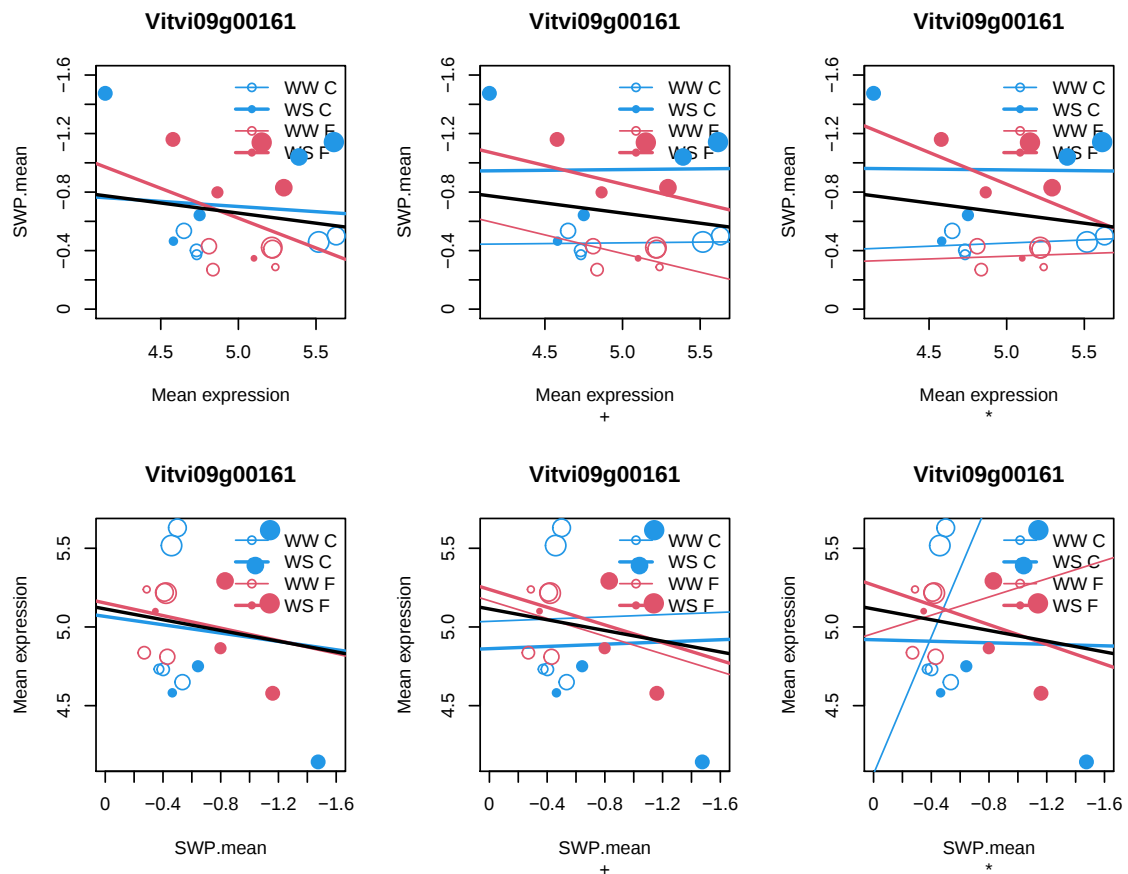
201606

Coefficient swp for Vitvi09g00161.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi09g00161	0.01323794	5.002242	0.01706073	0.9864299	0.9893508

B

Vitvi09g00161 -6.117647



Correlation of all measurements (not just means): $r = 0.0019$, $r^2 = 4e - 06$

Correlation of mean values (plots): $r_2 = -0.1534$

5.3.56 Vitvi13g02109

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

Vitvi13g02109

31.1

cell.organisation

Ankyrin repeat family protein |

Chr5:1354240-1356754 REVERSE LENGTH=669 |

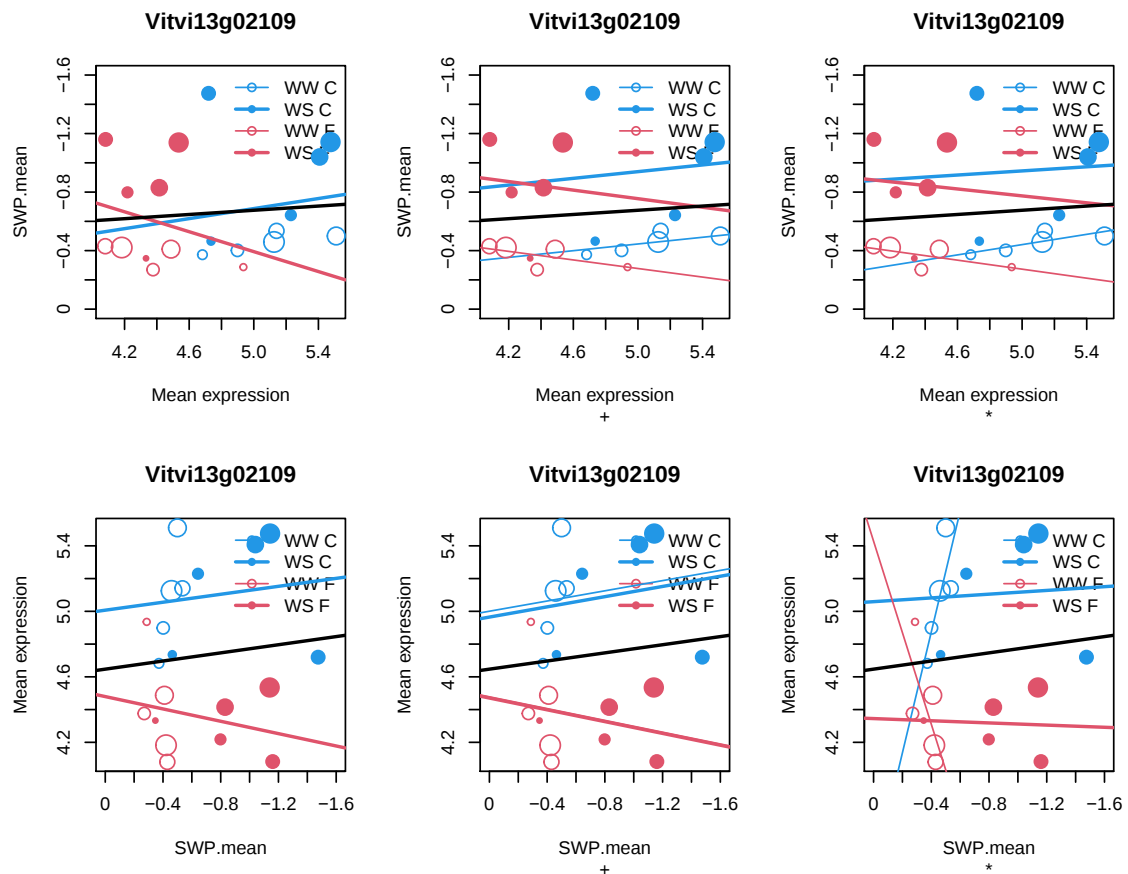
201606

Coefficient swp for Vitvi13g02109.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi13g02109	0.01572315	4.728483	0.01694934	0.9865185	0.9893746

B

Vitvi13g02109 -6.117649



Correlation of all measurements (not just means): $r = 0.0019$, $r^2 = 4e - 06$

Correlation of mean values (plots): $r_2 = 0.0945$

5.3.57 Vitvi12g02299

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

Vitvi12g02299

27.01.2002

RNA.processing.RNA helicase

Replication factor-A protein 1-like protein |

Chr5:24549682-24552641 REVERSE LENGTH=629 |

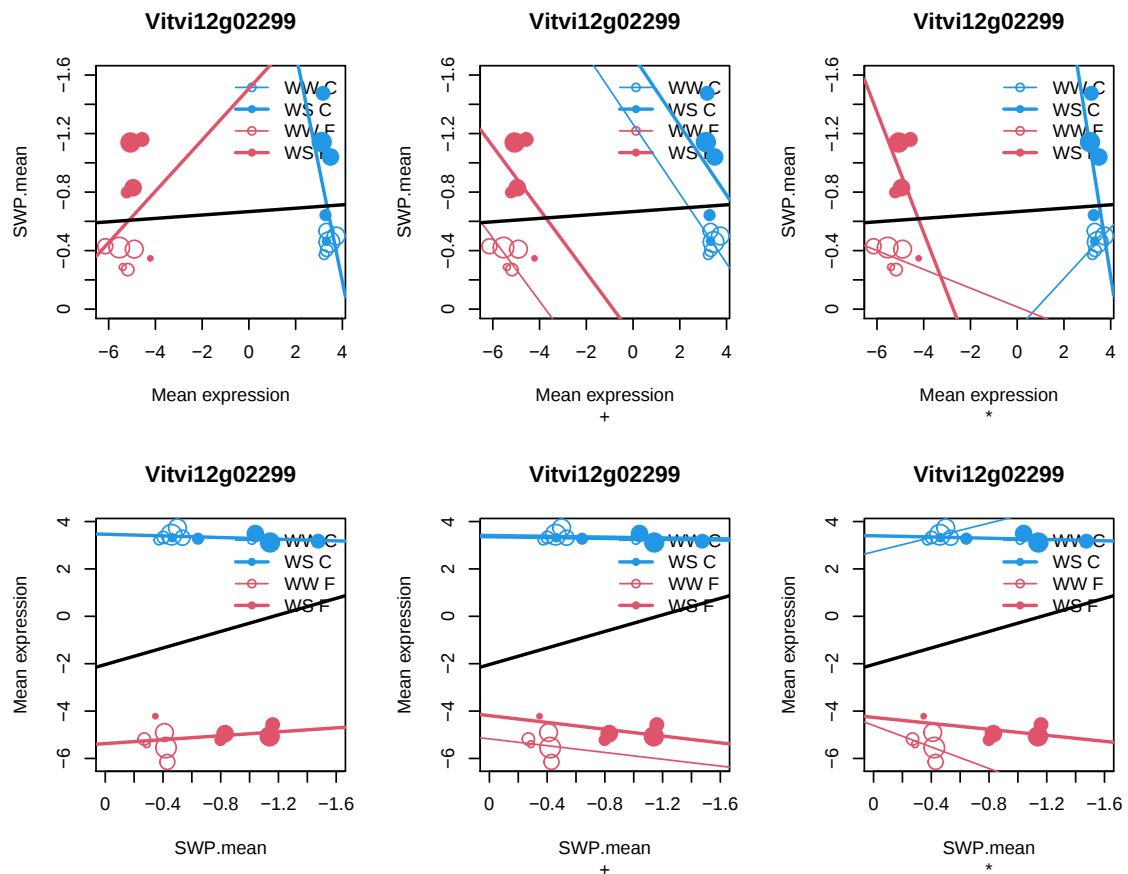
201606

Coefficient swp for Vitvi12g02299.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi12g02299	-0.1288029	-0.8895316	-0.01648571	0.9868872	0.9896792

B

Vitvi12g02299 -6.117656



Correlation of all measurements (not just means): $r = -0.0018$, $r^2 = 3e - 06$

Correlation of mean values (plots): $r_2 = 0.1423$

5.3.58 Vitvi12g00032

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

Vitvi12g00032

30.6

signalling.MAP kinases

MAP kinase 20 |

Chr2:17841070-17843947 REVERSE LENGTH=468 |

201606

Vitvi12g00032

29.4

protein.postranslational modification

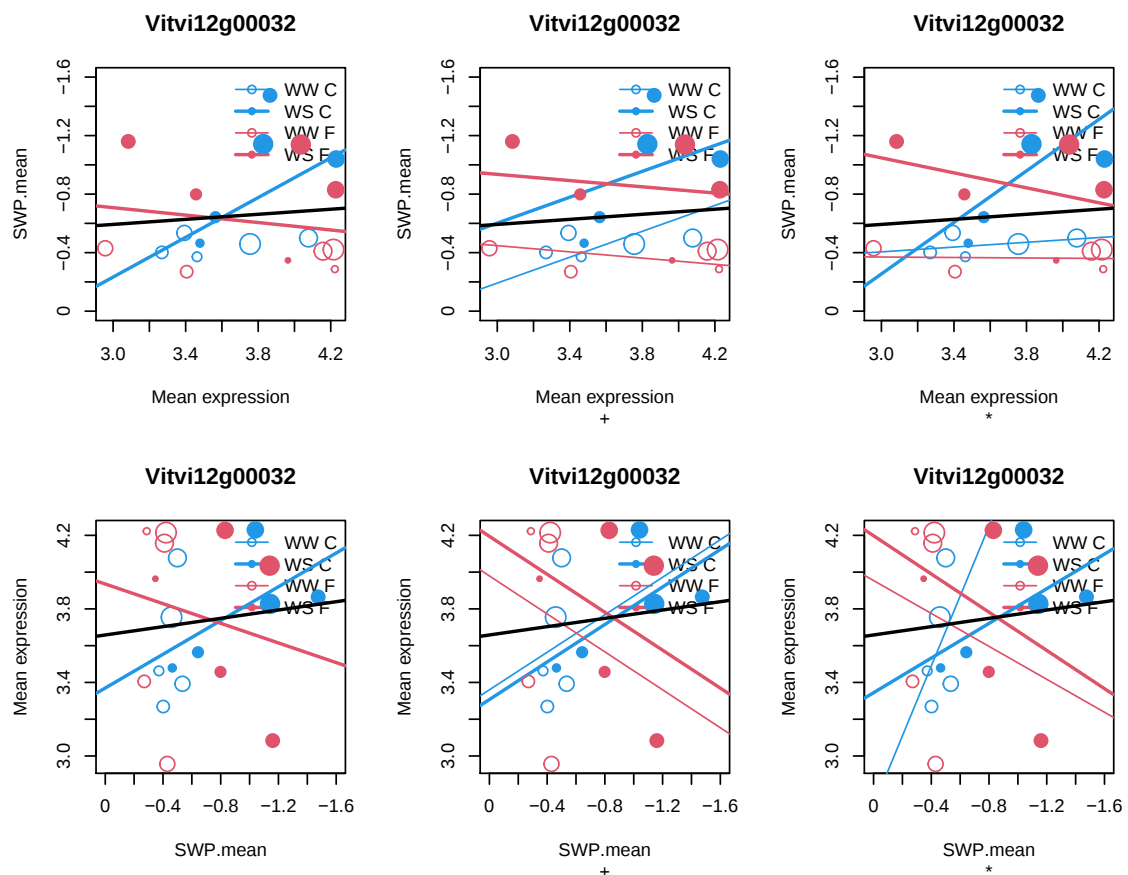
MAP kinase 20 |

Chr2:17841070-17843947 REVERSE LENGTH=468 |

201606

Coefficient swp for Vitvi12g00032.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi12g00032	-0.0132518	3.732406	-0.01574824	0.9874737	0.9901598
B					
Vitvi12g00032	-6.117668				



Correlation of all measurements (not just means): $r = -0.0018$, $r^2 = 3e - 06$
 Correlation of mean values (plots): $r_2 = 0.0989$

5.3.59 Vitvi18g01254

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

Vitvi18g01254

35.2

not assigned.unknown

Dof-type zinc finger DNA-binding family protein |

Chr3:19435390-19436190 FORWARD LENGTH=266 |

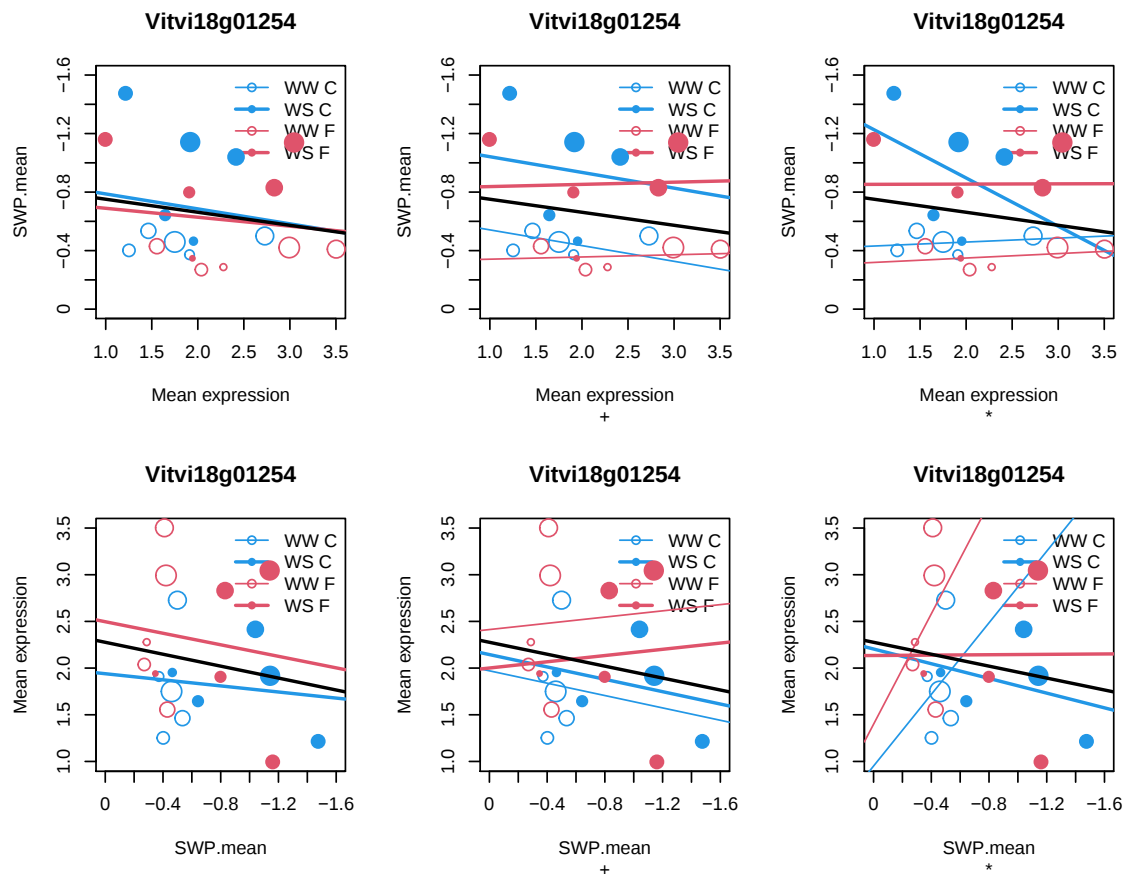
201606

Coefficient swp for Vitvi18g01254.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi18g01254	-0.02176195	2.066726	-0.01571988	0.9874963	0.9901598

B

Vitvi18g01254 -6.117668



Correlation of all measurements (not just means): $r = -0.0018$, $r^2 = 3e - 06$

Correlation of mean values (plots): $r_2 = -0.1687$

5.3.60 Vitvi04g01274

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

Vitvi04g01274

35.2

not assigned.unknown

Sulfite exporter TauE/Safe family protein |

Chr2:10977174-10979677 FORWARD LENGTH=476 |

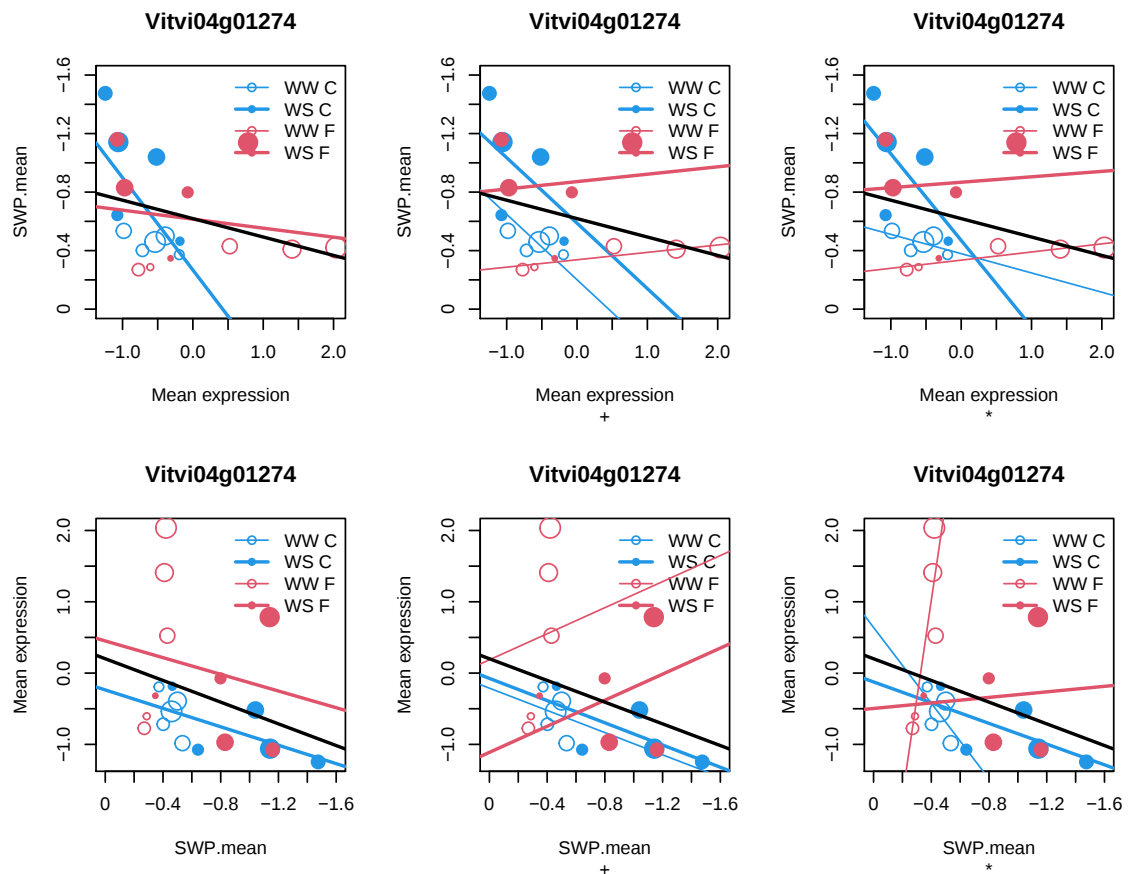
201606

Coefficient swp for Vitvi04g01274.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi04g01274	0.04421032	-0.2982016	0.01559262	0.9875975	0.9901961

B

Vitvi04g01274 -6.11767



Correlation of all measurements (not just means): $r = 0.0017$, $r^2 = 3e - 06$

Correlation of mean values (plots): $r_2 = -0.3094$

5.3.61 Vitvi10g00270

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

Vitvi10g00270

27.03.1932

RNA.regulation of transcription.WRKY domain transcription factor famil

WRKY family transcription factor family protein |

Chr4:13437298-13439774 REVERSE LENGTH=485 |

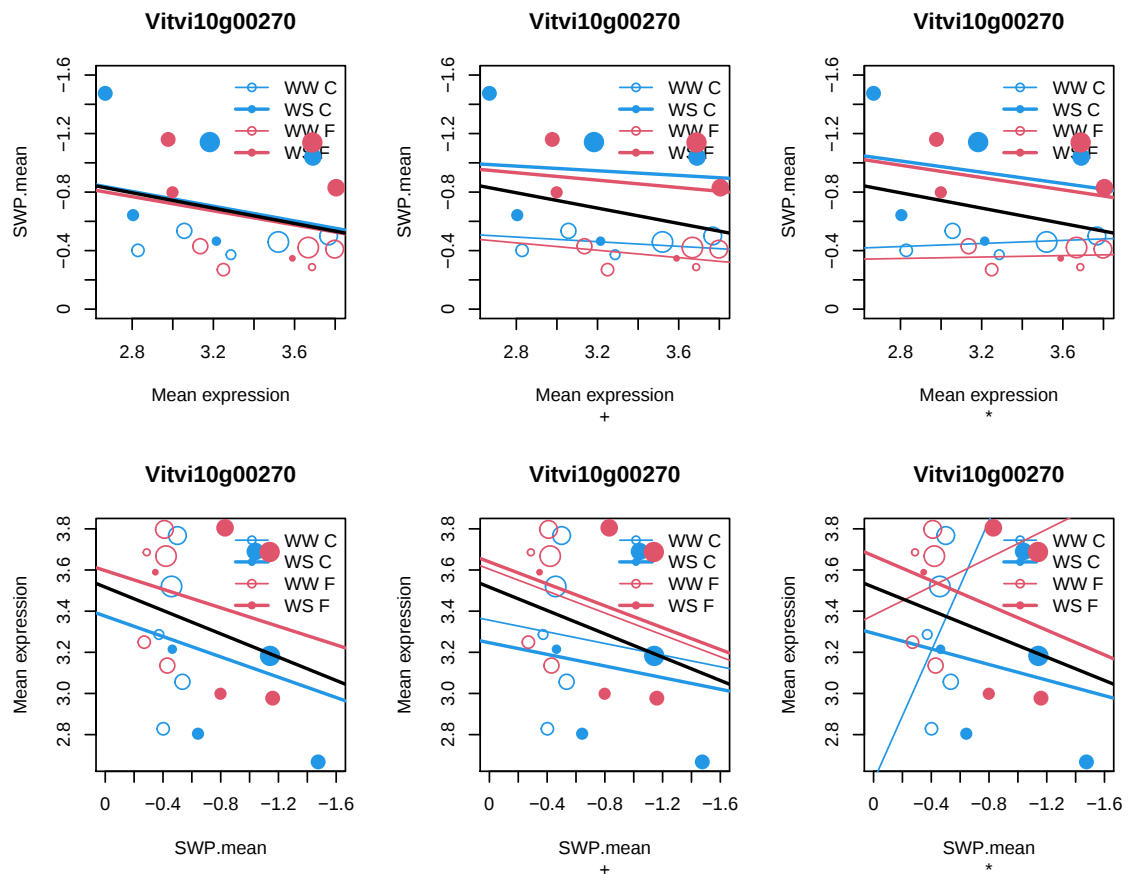
201606

Coefficient swp for Vitvi10g00270.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi10g00270	-0.01104934	3.330586	-0.01531274	0.9878201	0.9903542

B

Vitvi10g00270 -6.117674



Correlation of all measurements (not just means): $r = -0.0018$, $r^2 = 3e - 06$

Correlation of mean values (plots): $r_2 = -0.2725$

5.3.62 Vitvi07g00361

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

Vitvi07g00361

30.01.2001

signalling.in sugar and nutrient physiology.misc

EXORDIUM like 2 |

Chr5:25703980-25704897 FORWARD LENGTH=305 |

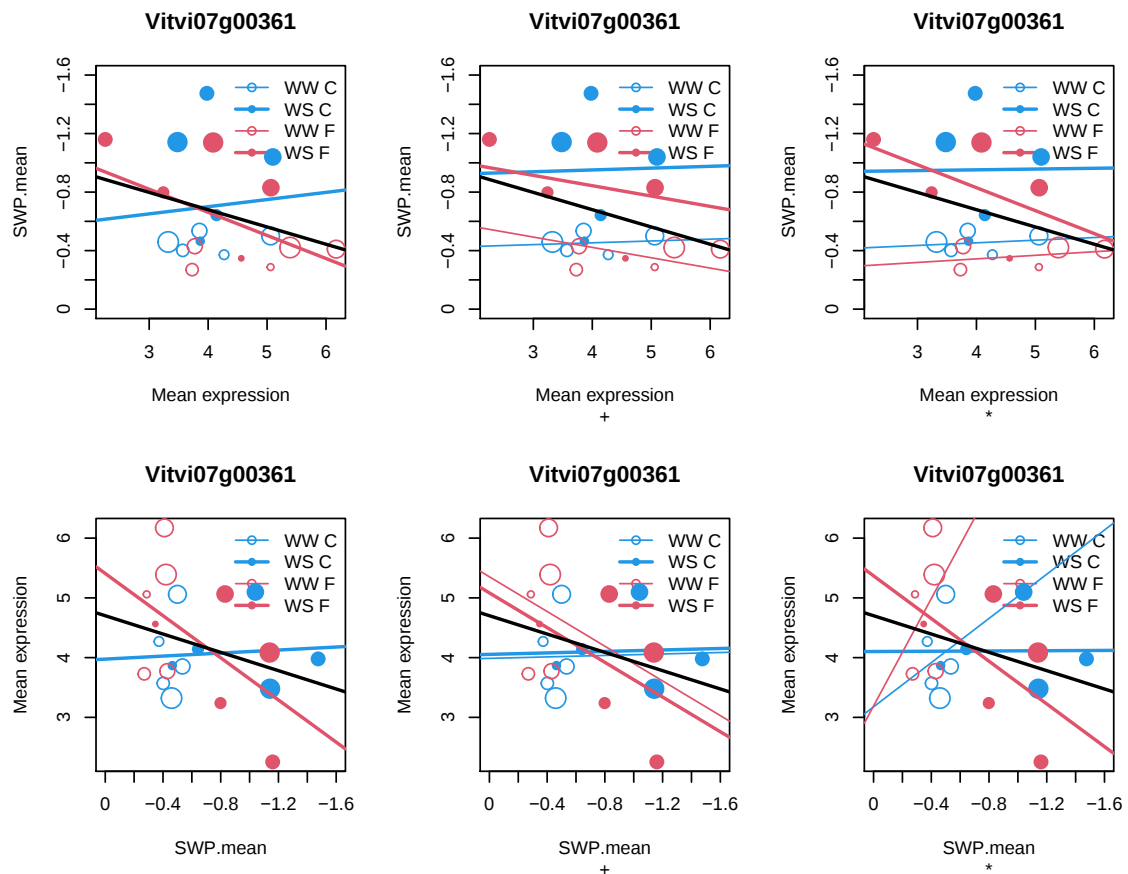
201606

Coefficient swp for Vitvi07g00361.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi07g00361	-0.02919931	4.198542	-0.01425395	0.9886622	0.9911332

B

Vitvi07g00361 -6.11769



Correlation of all measurements (not just means): $r = -0.0016$, $r^2 = 3e - 06$

Correlation of mean values (plots): $r_2 = -0.3008$

5.3.63 Vitvi17g01348

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

Vitvi17g01348

29.03.2001

protein.targeting.nucleus

Purple acid phosphatases superfamily protein |

Chr1:4715490-4718091 REVERSE LENGTH=613 |

201606

Vitvi17g01348

26.13

misc.acid and other phosphatases

Purple acid phosphatases superfamily protein |

Chr1:4715490-4718091 REVERSE LENGTH=613 |

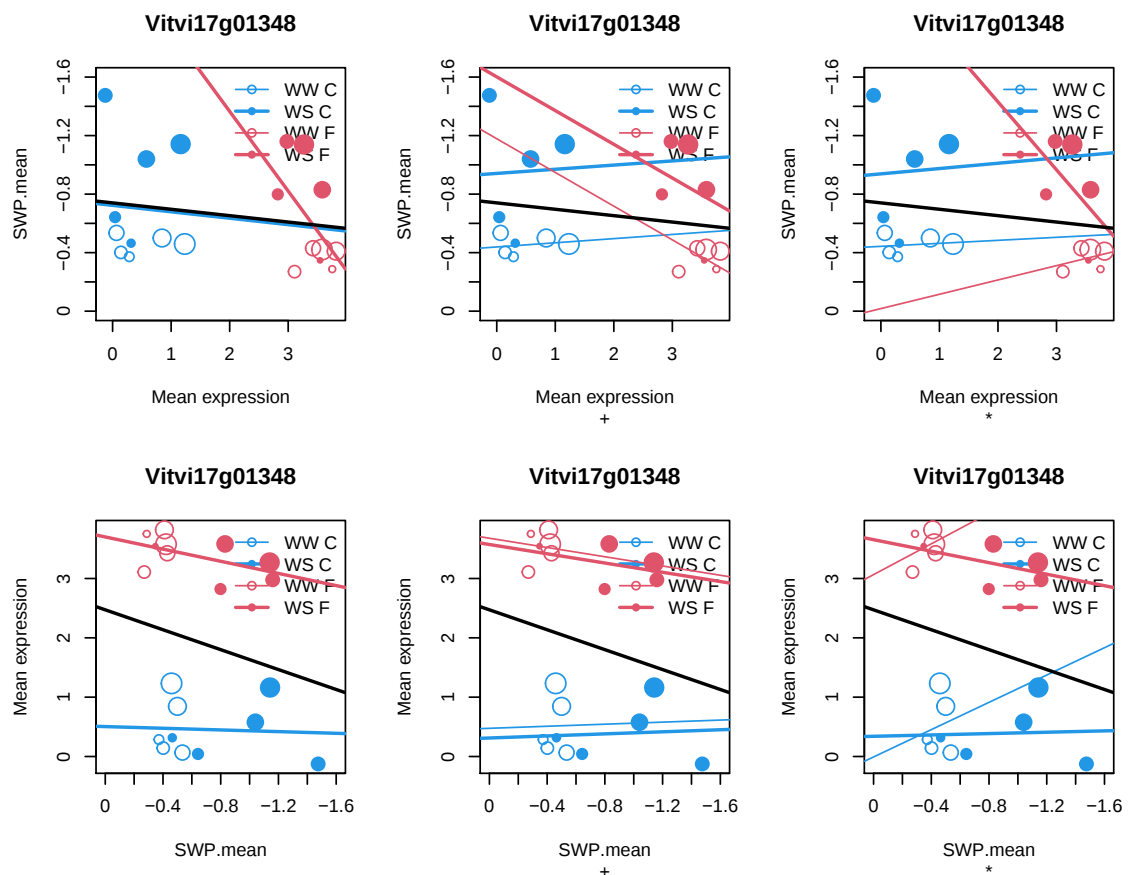
201606

Coefficient swp for Vitvi17g01348.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi17g01348	0.03708154	1.921248	0.01318308	0.989514	0.9919218

B

Vitvi17g01348	-6.117704
---------------	-----------



Correlation of all measurements (not just means): $r = 0.0015, r^2 = 2e - 06$
 Correlation of mean values (plots): $r_2 = -0.1914$

5.3.64 Vitvi05g00459

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

Vitvi05g00459

30.2.99

signalling.receptor kinases.misc

Leucine-rich repeat (LRR) family protein |

Chr3:1797116-1799732 REVERSE LENGTH=517 |

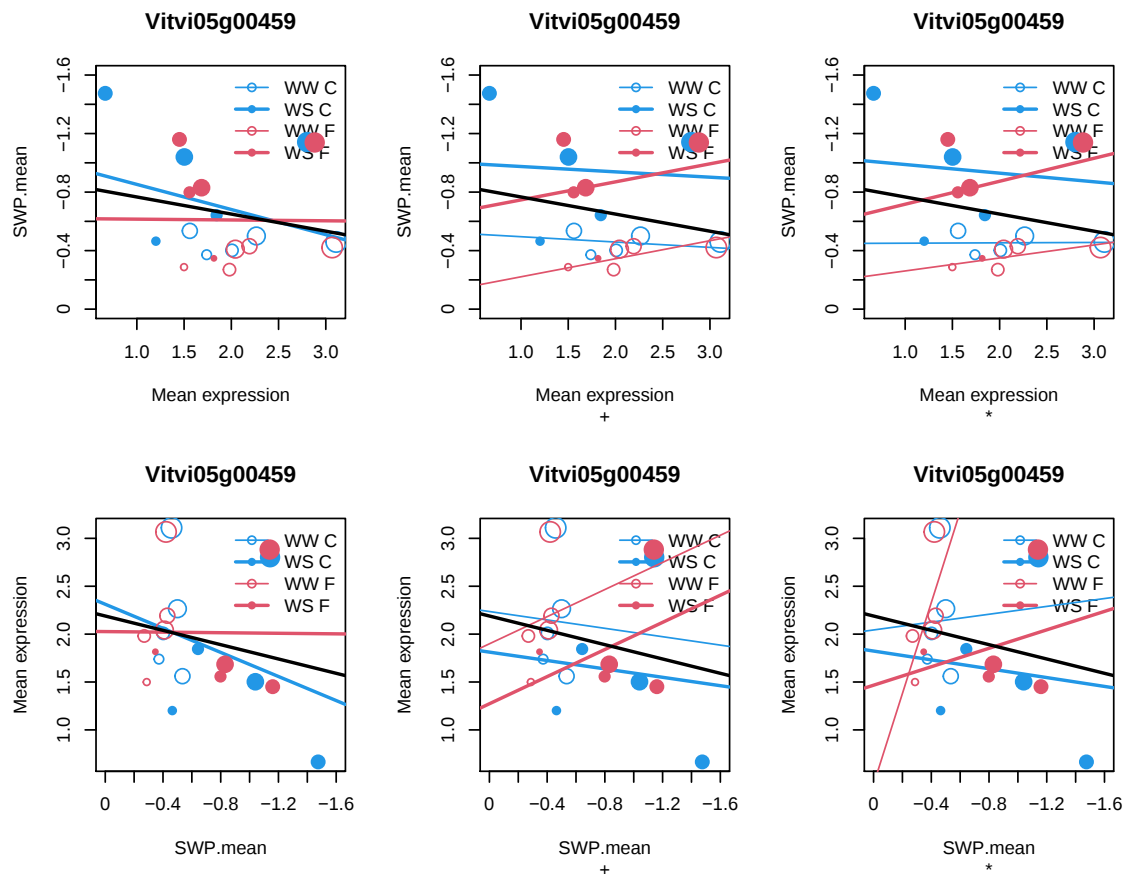
201606

Coefficient swp for Vitvi05g00459.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi05g00459	0.01647906	1.943617	0.01304292	0.9896254	0.9919684

B

Vitvi05g00459 -6.117705



Correlation of all measurements (not just means): $r = 0.0015$, $r^2 = 2e - 06$

Correlation of mean values (plots): $r_2 = -0.2091$

5.3.65 Vitvi15g00936

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

Vitvi15g00936

27.03.2008

RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family

Dof-type zinc finger DNA-binding family protein |

Chr3:22896212-22897150 FORWARD LENGTH=312 |

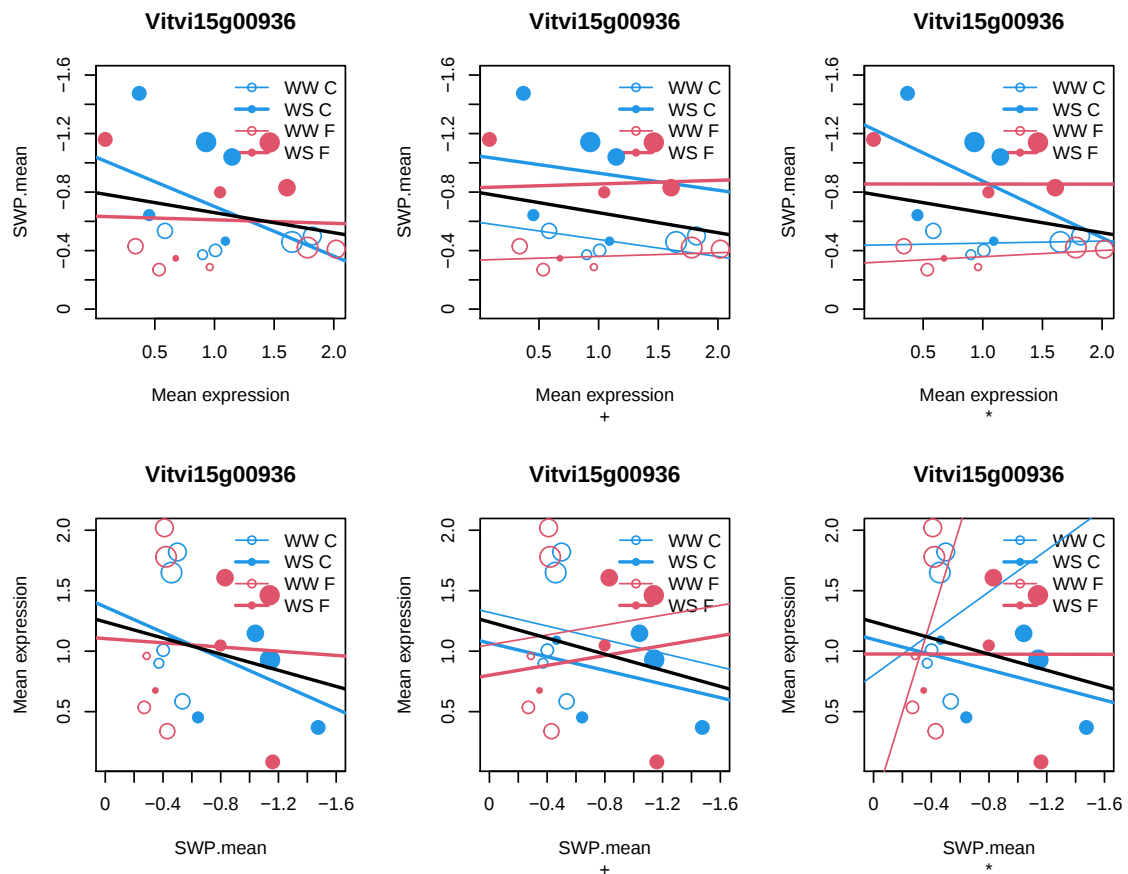
201606

Coefficient swp for Vitvi15g00936.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi15g00936	-0.01419403	1.023241	-0.01240148	0.9901356	0.992299

B

Vitvi15g00936 -6.117713



Correlation of all measurements (not just means): $r = -0.0014$, $r^2 = 2e - 06$

Correlation of mean values (plots): $r_2 = -0.2137$

5.3.66 Vitvi18g00410

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

Vitvi18g00410

35.2

not assigned.unknown

APR-like 4 |

Chr1:12748835-12750124 REVERSE LENGTH=310 |

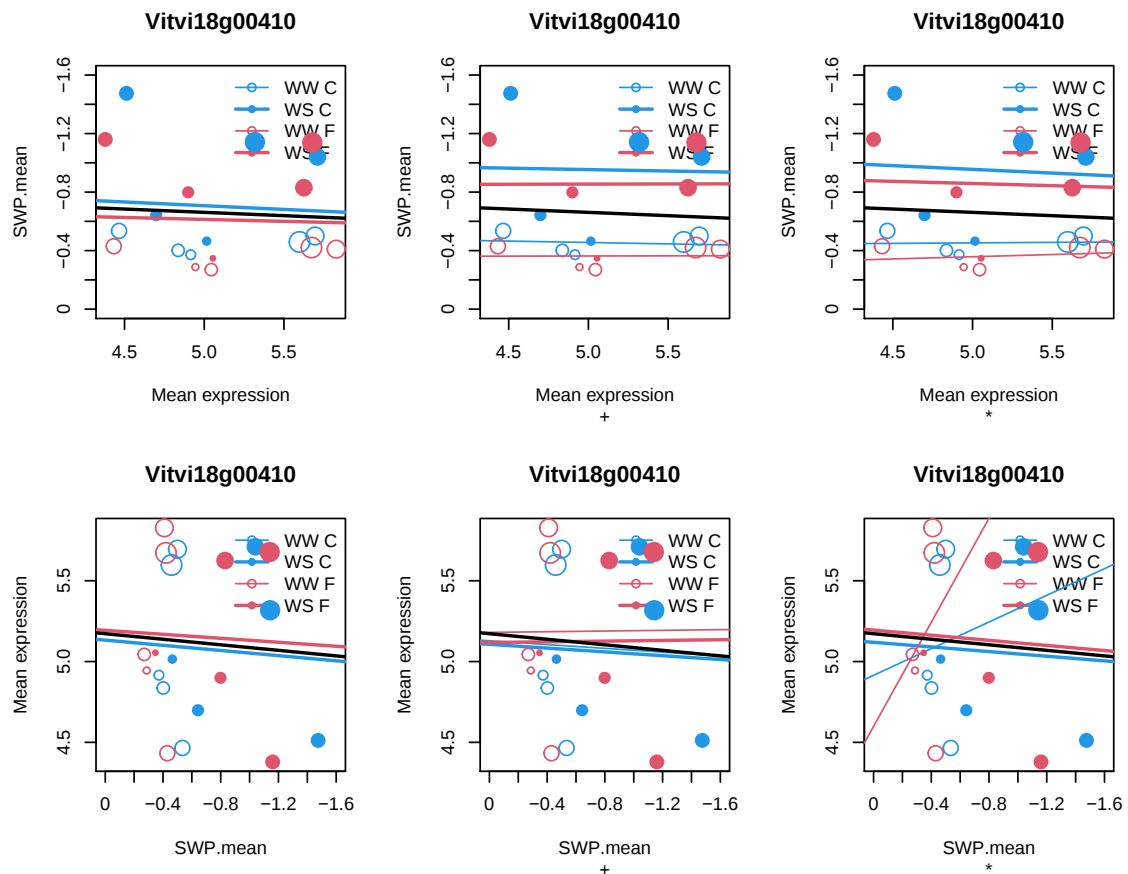
201606

Coefficient swp for Vitvi18g00410.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi18g00410	-0.0112071	5.115982	-0.01238571	0.9901482	0.992299

B

Vitvi18g00410 -6.117713



Correlation of all measurements (not just means): $r = -0.0014$, $r^2 = 2e - 06$

Correlation of mean values (plots): $r_2 = -0.0624$

5.3.67 Vitvi19g00271

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

Vitvi19g00271

27.03.2027

RNA.regulation of transcription.NAC domain transcription factor family

NAC domain containing protein 2 |

Chr3:5243696-5245037 FORWARD LENGTH=364 |

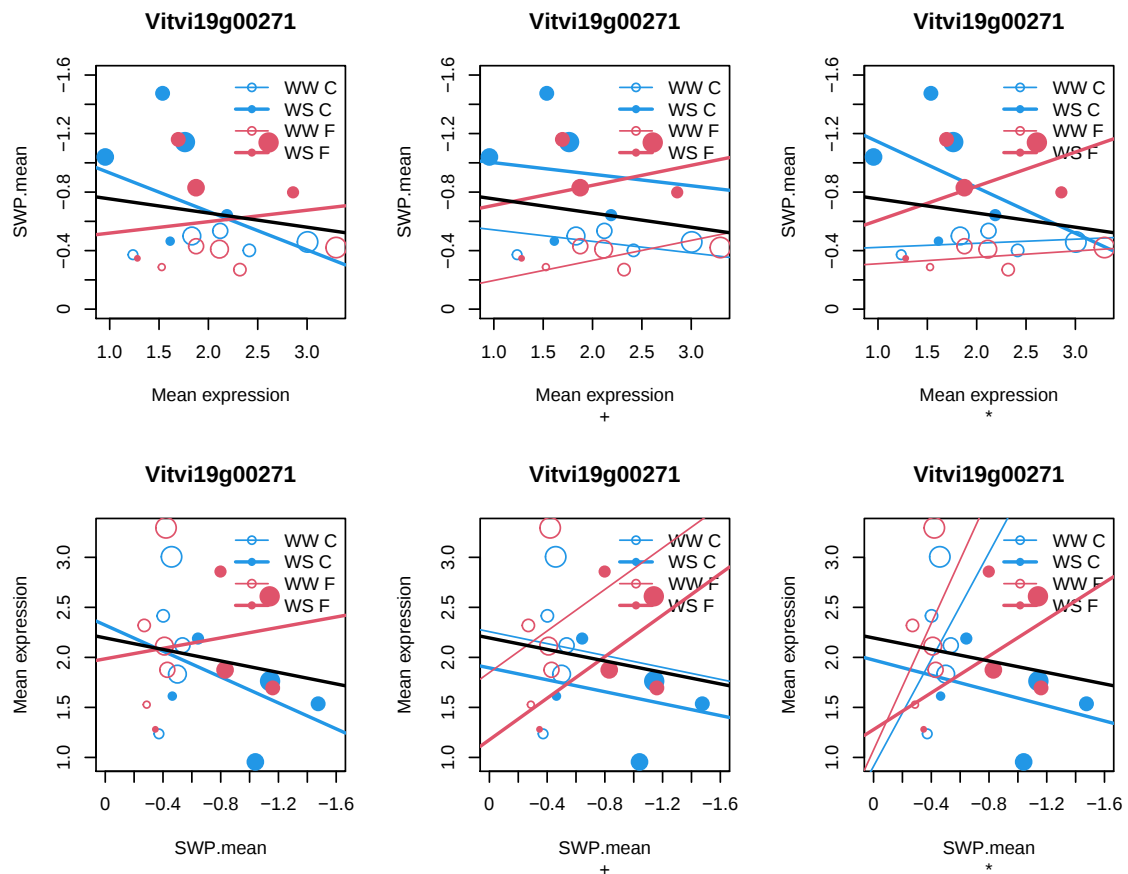
201606

Coefficient swp for Vitvi19g00271.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi19g00271	-0.01620898	2.005567	-0.01238261	0.9901506	0.992299

B

Vitvi19g00271 -6.117714



Correlation of all measurements (not just means): $r = -0.0014$, $r^2 = 2e - 06$

Correlation of mean values (plots): $r_2 = -0.1668$

5.3.68 Vitvi02g00828

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

Vitvi02g00828

29.3.4.3

protein.targeting.secretory pathway.vacuole

E2F/DP family winged-helix DNA-binding domain-containing protein |

Chr4:10407571-10408582 REVERSE LENGTH=179 |

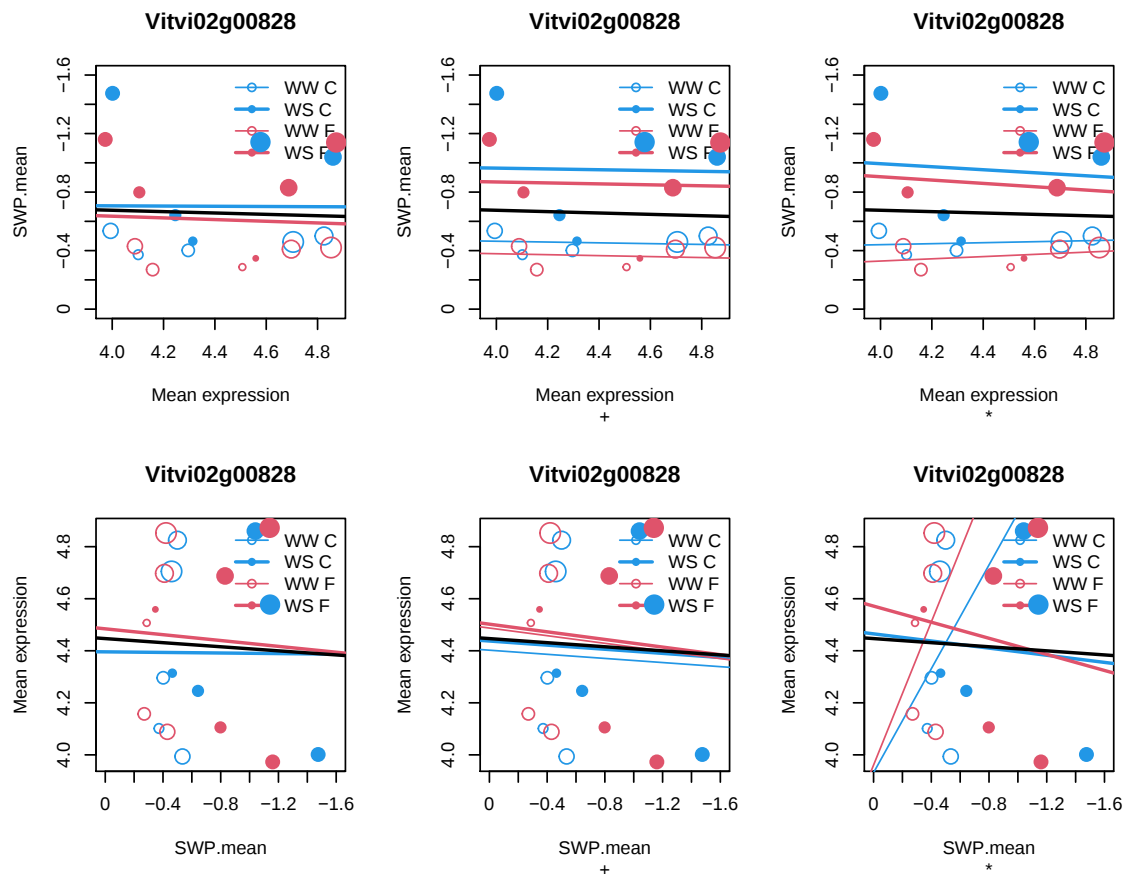
201606

Coefficient swp for Vitvi02g00828.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi02g00828	0.007716244	4.421039	0.01208943	0.9903838	0.9924675

B

Vitvi02g00828 -6.117717



Correlation of all measurements (not just means): $r = 0.0014$, $r^2 = 2e - 06$

Correlation of mean values (plots): $r_2 = -0.0427$

5.3.69 Vitvi11g00053

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

Vitvi11g00053

30.2.3

signalling.receptor kinases.leucine rich repeat III

Leucine-rich repeat protein kinase family protein |

Chr3:14954587-14956577 FORWARD LENGTH=633 |

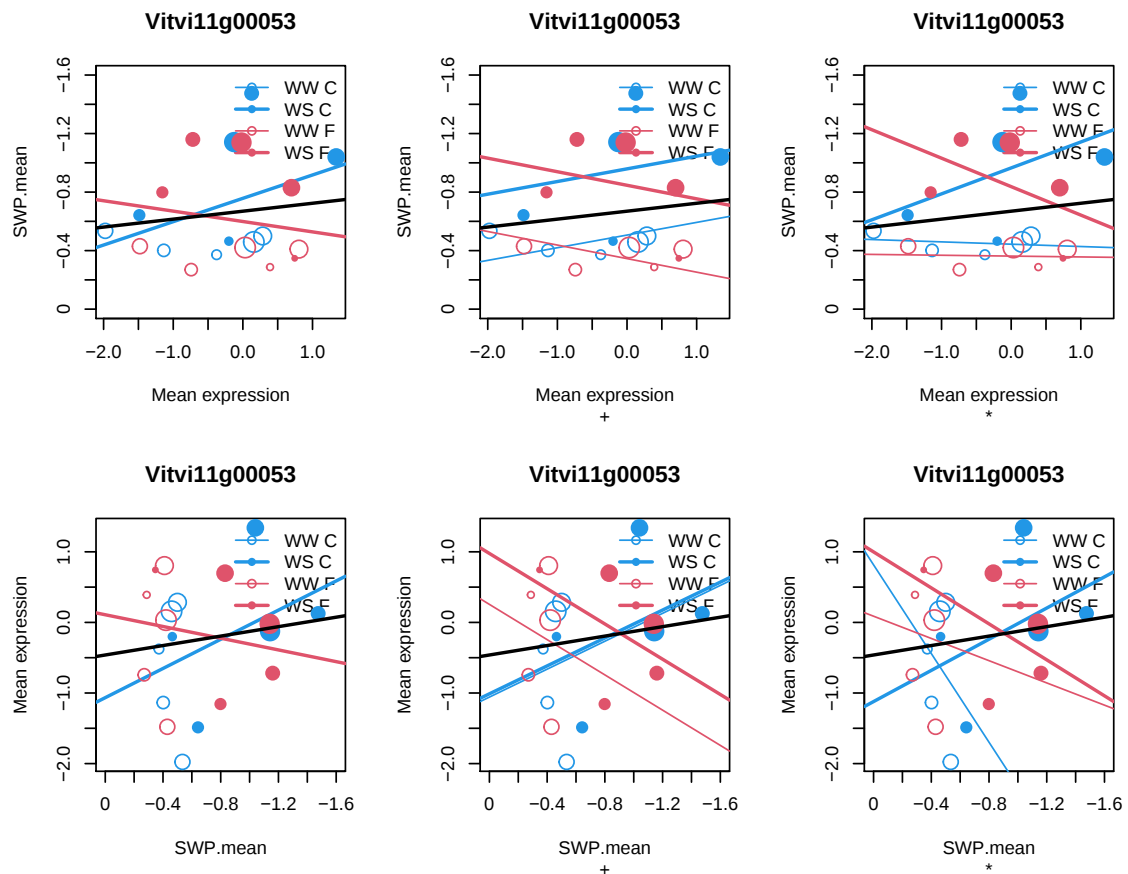
201606

Coefficient swp for Vitvi11g00053.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi11g00053	-0.0176124	-0.2419846	-0.009850811	0.9921644	0.9941864

B

Vitvi11g00053 -6.117741



Correlation of all measurements (not just means): $r = -0.0011$, $r^2 = 1e - 06$

Correlation of mean values (plots): $r_2 = 0.1348$

5.3.70 Vitvi12g00562

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

Vitvi12g00562

35.1.27

not assigned.no ontology.tetratricopeptide repeat (TPR)

Tetratricopeptide repeat (TPR)-like superfamily protein |

Chr4:17572040-17573938 REVERSE LENGTH=632 |

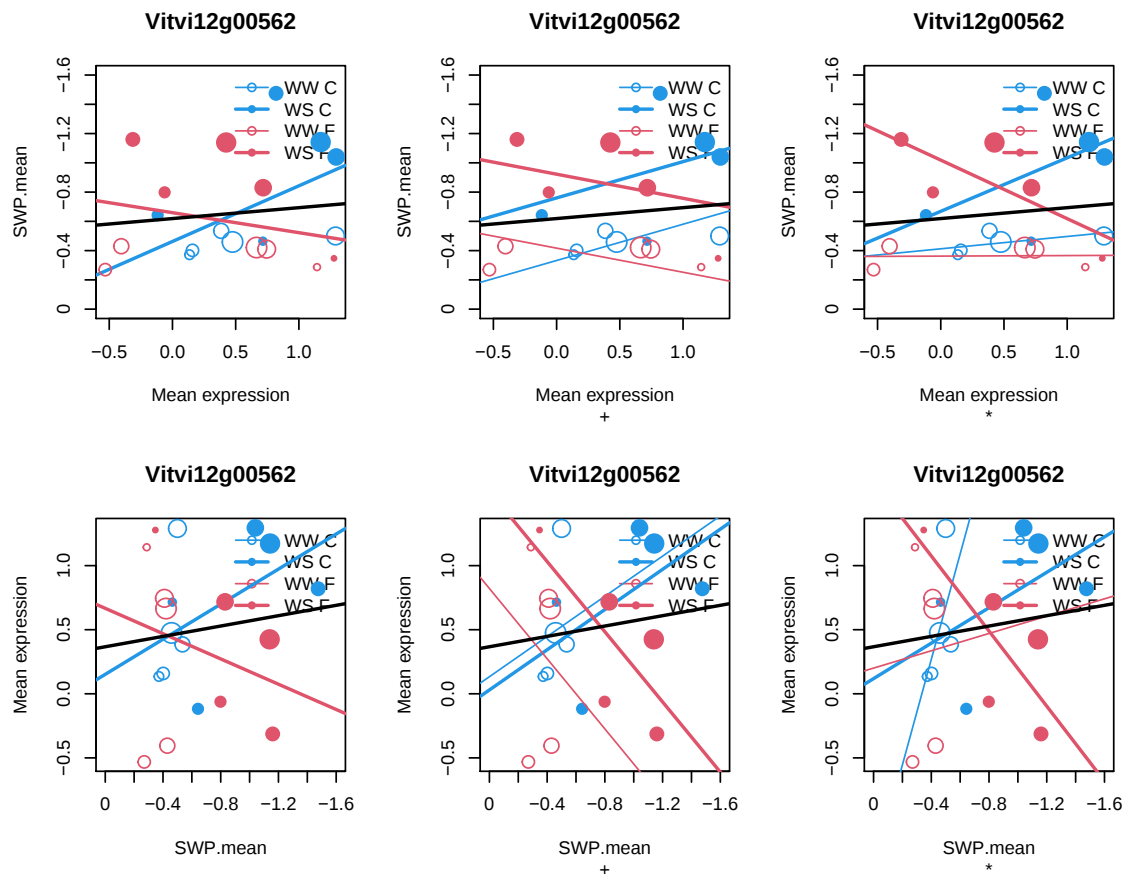
201606

Coefficient swp for Vitvi12g00562.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi12g00562	-0.01172975	0.4995579	-0.009690669	0.9922918	0.9942224

B

Vitvi12g00562 -6.117742



Correlation of all measurements (not just means): $r = -0.0011$, $r^2 = 1e - 06$

Correlation of mean values (plots): $r_2 = 0.1226$

5.3.71 Vitvi10g00022

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

Vitvi10g00022

20.02.2001

stress.abiotic.heat

Chaperone DnaJ-domain superfamily protein |

Chr1:22810220-22812370 FORWARD LENGTH=300 |

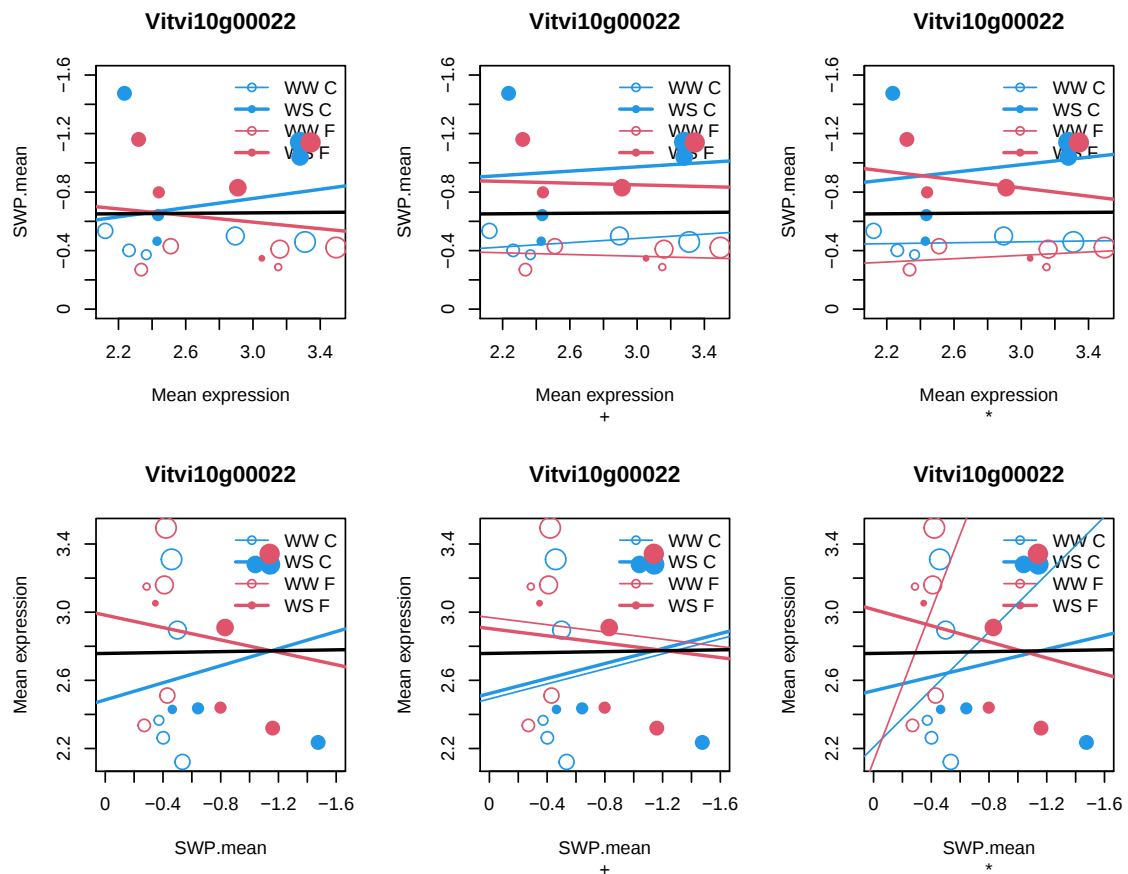
201606

Coefficient swp for Vitvi10g00022.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi10g00022	0.008758387	2.766618	0.009593208	0.9923693	0.9942224

B

Vitvi10g00022 -6.117743



Correlation of all measurements (not just means): $r = 0.0011$, $r^2 = 1e - 06$

Correlation of mean values (plots): $r_2 = 0.0102$

5.3.72 Vitvi19g00154

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

Vitvi19g00154

27.03.1936

RNA.regulation of transcription.argonaute transcription factor family

Stabilizer of iron transporter SufD / Polynucleotidyl transferase |

Chr1:17886285-17891892 REVERSE LENGTH=1048 |

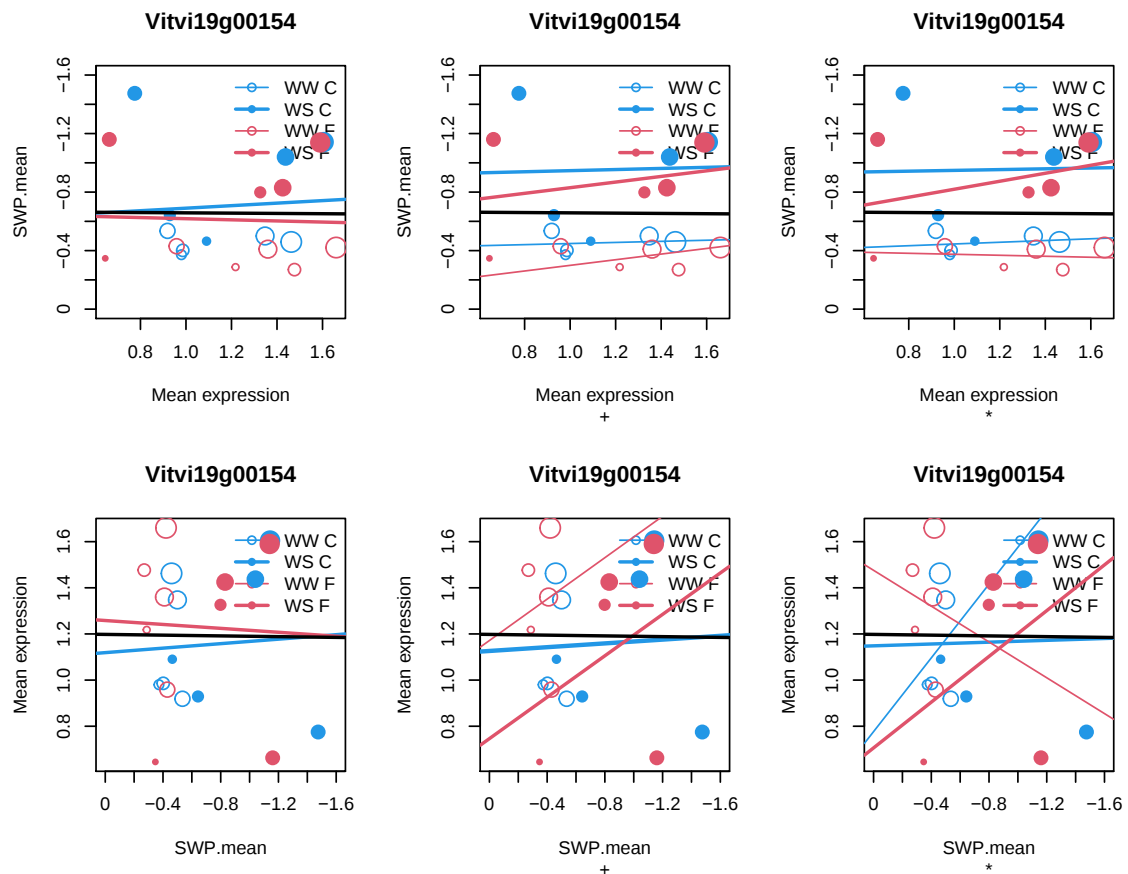
201606

Coefficient swp for Vitvi19g00154.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi19g00154	0.006931742	1.192741	0.009559713	0.9923959	0.9942224

B

Vitvi19g00154 -6.117743



Correlation of all measurements (not just means): $r = 0.0011$, $r^2 = 1e - 06$

Correlation of mean values (plots): $r_2 = -0.0090$

5.3.73 Vitvi07g02286

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

Vitvi07g02286

27.03.1999

RNA.regulation of transcription.unclassified

Mitochondrial transcription termination factor family protein |

Chr5:2520188-2521405 FORWARD LENGTH=405 |

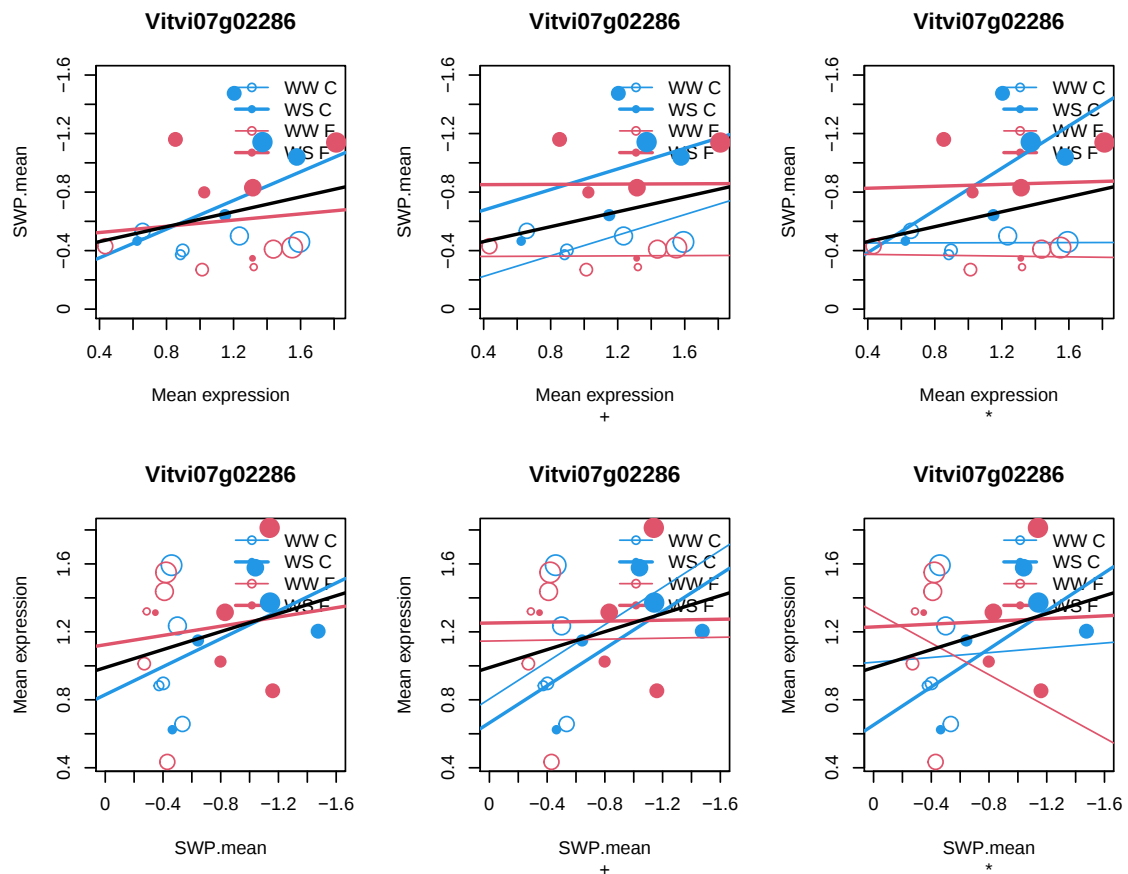
201606

Coefficient swp for Vitvi07g02286.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi07g02286	-0.007345489	1.16328	-0.009368765	0.9925478	0.9943092

B

Vitvi07g02286 -6.117745



Correlation of all measurements (not just means): $r = -0.0011$, $r^2 = 1e - 06$

Correlation of mean values (plots): $r_2 = 0.2597$

5.3.74 Vitvi09g00373

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

Vitvi09g00373

31.1

cell.organisation

ATP binding microtubule motor family protein |

Chr3:5447503-5451196 FORWARD LENGTH=684 |

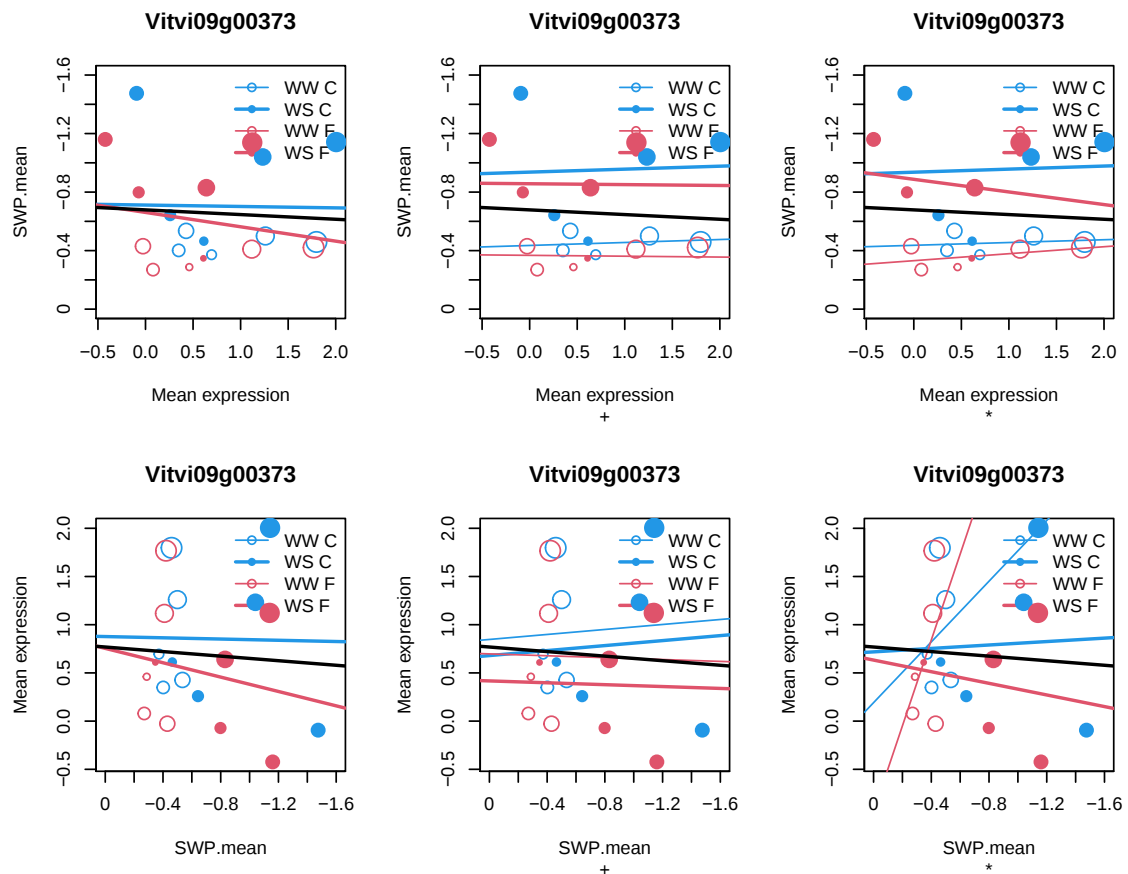
201606

Coefficient swp for Vitvi09g00373.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi09g00373	0.01320393	0.6909261	0.009255466	0.9926379	0.9943341

B

Vitvi09g00373 -6.117746



Correlation of all measurements (not just means): $r = 0.0010$, $r^2 = 1e - 06$

Correlation of mean values (plots): $r_2 = -0.0616$

5.3.75 Vitvi08g00642

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

Vitvi08g00642

30.04.2004

signalling.phosphinositides.phosphoinositide phospholipase C

Phosphoinositide-specific phospholipase C family protein |

Chr3:20747787-20750184 FORWARD LENGTH=584 |

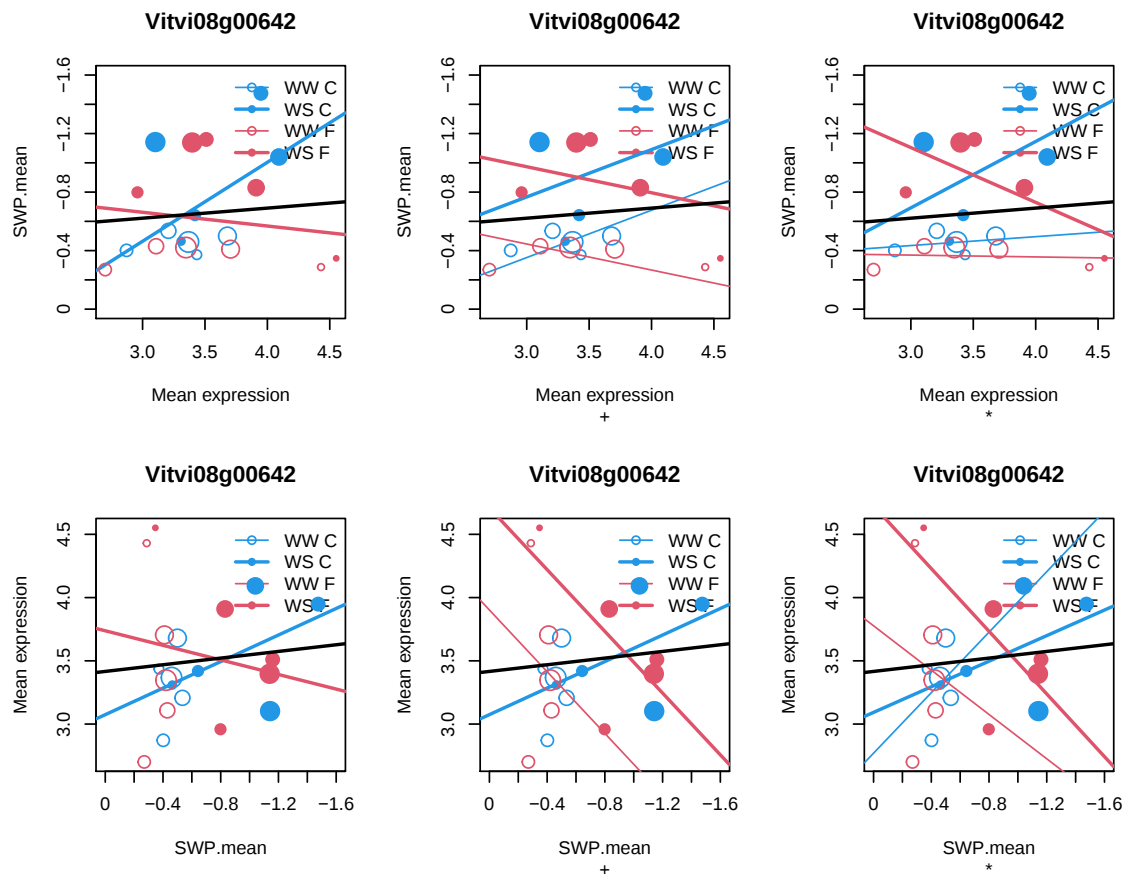
201606

Coefficient swp for Vitvi08g00642.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi08g00642	-0.008736877	3.502604	-0.009049968	0.9928014	0.9944325

B

Vitvi08g00642 -6.117748



Correlation of all measurements (not just means): $r = -0.0010$, $r^2 = 1e - 06$

Correlation of mean values (plots): $r_2 = 0.0952$

5.3.76 Vitvi19g01988

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

Vitvi19g01988

27.01.2002

RNA.processing.RNA helicase

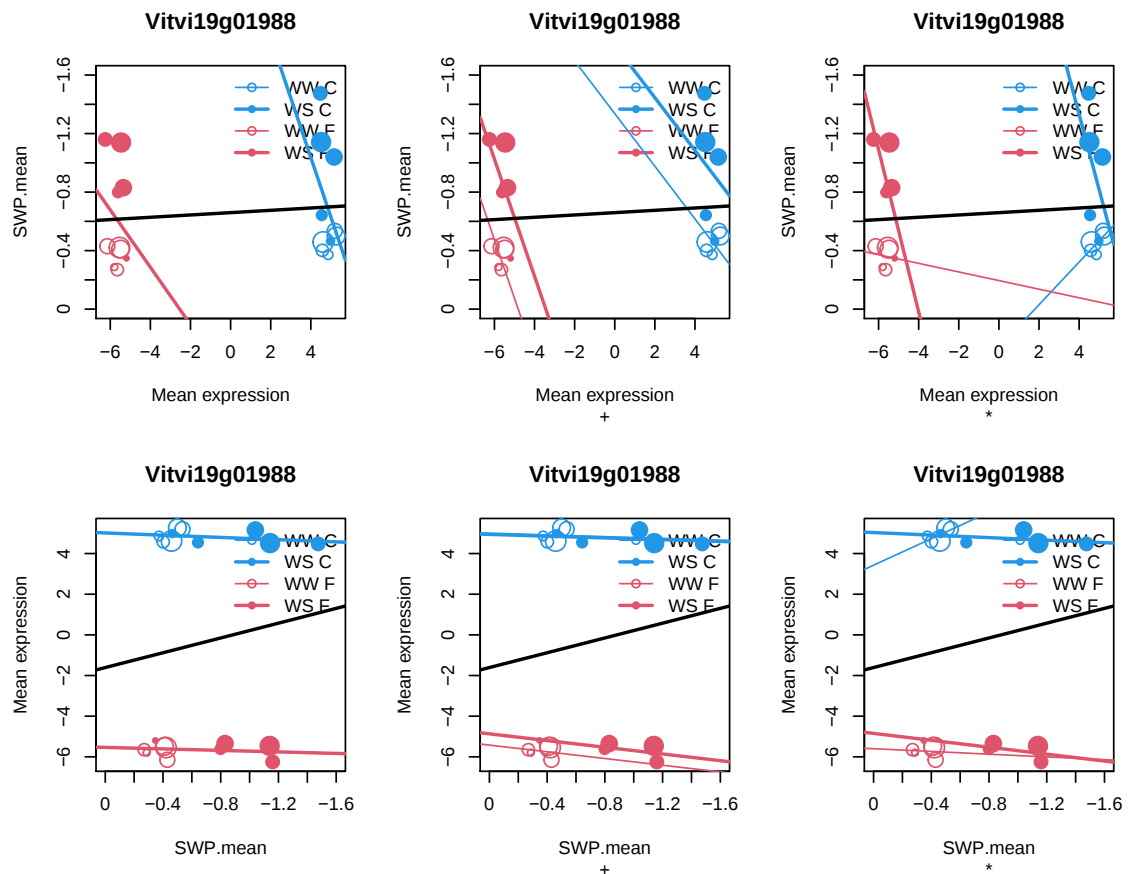
RPA70-kDa subunit B |

Chr5:2572107-2574879 FORWARD LENGTH=604 |

201606

Coefficient swp for Vitvi19g01988.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi19g01988	-0.0858519	-0.4147767	-0.008967217	0.9928672	0.994433
B					
Vitvi19g01988	-6.117749				



Correlation of all measurements (not just means): $r = -0.0010$, $r^2 = 1e - 06$

Correlation of mean values (plots): $r_2 = 0.1201$

5.3.77 Vitvi12g01812

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

Vitvi12g01812

35.2

not assigned.unknown

cysteine-rich RECEPTOR-like kinase |

Chr4:12129485-12133157 FORWARD LENGTH=1043 |

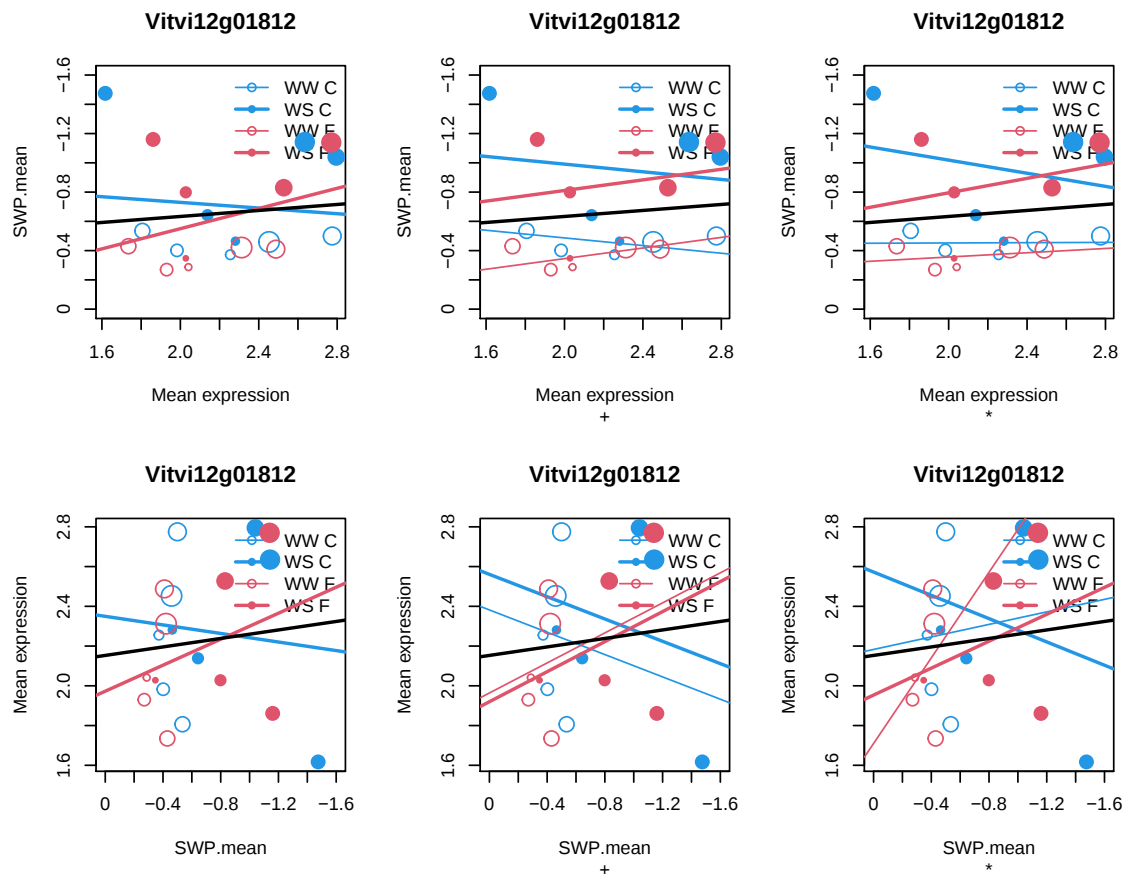
201606

Coefficient swp for Vitvi12g01812.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi12g01812	0.006233568	2.222929	0.00844228	0.9932848	0.9947859

B

Vitvi12g01812 -6.117753



Correlation of all measurements (not just means): $r = 0.0010$, $r^2 = 9e-07$

Correlation of mean values (plots): $r_2 = 0.1046$

5.3.78 Vitvi14g03090

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

Vitvi14g03090

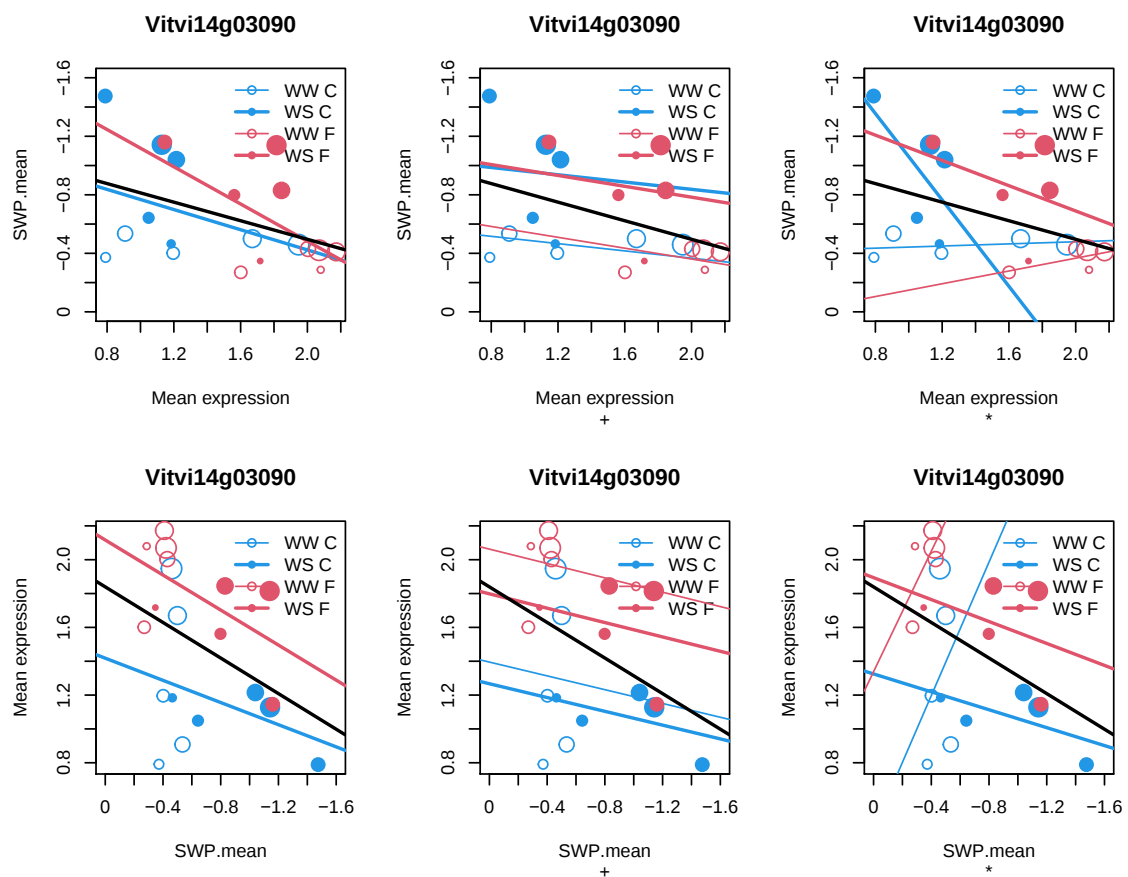
35.2

not assigned.unknown

NA

Coefficient swp for Vitvi14g03090.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi14g03090	-0.007003	1.494422	-0.007475143	0.994054	0.9954398
	B				
Vitvi14g03090	-6.117761				



Correlation of all measurements (not just means): $r = -8e - 04$, $r^2 = 7e - 07$
 Correlation of mean values (plots): $r_2 = -0.4084$

5.3.79 Vitvi05g00906

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

Vitvi05g00906

35.2

not assigned.unknown

cysteine-rich RLK (RECEPTOR-like protein kinase) 10 |

Chr4:12138171-12140780 FORWARD LENGTH=669 |

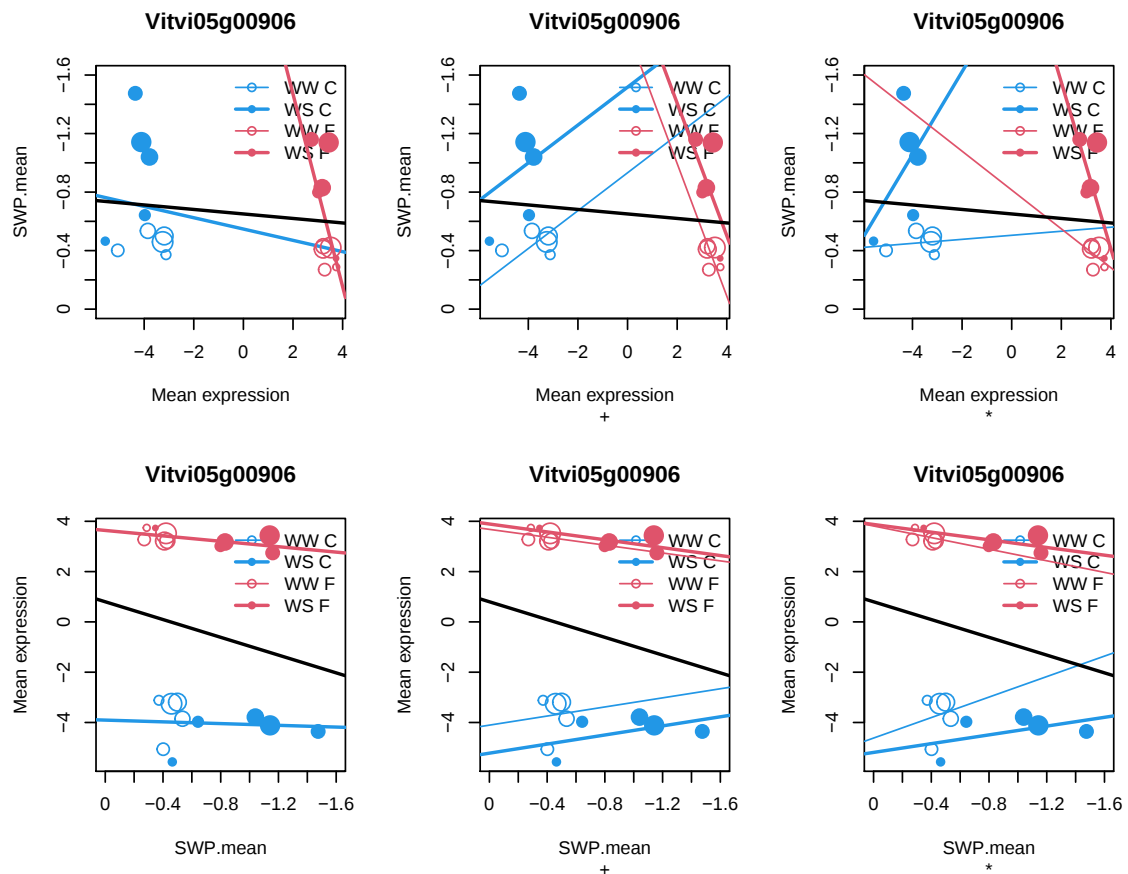
201606

Coefficient swp for Vitvi05g00906.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi05g00906	-0.05148312	-0.3596697	-0.007457227	0.9940683	0.9954398

B

Vitvi05g00906 -6.117761



Correlation of all measurements (not just means): $r = -8e - 04$, $r^2 = 7e - 07$

Correlation of mean values (plots): $r_2 = -0.1649$

5.3.80 Vitvi02g00473

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

Vitvi02g00473

35.1

not assigned.no ontology

Nucleotide-diphospho-sugar transferases superfamily protein |

Chr4:9350039-9352707 FORWARD LENGTH=494 |

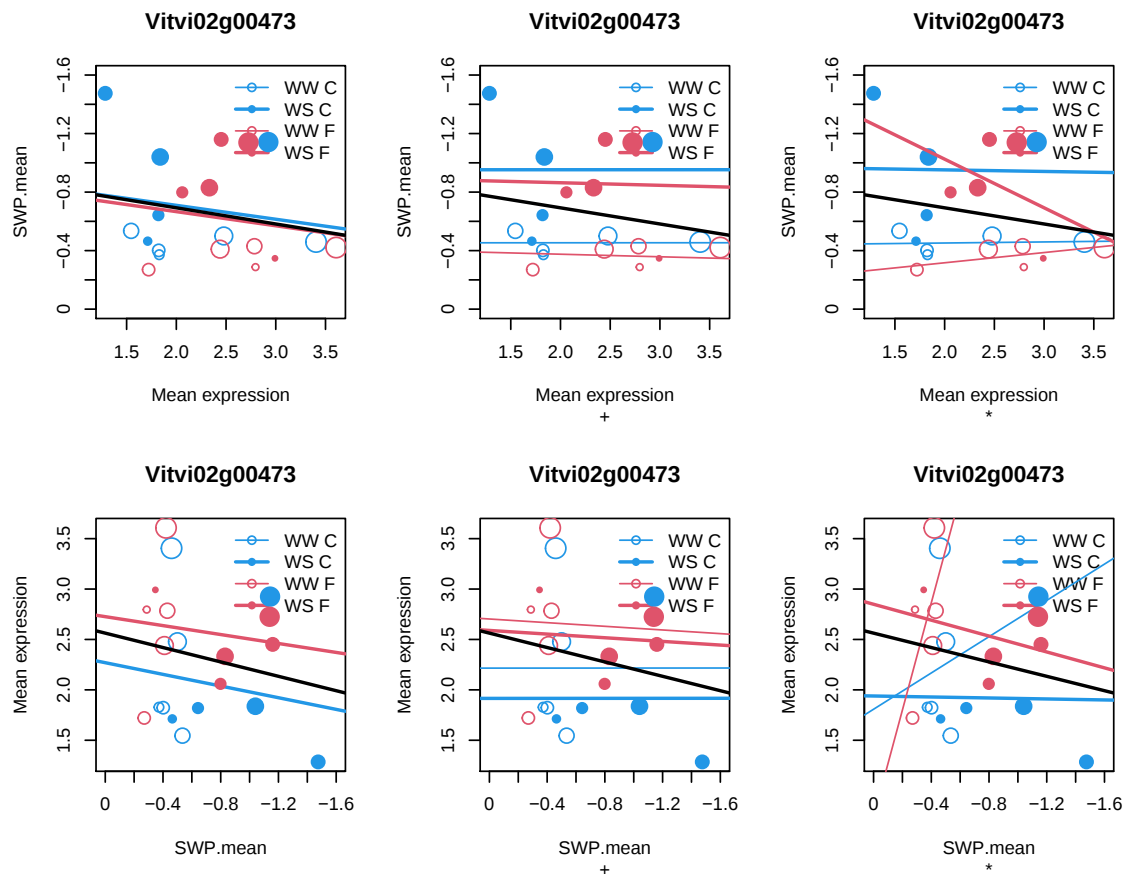
201606

Coefficient swp for Vitvi02g00473.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi02g00473	-0.008978635	2.328409	-0.007239205	0.9942417	0.995548

B

Vitvi02g00473 -6.117762



Correlation of all measurements (not just means): $r = -8e - 04$, $r^2 = 7e - 07$

Correlation of mean values (plots): $r_2 = -0.1986$

5.3.81 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 |

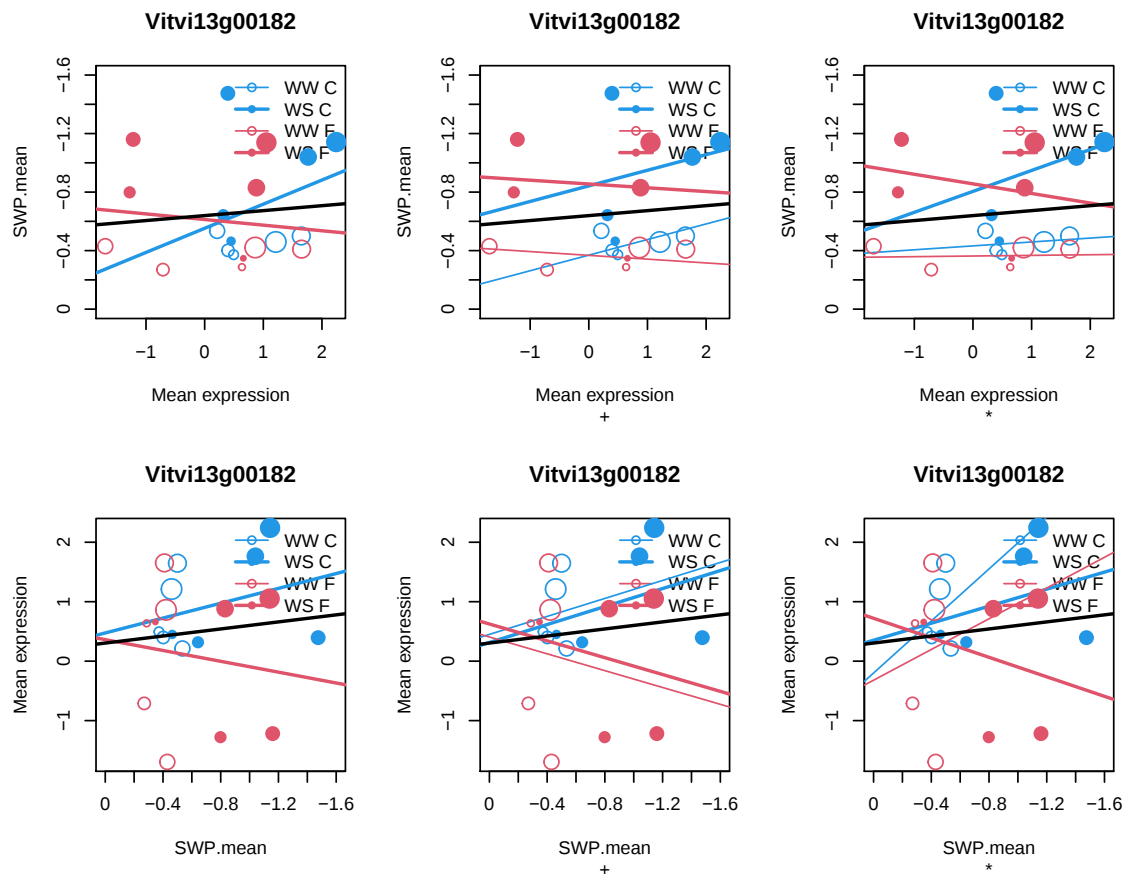
201606

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): $r_2 = 0.1003$

5.3.82 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 |

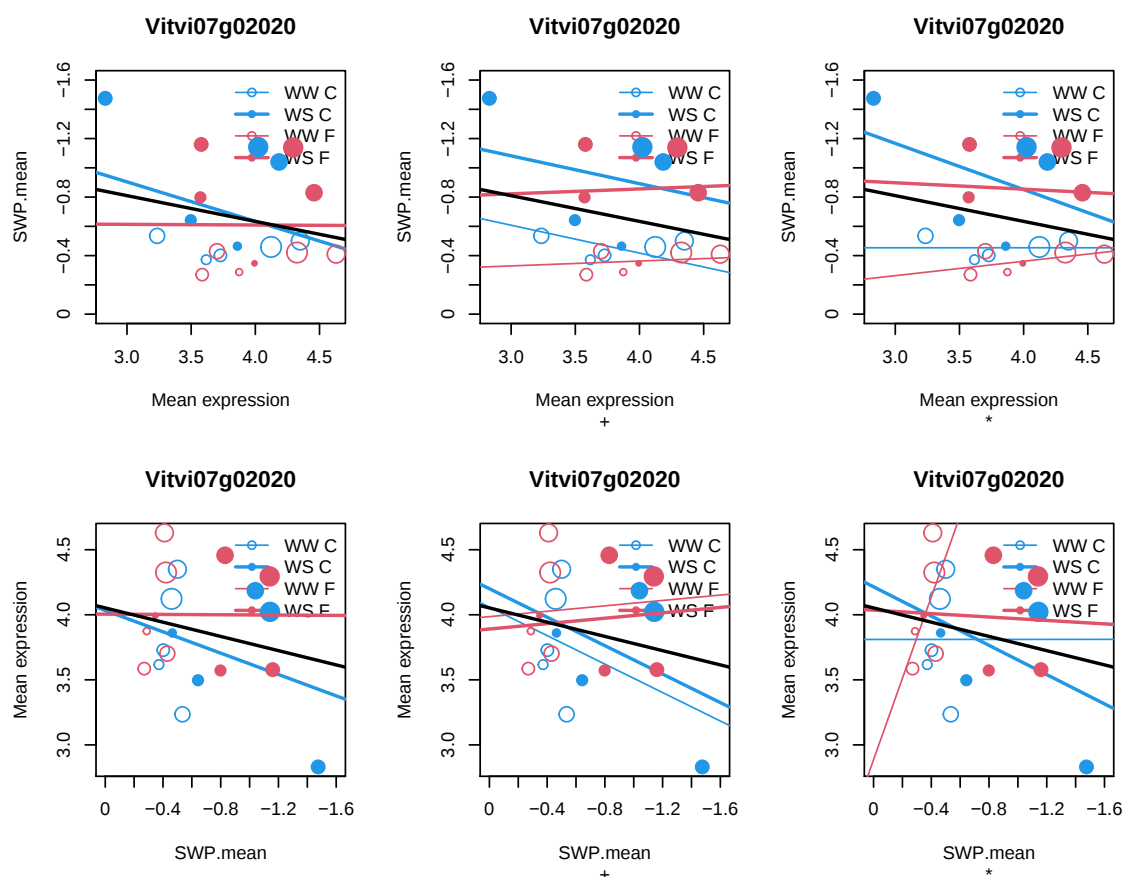
201606

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): $r_2 = -0.2195$

5.3.83 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 |

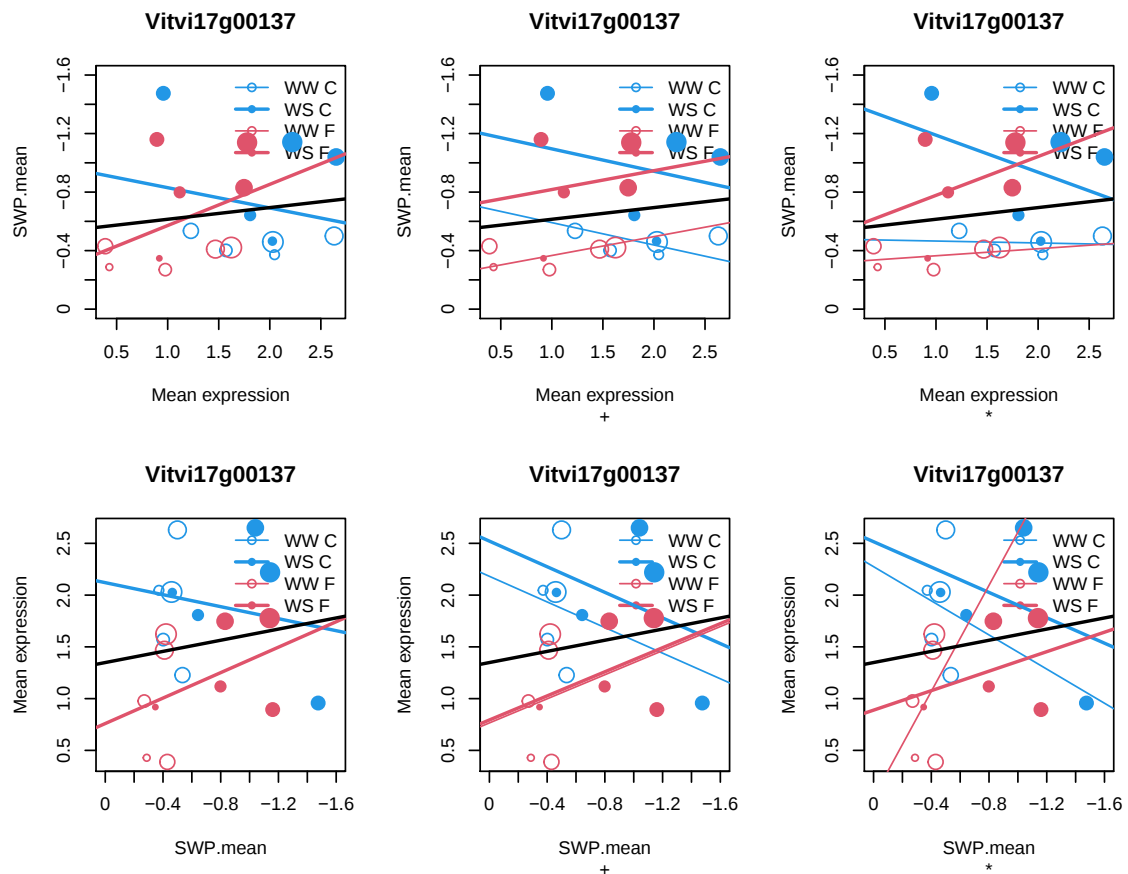
201606

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): $r_2 = 0.1466$

5.3.84 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 |

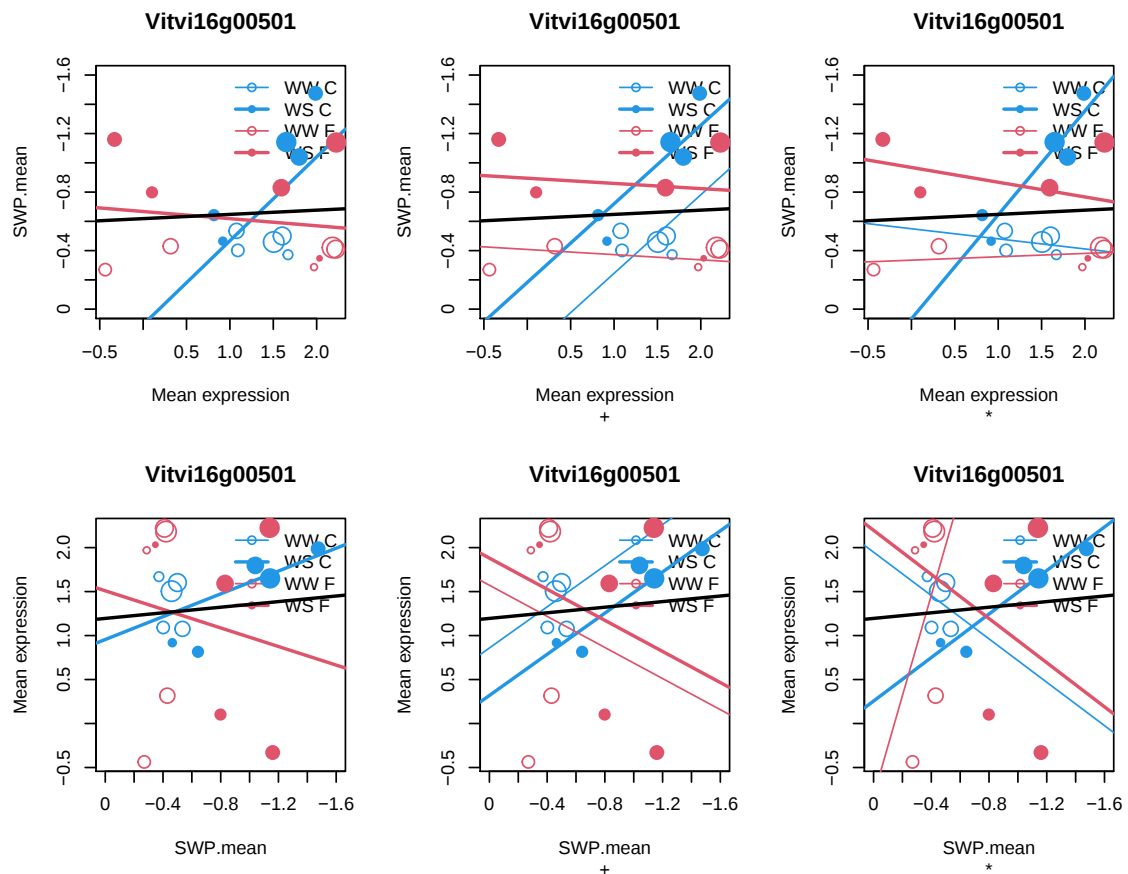
201606

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): $r_2 = 0.0679$

5.3.85 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

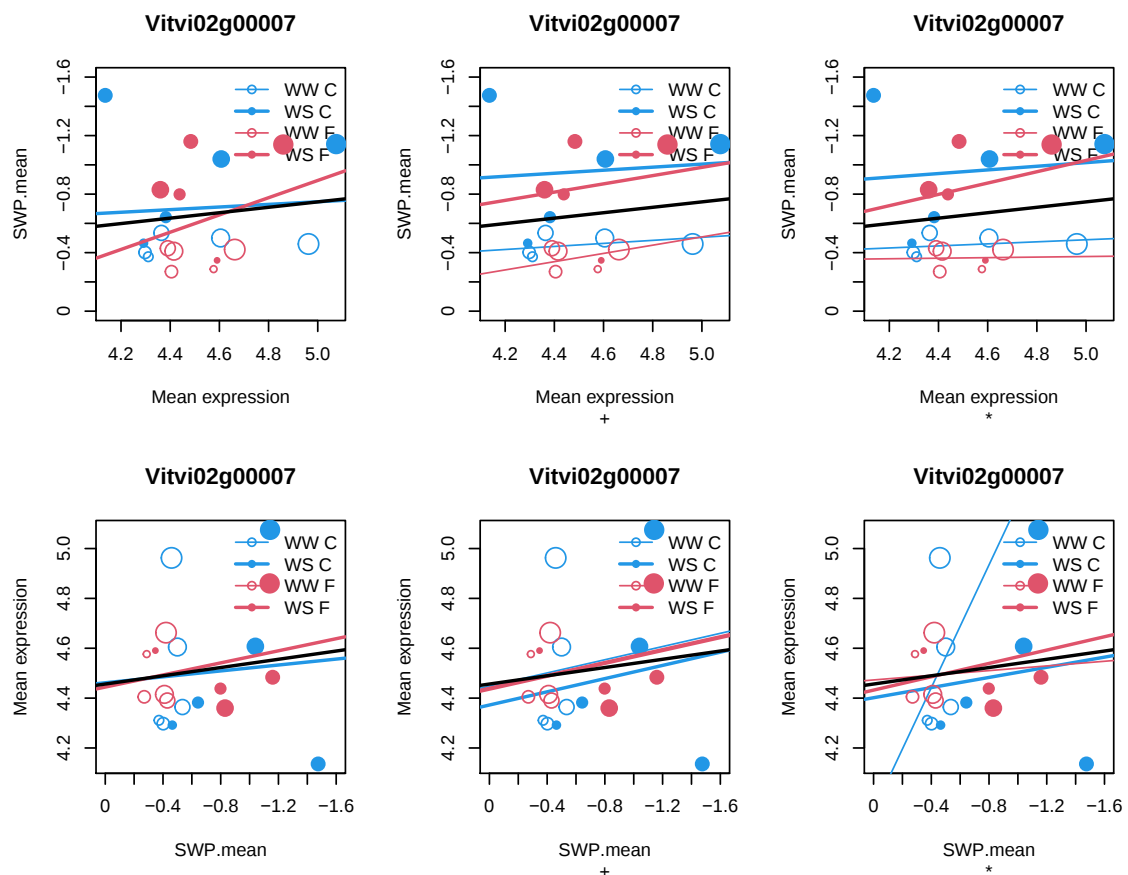
RNA-binding (RRM/RBD/RNP motifs) family protein |

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): $r_2 = 0.1238$

5.3.86 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 |

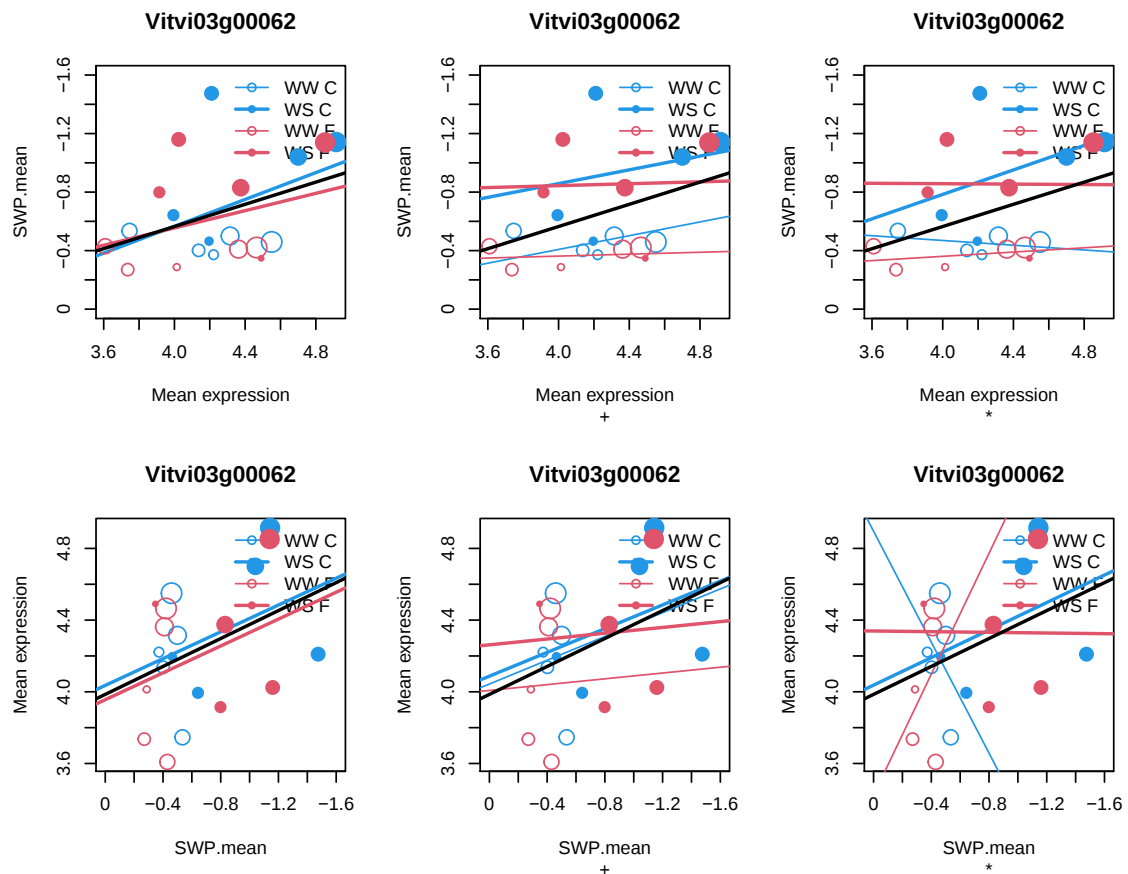
201606

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): $r_2 = 0.3844$

5.3.87 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 |

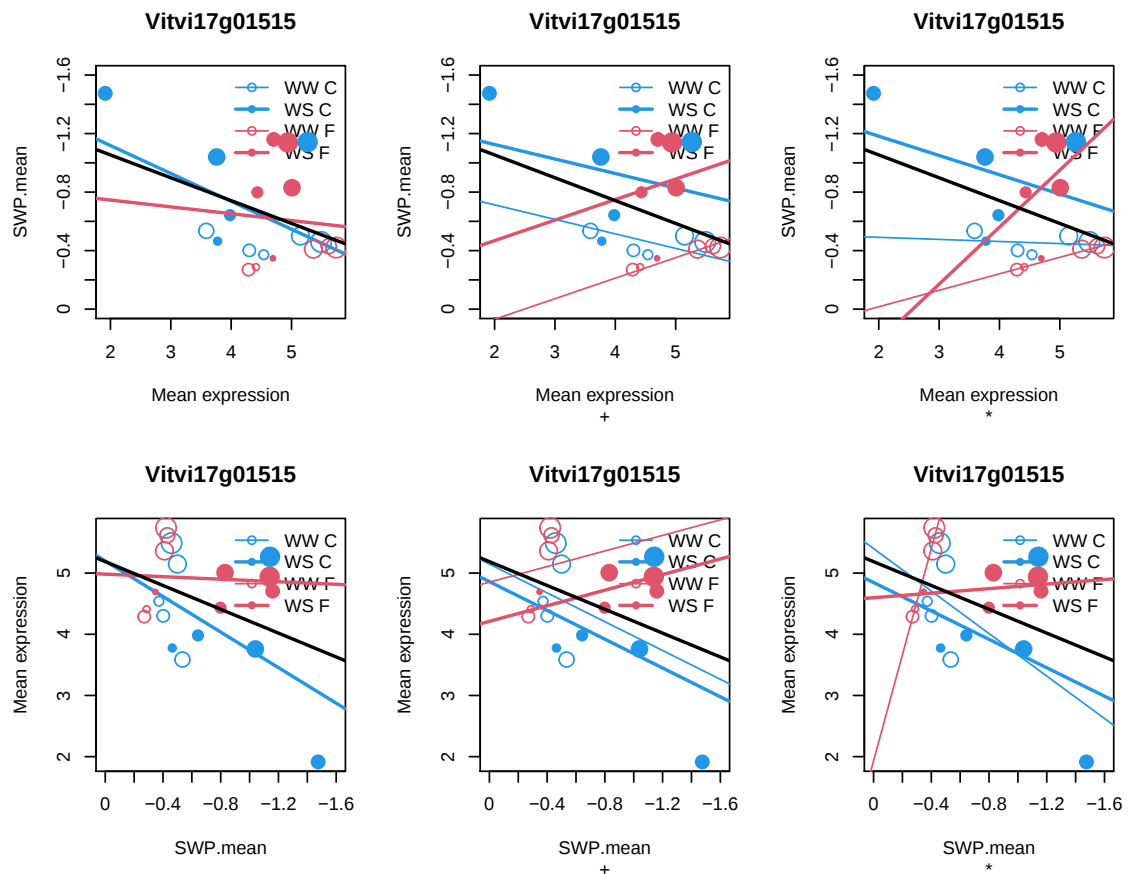
201606

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): $r_2 = -0.3898$

5.3.88 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 |

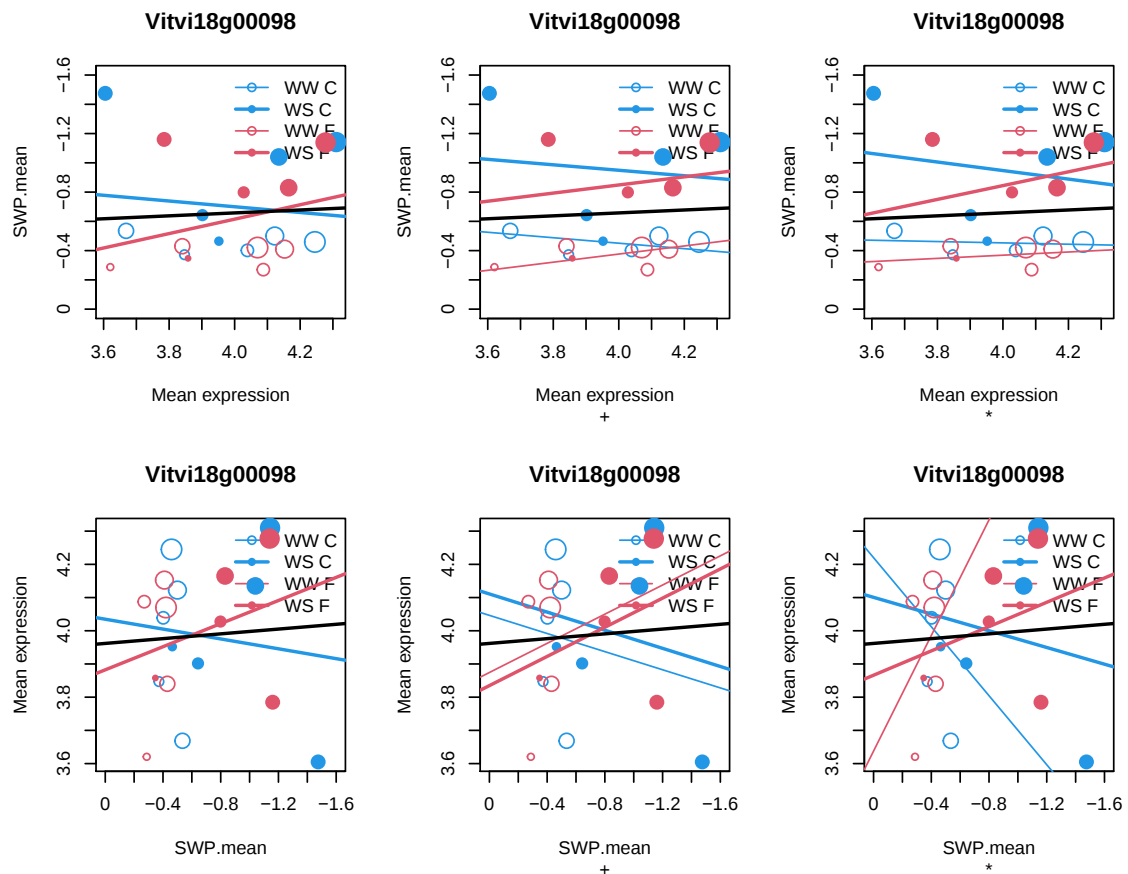
201606

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): $r_2 = 0.0599$

5.3.89 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 |

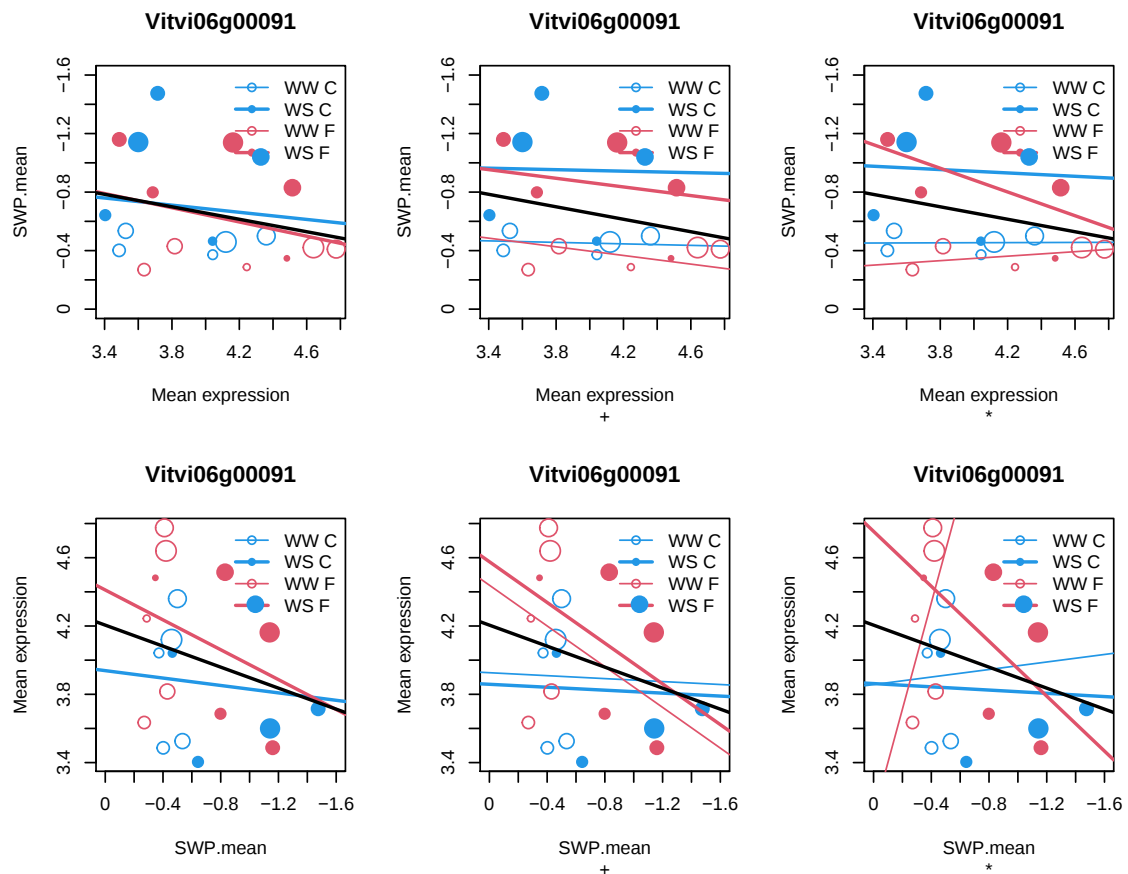
201606

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): $r_2 = -0.2560$

5.3.90 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 |

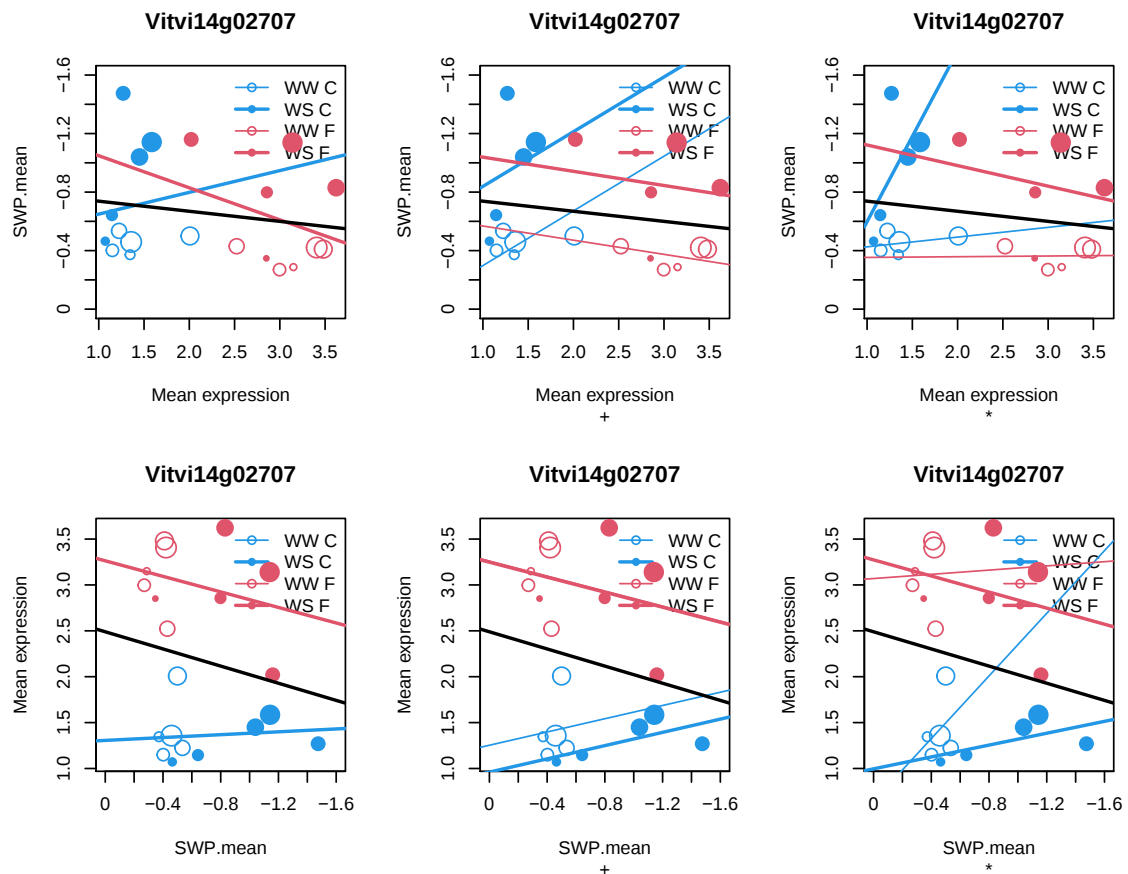
201606

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): $r_2 = -0.1795$

5.3.91 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 |

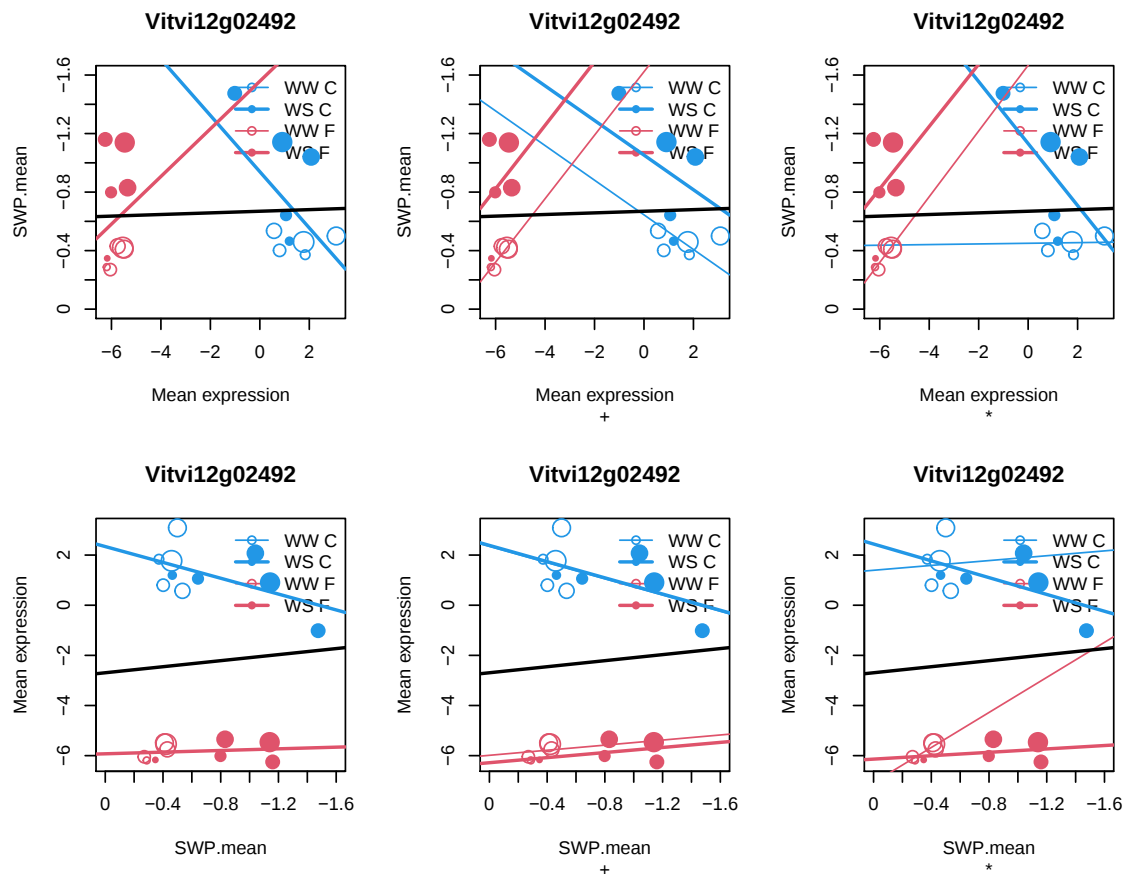
201606

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): $r_2 = 0.0579$

5.3.92 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 |

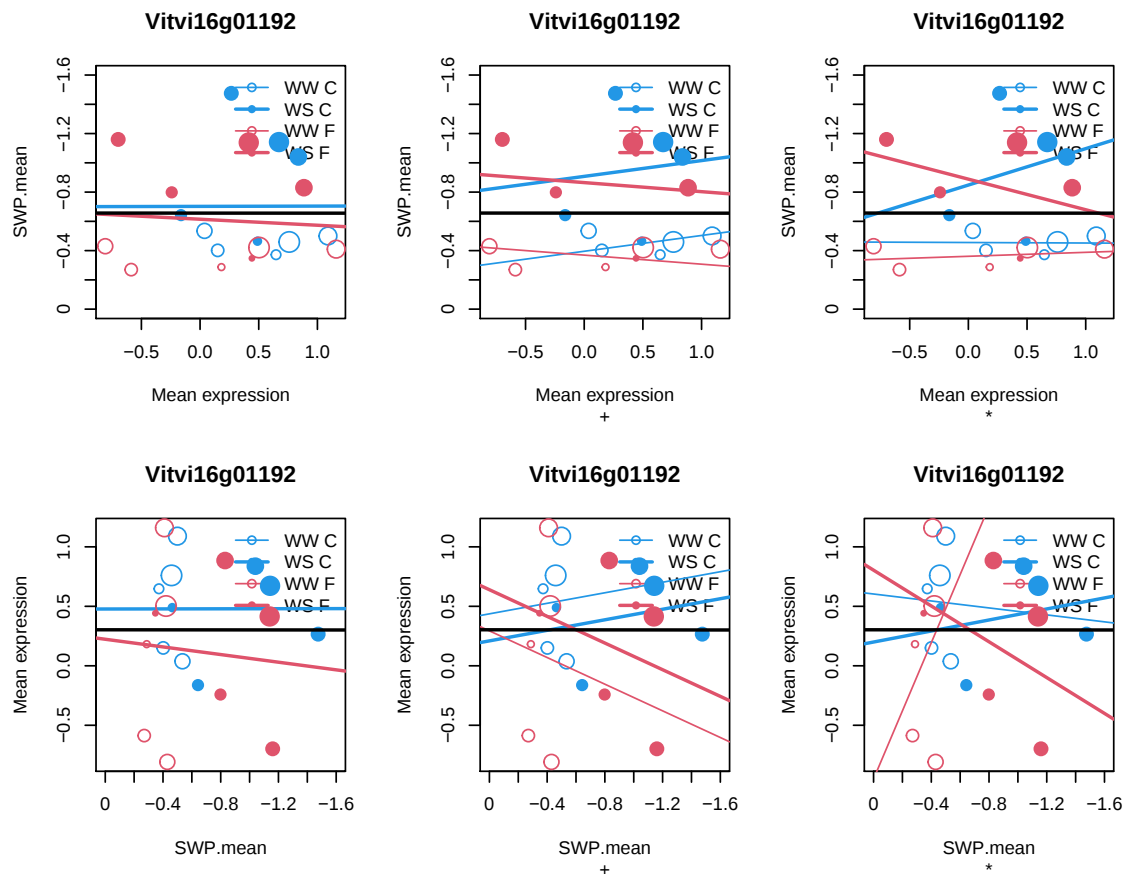
201606

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): $r_2 = -6e - 04$

5.3.93 Vitvi14g00080

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

Vitvi14g00080

35.2

not assigned.unknown

Polynucleotidyl transferase%2C ribonuclease H-like superfamily protein

Chr3:3946267-3946959 REVERSE LENGTH=230 |

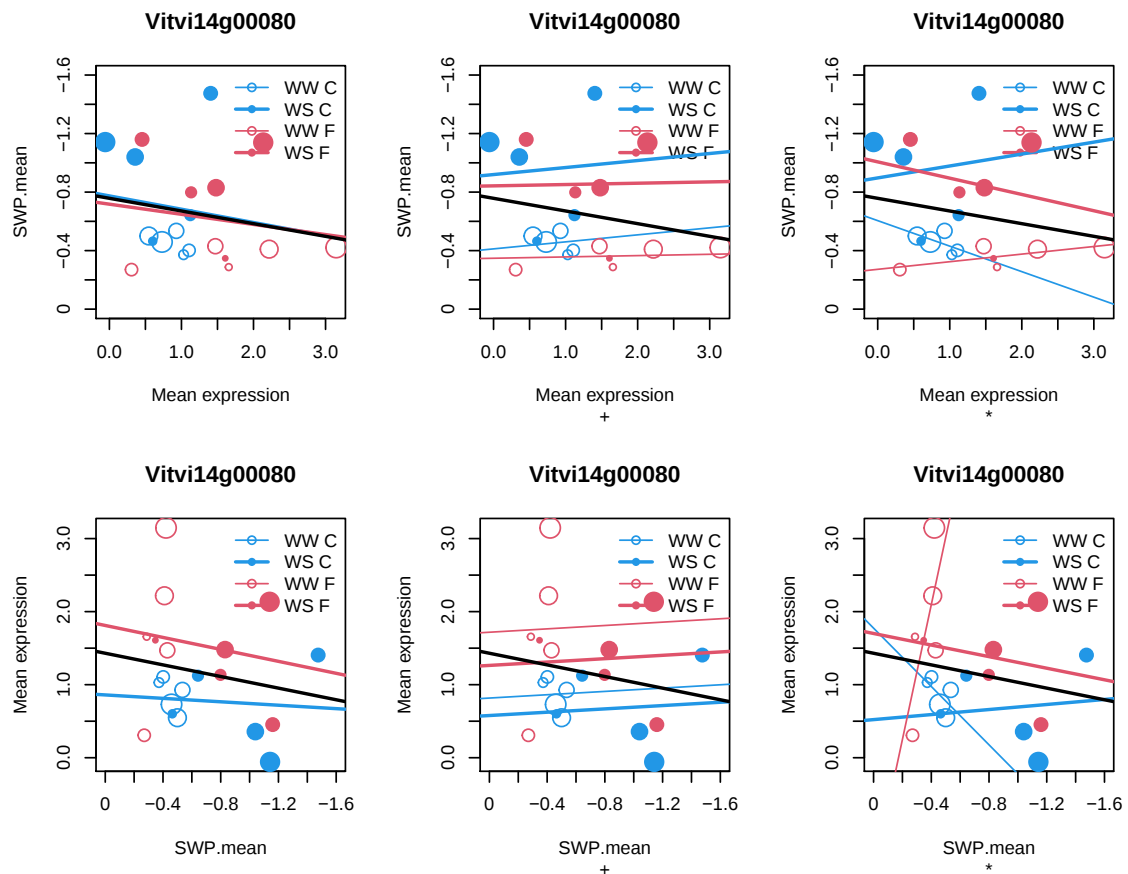
201606

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): $r_2 = -0.1857$

5.3.94 Vitvi18g02570

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

Vitvi18g02570

35.2

not assigned.unknown

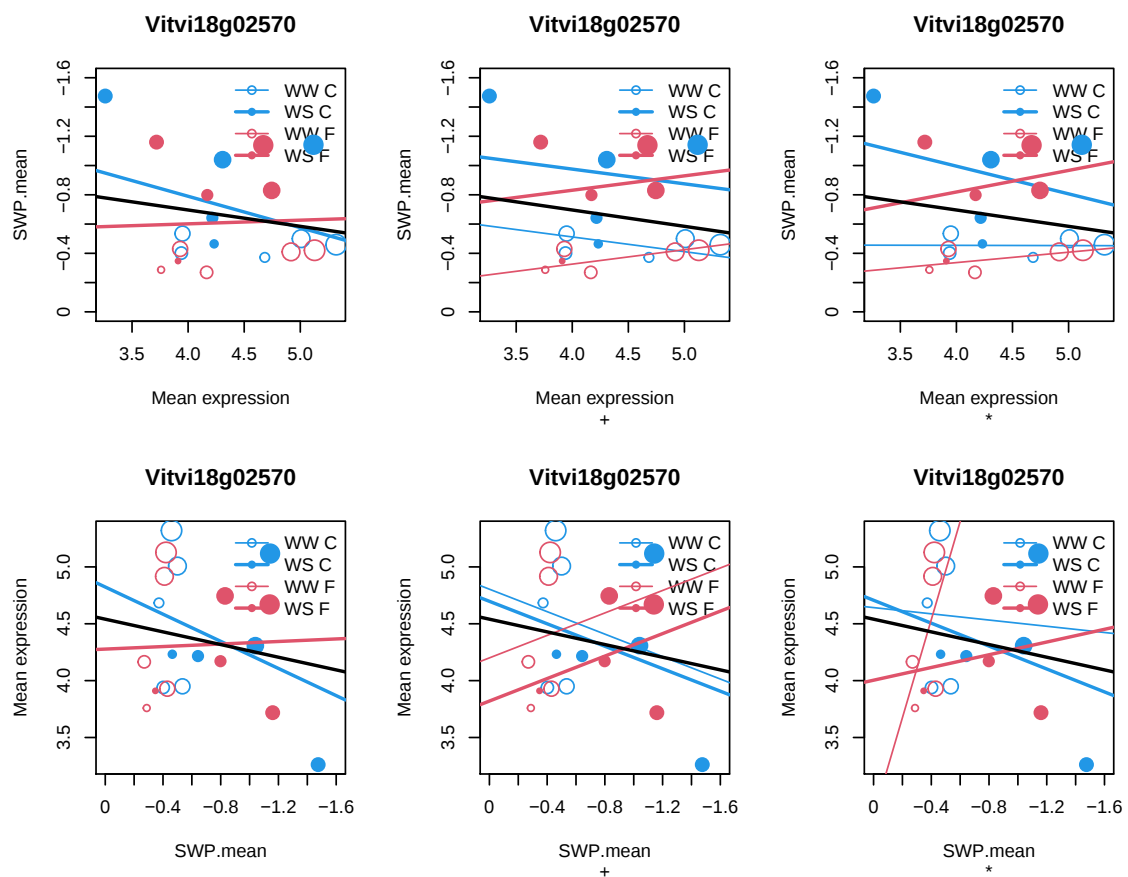
Glucan 1 3-beta-glucosidase IPR001547 Glycoside hydrolase, family 5

Coefficient swp for Vitvi18g02570.

	logFC	AveExpr	t	P.Value	adj.P.Val
Vitvi18g02570	0.002364193	4.35735	0.002093285	0.9983349	0.9987281

B

	B
Vitvi18g02570	-6.117785



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

5.3.95 Vitvi13g00387

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

Vitvi13g00387

35.2

not assigned.unknown

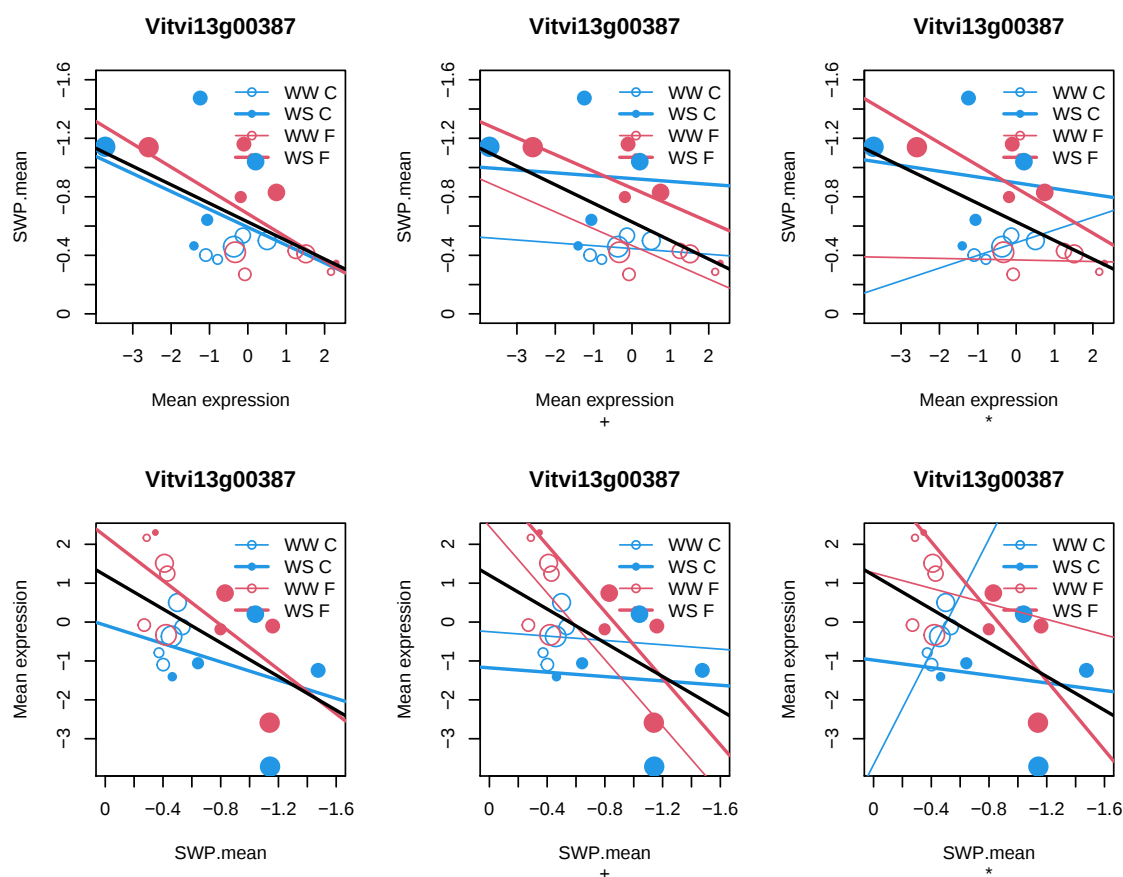
NA

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): $r_2 = -0.5247$

5.3.96 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 |

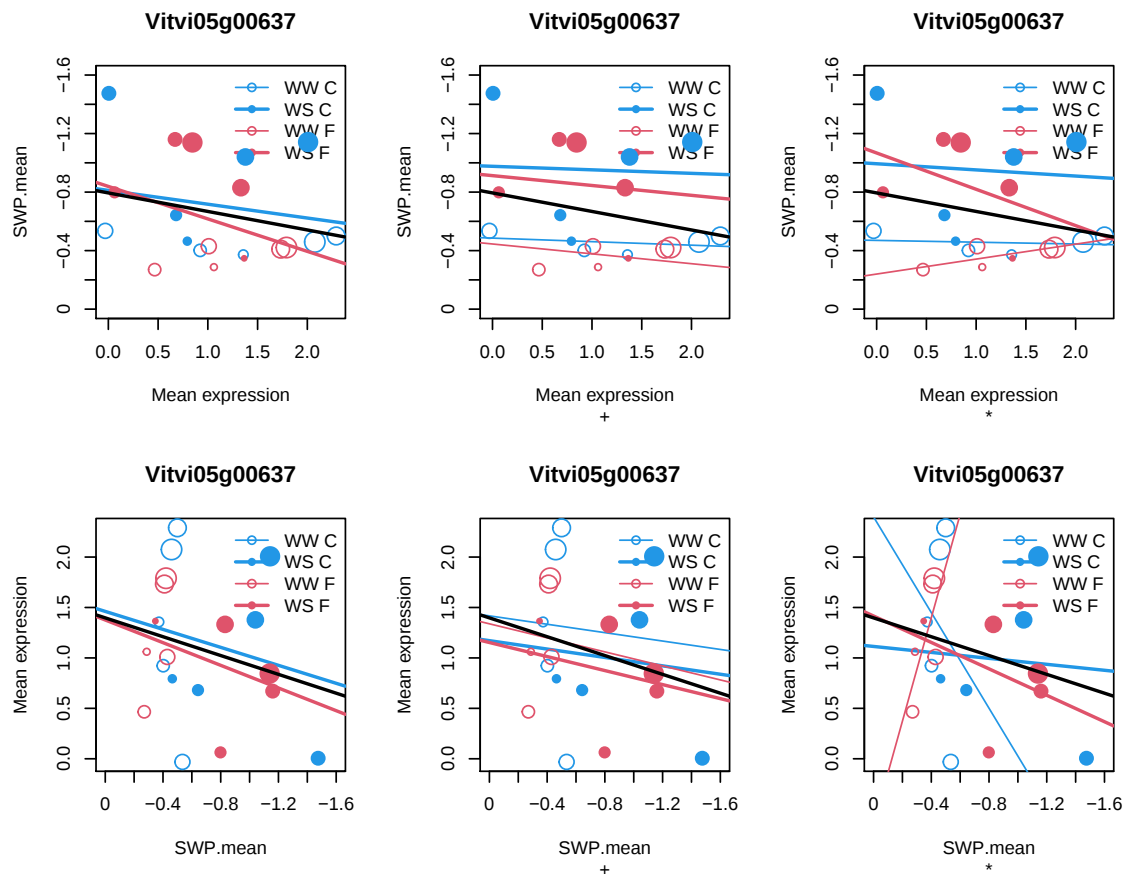
201606

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): $r_2 = -0.2430$

5.3.97 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 |

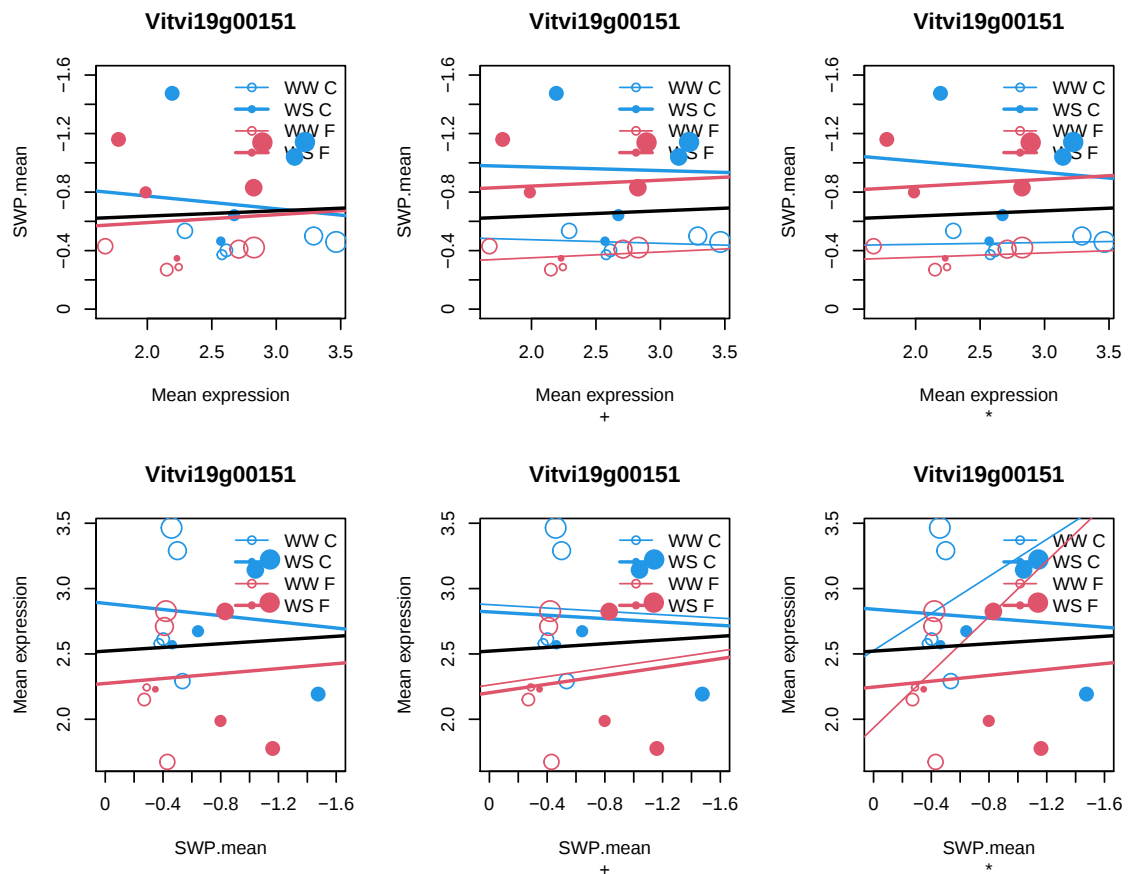
201606

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): $r_2 = 0.0506$

5.3.98 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 |

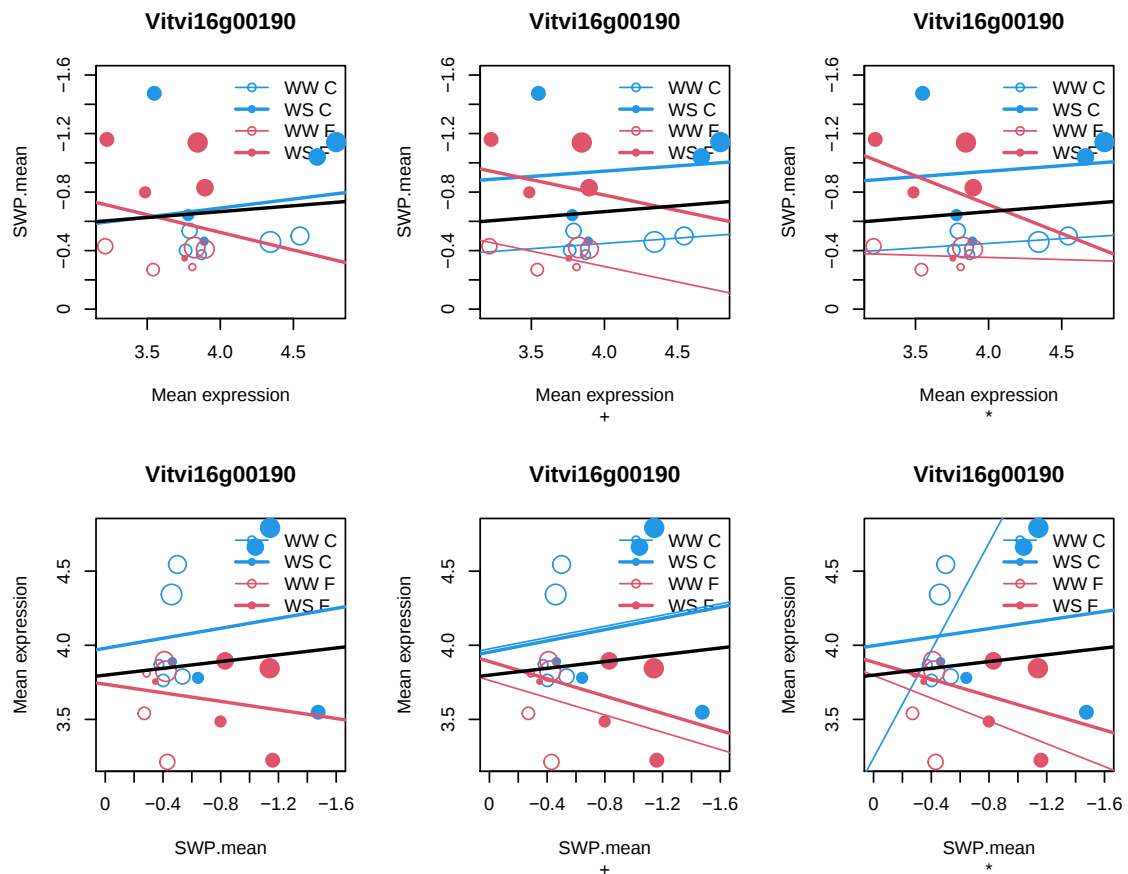
201606

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): $r_2 = 0.0960$

5.3.99 Vitvi01g01924

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

Vitvi01g01924

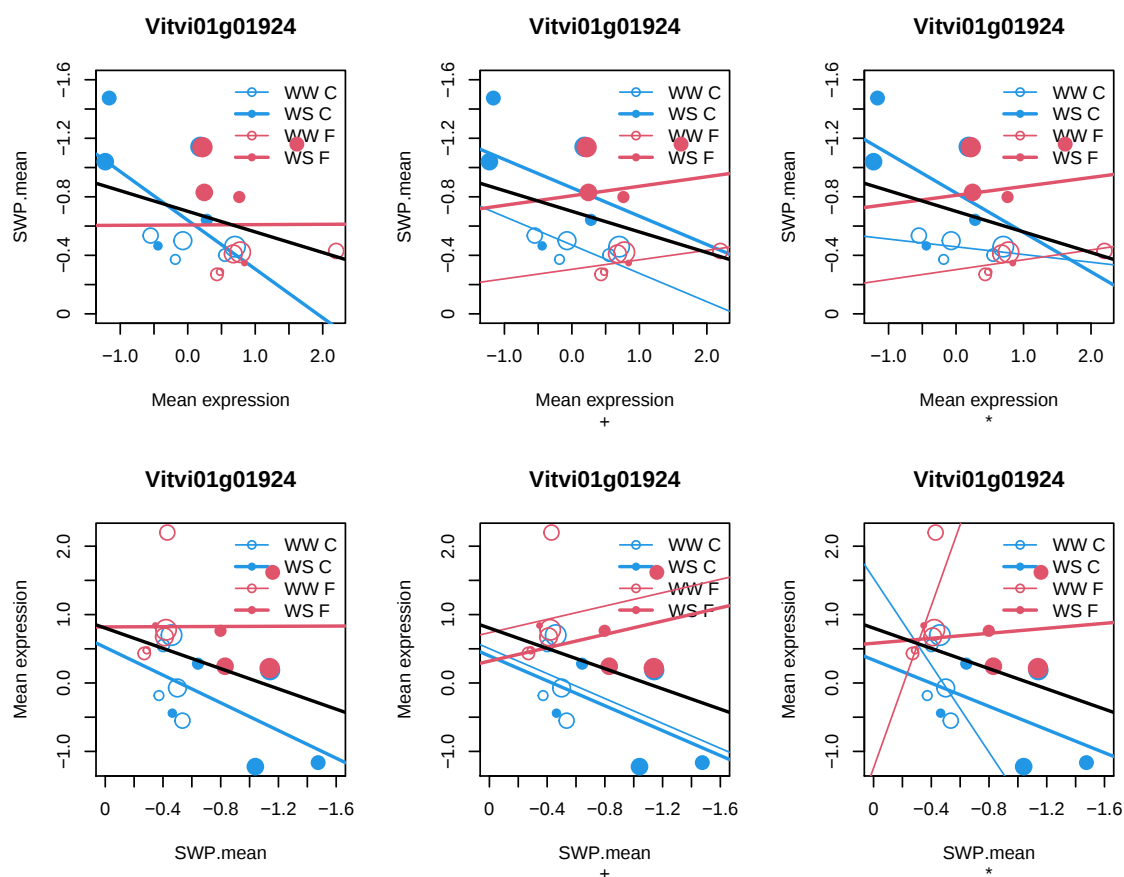
35.2

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): $r_2 = -0.3230$

5.3.100 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 |

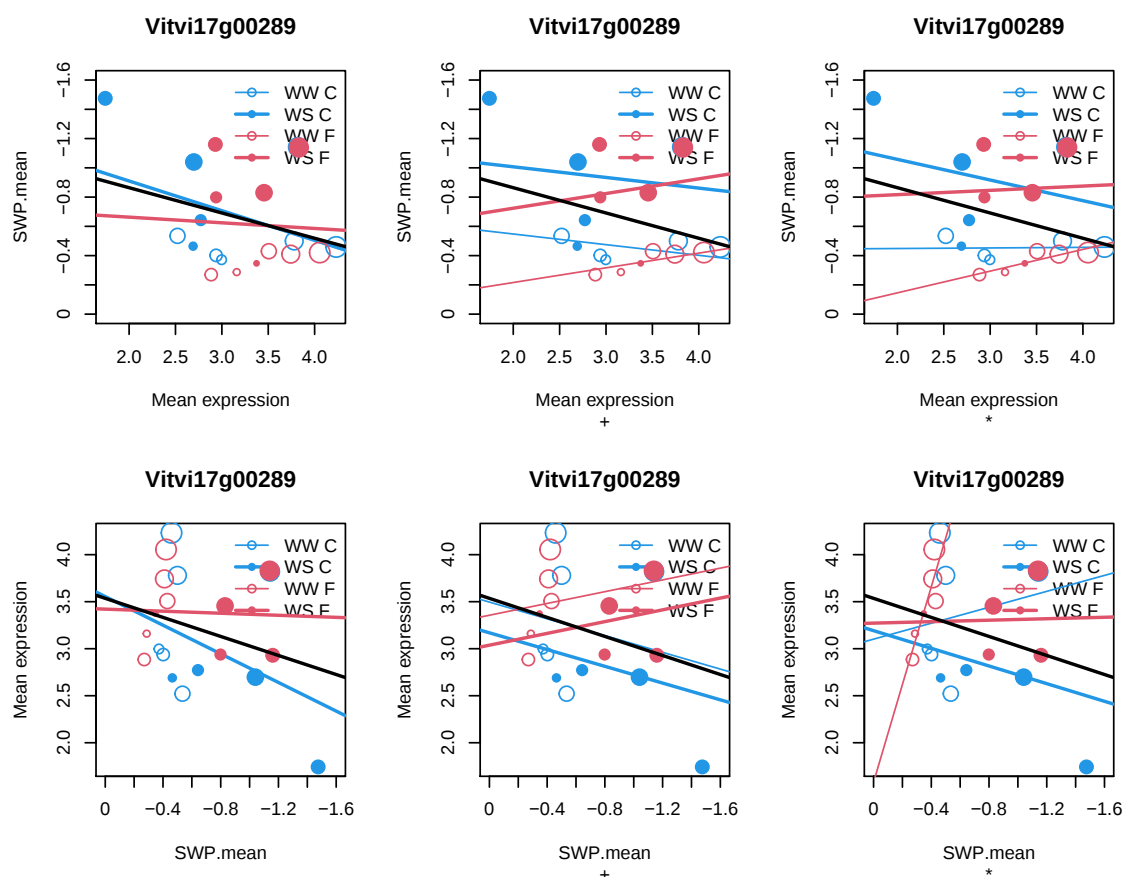
201606

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 perform preliminary data analyses to overview what we have.
pISA Assay creation date:	2020-11-13
pISA Assay creator:	Andrej Blejec
Analyst:	Andrej Blejec
Phenodata:	Phenodata_20201109.txt
Featuredata:	Transcripts1819-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_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

D:

DEJAVNOSTI

OMIKE

pISA-projects

_p_VinskaTrta

_I_EnViRoS

_S_01_Integ

_A_01_Desc-R

other

Network

O:

DEJAVNOSTI

OMIKE

pISA-projects

_p_VinskaTrta

_I_EnViRoS

_S_01_Integ

_A_01_Desc-R

other

Main file : [../doc/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=".")

```