

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

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7.4.30	Vitvi12g02451	234
7.4.31	Vitvi17g01328	235
7.4.32	Vitvi12g02491	236
7.4.33	Vitvi10g02381	237
7.4.34	Vitvi18g02485	238
7.4.35	Vitvi08g02231	239
7.4.36	Vitvi16g01756	240
7.4.37	Vitvi06g01781	241
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7.4.40	Vitvi10g01862	244
7.4.41	Vitvi12g02454	245
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7.4.45	Vitvi18g00878	249
7.4.46	Vitvi06g01743	250
7.4.47	Vitvi05g00038	251
7.4.48	Vitvi15g01643	252
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7.4.60	Vitvi10g02396	266
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7.4.82	Vitvi10g01739	290
7.4.83	Vitvi04g02192	291
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7.4.89	Vitvi11g00990	298
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7.5.23	Vitvi14g01809	329
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7.5.25	Vitvi13g00807	332
7.5.26	Vitvi05g00847	333
7.5.27	Vitvi15g00804	334
7.5.28	Vitvi05g00038	335
7.5.29	Vitvi12g02177	336
7.5.30	Vitvi07g03123	337
7.5.31	Vitvi12g00574	338
7.5.32	Vitvi18g02451	339
7.5.33	Vitvi13g00261	340
7.5.34	Vitvi04g01100	341
7.5.35	Vitvi15g01073	342
7.5.36	Vitvi07g02362	343
7.5.37	Vitvi01g02061	344
7.5.38	Vitvi07g02448	345
7.5.39	Vitvi19g01048	346
7.5.40	Vitvi03g00443	347
7.5.41	Vitvi09g01282	348
7.5.42	Vitvi03g01431	349
7.5.43	Vitvi07g02214	350
7.5.44	Vitvi19g02145	351
7.5.45	Vitvi01g00408	352
7.5.46	Vitvi07g02242	353
7.5.47	Vitvi04g01801	354
7.5.48	Vitvi16g01103	355
7.5.49	Vitvi08g02274	356
7.5.50	Vitvi04g01799	357
7.5.51	Vitvi04g01794	358
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7.6.8	Vitvi16g02098	370
7.6.9	Vitvi07g02989	371
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7.6.11	Vitvi09g01696	373
7.6.12	Vitvi00g02226	374
7.6.13	Vitvi16g01542	375
7.6.14	Vitvi16g02021	376
7.6.15	Vitvi18g01281	377
7.6.16	Vitvi16g01549	378
7.6.17	Vitvi09g00667	379

7.6.18	Vitvi05g01285	380
7.6.19	Vitvi16g00814	381
7.6.20	Vitvi10g00613	382
7.6.21	Vitvi19g02004	383
7.6.22	Vitvi01g01764	384
7.6.23	Vitvi17g01101	385
7.6.24	Vitvi18g00269	386
7.6.25	Vitvi19g02007	387
7.6.26	Vitvi13g00605	388
7.6.27	Vitvi04g01856	389
7.6.28	Vitvi16g00025	390
7.6.29	Vitvi19g00391	391
7.6.30	Vitvi05g01675	392
7.6.31	Vitvi07g01217	393
7.6.32	Vitvi06g01959	394
7.6.33	Vitvi14g03071	395
7.6.34	Vitvi06g01965	396
7.6.35	Vitvi06g00024	397
7.6.36	Vitvi05g01916	398
7.6.37	Vitvi19g01669	399
7.6.38	Vitvi02g00666	400
7.6.39	Vitvi10g01704	401
7.6.40	Vitvi07g00450	402
7.6.41	Vitvi16g01214	403
7.6.42	Vitvi06g00327	404
7.6.43	Vitvi04g01423	405
7.6.44	Vitvi10g00027	406
7.6.45	Vitvi03g00248	407
7.6.46	Vitvi11g00328	408
7.6.47	Vitvi14g01448	409
7.6.48	Vitvi02g00015	410
7.6.49	Vitvi01g01984	411
7.6.50	Vitvi14g01639	412
7.6.51	Vitvi13g00350	413
7.6.52	Vitvi09g01361	414
7.6.53	Vitvi01g00463	415
7.6.54	Vitvi07g01779	416
7.6.55	Vitvi07g01625	417
7.6.56	Vitvi01g01169	418
7.6.57	Vitvi18g02592	419
7.6.58	Vitvi09g01214	420
7.6.59	Vitvi14g01152	421
7.6.60	Vitvi05g00817	422
7.6.61	Vitvi08g01915	423
7.6.62	Vitvi12g02441	424
7.6.63	Vitvi14g02682	425
7.6.64	Vitvi14g03074	426
7.6.65	Vitvi16g01210	427
7.6.66	Vitvi15g00870	428
7.6.67	Vitvi01g00064	429

7.6.68	Vitvi06g01350	430
7.6.69	Vitvi09g02014	431
7.6.70	Vitvi09g01609	432
7.6.71	Vitvi03g00712	433
7.6.72	Vitvi10g00049	434
7.6.73	Vitvi01g01048	435
7.6.74	Vitvi02g00235	436
7.6.75	Vitvi13g02316	437
7.6.76	Vitvi02g00160	438
7.6.77	Vitvi18g00095	439
7.6.78	Vitvi03g00995	440
7.6.79	Vitvi12g00478	441
7.6.80	Vitvi08g01123	442
7.6.81	Vitvi13g00233	443
7.6.82	Vitvi08g01867	444
7.6.83	Vitvi03g00080	445
7.6.84	Vitvi14g02021	446
7.6.85	Vitvi01g00499	447
7.6.86	Vitvi18g02446	448
7.6.87	Vitvi07g02902	449
7.6.88	Vitvi03g00580	450
7.6.89	Vitvi00g00894	451
7.6.90	Vitvi03g00379	452
7.6.91	Vitvi01g02058	453
7.6.92	Vitvi15g00739	454
7.6.93	Vitvi08g01656	455
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1 Task

Final document in folder /reports:

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

2 Information from pISA

Data directory

```
> .inroot
```

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

Results directory

```
> .oroot
```

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

```
project:      _p_VinskaTrta
```

```
Investigation: _I_EnViRoS
```

```
Study:        _S_01_Integ
```

```
Assay:         _A_01_Desc-R
```

3 Data

Priporočljivo je najprej prebrati phenodata in feature-data, potem pa podatke. To omogoča izbor spremenljivk in vzorcev takoj za tem, ko podatke preberemo.

```
> cat(knit_child(file.path("../doc", "10a_Read-Data.Rnw"), quiet=TRUE))
```

List of data objects:

```
> my.objects
```

	name	description	class	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 Fleurtai
2018-06-04             2             2
2018-06-15             2             2
2018-06-21             2             2
2018-06-29             2             2
2018-07-04             2             2
2018-07-10             2             2
2018-07-16             2             2
2018-07-23             2             2
2018-07-31             2             2
2018-08-07             2             2
2019-06-18             2             2
2019-06-26             2             2
2019-07-08             2             2
2019-07-12             2             2
2019-07-17             2             2
2019-07-22             0             2
2019-07-30             2             2
2019-08-06             2             2
2019-08-12             2             2
2019-08-19             2             2

> table(pdata1819$date)
< table of extent 0 >
> pdata1819$date <- as_date(pdata1819$Date, format="%d.%m.%Y")
> table(pdata1819$date)

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

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

```

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

```

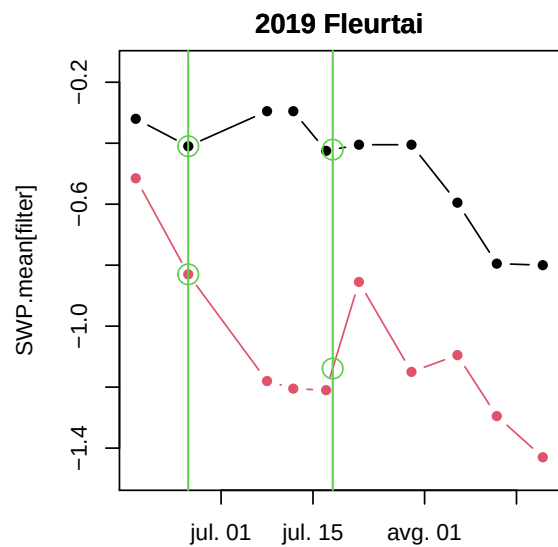
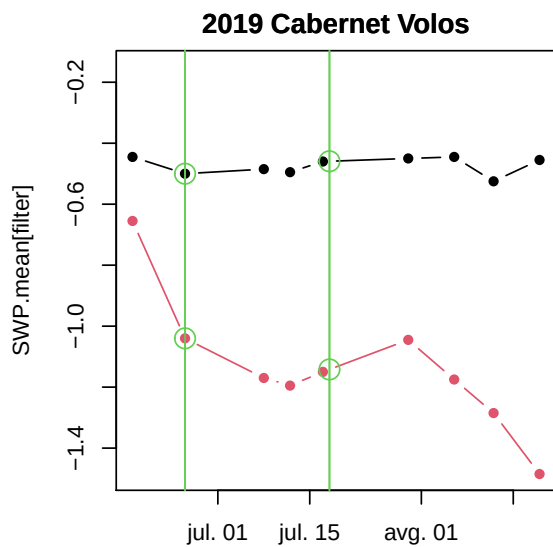
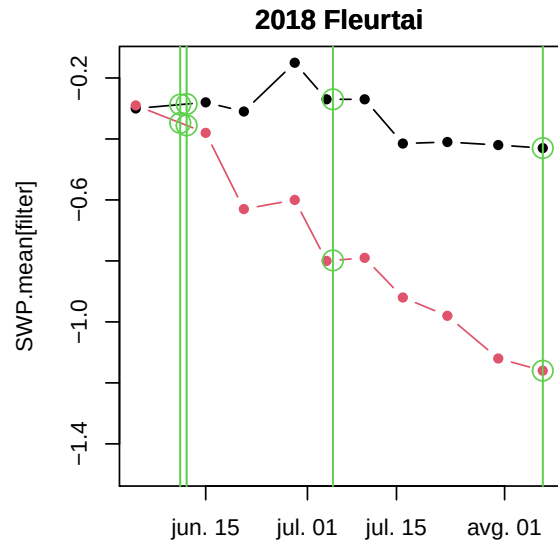
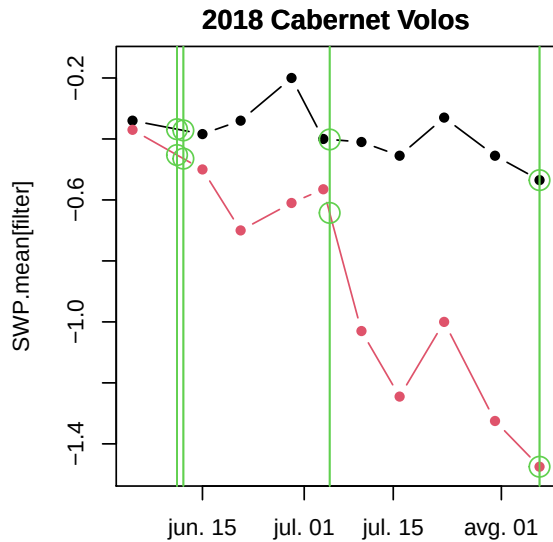
> wpas <- NULL
> par(mfrow=c(2,2),mar=c(3,4,2,1))
> for( yr in unique(wpdata$year)){
+   for (vari in levels(wpdata$variety)) {
+     with(wpdata, {
+       filter <- (wpdata$year==yr) & (variety== vari)
+       plot(date[filter], SWP.mean[filter], type="n",ylim=range(SWP.mean))
+       for(tr in levels(treat)){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

```

```

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

```



```

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

```

@

Order water potential data by date

```

> diff(wpas$date)

```

Time differences in days

```

[1] 23 33 -57 1 23 33 -57 1 23 33 -57 1 23 33 -57 380
[17] 22 -22 22 -22 22 -22 22

```

```

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

```

Time differences in days

```
[1] 0 0 0 1 0 0 0 23 0 0 0 33 0 0 0 323
[17] 0 0 0 22 0 0 0
```

Convert treatment and variety into factors

```
> (wpas$treat <- factor(wpas$treat, levels=c("WW", "WS")))
[1] WW WS WW WS WW WS WW WS WW WS WW WS WW WS WW WS WW WS WW WS
[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

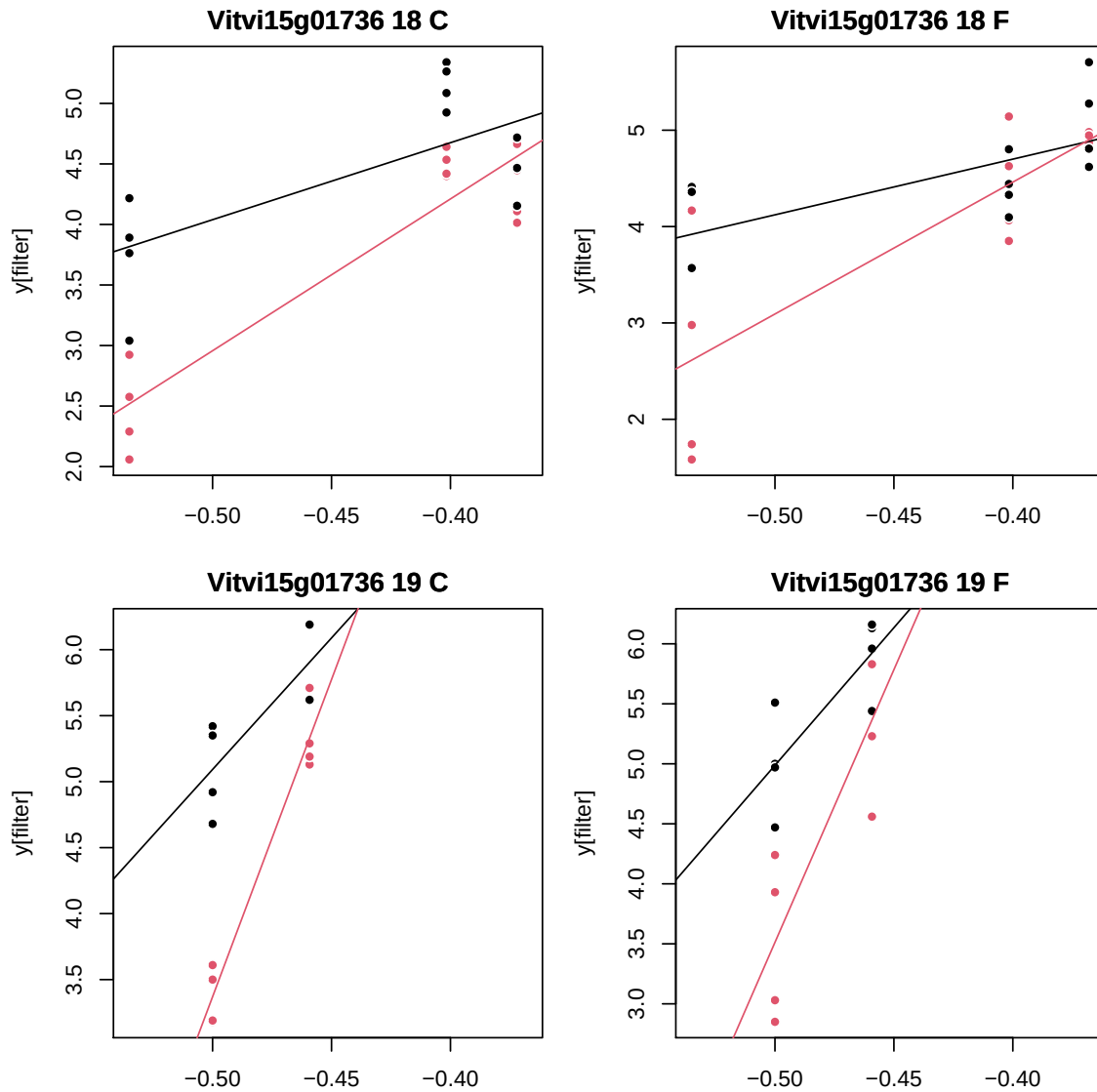
Call:

```
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  TRUE
[67] TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
[78] TRUE  TRUE  TRUE
[1] "2019-06-26" "2019-06-26" "2019-06-26" "2019-06-26" "2019-06-26"
[6] "2019-06-26" "2019-06-26" "2019-06-26" "2019-07-18" "2019-07-18"
[11] "2019-07-18" "2019-07-18" "2019-07-18" "2019-07-18" "2019-07-18"
[16] "2019-07-18"
```



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

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

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

```
Coefficients:
  (Intercept)  pd$swp[select]
      26.23          45.44
```

```
> .testing <- FALSE
```

4 Expression and water poential analysis

```

> varname <- rownames(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)

```

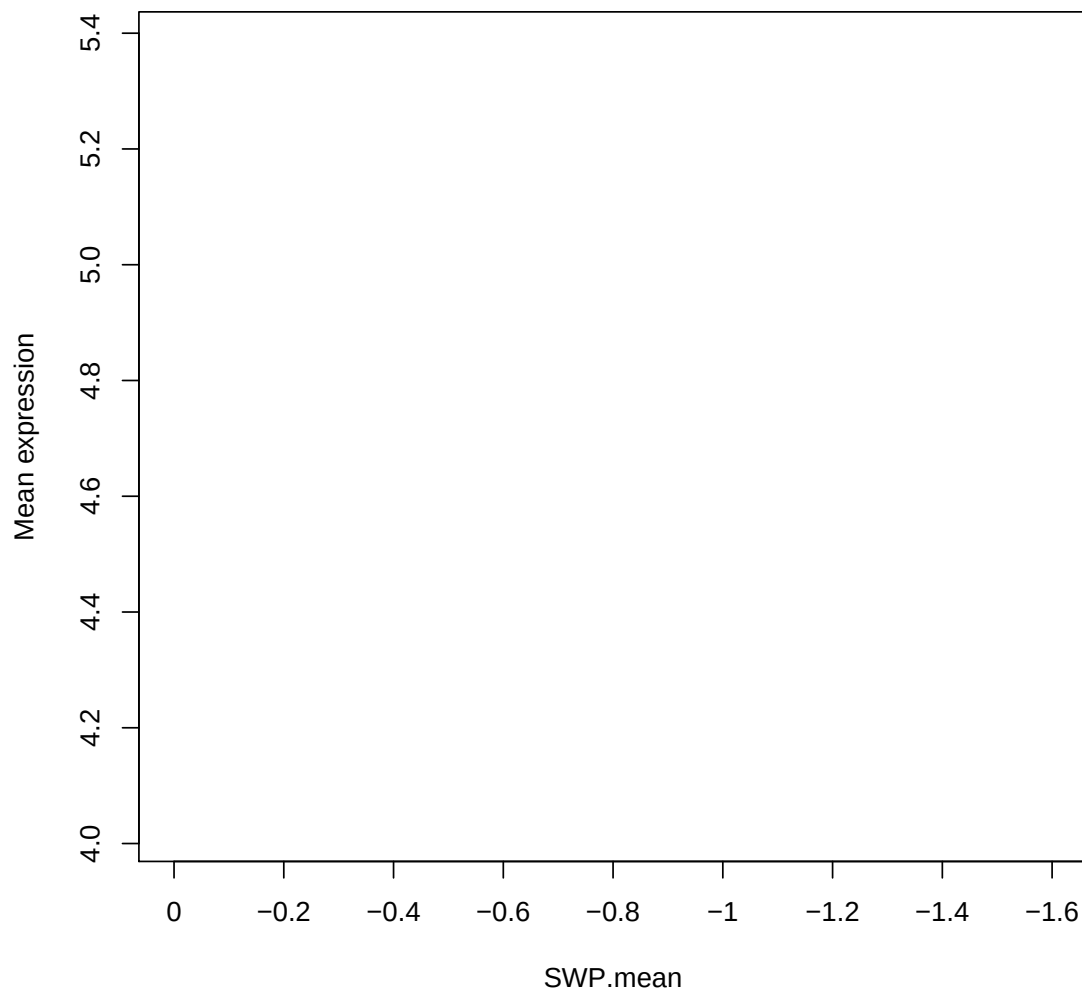
```
Error in tapply(pd$swp, pd[, c("date", "treat", "variety")], unique): argument
> means
, , variety = C

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

```

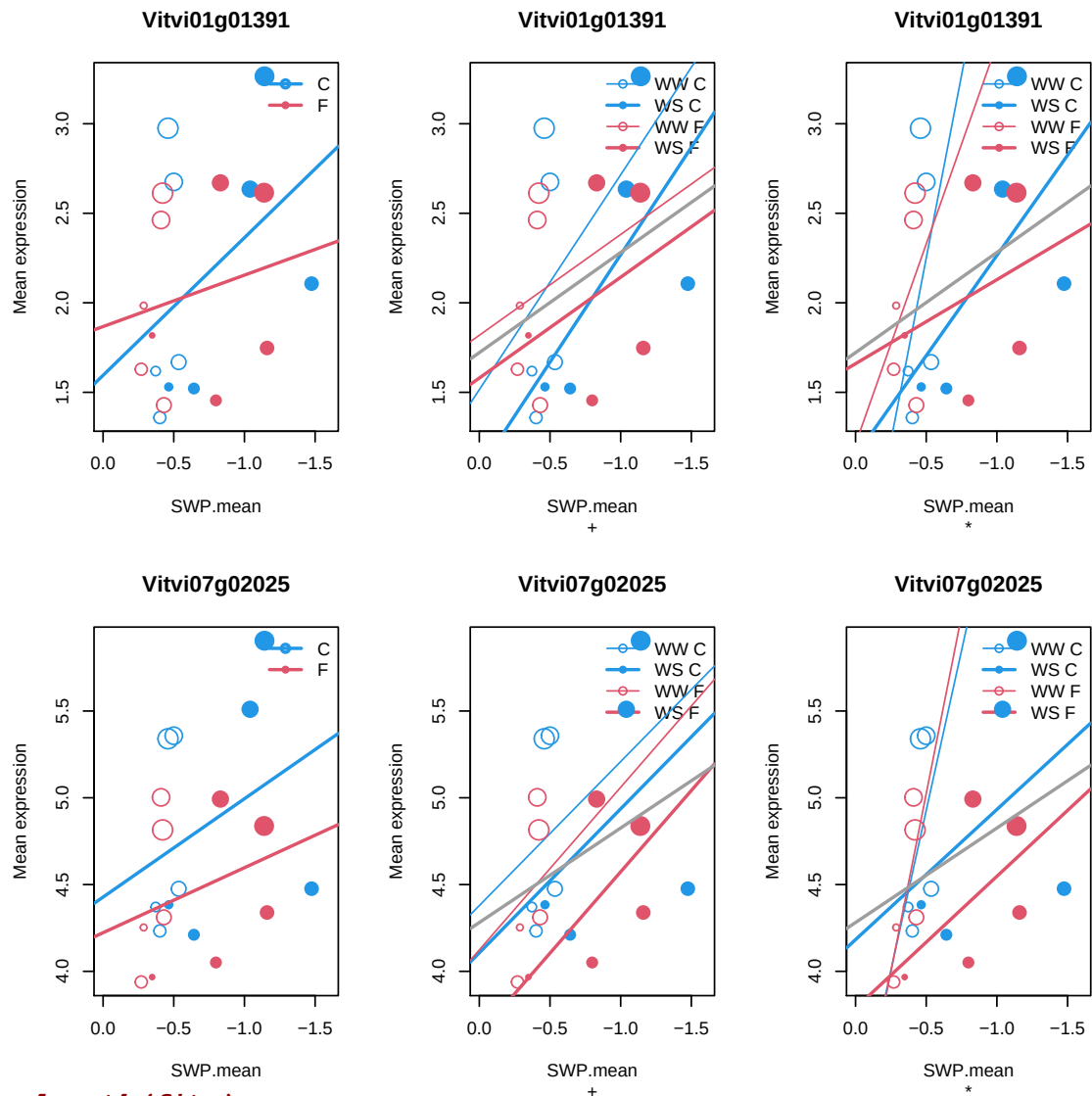
+       pch = pchs[as.numeric(mns$treat)]
+       , cex=cex
+     )
+ #   }
+   xx <- xx
+   if(model=="") fit <- lm(yy~xx)
+   if(model=="+") fit <- lm(yy~xx+mns$treat)
+   if(model=="*") fit <- lm(yy~xx*mns$treat)
+   if(verbose) print(summary(fit))
+   coef <- fit$coefficients
+ #   print(coef)
+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

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

[1] "Vitvi07g02767"

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

```

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

4.2 Water potential vs Expression

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

```

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

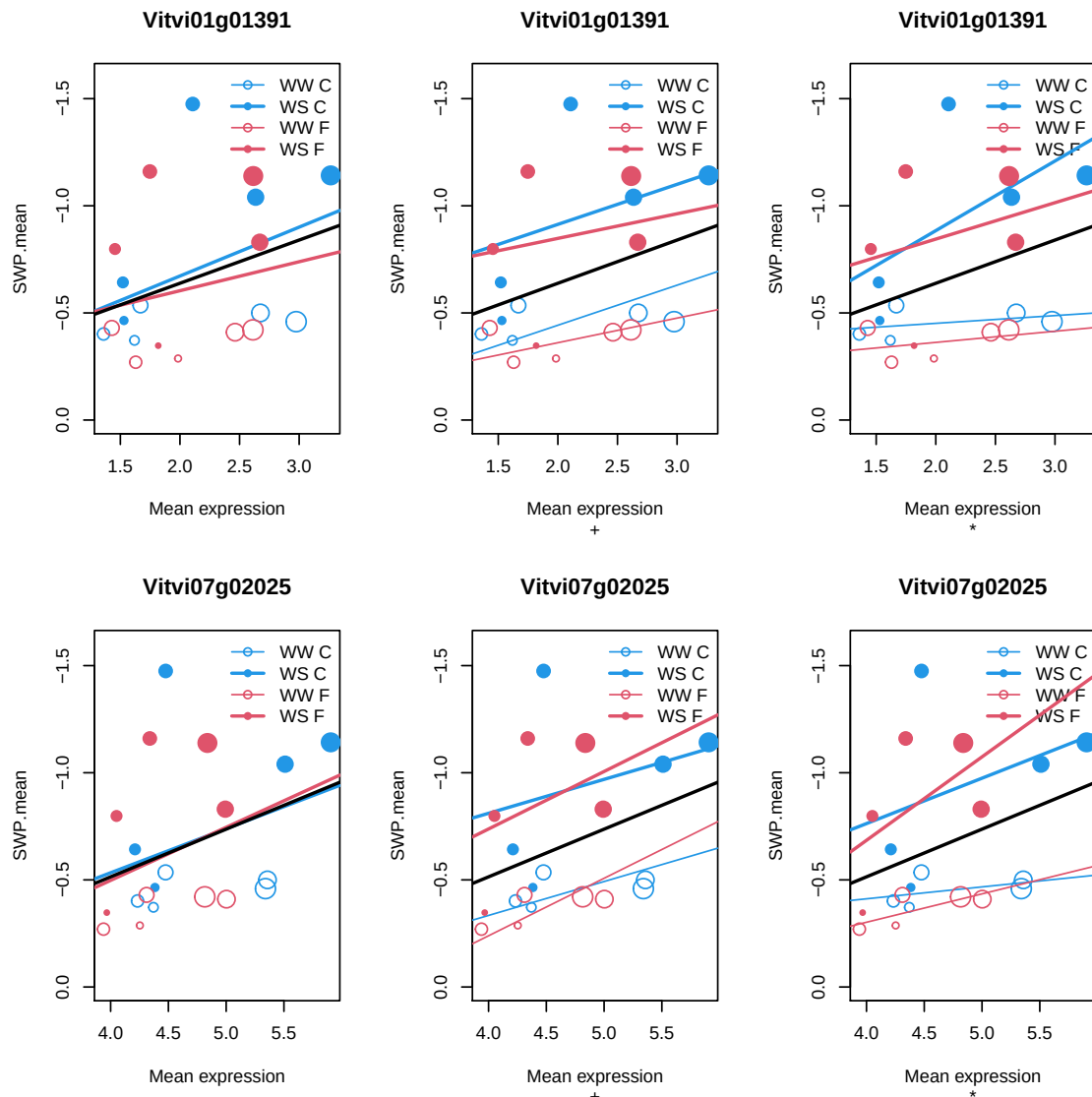
```

```

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

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

```



```

> length(fits)

```

```

[1] 5

```

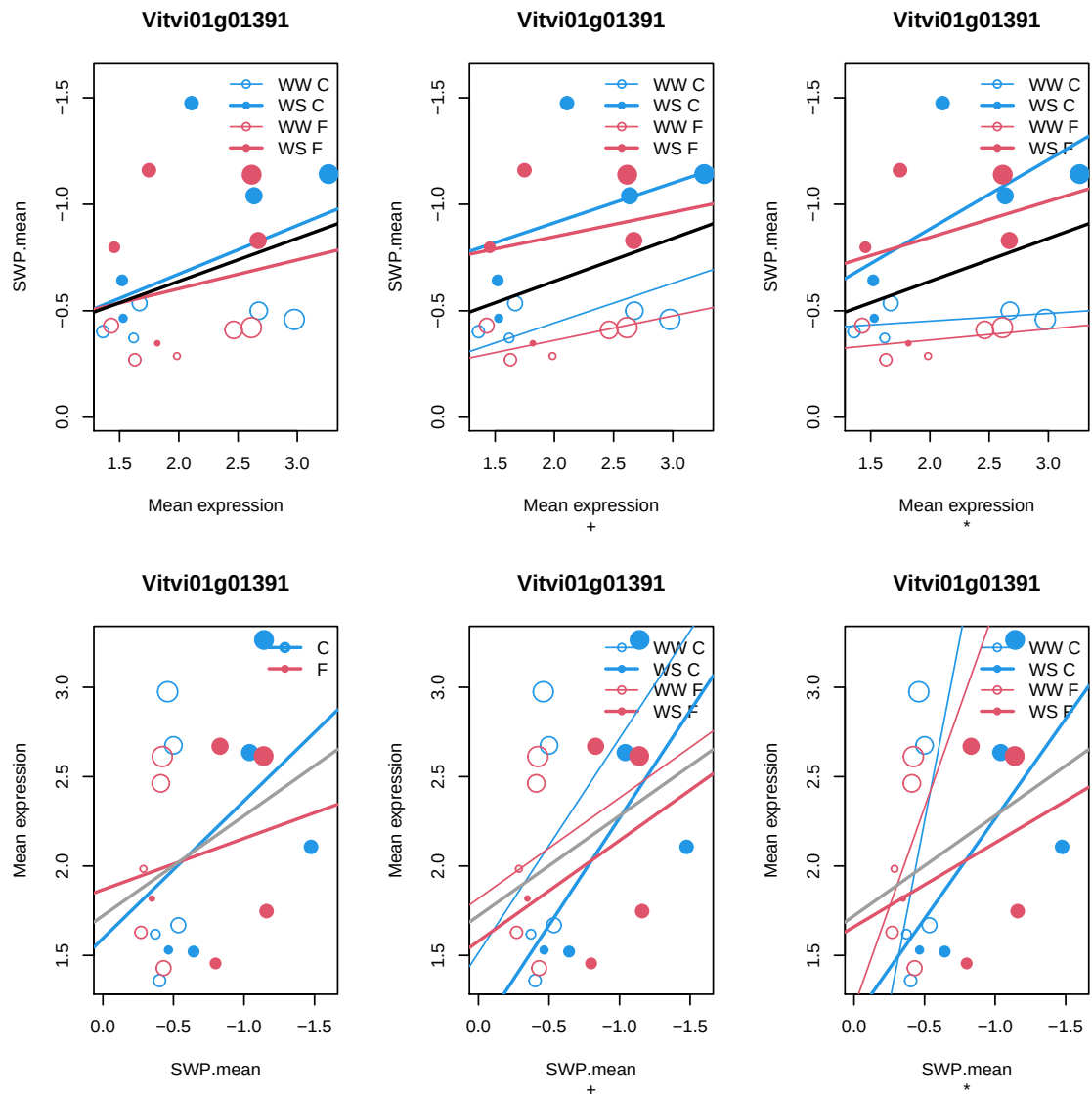
```

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

> testvar <- "Vitvi01g01391"

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

```



```

> fits

```

```
$name
[1] "Vitvi01g01391"
```

```
$C
```

```
Call:
lm(formula = yy ~ xx)
```

```
Coefficients:
(Intercept)          xx
      1.5950      -0.7686
```

```
$F
```

```
Call:
lm(formula = yy ~ xx)
```

```
Coefficients:
(Intercept)          xx
      1.8673      -0.2872
```

```
$all
```

```
Call:
lm(formula = ally ~ allx)
```

```
Coefficients:
(Intercept)        allx
      1.7218      -0.5594
```

```
$r
[1] -0.3359093
```

```
> varname
```

```
[1] "Vitvi01g01391"
```

```
> pd <- pdata1819
```

```
> (y <- unlist(t1819[varname,]))
```

```
C18_11d_WS1 C18_11d_WS2 C18_11d_WS3 C18_11d_WS4 C18_11d_WW1
      1.5776032      1.4525081      1.5639675      1.5265365      1.5687083
C18_11d_WW2 C18_11d_WW3 C18_11d_WW4 C18_34d_WS1 C18_34d_WS2
      1.5729410      1.3865447      1.9464369      1.7347063      1.2654132
C18_34d_WS3 C18_34d_WS4 C18_34d_WW1 C18_34d_WW2 C18_34d_WW3
      1.4874714      1.5978309      1.4698219      0.8040958      1.3141315
C18_34d_WW4 C18_67d_WS1 C18_67d_WS2 C18_67d_WS3 C18_67d_WS4
      1.8480061      2.4172910      2.2355638      2.1438253      1.6317226
C18_67d_WW1 C18_67d_WW2 C18_67d_WW3 C18_67d_WW4 F18_10d_WS1
      1.6332742      1.9178152      1.4992723      1.6246928      1.7805825
F18_10d_WS2 F18_10d_WS3 F18_10d_WS4 F18_10d_WW1 F18_10d_WW2
      1.8735295      1.9142822      1.7035168      2.0980960      2.1052765
```

```

F18_10d_WW3 F18_10d_WW4 F18_34d_WS1 F18_34d_WS2 F18_34d_WS3
  1.9447357   1.7887485   1.5892246   1.3699329   1.4469174
F18_34d_WS4 F18_34d_WW1 F18_34d_WW2 F18_34d_WW3 F18_34d_WW4
  1.4139991   1.5153857   1.4749029   1.9144891   1.6107161
F18_67d_WS1 F18_67d_WS2 F18_67d_WS3 F18_67d_WS4 F18_67d_WW1
  1.9483340   1.6580581   1.9058175   1.4784712   1.4242818
F18_67d_WW2 F18_67d_WW3 F18_67d_WW4 C19_22d_WS1 C19_22d_WS2
  1.3742853   1.4653761   1.4504864   2.8000000   2.6400000
C19_22d_WS3 C19_22d_WS4 C19_22d_WW1 C19_22d_WW2 C19_22d_WW3
  2.2900000   2.8100000   2.5900000   2.7900000   2.7500000
C19_22d_WW4 C19_44d_WS1 C19_44d_WS2 C19_44d_WS3 C19_44d_WS4
  2.5700000   2.9400000   3.3900000   3.3900000   3.3400000
C19_44d_WW1 C19_44d_WW2 C19_44d_WW3 C19_44d_WW4 F19_22d_WS1
  2.6900000   3.1600000   3.1200000   2.9300000   2.5900000
F19_22d_WS2 F19_22d_WS3 F19_22d_WS4 F19_22d_WW1 F19_22d_WW2
  2.9200000   2.8600000   2.3100000   2.4100000   2.1600000
F19_22d_WW3 F19_22d_WW4 F19_44d_WS1 F19_44d_WS2 F19_44d_WS3
  2.7200000   2.5600000   2.4800000   2.6400000   2.8200000
F19_44d_WS4 F19_44d_WW1 F19_44d_WW2 F19_44d_WW3 F19_44d_WW4
  2.5200000   2.6300000   2.5300000   2.6400000   2.6500000

> means <- tapply(y, pd[, c("date", "treat", "variety")], mean, na.rm=TRUE)
> means

, , variety = C

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

, , variety = F

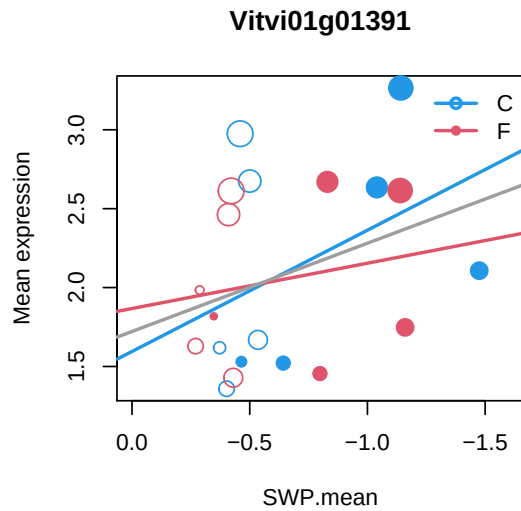
      treat
date      WW      WS
2018-06-11  1.984214 1.817978
2018-06-12    NA    NA
2018-07-05  1.628873 1.455019
2018-08-07  1.428607 1.747670
2019-06-26  2.462500 2.670000
2019-07-18  2.612500 2.615000

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

```

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

Error in eval(expr, envir, enclos): object 'wpa' not found



5 Linear models for water potential

```
> library(limma)
```

Warning: package 'limma' was built under R version 4.0.3

Attaching package: 'limma'

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

plotMA

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

We will use models on average expressions across replicates.

```
> varname <- testvar
> (y <- unlist(t1819[varname,]))

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

> means <- tapply(y,pd[,c("date", "treat", "variety")],mean,na.rm=TRUE)
> means

, , variety = C

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

, , variety = F
```



```

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

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

, , variety = C

```

```

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

, , variety = F

```

```

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

```

Small phenodata

```

> exp <- unlist(as.data.frame(means))
> swp <- unlist(as.data.frame(swps))
> treat <- factor(substr(names(swp), 1, 2), levels=levels(wpas$treat))
> variety <- factor(substr(names(swp), 4, 4))
> sday <- as.numeric(substr(names(swp), 5, 5))
> pd1 <- data.frame(swp, treat, variety, sday=sday, date=dimnames(swps)[[1]],
+   row.names=names(swp))
>
> str(pd1)
'data.frame':      24 obs. of  5 variables:
 $ swp      : num  -0.368 -0.372 -0.402 -0.535 -0.5 ...
 $ treat    : Factor w/ 2 levels "WW","WS": 1 1 1 1 1 1 2 2 2 2 ...
 $ variety  : Factor w/ 2 levels "C","F": 1 1 1 1 1 1 1 1 1 1 ...
 $ sday     : num   1 2 3 4 5 6 1 2 3 4 ...
 $ date     : chr   "2018-06-11" "2018-06-12" "2018-07-05" "2018-08-07" ...

```

5.1 Interpolated water potential data

```
> pd1
```

	swp	treat	variety	sday	date
WW.C1	-0.3680000	WW	C	1	2018-06-11
WW.C2	-0.3720000	WW	C	2	2018-06-12
WW.C3	-0.4016667	WW	C	3	2018-07-05
WW.C4	-0.5350000	WW	C	4	2018-08-07
WW.C5	-0.5000000	WW	C	5	2019-06-26
WW.C6	-0.4592308	WW	C	6	2019-07-18
WS.C1	-0.4527273	WS	C	1	2018-06-11
WS.C2	-0.4645455	WS	C	2	2018-06-12
WS.C3	-0.6425000	WS	C	3	2018-07-05
WS.C4	-1.4750000	WS	C	4	2018-08-07
WS.C5	-1.0400000	WS	C	5	2019-06-26
WS.C6	-1.1419231	WS	C	6	2019-07-18
WW.F1	-0.2872727	WW	F	1	2018-06-11
WW.F2	-0.2854545	WW	F	2	2018-06-12
WW.F3	-0.2700000	WW	F	3	2018-07-05
WW.F4	-0.4300000	WW	F	4	2018-08-07
WW.F5	-0.4100000	WW	F	5	2019-06-26
WW.F6	-0.4210000	WW	F	6	2019-07-18
WS.F1	-0.3472727	WS	F	1	2018-06-11
WS.F2	-0.3554545	WS	F	2	2018-06-12
WS.F3	-0.7983333	WS	F	3	2018-07-05
WS.F4	-1.1600000	WS	F	4	2018-08-07
WS.F5	-0.8300000	WS	F	5	2019-06-26
WS.F6	-1.1390000	WS	F	6	2019-07-18

```
> my.write.table(pd1,file=file.path(.oroot,"swp-interpolated.txt"),  
+   label="Interpolated swp data, considered as phenodata when swp is used"  
+   )
```

Object: pd1

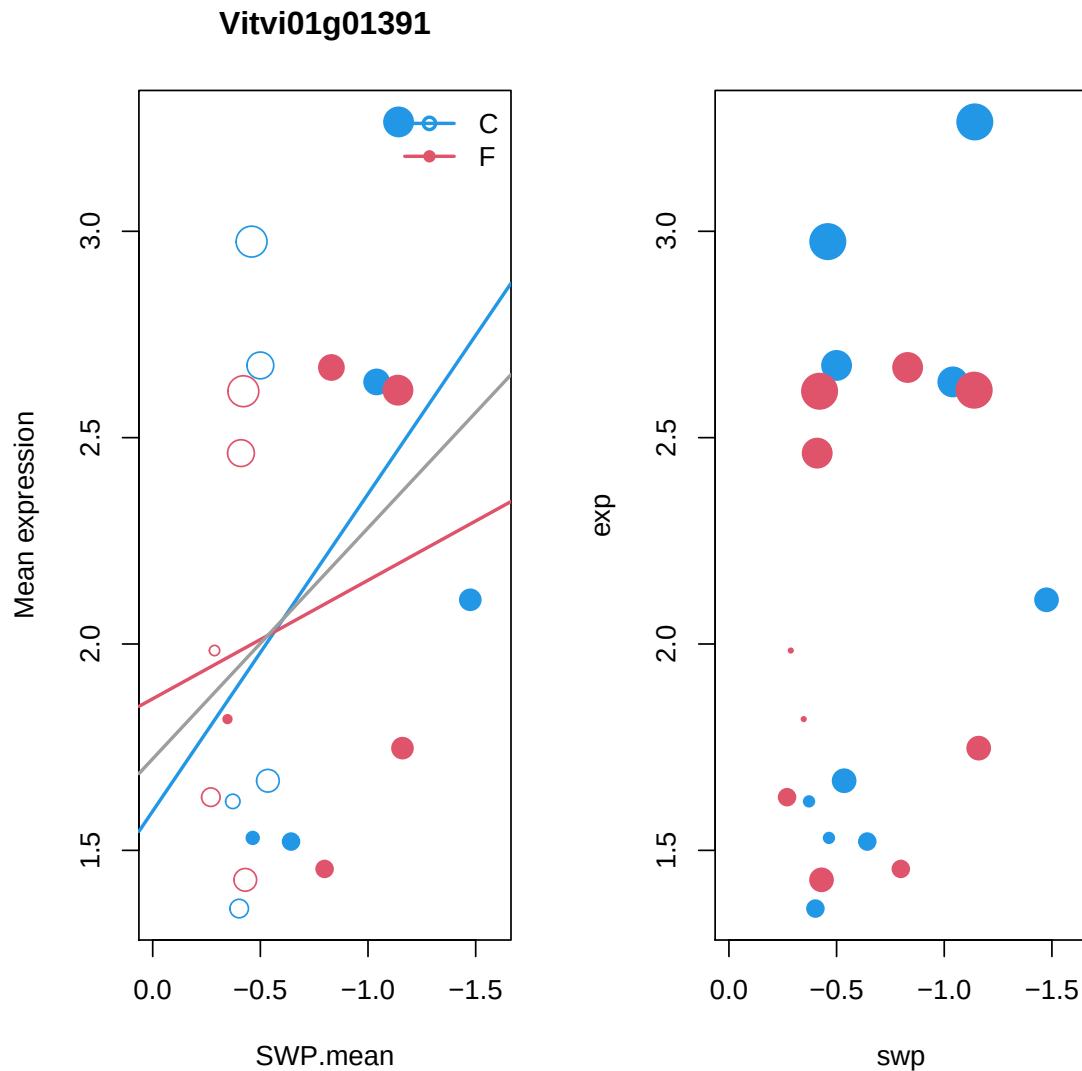
Label: Interpolated swp data, considered as phenodata when swp is used

File :

[../../output/50_Expression-water-stress-0.05-r/swp-interpolated.txt](#)

Graphical test, check the points positions

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



Aggregated expressions

```
> FUN <- function(x) unlist(as.data.frame(tapply(unlist(x),pd[,c("date","treat")],
> FUN(exprs[1,])
```

WW.C1	WW.C2	WW.C3	WW.C4	WW.C5	WW.C6	WS.C1
NA	4.453375	5.153464	3.727798	5.092500	5.905000	NA
WS.C2	WS.C3	WS.C4	WS.C5	WS.C6	WW.F1	WW.F2
4.309168	4.498764	2.461840	3.370000	5.330000	5.102229	NA
WW.F3	WW.F4	WW.F5	WW.F6	WS.F1	WS.F2	WS.F3
4.417362	3.974617	4.987500	5.922500	4.913018	NA	4.420979
WS.F4	WS.F5	WS.F6				
2.617199	3.512500	5.365000				

```
> expr <- t(apply(exprs,1, FUN=FUN))
> dim(expr)
```

```

[1] 15242    24
> str(expr)
num [1:15242, 1:24] NA NA NA NA NA NA NA NA NA NA ...
- attr(*, "dimnames")=List of 2
..$ : chr [1:15242] "Vitvi15g01736" "Vitvi07g02832" "Vitvi07g02830" "Vitvi07g02830" ...
..$ : chr [1:24] "WW.C1" "WW.C2" "WW.C3" "WW.C4" ...

> filter <- apply(expr,2,function(x) !all(is.na(x)))
> expr <- expr[,filter]
> pd1 <- pd1[filter,]
> dim(expr)
[1] 15242    20
> dim(pd1)
[1] 20    5
> str(expr)
num [1:15242, 1:20] 4.453 -2.47 -1.522 -0.894 2.059 ...
- attr(*, "dimnames")=List of 2
..$ : chr [1:15242] "Vitvi15g01736" "Vitvi07g02832" "Vitvi07g02830" "Vitvi07g02830" ...
..$ : chr [1:20] "WW.C2" "WW.C3" "WW.C4" "WW.C5" ...

> str(pd1)
'data.frame':    20 obs. of  5 variables:
 $ swp      : num  -0.372 -0.402 -0.535 -0.5 -0.459 ...
 $ treat    : Factor w/ 2 levels "WW","WS": 1 1 1 1 1 2 2 2 2 2 ...
 $ variety  : Factor w/ 2 levels "C","F": 1 1 1 1 1 1 1 1 1 1 ...
 $ sday     : num   2 3 4 5 6 2 3 4 5 6 ...
 $ date     : chr   "2018-06-12" "2018-07-05" "2018-08-07" "2019-06-26" ...

```

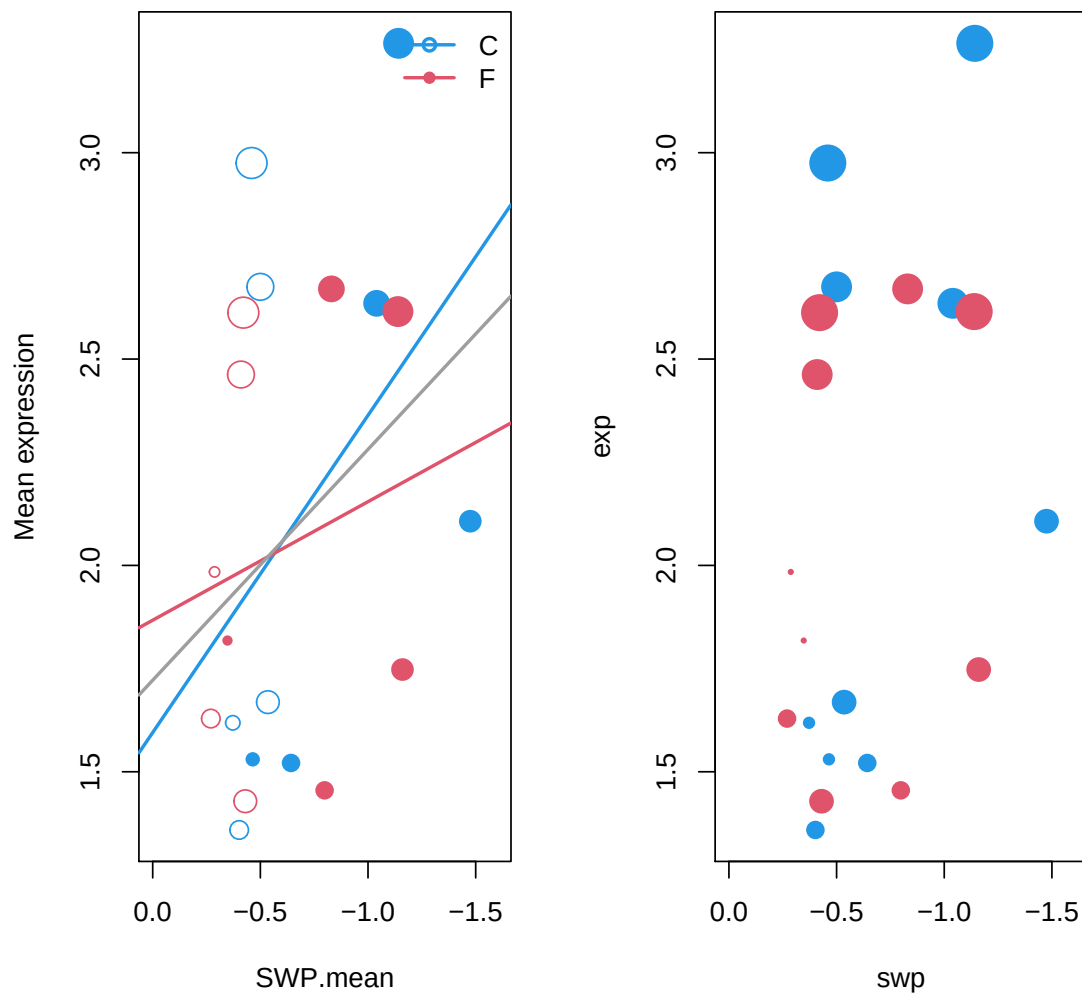
Check regressions

```

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

```

Vitvi01g01391



```
> lapply(fits[2:4], function(x) x$coefficients)
$C
(Intercept)          xx
  1.5950412   -0.7685916

$F
(Intercept)          xx
  1.8672599   -0.2871816

$all
(Intercept)          allx
  1.7217725   -0.5593981

> fitc <- lm(expr[varname,]~pd1$swp*pd1$variety)$coefficients
> fitc[c(1,2)]
(Intercept)    pd1$swp
  1.5950412   -0.7685916

> fitf <- c(fitc[1]+fitc[3],fitc[2]+fitc[4])
> fitf
(Intercept)    pd1$swp
  1.8672599   -0.2871816
```

```

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

(Intercept)      pd1$swp
    1.7217725   -0.5593981

```

Looks ok.

```

> all(colnames(expr)==rownames(pd1))
[1] TRUE

```

Replace expressions and phenodata with the reduced ones.

```

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

> exprs <- expr
> pd <- pd1
> swp <- pd$swp
> all(colnames(exprs)==rownames(pd))
[1] TRUE

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

> testvar <- "Vitvi01g01391"

```

5.2 Overall Model

Simple model with water potential for all data:

```
> design1 <- with(pd, model.matrix(~ swp))
> #design1[,2] <- (-design1[,2])
> head(design1)
      (Intercept)      swp
1             1 -0.3720000
2             1 -0.4016667
3             1 -0.5350000
4             1 -0.5000000
5             1 -0.4592308
6             1 -0.4645455

> tail(design1)
      (Intercept)      swp
15             1 -0.4210000
16             1 -0.3472727
17             1 -0.7983333
18             1 -1.1600000
19             1 -0.8300000
20             1 -1.1390000
```

Linear model

```
> fit1 <- lmFit(exprs, design1)
> fit1[testvar,]$coefficients
      (Intercept)      swp
Vitvi01g01391    1.721772 -0.5593981

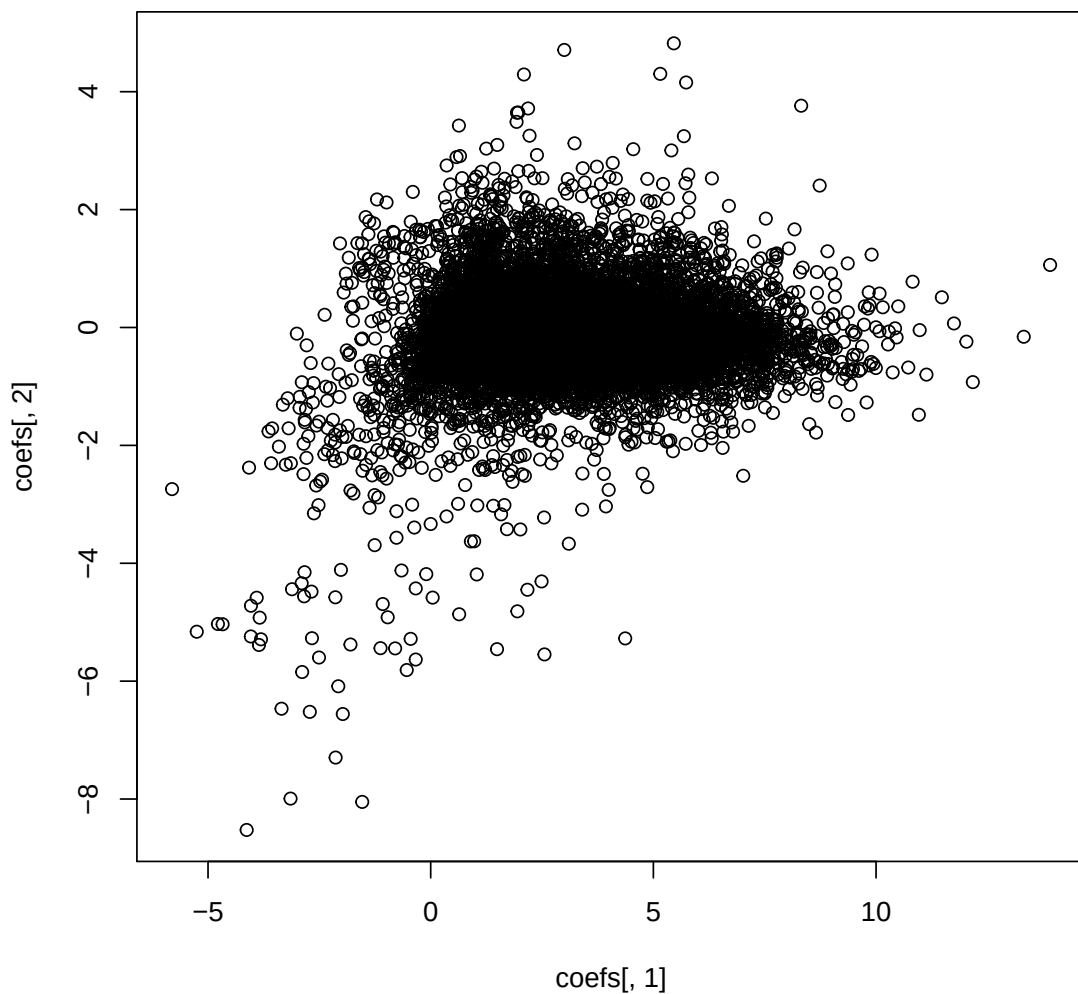
> fit1 <- eBayes(fit1)
> fit1[testvar,]$coefficients
      (Intercept)      swp
Vitvi01g01391    1.721772 -0.5593981

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

> fit <- fit1
> fit[testvar,]$coef
      (Intercept)      swp
Vitvi01g01391    1.721772 -0.5593981
```

Models for each variety

```
> coefs <- fit1$coefficients
> plot(coefs[,1], coefs[,2])
```



```
> dim(coefs[abs(coefs[, 2]) > 2, ])
[1] 252 2
```

Top table

```
> which <- 2
> tt <- topTable(fit1, coef=which, number=Inf)
> head(tt)
```

	logFC	AveExpr	t	P.Value
Vitvi16g01985	-5.241765	-0.5987979	-7.927163	7.223317e-08
Vitvi05g01740	-1.942843	2.4651929	-6.647068	1.145780e-06
Vitvi17g00152	-4.152022	-0.1074944	-6.643733	1.154385e-06
Vitvi05g00011	4.156807	3.0078249	6.335044	2.321195e-06
Vitvi17g01086	-1.698436	5.0044446	-6.317734	2.414762e-06
Vitvi07g01395	-1.403819	4.1341533	-6.181798	3.297561e-06

```

      adj.P.Val      B
Vitvi16g01985 0.001100978 7.653204
Vitvi05g01740 0.005865048 5.322334
Vitvi17g00152 0.005865048 5.315906
Vitvi05g00011 0.007278732 4.713350
Vitvi17g01086 0.007278732 4.679118
Vitvi07g01395 0.007278732 4.408716
```


5.3 Models for variety

Model with water potential by variety (slopes are of interest).

```
> design2 <- with(pd, model.matrix(~ swp*variety))
> head(design2)
```

	(Intercept)	swp	varietyF	swp:varietyF
1	1	-0.3720000	0	0
2	1	-0.4016667	0	0
3	1	-0.5350000	0	0
4	1	-0.5000000	0	0
5	1	-0.4592308	0	0
6	1	-0.4645455	0	0

```
> tail(design2)
```

	(Intercept)	swp	varietyF	swp:varietyF
15	1	-0.4210000	1	-0.4210000
16	1	-0.3472727	1	-0.3472727
17	1	-0.7983333	1	-0.7983333
18	1	-1.1600000	1	-1.1600000
19	1	-0.8300000	1	-0.8300000
20	1	-1.1390000	1	-1.1390000

Linear model

```
> fit2 <- lmFit(exprs, design2)
> fit2[testvar,]$coefficients
```

	(Intercept)	swp	varietyF	swp:varietyF
Vitvi01g01391	1.595041	-0.7685916	0.2722187	0.4814101

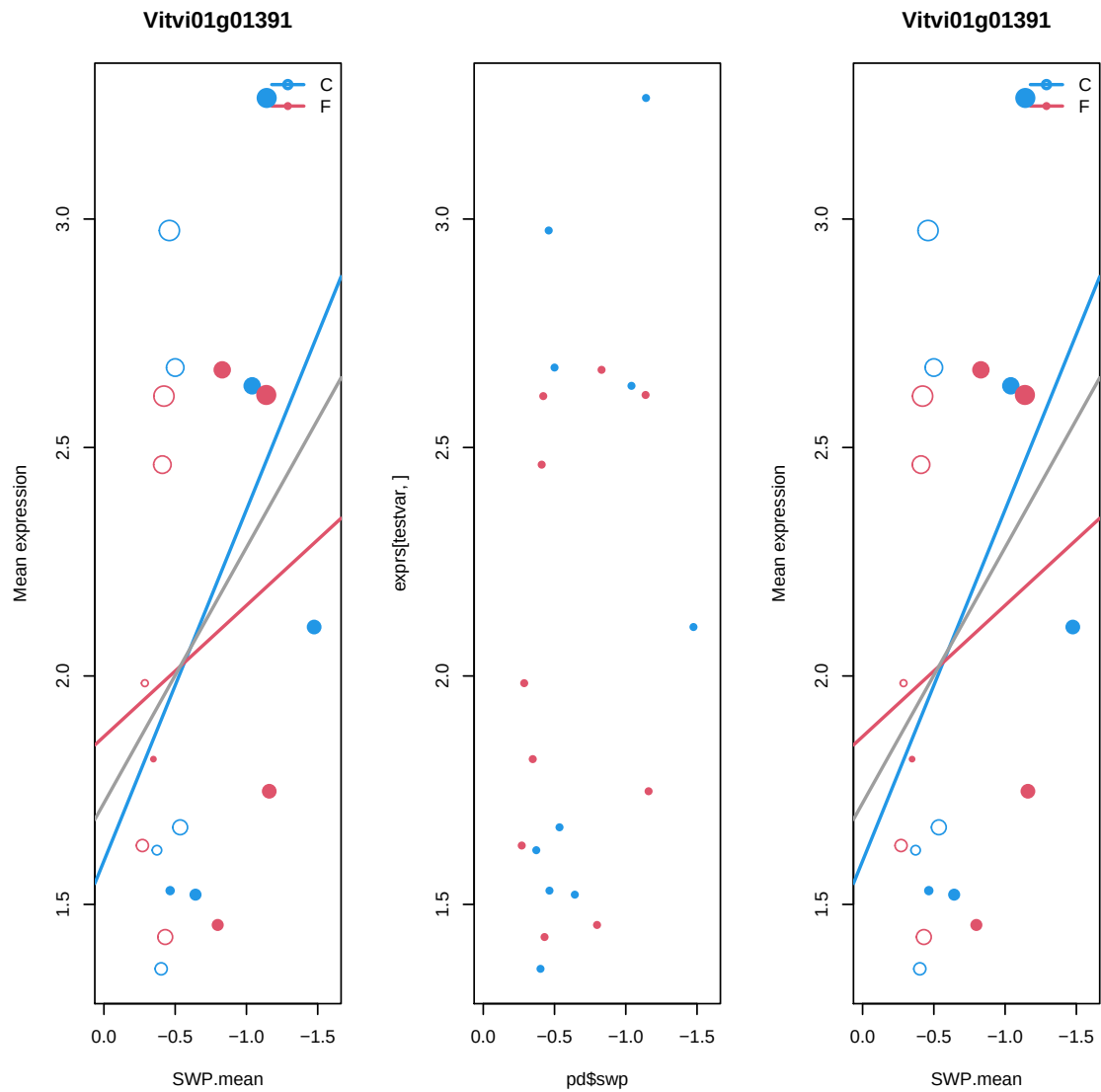
```
> varname <- testvar
> par(mfrow=c(1,3))
> p <- plot.ewp(varname,model="")
> plot(pd$swp,exprs[testvar,], xlim=c(0,-1.6),
+      ,pch=16, col=6-as.numeric(pd$variety)*2,cex=pd$day/2)
> c(p$C$coef[2],p$F$coef[2])
```

	xx	xx
	-0.7685916	-0.2871816

```
> fit2$coef[testvar,]
```

	(Intercept)	swp	varietyF	swp:varietyF
	1.5950412	-0.7685916	0.2722187	0.4814101

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



```
> #
> fit2 <- eBayes(fit2)
> fit2[testvar,]$coefficients
      (Intercept)          swp  varietyF  swp:varietyF
Vitvi01g01391    1.595041 -0.7685916  0.2722187    0.4814101
> head(fit2[1:6,]$coefficients)
      (Intercept)          swp  varietyF
Vitvi15g01736    5.550751  1.593545190 -0.2500355
Vitvi07g02832   -2.634115  0.508155686  5.4166972
Vitvi07g02830   -1.750650  1.548036562  4.3321685
Vitvi07g02812   -1.381363 -0.009794742  2.3030352
Vitvi07g02811    2.236177  0.566269561  1.2588734
Vitvi09g02033   -2.842837  0.419564483  4.1984533
      swp:varietyF
Vitvi15g01736   -0.31758915
Vitvi07g02832   -0.25109586
Vitvi07g02830   -0.90607176
Vitvi07g02812    0.40349136
Vitvi07g02811    0.02240192
Vitvi09g02033   -0.76028515
```

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

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

> fita[2]
      pd1$swp
-0.5593981

> fit1[testvar,]$coefficients[2]
[1] -0.5593981

> fitc[2]
      pd1$swp
-0.7685916

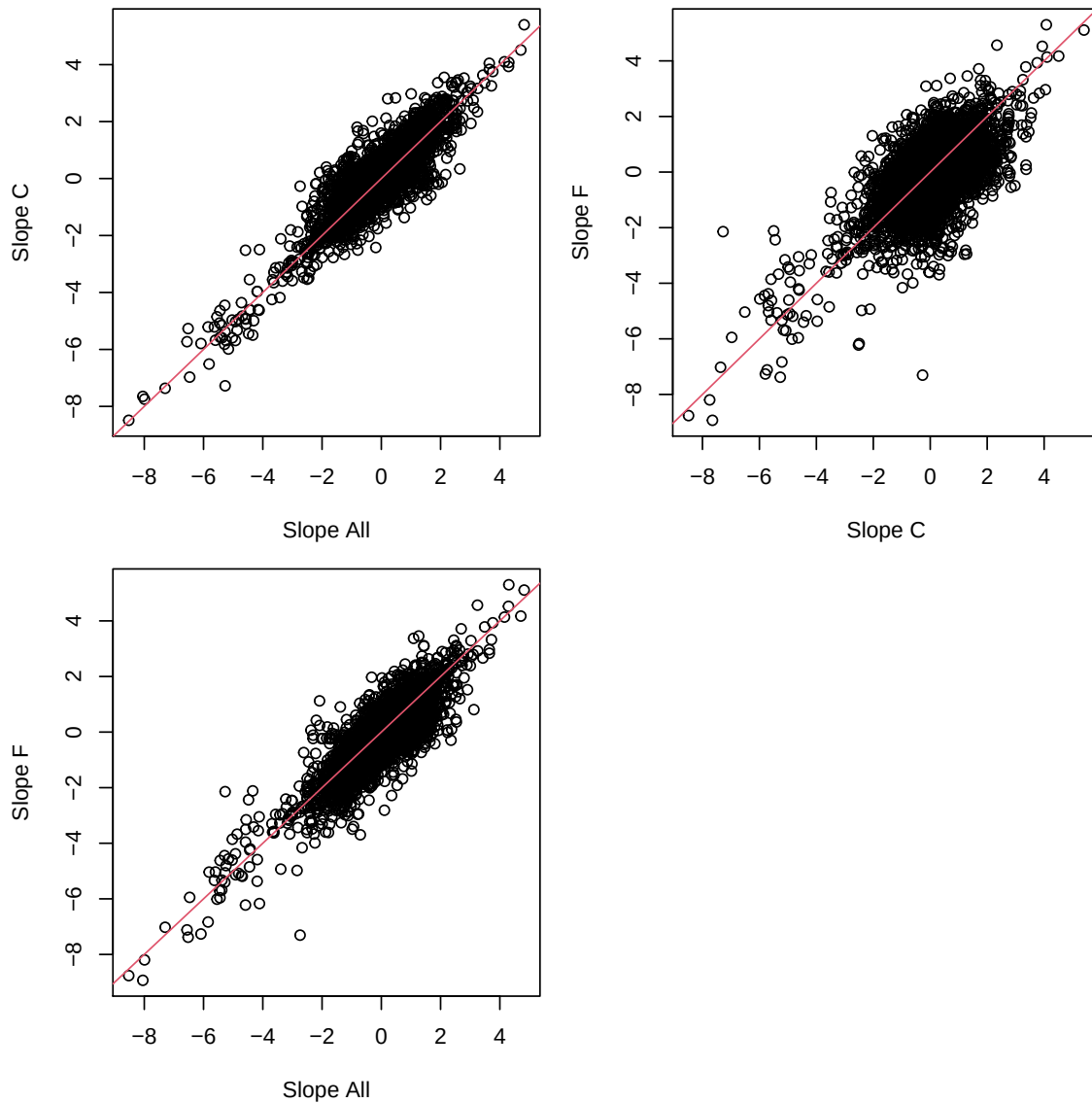
> fit2[testvar,]$coefficients[2]
[1] -0.7685916

> fitf[2]
      pd1$swp
-0.2871816

> fit2[testvar,]$coefficients[2]+fit2[testvar,]$coefficients[4]
[1] -0.2871816
```

Plots of coefficients

```
> oldpar <- par(mfrow=c(2,2), mar=c(4,4,1,1))
> coefs1 <- fit1$coefficients
> coefs2 <- fit2$coefficients
> plot(coefs1[,2], coefs2[,2], xlab="Slope All", ylab="Slope C")
> abline(c(0,1), col=2)
> cf24 <- coefs2[,2] + coefs2[,4]
> plot(coefs2[,2], cf24, xlab="Slope C", ylab="Slope F")
> abline(c(0,1), col=2)
> plot(coefs1[,2], cf24, xlab="Slope All", ylab="Slope F")
> abline(c(0,1), col=2)
> par(oldpar)
```



5.4 Mean expressions

```
> my.predict <- function(fit, x=1){
+   cf <- fit$coefficients
+   mc <- cf%%c(1,x,0,0)
+   mf <- cf%%c(1,x,1,x)
+   return(data.frame(mc=mc,mf=mf))
+ }
> fit2$coefficients[1:2,]
              (Intercept)          swp    varietyF  swp:varietyF
Vitvi15g01736    5.550751  1.5935452 -0.2500355   -0.3175892
Vitvi07g02832   -2.634115  0.5081557  5.4166972   -0.2510959

> my.predict(fit2)[1:2,]
              mc          mf
Vitvi15g01736  7.144296  6.576671
Vitvi07g02832 -2.125959  3.039642

> my.predict(fit2)[testvar,]
```

```

          mc      mf
Vitvi01g01391 0.8264496 1.580078

> ma <- fit1$coefficients%*%c(1,mean(swp))
> macf <- data.frame(ma=ma,my.predict(fit2, x=mean(swp)))
> head(macf)

```

```

          ma      mc      mf
Vitvi15g01736 4.4767407 4.505007 4.4633851
Vitvi07g02832 -0.1827419 -2.967585 2.6138903
Vitvi07g02830 -0.3244159 -2.766529 2.1602371
Vitvi07g02812 -0.3463388 -1.374935 0.6633139
Vitvi07g02811 2.4871819 1.864570 3.1087423
Vitvi09g02033 -0.7873280 -3.118171 1.5792098

```

```

> macf[testvar,]

```

```

          ma      mc      mf
Vitvi01g01391 2.08887 2.09942 2.055719

```

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

```

> design3 <- with(pd, model.matrix(~ 0+variety))
> head(design3)

```

```

  varietyC varietyF
1         1         0
2         1         0
3         1         0
4         1         0
5         1         0
6         1         0

```

```

> tail(design3)

```

```

  varietyC varietyF
15         0         1
16         0         1
17         0         1
18         0         1
19         0         1
20         0         1

```

```

> fit3 <- lmFit(exprs, design3)
> fit3[testvar,]$coefficients

```

```

          varietyC varietyF
Vitvi01g01391 2.135505 2.042236

```

```

> mswps <- with(pd, aggregate(swp, list(variety), mean) )$x
> my.predict(fit2, mswps[1])[testvar,1]

```

```

[1] 2.135505

```

```

> my.predict(fit2, mswps[2])[testvar,2]

```

```

[1] 2.042236

```

Object fit3 holds mean expressins for varieties.

5.4.1 Plots of variety coefficients

I will try to set the variety slopes compared to slope of complete data

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

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

Extract slopes

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

              A              C              F              ma
Vitvi15g01736 1.4417521  1.593545190  1.2759560  4.4767407
Vitvi07g02832 1.4868377  0.508155686  0.2570598 -0.1827419
Vitvi07g02830 2.1023461  1.548036562  0.6419648 -0.3244159
Vitvi07g02812 0.5715781 -0.009794742  0.3936966 -0.3463388
Vitvi07g02811 0.8198777  0.566269561  0.5886715  2.4871819
Vitvi09g02033 0.9949253  0.419564483 -0.3407207 -0.7873280

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

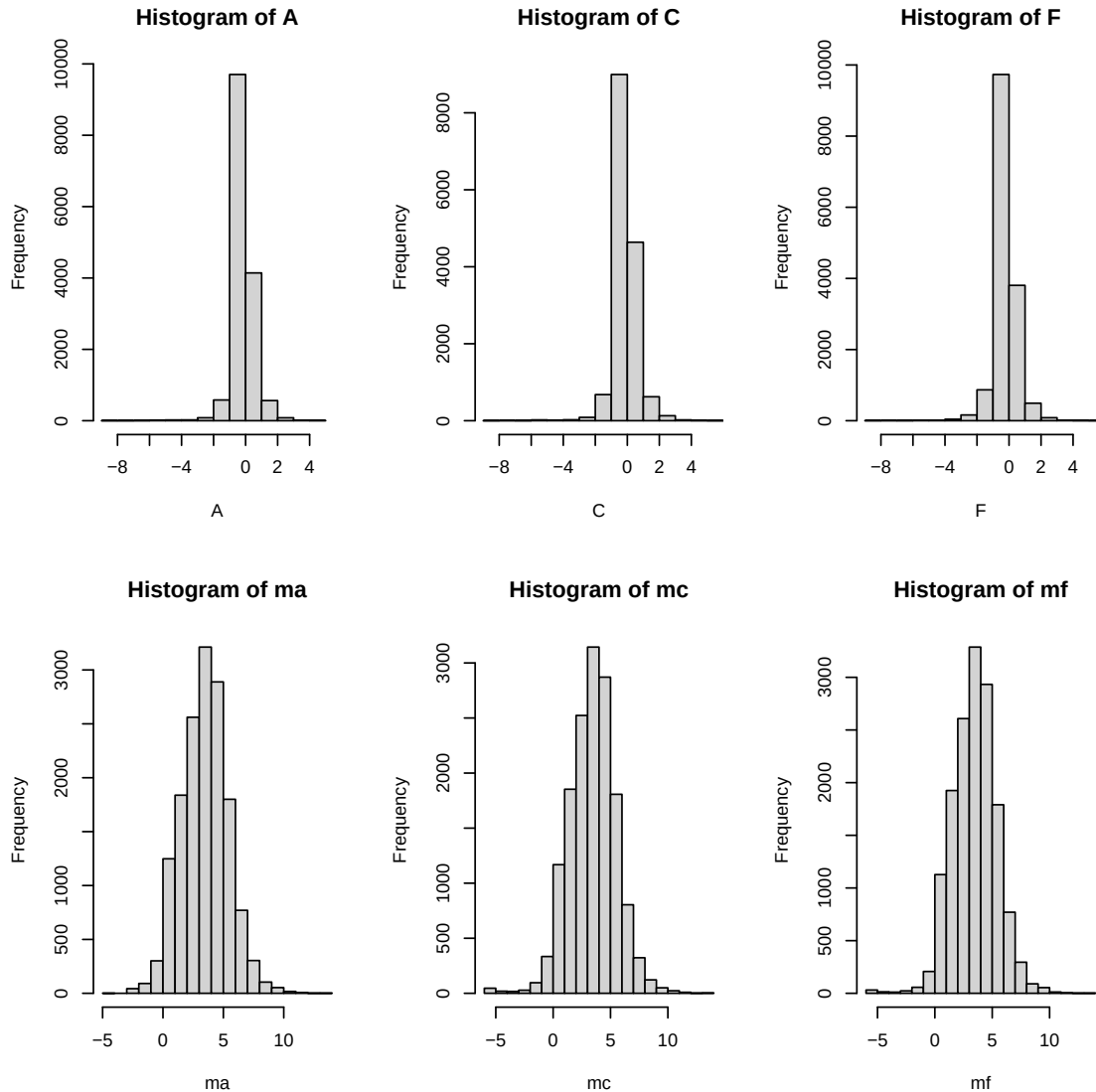
> ca <- C-A
> fa <- F-A
> fc <- F-C
> coefs <- data.frame(mc,mf,C,F)
> head(coefs)

              mc              mf              C              F
Vitvi15g01736  4.430191  4.5232904  1.593545190  1.2759560
Vitvi07g02832 -2.991443  2.6259591  0.508155686  0.2570598
Vitvi07g02830 -2.839209  2.1903769  1.548036562  0.6419648
Vitvi07g02812 -1.374475  0.6817977 -0.009794742  0.3936966
Vitvi07g02811  1.837984  3.1363800  0.566269561  0.5886715
Vitvi09g02033 -3.137869  1.5632132  0.419564483 -0.3407207
```

```

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

```



5.4.2 Types by effects

```

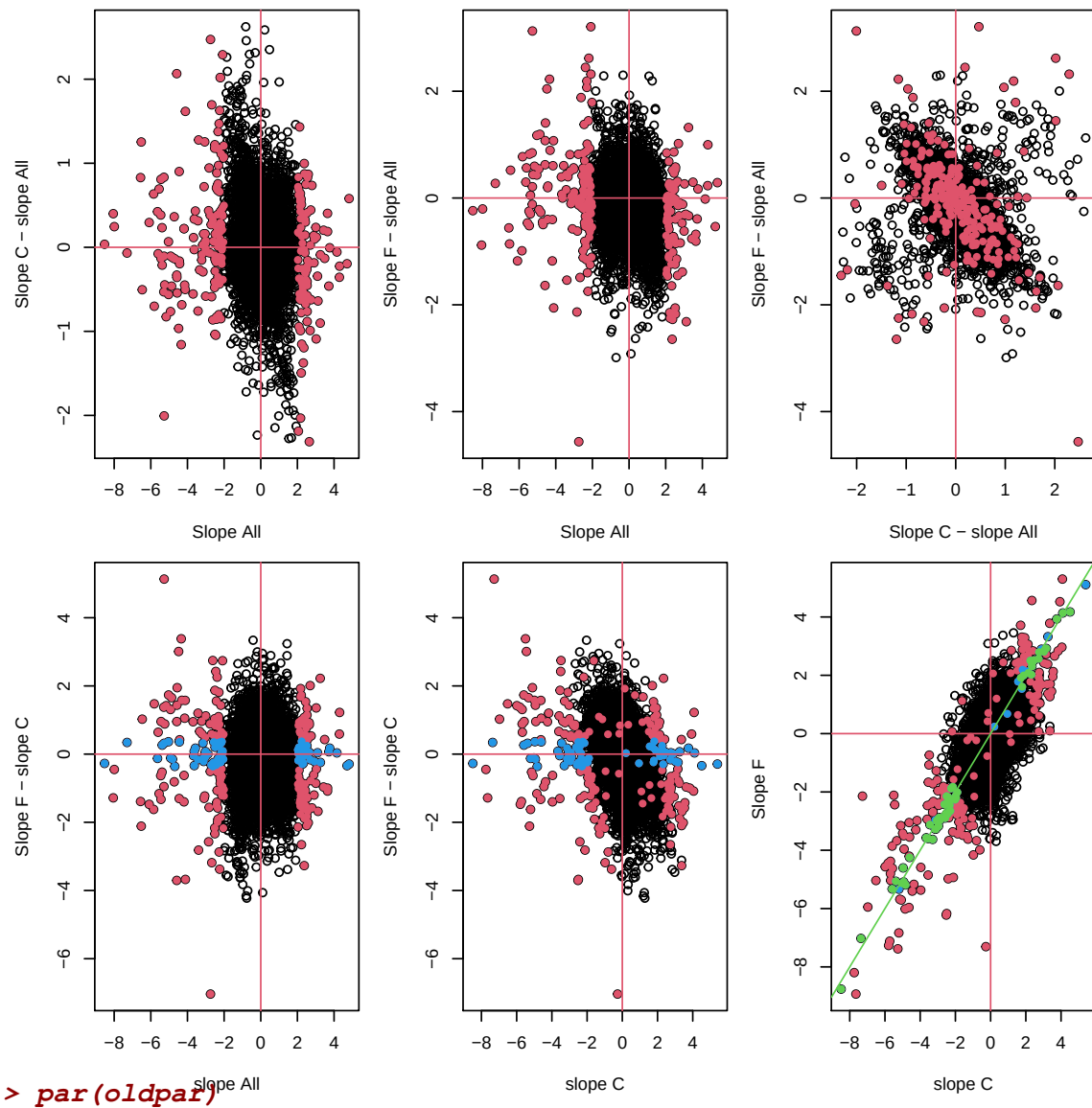
> delta <- 2
> large_abs_A <- abs(A) > delta
> small_fc <- abs(fc) < delta/5
> small_ca <- abs(ca) < delta/5
> oldpar <- par(mfrow=c(2,3), mar=c(4,4,1,1))
> plot(A,ca, xlab="Slope All",ylab="Slope C - slope All")
> points(A[large_abs_A],ca[large_abs_A],col=2,pch=16)
> abline(h=0,v=0,col=2)
> plot(A,fa, xlab="Slope All",ylab="Slope F - slope All")

```

```

> points(A[large_abs_A], fa[large_abs_A], col=2, pch=16)
> abline(h=0, v=0, col=2)
> plot(ca, fa, xlab="Slope C - slope All", ylab="Slope F - slope All")
> points(ca[large_abs_A], fa[large_abs_A], col=2, pch=16)
> abline(h=0, v=0, col=2)
> #
> plot(A, fc, xlab="slope All", ylab="Slope F - slope C")
> points(A[large_abs_A], fc[large_abs_A], col=2, pch=16)
> points(A[large_abs_A&small_fc], fc[large_abs_A&small_fc], col=4, pch=16)
> abline(h=0, v=0, col=2)
> #
> plot(C, fc, xlab="slope C", ylab="Slope F - slope C")
> points(C[large_abs_A], fc[large_abs_A], col=2, pch=16)
> points(C[large_abs_A&small_fc], fc[large_abs_A&small_fc], col=4, pch=16)
> abline(h=0, v=0, col=2)
> #
> plot(C, F, xlab="slope C", ylab="Slope F ")
> points(C[large_abs_A], F[large_abs_A], col=2, pch=16)
> points(C[large_abs_A&small_fc], F[large_abs_A&small_fc], col=4, pch=16)
> type1 <- large_abs_A&small_fc&small_ca
> points(
+   C[type1],
+   F[type1],
+   col=3, pch=16)
>
> abline(h=0, v=0, col=2)
> abline(c(0, 1), col=3)

```

6 Situation types and Type selection criteria

Boundaries:

min for at least ... (>)

max for at most ... (<)

delta difference at most ... (<)

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

```

> maxca <- maxfc # difference C - A smaller
> maxfa <- maxfc # difference F - A smaller
> #
> large_abs_A <- abs(A) > minA
> large_abs_C <- abs(C) > minC
> large_abs_F <- abs(F) > minF
> #
> small_fc <- abs(fc) < maxfc
> small_ca <- abs(ca) < maxca
> small_fa <- abs(fa) < maxfa
> plot(C,F, xlab="slope C",ylab="Slope F ")
> #points(C[large_abs_A],F[large_abs_A],col=2,pch=16)
> #
>
> type10 <- large_abs_A & small_fc & small_ca
> type1 <- (large_abs_C/large_abs_F) & small_fc & (abs(mc-mf)<deltam)
> table(type10,type1)

      type1
type10 FALSE TRUE
  FALSE 15149   13
   TRUE     8   72

> points(
+   C[type1],
+   F[type1],
+   col=2, pch=16)
> #
> type2 <- (large_abs_C & large_abs_F) & (abs(fc) > minfc) & (abs(mc-mf)>deltam)
> type2 <- type2 & ( (C*F >0) )
> points(
+   C[type2],
+   F[type2],
+   col=3,pch=16)
> #
> type30 <- ((abs(C)<maxC) | (abs(F)<maxF)) & (abs(fc)> minfc)
> type3 <- ((abs(C)<maxC) | (abs(F)<maxF)) & (abs(fc)> minfc) & (abs(mc-mf)>deltam)
> table(type3,type30)

      type30
type3  FALSE TRUE
  FALSE 14139 1009
   TRUE     0   94

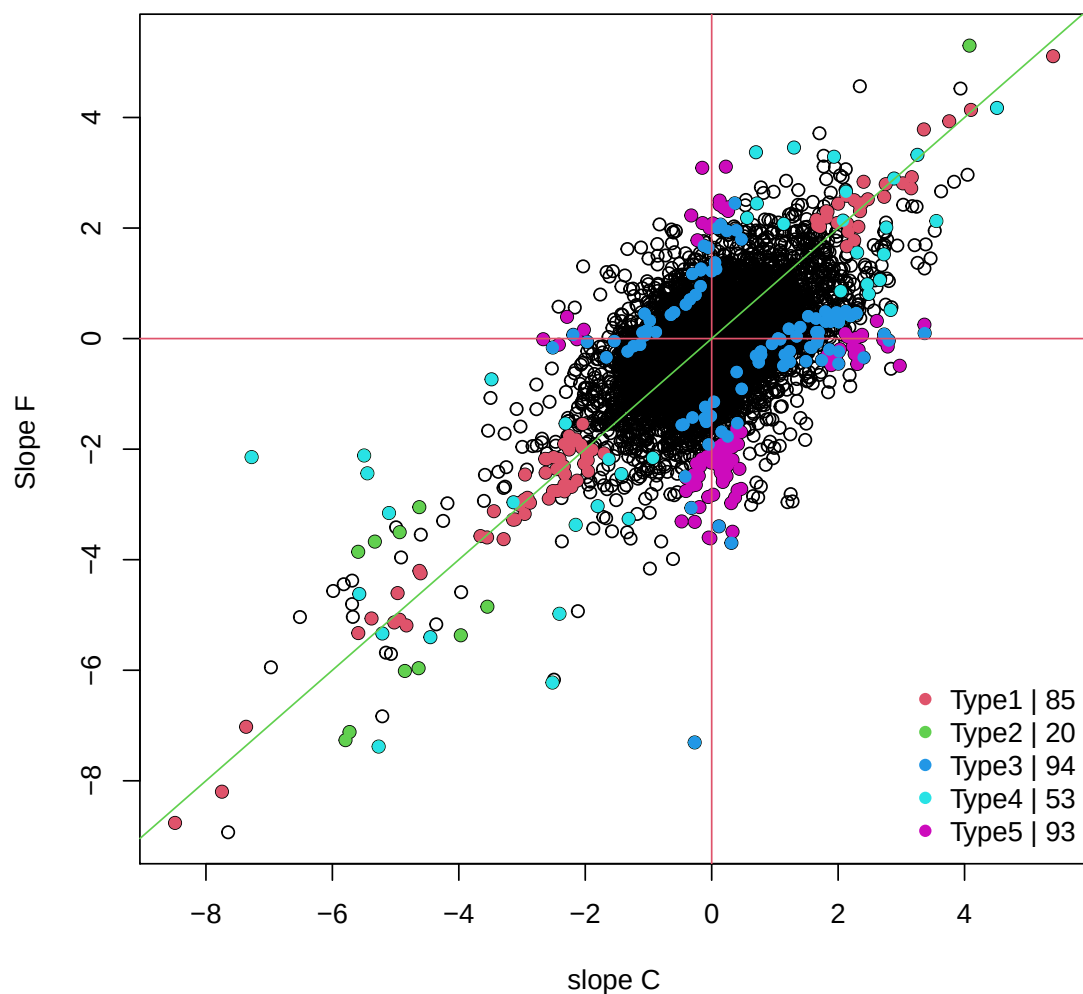
> points(
+   C[type3],
+   F[type3],
+   col=4,pch=16)
> #
> type4 <- (large_abs_C/large_abs_F) & (abs(mc-mf)>deltam) & (C*F>0)
> points(
+   C[type4],
+   F[type4],
+   col=5,pch=16)
> #
> type5 <- ((abs(C)<maxC) | (abs(F)<maxF)) & (abs(fc)> minfc*2) & (abs(mc-mf)<deltam)

```

```

> points(
+   C[type5],
+   F[type5],
+   col=6,pch=16)
>
> table(type3,type5)
      type5
type3 FALSE TRUE
FALSE 15055   93
TRUE    94    0
> points(
+   C[type3],
+   F[type3],
+   col=4,pch=16)
> # type 3 is a subset of type5, type3 & large mean difference
>
> #
> abline(h=0,v=0,col=2)
> abline(c(0,1),col=3)
> types <- data.frame(type1,type2,type3,type4,type5)
> nt <- apply(types,2,sum)
> legend("bottomright",pch=rep(16,5),col=2:6,legend=paste0("Type",1:5," | ",nt

```

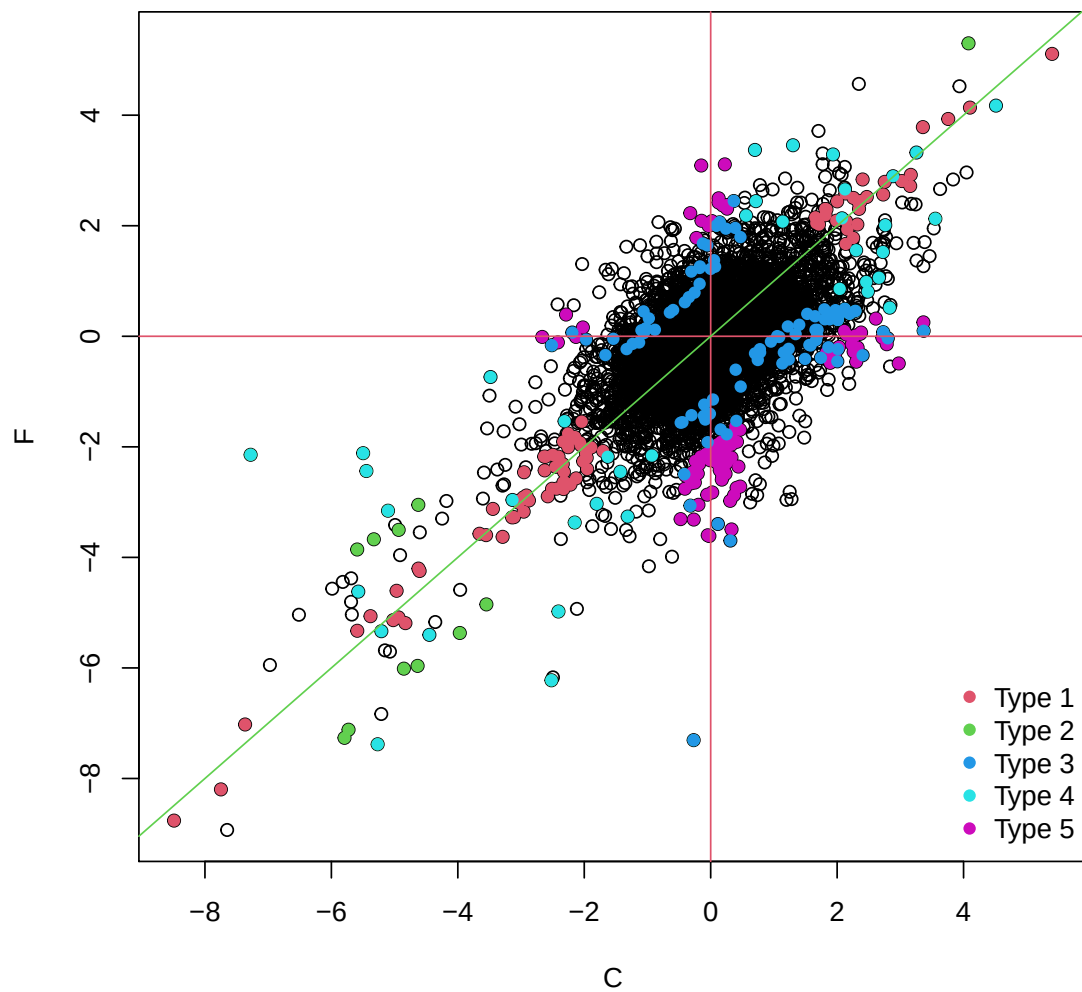


```

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

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

```



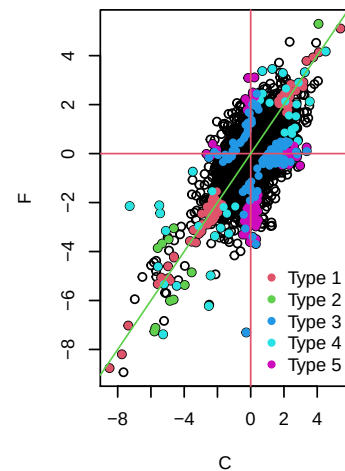
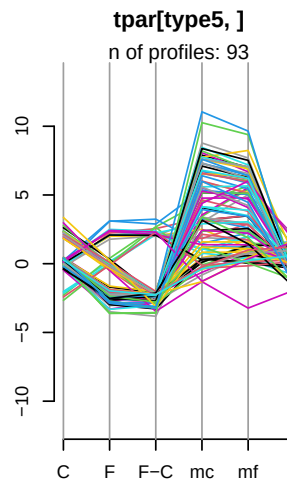
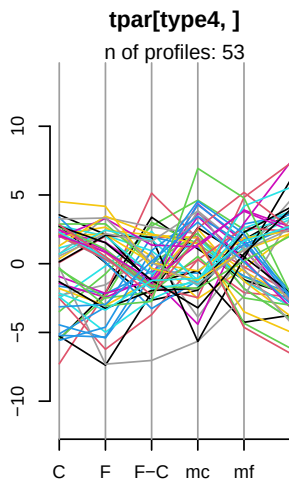
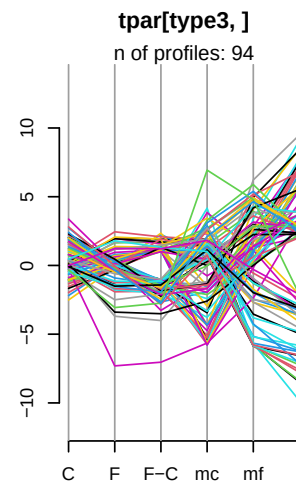
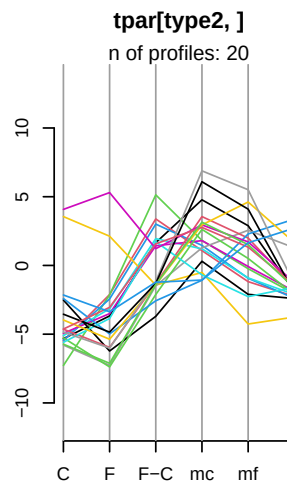
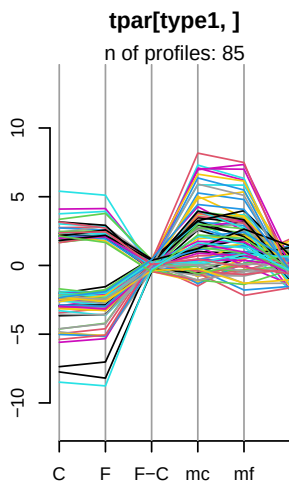
```
> x <- coefs[type1,]
> ylim <- range(x)
> my.paralleplot <- function(x, ylim = range(x), title, ...){
+ if(missing(title)) title <- deparse(substitute(x))
+ m <- ncol(x)
+ plot(0,0, type = "n"
+      , xlim = c(1,m)
+      , ylim = ylim
+      , axes = FALSE
+      , ann=FALSE
+      )
+ title(title)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

```

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

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

```



```

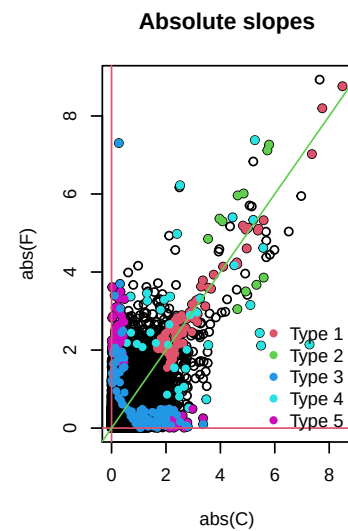
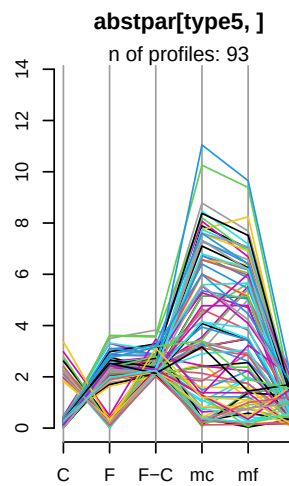
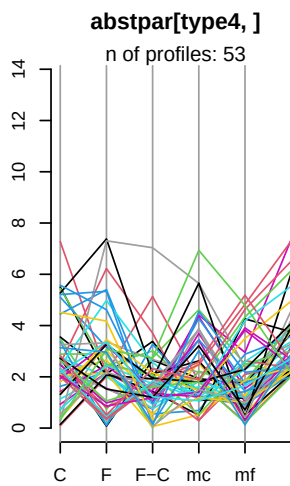
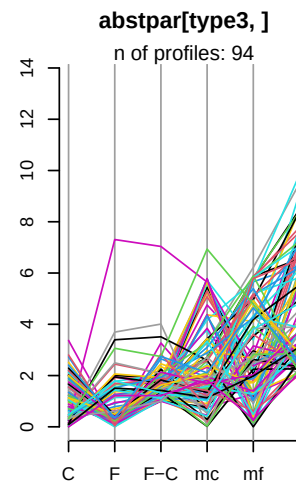
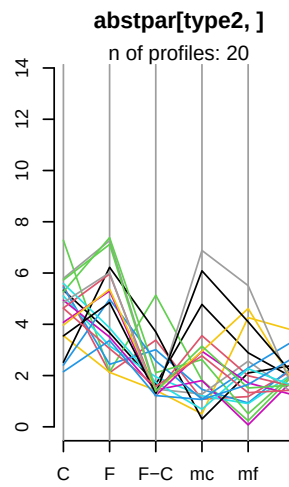
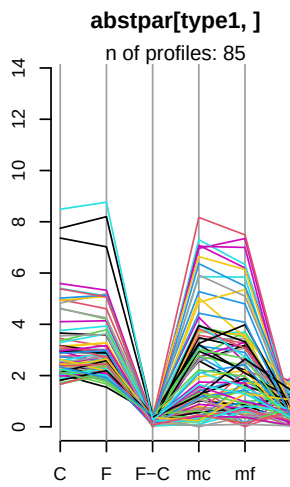
> par(mfrow=c(2,3))
> tpar <- data.frame(C,F,F-C,mc,mf,mf-mc)
> abstpar <- abs(tpar)
> ylim <- range(abstpar)
> my.parallelplot(abstpar[type1,], ylim=ylim)
> my.parallelplot(abstpar[type2,], ylim=ylim)

```

```

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

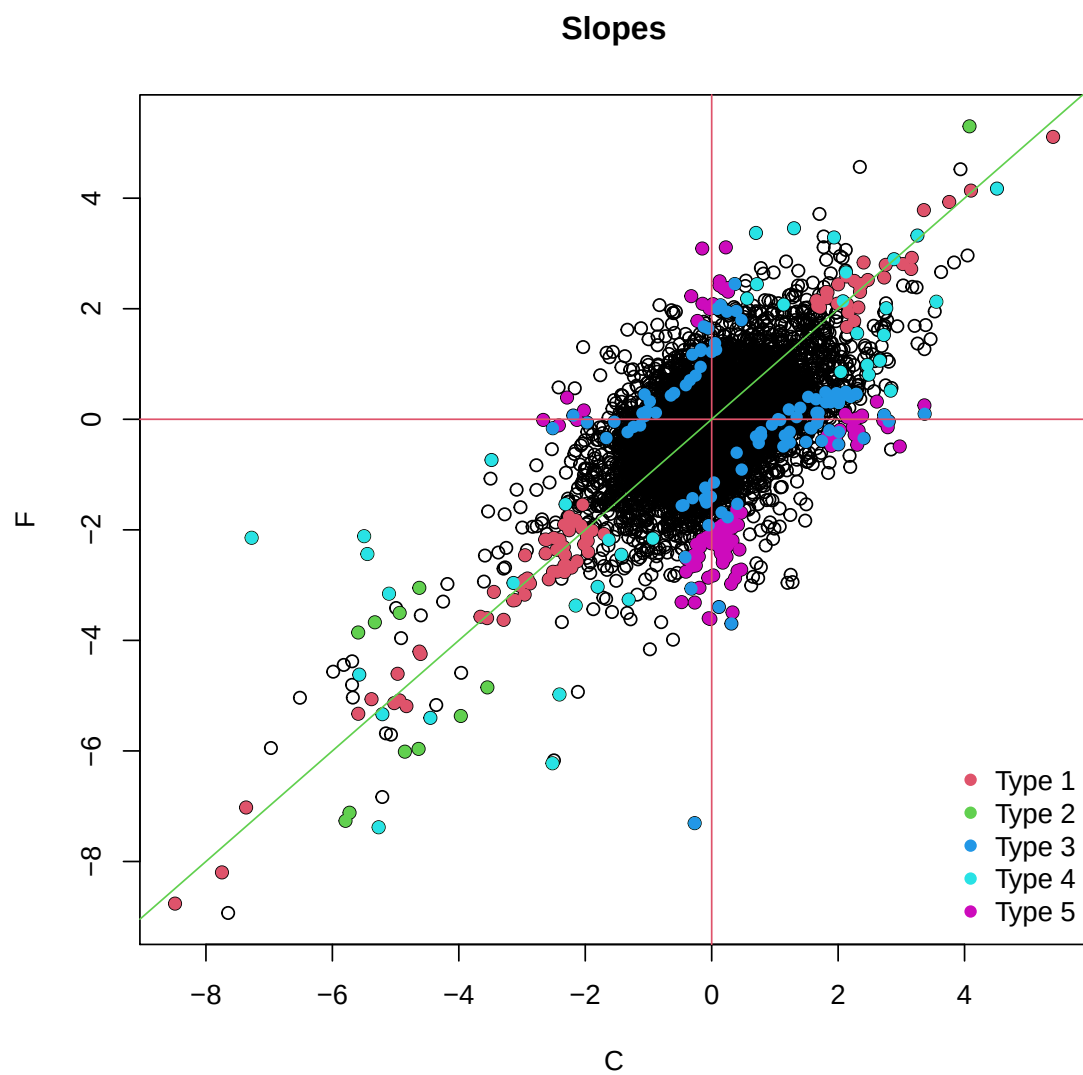
```



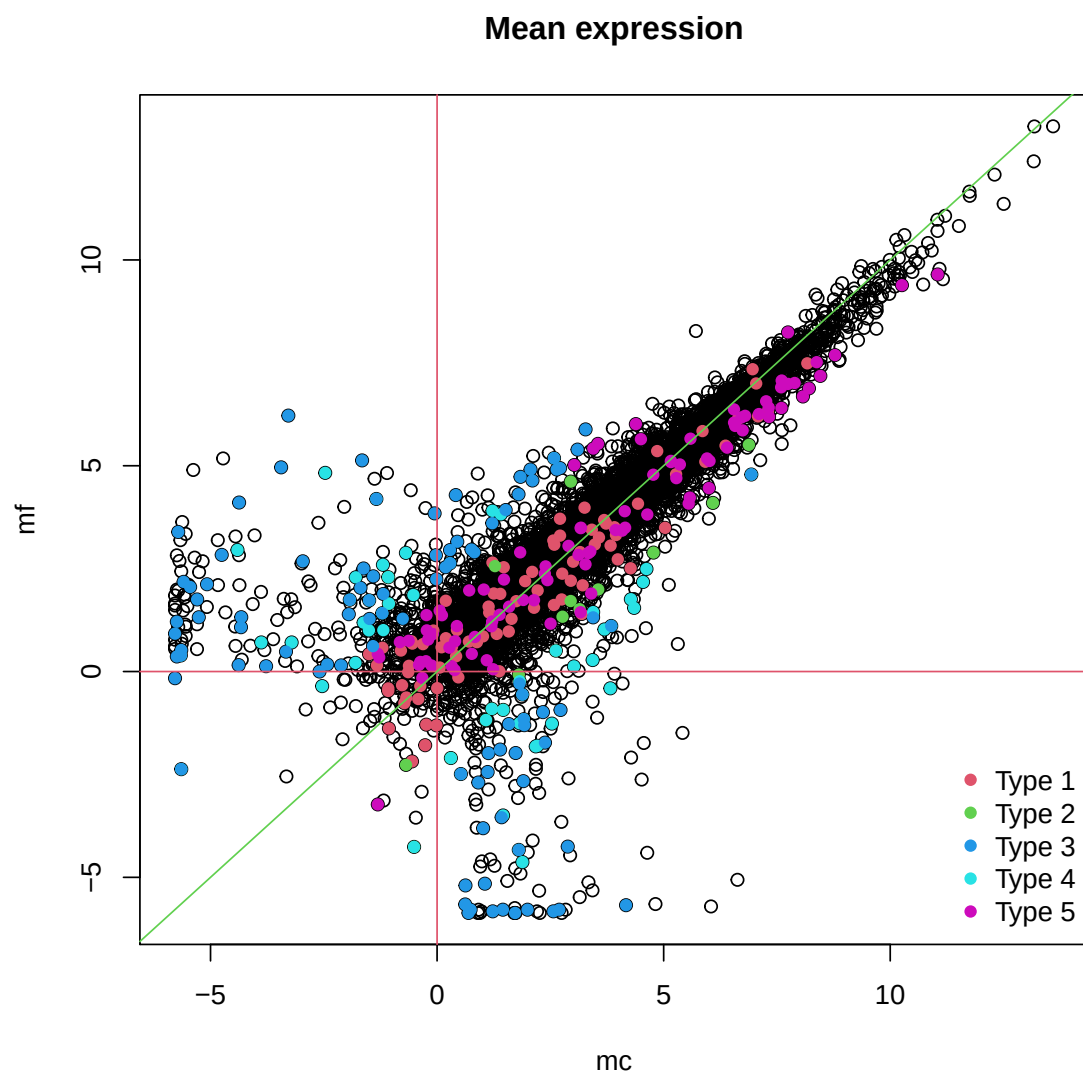
```

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

```

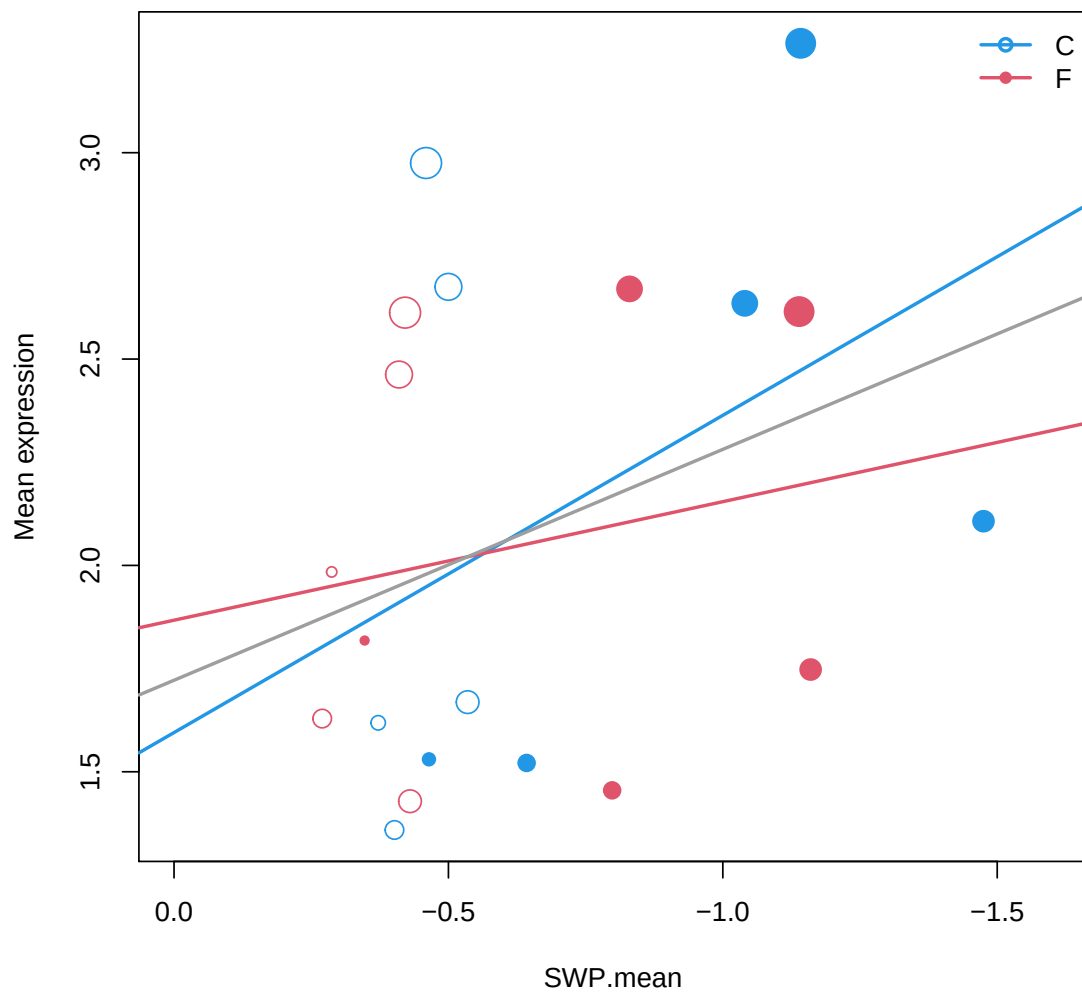


```
> plot.types(mc,mf,title="Mean expression")
```

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

Vitvi01g01391



```
> apply(data.frame(type1,type2,type3,type4, type5), 2, sum)
```

```
type1 type2 type3 type4 type5
   85    20    94    53    93
```

```
> par(mfrow=c(2,3))
```

```
> filt <- type1
```

```
> print(sum(filt))
```

```
[1] 85
```

```
> for(i in 1:min(sum(filt),6)){
```

```
+ varname <- rownames(exprs)[filt][i]
```

```
+ p <- plot.ewp(varname,model="", exprs=exprs, pd=pd, ylim=range(exprs)
```

```
+      , cex= 1.5
```

```
+      , pch = c(16,16)
```

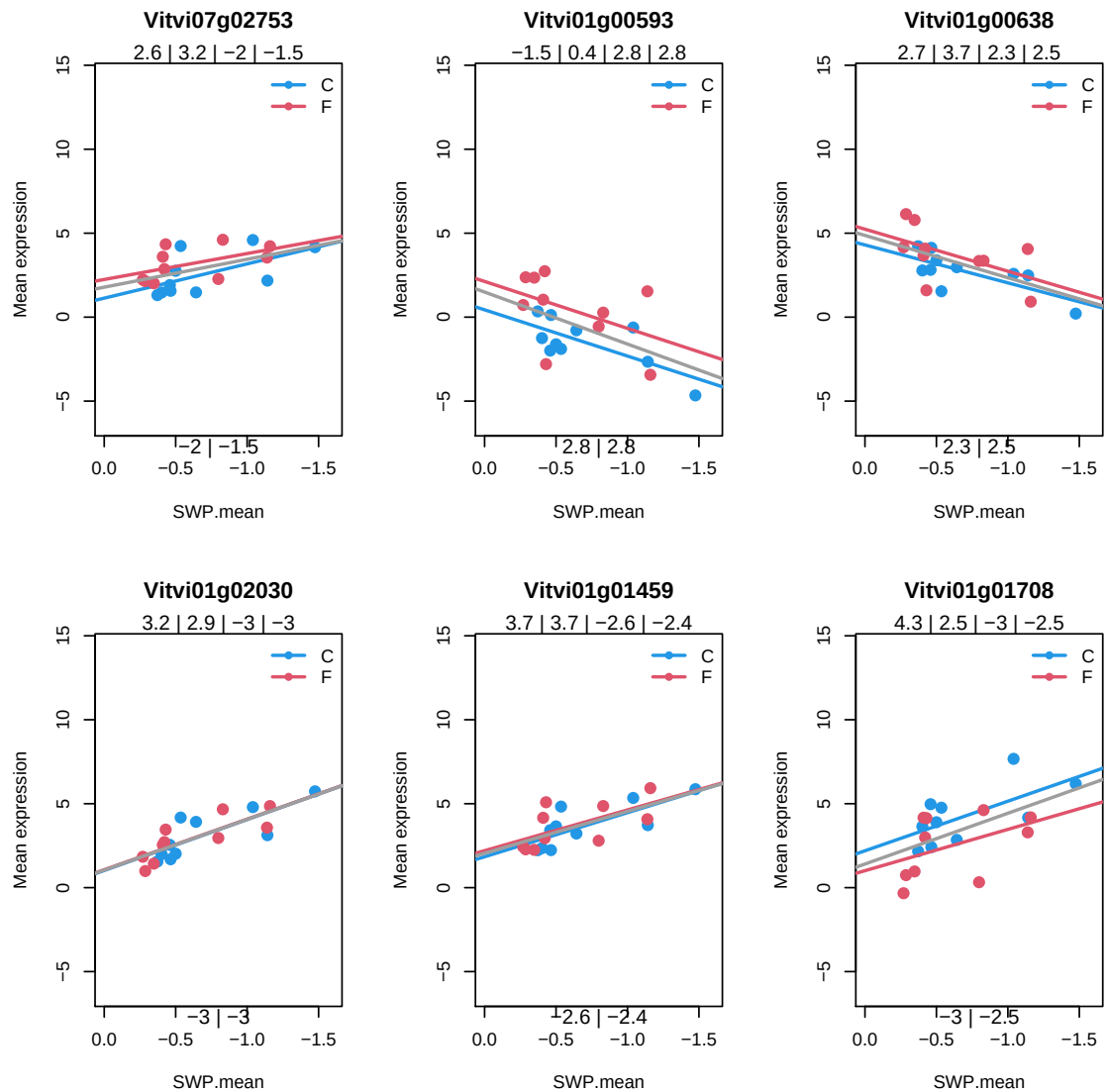
```
+      )
```

```
+ mtext(paste(round(coefs[varname,],1),collapse=" | "),cex=0.75)
```

```
+ mtext(paste(round(c(p$C$coefficients[2],p$F$coefficients[2]),1)
```

```
+ ,collapse=" | "),1,cex=0.75)
```

```
+ }
```



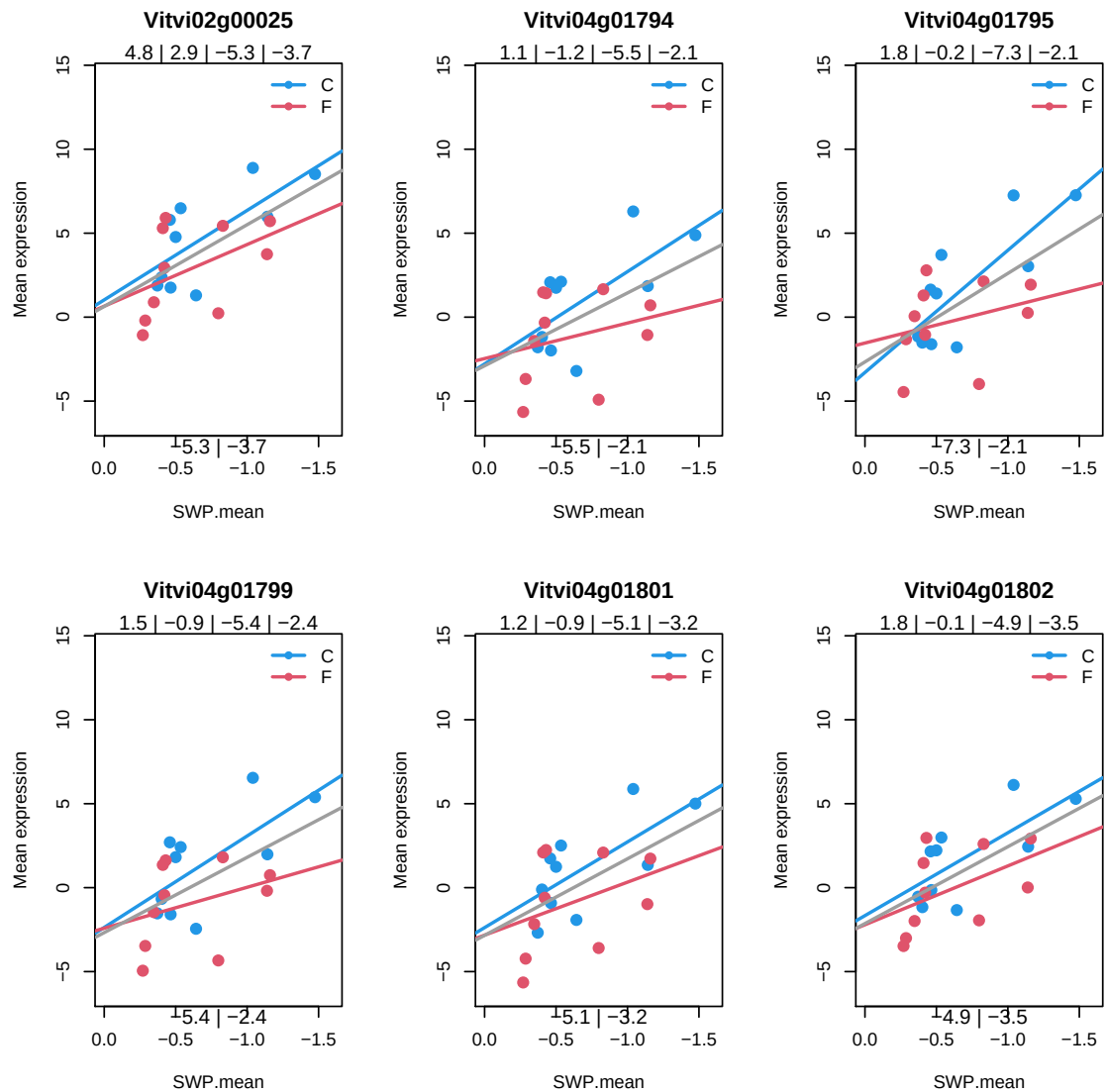
```

> par(mfrow=c(2,3))
> filt <- type2
> print(sum(filt))

[1] 20

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

```

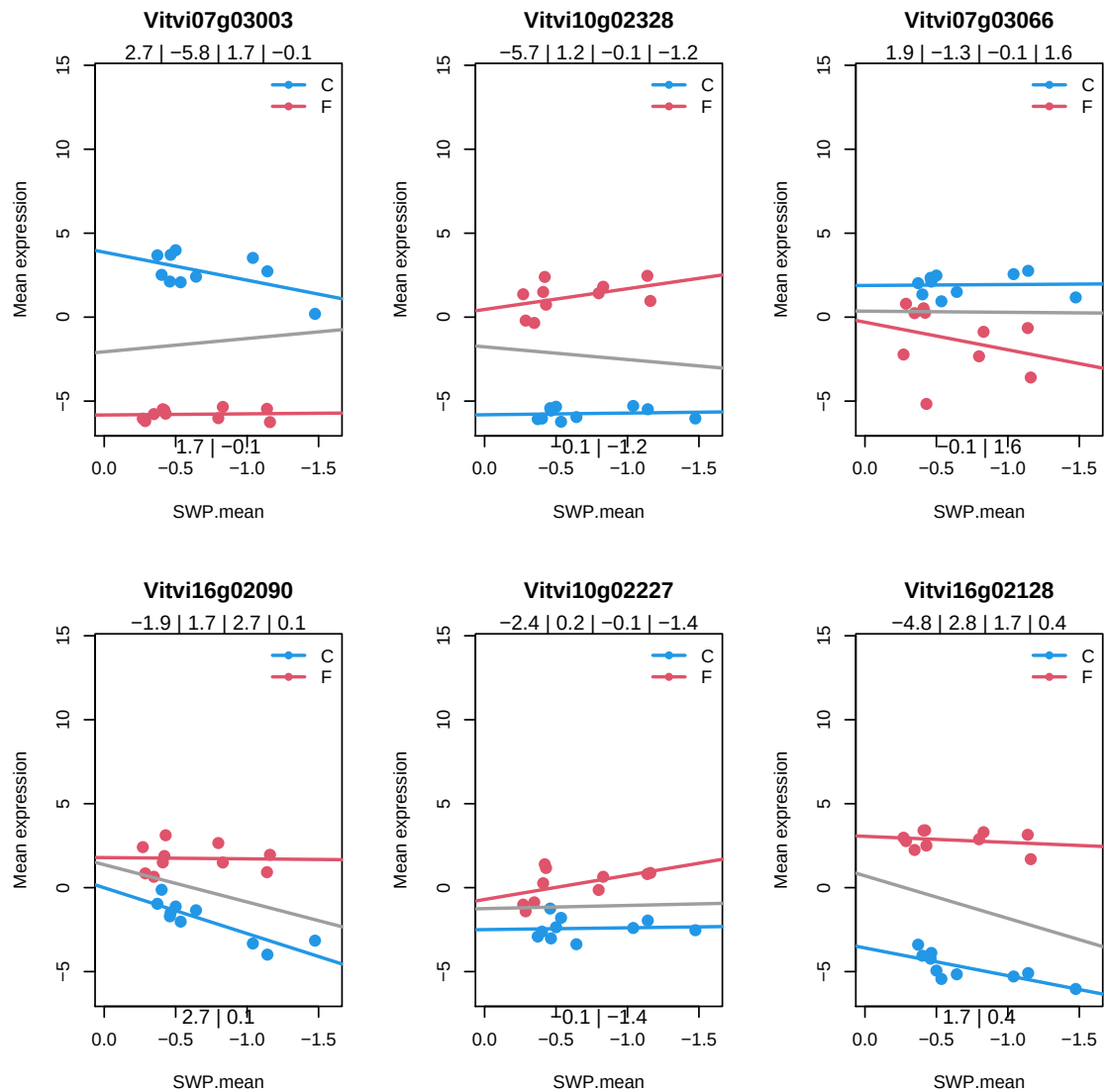


```

> par(mfrow=c(2,3))
> filt <- type3
> print(sum(filt))
[1] 94

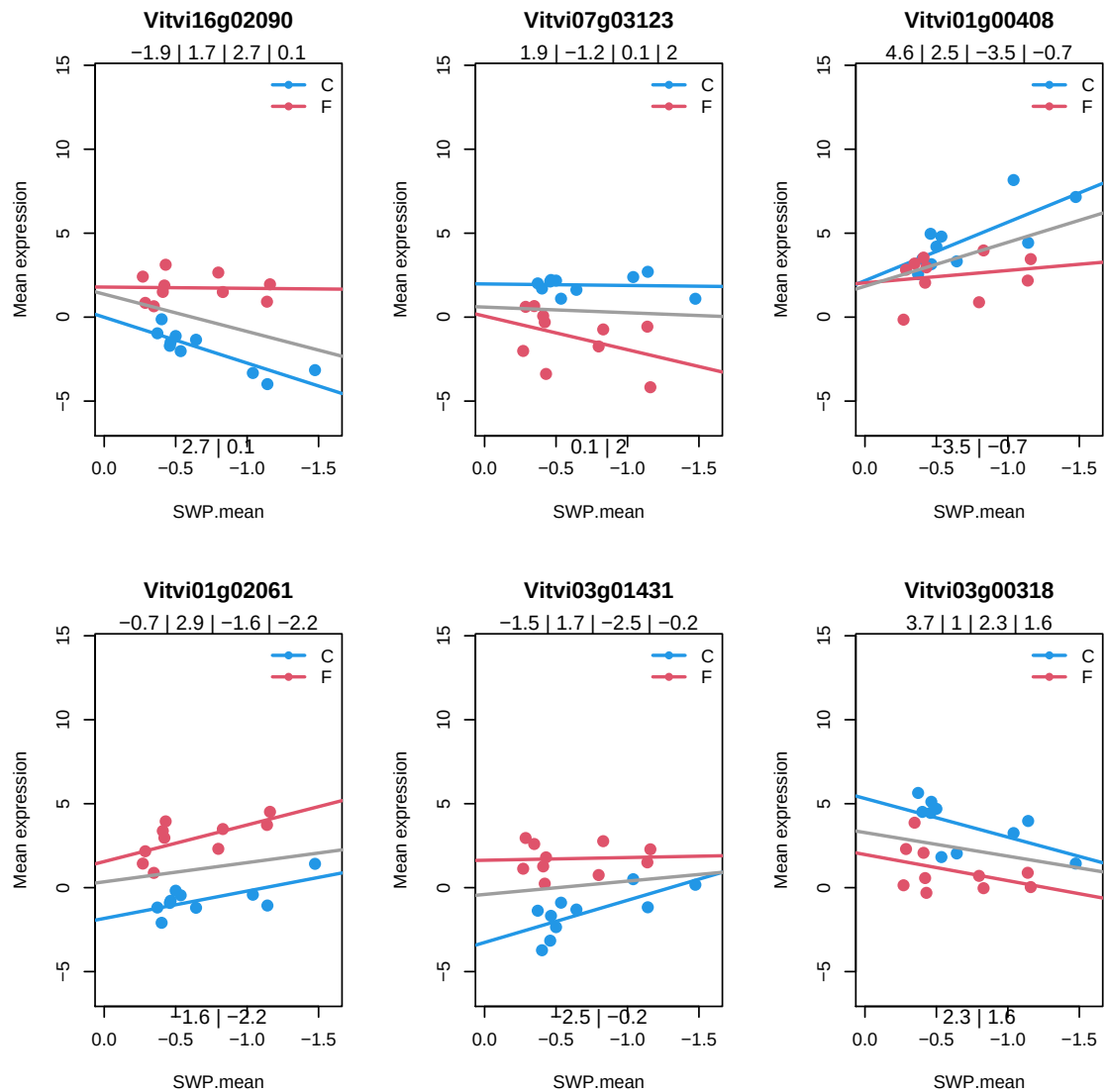
> for(i in 1:min(sum(filt),6)){
+   varname <- rownames(exprs)[filt][i]
+   p <- plot.ewp(varname,model="", exprs=exprs, pd=pd, ylim=range(exprs)
+     , cex= 1.5
+     , pch = c(16,16)
+     )
+   mtext(paste(round(coefs[varname,],1),collapse=" | "),cex=0.75)
+   mtext(paste(round(c(p$C$coefficients[2],p$F$coefficients[2]),1)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

```



```
> par(mfrow=c(2,3))
> filt <- type4
> print(sum(filt))
[1] 53

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

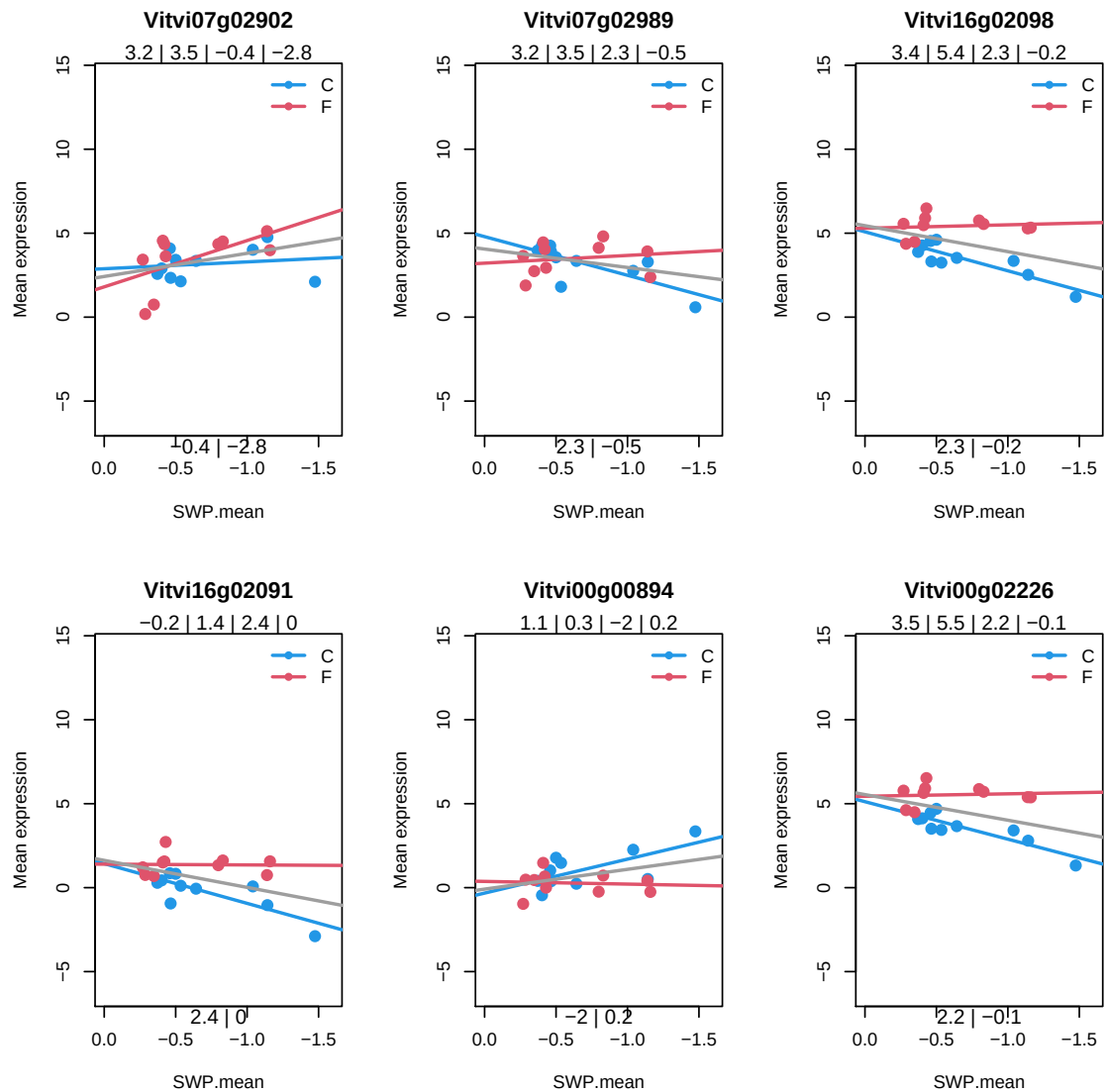


```

> par(mfrow=c(2,3))
> filt <- type5
> print(sum(filt))
[1] 93

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

```



```
> which <- 2
> tt <- topTable(fit,coef=which, number=Inf)
> head(tt)
```

	logFC	AveExpr	t	P.Value
Vitvi16g01985	-5.241765	-0.5987979	-7.927163	7.223317e-08
Vitvi05g01740	-1.942843	2.4651929	-6.647068	1.145780e-06
Vitvi17g00152	-4.152022	-0.1074944	-6.643733	1.154385e-06
Vitvi05g00011	4.156807	3.0078249	6.335044	2.321195e-06
Vitvi17g01086	-1.698436	5.0044446	-6.317734	2.414762e-06
Vitvi07g01395	-1.403819	4.1341533	-6.181798	3.297561e-06
	adj.P.Val	B		
Vitvi16g01985	0.001100978	7.653204		
Vitvi05g01740	0.005865048	5.322334		
Vitvi17g00152	0.005865048	5.315906		
Vitvi05g00011	0.007278732	4.713350		
Vitvi17g01086	0.007278732	4.679118		
Vitvi07g01395	0.007278732	4.408716		

6.0.1 Export output files

Export fit in a form:

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

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

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

Export top table

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

Removing intercept from test coefficients

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

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

Warning in write.table(x, file = file, col.names = col.names, sep = sep, : appending column names to file Object: ttext

Label:

File :

[../../output/50_Expression-water-stress-0.05-r/TopTable.txt](#)

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


7 Types by significance of contrasts

Starting point is fit2

Model with water potential by variety.

```
> design2 <- with(pd, model.matrix(~ swp*variety))
> head(design2)
```

	(Intercept)	swp	varietyF	swp:varietyF
1	1	-0.3720000	0	0
2	1	-0.4016667	0	0
3	1	-0.5350000	0	0
4	1	-0.5000000	0	0
5	1	-0.4592308	0	0
6	1	-0.4645455	0	0

```
> tail(design2)
```

	(Intercept)	swp	varietyF	swp:varietyF
15	1	-0.4210000	1	-0.4210000
16	1	-0.3472727	1	-0.3472727
17	1	-0.7983333	1	-0.7983333
18	1	-1.1600000	1	-1.1600000
19	1	-0.8300000	1	-0.8300000
20	1	-1.1390000	1	-1.1390000

Linear model

```
> fit2 <- lmFit(exprs, design2)
> fit2[testvar,]$coefficients
```

	(Intercept)	swp	varietyF	swp:varietyF
Vitvi01g01391	1.595041	-0.7685916	0.2722187	0.4814101

```
> design3 <- with(pd, model.matrix(~ 0+variety))
> head(design3)
```

	varietyC	varietyF
1	1	0
2	1	0
3	1	0
4	1	0
5	1	0
6	1	0

```
> tail(design3)
```

	varietyC	varietyF
15	0	1
16	0	1
17	0	1
18	0	1
19	0	1
20	0	1

```
> fit3 <- lmFit(exprs, design3)
> fit3[testvar,]$coefficients
```

	varietyC	varietyF
Vitvi01g01391	2.135505	2.042236

Combine design2 and design3: Replace intercepts with means in coefficients and standard deviations

```
> fit4 <- fit2
> fit4$coefficients[,1] <- fit3$coefficients[,1]
> fit4$coefficients[,3] <- fit3$coefficients[,2]
> fit4$stdev.unscaled[,1] <- fit3$stdev.unscaled[,1]
> fit4$stdev.unscaled[,3] <- fit3$stdev.unscaled[,2]
> dimnames(fit4$coefficients)[[2]] <- c("mc", "c1", "mf", "f1.c1")
> fit4[testvar,]$coefficients
```

	mc	c1	mf	f1.c1
Vitvi01g01391	2.135505	-0.7685916	2.042236	0.4814101

```
> fit2[testvar,]$coefficients
```

	(Intercept)	swp	varietyF	swp:varietyF
Vitvi01g01391	1.595041	-0.7685916	0.2722187	0.4814101

```
> fit3[testvar,]$coefficients
```

	varietyC	varietyF
Vitvi01g01391	2.135505	2.042236

```
> fit4<- eBayes(fit4)
> head(fit4)
```

An object of class "MArrayLM"

```
$coefficients
```

	mc	c1	mf	f1.c1
Vitvi15g01736	4.430191	1.593545190	4.5232904	-0.31758915
Vitvi07g02832	-2.991443	0.508155686	2.6259591	-0.25109586
Vitvi07g02830	-2.839209	1.548036562	2.1903769	-0.90607176
Vitvi07g02812	-1.374475	-0.009794742	0.6817977	0.40349136
Vitvi07g02811	1.837984	0.566269561	3.1363800	0.02240192
Vitvi09g02033	-3.137869	0.419564483	1.5632132	-0.76028515

```
$rank
[1] 4

$assign
[1] 0 1 2 3

$qqr
$qqr
```

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

```
15 more rows ...

$qqraux
[1] 1.223607 1.130819 1.182562 1.066939

$pivot
[1] 1 2 3 4
```

```

$tol
[1] 1e-07

$rank
[1] 4

$df.residual
[1] 16 16 16 16 16 16

$sigma
Vitvi15g01736 Vitvi07g02832 Vitvi07g02830 Vitvi07g02812
      0.8941832      0.7681327      0.5921856      0.8558602
Vitvi07g02811 Vitvi09g02033
      0.5294628      0.4728364

$cov.coefficients
              (Intercept)          swp  varietyF swp:varietyF
(Intercept)    0.4827337  0.5442848 -0.4827337   -0.5442848
swp             0.5442848  0.7740261 -0.5442848   -0.7740261
varietyF       -0.4827337 -0.5442848  0.9319295    1.1174059
swp:varietyF   -0.5442848 -0.7740261  1.1174059    1.7146670

$stdev.unscaled
              (Intercept)          swp  varietyF swp:varietyF
Vitvi15g01736    0.3162278  0.8797875  0.3162278    1.309453
Vitvi07g02832    0.3162278  0.8797875  0.3162278    1.309453
Vitvi07g02830    0.3162278  0.8797875  0.3162278    1.309453
Vitvi07g02812    0.3162278  0.8797875  0.3162278    1.309453
Vitvi07g02811    0.3162278  0.8797875  0.3162278    1.309453
Vitvi09g02033    0.3162278  0.8797875  0.3162278    1.309453

$pivot
[1] 1 2 3 4

$Amean
Vitvi15g01736 Vitvi07g02832 Vitvi07g02830 Vitvi07g02812
      4.4767407      -0.1827419      -0.3244159      -0.3463388
Vitvi07g02811 Vitvi09g02033
      2.4871819      -0.7873280

$method
[1] "ls"

$design
      (Intercept)          swp  varietyF swp:varietyF
1             1 -0.3720000          0          0
2             1 -0.4016667          0          0
3             1 -0.5350000          0          0
4             1 -0.5000000          0          0
5             1 -0.4592308          0          0
15 more rows ...

```

```

$df.prior
[1] 5.442291

$s2.prior
[1] 0.240232

$var.prior
[1] 66.60227703 10.07260620 66.60227703 0.04162642

$proportion
[1] 0.01

$s2.post
Vitvi15g01736 Vitvi07g02832 Vitvi07g02830 Vitvi07g02812
      0.6575990      0.5012458      0.3226499      0.6075545
Vitvi07g02811 Vitvi09g02033
      0.2701533      0.2278022

$t
      mc      c1      mf      fl.c1
Vitvi15g01736 17.275947 2.2336032 17.638998 -0.29908538
Vitvi07g02832 -13.361504 0.8158186 11.729043 -0.27084716
Vitvi07g02830 -15.806350 3.0976880 12.194194 -1.21816734
Vitvi07g02812 -5.576277 -0.0142831 2.766068 0.39532267
Vitvi07g02811 11.182439 1.2383410 19.081984 0.03291472
Vitvi09g02033 -20.790067 0.9991759 10.357126 -1.21648751

$df.total
[1] 21.44229 21.44229 21.44229 21.44229 21.44229 21.44229

$p.value
      mc      c1      mf
Vitvi15g01736 4.582548e-14 0.036281328 3.017391e-14
Vitvi07g02832 7.201069e-12 0.423574363 8.525719e-11
Vitvi07g02830 2.699108e-13 0.005361432 4.109529e-11
Vitvi07g02812 1.447097e-05 0.988736185 1.143671e-02
Vitvi07g02811 2.066890e-10 0.228976529 6.157627e-15
Vitvi09g02033 1.072274e-15 0.328852510 8.363470e-10
      fl.c1
Vitvi15g01736 0.7677545
Vitvi07g02832 0.7890987
Vitvi07g02830 0.2363952
Vitvi07g02812 0.6965102
Vitvi07g02811 0.9740471
Vitvi09g02033 0.2370210

$lods
      (Intercept)      swp  varietyF  swp:varietyF
Vitvi15g01736    22.24850 -3.752633 22.674807    -4.606008
Vitvi07g02832    17.06898 -5.596946 14.528954    -4.606206
Vitvi07g02830    20.43614 -2.117771 15.279322    -4.589886
Vitvi07g02812     2.18499 -5.915023 -4.428434    -4.605189

```

```

Vitvi07g02811    13.61819 -5.197139 24.293108    -4.607100
Vitvi09g02033    26.06635 -5.441685 12.180326    -4.589930

$F
[1] 2254.10642 247.98545 418.69222 43.13726 1749.02568
[6] 607.83918

$F.p.value
[1] 8.457058e-28 1.282015e-17 5.163533e-20 5.858488e-10
[5] 1.273489e-26 9.935192e-22
> fit4[testvar,]
An object of class "MArrayLM"
$coefficients
              mc              cl              mf              fl.cl
Vitvi01g01391 2.135505 -0.7685916 2.042236 0.4814101

$rank
[1] 4

$assign
[1] 0 1 2 3

$qqr
$qr
      (Intercept)          swp    varietyF swp:varietyF
1  -4.4721360    2.93478215 -2.2360680    1.36240911
2   0.2236068   -1.54891442 -0.3031114   -0.50167273
3   0.2236068    0.04473752  2.2154285   -1.44373971
4   0.2236068    0.06733399  0.1816105    0.76367769
5   0.2236068    0.09365515  0.1805019    0.08777677
15 more rows ...

$sraux
[1] 1.223607 1.130819 1.182562 1.066939

$pivot
[1] 1 2 3 4

$tol
[1] 1e-07

$rank
[1] 4

$df.residual
[1] 16

$sigma
Vitvi01g01391
      0.5999568

$cov.coefficients

```

	(Intercept)	swp	varietyF	swp:varietyF
(Intercept)	0.4827337	0.5442848	-0.4827337	-0.5442848
swp	0.5442848	0.7740261	-0.5442848	-0.7740261
varietyF	-0.4827337	-0.5442848	0.9319295	1.1174059
swp:varietyF	-0.5442848	-0.7740261	1.1174059	1.7146670

\$stddev.unscaled

	(Intercept)	swp	varietyF	swp:varietyF
Vitvi01g01391	0.3162278	0.8797875	0.3162278	1.309453

\$pivot

[1] 1 2 3 4

\$Amean

Vitvi01g01391
2.08887

\$method

[1] "ls"

\$design

	(Intercept)	swp	varietyF	swp:varietyF
1	1 -0.3720000	0	0	0
2	1 -0.4016667	0	0	0
3	1 -0.5350000	0	0	0
4	1 -0.5000000	0	0	0
5	1 -0.4592308	0	0	0
15 more rows ...				

\$df.prior

[1] 5.442291

\$s2.prior

[1] 0.240232

\$var.prior

[1] 66.60227703 10.07260620 66.60227703 0.04162642

\$proportion

[1] 0.01

\$s2.post

Vitvi01g01391
0.3295629

\$t

	mc	c1	mf	f1.c1
Vitvi01g01391	11.76336	-1.521769	11.24959	0.6404071

\$df.total

[1] 21.44229

\$p.value

	mc	c1	mf	f1.c1
Vitvi01g01391	8.072923e-11	0.1426785	1.850714e-10	0.5286929

\$lods

	(Intercept)	swp	varietyF	swp:varietyF
Vitvi01g01391	14.58507	-4.850464	13.73182	-4.602121

\$F

[1] 1143.211

\$F.p.value

[1] 1.193144e-24

```
> tt <- topTable(fit4, 2, number=Inf)
> tt[testvar,]
```

	logFC	AveExpr	t	P.Value
Vitvi01g01391	-0.7685916	2.08887	-1.521769	0.1426785

	adj.P.Val	B
Vitvi01g01391	0.6681823	-4.850464

With difference of means

```
> fit4 <- fit2
> fit4$coefficients[,1] <- fit3$coefficients[,1]
> fit4$coefficients[,3] <- fit3$coefficients[,2]-fit3$coefficients[,1]
> fit4$stdev.unscaled[,1] <- fit3$stdev.unscaled[,1]
> fit4$stdev.unscaled[,3] <- apply(fit3$stdev.unscaled[,1:2], 1
+ , function(x) sqrt(sum(x^2)) )
> dimnames(fit4$coefficients)[[2]] <- c("mc", "c", "mf.mc", "f.c")
> fit4[testvar,]$coefficients
```

	mc	c	mf.mc	f.c
Vitvi01g01391	2.135505	-0.7685916	-0.09326836	0.4814101

```
> fit3[testvar,]$stdev.unscaled
```

	varietyC	varietyF
Vitvi01g01391	0.3162278	0.3162278

```
> fit4[testvar,]$stdev.unscaled
```

	(Intercept)	swp	varietyF	swp:varietyF
Vitvi01g01391	0.3162278	0.8797875	0.4472136	1.309453

```
> #
```

```
> fit2[testvar,]$coefficients
```

	(Intercept)	swp	varietyF	swp:varietyF
Vitvi01g01391	1.595041	-0.7685916	0.2722187	0.4814101

```
> fit3[testvar,]$coefficients
```

	varietyC	varietyF
Vitvi01g01391	2.135505	2.042236

```
> fit4<- eBayes(fit4)
```

```
> head(fit4)
```

An object of class "MArrayLM"

\$coefficients

	mc	c	mf.mc	f.c
Vitvi15g01736	4.430191	1.593545190	0.09309953	-0.31758915
Vitvi07g02832	-2.991443	0.508155686	5.61740208	-0.25109586
Vitvi07g02830	-2.839209	1.548036562	5.02958569	-0.90607176
Vitvi07g02812	-1.374475	-0.009794742	2.05627305	0.40349136
Vitvi07g02811	1.837984	0.566269561	1.29839620	0.02240192
Vitvi09g02033	-3.137869	0.419564483	4.70108235	-0.76028515

\$rank

[1] 4

\$assign

[1] 0 1 2 3

\$qr

\$qr

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

15 more rows ...

\$sraux

[1] 1.223607 1.130819 1.182562 1.066939

\$pivot

[1] 1 2 3 4

\$tol

[1] 1e-07

\$rank

[1] 4

\$df.residual

[1] 16 16 16 16 16 16

\$sigma

Vitvi15g01736	Vitvi07g02832	Vitvi07g02830	Vitvi07g02812
0.8941832	0.7681327	0.5921856	0.8558602
Vitvi07g02811	Vitvi09g02033		
0.5294628	0.4728364		

\$cov.coefficients

	(Intercept)	swp	varietyF	swp:varietyF
(Intercept)	0.4827337	0.5442848	-0.4827337	-0.5442848
swp	0.5442848	0.7740261	-0.5442848	-0.7740261
varietyF	-0.4827337	-0.5442848	0.9319295	1.1174059


```
swp:varietyF -0.5442848 -0.7740261 1.1174059 1.7146670
```

```
$stdev.unscaled
```

```

      (Intercept)      swp  varietyF swp:varietyF
Vitvi15g01736    0.3162278 0.8797875 0.4472136    1.309453
Vitvi07g02832    0.3162278 0.8797875 0.4472136    1.309453
Vitvi07g02830    0.3162278 0.8797875 0.4472136    1.309453
Vitvi07g02812    0.3162278 0.8797875 0.4472136    1.309453
Vitvi07g02811    0.3162278 0.8797875 0.4472136    1.309453
Vitvi09g02033    0.3162278 0.8797875 0.4472136    1.309453

```

```
$pivot
```

```
[1] 1 2 3 4
```

```
$Amean
```

```

Vitvi15g01736 Vitvi07g02832 Vitvi07g02830 Vitvi07g02812
      4.4767407      -0.1827419      -0.3244159      -0.3463388
Vitvi07g02811 Vitvi09g02033
      2.4871819      -0.7873280

```

```
$method
```

```
[1] "ls"
```

```
$design
```

```

      (Intercept)      swp  varietyF swp:varietyF
1              1 -0.3720000          0          0
2              1 -0.4016667          0          0
3              1 -0.5350000          0          0
4              1 -0.5000000          0          0
5              1 -0.4592308          0          0
15 more rows ...

```

```
$df.prior
```

```
[1] 5.442291
```

```
$s2.prior
```

```
[1] 0.240232
```

```
$var.prior
```

```
[1] 66.60227703 10.07260620 66.60227703 0.04162642
```

```
$proportion
```

```
[1] 0.01
```

```
$s2.post
```

```

Vitvi15g01736 Vitvi07g02832 Vitvi07g02830 Vitvi07g02812
      0.6575990      0.5012458      0.3226499      0.6075545
Vitvi07g02811 Vitvi09g02033
      0.2701533      0.2278022

```

```
$t
```

```

              mc          c      mf.mc          f.c
Vitvi15g01736 17.275947 2.2336032 0.2567154 -0.29908538

```

```
Vitvi07g02832 -13.361504  0.8158186 17.7416959 -0.27084716
Vitvi07g02830 -15.806350  3.0976880 19.7993745 -1.21816734
Vitvi07g02812  -5.576277 -0.0142831  5.8989290  0.39532267
Vitvi07g02811  11.182439  1.2383410  5.5858219  0.03291472
Vitvi09g02033 -20.790067  0.9991759 22.0243909 -1.21648751
```

```
$df.total
```

```
[1] 21.44229 21.44229 21.44229 21.44229 21.44229 21.44229
```

```
$p.value
```

```

              mc              c              mf.mc
Vitvi15g01736 4.582548e-14 0.036281328 7.998456e-01
Vitvi07g02832 7.201069e-12 0.423574363 2.684665e-14
Vitvi07g02830 2.699108e-13 0.005361432 2.906795e-15
Vitvi07g02812 1.447097e-05 0.988736185 6.838803e-06
Vitvi07g02811 2.066890e-10 0.228976529 1.415145e-05
Vitvi09g02033 1.072274e-15 0.328852510 3.282724e-16
```

```

              f.c
Vitvi15g01736 0.7677545
Vitvi07g02832 0.7890987
Vitvi07g02830 0.2363952
Vitvi07g02812 0.6965102
Vitvi07g02811 0.9740471
Vitvi09g02033 0.2370210
```

```
$lods
```

```

      (Intercept)      swp  varietyF  swp:varietyF
Vitvi15g01736    22.24850 -3.752633 -7.466375    -4.606008
Vitvi07g02832    17.06898 -5.596946 22.901410    -4.606206
Vitvi07g02830    20.43614 -2.117771 25.106813    -4.589886
Vitvi07g02812     2.18499 -5.915023  3.264972    -4.605189
Vitvi07g02811    13.61819 -5.197139  2.529137    -4.607100
Vitvi09g02033    26.06635 -5.441685 27.247330    -4.589930
```

```
$F
```

```
[1] 602.7271 384.9793 557.1593  43.1426 512.2023 699.0823
```

```
$F.p.value
```

```
[1] 1.086743e-21 1.253785e-19 2.503334e-21 5.851652e-10
[5] 6.109721e-21 2.247742e-22
```

```
> fit4[testvar,]
```

```
An object of class "MArrayLM"
```

```
$coefficients
```

```

              mc              c              mf.mc              f.c
Vitvi01g01391 2.135505 -0.7685916 -0.09326836 0.4814101
```

```
$rank
```

```
[1] 4
```

```
$assign
```

```
[1] 0 1 2 3
```

```
$qr
```

```

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

$graux
[1] 1.223607 1.130819 1.182562 1.066939

$pivot
[1] 1 2 3 4

$tol
[1] 1e-07

$rank
[1] 4

$df.residual
[1] 16

$sigma
Vitvi01g01391
  0.5999568

$cov.coefficients
              (Intercept)          swp  varietyF swp:varietyF
(Intercept)  0.4827337  0.5442848 -0.4827337  -0.5442848
swp          0.5442848  0.7740261 -0.5442848  -0.7740261
varietyF     -0.4827337 -0.5442848  0.9319295   1.1174059
swp:varietyF -0.5442848 -0.7740261  1.1174059   1.7146670

$stdev.unscaled
              (Intercept)          swp  varietyF swp:varietyF
Vitvi01g01391  0.3162278  0.8797875  0.4472136   1.309453

$pivot
[1] 1 2 3 4

$Amean
Vitvi01g01391
  2.08887

$method
[1] "ls"

$design
  (Intercept)          swp  varietyF swp:varietyF
1           1 -0.3720000          0          0

```

```

2          1 -0.4016667          0          0
3          1 -0.5350000          0          0
4          1 -0.5000000          0          0
5          1 -0.4592308          0          0
15 more rows ...

$df.prior
[1] 5.442291

$s2.prior
[1] 0.240232

$var.prior
[1] 66.60227703 10.07260620 66.60227703 0.04162642

$proportion
[1] 0.01

$s2.post
Vitvi01g01391
      0.3295629

$t
              mc              c              mf.mc              f.c
Vitvi01g01391 11.76336 -1.521769 -0.3632873 0.6404071

$df.total
[1] 21.44229

$p.value
              mc              c              mf.mc              f.c
Vitvi01g01391 8.072923e-11 0.1426785 0.7199473 0.5286929

$lods
      (Intercept)      swp varietyF swp:varietyF
Vitvi01g01391    14.58507 -4.850464 -7.43206      -4.602121

$F
[1] 373.4584

$F.p.value
[1] 1.728022e-19

> fit4[testvar,]$coef
              mc              c              mf.mc              f.c
Vitvi01g01391 2.135505 -0.7685916 -0.09326836 0.4814101
> fit4[testvar,]$p.value
              mc              c              mf.mc              f.c
Vitvi01g01391 8.072923e-11 0.1426785 0.7199473 0.5286929
> #
> tt.mc <- topTable(fit4,1,number=Inf, sort.by="none", confint=TRUE)
> all(rownames(fit4)==rownames(tt.mc))

```

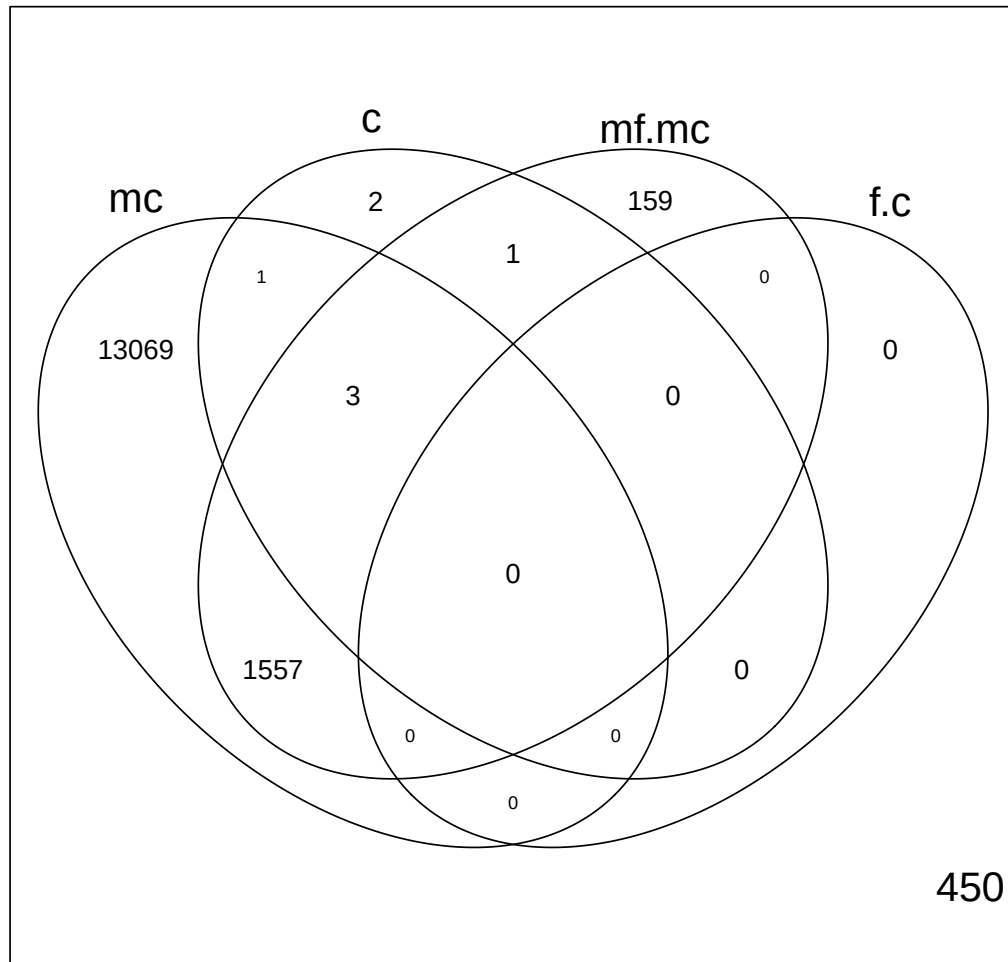
```

[1] TRUE
> tt.mc[testvar,]
      logFC      CI.L      CI.R AveExpr      t
Vitvi01g01391 2.135505 1.758448 2.512561 2.08887 11.76336
      P.Value      adj.P.Val      B
Vitvi01g01391 8.072923e-11 1.060206e-10 14.58507
> alpha <- as.numeric(.alpha)
> with(tt.mc, table(p=P.Value < alpha, adj.p=adj.P.Val < alpha))
      adj.p
p      FALSE  TRUE
FALSE    605    0
TRUE      7 14630
> #
> tt.c <- topTable(fit4,2,number=Inf, sort.by="none", confint=TRUE)
> tt.c[testvar,]
      logFC      CI.L      CI.R AveExpr
Vitvi01g01391 -0.7685916 -1.817613 0.2804301 2.08887
      t      P.Value      adj.P.Val      B
Vitvi01g01391 -1.521769 0.1426785 0.6681823 -4.850464
> with(tt.c, table(p=P.Value < alpha, adj.p=adj.P.Val < alpha))
      adj.p
p      FALSE  TRUE
FALSE 13748    0
TRUE   1487    7
> #
> tt.mf.mc <- topTable(fit4,3,number=Inf, sort.by="none", confint=TRUE)
> tt.mf.mc[testvar,]
      logFC      CI.L      CI.R AveExpr
Vitvi01g01391 -0.09326836 -0.6265071 0.4399704 2.08887
      t      P.Value      adj.P.Val      B
Vitvi01g01391 -0.3632873 0.7199473 0.9142513 -7.43206
> with(tt.mf.mc, table(p=P.Value < alpha, adj.p=adj.P.Val < alpha))
      adj.p
p      FALSE  TRUE
FALSE 12053    0
TRUE   1469 1720
> #
> tt.f.c <- topTable(fit4,4,number=Inf, sort.by="none", confint=TRUE)
> tt.f.c[testvar,]
      logFC      CI.L      CI.R AveExpr
Vitvi01g01391 0.4814101 -1.079927 2.042747 2.08887
      t      P.Value      adj.P.Val      B
Vitvi01g01391 0.6404071 0.5286929 0.9999488 -4.602121
> with(tt.f.c, table(p=P.Value < alpha, adj.p=adj.P.Val < alpha))
      adj.p
p      FALSE
FALSE 15083
TRUE   159

```

7.0.1 Write fit

```
> fit4fn <- "lm-fit-means-swpXvariety-statistics.txt"
> fit <- fit4
> decide0 <- decideTests(fit,lfc=0 )
> vennDiagram(decide0)
```



```
> #ind <- sapply(rownames(fit),FUN=function(x) match(x,fdata$geneID))
> ind <- match(rownames(fit),fdata$geneID)
> df4 <- as.data.frame(fit)
> write.fit(fit,file="../doc/tmp2.txt", adjust="BH")
> df4 <- read.table("../doc/tmp2.txt")
> colnames(df4)
[1] "A" "Coef.mc"
[3] "Coef.c" "Coef.mf.mc"
[5] "Coef.f.c" "t.mc"
[7] "t.c" "t.mf.mc"
[9] "t.f.c" "P.value.mc"
[11] "P.value.c" "P.value.mf.mc"
[13] "P.value.f.c" "P.value.adj.mc"
[15] "P.value.adj.c" "P.value.adj.mf.mc"
[17] "P.value.adj.f.c" "F"
[19] "F.p.value"
```

```

> df4$type <- ""
> types <- types[rownames(df4),]
> all(rownames(df4)==rownames(types))

[1] TRUE

> #ind <- sapply(rownames(tt),FUN=function(x) match(x,rownames(types)))
> for(i in 1:ncol(types)) df4$type[types[,i]] <- colnames(types)[i]
> stat4 <- data.frame(df4,fdata[ind,2:5] )

> my.write.table(stat4,file=file.path(.oroot,fit4fn),
+ label="WP x variety model statistics, types and gene annotation")

```

Warning in write.table(x, file = file, col.names = col.names, sep = sep, : appending column names to file Object: stat4

Label: WP x variety model statistics, types and gene annotation

File :

[../..output/50_Expression-water-stress-0.05-r/lm-fit-means-swpXvariety-statistics.txt](#)

Comparison with effects.

Large abs slope C

```
> alpha
[1] 0.05
> indp <- (tt.c$P.Value < alpha)
> sum(indp)
[1] 1494
> table(rownames(tt.c)[indp]%in%rownames(tt.c)[large_abs_c])
Error in rownames(tt.c)[indp] %in% rownames(tt.c)[large_abs_c]: object 'large_
> table(indp, large_abs_C)
      large_abs_C
indp  FALSE  TRUE
FALSE 13714   34
TRUE   1218  276
```

Small difference of slopes

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

FALSE  TRUE
4602 10481
> table(indp, small_fc)
      small_fc
indp  FALSE  TRUE
FALSE   159    0
TRUE   4602 10481
```

Large difference of mean expressions

```
> alpha
[1] 0.05
> range(tt.mf.mc$P.Value)
[1] 1.063003e-25 9.999648e-01
> indp <- (tt.mf.mc$P.Value < alpha)
> sum(indp)
[1] 3189
> table(rownames(tt.c)[indp]%in%rownames(tt.c)[(abs(mc-mf)<deltam)])

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


7.1 Genes in types

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

Figures caption:

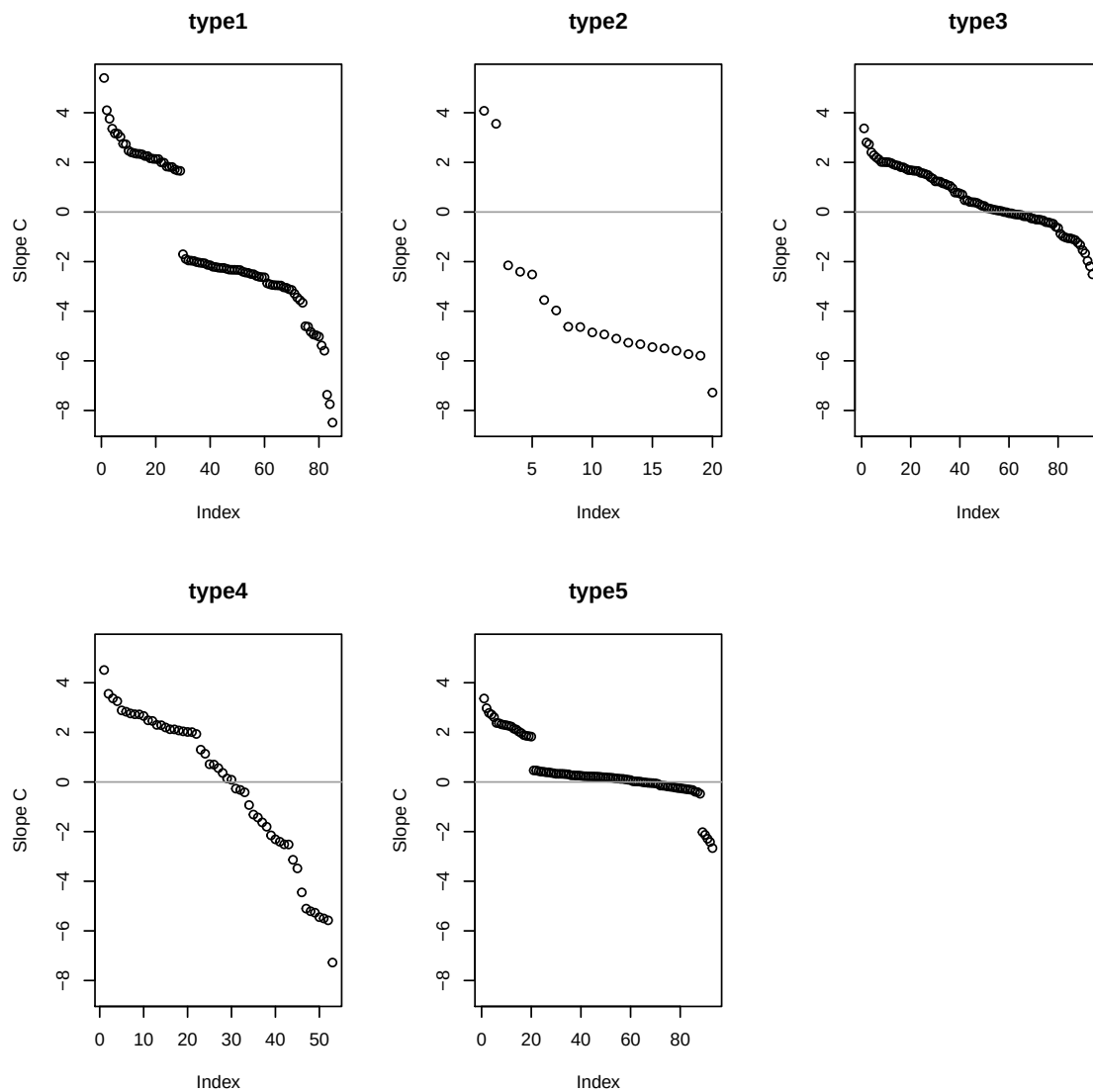
Mean expression (E) and mean water potential (WP). C (blue) and all F (red). Gray line (if present) is regression of all data, regardless of treatment and variety.

Order stat4 by swp

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

```
[1] TRUE
```

```
> par(mfrow=c(2,3))
> ylim <- range(stat4[, "Coef.c"])
> for(i in 1:ncol(types)){
+   varnames <- rownames(stat4)[types[,i]]
+   plot(stat4[varnames, "Coef.c"], ylab="Slope C",
+     ,ylim=ylim, main=colnames(types)[i])
+   abline(h=0, col=8)
+ }
```



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

```

[1] ""
> colnames(stat4)

[1] "A"                "Coef.mc"
[3] "Coef.c"           "Coef.mf.mc"
[5] "Coef.f.c"         "t.mc"
[7] "t.c"              "t.mf.mc"
[9] "t.f.c"            "P.value.mc"
[11] "P.value.c"        "P.value.mf.mc"
[13] "P.value.f.c"      "P.value.adj.mc"
[15] "P.value.adj.c"    "P.value.adj.mf.mc"
[17] "P.value.adj.f.c"  "F"
[19] "F.p.value"        "type"
[21] "geneID"           "BINCODE"
[23] "NAME"             "DESCRIPTION"

> tipi <- sort(unique(stat4$type))[-1]
> i <- 1
> for(i in 1:ncol(types)){
+ out <- paste(out, "
+ \\clearpage
+ \\subsection{", colnames(types)[i], "}\\")
+ varnames <- rownames(stat4)[types[,i]]
+ varname <- varnames[2]
+ for(varname in varnames)
+ out <- paste(out, knit_child(file.path("../doc/", "50aa_one-gene-plots.Rnw"),
+ }

```

7.2 type1

7.2.1 Vitvi03g00325

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

Vitvi03g00325

27.03.2025

RNA.regulation of transcription.MYB domain transcription factor family

RAD-like 1 |

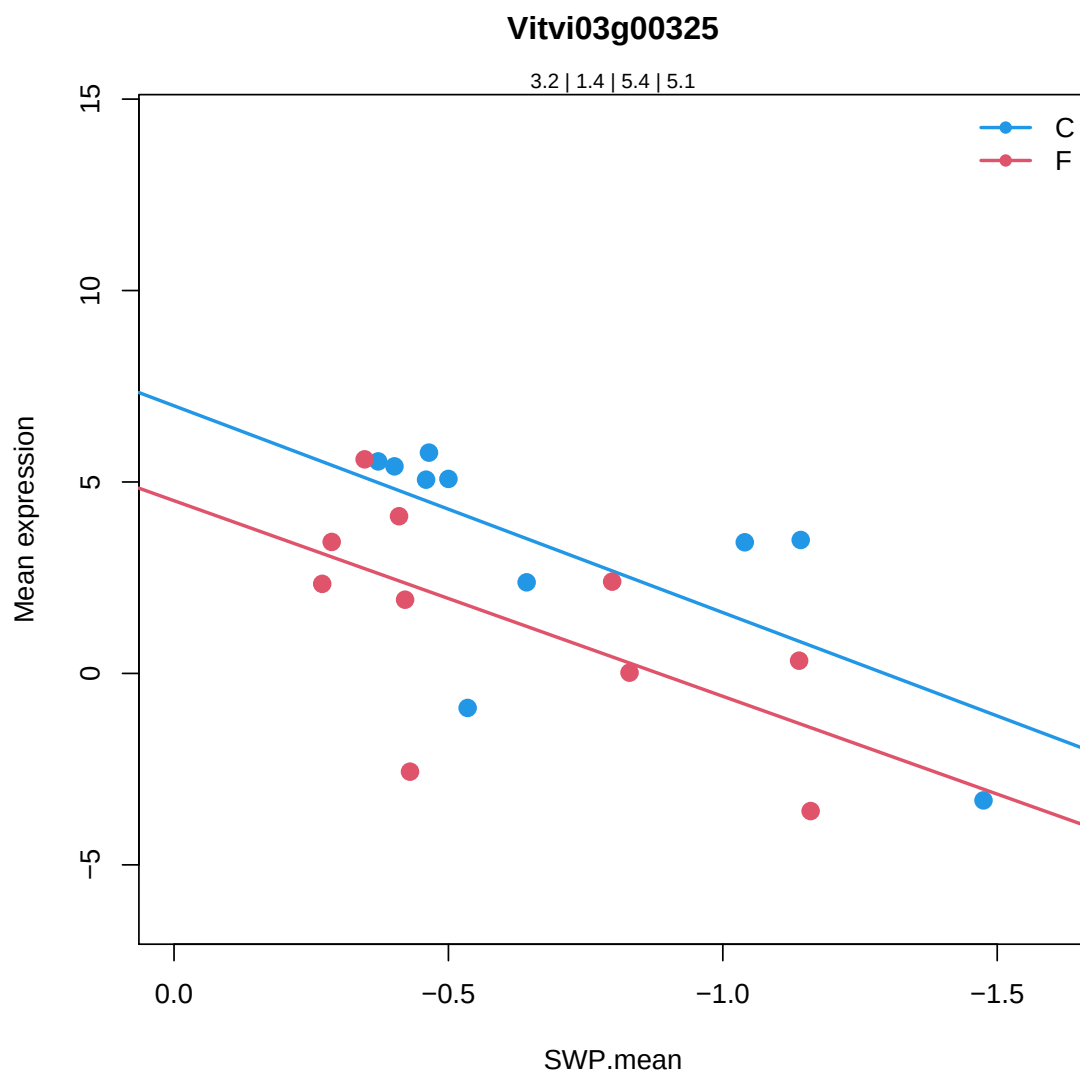
Chr4:18271457-18271857 REVERSE LENGTH=100 |

201606

Coefficients for Vitvi03g00325.

```
Error in symnum(x, corr = FALSE, na = FALSE, cutpoints = c(0, 0.001, 0.01, :
```

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.192321	9.103982e-05	***	0.0001006038	***
SlopeC	5.400429	0.008080928	**	0.2851146	
MeanF-MeanC	-1.794048	0.06988085	.	0.2960684	
SlopeF-SlopeC	-0.2916254	0.9166302		0.9999488	



7.2.2 Vitvi05g00011

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

```
Vitvi05g00011
```

```
35.2
```

```
not assigned.unknown
```

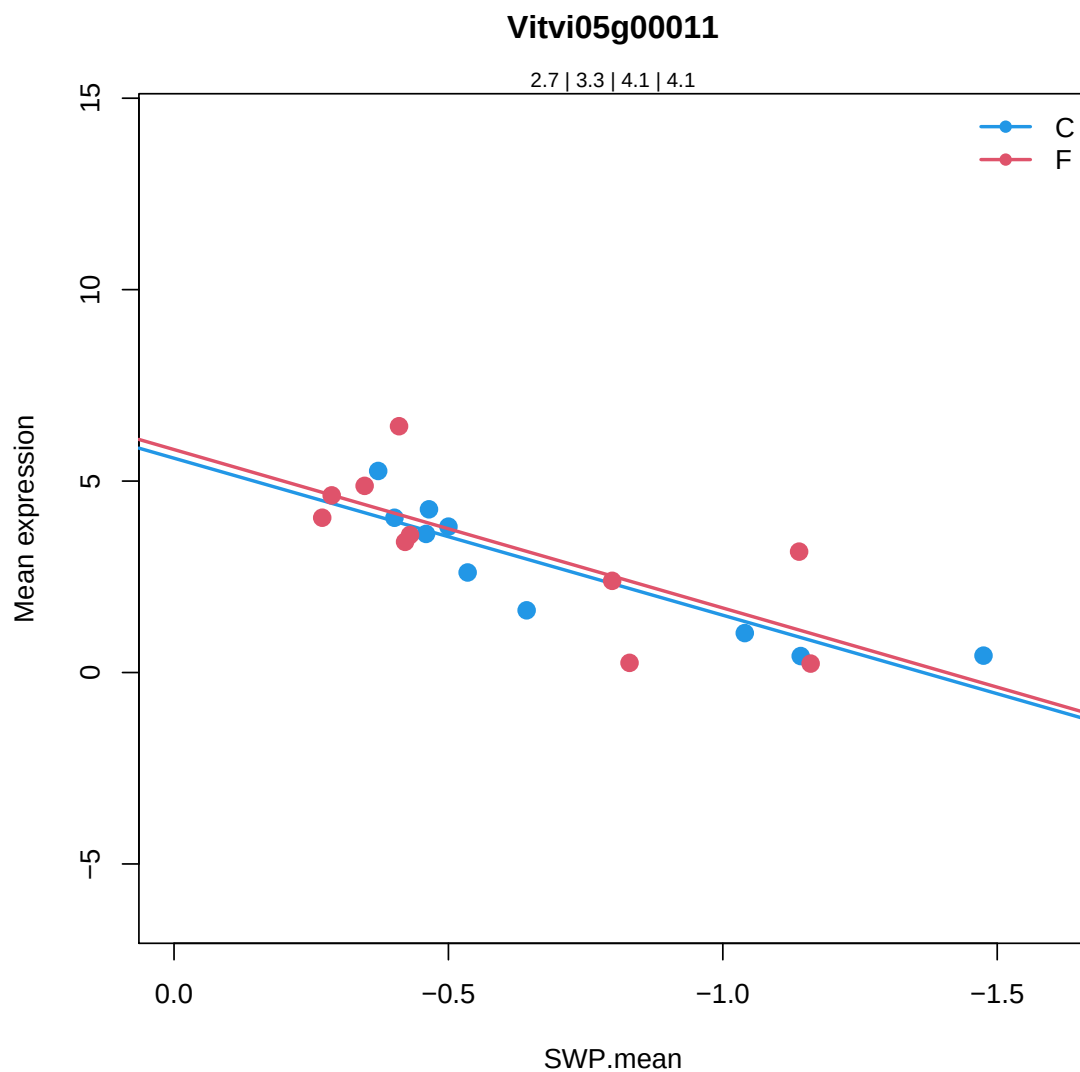
```
Pollen Ole e 1 allergen and extensin family protein |
```

```
Chr3:5676904-5677788 FORWARD LENGTH=180 |
```

```
201606
```

Coefficients for Vitvi05g00011.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.71363	3.60489e-08	***	4.329163e-08	***
SlopeC	4.101024	0.0001755321	***	0.07644173	.
MeanF-MeanC	0.5883901	0.2148664		0.5622308	
SlopeF-SlopeC	0.03610049	0.978881		0.9999488	



7.2.3 Vitvi05g01353

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

Vitvi05g01353

10.08.2001

cell wall.pectinesterases.PME

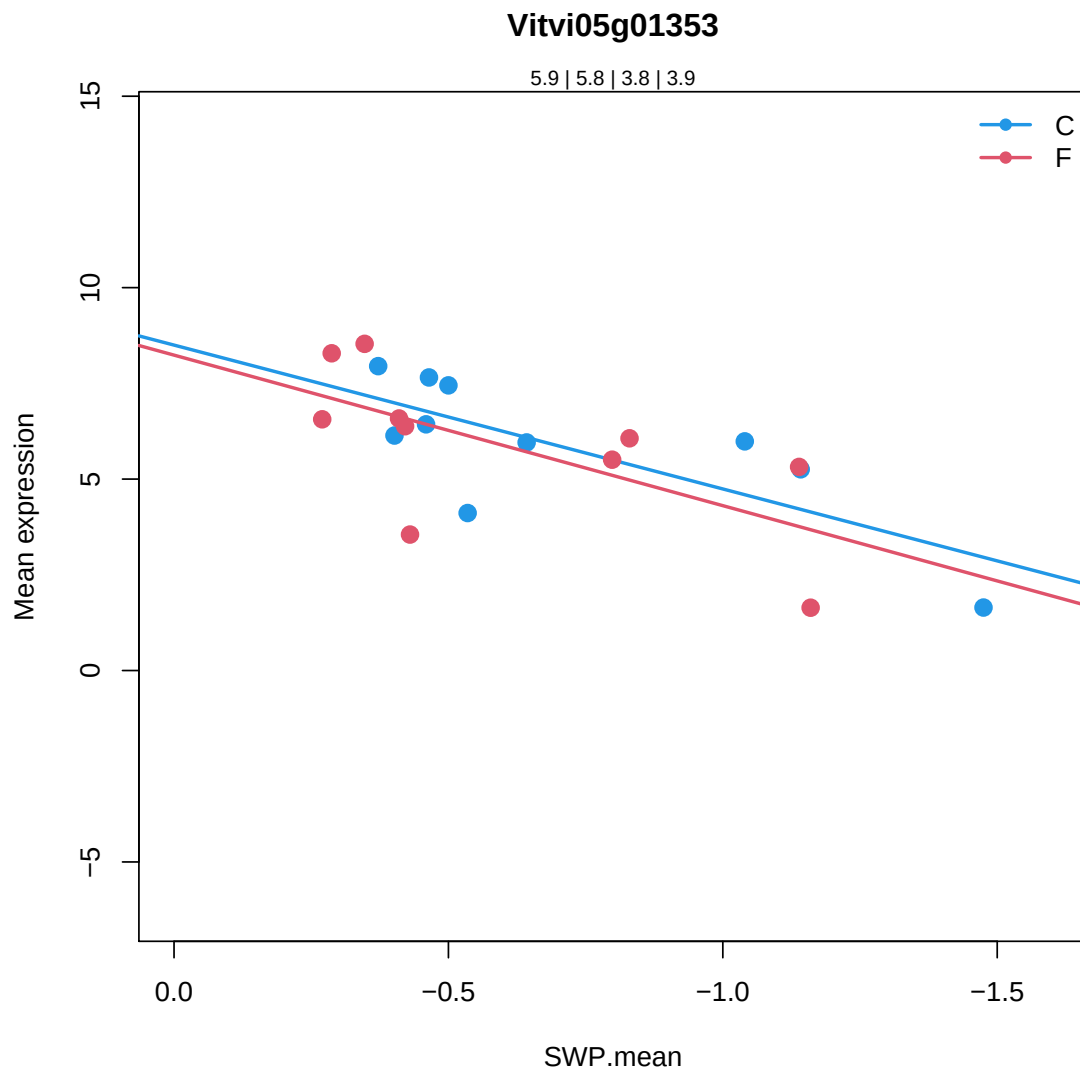
pectin methylesterase 61 |

Chr3:21803015-21805098 REVERSE LENGTH=529 |

201606

Coefficients for Vitvi05g01353.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.857325	2.084874e-12	***	2.936936e-12	***
SlopeC	3.757248	0.003467502	**	0.2238297	
MeanF-MeanC	-0.01519937	0.9793892		0.994731	
SlopeF-SlopeC	0.1744137	0.9193632		0.9999488	



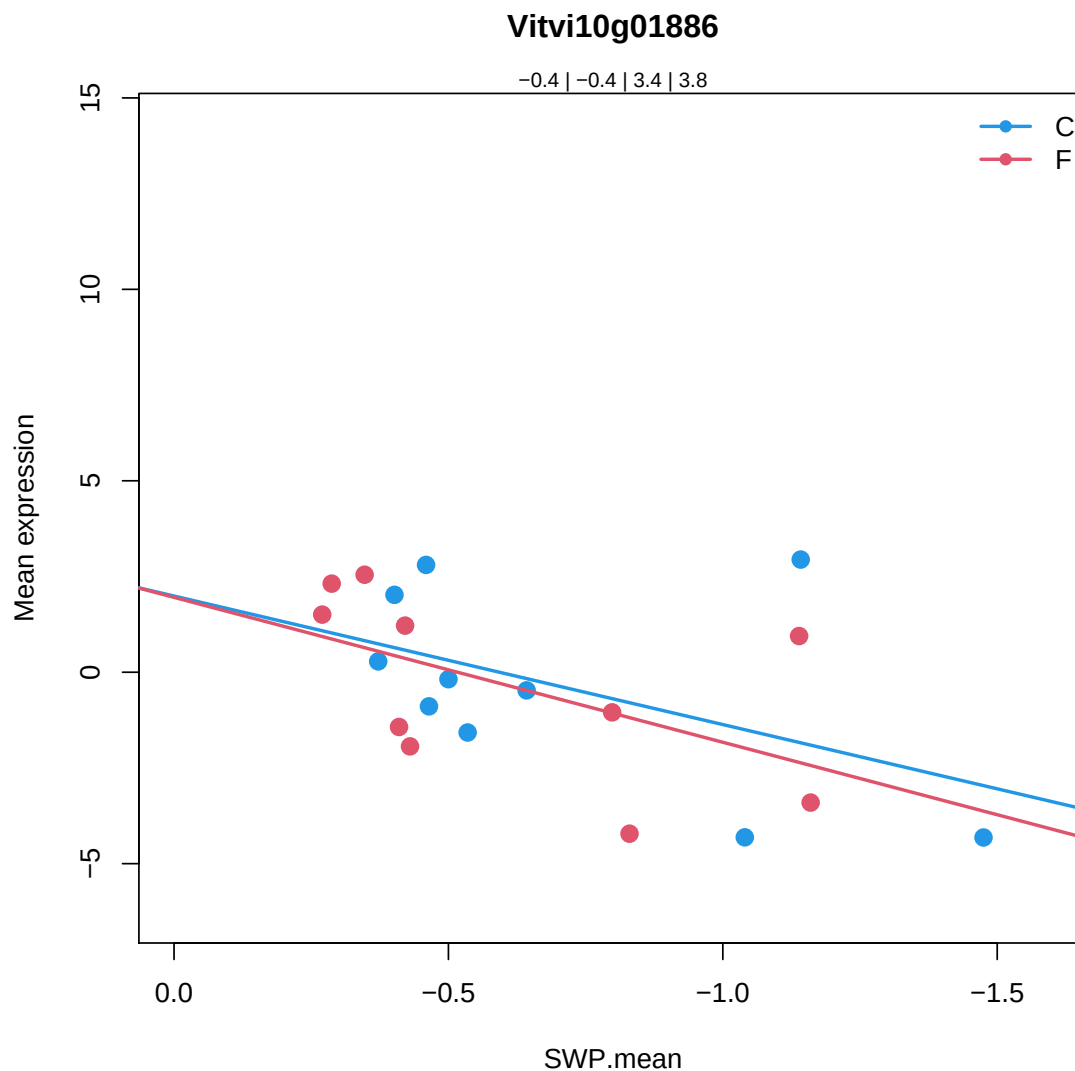
7.2.4 Vitvi10g01886

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

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

Coefficients for Vitvi10g01886.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.3703529	0.5581725		0.5640192	
SlopeC	3.356612	0.06592693	.	0.5539461	
MeanF-MeanC	0.01931686	0.9826998		0.9957601	
SlopeF-SlopeC	0.4277199	0.8697865		0.9999488	



7.2.5 Vitvi10g01616

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

Vitvi10g01616

35.2

not assigned.unknown

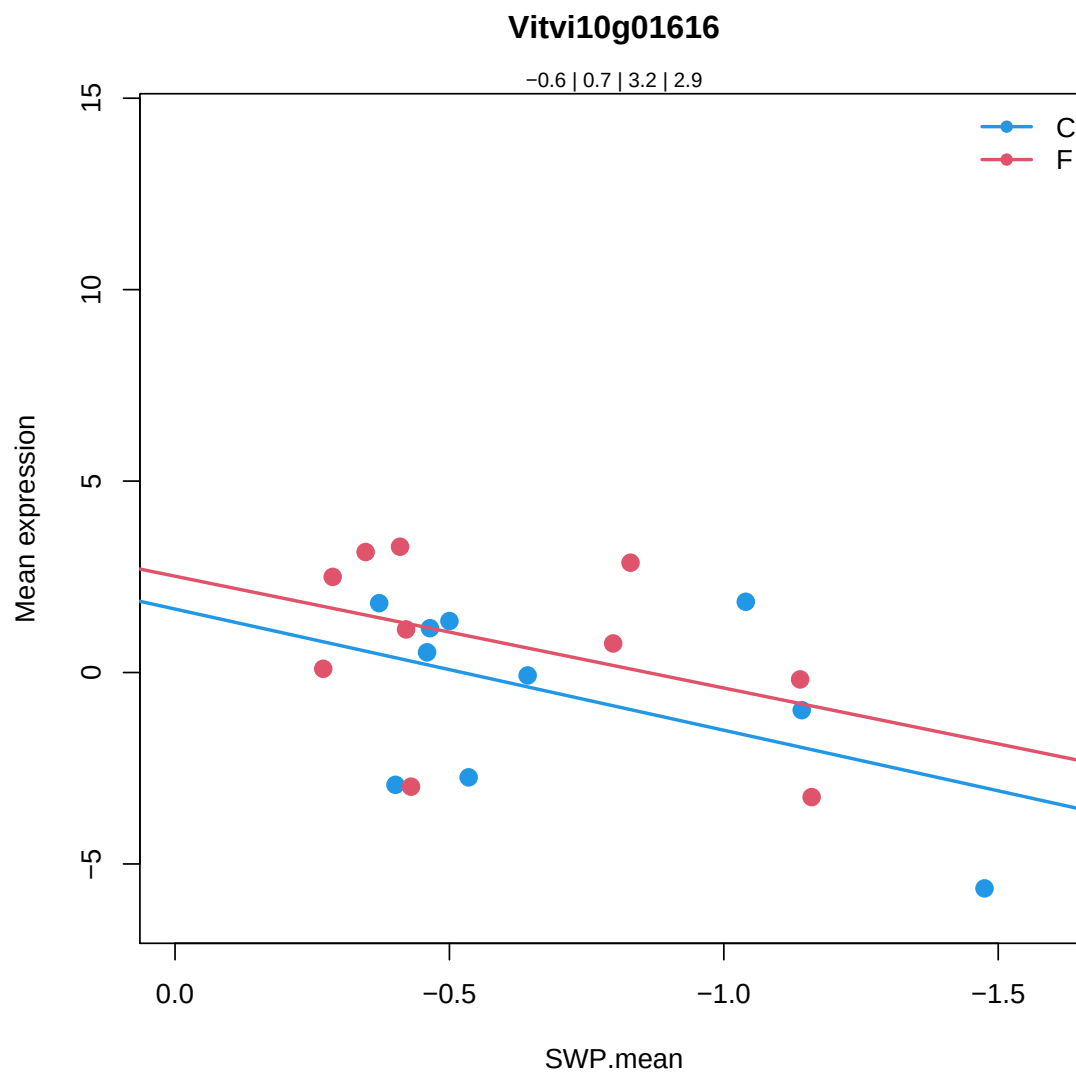
Stigma-specific Stig1 family protein |

Chr1:4026195-4026617 REVERSE LENGTH=140 |

201606

Coefficients for Vitvi10g01616.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.5679815	0.3801571		0.3862388	
SlopeC	3.165031	0.08679714	.	0.5916646	
MeanF-MeanC	1.30418	0.1601766		0.4837762	
SlopeF-SlopeC	-0.2446635	0.9265967		0.9999488	



7.2.6 Vitvi10g00436

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

Vitvi10g00436

3.08.2002

minor CHO metabolism.galactose.alpha-galactosidases

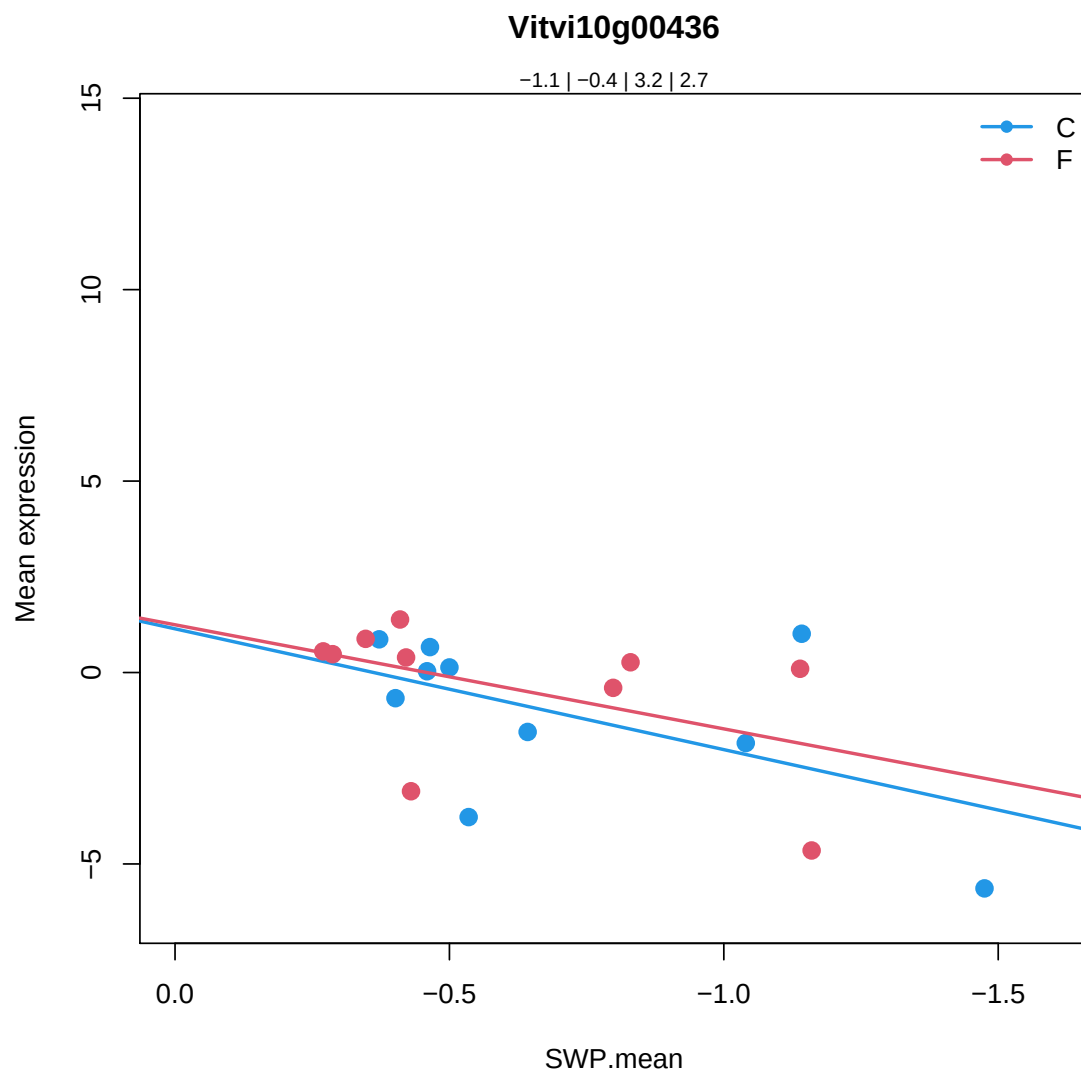
Melibiase family protein |

Chr3:20882886-20885745 FORWARD LENGTH=437 |

201606

Coefficients for Vitvi10g00436.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.077179	0.04821491	*	0.05022154	.
SlopeC	3.15566	0.03841712	*	0.4670907	
MeanF-MeanC	0.6675279	0.3688215		0.724094	
SlopeF-SlopeC	-0.4366108	0.8394522		0.9999488	



7.2.7 Vitvi04g02114

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

```
Vitvi04g02114
```

```
35.2
```

```
not assigned.unknown
```

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

```
Chr5:1232122-1233888 FORWARD LENGTH=401 |
```

```
201606
```

```
Vitvi04g02114
```

```
17.8.1.1.7
```

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

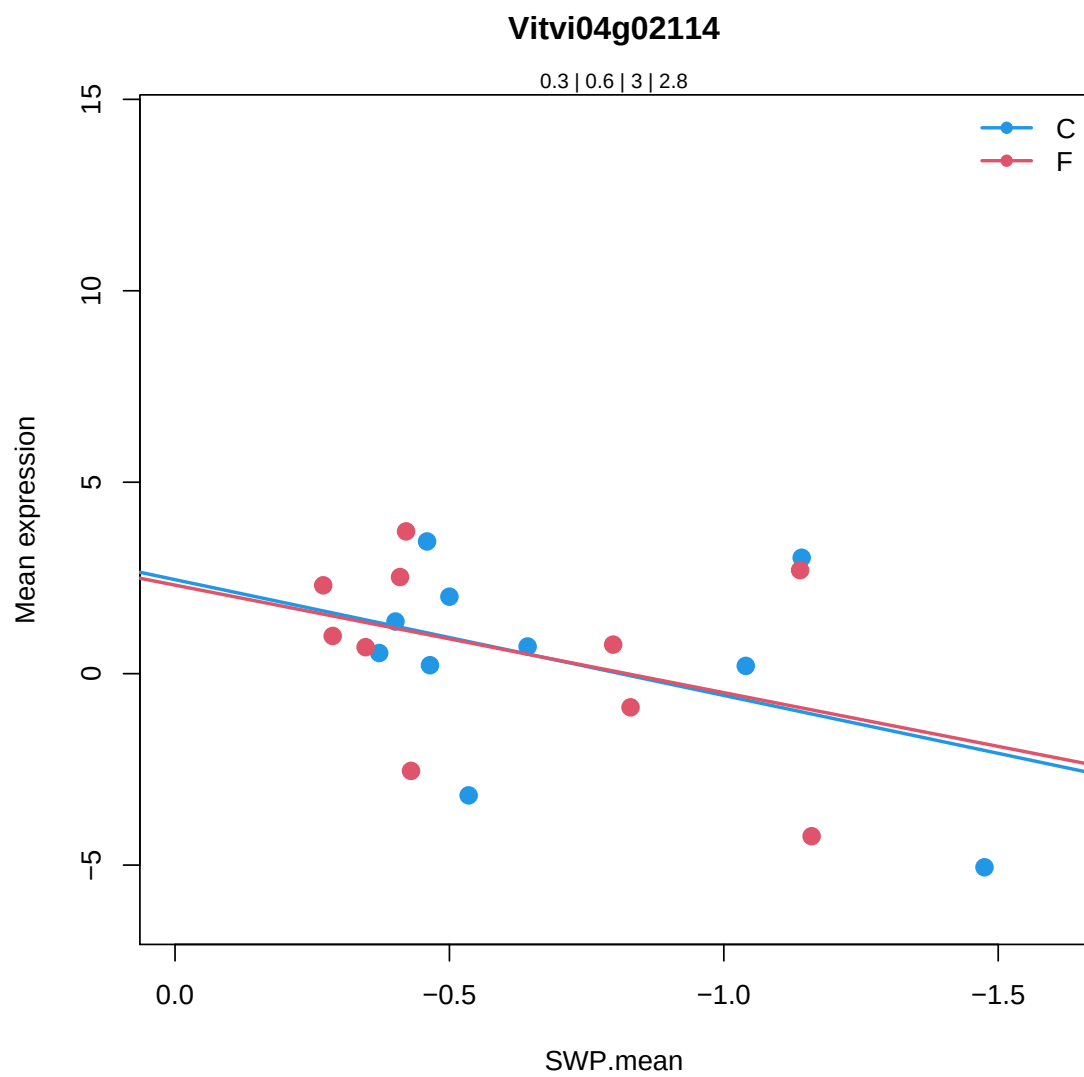
```
S-adenosyl-L-methionine-dependent methyltransferases superfamily prote
```

```
Chr5:1232122-1233888 FORWARD LENGTH=401 |
```

```
201606
```

Coefficients for Vitvi04g02114.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3284336	0.6354879		0.6405731	
SlopeC	3.024528	0.1260986		0.6471837	
MeanF-MeanC	0.2730671	0.7801191		0.9373729	
SlopeF-SlopeC	-0.2163602	0.9397313		0.9999488	



7.2.8 Vitvi01g00593

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

Vitvi01g00593

10.06.2003

cell wall.degradation.pectate lyases and polygalacturonases

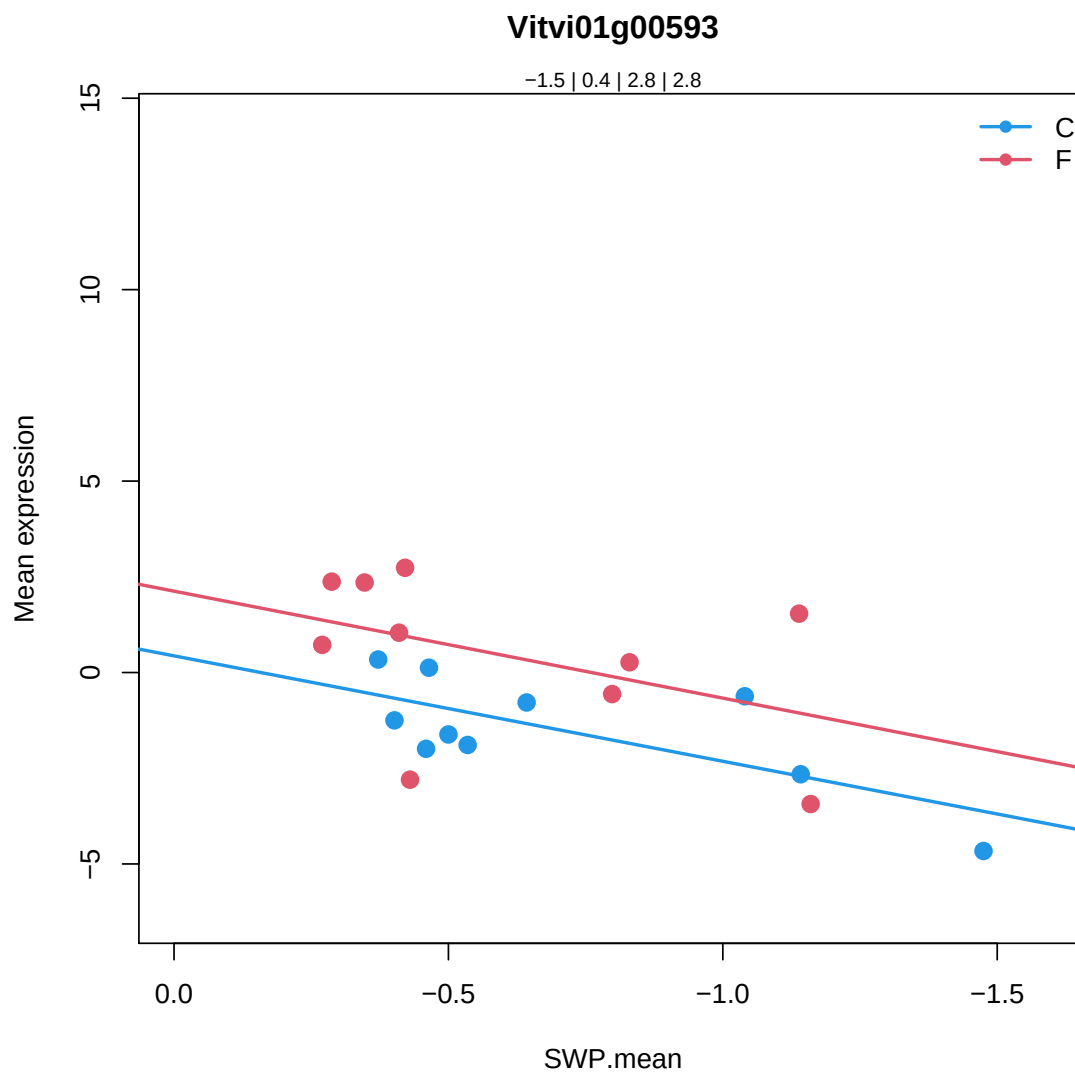
Pectate lyase family protein |

Chr1:25401660-25403165 FORWARD LENGTH=408 |

201606

Coefficients for Vitvi01g00593.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.500933	0.003006862	**	0.003221834	**
SlopeC	2.753643	0.03843906	*	0.4670907	
MeanF-MeanC	1.923883	0.006245072	**	0.0535965	.
SlopeF-SlopeC	0.04027117	0.9829088		0.9999488	



7.2.9 Vitvi03g00144

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

Vitvi03g00144

29.4.1.56

protein.postranslational modification.kinase.receptor like cytoplasmat

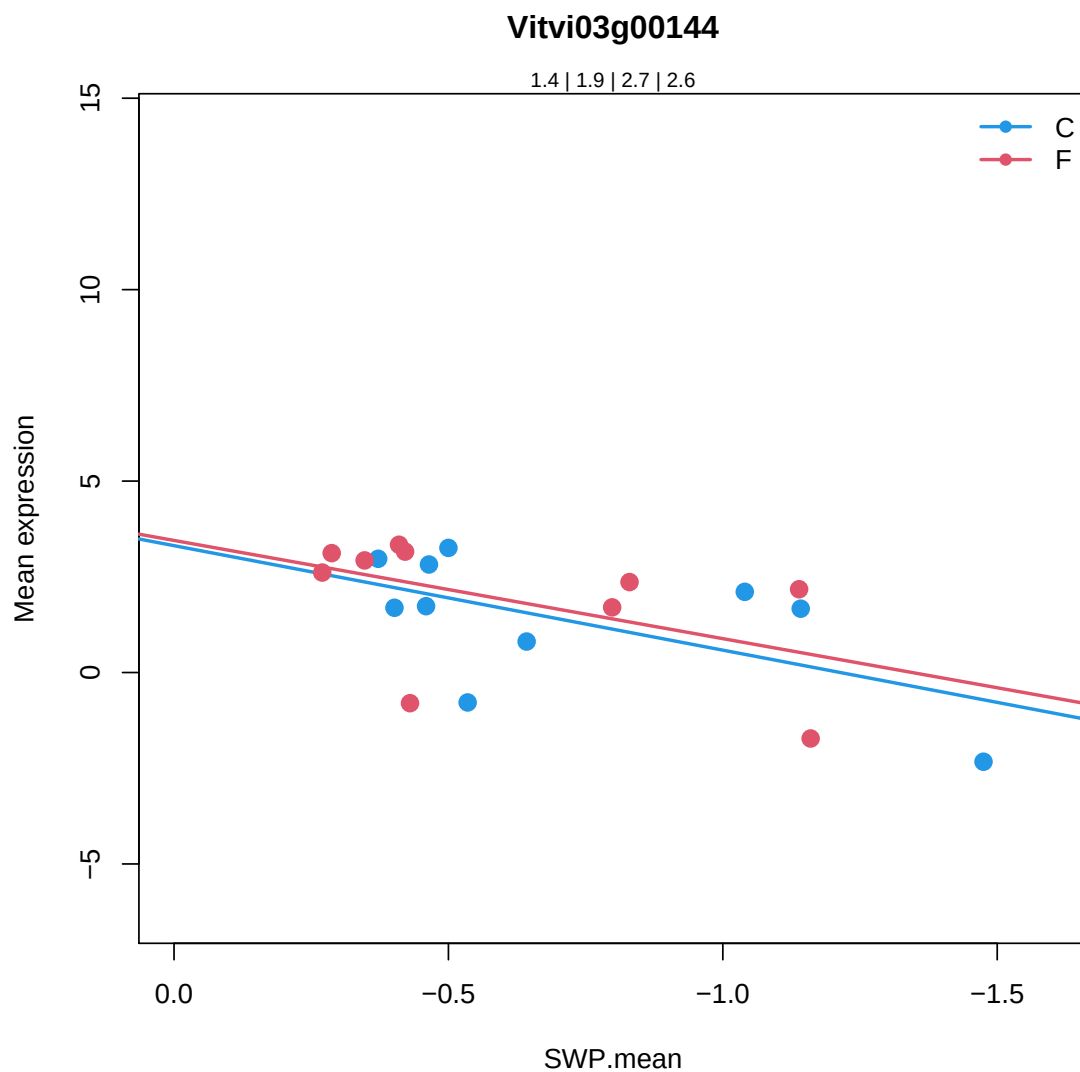
Protein kinase superfamily protein |

Chr4:16676234-16677962 FORWARD LENGTH=448 |

201606

Coefficients for Vitvi03g00144.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.394192	0.003904502	**	0.004175431	**
SlopeC	2.728777	0.03328153	*	0.4433084	
MeanF-MeanC	0.4924859	0.4281192		0.7634182	
SlopeF-SlopeC	-0.1638066	0.9277451		0.9999488	



7.2.10 Vitvi06g00790

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

Vitvi06g00790

10.7

cell wall.modification

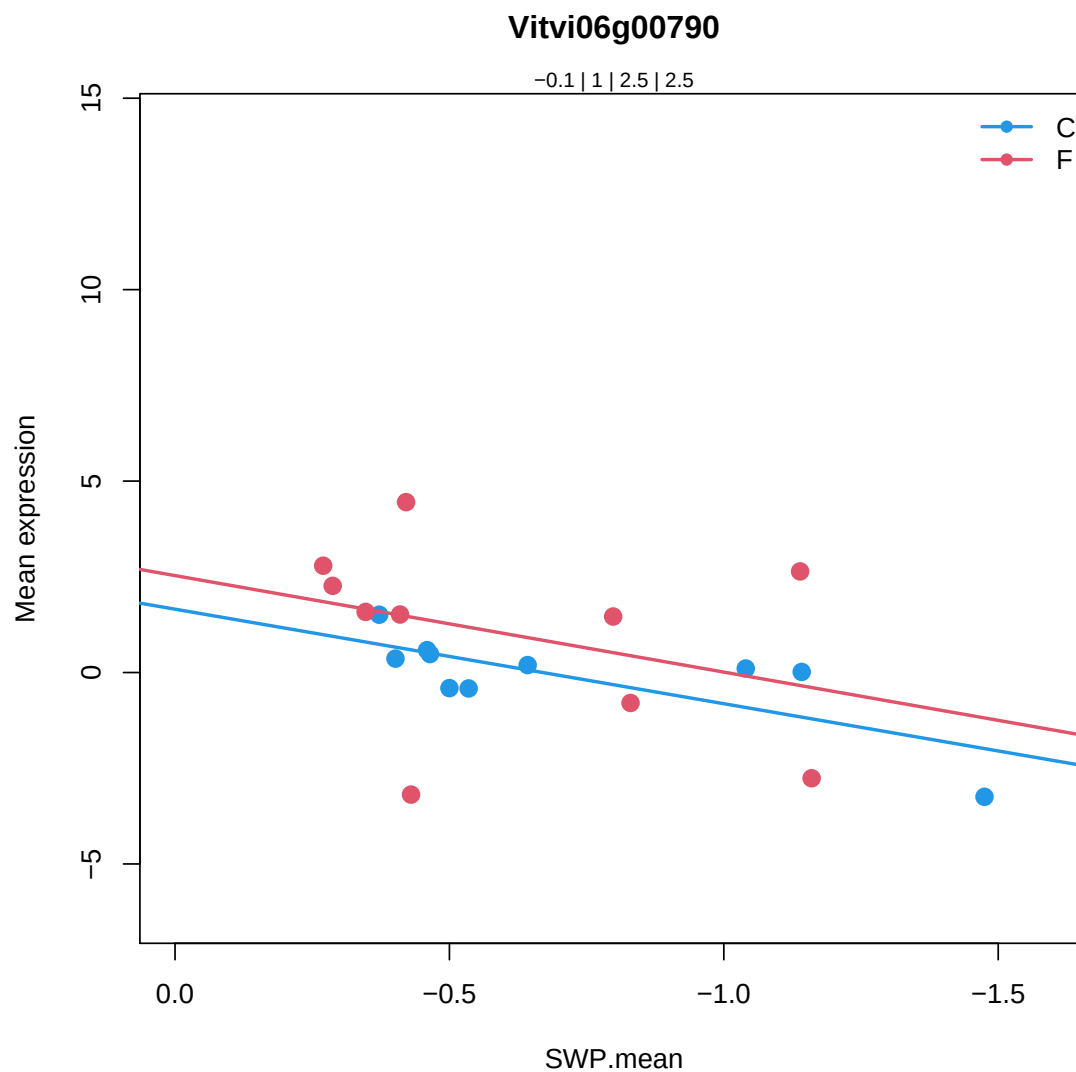
expansin A8 |

Chr2:16949121-16950472 REVERSE LENGTH=253 |

201606

Coefficients for Vitvi06g00790.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.08166594	0.8741388		0.8769003	
SlopeC	2.469095	0.09581708	.	0.6064284	
MeanF-MeanC	1.077543	0.1493144		0.4655993	
SlopeF-SlopeC	0.05143393	0.9807731		0.9999488	



7.2.11 Vitvi04g00060

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

Vitvi04g00060

29.4

protein.postranslational modification

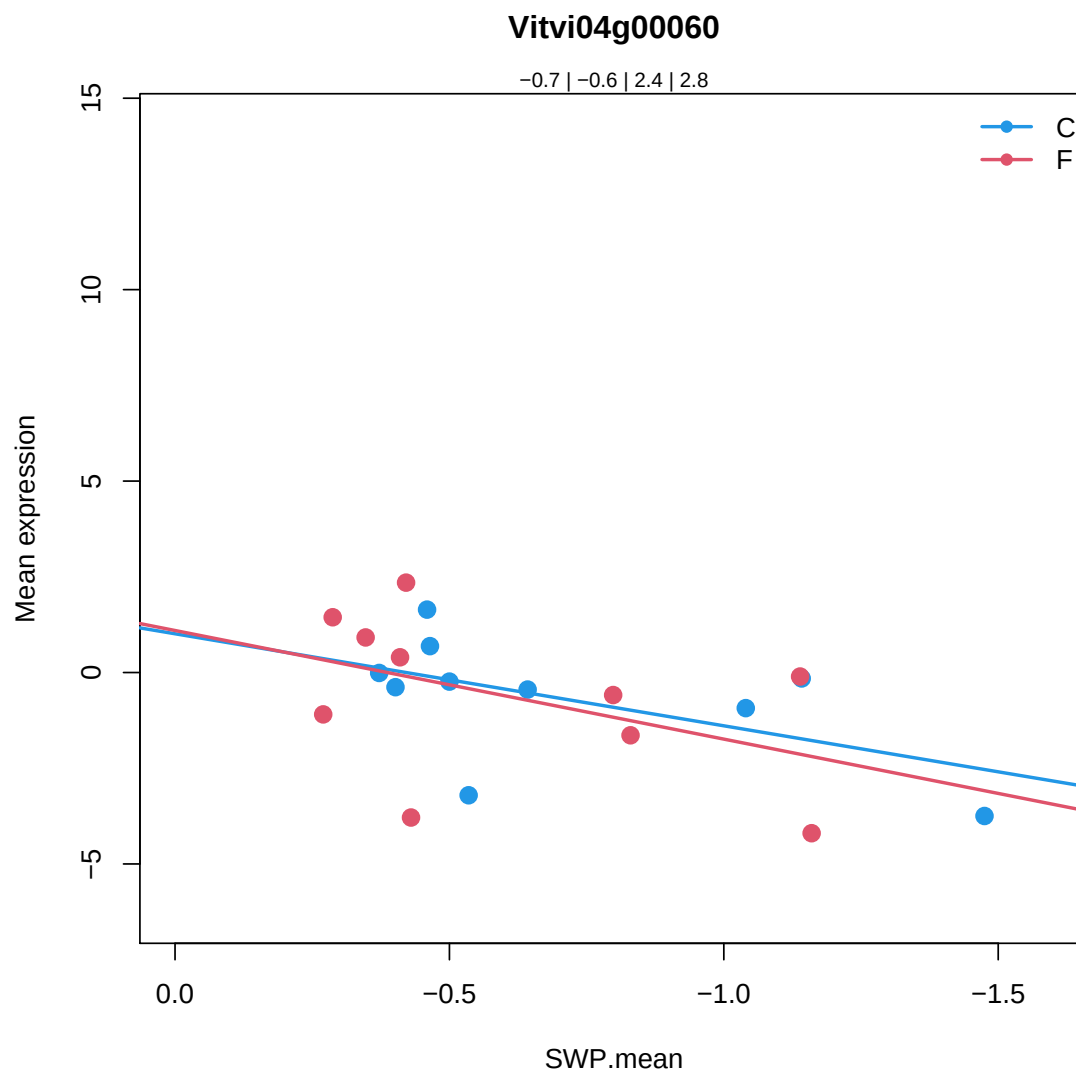
Protein phosphatase 2C family protein |

Chr5:9085512-9087372 REVERSE LENGTH=331 |

201606

Coefficients for Vitvi04g00060.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.6784558	0.1755229		0.1802533	
SlopeC	2.403369	0.0886092	.	0.5943767	
MeanF-MeanC	0.04771275	0.9451034		0.9857335	
SlopeF-SlopeC	0.4336031	0.8308518		0.9999488	



7.2.12 Vitvi18g00455

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

Vitvi18g00455

26.7

misc.oxidases - copper, flavone etc

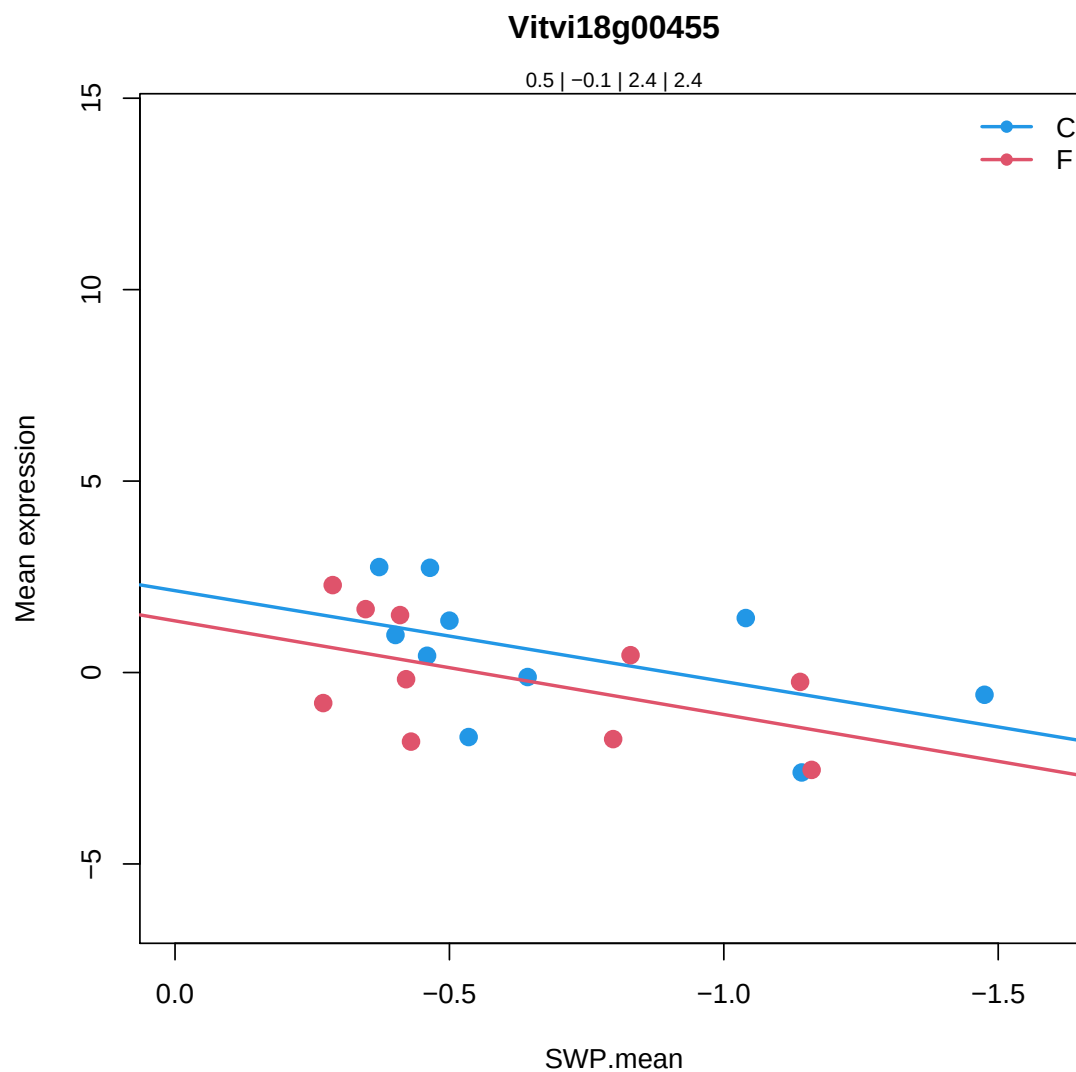
Cupredoxin superfamily protein |

Chr1:27188287-27189093 FORWARD LENGTH=181 |

201606

Coefficients for Vitvi18g00455.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4689391	0.2851456		0.2906956	
SlopeC	2.373306	0.059008	.	0.5387954	
MeanF-MeanC	-0.6103592	0.3242723		0.6848408	
SlopeF-SlopeC	0.07233783	0.9678037		0.9999488	



7.2.13 Vitvi11g01437

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

Vitvi11g01437

26.12

misc.peroxidases

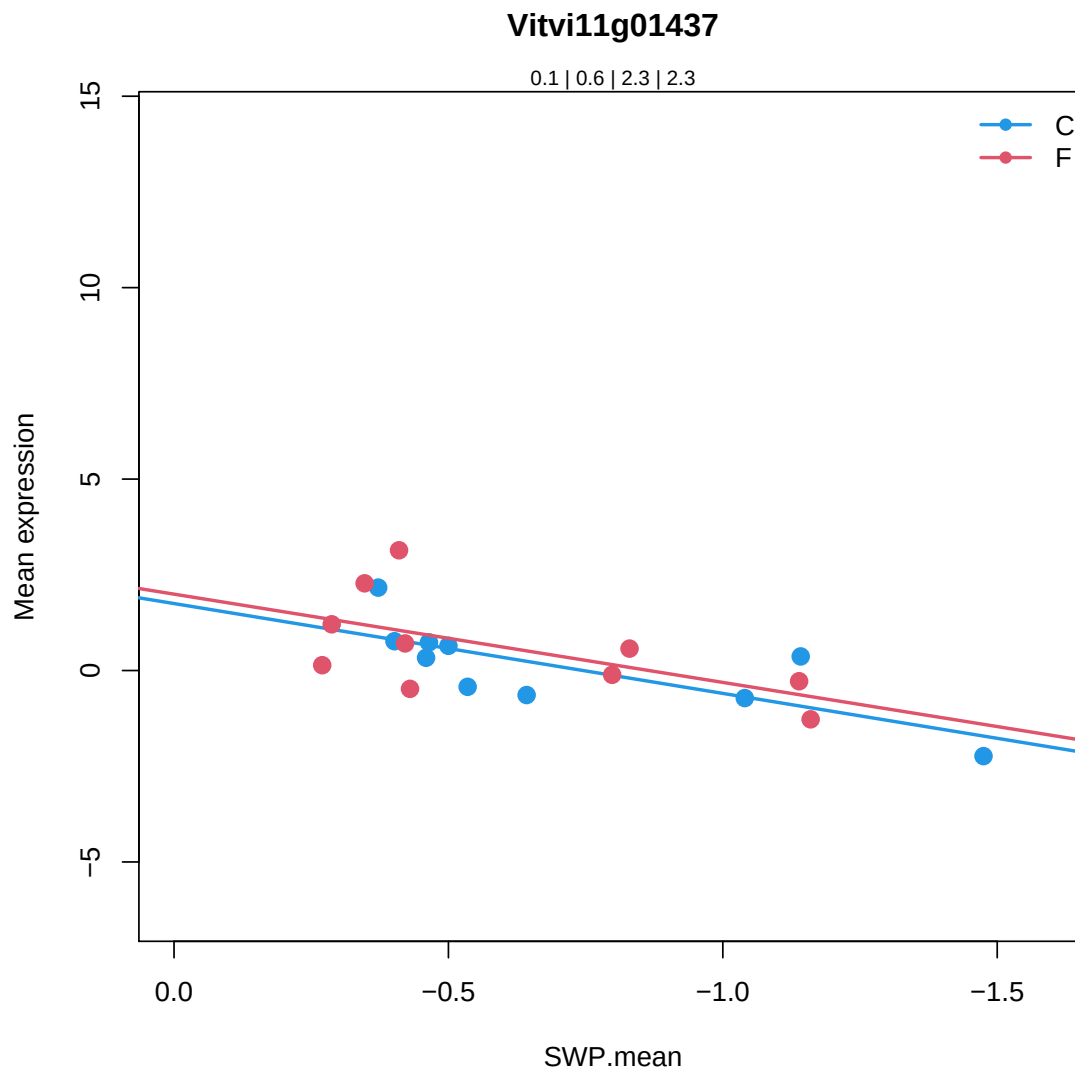
peroxidase superfamily protein |

Chr2:17296986-17298690 REVERSE LENGTH=328 |

201606

Coefficients for Vitvi11g01437.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.09876858	0.7280102		0.7325278	
SlopeC	2.346685	0.006578595	**	0.2702721	
MeanF-MeanC	0.4910265	0.2288586		0.5816886	
SlopeF-SlopeC	-0.04140832	0.9718717		0.9999488	



7.2.14 Vitvi03g00752

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

Vitvi03g00752

20.1.7.1

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

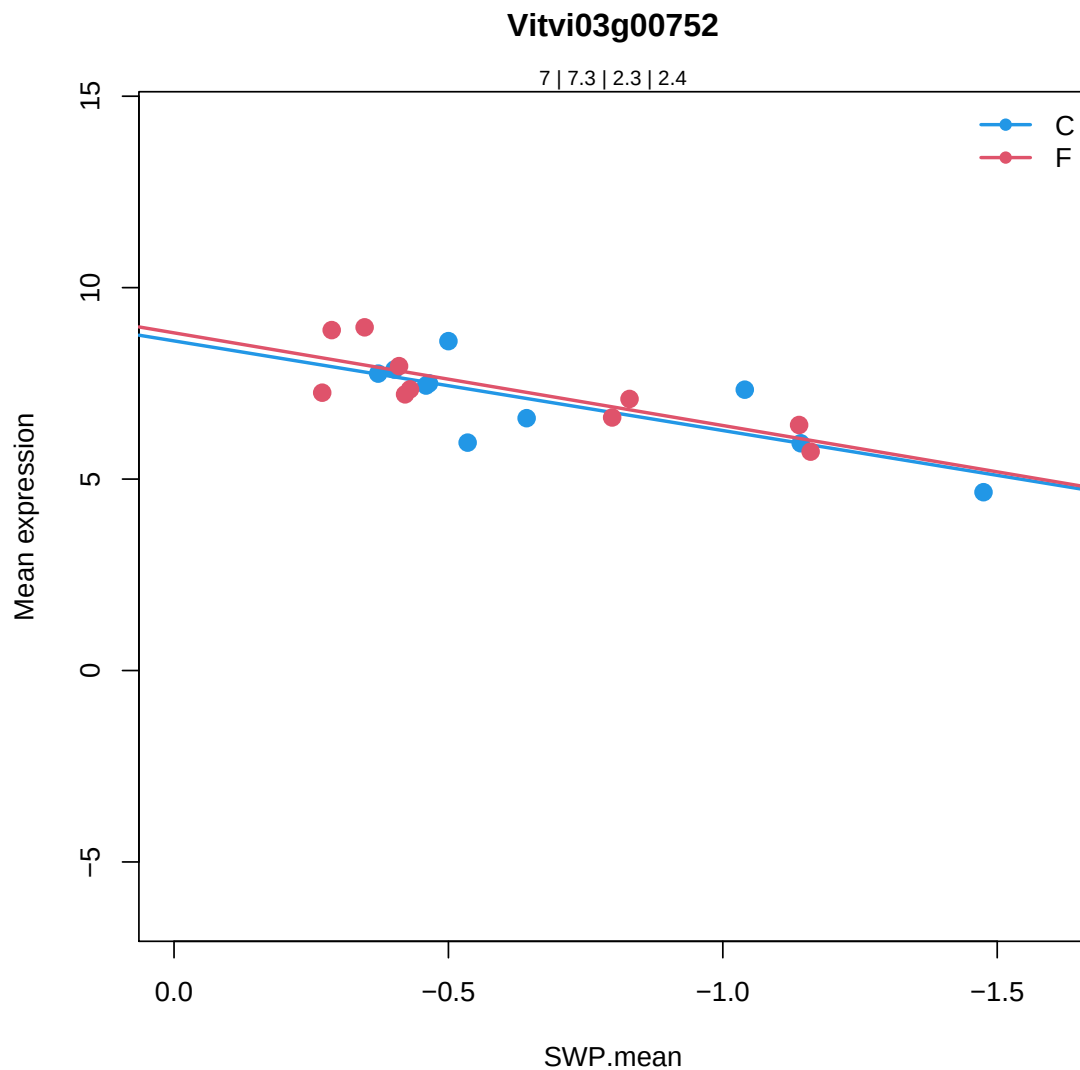
pathogenesis-related protein 1 |

Chr2:6241944-6242429 REVERSE LENGTH=161 |

201606

Coefficients for Vitvi03g00752.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.962961	9.923214e-20	***	4.751795e-19	***
SlopeC	2.340669	0.000749668	***	0.1076608	
MeanF-MeanC	0.3817999	0.2211937		0.5723025	
SlopeF-SlopeC	0.07947066	0.929457		0.9999488	



7.2.15 Vitvi06g00626

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

Vitvi06g00626

30.2.8.2

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

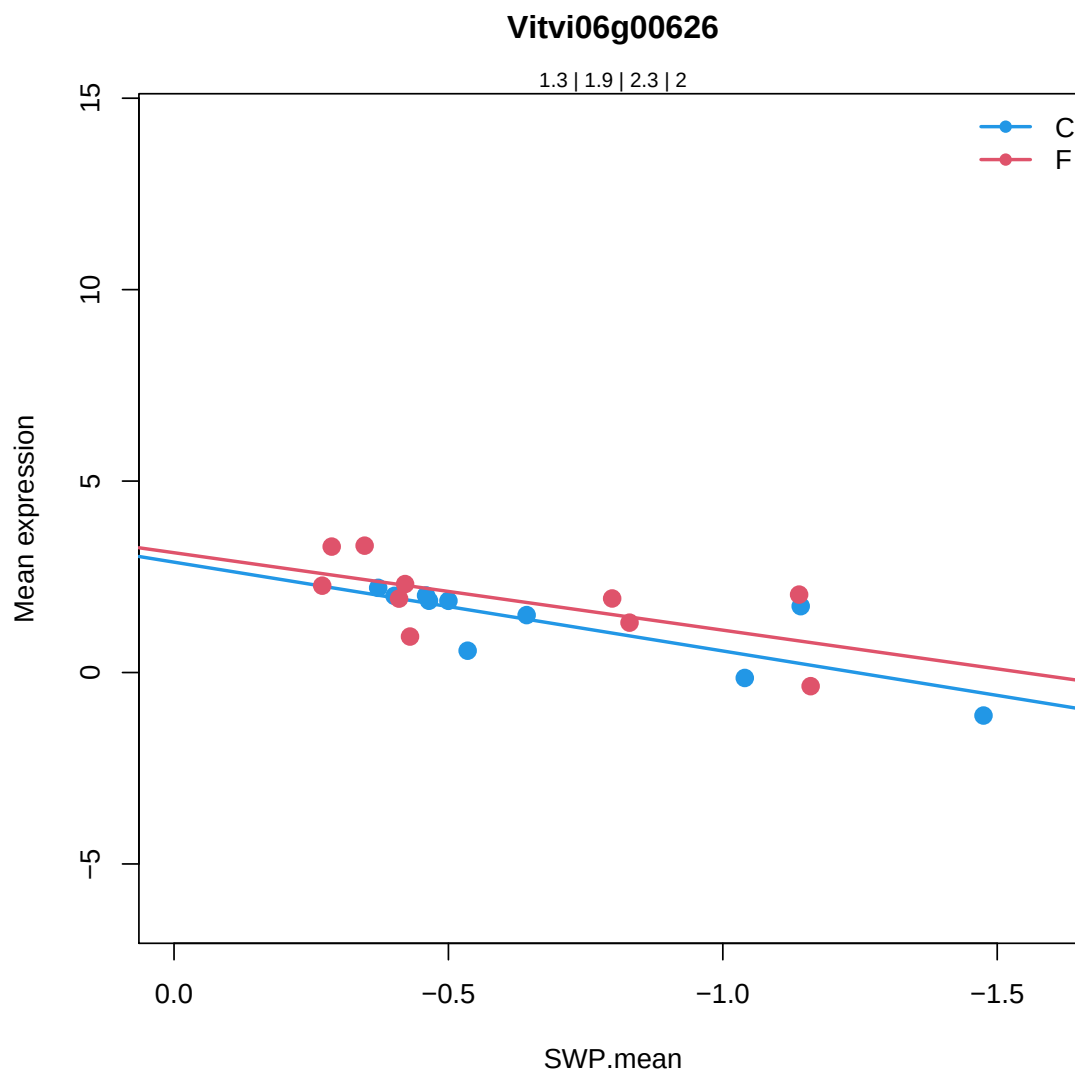
Protein kinase superfamily protein |

Chr3:2750285-2751674 FORWARD LENGTH=305 |

201606

Coefficients for Vitvi06g00626.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.250849	2.584959e-05	***	2.88983e-05	***
SlopeC	2.319803	0.00183732	**	0.160246	
MeanF-MeanC	0.6455885	0.06500153	.	0.2823463	
SlopeF-SlopeC	-0.297086	0.7627901		0.9999488	



7.2.16 Vitvi01g00638

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

Vitvi01g00638

35.2

not assigned.unknown

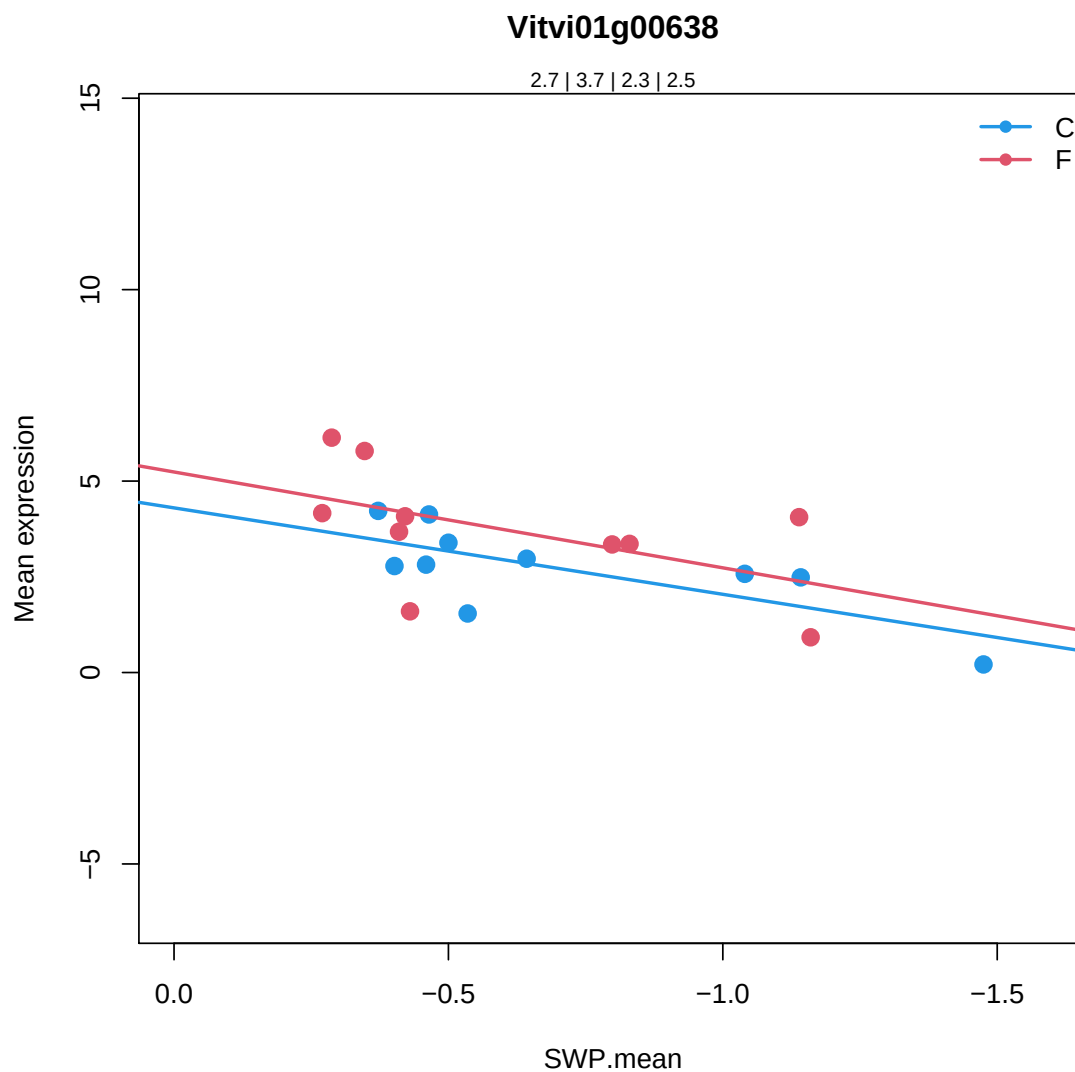
DUF868 family protein (DUF868) |

Chr4:7480896-7481753 FORWARD LENGTH=285 |

201606

Coefficients for Vitvi01g00638.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.712506	5.204179e-08	***	6.219877e-08	***
SlopeC	2.257332	0.0235059	*	0.3983963	
MeanF-MeanC	0.9995699	0.04541677	*	0.2251195	
SlopeF-SlopeC	0.2461278	0.8598843		0.9999488	



7.2.17 Vitvi03g01162

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

Vitvi03g01162

26.2

misc.UDP glucosyl and glucoronyl transferases

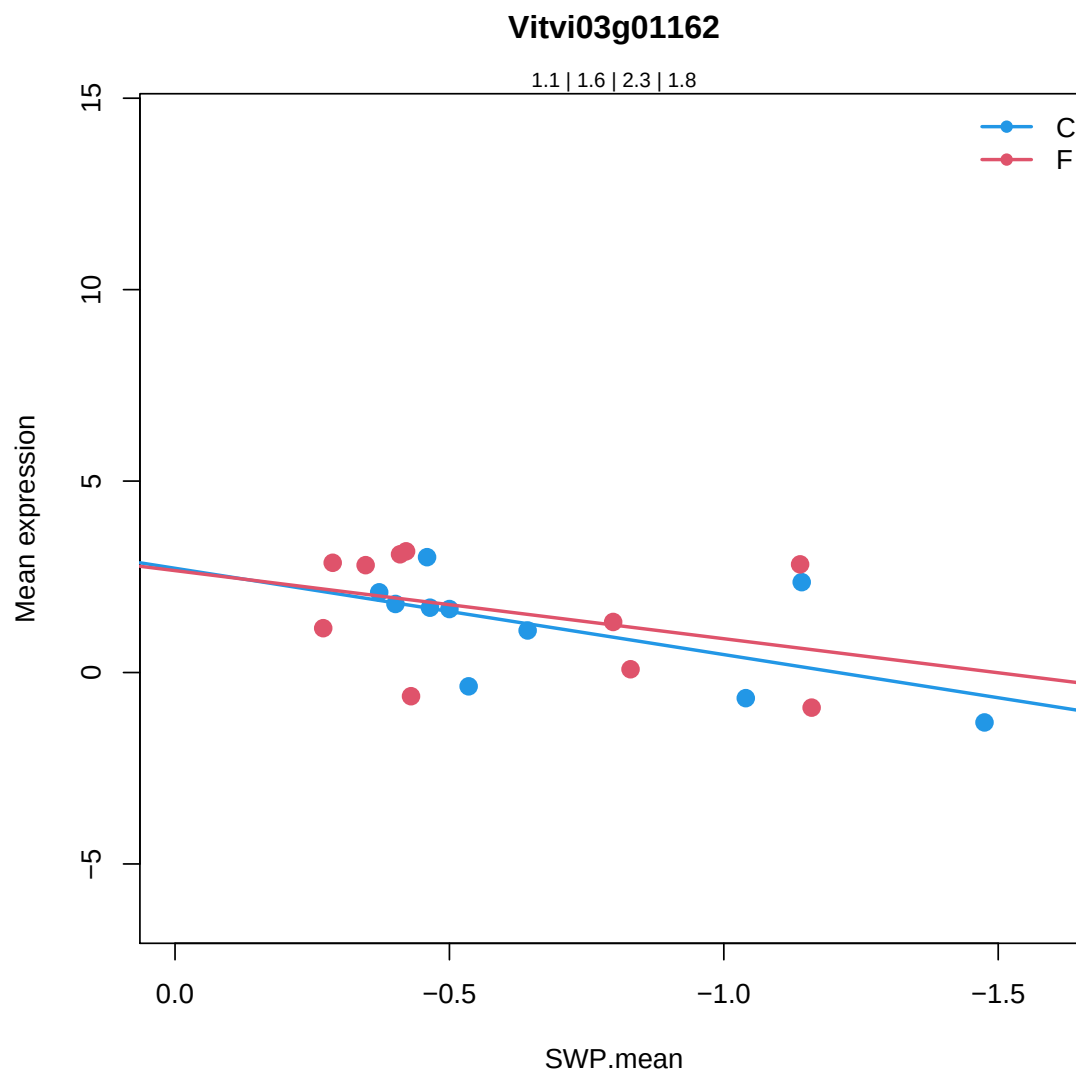
UDP-glucosyl transferase 85A3 |

Chr1:7900522-7902332 REVERSE LENGTH=488 |

201606

Coefficients for Vitvi03g01162.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.137076	0.008329468	**	0.008839838	**
SlopeC	2.254074	0.0506402	.	0.5104439	
MeanF-MeanC	0.4403571	0.4348589		0.7674876	
SlopeF-SlopeC	-0.4754753	0.7719849		0.9999488	



7.2.18 Vitvi07g00665

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

Vitvi07g00665

10.02.2001

cell wall.cellulose synthesis.cellulose synthase

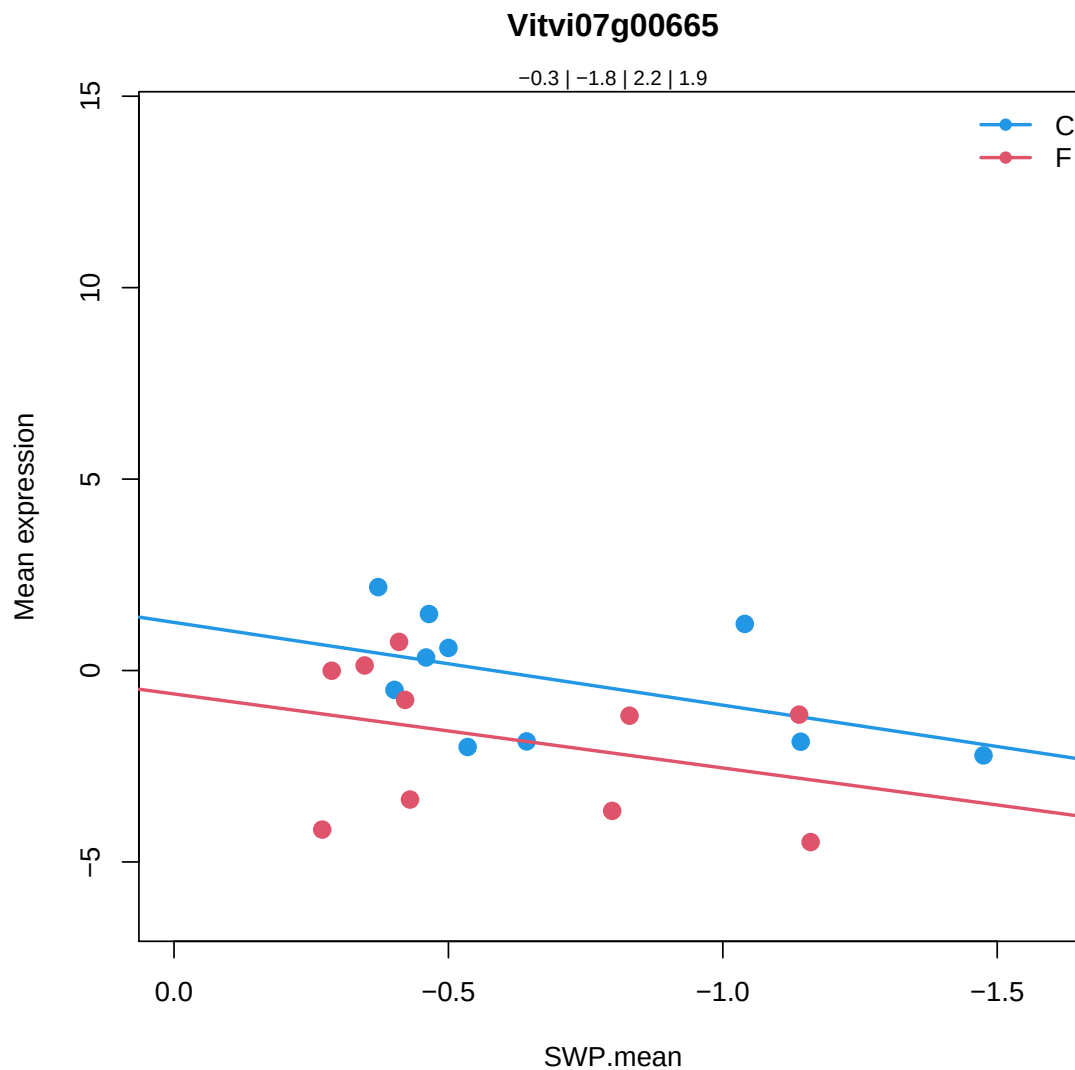
cellulose synthase A4 |

Chr5:17714713-17719564 FORWARD LENGTH=1078 |

201606

Coefficients for Vitvi07g00665.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.26307	0.5897013		0.5950498	
SlopeC	2.161511	0.1205218		0.6393992	
MeanF-MeanC	-1.52667	0.03531195	*	0.188458	
SlopeF-SlopeC	-0.228278	0.9097275		0.9999488	



7.2.19 Vitvi11g00365

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

Vitvi11g00365

15.2

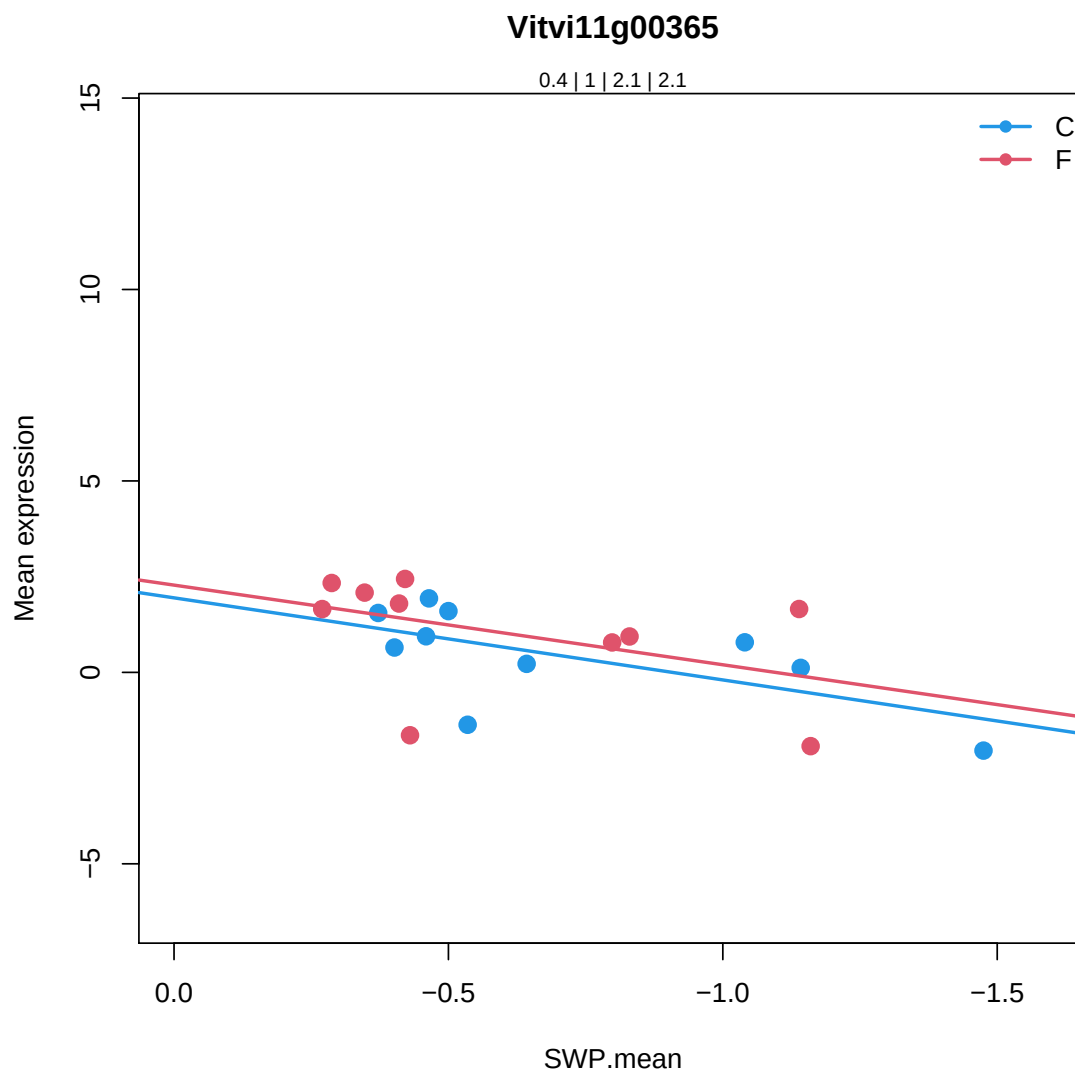
metal handling.binding, chelation and storage

[Sotub12g009040.1.1]: Metal ion binding protein [Sotub12g009040.1.1]:

[stNIB-v1_0017795]

Coefficients for Vitvi11g00365.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4387756	0.2354167		0.2407718	
SlopeC	2.144061	0.04362538	*	0.4850023	
MeanF-MeanC	0.5724837	0.2724907		0.6360341	
SlopeF-SlopeC	-0.06396351	0.9661169		0.9999488	



7.2.20 Vitvi18g01735

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

Vitvi18g01735

35.2

not assigned.unknown

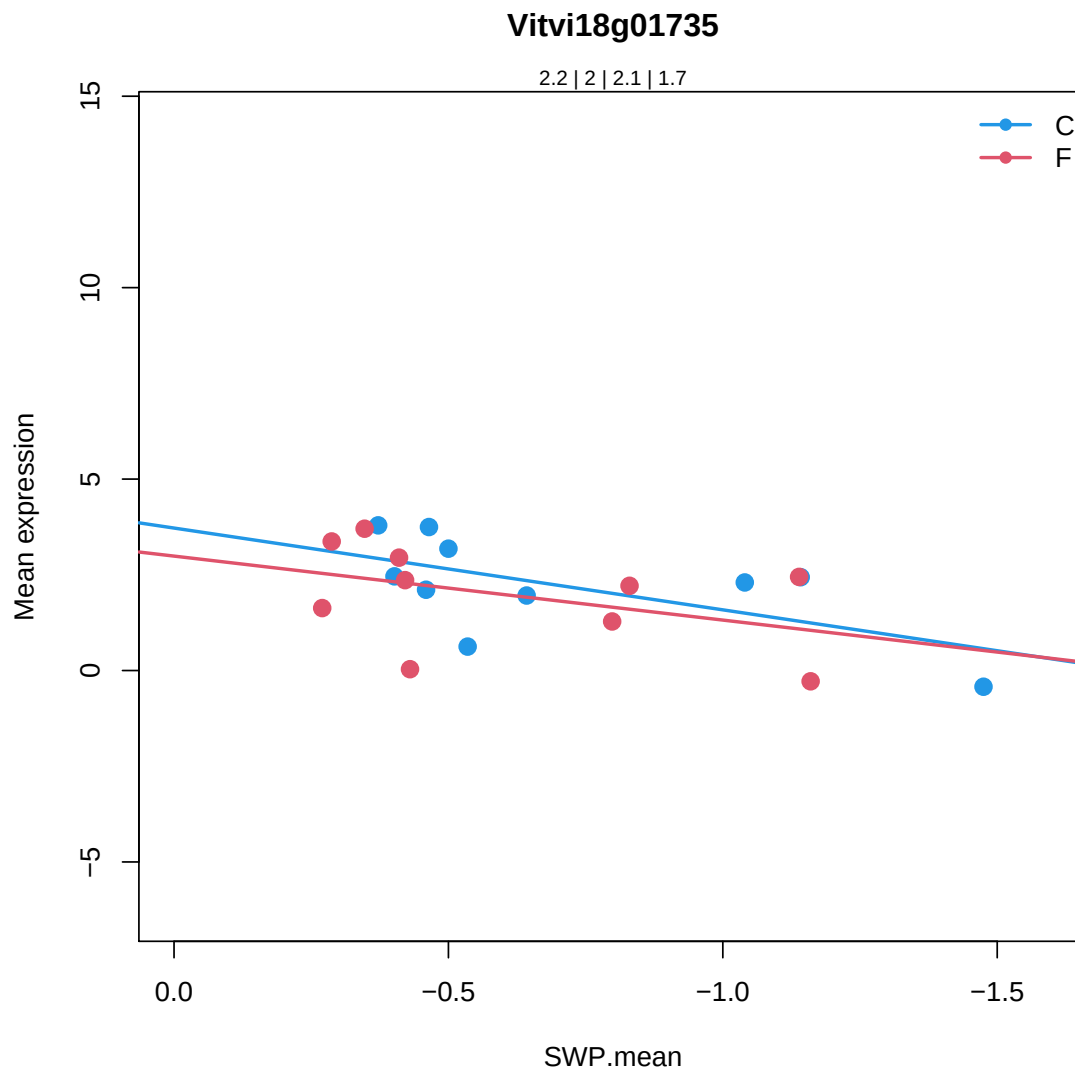
hypothetical protein |

Chr1:8025503-8026060 REVERSE LENGTH=185 |

201606

Coefficients for Vitvi18g01735.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.218754	1.174506e-06	***	1.353635e-06	***
SlopeC	2.136215	0.03083978	*	0.4322019	
MeanF-MeanC	-0.2484138	0.6024201		0.8612137	
SlopeF-SlopeC	-0.4651096	0.7385773		0.9999488	



7.2.21 Vitvi15g00812

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

Vitvi15g00812

26.7

misc.oxidases - copper, flavone etc

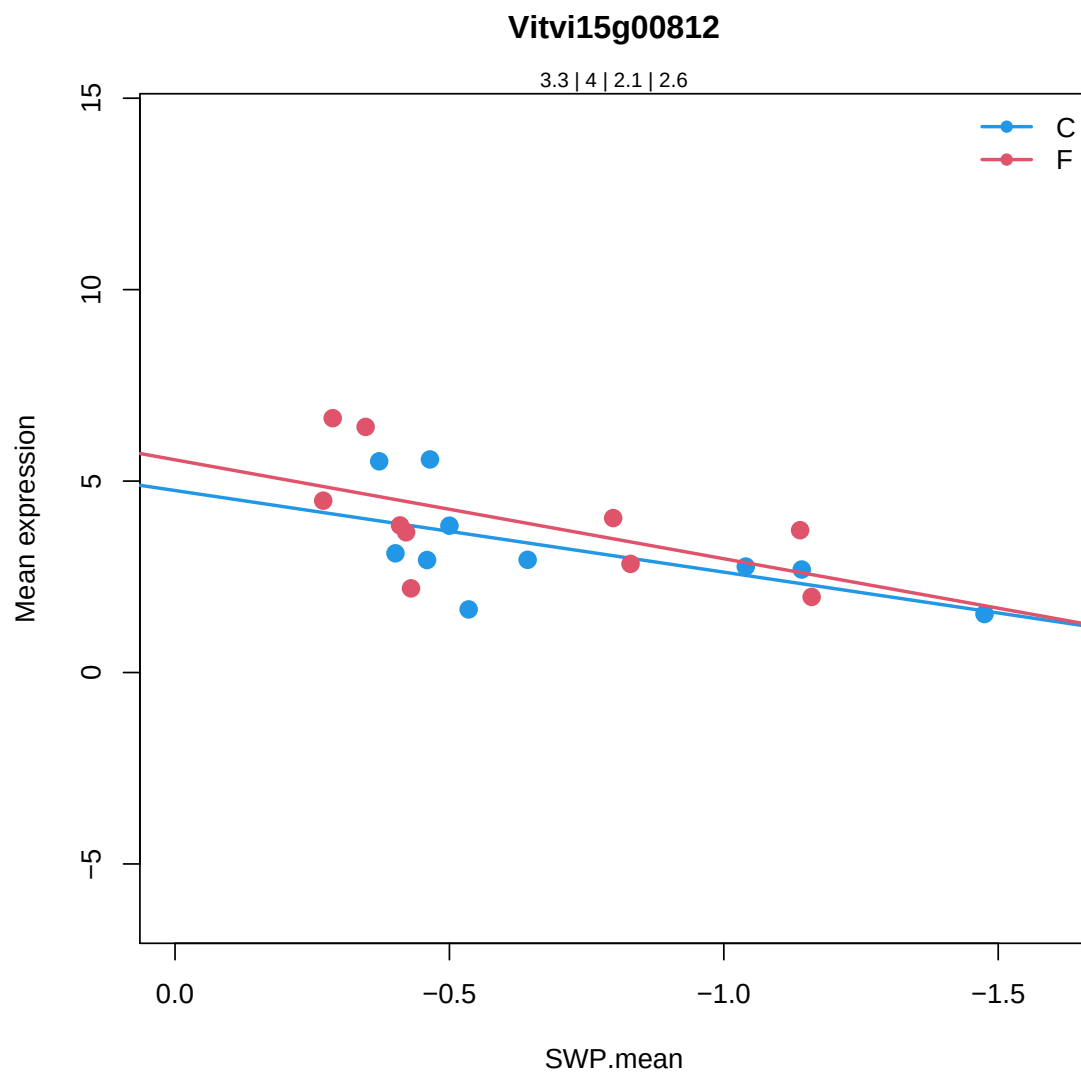
Oxidoreductase%2C zinc-binding dehydrogenase family protein |

Chr1:8398245-8399656 REVERSE LENGTH=386 |

201606

Coefficients for Vitvi15g00812.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.254347	8.246706e-09	***	1.008798e-08	***
SlopeC	2.132014	0.04382603	*	0.4861691	
MeanF-MeanC	0.7269828	0.1652003		0.4931388	
SlopeF-SlopeC	0.4515342	0.7634678		0.9999488	



7.2.22 Vitvi05g00089

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

Vitvi05g00089

10.06.2002

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

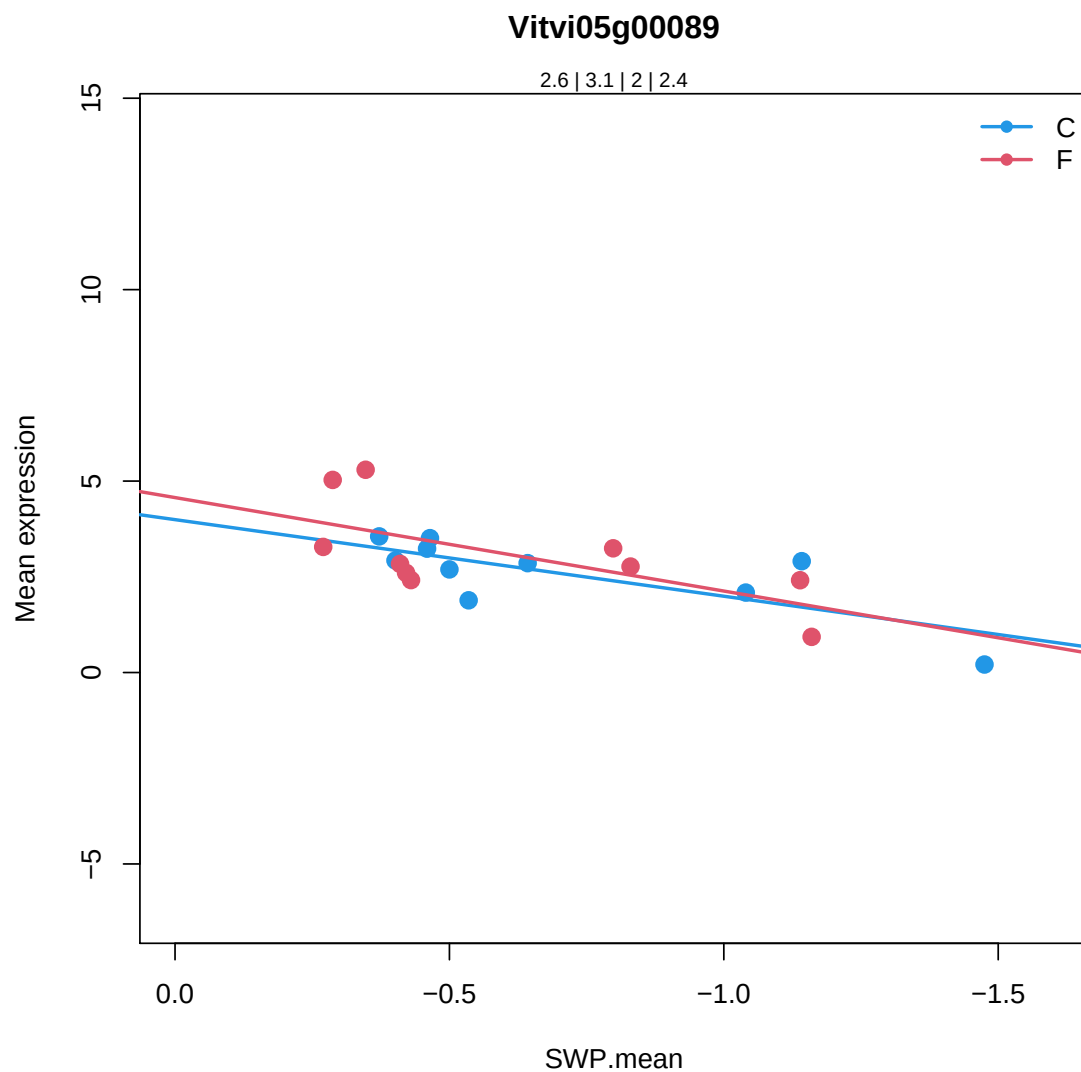
beta-xylosidase 1 |

Chr5:20012179-20016659 REVERSE LENGTH=774 |

201606

Coefficients for Vitvi05g00089.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.58641	8.431286e-10	***	1.065498e-09	***
SlopeC	2.000394	0.008881079	**	0.2903326	
MeanF-MeanC	0.4950349	0.1754928		0.507769	
SlopeF-SlopeC	0.4406078	0.6744241		0.9999488	



7.2.23 Vitvi14g01899

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

Vitvi14g01899

17.02.2002

hormone metabolism.auxin.signal transduction

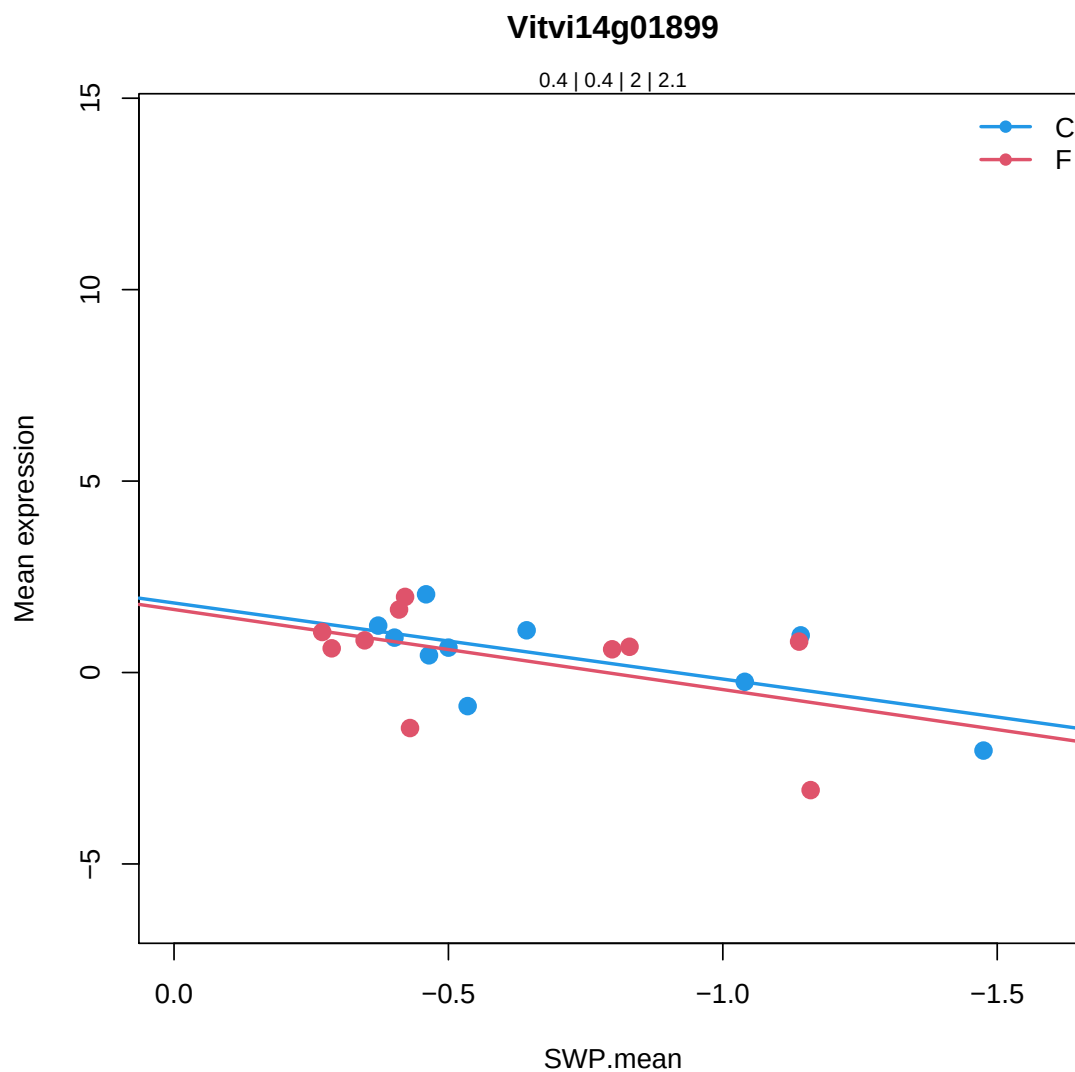
Auxin efflux carrier family protein |

Chr5:4892159-4893937 REVERSE LENGTH=367 |

201606

Coefficients for Vitvi14g01899.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4192037	0.228612		0.2339222	
SlopeC	1.986801	0.04665072	*	0.4955054	
MeanF-MeanC	-0.04772652	0.9214517		0.9796658	
SlopeF-SlopeC	0.1041887	0.9413919		0.9999488	



7.2.24 Vitvi05g01743

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

Vitvi05g01743

35.2

not assigned.unknown

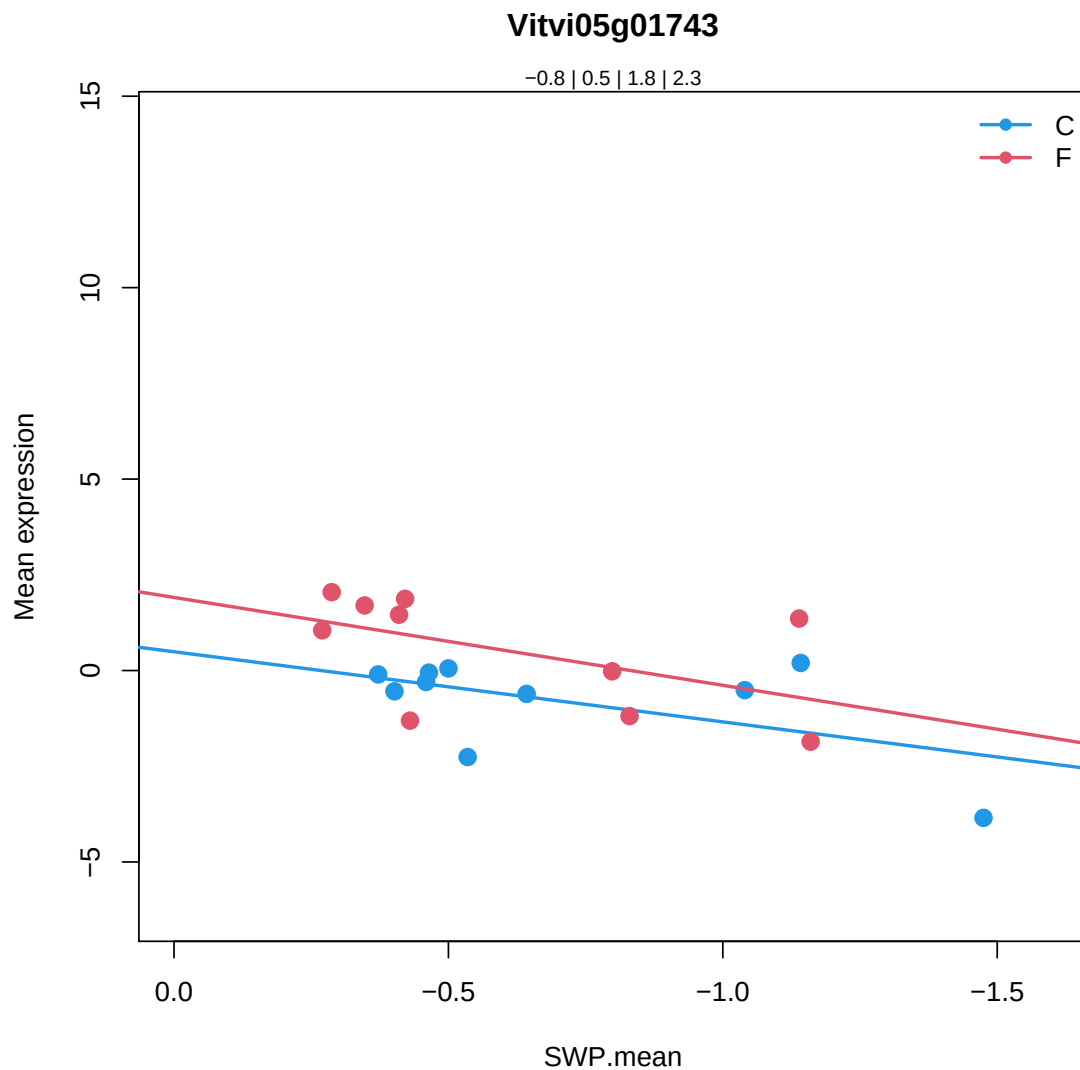
hypothetical protein |

Chr3:2156930-2157624 FORWARD LENGTH=187 |

201606

Coefficients for Vitvi05g01743.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.797796	0.03105648	*	0.03249333	*
SlopeC	1.831631	0.07034412	.	0.5604792	
MeanF-MeanC	1.308384	0.01397497	*	0.0970417	.
SlopeF-SlopeC	0.4631932	0.7493807		0.9999488	



7.2.25 Vitvi17g01520

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

Vitvi17g01520

20.1.7.1

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

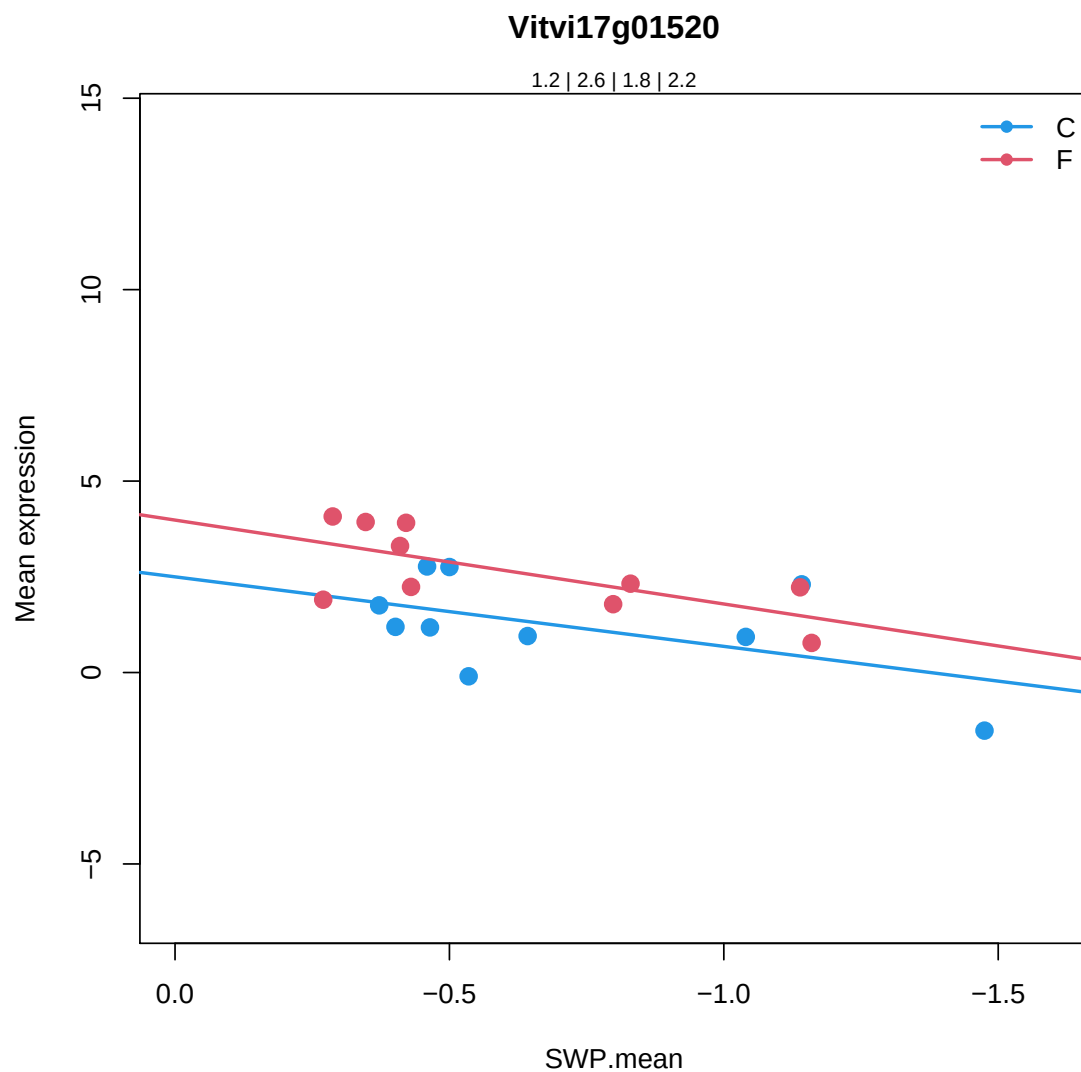
alpha/beta-Hydrolases superfamily protein |

Chr3:17755553-17757292 REVERSE LENGTH=515 |

201606

Coefficients for Vitvi17g01520.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.221775	0.0004318051	***	0.0004709533	***
SlopeC	1.815974	0.03731855	*	0.4620709	
MeanF-MeanC	1.424372	0.002485011	**	0.02626667	*
SlopeF-SlopeC	0.3752235	0.7609075		0.9999488	



7.2.26 Vitvi05g00953

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

```
Vitvi05g00953
```

```
35.2
```

```
not assigned.unknown
```

```
Pectin lyase-like superfamily protein |
```

```
Chr3:2212973-2214614 REVERSE LENGTH=383 |
```

```
201606
```

```
Vitvi05g00953
```

```
10.06.2003
```

```
cell wall.degradation.pectate lyases and polygalacturonases
```

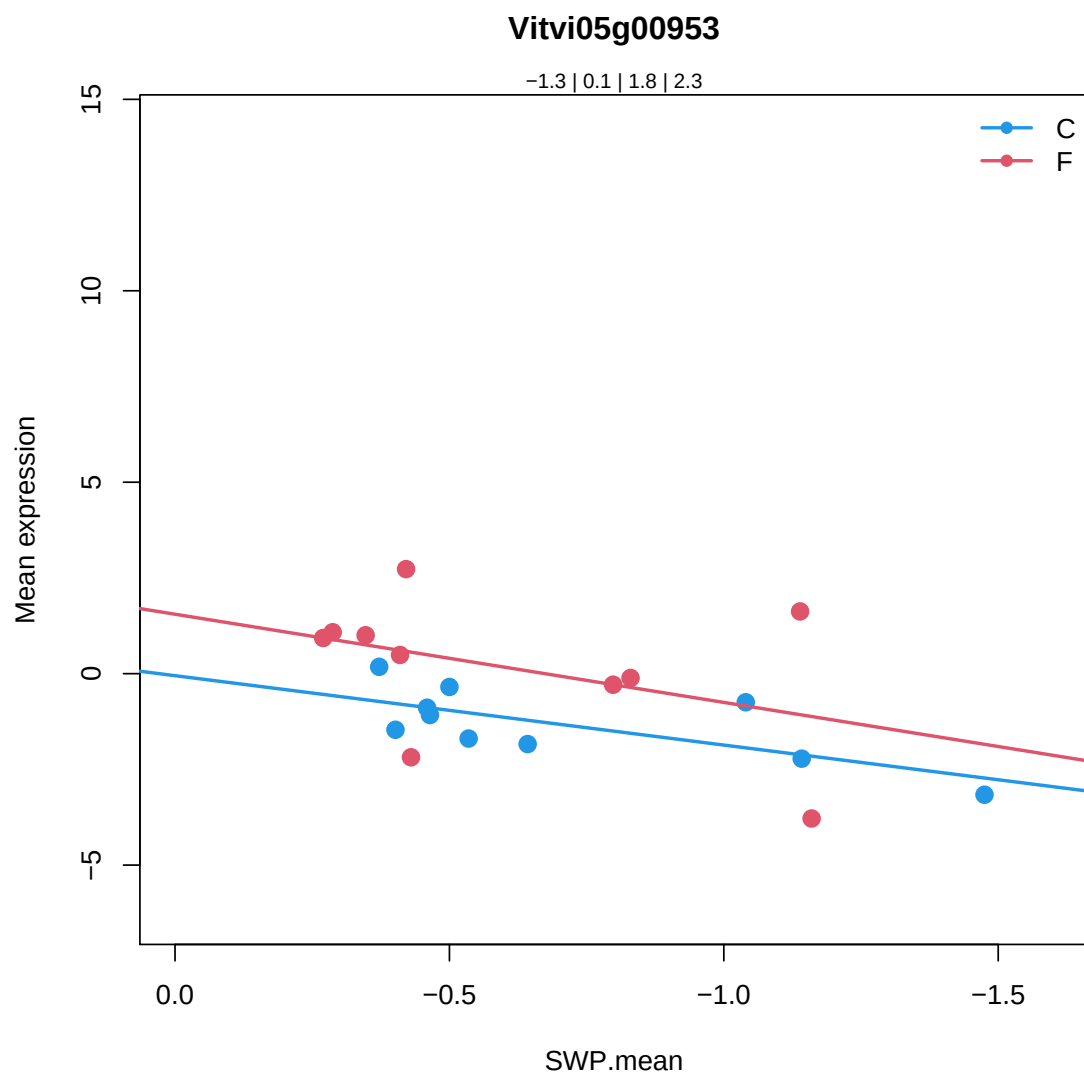
```
Pectin lyase-like superfamily protein |
```

```
Chr3:2212973-2214614 REVERSE LENGTH=383 |
```

```
201606
```

Coefficients for Vitvi05g00953.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.327067	0.002475979	**	0.002656732	**
SlopeC	1.81224	0.1070398		0.6223948	
MeanF-MeanC	1.475956	0.01340097	*	0.09434534	.
SlopeF-SlopeC	0.4911137	0.7623402		0.9999488	



7.2.27 Vitvi02g00327

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

Vitvi02g00327

31.1

cell.organisation

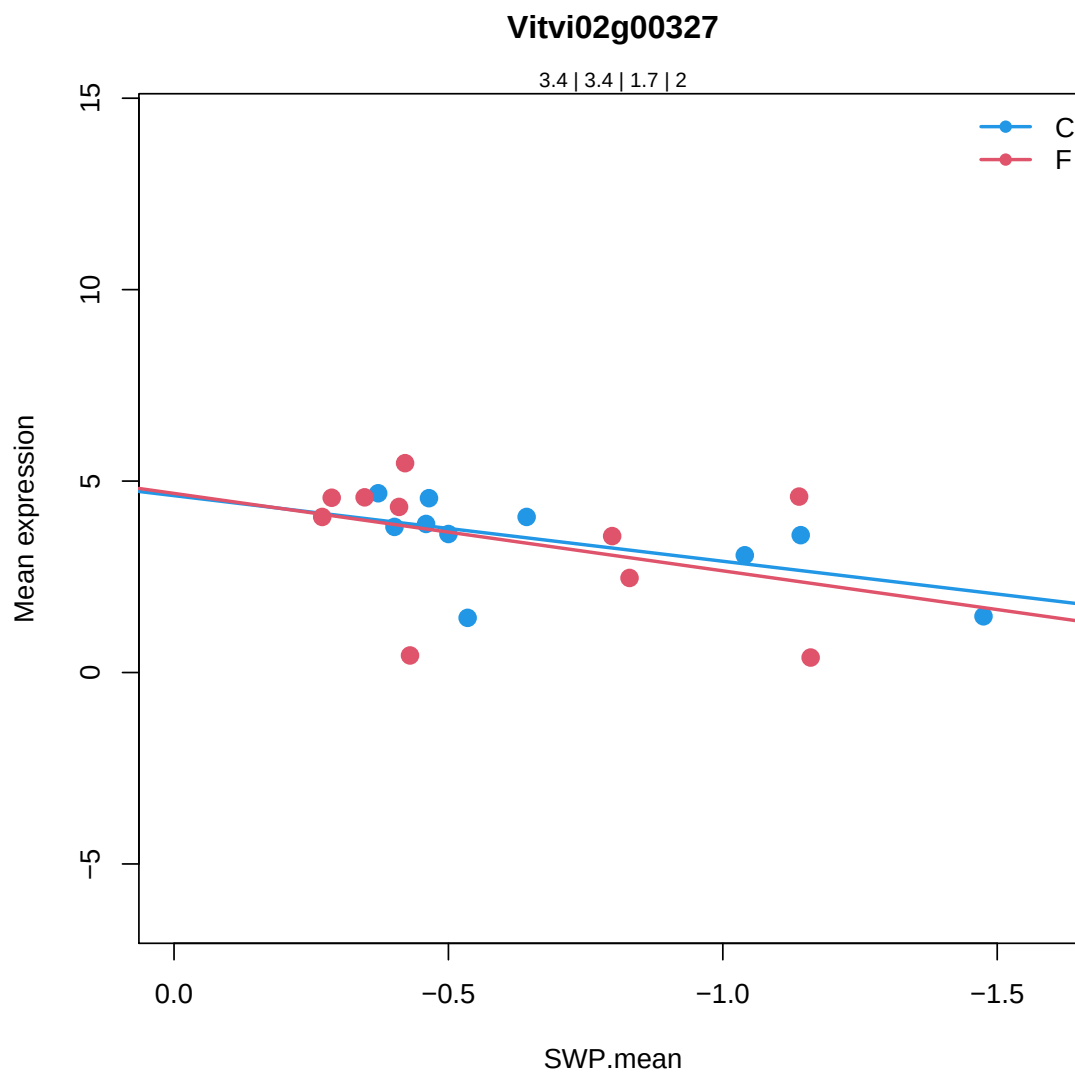
tubulin beta 8 |

Chr5:8042962-8044528 FORWARD LENGTH=449 |

201606

Coefficients for Vitvi02g00327.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.414548	1.831356e-08	***	2.218e-08	***
SlopeC	1.713415	0.1320727		0.6544384	
MeanF-MeanC	0.03133804	0.9555981		0.9897544	
SlopeF-SlopeC	0.3093124	0.8511772		0.9999488	



7.2.28 Vitvi02g01457

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

Vitvi02g01457

35.2

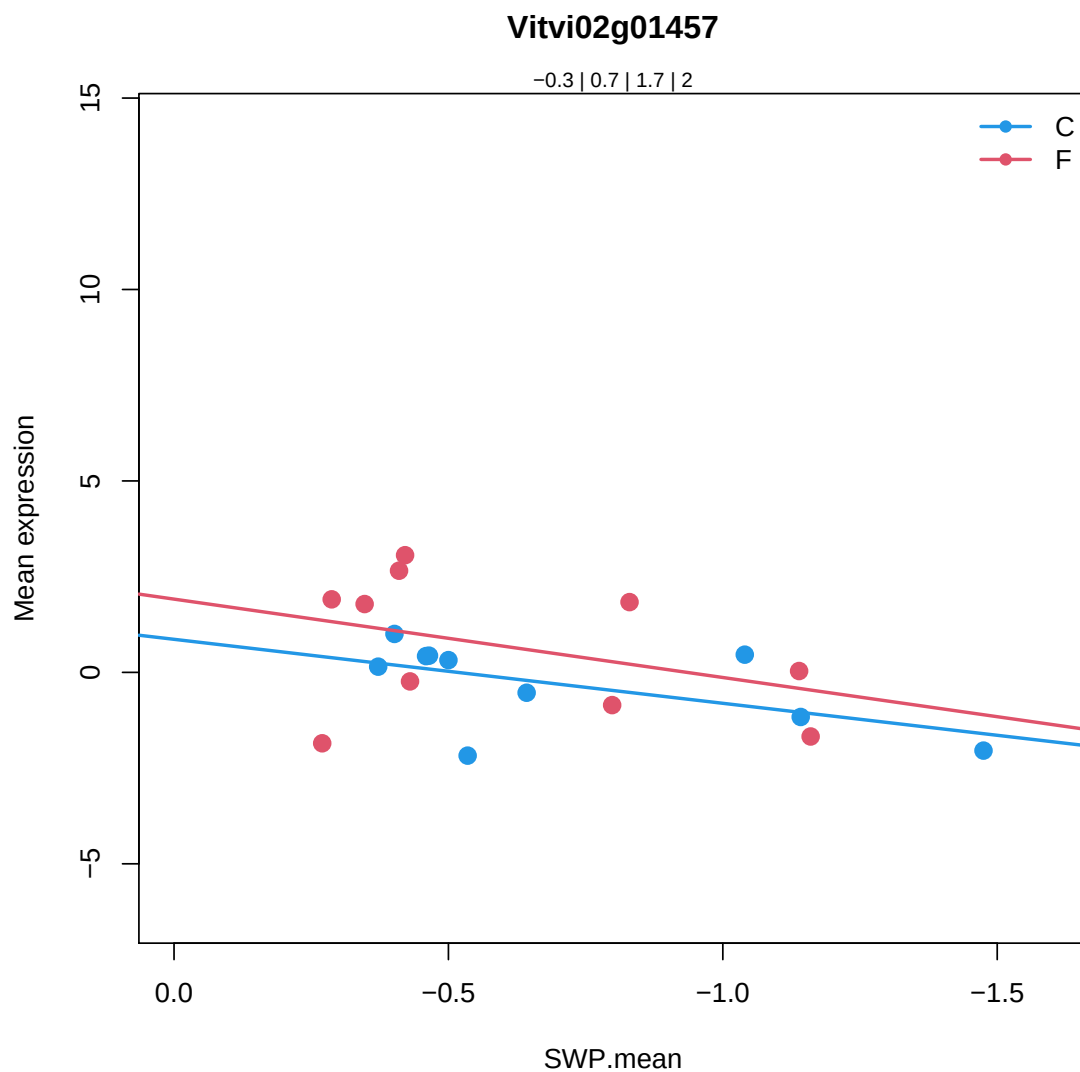
not assigned.unknown

[Sotub08g023330.1.1]: Cytochrome b [Sotub08g023340.1.1]: Unknown Prote

[stNIB-v1_0012210]

Coefficients for Vitvi02g01457.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.3118384	0.4402904		0.446471	
SlopeC	1.671346	0.1444288		0.6693663	
MeanF-MeanC	0.9776932	0.09561947	.	0.3555579	
SlopeF-SlopeC	0.3760593	0.8210411		0.9999488	



7.2.29 Vitvi13g01937

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

Vitvi13g01937

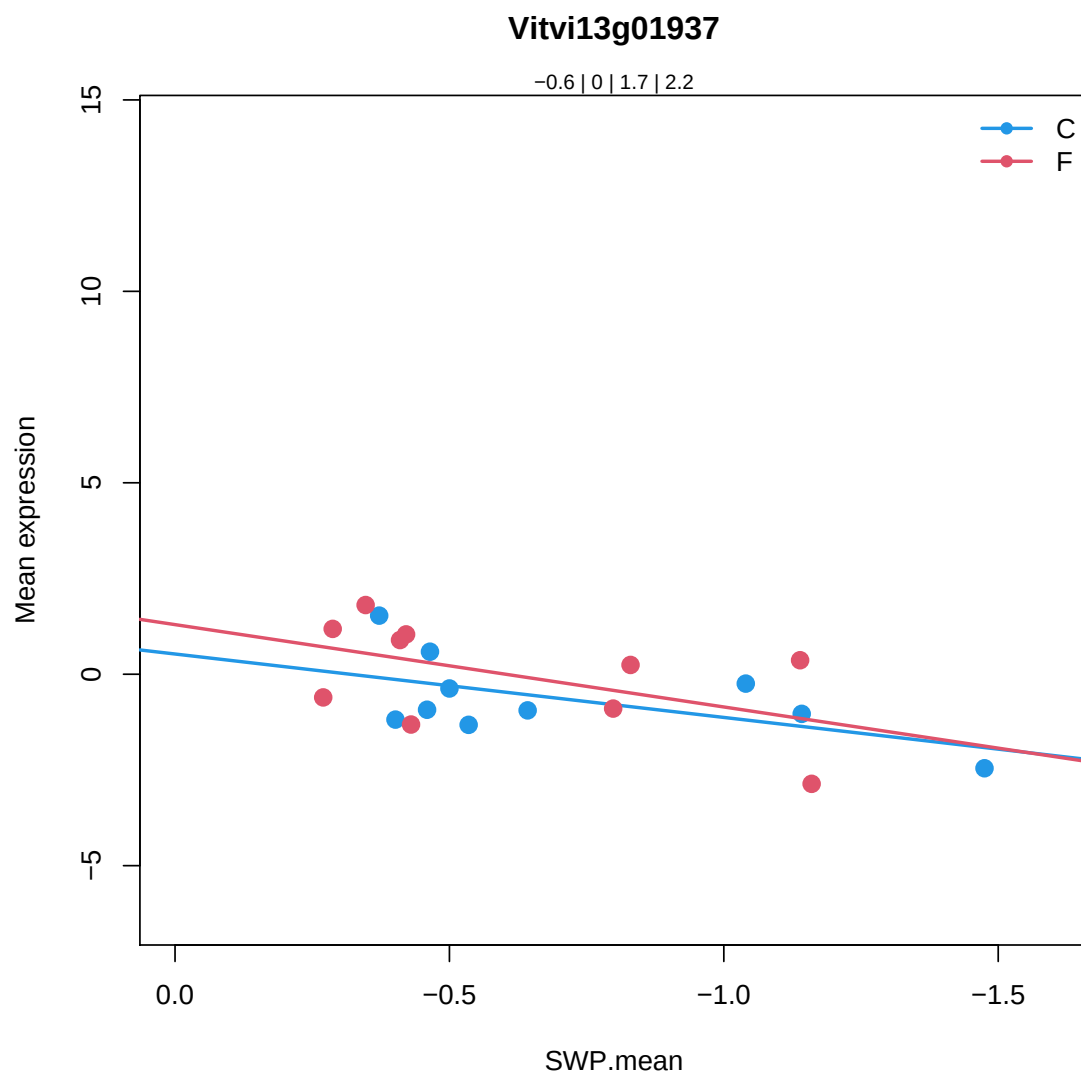
35.2

not assigned.unknown

Unknown Protein IPR007750 Protein of unknown function DUF674

Coefficients for Vitvi13g01937.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.63701	0.05704208	.	0.05931473	.
SlopeC	1.656786	0.07373898	.	0.5667824	.
MeanF-MeanC	0.6221561	0.1790991		0.5136084	
SlopeF-SlopeC	0.4941654	0.710037		0.9999488	



7.2.30 Vitvi04g01202

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

Vitvi04g01202

27.01.2020

RNA.processing.degradation dicer

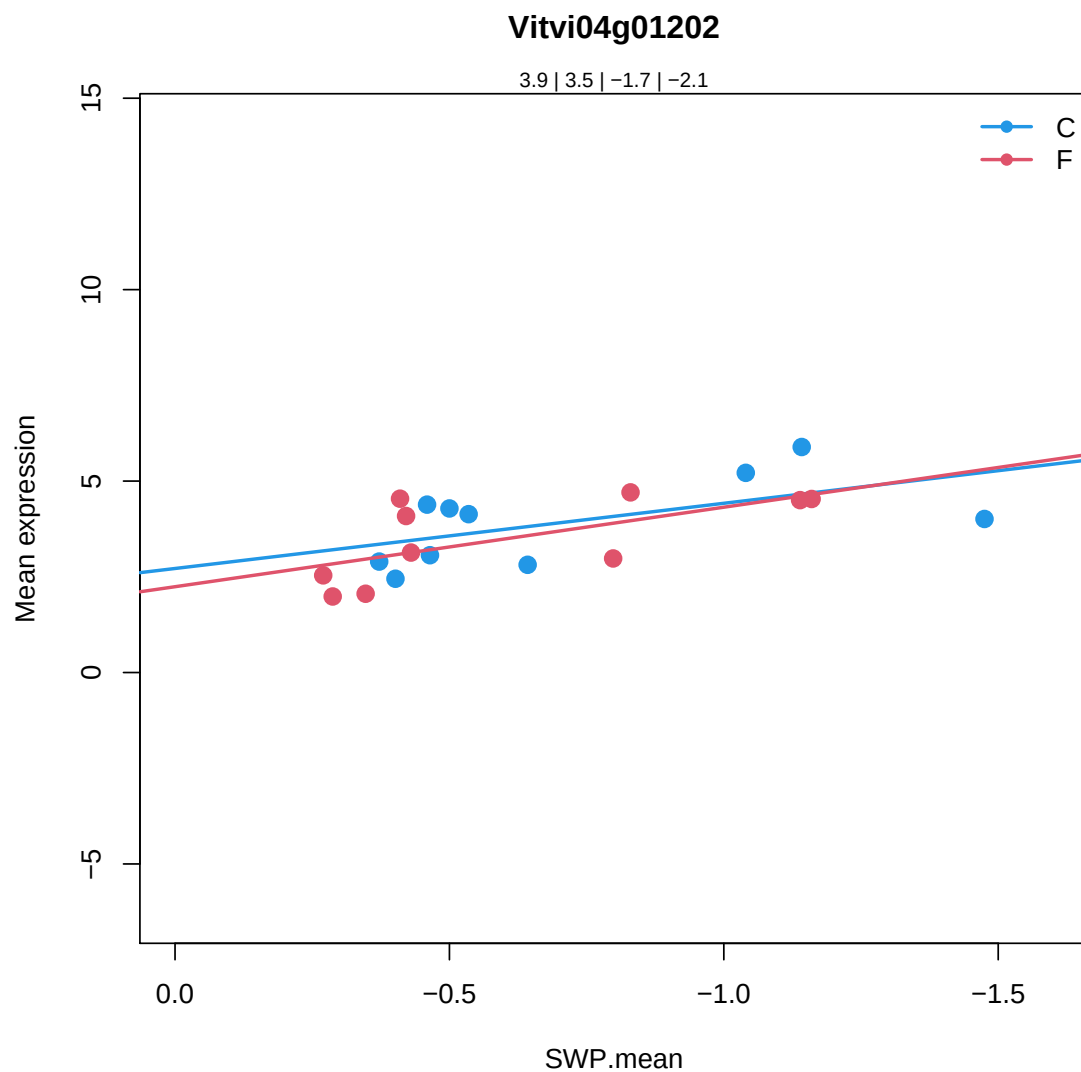
dicer-like 2 |

Chr3:768020-774525 REVERSE LENGTH=1374 |

201606

Coefficients for Vitvi04g01202.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.914467	8.449722e-13	***	1.218339e-12	***
SlopeC	-1.702794	0.02948553	*	0.4299803	
MeanF-MeanC	-0.4084844	0.2831982		0.6485007	
SlopeF-SlopeC	-0.3731589	0.7346169		0.9999488	



7.2.31 Vitvi08g02189

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

Vitvi08g02189

35.2

not assigned.unknown

heat shock cognate protein 70-1 |

Chr5:554055-556334 REVERSE LENGTH=651 |

201606

Vitvi08g02189

29.6

protein.folding

heat shock cognate protein 70-1 |

Chr5:554055-556334 REVERSE LENGTH=651 |

201606

Vitvi08g02189

20.02.2001

stress.abiotic.heat

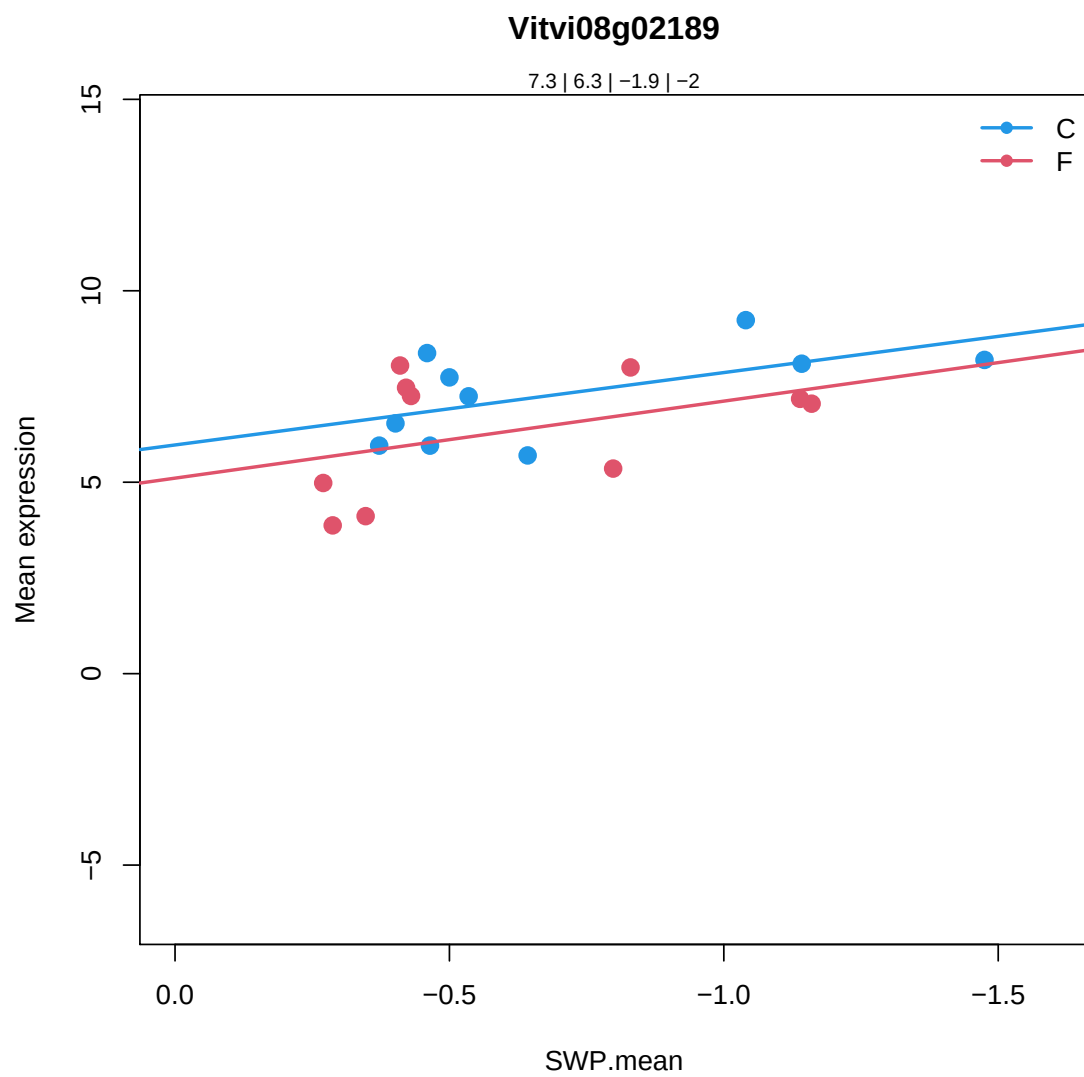
heat shock cognate protein 70-1 |

Chr5:554055-556334 REVERSE LENGTH=651 |

201606

Coefficients for Vitvi08g02189.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.302125	2.297086e-15	***	4.135623e-15	***
SlopeC	-1.890543	0.07608554	.	0.5694531	
MeanF-MeanC	-0.9706519	0.07339059	.	0.3042207	
SlopeF-SlopeC	-0.1210553	0.9368313		0.9999488	



7.2.32 Vitvi13g00255

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

Vitvi13g00255

34.19.2

transport.major intrinsic proteins.TIP

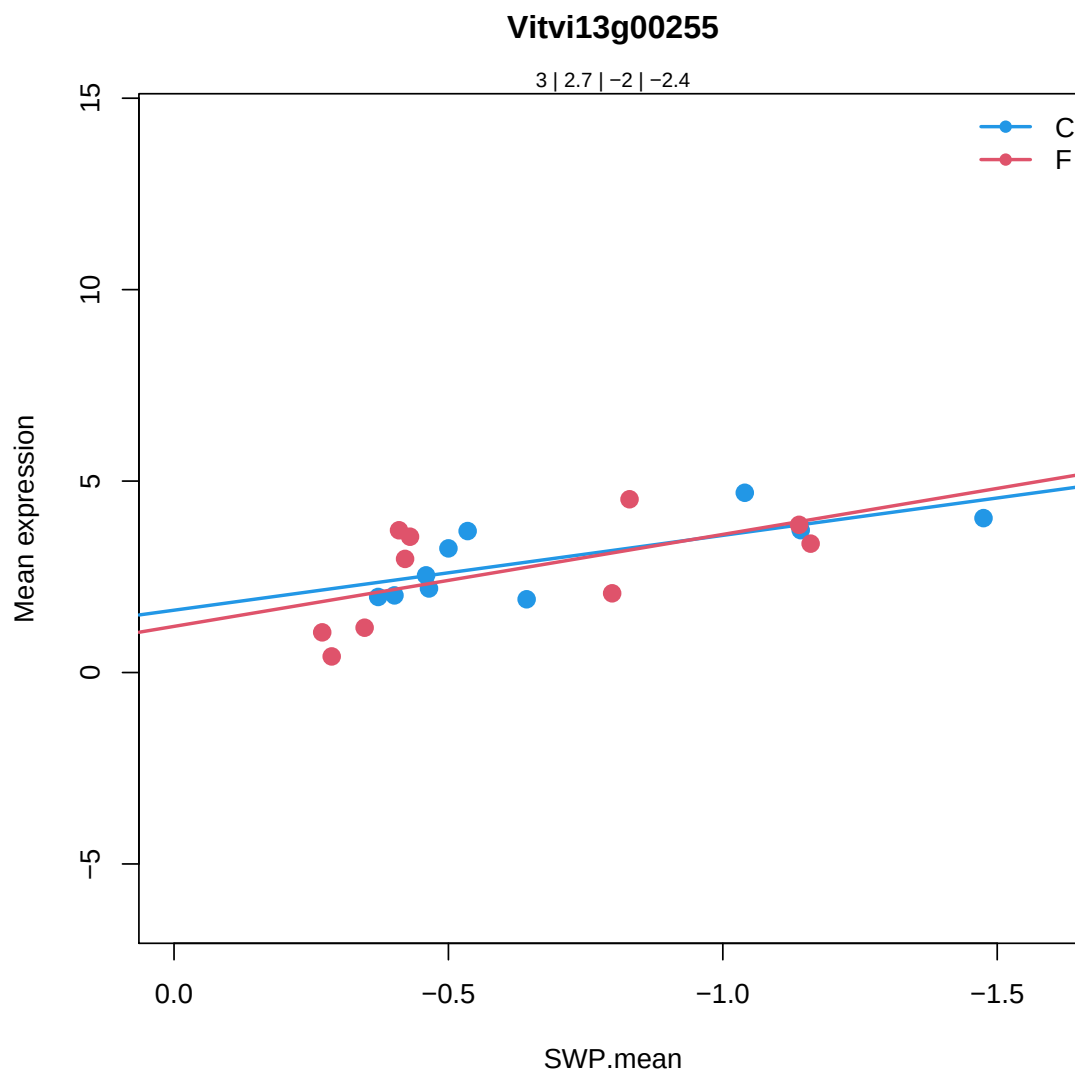
tonoplast intrinsic protein 1%3B3 |

Chr4:625092-625850 REVERSE LENGTH=252 |

201606

Coefficients for Vitvi13g00255.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.001449	4.678443e-10	***	5.969264e-10	***
SlopeC	-1.953979	0.02047822	*	0.3769674	
MeanF-MeanC	-0.3328085	0.4109846		0.7515148	
SlopeF-SlopeC	-0.4483182	0.7034636		0.9999488	



7.2.33 Vitvi06g01762

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

Vitvi06g01762

26.2

misc.UDP glucosyl and glucoronyl transferases

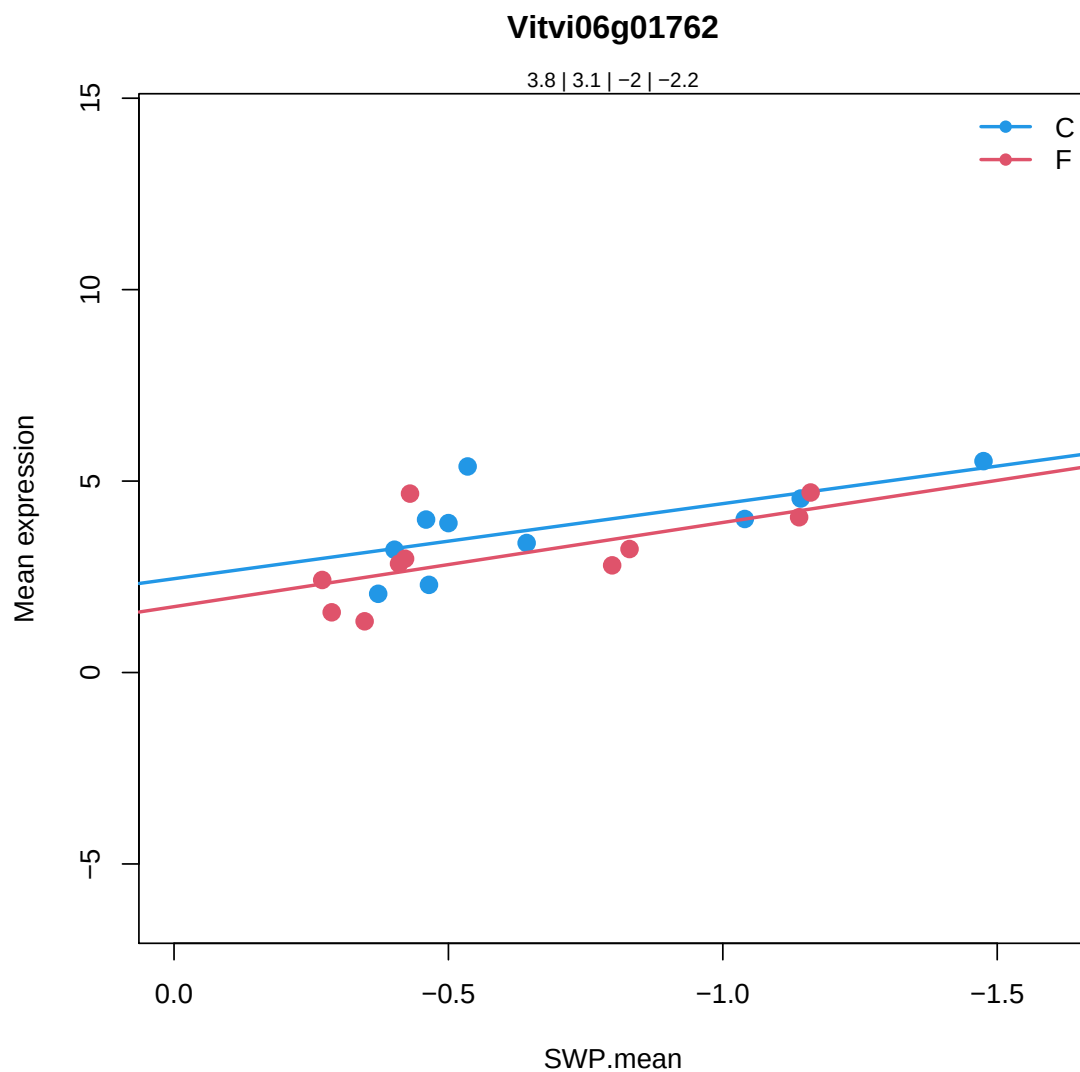
UDP-Glycosyltransferase superfamily protein |

Chr2:12872200-12873691 FORWARD LENGTH=454 |

201606

Coefficients for Vitvi06g01762.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.829051	1.707816e-12	***	2.417397e-12	***
SlopeC	-1.96081	0.0148532	*	0.3368935	
MeanF-MeanC	-0.7695267	0.05330879	.	0.2493196	
SlopeF-SlopeC	-0.2379683	0.8310348		0.9999488	



7.2.34 Vitvi11g01265

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

Vitvi11g01265

10.06.2002

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

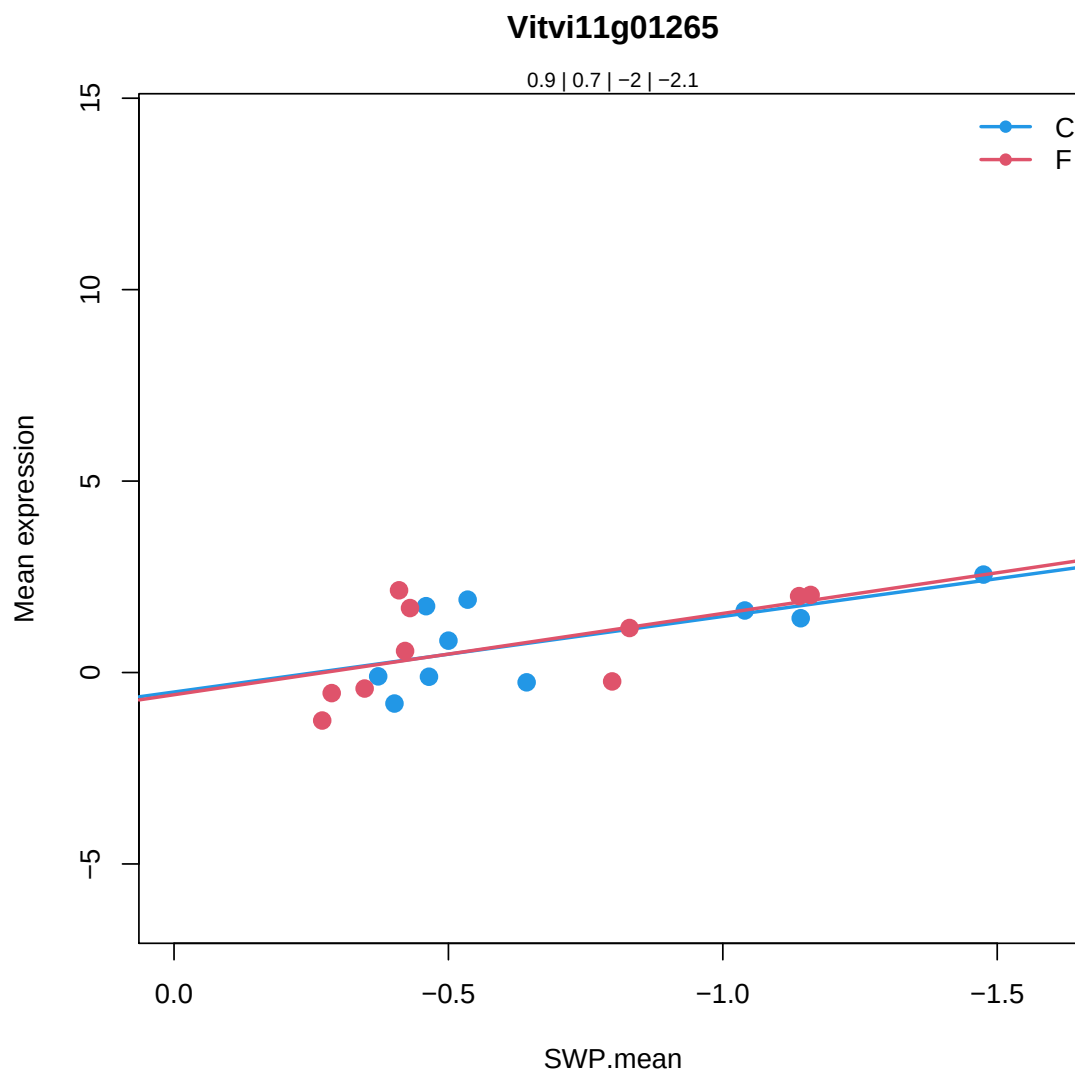
xyloglucan endotransglycosylase 6 |

Chr4:13128694-13129715 FORWARD LENGTH=286 |

201606

Coefficients for Vitvi11g01265.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8786255	0.00530675	**	0.005654745	**
SlopeC	-1.973338	0.02040242	*	0.3769378	
MeanF-MeanC	-0.1651298	0.6842467		0.89854	
SlopeF-SlopeC	-0.1505334	0.8990682		0.9999488	



7.2.35 Vitvi14g01824

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

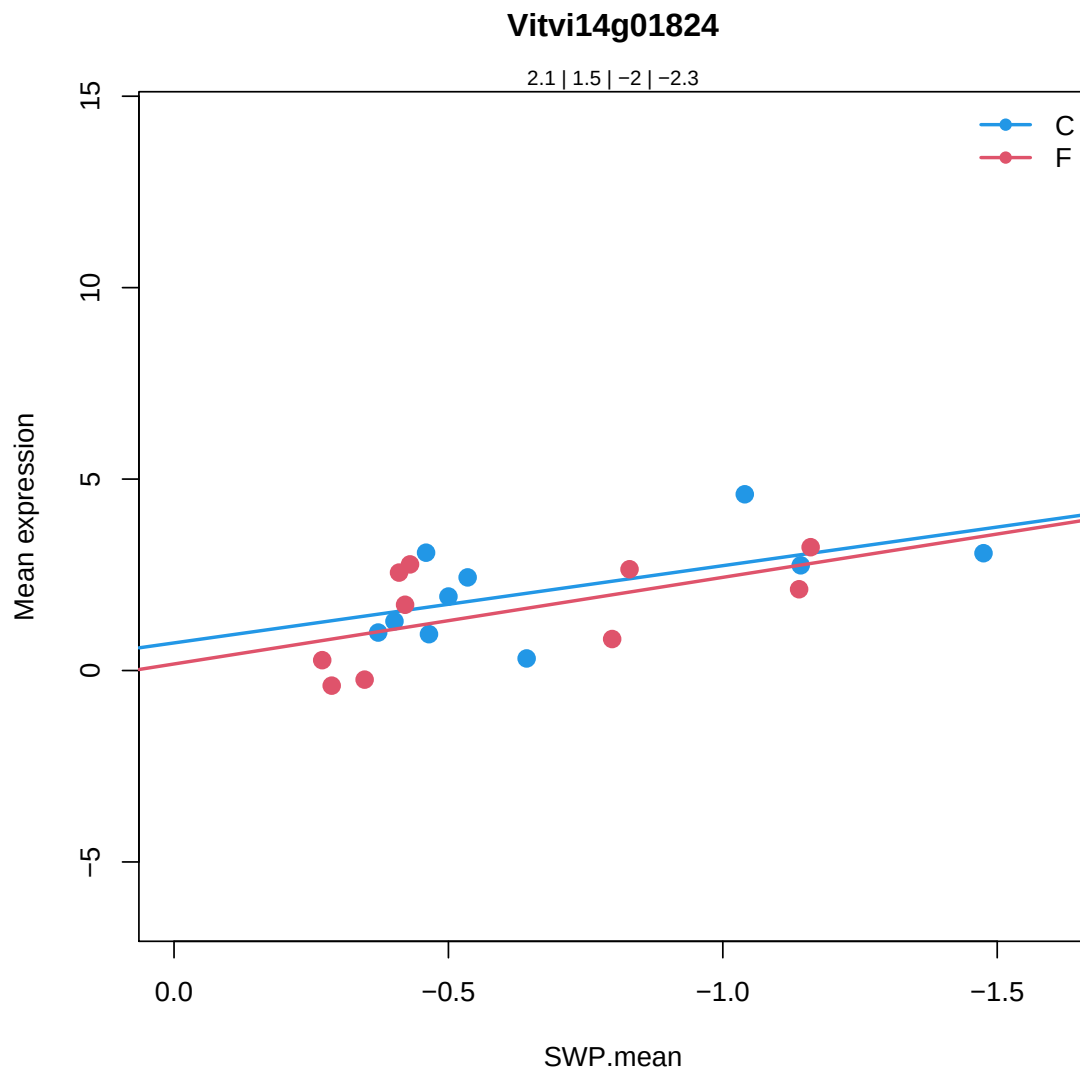
Vitvi14g01824

27.03.2011

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

Coefficients for Vitvi14g01824.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.139654	1.058859e-06	***	1.222014e-06	***
SlopeC	-2.017435	0.03297887	*	0.4417082	
MeanF-MeanC	-0.5902321	0.2034348		0.5476211	
SlopeF-SlopeC	-0.2450116	0.8542036		0.9999488	



7.2.36 Vitvi07g02753

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

Vitvi07g02753

35.2

not assigned.unknown

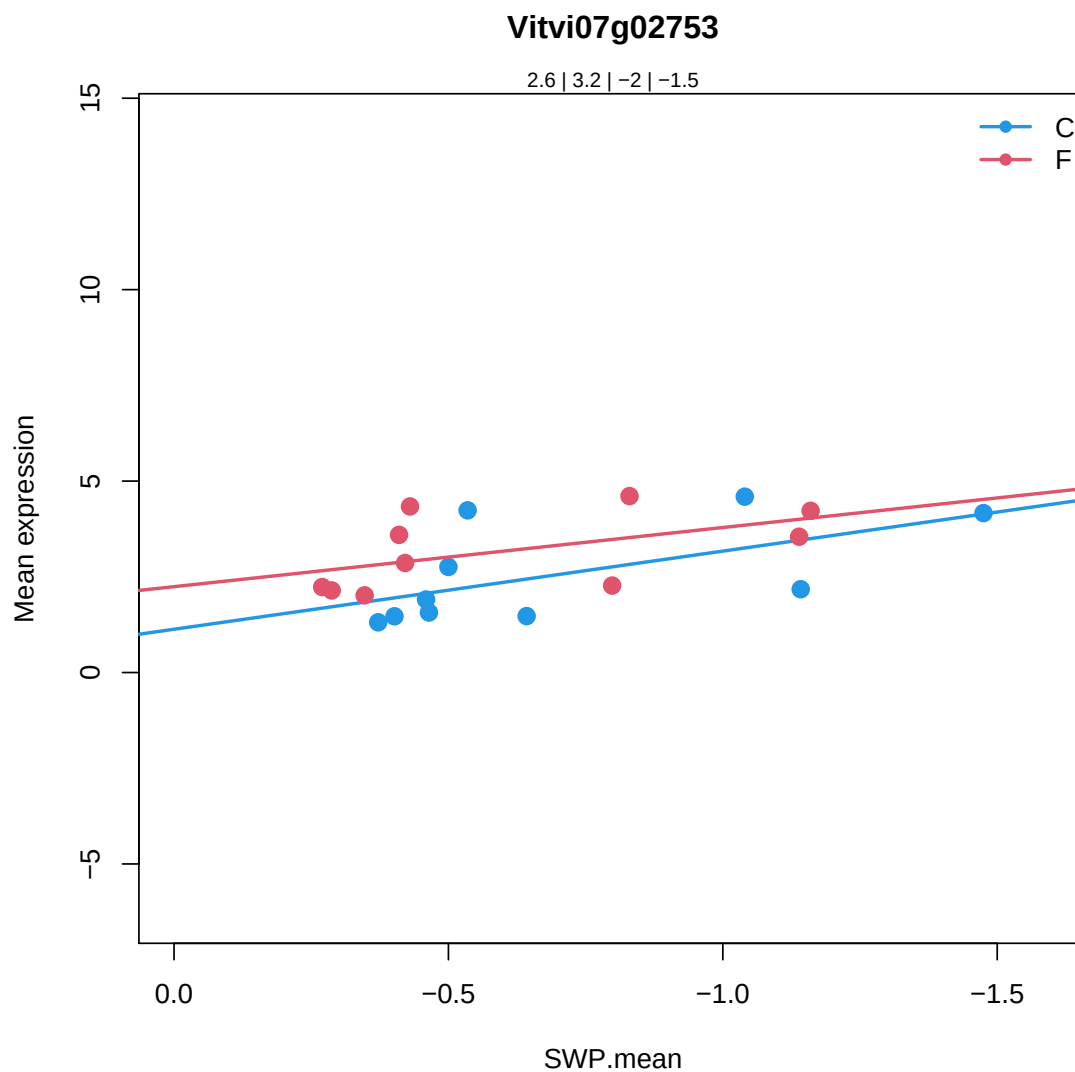
amino acid-ligase |

Chr3:2263806-2264576 REVERSE LENGTH=199 |

201606

Coefficients for Vitvi07g02753.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.56519	1.008754e-08	***	1.231315e-08	***
SlopeC	-2.040545	0.01765684	*	0.3571759	
MeanF-MeanC	0.6181004	0.1402064		0.448595	
SlopeF-SlopeC	0.4955967	0.6790587		0.9999488	



7.2.37 Vitvi13g00343

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

Vitvi13g00343

35.2

not assigned.unknown

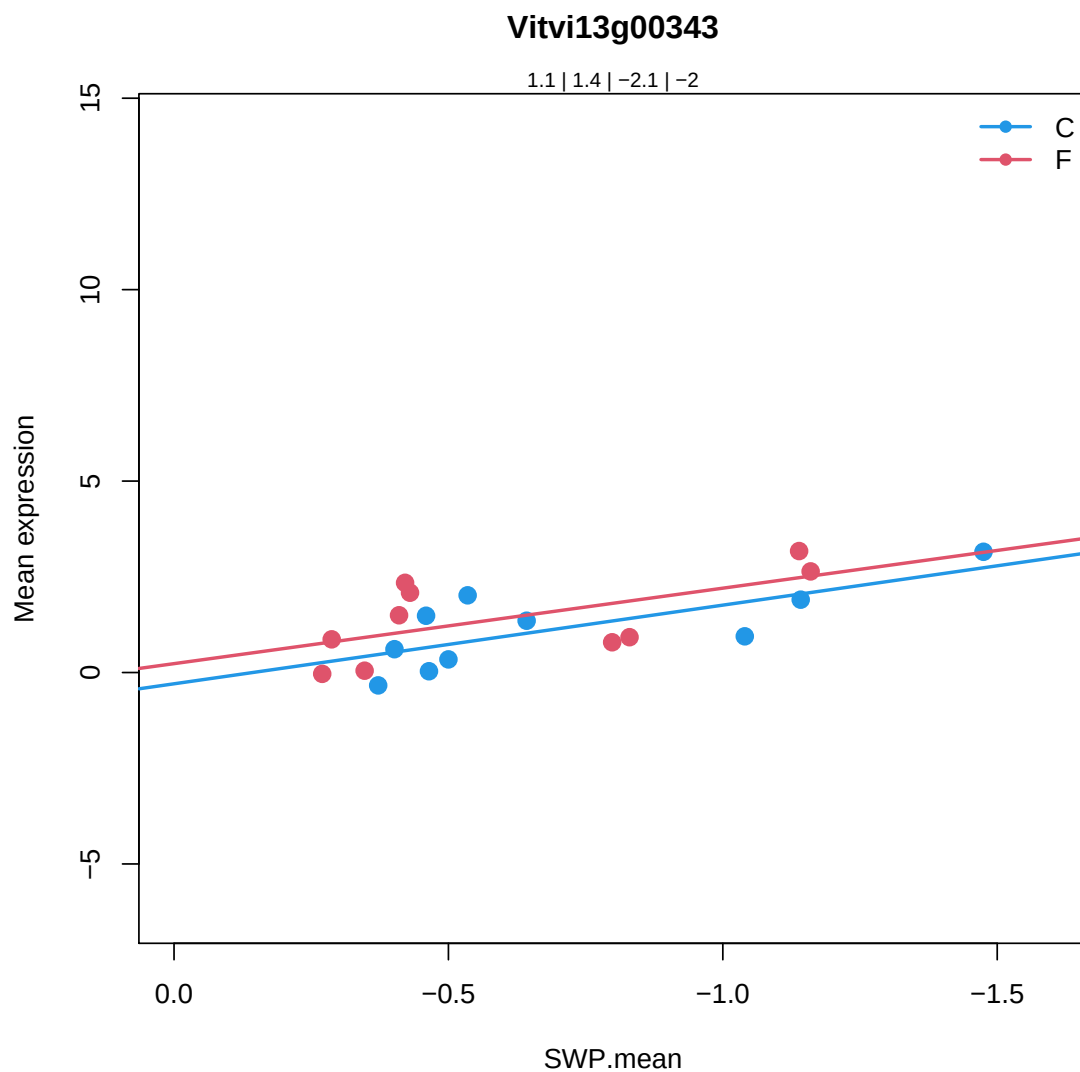
NAD(P)-binding Rossmann-fold superfamily protein |

Chr2:12582523-12583954 FORWARD LENGTH=322 |

201606

Coefficients for Vitvi13g00343.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.14993	9.794303e-05	***	0.0001081225	***
SlopeC	-2.05435	0.005803521	**	0.2626746	
MeanF-MeanC	0.2827783	0.4159279		0.7545314	
SlopeF-SlopeC	0.08342333	0.9341639		0.9999488	



7.2.38 Vitvi08g01890

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

Vitvi08g01890

3.1.2.2

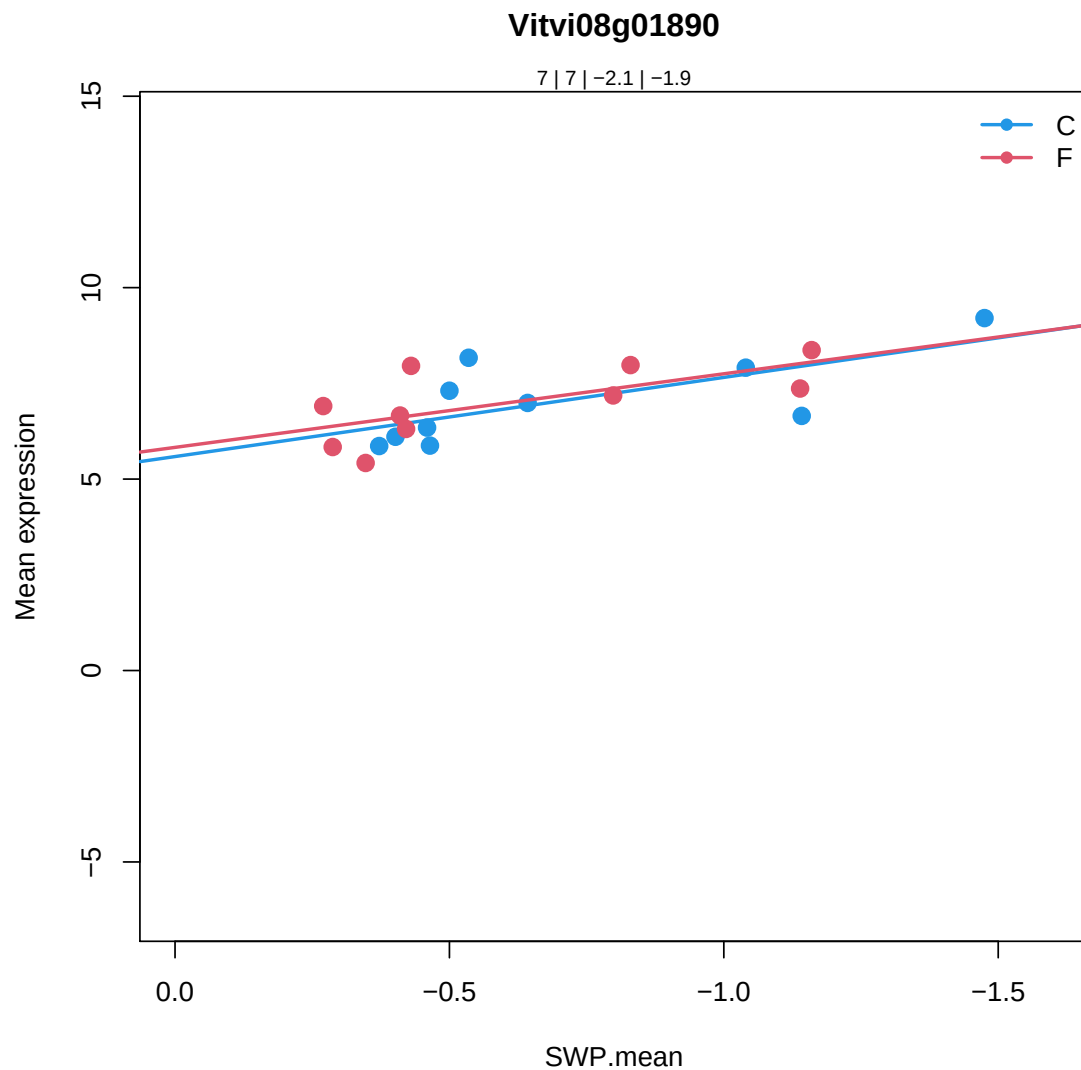
minor CHO metabolism.raffinose family.raffinose synthases.putative
seed imbibition 2 |

Chr3:21288982-21292694 REVERSE LENGTH=773 |

201606

Coefficients for Vitvi08g01890.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.041681	3.209318e-19	***	1.28999e-18	***
SlopeC	-2.067362	0.003819954	**	0.2269459	
MeanF-MeanC	-0.04310173	0.8954217		0.9727746	
SlopeF-SlopeC	0.1452297	0.8797751		0.9999488	



7.2.39 Vitvi12g02200

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

Vitvi12g02200

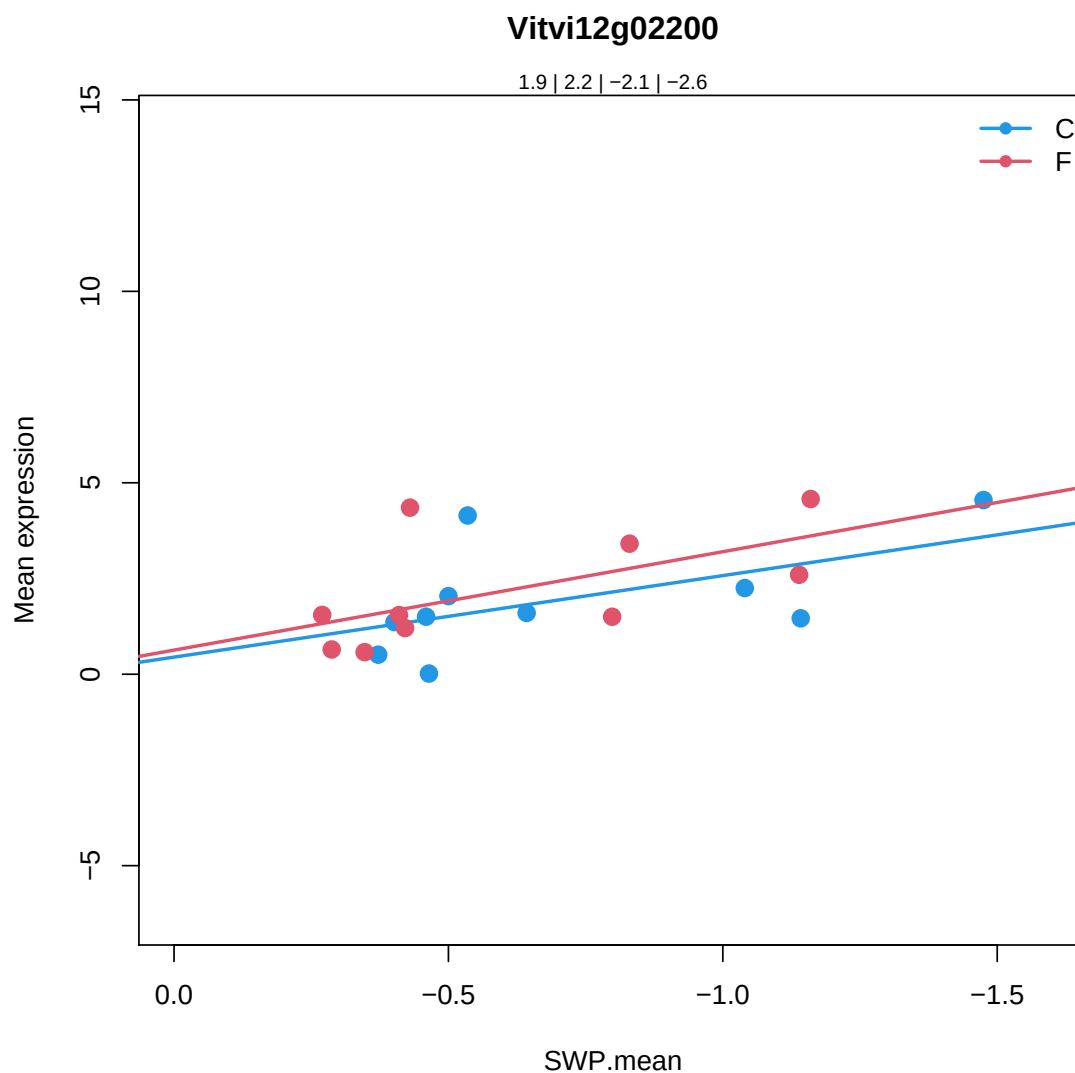
35.2

not assigned.unknown

NA

Coefficients for Vitvi12g02200.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.943816	1.461434e-05	***	1.644167e-05	***
SlopeC	-2.128876	0.039425	*	0.4699262	
MeanF-MeanC	0.251856	0.6149148		0.8669553	
SlopeF-SlopeC	-0.4414103	0.7628773		0.9999488	



7.2.40 Vitvi04g01296

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

Vitvi04g01296

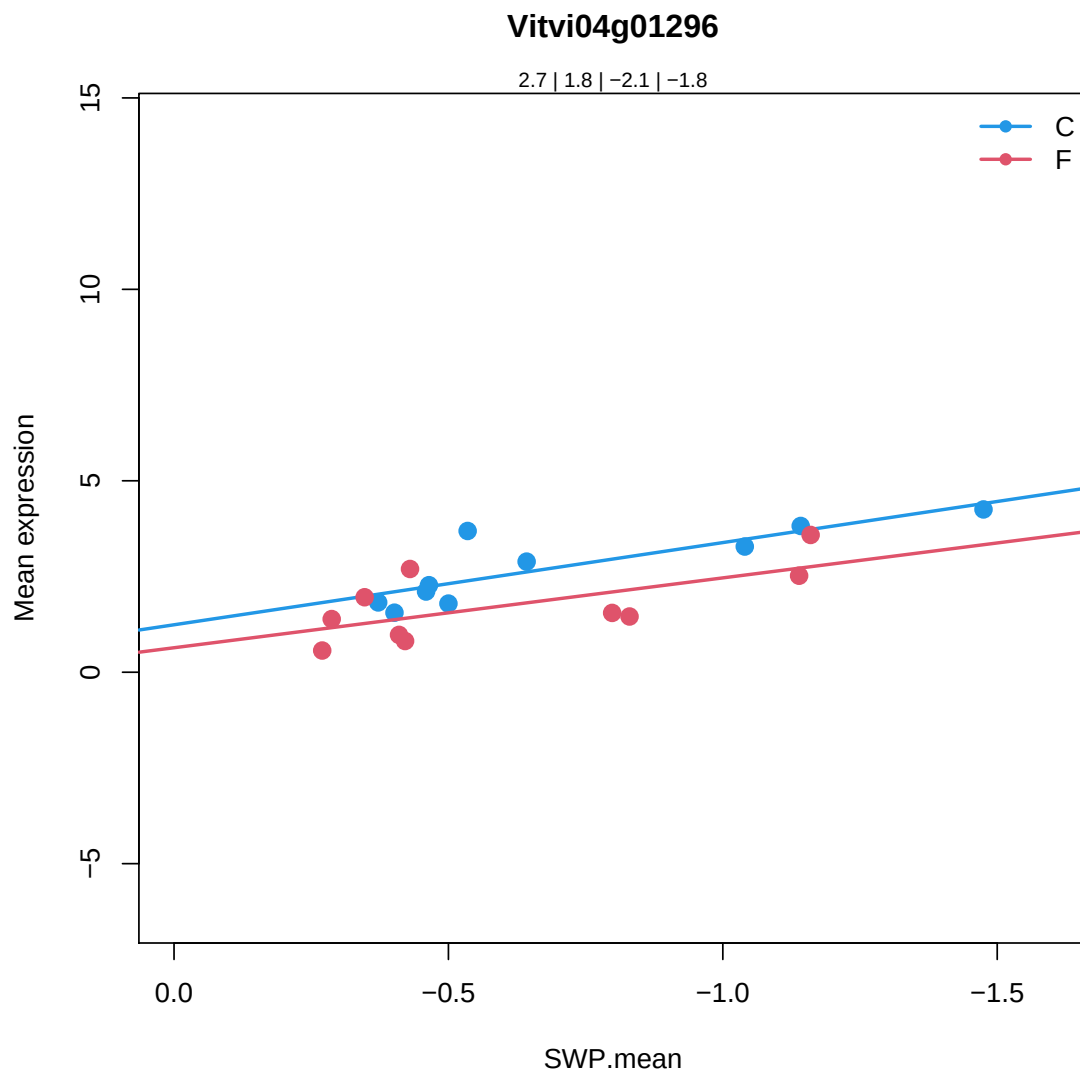
35.1

not assigned.no ontology

NA

Coefficients for Vitvi04g01296.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.74839	2.964505e-12	***	4.146934e-12	***
SlopeC	-2.146713	0.0007482566	***	0.1076608	
MeanF-MeanC	-0.9975088	0.001680168	**	0.01919724	*
SlopeF-SlopeC	0.3222407	0.6959423		0.9999488	



7.2.41 Vitvi07g02029

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

Vitvi07g02029

26.12

misc.peroxidases

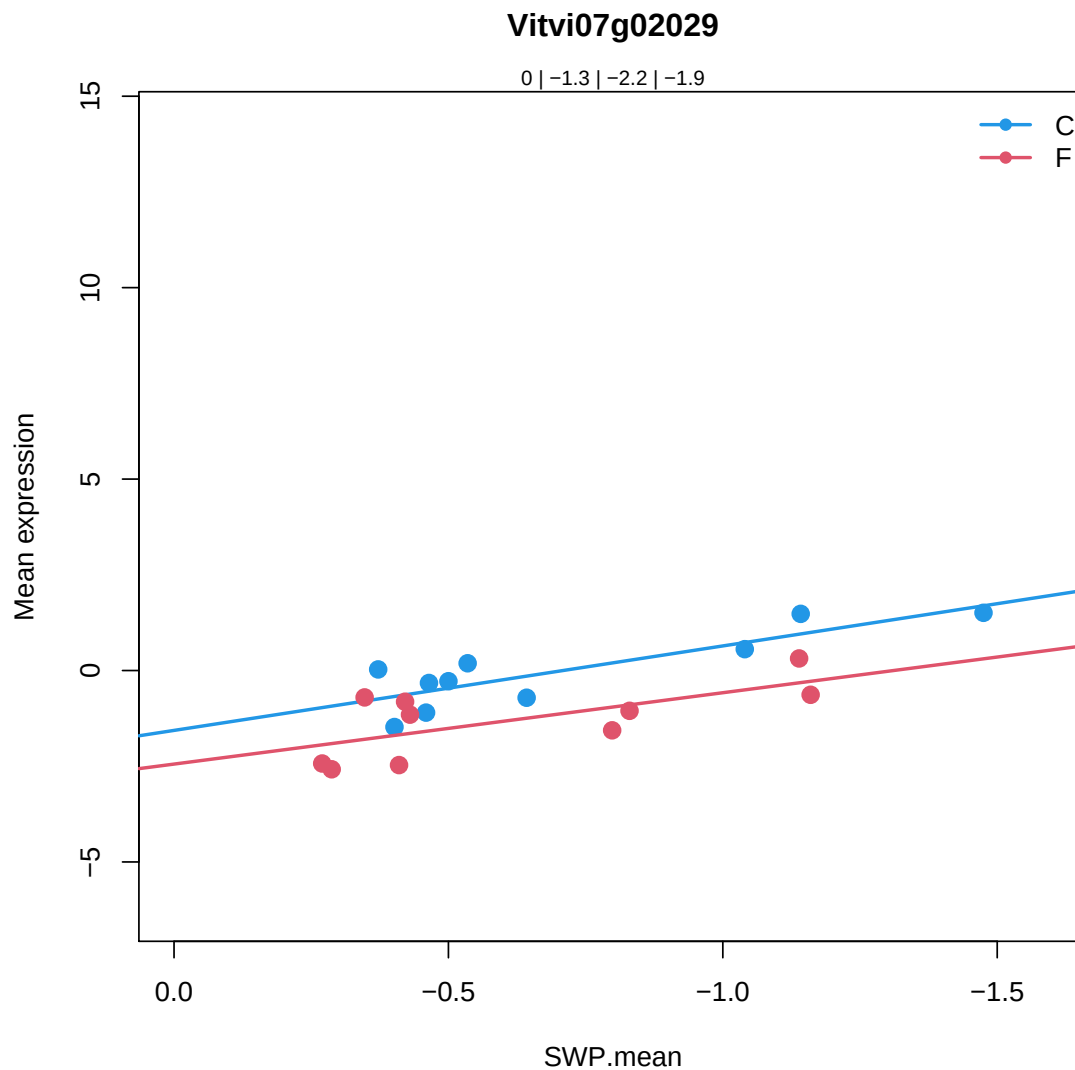
Peroxidase superfamily protein |

Chr4:16084856-16086105 FORWARD LENGTH=325 |

201606

Coefficients for Vitvi07g02029.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.01301875	0.9478156		0.9489362	
SlopeC	-2.206244	0.0005793016	***	0.1005065	
MeanF-MeanC	-1.295242	0.00012824	***	0.002228774	**
SlopeF-SlopeC	0.3426853	0.6779806		0.9999488	



7.2.42 Vitvi08g01143

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

Vitvi08g01143

21.02.2001

redox.ascorbate and glutathione.ascorbate

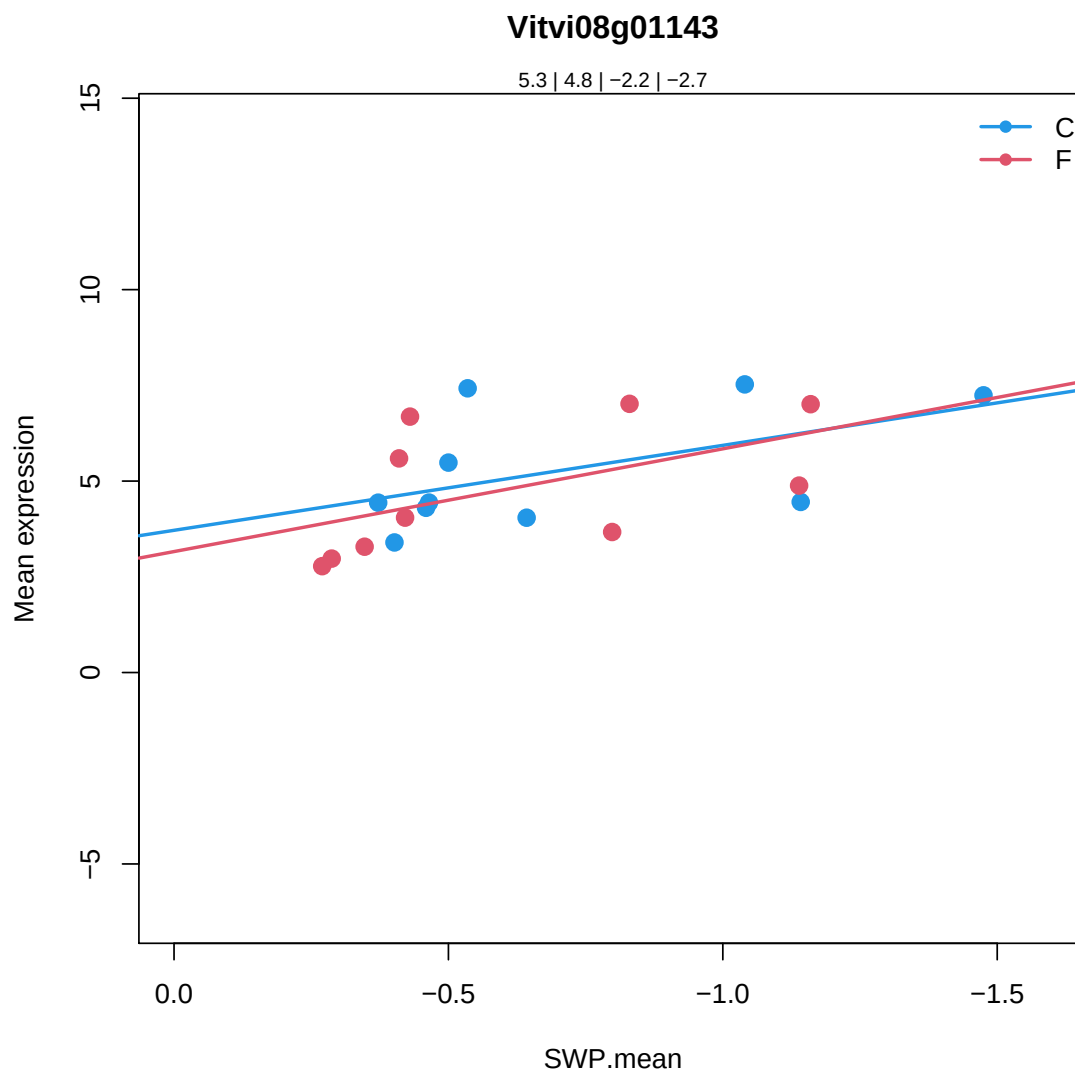
ascorbate peroxidase 2 |

Chr3:2956301-2958163 FORWARD LENGTH=251 |

201606

Coefficients for Vitvi08g01143.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.274202	9.724664e-12	***	1.328047e-11	***
SlopeC	-2.218766	0.05960803	.	0.5395912	
MeanF-MeanC	-0.4804745	0.4061604		0.7482679	
SlopeF-SlopeC	-0.4643908	0.7823844		0.9999488	



7.2.43 Vitvi15g01058

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

Vitvi15g01058

34.99

transport.misc

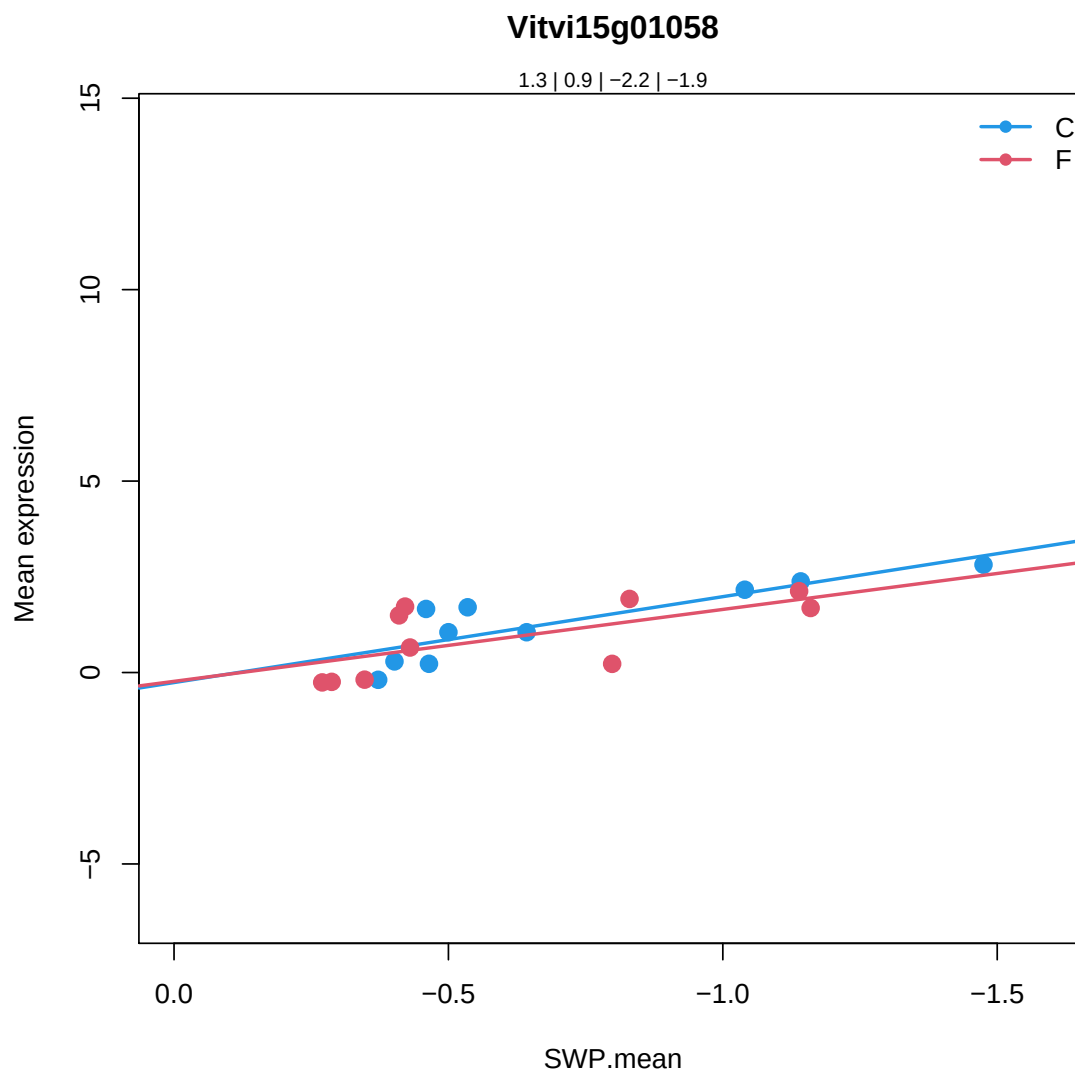
receptor-like protein kinase 4 |

Chr4:148958-151496 FORWARD LENGTH=818 |

201606

Coefficients for Vitvi15g01058.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.315457	1.50292e-06	***	1.727695e-06	***
SlopeC	-2.243262	0.0005907899	***	0.1005065	
MeanF-MeanC	-0.4016553	0.1705762		0.5001776	
SlopeF-SlopeC	0.3650419	0.6642526		0.9999488	



7.2.44 Vitvi14g02430

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

Vitvi14g02430

27.03.2025

RNA.regulation of transcription.MYB domain transcription factor family

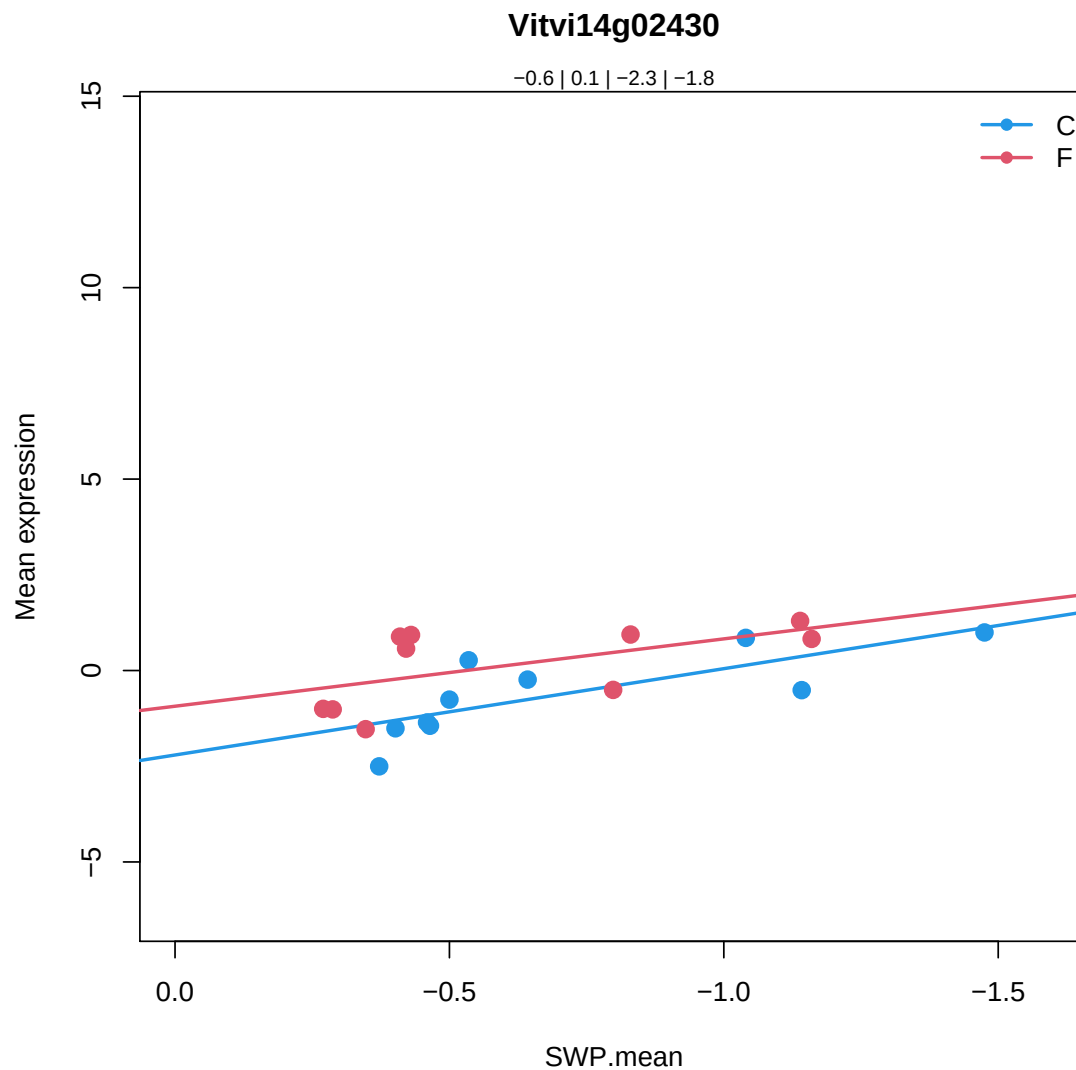
myb domain protein 43 |

Chr5:5438291-5440214 FORWARD LENGTH=327 |

201606

Coefficients for Vitvi14g02430.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.6209638	0.01722476	*	0.01813997	*
SlopeC	-2.254746	0.002837264	**	0.2035467	
MeanF-MeanC	0.7600814	0.03620843	*	0.1914287	
SlopeF-SlopeC	0.4955903	0.6238294		0.9999488	



7.2.45 Vitvi16g01167

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

Vitvi16g01167

30.2.24

signalling.receptor kinases.S-locus glycoprotein like

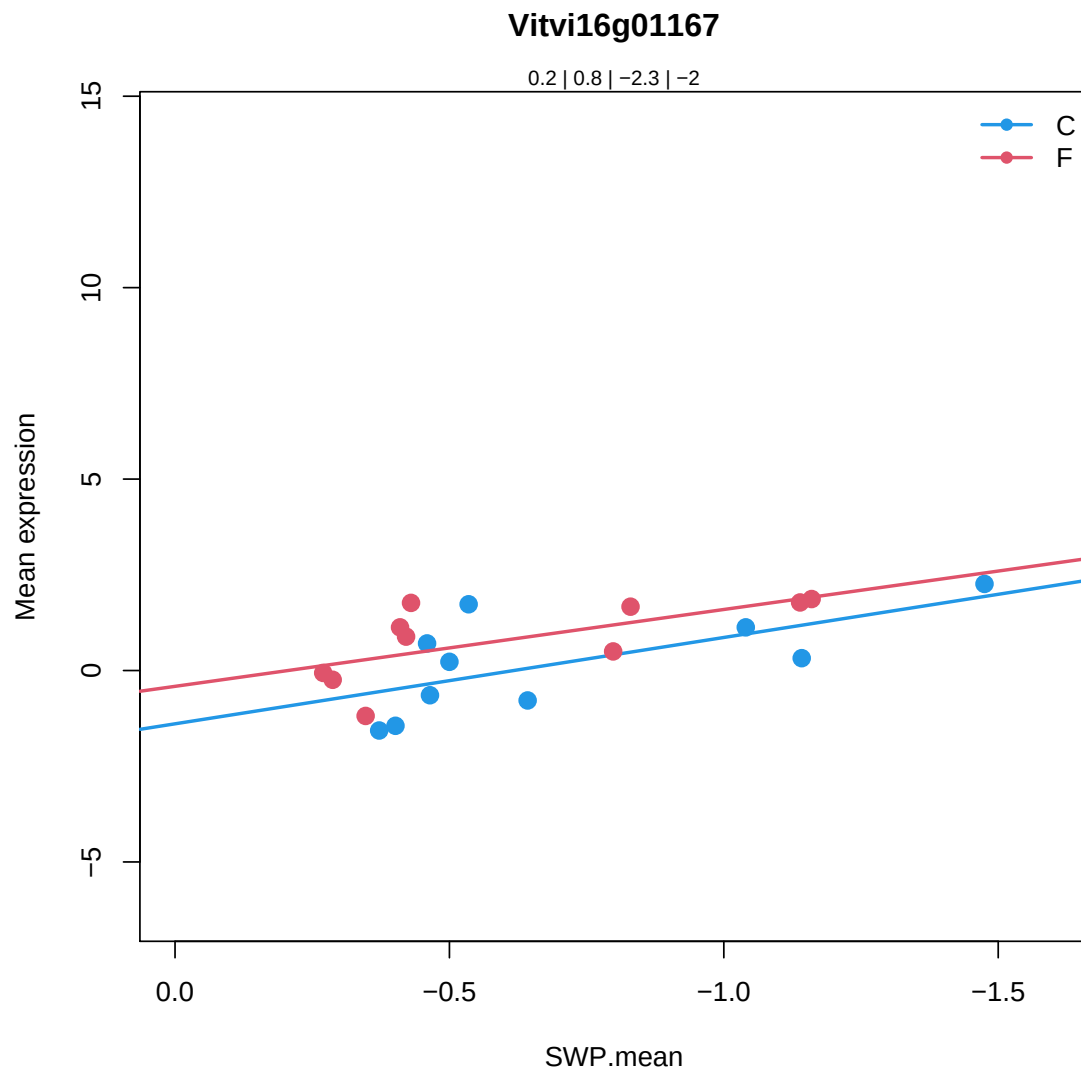
Protein kinase superfamily protein |

Chr5:8139334-8142391 REVERSE LENGTH=872 |

201606

Coefficients for Vitvi16g01167.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1937513	0.4781553		0.4843841	
SlopeC	-2.254897	0.006418653	**	0.2665752	
MeanF-MeanC	0.6160093	0.1192124		0.4059508	
SlopeF-SlopeC	0.2474672	0.8259004		0.9999488	



7.2.46 Vitvi17g00609

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

Vitvi17g00609

26.28

misc.GDSL-motif lipase

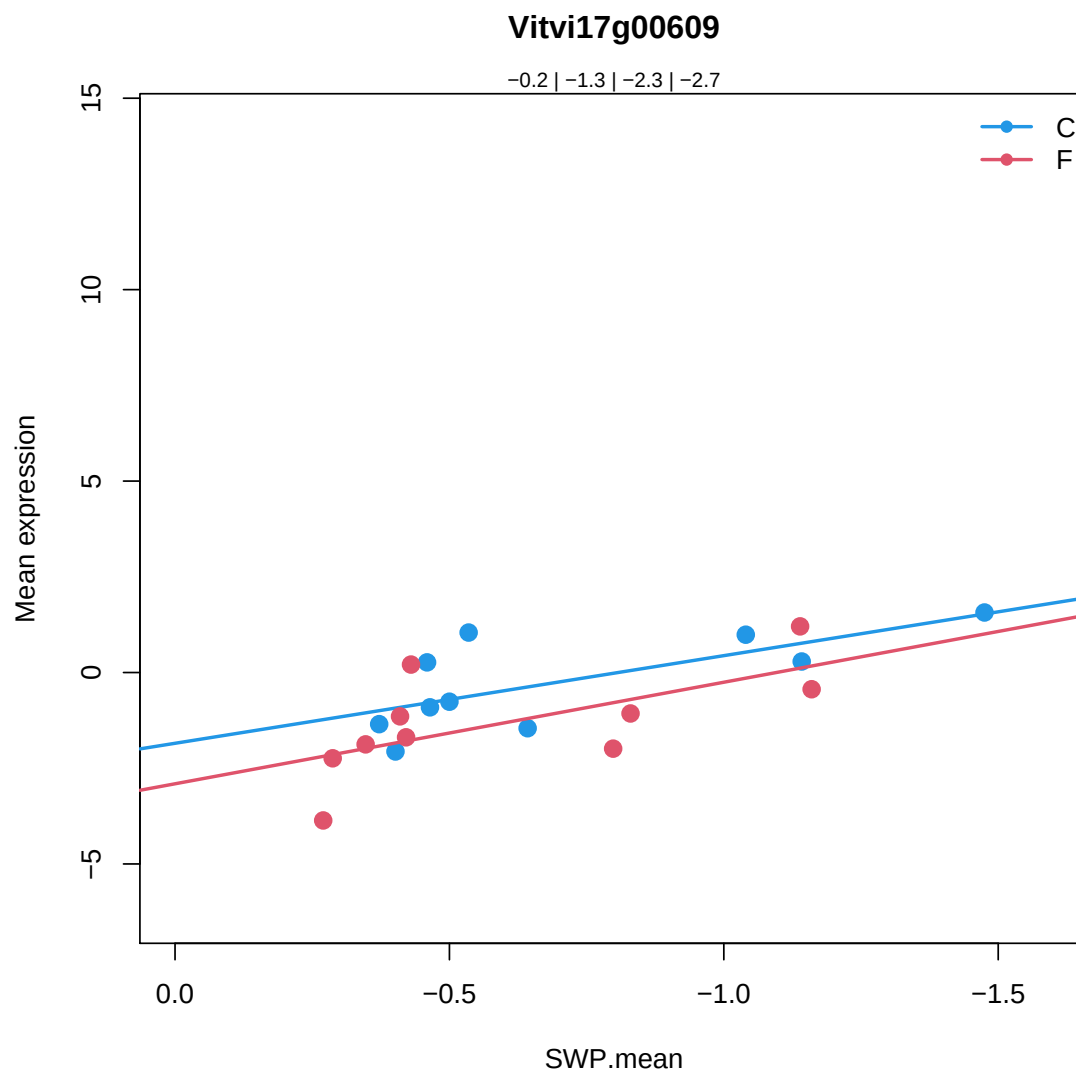
GDSL-like Lipase/Acylhydrolase superfamily protein |

Chr1:27988150-27989765 REVERSE LENGTH=366 |

201606

Coefficients for Vitvi17g00609.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.238655	0.426092		0.4321596	
SlopeC	-2.289082	0.01066502	*	0.3111585	
MeanF-MeanC	-1.051499	0.01938865	*	0.1233396	
SlopeF-SlopeC	-0.3631281	0.7684787		0.9999488	



7.2.47 Vitvi15g00763

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

Vitvi15g00763

29.05.2001

protein.degradation.subtilases

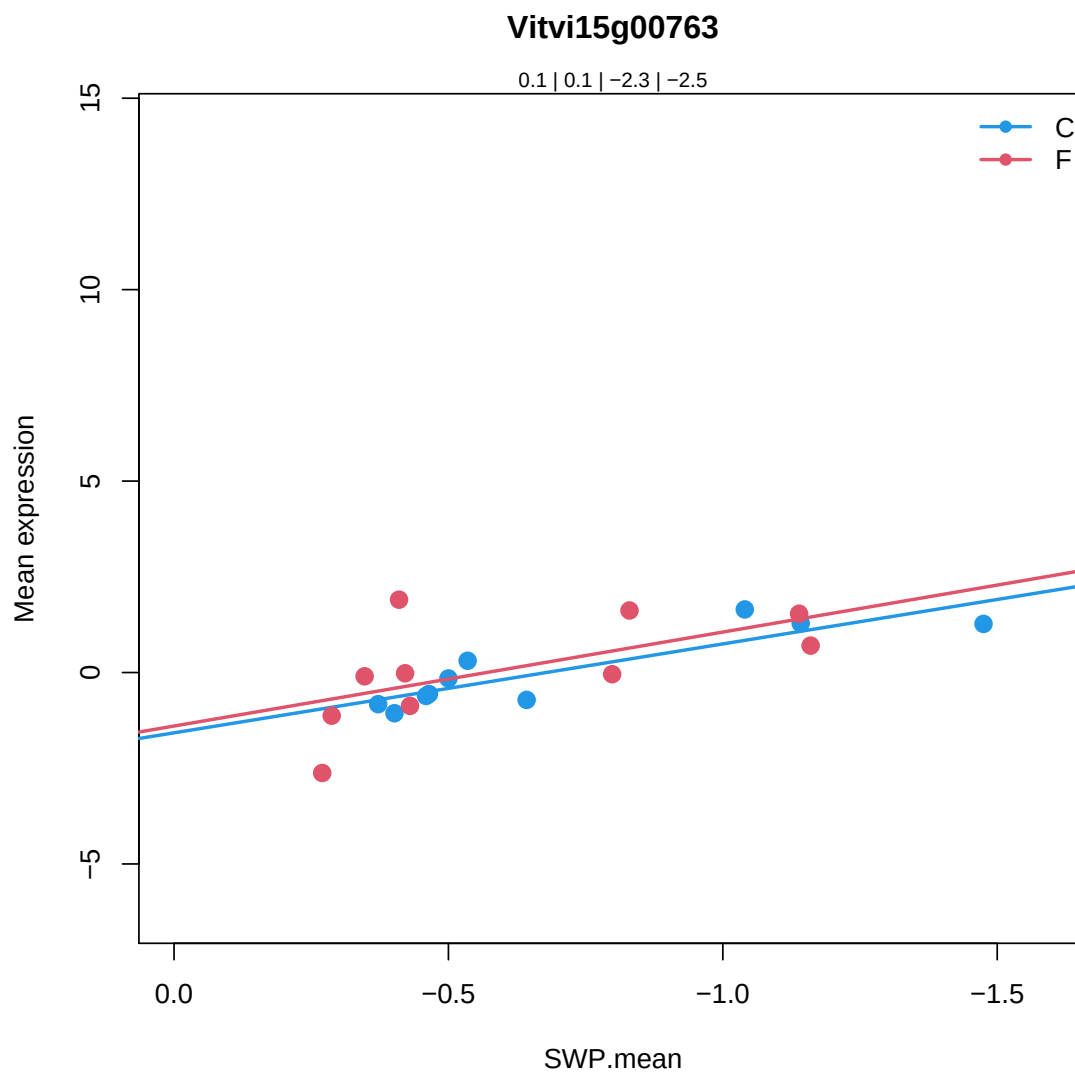
subtilase family protein |

Chr1:310332-313011 FORWARD LENGTH=774 |

201606

Coefficients for Vitvi15g00763.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.05752024	0.8295751		0.8329633	
SlopeC	-2.321806	0.00462461	**	0.2436609	
MeanF-MeanC	0.03992714	0.9158251		0.9772612	
SlopeF-SlopeC	-0.1323801	0.9047383		0.9999488	



7.2.48 Vitvi02g00263

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

Vitvi02g00263

26.6

misc.O-methyl transferases

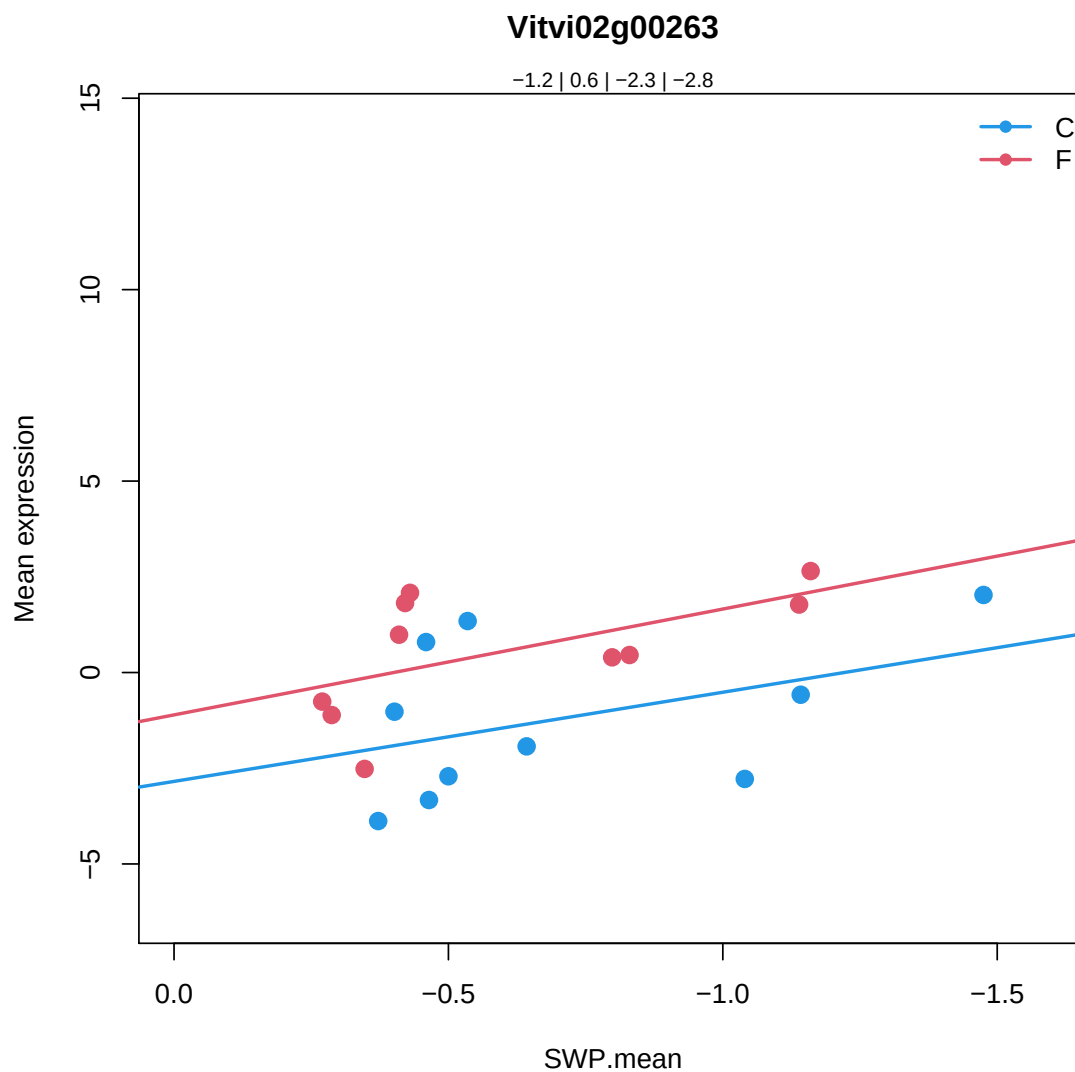
O-methyltransferase 1 |

Chr5:21982075-21984167 FORWARD LENGTH=363 |

201606

Coefficients for Vitvi02g00263.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.206661	0.01891324	*	0.0198948	*
SlopeC	-2.328381	0.09249281	.	0.6008919	
MeanF-MeanC	1.784135	0.01466739	*	0.1004817	
SlopeF-SlopeC	-0.4357503	0.826854		0.9999488	



7.2.49 Vitvi08g01112

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

Vitvi08g01112

34.16

transport.ABC transporters and multidrug resistance systems

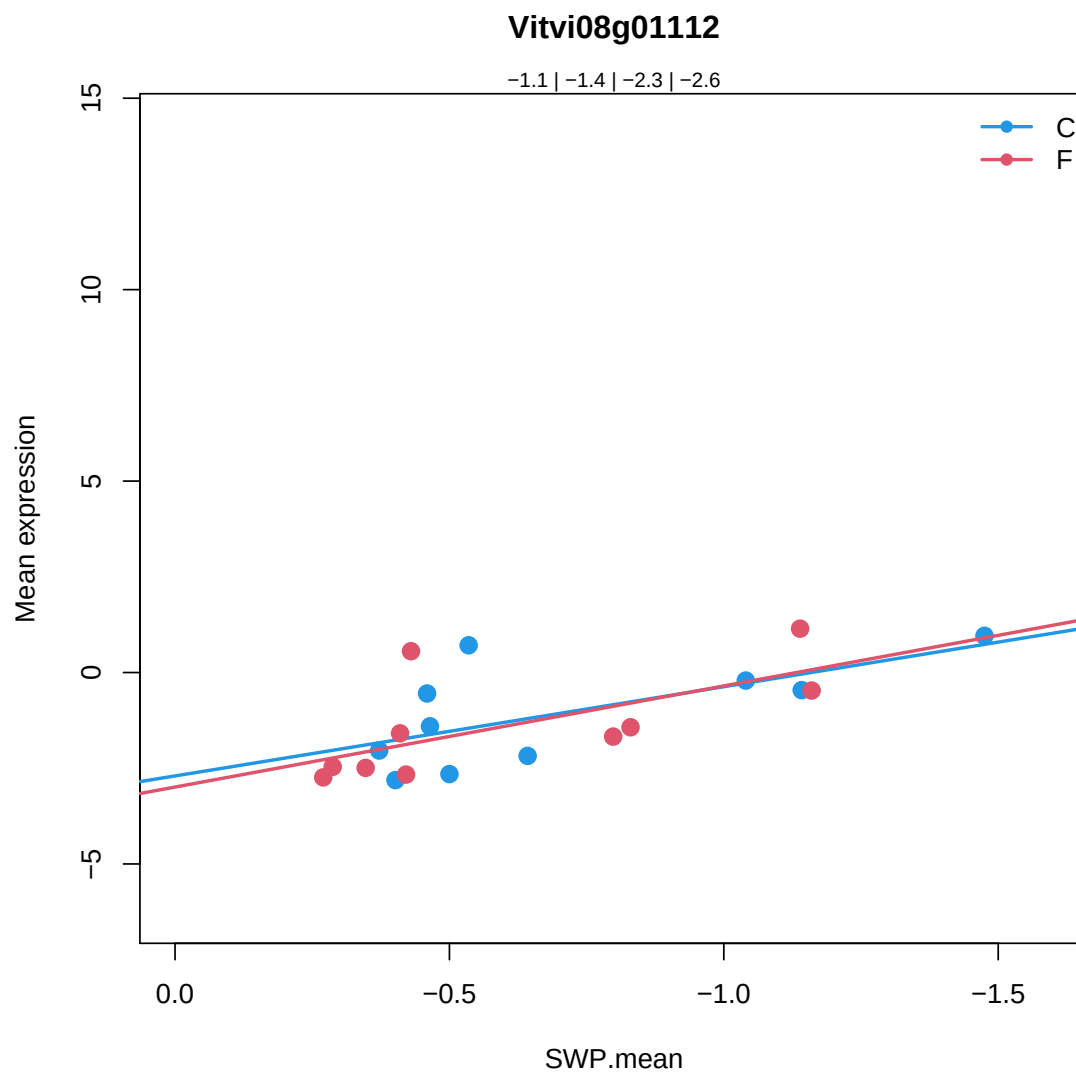
ABC-2 type transporter family protein |

Chr2:15673555-15675822 REVERSE LENGTH=755 |

201606

Coefficients for Vitvi08g01112.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.062956	0.002339767	**	0.002512698	**
SlopeC	-2.329875	0.01271304	*	0.3273178	
MeanF-MeanC	-0.3189805	0.471925		0.7897762	
SlopeF-SlopeC	-0.3120123	0.8090679		0.9999488	



7.2.50 Vitvi18g01966

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

Vitvi18g01966

35.1

not assigned.no ontology

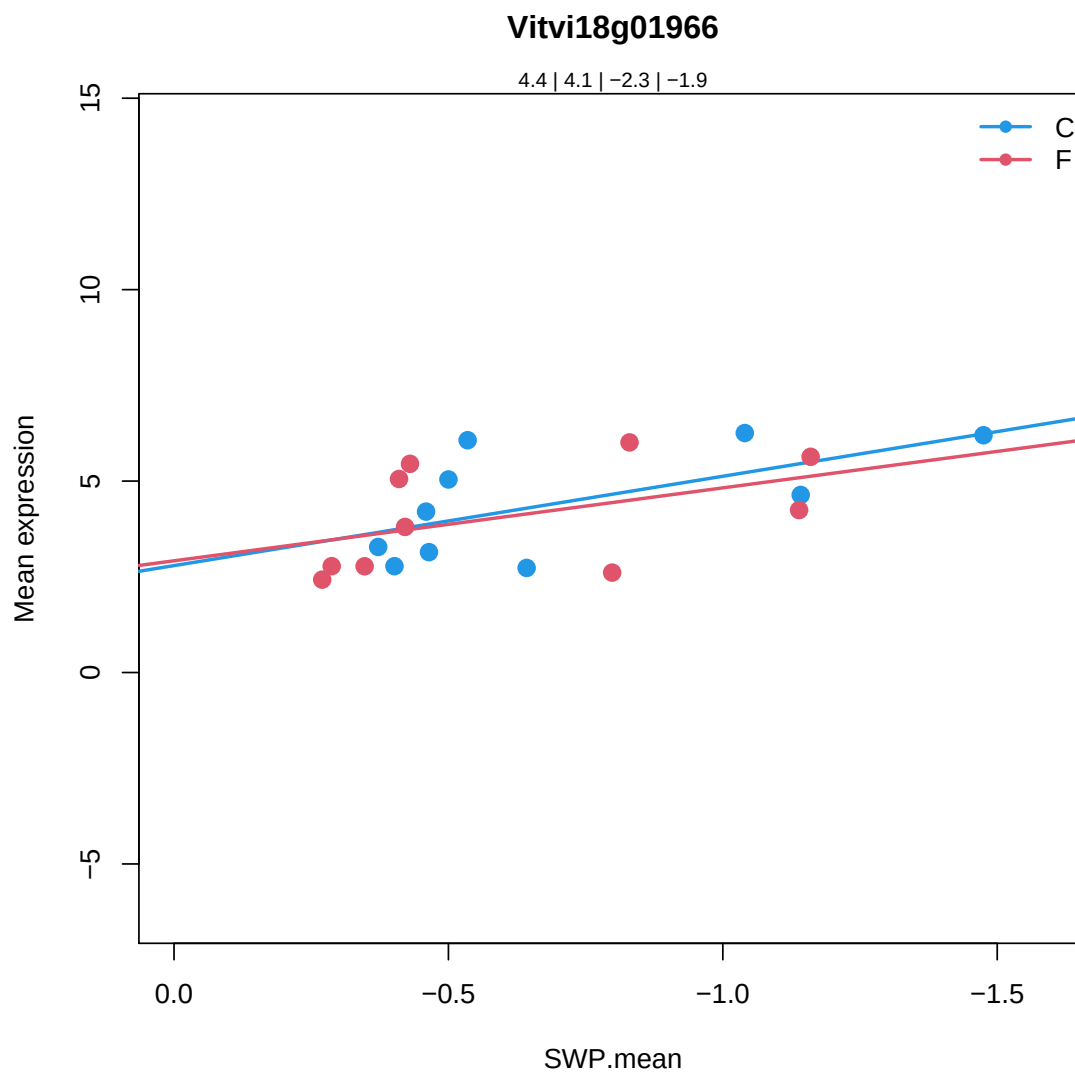
T-complex protein 11 |

Chr1:8118049-8121854 FORWARD LENGTH=1020 |

201606

Coefficients for Vitvi18g01966.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.433318	1.802502e-11	***	2.433242e-11	***
SlopeC	-2.333415	0.02502935	*	0.4079655	
MeanF-MeanC	-0.3550498	0.4785471		0.7941132	
SlopeF-SlopeC	0.4288107	0.768948		0.9999488	



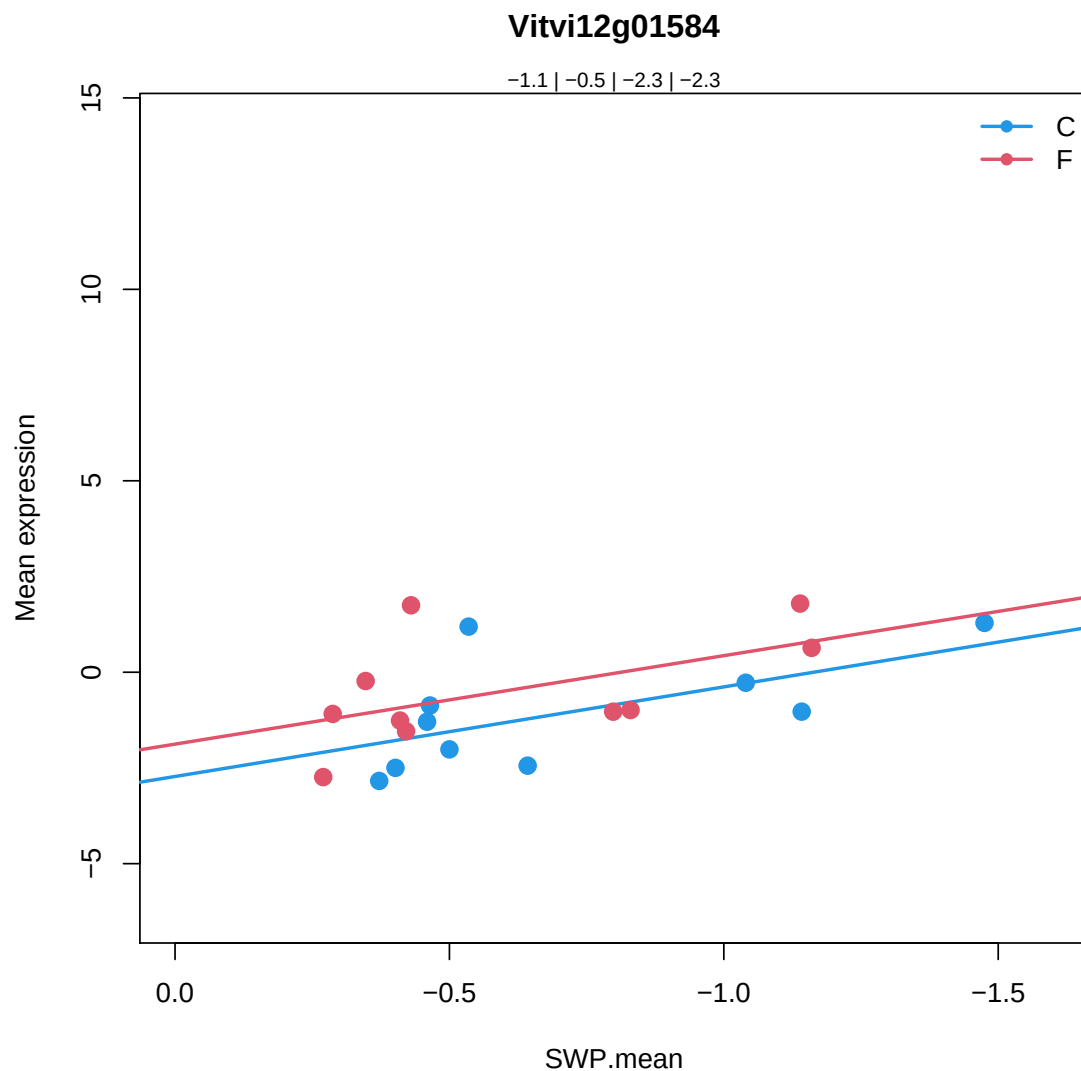
7.2.51 Vitvi12g01584

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

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

Coefficients for Vitvi12g01584.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.07798	0.006247541	**	0.006647006	**
SlopeC	-2.340025	0.02750159	*	0.4233169	
MeanF-MeanC	0.6075684	0.240133		0.5976418	
SlopeF-SlopeC	0.02913283	0.9843975		0.9999488	



7.2.52 Vitvi05g00218

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

Vitvi05g00218

34.9

transport.metabolite transporters at the mitochondrial membrane

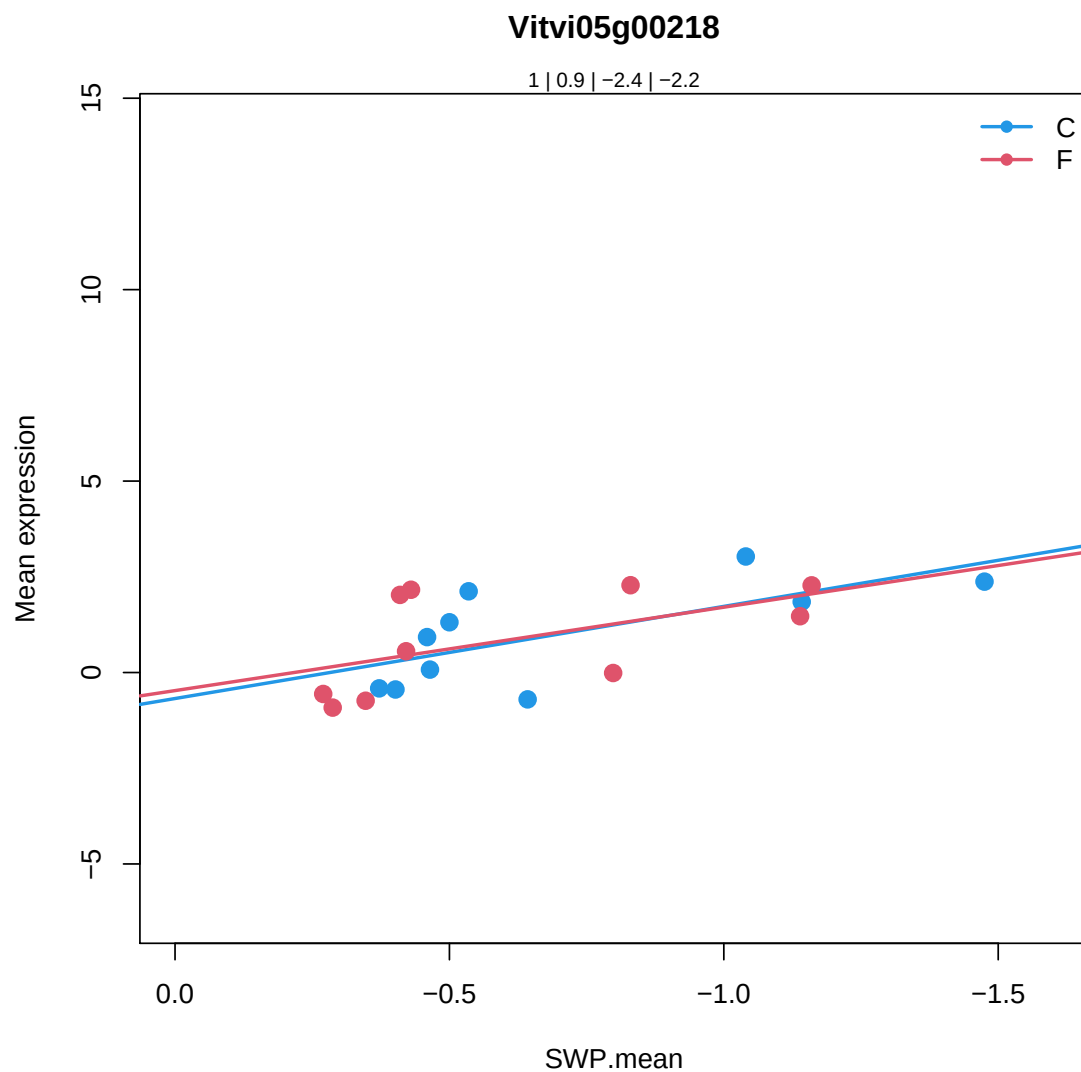
Mitochondrial substrate carrier family protein |

Chr5:5087822-5089677 FORWARD LENGTH=316 |

201606

Coefficients for Vitvi05g00218.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.01281	0.003695211	**	0.003952449	**
SlopeC	-2.406759	0.01103064	*	0.3143947	
MeanF-MeanC	-0.1584336	0.7221519		0.914736	
SlopeF-SlopeC	0.2287034	0.8606836		0.9999488	



7.2.53 Vitvi06g00443

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

```
Vitvi06g00443
```

```
29.6
```

```
protein.folding
```

```
heat shock cognate protein 70-1 |
```

```
Chr5:554055-556334 REVERSE LENGTH=651 |
```

```
201606
```

```
Vitvi06g00443
```

```
20.02.2001
```

```
stress.abiotic.heat
```

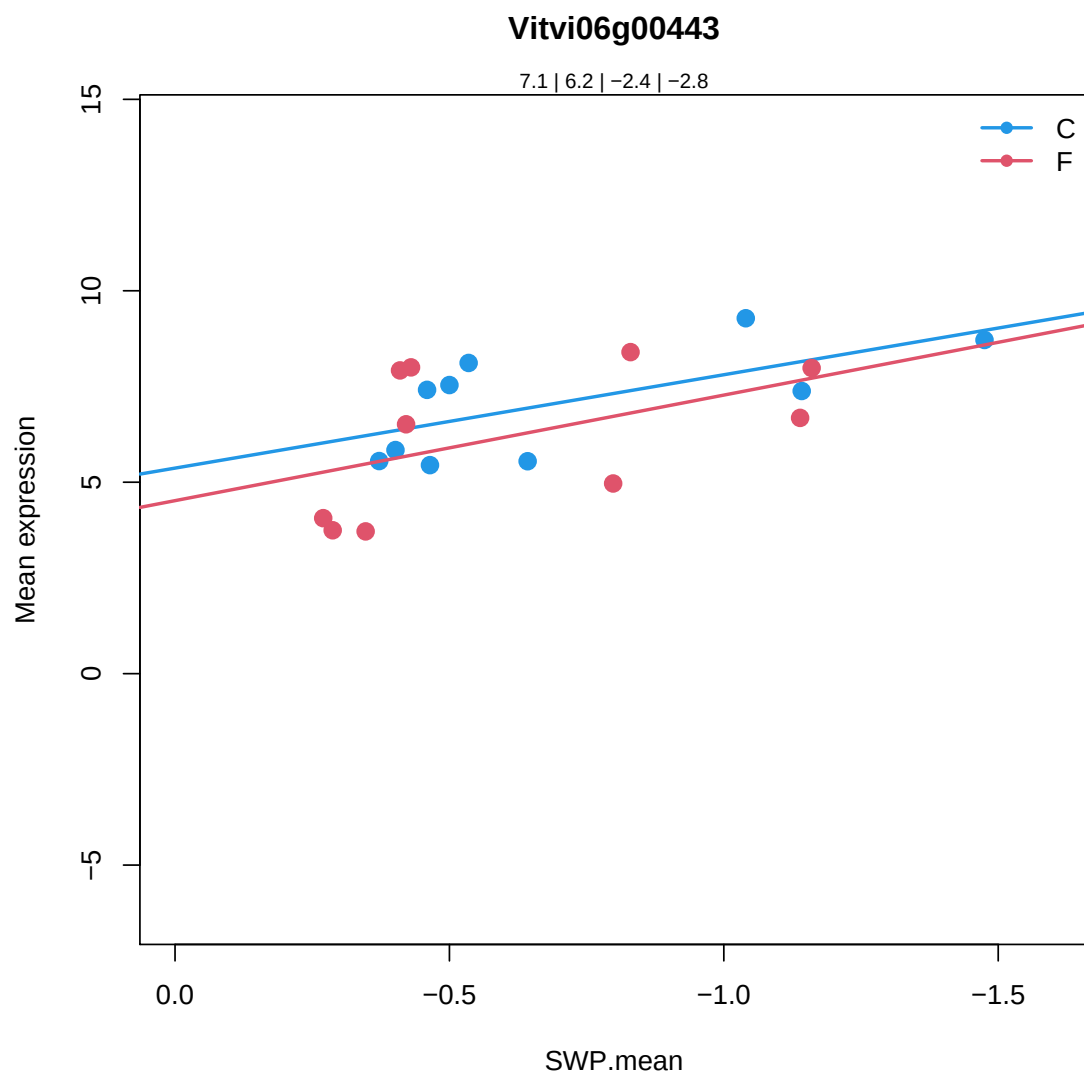
```
heat shock cognate protein 70-1 |
```

```
Chr5:554055-556334 REVERSE LENGTH=651 |
```

```
201606
```

Coefficients for Vitvi06g00443.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.083015	4.877361e-14	***	7.675863e-14	***
SlopeC	-2.438983	0.0447607	*	0.4901168	
MeanF-MeanC	-0.885021	0.1427101		0.4537312	
SlopeF-SlopeC	-0.3183393	0.8534745		0.9999488	



7.2.54 Vitvi07g01552

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

Vitvi07g01552

35.2

not assigned.unknown

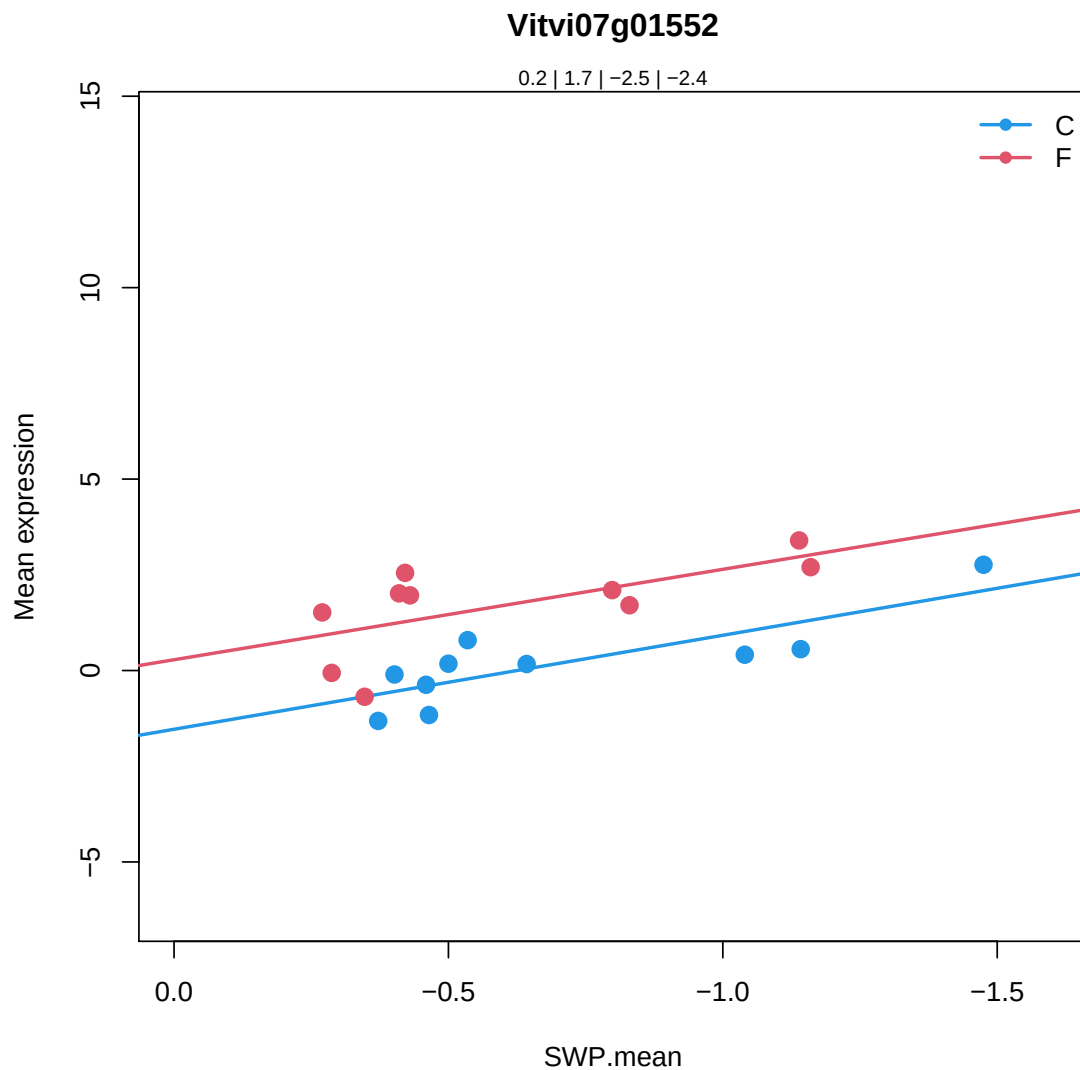
basic leucine-zipper 6 |

Chr2:9732601-9733284 REVERSE LENGTH=227 |

201606

Coefficients for Vitvi07g01552.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1917637	0.4448755		0.4510305	
SlopeC	-2.454713	0.001716853	**	0.1571259	
MeanF-MeanC	1.528104	0.0002476447	***	0.003915614	**
SlopeF-SlopeC	0.09286943	0.9283139		0.9999488	



7.2.55 Vitvi07g02597

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

Vitvi07g02597

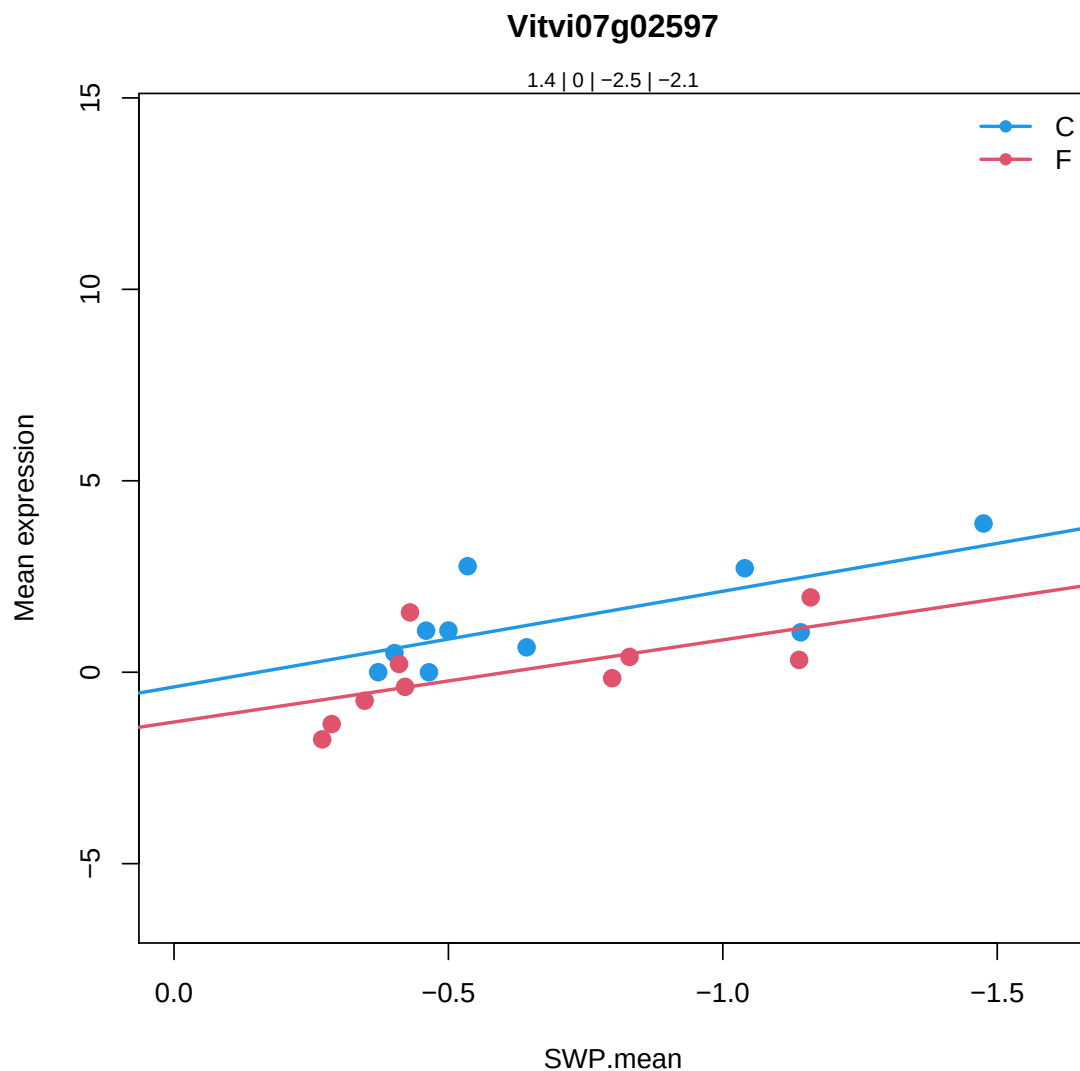
35.2

not assigned.unknown

NA

Coefficients for Vitvi07g02597.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.373304	5.182407e-05	***	5.755629e-05	***
SlopeC	-2.498658	0.00339104	**	0.2208813	
MeanF-MeanC	-1.366992	0.001871035	**	0.02090306	*
SlopeF-SlopeC	0.3531685	0.7574547		0.9999488	



7.2.56 Vitvi06g00605

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

Vitvi06g00605

26.1

misc.cytochrome P450

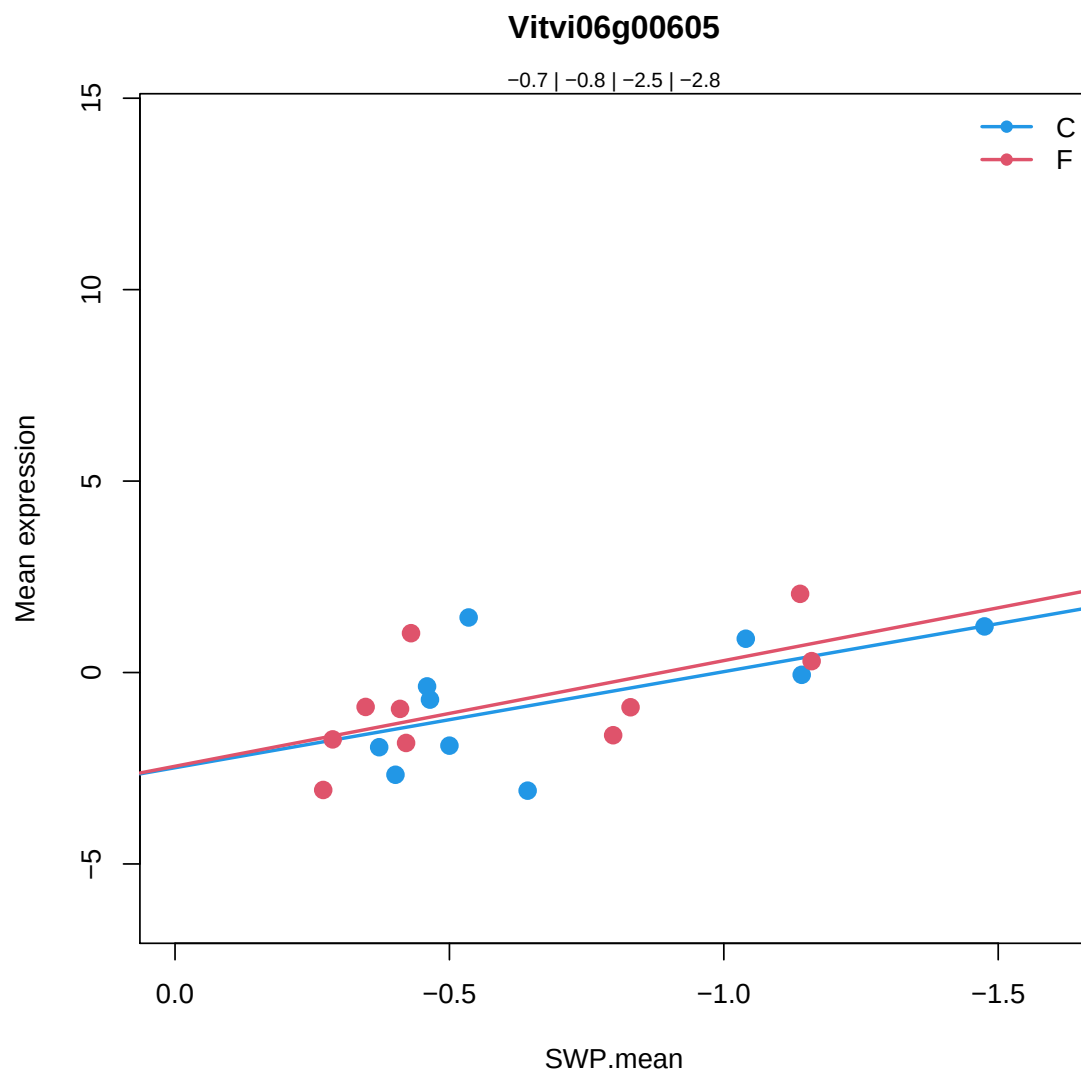
cytochrome P450%2C family 86%2C subfamily A%2C polypeptide 1 |

Chr5:23765999-23767997 REVERSE LENGTH=513 |

201606

Coefficients for Vitvi06g00605.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.7223887	0.06446106	.	0.06695622	.
SlopeC	-2.509662	0.02374058	*	0.3983963	
MeanF-MeanC	-0.04468309	0.9328475		0.981995	
SlopeF-SlopeC	-0.2491978	0.872519		0.9999488	



7.2.57 Vitvi07g01120

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

Vitvi07g01120

35.2

not assigned.unknown

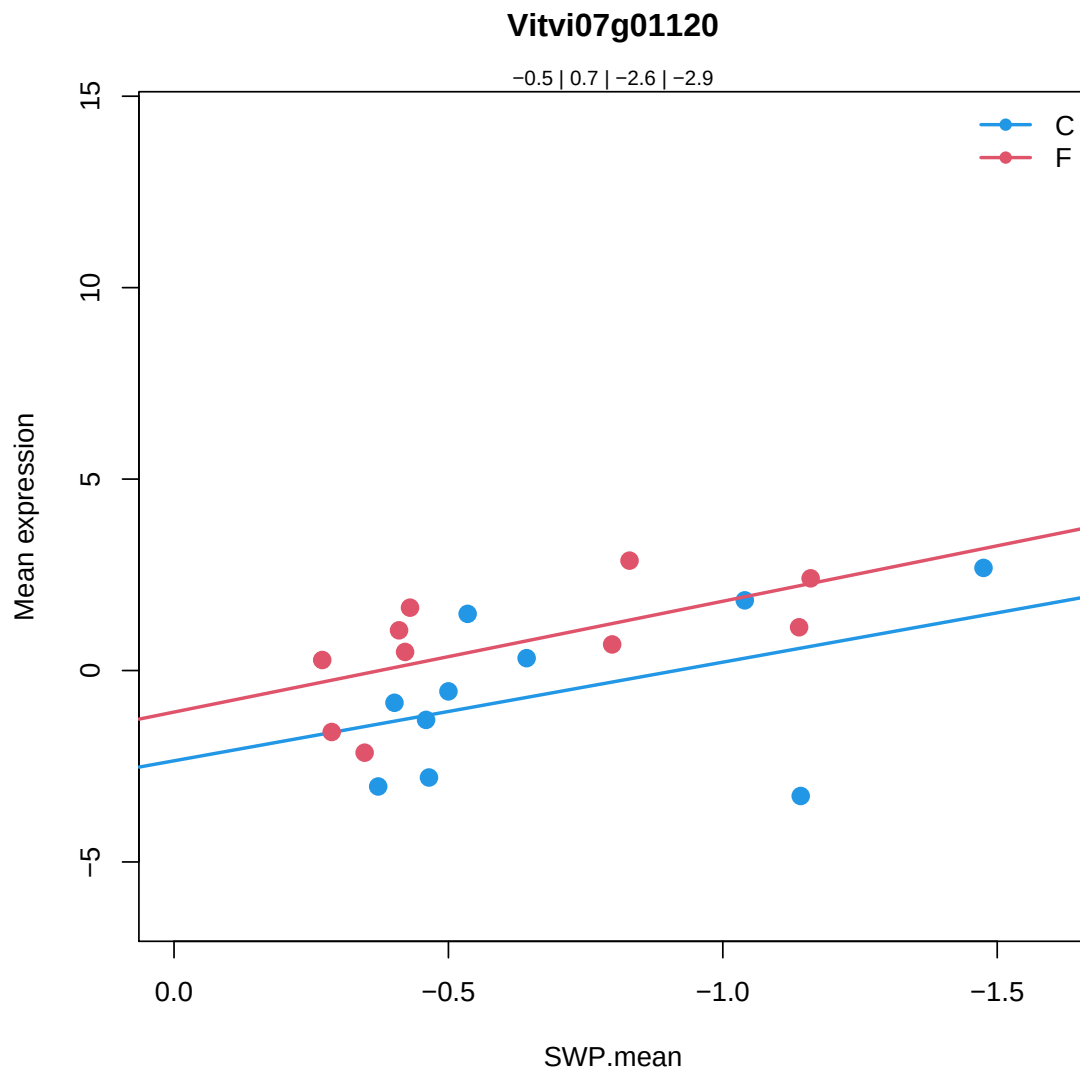
nuclear transport factor 2/RNA recognition motif protein |

Chr3:2307289-2308326 REVERSE LENGTH=293 |

201606

Coefficients for Vitvi07g01120.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.5464727	0.2536031		0.2590069	
SlopeC	-2.576419	0.05972457	.	0.5396099	
MeanF-MeanC	1.225249	0.07667075	.	0.3124641	
SlopeF-SlopeC	-0.318679	0.8703226		0.9999488	



7.2.58 Vitvi04g00522

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

Vitvi04g00522

20.02.2001

stress.abiotic.heat

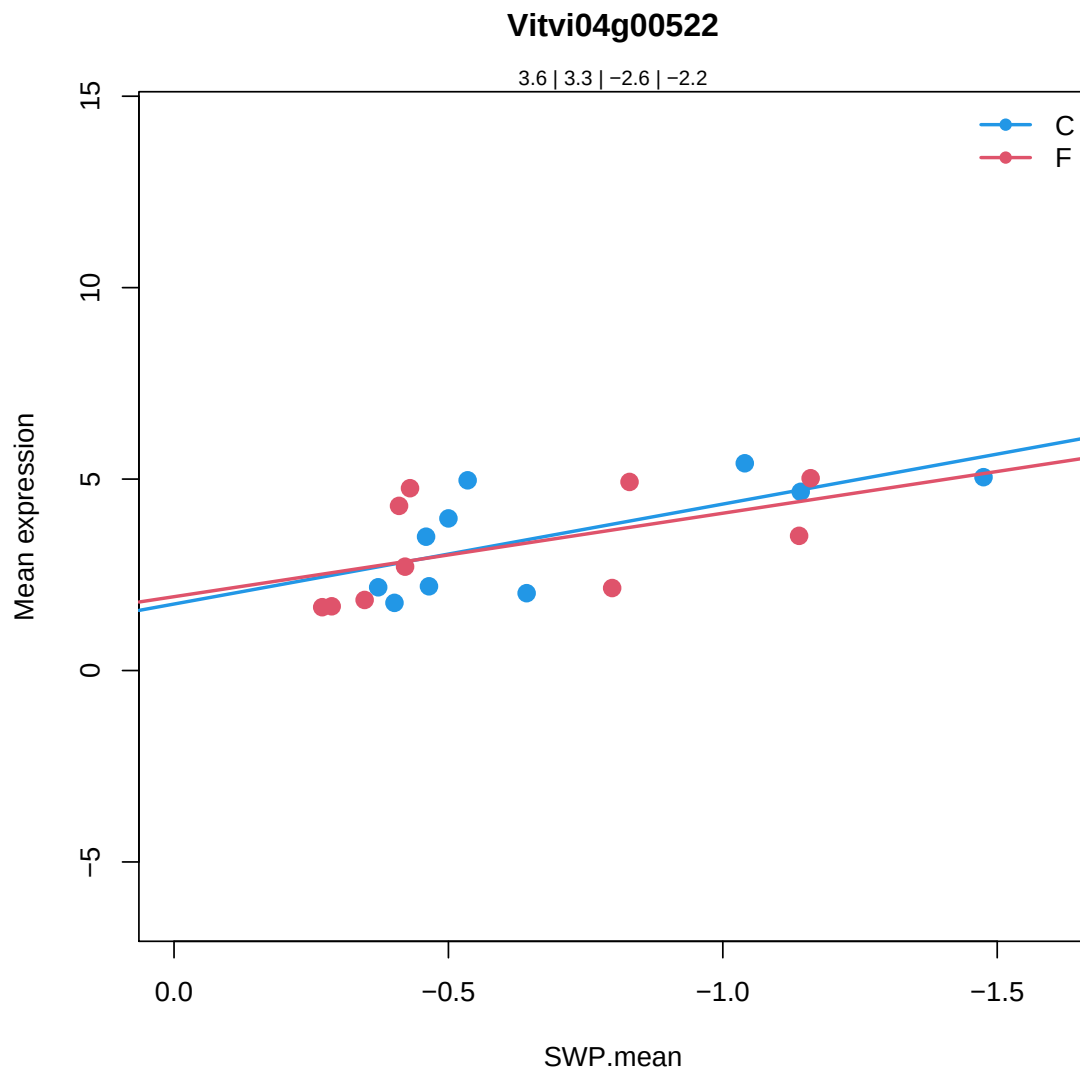
casein lytic proteinase B4 |

Chr2:10697877-10701998 REVERSE LENGTH=964 |

201606

Coefficients for Vitvi04g00522.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.572372	4.357544e-10	***	5.565884e-10	***
SlopeC	-2.610525	0.01012679	*	0.3042563	
MeanF-MeanC	-0.3157466	0.5093765		0.812391	
SlopeF-SlopeC	0.4302342	0.7578561		0.9999488	



7.2.59 Vitvi01g01459

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

Vitvi01g01459

17.01.2003

hormone metabolism.abscisic acid.induced-regulated-responsive-activate

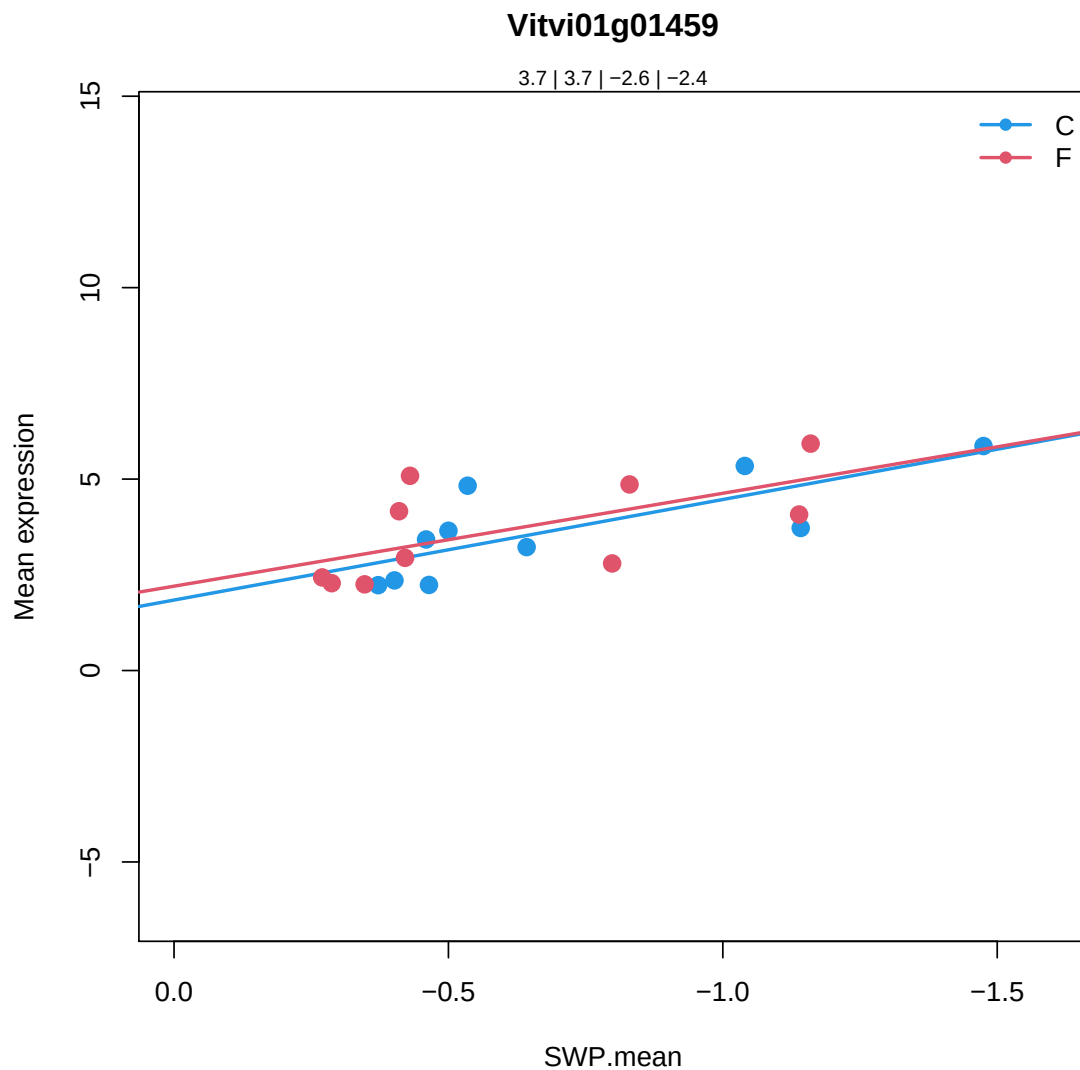
GRAM domain family protein |

Chr5:4207081-4207812 FORWARD LENGTH=213 |

201606

Coefficients for Vitvi01g01459.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.686915	1.001241e-11	***	1.366363e-11	***
SlopeC	-2.625931	0.002885634	**	0.2045713	
MeanF-MeanC	-0.006086896	0.9879085		0.9967265	
SlopeF-SlopeC	0.1996119	0.8652634		0.9999488	



7.2.60 Vitvi14g02026

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

Vitvi14g02026

20.02.2001

stress.abiotic.heat

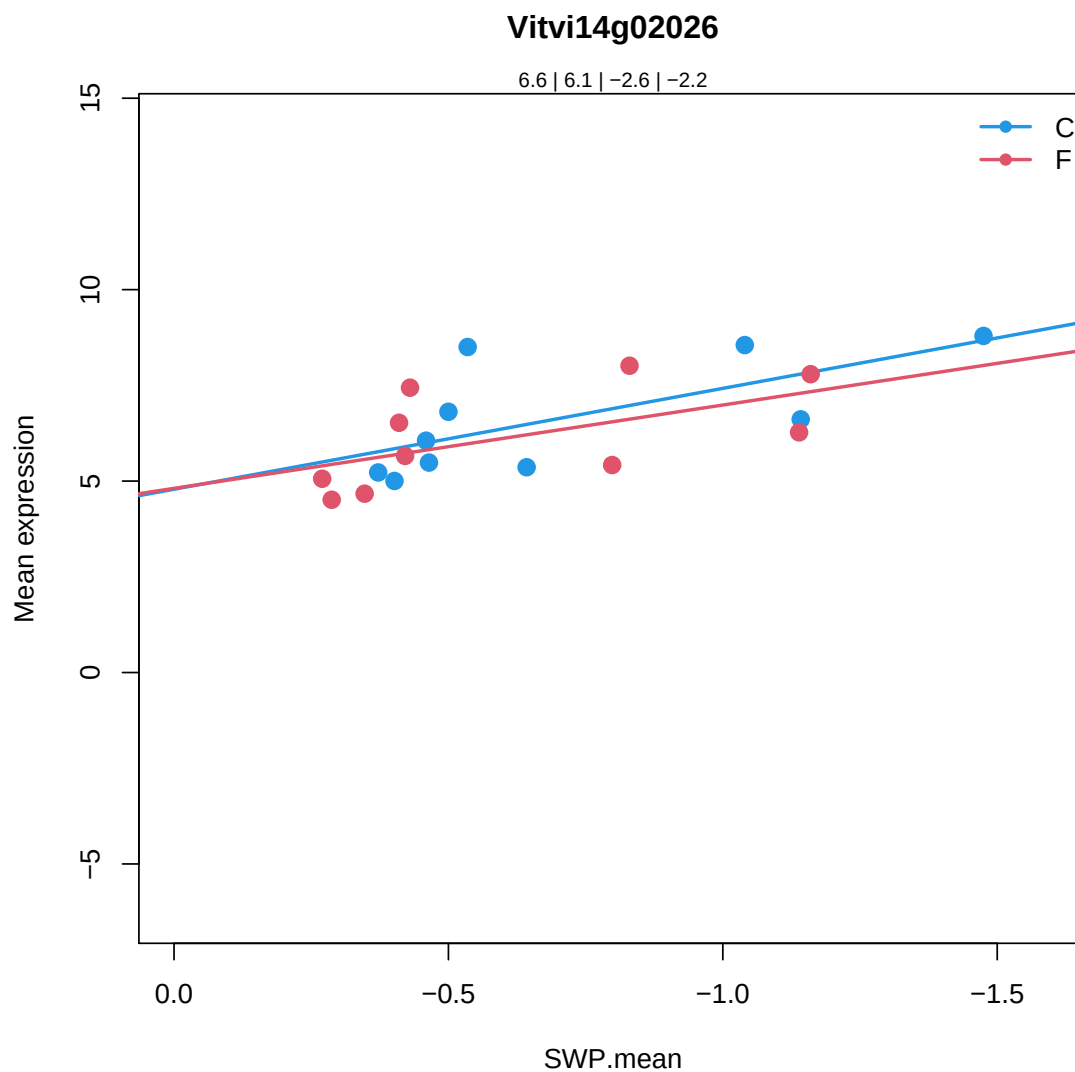
casein lytic proteinase B3 |

Chr5:5014399-5018255 REVERSE LENGTH=968 |

201606

Coefficients for Vitvi14g02026.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.639492	1.082566e-15	***	2.018406e-15	***
SlopeC	-2.634207	0.007307227	**	0.2775469	
MeanF-MeanC	-0.5036664	0.2773301		0.6412508	
SlopeF-SlopeC	0.4582077	0.7324697		0.9999488	



7.2.61 Vitvi16g00681

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

Vitvi16g00681

20.02.2001

stress.abiotic.heat

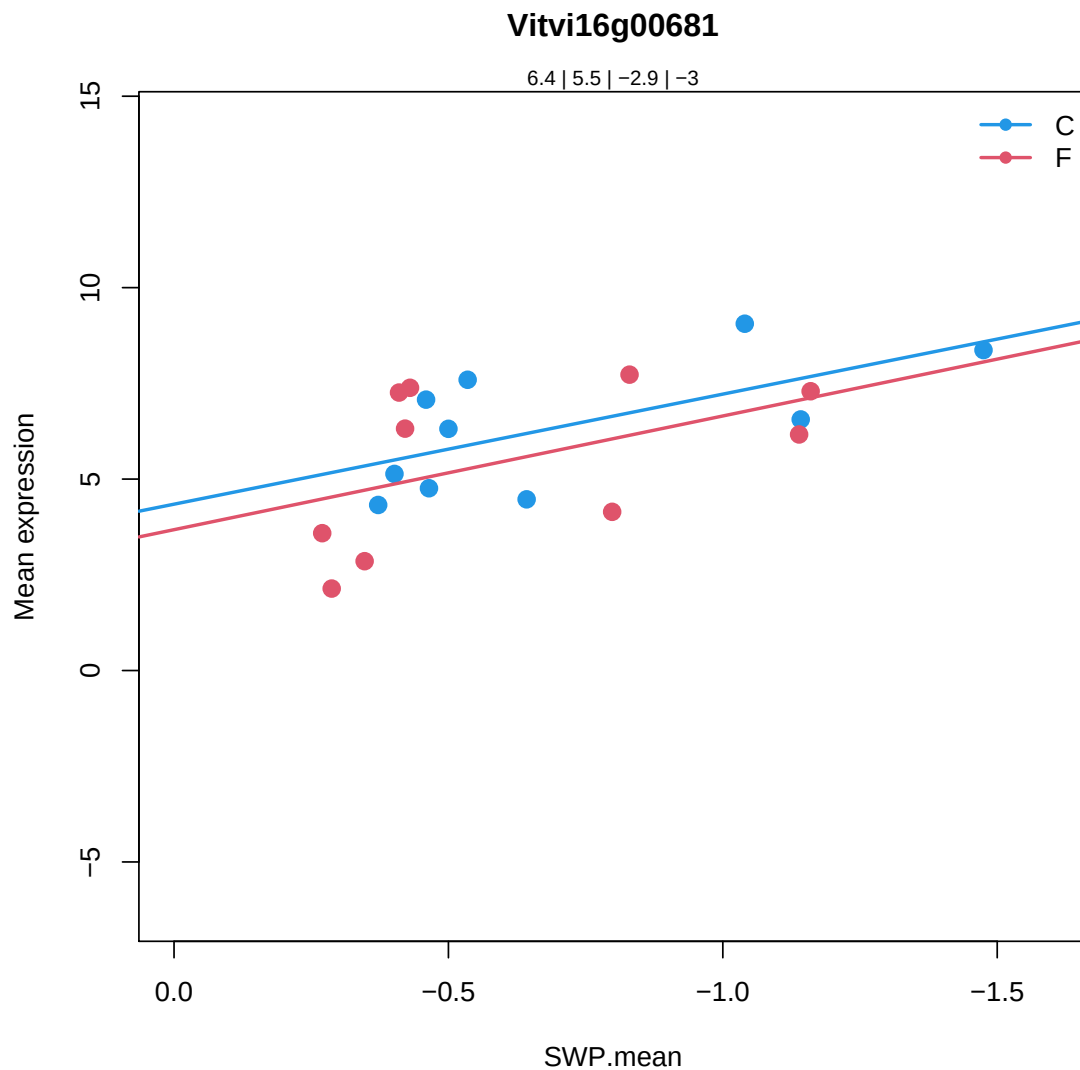
mitochondrion-localized small heat shock protein 23.6 |

Chr4:12917089-12917858 FORWARD LENGTH=210 |

201606

Coefficients for Vitvi16g00681.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.365536	4.303294e-12	***	5.964428e-12	***
SlopeC	-2.874618	0.03674623	*	0.4602035	
MeanF-MeanC	-0.8780277	0.1947686		0.5358599	
SlopeF-SlopeC	-0.09509428	0.9609728		0.9999488	



7.2.62 Vitvi08g00689

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

Vitvi08g00689

20.02.2001

stress.abiotic.heat

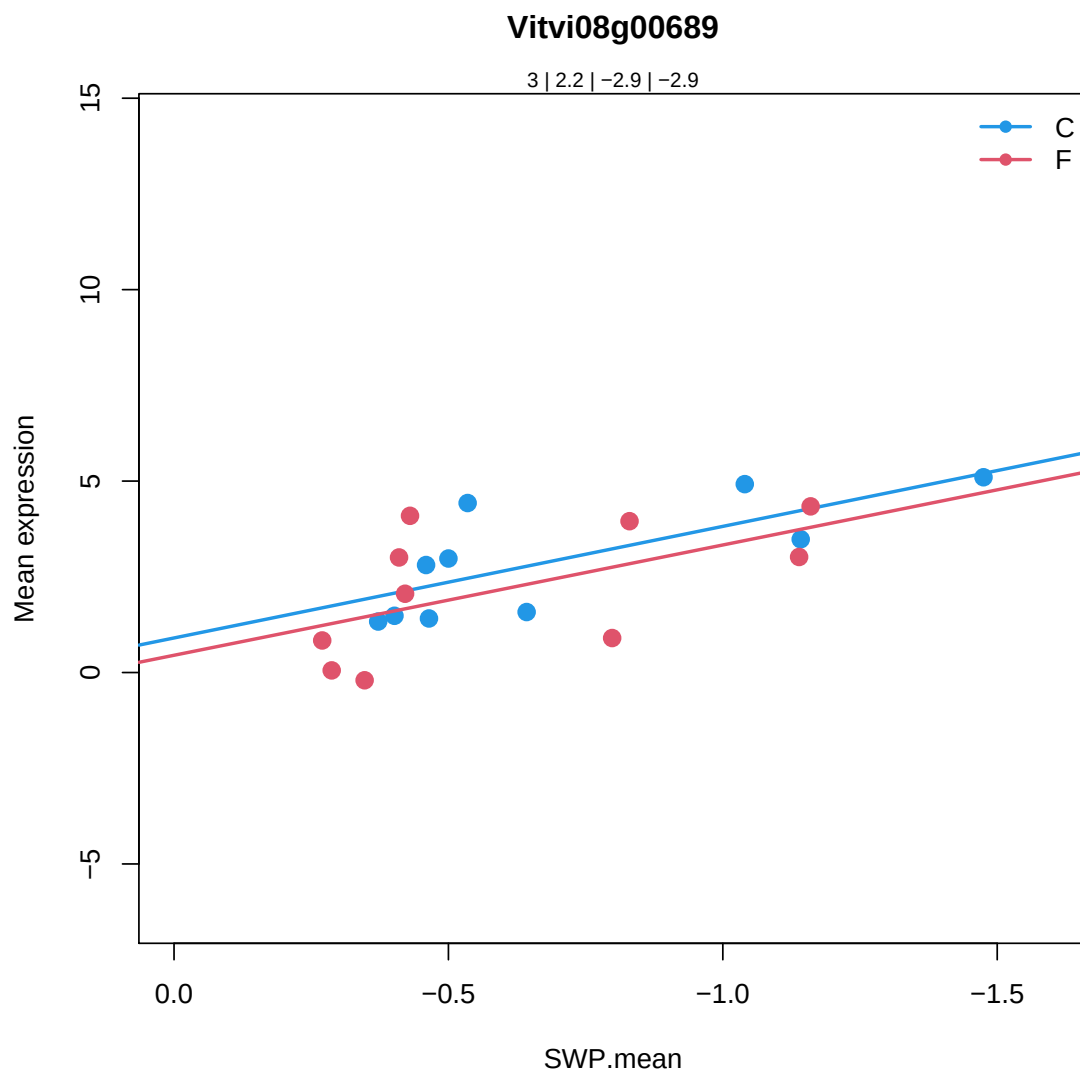
DNAJ heat shock N-terminal domain-containing protein |

Chr3:2737589-2740265 FORWARD LENGTH=572 |

201606

Coefficients for Vitvi08g00689.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.951604	5.060499e-08	***	6.049579e-08	***
SlopeC	-2.914322	0.008477063	**	0.2890546	
MeanF-MeanC	-0.7461071	0.1588471		0.4815329	
SlopeF-SlopeC	0.03394978	0.9821109		0.9999488	



7.2.63 Vitvi05g01833

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

Vitvi05g01833

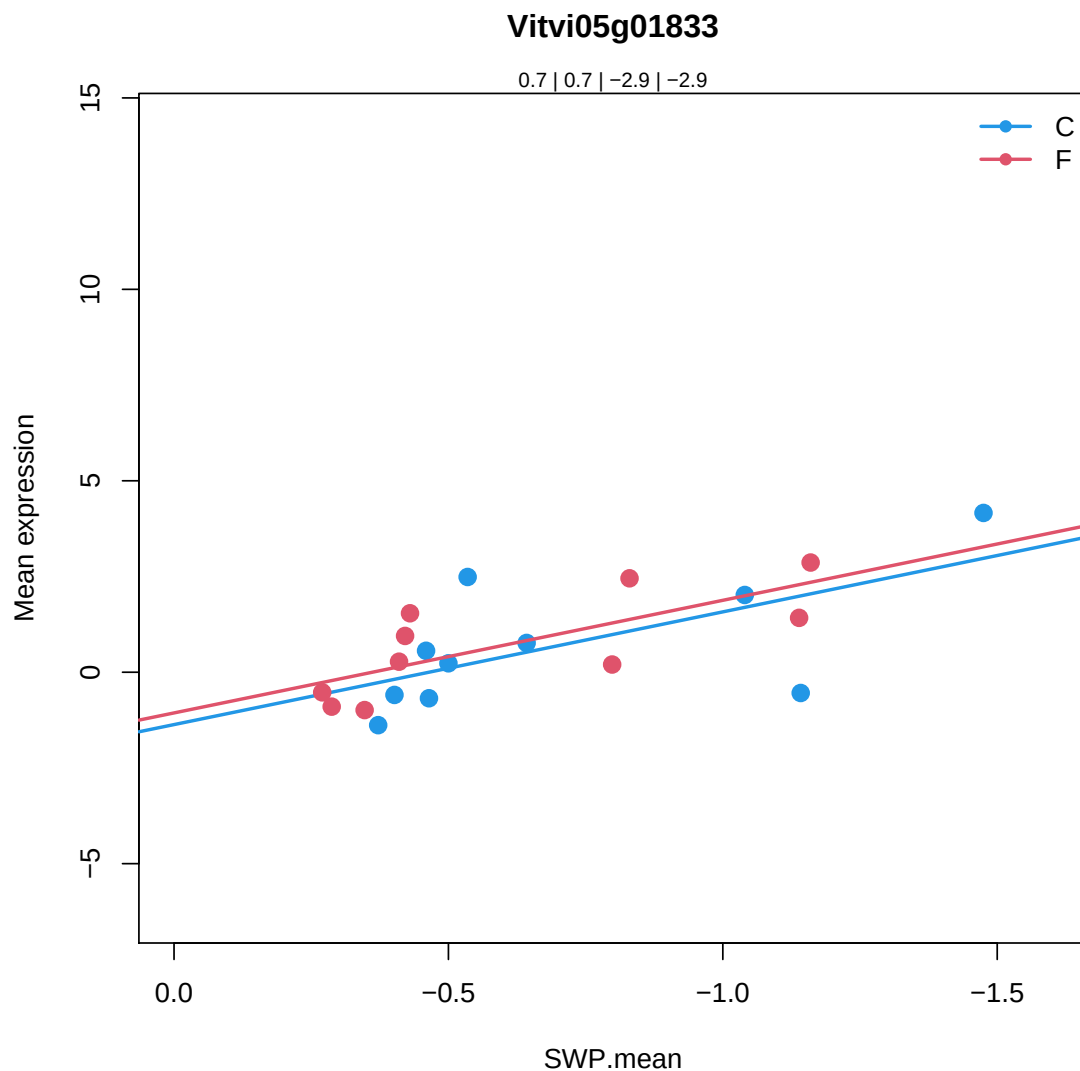
35.2

not assigned.unknown

NA

Coefficients for Vitvi05g01833.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.7023488	0.0473538	*	0.04934819	*
SlopeC	-2.943432	0.004540305	**	0.2419697	
MeanF-MeanC	0.02632047	0.9560566		0.9899375	
SlopeF-SlopeC	0.002075687	0.9988158		0.9999488	



7.2.64 Vitvi01g01708

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

Vitvi01g01708

20.02.2001

stress.abiotic.heat

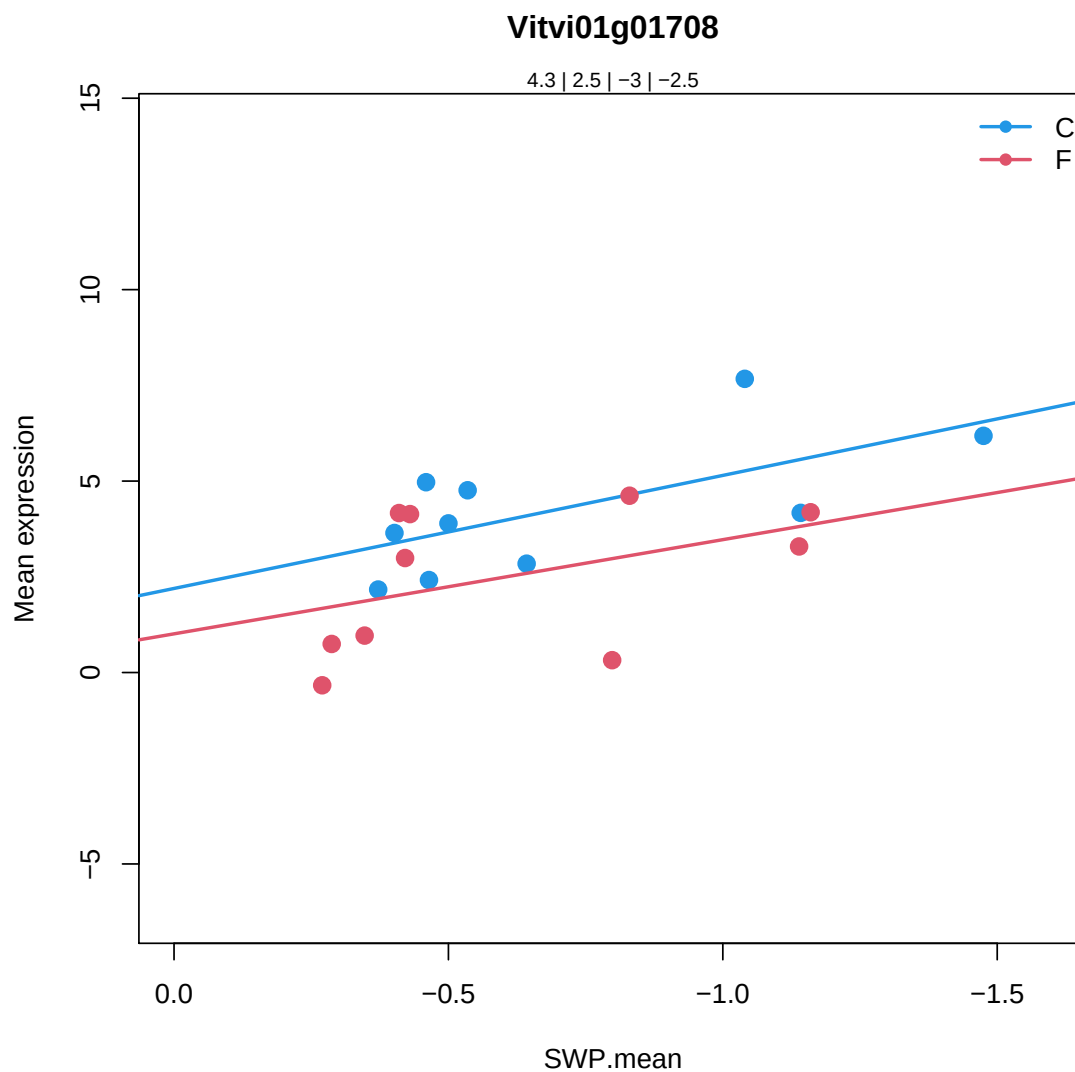
BCL-2-associated athanogene 5 |

Chr1:4076334-4076981 FORWARD LENGTH=215 |

201606

Coefficients for Vitvi01g01708.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.271601	2.851353e-09	***	3.543732e-09	***
SlopeC	-2.952446	0.02543851	*	0.4079655	
MeanF-MeanC	-1.762888	0.01009625	*	0.07663695	.
SlopeF-SlopeC	0.4926336	0.7902962		0.9999488	



7.2.65 Vitvi17g00085

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

Vitvi17g00085

17.01.2003

hormone metabolism.abscisic acid.induced-regulated-responsive-activate

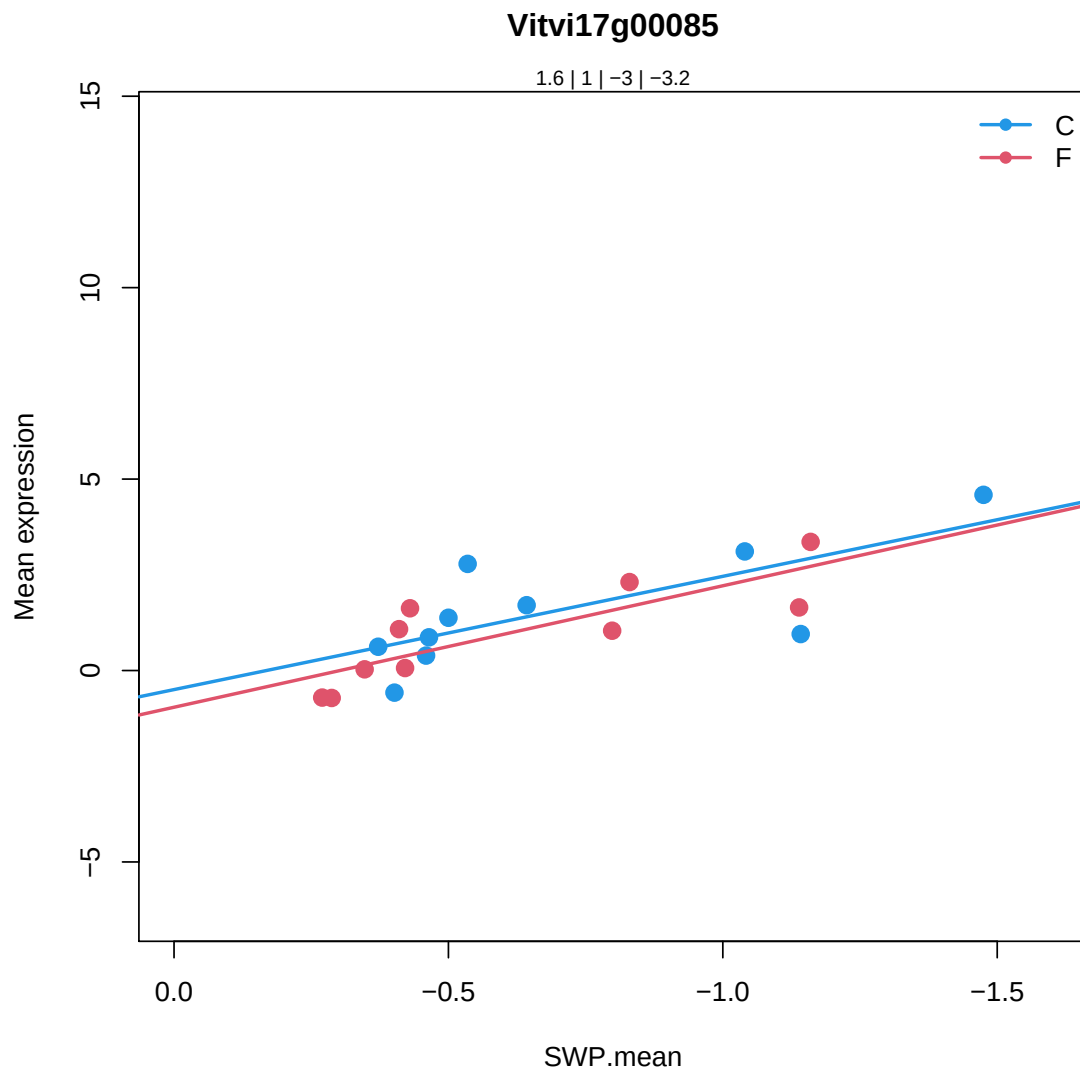
HVA22 homologue D |

Chr4:12828237-12829019 FORWARD LENGTH=135 |

201606

Coefficients for Vitvi17g00085.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.581834	8.293491e-06	***	9.383817e-06	***
SlopeC	-2.957952	0.0007828248	***	0.1097382	
MeanF-MeanC	-0.608472	0.1283374		0.4255208	
SlopeF-SlopeC	-0.2145244	0.8507385		0.9999488	



7.2.66 Vitvi13g01107

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

Vitvi13g01107

35.2

not assigned.unknown

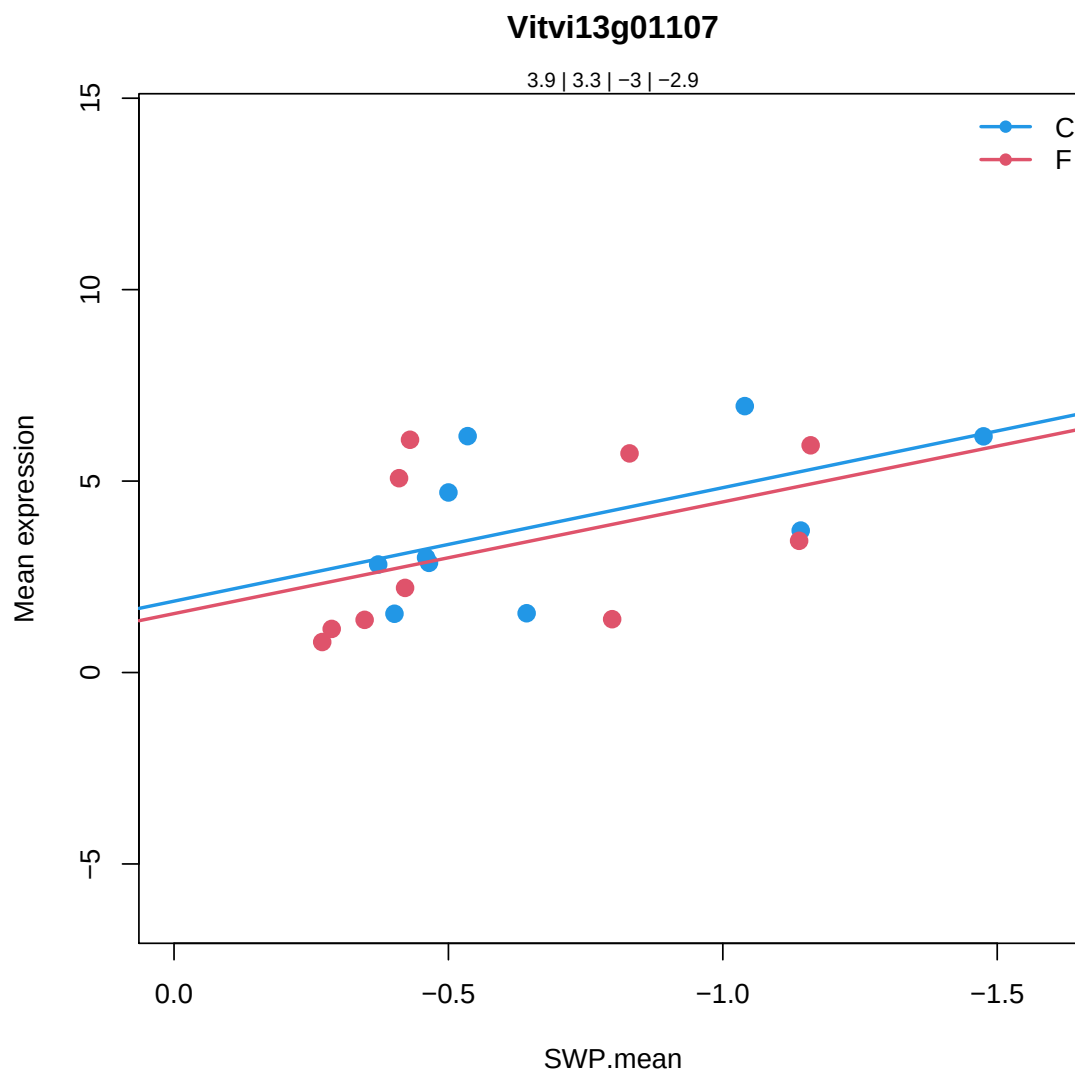
HSP20-like chaperones superfamily protein |

Chr3:951885-953490 FORWARD LENGTH=150 |

201606

Coefficients for Vitvi13g01107.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.94795	1.781634e-07	***	2.098907e-07	***
SlopeC	-2.964306	0.05399201	.	0.5205226	
MeanF-MeanC	-0.6315872	0.4022459		0.7465943	
SlopeF-SlopeC	0.04693335	0.9828977		0.9999488	



7.2.67 Vitvi01g02030

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

Vitvi01g02030

29.5.11.4.2

protein.degradation.ubiquitin.E3.RING

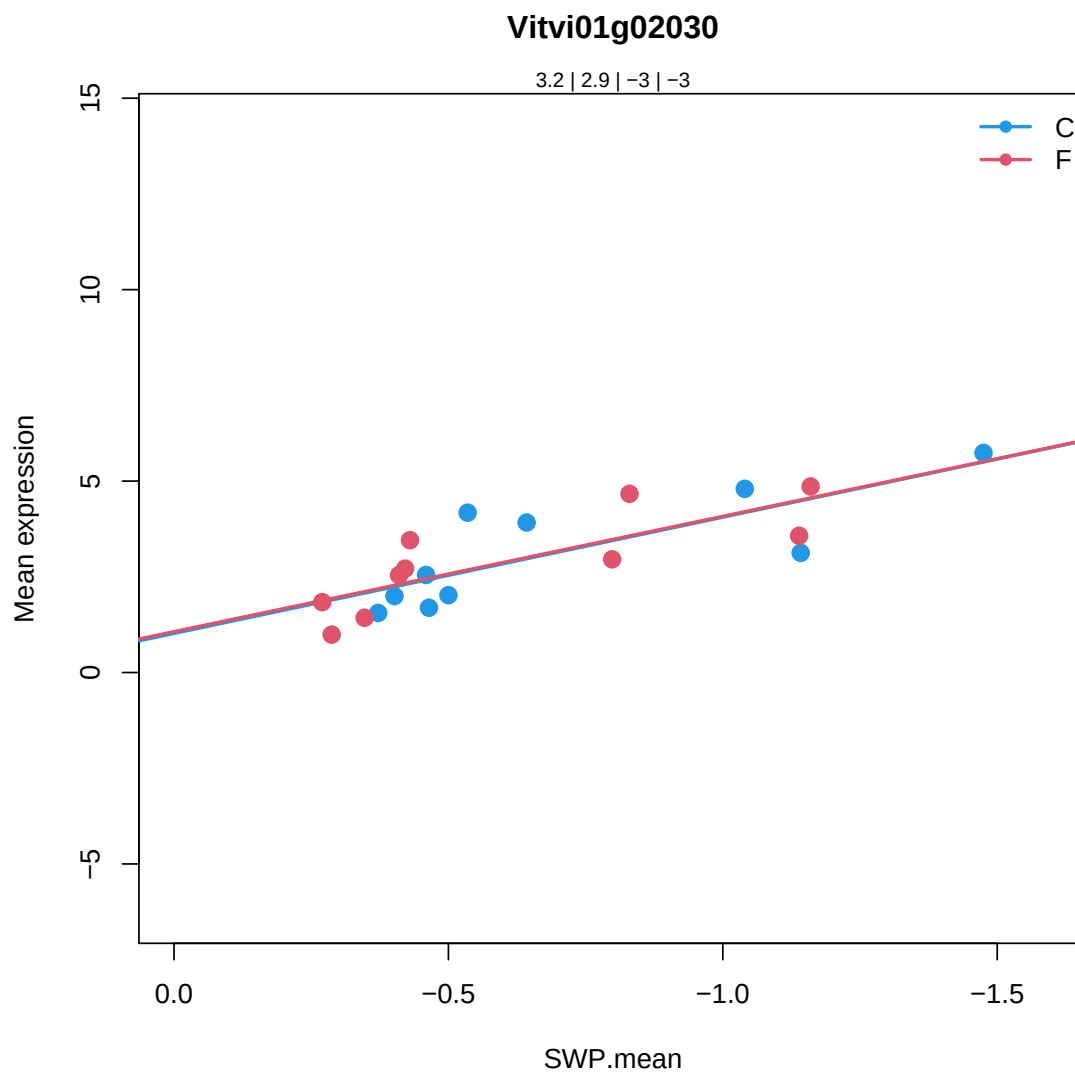
RING/U-box superfamily protein |

Chr1:25442486-25442887 FORWARD LENGTH=133 |

201606

Coefficients for Vitvi01g02030.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.155968	1.931528e-11	***	2.603728e-11	***
SlopeC	-3.035038	0.0002471739	***	0.08263916	.
MeanF-MeanC	-0.2534253	0.4789676		0.7941132	
SlopeF-SlopeC	0.02234586	0.9828888		0.9999488	



7.2.68 Vitvi13g01839

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

```
Vitvi13g01839
```

```
26.21
```

```
misc.protease inhibitor/seed storage/lipid transfer protein (LTP) fami
```

```
Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin
```

```
Chr2:18305418-18306202 REVERSE LENGTH=205 |
```

```
201606
```

```
Vitvi13g01839
```

```
11.6
```

```
lipid metabolism.lipid transfer proteins etc
```

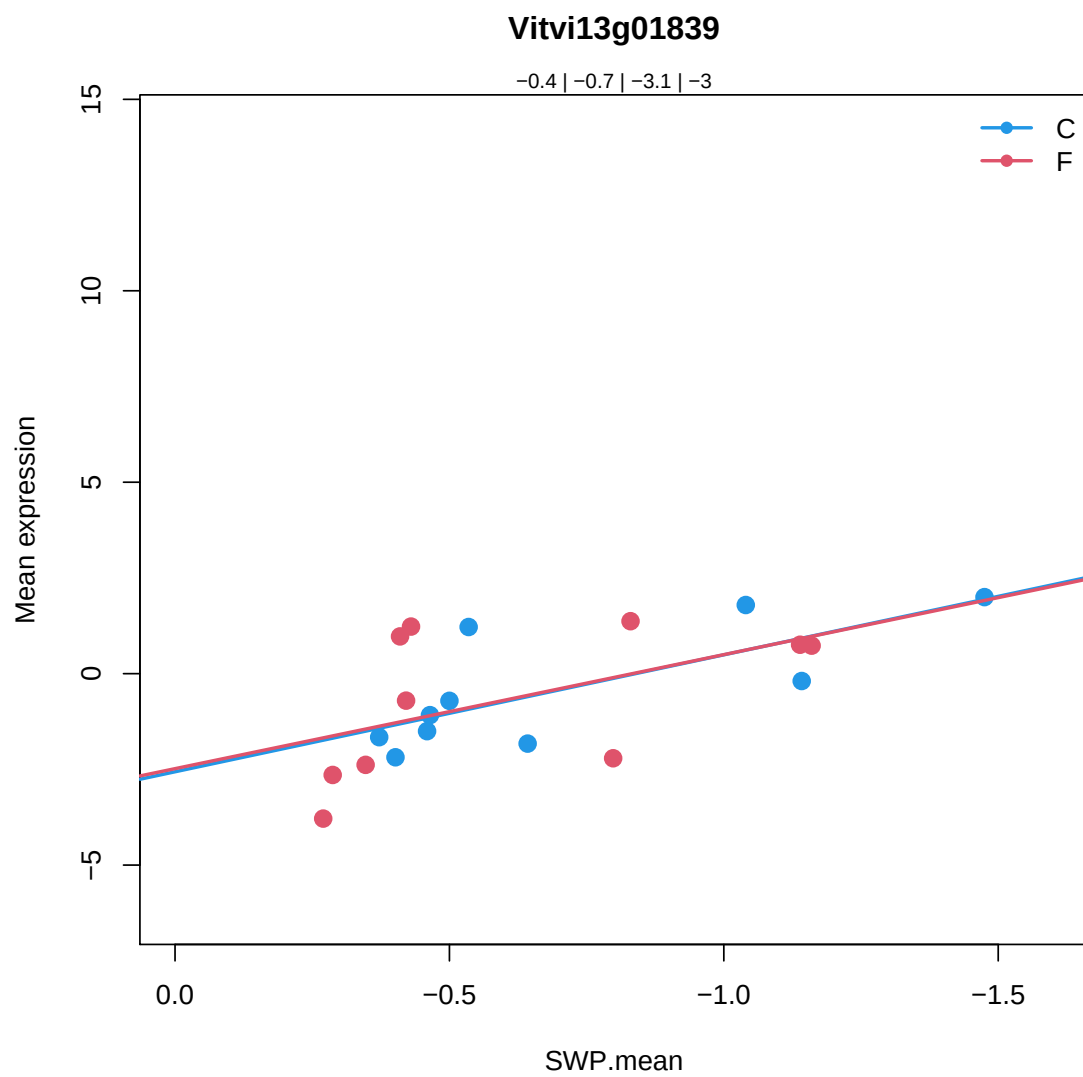
```
Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin
```

```
Chr2:18305418-18306202 REVERSE LENGTH=205 |
```

```
201606
```

Coefficients for Vitvi13g01839.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.4151178	0.3157402		0.321477	
SlopeC	-3.054071	0.01277848	*	0.3284478	
MeanF-MeanC	-0.2519902	0.6636665		0.8886547	
SlopeF-SlopeC	0.07550815	0.9644251		0.9999488	



7.2.69 Vitvi09g00045

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

Vitvi09g00045

20.02.2001

stress.abiotic.heat

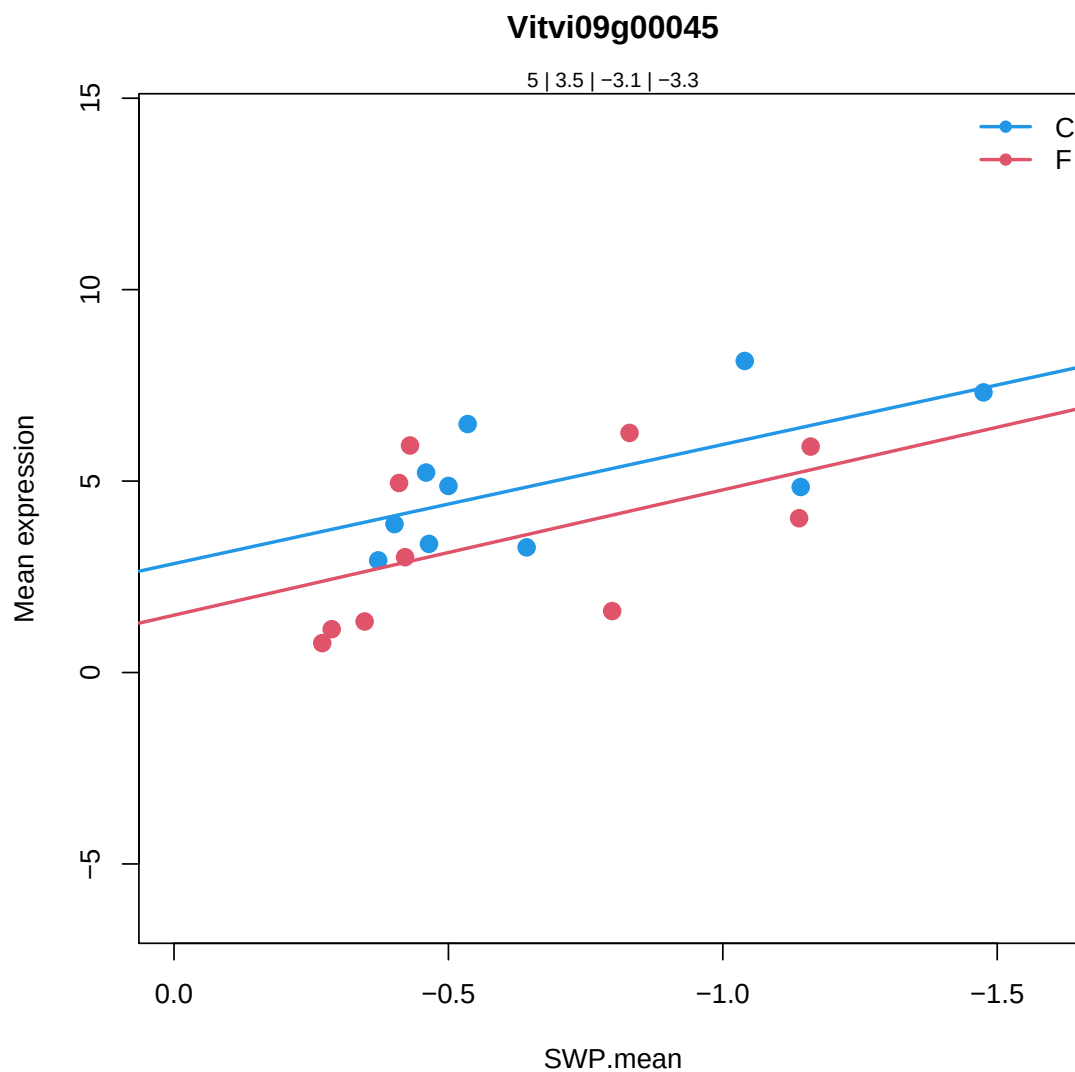
HSP20-like chaperones superfamily protein |

Chr1:20179558-20180122 REVERSE LENGTH=155 |

201606

Coefficients for Vitvi09g00045.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.031606	6.76044e-10	***	8.576166e-10	***
SlopeC	-3.111025	0.02970244	*	0.4299803	
MeanF-MeanC	-1.539846	0.03378118	*	0.1831436	
SlopeF-SlopeC	-0.1609299	0.9362353		0.9999488	



7.2.70 Vitvi06g00533

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

Vitvi06g00533

29.4

protein.postranslational modification

highly ABA-induced PP2C protein 3 |

Chr2:12608855-12610124 FORWARD LENGTH=362 |

201606

Vitvi06g00533

17.01.2002

hormone metabolism.abscisic acid.signal transduction

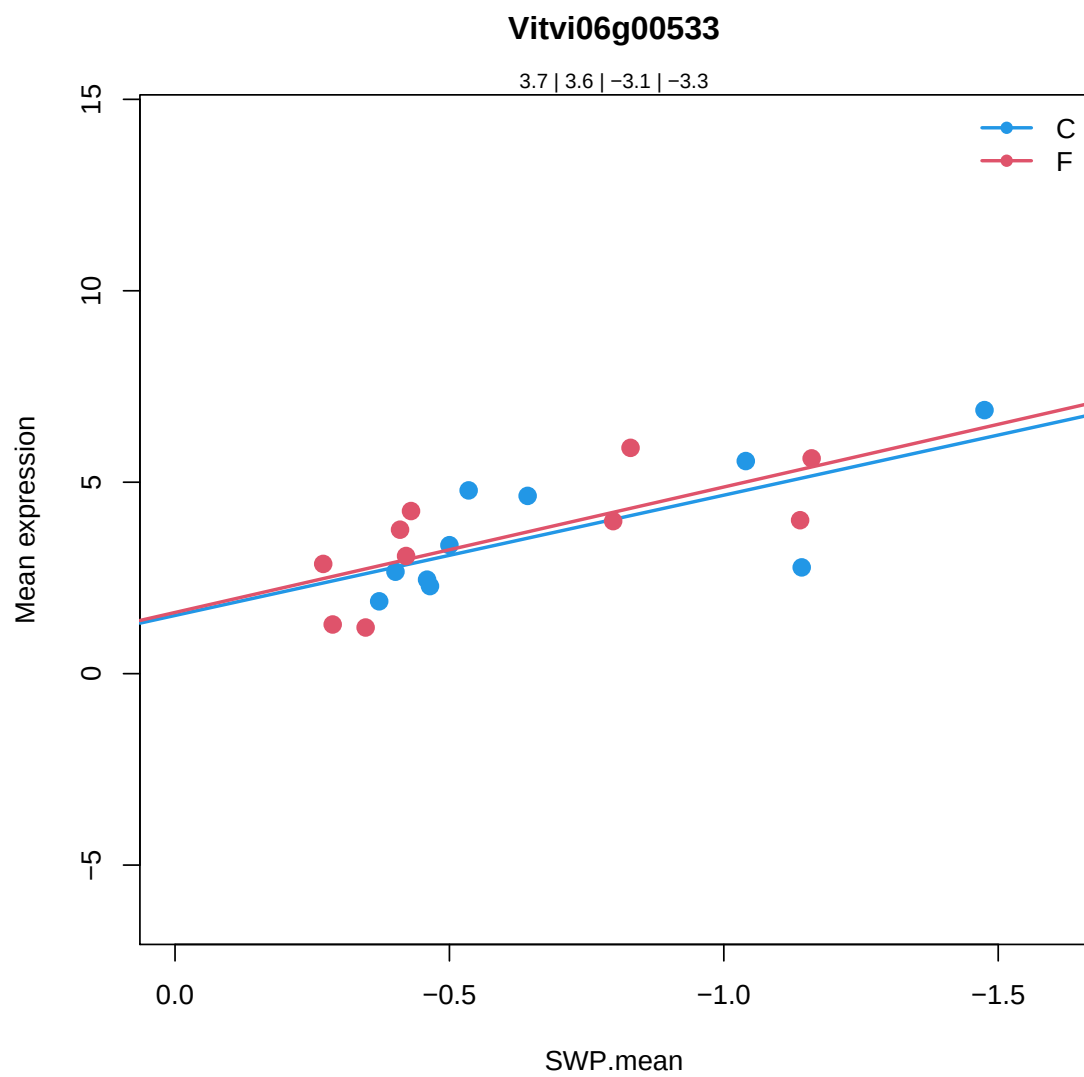
highly ABA-induced PP2C protein 3 |

Chr2:12608855-12610124 FORWARD LENGTH=362 |

201606

Coefficients for Vitvi06g00533.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.728735	1.948614e-10	***	2.522359e-10	***
SlopeC	-3.141484	0.002657744	**	0.1966472	
MeanF-MeanC	-0.1342722	0.7778878		0.9365376	
SlopeF-SlopeC	-0.1347465	0.9229198		0.9999488	



7.2.71 Vitvi13g02014

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

Vitvi13g02014

20.02.2001

stress.abiotic.heat

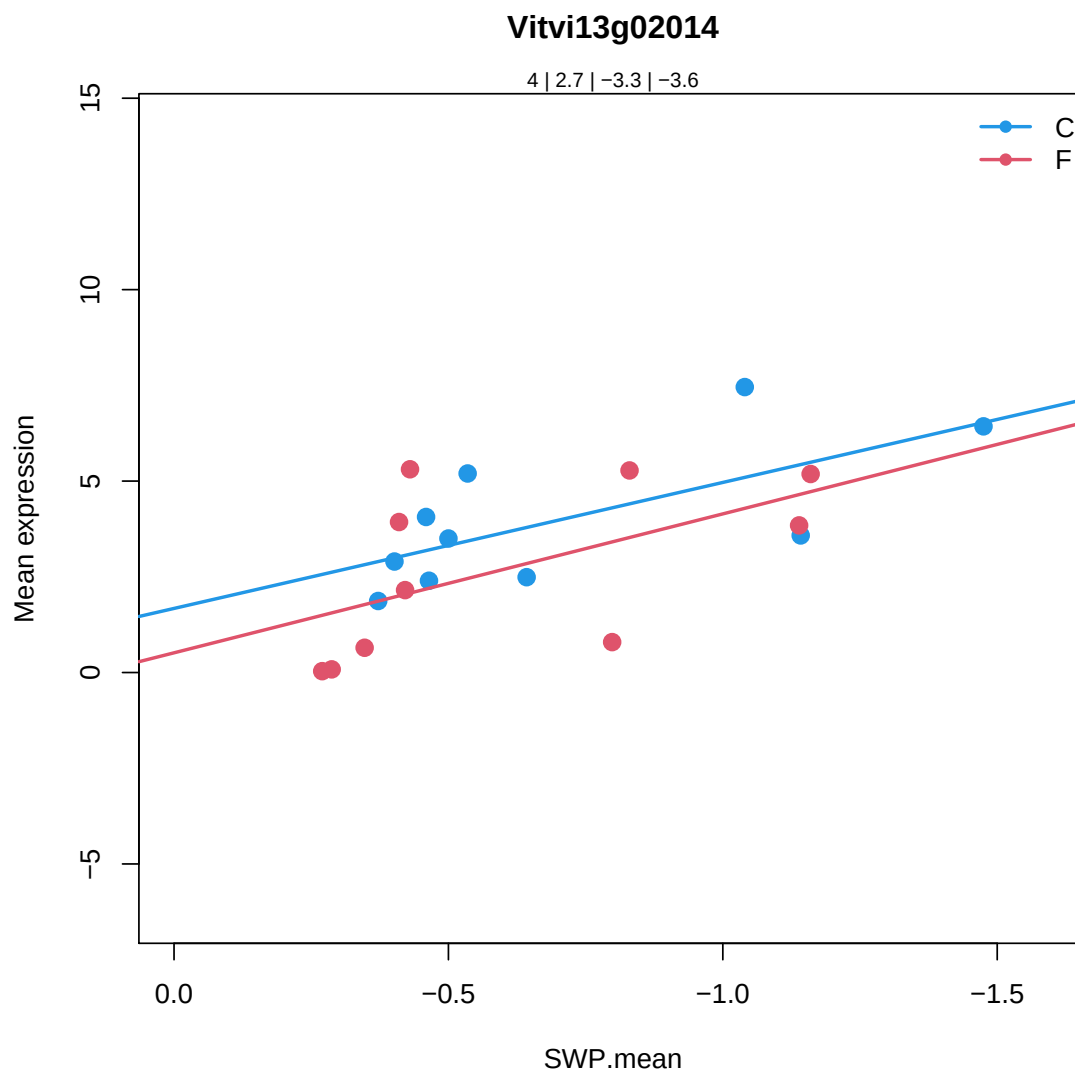
heat shock protein 18.2 |

Chr5:24062632-24063117 FORWARD LENGTH=161 |

201606

Coefficients for Vitvi13g02014.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.987802	3.089219e-08	***	3.715155e-08	***
SlopeC	-3.29079	0.02078355	*	0.378927	
MeanF-MeanC	-1.26242	0.07326951	.	0.3040495	
SlopeF-SlopeC	-0.3375916	0.8650362		0.9999488	



7.2.72 Vitvi02g00436

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

Vitvi02g00436

1.02.2006

PS.photorespiration.hydroxypyruvate reductase

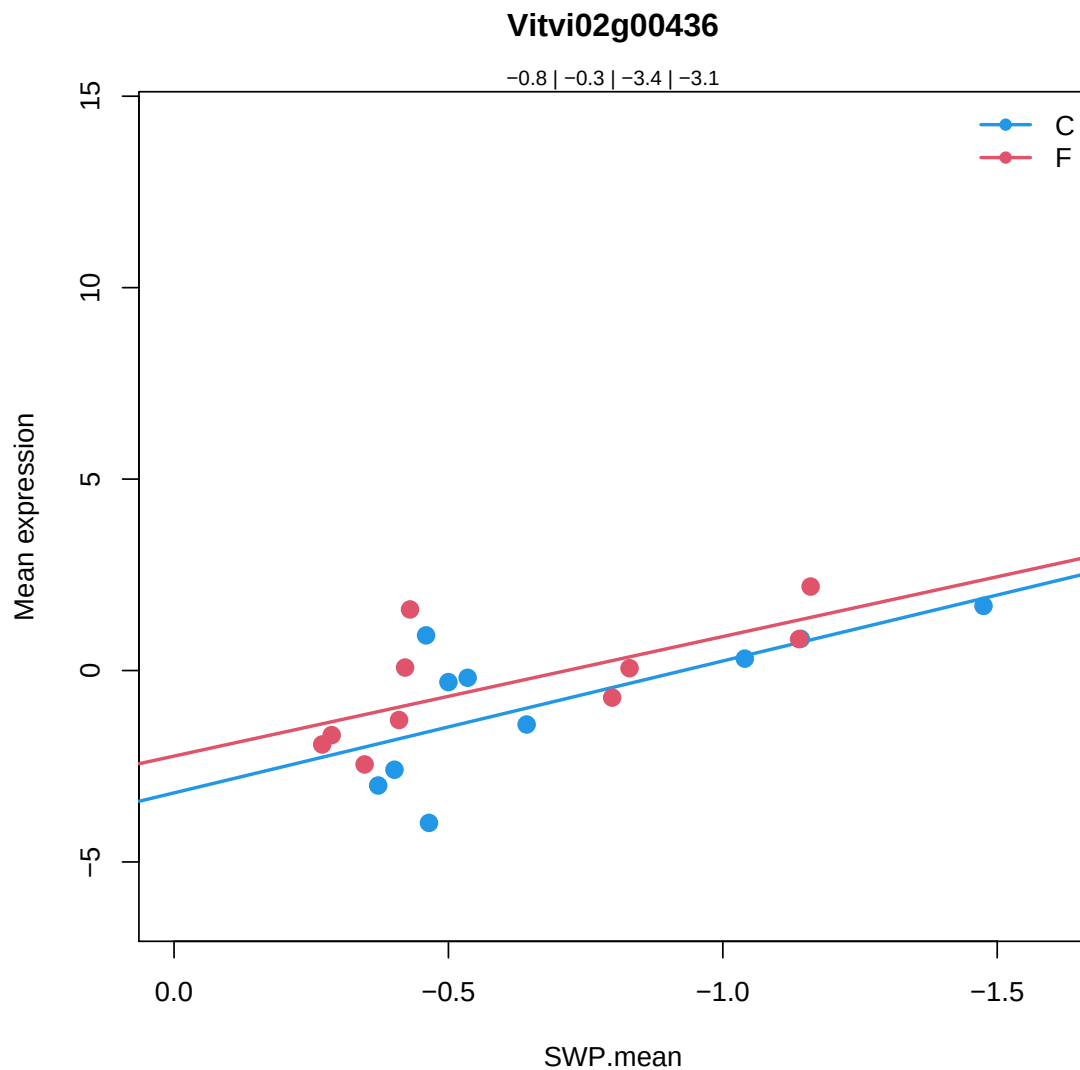
D-isomer specific 2-hydroxyacid dehydrogenase family protein |

Chr1:4274649-4275831 FORWARD LENGTH=323 |

201606

Coefficients for Vitvi02g00436.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.7732662	0.04915228	*	0.05118742	.
SlopeC	-3.44536	0.003042667	**	0.2098476	
MeanF-MeanC	0.4405752	0.4100686		0.7507664	
SlopeF-SlopeC	0.3224828	0.8356227		0.9999488	



7.2.73 Vitvi17g00695

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

Vitvi17g00695

20.02.2001

stress.abiotic.heat

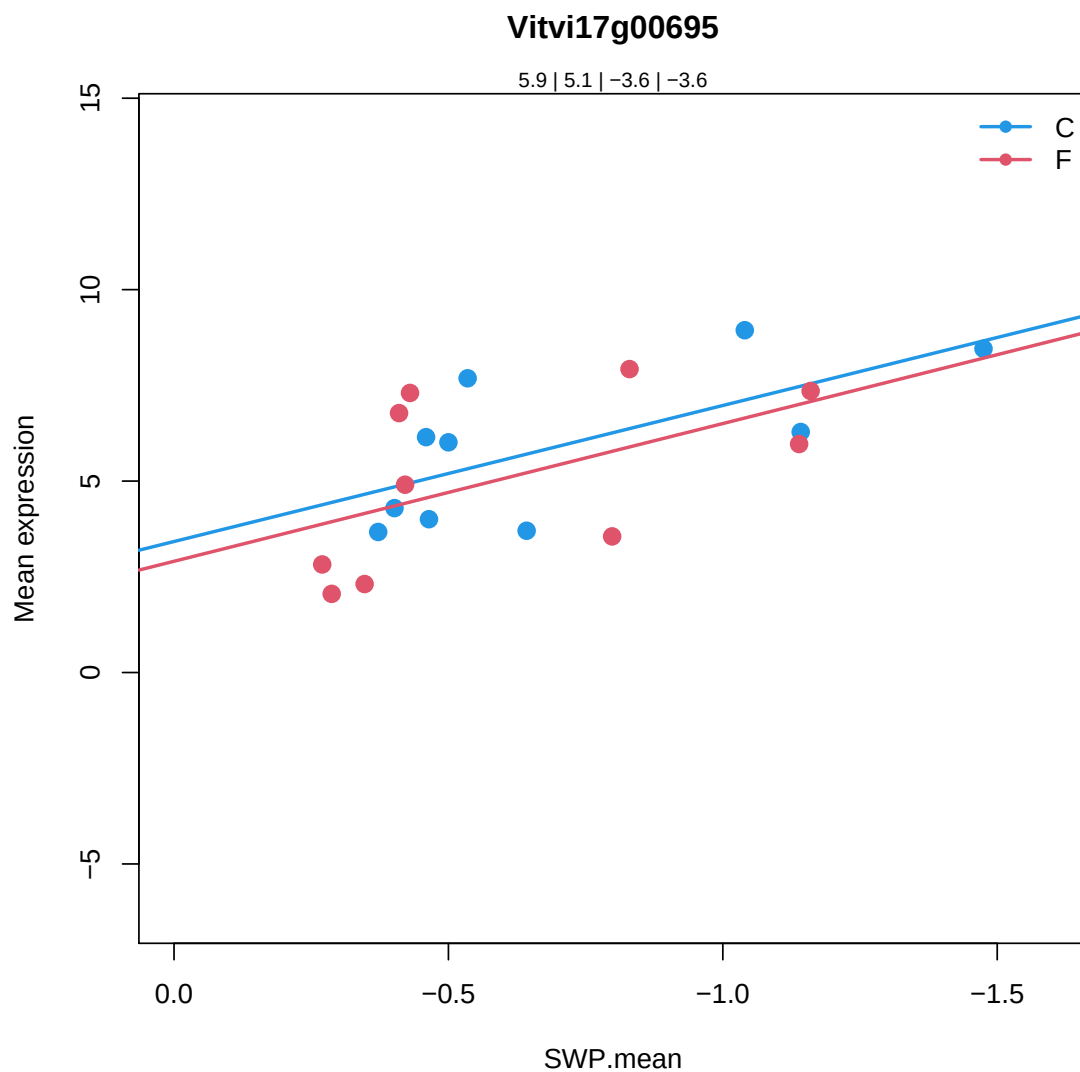
heat shock protein 101 |

Chr1:27936715-27939862 REVERSE LENGTH=911 |

201606

Coefficients for Vitvi17g00695.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.919457	5.917164e-11	***	7.808607e-11	***
SlopeC	-3.552929	0.01728155	*	0.3551322	
MeanF-MeanC	-0.822455	0.252864		0.6127344	
SlopeF-SlopeC	-0.04441921	0.9829086		0.9999488	



7.2.74 Vitvi02g00374

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

Vitvi02g00374

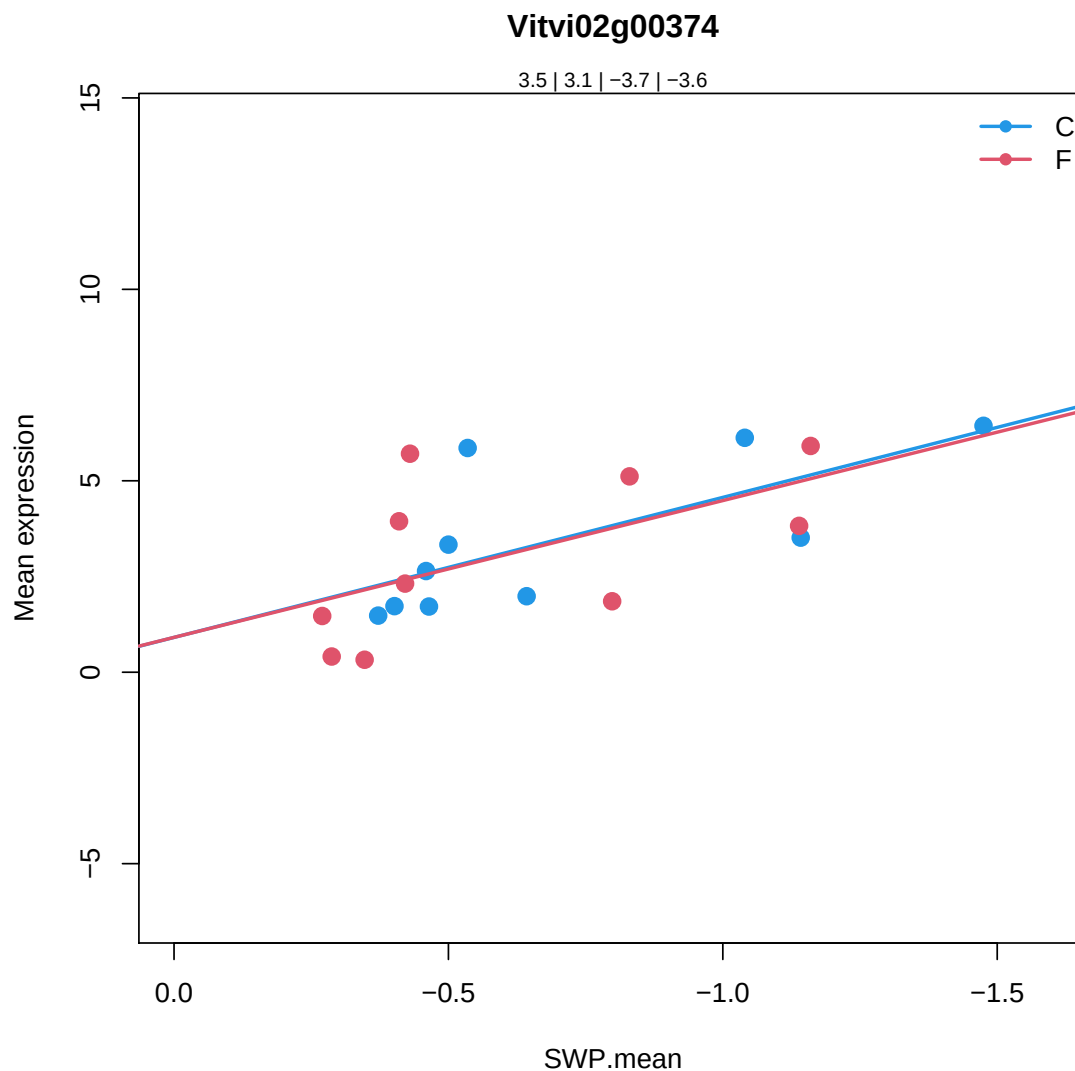
29.05.2011

protein.degradation.ubiquitin

UBX domain-containing protein IPR001012 UBX

Coefficients for Vitvi02g00374.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.480907	1.548508e-07	***	1.828223e-07	***
SlopeC	-3.65719	0.008877934	**	0.2903326	
MeanF-MeanC	-0.3940523	0.548229		0.832362	
SlopeF-SlopeC	0.08429943	0.96486		0.9999488	



7.2.75 Vitvi13g00471

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

Vitvi13g00471

20.02.2001

stress.abiotic.heat

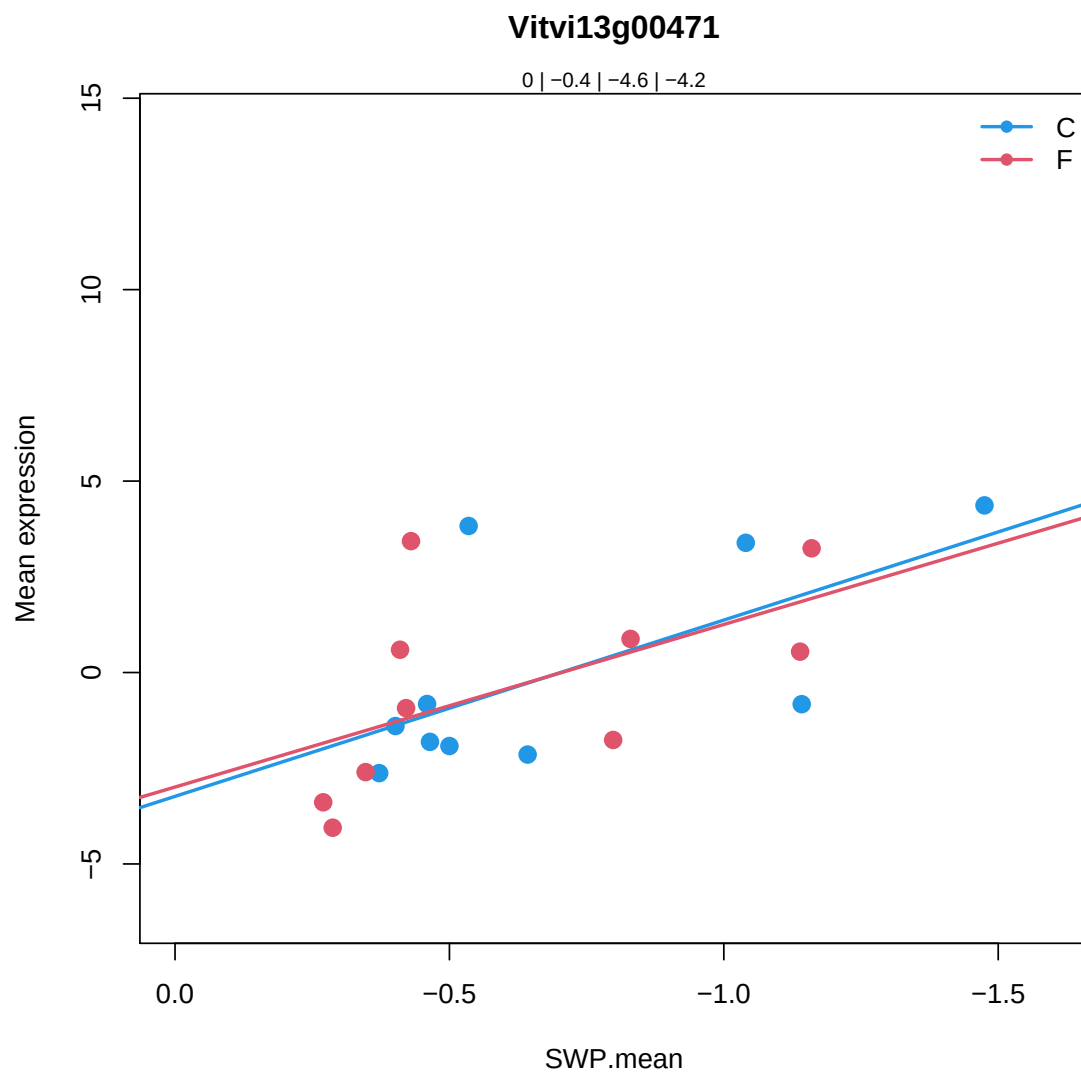
heat shock protein 18.2 |

Chr5:24062632-24063117 FORWARD LENGTH=161 |

201606

Coefficients for Vitvi13g00471.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.00289999	0.9963119		0.9965734	
SlopeC	-4.604229	0.01421304	*	0.3359386	
MeanF-MeanC	-0.4070974	0.6471743		0.8804711	
SlopeF-SlopeC	0.3580492	0.8904042		0.9999488	



7.2.76 Vitvi05g00486

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

Vitvi05g00486

20.02.2001

stress.abiotic.heat

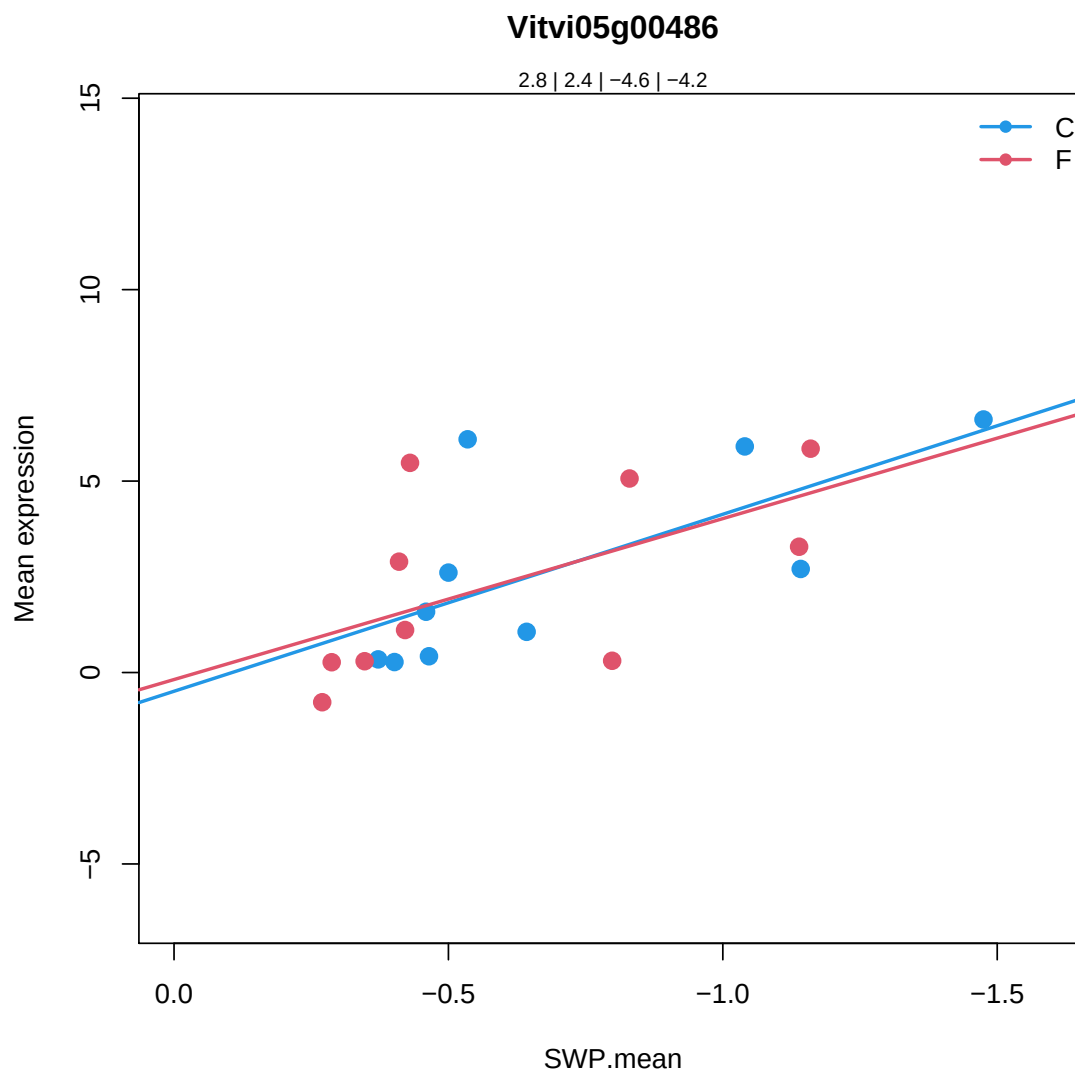
heat-shock protein 70T-2 |

Chr2:13651720-13653411 REVERSE LENGTH=563 |

201606

Coefficients for Vitvi05g00486.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.761098	6.57414e-05	***	7.285905e-05	***
SlopeC	-4.622837	0.007179199	**	0.2775469	
MeanF-MeanC	-0.3837781	0.6324297		0.8748606	
SlopeF-SlopeC	0.4200715	0.8577626		0.9999488	



7.2.77 Vitvi09g00599

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

Vitvi09g00599

20.02.2001

stress.abiotic.heat

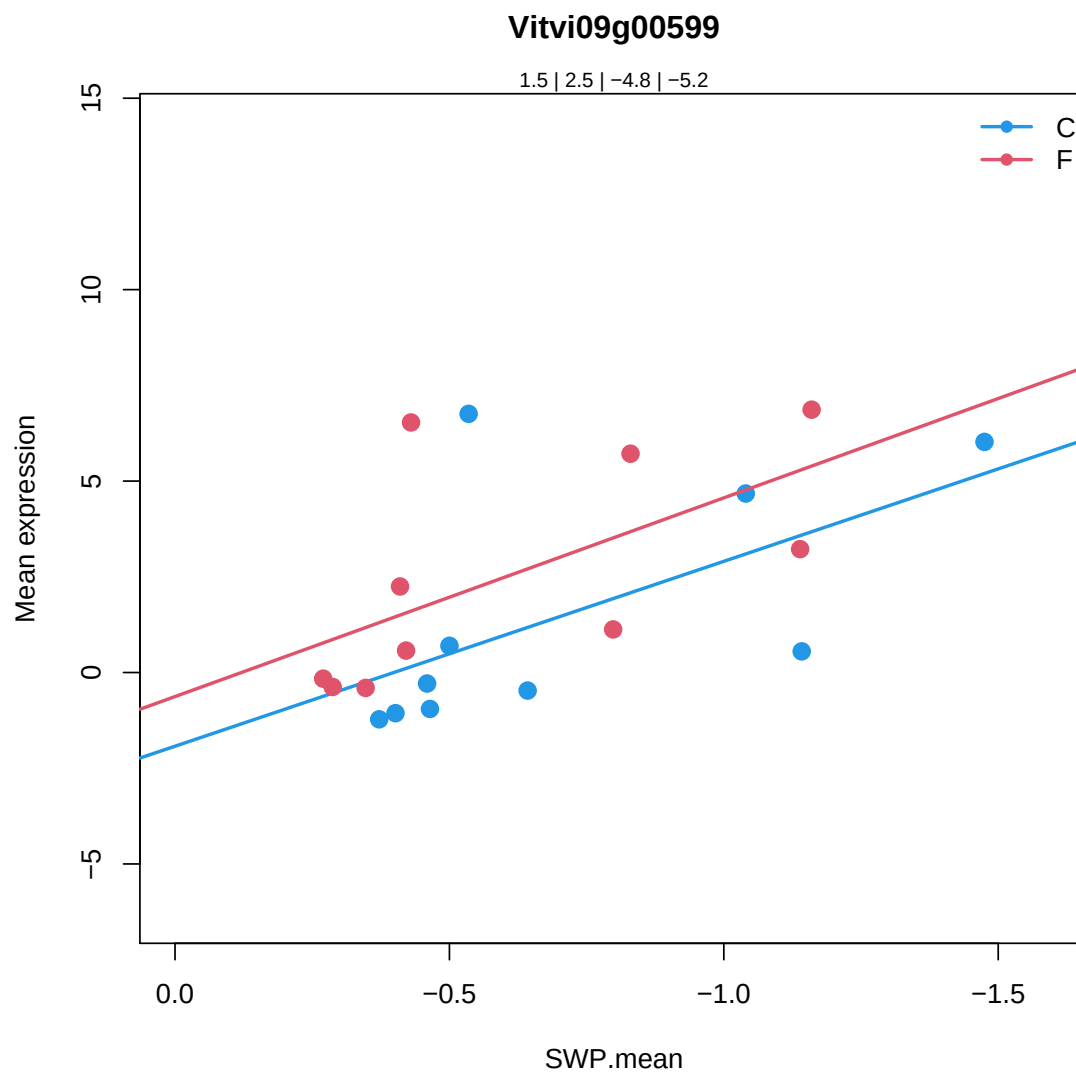
HSP20-like chaperones superfamily protein |

Chr1:19574783-19575766 REVERSE LENGTH=232 |

201606

Coefficients for Vitvi09g00599.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.470814	0.04748063	*	0.0494736	*
SlopeC	-4.828826	0.02144893	*	0.386893	
MeanF-MeanC	1.063106	0.294488		0.661003	
SlopeF-SlopeC	-0.3605426	0.9021035		0.9999488	



7.2.78 Vitvi13g02024

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

Vitvi13g02024

26.2

misc.UDP glucosyl and glucoronyl transferases

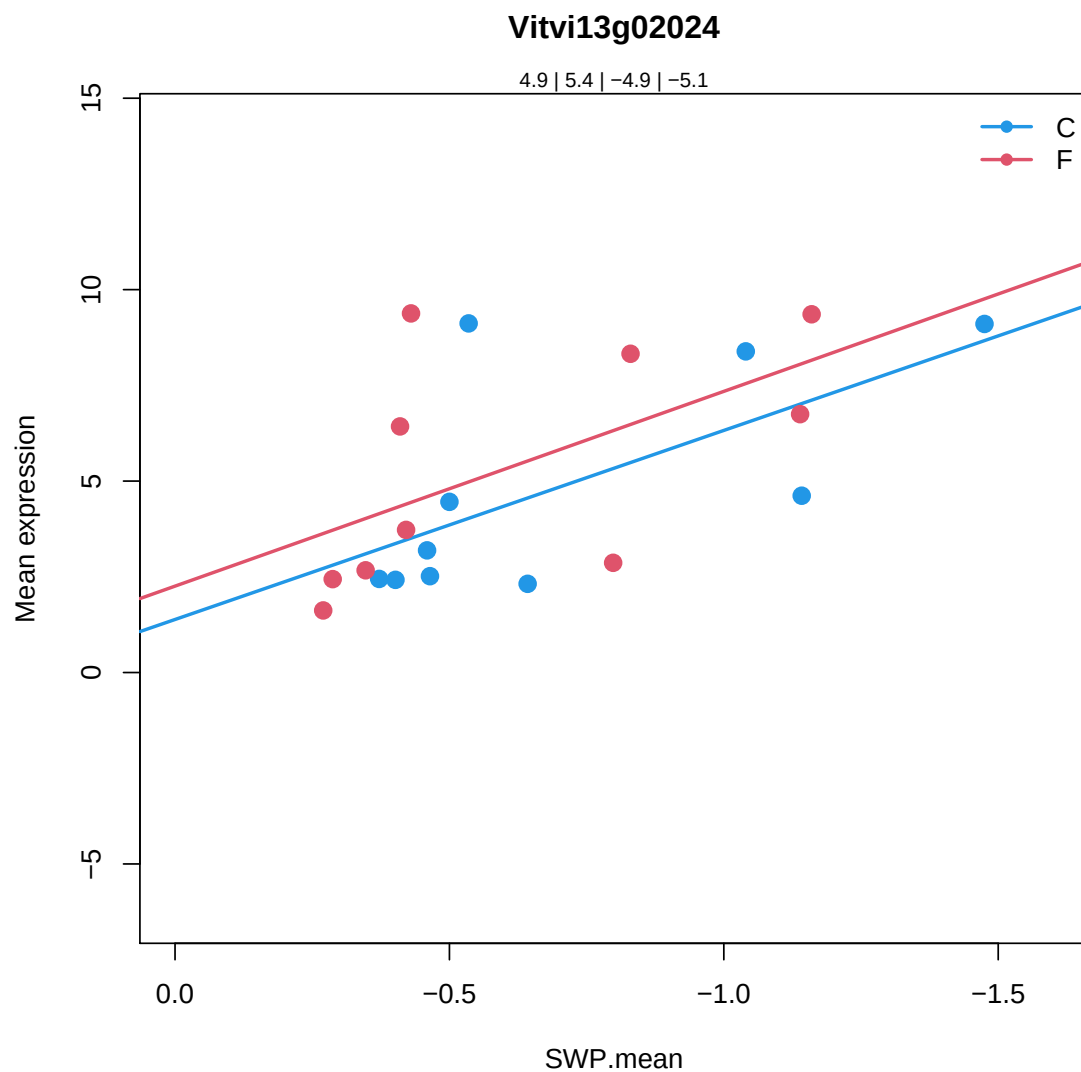
heat shock protein 18.2 |

Chr5:24062632-24063117 FORWARD LENGTH=161 |

201606

Coefficients for Vitvi13g02024.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.85719	4.650855e-07	***	5.414217e-07	***
SlopeC	-4.938026	0.01671165	*	0.3523917	
MeanF-MeanC	0.4983951	0.6115774		0.8646381	
SlopeF-SlopeC	-0.1483944	0.9586909		0.9999488	



7.2.79 Vitvi08g00731

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

Vitvi08g00731

20.02.2001

stress.abiotic.heat

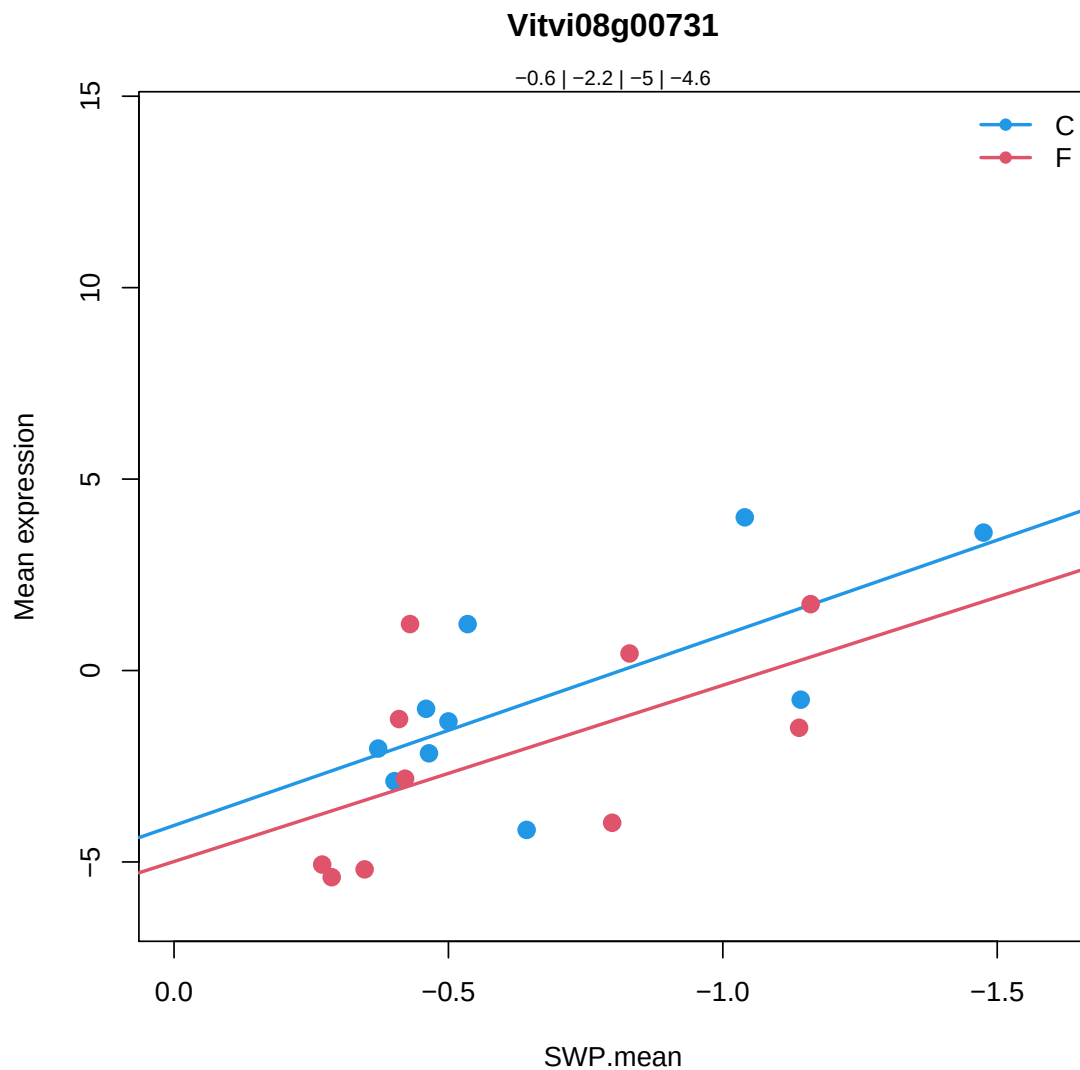
HSP20-like chaperones superfamily protein |

Chr1:19980510-19980983 FORWARD LENGTH=157 |

201606

Coefficients for Vitvi08g00731.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.5532469	0.3709281		0.3770381	
SlopeC	-4.968213	0.007536943	**	0.2777732	
MeanF-MeanC	-1.630057	0.07041397	.	0.2973667	
SlopeF-SlopeC	0.3636611	0.8860073		0.9999488	



7.2.80 Vitvi14g02990

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

Vitvi14g02990

35.2

not assigned.unknown

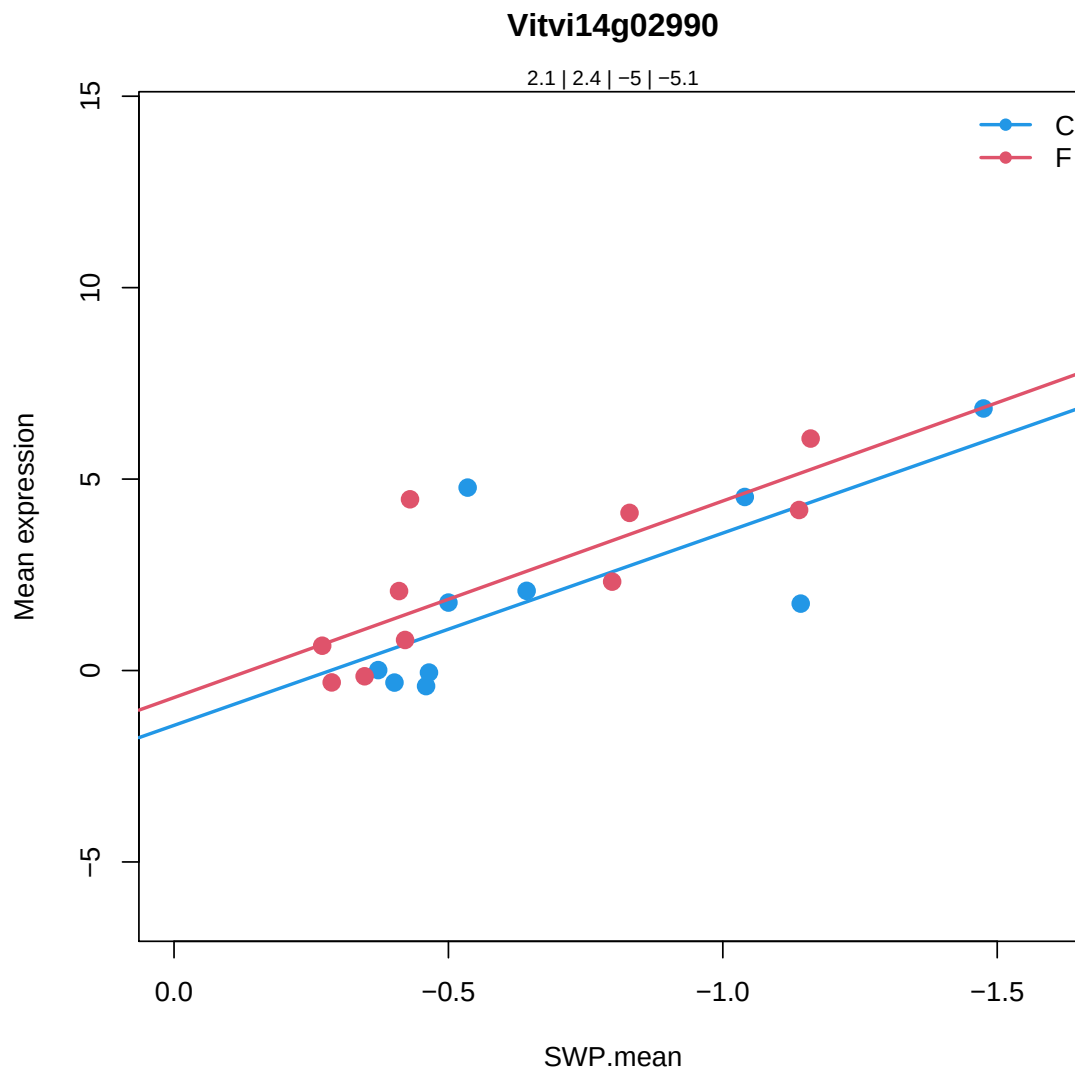
hypothetical protein |

Chr3:10061633-10062481 FORWARD LENGTH=282 |

201606

Coefficients for Vitvi14g02990.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.099223	9.197532e-05	***	0.0001016303	***
SlopeC	-5.022153	0.0004647919	***	0.1005065	
MeanF-MeanC	0.3227609	0.6073488		0.8620981	
SlopeF-SlopeC	-0.1129527	0.9508756		0.9999488	



7.2.81 Vitvi15g01034

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

Vitvi15g01034

20.02.2001

stress.abiotic.heat

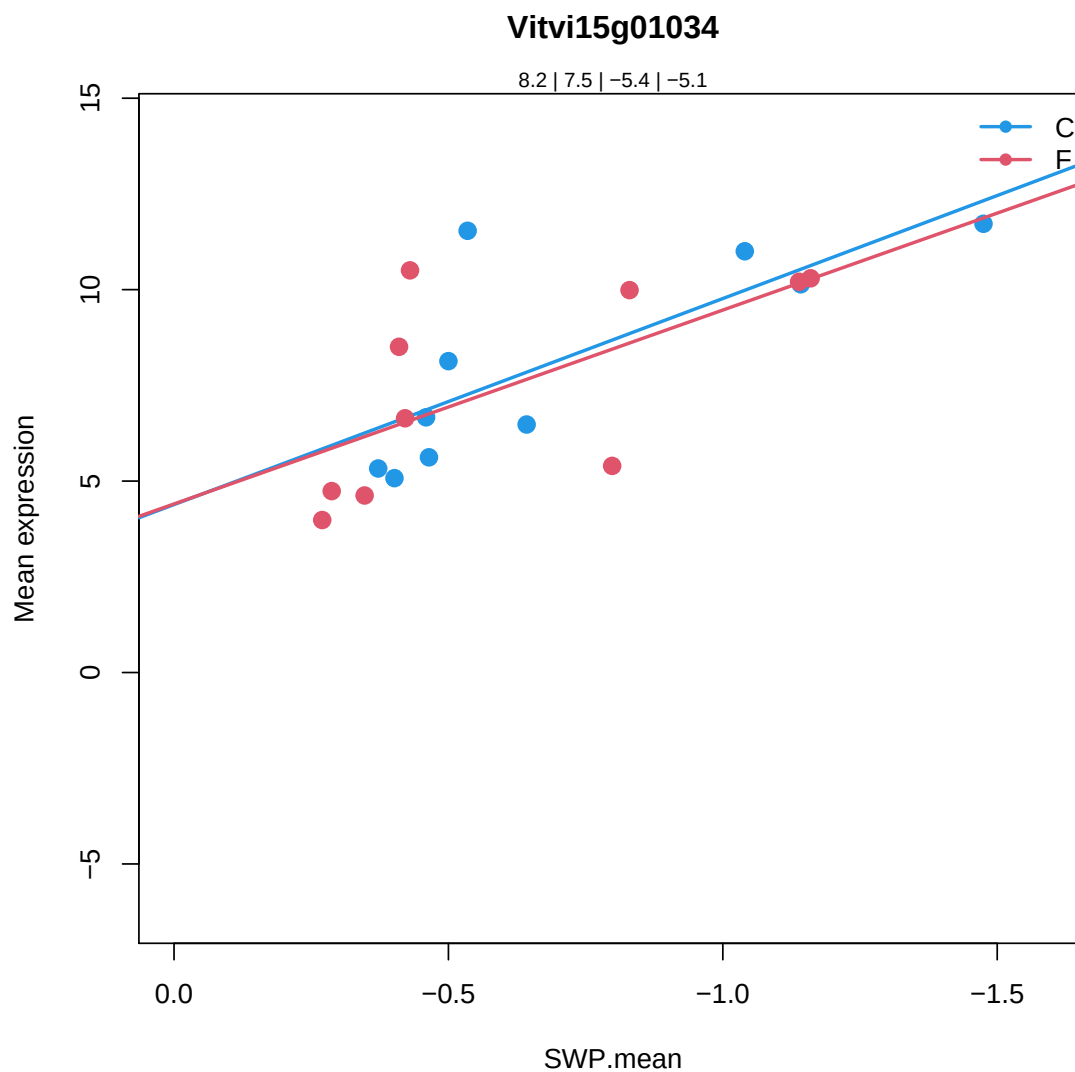
BCL-2-associated athanogene 6 |

Chr2:18986586-18989827 FORWARD LENGTH=1043 |

201606

Coefficients for Vitvi15g01034.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	8.170016	1.181955e-12	***	1.687937e-12	***
SlopeC	-5.38071	0.002228703	**	0.1816214	
MeanF-MeanC	-0.6819577	0.3963123		0.7423612	
SlopeF-SlopeC	0.316925	0.8920127		0.9999488	



7.2.82 Vitvi13g02017

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

Vitvi13g02017

20.02.2001

stress.abiotic.heat

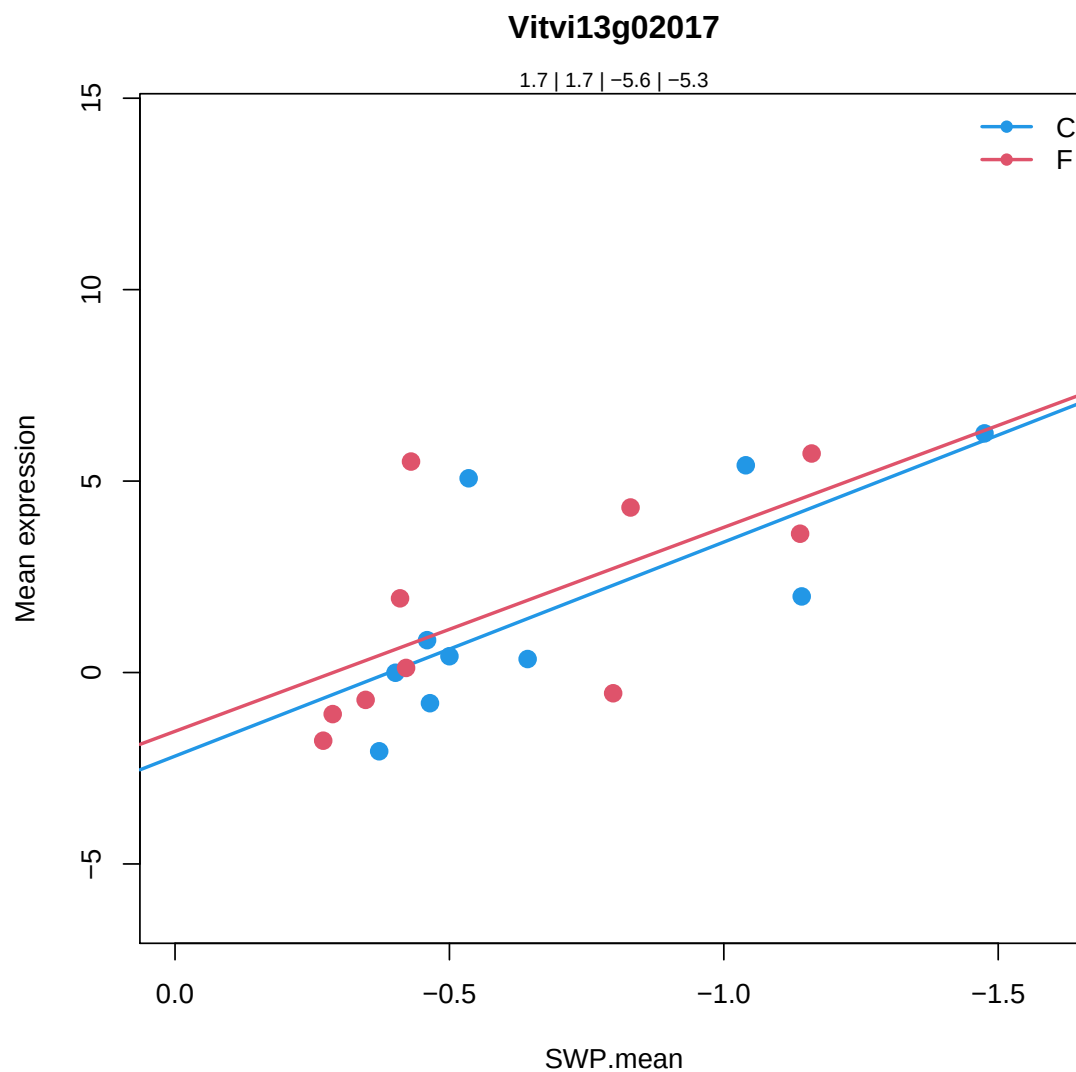
heat shock protein 18.2 |

Chr5:24062632-24063117 FORWARD LENGTH=161 |

201606

Coefficients for Vitvi13g02017.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.747598	0.008703427	**	0.009234138	**
SlopeC	-5.59067	0.003192727	**	0.2103859	
MeanF-MeanC	-0.03771032	0.9652737		0.9919971	
SlopeF-SlopeC	0.2632103	0.9173508		0.9999488	



7.2.83 Vitvi12g02138

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

Vitvi12g02138

20.02.2001

stress.abiotic.heat

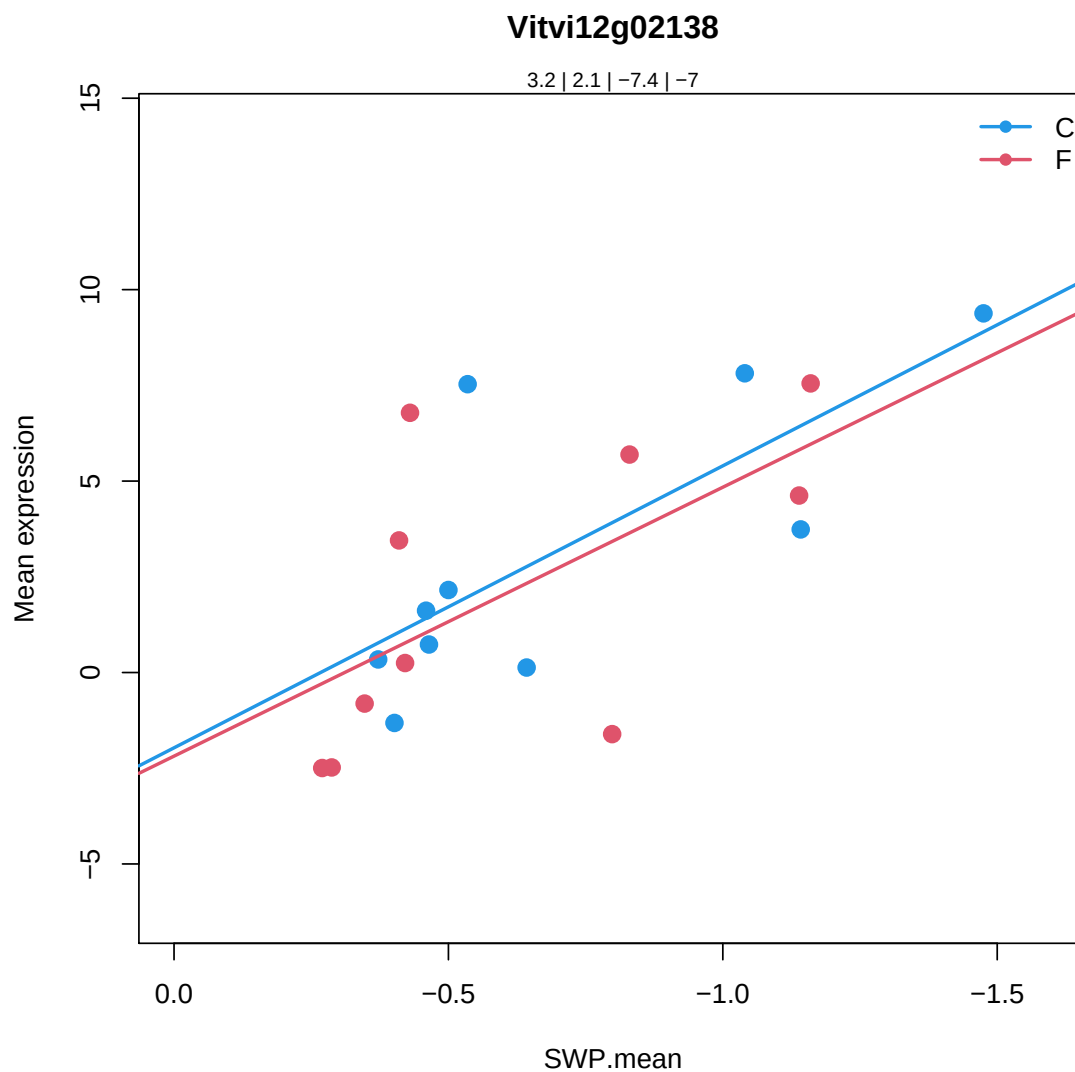
HSP20-like chaperones superfamily protein |

Chr4:6370537-6371124 FORWARD LENGTH=195 |

201606

Coefficients for Vitvi12g02138.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.21186	0.0008015218	***	0.0008698943	***
SlopeC	-7.364735	0.004094778	**	0.2328828	
MeanF-MeanC	-1.11679	0.3484371		0.7079025	
SlopeF-SlopeC	0.3417037	0.9211381		0.9999488	



7.2.84 Vitvi04g00135

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

Vitvi04g00135

20.02.2001

stress.abiotic.heat

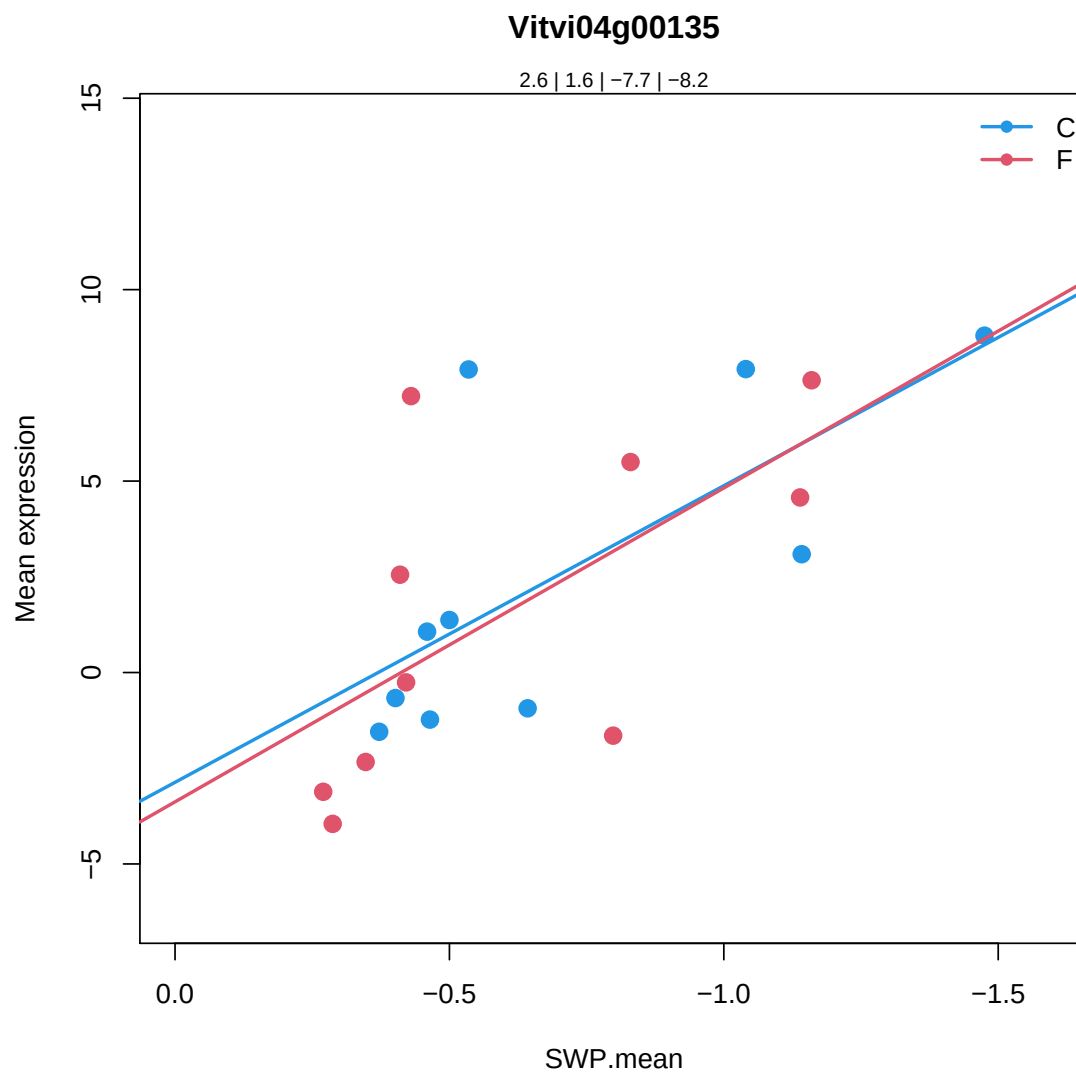
17.6 kDa class II heat shock protein |

Chr5:3882409-3882876 REVERSE LENGTH=155 |

201606

Coefficients for Vitvi04g00135.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.578927	0.01060559	*	0.01122885	*
SlopeC	-7.746727	0.006376148	**	0.2661465	
MeanF-MeanC	-0.9622751	0.4681276		0.7878981	
SlopeF-SlopeC	-0.4507473	0.9070348		0.9999488	



7.2.85 Vitvi18g02423

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

Vitvi18g02423

35.2

not assigned.unknown

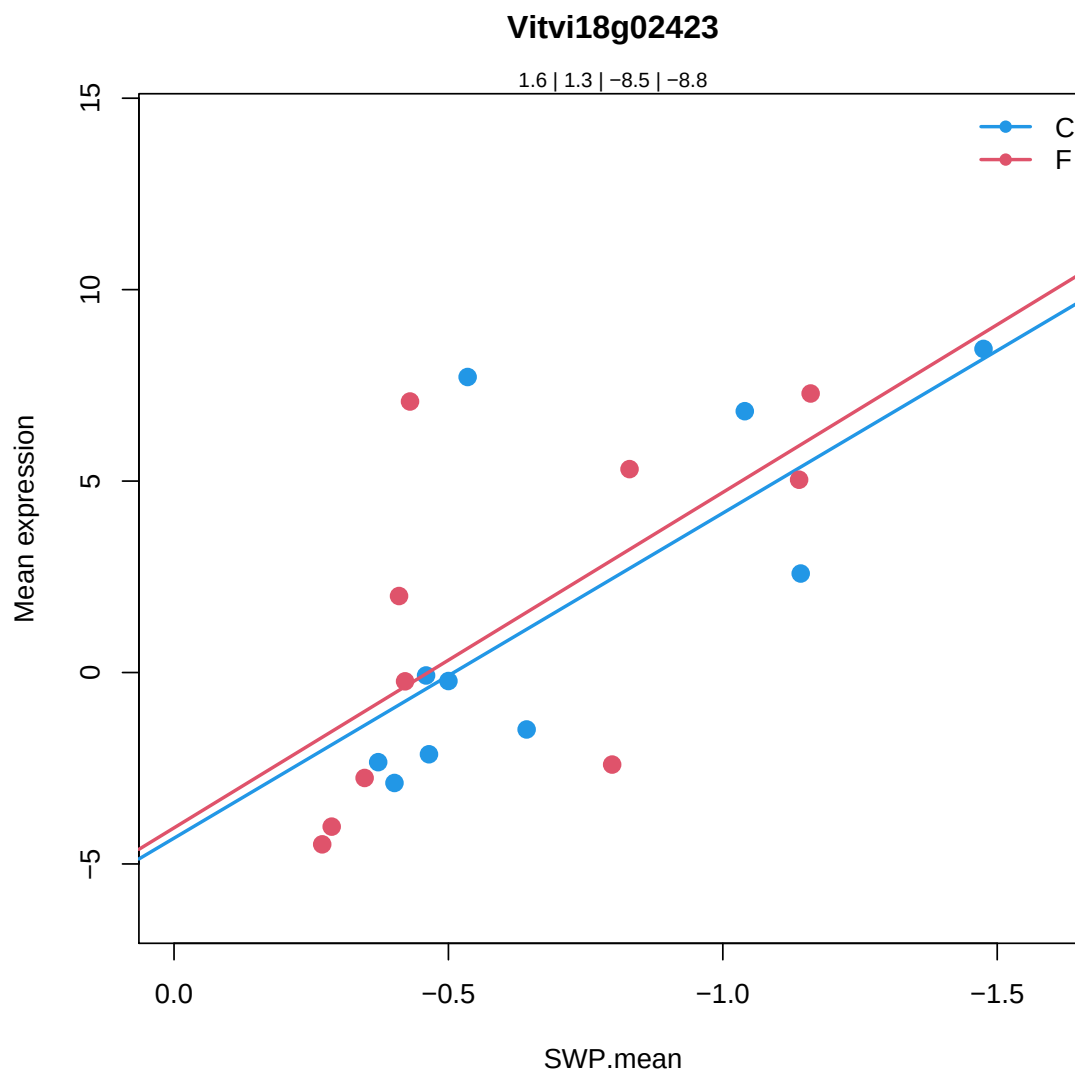
HSP20-like chaperones superfamily protein |

Chr4:6370537-6371124 FORWARD LENGTH=195 |

201606

Coefficients for Vitvi18g02423.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.643122	0.1022202		0.1056729	
SlopeC	-8.488894	0.004528886	**	0.2419697	
MeanF-MeanC	-0.3621322	0.7927368		0.9414753	
SlopeF-SlopeC	-0.2732159	0.9459792		0.9999488	



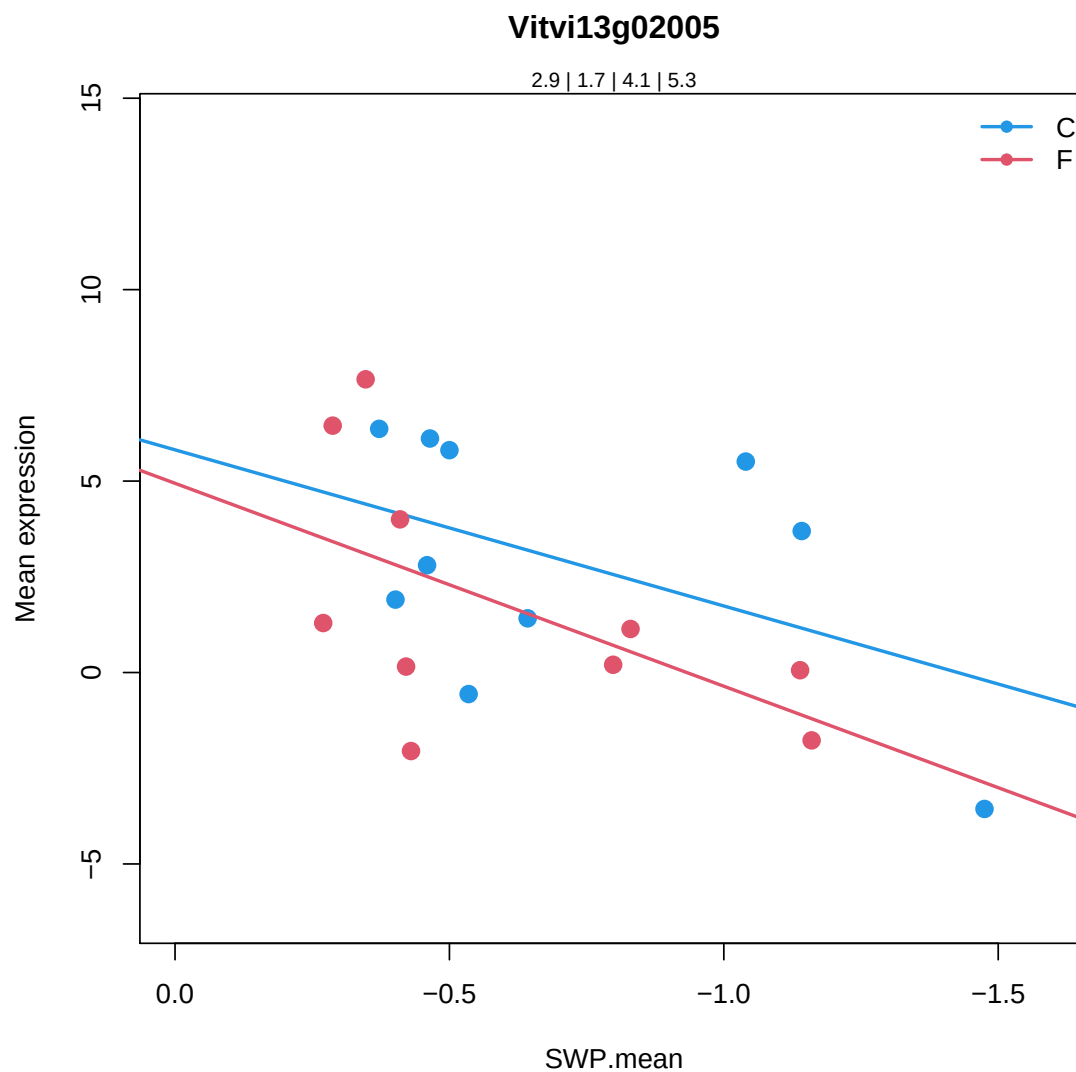
7.3 type2

7.3.1 Vitvi13g02005

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
Vitvi13g02005
29.05.2001
protein.degradation.subtilases
Subtilisin-like serine endopeptidase family protein |
Chr5:23755787-23758600 FORWARD LENGTH=710 |
201606
```

Coefficients for Vitvi13g02005.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.948421	0.001571115	**	0.001694639	**
SlopeC	4.07808	0.08613381	.	0.5889741	
MeanF-MeanC	-1.235611	0.2955399		0.6617627	
SlopeF-SlopeC	1.221977	0.7207826		0.9999488	



7.3.2 Vitvi05g01577

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

Vitvi05g01577

20.1.7.3

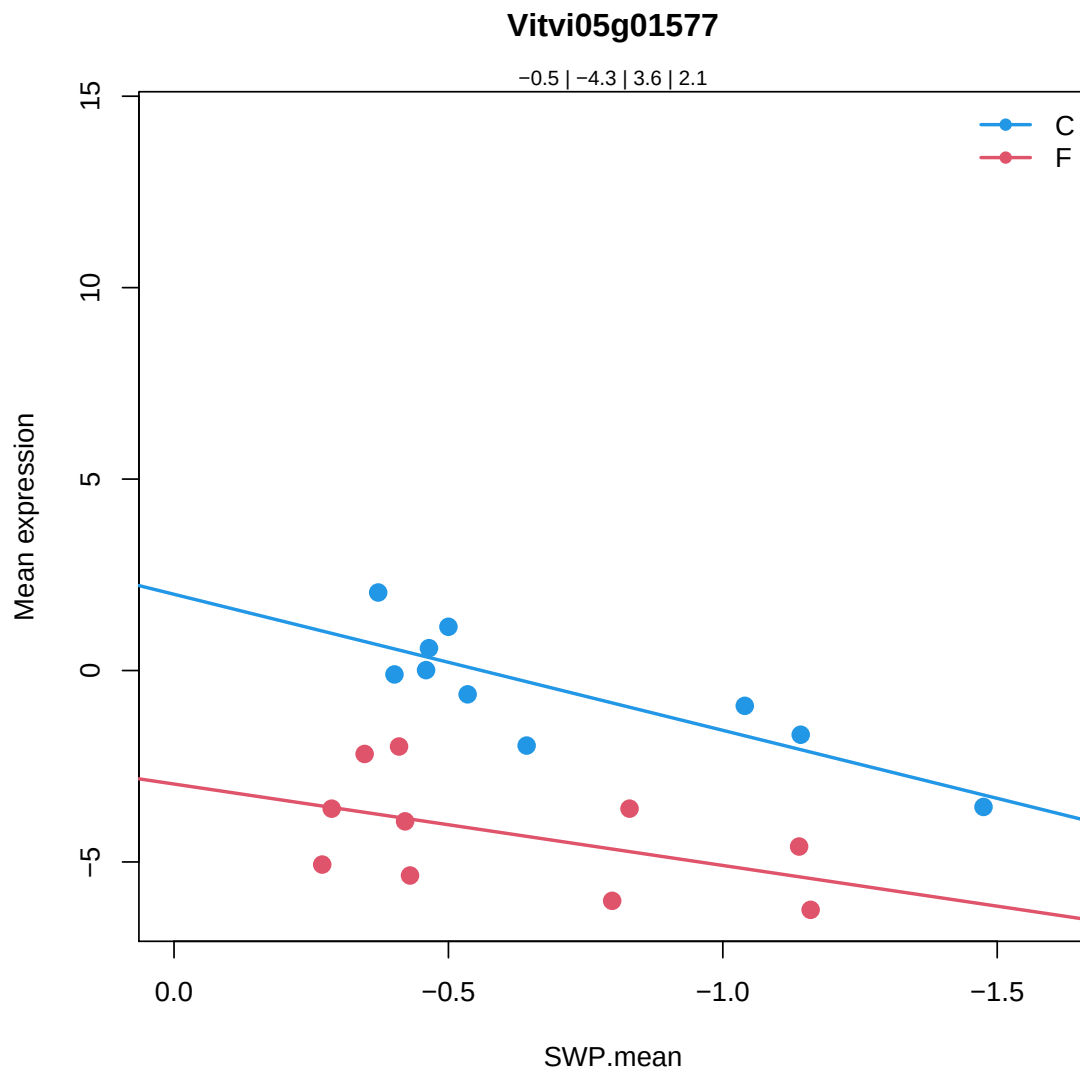
stress.biotic.PR-proteins.PR3/4/8/11 (chitinases and chitin binding pr
homolog of carrot EP3-3 chitinase |

Chr3:20145935-20147034 FORWARD LENGTH=273 |

201606

Coefficients for Vitvi05g01577.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.5075609	0.1396409		0.1438405	
SlopeC	3.553568	0.0008792532	***	0.118598	
MeanF-MeanC	-3.752991	6.802344e-08	***	2.920601e-06	***
SlopeF-SlopeC	-1.42671	0.3093121		0.9999488	



7.3.3 Vitvi19g01048

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

Vitvi19g01048

26.9

misc.glutathione S transferases

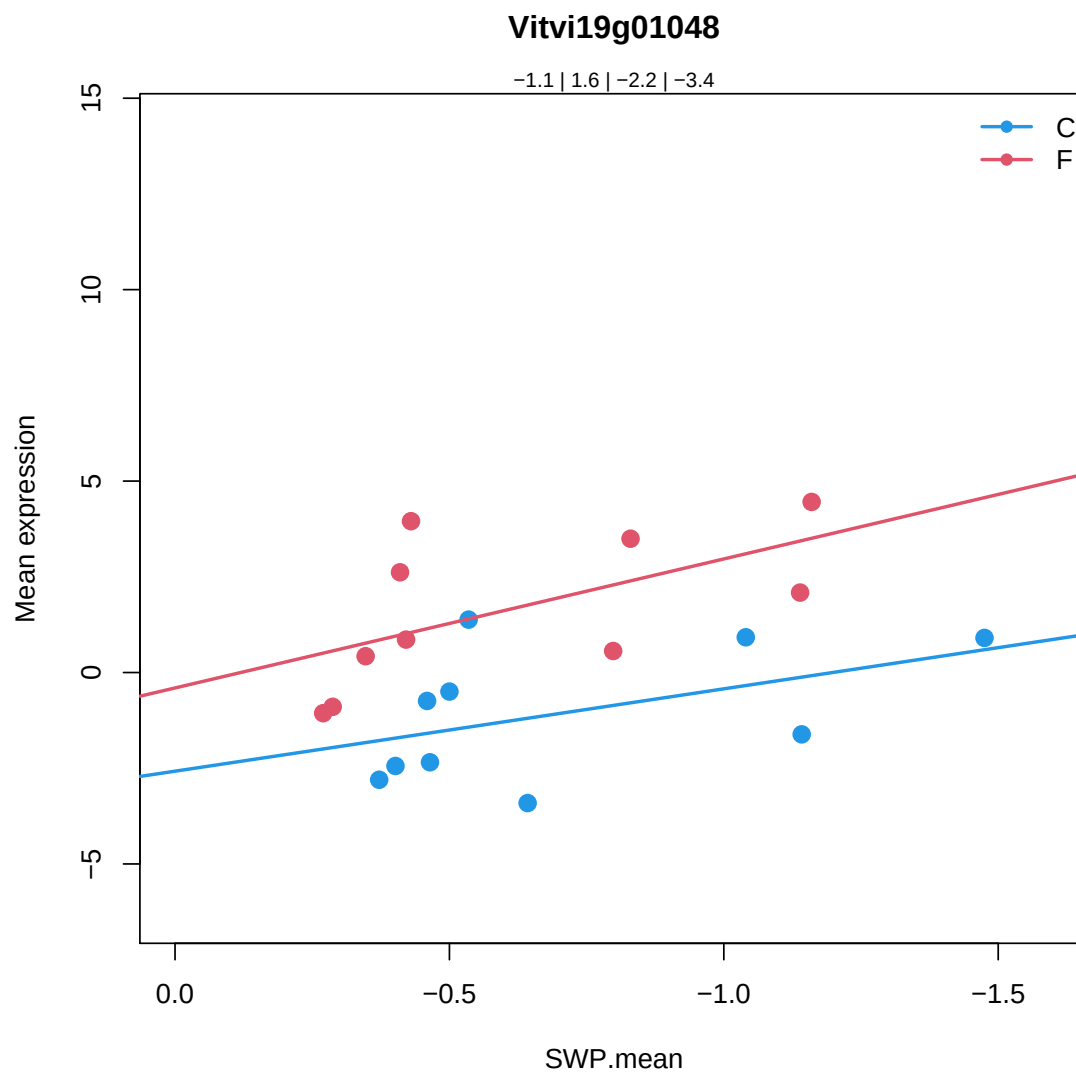
glutathione S-transferase TAU 25 |

Chr1:5872208-5872958 FORWARD LENGTH=221 |

201606

Coefficients for Vitvi19g01048.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.064541	0.02951157	*	0.03089603	*
SlopeC	-2.150775	0.1048283		0.6181019	
MeanF-MeanC	2.714192	0.0003836245	***	0.005633145	**
SlopeF-SlopeC	-1.218795	0.5258973		0.9999488	



7.3.4 Vitvi09g01282

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

Vitvi09g01282

26.13

misc.acid and other phosphatases

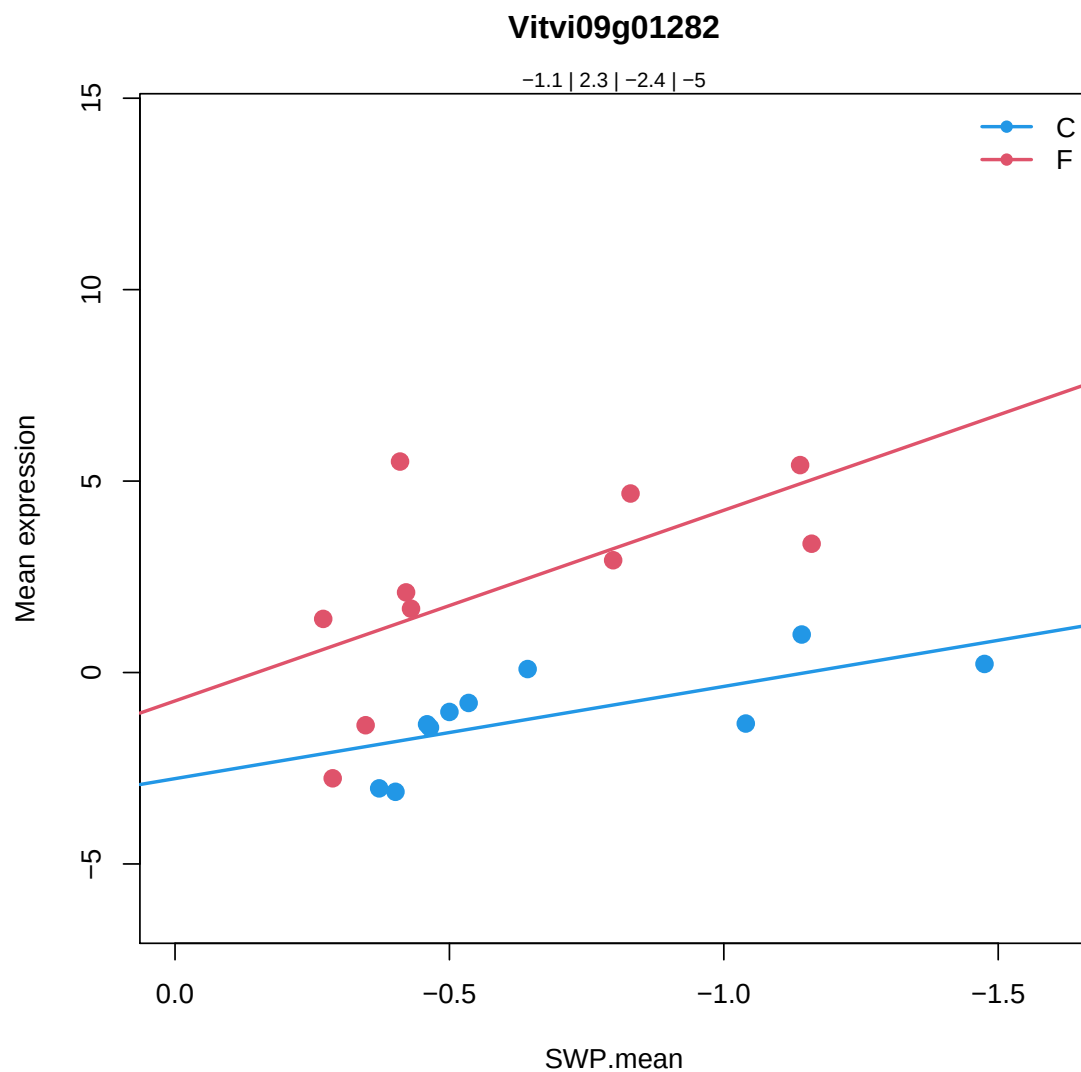
HAD superfamily%2C subfamily IIIB acid phosphatase |

Chr4:12901736-12902882 REVERSE LENGTH=260 |

201606

Coefficients for Vitvi09g01282.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.078226	0.03754027	*	0.03919906	*
SlopeC	-2.408129	0.08927348	.	0.5953805	
MeanF-MeanC	3.37008	7.180676e-05	***	0.001351208	**
SlopeF-SlopeC	-2.570707	0.2154002		0.9999488	



7.3.5 Vitvi07g02214

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

Vitvi07g02214

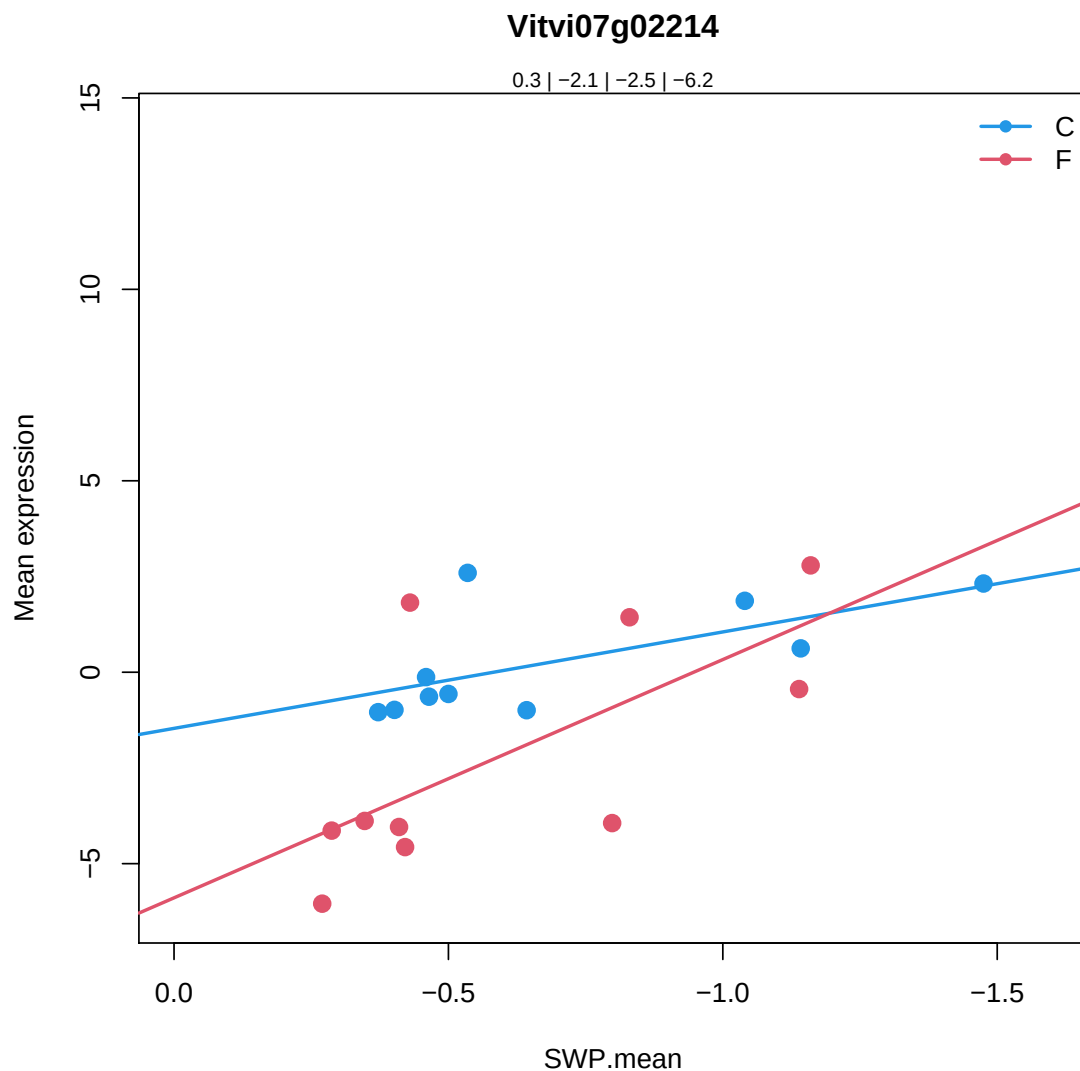
35.2

not assigned.unknown

GATA transcription factor 22 IPR000679 Zinc finger, GATA-type

Coefficients for Vitvi07g02214.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3045917	0.5752195		0.5808597	
SlopeC	-2.518808	0.1052292		0.619507	
MeanF-MeanC	-2.405858	0.004444061	**	0.04150513	*
SlopeF-SlopeC	-3.70436	0.1091801		0.9999488	



7.3.6 Vitvi13g00451

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

Vitvi13g00451

20.02.2001

stress.abiotic.heat

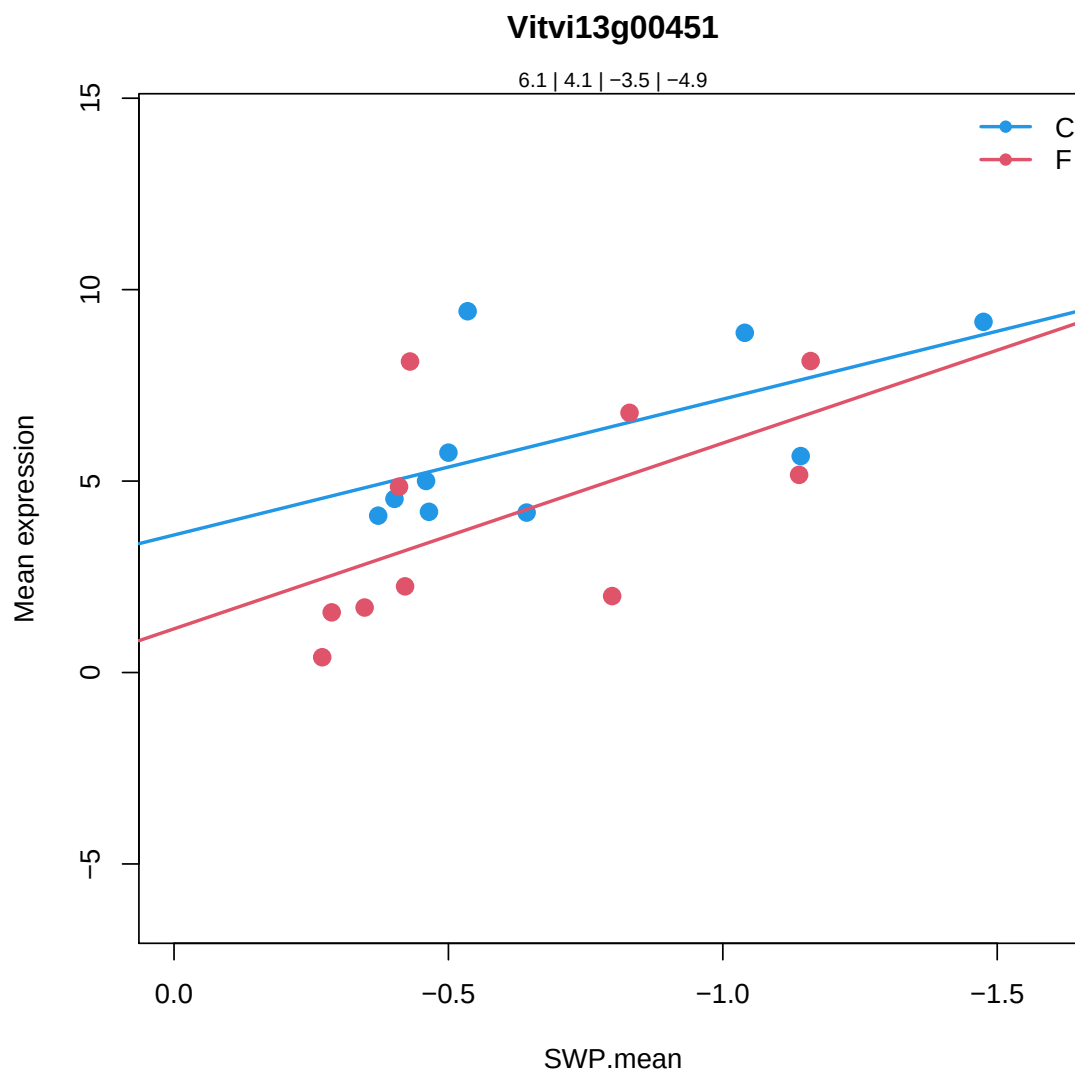
heat shock protein 18.2 |

Chr5:24062632-24063117 FORWARD LENGTH=161 |

201606

Coefficients for Vitvi13g00451.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.08702	1.42437e-09	***	1.78744e-09	***
SlopeC	-3.548031	0.04710944	*	0.4986403	
MeanF-MeanC	-1.990168	0.02999342	*	0.1689493	
SlopeF-SlopeC	-1.302419	0.60872		0.9999488	



7.3.7 Vitvi13g02018

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

Vitvi13g02018

20.02.2001

stress.abiotic.heat

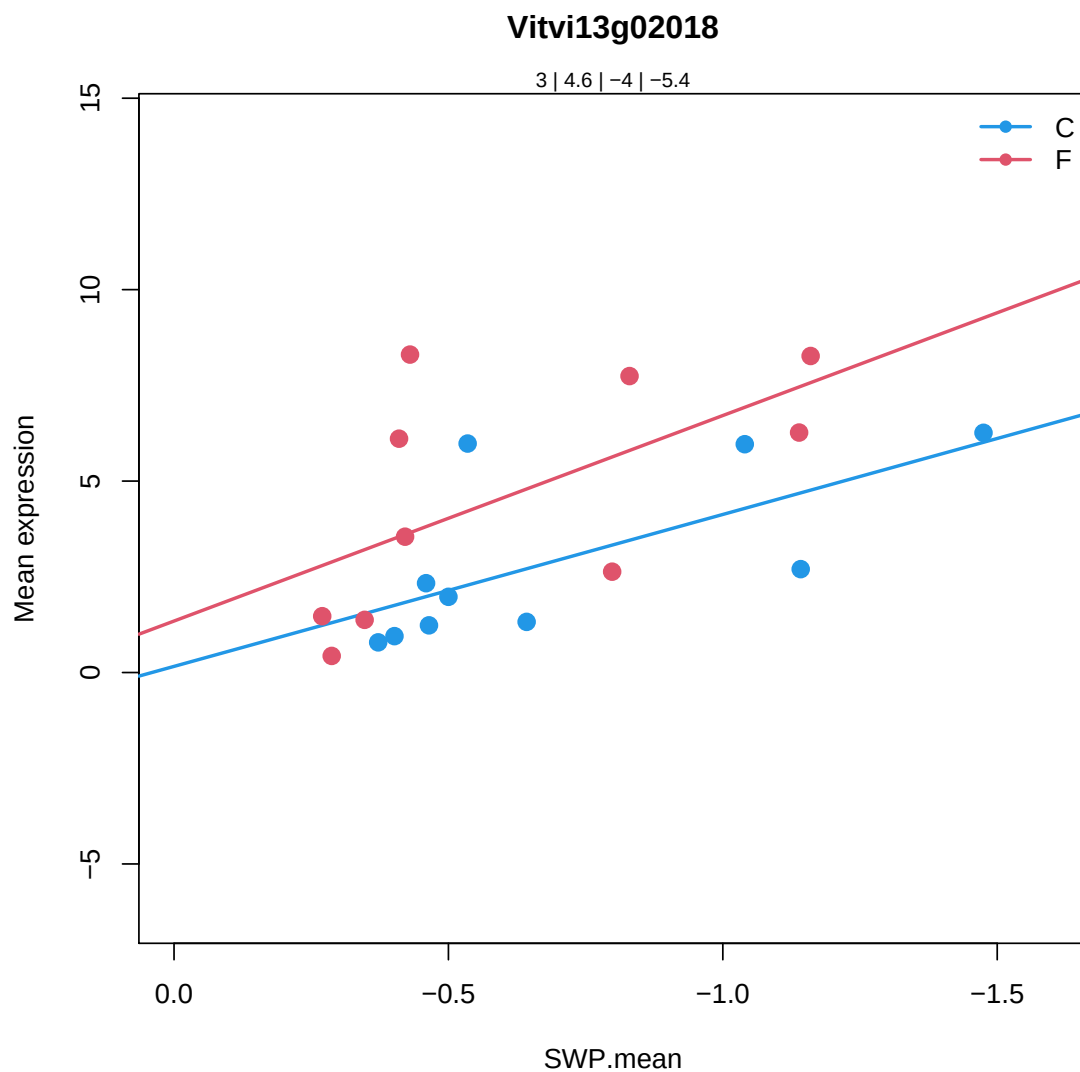
heat shock protein 18.2 |

Chr5:24062632-24063117 FORWARD LENGTH=161 |

201606

Coefficients for Vitvi13g02018.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.950521	8.38613e-05	***	9.27519e-05	***
SlopeC	-3.968203	0.02917498	*	0.4292327	
MeanF-MeanC	1.664414	0.06710013	.	0.2880958	
SlopeF-SlopeC	-1.399499	0.5853876		0.9999488	



7.3.8 Vitvi13g00490

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

Vitvi13g00490

20.02.2001

stress.abiotic.heat

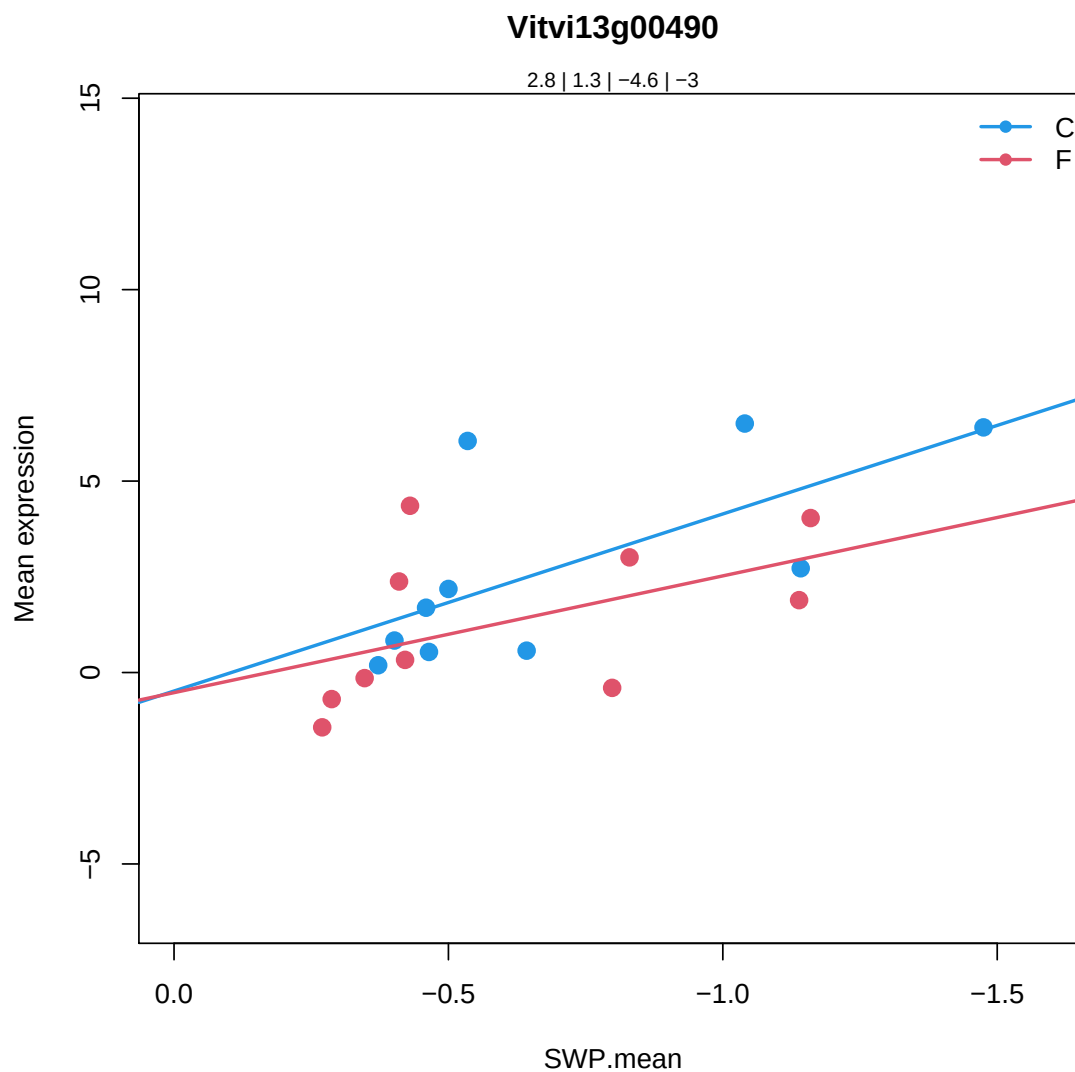
heat shock protein 18.2 |

Chr5:24062632-24063117 FORWARD LENGTH=161 |

201606

Coefficients for Vitvi13g00490.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.768364	3.965659e-05	***	4.415558e-05	***
SlopeC	-4.624813	0.005434675	**	0.2577627	
MeanF-MeanC	-1.436279	0.07249786	.	0.3024112	
SlopeF-SlopeC	1.575339	0.486818		0.9999488	



7.3.9 Vitvi07g00457

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

Vitvi07g00457

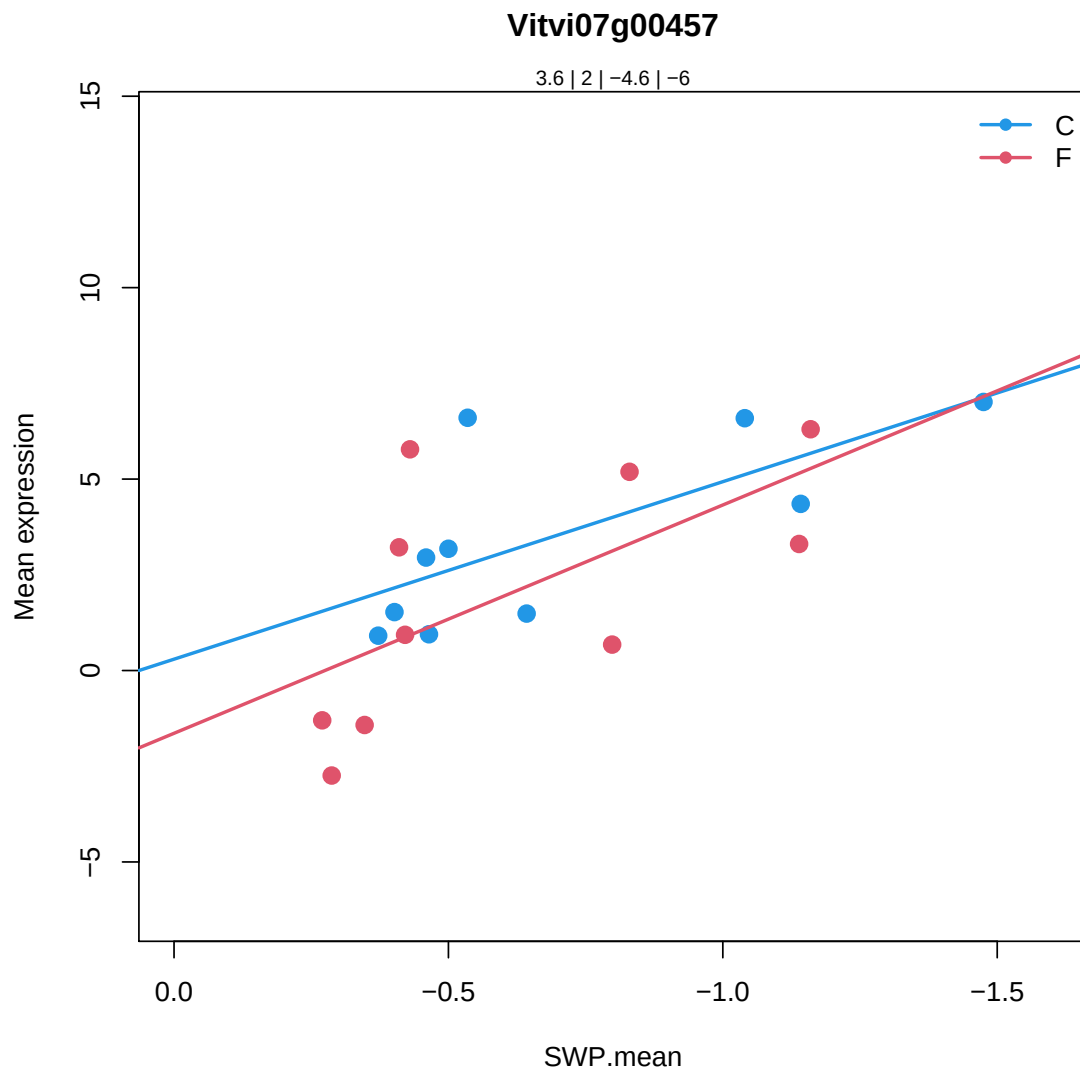
3.1.1.1

minor CHO metabolism.raffinose family.galactinol synthases.known
galactinol synthase 1 |

Chr2:19369049-19370372 REVERSE LENGTH=344 |
201606

Coefficients for Vitvi07g00457.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.555754	1.102899e-05	***	1.244477e-05	***
SlopeC	-4.635979	0.01424512	*	0.3359386	
MeanF-MeanC	-1.562377	0.09116898	.	0.3456204	
SlopeF-SlopeC	-1.327112	0.6131283		0.9999488	



7.3.10 Vitvi13g00410

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

Vitvi13g00410

35.2

not assigned.unknown

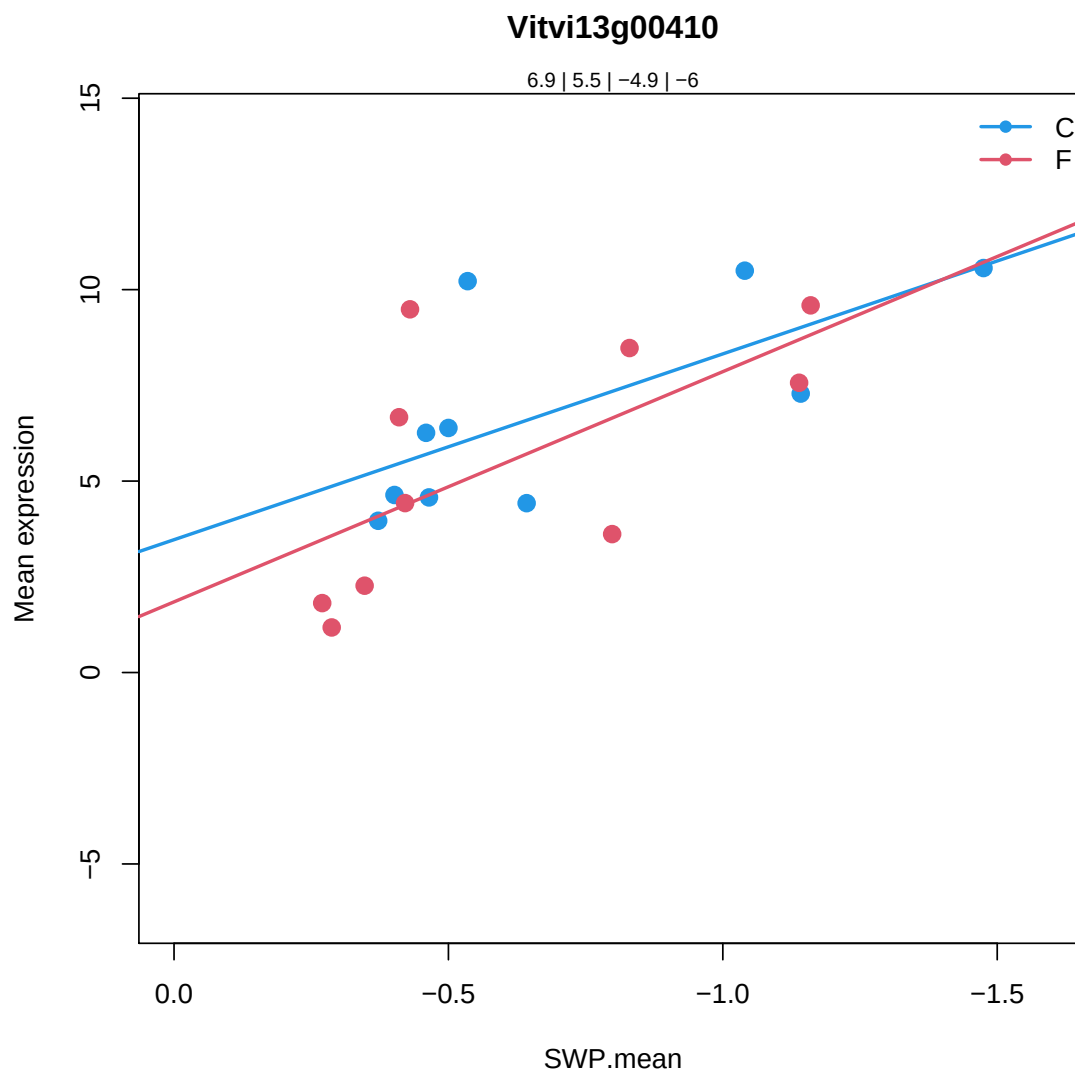
heat shock protein 18.2 |

Chr5:24062632-24063117 FORWARD LENGTH=161 |

201606

Coefficients for Vitvi13g00410.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.880973	5.561548e-10	***	7.077067e-10	***
SlopeC	-4.853089	0.01369382	*	0.3344891	
MeanF-MeanC	-1.372646	0.1496748		0.4660558	
SlopeF-SlopeC	-1.160051	0.6705588		0.9999488	



7.3.11 Vitvi04g01802

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

Vitvi04g01802

20.02.2001

stress.abiotic.heat

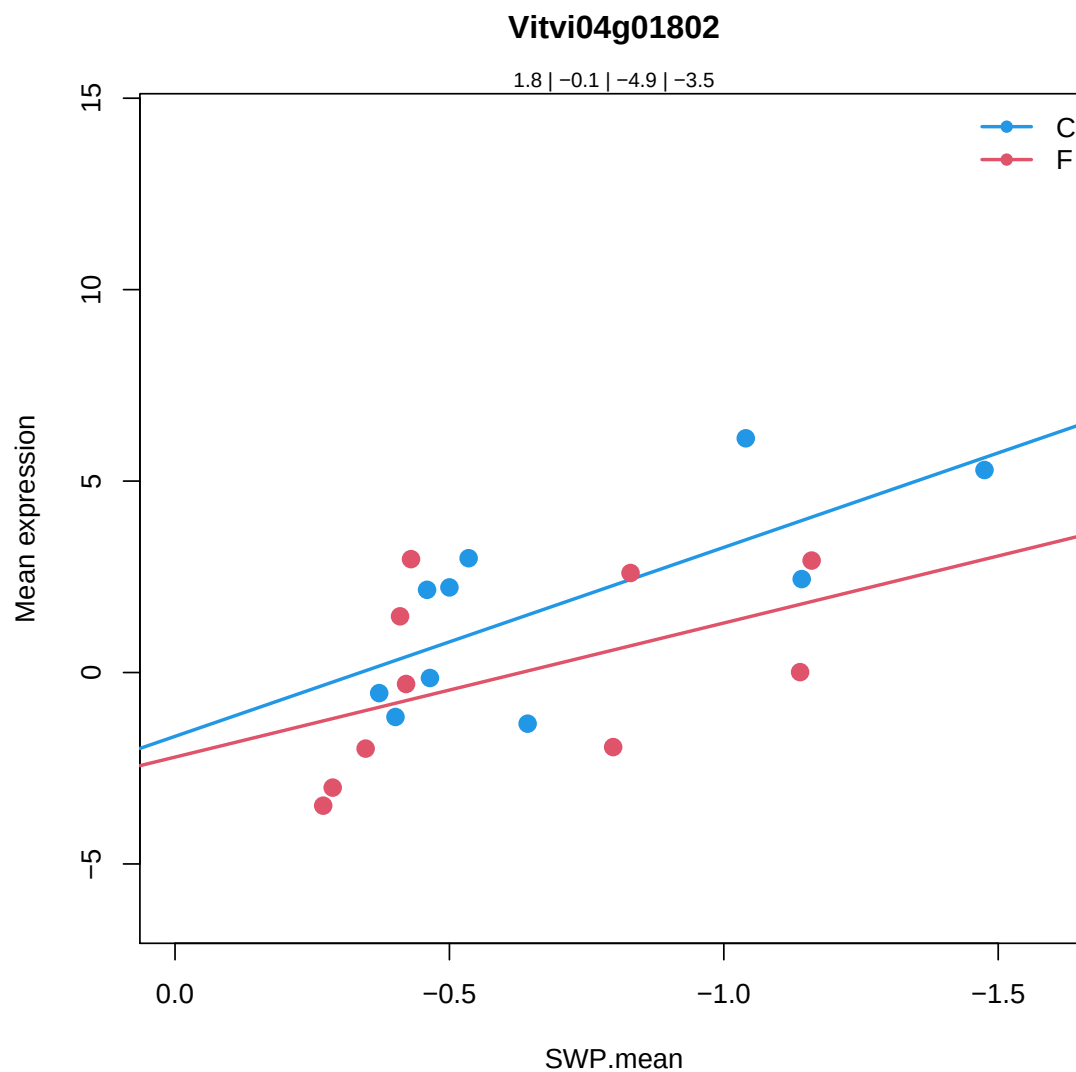
17.6 kDa class II heat shock protein |

Chr5:3882409-3882876 REVERSE LENGTH=155 |

201606

Coefficients for Vitvi04g01802.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.803501	0.00537385	**	0.005725846	**
SlopeC	-4.935441	0.00604259	**	0.2647742	
MeanF-MeanC	-1.879083	0.03283183	*	0.179723	
SlopeF-SlopeC	1.433256	0.5585218		0.9999488	



7.3.12 Vitvi04g01801

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

Vitvi04g01801

20.02.2001

stress.abiotic.heat

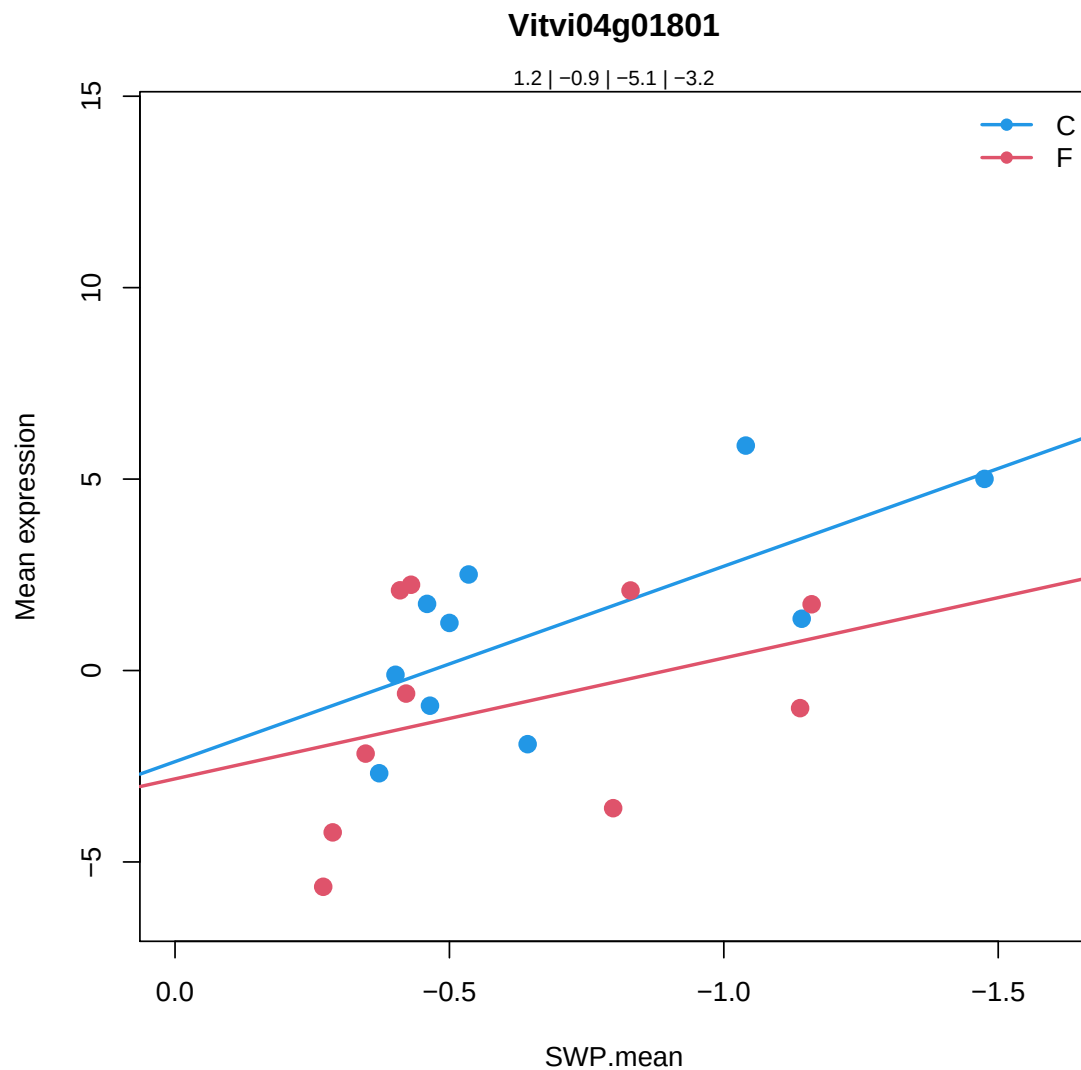
17.6 kDa class II heat shock protein |

Chr5:3882409-3882876 REVERSE LENGTH=155 |

201606

Coefficients for Vitvi04g01801.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.208586	0.09664858	.	0.09995371	.
SlopeC	-5.104125	0.01523524	*	0.3393703	
MeanF-MeanC	-2.115849	0.04303485	*	0.2168388	
SlopeF-SlopeC	1.948595	0.5059525		0.9999488	



7.3.13 Vitvi08g02274

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

Vitvi08g02274

35.2

not assigned.unknown

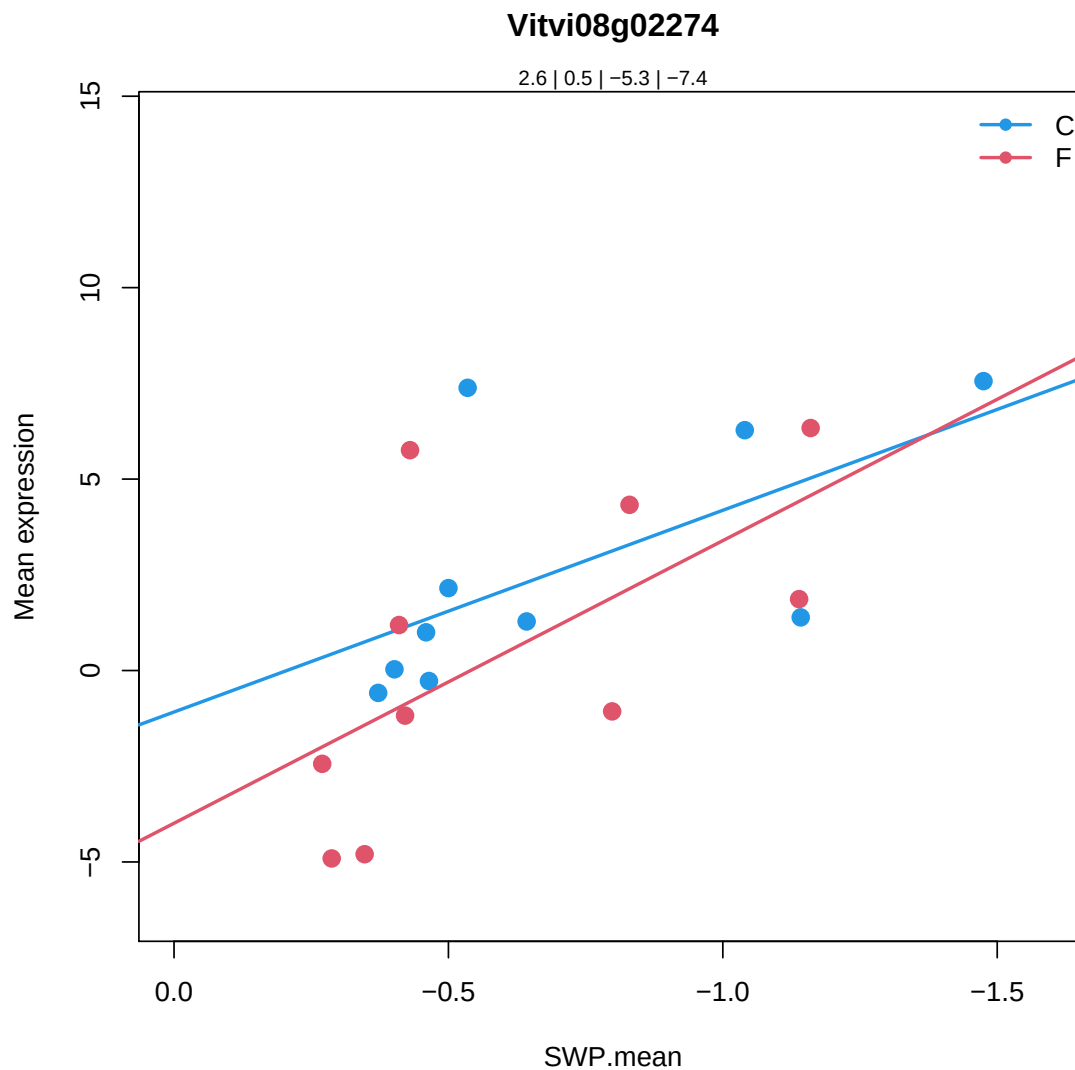
plant/protein |

Chr3:3091225-3091674 REVERSE LENGTH=149 |

201606

Coefficients for Vitvi08g02274.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.621184	0.004851113	**	0.005175743	**
SlopeC	-5.267913	0.03371344	*	0.4433084	
MeanF-MeanC	-2.113039	0.08753536	.	0.337434	
SlopeF-SlopeC	-2.113051	0.5473344		0.9999488	



7.3.14 Vitvi02g00025

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

Vitvi02g00025

20.02.2001

stress.abiotic.heat

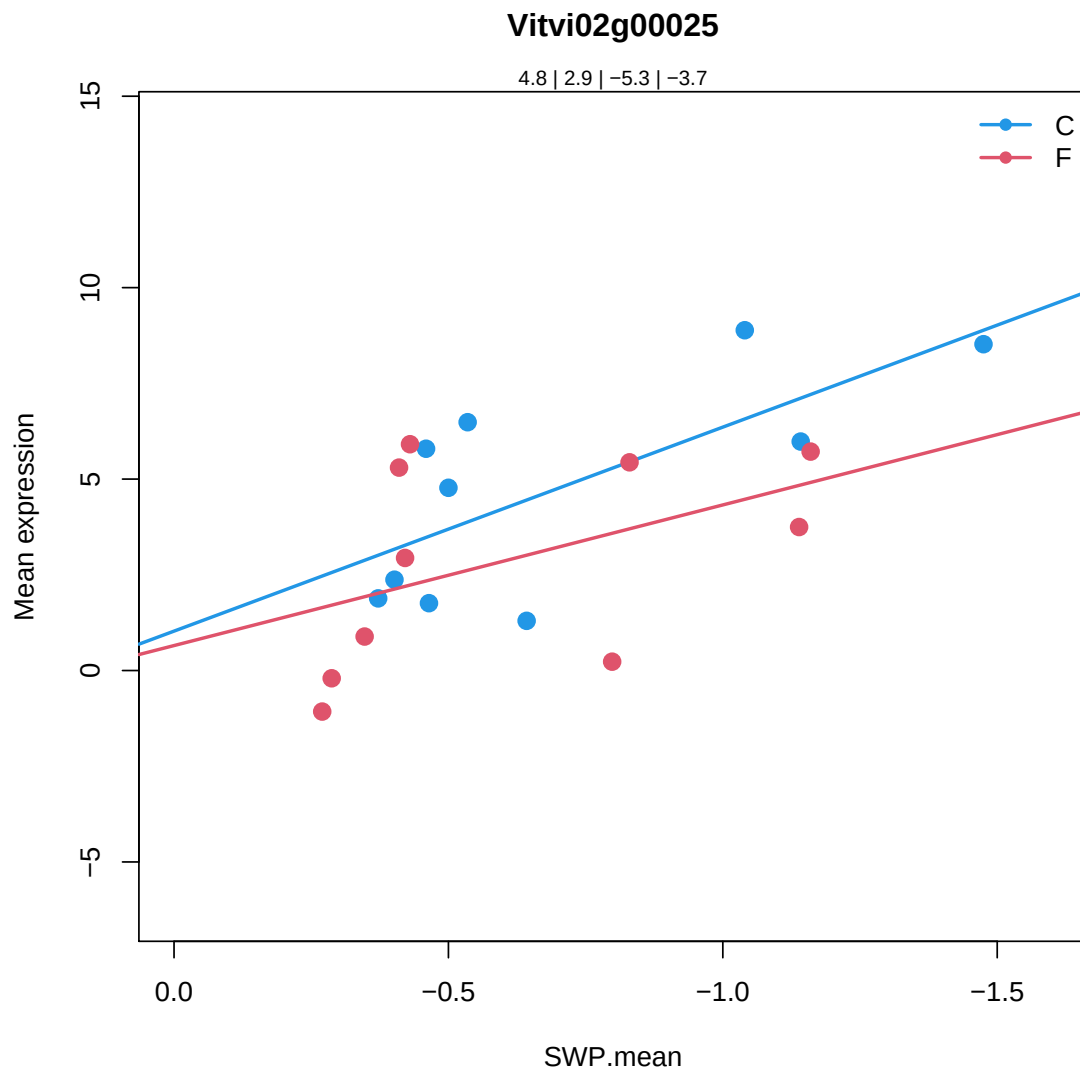
heat shock-like protein |

Chr5:21352557-21355147 FORWARD LENGTH=700 |

201606

Coefficients for Vitvi02g00025.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.775282	2.294969e-07	***	2.694701e-07	***
SlopeC	-5.328021	0.00701325	**	0.2775469	
MeanF-MeanC	-1.885708	0.05012567	.	0.2392782	
SlopeF-SlopeC	1.655038	0.5403657		0.9999488	



7.3.15 Vitvi04g01799

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

Vitvi04g01799

20.02.2001

stress.abiotic.heat

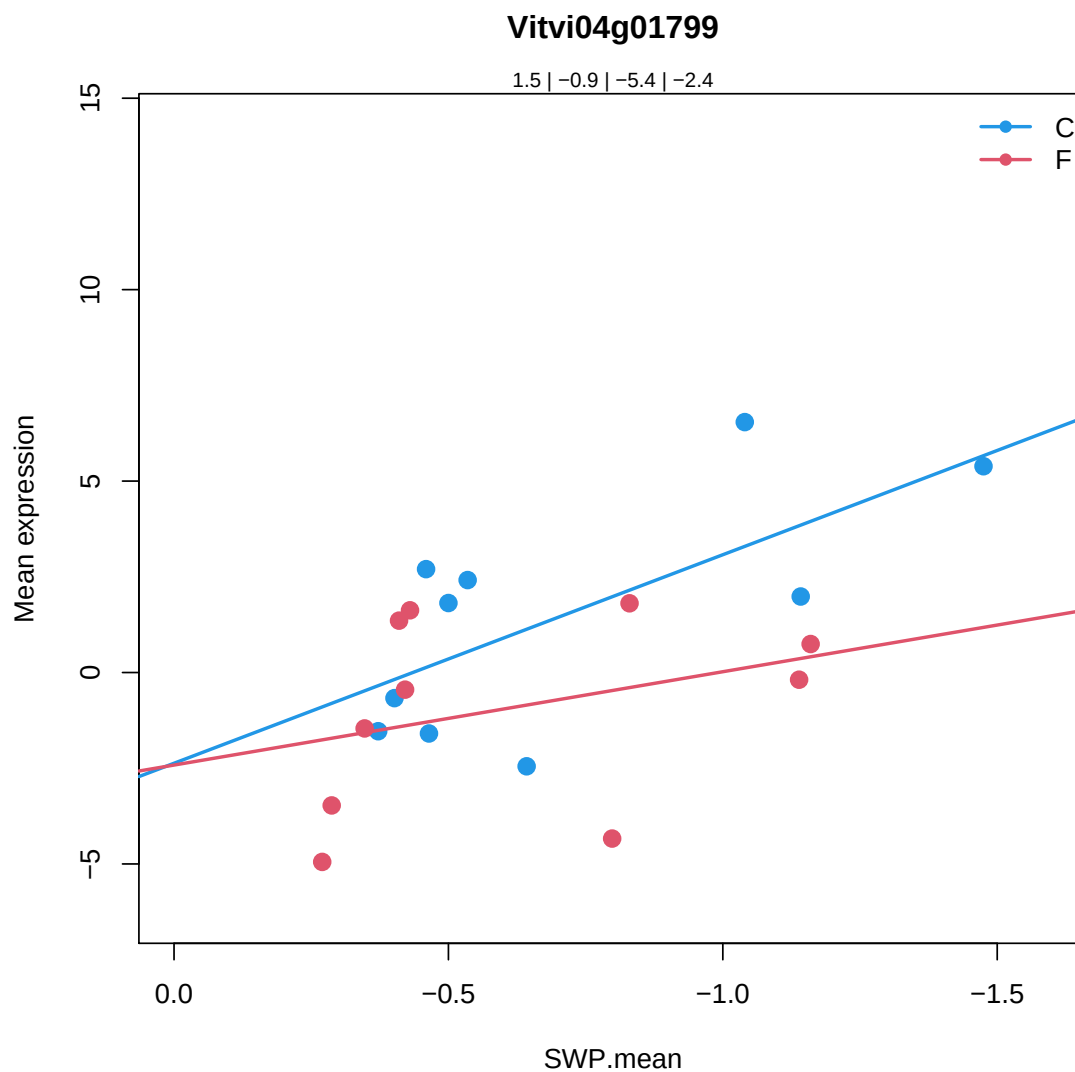
17.6 kDa class II heat shock protein |

Chr5:3882409-3882876 REVERSE LENGTH=155 |

201606

Coefficients for Vitvi04g01799.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.459784	0.04054411	*	0.04232114	*
SlopeC	-5.446372	0.008008975	**	0.2832315	
MeanF-MeanC	-2.391652	0.01948465	*	0.1236922	
SlopeF-SlopeC	3.008905	0.2899314		0.9999488	



7.3.16 Vitvi04g01794

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

Vitvi04g01794

20.02.2001

stress.abiotic.heat

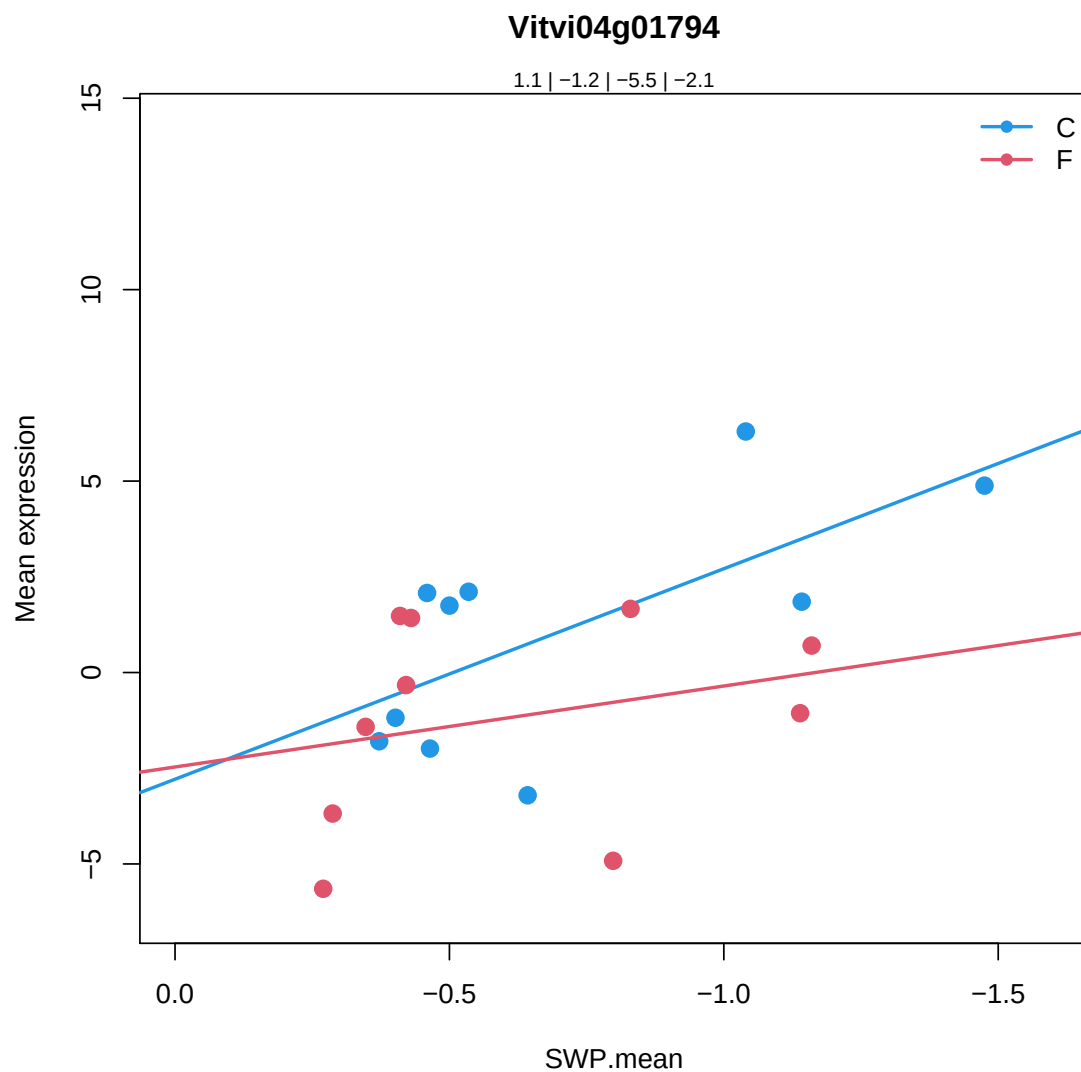
17.6 kDa class II heat shock protein |

Chr5:3882409-3882876 REVERSE LENGTH=155 |

201606

Coefficients for Vitvi04g01794.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.079134	0.1462899		0.1505876	
SlopeC	-5.497568	0.01158549	*	0.318473	
MeanF-MeanC	-2.25819	0.03651267	*	0.192703	
SlopeF-SlopeC	3.382727	0.2663928		0.9999488	



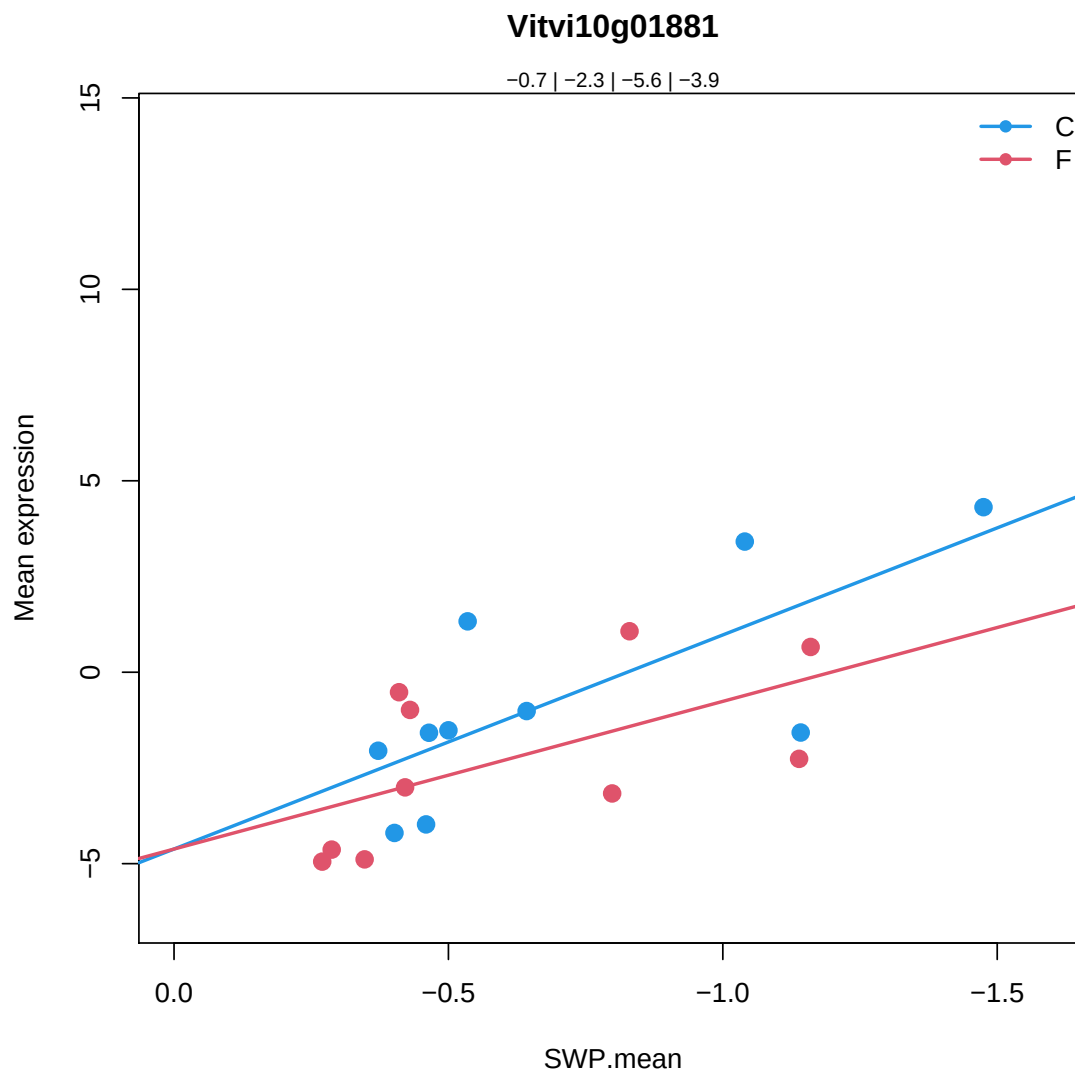
7.3.17 Vitvi10g01881

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

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

Coefficients for Vitvi10g01881.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.6859056	0.2218556		0.2272071	
SlopeC	-5.591522	0.00133436	**	0.1432275	
MeanF-MeanC	-1.582313	0.05253977	.	0.2472403	
SlopeF-SlopeC	1.734231	0.4507249		0.9999488	



7.3.18 Vitvi14g01942

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

Vitvi14g01942

29.05.2007

protein.degradation.metalloprotease

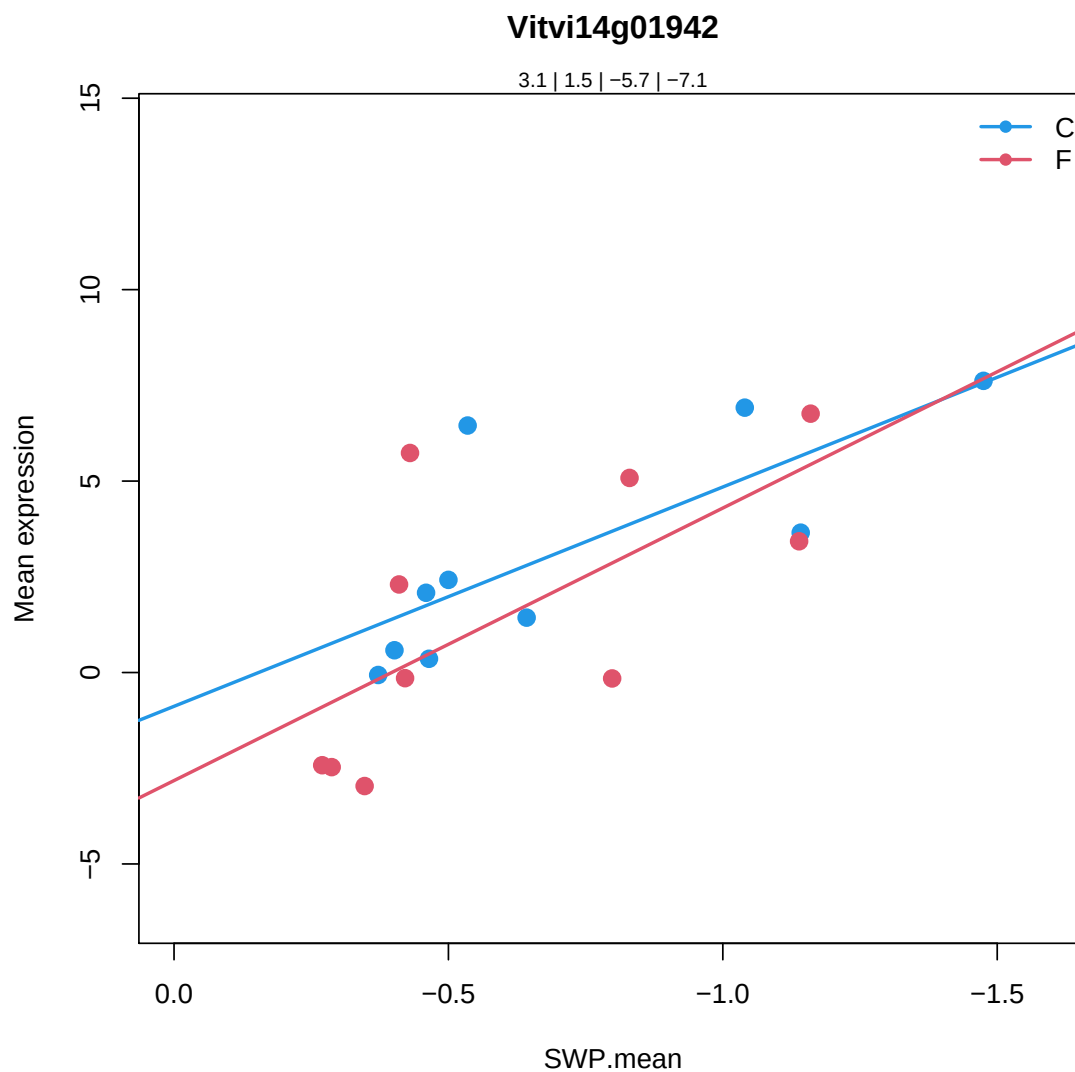
FTSH protease 6 |

Chr5:4951071-4952777 REVERSE LENGTH=514 |

201606

Coefficients for Vitvi14g01942.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.144964	0.0001381096	***	0.0001521111	***
SlopeC	-5.728533	0.00627106	**	0.2647742	
MeanF-MeanC	-1.630516	0.1042469		0.373954	
SlopeF-SlopeC	-1.388999	0.6266054		0.9999488	



7.3.19 Vitvi06g00561

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

Vitvi06g00561

35.2

not assigned.unknown

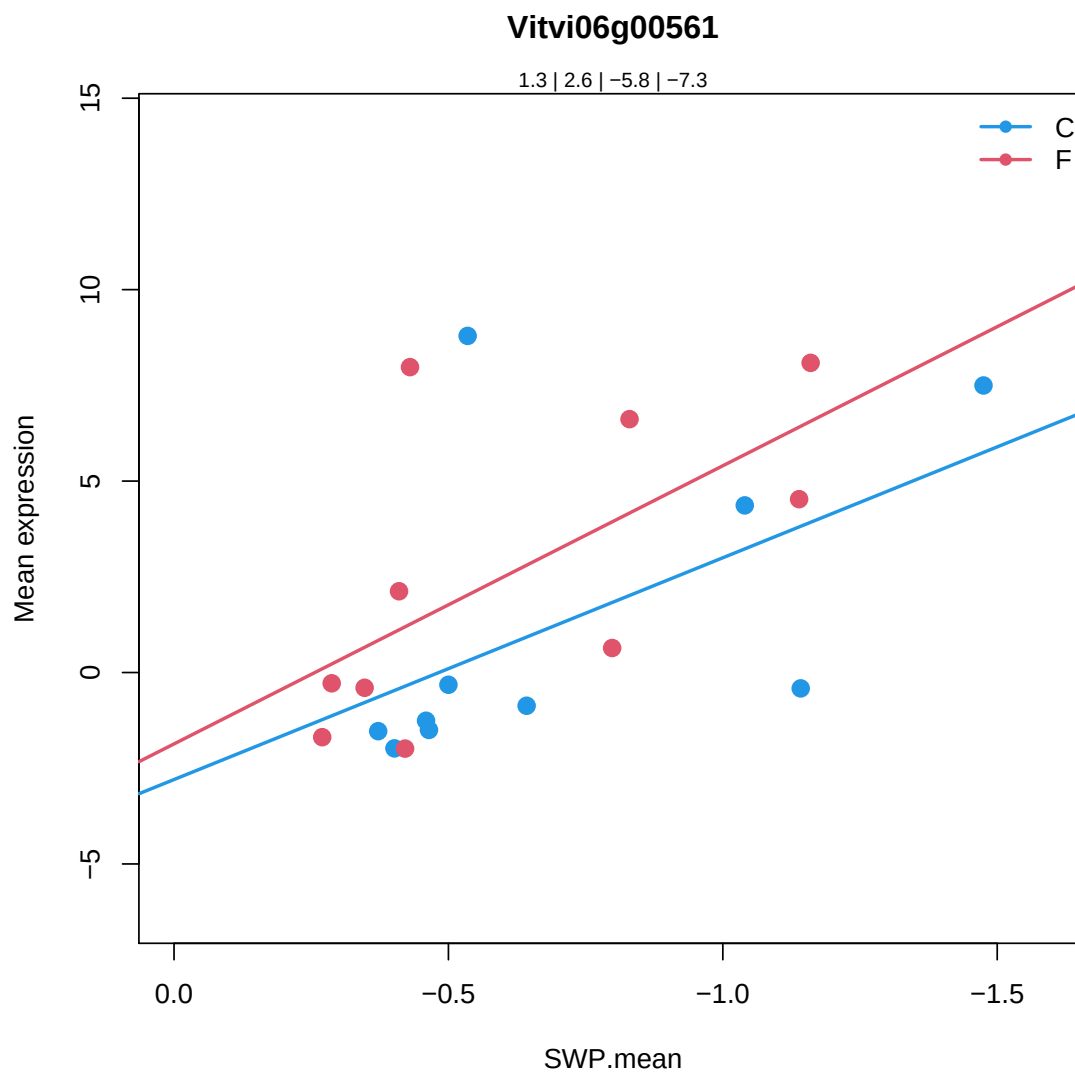
HSP20-like chaperones superfamily protein |

Chr2:12633279-12633740 REVERSE LENGTH=153 |

201606

Coefficients for Vitvi06g00561.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.277783	0.1875177		0.1923899	
SlopeC	-5.792331	0.03745657	*	0.4626524	
MeanF-MeanC	1.283774	0.3442368		0.7038982	
SlopeF-SlopeC	-1.47236	0.7085305		0.9999488	



7.3.20 Vitvi04g01795

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

Vitvi04g01795

35.2

not assigned.unknown

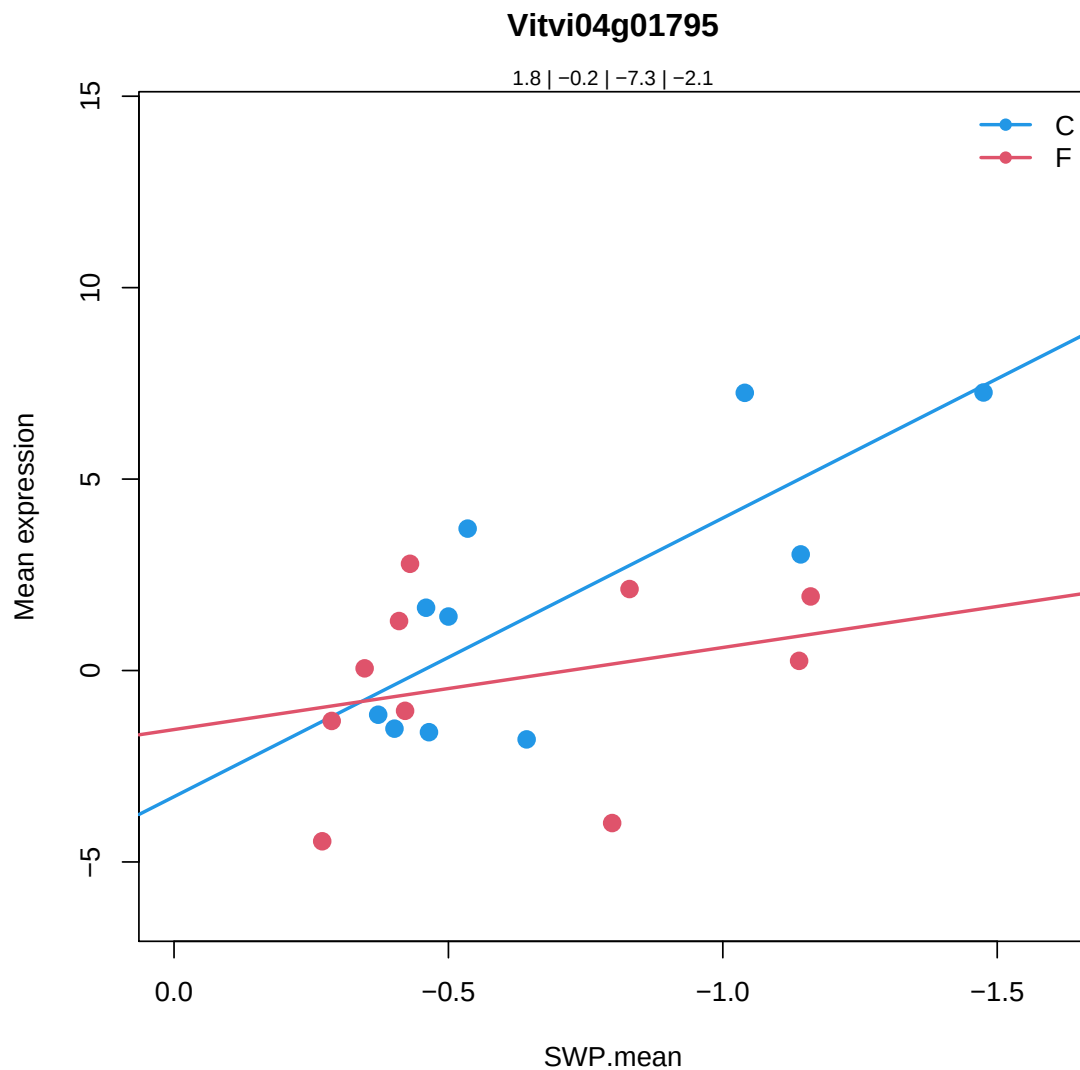
17.6 kDa class II heat shock protein |

Chr5:3882409-3882876 REVERSE LENGTH=155 |

201606

Coefficients for Vitvi04g01795.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.821988	0.01144052	*	0.01210359	*
SlopeC	-7.277261	0.0006740302	***	0.1037734	
MeanF-MeanC	-2.058336	0.03814072	*	0.1995898	
SlopeF-SlopeC	5.133591	0.07347637	.	0.9999488	



7.4 type3

7.4.1 Vitvi09g01874

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

Vitvi09g01874

35.2

not assigned.unknown

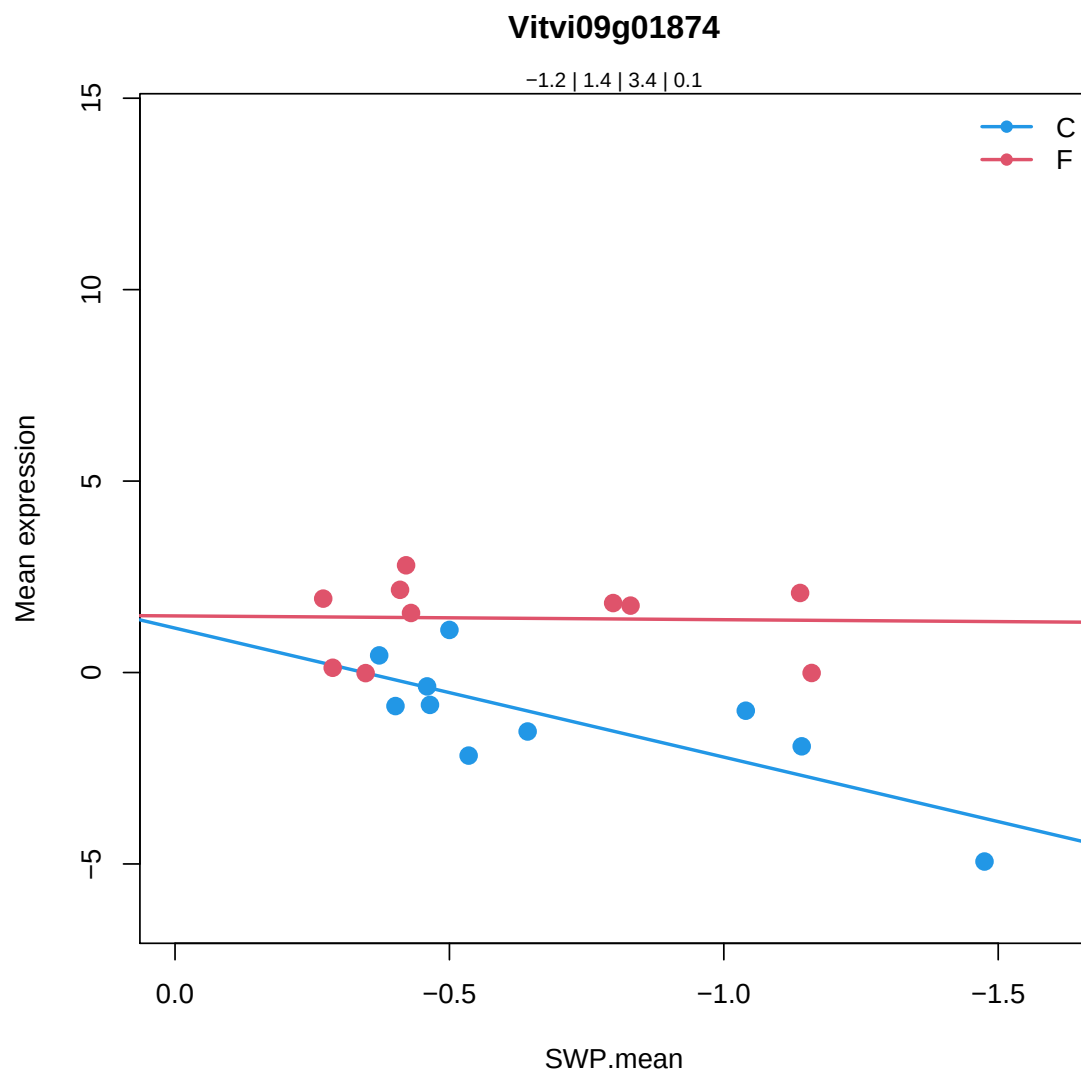
disease resistance family protein / LRR family protein |

Chr2:14737169-14739886 REVERSE LENGTH=905 |

201606

Coefficients for Vitvi09g01874.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.209693	0.0007634725	***	0.0008287763	***
SlopeC	3.369133	0.0007557867	***	0.1076608	
MeanF-MeanC	2.627733	5.179869e-06	***	0.0001389992	***
SlopeF-SlopeC	-3.270373	0.01811727	*	0.9999488	



7.4.2 Vitvi18g03084

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

Vitvi18g03084

30.2.25

signalling.receptor kinases.wall associated kinase

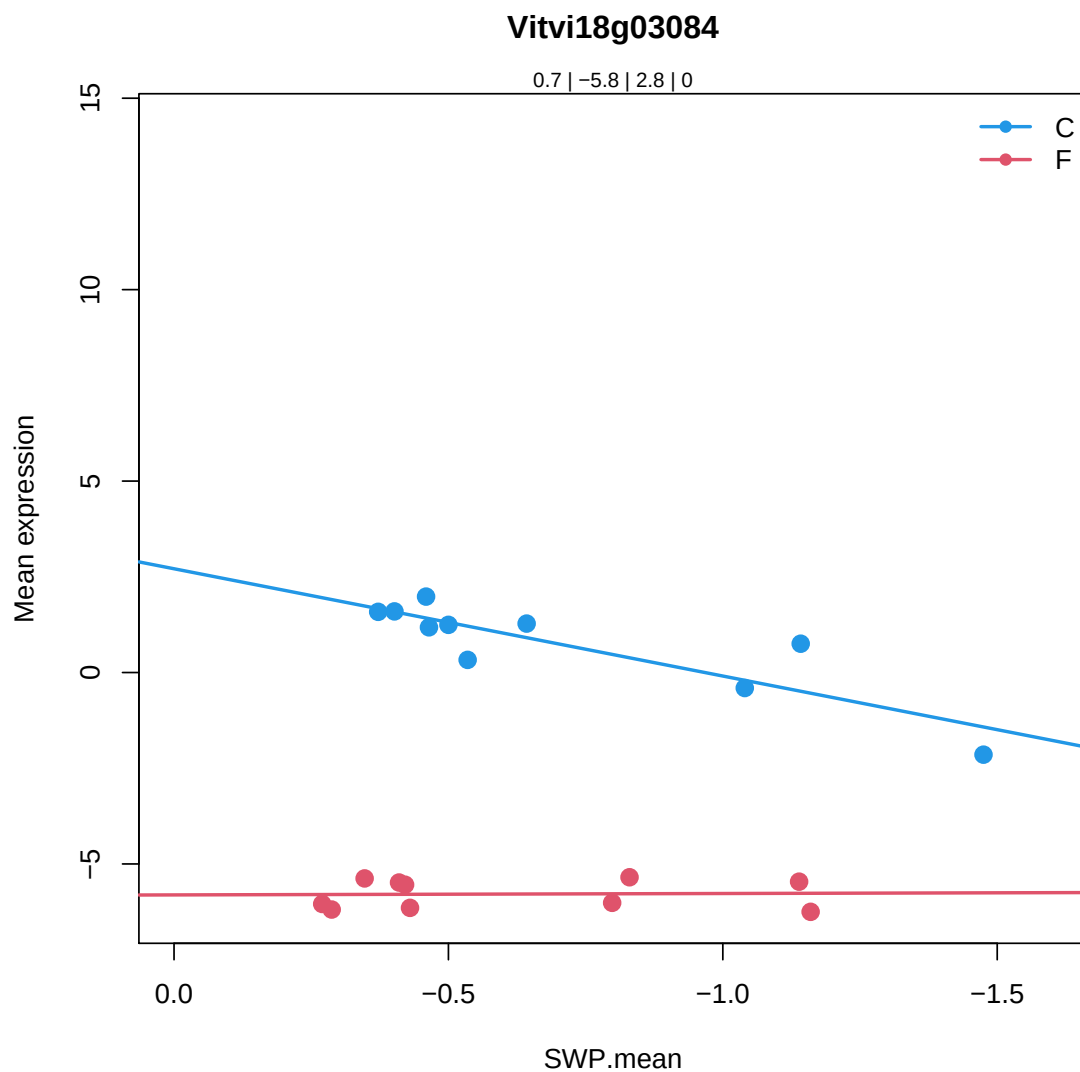
Protein kinase family protein |

Chr3:9241725-9243113 FORWARD LENGTH=433 |

201606

Coefficients for Vitvi18g03084.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.7399658	0.0002141846	***	0.0002349817	***
SlopeC	2.801771	4.827114e-06	***	0.01839372	*
MeanF-MeanC	-6.526298	2.769532e-18	***	6.920199e-16	***
SlopeF-SlopeC	-2.838533	0.0004720067	***	0.9999488	



7.4.3 Vitvi16g02090

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

```
Vitvi16g02090
```

```
35.2
```

```
not assigned.unknown
```

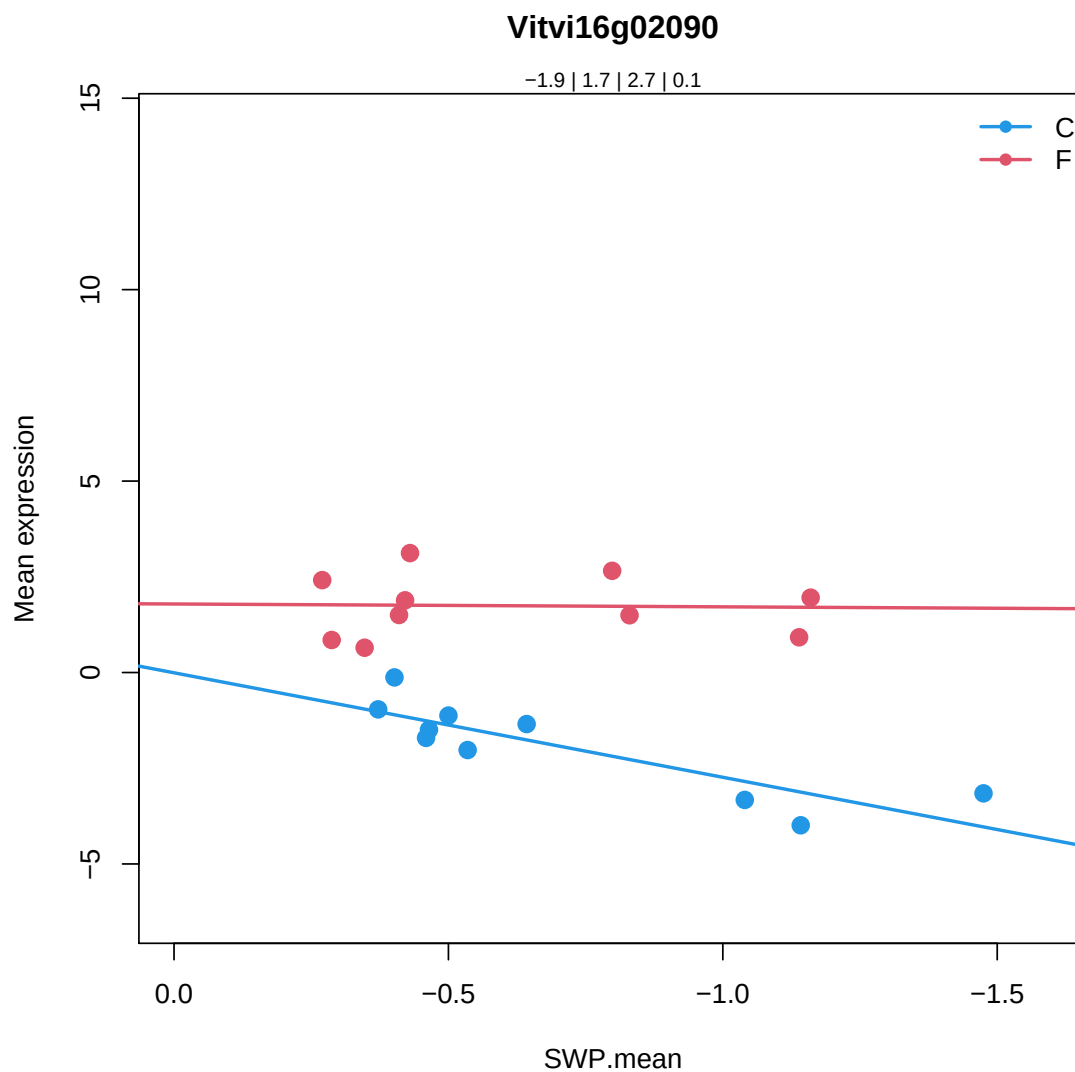
```
PR5-like receptor kinase |
```

```
Chr5:15293325-15295838 REVERSE LENGTH=665 |
```

```
201606
```

Coefficients for Vitvi16g02090.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.926199	2.28078e-08	***	2.753775e-08	***
SlopeC	2.729033	0.0002614243	***	0.08298279	.
MeanF-MeanC	3.670552	1.144627e-10	***	7.8943e-09	***
SlopeF-SlopeC	-2.654757	0.009425042	**	0.9999488	



7.4.4 Vitvi18g03250

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

Vitvi18g03250

26.1

misc.cytochrome P450

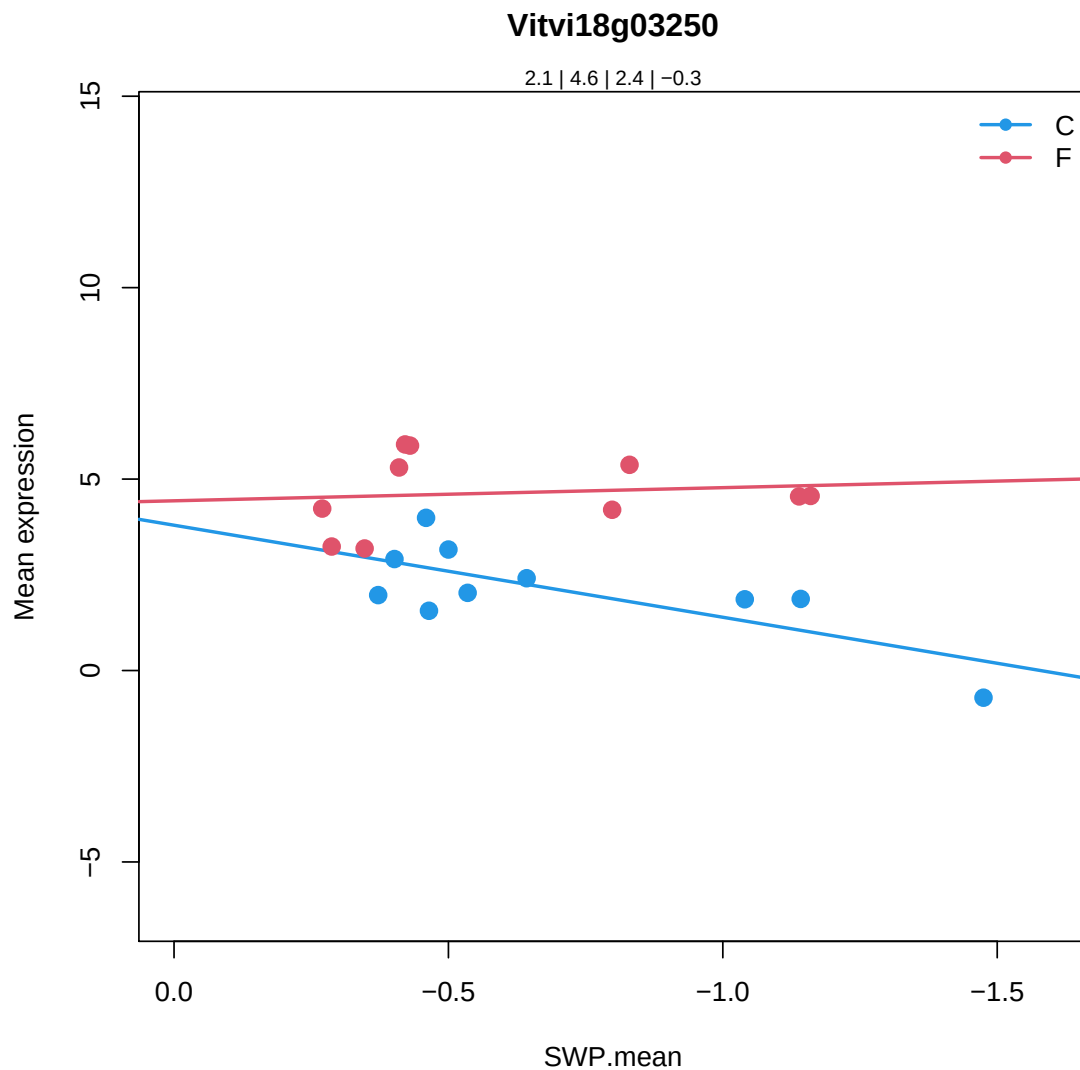
cytochrome P450%2C family 714%2C subfamily A%2C polypeptide 1 |

Chr5:8567674-8570260 REVERSE LENGTH=532 |

201606

Coefficients for Vitvi18g03250.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.104769	1.319663e-07	***	1.560942e-07	***
SlopeC	2.403889	0.004635983	**	0.2436609	
MeanF-MeanC	2.536661	1.526731e-06	***	4.778322e-05	***
SlopeF-SlopeC	-2.746937	0.02414396	*	0.9999488	



7.4.5 Vitvi16g02003

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

Vitvi16g02003

35.2

not assigned.unknown

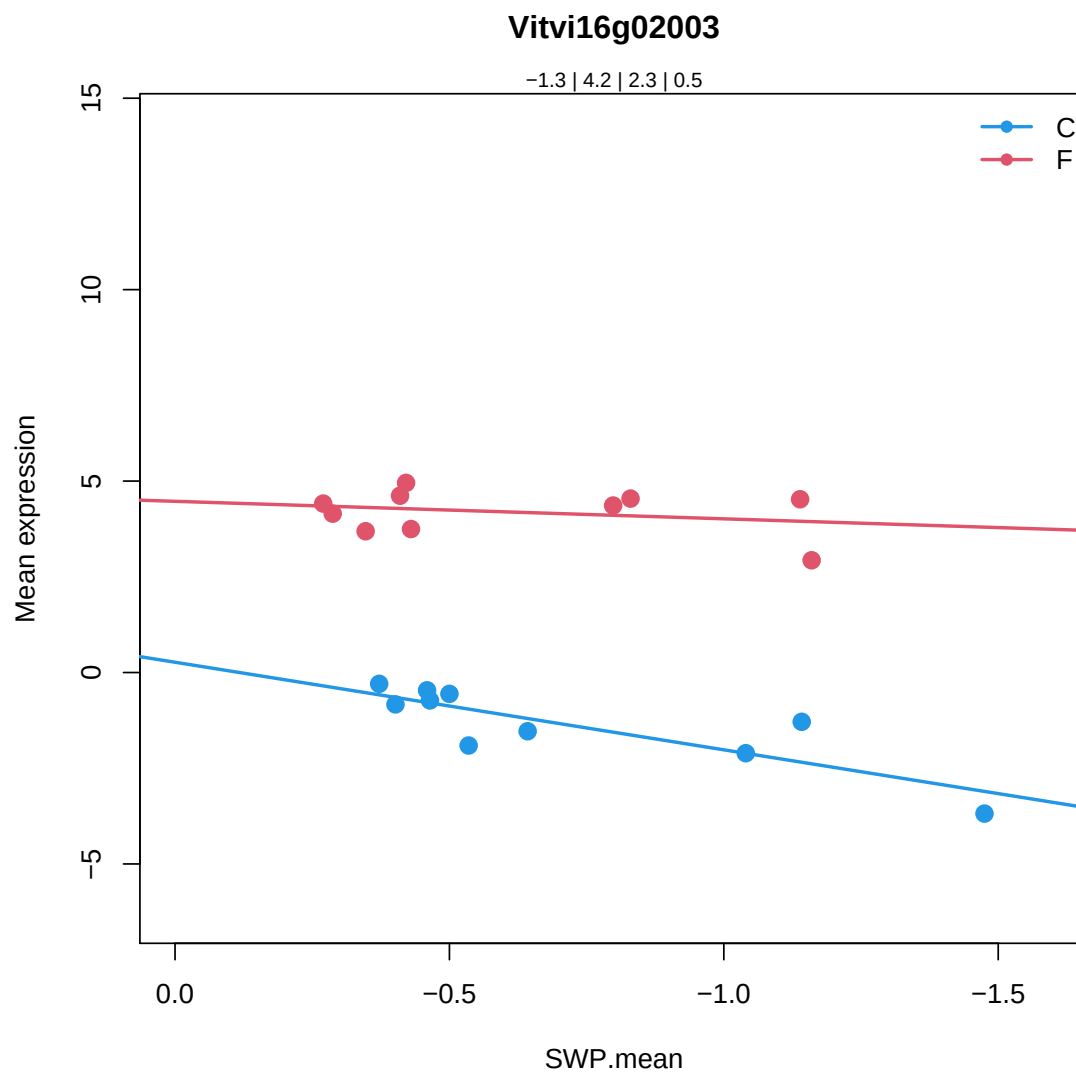
PR5-like receptor kinase |

Chr5:15293325-15295838 REVERSE LENGTH=665 |

201606

Coefficients for Vitvi16g02003.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.339973	2.33912e-07	***	2.745485e-07	***
SlopeC	2.2875	0.000164243	***	0.07644173	.
MeanF-MeanC	5.532948	4.544274e-16	***	7.214982e-14	***
SlopeF-SlopeC	-1.830222	0.02298766	*	0.9999488	



7.4.6 Vitvi16g01548

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

Vitvi16g01548

35.2

not assigned.unknown

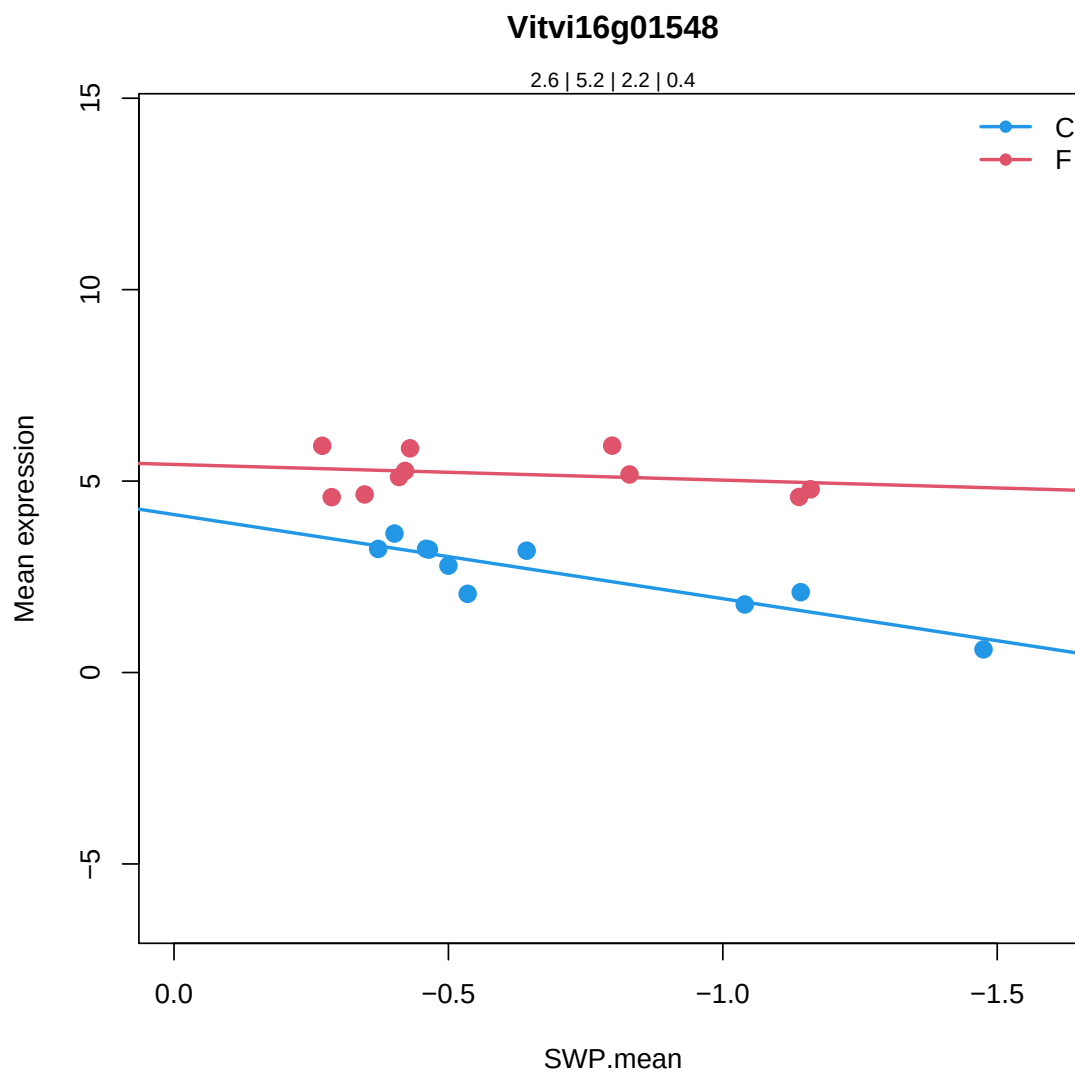
dihydroflavonol 4-reductase |

Chr5:17164296-17165864 REVERSE LENGTH=382 |

201606

Coefficients for Vitvi16g01548.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.580398	1.607866e-13	***	2.431742e-13	***
SlopeC	2.196869	6.152636e-05	***	0.07213729	.
MeanF-MeanC	2.60436	1.084352e-10	***	7.546893e-09	***
SlopeF-SlopeC	-1.787469	0.0128491	*	0.9999488	



7.4.7 Vitvi09g00681

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

Vitvi09g00681

20.01.2002

stress.biotic.receptors

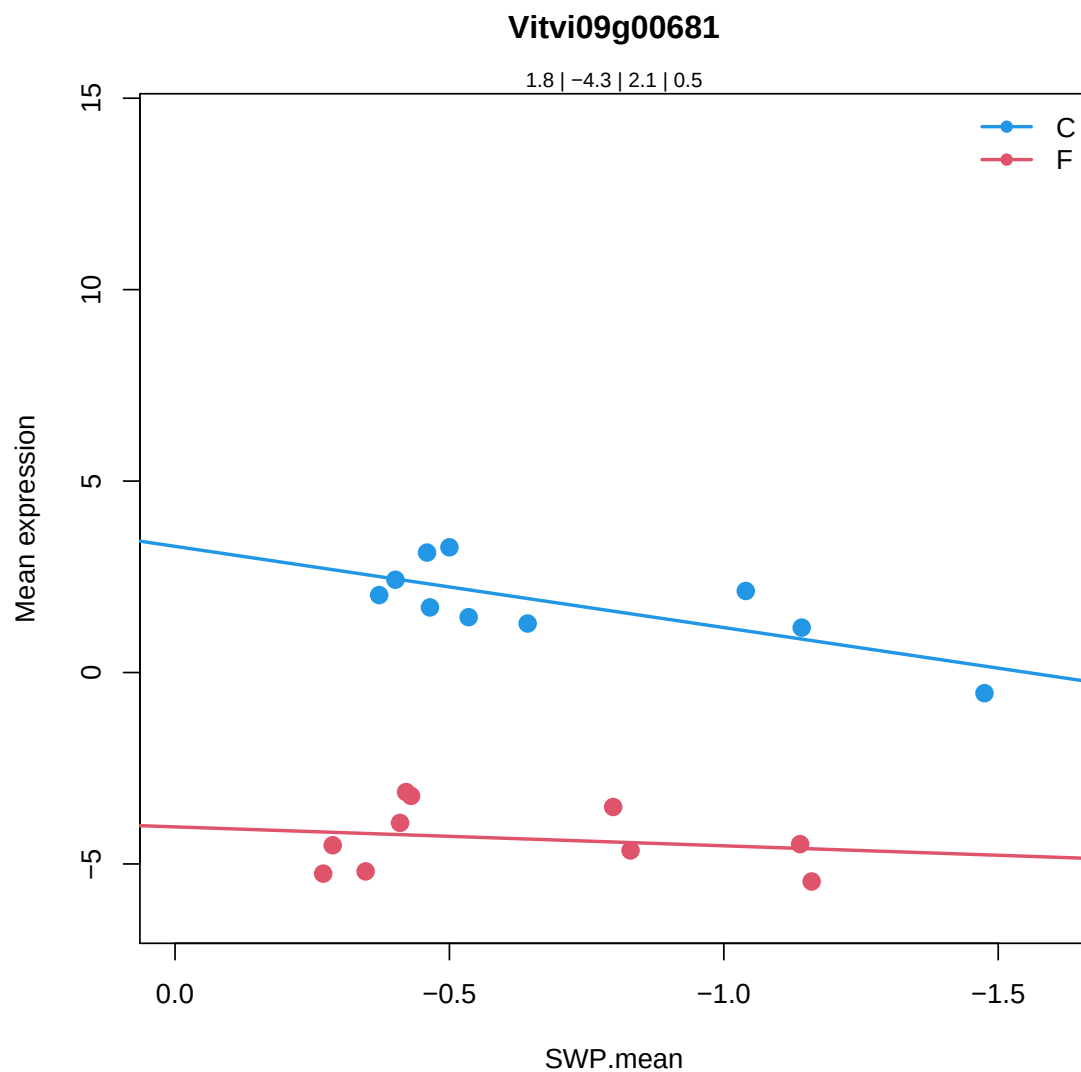
receptor like protein 1 |

Chr1:2270633-2274654 FORWARD LENGTH=913 |

201606

Coefficients for Vitvi09g00681.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.80362	2.175092e-07	***	2.556307e-07	***
SlopeC	2.121009	0.004715187	**	0.2454895	
MeanF-MeanC	-6.136671	2.131152e-14	***	2.537736e-12	***
SlopeF-SlopeC	-1.626761	0.1188241		0.9999488	



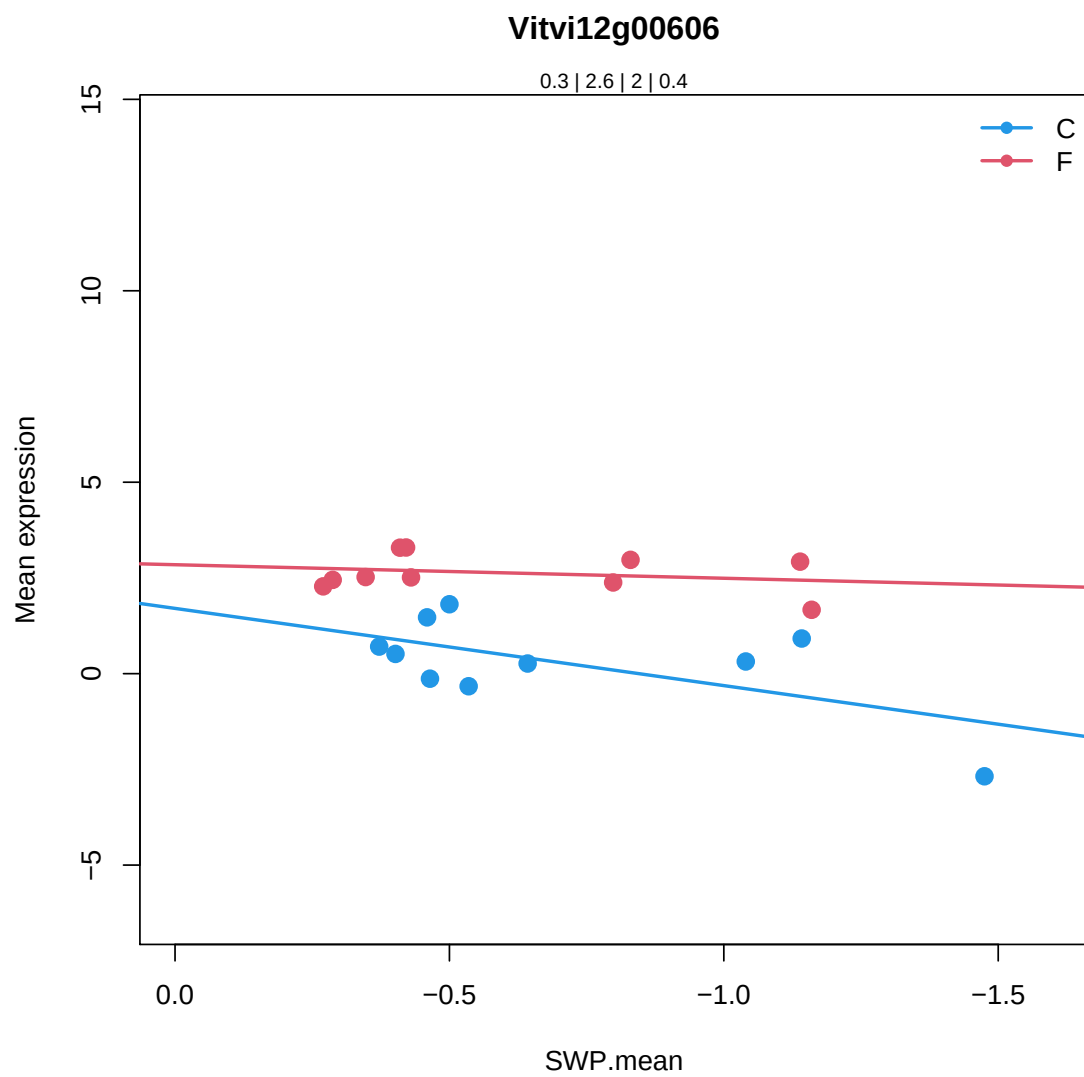
7.4.8 Vitvi12g00606

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
Vitvi12g00606
  29.4
  protein.postranslational modification
  G-type lectin S-receptor-like Serine/Threonine-kinase |
  Chr4:1419278-1422828 REVERSE LENGTH=1010 |
  201606

Vitvi12g00606
  30.2.24
  signalling.receptor kinases.S-locus glycoprotein like
  G-type lectin S-receptor-like Serine/Threonine-kinase |
  Chr4:1419278-1422828 REVERSE LENGTH=1010 |
  201606
```

Coefficients for Vitvi12g00606.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.2862625	0.2372891		0.2426379	
SlopeC	2.016467	0.005608764	**	0.2614336	
MeanF-MeanC	2.343448	5.354432e-07	***	1.871841e-05	***
SlopeF-SlopeC	-1.662881	0.1025429		0.9999488	



7.4.9 Vitvi07g02459

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

Vitvi07g02459

35.2

not assigned.unknown

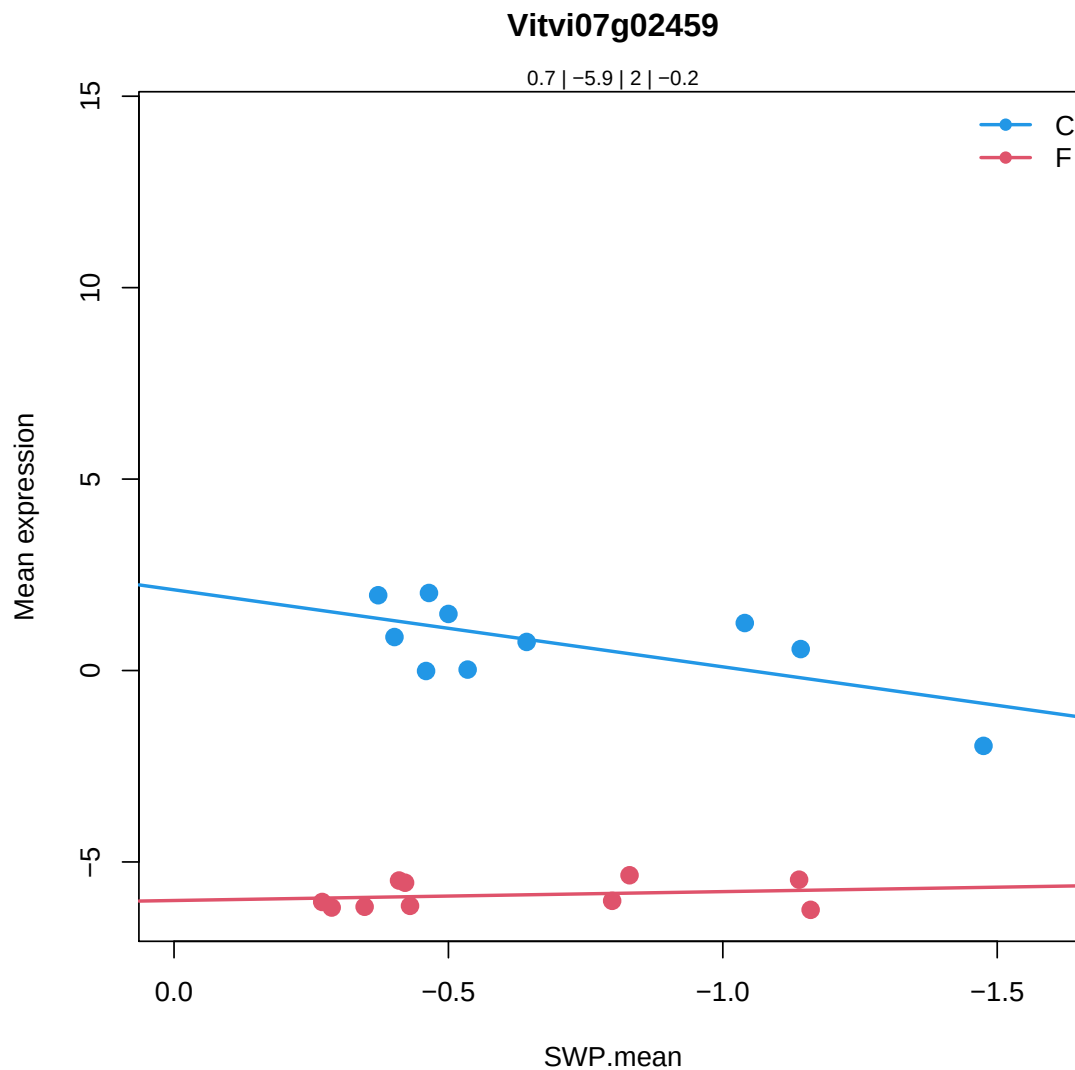
Ankyrin repeat family protein |

Chr5:1349781-1352525 REVERSE LENGTH=625 |

201606

Coefficients for Vitvi07g02459.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6932742	0.003485594	**	0.003730073	**
SlopeC	2.012497	0.002490803	**	0.1896965	
MeanF-MeanC	-6.558855	3.497533e-16	***	5.611515e-14	***
SlopeF-SlopeC	-2.244575	0.01782121	*	0.9999488	



7.4.10 Vitvi08g00723

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

Vitvi08g00723

34.5

transport.ammonium

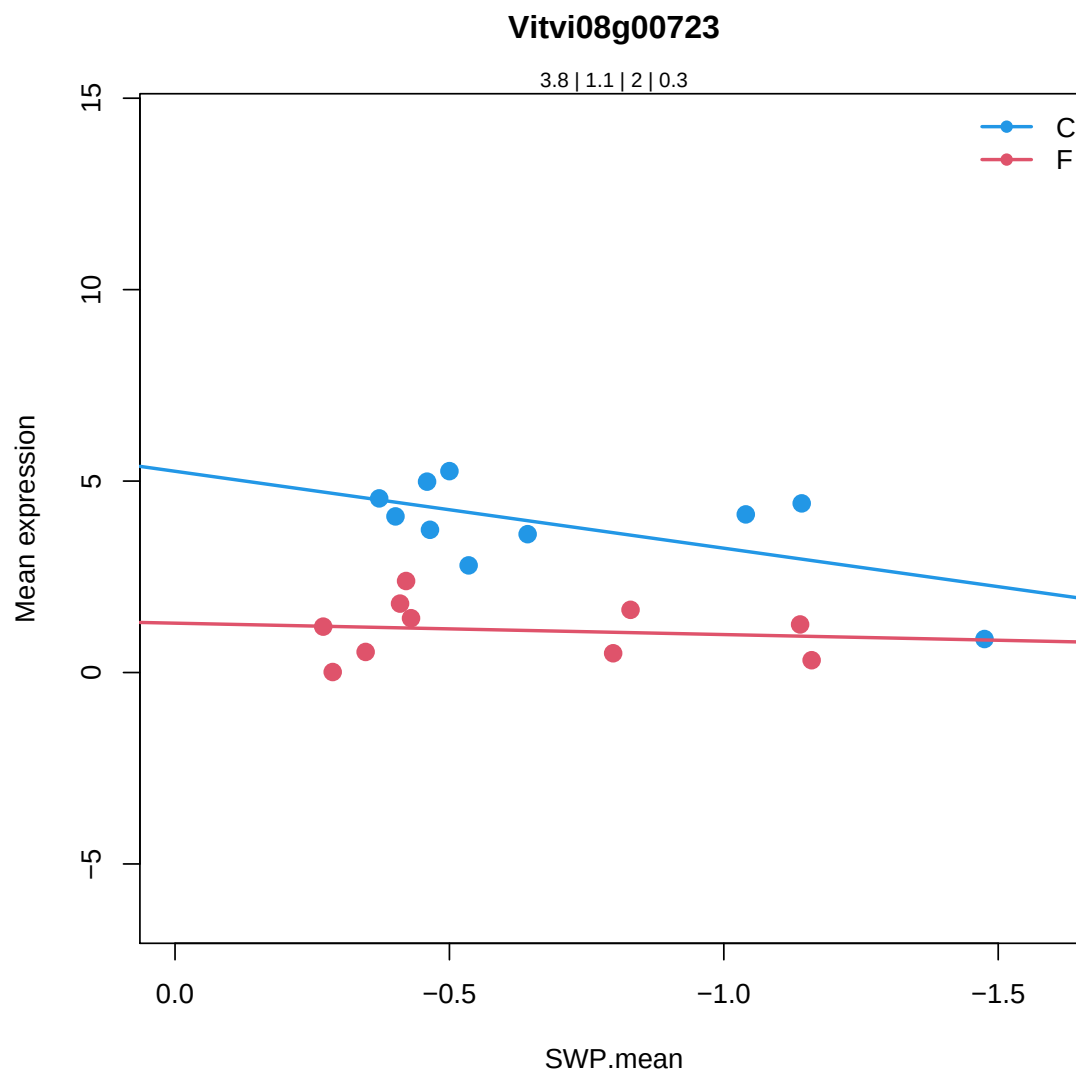
ammonium transporter 2 |

Chr2:16039672-16042291 REVERSE LENGTH=475 |

201606

Coefficients for Vitvi08g00723.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.8431	1.699178e-12	***	2.40584e-12	***
SlopeC	2.009066	0.01311545	*	0.3305597	
MeanF-MeanC	-2.73582	3.419843e-07	***	1.241077e-05	***
SlopeF-SlopeC	-1.711553	0.1362029		0.9999488	



7.4.11 Vitvi16g01010

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

Vitvi16g01010

35.2

not assigned.unknown

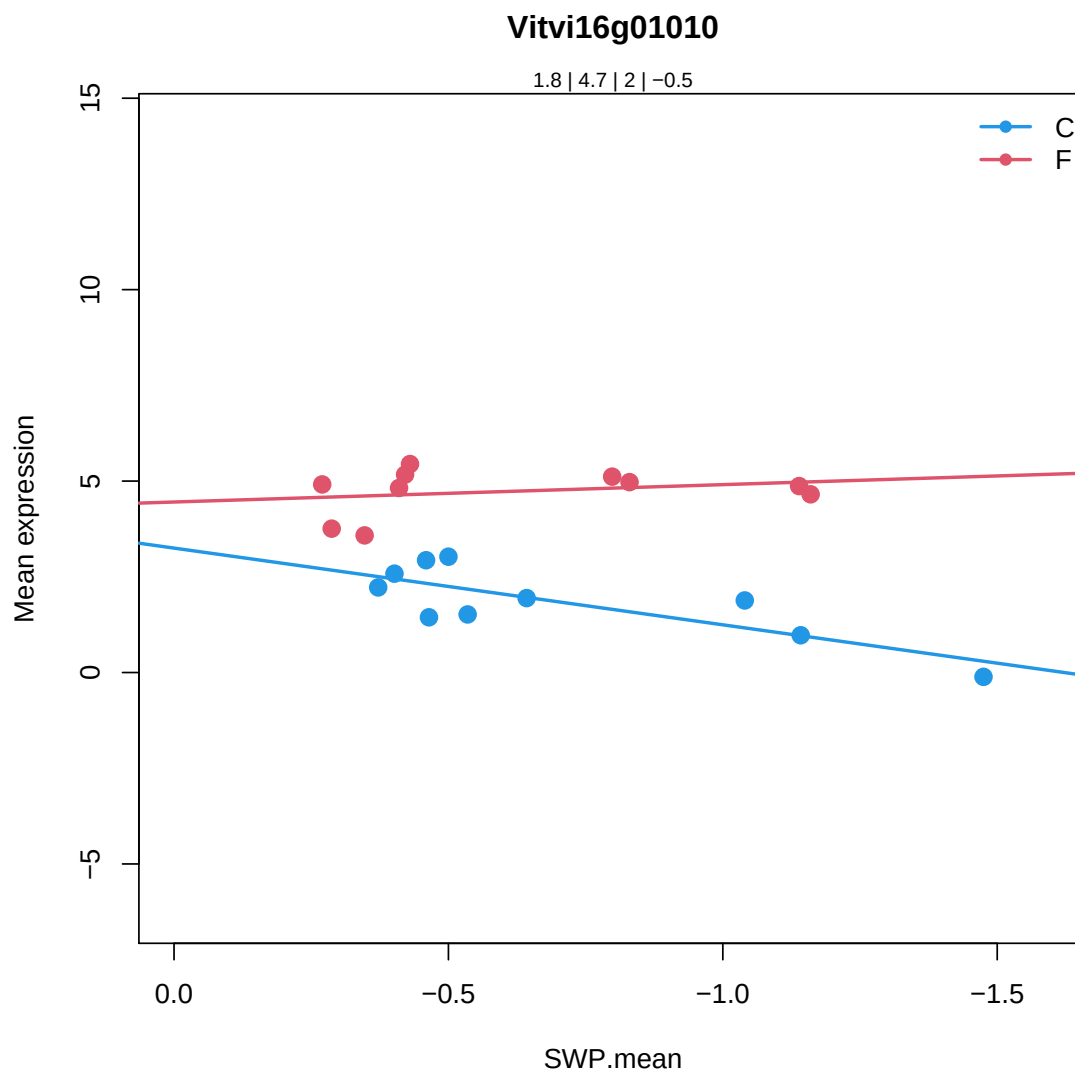
suppressor of npr1-1 constitutive 4 |

Chr1:24997491-25001961 REVERSE LENGTH=1101 |

201606

Coefficients for Vitvi16g01010.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.840664	1.600078e-09	***	2.004306e-09	***
SlopeC	2.003371	0.00078477	***	0.1097382	
MeanF-MeanC	2.889029	2.424297e-10	***	1.585886e-08	***
SlopeF-SlopeC	-2.457307	0.004028662	**	0.9999488	



7.4.12 Vitvi14g03027

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

Vitvi14g03027

35.2

not assigned.unknown

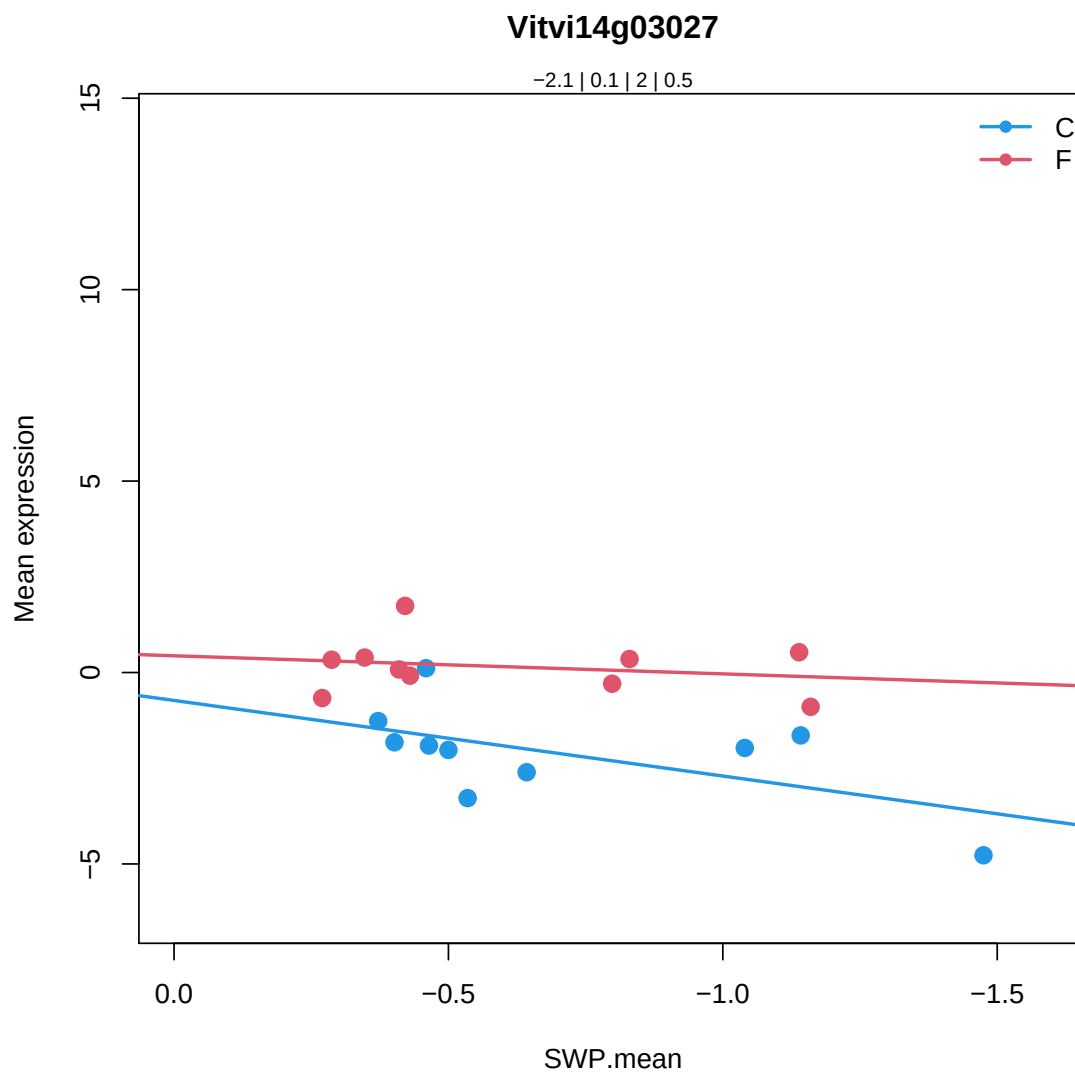
transmembrane protein |

Chr1:8425981-8427045 REVERSE LENGTH=354 |

201606

Coefficients for Vitvi14g03027.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-2.117932	9.501523e-08	***	1.12825e-07	***
SlopeC	1.973808	0.01542005	*	0.3393703	
MeanF-MeanC	2.267038	6.121502e-06	***	0.000160592	***
SlopeF-SlopeC	-1.501193	0.1926976		0.9999488	



7.4.13 Vitvi12g02241

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

Vitvi12g02241

26.6

misc.O-methyl transferases

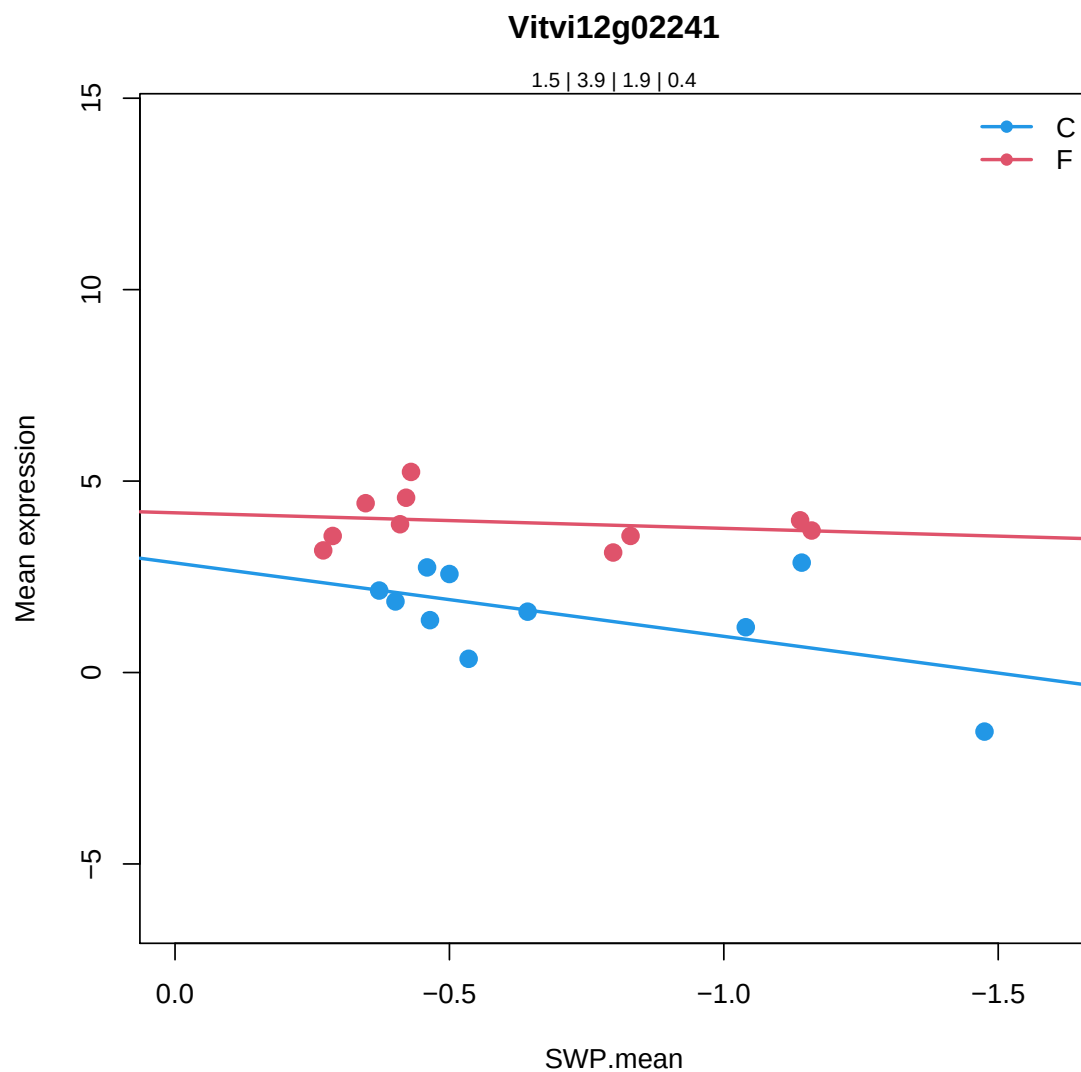
O-methyltransferase family protein |

Chr4:16730989-16732808 REVERSE LENGTH=382 |

201606

Coefficients for Vitvi12g02241.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.513909	1.593673e-05	***	1.791222e-05	***
SlopeC	1.917744	0.01970617	*	0.374907	
MeanF-MeanC	2.40998	3.204087e-06	***	9.094357e-05	***
SlopeF-SlopeC	-1.511665	0.195969		0.9999488	



7.4.14 Vitvi16g01695

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

Vitvi16g01695

35.2

not assigned.unknown

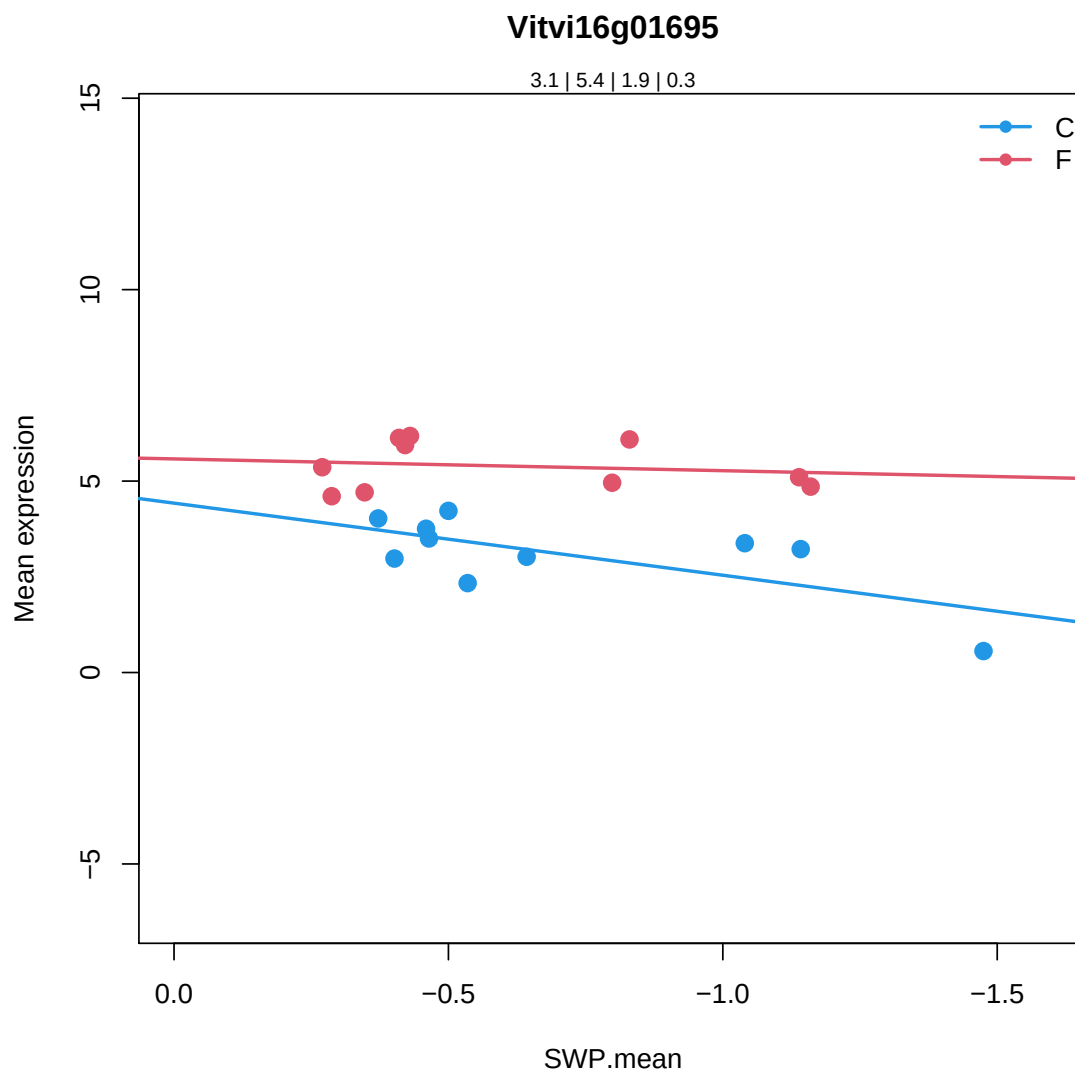
receptor like protein 6 |

Chr1:17183550-17186534 REVERSE LENGTH=994 |

201606

Coefficients for Vitvi16g01695.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.099689	1.944845e-12	***	2.745261e-12	***
SlopeC	1.88261	0.005080912	**	0.2530826	
MeanF-MeanC	2.292059	2.105269e-07	***	7.903575e-06	***
SlopeF-SlopeC	-1.575394	0.09360147	.	0.9999488	

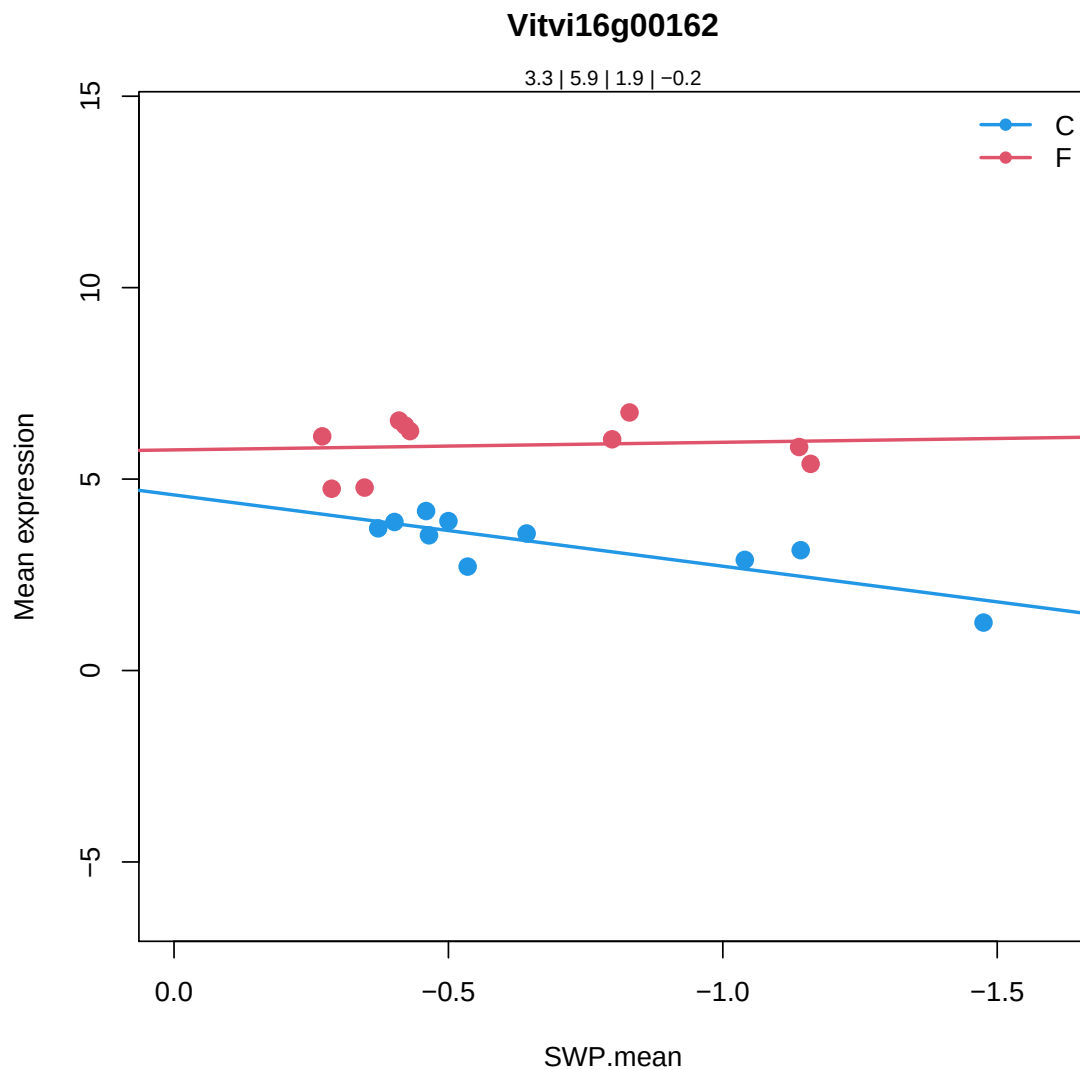


7.4.15 Vitvi16g00162

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
Vitvi16g00162
35.2
not assigned.unknown
NB-ARC domain-containing disease resistance protein |
Chr4:13633953-13636736 REVERSE LENGTH=927 |
201606
```

Coefficients for Vitvi16g00162.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.27686	4.140595e-14	***	6.560389e-14	***
SlopeC	1.862536	0.00186088	**	0.160246	
MeanF-MeanC	2.606492	2.387076e-09	***	1.285647e-07	***
SlopeF-SlopeC	-2.06133	0.01522443	*	0.9999488	



7.4.16 Vitvi07g01975

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

Vitvi07g01975

35.2

not assigned.unknown

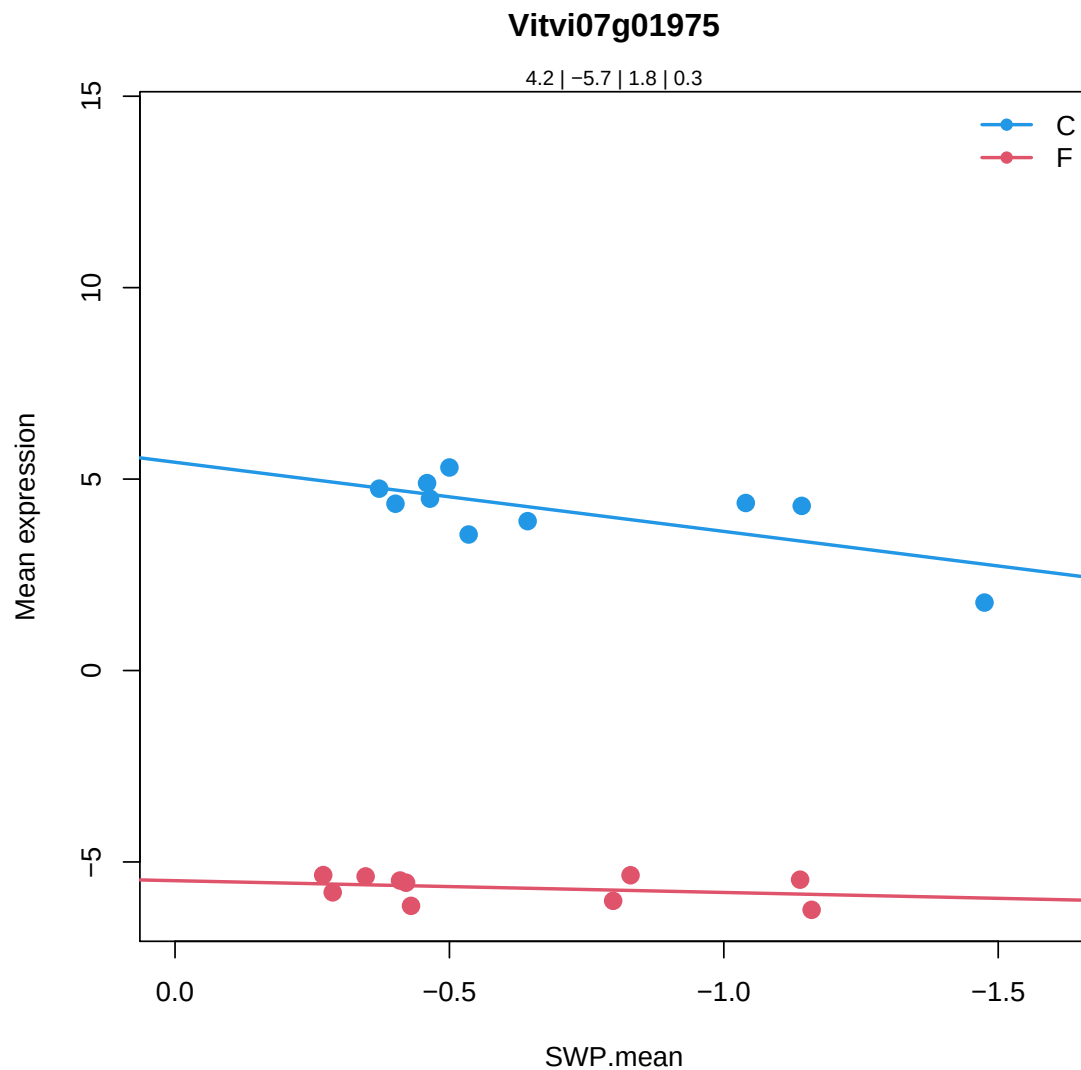
ammonium transporter 2 |

Chr2:16039672-16042291 REVERSE LENGTH=475 |

201606

Coefficients for Vitvi07g01975.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.169379	6.951417e-17	***	1.554254e-16	***
SlopeC	1.805957	0.001302019	**	0.1417527	
MeanF-MeanC	-9.845904	1.491184e-21	***	9.882012e-19	***
SlopeF-SlopeC	-1.498707	0.05160997	.	0.9999488	



7.4.17 Vitvi12g02434

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

```
Vitvi12g02434
```

```
29.4
```

```
protein.postranslational modification
```

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

```
Chr4:1419278-1422828 REVERSE LENGTH=1010 |
```

```
201606
```

```
Vitvi12g02434
```

```
30.2.24
```

```
signalling.receptor kinases.S-locus glycoprotein like
```

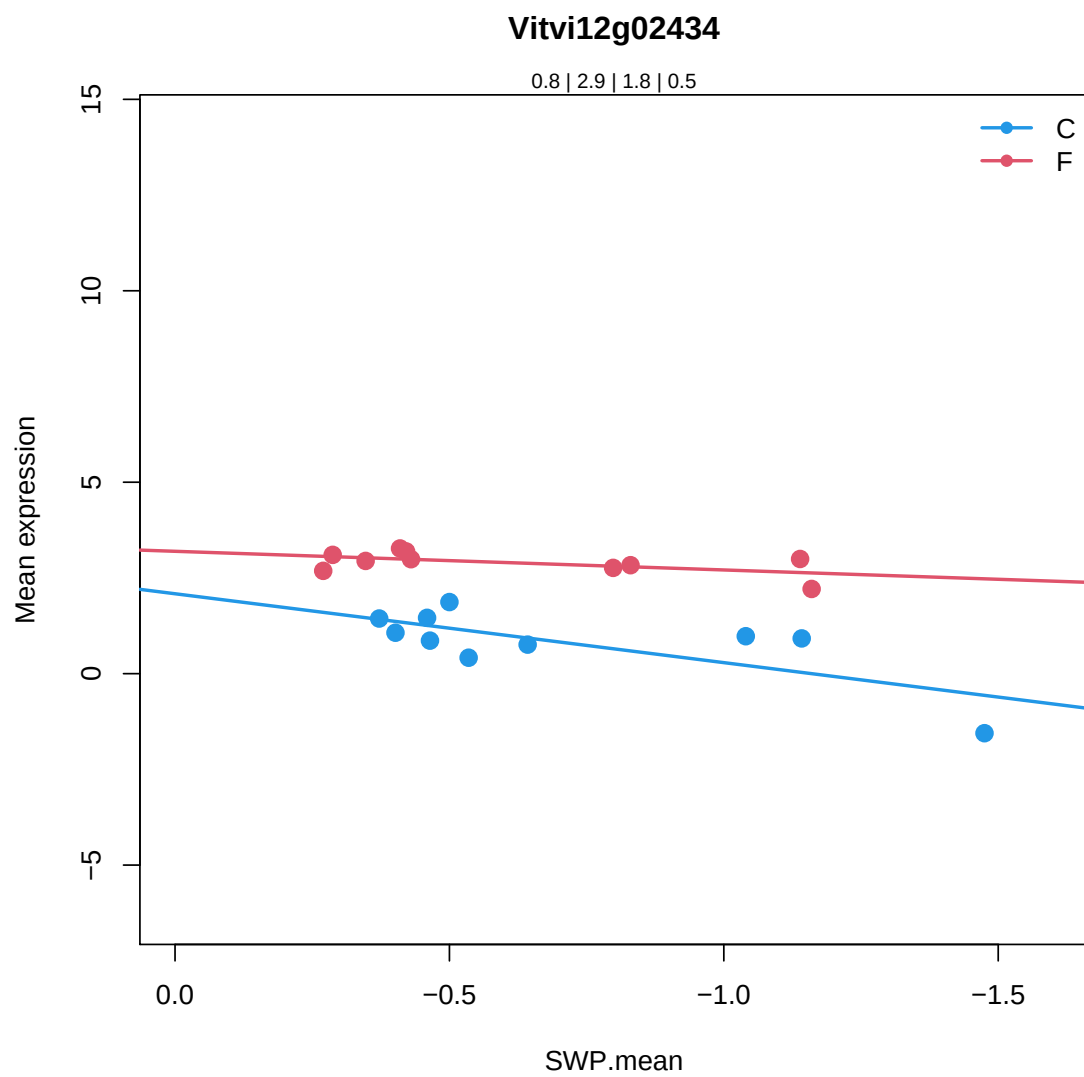
```
G-type lectin S-receptor-like Serine/Threonine-kinase |
```

```
Chr4:1419278-1422828 REVERSE LENGTH=1010 |
```

```
201606
```

Coefficients for Vitvi12g02434.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8214444	4.165707e-05	***	4.635592e-05	***
SlopeC	1.798958	0.0005749267	***	0.1005065	
MeanF-MeanC	2.077066	7.184554e-09	***	3.638105e-07	***
SlopeF-SlopeC	-1.311562	0.06099283	.	0.9999488	



7.4.18 Vitvi17g01499

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

Vitvi17g01499

26.2

misc.UDP glucosyl and glucoronyl transferases

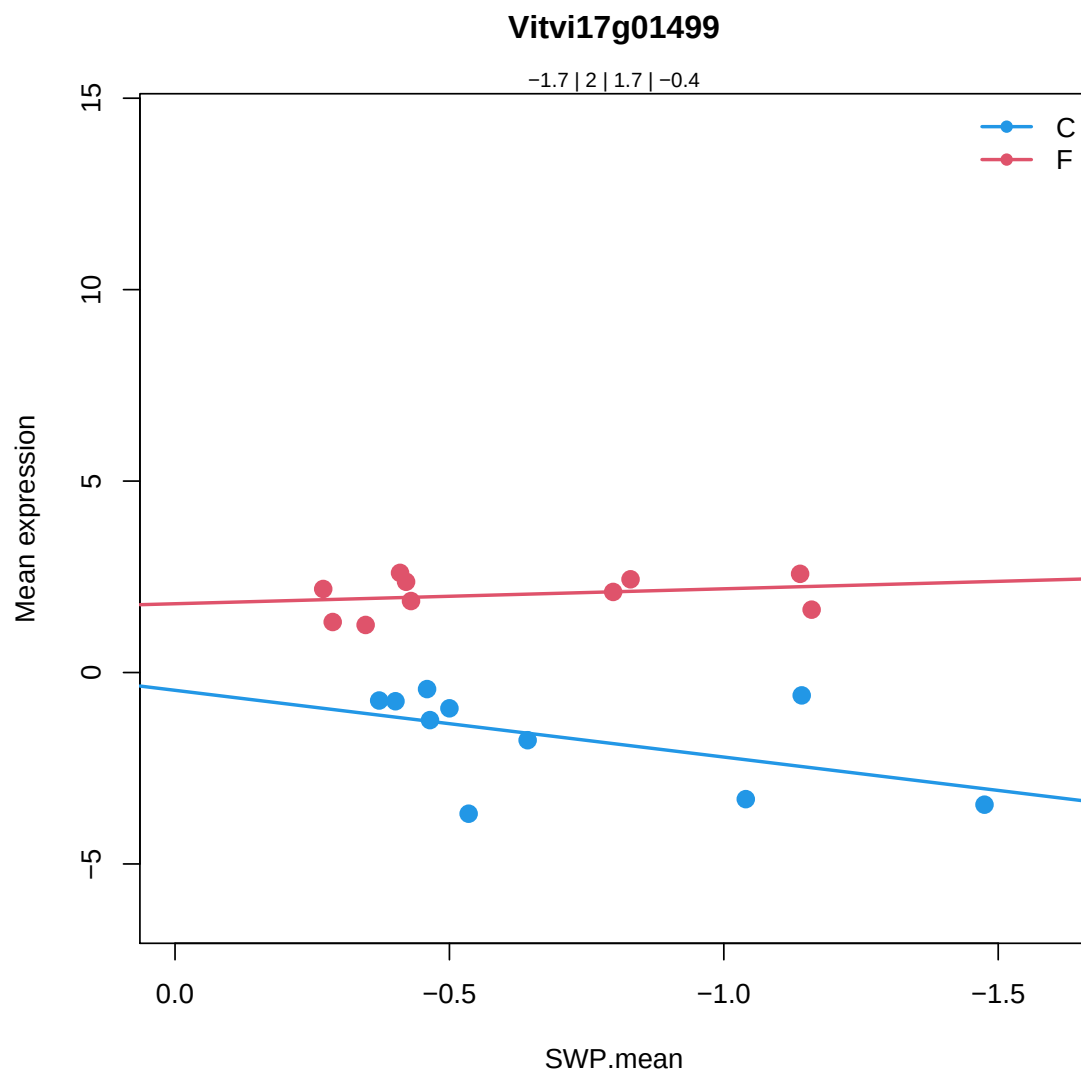
UDP-Glycosyltransferase superfamily protein |

Chr3:368840-370484 REVERSE LENGTH=464 |

201606

Coefficients for Vitvi17g01499.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.690499	1.763896e-06	***	2.024953e-06	***
SlopeC	1.743445	0.02511451	*	0.4079655	
MeanF-MeanC	3.724487	1.268641e-09	***	7.215157e-08	***
SlopeF-SlopeC	-2.133583	0.06070084	.	0.9999488	



7.4.19 Vitvi09g00253

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

```
Vitvi09g00253
```

```
29.4
```

```
protein.postranslational modification
```

```
Leucine-rich repeat transmembrane protein kinase protein |
```

```
Chr4:14665802-14669438 REVERSE LENGTH=876 |
```

```
201606
```

```
Vitvi09g00253
```

```
30.2.1
```

```
signalling.receptor kinases.leucine rich repeat I
```

```
Leucine-rich repeat transmembrane protein kinase protein |
```

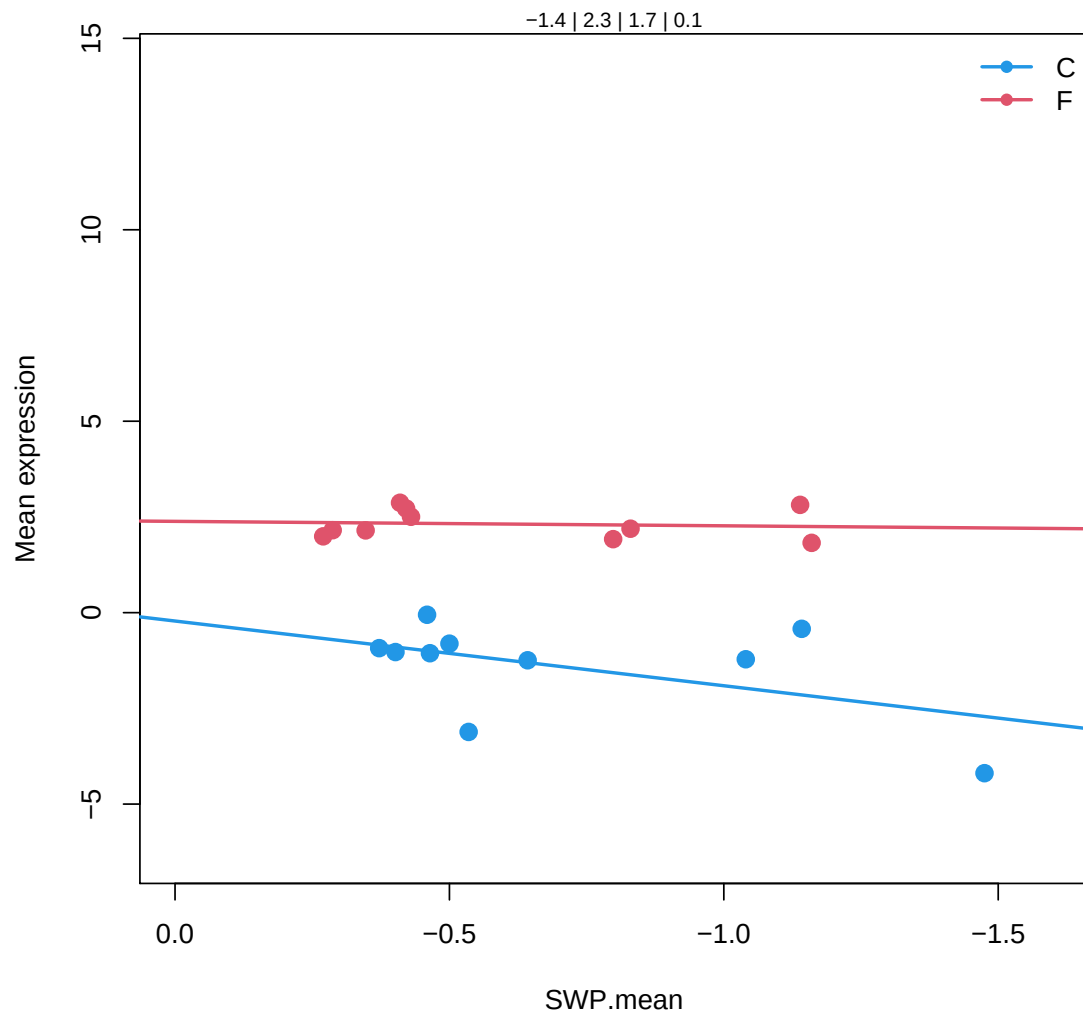
```
Chr4:14665802-14669438 REVERSE LENGTH=876 |
```

```
201606
```

Coefficients for Vitvi09g00253.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.407384	1.22789e-05	***	1.383771e-05	***
SlopeC	1.690283	0.02356607	*	0.3983963	
MeanF-MeanC	3.721139	5.921833e-10	***	3.639539e-08	***
SlopeF-SlopeC	-1.574086	0.1418375		0.9999488	

Vitvi09g00253



7.4.20 Vitvi07g02479

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

Vitvi07g02479

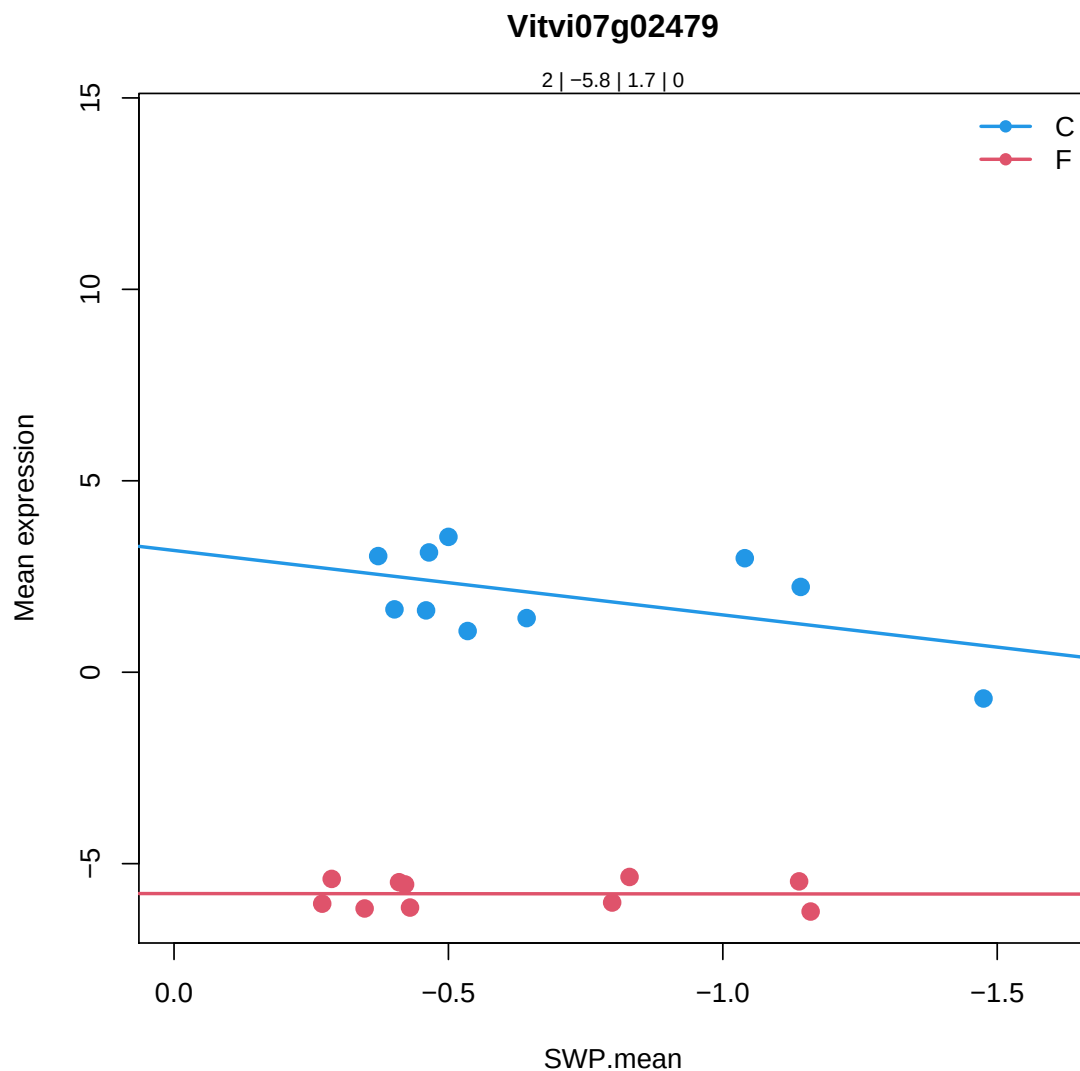
35.2

not assigned.unknown

Serine_threonine-protein phosphatase 6 regulatory ankyrin repeat subun

Coefficients for Vitvi07g02479.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.996167	6.687837e-08	***	7.966241e-08	***
SlopeC	1.683394	0.02375949	*	0.3983963	
MeanF-MeanC	-7.7825	2.962028e-16	***	4.961235e-14	***
SlopeF-SlopeC	-1.67543	0.1182497		0.9999488	



7.4.21 Vitvi07g03003

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

Vitvi07g03003

31.1

cell.organisation

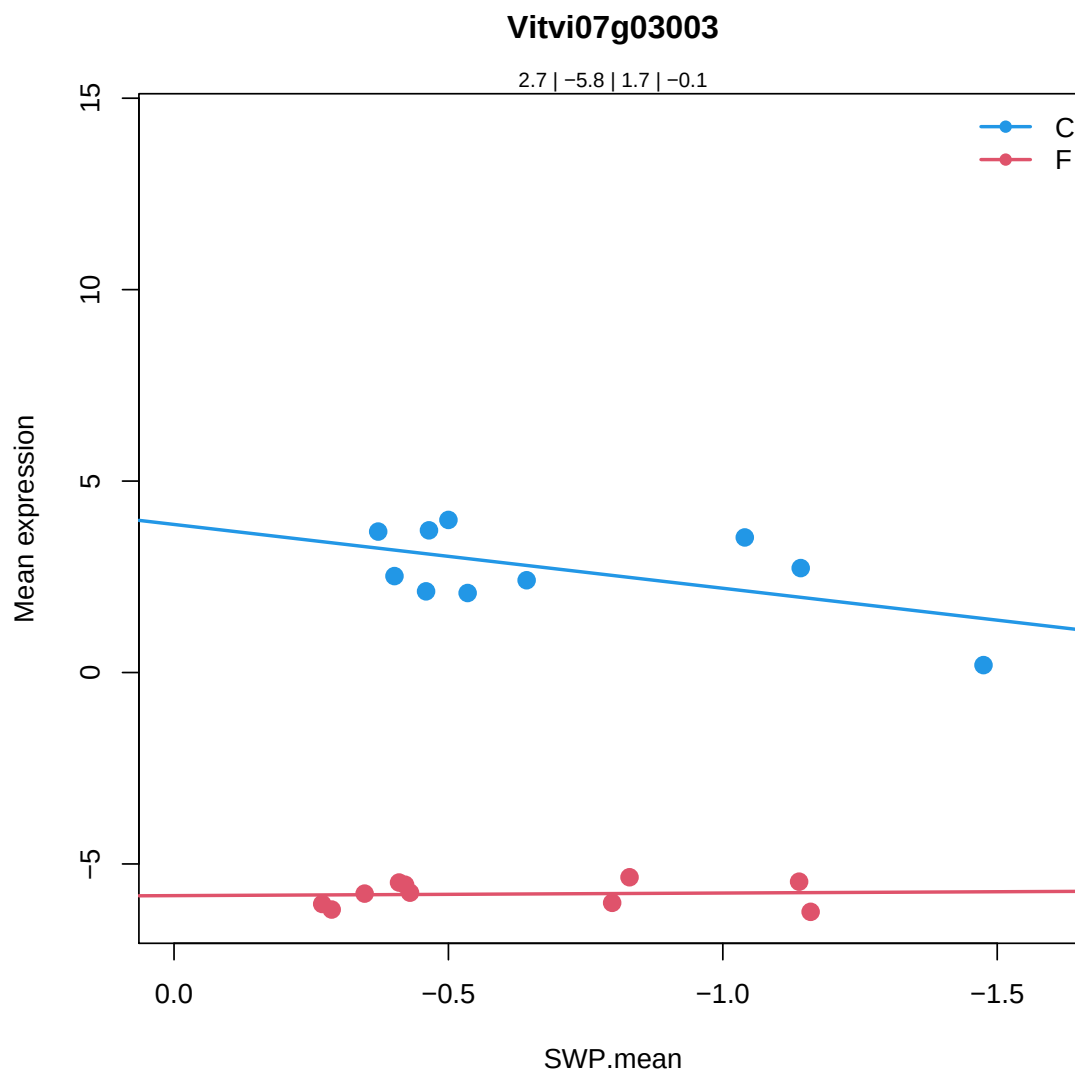
Ankyrin repeat family protein |

Chr3:6424135-6426471 REVERSE LENGTH=653 |

201606

Coefficients for Vitvi07g03003.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.695259	2.950611e-11	***	3.947789e-11	***
SlopeC	1.666543	0.01164374	*	0.318473	
MeanF-MeanC	-8.481592	3.014671e-18	***	7.411229e-16	***
SlopeF-SlopeC	-1.734139	0.0671711	.	0.9999488	



7.4.22 Vitvi11g00749

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

Vitvi11g00749

30.2.12

signalling.receptor kinases.leucine rich repeat XII

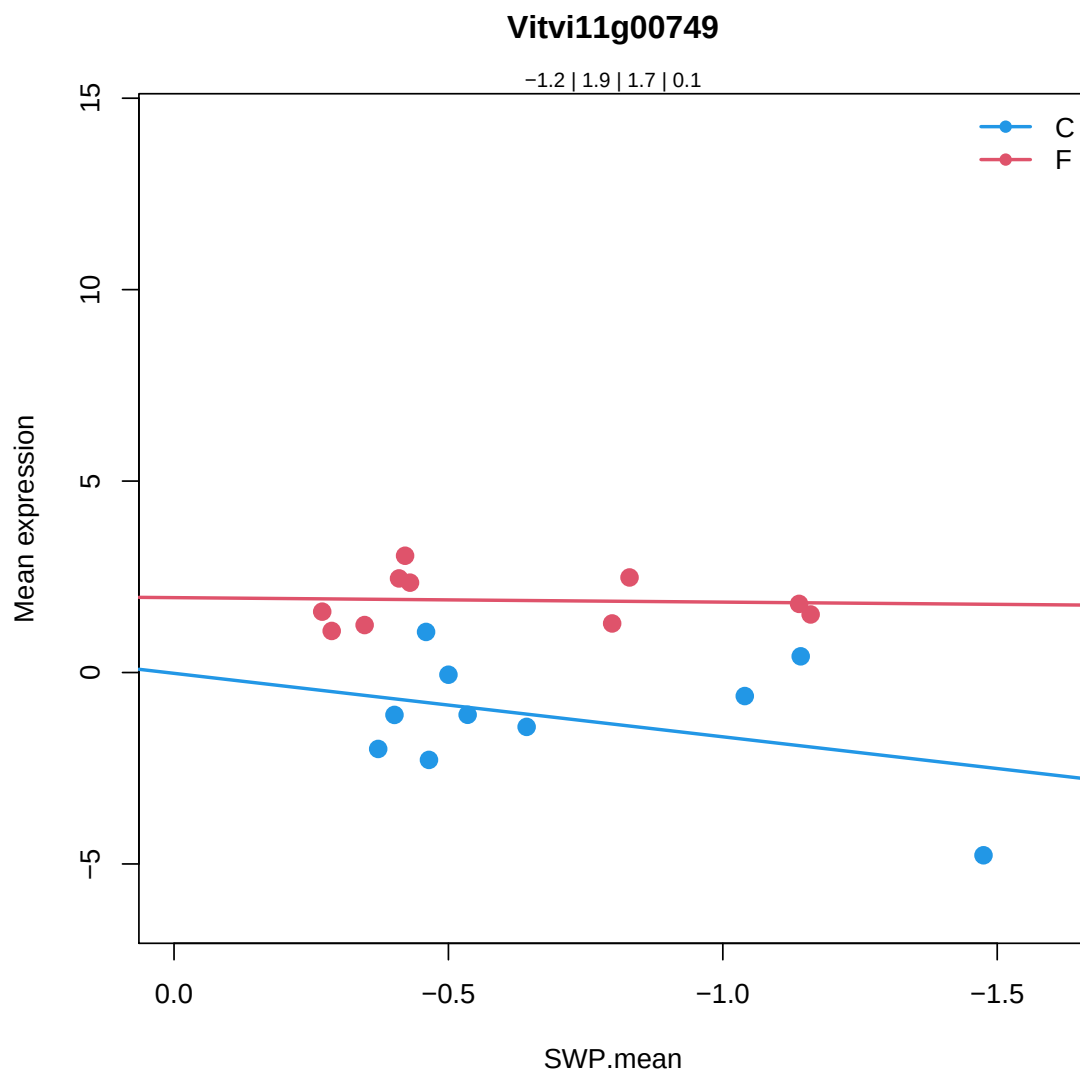
kinase family with leucine-rich repeat domain-containing protein |

Chr1:13220940-13224386 FORWARD LENGTH=1120 |

201606

Coefficients for Vitvi11g00749.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.187309	0.002453198	**	0.002632658	**
SlopeC	1.657462	0.09954394	.	0.6110181	
MeanF-MeanC	3.071475	2.889466e-06	***	8.264173e-05	***
SlopeF-SlopeC	-1.540859	0.2941879		0.9999488	



7.4.23 Vitvi16g02128

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

Vitvi16g02128

35.2

not assigned.unknown

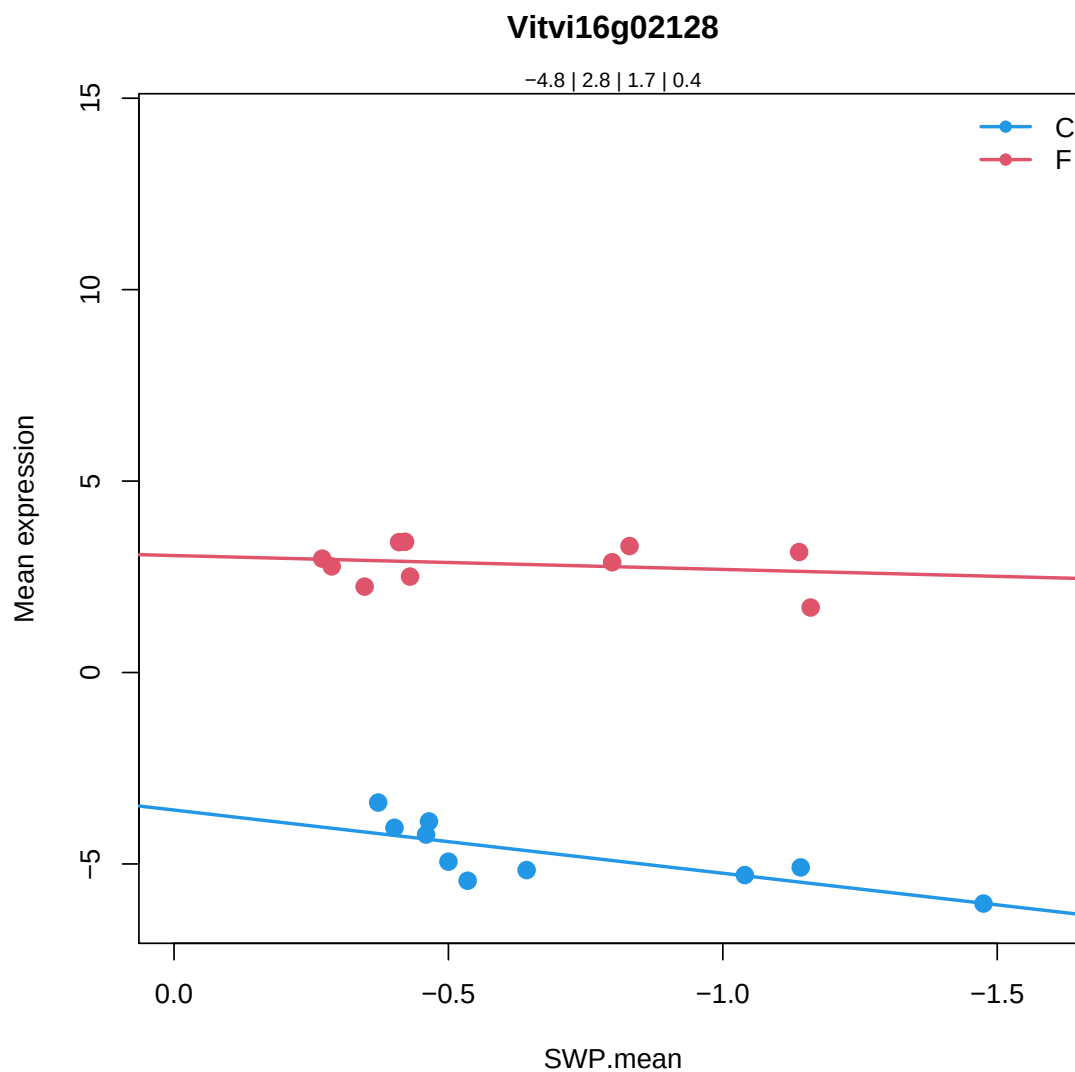
PR5-like receptor kinase |

Chr5:15293325-15295838 REVERSE LENGTH=665 |

201606

Coefficients for Vitvi16g02128.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-4.752626	3.621096e-18	***	1.065291e-17	***
SlopeC	1.650819	0.002533182	**	0.1902008	
MeanF-MeanC	7.586807	2.867599e-19	***	8.405375e-17	***
SlopeF-SlopeC	-1.288502	0.08722927	.	0.9999488	



7.4.24 Vitvi12g02492

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

Vitvi12g02492

30.2.12

signalling.receptor kinases.leucine rich repeat XII

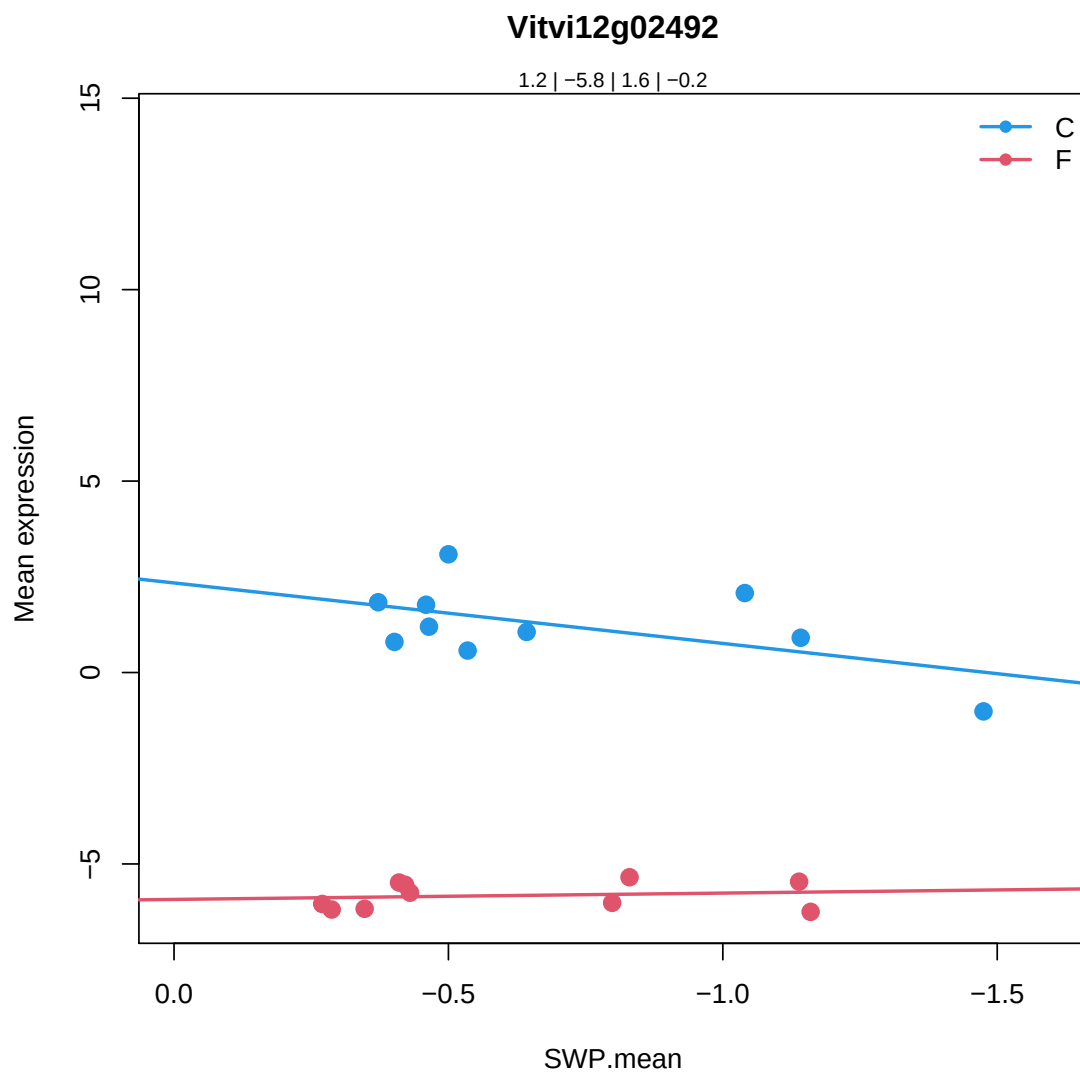
receptor like protein 22 |

Chr2:13853897-13855666 REVERSE LENGTH=589 |

201606

Coefficients for Vitvi12g02492.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.228831	9.368109e-06	***	1.058714e-05	***
SlopeC	1.579994	0.01438592	*	0.3359386	
MeanF-MeanC	-7.054787	9.455527e-17	***	1.736399e-14	***
SlopeF-SlopeC	-1.745248	0.06109156	.	0.9999488	



7.4.25 Vitvi16g02015

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

```
Vitvi16g02015
```

```
35.2
```

```
not assigned.unknown
```

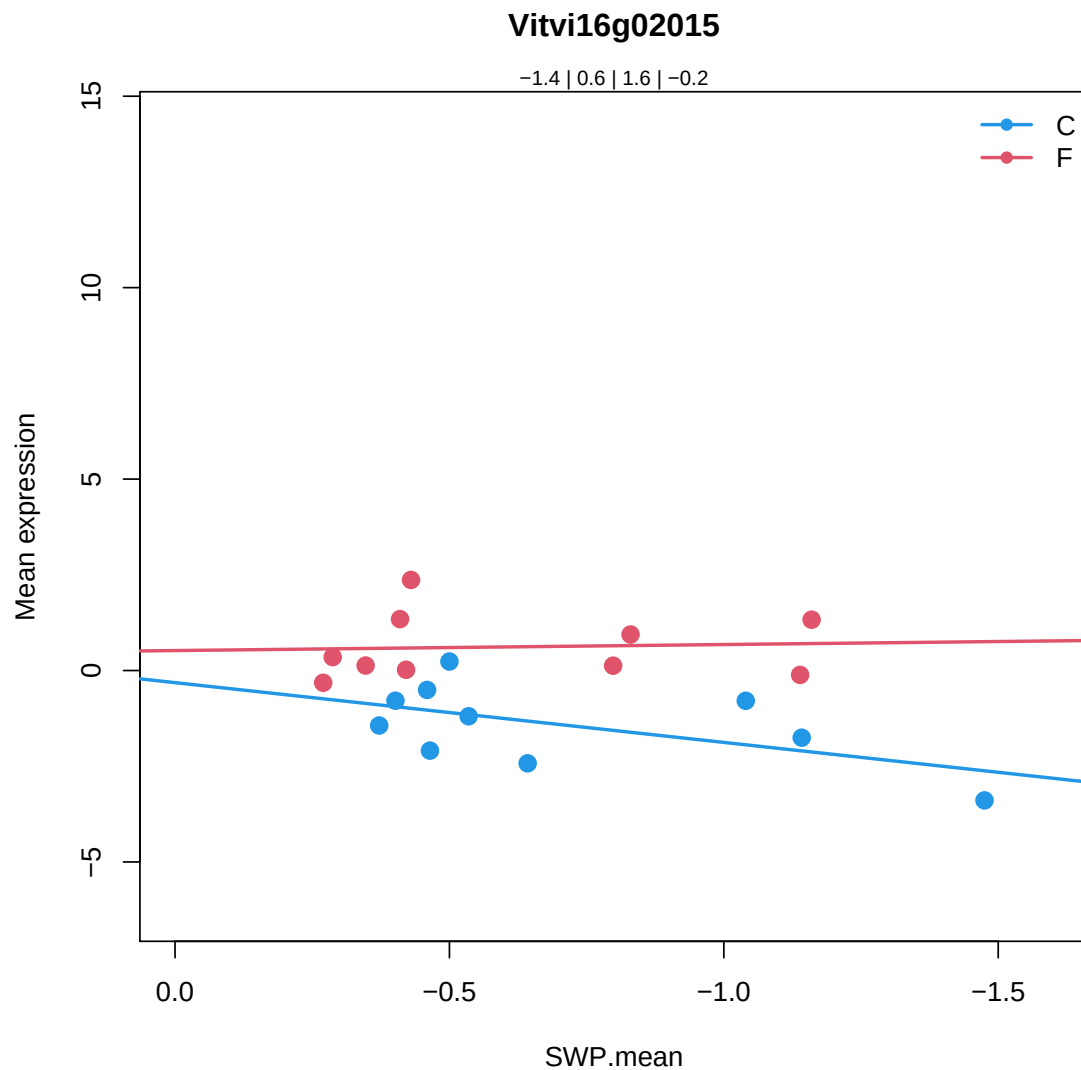
```
PR5-like receptor kinase |
```

```
Chr5:15293325-15295838 REVERSE LENGTH=665 |
```

```
201606
```

Coefficients for Vitvi16g02015.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.41461	2.01347e-05	***	2.257729e-05	***
SlopeC	1.561065	0.04258379	*	0.48214	
MeanF-MeanC	2.031392	1.653779e-05	***	0.0003908047	***
SlopeF-SlopeC	-1.71816	0.1254976		0.9999488	



7.4.26 Vitvi07g01880

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

Vitvi07g01880

29.2.1.2.2.3

protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L3

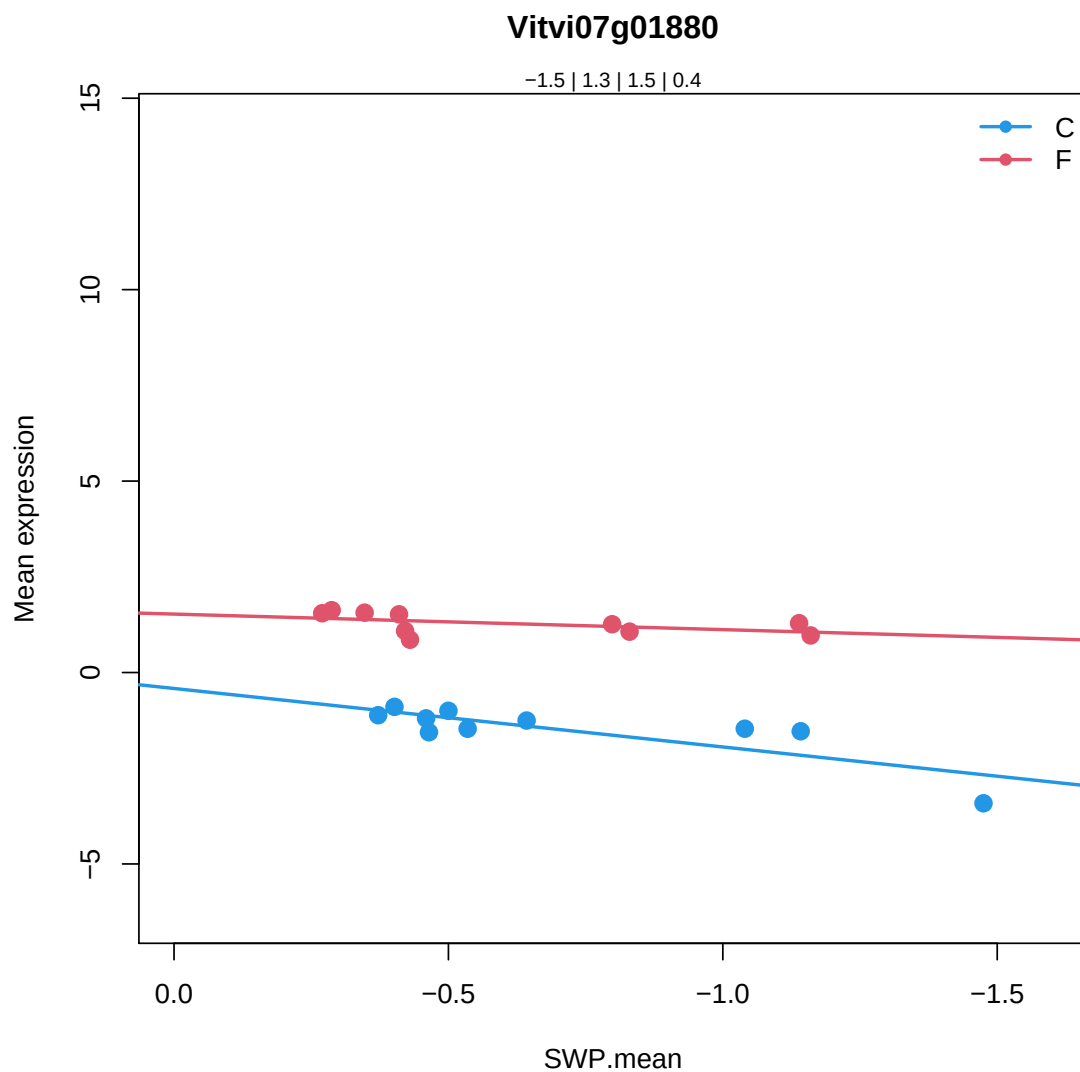
cysteine-rich RECEPTOR-like kinase |

Chr4:12129485-12133157 FORWARD LENGTH=1043 |

201606

Coefficients for Vitvi07g01880.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.491084	7.084737e-11	***	9.323568e-11	***
SlopeC	1.527266	0.0002627845	***	0.08298279	.
MeanF-MeanC	2.769697	3.688811e-13	***	3.627411e-11	***
SlopeF-SlopeC	-1.121594	0.04294883	*	0.9999488	



7.4.27 Vitvi09g01427

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

Vitvi09g01427

16.01.2005

secondary metabolism.isoprenoids.terpenoids

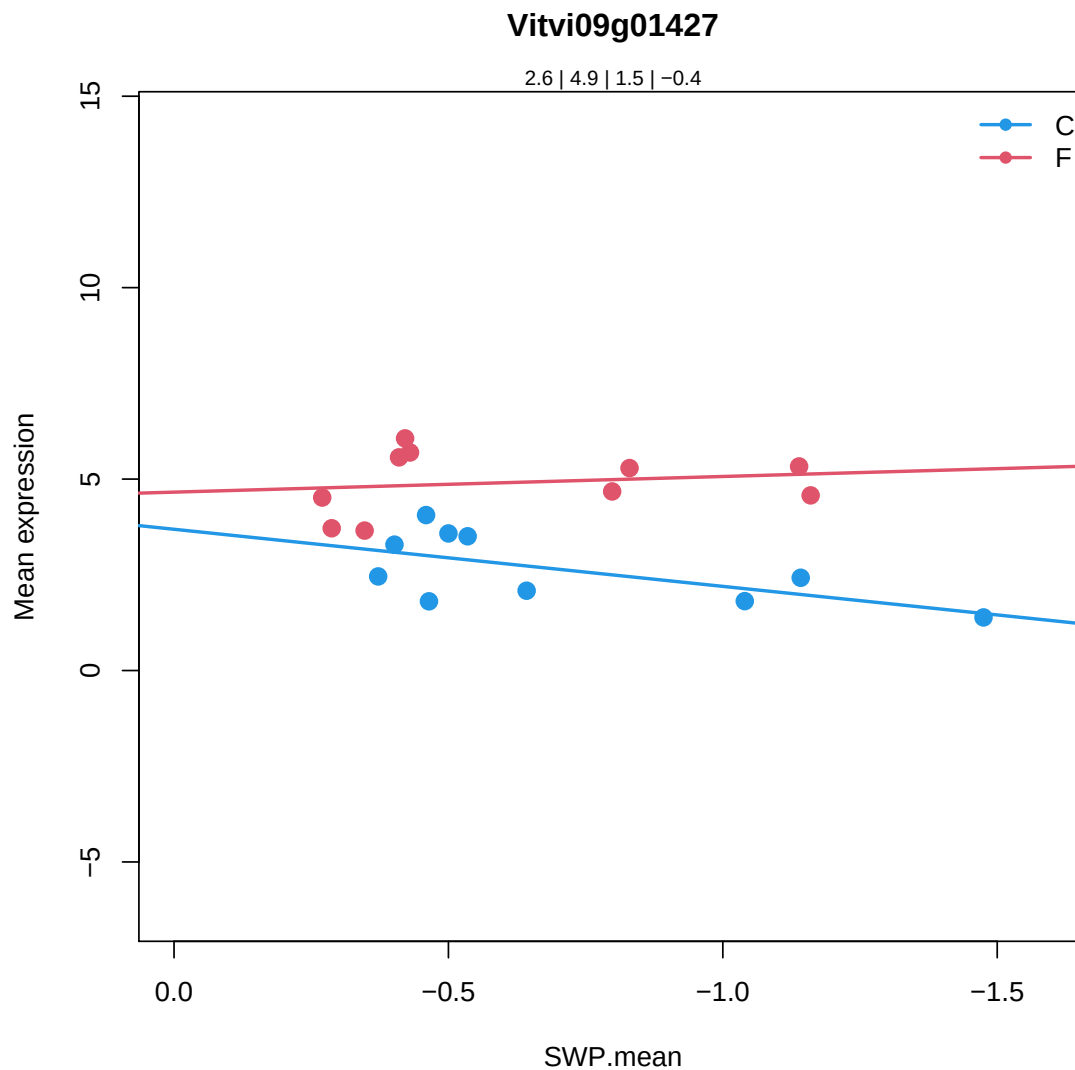
lupeol synthase 2 |

Chr1:29696722-29701024 FORWARD LENGTH=763 |

201606

Coefficients for Vitvi09g01427.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.640377	1.670713e-10	***	2.168157e-10	***
SlopeC	1.49161	0.03178072	*	0.4343406	
MeanF-MeanC	2.267754	7.710756e-07	***	2.577354e-05	***
SlopeF-SlopeC	-1.90059	0.06232887	.	0.9999488	



7.4.28 Vitvi07g00060

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

Vitvi07g00060

35.2

not assigned.unknown

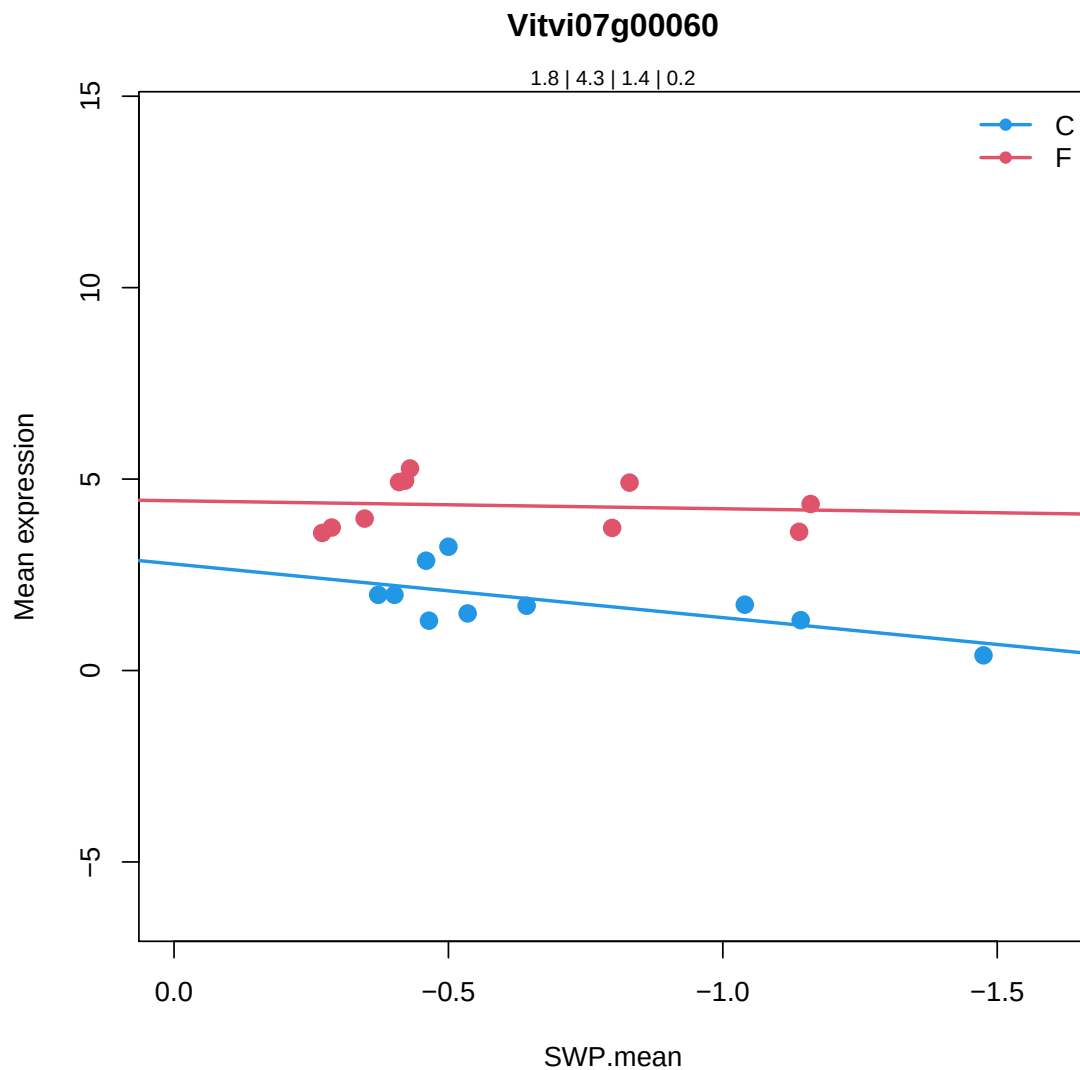
Ubiquitin-conjugating enzyme/RWD-like protein |

Chr2:16225777-16226772 FORWARD LENGTH=331 |

201606

Coefficients for Vitvi07g00060.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.797056	8.679692e-09	***	1.061253e-08	***
SlopeC	1.400516	0.01885436	*	0.3679617	
MeanF-MeanC	2.508855	1.082839e-08	***	5.358644e-07	***
SlopeF-SlopeC	-1.192193	0.1607068		0.9999488	



7.4.29 Vitvi15g00017

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

Vitvi15g00017

35.2

not assigned.unknown

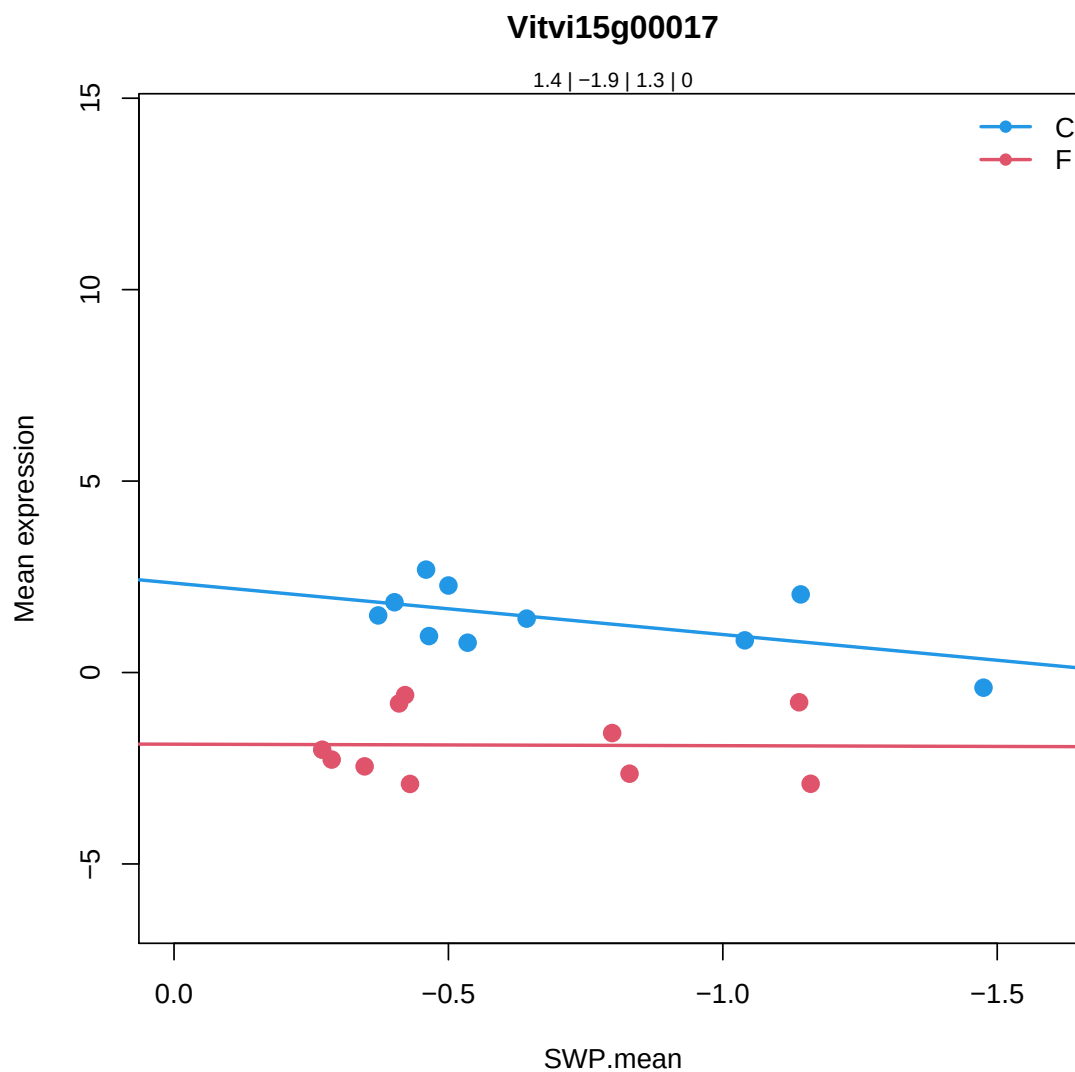
NB-ARC domain-containing disease resistance protein |

Chr3:4857940-4861104 FORWARD LENGTH=1054 |

201606

Coefficients for Vitvi15g00017.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.390779	1.520535e-05	***	1.710027e-05	***
SlopeC	1.343637	0.06706753	.	0.5552652	
MeanF-MeanC	-3.286505	5.811022e-09	***	2.972201e-07	***
SlopeF-SlopeC	-1.304475	0.2218154		0.9999488	



7.4.30 Vitvi12g02451

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

Vitvi12g02451

16.8.1.21

secondary metabolism.flavonoids.anthocyanins.anthocyanin 5-aromatic ac

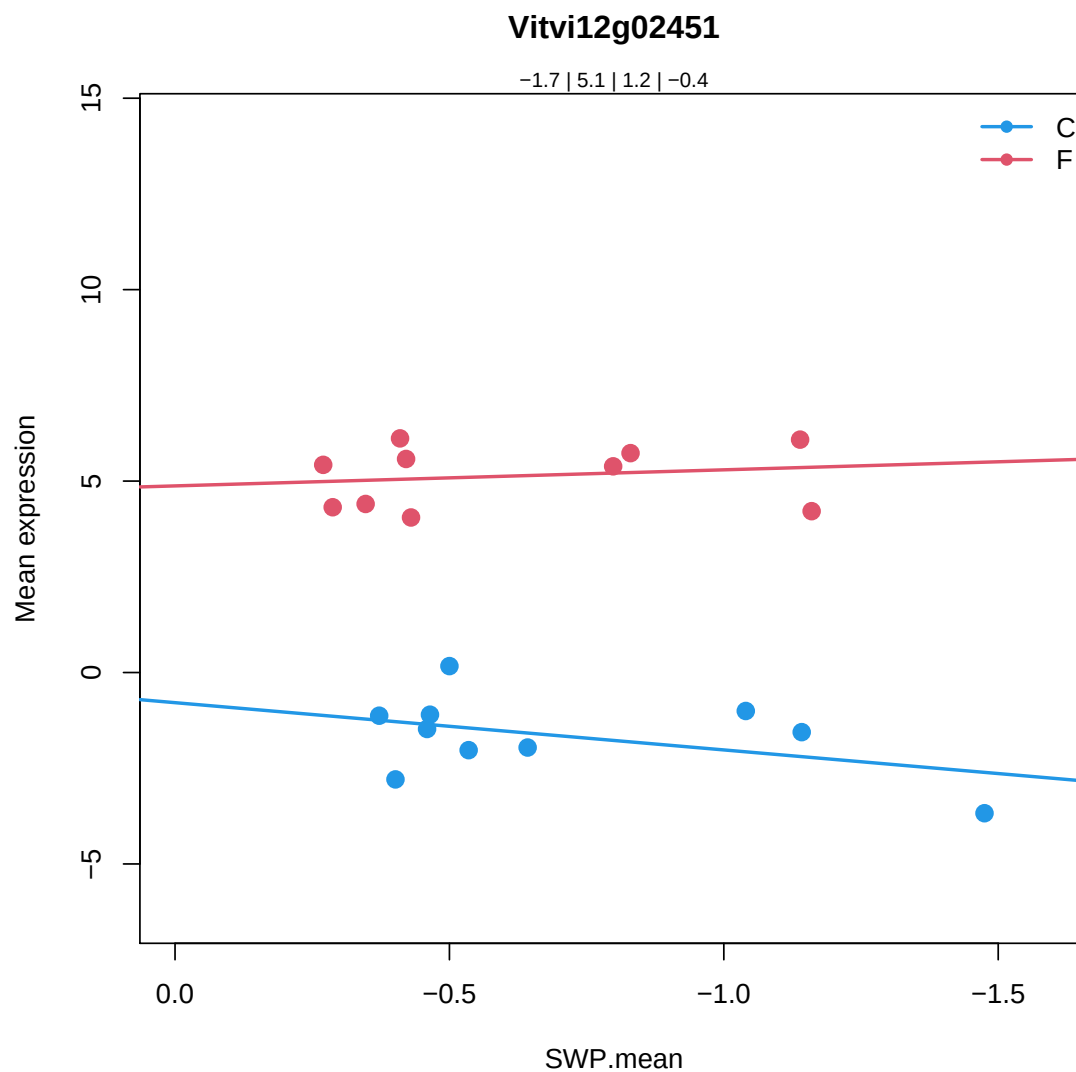
HXXXD-type acyl-transferase family protein |

Chr1:1009542-1010951 REVERSE LENGTH=469 |

201606

Coefficients for Vitvi12g02451.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.655451	2.884365e-06	***	3.294626e-06	***
SlopeC	1.234009	0.1071191		0.6223948	
MeanF-MeanC	6.785157	1.620031e-14	***	2.019201e-12	***
SlopeF-SlopeC	-1.654182	0.1444542		0.9999488	



7.4.31 Vitvi17g01328

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

Vitvi17g01328

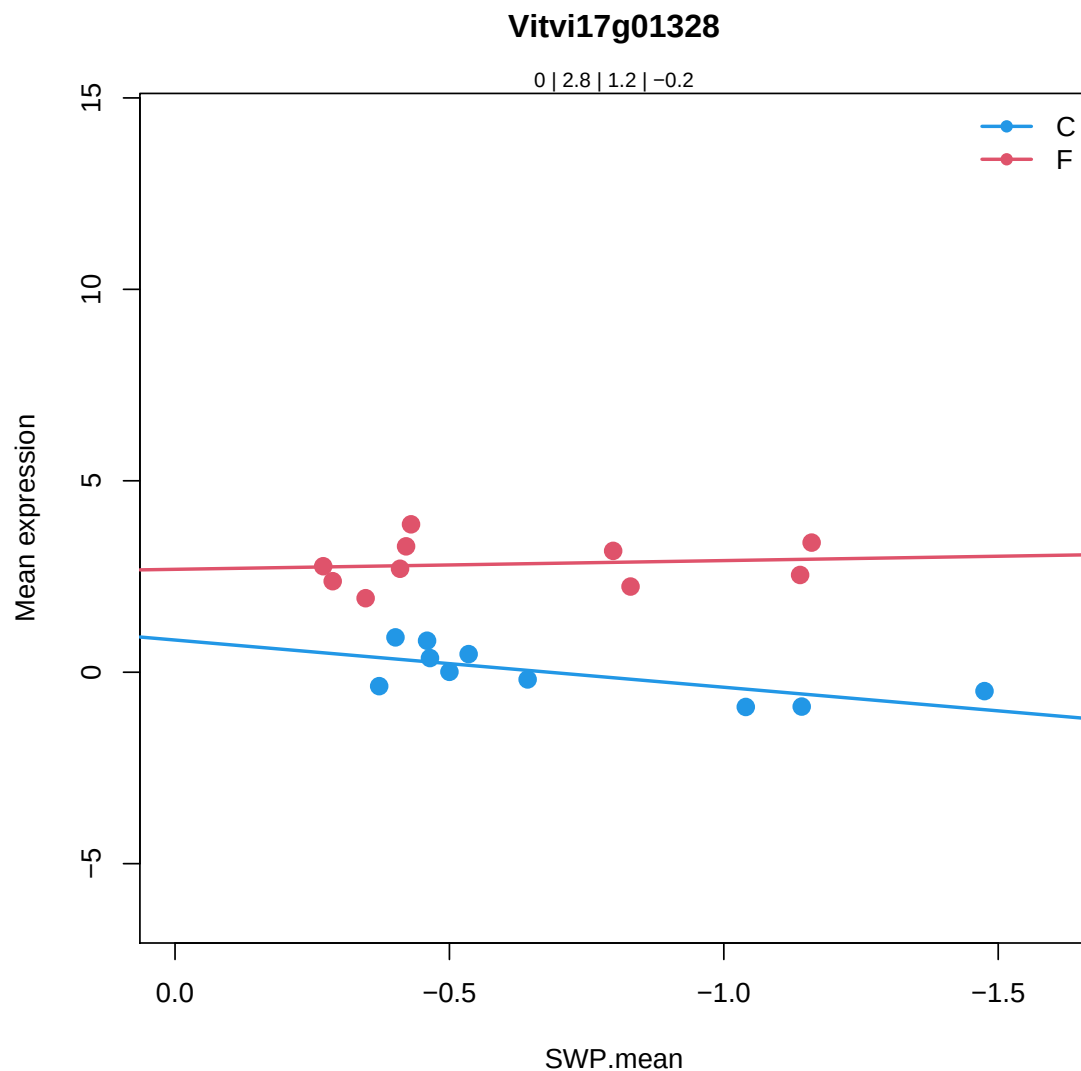
35.2

not assigned.unknown

NA

Coefficients for Vitvi17g01328.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.02650758	0.8790298		0.8816908	
SlopeC	1.233294	0.01745139	*	0.3551322	
MeanF-MeanC	2.852842	8.627588e-11	***	6.144939e-09	***
SlopeF-SlopeC	-1.460876	0.05279348	.	0.9999488	



7.4.32 Vitvi12g02491

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

Vitvi12g02491

30.2.12

signalling.receptor kinases.leucine rich repeat XII

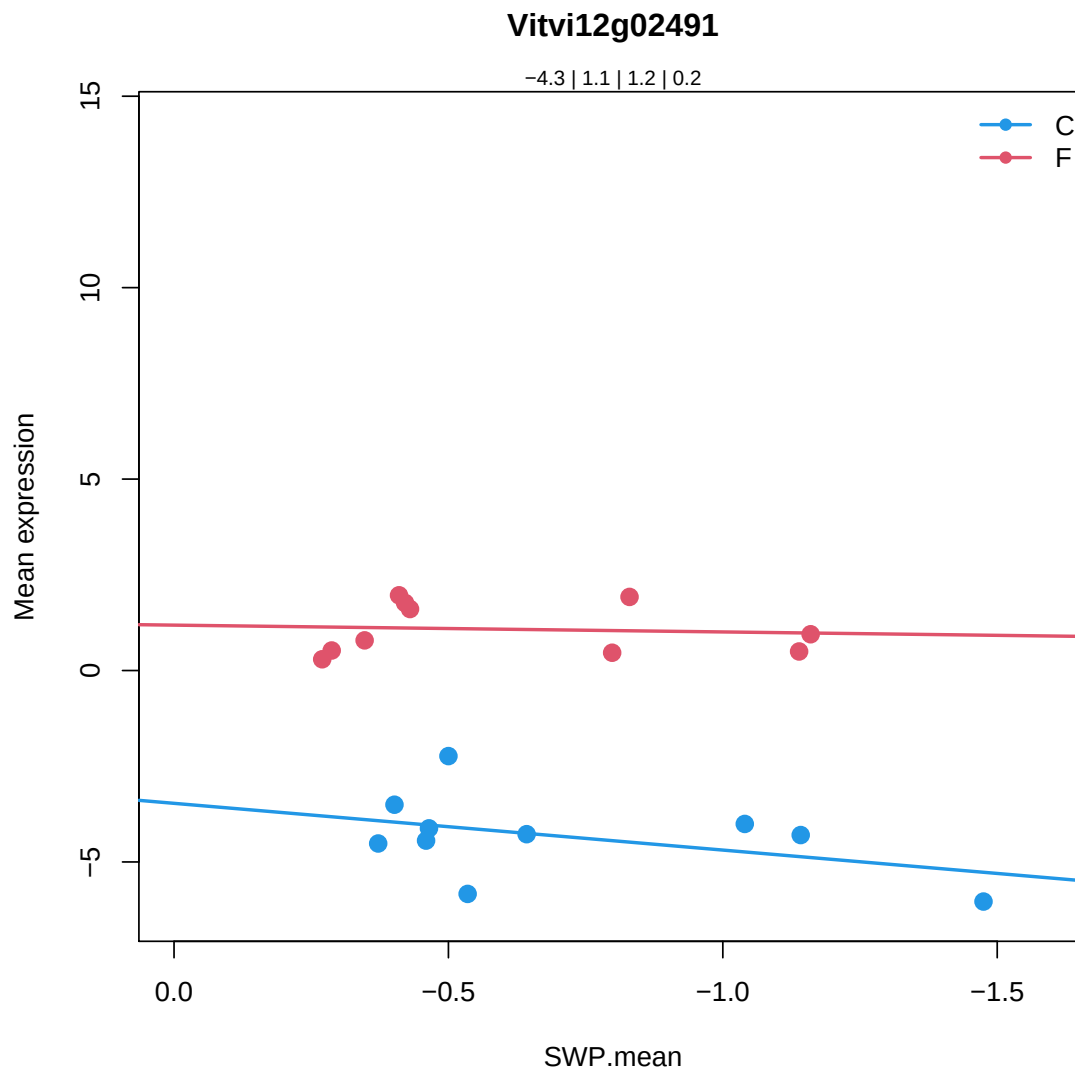
receptor like protein 6 |

Chr1:17183550-17186534 REVERSE LENGTH=994 |

201606

Coefficients for Vitvi12g02491.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-4.327187	5.817118e-14	***	9.090067e-14	***
SlopeC	1.220752	0.09780238	.	0.6084506	
MeanF-MeanC	5.404248	6.868441e-13	***	6.374487e-11	***
SlopeF-SlopeC	-1.042901	0.331487		0.9999488	



7.4.33 Vitvi10g02381

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

```
Vitvi10g02381
```

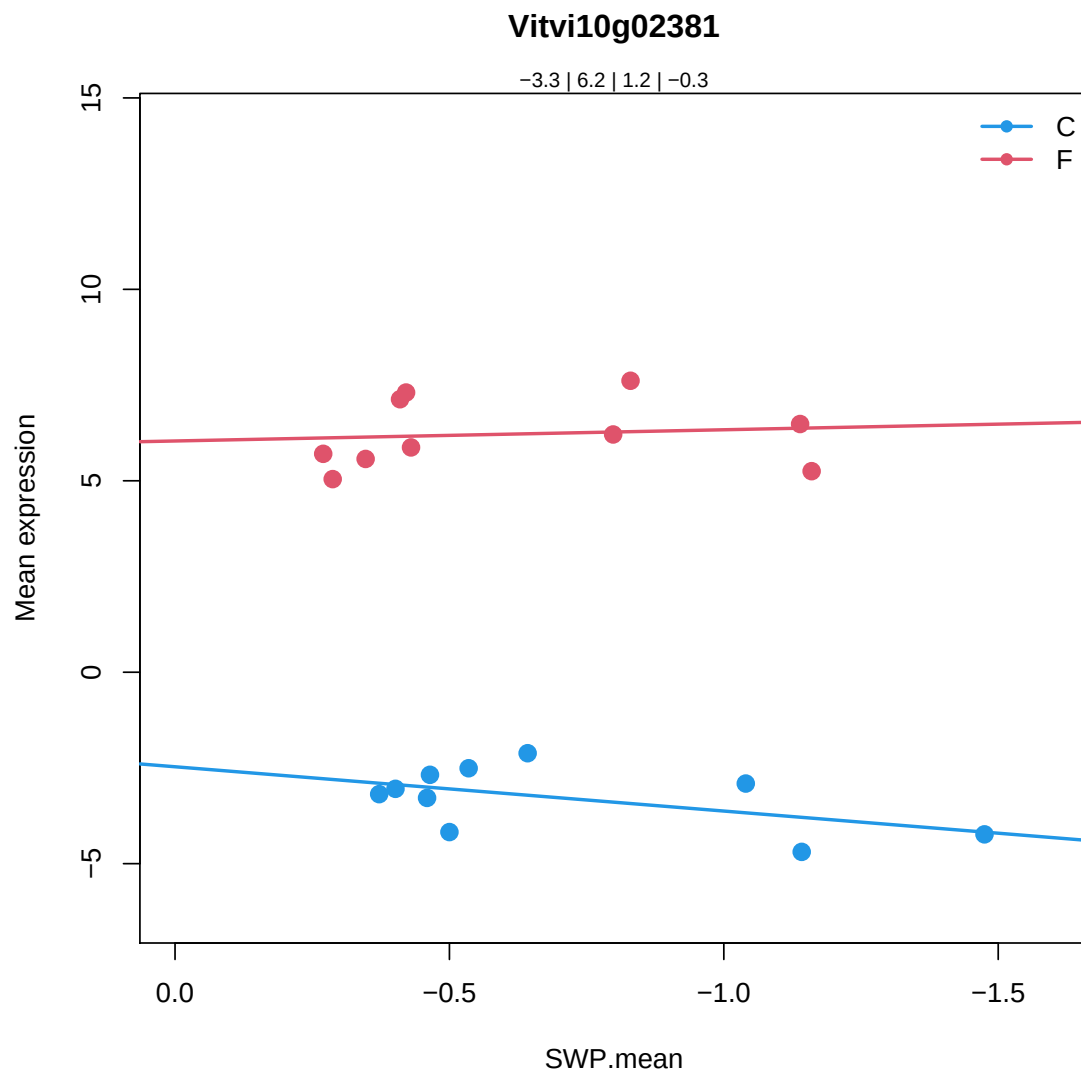
```
35.2
```

```
not assigned.unknown
```

```
NA
```

Coefficients for Vitvi10g02381.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-3.282562	6.75514e-12	***	9.297619e-12	***
SlopeC	1.156847	0.1039412		0.6157294	
MeanF-MeanC	9.500513	3.451249e-18	***	8.219364e-16	***
SlopeF-SlopeC	-1.44987	0.1671388		0.9999488	



7.4.34 Vitvi18g02485

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

Vitvi18g02485

17.7.1.5

hormone metabolism.jasmonate.synthesis-degradation.12-oxophytodienoate

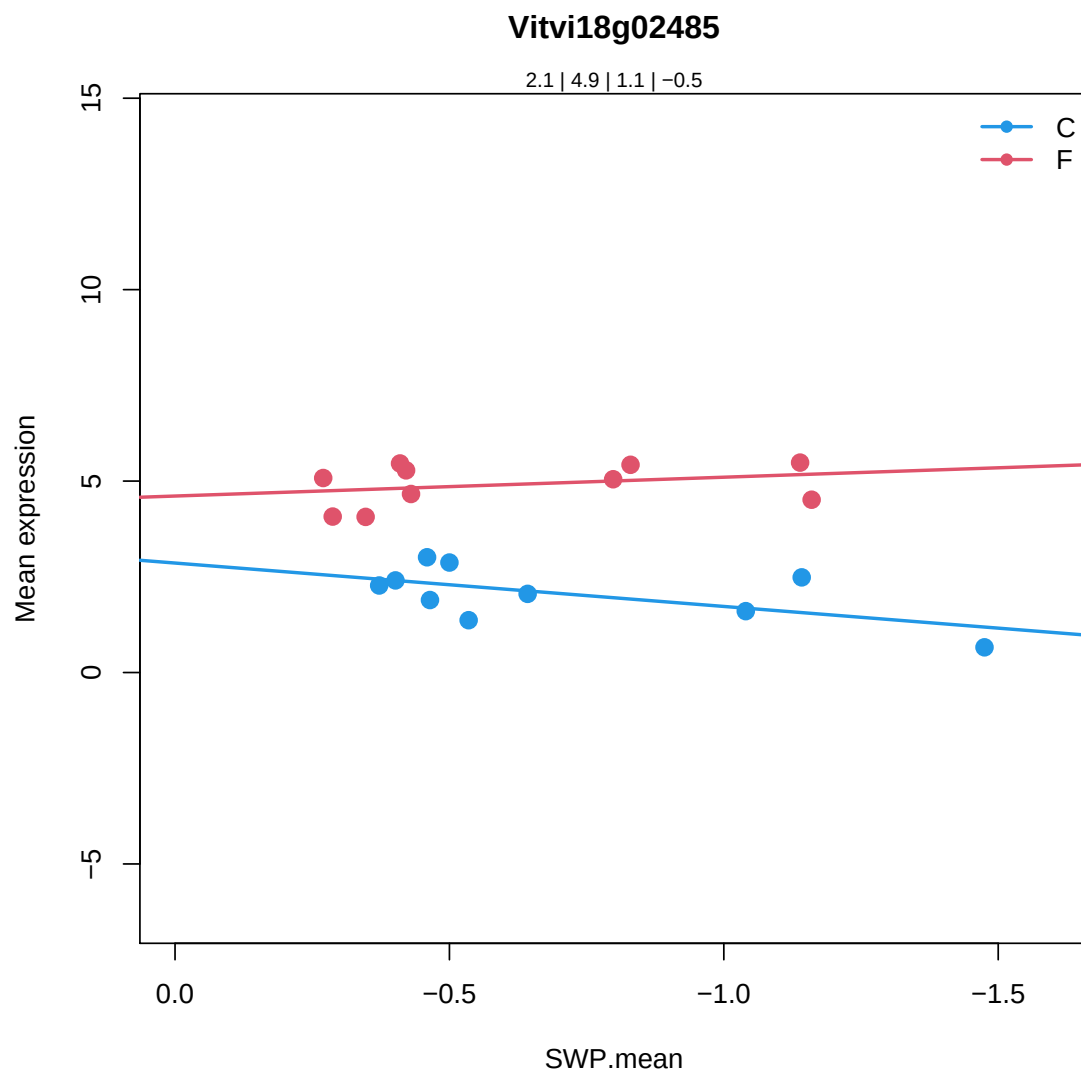
12-oxophytodienoate reductase 2 |

Chr1:28778976-28780355 FORWARD LENGTH=374 |

201606

Coefficients for Vitvi18g02485.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.062013	9.401842e-11	***	1.231548e-10	***
SlopeC	1.13339	0.0312388	*	0.4322019	
MeanF-MeanC	2.84682	1.470283e-10	***	9.915952e-09	***
SlopeF-SlopeC	-1.625173	0.03726078	*	0.9999488	



7.4.35 Vitvi08g02231

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

Vitvi08g02231

1.03.2007

PS.calvin cycle.FBPase

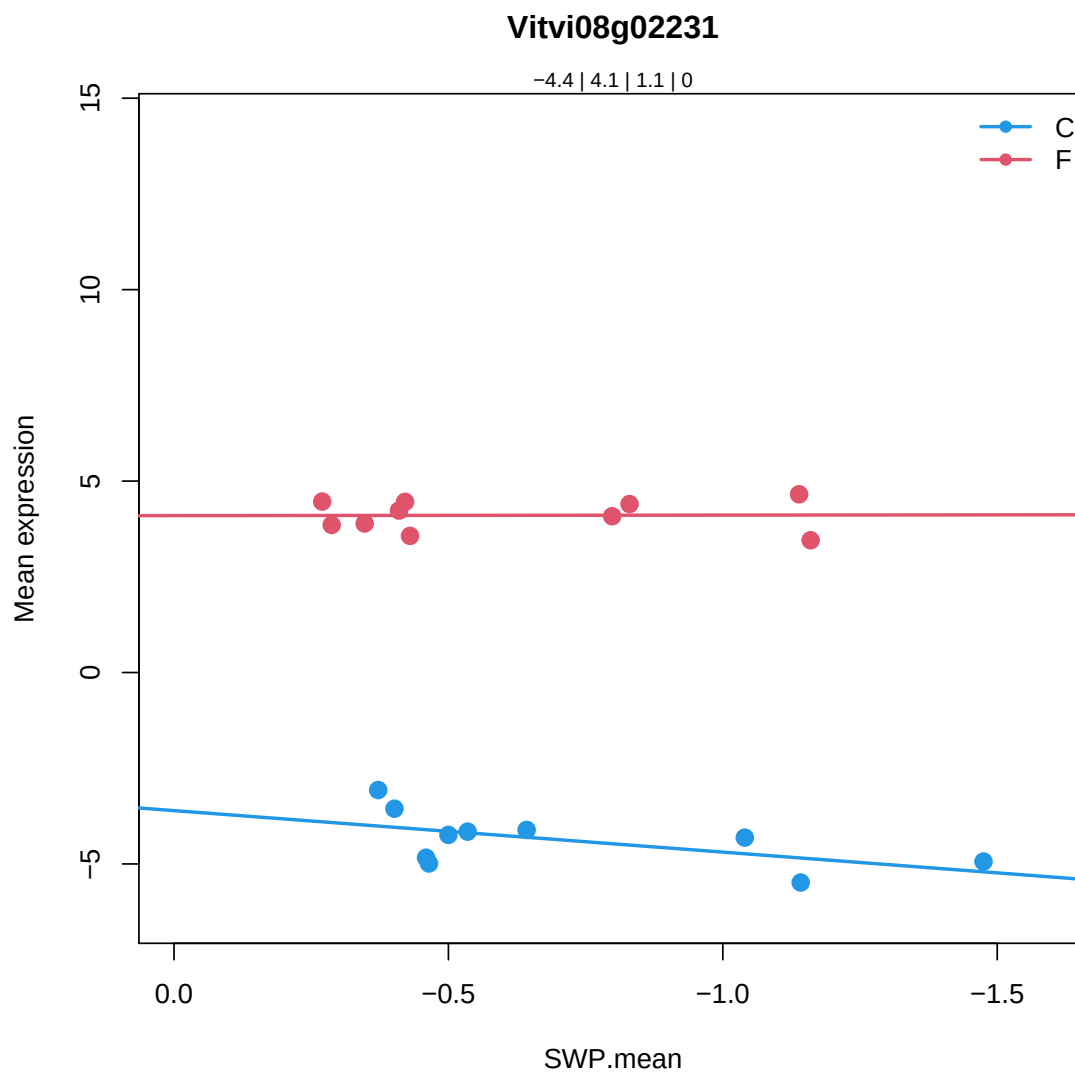
high cyclic electron flow 1 |

Chr3:20016951-20018527 FORWARD LENGTH=417 |

201606

Coefficients for Vitvi08g02231.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-4.369236	8.352797e-18	***	2.245781e-17	***
SlopeC	1.083398	0.02879223	*	0.4275443	
MeanF-MeanC	8.475029	1.103454e-20	***	5.425435e-18	***
SlopeF-SlopeC	-1.096231	0.1257159		0.9999488	



7.4.36 Vitvi16g01756

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

Vitvi16g01756

20.1.2.1

stress.biotic.receptors.CC-NBS-LRR

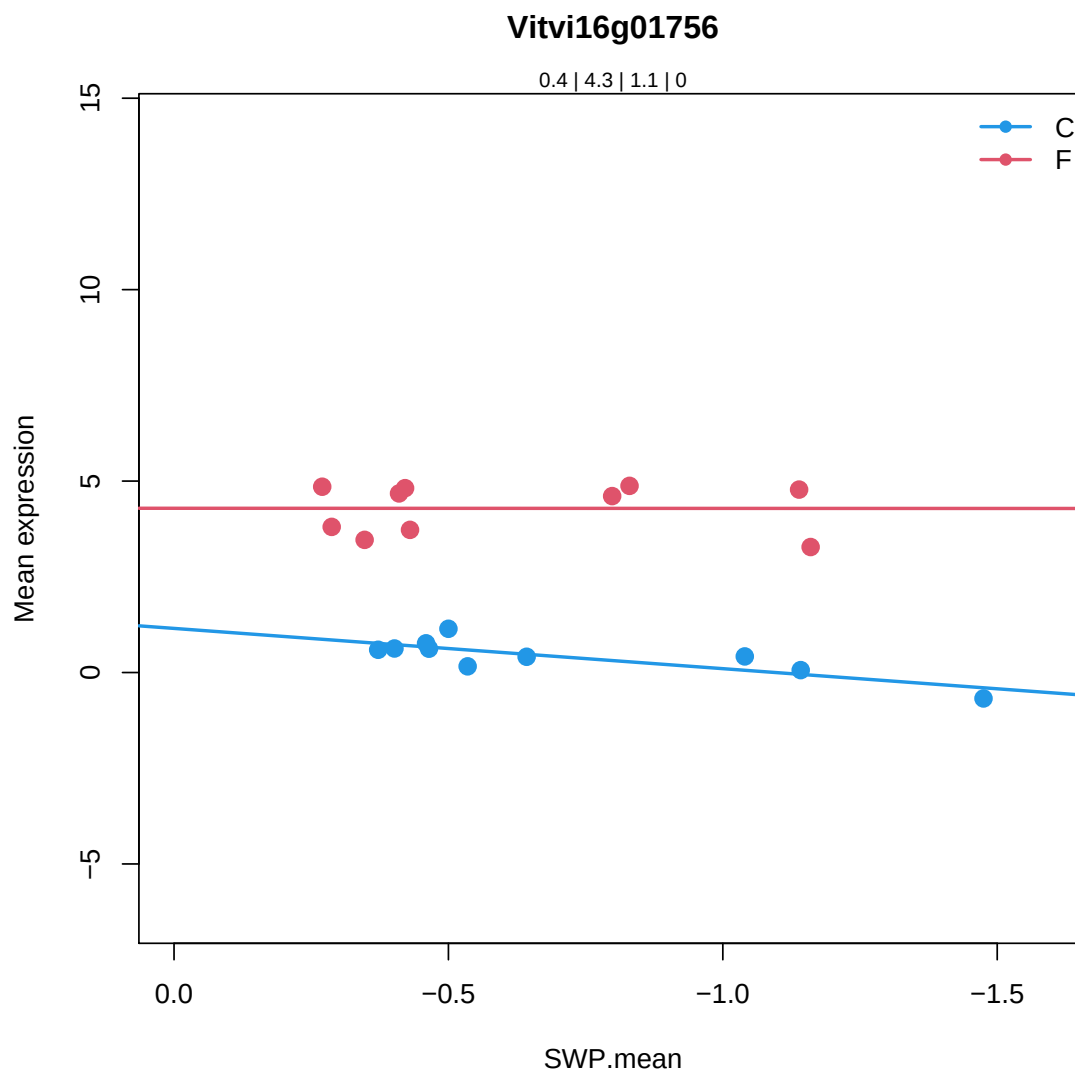
NB-ARC domain-containing disease resistance protein |

Chr3:4857940-4861104 FORWARD LENGTH=1054 |

201606

Coefficients for Vitvi16g01756.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4126079	0.01939715	*	0.0203996	*
SlopeC	1.051572	0.03057608	*	0.4321285	
MeanF-MeanC	3.875102	8.16547e-14	***	8.703363e-12	***
SlopeF-SlopeC	-1.048555	0.1355052		0.9999488	



7.4.37 Vitvi06g01781

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

```
Vitvi06g01781
```

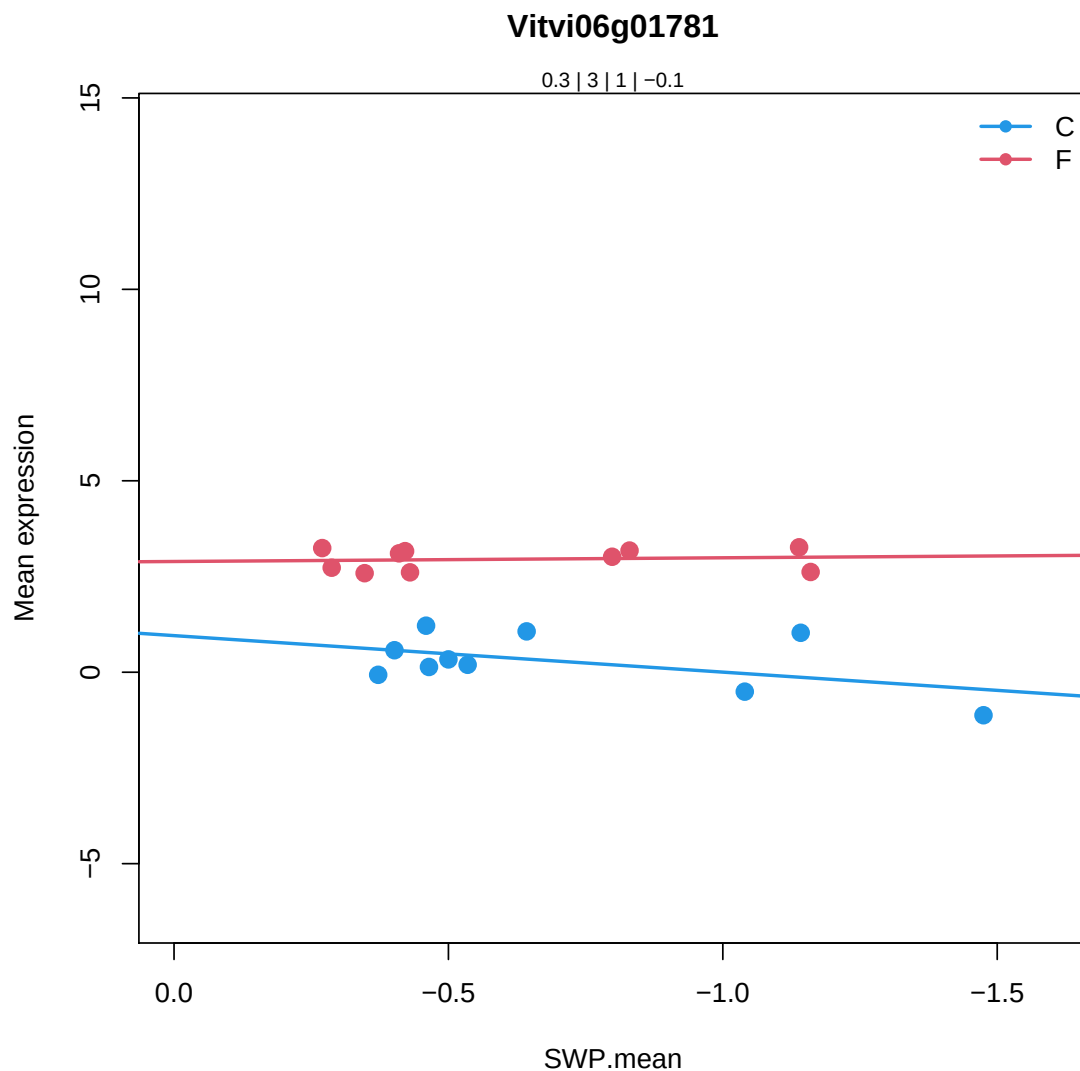
```
35.2
```

```
not assigned.unknown
```

```
NA
```

Coefficients for Vitvi06g01781.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.2854014	0.09493677	.	0.09822334	.
SlopeC	0.9534047	0.04794865	*	0.5005708	
MeanF-MeanC	2.665455	1.158902e-10	***	7.956748e-09	***
SlopeF-SlopeC	-1.049892	0.1352856		0.9999488	



7.4.38 Vitvi16g01762

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

Vitvi16g01762

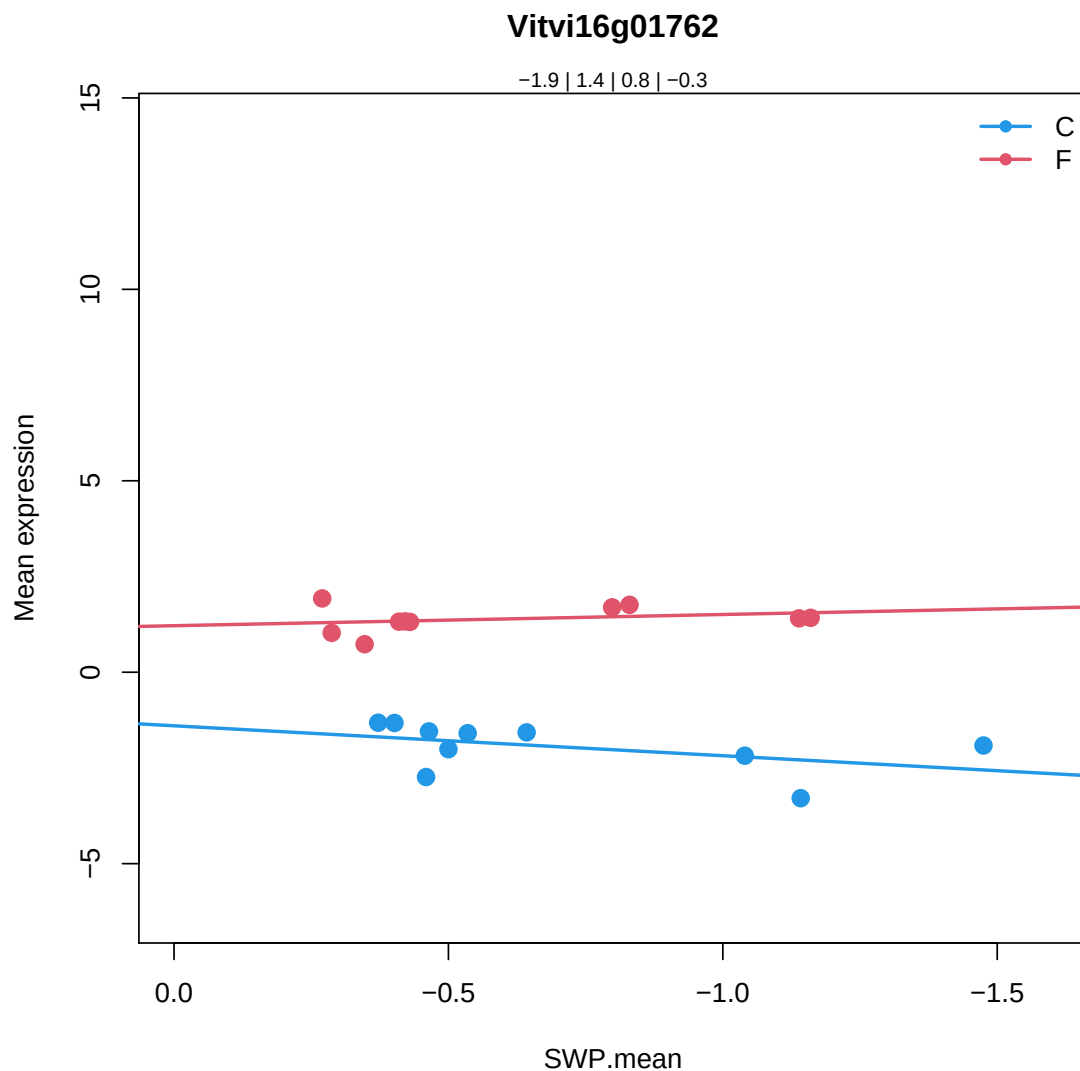
35.2

not assigned.unknown

NA

Coefficients for Vitvi16g01762.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.948574	2.626243e-11	***	3.521837e-11	***
SlopeC	0.7816522	0.08589085	.	0.5889741	
MeanF-MeanC	3.341787	6.303147e-13	***	5.894023e-11	***
SlopeF-SlopeC	-1.074305	0.1109652		0.9999488	



7.4.39 Vitvi08g02288

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

Vitvi08g02288

26.2

misc.UDP glucosyl and glucoronyl transferases

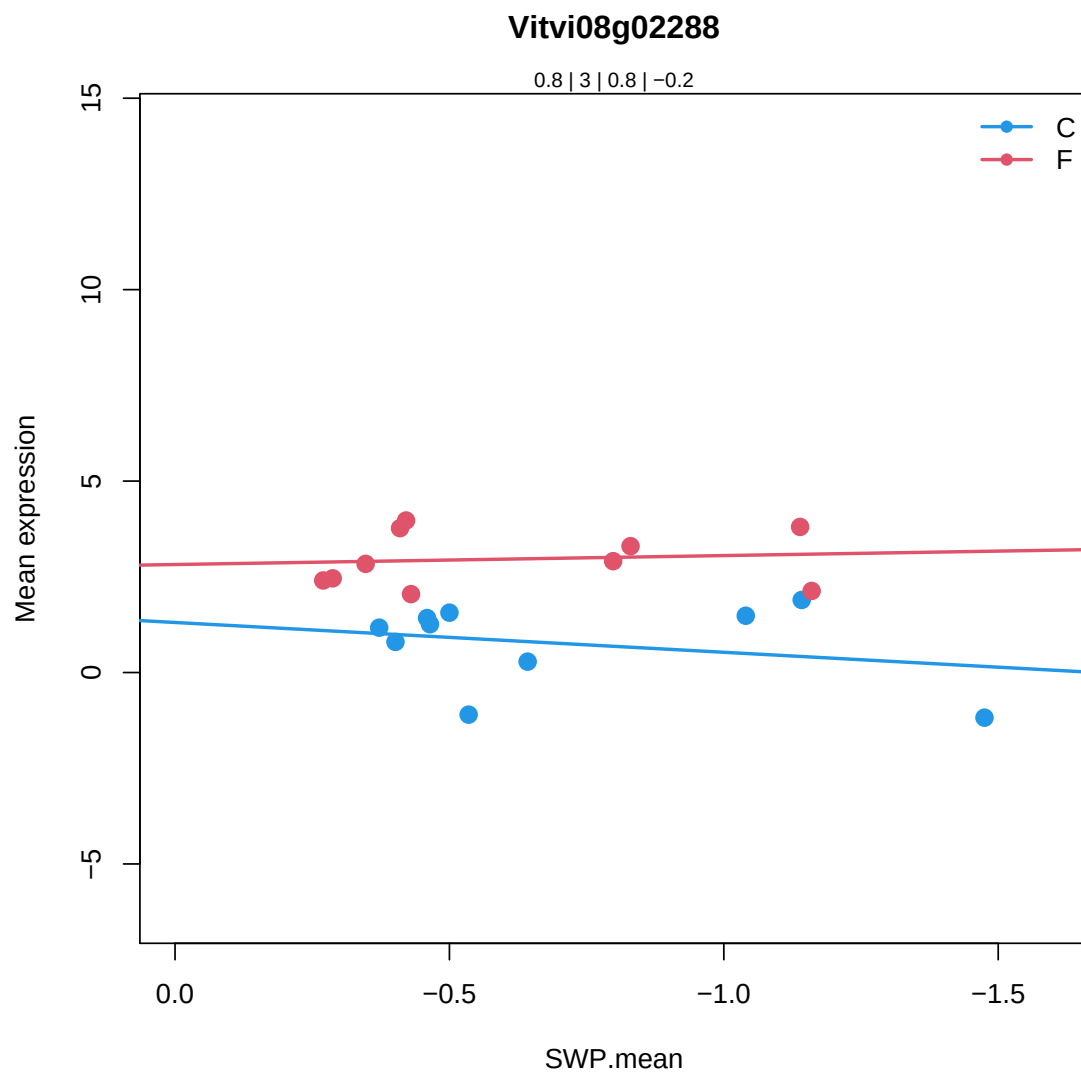
UDP-Glycosyltransferase superfamily protein |

Chr2:15415227-15416717 REVERSE LENGTH=496 |

201606

Coefficients for Vitvi08g02288.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.7597769	0.01067766	*	0.01130436	*
SlopeC	0.7784241	0.3145507		0.7945612	
MeanF-MeanC	2.203336	1.000257e-05	***	0.0002528345	***
SlopeF-SlopeC	-1.012031	0.3783293		0.9999488	



7.4.40 Vitvi10g01862

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

Vitvi10g01862

16.01.2005

secondary metabolism.isoprenoids.terpenoids

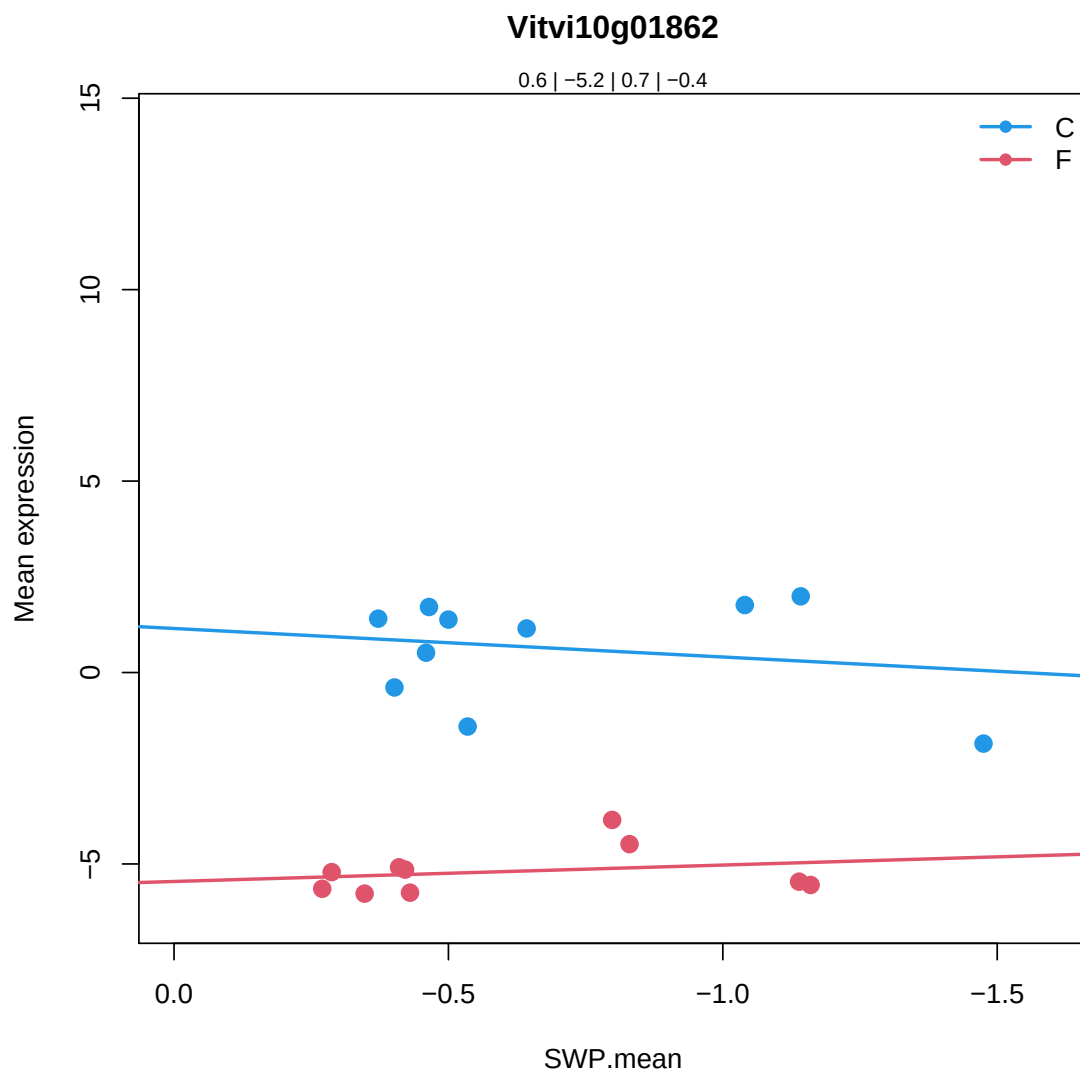
Terpenoid cyclases family protein |

Chr1:29684558-29688673 REVERSE LENGTH=759 |

201606

Coefficients for Vitvi10g01862.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6263385	0.0577119	.	0.05999896	.
SlopeC	0.7447214	0.4009091		0.835066	
MeanF-MeanC	-5.822896	9.330016e-12	***	7.604711e-10	***
SlopeF-SlopeC	-1.173754	0.3742103		0.9999488	



7.4.41 Vitvi12g02454

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

Vitvi12g02454

16.8.1.21

secondary metabolism.flavonoids.anthocyanins.anthocyanin 5-aromatic ac

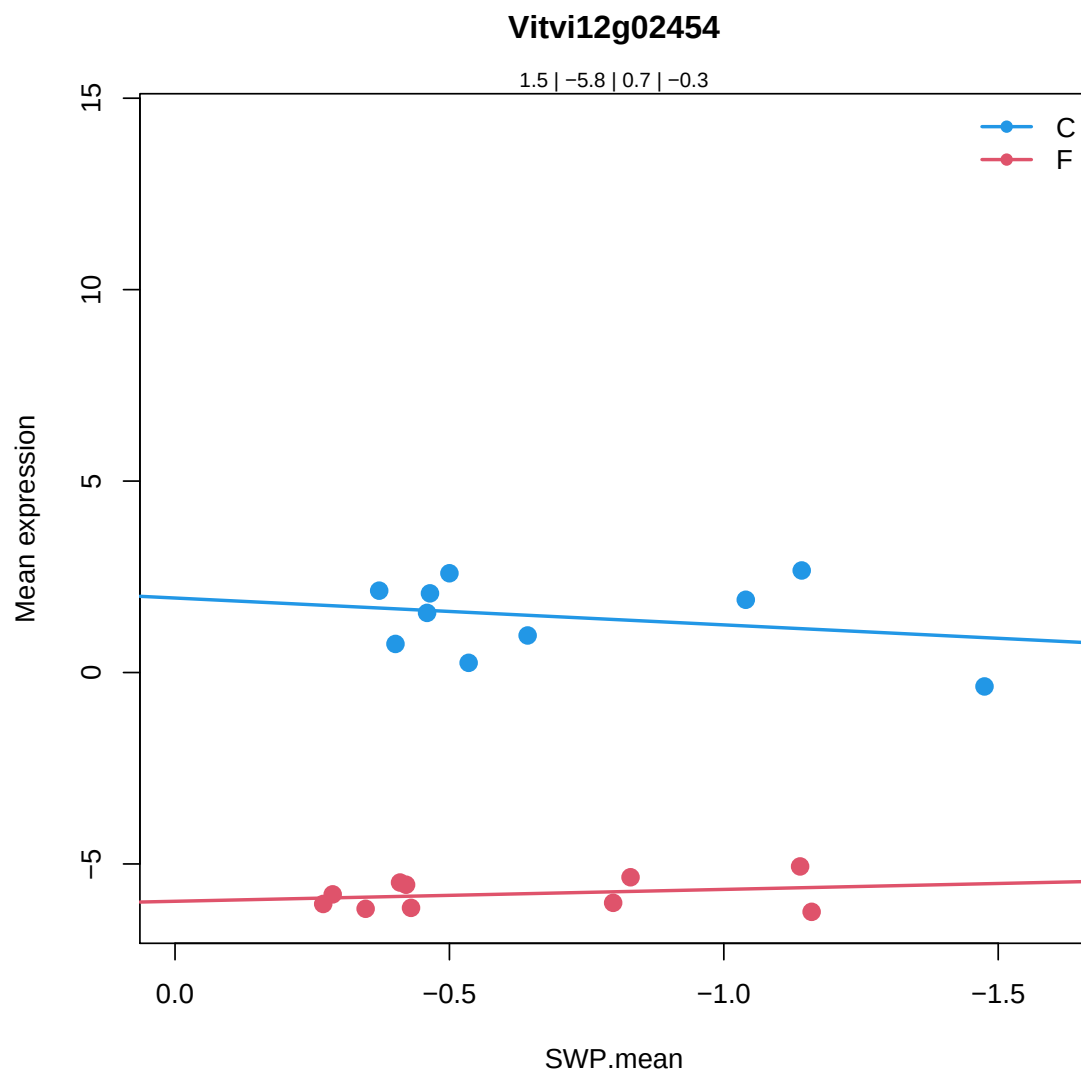
HXXXD-type acyl-transferase family protein |

Chr1:1009542-1010951 REVERSE LENGTH=469 |

201606

Coefficients for Vitvi12g02454.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.45233	2.652875e-06	***	3.031801e-06	***
SlopeC	0.7013162	0.2852786		0.7782707	
MeanF-MeanC	-7.238537	2.656374e-16	***	4.498717e-14	***
SlopeF-SlopeC	-1.011435	0.3000955		0.9999488	



7.4.42 Vitvi10g01786

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

Vitvi10g01786

35.2

not assigned.unknown

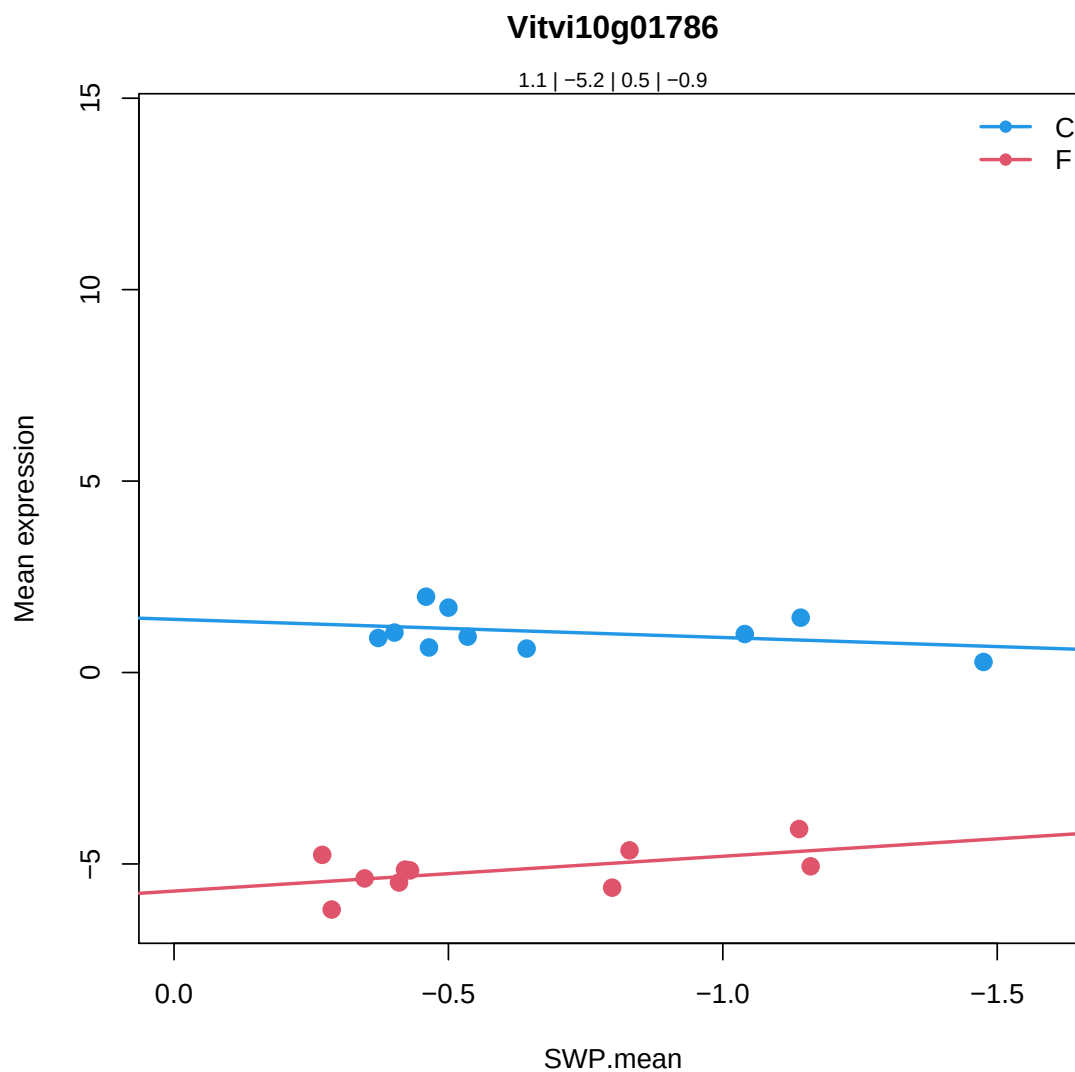
glutamate receptor 2.9 |

Chr2:12501092-12504912 REVERSE LENGTH=940 |

201606

Coefficients for Vitvi10g01786.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.054962	1.528935e-06	***	1.757336e-06	***
SlopeC	0.4742976	0.3009198		0.7855144	
MeanF-MeanC	-6.209645	3.820353e-18	***	8.958434e-16	***
SlopeF-SlopeC	-1.384343	0.04982324	*	0.9999488	

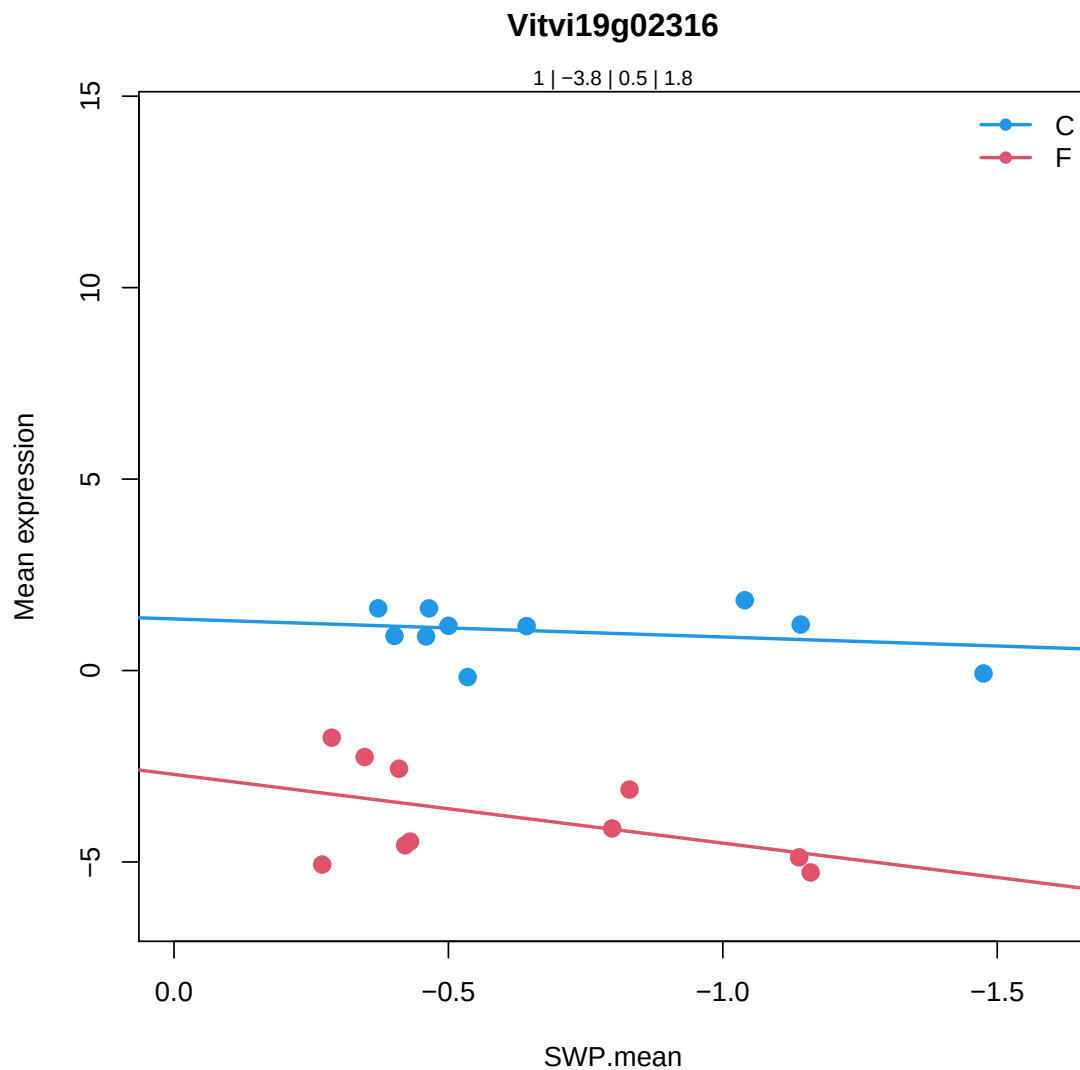


7.4.43 Vitvi19g02316

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
Vitvi19g02316
35.2
not assigned.unknown
Disease resistance protein (CC-NBS-LRR class) family |
Chr1:4145011-4147680 FORWARD LENGTH=889 |
201606
```

Coefficients for Vitvi19g02316.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.015579	0.001366712	**	0.001476046	**
SlopeC	0.4709163	0.5464691		0.8857058	
MeanF-MeanC	-4.822373	3.259702e-11	***	2.400211e-09	***
SlopeF-SlopeC	1.323198	0.2600661		0.9999488	



7.4.44 Vitvi17g00175

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

Vitvi17g00175

30.2.25

signalling.receptor kinases.wall associated kinase

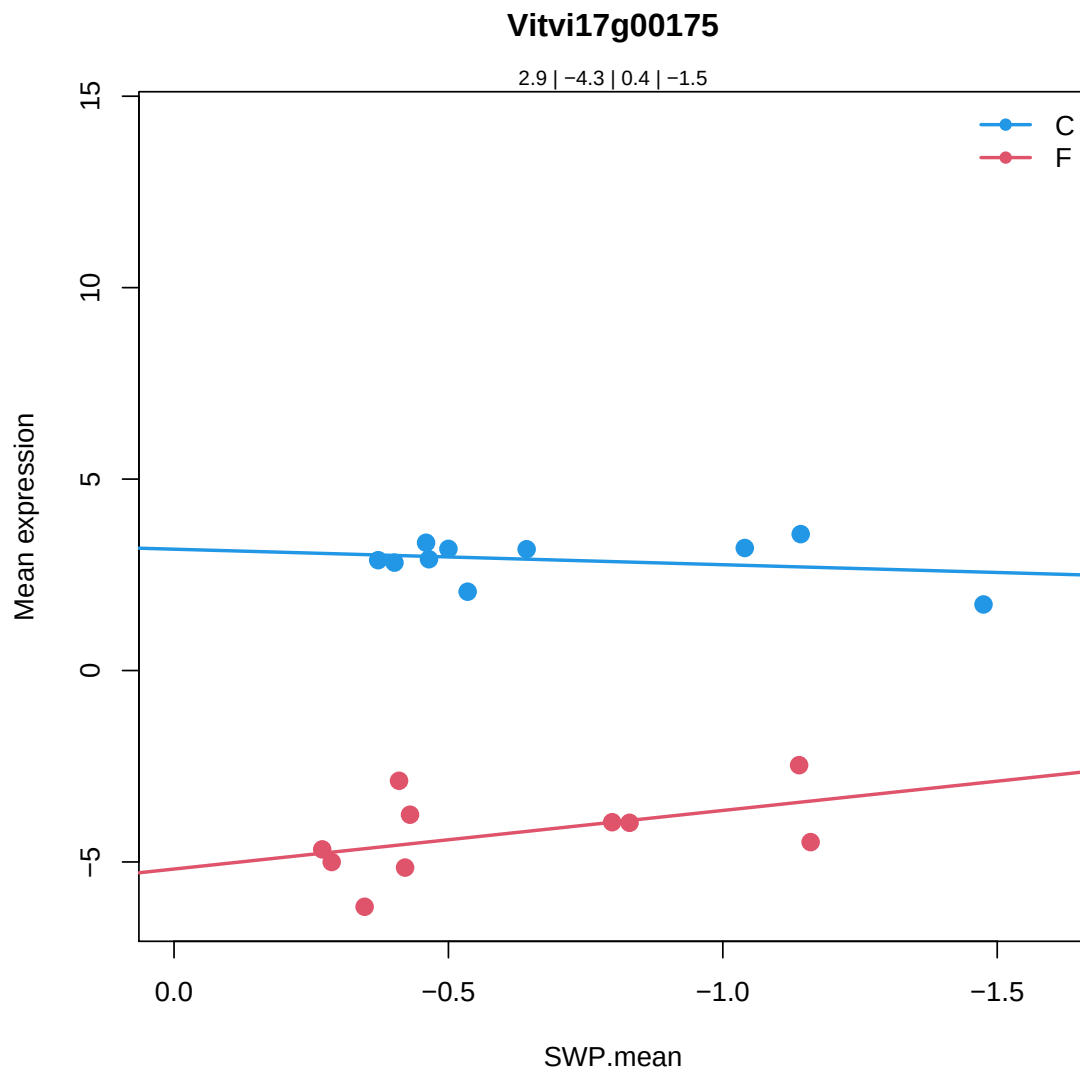
wall associated kinase 5 |

Chr1:7429980-7432346 FORWARD LENGTH=733 |

201606

Coefficients for Vitvi17g00175.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.883592	5.172864e-11	***	6.845355e-11	***
SlopeC	0.4052957	0.5492078		0.8871925	
MeanF-MeanC	-7.136685	8.065835e-16	***	1.193587e-13	***
SlopeF-SlopeC	-1.935313	0.06406735	.	0.9999488	



7.4.45 Vitvi18g00878

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

Vitvi18g00878

26.1

misc.cytochrome P450

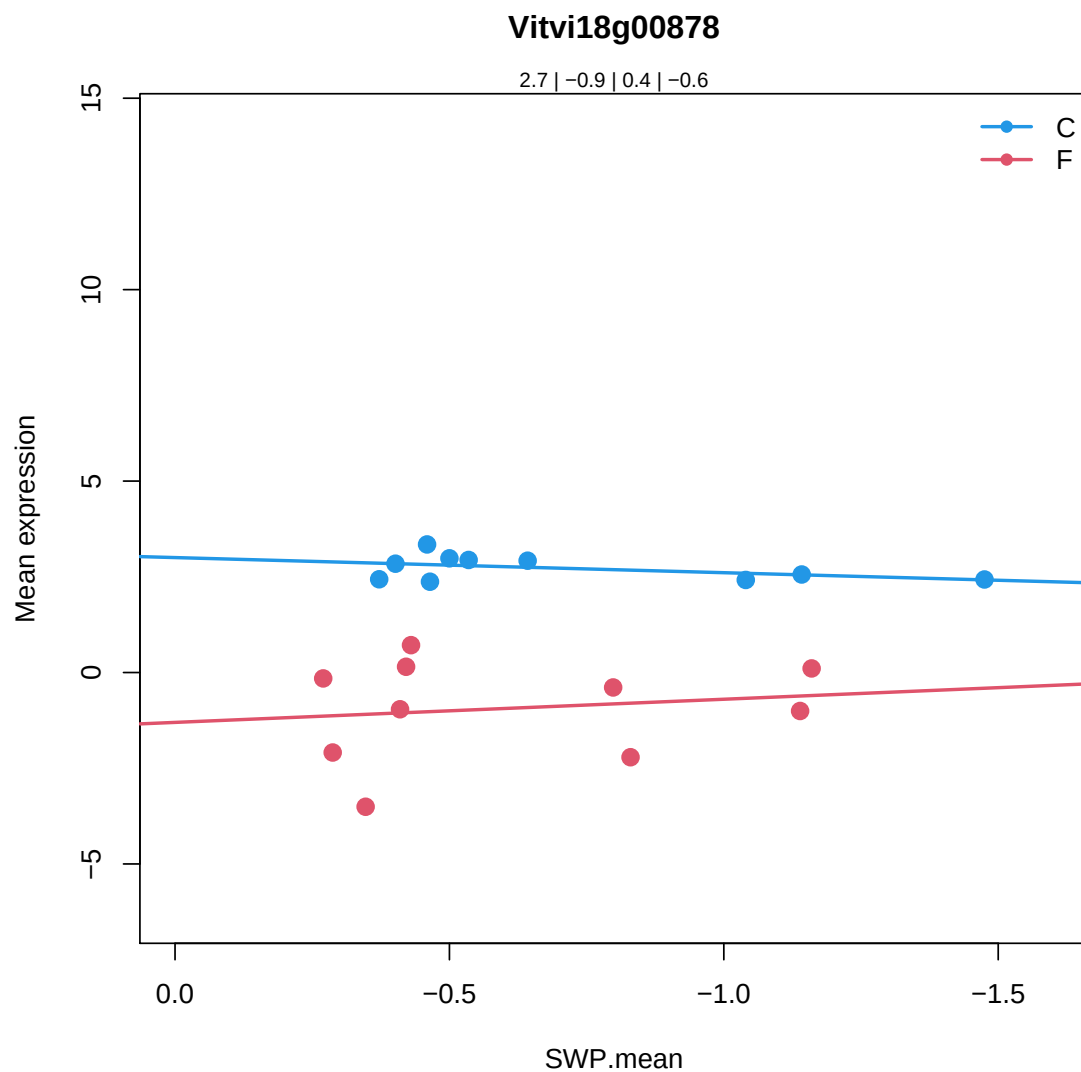
cytochrome P450%2C family 82%2C subfamily C%2C polypeptide 4 |

Chr4:15452040-15453966 FORWARD LENGTH=524 |

201606

Coefficients for Vitvi18g00878.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.724363	3.048733e-09	***	3.785029e-09	***
SlopeC	0.3950882	0.6207516		0.9092346	
MeanF-MeanC	-3.65896	7.494057e-09	***	3.769783e-07	***
SlopeF-SlopeC	-1.000008	0.4026699		0.9999488	



7.4.46 Vitvi06g01743

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

Vitvi06g01743

35.2

not assigned.unknown

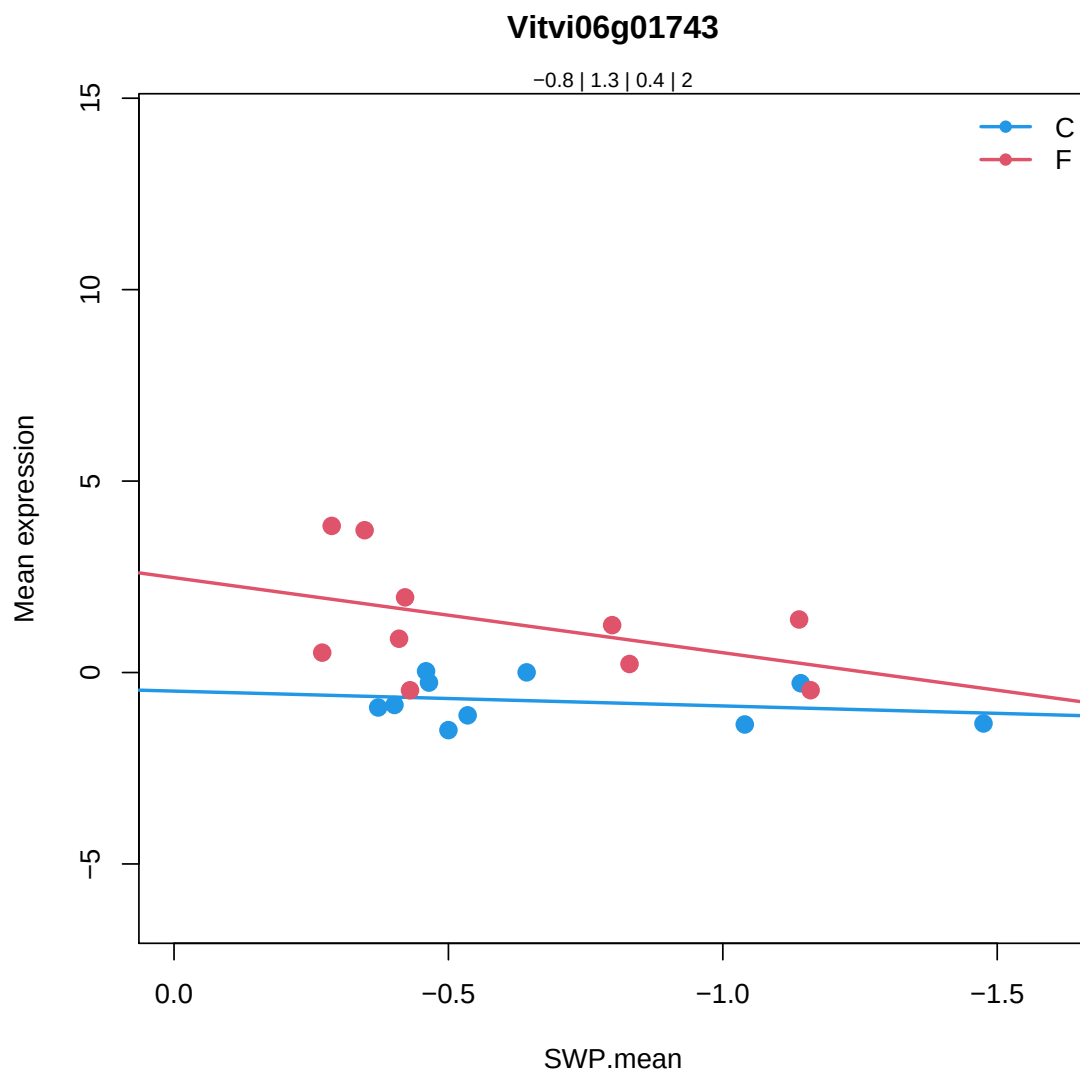
UDP-glucosyl transferase 71C4 |

Chr1:2225963-2227402 FORWARD LENGTH=479 |

201606

Coefficients for Vitvi06g01743.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.7579229	0.02425504	*	0.02545585	*
SlopeC	0.3874884	0.6604477		0.9219292	
MeanF-MeanC	2.040905	0.0001421972	***	0.002421403	**
SlopeF-SlopeC	1.572361	0.2377642		0.9999488	



7.4.47 Vitvi05g00038

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

Vitvi05g00038

26.03.2005

misc.gluco-, galacto- and mannosidases.glycosyl hydrolase family 5

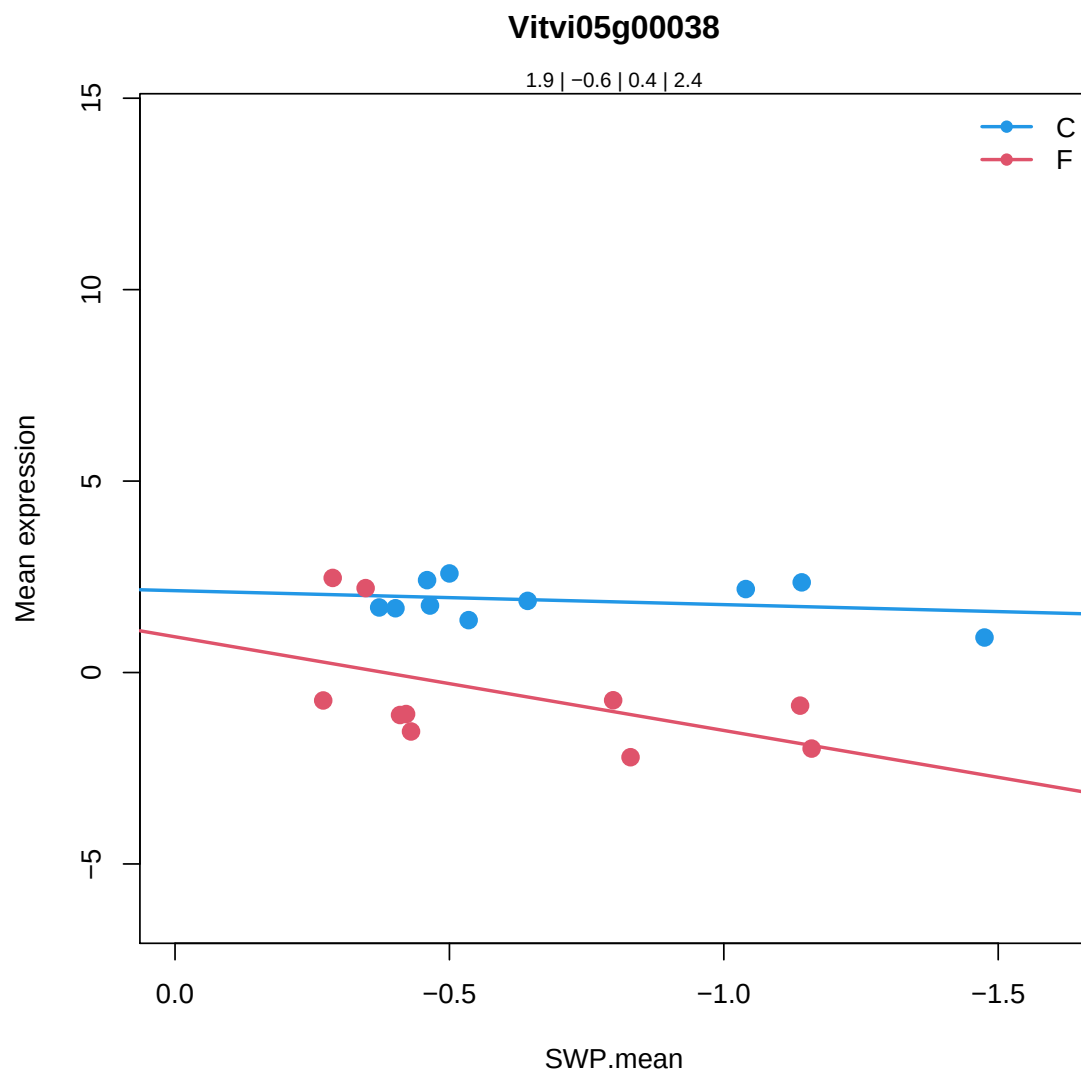
alpha/beta-Hydrolases superfamily protein |

Chr4:1035722-1037403 FORWARD LENGTH=324 |

201606

Coefficients for Vitvi05g00038.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.881532	4.363251e-06	***	4.964146e-06	***
SlopeC	0.3647677	0.6752848		0.9252688	
MeanF-MeanC	-2.439425	1.40955e-05	***	0.0003437499	***
SlopeF-SlopeC	2.082283	0.1179377		0.9999488	



7.4.48 Vitvi15g01643

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

Vitvi15g01643

16.8.1.12

secondary metabolism.flavonoids.anthocyanins.anthocyanidin 3-O-glucosyl

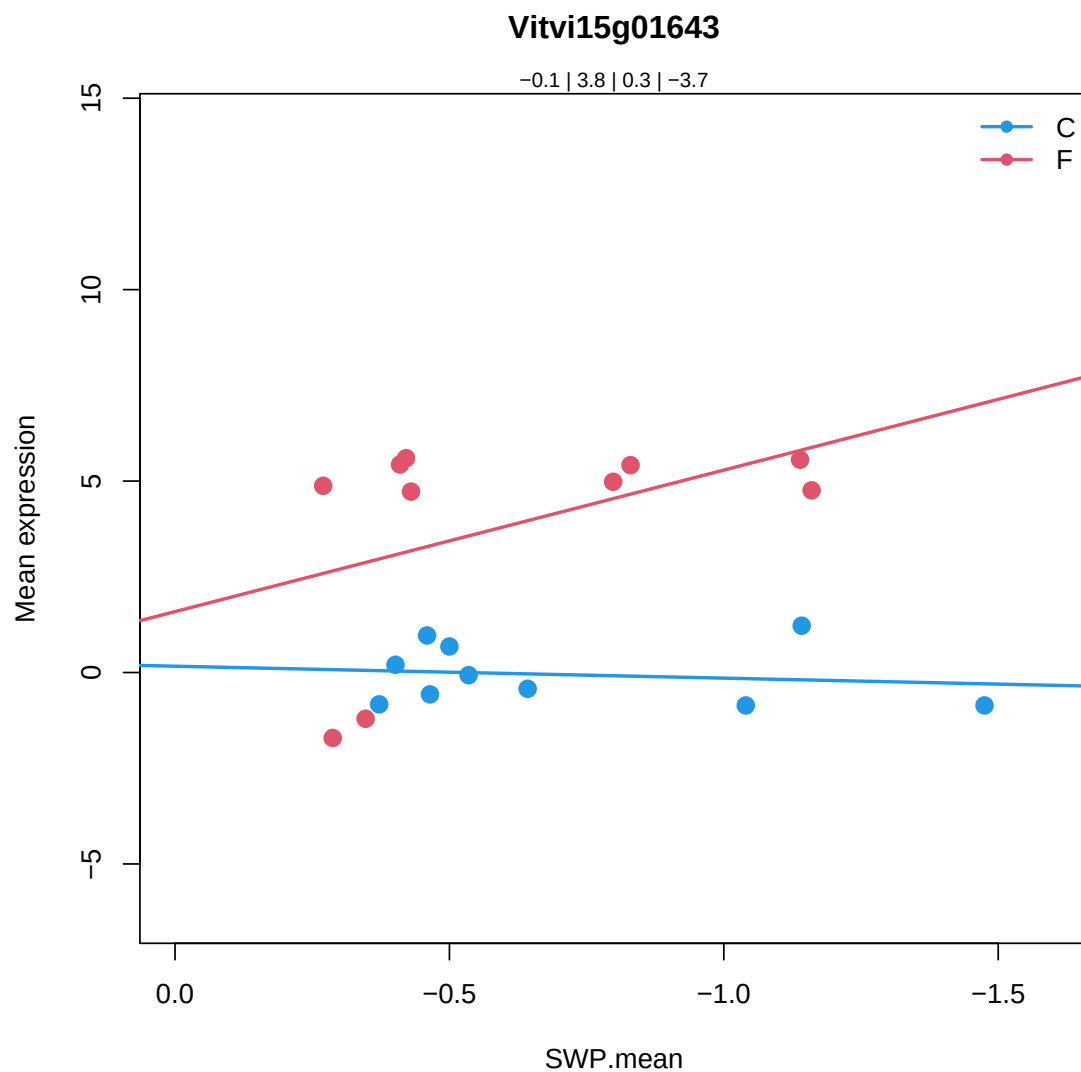
UDP-Glycosyltransferase superfamily protein |

Chr2:9593012-9594424 FORWARD LENGTH=470 |

201606

Coefficients for Vitvi15g01643.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.05461697	0.9210385		0.922673	
SlopeC	0.3115766	0.8389936		0.9693055	
MeanF-MeanC	3.897101	4.895259e-05	***	0.0009663134	***
SlopeF-SlopeC	-4.007713	0.08969632	.	0.9999488	



7.4.49 Vitvi05g01578

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

Vitvi05g01578

35.2

not assigned.unknown

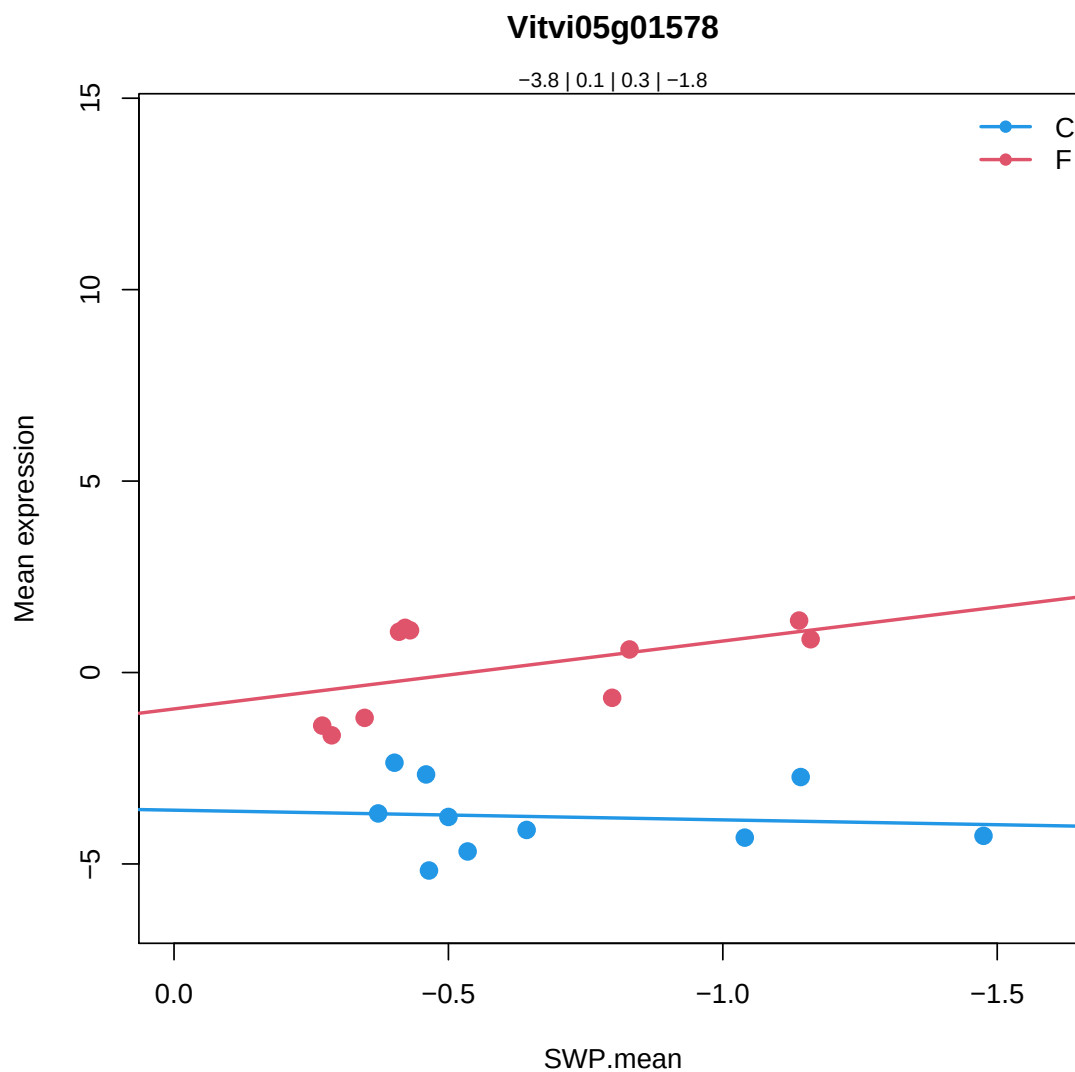
homolog of carrot EP3-3 chitinase |

Chr3:20145935-20147034 FORWARD LENGTH=273 |

201606

Coefficients for Vitvi05g01578.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-3.773614	1.602428e-11	***	2.168121e-11	***
SlopeC	0.2532287	0.7602289		0.9479775	
MeanF-MeanC	3.902919	4.915293e-09	***	2.531044e-07	***
SlopeF-SlopeC	-2.026263	0.1111117		0.9999488	



7.4.50 Vitvi11g00865

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

```
Vitvi11g00865
```

```
20
```

```
stress
```

```
Ankyrin repeat family protein |
```

```
Chr5:1354240-1356754 REVERSE LENGTH=669 |
```

```
201606
```

```
Vitvi11g00865
```

```
19.99
```

```
tetrapyrrole synthesis.unspecified
```

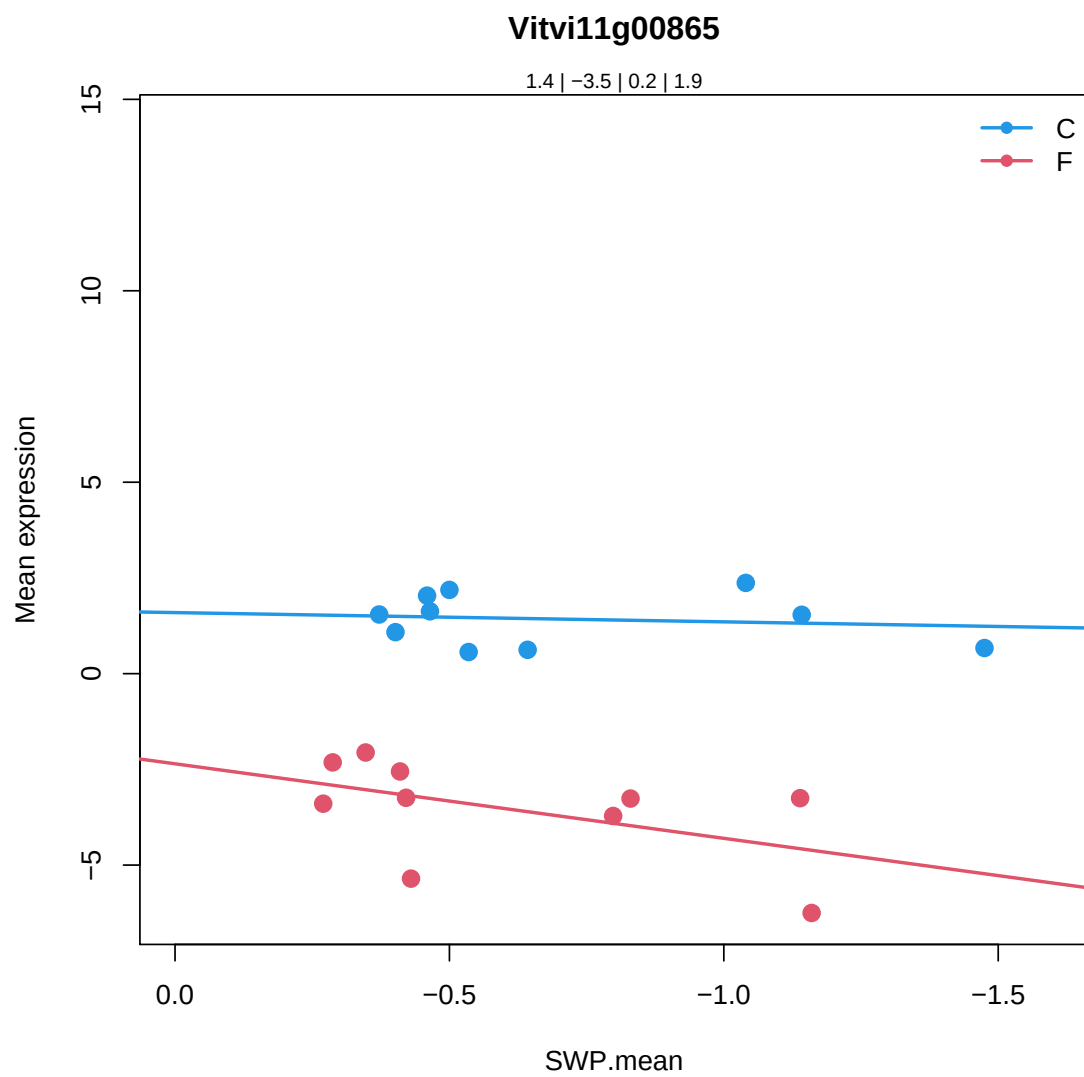
```
Ankyrin repeat family protein |
```

```
Chr5:1354240-1356754 REVERSE LENGTH=669 |
```

```
201606
```

Coefficients for Vitvi11g00865.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.424545	4.543505e-05	***	5.050843e-05	***
SlopeC	0.241433	0.7594168		0.9479775	
MeanF-MeanC	-4.965309	2.386458e-11	***	1.774361e-09	***
SlopeF-SlopeC	1.705682	0.1554573		0.9999488	



7.4.51 Vitvi10g00313

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

Vitvi10g00313

29.5.11.4.2

protein.degradation.ubiquitin.E3.RING

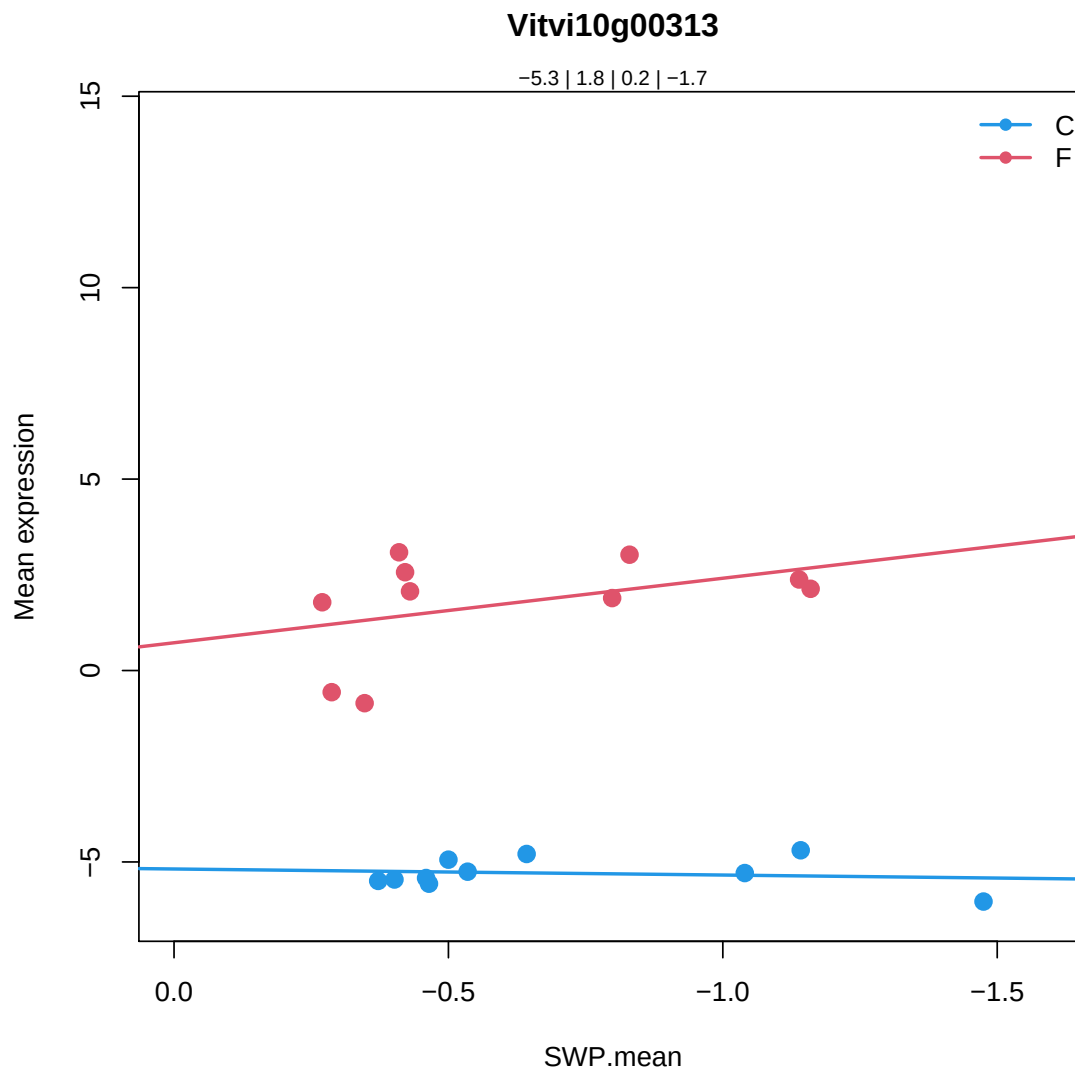
plant U-box 8 |

Chr4:11356143-11357267 REVERSE LENGTH=374 |

201606

Coefficients for Vitvi10g00313.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.2947	6.44878e-15	***	1.098975e-14	***
SlopeC	0.1580878	0.8400291		0.9694858	
MeanF-MeanC	7.046217	2.205385e-14	***	2.605774e-12	***
SlopeF-SlopeC	-1.843471	0.12405		0.9999488	



7.4.52 Vitvi12g02177

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

Vitvi12g02177

16.01.2005

secondary metabolism.isoprenoids.terpenoids

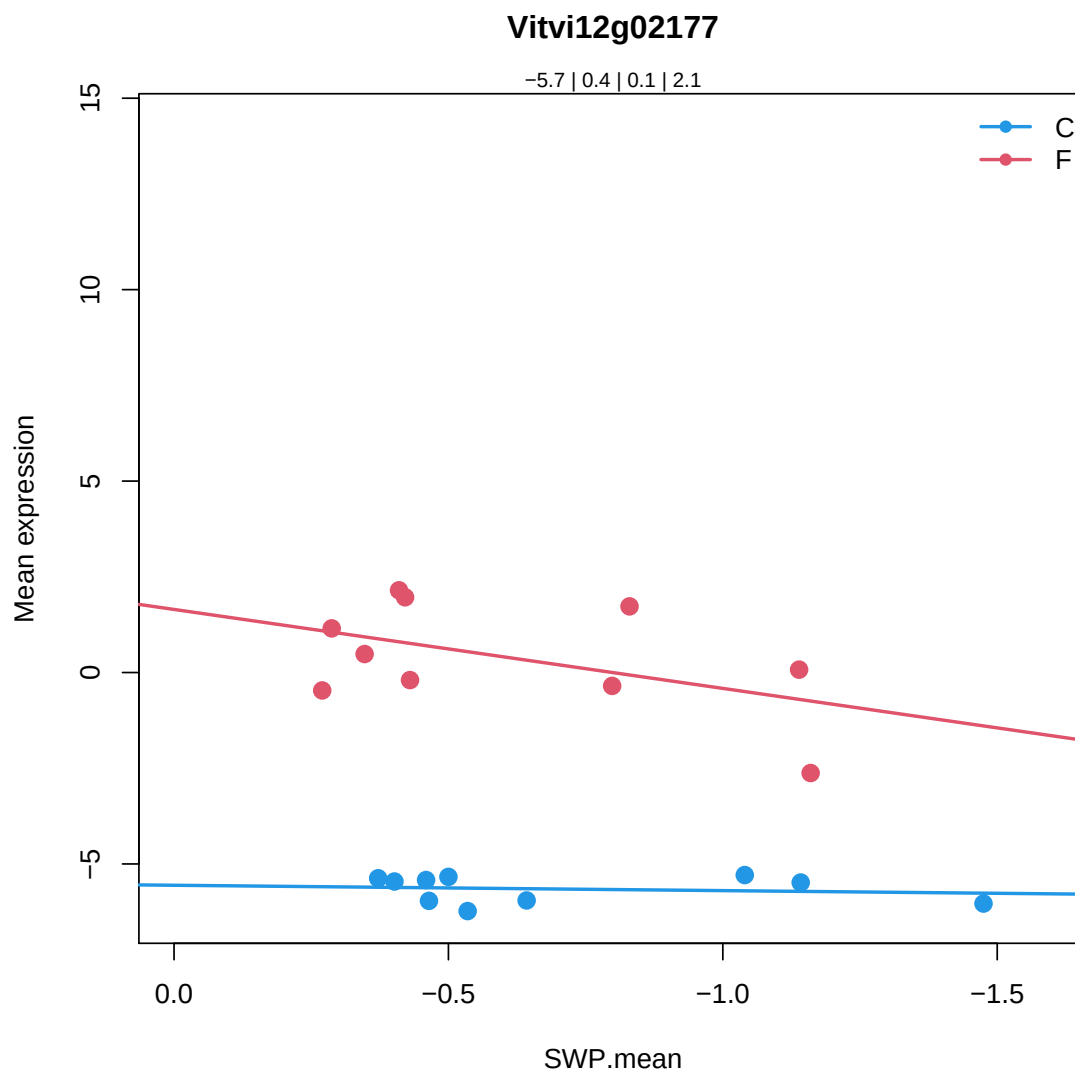
terpene synthase 21 |

Chr5:8092969-8095128 FORWARD LENGTH=545 |

201606

Coefficients for Vitvi12g02177.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.654707	1.734801e-15	***	3.157989e-15	***
SlopeC	0.1400847	0.8582087		0.9733541	
MeanF-MeanC	6.045631	4.807264e-13	***	4.608322e-11	***
SlopeF-SlopeC	1.922026	0.1100849		0.9999488	



7.4.53 Vitvi15g01075

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

Vitvi15g01075

16.8.1.12

secondary metabolism.flavonoids.anthocyanins.anthocyanidin 3-O-glucosyl

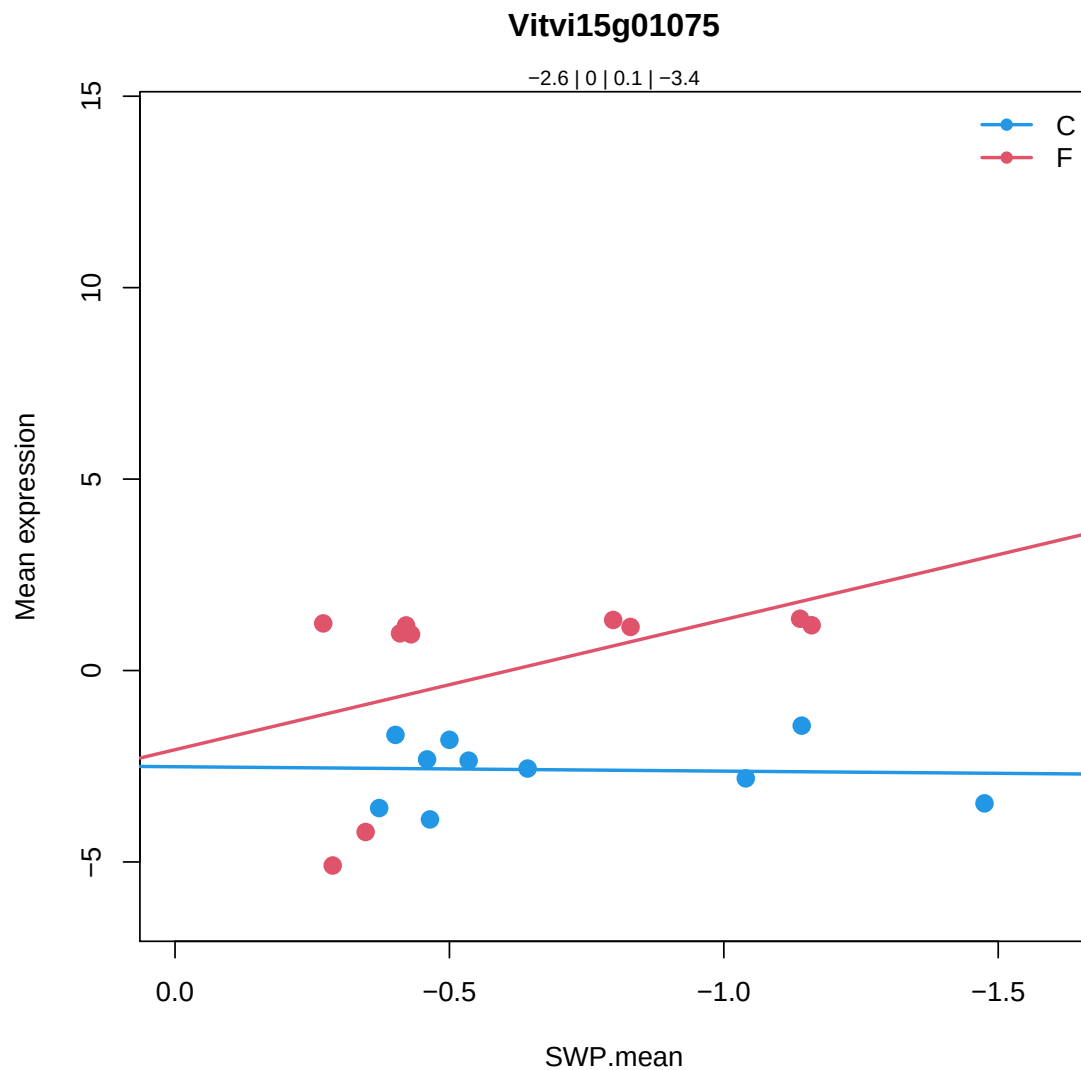
UDP-Glycosyltransferase superfamily protein |

Chr2:9593012-9594424 FORWARD LENGTH=470 |

201606

Coefficients for Vitvi15g01075.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-2.593823	2.386606e-05	***	2.671022e-05	***
SlopeC	0.1146464	0.9328867		0.988165	
MeanF-MeanC	2.594459	0.001032986	**	0.01287389	*
SlopeF-SlopeC	-3.510991	0.09385012	.	0.9999488	



7.4.54 Vitvi07g03123

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

Vitvi07g03123

31.1

cell.organisation

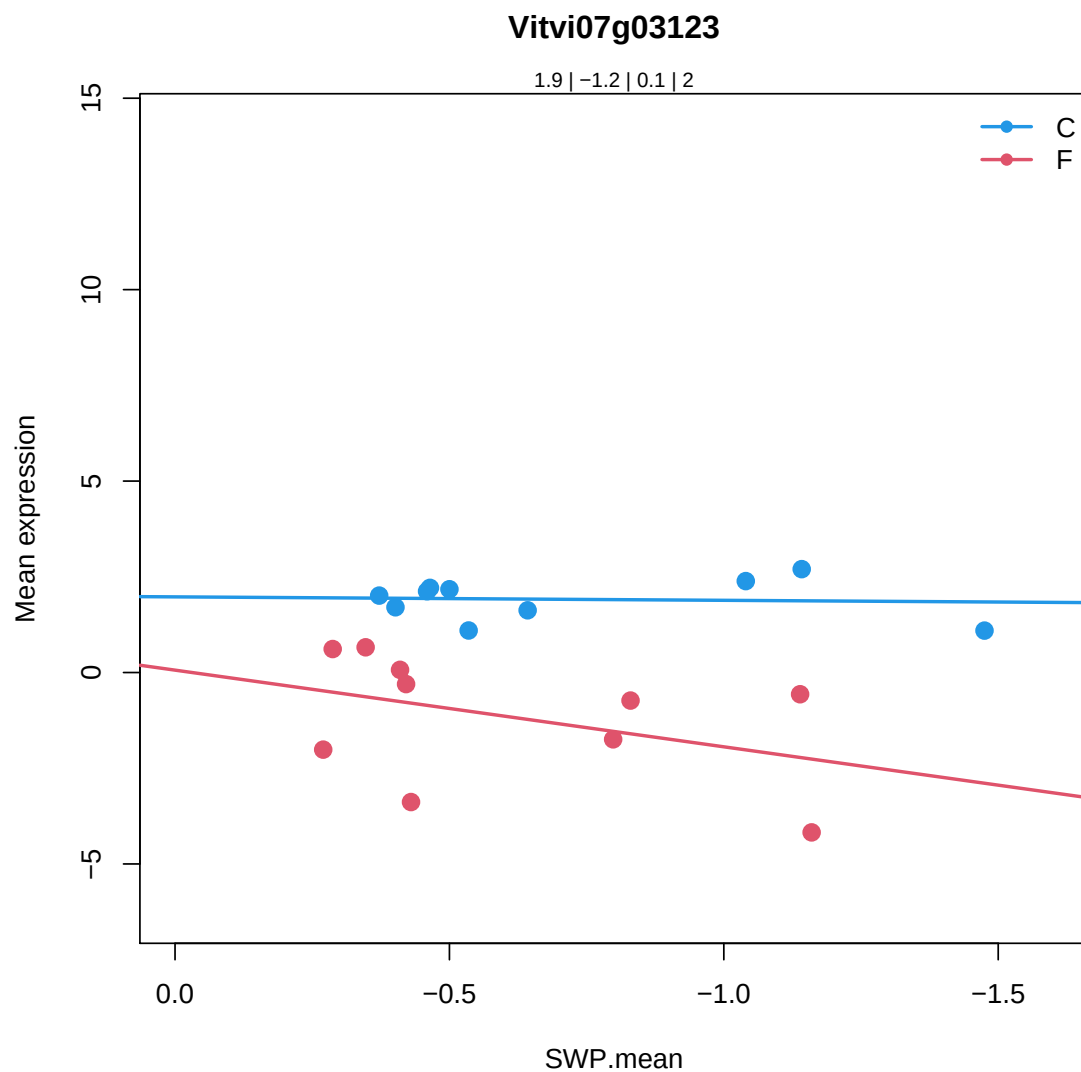
tubulin alpha-5 |

Chr5:6687212-6688926 FORWARD LENGTH=450 |

201606

Coefficients for Vitvi07g03123.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.912632	1.0113e-05	***	1.14188e-05	***
SlopeC	0.0898298	0.9238393		0.9860755	
MeanF-MeanC	-3.070558	1.72904e-06	***	5.302623e-05	***
SlopeF-SlopeC	1.912759	0.1806418		0.9999488	



7.4.55 Vitvi00g02347

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

Vitvi00g02347

35.2

not assigned.unknown

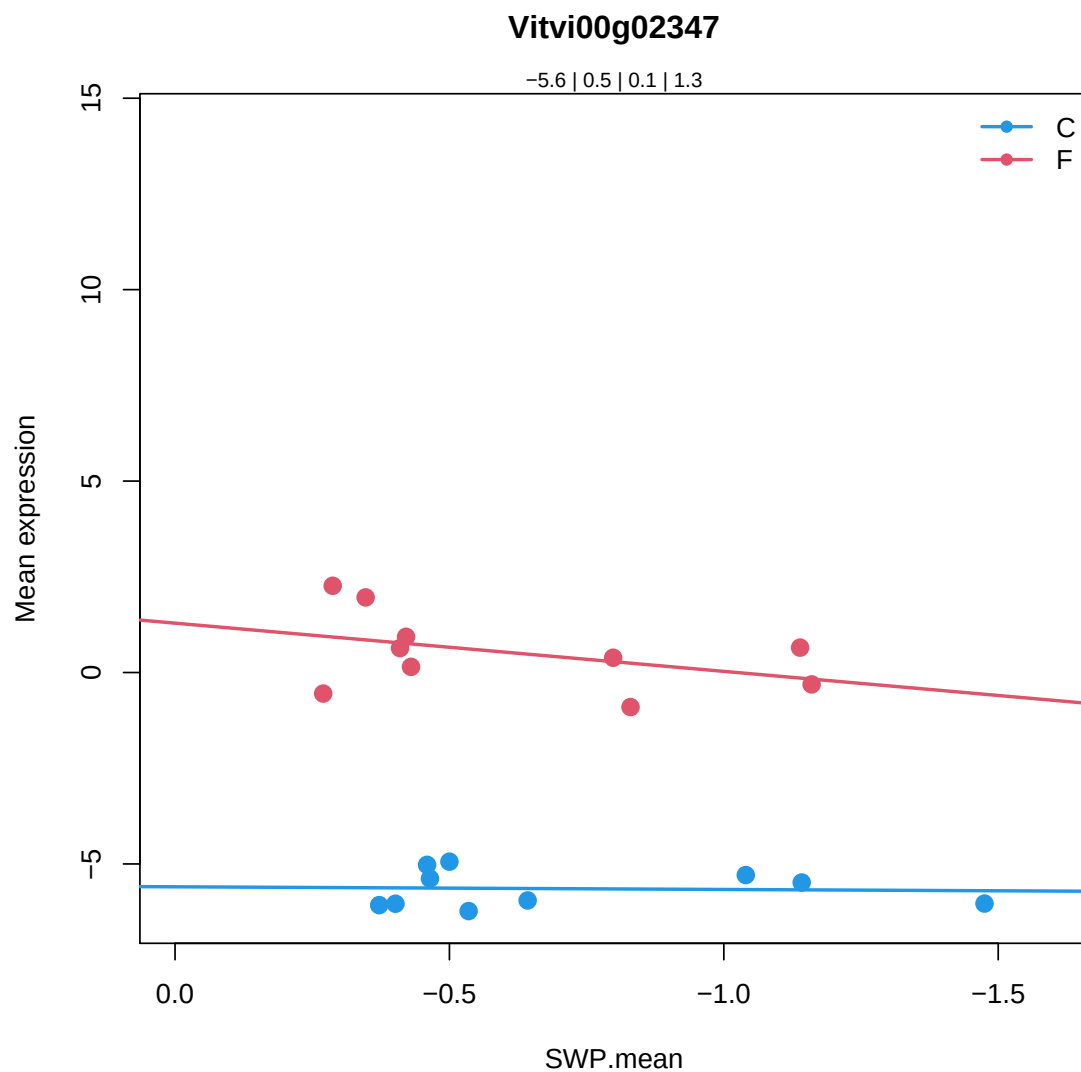
S-locus lectin protein kinase family protein |

Chr1:3810372-3813053 FORWARD LENGTH=748 |

201606

Coefficients for Vitvi00g02347.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.645391	2.520357e-17	***	6.120006e-17	***
SlopeC	0.06949314	0.9131709		0.9839968	
MeanF-MeanC	6.167235	5.084148e-15	***	6.680395e-13	***
SlopeF-SlopeC	1.189664	0.2180264		0.9999488	



7.4.56 Vitvi11g00001

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

```
Vitvi11g00001
```

```
11.10.2002
```

```
lipid metabolism.glycolipid synthesis.DGDG synthase
```

```
digalactosyl diacylglycerol deficient 2 |
```

```
Chr4:238154-240019 REVERSE LENGTH=473 |
```

```
201606
```

```
Vitvi11g00001
```

```
35.2
```

```
not assigned.unknown
```

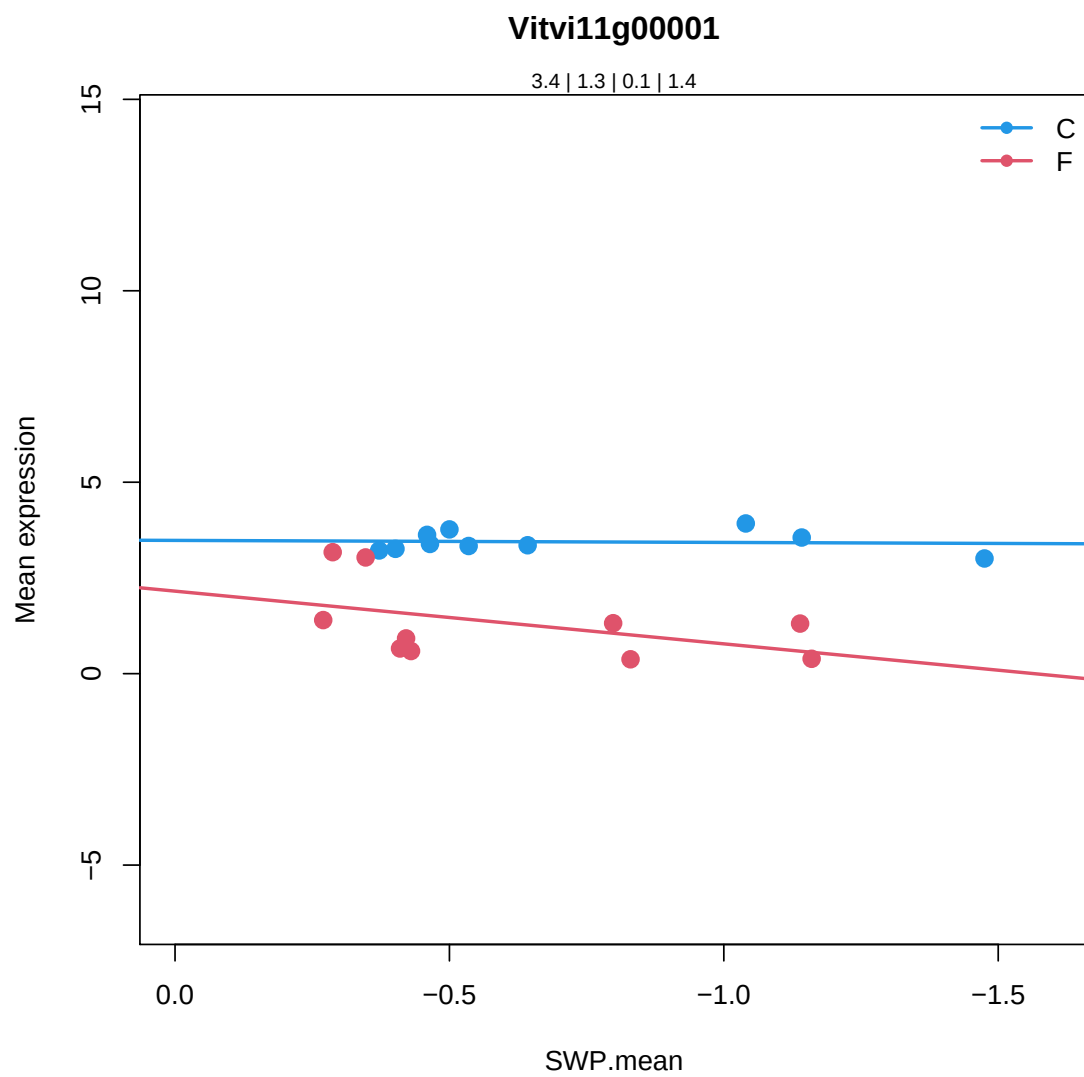
```
digalactosyl diacylglycerol deficient 2 |
```

```
Chr4:238154-240019 REVERSE LENGTH=473 |
```

```
201606
```

Coefficients for Vitvi11g00001.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.442962	1.035011e-13	***	1.587566e-13	***
SlopeC	0.05303929	0.927675		0.9869214	
MeanF-MeanC	-2.126774	3.428407e-07	***	1.24123e-05	***
SlopeF-SlopeC	1.323482	0.1382439		0.9999488	



7.4.57 Vitvi12g00573

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

Vitvi12g00573

16.01.2005

secondary metabolism.isoprenoids.terpenoids

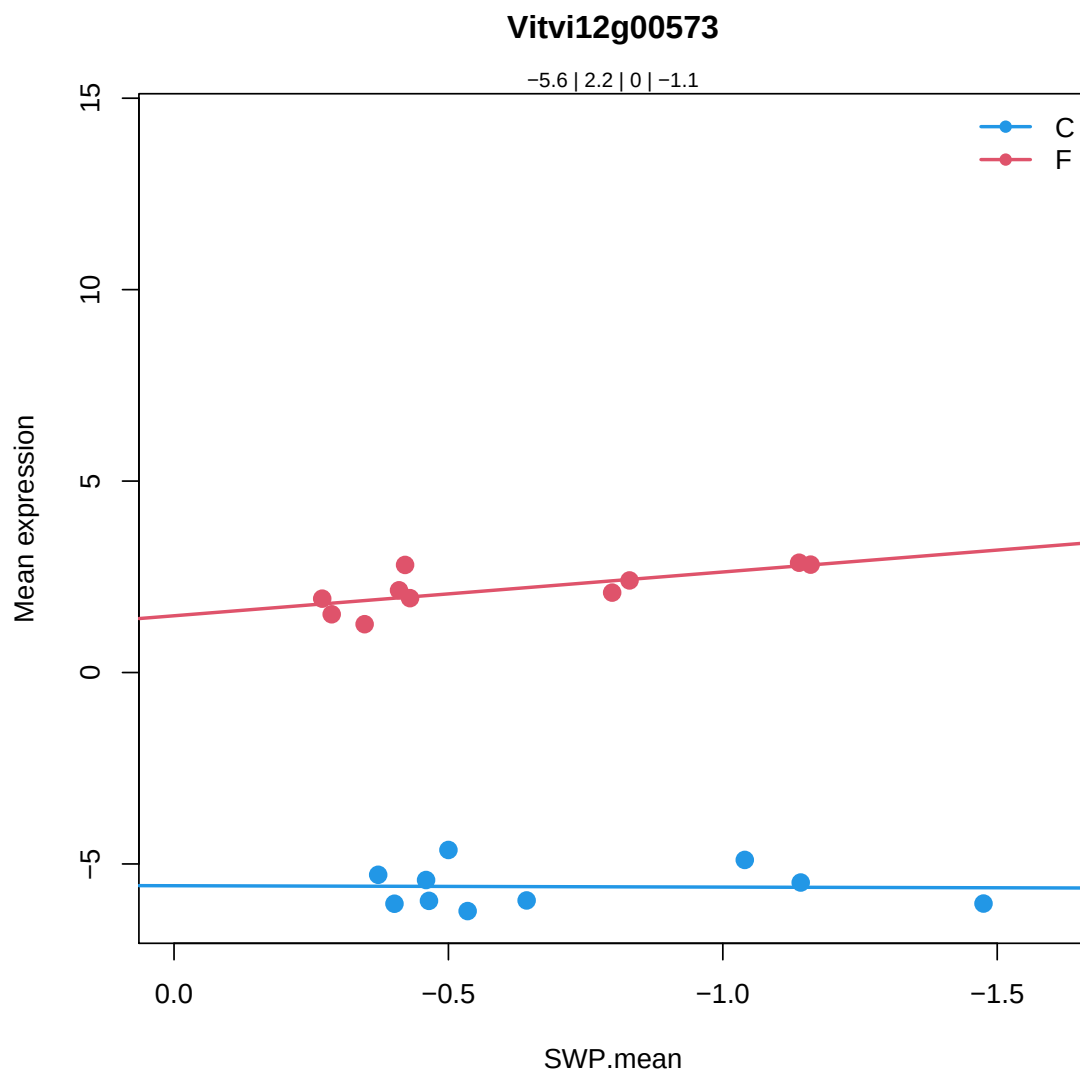
Terpenoid cyclases/Protein prenyltransferases superfamily protein |

Chr3:9430805-9433844 FORWARD LENGTH=598 |

201606

Coefficients for Vitvi12g00573.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.593941	1.355898e-20	***	9.122575e-20	***
SlopeC	0.0353512	0.9360889		0.9889957	
MeanF-MeanC	7.77276	1.966886e-20	***	8.102506e-18	***
SlopeF-SlopeC	-1.179046	0.08305281	.	0.9999488	



7.4.58 Vitvi19g02329

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

Vitvi19g02329

26.03.2005

misc.gluco-, galacto- and mannosidases.glycosyl hydrolase family 5

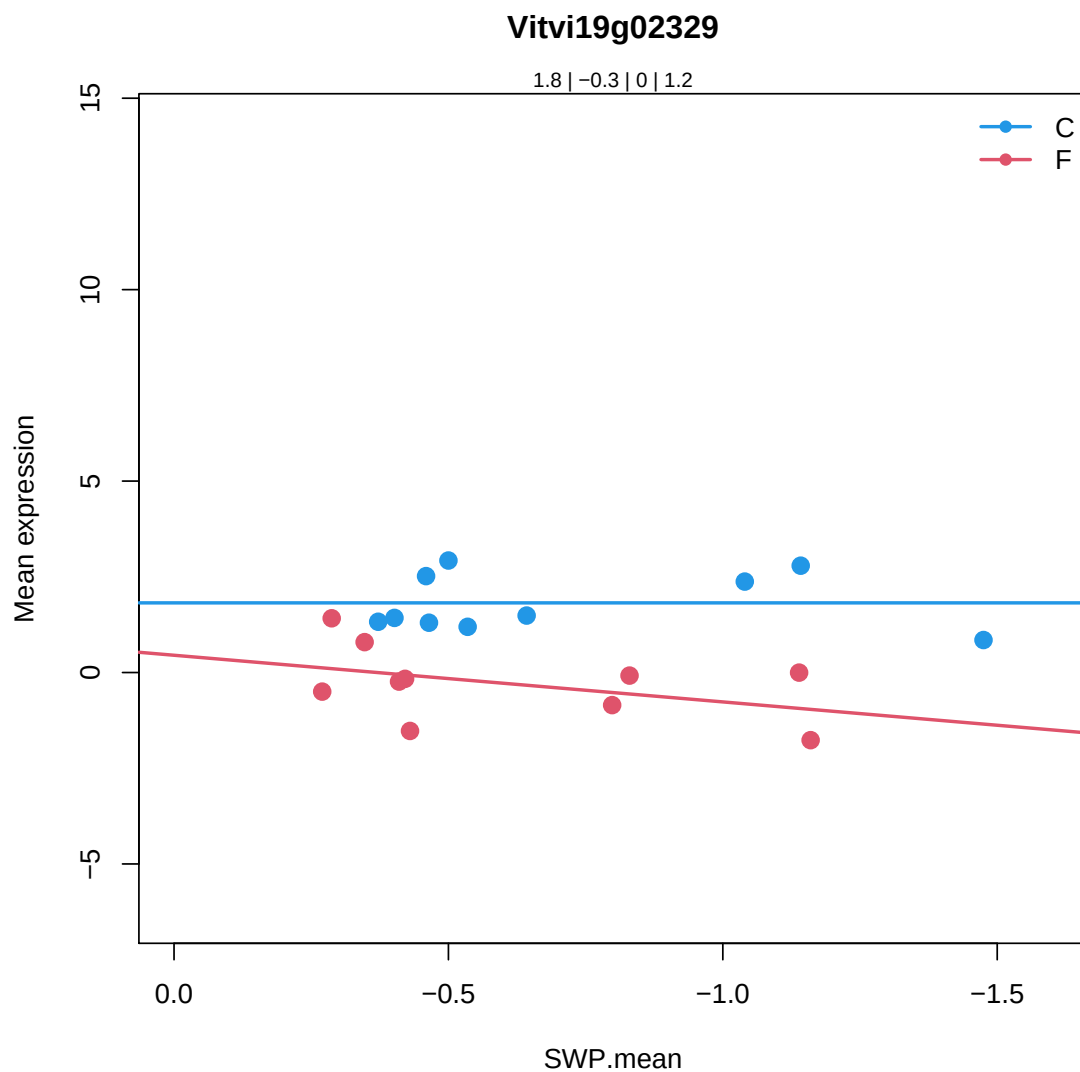
NB-ARC domain-containing disease resistance protein |

Chr3:4857940-4861104 FORWARD LENGTH=1054 |

201606

Coefficients for Vitvi19g02329.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.818909	2.689727e-07	***	3.15142e-07	***
SlopeC	0.0001976475	0.9997733		0.9998964	
MeanF-MeanC	-2.110744	4.96342e-06	***	0.0001341356	***
SlopeF-SlopeC	1.21853	0.2468431		0.9999488	



7.4.59 Vitvi10g01642

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

Vitvi10g01642

35.2

not assigned.unknown

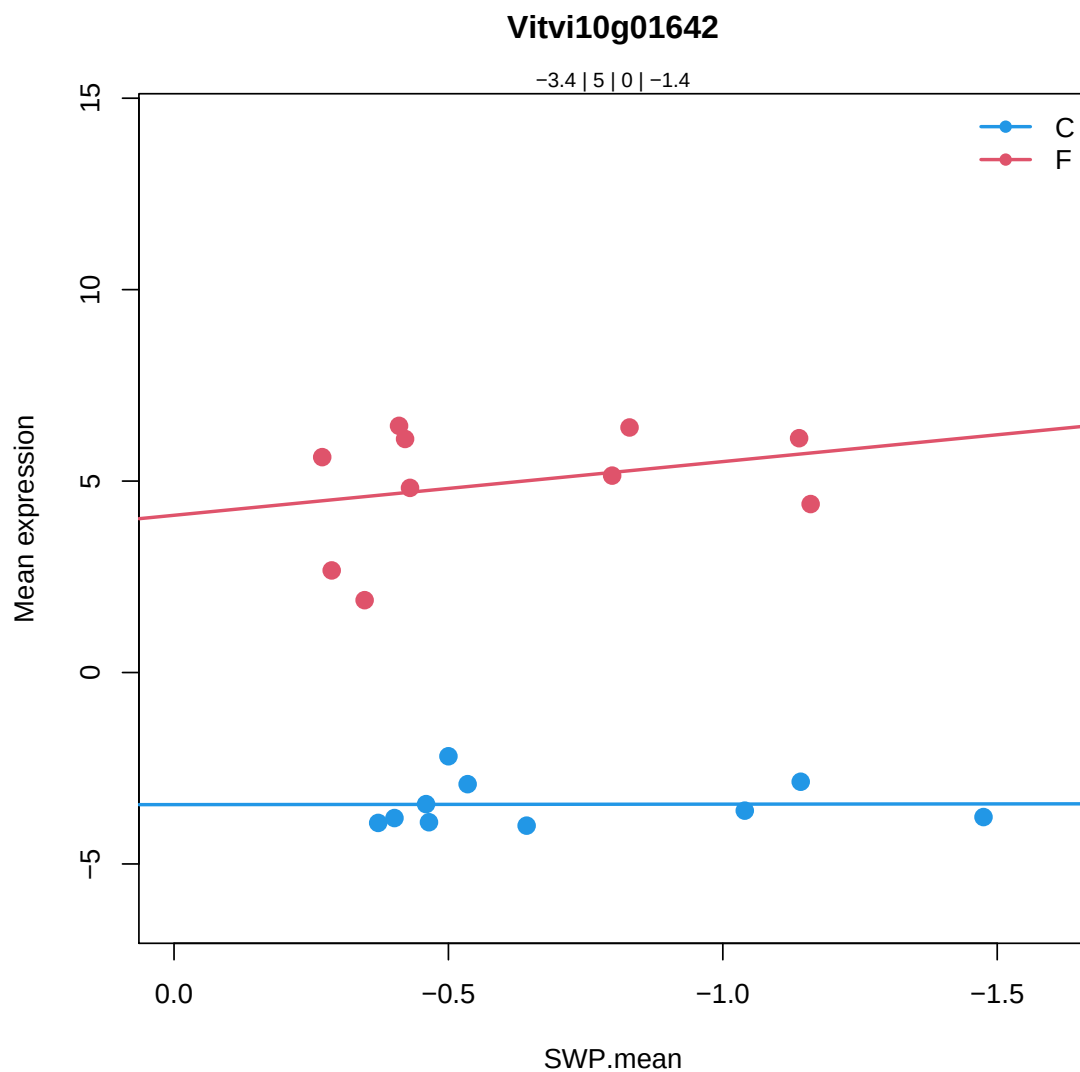
senescence regulator (Protein of unknown function%2C DUF584) |

Chr1:3945852-3946457 FORWARD LENGTH=201 |

201606

Coefficients for Vitvi10g01642.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-3.441614	1.297633e-09	***	1.631084e-09	***
SlopeC	-0.01243179	0.9896517		0.9983274	
MeanF-MeanC	8.402486	3.756324e-14	***	4.179116e-12	***
SlopeF-SlopeC	-1.389259	0.3354931		0.9999488	



7.4.60 Vitvi10g02396

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

Vitvi10g02396

14.2

S-assimilation.APR

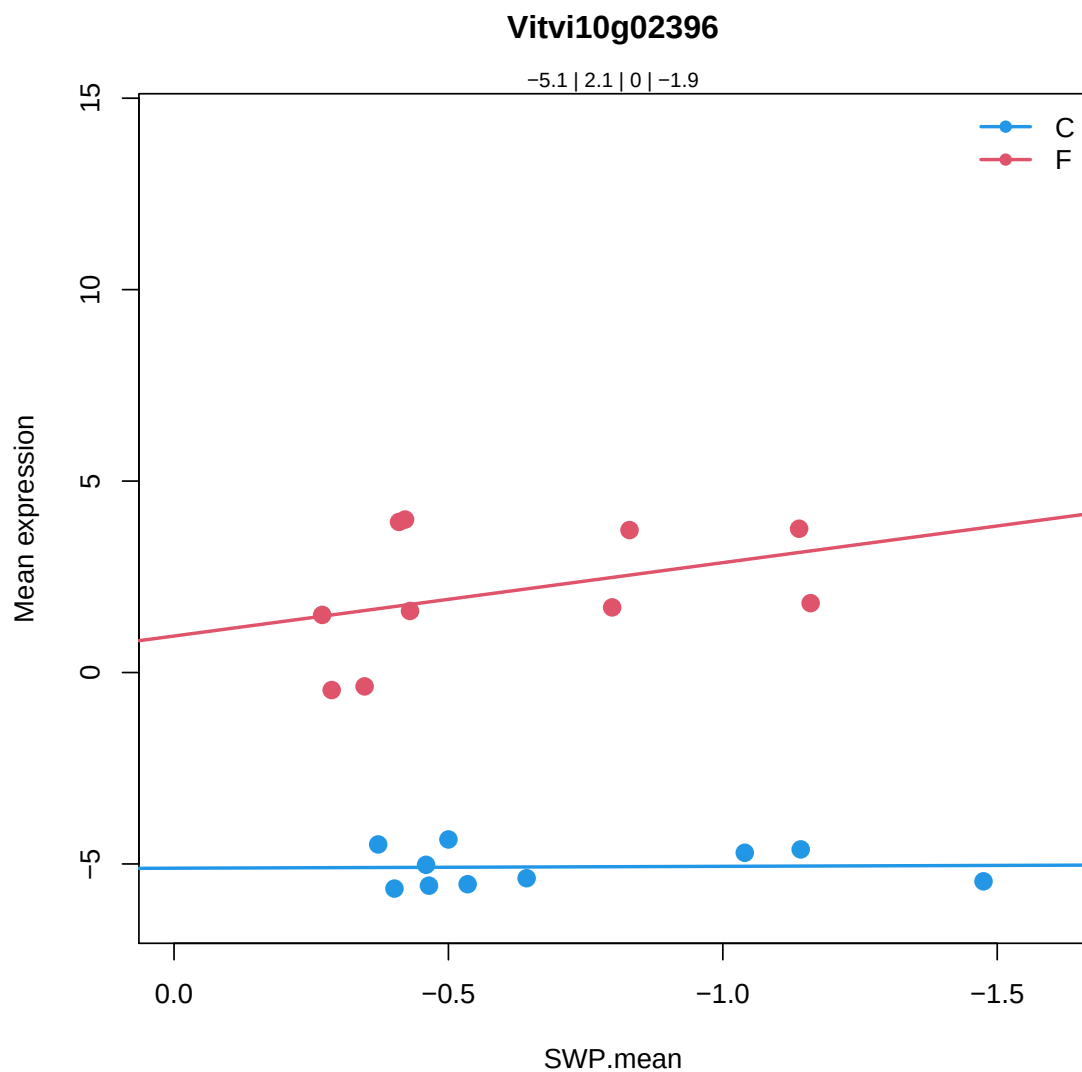
APS reductase 1 |

Chr4:2325069-2326718 FORWARD LENGTH=465 |

201606

Coefficients for Vitvi10g02396.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.076664	1.036555e-12	***	1.485024e-12	***
SlopeC	-0.04830116	0.9602008		0.9937458	
MeanF-MeanC	7.197329	9.873187e-13	***	8.749251e-11	***
SlopeF-SlopeC	-1.867763	0.2034859		0.9999488	



7.4.61 Vitvi07g03066

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

Vitvi07g03066

35.2

not assigned.unknown

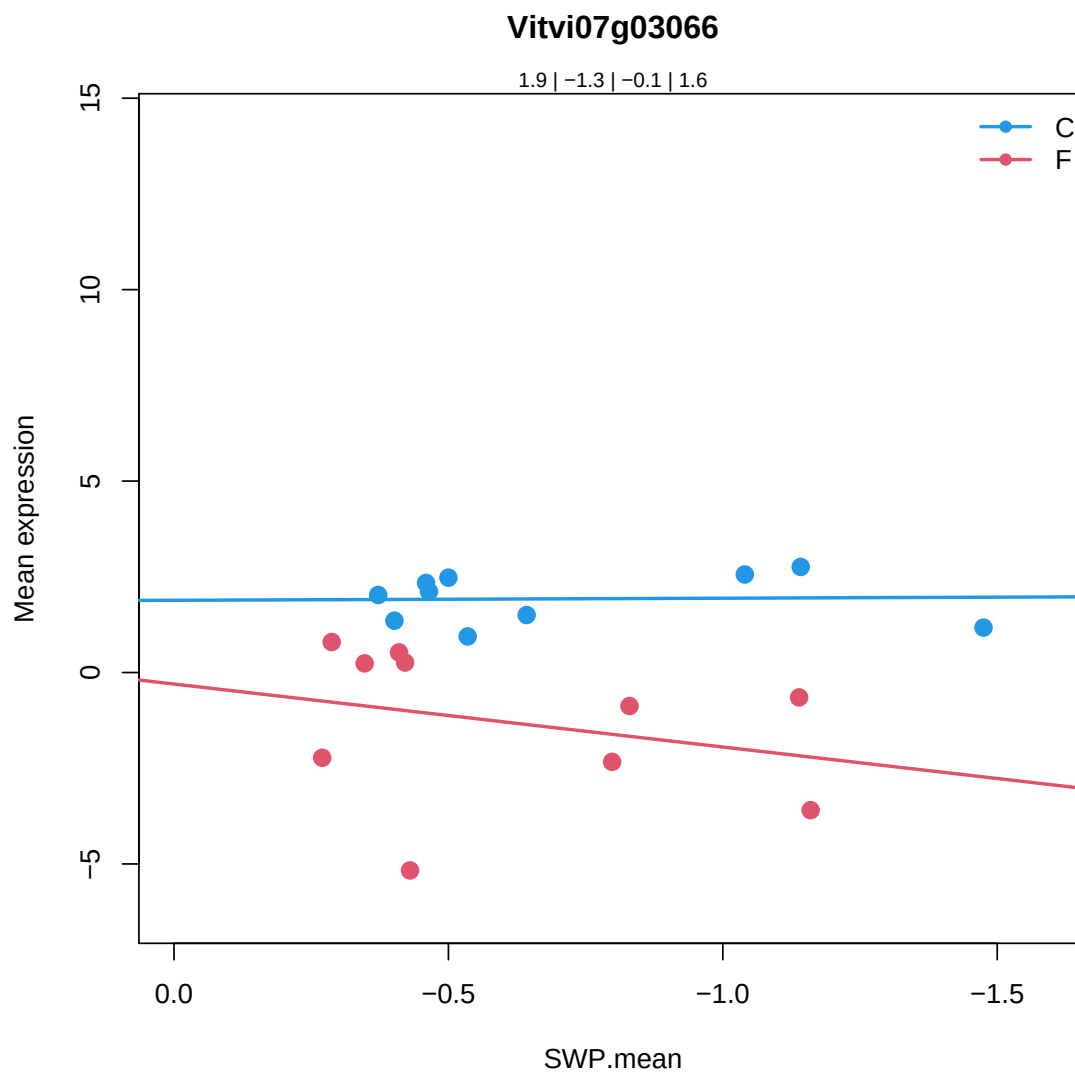
tubulin alpha-5 |

Chr5:6687212-6688926 FORWARD LENGTH=450 |

201606

Coefficients for Vitvi07g03066.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.924411	0.0001445351	***	0.0001590961	***
SlopeC	-0.0543839	0.9630928		0.9939741	
MeanF-MeanC	-3.22752	1.874679e-05	***	0.0004355772	***
SlopeF-SlopeC	1.698955	0.3367385		0.9999488	



7.4.62 Vitvi18g01877

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

Vitvi18g01877

20.1.2.2

stress.biotic.receptors.TIR-NBS-LRR

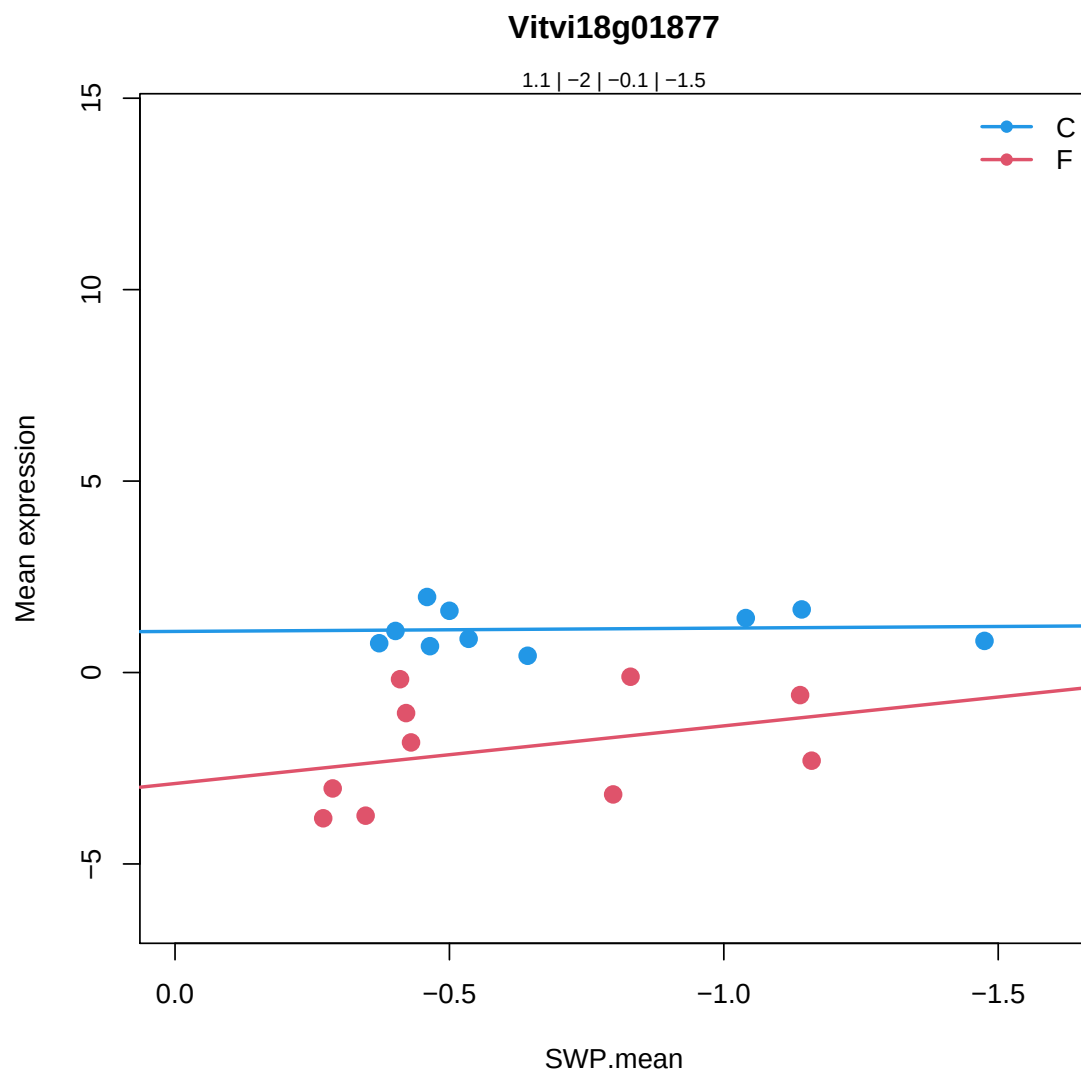
Disease resistance protein (TIR-NBS-LRR class) family |

Chr5:14568141-14571907 REVERSE LENGTH=1125 |

201606

Coefficients for Vitvi18g01877.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.133662	0.001197745	**	0.001295489	**
SlopeC	-0.08588147	0.9200083		0.9853314	
MeanF-MeanC	-3.115832	3.373809e-07	***	1.227294e-05	***
SlopeF-SlopeC	-1.420387	0.2713186		0.9999488	



7.4.63 Vitvi10g02328

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

Vitvi10g02328

35.2

not assigned.unknown

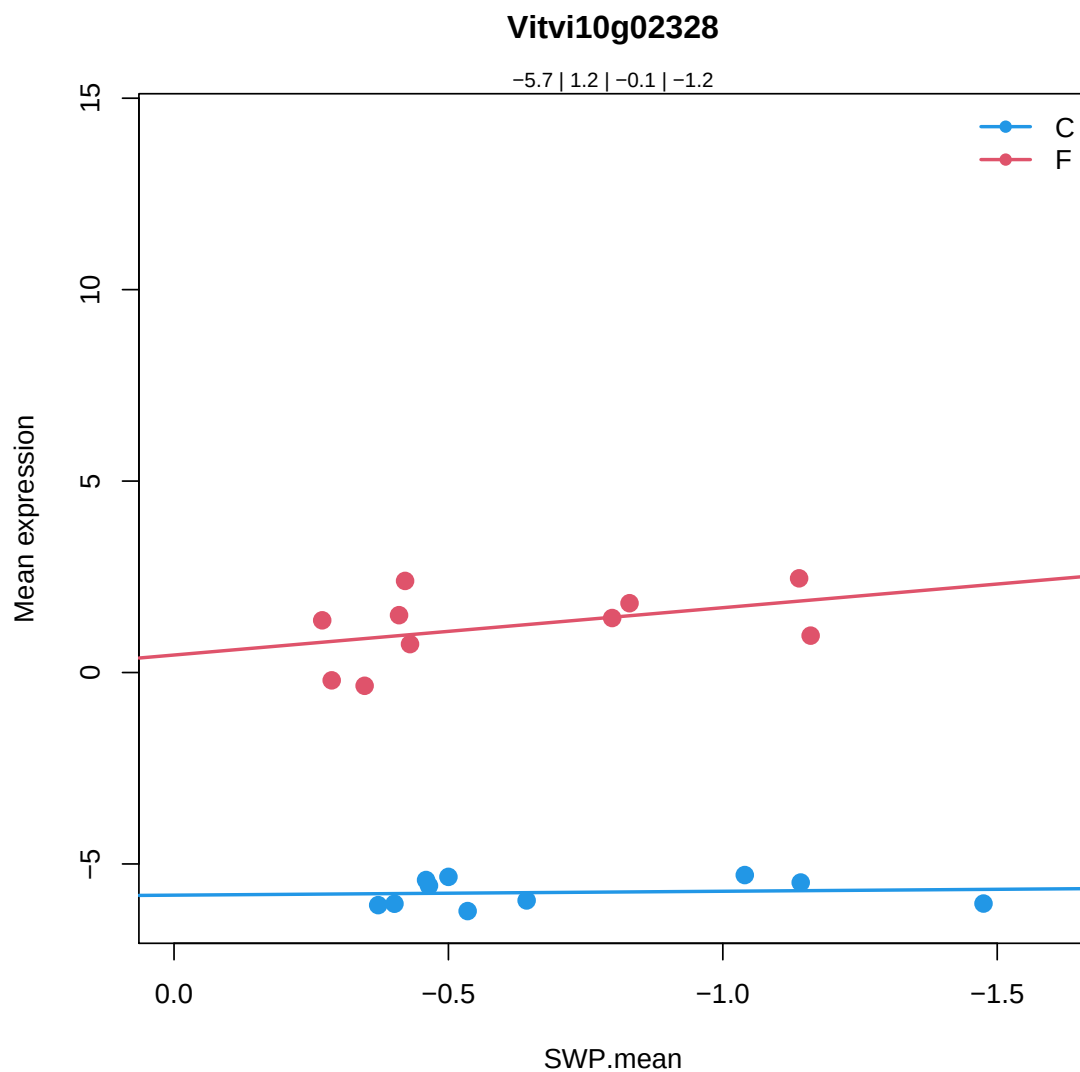
B-box type zinc finger family protein |

Chr4:13675853-13676616 FORWARD LENGTH=223 |

201606

Coefficients for Vitvi10g02328.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.743315	2.15372e-18	***	6.743426e-18	***
SlopeC	-0.1021136	0.8593585		0.9737381	
MeanF-MeanC	6.953263	5.463107e-17	***	1.051375e-14	***
SlopeF-SlopeC	-1.134082	0.1948572		0.9999488	



7.4.64 Vitvi10g02227

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

Vitvi10g02227

30.2.17

signalling.receptor kinases.DUF 26

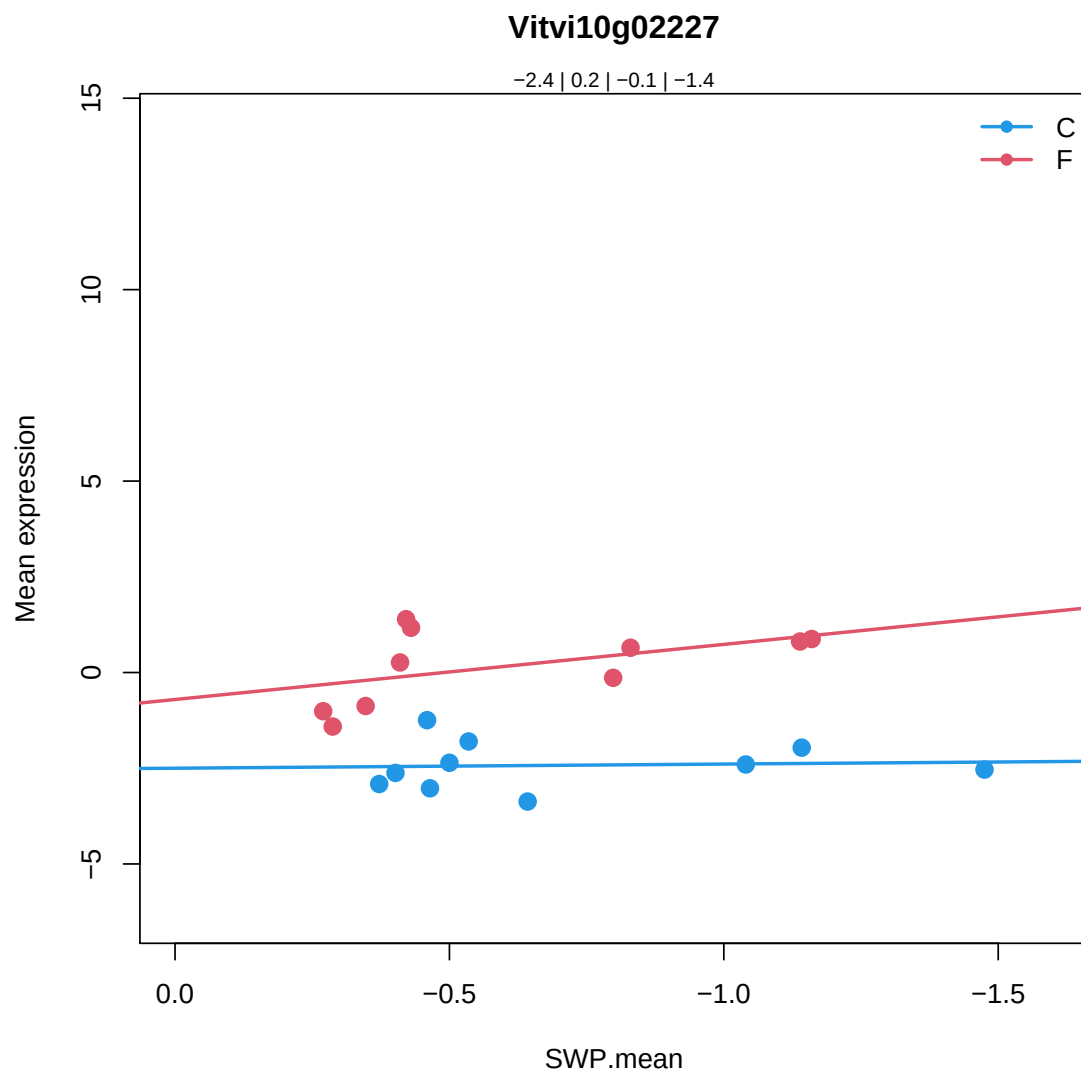
Receptor-like protein kinase-related family protein |

Chr3:7771065-7772137 FORWARD LENGTH=252 |

201606

Coefficients for Vitvi10g02227.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-2.423304	6.172705e-10	***	7.843632e-10	***
SlopeC	-0.1082359	0.8673084		0.9757404	
MeanF-MeanC	2.595396	7.441044e-08	***	3.150455e-06	***
SlopeF-SlopeC	-1.330957	0.1766957		0.9999488	



7.4.65 Vitvi08g02249

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

```
Vitvi08g02249
```

```
29.5
```

```
protein.degradation
```

```
Eukaryotic aspartyl protease family protein |
```

```
Chr3:19465644-19467053 REVERSE LENGTH=469 |
```

```
201606
```

```
Vitvi08g02249
```

```
35.2
```

```
not assigned.unknown
```

```
Eukaryotic aspartyl protease family protein |
```

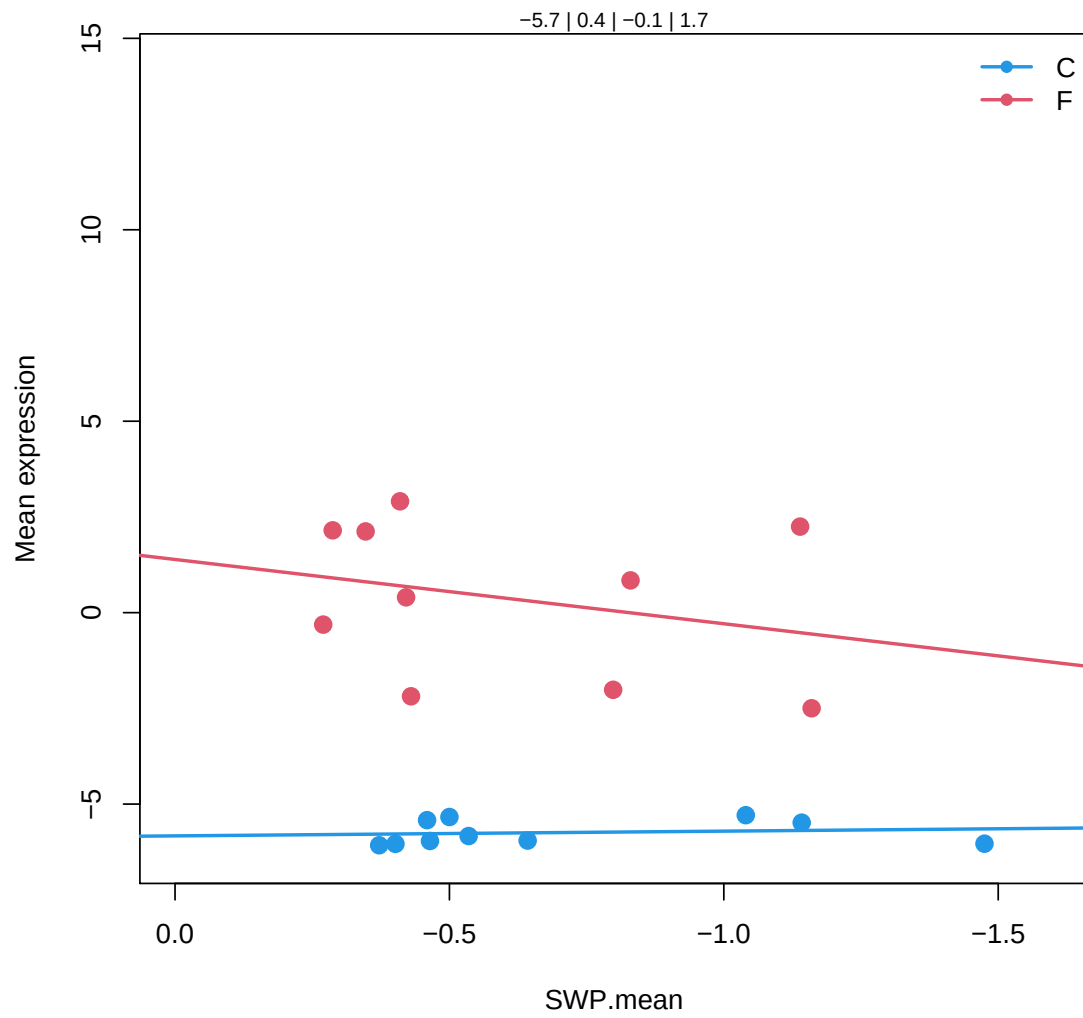
```
Chr3:19465644-19467053 REVERSE LENGTH=469 |
```

```
201606
```

Coefficients for Vitvi08g02249.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.743315	3.296028e-12	***	4.598028e-12	***
SlopeC	-0.1237221	0.9152126		0.9842726	
MeanF-MeanC	6.109273	6.937645e-10	***	4.179588e-08	***
SlopeF-SlopeC	1.802499	0.3033914		0.9999488	

Vitvi08g02249



7.4.66 Vitvi01g01811

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

```
Vitvi01g01811
```

```
35.2
```

```
not assigned.unknown
```

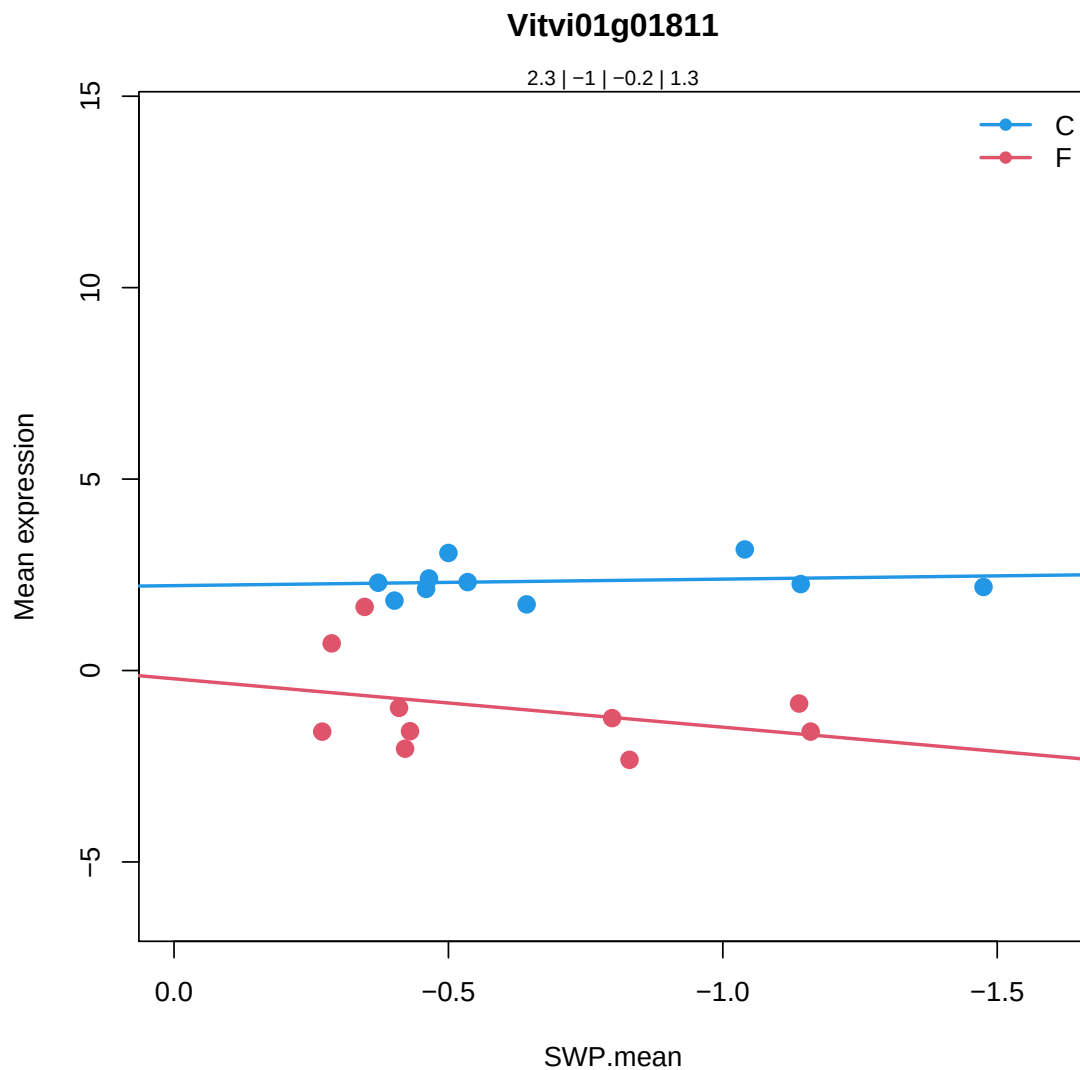
```
heparan-alpha-glucosaminide N-acetyltransferase-like protein (DUF1624)
```

```
Chr5:19392408-19394689 FORWARD LENGTH=403 |
```

```
201606
```

Coefficients for Vitvi01g01811.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.336578	1.790596e-08	***	2.169669e-08	***
SlopeC	-0.1698524	0.822491		0.9640425	
MeanF-MeanC	-3.322936	1.629062e-08	***	7.857644e-07	***
SlopeF-SlopeC	1.433989	0.2113931		0.9999488	



7.4.67 Vitvi12g02563

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

Vitvi12g02563

35.2

not assigned.unknown

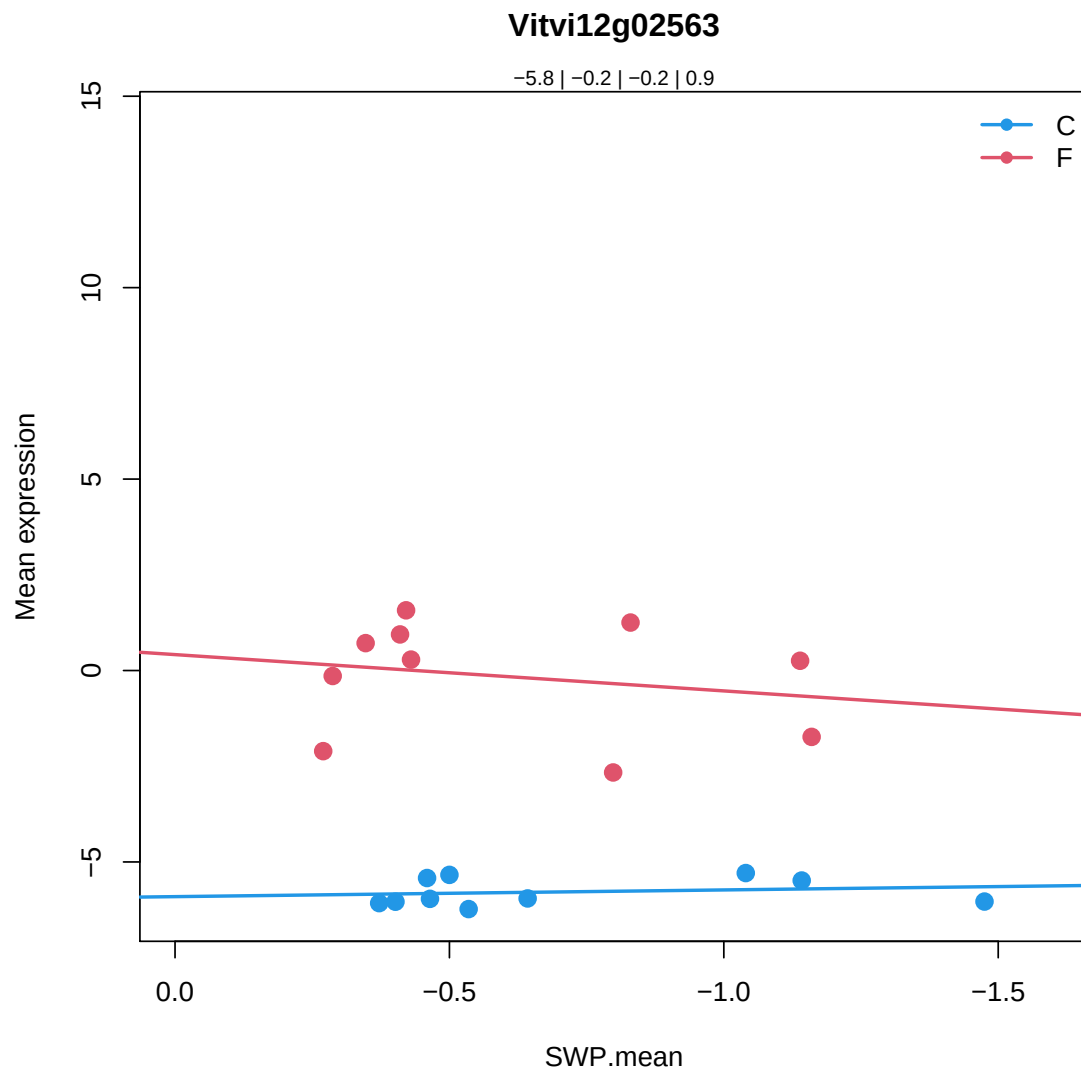
Peroxidase superfamily protein |

Chr5:25659551-25660946 REVERSE LENGTH=328 |

201606

Coefficients for Vitvi12g02563.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.782939	1.37936e-14	***	2.273133e-14	***
SlopeC	-0.175305	0.8435181		0.9700368	
MeanF-MeanC	5.620778	2.202456e-11	***	1.653686e-09	***
SlopeF-SlopeC	1.123919	0.3989503		0.9999488	



7.4.68 Vitvi09g00260

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

Vitvi09g00260

35.2

not assigned.unknown

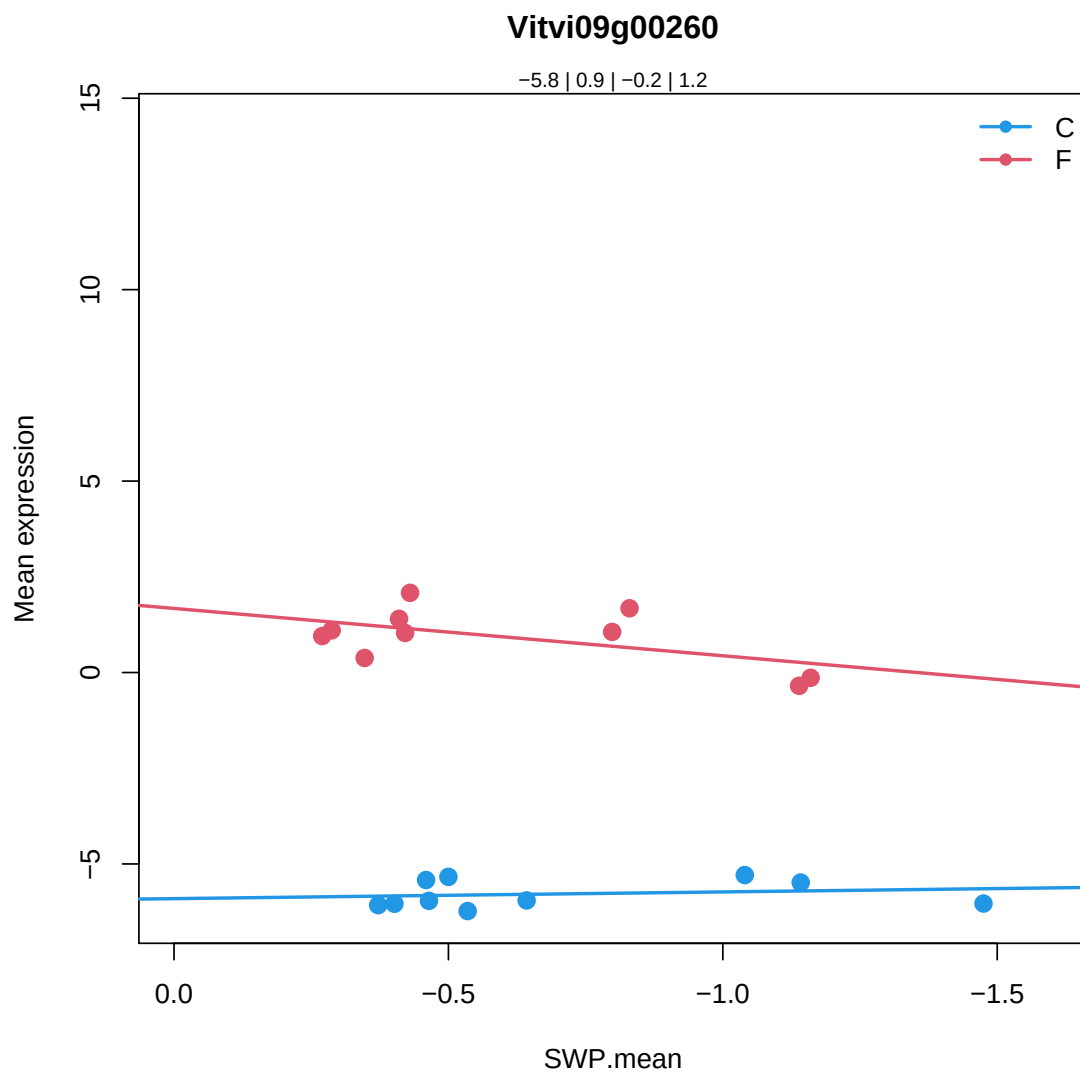
root hair specific 16 |

Chr4:14385631-14389524 FORWARD LENGTH=911 |

201606

Coefficients for Vitvi09g00260.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.782939	2.796541e-20	***	1.639624e-19	***
SlopeC	-0.175305	0.7105724		0.935038	
MeanF-MeanC	6.703427	1.820469e-18	***	4.624598e-16	***
SlopeF-SlopeC	1.411262	0.05450845	.	0.9999488	



7.4.69 Vitvi05g00909

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

Vitvi05g00909

20.1.2.2

stress.biotic.receptors.TIR-NBS-LRR

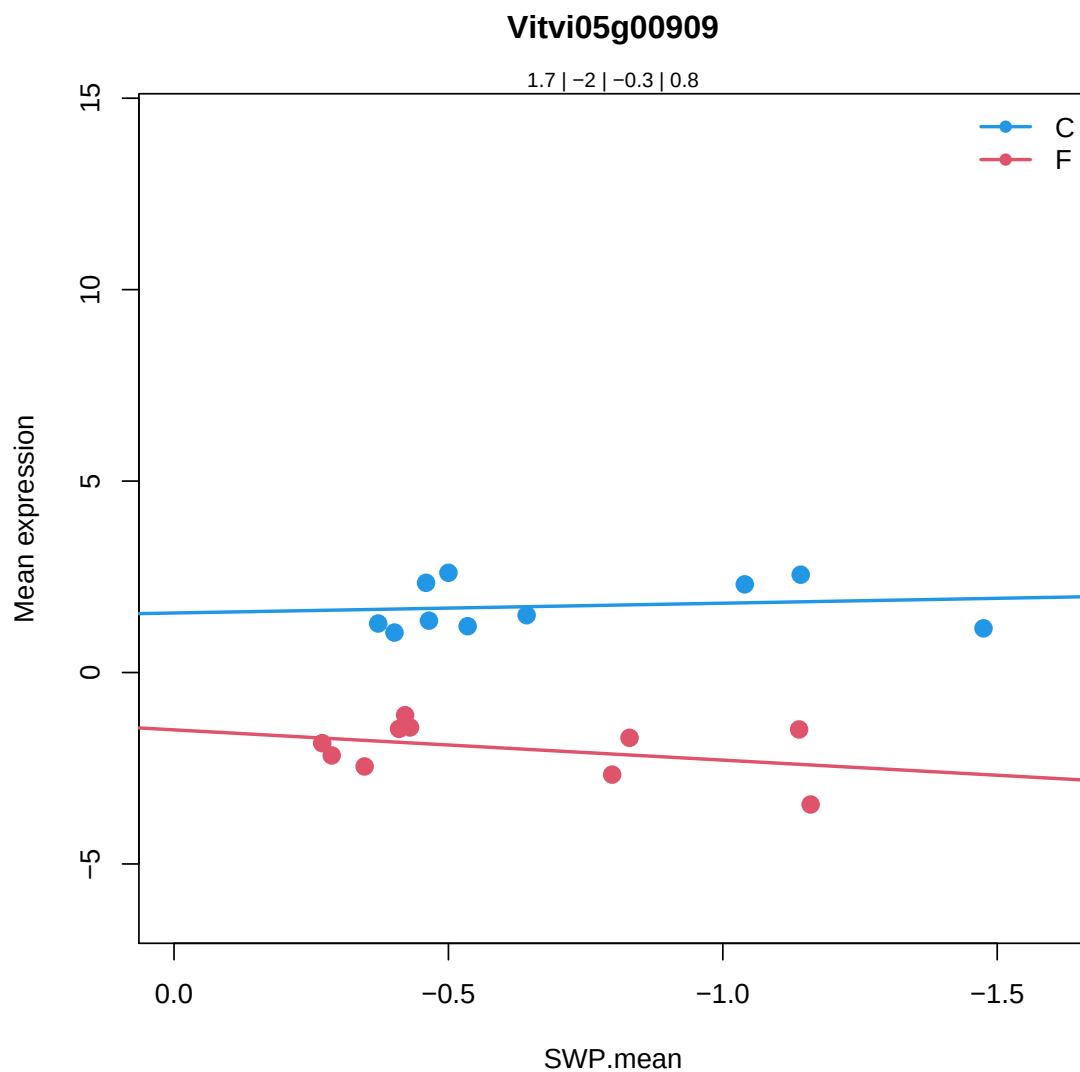
disease resistance protein (TIR-NBS-LRR class) |

Chr5:5822999-5827153 FORWARD LENGTH=1295 |

201606

Coefficients for Vitvi05g00909.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.734407	2.101861e-08	***	2.540165e-08	***
SlopeC	-0.2554092	0.6531717		0.919605	
MeanF-MeanC	-3.713598	1.157191e-11	***	9.234507e-10	***
SlopeF-SlopeC	1.045479	0.2235796		0.9999488	



7.4.70 Vitvi12g00574

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

Vitvi12g00574

16.01.2005

secondary metabolism.isoprenoids.terpenoids

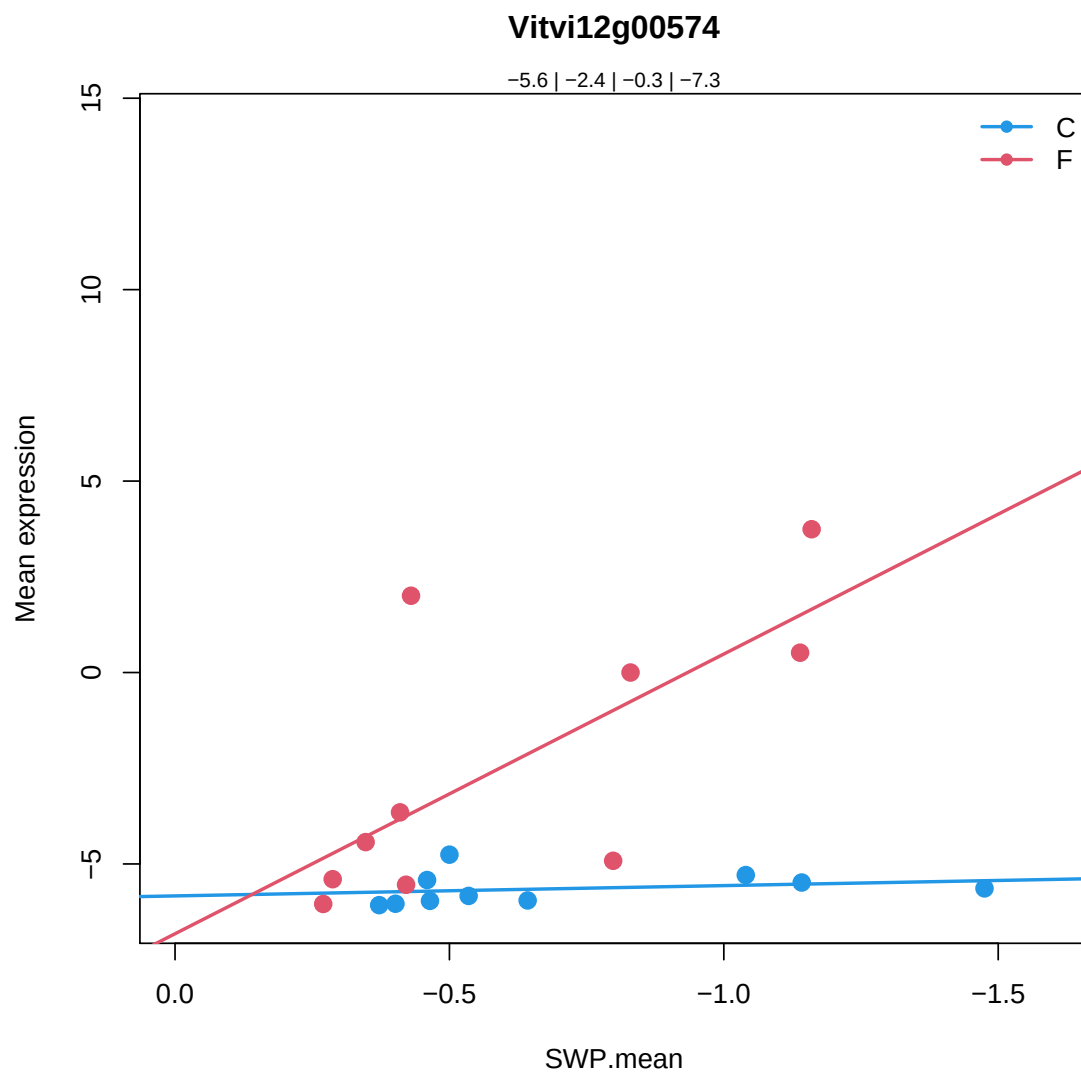
terpene synthase-like sequence-1%2C8-cineole |

Chr3:9447545-9450316 FORWARD LENGTH=600 |

201606

Coefficients for Vitvi12g00574.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.645691	6.169158e-10	***	7.839779e-10	***
SlopeC	-0.2692201	0.8584264		0.9734036	
MeanF-MeanC	3.273791	0.0002909881	***	0.004497484	**
SlopeF-SlopeC	-7.036961	0.004526106	**	0.9999488	



7.4.71 Vitvi15g00110

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

Vitvi15g00110

35.2

not assigned.unknown

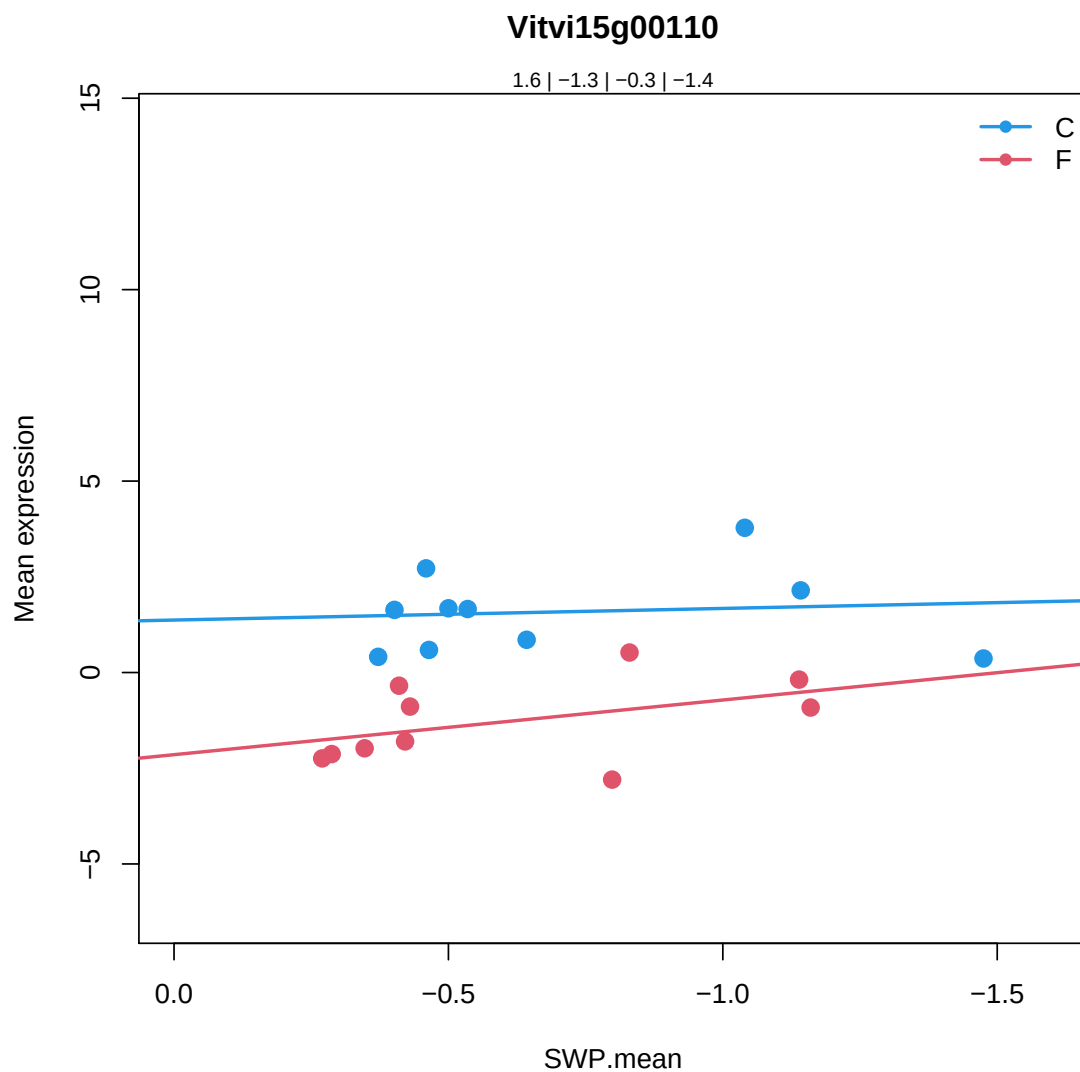
Pentatricopeptide repeat (PPR) superfamily protein |

Chr4:14962617-14964995 REVERSE LENGTH=792 |

201606

Coefficients for Vitvi15g00110.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.58373	3.827328e-05	***	4.26309e-05	***
SlopeC	-0.3035374	0.7255101		0.9394623	
MeanF-MeanC	-2.859953	1.41705e-06	***	4.481054e-05	***
SlopeF-SlopeC	-1.124079	0.385905		0.9999488	



7.4.72 Vitvi16g01081

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

Vitvi16g01081

35.1

not assigned.no ontology

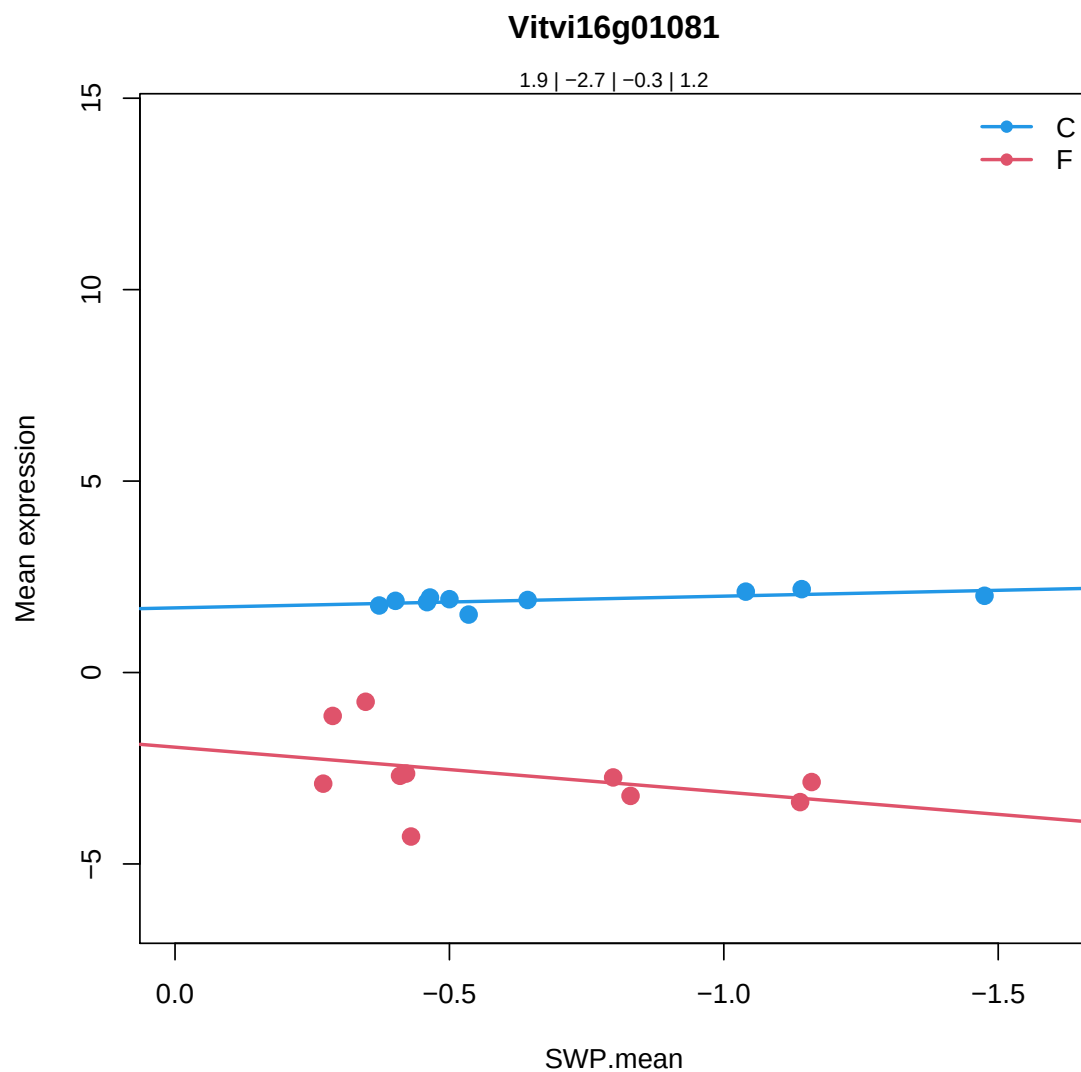
Ribosomal protein L31 |

Chr1:28272163-28272687 FORWARD LENGTH=144 |

201606

Coefficients for Vitvi16g01081.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.903497	9.543851e-09	***	1.165511e-08	***
SlopeC	-0.3059787	0.6076322		0.9048393	
MeanF-MeanC	-4.566578	5.138006e-13	***	4.894593e-11	***
SlopeF-SlopeC	1.476801	0.1055467		0.9999488	



7.4.73 Vitvi18g02451

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

Vitvi18g02451

16.01.2005

secondary metabolism.isoprenoids.terpenoids

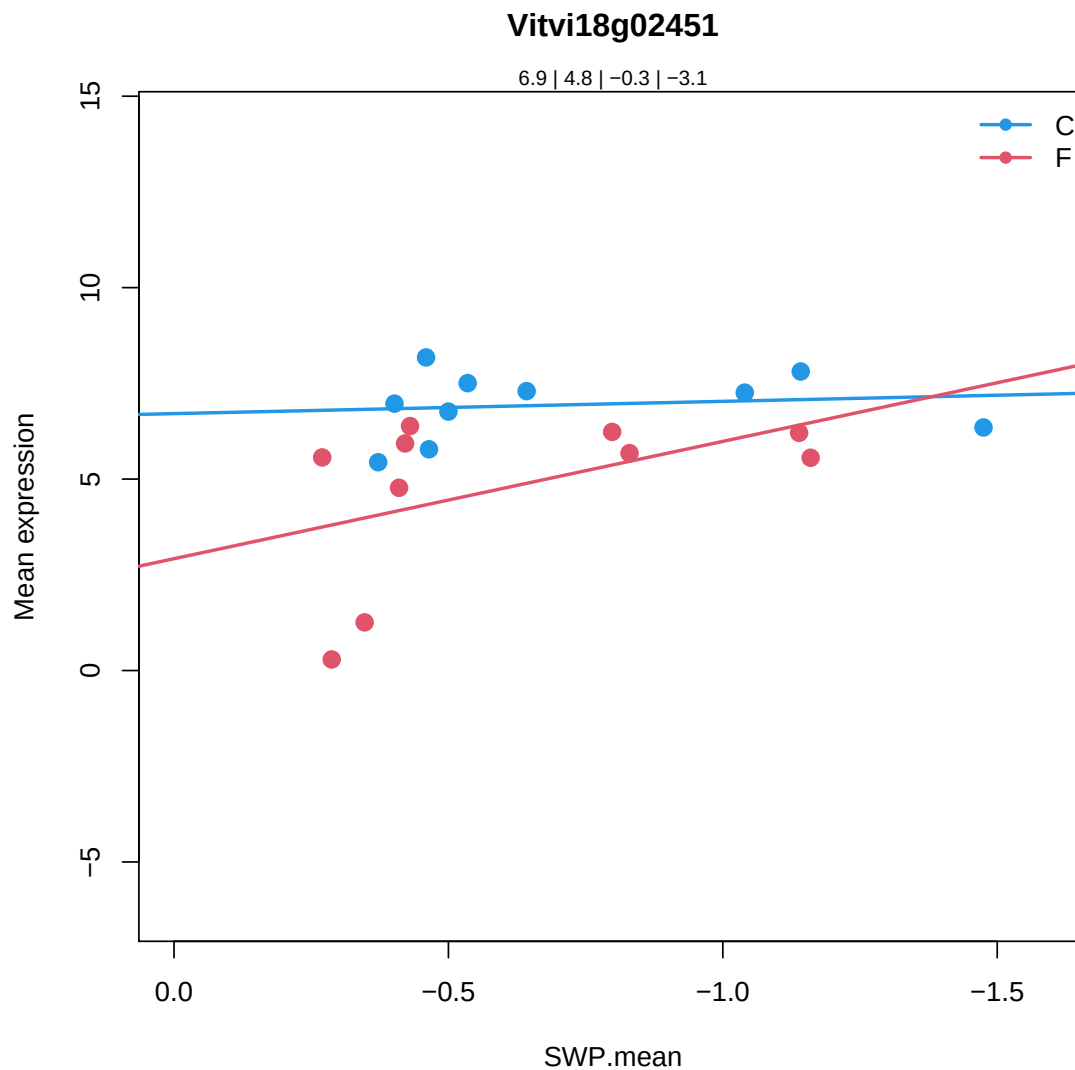
terpene synthase 21 |

Chr5:8092969-8095128 FORWARD LENGTH=545 |

201606

Coefficients for Vitvi18g02451.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.934609	2.33132e-13	***	3.491597e-13	***
SlopeC	-0.3205063	0.7938969		0.9552081	
MeanF-MeanC	-2.147399	0.00214966	**	0.02330378	*
SlopeF-SlopeC	-2.742855	0.1428692		0.9999488	



7.4.74 Vitvi09g01930

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

Vitvi09g01930

29.2.1.2.2.7

protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L7

disease resistance family protein / LRR family protein |

Chr2:14737169-14739886 REVERSE LENGTH=905 |

201606

Vitvi09g01930

20.01.2002

stress.biotic.receptors

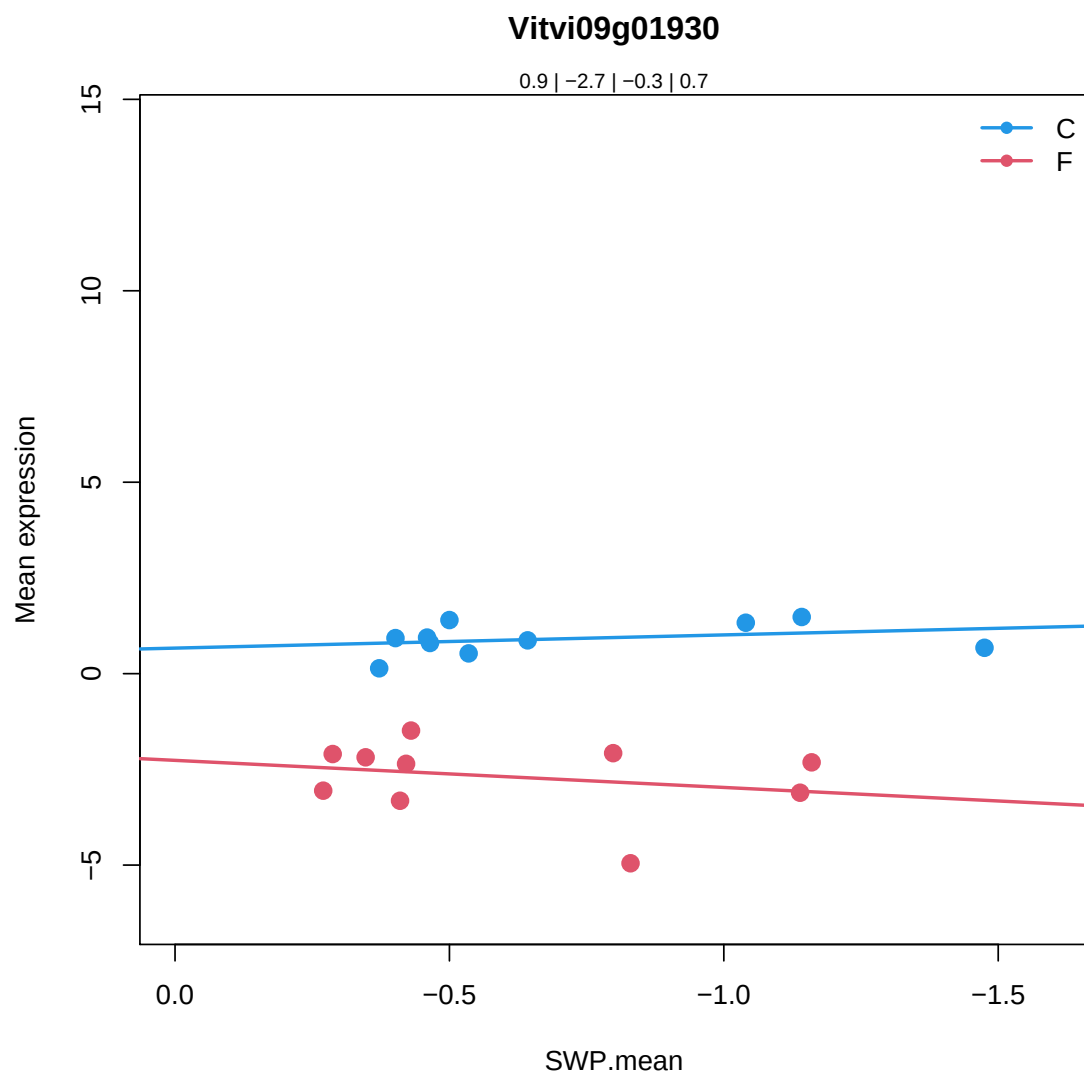
disease resistance family protein / LRR family protein |

Chr2:14737169-14739886 REVERSE LENGTH=905 |

201606

Coefficients for Vitvi09g01930.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.9094944	0.0005236805	***	0.0005699349	***
SlopeC	-0.3447382	0.5844654		0.8963999	
MeanF-MeanC	-3.605352	1.392337e-10	***	9.432003e-09	***
SlopeF-SlopeC	1.051695	0.2676335		0.9999488	



7.4.75 Vitvi10g00932

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

Vitvi10g00932

30.2.12

signalling.receptor kinases.leucine rich repeat XII

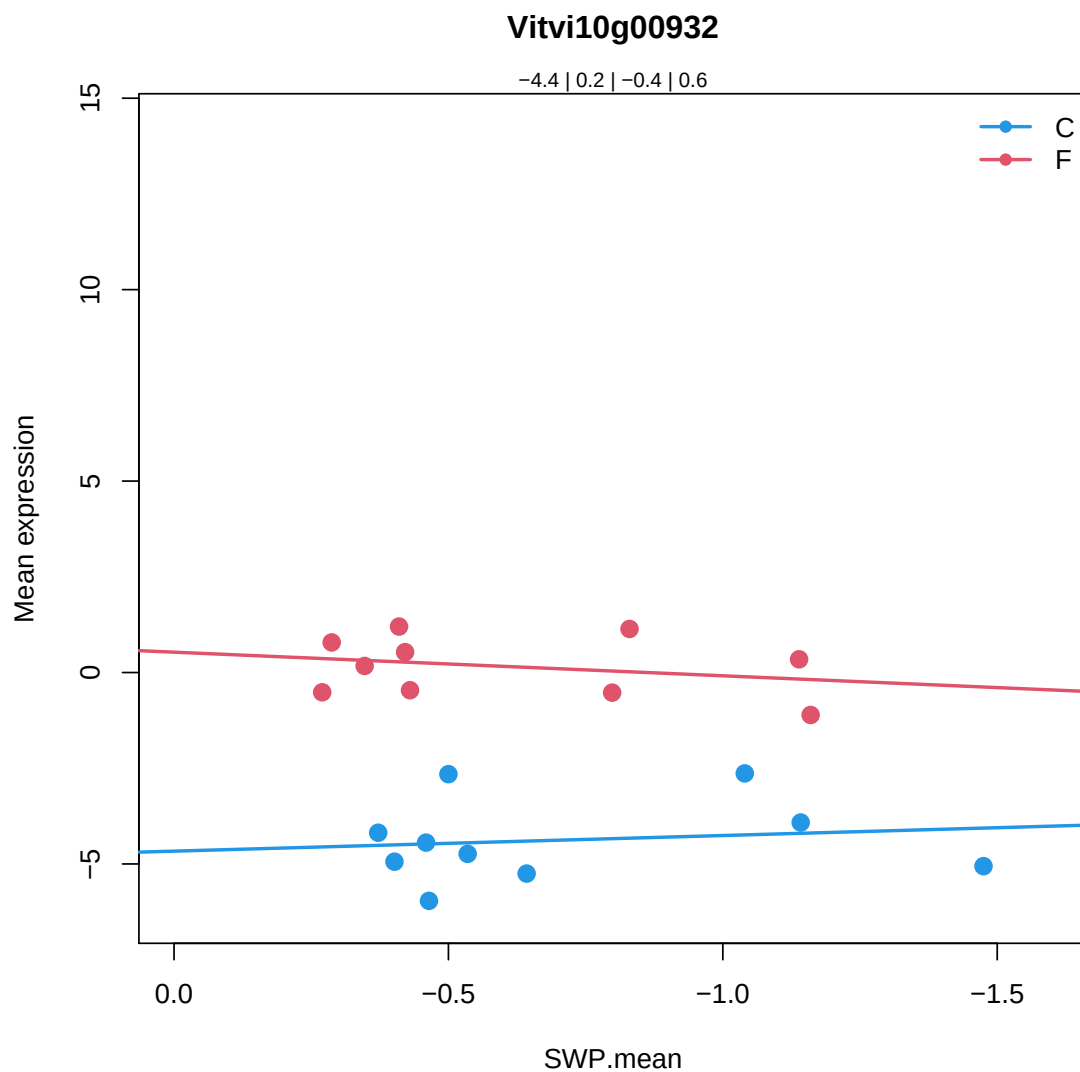
Leucine-rich receptor-like protein kinase family protein |

Chr2:11208367-11213895 REVERSE LENGTH=976 |

201606

Coefficients for Vitvi10g00932.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-4.378537	3.058643e-13	***	4.544286e-13	***
SlopeC	-0.4084059	0.6038814		0.9046943	
MeanF-MeanC	4.534266	1.228068e-10	***	8.393817e-09	***
SlopeF-SlopeC	1.024973	0.3844253		0.9999488	



7.4.76 Vitvi13g00261

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

Vitvi13g00261

35.2

not assigned.unknown

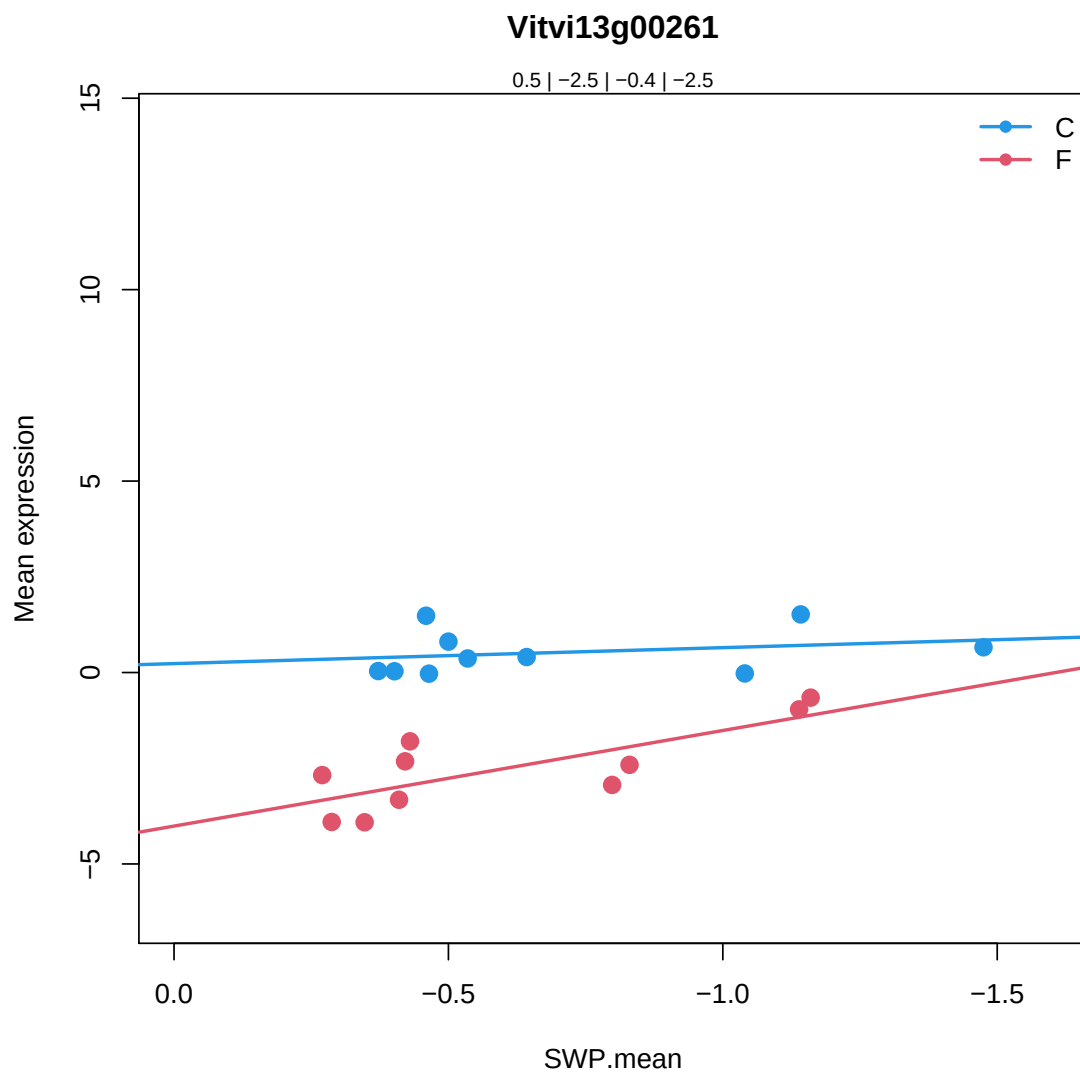
PIF / Ping-Pong family of plant transposase |

Chr3:20518518-20520690 FORWARD LENGTH=406 |

201606

Coefficients for Vitvi13g00261.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.5253927	0.0164883	*	0.01737758	*
SlopeC	-0.4169403	0.4660837		0.8618199	
MeanF-MeanC	-3.015297	5.911452e-10	***	3.639539e-08	***
SlopeF-SlopeC	-2.079326	0.02120173	*	0.9999488	



7.4.77 Vitvi00g02022

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

Vitvi00g02022

17.01.2002

hormone metabolism.abscisic acid.signal transduction

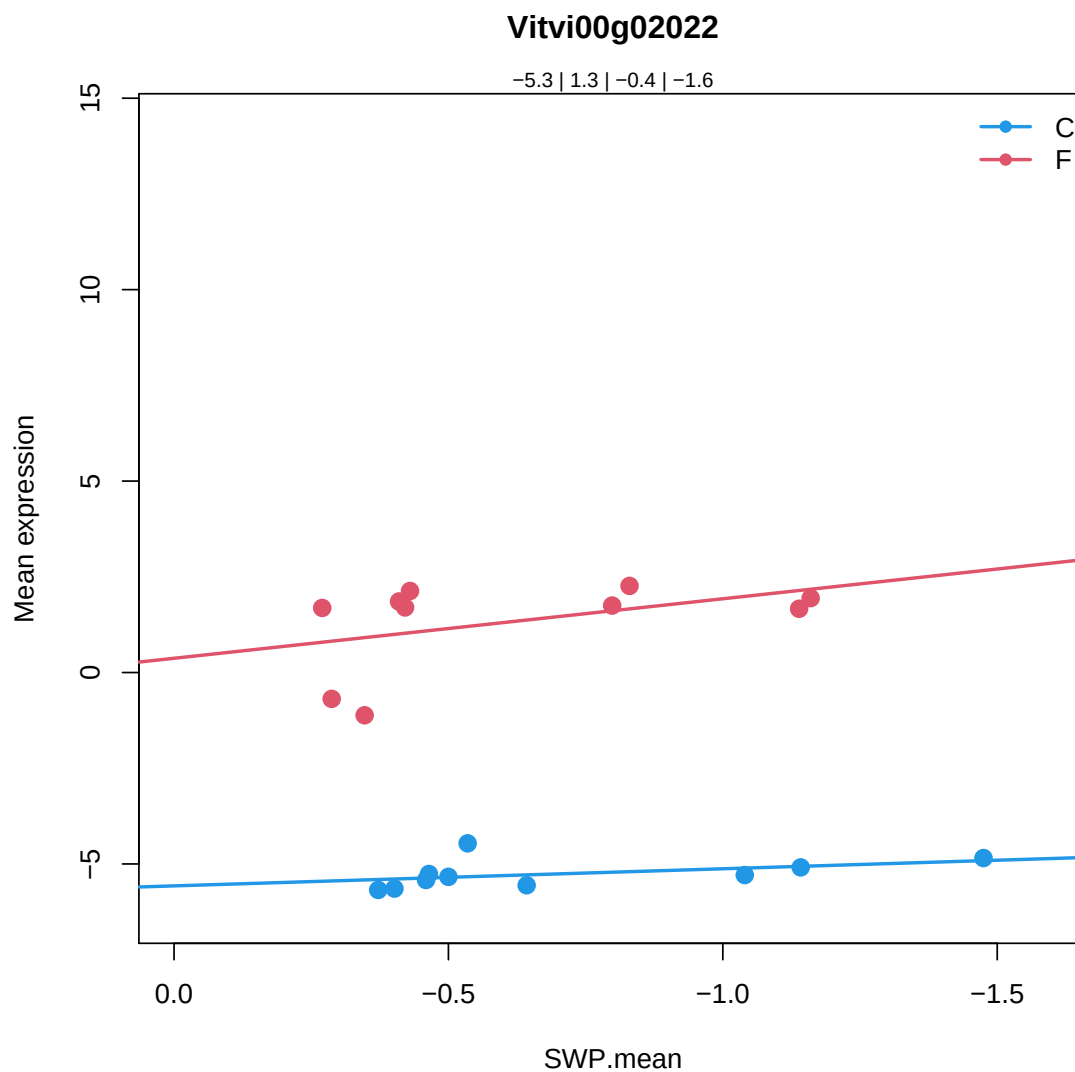
GCR2-like 1 |

Chr5:26086129-26087304 REVERSE LENGTH=311 |

201606

Coefficients for Vitvi00g02022.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.25859	4.249314e-16	***	8.367965e-16	***
SlopeC	-0.446971	0.5134631		0.8711742	
MeanF-MeanC	6.577033	5.234018e-15	***	6.818539e-13	***
SlopeF-SlopeC	-1.107401	0.2809345		0.9999488	



7.4.78 Vitvi17g01497

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

Vitvi17g01497

26.2

misc.UDP glucosyl and glucoronyl transferases

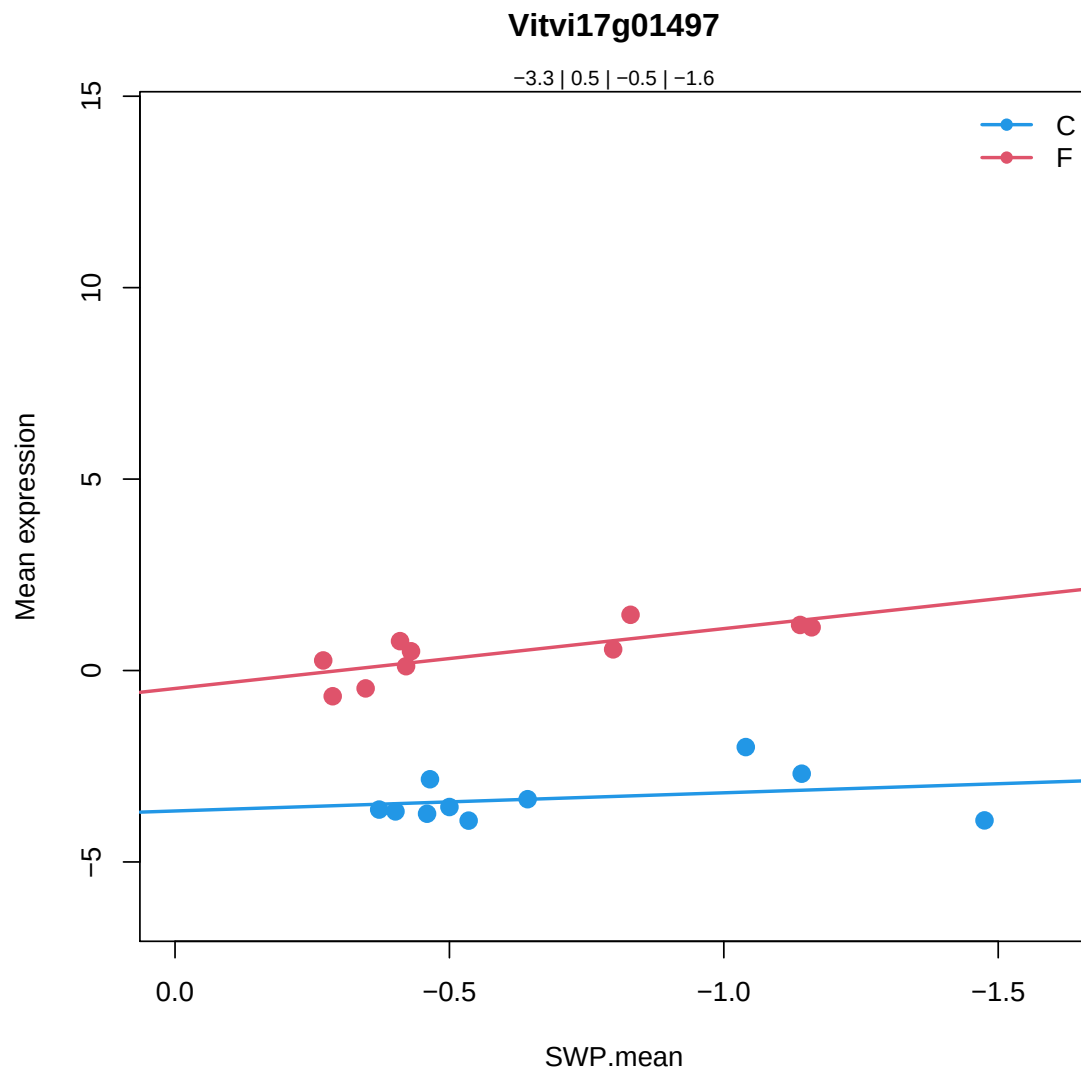
UDP-Glycosyltransferase superfamily protein |

Chr3:368840-370484 REVERSE LENGTH=464 |

201606

Coefficients for Vitvi17g01497.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-3.334798	4.342005e-15	***	7.574779e-15	***
SlopeC	-0.4744792	0.331881		0.801141	
MeanF-MeanC	3.817918	3.025e-13	***	3.053447e-11	***
SlopeF-SlopeC	-1.089142	0.1403554		0.9999488	



7.4.79 Vitvi01g01006

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

Vitvi01g01006

35.2

not assigned.unknown

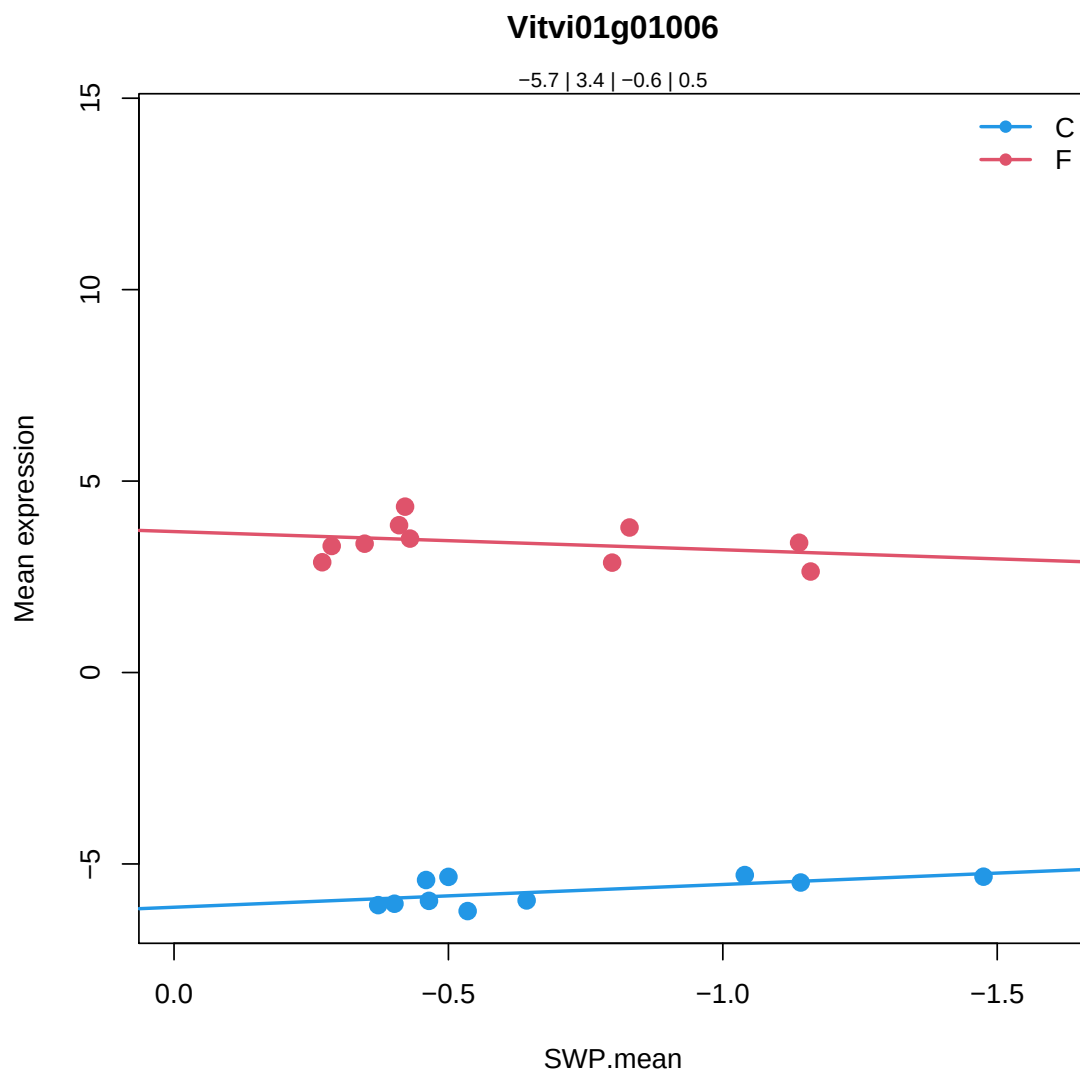
disease resistance family protein / LRR family protein |

Chr2:14737169-14739886 REVERSE LENGTH=905 |

201606

Coefficients for Vitvi01g01006.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.712755	8.273396e-22	***	9.813471e-21	***
SlopeC	-0.594586	0.141829		0.6676582	
MeanF-MeanC	9.104039	6.568669e-23	***	7.701512e-20	***
SlopeF-SlopeC	1.070103	0.07900839	.	0.9999488	



7.4.80 Vitvi12g02328

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

Vitvi12g02328

35.2

not assigned.unknown

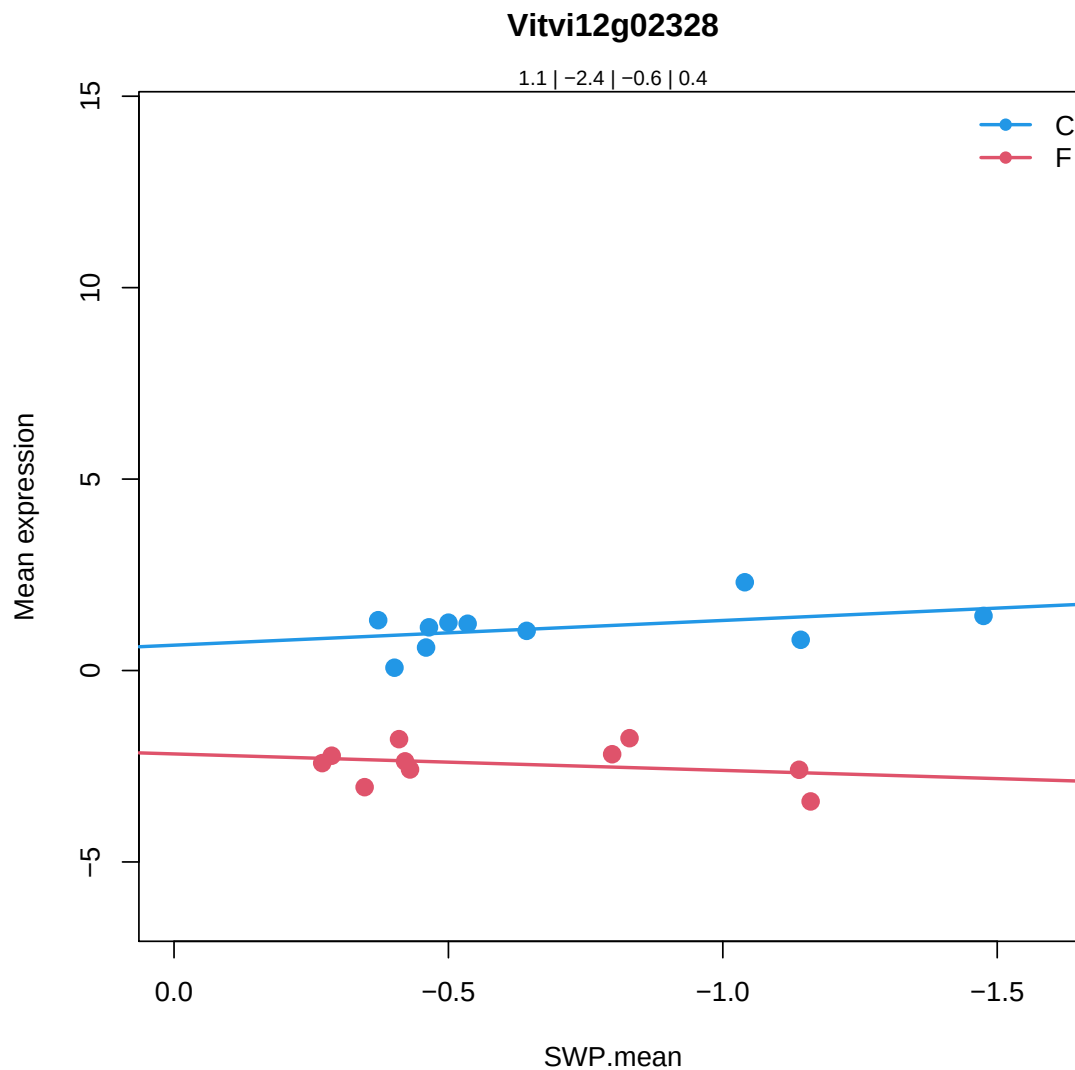
Ankyrin repeat family protein |

Chr4:1524199-1527133 REVERSE LENGTH=751 |

201606

Coefficients for Vitvi12g02328.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.115688	1.152208e-06	***	1.328137e-06	***
SlopeC	-0.645458	0.1786171		0.7108306	
MeanF-MeanC	-3.556267	6.900606e-13	***	6.374487e-11	***
SlopeF-SlopeC	1.075452	0.1341766		0.9999488	



7.4.81 Vitvi15g00245

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

Vitvi15g00245

20.1.2.2

stress.biotic.receptors.TIR-NBS-LRR

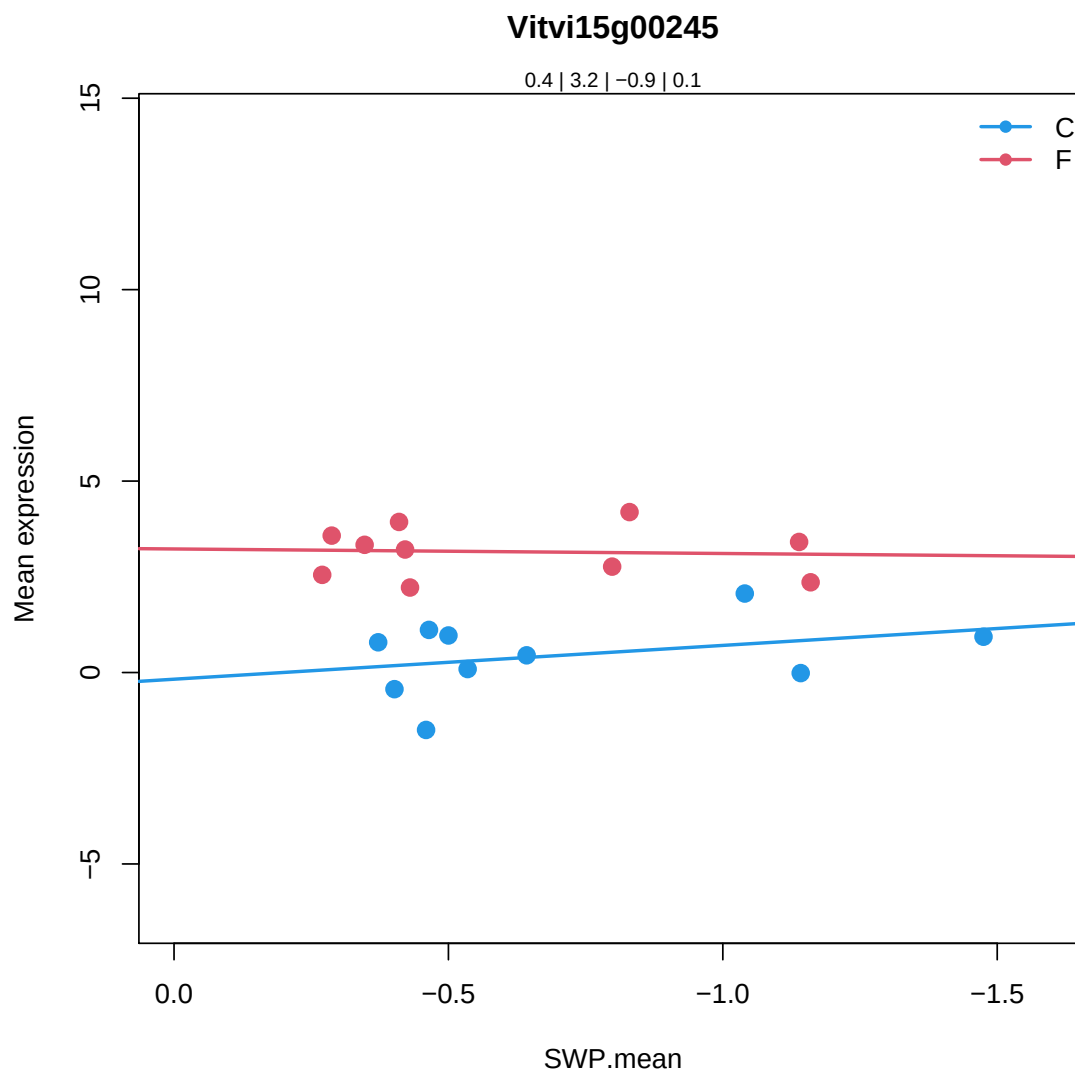
disease resistance protein (TIR-NBS-LRR class) |

Chr5:5822999-5827153 FORWARD LENGTH=1295 |

201606

Coefficients for Vitvi15g00245.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4456436	0.08275899	.	0.08575205	.
SlopeC	-0.8828349	0.2087882		0.7320795	
MeanF-MeanC	2.709153	1.018959e-07	***	4.152665e-06	***
SlopeF-SlopeC	1.000898	0.3345948		0.9999488	



7.4.82 Vitvi10g01739

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

Vitvi10g01739

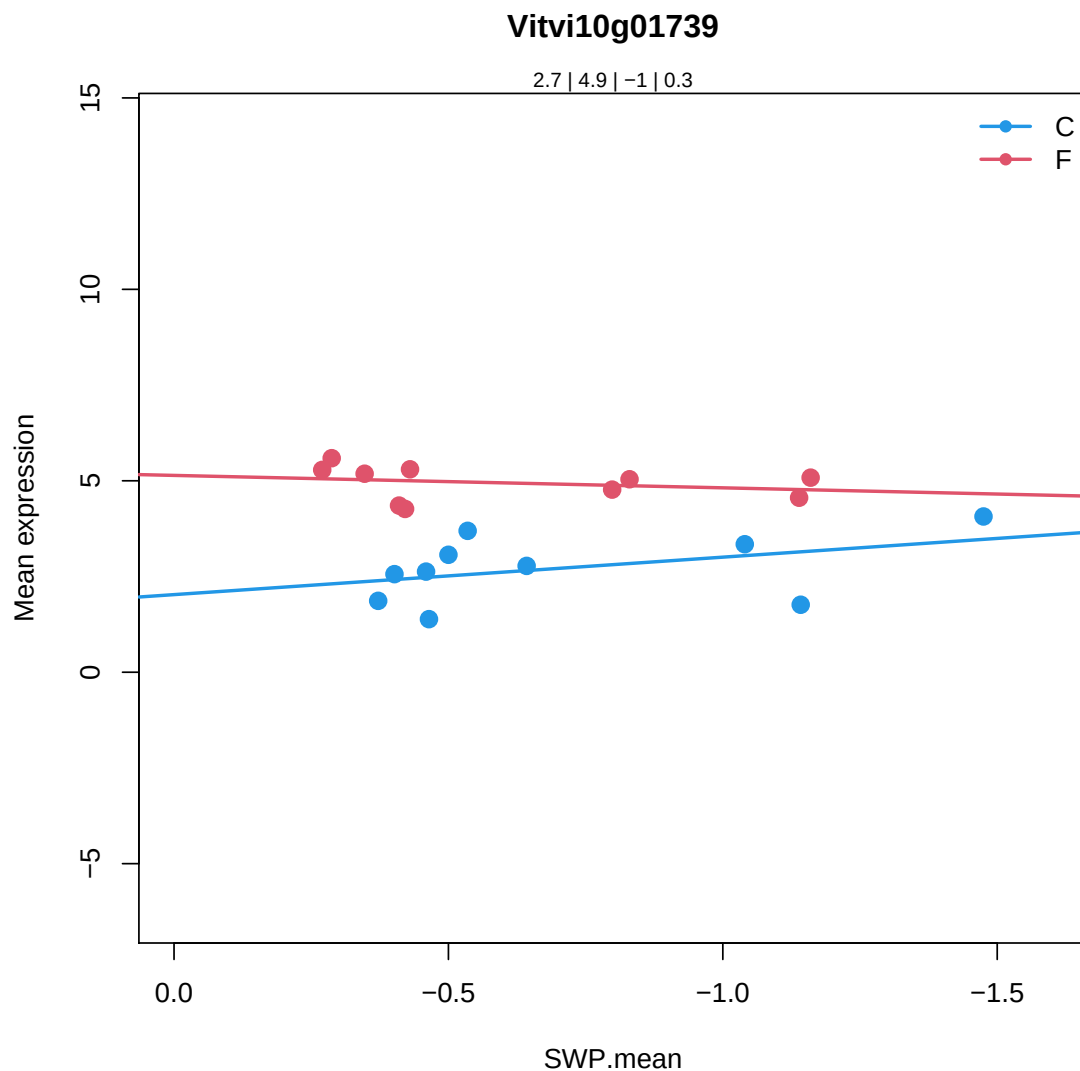
35.2

not assigned.unknown

NA

Coefficients for Vitvi10g01739.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.714859	4.496605e-12	***	6.225001e-12	***
SlopeC	-0.9783917	0.09034051	.	0.5961693	
MeanF-MeanC	2.227631	7.953729e-08	***	3.33969e-06	***
SlopeF-SlopeC	1.302982	0.1271647		0.9999488	



7.4.83 Vitvi04g02192

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

Vitvi04g02192

16.04.2001

secondary metabolism.N misc.alkaloid-like

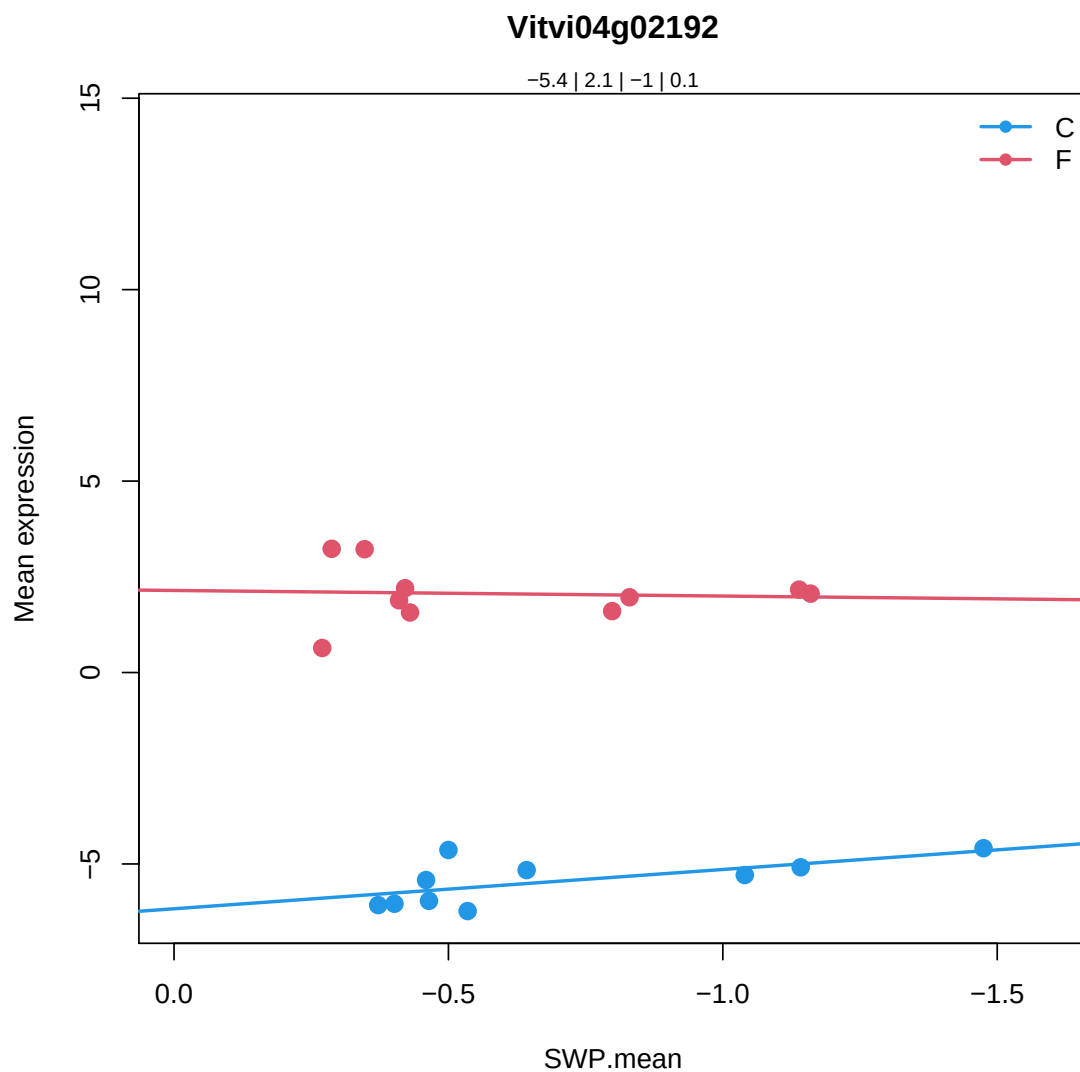
Calcium-dependent phosphotriesterase superfamily protein |

Chr3:19086548-19087909 FORWARD LENGTH=371 |

201606

Coefficients for Vitvi04g02192.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.449157	3.37321e-18	***	1.001646e-17	***
SlopeC	-1.026036	0.07682635	.	0.5706566	
MeanF-MeanC	7.503254	5.887175e-18	***	1.300468e-15	***
SlopeF-SlopeC	1.171818	0.1681586		0.9999488	



7.4.84 Vitvi12g01845

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

Vitvi12g01845

20.1.2.1

stress.biotic.receptors.CC-NBS-LRR

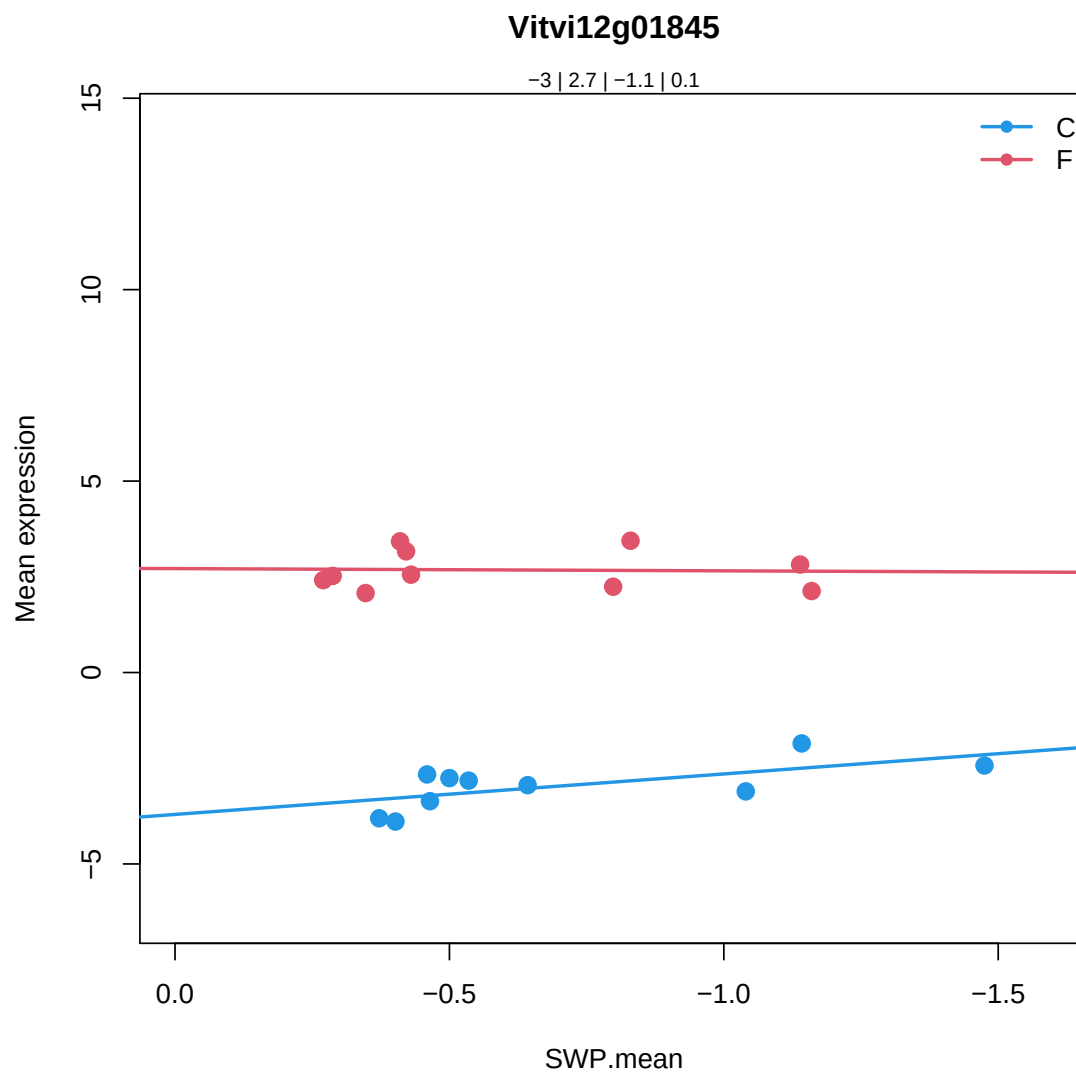
NB-ARC domain-containing disease resistance protein |

Chr3:4857940-4861104 FORWARD LENGTH=1054 |

201606

Coefficients for Vitvi12g01845.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-2.963099	1.512192e-14	***	2.483978e-14	***
SlopeC	-1.057327	0.02894713	*	0.4283614	
MeanF-MeanC	5.641784	3.409841e-17	***	6.838525e-15	***
SlopeF-SlopeC	1.115801	0.1114708		0.9999488	



7.4.85 Vitvi15g01514

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

Vitvi15g01514

35.2

not assigned.unknown

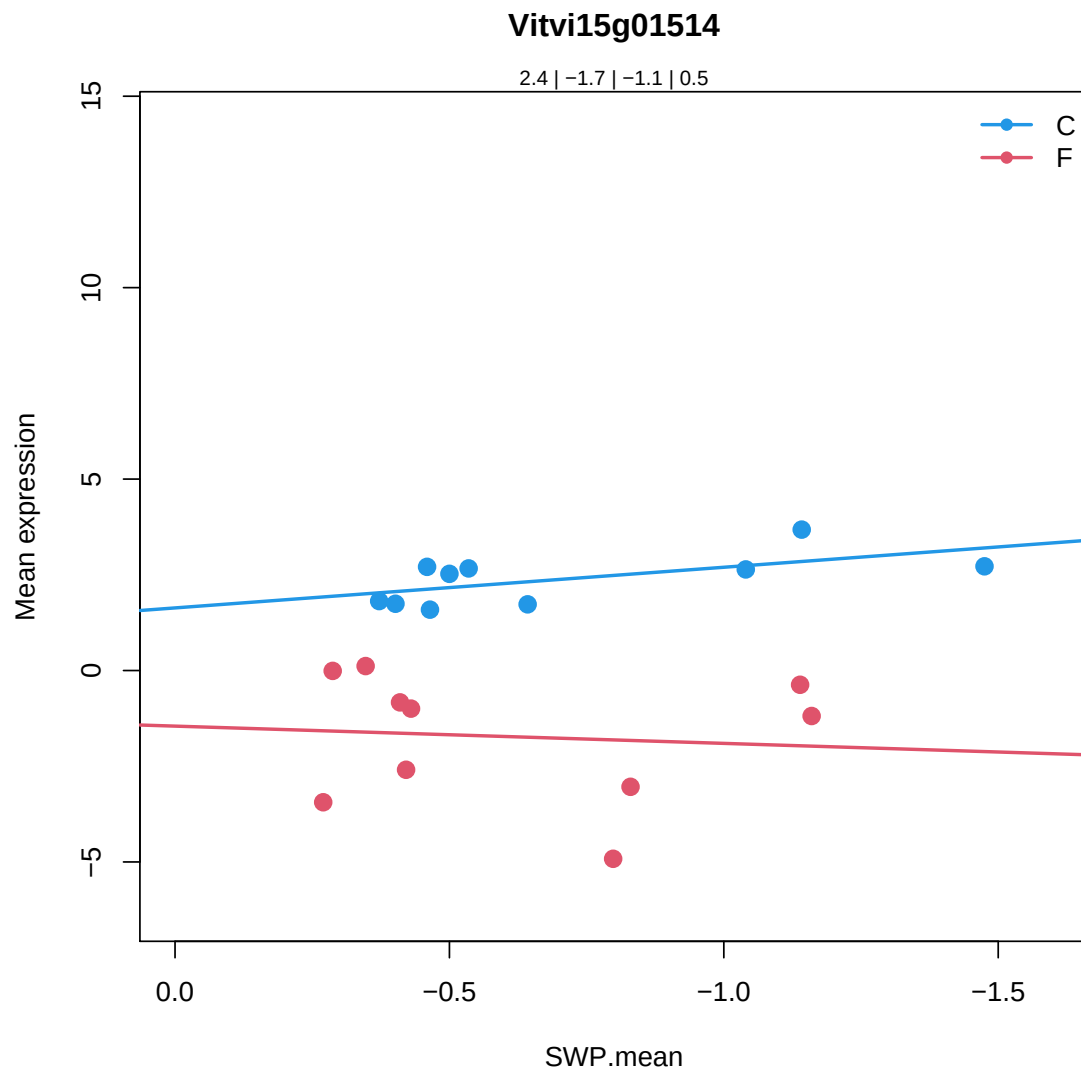
cytochrome P450%2C family 76%2C subfamily C%2C polypeptide 1 |

Chr2:18776391-18778354 REVERSE LENGTH=512 |

201606

Coefficients for Vitvi15g01514.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.381574	1.79077e-06	***	2.05565e-06	***
SlopeC	-1.06173	0.3100232		0.7925436	
MeanF-MeanC	-4.108615	8.428322e-08	***	3.509959e-06	***
SlopeF-SlopeC	1.512169	0.330839		0.9999488	



7.4.86 Vitvi05g01820

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

Vitvi05g01820

35.2

not assigned.unknown

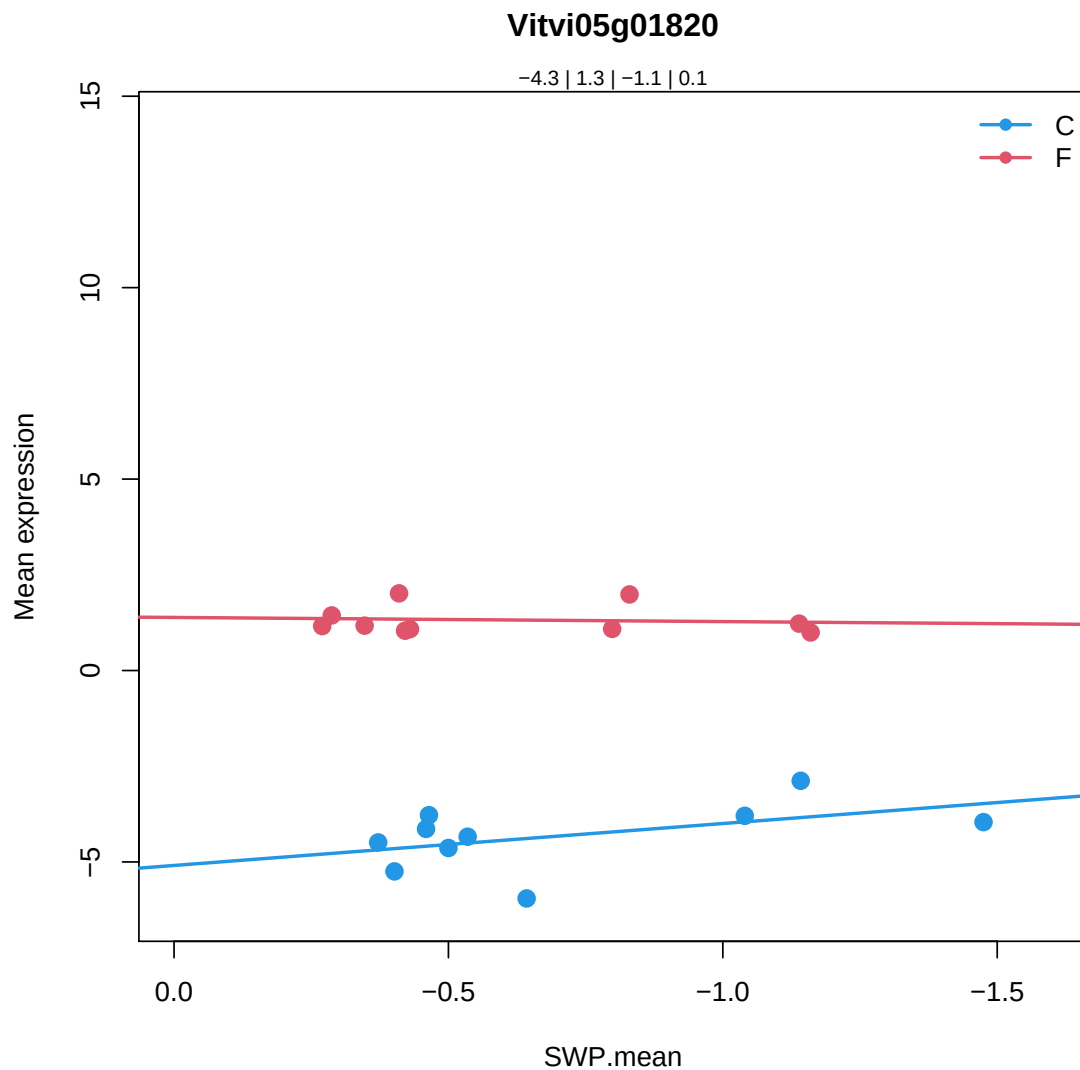
RNA-directed DNA polymerase (reverse transcriptase)-related family pro

Chr3:8789309-8790907 FORWARD LENGTH=532 |

201606

Coefficients for Vitvi05g01820.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-4.321537	1.221516e-16	***	2.614202e-16	***
SlopeC	-1.095343	0.04724099	*	0.4993392	
MeanF-MeanC	5.641628	6.341921e-16	***	9.570649e-14	***
SlopeF-SlopeC	1.203532	0.1348108		0.9999488	



7.4.87 Vitvi07g01569

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

```
Vitvi07g01569
```

```
26.24
```

```
misc.GCN5-related N-acetyltransferase
```

```
N-acetyl-l-glutamate synthase 1 |
```

```
Chr2:9749988-9752737 FORWARD LENGTH=609 |
```

```
201606
```

```
Vitvi07g01569
```

```
35.2
```

```
not assigned.unknown
```

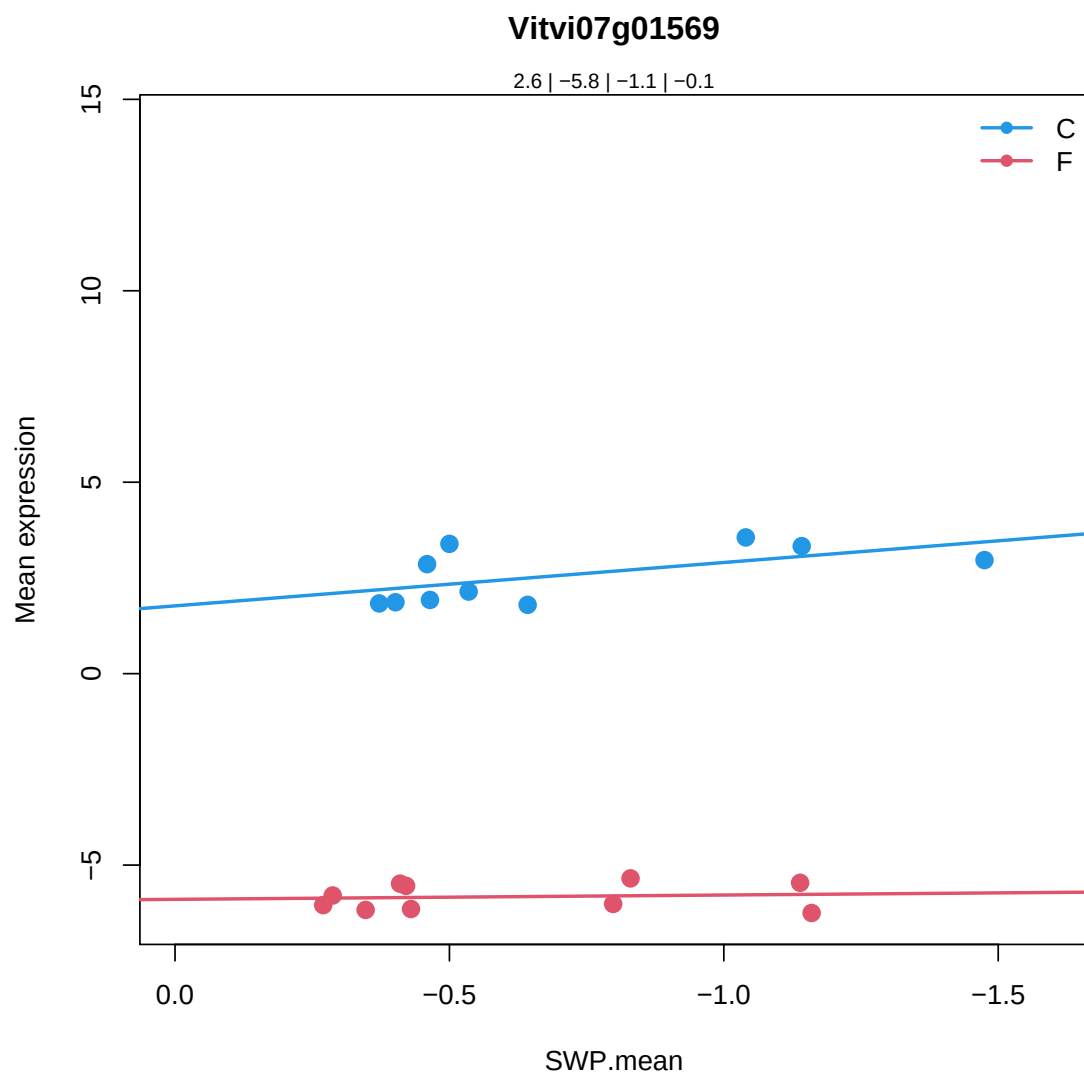
```
N-acetyl-l-glutamate synthase 1 |
```

```
Chr2:9749988-9752737 FORWARD LENGTH=609 |
```

```
201606
```

Coefficients for Vitvi07g01569.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.566733	1.653028e-13	***	2.497319e-13	***
SlopeC	-1.132495	0.01769768	*	0.3571759	
MeanF-MeanC	-8.39269	4.961717e-21	***	2.800981e-18	***
SlopeF-SlopeC	1.020438	0.1344627		0.9999488	



7.4.88 Vitvi04g00189

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

Vitvi04g00189

28.2

DNA.repair

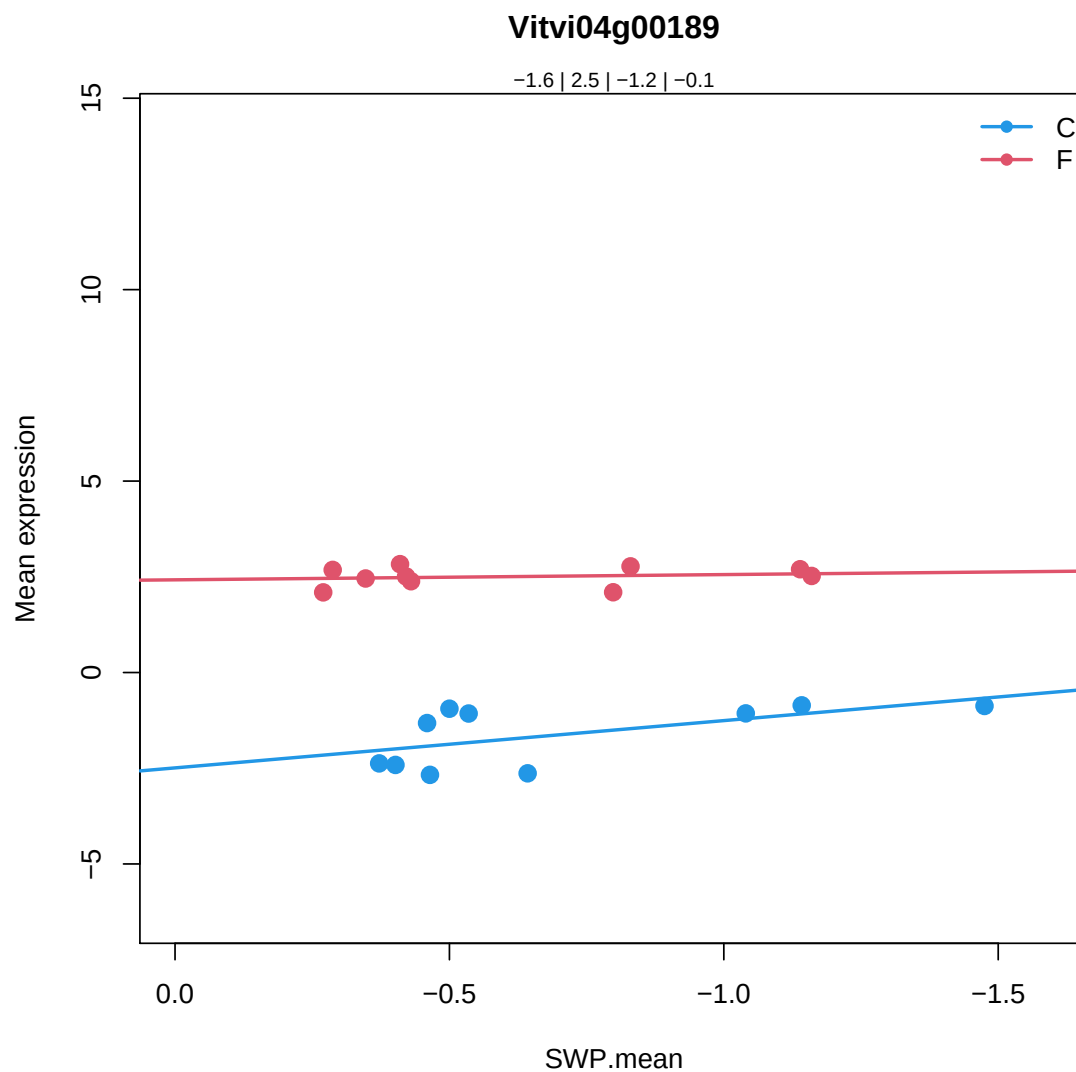
sterile alpha motif (SAM) domain-containing protein |

Chr2:18827761-18830505 REVERSE LENGTH=631 |

201606

Coefficients for Vitvi04g00189.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.622777	1.322004e-09	***	1.661169e-09	***
SlopeC	-1.235233	0.01153378	*	0.318473	
MeanF-MeanC	4.126921	1.686347e-14	***	2.072846e-12	***
SlopeF-SlopeC	1.098512	0.1134135		0.9999488	



7.4.89 Vitvi11g00990

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

Vitvi11g00990

35.2

not assigned.unknown

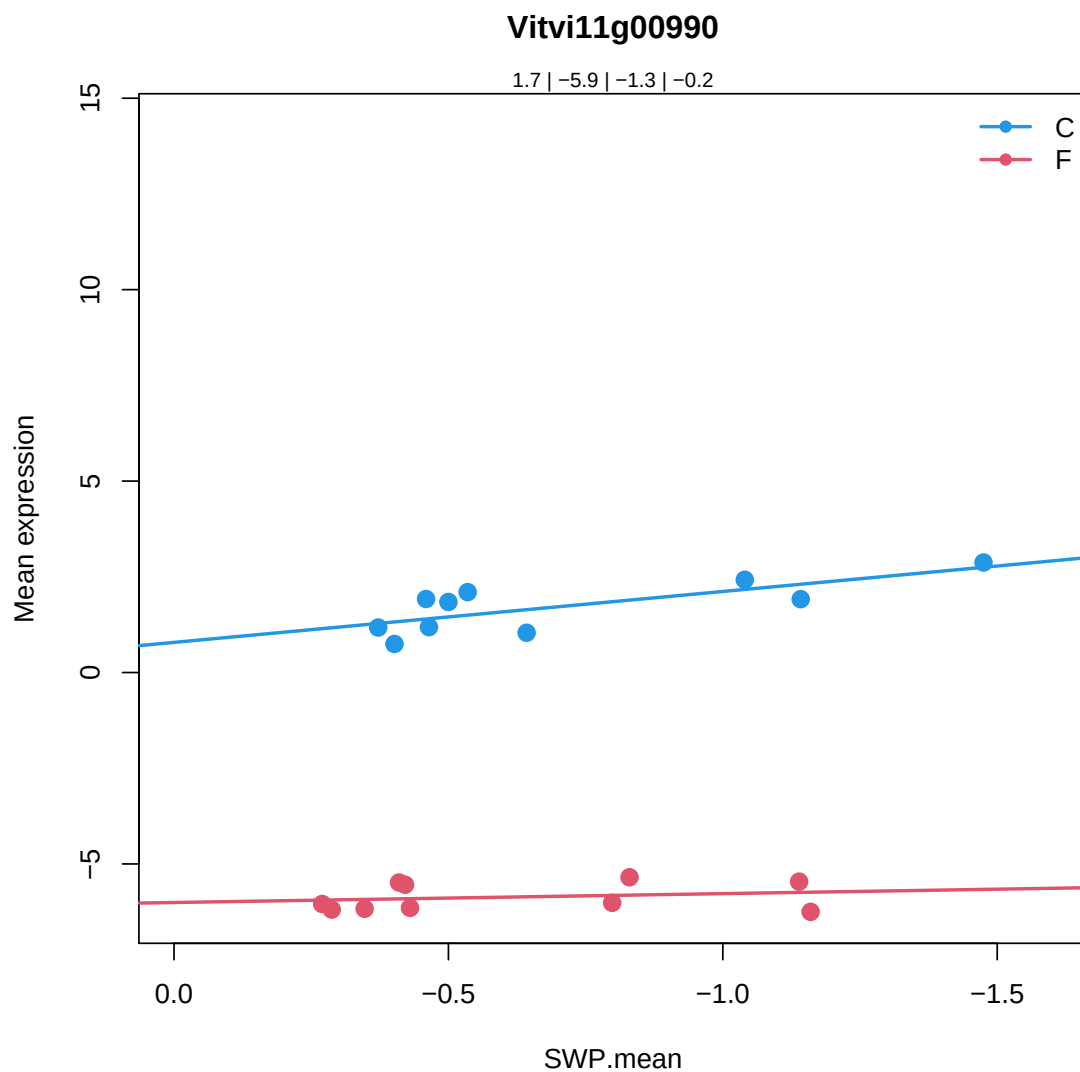
RING/U-box superfamily protein |

Chr2:8093469-8094452 FORWARD LENGTH=181 |

201606

Coefficients for Vitvi11g00990.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.721796	3.353624e-11	***	4.473259e-11	***
SlopeC	-1.330176	0.002501574	**	0.1896965	
MeanF-MeanC	-7.587376	2.924031e-21	***	1.714157e-18	***
SlopeF-SlopeC	1.098097	0.07117897	.	0.9999488	



7.4.90 Vitvi09g00038

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

Vitvi09g00038

26.28

misc.GDSL-motif lipase

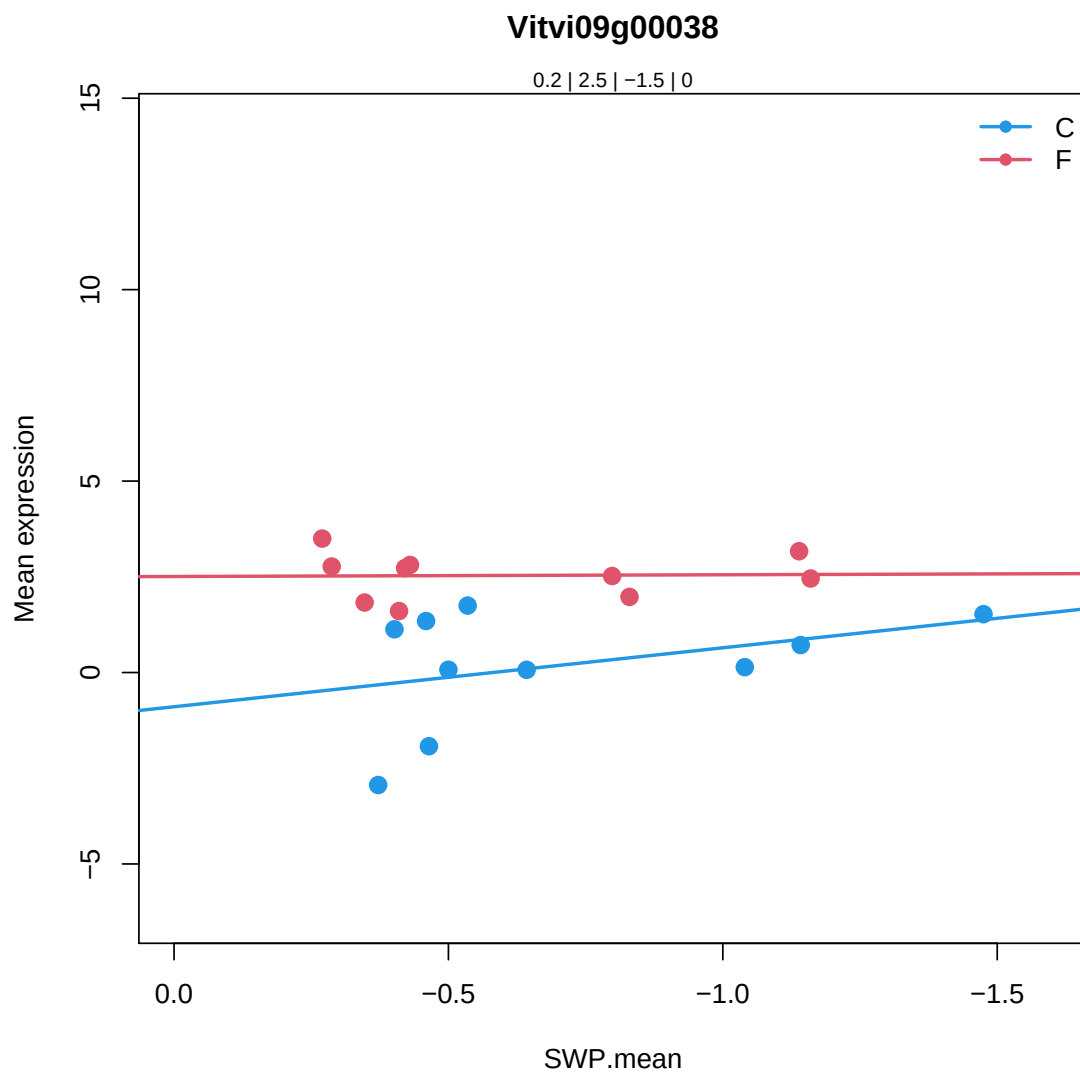
GDSL lipase 1 |

Chr5:16418920-16420400 FORWARD LENGTH=374 |

201606

Coefficients for Vitvi09g00038.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1883609	0.5662382		0.5720935	
SlopeC	-1.539814	0.1013475		0.6135572	
MeanF-MeanC	2.347224	4.113761e-05	***	0.0008326951	***
SlopeF-SlopeC	1.494714	0.2765741		0.9999488	



7.4.91 Vitvi14g00488

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

Vitvi14g00488

20.01.2007

stress.biotic.PR-proteins

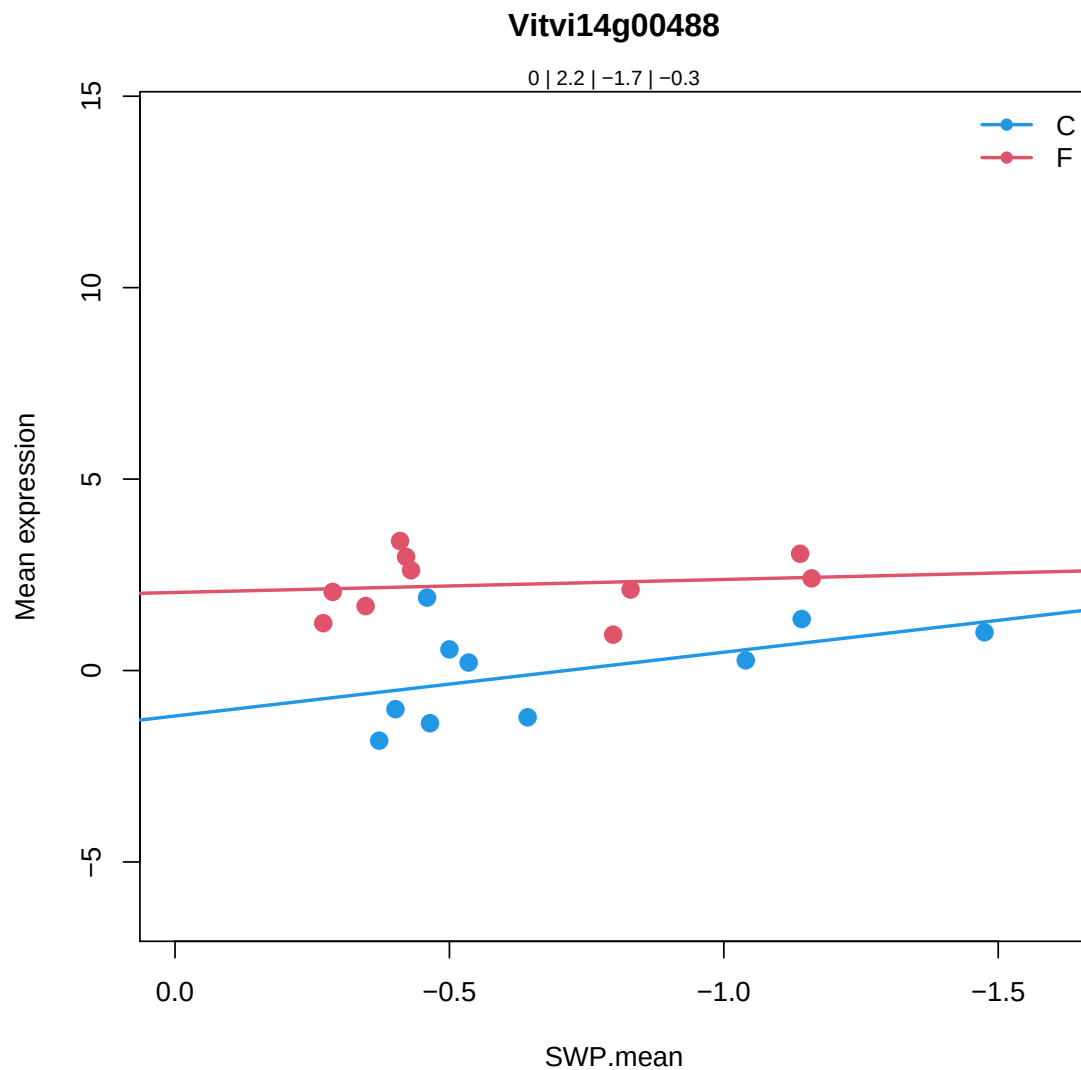
pathogenesis-related 4 |

Chr3:1285691-1286531 REVERSE LENGTH=212 |

201606

Coefficients for Vitvi14g00488.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.01658827	0.954802		0.9555543	
SlopeC	-1.665567	0.0507581	.	0.5104439	
MeanF-MeanC	2.2616	1.619289e-05	***	0.0003838445	***
SlopeF-SlopeC	1.326057	0.2805442		0.9999488	



7.4.92 Vitvi14g01560

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

Vitvi14g01560

34.18

transport.unspecified anions

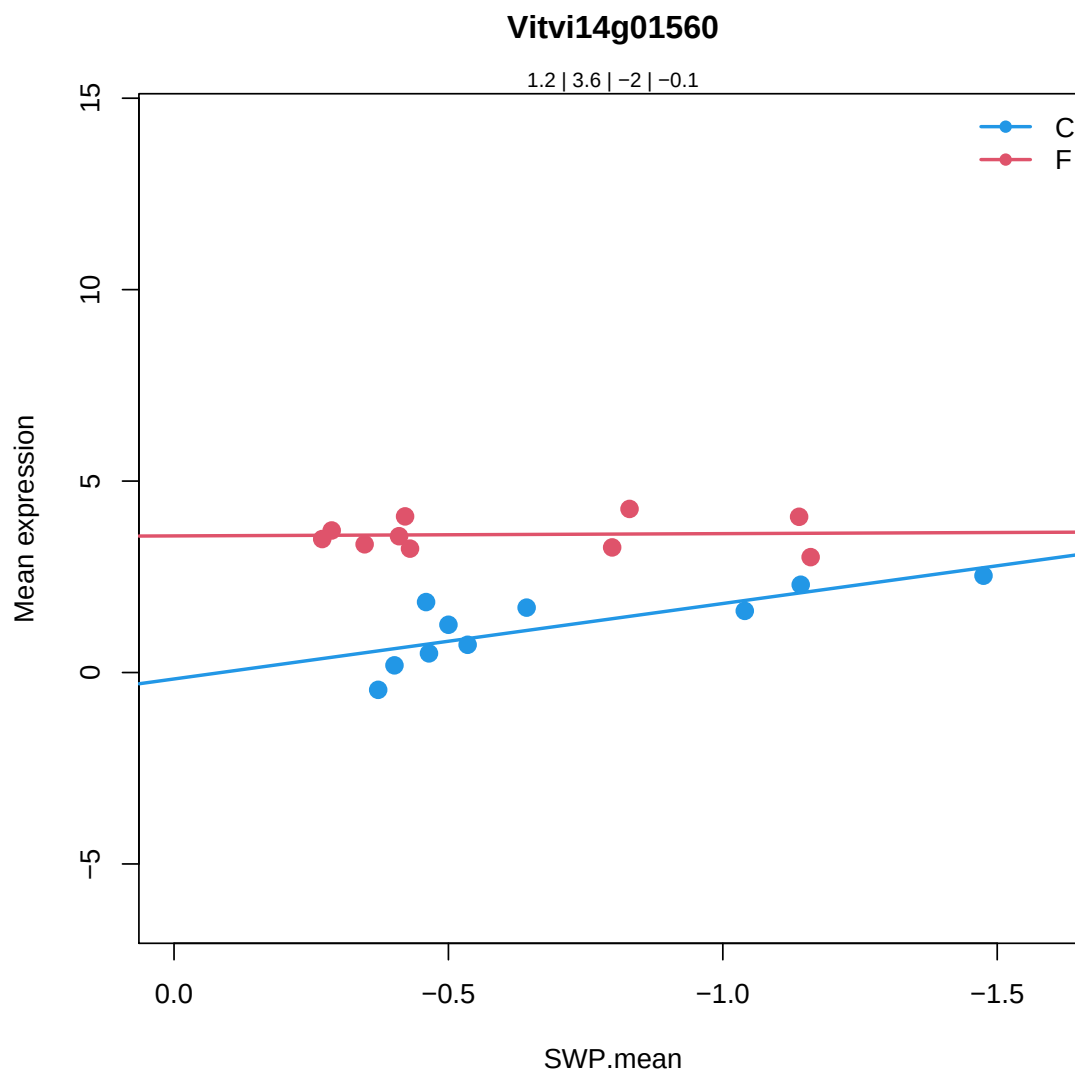
chloride channel B |

Chr3:10024147-10026921 FORWARD LENGTH=780 |

201606

Coefficients for Vitvi14g01560.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.217239	3.697346e-07	***	4.316072e-07	***
SlopeC	-1.971048	0.0003913296	***	0.09467692	.
MeanF-MeanC	2.386564	1.581577e-09	***	8.765963e-08	***
SlopeF-SlopeC	1.911944	0.01226789	*	0.9999488	



7.4.93 Vitvi01g01977

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

Vitvi01g01977

20.1

stress.biotic

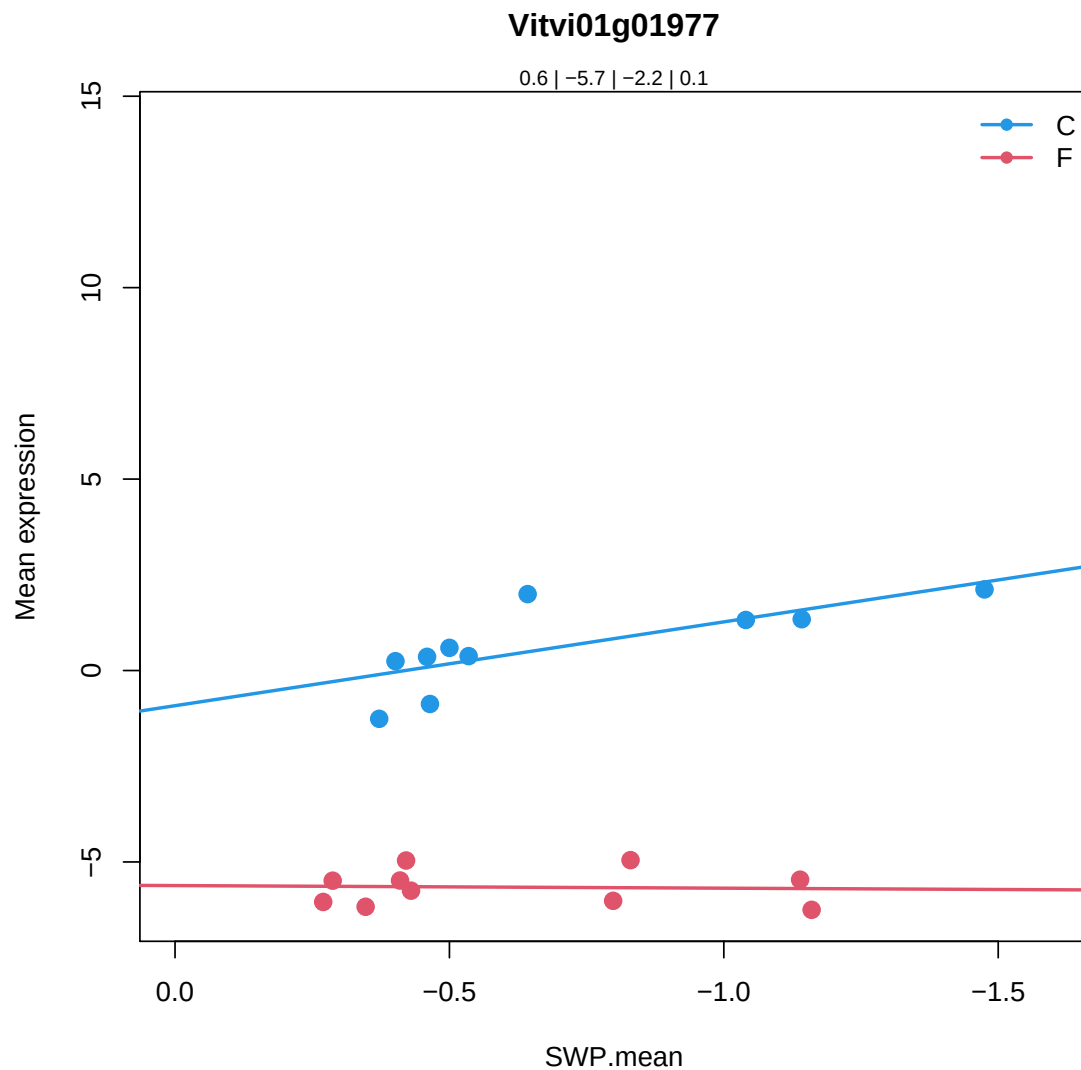
Polyketide cyclase/dehydrase and lipid transport superfamily protein |

Chr1:8198788-8199359 FORWARD LENGTH=148 |

201606

Coefficients for Vitvi01g01977.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6206962	0.004645355	**	0.004958298	**
SlopeC	-2.189318	0.0006200866	***	0.1005065	
MeanF-MeanC	-6.278969	1.930905e-16	***	3.344415e-14	***
SlopeF-SlopeC	2.257369	0.01121402	*	0.9999488	



7.4.94 Vitvi03g01431

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

Vitvi03g01431

26.7

misc.oxidases - copper, flavone etc

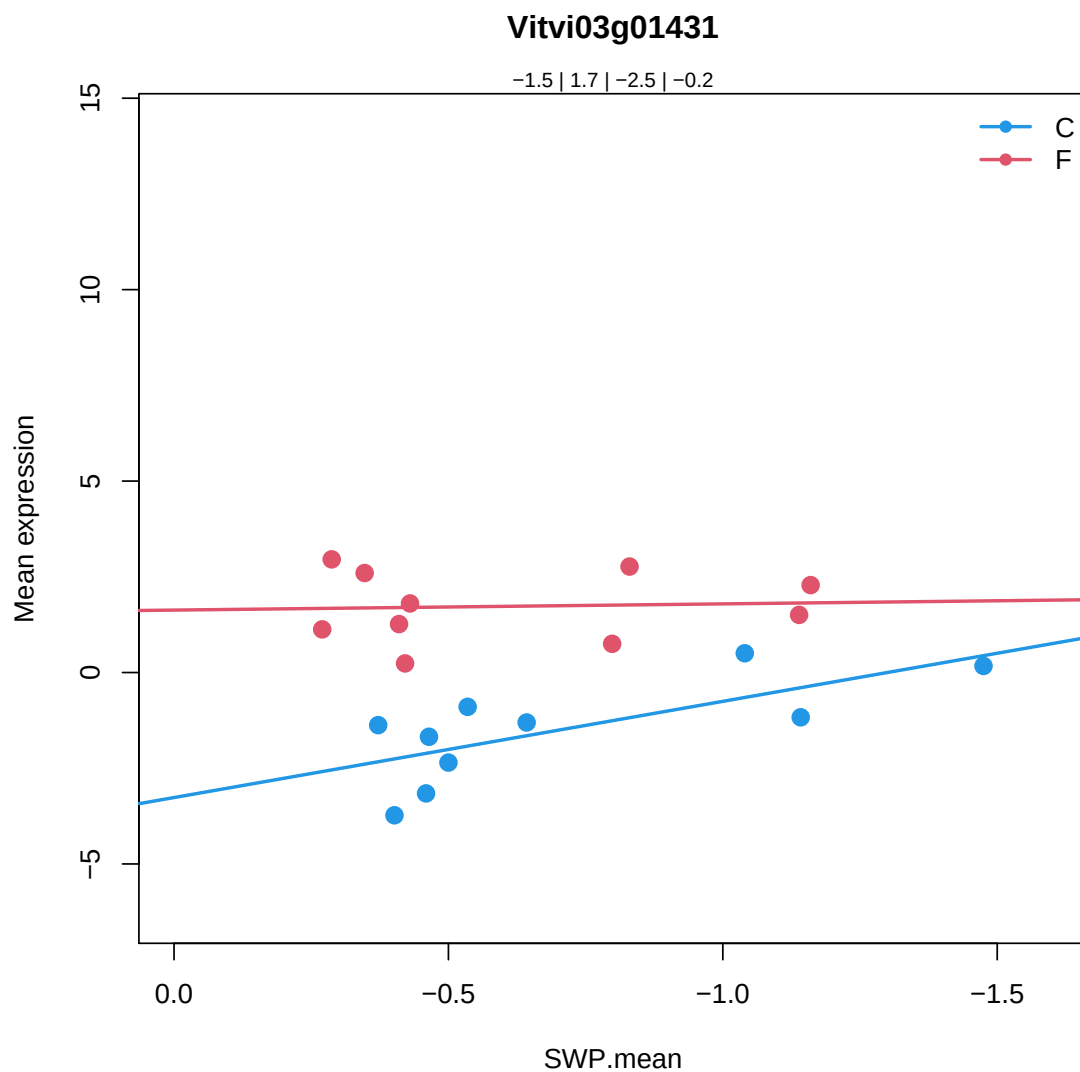
flavin-dependent monooxygenase 1 |

Chr1:6650656-6653053 REVERSE LENGTH=530 |

201606

Coefficients for Vitvi03g01431.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.498922	2.078617e-05	***	2.330265e-05	***
SlopeC	-2.513015	0.003608732	**	0.2248659	
MeanF-MeanC	3.228153	4.224193e-08	***	1.877118e-06	***
SlopeF-SlopeC	2.351136	0.05238461	.	0.9999488	



7.5 type4

7.5.1 Vitvi17g00601

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

Vitvi17g00601

17.06.2003

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

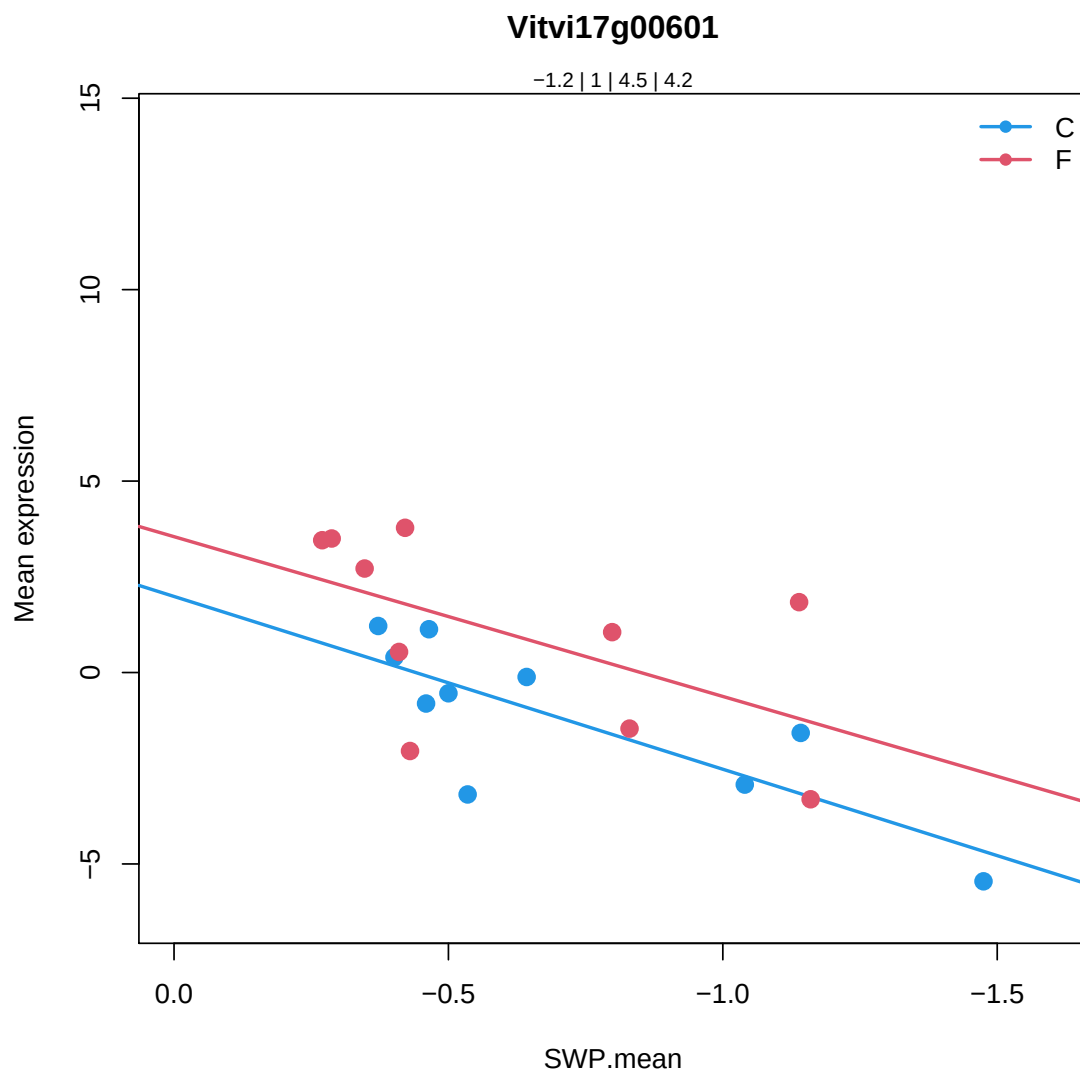
Gibberellin-regulated family protein |

Chr1:28053378-28053893 FORWARD LENGTH=101 |

201606

Coefficients for Vitvi17g00601.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.186615	0.02892715	*	0.03029669	*
SlopeC	4.512791	0.004217337	**	0.2376222	
MeanF-MeanC	2.192138	0.005867102	**	0.05151288	.
SlopeF-SlopeC	-0.3397197	0.8729075		0.9999488	



7.5.2 Vitvi05g01577

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

Vitvi05g01577

20.1.7.3

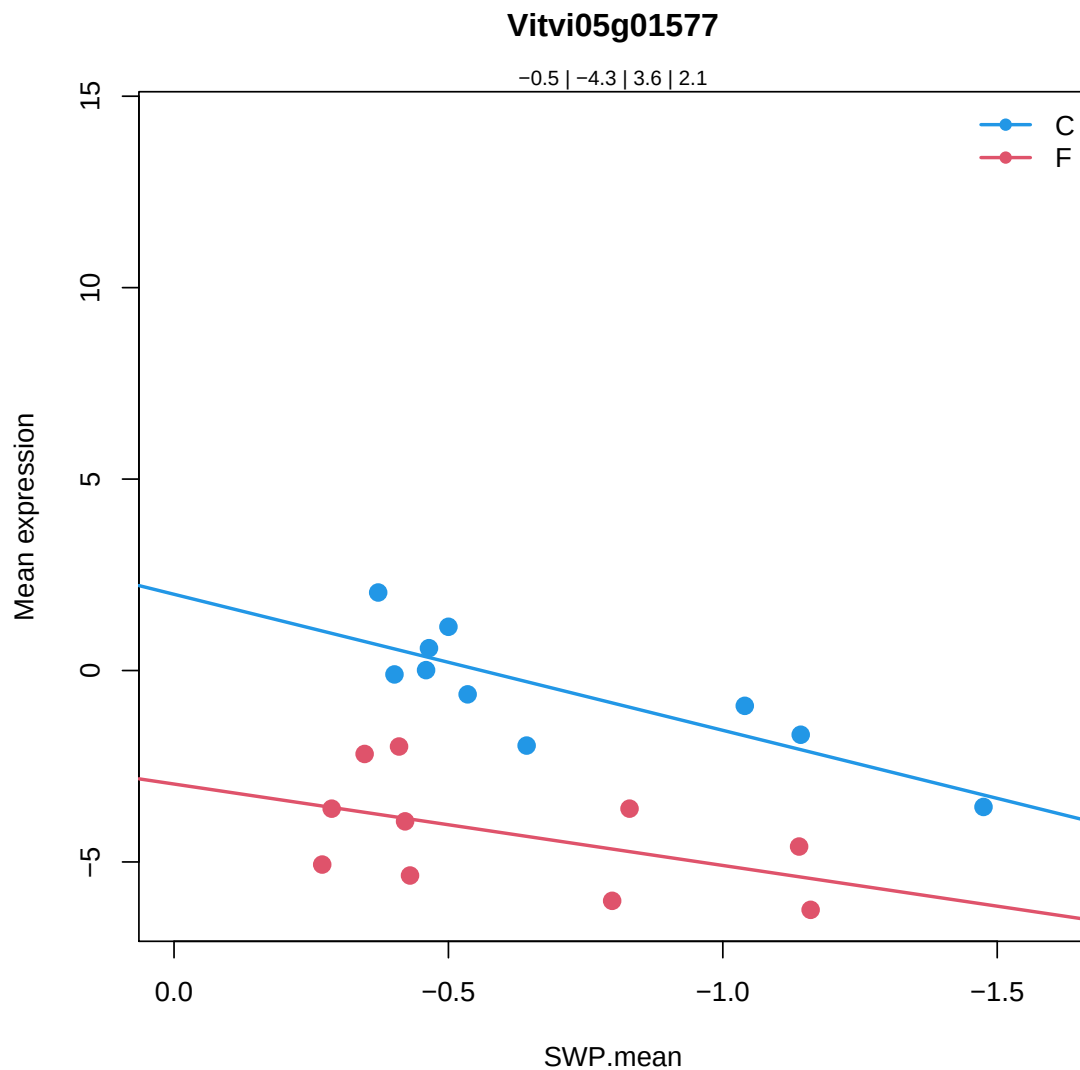
stress.biotic.PR-proteins.PR3/4/8/11 (chitinases and chitin binding pr
homolog of carrot EP3-3 chitinase |

Chr3:20145935-20147034 FORWARD LENGTH=273 |

201606

Coefficients for Vitvi05g01577.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.5075609	0.1396409		0.1438405	
SlopeC	3.553568	0.0008792532	***	0.118598	
MeanF-MeanC	-3.752991	6.802344e-08	***	2.920601e-06	***
SlopeF-SlopeC	-1.42671	0.3093121		0.9999488	



7.5.3 Vitvi09g01874

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

Vitvi09g01874

35.2

not assigned.unknown

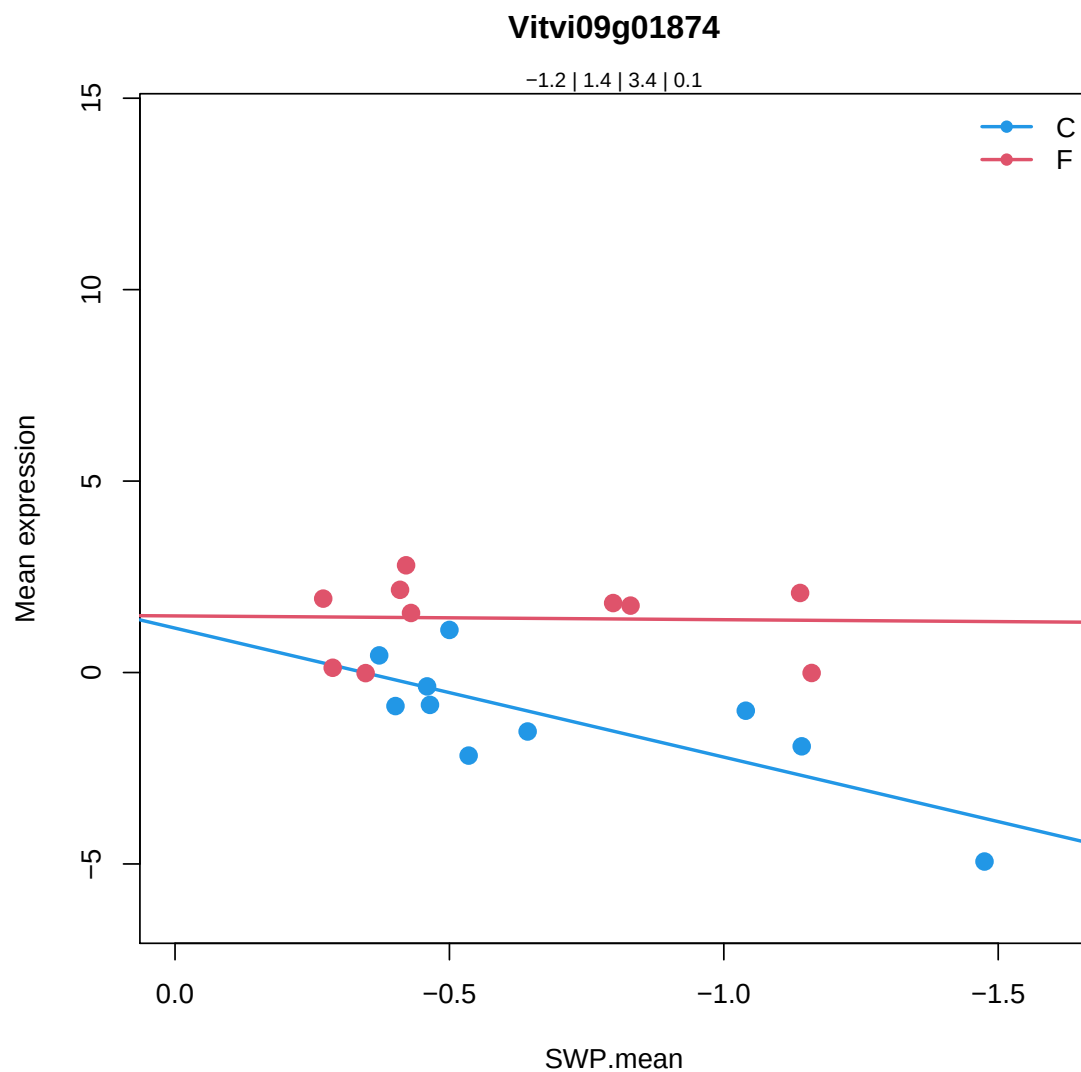
disease resistance family protein / LRR family protein |

Chr2:14737169-14739886 REVERSE LENGTH=905 |

201606

Coefficients for Vitvi09g01874.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.209693	0.0007634725	***	0.0008287763	***
SlopeC	3.369133	0.0007557867	***	0.1076608	
MeanF-MeanC	2.627733	5.179869e-06	***	0.0001389992	***
SlopeF-SlopeC	-3.270373	0.01811727	*	0.9999488	



7.5.4 Vitvi17g01596

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

```
Vitvi17g01596
```

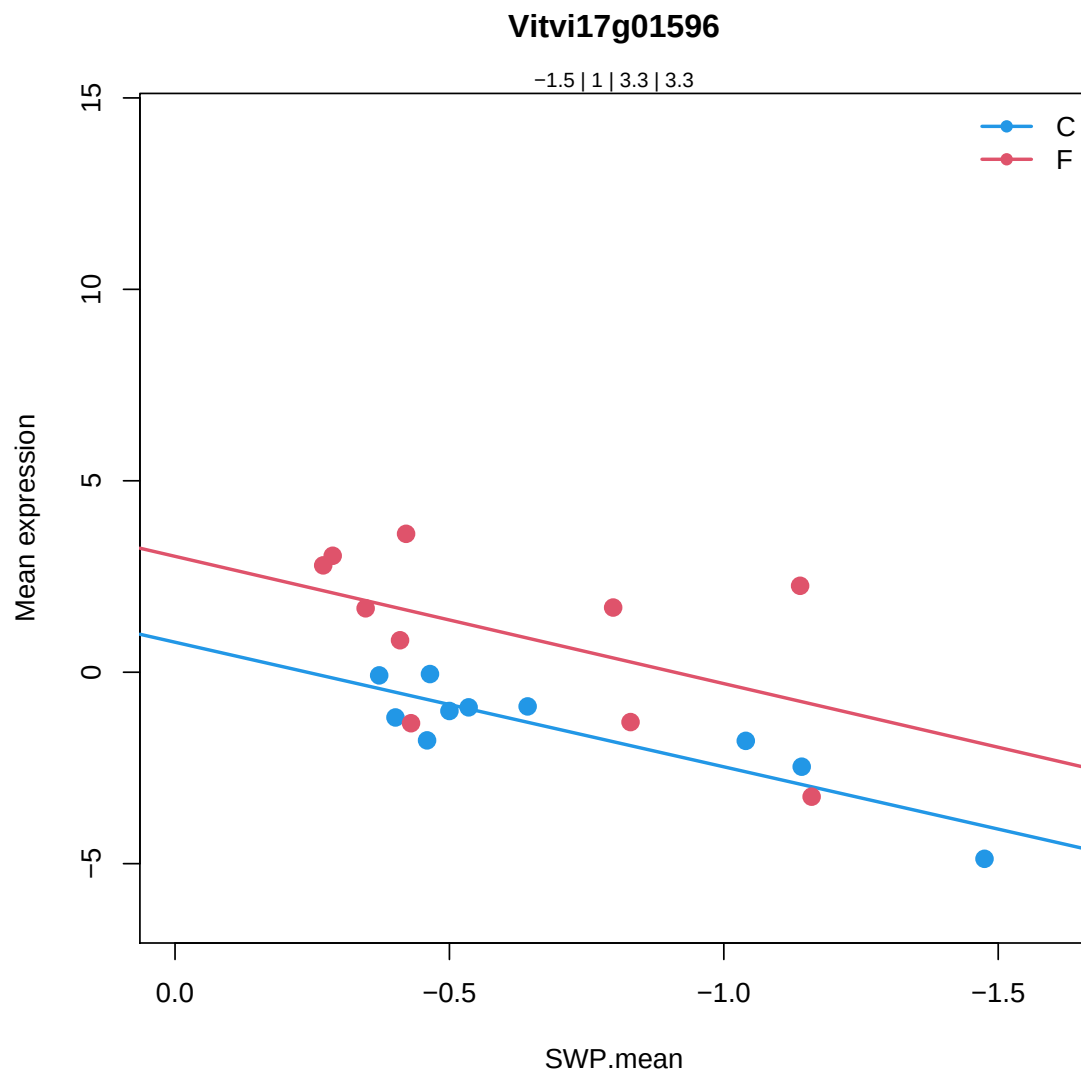
```
35.2
```

```
not assigned.unknown
```

```
NA
```

Coefficients for Vitvi17g01596.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.504888	0.00196087	**	0.002109513	**
SlopeC	3.254213	0.01212222	*	0.3229093	
MeanF-MeanC	2.506095	0.0004361519	***	0.006295291	**
SlopeF-SlopeC	0.07011039	0.9687282		0.9999488	



7.5.5 Vitvi07g00445

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

Vitvi07g00445

11.01.2009

lipid metabolism.FA synthesis and FA elongation.long chain fatty acid

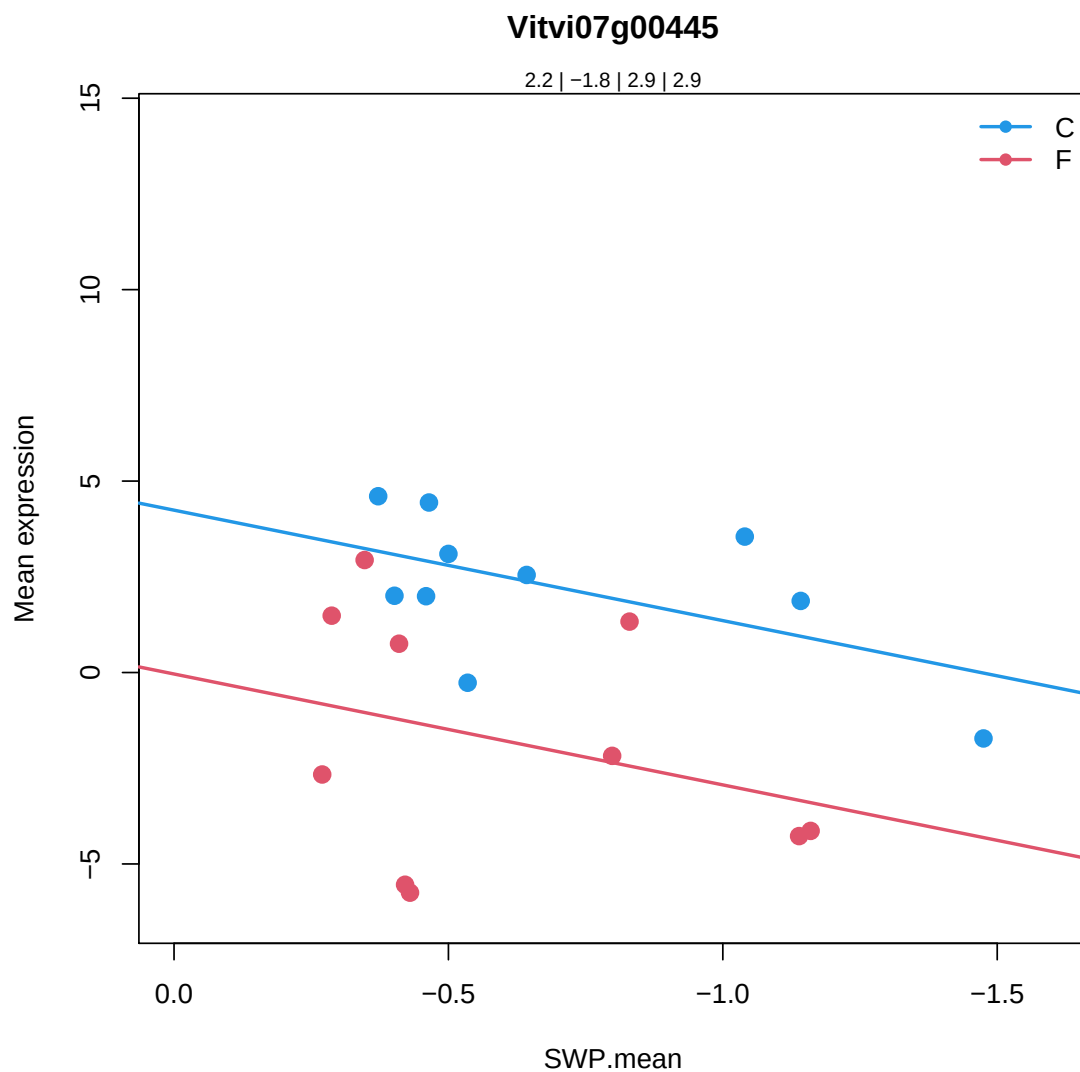
AMP-dependent synthetase and ligase family protein |

Chr2:19393835-19397616 FORWARD LENGTH=660 |

201606

Coefficients for Vitvi07g00445.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.211746	0.005213937	**	0.005558566	**
SlopeC	2.884577	0.1593951		0.6889929	
MeanF-MeanC	-4.015337	0.0006405182	***	0.008670318	**
SlopeF-SlopeC	0.01163635	0.9968841		0.9999488	



7.5.6 Vitvi18g01938

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

Vitvi18g01938

30.2.25

signalling.receptor kinases.wall associated kinase

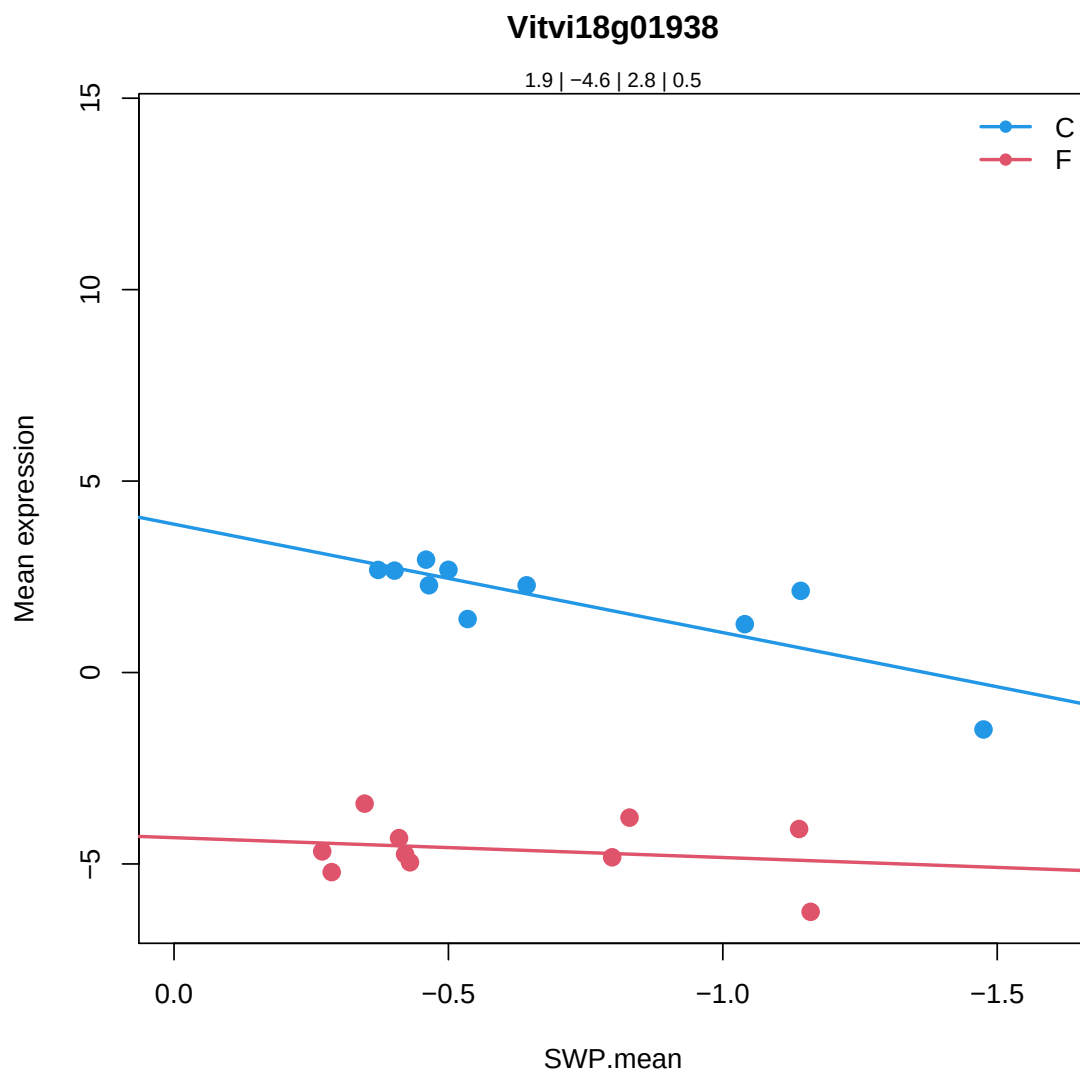
wall associated kinase 3 |

Chr1:7434303-7436702 FORWARD LENGTH=741 |

201606

Coefficients for Vitvi18g01938.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.88307	6.297909e-08	***	7.509993e-08	***
SlopeC	2.831106	0.0002667732	***	0.08298279	.
MeanF-MeanC	-6.512595	3.19492e-15	***	4.23452e-13	***
SlopeF-SlopeC	-2.313519	0.02603853	*	0.9999488	



7.5.7 Vitvi07g00586

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

Vitvi07g00586

29.05.2004

protein.degradation.aspartate protease

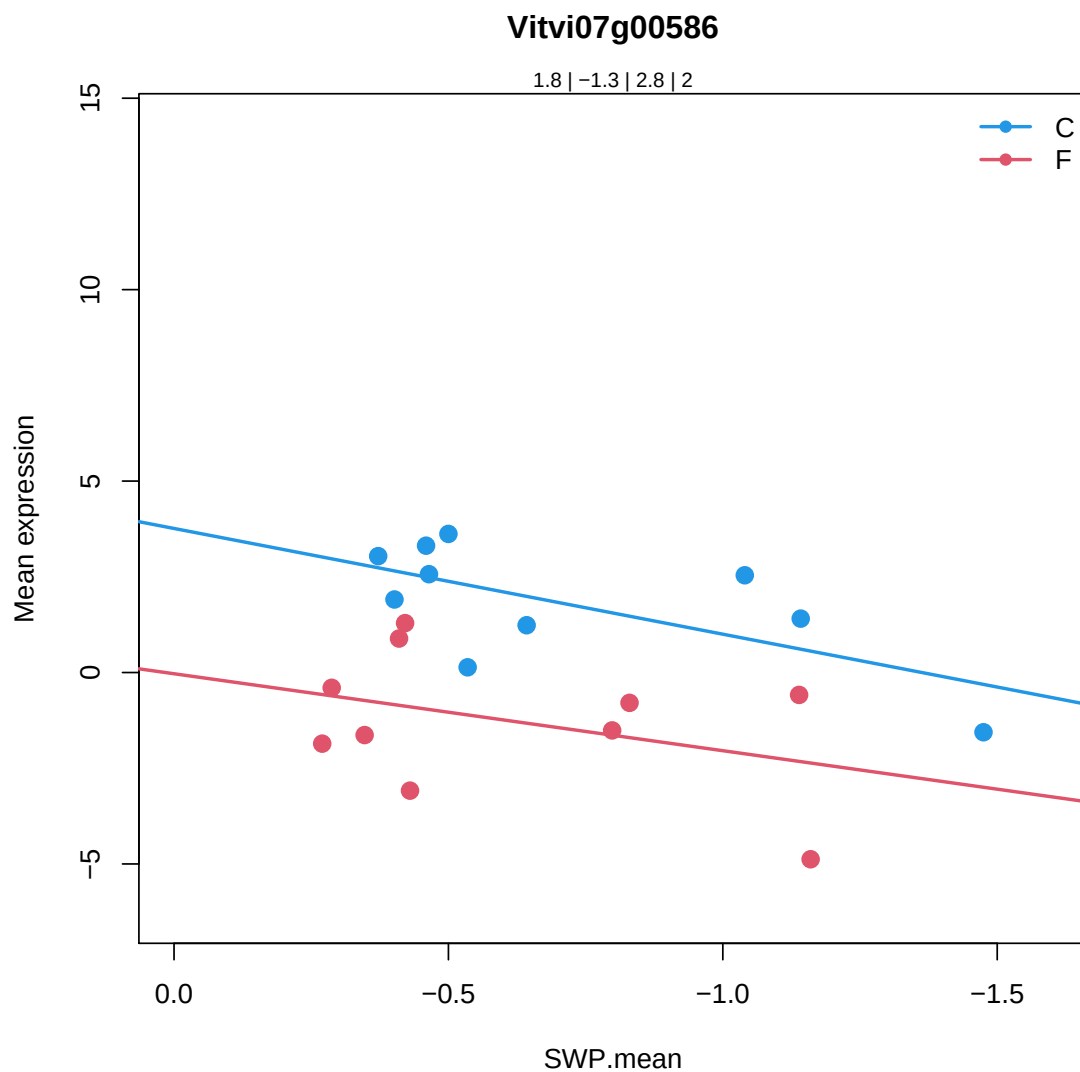
Eukaryotic aspartyl protease family protein |

Chr2:966506-967891 REVERSE LENGTH=461 |

201606

Coefficients for Vitvi07g00586.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.820575	0.0003499595	***	0.0003821523	***
SlopeC	2.761208	0.03074027	*	0.4322019	
MeanF-MeanC	-3.07708	4.782582e-05	***	0.0009503821	***
SlopeF-SlopeC	-0.7514262	0.6766004		0.9999488	



7.5.8 Vitvi16g02090

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

Vitvi16g02090

35.2

not assigned.unknown

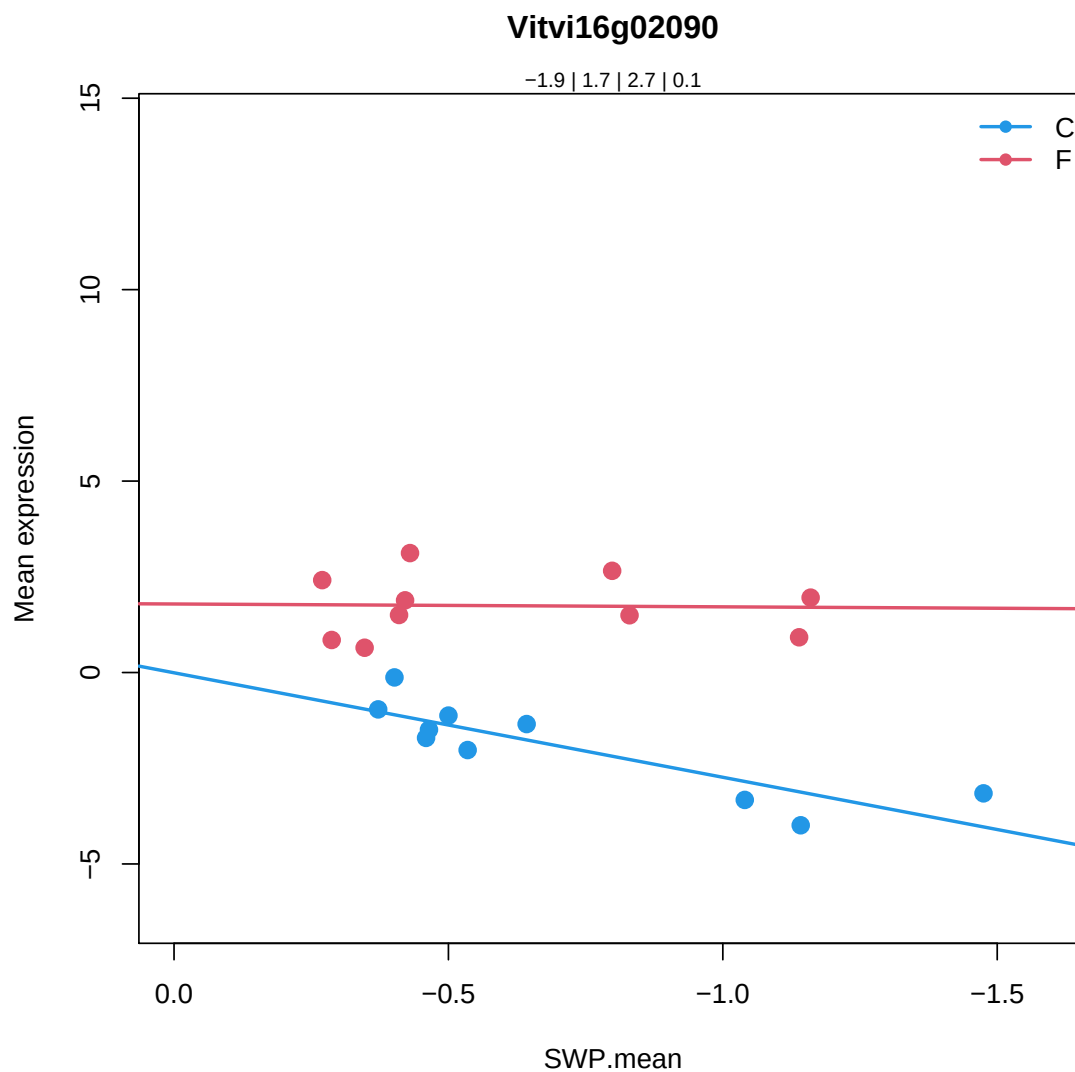
PR5-like receptor kinase |

Chr5:15293325-15295838 REVERSE LENGTH=665 |

201606

Coefficients for Vitvi16g02090.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.926199	2.28078e-08	***	2.753775e-08	***
SlopeC	2.729033	0.0002614243	***	0.08298279	.
MeanF-MeanC	3.670552	1.144627e-10	***	7.8943e-09	***
SlopeF-SlopeC	-2.654757	0.009425042	**	0.9999488	



7.5.9 Vitvi18g02709

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

Vitvi18g02709

35.1.40

not assigned.no ontology.glycine rich proteins

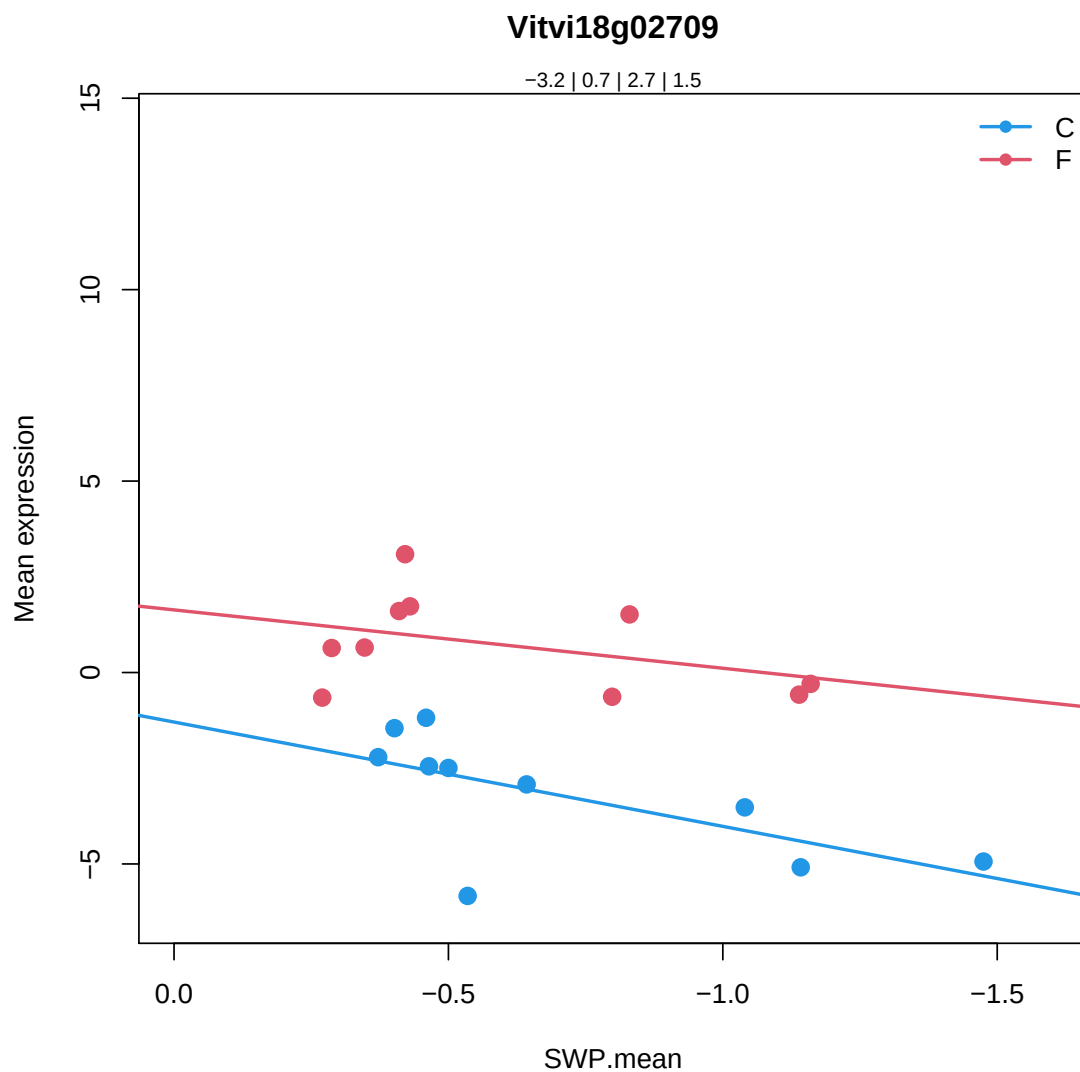
Cupredoxin superfamily protein |

Chr2:6873666-6874701 REVERSE LENGTH=257 |

201606

Coefficients for Vitvi18g02709.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-3.209467	8.027118e-09	***	9.824888e-09	***
SlopeC	2.724042	0.01110047	*	0.3143947	
MeanF-MeanC	3.91652	9.423432e-08	***	3.871481e-06	***
SlopeF-SlopeC	-1.199916	0.4198128		0.9999488	



7.5.10 Vitvi16g01470

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

Vitvi16g01470

35.2

not assigned.unknown

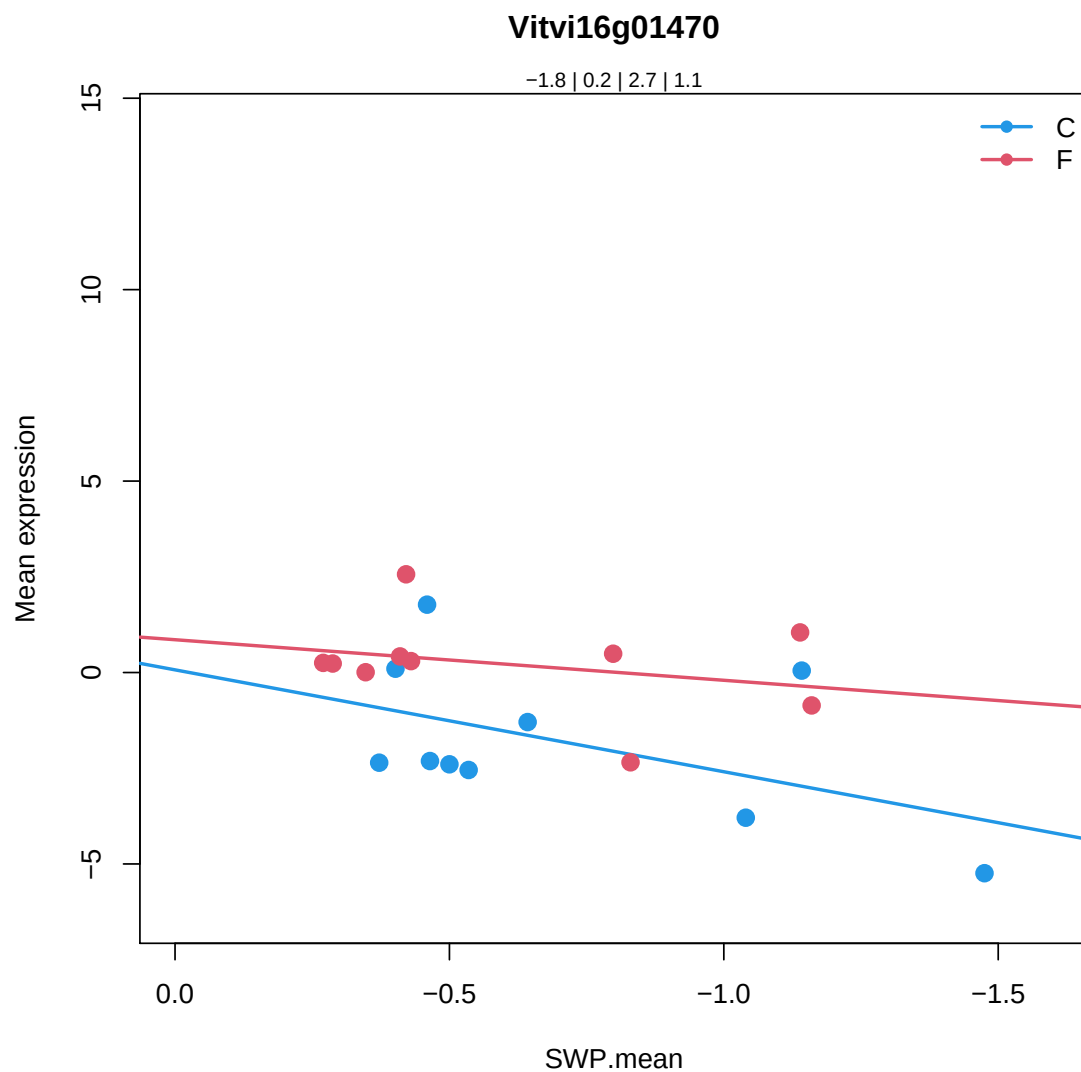
Chalcone and stilbene synthase family protein |

Chr5:4488762-4490035 FORWARD LENGTH=395 |

201606

Coefficients for Vitvi16g01470.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.801762	0.0005550164	***	0.0006037799	***
SlopeC	2.661094	0.04304173	*	0.48214	
MeanF-MeanC	2.012758	0.004222528	**	0.03986124	*
SlopeF-SlopeC	-1.601562	0.3941009		0.9999488	



7.5.11 Vitvi09g00258

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

```
Vitvi09g00258
```

```
30.2.1
```

```
signalling.receptor kinases.leucine rich repeat I
```

```
root hair specific 6 |
```

```
Chr1:19270193-19274122 REVERSE LENGTH=890 |
```

```
201606
```

```
Vitvi09g00258
```

```
29.4
```

```
protein.postranslational modification
```

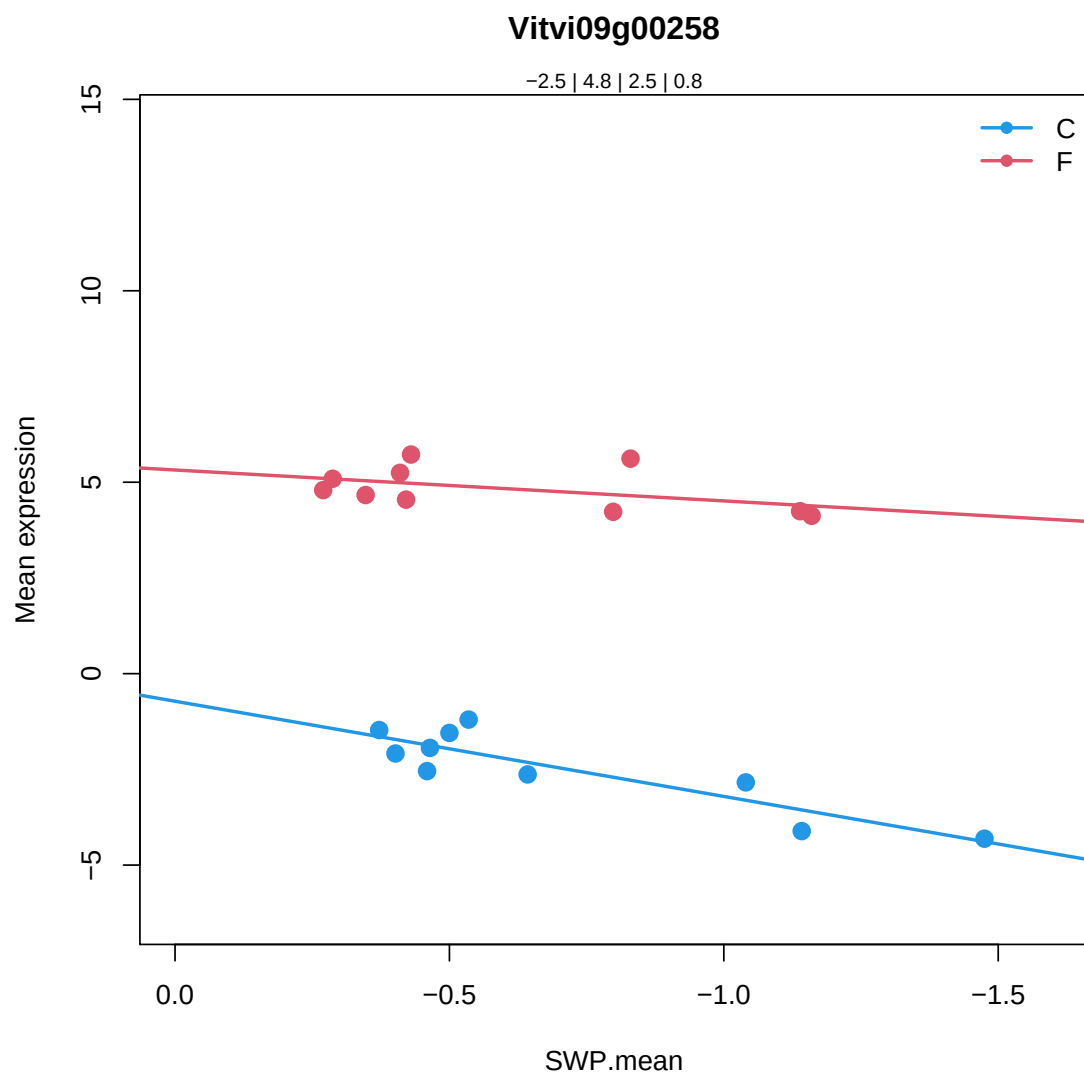
```
root hair specific 6 |
```

```
Chr1:19270193-19274122 REVERSE LENGTH=890 |
```

```
201606
```

Coefficients for Vitvi09g00258.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-2.468524	6.812044e-13	***	9.893204e-13	***
SlopeC	2.485974	1.903022e-05	***	0.04768143	*
MeanF-MeanC	7.295481	1.887833e-19	***	5.860462e-17	***
SlopeF-SlopeC	-1.678231	0.02167859	*	0.9999488	



7.5.12 Vitvi09g01932

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

Vitvi09g01932

20.01.2002

stress.biotic.receptors

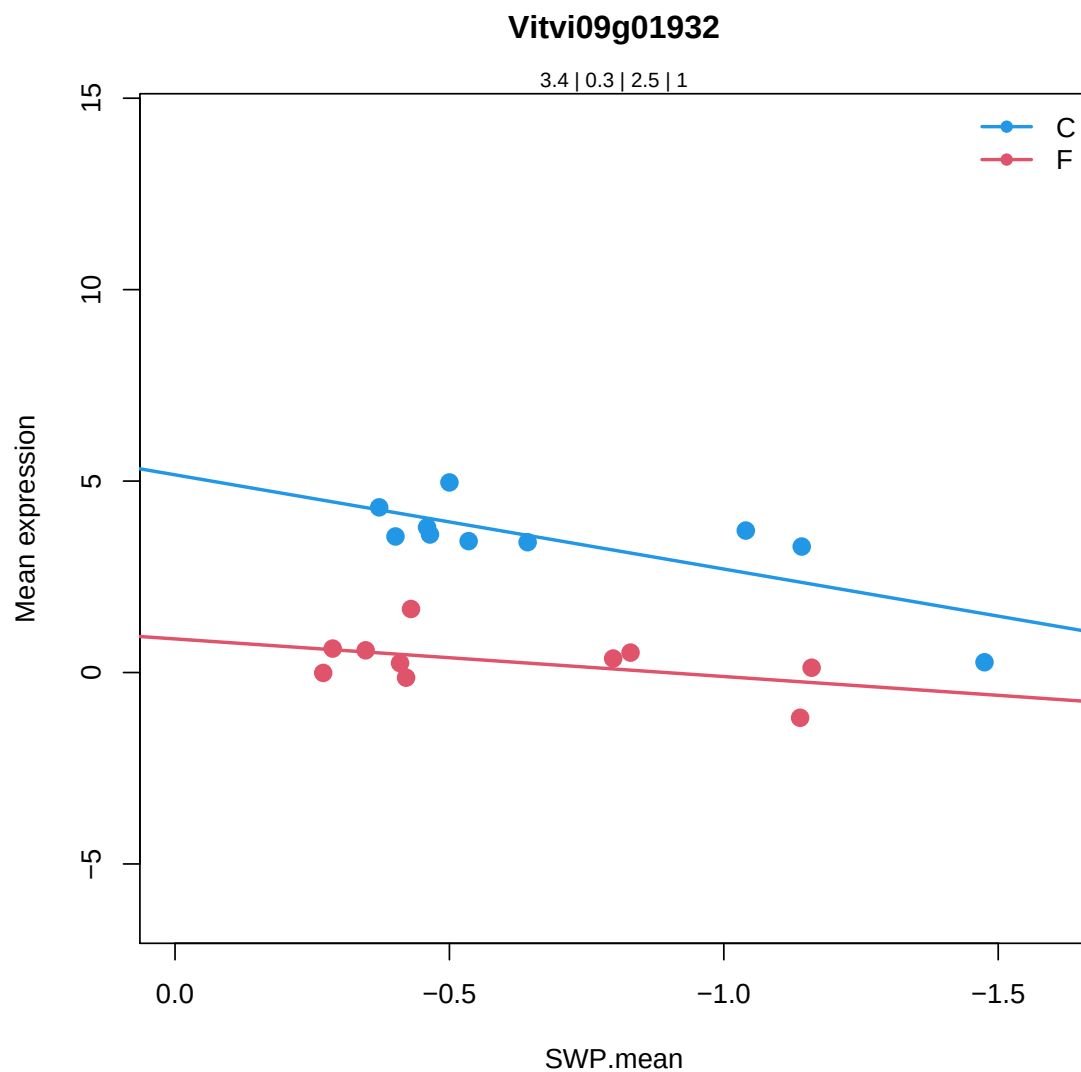
disease resistance family protein / LRR family protein |

Chr2:14737169-14739886 REVERSE LENGTH=905 |

201606

Coefficients for Vitvi09g01932.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.433029	3.782626e-13	***	5.580756e-13	***
SlopeC	2.460612	0.000623382	***	0.1005065	
MeanF-MeanC	-3.153777	1.327157e-09	***	7.464401e-08	***
SlopeF-SlopeC	-1.478196	0.120754		0.9999488	



7.5.13 Vitvi03g00318

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

Vitvi03g00318

27.03.2025

RNA.regulation of transcription.MYB domain transcription factor family

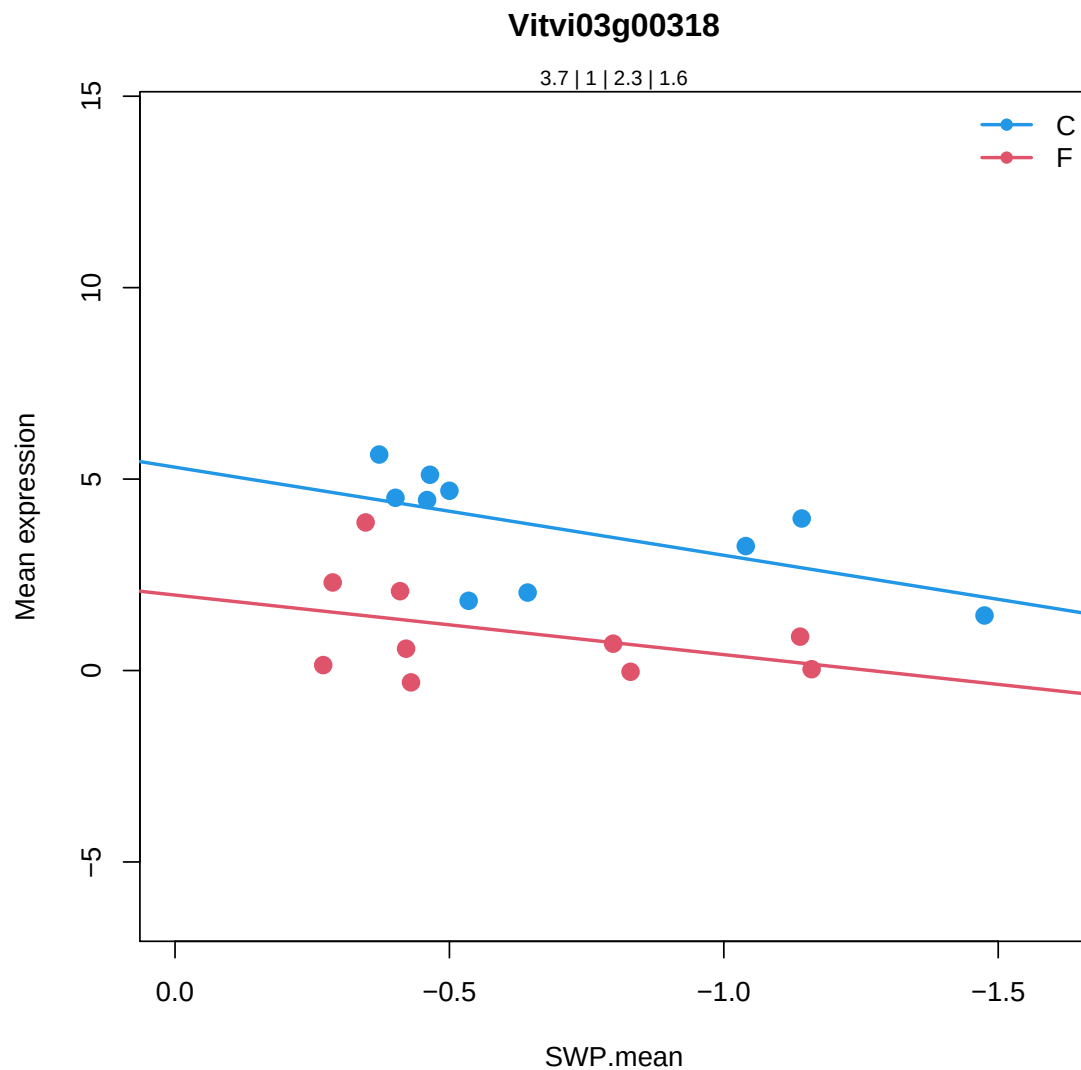
RAD-like 6 |

Chr1:28245073-28245453 REVERSE LENGTH=126 |

201606

Coefficients for Vitvi03g00318.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.692558	8.664173e-10	***	1.094475e-09	***
SlopeC	2.300824	0.03059091	*	0.4321285	
MeanF-MeanC	-2.669643	2.876014e-05	***	0.0006253381	***
SlopeF-SlopeC	-0.7449947	0.6196467		0.9999488	



7.5.14 Vitvi16g02003

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

Vitvi16g02003

35.2

not assigned.unknown

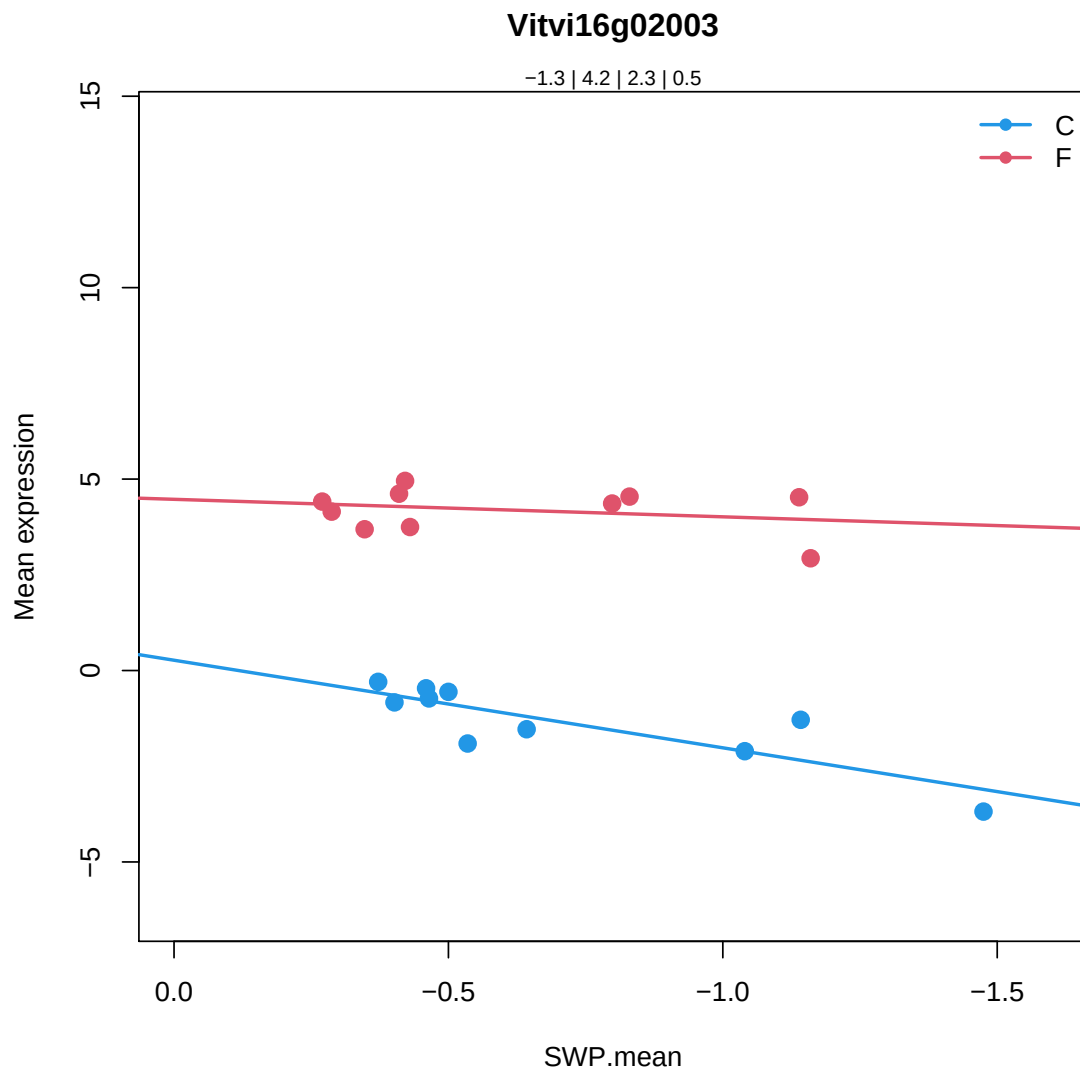
PR5-like receptor kinase |

Chr5:15293325-15295838 REVERSE LENGTH=665 |

201606

Coefficients for Vitvi16g02003.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.339973	2.33912e-07	***	2.745485e-07	***
SlopeC	2.2875	0.000164243	***	0.07644173	.
MeanF-MeanC	5.532948	4.544274e-16	***	7.214982e-14	***
SlopeF-SlopeC	-1.830222	0.02298766	*	0.9999488	



7.5.15 Vitvi16g01548

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

Vitvi16g01548

35.2

not assigned.unknown

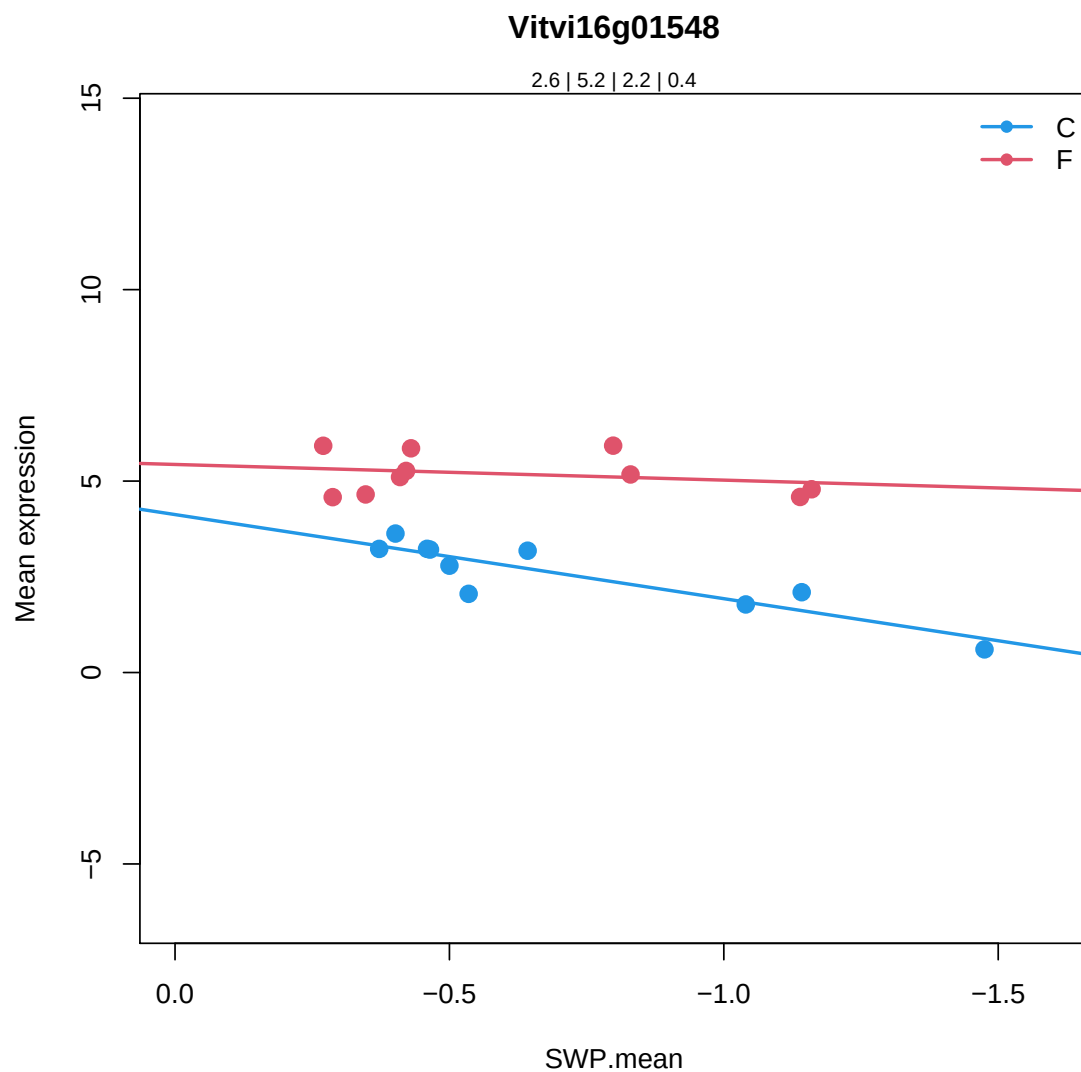
dihydroflavonol 4-reductase |

Chr5:17164296-17165864 REVERSE LENGTH=382 |

201606

Coefficients for Vitvi16g01548.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.580398	1.607866e-13	***	2.431742e-13	***
SlopeC	2.196869	6.152636e-05	***	0.07213729	.
MeanF-MeanC	2.60436	1.084352e-10	***	7.546893e-09	***
SlopeF-SlopeC	-1.787469	0.0128491	*	0.9999488	



7.5.16 Vitvi03g01503

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

Vitvi03g01503

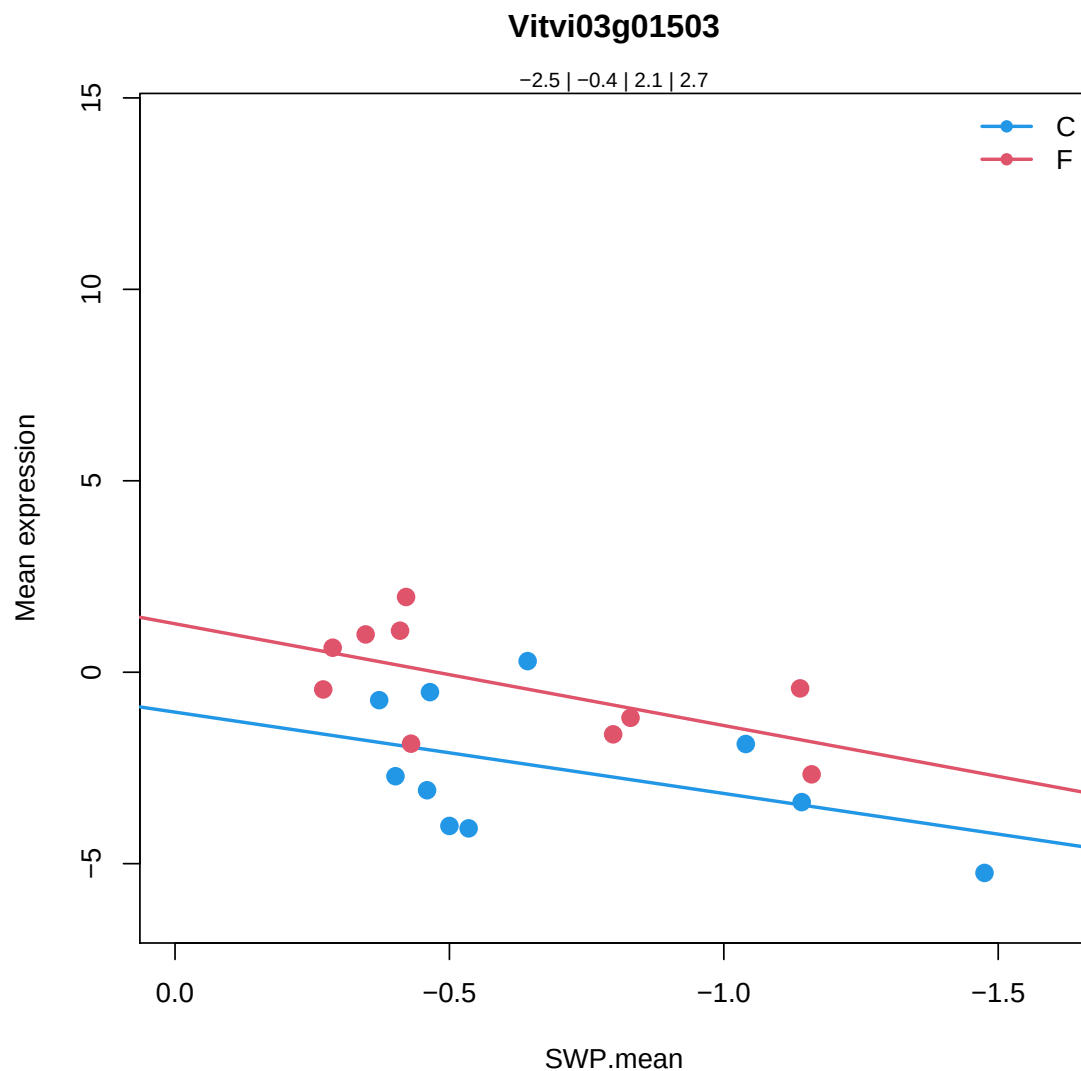
35.2

not assigned.unknown

Organ-specific protein S2

Coefficients for Vitvi03g01503.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-2.536121	4.151528e-06	***	4.725735e-06	***
SlopeC	2.124611	0.07938146	.	0.5748584	
MeanF-MeanC	2.181984	0.00122855	**	0.01484977	*
SlopeF-SlopeC	0.5331686	0.7591512		0.9999488	



7.5.17 Vitvi09g00681

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

Vitvi09g00681

20.01.2002

stress.biotic.receptors

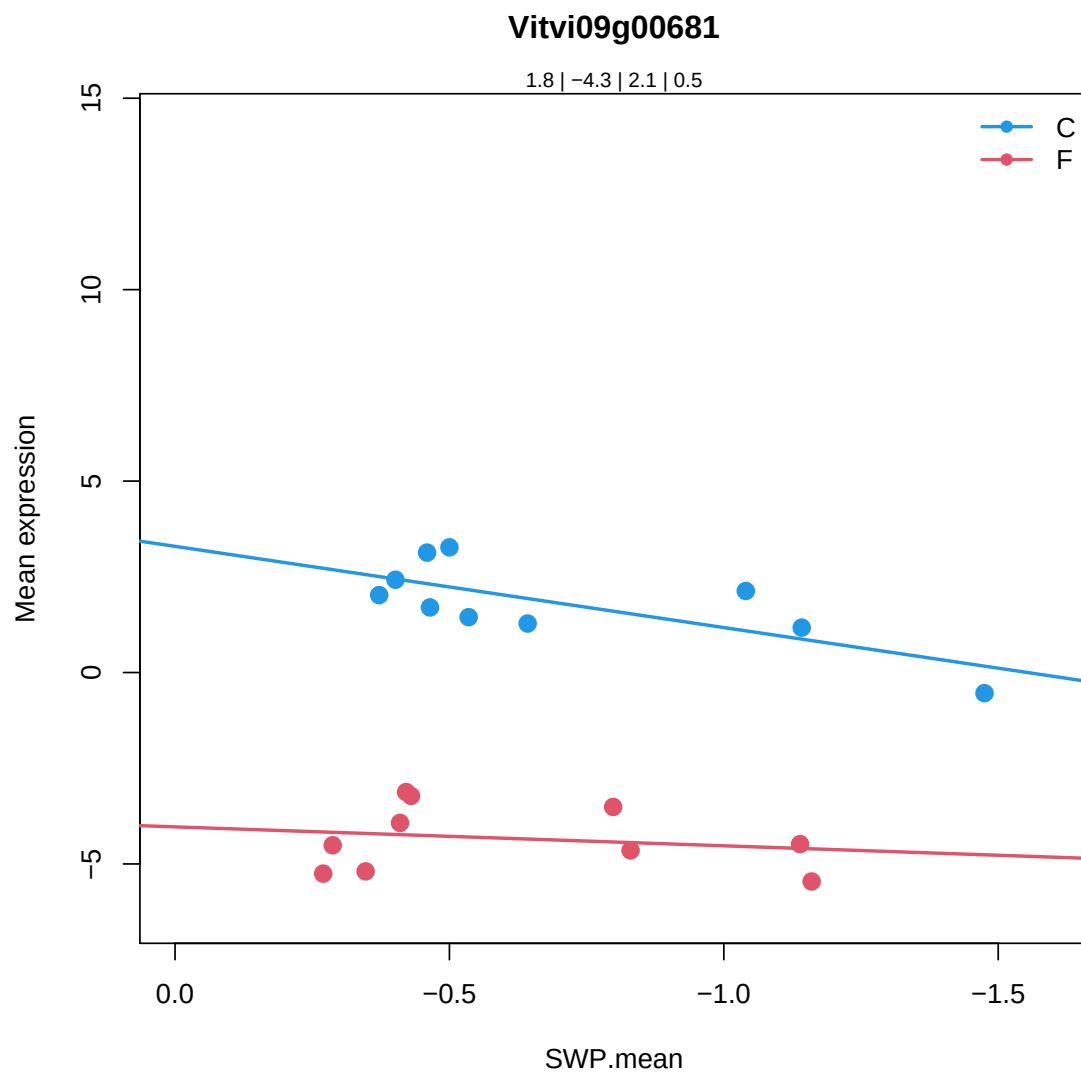
receptor like protein 1 |

Chr1:2270633-2274654 FORWARD LENGTH=913 |

201606

Coefficients for Vitvi09g00681.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.80362	2.175092e-07	***	2.556307e-07	***
SlopeC	2.121009	0.004715187	**	0.2454895	
MeanF-MeanC	-6.136671	2.131152e-14	***	2.537736e-12	***
SlopeF-SlopeC	-1.626761	0.1188241		0.9999488	



7.5.18 Vitvi10g01685

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

Vitvi10g01685

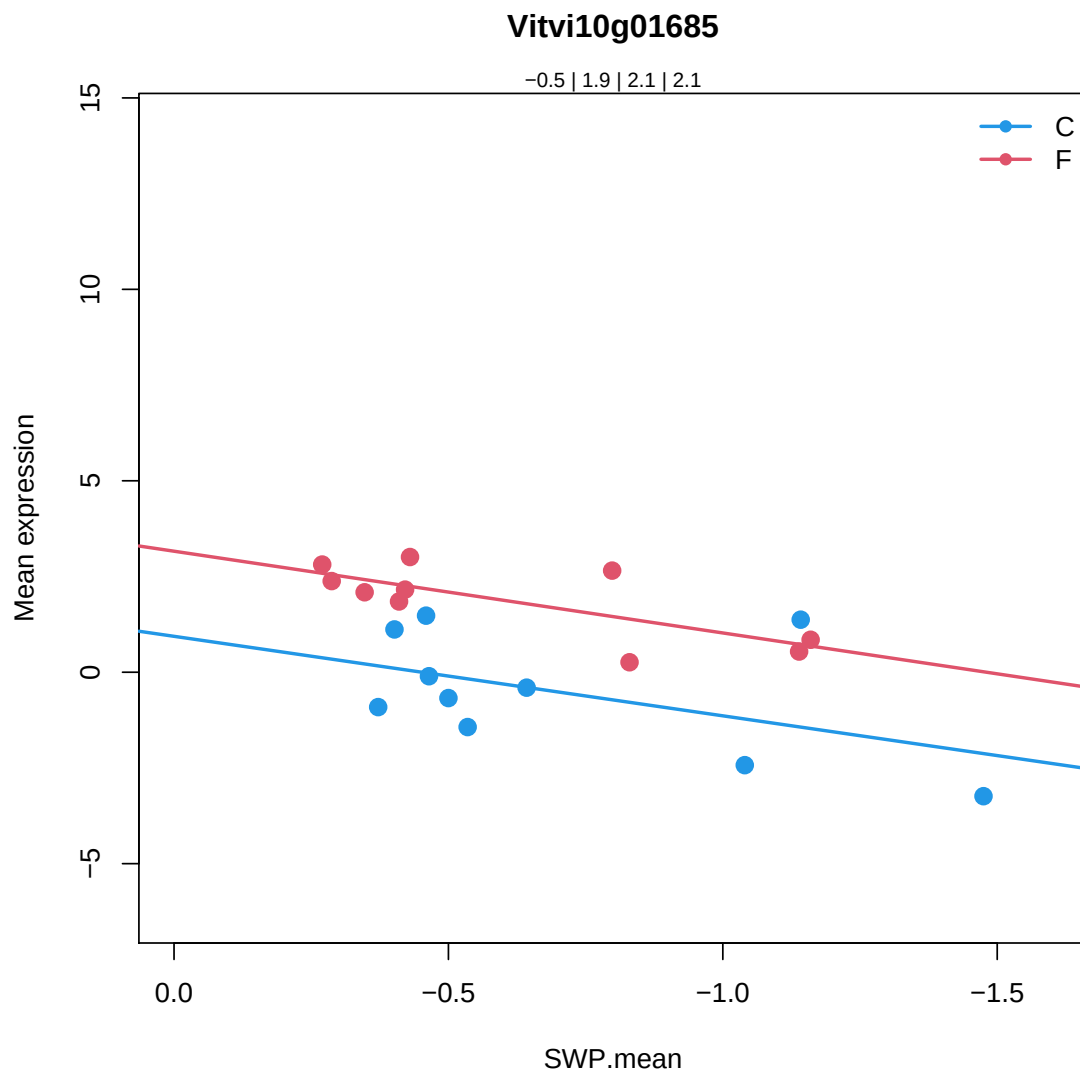
35.2

not assigned.unknown

NA

Coefficients for Vitvi10g01685.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.5224823	0.1171482		0.1209328	
SlopeC	2.076279	0.02951921	*	0.4299803	
MeanF-MeanC	2.382122	3.023132e-05	***	0.0006517479	***
SlopeF-SlopeC	0.05856843	0.9651568		0.9999488	



7.5.19 Vitvi16g01251

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

Vitvi16g01251

35.2

not assigned.unknown

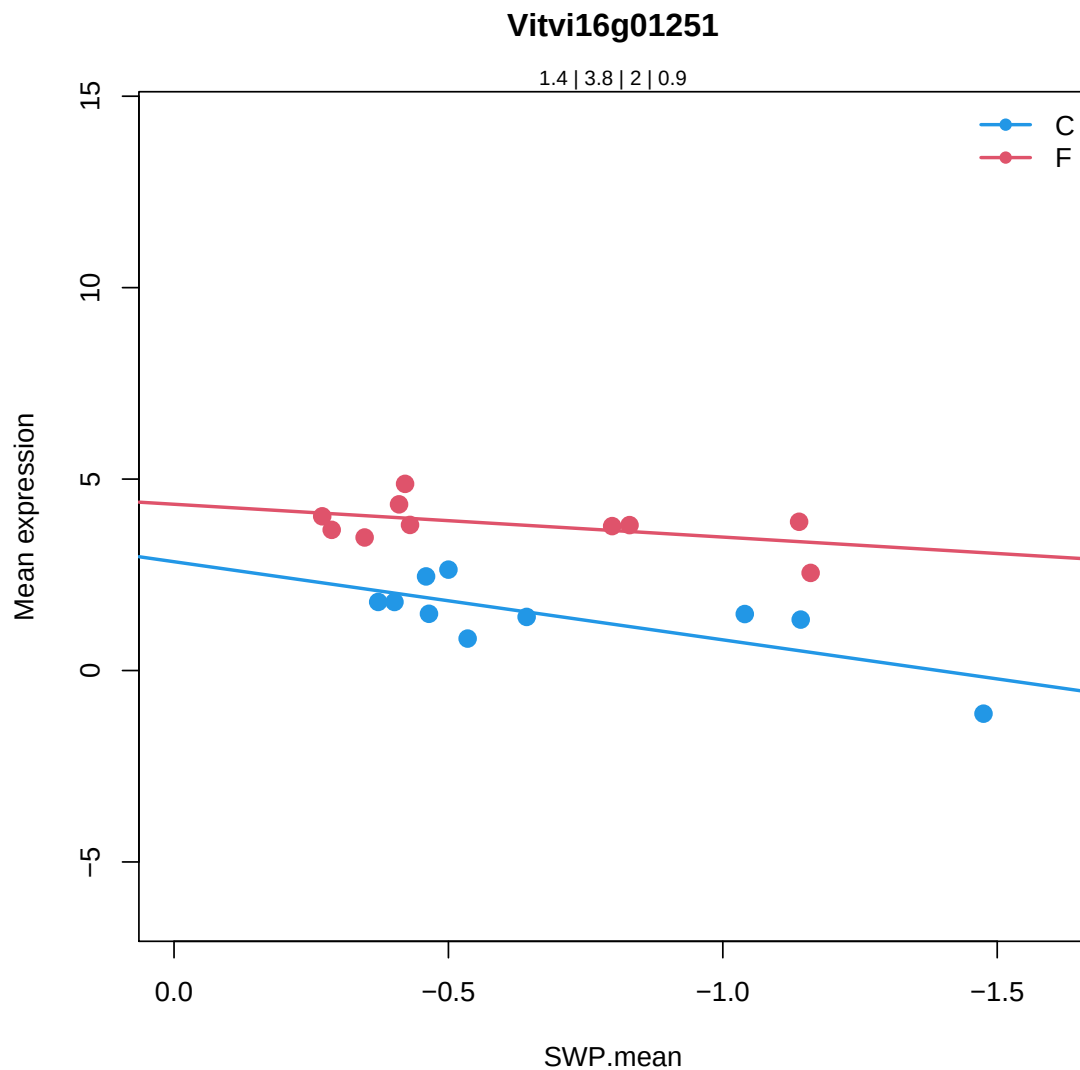
PR5-like receptor kinase |

Chr5:15293325-15295838 REVERSE LENGTH=665 |

201606

Coefficients for Vitvi16g01251.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.406554	3.194893e-07	***	3.734972e-07	***
SlopeC	2.040488	0.001029046	**	0.1273773	
MeanF-MeanC	2.413194	1.372374e-08	***	6.661697e-07	***
SlopeF-SlopeC	-1.182968	0.1538897		0.9999488	



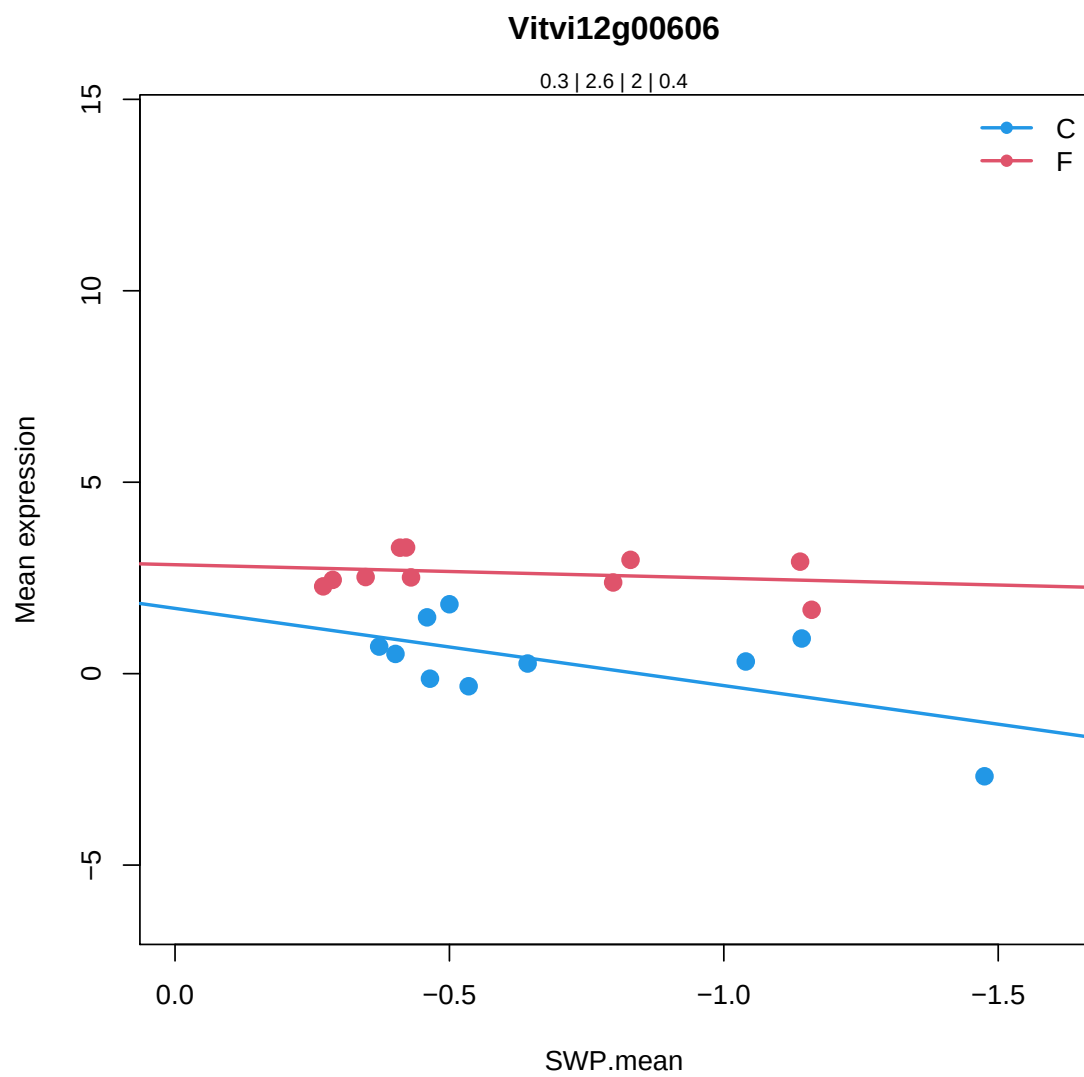
7.5.20 Vitvi12g00606

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
Vitvi12g00606
  29.4
protein.postranslational modification
G-type lectin S-receptor-like Serine/Threonine-kinase |
Chr4:1419278-1422828 REVERSE LENGTH=1010 |
201606

Vitvi12g00606
  30.2.24
signalling.receptor kinases.S-locus glycoprotein like
G-type lectin S-receptor-like Serine/Threonine-kinase |
Chr4:1419278-1422828 REVERSE LENGTH=1010 |
201606
```

Coefficients for Vitvi12g00606.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.2862625	0.2372891		0.2426379	
SlopeC	2.016467	0.005608764	**	0.2614336	
MeanF-MeanC	2.343448	5.354432e-07	***	1.871841e-05	***
SlopeF-SlopeC	-1.662881	0.1025429		0.9999488	



7.5.21 Vitvi08g00723

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

Vitvi08g00723

34.5

transport.ammonium

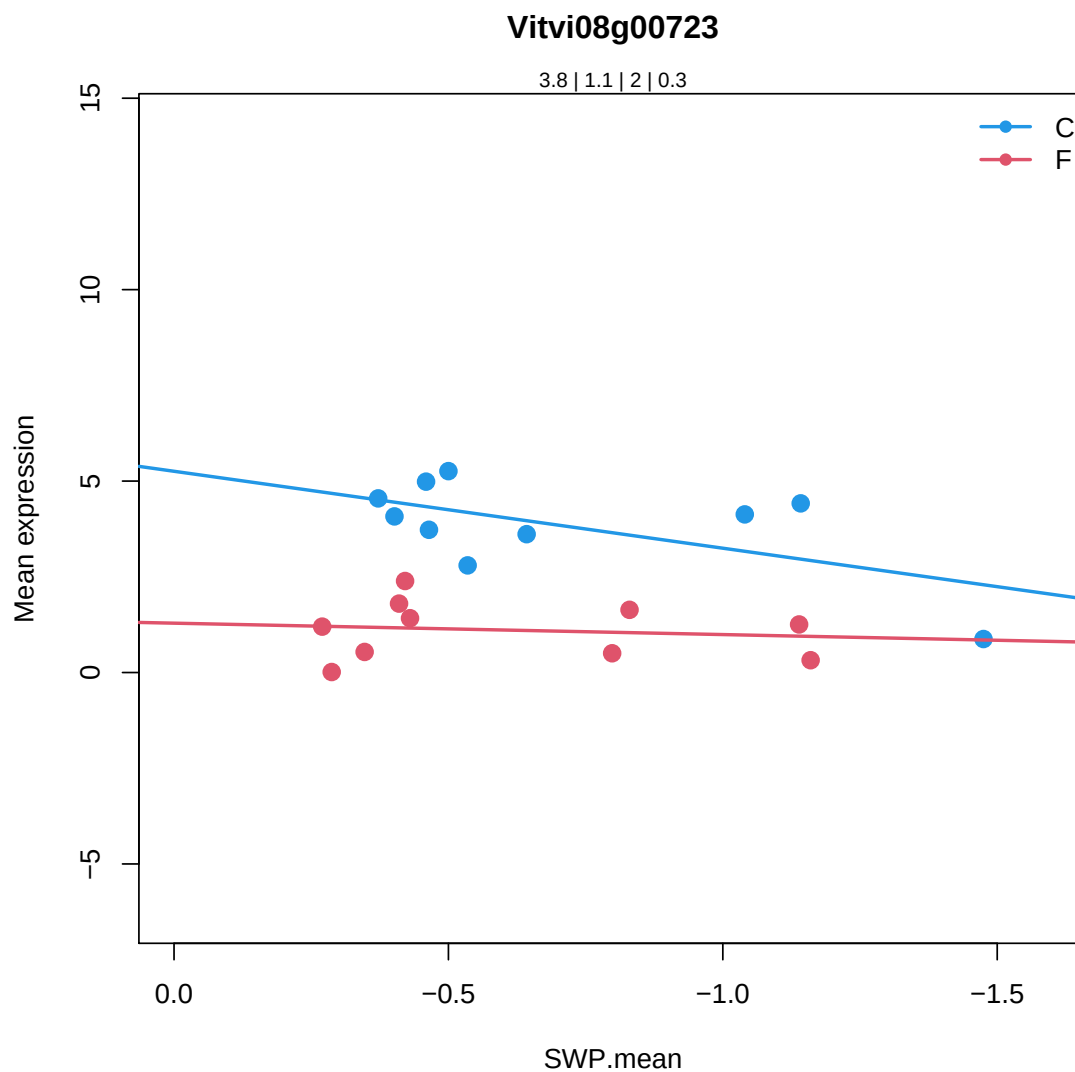
ammonium transporter 2 |

Chr2:16039672-16042291 REVERSE LENGTH=475 |

201606

Coefficients for Vitvi08g00723.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.8431	1.699178e-12	***	2.40584e-12	***
SlopeC	2.009066	0.01311545	*	0.3305597	
MeanF-MeanC	-2.73582	3.419843e-07	***	1.241077e-05	***
SlopeF-SlopeC	-1.711553	0.1362029		0.9999488	



7.5.22 Vitvi14g02893

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

Vitvi14g02893

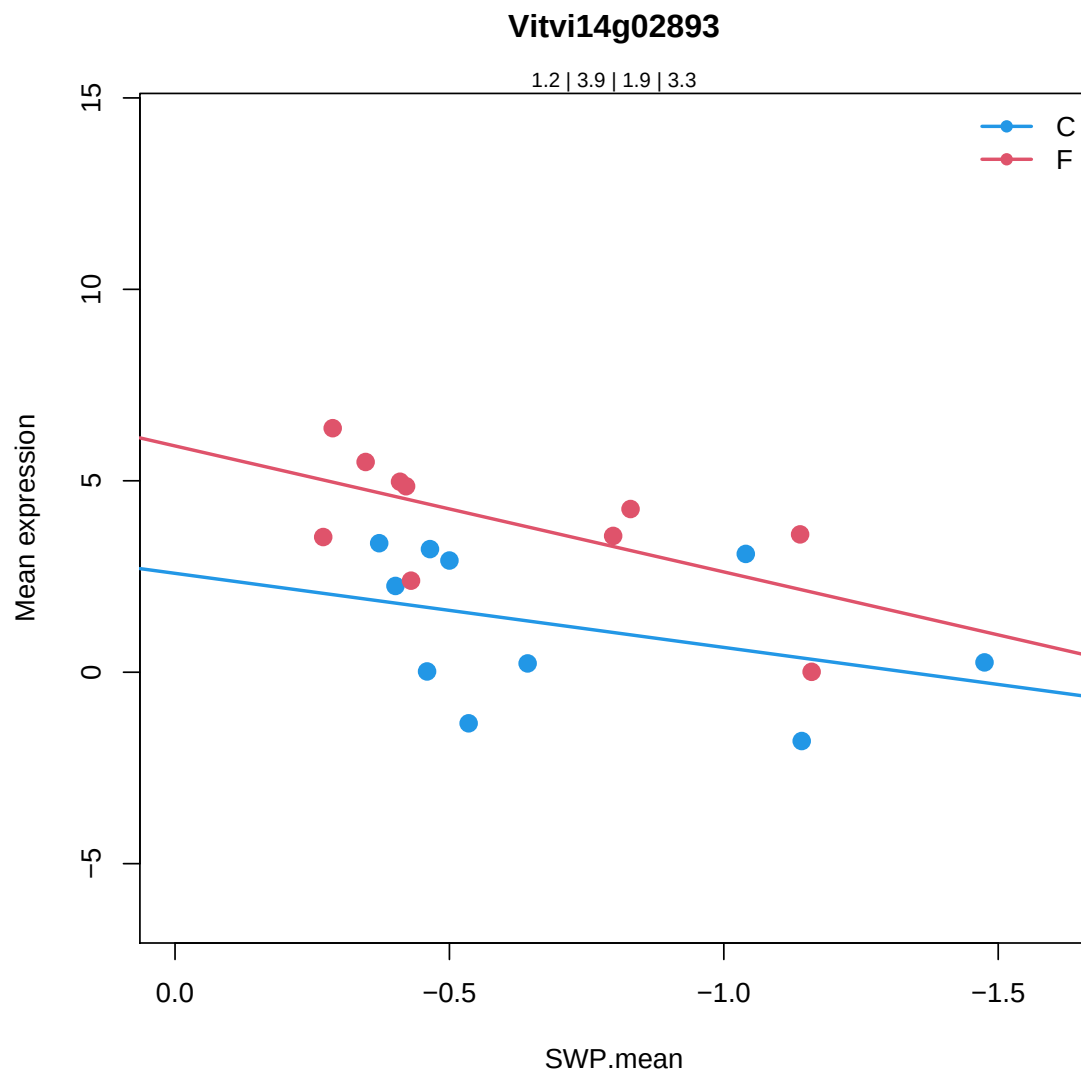
35.2

not assigned.unknown

NA

Coefficients for Vitvi14g02893.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.221987	0.017794	*	0.01873169	*
SlopeC	1.934911	0.1585324		0.6889929	
MeanF-MeanC	2.683206	0.0006505913	***	0.008798857	**
SlopeF-SlopeC	1.355003	0.4992098		0.9999488	



7.5.23 Vitvi14g01809

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

```
Vitvi14g01809
```

```
26.14
```

```
misc.oxygenases
```

```
Peroxidase superfamily protein |
```

```
Chr3:159689-162726 REVERSE LENGTH=639 |
```

```
201606
```

```
Vitvi14g01809
```

```
35.2
```

```
not assigned.unknown
```

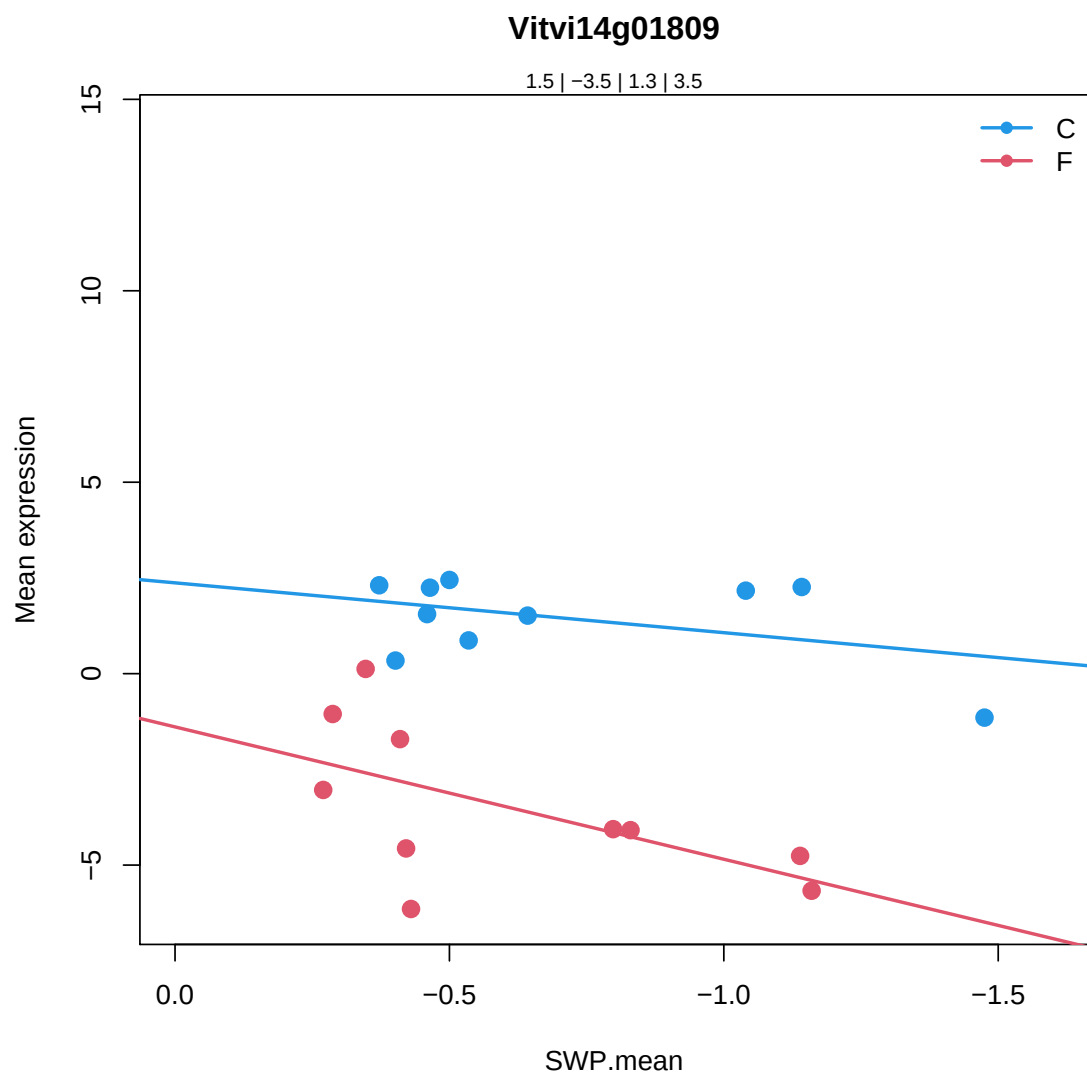
```
Peroxidase superfamily protein |
```

```
Chr3:159689-162726 REVERSE LENGTH=639 |
```

```
201606
```

Coefficients for Vitvi14g01809.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.456259	0.001813832	**	0.001952569	**
SlopeC	1.301701	0.265568		0.7701943	
MeanF-MeanC	-4.953091	2.328898e-08	***	1.092217e-06	***
SlopeF-SlopeC	2.154381	0.2172755		0.9999488	



7.5.24 Vitvi04g01937

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

Vitvi04g01937

27.03.1999

RNA.regulation of transcription.unclassified

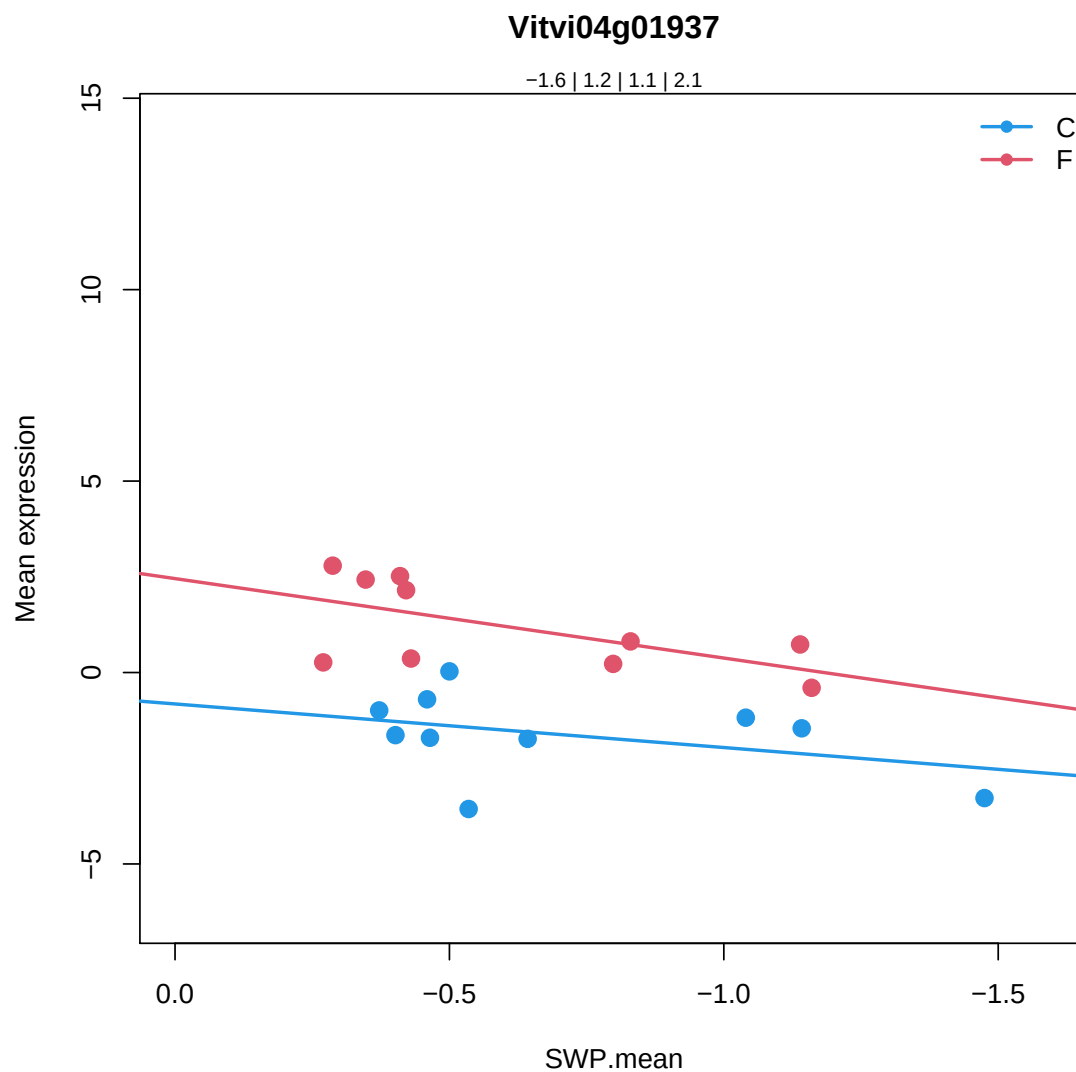
Eukaryotic aspartyl protease family protein |

Chr5:3403331-3405331 REVERSE LENGTH=474 |

201606

Coefficients for Vitvi04g01937.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.621219	1.342132e-05	***	1.510841e-05	***
SlopeC	1.13847	0.1712478		0.7015862	
MeanF-MeanC	2.809877	7.652417e-07	***	2.563476e-05	***
SlopeF-SlopeC	0.9367621	0.4424164		0.9999488	



7.5.25 Vitvi13g00807

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

Vitvi13g00807

35.2

not assigned.unknown

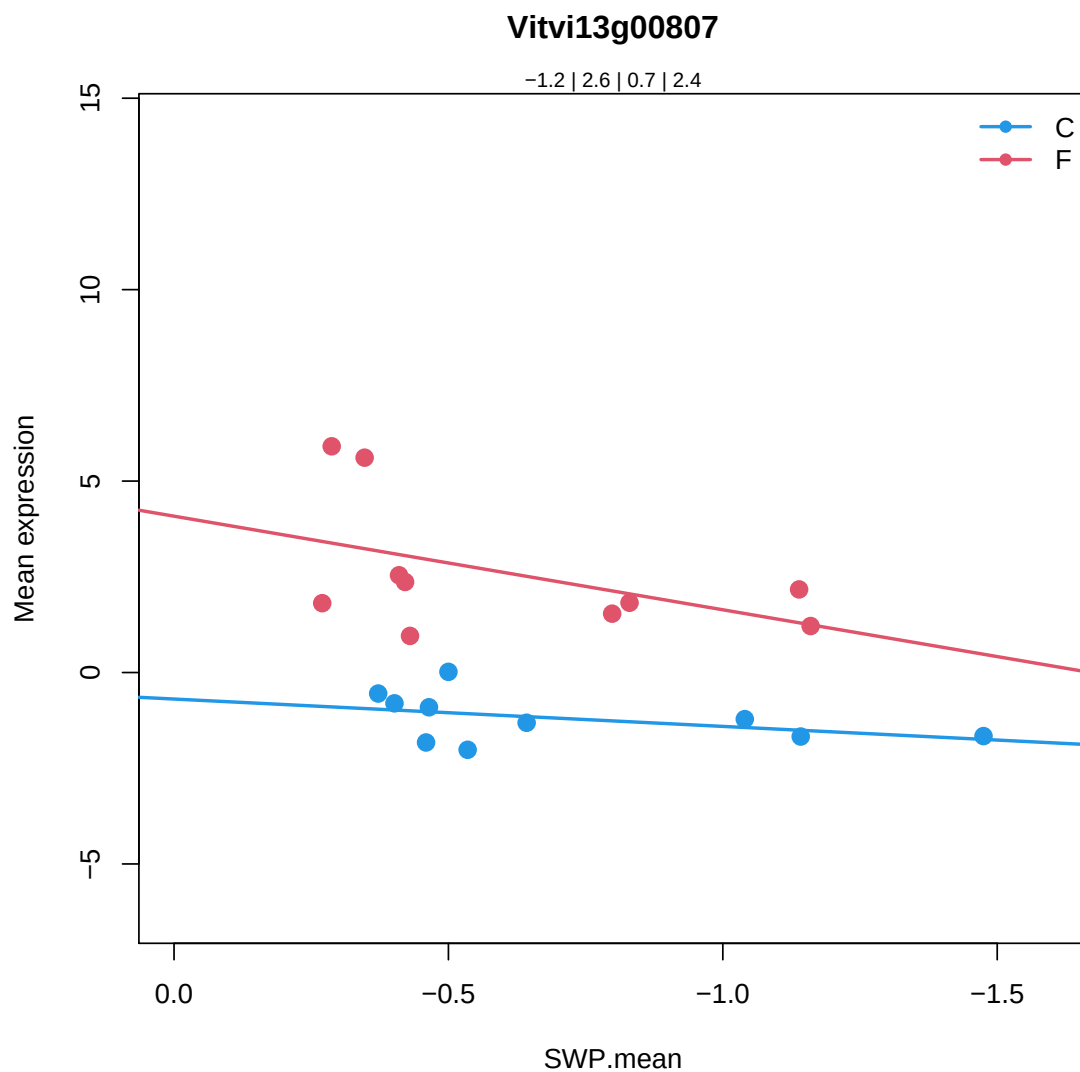
Ankyrin repeat family protein |

Chr5:1354240-1356754 REVERSE LENGTH=669 |

201606

Coefficients for Vitvi13g00807.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.195329	0.00214581	**	0.002306193	**
SlopeC	0.7145515	0.4617959		0.8604478	
MeanF-MeanC	3.788788	1.033391e-07	***	4.200254e-06	***
SlopeF-SlopeC	1.730151	0.2360724		0.9999488	



7.5.26 Vitvi05g00847

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

Vitvi05g00847

30.3

signalling.calcium

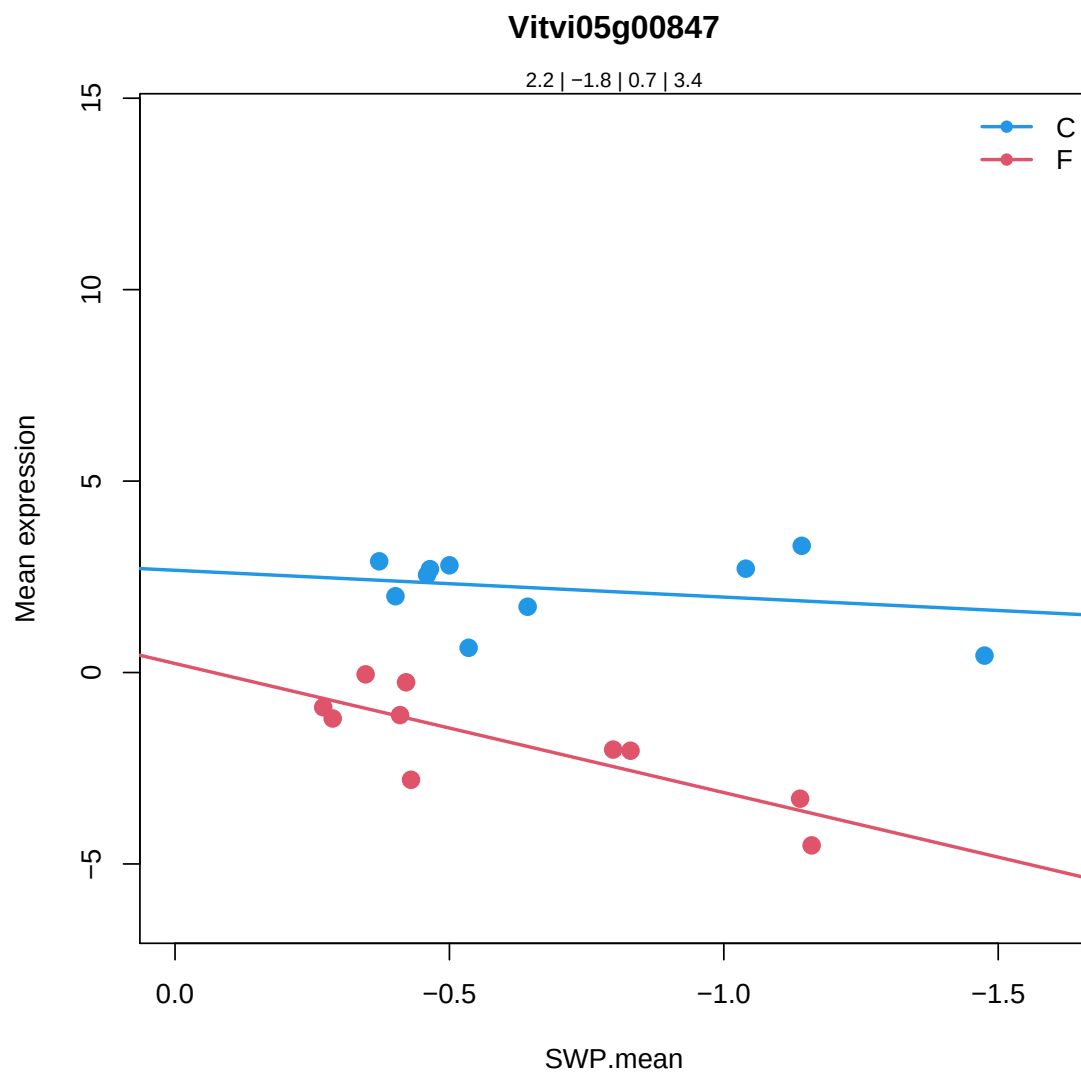
Calcium-binding EF-hand family protein |

Chr4:7810215-7810679 FORWARD LENGTH=154 |

201606

Coefficients for Vitvi05g00847.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.177676	4.164641e-08	***	4.991151e-08	***
SlopeC	0.7001947	0.3501821		0.8124192	
MeanF-MeanC	-3.99674	4.445221e-10	***	2.821747e-08	***
SlopeF-SlopeC	2.671128	0.02304466	*	0.9999488	



7.5.27 Vitvi15g00804

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

Vitvi15g00804

26.1

misc.cytochrome P450

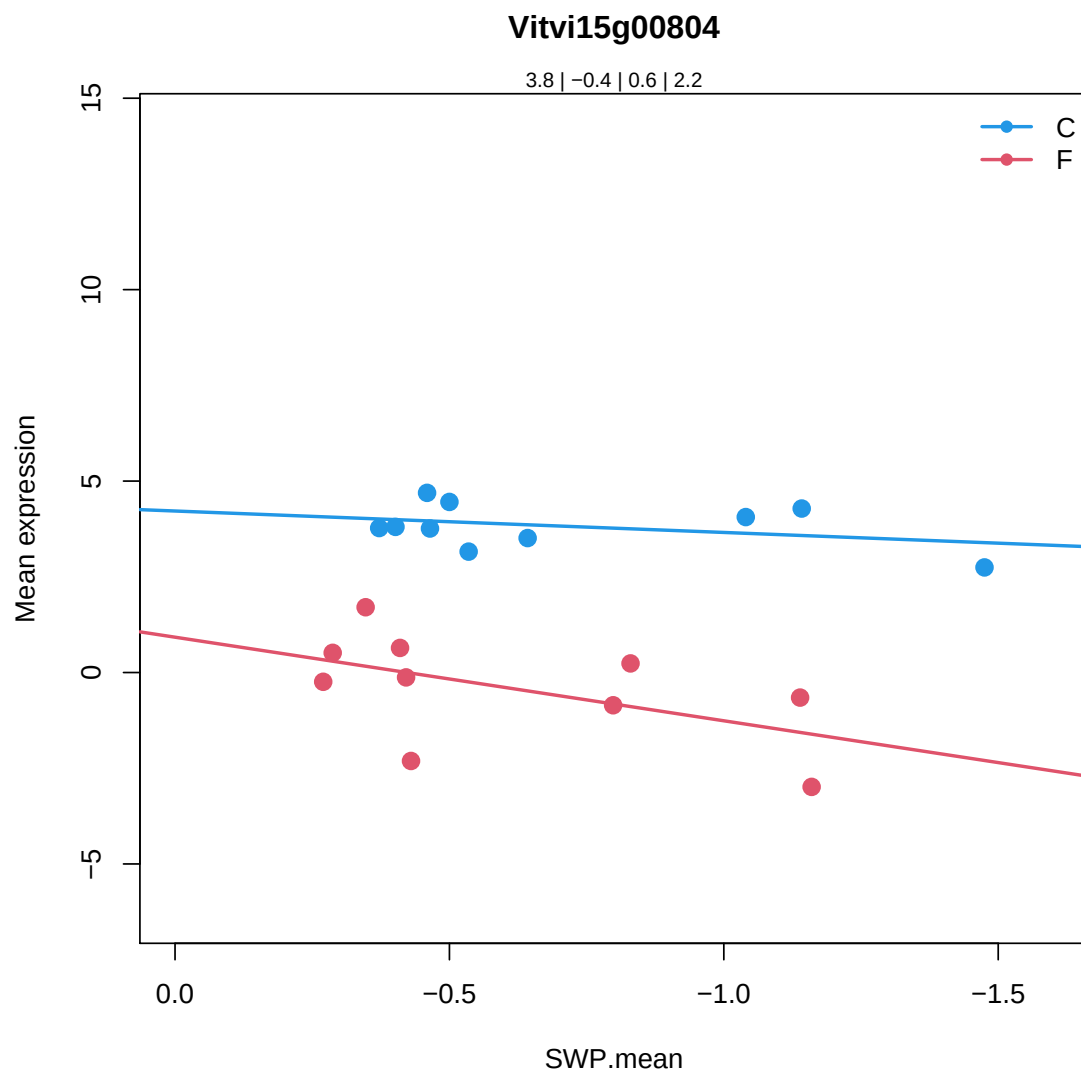
cytochrome P450%2C family 76%2C subfamily C%2C polypeptide 2 |

Chr2:18779935-18781922 REVERSE LENGTH=512 |

201606

Coefficients for Vitvi15g00804.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.824202	3.801638e-12	***	5.28402e-12	***
SlopeC	0.5598445	0.4752488		0.8622843	
MeanF-MeanC	-4.23207	3.864461e-10	***	2.464524e-08	***
SlopeF-SlopeC	1.623612	0.1711245		0.9999488	



7.5.28 Vitvi05g00038

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

Vitvi05g00038

26.03.2005

misc.gluco-, galacto- and mannosidases.glycosyl hydrolase family 5

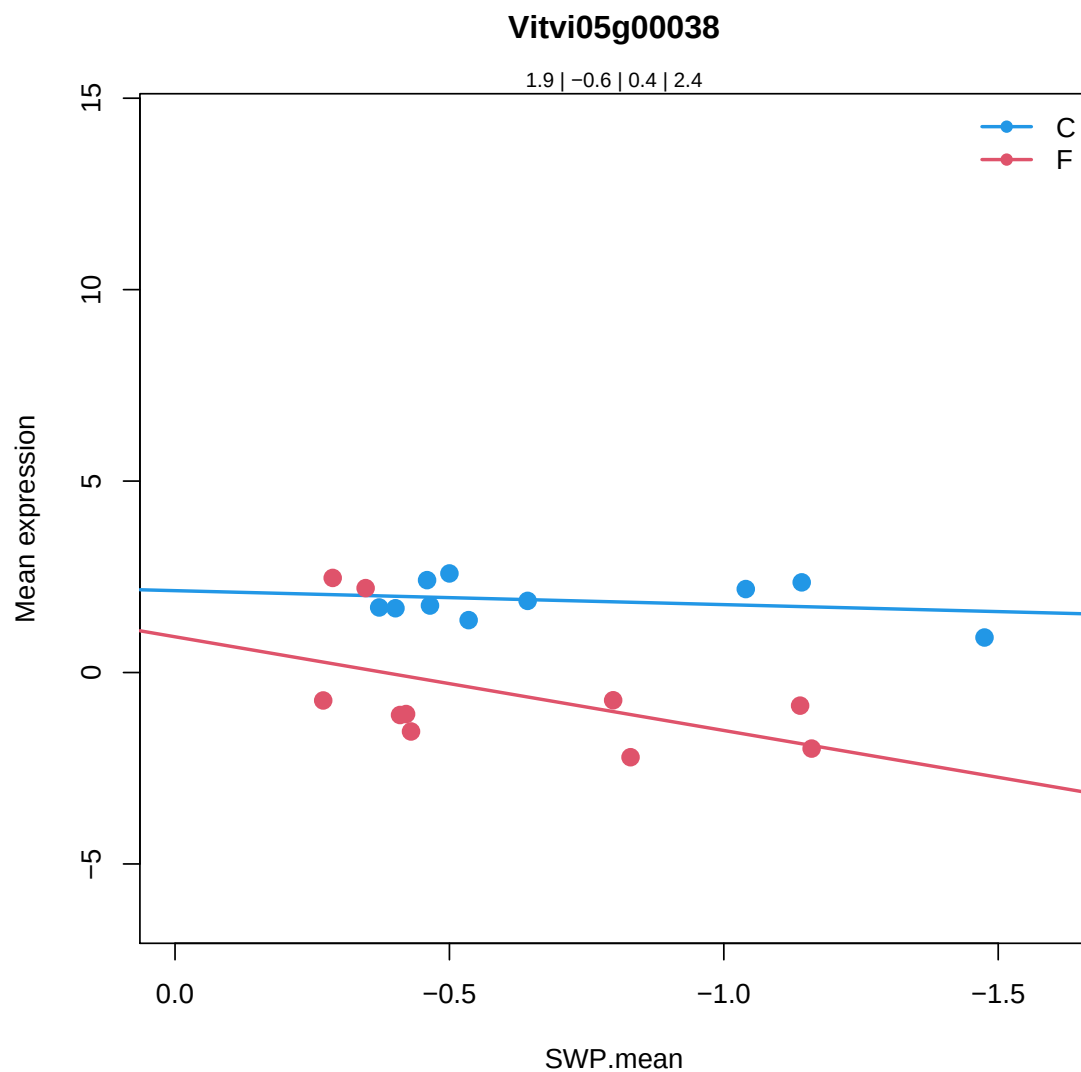
alpha/beta-Hydrolases superfamily protein |

Chr4:1035722-1037403 FORWARD LENGTH=324 |

201606

Coefficients for Vitvi05g00038.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.881532	4.363251e-06	***	4.964146e-06	***
SlopeC	0.3647677	0.6752848		0.9252688	
MeanF-MeanC	-2.439425	1.40955e-05	***	0.0003437499	***
SlopeF-SlopeC	2.082283	0.1179377		0.9999488	



7.5.29 Vitvi12g02177

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

Vitvi12g02177

16.01.2005

secondary metabolism.isoprenoids.terpenoids

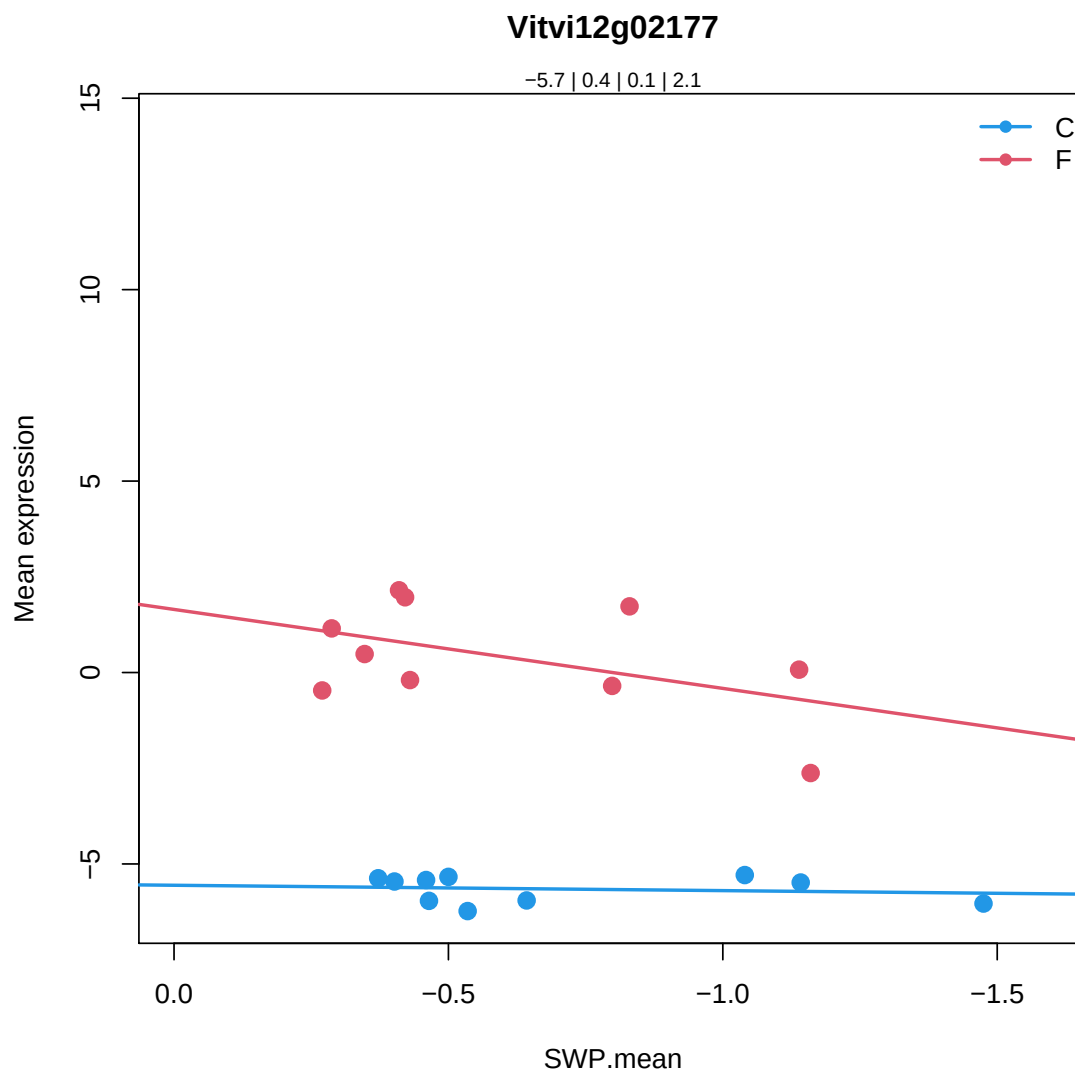
terpene synthase 21 |

Chr5:8092969-8095128 FORWARD LENGTH=545 |

201606

Coefficients for Vitvi12g02177.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.654707	1.734801e-15	***	3.157989e-15	***
SlopeC	0.1400847	0.8582087		0.9733541	
MeanF-MeanC	6.045631	4.807264e-13	***	4.608322e-11	***
SlopeF-SlopeC	1.922026	0.1100849		0.9999488	



7.5.30 Vitvi07g03123

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

Vitvi07g03123

31.1

cell.organisation

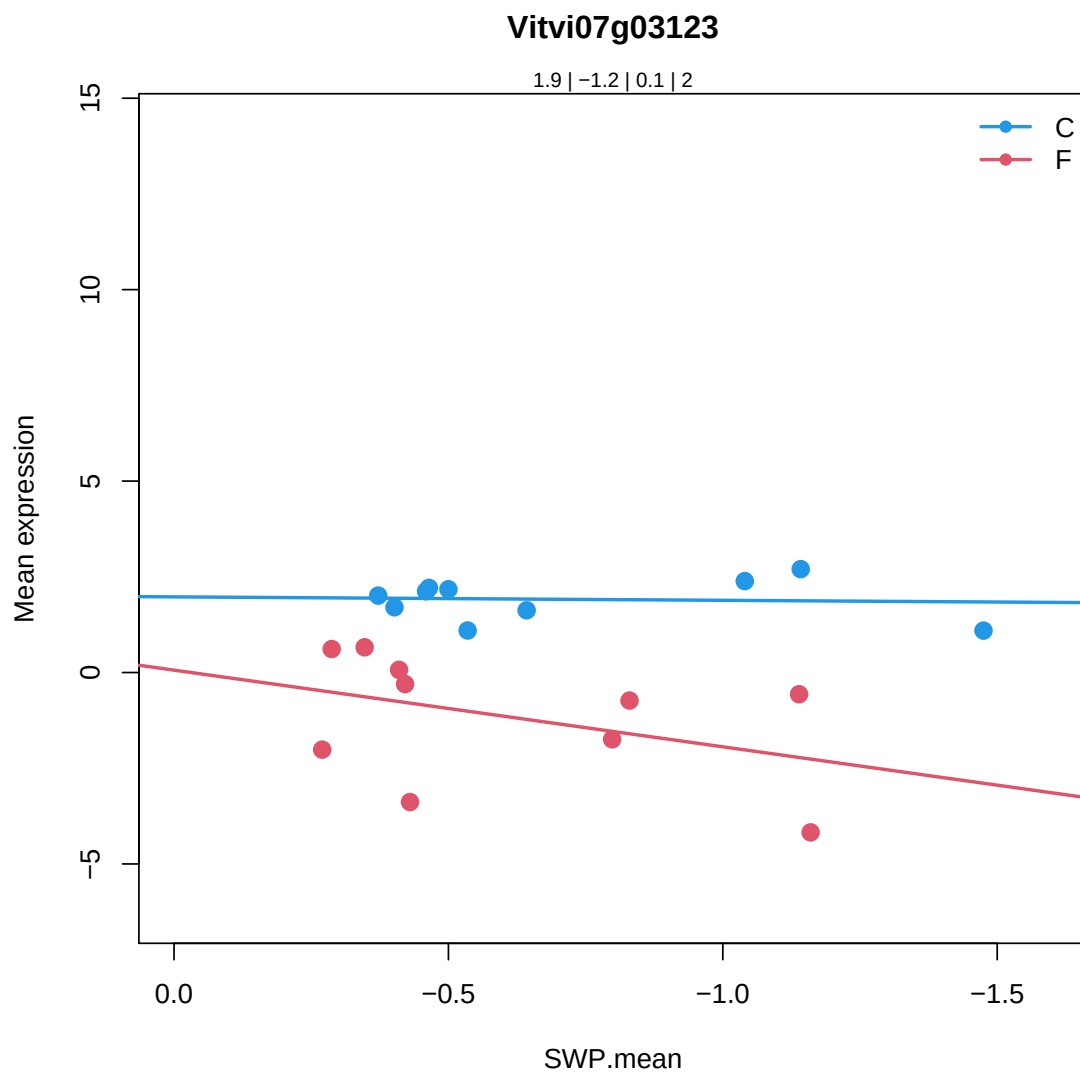
tubulin alpha-5 |

Chr5:6687212-6688926 FORWARD LENGTH=450 |

201606

Coefficients for Vitvi07g03123.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.912632	1.0113e-05	***	1.14188e-05	***
SlopeC	0.0898298	0.9238393		0.9860755	
MeanF-MeanC	-3.070558	1.72904e-06	***	5.302623e-05	***
SlopeF-SlopeC	1.912759	0.1806418		0.9999488	



7.5.31 Vitvi12g00574

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

Vitvi12g00574

16.01.2005

secondary metabolism.isoprenoids.terpenoids

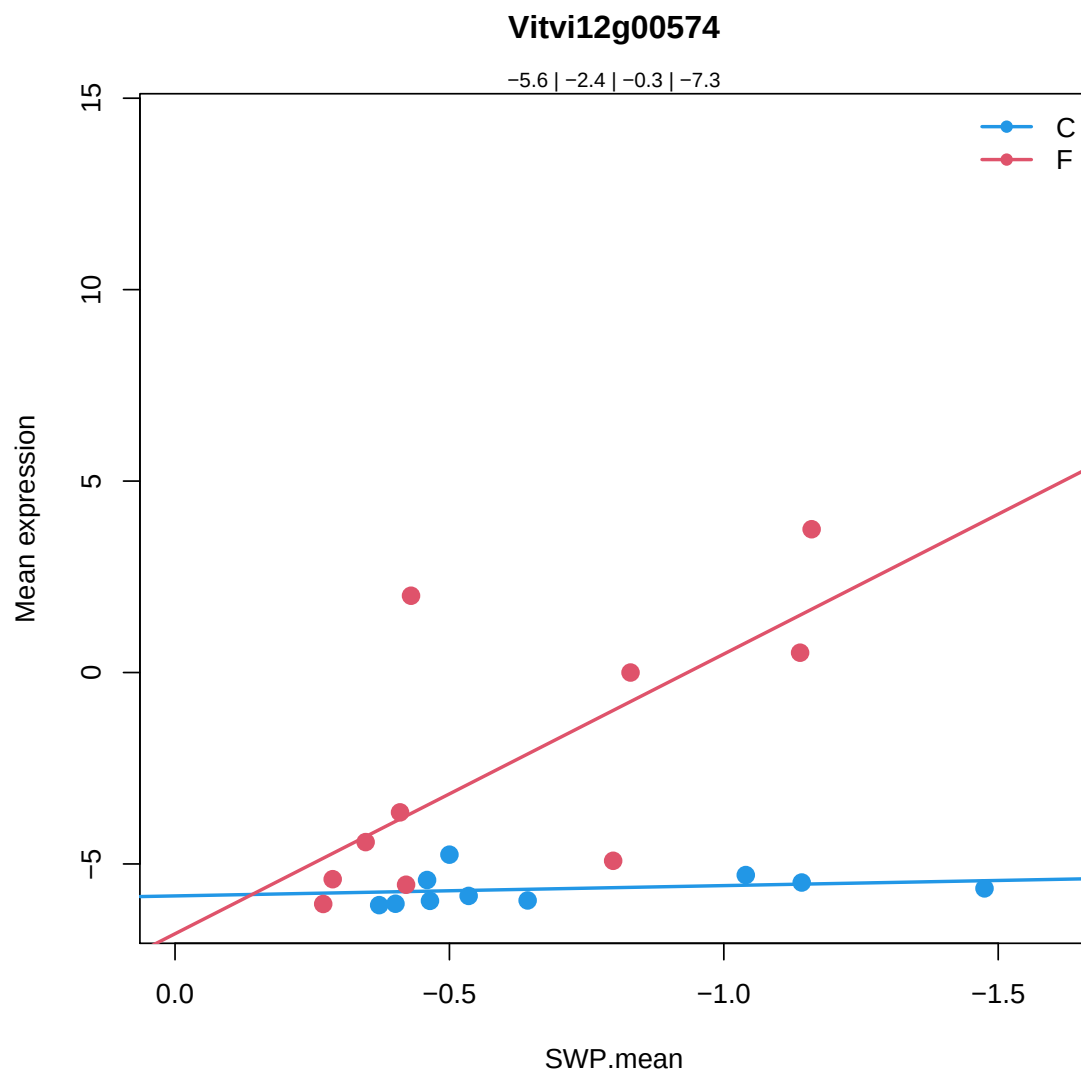
terpene synthase-like sequence-1%2C8-cineole |

Chr3:9447545-9450316 FORWARD LENGTH=600 |

201606

Coefficients for Vitvi12g00574.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.645691	6.169158e-10	***	7.839779e-10	***
SlopeC	-0.2692201	0.8584264		0.9734036	
MeanF-MeanC	3.273791	0.0002909881	***	0.004497484	**
SlopeF-SlopeC	-7.036961	0.004526106	**	0.9999488	



7.5.32 Vitvi18g02451

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

Vitvi18g02451

16.01.2005

secondary metabolism.isoprenoids.terpenoids

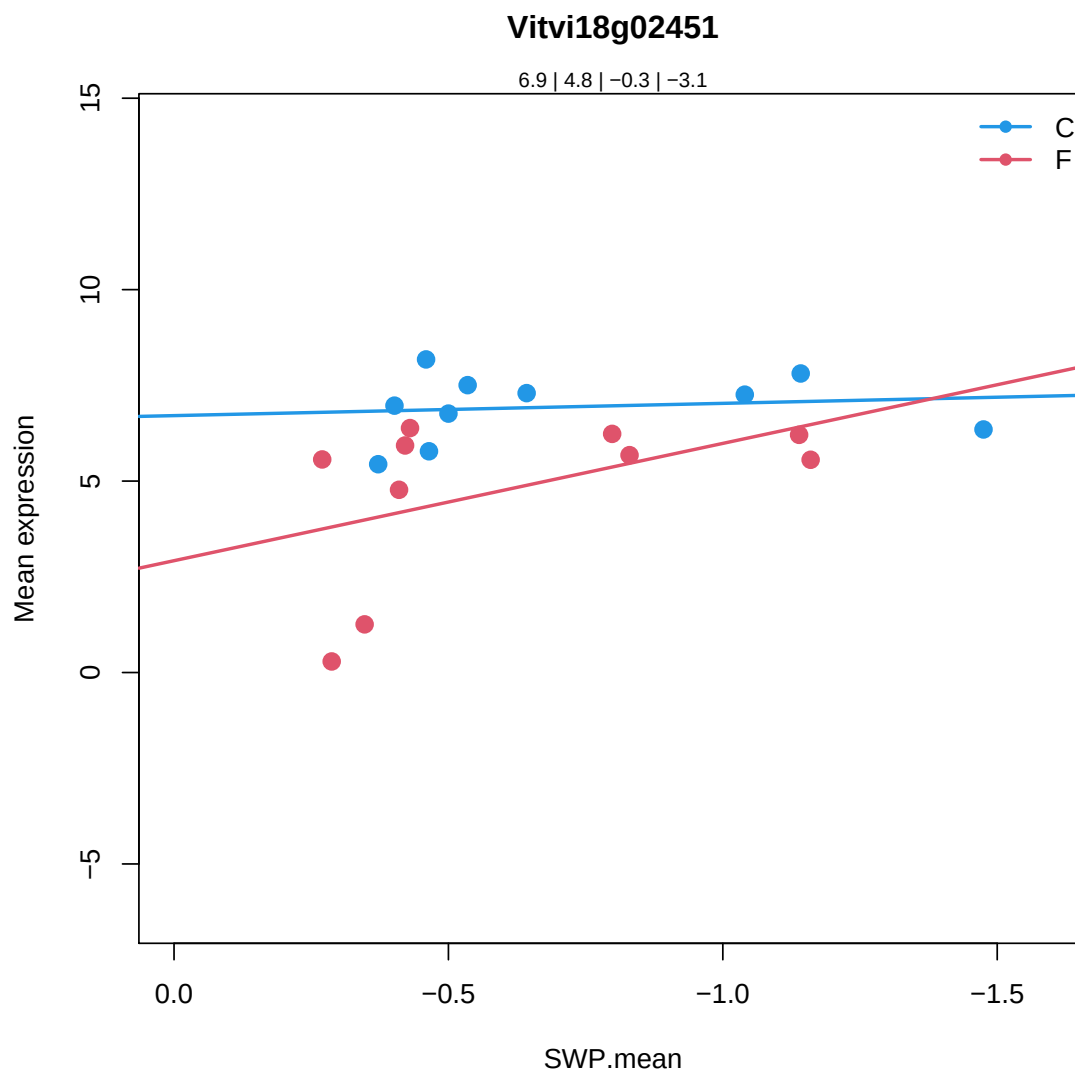
terpene synthase 21 |

Chr5:8092969-8095128 FORWARD LENGTH=545 |

201606

Coefficients for Vitvi18g02451.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.934609	2.33132e-13	***	3.491597e-13	***
SlopeC	-0.3205063	0.7938969		0.9552081	
MeanF-MeanC	-2.147399	0.00214966	**	0.02330378	*
SlopeF-SlopeC	-2.742855	0.1428692		0.9999488	



7.5.33 Vitvi13g00261

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

Vitvi13g00261

35.2

not assigned.unknown

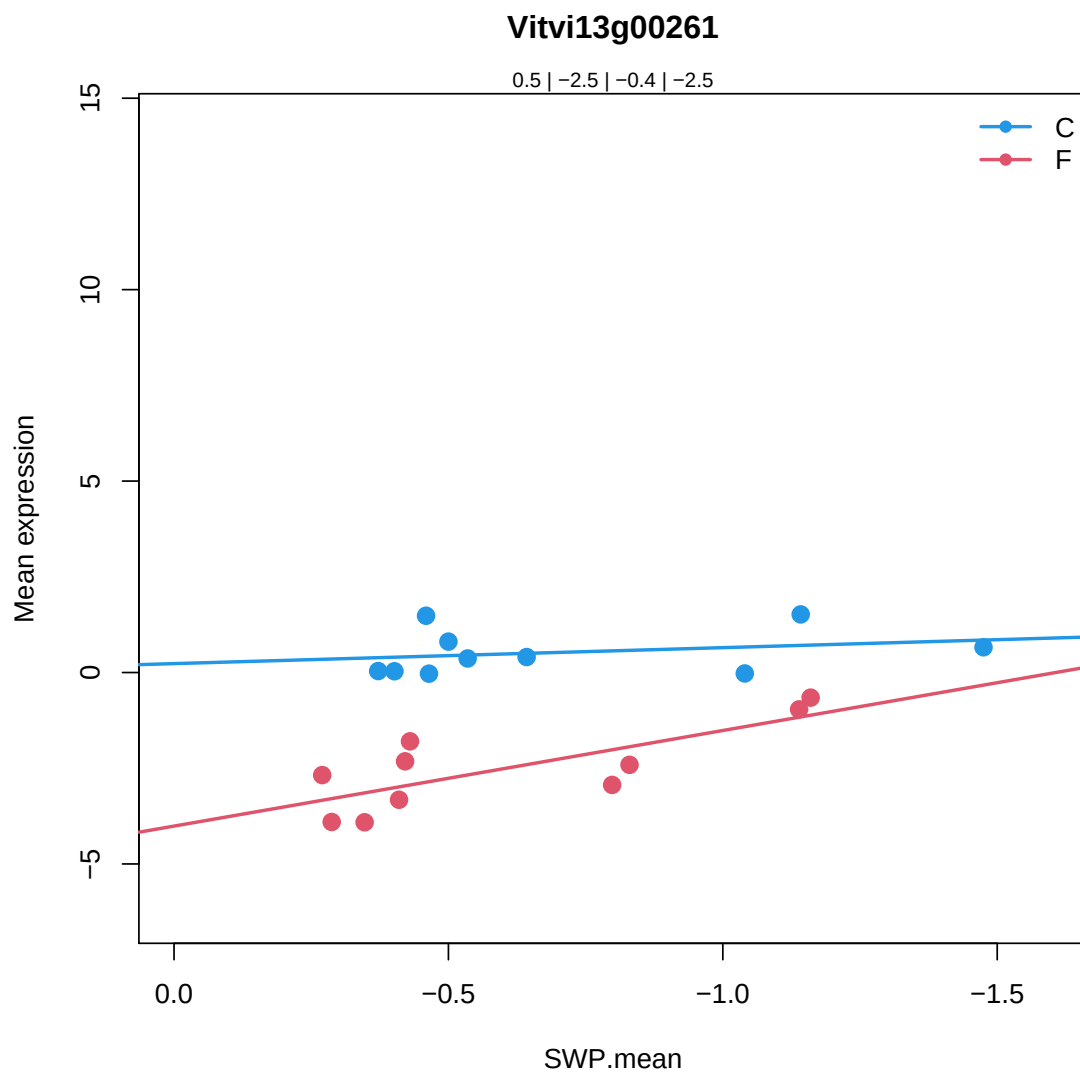
PIF / Ping-Pong family of plant transposase |

Chr3:20518518-20520690 FORWARD LENGTH=406 |

201606

Coefficients for Vitvi13g00261.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.5253927	0.0164883	*	0.01737758	*
SlopeC	-0.4169403	0.4660837		0.8618199	
MeanF-MeanC	-3.015297	5.911452e-10	***	3.639539e-08	***
SlopeF-SlopeC	-2.079326	0.02120173	*	0.9999488	



7.5.34 Vitvi04g01100

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

Vitvi04g01100

31.1

cell.organisation

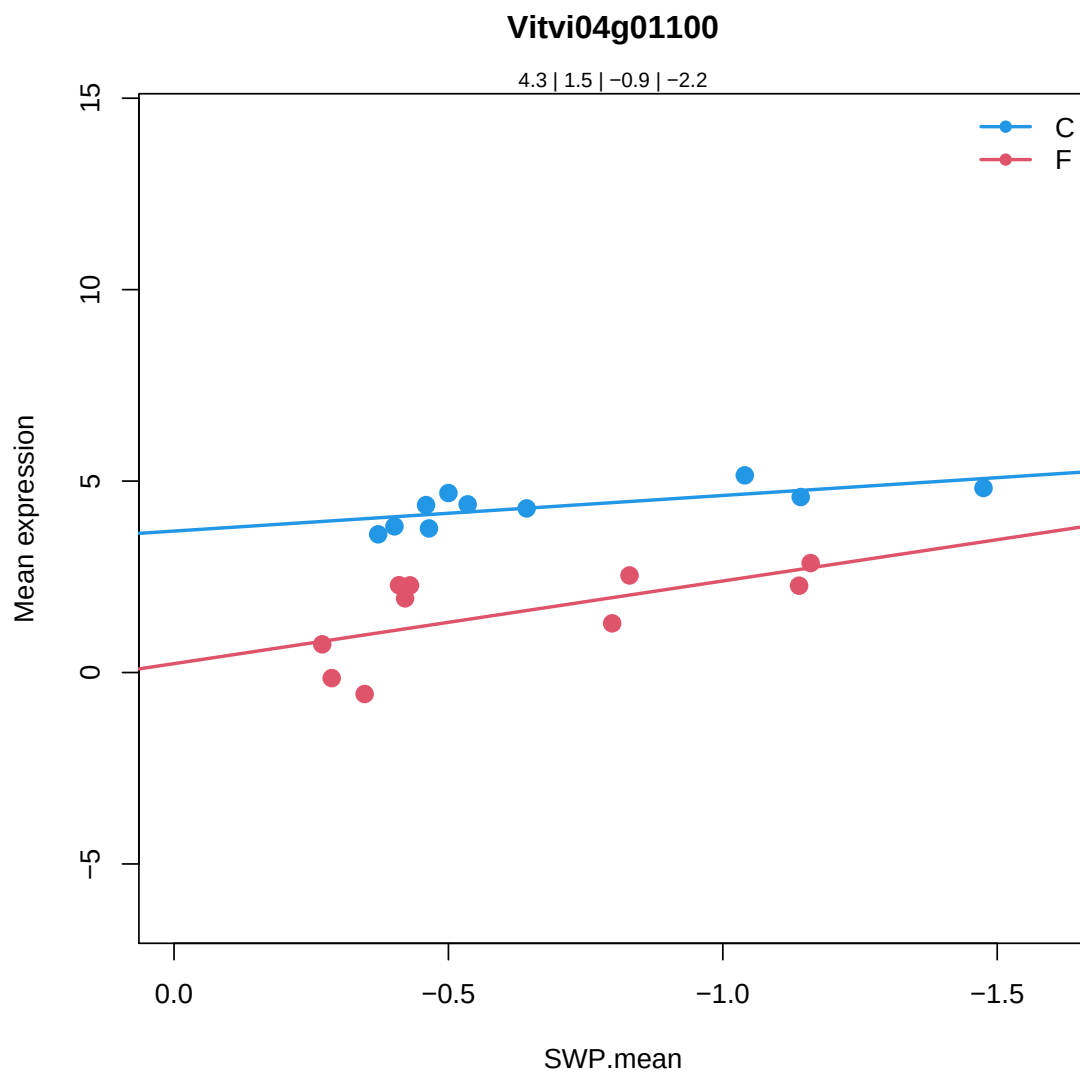
phloem protein 2-B1 |

Chr2:590393-591595 REVERSE LENGTH=336 |

201606

Coefficients for Vitvi04g01100.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.348044	1.905579e-15	***	3.458543e-15	***
SlopeC	-0.9302426	0.1347228		0.6596656	
MeanF-MeanC	-2.801248	6.673827e-09	***	3.402089e-07	***
SlopeF-SlopeC	-1.228185	0.1821518		0.9999488	



7.5.35 Vitvi15g01073

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

Vitvi15g01073

16.8.1.12

secondary metabolism.flavonoids.anthocyanins.anthocyanidin 3-O-glucosyl

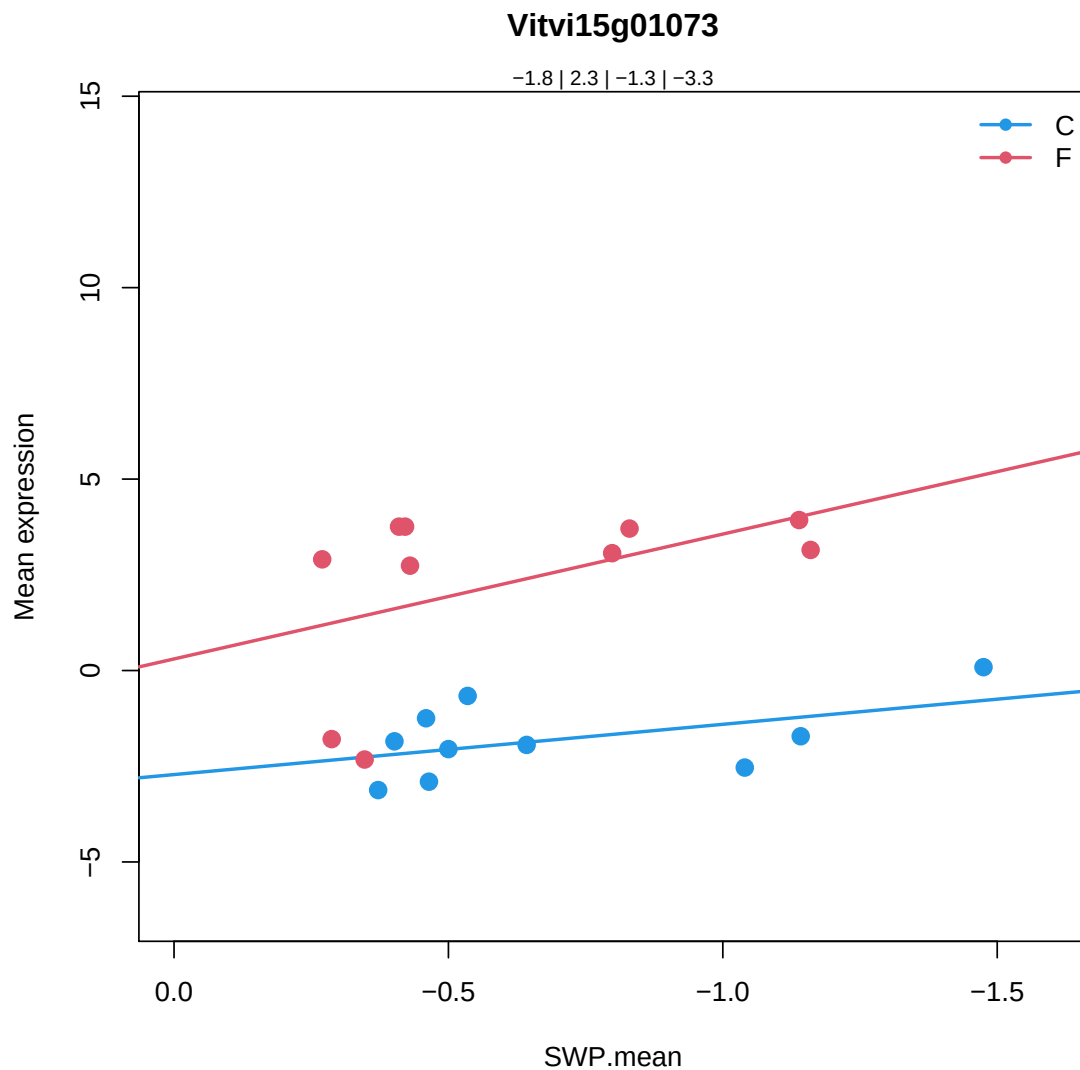
UDP-Glycosyltransferase superfamily protein |

Chr2:9593012-9594424 FORWARD LENGTH=470 |

201606

Coefficients for Vitvi15g01073.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.794704	0.0007996753	***	0.000867952	***
SlopeC	-1.312703	0.316654		0.7963375	
MeanF-MeanC	4.084005	2.895334e-06	***	8.264173e-05	***
SlopeF-SlopeC	-1.948958	0.317825		0.9999488	



7.5.36 Vitvi07g02362

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

Vitvi07g02362

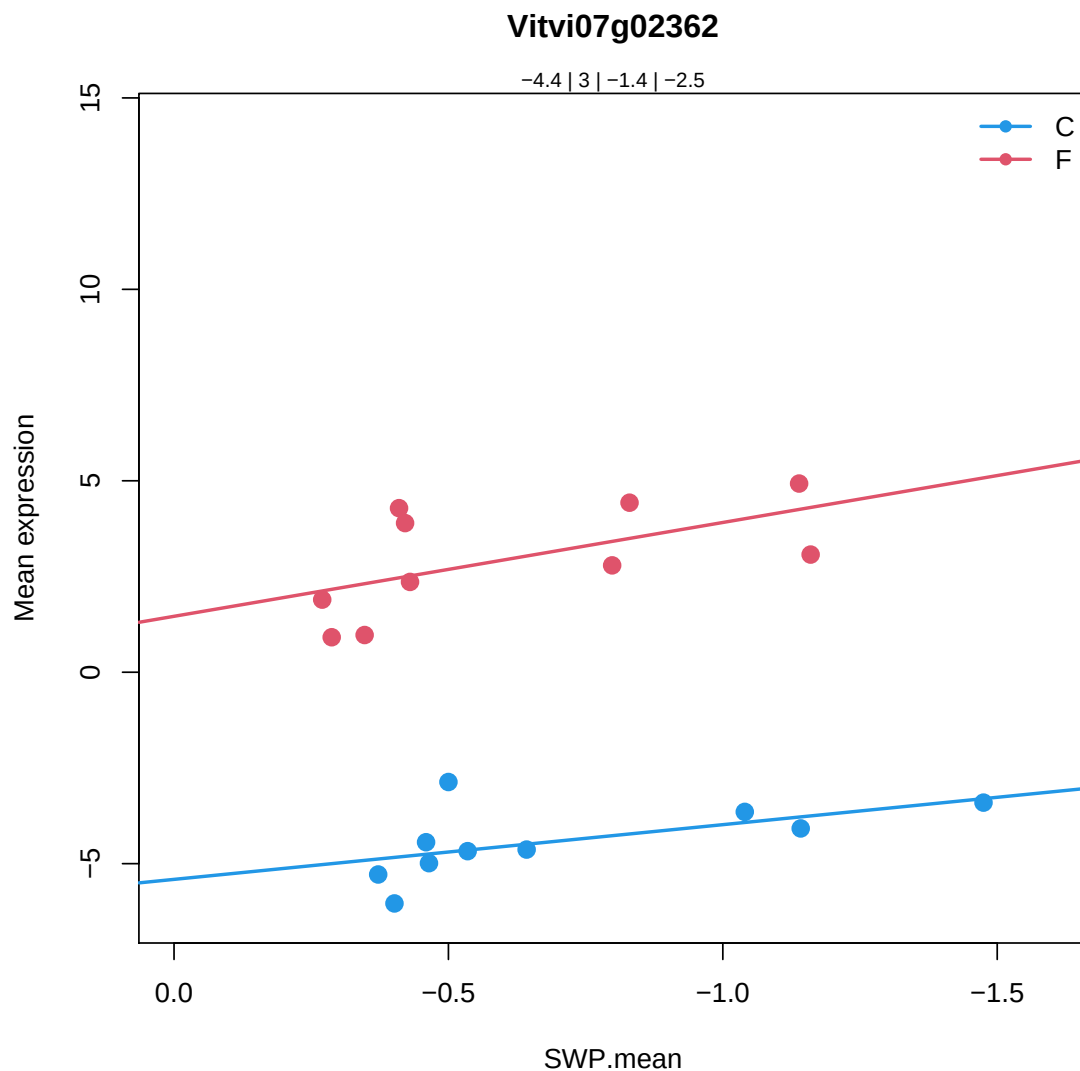
35.2

not assigned.unknown

NA

Coefficients for Vitvi07g02362.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-4.405545	7.862665e-13	***	1.136489e-12	***
SlopeC	-1.429156	0.09515211	.	0.6053158	
MeanF-MeanC	7.359295	2.860697e-14	***	3.303238e-12	***
SlopeF-SlopeC	-1.021377	0.4111096		0.9999488	



7.5.37 Vitvi01g02061

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

Vitvi01g02061

35.1.26

not assigned.no ontology.DC1 domain containing protein

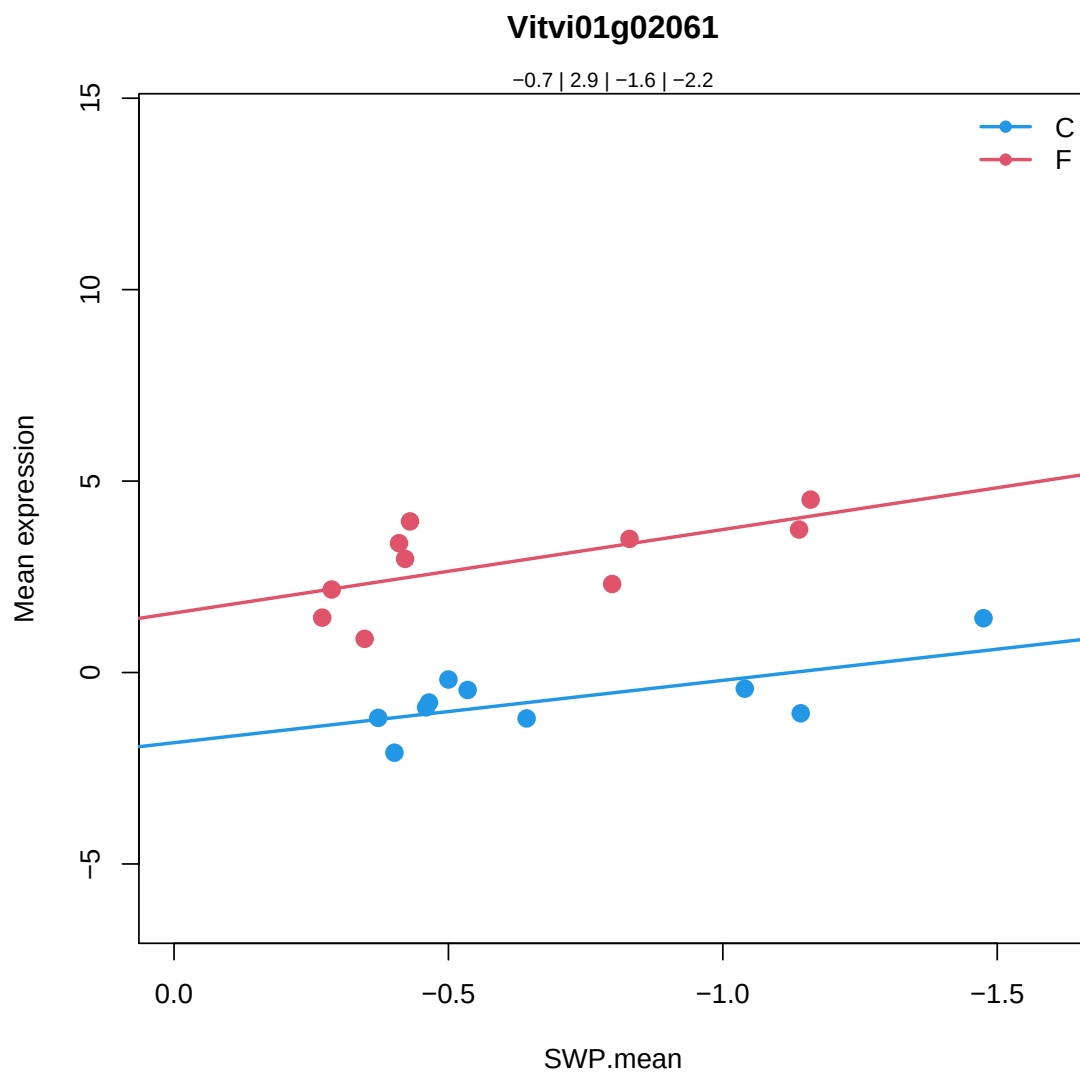
DC1 domain-containing protein |

Chr1:22261978-22264243 FORWARD LENGTH=578 |

201606

Coefficients for Vitvi01g02061.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.6880274	0.009278023	**	0.009836925	**
SlopeC	-1.628569	0.02384104	*	0.3984486	
MeanF-MeanC	3.570542	6.641649e-10	***	4.033148e-08	***
SlopeF-SlopeC	-0.5520575	0.5853545		0.9999488	



7.5.38 Vitvi07g02448

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

Vitvi07g02448

26.2

misc.UDP glucosyl and glucoronyl transferases

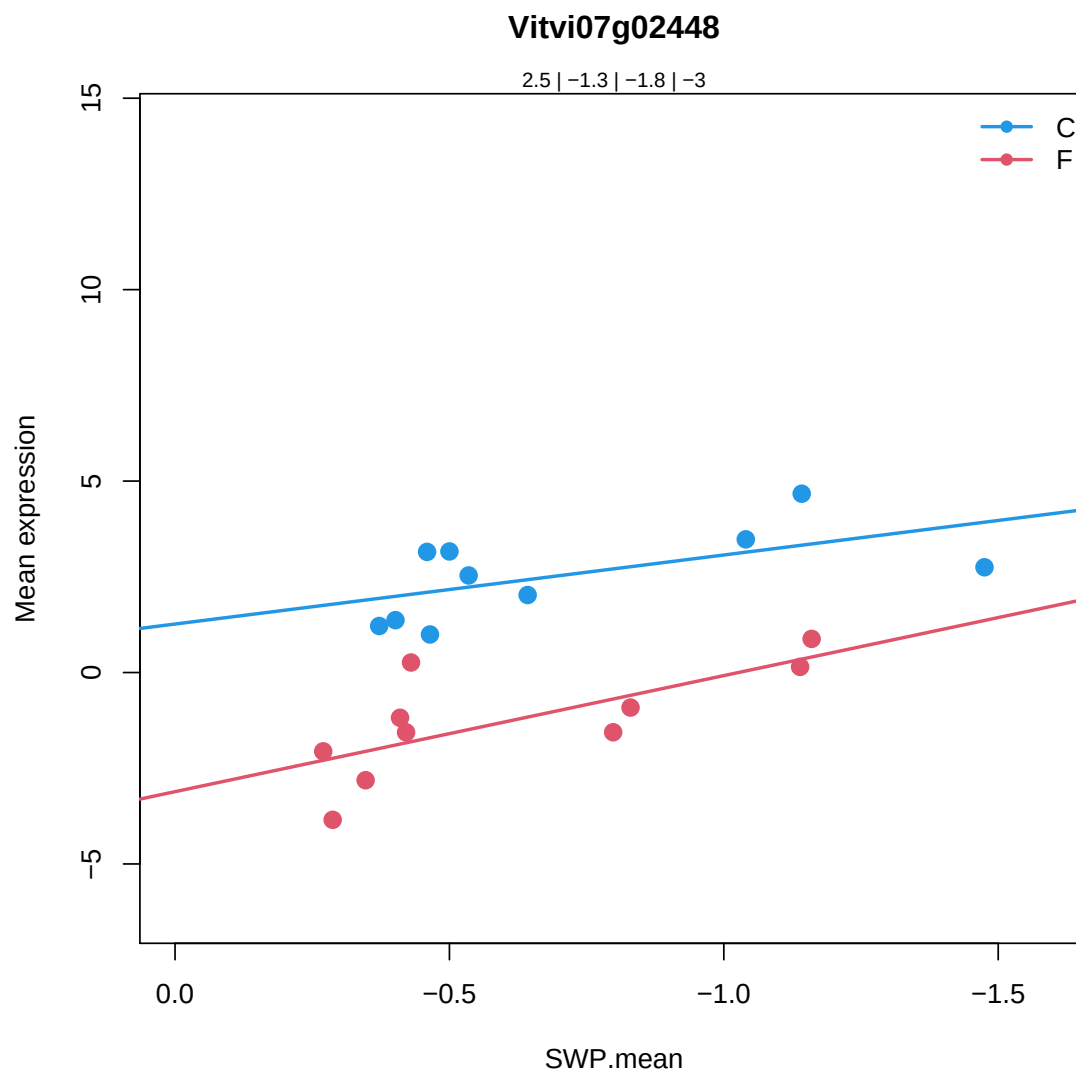
Uridine diphosphate glycosyltransferase 74E2 |

Chr1:1703196-1704639 REVERSE LENGTH=453 |

201606

Coefficients for Vitvi07g02448.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.534319	1.823511e-08	***	2.209025e-08	***
SlopeC	-1.803435	0.03725763	*	0.4620709	
MeanF-MeanC	-3.799573	6.720516e-09	***	3.41447e-07	***
SlopeF-SlopeC	-1.227884	0.3209972		0.9999488	



7.5.39 Vitvi19g01048

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

Vitvi19g01048

26.9

misc.glutathione S transferases

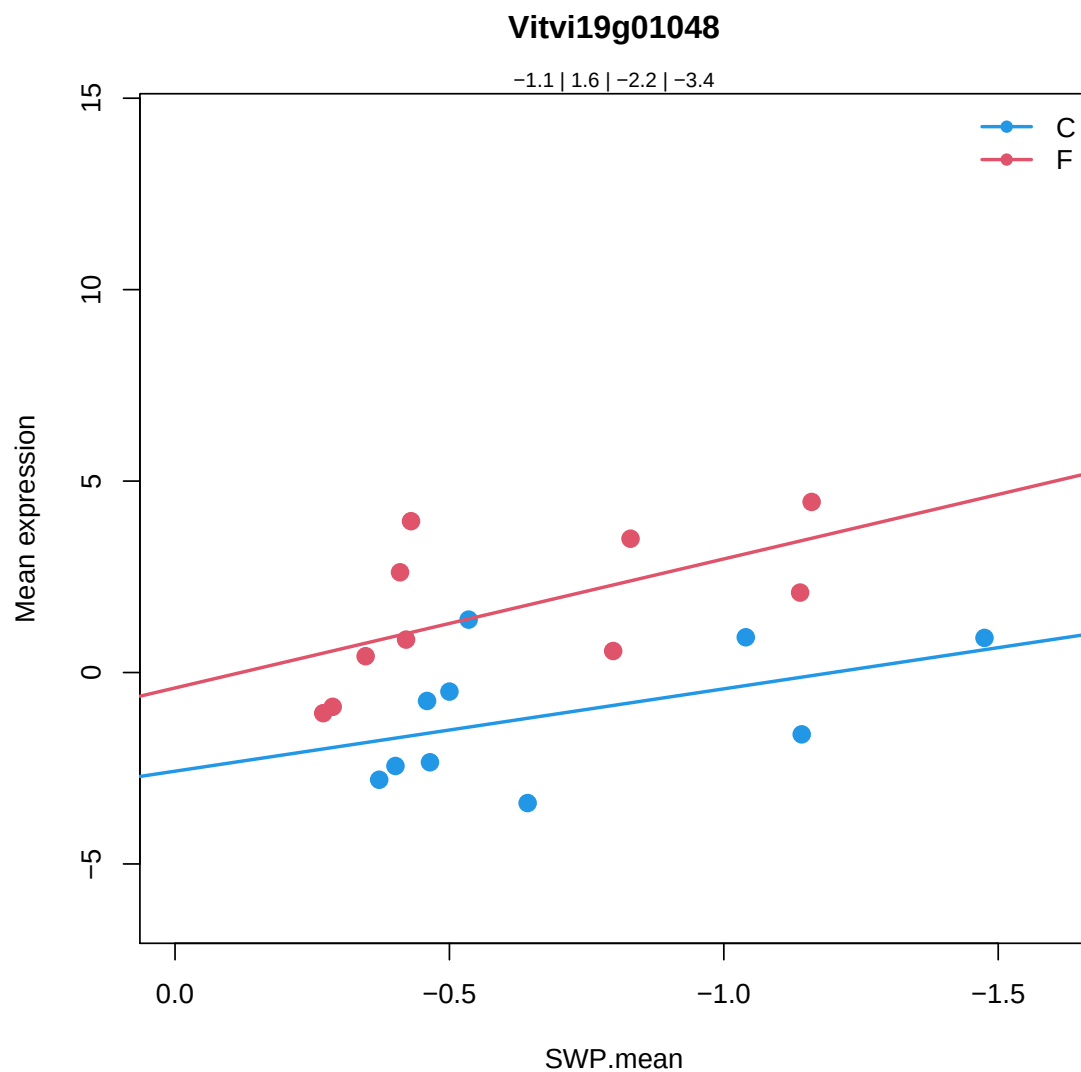
glutathione S-transferase TAU 25 |

Chr1:5872208-5872958 FORWARD LENGTH=221 |

201606

Coefficients for Vitvi19g01048.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.064541	0.02951157	*	0.03089603	*
SlopeC	-2.150775	0.1048283		0.6181019	
MeanF-MeanC	2.714192	0.0003836245	***	0.005633145	**
SlopeF-SlopeC	-1.218795	0.5258973		0.9999488	



7.5.40 Vitvi03g00443

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

Vitvi03g00443

26.8

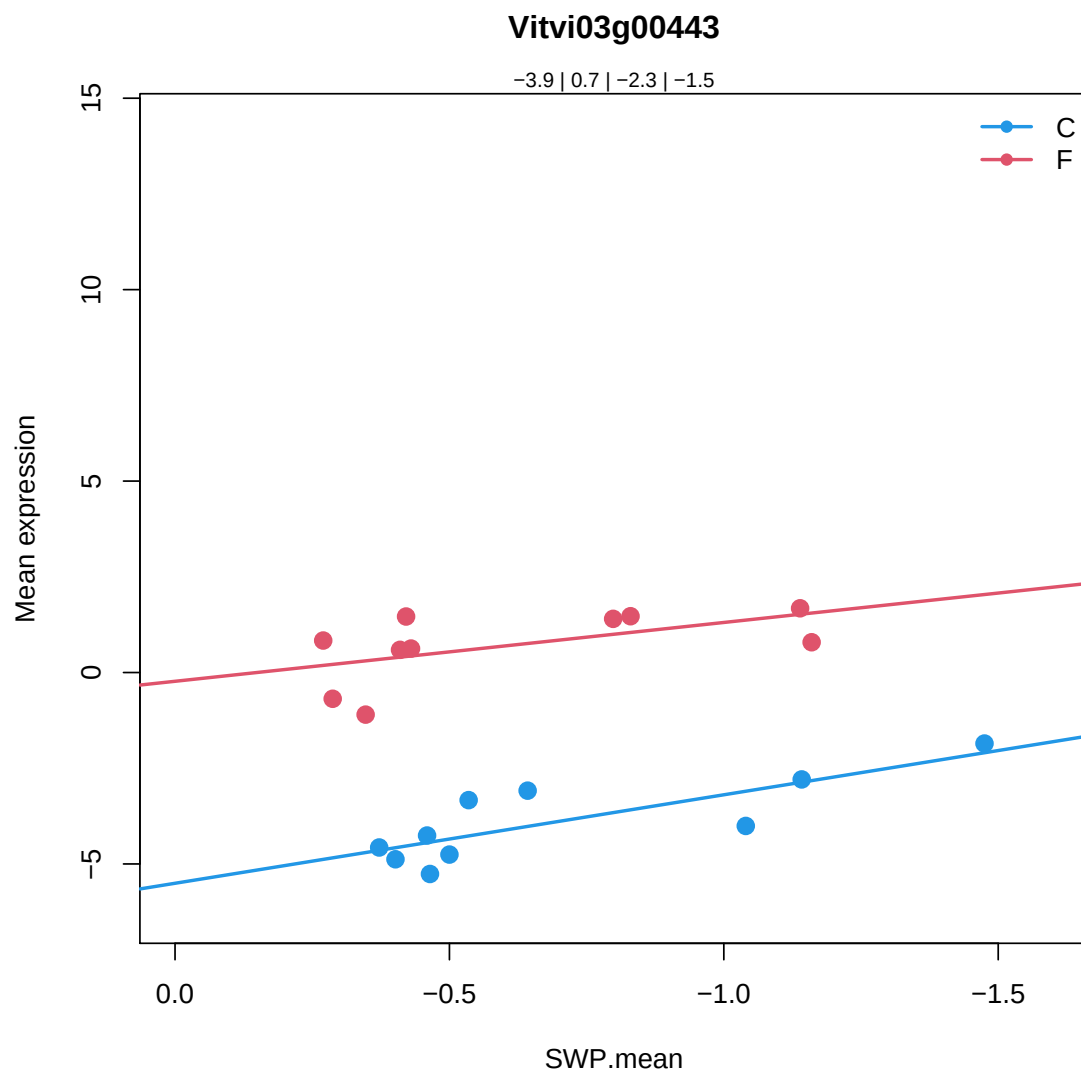
misc.nitrilases, nitrile lyases, berberine bridge enzymes, reticuline
acetone-cyanohydrin lyase |

Chr2:10042681-10043686 REVERSE LENGTH=187 |

201606

Coefficients for Vitvi03g00443.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-3.879575	2.657365e-14	***	4.276136e-14	***
SlopeC	-2.311521	0.001013174	**	0.1271346	
MeanF-MeanC	4.586549	9.379116e-13	***	8.360029e-11	***
SlopeF-SlopeC	0.7750986	0.401223		0.9999488	



7.5.41 Vitvi09g01282

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

Vitvi09g01282

26.13

misc.acid and other phosphatases

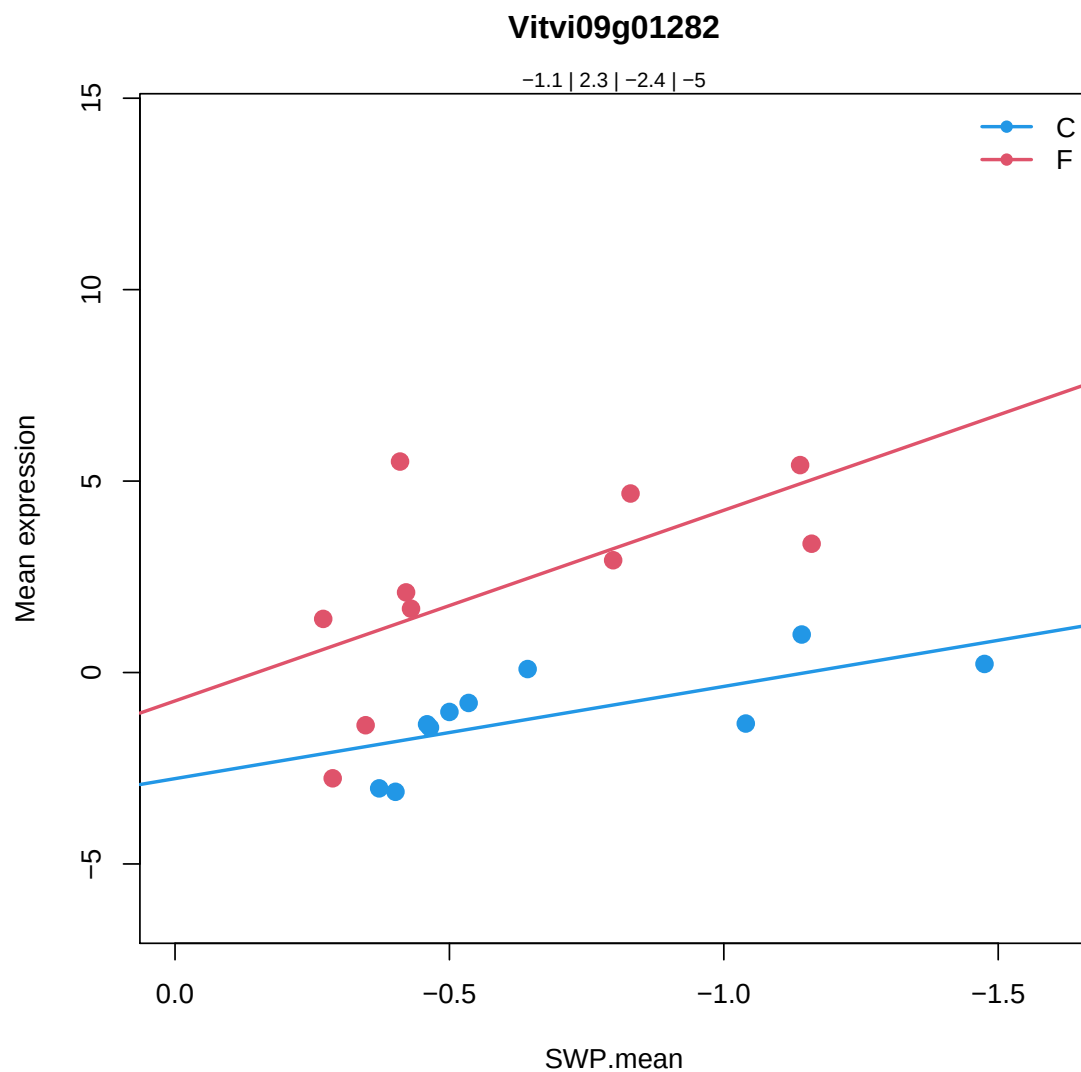
HAD superfamily%2C subfamily IIIB acid phosphatase |

Chr4:12901736-12902882 REVERSE LENGTH=260 |

201606

Coefficients for Vitvi09g01282.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.078226	0.03754027	*	0.03919906	*
SlopeC	-2.408129	0.08927348	.	0.5953805	
MeanF-MeanC	3.37008	7.180676e-05	***	0.001351208	**
SlopeF-SlopeC	-2.570707	0.2154002		0.9999488	



7.5.42 Vitvi03g01431

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

Vitvi03g01431

26.7

misc.oxidases - copper, flavone etc

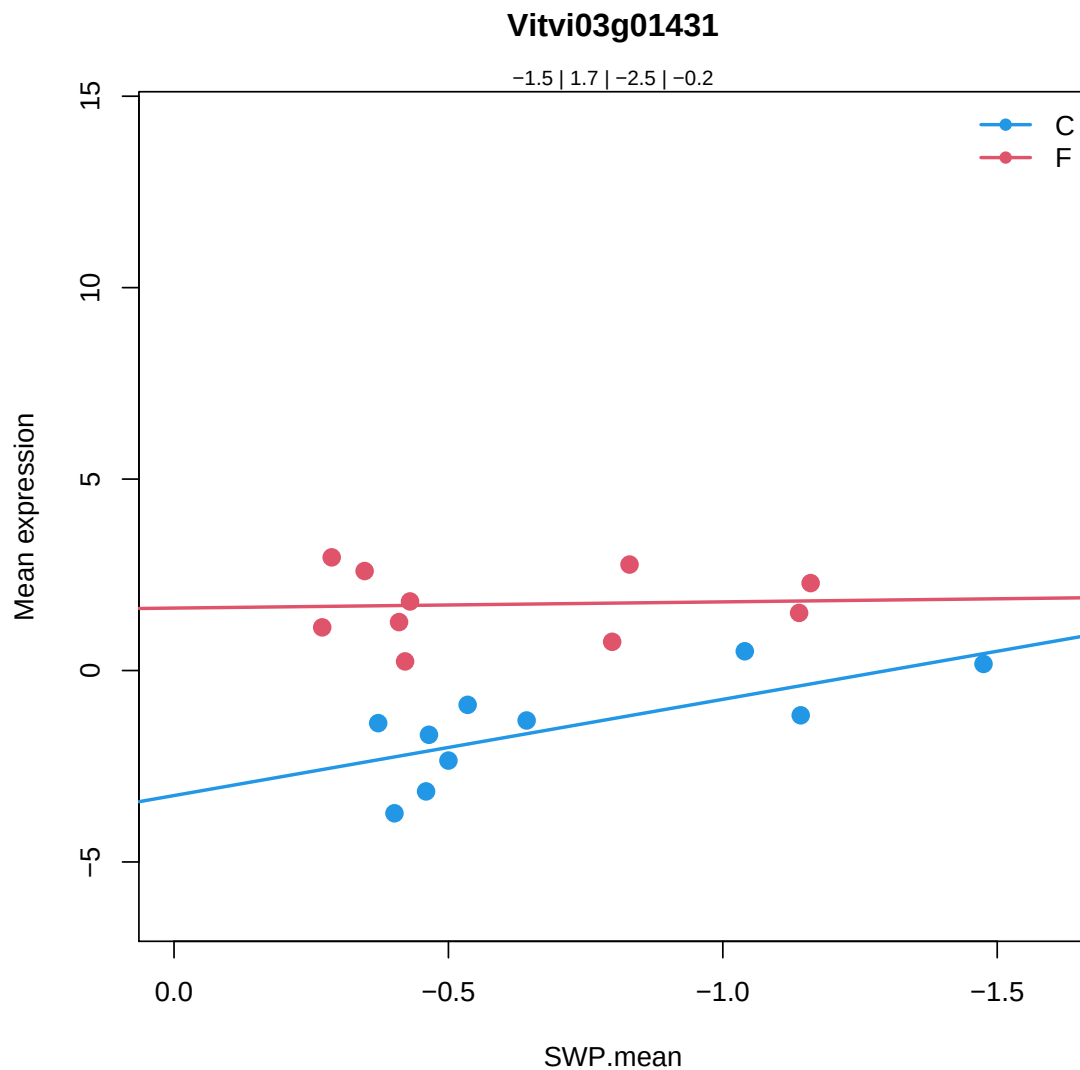
flavin-dependent monooxygenase 1 |

Chr1:6650656-6653053 REVERSE LENGTH=530 |

201606

Coefficients for Vitvi03g01431.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.498922	2.078617e-05	***	2.330265e-05	***
SlopeC	-2.513015	0.003608732	**	0.2248659	
MeanF-MeanC	3.228153	4.224193e-08	***	1.877118e-06	***
SlopeF-SlopeC	2.351136	0.05238461	.	0.9999488	



7.5.43 Vitvi07g02214

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

Vitvi07g02214

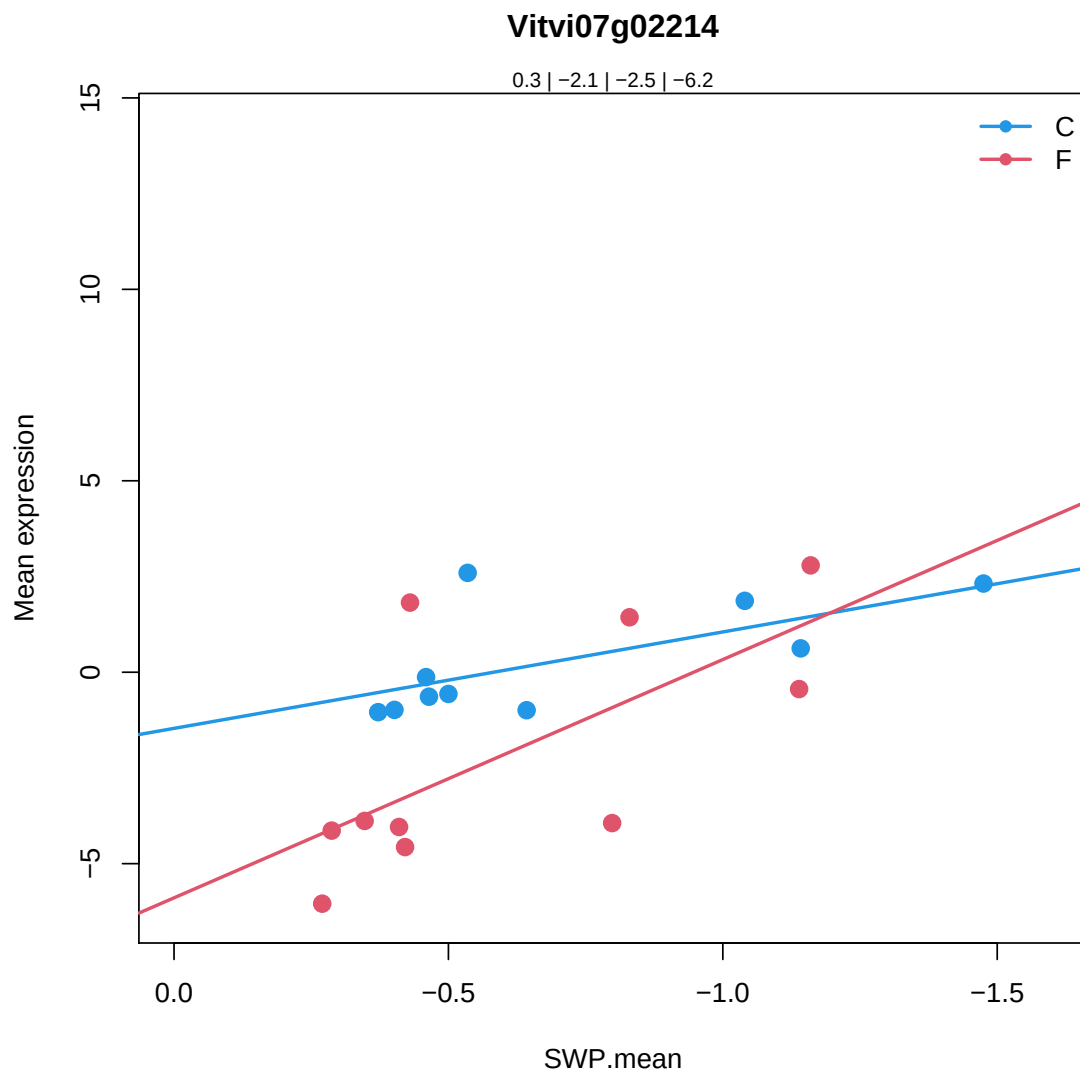
35.2

not assigned.unknown

GATA transcription factor 22 IPR000679 Zinc finger, GATA-type

Coefficients for Vitvi07g02214.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3045917	0.5752195		0.5808597	
SlopeC	-2.518808	0.1052292		0.619507	
MeanF-MeanC	-2.405858	0.004444061	**	0.04150513	*
SlopeF-SlopeC	-3.70436	0.1091801		0.9999488	



7.5.44 Vitvi19g02145

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

Vitvi19g02145

26.9

misc.glutathione S transferases

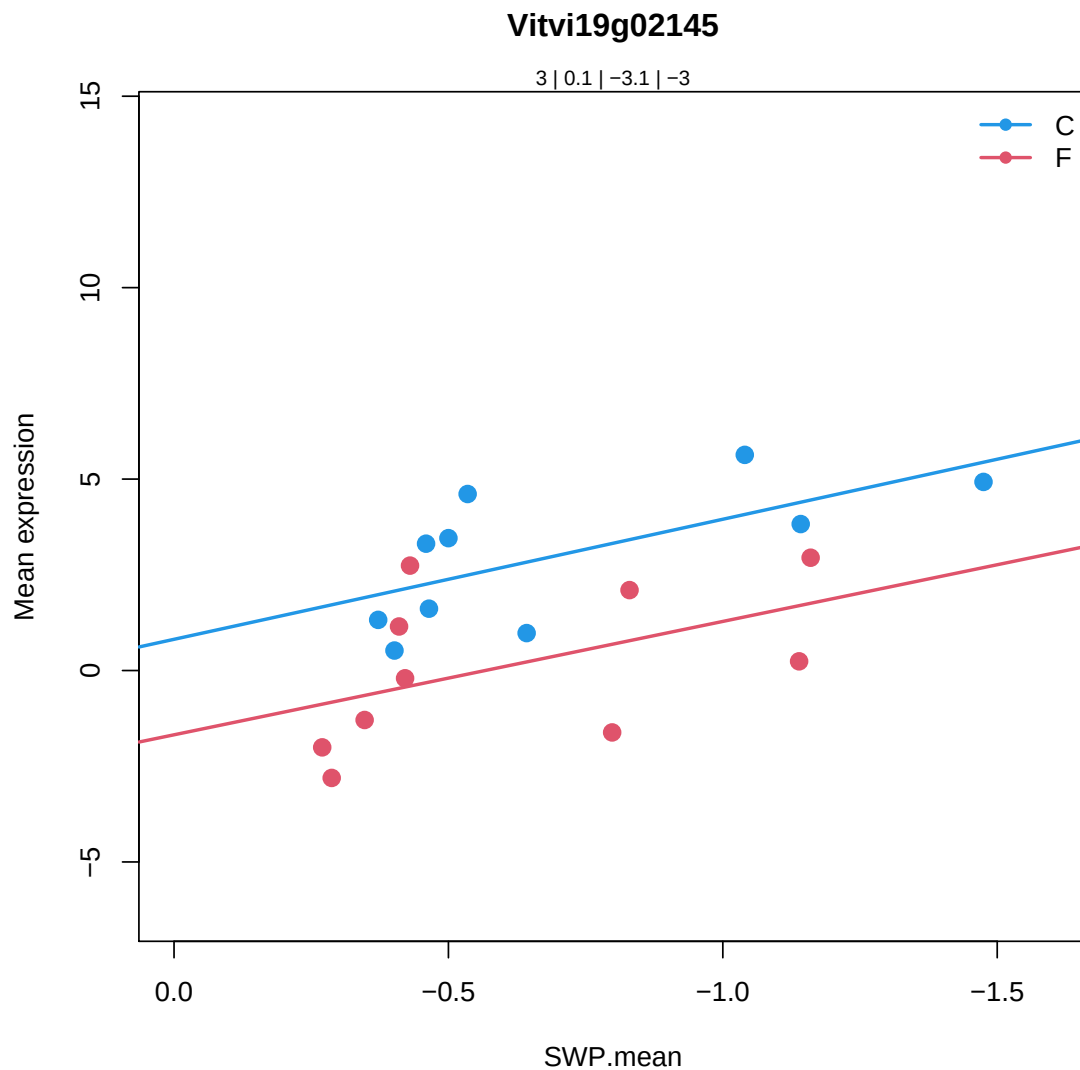
glutathione S-transferase TAU 25 |

Chr1:5872208-5872958 FORWARD LENGTH=221 |

201606

Coefficients for Vitvi19g02145.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.020018	1.808191e-06	***	2.075492e-06	***
SlopeC	-3.135408	0.02447993	*	0.4039715	
MeanF-MeanC	-2.894891	0.0002419684	***	0.003857827	**
SlopeF-SlopeC	0.1742035	0.9288624		0.9999488	



7.5.45 Vitvi01g00408

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

Vitvi01g00408

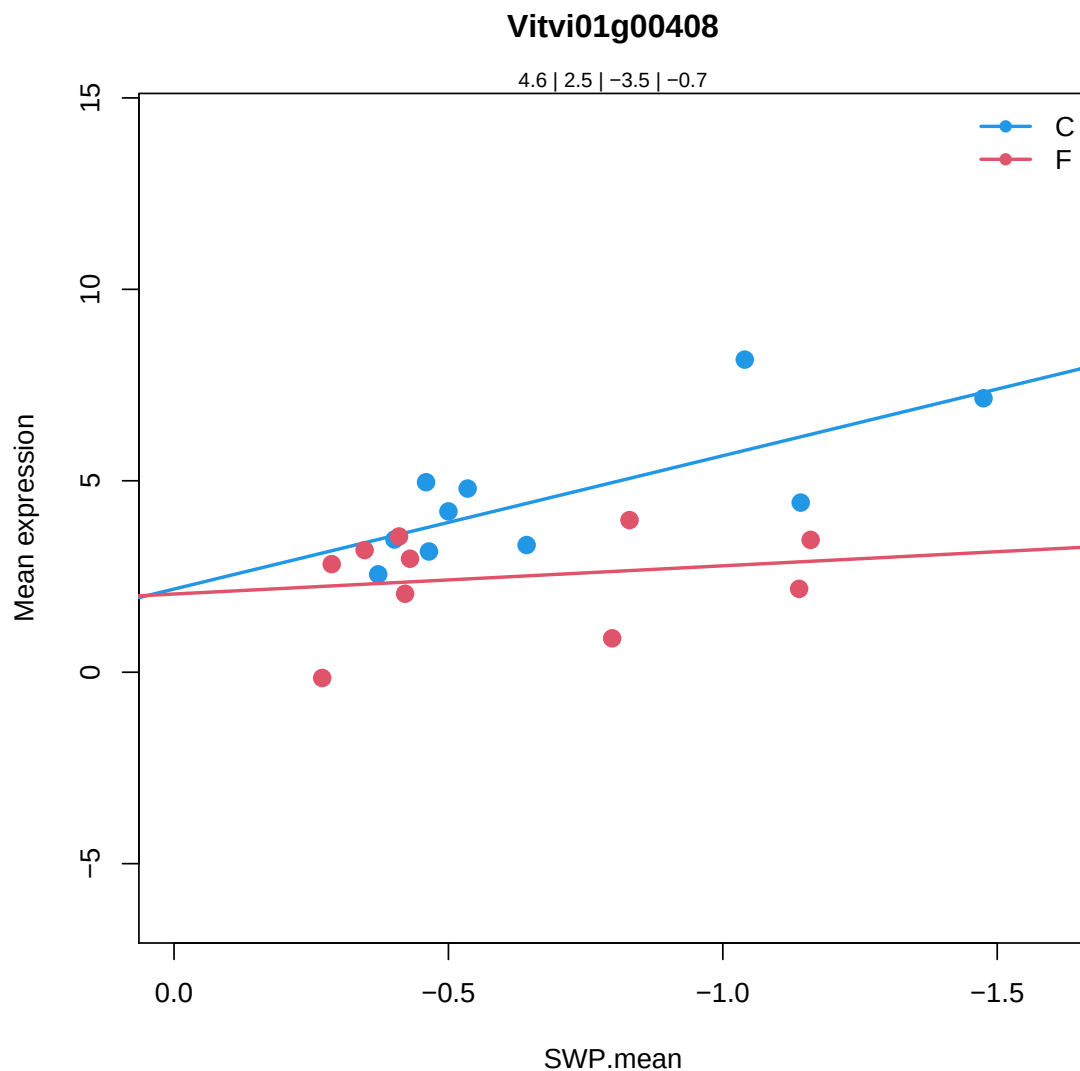
20.02.2001

stress.abiotic.heat

Chaperone protein dnaJ IPR001623 Heat shock protein DnaJ, N-terminal

Coefficients for Vitvi01g00408.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.620739	2.147964e-11	***	2.890884e-11	***
SlopeC	-3.482485	0.002526958	**	0.1902008	
MeanF-MeanC	-2.129225	0.0004797738	***	0.006808857	**
SlopeF-SlopeC	2.745564	0.08420911	.	0.9999488	



7.5.46 Vitvi07g02242

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

Vitvi07g02242

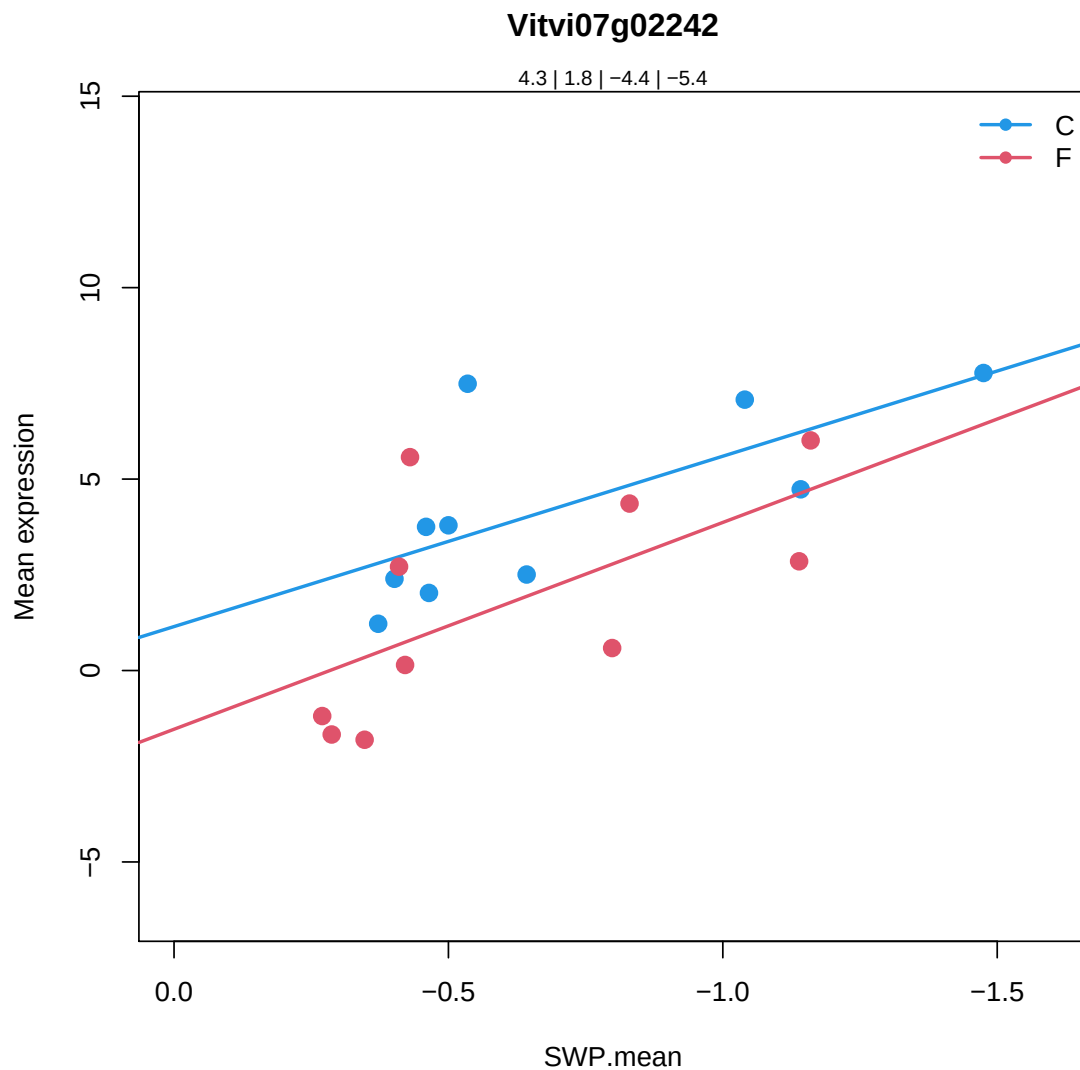
3.1.1.1

minor CHO metabolism.raffinose family.galactinol synthases.known
galactinol synthase 1 |

Chr2:19369049-19370372 REVERSE LENGTH=344 |
201606

Coefficients for Vitvi07g02242.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.276297	3.725657e-07	***	4.348787e-07	***
SlopeC	-4.449677	0.01340344	*	0.3305597	
MeanF-MeanC	-2.519255	0.00668982	**	0.05649099	.
SlopeF-SlopeC	-0.9519606	0.7022784		0.9999488	



7.5.47 Vitvi04g01801

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

Vitvi04g01801

20.02.2001

stress.abiotic.heat

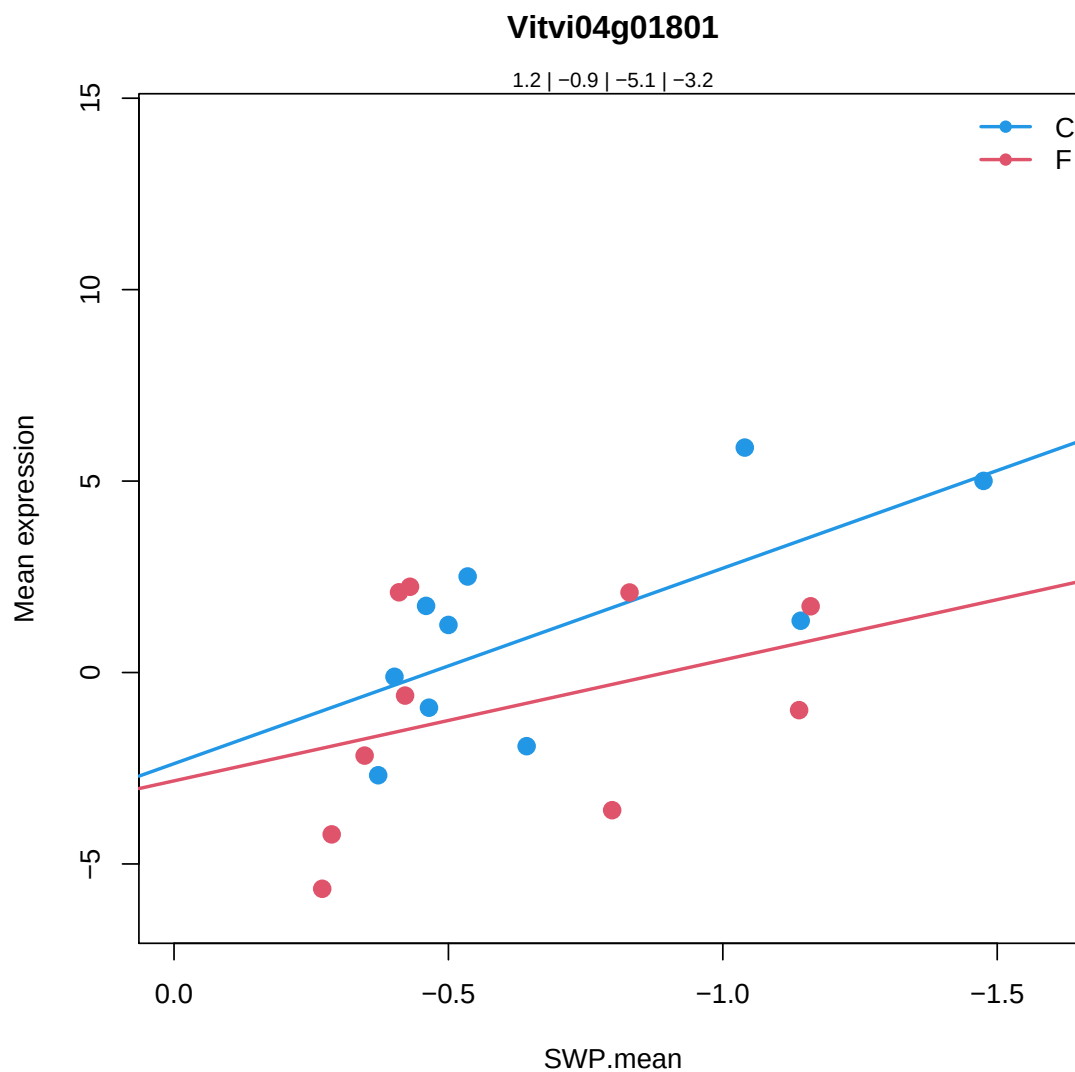
17.6 kDa class II heat shock protein |

Chr5:3882409-3882876 REVERSE LENGTH=155 |

201606

Coefficients for Vitvi04g01801.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.208586	0.09664858	.	0.09995371	.
SlopeC	-5.104125	0.01523524	*	0.3393703	
MeanF-MeanC	-2.115849	0.04303485	*	0.2168388	
SlopeF-SlopeC	1.948595	0.5059525		0.9999488	



7.5.48 Vitvi16g01103

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

Vitvi16g01103

20.02.2001

stress.abiotic.heat

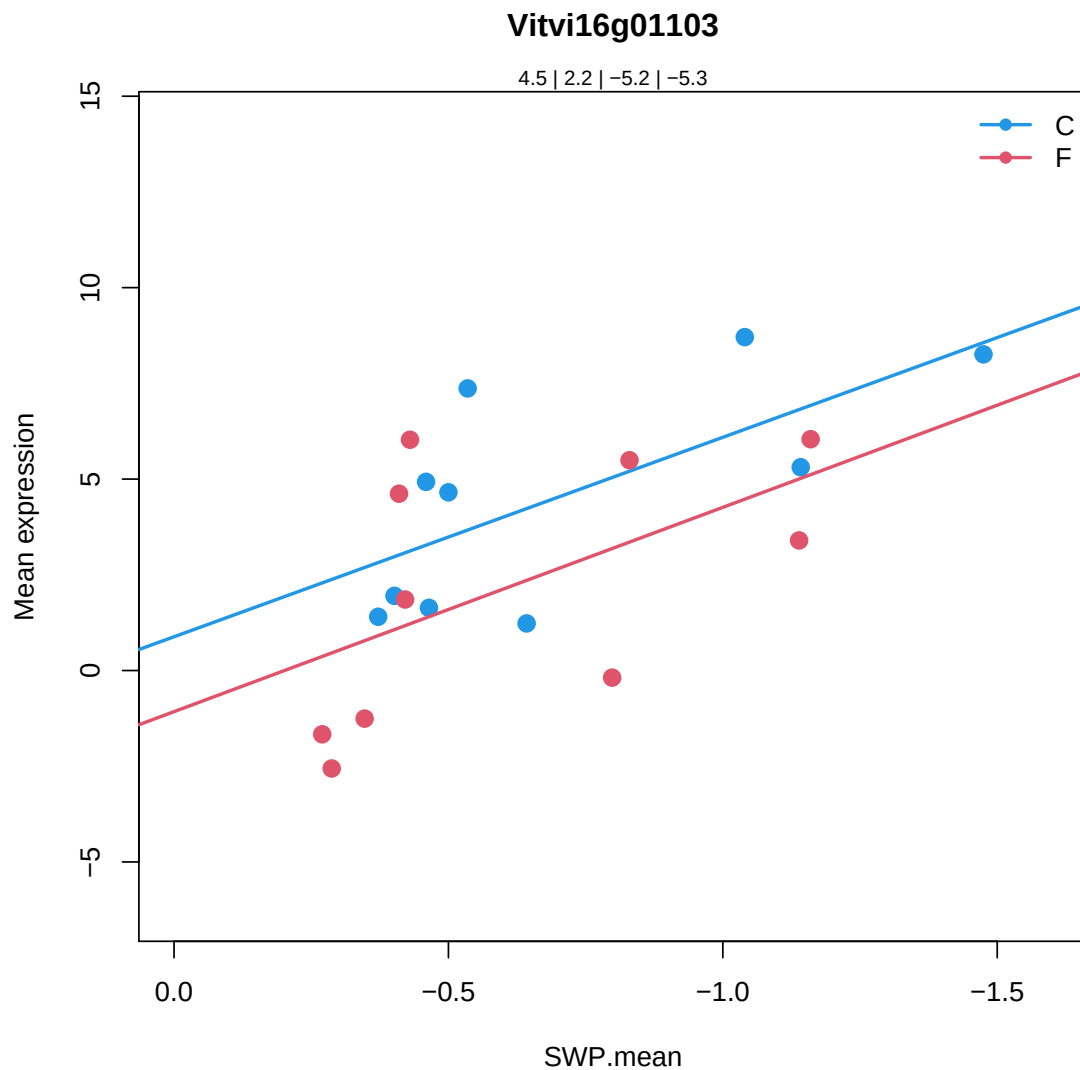
heat shock-like protein |

Chr5:21352557-21355147 FORWARD LENGTH=700 |

201606

Coefficients for Vitvi16g01103.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.544681	3.332247e-06	***	3.801939e-06	***
SlopeC	-5.209495	0.01806874	*	0.3612388	
MeanF-MeanC	-2.368196	0.03229181	*	0.1781367	
SlopeF-SlopeC	-0.1260899	0.9671792		0.9999488	



7.5.49 Vitvi08g02274

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

Vitvi08g02274

35.2

not assigned.unknown

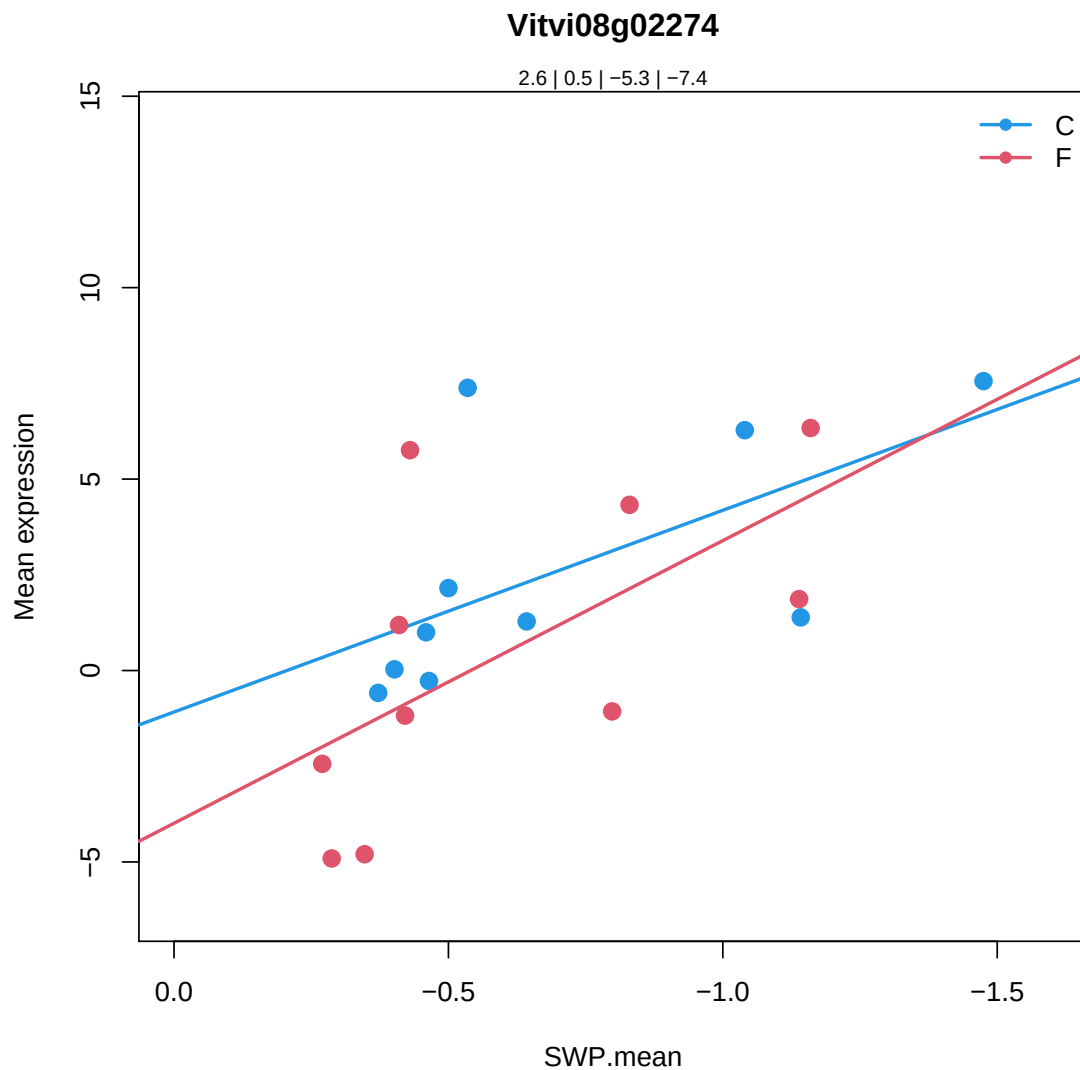
plant/protein |

Chr3:3091225-3091674 REVERSE LENGTH=149 |

201606

Coefficients for Vitvi08g02274.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.621184	0.004851113	**	0.005175743	**
SlopeC	-5.267913	0.03371344	*	0.4433084	
MeanF-MeanC	-2.113039	0.08753536	.	0.337434	
SlopeF-SlopeC	-2.113051	0.5473344		0.9999488	



7.5.50 Vitvi04g01799

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

Vitvi04g01799

20.02.2001

stress.abiotic.heat

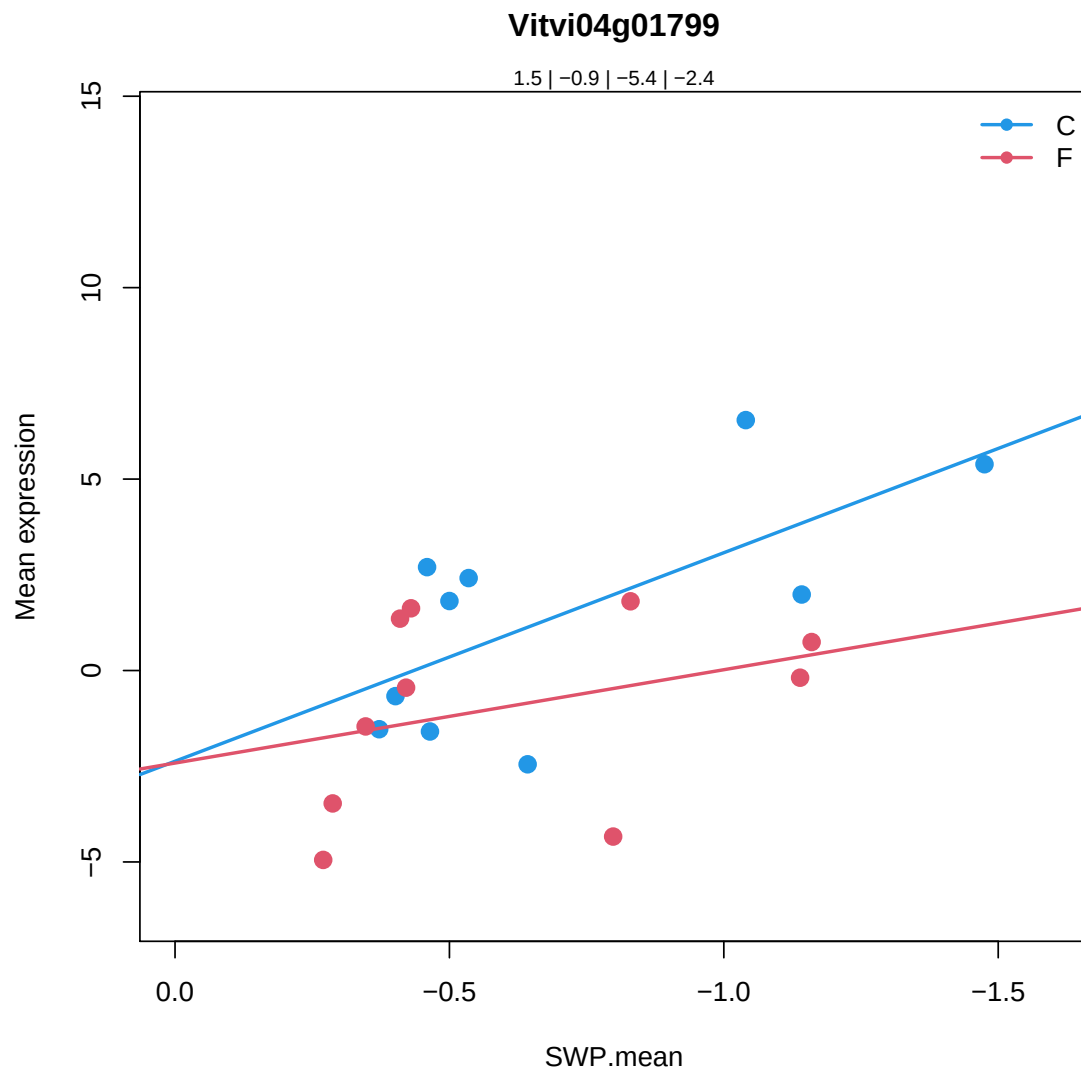
17.6 kDa class II heat shock protein |

Chr5:3882409-3882876 REVERSE LENGTH=155 |

201606

Coefficients for Vitvi04g01799.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.459784	0.04054411	*	0.04232114	*
SlopeC	-5.446372	0.008008975	**	0.2832315	
MeanF-MeanC	-2.391652	0.01948465	*	0.1236922	
SlopeF-SlopeC	3.008905	0.2899314		0.9999488	



7.5.51 Vitvi04g01794

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

Vitvi04g01794

20.02.2001

stress.abiotic.heat

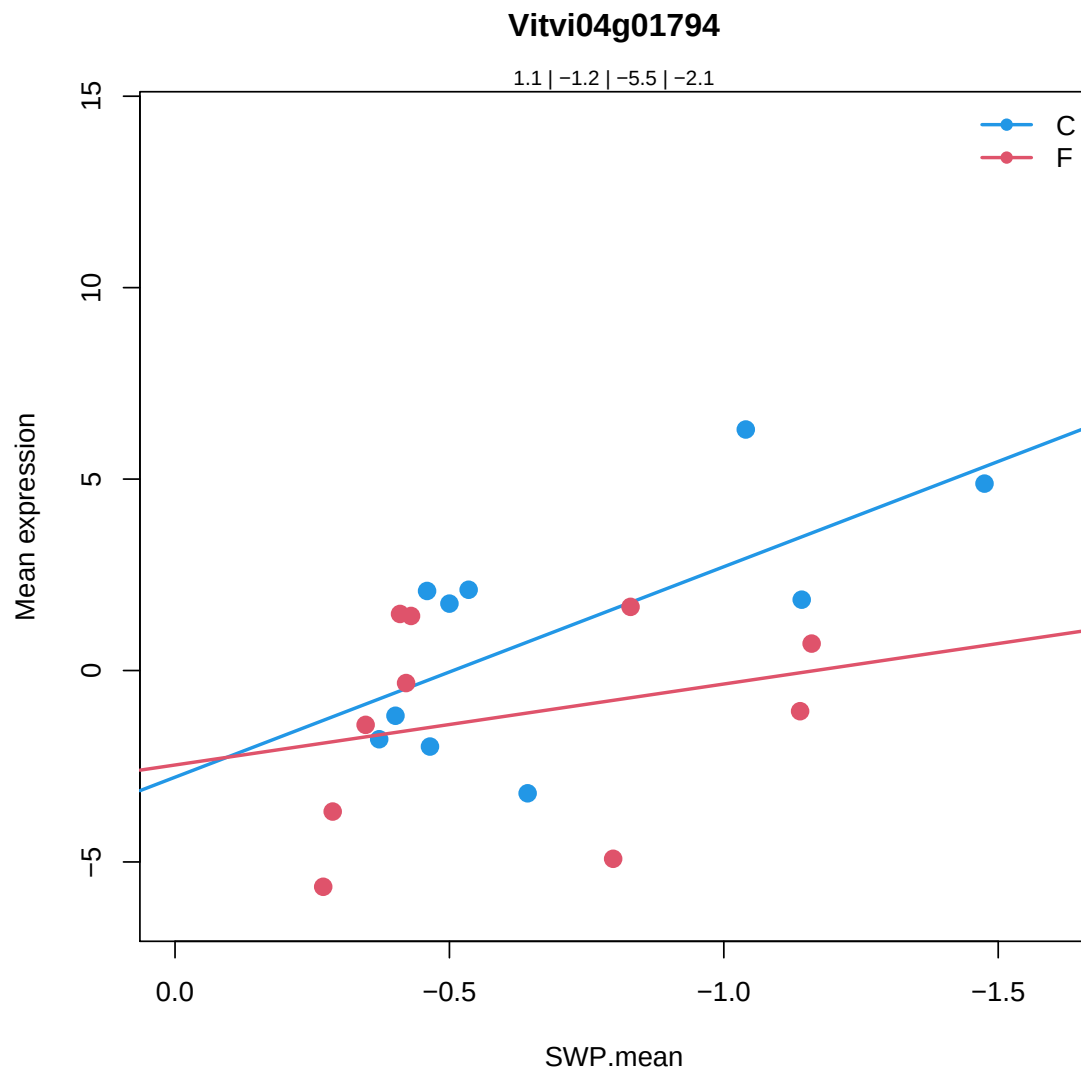
17.6 kDa class II heat shock protein |

Chr5:3882409-3882876 REVERSE LENGTH=155 |

201606

Coefficients for Vitvi04g01794.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.079134	0.1462899		0.1505876	
SlopeC	-5.497568	0.01158549	*	0.318473	
MeanF-MeanC	-2.25819	0.03651267	*	0.192703	
SlopeF-SlopeC	3.382727	0.2663928		0.9999488	



7.5.52 Vitvi13g00409

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

Vitvi13g00409

35.2

not assigned.unknown

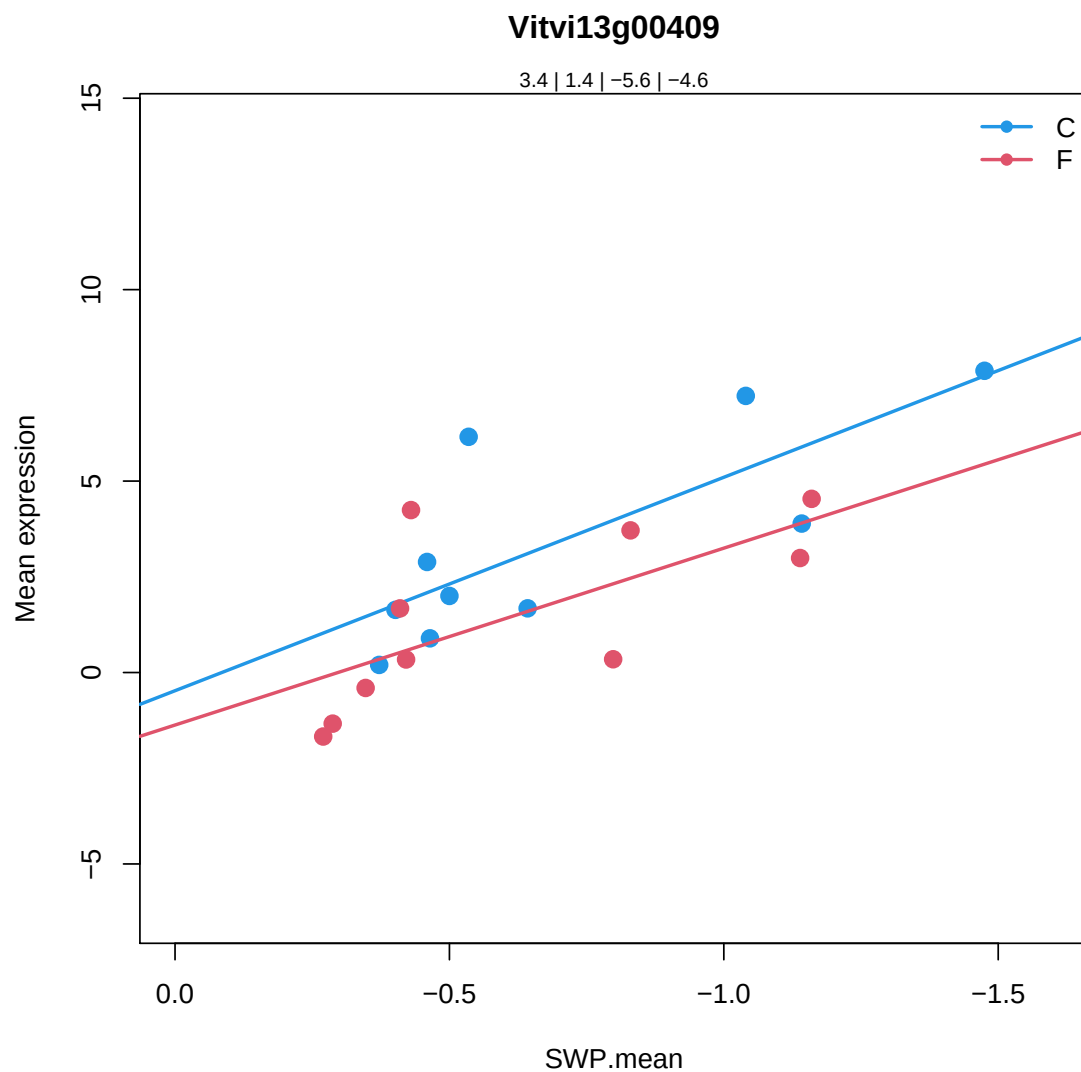
heat shock protein 18.2 |

Chr5:24062632-24063117 FORWARD LENGTH=161 |

201606

Coefficients for Vitvi13g00409.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.444287	7.91282e-07	***	9.154942e-07	***
SlopeC	-5.574561	0.0006440829	***	0.1015345	
MeanF-MeanC	-2.001179	0.01018303	*	0.0770272	.
SlopeF-SlopeC	0.9551048	0.650661		0.9999488	



7.5.53 Vitvi04g01795

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

Vitvi04g01795

35.2

not assigned.unknown

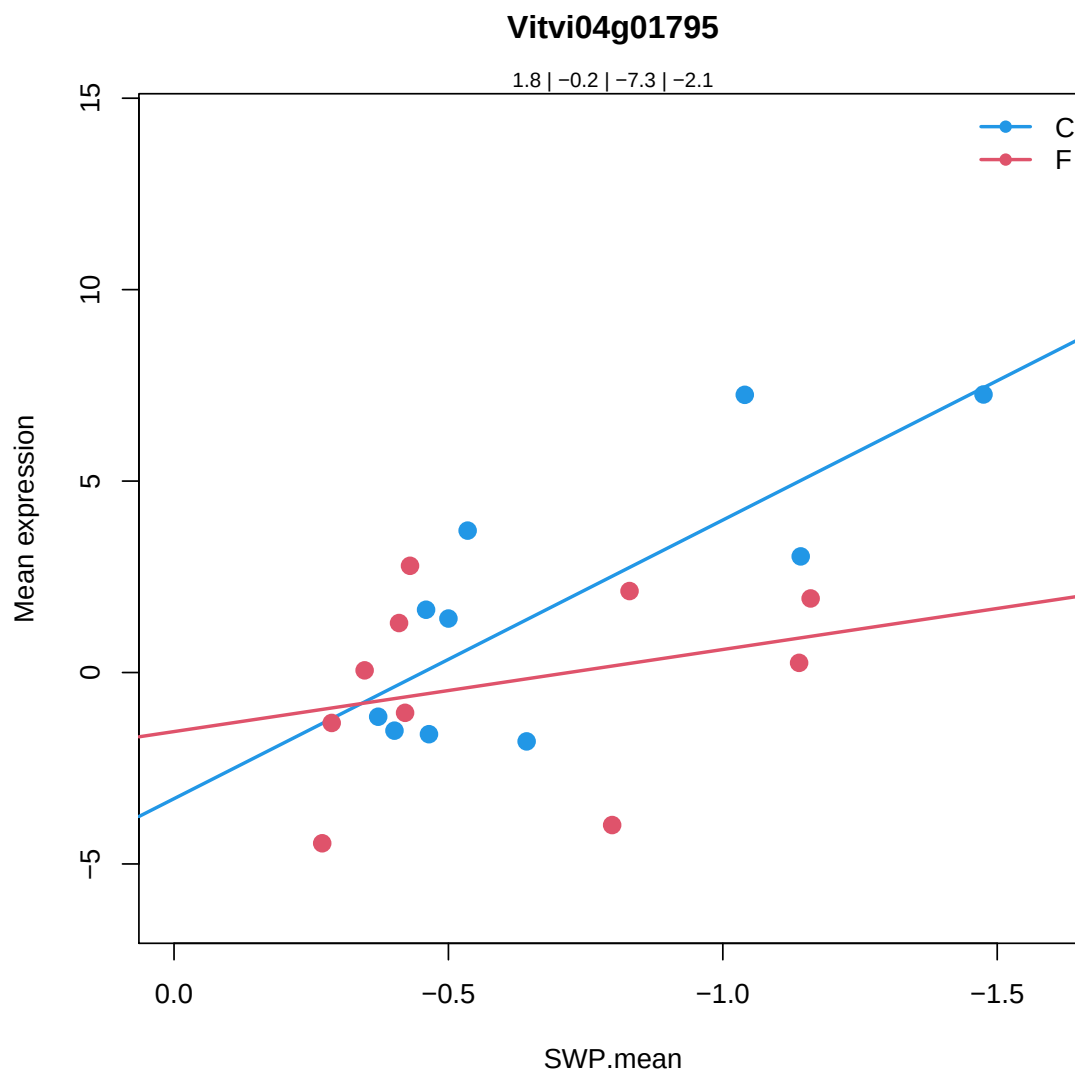
17.6 kDa class II heat shock protein |

Chr5:3882409-3882876 REVERSE LENGTH=155 |

201606

Coefficients for Vitvi04g01795.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.821988	0.01144052	*	0.01210359	*
SlopeC	-7.277261	0.0006740302	***	0.1037734	
MeanF-MeanC	-2.058336	0.03814072	*	0.1995898	
SlopeF-SlopeC	5.133591	0.07347637	.	0.9999488	



7.6 type5

7.6.1 Vitvi18g02730

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

Vitvi18g02730

35.2

not assigned.unknown

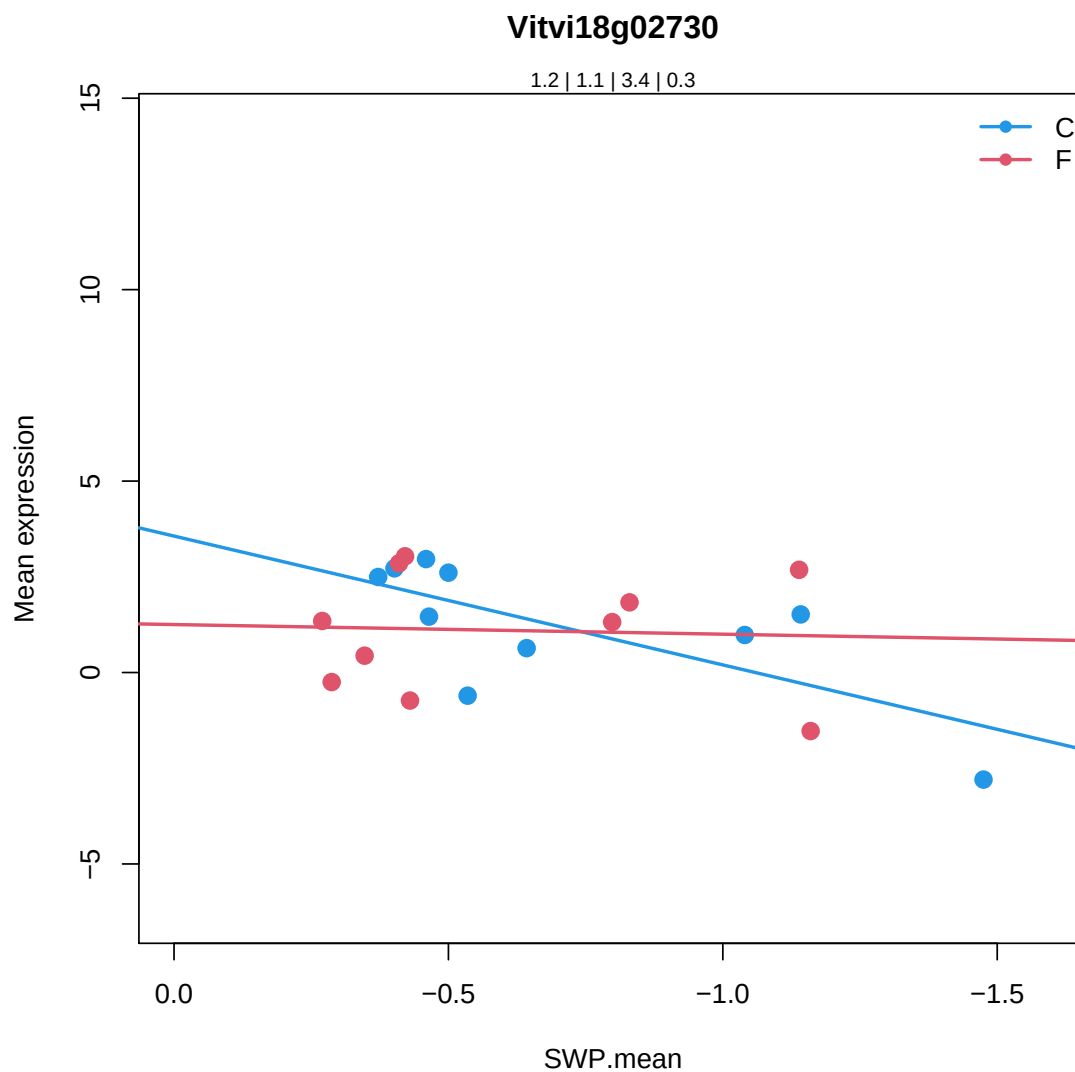
calcium uniporter (DUF607) |

Chr5:17062507-17063934 FORWARD LENGTH=293 |

201606

Coefficients for Vitvi18g02730.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.197709	0.009522617	**	0.01009064	*
SlopeC	3.364707	0.008940607	**	0.2903326	
MeanF-MeanC	-0.09823464	0.8703899		0.9660555	
SlopeF-SlopeC	-3.112693	0.08808841	.	0.9999488	



7.6.2 Vitvi14g01770

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

Vitvi14g01770

28.99

DNA.unspecified

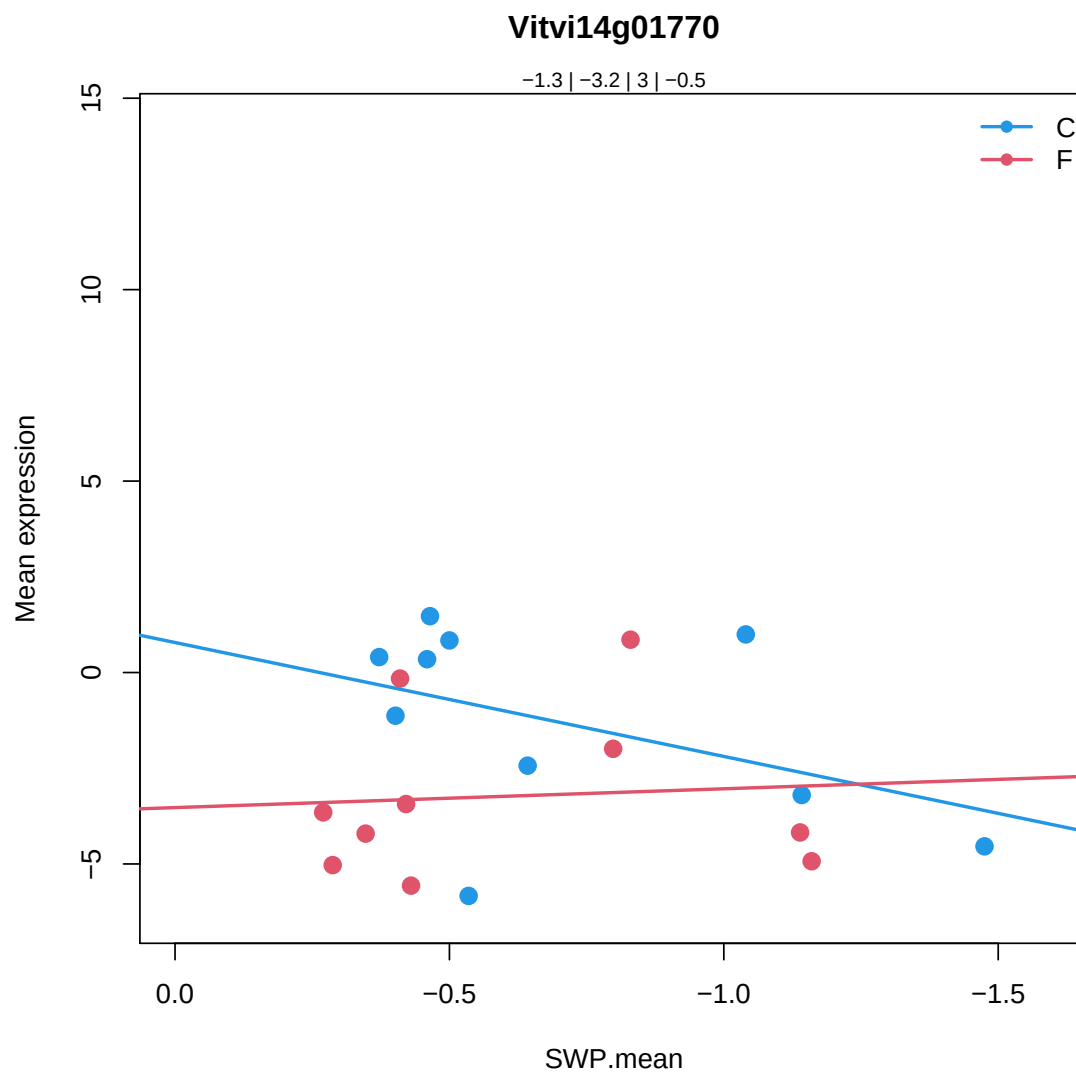
Exonuclease family protein |

Chr3:10389609-10391544 FORWARD LENGTH=357 |

201606

Coefficients for Vitvi14g01770.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.308148	0.05623463	.	0.05849108	.
SlopeC	2.974912	0.113551		0.6305081	
MeanF-MeanC	-1.920874	0.04814758	*	0.2335663	
SlopeF-SlopeC	-3.466655	0.2102088		0.9999488	



7.6.3 Vitvi14g02934

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

Vitvi14g02934

34.16

transport.ABC transporters and multidrug resistance systems

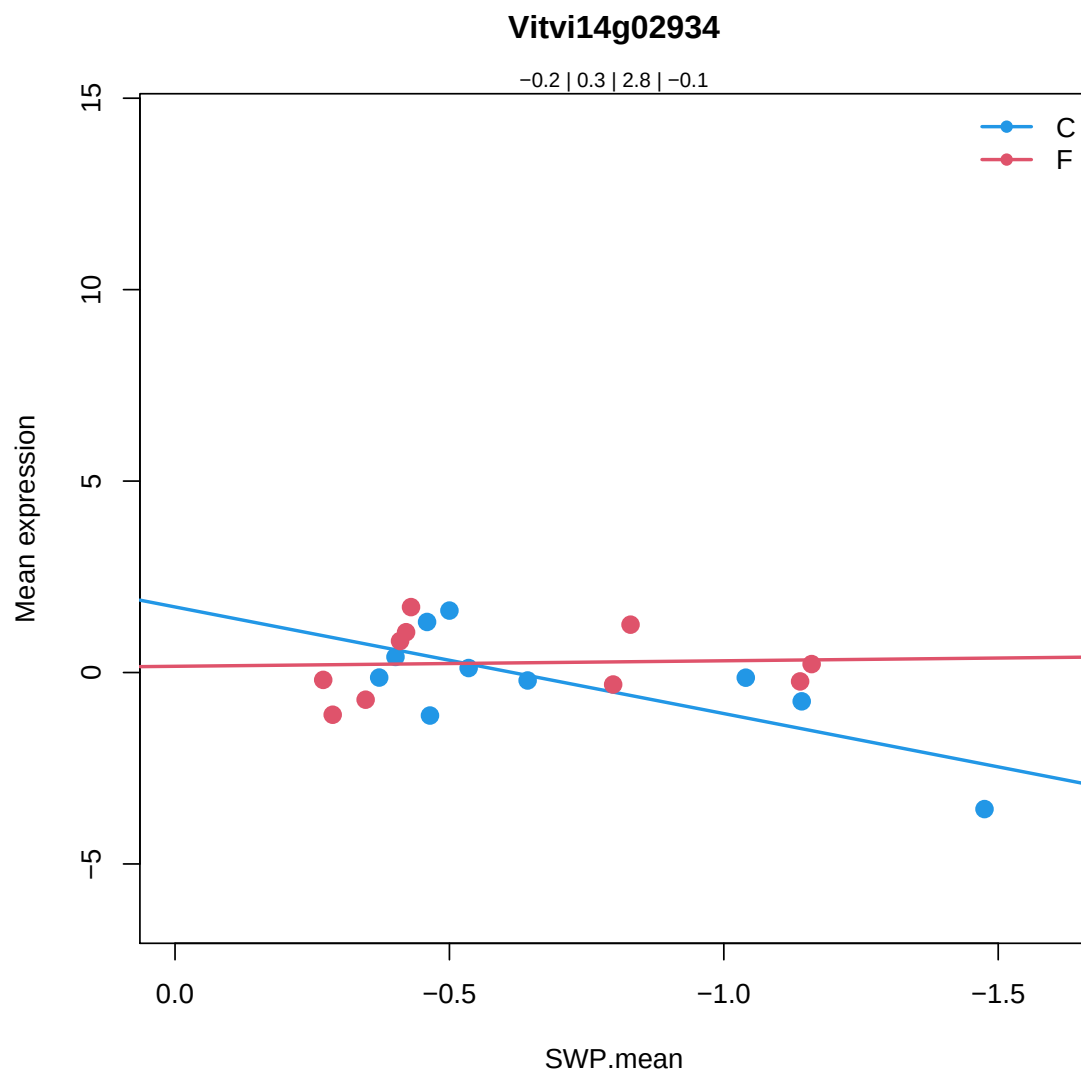
transporter associated with antigen processing protein 2 |

Chr5:15625660-15629621 FORWARD LENGTH=644 |

201606

Coefficients for Vitvi14g02934.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.2456549	0.3984604		0.4045922	
SlopeC	2.784639	0.002032099	**	0.1701827	
MeanF-MeanC	0.4958826	0.2321044		0.5863973	
SlopeF-SlopeC	-2.928269	0.02149545	*	0.9999488	



7.6.4 Vitvi10g00663

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

```
Vitvi10g00663
```

```
33.99
```

```
development.unspecified
```

```
K-box region and MADS-box transcription factor family protein |
```

```
Chr3:21739150-21741766 FORWARD LENGTH=241 |
```

```
201606
```

```
Vitvi10g00663
```

```
27.03.2024
```

```
RNA.regulation of transcription.MADS box transcription factor family
```

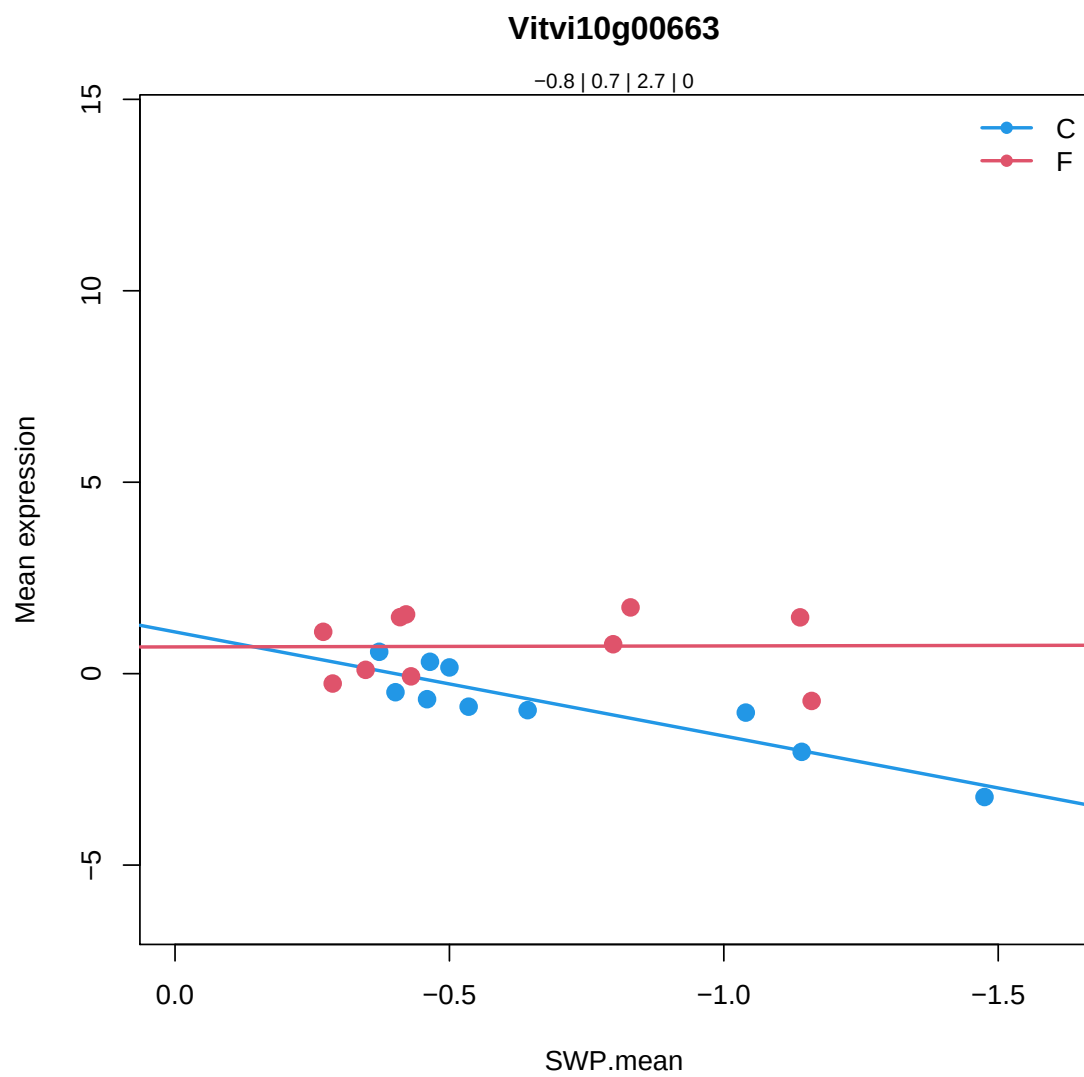
```
K-box region and MADS-box transcription factor family protein |
```

```
Chr3:21739150-21741766 FORWARD LENGTH=241 |
```

```
201606
```

Coefficients for Vitvi10g00663.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.8209171	0.001213348	**	0.001311992	**
SlopeC	2.716708	0.0002212026	***	0.08109226	.
MeanF-MeanC	1.534975	6.737202e-05	***	0.001277494	**
SlopeF-SlopeC	-2.742007	0.00662921	**	0.9999488	



7.6.5 Vitvi11g00243

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

Vitvi11g00243

10.05.2003

cell wall.cell wall proteins.LRR

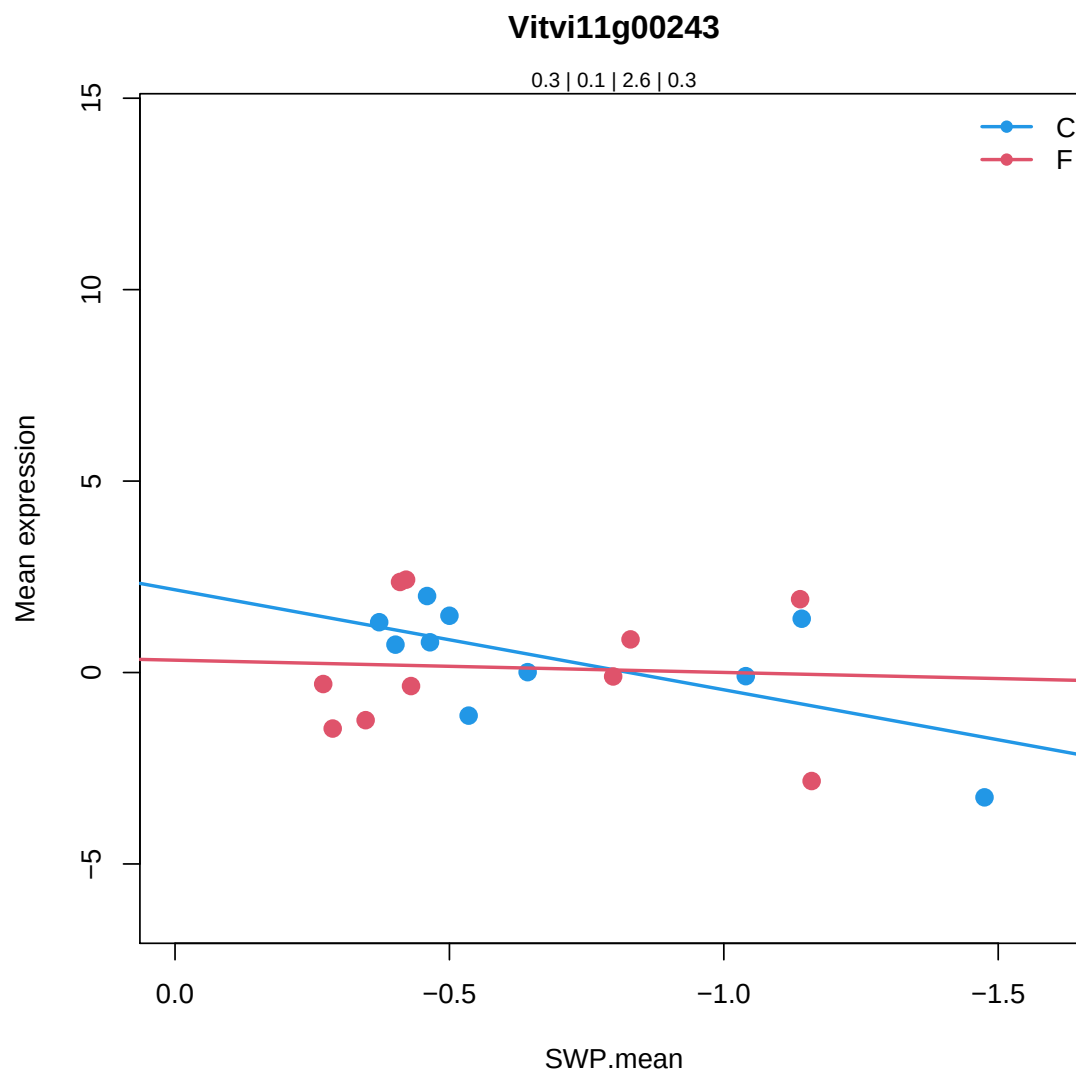
Leucine-rich repeat (LRR) family protein |

Chr4:14418826-14420073 FORWARD LENGTH=415 |

201606

Coefficients for Vitvi11g00243.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3244235	0.4712635		0.4774978	
SlopeC	2.612418	0.04557967	*	0.4926906	
MeanF-MeanC	-0.1974358	0.7553592		0.9285435	
SlopeF-SlopeC	-2.292601	0.2242025		0.9999488	



7.6.6 Vitvi05g01758

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

Vitvi05g01758

35.2

not assigned.unknown

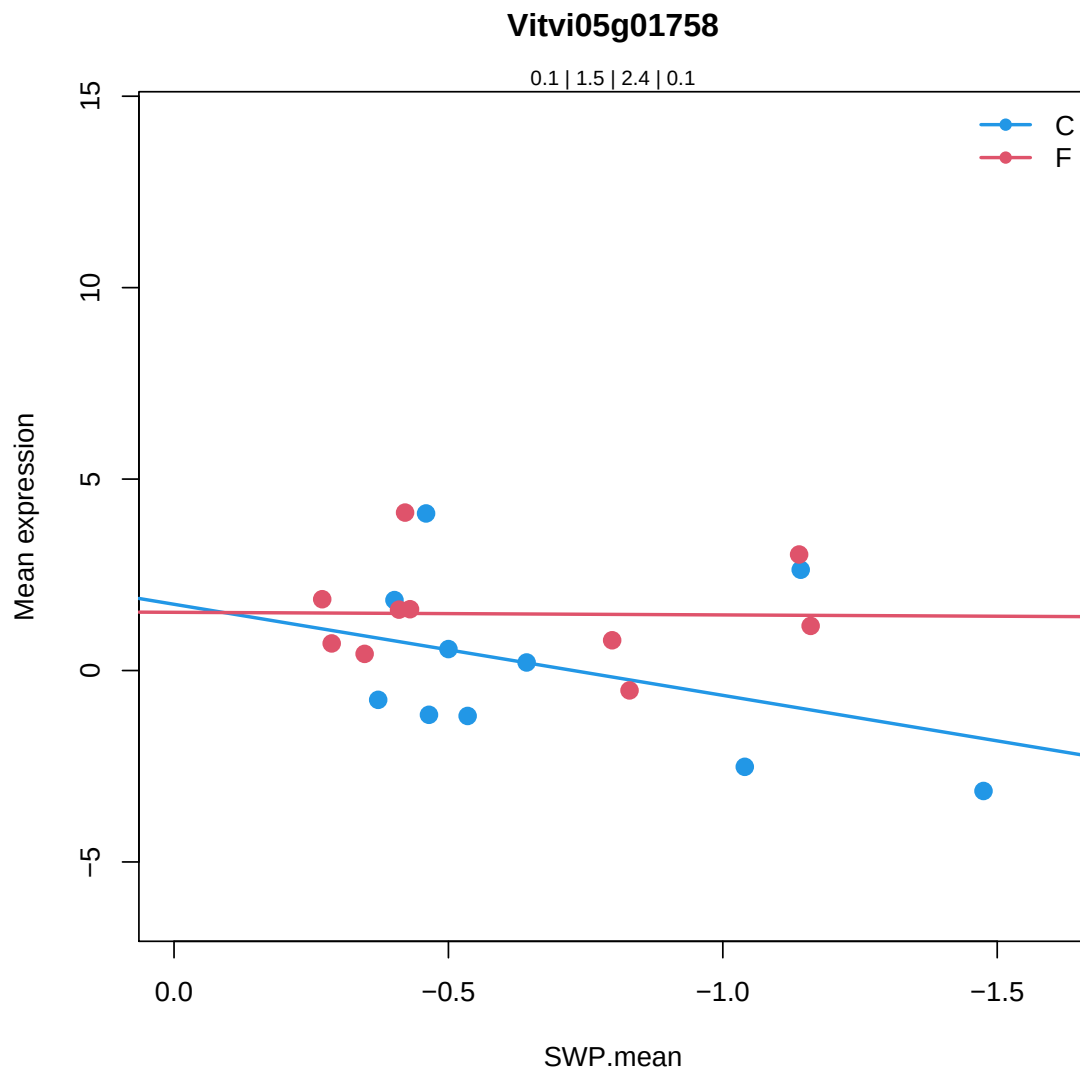
MLP-like protein 423 |

Chr1:8500653-8501458 REVERSE LENGTH=155 |

201606

Coefficients for Vitvi05g01758.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.0573489	0.9123565		0.914276	
SlopeC	2.378762	0.1113767		0.6258604	
MeanF-MeanC	1.421246	0.06415951	.	0.2806081	
SlopeF-SlopeC	-2.310635	0.2905474		0.9999488	



7.6.7 Vitvi16g02091

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

Vitvi16g02091

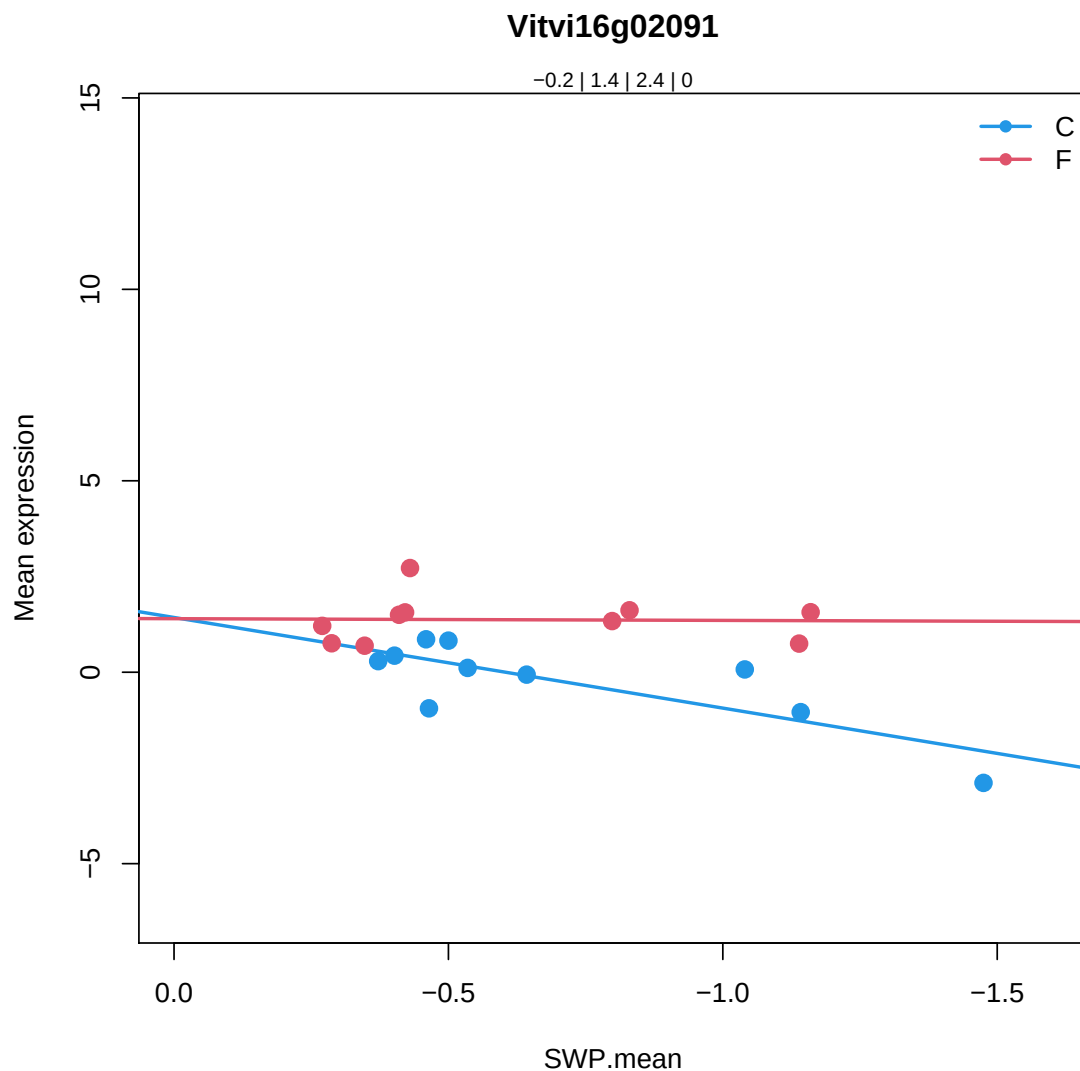
35.2

not assigned.unknown

Receptor-like protein kinase

Coefficients for Vitvi16g02091.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.2346616	0.2592422		0.2646775	
SlopeC	2.366765	0.0003865785	***	0.09467692	.
MeanF-MeanC	1.605684	1.346083e-05	***	0.0003309194	***
SlopeF-SlopeC	-2.321945	0.01135478	*	0.9999488	



7.6.8 Vitvi16g02098

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

Vitvi16g02098

35.2

not assigned.unknown

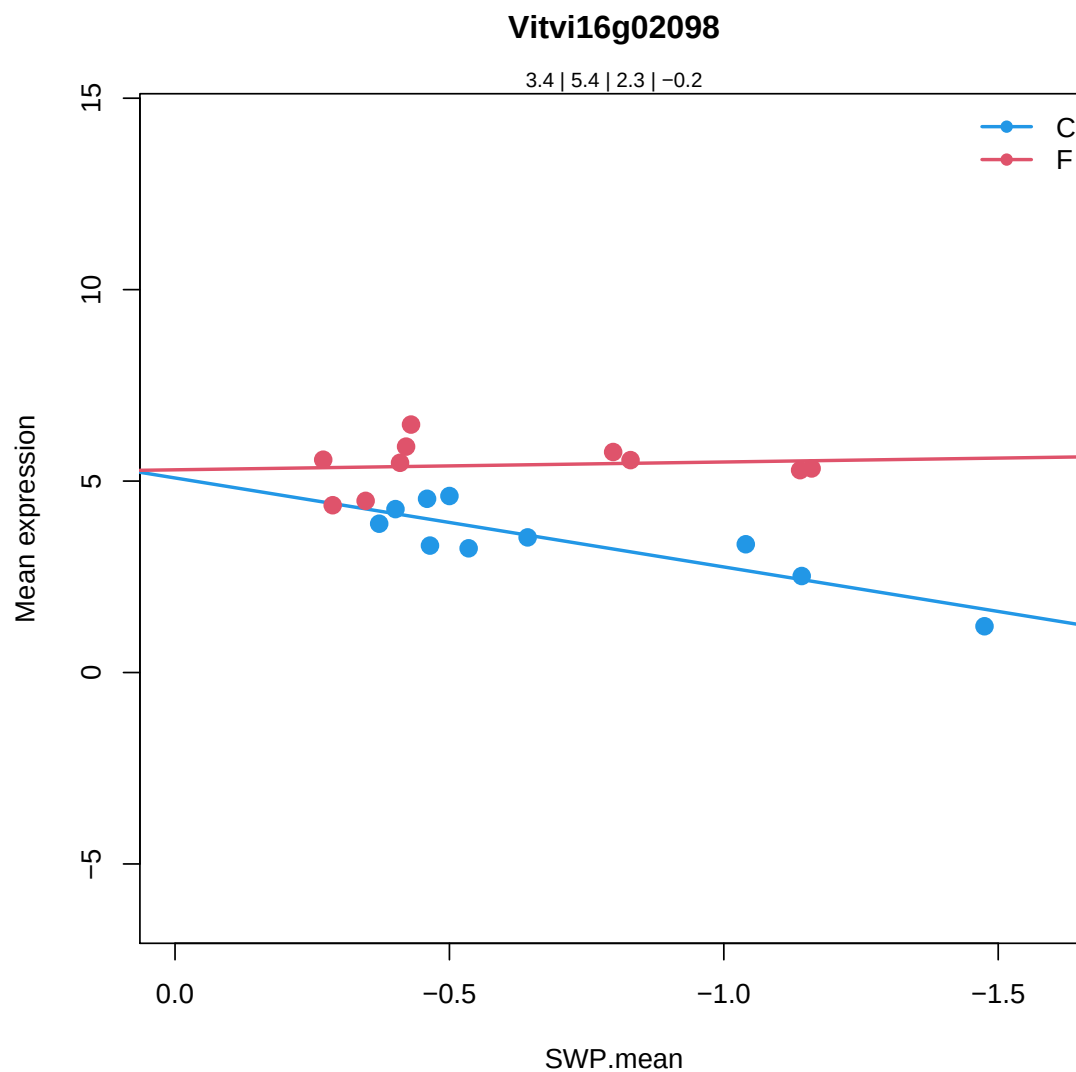
PR5-like receptor kinase |

Chr5:15293325-15295838 REVERSE LENGTH=665 |

201606

Coefficients for Vitvi16g02098.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.446831	7.658968e-15	***	1.295793e-14	***
SlopeC	2.32385	0.000156973	***	0.07644173	.
MeanF-MeanC	1.97166	1.502738e-07	***	5.828175e-06	***
SlopeF-SlopeC	-2.527587	0.003019792	**	0.9999488	



7.6.9 Vitvi07g02989

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

Vitvi07g02989

29.7

protein.glycosylation

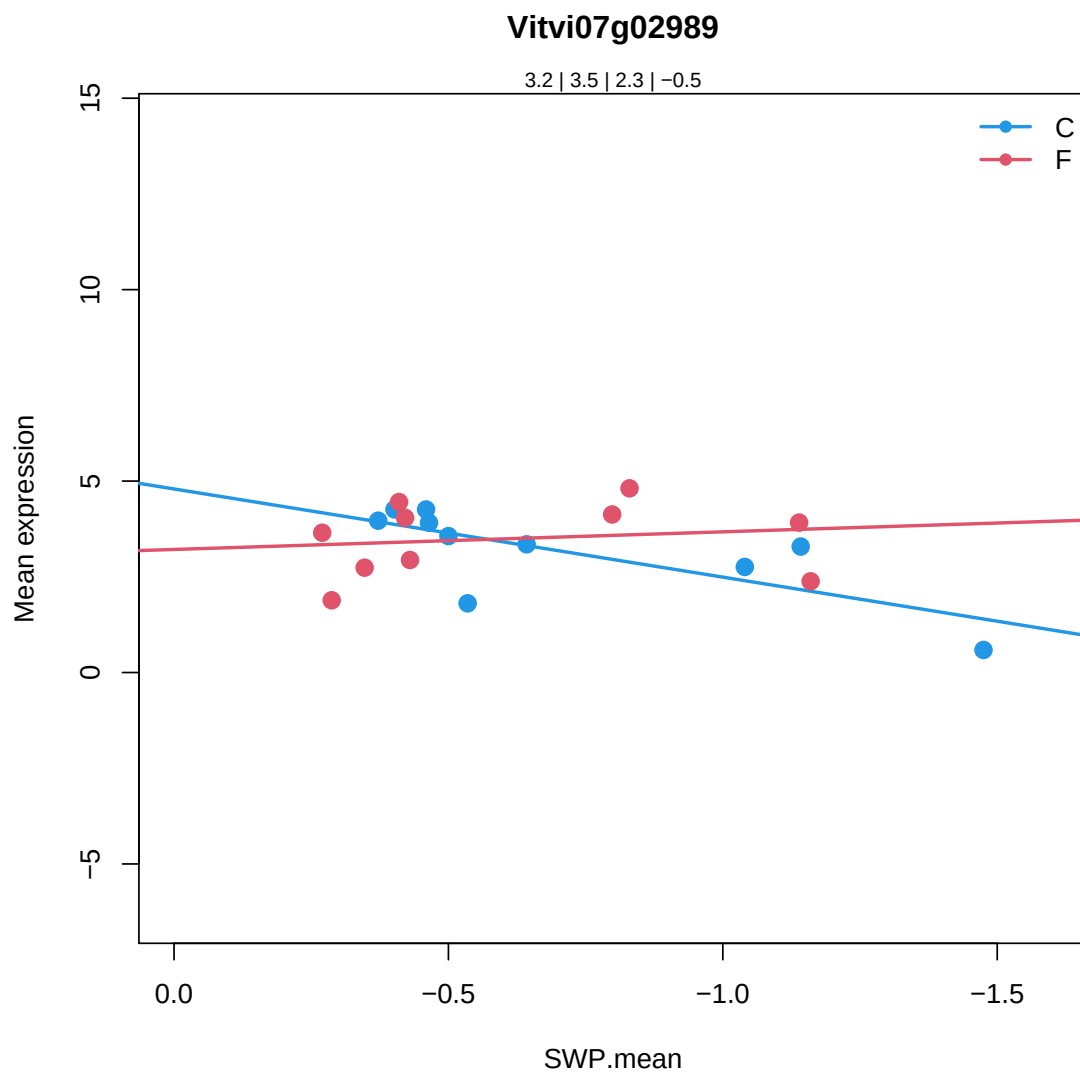
cysteine-rich RECEPTOR-like kinase |

Chr4:12129485-12133157 FORWARD LENGTH=1043 |

201606

Coefficients for Vitvi07g02989.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.174867	5.288199e-11	***	6.993122e-11	***
SlopeC	2.302397	0.004902096	**	0.2503311	
MeanF-MeanC	0.3194933	0.4013746		0.7457035	
SlopeF-SlopeC	-2.762497	0.01936364	*	0.9999488	



7.6.10 Vitvi05g01581

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

Vitvi05g01581

20.1.7.3

stress.biotic.PR-proteins.PR3/4/8/11 (chitinases and chitin binding pr

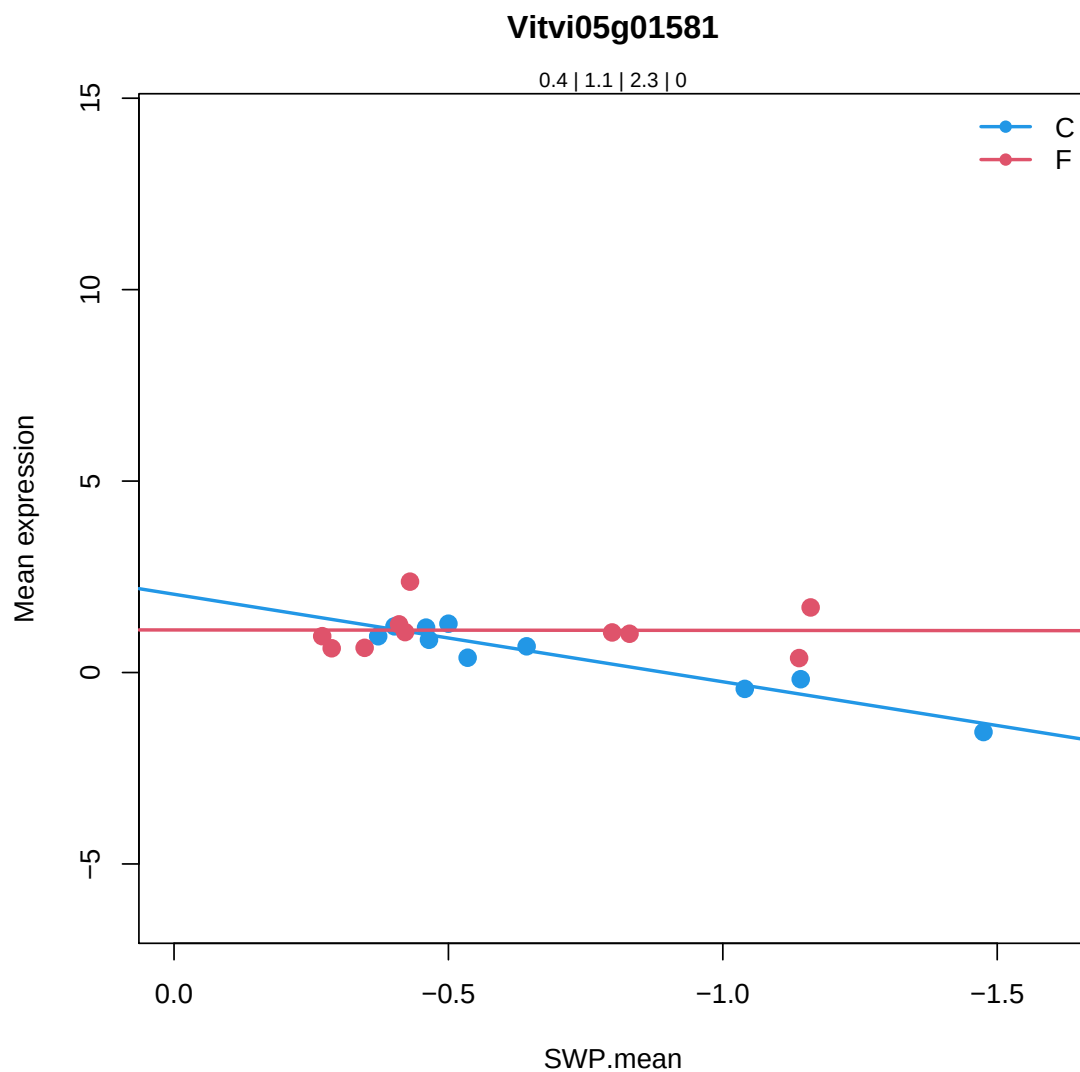
homolog of carrot EP3-3 chitinase |

Chr3:20145935-20147034 FORWARD LENGTH=273 |

201606

Coefficients for Vitvi05g01581.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4368721	0.009024529	**	0.009570157	**
SlopeC	2.2861	2.189805e-05	***	0.04768143	*
MeanF-MeanC	0.6679842	0.005283957	**	0.04768388	*
SlopeF-SlopeC	-2.274535	0.001603921	**	0.9999488	



7.6.11 Vitvi09g01696

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

Vitvi09g01696

20.01.2002

stress.biotic.receptors

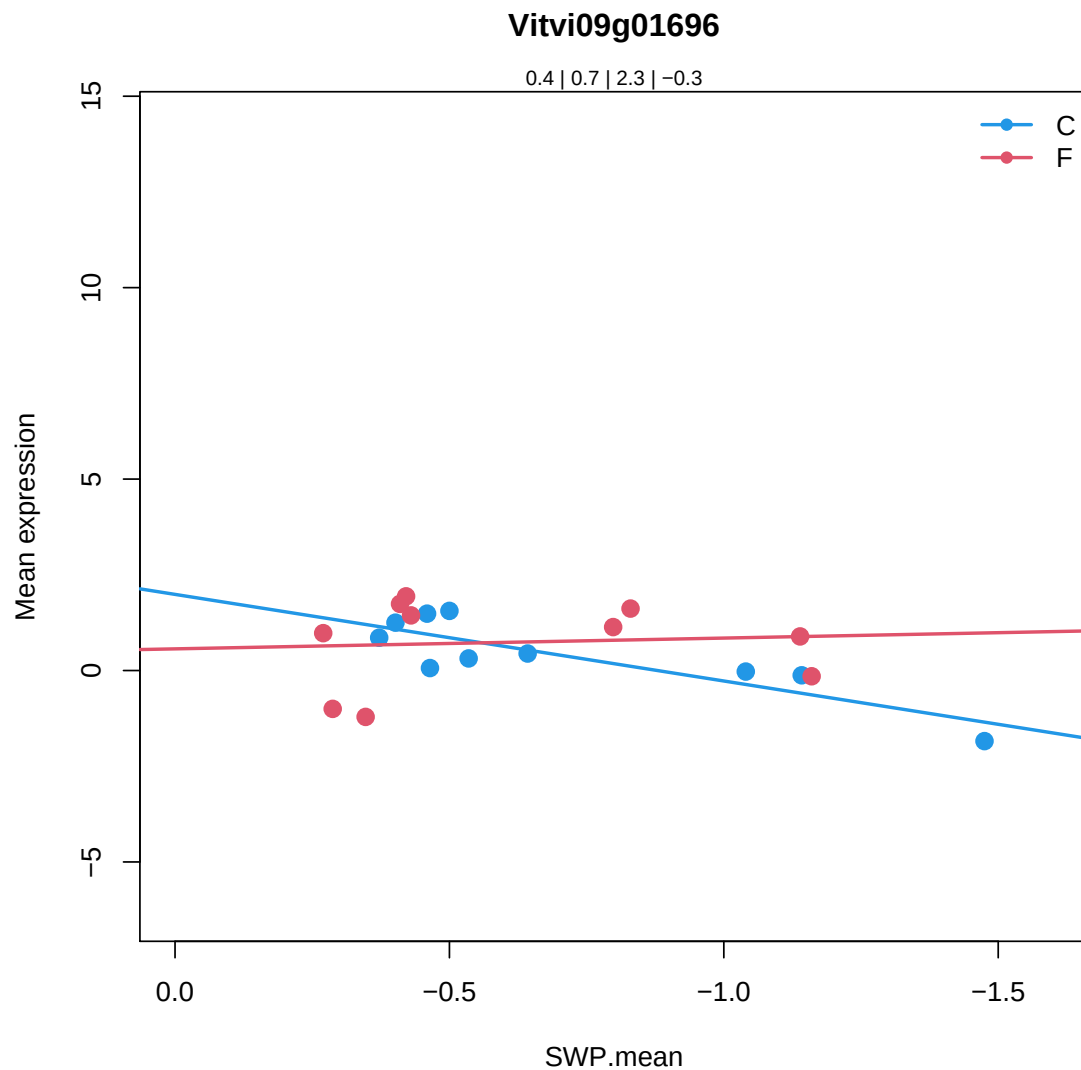
receptor like protein 1 |

Chr1:2270633-2274654 FORWARD LENGTH=913 |

201606

Coefficients for Vitvi09g01696.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3976992	0.1502863		0.15467	
SlopeC	2.261964	0.005987002	**	0.2647742	
MeanF-MeanC	0.3394621	0.3778739		0.7294269	
SlopeF-SlopeC	-2.543567	0.03129144	*	0.9999488	



7.6.12 Vitvi00g02226

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

Vitvi00g02226

35.2

not assigned.unknown

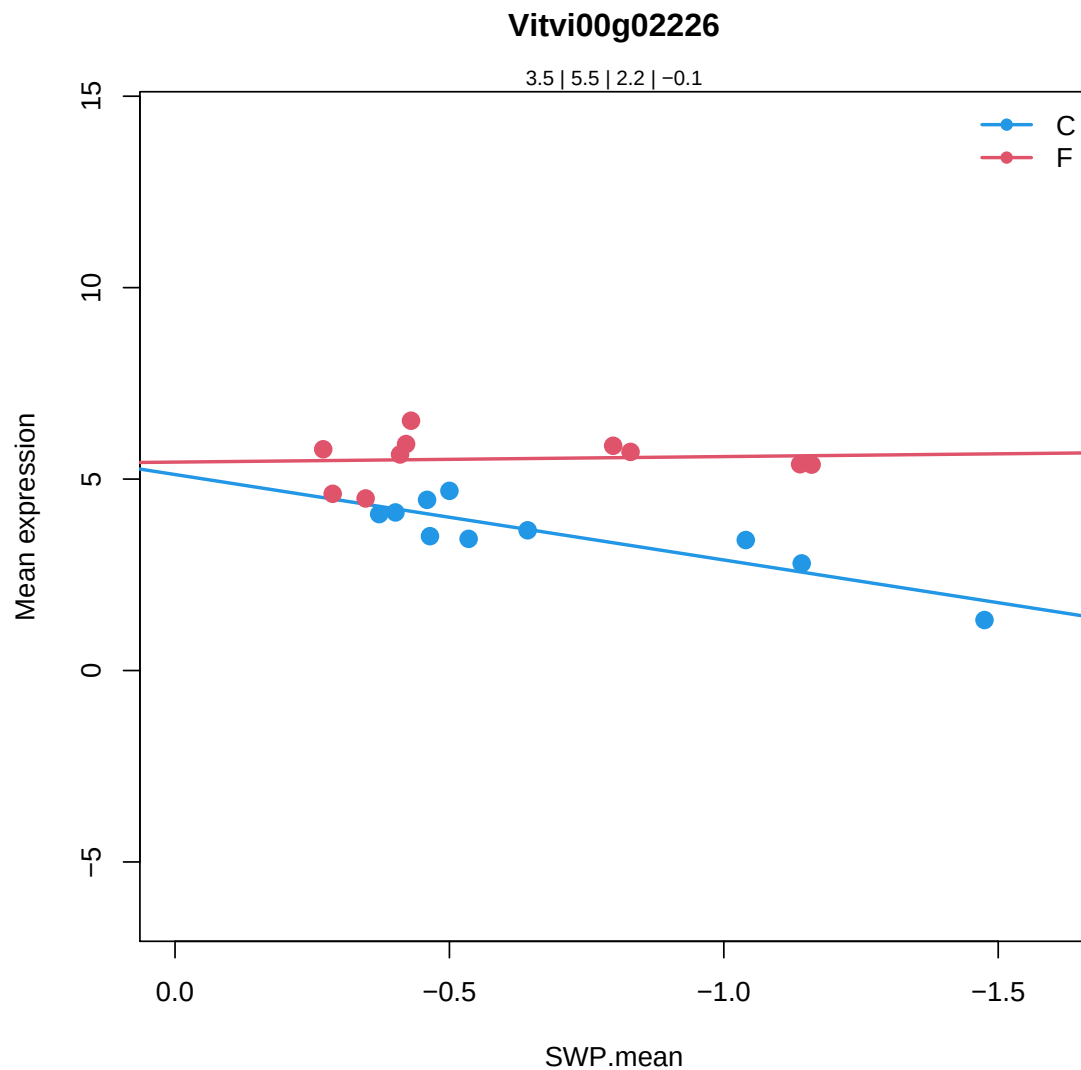
PR5-like receptor kinase |

Chr5:15293325-15295838 REVERSE LENGTH=665 |

201606

Coefficients for Vitvi00g02226.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.549584	1.613386e-15	***	2.94647e-15	***
SlopeC	2.231859	0.0001456927	***	0.07644173	.
MeanF-MeanC	1.981757	6.472083e-08	***	2.794547e-06	***
SlopeF-SlopeC	-2.375927	0.003388446	**	0.9999488	



7.6.13 Vitvi16g01542

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

Vitvi16g01542

35.2

not assigned.unknown

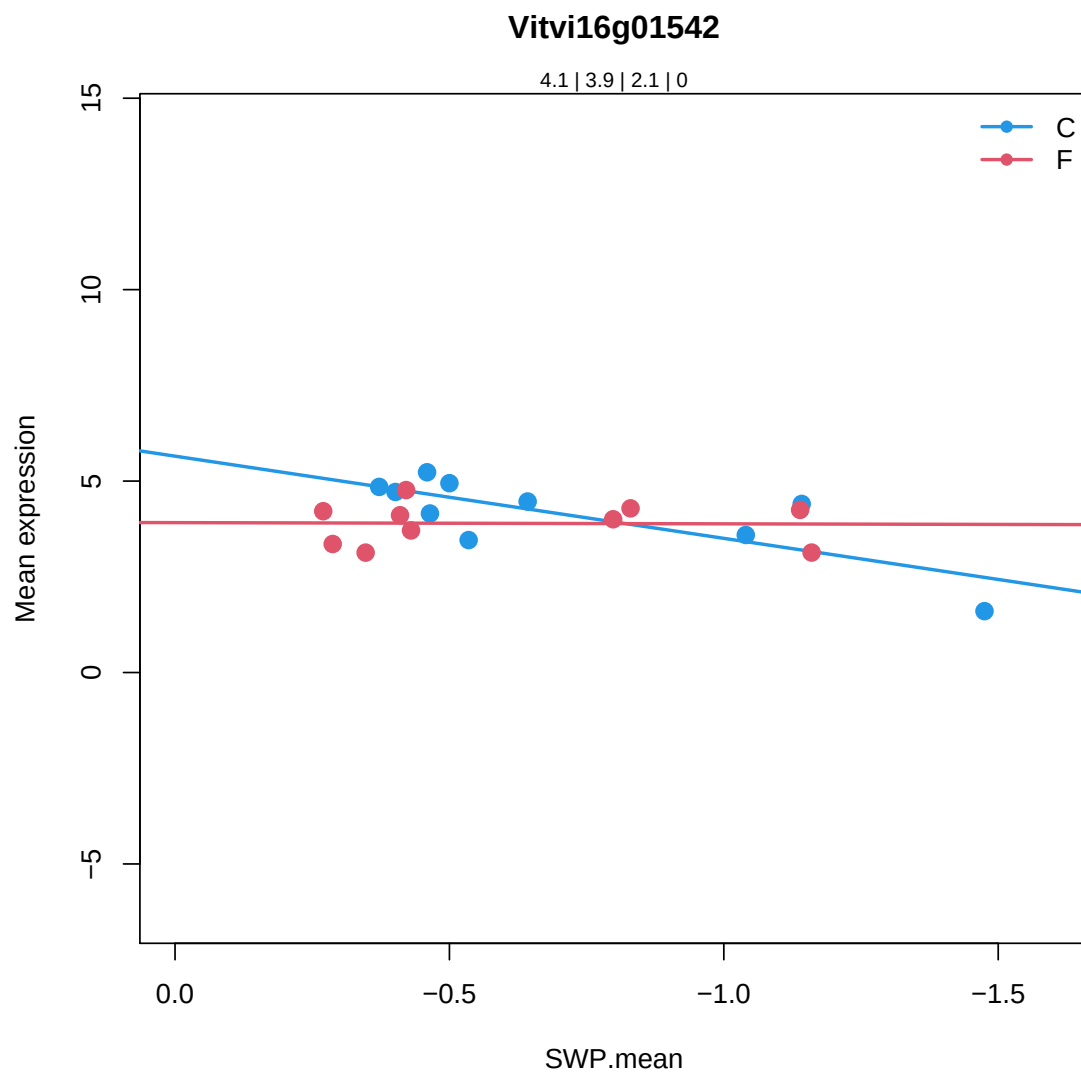
disease resistance family protein / LRR family protein |

Chr2:14737169-14739886 REVERSE LENGTH=905 |

201606

Coefficients for Vitvi16g01542.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.141452	6.308257e-16	***	1.211421e-15	***
SlopeC	2.146633	0.0006675167	***	0.1037734	
MeanF-MeanC	-0.2460853	0.3799787		0.7316365	
SlopeF-SlopeC	-2.115503	0.01542334	*	0.9999488	



7.6.14 Vitvi16g02021

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

Vitvi16g02021

35.2

not assigned.unknown

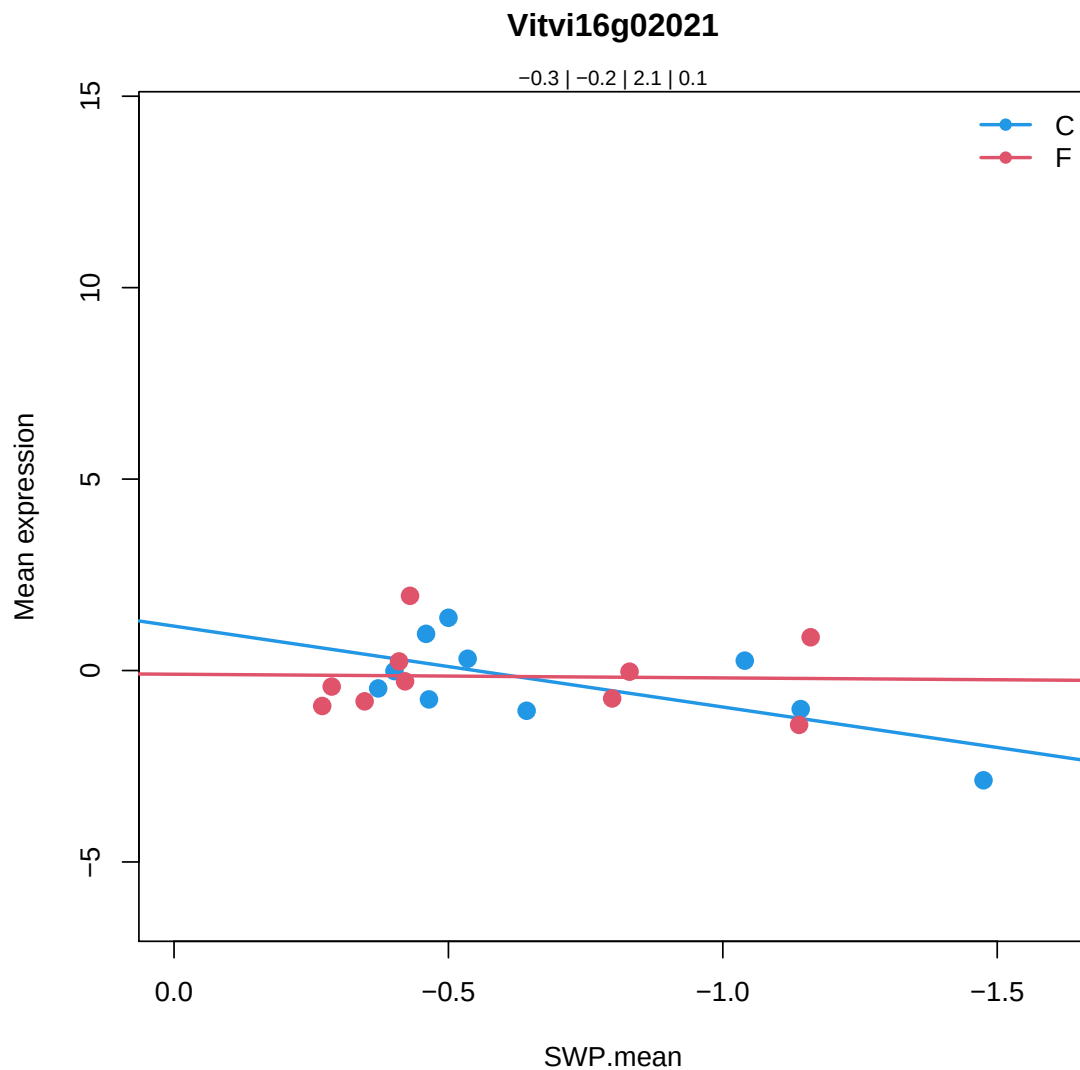
PR5-like receptor kinase |

Chr5:15293325-15295838 REVERSE LENGTH=665 |

201606

Coefficients for Vitvi16g02021.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.3262667	0.262738		0.2681208	
SlopeC	2.113053	0.01394122	*	0.3359386	
MeanF-MeanC	0.1706188	0.6748503		0.8949163	
SlopeF-SlopeC	-2.016905	0.1003787		0.9999488	



7.6.15 Vitvi18g01281

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

Vitvi18g01281

29.4

protein.postranslational modification

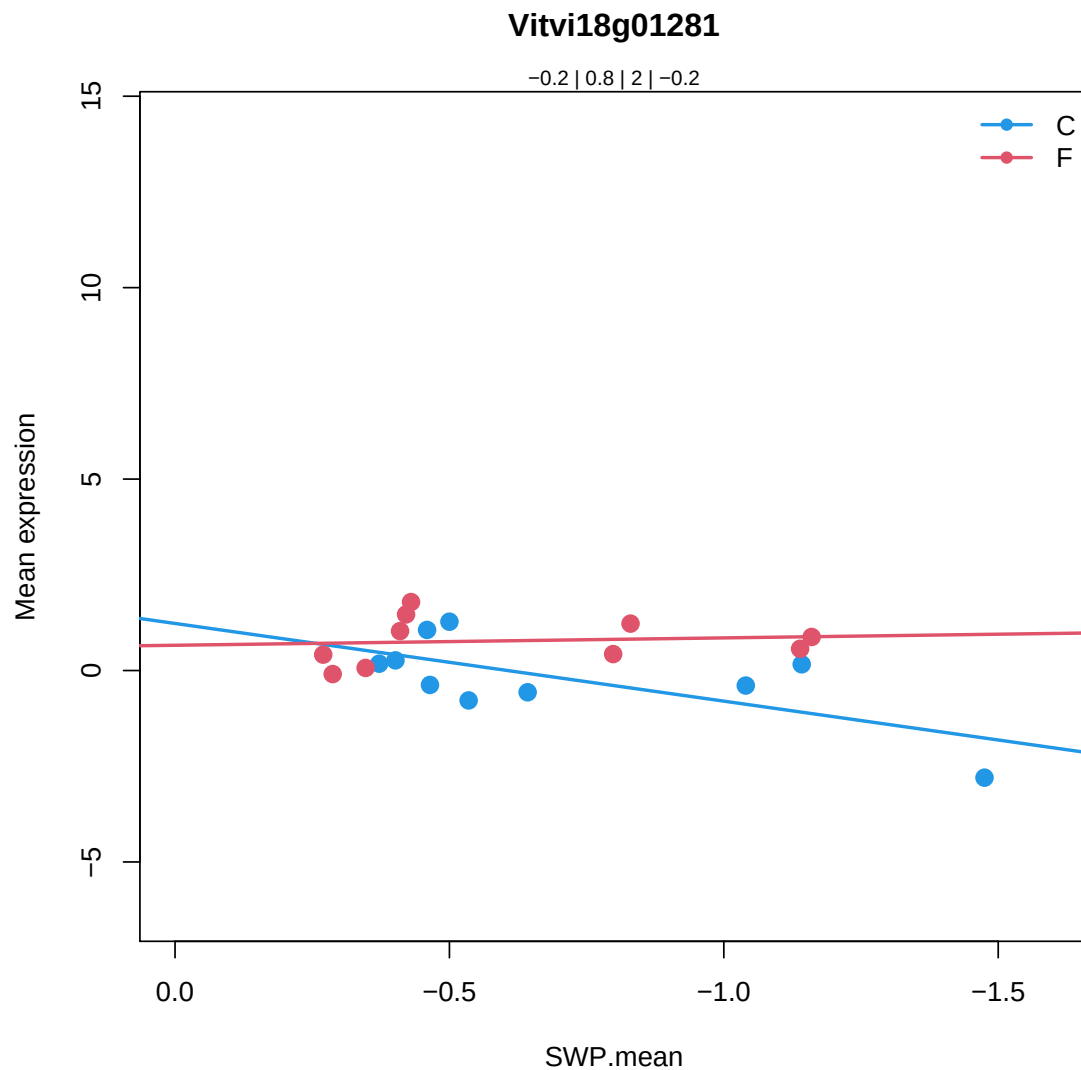
receptor-like protein kinase 1 |

Chr5:24498467-24501494 REVERSE LENGTH=832 |

201606

Coefficients for Vitvi18g01281.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.1976097	0.3888288		0.3949176	
SlopeC	2.029457	0.003785477	**	0.2269459	
MeanF-MeanC	0.9745386	0.005751961	**	0.05076513	.
SlopeF-SlopeC	-2.221749	0.02619175	*	0.9999488	



7.6.16 Vitvi16g01549

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

Vitvi16g01549

35.2

not assigned.unknown

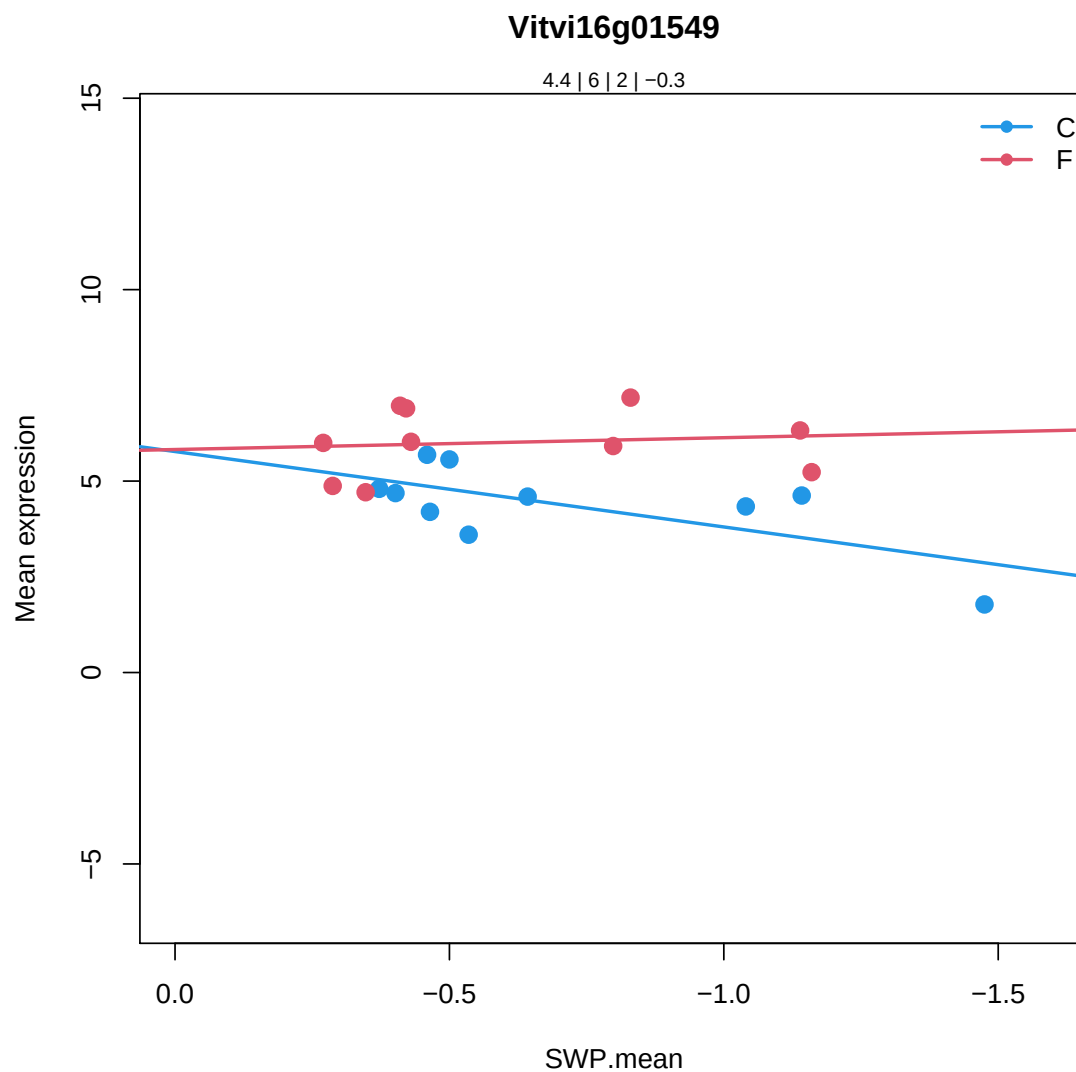
receptor like protein 34 |

Chr3:3450988-3453672 REVERSE LENGTH=894 |

201606

Coefficients for Vitvi16g01549.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.386477	4.739072e-14	***	7.467481e-14	***
SlopeC	1.969869	0.01098639	*	0.3141738	
MeanF-MeanC	1.62591	0.0001789125	***	0.002941731	**
SlopeF-SlopeC	-2.278492	0.0419335	*	0.9999488	



7.6.17 Vitvi09g00667

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

Vitvi09g00667

20.01.2002

stress.biotic.receptors

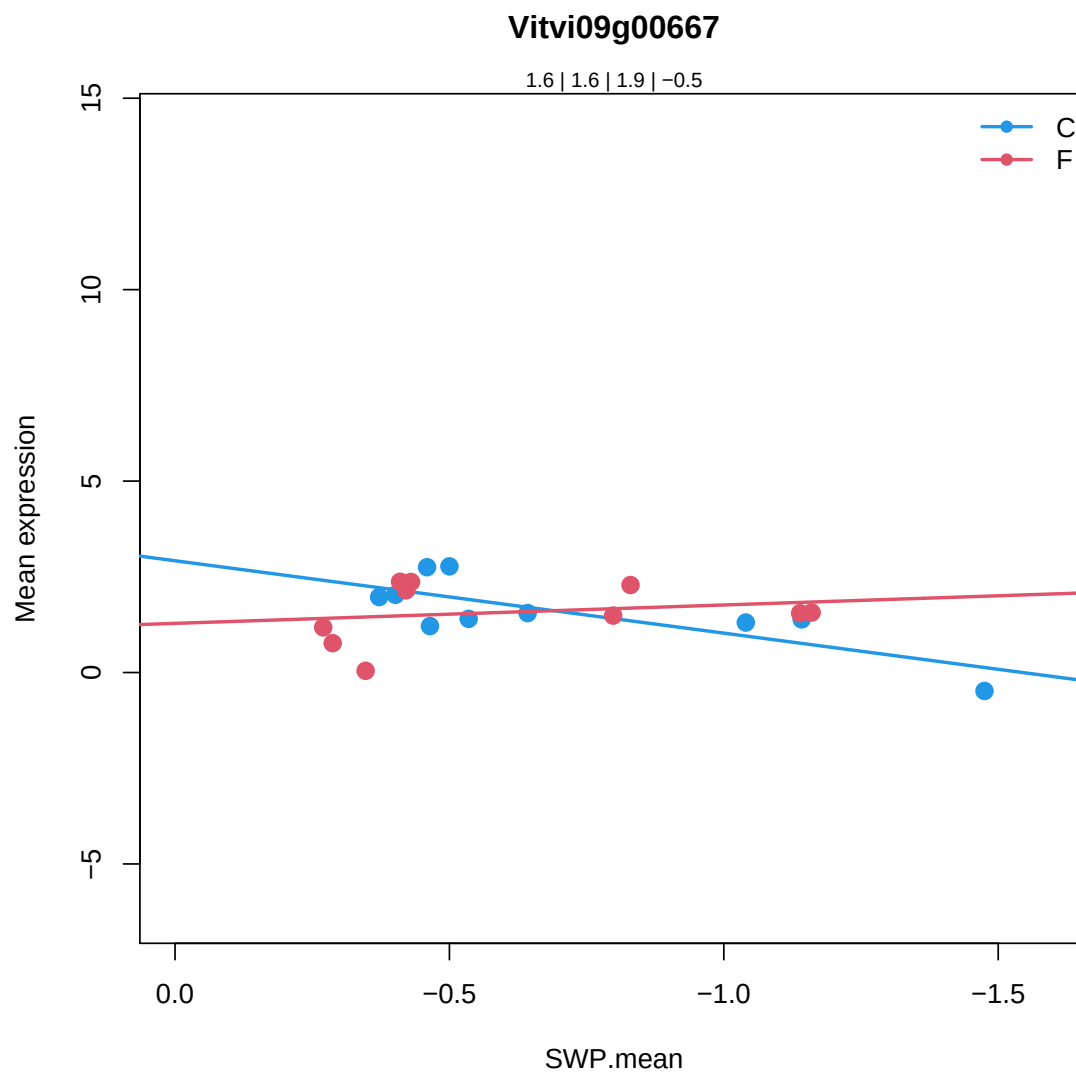
receptor like protein 1 |

Chr1:2270633-2274654 FORWARD LENGTH=913 |

201606

Coefficients for Vitvi09g00667.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.590052	1.599417e-07	***	1.887013e-07	***
SlopeC	1.889958	0.003763512	**	0.2269459	
MeanF-MeanC	-0.01386751	0.9630231		0.9915927	
SlopeF-SlopeC	-2.370296	0.01217728	*	0.9999488	



7.6.18 Vitvi05g01285

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

Vitvi05g01285

35.2

not assigned.unknown

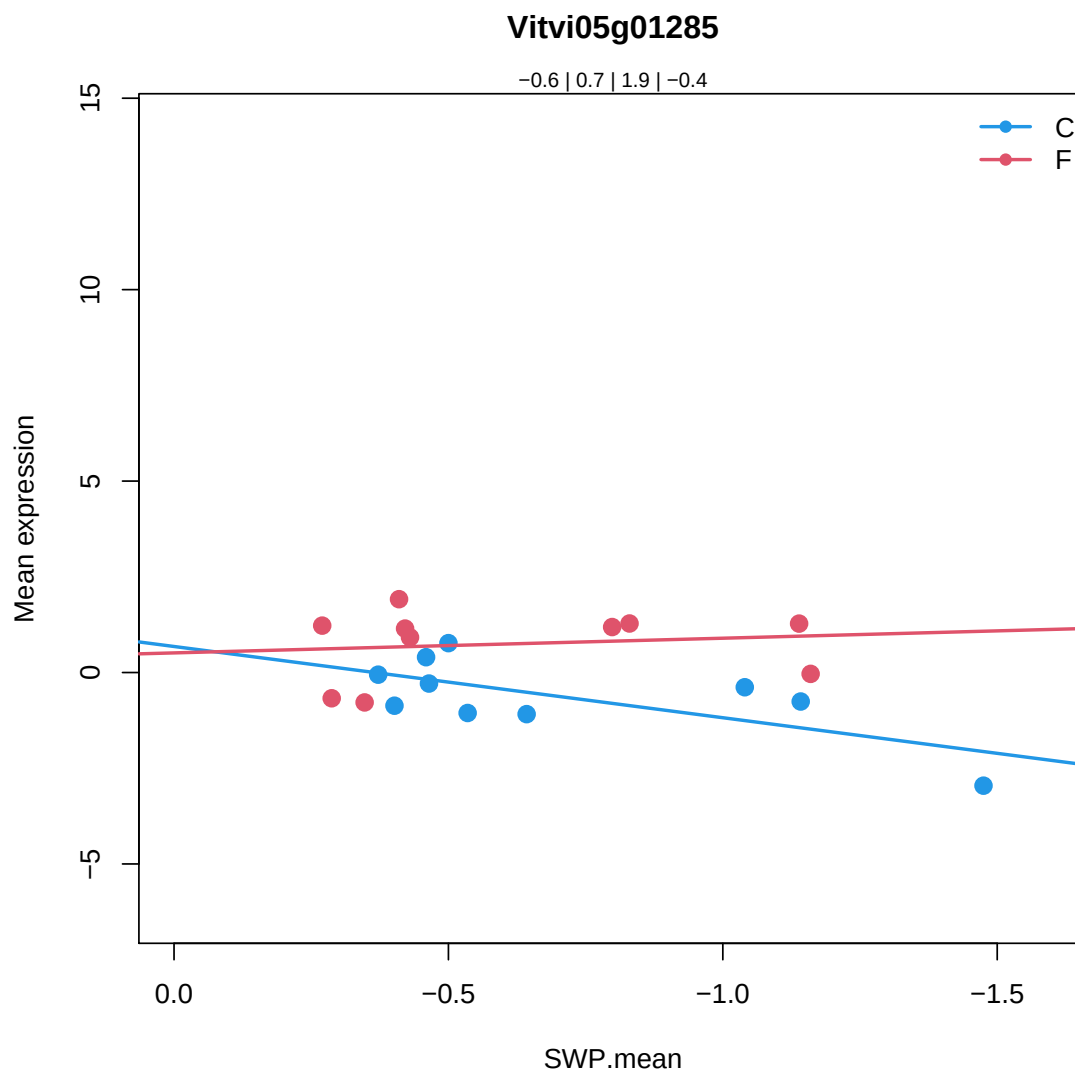
indole-3-acetate beta-D-glucosyltransferase |

Chr4:8877877-8879301 REVERSE LENGTH=474 |

201606

Coefficients for Vitvi05g01285.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.6285472	0.02067477	*	0.02173275	*
SlopeC	1.860691	0.01455316	*	0.3359386	
MeanF-MeanC	1.374557	0.0008738596	***	0.01117397	*
SlopeF-SlopeC	-2.244205	0.04275548	*	0.9999488	



7.6.19 Vitvi16g00814

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

Vitvi16g00814

35.2

not assigned.unknown

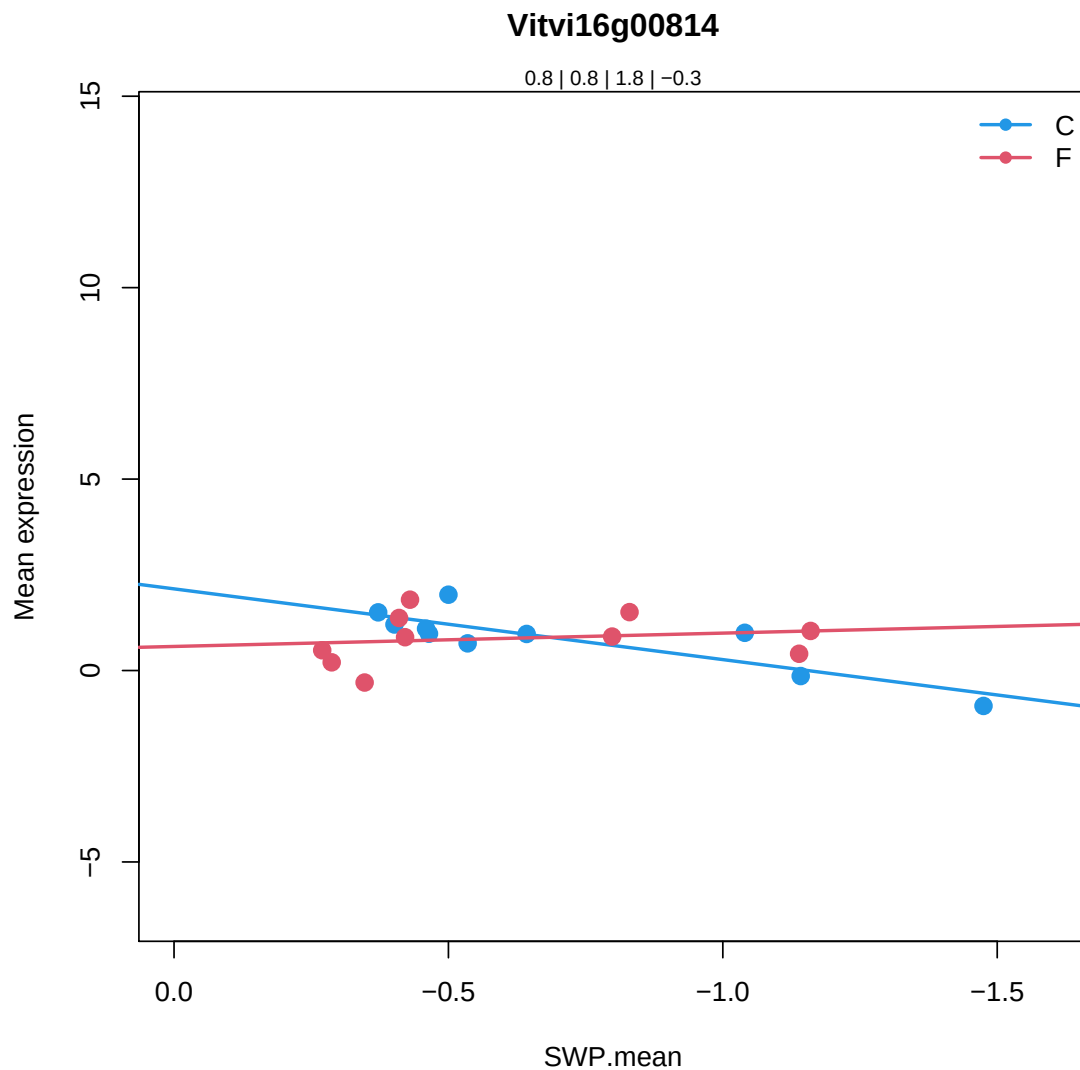
Protein kinase superfamily protein |

Chr1:24961634-24963941 REVERSE LENGTH=666 |

201606

Coefficients for Vitvi16g00814.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8334508	0.0001093319	***	0.0001206427	***
SlopeC	1.847189	0.001108435	**	0.1330296	
MeanF-MeanC	0.006900955	0.978186		0.994504	
SlopeF-SlopeC	-2.195694	0.006624803	**	0.9999488	



7.6.20 Vitvi10g00613

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

Vitvi10g00613

10.02.2001

cell wall.cellulose synthesis.cellulose synthase

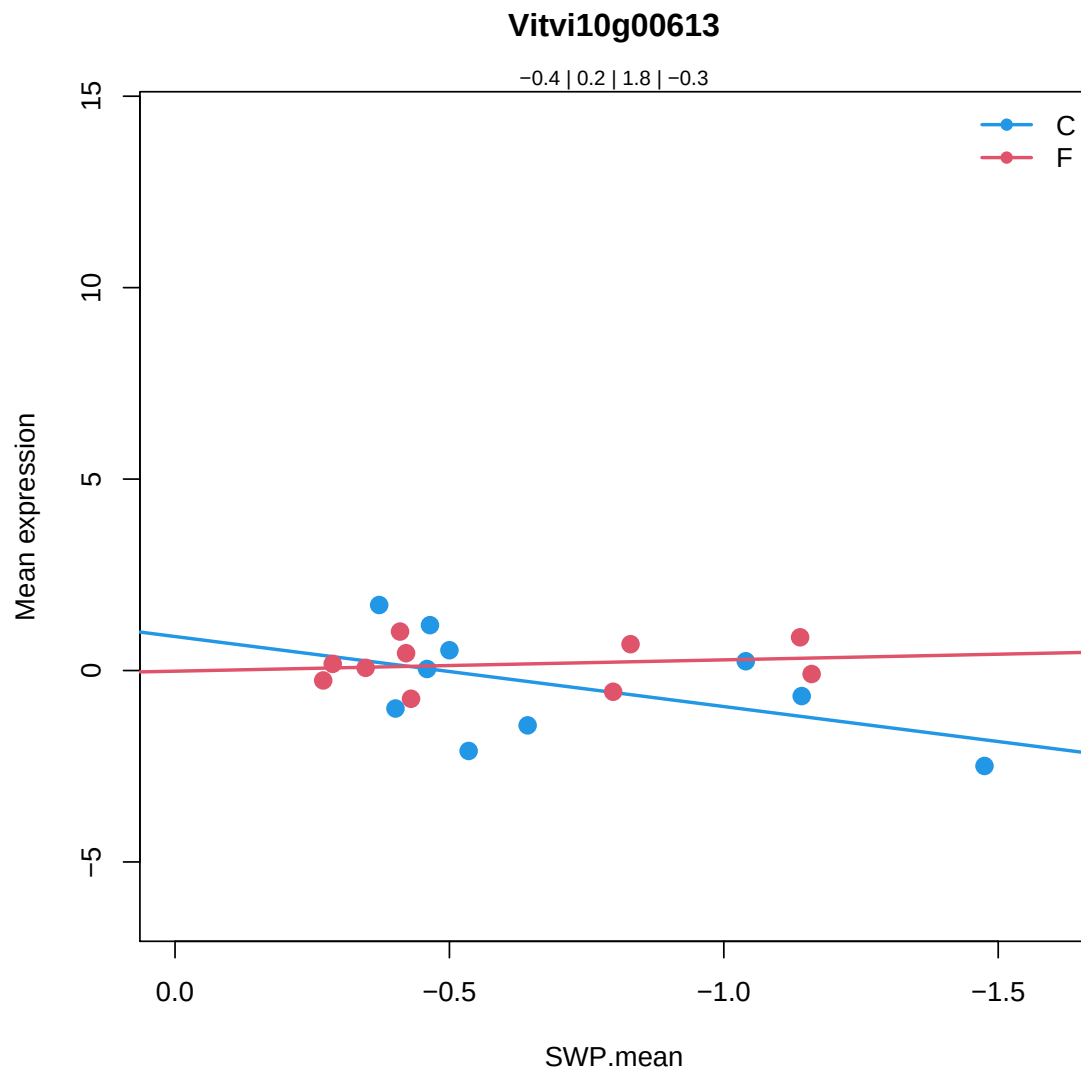
cellulose synthase family protein |

Chr4:10312846-10316719 REVERSE LENGTH=985 |

201606

Coefficients for Vitvi10g00613.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.3978763	0.1750966		0.1798519	
SlopeC	1.828719	0.03047437	*	0.4320841	
MeanF-MeanC	0.5603847	0.1767898		0.5101322	
SlopeF-SlopeC	-2.124476	0.08458891	.	0.9999488	



7.6.21 Vitvi19g02004

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

Vitvi19g02004

35.2

not assigned.unknown

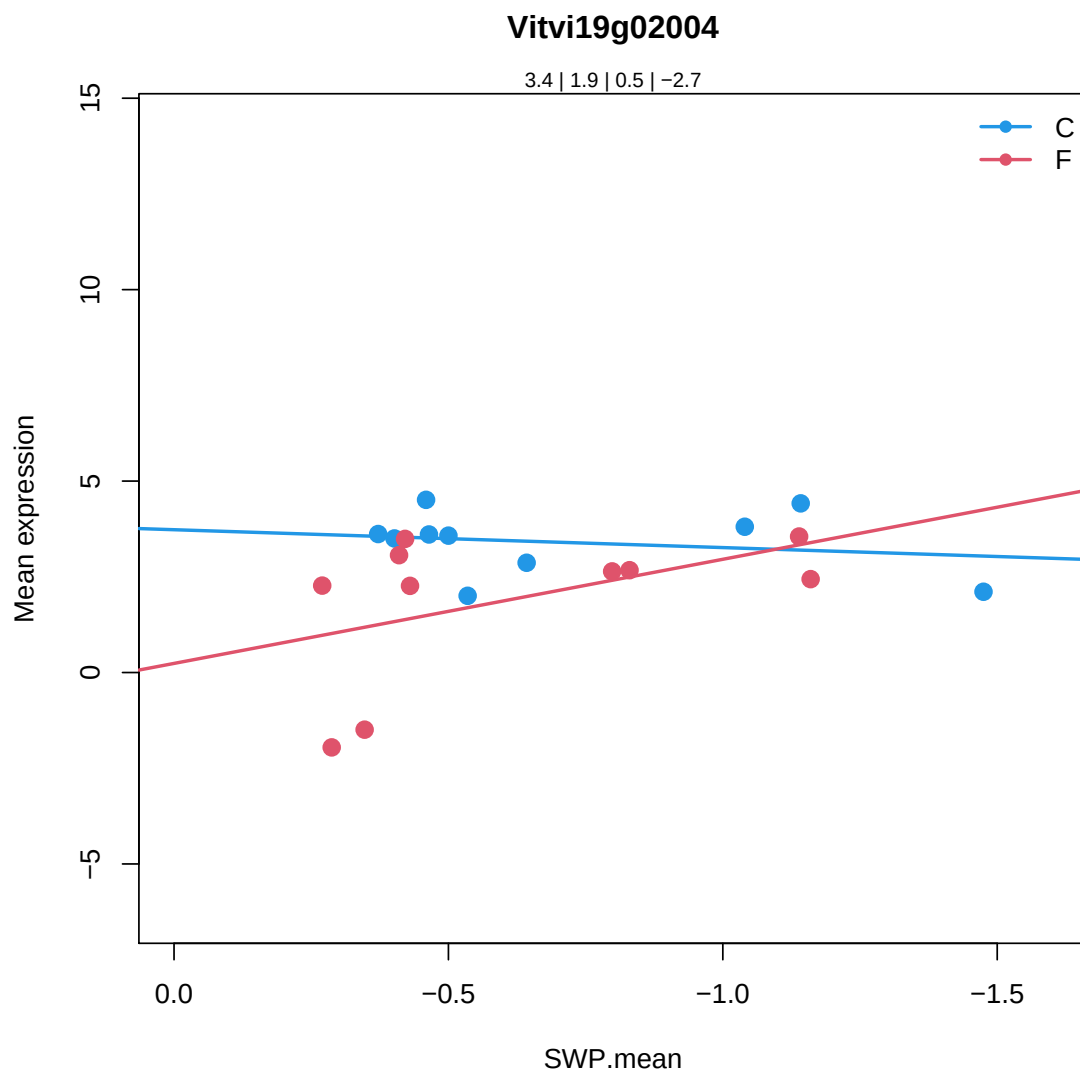
fatty acid desaturase A |

Chr4:13571951-13572922 FORWARD LENGTH=323 |

201606

Coefficients for Vitvi19g02004.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.401391	2.600455e-08	***	3.135026e-08	***
SlopeC	0.4667448	0.6791641		0.9268622	
MeanF-MeanC	-1.506922	0.01439005	*	0.09906648	.
SlopeF-SlopeC	-3.186127	0.06784855	.	0.9999488	



7.6.22 Vitvi01g01764

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

Vitvi01g01764

19.99

tetrapyrrole synthesis.unspecified

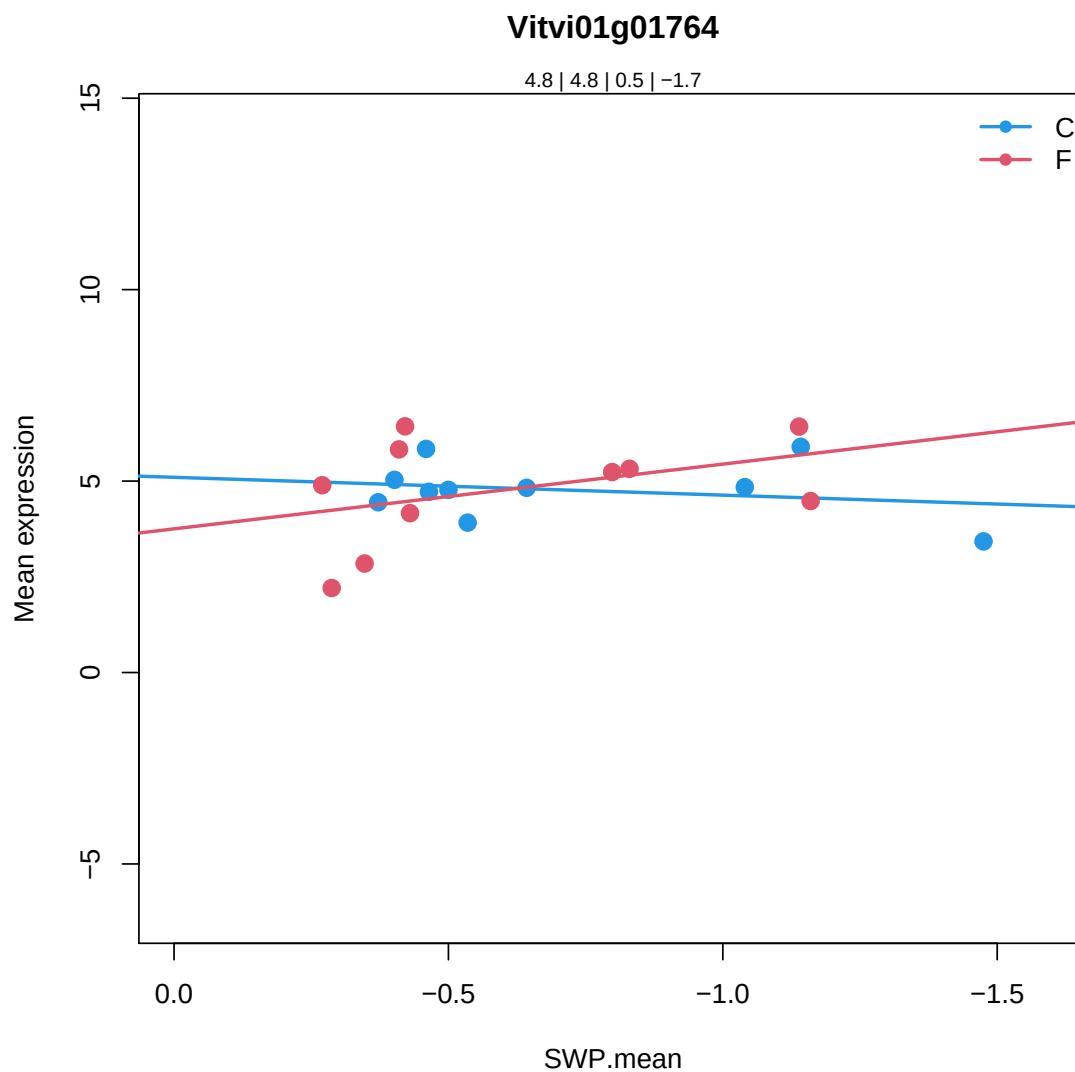
SOUL heme-binding family protein |

Chr1:5844766-5845539 FORWARD LENGTH=232 |

201606

Coefficients for Vitvi01g01764.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.771117	5.468395e-13	***	7.984412e-13	***
SlopeC	0.4655929	0.5981785		0.9034321	
MeanF-MeanC	0.01100363	0.9803868		0.9949434	
SlopeF-SlopeC	-2.156261	0.1105399		0.9999488	



7.6.23 Vitvi17g01101

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

Vitvi17g01101

34.14

transport.unspecified cations

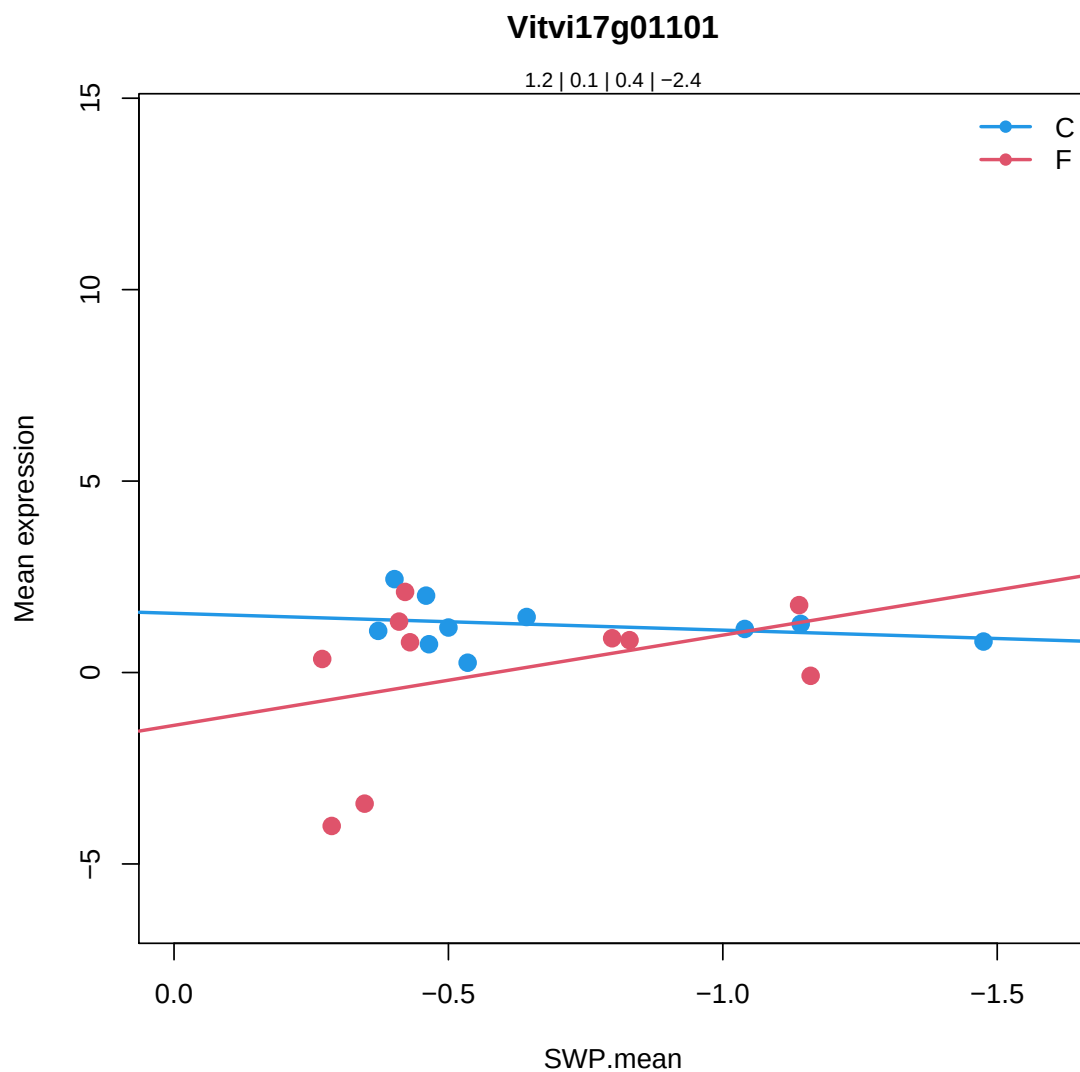
organic cation/carnitine transporter1 |

Chr1:27538387-27540109 FORWARD LENGTH=539 |

201606

Coefficients for Vitvi17g01101.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.237068	0.0077324	**	0.008213048	**
SlopeC	0.4385322	0.7117525		0.9350571	
MeanF-MeanC	-1.181232	0.06018117	.	0.2686036	
SlopeF-SlopeC	-2.79515	0.1234474		0.9999488	



7.6.24 Vitvi18g00269

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

Vitvi18g00269

19.16

tetrapyrrole synthesis.chlorophyll b synthase

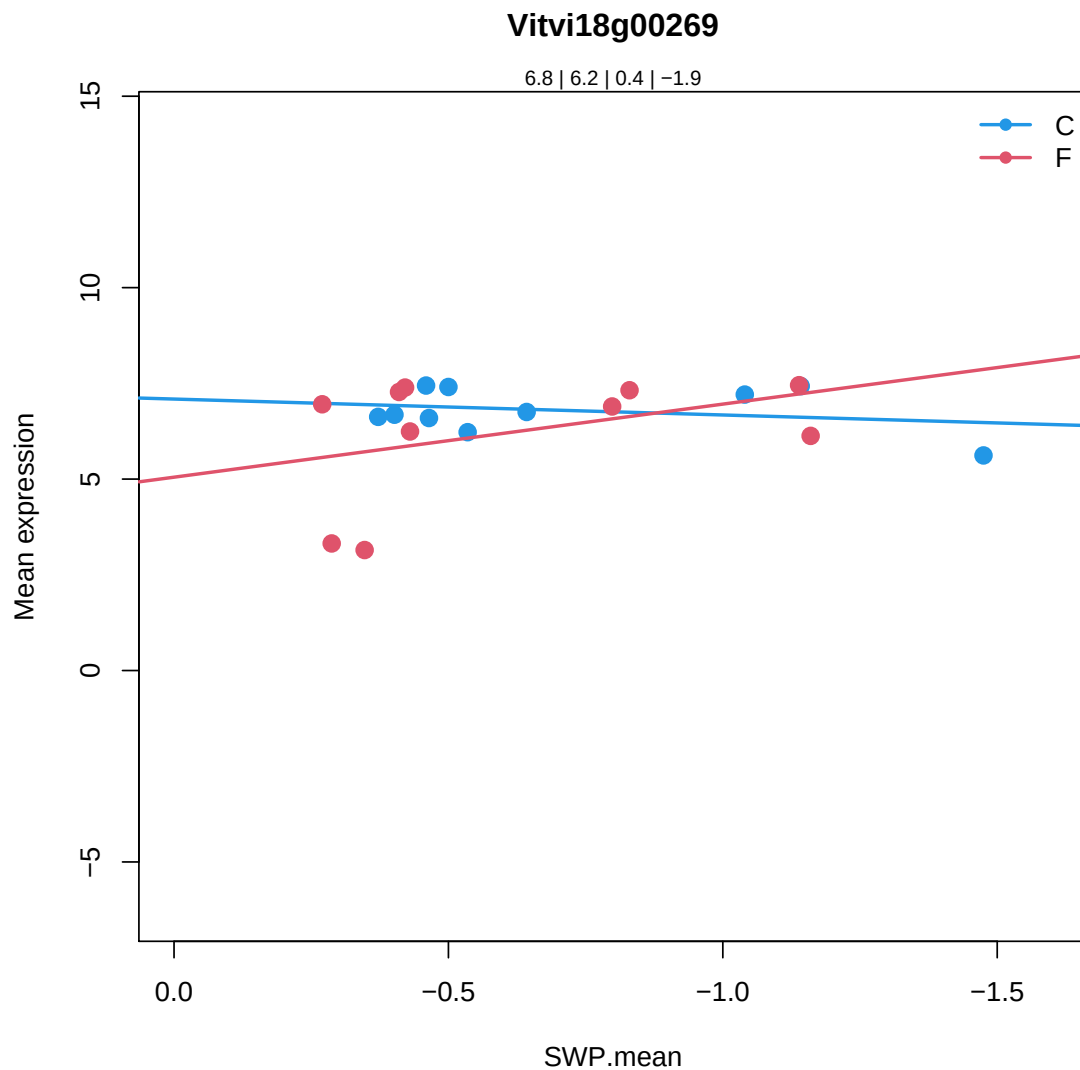
Pheophorbide a oxygenase family protein with Rieske 2Fe-2S domain-cont

Chr1:16848664-16850718 REVERSE LENGTH=434 |

201606

Coefficients for Vitvi18g00269.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.797749	2.06861e-15	***	3.739741e-15	***
SlopeC	0.4156576	0.6625771		0.9225525	
MeanF-MeanC	-0.5854615	0.2334692		0.5882853	
SlopeF-SlopeC	-2.324171	0.1110042		0.9999488	



7.6.25 Vitvi19g02007

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

Vitvi19g02007

35.2

not assigned.unknown

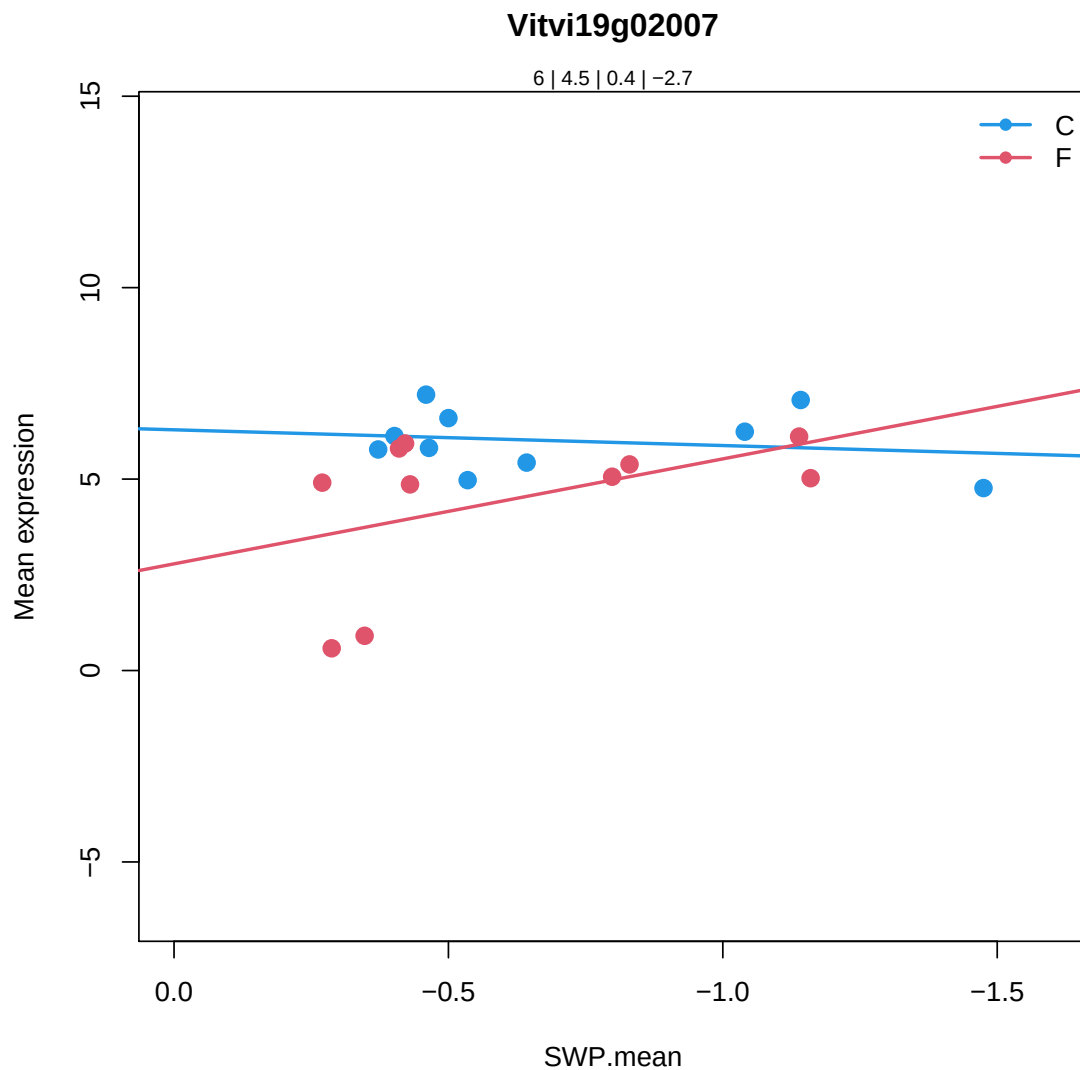
fatty acid desaturase A |

Chr4:13571951-13572922 FORWARD LENGTH=323 |

201606

Coefficients for Vitvi19g02007.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.99801	1.023182e-12	***	1.466555e-12	***
SlopeC	0.4107341	0.7197001		0.9380929	
MeanF-MeanC	-1.541676	0.01370917	*	0.09580703	.
SlopeF-SlopeC	-3.15221	0.07448352	.	0.9999488	



7.6.26 Vitvi13g00605

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

Vitvi13g00605

34.19.1

transport.major intrinsic proteins.PIP

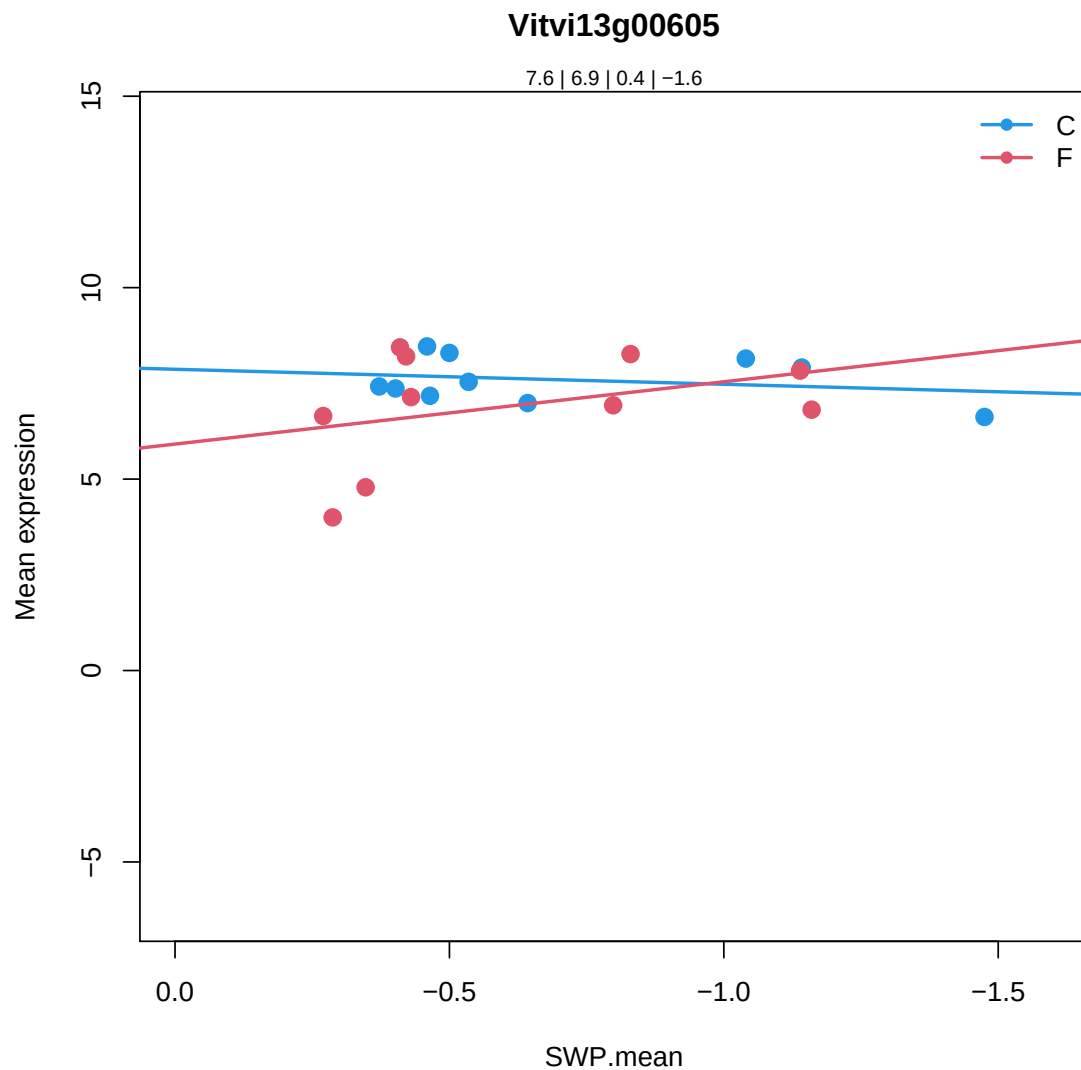
plasma membrane intrinsic protein 2 |

Chr2:15613624-15614791 REVERSE LENGTH=285 |

201606

Coefficients for Vitvi13g00605.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.592703	5.28452e-17	***	1.207234e-16	***
SlopeC	0.3913983	0.6601853		0.9218432	
MeanF-MeanC	-0.6872399	0.1381836		0.4448345	
SlopeF-SlopeC	-2.019107	0.1369143		0.9999488	



7.6.27 Vitvi04g01856

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

Vitvi04g01856

31.1

cell.organisation

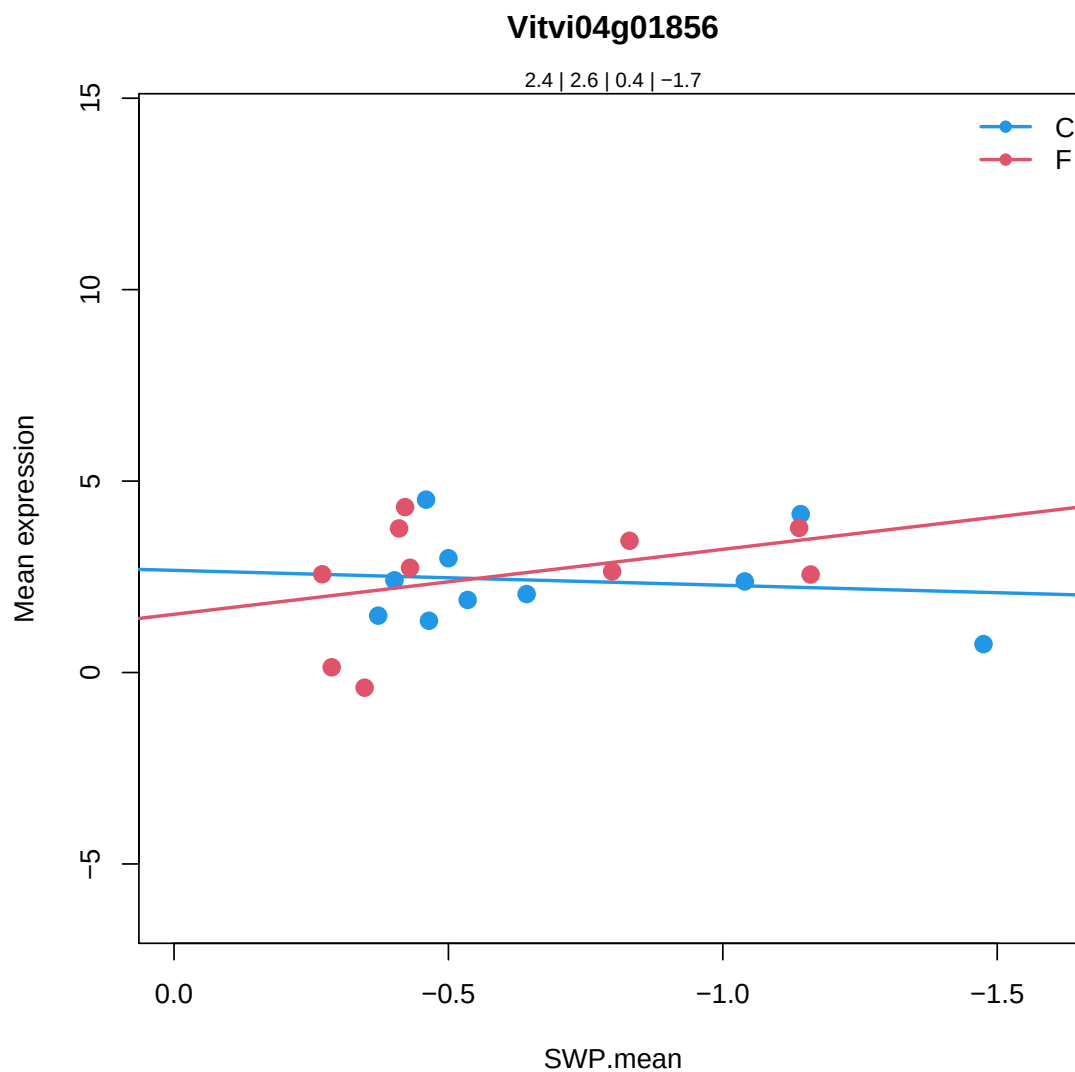
Ankyrin repeat family protein |

Chr1:3390475-3392481 REVERSE LENGTH=578 |

201606

Coefficients for Vitvi04g01856.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.394766	3.749757e-06	***	4.272862e-06	***
SlopeC	0.3888641	0.7226597		0.9392454	
MeanF-MeanC	0.1594426	0.7745531		0.9355874	
SlopeF-SlopeC	-2.085775	0.2087743		0.9999488	



7.6.28 Vitvi16g00025

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

Vitvi16g00025

28.99

DNA.unspecified

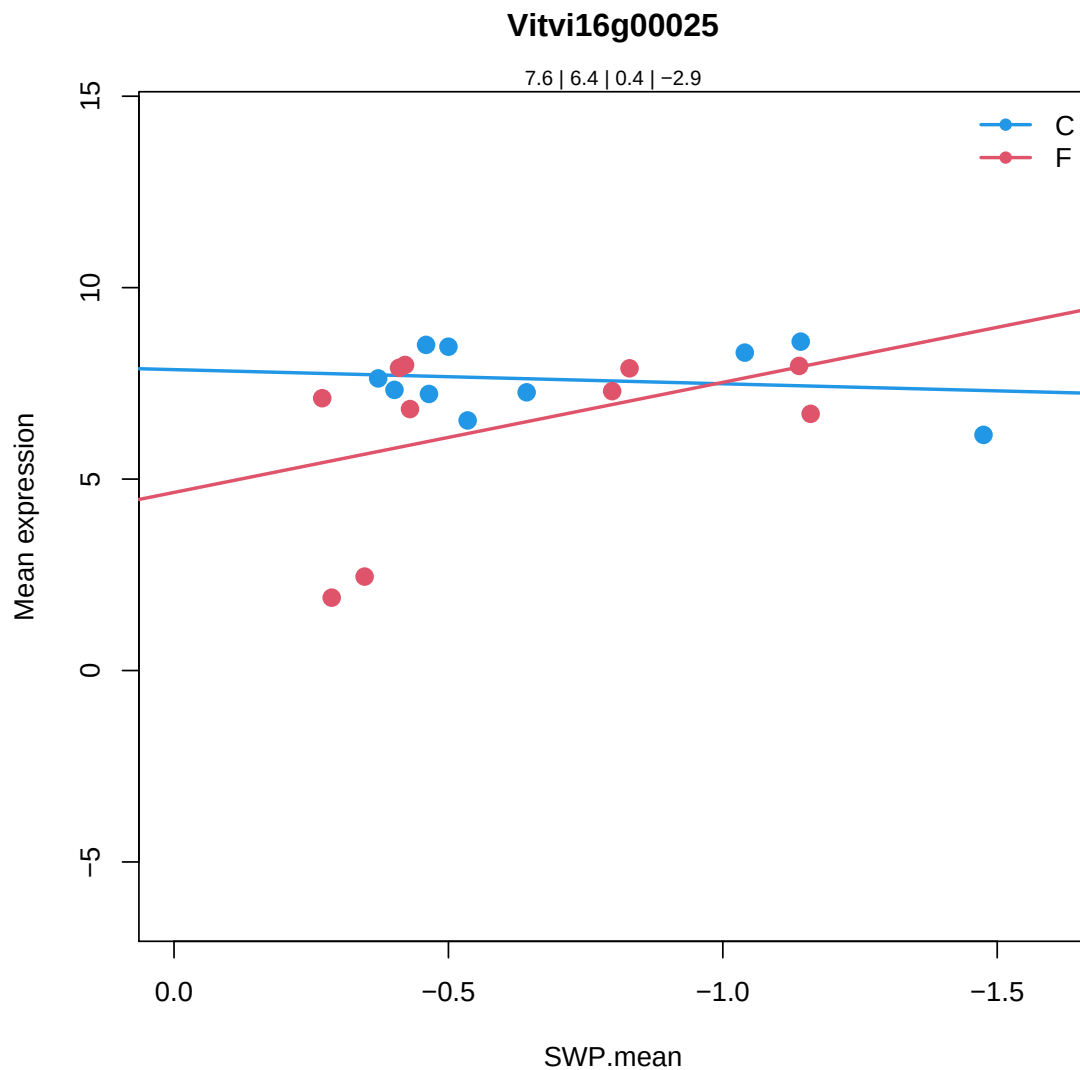
P-loop containing nucleoside triphosphate hydrolases superfamily prote

Chr5:14119060-14123078 REVERSE LENGTH=961 |

201606

Coefficients for Vitvi16g00025.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.598812	1.213612e-13	***	1.851824e-13	***
SlopeC	0.36987	0.7761981		0.9513135	
MeanF-MeanC	-1.19583	0.0810236	.	0.3225285	
SlopeF-SlopeC	-3.244807	0.1041917		0.9999488	



7.6.29 Vitvi19g00391

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

Vitvi19g00391

16.01.2005

secondary metabolism.isoprenoids.terpenoids

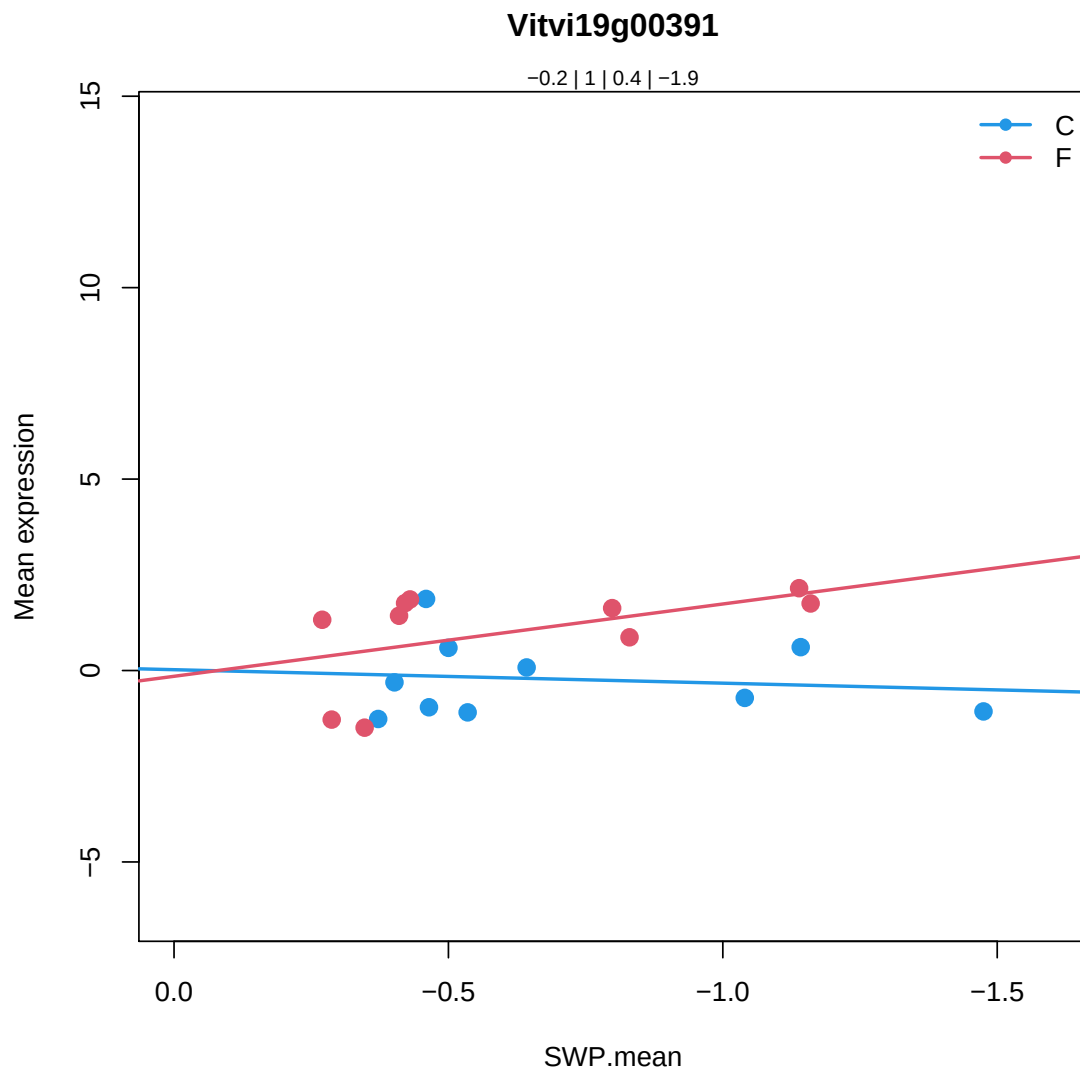
terpene synthase 21 |

Chr5:8092969-8095128 FORWARD LENGTH=545 |

201606

Coefficients for Vitvi19g00391.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.2259877	0.4867558		0.4929328	
SlopeC	0.3515541	0.6962291		0.9317974	
MeanF-MeanC	1.225536	0.01285799	*	0.09162296	.
SlopeF-SlopeC	-2.240139	0.1047179		0.9999488	



7.6.30 Vitvi05g01675

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

Vitvi05g01675

26.11.2001

misc.alcohol dehydrogenases.cinnamyl alcohol dehydrogenase

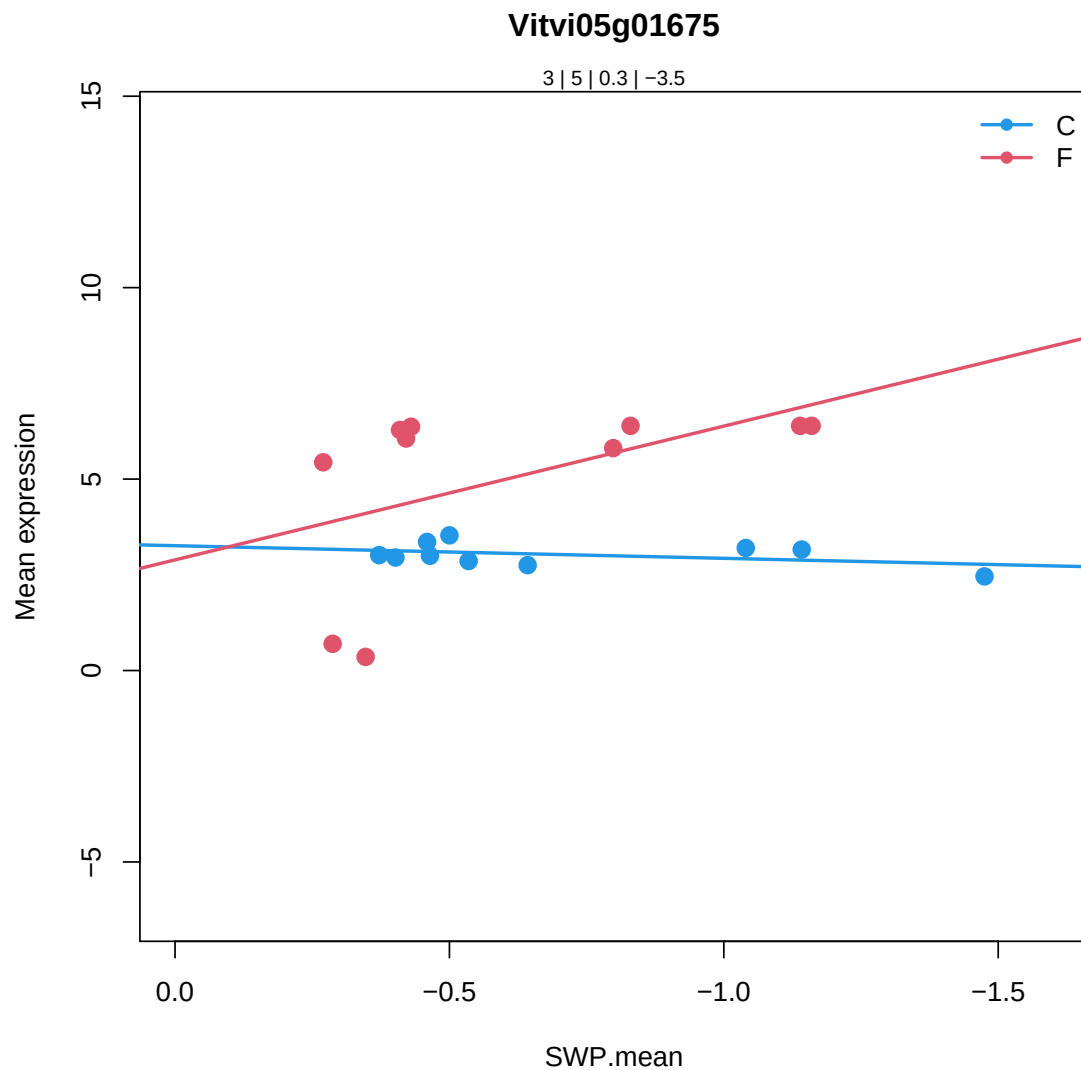
Zinc-binding dehydrogenase family protein |

Chr5:5584983-5586991 REVERSE LENGTH=345 |

201606

Coefficients for Vitvi05g01675.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.027901	6.100684e-07	***	7.084695e-07	***
SlopeC	0.3297008	0.7874006		0.9533712	
MeanF-MeanC	1.9902	0.003821472	**	0.03702916	*
SlopeF-SlopeC	-3.824121	0.04507823	*	0.9999488	



7.6.31 Vitvi07g01217

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

Vitvi07g01217

20.1.3.1

stress.biotic.signalling.MLO-like

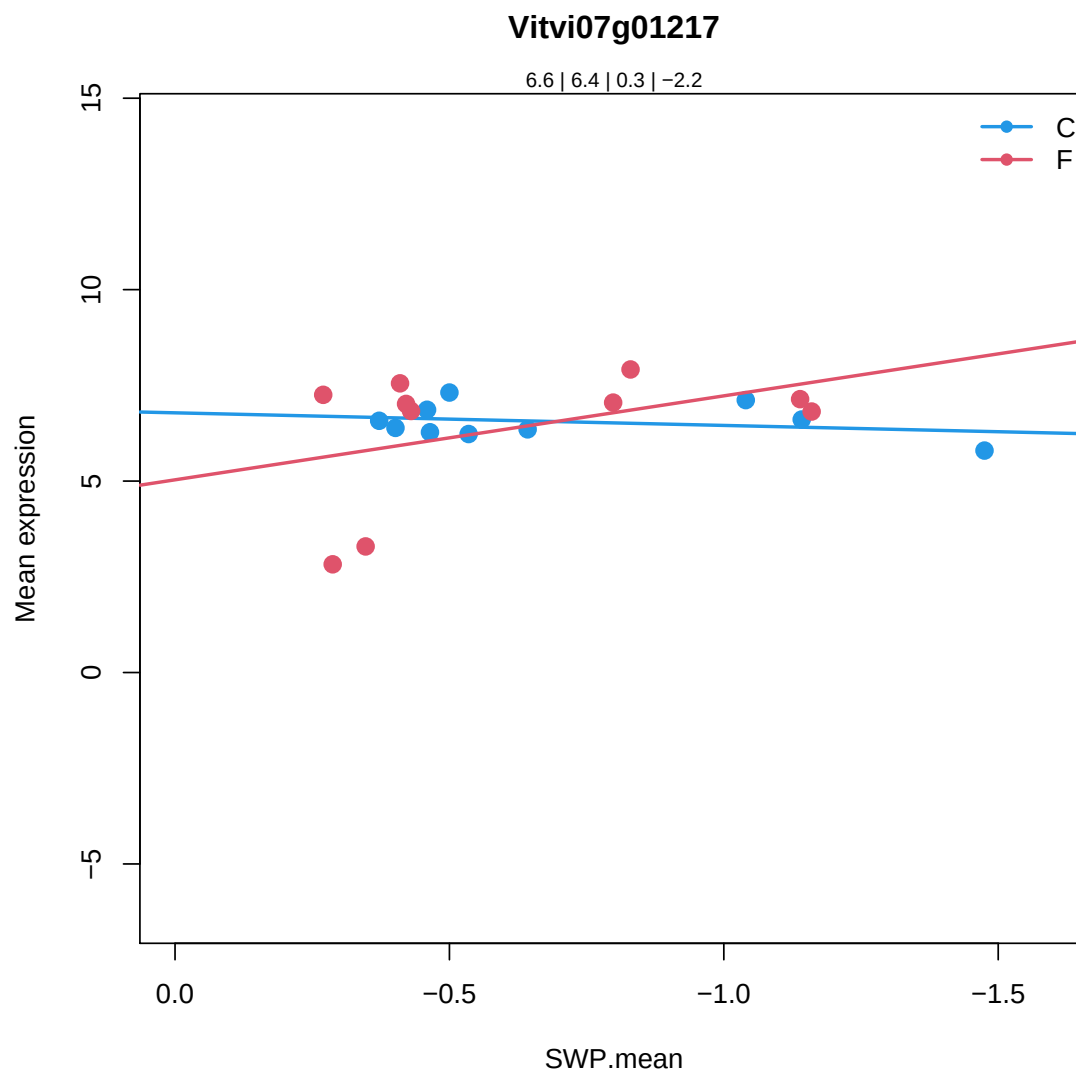
Seven transmembrane MLO family protein |

Chr4:1144141-1147156 FORWARD LENGTH=526 |

201606

Coefficients for Vitvi07g01217.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.551282	9.371349e-15	***	1.572068e-14	***
SlopeC	0.3290549	0.739068		0.9434568	
MeanF-MeanC	-0.1821918	0.7168116		0.9128164	
SlopeF-SlopeC	-2.522145	0.09660126	.	0.9999488	



7.6.32 Vitvi06g01959

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

Vitvi06g01959

35.2

not assigned.unknown

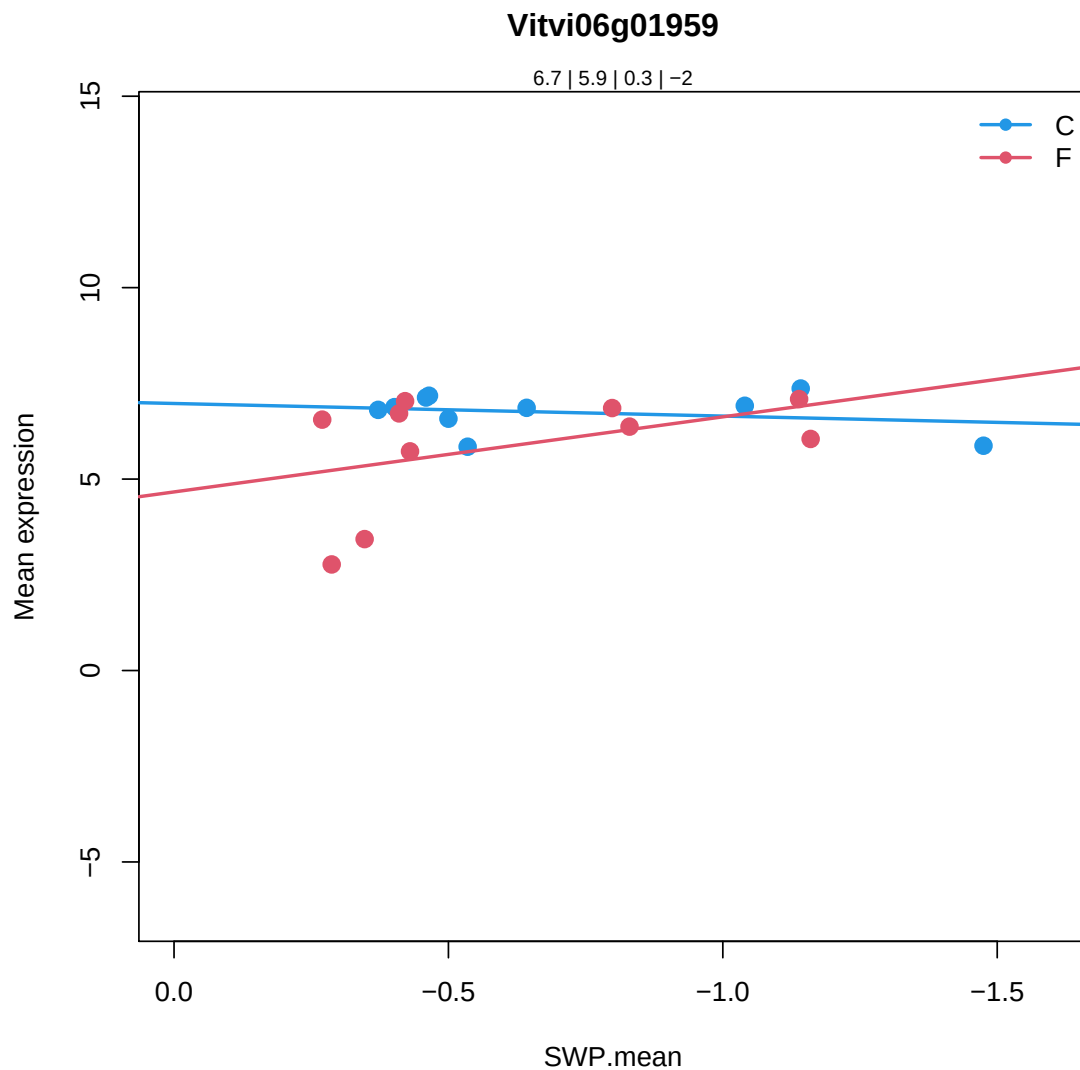
hypothetical protein |

Chr3:19546446-19546868 REVERSE LENGTH=140 |

201606

Coefficients for Vitvi06g01959.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.742876	3.661843e-16	***	7.287349e-16	***
SlopeC	0.3287882	0.7047868		0.9342808	
MeanF-MeanC	-0.8836593	0.05493261	.	0.2540454	
SlopeF-SlopeC	-2.289575	0.08652596	.	0.9999488	



7.6.33 Vitvi14g03071

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

Vitvi14g03071

35.2

not assigned.unknown

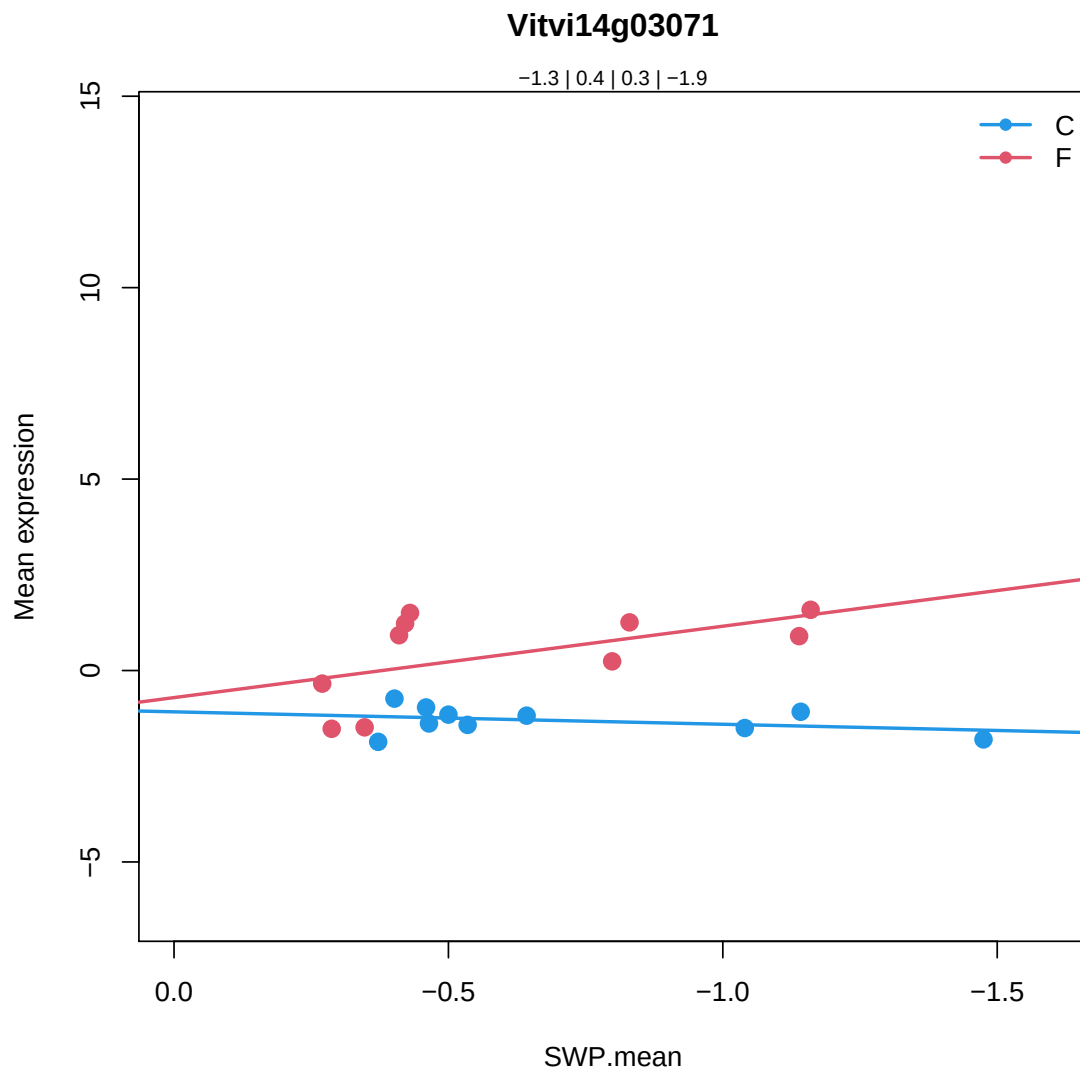
kinase family with leucine-rich repeat domain-containing protein |

Chr1:13220940-13224386 FORWARD LENGTH=1120 |

201606

Coefficients for Vitvi14g03071.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.307629	9.148178e-06	***	1.034165e-05	***
SlopeC	0.3246997	0.6116398		0.9065647	
MeanF-MeanC	1.736141	2.088562e-05	***	0.0004765548	***
SlopeF-SlopeC	-2.188816	0.02941108	*	0.9999488	



7.6.34 Vitvi06g01965

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

Vitvi06g01965

35.2

not assigned.unknown

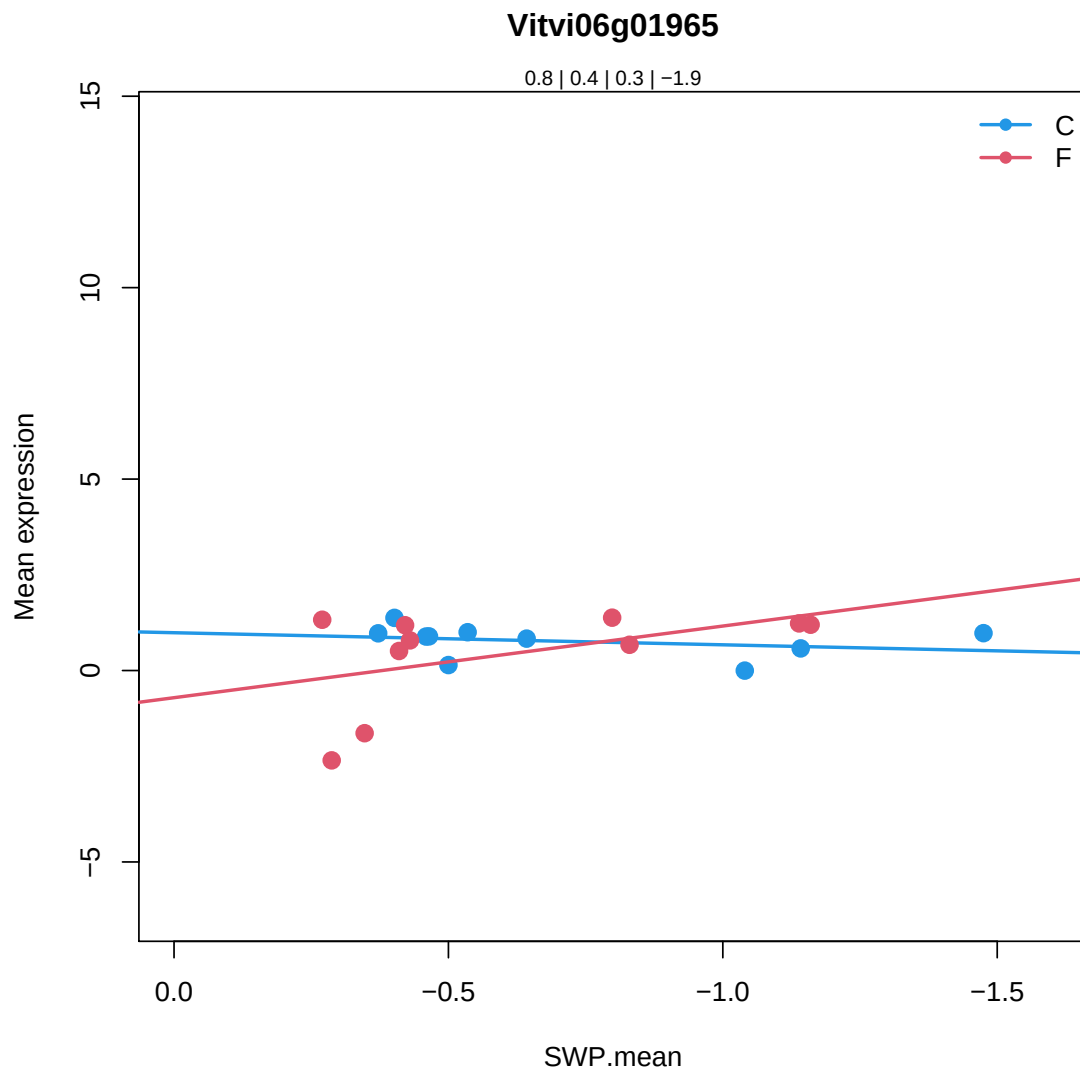
BED zinc finger and hAT dimerization domain-containing protein DAYSLEE

Chr3:14321838-14323928 FORWARD LENGTH=696 |

201606

Coefficients for Vitvi06g01965.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.7651484	0.008021156	**	0.008514413	**
SlopeC	0.3157152	0.6690095		0.9237671	
MeanF-MeanC	-0.3351699	0.3753781		0.7282614	
SlopeF-SlopeC	-2.186908	0.05635322	.	0.9999488	



7.6.35 Vitvi06g00024

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

Vitvi06g00024

27.03.2025

RNA.regulation of transcription.MYB domain transcription factor family

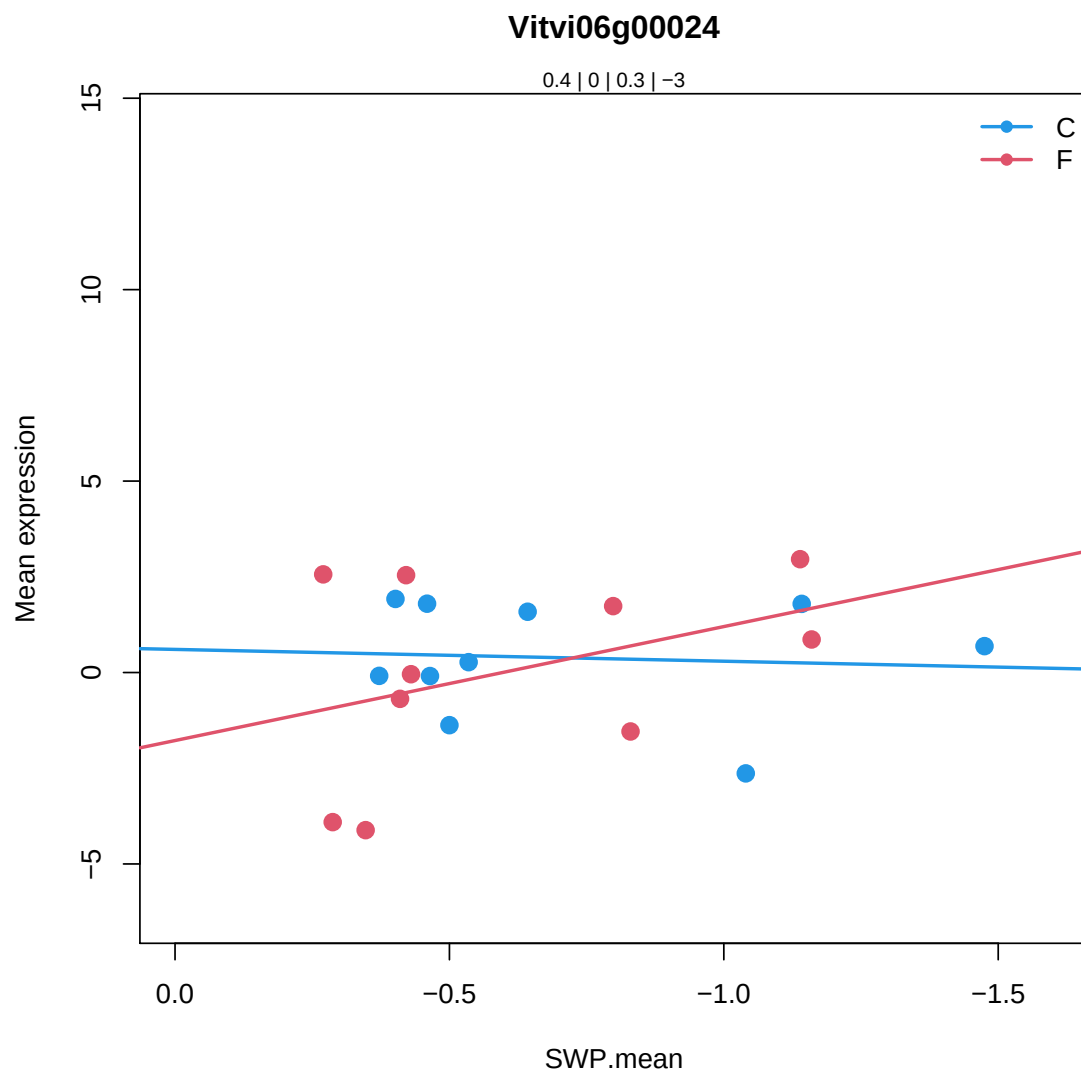
Homeodomain-like superfamily protein |

Chr3:1042920-1044574 REVERSE LENGTH=388 |

201606

Coefficients for Vitvi06g00024.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3868611	0.5141566		0.5201975	
SlopeC	0.3085189	0.8509751		0.9721955	
MeanF-MeanC	-0.3502342	0.6753086		0.8951087	
SlopeF-SlopeC	-3.285553	0.1877762		0.9999488	



7.6.36 Vitvi05g01916

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

Vitvi05g01916

35.2

not assigned.unknown

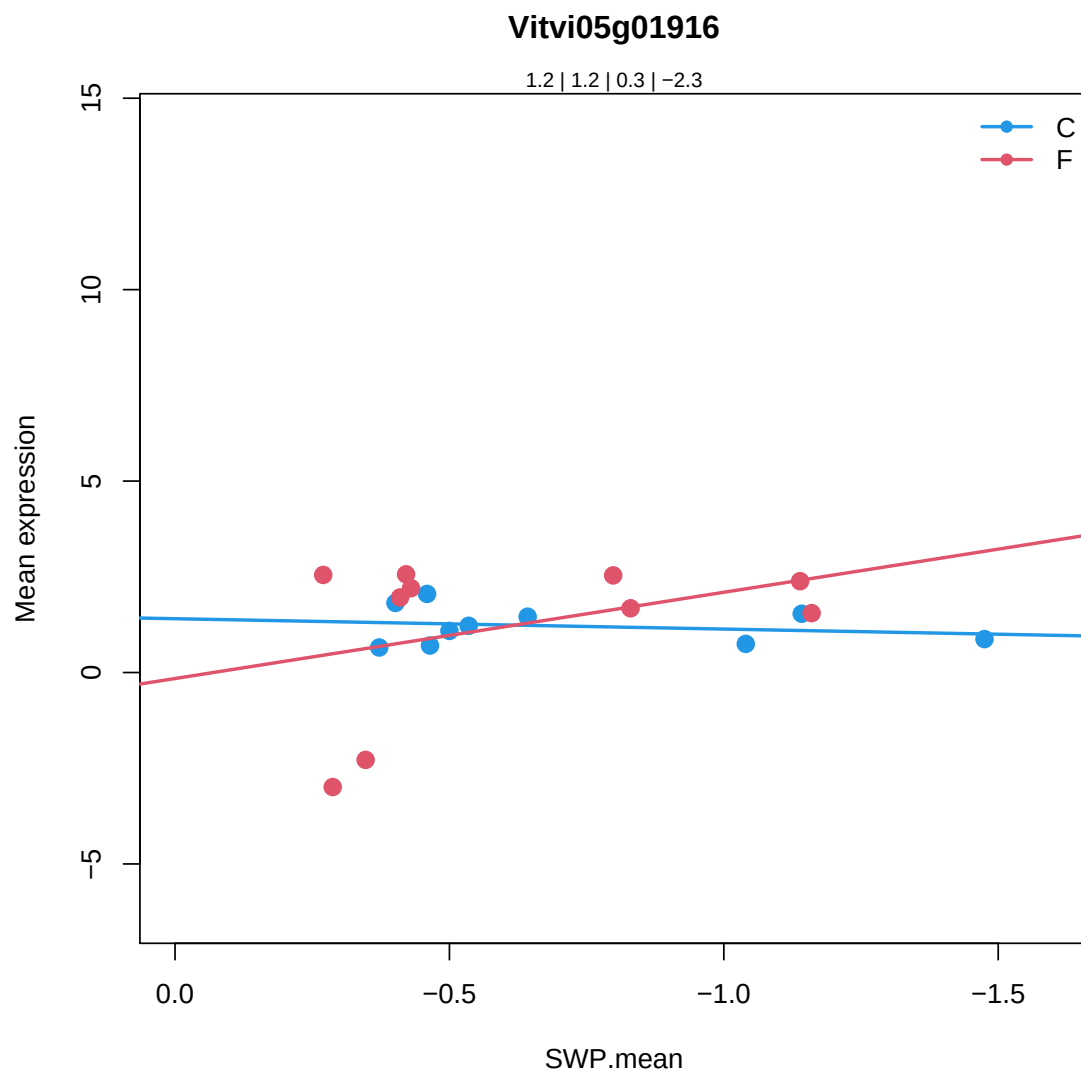
AT-hook motif nuclear-localized protein 20 |

Chr4:8320972-8321817 FORWARD LENGTH=281 |

201606

Coefficients for Vitvi05g01916.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.214898	0.007602167	**	0.008075846	**
SlopeC	0.2702258	0.8160264		0.9600088	
MeanF-MeanC	0.0005460515	0.9992616		0.9999176	
SlopeF-SlopeC	-2.523015	0.1540676		0.9999488	



7.6.37 Vitvi19g01669

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

Vitvi19g01669

27.03.2025

RNA.regulation of transcription.MYB domain transcription factor family

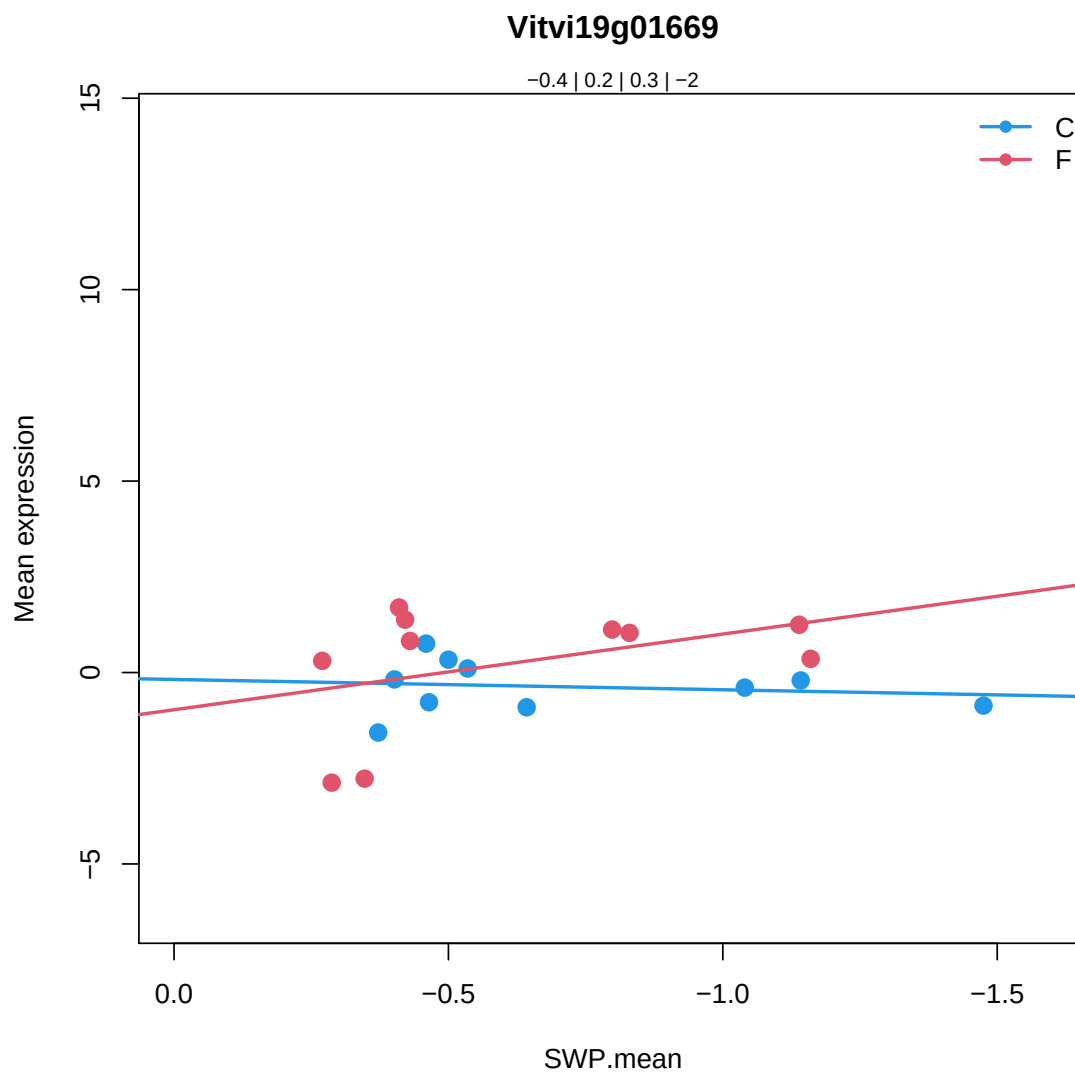
myb domain protein 58 |

Chr1:5629859-5630844 REVERSE LENGTH=274 |

201606

Coefficients for Vitvi19g01669.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.3703981	0.3013836		0.3071264	
SlopeC	0.2686673	0.7851157		0.9533712	
MeanF-MeanC	0.6025199	0.2364189		0.592388	
SlopeF-SlopeC	-2.245104	0.1357397		0.9999488	



7.6.38 Vitvi02g00666

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

Vitvi02g00666

27.03.1999

RNA.regulation of transcription.unclassified

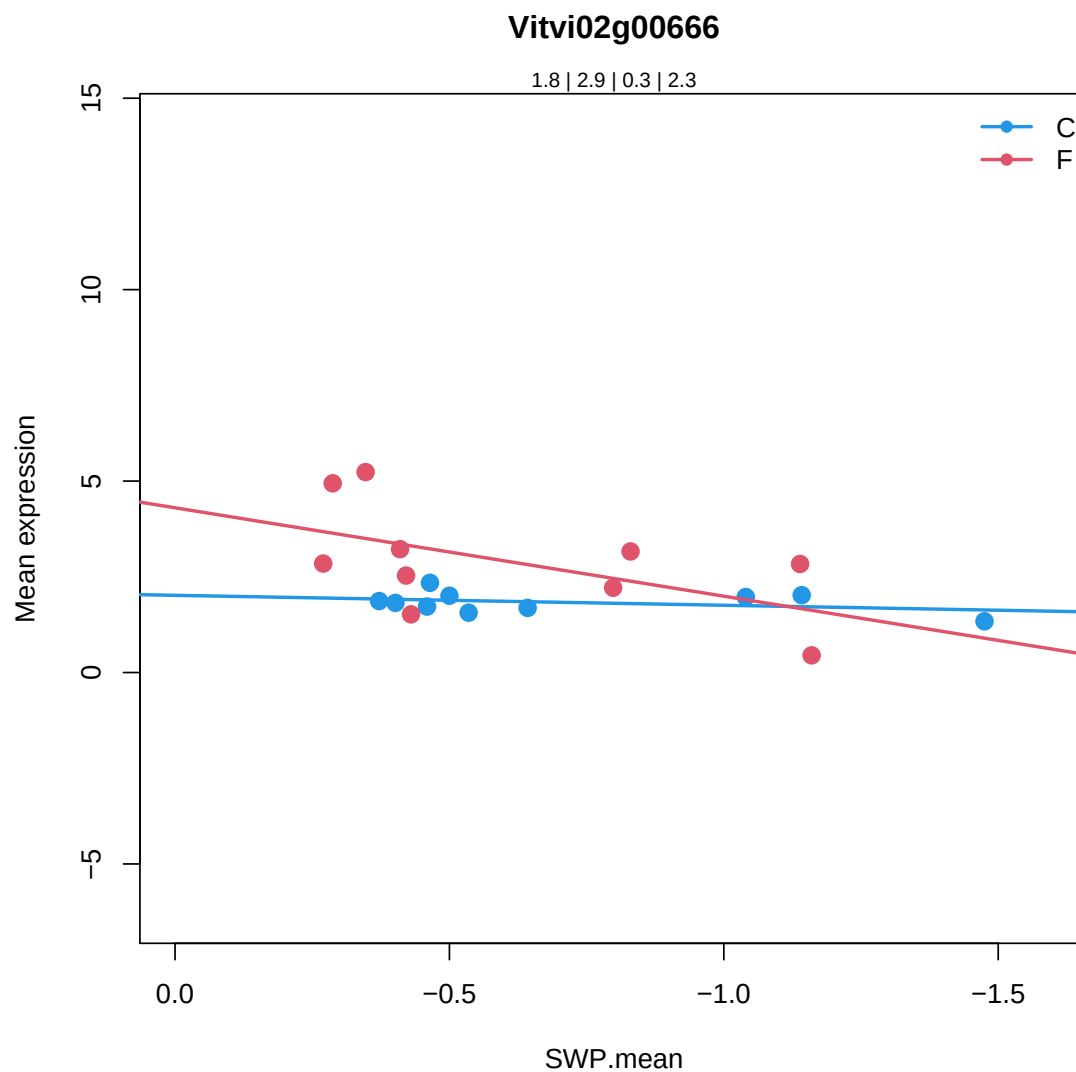
lsd one like 1 |

Chr1:11768253-11769591 FORWARD LENGTH=187 |

201606

Coefficients for Vitvi02g00666.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.833759	5.370324e-07	***	6.245573e-07	***
SlopeC	0.2596456	0.7237702		0.9393482	
MeanF-MeanC	1.061972	0.008812576	**	0.06916647	.
SlopeF-SlopeC	2.048877	0.07116225	.	0.9999488	



7.6.39 Vitvi10g01704

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

Vitvi10g01704

35.2

not assigned.unknown

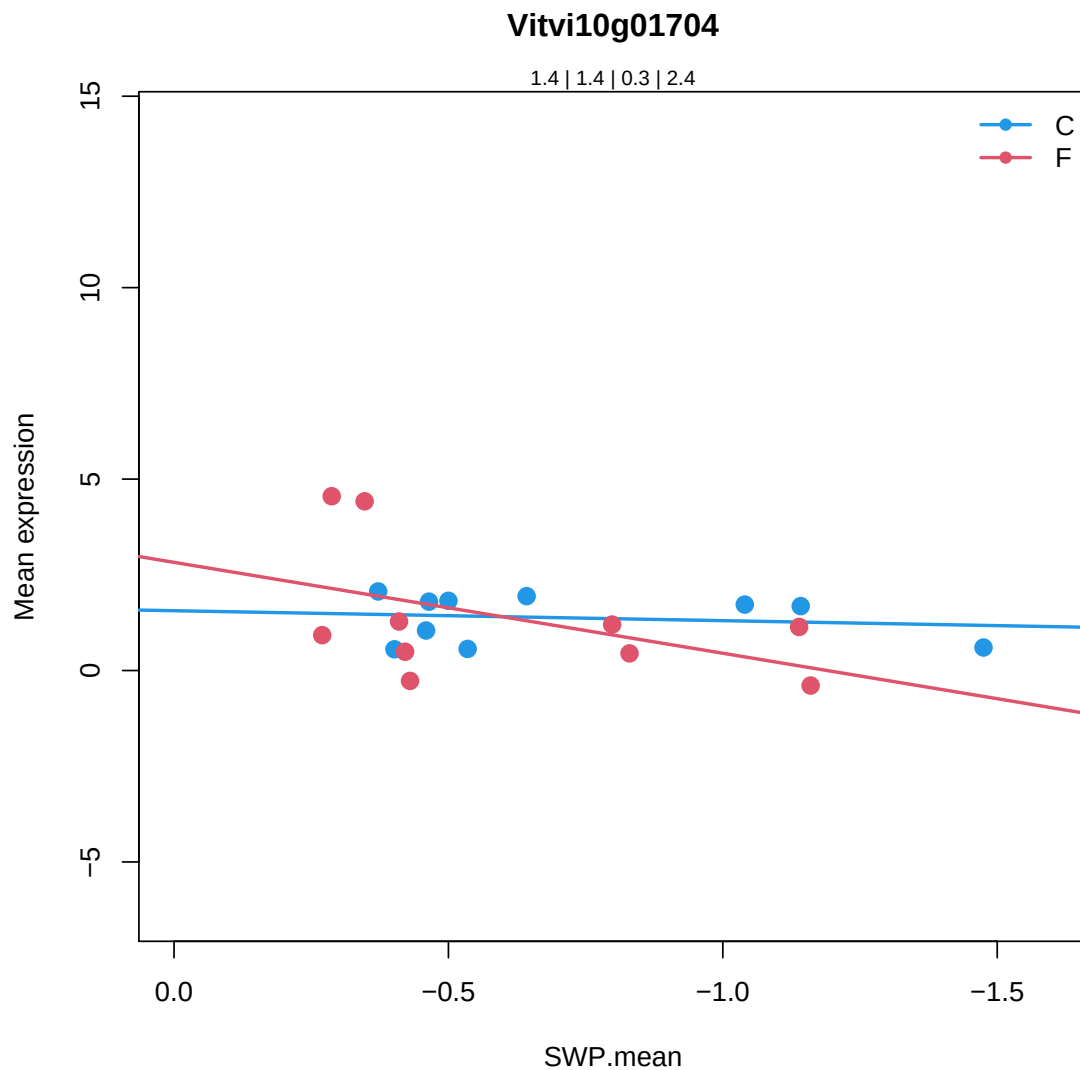
Heavy metal transport/detoxification superfamily protein |

Chr4:9255062-9255955 FORWARD LENGTH=261 |

201606

Coefficients for Vitvi10g01704.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.379404	0.0006645531	***	0.0007224248	***
SlopeC	0.2596266	0.7904758		0.9536839	
MeanF-MeanC	-0.0007762402	0.9987521		0.9998558	
SlopeF-SlopeC	2.11457	0.1554937		0.9999488	



7.6.40 Vitvi07g00450

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

Vitvi07g00450

35.2

not assigned.unknown

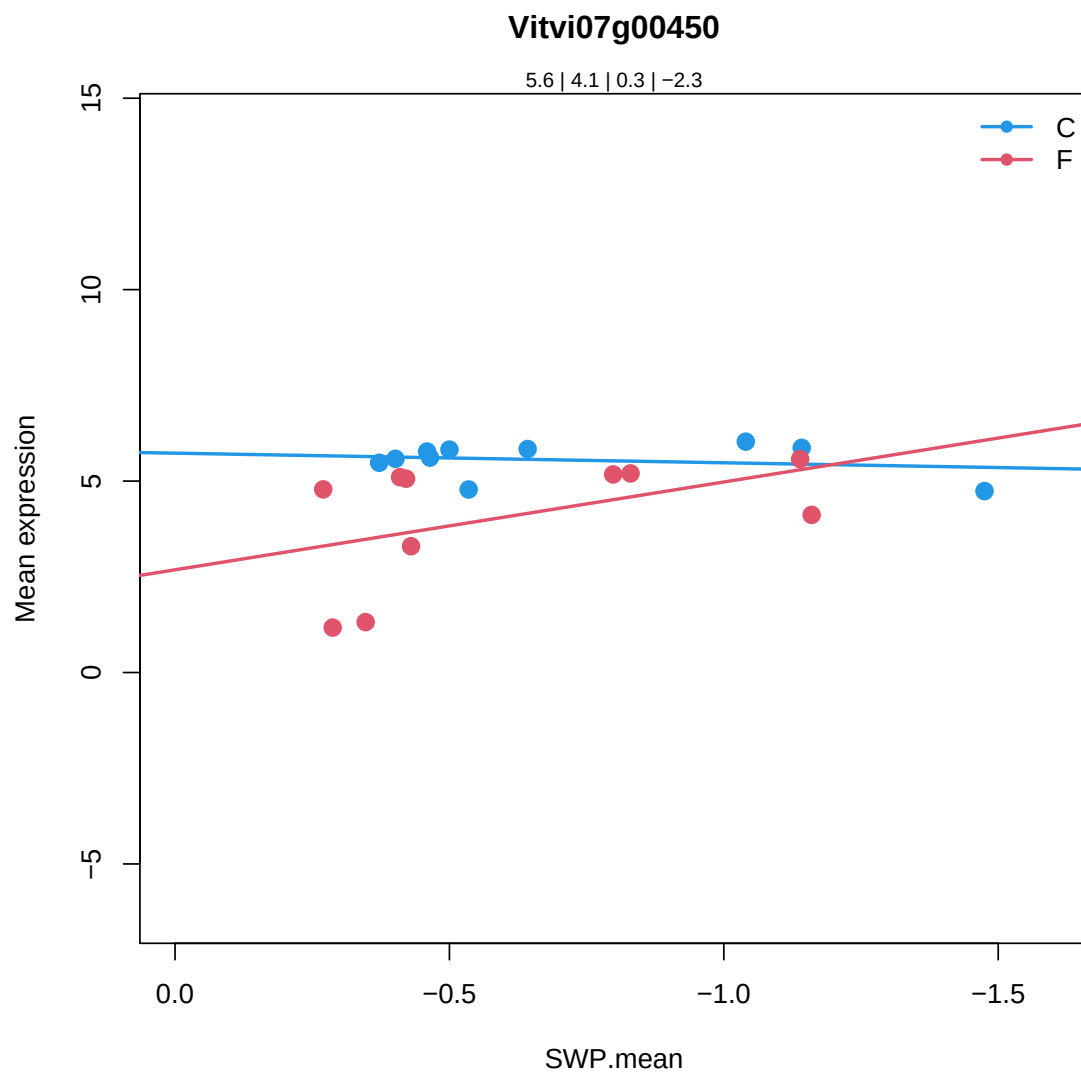
insulin-induced protein |

Chr4:841102-842228 FORWARD LENGTH=256 |

201606

Coefficients for Vitvi07g00450.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.552274	3.119128e-14	***	4.988641e-14	***
SlopeC	0.2505644	0.7778902		0.9513135	
MeanF-MeanC	-1.47195	0.003333318	**	0.03333755	*
SlopeF-SlopeC	-2.544415	0.06451323	.	0.9999488	



7.6.41 Vitvi16g01214

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

Vitvi16g01214

27.03.1985

RNA.regulation of transcription.sigma like plant

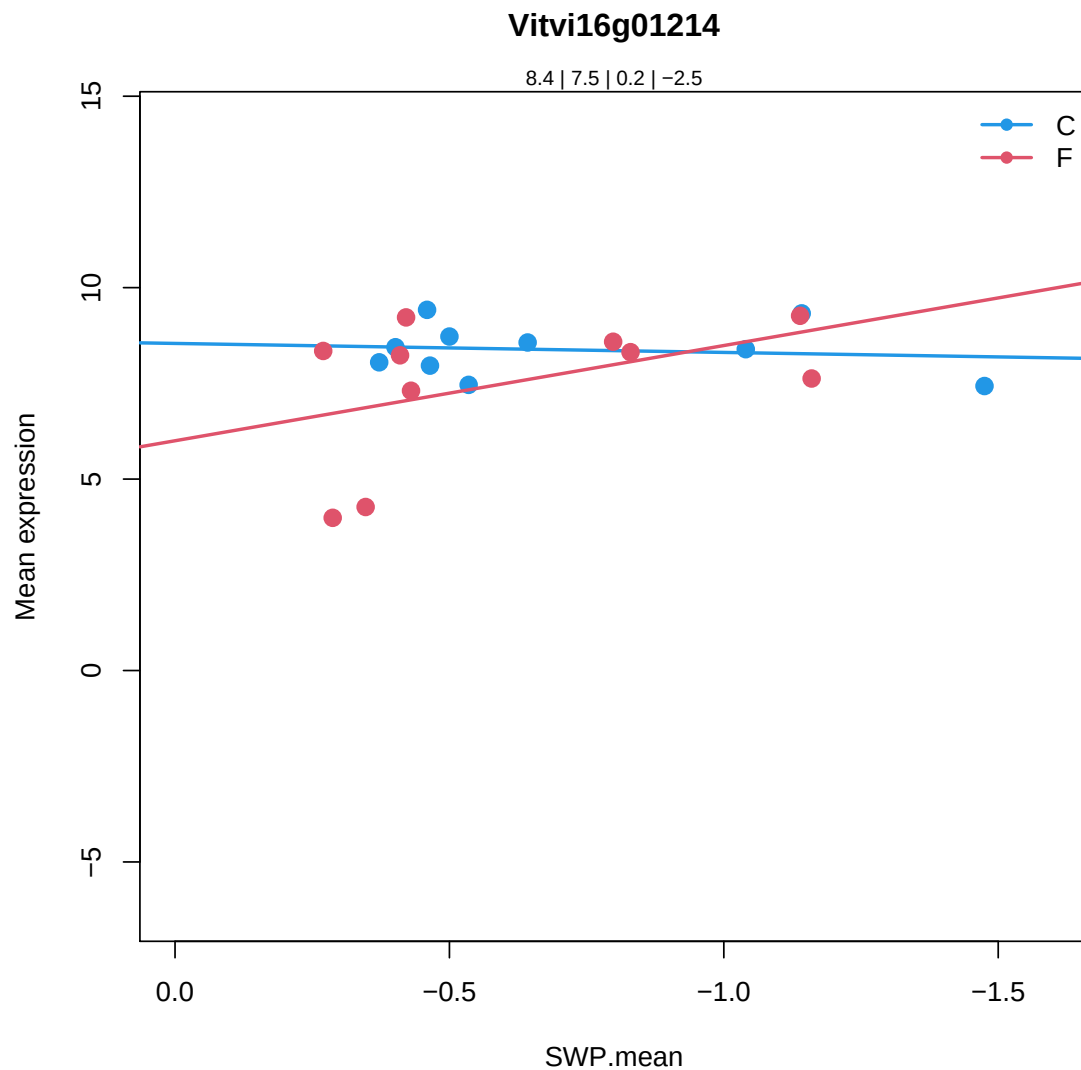
sigma factor E |

Chr5:8157794-8159746 REVERSE LENGTH=517 |

201606

Coefficients for Vitvi16g01214.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	8.377712	3.064361e-16	***	6.160247e-16	***
SlopeC	0.2347942	0.8259473		0.9653997	
MeanF-MeanC	-0.8615797	0.1226846		0.4136162	
SlopeF-SlopeC	-2.721939	0.09729539	.	0.9999488	



7.6.42 Vitvi06g00327

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

Vitvi06g00327

35.2

not assigned.unknown

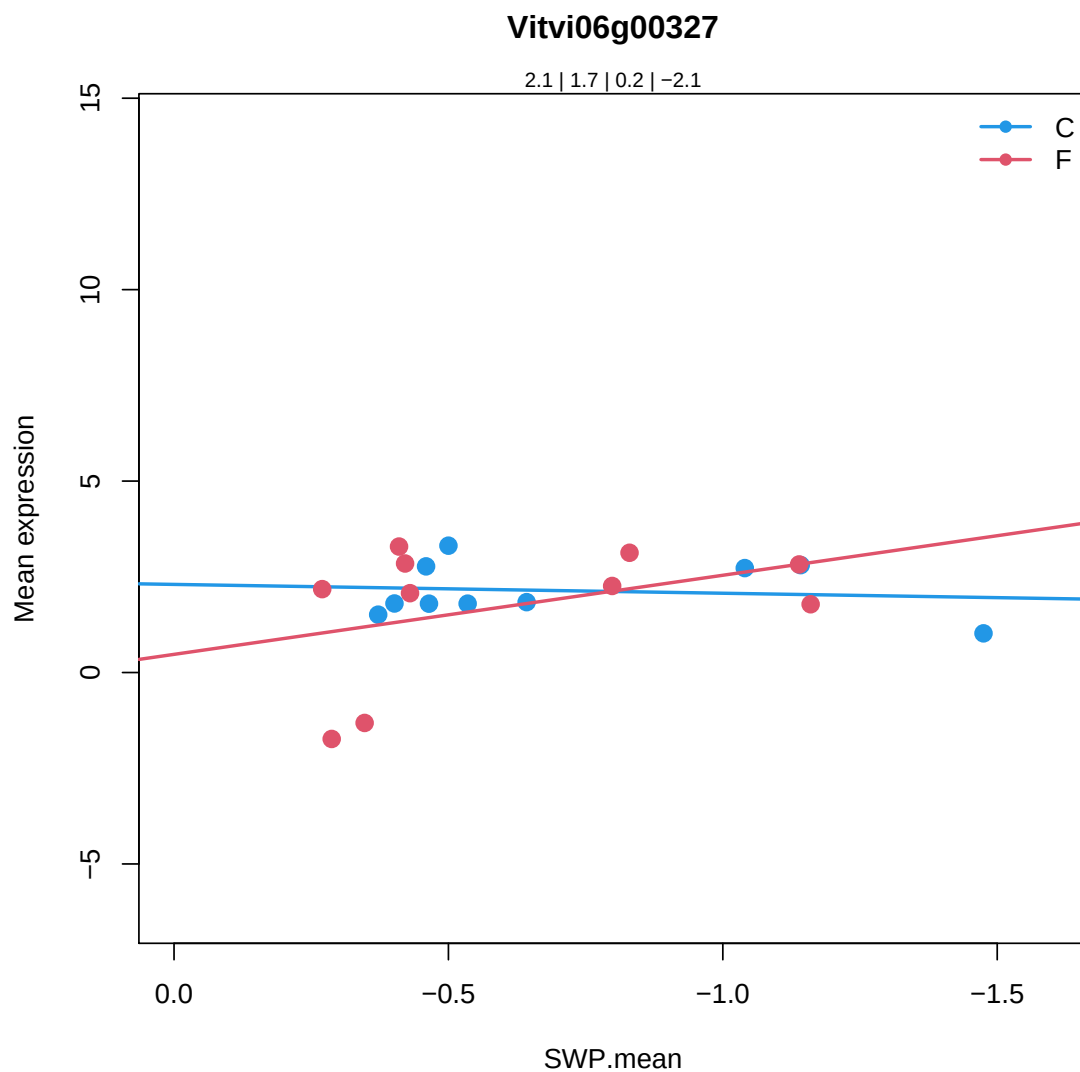
lectin protein kinase family protein |

Chr1:12503450-12505939 FORWARD LENGTH=829 |

201606

Coefficients for Vitvi06g00327.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.138951	1.054237e-05	***	1.190008e-05	***
SlopeC	0.230431	0.8270416		0.9656897	
MeanF-MeanC	-0.4060912	0.4515428		0.77888	
SlopeF-SlopeC	-2.296154	0.1532		0.9999488	



7.6.43 Vitvi04g01423

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

Vitvi04g01423

27.03.2007

RNA.regulation of transcription.C2C2(Zn) Constans-like zinc finger fam

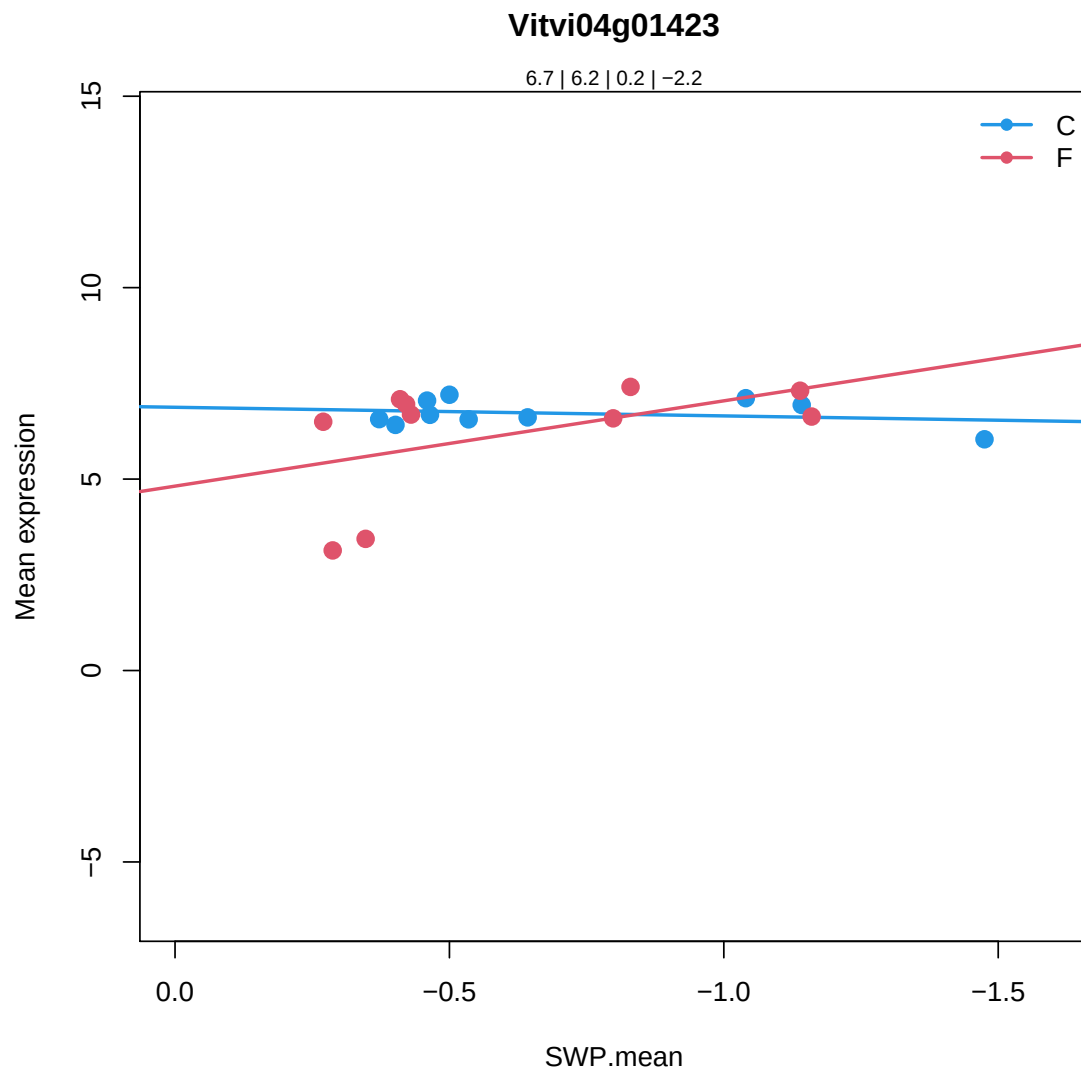
B-box type zinc finger family protein |

Chr4:18161576-18163045 FORWARD LENGTH=183 |

201606

Coefficients for Vitvi04g01423.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.716982	1.815366e-16	***	3.776932e-16	***
SlopeC	0.2254381	0.7871277		0.9533712	
MeanF-MeanC	-0.5438791	0.2081442		0.5525589	
SlopeF-SlopeC	-2.453074	0.05842625	.	0.9999488	



7.6.44 Vitvi10g00027

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

Vitvi10g00027

18.2

Co-factor and vitamine metabolism.thiamine

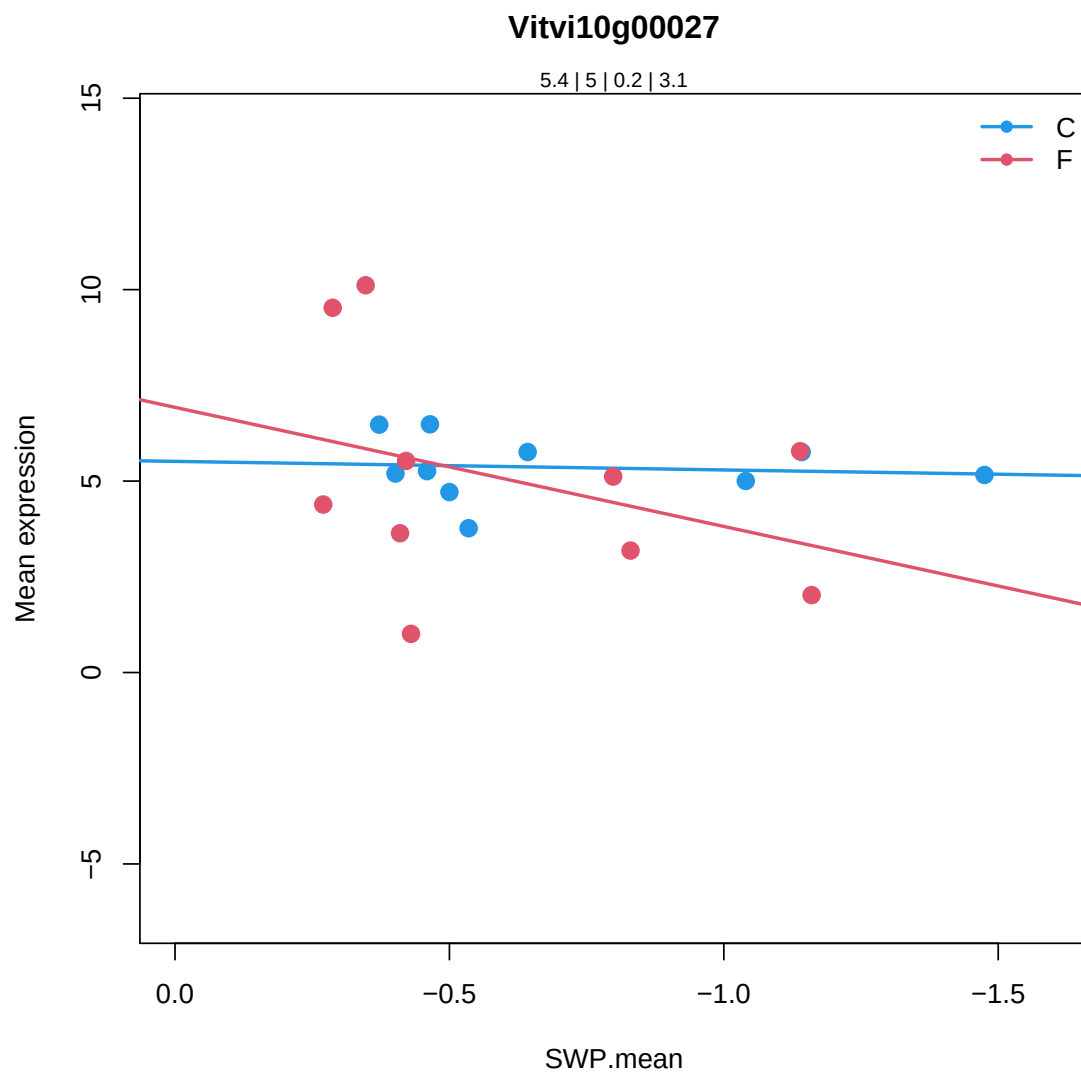
thiazole biosynthetic enzyme%2C chloroplast (ARA6) (THI1) (THI4) |

Chr5:22246634-22247891 FORWARD LENGTH=349 |

201606

Coefficients for Vitvi10g00027.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.357273	8.634117e-09	***	1.055766e-08	***
SlopeC	0.2236902	0.8929712		0.9805249	
MeanF-MeanC	-0.3265925	0.6996094		0.9062933	
SlopeF-SlopeC	2.886813	0.2507124		0.9999488	



7.6.45 Vitvi03g00248

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

Vitvi03g00248

34.9

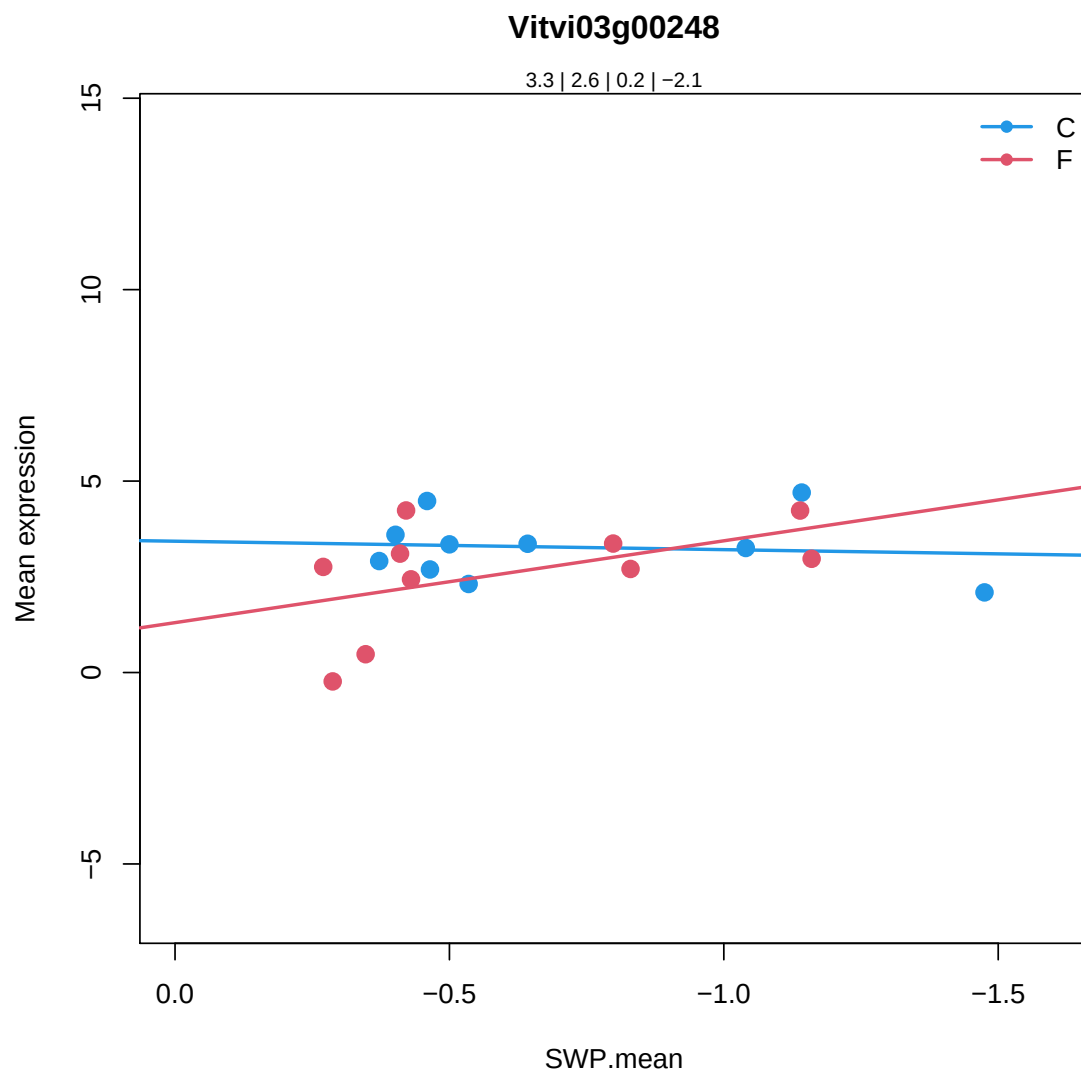
transport.metabolite transporters at the mitochondrial membrane
phosphate transporter 3%3B3 |

Chr2:7510456-7512118 FORWARD LENGTH=309 |

201606

Coefficients for Vitvi03g00248.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.274755	9.271225e-10	***	1.170092e-09	***
SlopeC	0.2201906	0.8058195		0.9575465	
MeanF-MeanC	-0.6699213	0.1508798		0.4679293	
SlopeF-SlopeC	-2.357623	0.08751471	.	0.9999488	



7.6.46 Vitvi11g00328

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

Vitvi11g00328

29.4

protein.postranslational modification

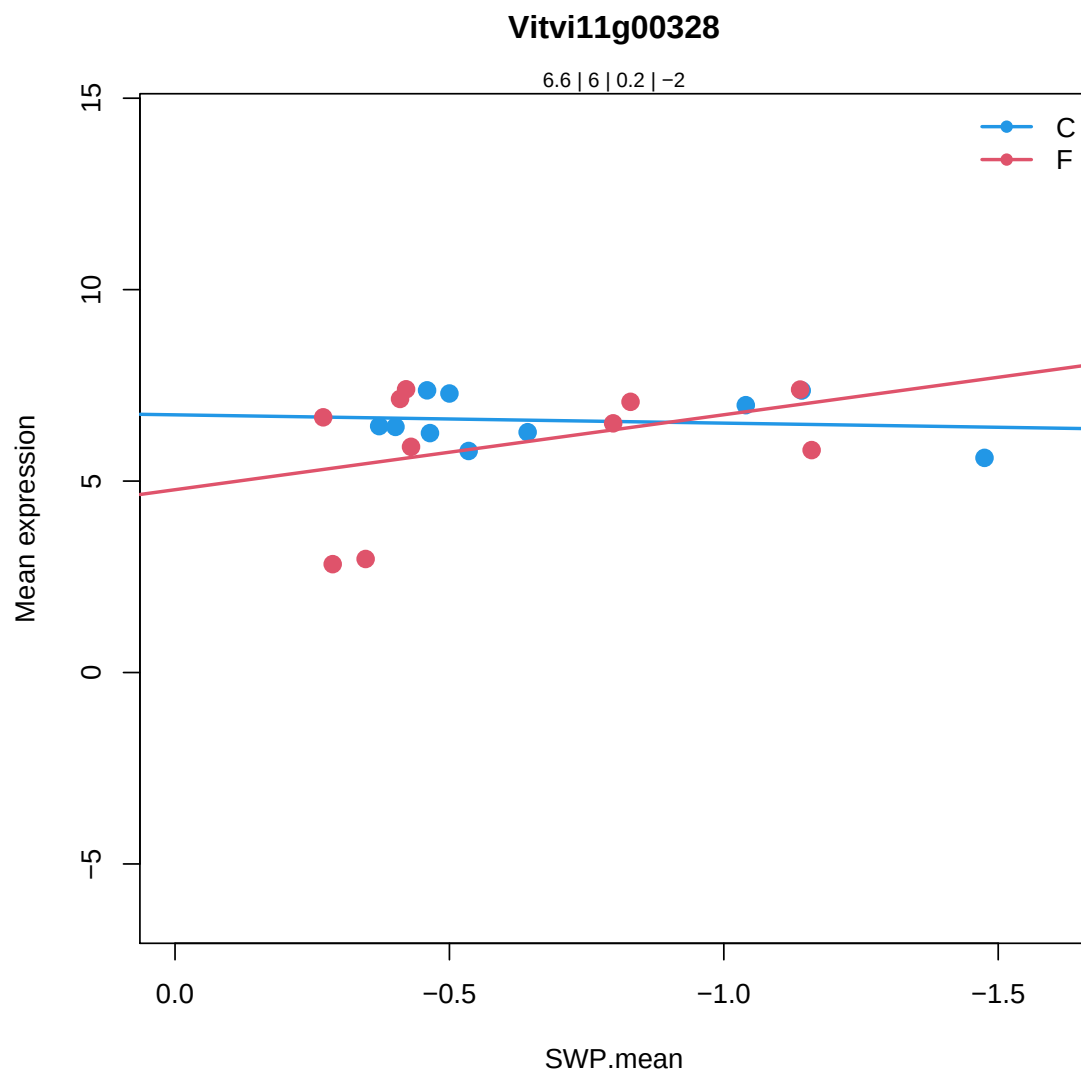
protein kinase family protein |

Chr5:7209422-7213700 FORWARD LENGTH=831 |

201606

Coefficients for Vitvi11g00328.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.577758	1.211049e-14	***	2.007265e-14	***
SlopeC	0.2169187	0.8289055		0.9662319	
MeanF-MeanC	-0.6102972	0.2391458		0.5962654	
SlopeF-SlopeC	-2.174644	0.1551483		0.9999488	



7.6.47 Vitvi14g01448

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

Vitvi14g01448

16.8.2.1

secondary metabolism.flavonoids.chalcones.naringenin-chalcone synthase

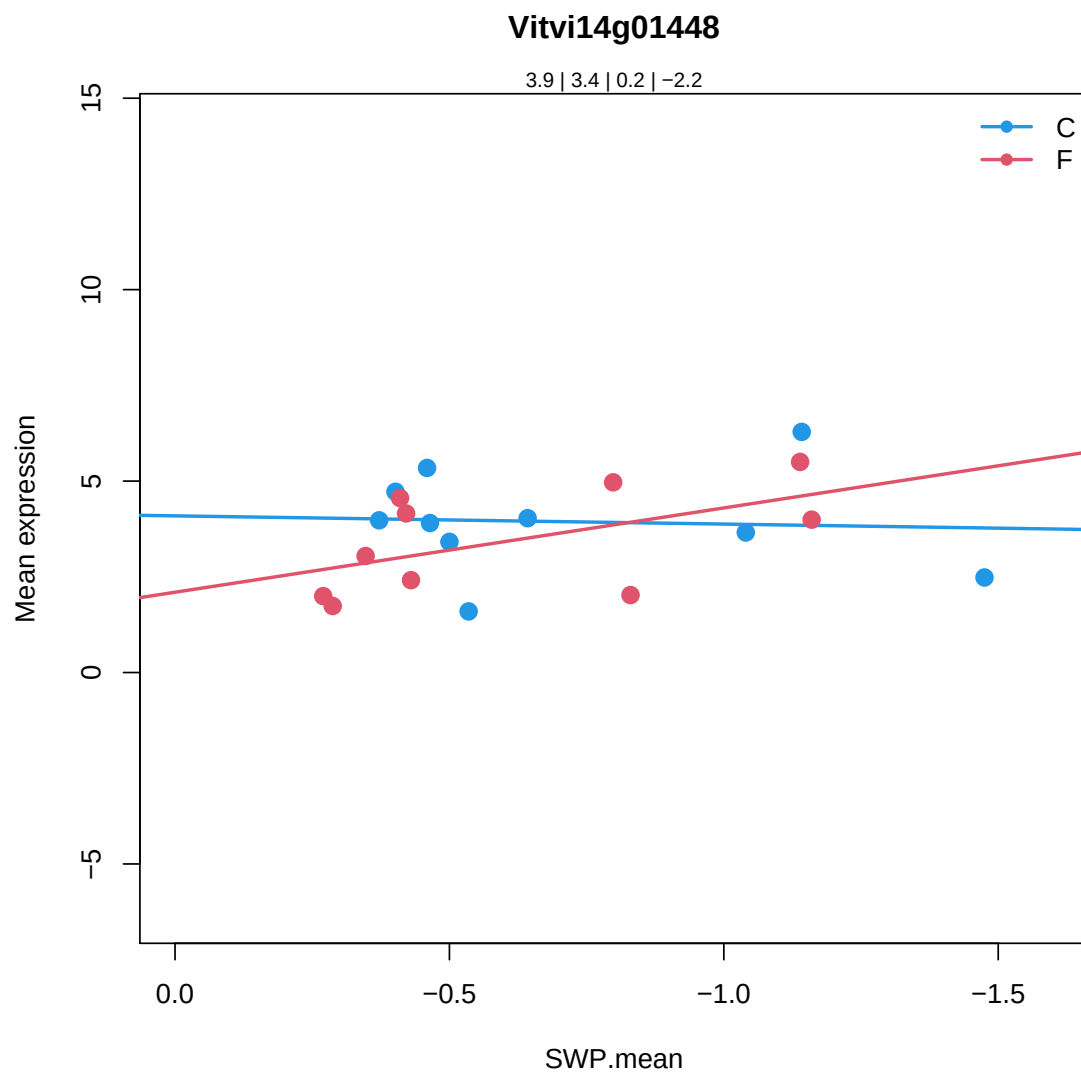
Chalcone and stilbene synthase family protein |

Chr5:4488762-4490035 FORWARD LENGTH=395 |

201606

Coefficients for Vitvi14g01448.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.940695	4.532478e-10	***	5.785932e-10	***
SlopeC	0.214132	0.8362316		0.9691182	
MeanF-MeanC	-0.5024314	0.344882		0.7045706	
SlopeF-SlopeC	-2.415744	0.1273688		0.9999488	



7.6.48 Vitvi02g00015

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

Vitvi02g00015

4.01.2012

glycolysis.cytosolic branch.phosphoglycerate mutase

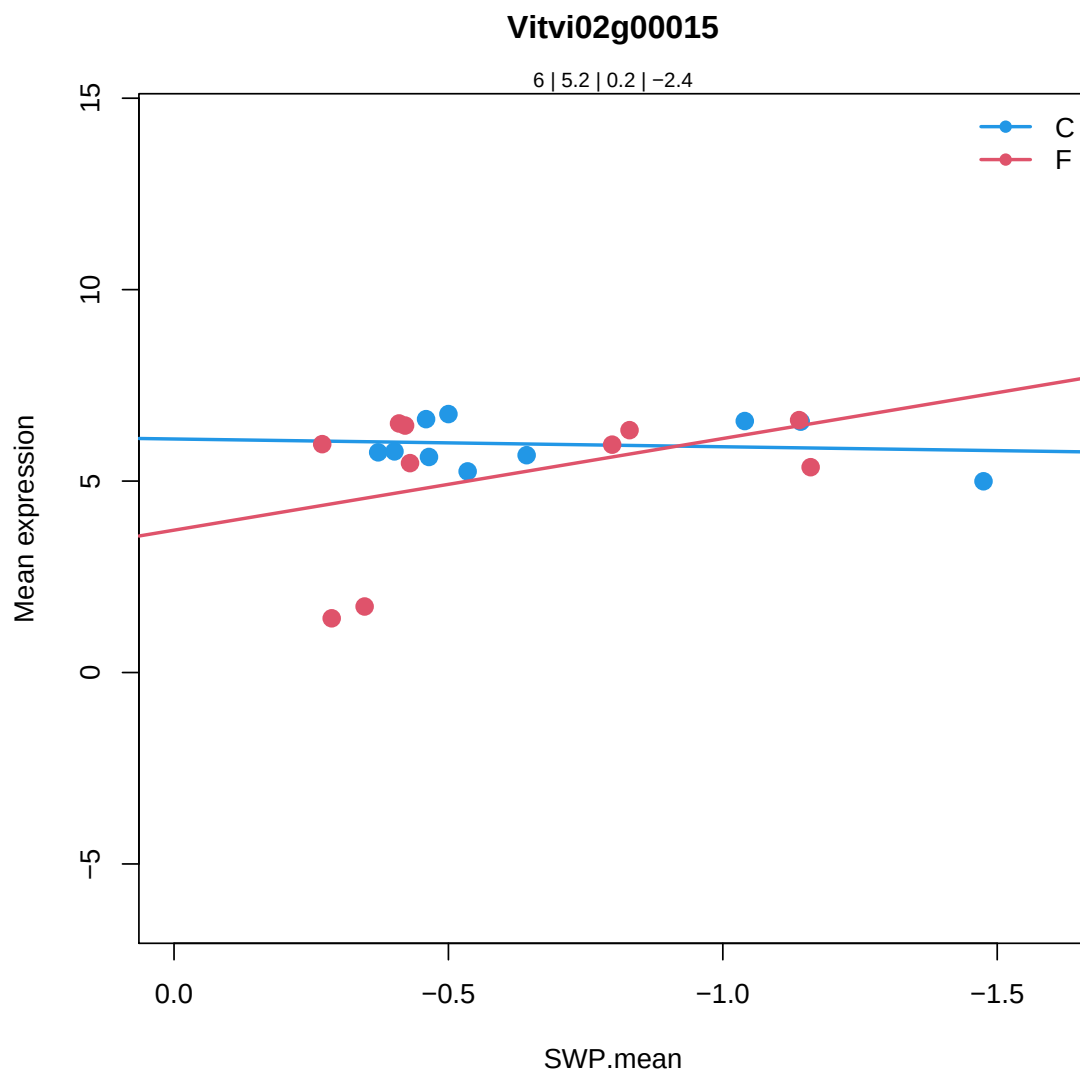
Phosphoglycerate mutase family protein |

Chr3:1466738-1468219 FORWARD LENGTH=316 |

201606

Coefficients for Vitvi02g00015.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.956586	5.565937e-13	***	8.124499e-13	***
SlopeC	0.2023908	0.8541168		0.972509	
MeanF-MeanC	-0.7801629	0.1725201		0.5031349	
SlopeF-SlopeC	-2.596304	0.1233502		0.9999488	



7.6.49 Vitvi01g01984

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

Vitvi01g01984

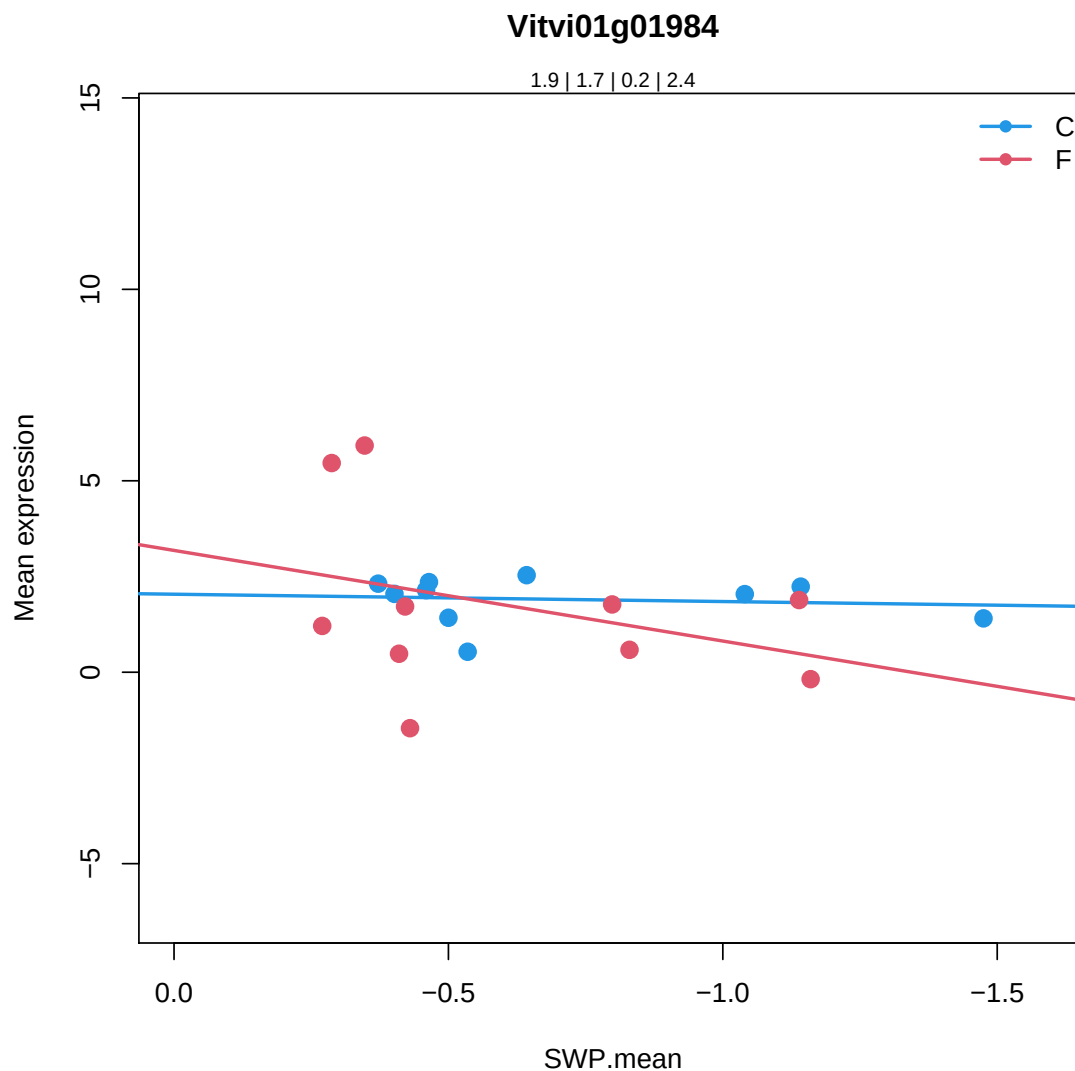
1.01.2006

PS.lightreaction.NADH DH

Unknown Protein

Coefficients for Vitvi01g01984.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.902803	0.0005459532	***	0.0005940052	***
SlopeC	0.1912234	0.8848239		0.9789842	
MeanF-MeanC	-0.1637473	0.8072977		0.9465338	
SlopeF-SlopeC	2.175521	0.2748866		0.9999488	



7.6.50 Vitvi14g01639

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

Vitvi14g01639

11.05.2002

lipid metabolism.glycerol metabolism.glycerol-3-phosphate dehydrogenas

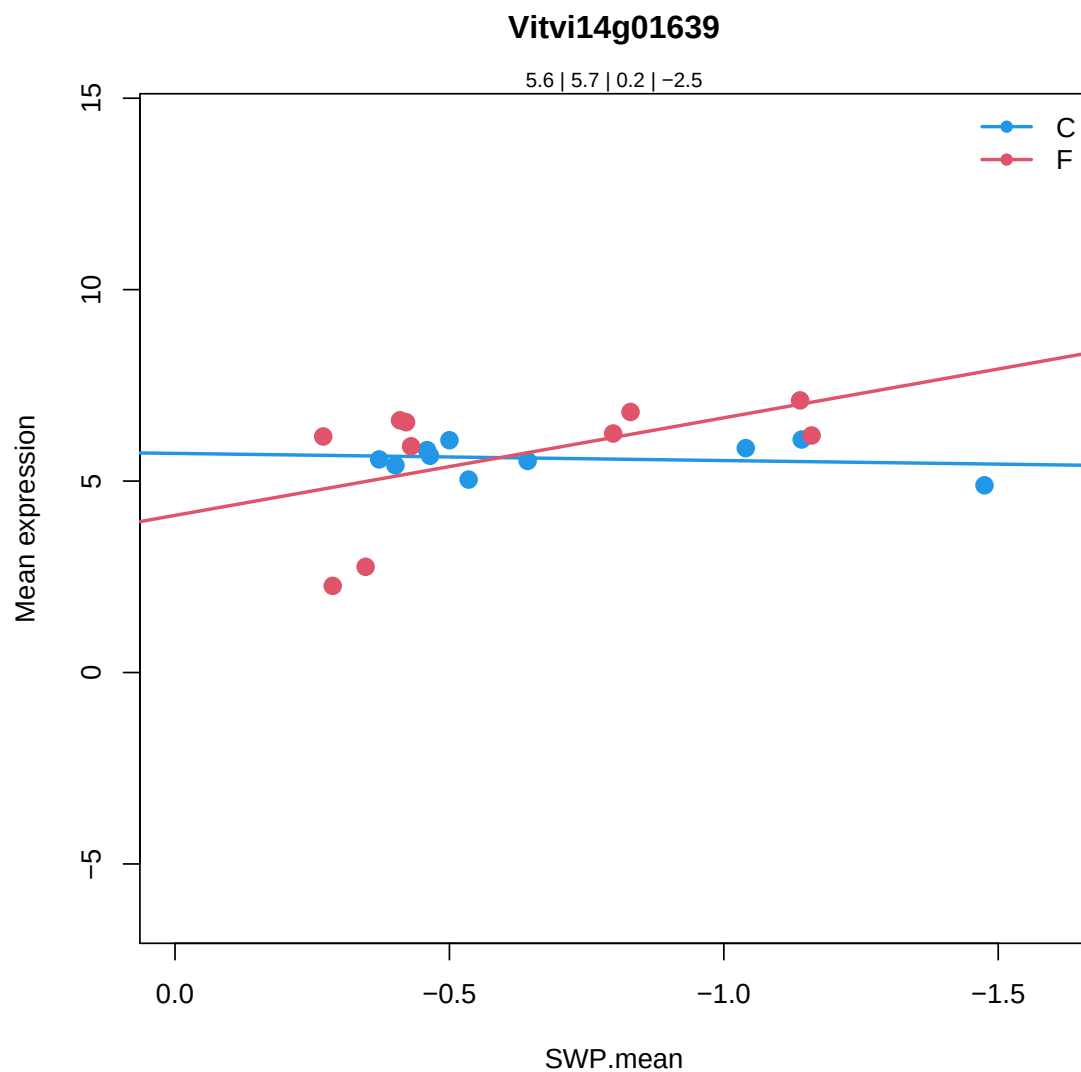
NAD-dependent glycerol-3-phosphate dehydrogenase family protein |

Chr5:16265071-16267258 REVERSE LENGTH=400 |

201606

Coefficients for Vitvi14g01639.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.591318	3.253981e-14	***	5.195597e-14	***
SlopeC	0.1867008	0.8349487		0.9683677	
MeanF-MeanC	0.06538842	0.8858182		0.9703262	
SlopeF-SlopeC	-2.735318	0.05009161	.	0.9999488	



7.6.51 Vitvi13g00350

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

Vitvi13g00350

31.2

cell.division

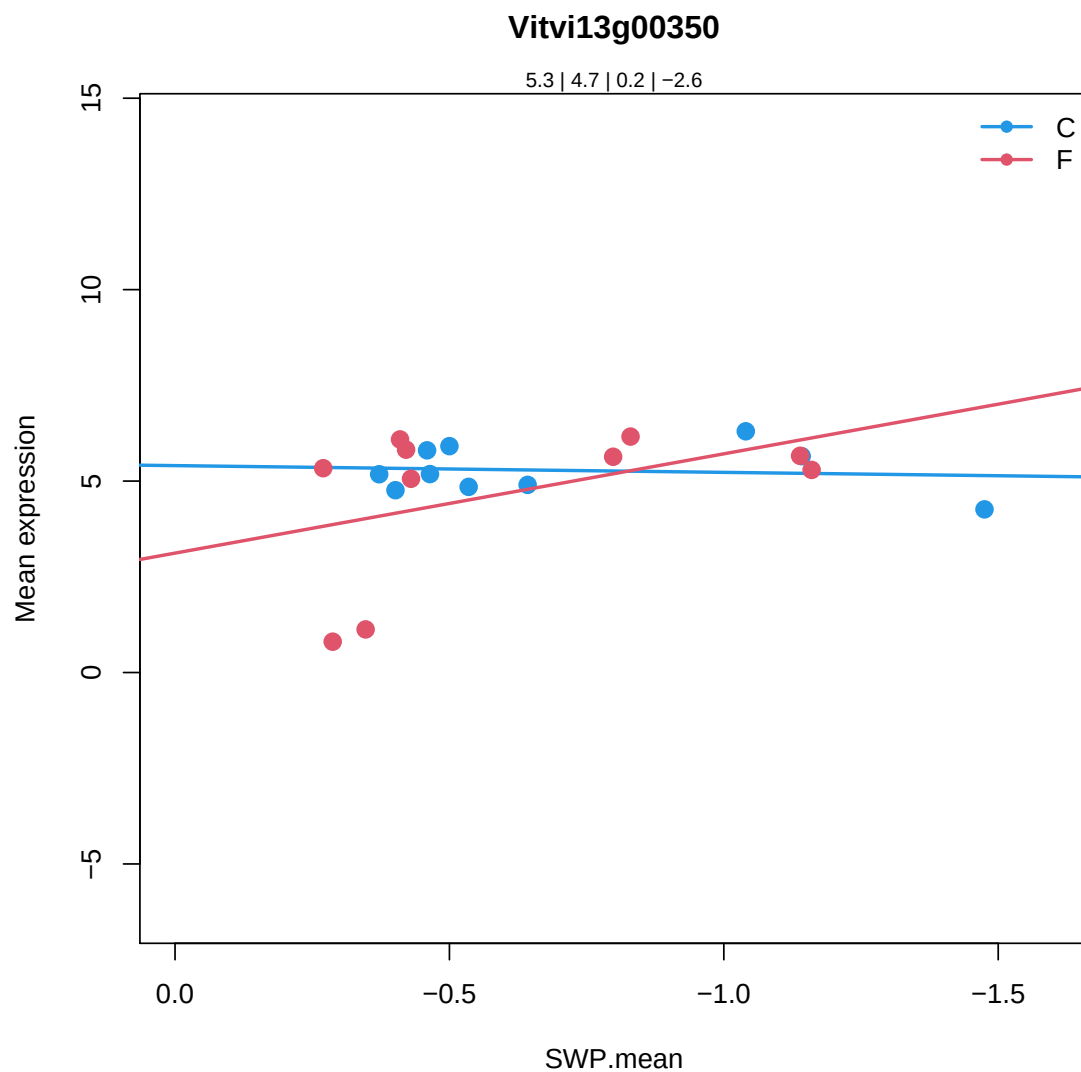
Regulator of chromosome condensation (RCC1) family protein |

Chr3:20612766-20615730 FORWARD LENGTH=488 |

201606

Coefficients for Vitvi13g00350.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.279791	7.387094e-12	***	1.015276e-11	***
SlopeC	0.1761415	0.8743711		0.9763383	
MeanF-MeanC	-0.5812761	0.3104724		0.6744662	
SlopeF-SlopeC	-2.769591	0.1054393		0.9999488	



7.6.52 Vitvi09g01361

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

Vitvi09g01361

35.2

not assigned.unknown

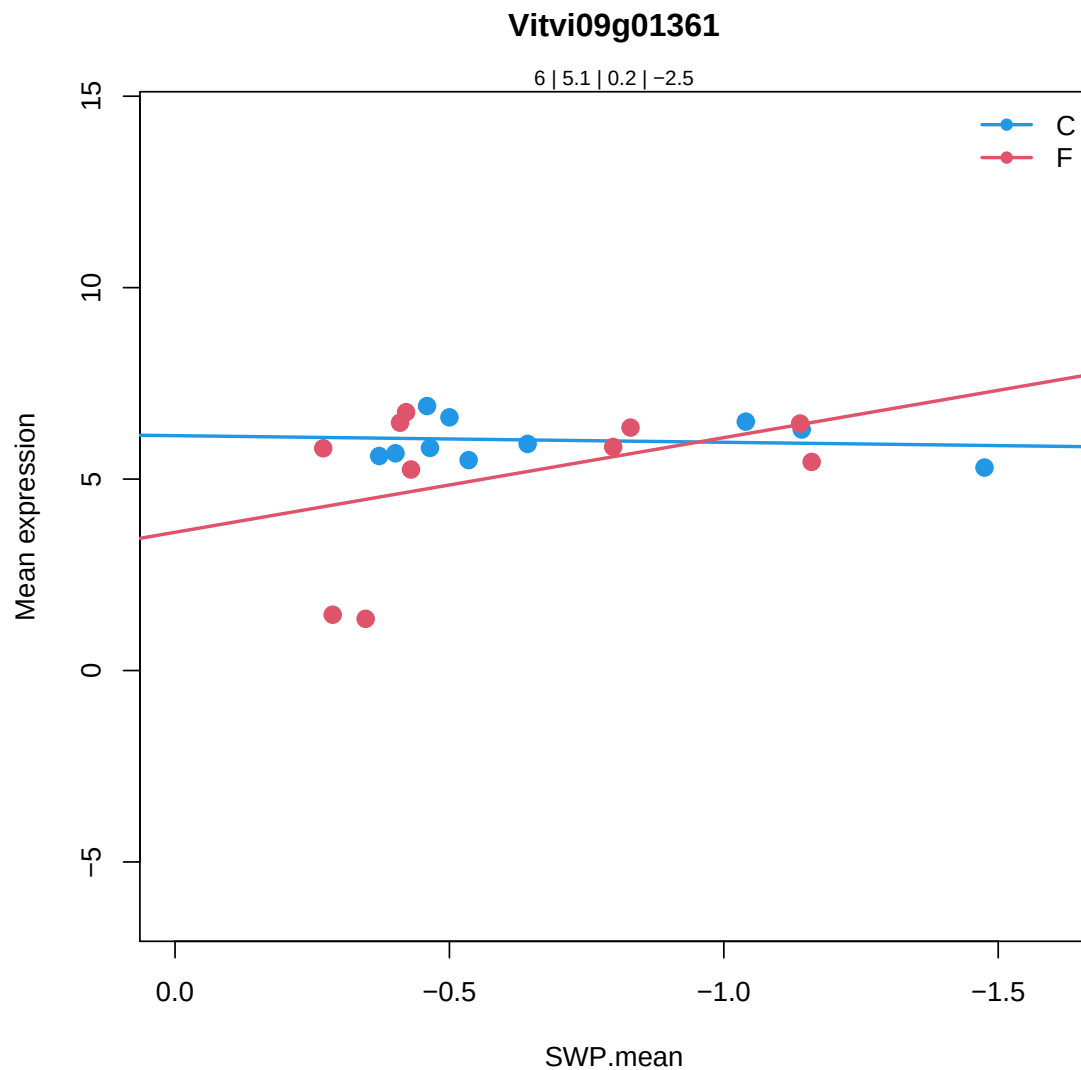
B-box 32 |

Chr3:7412713-7413390 REVERSE LENGTH=225 |

201606

Coefficients for Vitvi09g01361.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.011911	6.380595e-13	***	9.285966e-13	***
SlopeC	0.172968	0.8771097		0.9764303	
MeanF-MeanC	-0.8955918	0.1255631		0.4194242	
SlopeF-SlopeC	-2.644642	0.1225477		0.9999488	



7.6.53 Vitvi01g00463

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

Vitvi01g00463

35.1

not assigned.no ontology

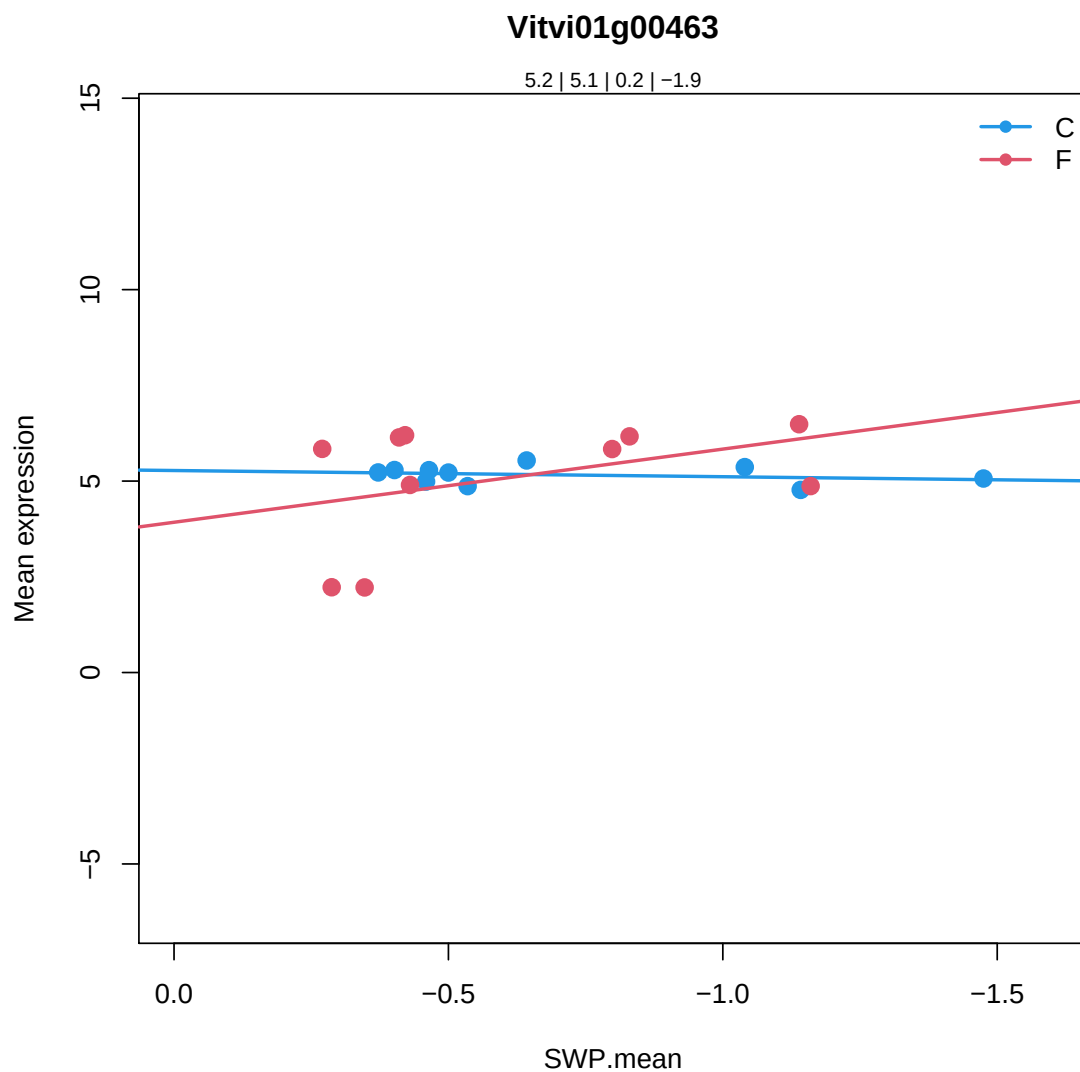
PLANT CADMIUM RESISTANCE 2 |

Chr1:5128591-5129458 REVERSE LENGTH=152 |

201606

Coefficients for Vitvi01g00463.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.161753	1.136374e-13	***	1.737796e-13	***
SlopeC	0.1617388	0.8542417		0.972509	
MeanF-MeanC	-0.07328533	0.8699129		0.9657814	
SlopeF-SlopeC	-2.072604	0.1240367		0.9999488	



7.6.54 Vitvi07g01779

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

Vitvi07g01779

34.6

transport.sulphate

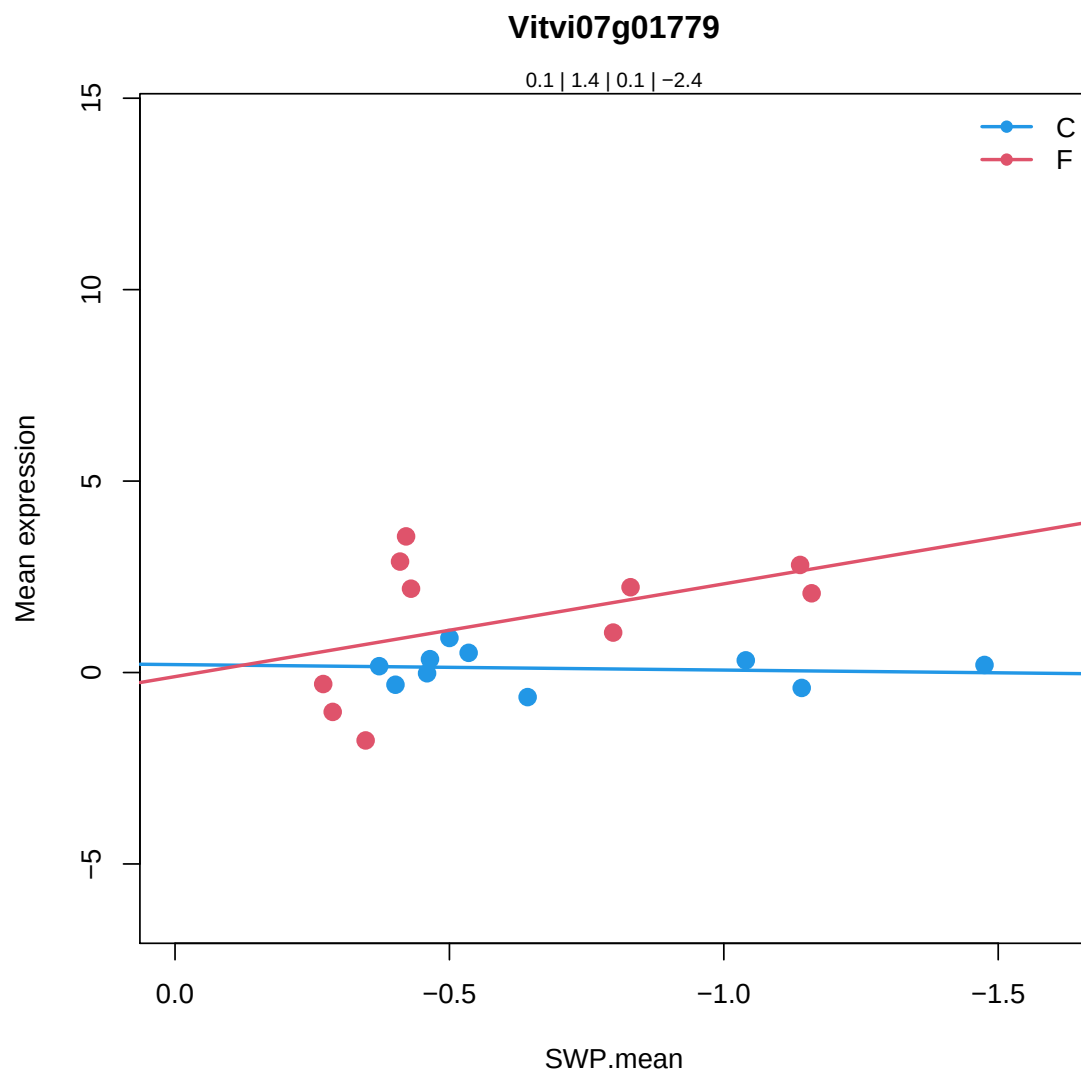
STAS domain / Sulfate transporter family |

Chr1:29317965-29323249 REVERSE LENGTH=677 |

201606

Coefficients for Vitvi07g01779.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1061768	0.7659189		0.7703158	
SlopeC	0.1430805	0.8852476		0.9789972	
MeanF-MeanC	1.262582	0.01906637	*	0.1219474	
SlopeF-SlopeC	-2.565898	0.09271658	.	0.9999488	



7.6.55 Vitvi07g01625

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

Vitvi07g01625

35.2

not assigned.unknown

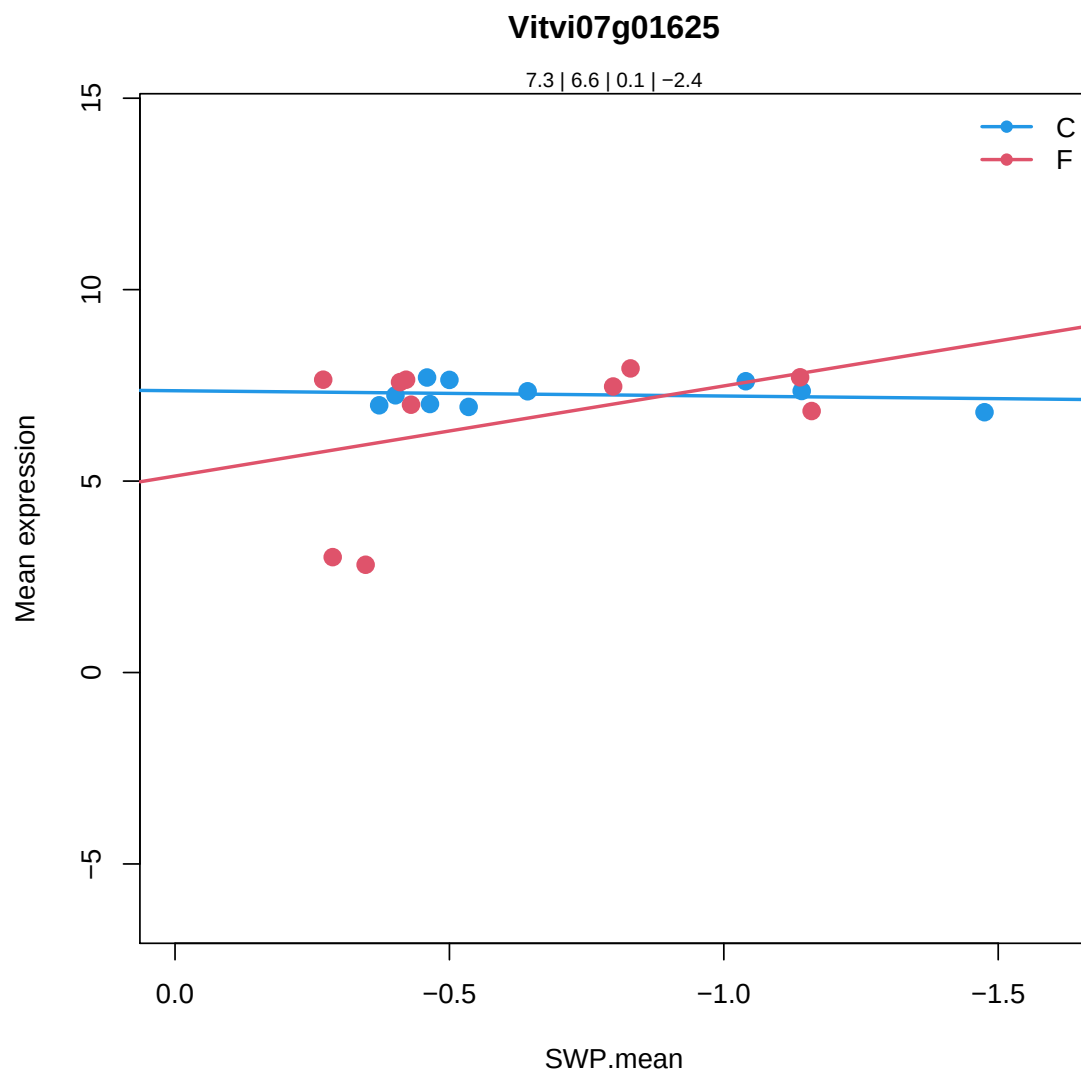
DUF1230 family protein (DUF1230) |

Chr5:26877667-26879465 REVERSE LENGTH=327 |

201606

Coefficients for Vitvi07g01625.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.262097	5.444524e-15	***	9.375825e-15	***
SlopeC	0.1377329	0.8970951		0.9815383	
MeanF-MeanC	-0.6966094	0.2066727		0.5512875	
SlopeF-SlopeC	-2.491219	0.1263736		0.9999488	



7.6.56 Vitvi01g01169

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

Vitvi01g01169

28.2

DNA.repair

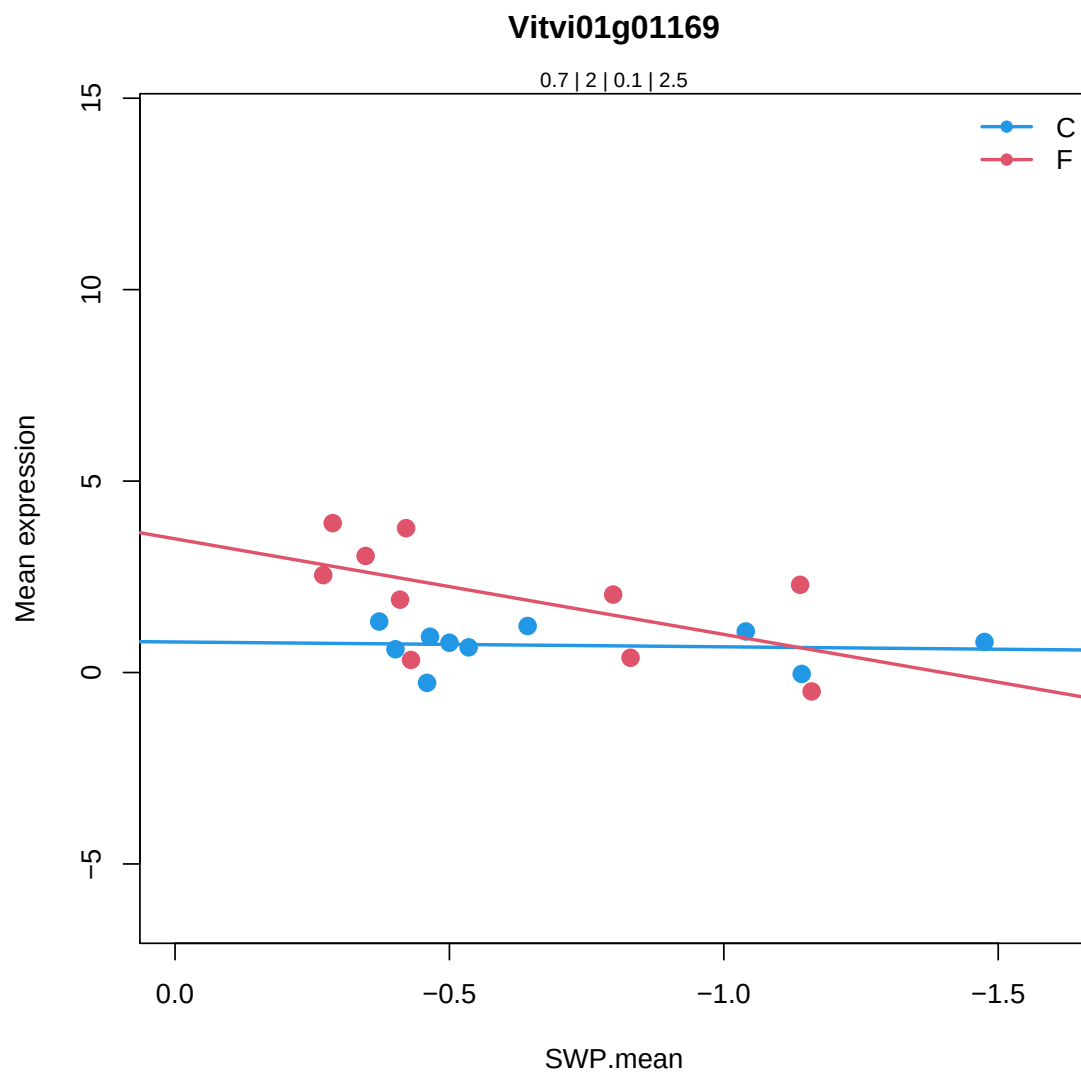
DNA glycosylase superfamily protein |

Chr5:18024461-18025893 REVERSE LENGTH=353 |

201606

Coefficients for Vitvi01g01169.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.7085306	0.01947902	*	0.02048428	*
SlopeC	0.1261609	0.8731049		0.9762394	
MeanF-MeanC	1.262078	0.004416771	**	0.04135161	*
SlopeF-SlopeC	2.370177	0.05383022	.	0.9999488	



7.6.57 Vitvi18g02592

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

Vitvi18g02592

26.12

misc.peroxidases

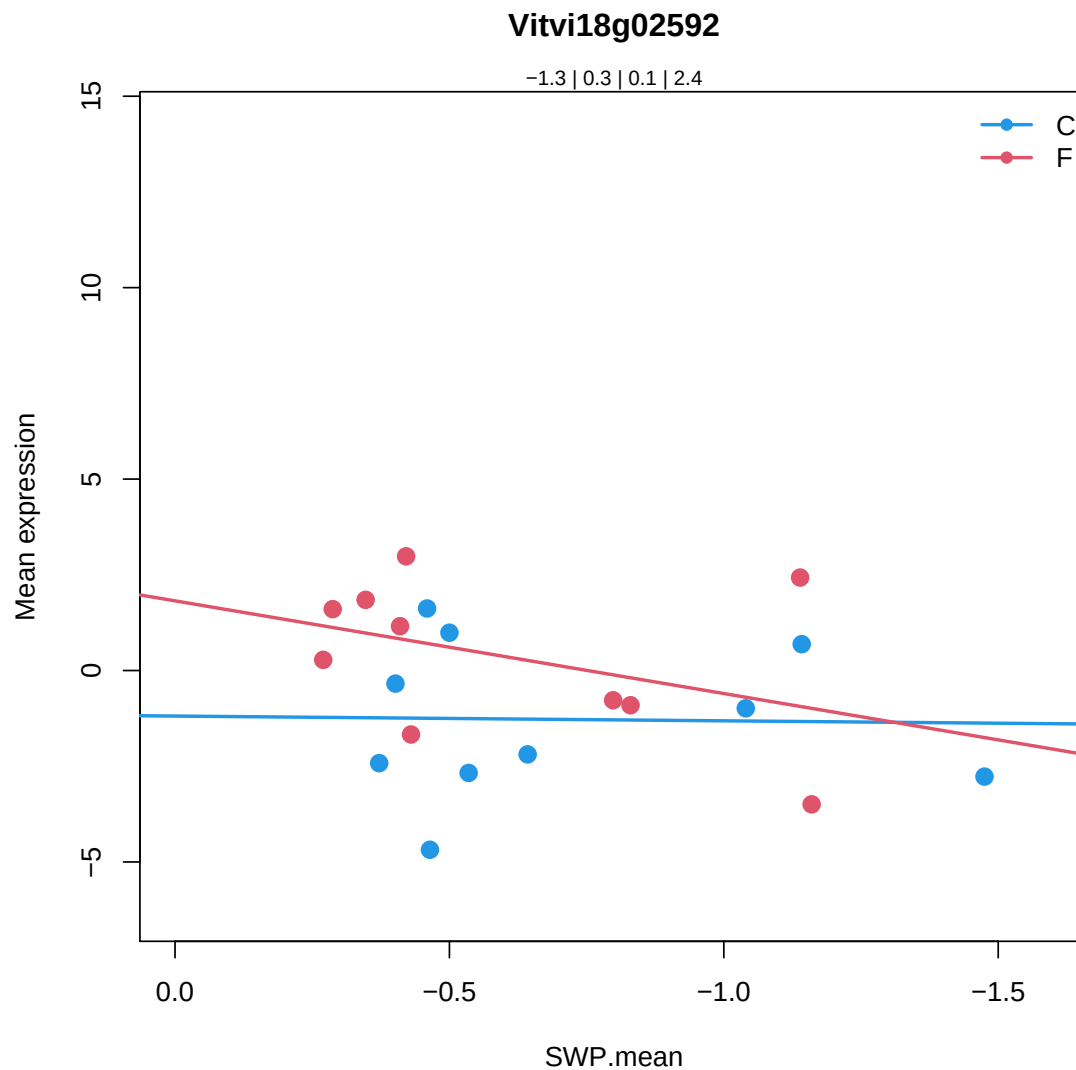
Peroxidase superfamily protein |

Chr5:1579142-1580819 REVERSE LENGTH=324 |

201606

Coefficients for Vitvi18g02592.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.277313	0.03463876	*	0.03620407	*
SlopeC	0.1244362	0.9377718		0.9891708	
MeanF-MeanC	1.621751	0.05546714	.	0.256018	
SlopeF-SlopeC	2.296027	0.3383703		0.9999488	



7.6.58 Vitvi09g01214

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

Vitvi09g01214

30.2.12

signalling.receptor kinases.leucine rich repeat XII

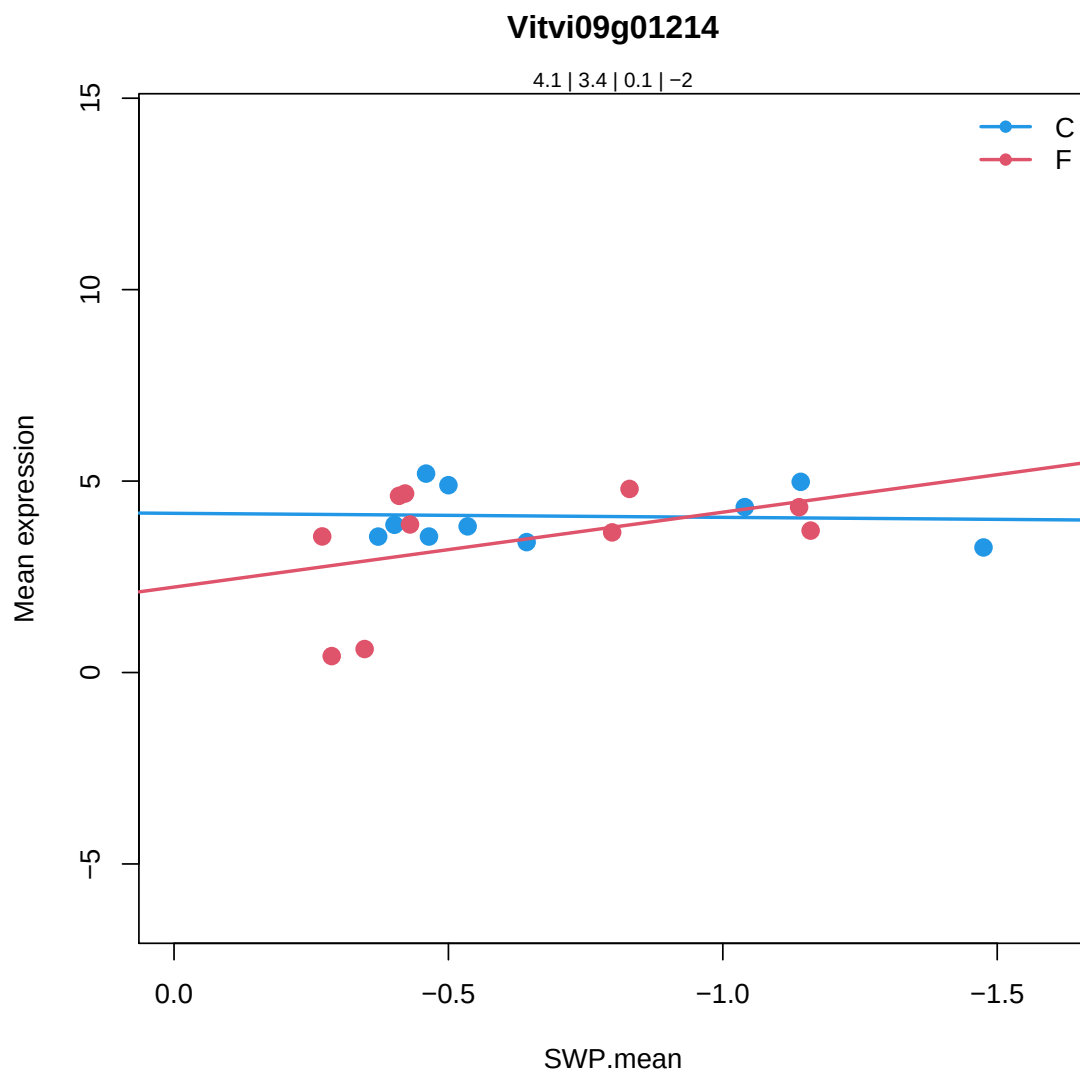
Leucine-rich repeat protein kinase family protein |

Chr3:17527611-17530748 FORWARD LENGTH=1010 |

201606

Coefficients for Vitvi09g01214.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.083621	5.230828e-11	***	6.919056e-11	***
SlopeC	0.105182	0.9122911		0.9839968	
MeanF-MeanC	-0.6604063	0.1828124		0.5186478	
SlopeF-SlopeC	-2.062439	0.156524		0.9999488	



7.6.59 Vitvi14g01152

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

Vitvi14g01152

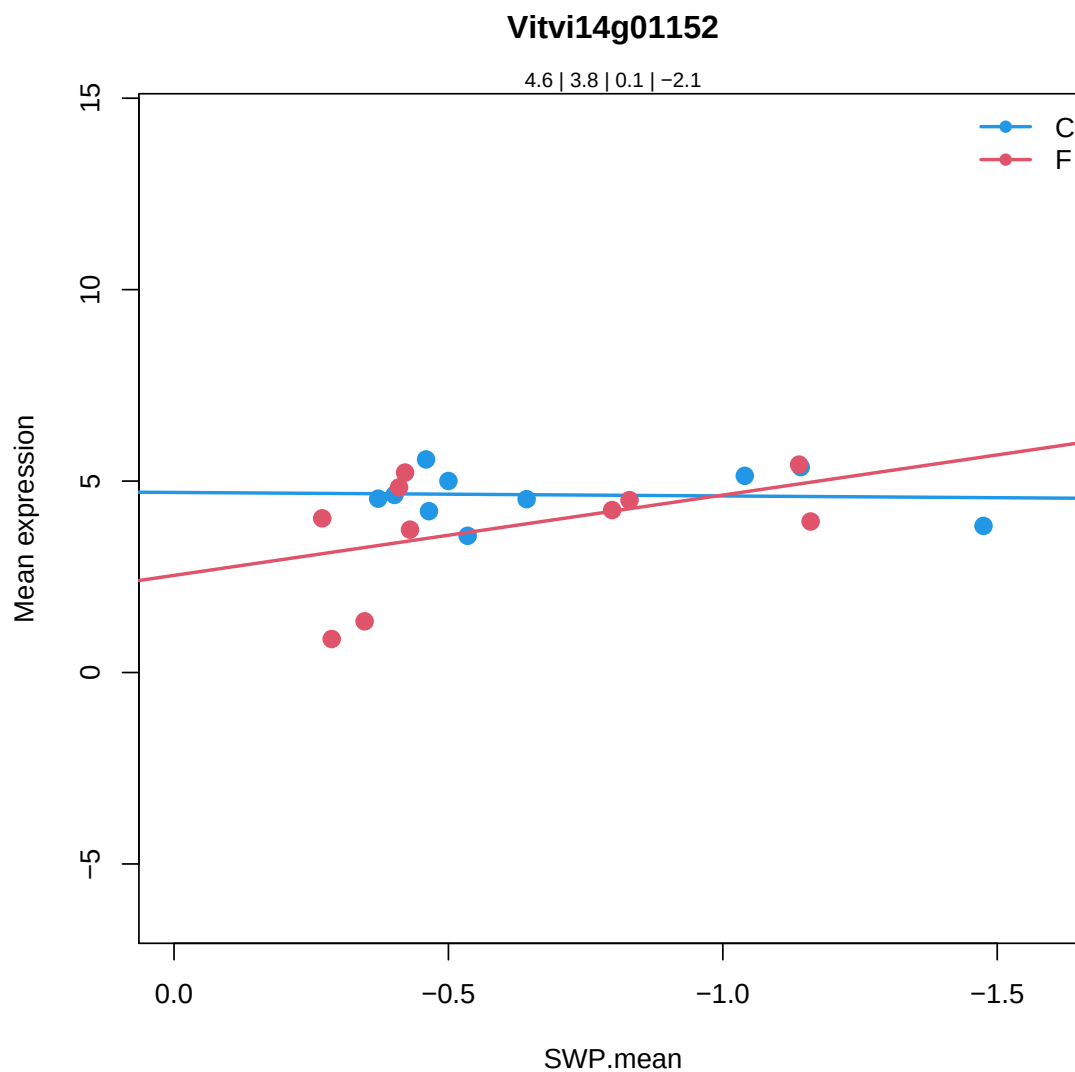
17.3.1.2.6

hormone metabolism.brassinosteroid.synthesis-degradation.sterols.DWF7
sterol 1 |

Chr3:547048-548615 FORWARD LENGTH=281 |
201606

Coefficients for Vitvi14g01152.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.638805	1.22124e-12	***	1.742408e-12	***
SlopeC	0.09131105	0.9184623		0.9851716	
MeanF-MeanC	-0.8241429	0.07977182	.	0.3193704	
SlopeF-SlopeC	-2.189018	0.1097702		0.9999488	



7.6.60 Vitvi05g00817

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

Vitvi05g00817

1.01.1940

PS.lightreaction.cyclic electron flow-chlororespiration

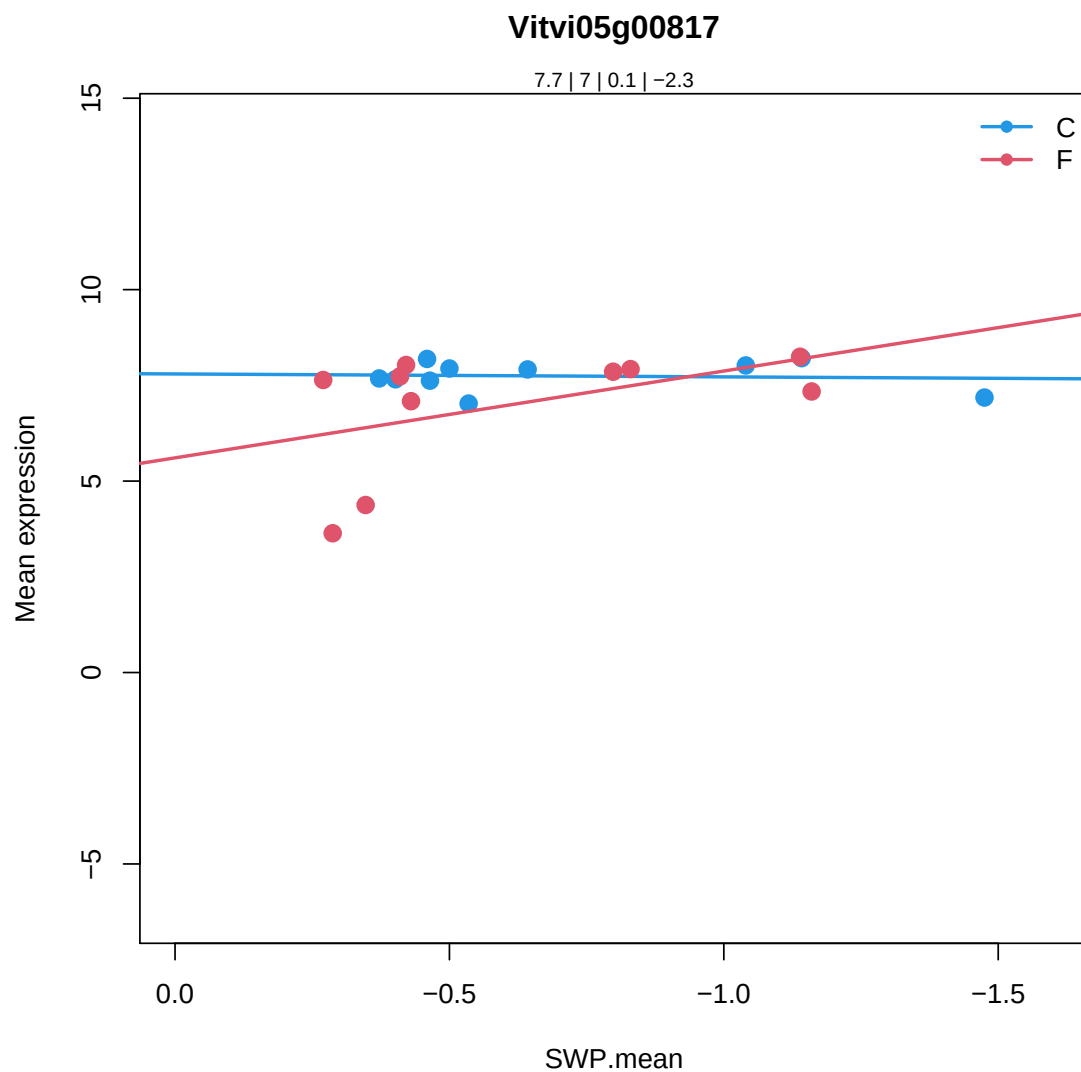
proton gradient regulation 5 |

Chr2:2081204-2081687 REVERSE LENGTH=133 |

201606

Coefficients for Vitvi05g00817.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.744301	2.589511e-17	***	6.274933e-17	***
SlopeC	0.07654634	0.9303178		0.987284	
MeanF-MeanC	-0.7566705	0.09972295	.	0.3635439	
SlopeF-SlopeC	-2.344279	0.08265792	.	0.9999488	



7.6.61 Vitvi08g01915

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

Vitvi08g01915

19.1

tetrapyrrole synthesis.magnesium chelatase

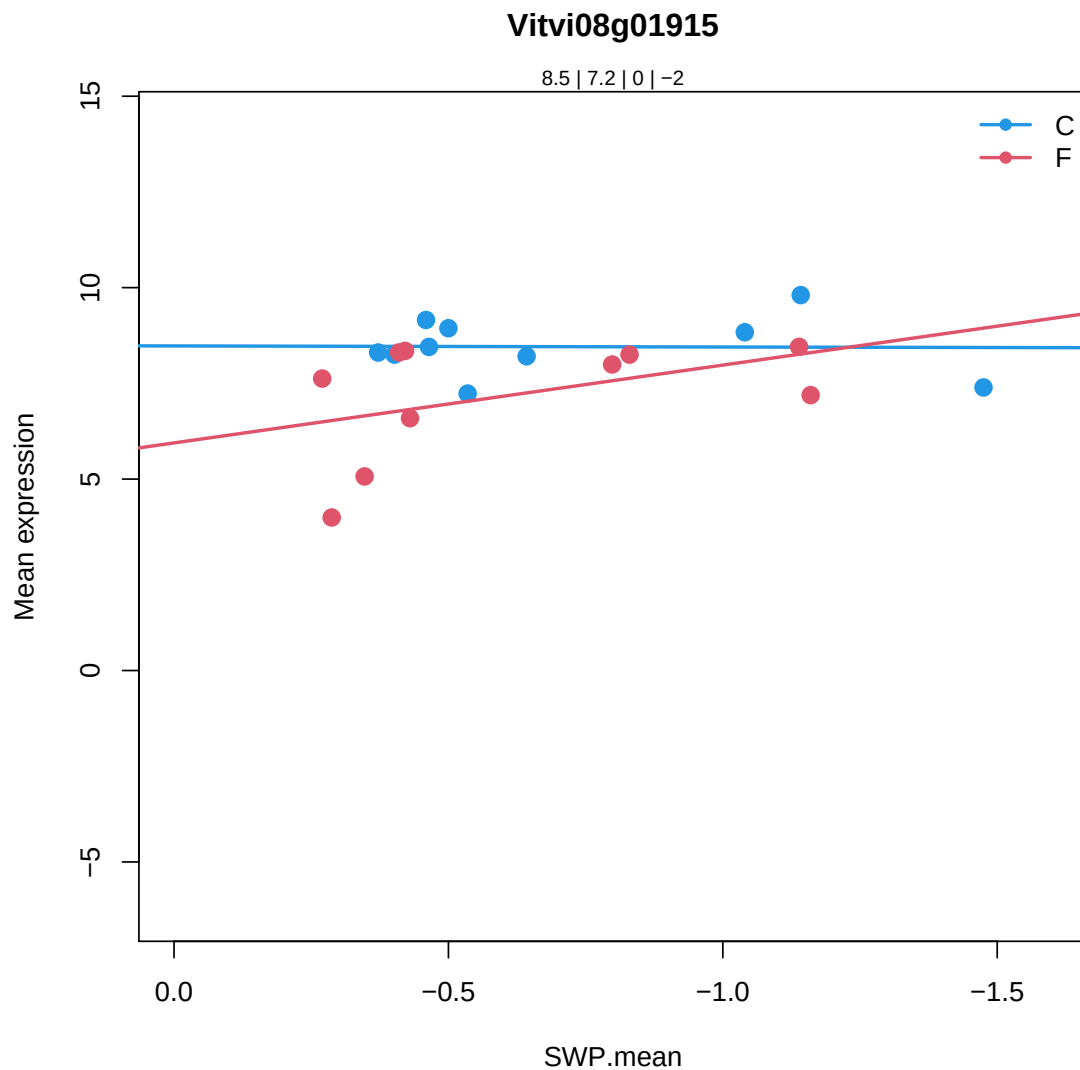
magnesium-chelatase subunit chlH%2C chloroplast%2C putative / Mg-proto

Chr5:4387567-4392082 REVERSE LENGTH=1381 |

201606

Coefficients for Vitvi08g01915.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	8.457666	1.560842e-17	***	3.949917e-17	***
SlopeC	0.02775976	0.9762615		0.9963787	
MeanF-MeanC	-1.274937	0.01267845	*	0.09068273	.
SlopeF-SlopeC	-2.060202	0.1478986		0.9999488	



7.6.62 Vitvi12g02441

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

Vitvi12g02441

27.03.2007

RNA.regulation of transcription.C2C2(Zn) Constans-like zinc finger fam

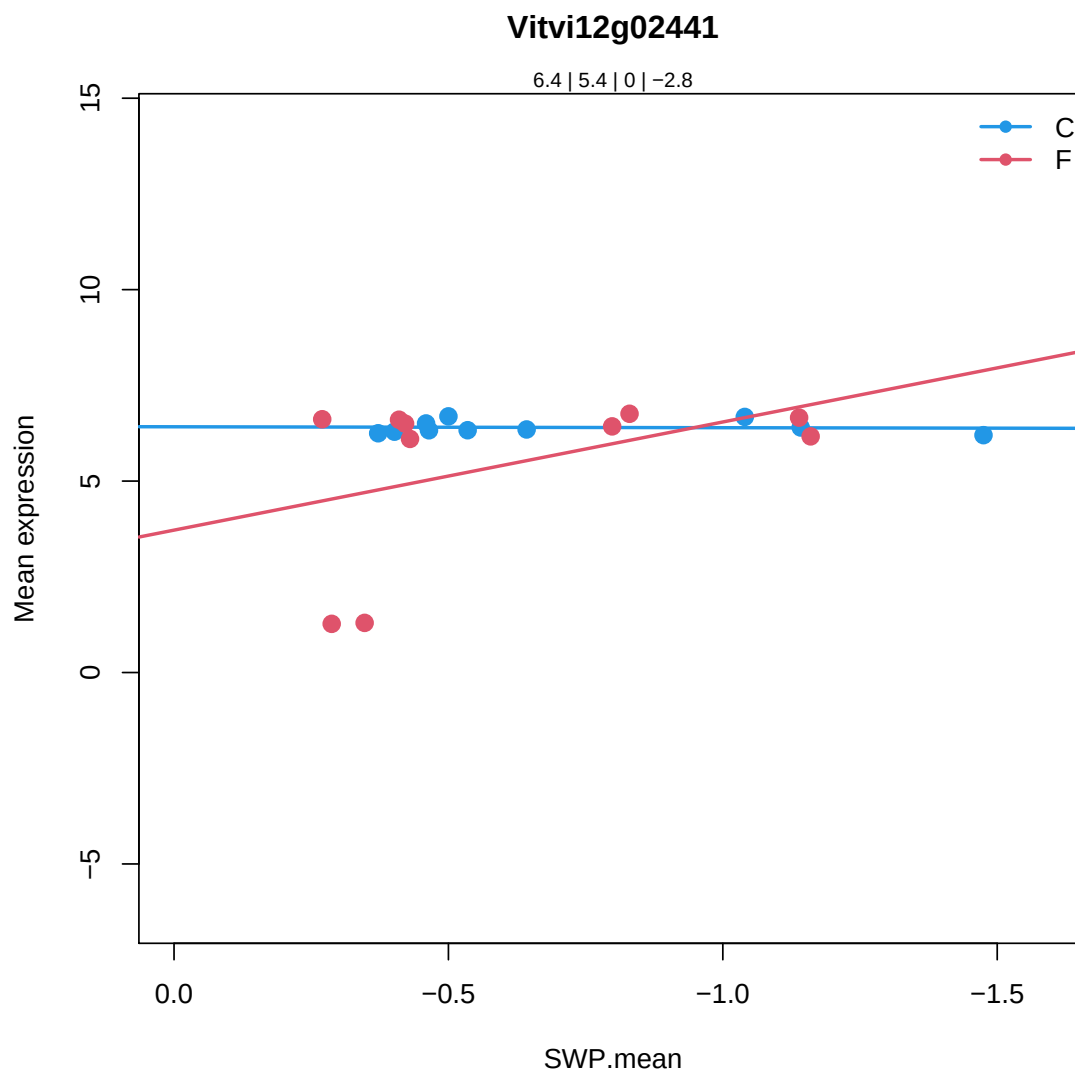
B-box type zinc finger family protein |

Chr4:13675853-13676616 FORWARD LENGTH=223 |

201606

Coefficients for Vitvi12g02441.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.401049	4.065163e-13	***	5.983122e-13	***
SlopeC	0.02401503	0.9835357		0.9979351	
MeanF-MeanC	-0.9613183	0.114726		0.396071	
SlopeF-SlopeC	-2.848841	0.1106466		0.9999488	



7.6.63 Vitvi14g02682

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

Vitvi14g02682

31.1

cell.organisation

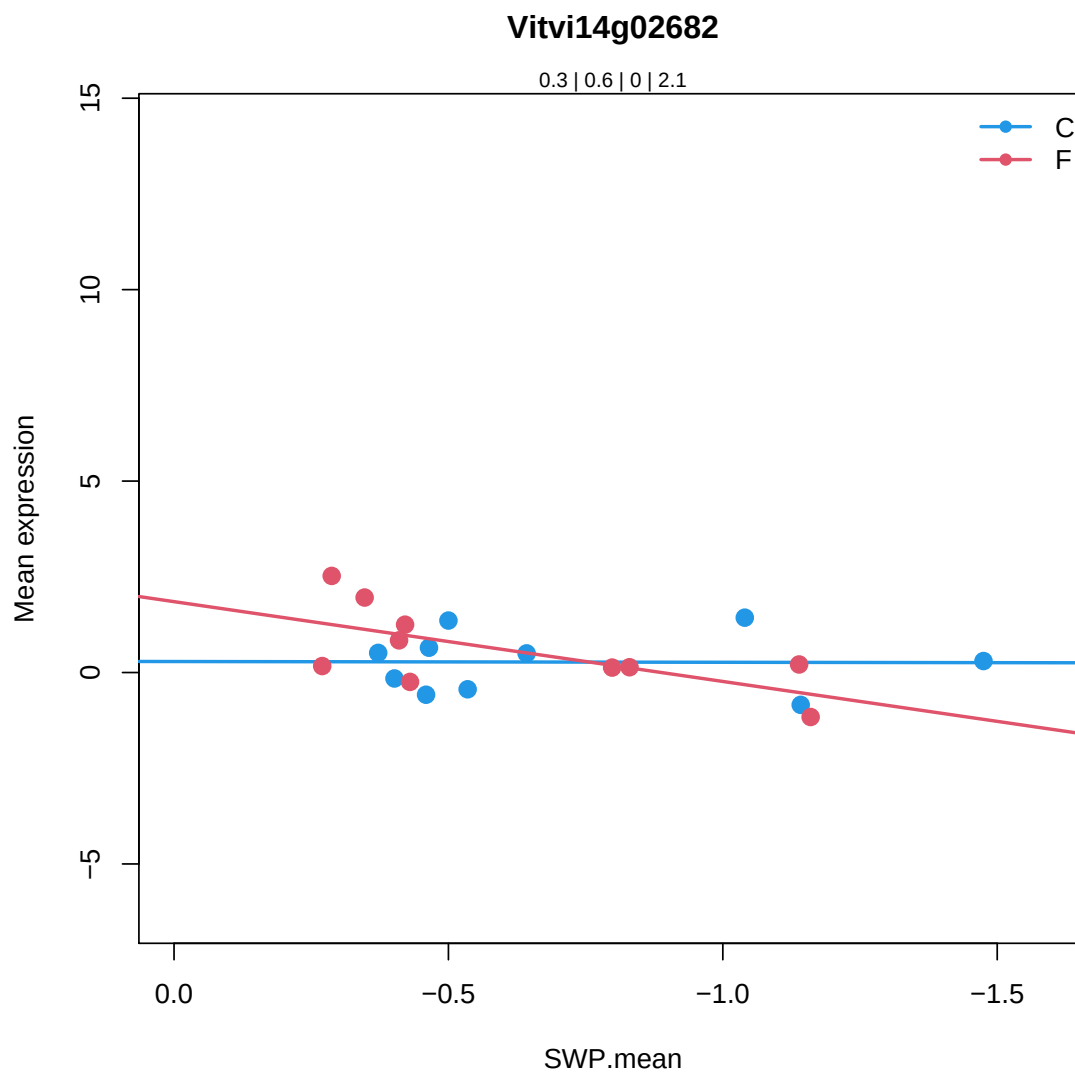
Ankyrin repeat family protein |

Chr4:1554420-1556571 FORWARD LENGTH=629 |

201606

Coefficients for Vitvi14g02682.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.2730829	0.2749453		0.280428	
SlopeC	0.01968125	0.9771146		0.9966352	
MeanF-MeanC	0.3078497	0.3817249		0.7331307	
SlopeF-SlopeC	2.064588	0.05326133	.	0.9999488	



7.6.64 Vitvi14g03074

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

Vitvi14g03074

35.2

not assigned.unknown

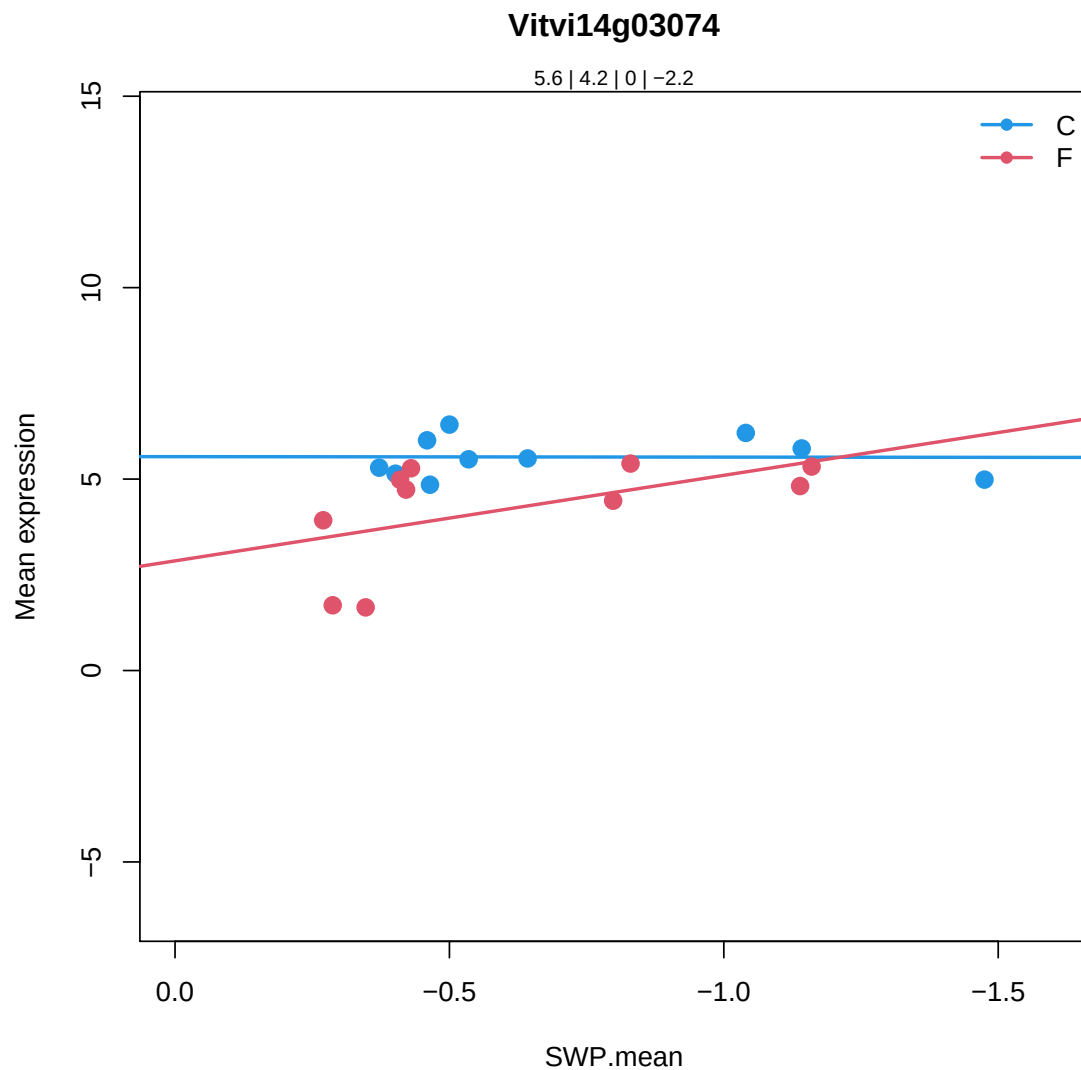
Leucine-rich repeat receptor-like protein kinase family protein |

Chr4:5637467-5640496 REVERSE LENGTH=1009 |

201606

Coefficients for Vitvi14g03074.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.577211	2.156211e-15	***	3.89257e-15	***
SlopeC	0.01214811	0.9875953		0.9983274	
MeanF-MeanC	-1.352187	0.002376485	**	0.02527731	*
SlopeF-SlopeC	-2.246425	0.06382701	.	0.9999488	



7.6.65 Vitvi16g01210

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

Vitvi16g01210

34.16

transport.ABC transporters and multidrug resistance systems

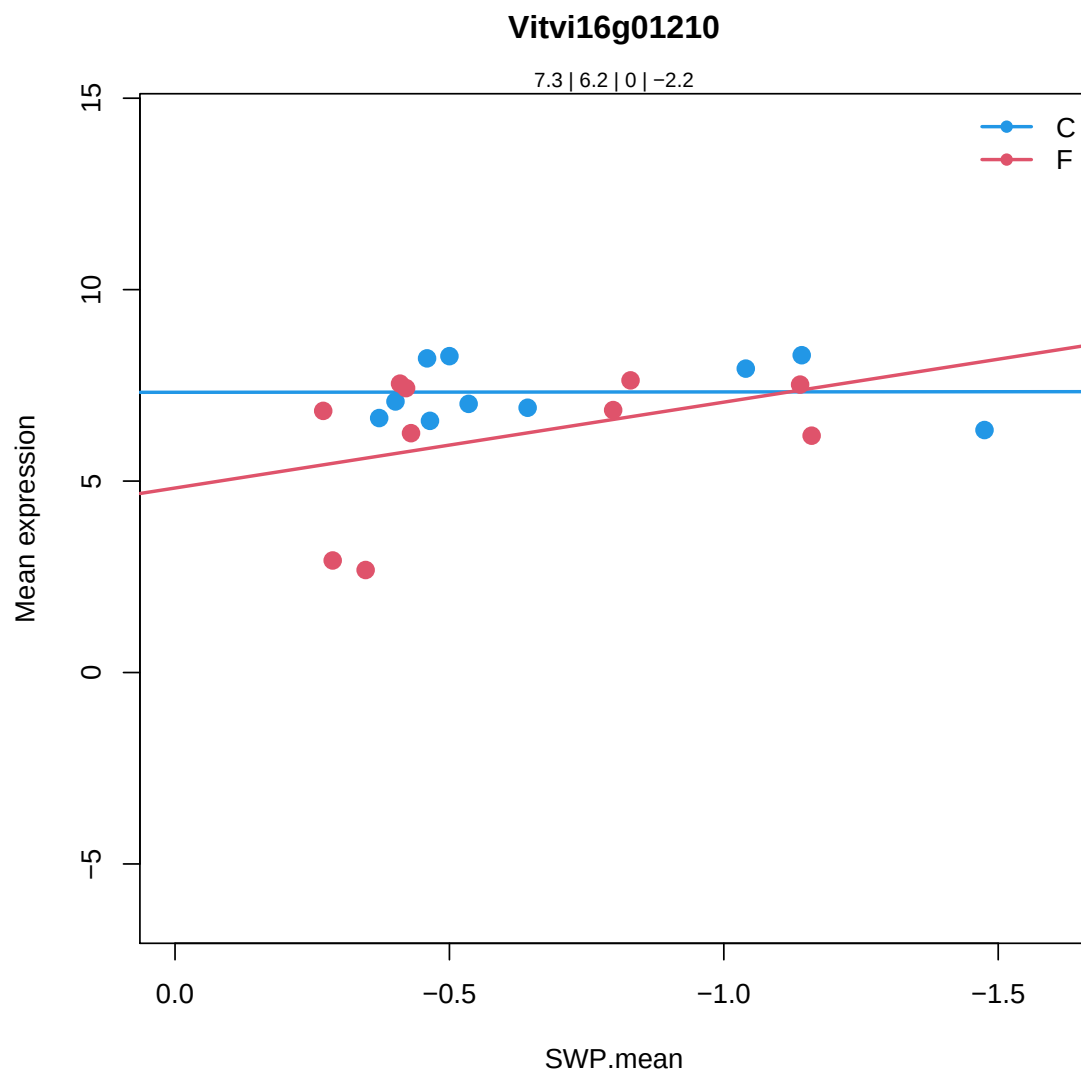
multidrug resistance-associated protein 14 |

Chr3:21863519-21868701 REVERSE LENGTH=1453 |

201606

Coefficients for Vitvi16g01210.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.325649	7.702025e-15	***	1.302644e-14	***
SlopeC	-0.009695296	0.9929198		0.9989481	
MeanF-MeanC	-1.140561	0.04992636	*	0.2387006	
SlopeF-SlopeC	-2.233358	0.1789447		0.9999488	



7.6.66 Vitvi15g00870

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

Vitvi15g00870

35.2

not assigned.unknown

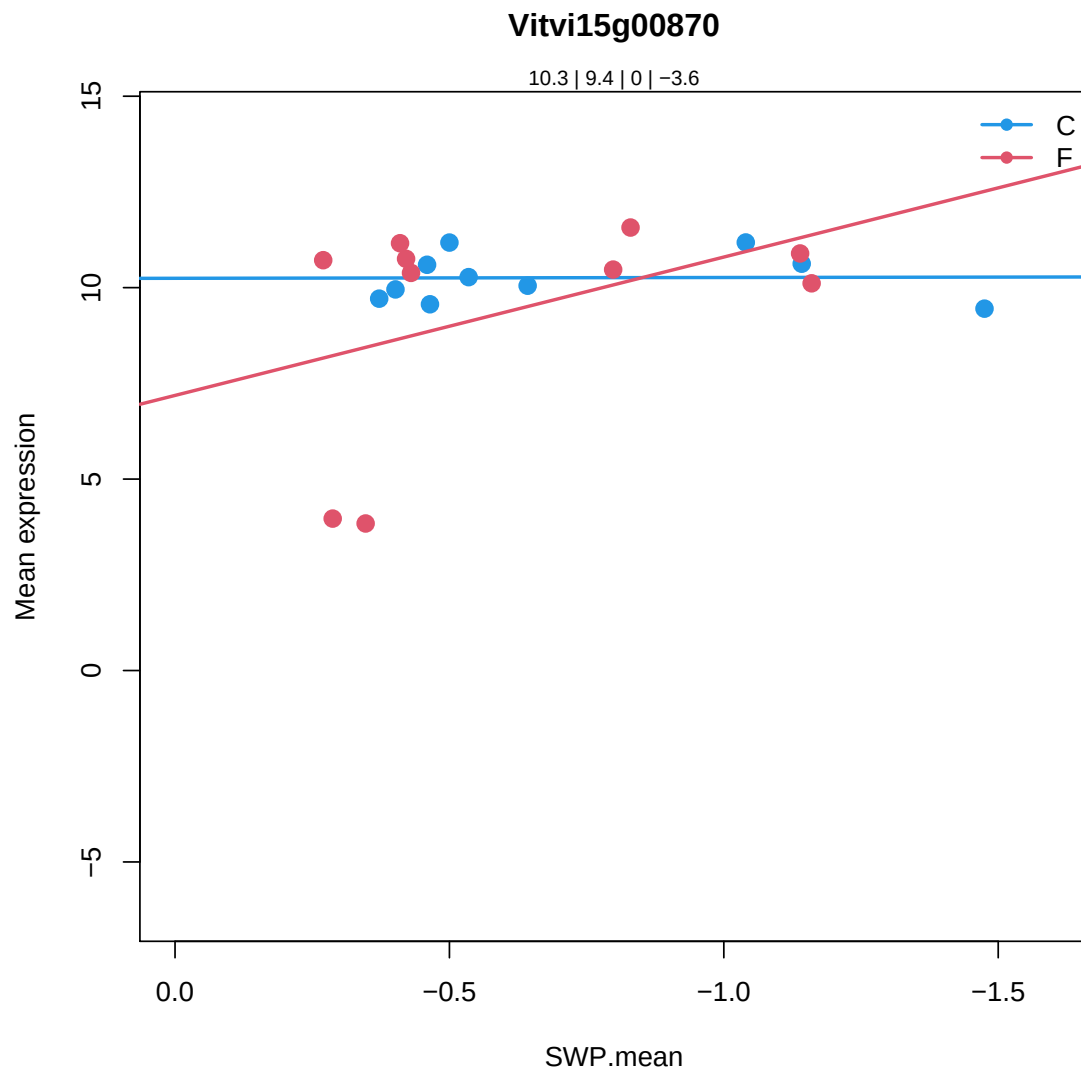
Homeodomain-like superfamily protein |

Chr1:33992-37061 REVERSE LENGTH=645 |

201606

Coefficients for Vitvi15g00870.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	10.25864	1.478874e-14	***	2.431869e-14	***
SlopeC	-0.02089706	0.9894484		0.9983274	
MeanF-MeanC	-0.8716246	0.2844279		0.6495729	
SlopeF-SlopeC	-3.592952	0.1368253		0.9999488	



7.6.67 Vitvi01g00064

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

Vitvi01g00064

2.2.2.2

major CHO metabolism.degradation.starch.starch phosphorylase

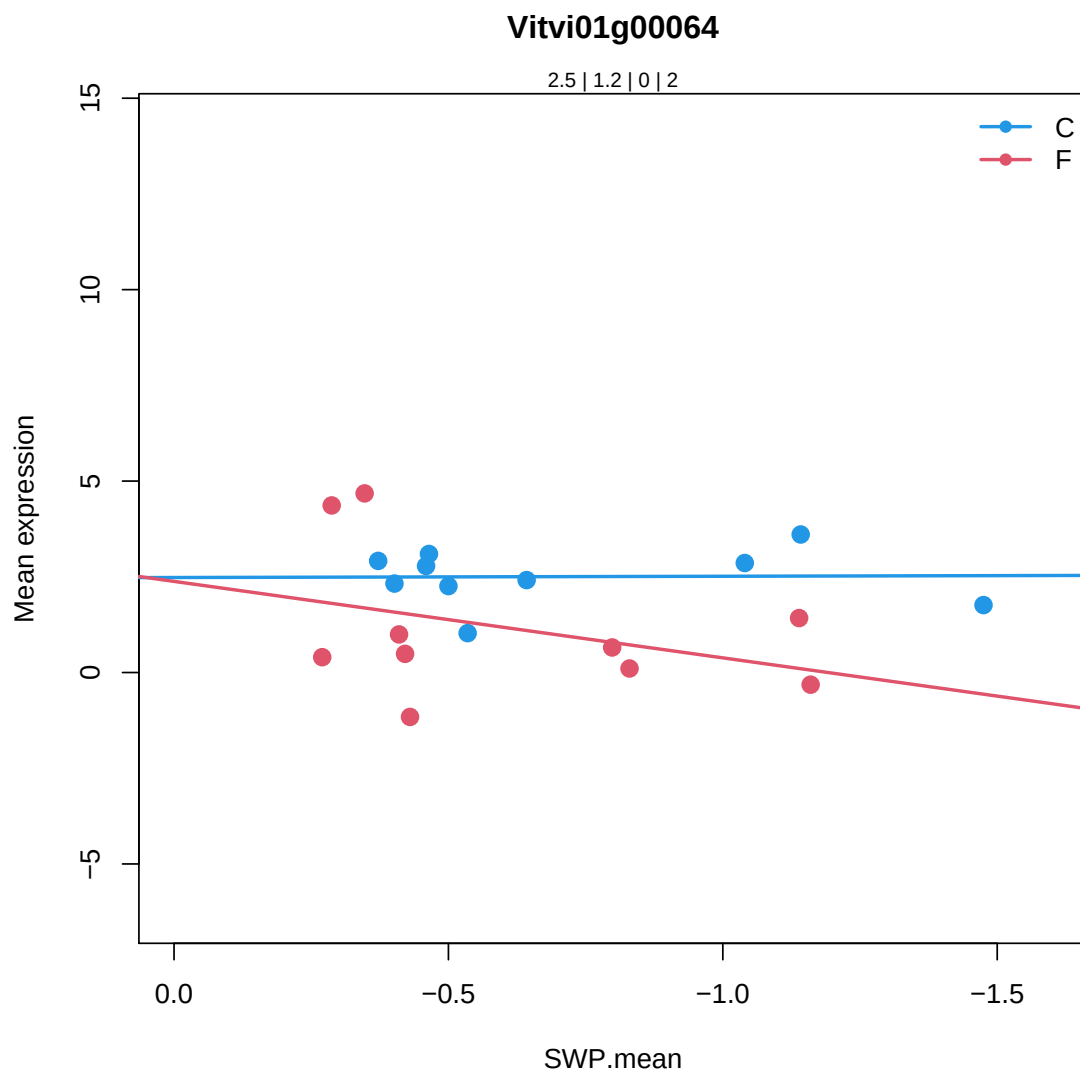
Glycosyl transferase%2C family 35 |

Chr3:11252871-11257587 FORWARD LENGTH=962 |

201606

Coefficients for Vitvi01g00064.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.50421	3.137274e-06	***	3.580556e-06	***
SlopeC	-0.03291293	0.9767566		0.9965809	
MeanF-MeanC	-1.341287	0.02762602	*	0.1599574	
SlopeF-SlopeC	2.030061	0.2351312		0.9999488	



7.6.68 Vitvi06g01350

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

Vitvi06g01350

27.03.2011

RNA.regulation of transcription.C2H2 zinc finger family

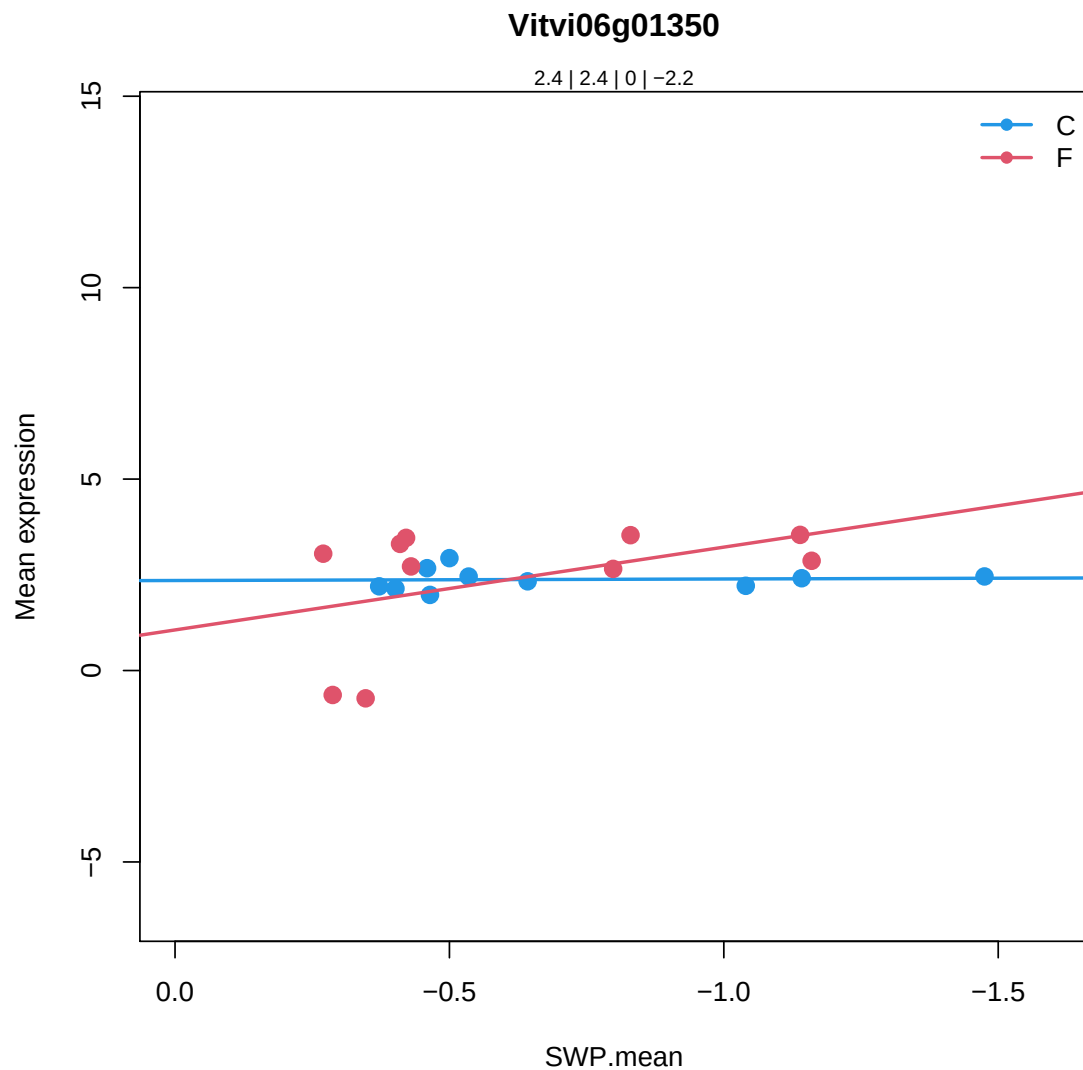
C2H2-type zinc finger family protein |

Chr2:12024321-12025181 FORWARD LENGTH=286 |

201606

Coefficients for Vitvi06g01350.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.378478	1.871945e-07	***	2.204279e-07	***
SlopeC	-0.03982735	0.9642676		0.9943773	
MeanF-MeanC	-0.001000824	0.9982329		0.9998558	
SlopeF-SlopeC	-2.122684	0.1191913		0.9999488	



7.6.69 Vitvi09g02014

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

Vitvi09g02014

35.2

not assigned.unknown

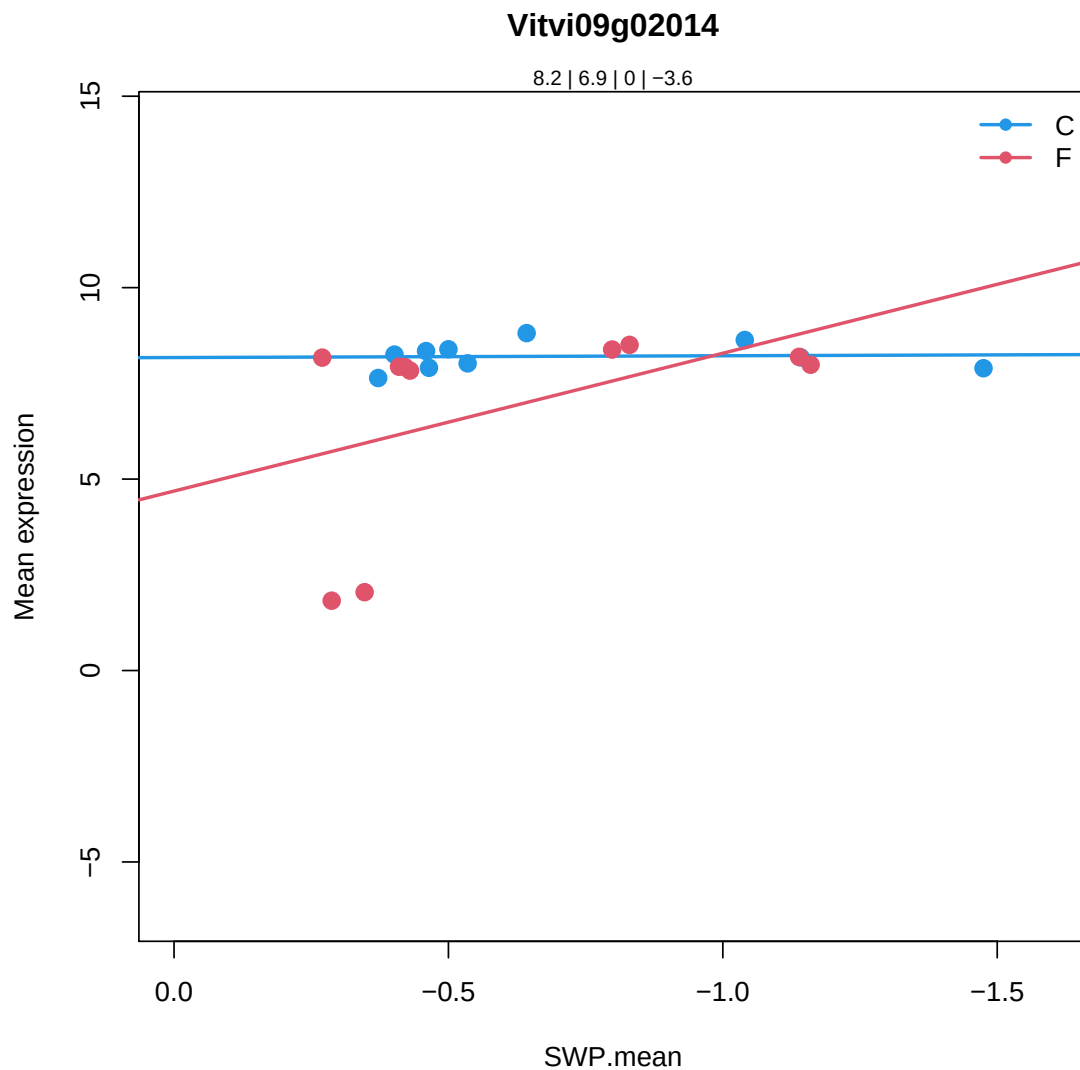
hypothetical protein |

Chr1:5726617-5727312 REVERSE LENGTH=202 |

201606

Coefficients for Vitvi09g02014.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	8.206843	6.668827e-14	***	1.037524e-13	***
SlopeC	-0.04628244	0.9729004		0.9962426	
MeanF-MeanC	-1.326783	0.06586435	.	0.2847474	
SlopeF-SlopeC	-3.553714	0.09042245	.	0.9999488	



7.6.70 Vitvi09g01609

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

Vitvi09g01609

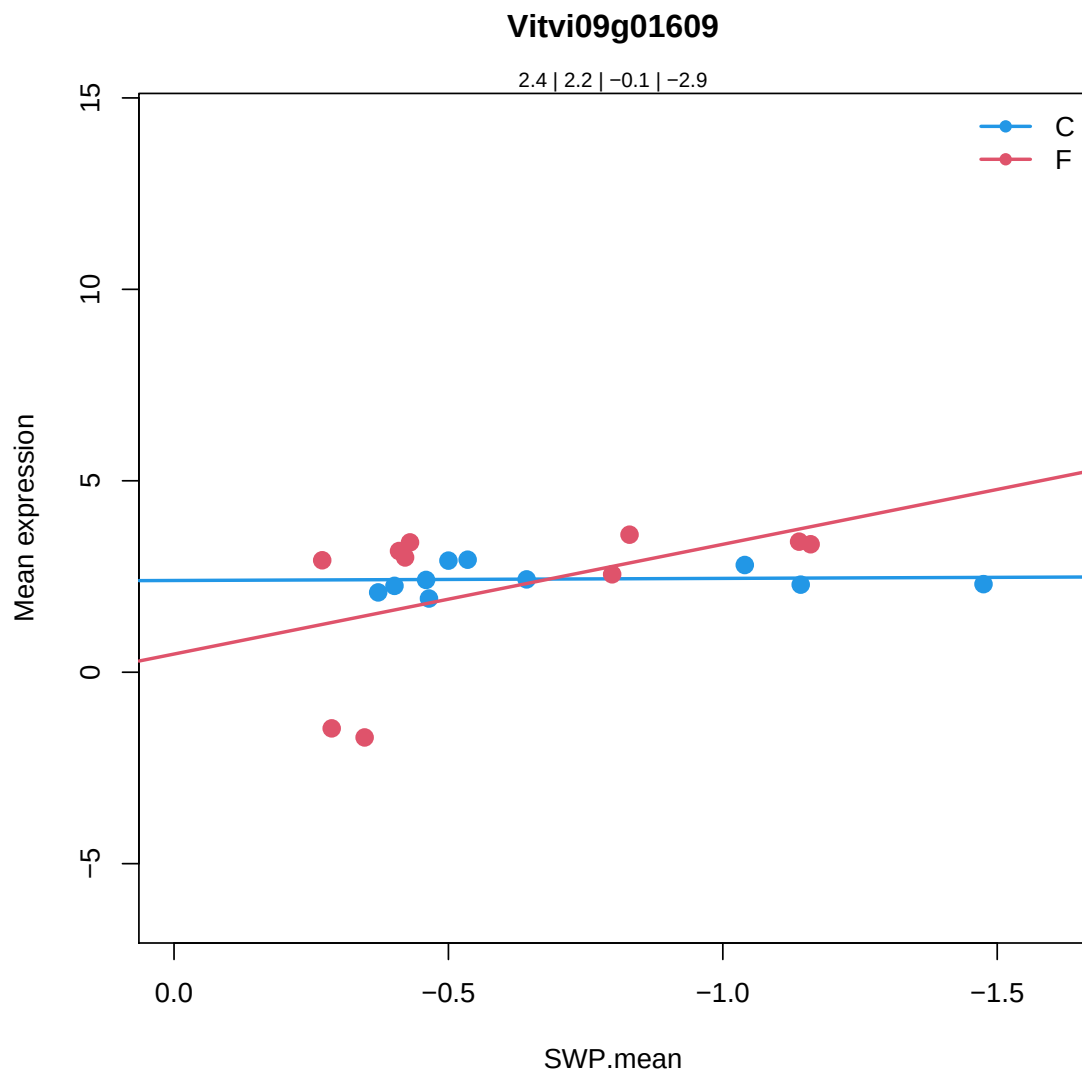
35.2

not assigned.unknown

Unknown Protein

Coefficients for Vitvi09g01609.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.434131	2.014194e-06	***	2.309338e-06	***
SlopeC	-0.05467525	0.9590377		0.9933601	
MeanF-MeanC	-0.2132905	0.6939848		0.903615	
SlopeF-SlopeC	-2.811312	0.08672848	.	0.9999488	



7.6.71 Vitvi03g00712

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

Vitvi03g00712

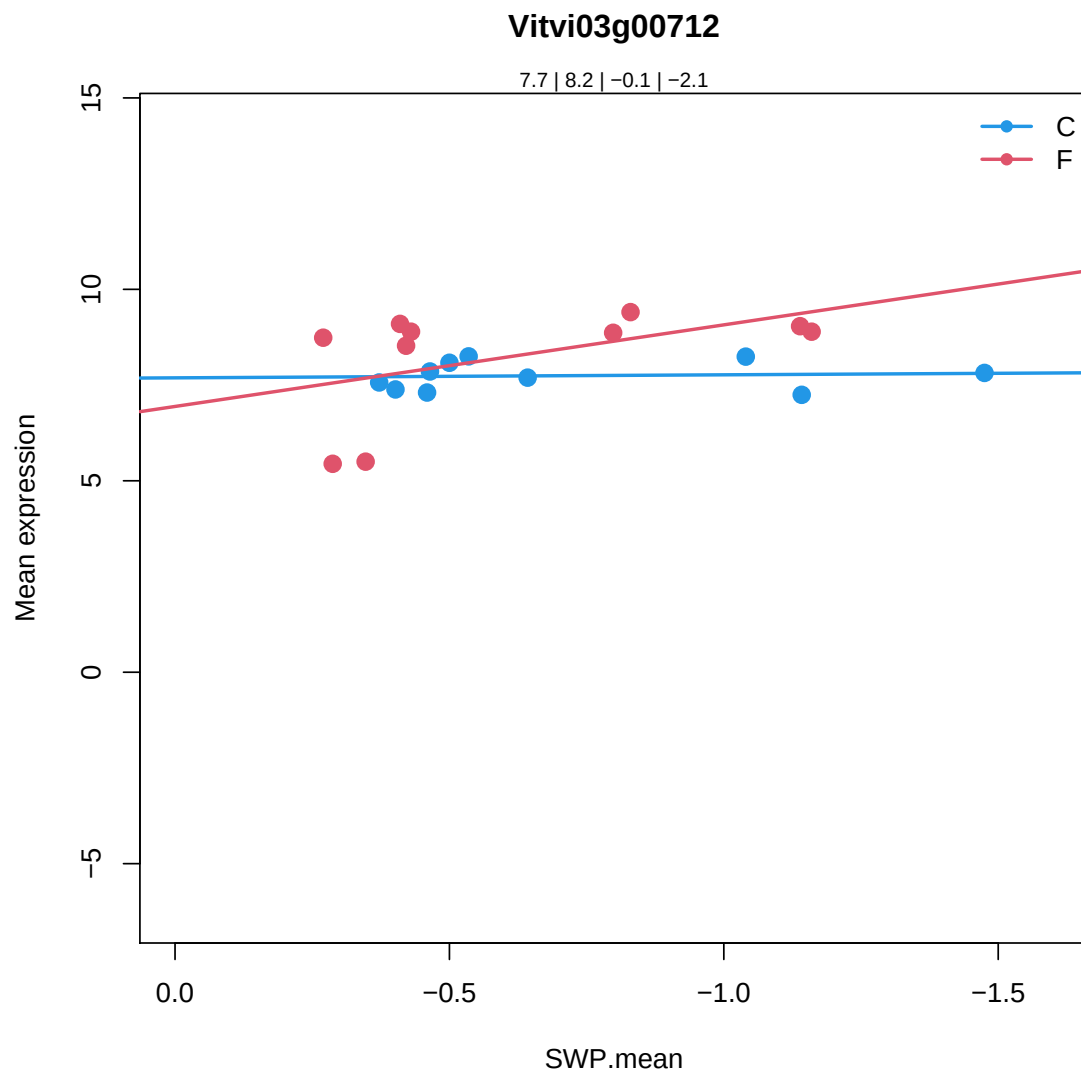
35.2

not assigned.unknown

NA

Coefficients for Vitvi03g00712.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.744266	4.044006e-18	***	1.173624e-17	***
SlopeC	-0.07900518	0.9213969		0.985539	
MeanF-MeanC	0.4957387	0.2311173		0.584776	
SlopeF-SlopeC	-2.052156	0.09575741	.	0.9999488	



7.6.72 Vitvi10g00049

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

Vitvi10g00049

35.2

not assigned.unknown

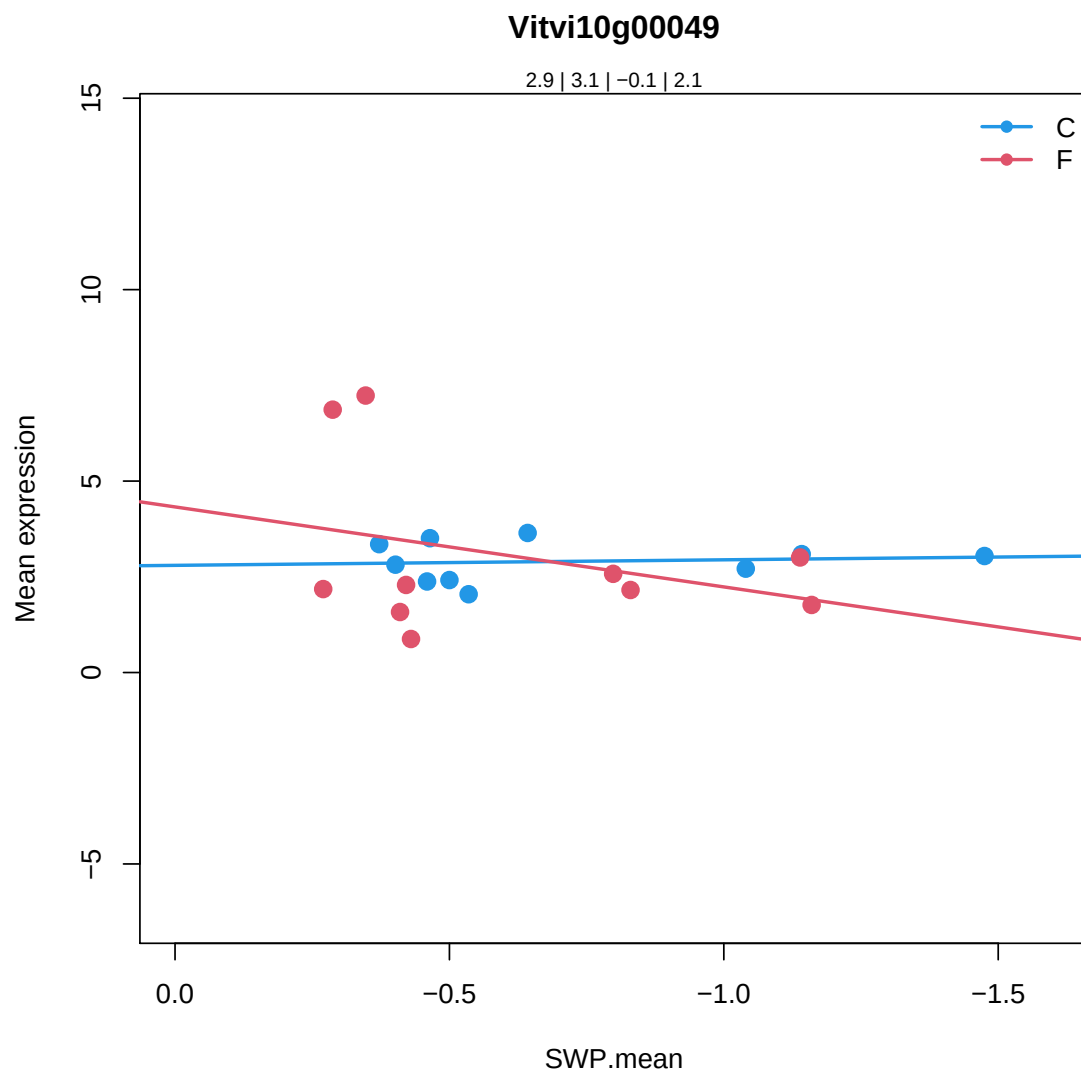
Chaperonin-like RbcX protein |

Chr4:2116700-2118563 REVERSE LENGTH=174 |

201606

Coefficients for Vitvi10g00049.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.900545	1.569081e-06	***	1.803207e-06	***
SlopeC	-0.1446943	0.9076268		0.9837899	
MeanF-MeanC	0.1517371	0.8109098		0.9474118	
SlopeF-SlopeC	2.234213	0.2364319		0.9999488	



7.6.73 Vitvi01g01048

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

Vitvi01g01048

35.2

not assigned.unknown

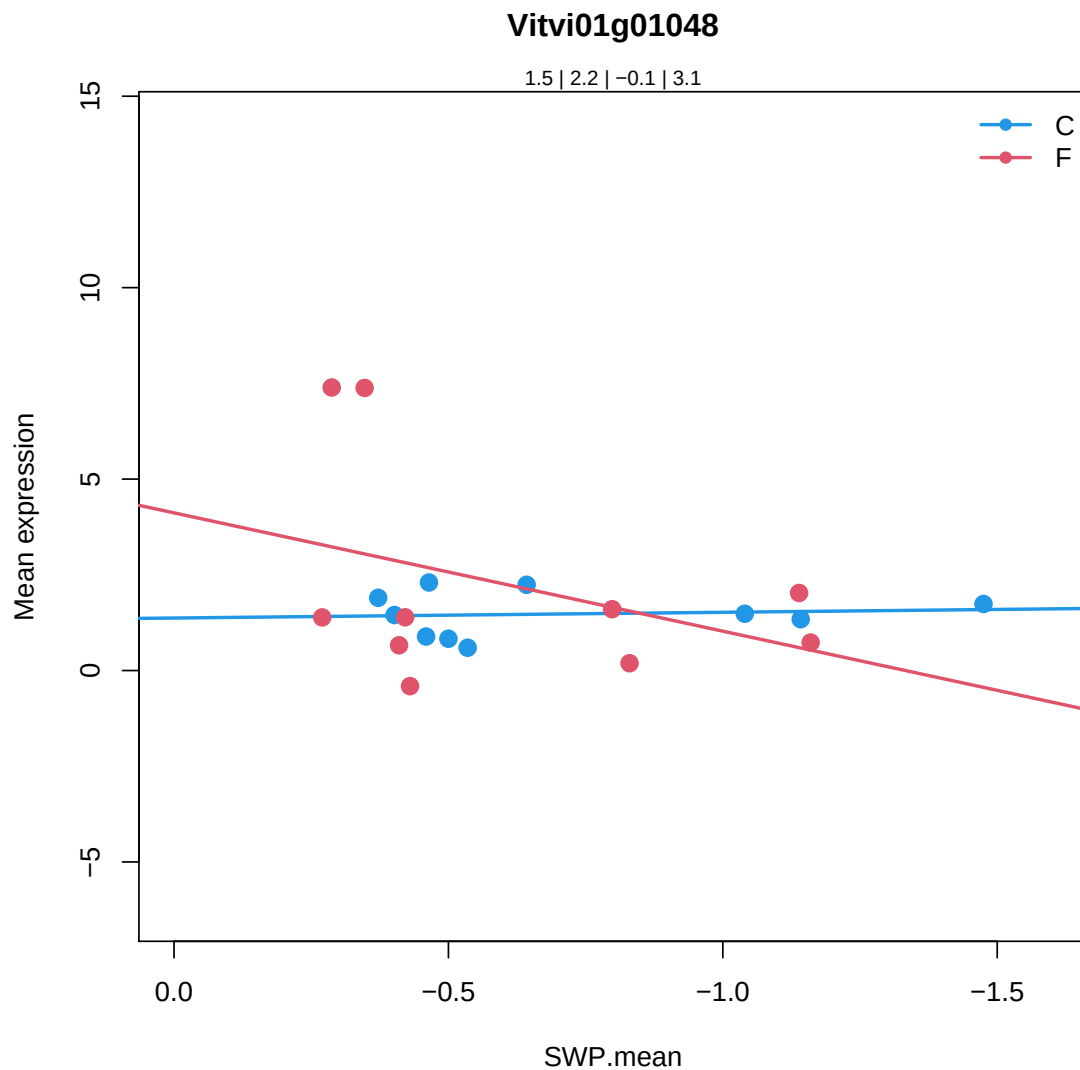
cysteine-rich RECEPTOR-like kinase |

Chr4:12129485-12133157 FORWARD LENGTH=1043 |

201606

Coefficients for Vitvi01g01048.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.475931	0.0138706	*	0.01464402	*
SlopeC	-0.1494626	0.9232035		0.9858811	
MeanF-MeanC	0.7591408	0.3406161		0.7000202	
SlopeF-SlopeC	3.239226	0.1698987		0.9999488	



7.6.74 Vitvi02g00235

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

Vitvi02g00235

35.2

not assigned.unknown

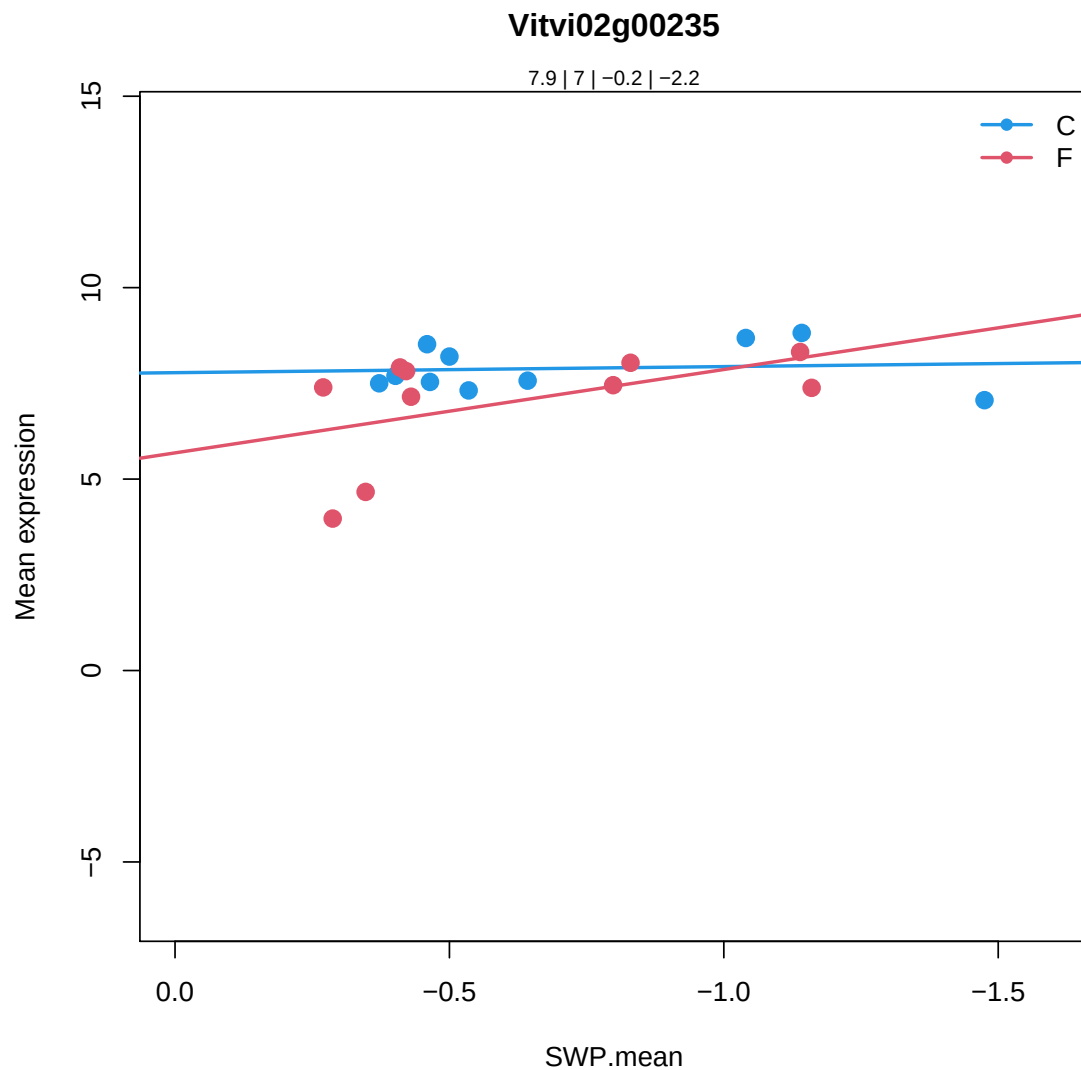
beta-carotene isomerase D27 |

Chr1:24036071-24036768 FORWARD LENGTH=204 |

201606

Coefficients for Vitvi02g00235.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.890663	7.696105e-18	***	2.084293e-17	***
SlopeC	-0.1585789	0.8505488		0.9719233	
MeanF-MeanC	-0.8800076	0.04950307	*	0.237403	
SlopeF-SlopeC	-2.019059	0.1174086		0.9999488	



7.6.75 Vitvi13g02316

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

Vitvi13g02316

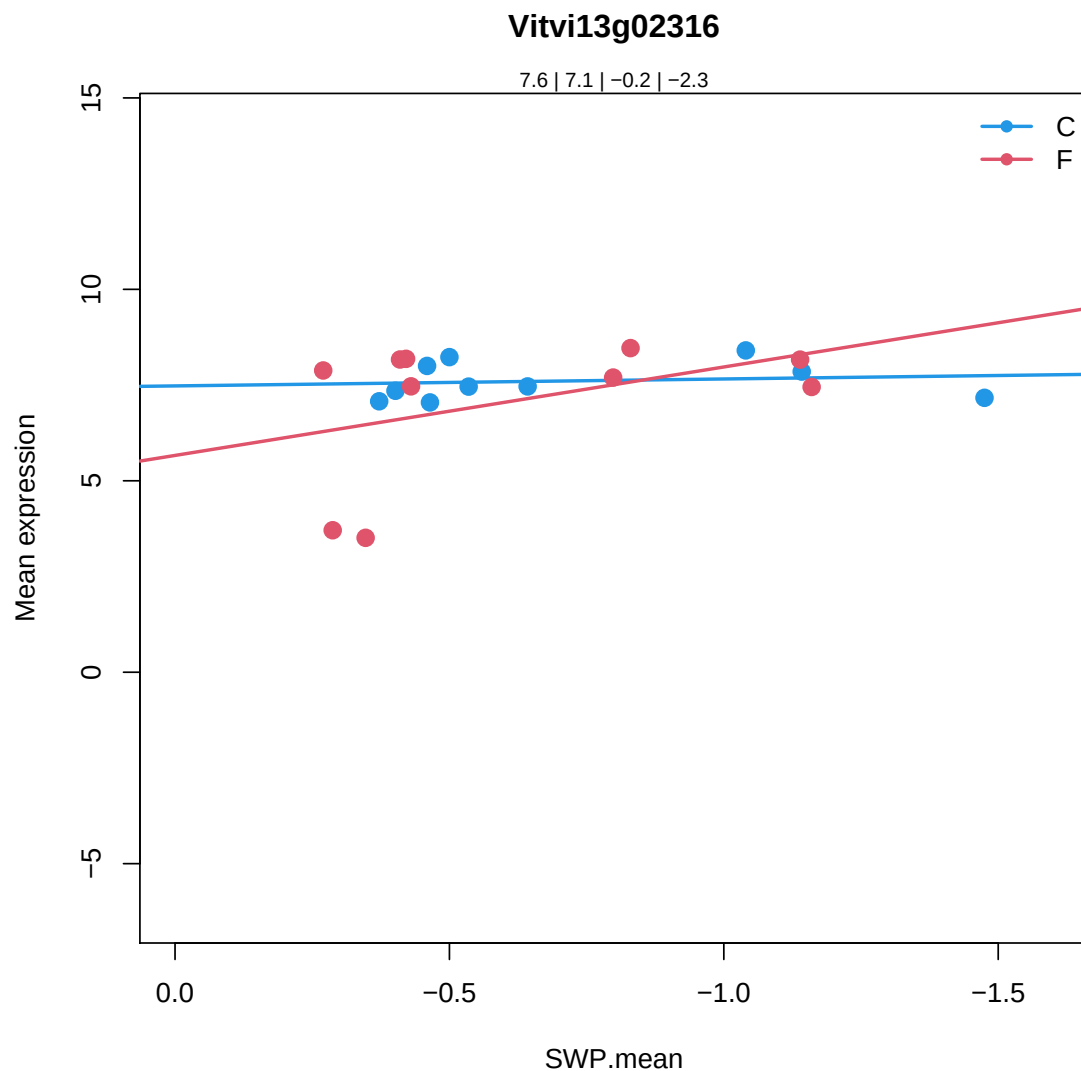
35.2

not assigned.unknown

NA

Coefficients for Vitvi13g02316.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.605129	1.054538e-15	***	1.968557e-15	***
SlopeC	-0.1815475	0.8599814		0.9737594	
MeanF-MeanC	-0.5356114	0.3116603		0.6758182	
SlopeF-SlopeC	-2.128751	0.1739056		0.9999488	



7.6.76 Vitvi02g00160

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

Vitvi02g00160

21.4

redox.glutaredoxins

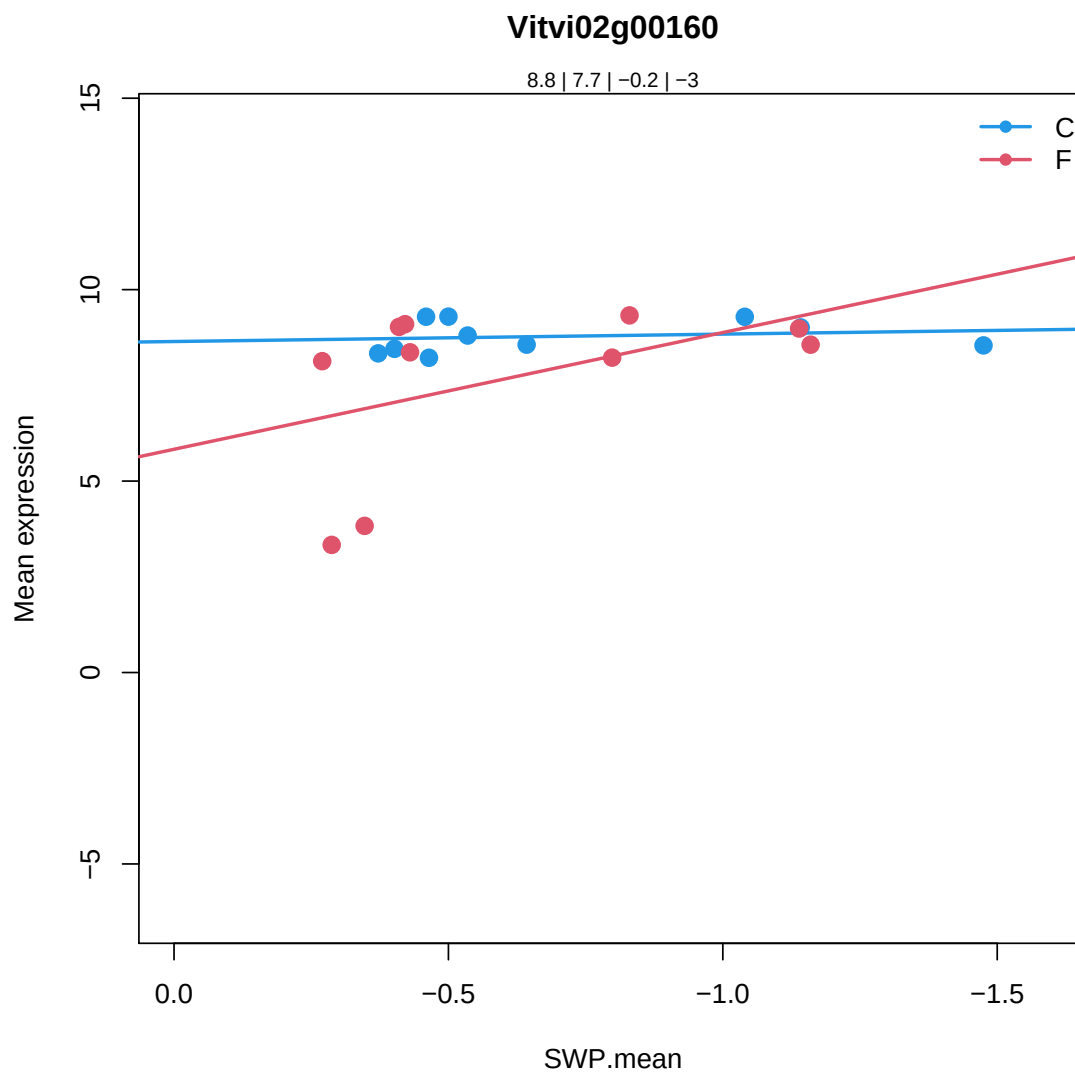
Glutaredoxin family protein |

Chr1:23953270-23954376 FORWARD LENGTH=368 |

201606

Coefficients for Vitvi02g00160.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	8.780784	6.921898e-16	***	1.323759e-15	***
SlopeC	-0.1937055	0.8678407		0.9758833	
MeanF-MeanC	-1.092576	0.07539069	.	0.3088952	
SlopeF-SlopeC	-2.854744	0.1099476		0.9999488	



7.6.77 Vitvi18g00095

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

Vitvi18g00095

21.6

redox.dismutases and catalases

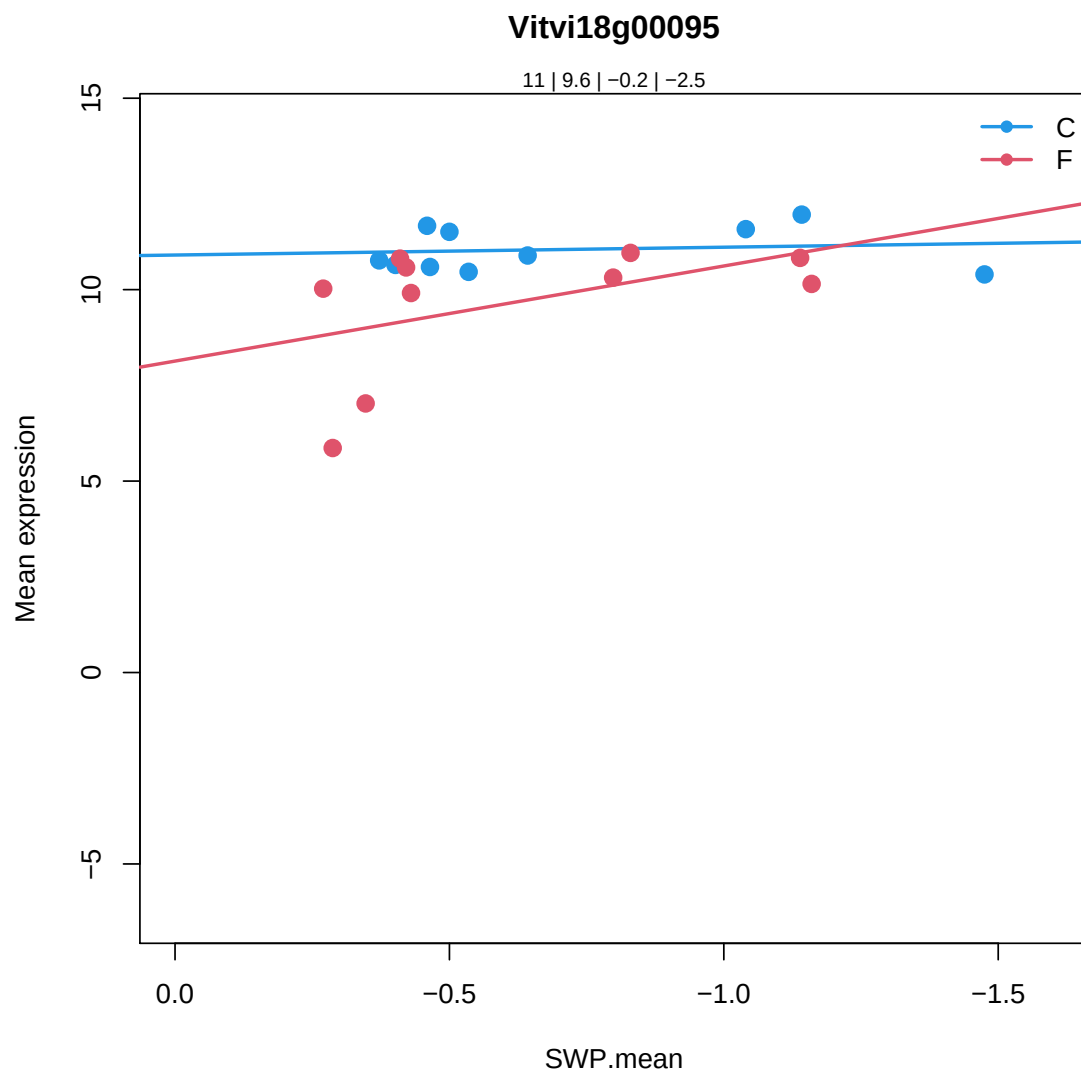
catalase 2 |

Chr4:16700937-16702955 REVERSE LENGTH=492 |

201606

Coefficients for Vitvi18g00095.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	11.04727	1.126924e-19	***	5.270503e-19	***
SlopeC	-0.2041556	0.8321327		0.9669878	
MeanF-MeanC	-1.399968	0.008552013	**	0.06760881	.
SlopeF-SlopeC	-2.279565	0.1220916		0.9999488	



7.6.78 Vitvi03g00995

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

Vitvi03g00995

35.2

not assigned.unknown

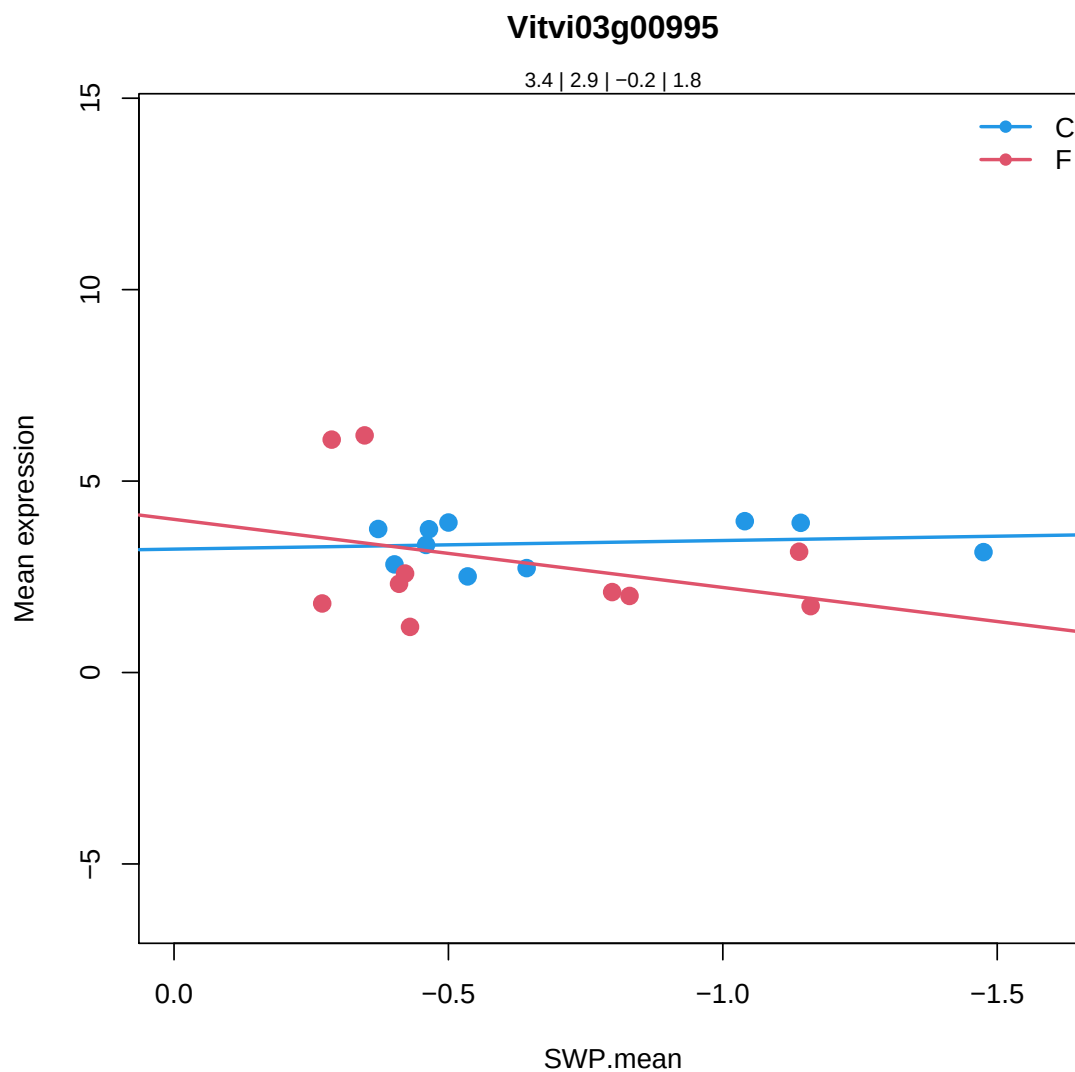
nicotinamidase 1 |

Chr2:9589604-9590846 REVERSE LENGTH=244 |

201606

Coefficients for Vitvi03g00995.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.380909	6.864526e-09	***	8.423566e-09	***
SlopeC	-0.2252086	0.8278634		0.9659517	
MeanF-MeanC	-0.4645233	0.3816796		0.7331307	
SlopeF-SlopeC	2.00419	0.2020341		0.9999488	



7.6.79 Vitvi12g00478

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

Vitvi12g00478

35.1

not assigned.no ontology

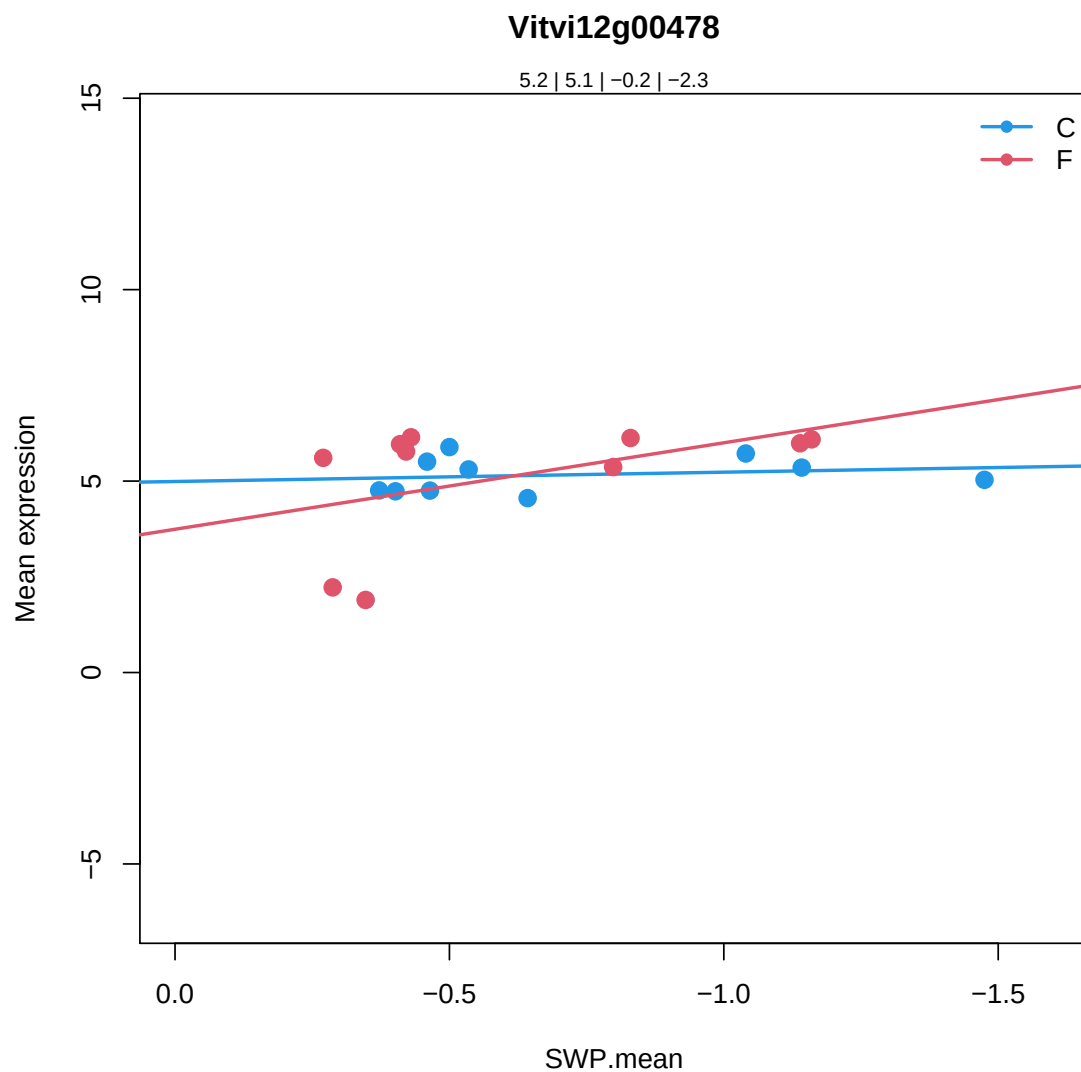
Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein |

Chr4:1501907-1503503 FORWARD LENGTH=361 |

201606

Coefficients for Vitvi12g00478.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.160011	1.616356e-13	***	2.443855e-13	***
SlopeC	-0.2434733	0.7858833		0.9533712	
MeanF-MeanC	-0.04277148	0.9251437		0.9803281	
SlopeF-SlopeC	-2.014384	0.140849		0.9999488	



7.6.80 Vitvi08g01123

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

Vitvi08g01123

35.1.5

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

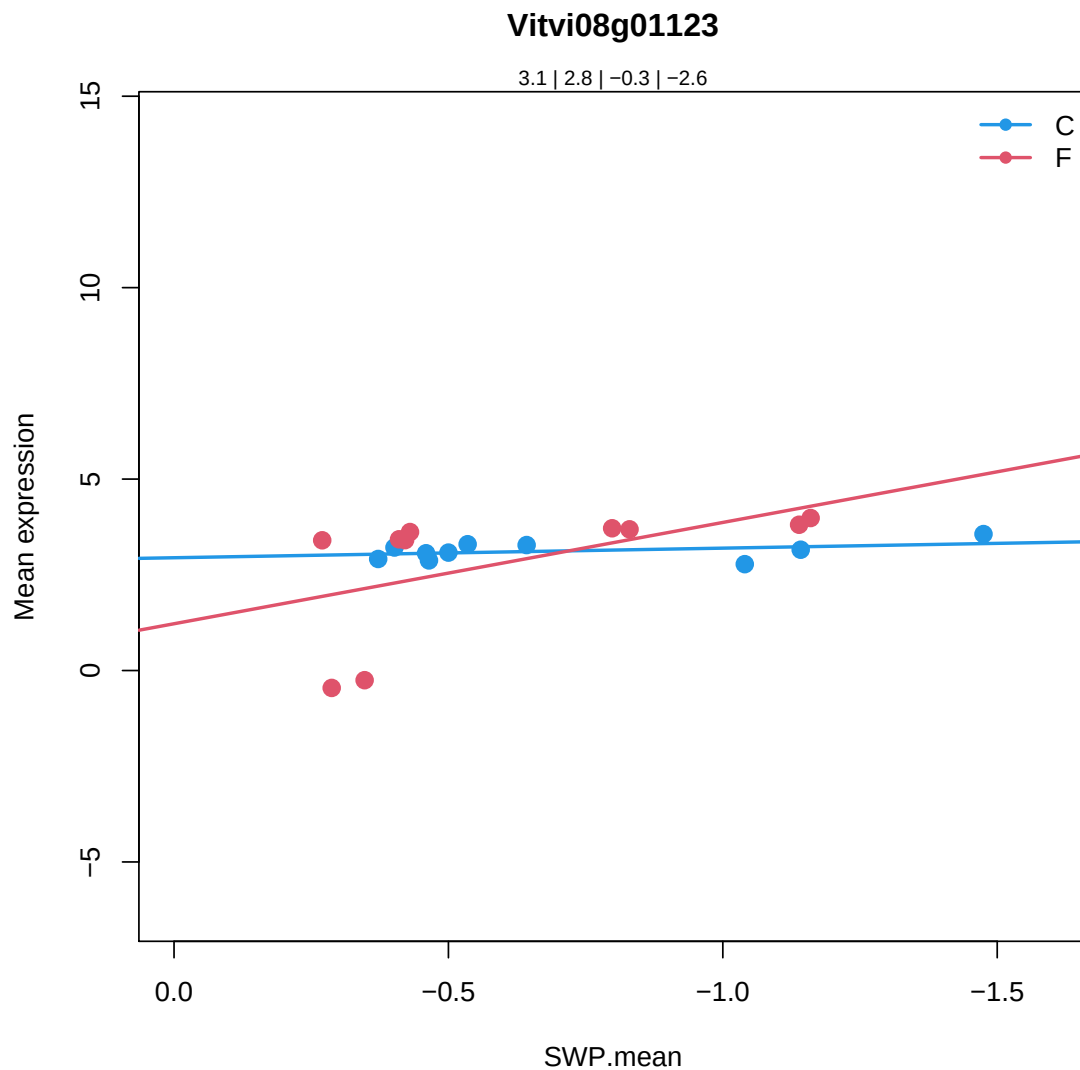
RING/U-box superfamily protein |

Chr5:620101-620952 FORWARD LENGTH=283 |

201606

Coefficients for Vitvi08g01123.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.121527	1.06218e-09	***	1.338438e-09	***
SlopeC	-0.2506405	0.7708566		0.9509831	
MeanF-MeanC	-0.2879987	0.512032		0.8136412	
SlopeF-SlopeC	-2.395258	0.07180596	.	0.9999488	



7.6.81 Vitvi13g00233

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

Vitvi13g00233

35.2

not assigned.unknown

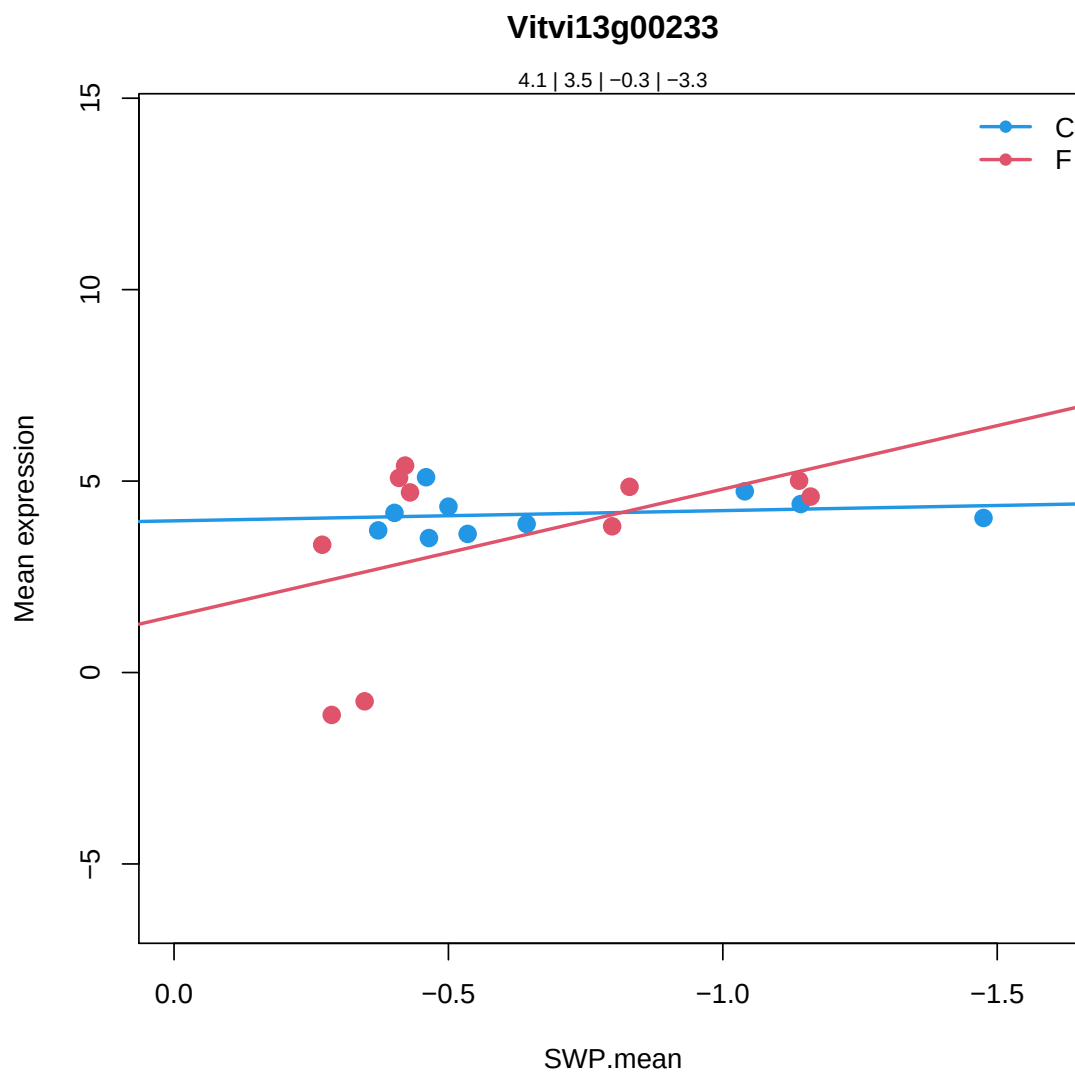
exocyst subunit exo70 family protein H2 |

Chr2:16447096-16449009 REVERSE LENGTH=637 |

201606

Coefficients for Vitvi13g00233.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.149428	7.549148e-09	***	9.24804e-09	***
SlopeC	-0.2676308	0.8341394		0.967871	
MeanF-MeanC	-0.6551813	0.3187257		0.6800137	
SlopeF-SlopeC	-3.048163	0.1194204		0.9999488	



7.6.82 Vitvi08g01867

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

Vitvi08g01867

29.5

protein.degradation

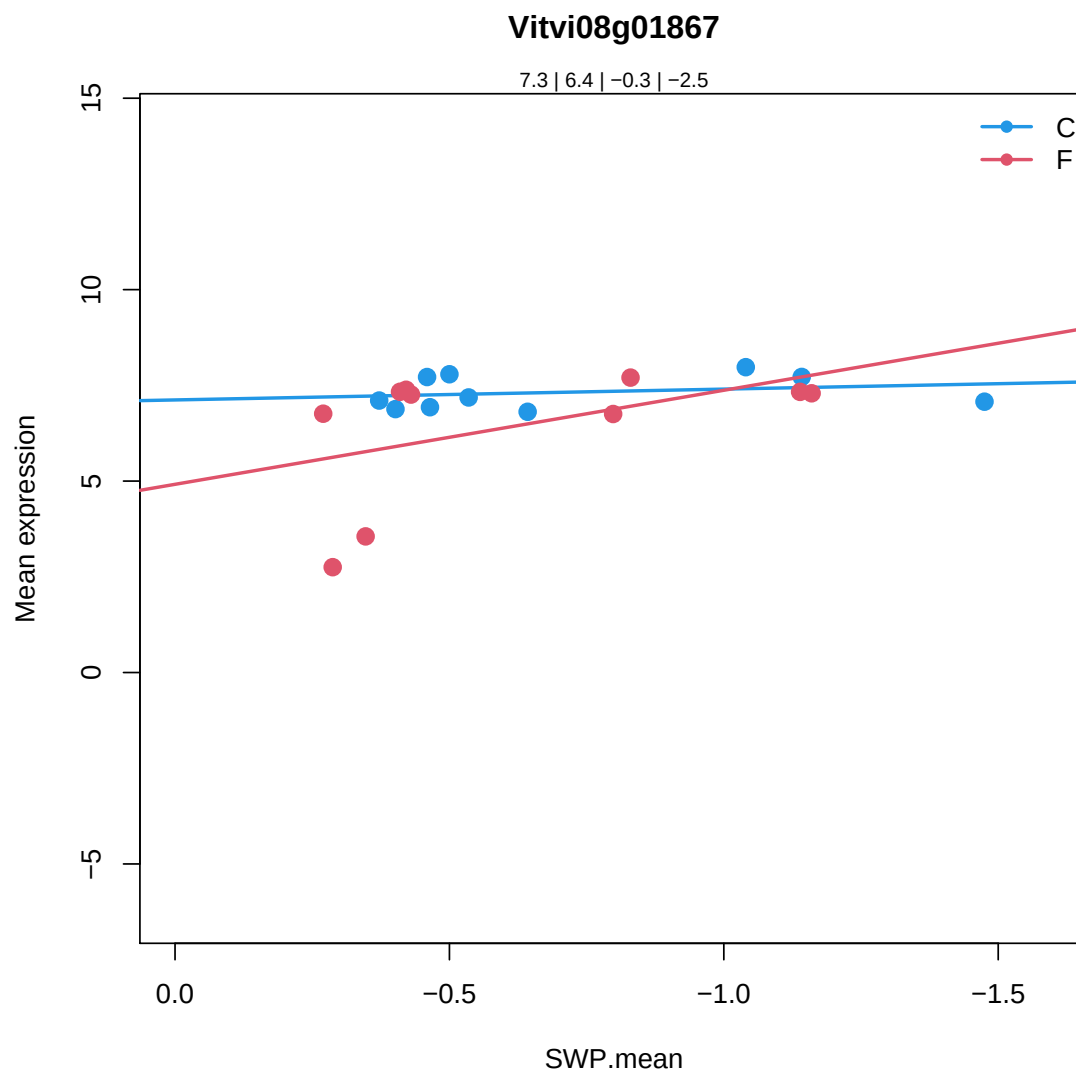
Peptidase S41 family protein |

Chr3:21381664-21383629 FORWARD LENGTH=370 |

201606

Coefficients for Vitvi08g01867.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.318216	3.920092e-16	***	7.753703e-16	***
SlopeC	-0.2826572	0.7647097		0.9491522	
MeanF-MeanC	-0.9062074	0.06934472	.	0.2946414	
SlopeF-SlopeC	-2.173633	0.1319412		0.9999488	



7.6.83 Vitvi03g00080

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

Vitvi03g00080

30.3

signalling.calcium

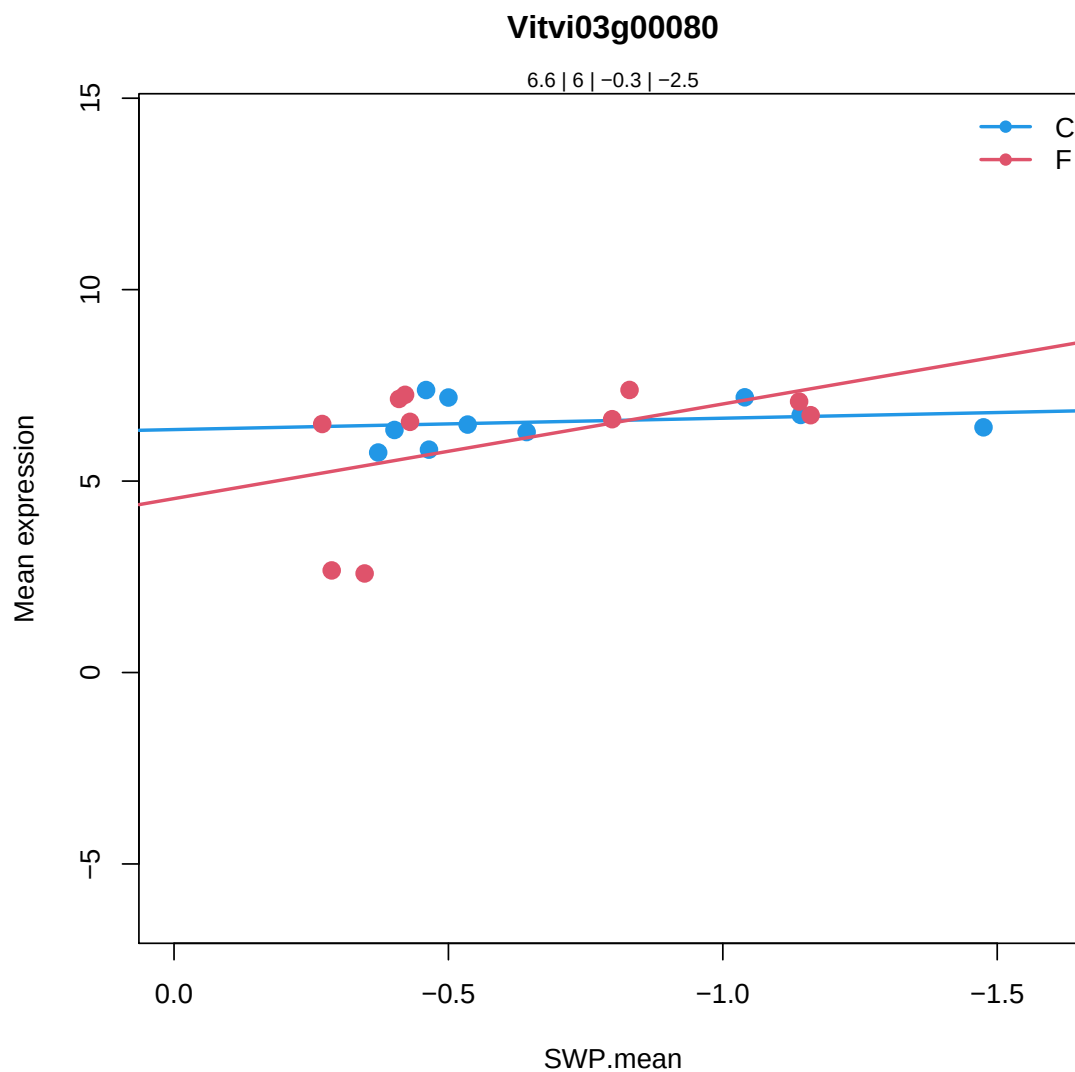
Calcium-binding EF-hand family protein |

Chr4:18115607-18118860 REVERSE LENGTH=375 |

201606

Coefficients for Vitvi03g00080.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.5536	1.528656e-14	***	2.51021e-14	***
SlopeC	-0.2966889	0.7694223		0.9502904	
MeanF-MeanC	-0.505334	0.3309596		0.6907427	
SlopeF-SlopeC	-2.1751	0.1581657		0.9999488	



7.6.84 Vitvi14g02021

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

Vitvi14g02021

35.2

not assigned.unknown

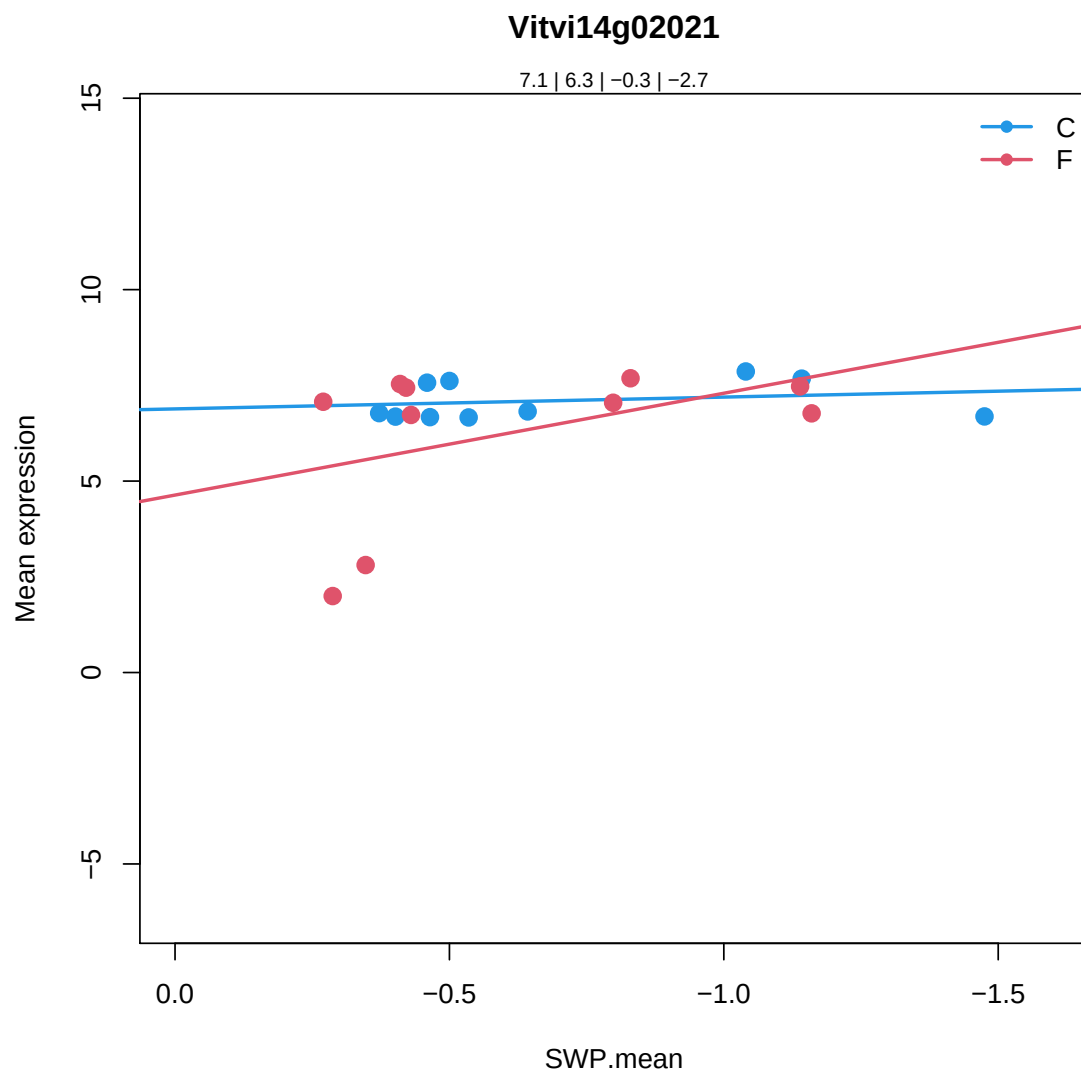
lysine-tRNA ligase |

Chr3:17055-18782 REVERSE LENGTH=372 |

201606

Coefficients for Vitvi14g02021.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.102064	2.663483e-14	***	4.285528e-14	***
SlopeC	-0.3086503	0.7842441		0.9533027	
MeanF-MeanC	-0.8470095	0.1490293		0.4650909	
SlopeF-SlopeC	-2.350934	0.17032		0.9999488	



7.6.85 Vitvi01g00499

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

Vitvi01g00499

29.5.11.4.3.2

protein.degradation.ubiquitin.E3.SCF.FBOX

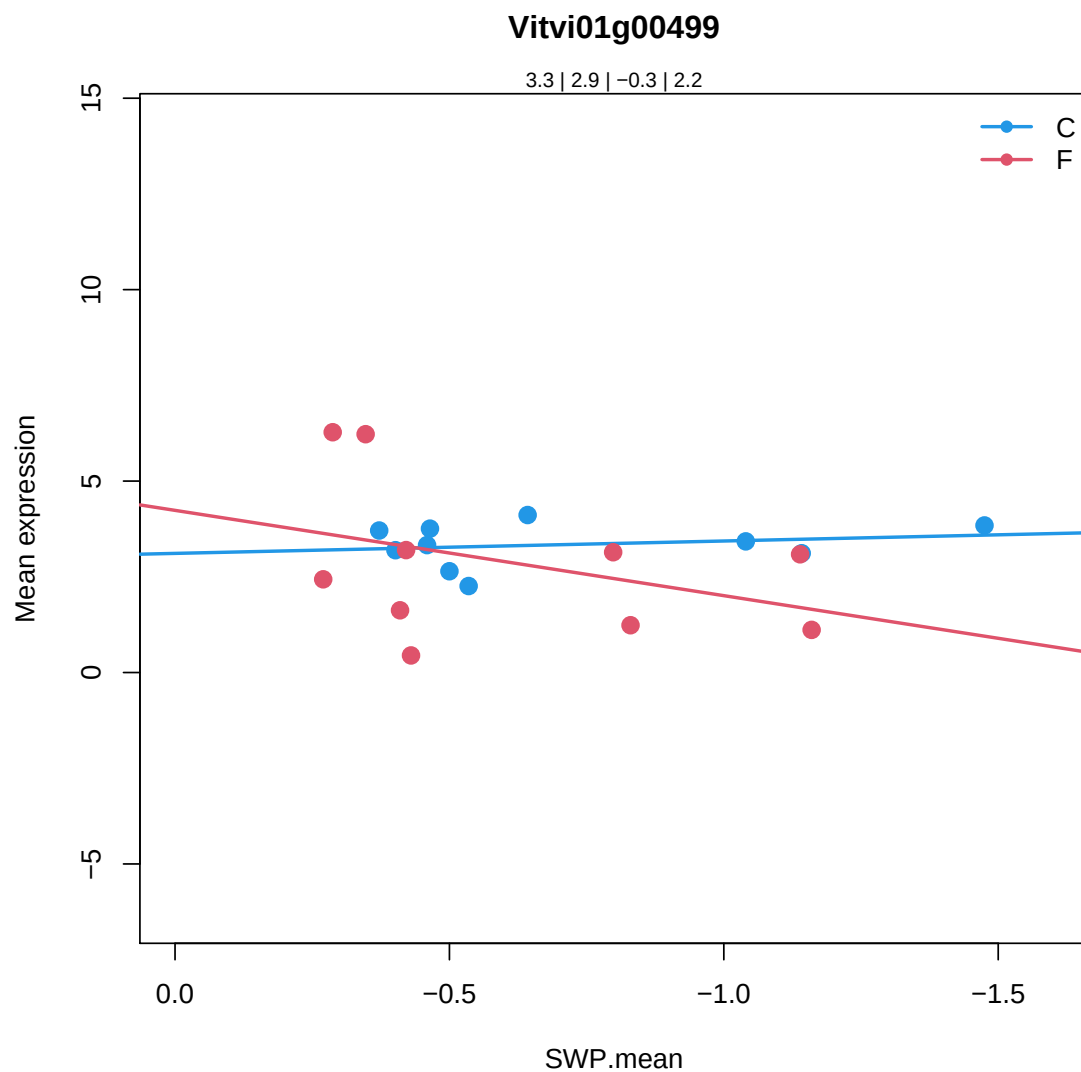
flavin-binding%2C kelch repeat%2C f box 1 |

Chr1:25508737-25510697 FORWARD LENGTH=619 |

201606

Coefficients for Vitvi01g00499.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.338622	4.411033e-08	***	5.282703e-08	***
SlopeC	-0.323465	0.7770267		0.9513135	
MeanF-MeanC	-0.4605614	0.4306082		0.7652319	
SlopeF-SlopeC	2.551102	0.1432014		0.9999488	



7.6.86 Vitvi18g02446

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

Vitvi18g02446

16.01.2005

secondary metabolism.isoprenoids.terpenoids

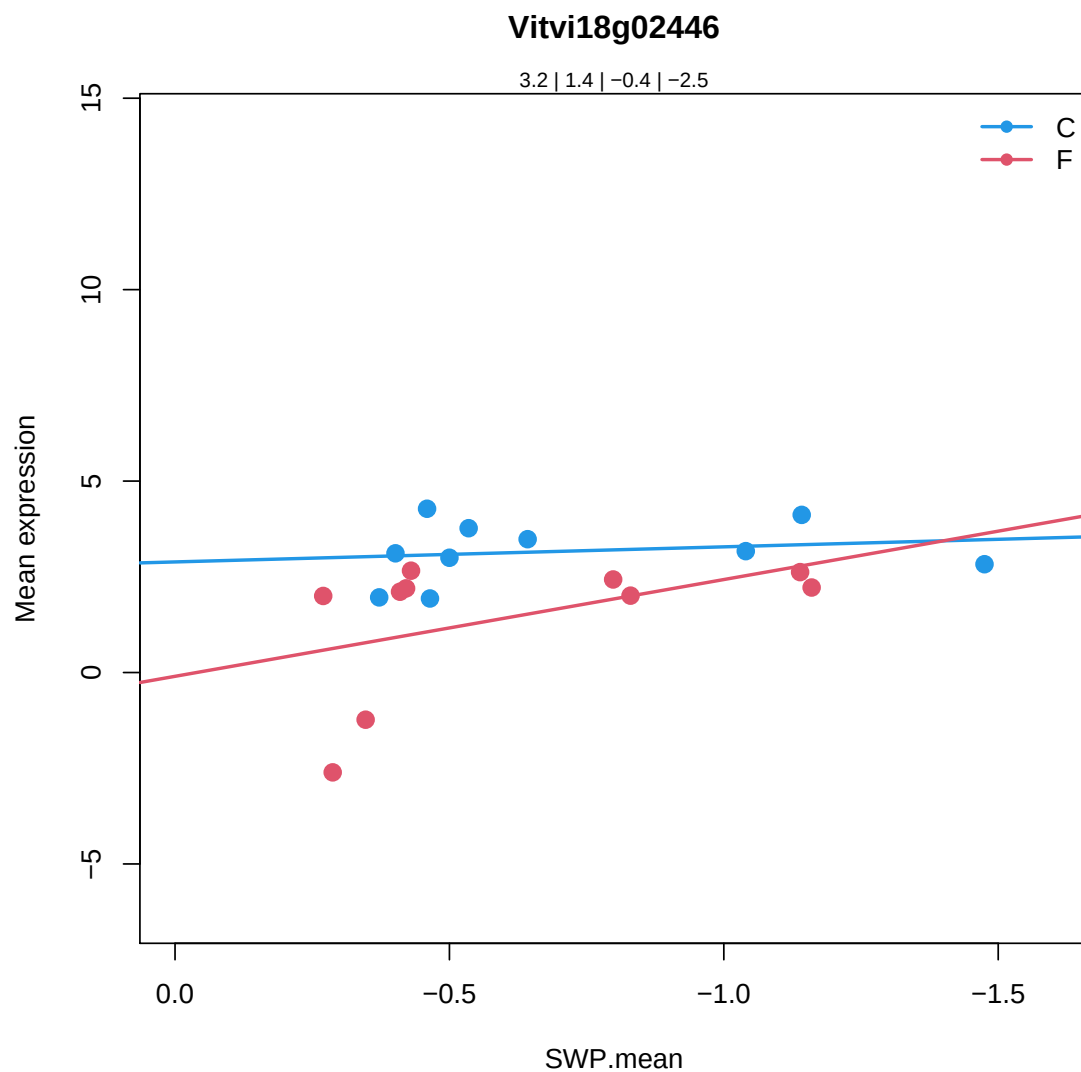
terpene synthase 21 |

Chr5:8092969-8095128 FORWARD LENGTH=547 |

201606

Coefficients for Vitvi18g02446.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.165086	2.576314e-08	***	3.106413e-08	***
SlopeC	-0.3940815	0.7071927		0.9346979	
MeanF-MeanC	-1.724404	0.003528654	**	0.03482595	*
SlopeF-SlopeC	-2.13365	0.1803668		0.9999488	



7.6.87 Vitvi07g02902

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

Vitvi07g02902

35.2

not assigned.unknown

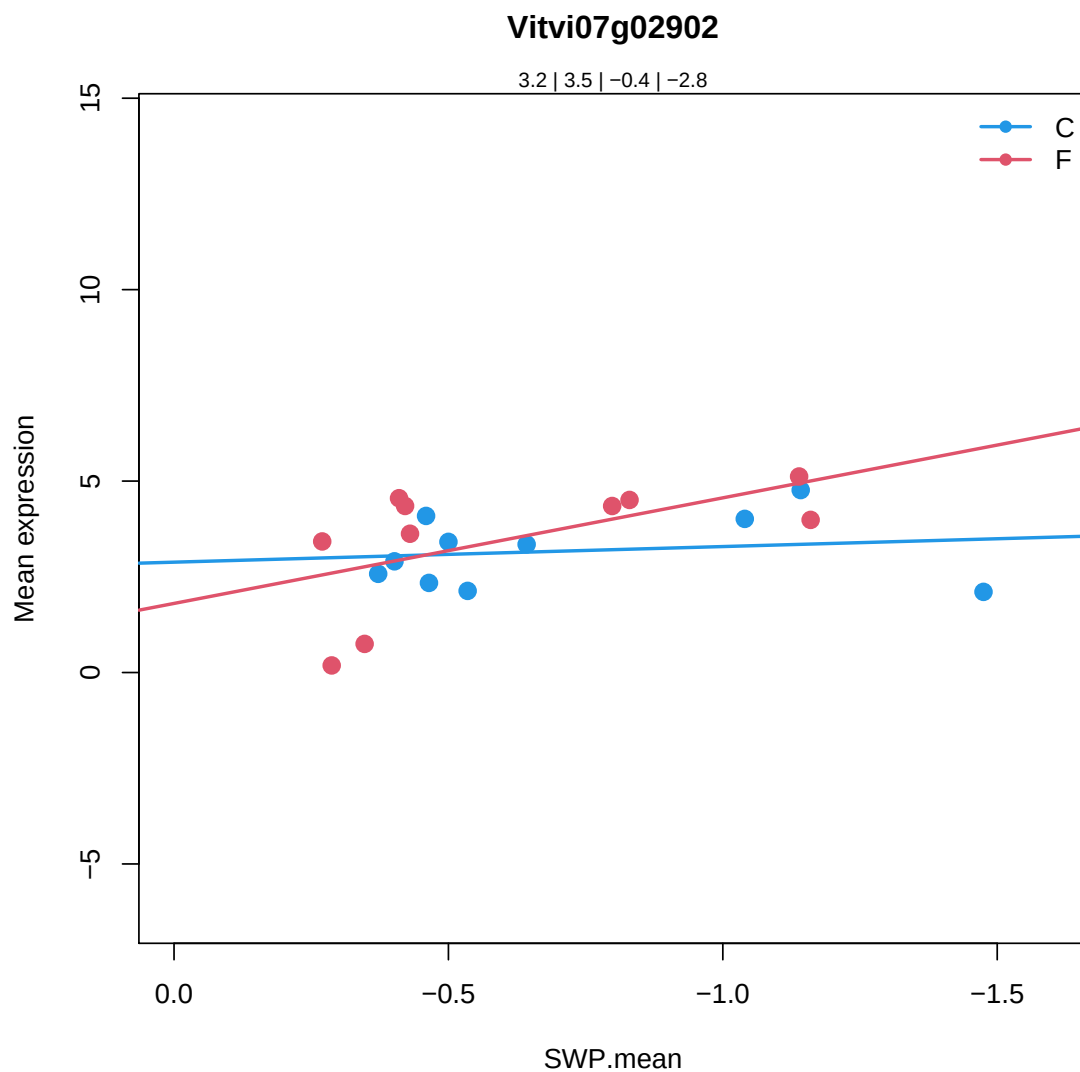
cysteine-rich RECEPTOR-like kinase |

Chr4:12129485-12133157 FORWARD LENGTH=1043 |

201606

Coefficients for Vitvi07g02902.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.168757	6.998453e-09	***	8.586527e-09	***
SlopeC	-0.4080718	0.6750206		0.9250732	
MeanF-MeanC	0.3157186	0.5245143		0.8203845	
SlopeF-SlopeC	-2.349575	0.1146809		0.9999488	



7.6.88 Vitvi03g00580

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

Vitvi03g00580

35.2

not assigned.unknown

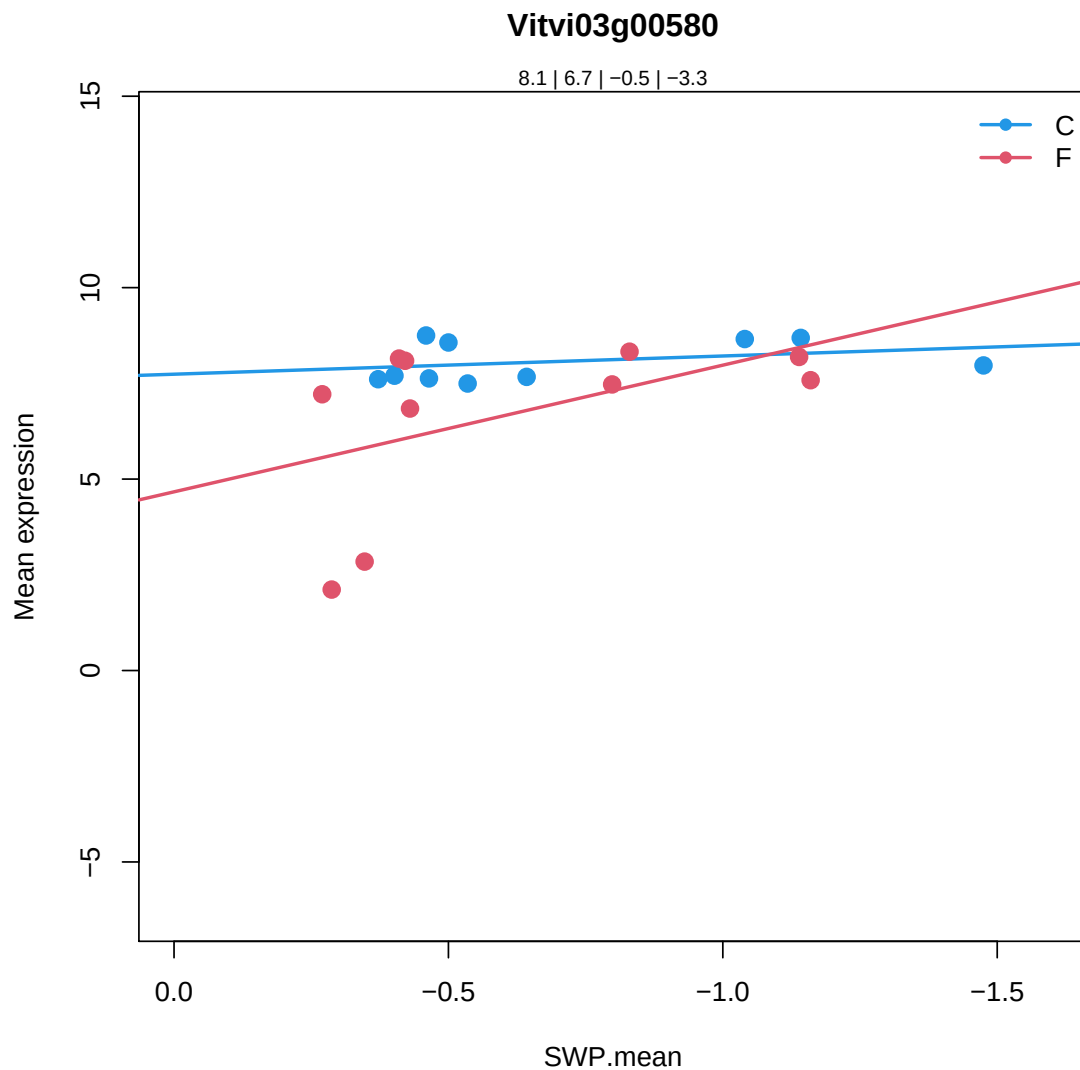
hypothetical protein |

Chr2:6491706-6493286 REVERSE LENGTH=526 |

201606

Coefficients for Vitvi03g00580.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	8.073395	6.043421e-15	***	1.033477e-14	***
SlopeC	-0.475253	0.6901238		0.9312028	
MeanF-MeanC	-1.390809	0.02985651	*	0.1685188	
SlopeF-SlopeC	-2.832606	0.1202108		0.9999488	



7.6.89 Vitvi00g00894

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

Vitvi00g00894

26.1

misc.cytochrome P450

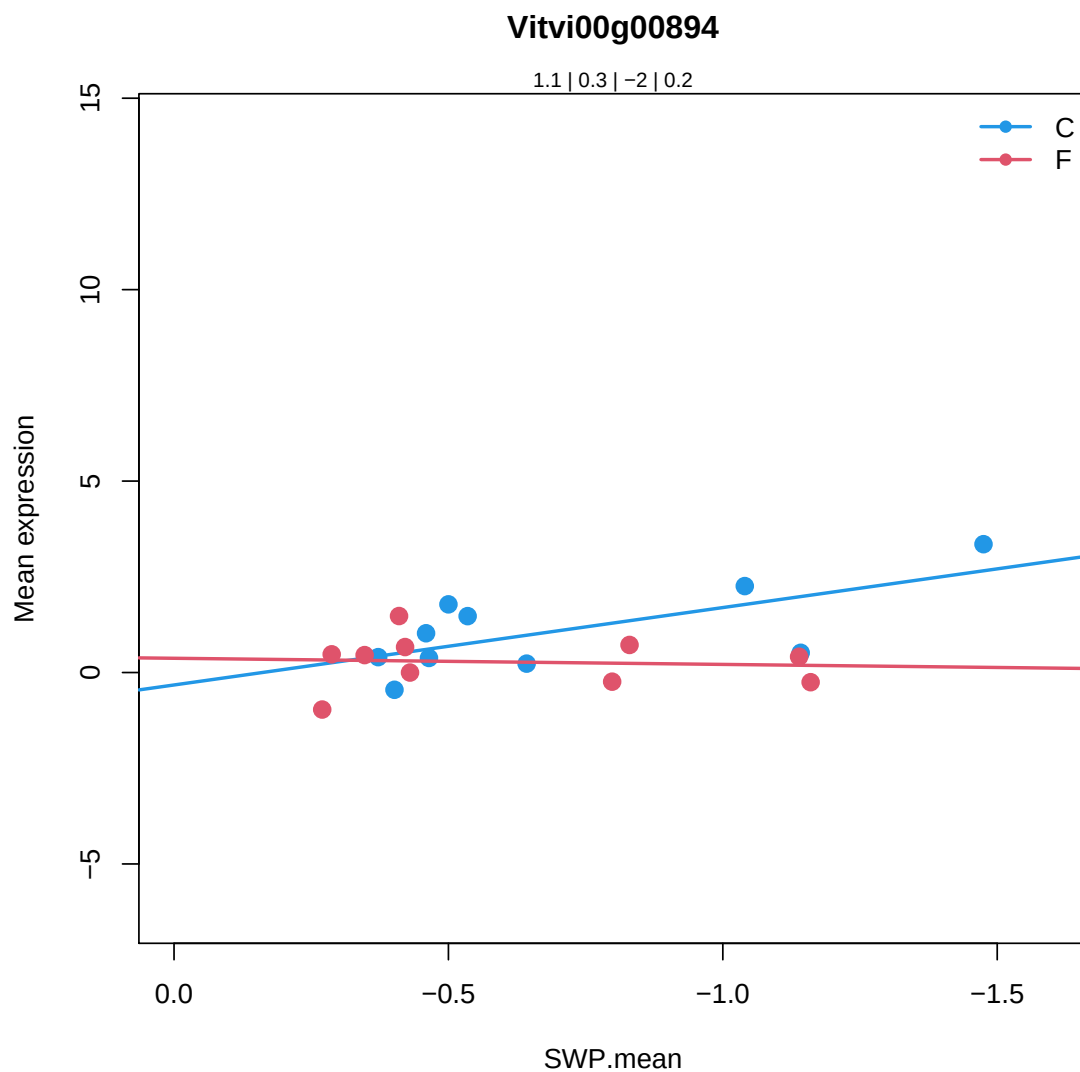
cytochrome P450%2C family 81%2C subfamily D%2C polypeptide 3 |

Chr4:17564953-17566706 REVERSE LENGTH=500 |

201606

Coefficients for Vitvi00g00894.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.096441	0.0001105001	***	0.0001219229	***
SlopeC	-2.021627	0.004991736	**	0.2519339	
MeanF-MeanC	-0.8222664	0.02044618	*	0.1283229	
SlopeF-SlopeC	2.181716	0.03374317	*	0.9999488	



7.6.90 Vitvi03g00379

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

Vitvi03g00379

21.3

redox.heme

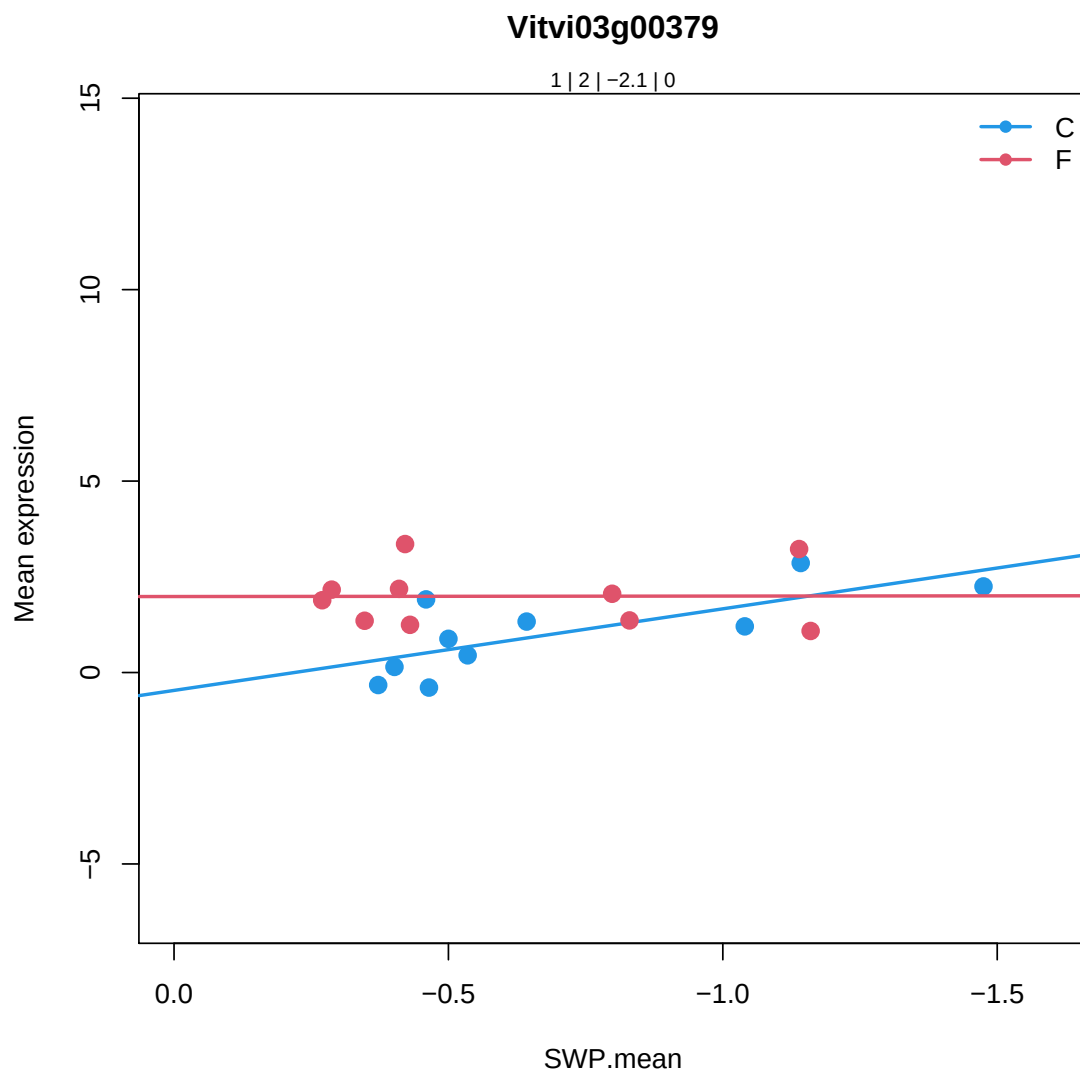
hemoglobin 1 |

Chr2:6982782-6983522 REVERSE LENGTH=160 |

201606

Coefficients for Vitvi03g00379.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.030871	0.0002454846	***	0.0002690692	***
SlopeC	-2.130936	0.003660677	**	0.224984	
MeanF-MeanC	0.9607862	0.008587949	**	0.06775747	.
SlopeF-SlopeC	2.119206	0.04061071	*	0.9999488	



7.6.91 Vitvi01g02058

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

Vitvi01g02058

35.1.26

not assigned.no ontology.DC1 domain containing protein

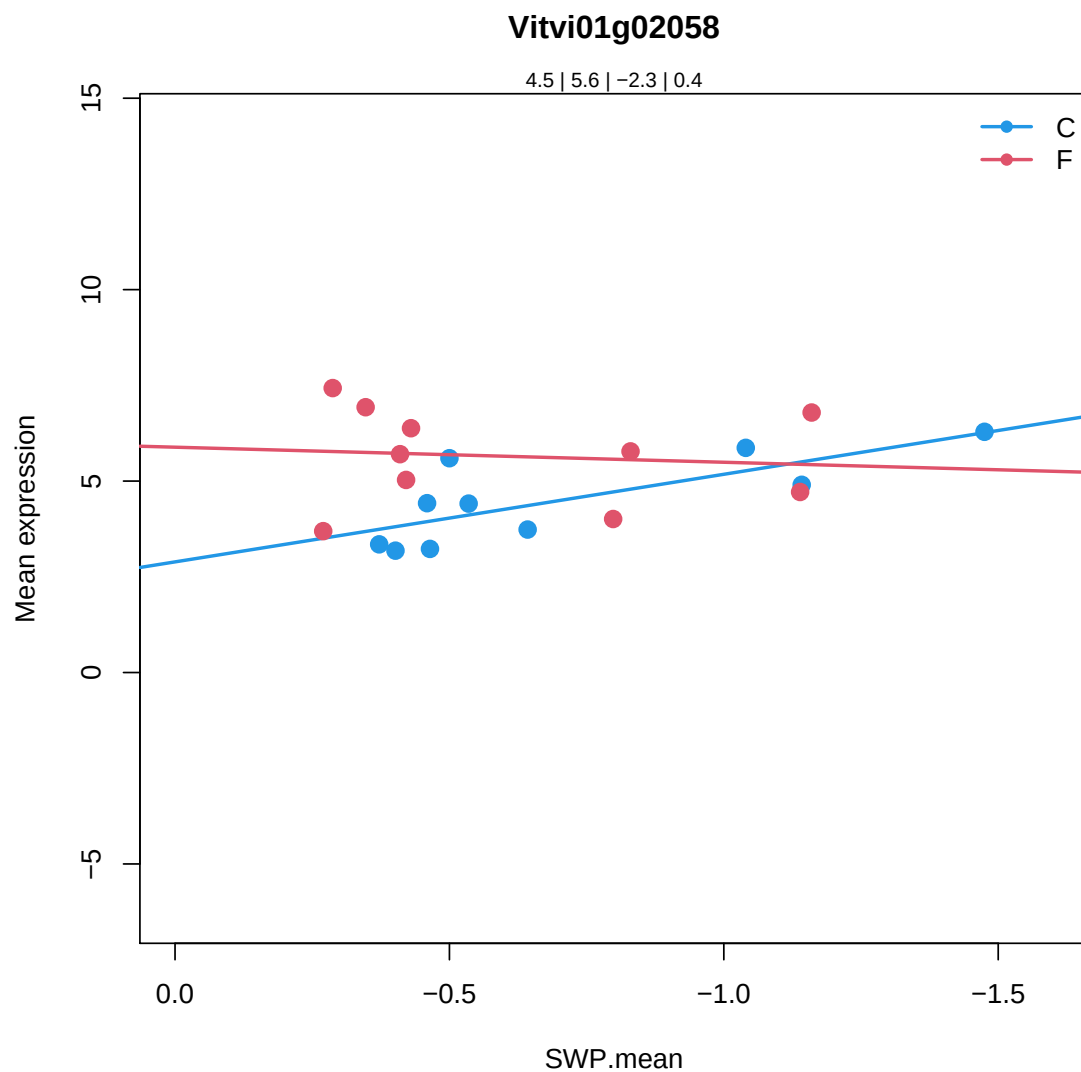
DC1 domain-containing protein |

Chr1:22261978-22264243 FORWARD LENGTH=578 |

201606

Coefficients for Vitvi01g02058.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.498078	1.402763e-12	***	1.995232e-12	***
SlopeC	-2.287997	0.01456258	*	0.3359386	
MeanF-MeanC	1.147159	0.01577985	*	0.1054434	
SlopeF-SlopeC	2.681258	0.04844408	*	0.9999488	



7.6.92 Vitvi15g00739

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

Vitvi15g00739

31.1

cell.organisation

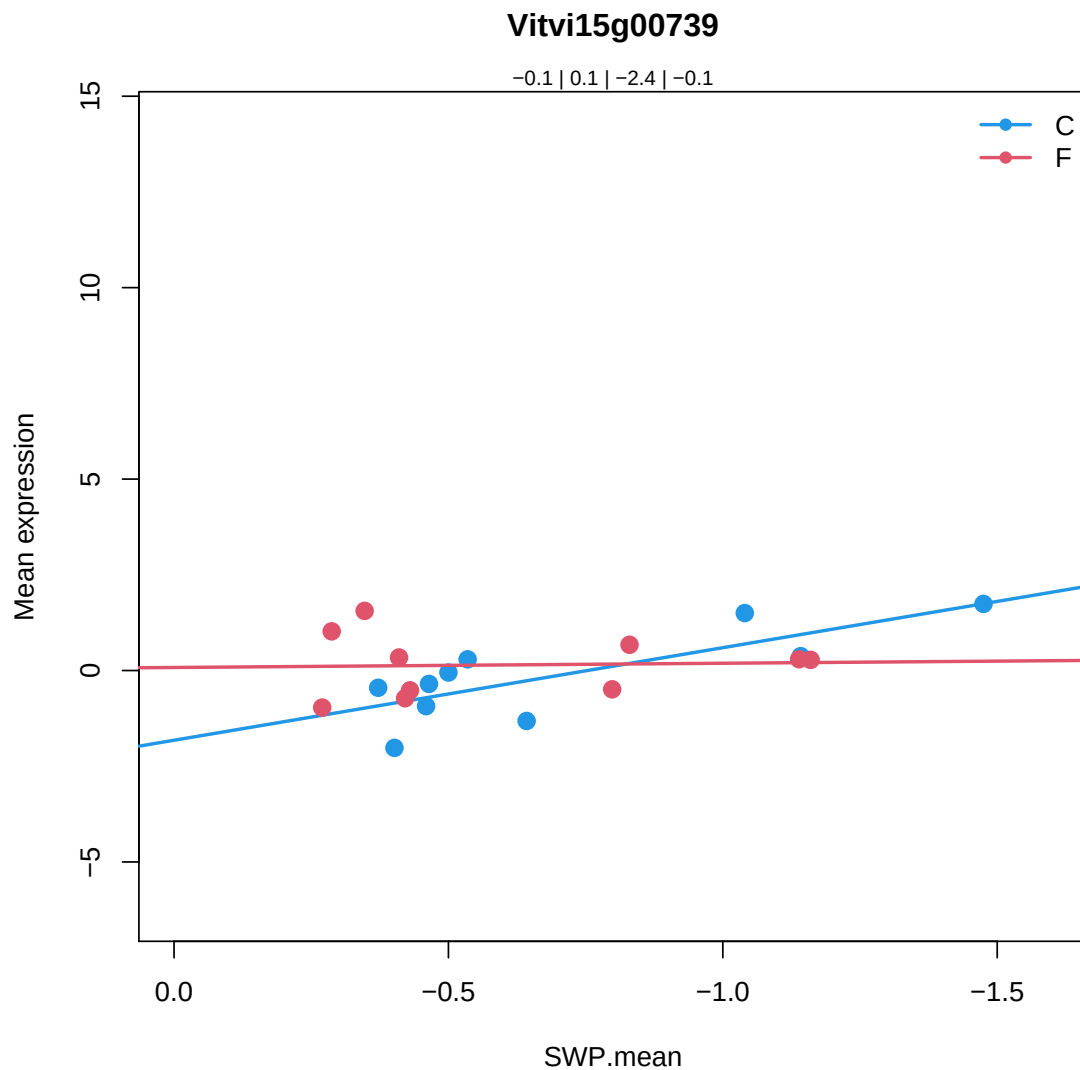
microtubule-associated protein 65-9 |

Chr5:25005756-25008096 FORWARD LENGTH=549 |

201606

Coefficients for Vitvi15g00739.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.121504	0.6138651		0.6191869	
SlopeC	-2.417377	0.001416796	**	0.1479249	
MeanF-MeanC	0.2679126	0.4334342		0.7672943	
SlopeF-SlopeC	2.306901	0.02855227	*	0.9999488	



7.6.93 Vitvi08g01656

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

Vitvi08g01656

16.04.2001

secondary metabolism.N misc.alkaloid-like

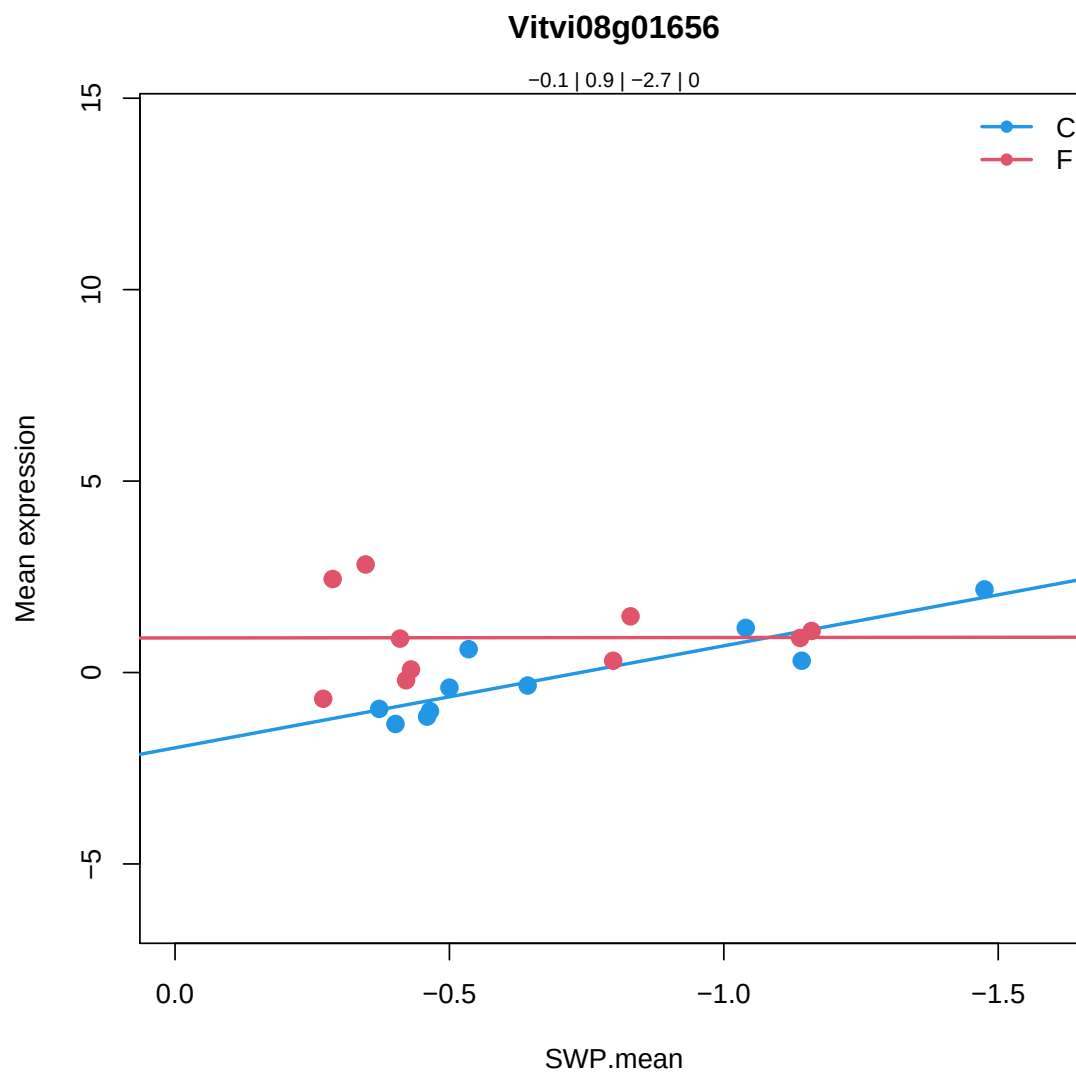
strictosidine synthase-like 2 |

Chr2:17210599-17212904 REVERSE LENGTH=376 |

201606

Coefficients for Vitvi08g01656.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.09373959	0.7272465		0.7318077	
SlopeC	-2.664662	0.001599851	**	0.1556102	
MeanF-MeanC	1.003909	0.01398203	*	0.0970465	.
SlopeF-SlopeC	2.653252	0.02470524	*	0.9999488	



```

> #
> fit2 <- eBayes(fit2)
> fit2[testvar,]$coefficients
              (Intercept)              swp  varietyF swp:varietyF
Vitvi01g01391    1.595041 -0.7685916  0.2722187    0.4814101
> head(fit2[1:6,]$coefficients)
              (Intercept)              swp  varietyF swp:varietyF
Vitvi15g01736    5.550751  1.593545190 -0.2500355  -0.31758915
Vitvi07g02832   -2.634115  0.508155686  5.4166972  -0.25109586
Vitvi07g02830   -1.750650  1.548036562  4.3321685  -0.90607176
Vitvi07g02812   -1.381363 -0.009794742  2.3030352   0.40349136
Vitvi07g02811    2.236177  0.566269561  1.2588734   0.02240192
Vitvi09g02033   -2.842837  0.419564483  4.1984533  -0.76028515

```

A Metadata files

A.1 Project metadata

Table 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_MONETARY=Slovenian_Slovenia.1250, LC_NUMERIC=C, LC_TIME=Slovenian_Slovenia.1250
- Running under: Windows 10 x64 (build 19041)
- Matrix products: default
- Base packages: base, datasets, graphics, grDevices, grid, methods, parallel, stats, utils
- Other packages: amisc 0.1.0, Biobase 2.50.0, BiocGenerics 0.36.0, dotCall64 1.0-0, fields 11.6, Formula 1.2-4, ggplot2 3.3.3, Hmisc 4.4-1, knitr 1.30, lattice 0.20-41, limma 3.46.0, lubridate 1.7.9.2, reshape2 1.4.4, spam 2.6-0, survival 3.2-7, xtable 1.8-4
- Loaded via a namespace (and not attached): backports 1.2.0, base64enc 0.1-3, checkmate 2.0.0, cluster 2.1.0, colorspace 1.4-1, compiler 4.0.2, crayon 1.3.4, data.table 1.13.2, digest 0.6.27, dplyr 1.0.2, ellipsis 0.3.1, evaluate 0.14, foreign 0.8-80, generics 0.1.0, glue 1.4.2, gridExtra 2.3, gtable 0.3.0, highr 0.8, htmlTable 2.1.0, htmltools 0.5.0, htmlwidgets 1.5.3, jpeg 0.1-8.1, latticeExtra 0.6-29, lifecycle 0.2.0, magrittr 2.0.1, maps 3.3.0, Matrix 1.2-18, munsell 0.5.0, nnet 7.3-14, pillar 1.4.7, pkgconfig 2.0.3, plyr 1.8.6, png 0.1-7, purrr 0.3.4, R6 2.5.0, RColorBrewer 1.1-2, Rcpp 1.0.5, rlang 0.4.8, rpart 4.1-15, rstudioapi 0.13, scales 1.1.1, splines 4.0.2, stringi 1.5.3, stringr 1.4.0, tibble 3.0.4, tidyselect 1.1.0, tools 4.0.2, vctrs 0.3.4, withr 2.3.0, xfun 0.19

Analysis project path: [\[link\]](#)

Local

D:

DEJAVNOSTI

OMIKE

pISA-projects

_p_VinskaTrta

_I_EnViRoS

_S_01_Integ

_A_01_Desc-R

other

Network

O:

DEJAVNOSTI

OMIKE

pISA-projects

_p_VinskaTrta

_I_EnViRoS

_S_01_Integ

_A_01_Desc-R

other

Main file : [../doc/50_Expression-water-stress.Rnw](#)

Main file : [../scripts/50_Expression-water-stress.Rnw](#)

Project file: [\[link\]](#)

View as vignette

Source files can be viewed by pasting this code to R console:

```
projectName <-"other"
mainFile <-"50_Expression-water-stress"
commandArgs()
library(tkWidgets)
openPDF(file.path(dirname(getwd()),"doc",
paste(mainFile,"PDF",sep=".")
viewVignette("viewVignette", projectName,
file.path("../doc",paste(mainFile,"Rnw",sep=".")))
```