

Expression analysis - water potential

A. Blejec

February 13, 2021

Parameters:

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

Contents

1	Task	12
2	Information from pISA	13
3	Data	14
3.1	Phenodata	15
3.2	Declare factor types	16
3.3	Select samples	18
3.4	Featuredata	21
3.5	Transcripts measurements	28
3.5.1	Normalized values	28
3.5.2	Keep genes in the intersection	32
3.6	Metabolite measurements	36
3.7	Visualize metabolites	39
3.8	Standardization	48
3.9	Featuredata for metabolites	59
3.10	Interesting bins	62
3.10.1	Genes in bins of interest	63
3.10.2	Metabolites in bins of interest	64
3.11	Created objects overview	67
3.12	Data overview	71
3.13	Water potential	97
4	Expression and water poential analysis	107
4.1	Expression vs water potential	111
4.2	Water potential vs Expression	113
5	Linear models for water potential	119
5.1	Interpolated water potential data	122
5.2	Overall Model	127
5.3	Models for variety	129
5.4	Mean expressions	132
5.4.1	Plots of variety coefficients	134
5.4.2	Types by effects	136
6	Situation types and Type selection criteria	138
6.1	Old Types	138
6.2	New type definitions	141
6.2.1	Parameter explanation	144
6.2.2	Type1	148
6.2.3	Type2	152
6.2.4	Type3	156
6.2.5	Type4	161
6.2.6	Type5	165
6.2.7	Type6	169
6.3	Export output files	194
7	Types and significance of contrasts	195
7.1	Export fit statistics, types and descriptions	208

8	Detailed plots, stats and info of Genes by types	213
8.1	Type1	217
8.1.1	Vitvi05g00011: * Type1	218
8.1.2	Vitvi14g01381: Type1	219
8.1.3	Vitvi05g01353: * Type1	220
8.1.4	Vitvi10g01886: Type1	221
8.1.5	Vitvi08g00768: * Type1	222
8.1.6	Vitvi10g00436: * Type1	223
8.1.7	Vitvi04g02114: Type1	224
8.1.8	Vitvi03g00144: * Type1	226
8.1.9	Vitvi06g00790: Type1	227
8.1.10	Vitvi04g00060: Type1	228
8.1.11	Vitvi18g00455: Type1	229
8.1.12	Vitvi11g01437: * Type1	230
8.1.13	Vitvi03g00752: * Type1	231
8.1.14	Vitvi06g00626: * Type1	232
8.1.15	Vitvi01g00638: * Type1	233
8.1.16	Vitvi03g01162: Type1	234
8.1.17	Vitvi11g00365: * Type1	235
8.1.18	Vitvi18g01735: * Type1	236
8.1.19	Vitvi15g00812: * Type1	237
8.1.20	Vitvi19g00041: Type1	238
8.1.21	Vitvi13g02129: Type1	239
8.1.22	Vitvi15g00641: Type1	240
8.1.23	Vitvi05g00089: * Type1	241
8.1.24	Vitvi14g01899: * Type1	242
8.1.25	Vitvi08g01702: * Type1	243
8.1.26	Vitvi18g00739: Type1	244
8.1.27	Vitvi18g02692: * Type1	245
8.1.28	Vitvi09g00528: * Type1	246
8.1.29	Vitvi05g01949: Type1	247
8.1.30	Vitvi19g01964: * Type1	248
8.1.31	Vitvi16g01418: Type1	250
8.1.32	Vitvi11g00708: Type1	251
8.1.33	Vitvi14g02920: * Type1	252
8.1.34	Vitvi11g00417: * Type1	253
8.1.35	Vitvi19g00445: Type1	254
8.1.36	Vitvi02g00327: Type1	255
8.1.37	Vitvi14g00483: Type1	256
8.1.38	Vitvi04g00005: * Type1	257
8.1.39	Vitvi13g01937: Type1	258
8.1.40	Vitvi05g01941: Type1	259
8.1.41	Vitvi18g02815: Type1	260
8.1.42	Vitvi11g00178: * Type1	261
8.1.43	Vitvi17g00217: Type1	262
8.1.44	Vitvi08g01789: Type1	263
8.1.45	Vitvi13g00367: * Type1	264
8.1.46	Vitvi13g02006: Type1	265
8.1.47	Vitvi07g00905: Type1	266
8.1.48	Vitvi09g00177: * Type1	267

8.1.49	Vitvi12g02375: Type1	268
8.1.50	Vitvi14g02930: Type1	269
8.1.51	Vitvi07g00421: Type1	270
8.1.52	Vitvi05g01314: * Type1	271
8.1.53	Vitvi02g00991: * Type1	272
8.1.54	Vitvi10g01544: * Type1	273
8.1.55	Vitvi07g03049: * Type1	274
8.1.56	Vitvi08g00877: * Type1	275
8.1.57	Vitvi13g00241: * Type1	276
8.1.58	Vitvi13g02576: * Type1	277
8.1.59	Vitvi10g00798: * Type1	278
8.1.60	Vitvi04g01202: * Type1	279
8.1.61	Vitvi17g01012: * Type1	280
8.1.62	Vitvi02g00983: * Type1	281
8.1.63	Vitvi17g01086: * Type1	282
8.1.64	Vitvi02g01261: * Type1	283
8.1.65	Vitvi18g02167: Type1	284
8.1.66	Vitvi10g01342: * Type1	285
8.1.67	Vitvi02g00228: * Type1	286
8.1.68	Vitvi05g01740: * Type1	287
8.1.69	Vitvi18g00596: * Type1	288
8.1.70	Vitvi08g02189: Type1	289
8.1.71	Vitvi07g01297: Type1	291
8.1.72	Vitvi08g01234: * Type1	292
8.1.73	Vitvi01g02009: * Type1	293
8.1.74	Vitvi07g00087: * Type1	294
8.1.75	Vitvi09g01273: * Type1	295
8.1.76	Vitvi13g00255: * Type1	296
8.1.77	Vitvi17g00078: Type1	297
8.1.78	Vitvi06g01762: * Type1	298
8.1.79	Vitvi11g01265: * Type1	299
8.1.80	Vitvi18g02607: Type1	300
8.1.81	Vitvi05g00539: * Type1	301
8.1.82	Vitvi10g02382: * Type1	302
8.1.83	Vitvi14g01824: * Type1	303
8.1.84	Vitvi13g00343: * Type1	304
8.1.85	Vitvi08g01890: * Type1	305
8.1.86	Vitvi08g01757: * Type1	306
8.1.87	Vitvi12g02200: * Type1	307
8.1.88	Vitvi08g01143: Type1	308
8.1.89	Vitvi15g01058: * Type1	309
8.1.90	Vitvi16g01167: * Type1	310
8.1.91	Vitvi15g00763: * Type1	311
8.1.92	Vitvi08g01112: * Type1	312
8.1.93	Vitvi18g01966: * Type1	313
8.1.94	Vitvi12g01584: * Type1	314
8.1.95	Vitvi05g00218: * Type1	315
8.1.96	Vitvi06g00443: * Type1	316
8.1.97	Vitvi11g00513: * Type1	318
8.1.98	Vitvi06g00440: * Type1	319

8.1.99	Vitvi06g00605: * Type1	320
8.1.100	Vitvi04g00522: * Type1	321
8.1.101	Vitvi01g01459: * Type1	322
8.1.102	Vitvi14g02026: * Type1	323
8.1.103	Vitvi04g02184: * Type1	324
8.1.104	Vitvi01g00424: * Type1	325
8.1.105	Vitvi16g00681: * Type1	326
8.1.106	Vitvi08g00689: * Type1	327
8.1.107	Vitvi05g01833: * Type1	328
8.1.108	Vitvi17g00085: * Type1	329
8.1.109	Vitvi13g01107: Type1	330
8.1.110	Vitvi01g02030: * Type1	331
8.1.111	Vitvi13g01839: * Type1	332
8.1.112	Vitvi06g00533: * Type1	334
8.1.113	Vitvi02g00436: * Type1	336
8.1.114	Vitvi17g00695: * Type1	337
8.1.115	Vitvi19g00514: * Type1	338
8.1.116	Vitvi02g00374: * Type1	339
8.1.117	Vitvi18g01510: * Type1	340
8.1.118	Vitvi14g00063: * Type1	341
8.1.119	Vitvi13g00471: * Type1	342
8.1.120	Vitvi05g00486: * Type1	343
8.1.121	Vitvi14g02990: * Type1	344
8.1.122	Vitvi11g00724: * Type1	345
8.1.123	Vitvi05g00170: * Type1	347
8.1.124	Vitvi15g01034: * Type1	348
8.1.125	Vitvi13g02017: * Type1	349
8.1.126	Vitvi16g01985: * Type1	350
8.1.127	Vitvi12g02138: * Type1	351
8.1.128	Vitvi04g00135: * Type1	352
8.1.129	Vitvi18g02423: * Type1	353
8.2	Type1.2	354
8.2.1	Vitvi10g02300: * Type1.2	355
8.2.2	Vitvi14g01717: Type1.2	356
8.2.3	Vitvi07g03083: Type1.2	357
8.2.4	Vitvi04g01126: * Type1.2	358
8.2.5	Vitvi05g00681: * Type1.2	359
8.2.6	Vitvi13g00451: * Type1.2	360
8.2.7	Vitvi13g00278: * Type1.2	361
8.2.8	Vitvi07g00457: * Type1.2	362
8.3	Type1.4	363
8.3.1	Vitvi09g01874: * Type3.C	364
8.3.2	Vitvi10g00663: * Type3.C	365
8.3.3	Vitvi18g03250: * Type3.C	367
8.3.4	Vitvi05g01758: Type3.C	368
8.3.5	Vitvi16g02091: * Type3.C	369
8.3.6	Vitvi16g02098: * Type3.C	370
8.3.7	Vitvi00g02226: * Type3.C	371
8.3.8	Vitvi09g01948: * Type3.C	372
8.3.9	Vitvi09g01335: * Type3.C	373

8.3.10	Vitvi16g01549: * Type3.C	374
8.3.11	Vitvi16g01995: * Type3.C	375
8.3.12	Vitvi14g03032: * Type3.C	376
8.3.13	Vitvi05g01285: * Type3.C	377
8.3.14	Vitvi14g03057: * Type3.C	378
8.3.15	Vitvi08g02300: Type3.C	379
8.3.16	Vitvi18g00973: * Type3.C	380
8.3.17	Vitvi16g01960: * Type3.C	381
8.3.18	Vitvi18g01262: * Type3.C	382
8.3.19	Vitvi11g00766: * Type3.C	383
8.3.20	Vitvi08g00630: * Type3.C	384
8.3.21	Vitvi16g02010: * Type3.C	385
8.3.22	Vitvi01g02251: * Type3.C	386
8.3.23	Vitvi18g01321: * Type3.C	387
8.3.24	Vitvi01g01520: * Type3.C	388
8.3.25	Vitvi14g01615: * Type3.C	389
8.3.26	Vitvi02g00514: * Type3.C	390
8.3.27	Vitvi18g03246: * Type3.C	391
8.3.28	Vitvi13g00085: Type3.C	392
8.3.29	Vitvi16g02015: * Type3.C	393
8.3.30	Vitvi16g02019: * Type3.C	394
8.3.31	Vitvi17g00400: * Type3.C	395
8.3.32	Vitvi13g02359: * Type3.C	396
8.3.33	Vitvi07g01329: * Type3.C	397
8.3.34	Vitvi06g00668: Type3.C	398
8.3.35	Vitvi14g01560: * Type3.C	400
8.3.36	Vitvi05g01789: * Type3.C	401
8.4	Type3.C	402
8.4.1	Vitvi06g01743: Type3.F	403
8.4.2	Vitvi19g01966: Type3.F	404
8.4.3	Vitvi05g01780: Type3.F	406
8.4.4	Vitvi19g00391: Type3.F	407
8.4.5	Vitvi05g01675: + Type3.F	408
8.4.6	Vitvi14g03071: + Type3.F	409
8.4.7	Vitvi01g02299: Type3.F	410
8.4.8	Vitvi13g00600: Type3.F	411
8.4.9	Vitvi07g01779: Type3.F	412
8.4.10	Vitvi15g00727: Type3.F	413
8.4.11	Vitvi15g01075: Type3.F	414
8.4.12	Vitvi18g02012: Type3.F	415
8.4.13	Vitvi04g01421: Type3.F	416
8.4.14	Vitvi01g00064: Type3.F	417
8.4.15	Vitvi18g00154: Type3.F	418
8.4.16	Vitvi08g00662: Type3.F	419
8.4.17	Vitvi15g00795: Type3.F	420
8.4.18	Vitvi00g01320: Type3.F	421
8.4.19	Vitvi19g01715: Type3.F	423
8.4.20	Vitvi12g00574: + Type3.F	424
8.4.21	Vitvi01g01284: Type3.F	425
8.4.22	Vitvi19g02155: Type3.F	426

8.4.23	Vitvi18g02446: Type3.F	427
8.4.24	Vitvi09g00303: Type3.F	428
8.4.25	Vitvi01g01021: Type3.F	429
8.5	Type3.F	430
8.5.1	Vitvi13g02005: Type1.4	431
8.5.2	Vitvi02g00391: * Type1.4	432
8.5.3	Vitvi02g01404: * Type1.4	433
8.5.4	Vitvi12g02414: * Type1.4	434
8.5.5	Vitvi13g00490: * Type1.4	435
8.5.6	Vitvi04g01802: * Type1.4	436
8.5.7	Vitvi04g01801: * Type1.4	437
8.5.8	Vitvi02g00025: * Type1.4	438
8.5.9	Vitvi04g01799: * Type1.4	439
8.5.10	Vitvi04g01794: * Type1.4	440
8.5.11	Vitvi10g01881: * Type1.4	441
8.5.12	Vitvi06g00561: * Type1.4	442
8.5.13	Vitvi16g01352: * Type1.4	443
8.6	Type5	444
8.6.1	Vitvi03g00325: * Type5	445
8.6.2	Vitvi17g00601: * Type5	446
8.6.3	Vitvi05g01577: * Type5	447
8.6.4	Vitvi17g01596: * Type5	448
8.6.5	Vitvi07g00445: Type5	449
8.6.6	Vitvi07g00586: * Type5	450
8.6.7	Vitvi15g00714: Type5	451
8.6.8	Vitvi01g00593: * Type5	452
8.6.9	Vitvi18g02709: * Type5	453
8.6.10	Vitvi03g00318: * Type5	454
8.6.11	Vitvi05g00094: Type5	455
8.6.12	Vitvi07g00665: Type5	456
8.6.13	Vitvi16g02137: * Type5	457
8.6.14	Vitvi03g01503: Type5	458
8.6.15	Vitvi10g01685: * Type5	459
8.6.16	Vitvi11g00726: Type5	460
8.6.17	Vitvi14g02893: Type5	461
8.6.18	Vitvi01g00784: Type5	462
8.6.19	Vitvi18g01019: Type5	463
8.6.20	Vitvi04g00644: * Type5	465
8.6.21	Vitvi16g01118: * Type5	466
8.6.22	Vitvi13g01760: Type5	467
8.6.23	Vitvi10g00650: * Type5	468
8.6.24	Vitvi05g01951: Type5	469
8.6.25	Vitvi12g00036: Type5	470
8.6.26	Vitvi14g02924: Type5	471
8.6.27	Vitvi01g02061: * Type5	472
8.6.28	Vitvi05g01116: * Type5	473
8.6.29	Vitvi18g00508: * Type5	474
8.6.30	Vitvi07g02448: * Type5	475
8.6.31	Vitvi19g01048: Type5	476
8.6.32	Vitvi03g00443: * Type5	477

8.6.33	Vitvi02g00263: Type5	478
8.6.34	Vitvi09g01282: Type5	479
8.6.35	Vitvi07g01552: * Type5	480
8.6.36	Vitvi07g01120: Type5	481
8.6.37	Vitvi05g00421: * Type5	482
8.6.38	Vitvi01g01708: * Type5	483
8.6.39	Vitvi09g00045: * Type5	484
8.6.40	Vitvi19g02145: * Type5	485
8.6.41	Vitvi11g01516: * Type5	486
8.6.42	Vitvi05g00857: * Type5	487
8.6.43	Vitvi13g02018: * Type5	488
8.6.44	Vitvi07g02242: * Type5	489
8.6.45	Vitvi09g00599: * Type5	490
8.6.46	Vitvi16g01103: * Type5	491
8.7	Type6.C	492
8.7.1	Vitvi18g03084: * Type6.C	493
8.7.2	Vitvi16g02090: * Type6.C	494
8.7.3	Vitvi16g02003: * Type6.C	495
8.7.4	Vitvi16g01548: * Type6.C	496
8.7.5	Vitvi09g00681: * Type6.C	497
8.7.6	Vitvi12g00606: * Type6.C	498
8.7.7	Vitvi07g02459: * Type6.C	500
8.7.8	Vitvi08g00723: * Type6.C	501
8.7.9	Vitvi16g01010: * Type6.C	502
8.7.10	Vitvi14g03027: * Type6.C	503
8.7.11	Vitvi12g02241: * Type6.C	504
8.7.12	Vitvi16g01695: * Type6.C	505
8.7.13	Vitvi16g00162: * Type6.C	506
8.7.14	Vitvi07g01975: * Type6.C	507
8.7.15	Vitvi12g02434: * Type6.C	508
8.7.16	Vitvi17g01499: * Type6.C	510
8.7.17	Vitvi09g00253: * Type6.C	511
8.7.18	Vitvi07g02479: * Type6.C	513
8.7.19	Vitvi07g03003: * Type6.C	514
8.7.20	Vitvi11g00749: Type6.C	515
8.7.21	Vitvi16g02128: * Type6.C	516
8.7.22	Vitvi12g02492: * Type6.C	517
8.7.23	Vitvi07g01880: * Type6.C	518
8.7.24	Vitvi09g00038: Type6.C	519
8.7.25	Vitvi14g00488: Type6.C	520
8.7.26	Vitvi01g01977: * Type6.C	521
8.7.27	Vitvi03g01431: * Type6.C	522
8.8	Type6.F	523
8.8.1	Vitvi19g02316: Type6.F	524
8.8.2	Vitvi17g00175: Type6.F	525
8.8.3	Vitvi05g00038: Type6.F	526
8.8.4	Vitvi15g01643: Type6.F	527
8.8.5	Vitvi05g01578: Type6.F	528
8.8.6	Vitvi11g00865: Type6.F	529
8.8.7	Vitvi10g00313: Type6.F	531

8.8.8	Vitvi12g02177: Type6.F	532
8.8.9	Vitvi07g03123: Type6.F	533
8.8.10	Vitvi10g02396: Type6.F	534
8.8.11	Vitvi07g03066: Type6.F	535
8.8.12	Vitvi18g01877: Type6.F	536
8.8.13	Vitvi08g02249: Type6.F	537
8.8.14	Vitvi13g00261: + Type6.F	539
8.8.15	Vitvi00g02022: Type6.F	540
8.8.16	Vitvi17g01497: Type6.F	541
Appendix		543
A Metadata files		543
A.1	Project metadata	543
A.2	Investigation metadata	544
A.3	Study metadata	544
A.4	Assay metadata	545
B SessionInfo		546

List of Tables

1	Table of new types.	174
2	Project metadata	543
3	Investigation metadata	544
4	Study metadata	544
5	Assay metadata	545

List of Figures

1 Task

Final document in folder /reports:

```
> fileName(outputFile)
```

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


2 Information from pISA

Data directory

```
> .inroot
```

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

Results directory

```
> .oroot
```

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

```
project:      _p_VinskaTrta
```

```
Investigation: _I_EnViRoS
```

```
Study:        _S_01_Integ
```

```
Assay:         _A_01_Desc-R
```

3 Data

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

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

Entered 10a-ReadData.Rnw

3.1 Phenodata

Two incomplete lines in original phenodata were manually completed. Sample ids (ID) were parsed in Excel to form factors of interest: variety, year and day.

```
> (pfn <- getDesc(.adesc
+           , "Phenodata"))
[1] "Phenodata_20201109.txt"
> dir(file.path(.iroot), pattern = pfn)
[1] "Phenodata_20201109.txt"
> phdata <- read.table(file.path(.iroot, pfn)
+   , header = TRUE
+   , sep = "\t"
+   , stringsAsFactors = FALSE
+   )
> rownames(phdata) <- phdata[,1]
> my.summary(phdata)
```

ID	Variety	Date	variety
C18_11d_WS1: 1	Cabernet Volos:134	21.06.2018: 20	C:134
C18_11d_WS2: 1	Fleurtai :136	26.06.2019: 20	F:136
C18_11d_WS3: 1		7.08.2018 : 20	
C18_11d_WS4: 1		8.07.2019 : 20	
C18_11d_WW1: 1		1.08.2018 : 16	
C18_11d_WW2: 1		18.07.2019: 16	
(Other) :264		(Other) :158	

year	day	treat	rep	project.name
18:136	34 : 36	WS:135	1 :48	EnViros:270
19:134	49 : 24	WW:135	2 :48	
	20 : 20		3 :48	
	22 : 20		4 :48	
	67 : 20		NA's:78	
	44 : 16			
	(Other):134			

species	plant.name	tissue	health.status
Vitis vinifera:270	grapevine:270	: 78	water stress:134
		leaf:192	well watered:136

plant.number	growth.location	growth.conditions
:78	Udine:270	outside:270
R1:48		
R2:48		
R3:48		
R4:48		

several leaves ground together and stored at -80oC; an aliquot was received f

```

Metabolites.Order                                Metabolites.File.Name
2          : 2                                : 80
3          : 2          1019Cabernet Volos_6_12_WS1.D: 1
4          : 2          1019Cabernet Volos_6_12_WS2.D: 1
5          : 2          1019Cabernet Volos_6_12_WW1.D: 1
6          : 2          1019Cabernet Volos_6_12_WW2.D: 1
(Other):180          1019Cabernet Volos_6_21_WS1.D: 1
NA's      : 80          (Other)                :185

          Metabolites.File Transcripts.ID
          : 80                :190
Cabernet Volos08_07WS: 4      C1_S1 : 1
Cabernet Volos08_07WW: 4      C1_S2 : 1
Cabernet Volos08_08WS: 4      C1_S3 : 1
Cabernet Volos08_08WW: 4      C1_S4 : 1
Cabernet Volos18_07WS: 4      C1_W1 : 1
(Other)                :170      (Other): 75

> dim(phdata)
[1] 270  21

> names(phdata)
[1] "ID"                "Variety"
[3] "Date"              "variety"
[5] "year"              "day"
[7] "treat"             "rep"
[9] "project.name"      "species"
[11] "plant.name"        "tissue"
[13] "health.status"     "plant.number"
[15] "growth.location"   "growth.conditions"
[17] "sampling"          "Metabolites.Order"
[19] "Metabolites.File.Name" "Metabolites.File"
[21] "Transcripts.ID"

```

3.2 Declare factor types

In 2018, day 11 is present only for C and day 10 only for F. The two day points coincide and are changed to a common value 11.

```

> for(yr in levels(phdata$year)){
+   cat("\n\nYear:", yr, "\n")
+   print(
+     with(phdata[phdata$year==yr, ], ftable(treat, variety, factor(day)))
+   )
+ }
> phdata[phdata$day==10, "day"] <- 11

```

Factors

```

> factors <- colnames(phdata)[4:8]
> factors

[1] "variety" "year"      "day"      "treat"    "rep"

> for (varname in factors)
+ phdata[,varname] <- factor(phdata[,varname])
> #
> # Change the order of levels for treatment
> phdata$treat <- factor(phdata$treat, levels=c("WW", "WS"))
> str(phdata[,factors])

'data.frame':      270 obs. of  5 variables:
 $ variety: Factor w/ 2 levels "C","F": 1 1 1 1 1 1 1 1 1 1 ...
 $ year   : Factor w/ 2 levels "18","19": 1 1 1 1 1 1 1 1 1 1 ...
 $ day    : Factor w/ 26 levels "3","11","14",..: 2 2 2 2 2 2 2 2 2 4 4 ...
 $ treat  : Factor w/ 2 levels "WW","WS": 2 2 2 2 1 1 1 1 2 2 ...
 $ rep    : Factor w/ 4 levels "1","2","3","4": 1 2 3 4 1 2 3 4 1 2 ...

```

Date of sampling might be useful as well

```
> library(lubridate)
```

```
Warning: package 'lubridate' was built under R version 4.0.3
```

```
Attaching package: 'lubridate'
```

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

```
intersect, setdiff, union
```

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

```
date, intersect, setdiff, union
```

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

```
Error in h(simpleError(msg, call)): error in evaluating the argument 'x' in se
```

```
> table(data.frame(pdata$date, "Count"=1))
```

```
Error in data.frame(pdata$date, Count = 1): object 'pdata' not found
```

3.3 Select samples

Check for assay specific sample selection column (assay name)

```
> .aName
[1] "_A_01_Desc-R"
> selectId <- substr(gsub("-", ".", .aName), 2, nchar(.aName))
> selectId <- .vzorci

Error in eval(expr, envir, enclos): object '.vzorci' not found
> selectId
[1] "A_01_Desc.R"
> #
> if(selectId %in% names(phdata)){
+ pdata <- phdata[!is.na(phdata[,selectId]),]
+ cat("Sample selection column found (", selectId, ")\n",
+ nrow(pdata), "samples will be used.\n")
+ } else {
+ pdata <- phdata
+ cat("No sample selection column found,\n",
+     nrow(pdata), "samples will be used.\n")
+ }
No sample selection column found,
  270 samples will be used.
> dim(pdata)
[1] 270  21
```

Table of sample conditions

```
> head(pdata[, factors])
```

	variety	year	day	treat	rep
C18_11d_WS1	C	18	11	WS	1
C18_11d_WS2	C	18	11	WS	2
C18_11d_WS3	C	18	11	WS	3
C18_11d_WS4	C	18	11	WS	4
C18_11d_WW1	C	18	11	WW	1
C18_11d_WW2	C	18	11	WW	2

```
> for(yr in levels(pdata$year)){
+ cat("\n\nYear: ", yr, "\n")
+ print(
+ with(pdata[pdata$year==yr, ], ftable(treat, variety, factor(day)))
+ )
+ }
```

Year: 18

		3	11	14	20	28	33	34	39	45	49	52	60	61	67
treat	variety														
WW	C	1	4	1	5	1	1	4	1	1	4	1	1	4	5
	F	1	4	1	5	1	1	4	1	1	4	1	1	4	5
WS	C	1	4	1	5	1	1	4	1	1	4	1	1	4	5
	F	1	4	1	5	1	1	4	1	1	4	1	1	4	5

Year: 19

		14	22	34	38	43	44	47	48	49	55	56	63	65	69	76
treat	variety															
WW	C	1	5	5	1	1	4	0	0	4	4	1	1	4	1	1
	F	1	5	5	1	1	4	4	1	0	4	1	1	4	1	1
WS	C	1	5	5	1	1	4	0	0	4	4	1	1	4	1	1
	F	1	5	5	1	1	4	4	1	0	4	1	1	4	1	1

> my.summary(pdata)

ID	Variety	Date	variety	
C18_11d_WS1: 1	Cabernet Volos:134	21.06.2018: 20	C:134	
C18_11d_WS2: 1	Fleurtai :136	26.06.2019: 20	F:136	
C18_11d_WS3: 1		7.08.2018 : 20		
C18_11d_WS4: 1		8.07.2019 : 20		
C18_11d_WW1: 1		1.08.2018 : 16		
C18_11d_WW2: 1		18.07.2019: 16		
(Other) :264		(Other) :158		
year	day	treat	rep	project.name
18:136	34 : 36	WW:135	1 :48	EnViros:270
19:134	49 : 24	WS:135	2 :48	
	20 : 20		3 :48	
	22 : 20		4 :48	
	67 : 20		NA's:78	
	11 : 16			
	(Other):134			
species	plant.name	tissue	health.status	
Vitis vinifera:270	grapevine:270	: 78	water stress:134	
		leaf:192	well watered:136	

plant.number	growth.location	growth.conditions
:78	Udine:270	outside:270
R1:48		
R2:48		
R3:48		
R4:48		

several leaves ground together and stored at -80°C ; an aliquot was received f

```

Metabolites.Order                      Metabolites.File.Name
2      : 2                               : 80
3      : 2      1019Cabernet Volos_6_12_WS1.D: 1
4      : 2      1019Cabernet Volos_6_12_WS2.D: 1
5      : 2      1019Cabernet Volos_6_12_WW1.D: 1
6      : 2      1019Cabernet Volos_6_12_WW2.D: 1
(Other):180      1019Cabernet Volos_6_21_WS1.D: 1
NA's   : 80      (Other)                  :185

      Metabolites.File Transcripts.ID
      : 80                  :190
Cabernet Volos08_07WS: 4      C1_S1      : 1
Cabernet Volos08_07WW: 4      C1_S2      : 1
Cabernet Volos08_08WS: 4      C1_S3      : 1
Cabernet Volos08_08WW: 4      C1_S4      : 1
Cabernet Volos18_07WS: 4      C1_W1      : 1
(Other)              :170      (Other) : 75

```

For separate yearly analyses, it will be handy to have two, separate phenodata objects.

```

> dim(pdata)
[1] 270 21
> table(pdata$year)

18 19
136 134
> pdata18 <- pdata[pdata$year==18,]
> dim(pdata18)
[1] 136 21
> pdata18[1:5,1:6]
      ID      Variety      Date variety year day
C18_11d_WS1 C18_11d_WS1 Cabernet Volos 12.06.2018      C    18 11
C18_11d_WS2 C18_11d_WS2 Cabernet Volos 12.06.2018      C    18 11
C18_11d_WS3 C18_11d_WS3 Cabernet Volos 12.06.2018      C    18 11
C18_11d_WS4 C18_11d_WS4 Cabernet Volos 12.06.2018      C    18 11
C18_11d_WW1 C18_11d_WW1 Cabernet Volos 12.06.2018      C    18 11
> #
> pdata19 <- pdata[pdata$year==19,]
> dim(pdata19)
[1] 134 21
> pdata19[1:5,1:6]
      ID      Variety      Date variety year day
C19_22d_WS1 C19_22d_WS1 Cabernet Volos 26.06.2019      C    19 22
C19_22d_WS2 C19_22d_WS2 Cabernet Volos 26.06.2019      C    19 22
C19_22d_WS3 C19_22d_WS3 Cabernet Volos 26.06.2019      C    19 22
C19_22d_WS4 C19_22d_WS4 Cabernet Volos 26.06.2019      C    19 22
C19_22d_WW1 C19_22d_WW1 Cabernet Volos 26.06.2019      C    19 22

```


3.4 Featuredata

```
> (ffn <- getDesc(.adesc, "Featuredata"))
[1] "Transcripts1819-02.txt"
> if(ffn=="") {
+   cat("No feature data declared in the assay metadata file.\\\\"")
+   fdata <- NULL
+ }

> fdata <- read.table(file.path(.iroot, ffn)
+   , sep = "\t"
+   , header = TRUE
+   , na.strings = c("", "-", "NA")
+   , stringsAsFactors = FALSE
+   , quote = "\"",
+   #   , row.names = 1
+   )
> if(interactive()) my.summary(fdata)
> #"
```

Some genes are listed more than once. Is it OK? Column geneID can not be used as row names.

```
> tbl <- table(fdata$geneID)
> tbl[tbl>3]
named integer(0)
> tbl[tbl==3]
```

```
Vitvi01g01443 Vitvi03g00845 Vitvi04g02157 Vitvi05g01641 Vitvi06g01689
      3          3          3          3          3
Vitvi07g01861 Vitvi08g01514 Vitvi08g01692 Vitvi08g02189 Vitvi12g01199
      3          3          3          3          3
Vitvi16g00114 Vitvi17g01011 Vitvi19g00061 Vitvi19g01931 Vitvi19g01936
      3          3          3          3          3
Vitvi19g01964
      3
```

```
> tbl[tbl==2]
```

```
Vitvi00g00711 Vitvi00g00822 Vitvi00g00983 Vitvi00g01149 Vitvi00g01320
      2          2          2          2          2
Vitvi00g01329 Vitvi00g01996 Vitvi00g01999 Vitvi00g02041 Vitvi01g00036
      2          2          2          2          2
Vitvi01g00137 Vitvi01g00165 Vitvi01g00274 Vitvi01g00301 Vitvi01g00348
      2          2          2          2          2
Vitvi01g00373 Vitvi01g00397 Vitvi01g00398 Vitvi01g00417 Vitvi01g00478
      2          2          2          2          2
Vitvi01g00553 Vitvi01g00625 Vitvi01g00681 Vitvi01g00696 Vitvi01g00793
      2          2          2          2          2
Vitvi01g00814 Vitvi01g00828 Vitvi01g00861 Vitvi01g00885 Vitvi01g00993
      2          2          2          2          2
Vitvi01g01351 Vitvi01g01436 Vitvi01g01632 Vitvi01g01645 Vitvi01g01671
      2          2          2          2          2
```

Vitvi01g01773	Vitvi01g01814	Vitvi01g01956	Vitvi01g01982	Vitvi01g02258
2	2	2	2	2
Vitvi01g02269	Vitvi02g00007	Vitvi02g00023	Vitvi02g00085	Vitvi02g00187
2	2	2	2	2
Vitvi02g00220	Vitvi02g00222	Vitvi02g00278	Vitvi02g00380	Vitvi02g00387
2	2	2	2	2
Vitvi02g00485	Vitvi02g00561	Vitvi02g00739	Vitvi02g01143	Vitvi02g01273
2	2	2	2	2
Vitvi02g01365	Vitvi02g01416	Vitvi02g01458	Vitvi02g01751	Vitvi03g00042
2	2	2	2	2
Vitvi03g00059	Vitvi03g00097	Vitvi03g00121	Vitvi03g00167	Vitvi03g00273
2	2	2	2	2
Vitvi03g00278	Vitvi03g00375	Vitvi03g00432	Vitvi03g00442	Vitvi03g00464
2	2	2	2	2
Vitvi03g00521	Vitvi03g00532	Vitvi03g00537	Vitvi03g00541	Vitvi03g00757
2	2	2	2	2
Vitvi03g00785	Vitvi03g00804	Vitvi03g00855	Vitvi03g00900	Vitvi03g00936
2	2	2	2	2
Vitvi03g01059	Vitvi03g01228	Vitvi03g01320	Vitvi04g00092	Vitvi04g00112
2	2	2	2	2
Vitvi04g00113	Vitvi04g00127	Vitvi04g00199	Vitvi04g00205	Vitvi04g00227
2	2	2	2	2
Vitvi04g00279	Vitvi04g00314	Vitvi04g00371	Vitvi04g00450	Vitvi04g00483
2	2	2	2	2
Vitvi04g00520	Vitvi04g00888	Vitvi04g01149	Vitvi04g01257	Vitvi04g01359
2	2	2	2	2
Vitvi04g01462	Vitvi04g01469	Vitvi04g01474	Vitvi04g01560	Vitvi04g01624
2	2	2	2	2
Vitvi04g01633	Vitvi04g01668	Vitvi04g01671	Vitvi04g01694	Vitvi04g01695
2	2	2	2	2
Vitvi04g01709	Vitvi04g01746	Vitvi04g01763	Vitvi04g02022	Vitvi04g02037
2	2	2	2	2
Vitvi04g02038	Vitvi04g02099	Vitvi04g02114	Vitvi04g02185	Vitvi05g00115
2	2	2	2	2
Vitvi05g00132	Vitvi05g00144	Vitvi05g00210	Vitvi05g00239	Vitvi05g00390
2	2	2	2	2
Vitvi05g00409	Vitvi05g00418	Vitvi05g00436	Vitvi05g00443	Vitvi05g00503
2	2	2	2	2
Vitvi05g00541	Vitvi05g00556	Vitvi05g00652	Vitvi05g00737	Vitvi05g00790
2	2	2	2	2
Vitvi05g00953	Vitvi05g00991	Vitvi05g01068	Vitvi05g01130	Vitvi05g01255
2	2	2	2	2
Vitvi05g01369	Vitvi05g01562	Vitvi05g01570	Vitvi05g01603	Vitvi05g01634
2	2	2	2	2
Vitvi05g02135	Vitvi06g00022	Vitvi06g00089	Vitvi06g00200	Vitvi06g00201
2	2	2	2	2
Vitvi06g00212	Vitvi06g00213	Vitvi06g00215	Vitvi06g00243	Vitvi06g00259
2	2	2	2	2
Vitvi06g00319	Vitvi06g00337	Vitvi06g00356	Vitvi06g00365	Vitvi06g00414
2	2	2	2	2
Vitvi06g00439	Vitvi06g00443	Vitvi06g00454	Vitvi06g00472	Vitvi06g00512
2	2	2	2	2
Vitvi06g00525	Vitvi06g00533	Vitvi06g00652	Vitvi06g00668	Vitvi06g00701

2	2	2	2	2
Vitvi06g00789	Vitvi06g01242	Vitvi06g01279	Vitvi06g01469	Vitvi06g01486
2	2	2	2	2
Vitvi06g01604	Vitvi06g01690	Vitvi06g01693	Vitvi06g01718	Vitvi06g01739
2	2	2	2	2
Vitvi06g01836	Vitvi07g00067	Vitvi07g00078	Vitvi07g00080	Vitvi07g00205
2	2	2	2	2
Vitvi07g00316	Vitvi07g00406	Vitvi07g00416	Vitvi07g00464	Vitvi07g00594
2	2	2	2	2
Vitvi07g00630	Vitvi07g00636	Vitvi07g00708	Vitvi07g00908	Vitvi07g00916
2	2	2	2	2
Vitvi07g01028	Vitvi07g01205	Vitvi07g01306	Vitvi07g01340	Vitvi07g01364
2	2	2	2	2
Vitvi07g01402	Vitvi07g01441	Vitvi07g01524	Vitvi07g01569	Vitvi07g01737
2	2	2	2	2
Vitvi07g01749	Vitvi07g01817	Vitvi07g01903	Vitvi07g01937	Vitvi07g01973
2	2	2	2	2
Vitvi07g01983	Vitvi07g01996	Vitvi07g02049	Vitvi07g02102	Vitvi07g02119
2	2	2	2	2
Vitvi07g02123	Vitvi07g02135	Vitvi07g02302	Vitvi07g02394	Vitvi07g02412
2	2	2	2	2
Vitvi07g02447	Vitvi07g02491	Vitvi07g02523	Vitvi07g02528	Vitvi07g02557
2	2	2	2	2
Vitvi07g02631	Vitvi07g02863	Vitvi07g03034	Vitvi07g03040	Vitvi07g03070
2	2	2	2	2
Vitvi07g03110	Vitvi08g00215	Vitvi08g00703	Vitvi08g00740	Vitvi08g00744
2	2	2	2	2
Vitvi08g00799	Vitvi08g00853	Vitvi08g00935	Vitvi08g00961	Vitvi08g00981
2	2	2	2	2
Vitvi08g00983	Vitvi08g00999	Vitvi08g01042	Vitvi08g01082	Vitvi08g01108
2	2	2	2	2
Vitvi08g01206	Vitvi08g01241	Vitvi08g01243	Vitvi08g01302	Vitvi08g01346
2	2	2	2	2
Vitvi08g01376	Vitvi08g01395	Vitvi08g01417	Vitvi08g01506	Vitvi08g01513
2	2	2	2	2
Vitvi08g01519	Vitvi08g01766	Vitvi08g01833	Vitvi08g01864	Vitvi08g01884
2	2	2	2	2
Vitvi08g01931	Vitvi08g01959	Vitvi08g02249	Vitvi08g02367	Vitvi08g02413
2	2	2	2	2
Vitvi09g00067	Vitvi09g00156	Vitvi09g00233	Vitvi09g00239	Vitvi09g00243
2	2	2	2	2
Vitvi09g00249	Vitvi09g00253	Vitvi09g00258	Vitvi09g00277	Vitvi09g00292
2	2	2	2	2
Vitvi09g00297	Vitvi09g00446	Vitvi09g00490	Vitvi09g00653	Vitvi09g00675
2	2	2	2	2
Vitvi09g00816	Vitvi09g00861	Vitvi09g01320	Vitvi09g01500	Vitvi09g01555
2	2	2	2	2
Vitvi09g01556	Vitvi09g01557	Vitvi09g01559	Vitvi09g01930	Vitvi09g01933
2	2	2	2	2
Vitvi09g02012	Vitvi10g00078	Vitvi10g00087	Vitvi10g00125	Vitvi10g00154
2	2	2	2	2
Vitvi10g00219	Vitvi10g00290	Vitvi10g00303	Vitvi10g00316	Vitvi10g00317
2	2	2	2	2

Vitvi10g00336	Vitvi10g00365	Vitvi10g00457	Vitvi10g00554	Vitvi10g00582
2	2	2	2	2
Vitvi10g00605	Vitvi10g00635	Vitvi10g00662	Vitvi10g00663	Vitvi10g00784
2	2	2	2	2
Vitvi10g01029	Vitvi10g01098	Vitvi10g02139	Vitvi10g02141	Vitvi10g02143
2	2	2	2	2
Vitvi10g02151	Vitvi10g02152	Vitvi10g02155	Vitvi10g02157	Vitvi10g02322
2	2	2	2	2
Vitvi10g02324	Vitvi10g02368	Vitvi10g02370	Vitvi10g02408	Vitvi11g00001
2	2	2	2	2
Vitvi11g00068	Vitvi11g00102	Vitvi11g00136	Vitvi11g00137	Vitvi11g00198
2	2	2	2	2
Vitvi11g00270	Vitvi11g00339	Vitvi11g00360	Vitvi11g00480	Vitvi11g00517
2	2	2	2	2
Vitvi11g00597	Vitvi11g00614	Vitvi11g00692	Vitvi11g00724	Vitvi11g00812
2	2	2	2	2
Vitvi11g00865	Vitvi11g01141	Vitvi11g01176	Vitvi12g00021	Vitvi12g00032
2	2	2	2	2
Vitvi12g00089	Vitvi12g00121	Vitvi12g00157	Vitvi12g00220	Vitvi12g00229
2	2	2	2	2
Vitvi12g00284	Vitvi12g00596	Vitvi12g00598	Vitvi12g00606	Vitvi12g00615
2	2	2	2	2
Vitvi12g00628	Vitvi12g00646	Vitvi12g00689	Vitvi12g00691	Vitvi12g00694
2	2	2	2	2
Vitvi12g00837	Vitvi12g01277	Vitvi12g01467	Vitvi12g01780	Vitvi12g01840
2	2	2	2	2
Vitvi12g01863	Vitvi12g01897	Vitvi12g01952	Vitvi12g02074	Vitvi12g02434
2	2	2	2	2
Vitvi12g02435	Vitvi12g02440	Vitvi13g00019	Vitvi13g00031	Vitvi13g00053
2	2	2	2	2
Vitvi13g00095	Vitvi13g00096	Vitvi13g00111	Vitvi13g00149	Vitvi13g00288
2	2	2	2	2
Vitvi13g00328	Vitvi13g00332	Vitvi13g00334	Vitvi13g00344	Vitvi13g00510
2	2	2	2	2
Vitvi13g00627	Vitvi13g00628	Vitvi13g00636	Vitvi13g00637	Vitvi13g00700
2	2	2	2	2
Vitvi13g00744	Vitvi13g01070	Vitvi13g01077	Vitvi13g01233	Vitvi13g01272
2	2	2	2	2
Vitvi13g01327	Vitvi13g01364	Vitvi13g01839	Vitvi13g01854	Vitvi13g02272
2	2	2	2	2
Vitvi14g00020	Vitvi14g00025	Vitvi14g00053	Vitvi14g00160	Vitvi14g00185
2	2	2	2	2
Vitvi14g00237	Vitvi14g00281	Vitvi14g00327	Vitvi14g00380	Vitvi14g00383
2	2	2	2	2
Vitvi14g00397	Vitvi14g00404	Vitvi14g00439	Vitvi14g00484	Vitvi14g00535
2	2	2	2	2
Vitvi14g00562	Vitvi14g00627	Vitvi14g00654	Vitvi14g00658	Vitvi14g00763
2	2	2	2	2
Vitvi14g00841	Vitvi14g01061	Vitvi14g01128	Vitvi14g01280	Vitvi14g01294
2	2	2	2	2
Vitvi14g01321	Vitvi14g01472	Vitvi14g01520	Vitvi14g01596	Vitvi14g01678
2	2	2	2	2
Vitvi14g01746	Vitvi14g01758	Vitvi14g01809	Vitvi14g01983	Vitvi14g02002

2	2	2	2	2
Vitvi14g02027	Vitvi14g02478	Vitvi14g02644	Vitvi14g02869	Vitvi15g00225
2	2	2	2	2
Vitvi15g00526	Vitvi15g00563	Vitvi15g00690	Vitvi15g00827	Vitvi15g00840
2	2	2	2	2
Vitvi15g00878	Vitvi15g00908	Vitvi15g00974	Vitvi15g01077	Vitvi15g01403
2	2	2	2	2
Vitvi15g01468	Vitvi15g01491	Vitvi15g01537	Vitvi15g01539	Vitvi16g00018
2	2	2	2	2
Vitvi16g00048	Vitvi16g00095	Vitvi16g00461	Vitvi16g00796	Vitvi16g00857
2	2	2	2	2
Vitvi16g00935	Vitvi16g00949	Vitvi16g00982	Vitvi16g01025	Vitvi16g01083
2	2	2	2	2
Vitvi16g01089	Vitvi16g01211	Vitvi16g01323	Vitvi16g01326	Vitvi16g01348
2	2	2	2	2
Vitvi16g01358	Vitvi16g01371	Vitvi16g01375	Vitvi16g01391	Vitvi17g00038
2	2	2	2	2
Vitvi17g00161	Vitvi17g00210	Vitvi17g00222	Vitvi17g00225	Vitvi17g00240
2	2	2	2	2
Vitvi17g00253	Vitvi17g00263	Vitvi17g00277	Vitvi17g00287	Vitvi17g00299
2	2	2	2	2
Vitvi17g00428	Vitvi17g00468	Vitvi17g00519	Vitvi17g00548	Vitvi17g00603
2	2	2	2	2
Vitvi17g00614	Vitvi17g00869	Vitvi17g00905	Vitvi17g01148	Vitvi17g01183
2	2	2	2	2
Vitvi17g01348	Vitvi17g01399	Vitvi17g01407	Vitvi18g00056	Vitvi18g00132
2	2	2	2	2
Vitvi18g00177	Vitvi18g00234	Vitvi18g00310	Vitvi18g00358	Vitvi18g00444
2	2	2	2	2
Vitvi18g00507	Vitvi18g00517	Vitvi18g00534	Vitvi18g00579	Vitvi18g00743
2	2	2	2	2
Vitvi18g00762	Vitvi18g00784	Vitvi18g00838	Vitvi18g00909	Vitvi18g00960
2	2	2	2	2
Vitvi18g00966	Vitvi18g01002	Vitvi18g01004	Vitvi18g01019	Vitvi18g01095
2	2	2	2	2
Vitvi18g01103	Vitvi18g01223	Vitvi18g01226	Vitvi18g01242	Vitvi18g01299
2	2	2	2	2
Vitvi18g01309	Vitvi18g01430	Vitvi18g01436	Vitvi18g01634	Vitvi18g01677
2	2	2	2	2
Vitvi18g02066	Vitvi18g02228	Vitvi18g02237	Vitvi18g02378	Vitvi18g03244
2	2	2	2	2
Vitvi19g00015	Vitvi19g00020	Vitvi19g00094	Vitvi19g00138	Vitvi19g00155
2	2	2	2	2
Vitvi19g00197	Vitvi19g00226	Vitvi19g00337	Vitvi19g00339	Vitvi19g00341
2	2	2	2	2
Vitvi19g00353	Vitvi19g00421	Vitvi19g00531	Vitvi19g00539	Vitvi19g00552
2	2	2	2	2
Vitvi19g00602	Vitvi19g00612	Vitvi19g00621	Vitvi19g00675	Vitvi19g00706
2	2	2	2	2
Vitvi19g00745	Vitvi19g00782	Vitvi19g00904	Vitvi19g00928	Vitvi19g01352
2	2	2	2	2
Vitvi19g01464	Vitvi19g01552	Vitvi19g01690	Vitvi19g01692	Vitvi19g01725
2	2	2	2	2

Vitvi19g01864	Vitvi19g01933	Vitvi19g01937	Vitvi19g01940	Vitvi19g01952
2	2	2	2	2
Vitvi19g01957	Vitvi19g01959	Vitvi19g01963	Vitvi19g01965	Vitvi19g01966
2	2	2	2	2
Vitvi19g01969	Vitvi19g01970	Vitvi19g02001	Vitvi19g02292	
2	2	2	2	

A glimpse into feature data (or NULL if nonexistent)

```
> fdata[1:6,]
```

	YEAR	geneID	BINCODE	NAME
1	2018	Vitvi15g01736	26.9	misc.glutathione S transferases
2	2018	Vitvi07g02832	35.2	not assigned.unknown
3	2018	Vitvi07g02830	35.2	not assigned.unknown
4	2018	Vitvi07g02812	35.2	not assigned.unknown
5	2018	Vitvi07g02811	35.2	not assigned.unknown
6	2018	Vitvi09g02033	35.2	not assigned.unknown

```
1          glutathione S-transferase tau 7 | Chr2:12618111-12618871
2 Disease resistance protein (TIR-NBS-LRR class) family | Chr4:7197325-7201393
3
4
5
```

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

```
> cat(gsub("\\| ", " |\\|\\n\\|\\t", fdata$DESCRIPTION[1:6]), sep="\n\n")
```

```
glutathione S-transferase tau 7 |
      Chr2:12618111-12618871 REVERSE LENGTH=227 |
      201606
```

```
Disease resistance protein (TIR-NBS-LRR class) family |
      Chr4:7197325-7201393 REVERSE LENGTH=1219 |
      201606
```

```
NA
```

```
Tir-nbs-lrr, resistance protein
```

```
NA
```

```
Disease resistance protein (CC-NBS-LRR class) family |
      Chr1:4145374-4147680 FORWARD LENGTH=768 |
      201606
```

```
> fd <- (apply(fdata[1:6, c(2:5)], 1, paste, collapse="\n\t"))
```

```
> cat(gsub("\\| ", " |\\|\\n\\|\\t", fd[1:6]), sep="\n\n")
```

```
Vitvi15g01736
      26.9
      misc.glutathione S transferases
      glutathione S-transferase tau 7 |
      Chr2:12618111-12618871 REVERSE LENGTH=227 |
      201606
```

```
Vitvi07g02832
      35.2
```

```

not assigned.unknown
Disease resistance protein (TIR-NBS-LRR class) family |
Chr4:7197325-7201393 REVERSE LENGTH=1219 |
201606

Vitvi07g02830
35.2
not assigned.unknown
NA

Vitvi07g02812
35.2
not assigned.unknown
Tir-nbs-lrr, resistance protein

Vitvi07g02811
35.2
not assigned.unknown
NA

Vitvi09g02033
35.2
not assigned.unknown
Disease resistance protein (CC-NBS-LRR class) family |
Chr1:4145374-4147680 FORWARD LENGTH=768 |
201606

> cat.feature <- function(x,...) {
+ #x <- t(apply(x,1, FUN=function(x) paste(names(x),x,sep=":\t") ))
+ #cat(x)
+ fd <- (apply(x,1,paste,collapse="\n\t"))
+ cat(gsub(" \\| ", " |\\n\\|\\t", fd), sep="\n\n")
+ }
> cat.feature(fdata[1,2:5])
Vitvi15g01736
26.9
misc.glutathione S transferases
glutathione S-transferase tau 7 |
Chr2:12618111-12618871 REVERSE LENGTH=227 |
201606
> cat.feature(fdata[1:2,2:5])
Vitvi15g01736
26.9
misc.glutathione S transferases
glutathione S-transferase tau 7 |
Chr2:12618111-12618871 REVERSE LENGTH=227 |
201606

Vitvi07g02832
35.2
not assigned.unknown
Disease resistance protein (TIR-NBS-LRR class) family |
Chr4:7197325-7201393 REVERSE LENGTH=1219 |
201606

```

3.5 Transcripts measurements

Normalised transcript measurements for each year are available in two separate files. The first few lines contain factor values and are commented out (by a hash). The first effective line is the table header line with sample ids.

3.5.1 Normalized values

Data for year 2018:

```
> (t18fn <- getDesc(.adesc, "Transcript data 18"))
[1] "/input/Transcripts 2018.txt"
> td <- read.table(file.path(.aroot, t18fn),
+   header = TRUE,
+   sep = "\t",
+   row.names = 1
+   )
> head(td)
```

	C18_11d_WS1	C18_11d_WS2	C18_11d_WS3	C18_11d_WS4
Vitvi15g01736	4.6646023	4.109897	4.4482203	4.013955
Vitvi07g02832	-2.4786650	-1.601359	-1.4274193	-2.066419
Vitvi07g02830	-1.8506337	-2.218030	-1.0648492	-1.580992
Vitvi07g02812	-0.5805446	-1.266940	-0.3278837	-1.019113
Vitvi07g02811	2.2762225	1.823447	1.9550503	1.648742
Vitvi09g02033	-1.6901691	-2.218030	-2.6498117	-1.449747
	C18_11d_WW1	C18_11d_WW2	C18_11d_WW3	C18_11d_WW4
Vitvi15g01736	4.717536	4.154237	4.475261	4.466465
Vitvi07g02832	-2.608485	-1.801183	-1.886474	-3.583384
Vitvi07g02830	-1.544354	-1.405255	-1.755229	-1.381750
Vitvi07g02812	-0.858463	-0.434401	-1.234397	-1.047331
Vitvi07g02811	2.086902	2.105707	2.134837	1.908469
Vitvi09g02033	-2.608485	-1.961648	-3.108866	-4.320350
	C18_34d_WS1	C18_34d_WS2	C18_34d_WS3	C18_34d_WS4
Vitvi15g01736	4.400333	4.641164	4.4191231	4.534438
Vitvi07g02832	-5.683146	-2.452000	-4.4274120	-1.876949
Vitvi07g02830	-2.513221	-2.452000	-4.4274120	-2.263972
Vitvi07g02812	-2.875791	-2.693008	-2.5529429	-3.157057
Vitvi07g02811	1.414886	1.409803	0.3970164	1.273993
Vitvi09g02033	-2.513221	-3.345084	-2.1054839	-1.716484
	C18_34d_WW1	C18_34d_WW2	C18_34d_WW3	C18_34d_WW4
Vitvi15g01736	4.924801	5.085690	5.3397350	5.263629
Vitvi07g02832	-2.827859	-3.130016	-4.6322874	-3.196388
Vitvi07g02830	-3.190429	-1.545054	-2.1297871	-3.196388
Vitvi07g02812	-2.827859	-1.182484	-3.4098950	-2.303303
Vitvi07g02811	1.517916	1.357250	0.9626591	1.344985
Vitvi09g02033	-4.412821	-3.130016	-2.3103594	-4.418780
	C18_67d_WS1	C18_67d_WS2	C18_67d_WS3	C18_67d_WS4
Vitvi15g01736	2.05871733	2.2895026	2.9234830	2.575657
Vitvi07g02832	-5.85417200	-4.4786818	-4.4659691	-2.468738
Vitvi07g02830	-2.15373228	-3.2562893	-3.7290035	-2.709746
Vitvi07g02812	-1.21031581	-2.3632045	-2.3504919	-2.999252
Vitvi07g02811	0.02847105	0.5362686	0.9824914	1.231702
Vitvi09g02033	-4.26920950	-3.7417162	-2.5915000	-3.847249

	C18_67d_WW1	C18_67d_WW2	C18_67d_WW3	C18_67d_WW4
Vitvi15g01736	3.891121	3.040087	4.216897	3.763086
Vitvi07g02832	-2.726982	-4.610965	-2.436913	-3.355855
Vitvi07g02830	-2.726982	-3.873999	-1.493496	-2.075747
Vitvi07g02812	-1.672534	-3.388572	-2.230462	-2.462770
Vitvi07g02811	1.436764	1.552266	1.811015	1.352490
Vitvi09g02033	-2.520531	-2.736495	-3.815424	-2.993285
	F18_10d_WS1	F18_10d_WS2	F18_10d_WS3	F18_10d_WS4
Vitvi15g01736	4.8591409	4.8669435	4.9805904	4.9453953
Vitvi07g02832	2.8881443	2.7032394	2.2757651	2.0553154
Vitvi07g02830	2.8426117	2.4130023	2.2135368	2.0169691
Vitvi07g02812	0.8222302	0.9363895	0.7209384	0.3104447
Vitvi07g02811	3.5853480	3.5007015	3.2965509	3.2141610
Vitvi09g02033	1.0793880	1.0850336	0.6285743	0.8579324
	F18_10d_WW1	F18_10d_WW2	F18_10d_WW3	F18_10d_WW4
Vitvi15g01736	5.705006	4.619238	4.808548	5.276124
Vitvi07g02832	2.747538	3.349854	2.537311	2.621336
Vitvi07g02830	2.287722	3.464855	1.989824	2.321031
Vitvi07g02812	1.073767	1.384521	1.472076	1.016877
Vitvi07g02811	3.818074	4.000053	3.198197	3.501954
Vitvi09g02033	1.073767	1.566041	1.237985	1.268416
	F18_34d_WS1	F18_34d_WS2	F18_34d_WS3	F18_34d_WS4
Vitvi15g01736	4.0647184	3.8504580	5.1418322	4.6269091
Vitvi07g02832	2.2592790	2.1761360	2.3686660	1.2127920
Vitvi07g02830	2.1186455	1.9359657	2.6356368	1.5129655
Vitvi07g02812	0.4316833	-0.6220298	-0.5985972	-0.2055206
Vitvi07g02811	2.9490282	2.7595613	3.1300210	2.4602029
Vitvi09g02033	1.5459405	1.3699329	1.4288835	1.4477479
	F18_34d_WW1	F18_34d_WW2	F18_34d_WW3	F18_34d_WW4
Vitvi15g01736	4.0961725	4.80222138	4.3291524	4.4419027
Vitvi07g02832	1.8816574	1.82887526	1.7895023	1.6490200
Vitvi07g02830	2.1414534	1.62149541	2.1153419	2.1541121
Vitvi07g02812	0.1031253	-0.09471163	0.3053805	0.2855497
Vitvi07g02811	3.0025984	2.73213947	2.8750439	3.0458304
Vitvi09g02033	1.7460934	1.45938991	2.0072243	1.2444445
	F18_67d_WS1	F18_67d_WS2	F18_67d_WS3	F18_67d_WS4
Vitvi15g01736	1.5831276	1.7408584	2.97840555	4.1664059
Vitvi07g02832	1.3093668	1.9241330	2.01456521	2.9813855
Vitvi07g02830	0.8382242	1.4203666	2.18501915	2.8731326
Vitvi07g02812	0.1974739	0.4558154	-0.03878421	-0.0111843
Vitvi07g02811	1.8823168	2.5341865	2.65708760	2.9461961
Vitvi09g02033	1.6066824	1.5040245	1.25520700	0.9986635
	F18_67d_WW1	F18_67d_WW2	F18_67d_WW3	F18_67d_WW4
Vitvi15g01736	3.5580430	3.569471	4.4112089	4.3597440
Vitvi07g02832	2.5563386	2.180583	2.6637430	2.7538173
Vitvi07g02830	2.0265816	2.154972	2.7552617	2.3663511
Vitvi07g02812	0.6773148	0.106805	-0.2413317	-0.1063251
Vitvi07g02811	3.0678390	2.949349	2.9761917	2.9625700
Vitvi09g02033	1.7205680	1.541742	1.6527997	1.3320450

```
> dim(td)
```

```
[1] 16005    48
```

```
> t18 <- td
```

```
> (t19fn <- getDesc(.adesc, "Transcript data 19"))
```

```
[1] "/input/Transcripts 2019.txt"
```

```
> td <- read.table(file.path(.aroot, t19fn),
+   header = TRUE,
+   sep = "\t",
+   row.names = 1
+   )
> head(td)
```

	C19_22d_WS1	C19_22d_WS2	C19_22d_WS3	C19_22d_WS4
Vitvi15g01736	3.18	3.50	3.19	3.61
Vitvi07g02832	-5.05	-3.02	-0.80	-0.02
Vitvi07g02830	-5.05	-5.35	-2.39	-3.99
Vitvi07g02812	-1.35	-0.95	-0.15	0.26
Vitvi07g02811	2.09	2.29	2.34	2.63
Vitvi09g02033	-5.05	-3.76	-2.39	-2.76
	C19_22d_WW1	C19_22d_WW2	C19_22d_WW3	C19_22d_WW4
Vitvi15g01736	5.42	5.35	4.68	4.92
Vitvi07g02832	-1.36	-2.10	-1.15	-3.81
Vitvi07g02830	-2.28	-1.81	-2.07	-2.59
Vitvi07g02812	-1.36	0.16	-0.29	-0.75
Vitvi07g02811	2.85	3.16	3.09	2.89
Vitvi09g02033	-5.45	-3.68	-1.78	-3.81
	C19_44d_WS1	C19_44d_WS2	C19_44d_WS3	C19_44d_WS4
Vitvi15g01736	5.13	5.19	5.71	5.29
Vitvi07g02832	-3.13	-1.28	-3.18	-2.29
Vitvi07g02830	-3.87	-5.53	-5.50	-2.29
Vitvi07g02812	-0.10	-1.01	-0.29	-0.04
Vitvi07g02811	2.11	1.92	2.40	2.29
Vitvi09g02033	-3.87	-3.95	-2.69	-2.00
	C19_44d_WW1	C19_44d_WW2	C19_44d_WW3	C19_44d_WW4
Vitvi15g01736	6.19	5.62	5.62	6.19
Vitvi07g02832	-5.54	-5.31	-3.73	-1.81
Vitvi07g02830	-3.22	-5.31	-3.73	-2.05
Vitvi07g02812	-0.59	-0.45	-1.07	-0.55
Vitvi07g02811	2.44	2.13	2.08	2.26
Vitvi09g02033	-3.22	-3.72	-3.73	-3.18
	F19_22d_WS1	F19_22d_WS2	F19_22d_WS3	F19_22d_WS4
Vitvi15g01736	3.03	3.93	4.24	2.85
Vitvi07g02832	3.35	3.23	3.02	2.98
Vitvi07g02830	2.28	2.39	1.75	1.35
Vitvi07g02812	2.19	1.04	0.89	1.56
Vitvi07g02811	3.84	3.72	3.01	3.43
Vitvi09g02033	2.70	1.61	1.94	2.47
	F19_22d_WW1	F19_22d_WW2	F19_22d_WW3	F19_22d_WW4
Vitvi15g01736	5.00	4.97	4.47	5.51
Vitvi07g02832	3.18	3.04	2.81	3.05
Vitvi07g02830	2.59	2.07	1.81	2.20
Vitvi07g02812	1.72	1.08	1.42	1.35
Vitvi07g02811	3.79	3.43	3.24	3.33
Vitvi09g02033	2.24	1.90	2.08	1.25
	F19_44d_WS1	F19_44d_WS2	F19_44d_WS3	F19_44d_WS4
Vitvi15g01736	5.84	5.83	4.56	5.23

Vitvi07g02832	2.54	3.14	3.01	2.16
Vitvi07g02830	1.13	2.25	2.18	1.90
Vitvi07g02812	0.99	0.84	0.85	0.22
Vitvi07g02811	2.91	3.10	3.18	2.61
Vitvi09g02033	1.21	1.67	2.52	2.21
	F19_44d_WW1	F19_44d_WW2	F19_44d_WW3	F19_44d_WW4
Vitvi15g01736	5.44	6.13	5.96	6.16
Vitvi07g02832	3.84	3.05	3.89	4.02
Vitvi07g02830	2.74	2.79	2.90	2.88
Vitvi07g02812	1.03	0.93	1.49	1.29
Vitvi07g02811	3.32	2.89	3.35	3.26
Vitvi09g02033	1.99	1.14	1.65	1.29

```
> dim(td)
```

```
[1] 15562    32
```

```
> t19 <- td
```

```
> dim(t18)-dim(t19)
```

```
[1] 443  16
```

Data for year 2018 have more genes than data for year 2019.

```
> allNames <- unique(c(rownames(t18), rownames(t19)))
```

```
> length(allNames)
```

```
[1] 16325
```

```
> sum(allNames %in% rownames(t18))
```

```
[1] 16005
```

```
> sum(allNames %in% rownames(t19))
```

```
[1] 15562
```

```
> tbl <- table(gene.in.18=allNames %in% rownames(t18),
+              gene.in.19=allNames %in% rownames(t19))
> tbl
```

	gene.in.19	
gene.in.18	FALSE	TRUE
FALSE	0	320
TRUE	763	15242

We have complete yearly data on 15242 genes. At the meeting on Nov. 19 we decided to use only the genes in the intersection. This will allow us to use the combined set of data.

3.5.2 Keep genes in the intersection

```
> gene.keep <- (allNames %in% rownames(t18)) & (allNames %in% rownames(t19))
> sum(gene.keep)
[1] 15242
> t18 <- t18[allNames[gene.keep], ]
> t19 <- t19[allNames[gene.keep], ]
> all(rownames(t18) == rownames(t19))
[1] TRUE
> dim(t18)
[1] 15242    48
> dim(t19)
[1] 15242    32
```

Order rows of yearly phenodata according to the sequence of samples (columns) in the measurements.

Year 2018

```
> dim(pdata18)
[1] 136  21
> dim(t18)
[1] 15242    48
> pdata18 <- pdata18[colnames(t18), ]
> dim(pdata18)
[1] 48 21
> dim(t18)
[1] 15242    48
> pdata18[, 4:8]
```

	variety	year	day	treat	rep
C18_11d_WS1	C	18	11	WS	1
C18_11d_WS2	C	18	11	WS	2
C18_11d_WS3	C	18	11	WS	3
C18_11d_WS4	C	18	11	WS	4
C18_11d_WW1	C	18	11	WW	1
C18_11d_WW2	C	18	11	WW	2
C18_11d_WW3	C	18	11	WW	3
C18_11d_WW4	C	18	11	WW	4
C18_34d_WS1	C	18	34	WS	1
C18_34d_WS2	C	18	34	WS	2
C18_34d_WS3	C	18	34	WS	3
C18_34d_WS4	C	18	34	WS	4
C18_34d_WW1	C	18	34	WW	1
C18_34d_WW2	C	18	34	WW	2
C18_34d_WW3	C	18	34	WW	3
C18_34d_WW4	C	18	34	WW	4
C18_67d_WS1	C	18	67	WS	1
C18_67d_WS2	C	18	67	WS	2
C18_67d_WS3	C	18	67	WS	3
C18_67d_WS4	C	18	67	WS	4
C18_67d_WW1	C	18	67	WW	1
C18_67d_WW2	C	18	67	WW	2

C18_67d_WW3	C	18	67	WW	3
C18_67d_WW4	C	18	67	WW	4
F18_10d_WS1	F	18	11	WS	1
F18_10d_WS2	F	18	11	WS	2
F18_10d_WS3	F	18	11	WS	3
F18_10d_WS4	F	18	11	WS	4
F18_10d_WW1	F	18	11	WW	1
F18_10d_WW2	F	18	11	WW	2
F18_10d_WW3	F	18	11	WW	3
F18_10d_WW4	F	18	11	WW	4
F18_34d_WS1	F	18	34	WS	1
F18_34d_WS2	F	18	34	WS	2
F18_34d_WS3	F	18	34	WS	3
F18_34d_WS4	F	18	34	WS	4
F18_34d_WW1	F	18	34	WW	1
F18_34d_WW2	F	18	34	WW	2
F18_34d_WW3	F	18	34	WW	3
F18_34d_WW4	F	18	34	WW	4
F18_67d_WS1	F	18	67	WS	1
F18_67d_WS2	F	18	67	WS	2
F18_67d_WS3	F	18	67	WS	3
F18_67d_WS4	F	18	67	WS	4
F18_67d_WW1	F	18	67	WW	1
F18_67d_WW2	F	18	67	WW	2
F18_67d_WW3	F	18	67	WW	3
F18_67d_WW4	F	18	67	WW	4

```
> all(rownames(pdata18)==colnames(t18))
```

```
[1] TRUE
```

Get rid of unused factors

```
> str(pdata18[,factors])
```

```
'data.frame':      48 obs. of  5 variables:
 $ variety: Factor w/ 2 levels "C","F": 1 1 1 1 1 1 1 1 1 1 ...
 $ year   : Factor w/ 2 levels "18","19": 1 1 1 1 1 1 1 1 1 1 ...
 $ day    : Factor w/ 26 levels "3","11","14",...: 2 2 2 2 2 2 2 2 8 8 ...
 $ treat  : Factor w/ 2 levels "WW","WS": 2 2 2 2 1 1 1 1 2 2 ...
 $ rep    : Factor w/ 4 levels "1","2","3","4": 1 2 3 4 1 2 3 4 1 2 ...
```

```
> for (var in factors) pdata18[,var] <- factor(pdata18[,var])
```

```
> str(pdata18[,factors])
```

```
'data.frame':      48 obs. of  5 variables:
 $ variety: Factor w/ 2 levels "C","F": 1 1 1 1 1 1 1 1 1 1 ...
 $ year   : Factor w/ 1 level "18": 1 1 1 1 1 1 1 1 1 1 ...
 $ day    : Factor w/ 3 levels "11","34","67": 1 1 1 1 1 1 1 1 2 2 ...
 $ treat  : Factor w/ 2 levels "WW","WS": 2 2 2 2 1 1 1 1 2 2 ...
 $ rep    : Factor w/ 4 levels "1","2","3","4": 1 2 3 4 1 2 3 4 1 2 ...
```

Year 2019

```
> dim(pdata19)
```

```
[1] 134  21
```

```
> dim(t19)
```

```
[1] 15242  32
```

```
> pdata19 <- pdata19[colnames(t19),]
> dim(pdata19)
[1] 32 21
> dim(t19)
[1] 15242 32
> pdata19[,4:9]
```

	variety	year	day	treat	rep	project.name
C19_22d_WS1	C	19	22	WS	1	EnViros
C19_22d_WS2	C	19	22	WS	2	EnViros
C19_22d_WS3	C	19	22	WS	3	EnViros
C19_22d_WS4	C	19	22	WS	4	EnViros
C19_22d_WW1	C	19	22	WW	1	EnViros
C19_22d_WW2	C	19	22	WW	2	EnViros
C19_22d_WW3	C	19	22	WW	3	EnViros
C19_22d_WW4	C	19	22	WW	4	EnViros
C19_44d_WS1	C	19	44	WS	1	EnViros
C19_44d_WS2	C	19	44	WS	2	EnViros
C19_44d_WS3	C	19	44	WS	3	EnViros
C19_44d_WS4	C	19	44	WS	4	EnViros
C19_44d_WW1	C	19	44	WW	1	EnViros
C19_44d_WW2	C	19	44	WW	2	EnViros
C19_44d_WW3	C	19	44	WW	3	EnViros
C19_44d_WW4	C	19	44	WW	4	EnViros
F19_22d_WS1	F	19	22	WS	1	EnViros
F19_22d_WS2	F	19	22	WS	2	EnViros
F19_22d_WS3	F	19	22	WS	3	EnViros
F19_22d_WS4	F	19	22	WS	4	EnViros
F19_22d_WW1	F	19	22	WW	1	EnViros
F19_22d_WW2	F	19	22	WW	2	EnViros
F19_22d_WW3	F	19	22	WW	3	EnViros
F19_22d_WW4	F	19	22	WW	4	EnViros
F19_44d_WS1	F	19	44	WS	1	EnViros
F19_44d_WS2	F	19	44	WS	2	EnViros
F19_44d_WS3	F	19	44	WS	3	EnViros
F19_44d_WS4	F	19	44	WS	4	EnViros
F19_44d_WW1	F	19	44	WW	1	EnViros
F19_44d_WW2	F	19	44	WW	2	EnViros
F19_44d_WW3	F	19	44	WW	3	EnViros
F19_44d_WW4	F	19	44	WW	4	EnViros

```
> all(rownames(pdata19)==colnames(t19))
[1] TRUE
```

Get rid of unused factors levels

```
> str(pdata19[,factors])
```

```
'data.frame':      32 obs. of  5 variables:
 $ variety: Factor w/ 2 levels "C","F": 1 1 1 1 1 1 1 1 1 1 ...
 $ year   : Factor w/ 2 levels "18","19": 2 2 2 2 2 2 2 2 2 2 ...
 $ day    : Factor w/ 26 levels "3","11","14",...: 5 5 5 5 5 5 5 5 12 12 ...
 $ treat  : Factor w/ 2 levels "WW","WS": 2 2 2 2 1 1 1 1 2 2 ...
 $ rep    : Factor w/ 4 levels "1","2","3","4": 1 2 3 4 1 2 3 4 1 2 ...
```

```

> for (var in factors) pdata19[,var] <- factor(pdata19[,var])
> str(pdata19[,factors])

'data.frame':      32 obs. of  5 variables:
 $ variety: Factor w/ 2 levels "C","F": 1 1 1 1 1 1 1 1 1 1 ...
 $ year   : Factor w/ 1 level "19": 1 1 1 1 1 1 1 1 1 1 ...
 $ day    : Factor w/ 2 levels "22","44": 1 1 1 1 1 1 1 1 2 2 ...
 $ treat  : Factor w/ 2 levels "WW","WS": 2 2 2 2 1 1 1 1 2 2 ...
 $ rep    : Factor w/ 4 levels "1","2","3","4": 1 2 3 4 1 2 3 4 1 2 ...

> t1819 <- data.frame(t18, t19)
> pdata1819 <- rbind(pdata18, pdata19)
> str(pdata1819[,factors])

'data.frame':      80 obs. of  5 variables:
 $ variety: Factor w/ 2 levels "C","F": 1 1 1 1 1 1 1 1 1 1 ...
 $ year   : Factor w/ 2 levels "18","19": 1 1 1 1 1 1 1 1 1 1 ...
 $ day    : Factor w/ 5 levels "11","34","67",..: 1 1 1 1 1 1 1 1 2 2 ...
 $ treat  : Factor w/ 2 levels "WW","WS": 2 2 2 2 1 1 1 1 2 2 ...
 $ rep    : Factor w/ 4 levels "1","2","3","4": 1 2 3 4 1 2 3 4 1 2 ...

> catln("Sample names ",
+ c("different", "OK")[1+all(rownames(pdata1819)==colnames(t1819))])
Sample names  OK

```

3.6 Metabolite measurements

Normalised transcript measurements for each year are available in two separate files. The first few lines contains variable names

```
> (mfn18 <- getMeta(.adesc, "Metabolite data 18"))
[1] "/input/Metabolites_2018_raw_data.txt"
> (mfn19 <- getMeta(.adesc, "Metabolite data 19"))
[1] "/input/Metabolites_2019_raw_data.txt"
```

Read the metabolomics data

```
> m18 <- read.table(file.path(.aroot, mfn18), sep="\t", header=TRUE)
> dim(m18)
[1] 96 60
> m19 <- read.table(file.path(.aroot, mfn19), sep="\t", header=TRUE)
> dim(m19)
[1] 96 60
```

Check consistency of column names

```
> ok <- all(colnames(m18)==colnames(m19))
> if(ok) {catln("Column names match")} else {
+   catln("Column names do not match")}
```

Column names match

```
> cbind(names18=colnames(m18), names19=colnames(m19))
      names18      names19
[1,] "ID"      "ID"
[2,] "Variety"  "Variety"
[3,] "Date"     "Date"
[4,] "Treat"    "Treat"
[5,] "Rep"      "Rep"
[6,] "Alanine"  "Alanine"
[7,] "Arabinose" "Arabinose"
[8,] "Ascorbic.acid" "Ascorbic.acid"
[9,] "Aspartic.acid" "Aspartic.acid"
[10,] "GABA"     "GABA"
[11,] "Trans.Caffeic.acid" "Trans.Caffeic.acid"
[12,] "Catechin" "Catechin"
[13,] "Citric.acid" "Citric.acid"
[14,] "Erythronic.acid" "Erythronic.acid"
[15,] "Ethanolamine" "Ethanolamine"
[16,] "Fructose"   "Fructose"
[17,] "Fructose.6.phosphate" "Fructose.6.phosphate"
[18,] "Fumaric.acid" "Fumaric.acid"
[19,] "Galactinol"  "Galactinol"
[20,] "Galactose"   "Galactose"
[21,] "Gallic.acid" "Gallic.acid"
[22,] "Gluconic.acid" "Gluconic.acid"
[23,] "Glucopyranose..H2O." "Glucopyranose..H2O."
[24,] "Glucose"     "Glucose"
[25,] "Glutamic.acid" "Glutamic.acid"
[26,] "Glyceric.acid" "Glyceric.acid"
```


[27,]	"Glycine"	"Glycine"
[28,]	"Hydroquinone"	"Hydroquinone"
[29,]	"Myo.Inostol"	"Myo.Inostol"
[30,]	"Isoleucine"	"Isoleucine"
[31,]	"Leucine"	"Leucine"
[32,]	"Lyxonic.acid"	"Lyxonic.acid"
[33,]	"Maleic.acid"	"Maleic.acid"
[34,]	"Malic.acid"	"Malic.acid"
[35,]	"Malonic.acid"	"Malonic.acid"
[36,]	"Mannose.6.phosphate"	"Mannose.6.phosphate"
[37,]	"Melibiose"	"Melibiose"
[38,]	"Phenylalanine"	"Phenylalanine"
[39,]	"Phosphoric.acid"	"Phosphoric.acid"
[40,]	"Proline"	"Proline"
[41,]	"Putrescine"	"Putrescine"
[42,]	"Pyroglutamic.acid"	"Pyroglutamic.acid"
[43,]	"Quinic.acid"	"Quinic.acid"
[44,]	"X3.caffeoylquinic.acid"	"X3.caffeoylquinic.acid"
[45,]	"Raffinose"	"Raffinose"
[46,]	"Rhamnose"	"Rhamnose"
[47,]	"Ribonic.acid"	"Ribonic.acid"
[48,]	"Ribose"	"Ribose"
[49,]	"Serine"	"Serine"
[50,]	"Shikimic.acid"	"Shikimic.acid"
[51,]	"Succinic.acid"	"Succinic.acid"
[52,]	"Sucrose"	"Sucrose"
[53,]	"Tartaric.acid"	"Tartaric.acid"
[54,]	"Threitol"	"Threitol"
[55,]	"Threonic.acid"	"Threonic.acid"
[56,]	"Threonolactone"	"Threonolactone"
[57,]	"Threonine"	"Threonine"
[58,]	"Uracil"	"Uracil"
[59,]	"Valine"	"Valine"
[60,]	"Xylose"	"Xylose"

Use first column as row names

```
> rownames(m18) <- m18[,1]
> rownames(m19) <- m19[,1]
```

Both years together

```
> m1819 <- rbind(m18,m19)
> dim(m1819)
[1] 192 60
> colnames(m1819)[1:7]
[1] "ID"          "Variety"     "Date"        "Treat"       "Rep"
[6] "Alanine"     "Arabinose"
> rownames(m1819) <- m1819[,1]
> head(rownames(m1819))
[1] "C18_11d_WS1" "C18_11d_WS2" "C18_11d_WS3" "C18_11d_WS4"
[5] "C18_11d_WW1" "C18_11d_WW2"
> length(rownames(m1819))
```

```
[1] 192
```

At some point, we will not need the first five descriptive columns.
Intersection of transcriptomics and metabolomics samples

```
> dim(m1819)
[1] 192  60

> dim(t1819)
[1] 15242    80

> head(colnames(t1819))
[1] "C18_11d_WS1" "C18_11d_WS2" "C18_11d_WS3" "C18_11d_WS4"
[5] "C18_11d_WW1" "C18_11d_WW2"

> head(rownames(m1819))
[1] "C18_11d_WS1" "C18_11d_WS2" "C18_11d_WS3" "C18_11d_WS4"
[5] "C18_11d_WW1" "C18_11d_WW2"

> sum(colnames(t1819) %in% rownames(m1819))
[1] 80

> sum(rownames(m1819) %in% colnames(t1819))
[1] 80

> all(sort(colnames(t1819)[(colnames(t1819) %in% rownames(m1819))]) ==
+ sort(rownames(m1819)[(rownames(m1819) %in% colnames(t1819))]))
[1] TRUE

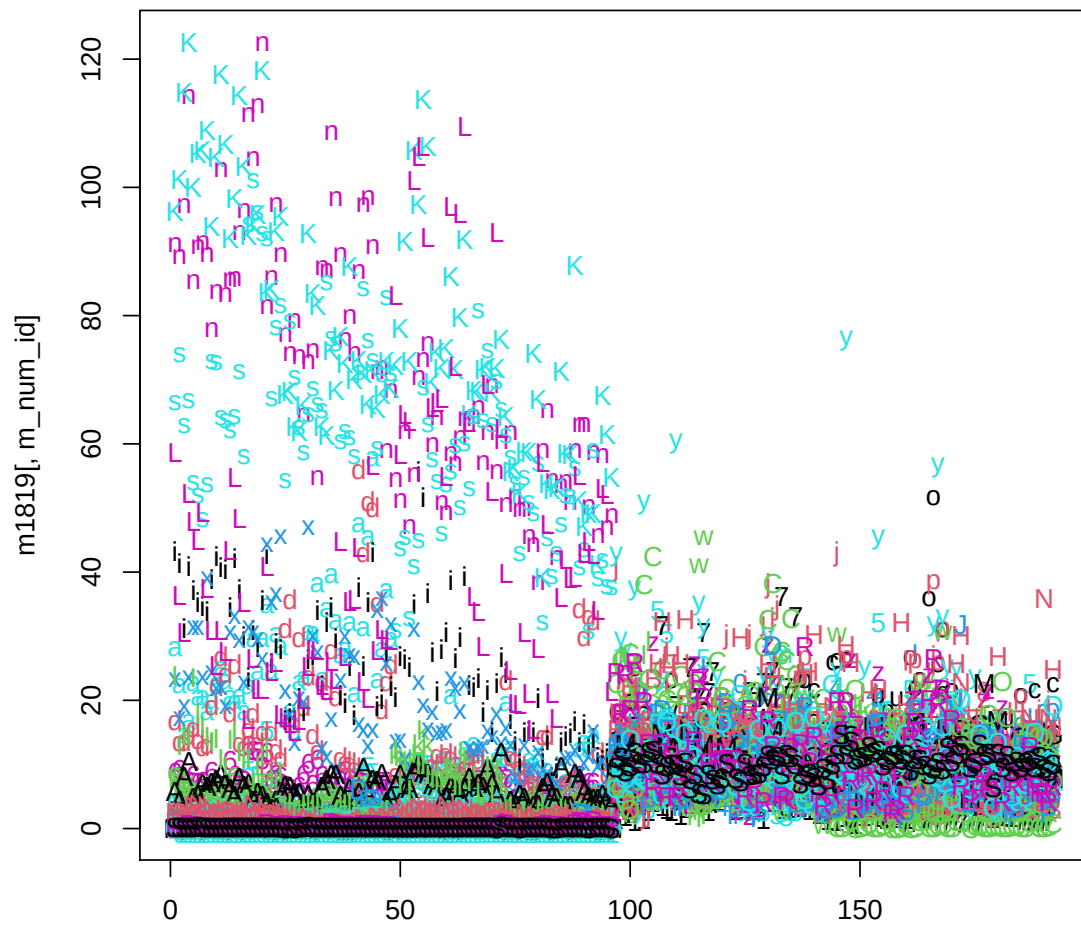
> m_num_id <- 6:ncol(m1819)
> colnames(m1819)[-m_num_id]
[1] "ID"          "Variety" "Date"      "Treat"     "Rep"
```

We end up with 80 samples

Phenodata for metabolomics data will be prepared when needed from the total phenodata. Selection of needed metabolomics data will be finalized in data analysis scripts.

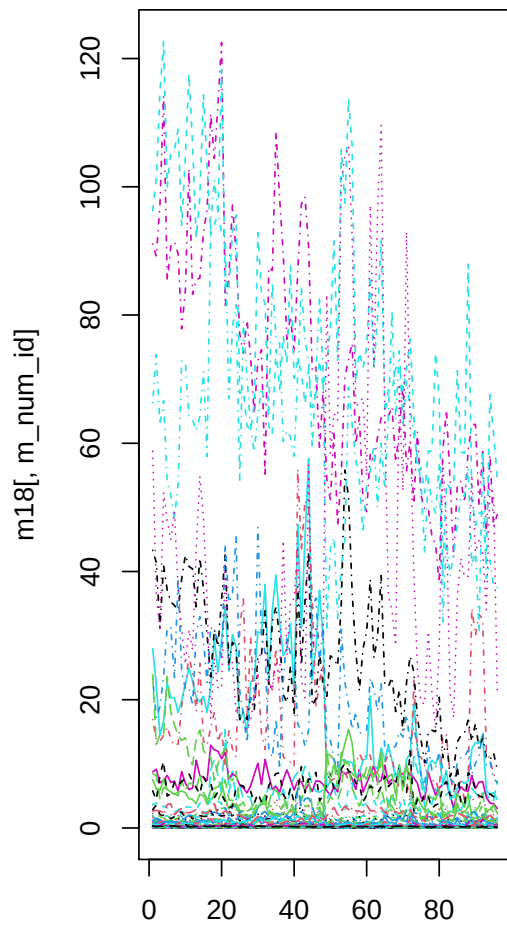
3.7 Visualize metabolites

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

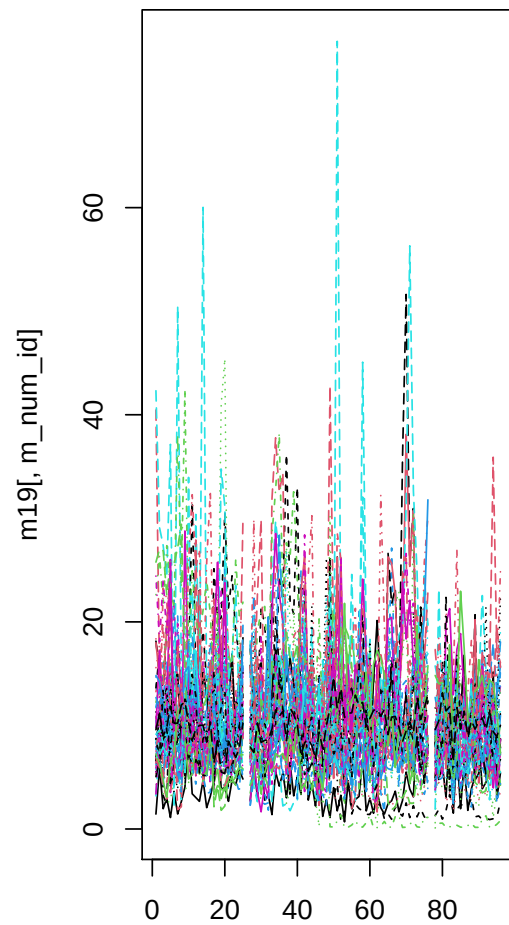


```
> par(mfrow=c(1,2))
> matplot(m18[,m_num_id], main="2018", type="l")
> matplot(m19[,m_num_id], main="2019", type="l")
```

2018



2019



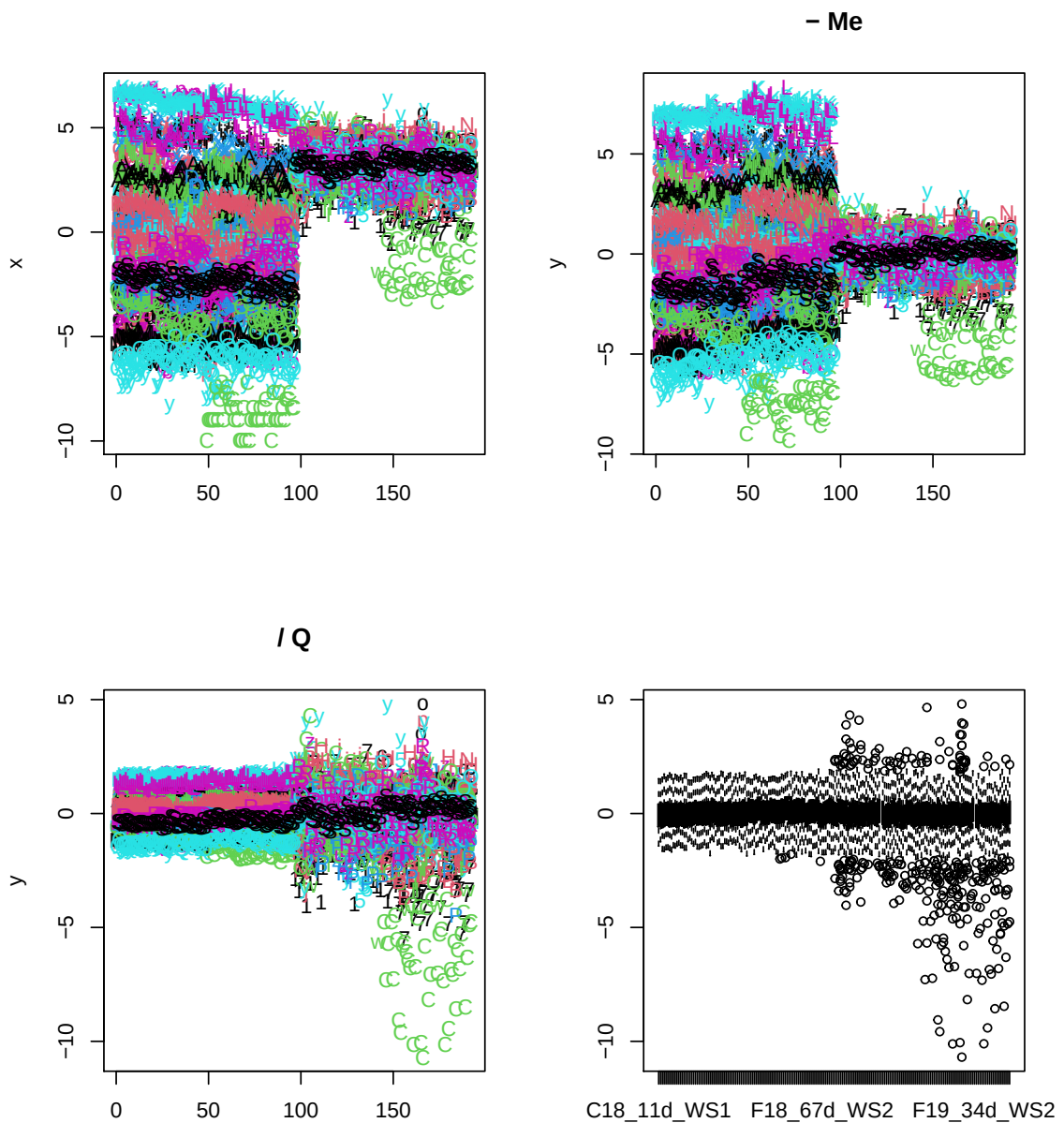
Median standardization of samples

```
> my.parallel <- function(x, m=1:ncol(x), ...){
+ m <- m[m<ncol(x)]
+ par(mar=c(4,8,3,1))
+ xlim <- range(x,na.rm=TRUE)
+ n1 <- nrow(x)
+ plot(0,0,xlim=xlim,ylim=c(n1,1) , type="n", axes=FALSE, ann=FALSE)
+ title(paste(range(m),collapse=":"))
+ axis(1)
+ axis(2,at=1:n1,labels=rownames(x), las=2)
+ box()
+ for(i in m)
+   lines(x[,i],1:n1 , col=i)
+ }
> #
> my.parallel(x)
Error in h(simpleError(msg, call)): error in evaluating the argument 'x' in se
```

```

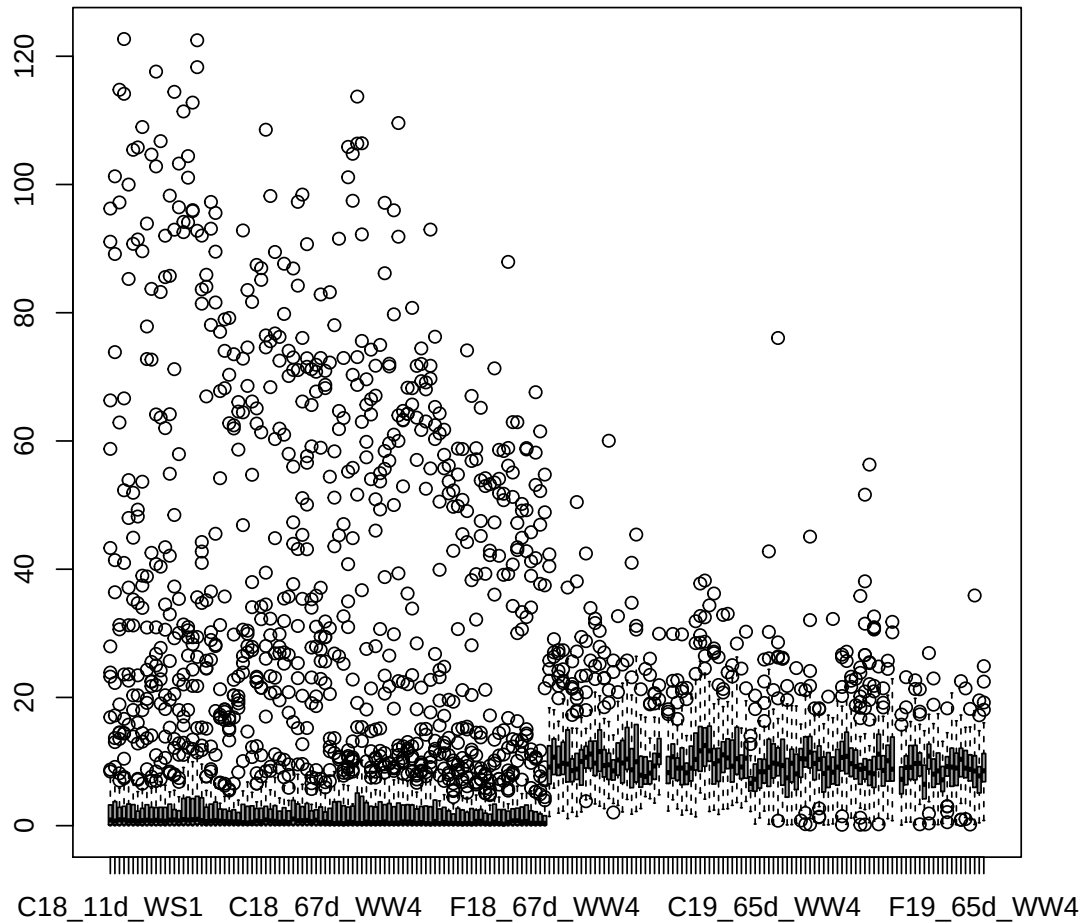
> for(k in seq(1,ncol(x),10)) {
+ if(interactive()) windows()
+   my.parallel( x, k:(k+9))
+ }
Error in h(simpleError(msg, call)): error in evaluating the argument 'x' in se
> par(mfrow=c(2,2))
> x <- log2(m1819[,m_num_id])
> matplot(x)
}1 dim(x) 55
Me <- apply(x,1,median, na.rm=TRUE)
> Q <- apply(x,1,function(x) diff(quantile(x, probs=c(0.25,0.75), na.rm=TRUE)))
> y <- sweep(x,1,Me)
> matplot(y, main="- Me")
> y <- sweep(y,1,Q, "/" )
> matplot(y, main="/ Q")
> boxplot(t(y))

```



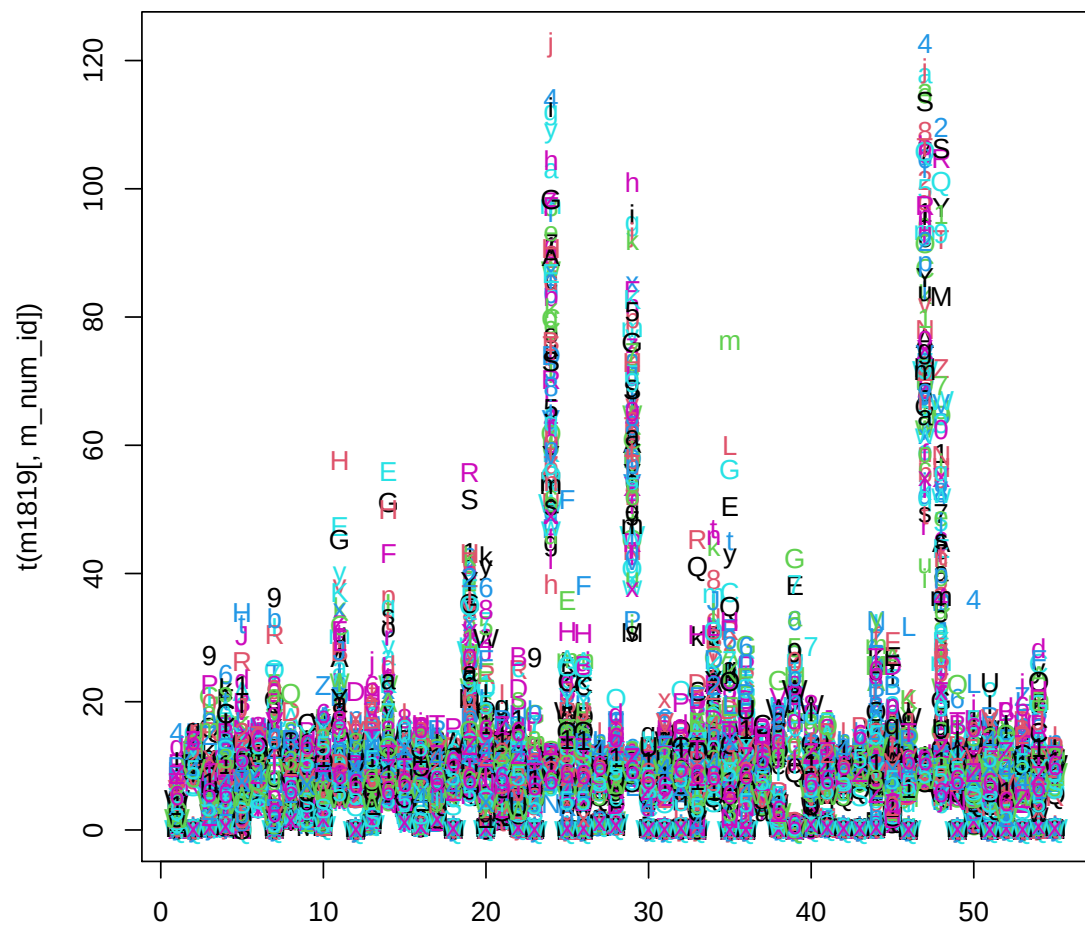
Data are highly skewed with marked differences between years

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

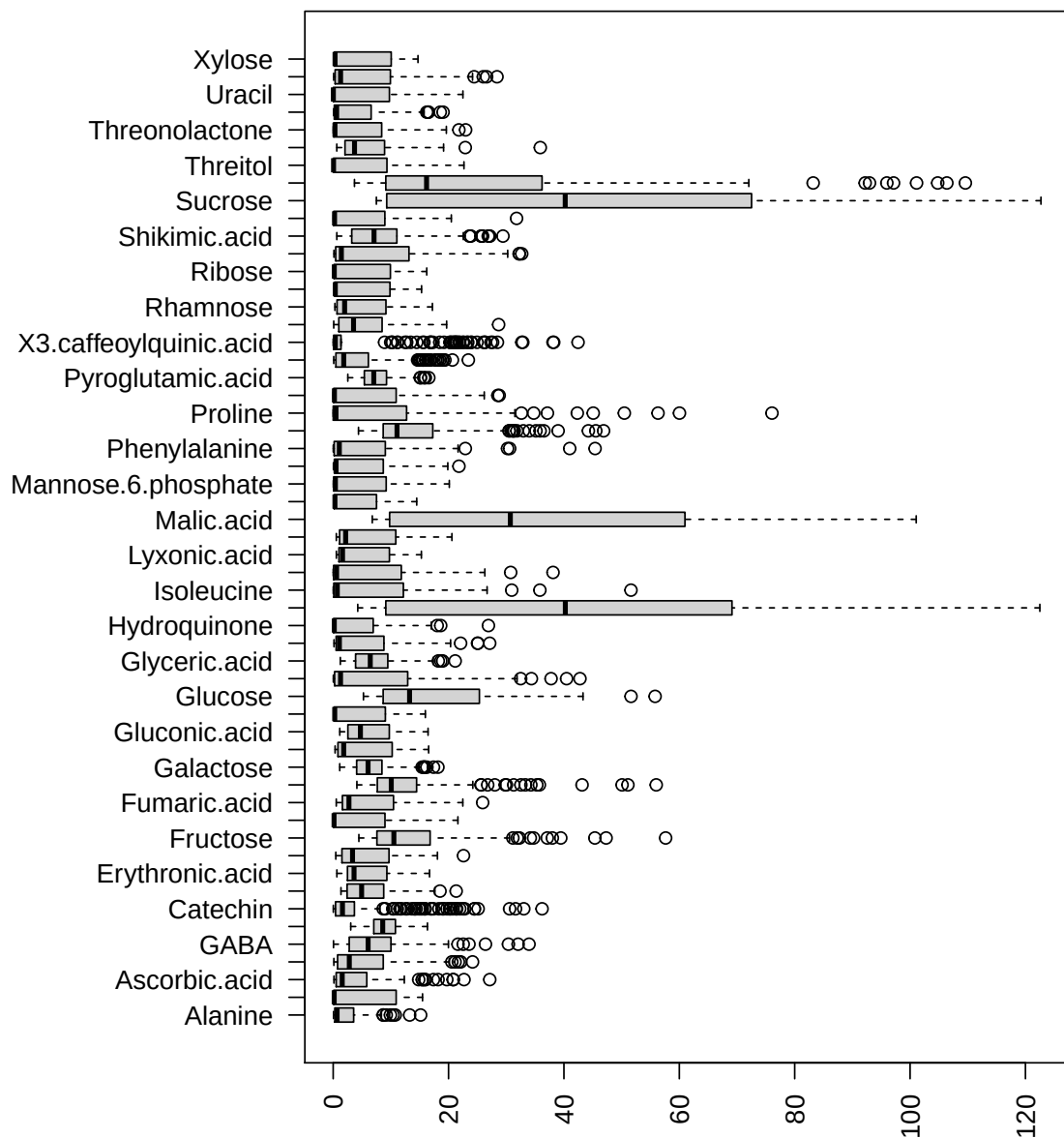


```
> matplot(t(m1819[,m_num_id]))
```

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



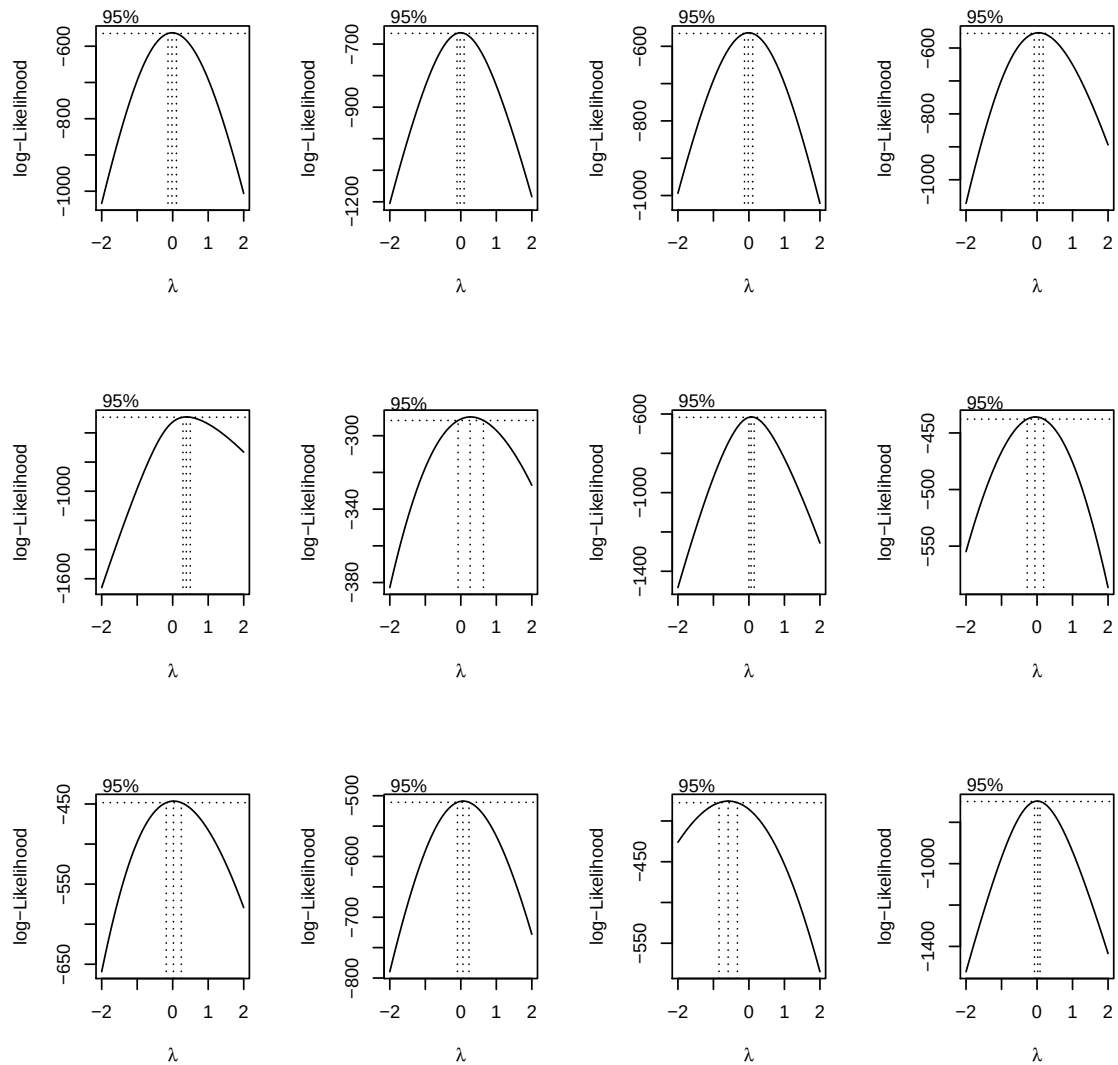
```
> par(mar=c(4,10,3,1))
> boxplot(m1819[,m_num_id], horizontal=TRUE, las=2)
```



Box-Cox transformation

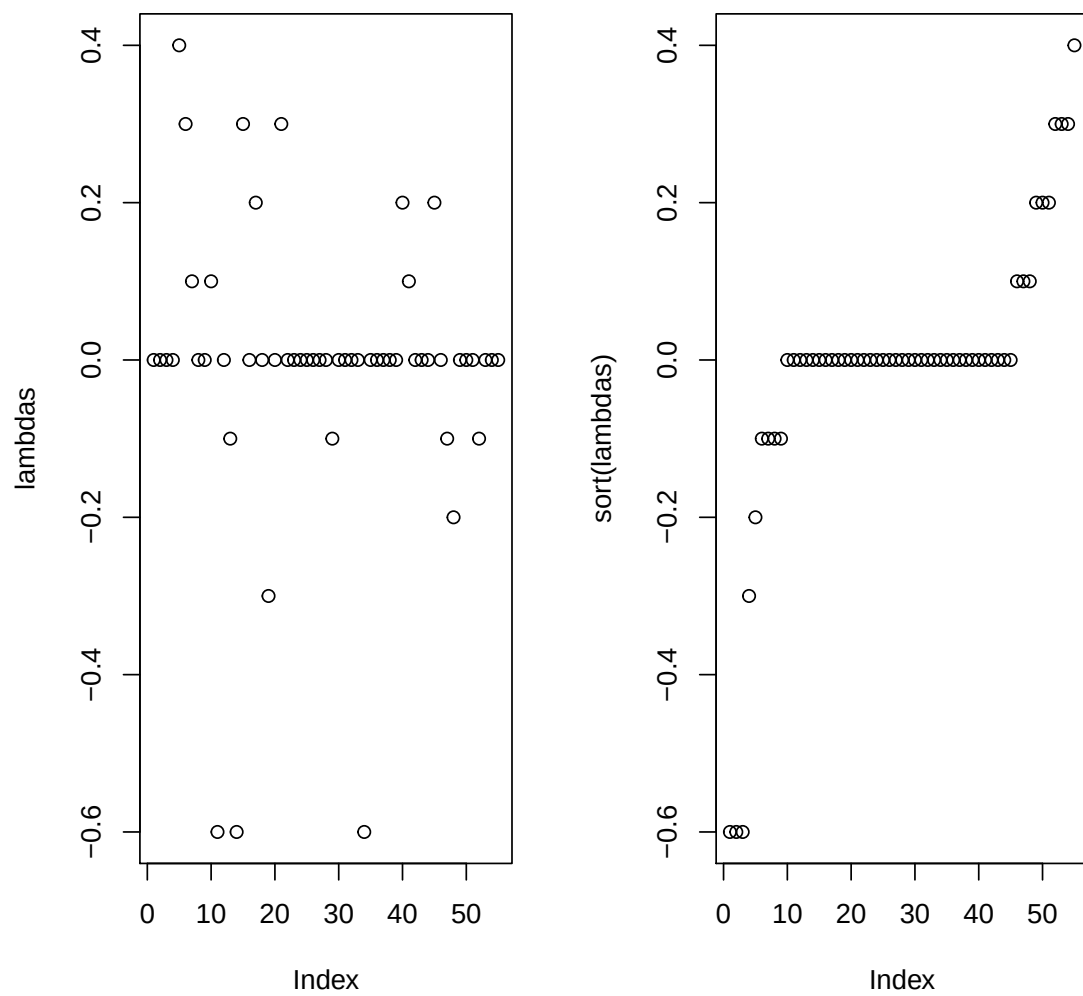
```
> library(MASS)
> par(mfrow=c(3,2))
> my.boxcox <- function(x, plotit=FALSE,...) {
+   require(MASS)
+   bc <- boxcox(x ~1, plotit=plotit, ...)
+   bc$x[which.max(bc$y)]
+ }

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

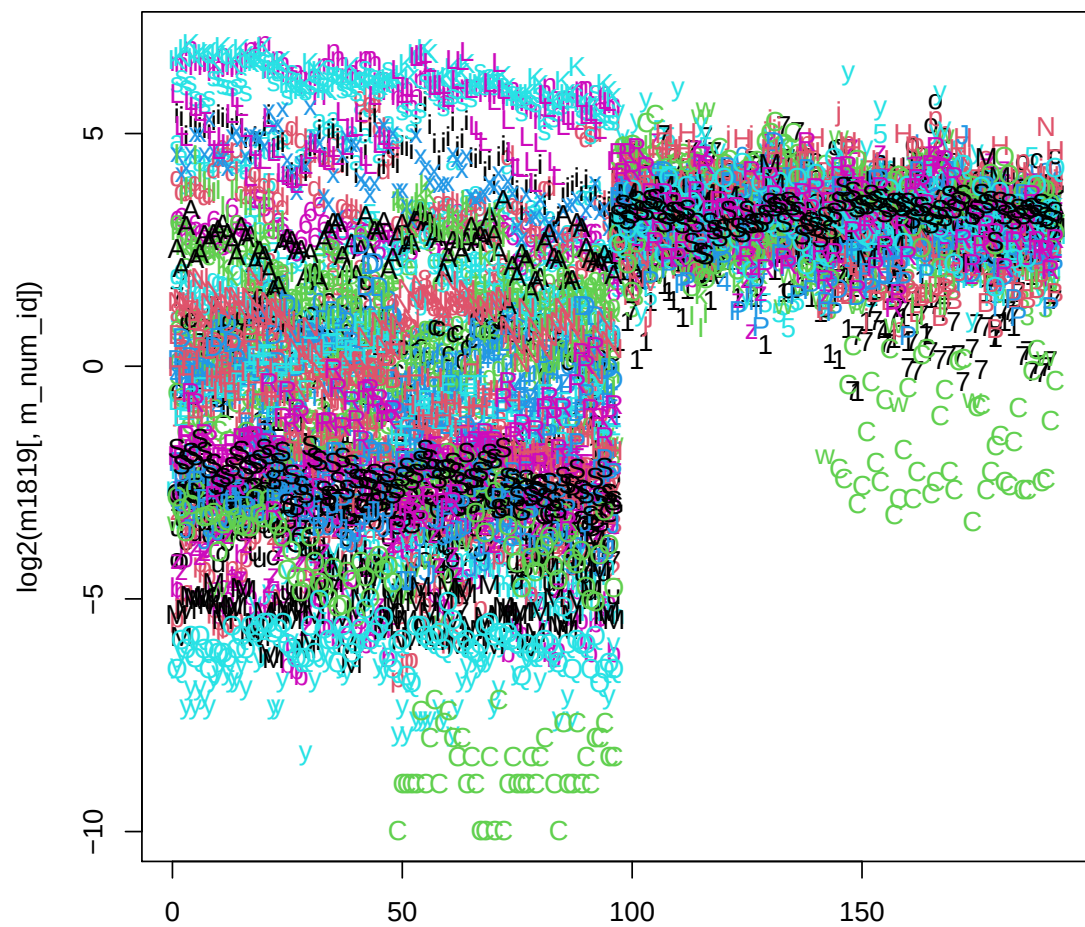
Alanine	Arabinose	Ascorbic.acid
-0.02020202	-0.02020202	-0.02020202
Aspartic.acid	GABA	Trans.Caffeic.acid
0.06060606	0.38383838	0.26262626
Catechin	Citric.acid	Erythronic.acid
0.06060606	-0.06060606	0.02020202
Ethanolamine	Fructose	Fructose.6.phosphate
0.06060606	-0.58585859	0.02020202

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



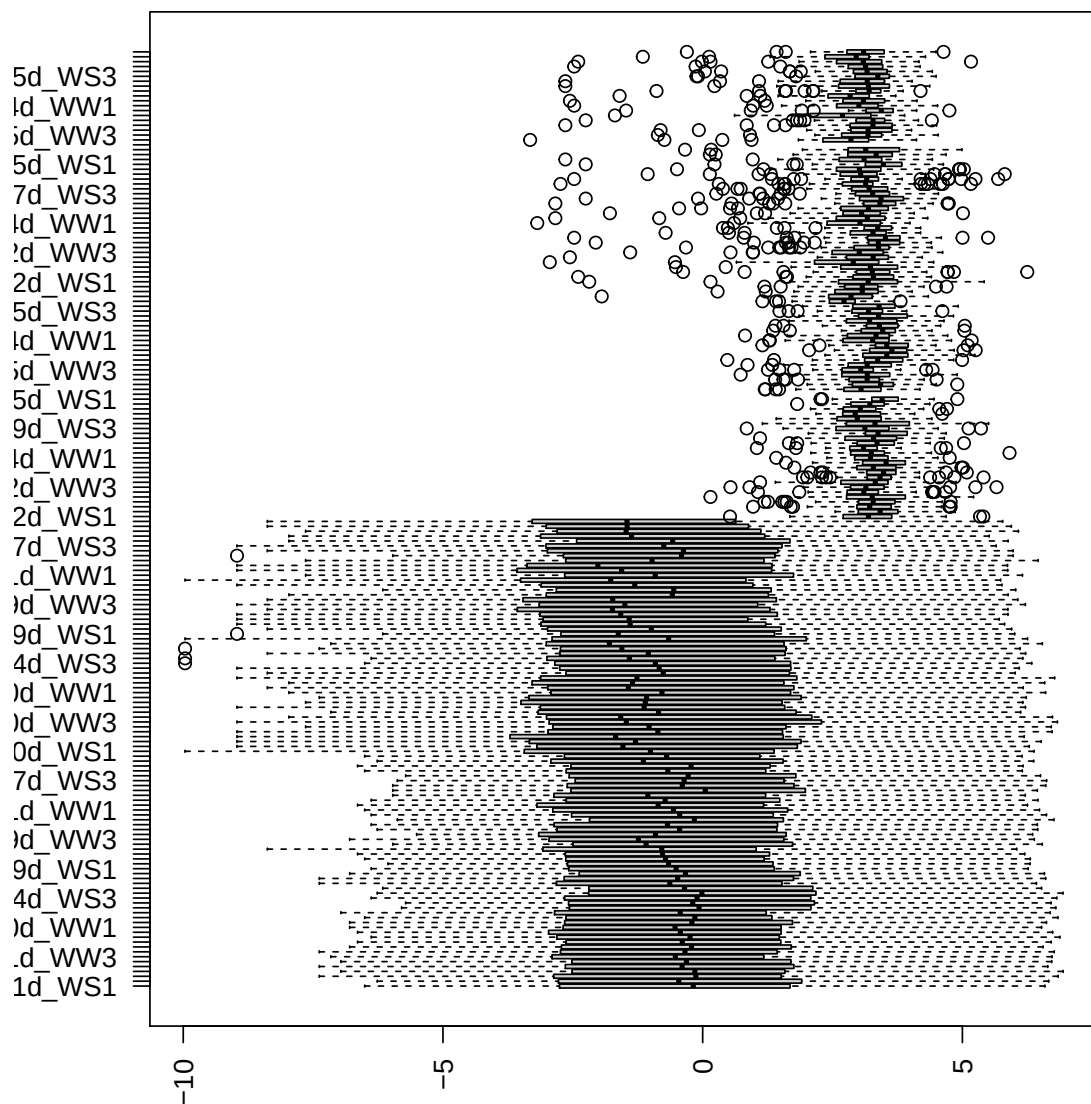
It seems that logarithm is adequate.

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



Data are highly skewed with marked differences between years

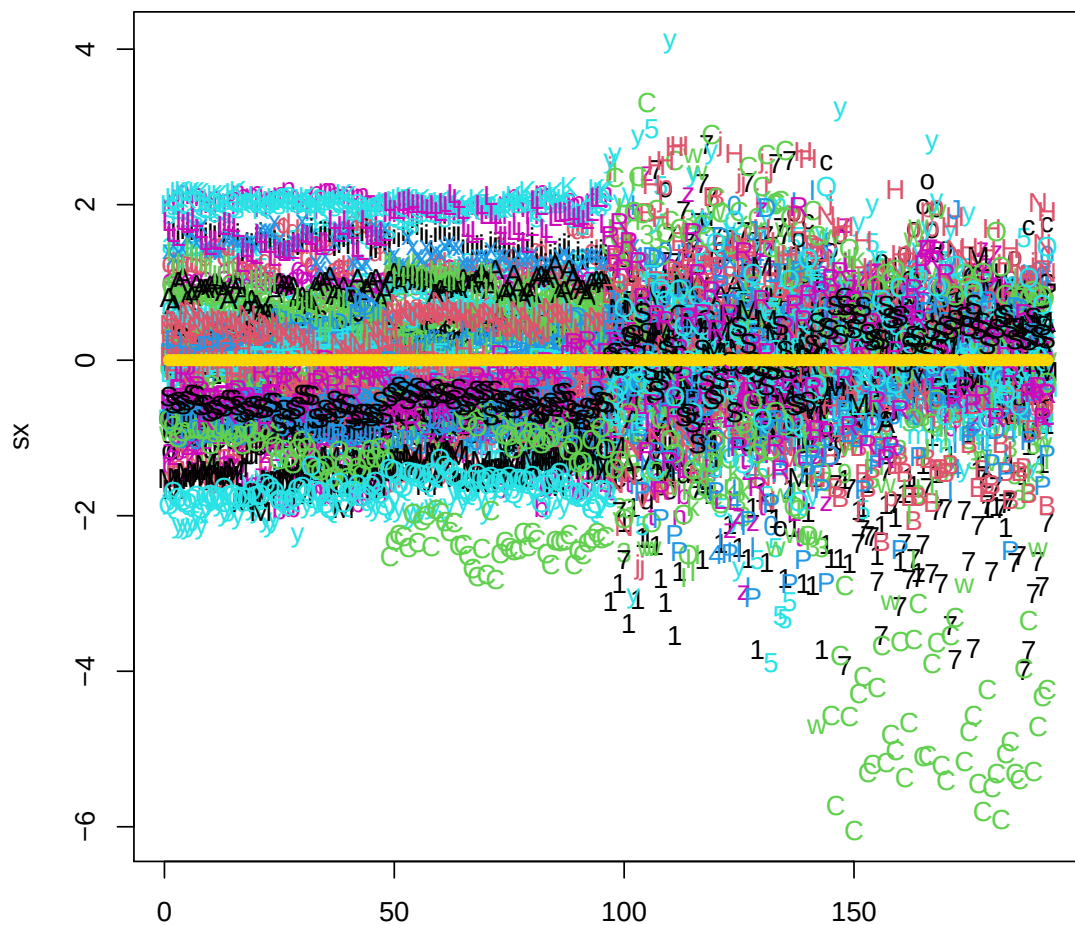
```
> boxplot(t(log2(m1819[,m_num_id])))
+ , horizontal=TRUE, las=2)
```



3.8 Standardization

For CCA standardized values are needed
Standardization across samples

```
> x <- t(log2(m1819[,m_num_id]))
> dim(x)
[1] 55 192
> sx <- t(scale(x))
> matplot(sx)
> points(1:nrow(sx), apply(sx,1,mean, na.rm=TRUE), col="gold", pch=16)
```

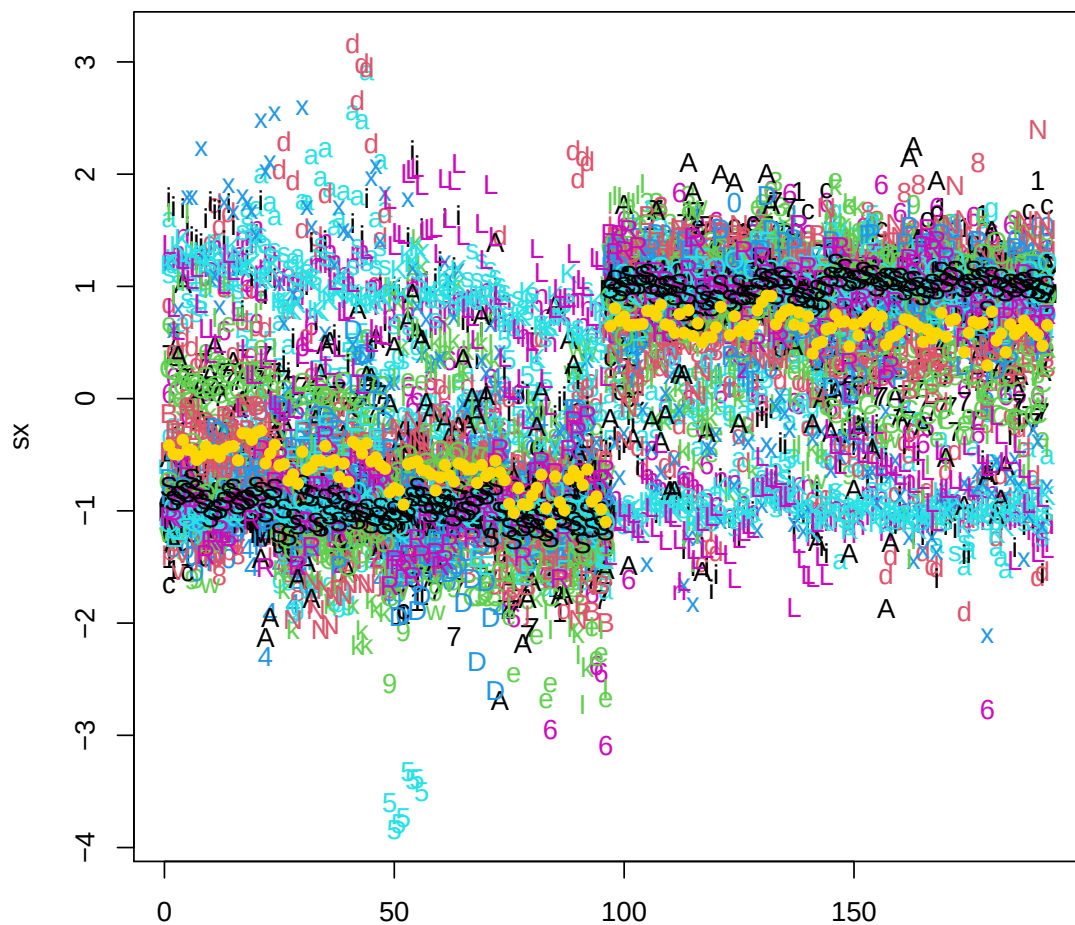


```
> head(apply(sx,1,mean, na.rm=TRUE))
  C18_11d_WS1  C18_11d_WS2  C18_11d_WS3  C18_11d_WS4  C18_11d_WW1
3.156507e-18 2.714645e-17 -5.391442e-19 2.231091e-17 9.791331e-18
  C18_11d_WW2
-2.039877e-17

> head(apply(sx,1,sd, na.rm=TRUE))
C18_11d_WS1 C18_11d_WS2 C18_11d_WS3 C18_11d_WS4 C18_11d_WW1
          1          1          1          1          1
C18_11d_WW2
          1
```

Standardization across variables

```
> x <- log2(m1819[,m_num_id])
> sx <- scale(x)
> matplot(sx)
> points(1:nrow(sx), apply(sx,1,mean, na.rm=TRUE), col="gold", pch=16)
```



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

Alanine	Arabinose	Ascorbic.acid
-3.395835e-18	-1.762114e-17	-2.402592e-17
Aspartic.acid	GABA	Trans.Caffeic.acid
4.406198e-17	-1.204206e-17	1.468649e-16

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

Alanine	Arabinose	Ascorbic.acid
1	1	1
Aspartic.acid	GABA	Trans.Caffeic.acid
1	1	1

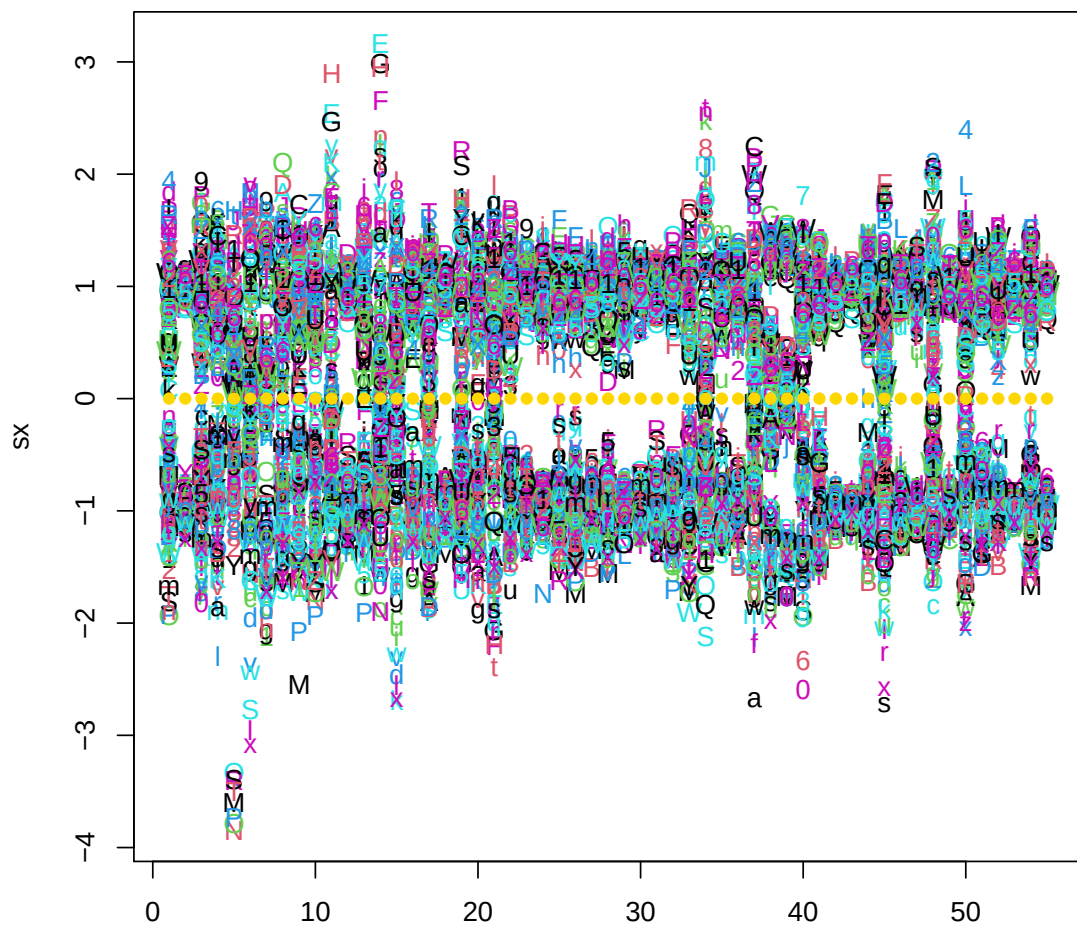
```
> x <- log2(m1819[,m_num_id])
```

```
> sx <- t(scale(x))
```

```
> matplot(sx)
```

Warning in matplot(sx): default 'pch' is smaller than number of columns and he

```
> points(1:nrow(sx), apply(sx,1,mean, na.rm=TRUE), col="gold", pch=16)
```

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

```
C18_11d_WS1 C18_11d_WS2 C18_11d_WS3 C18_11d_WS4 C18_11d_WW1
-0.4172622 -0.4925258 -0.4993865 -0.3693033 -0.4525290
C18_11d_WW2
-0.4644972
```

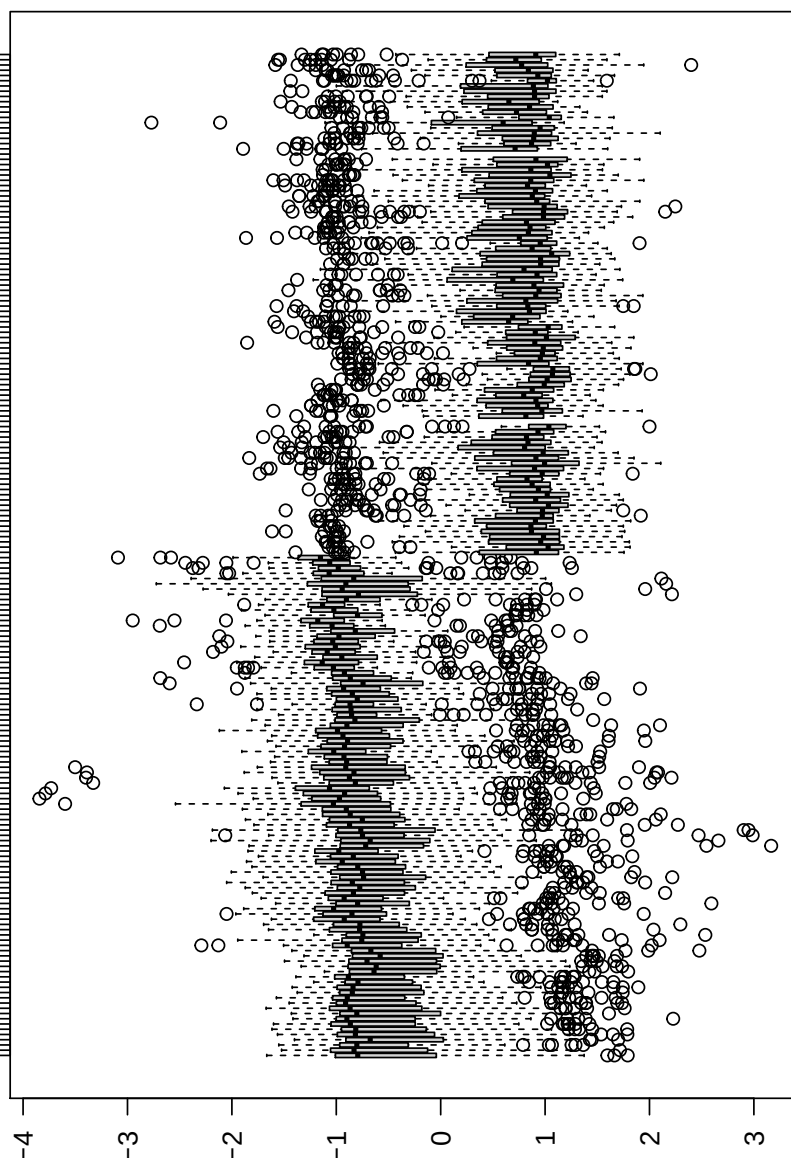
```
> head(apply(sx,2,sd, na.rm=TRUE))
```

```
C18_11d_WS1 C18_11d_WS2 C18_11d_WS3 C18_11d_WS4 C18_11d_WW1
0.9061152 0.8297170 0.7423594 0.8131148 0.8619359
C18_11d_WW2
0.8126080
```

```
> par(mar=c(4,10,3,1))
```

```
> boxplot(sx, horizontal=TRUE, las=2)
```

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



```

> sm1819 <- sx
> head(sm1819)

```

	C18_11d_WS1	C18_11d_WS2	C18_11d_WS3	C18_11d_WS4
Alanine	-1.42040510	-1.5237244	-0.3221074	-0.2941971
Arabinose	-0.89096253	-0.8768234	-0.9786693	-0.9055979
Ascorbic.acid	-0.48475127	-0.3013277	-0.3439011	-0.0716600
Aspartic.acid	-0.79435180	-1.0652846	-0.9506661	-0.8422994
GABA	-0.79478369	-1.3283418	-1.0815306	-0.9112230
Trans.Caffeic.acid	0.04856765	0.1856718	-0.5986832	-0.4584358
	C18_11d_WW1	C18_11d_WW2	C18_11d_WW3	C18_11d_WW4
Alanine	-1.4045568	-1.0312407	-0.8260696	-0.9777046
Arabinose	-0.7568413	-0.7921839	-0.9055979	-0.8982160
Ascorbic.acid	-0.5841291	-0.4705092	-0.5050201	-0.4658249
Aspartic.acid	-1.1473972	-1.0508478	-1.2872479	-1.0472819
GABA	-0.8041739	-1.0148328	-0.8827044	-1.2282093

Trans.Caffeic.acid	-0.1458728	-0.5759619	-0.4884020	-1.1855997
	C18_20d_WS1	C18_20d_WS2	C18_20d_WS3	C18_20d_WS4
Alanine	-1.30253488	-1.1485305	-0.4301155	-0.4301155
Arabinose	-0.82156681	-0.9093384	-0.9487134	-0.8945735
Ascorbic.acid	-0.40759378	-0.3990459	-0.2193190	-0.3969249
Aspartic.acid	-0.68028375	-1.1419912	-0.7477177	-1.0665004
GABA	-0.55840143	-0.6637706	-0.8598745	-0.8432557
Trans.Caffeic.acid	0.06651981	-0.6147770	-1.0784674	-0.9712290
	C18_20d_WW1	C18_20d_WW2	C18_20d_WW3	C18_20d_WW4
Alanine	-1.1669862	-1.1745048	-0.7070211	-0.67637466
Arabinose	-0.8733622	-0.9612891	-0.8277002	-0.96988871
Ascorbic.acid	-0.1710309	-0.3976312	-0.3309222	-0.08880282
Aspartic.acid	-0.9979629	-1.0091444	-0.8262651	-1.22149861
GABA	-0.9178608	-0.9071634	-0.5883746	-0.86516407
Trans.Caffeic.acid	0.6097629	-0.1444223	-0.2703104	-0.43635765
	C18_34d_WS1	C18_34d_WS2	C18_34d_WS3	C18_34d_WS4
Alanine	-0.6524125	-0.7493615	-0.5607169	-0.65060226
Arabinose	-0.8434404	-0.9285614	-0.8803135	-0.90559788
Ascorbic.acid	-0.3934041	-0.3618092	-0.4391011	-0.57954495
Aspartic.acid	-0.5681871	-1.3362907	-1.4955004	-1.23969930
GABA	0.5383838	0.6785329	0.4481893	0.08421358
Trans.Caffeic.acid	1.2085257	1.0325340	0.9791050	0.67184120
	C18_34d_WW1	C18_34d_WW2	C18_34d_WW3	C18_34d_WW4
Alanine	-0.4938681	-0.7208561	-0.57357704	-0.17365428
Arabinose	-0.8499066	-1.0407476	-0.92464525	-0.84666098
Ascorbic.acid	-0.8649740	-0.2872844	-0.49847064	-0.57499031
Aspartic.acid	-0.8642301	-2.2922701	-1.90683969	-0.97716973
GABA	0.9929407	0.1022634	0.51365512	-0.08629024
Trans.Caffeic.acid	0.9342980	-0.3488723	-0.05127649	-0.20189133
	C18_49d_WS1	C18_49d_WS2	C18_49d_WS3	C18_49d_WS4
Alanine	-0.2726324	-0.35831179	-0.58173446	-0.61190189
Arabinose	-1.0255800	-0.92856138	-0.94871336	-1.00617809
Ascorbic.acid	-0.6890378	-0.72067394	-0.74913040	-0.77756970
Aspartic.acid	-1.4783807	-1.33979505	-1.52418769	-1.82838040
GABA	0.2730391	-0.05768882	0.01397647	-0.01902277
Trans.Caffeic.acid	-0.7596655	-0.95833043	-1.34574708	-0.80549633
	C18_49d_WW1	C18_49d_WW2	C18_49d_WW3	C18_49d_WW4
Alanine	-0.78777647	-0.8640990	-0.8123175	-1.01596046
Arabinose	-1.02557995	-0.7674005	-0.9246452	-0.82770022
Ascorbic.acid	-0.63168277	-0.9822666	-1.0052447	-0.84341555
Aspartic.acid	-1.64349297	-1.5802398	-1.4372280	-1.68141186
GABA	-0.89011882	-0.3070515	-0.2091395	-0.03424594
Trans.Caffeic.acid	-0.09552259	0.4665606	-0.6970157	0.64777629
	C18_61d_WS1	C18_61d_WS2	C18_61d_WS3	C18_61d_WS4
Alanine	-0.3989935	-0.48953135	-0.9199530	-0.8991309
Arabinose	-1.0014654	-0.95705493	-0.9698887	-1.0061781
Ascorbic.acid	-0.8649740	-1.07533485	-1.2382552	-1.0429323
Aspartic.acid	-0.5700590	-0.60196936	-0.3984122	-0.5020430
GABA	0.2573183	0.03096133	0.2921707	-0.1017523
Trans.Caffeic.acid	-0.1502284	-1.07152665	-0.8442359	-1.2882030
	C18_61d_WW1	C18_61d_WW2	C18_61d_WW3	C18_61d_WW4
Alanine	-0.6973013	-0.7109465	-1.3993516	-1.2173427
Arabinose	-0.8499066	-0.9365057	-0.9169216	-1.0841181

Ascorbic.acid	-0.5713676	-0.4823576	-0.8554612	-0.7584837
Aspartic.acid	-0.9913337	-1.3720993	-1.0616491	-1.3328028
GABA	0.1848340	-0.3855115	0.1932726	0.4195016
Trans.Caffeic.acid	-0.4069089	0.1514097	-0.3879618	-1.1184425
	C18_67d_WS1	C18_67d_WS2	C18_67d_WS3	C18_67d_WS4
Alanine	-0.2683969	-0.2996921	-1.0099392	-0.9834577
Arabinose	-1.0511748	-0.9405354	-0.9968055	-0.9528633
Ascorbic.acid	-1.2546783	-0.9234174	-0.9445333	-1.0808826
Aspartic.acid	-0.6752302	-0.7219964	-0.8849168	-0.8531840
GABA	0.4999725	0.4293145	0.5888935	0.5085247
Trans.Caffeic.acid	-0.4596448	-0.5297954	-1.1254938	-0.6948336
	C18_67d_WW1	C18_67d_WW2	C18_67d_WW3	C18_67d_WW4
Alanine	-0.4668387	-0.4710387	-1.1412804	-1.1164723
Arabinose	-0.9876388	-1.0109446	-0.8665250	-0.9786693
Ascorbic.acid	-0.8663435	-1.2546783	-1.4019136	-0.9969523
Aspartic.acid	-1.0472819	-0.7572957	-1.6023971	-1.0592352
GABA	0.2650833	0.1418167	0.1148187	0.1764576
Trans.Caffeic.acid	-1.2192354	-0.4762171	-0.4916597	-0.7092651
	F18_10d_WS1	F18_10d_WS2	F18_10d_WS3	F18_10d_WS4
Alanine	-0.6801339	-0.7855869	-1.9290988	-1.9182512
Arabinose	-1.1325277	-1.0673212	-0.9921970	-1.0784436
Ascorbic.acid	-0.6795006	-0.6763499	-0.5668652	-0.8368111
Aspartic.acid	-0.2260179	-0.5146942	-0.4114244	-0.6291963
GABA	-3.5975121	-3.8432554	-3.7854179	-3.7311978
Trans.Caffeic.acid	-1.1712269	-1.5566942	-0.8241195	-1.2690901
	F18_10d_WW1	F18_10d_WW2	F18_10d_WW3	F18_10d_WW4
Alanine	-1.0189903	-1.11647226	-1.80872651	-1.7554137
Arabinose	-0.8982160	-0.91311277	-0.83080109	-0.9093384
Ascorbic.acid	-0.4550139	-0.59525382	-0.45348288	-0.3399824
Aspartic.acid	-0.3429779	-0.32748229	-0.32433165	-0.2883839
GABA	-3.3285334	-3.39726159	-3.38836674	-3.5016458
Trans.Caffeic.acid	0.1091013	-0.06183566	0.02982272	-0.3442159
	F18_20d_WS1	F18_20d_WS2	F18_20d_WS3	F18_20d_WS4
Alanine	-0.3989935	-0.4367744	-1.3639455	-1.1707356
Arabinose	-1.0511748	-0.9968055	-0.9968055	-0.6679676
Ascorbic.acid	-0.8704679	-0.8677156	-1.0607502	-0.9838834
Aspartic.acid	-0.6151265	-0.5961236	-1.0437330	-0.9611546
GABA	-0.8901188	-0.9636402	-0.8109439	-0.8724295
Trans.Caffeic.acid	-1.0670733	0.1618934	-1.2775696	-0.6335214
	F18_20d_WW1	F18_20d_WW2	F18_20d_WW3	F18_20d_WW4
Alanine	-0.8689990	-0.6915326	-1.1199637	-1.2054012
Arabinose	-1.0728454	-1.0157662	-1.0014654	-0.9246452
Ascorbic.acid	-0.7206739	-0.6879717	-0.8315716	-1.3566288
Aspartic.acid	-0.8019896	-0.8716862	-0.9696531	-0.7143743
GABA	-1.4867876	-1.1085653	-0.6976926	-0.5317253
Trans.Caffeic.acid	-0.1044514	0.3399237	-0.5600763	-0.4463728
	F18_34d_WS1	F18_34d_WS2	F18_34d_WS3	F18_34d_WS4
Alanine	-1.14853050	-1.00100193	-1.1164723	-1.1975502
Arabinose	-1.00146544	-1.01094460	-0.9612891	-0.9285614
Ascorbic.acid	-0.77035196	-0.80594079	-0.8447439	-1.0052447
Aspartic.acid	-0.08906787	-0.47296796	-0.3583326	-0.6157905
GABA	-0.71172267	-0.08786346	-0.4482032	-0.7101077
Trans.Caffeic.acid	0.38304173	-0.64636973	-0.3687437	-0.5260834

	F18_34d_WW1	F18_34d_WW2	F18_34d_WW3	F18_34d_WW4
Alanine	-0.798826516	-0.6763747	-0.9468693	-0.7966027
Arabinose	-0.786547801	-1.0618693	-1.0673212	-0.8597980
Ascorbic.acid	-1.754522307	-1.7216172	-1.6112704	-1.8200162
Aspartic.acid	-0.139533413	-0.3959358	-0.9190598	0.1918374
GABA	-0.832505609	-1.1659845	-0.9086835	-0.7763030
Trans.Caffeic.acid	-0.007332999	-0.0951660	0.1746206	-0.1098216
	F18_49d_WS1	F18_49d_WS2	F18_49d_WS3	F18_49d_WS4
Alanine	-0.8813990	-0.9359801	-0.8689990	-0.6839132
Arabinose	-1.0459286	-1.1016199	-1.0511748	-1.1729203
Ascorbic.acid	-1.2523087	-1.4287209	-1.6685424	-1.3649018
Aspartic.acid	-1.8737376	-0.5322996	-0.9362259	-0.8877828
GABA	0.7166446	0.5230477	0.3452471	-0.3126450
Trans.Caffeic.acid	-0.2820581	-0.6232825	-1.7938439	-1.9520321
	F18_49d_WW1	F18_49d_WW2	F18_49d_WW3	F18_49d_WW4
Alanine	-1.20935940	-1.2054012	-0.9359801	-1.08247037
Arabinose	-1.02064421	-1.1455620	-1.0564878	-0.97425592
Ascorbic.acid	-1.29874782	-0.6455914	-1.1911571	-1.22903904
Aspartic.acid	-0.81750417	-1.1487549	-1.0091444	-0.90130513
GABA	-0.15176956	-0.2414255	0.2016299	0.03950059
Trans.Caffeic.acid	0.03460538	-0.6957063	-1.5433162	-0.96405620
	F18_61d_WS1	F18_61d_WS2	F18_61d_WS3	F18_61d_WS4
Alanine	-1.34929542	-0.93868678	-0.6763747	-0.7309058
Arabinose	-1.23369161	-1.13899393	-1.1016199	-1.1590169
Ascorbic.acid	-1.26906519	-1.31406969	-1.3704714	-1.4888883
Aspartic.acid	-0.21430282	-0.19480061	-0.7851219	-0.9990735
GABA	-0.02029638	0.05699739	0.1523252	-0.5607751
Trans.Caffeic.acid	-0.70269666	-0.52361129	-1.5901101	-2.9498706
	F18_61d_WW1	F18_61d_WW2	F18_61d_WW3	F18_61d_WW4
Alanine	-1.6822688	-1.9075667	-1.2014648	-0.5559537
Arabinose	-1.0898708	-1.1590169	-1.1137095	-1.0109446
Ascorbic.acid	-1.2666470	-1.3270964	-1.2475931	-1.1634985
Aspartic.acid	-0.3489890	-0.8849168	-0.5813898	-0.6058921
GABA	-0.5567099	-0.4547891	-0.1848092	-0.3841255
Trans.Caffeic.acid	-1.4116358	-0.8760588	-1.1559043	-1.2052175
	F18_67d_WS1	F18_67d_WS2	F18_67d_WS3	F18_67d_WS4
Alanine	-1.2335835	-1.11996369	-0.50409137	-0.87641303
Arabinose	-1.1590169	-1.06732124	-1.20985284	-1.13899393
Ascorbic.acid	-1.5124122	-1.74023228	-1.03245310	-1.07717926
Aspartic.acid	-0.5406601	-0.93929677	-1.34862878	-0.87168620
GABA	0.2083702	0.09671283	-0.02981653	0.09527977
Trans.Caffeic.acid	-0.1524087	-0.99816120	-0.53930272	-0.52649560
	F18_67d_WW1	F18_67d_WW2	F18_67d_WW3	F18_67d_WW4
Alanine	-0.68771273	-0.8145911	-0.9120730	-0.4301155
Arabinose	-1.05648778	-1.0957039	-1.1198884	-1.2589760
Ascorbic.acid	-1.44717412	-1.6434274	-1.3931989	-1.3403676
Aspartic.acid	-1.06407077	-0.9600991	-0.9869468	-1.2856130
GABA	0.09272624	-0.1293893	-0.1176987	0.3447692
Trans.Caffeic.acid	-1.74127656	-2.3749262	-2.4456161	-3.0910196
	C19_22d_WS1	C19_22d_WS2	C19_22d_WS3	C19_22d_WS4
Alanine	0.2720501	1.2824603	0.4910994	0.7887854
Arabinose	1.0854730	1.1410463	0.9948382	1.0441785
Ascorbic.acid	0.5077076	1.2996969	0.4546839	0.2179557

Aspartic.acid	1.3002167	1.0138284	1.1871125	1.3693923
GABA	-0.3652211	0.4540044	0.5683581	0.2222463
Trans.Caffeic.acid	-0.9856266	1.0291158	0.2102271	1.5825560
	C19_22d_WW1	C19_22d_WW2	C19_22d_WW3	C19_22d_WW4
Alanine	0.08711792	0.9289745	0.2769671	0.7027119
Arabinose	1.14132150	1.0867292	1.0819988	1.0329153
Ascorbic.acid	0.34494184	0.6917733	0.9890956	0.5804620
Aspartic.acid	1.34162557	0.9135394	1.5509238	1.1114018
GABA	0.64266257	0.4196112	0.1871306	-0.4626375
Trans.Caffeic.acid	-1.61556947	0.1286776	0.2005584	1.4285608
	C19_44d_WS1	C19_44d_WS2	C19_44d_WS3	C19_44d_WS4
Alanine	1.0050069	1.589722	0.8824669	0.8029488
Arabinose	0.9092302	1.045219	0.8819613	1.0608565
Ascorbic.acid	1.7487219	1.213896	1.7487219	1.2801920
Aspartic.acid	1.2843338	1.096224	0.8750735	0.8839919
GABA	0.6856613	1.682973	0.4508374	1.5866186
Trans.Caffeic.acid	0.5475100	-0.466101	0.3607963	1.7095972
	C19_44d_WW1	C19_44d_WW2	C19_44d_WW3	C19_44d_WW4
Alanine	0.7107403	1.1125188	0.5264551	0.8304556
Arabinose	0.9789026	1.0213394	0.9797140	1.0146840
Ascorbic.acid	1.3785054	1.5556943	1.1228496	0.8010254
Aspartic.acid	0.5339921	0.4810936	0.5672792	0.7640104
GABA	0.9245993	0.7243169	0.6443564	0.6443564
Trans.Caffeic.acid	-0.0908902	0.3851661	0.3851661	1.8388831
	C19_49d_WS1	C19_49d_WS2	C19_49d_WS3	C19_49d_WS4
Alanine	1.1079692	1.675464089	0.9633604	1.0067634
Arabinose	1.0791345	1.012816267	0.9252369	0.9817356
Ascorbic.acid	1.2854461	1.809587711	1.5636868	1.5389760
Aspartic.acid	0.7460909	1.178805258	1.0565169	0.6814897
GABA	0.8617421	0.610714821	0.1885628	1.4648404
Trans.Caffeic.acid	-0.6882969	-0.006640693	0.8659242	1.6067934
	C19_49d_WW1	C19_49d_WW2	C19_49d_WW3	C19_49d_WW4
Alanine	0.71074026	1.1125188	1.0460089	1.2458283
Arabinose	0.99717689	1.0124417	0.8214110	0.9321080
Ascorbic.acid	0.90241827	1.2196641	1.3575459	1.3054450
Aspartic.acid	0.31834284	0.5886717	0.4672602	0.2384083
GABA	-0.07535686	0.7774375	0.5169933	0.6246747
Trans.Caffeic.acid	-0.26690844	-0.5856183	0.9473843	1.5784971
	C19_55d_WS1	C19_55d_WS2	C19_55d_WS3	C19_55d_WS4
Alanine	1.13043165	NA	0.7368647	1.3240626
Arabinose	1.00602230	NA	0.9631780	0.9302867
Ascorbic.acid	1.24018846	NA	0.8036164	1.5086137
Aspartic.acid	1.02271128	NA	0.5452540	0.4323224
GABA	0.12780899	NA	0.2139473	0.7509098
Trans.Caffeic.acid	0.04142443	NA	0.8400033	1.3308596
	C19_55d_WW1	C19_55d_WW2	C19_55d_WW3	C19_55d_WW4
Alanine	0.7982590	1.37285782	0.7394250	0.8590999
Arabinose	1.0044974	1.05004056	0.8995193	1.0094331
Ascorbic.acid	0.5606877	0.34246432	1.0371665	0.8126107
Aspartic.acid	0.7681648	1.38403013	0.7178225	0.3695937
GABA	0.2586393	0.05583074	0.2625903	0.2612753
Trans.Caffeic.acid	0.3821308	1.00950745	1.0943552	1.5252216
	C19_34d_WS1	C19_34d_WS2	C19_34d_WS3	C19_34d_WS4

Alanine	0.24694130	1.22934840	1.0223795	1.2124772
Arabinose	1.02861189	0.99795354	1.0978681	1.0697692
Ascorbic.acid	1.23528856	0.98710311	1.1843270	1.2239597
Aspartic.acid	1.59074795	1.67071566	1.2894944	1.1576225
GABA	-0.54863624	0.21948879	0.1726762	-0.6823219
Trans.Caffeic.acid	0.02434738	-0.04495894	0.9624127	1.8518783
C19_34d_WW1 C19_34d_WW2 C19_34d_WW3 C19_34d_WW4				
Alanine	0.7959024	1.3206873	0.8393928	1.1621430
Arabinose	0.9833459	1.0224384	1.0187638	0.9825415
Ascorbic.acid	1.9365717	1.7099495	1.6531531	1.6213218
Aspartic.acid	0.5939251	0.4991472	0.7524648	0.4901751
GABA	-0.5968286	-0.8836893	-0.5587401	-0.5320537
Trans.Caffeic.acid	0.3423869	0.6044133	0.9448722	1.8220911
C19_65d_WS1 C19_65d_WS2 C19_65d_WS3 C19_65d_WS4				
Alanine	0.86981662	1.84944595	0.7419762	1.0656555
Arabinose	1.04521895	0.98495000	0.9097098	1.0195013
Ascorbic.acid	0.97299630	1.11206313	0.6856887	0.9439095
Aspartic.acid	0.85322328	1.30526880	0.5577232	0.8354587
GABA	1.20433121	1.36540008	0.7150083	1.2007751
Trans.Caffeic.acid	-0.03445944	-0.05549566	1.0847800	1.4646504
C19_65d_WW1 C19_65d_WW2 C19_65d_WW3 C19_65d_WW4				
Alanine	0.57960166	1.1992211	0.1542540	0.7520903
Arabinose	0.91257627	0.9516337	0.9516337	0.9998889
Ascorbic.acid	0.29366343	0.6826267	0.1969294	0.5945038
Aspartic.acid	0.64083931	0.2913310	0.4547444	0.5225574
GABA	0.42942294	0.3428547	0.7803355	0.5515722
Trans.Caffeic.acid	0.05840396	0.4894964	1.1884487	1.7482095
F19_22d_WS1 F19_22d_WS2 F19_22d_WS3 F19_22d_WS4				
Alanine	0.08711792	0.9961587	0.4105789	0.8525914
Arabinose	1.13438644	1.1432428	1.0531110	1.1503027
Ascorbic.acid	0.62177779	1.1895916	1.5380609	0.8049083
Aspartic.acid	1.60434969	1.4023739	1.3957151	1.2718004
GABA	0.21255637	0.7219991	0.8669941	0.1028955
Trans.Caffeic.acid	-0.08377750	0.3730062	0.2262719	1.4200051
F19_22d_WW1 F19_22d_WW2 F19_22d_WW3 F19_22d_WW4				
Alanine	-0.25067245	1.1049198	0.48746506	0.7570939
Arabinose	1.10483199	1.0571701	1.13911481	1.1481431
Ascorbic.acid	0.51357764	1.1659735	1.29195938	0.8389273
Aspartic.acid	0.90840960	1.0901997	1.22675356	0.9621851
GABA	-0.07535686	0.1871306	0.07887073	-0.4872417
Trans.Caffeic.acid	0.10543713	0.5475100	0.46005943	1.5231533
F19_44d_WS1 F19_44d_WS2 F19_44d_WS3 F19_44d_WS4				
Alanine	0.8259444	1.36442444	0.4105789	0.7887854
Arabinose	0.9563756	1.06681937	1.0033500	1.0531110
Ascorbic.acid	1.0591295	0.39506053	0.6300897	0.8339895
Aspartic.acid	1.5709259	1.53408190	1.3305144	1.2103491
GABA	1.0629968	1.63329752	0.8199230	1.1475028
Trans.Caffeic.acid	0.1120958	0.09542104	0.7068967	1.9051184
F19_44d_WW1 F19_44d_WW2 F19_44d_WW3 F19_44d_WW4				
Alanine	0.3104650	0.9131409	0.5264551	0.2720501
Arabinose	1.0674767	0.9913054	0.9402066	1.0835816
Ascorbic.acid	0.3399781	1.3168030	1.0202349	0.5289969
Aspartic.acid	0.7535218	0.7825253	0.5820523	0.7671283

GABA	0.2922977	0.8397348	0.4971698	0.5866357
Trans.Caffeic.acid	0.2358574	0.8400033	0.8555830	1.6566622
	F19_47d_WS1	F19_47d_WS2	F19_47d_WS3	F19_47d_WS4
Alanine	0.643819879	0.7265299	0.9328784	0.3730656
Arabinose	0.984549552	0.9116230	0.9627561	1.0794538
Ascorbic.acid	1.115399611	0.7228861	1.1011096	0.3740144
Aspartic.acid	1.477155992	1.3310010	1.4589479	0.9228533
GABA	1.292014347	1.2231993	0.6742929	0.7583604
Trans.Caffeic.acid	0.003724593	-0.3049282	1.2275540	1.3725035
	F19_47d_WW1	F19_47d_WW2	F19_47d_WW3	F19_47d_WW4
Alanine	0.7317161	1.2241998	0.9726240	0.8168353
Arabinose	0.9361769	0.9849500	0.9813321	0.9572320
Ascorbic.acid	0.6560497	0.8189660	0.7945062	1.0390231
Aspartic.acid	1.0408838	1.2011413	0.9541606	0.9278849
GABA	0.5430559	0.2331895	0.8136814	0.3185607
Trans.Caffeic.acid	-0.3982098	-0.2518356	0.8736566	1.7018142
	F19_55d_WS1	F19_55d_WS2	F19_55d_WS3	F19_55d_WS4
Alanine	1.7003494	1.5492019	1.0656555	1.4966108
Arabinose	0.9158957	0.8689514	1.0228041	0.9063406
Ascorbic.acid	0.4589067	0.4132566	0.5892707	0.9831012
Aspartic.acid	1.4023739	0.8633176	0.8401748	0.2913310
GABA	1.2175382	1.1873084	1.0482528	1.0795457
Trans.Caffeic.acid	0.1940951	-0.5026811	1.1038997	1.5560739
	F19_55d_WW1	F19_55d_WW2	F19_55d_WW3	F19_55d_WW4
Alanine	NA	1.52169511	1.1245108	1.3070234
Arabinose	NA	0.80939103	0.9252369	1.0154288
Ascorbic.acid	NA	0.54221849	0.6749130	0.5839986
Aspartic.acid	NA	1.03800586	0.5978411	1.0093469
GABA	NA	1.01689035	0.9091511	0.8908794
Trans.Caffeic.acid	NA	0.09207483	1.2548512	1.6208412
	F19_34d_WS1	F19_34d_WS2	F19_34d_WS3	F19_34d_WS4
Alanine	0.7982590	1.6432584	0.3151241	1.4455128
Arabinose	1.0848435	1.0064027	0.8057164	1.0476367
Ascorbic.acid	0.5661358	0.8642997	0.5327998	1.1518890
Aspartic.acid	1.0621212	1.1758158	1.1823768	0.7629681
GABA	0.2922977	0.3688149	-0.1252694	0.5893444
Trans.Caffeic.acid	-0.3087571	0.1843738	-2.7709424	1.4709739
	F19_34d_WW1	F19_34d_WW2	F19_34d_WW3	F19_34d_WW4
Alanine	0.4910994	1.3318766	0.43059441	0.9799488
Arabinose	0.9861490	0.8855325	0.95422686	1.0601886
Ascorbic.acid	0.8853459	1.1605295	0.70080322	0.6480391
Aspartic.acid	0.5686344	0.6518175	0.34440911	0.4841331
GABA	0.6644284	0.4412663	0.06907130	0.3917591
Trans.Caffeic.acid	0.5503812	0.4511712	0.02434738	1.5478779
	F19_65d_WS1	F19_65d_WS2	F19_65d_WS3	F19_65d_WS4
Alanine	1.1691569	1.54838383	0.9781247	1.0816225
Arabinose	1.0406913	1.10960874	0.9669562	1.0242637
Ascorbic.acid	0.3015962	0.13316265	1.0240327	0.4243959
Aspartic.acid	0.5899885	0.95818365	1.0365627	0.8839919
GABA	0.9511372	0.90352165	1.3277535	0.9911842
Trans.Caffeic.acid	-0.1922971	0.04142443	1.0315578	1.5293538
	F19_65d_WW1	F19_65d_WW2	F19_65d_WW3	F19_65d_WW4
Alanine	1.2280647	1.94458838	0.7767631	1.2137893

Arabinose	0.8850242	0.94065190	0.9388677	1.1084197
Ascorbic.acid	0.4958194	0.22090909	0.5057401	0.8487006
Aspartic.acid	1.0962240	0.77537968	0.4531650	0.5873525
GABA	0.7258587	0.61510148	0.7196751	0.7304676
Trans.Caffeic.acid	0.6324617	0.02434738	1.2751610	1.3898648

3.9 Featuredata for metabolites

!!! Rows in featuredata and columns of metabolite data ARE in the same order !!!

```
> (fmfn <- getMeta(.adesc, "Featuredata metabolites"))
[1] "Featuredata_metabolites_210127.txt"
> mfddata <- read.table(file.path(.iroot, fmfn), sep="\t", header=TRUE)
> cbind(rownames(sm1819), make.names(mfddata[,1]), mfddata[,1])
```

	[,1]	[,2]
[1,]	"Alanine"	"Alanine"
[2,]	"Arabinose"	"Arabinose"
[3,]	"Ascorbic.acid"	"Ascorbic.acid"
[4,]	"Aspartic.acid"	"Aspartic.acid"
[5,]	"GABA"	"GABA"
[6,]	"Trans.Caffeic.acid"	"Trans.Caffeic.acid"
[7,]	"Catechin"	"Catechin"
[8,]	"Citric.acid"	"Citric.acid"
[9,]	"Erythronic.acid"	"Erythronic.acid"
[10,]	"Ethanolamine"	"Ethanolamine"
[11,]	"Fructose"	"Fructose"
[12,]	"Fructose.6.phosphate"	"Fructose.6.phosphate"
[13,]	"Fumaric.acid"	"Fumaric.acid"
[14,]	"Galactinol"	"Galactinol"
[15,]	"Galactose"	"Galactose"
[16,]	"Gallic.acid"	"Gallic.acid"
[17,]	"Gluconic.acid"	"Gluconic.acid"
[18,]	"Glucopyranose..H2O."	"Glucopyranose..H2O."
[19,]	"Glucose"	"Glucose"
[20,]	"Glutamic.acid"	"Glutamic.acid"
[21,]	"Glyceric.acid"	"Glyceric.acid"
[22,]	"Glycine"	"Glycine"
[23,]	"Hydroquinone"	"Hydroquinone"
[24,]	"Myo.Inostol"	"Myo.Inostol"
[25,]	"Isoleucine"	"Isoleucine"
[26,]	"Leucine"	"Leucine"
[27,]	"Lyxonic.acid"	"Lyxonic.acid"
[28,]	"Maleic.acid"	"Maleic.acid"
[29,]	"Malic.acid"	"Malic.acid"
[30,]	"Malonic.acid"	"Malonic.acid"
[31,]	"Mannose.6.phosphate"	"Mannose.6.phosphate"
[32,]	"Melibiose"	"Melibiose"
[33,]	"Phenylalanine"	"Phenylalanine"
[34,]	"Phosphoric.acid"	"Phosphoric.acid"
[35,]	"Proline"	"Proline"
[36,]	"Putrescine"	"Putrescine"

[37,]	"Pyroglutamic.acid"	"Pyroglutamic.acid"
[38,]	"Quinic.acid"	"Quinic.acid"
[39,]	"X3.caffeoylquinic.acid"	"X3.caffeoylquinic.acid"
[40,]	"Raffinose"	"Raffinose"
[41,]	"Rhamnose"	"Rhamnose"
[42,]	"Ribonic.acid"	"Ribonic.acid"
[43,]	"Ribose"	"Ribose"
[44,]	"Serine"	"Serine"
[45,]	"Shikimic.acid"	"Shikimic.acid"
[46,]	"Succinic.acid"	"Succinic.acid"
[47,]	"Sucrose"	"Sucrose"
[48,]	"Tartaric.acid"	"Tartaric.acid"
[49,]	"Threitol"	"Threitol"
[50,]	"Threonic.acid"	"Threonic.acid"
[51,]	"Threonolactone"	"Threonolactone"
[52,]	"Threonine"	"Threonine"
[53,]	"Uracil"	"Uracil"
[54,]	"Valine"	"Valine"
[55,]	"Xylose"	"Xylose"
	[,3]	
[1,]	"Alanine"	
[2,]	"Arabinose"	
[3,]	"Ascorbic acid"	
[4,]	"Aspartic acid"	
[5,]	"GABA"	
[6,]	"Trans-Caffeic acid"	
[7,]	"Catechin"	
[8,]	"Citric acid"	
[9,]	"Erythronic acid"	
[10,]	"Ethanolamine"	
[11,]	"Fructose"	
[12,]	"Fructose-6-phosphate"	
[13,]	"Fumaric acid"	
[14,]	"Galactinol"	
[15,]	"Galactose"	
[16,]	"Gallic acid"	
[17,]	"Gluconic acid"	
[18,]	"Glucopyranose[-H20]"	
[19,]	"Glucose"	
[20,]	"Glutamic acid"	
[21,]	"Glyceric acid"	
[22,]	"Glycine"	
[23,]	"Hydroquinone"	
[24,]	"Myo-Inositol"	
[25,]	"Isoleucine"	
[26,]	"Leucine"	
[27,]	"Lyxonic acid"	
[28,]	"Maleic acid"	
[29,]	"Malic acid"	
[30,]	"Malonic acid"	
[31,]	"Mannose-6-phosphate"	
[32,]	"Melibiose"	
[33,]	"Phenylalanine"	


```

[34,] "Phosphoric acid"
[35,] "Proline"
[36,] "Putrescine"
[37,] "Pyroglutamic acid"
[38,] "Quinic acid"
[39,] "3-caffeoylquinic acid"
[40,] "Raffinose"
[41,] "Rhamnose"
[42,] "Ribonic acid"
[43,] "Ribose"
[44,] "Serine"
[45,] "Shikimic acid"
[46,] "Succinic acid"
[47,] "Sucrose"
[48,] "Tartaric acid"
[49,] "Threitol"
[50,] "Threonic acid"
[51,] "Threonolactone"
[52,] "Threonine"
[53,] "Uracil"
[54,] "Valine"
[55,] "Xylose"

```

```
> all(rownames(sm1819) == make.names(mfdata[,1]))
```

```
[1] TRUE
```

```
> rownames(mfdata) <- make.names(mfdata[,1])
```

```
> # to be sure, that the fdata rows are in the same order as data
```

```
> mfdata <- mfdata[rownames(sm1819),]
```

```
> head(mfdata)
```

	Metabolite	Bin
Alanine	Alanine	5.1001
Arabinose	Arabinose	10.6.1001
Ascorbic.acid	Ascorbic acid	17.5.1001
Aspartic.acid	Aspartic acid	13.1.1.2.1001
GABA	GABA	22.1002
Trans.Caffeic.acid	Trans-Caffeic acid	16.2.1.1006

```
Alanine
```

```
Arabinose
```

```
Ascorbic.acid
```

```
Aspartic.acid
```

```
GABA
```

```
Trans.Caffeic.acid
```

```
cell wall
```

```
hormone metabol
```

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

```
pol
```

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

3.10 Interesting bins

For Canonical Correlation Analysis (CCA) we will need to restrict the number of genes (and metabolites) to those that are of more interest. The Mapman bins of interest are provided in the file (at the investigation layer).

List of bins for metabolite and transcripts:

```
>1 (bfn <- getMeta( adesc, "Interesting bins"))
> bindata <- read.table(file.path(.iroot, bfn), sep="\t", header=TRUE, dec="$")
> head(bindata)
      bin description
1 1.2      PS.photorespiration
2 1.3      PS.calvin cycle
3 2.1      major CHO metabolism.synthesis
4 2.2      major CHO metabolism.degradation
5 3.1 minor CHO metabolism.raffinose family.
6 3.3 minor CHO metabolism.sugar alcohols
data.frame:      22 obs. of  2 variables:
 $ bin      : chr  "1.2" "1.3" "2.1" "2.2" ...
 $ description: chr  "PS.photorespiration" "PS.calvin cycle" "major CHO metabo
```

At some point, the transcripts and metabolites that correspond to the bins of interest (including the sub-bins) will be selected. Let us try to find them for the first bin:

```
> bindata$bin
[1] "1.2" "1.3" "2.1" "2.2" "3.1" "3.3" "3.4" "3.99" "5"
[10] "6" "8.1" "10.6" "11" "12.2" "13.1" "16.1" "16.2" "16.8"
[19] "17.5" "21" "22"
> paste0("1", bindata$bin[1])
[1] "11"
> ind <- grep(paste0("1", bindata$bin[1]), fdata$BINCODE)
> ind
[1] 396 596 1785 1786 1882 1953 2240 2749 2817 2856 6436
[12] 6438 6439 7892 7894 8114 8161 8530 8627 8992 9343 15061
[23] 16469 16736
> fdata[ind, 2]
      geneID BINCODE
396  Vitvi07g03141  1.2.1
596  Vitvi01g00157 1.2.4.4
1785 Vitvi02g00436  1.2.6
1786 Vitvi02g00437  1.2.6
1882 Vitvi02g00572   1.2
1953 Vitvi02g00680 1.2.4.4
2240 Vitvi03g00154  1.2.6
2749 Vitvi03g01231 1.2.4.4
2817 Vitvi04g00063  1.2.5
2856 Vitvi04g00112 1.2.4.1
6436 Vitvi07g01511  1.2.5
6438 Vitvi07g02608  1.2.5
6439 Vitvi07g02610  1.2.5
7892 Vitvi09g01499  1.2.2
7894 Vitvi09g01500  1.2.2
8114 Vitvi09g00358  1.2.6
8161 Vitvi09g00439  1.2.7
8530 Vitvi10g00078 1.2.4.2
8627 Vitvi10g00223  1.2.1
8992 Vitvi10g00829  1.2.2
9343 Vitvi11g00186 1.2.4.1
15061 Vitvi18g00560  1.2.5
16469 Vitvi19g01352  1.2.2
16736 Vitvi07g02607  1.2.5
```

3.10.1 Genes in bins of interest

```
> intgenes <- sapply(bindata$bin, function(x) fdata$geneID[grep(paste0("^",x),
> str(intgenes)
```

```
List of 22
```

```
$ 1.2 : chr [1:24] "Vitvi07g03141" "Vitvi01g00157" "Vitvi02g00436" "Vitvi02g0
$ 1.3 : chr [1:33] "Vitvi01g00086" "Vitvi01g00360" "Vitvi01g01058" "Vitvi02g0
$ 2.1 : chr [1:29] "Vitvi02g00250" "Vitvi03g00304" "Vitvi05g00442" "Vitvi05g0
$ 2.2 : chr [1:53] "Vitvi02g01845" "Vitvi01g00025" "Vitvi01g00052" "Vitvi01g0
$ 3.1 : chr [1:16] "Vitvi10g02295" "Vitvi00g01259" "Vitvi01g00714" "Vitvi05g0
$ 3.3 : chr [1:3] "Vitvi11g01277" "Vitvi16g01858" "Vitvi16g00929"
$ 3.4 : chr [1:6] "Vitvi01g00140" "Vitvi03g00287" "Vitvi07g01777" "Vitvi09g00
$ 3.99: chr(0)
$ 5    : chr [1:22] "Vitvi01g00787" "Vitvi04g01402" "Vitvi04g01668" "Vitvi06g0
$ 6    : chr [1:9] "Vitvi07g03070" "Vitvi00g01243" "Vitvi00g01382" "Vitvi03g00
$ 8.1  : chr [1:36] "Vitvi07g03070" "Vitvi01g00274" "Vitvi01g00861" "Vitvi01g0
$ 10.6: chr [1:57] "Vitvi07g02990" "Vitvi01g00593" "Vitvi01g00708" "Vitvi01g0
$ 11   : chr [1:251] "Vitvi02g01774" "Vitvi07g02896" "Vitvi02g01724" "Vitvi02g
$ 12.2: chr [1:12] "Vitvi01g00175" "Vitvi05g00403" "Vitvi07g00187" "Vitvi07g0
$ 13.1: chr [1:134] "Vitvi07g03049" "Vitvi00g00869" "Vitvi02g01749" "Vitvi01g
$ 16.1: chr [1:83] "Vitvi10g02269" "Vitvi02g00020" "Vitvi02g00034" "Vitvi02g0
$ 16.2: chr [1:33] "Vitvi07g03081" "Vitvi07g03083" "Vitvi01g02214" "Vitvi01g0
$ 16.8: chr [1:71] "Vitvi10g02185" "Vitvi01g00556" "Vitvi01g02009" "Vitvi01g0
$ 17.5: chr [1:53] "Vitvi02g01780" "Vitvi10g02409" "Vitvi01g00481" "Vitvi01g0
$ 21   : chr [1:134] "Vitvi10g02216" "Vitvi04g02274" "Vitvi01g00023" "Vitvi01g
$ 22   : chr [1:8] "Vitvi01g00739" "Vitvi01g00789" "Vitvi03g00054" "Vitvi06g01
$ 23   : chr [1:123] "Vitvi01g00048" "Vitvi01g00115" "Vitvi01g00201" "Vitvi01g
```

```
> nn <- t(t(sapply(intgenes, length)))
```

```
> nn
```

```
      [,1]
1.2      24
1.3      33
2.1      29
2.2      53
3.1      16
3.3       3
3.4       6
3.99     0
5         22
6         9
8.1      36
10.6     57
11       251
12.2     12
13.1    134
16.1     83
16.2     33
16.8     71
17.5     53
21      134
22       8
23     123
```

```

> # unlist(intgenes)
> head(fdata[fdata[, "geneID"] %in% unlist(intgenes), 2:3], 10)
  geneID BINCODE
35 Vitvi02g01774 11.9.4.3
38 Vitvi02g01780 17.5.2
43 Vitvi07g02896 11.1.7
80 Vitvi02g01724 11.9.4.2
103 Vitvi07g02990 10.6.1
126 Vitvi10g02185 16.8.3.1
139 Vitvi07g03081 16.2.1.10
142 Vitvi07g03070 6.3
143 Vitvi07g03070 8.1.9
159 Vitvi07g03049 13.1.6.1.1
> tail(fdata[fdata[, "geneID"] %in% unlist(intgenes), 2:3], 10)
  geneID BINCODE
16883 Vitvi16g01457 16.8.2.1
16886 Vitvi16g01461 16.8.2.1
16887 Vitvi16g01465 16.8.2.1
16888 Vitvi16g01467 16.8.2.1
16890 Vitvi16g01469 16.8.2.1
16891 Vitvi16g01484 16.8.2.1
16897 Vitvi17g00109 23.2
16907 Vitvi18g00124 16.2.1.3
16915 Vitvi18g00759 16.2
16930 Vitvi19g02064 2.2.2.1.2
> length(unique(unlist(intgenes)))
[1] 1183

```

Number of interesting genes: 1183.

3.10.2 Metabolites in bins of interest

```

> intmtbs <- sapply(bindata$bin, function(x) rownames(mfdata)[grep(paste0("^(x)",
> str(intmtbs)
List of 22
 $ 1.2 : chr [1:3] "Glyceric.acid" "Glycine" "Serine"
 $ 1.3 : chr "Fructose.6.phosphate"
 $ 2.1 : chr "Sucrose"
 $ 2.2 : chr [1:2] "Fructose" "Glucose"
 $ 3.1 : chr [1:2] "Galactinol" "Raffinose"
 $ 3.3 : chr "Threitol"
 $ 3.4 : chr "Myo.Inostol"
 $ 3.99: chr [1:3] "Erythronic.acid" "Galactose" "Xylose"
 $ 5   : chr "Alanine"
 $ 6   : chr [1:2] "Citric.acid" "Malic.acid"
 $ 8.1 : chr [1:2] "Fumaric.acid" "Succinic.acid"
 $ 10.6: chr [1:5] "Arabinose" "Melibiose" "Rhamnose" "Ribonic.acid" ...
 $ 11  : chr "Ethanolamine"
 $ 12.2: chr "Glutamic.acid"
 $ 13.1: chr [1:8] "Aspartic.acid" "Isoleucine" "Leucine" "Phenylalanine" ...
 $ 16.1: chr "Hydroquinone"
 $ 16.2: chr [1:4] "Trans.Caffeic.acid" "Gallic.acid" "Quinic.acid" "X3.caffeo
 $ 16.8: chr "Catechin"
 $ 17.5: chr "Ascorbic.acid"
 $ 21  : chr [1:3] "Mannose.6.phosphate" "Pyroglutamic.acid" "Threonic.acid"
 $ 22  : chr [1:2] "GABA" "Putrescine"
 $ 23  : chr "Uracil"

```

```

> nn <- t(t(sapply(intmtbs,length)))
> nn
      [,1]
1.2      3
1.3      1
2.1      1
2.2      2
3.1      2
3.3      1
3.4      1
3.99     3
5         1
6         2
8.1       2
10.6      5
11        1
12.2      1
13.1      8
16.1      1
16.2      4
16.8      1
17.5      1
21        3
22        2
23        1

> # unlist(intmtbs)
> head(mfdata[unlist(intmtbs),2:3], 10)

      Bin
Glyceric.acid      1.2.1001
Glycine             1.2.1002
Serine              1.2.1006
Fructose.6.phosphate 1.3.1002
Sucrose             2.1.1.1006
Fructose            2.2.1.1001
Glucose             2.2.1.1002
Galactinol          3.1.1001
Raffinose           3.1.1002
Threitol            3.3.1011

      Description
Glyceric.acid      PS.photorespiration.glycerate
Glycine            PS.photorespiration.glycine
Serine             PS.photorespiration.serine
Fructose.6.phosphate PS.calvin cycle.fructose 6-phosphate
Sucrose            major CHO metabolism.synthesis.sucrose.sucrose
Fructose           major CHO metabolism.degradation.sucrose.fructose
Glucose            major CHO metabolism.degradation.sucrose.glucose
Galactinol         minor CHO metabolism.raffinose family.galactinol
Raffinose          minor CHO metabolism.raffinose family.raffinose
Threitol           minor CHO metabolism.sugar alcohols.threitol

> tail(mfdata[unlist(intmtbs),2:3], 10)

```

```

                                Bin
Quinic.acid                    16.2.99.1044
X3.caffeoylquinic.acid 16.2.99.1008
Catechin                      16.8.7.1001
Ascorbic.acid                 17.5.1001
Mannose.6.phosphate          21.1009
Pyroglutamic.acid           21.1010
Threonic.acid                21.1011
GABA                         22.1002
Putrescine                   22.1003
Uracil                       23.2.1002

Quinic.acid                    secondary metabolism.phenylpropanoids.unspecified
X3.caffeoylquinic.acid secondary metabolism.phenylpropanoids.unspecified.3-caf
Catechin                      secondary metabolism.flavonoids.flavan 3
Ascorbic.acid                 hormone metabolism.ethyle
Mannose.6.phosphate          redox
Pyroglutamic.acid           redox.p
Threonic.acid                red
GABA                         polyamine met
Putrescine                   polyamine metabolis
Uracil                       nucleotide metabolism.degrad

> length(unique(unlist(intmtbs)))
[1] 47

```

3.11 Created objects overview

```
> #if(!exists("addObject")) {
> addObject <- function(x=NULL, desc="", x0=my.objects) {
+ if(is.null(x)) x0 <- data.frame(name="", description="", class="", nrow=NA, ncol=NA)
+ nr <- length(x)
+ nc <- ncol(x)
+ if(is.data.frame(x) | is.matrix(x) | is.array(x) ) {
+   nr <- nrow(x)
+   nc <- ncol(x)
+ }
+ if(is.null(nc)) nc <- NA
+ x0 <- rbind(x0, c(deparse(substitute(x)), desc, class(x)[1], nr, nc))
+ x0 <- x0[x0$name!="", ]
+ }
+ rownames(x0) <- 1:nrow(x0)
+ return(x0)
+ }
> #}

> (my.objects <- addObject())
  name description class nrow ncol
1      NA      NA
> (my.objects <- addObject(t18, "Transcripts for 2018"))
  name      description      class  nrow ncol
1  t18 Transcripts for 2018 data.frame 15242   48
> (my.objects <- addObject(t19, "Transcripts for 2019"))
  name      description      class  nrow ncol
1  t18 Transcripts for 2018 data.frame 15242   48
2  t19 Transcripts for 2019 data.frame 15242   32
> (my.objects <- addObject(t1819, "Transcripts for 18/19"))
  name      description      class  nrow ncol
1  t18 Transcripts for 2018 data.frame 15242   48
2  t19 Transcripts for 2019 data.frame 15242   32
3 t1819 Transcripts for 18/19 data.frame 15242   80
> (my.objects <- addObject(pdata18, "Phenodata for 2018"))
  name      description      class  nrow ncol
1  t18 Transcripts for 2018 data.frame 15242   48
2  t19 Transcripts for 2019 data.frame 15242   32
3 t1819 Transcripts for 18/19 data.frame 15242   80
4 pdata18 Phenodata for 2018 data.frame    48   21
> (my.objects <- addObject(pdata19, "Phenodata for 2019"))
  name      description      class  nrow ncol
1  t18 Transcripts for 2018 data.frame 15242   48
2  t19 Transcripts for 2019 data.frame 15242   32
3 t1819 Transcripts for 18/19 data.frame 15242   80
4 pdata18 Phenodata for 2018 data.frame    48   21
5 pdata19 Phenodata for 2019 data.frame    32   21
> (my.objects <- addObject(pdata1819, "Phenodata for 2018/19"))
```

```

      name      description      class  nrow ncol
1      t18  Transcripts for 2018 data.frame 15242  48
2      t19  Transcripts for 2019 data.frame 15242  32
3      t1819 Transcripts for 18/19 data.frame 15242  80
4      pdata18  Phenodata for 2018 data.frame  48  21
5      pdata19  Phenodata for 2019 data.frame  32  21
6      pdata1819 Phenodata for 2018/19 data.frame  80  21
> (my.objects <- addObject(fdata,"Trans. featuredata 18/19"))

      name      description      class  nrow ncol
1      t18  Transcripts for 2018 data.frame 15242  48
2      t19  Transcripts for 2019 data.frame 15242  32
3      t1819  Transcripts for 18/19 data.frame 15242  80
4      pdata18  Phenodata for 2018 data.frame  48  21
5      pdata19  Phenodata for 2019 data.frame  32  21
6      pdata1819 Phenodata for 2018/19 data.frame  80  21
7      fdata Trans. featuredata 18/19 data.frame 16936  5
> (my.objects <- addObject(m18,"Metabolites for 2018"))

      name      description      class  nrow ncol
1      t18  Transcripts for 2018 data.frame 15242  48
2      t19  Transcripts for 2019 data.frame 15242  32
3      t1819  Transcripts for 18/19 data.frame 15242  80
4      pdata18  Phenodata for 2018 data.frame  48  21
5      pdata19  Phenodata for 2019 data.frame  32  21
6      pdata1819 Phenodata for 2018/19 data.frame  80  21
7      fdata Trans. featuredata 18/19 data.frame 16936  5
8      m18  Metabolites for 2018 data.frame  96  60
> (my.objects <- addObject(m19,"Metabolites for 2019"))

      name      description      class  nrow ncol
1      t18  Transcripts for 2018 data.frame 15242  48
2      t19  Transcripts for 2019 data.frame 15242  32
3      t1819  Transcripts for 18/19 data.frame 15242  80
4      pdata18  Phenodata for 2018 data.frame  48  21
5      pdata19  Phenodata for 2019 data.frame  32  21
6      pdata1819 Phenodata for 2018/19 data.frame  80  21
7      fdata Trans. featuredata 18/19 data.frame 16936  5
8      m18  Metabolites for 2018 data.frame  96  60
9      m19  Metabolites for 2019 data.frame  96  60
> (my.objects <- addObject(m1819,"Metabolites for 18/19"))

      name      description      class  nrow ncol
1      t18  Transcripts for 2018 data.frame 15242  48
2      t19  Transcripts for 2019 data.frame 15242  32
3      t1819  Transcripts for 18/19 data.frame 15242  80
4      pdata18  Phenodata for 2018 data.frame  48  21
5      pdata19  Phenodata for 2019 data.frame  32  21
6      pdata1819 Phenodata for 2018/19 data.frame  80  21
7      fdata Trans. featuredata 18/19 data.frame 16936  5
8      m18  Metabolites for 2018 data.frame  96  60
9      m19  Metabolites for 2019 data.frame  96  60
10     m1819  Metabolites for 18/19 data.frame  192  60
> (my.objects <- addObject(sm1819,"Standardized metabolites 18/19"))

```



```

      name                description      class  nrow ncol
1      t18      Transcripts for 2018 data.frame 15242   48
2      t19      Transcripts for 2019 data.frame 15242   32
3     t1819      Transcripts for 18/19 data.frame 15242   80
4    pdata18      Phenodata for 2018 data.frame    48   21
5    pdata19      Phenodata for 2019 data.frame    32   21
6  pdata1819      Phenodata for 2018/19 data.frame    80   21
7      fdata      Trans. featuredata 18/19 data.frame 16936    5
8      m18      Metabolites for 2018 data.frame    96   60
9      m19      Metabolites for 2019 data.frame    96   60
10     m1819      Metabolites for 18/19 data.frame   192   60
11    sm1819 Standardized metabolites 18/19      matrix    55  192
> (my.objects <- addObject(mfdata,"Metabolites featuredata 18/19"))

      name                description      class  nrow ncol
1      t18      Transcripts for 2018 data.frame 15242   48
2      t19      Transcripts for 2019 data.frame 15242   32
3     t1819      Transcripts for 18/19 data.frame 15242   80
4    pdata18      Phenodata for 2018 data.frame    48   21
5    pdata19      Phenodata for 2019 data.frame    32   21
6  pdata1819      Phenodata for 2018/19 data.frame    80   21
7      fdata      Trans. featuredata 18/19 data.frame 16936    5
8      m18      Metabolites for 2018 data.frame    96   60
9      m19      Metabolites for 2019 data.frame    96   60
10     m1819      Metabolites for 18/19 data.frame   192   60
11    sm1819 Standardized metabolites 18/19      matrix    55  192
12    mfdata      Metabolites featuredata 18/19 data.frame    55    3
> (my.objects <- addObject(intgenes,"Names of genes in bins"))

      name                description      class  nrow ncol
1      t18      Transcripts for 2018 data.frame 15242   48
2      t19      Transcripts for 2019 data.frame 15242   32
3     t1819      Transcripts for 18/19 data.frame 15242   80
4    pdata18      Phenodata for 2018 data.frame    48   21
5    pdata19      Phenodata for 2019 data.frame    32   21
6  pdata1819      Phenodata for 2018/19 data.frame    80   21
7      fdata      Trans. featuredata 18/19 data.frame 16936    5
8      m18      Metabolites for 2018 data.frame    96   60
9      m19      Metabolites for 2019 data.frame    96   60
10     m1819      Metabolites for 18/19 data.frame   192   60
11    sm1819 Standardized metabolites 18/19      matrix    55  192
12    mfdata      Metabolites featuredata 18/19 data.frame    55    3
13  intgenes      Names of genes in bins      list    22 <NA>
> (my.objects <- addObject(intmtbs,"Names of metabolites in bins"))

      name                description      class  nrow ncol
1      t18      Transcripts for 2018 data.frame 15242   48
2      t19      Transcripts for 2019 data.frame 15242   32
3     t1819      Transcripts for 18/19 data.frame 15242   80
4    pdata18      Phenodata for 2018 data.frame    48   21
5    pdata19      Phenodata for 2019 data.frame    32   21
6  pdata1819      Phenodata for 2018/19 data.frame    80   21
7      fdata      Trans. featuredata 18/19 data.frame 16936    5
8      m18      Metabolites for 2018 data.frame    96   60
9      m19      Metabolites for 2019 data.frame    96   60

```

10	m1819	Metabolites for 18/19	data.frame	192	60
11	sm1819	Standardized metabolites 18/19	matrix	55	192
12	mfddata	Metabolites featuredata 18/19	data.frame	55	3
13	intgenes	Names of genes in bins	list	22	<NA>
14	intmtbs	Names of metabolites in bins	list	22	<NA>

> *my.objects*

	name	description	class	nrow	ncol
1	t18	Transcripts for 2018	data.frame	15242	48
2	t19	Transcripts for 2019	data.frame	15242	32
3	t1819	Transcripts for 18/19	data.frame	15242	80
4	pdata18	Phenodata for 2018	data.frame	48	21
5	pdata19	Phenodata for 2019	data.frame	32	21
6	pdata1819	Phenodata for 2018/19	data.frame	80	21
7	fdata	Trans. featuredata 18/19	data.frame	16936	5
8	m18	Metabolites for 2018	data.frame	96	60
9	m19	Metabolites for 2019	data.frame	96	60
10	m1819	Metabolites for 18/19	data.frame	192	60
11	sm1819	Standardized metabolites 18/19	matrix	55	192
12	mfddata	Metabolites featuredata 18/19	data.frame	55	3
13	intgenes	Names of genes in bins	list	22	<NA>
14	intmtbs	Names of metabolites in bins	list	22	<NA>

List of data objects:

> *my.objects*

	name	description	class	nrow	ncol
1	t18	Transcripts for 2018	data.frame	15242	48
2	t19	Transcripts for 2019	data.frame	15242	32
3	t1819	Transcripts for 18/19	data.frame	15242	80
4	pdata18	Phenodata for 2018	data.frame	48	21
5	pdata19	Phenodata for 2019	data.frame	32	21
6	pdata1819	Phenodata for 2018/19	data.frame	80	21
7	fdata	Trans. featuredata 18/19	data.frame	16936	5
8	m18	Metabolites for 2018	data.frame	96	60
9	m19	Metabolites for 2019	data.frame	96	60
10	m1819	Metabolites for 18/19	data.frame	192	60
11	sm1819	Standardized metabolites 18/19	matrix	55	192
12	mfddata	Metabolites featuredata 18/19	data.frame	55	3
13	intgenes	Names of genes in bins	list	22	<NA>
14	intmtbs	Names of metabolites in bins	list	22	<NA>

3.12 Data overview

```
> x <- my.objects
> x$name[1]
[1] "t18"
> for(i in 1:nrow(x)){
+ cat("\n\n----- ", x[i,1], ": ", x[i,2], " -----")
+ print(x[i,])
+ cat("\n")
+ print(head(eval(as.name(x[i,1]))))
+ }
```

```
----- t18: Transcripts for 2018 -----
```

name	description	class	nrow	ncol
1 t18	Transcripts for 2018	data.frame	15242	48
	C18_11d_WS1 C18_11d_WS2 C18_11d_WS3 C18_11d_WS4			
Vitvi15g01736	4.6646023 4.109897 4.4482203 4.013955			
Vitvi07g02832	-2.4786650 -1.601359 -1.4274193 -2.066419			
Vitvi07g02830	-1.8506337 -2.218030 -1.0648492 -1.580992			
Vitvi07g02812	-0.5805446 -1.266940 -0.3278837 -1.019113			
Vitvi07g02811	2.2762225 1.823447 1.9550503 1.648742			
Vitvi09g02033	-1.6901691 -2.218030 -2.6498117 -1.449747			
	C18_11d_WW1 C18_11d_WW2 C18_11d_WW3 C18_11d_WW4			
Vitvi15g01736	4.717536 4.154237 4.475261 4.466465			
Vitvi07g02832	-2.608485 -1.801183 -1.886474 -3.583384			
Vitvi07g02830	-1.544354 -1.405255 -1.755229 -1.381750			
Vitvi07g02812	-0.858463 -0.434401 -1.234397 -1.047331			
Vitvi07g02811	2.086902 2.105707 2.134837 1.908469			
Vitvi09g02033	-2.608485 -1.961648 -3.108866 -4.320350			
	C18_34d_WS1 C18_34d_WS2 C18_34d_WS3 C18_34d_WS4			
Vitvi15g01736	4.400333 4.641164 4.4191231 4.534438			
Vitvi07g02832	-5.683146 -2.452000 -4.4274120 -1.876949			
Vitvi07g02830	-2.513221 -2.452000 -4.4274120 -2.263972			
Vitvi07g02812	-2.875791 -2.693008 -2.5529429 -3.157057			
Vitvi07g02811	1.414886 1.409803 0.3970164 1.273993			
Vitvi09g02033	-2.513221 -3.345084 -2.1054839 -1.716484			
	C18_34d_WW1 C18_34d_WW2 C18_34d_WW3 C18_34d_WW4			
Vitvi15g01736	4.924801 5.085690 5.3397350 5.263629			
Vitvi07g02832	-2.827859 -3.130016 -4.6322874 -3.196388			
Vitvi07g02830	-3.190429 -1.545054 -2.1297871 -3.196388			
Vitvi07g02812	-2.827859 -1.182484 -3.4098950 -2.303303			
Vitvi07g02811	1.517916 1.357250 0.9626591 1.344985			
Vitvi09g02033	-4.412821 -3.130016 -2.3103594 -4.418780			
	C18_67d_WS1 C18_67d_WS2 C18_67d_WS3 C18_67d_WS4			
Vitvi15g01736	2.05871733 2.2895026 2.9234830 2.575657			
Vitvi07g02832	-5.85417200 -4.4786818 -4.4659691 -2.468738			
Vitvi07g02830	-2.15373228 -3.2562893 -3.7290035 -2.709746			
Vitvi07g02812	-1.21031581 -2.3632045 -2.3504919 -2.999252			
Vitvi07g02811	0.02847105 0.5362686 0.9824914 1.231702			
Vitvi09g02033	-4.26920950 -3.7417162 -2.5915000 -3.847249			

	C18_67d_WW1	C18_67d_WW2	C18_67d_WW3	C18_67d_WW4
Vitvi15g01736	3.891121	3.040087	4.216897	3.763086
Vitvi07g02832	-2.726982	-4.610965	-2.436913	-3.355855
Vitvi07g02830	-2.726982	-3.873999	-1.493496	-2.075747
Vitvi07g02812	-1.672534	-3.388572	-2.230462	-2.462770
Vitvi07g02811	1.436764	1.552266	1.811015	1.352490
Vitvi09g02033	-2.520531	-2.736495	-3.815424	-2.993285
	F18_10d_WS1	F18_10d_WS2	F18_10d_WS3	F18_10d_WS4
Vitvi15g01736	4.8591409	4.8669435	4.9805904	4.9453953
Vitvi07g02832	2.8881443	2.7032394	2.2757651	2.0553154
Vitvi07g02830	2.8426117	2.4130023	2.2135368	2.0169691
Vitvi07g02812	0.8222302	0.9363895	0.7209384	0.3104447
Vitvi07g02811	3.5853480	3.5007015	3.2965509	3.2141610
Vitvi09g02033	1.0793880	1.0850336	0.6285743	0.8579324
	F18_10d_WW1	F18_10d_WW2	F18_10d_WW3	F18_10d_WW4
Vitvi15g01736	5.705006	4.619238	4.808548	5.276124
Vitvi07g02832	2.747538	3.349854	2.537311	2.621336
Vitvi07g02830	2.287722	3.464855	1.989824	2.321031
Vitvi07g02812	1.073767	1.384521	1.472076	1.016877
Vitvi07g02811	3.818074	4.000053	3.198197	3.501954
Vitvi09g02033	1.073767	1.566041	1.237985	1.268416
	F18_34d_WS1	F18_34d_WS2	F18_34d_WS3	F18_34d_WS4
Vitvi15g01736	4.0647184	3.8504580	5.1418322	4.6269091
Vitvi07g02832	2.2592790	2.1761360	2.3686660	1.2127920
Vitvi07g02830	2.1186455	1.9359657	2.6356368	1.5129655
Vitvi07g02812	0.4316833	-0.6220298	-0.5985972	-0.2055206
Vitvi07g02811	2.9490282	2.7595613	3.1300210	2.4602029
Vitvi09g02033	1.5459405	1.3699329	1.4288835	1.4477479
	F18_34d_WW1	F18_34d_WW2	F18_34d_WW3	F18_34d_WW4
Vitvi15g01736	4.0961725	4.80222138	4.3291524	4.4419027
Vitvi07g02832	1.8816574	1.82887526	1.7895023	1.6490200
Vitvi07g02830	2.1414534	1.62149541	2.1153419	2.1541121
Vitvi07g02812	0.1031253	-0.09471163	0.3053805	0.2855497
Vitvi07g02811	3.0025984	2.73213947	2.8750439	3.0458304
Vitvi09g02033	1.7460934	1.45938991	2.0072243	1.2444445
	F18_67d_WS1	F18_67d_WS2	F18_67d_WS3	F18_67d_WS4
Vitvi15g01736	1.5831276	1.7408584	2.97840555	4.1664059
Vitvi07g02832	1.3093668	1.9241330	2.01456521	2.9813855
Vitvi07g02830	0.8382242	1.4203666	2.18501915	2.8731326
Vitvi07g02812	0.1974739	0.4558154	-0.03878421	-0.0111843
Vitvi07g02811	1.8823168	2.5341865	2.65708760	2.9461961
Vitvi09g02033	1.6066824	1.5040245	1.25520700	0.9986635
	F18_67d_WW1	F18_67d_WW2	F18_67d_WW3	F18_67d_WW4
Vitvi15g01736	3.5580430	3.569471	4.4112089	4.3597440
Vitvi07g02832	2.5563386	2.180583	2.6637430	2.7538173
Vitvi07g02830	2.0265816	2.154972	2.7552617	2.3663511
Vitvi07g02812	0.6773148	0.106805	-0.2413317	-0.1063251
Vitvi07g02811	3.0678390	2.949349	2.9761917	2.9625700
Vitvi09g02033	1.7205680	1.541742	1.6527997	1.3320450

----- t19: Transcripts for 2019 -----

name	description	class	nrow	ncol
2	t19 Transcripts for 2019	data.frame	15242	32
	C19_22d_WS1	C19_22d_WS2	C19_22d_WS3	C19_22d_WS4
Vitvi15g01736	3.18	3.50	3.19	3.61
Vitvi07g02832	-5.05	-3.02	-0.80	-0.02
Vitvi07g02830	-5.05	-5.35	-2.39	-3.99
Vitvi07g02812	-1.35	-0.95	-0.15	0.26
Vitvi07g02811	2.09	2.29	2.34	2.63
Vitvi09g02033	-5.05	-3.76	-2.39	-2.76
	C19_22d_WW1	C19_22d_WW2	C19_22d_WW3	C19_22d_WW4
Vitvi15g01736	5.42	5.35	4.68	4.92
Vitvi07g02832	-1.36	-2.10	-1.15	-3.81
Vitvi07g02830	-2.28	-1.81	-2.07	-2.59
Vitvi07g02812	-1.36	0.16	-0.29	-0.75
Vitvi07g02811	2.85	3.16	3.09	2.89
Vitvi09g02033	-5.45	-3.68	-1.78	-3.81
	C19_44d_WS1	C19_44d_WS2	C19_44d_WS3	C19_44d_WS4
Vitvi15g01736	5.13	5.19	5.71	5.29
Vitvi07g02832	-3.13	-1.28	-3.18	-2.29
Vitvi07g02830	-3.87	-5.53	-5.50	-2.29
Vitvi07g02812	-0.10	-1.01	-0.29	-0.04
Vitvi07g02811	2.11	1.92	2.40	2.29
Vitvi09g02033	-3.87	-3.95	-2.69	-2.00
	C19_44d_WW1	C19_44d_WW2	C19_44d_WW3	C19_44d_WW4
Vitvi15g01736	6.19	5.62	5.62	6.19
Vitvi07g02832	-5.54	-5.31	-3.73	-1.81
Vitvi07g02830	-3.22	-5.31	-3.73	-2.05
Vitvi07g02812	-0.59	-0.45	-1.07	-0.55
Vitvi07g02811	2.44	2.13	2.08	2.26
Vitvi09g02033	-3.22	-3.72	-3.73	-3.18
	F19_22d_WS1	F19_22d_WS2	F19_22d_WS3	F19_22d_WS4
Vitvi15g01736	3.03	3.93	4.24	2.85
Vitvi07g02832	3.35	3.23	3.02	2.98
Vitvi07g02830	2.28	2.39	1.75	1.35
Vitvi07g02812	2.19	1.04	0.89	1.56
Vitvi07g02811	3.84	3.72	3.01	3.43
Vitvi09g02033	2.70	1.61	1.94	2.47
	F19_22d_WW1	F19_22d_WW2	F19_22d_WW3	F19_22d_WW4
Vitvi15g01736	5.00	4.97	4.47	5.51
Vitvi07g02832	3.18	3.04	2.81	3.05
Vitvi07g02830	2.59	2.07	1.81	2.20
Vitvi07g02812	1.72	1.08	1.42	1.35
Vitvi07g02811	3.79	3.43	3.24	3.33
Vitvi09g02033	2.24	1.90	2.08	1.25
	F19_44d_WS1	F19_44d_WS2	F19_44d_WS3	F19_44d_WS4
Vitvi15g01736	5.84	5.83	4.56	5.23
Vitvi07g02832	2.54	3.14	3.01	2.16
Vitvi07g02830	1.13	2.25	2.18	1.90
Vitvi07g02812	0.99	0.84	0.85	0.22
Vitvi07g02811	2.91	3.10	3.18	2.61
Vitvi09g02033	1.21	1.67	2.52	2.21
	F19_44d_WW1	F19_44d_WW2	F19_44d_WW3	F19_44d_WW4

Vitvi15g01736	5.44	6.13	5.96	6.16
Vitvi07g02832	3.84	3.05	3.89	4.02
Vitvi07g02830	2.74	2.79	2.90	2.88
Vitvi07g02812	1.03	0.93	1.49	1.29
Vitvi07g02811	3.32	2.89	3.35	3.26
Vitvi09g02033	1.99	1.14	1.65	1.29

----- t1819: Transcripts for 18/19 -----

name	description	class	nrow	ncol
3 t1819	Transcripts for 18/19	data.frame	15242	80

	C18_11d_WS1	C18_11d_WS2	C18_11d_WS3	C18_11d_WS4
Vitvi15g01736	4.6646023	4.109897	4.4482203	4.013955
Vitvi07g02832	-2.4786650	-1.601359	-1.4274193	-2.066419
Vitvi07g02830	-1.8506337	-2.218030	-1.0648492	-1.580992
Vitvi07g02812	-0.5805446	-1.266940	-0.3278837	-1.019113
Vitvi07g02811	2.2762225	1.823447	1.9550503	1.648742
Vitvi09g02033	-1.6901691	-2.218030	-2.6498117	-1.449747
	C18_11d_WW1	C18_11d_WW2	C18_11d_WW3	C18_11d_WW4
Vitvi15g01736	4.717536	4.154237	4.475261	4.466465
Vitvi07g02832	-2.608485	-1.801183	-1.886474	-3.583384
Vitvi07g02830	-1.544354	-1.405255	-1.755229	-1.381750
Vitvi07g02812	-0.858463	-0.434401	-1.234397	-1.047331
Vitvi07g02811	2.086902	2.105707	2.134837	1.908469
Vitvi09g02033	-2.608485	-1.961648	-3.108866	-4.320350
	C18_34d_WS1	C18_34d_WS2	C18_34d_WS3	C18_34d_WS4
Vitvi15g01736	4.400333	4.641164	4.4191231	4.534438
Vitvi07g02832	-5.683146	-2.452000	-4.4274120	-1.876949
Vitvi07g02830	-2.513221	-2.452000	-4.4274120	-2.263972
Vitvi07g02812	-2.875791	-2.693008	-2.5529429	-3.157057
Vitvi07g02811	1.414886	1.409803	0.3970164	1.273993
Vitvi09g02033	-2.513221	-3.345084	-2.1054839	-1.716484
	C18_34d_WW1	C18_34d_WW2	C18_34d_WW3	C18_34d_WW4
Vitvi15g01736	4.924801	5.085690	5.3397350	5.263629
Vitvi07g02832	-2.827859	-3.130016	-4.6322874	-3.196388
Vitvi07g02830	-3.190429	-1.545054	-2.1297871	-3.196388
Vitvi07g02812	-2.827859	-1.182484	-3.4098950	-2.303303
Vitvi07g02811	1.517916	1.357250	0.9626591	1.344985
Vitvi09g02033	-4.412821	-3.130016	-2.3103594	-4.418780
	C18_67d_WS1	C18_67d_WS2	C18_67d_WS3	C18_67d_WS4
Vitvi15g01736	2.05871733	2.2895026	2.9234830	2.575657
Vitvi07g02832	-5.85417200	-4.4786818	-4.4659691	-2.468738
Vitvi07g02830	-2.15373228	-3.2562893	-3.7290035	-2.709746
Vitvi07g02812	-1.21031581	-2.3632045	-2.3504919	-2.999252
Vitvi07g02811	0.02847105	0.5362686	0.9824914	1.231702
Vitvi09g02033	-4.26920950	-3.7417162	-2.5915000	-3.847249
	C18_67d_WW1	C18_67d_WW2	C18_67d_WW3	C18_67d_WW4
Vitvi15g01736	3.891121	3.040087	4.216897	3.763086
Vitvi07g02832	-2.726982	-4.610965	-2.436913	-3.355855
Vitvi07g02830	-2.726982	-3.873999	-1.493496	-2.075747
Vitvi07g02812	-1.672534	-3.388572	-2.230462	-2.462770

Vitvi07g02811	1.436764	1.552266	1.811015	1.352490
Vitvi09g02033	-2.520531	-2.736495	-3.815424	-2.993285
F18_10d_WS1	F18_10d_WS2	F18_10d_WS3	F18_10d_WS4	
Vitvi15g01736	4.8591409	4.8669435	4.9805904	4.9453953
Vitvi07g02832	2.8881443	2.7032394	2.2757651	2.0553154
Vitvi07g02830	2.8426117	2.4130023	2.2135368	2.0169691
Vitvi07g02812	0.8222302	0.9363895	0.7209384	0.3104447
Vitvi07g02811	3.5853480	3.5007015	3.2965509	3.2141610
Vitvi09g02033	1.0793880	1.0850336	0.6285743	0.8579324
F18_10d_WW1	F18_10d_WW2	F18_10d_WW3	F18_10d_WW4	
Vitvi15g01736	5.705006	4.619238	4.808548	5.276124
Vitvi07g02832	2.747538	3.349854	2.537311	2.621336
Vitvi07g02830	2.287722	3.464855	1.989824	2.321031
Vitvi07g02812	1.073767	1.384521	1.472076	1.016877
Vitvi07g02811	3.818074	4.000053	3.198197	3.501954
Vitvi09g02033	1.073767	1.566041	1.237985	1.268416
F18_34d_WS1	F18_34d_WS2	F18_34d_WS3	F18_34d_WS4	
Vitvi15g01736	4.0647184	3.8504580	5.1418322	4.6269091
Vitvi07g02832	2.2592790	2.1761360	2.3686660	1.2127920
Vitvi07g02830	2.1186455	1.9359657	2.6356368	1.5129655
Vitvi07g02812	0.4316833	-0.6220298	-0.5985972	-0.2055206
Vitvi07g02811	2.9490282	2.7595613	3.1300210	2.4602029
Vitvi09g02033	1.5459405	1.3699329	1.4288835	1.4477479
F18_34d_WW1	F18_34d_WW2	F18_34d_WW3	F18_34d_WW4	
Vitvi15g01736	4.0961725	4.80222138	4.3291524	4.4419027
Vitvi07g02832	1.8816574	1.82887526	1.7895023	1.6490200
Vitvi07g02830	2.1414534	1.62149541	2.1153419	2.1541121
Vitvi07g02812	0.1031253	-0.09471163	0.3053805	0.2855497
Vitvi07g02811	3.0025984	2.73213947	2.8750439	3.0458304
Vitvi09g02033	1.7460934	1.45938991	2.0072243	1.2444445
F18_67d_WS1	F18_67d_WS2	F18_67d_WS3	F18_67d_WS4	
Vitvi15g01736	1.5831276	1.7408584	2.97840555	4.1664059
Vitvi07g02832	1.3093668	1.9241330	2.01456521	2.9813855
Vitvi07g02830	0.8382242	1.4203666	2.18501915	2.8731326
Vitvi07g02812	0.1974739	0.4558154	-0.03878421	-0.0111843
Vitvi07g02811	1.8823168	2.5341865	2.65708760	2.9461961
Vitvi09g02033	1.6066824	1.5040245	1.25520700	0.9986635
F18_67d_WW1	F18_67d_WW2	F18_67d_WW3	F18_67d_WW4	
Vitvi15g01736	3.5580430	3.569471	4.4112089	4.3597440
Vitvi07g02832	2.5563386	2.180583	2.6637430	2.7538173
Vitvi07g02830	2.0265816	2.154972	2.7552617	2.3663511
Vitvi07g02812	0.6773148	0.106805	-0.2413317	-0.1063251
Vitvi07g02811	3.0678390	2.949349	2.9761917	2.9625700
Vitvi09g02033	1.7205680	1.541742	1.6527997	1.3320450
C19_22d_WS1	C19_22d_WS2	C19_22d_WS3	C19_22d_WS4	
Vitvi15g01736	3.18	3.50	3.19	3.61
Vitvi07g02832	-5.05	-3.02	-0.80	-0.02
Vitvi07g02830	-5.05	-5.35	-2.39	-3.99
Vitvi07g02812	-1.35	-0.95	-0.15	0.26
Vitvi07g02811	2.09	2.29	2.34	2.63
Vitvi09g02033	-5.05	-3.76	-2.39	-2.76
C19_22d_WW1	C19_22d_WW2	C19_22d_WW3	C19_22d_WW4	
Vitvi15g01736	5.42	5.35	4.68	4.92

Vitvi07g02832	-1.36	-2.10	-1.15	-3.81
Vitvi07g02830	-2.28	-1.81	-2.07	-2.59
Vitvi07g02812	-1.36	0.16	-0.29	-0.75
Vitvi07g02811	2.85	3.16	3.09	2.89
Vitvi09g02033	-5.45	-3.68	-1.78	-3.81
C19_44d_WS1	C19_44d_WS2	C19_44d_WS3	C19_44d_WS4	
Vitvi15g01736	5.13	5.19	5.71	5.29
Vitvi07g02832	-3.13	-1.28	-3.18	-2.29
Vitvi07g02830	-3.87	-5.53	-5.50	-2.29
Vitvi07g02812	-0.10	-1.01	-0.29	-0.04
Vitvi07g02811	2.11	1.92	2.40	2.29
Vitvi09g02033	-3.87	-3.95	-2.69	-2.00
C19_44d_WW1	C19_44d_WW2	C19_44d_WW3	C19_44d_WW4	
Vitvi15g01736	6.19	5.62	5.62	6.19
Vitvi07g02832	-5.54	-5.31	-3.73	-1.81
Vitvi07g02830	-3.22	-5.31	-3.73	-2.05
Vitvi07g02812	-0.59	-0.45	-1.07	-0.55
Vitvi07g02811	2.44	2.13	2.08	2.26
Vitvi09g02033	-3.22	-3.72	-3.73	-3.18
F19_22d_WS1	F19_22d_WS2	F19_22d_WS3	F19_22d_WS4	
Vitvi15g01736	3.03	3.93	4.24	2.85
Vitvi07g02832	3.35	3.23	3.02	2.98
Vitvi07g02830	2.28	2.39	1.75	1.35
Vitvi07g02812	2.19	1.04	0.89	1.56
Vitvi07g02811	3.84	3.72	3.01	3.43
Vitvi09g02033	2.70	1.61	1.94	2.47
F19_22d_WW1	F19_22d_WW2	F19_22d_WW3	F19_22d_WW4	
Vitvi15g01736	5.00	4.97	4.47	5.51
Vitvi07g02832	3.18	3.04	2.81	3.05
Vitvi07g02830	2.59	2.07	1.81	2.20
Vitvi07g02812	1.72	1.08	1.42	1.35
Vitvi07g02811	3.79	3.43	3.24	3.33
Vitvi09g02033	2.24	1.90	2.08	1.25
F19_44d_WS1	F19_44d_WS2	F19_44d_WS3	F19_44d_WS4	
Vitvi15g01736	5.84	5.83	4.56	5.23
Vitvi07g02832	2.54	3.14	3.01	2.16
Vitvi07g02830	1.13	2.25	2.18	1.90
Vitvi07g02812	0.99	0.84	0.85	0.22
Vitvi07g02811	2.91	3.10	3.18	2.61
Vitvi09g02033	1.21	1.67	2.52	2.21
F19_44d_WW1	F19_44d_WW2	F19_44d_WW3	F19_44d_WW4	
Vitvi15g01736	5.44	6.13	5.96	6.16
Vitvi07g02832	3.84	3.05	3.89	4.02
Vitvi07g02830	2.74	2.79	2.90	2.88
Vitvi07g02812	1.03	0.93	1.49	1.29
Vitvi07g02811	3.32	2.89	3.35	3.26
Vitvi09g02033	1.99	1.14	1.65	1.29

----- pdata18: Phenodata for 2018 -----

name	description	class	nrow	ncol
4	pdata18 Phenodata for 2018	data.frame	48	21

	ID	Variety	Date	variety	year	day
C18_11d_WS1	C18_11d_WS1	Cabernet Volos	12.06.2018	C	18	11
C18_11d_WS2	C18_11d_WS2	Cabernet Volos	12.06.2018	C	18	11
C18_11d_WS3	C18_11d_WS3	Cabernet Volos	12.06.2018	C	18	11
C18_11d_WS4	C18_11d_WS4	Cabernet Volos	12.06.2018	C	18	11
C18_11d_WW1	C18_11d_WW1	Cabernet Volos	12.06.2018	C	18	11
C18_11d_WW2	C18_11d_WW2	Cabernet Volos	12.06.2018	C	18	11
	treat	rep	project.name	species	plant.name	tissue
C18_11d_WS1	WS	1	EnViros Vitis	vinifera	grapevine	leaf
C18_11d_WS2	WS	2	EnViros Vitis	vinifera	grapevine	leaf
C18_11d_WS3	WS	3	EnViros Vitis	vinifera	grapevine	leaf
C18_11d_WS4	WS	4	EnViros Vitis	vinifera	grapevine	leaf
C18_11d_WW1	WW	1	EnViros Vitis	vinifera	grapevine	leaf
C18_11d_WW2	WW	2	EnViros Vitis	vinifera	grapevine	leaf
	health.status	plant.number	growth.location			
C18_11d_WS1	water stress		R1	Udine		
C18_11d_WS2	water stress		R2	Udine		
C18_11d_WS3	water stress		R3	Udine		
C18_11d_WS4	water stress		R4	Udine		
C18_11d_WW1	well watered		R1	Udine		
C18_11d_WW2	well watered		R2	Udine		
	growth.conditions					
C18_11d_WS1	outside					
C18_11d_WS2	outside					
C18_11d_WS3	outside					
C18_11d_WS4	outside					
C18_11d_WW1	outside					
C18_11d_WW2	outside					
C18_11d_WS1	several leaves ground together and stored at -80oC; an aliquot was					
C18_11d_WS2	several leaves ground together and stored at -80oC; an aliquot was					
C18_11d_WS3	several leaves ground together and stored at -80oC; an aliquot was					
C18_11d_WS4	several leaves ground together and stored at -80oC; an aliquot was					
C18_11d_WW1	several leaves ground together and stored at -80oC; an aliquot was					
C18_11d_WW2	several leaves ground together and stored at -80oC; an aliquot was					
	Metabolites.Order	Metabolites.File.Name				
C18_11d_WS1	2	1019Cabernet Volos_6_12_WS1.D				
C18_11d_WS2	4	1019Cabernet Volos_6_12_WS2.D				
C18_11d_WS3	102	1219Cabernet Volos_6_12_WS3.D				
C18_11d_WS4	100	1219Cabernet Volos_6_12_WS4.D				
C18_11d_WW1	6	1019Cabernet Volos_6_12_WW1.D				
C18_11d_WW2	8	1019Cabernet Volos_6_12_WW2.D				
	Metabolites.File	Transcripts.ID				
C18_11d_WS1	Cabernet Volos6_12WS	C1_S1				
C18_11d_WS2	Cabernet Volos6_12WS	C1_S2				
C18_11d_WS3	Cabernet Volos6_12WS	C1_S3				
C18_11d_WS4	Cabernet Volos6_12WS	C1_S4				
C18_11d_WW1	Cabernet Volos6_12WW	C1_W1				
C18_11d_WW2	Cabernet Volos6_12WW	C1_W2				

----- pdata19: Phenodata for 2019 -----

name	description	class	nrow	ncol
5 pdata19	Phenodata for 2019 data.frame		32	21

	ID	Variety	Date	variety	year	day
C19_22d_WS1	C19_22d_WS1	Cabernet Volos	26.06.2019	C	19	22
C19_22d_WS2	C19_22d_WS2	Cabernet Volos	26.06.2019	C	19	22
C19_22d_WS3	C19_22d_WS3	Cabernet Volos	26.06.2019	C	19	22
C19_22d_WS4	C19_22d_WS4	Cabernet Volos	26.06.2019	C	19	22
C19_22d_WW1	C19_22d_WW1	Cabernet Volos	26.06.2019	C	19	22
C19_22d_WW2	C19_22d_WW2	Cabernet Volos	26.06.2019	C	19	22

	treat	rep	project.name	species	plant.name	tissue
C19_22d_WS1	WS	1	EnViros Vitis	vinifera	grapevine	leaf
C19_22d_WS2	WS	2	EnViros Vitis	vinifera	grapevine	leaf
C19_22d_WS3	WS	3	EnViros Vitis	vinifera	grapevine	leaf
C19_22d_WS4	WS	4	EnViros Vitis	vinifera	grapevine	leaf
C19_22d_WW1	WW	1	EnViros Vitis	vinifera	grapevine	leaf
C19_22d_WW2	WW	2	EnViros Vitis	vinifera	grapevine	leaf

	health.status	plant.number	growth.location
C19_22d_WS1	water stress	R1	Udine
C19_22d_WS2	water stress	R2	Udine
C19_22d_WS3	water stress	R3	Udine
C19_22d_WS4	water stress	R4	Udine
C19_22d_WW1	well watered	R1	Udine
C19_22d_WW2	well watered	R2	Udine

	growth.conditions
C19_22d_WS1	outside
C19_22d_WS2	outside
C19_22d_WS3	outside
C19_22d_WS4	outside
C19_22d_WW1	outside
C19_22d_WW2	outside

C19_22d_WS1 several leaves ground together and stored at -80oC; an aliquot was

C19_22d_WS2 several leaves ground together and stored at -80oC; an aliquot was

C19_22d_WS3 several leaves ground together and stored at -80oC; an aliquot was

C19_22d_WS4 several leaves ground together and stored at -80oC; an aliquot was

C19_22d_WW1 several leaves ground together and stored at -80oC; an aliquot was

C19_22d_WW2 several leaves ground together and stored at -80oC; an aliquot was

	Metabolites.Order	Metabolites.File.Name
C19_22d_WS1	2	11120Cabernet_Volos_26_06_2019WS_1.D
C19_22d_WS2	27	11120Cabernet_Volos_26_06_2019WS_2.D
C19_22d_WS3	53	11420Cabernet_Volos_26_06_2019WS_3.D
C19_22d_WS4	79	11420Cabernet_Volos_26_06_2019WS_4.D
C19_22d_WW1	3	11120Cabernet_Volos_26_06_2019WW_1.D
C19_22d_WW2	28	11120Cabernet_Volos_26_06_2019WW_2.D

	Metabolites.File	Transcripts.ID
C19_22d_WS1	Cabernet Volos26_06WS	C1S1
C19_22d_WS2	Cabernet Volos26_06WS	C1S2
C19_22d_WS3	Cabernet Volos26_06WS	C1S3
C19_22d_WS4	Cabernet Volos26_06WS	C1S4
C19_22d_WW1	Cabernet Volos26_06WW	C1W1
C19_22d_WW2	Cabernet Volos26_06WW	C1W2

----- pdata1819: Phenodata for 2018/19 -----

	name	description	class	nrow	ncol
6	pdata1819	Phenodata for 2018/19	data.frame	80	21

	ID	Variety	Date	variety	year	day
C18_11d_WS1	C18_11d_WS1	Cabernet Volos	12.06.2018	C	18	11
C18_11d_WS2	C18_11d_WS2	Cabernet Volos	12.06.2018	C	18	11
C18_11d_WS3	C18_11d_WS3	Cabernet Volos	12.06.2018	C	18	11
C18_11d_WS4	C18_11d_WS4	Cabernet Volos	12.06.2018	C	18	11
C18_11d_WW1	C18_11d_WW1	Cabernet Volos	12.06.2018	C	18	11
C18_11d_WW2	C18_11d_WW2	Cabernet Volos	12.06.2018	C	18	11

	treat	rep	project.name	species	plant.name	tissue
C18_11d_WS1	WS	1	EnViros Vitis	vinifera	grapevine	leaf
C18_11d_WS2	WS	2	EnViros Vitis	vinifera	grapevine	leaf
C18_11d_WS3	WS	3	EnViros Vitis	vinifera	grapevine	leaf
C18_11d_WS4	WS	4	EnViros Vitis	vinifera	grapevine	leaf
C18_11d_WW1	WW	1	EnViros Vitis	vinifera	grapevine	leaf
C18_11d_WW2	WW	2	EnViros Vitis	vinifera	grapevine	leaf

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

	growth.conditions
C18_11d_WS1	outside
C18_11d_WS2	outside
C18_11d_WS3	outside
C18_11d_WS4	outside
C18_11d_WW1	outside
C18_11d_WW2	outside

C18_11d_WS1	several leaves ground together and stored at -80oC; an aliquot was
C18_11d_WS2	several leaves ground together and stored at -80oC; an aliquot was
C18_11d_WS3	several leaves ground together and stored at -80oC; an aliquot was
C18_11d_WS4	several leaves ground together and stored at -80oC; an aliquot was
C18_11d_WW1	several leaves ground together and stored at -80oC; an aliquot was
C18_11d_WW2	several leaves ground together and stored at -80oC; an aliquot was

	Metabolites.Order	Metabolites.File.Name
C18_11d_WS1	2	1019Cabernet Volos_6_12_WS1.D
C18_11d_WS2	4	1019Cabernet Volos_6_12_WS2.D
C18_11d_WS3	102	1219Cabernet Volos_6_12_WS3.D
C18_11d_WS4	100	1219Cabernet Volos_6_12_WS4.D
C18_11d_WW1	6	1019Cabernet Volos_6_12_WW1.D
C18_11d_WW2	8	1019Cabernet Volos_6_12_WW2.D

	Metabolites.File	Transcripts.ID
C18_11d_WS1	Cabernet Volos6_12WS	C1_S1
C18_11d_WS2	Cabernet Volos6_12WS	C1_S2
C18_11d_WS3	Cabernet Volos6_12WS	C1_S3

C18_11d_WS4	Cabernet Volos6_12WS	C1_S4
C18_11d_WW1	Cabernet Volos6_12WW	C1_W1
C18_11d_WW2	Cabernet Volos6_12WW	C1_W2

----- fdata: Trans. featuredata 18/19 -----

name	description	class	nrow	ncol
7 fdata	Trans. featuredata 18/19	data.frame	16936	5

YEAR	geneID	BINCODE	NAME
1 2018	Vitvi15g01736	26.9	misc.glutathione S transferases
2 2018	Vitvi07g02832	35.2	not assigned.unknown
3 2018	Vitvi07g02830	35.2	not assigned.unknown
4 2018	Vitvi07g02812	35.2	not assigned.unknown
5 2018	Vitvi07g02811	35.2	not assigned.unknown
6 2018	Vitvi09g02033	35.2	not assigned.unknown

1	glutathione S-transferase tau 7 Chr2:12618111-1261887
2	Disease resistance protein (TIR-NBS-LRR class) family Chr4:7197325-7201393
3	
4	
5	
6	Disease resistance protein (CC-NBS-LRR class) family Chr1:4145374-414768

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

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

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

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

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

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

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

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

C19_22d_WS2	10.69	12.24		7.71	8.39
C19_22d_WS3	8.34	10.82		8.21	4.05
C19_22d_WS4	5.94	10.75		9.73	11.80
C19_22d_WW1	8.68	14.73		13.54	3.79
C19_22d_WW2	6.65	15.20		21.62	5.53
Galactinol Galactose Gallic.acid Gluconic.acid					
C19_22d_WS1	18.37	12.24	8.35	10.27	
C19_22d_WS2	14.63	13.59	6.97	11.45	
C19_22d_WS3	19.87	11.75	4.26	9.88	
C19_22d_WS4	12.76	12.42	11.59	8.80	
C19_22d_WW1	11.17	15.85	8.83	8.55	
C19_22d_WW2	12.18	14.85	10.23	7.69	
Glucopyranose..H2O. Glucose Glutamic.acid Glyceric.acid					
C19_22d_WS1		7.92	11.29	40.46	6.60
C19_22d_WS2		13.10	12.31	14.61	7.73
C19_22d_WS3		10.09	11.09	4.98	9.26
C19_22d_WS4		9.05	11.56	7.01	8.10
C19_22d_WW1		6.55	13.44	22.22	6.49
C19_22d_WW2		8.59	12.87	10.24	5.66
Glycine Hydroquinone Myo.Inostol Isoleucine Leucine					
C19_22d_WS1	7.71	5.76	9.85	18.14	17.99
C19_22d_WS2	8.66	9.66	10.15	14.90	14.61
C19_22d_WS3	16.27	8.18	9.06	13.60	13.96
C19_22d_WS4	16.39	6.41	9.00	19.76	19.64
C19_22d_WW1	9.61	5.49	9.09	24.93	24.59
C19_22d_WW2	22.09	7.93	8.50	6.72	6.62
Lyxonic.acid Maleic.acid Malic.acid Malonic.acid					
C19_22d_WS1	10.61	10.45	9.97	3.38	
C19_22d_WS2	11.95	6.52	9.34	9.58	
C19_22d_WS3	9.29	5.28	9.45	7.40	
C19_22d_WS4	9.88	10.07	8.48	9.60	
C19_22d_WW1	9.79	5.66	10.31	3.53	
C19_22d_WW2	10.41	4.09	9.20	7.04	
Mannose.6.phosphate Melibiose Phenylalanine					
C19_22d_WS1		5.06	6.44	10.84	
C19_22d_WS2		6.60	6.69	9.08	
C19_22d_WS3		8.72	5.63	15.50	
C19_22d_WS4		9.13	4.52	19.50	
C19_22d_WW1		10.64	6.69	15.80	
C19_22d_WW2		14.61	6.01	7.75	
Phosphoric.acid Proline Putrescine Pyroglutamic.acid					
C19_22d_WS1	8.37	42.32	9.77	6.61	
C19_22d_WS2	10.42	29.09	17.21	11.75	
C19_22d_WS3	8.93	27.38	11.09	12.15	
C19_22d_WS4	10.84	24.39	11.07	13.65	
C19_22d_WW1	16.18	37.14	26.02	4.01	
C19_22d_WW2	17.27	2.09	6.03	6.17	
Quinic.acid X3.caffeoylquinic.acid Raffinose Rhamnose					
C19_22d_WS1	15.57		22.62	12.69	8.65
C19_22d_WS2	17.79		26.34	11.81	7.16
C19_22d_WS3	16.01		21.82	12.97	7.92
C19_22d_WS4	13.27		27.36	8.93	7.18
C19_22d_WW1	13.87		23.22	9.27	8.09

C19_22d_WW2	14.48			21.36	9.21	7.63
	Ribonic.acid	Ribose	Serine	Shikimic.acid	Succinic.acid	
C19_22d_WS1	10.72	8.67	7.52	25.77		14.82
C19_22d_WS2	12.01	10.68	10.27	27.03		14.23
C19_22d_WS3	9.29	8.24	23.26	26.88		12.09
C19_22d_WS4	9.88	8.45	22.24	22.56		8.96
C19_22d_WW1	9.90	8.22	10.73	25.90		11.32
C19_22d_WW2	10.44	9.96	7.29	25.63		10.23
	Sucrose	Tartaric.acid	Threitol	Threonic.acid		
C19_22d_WS1	9.14		5.49	8.74	6.89	
C19_22d_WS2	9.58		7.20	7.03	5.86	
C19_22d_WS3	8.30		7.11	13.37	4.25	
C19_22d_WS4	9.41		7.89	9.49	2.89	
C19_22d_WW1	9.33		6.96	7.26	3.78	
C19_22d_WW2	9.51		7.55	12.28	5.13	
	Threonolactone	Threonine	Uracil	Valine	Xylose	
C19_22d_WS1	7.24	11.78	6.22	24.43	9.58	
C19_22d_WS2	6.31	13.48	9.03	18.07	11.19	
C19_22d_WS3	4.64	9.94	7.75	24.16	8.97	
C19_22d_WS4	3.07	7.60	13.93	18.60	9.80	
C19_22d_WW1	6.32	7.58	9.59	26.02	11.86	
C19_22d_WW2	7.49	7.14	8.35	9.35	10.21	

----- m1819: Metabolites for 18/19 -----

name	description	class	nrow	ncol
10 m1819	Metabolites for 18/19	data.frame	192	60

	ID	Variety	Date	Treat	Rep	Alanine
C18_11d_WS1	C18_11d_WS1	Cabernet Volos	12.06.2018	WS	1	0.133
C18_11d_WS2	C18_11d_WS2	Cabernet Volos	12.06.2018	WS	2	0.115
C18_11d_WS3	C18_11d_WS3	Cabernet Volos	12.06.2018	WS	3	0.624
C18_11d_WS4	C18_11d_WS4	Cabernet Volos	12.06.2018	WS	4	0.649
C18_11d_WW1	C18_11d_WW1	Cabernet Volos	12.06.2018	WW	1	0.136
C18_11d_WW2	C18_11d_WW2	Cabernet Volos	12.06.2018	WW	2	0.230
	Arabinose	Ascorbic.acid	Aspartic.acid	GABA		
C18_11d_WS1	0.116	0.885	0.882	1.950		
C18_11d_WS2	0.120	1.147	0.613	1.054		
C18_11d_WS3	0.094	1.080	0.715	1.401		
C18_11d_WS4	0.112	1.587	0.827	1.705		
C18_11d_WW1	0.160	0.769	0.549	1.929		
C18_11d_WW2	0.147	0.903	0.625	1.513		
	Trans.Caffeic.acid	Catechin	Citric.acid	Erythronic.acid		
C18_11d_WS1	8.751	2.828	2.236			1.696
C18_11d_WS2	9.164	3.595	2.152			2.039
C18_11d_WS3	7.039	2.059	1.996			1.791
C18_11d_WS4	7.379	1.880	2.619			1.587
C18_11d_WW1	8.197	1.930	2.290			1.999
C18_11d_WW2	7.093	1.419	2.056			1.301
	Ethanolamine	Fructose	Fructose.6.phosphate	Fumaric.acid		
C18_11d_WS1	1.052	27.962	0.037			0.683
C18_11d_WS2	0.865	22.260	0.035			1.069

C18_11d_WS3	1.335	14.477		0.058	1.907
C18_11d_WS4	0.901	16.651		0.079	2.009
C18_11d_WW1	0.861	22.621		0.033	0.760
C18_11d_WW2	0.805	20.318		0.089	1.094
Galactinol Galactose Gallic.acid Gluconic.acid					
C18_11d_WS1	16.908	8.455	1.002	3.640	
C18_11d_WS2	13.660	8.218	0.958	3.911	
C18_11d_WS3	13.524	4.445	0.936	3.079	
C18_11d_WS4	14.463	6.358	0.905	3.421	
C18_11d_WW1	15.754	6.071	1.143	3.133	
C18_11d_WW2	13.891	5.467	0.917	2.805	
Glucopyranose..H2O. Glucose Glutamic.acid Glyceric.acid					
C18_11d_WS1		0.143	43.309	0.491	7.540
C18_11d_WS2		0.155	41.412	0.298	6.082
C18_11d_WS3		0.178	31.305	0.140	5.876
C18_11d_WS4		0.153	40.981	0.202	7.596
C18_11d_WW1		0.169	37.135	0.303	6.008
C18_11d_WW2		0.156	35.269	0.263	5.638
Glycine Hydroquinone Myo.Inostol Isoleucine Leucine					
C18_11d_WS1	0.742	0.161	91.071	0.055	0.022
C18_11d_WS2	0.727	0.208	89.166	0.054	0.027
C18_11d_WS3	0.913	0.099	97.202	0.072	0.033
C18_11d_WS4	0.742	0.176	114.143	0.150	0.079
C18_11d_WW1	1.031	0.101	85.266	0.146	0.077
C18_11d_WW2	0.847	0.161	90.745	0.096	0.050
Lyxonic.acid Maleic.acid Malic.acid Malonic.acid					
C18_11d_WS1	1.028	1.093	66.326	0.166	
C18_11d_WS2	1.187	1.486	73.855	0.140	
C18_11d_WS3	1.237	1.108	62.877	0.183	
C18_11d_WS4	1.020	1.084	66.638	0.233	
C18_11d_WW1	1.205	0.879	53.894	0.156	
C18_11d_WW2	1.096	1.202	51.917	0.170	
Mannose.6.phosphate Melibiose Phenylalanine					
C18_11d_WS1		0.088	0.227	0.095	
C18_11d_WS2		0.102	0.204	0.116	
C18_11d_WS3		0.134	0.069	0.103	
C18_11d_WS4		0.174	0.092	0.203	
C18_11d_WW1		0.082	0.178	0.104	
C18_11d_WW2		0.198	0.164	0.179	
Phosphoric.acid Proline Putrescine Pyroglutamic.acid					
C18_11d_WS1	23.244	0.011	0.054	5.790	
C18_11d_WS2	17.190	0.013	0.046	4.354	
C18_11d_WS3	18.909	0.006	0.104	8.169	
C18_11d_WS4	23.579	0.008	0.111	10.445	
C18_11d_WW1	31.264	0.006	0.066	4.966	
C18_11d_WW2	31.233	0.008	0.058	5.408	
Quinic.acid X3.caffeoylquinic.acid Raffinose Rhamnose					
C18_11d_WS1	1.615		0.677	1.117	0.603
C18_11d_WS2	1.304		0.635	1.544	0.472
C18_11d_WS3	1.254		0.378	0.961	0.516
C18_11d_WS4	1.106		0.423	1.164	0.634
C18_11d_WW1	1.985		0.576	0.870	0.534
C18_11d_WW2	1.513		0.462	1.001	0.747

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

----- sm1819: Standardized metabolites 18/19 -----

name	description	class	nrow	ncol
11 sm1819	Standardized metabolites 18/19 matrix		55	192

	C18_11d_WS1	C18_11d_WS2	C18_11d_WS3	C18_11d_WS4
Alanine	-1.42040510	-1.5237244	-0.3221074	-0.2941971
Arabinose	-0.89096253	-0.8768234	-0.9786693	-0.9055979
Ascorbic.acid	-0.48475127	-0.3013277	-0.3439011	-0.0716600
Aspartic.acid	-0.79435180	-1.0652846	-0.9506661	-0.8422994
GABA	-0.79478369	-1.3283418	-1.0815306	-0.9112230
Trans.Caffeic.acid	0.04856765	0.1856718	-0.5986832	-0.4584358
	C18_11d_WW1	C18_11d_WW2	C18_11d_WW3	C18_11d_WW4
Alanine	-1.4045568	-1.0312407	-0.8260696	-0.9777046
Arabinose	-0.7568413	-0.7921839	-0.9055979	-0.8982160
Ascorbic.acid	-0.5841291	-0.4705092	-0.5050201	-0.4658249
Aspartic.acid	-1.1473972	-1.0508478	-1.2872479	-1.0472819
GABA	-0.8041739	-1.0148328	-0.8827044	-1.2282093
Trans.Caffeic.acid	-0.1458728	-0.5759619	-0.4884020	-1.1855997
	C18_20d_WS1	C18_20d_WS2	C18_20d_WS3	C18_20d_WS4
Alanine	-1.30253488	-1.1485305	-0.4301155	-0.4301155
Arabinose	-0.82156681	-0.9093384	-0.9487134	-0.8945735
Ascorbic.acid	-0.40759378	-0.3990459	-0.2193190	-0.3969249
Aspartic.acid	-0.68028375	-1.1419912	-0.7477177	-1.0665004
GABA	-0.55840143	-0.6637706	-0.8598745	-0.8432557
Trans.Caffeic.acid	0.06651981	-0.6147770	-1.0784674	-0.9712290
	C18_20d_WW1	C18_20d_WW2	C18_20d_WW3	C18_20d_WW4
Alanine	-1.1669862	-1.1745048	-0.7070211	-0.67637466
Arabinose	-0.8733622	-0.9612891	-0.8277002	-0.96988871
Ascorbic.acid	-0.1710309	-0.3976312	-0.3309222	-0.08880282

Aspartic.acid	-0.9979629	-1.0091444	-0.8262651	-1.22149861
GABA	-0.9178608	-0.9071634	-0.5883746	-0.86516407
Trans.Caffeic.acid	0.6097629	-0.1444223	-0.2703104	-0.43635765
	C18_34d_WS1	C18_34d_WS2	C18_34d_WS3	C18_34d_WS4
Alanine	-0.6524125	-0.7493615	-0.5607169	-0.65060226
Arabinose	-0.8434404	-0.9285614	-0.8803135	-0.90559788
Ascorbic.acid	-0.3934041	-0.3618092	-0.4391011	-0.57954495
Aspartic.acid	-0.5681871	-1.3362907	-1.4955004	-1.23969930
GABA	0.5383838	0.6785329	0.4481893	0.08421358
Trans.Caffeic.acid	1.2085257	1.0325340	0.9791050	0.67184120
	C18_34d_WW1	C18_34d_WW2	C18_34d_WW3	C18_34d_WW4
Alanine	-0.4938681	-0.7208561	-0.57357704	-0.17365428
Arabinose	-0.8499066	-1.0407476	-0.92464525	-0.84666098
Ascorbic.acid	-0.8649740	-0.2872844	-0.49847064	-0.57499031
Aspartic.acid	-0.8642301	-2.2922701	-1.90683969	-0.97716973
GABA	0.9929407	0.1022634	0.51365512	-0.08629024
Trans.Caffeic.acid	0.9342980	-0.3488723	-0.05127649	-0.20189133
	C18_49d_WS1	C18_49d_WS2	C18_49d_WS3	C18_49d_WS4
Alanine	-0.2726324	-0.35831179	-0.58173446	-0.61190189
Arabinose	-1.0255800	-0.92856138	-0.94871336	-1.00617809
Ascorbic.acid	-0.6890378	-0.72067394	-0.74913040	-0.77756970
Aspartic.acid	-1.4783807	-1.33979505	-1.52418769	-1.82838040
GABA	0.2730391	-0.05768882	0.01397647	-0.01902277
Trans.Caffeic.acid	-0.7596655	-0.95833043	-1.34574708	-0.80549633
	C18_49d_WW1	C18_49d_WW2	C18_49d_WW3	C18_49d_WW4
Alanine	-0.78777647	-0.8640990	-0.8123175	-1.01596046
Arabinose	-1.02557995	-0.7674005	-0.9246452	-0.82770022
Ascorbic.acid	-0.63168277	-0.9822666	-1.0052447	-0.84341555
Aspartic.acid	-1.64349297	-1.5802398	-1.4372280	-1.68141186
GABA	-0.89011882	-0.3070515	-0.2091395	-0.03424594
Trans.Caffeic.acid	-0.09552259	0.4665606	-0.6970157	0.64777629
	C18_61d_WS1	C18_61d_WS2	C18_61d_WS3	C18_61d_WS4
Alanine	-0.3989935	-0.48953135	-0.9199530	-0.8991309
Arabinose	-1.0014654	-0.95705493	-0.9698887	-1.0061781
Ascorbic.acid	-0.8649740	-1.07533485	-1.2382552	-1.0429323
Aspartic.acid	-0.5700590	-0.60196936	-0.3984122	-0.5020430
GABA	0.2573183	0.03096133	0.2921707	-0.1017523
Trans.Caffeic.acid	-0.1502284	-1.07152665	-0.8442359	-1.2882030
	C18_61d_WW1	C18_61d_WW2	C18_61d_WW3	C18_61d_WW4
Alanine	-0.6973013	-0.7109465	-1.3993516	-1.2173427
Arabinose	-0.8499066	-0.9365057	-0.9169216	-1.0841181
Ascorbic.acid	-0.5713676	-0.4823576	-0.8554612	-0.7584837
Aspartic.acid	-0.9913337	-1.3720993	-1.0616491	-1.3328028
GABA	0.1848340	-0.3855115	0.1932726	0.4195016
Trans.Caffeic.acid	-0.4069089	0.1514097	-0.3879618	-1.1184425
	C18_67d_WS1	C18_67d_WS2	C18_67d_WS3	C18_67d_WS4
Alanine	-0.2683969	-0.2996921	-1.0099392	-0.9834577
Arabinose	-1.0511748	-0.9405354	-0.9968055	-0.9528633
Ascorbic.acid	-1.2546783	-0.9234174	-0.9445333	-1.0808826
Aspartic.acid	-0.6752302	-0.7219964	-0.8849168	-0.8531840
GABA	0.4999725	0.4293145	0.5888935	0.5085247
Trans.Caffeic.acid	-0.4596448	-0.5297954	-1.1254938	-0.6948336
	C18_67d_WW1	C18_67d_WW2	C18_67d_WW3	C18_67d_WW4

Alanine	-0.4668387	-0.4710387	-1.1412804	-1.1164723
Arabinose	-0.9876388	-1.0109446	-0.8665250	-0.9786693
Ascorbic.acid	-0.8663435	-1.2546783	-1.4019136	-0.9969523
Aspartic.acid	-1.0472819	-0.7572957	-1.6023971	-1.0592352
GABA	0.2650833	0.1418167	0.1148187	0.1764576
Trans.Caffeic.acid	-1.2192354	-0.4762171	-0.4916597	-0.7092651
F18_10d_WS1	F18_10d_WS2	F18_10d_WS3	F18_10d_WS4	
Alanine	-0.6801339	-0.7855869	-1.9290988	-1.9182512
Arabinose	-1.1325277	-1.0673212	-0.9921970	-1.0784436
Ascorbic.acid	-0.6795006	-0.6763499	-0.5668652	-0.8368111
Aspartic.acid	-0.2260179	-0.5146942	-0.4114244	-0.6291963
GABA	-3.5975121	-3.8432554	-3.7854179	-3.7311978
Trans.Caffeic.acid	-1.1712269	-1.5566942	-0.8241195	-1.2690901
F18_10d_WW1	F18_10d_WW2	F18_10d_WW3	F18_10d_WW4	
Alanine	-1.0189903	-1.11647226	-1.80872651	-1.7554137
Arabinose	-0.8982160	-0.91311277	-0.83080109	-0.9093384
Ascorbic.acid	-0.4550139	-0.59525382	-0.45348288	-0.3399824
Aspartic.acid	-0.3429779	-0.32748229	-0.32433165	-0.2883839
GABA	-3.3285334	-3.39726159	-3.38836674	-3.5016458
Trans.Caffeic.acid	0.1091013	-0.06183566	0.02982272	-0.3442159
F18_20d_WS1	F18_20d_WS2	F18_20d_WS3	F18_20d_WS4	
Alanine	-0.3989935	-0.4367744	-1.3639455	-1.1707356
Arabinose	-1.0511748	-0.9968055	-0.9968055	-0.6679676
Ascorbic.acid	-0.8704679	-0.8677156	-1.0607502	-0.9838834
Aspartic.acid	-0.6151265	-0.5961236	-1.0437330	-0.9611546
GABA	-0.8901188	-0.9636402	-0.8109439	-0.8724295
Trans.Caffeic.acid	-1.0670733	0.1618934	-1.2775696	-0.6335214
F18_20d_WW1	F18_20d_WW2	F18_20d_WW3	F18_20d_WW4	
Alanine	-0.8689990	-0.6915326	-1.1199637	-1.2054012
Arabinose	-1.0728454	-1.0157662	-1.0014654	-0.9246452
Ascorbic.acid	-0.7206739	-0.6879717	-0.8315716	-1.3566288
Aspartic.acid	-0.8019896	-0.8716862	-0.9696531	-0.7143743
GABA	-1.4867876	-1.1085653	-0.6976926	-0.5317253
Trans.Caffeic.acid	-0.1044514	0.3399237	-0.5600763	-0.4463728
F18_34d_WS1	F18_34d_WS2	F18_34d_WS3	F18_34d_WS4	
Alanine	-1.14853050	-1.00100193	-1.1164723	-1.1975502
Arabinose	-1.00146544	-1.01094460	-0.9612891	-0.9285614
Ascorbic.acid	-0.77035196	-0.80594079	-0.8447439	-1.0052447
Aspartic.acid	-0.08906787	-0.47296796	-0.3583326	-0.6157905
GABA	-0.71172267	-0.08786346	-0.4482032	-0.7101077
Trans.Caffeic.acid	0.38304173	-0.64636973	-0.3687437	-0.5260834
F18_34d_WW1	F18_34d_WW2	F18_34d_WW3	F18_34d_WW4	
Alanine	-0.798826516	-0.6763747	-0.9468693	-0.7966027
Arabinose	-0.786547801	-1.0618693	-1.0673212	-0.8597980
Ascorbic.acid	-1.754522307	-1.7216172	-1.6112704	-1.8200162
Aspartic.acid	-0.139533413	-0.3959358	-0.9190598	0.1918374
GABA	-0.832505609	-1.1659845	-0.9086835	-0.7763030
Trans.Caffeic.acid	-0.007332999	-0.0951660	0.1746206	-0.1098216
F18_49d_WS1	F18_49d_WS2	F18_49d_WS3	F18_49d_WS4	
Alanine	-0.8813990	-0.9359801	-0.8689990	-0.6839132
Arabinose	-1.0459286	-1.1016199	-1.0511748	-1.1729203
Ascorbic.acid	-1.2523087	-1.4287209	-1.6685424	-1.3649018
Aspartic.acid	-1.8737376	-0.5322996	-0.9362259	-0.8877828

GABA	0.7166446	0.5230477	0.3452471	-0.3126450
Trans.Caffeic.acid	-0.2820581	-0.6232825	-1.7938439	-1.9520321
	F18_49d_WW1	F18_49d_WW2	F18_49d_WW3	F18_49d_WW4
Alanine	-1.20935940	-1.2054012	-0.9359801	-1.08247037
Arabinose	-1.02064421	-1.1455620	-1.0564878	-0.97425592
Ascorbic.acid	-1.29874782	-0.6455914	-1.1911571	-1.22903904
Aspartic.acid	-0.81750417	-1.1487549	-1.0091444	-0.90130513
GABA	-0.15176956	-0.2414255	0.2016299	0.03950059
Trans.Caffeic.acid	0.03460538	-0.6957063	-1.5433162	-0.96405620
	F18_61d_WS1	F18_61d_WS2	F18_61d_WS3	F18_61d_WS4
Alanine	-1.34929542	-0.93868678	-0.6763747	-0.7309058
Arabinose	-1.23369161	-1.13899393	-1.1016199	-1.1590169
Ascorbic.acid	-1.26906519	-1.31406969	-1.3704714	-1.4888883
Aspartic.acid	-0.21430282	-0.19480061	-0.7851219	-0.9990735
GABA	-0.02029638	0.05699739	0.1523252	-0.5607751
Trans.Caffeic.acid	-0.70269666	-0.52361129	-1.5901101	-2.9498706
	F18_61d_WW1	F18_61d_WW2	F18_61d_WW3	F18_61d_WW4
Alanine	-1.6822688	-1.9075667	-1.2014648	-0.5559537
Arabinose	-1.0898708	-1.1590169	-1.1137095	-1.0109446
Ascorbic.acid	-1.2666470	-1.3270964	-1.2475931	-1.1634985
Aspartic.acid	-0.3489890	-0.8849168	-0.5813898	-0.6058921
GABA	-0.5567099	-0.4547891	-0.1848092	-0.3841255
Trans.Caffeic.acid	-1.4116358	-0.8760588	-1.1559043	-1.2052175
	F18_67d_WS1	F18_67d_WS2	F18_67d_WS3	F18_67d_WS4
Alanine	-1.2335835	-1.11996369	-0.50409137	-0.87641303
Arabinose	-1.1590169	-1.06732124	-1.20985284	-1.13899393
Ascorbic.acid	-1.5124122	-1.74023228	-1.03245310	-1.07717926
Aspartic.acid	-0.5406601	-0.93929677	-1.34862878	-0.87168620
GABA	0.2083702	0.09671283	-0.02981653	0.09527977
Trans.Caffeic.acid	-0.1524087	-0.99816120	-0.53930272	-0.52649560
	F18_67d_WW1	F18_67d_WW2	F18_67d_WW3	F18_67d_WW4
Alanine	-0.68771273	-0.8145911	-0.9120730	-0.4301155
Arabinose	-1.05648778	-1.0957039	-1.1198884	-1.2589760
Ascorbic.acid	-1.44717412	-1.6434274	-1.3931989	-1.3403676
Aspartic.acid	-1.06407077	-0.9600991	-0.9869468	-1.2856130
GABA	0.09272624	-0.1293893	-0.1176987	0.3447692
Trans.Caffeic.acid	-1.74127656	-2.3749262	-2.4456161	-3.0910196
	C19_22d_WS1	C19_22d_WS2	C19_22d_WS3	C19_22d_WS4
Alanine	0.2720501	1.2824603	0.4910994	0.7887854
Arabinose	1.0854730	1.1410463	0.9948382	1.0441785
Ascorbic.acid	0.5077076	1.2996969	0.4546839	0.2179557
Aspartic.acid	1.3002167	1.0138284	1.1871125	1.3693923
GABA	-0.3652211	0.4540044	0.5683581	0.2222463
Trans.Caffeic.acid	-0.9856266	1.0291158	0.2102271	1.5825560
	C19_22d_WW1	C19_22d_WW2	C19_22d_WW3	C19_22d_WW4
Alanine	0.08711792	0.9289745	0.2769671	0.7027119
Arabinose	1.14132150	1.0867292	1.0819988	1.0329153
Ascorbic.acid	0.34494184	0.6917733	0.9890956	0.5804620
Aspartic.acid	1.34162557	0.9135394	1.5509238	1.1114018
GABA	0.64266257	0.4196112	0.1871306	-0.4626375
Trans.Caffeic.acid	-1.61556947	0.1286776	0.2005584	1.4285608
	C19_44d_WS1	C19_44d_WS2	C19_44d_WS3	C19_44d_WS4
Alanine	1.0050069	1.589722	0.8824669	0.8029488

Arabinose	0.9092302	1.045219	0.8819613	1.0608565
Ascorbic.acid	1.7487219	1.213896	1.7487219	1.2801920
Aspartic.acid	1.2843338	1.096224	0.8750735	0.8839919
GABA	0.6856613	1.682973	0.4508374	1.5866186
Trans.Caffeic.acid	0.5475100	-0.466101	0.3607963	1.7095972
C19_44d_WW1 C19_44d_WW2 C19_44d_WW3 C19_44d_WW4				
Alanine	0.7107403	1.1125188	0.5264551	0.8304556
Arabinose	0.9789026	1.0213394	0.9797140	1.0146840
Ascorbic.acid	1.3785054	1.5556943	1.1228496	0.8010254
Aspartic.acid	0.5339921	0.4810936	0.5672792	0.7640104
GABA	0.9245993	0.7243169	0.6443564	0.6443564
Trans.Caffeic.acid	-0.0908902	0.3851661	0.3851661	1.8388831
C19_49d_WS1 C19_49d_WS2 C19_49d_WS3 C19_49d_WS4				
Alanine	1.1079692	1.675464089	0.9633604	1.0067634
Arabinose	1.0791345	1.012816267	0.9252369	0.9817356
Ascorbic.acid	1.2854461	1.809587711	1.5636868	1.5389760
Aspartic.acid	0.7460909	1.178805258	1.0565169	0.6814897
GABA	0.8617421	0.610714821	0.1885628	1.4648404
Trans.Caffeic.acid	-0.6882969	-0.006640693	0.8659242	1.6067934
C19_49d_WW1 C19_49d_WW2 C19_49d_WW3 C19_49d_WW4				
Alanine	0.71074026	1.1125188	1.0460089	1.2458283
Arabinose	0.99717689	1.0124417	0.8214110	0.9321080
Ascorbic.acid	0.90241827	1.2196641	1.3575459	1.3054450
Aspartic.acid	0.31834284	0.5886717	0.4672602	0.2384083
GABA	-0.07535686	0.7774375	0.5169933	0.6246747
Trans.Caffeic.acid	-0.26690844	-0.5856183	0.9473843	1.5784971
C19_55d_WS1 C19_55d_WS2 C19_55d_WS3 C19_55d_WS4				
Alanine	1.13043165	NA	0.7368647	1.3240626
Arabinose	1.00602230	NA	0.9631780	0.9302867
Ascorbic.acid	1.24018846	NA	0.8036164	1.5086137
Aspartic.acid	1.02271128	NA	0.5452540	0.4323224
GABA	0.12780899	NA	0.2139473	0.7509098
Trans.Caffeic.acid	0.04142443	NA	0.8400033	1.3308596
C19_55d_WW1 C19_55d_WW2 C19_55d_WW3 C19_55d_WW4				
Alanine	0.7982590	1.37285782	0.7394250	0.8590999
Arabinose	1.0044974	1.05004056	0.8995193	1.0094331
Ascorbic.acid	0.5606877	0.34246432	1.0371665	0.8126107
Aspartic.acid	0.7681648	1.38403013	0.7178225	0.3695937
GABA	0.2586393	0.05583074	0.2625903	0.2612753
Trans.Caffeic.acid	0.3821308	1.00950745	1.0943552	1.5252216
C19_34d_WS1 C19_34d_WS2 C19_34d_WS3 C19_34d_WS4				
Alanine	0.24694130	1.22934840	1.0223795	1.2124772
Arabinose	1.02861189	0.99795354	1.0978681	1.0697692
Ascorbic.acid	1.23528856	0.98710311	1.1843270	1.2239597
Aspartic.acid	1.59074795	1.67071566	1.2894944	1.1576225
GABA	-0.54863624	0.21948879	0.1726762	-0.6823219
Trans.Caffeic.acid	0.02434738	-0.04495894	0.9624127	1.8518783
C19_34d_WW1 C19_34d_WW2 C19_34d_WW3 C19_34d_WW4				
Alanine	0.7959024	1.3206873	0.8393928	1.1621430
Arabinose	0.9833459	1.0224384	1.0187638	0.9825415
Ascorbic.acid	1.9365717	1.7099495	1.6531531	1.6213218
Aspartic.acid	0.5939251	0.4991472	0.7524648	0.4901751
GABA	-0.5968286	-0.8836893	-0.5587401	-0.5320537

Trans.Caffeic.acid	0.3423869	0.6044133	0.9448722	1.8220911
	C19_65d_WS1	C19_65d_WS2	C19_65d_WS3	C19_65d_WS4
Alanine	0.86981662	1.84944595	0.7419762	1.0656555
Arabinose	1.04521895	0.98495000	0.9097098	1.0195013
Ascorbic.acid	0.97299630	1.11206313	0.6856887	0.9439095
Aspartic.acid	0.85322328	1.30526880	0.5577232	0.8354587
GABA	1.20433121	1.36540008	0.7150083	1.2007751
Trans.Caffeic.acid	-0.03445944	-0.05549566	1.0847800	1.4646504
	C19_65d_WW1	C19_65d_WW2	C19_65d_WW3	C19_65d_WW4
Alanine	0.57960166	1.1992211	0.1542540	0.7520903
Arabinose	0.91257627	0.9516337	0.9516337	0.9998889
Ascorbic.acid	0.29366343	0.6826267	0.1969294	0.5945038
Aspartic.acid	0.64083931	0.2913310	0.4547444	0.5225574
GABA	0.42942294	0.3428547	0.7803355	0.5515722
Trans.Caffeic.acid	0.05840396	0.4894964	1.1884487	1.7482095
	F19_22d_WS1	F19_22d_WS2	F19_22d_WS3	F19_22d_WS4
Alanine	0.08711792	0.9961587	0.4105789	0.8525914
Arabinose	1.13438644	1.1432428	1.0531110	1.1503027
Ascorbic.acid	0.62177779	1.1895916	1.5380609	0.8049083
Aspartic.acid	1.60434969	1.4023739	1.3957151	1.2718004
GABA	0.21255637	0.7219991	0.8669941	0.1028955
Trans.Caffeic.acid	-0.08377750	0.3730062	0.2262719	1.4200051
	F19_22d_WW1	F19_22d_WW2	F19_22d_WW3	F19_22d_WW4
Alanine	-0.25067245	1.1049198	0.48746506	0.7570939
Arabinose	1.10483199	1.0571701	1.13911481	1.1481431
Ascorbic.acid	0.51357764	1.1659735	1.29195938	0.8389273
Aspartic.acid	0.90840960	1.0901997	1.22675356	0.9621851
GABA	-0.07535686	0.1871306	0.07887073	-0.4872417
Trans.Caffeic.acid	0.10543713	0.5475100	0.46005943	1.5231533
	F19_44d_WS1	F19_44d_WS2	F19_44d_WS3	F19_44d_WS4
Alanine	0.8259444	1.36442444	0.4105789	0.7887854
Arabinose	0.9563756	1.06681937	1.0033500	1.0531110
Ascorbic.acid	1.0591295	0.39506053	0.6300897	0.8339895
Aspartic.acid	1.5709259	1.53408190	1.3305144	1.2103491
GABA	1.0629968	1.63329752	0.8199230	1.1475028
Trans.Caffeic.acid	0.1120958	0.09542104	0.7068967	1.9051184
	F19_44d_WW1	F19_44d_WW2	F19_44d_WW3	F19_44d_WW4
Alanine	0.3104650	0.9131409	0.5264551	0.2720501
Arabinose	1.0674767	0.9913054	0.9402066	1.0835816
Ascorbic.acid	0.3399781	1.3168030	1.0202349	0.5289969
Aspartic.acid	0.7535218	0.7825253	0.5820523	0.7671283
GABA	0.2922977	0.8397348	0.4971698	0.5866357
Trans.Caffeic.acid	0.2358574	0.8400033	0.8555830	1.6566622
	F19_47d_WS1	F19_47d_WS2	F19_47d_WS3	F19_47d_WS4
Alanine	0.643819879	0.7265299	0.9328784	0.3730656
Arabinose	0.984549552	0.9116230	0.9627561	1.0794538
Ascorbic.acid	1.115399611	0.7228861	1.1011096	0.3740144
Aspartic.acid	1.477155992	1.3310010	1.4589479	0.9228533
GABA	1.292014347	1.2231993	0.6742929	0.7583604
Trans.Caffeic.acid	0.003724593	-0.3049282	1.2275540	1.3725035
	F19_47d_WW1	F19_47d_WW2	F19_47d_WW3	F19_47d_WW4
Alanine	0.7317161	1.2241998	0.9726240	0.8168353
Arabinose	0.9361769	0.9849500	0.9813321	0.9572320

Ascorbic.acid	0.6560497	0.8189660	0.7945062	1.0390231
Aspartic.acid	1.0408838	1.2011413	0.9541606	0.9278849
GABA	0.5430559	0.2331895	0.8136814	0.3185607
Trans.Caffeic.acid	-0.3982098	-0.2518356	0.8736566	1.7018142
	F19_55d_WS1	F19_55d_WS2	F19_55d_WS3	F19_55d_WS4
Alanine	1.7003494	1.5492019	1.0656555	1.4966108
Arabinose	0.9158957	0.8689514	1.0228041	0.9063406
Ascorbic.acid	0.4589067	0.4132566	0.5892707	0.9831012
Aspartic.acid	1.4023739	0.8633176	0.8401748	0.2913310
GABA	1.2175382	1.1873084	1.0482528	1.0795457
Trans.Caffeic.acid	0.1940951	-0.5026811	1.1038997	1.5560739
	F19_55d_WW1	F19_55d_WW2	F19_55d_WW3	F19_55d_WW4
Alanine	NA	1.52169511	1.1245108	1.3070234
Arabinose	NA	0.80939103	0.9252369	1.0154288
Ascorbic.acid	NA	0.54221849	0.6749130	0.5839986
Aspartic.acid	NA	1.03800586	0.5978411	1.0093469
GABA	NA	1.01689035	0.9091511	0.8908794
Trans.Caffeic.acid	NA	0.09207483	1.2548512	1.6208412
	F19_34d_WS1	F19_34d_WS2	F19_34d_WS3	F19_34d_WS4
Alanine	0.7982590	1.6432584	0.3151241	1.4455128
Arabinose	1.0848435	1.0064027	0.8057164	1.0476367
Ascorbic.acid	0.5661358	0.8642997	0.5327998	1.1518890
Aspartic.acid	1.0621212	1.1758158	1.1823768	0.7629681
GABA	0.2922977	0.3688149	-0.1252694	0.5893444
Trans.Caffeic.acid	-0.3087571	0.1843738	-2.7709424	1.4709739
	F19_34d_WW1	F19_34d_WW2	F19_34d_WW3	F19_34d_WW4
Alanine	0.4910994	1.3318766	0.43059441	0.9799488
Arabinose	0.9861490	0.8855325	0.95422686	1.0601886
Ascorbic.acid	0.8853459	1.1605295	0.70080322	0.6480391
Aspartic.acid	0.5686344	0.6518175	0.34440911	0.4841331
GABA	0.6644284	0.4412663	0.06907130	0.3917591
Trans.Caffeic.acid	0.5503812	0.4511712	0.02434738	1.5478779
	F19_65d_WS1	F19_65d_WS2	F19_65d_WS3	F19_65d_WS4
Alanine	1.1691569	1.54838383	0.9781247	1.0816225
Arabinose	1.0406913	1.10960874	0.9669562	1.0242637
Ascorbic.acid	0.3015962	0.13316265	1.0240327	0.4243959
Aspartic.acid	0.5899885	0.95818365	1.0365627	0.8839919
GABA	0.9511372	0.90352165	1.3277535	0.9911842
Trans.Caffeic.acid	-0.1922971	0.04142443	1.0315578	1.5293538
	F19_65d_WW1	F19_65d_WW2	F19_65d_WW3	F19_65d_WW4
Alanine	1.2280647	1.94458838	0.7767631	1.2137893
Arabinose	0.8850242	0.94065190	0.9388677	1.1084197
Ascorbic.acid	0.4958194	0.22090909	0.5057401	0.8487006
Aspartic.acid	1.0962240	0.77537968	0.4531650	0.5873525
GABA	0.7258587	0.61510148	0.7196751	0.7304676
Trans.Caffeic.acid	0.6324617	0.02434738	1.2751610	1.3898648

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

name	description	class	nrow	ncol
12 mldata Metabolites featuredata 18/19	data.frame		55	3

	Metabolite	Bin
Alanine	Alanine	5.1001
Arabinose	Arabinose	10.6.1001
Ascorbic.acid	Ascorbic acid	17.5.1001
Aspartic.acid	Aspartic acid	13.1.1.2.1001
GABA	GABA	22.1002
Trans.Caffeic.acid	Trans-Caffeic acid	16.2.1.1006

Alanine	
Arabinose	cell wall
Ascorbic.acid	hormone metabol
Aspartic.acid	amino acid metabolism.synthesis.central amino acid metaboli
GABA	pol
Trans.Caffeic.acid	secondary metabolism.phenylpropanoids.lignin

----- intgenes: Names of genes in bins -----

name	description	class	nrow	ncol
13 intgenes	Names of genes in bins	list	22	<NA>

\$`1.2`

```
[1] "Vitvi07g03141" "Vitvi01g00157" "Vitvi02g00436" "Vitvi02g00437"
[5] "Vitvi02g00572" "Vitvi02g00680"
```

\$`1.3`

```
[1] "Vitvi01g00086" "Vitvi01g00360" "Vitvi01g01058" "Vitvi02g00915"
[5] "Vitvi03g00048" "Vitvi03g00097"
```

\$`2.1`

```
[1] "Vitvi02g00250" "Vitvi03g00304" "Vitvi05g00442" "Vitvi05g01193"
[5] "Vitvi07g00167" "Vitvi07g00544"
```

\$`2.2`

```
[1] "Vitvi02g01845" "Vitvi01g00025" "Vitvi01g00052" "Vitvi01g00053"
[5] "Vitvi01g00064" "Vitvi01g00681"
```

\$`3.1`

```
[1] "Vitvi10g02295" "Vitvi00g01259" "Vitvi01g00714" "Vitvi05g00170"
[5] "Vitvi05g00204" "Vitvi07g00431"
```

\$`3.3`

```
[1] "Vitvi11g01277" "Vitvi16g01858" "Vitvi16g00929"
```

\$`3.4`

```
[1] "Vitvi01g00140" "Vitvi03g00287" "Vitvi07g01777" "Vitvi09g00246"
[5] "Vitvi17g00279" "Vitvi18g00994"
```

\$`3.99`

character(0)

\$`5`

```
[1] "Vitvi01g00787" "Vitvi04g01402" "Vitvi04g01668" "Vitvi06g00210"
```

[5] "Vitvi06g01689" "Vitvi06g01690"

\$`6`

[1] "Vitvi07g03070" "Vitvi00g01243" "Vitvi00g01382" "Vitvi03g00785"

[5] "Vitvi05g00387" "Vitvi05g00388"

\$`8.1`

[1] "Vitvi07g03070" "Vitvi01g00274" "Vitvi01g00861" "Vitvi01g01724"

[5] "Vitvi03g00197" "Vitvi03g00785"

\$`10.6`

[1] "Vitvi07g02990" "Vitvi01g00593" "Vitvi01g00708" "Vitvi01g01805"

[5] "Vitvi02g00118" "Vitvi02g00125"

\$`11`

[1] "Vitvi02g01774" "Vitvi07g02896" "Vitvi02g01724" "Vitvi02g01739"

[5] "Vitvi07g02982" "Vitvi07g02994"

\$`12.2`

[1] "Vitvi01g00175" "Vitvi05g00403" "Vitvi07g00187" "Vitvi07g02204"

[5] "Vitvi08g01586" "Vitvi08g01646"

\$`13.1`

[1] "Vitvi07g03049" "Vitvi00g00869" "Vitvi02g01749" "Vitvi01g00035"

[5] "Vitvi01g00502" "Vitvi01g00536"

\$`16.1`

[1] "Vitvi10g02269" "Vitvi02g00020" "Vitvi02g00034" "Vitvi02g00420"

[5] "Vitvi02g00831" "Vitvi03g00262"

\$`16.2`

[1] "Vitvi07g03081" "Vitvi07g03083" "Vitvi01g02214" "Vitvi01g01561"

[5] "Vitvi02g00283" "Vitvi02g00717"

\$`16.8`

[1] "Vitvi10g02185" "Vitvi01g00556" "Vitvi01g02009" "Vitvi01g00557"

[5] "Vitvi01g00558" "Vitvi02g00270"

\$`17.5`

[1] "Vitvi02g01780" "Vitvi10g02409" "Vitvi01g00481" "Vitvi01g01671"

[5] "Vitvi02g00032" "Vitvi04g01895"

\$`21`

[1] "Vitvi10g02216" "Vitvi04g02274" "Vitvi01g00023" "Vitvi01g01866"

[5] "Vitvi01g01867" "Vitvi01g00133"

\$`22`

[1] "Vitvi01g00739" "Vitvi01g00789" "Vitvi03g00054" "Vitvi06g01502"

[5] "Vitvi13g01673" "Vitvi14g01289"

\$`23`

[1] "Vitvi01g00048" "Vitvi01g00115" "Vitvi01g00201" "Vitvi01g00421"

[5] "Vitvi01g00483" "Vitvi01g00663"

----- intmtbs: Names of metabolites in bins -----

name	description	class	nrow	ncol
14 intmtbs	Names of metabolites in bins	list	22	<NA>
\$`1.2`				
[1]	"Glyceric.acid"	"Glycine"	"Serine"	
\$`1.3`				
[1]	"Fructose.6.phosphate"			
\$`2.1`				
[1]	"Sucrose"			
\$`2.2`				
[1]	"Fructose"	"Glucose"		
\$`3.1`				
[1]	"Galactinol"	"Raffinose"		
\$`3.3`				
[1]	"Threitol"			
\$`3.4`				
[1]	"Myo.Inostol"			
\$`3.99`				
[1]	"Erythronic.acid"	"Galactose"	"Xylose"	
\$`5`				
[1]	"Alanine"			
\$`6`				
[1]	"Citric.acid"	"Malic.acid"		
\$`8.1`				
[1]	"Fumaric.acid"	"Succinic.acid"		
\$`10.6`				
[1]	"Arabinose"	"Melibiose"	"Rhamnose"	"Ribonic.acid"
[5]	"Ribose"			
\$`11`				
[1]	"Ethanolamine"			
\$`12.2`				
[1]	"Glutamic.acid"			
\$`13.1`				
[1]	"Aspartic.acid"	"Isoleucine"	"Leucine"	"Phenylalanine"

```

[5] "Proline"          "Shikimic.acid"

$`16.1`
[1] "Hydroquinone"

$`16.2`
[1] "Trans.Caffeic.acid"      "Gallic.acid"
[3] "Quinic.acid"            "X3.caffeoylquinic.acid"

$`16.8`
[1] "Catechin"

$`17.5`
[1] "Ascorbic.acid"

$`21`
[1] "Mannose.6.phosphate" "Pyroglutamic.acid"  "Threonic.acid"

$`22`
[1] "GABA"          "Putrescine"

$`23`
[1] "Uracil"

```

Factor for days within the year

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

3.13 Water potential

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

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

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

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

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

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

```
      Count
X.date    1
2018-06-04 4
2018-06-15 4
2018-06-21 4
2018-06-29 4
2018-07-04 4
2018-07-10 4
2018-07-16 4
2018-07-23 4
2018-07-31 4
2018-08-07 4
```

```

2019-06-18 4
2019-06-26 4
2019-07-08 4
2019-07-12 4
2019-07-17 4
2019-07-22 2
2019-07-30 4
2019-08-06 4
2019-08-12 4
2019-08-19 4

```

```
> str(X)
```

```

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

```

Order by date

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

```
> wpdata <- X
```

Tidy dates ...

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

	Cabernet Volos	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 >
```

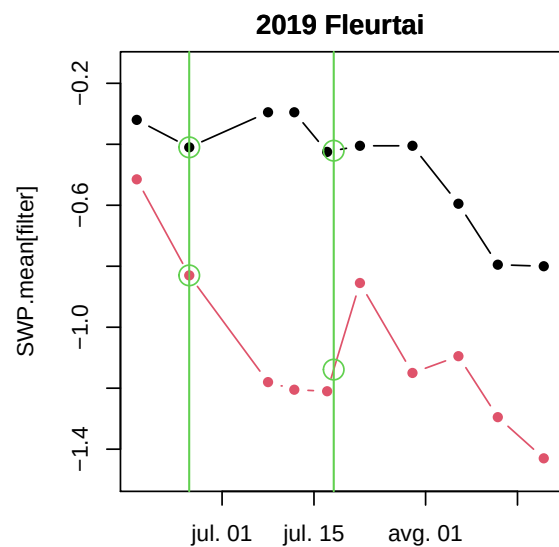
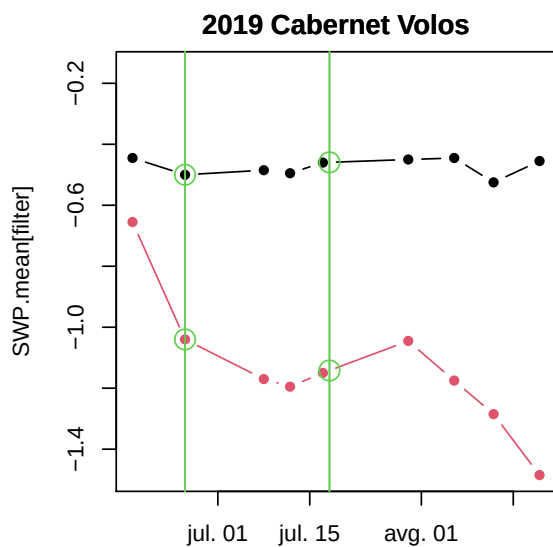
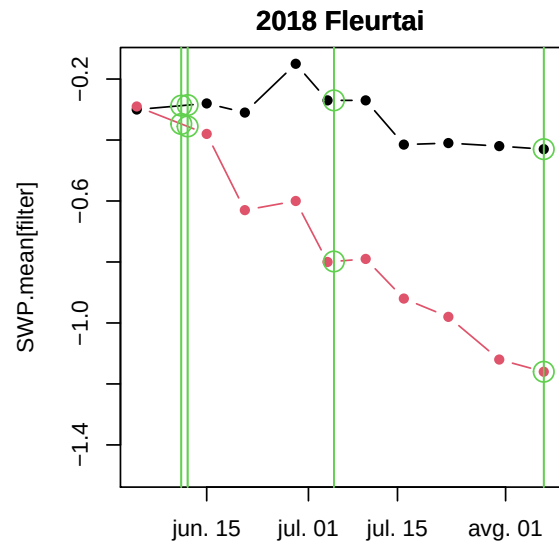
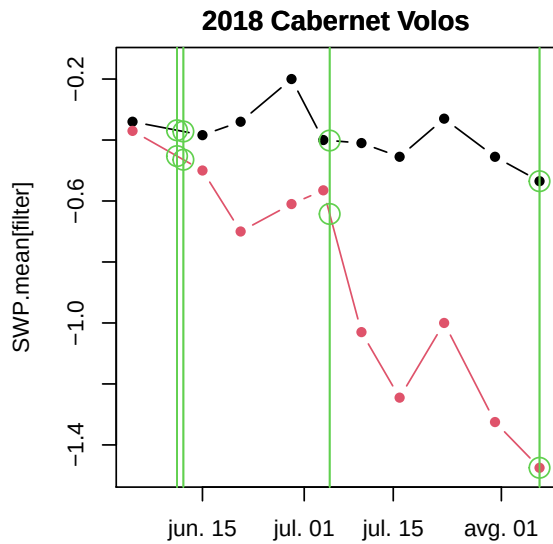
```
> pdata1819$date <- as_date(pdata1819$Date, format="%d.%m.%Y")
> table(pdata1819$date)
```

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

@ @

Order water potential data by date

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

Time differences in days

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

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

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

Time differences in days

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

Convert treatment and variety into factors

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

```
[1] WW WS WW WS WW WS WW WS WW WS WW WS WW WS WW WS WW WS WW WS
[23] WW WS
Levels: WW WS
```

```
> (wpas$variety <- factor(wpas$variety))
```

```
[1] C C F F C C F F C C F F C C F F C C F F C C F F
Levels: C F
```

```
> with(wpas, ftable(yr, variety, treat, date))
```

			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"
```

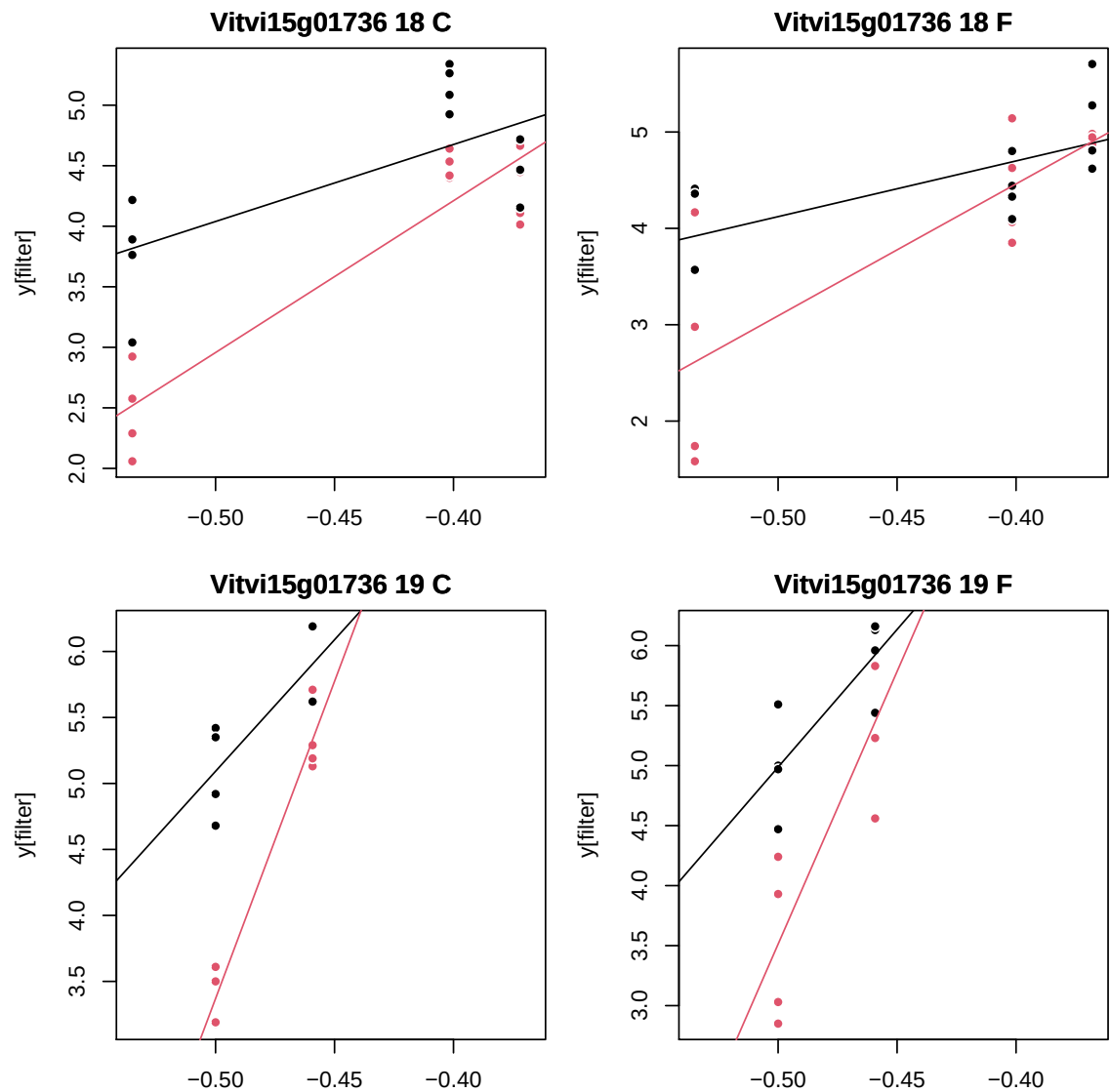
```
Call:
lm(formula = y[select] ~ pd$swp[select])
```

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



```
Call:
```



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

Coefficients:

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

Call:

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

Coefficients:

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

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

4 Expression and water poential analysis

```
> varname <- rownames(tl1819)[10]
```

```
> pd <- pdata1819
```

```
> (y <- unlist(tl1819[varname,]))
```

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

```

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

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

, , variety = F

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

> tfilter <- wpas$treat %in% "WW"
> vfilter <- wpas$variety %in% "C"
> (swp <- wpas$swp[as.character(wpas$date) %in% dimnames(means)[[1]]])
[1] -0.3680000 -0.4527273 -0.2872727 -0.3472727 -0.3720000 -0.4645455
[7] -0.2854545 -0.3554545 -0.4016667 -0.6425000 -0.2700000 -0.7983333
[13] -0.5350000 -1.4750000 -0.4300000 -1.1600000 -0.5000000 -1.0400000
[19] -0.4100000 -0.8300000 -0.4592308 -1.1419231 -0.4210000 -1.1390000

> varname <- rownames(t1819)[10]
> #varname <- rownames(t1819)[runif(1, 1, 10000)]
> (y <- unlist(t1819[varname,]))
C18_11d_WS1 C18_11d_WS2 C18_11d_WS3 C18_11d_WS4 C18_11d_WW1
  4.088427    3.961216    4.127170    3.916955    4.472212
C18_11d_WW2 C18_11d_WW3 C18_11d_WW4 C18_34d_WS1 C18_34d_WS2
  4.309540    4.212060    4.154032    4.086692    3.914995
C18_34d_WS3 C18_34d_WS4 C18_34d_WW1 C18_34d_WW2 C18_34d_WW3
  4.065776    4.081348    4.313965    4.041339    4.318997
C18_34d_WW4 C18_67d_WS1 C18_67d_WS2 C18_67d_WS3 C18_67d_WS4
  4.238240    4.441597    4.248104    4.242540    3.969094
C18_67d_WW1 C18_67d_WW2 C18_67d_WW3 C18_67d_WW4 F18_10d_WS1
  4.160356    4.676748    4.467201    4.359372    4.102511
F18_10d_WS2 F18_10d_WS3 F18_10d_WS4 F18_10d_WW1 F18_10d_WW2
  4.307786    4.261419    4.248699    4.239323    4.289799
F18_10d_WW3 F18_10d_WW4 F18_34d_WS1 F18_34d_WS2 F18_34d_WS3
  4.620659    4.532309    4.114948    4.149386    4.350818
F18_34d_WS4 F18_34d_WW1 F18_34d_WW2 F18_34d_WW3 F18_34d_WW4
  4.075166    4.239367    4.109161    4.460006    4.507653
F18_67d_WS1 F18_67d_WS2 F18_67d_WS3 F18_67d_WS4 F18_67d_WW1
  4.443768    4.392282    4.258226    4.311732    4.659167

```

```

F18_67d_WW2 F18_67d_WW3 F18_67d_WW4 C19_22d_WS1 C19_22d_WS2
  4.584738    4.404701    4.488189    5.160000    5.040000
C19_22d_WS3 C19_22d_WS4 C19_22d_WW1 C19_22d_WW2 C19_22d_WW3
  4.950000    4.920000    5.060000    4.710000    5.410000
C19_22d_WW4 C19_44d_WS1 C19_44d_WS2 C19_44d_WS3 C19_44d_WS4
  5.070000    4.420000    4.480000    4.490000    4.570000
C19_44d_WW1 C19_44d_WW2 C19_44d_WW3 C19_44d_WW4 F19_22d_WS1
  4.930000    5.000000    4.820000    4.770000    5.560000
F19_22d_WS2 F19_22d_WS3 F19_22d_WS4 F19_22d_WW1 F19_22d_WW2
  5.150000    5.130000    5.690000    5.060000    5.160000
F19_22d_WW3 F19_22d_WW4 F19_44d_WS1 F19_44d_WS2 F19_44d_WS3
  5.250000    4.940000    4.710000    4.320000    4.910000
F19_44d_WS4 F19_44d_WW1 F19_44d_WW2 F19_44d_WW3 F19_44d_WW4
  4.540000    5.030000    4.700000    4.820000    4.720000

```

```

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

```

```

, , variety = C

```

```

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

```

```

, , variety = F

```

```

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

```

```

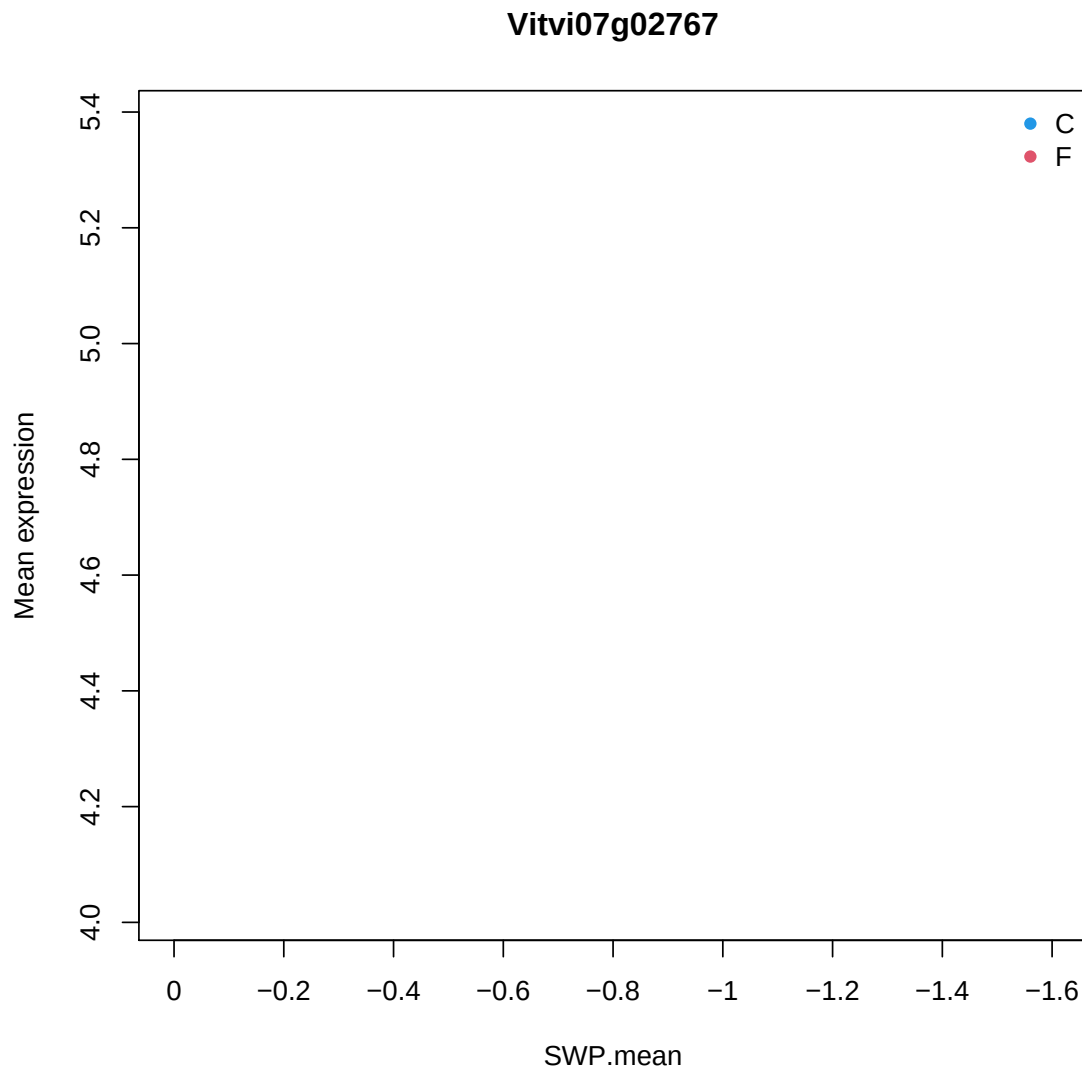
> ylim <- range(means, na.rm=TRUE)
> xlim <- c(min(wpas$swp, -1.6, na.rm=TRUE), max(wpas$swp, 0, na.rm=TRUE))
> vlvs <- unique(wpas$variety)
> tlvs <- rev(unique(wpas$treat))
> cols <- c(4, 2)
> pchs <- c(16, 16)
> plot(1, 1, #wpas$swp[tfilter & vfilter], means[, "WS", vlvs[i]],
+      ylim=ylim,
+ 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

```

```

> axis(2)
> box()
> axis(1,at=seq(0,2,0.2),labels=-(seq(0,2,0.2)))
> title(varname)
> legend("topright", bty="n", pch=pchs, col=cols,legend = vlvs)

```



```

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

```

4.1 Expression vs water potential

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

```

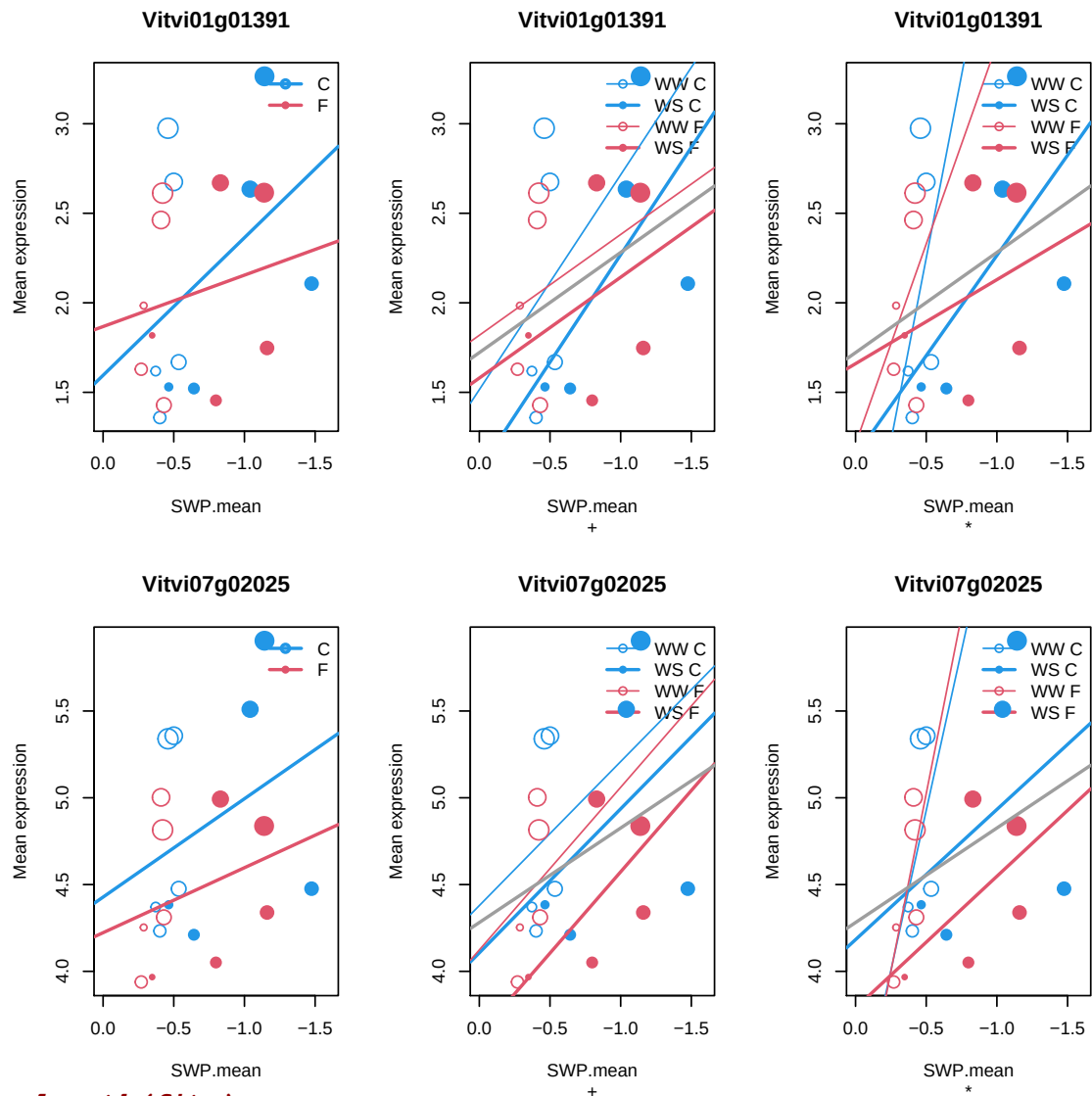
+       col = cols[i],
+       pch = pchs[as.numeric(mns$treat)]
+       , cex=cex
+     )
+ #   }
+   xx <- xx
+   if(model=="") fit <- lm(yy~xx)
+   if(model=="+") fit <- lm(yy~xx+mns$treat)
+   if(model=="*") fit <- lm(yy~xx*mns$treat)
+   if(verbose) print(summary(fit))
+   coef <- fit$coefficients
+ #   print(coef)
+   if(length(coef)<3) coef[3] <- 0
+   if(length(coef)<4) coef[4] <- 0
+   abline(coef[1:2], col=cols[i],lwd=1)
+   abline(coef[1:2]+coef[3:4],col=cols[i],lwd=2,lty=1)
+   ally <- c(ally,yy)
+   allx <- c(allx,xx)
+   fits[[v1vls[i]]] <- fit
+ }
+ fit <- lm(ally~allx)
+ fits[["all"]] <- fit
+ fits[["r"]] <- cor(ally,allx,use="complete")
+ if(verbose) print(summary(fit))
+ if(all) abline(fit$coefficients,lwd=2,col=8)
+ #points(-swps,means,cex=1.5)
+ invisible(fits)
+ }

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

[1] "Vitvi07g02767"

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

```



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

4.2 Water potential vs Expression

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

```

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

```

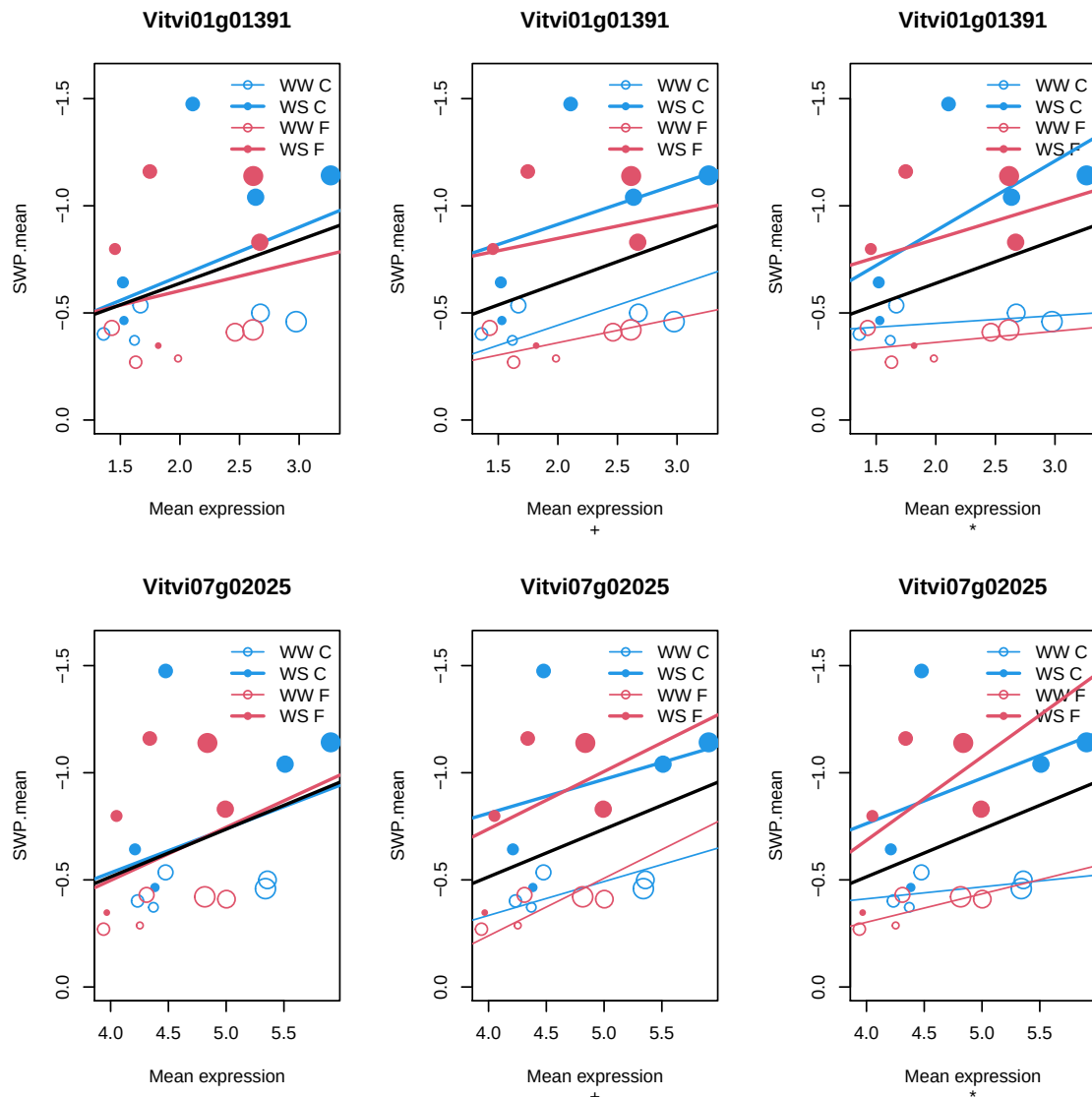


```

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

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

```



```

> length(fits)

```

```

[1] 5

```

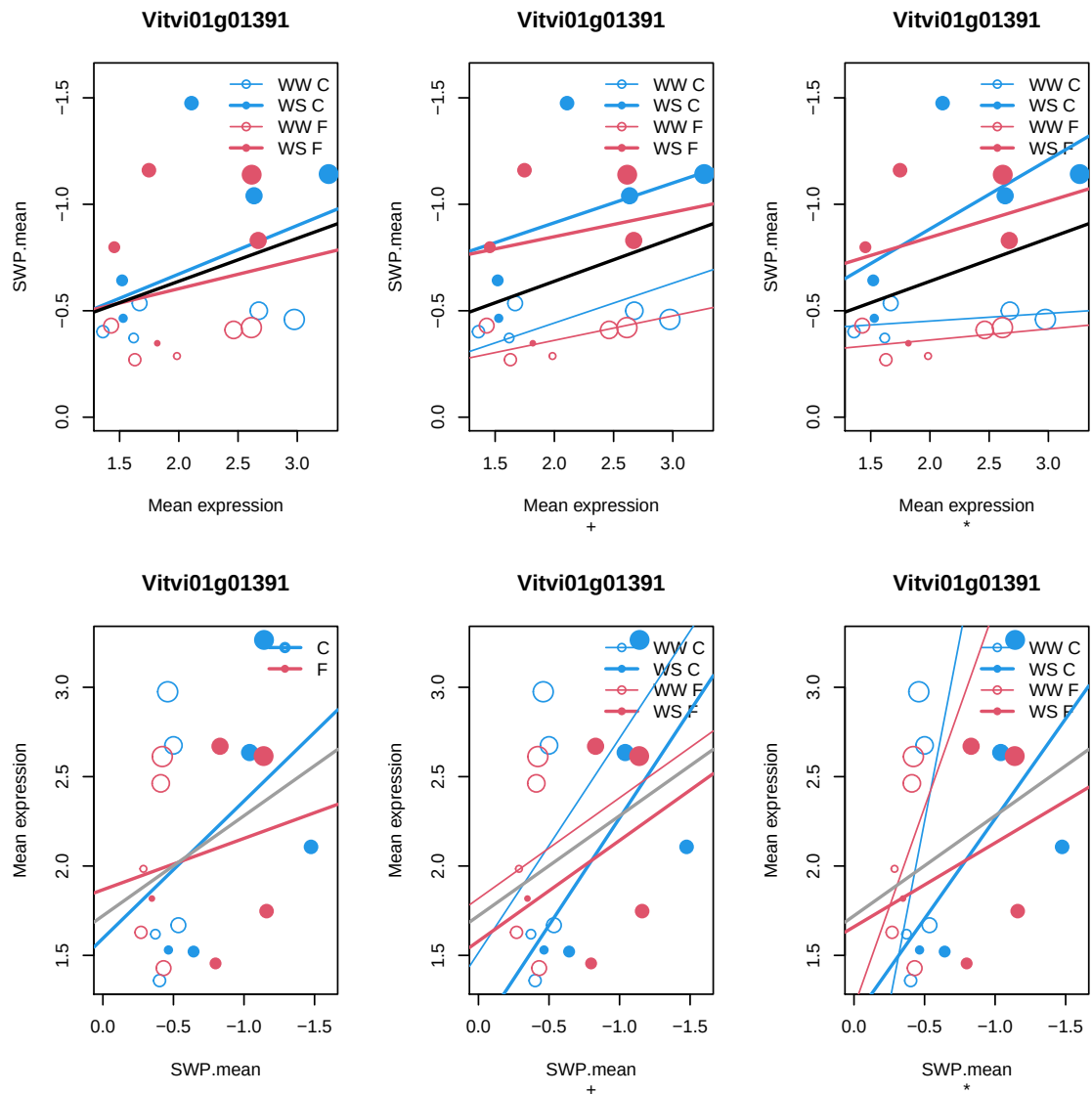
```

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

> testvar <- "Vitvi01g01391"

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

```



```

> fits

```

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

```
$C
```

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

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

```
$F
```

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

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

```
$all
```

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

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

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

```
> varname
```

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

```
> pd <- pdata1819
```

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

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

```

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

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

, , variety = C

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

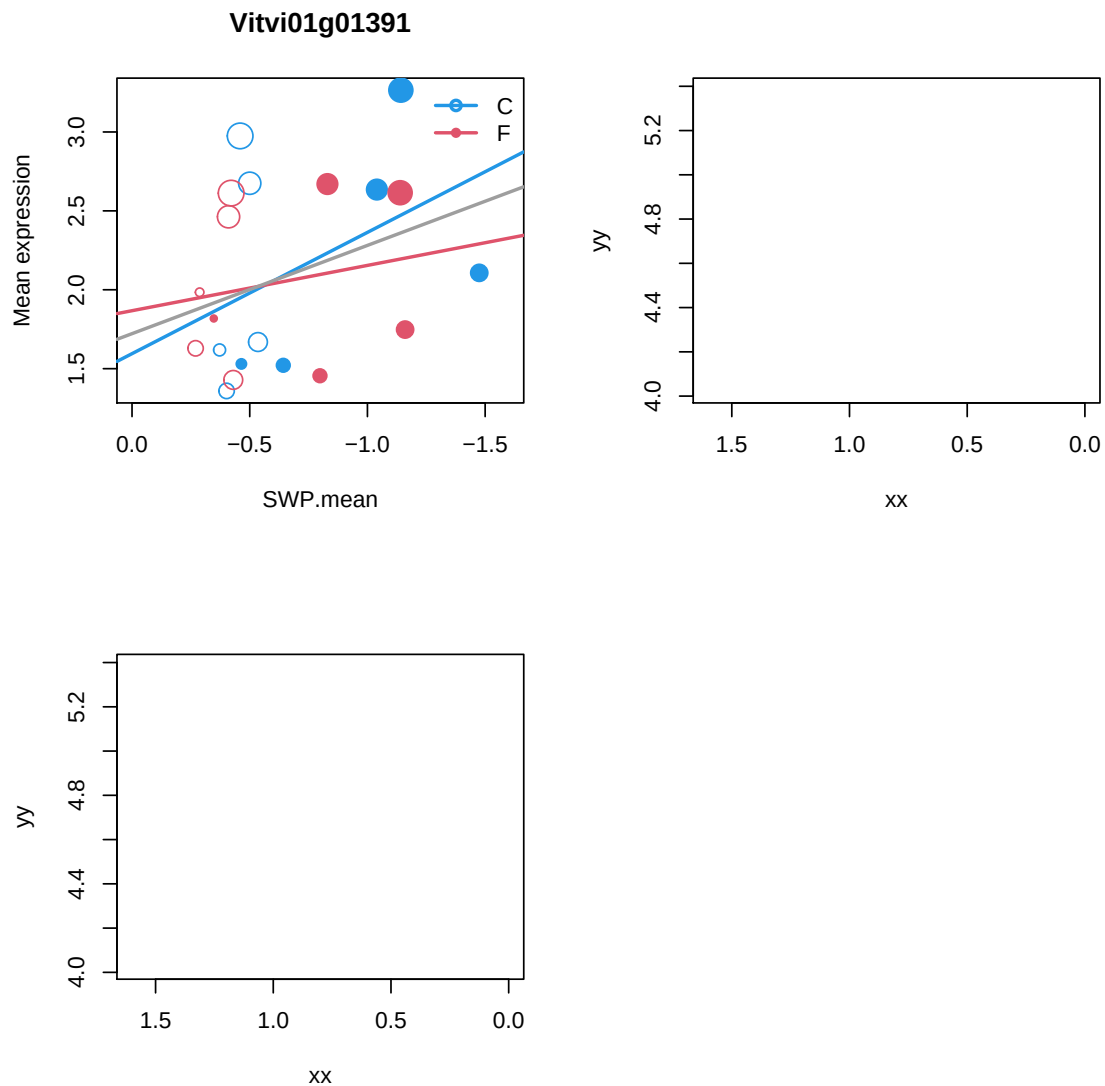
, , variety = F

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

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

```

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



5 Linear models for water potential

```
> library(limma)
```

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

```
Attaching package: 'limma'
```

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

```
plotMA
```

```
> exprs <- t1819
```

```
> pd <- pdata1819w
```

We will use models on average expressions across replicates.

```
> varname <- testvar
> (y <- unlist(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
```

	variety = F	
	treat	
date	WW	WS

```

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

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

, , variety = C

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

, , variety = F

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

```

Small phenodata

```

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

```

5.1 Interpolated water potential data

```
> pd1
```

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

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

Object: pd1

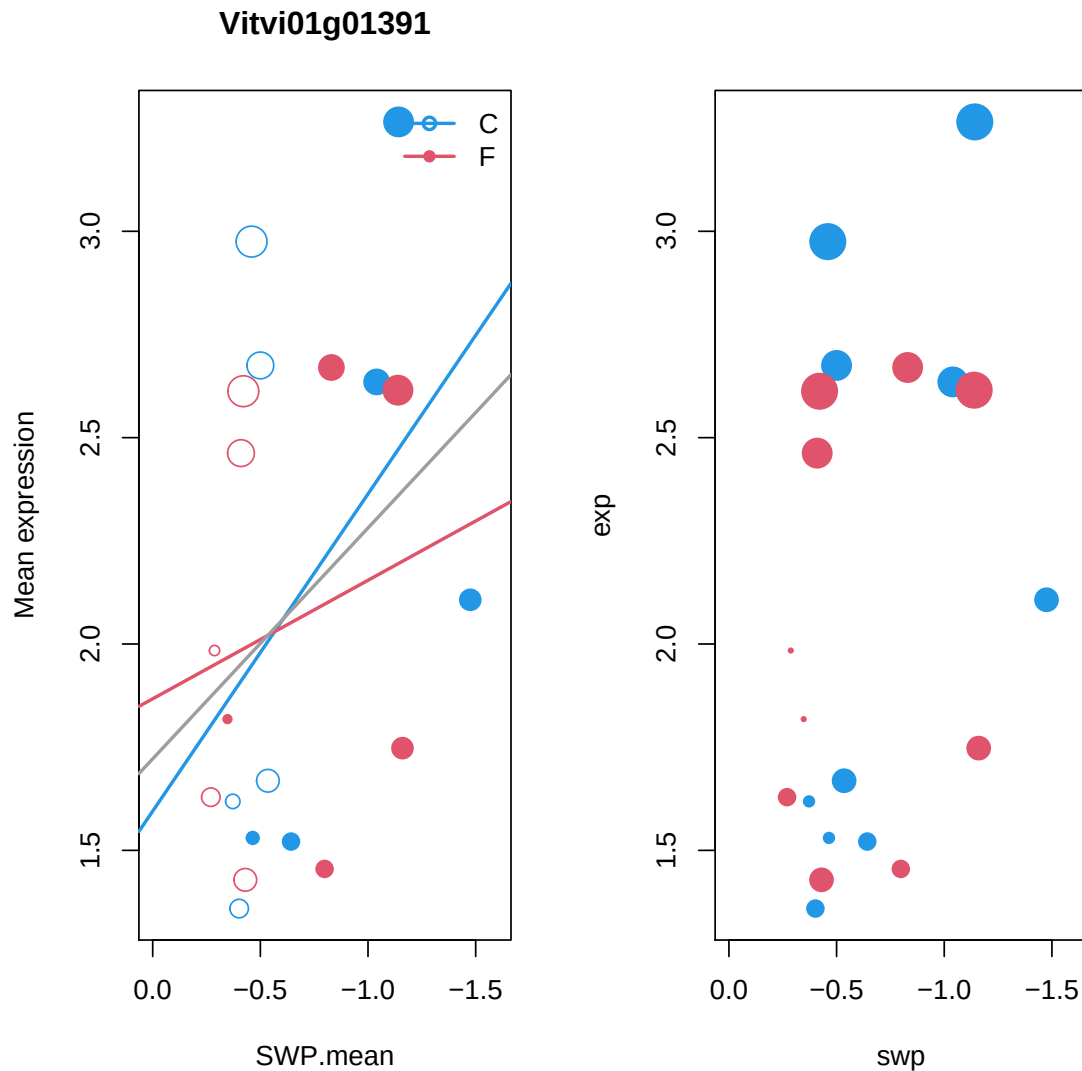
Label: Interpolated swp data, considered as phenodata when swp is used.

File :

[../../output/50_Expression-water-stress-0.05-1.5-0.5-1-1/swp-interpolated.txt](#)

Graphical test, check the points positions

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



Aggregated expressions

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

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

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

```

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

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

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

```

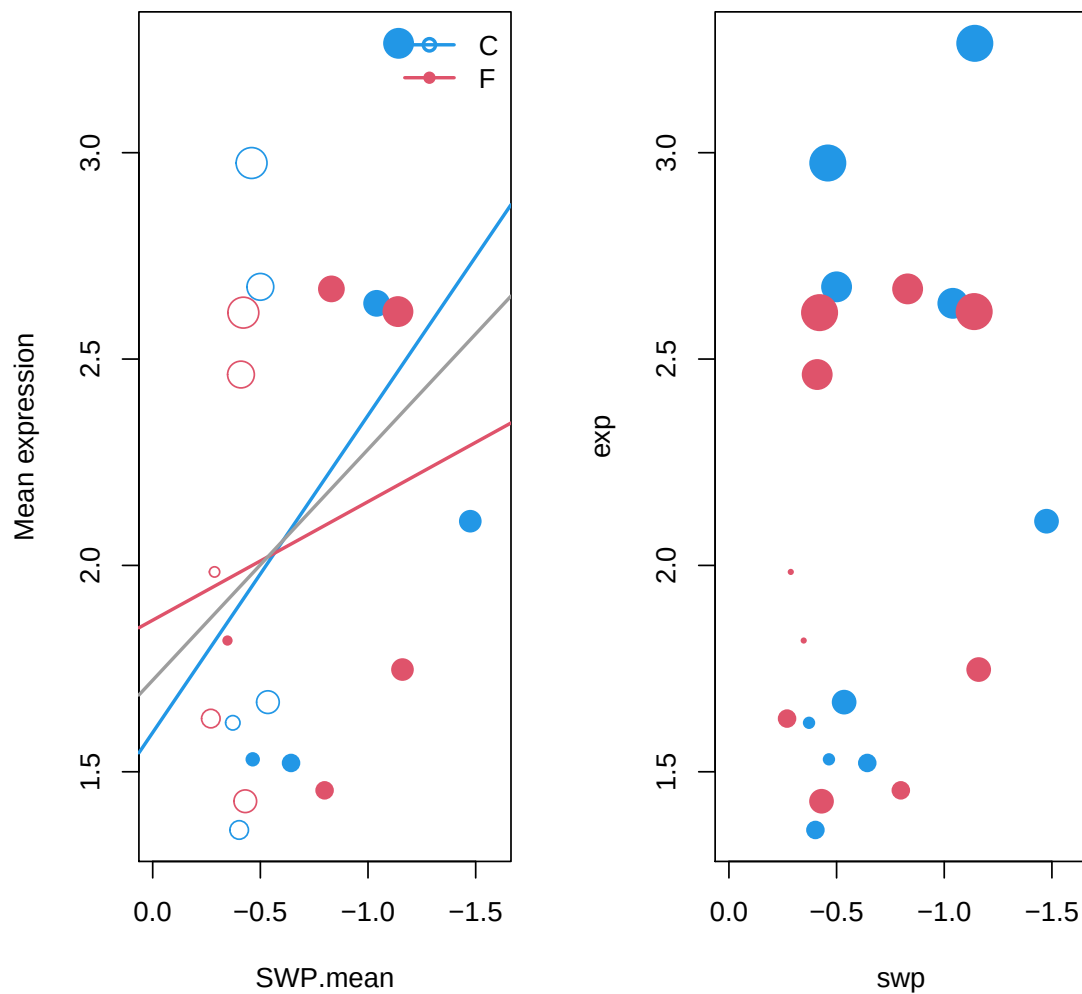
Check regressions

```

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

```

Vitvi01g01391



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

$F
(Intercept)          xx
  1.8672599   -0.2871816

$all
(Intercept)          allx
  1.7217725   -0.5593981

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

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

```

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

(Intercept)      pd1$swp
    1.7217725    -0.5593981

```

Looks ok.

```

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

```

Replace expressions and phenodata with the reduced ones.

```

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

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

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

> testvar <- "Vitvi01g01391"

```

5.2 Overall Model

Simple model with water potential for all data:

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

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

Linear model

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

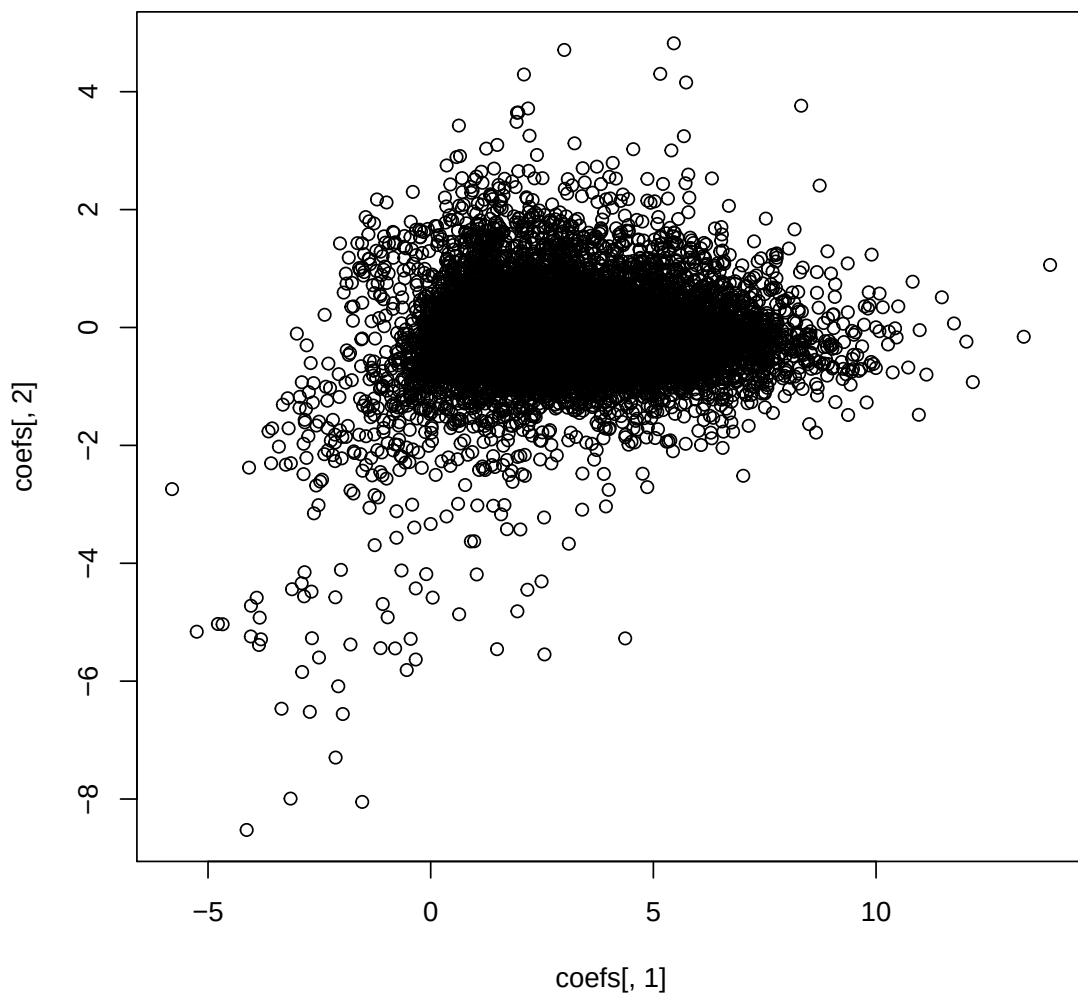
> fit1 <- eBayes(fit1)
> fit1[testvar,]$coefficients
      (Intercept)      swp
Vitvi01g01391    1.721772 -0.5593981

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

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

Models for each variety

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



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

Top table

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

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

```

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

5.3 Models for variety

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

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

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

```
> tail(design2)
```

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

Linear model

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

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

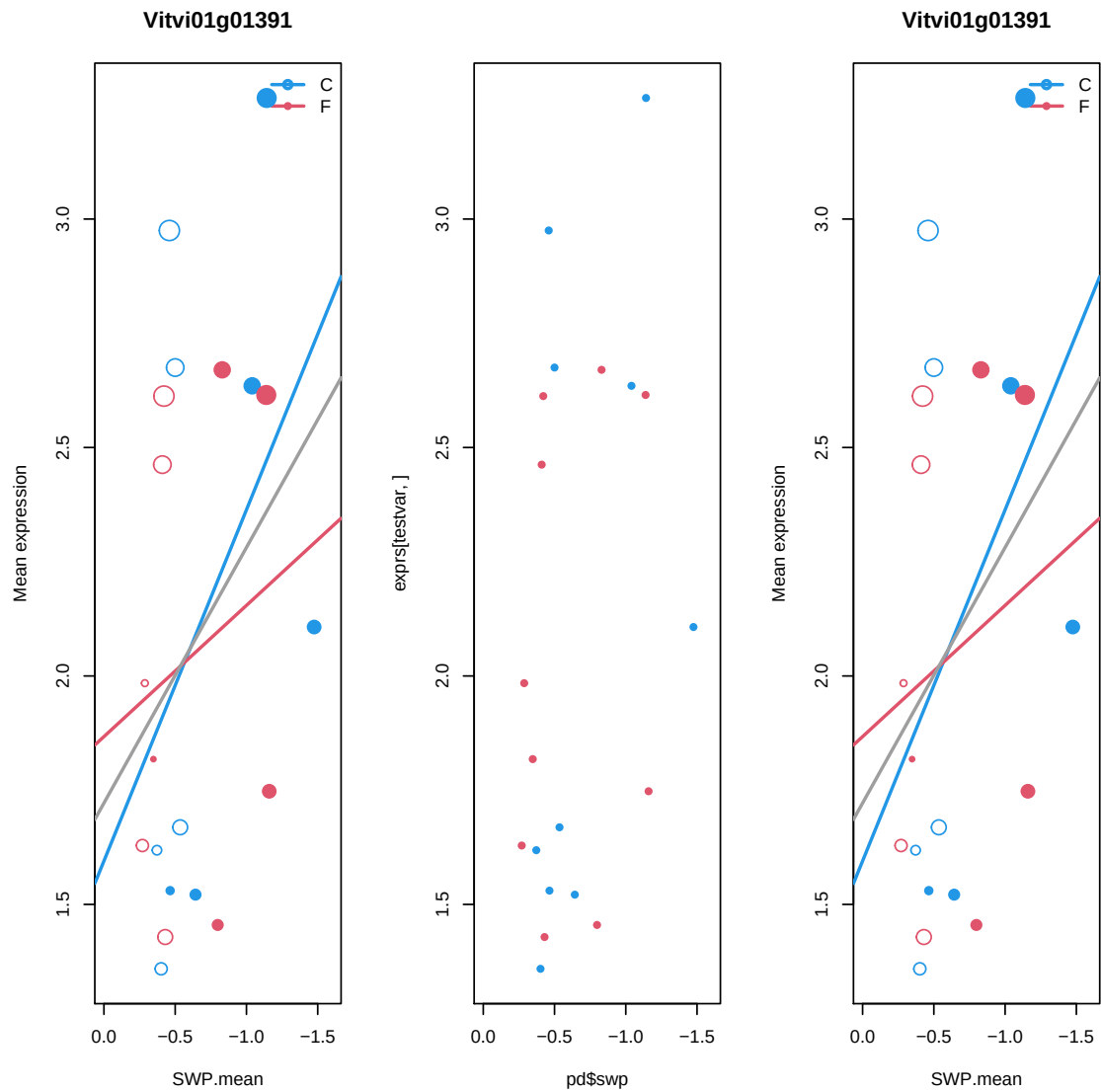
```
> varname <- testvar
> par(mfrow=c(1,3))
> p <- plot.ewp(varname,model="")
> plot(pd$swp,exprs[testvar,], xlim=c(0,-1.6),
+      ,pch=16, col=6-as.numeric(pd$variety)*2,cex=pd$day/2)
> c(p$C$coef[2],p$F$coef[2])
```

	xx	xx
	-0.7685916	-0.2871816

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

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

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



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


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

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

> fita[2]
      pd1$swp
-0.5593981

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

> fitc[2]
      pd1$swp
-0.7685916

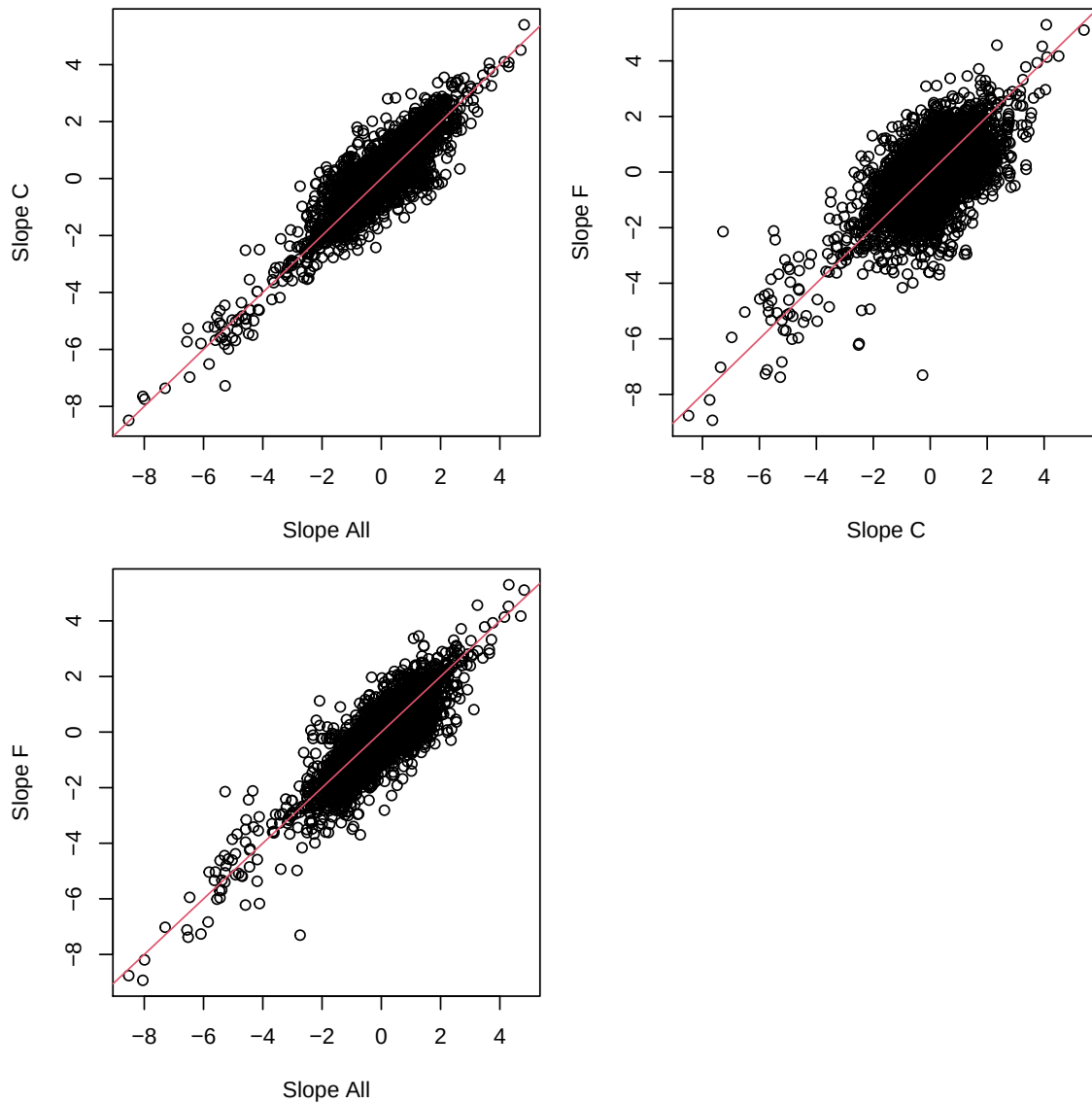
> fit2[testvar,]$coefficients[2]
[1] -0.7685916

> fitf[2]
      pd1$swp
-0.2871816

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

Plots of coefficients

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



5.4 Mean expressions

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

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

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

```

          mc      mf
Vitvi01g01391 0.8264496 1.580078
> ma <- fit1$coefficients%*%c(1,mean(swp))
> macf <- data.frame(ma=ma,my.predict(fit2, x=mean(swp)))
> head(macf)

```

```

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

```

```

> macf[testvar,]

```

```

          ma      mc      mf
Vitvi01g01391 2.08887 2.09942 2.055719

```

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

```

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

```

```

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

```

```

> tail(design3)

```

```

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

```

```

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

```

```

          varietyC varietyF
Vitvi01g01391 2.135505 2.042236

```

```

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

```

```

[1] 2.135505

```

```

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

```

```

[1] 2.042236

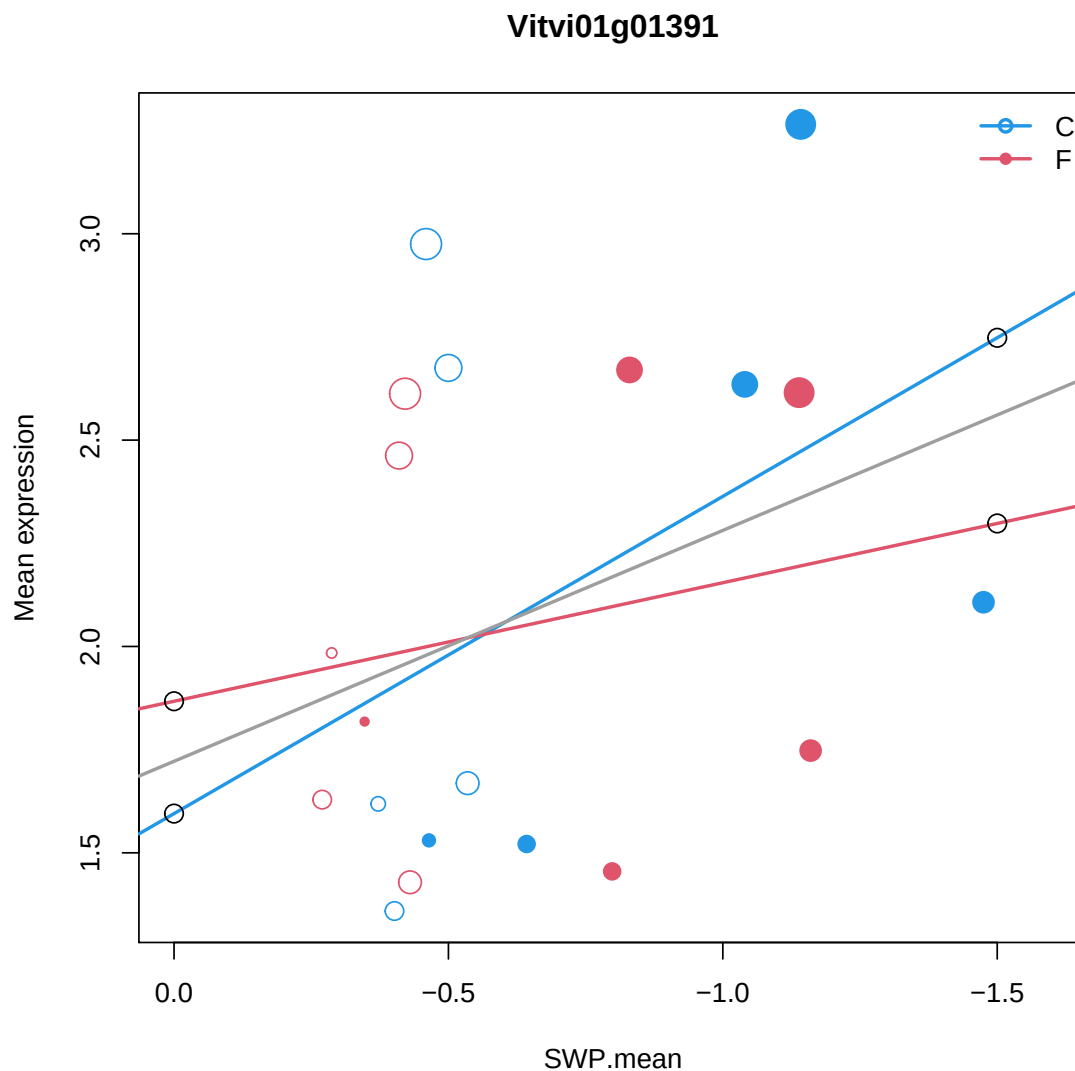
```

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

```

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

```



5.4.1 Plots of variety coefficients

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

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

```

> head(fit1[1:6,]$coefficients)

```

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

Extract slopes

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

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

```

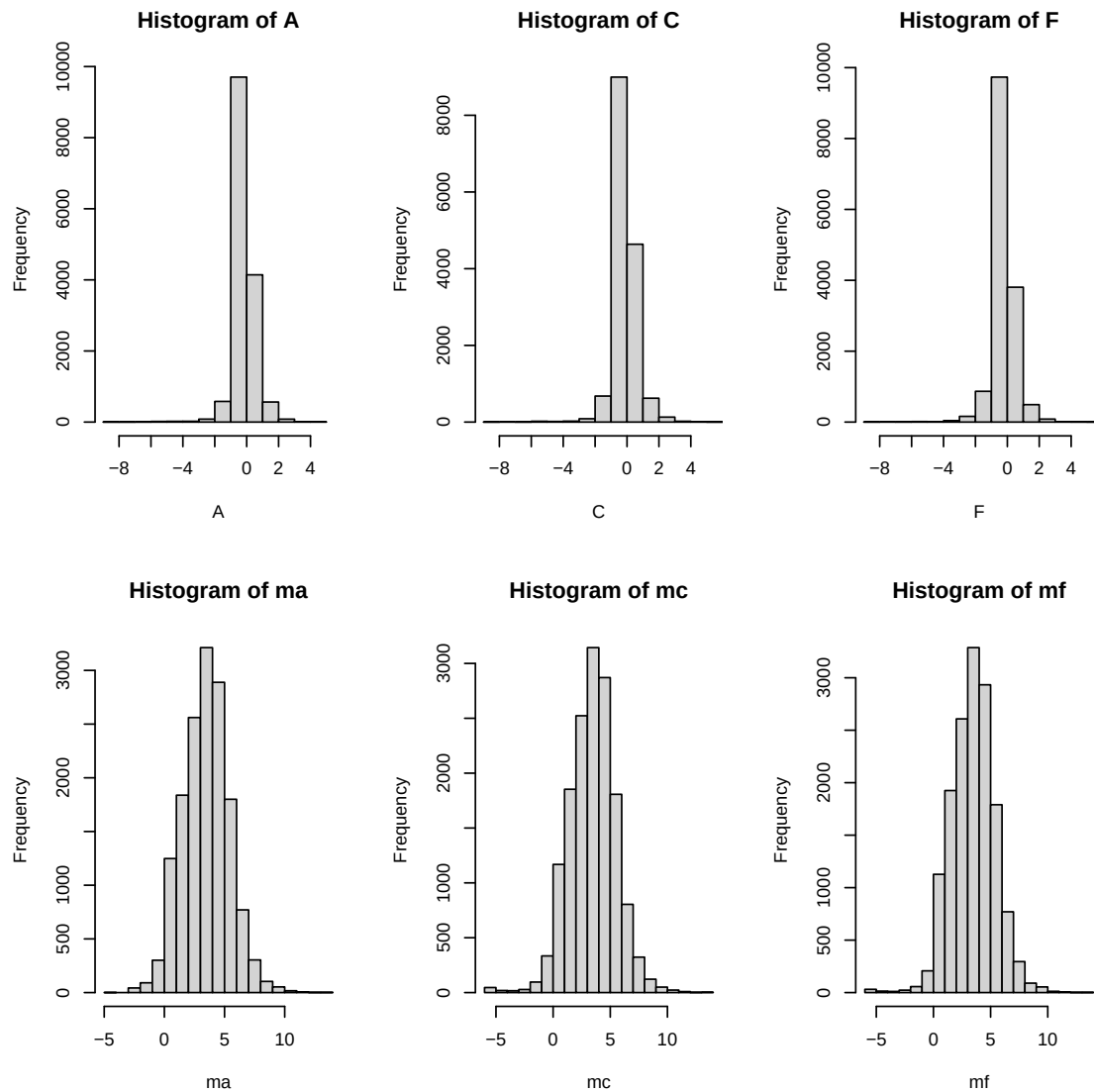
      mc      mf
Vitvi15g01736  4.430191 4.5232904
Vitvi07g02832 -2.991443 2.6259591
Vitvi07g02830 -2.839209 2.1903769
Vitvi07g02812 -1.374475 0.6817977
Vitvi07g02811  1.837984 3.1363800
Vitvi09g02033 -3.137869 1.5632132

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

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

```

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



5.4.2 Types by effects

```

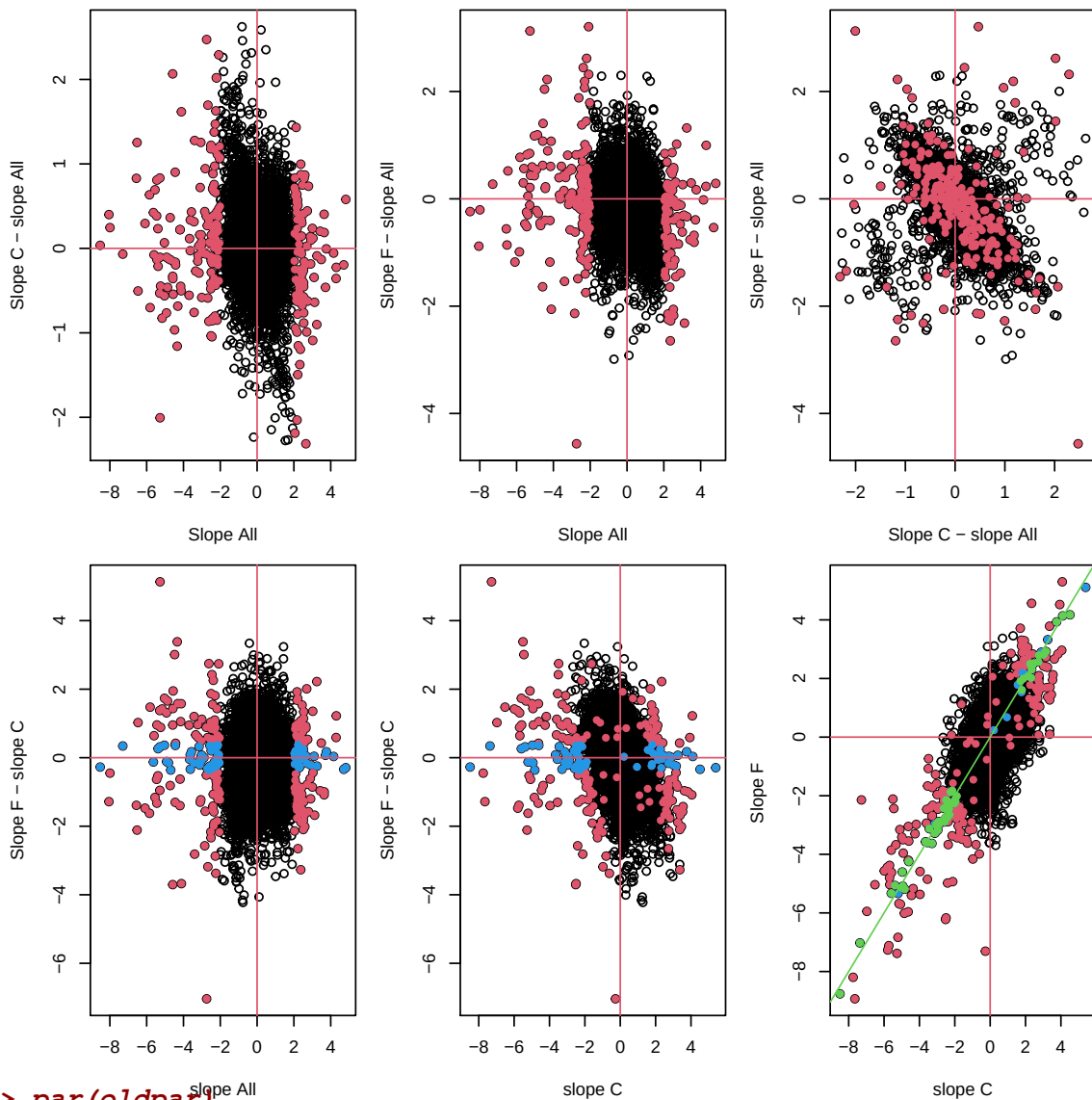
> delta <- 2
> large_abs_A <- abs(A) > delta
> small_fc <- abs(fc) < delta/5
> small_ca <- abs(ca) < delta/5
> oldpar <- par(mfrow=c(2, 3), mar=c(4, 4, 1, 1))
> plot(A, ca, xlab="Slope All", ylab="Slope C - slope All")
> points(A[large_abs_A], ca[large_abs_A], col=2, pch=16)
> abline(h=0, v=0, col=2)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

```

```

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

```



```

> par(oldpar)

```

6 Situation types and Type selection criteria

Boundaries:

minX X at least ... ($>$)

maxX X at most ... ($<$)

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

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

6.1 Old Types

Type1

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

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

Type2

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

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

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



```

[1] 1.5
> (max.slope <- as.numeric(.max.slope))      # slope C smaller
[1] 0.5
> min.slope <- min.slope      # slope F larger
> max.slope <- max.slope      # slope F smaller
> minA <- min.slope           # slope A larger
> (diff.slope <- as.numeric(.diff.slope)) # 1      # difference F - C larger
[1] 1
> (diff.slope5 <- as.numeric(.diff.slope5)) # difference for F - C larger for
[1] 2
> (maxfc <- as.numeric(.maxfc))      # difference F - C smaller
[1] 1
> maxca <- maxfc # difference C - A smaller
> maxfa <- maxfc # difference F - A smaller
> #
> large_abs_A <- abs(A) > minA
> large_abs_C <- abs(C) > min.slope
> large_abs_F <- abs(F) > min.slope
> #
> small_fc <- abs(fc) < maxfc
> small_ca <- abs(ca) < maxca
> small_fa <- abs(fa) < maxfa
> plot(C,F, xlab="slope C",ylab="Slope F ")
> #points(C[large_abs_A],F[large_abs_A],col=2,pch=16)
> #
> type10 <- large_abs_A & small_fc & small_ca
> type1 <- (large_abs_C/large_abs_F) & small_fc & (abs(mc-mf)<deltam)
> table(type10,type1)

      type1
type10 FALSE TRUE
FALSE 14775  146
TRUE    28  293

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

```

```

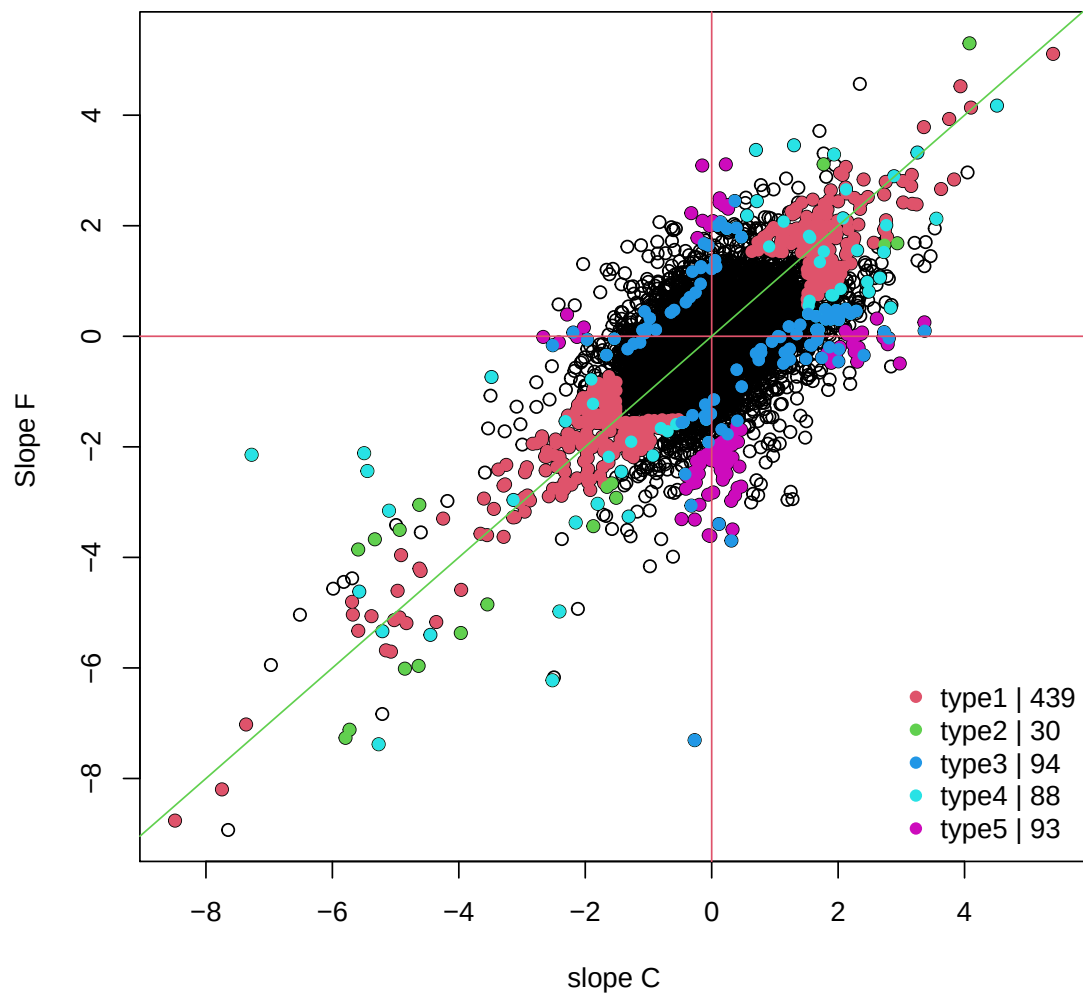
      type30
type3  FALSE  TRUE
      FALSE 14139 1009
      TRUE   0    94

> points(
+   C[type3],
+   F[type3],
+   col=4,pch=16)
> #
> type4 <- (large_abs_C/large_abs_F) & (abs(mc-mf)>deltam) & (C*F>0)
> points(
+   C[type4],
+   F[type4],
+   col=5,pch=16)
> #
> type5 <- ((abs(C)<max.slope) | (abs(F)<max.slope)) & (abs(fc)> diff.slope5) & (a
> points(
+   C[type5],
+   F[type5],
+   col=6,pch=16)
>
> table(type3,type5)

      type5
type3  FALSE  TRUE
      FALSE 15055   93
      TRUE   94    0

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

```



6.2 New type definitions

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

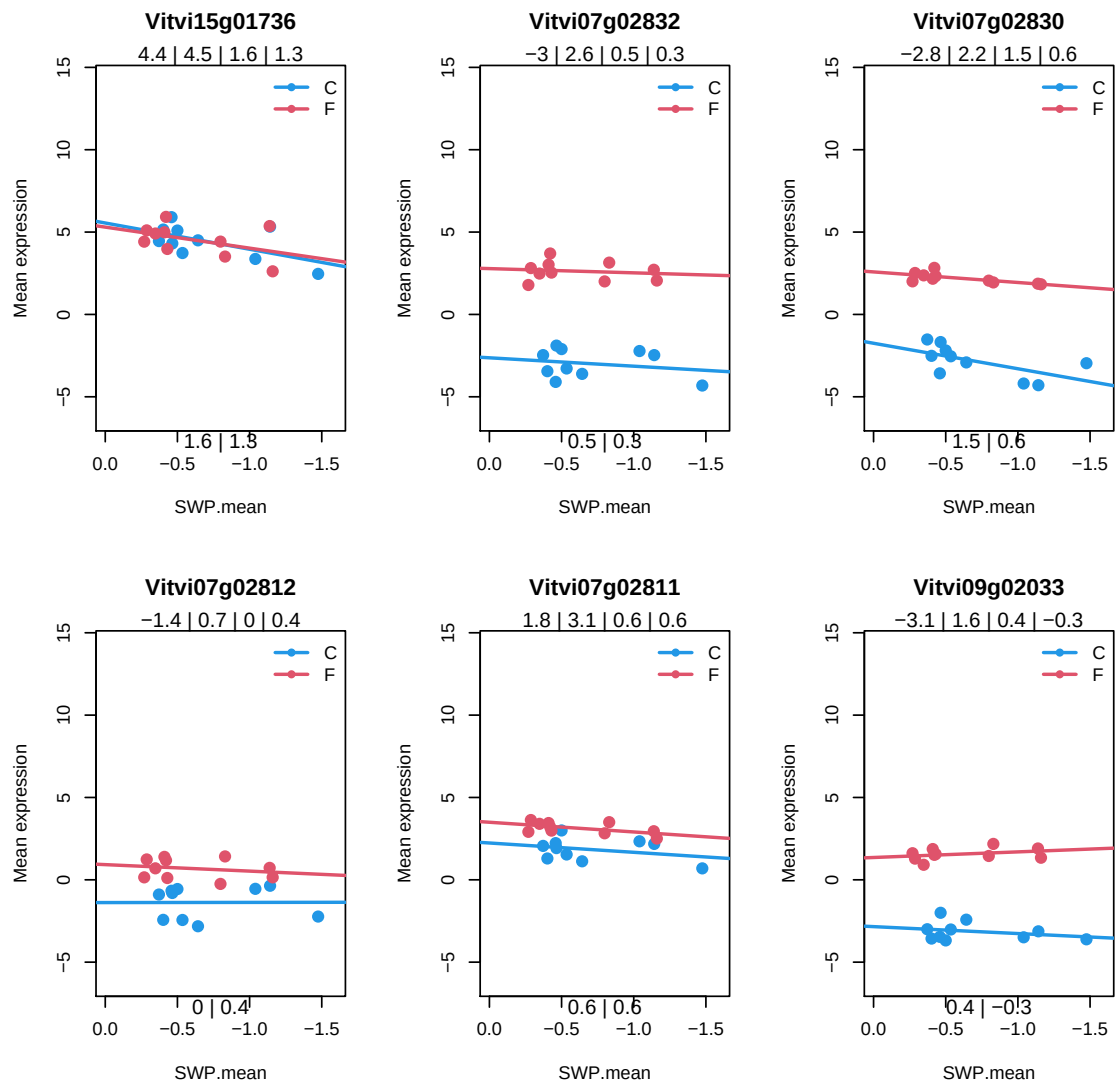
Function to plot the overview for types

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

```

> #' plot.type() # TRUE most of the time
>
> plot.type <- function( filt=rep(TRUE,6), ...){
+ par(mfrow=c(2,3), oma=c(0,0,1,0))
+ #filt <- type1
+ print(sum(filt))
+ for(i in 1:min(sum(filt),6)){
+ varname <- rownames(exprs)[filt][i]
+ p <- plot.ewp(varname,model="", exprs=exprs, pd=pd, ylim=range(exprs)
+ , cex= 1.5
+ , pch = c(16,16)
+ , all = FALSE
+ )
+ mtext(paste(round(coefs[varname,],1),collapse=" | "),cex=0.75)
+ mtext(paste(round(c(p$C$coefficients[2],p$F$coefficients[2]),1)
+ ,collapse=" | "),1,cex=0.75)
+ }
+ }
> plot.type()
[1] 6

```



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

6.2.1 Parameter explanation

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

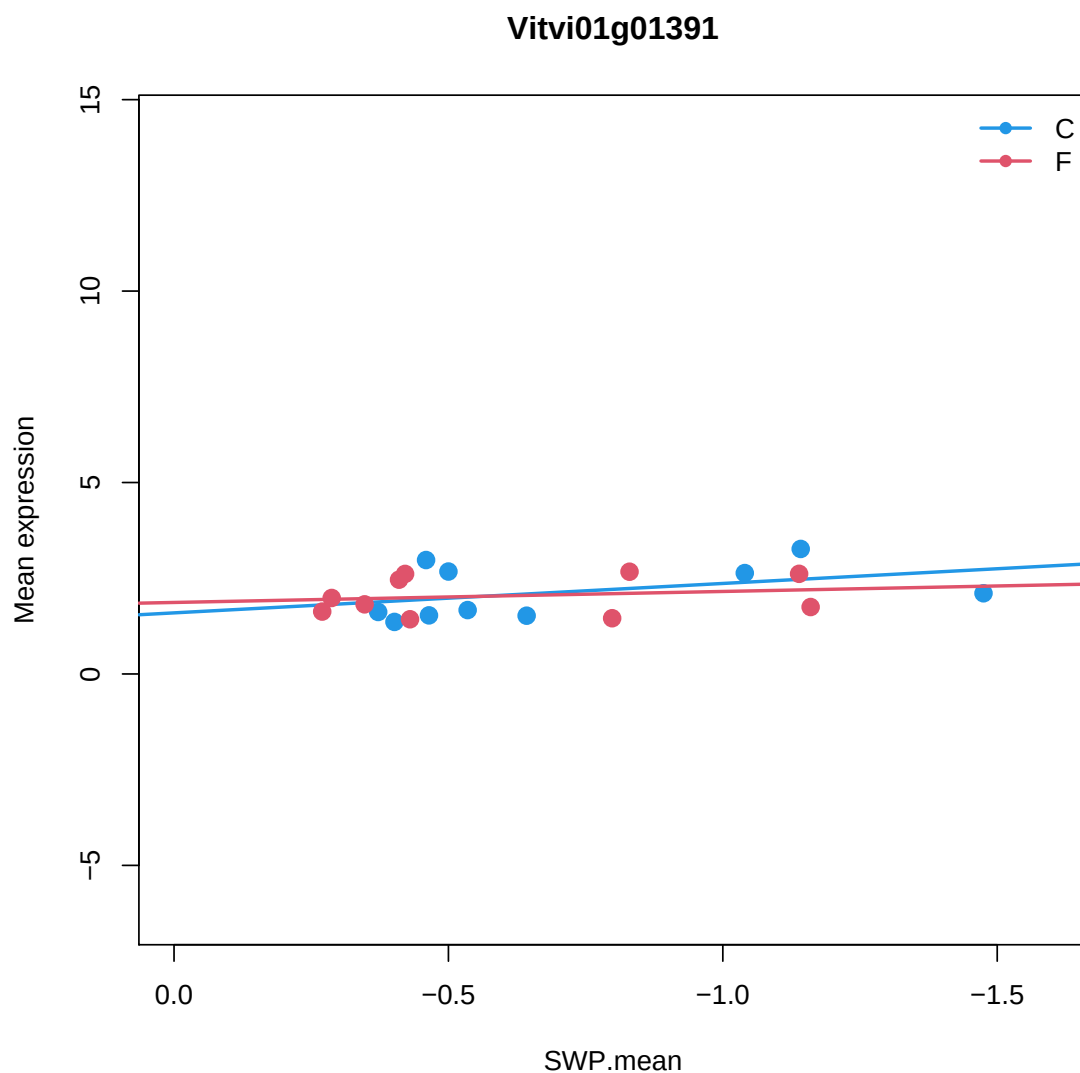
.max.slope (0.5) Upper level for small slope

.diff.slope (1) Threshold for slope difference

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

Preparation for decision rules

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

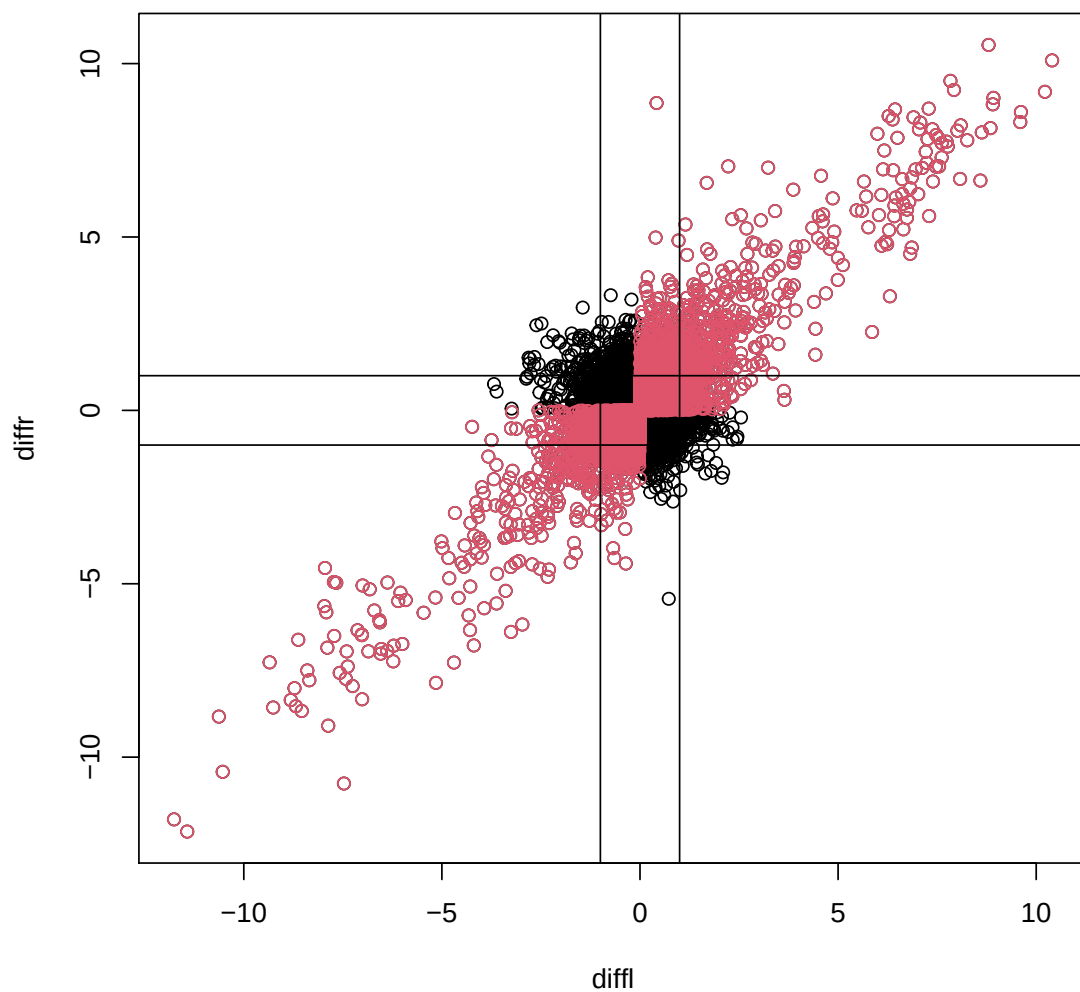


```

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

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

```

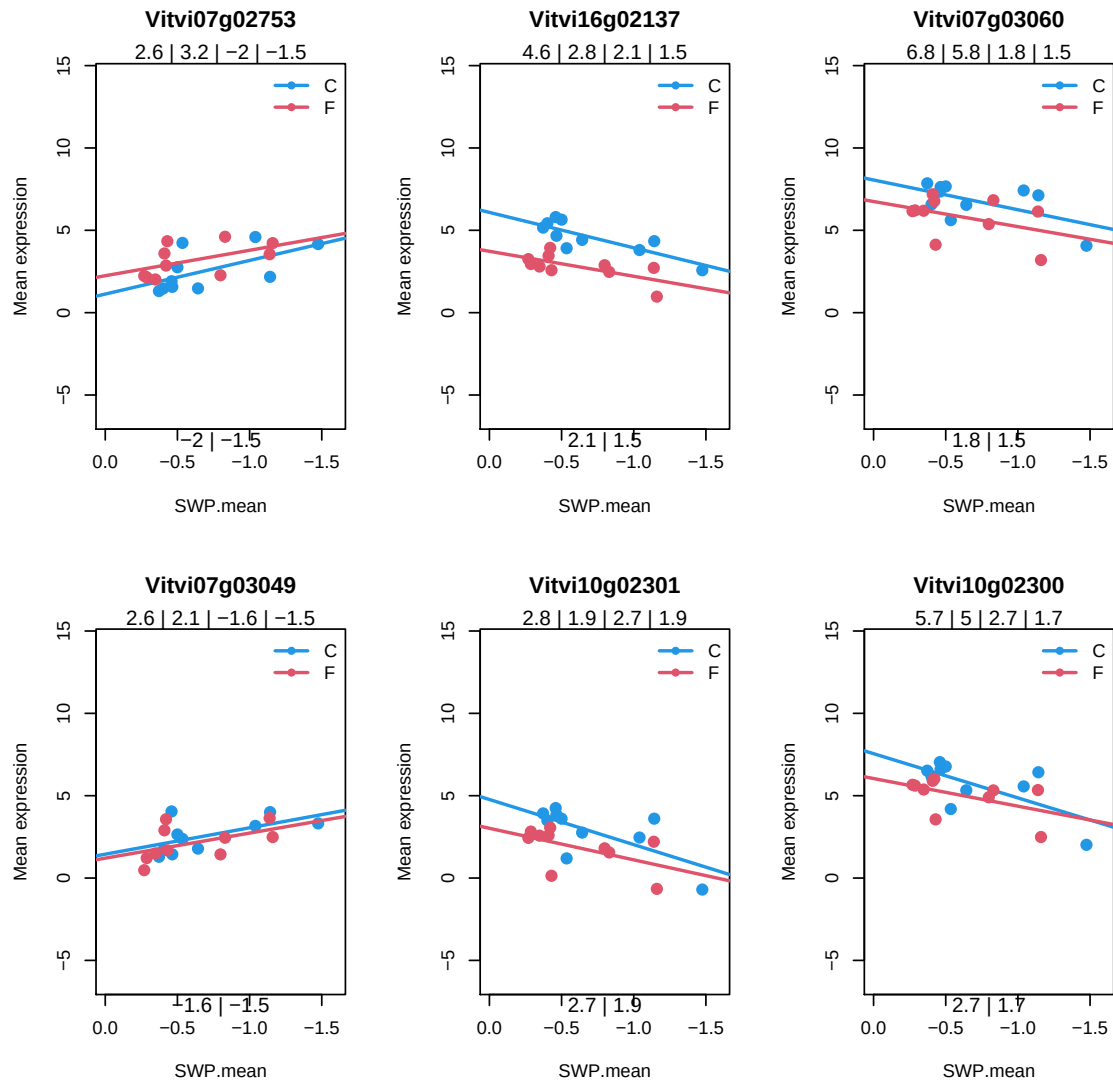


Function to plot coefficients for types

```

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

```



```
> head(types)
```

```

      type1 type2 type3 type4 type5
Vitvi15g01736 TRUE FALSE FALSE FALSE FALSE
Vitvi07g02832 FALSE FALSE FALSE FALSE FALSE
Vitvi07g02830 FALSE FALSE FALSE TRUE FALSE
Vitvi07g02812 FALSE FALSE FALSE FALSE FALSE
Vitvi07g02811 FALSE FALSE FALSE FALSE FALSE
Vitvi09g02033 FALSE FALSE FALSE FALSE FALSE

```

```

> plot.types <- function(x=C, y=F, type=types,title,...){
+   xlab <- deparse(substitute(x))
+   ylab <- deparse(substitute(y))
+   plot(x,y, xlab=xlab,ylab=ylab, col=8)
+   m <- ncol(type)
+   sek <- 1:ncol(type)
+   for( i in sek){
+     points(
+       x[type[,i]],
+       y[type[,i]],
+       col=i+1,pch=16)
+   }
+ }

```



```

+     }
+     abline(h=0,v=0,col=2)
+ abline(c(0,1),col=3)
+ if(!missing(title)) title(title)
+ nt <- apply(type,2,sum)
+ pre <- "" # substr(rep(" ",length(nt)),1,(3-nchar(nt))*2.3)
+ legend("bottomright",pch=rep(16,m),col=2:(m+1),legend=paste0(colnames(type),
+ }
> #plot.types(type=Types)

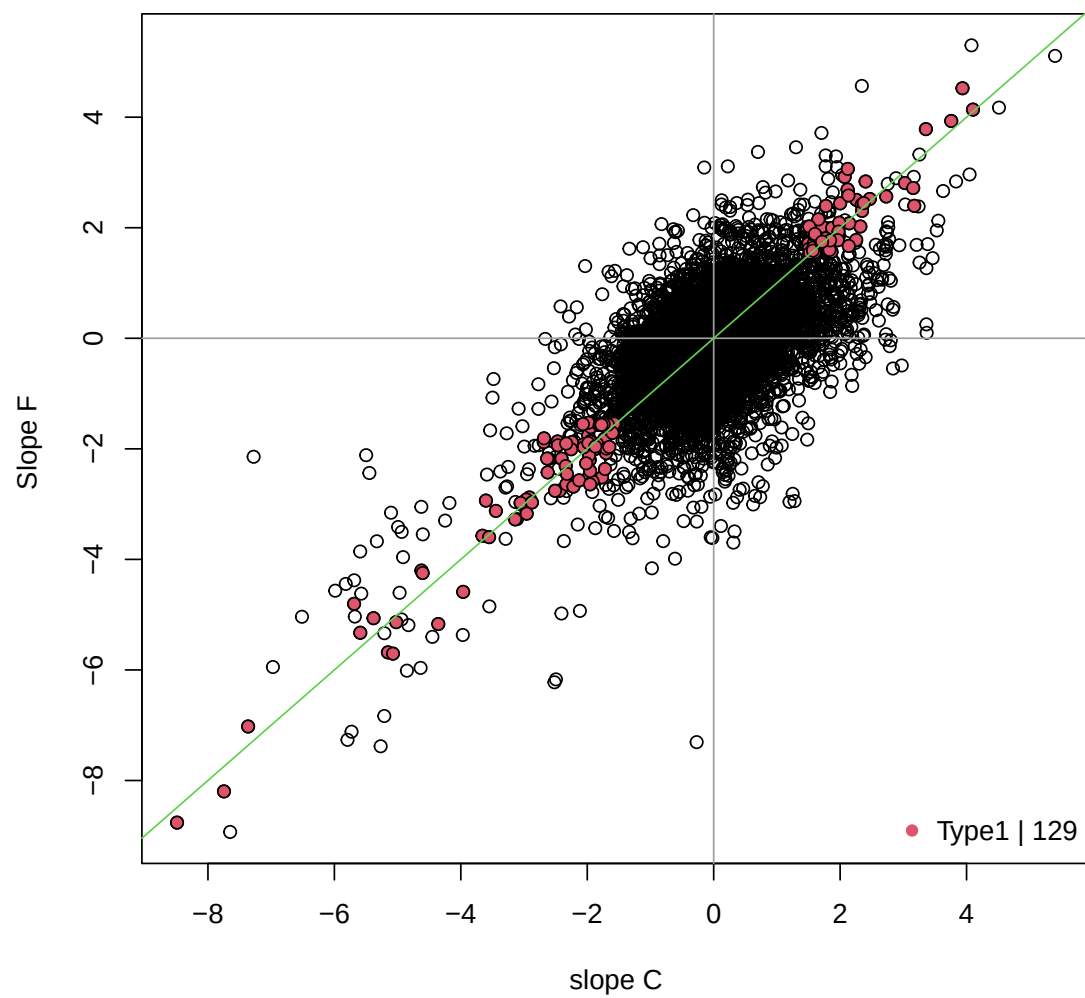
```

6.2.2 Type1

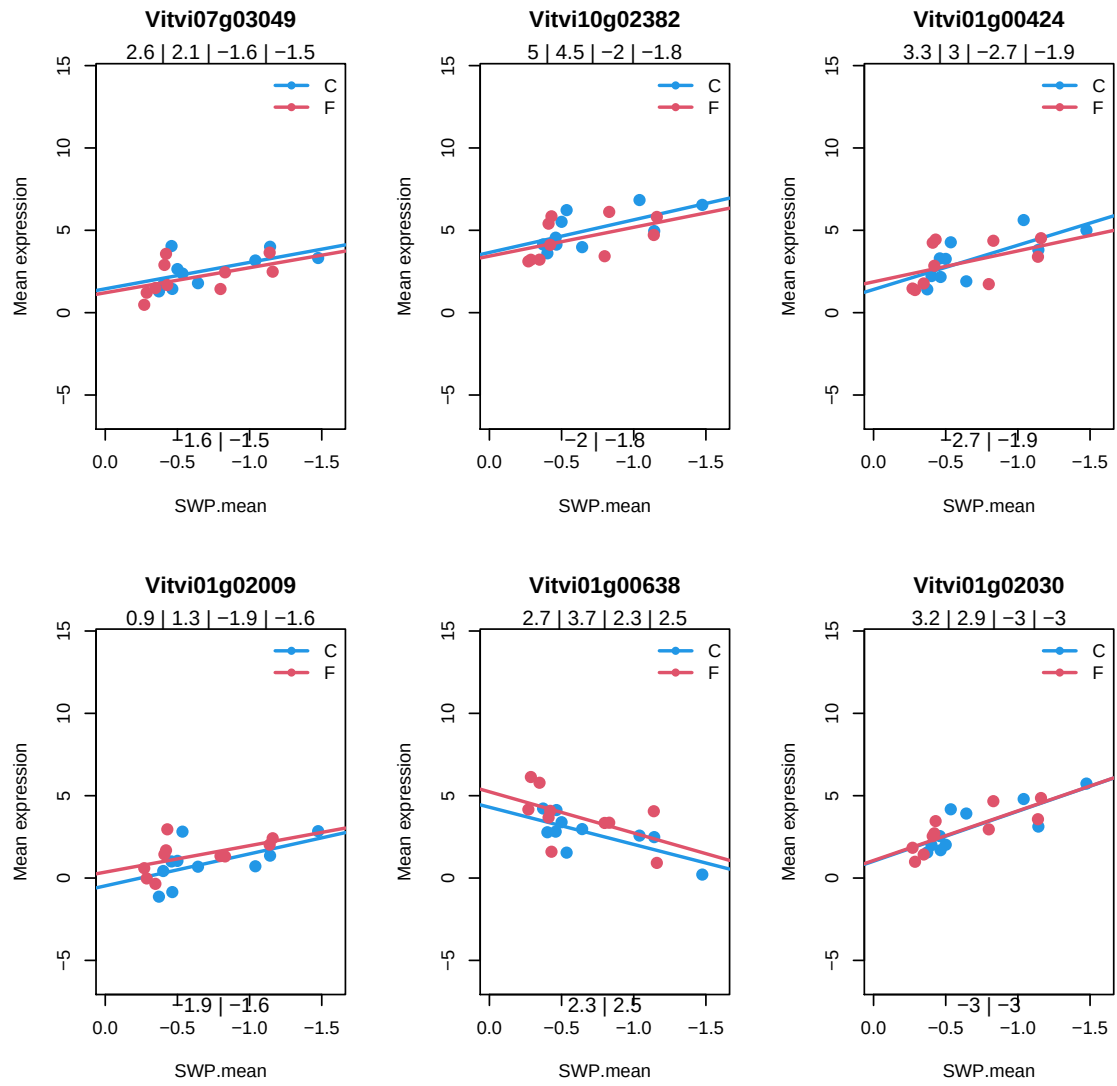
```
> plot(C,F, xlab="slope C",ylab="Slope F ")
> abline(h=0,v=0,col=8)
> #points(C[large_abs_A],F[large_abs_A],col=2,pch=16)
> #
> type10 <- large_abs_A & small_fc & small_ca
> type1 <- (large_abs_C/large_abs_F) & small_fc & (abs(mc-mf)<deltam)
> #
> Type1 <- C*F > 0
> Type1 <- Type1 & ( abs(C) > min.slope)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

      type1
Type1  FALSE  TRUE
FALSE 14803   310
TRUE     0   129

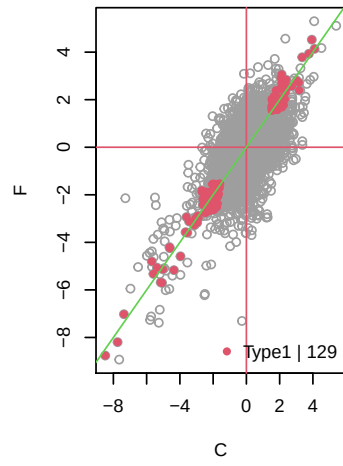
> points(
+   C[Type1],
+   F[Type1],
+   bg=2, pch=21, col=1)
> abline(c(0,1),col=3)
> Types <- data.frame(Type1)
> nt <- apply(Types,2,sum)
> legend("bottomright",pch=rep(16,5),col=2:7,legend=paste0("Type",1:ncol(Types
```



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



> plot.types (type=Types)

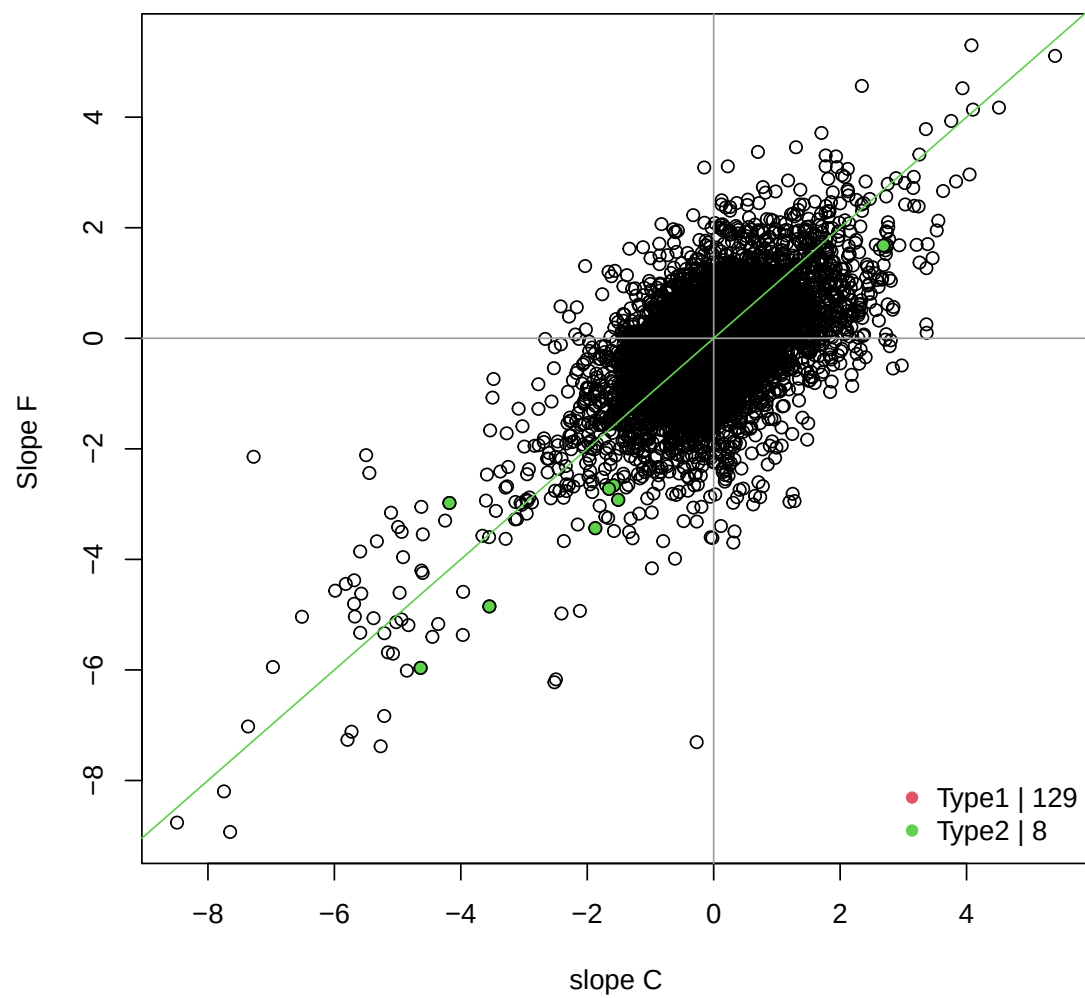


6.2.3 Type2

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

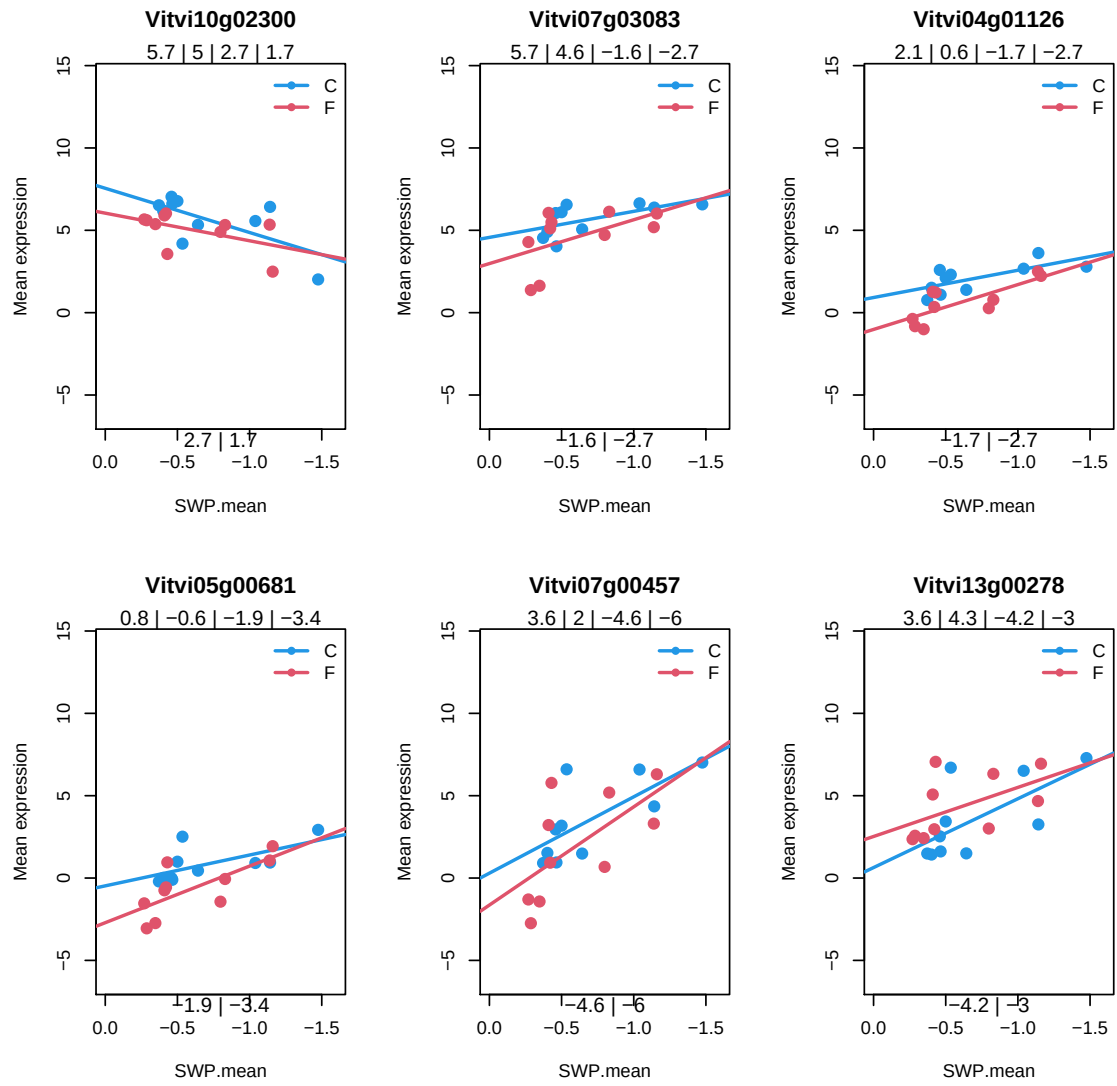
      type2
Type2  FALSE  TRUE
  FALSE 15210   24
   TRUE     2    6

> points(
+   C[Type2],
+   F[Type2],
+   bg=3, pch=21, col=1)
>       abline(c(0,1),col=3)
> Type1.2 <- Type2
> Types <- data.frame(Type1,Type1.2)
> nt <- apply(Types,2,sum)
> legend("bottomright",pch=rep(16,5),col=2:7,legend=paste0("Type",1:ncol(Types
```

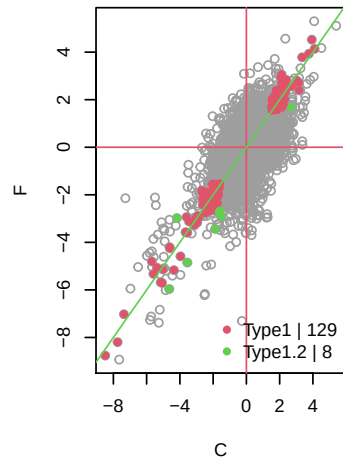


```
> nt
  Type1 Type1.2
    129      8

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



> plot.types (type=Types)



6.2.4 Type3

```

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

      FALSE TRUE
FALSE  5011 9572
TRUE   517  142

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

[1] TRUE

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

      Type3 Type3.C Type3.F
[1,]      0      0      0

> sum((Type3 != (Type3.C|Type3.F)))

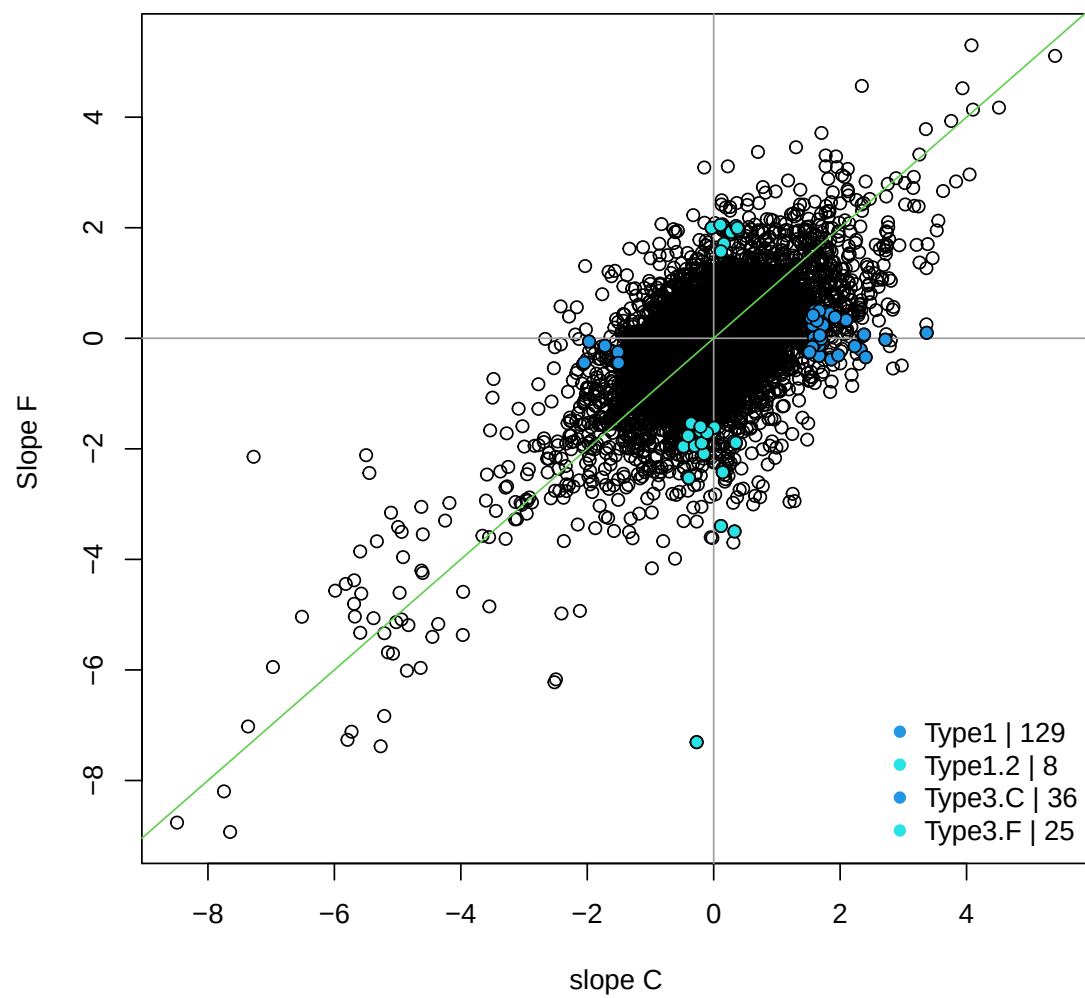
[1] 0

> #
> table(Type3,type3)

      type3
Type3  FALSE  TRUE
FALSE 15094    87
TRUE   54     7

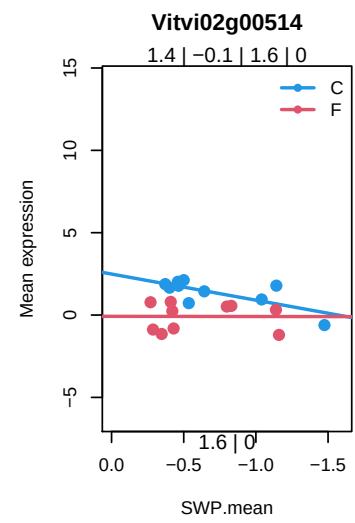
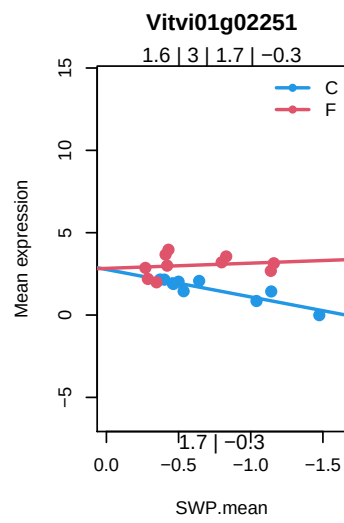
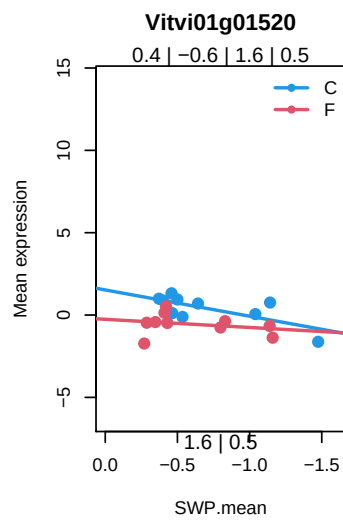
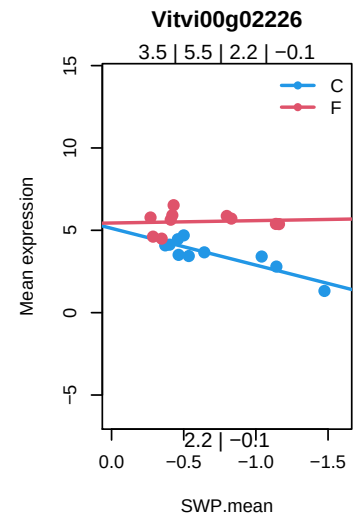
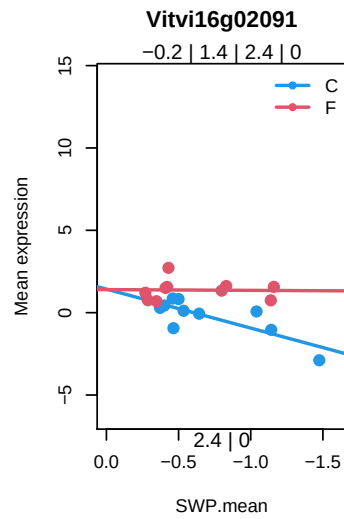
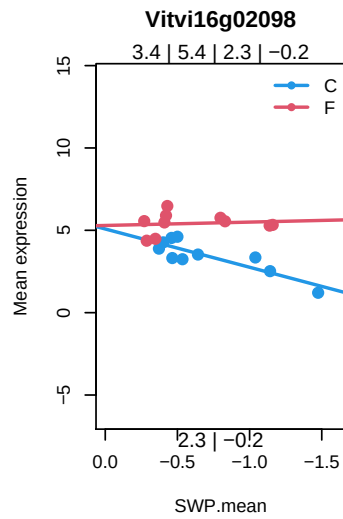
> points(
+   C[Type3.C],
+   F[Type3.C],
+   bg=4, pch=21, col=1)
> points(
+   C[Type3.F],
+   F[Type3.F],
+   bg=5, pch=21, col=1)
> abline(c(0,1),col=3)
> Types <- data.frame(Type1,Type1.2,Type3.C, Type3.F)
> nt <- apply(Types,2,sum)
> legend("bottomright",pch=rep(16,ncol(Types)),col=c(4,5),legend=paste0(colnam

```



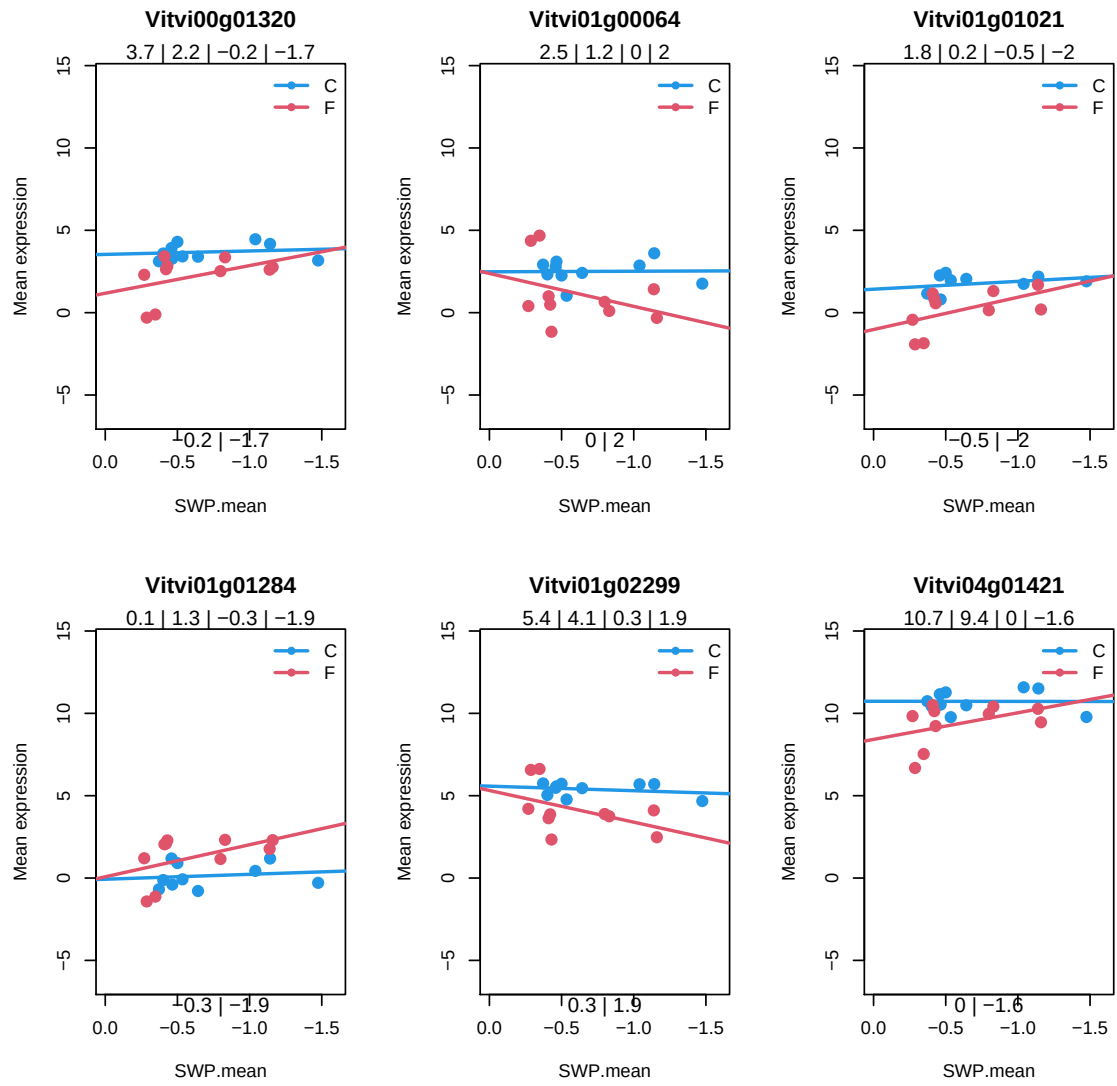
```
> nt
  Type1 Type1.2 Type3.C Type3.F
    129      8     36     25

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

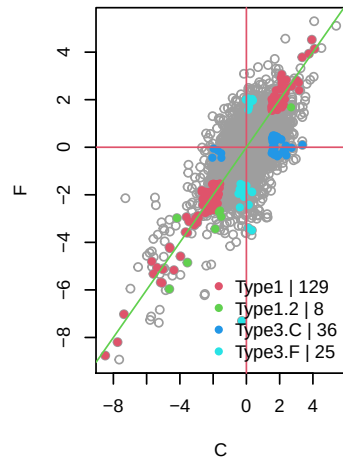


> plot.type(Type3.F)

[1] 25



> plot.types (type=Types)

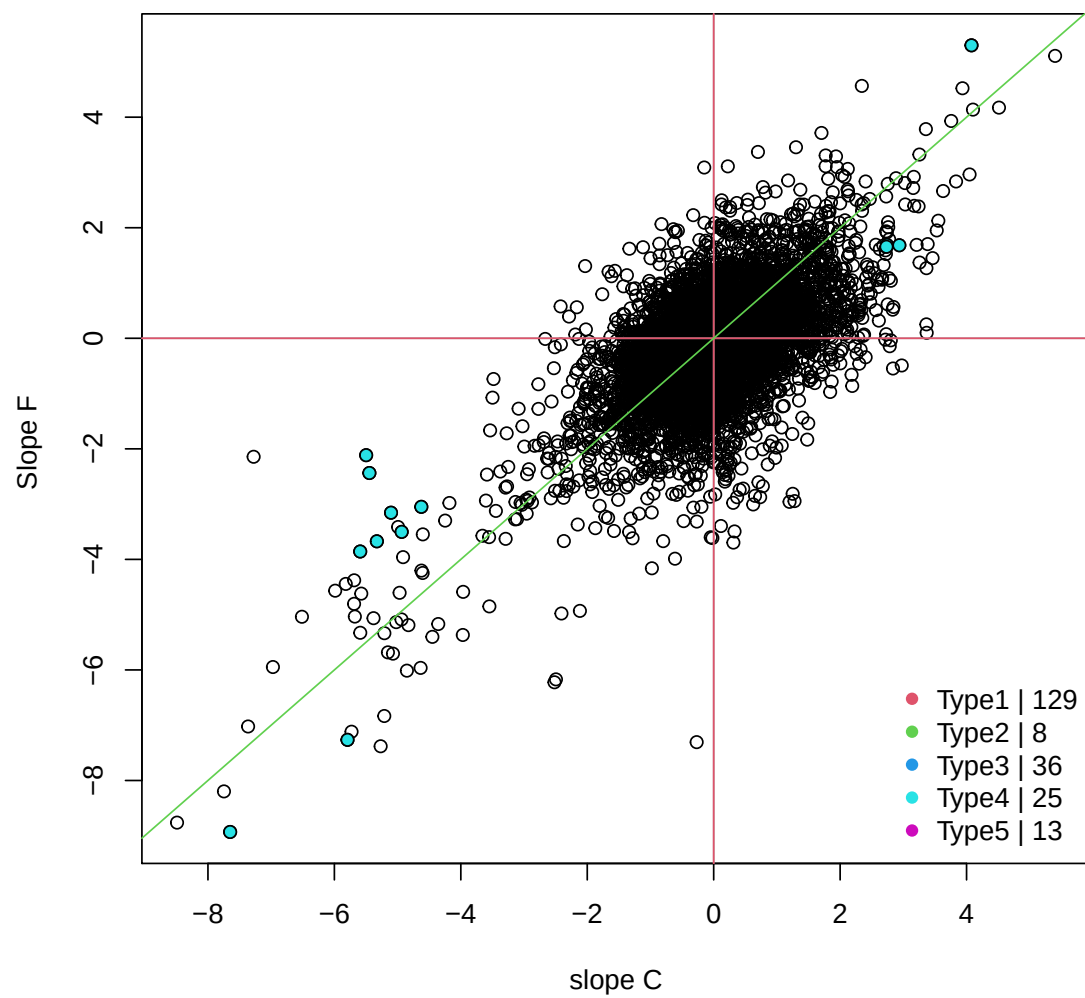


6.2.5 Type4

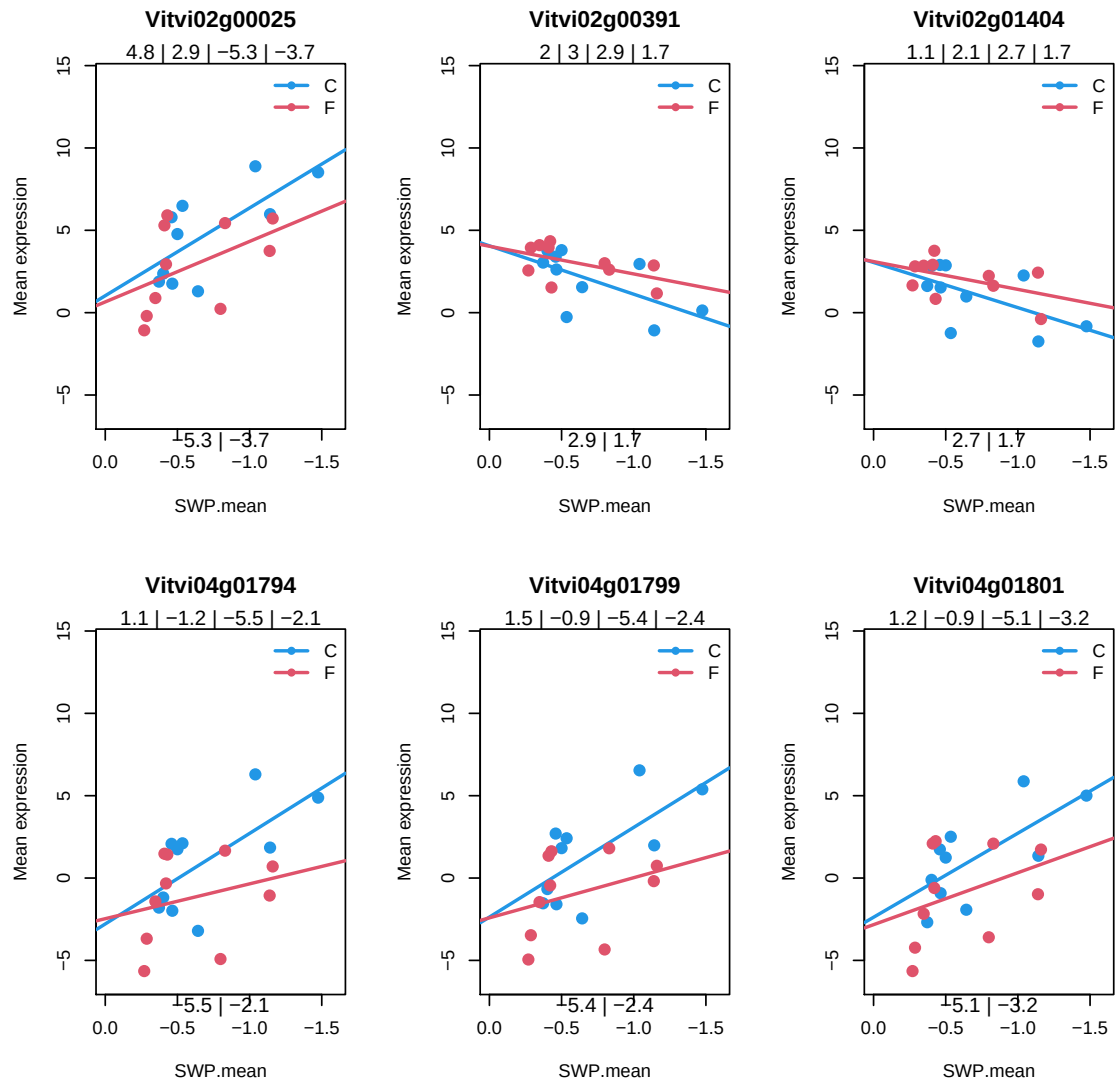
```
> plot(C,F, xlab="slope C",ylab="Slope F ")
>       abline(h=0,v=0,col=8)
> #
> type4 <- (large_abs_C/large_abs_F) & (abs(mc-mf)>deltam) & (C*F>0)
> #
> Type4 <- C*F > 0
> Type4 <- Type4 & ( abs(C) > min.slope) & (abs(F) > min.slope )
> Type4 <- Type4 & ( abs(F-C) > diff.slope )
> Type4 <- Type4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

	type4	
Type4	FALSE	TRUE
FALSE	15144	85
TRUE	10	3

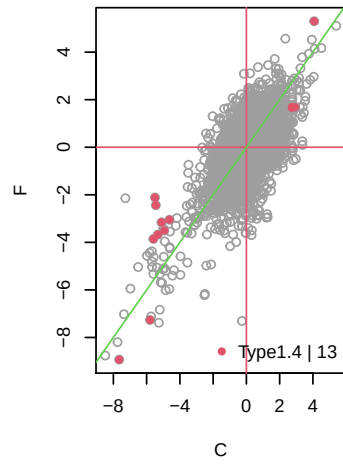
```
> points(
+   C[Type4],
+   F[Type4],
+   bg=5, pch=21, col=1)
>       abline(h=0,v=0,col=2)
> abline(c(0,1),col=3)
> Types <- data.frame(Type1,Type1.2,Type3.C, Type3.F, Type1.4)
> nt <- apply(Types,2,sum)
> legend("bottomright",pch=rep(16,5),col=2:7,legend=paste0("Type",1:ncol(Types))
```



```
> nt
  Type1 Type1.2 Type3.C Type3.F Type1.4
    129      8     36    25     13
> plot.type(Type1.4)
[1] 13
```

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



6.2.6 Type5

```

> plot(C,F, xlab="slope C",ylab="Slope F ")
>       abline(h=0,v=0,col=8)
> #
> type5 <- ((abs(C)<max.slope)|(abs(F)<max.slope)) & (abs(fc)> diff.slope5)&(a
> #
> Type5 <- C*F > 0
> Type5 <- Type5 & ( abs(C) > min.slope) & (abs(F) > min.slope )
> Type5 <- Type5 & ( ( abs(diff0) > diff01 ) & ( abs(diff1) > diff01 ) )
> Type5 <- Type5 & nocross
> #
> table(Type5,type5)

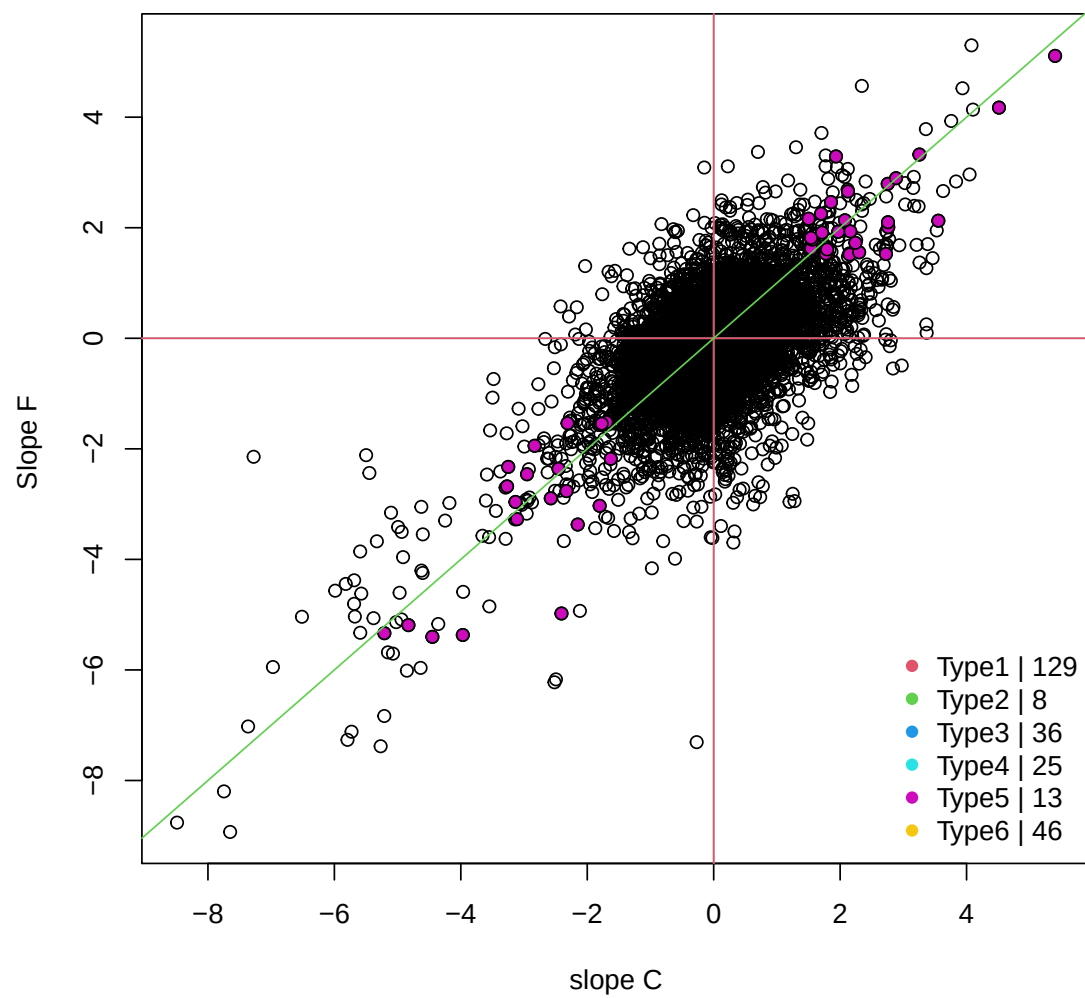
      type5
Type5  FALSE  TRUE
  FALSE 15103   93
   TRUE   46    0

> # type 3 is a subset of type5, type3 & large mean difference
> table(type5,Type5)

      Type5
type5  FALSE  TRUE
  FALSE 15103   46
   TRUE   93    0

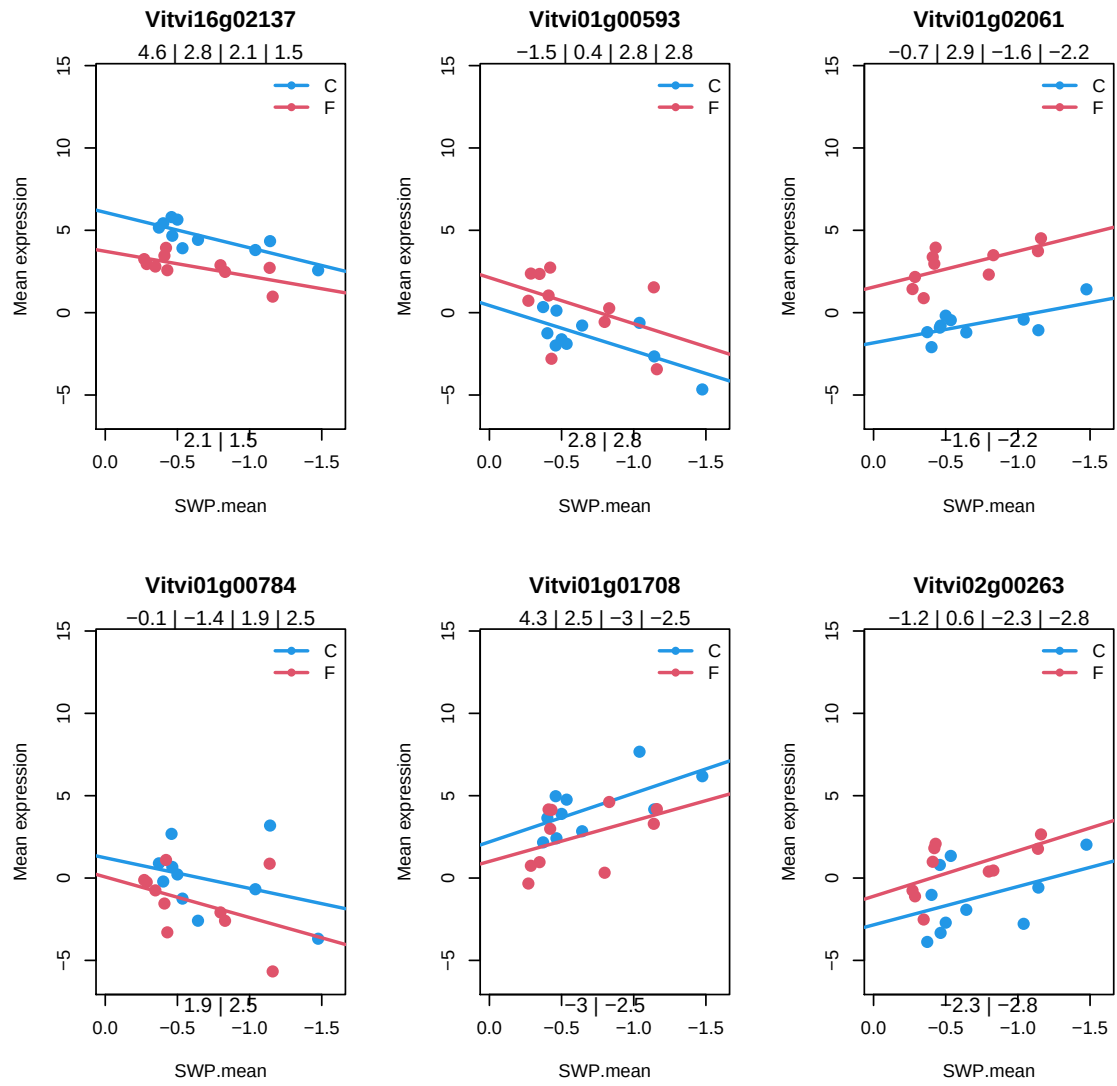
> points(
+   C[Type5],
+   F[Type5],
+   bg=6, pch=21, col=1)
> #
> abline(h=0,v=0,col=2)
> abline(c(0,1),col=3)
> Types <- data.frame(Type1,Type1.2,Type3.C, Type3.F, Type1.4, Type5)
> nt <- apply(Types,2,sum)
> legend("bottomright",pch=rep(16,5),col=2:7,legend=paste0("Type",1:ncol(Types

```

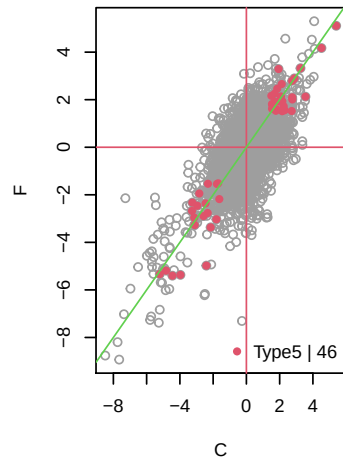


```
> nt
  Type1 Type1.2 Type3.C Type3.F Type1.4  Type5
    129      8     36    25     13     46

> plot.type(Type5)
[1] 46
```



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



6.2.7 Type6

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

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

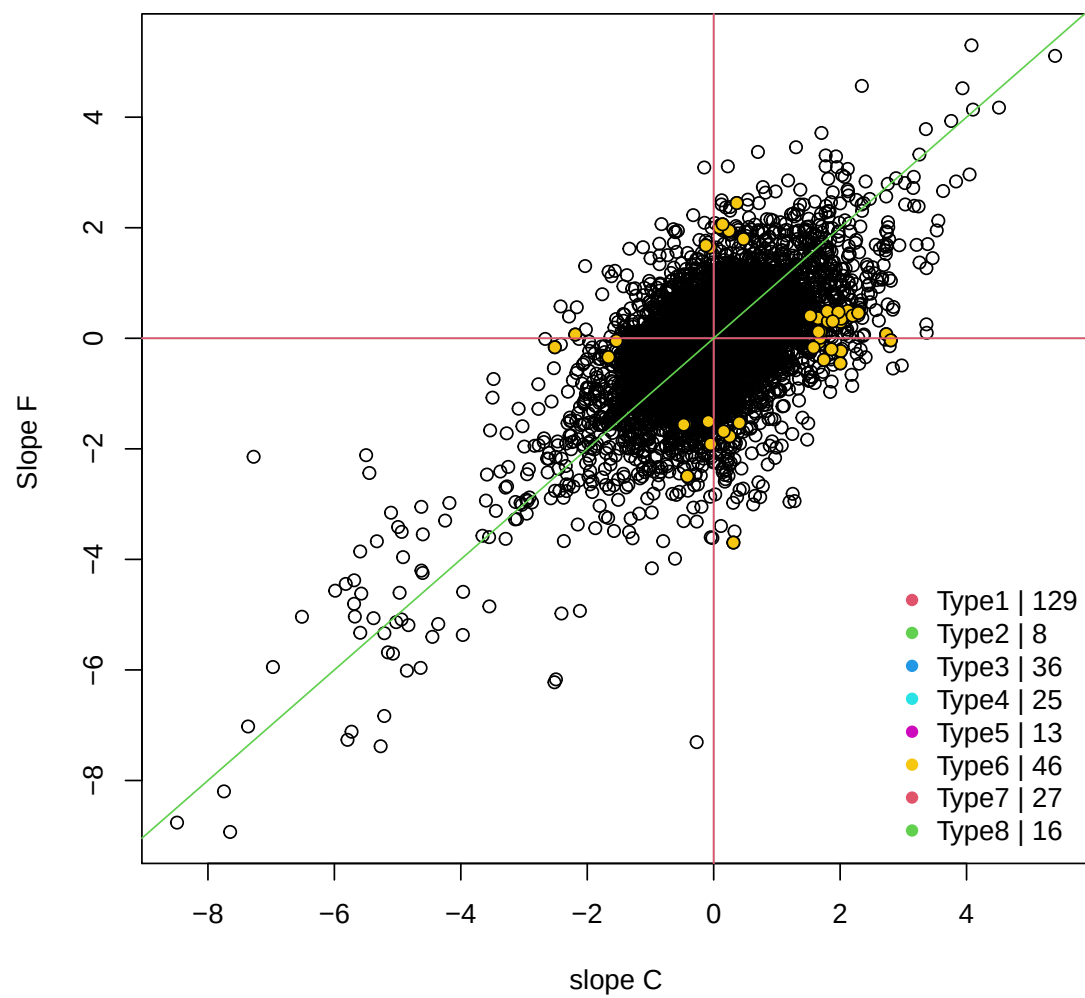
      Type6.F = FALSE

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

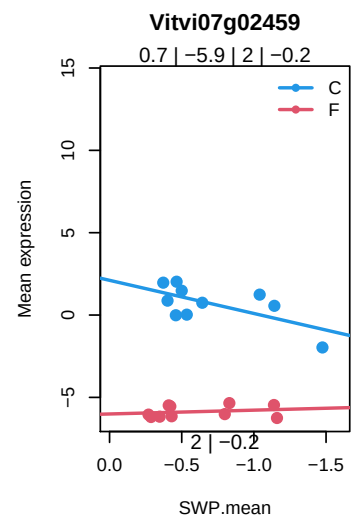
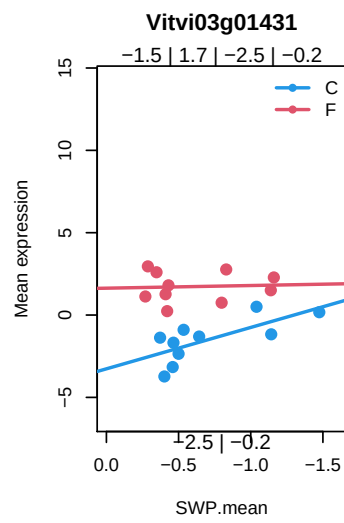
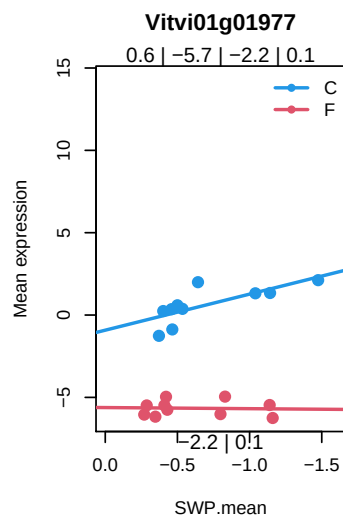
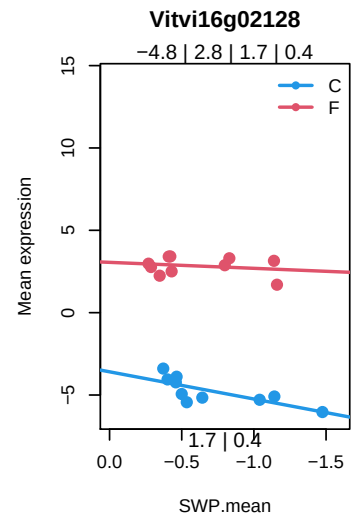
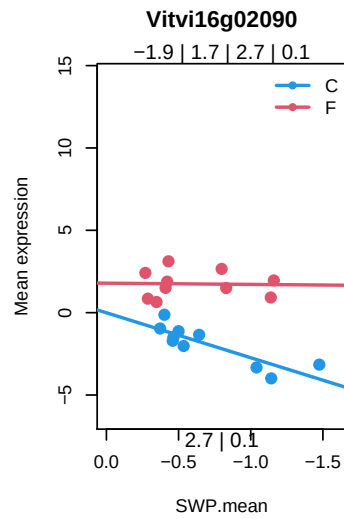
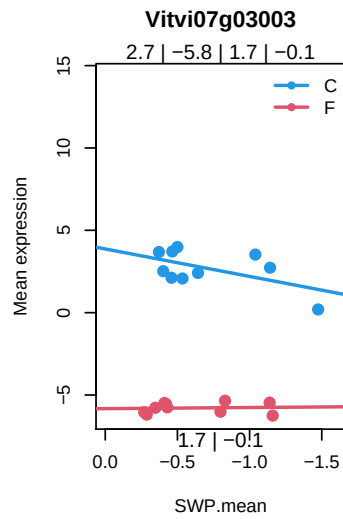
> # type 3 is a subset of Type6, type3 & large mean difference
> table(Type3,Type6)

      Type6
Type3  FALSE  TRUE
  FALSE 15138   43
   TRUE   61    0

> points(
+   C[Type6.C],
+   F[Type6.C],
+   bg=7, pch=21, col=1)
> points(
+   C[Type6.F],
+   F[Type6.F],
+   bg=7, pch=21, col=1)
> #
> abline(h=0,v=0,col=2)
> abline(c(0,1),col=3)
> Types <- data.frame(Type1,Type1.2,Type3.C,Type3.F, Type1.4,Type5, Type6.C, Type6.F)
> nt <- apply(Types,2,sum)
> legend("bottomright",pch=rep(16,5),col=2:7,legend=paste0("Type",1:ncol(Types))
```

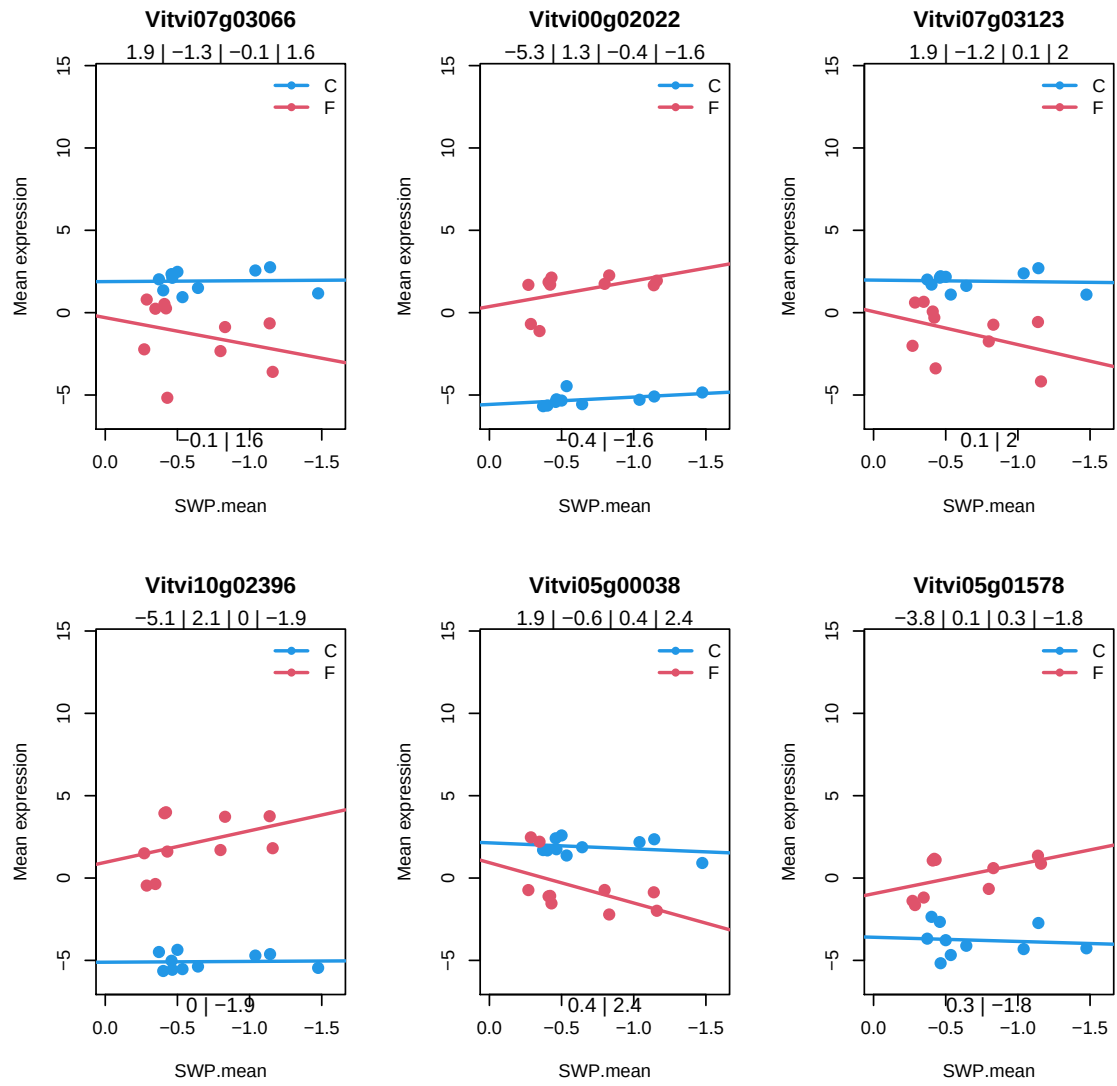


```
> nt
  Type1 Type1.2 Type3.C Type3.F Type1.4  Type5 Type6.C
    129      8     36     25     13     46     27
Type6.F
    16
> plot.type(Type6.C)
[1] 27
```

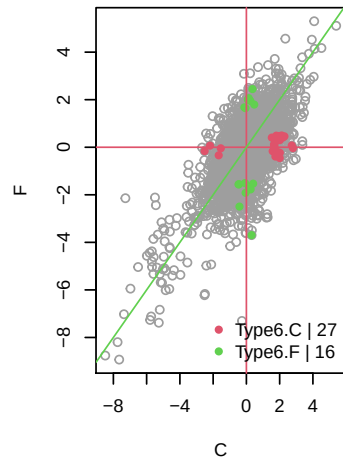



```
> plot.type(Type6.F)
```

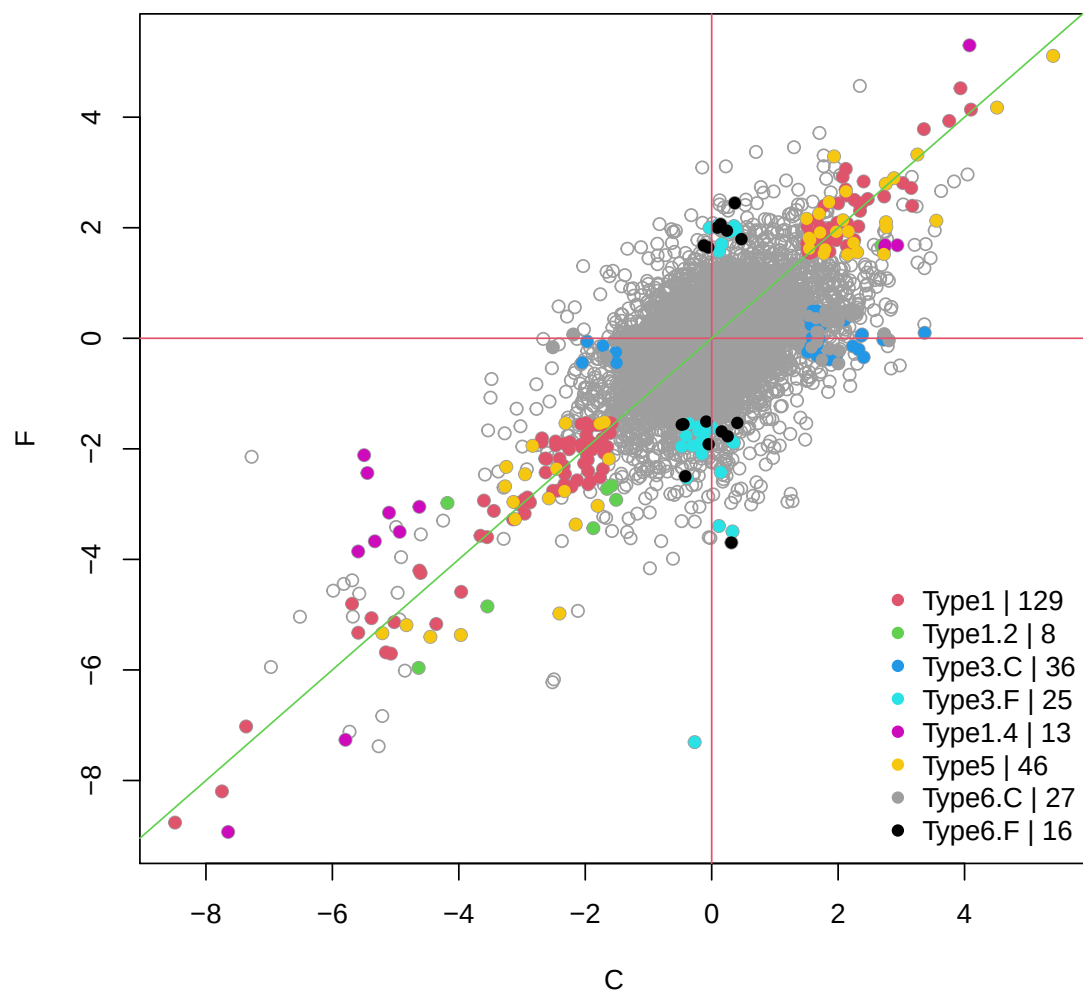
```
[1] 16
```



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



```
> plot.types (type=Types)
```



```
> nts <- apply(Types, 2, sum)
[1] 300
> sum(nts)
[1] 300
> xtable( data.frame(Count=t(t(addmargins(apply(Types, 2, table), 2) [2, ]))), auto = TRUE)
```

	Count
Type1	129
Type1.2	8
Type3.C	36
Type3.F	25
Type1.4	13
Type5	46
Type6.C	27
Type6.F	16
Sum	300

Table 1: Table of new types.

Override old types

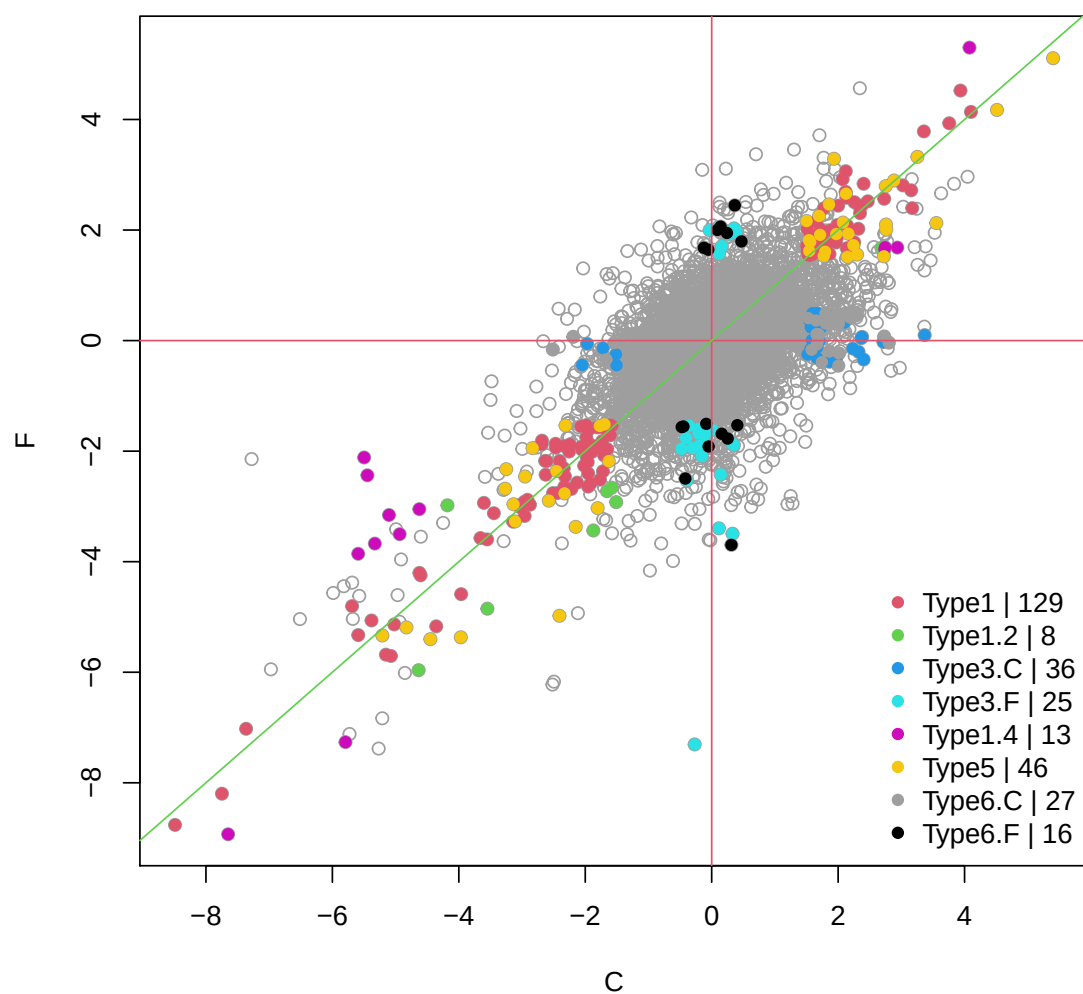
```
> types.old <- types
> types.new <- Types
> types <- types.new
```

```
> head(types)
```

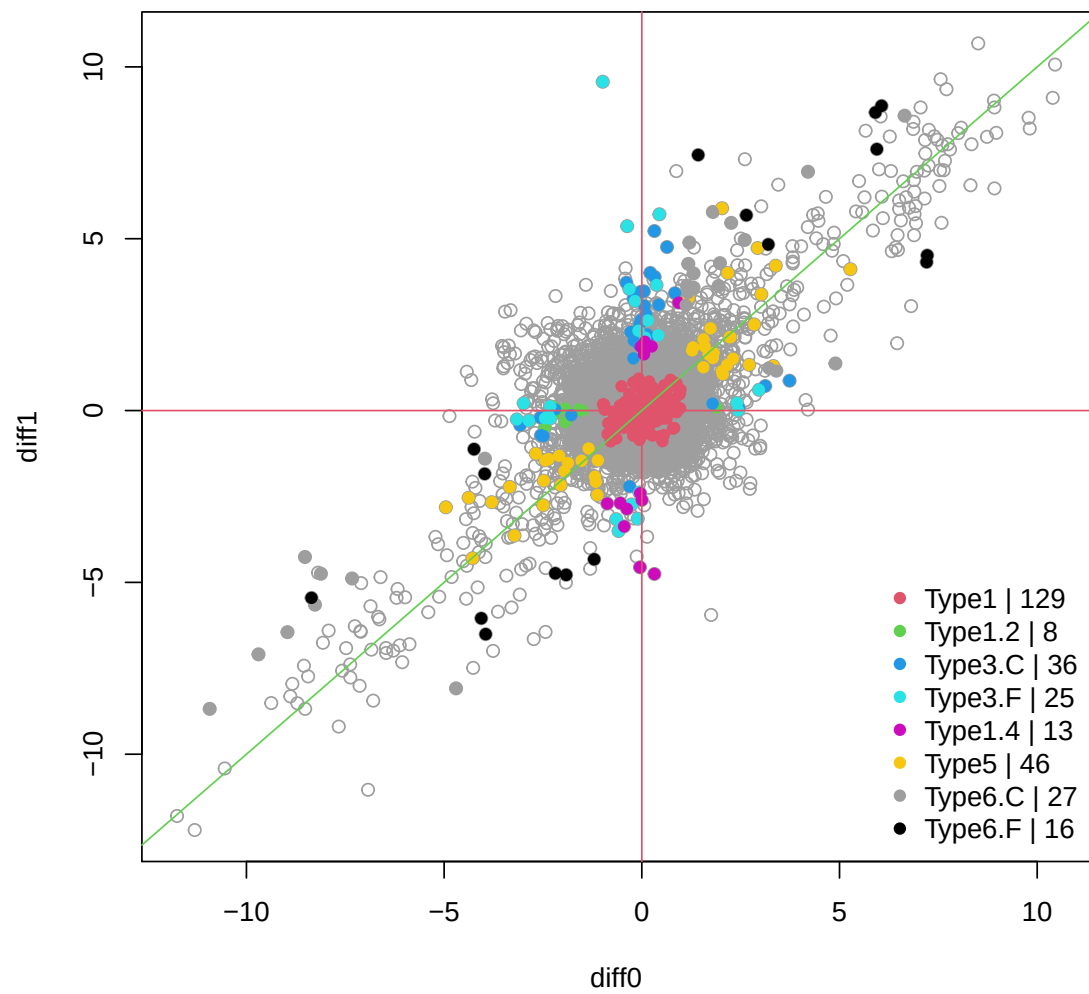
	Type1	Type1.2	Type3.C	Type3.F	Type1.4	Type5
Vitvi15g01736	FALSE	FALSE	FALSE	FALSE	FALSE	FALSE
Vitvi07g02832	FALSE	FALSE	FALSE	FALSE	FALSE	FALSE
Vitvi07g02830	FALSE	FALSE	FALSE	FALSE	FALSE	FALSE
Vitvi07g02812	FALSE	FALSE	FALSE	FALSE	FALSE	FALSE
Vitvi07g02811	FALSE	FALSE	FALSE	FALSE	FALSE	FALSE
Vitvi09g02033	FALSE	FALSE	FALSE	FALSE	FALSE	FALSE

	Type6.C	Type6.F
Vitvi15g01736	FALSE	FALSE
Vitvi07g02832	FALSE	FALSE
Vitvi07g02830	FALSE	FALSE
Vitvi07g02812	FALSE	FALSE
Vitvi07g02811	FALSE	FALSE
Vitvi09g02033	FALSE	FALSE

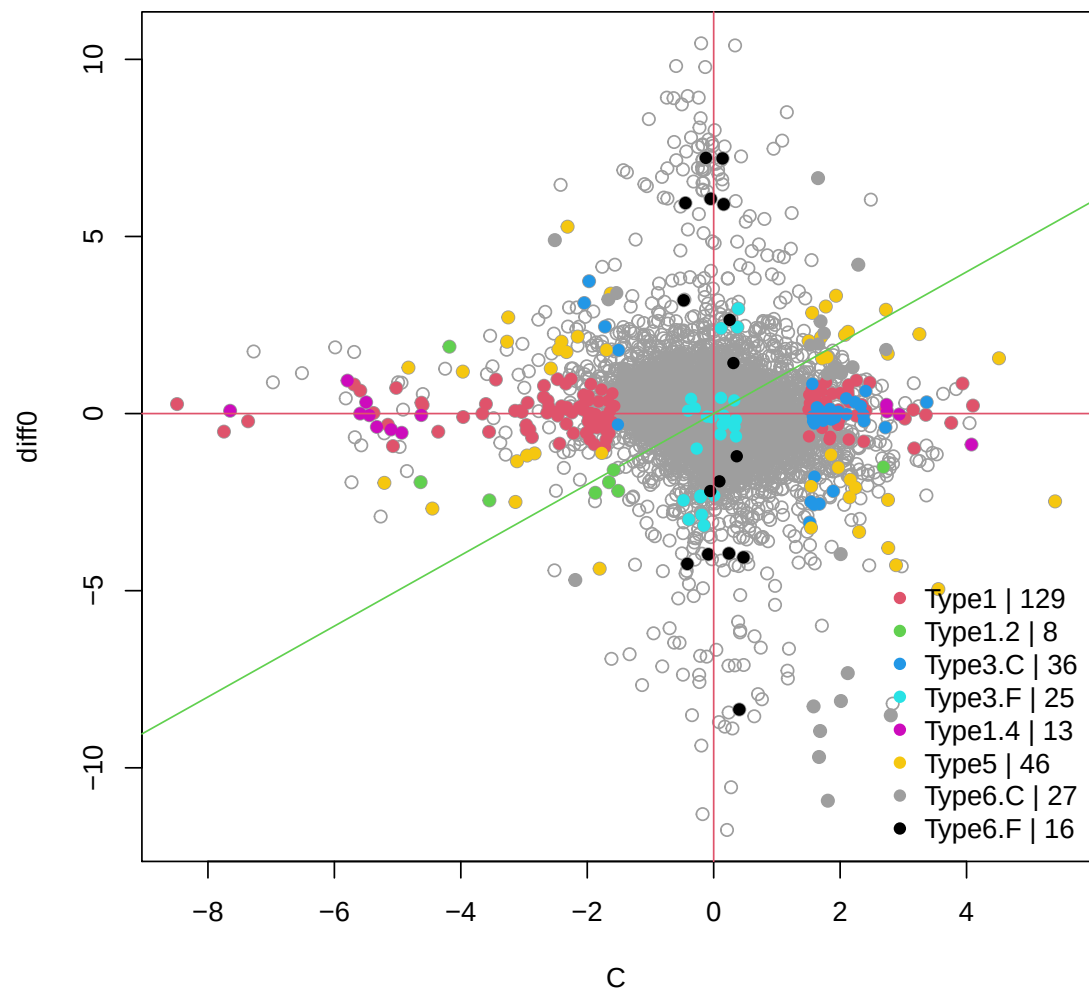
```
> plot.types()
```



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



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



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

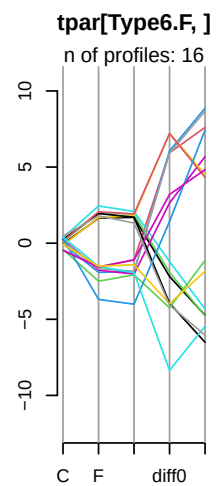
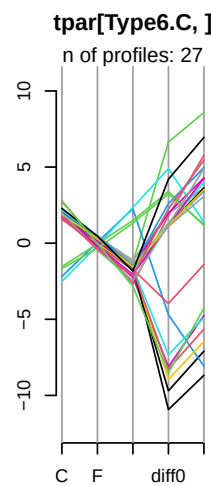
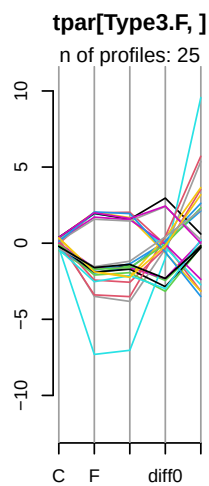
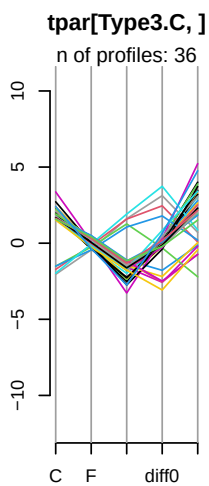
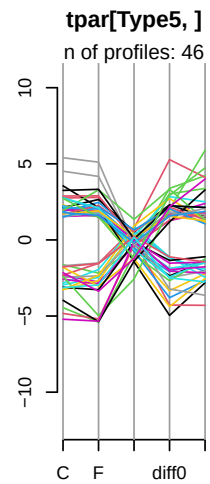
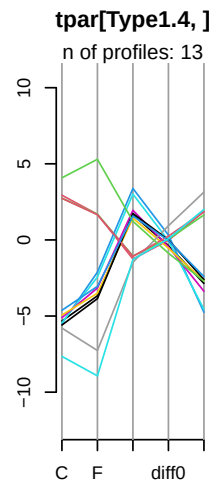
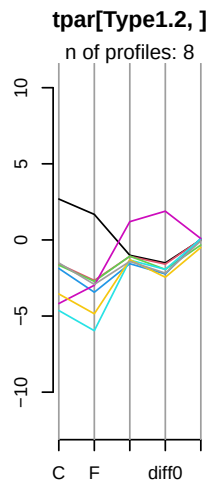
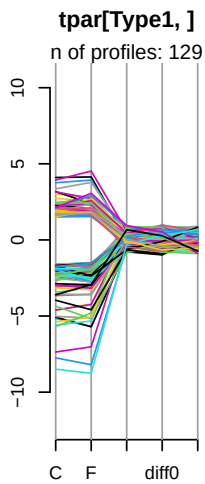


```

+ x$col <- 1:nrow(x)
+ apply(x,1,function(y) lines(1:m,y[-(m+1)],col=y[m+1]))
+ invisible(nrow(x))
+ }
> if(interactive()) my.parallelplot(coefs[Type1,])

> par(mfrow=c(2,4))
> tpar <- data.frame(C,F,F-C,diff0,diff1)
> ylim <- range(tpar)
> my.parallelplot(tpar[Type1,], ylim=ylim)
> my.parallelplot(tpar[Type1.2,], ylim=ylim)
> my.parallelplot(tpar[Type1.4,], ylim=ylim)
> my.parallelplot(tpar[Type5,], ylim=ylim)
> my.parallelplot(tpar[Type3.C,], ylim=ylim)
> my.parallelplot(tpar[Type3.F,], ylim=ylim)
> my.parallelplot(tpar[Type6.C,], ylim=ylim)
> my.parallelplot(tpar[Type6.F,], ylim=ylim)

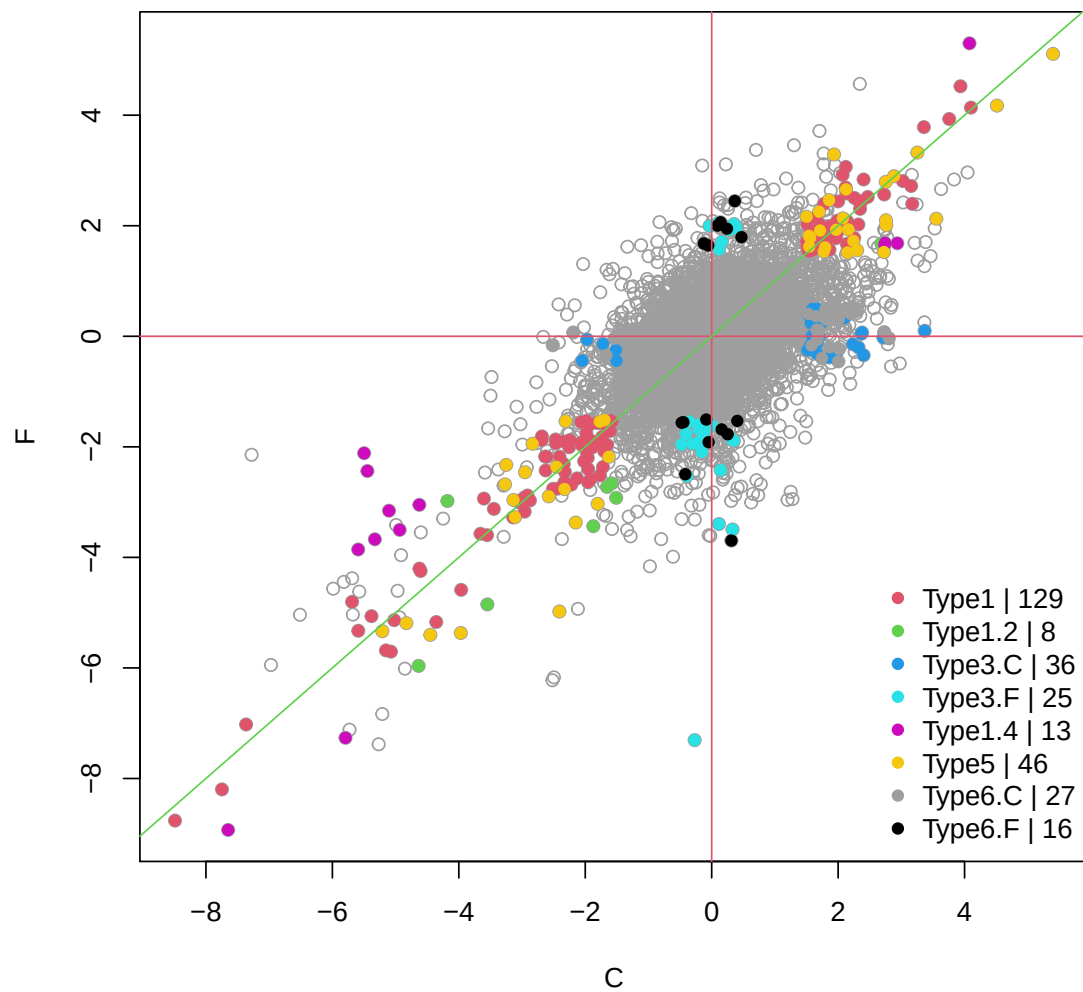
```



```

> plot.types()

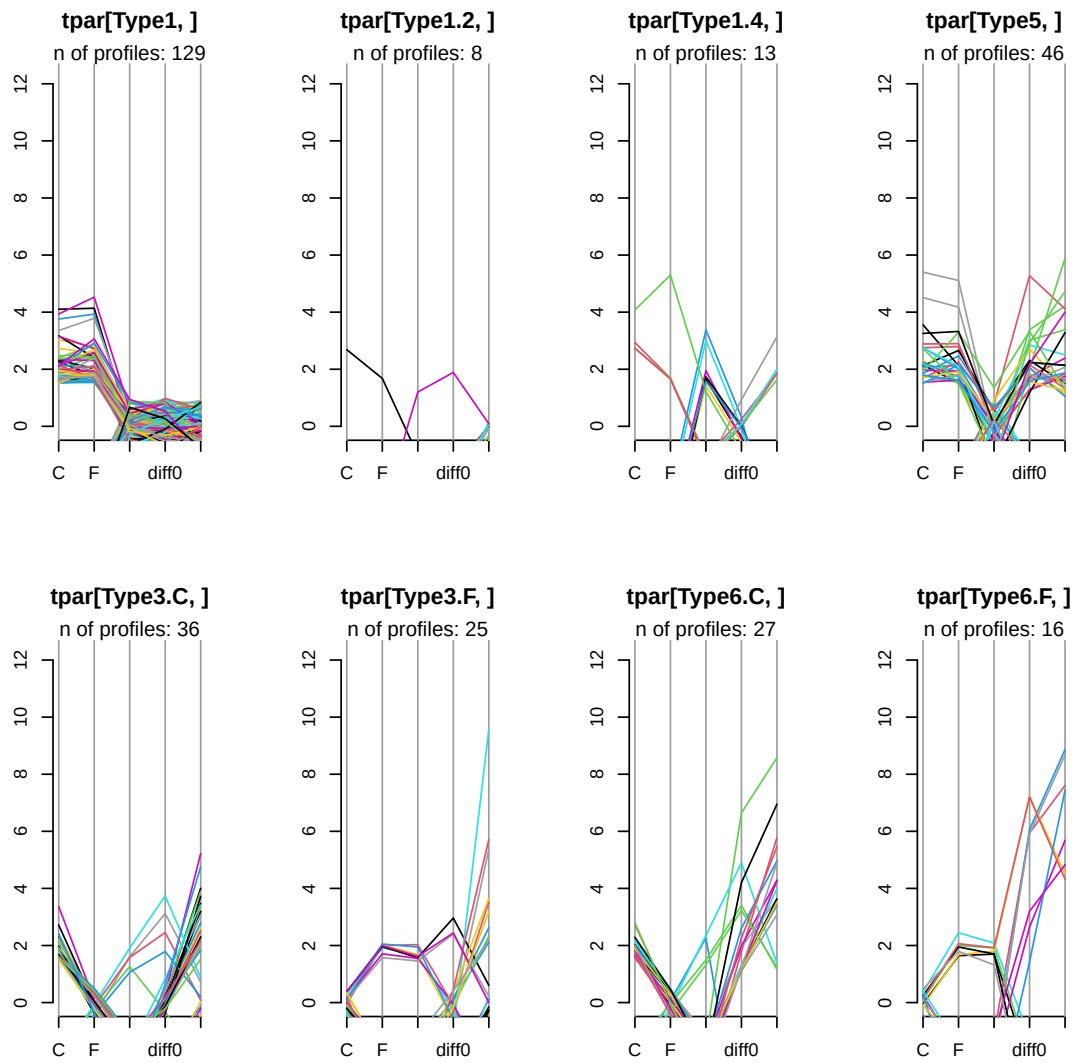
```



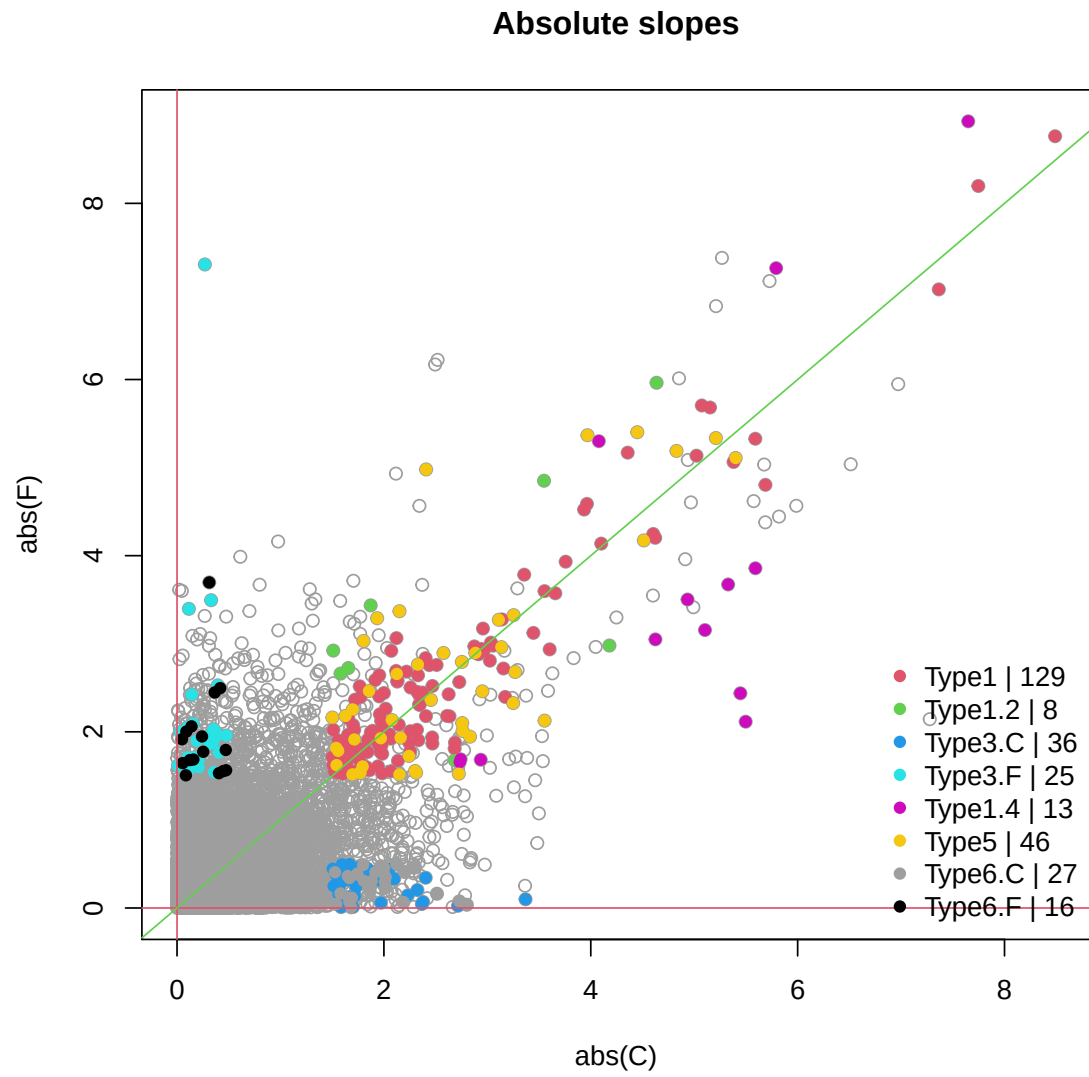
```

> par(mfrow=c(2,4))
> tpar <- data.frame(C,F,F-C,diff0,diff1)
> abstpar <- abs(tpar)
> ylim <- range(abstpar)
> my.parallelplot(tpar[Type1,], ylim=ylim)
> my.parallelplot(tpar[Type1.2,], ylim=ylim)
> my.parallelplot(tpar[Type1.4,], ylim=ylim)
> my.parallelplot(tpar[Type5,], ylim=ylim)
> my.parallelplot(tpar[Type3.C,], ylim=ylim)
> my.parallelplot(tpar[Type3.F,], ylim=ylim)
> my.parallelplot(tpar[Type6.C,], ylim=ylim)
> my.parallelplot(tpar[Type6.F,], ylim=ylim)

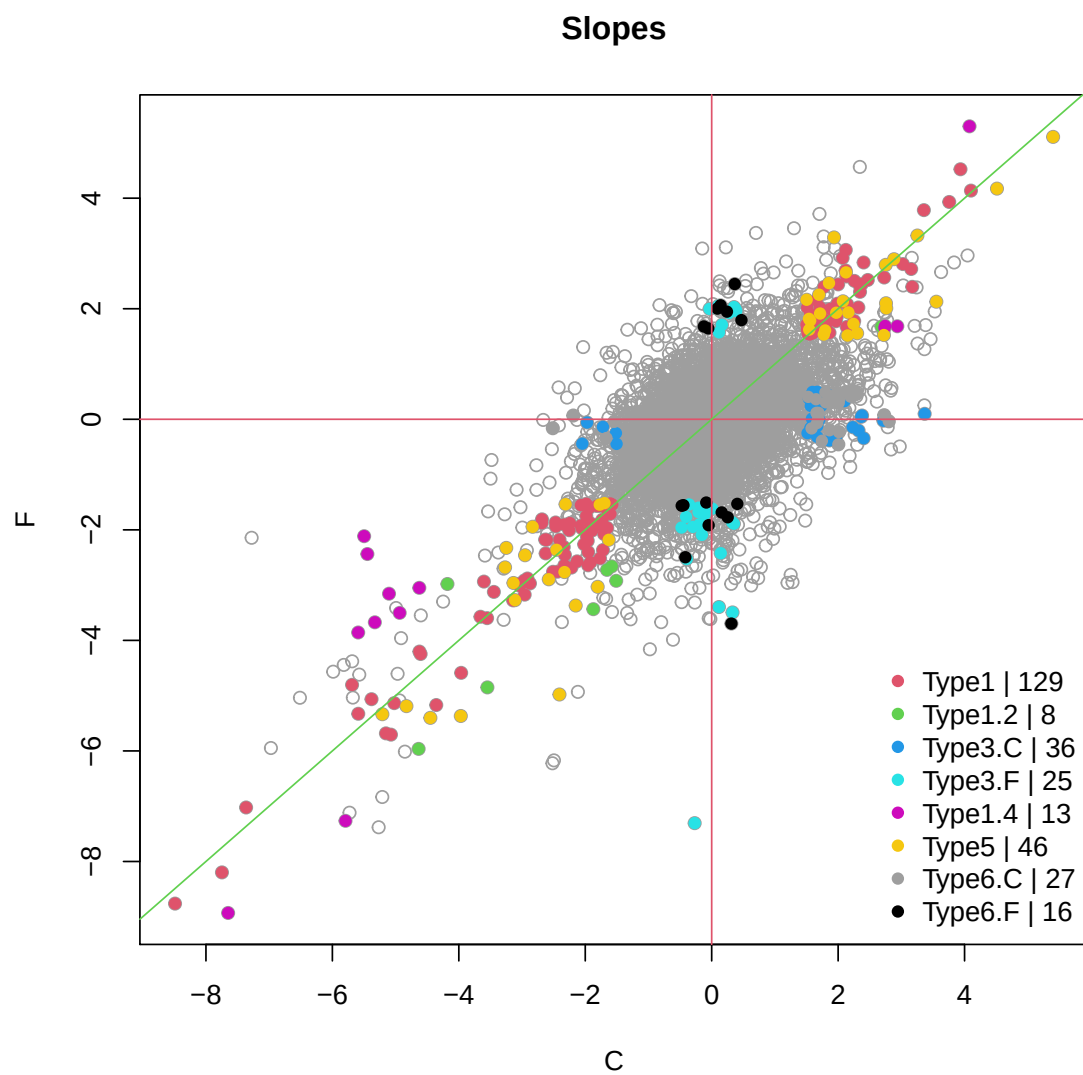
```



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

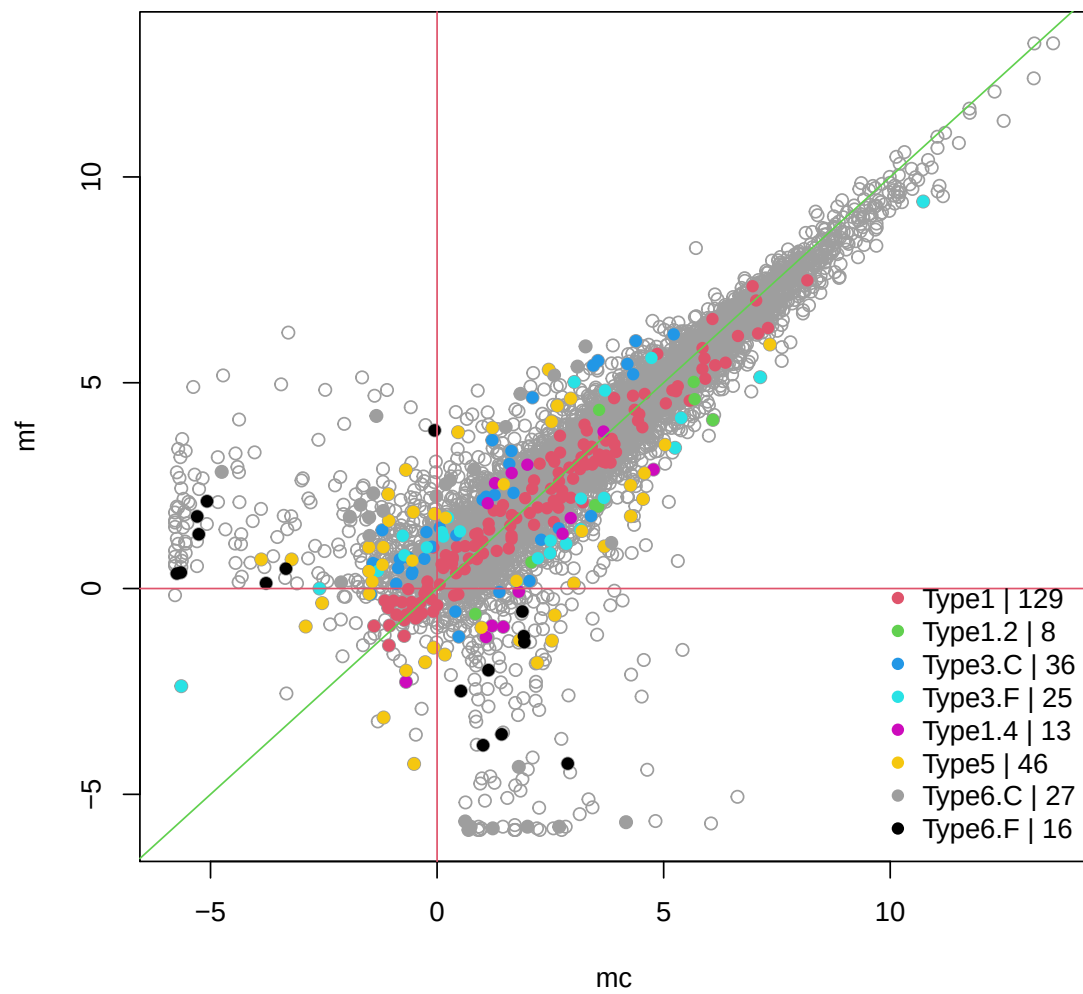


```
> plot.types(C,F,title="Slopes")
```



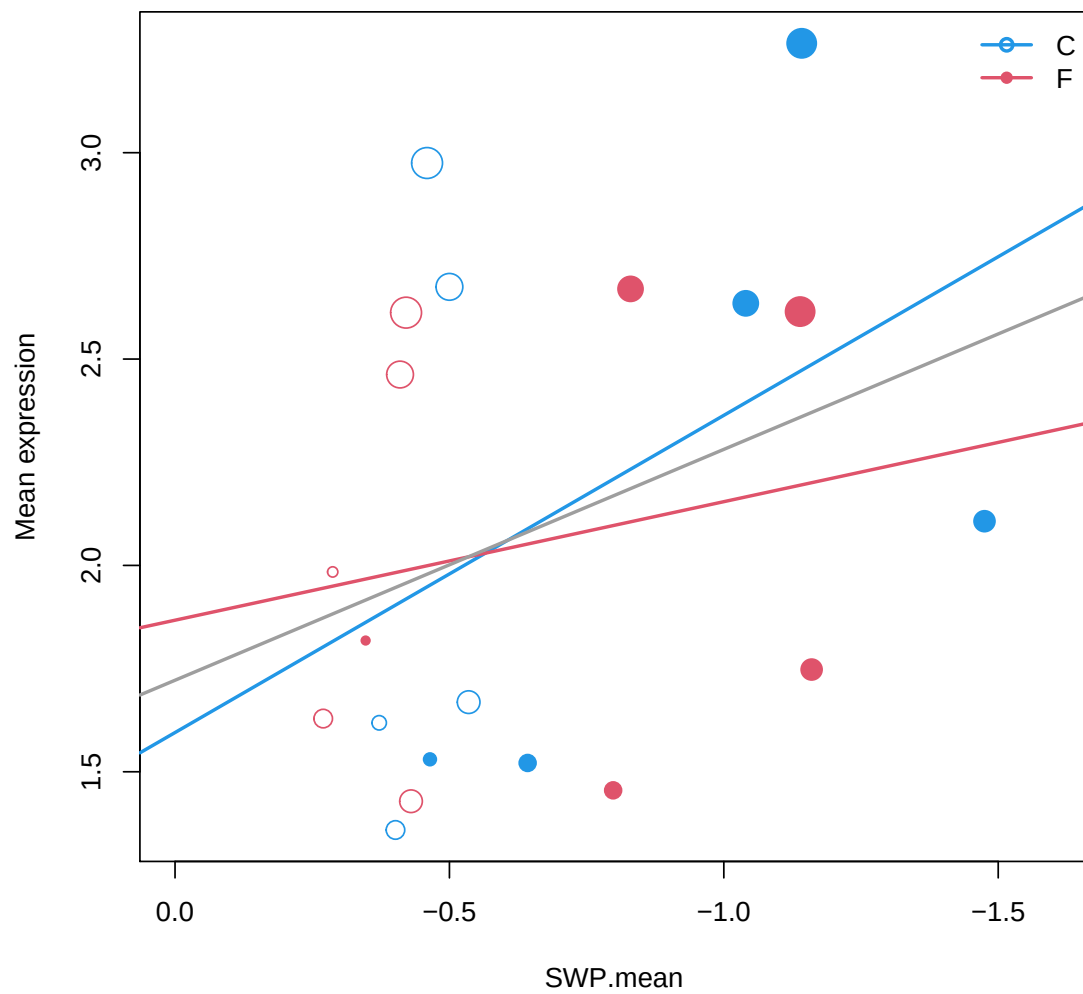
```
> plot.types(mc,mf,title="Mean expression")
```

Mean expression



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

Vitvi01g01391



```
> apply(types, 2, sum)
```

```

Type1 Type1.2 Type3.C Type3.F Type1.4 Type5 Type6.C
129      8      36      25      13      46      27
Type6.F
16

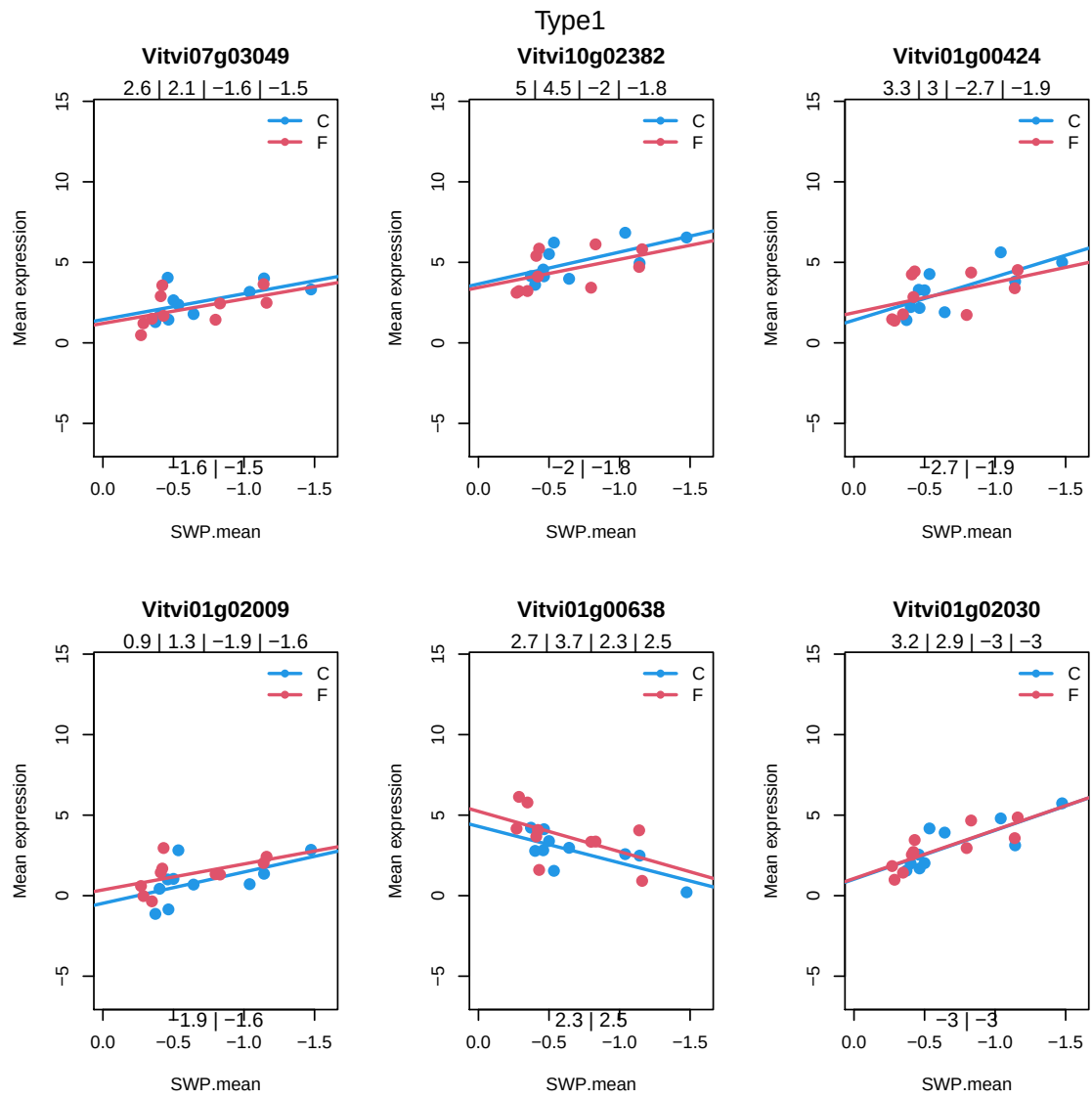
```

```

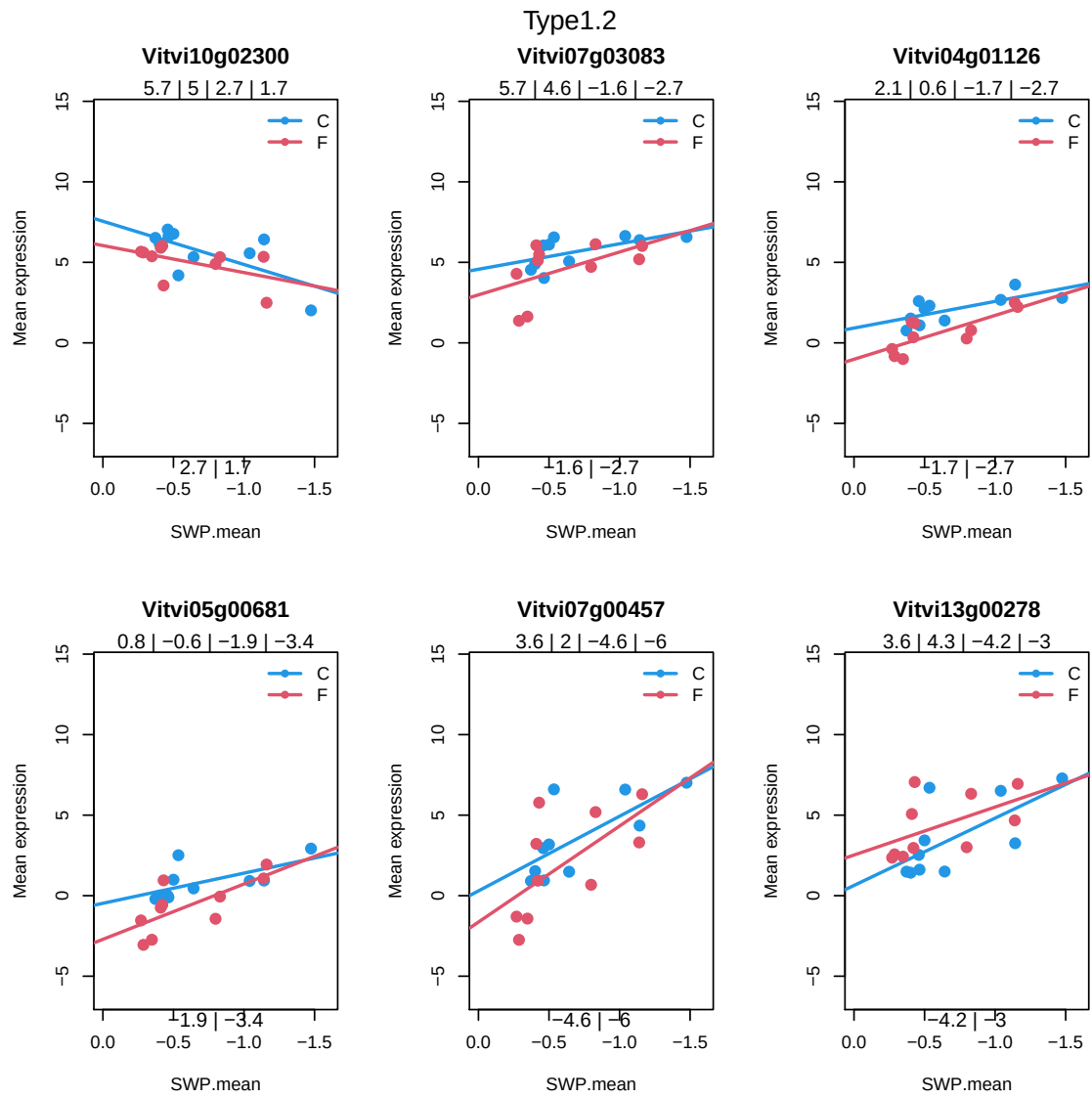
> for(i in 1:ncol(types)) {
+ plot.type(types[,i])
+ mtext(names(types[i]), outer=TRUE, line=-1)
+ }

```

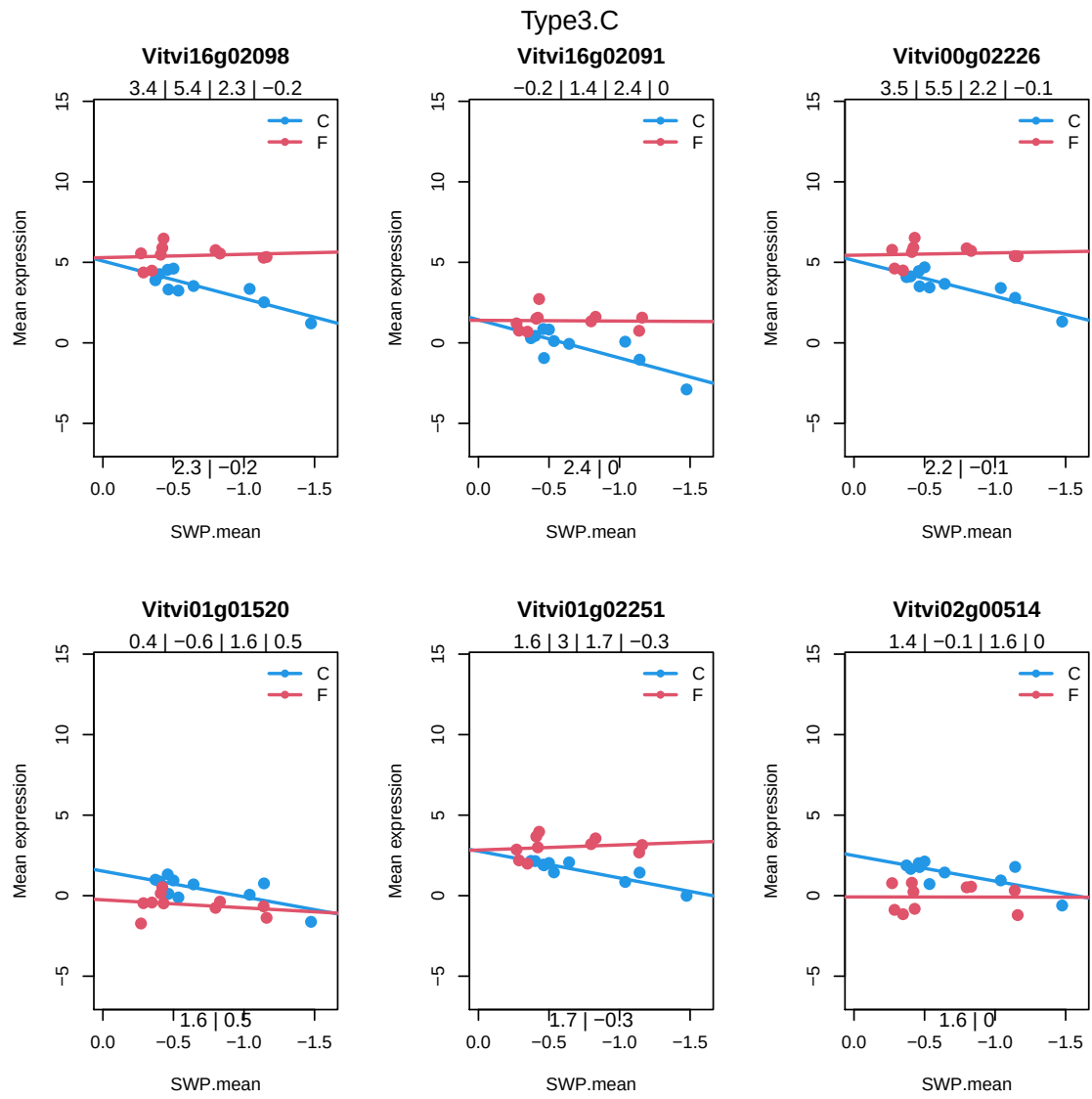
```
[1] 129
```



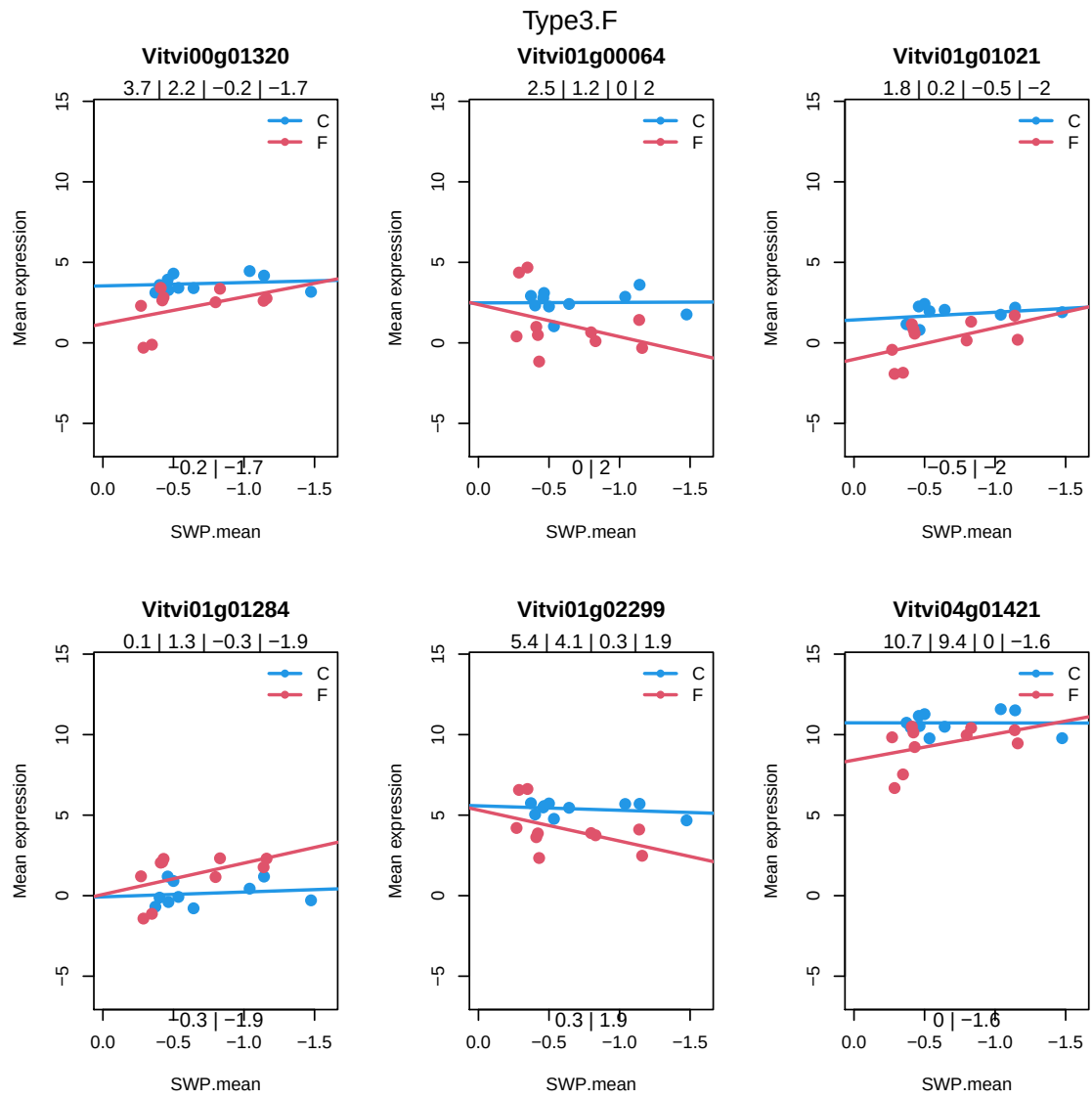
[1] 8



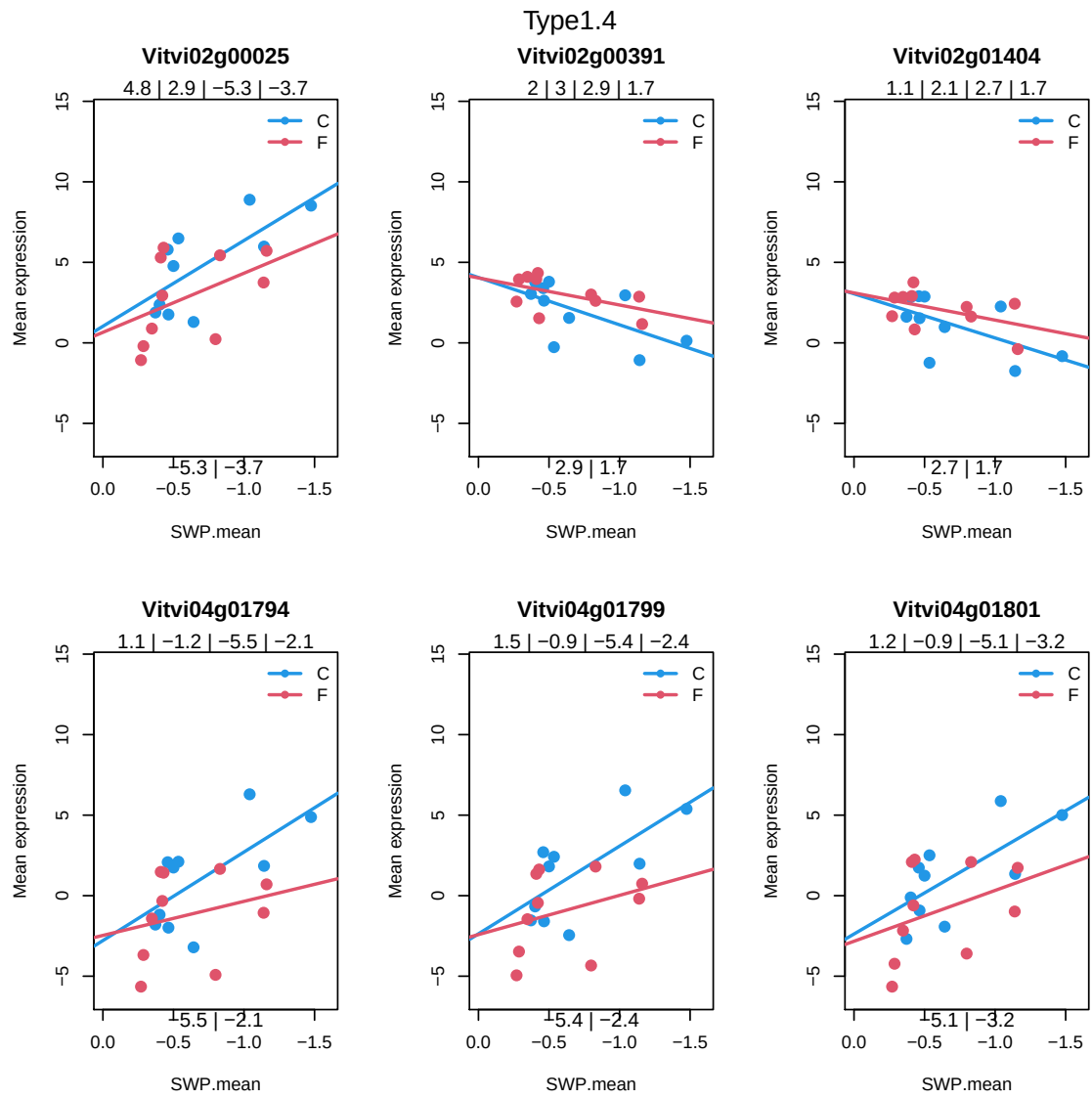
[1] 36



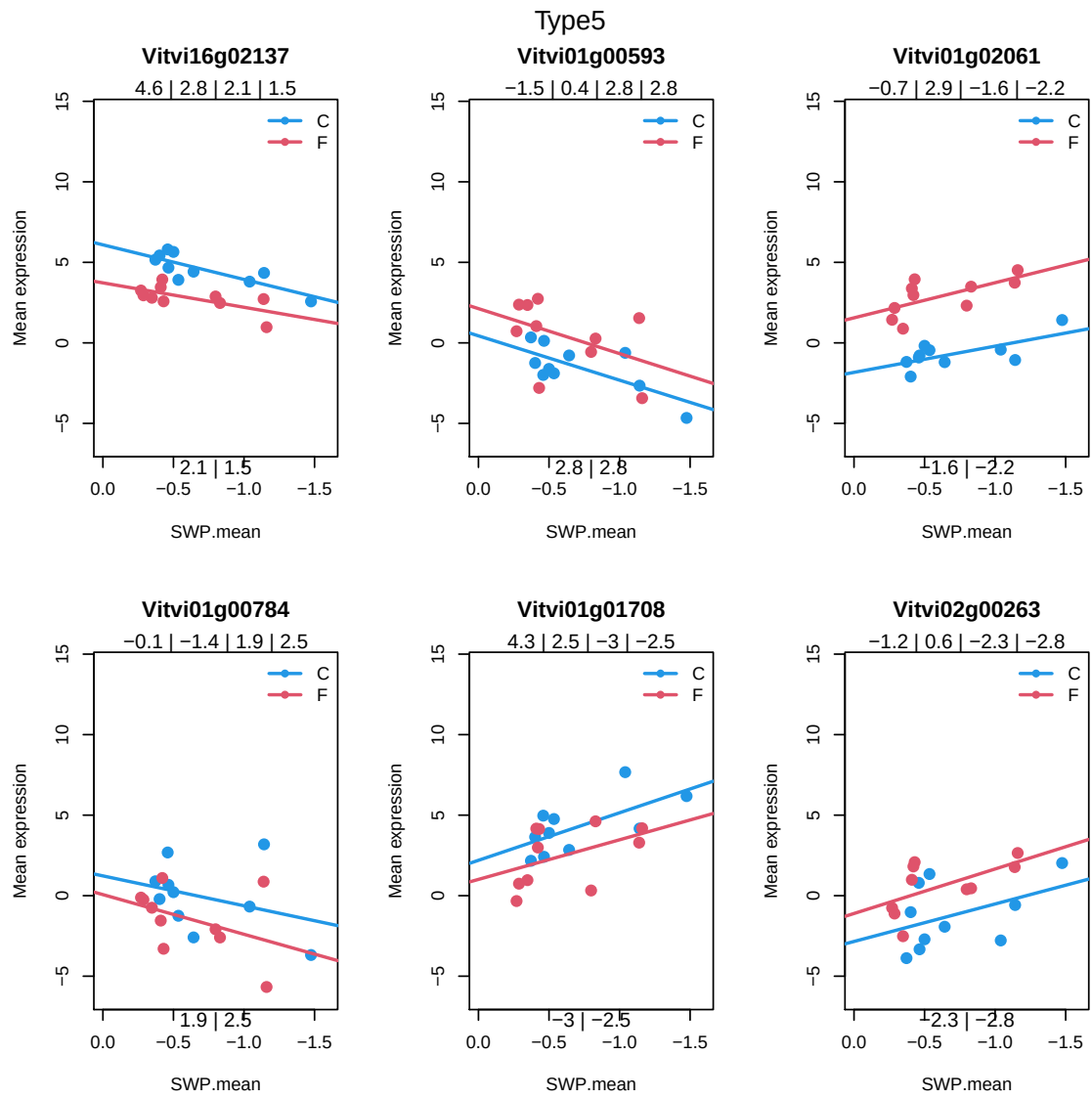
[1] 25



[1] 13

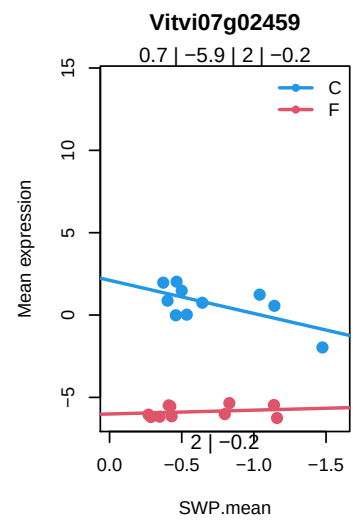
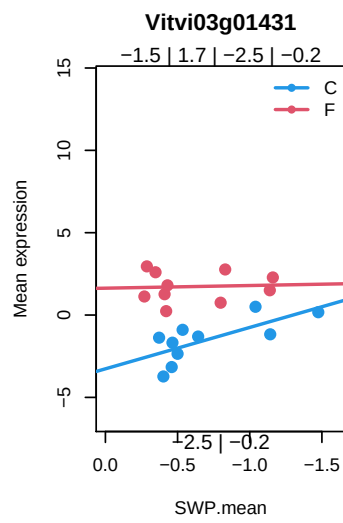
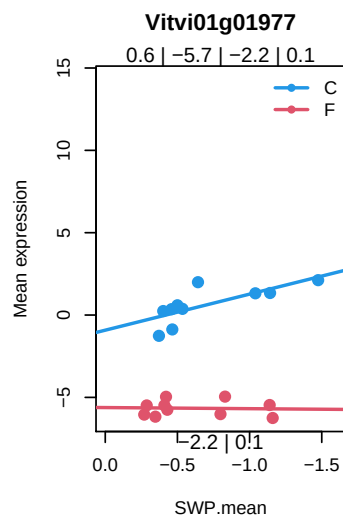
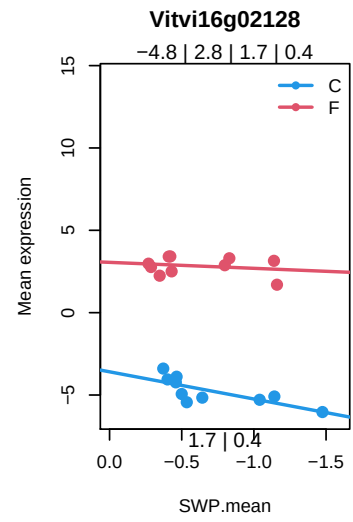
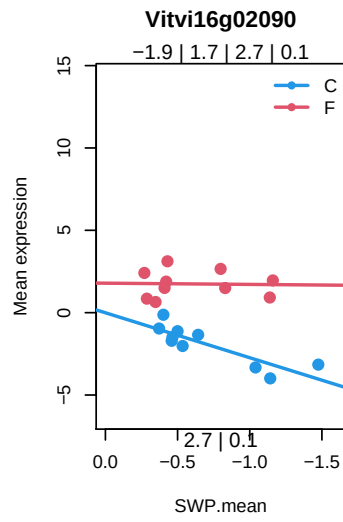
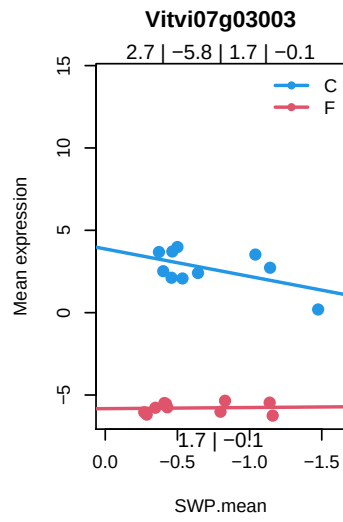


[1] 46

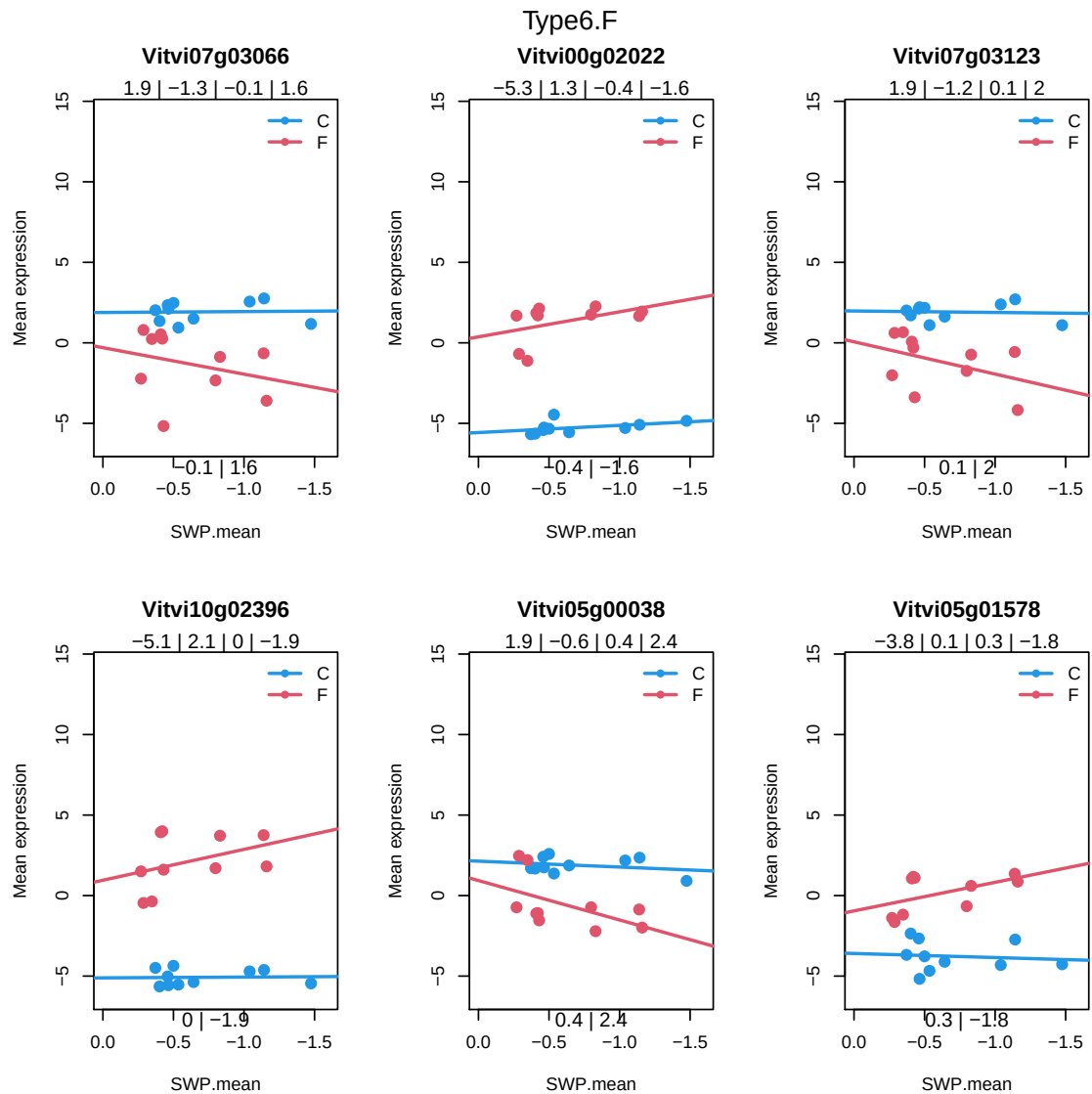


[1] 27

Type6.C



[1] 16



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

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

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

6.3 Export output files

Export fit in a form:

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

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

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

Export top table

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

Removing intercept from test coefficients

```
> #
> types <- types.new
> tt$Type <- ""
> types <- types[rownames(tt), ]
> all(rownames(tt) == rownames(types))
```

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

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

Label:

File :

../output/50_Expression-water-stress-0.05-1.5-0.5-1-1/TopTable.txt

```
> types <- types.new

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


7 Types and significance of contrasts

Starting point is fit2

Model with water potential by variety.

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

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

```
> tail(design2)
```

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

Linear model

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

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

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

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

```
> tail(design3)
```

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

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

	varietyC	varietyF
Vitvi01g01391	2.135505	2.042236

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

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

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

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

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

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

	varietyC	varietyF
Vitvi01g01391	2.135505	2.042236

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

An object of class "MArrayLM"

```
$coefficients
```

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

```
$rank
[1] 4

$assign
[1] 0 1 2 3

$qqr
$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

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

$sraux
[1] 1.223607 1.130819 1.182562 1.066939

$pivot
[1] 1 2 3 4

$tol
[1] 1e-07

$rank
[1] 4

$df.residual
[1] 16

$sigma
Vitvi01g01391
      0.5999568

$cov.coefficients

```

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

\$stddev.unscaled

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

\$pivot

[1] 1 2 3 4

\$Amean

Vitvi01g01391
2.08887

\$method

[1] "ls"

\$design

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

\$df.prior

[1] 5.442291

\$s2.prior

[1] 0.240232

\$var.prior

[1] 66.60227703 10.07260620 66.60227703 0.04162642

\$proportion

[1] 0.01

\$s2.post

Vitvi01g01391
0.3295629

\$t

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

\$df.total

[1] 21.44229

\$p.value

```

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

```

```
$lods
```

```

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

```

```
$F
```

```
[1] 1143.211
```

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

```
[1] 1.193144e-24
```

```

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

```

```

              logFC AveExpr          t    P.Value
Vitvi01g01391 -0.7685916 2.08887 -1.521769 0.1426785
              adj.P.Val          B
Vitvi01g01391 0.6681823 -4.850464

```

With difference of means

```

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

```

```

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

```

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

```

              varietyC varietyF
Vitvi01g01391 0.3162278 0.3162278

```

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

```

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

```

```
> #
```

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

```

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

```

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

```

              varietyC varietyF
Vitvi01g01391 2.135505 2.042236

```

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

```
> head(fit4)
```

An object of class "MArrayLM"

\$coefficients

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

\$rank

[1] 4

\$assign

[1] 0 1 2 3

\$qr

\$qr

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

15 more rows ...

\$sraux

[1] 1.223607 1.130819 1.182562 1.066939

\$pivot

[1] 1 2 3 4

\$tol

[1] 1e-07

\$rank

[1] 4

\$df.residual

[1] 16 16 16 16 16 16

\$sigma

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

\$cov.coefficients

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


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

```
$stdev.unscaled
```

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

```
$pivot
```

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

```
$Amean
```

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

```
$method
```

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

```
$design
```

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

```
$df.prior
```

```
[1] 5.442291
```

```
$s2.prior
```

```
[1] 0.240232
```

```
$var.prior
```

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

```
$proportion
```

```
[1] 0.01
```

```
$s2.post
```

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

```
$t
```

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

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

```
$df.total
```

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

```
$p.value
```

```

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

```

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

```
$lods
```

```

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

```
$F
```

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

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

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

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

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

```
$coefficients
```

```

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

```
$rank
```

```
[1] 4
```

```
$assign
```

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

```
$qr
```

```

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

$graux
[1] 1.223607 1.130819 1.182562 1.066939

$pivot
[1] 1 2 3 4

$tol
[1] 1e-07

$rank
[1] 4

$df.residual
[1] 16

$sigma
Vitvi01g01391
  0.5999568

$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))

```

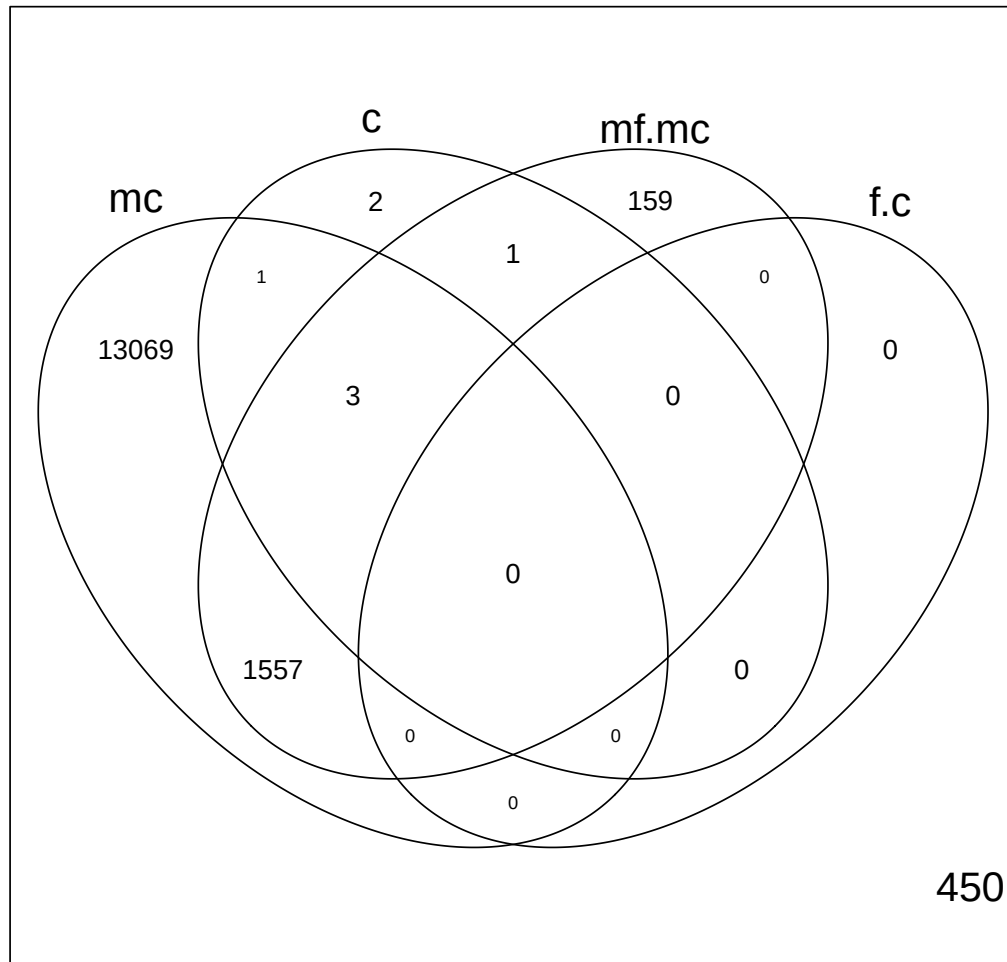
```

[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

```

7.1 Export fit statistics, types and descriptions

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



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

```

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

[1] TRUE

> #ind <- sapply(rownames(tt), FUN=function(x) match(x, rownames(types)))
> for(i in 1:ncol(types)) {
+     df4$Type[types[,i]] <- paste(df4$Type[types[,i]], colnames(types)[i],
+     print(table(df4$Type))
+     }

```

```

|Type1
15113      129

      |Type1 |Type1.2
15105      129      8

      |Type1 |Type1.2 |Type3.C
15069      129      8      36

      |Type1 |Type1.2 |Type3.C |Type3.F
15044      129      8      36      25

      |Type1 |Type1.2 |Type1.4 |Type3.C |Type3.F
15031      129      8      13      36      25

      |Type1 |Type1.2 |Type1.4 |Type3.C |Type3.F
14985      129      8      13      36      25
|Type5
46

      |Type1 |Type1.2 |Type1.4 |Type3.C |Type3.F
14958      129      8      13      36      25
|Type5 |Type6.C
46      27

      |Type1 |Type1.2 |Type1.4 |Type3.C |Type3.F

```

```

      14942      129      8      13      36      25
|Type5 |Type6.C |Type6.F
      46      27      16

```

```

> df4$Type <- gsub("^\\|", "", df4$Type)
> types <- types.new
> #
> # Mark interesting genes:
> stat4 <- data.frame(df4, fdata[ind, 2:5] )
> pc <- stat4[, "P.value.c"]
> pfc <- stat4[, "P.value.f.c"]
> inc <- c("", "*")[(pc < alpha)+1]
> incf <- c("", "+")[((pc > alpha)&(pfc < alpha))+1]
> df4$interestingC <- inc
> df4$interestingFC <- incf
> #
> stat4 <- data.frame(df4, fdata[ind, 2:5] )
> table(stat4$interestingC, stat4$interestingFC)

```

```

      +
      13700      48
* 1494      0

```

```

> print(table(stat4$type, stat4$Type), zero.print=".")

```

Error in h(simpleError(msg, call)): error in evaluating the argument 'x' in se

Some genes are classified into two types:

```

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

```

```

      [,1]
      14942
Type1      129
Type1.2      8
Type1.4      13
Type3.C      36
Type3.F      25
Type5      46
Type6.C      27
Type6.F      16

```

```

> summary(types)

```

Type1	Type1.2	Type3.C
Mode :logical	Mode :logical	Mode :logical
FALSE:15113	FALSE:15234	FALSE:15206
TRUE :129	TRUE :8	TRUE :36
Type3.F	Type1.4	Type5
Mode :logical	Mode :logical	Mode :logical
FALSE:15217	FALSE:15229	FALSE:15196
TRUE :25	TRUE :13	TRUE :46
Type6.C	Type6.F	
Mode :logical	Mode :logical	
FALSE:15215	FALSE:15226	
TRUE :27	TRUE :16	

Order stat4 and types by decreasing coefficient for C

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

[1] TRUE
```

Genes from interesting bins are marked by
'*' (for significant slope C) and
'+' (for significant difference in slopes)

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

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

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

File :

[../..output/50_Expression-water-stress-0.05-1.5-0.5-1-1/lm-fit-means-swpXvariety-
statistics.txt](#)

Comparison with effects.
Large abs slope C

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

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

Small difference of slopes

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

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

Large difference of mean expressions

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

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

8 Detailed plots, stats and info of Genes by types

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

Figures caption:

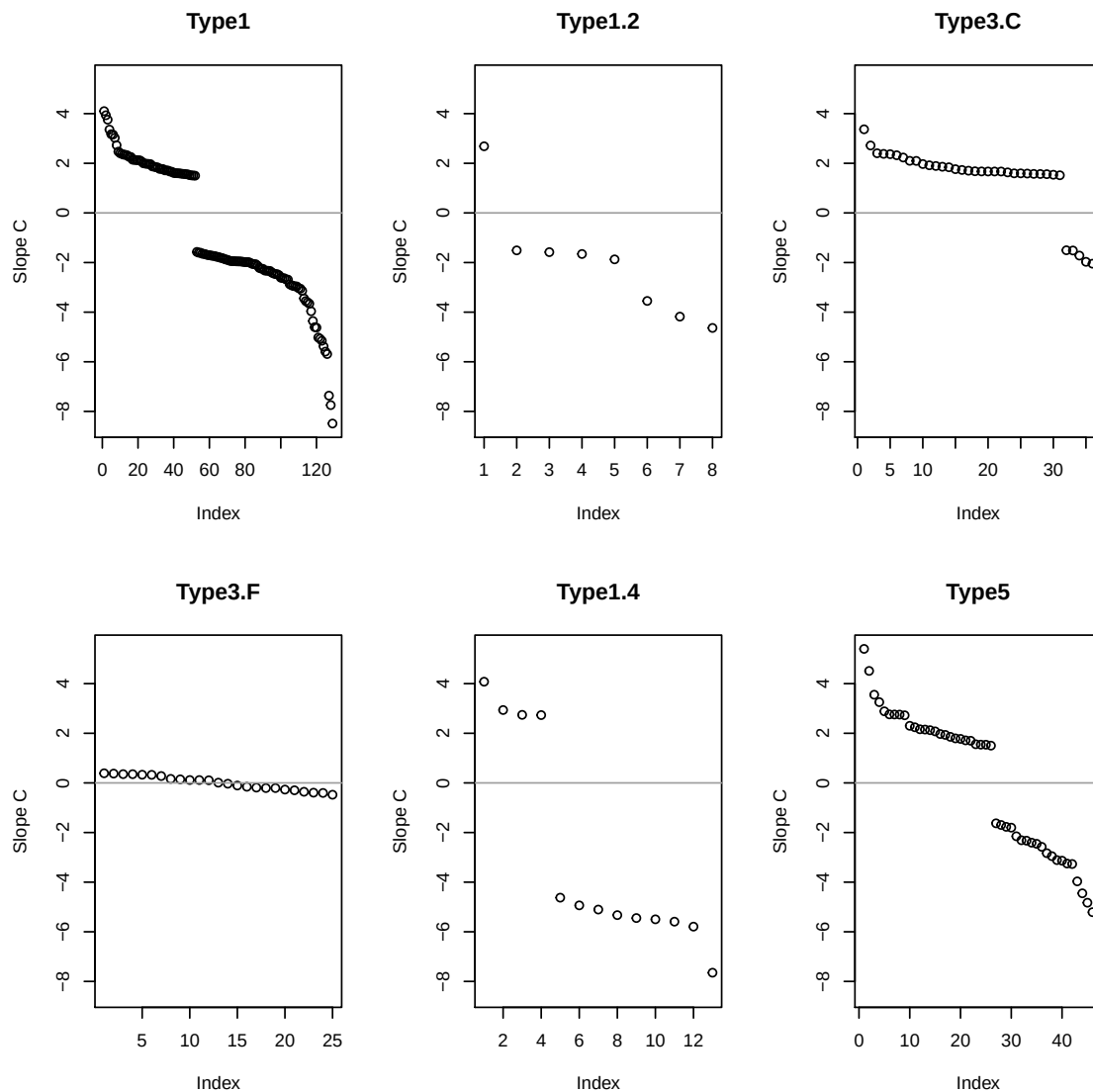
Mean expression (E) and mean water potential (WP). C (blue) and all F (red). Gray line (if present) is regression of all data, regardless of treatment and variety.

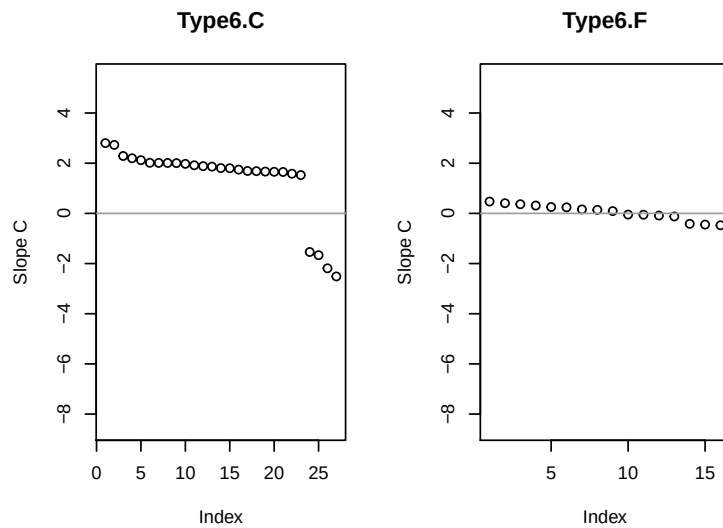
Order stat4 and types by decreasing coefficient for C

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

```
[1] TRUE
```

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





```
> # Report for selected genes
> out <- ""
> (cname <- "")
[1] ""
> colnames(stat4)
[1] "A" "Coef.mc"
[3] "Coef.c" "Coef.mf.mc"
[5] "Coef.f.c" "Kcoef.f"
[7] "t.mc" "t.c"
[9] "t.mf.mc" "t.f.c"
[11] "P.value.mc" "P.value.c"
[13] "P.value.mf.mc" "P.value.f.c"
[15] "P.value.adj.mc" "P.value.adj.c"
[17] "P.value.adj.mf.mc" "P.value.adj.f.c"
[19] "F" "F.p.value"
[21] "Type" "interestingC"
[23] "interestingFC" "geneID"
[25] "BINCODE" "NAME"
[27] "DESCRIPTION"
```

```

> i <- 1
> (typevar <- substr(names(types)[1],1,4))
[1] "Type"
> tipi <- sort(unique(stat4[,typevar]))[-1]
> # reorder type names
> types <- types[,sort(colnames(types))]
> for(i in 1:ncol(types)){
+ type.name <- colnames(types)[i]
+ out <- paste(out, "
+ \\clearpage
+ \\subsection{",type.name,"}\\")
+ varnames <- rownames(stat4)[types[,i]]
+ varname <- varnames[2]
+ for(varname in varnames)
+ out <- paste(out,knit_child(file.path("../doc/", "50aa_one-gene-plots.Rnw"),
+ }

```

8.1 Type1

8.1.1 Vitvi05g00011: * Type1

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

```
Vitvi05g00011
```

```
35.2
```

```
not assigned.unknown
```

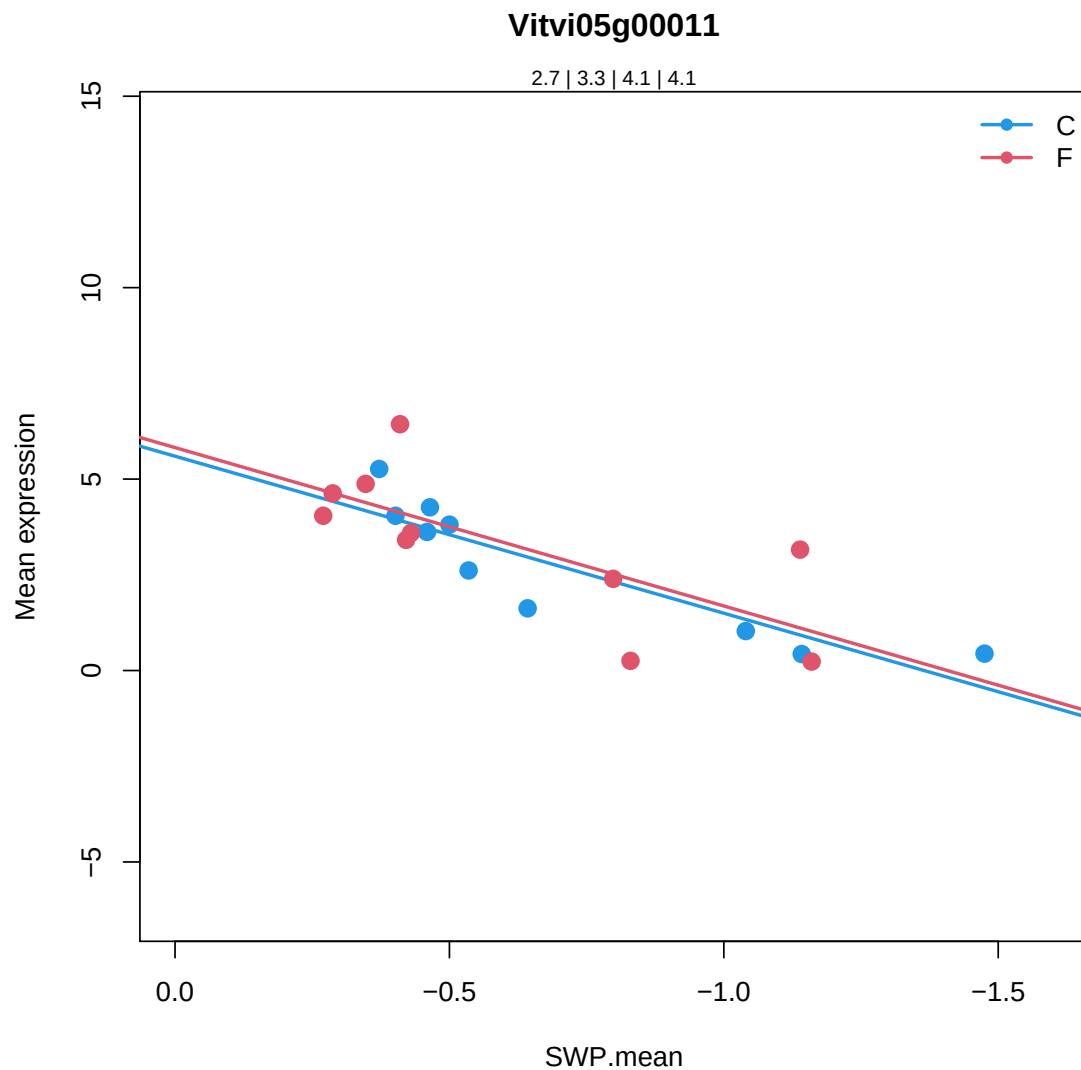
```
Pollen Ole e 1 allergen and extensin family protein |
```

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

```
201606
```

Coefficients for Vitvi05g00011.

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



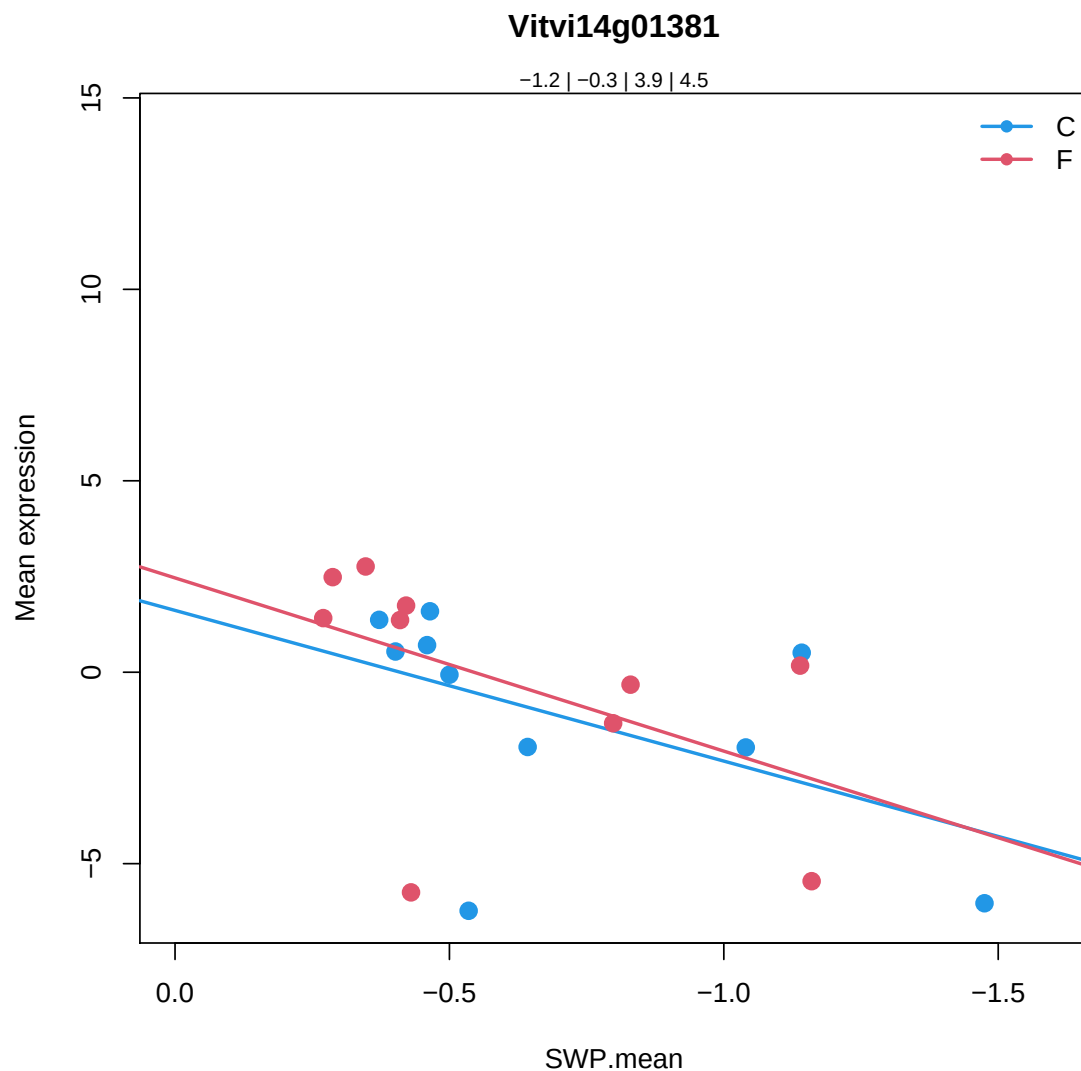
8.1.2 Vitvi14g01381: Type1

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

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

Coefficients for Vitvi14g01381.

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



8.1.3 Vitvi05g01353: * Type1

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

Vitvi05g01353

10.8.1

cell wall.pectinesterases.PME

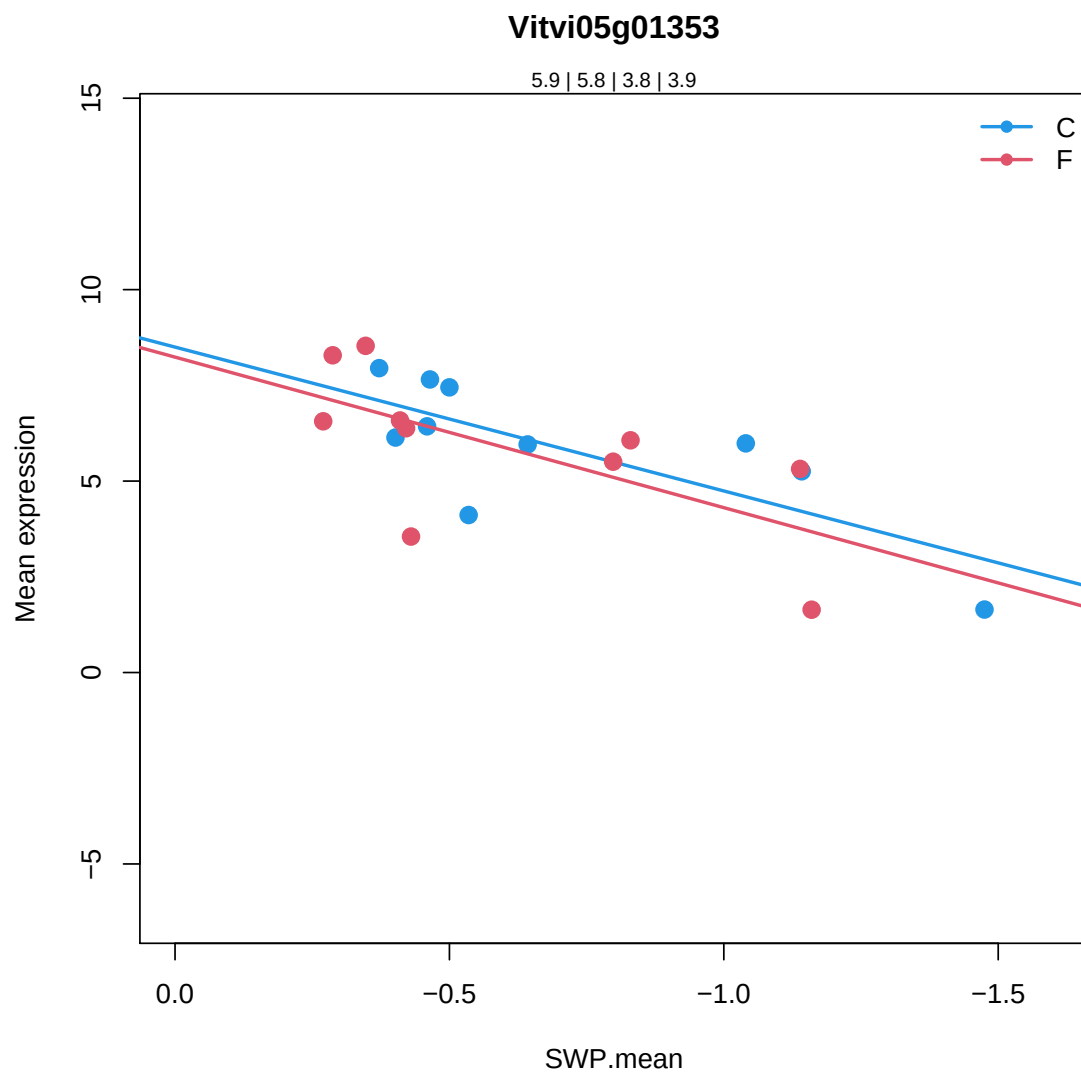
pectin methylesterase 61 |

Chr3:21803015-21805098 REVERSE LENGTH=529 |

201606

Coefficients for Vitvi05g01353.

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



8.1.4 Vitvi10g01886: Type1

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

Vitvi10g01886

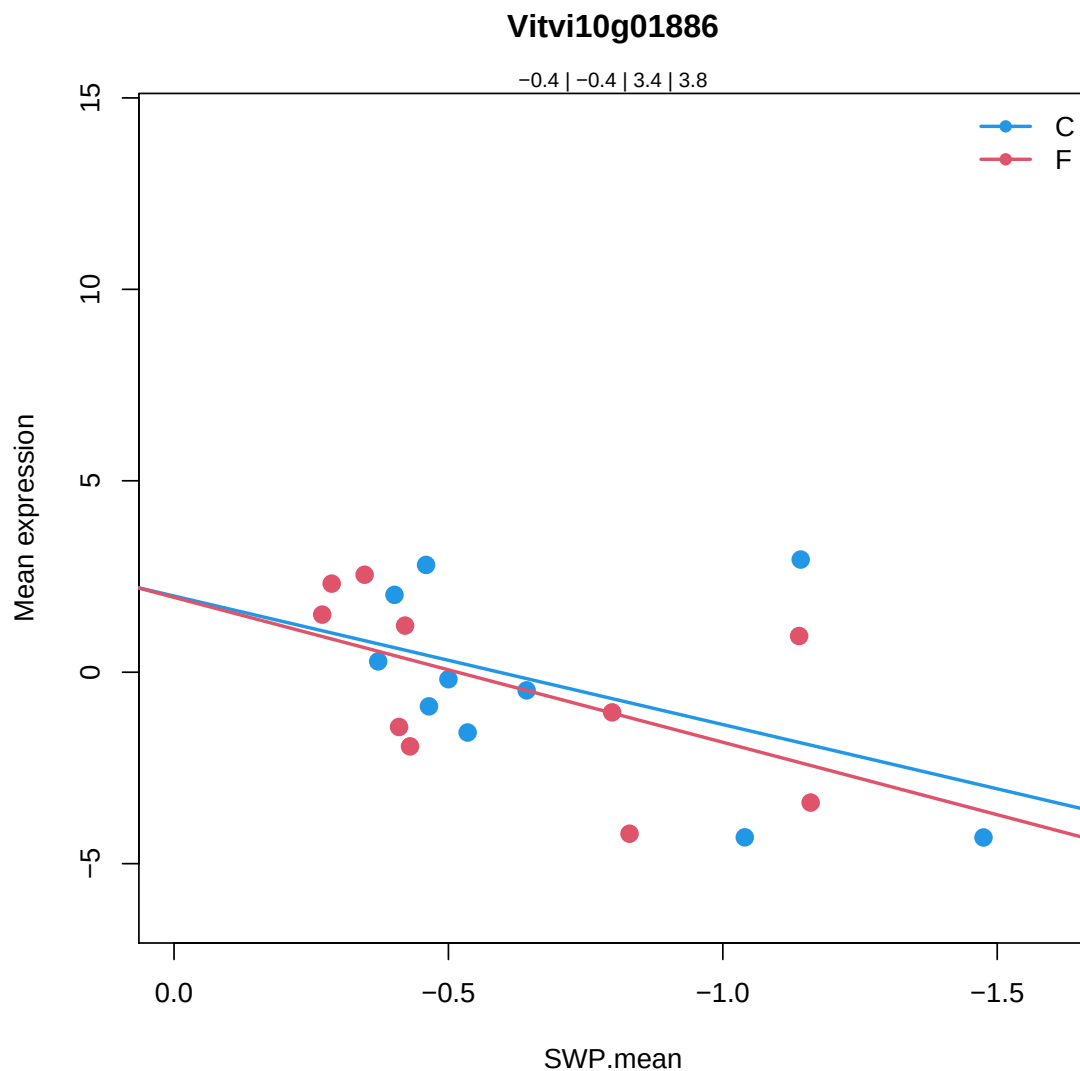
35.2

not assigned.unknown

NA

Coefficients for Vitvi10g01886.

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



8.1.5 Vitvi08g00768: * Type1

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

Vitvi08g00768

35.2

not assigned.unknown

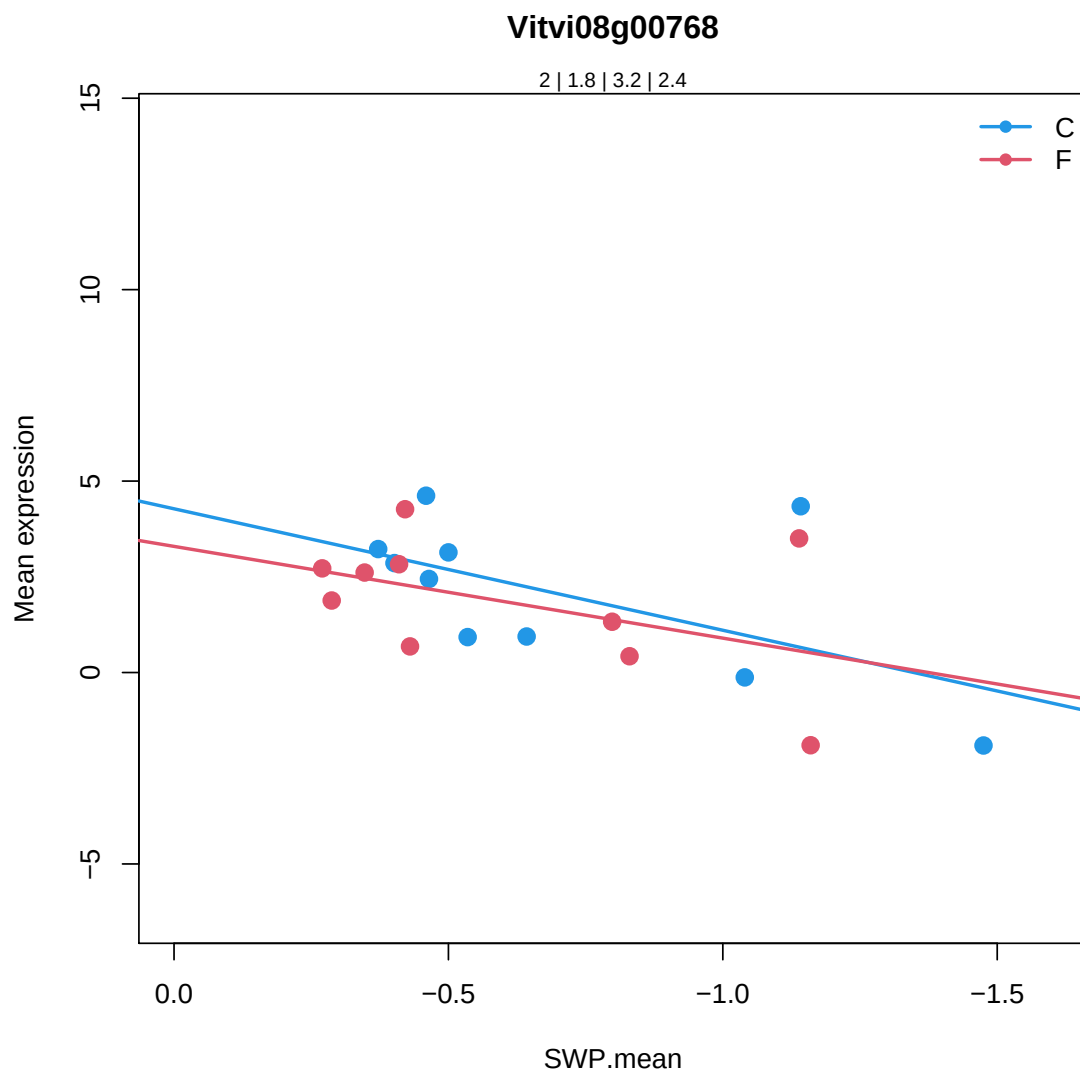
PYR1-like 4 |

Chr2:16050251-16050874 FORWARD LENGTH=207 |

201606

Coefficients for Vitvi08g00768.

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



8.1.6 Vitvi10g00436: * Type1

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

Vitvi10g00436

3.8.2

minor CHO metabolism.galactose.alpha-galactosidases

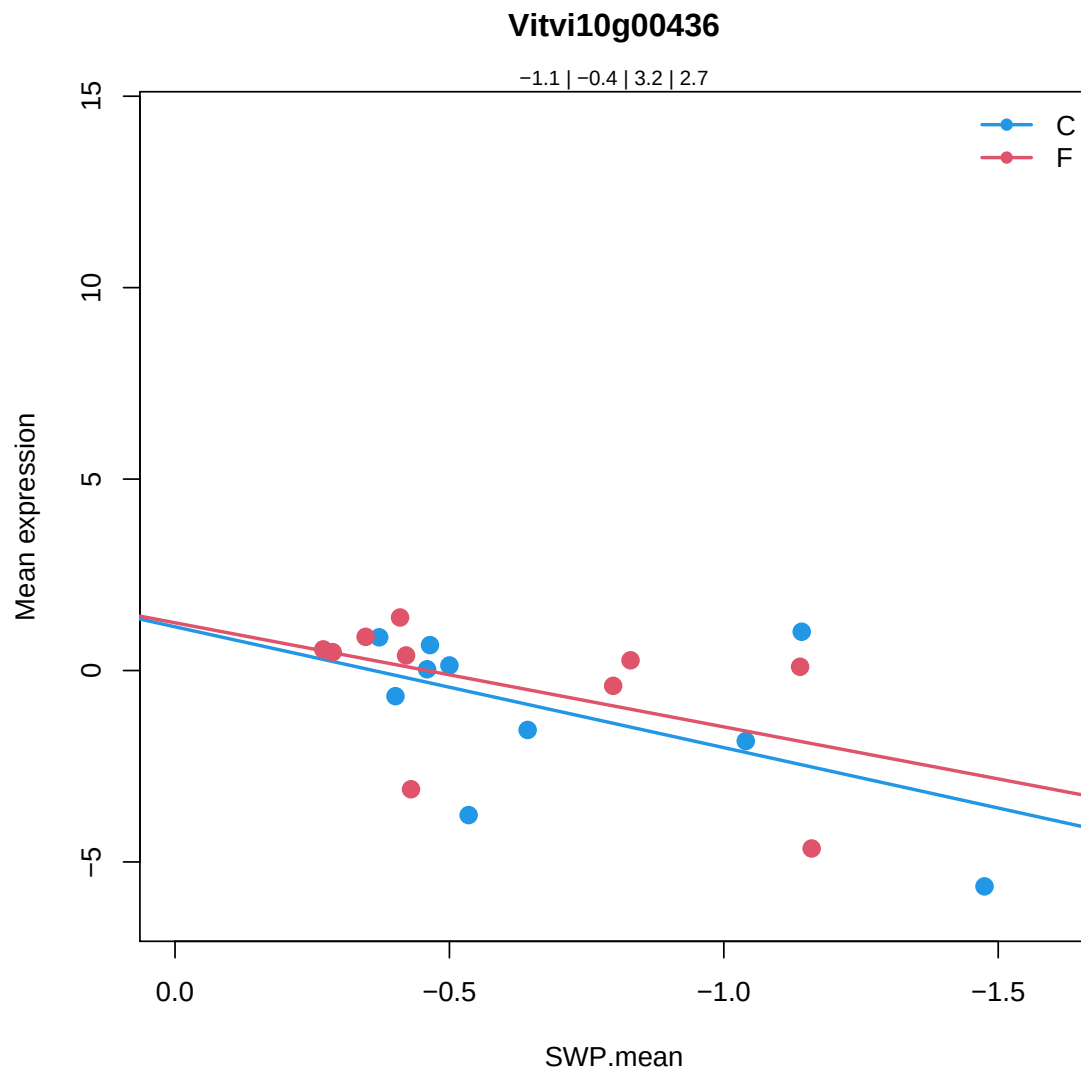
Melibiase family protein |

Chr3:20882886-20885745 FORWARD LENGTH=437 |

201606

Coefficients for Vitvi10g00436.

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



8.1.7 Vitvi04g02114: Type1

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

```
Vitvi04g02114
```

```
35.2
```

```
not assigned.unknown
```

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

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

```
201606
```

```
Vitvi04g02114
```

```
17.8.1.1.7
```

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

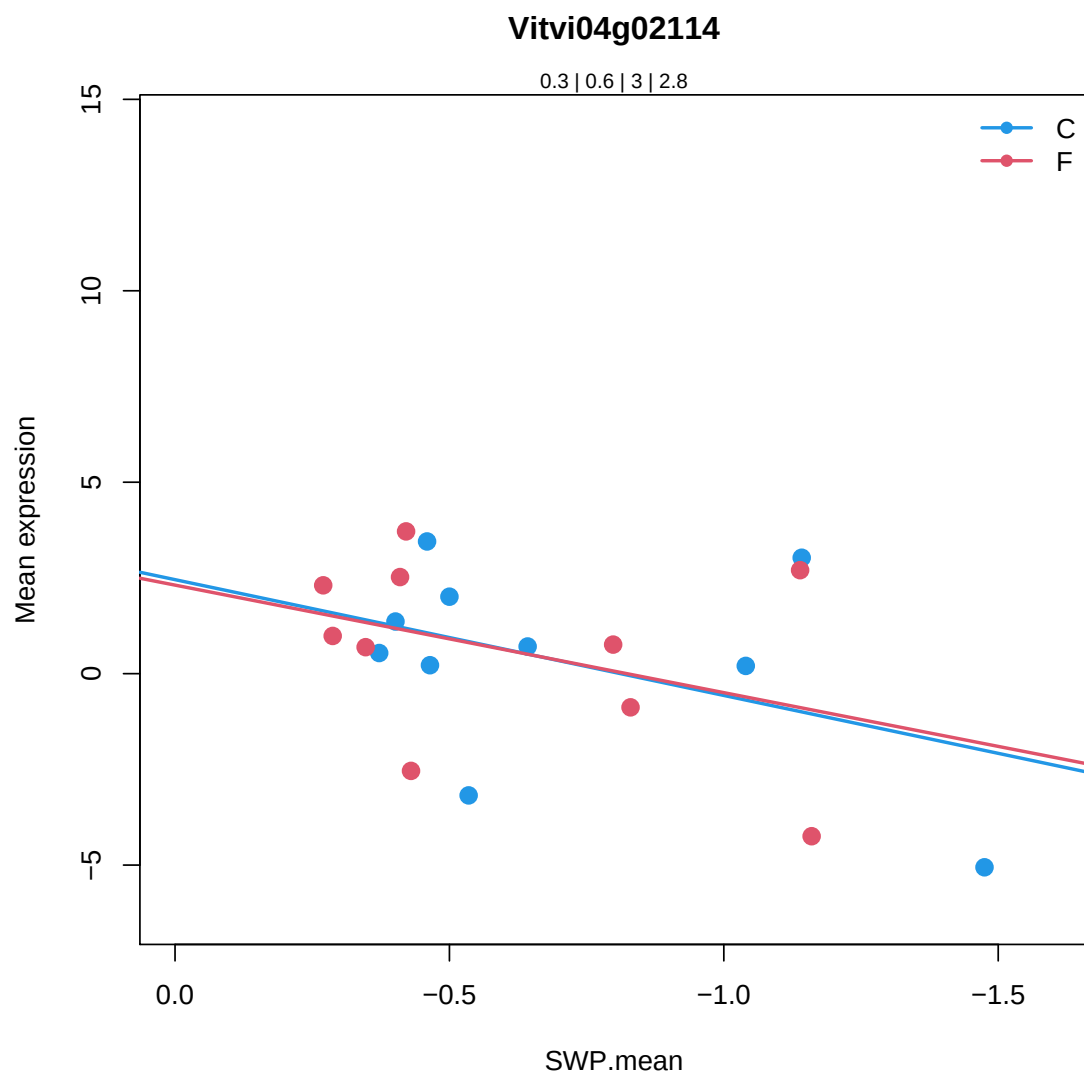
```
S-adenosyl-L-methionine-dependent methyltransferases superfamily prote
```

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

```
201606
```

Coefficients for Vitvi04g02114.

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



8.1.8 Vitvi03g00144: * Type1

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

Vitvi03g00144

29.4.1.56

protein.postranslational modification.kinase.receptor like cytoplasmat

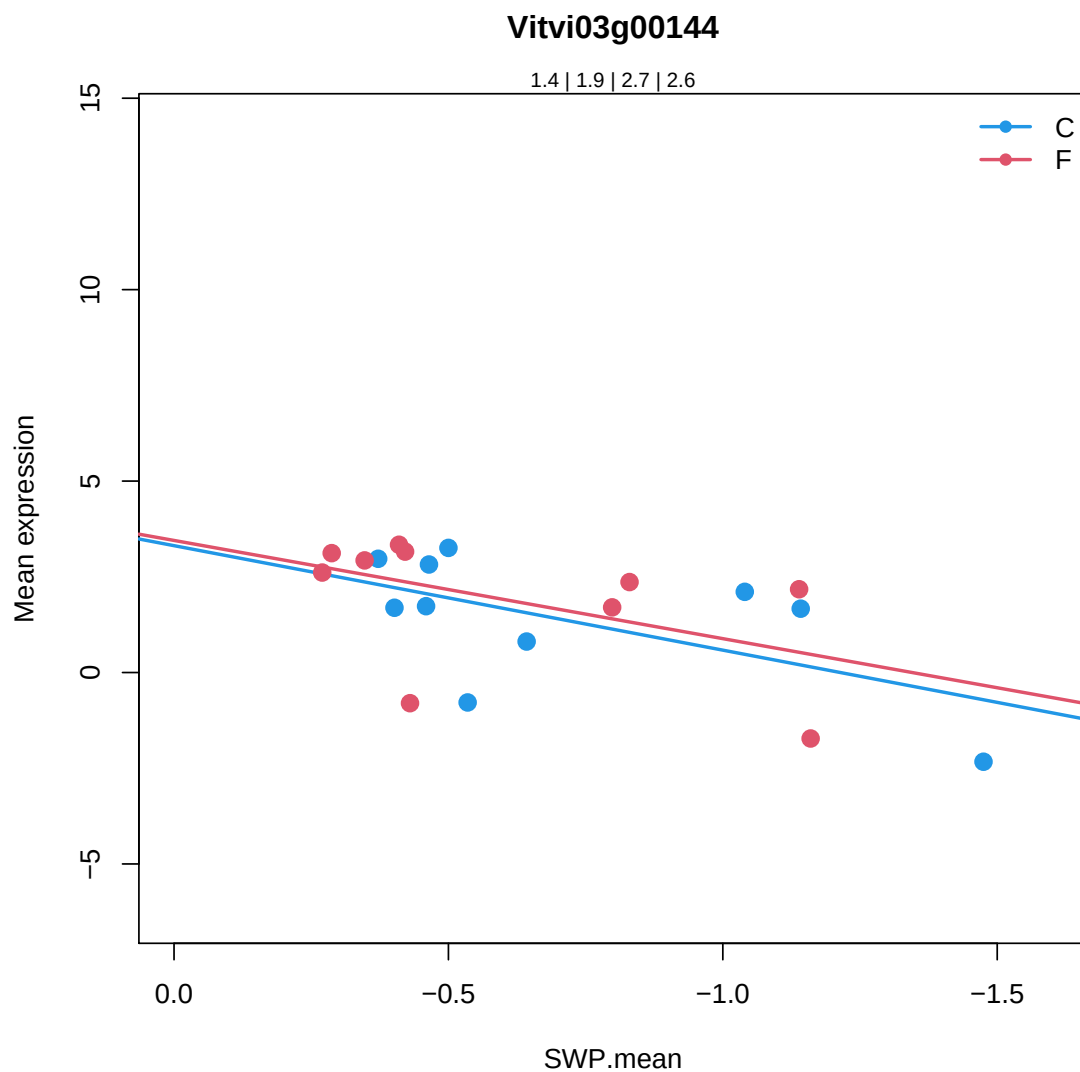
Protein kinase superfamily protein |

Chr4:16676234-16677962 FORWARD LENGTH=448 |

201606

Coefficients for Vitvi03g00144.

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



8.1.9 Vitvi06g00790: Type1

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

Vitvi06g00790

10.7

cell wall.modification

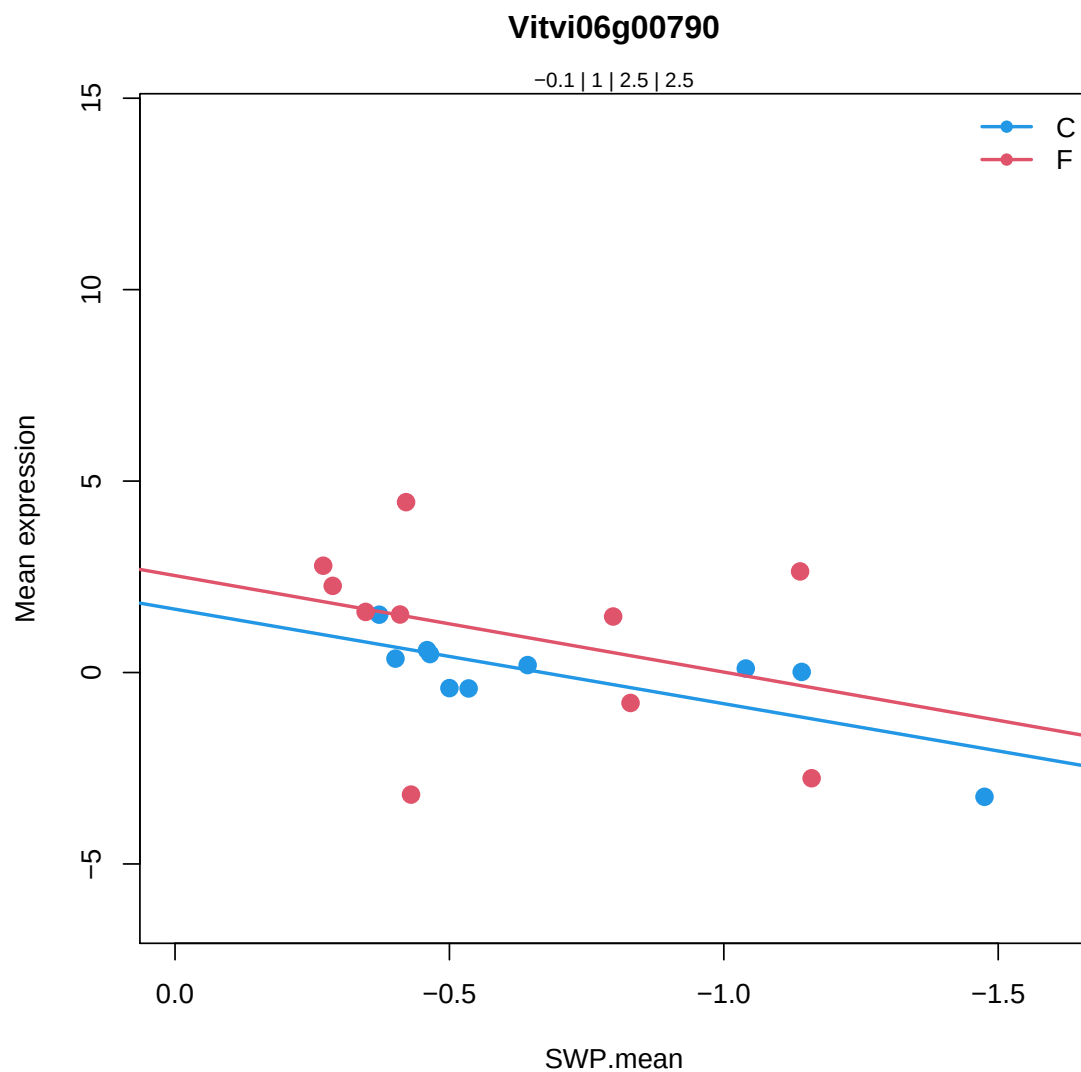
expansin A8 |

Chr2:16949121-16950472 REVERSE LENGTH=253 |

201606

Coefficients for Vitvi06g00790.

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



8.1.10 Vitvi04g00060: Type1

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

Vitvi04g00060

29.4

protein.postranslational modification

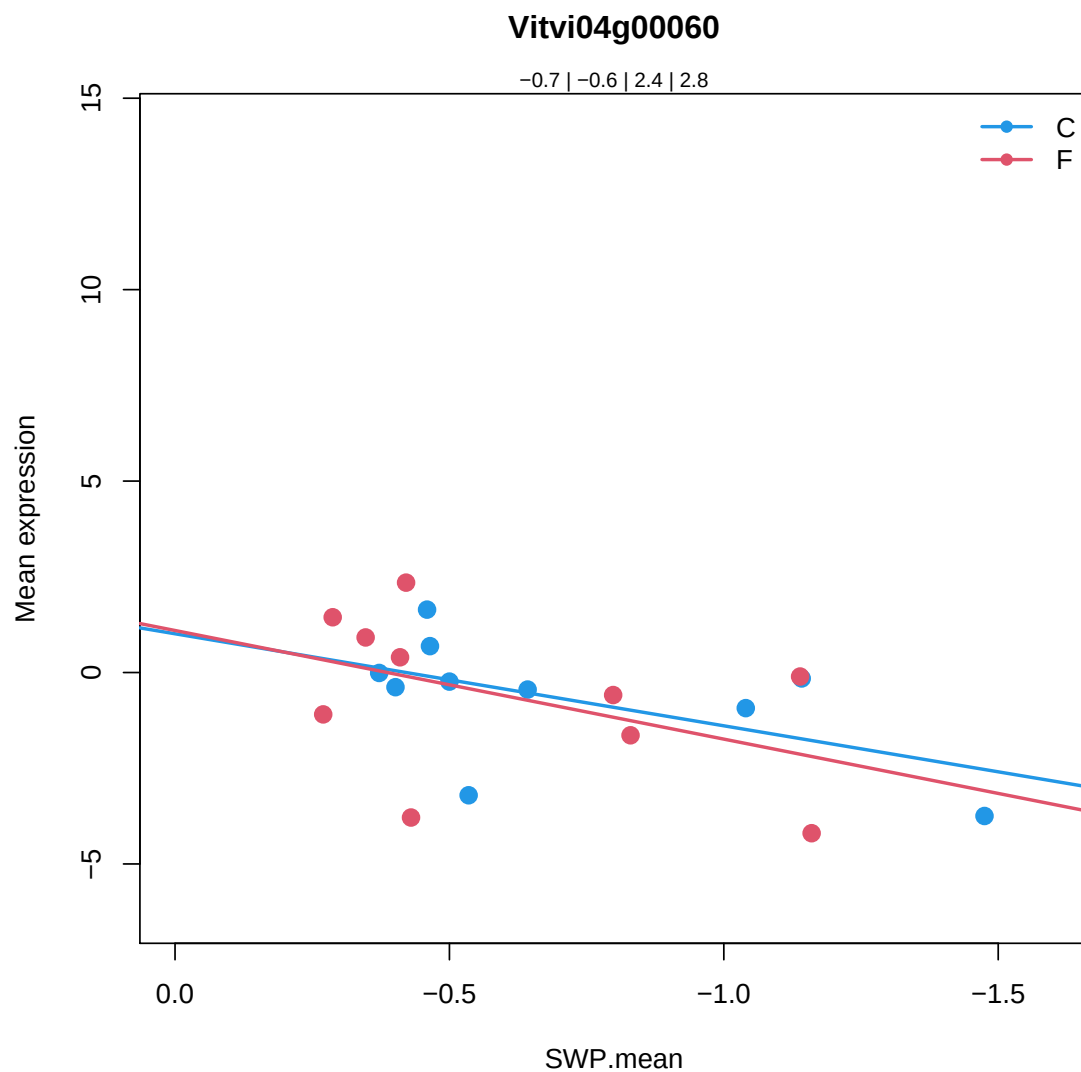
Protein phosphatase 2C family protein |

Chr5:9085512-9087372 REVERSE LENGTH=331 |

201606

Coefficients for Vitvi04g00060.

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



8.1.11 Vitvi18g00455: Type1

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

Vitvi18g00455

26.7

misc.oxidases - copper, flavone etc

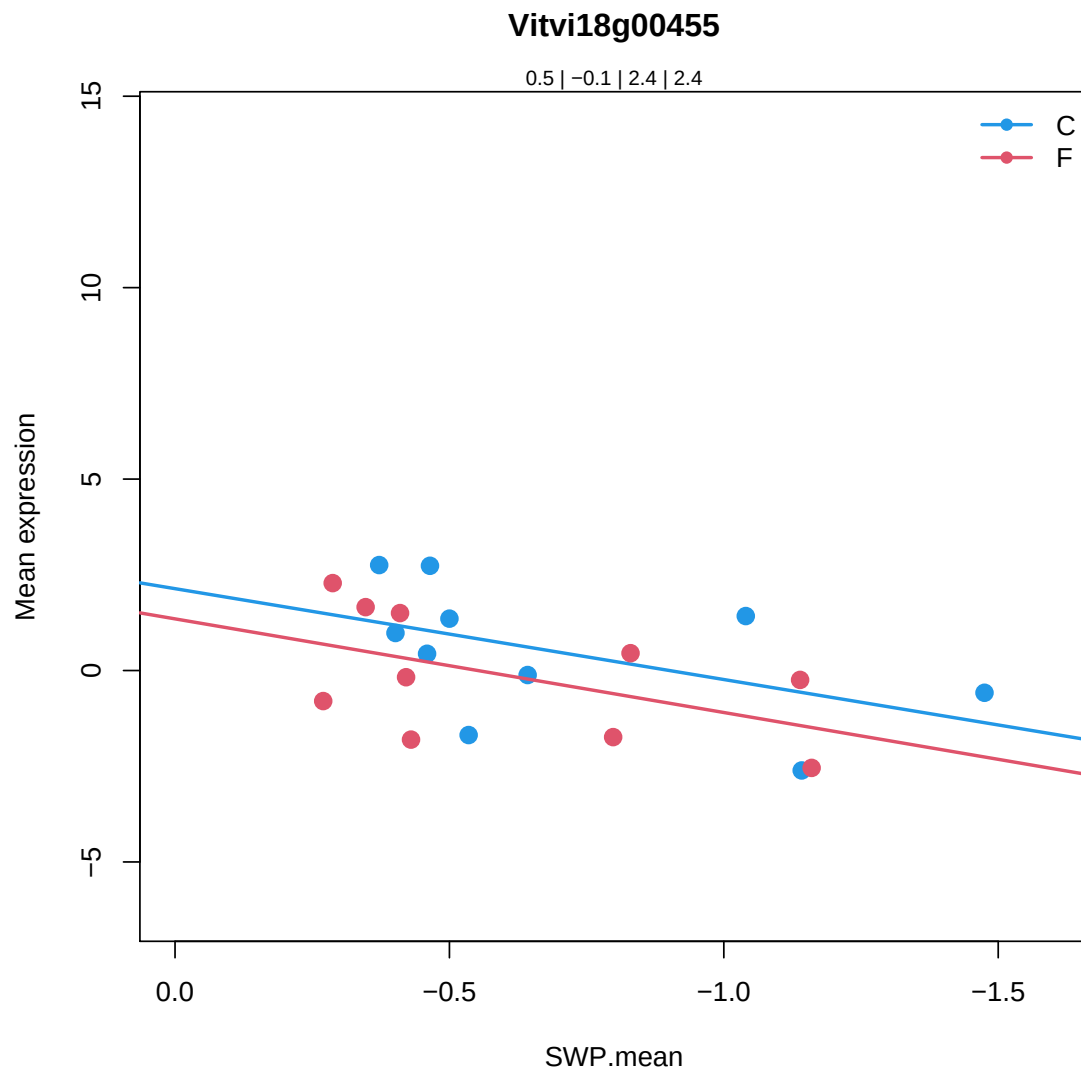
Cupredoxin superfamily protein |

Chr1:27188287-27189093 FORWARD LENGTH=181 |

201606

Coefficients for Vitvi18g00455.

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



8.1.12 Vitvi11g01437: * Type1

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

Vitvi11g01437

26.12

misc.peroxidases

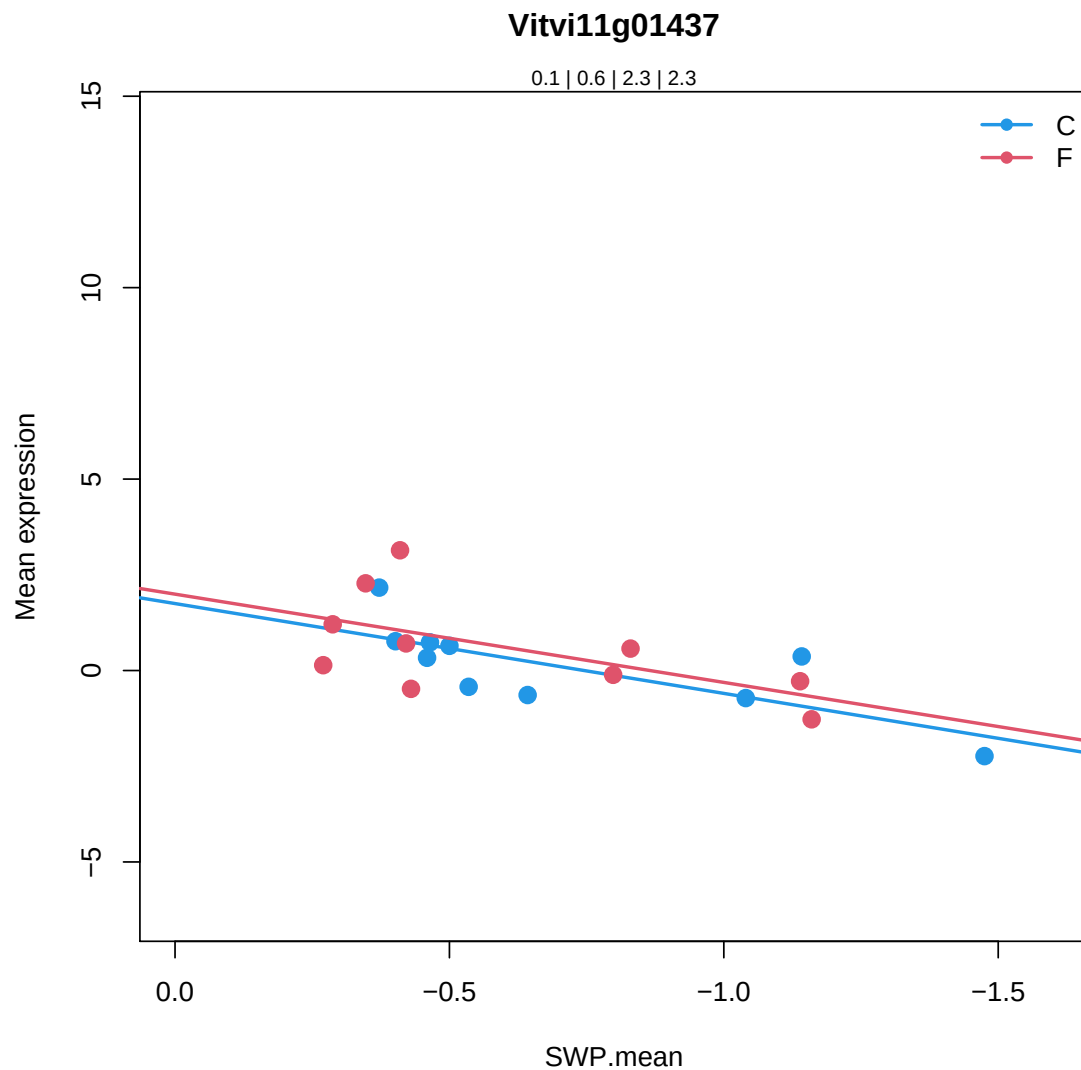
peroxidase superfamily protein |

Chr2:17296986-17298690 REVERSE LENGTH=328 |

201606

Coefficients for Vitvi11g01437.

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



8.1.13 Vitvi03g00752: * Type1

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

Vitvi03g00752

20.1.7.1

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

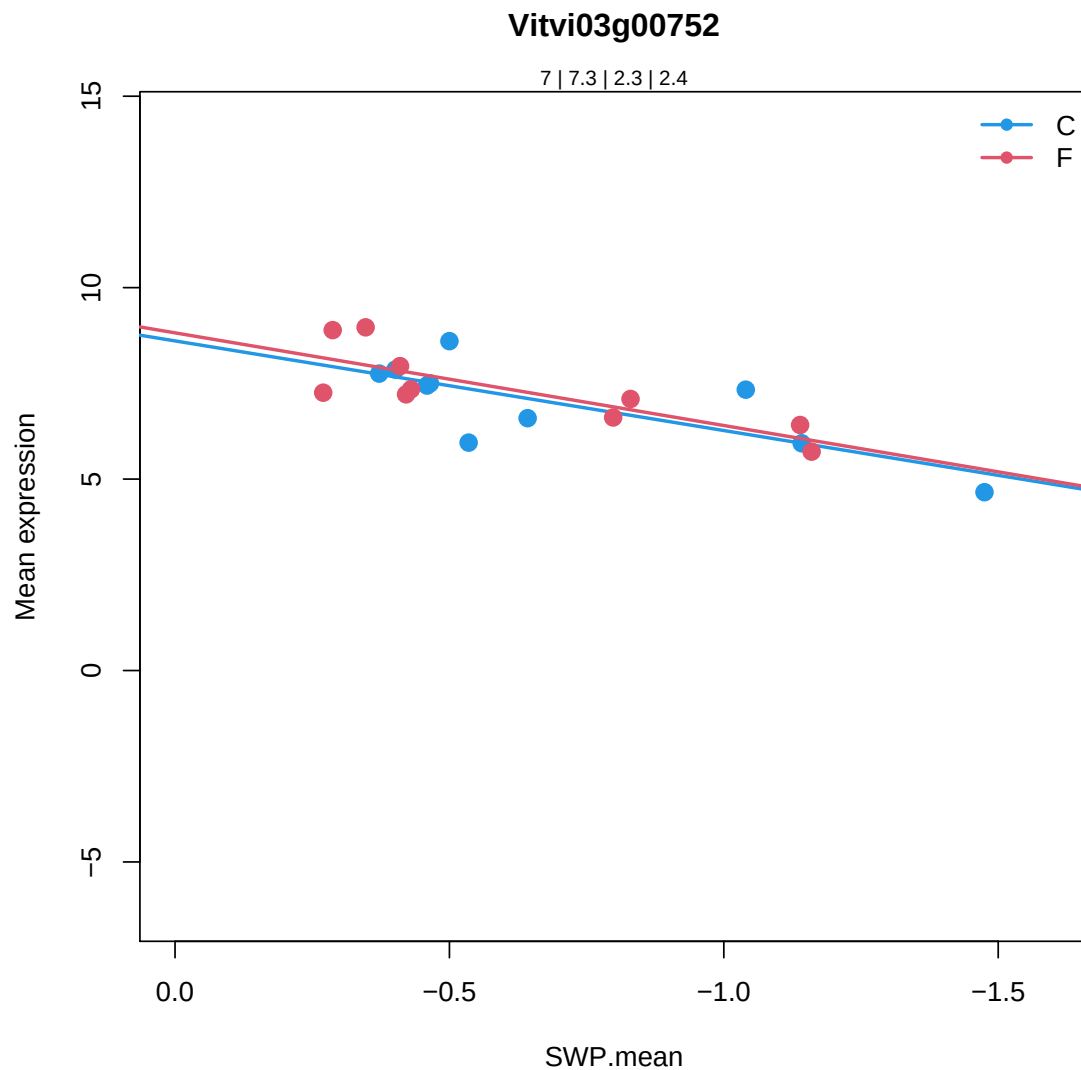
pathogenesis-related protein 1 |

Chr2:6241944-6242429 REVERSE LENGTH=161 |

201606

Coefficients for Vitvi03g00752.

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



8.1.14 Vitvi06g00626: * Type1

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

Vitvi06g00626

30.2.8.2

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

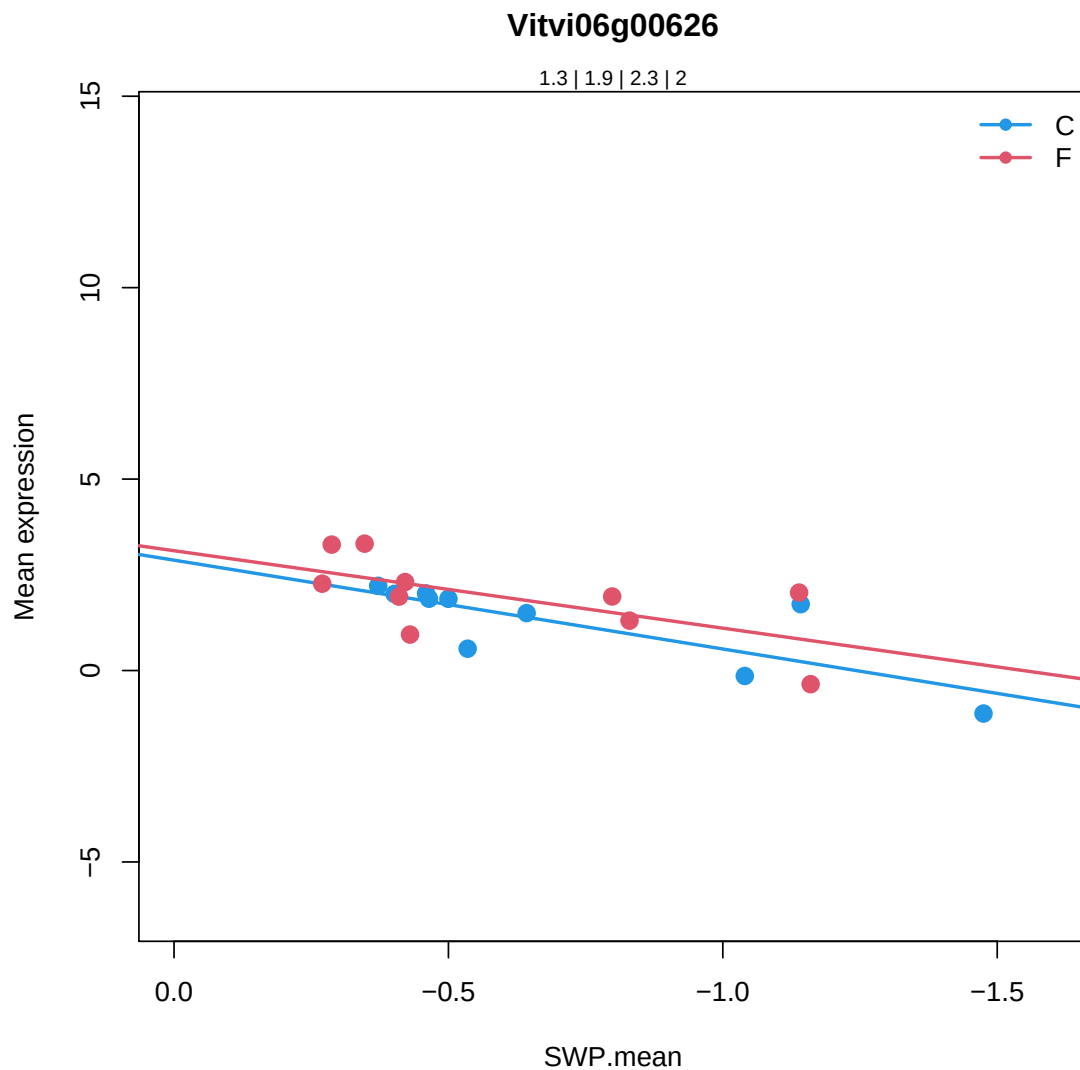
Protein kinase superfamily protein |

Chr3:2750285-2751674 FORWARD LENGTH=305 |

201606

Coefficients for Vitvi06g00626.

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



8.1.15 Vitvi01g00638: * Type1

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

Vitvi01g00638

35.2

not assigned.unknown

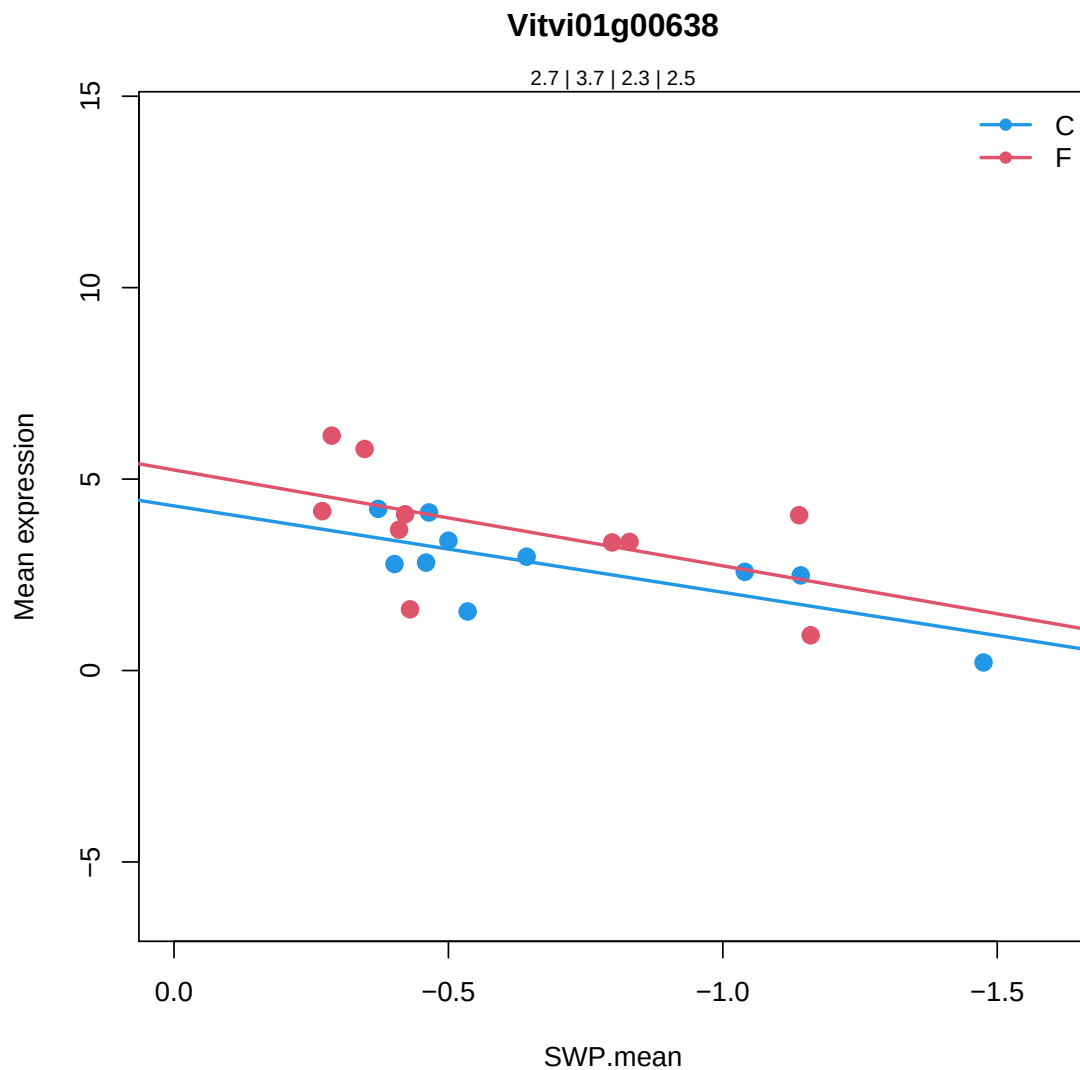
DUF868 family protein (DUF868) |

Chr4:7480896-7481753 FORWARD LENGTH=285 |

201606

Coefficients for Vitvi01g00638.

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



8.1.16 Vitvi03g01162: Type1

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

Vitvi03g01162

26.2

misc.UDP glucosyl and glucoronyl transferases

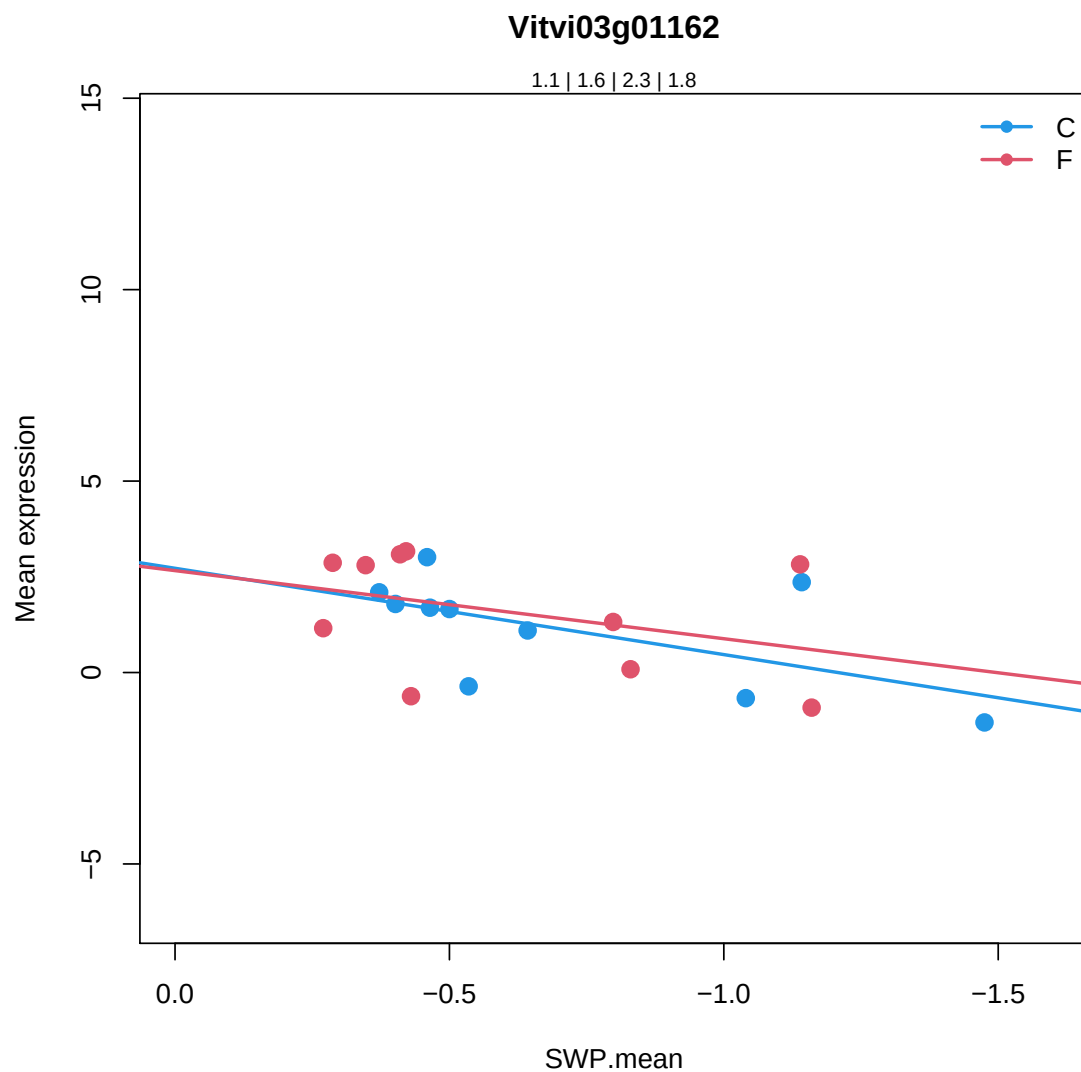
UDP-glucosyl transferase 85A3 |

Chr1:7900522-7902332 REVERSE LENGTH=488 |

201606

Coefficients for Vitvi03g01162.

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



8.1.17 Vitvi11g00365: * Type1

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

Vitvi11g00365

15.2

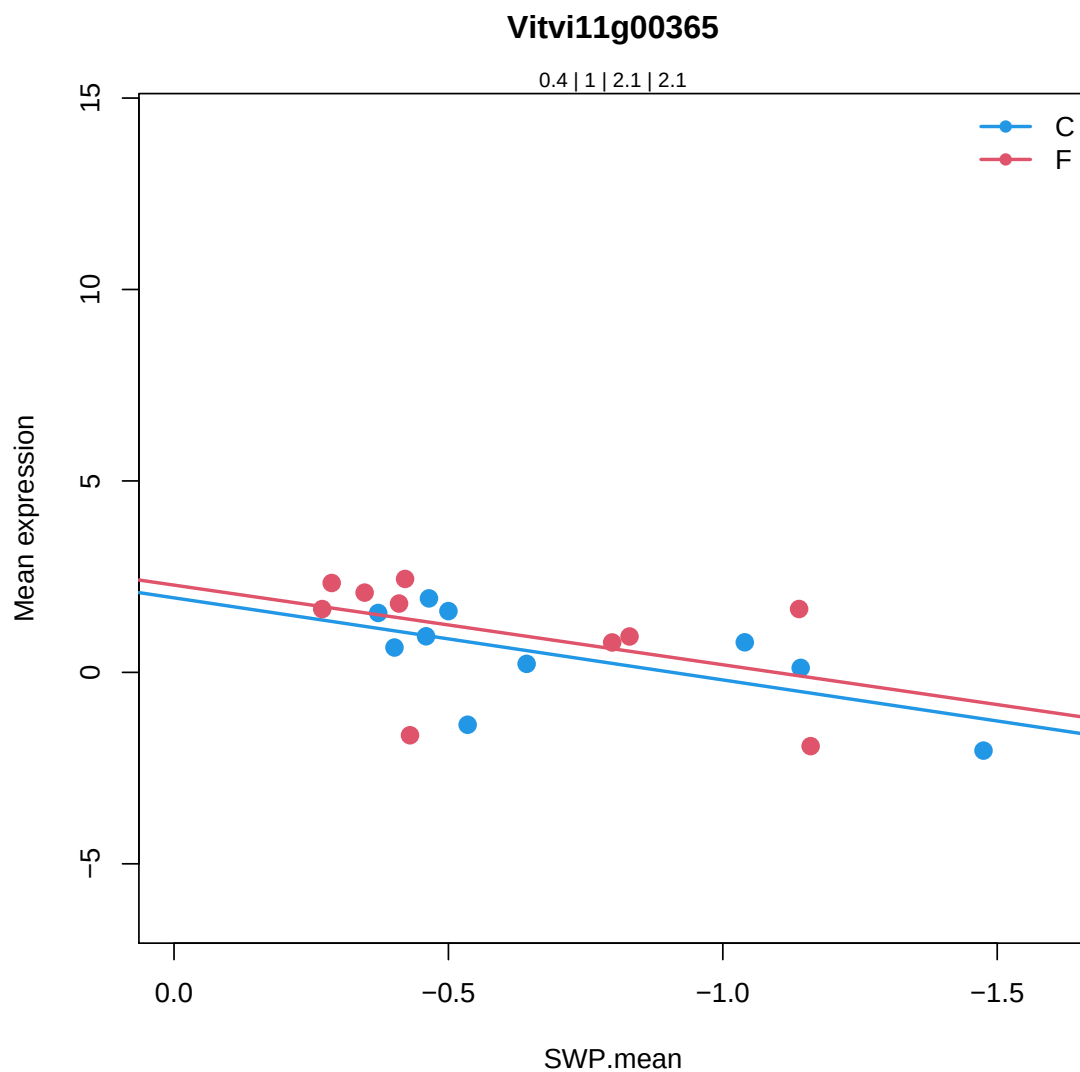
metal handling.binding, chelation and storage

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

[stNIB-v1_0017795]

Coefficients for Vitvi11g00365.

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



8.1.18 Vitvi18g01735: * Type1

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

Vitvi18g01735

35.2

not assigned.unknown

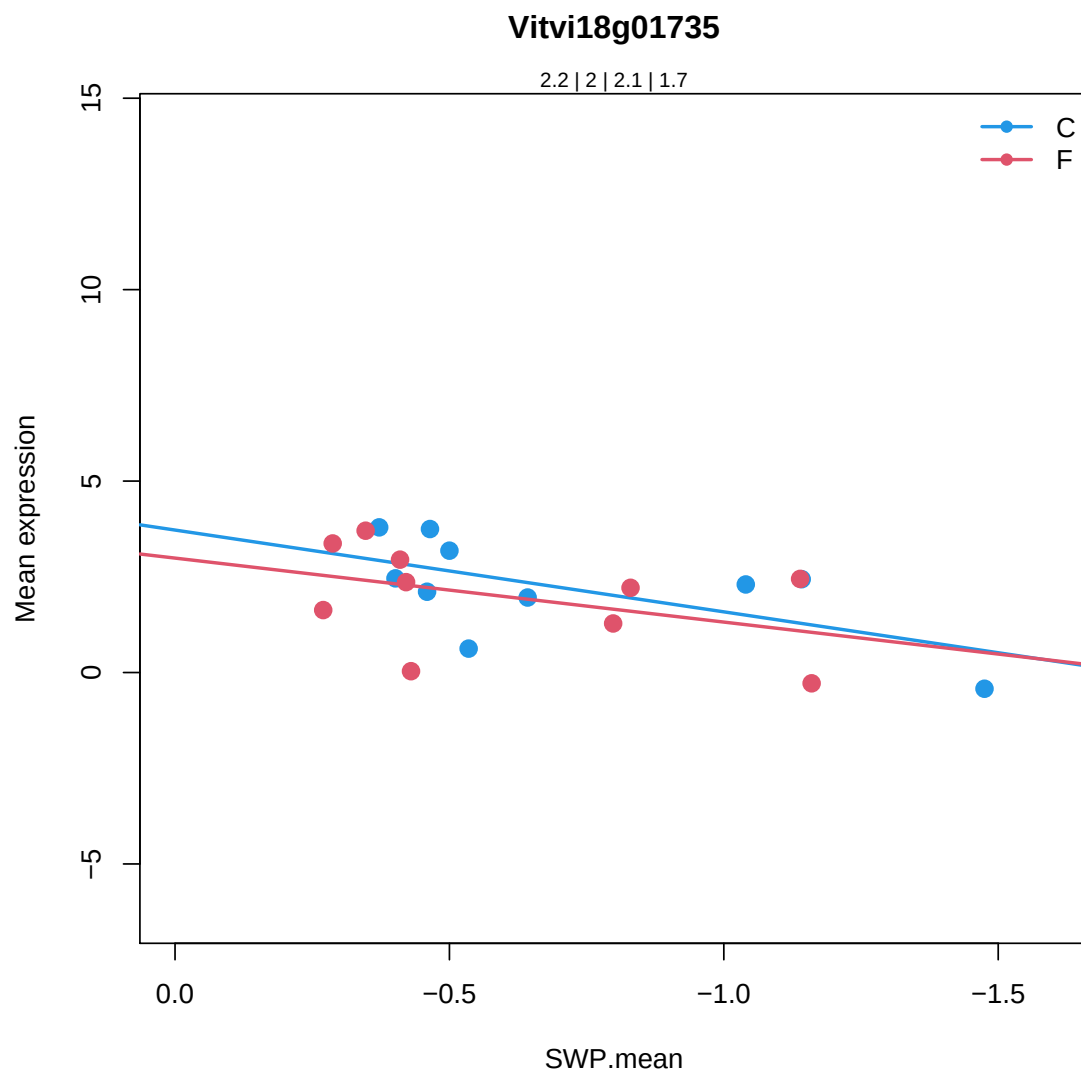
hypothetical protein |

Chr1:8025503-8026060 REVERSE LENGTH=185 |

201606

Coefficients for Vitvi18g01735.

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



8.1.19 Vitvi15g00812: * Type1

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

Vitvi15g00812

26.7

misc.oxidases - copper, flavone etc

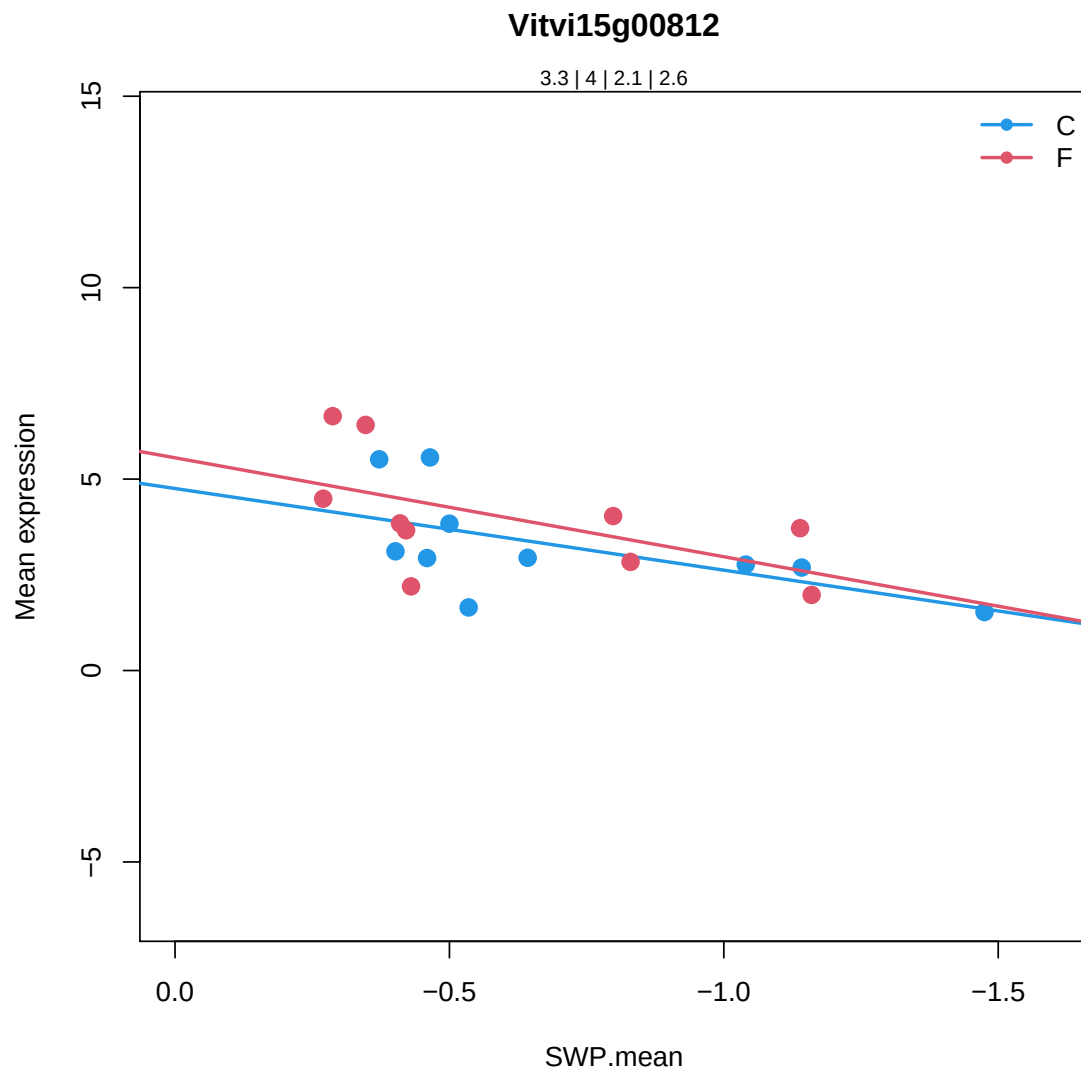
Oxidoreductase%2C zinc-binding dehydrogenase family protein |

Chr1:8398245-8399656 REVERSE LENGTH=386 |

201606

Coefficients for Vitvi15g00812.

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



8.1.20 Vitvi19g00041: Type1

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

Vitvi19g00041

35.2

not assigned.unknown

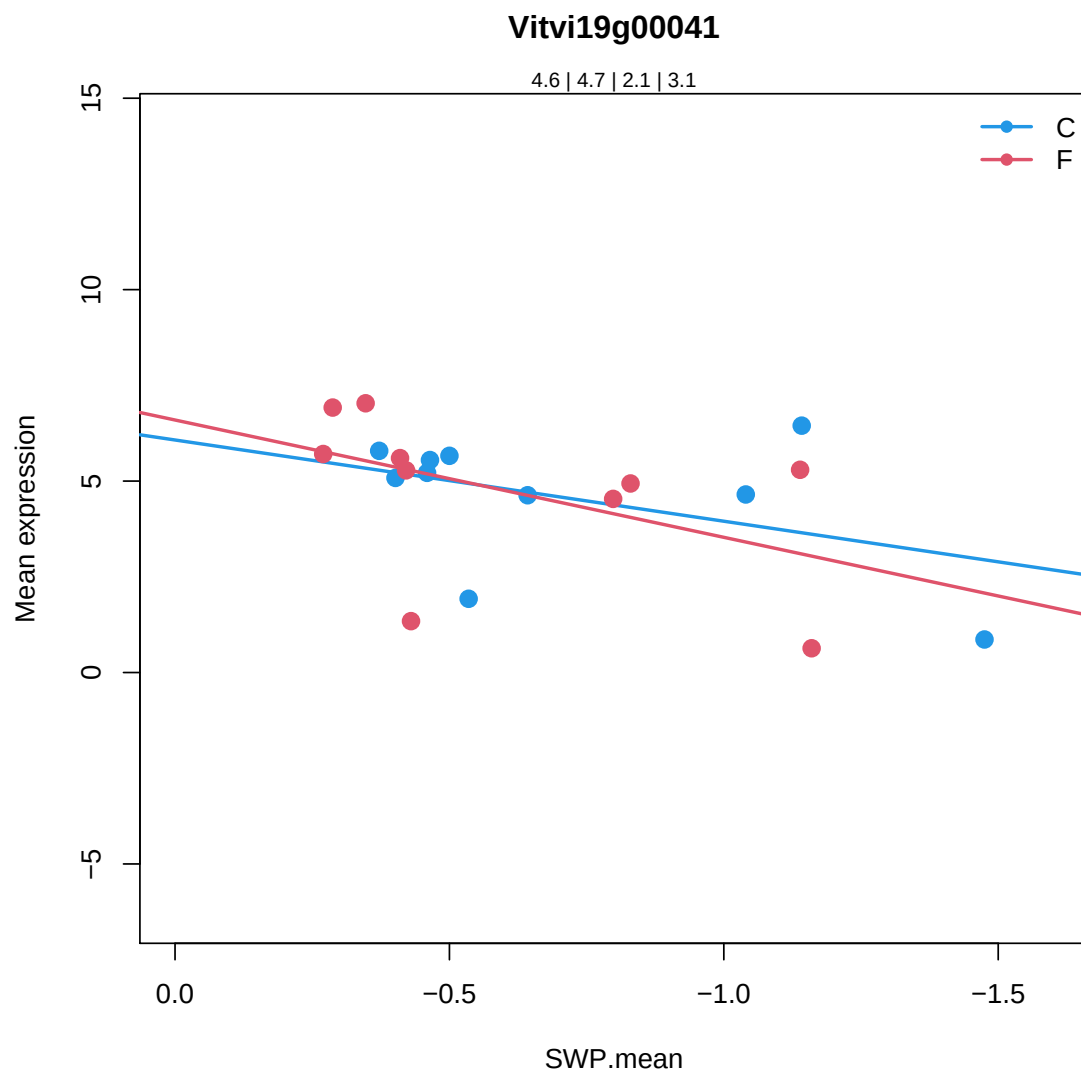
TRICHOME BIREFRINGENCE-LIKE 42 |

Chr1:29602708-29604557 FORWARD LENGTH=359 |

201606

Coefficients for Vitvi19g00041.

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



8.1.21 Vitvi13g02129: Type1

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

Vitvi13g02129

26.28

misc.GDSL-motif lipase

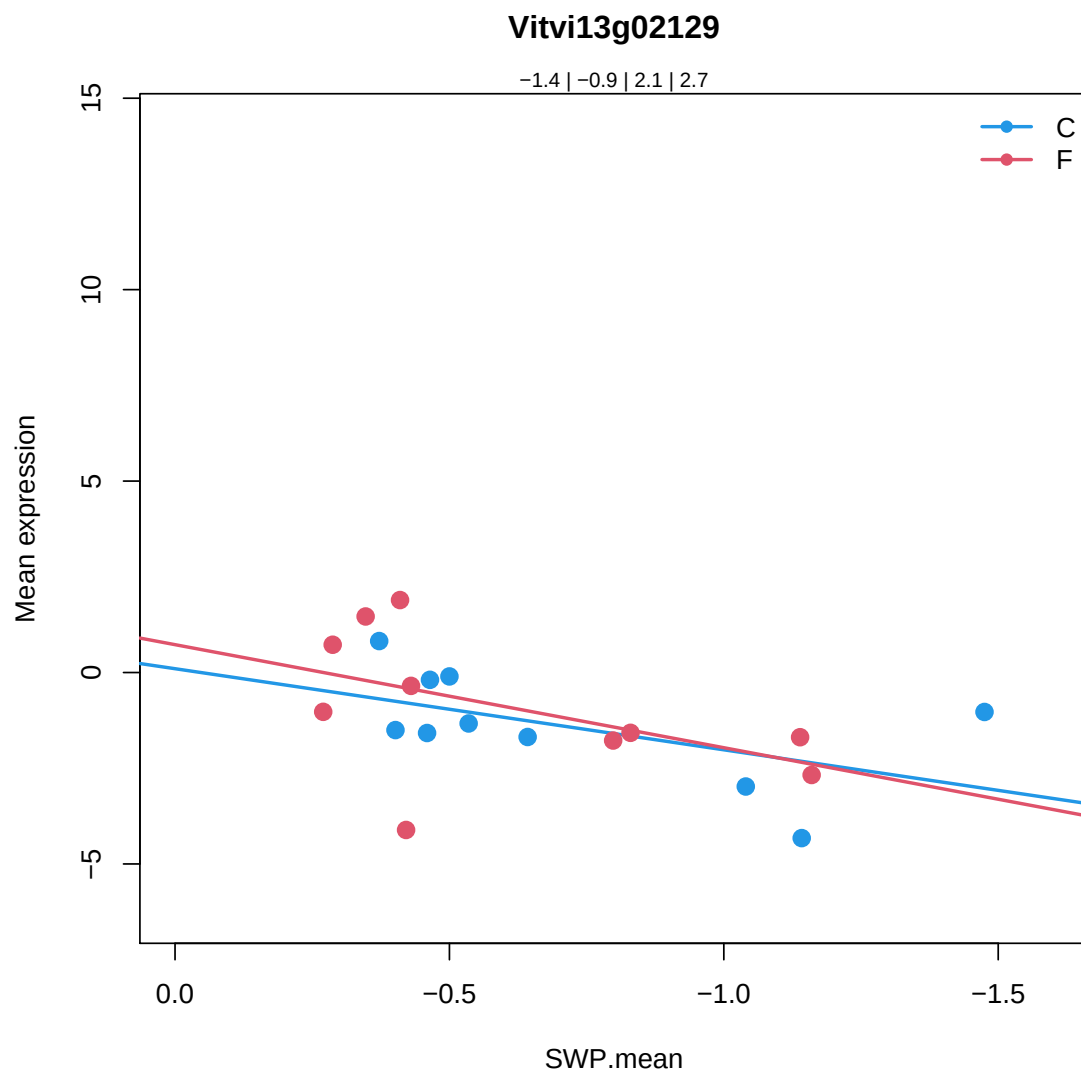
GDSL-like Lipase/Acylhydrolase superfamily protein |

Chr5:915650-918326 FORWARD LENGTH=359 |

201606

Coefficients for Vitvi13g02129.

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



8.1.22 Vitvi15g00641: Type1

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

Vitvi15g00641

31.3

cell.cycle

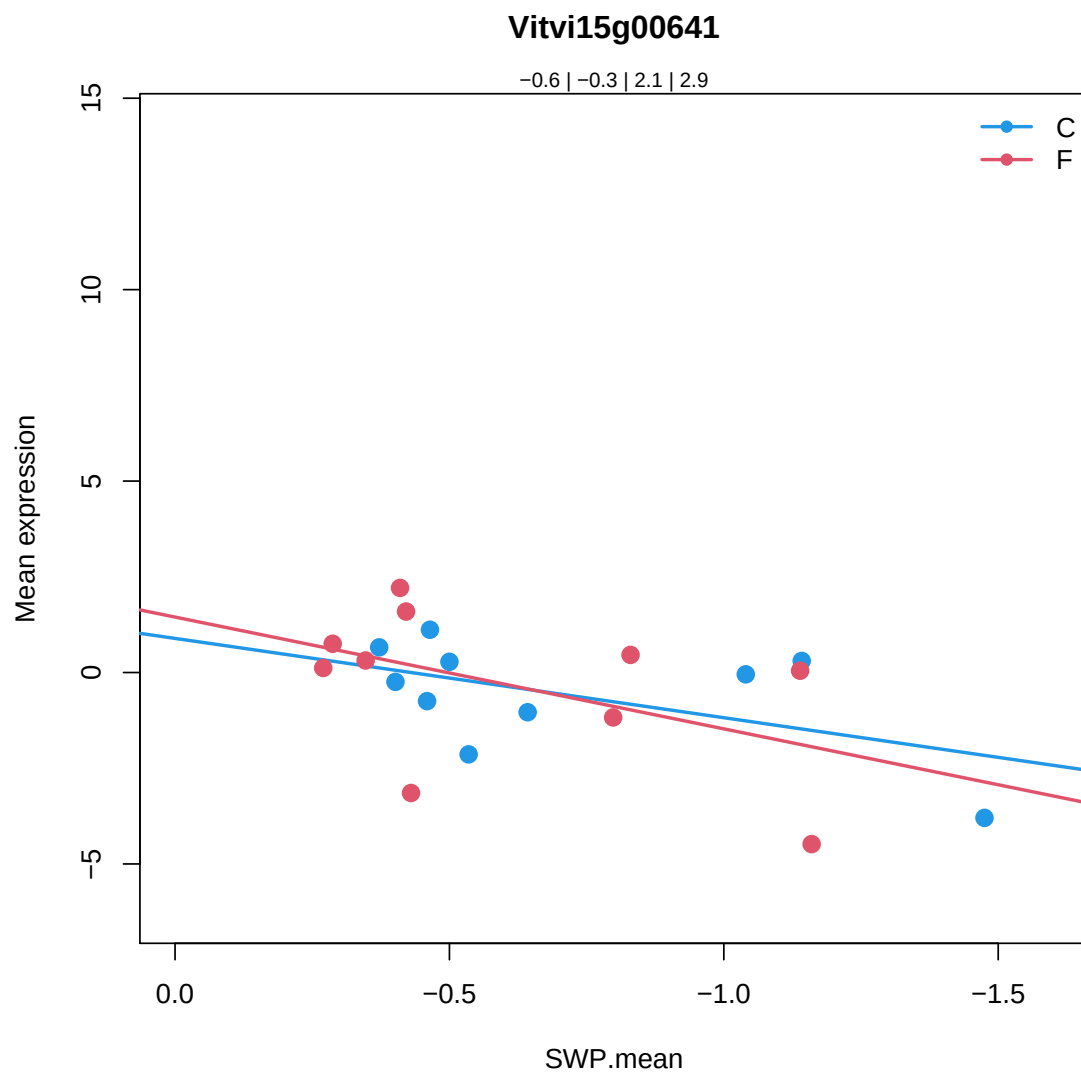
cyclin p3%3B1 |

Chr2:18591688-18592443 FORWARD LENGTH=222 |

201606

Coefficients for Vitvi15g00641.

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



8.1.23 Vitvi05g00089: * Type1

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

Vitvi05g00089

10.6.2

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

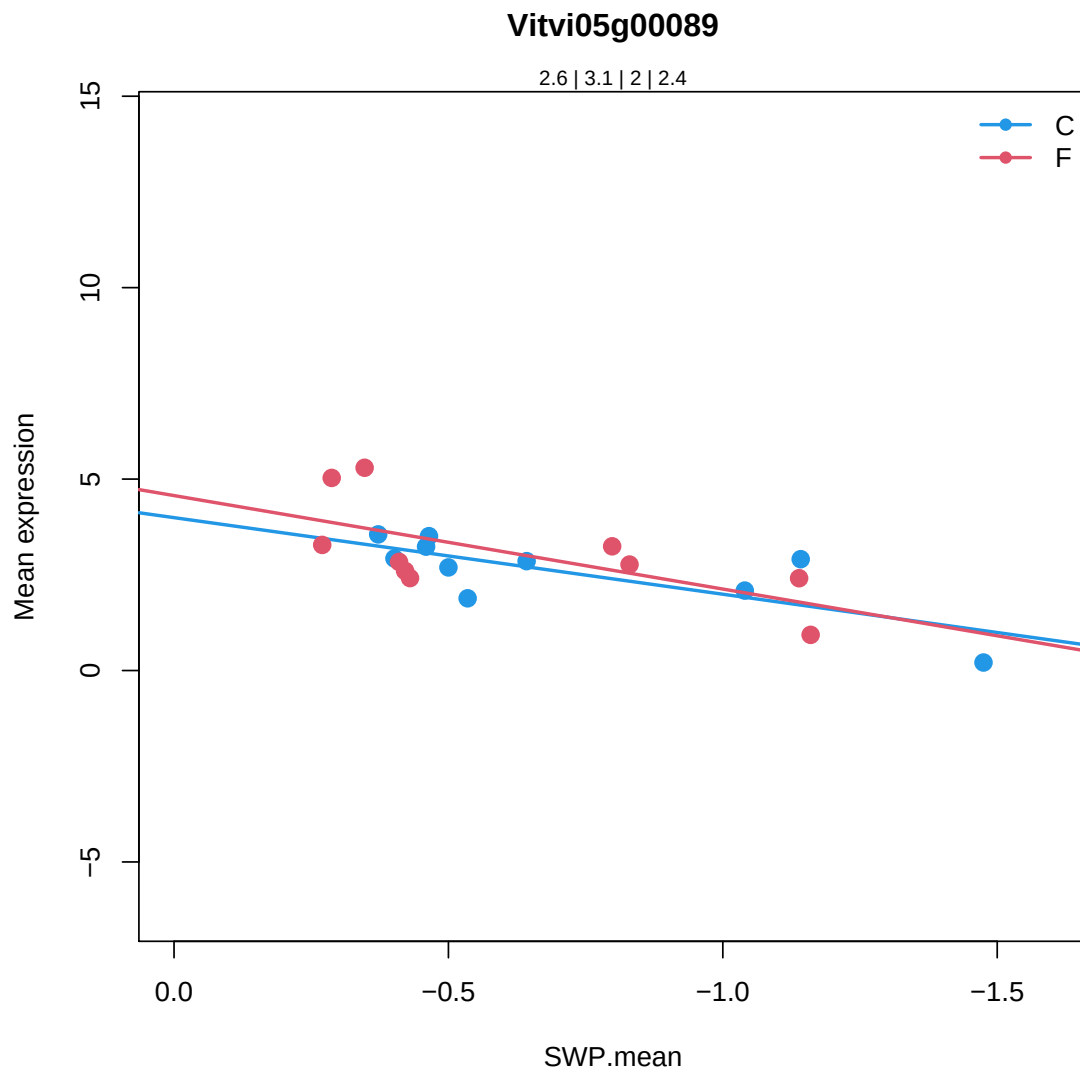
beta-xylosidase 1 |

Chr5:20012179-20016659 REVERSE LENGTH=774 |

201606

Coefficients for Vitvi05g00089.

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



8.1.24 Vitvi14g01899: * Type1

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

Vitvi14g01899

17.2.2

hormone metabolism.auxin.signal transduction

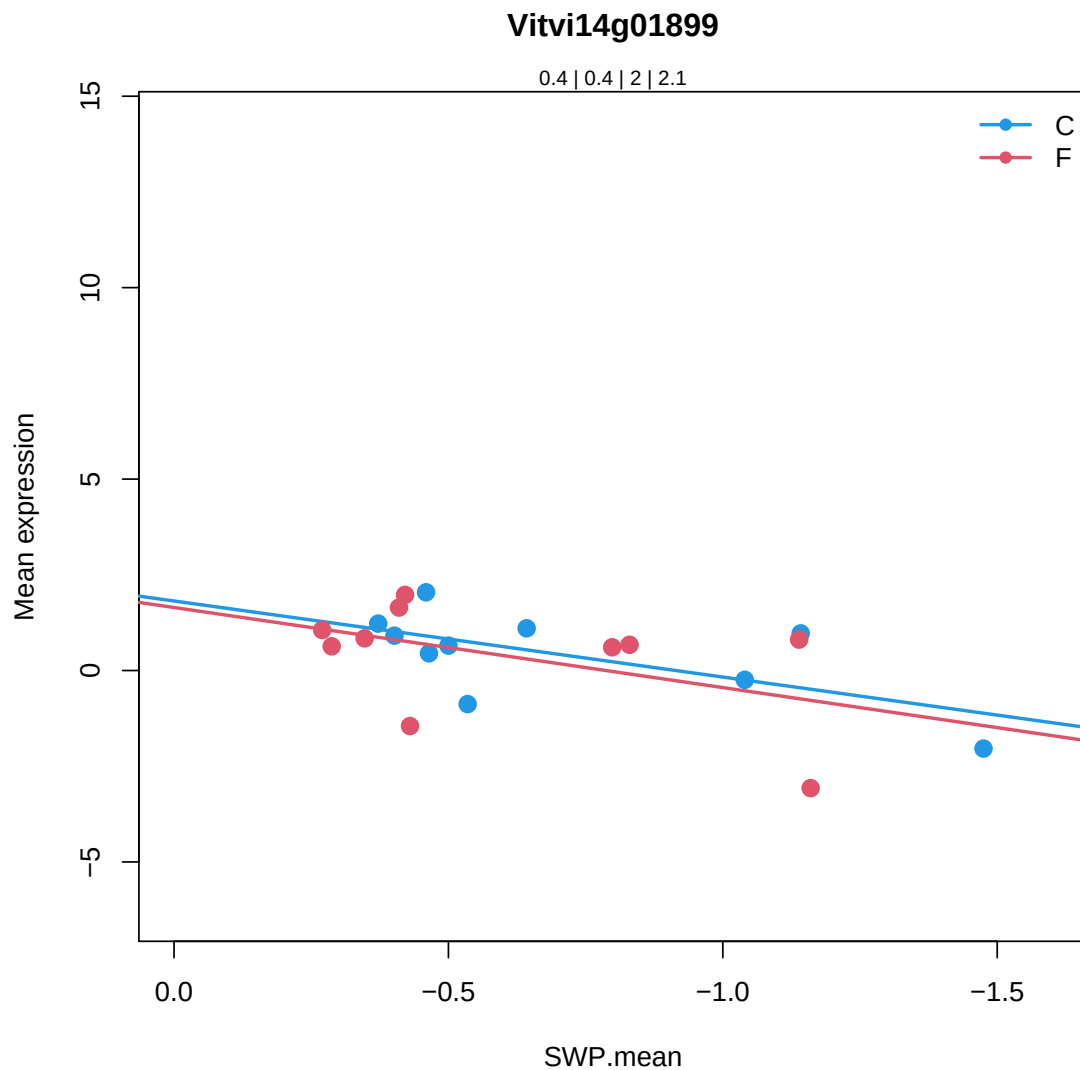
Auxin efflux carrier family protein |

Chr5:4892159-4893937 REVERSE LENGTH=367 |

201606

Coefficients for Vitvi14g01899.

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



8.1.25 Vitvi08g01702: * Type1

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

Vitvi08g01702

26.4.1

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

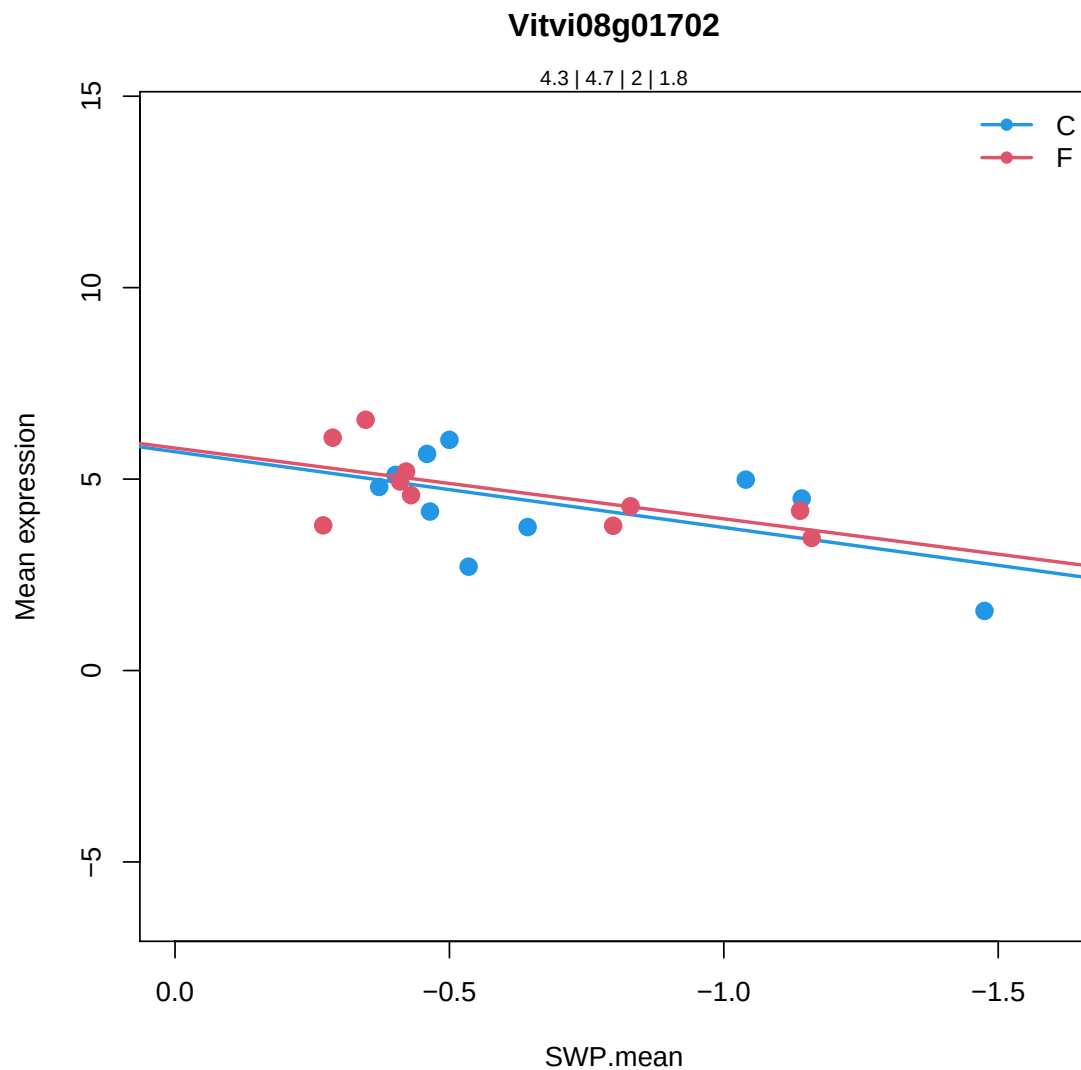
beta-1%2C3-glucanase 3 |

Chr3:21181916-21183045 REVERSE LENGTH=341 |

201606

Coefficients for Vitvi08g01702.

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



8.1.26 Vitvi18g00739: Type1

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

Vitvi18g00739

35.2

not assigned.unknown

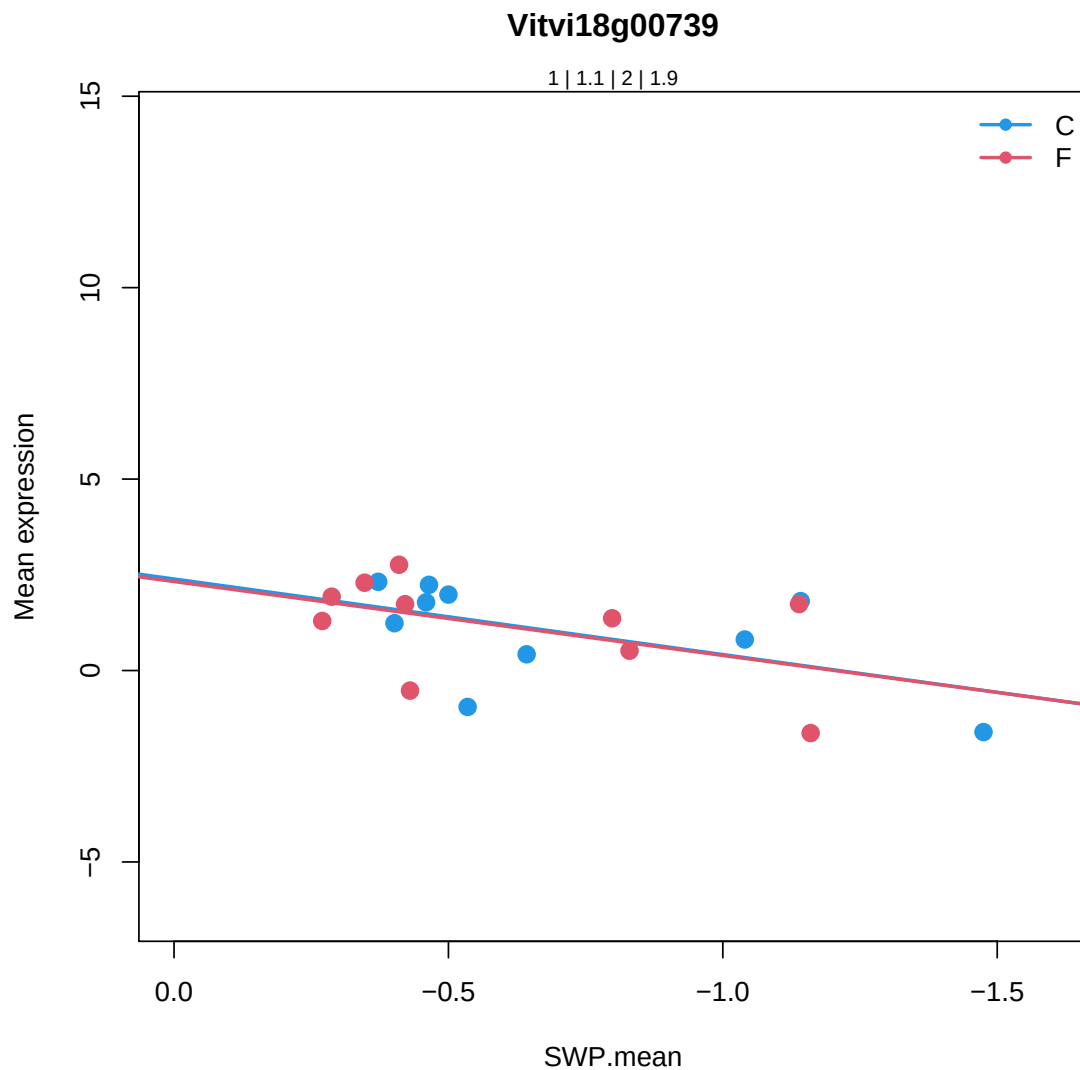
Serine/threonine-protein kinase WNK (With No Lysine)-like protein |

Chr1:22139282-22141585 FORWARD LENGTH=386 |

201606

Coefficients for Vitvi18g00739.

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



8.1.27 Vitvi18g02692: * Type1

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

Vitvi18g02692

33.1

development.storage proteins

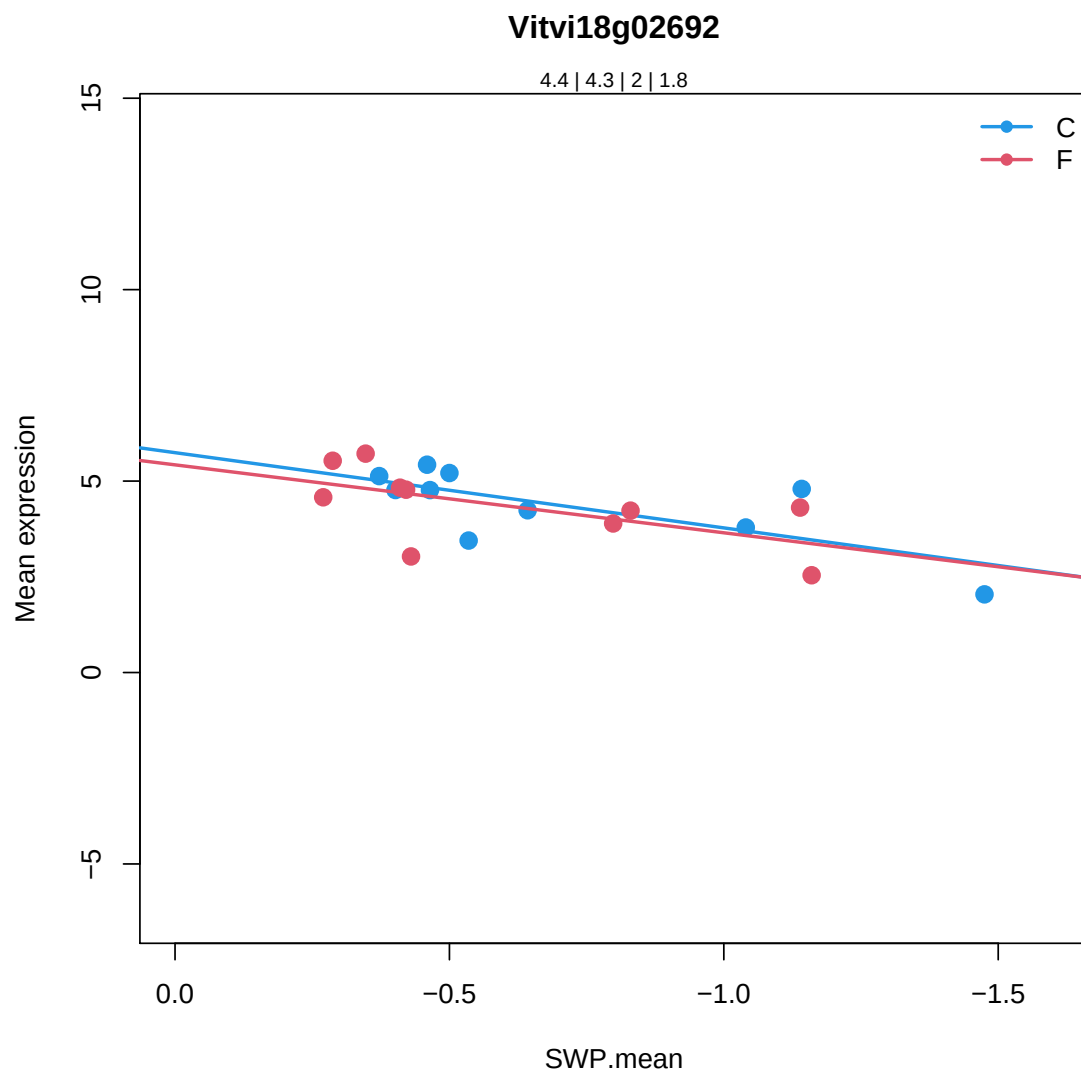
phospholipase A 2A |

Chr2:11293912-11295708 REVERSE LENGTH=407 |

201606

Coefficients for Vitvi18g02692.

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



8.1.28 Vitvi09g00528: * Type1

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

Vitvi09g00528

27.4

RNA.RNA binding

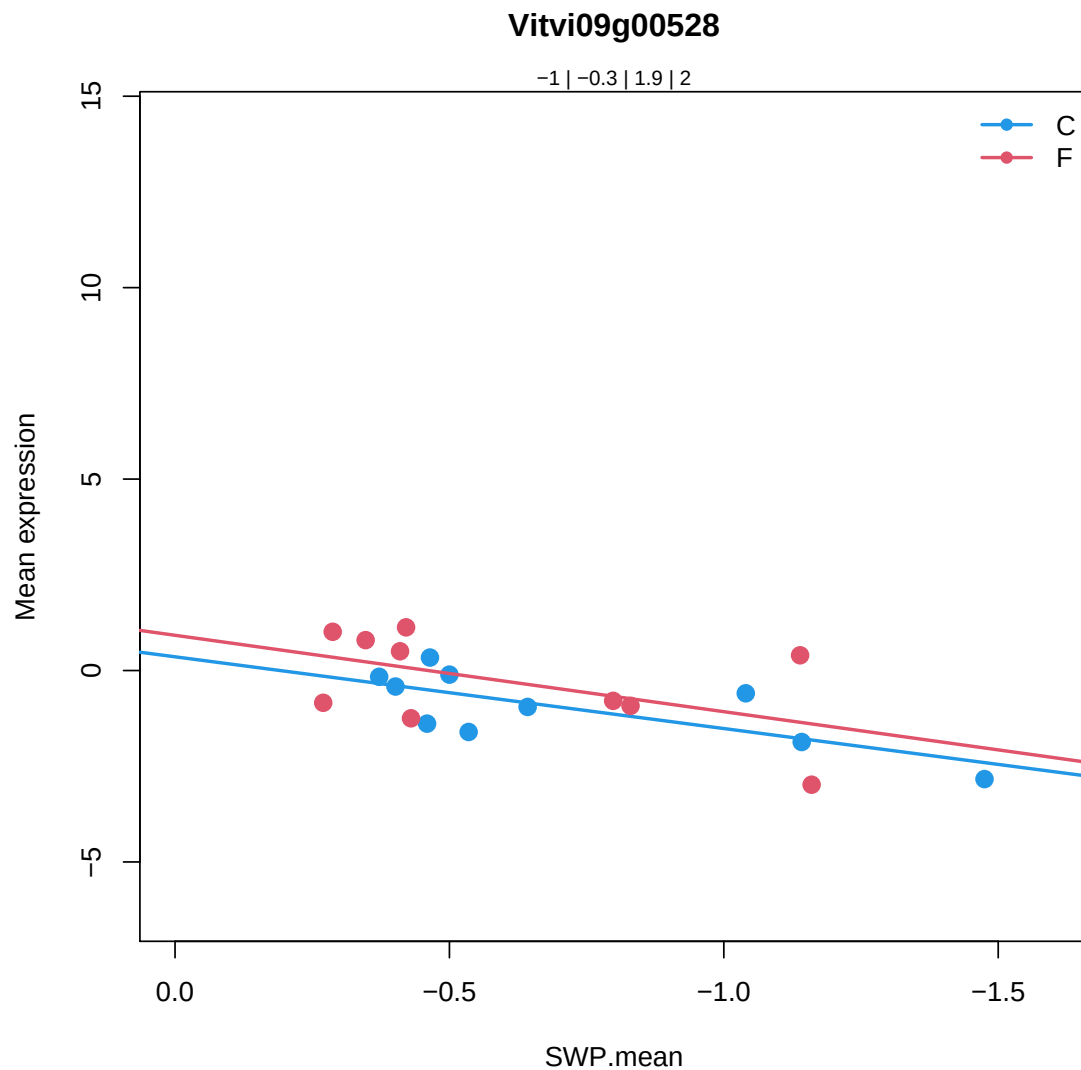
Ran BP2/NZF zinc finger-like superfamily protein |

Chr3:5315437-5316048 FORWARD LENGTH=164 |

201606

Coefficients for Vitvi09g00528.

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



8.1.29 Vitvi05g01949: Type1

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

Vitvi05g01949

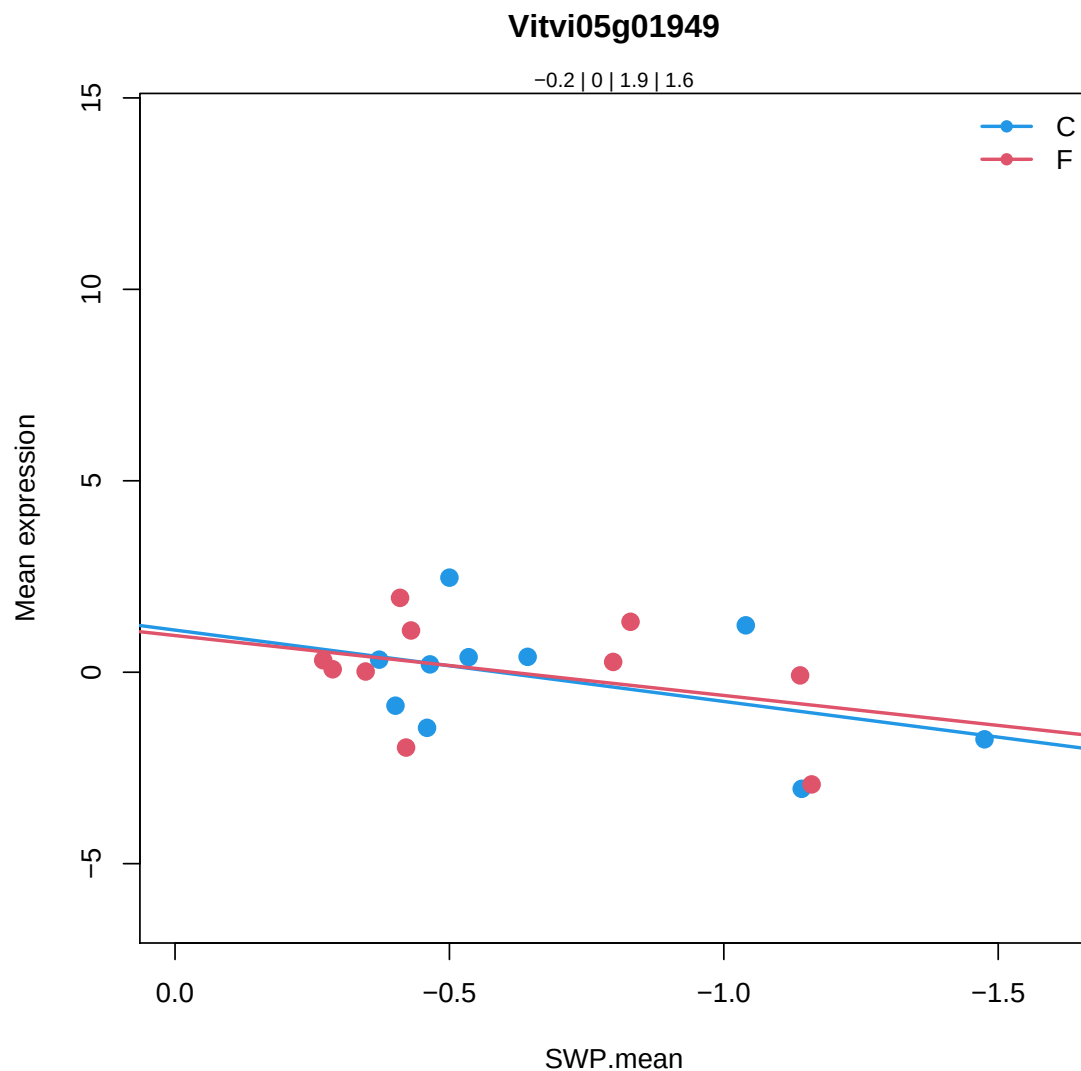
35.2

not assigned.unknown

NA

Coefficients for Vitvi05g01949.

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



8.1.30 Vitvi19g01964: * Type1

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

Vitvi19g01964

29.4

protein.postranslational modification

S-locus lectin protein kinase family protein |

Chr4:13666281-13669202 FORWARD LENGTH=829 |

201606

Vitvi19g01964

35.2

not assigned.unknown

S-locus lectin protein kinase family protein |

Chr4:13666281-13669202 FORWARD LENGTH=829 |

201606

Vitvi19g01964

30.2.24

signalling.receptor kinases.S-locus glycoprotein like

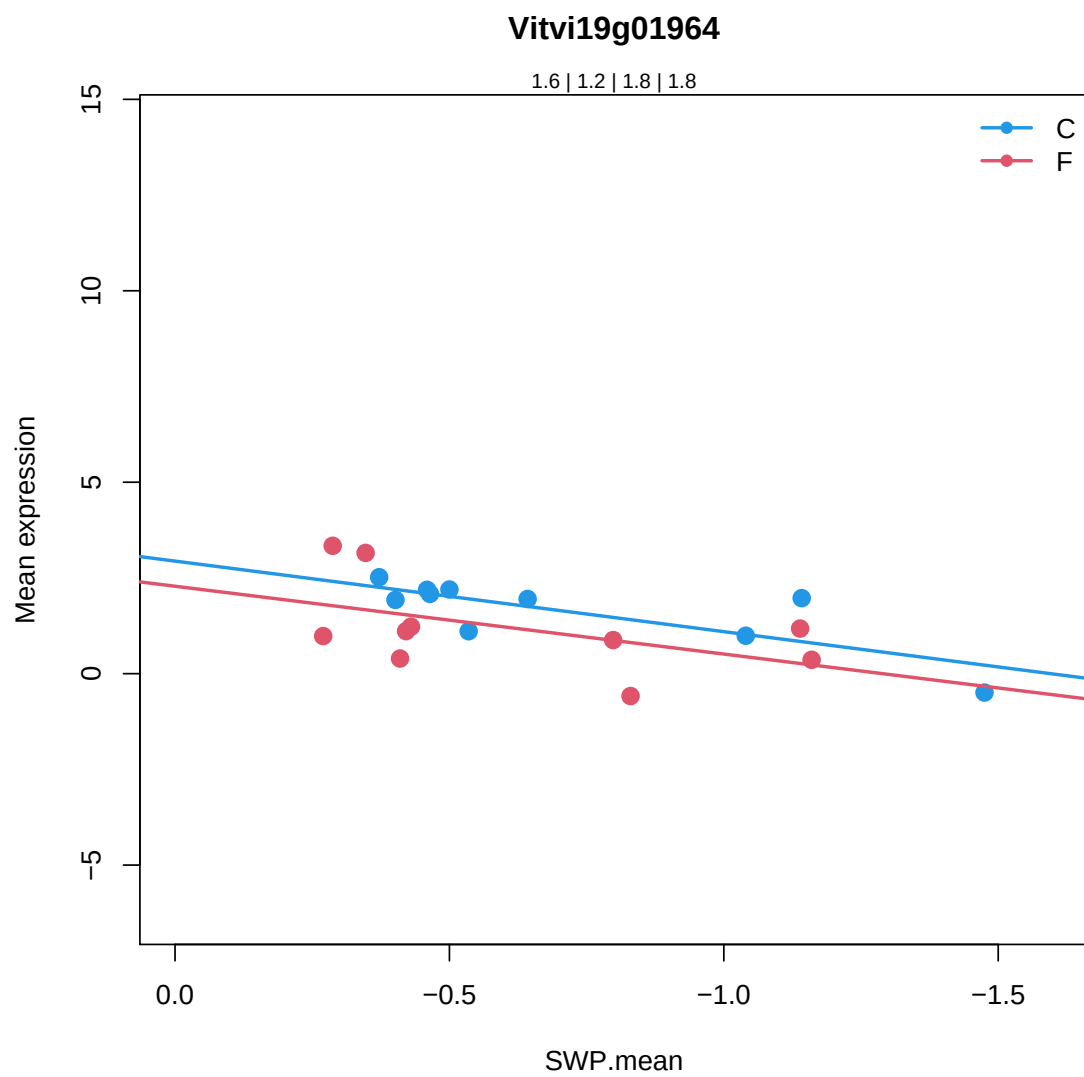
S-locus lectin protein kinase family protein |

Chr4:13666281-13669202 FORWARD LENGTH=829 |

201606

Coefficients for Vitvi19g01964.

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



8.1.31 Vitvi16g01418: Type1

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

Vitvi16g01418

10.8.1

cell wall.pectinesterases.PME

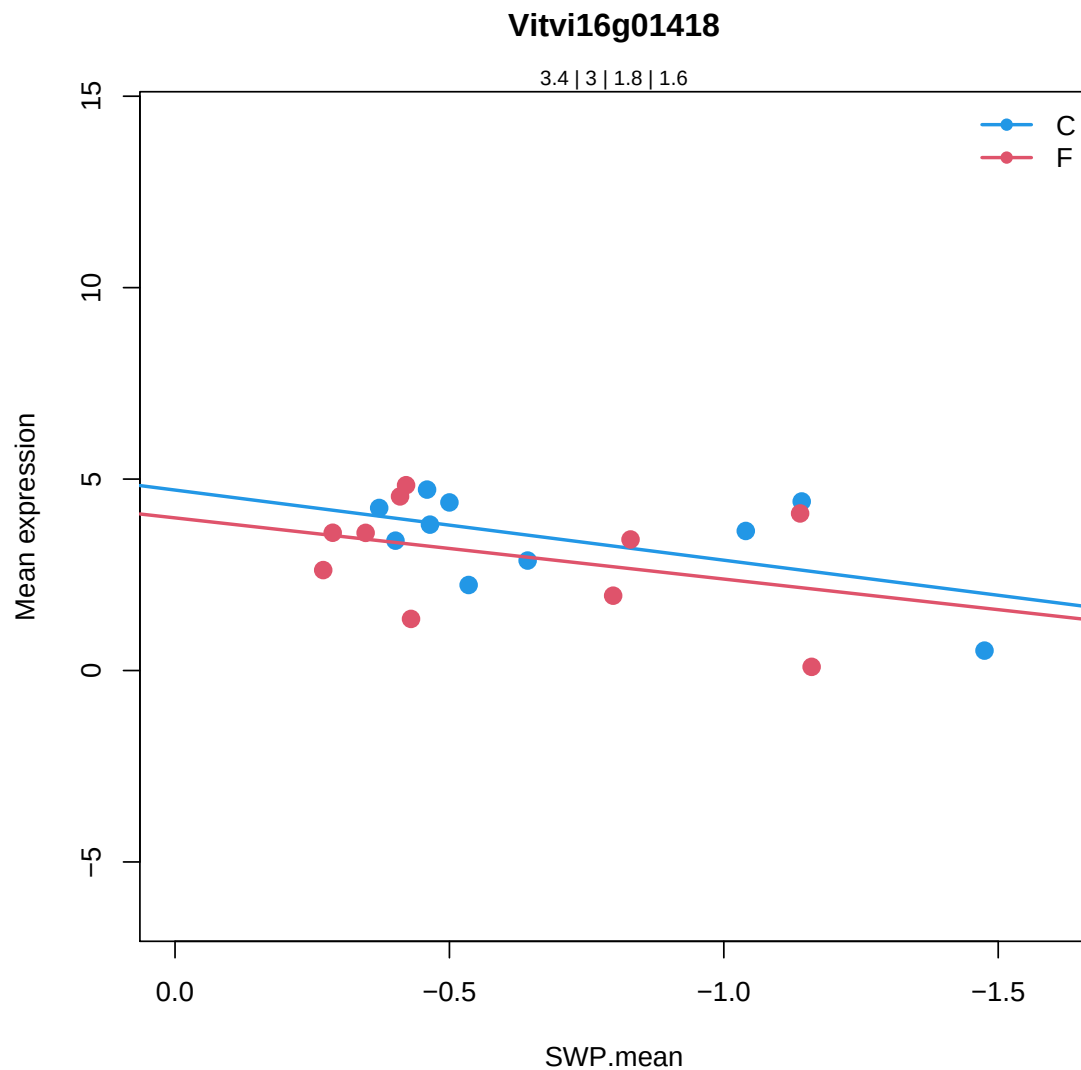
Plant invertase/pectin methylesterase inhibitor superfamily |

Chr3:18249840-18253647 FORWARD LENGTH=598 |

201606

Coefficients for Vitvi16g01418.

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



8.1.32 Vitvi11g00708: Type1

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

Vitvi11g00708

35.2

not assigned.unknown

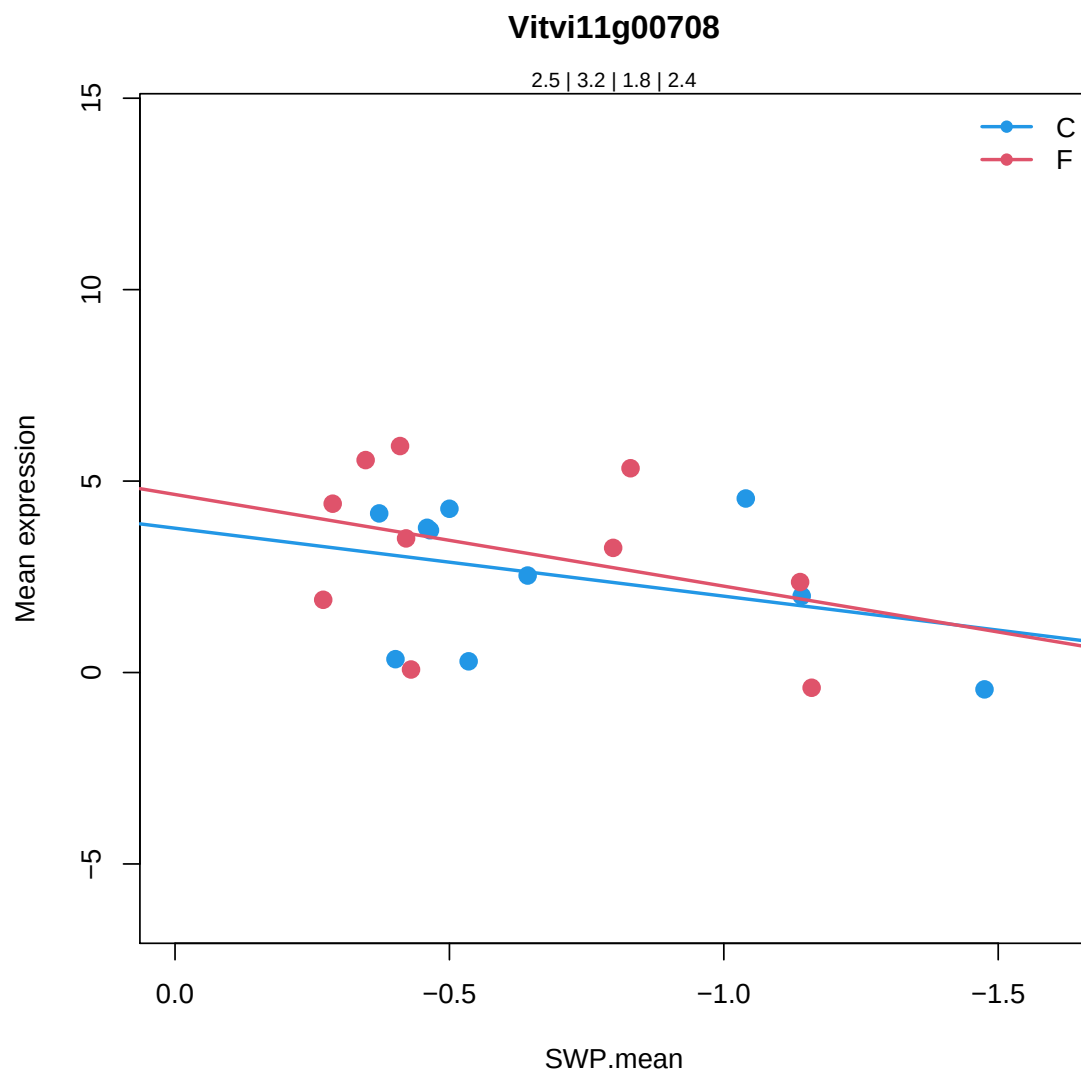
early nodulin-like protein 15 |

Chr4:15401798-15402426 FORWARD LENGTH=177 |

201606

Coefficients for Vitvi11g00708.

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



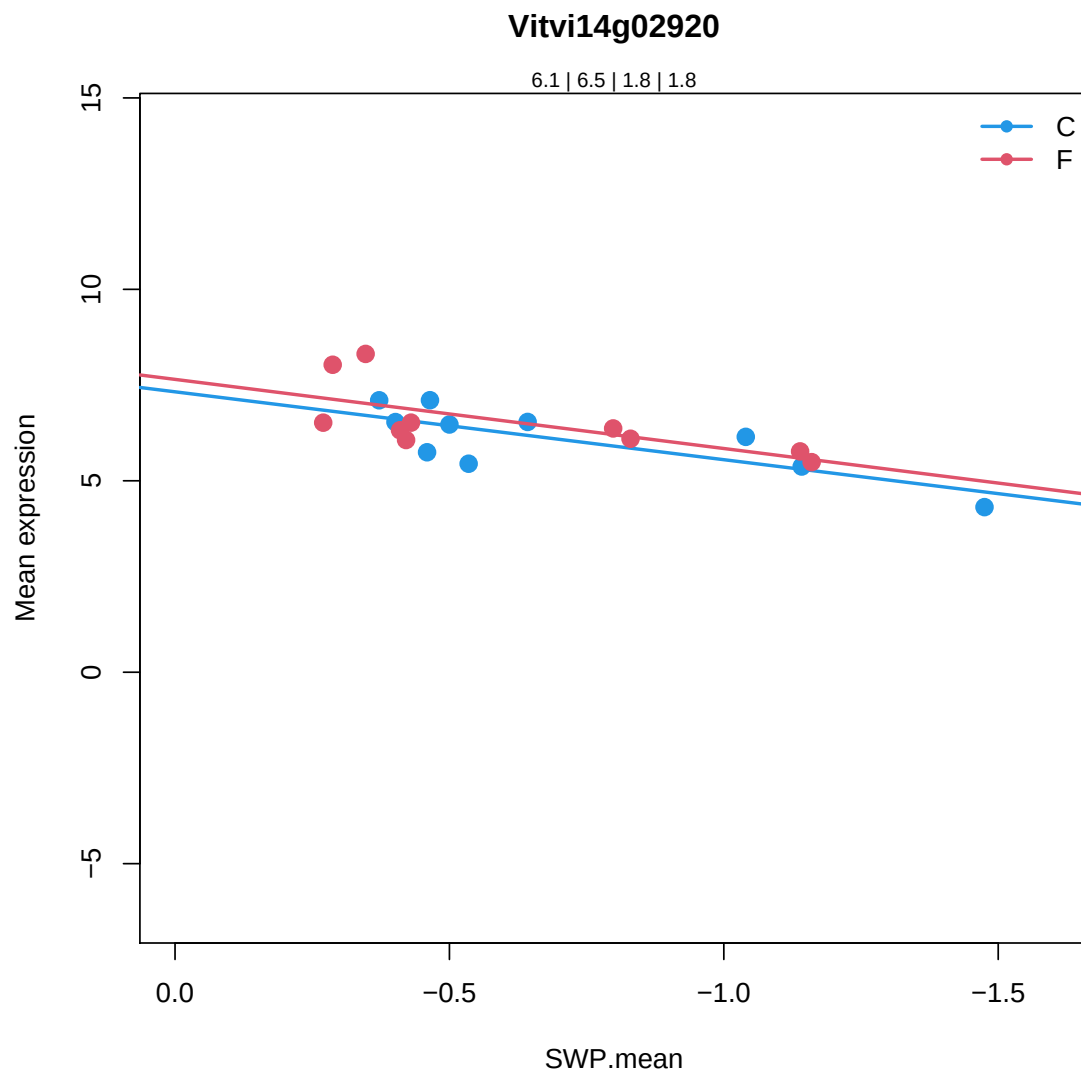
8.1.33 Vitvi14g02920: * Type1

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

```
Vitvi14g02920
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi14g02920.

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



8.1.34 Vitvi11g00417: * Type1

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

Vitvi11g00417

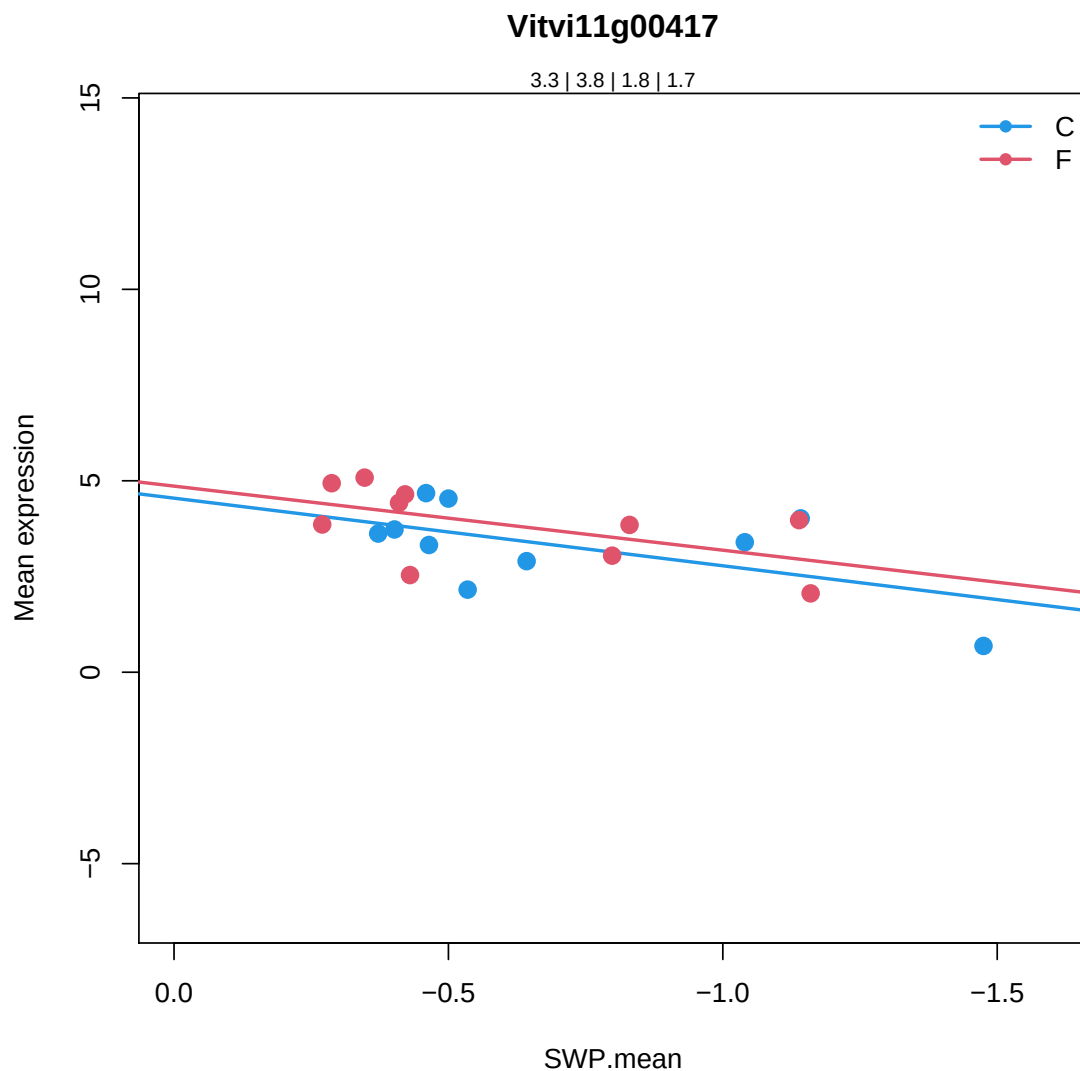
35.2

not assigned.unknown

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

Coefficients for Vitvi11g00417.

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



8.1.35 Vitvi19g00445: Type1

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

Vitvi19g00445

26.19

misc.plastocyanin-like

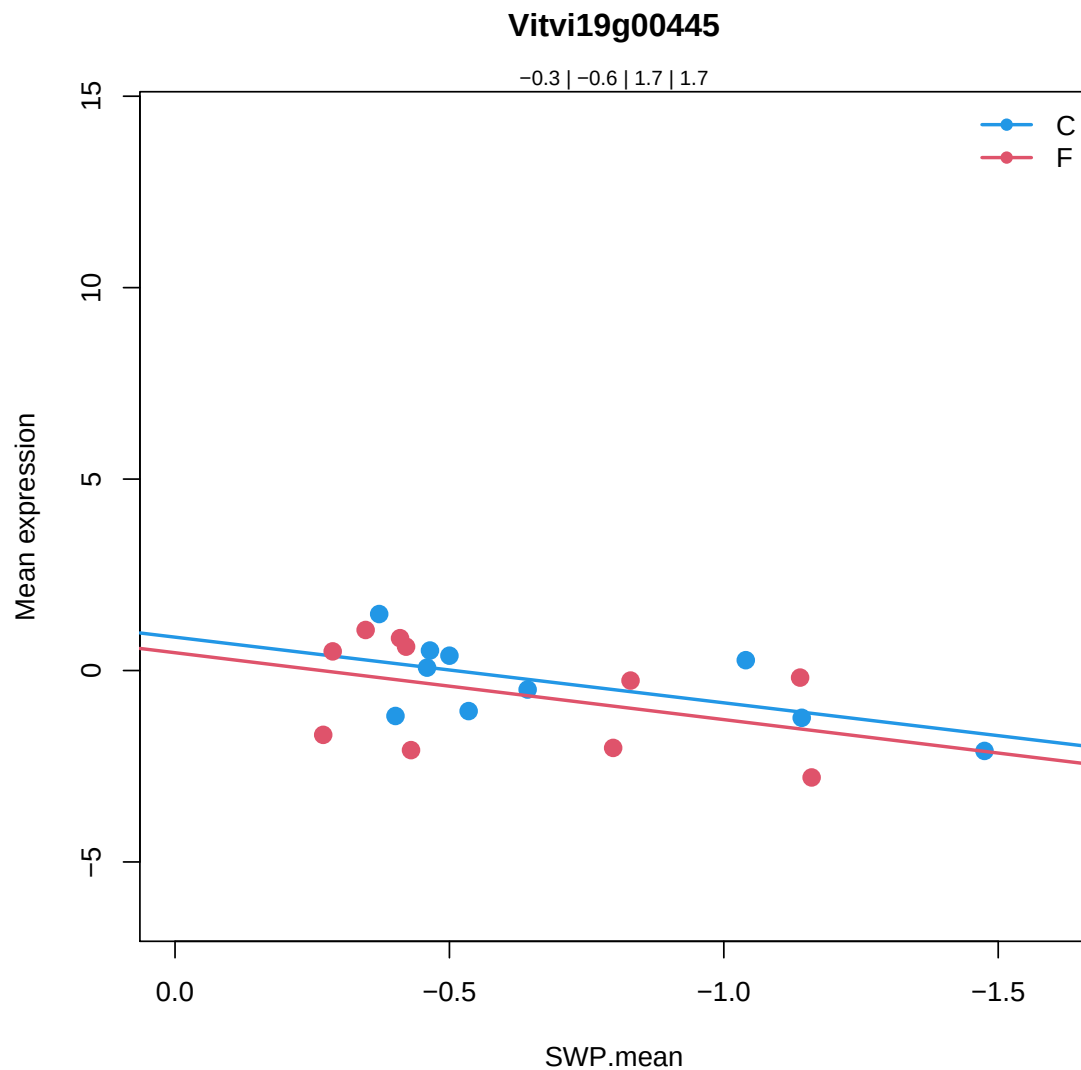
early nodulin-like protein 9 |

Chr3:7186754-7187453 REVERSE LENGTH=203 |

201606

Coefficients for Vitvi19g00445.

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



8.1.36 Vitvi02g00327: Type1

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

Vitvi02g00327

31.1

cell.organisation

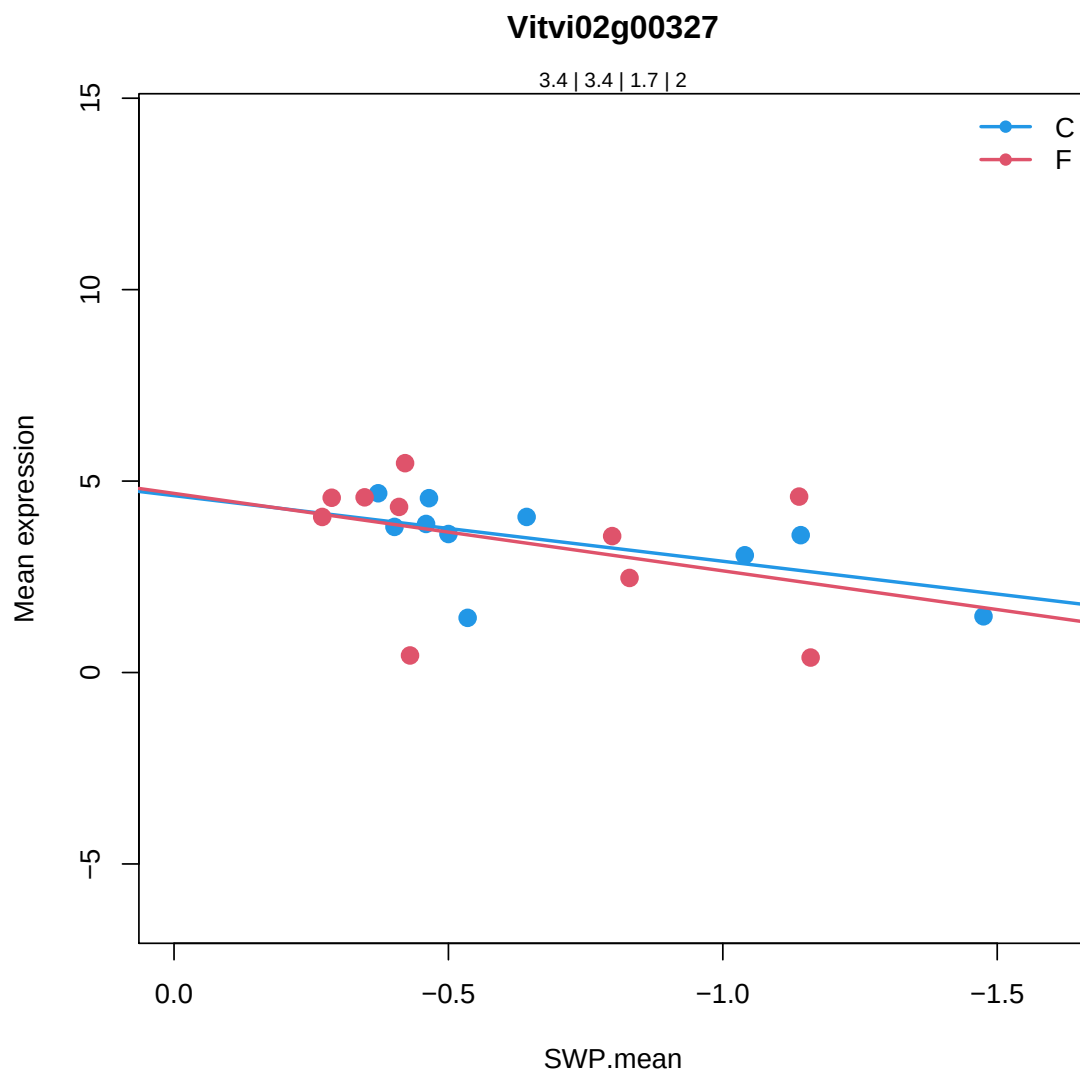
tubulin beta 8 |

Chr5:8042962-8044528 FORWARD LENGTH=449 |

201606

Coefficients for Vitvi02g00327.

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



8.1.37 Vitvi14g00483: Type1

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

Vitvi14g00483

27.3.40

RNA.regulation of transcription.AUX/IAA family

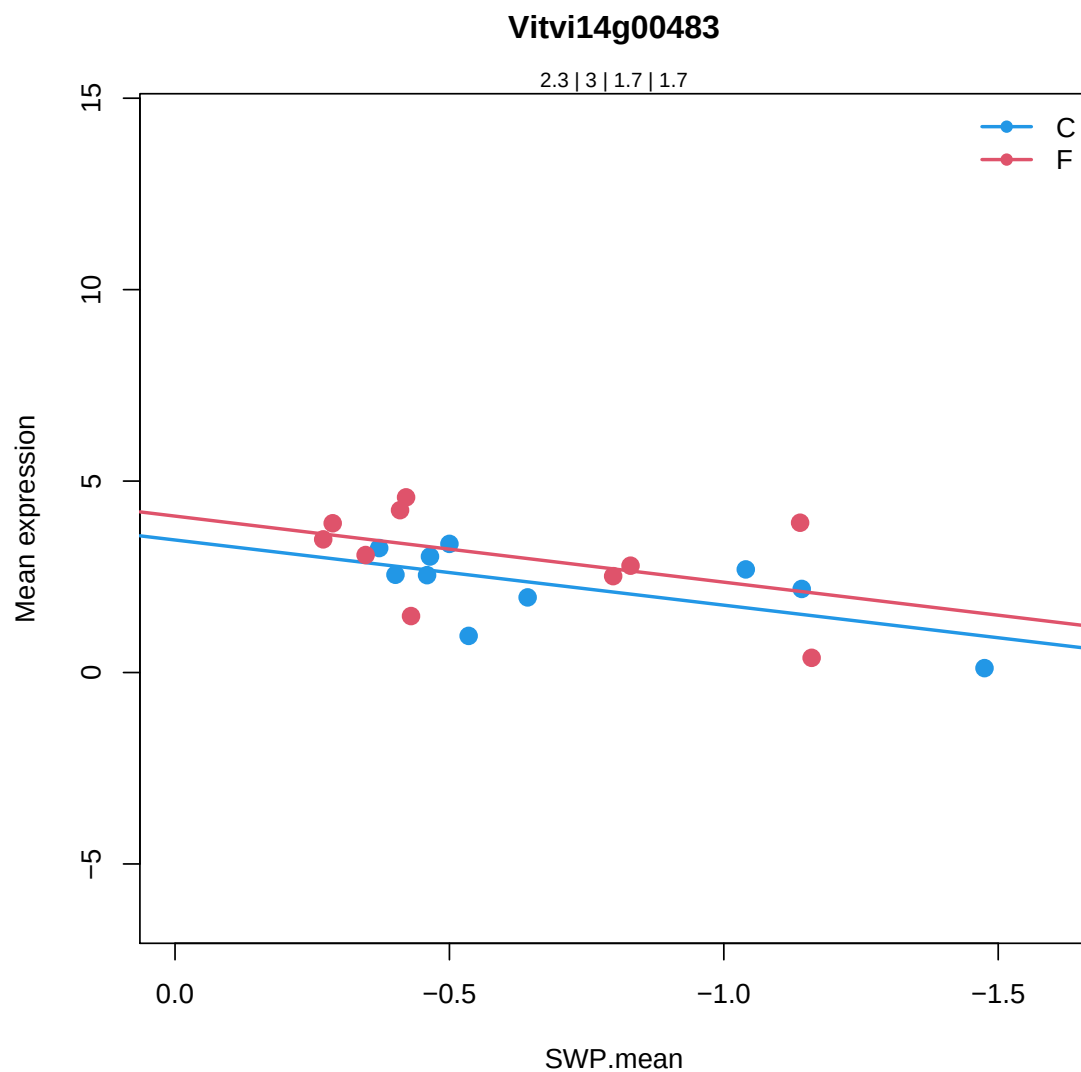
AUX/IAA transcriptional regulator family protein |

Chr5:17550465-17551206 FORWARD LENGTH=186 |

201606

Coefficients for Vitvi14g00483.

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



8.1.38 Vitvi04g00005: * Type1

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

Vitvi04g00005

35.2

not assigned.unknown

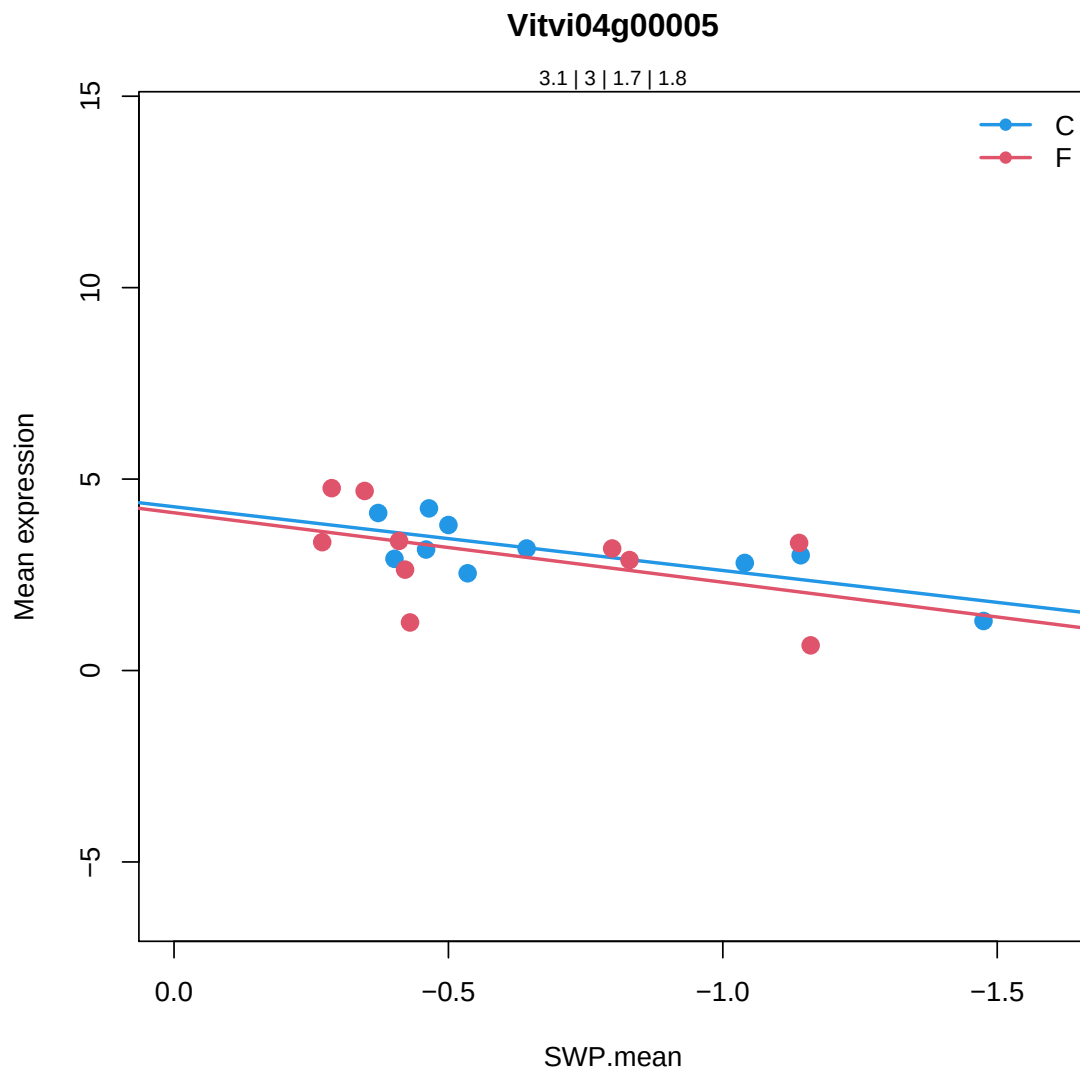
Avr9/Cf-9 rapidly elicited protein |

Chr1:19407559-19408185 REVERSE LENGTH=208 |

201606

Coefficients for Vitvi04g00005.

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



8.1.39 Vitvi13g01937: Type1

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

Vitvi13g01937

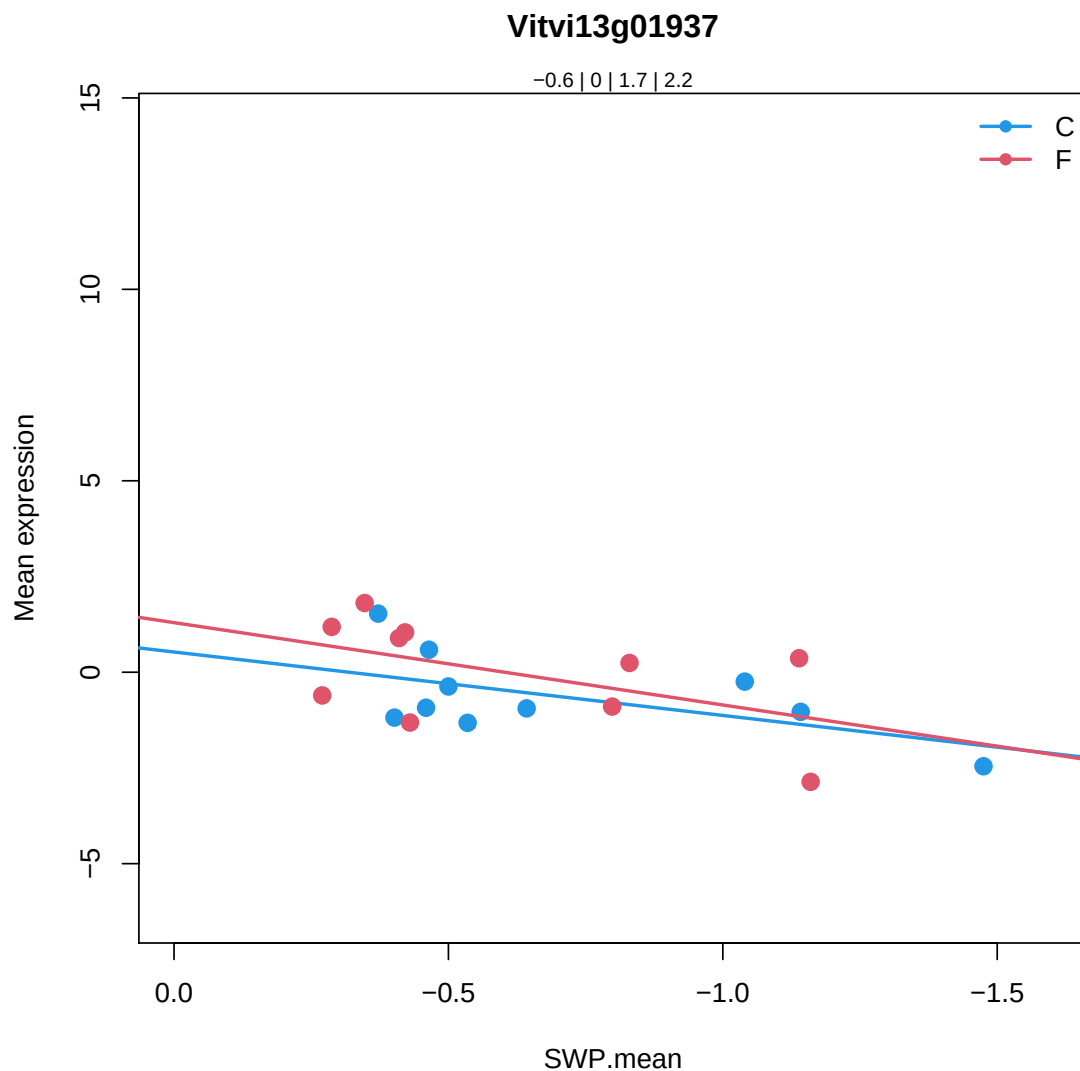
35.2

not assigned.unknown

Unknown Protein IPR007750 Protein of unknown function DUF674

Coefficients for Vitvi13g01937.

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



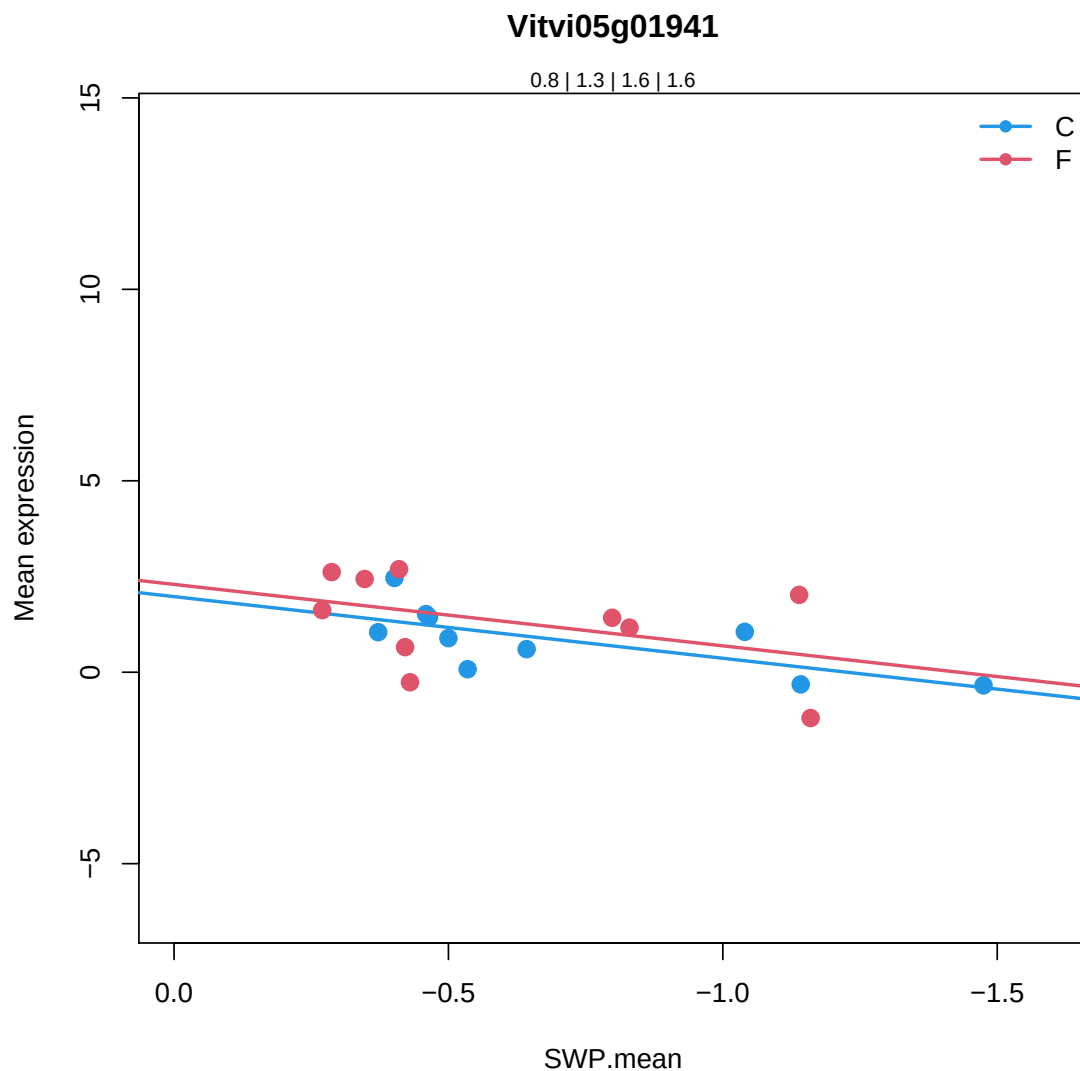
8.1.40 Vitvi05g01941: Type1

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

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

Coefficients for Vitvi05g01941.

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



8.1.41 Vitvi18g02815: Type1

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

Vitvi18g02815

26.28

misc.GDSL-motif lipase

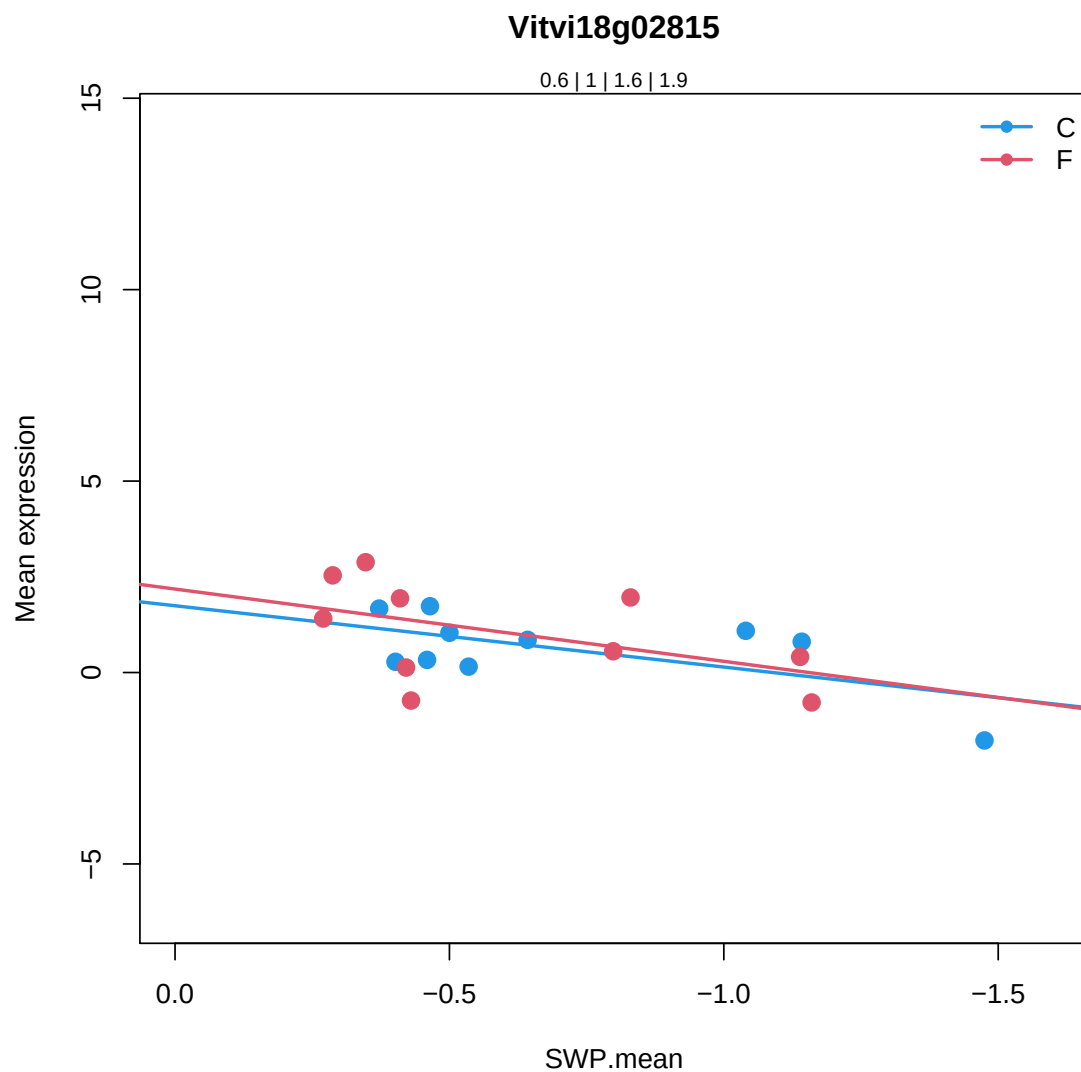
GDSL-like Lipase/Acylhydrolase superfamily protein |

Chr1:28499179-28500943 FORWARD LENGTH=364 |

201606

Coefficients for Vitvi18g02815.

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



8.1.42 Vitvi11g00178: * Type1

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

Vitvi11g00178

26.3.2

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

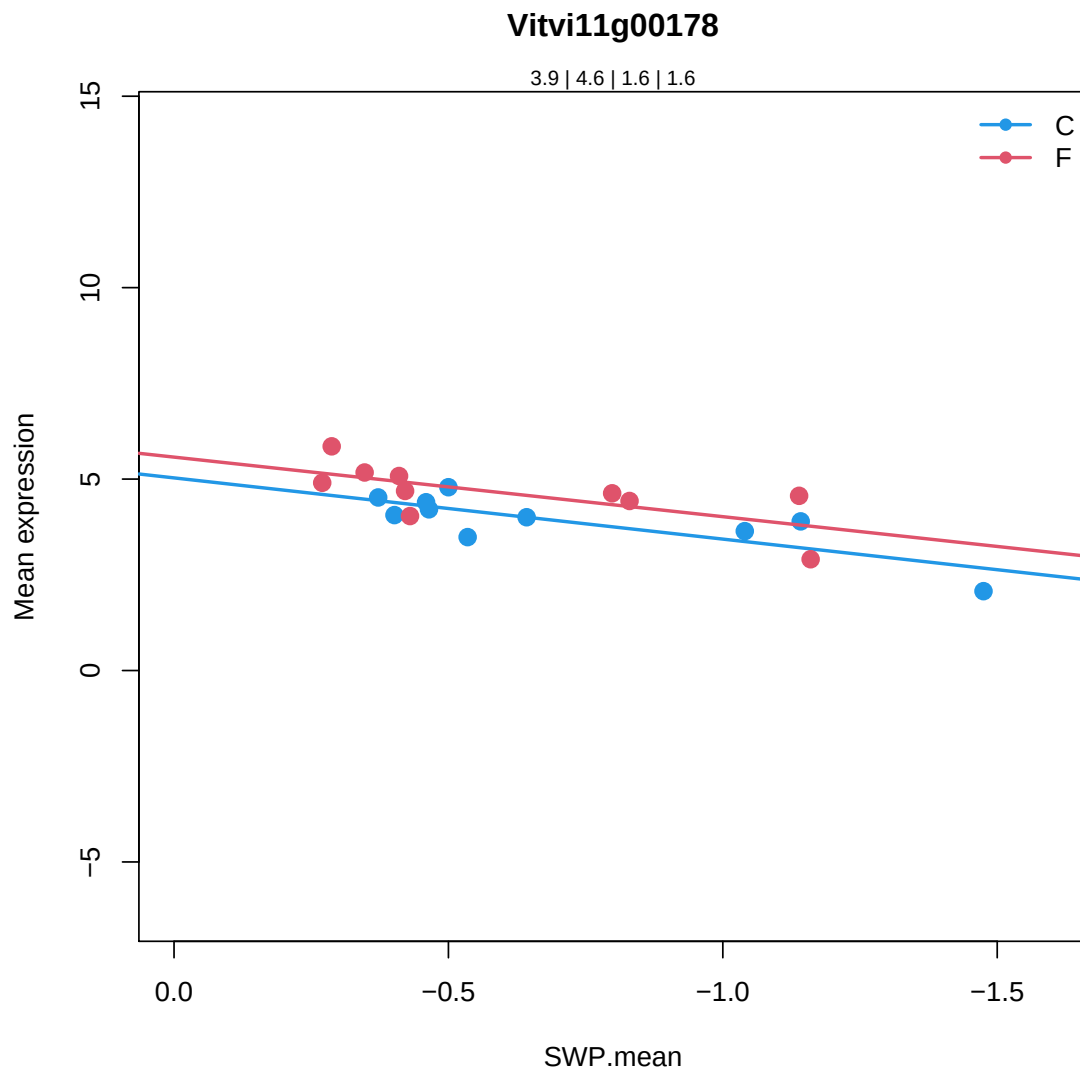
beta galactosidase 1 |

Chr3:4511192-4515756 FORWARD LENGTH=847 |

201606

Coefficients for Vitvi11g00178.

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



8.1.43 Vitvi17g00217: Type1

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

Vitvi17g00217

20.1.7.5

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

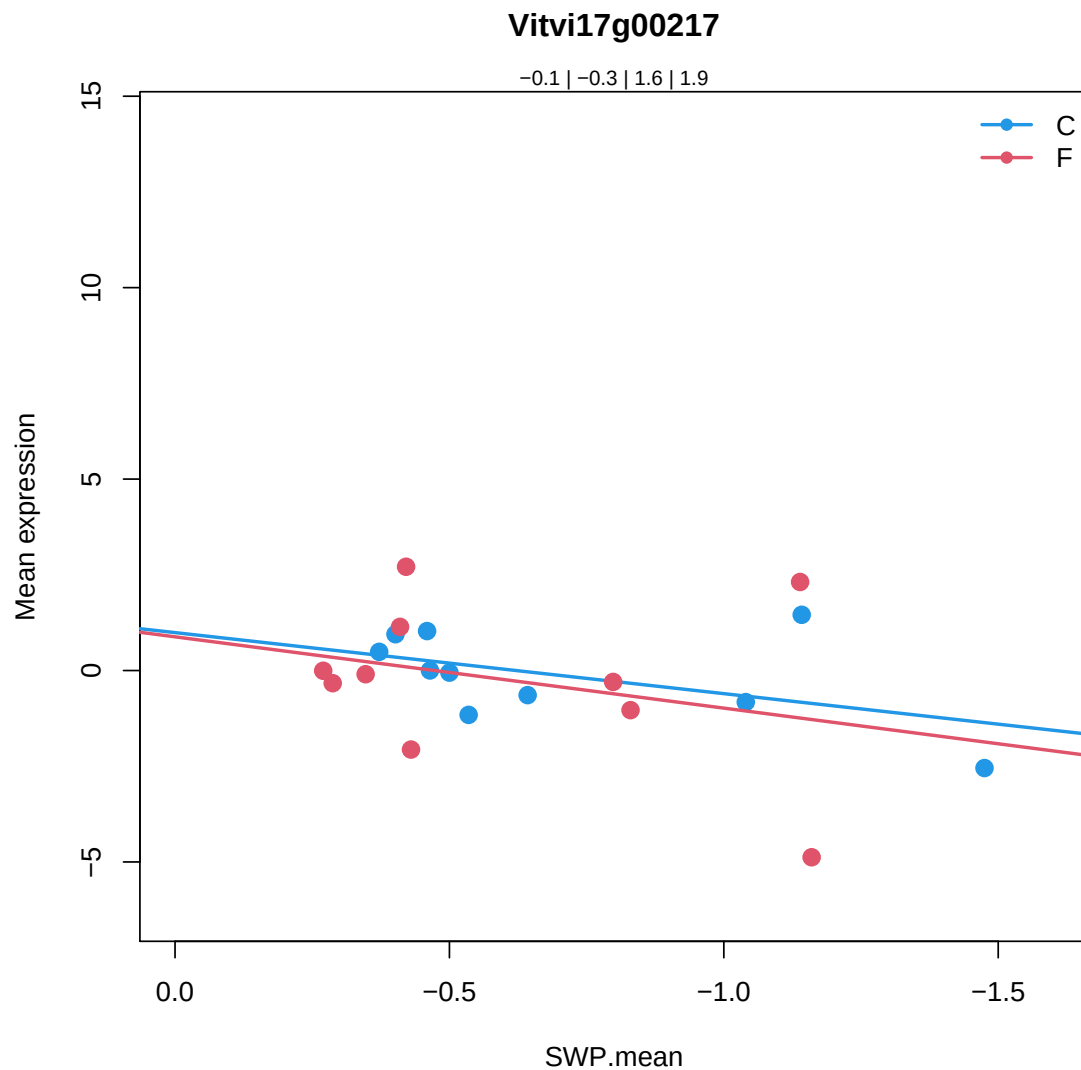
Pathogenesis-related thaumatin superfamily protein |

Chr1:6277024-6278005 REVERSE LENGTH=243 |

201606

Coefficients for Vitvi17g00217.

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



8.1.44 Vitvi08g01789: Type1

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

Vitvi08g01789

26.3.5

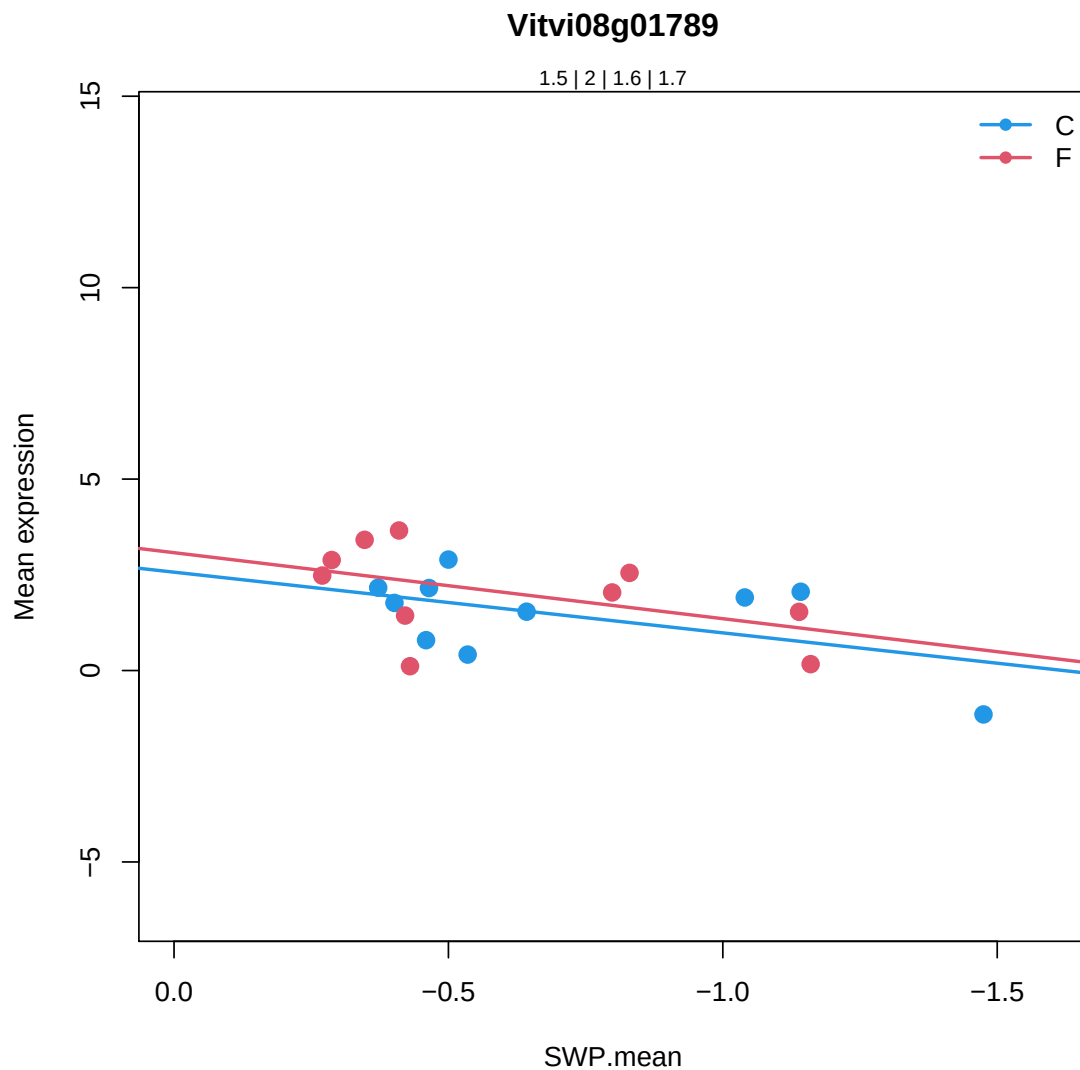
misc.gluco-, galacto- and mannosidases.glycosyl hydrolase family 5
alpha/beta-Hydrolases superfamily protein |

Chr3:1033788-1034591 FORWARD LENGTH=267 |

201606

Coefficients for Vitvi08g01789.

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



8.1.45 Vitvi13g00367: * Type1

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

Vitvi13g00367

34.13

transport.peptides and oligopeptides

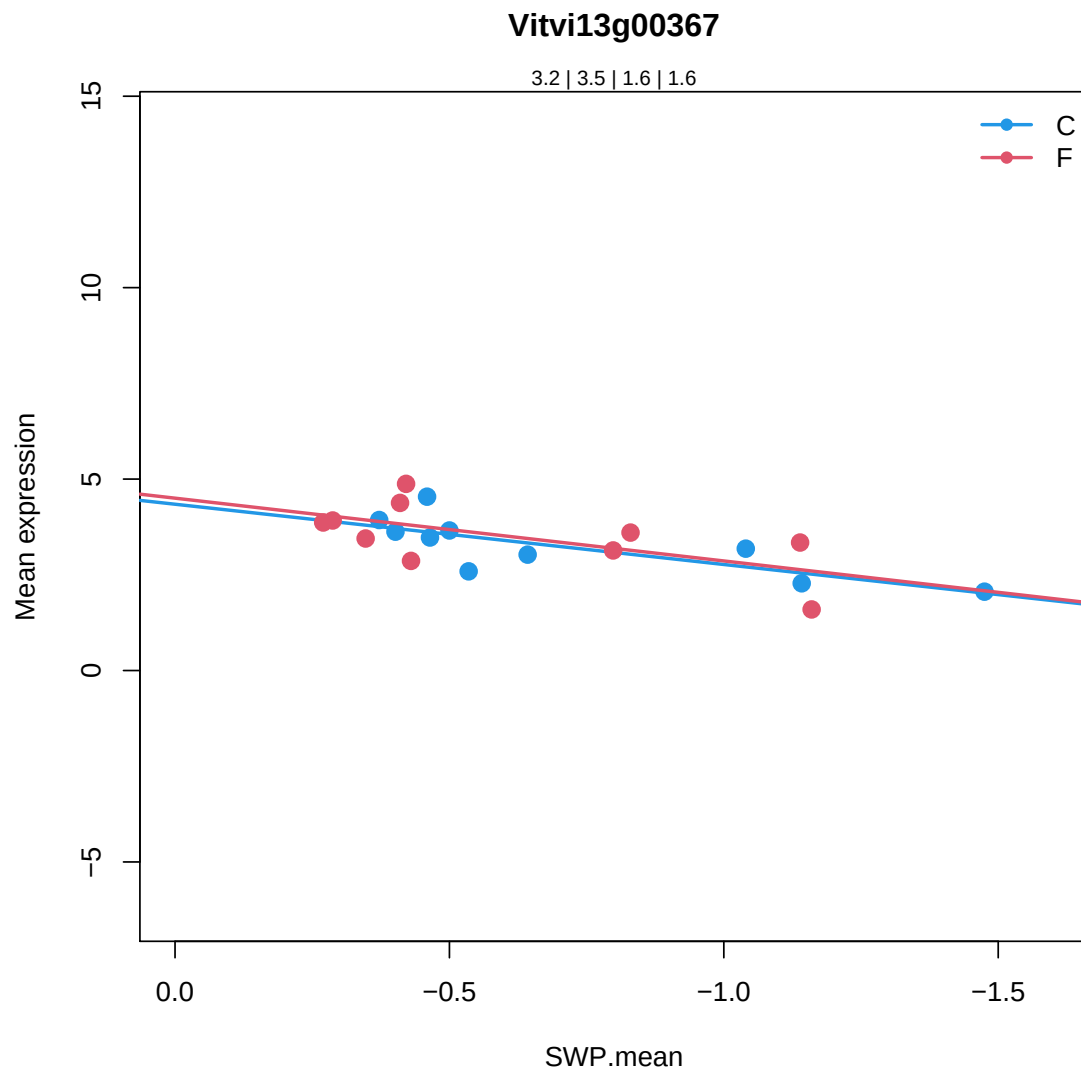
Major facilitator superfamily protein |

Chr2:15864396-15866408 REVERSE LENGTH=575 |

201606

Coefficients for Vitvi13g00367.

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



8.1.46 Vitvi13g02006: Type1

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

Vitvi13g02006

35.2

not assigned.unknown

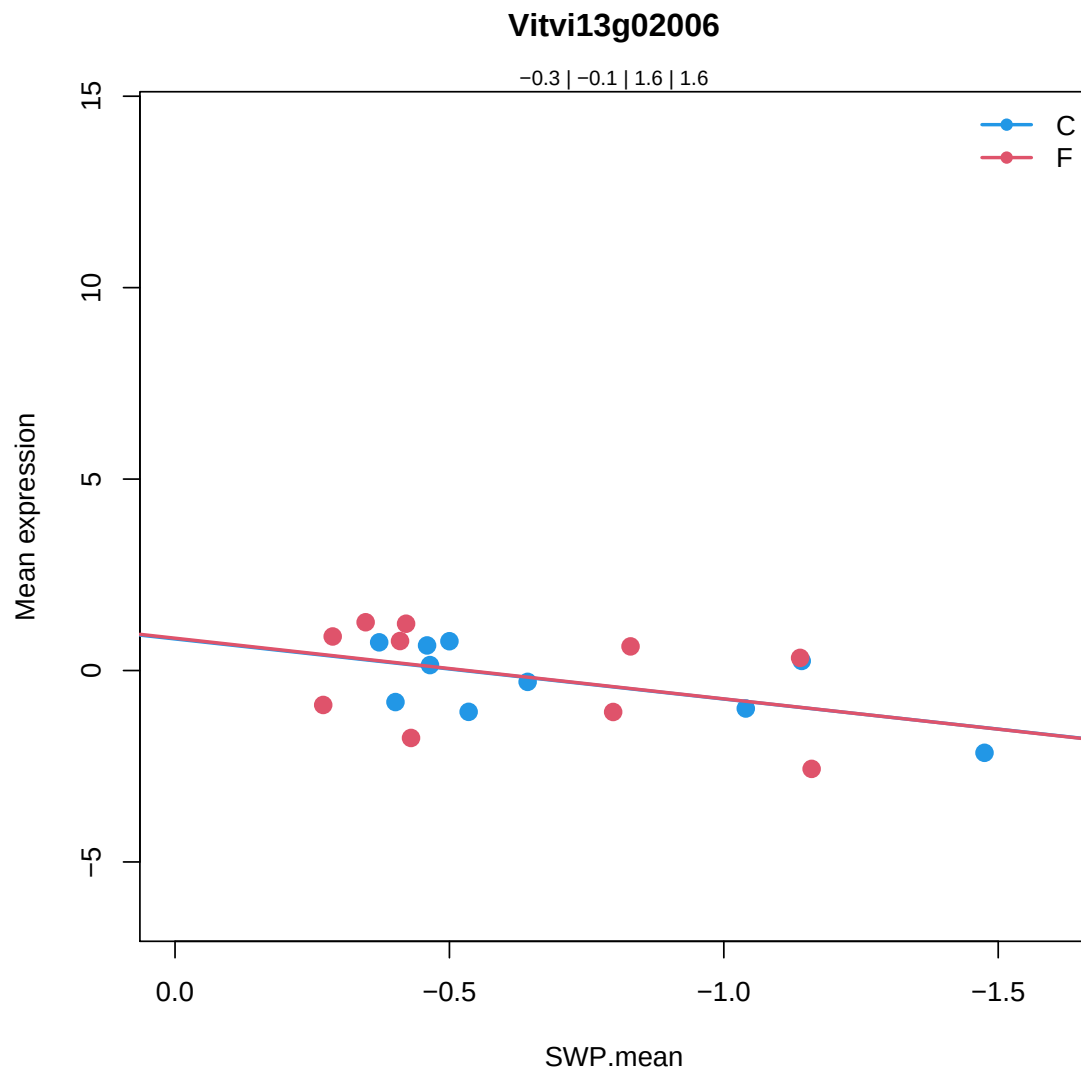
Subtilisin-like serine endopeptidase family protein |

Chr5:23858951-23862087 REVERSE LENGTH=741 |

201606

Coefficients for Vitvi13g02006.

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



8.1.47 Vitvi07g00905: Type1

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

Vitvi07g00905

30.11

signalling.light

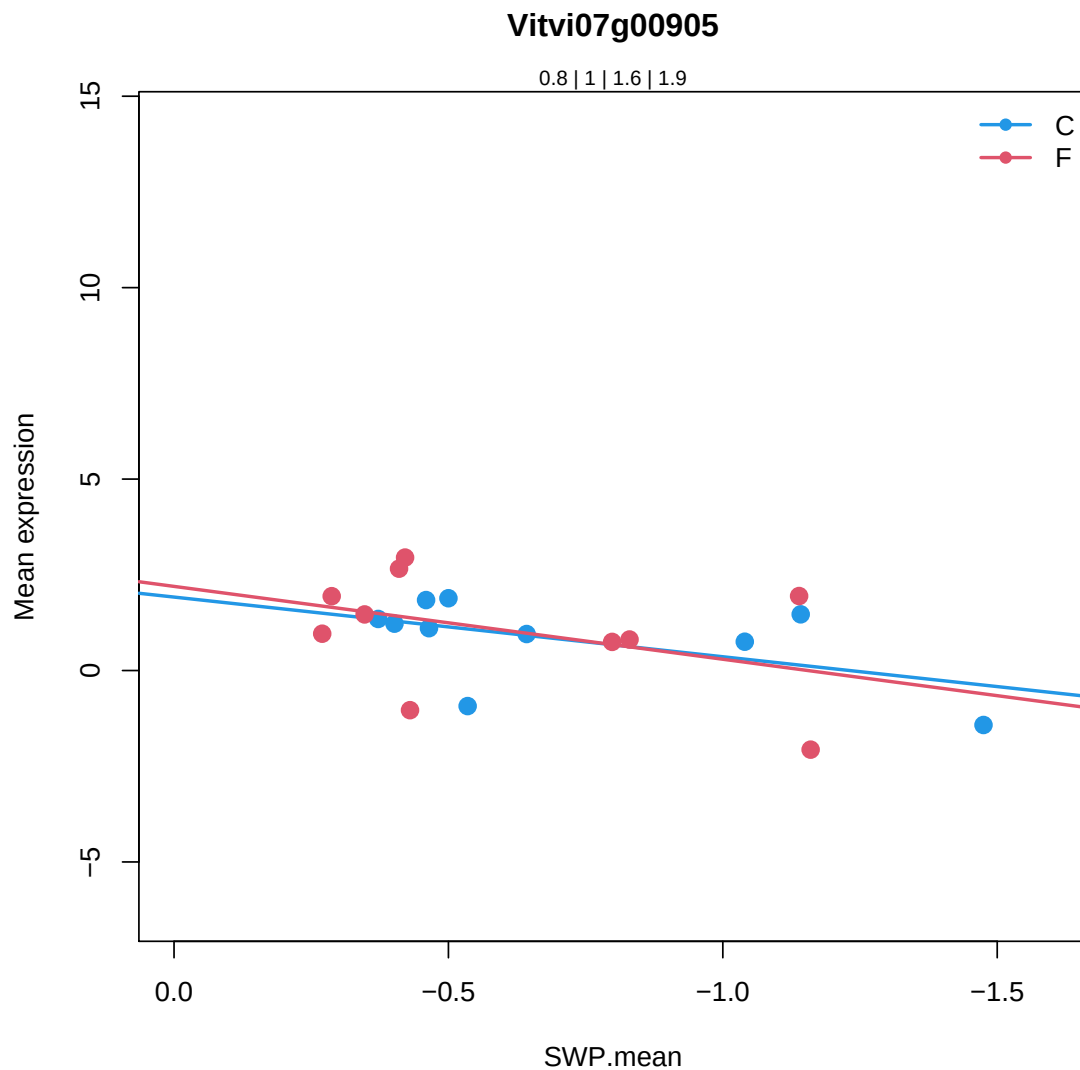
Phototropic-responsive NPH3 family protein |

Chr5:19786881-19789003 FORWARD LENGTH=614 |

201606

Coefficients for Vitvi07g00905.

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



8.1.48 Vitvi09g00177: * Type1

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

Vitvi09g00177

26.3.2

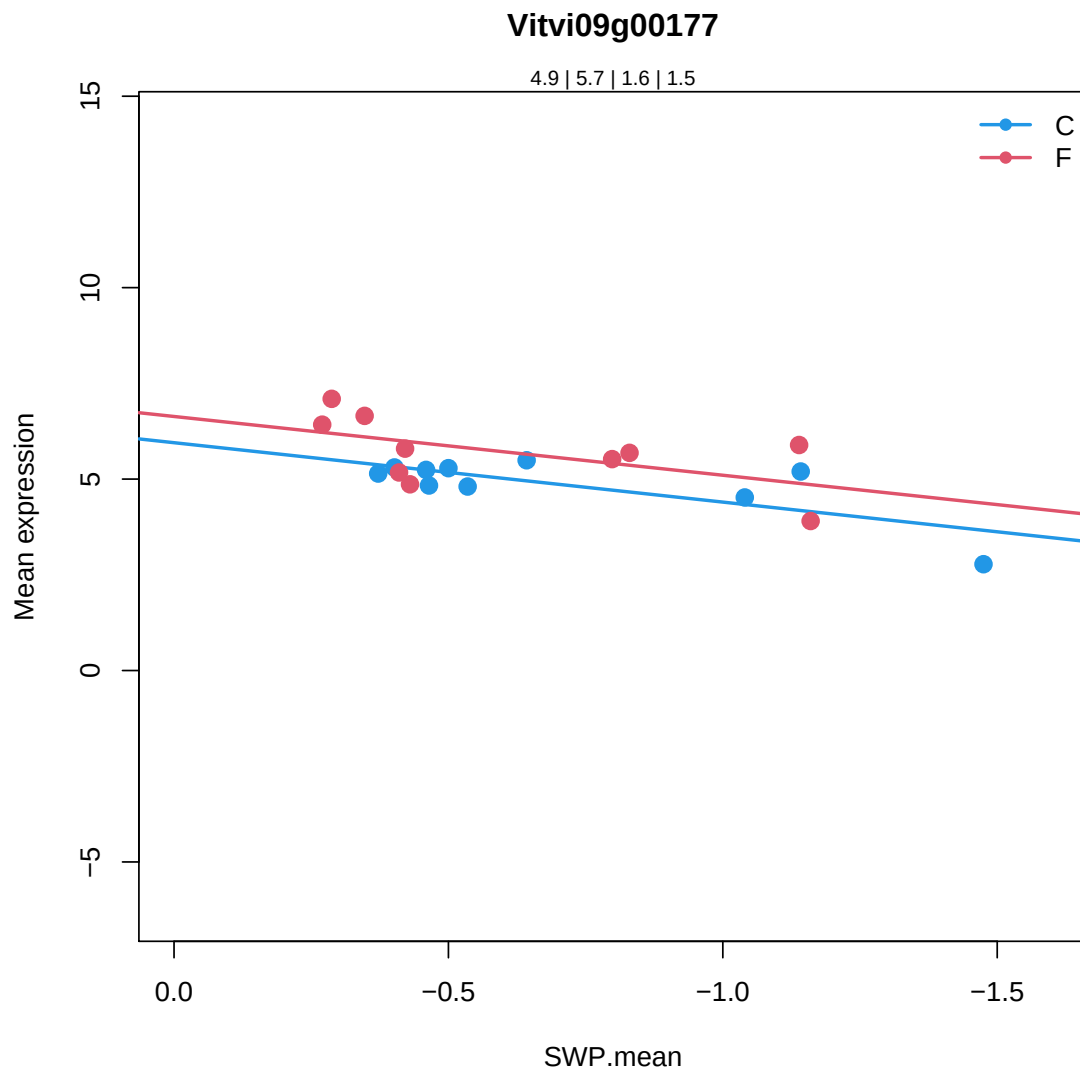
misc.gluco-, galacto- and mannosidases.beta-galactosidase
beta galactosidase 1 |

Chr3:4511192-4515756 FORWARD LENGTH=847 |

201606

Coefficients for Vitvi09g00177.

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



8.1.49 Vitvi12g02375: Type1

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

Vitvi12g02375

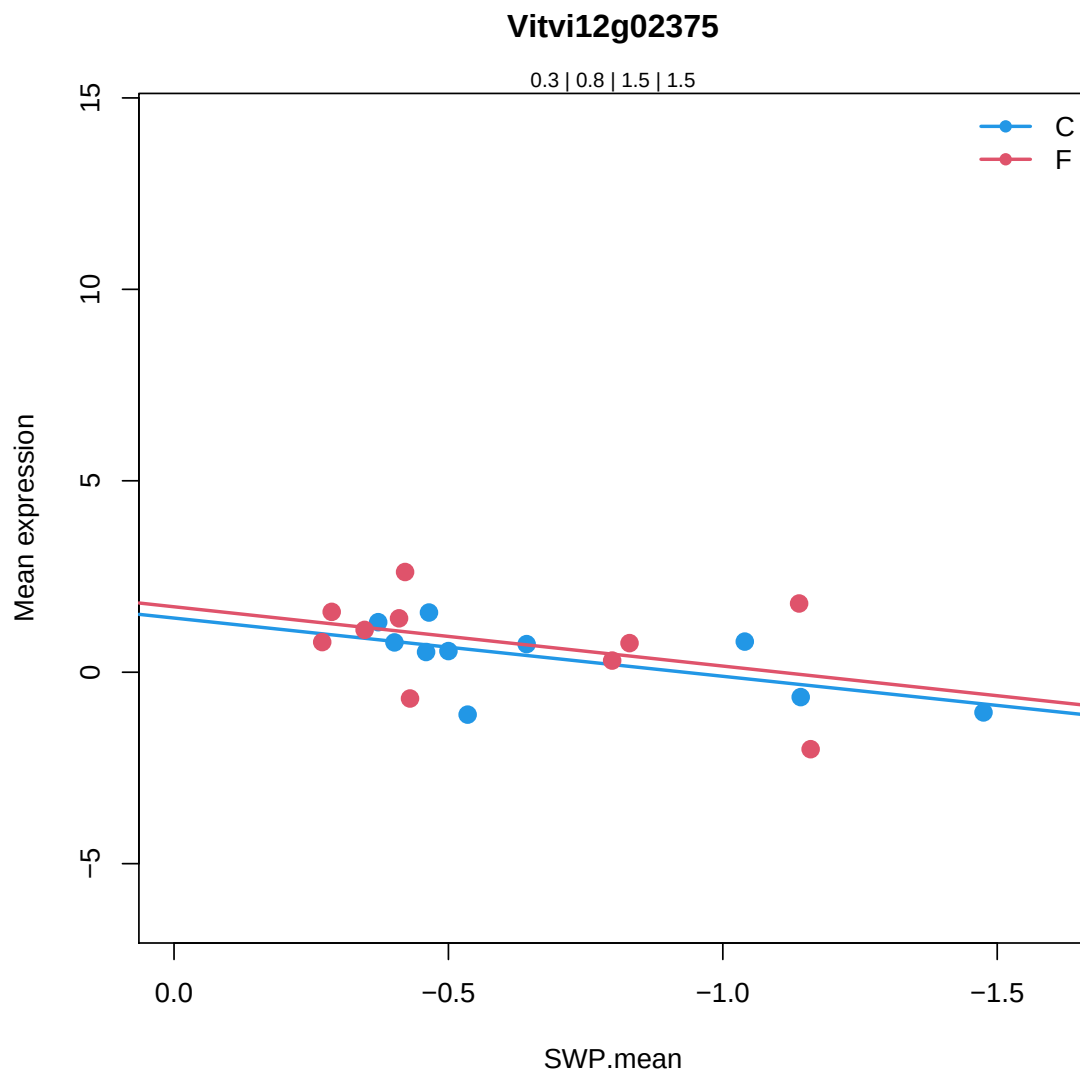
26.10

misc.cytochrome P450

NA

Coefficients for Vitvi12g02375.

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



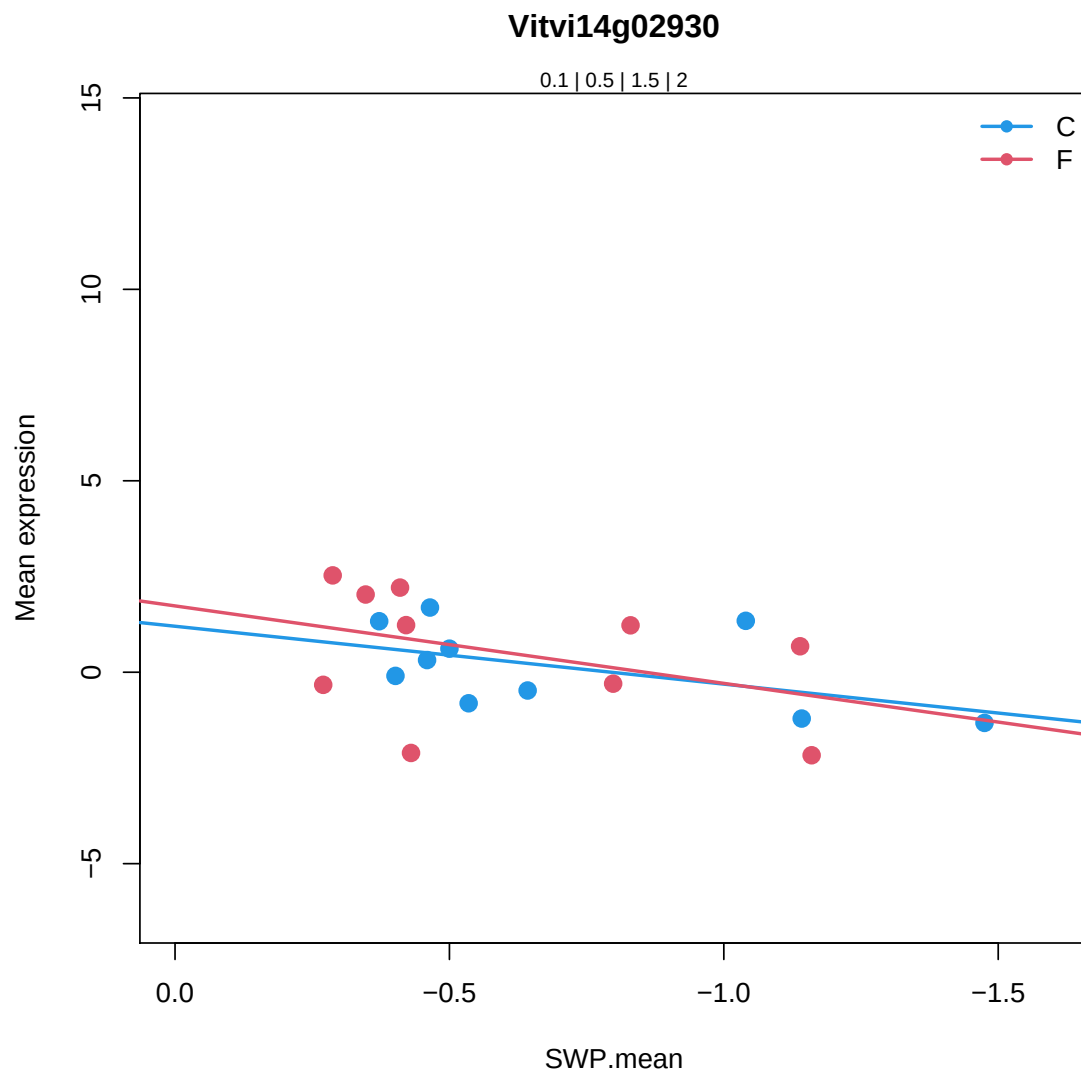
8.1.50 Vitvi14g02930: Type1

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

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

Coefficients for Vitvi14g02930.

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



8.1.51 Vitvi07g00421: Type1

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

Vitvi07g00421

27.3.32

RNA.regulation of transcription.WRKY domain transcription factor famil

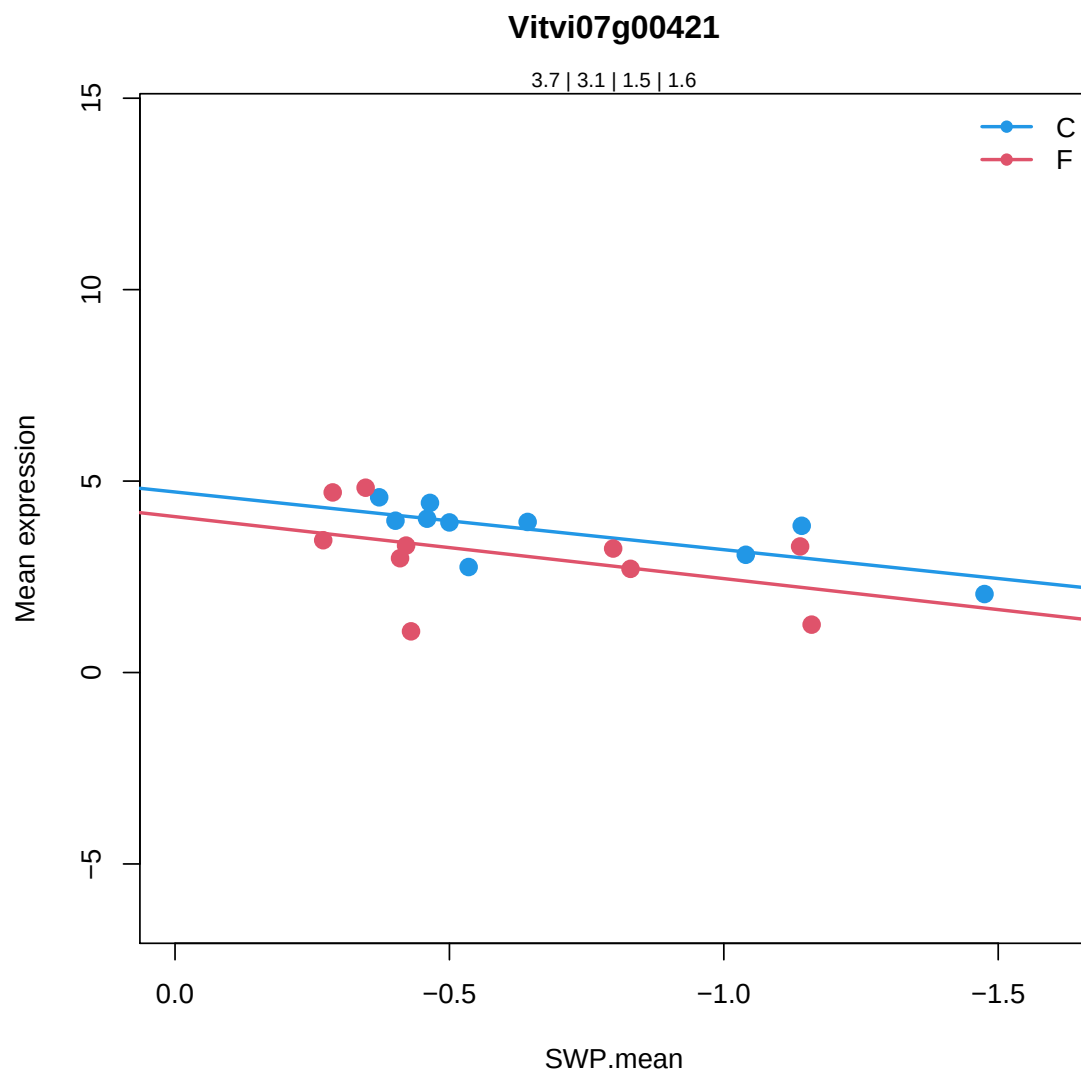
WRKY DNA-binding protein 35 |

Chr2:14693839-14696378 REVERSE LENGTH=427 |

201606

Coefficients for Vitvi07g00421.

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



8.1.52 Vitvi05g01314: * Type1

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

Vitvi05g01314

35.2

not assigned.unknown

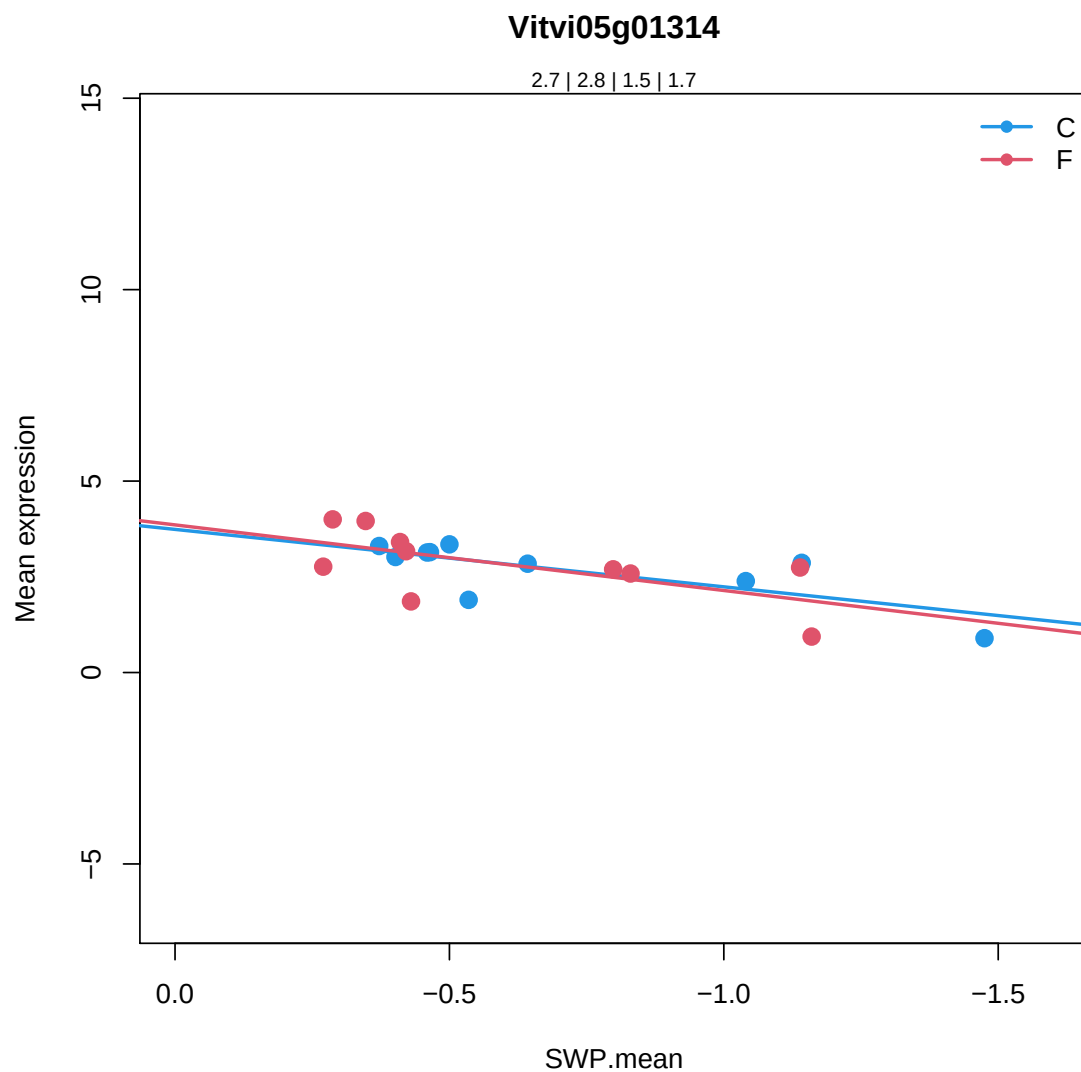
dCTP pyrophosphatase-like protein |

Chr3:9213236-9214144 FORWARD LENGTH=141 |

201606

Coefficients for Vitvi05g01314.

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



8.1.53 Vitvi02g00991: * Type1

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

Vitvi02g00991

35.2

not assigned.unknown

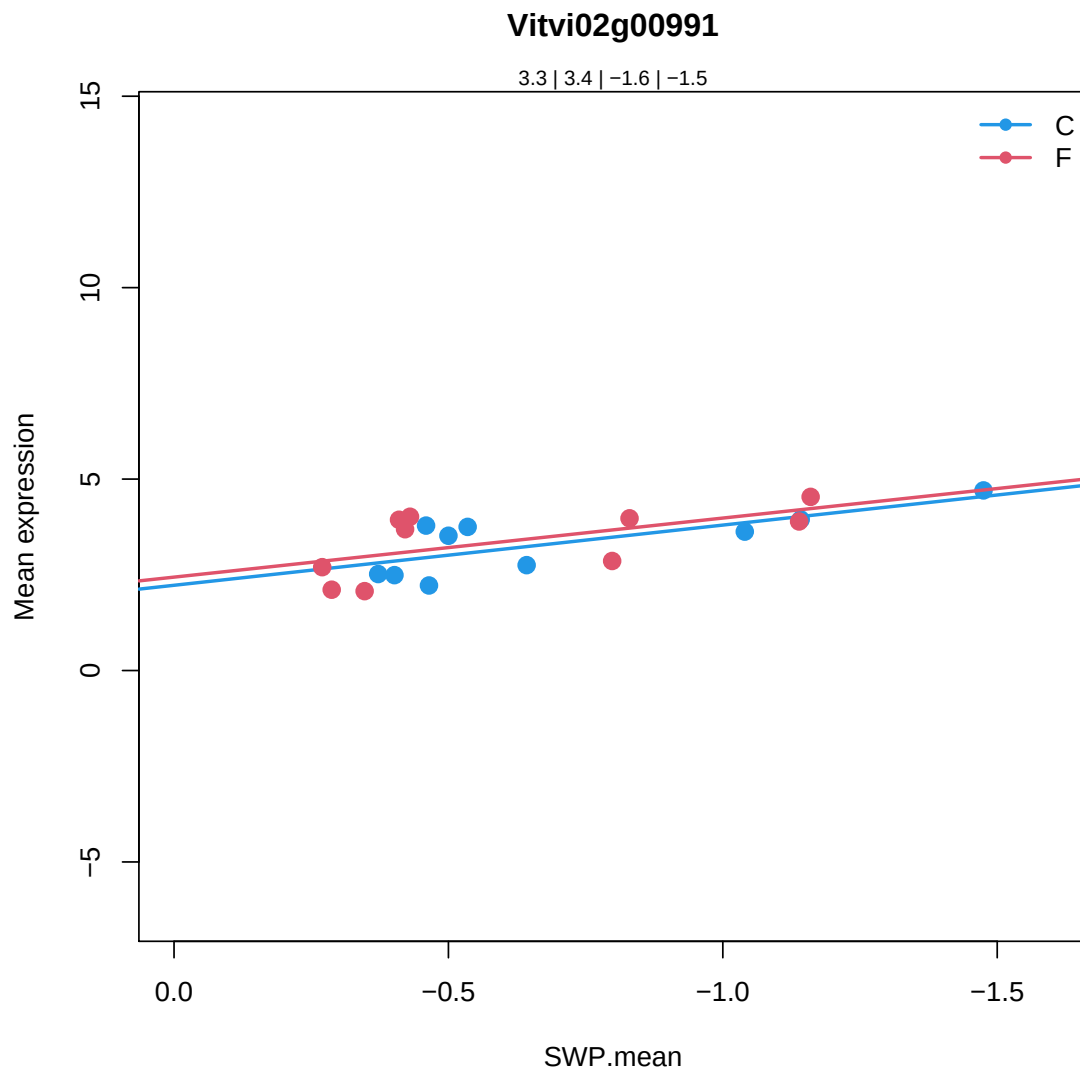
UDP-Glycosyltransferase superfamily protein |

Chr2:15417618-15419108 REVERSE LENGTH=496 |

201606

Coefficients for Vitvi02g00991.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.33156	5.382133e-14	***	8.43976e-14	***
SlopeC	-1.572287	0.008310277	**	0.2862911	
MeanF-MeanC	0.04742068	0.8646699		0.964386	
SlopeF-SlopeC	0.02977909	0.9708319		0.9999488	



8.1.54 Vitvi10g01544: * Type1

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

Vitvi10g01544

35.2

not assigned.unknown

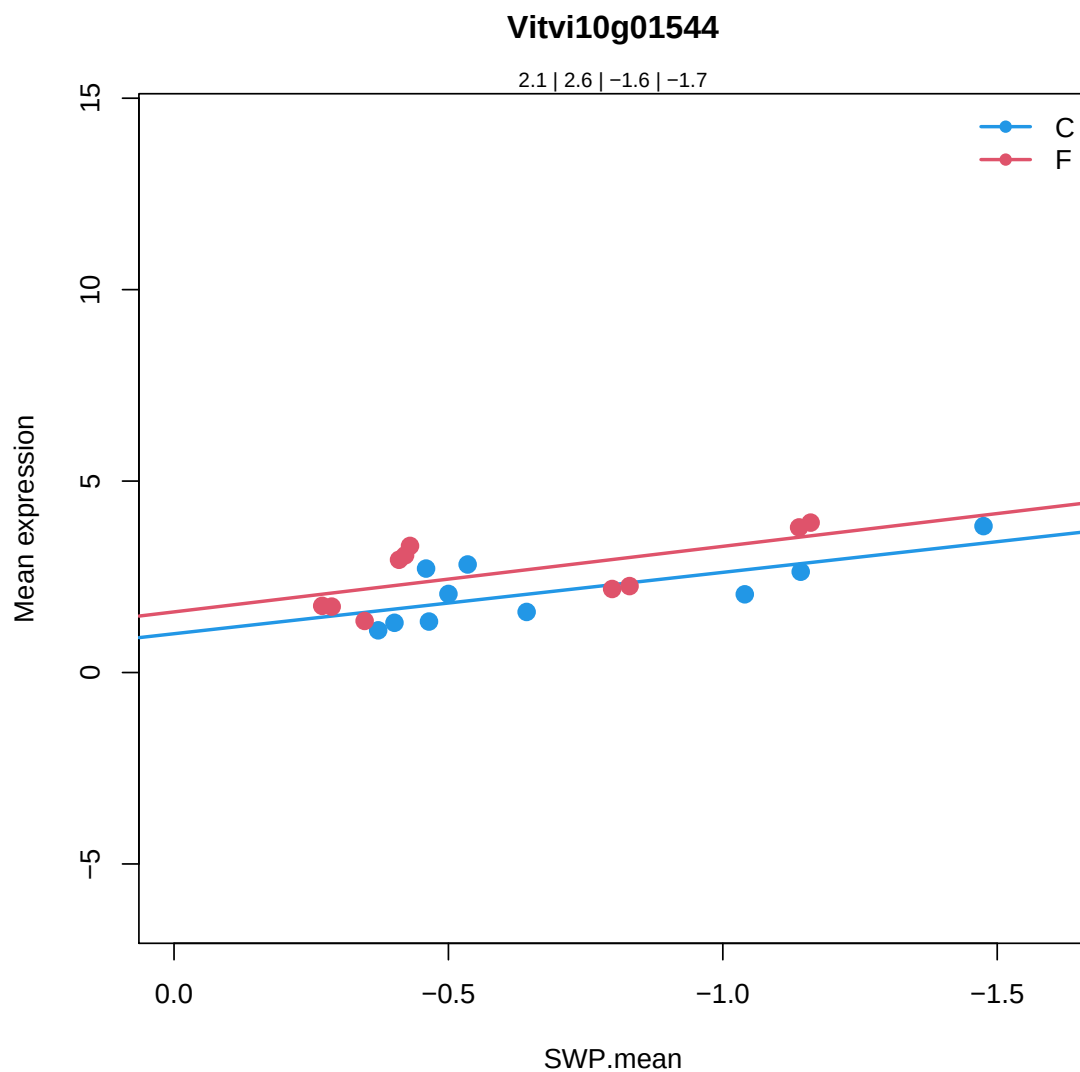
E3 ubiquitin-protein ligase |

Chr3:6965671-6967102 FORWARD LENGTH=425 |

201606

Coefficients for Vitvi10g01544.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.140199	6.191029e-10	***	7.865179e-10	***
SlopeC	-1.602621	0.009802541	**	0.3011737	
MeanF-MeanC	0.4864314	0.1050379		0.3758187	
SlopeF-SlopeC	-0.1098173	0.8973909		0.9999488	



8.1.55 Vitvi07g03049: * Type1

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

Vitvi07g03049

13.1.6.1.1

amino acid metabolism.synthesis.aromatic aa.chorismate.3-deoxy-D-arabi

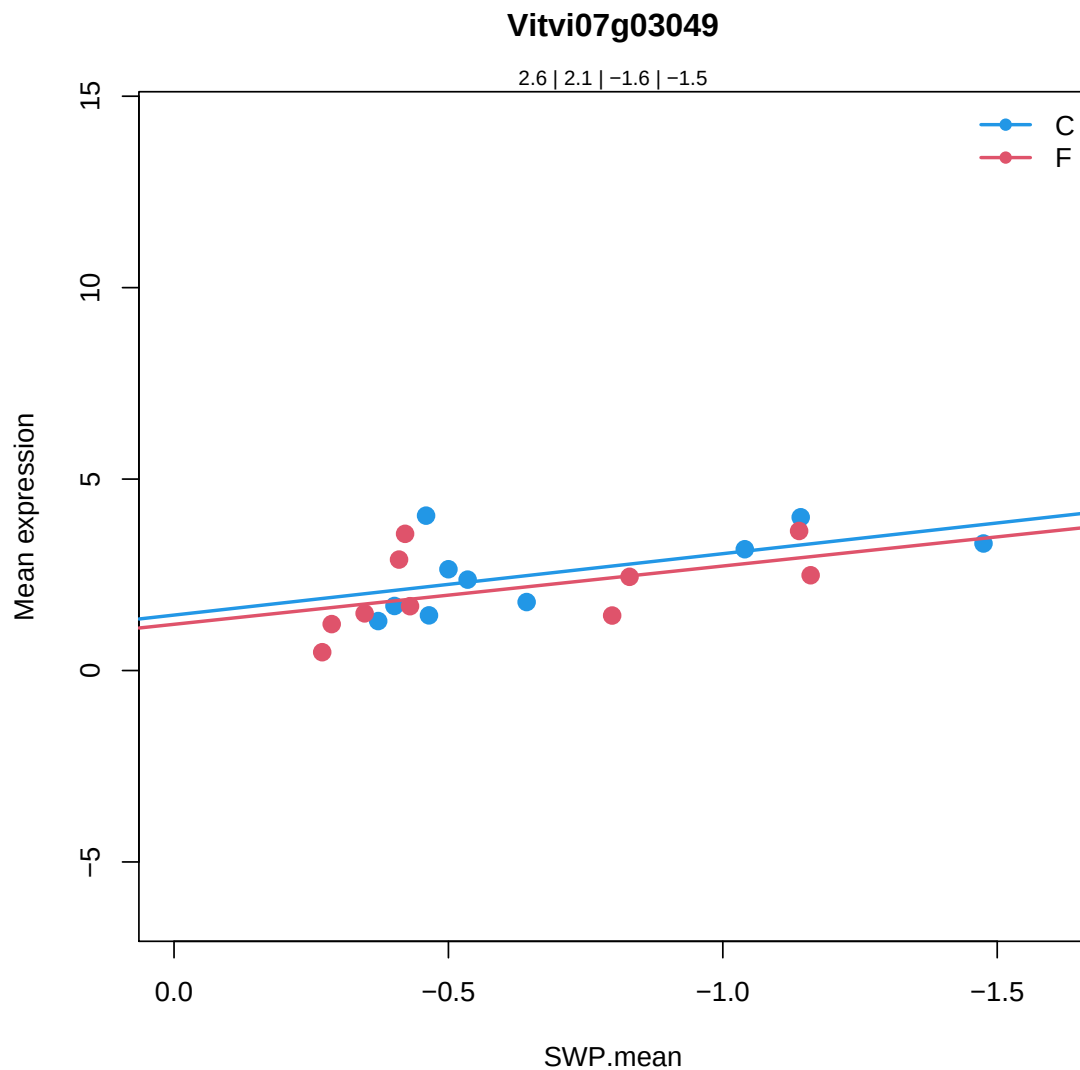
3-deoxy-D-arabino-heptulosonate 7-phosphate synthase 1 |

Chr4:18539654-18541832 FORWARD LENGTH=525 |

201606

Coefficients for Vitvi07g03049.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.575644	2.315396e-09	***	2.884451e-09	***
SlopeC	-1.603605	0.03976744	*	0.4708616	
MeanF-MeanC	-0.4410604	0.2491464		0.6091793	
SlopeF-SlopeC	0.08108974	0.9413972		0.9999488	



8.1.56 Vitvi08g00877: * Type1

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

Vitvi08g00877

10.6.2

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

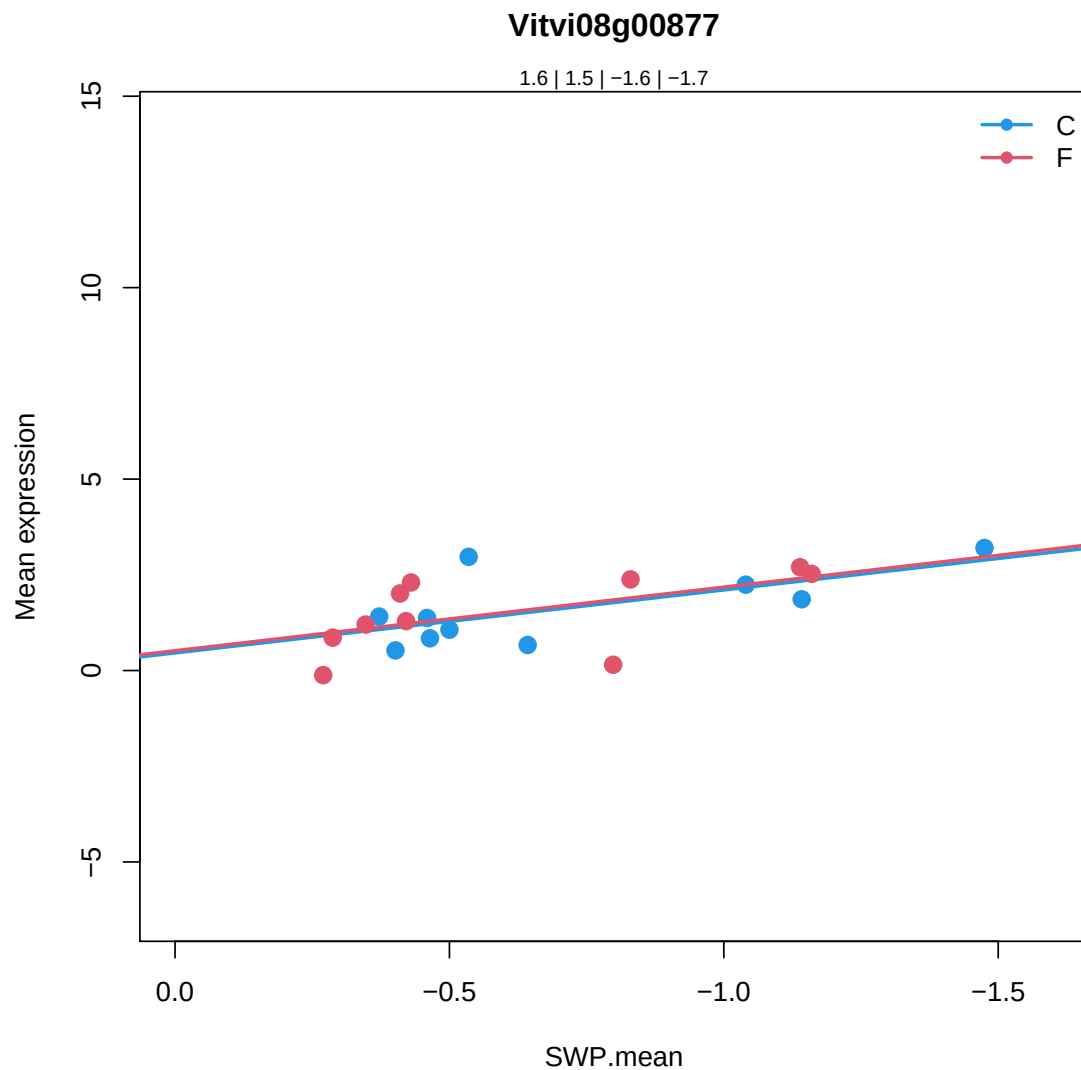
Glycosyl hydrolase superfamily protein |

Chr5:361189-362867 REVERSE LENGTH=448 |

201606

Coefficients for Vitvi08g00877.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.615209	8.009752e-07	***	9.266386e-07	***
SlopeC	-1.645206	0.0202006	*	0.3764029	
MeanF-MeanC	-0.08594045	0.7990073		0.9437748	
SlopeF-SlopeC	-0.01592818	0.9871305		0.9999488	



8.1.57 Vitvi13g00241: * Type1

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

Vitvi13g00241

21.2.1

redox.ascorbate and glutathione.ascorbate

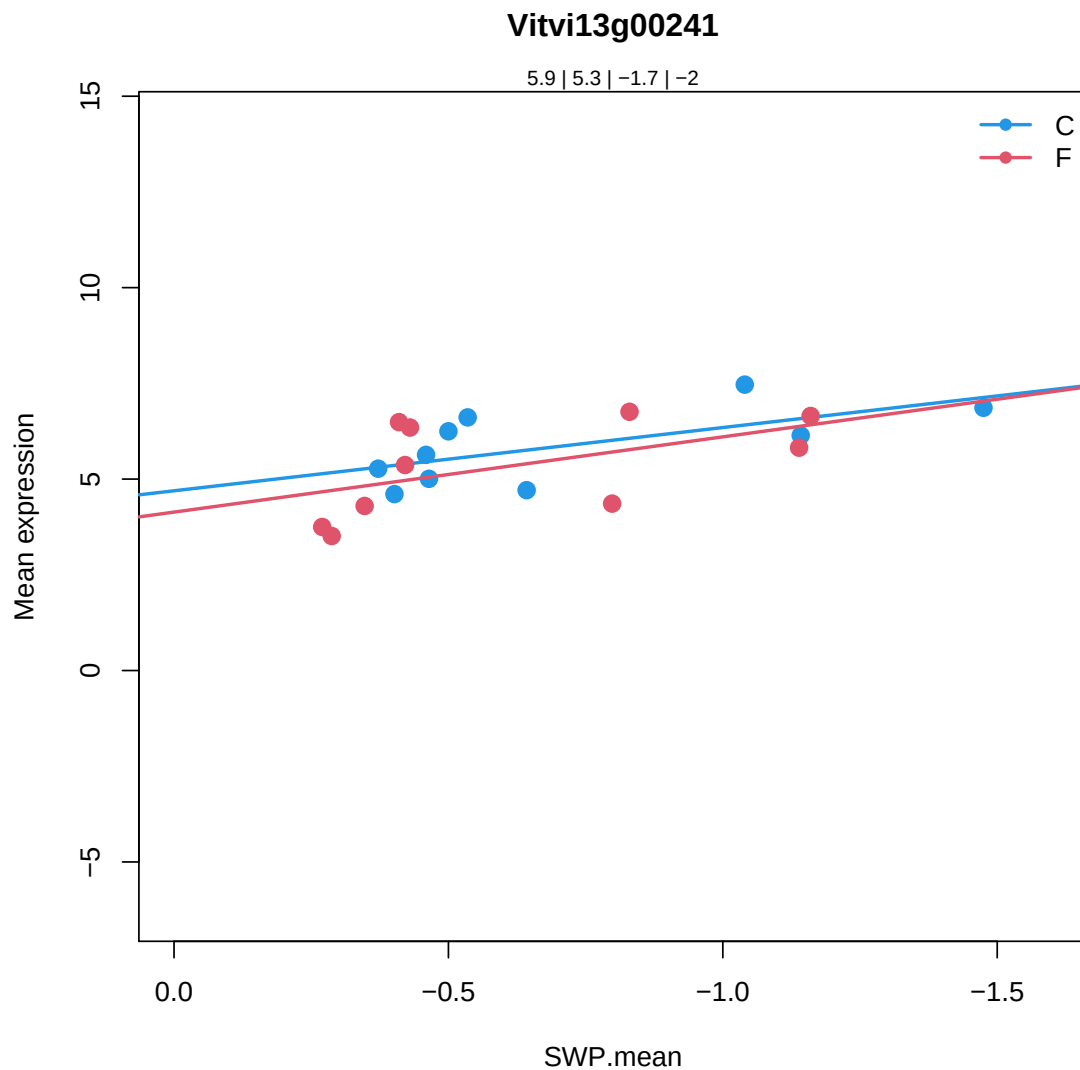
dehydroascorbate reductase 2 |

Chr1:28250255-28251237 REVERSE LENGTH=213 |

201606

Coefficients for Vitvi13g00241.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.855599	6.807616e-16	***	1.302557e-15	***
SlopeC	-1.65169	0.04266318	*	0.48214	
MeanF-MeanC	-0.5209892	0.1951408		0.5362063	
SlopeF-SlopeC	-0.3134823	0.7860909		0.9999488	



8.1.58 Vitvi13g02576: * Type1

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

Vitvi13g02576

35.2

not assigned.unknown

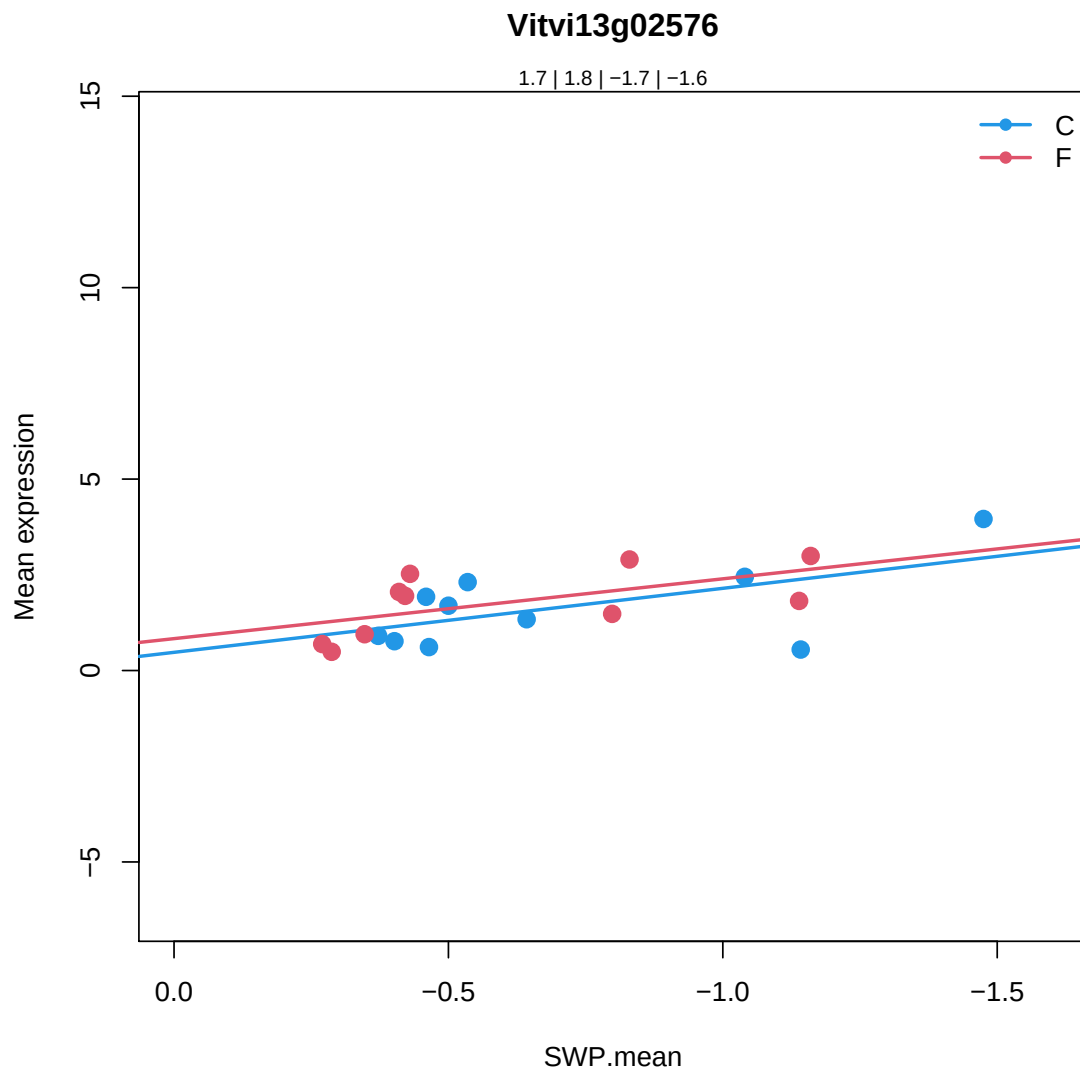
oxidoreductase/transition metal ion-binding protein |

Chr2:13580600-13580962 FORWARD LENGTH=120 |

201606

Coefficients for Vitvi13g02576.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.650056	7.486693e-07	***	8.667845e-07	***
SlopeC	-1.671749	0.02029366	*	0.3768116	
MeanF-MeanC	0.1341797	0.6961594		0.9046669	
SlopeF-SlopeC	0.1094618	0.9132158		0.9999488	



8.1.59 Vitvi10g00798: * Type1

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

Vitvi10g00798

29.5.11.4.3.3

protein.degradation.ubiquitin.E3.SCF.cullin

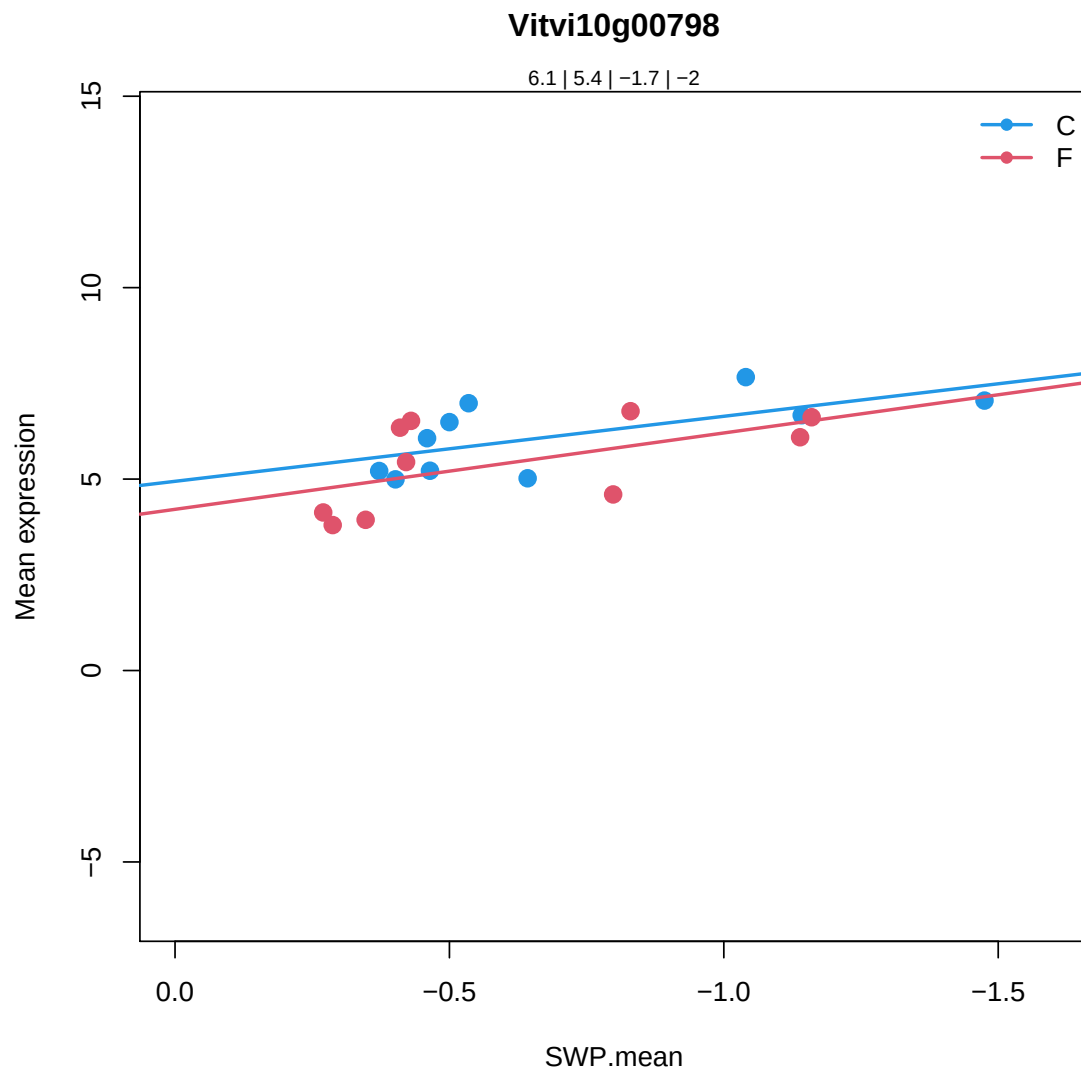
SGS domain-containing protein |

Chr1:10546794-10548072 REVERSE LENGTH=229 |

201606

Coefficients for Vitvi10g00798.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	6.135884	1.006157e-16	***	2.18615e-16	***
SlopeC	-1.69829	0.03024769	*	0.4320841	
MeanF-MeanC	-0.7109646	0.06946186	.	0.2947488	
SlopeF-SlopeC	-0.296639	0.7879845		0.9999488	



8.1.60 Vitvi04g01202: * Type1

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

Vitvi04g01202

27.1.20

RNA.processing.degradation dicer

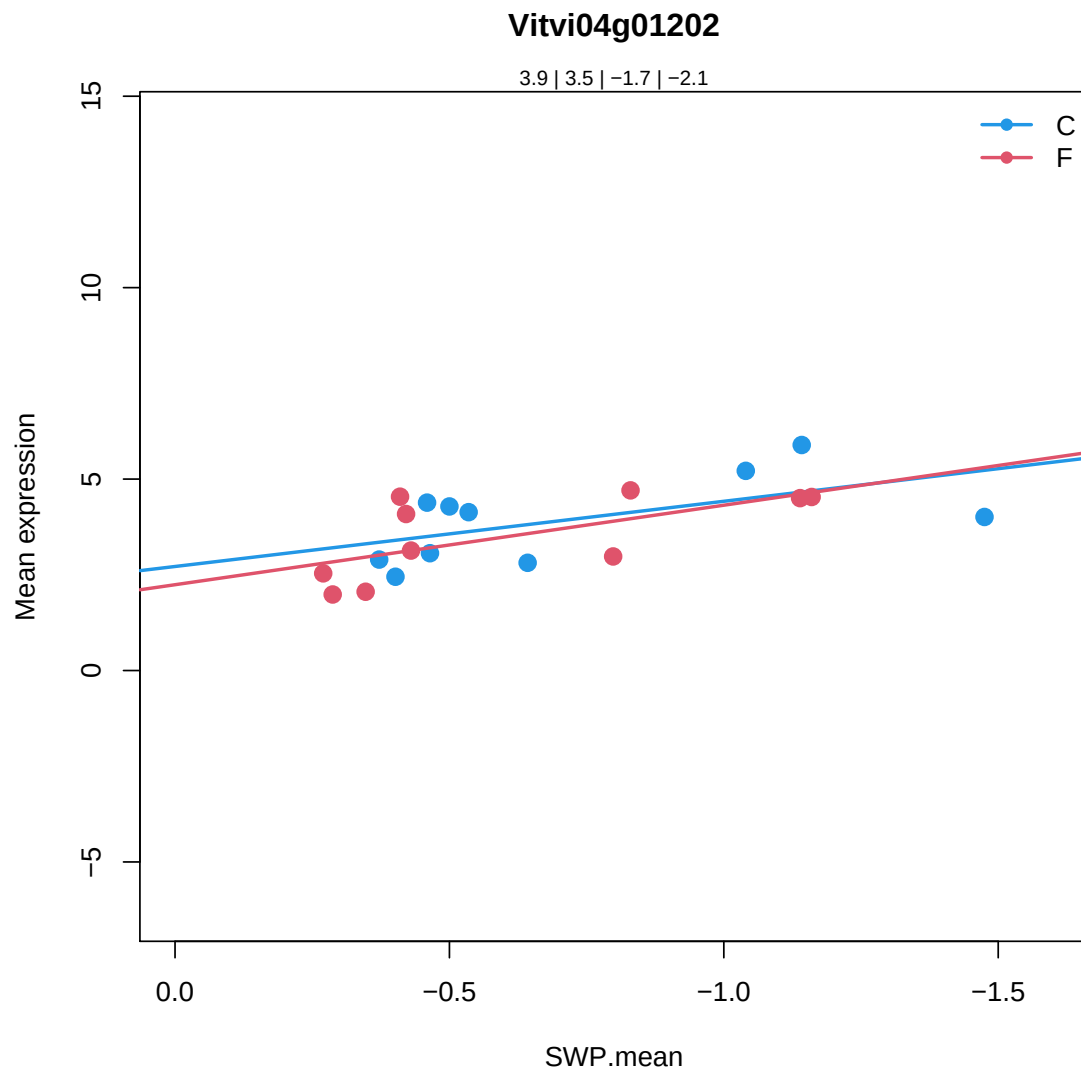
dicer-like 2 |

Chr3:768020-774525 REVERSE LENGTH=1374 |

201606

Coefficients for Vitvi04g01202.

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



8.1.61 Vitvi17g01012: * Type1

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

Vitvi17g01012

26.28

misc.GDSL-motif lipase

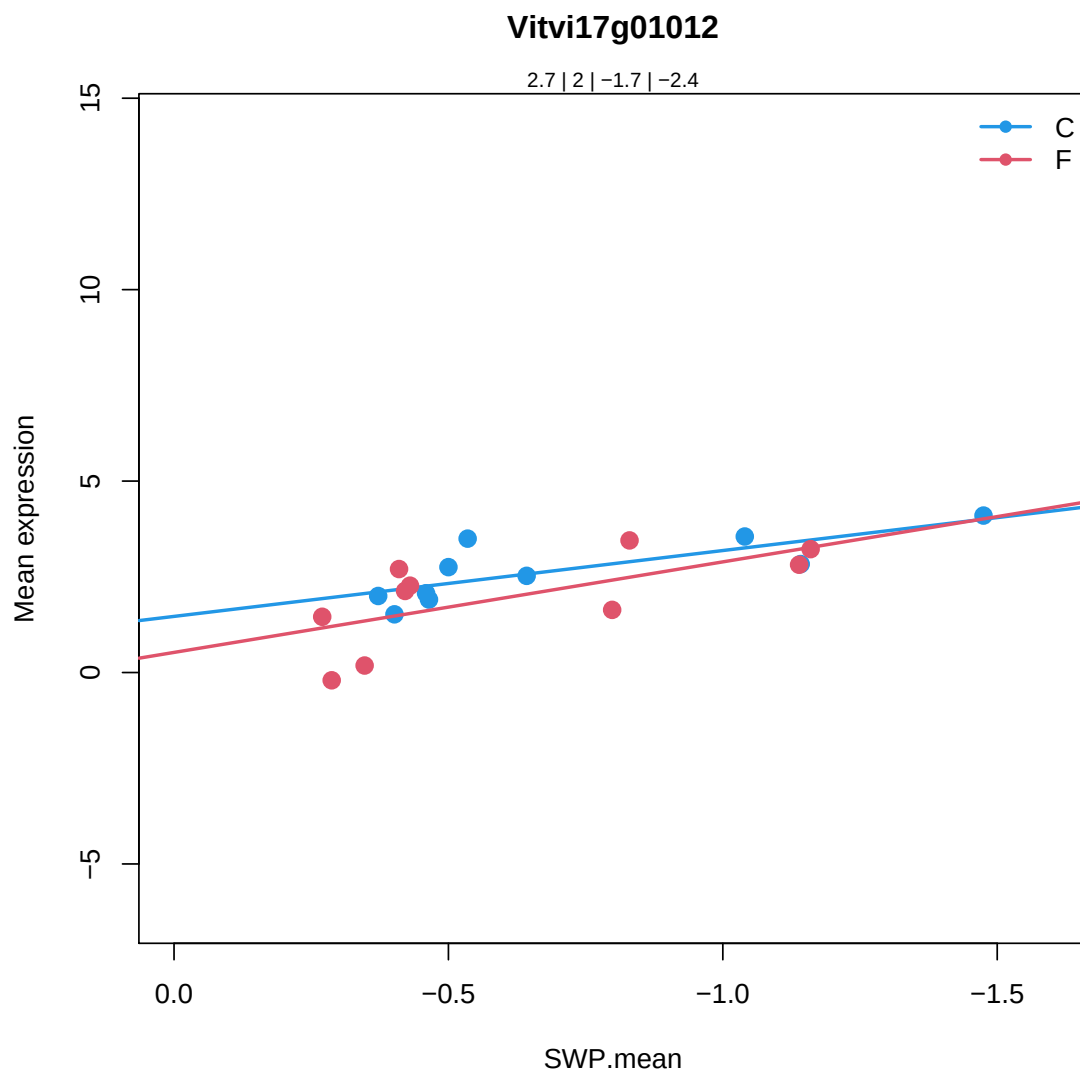
GDSL-like Lipase/Acylhydrolase superfamily protein |

Chr3:17949496-17951082 FORWARD LENGTH=381 |

201606

Coefficients for Vitvi17g01012.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.675271	9.1069e-11	***	1.193631e-10	***
SlopeC	-1.720188	0.01322339	*	0.3305597	
MeanF-MeanC	-0.7093721	0.0395954	*	0.204845	
SlopeF-SlopeC	-0.6447263	0.5036476		0.9999488	



8.1.62 Vitvi02g00983: * Type1

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

Vitvi02g00983

35.2

not assigned.unknown

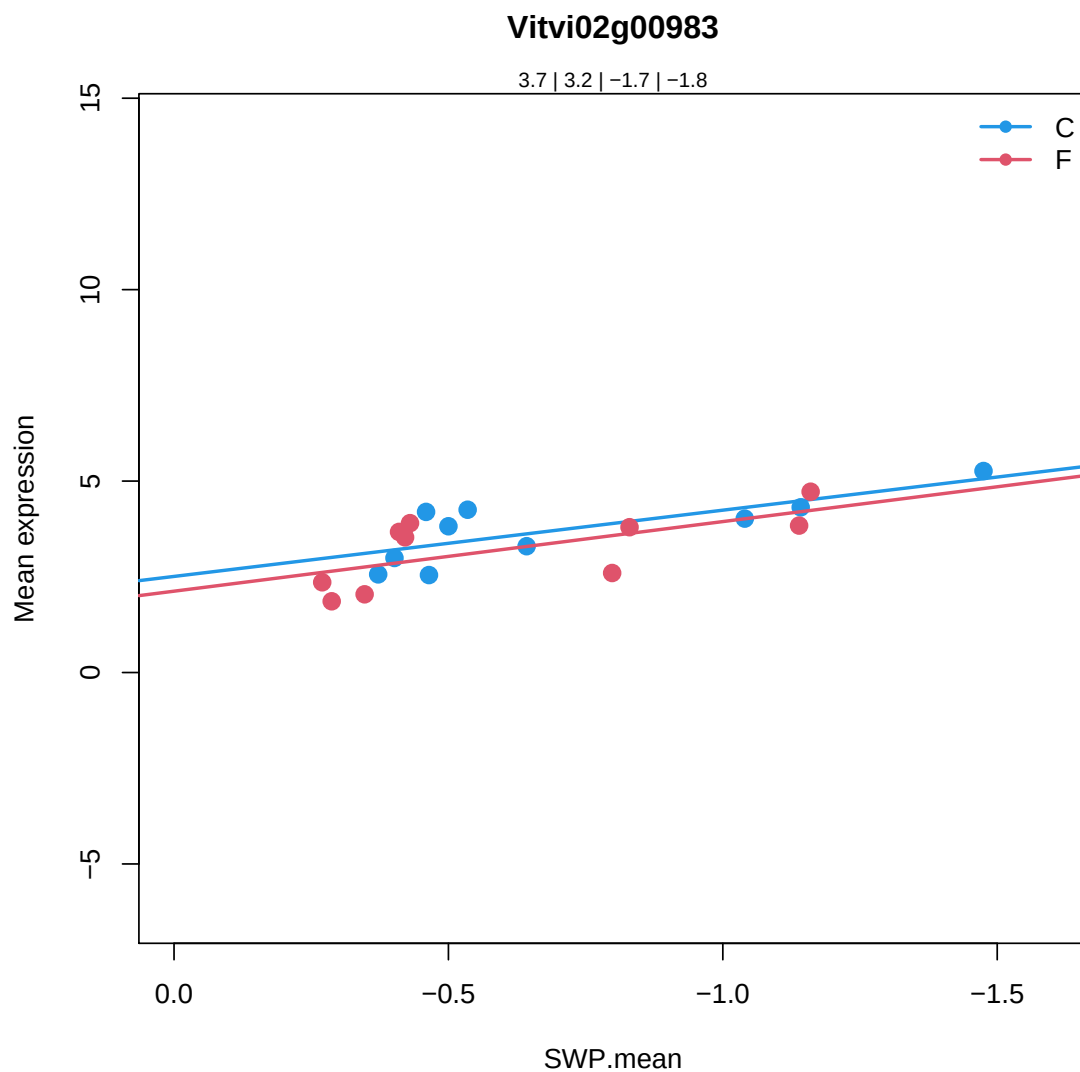
UDP-Glycosyltransferase superfamily protein |

Chr2:15417618-15419108 REVERSE LENGTH=496 |

201606

Coefficients for Vitvi02g00983.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.726364	1.280806e-14	***	2.117818e-14	***
SlopeC	-1.730352	0.005692474	**	0.2614474	
MeanF-MeanC	-0.4946906	0.0984271	.	0.3613261	
SlopeF-SlopeC	-0.08771546	0.9176478		0.9999488	



8.1.63 Vitvi17g01086: * Type1

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

Vitvi17g01086

13.1.1.1.1

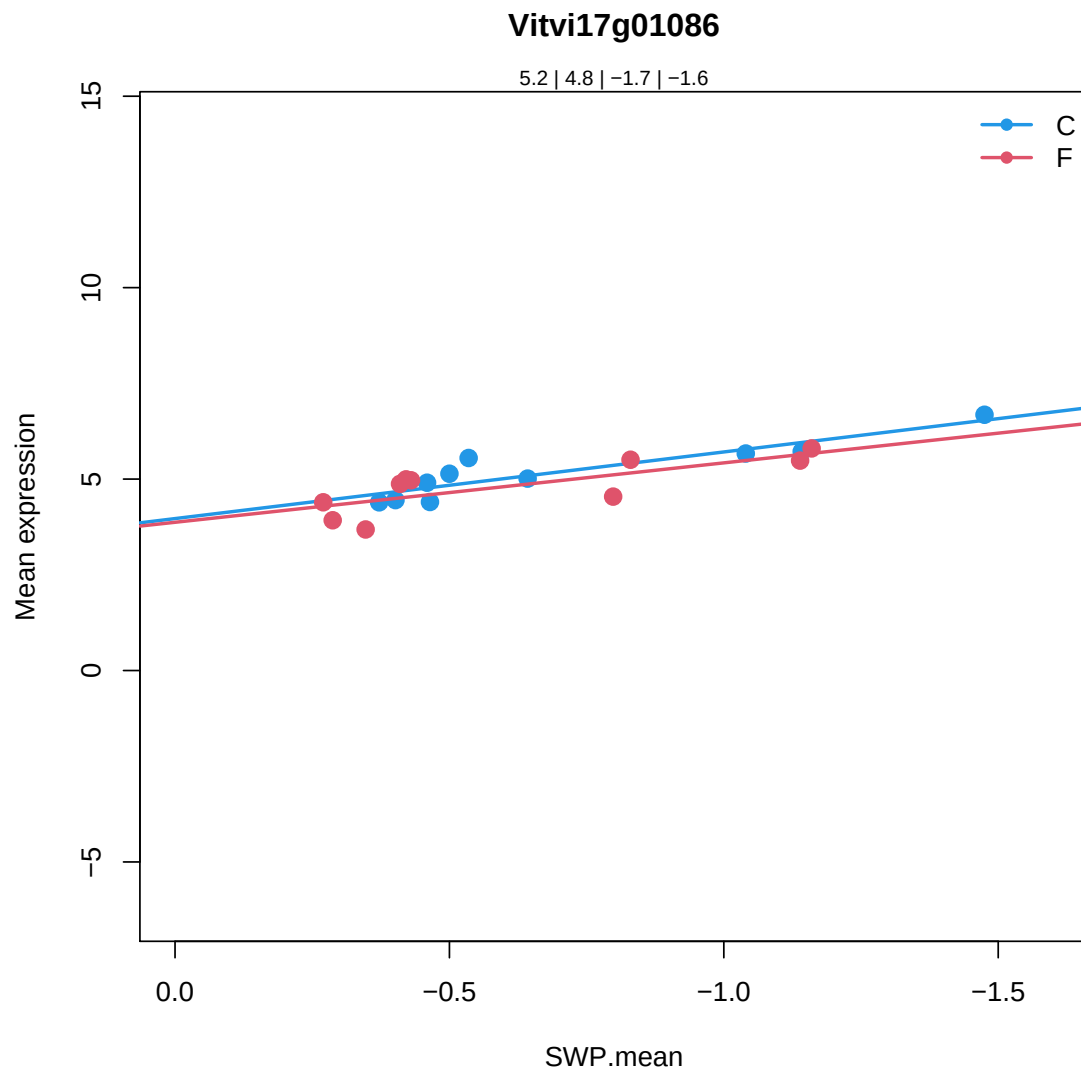
amino acid metabolism.synthesis.central amino acid metabolism.GABA.glu
glutamate decarboxylase |

Chr5:5711141-5714839 FORWARD LENGTH=502 |

201606

Coefficients for Vitvi17g01086.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.192026	2.69292e-21	***	2.468827e-20	***
SlopeC	-1.740421	0.0001322915	***	0.07644173	.
MeanF-MeanC	-0.3751626	0.06188059	.	0.2742611	
SlopeF-SlopeC	0.1882582	0.7389244		0.9999488	



8.1.64 Vitvi02g01261: * Type1

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

Vitvi02g01261

29.2.1.99.99

protein.synthesis.ribosomal protein.unknown.unknown

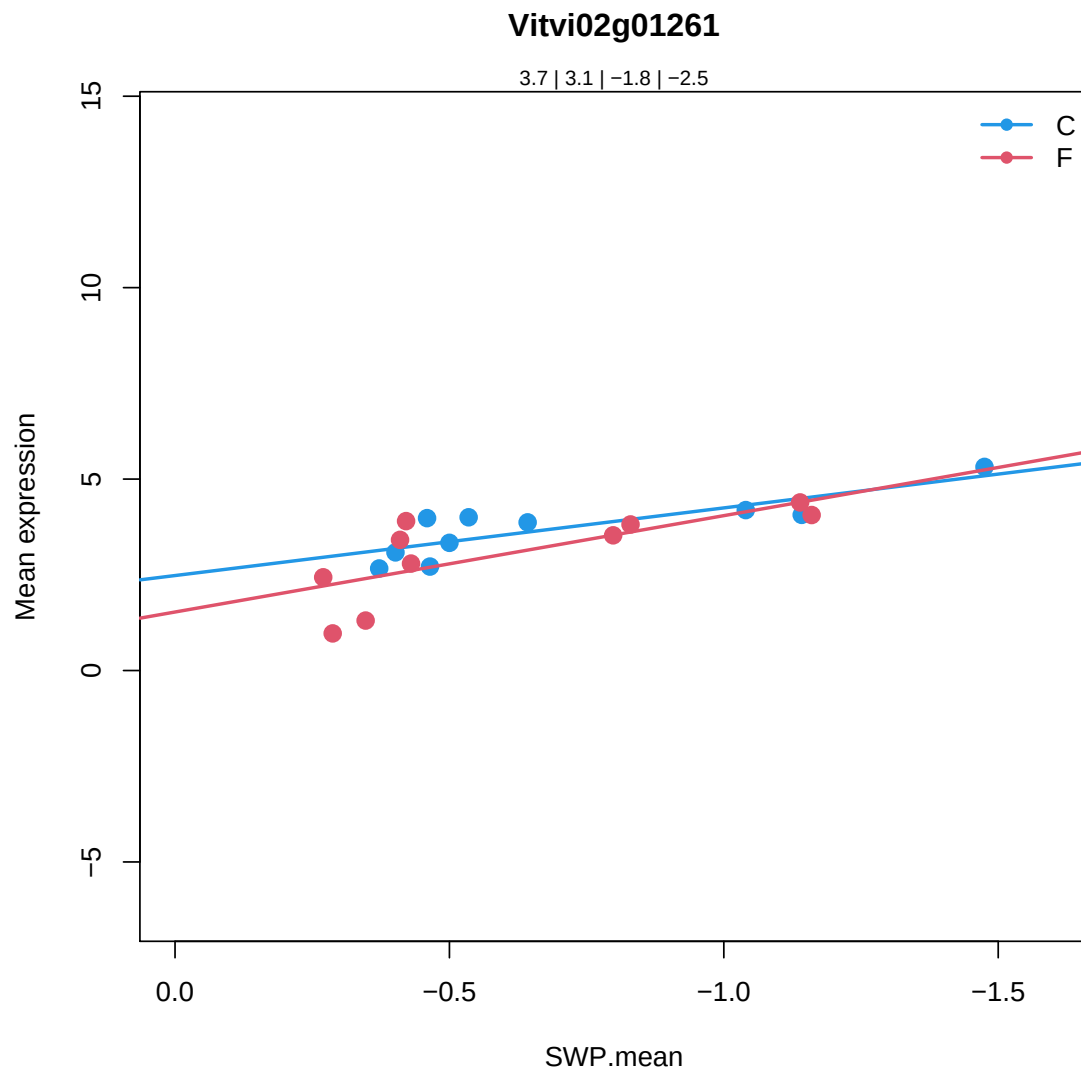
Uncharacterized protein family (UPF0114) |

Chr4:10574903-10577267 REVERSE LENGTH=185 |

201606

Coefficients for Vitvi02g01261.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.722424	1.037277e-14	***	1.731483e-14	***
SlopeC	-1.766391	0.004510503	**	0.2419697	
MeanF-MeanC	-0.6610484	0.0293114	*	0.1663141	
SlopeF-SlopeC	-0.7504356	0.3753056		0.9999488	



8.1.65 Vitvi18g02167: Type1

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

Vitvi18g02167

17.1.1.1.12

hormone metabolism.abscisic acid.synthesis-degradation.synthesis.absci

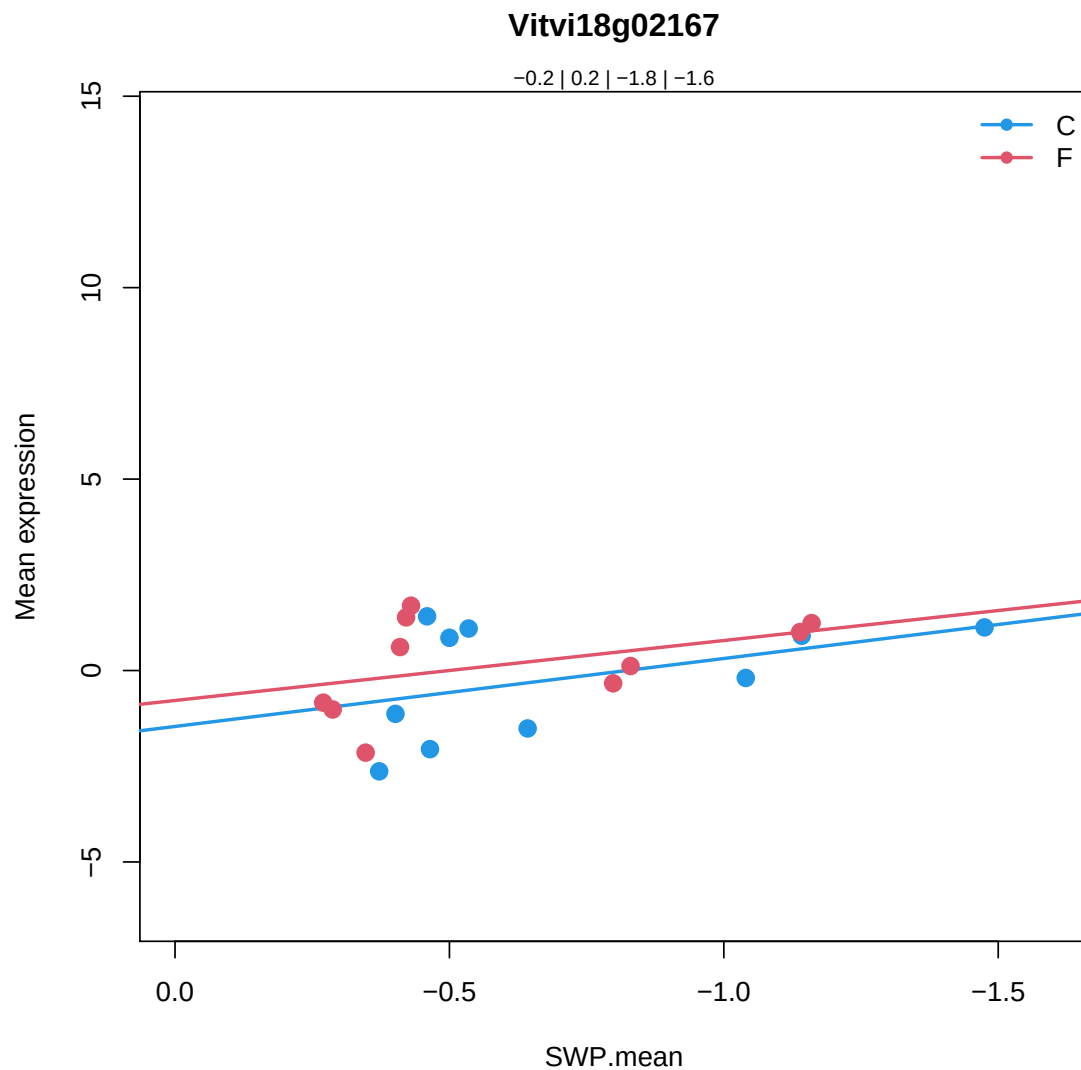
aldehyde oxidase 1 |

Chr5:7116783-7122338 FORWARD LENGTH=1368 |

201606

Coefficients for Vitvi18g02167.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.2128345	0.5677555		0.5735505	
SlopeC	-1.774895	0.09629287	.	0.6067366	
MeanF-MeanC	0.3844787	0.4665734		0.7876703	
SlopeF-SlopeC	0.2086531	0.8920053		0.9999488	



8.1.66 Vitvi10g01342: * Type1

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

Vitvi10g01342

27.3.36

RNA.regulation of transcription.argonaute transcription factor family

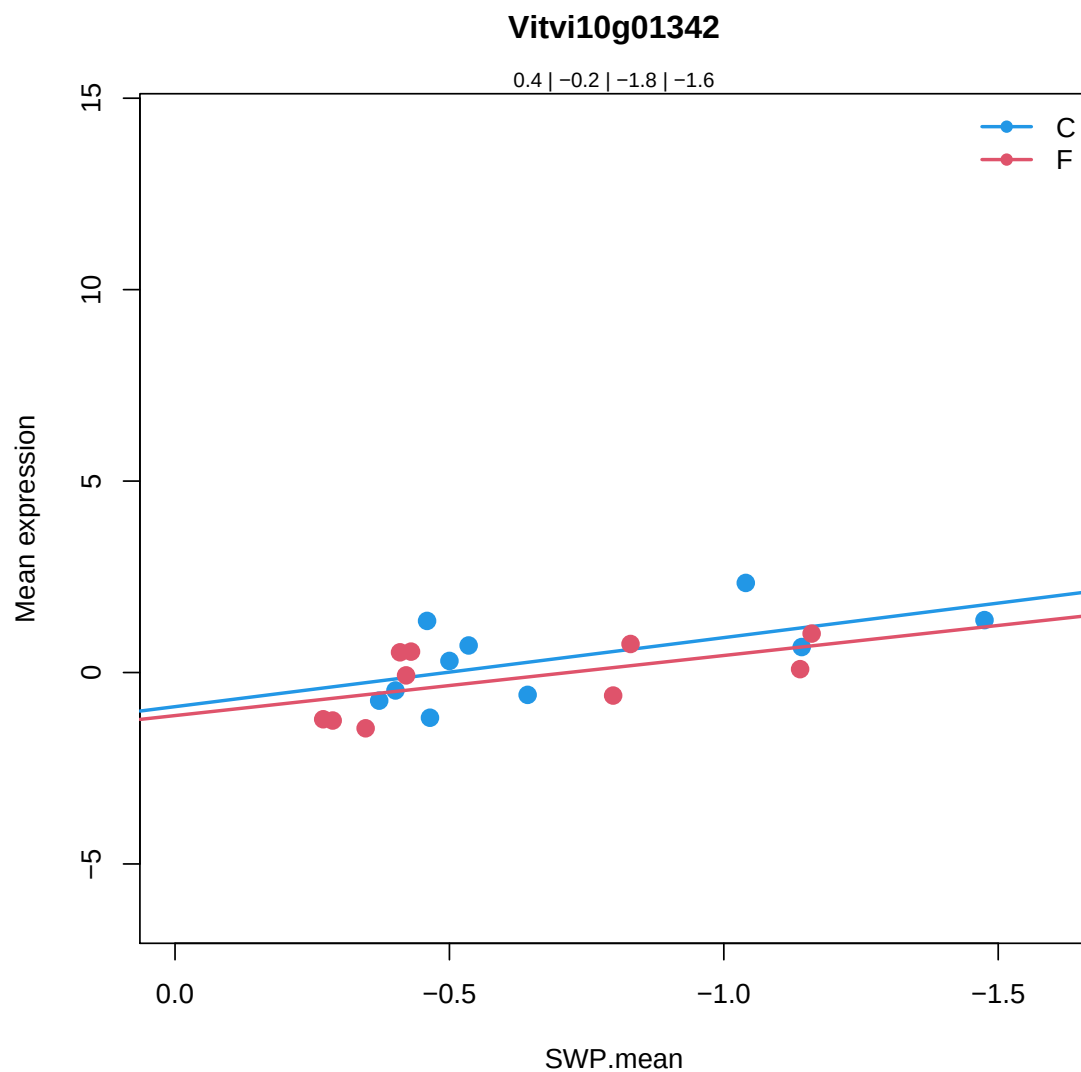
Argonaute family protein |

Chr1:11181777-11185112 FORWARD LENGTH=1014 |

201606

Coefficients for Vitvi10g01342.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3761012	0.144305		0.1485645	
SlopeC	-1.802985	0.0161523	*	0.3486596	
MeanF-MeanC	-0.5447118	0.1353421		0.4400114	
SlopeF-SlopeC	0.2340175	0.8220433		0.9999488	



8.1.67 Vitvi02g00228: * Type1

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

Vitvi02g00228

27.3.35

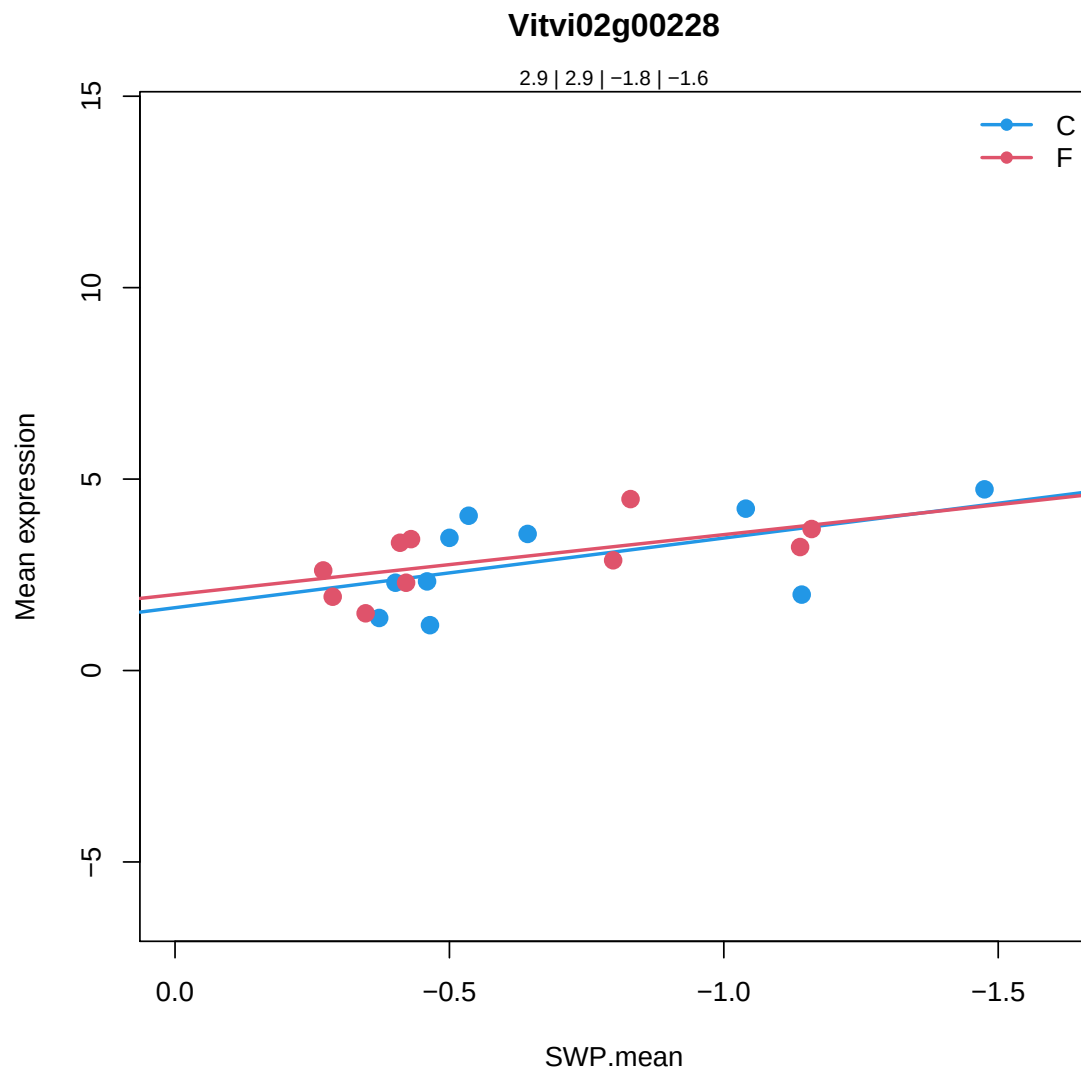
RNA.regulation of transcription.bZIP transcription factor family
homeobox 7 |

Chr2:19165777-19166773 REVERSE LENGTH=258 |

201606

Coefficients for Vitvi02g00228.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.91942	3.526112e-10	***	4.517906e-10	***
SlopeC	-1.818326	0.02386796	*	0.3984616	
MeanF-MeanC	0.01795977	0.9627522		0.9915437	
SlopeF-SlopeC	0.2522321	0.8228588		0.9999488	



8.1.68 Vitvi05g01740: * Type1

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

Vitvi05g01740

16.8.2

secondary metabolism.flavonoids.chalcones

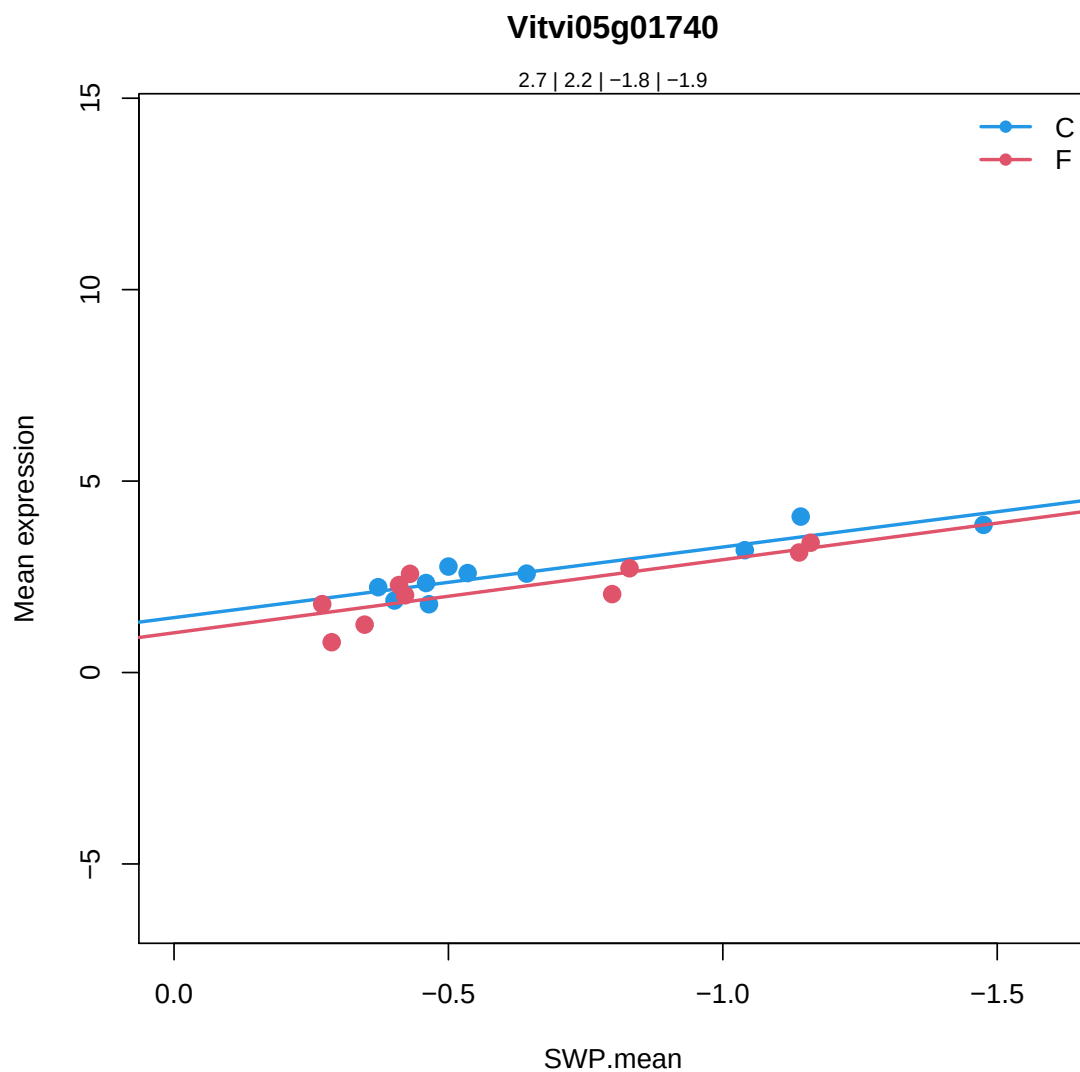
NAD(P)-linked oxidoreductase superfamily protein |

Chr1:22071410-22073067 REVERSE LENGTH=326 |

201606

Coefficients for Vitvi05g01740.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.730013	4.118221e-15	***	7.20665e-15	***
SlopeC	-1.844095	0.0001091579	***	0.07644173	.
MeanF-MeanC	-0.5296411	0.01417235	*	0.09792158	.
SlopeF-SlopeC	-0.06541604	0.9113725		0.9999488	



8.1.69 Vitvi18g00596: * Type1

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

Vitvi18g00596

35.2

not assigned.unknown

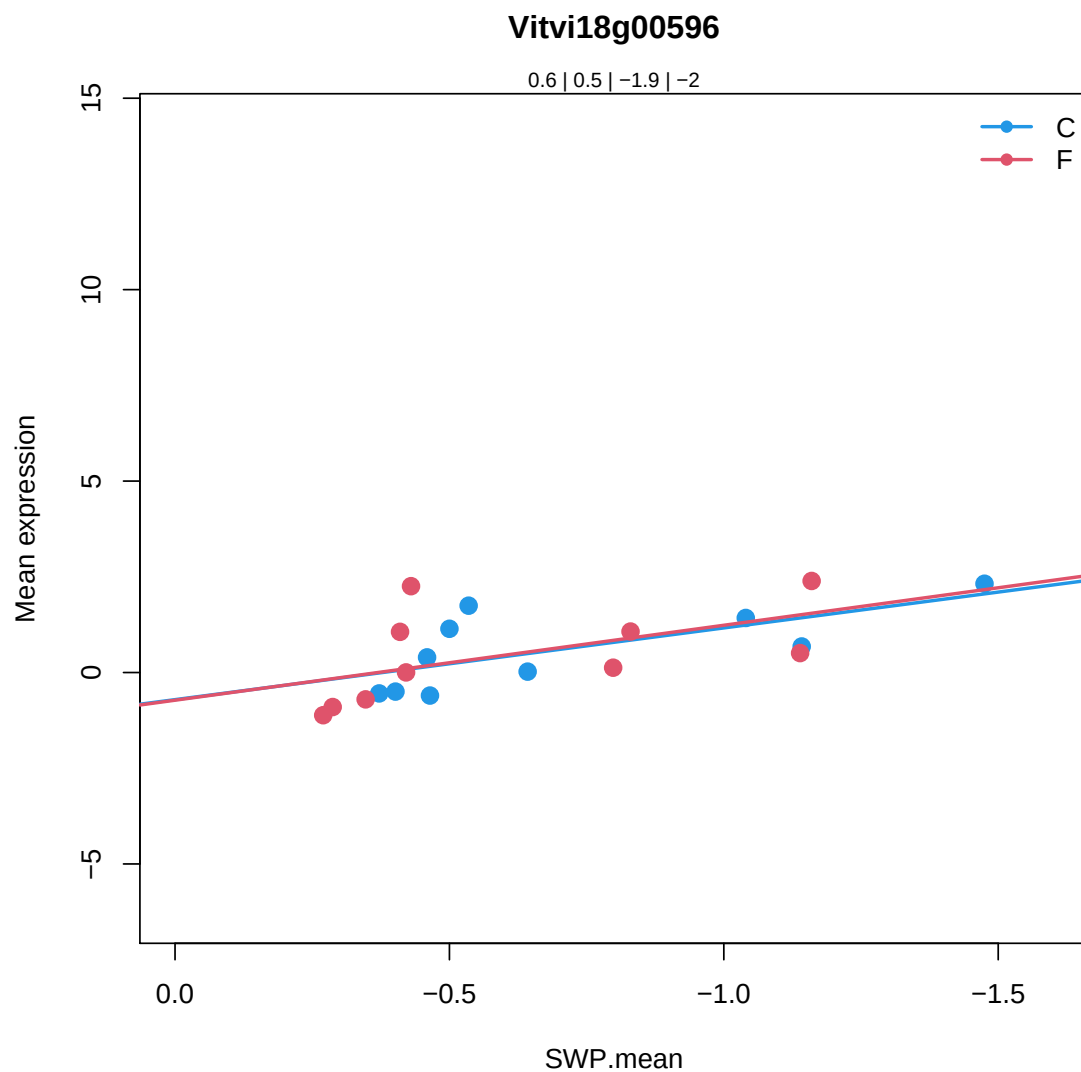
tubulin alpha-6 chain |

Chr1:18520144-18521600 REVERSE LENGTH=209 |

201606

Coefficients for Vitvi18g00596.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6083869	0.03667248	*	0.03830343	*
SlopeC	-1.872526	0.02219784	*	0.3929231	
MeanF-MeanC	-0.1388005	0.7227382		0.9149482	
SlopeF-SlopeC	-0.08545914	0.9404426		0.9999488	



8.1.70 Vitvi08g02189: Type1

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

Vitvi08g02189

35.2

not assigned.unknown

heat shock cognate protein 70-1 |

Chr5:554055-556334 REVERSE LENGTH=651 |

201606

Vitvi08g02189

29.6

protein.folding

heat shock cognate protein 70-1 |

Chr5:554055-556334 REVERSE LENGTH=651 |

201606

Vitvi08g02189

20.2.1

stress.abiotic.heat

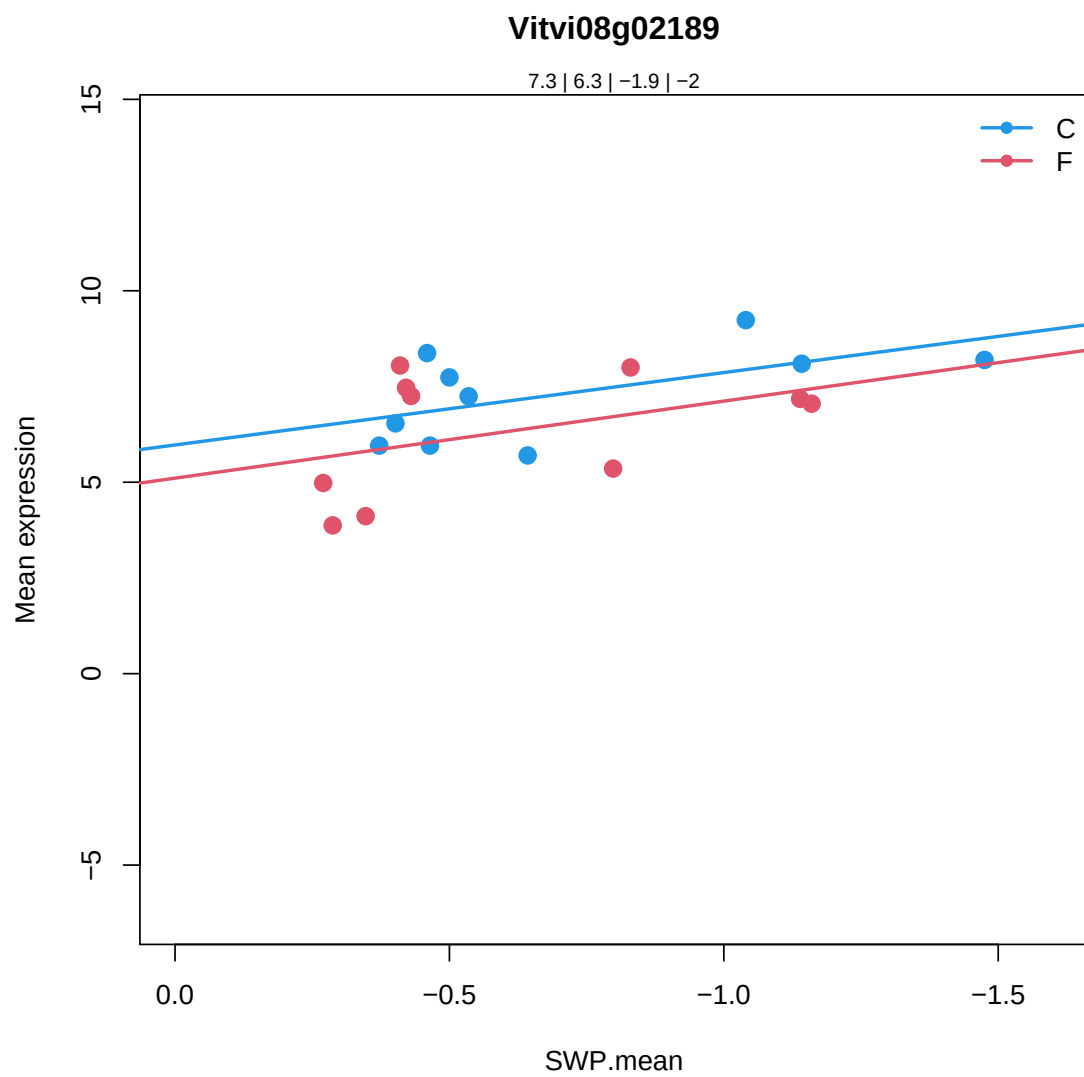
heat shock cognate protein 70-1 |

Chr5:554055-556334 REVERSE LENGTH=651 |

201606

Coefficients for Vitvi08g02189.

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



8.1.71 Vitvi07g01297: Type1

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

Vitvi07g01297

26.28

misc.GDSL-motif lipase

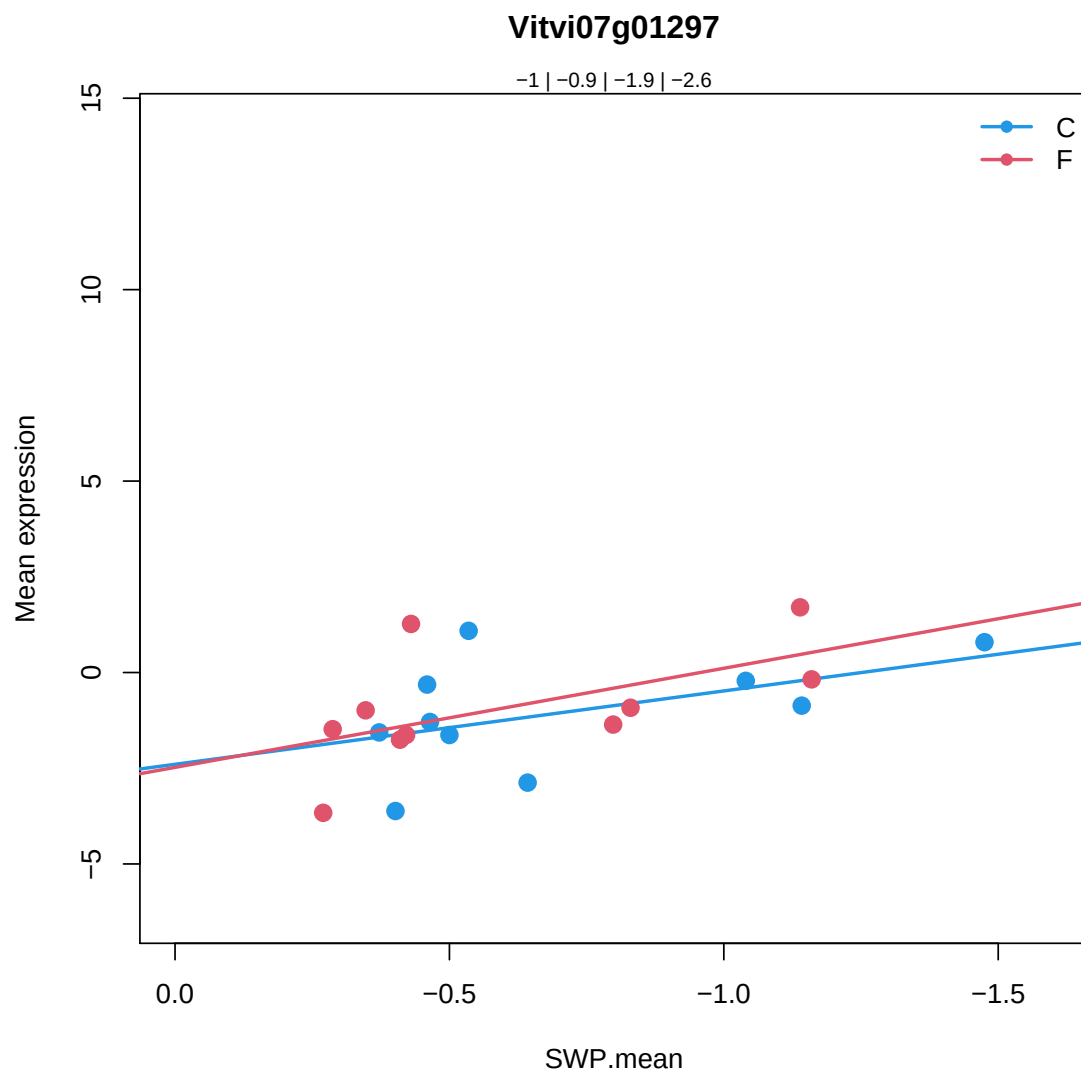
GDSL-like Lipase/Acylhydrolase superfamily protein |

Chr2:10024366-10026058 FORWARD LENGTH=387 |

201606

Coefficients for Vitvi07g01297.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.049876	0.01124818	*	0.0119034	*
SlopeC	-1.916124	0.08284178	.	0.5803324	
MeanF-MeanC	0.149202	0.7831418		0.9384607	
SlopeF-SlopeC	-0.6721018	0.6723638		0.9999488	



8.1.72 Vitvi08g01234: * Type1

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

Vitvi08g01234

35.1.3

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

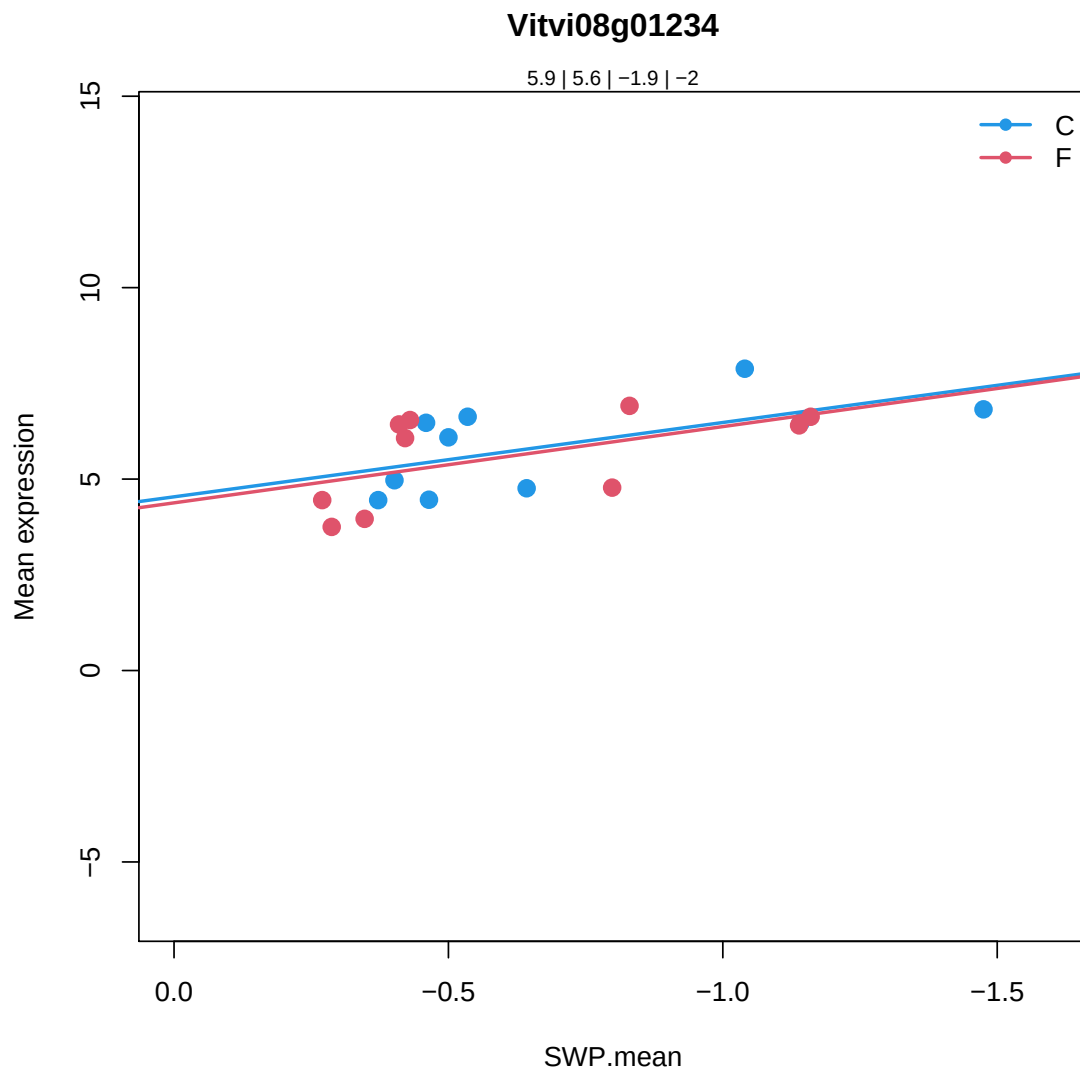
Fes1A |

Chr3:2871710-2873109 FORWARD LENGTH=327 |

201606

Coefficients for Vitvi08g01234.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.90145	1.529707e-15	***	2.79868e-15	***
SlopeC	-1.940814	0.02472301	*	0.4060648	
MeanF-MeanC	-0.3092112	0.4572898		0.7825787	
SlopeF-SlopeC	-0.05059603	0.9666479		0.9999488	



8.1.73 Vitvi01g02009: * Type1

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

Vitvi01g02009

16.8.2

secondary metabolism.flavonoids.chalcones

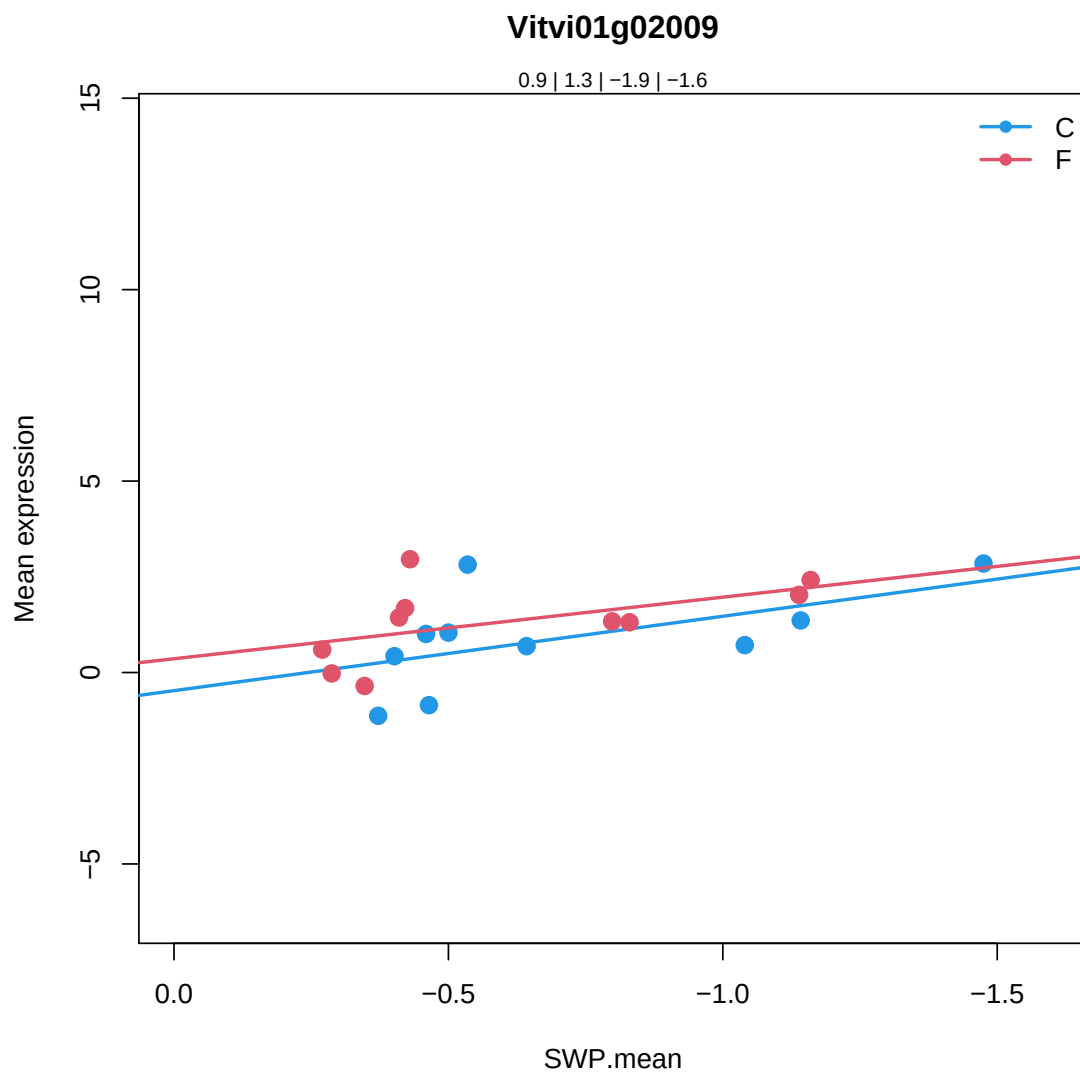
NAD(P)-linked oxidoreductase superfamily protein |

Chr1:22071410-22073067 REVERSE LENGTH=326 |

201606

Coefficients for Vitvi01g02009.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8920748	0.006206541	**	0.006605229	**
SlopeC	-1.942709	0.02693091	*	0.4184311	
MeanF-MeanC	0.4474214	0.2938199		0.6604339	
SlopeF-SlopeC	0.3343367	0.7862208		0.9999488	



8.1.74 Vitvi07g00087: * Type1

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

Vitvi07g00087

35.1

not assigned.no ontology

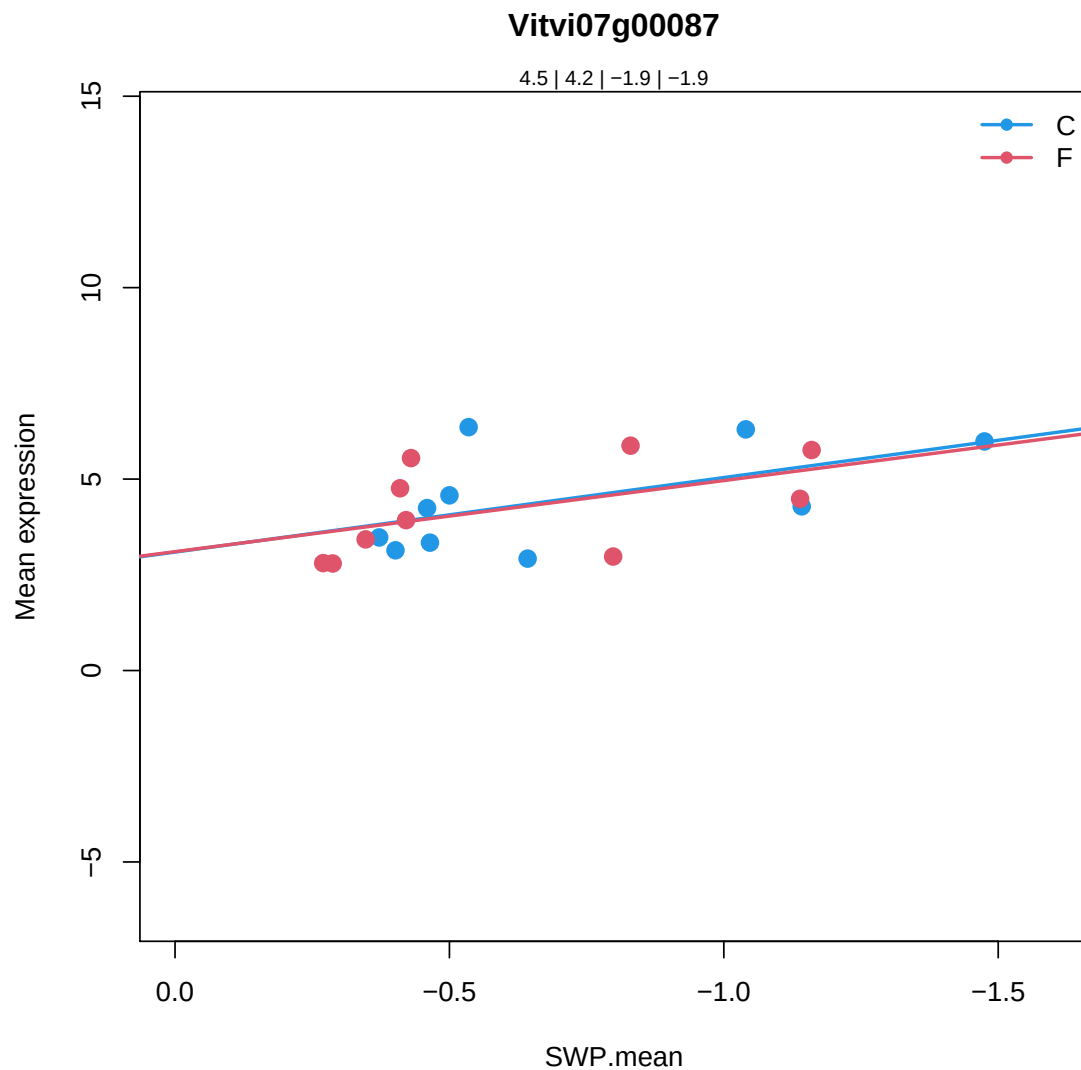
Bax inhibitor-1 family protein |

Chr1:730148-731379 FORWARD LENGTH=247 |

201606

Coefficients for Vitvi07g00087.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.461907	3.187147e-12	***	4.45021e-12	***
SlopeC	-1.946211	0.04011329	*	0.472859	
MeanF-MeanC	-0.2263095	0.6222682		0.8698761	
SlopeF-SlopeC	0.08953531	0.9467777		0.9999488	



8.1.75 Vitvi09g01273: * Type1

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

Vitvi09g01273

35.2

not assigned.unknown

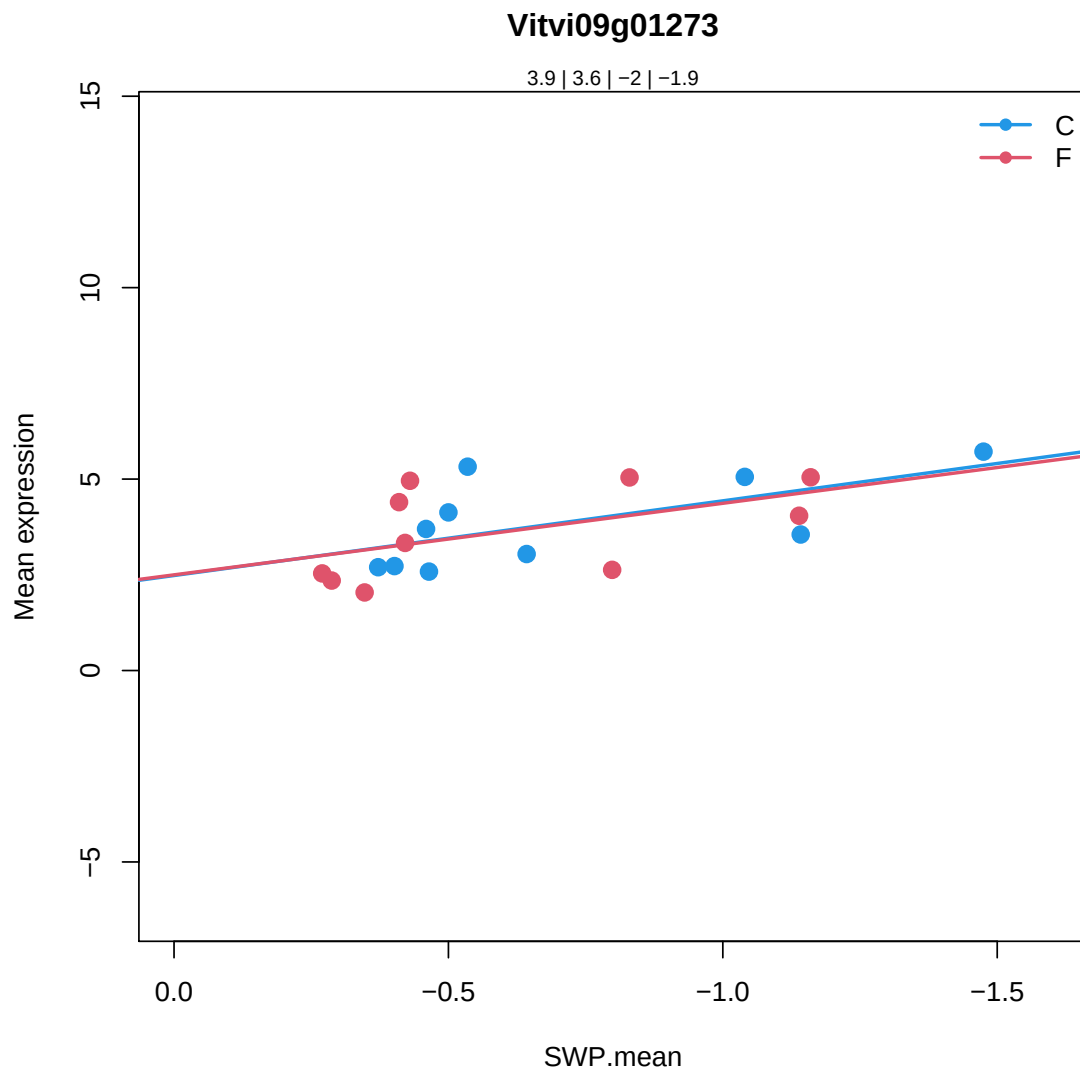
ATP-dependent DNA helicase |

Chr4:14990523-14992855 FORWARD LENGTH=589 |

201606

Coefficients for Vitvi09g01273.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.852927	7.081238e-12	***	9.740297e-12	***
SlopeC	-1.951126	0.02373849	*	0.3983963	
MeanF-MeanC	-0.2157831	0.6018321		0.8611337	
SlopeF-SlopeC	0.08240906	0.9455691		0.9999488	



8.1.76 Vitvi13g00255: * Type1

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

Vitvi13g00255

34.19.2

transport.major intrinsic proteins.TIP

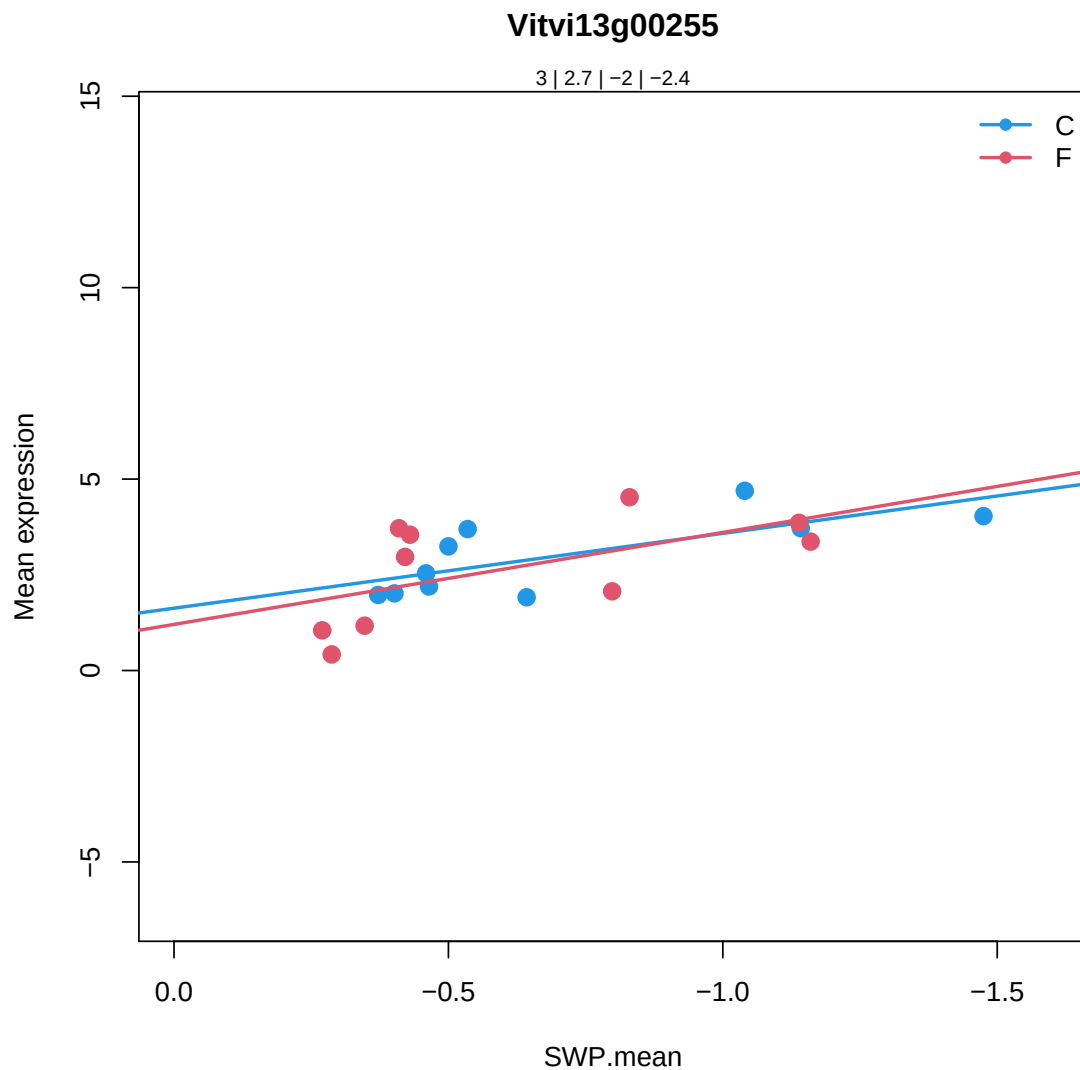
tonoplast intrinsic protein 1%3B3 |

Chr4:625092-625850 REVERSE LENGTH=252 |

201606

Coefficients for Vitvi13g00255.

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



8.1.77 Vitvi17g00078: Type1

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

Vitvi17g00078

35.1

not assigned.no ontology

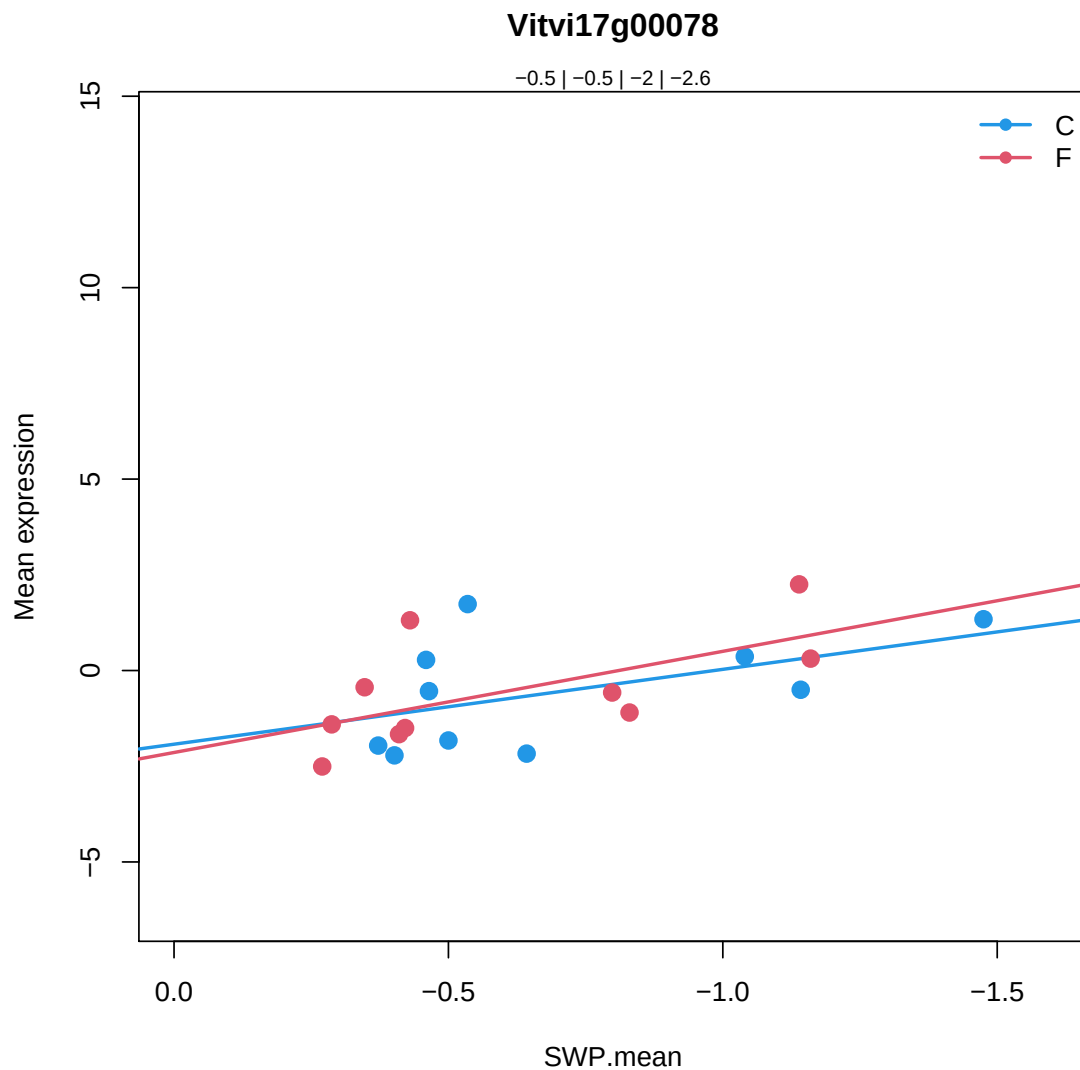
HXXXD-type acyl-transferase family protein |

Chr5:16431448-16433086 FORWARD LENGTH=457 |

201606

Coefficients for Vitvi17g00078.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.5499436	0.1382099		0.142376	
SlopeC	-1.955218	0.06215032	.	0.5453628	
MeanF-MeanC	0.01843645	0.9712182		0.9933672	
SlopeF-SlopeC	-0.6870146	0.6469197		0.9999488	



8.1.78 Vitvi06g01762: * Type1

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

Vitvi06g01762

26.2

misc.UDP glucosyl and glucoronyl transferases

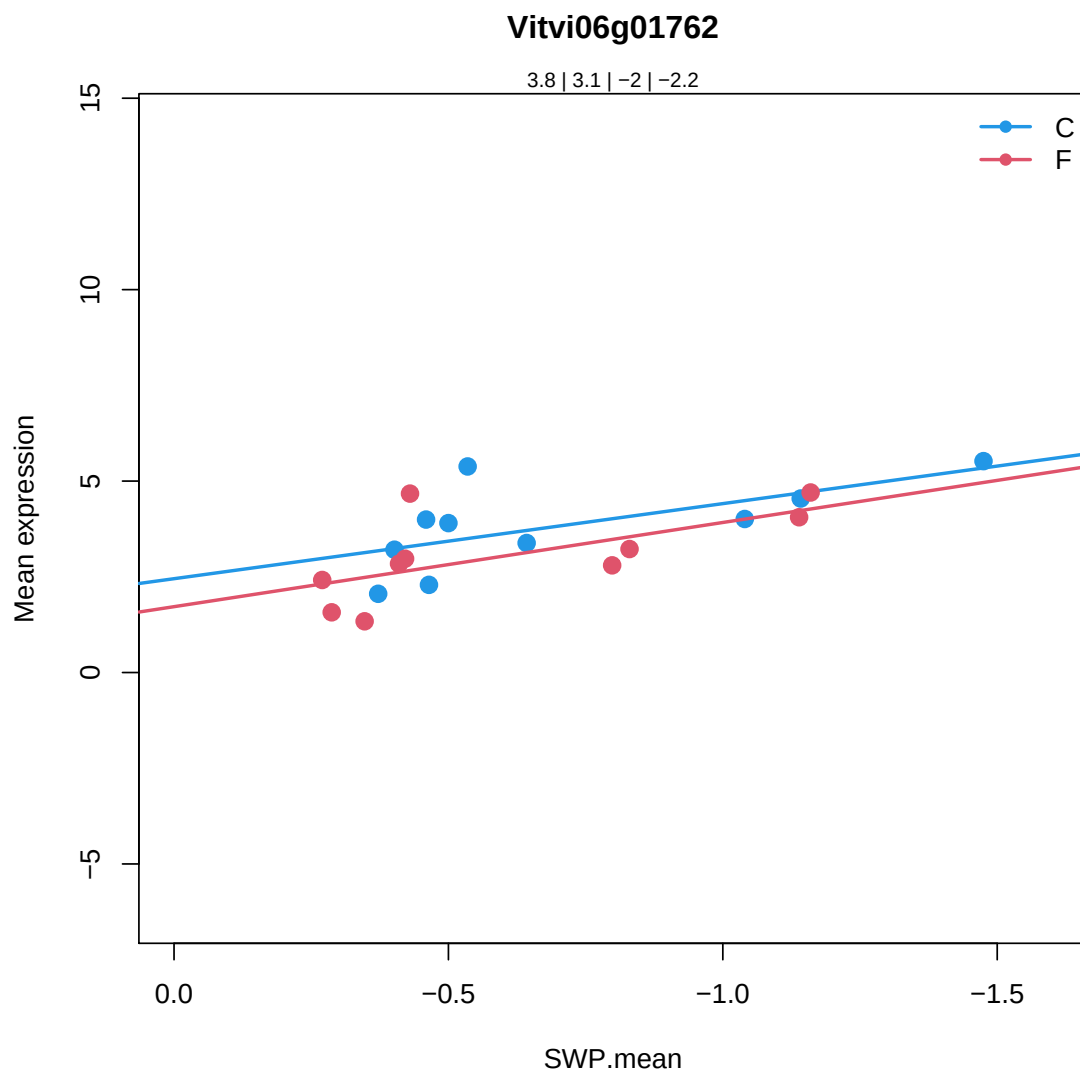
UDP-Glycosyltransferase superfamily protein |

Chr2:12872200-12873691 FORWARD LENGTH=454 |

201606

Coefficients for Vitvi06g01762.

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



8.1.79 Vitvi11g01265: * Type1

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

Vitvi11g01265

10.6.2

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

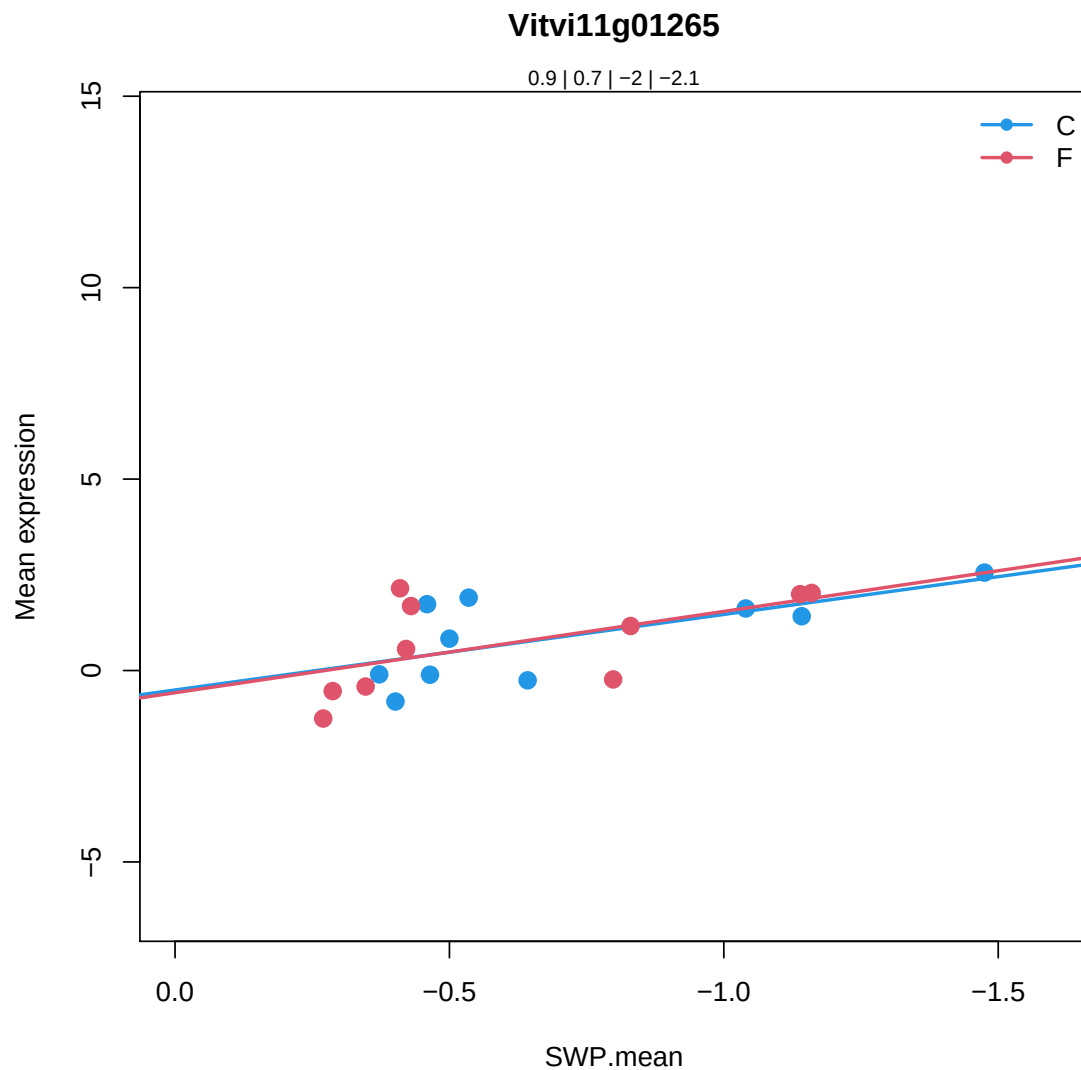
xyloglucan endotransglycosylase 6 |

Chr4:13128694-13129715 FORWARD LENGTH=286 |

201606

Coefficients for Vitvi11g01265.

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



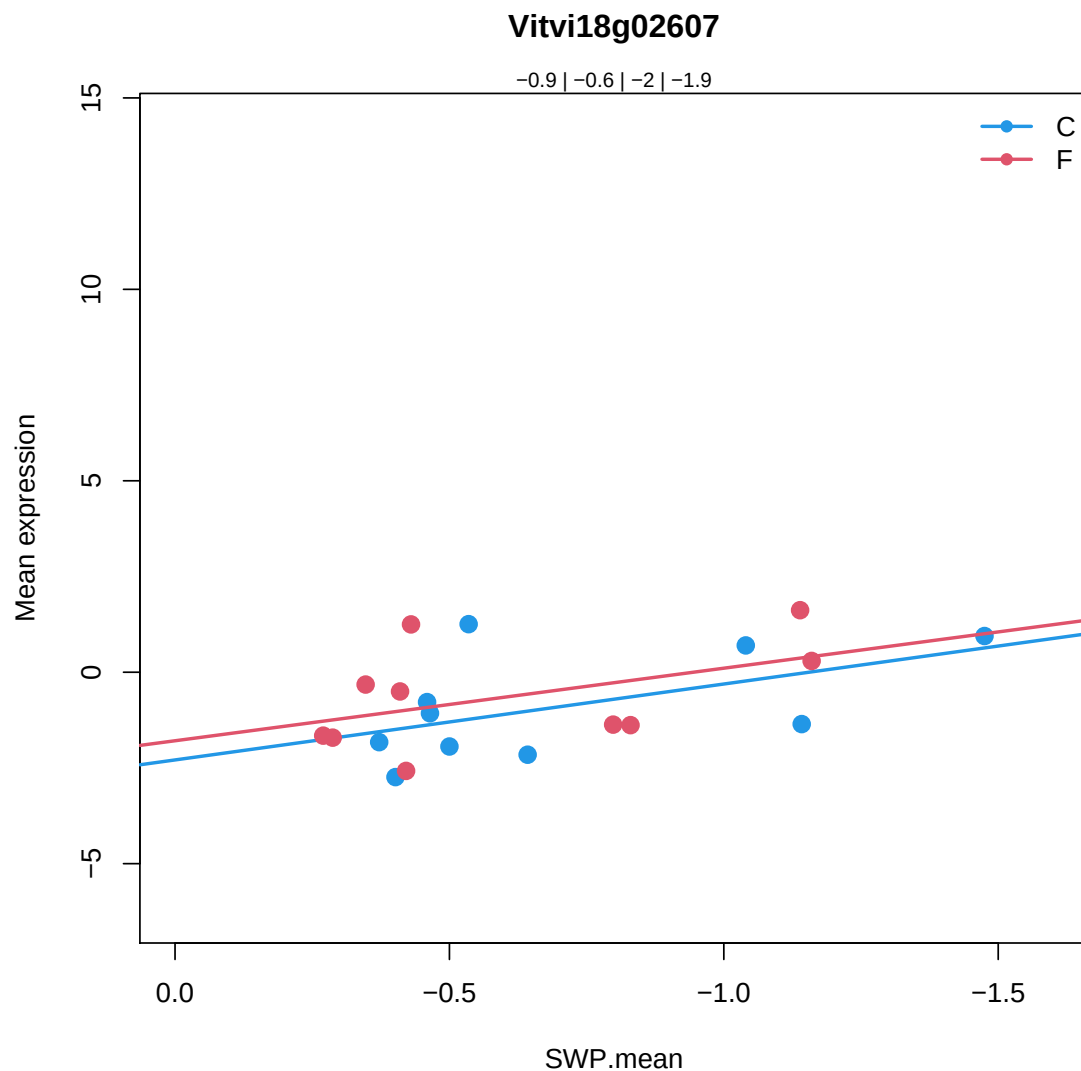
8.1.80 Vitvi18g02607: Type1

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

```
Vitvi18g02607
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi18g02607.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.8967429	0.01911297	*	0.02010211	*
SlopeC	-1.98267	0.0567301	.	0.5329089	
MeanF-MeanC	0.2611649	0.6070969		0.8620618	
SlopeF-SlopeC	0.08735273	0.9530133		0.9999488	



8.1.81 Vitvi05g00539: * Type1

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

Vitvi05g00539

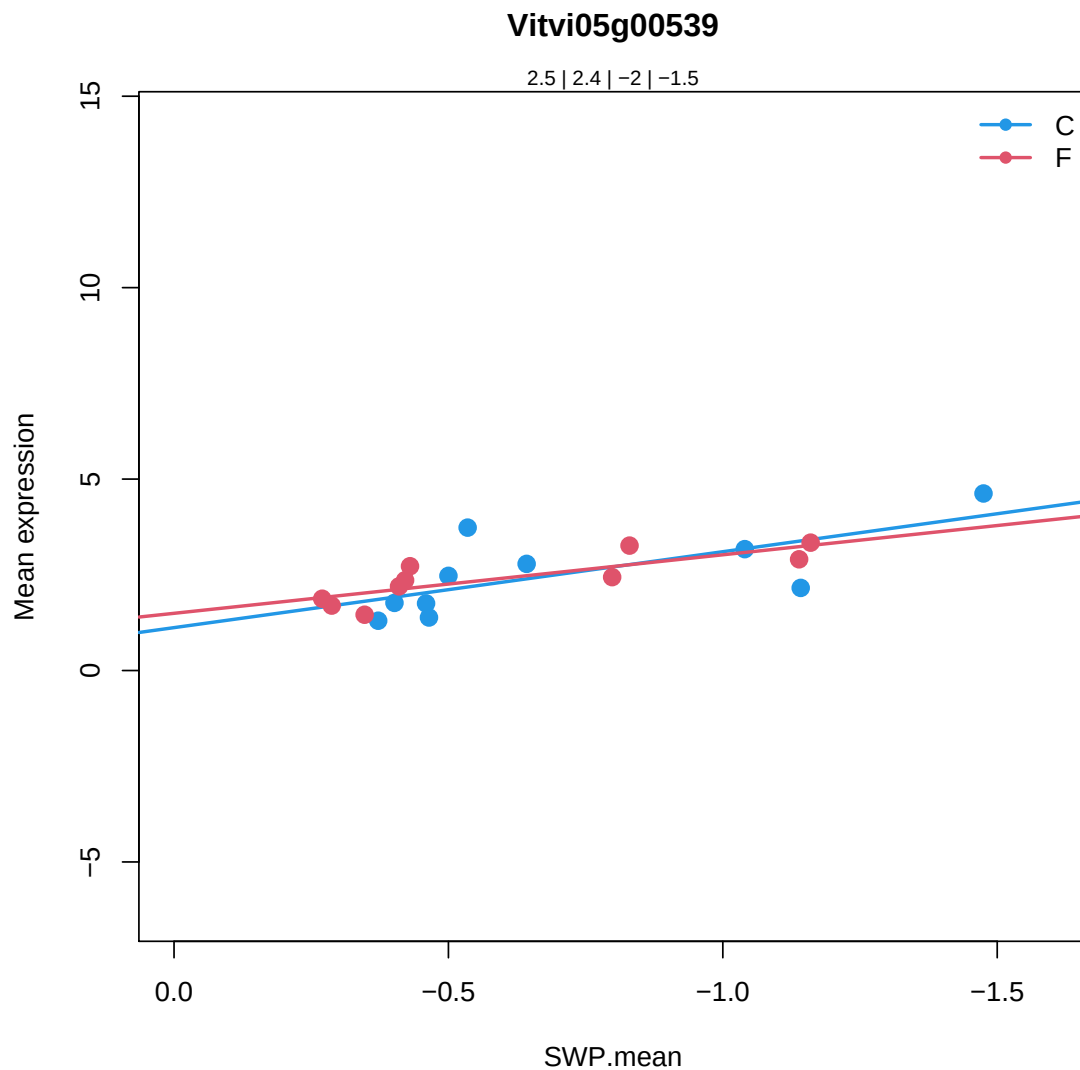
13.1.3.4.12

amino acid metabolism.synthesis.aspartate family.methionine.homocysteine
homocysteine methyltransferase 2 |

Chr3:23370575-23371974 REVERSE LENGTH=293 |
201606

Coefficients for Vitvi05g00539.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.514555	1.026531e-11	***	1.399873e-11	***
SlopeC	-1.983181	0.001236499	**	0.1365704	
MeanF-MeanC	-0.08927246	0.7451312		0.9250114	
SlopeF-SlopeC	0.4546535	0.57277		0.9999488	



8.1.82 Vitvi10g02382: * Type1

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

Vitvi10g02382

20.2.1

stress.abiotic.heat

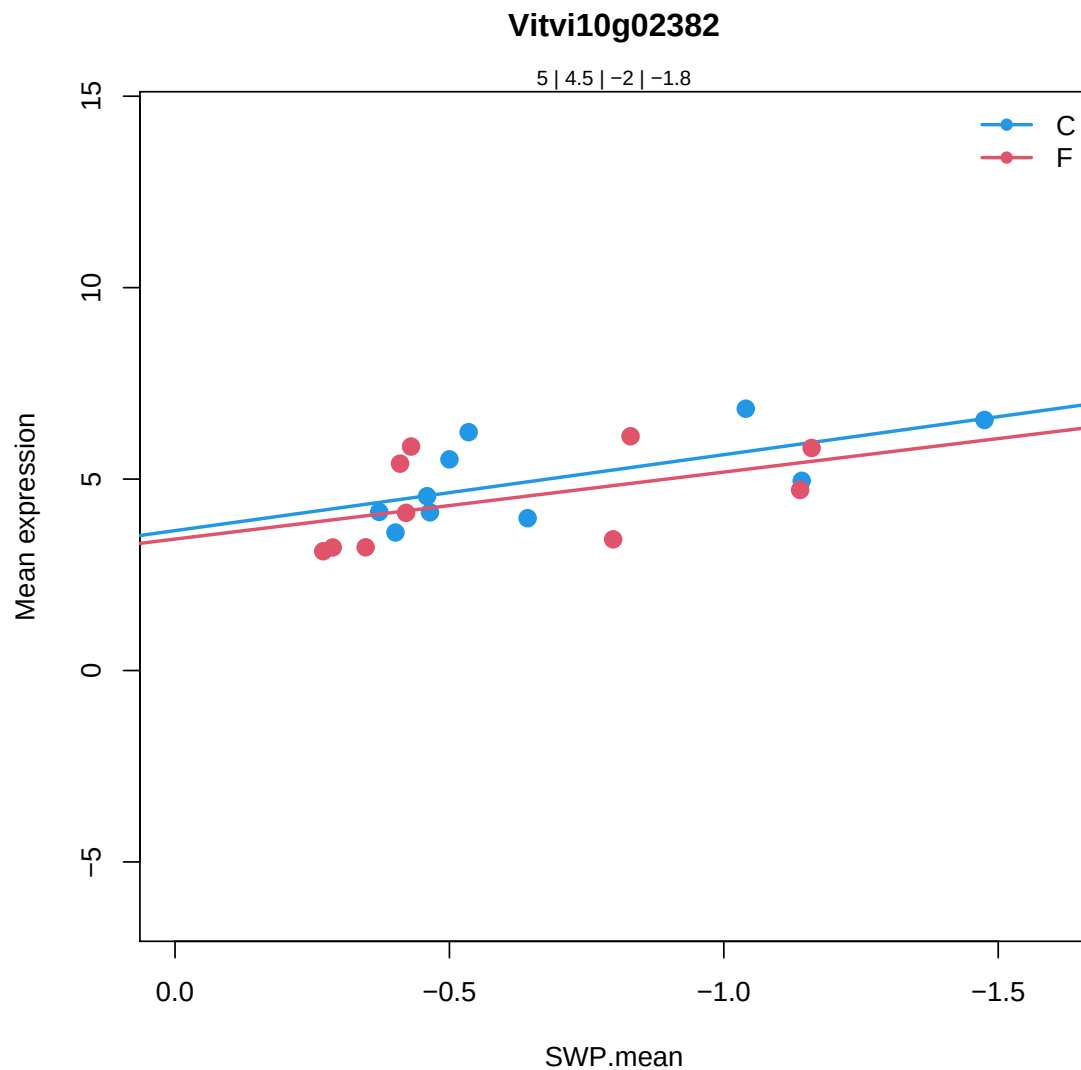
Aldolase-type TIM barrel family protein |

Chr4:11340492-11341732 FORWARD LENGTH=286 |

201606

Coefficients for Vitvi10g02382.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.048511	5.62629e-14	***	8.804509e-14	***
SlopeC	-1.983972	0.02471352	*	0.4060648	
MeanF-MeanC	-0.5497127	0.2018712		0.5452933	
SlopeF-SlopeC	0.2334417	0.8503601		0.9999488	



8.1.83 Vitvi14g01824: * Type1

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

Vitvi14g01824

27.3.11

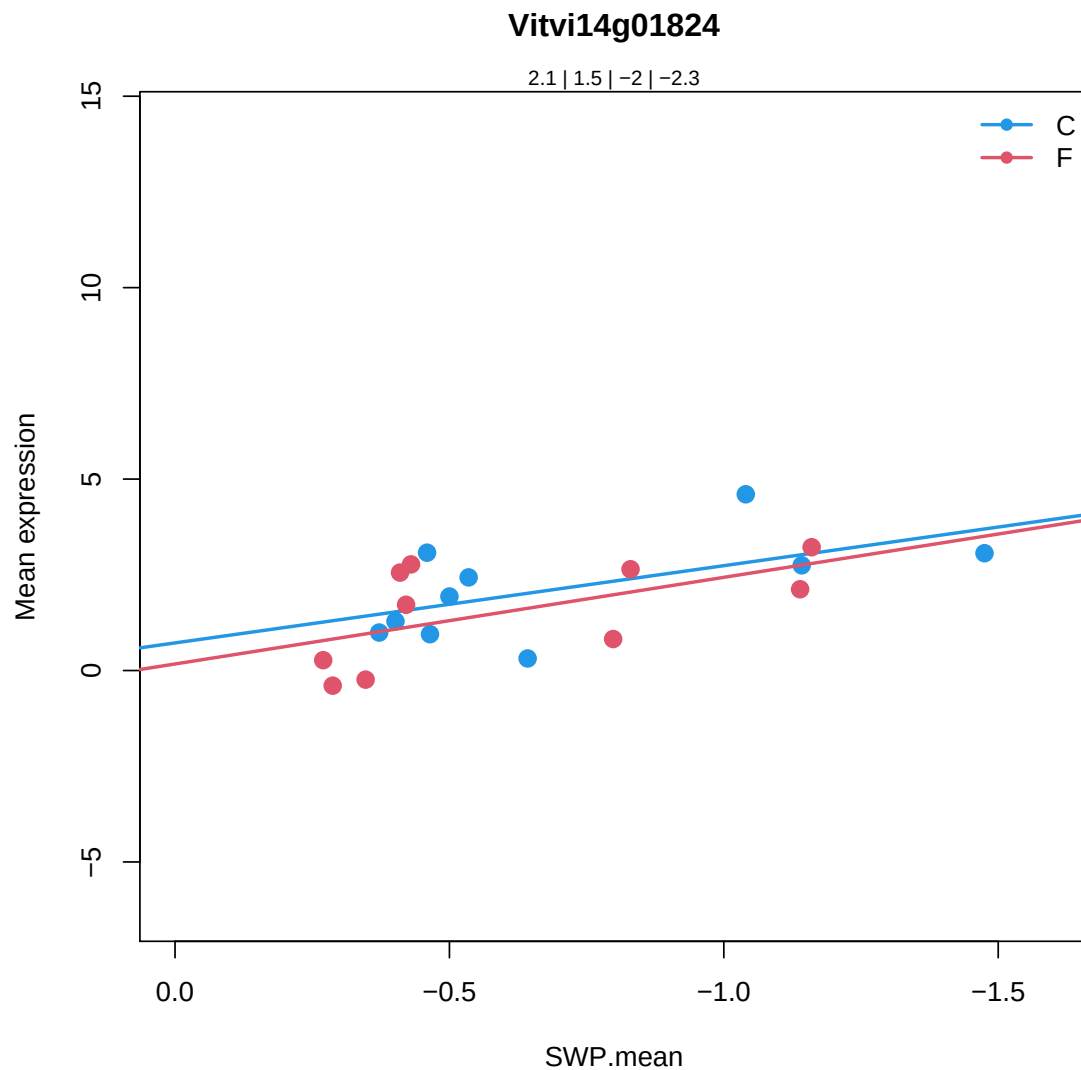
RNA.regulation of transcription.C2H2 zinc finger family
zinc finger (AN1-like) family protein |

Chr3:10520585-10521223 FORWARD LENGTH=186 |

201606

Coefficients for Vitvi14g01824.

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



8.1.84 Vitvi13g00343: * Type1

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

Vitvi13g00343

35.2

not assigned.unknown

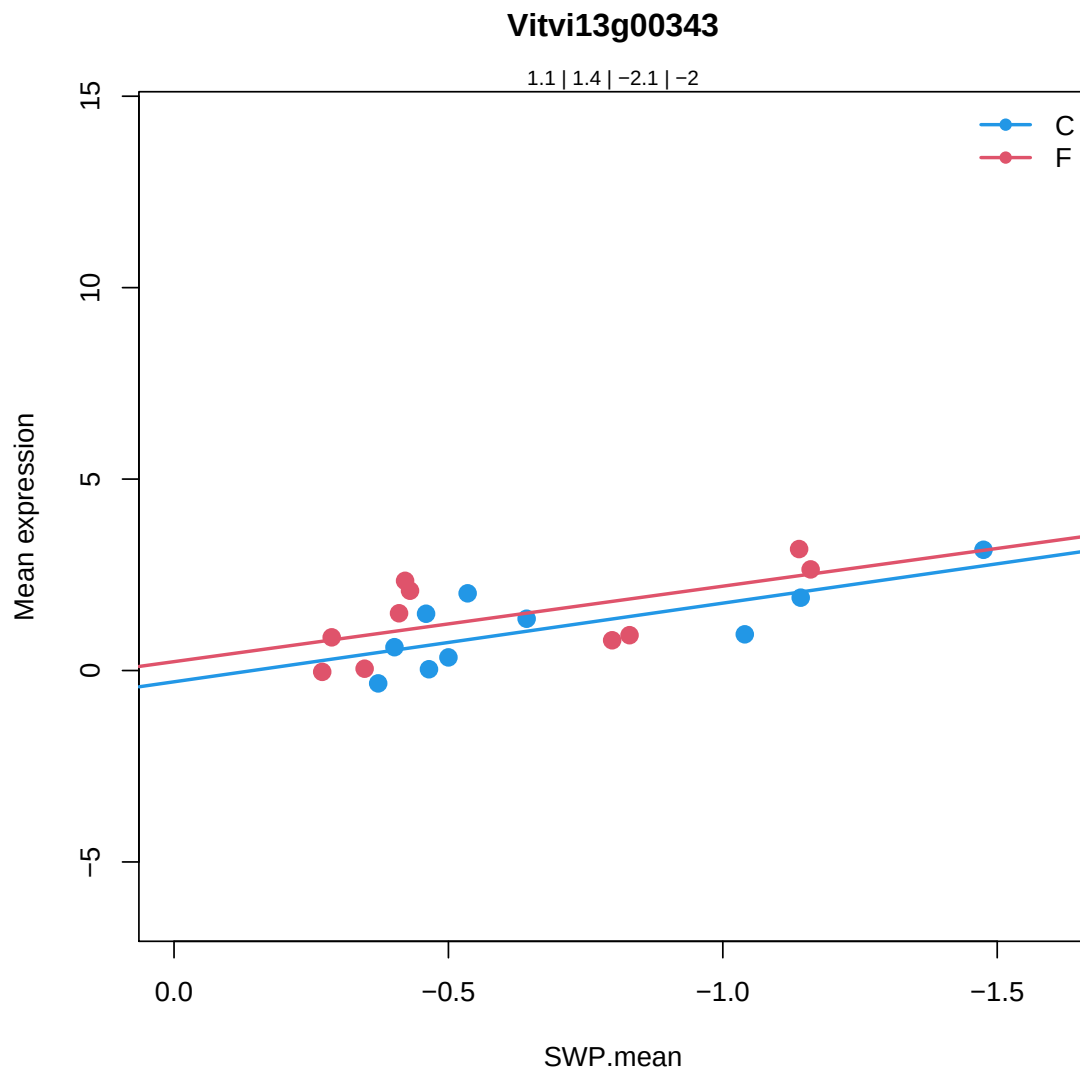
NAD(P)-binding Rossmann-fold superfamily protein |

Chr2:12582523-12583954 FORWARD LENGTH=322 |

201606

Coefficients for Vitvi13g00343.

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



8.1.85 Vitvi08g01890: * Type1

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

Vitvi08g01890

3.1.2.2

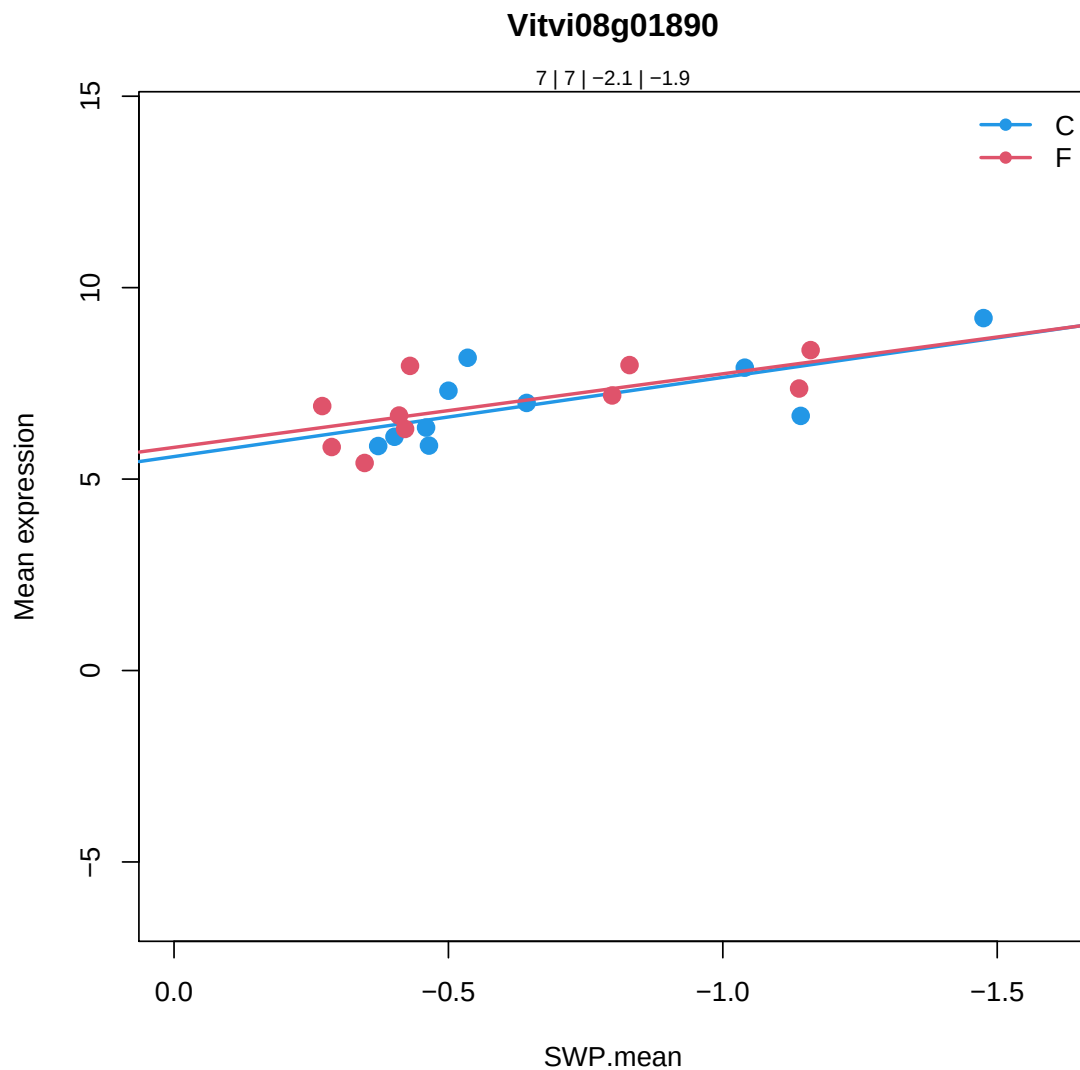
minor CHO metabolism.raffinose family.raffinose synthases.putative
seed imbibition 2 |

Chr3:21288982-21292694 REVERSE LENGTH=773 |

201606

Coefficients for Vitvi08g01890.

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



8.1.86 Vitvi08g01757: * Type1

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

Vitvi08g01757

35.1

not assigned.no ontology

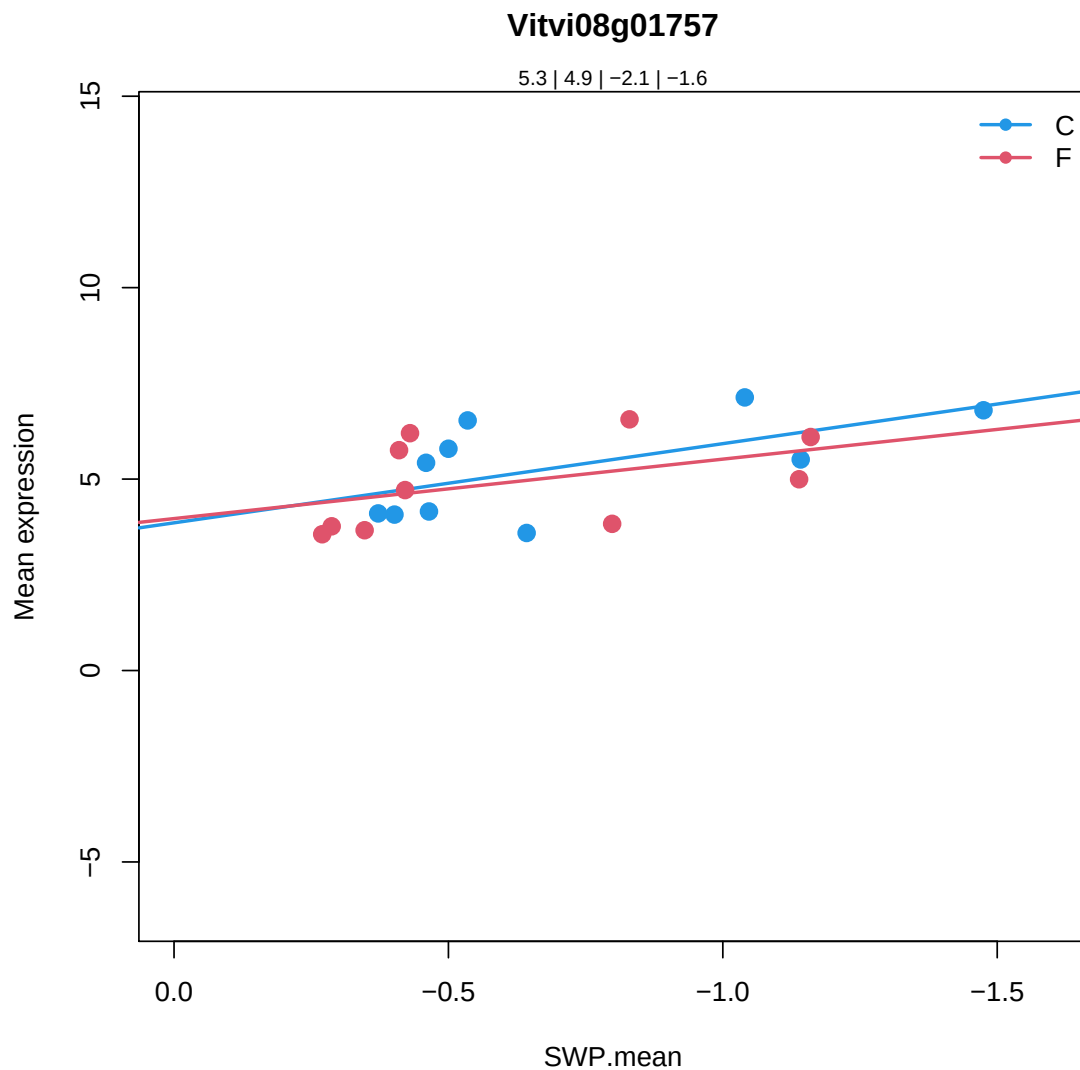
Ahal domain-containing protein |

Chr3:3839289-3841303 FORWARD LENGTH=360 |

201606

Coefficients for Vitvi08g01757.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.311265	4.460549e-14	***	7.040978e-14	***
SlopeC	-2.068001	0.0244177	*	0.4039715	
MeanF-MeanC	-0.397333	0.3703171		0.7247527	
SlopeF-SlopeC	0.5152747	0.6892723		0.9999488	



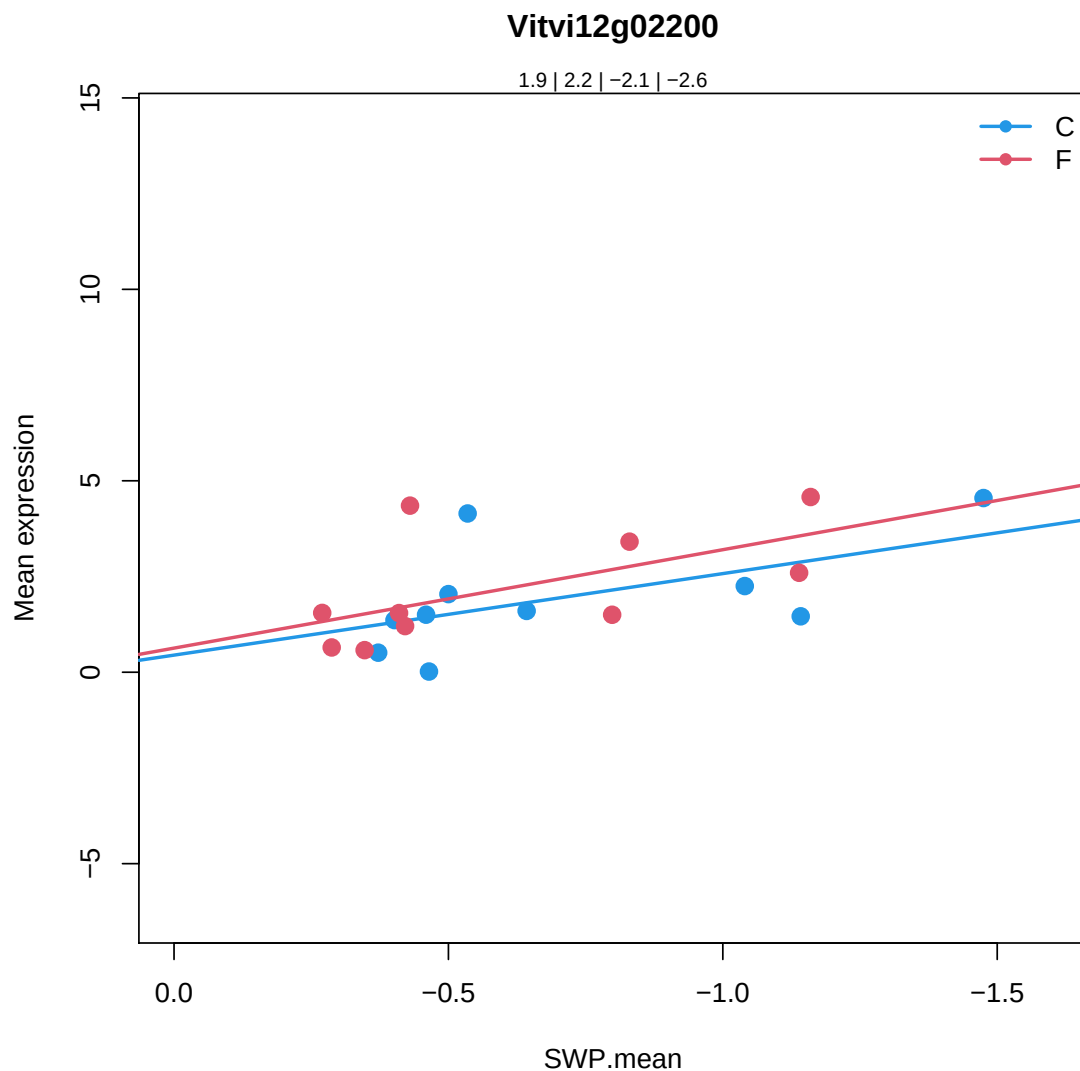
8.1.87 Vitvi12g02200: * Type1

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

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

Coefficients for Vitvi12g02200.

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



8.1.88 Vitvi08g01143: Type1

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

Vitvi08g01143

21.2.1

redox.ascorbate and glutathione.ascorbate

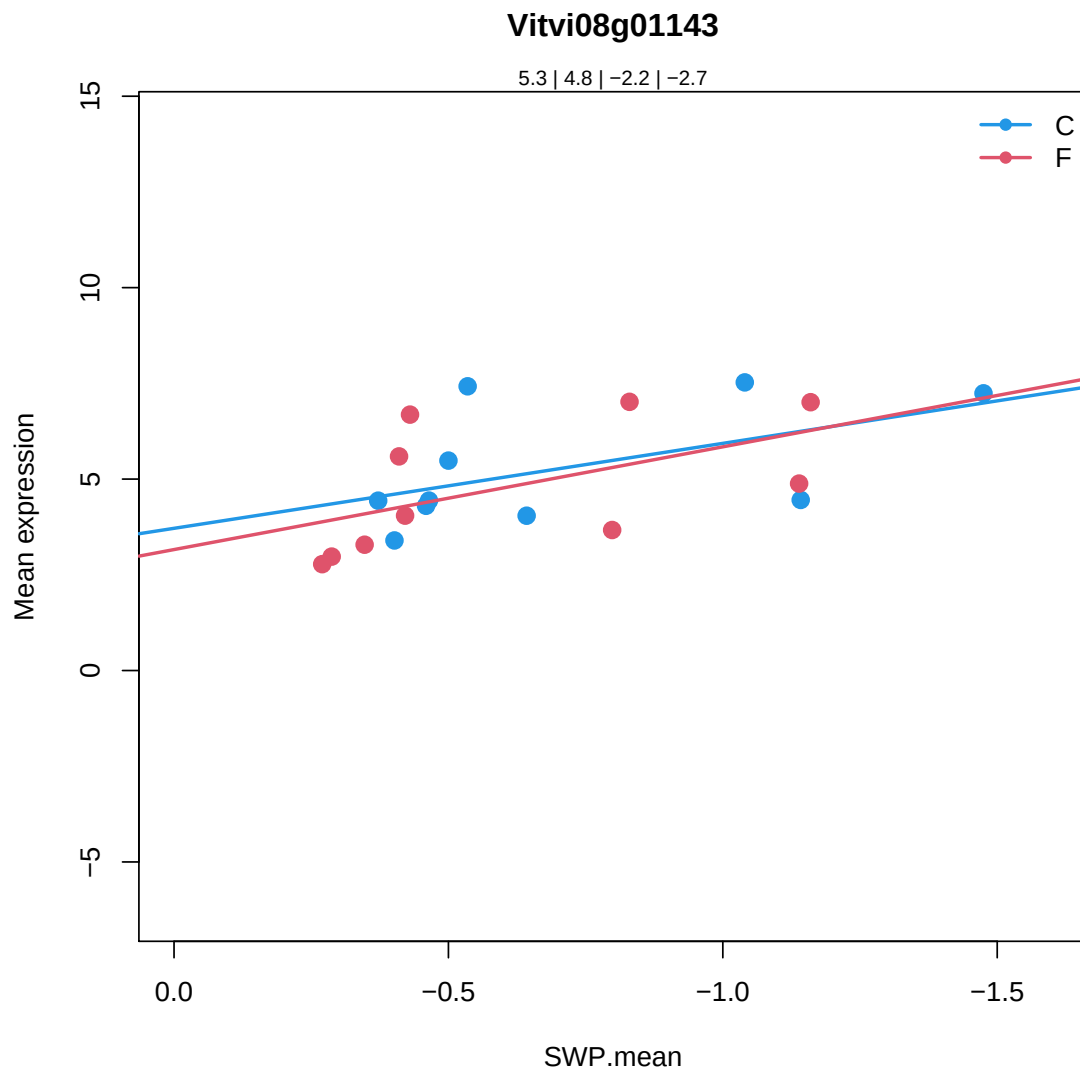
ascorbate peroxidase 2 |

Chr3:2956301-2958163 FORWARD LENGTH=251 |

201606

Coefficients for Vitvi08g01143.

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



8.1.89 Vitvi15g01058: * Type1

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

Vitvi15g01058

34.99

transport.misc

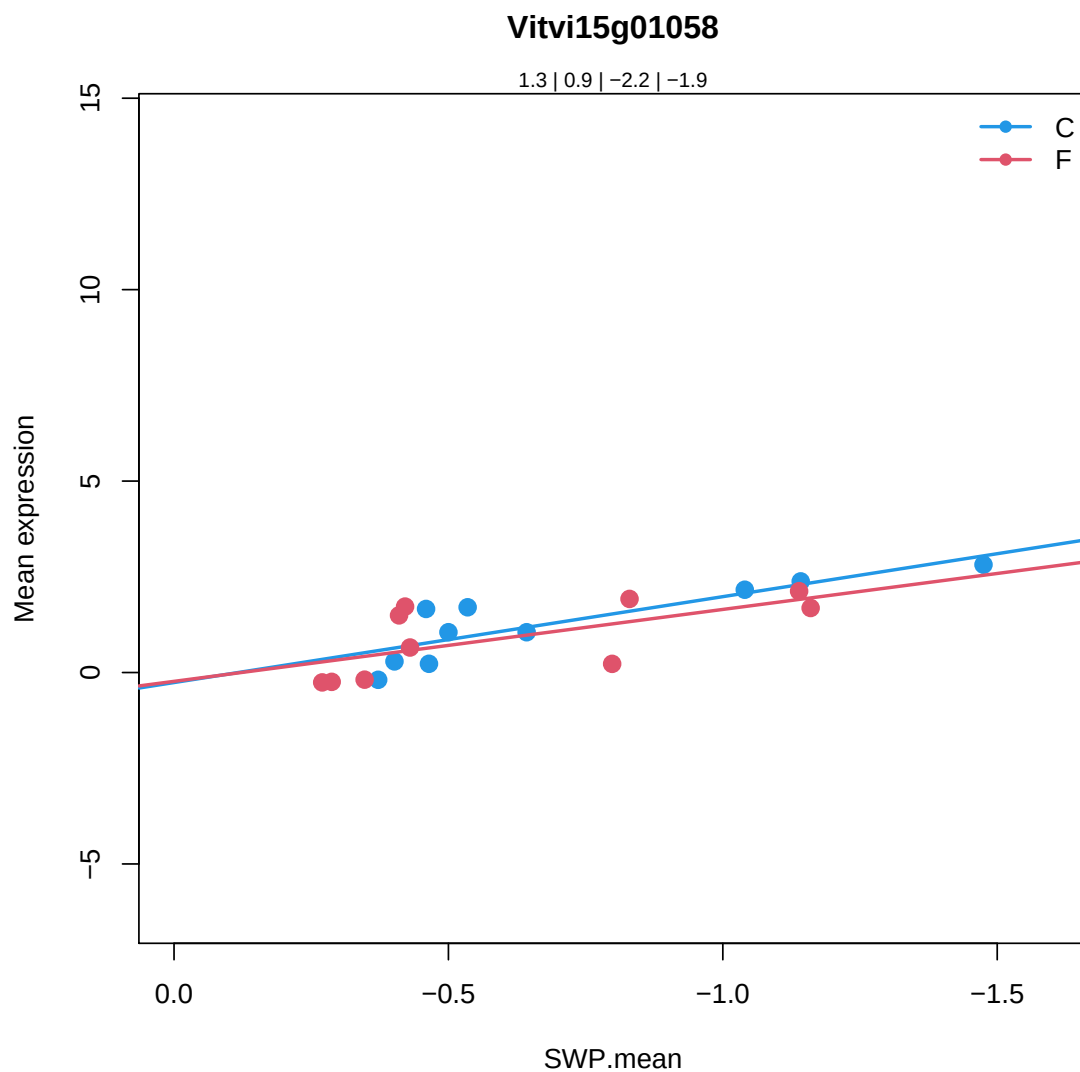
receptor-like protein kinase 4 |

Chr4:148958-151496 FORWARD LENGTH=818 |

201606

Coefficients for Vitvi15g01058.

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



8.1.90 Vitvi16g01167: * Type1

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

Vitvi16g01167

30.2.24

signalling.receptor kinases.S-locus glycoprotein like

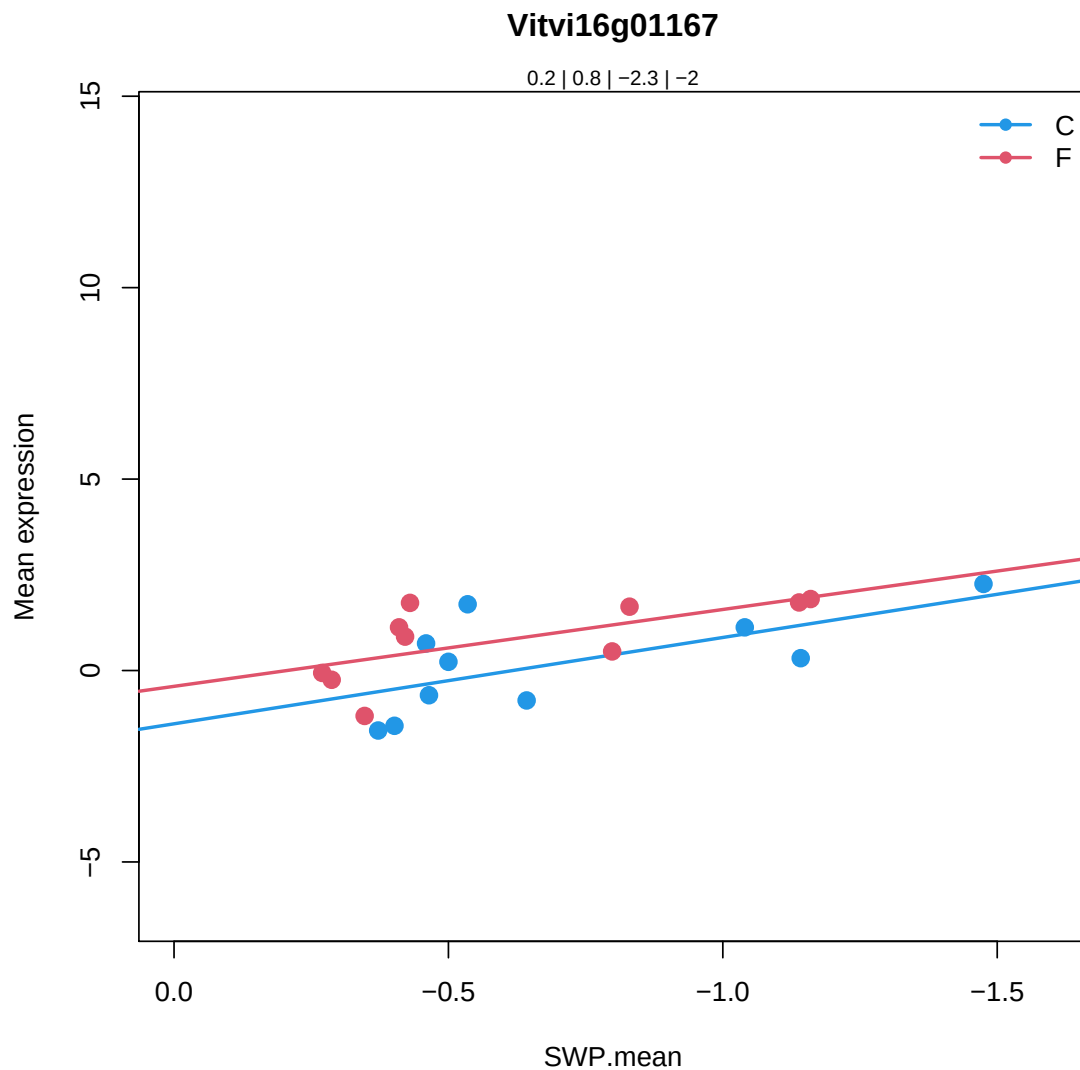
Protein kinase superfamily protein |

Chr5:8139334-8142391 REVERSE LENGTH=872 |

201606

Coefficients for Vitvi16g01167.

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



8.1.91 Vitvi15g00763: * Type1

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

Vitvi15g00763

29.5.1

protein.degradation.subtilases

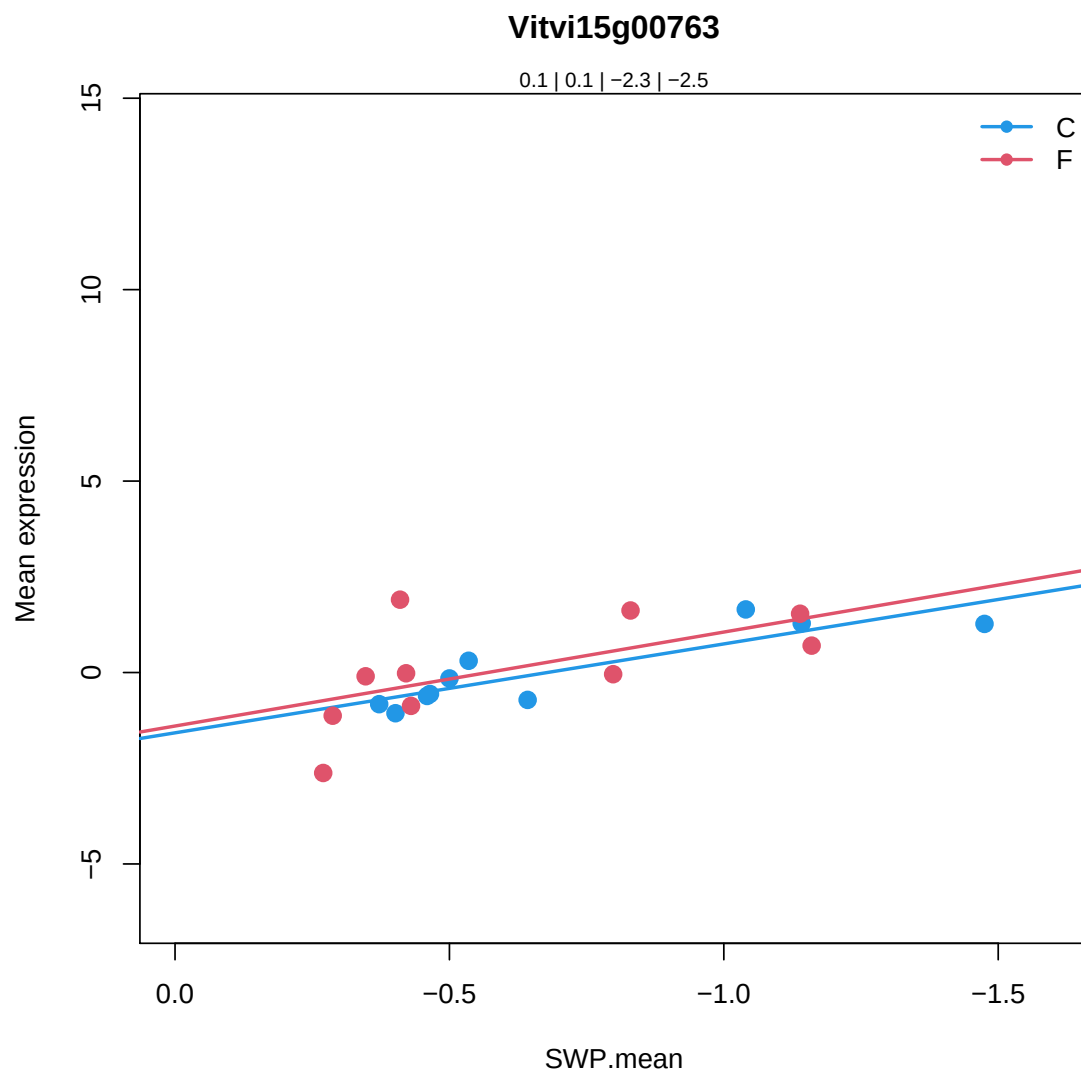
subtilase family protein |

Chr1:310332-313011 FORWARD LENGTH=774 |

201606

Coefficients for Vitvi15g00763.

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



8.1.92 Vitvi08g01112: * Type1

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

Vitvi08g01112

34.16

transport.ABC transporters and multidrug resistance systems

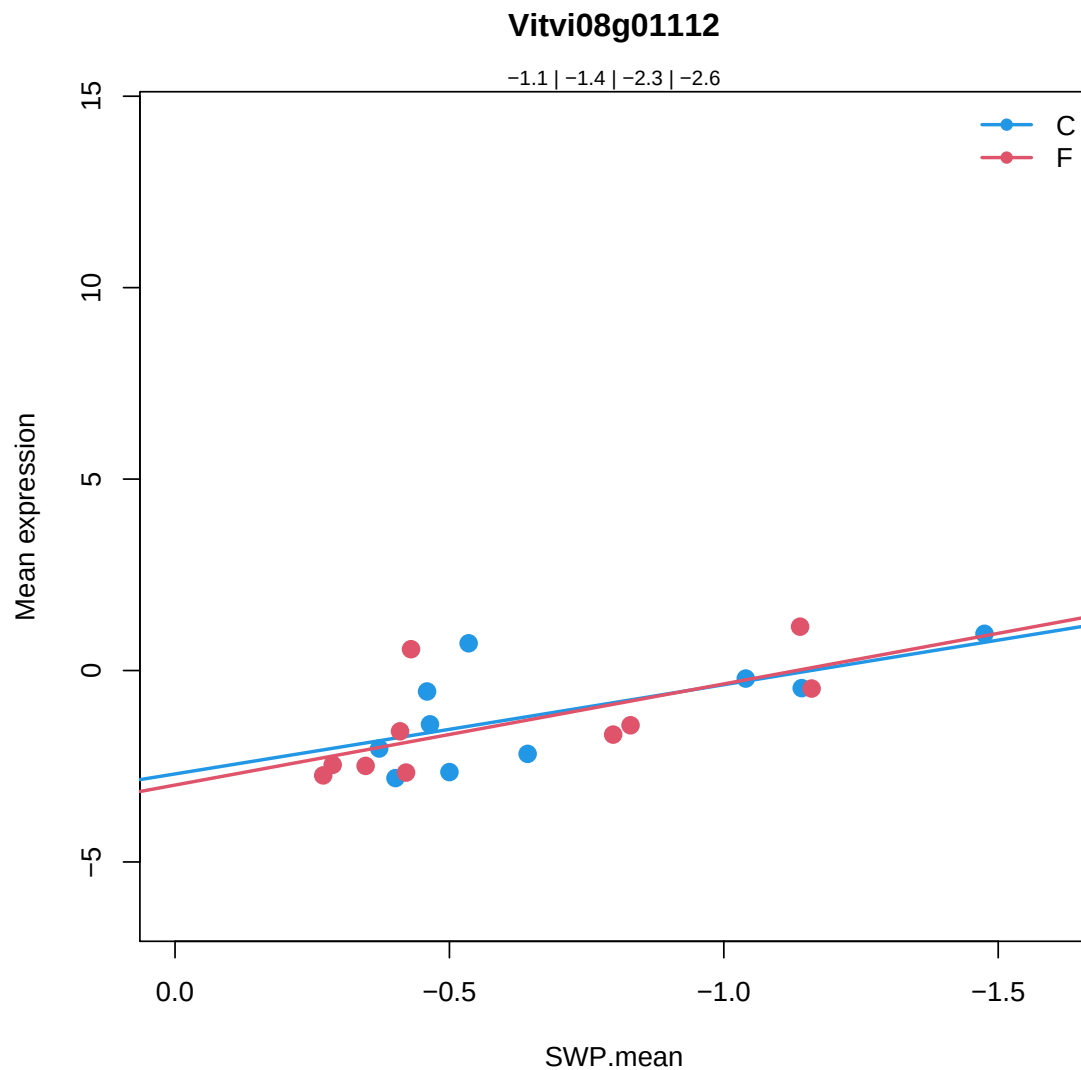
ABC-2 type transporter family protein |

Chr2:15673555-15675822 REVERSE LENGTH=755 |

201606

Coefficients for Vitvi08g01112.

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



8.1.93 Vitvi18g01966: * Type1

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

Vitvi18g01966

35.1

not assigned.no ontology

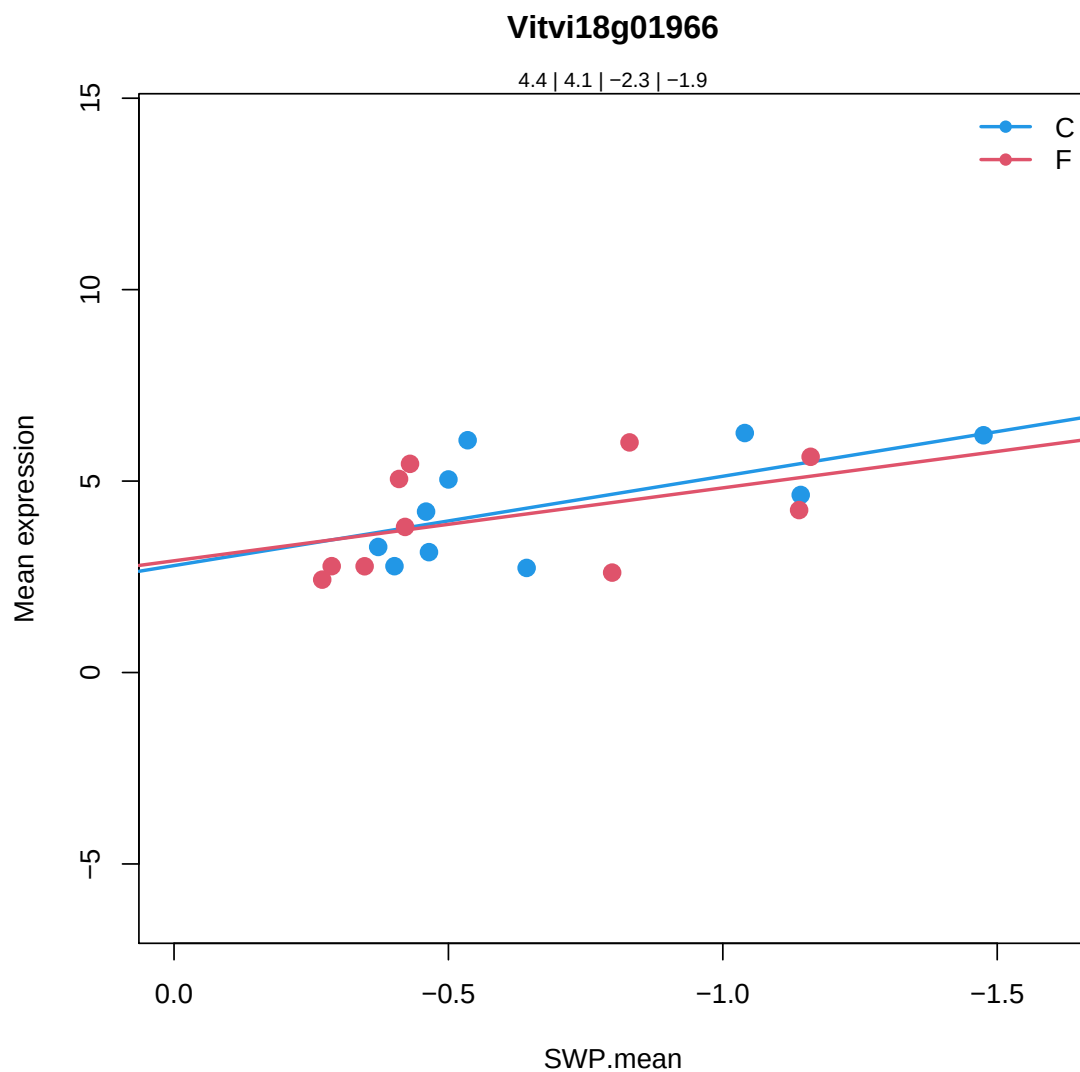
T-complex protein 11 |

Chr1:8118049-8121854 FORWARD LENGTH=1020 |

201606

Coefficients for Vitvi18g01966.

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



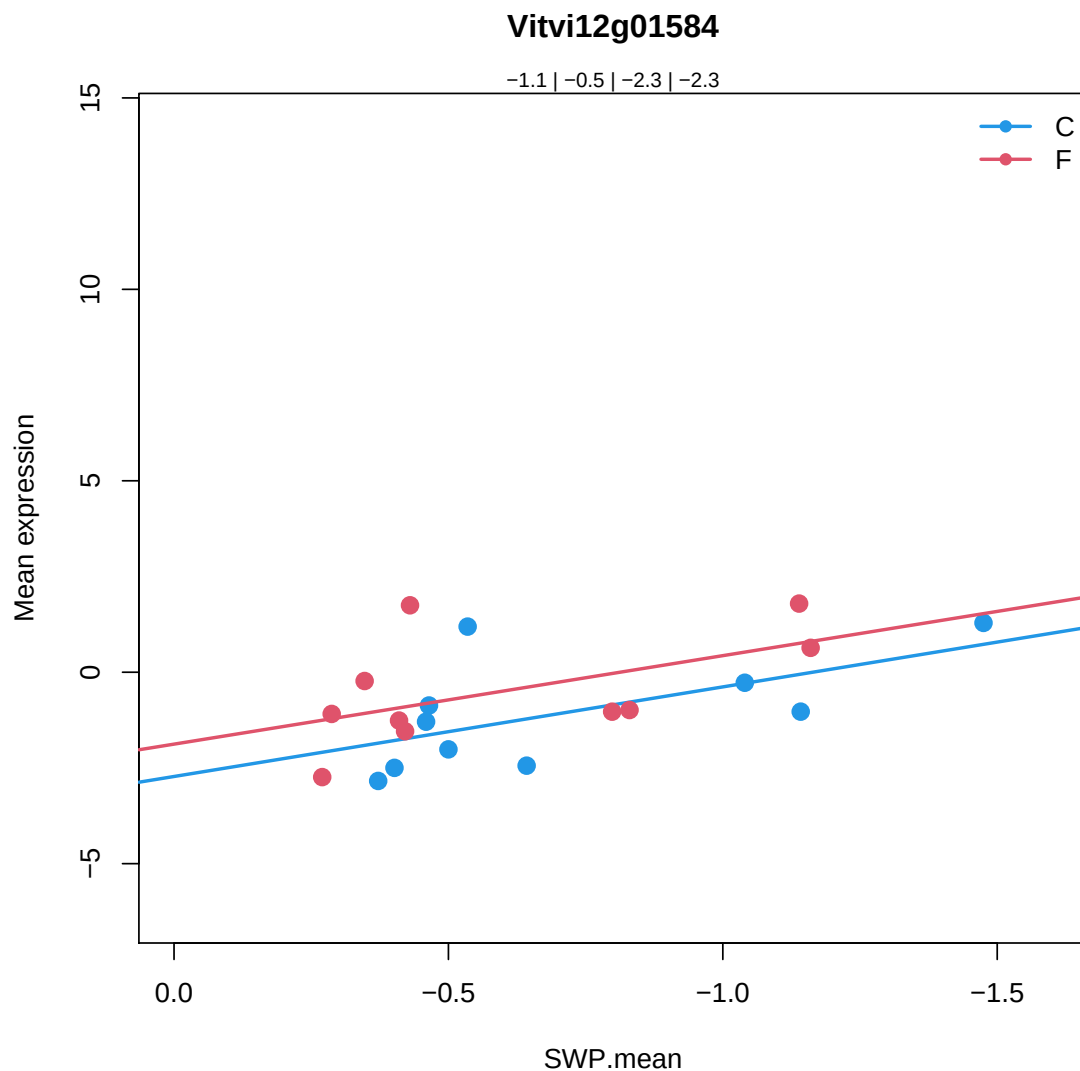
8.1.94 Vitvi12g01584: * Type1

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

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

Coefficients for Vitvi12g01584.

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



8.1.95 Vitvi05g00218: * Type1

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

Vitvi05g00218

34.9

transport.metabolite transporters at the mitochondrial membrane

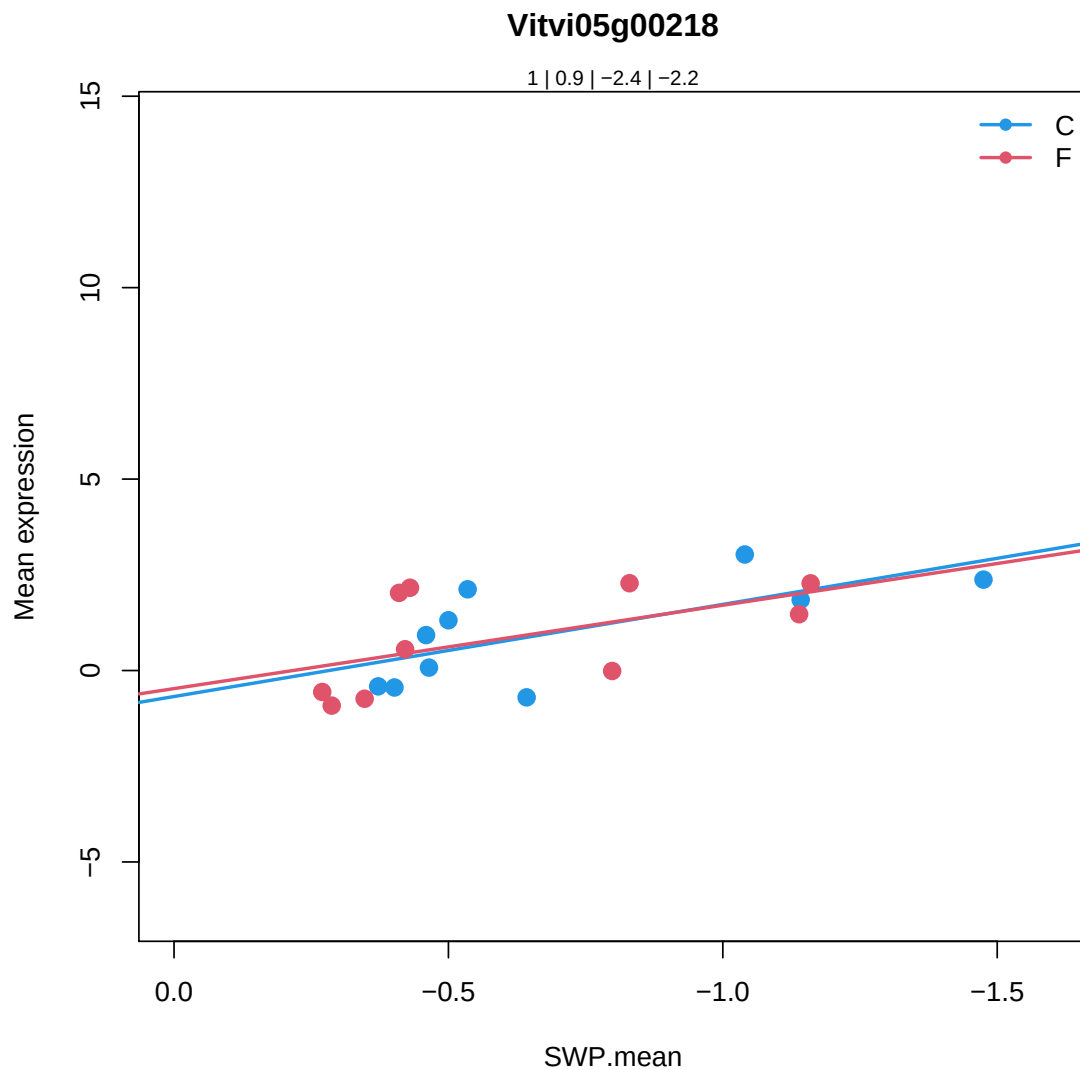
Mitochondrial substrate carrier family protein |

Chr5:5087822-5089677 FORWARD LENGTH=316 |

201606

Coefficients for Vitvi05g00218.

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



8.1.96 Vitvi06g00443: * Type1

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

```
Vitvi06g00443
```

```
29.6
```

```
protein.folding
```

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

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

```
201606
```

```
Vitvi06g00443
```

```
20.2.1
```

```
stress.abiotic.heat
```

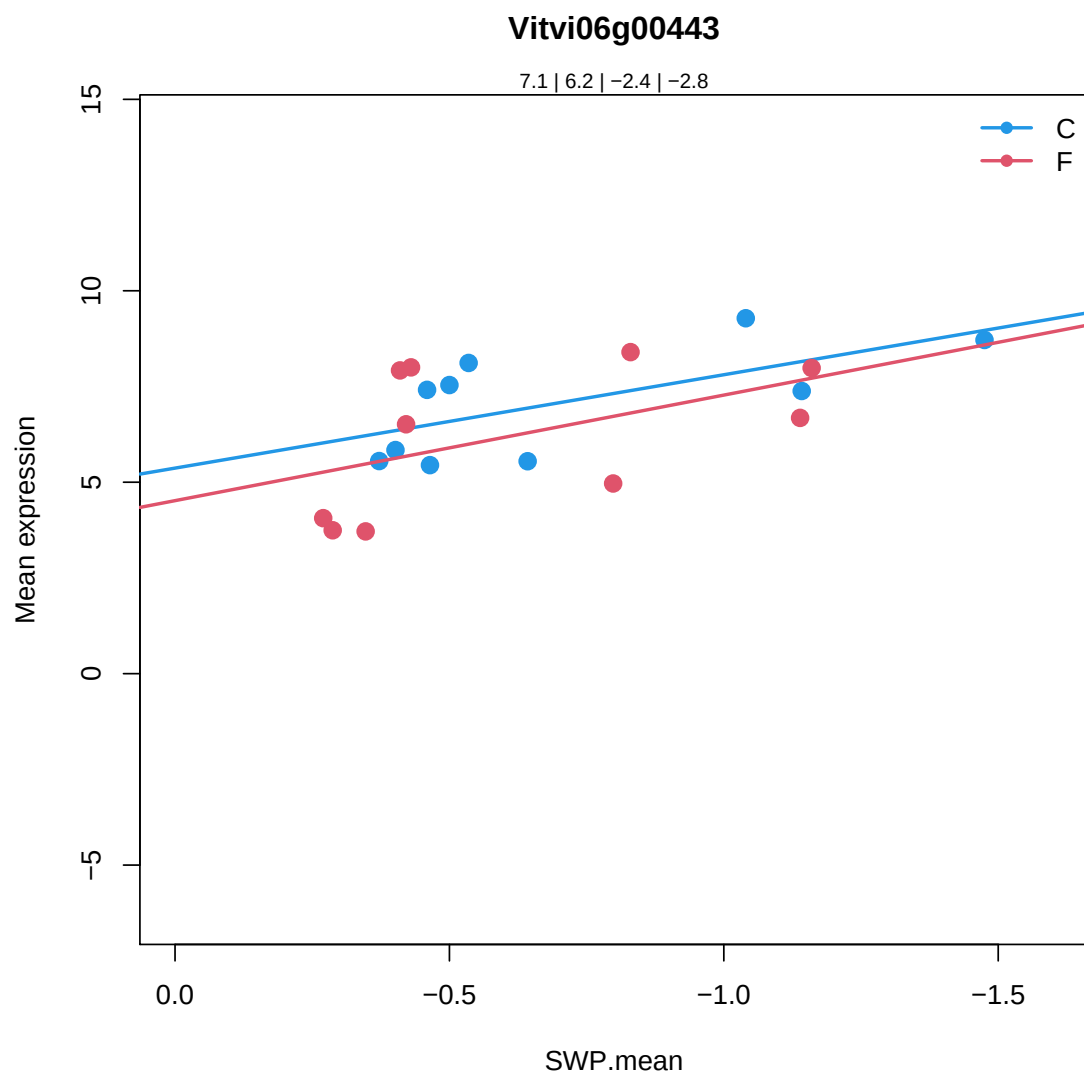
```
heat shock cognate protein 70-1 |
```

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

```
201606
```

Coefficients for Vitvi06g00443.

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



8.1.97 Vitvi11g00513: * Type1

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

Vitvi11g00513

3.1.2.2

minor CHO metabolism.raffinose family.raffinose synthases.putative

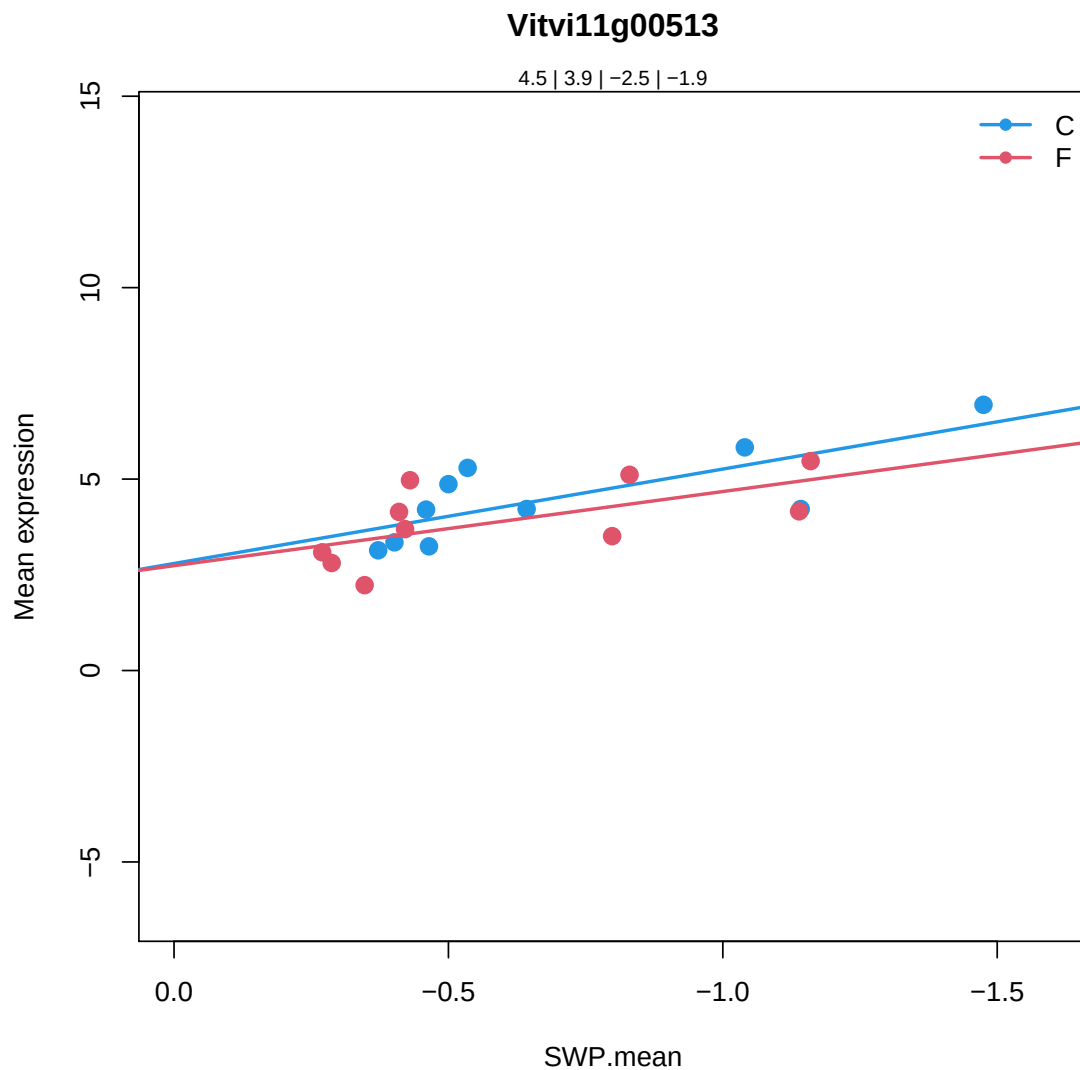
Raffinose synthase family protein |

Chr5:6833730-6836635 FORWARD LENGTH=844 |

201606

Coefficients for Vitvi11g00513.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.529491	1.273499e-14	***	2.106421e-14	***
SlopeC	-2.466365	0.001629253	**	0.1556102	
MeanF-MeanC	-0.6117002	0.09301346	.	0.3495771	
SlopeF-SlopeC	0.5296637	0.6084689		0.9999488	



8.1.98 Vitvi06g00440: * Type1

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

Vitvi06g00440

35.2

not assigned.unknown

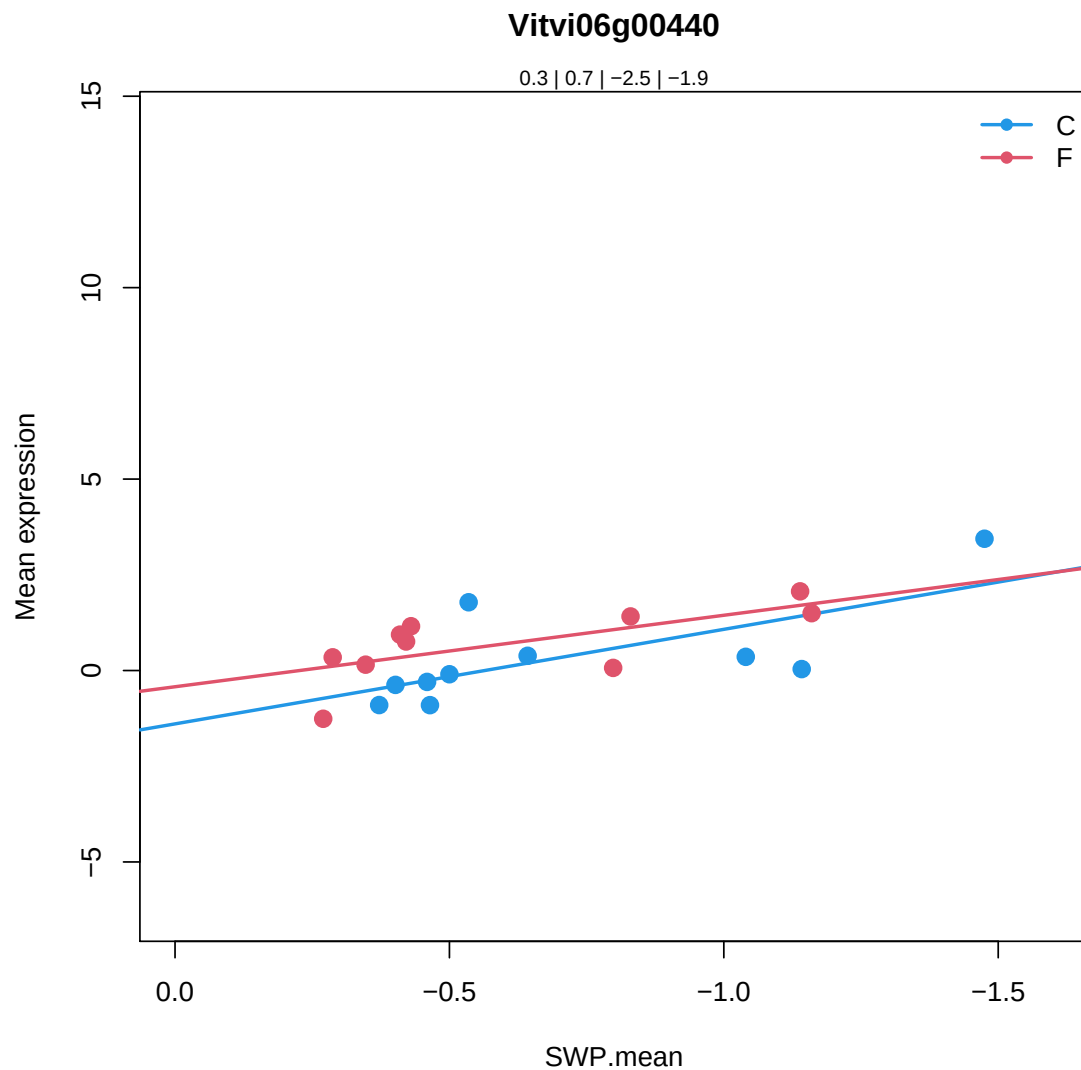
Pathogenesis-related thaumatin superfamily protein |

Chr2:12354664-12355488 REVERSE LENGTH=274 |

201606

Coefficients for Vitvi06g00440.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.3426808	0.1888425		0.1937231	
SlopeC	-2.469205	0.002009926	**	0.1692557	
MeanF-MeanC	0.3706863	0.3107926		0.6747237	
SlopeF-SlopeC	0.6023688	0.570529		0.9999488	



8.1.99 Vitvi06g00605: * Type1

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

Vitvi06g00605

26.10

misc.cytochrome P450

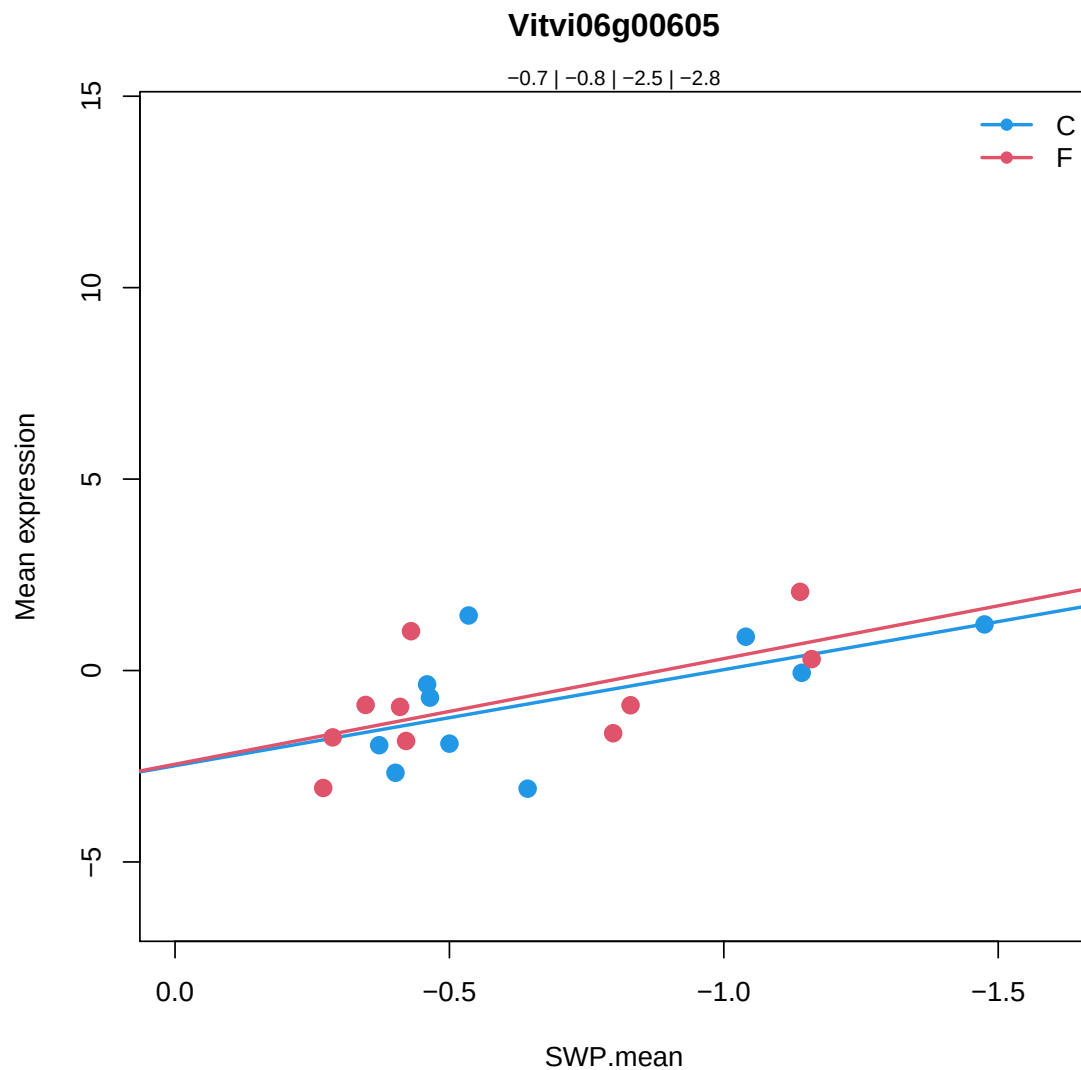
cytochrome P450%2C family 86%2C subfamily A%2C polypeptide 1 |

Chr5:23765999-23767997 REVERSE LENGTH=513 |

201606

Coefficients for Vitvi06g00605.

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



8.1.100 Vitvi04g00522: * Type1

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

Vitvi04g00522

20.2.1

stress.abiotic.heat

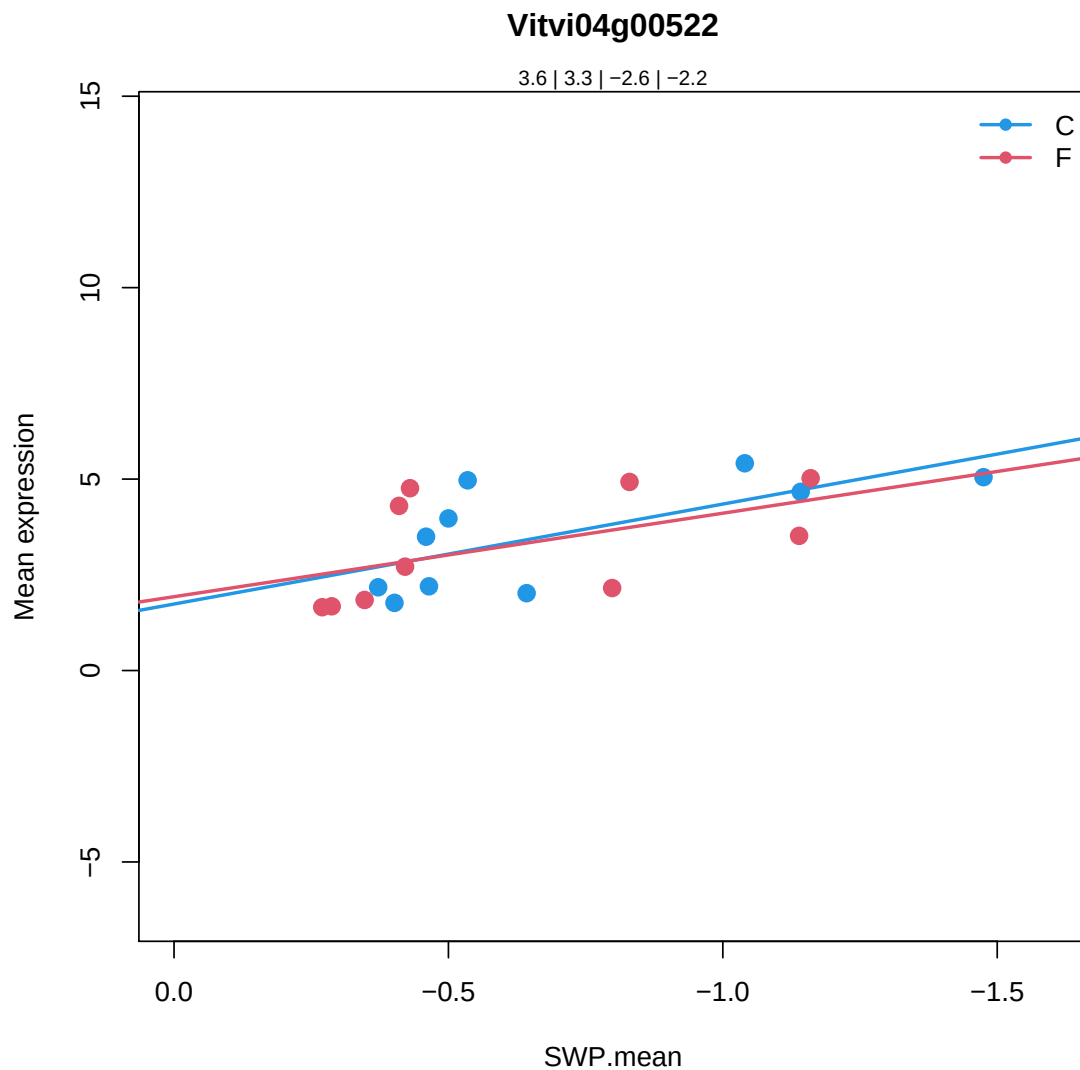
casein lytic proteinase B4 |

Chr2:10697877-10701998 REVERSE LENGTH=964 |

201606

Coefficients for Vitvi04g00522.

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



8.1.101 Vitvi01g01459: * Type1

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

Vitvi01g01459

17.1.3

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

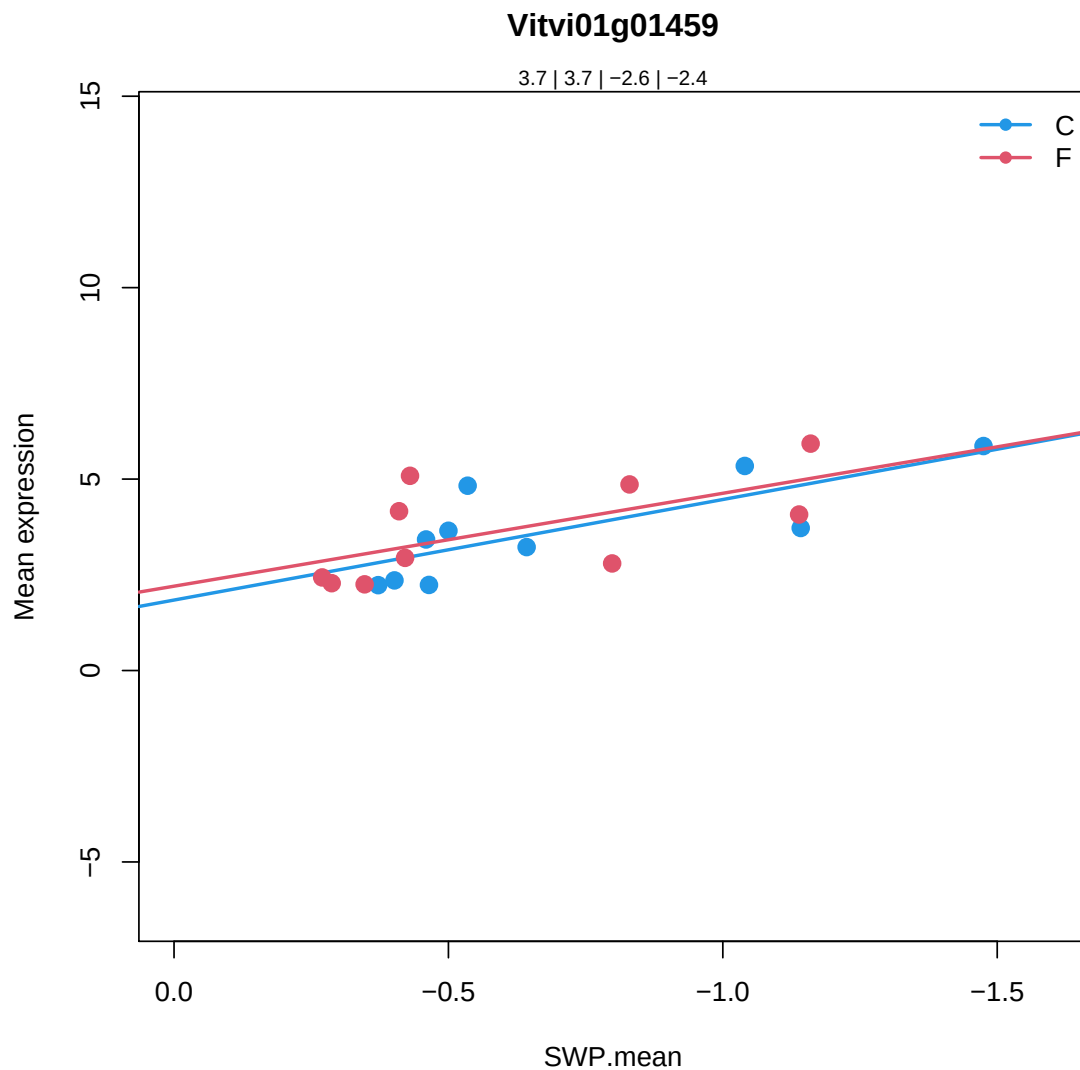
GRAM domain family protein |

Chr5:4207081-4207812 FORWARD LENGTH=213 |

201606

Coefficients for Vitvi01g01459.

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



8.1.102 Vitvi14g02026: * Type1

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

Vitvi14g02026

20.2.1

stress.abiotic.heat

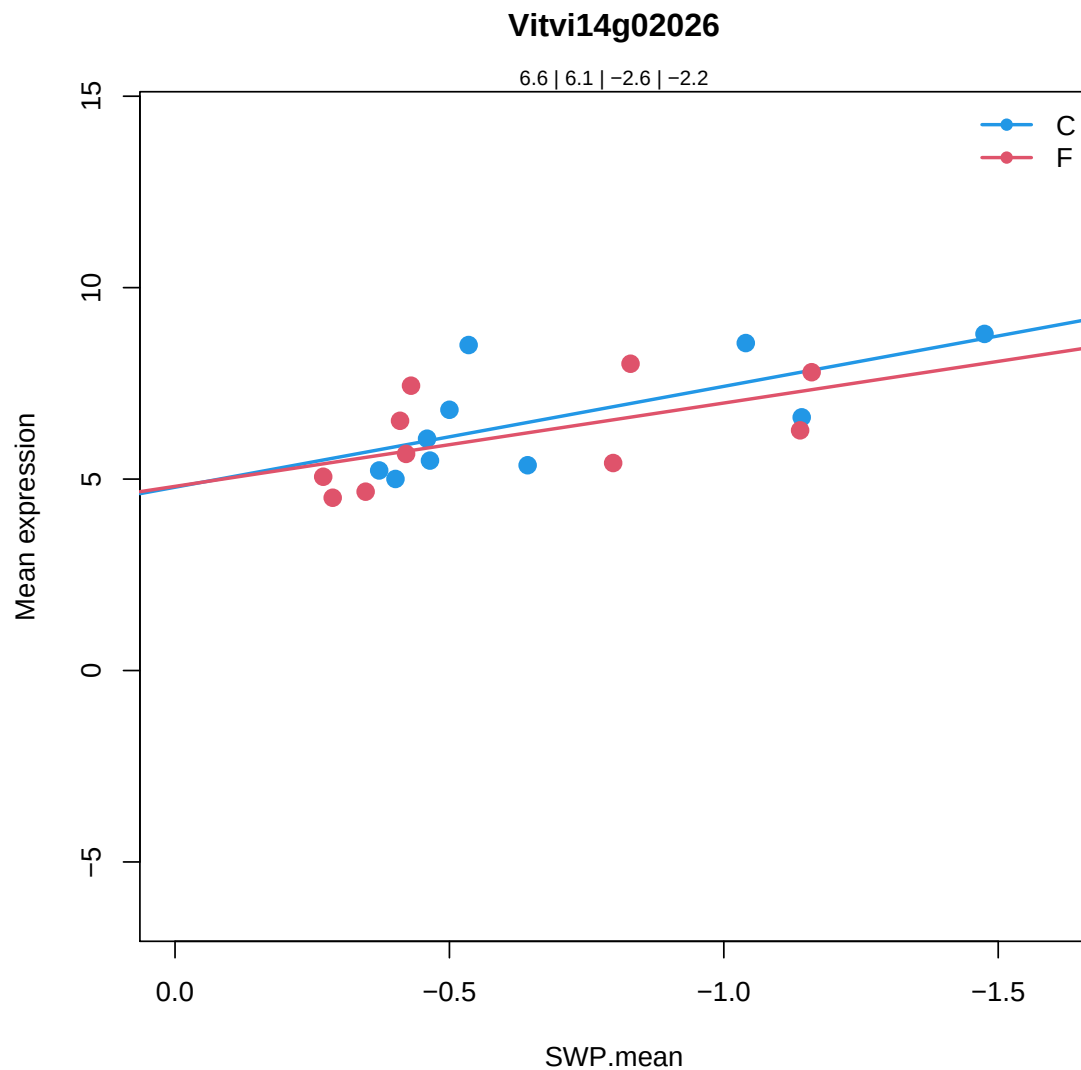
casein lytic proteinase B3 |

Chr5:5014399-5018255 REVERSE LENGTH=968 |

201606

Coefficients for Vitvi14g02026.

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



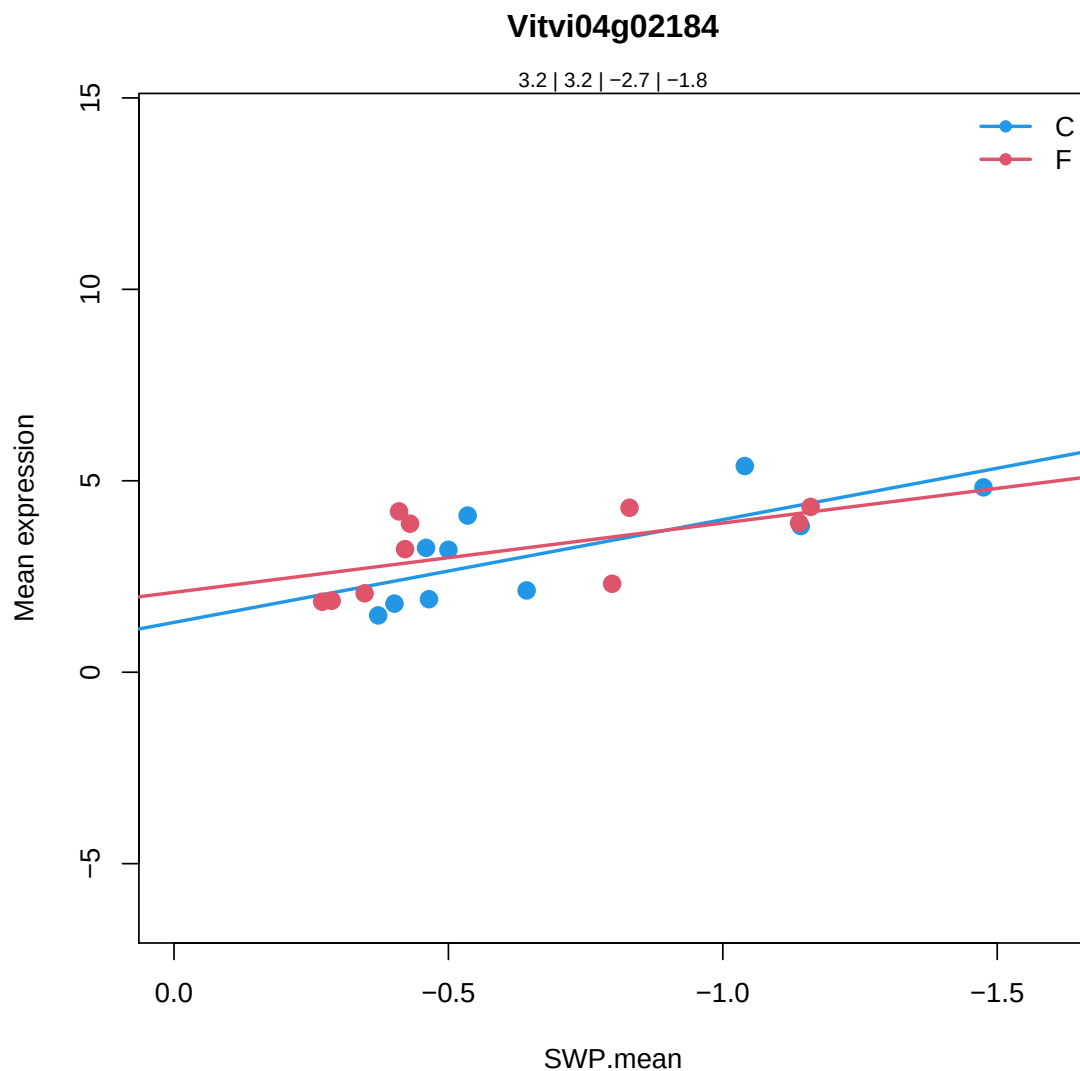
8.1.103 Vitvi04g02184: * Type1

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

```
Vitvi04g02184
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi04g02184.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.188648	4.960672e-11	***	6.572546e-11	***
SlopeC	-2.684272	0.001446058	**	0.1479249	
MeanF-MeanC	4.405018e-05	0.999907		0.9999648	
SlopeF-SlopeC	0.8740834	0.4329252		0.9999488	



8.1.104 Vitvi01g00424: * Type1

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

Vitvi01g00424

29

protein

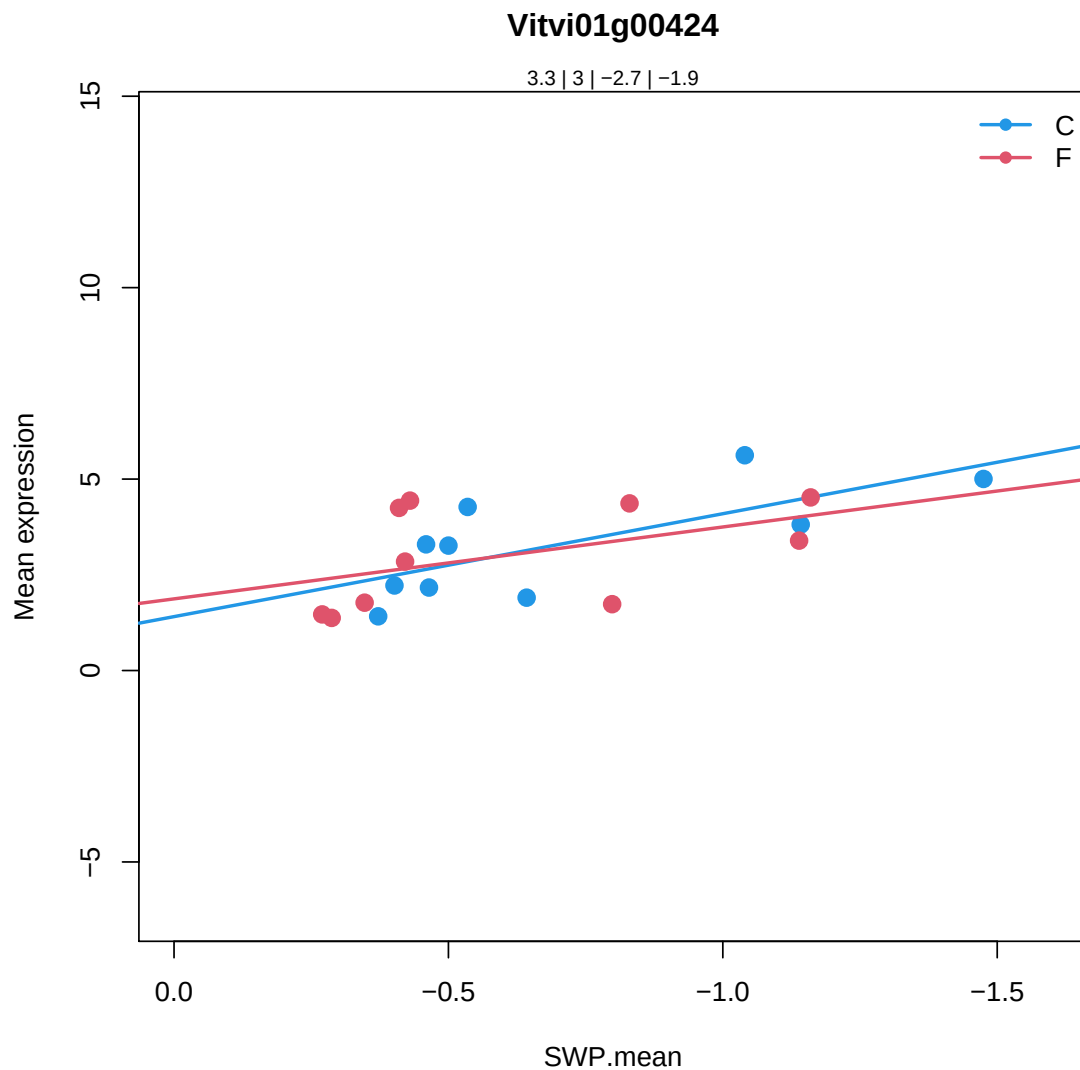
GroES-like family protein |

Chr1:8195867-8196336 FORWARD LENGTH=97 |

201606

Coefficients for Vitvi01g00424.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.297455	8.49922e-10	***	1.073905e-09	***
SlopeC	-2.687409	0.006251116	**	0.2647742	
MeanF-MeanC	-0.2822733	0.5376877		0.8284076	
SlopeF-SlopeC	0.8097099	0.5459104		0.9999488	



8.1.105 Vitvi16g00681: * Type1

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

Vitvi16g00681

20.2.1

stress.abiotic.heat

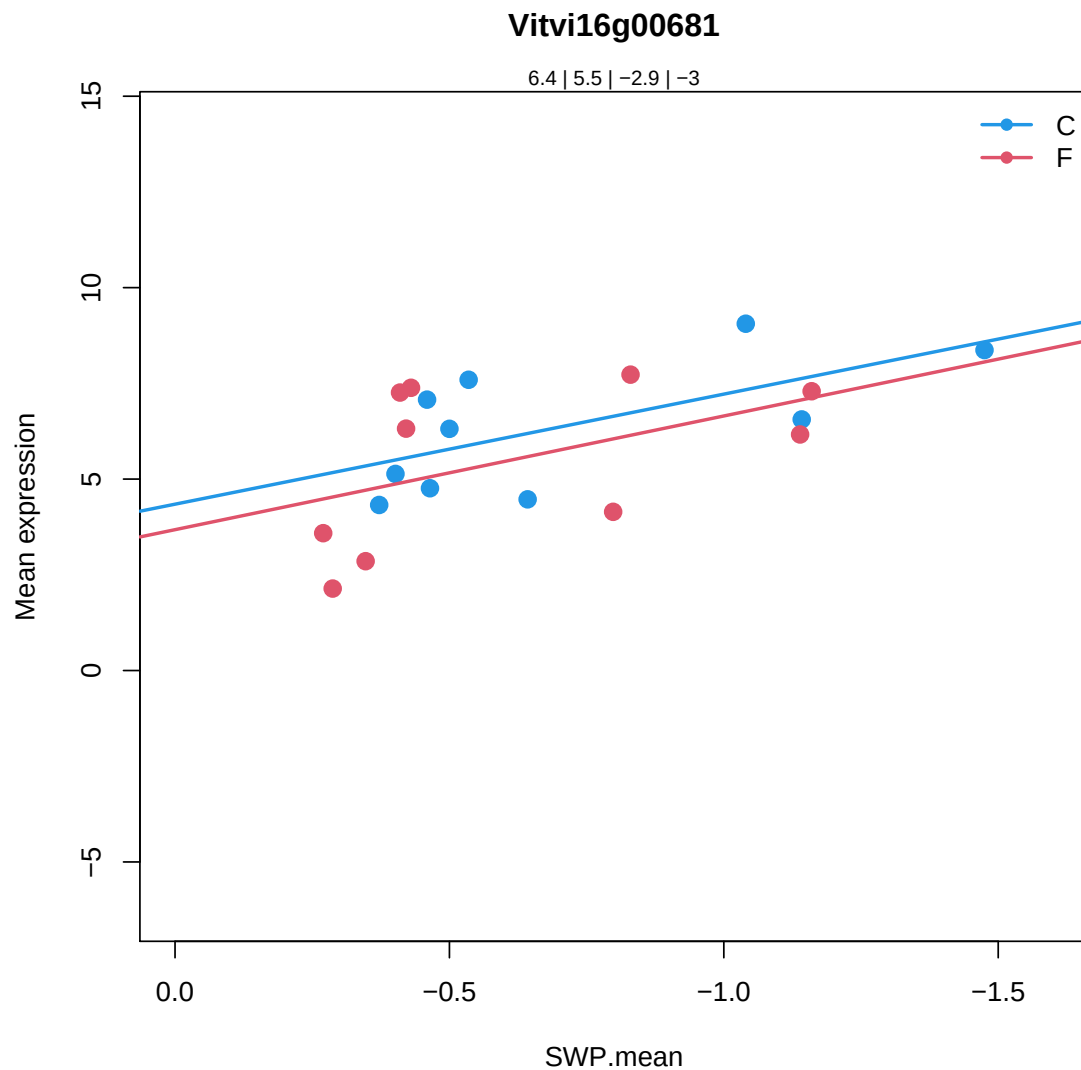
mitochondrion-localized small heat shock protein 23.6 |

Chr4:12917089-12917858 FORWARD LENGTH=210 |

201606

Coefficients for Vitvi16g00681.

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



8.1.106 Vitvi08g00689: * Type1

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

Vitvi08g00689

20.2.1

stress.abiotic.heat

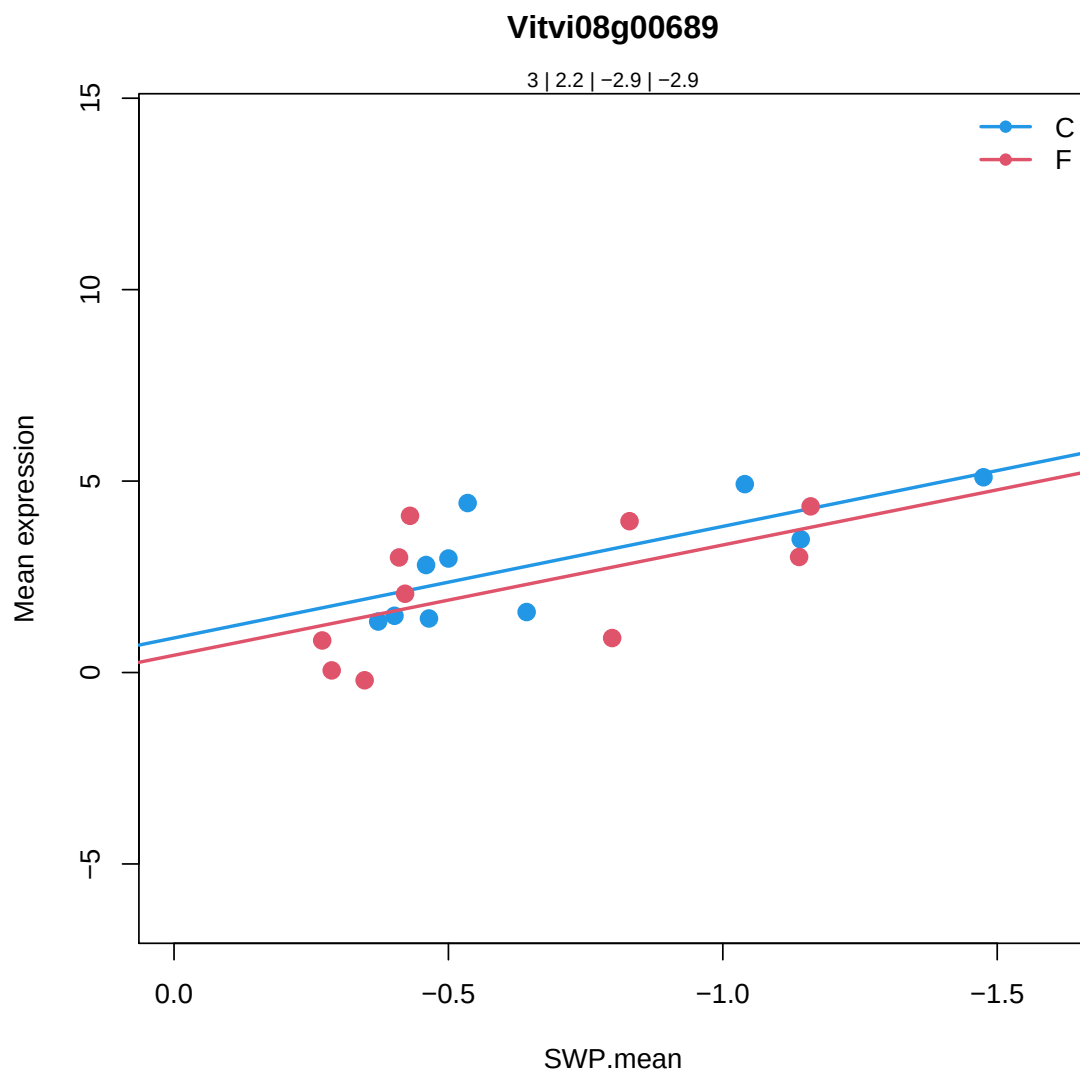
DNAJ heat shock N-terminal domain-containing protein |

Chr3:2737589-2740265 FORWARD LENGTH=572 |

201606

Coefficients for Vitvi08g00689.

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



8.1.107 Vitvi05g01833: * Type1

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

Vitvi05g01833

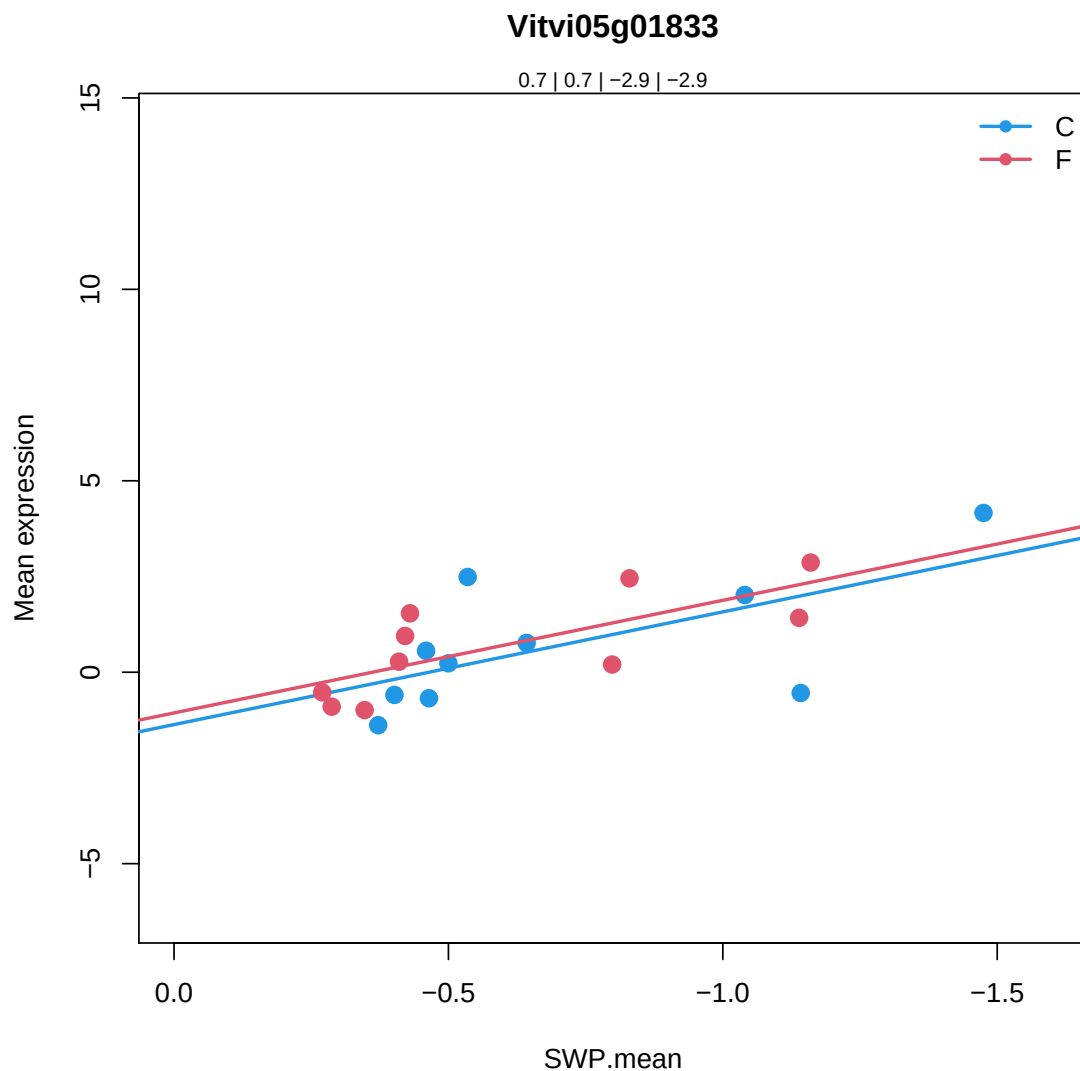
35.2

not assigned.unknown

NA

Coefficients for Vitvi05g01833.

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



8.1.108 Vitvi17g00085: * Type1

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

Vitvi17g00085

17.1.3

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

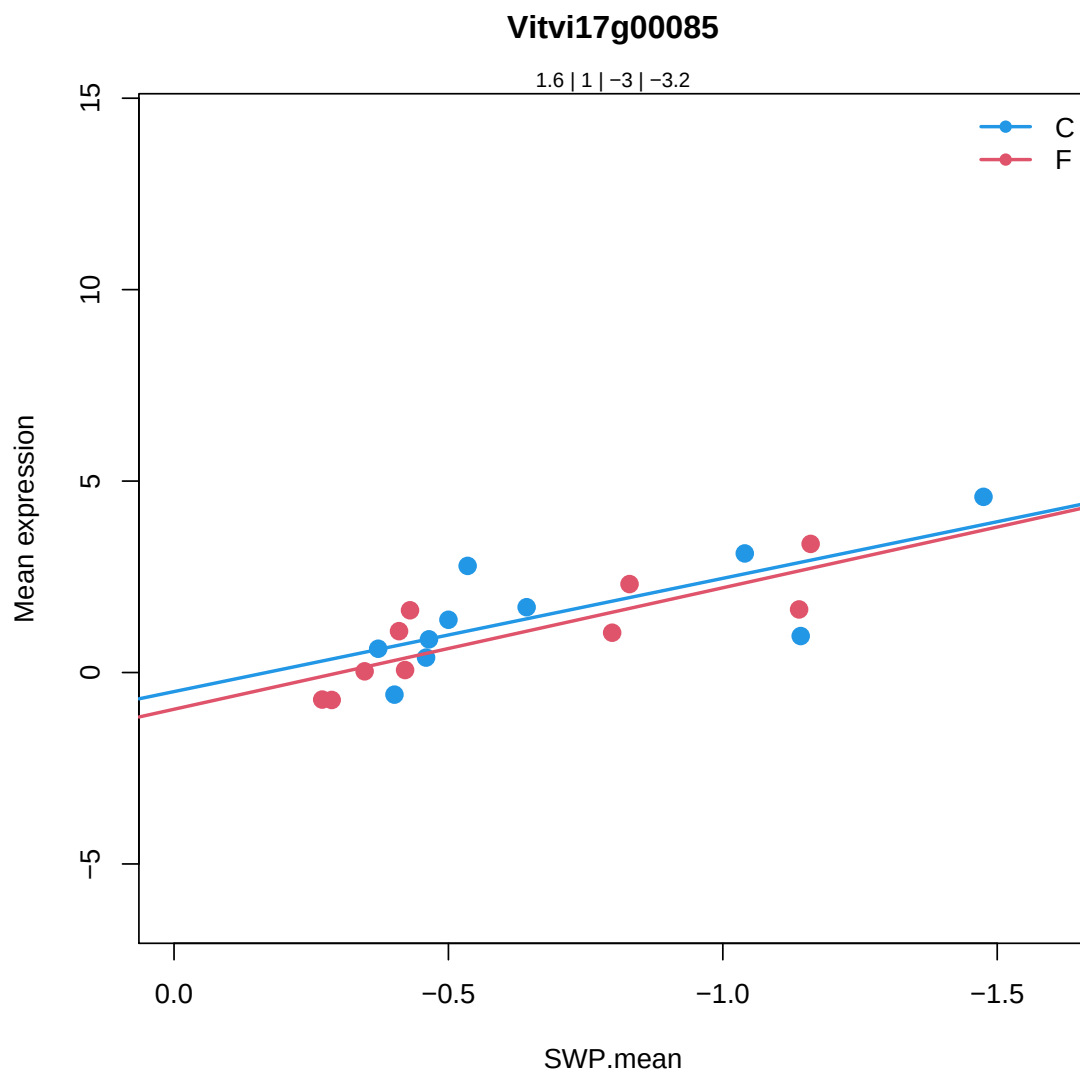
HVA22 homologue D |

Chr4:12828237-12829019 FORWARD LENGTH=135 |

201606

Coefficients for Vitvi17g00085.

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



8.1.109 Vitvi13g01107: Type1

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

Vitvi13g01107

35.2

not assigned.unknown

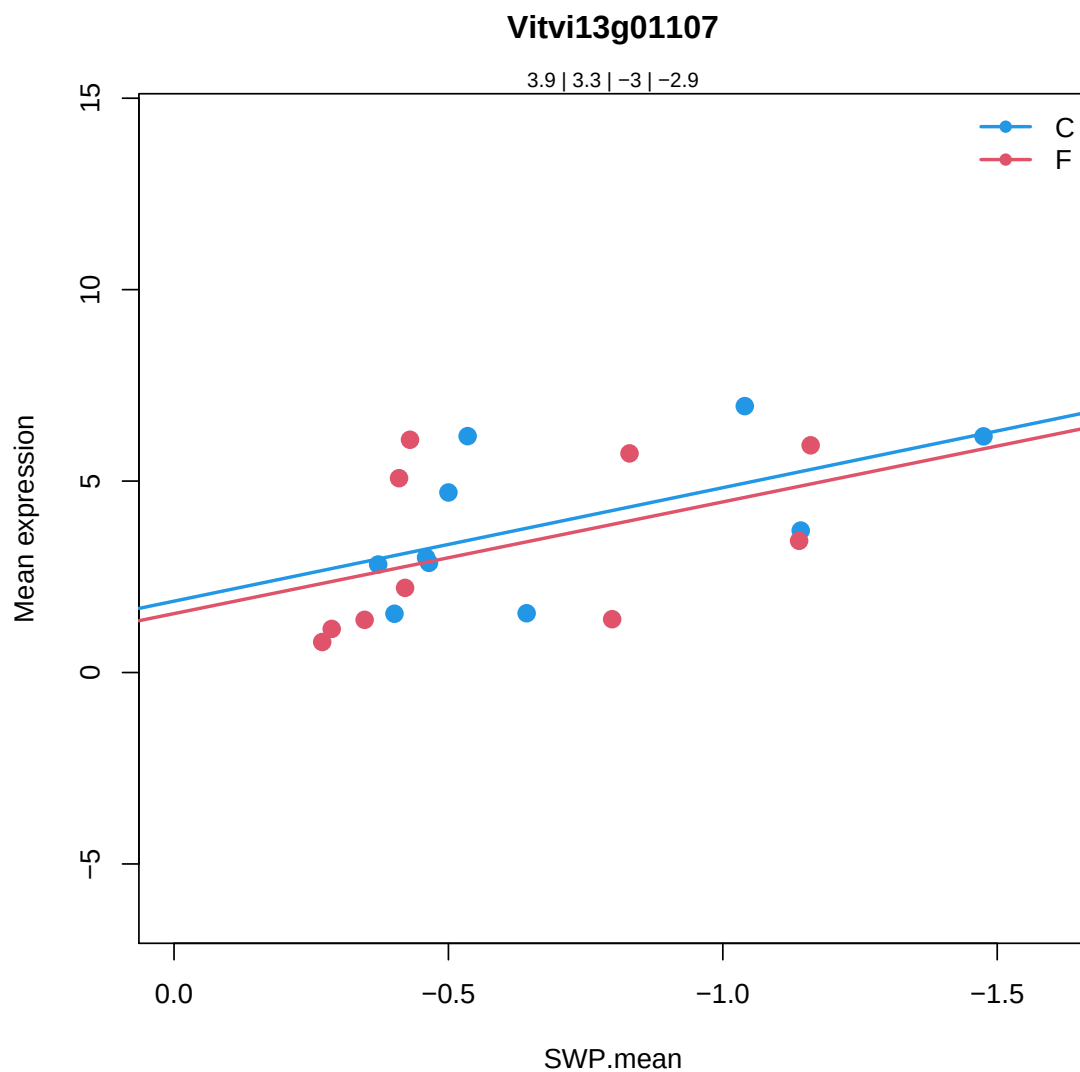
HSP20-like chaperones superfamily protein |

Chr3:951885-953490 FORWARD LENGTH=150 |

201606

Coefficients for Vitvi13g01107.

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



8.1.110 Vitvi01g02030: * Type1

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

Vitvi01g02030

29.5.11.4.2

protein.degradation.ubiquitin.E3.RING

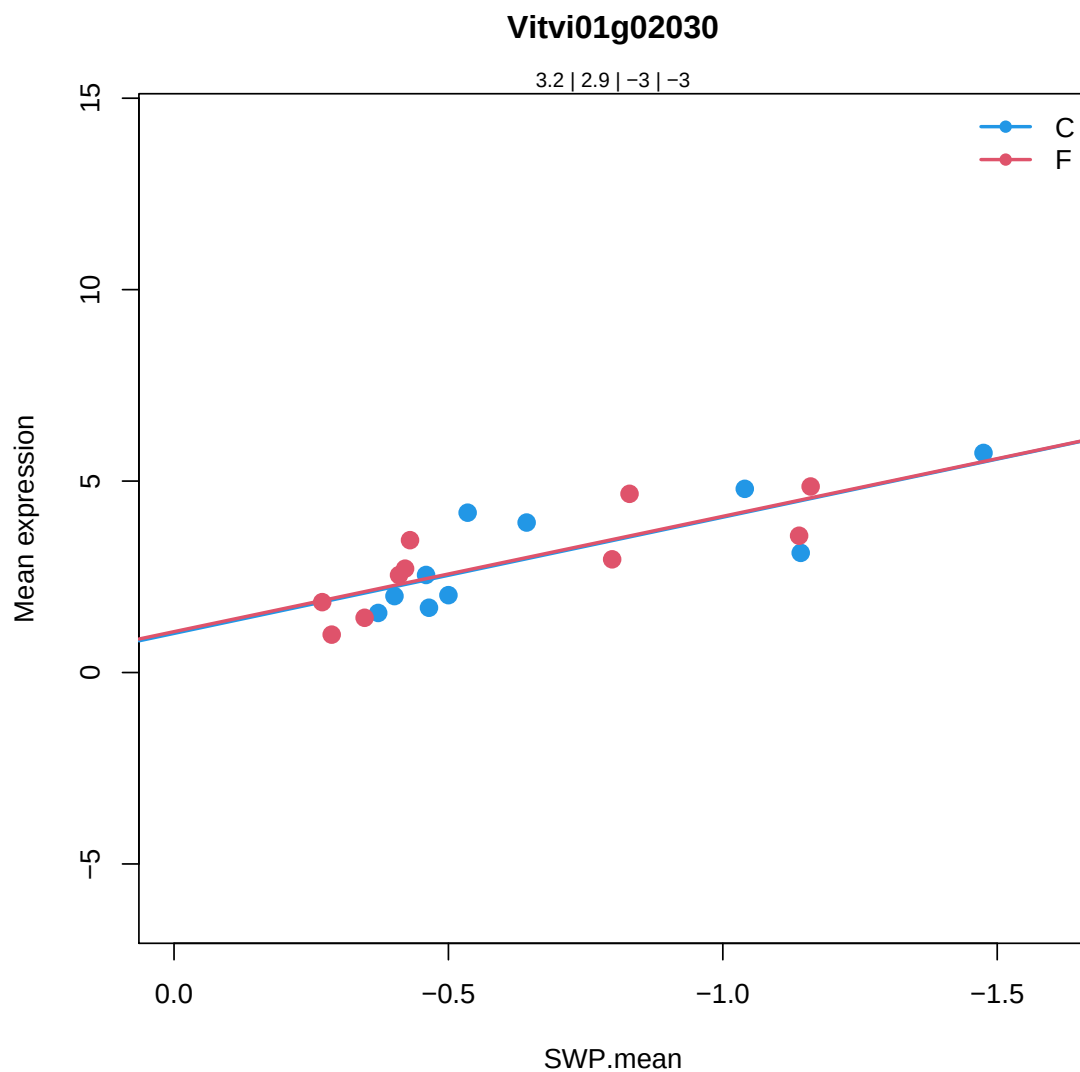
RING/U-box superfamily protein |

Chr1:25442486-25442887 FORWARD LENGTH=133 |

201606

Coefficients for Vitvi01g02030.

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



8.1.111 Vitvi13g01839: * Type1

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

Vitvi13g01839

26.21

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

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

Chr2:18305418-18306202 REVERSE LENGTH=205 |

201606

Vitvi13g01839

11.6

lipid metabolism.lipid transfer proteins etc

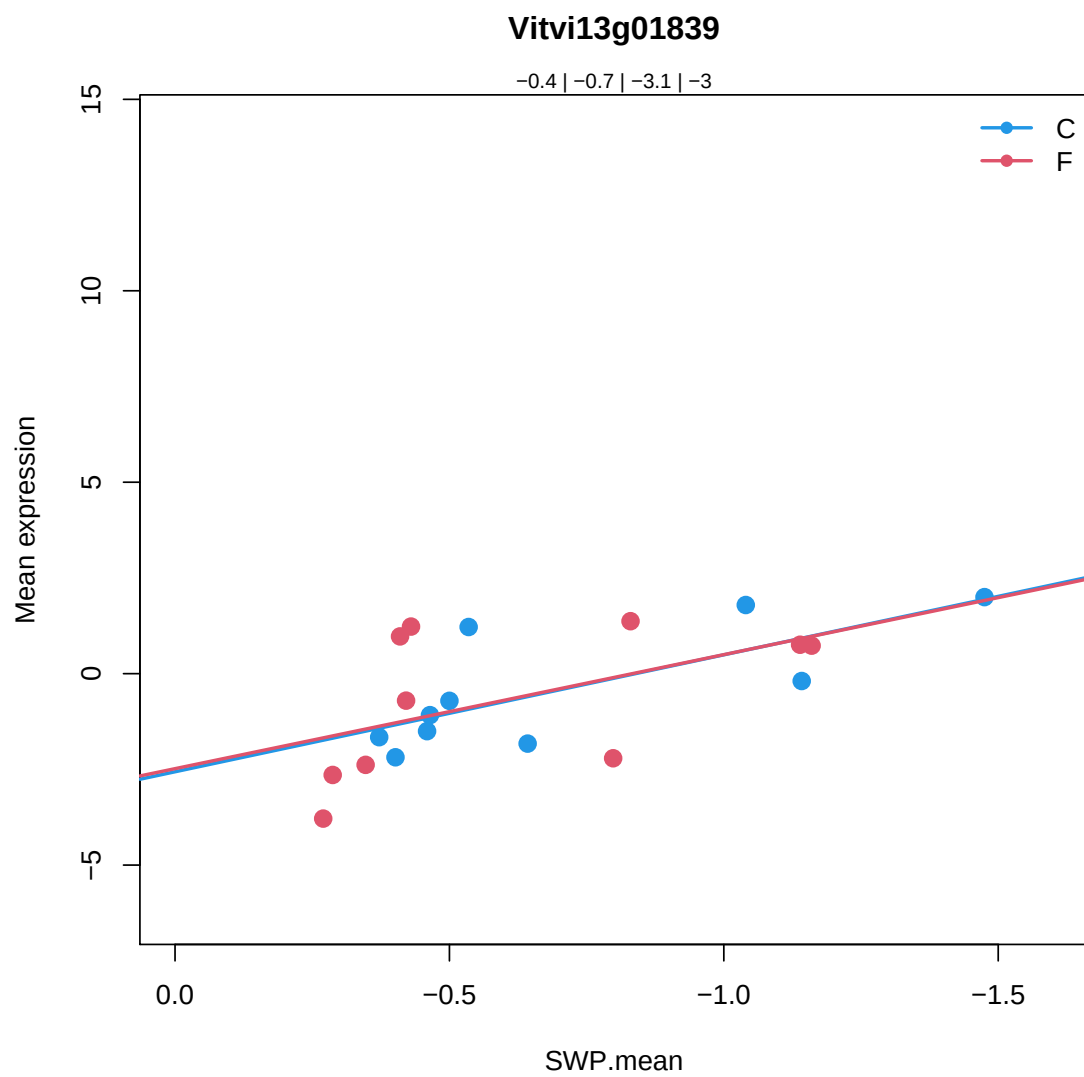
Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin

Chr2:18305418-18306202 REVERSE LENGTH=205 |

201606

Coefficients for Vitvi13g01839.

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



8.1.112 Vitvi06g00533: * Type1

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

Vitvi06g00533

29.4

protein.postranslational modification

highly ABA-induced PP2C protein 3 |

Chr2:12608855-12610124 FORWARD LENGTH=362 |

201606

Vitvi06g00533

17.1.2

hormone metabolism.abscisic acid.signal transduction

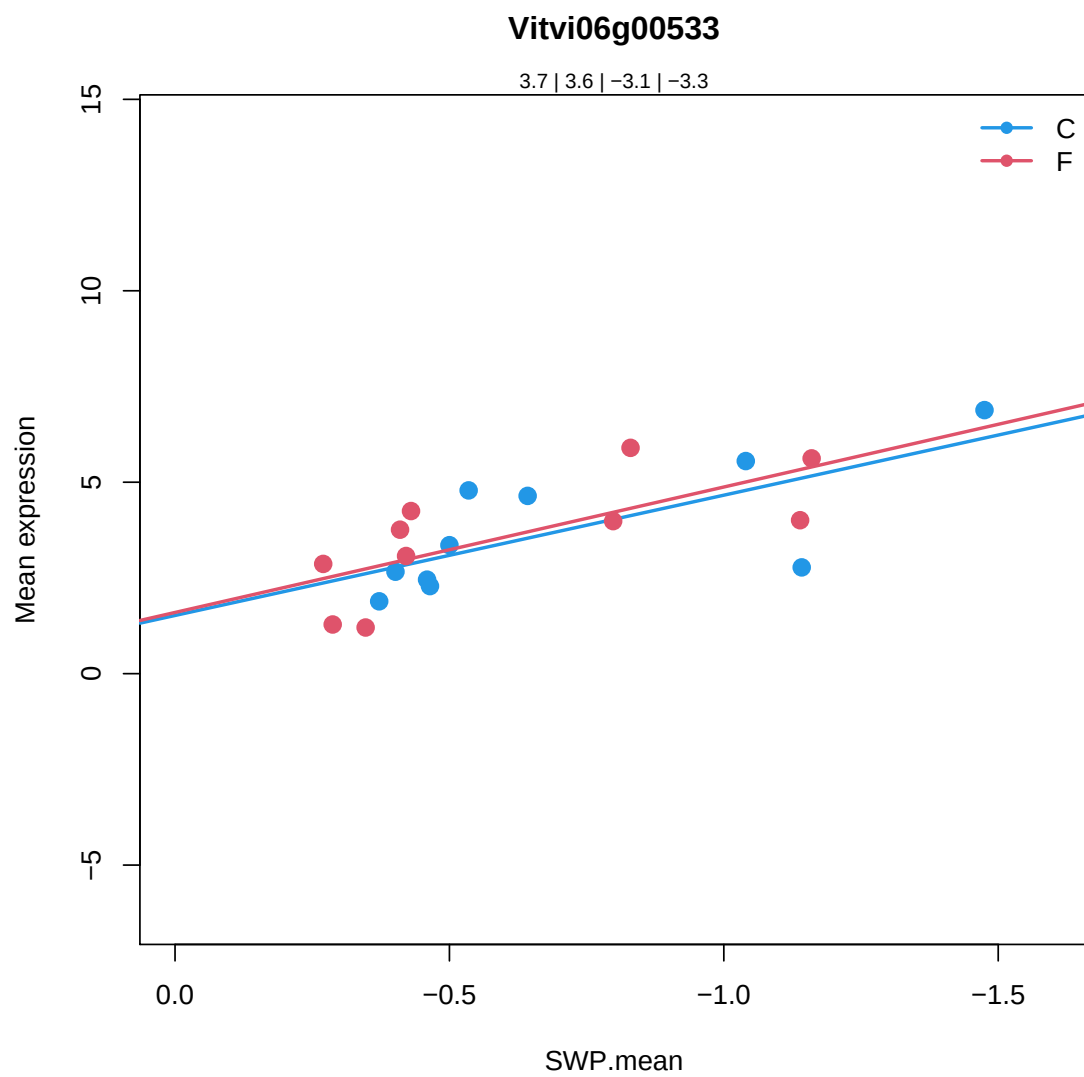
highly ABA-induced PP2C protein 3 |

Chr2:12608855-12610124 FORWARD LENGTH=362 |

201606

Coefficients for Vitvi06g00533.

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



8.1.113 Vitvi02g00436: * Type1

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

Vitvi02g00436

1.2.6

PS.photorespiration.hydroxypyruvate reductase

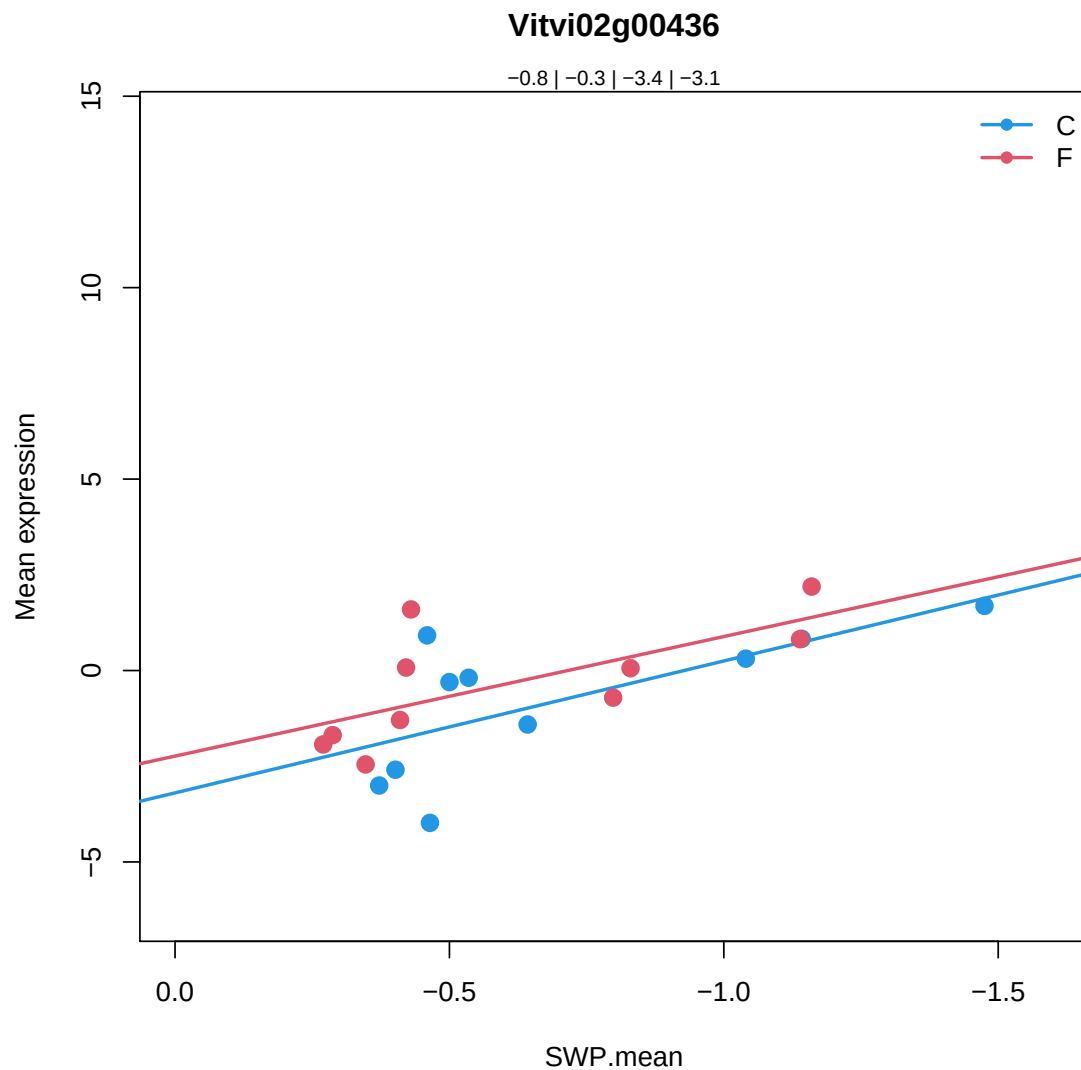
D-isomer specific 2-hydroxyacid dehydrogenase family protein |

Chr1:4274649-4275831 FORWARD LENGTH=323 |

201606

Coefficients for Vitvi02g00436.

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



8.1.114 Vitvi17g00695: * Type1

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

Vitvi17g00695

20.2.1

stress.abiotic.heat

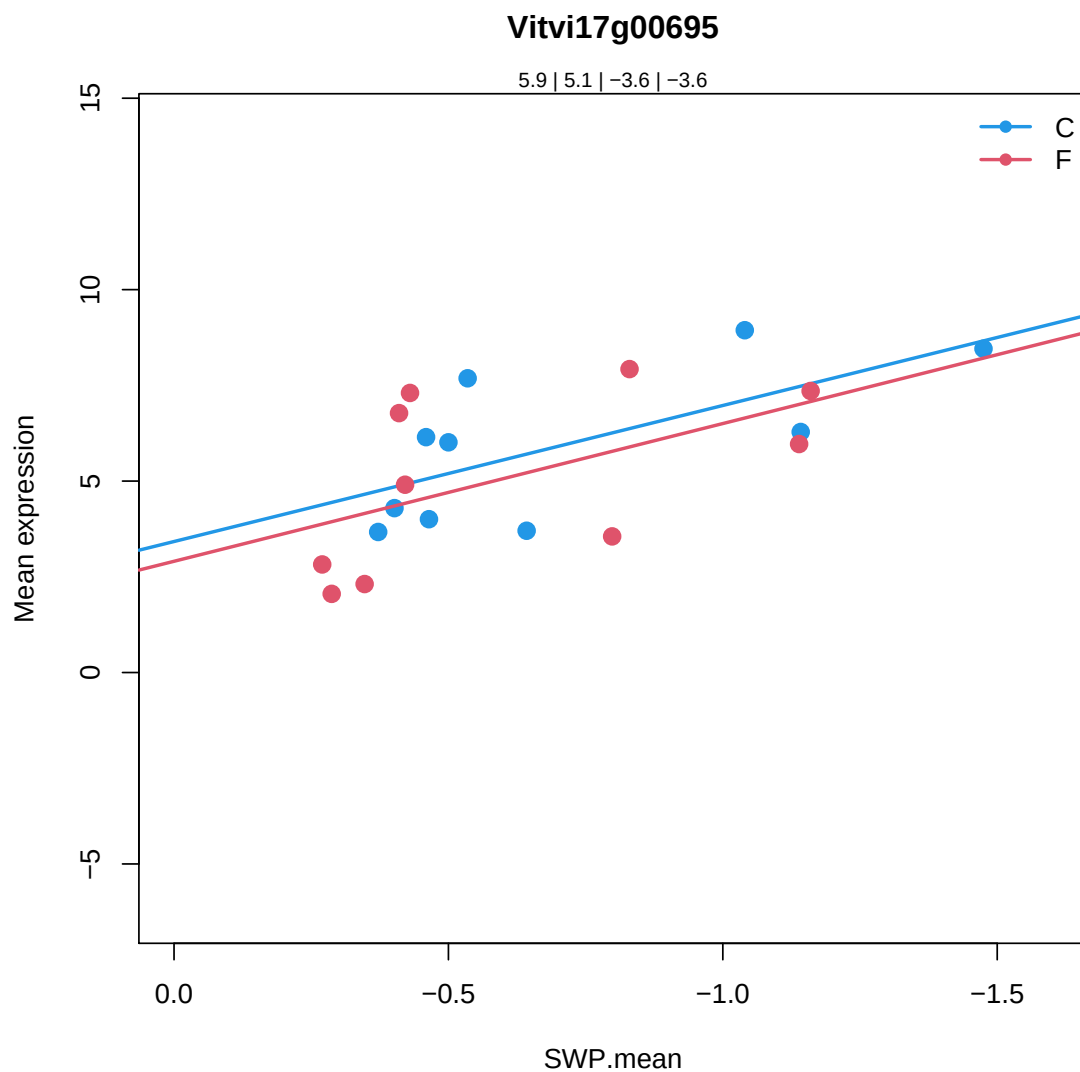
heat shock protein 101 |

Chr1:27936715-27939862 REVERSE LENGTH=911 |

201606

Coefficients for Vitvi17g00695.

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



8.1.115 Vitvi19g00514: * Type1

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

Vitvi19g00514

26.28

misc.GDSL-motif lipase

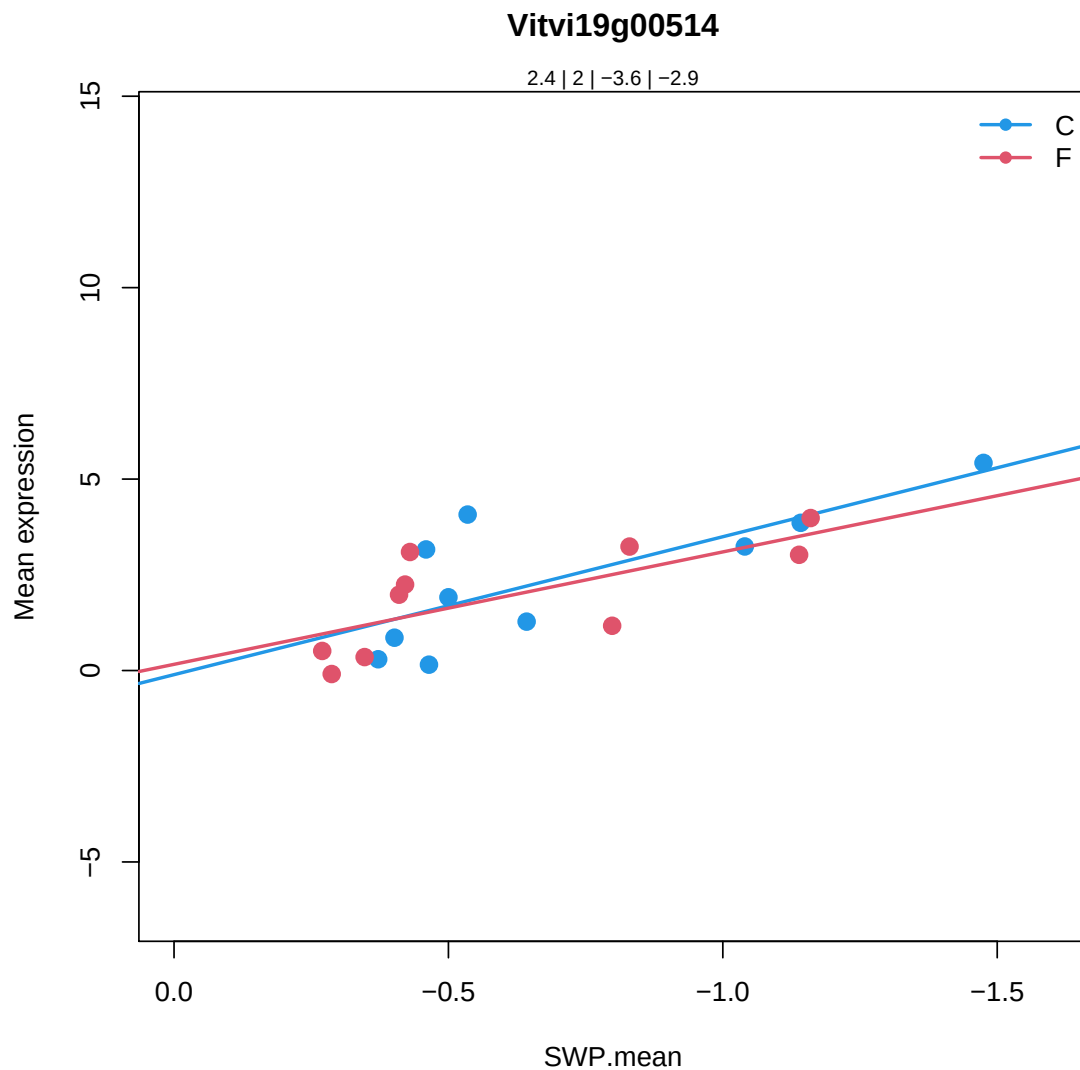
GDSL-like Lipase/Acylhydrolase superfamily protein |

Chr5:22337745-22339741 FORWARD LENGTH=376 |

201606

Coefficients for Vitvi19g00514.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.424878	1.617823e-07	***	1.90799e-07	***
SlopeC	-3.602676	0.0005453082	***	0.1005065	
MeanF-MeanC	-0.4746797	0.3044957		0.6685796	
SlopeF-SlopeC	0.6663077	0.619161		0.9999488	



8.1.116 Vitvi02g00374: * Type1

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

Vitvi02g00374

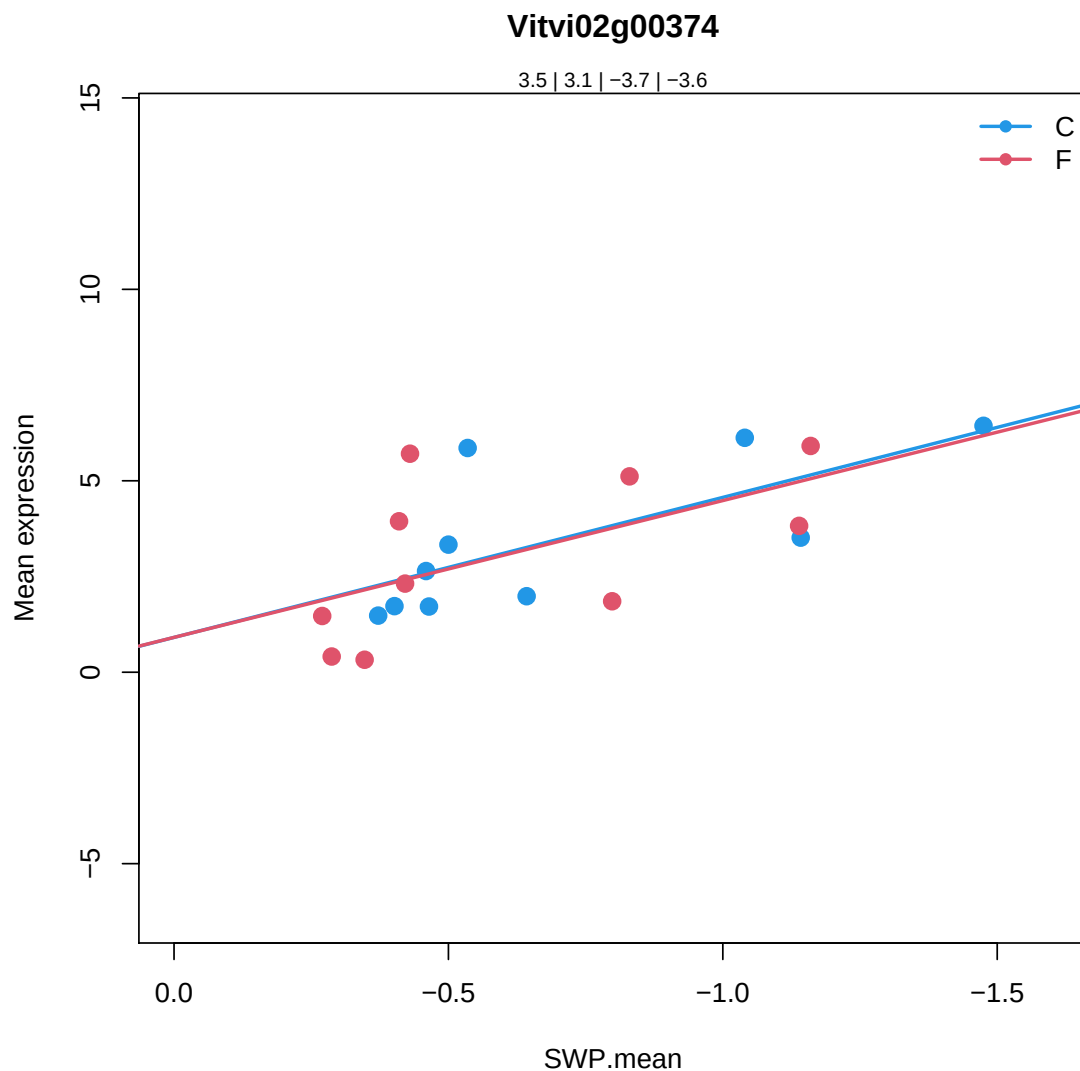
29.5.11

protein.degradation.ubiquitin

UBX domain-containing protein IPR001012 UBX

Coefficients for Vitvi02g00374.

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



8.1.117 Vitvi18g01510: * Type1

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

Vitvi18g01510

20.2.1

stress.abiotic.heat

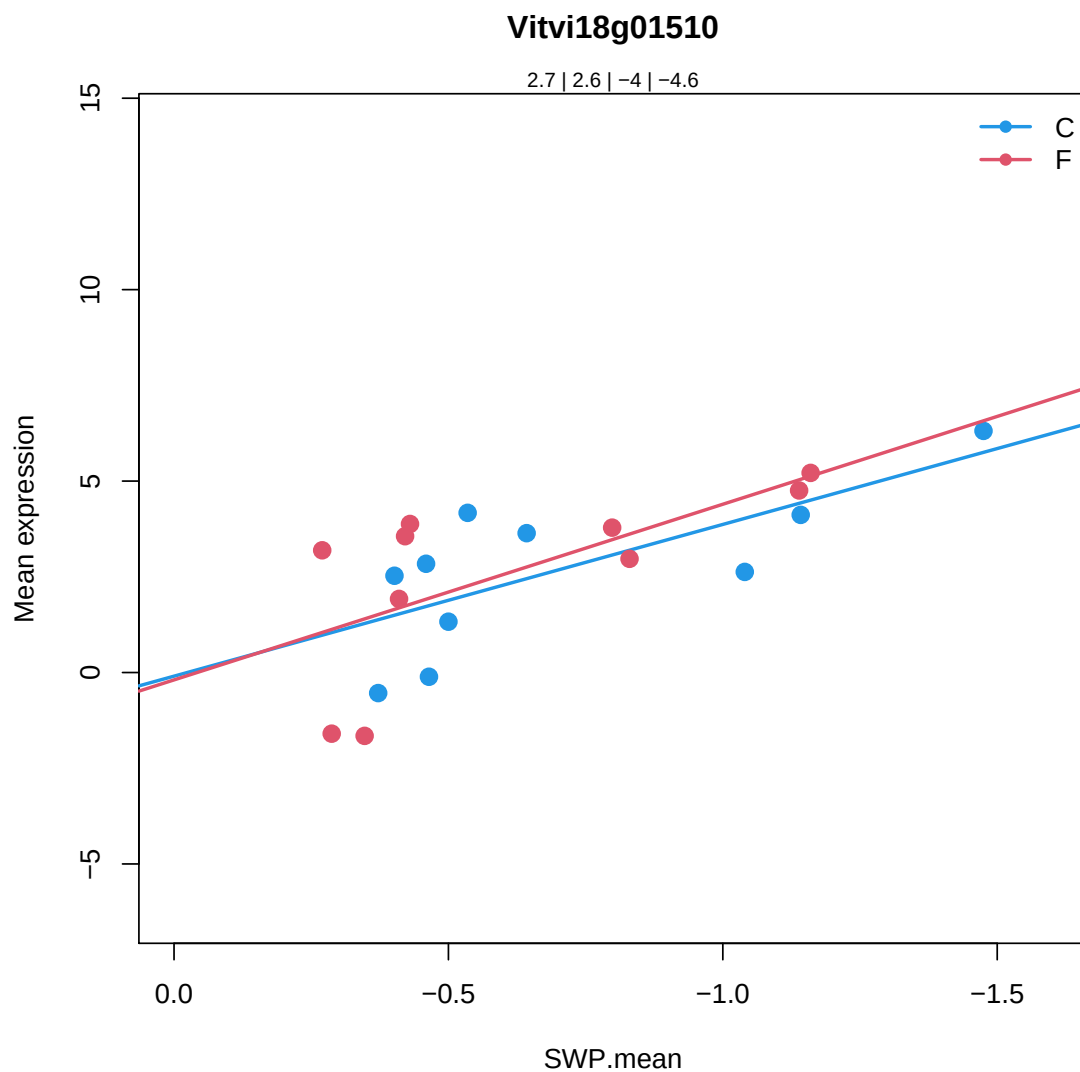
HSP20-like chaperones superfamily protein |

Chr1:19980510-19980983 FORWARD LENGTH=157 |

201606

Coefficients for Vitvi18g01510.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.691284	1.303921e-05	***	1.468259e-05	***
SlopeC	-3.963027	0.007114891	**	0.2775469	
MeanF-MeanC	-0.0887675	0.8969235		0.9730614	
SlopeF-SlopeC	-0.6245041	0.755819		0.9999488	



8.1.118 Vitvi14g00063: * Type1

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

Vitvi14g00063

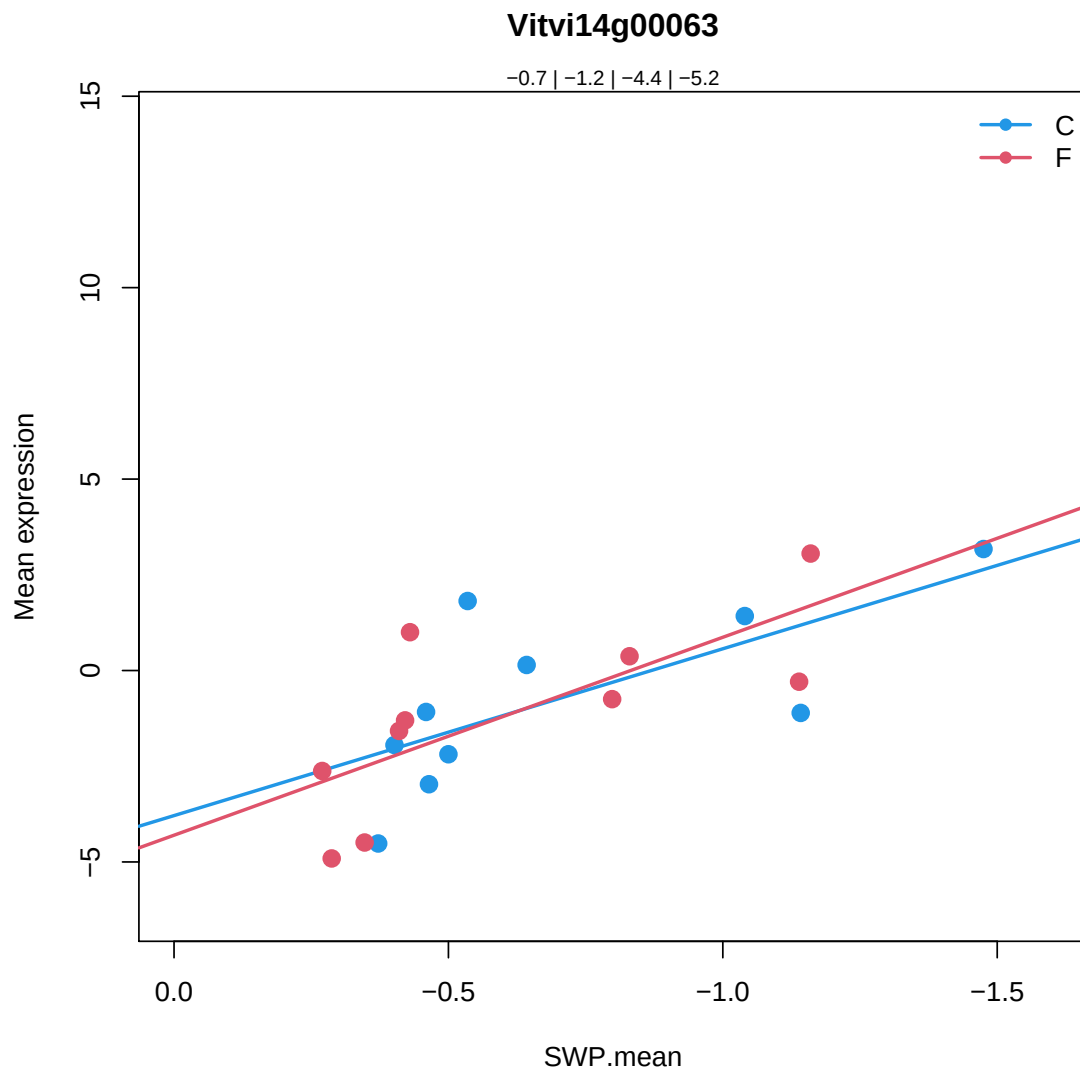
3.1.1.1

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

Chr2:19369049-19370372 REVERSE LENGTH=344 |
201606

Coefficients for Vitvi14g00063.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.7256696	0.1547876		0.1592704	
SlopeC	-4.356928	0.004398415	**	0.2399107	
MeanF-MeanC	-0.42607	0.5467705		0.8315272	
SlopeF-SlopeC	-0.8128272	0.6938776		0.9999488	



8.1.119 Vitvi13g00471: * Type1

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

Vitvi13g00471

20.2.1

stress.abiotic.heat

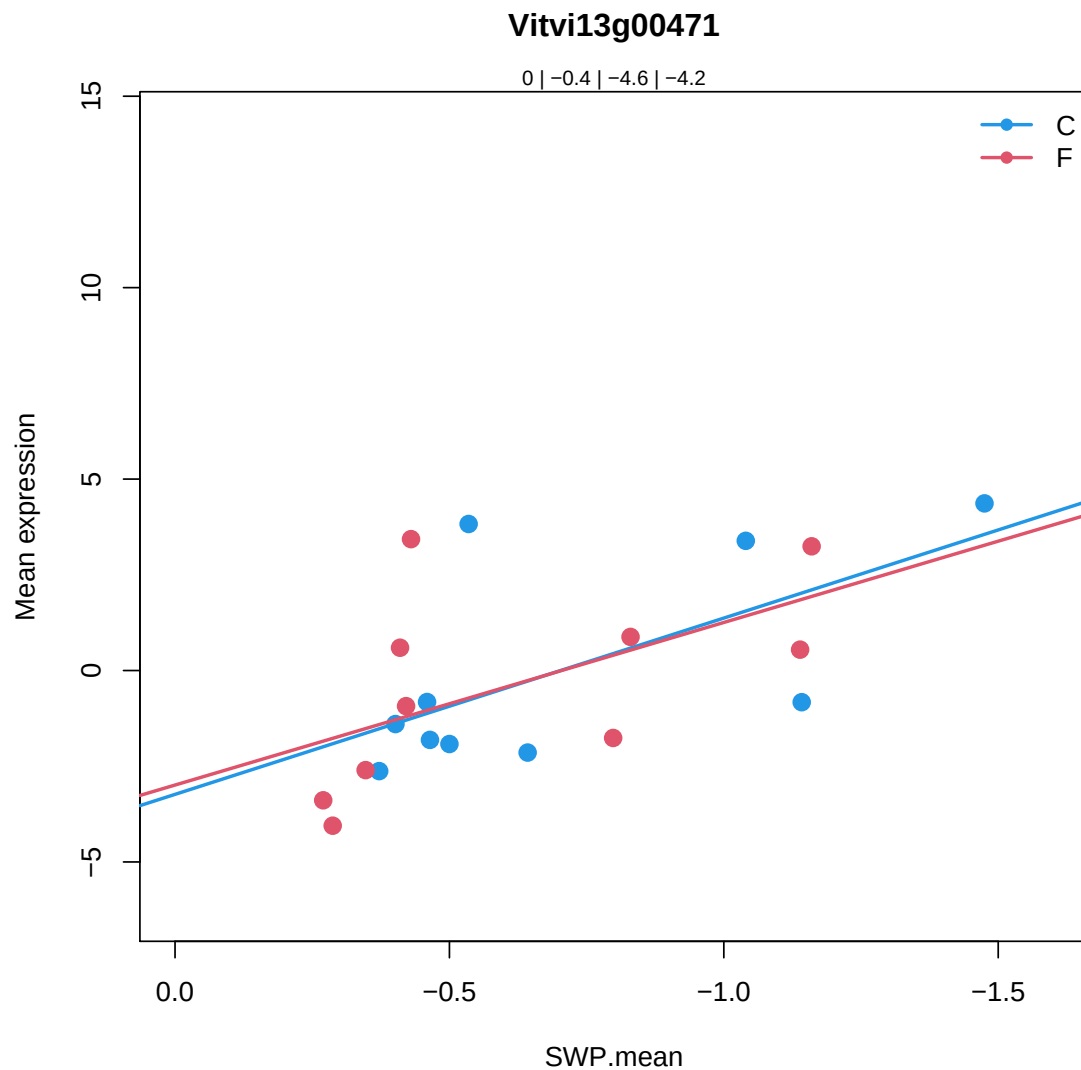
heat shock protein 18.2 |

Chr5:24062632-24063117 FORWARD LENGTH=161 |

201606

Coefficients for Vitvi13g00471.

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



8.1.120 Vitvi05g00486: * Type1

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

Vitvi05g00486

20.2.1

stress.abiotic.heat

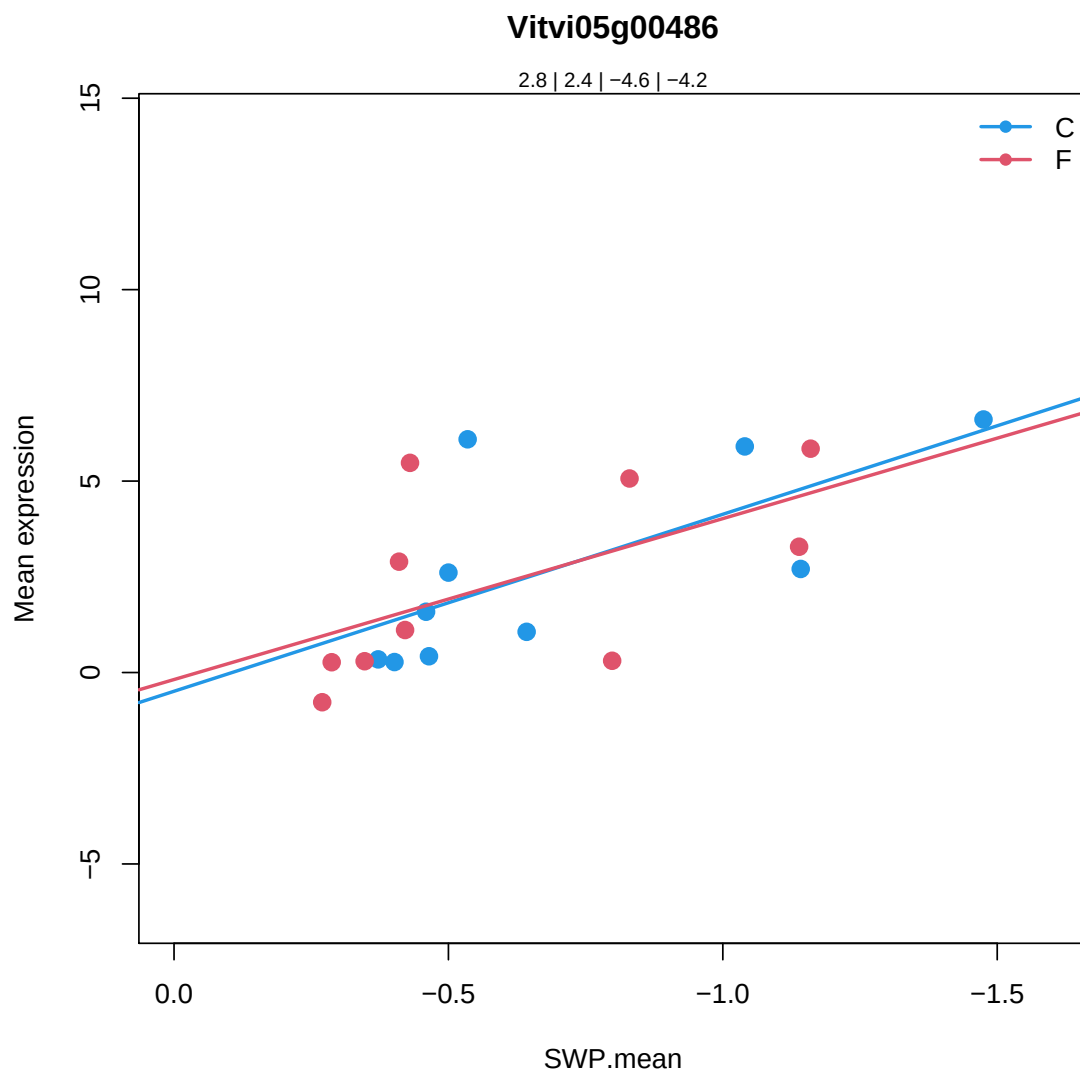
heat-shock protein 70T-2 |

Chr2:13651720-13653411 REVERSE LENGTH=563 |

201606

Coefficients for Vitvi05g00486.

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



8.1.121 Vitvi14g02990: * Type1

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

Vitvi14g02990

35.2

not assigned.unknown

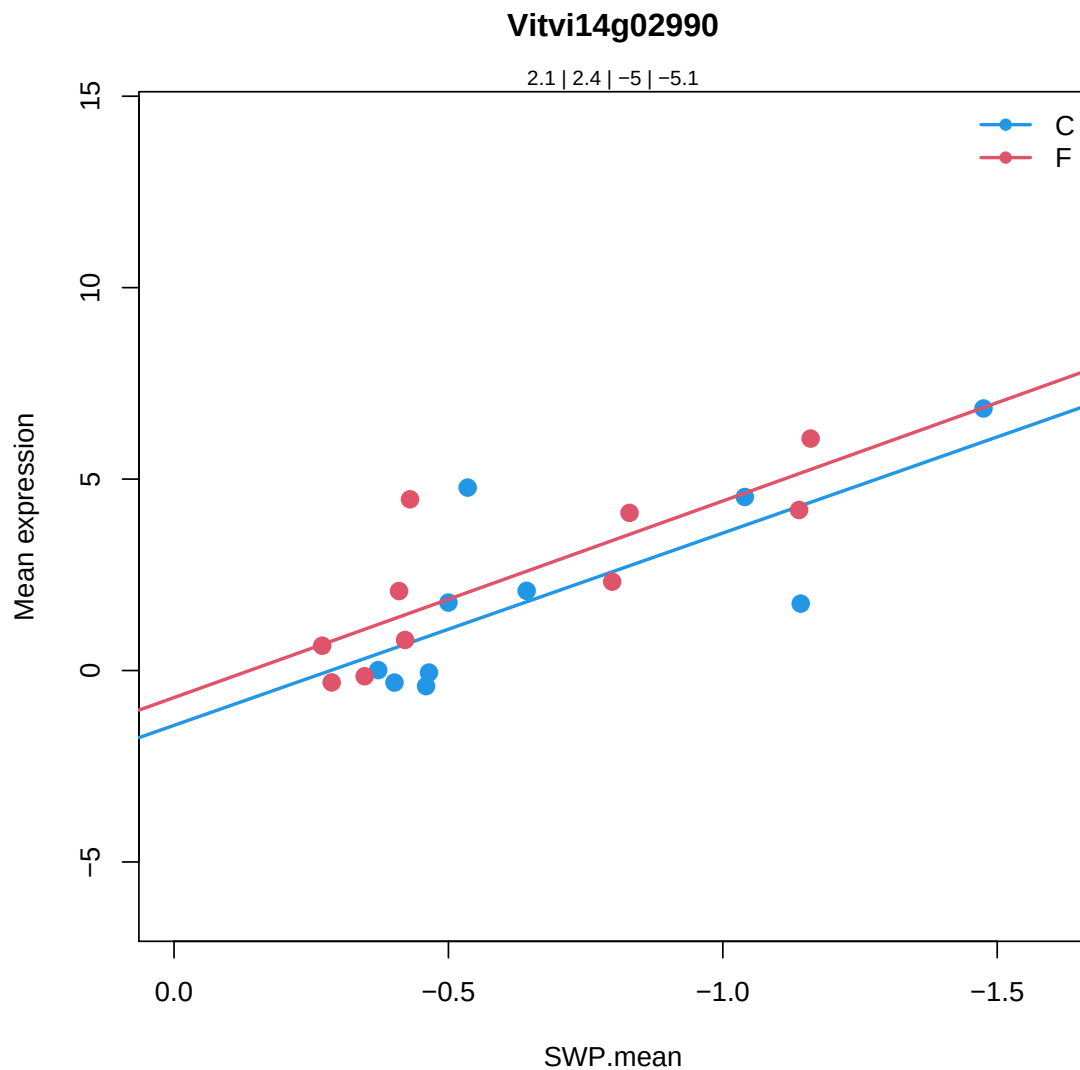
hypothetical protein |

Chr3:10061633-10062481 FORWARD LENGTH=282 |

201606

Coefficients for Vitvi14g02990.

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



8.1.122 Vitvi11g00724: * Type1

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

```
Vitvi11g00724
```

```
20.2.1
```

```
stress.abiotic.heat
```

```
heat shock protein 70B |
```

```
Chr1:5502386-5504326 REVERSE LENGTH=646 |
```

```
201606
```

```
Vitvi11g00724
```

```
29.6
```

```
protein.folding
```

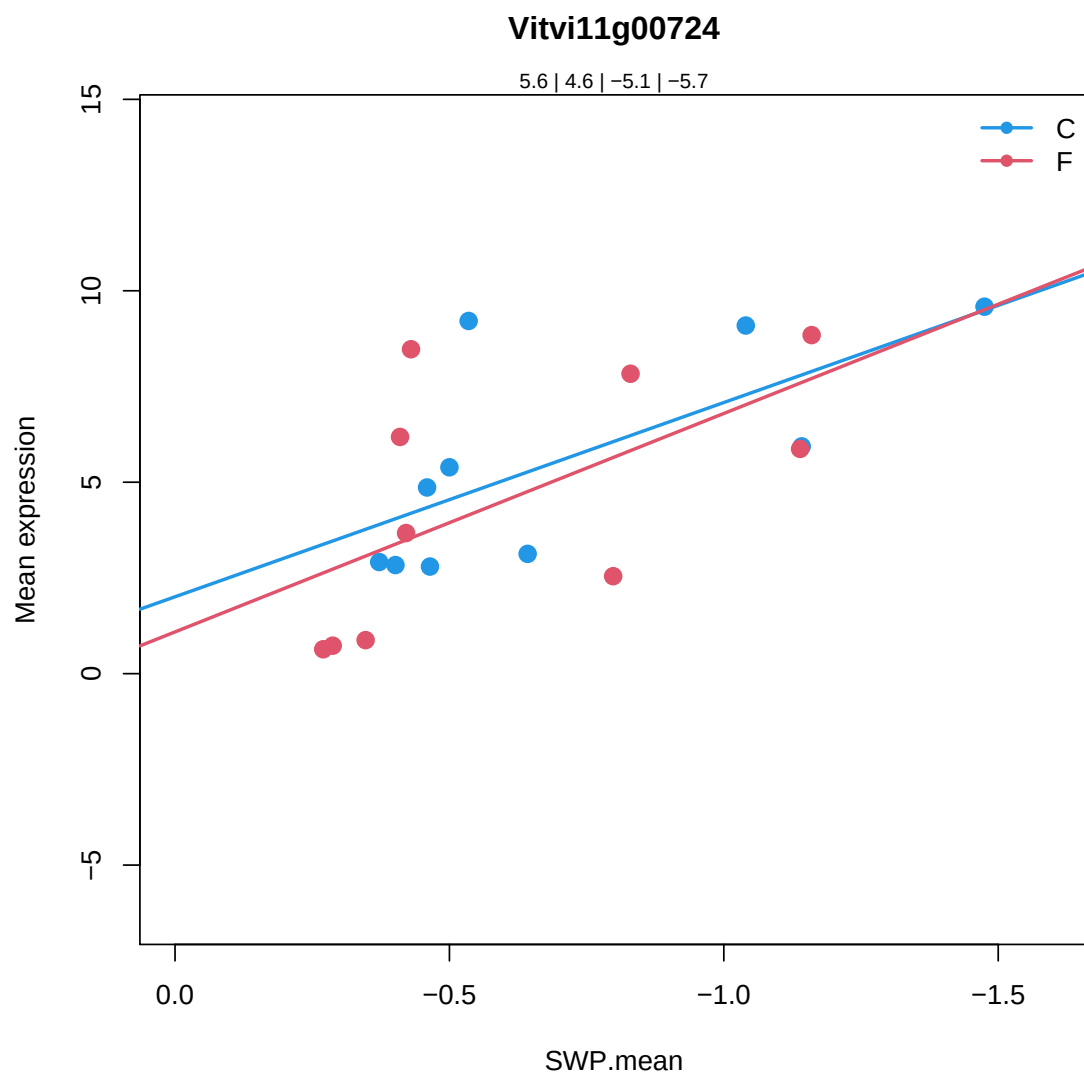
```
heat shock protein 70B |
```

```
Chr1:5502386-5504326 REVERSE LENGTH=646 |
```

```
201606
```

Coefficients for Vitvi11g00724.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.57538	5.63319e-08	***	6.726816e-08	***
SlopeC	-5.073527	0.01469064	*	0.3359386	
MeanF-MeanC	-1.009405	0.3105058		0.6744662	
SlopeF-SlopeC	-0.6317686	0.8263893		0.9999488	



8.1.123 Vitvi05g00170: * Type1

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

Vitvi05g00170

3.1.1.1

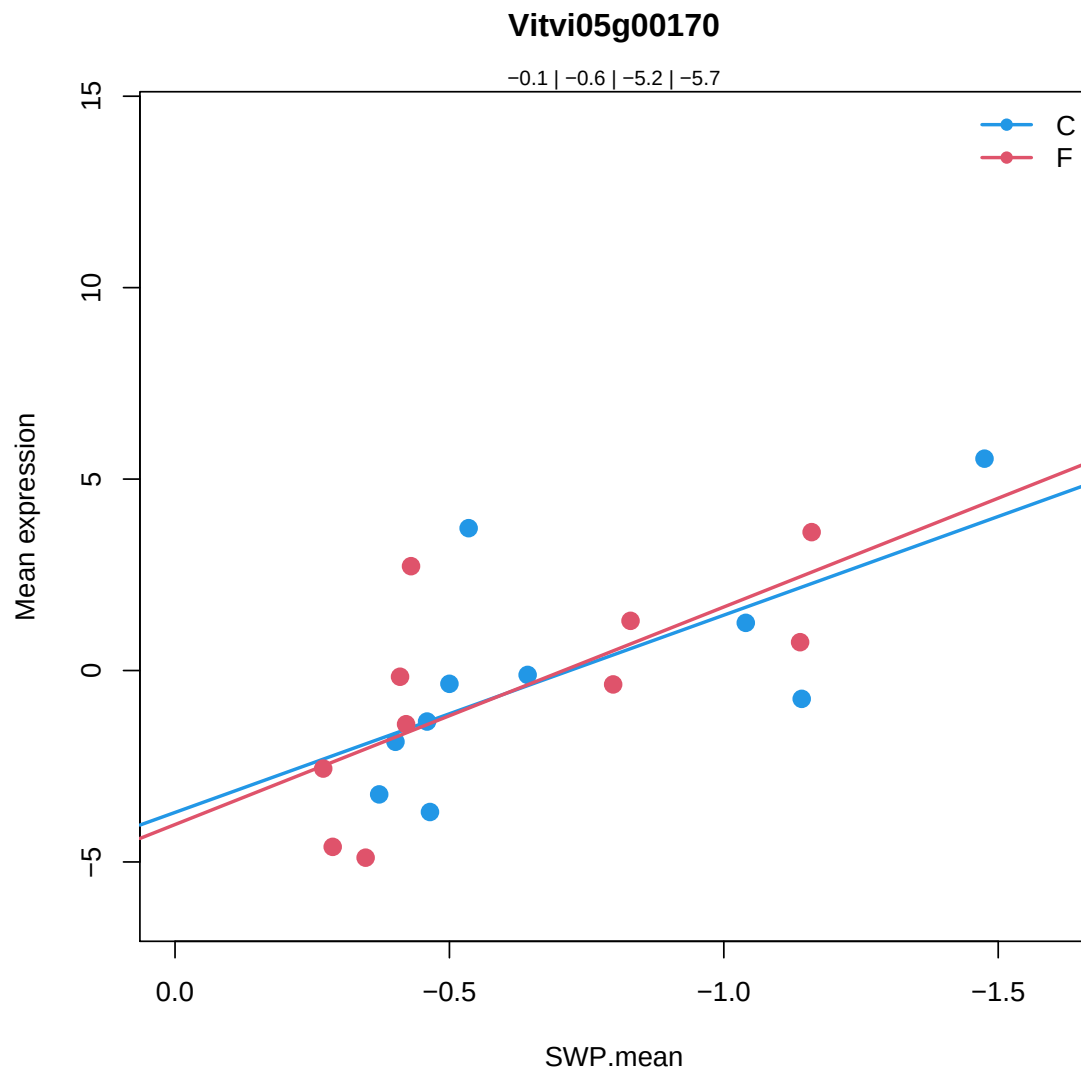
minor CHO metabolism.raffinose family.galactinol synthases.known
galactinol synthase 3 |

Chr1:3019888-3021214 FORWARD LENGTH=334 |

201606

Coefficients for Vitvi05g00170.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.08316482	0.8942845		0.8967556	
SlopeC	-5.15293	0.006799412	**	0.2748982	
MeanF-MeanC	-0.4774518	0.5907784		0.8569322	
SlopeF-SlopeC	-0.5293673	0.8381889		0.9999488	



8.1.124 Vitvi15g01034: * Type1

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

Vitvi15g01034

20.2.1

stress.abiotic.heat

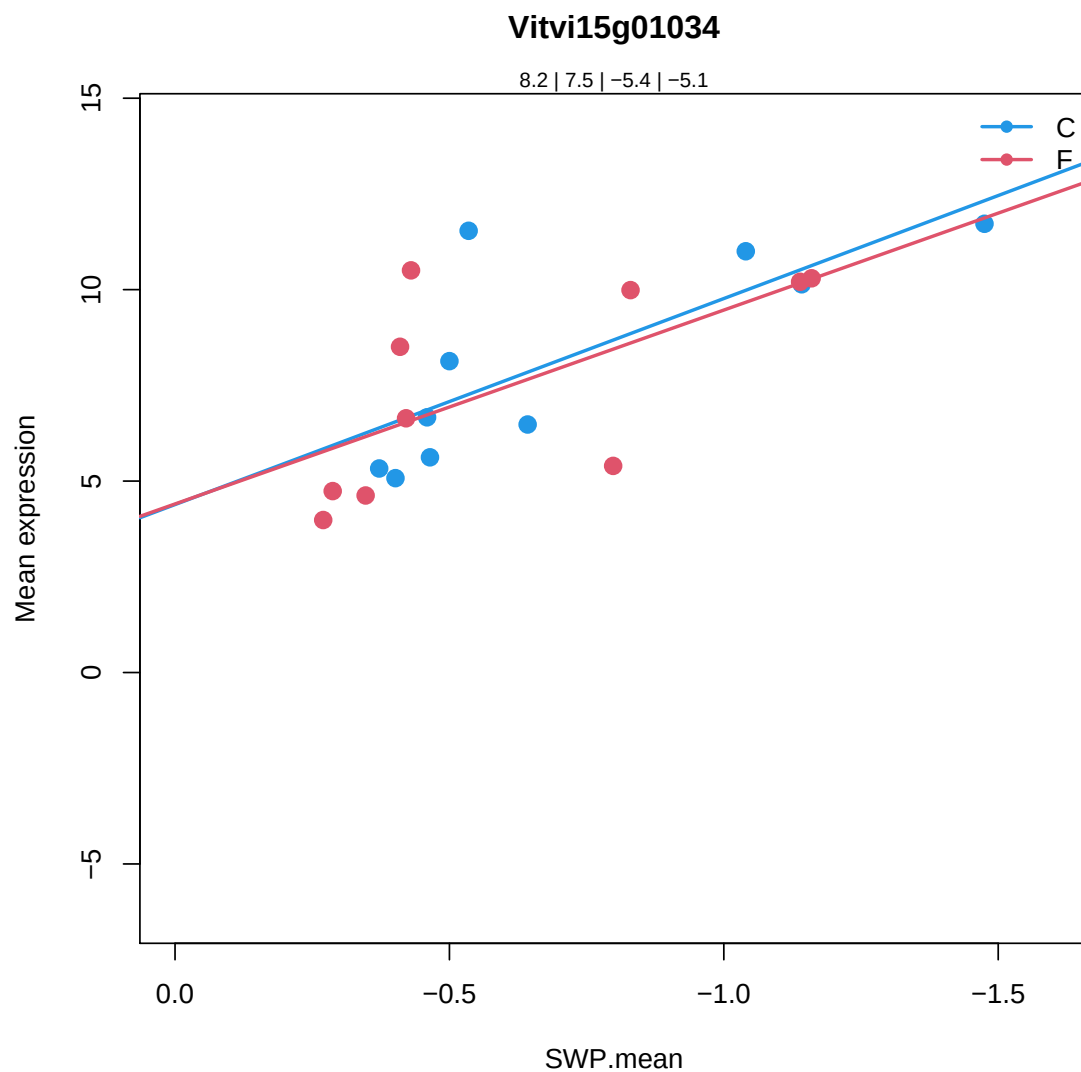
BCL-2-associated athanogene 6 |

Chr2:18986586-18989827 FORWARD LENGTH=1043 |

201606

Coefficients for Vitvi15g01034.

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



8.1.125 Vitvi13g02017: * Type1

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

Vitvi13g02017

20.2.1

stress.abiotic.heat

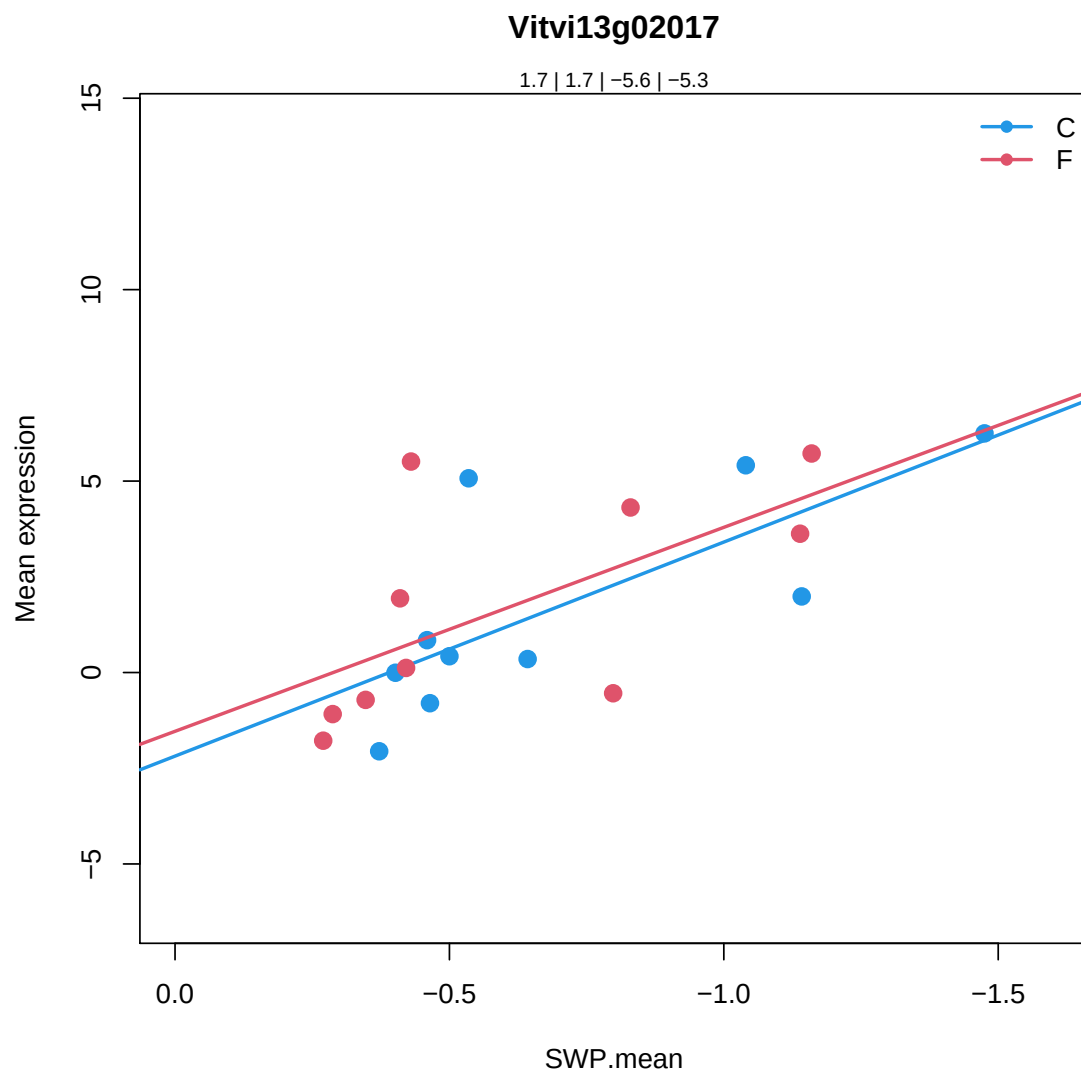
heat shock protein 18.2 |

Chr5:24062632-24063117 FORWARD LENGTH=161 |

201606

Coefficients for Vitvi13g02017.

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



8.1.126 Vitvi16g01985: * Type1

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

Vitvi16g01985

35.2

not assigned.unknown

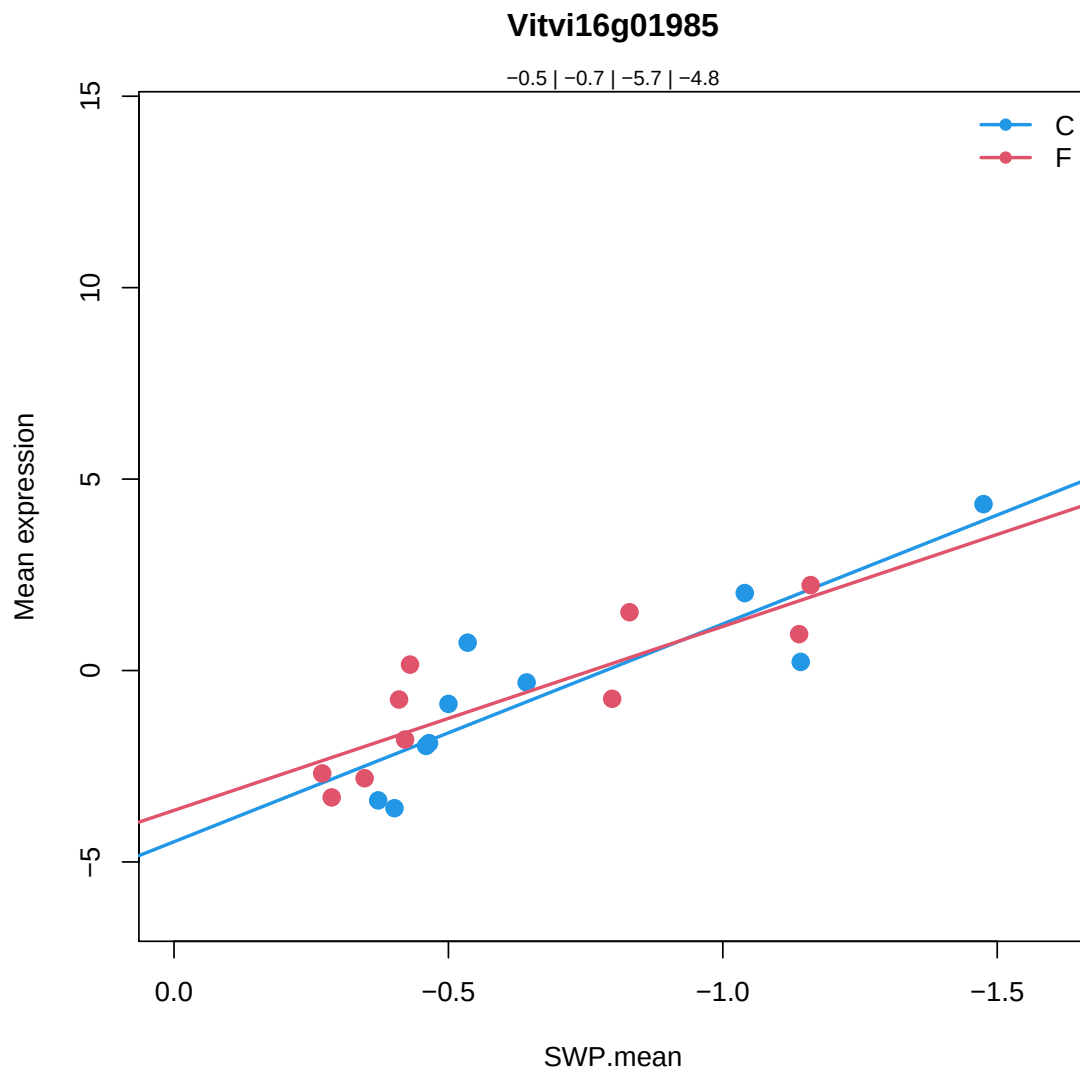
highly ABA-induced PP2C protein 3 |

Chr2:12608855-12610124 FORWARD LENGTH=362 |

201606

Coefficients for Vitvi16g01985.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.4719704	0.159837		0.1643662	
SlopeC	-5.688522	2.68669e-06	***	0.01365018	*
MeanF-MeanC	-0.2536551	0.5857293		0.8542535	
SlopeF-SlopeC	0.8843373	0.5169724		0.9999488	



8.1.127 Vitvi12g02138: * Type1

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

Vitvi12g02138

20.2.1

stress.abiotic.heat

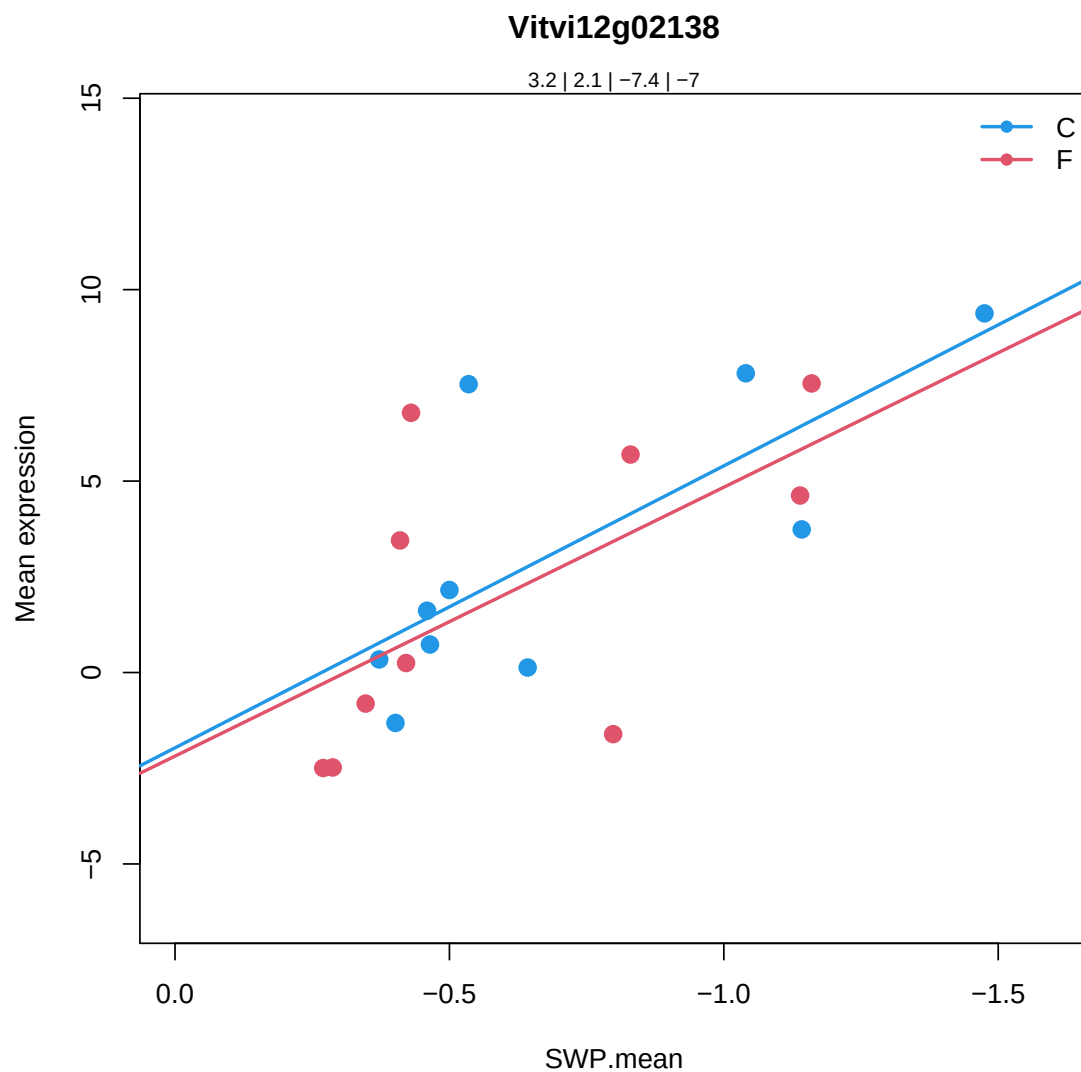
HSP20-like chaperones superfamily protein |

Chr4:6370537-6371124 FORWARD LENGTH=195 |

201606

Coefficients for Vitvi12g02138.

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



8.1.128 Vitvi04g00135: * Type1

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

Vitvi04g00135

20.2.1

stress.abiotic.heat

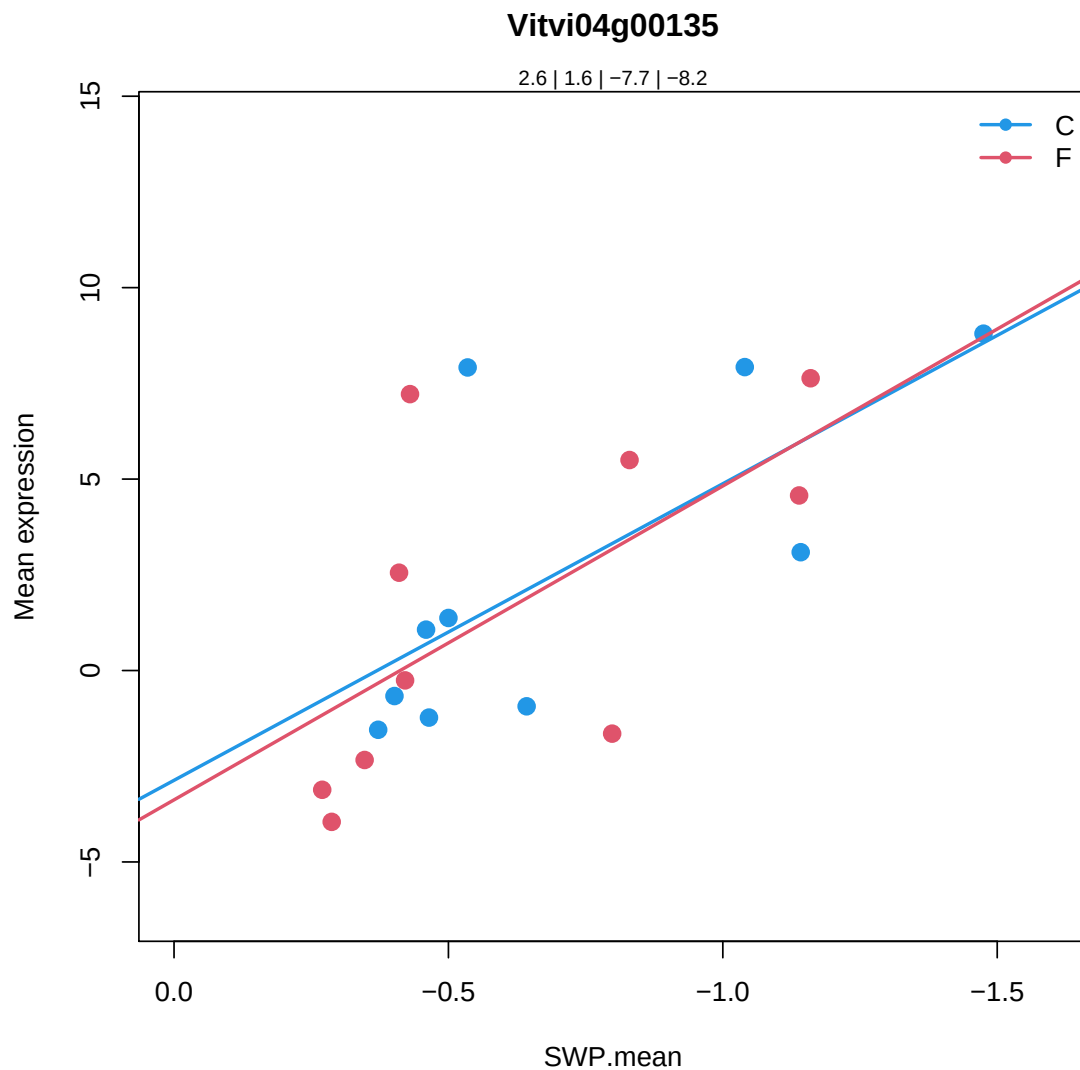
17.6 kDa class II heat shock protein |

Chr5:3882409-3882876 REVERSE LENGTH=155 |

201606

Coefficients for Vitvi04g00135.

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



8.1.129 Vitvi18g02423: * Type1

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

Vitvi18g02423

35.2

not assigned.unknown

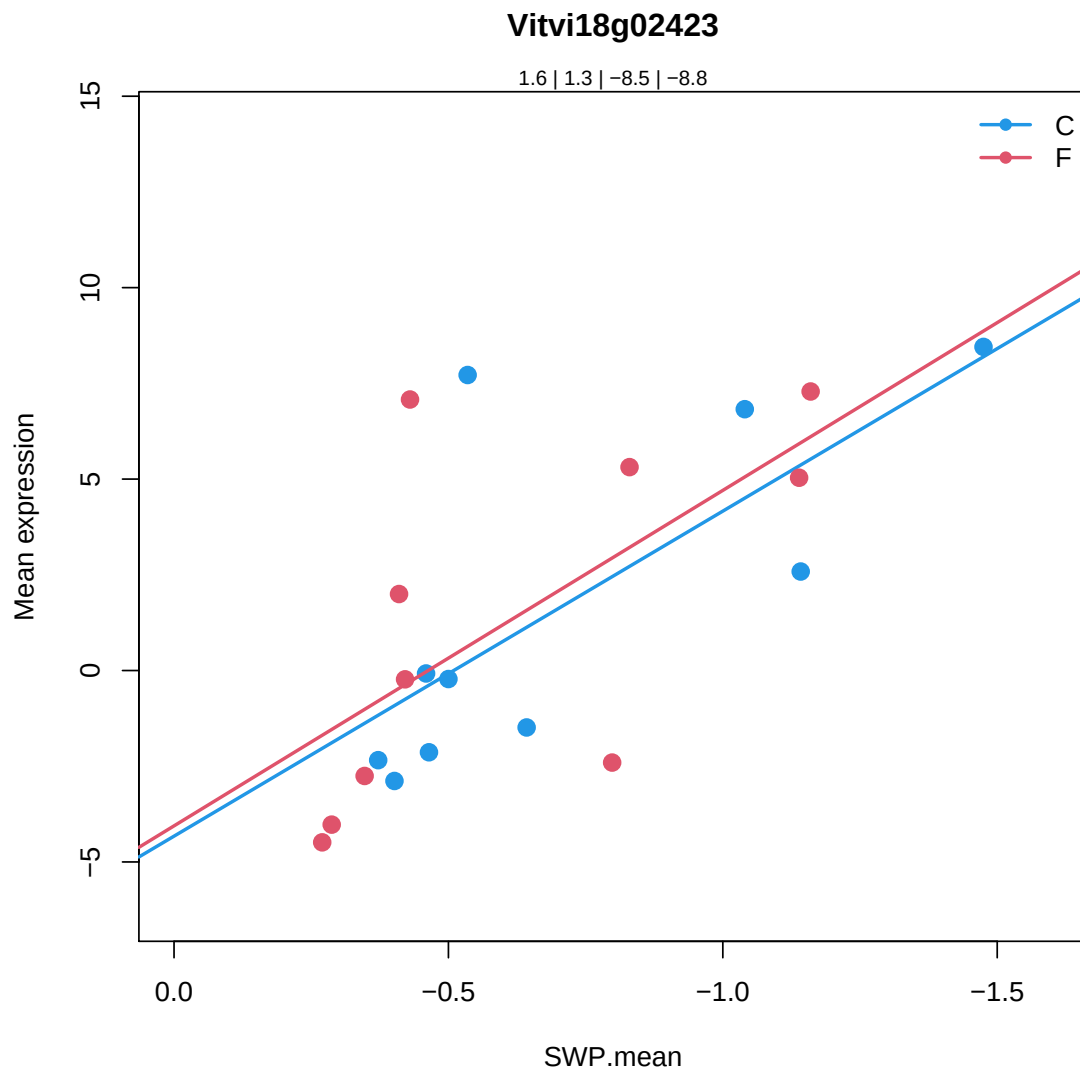
HSP20-like chaperones superfamily protein |

Chr4:6370537-6371124 FORWARD LENGTH=195 |

201606

Coefficients for Vitvi18g02423.

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



8.2 Type1.2

8.2.1 Vitvi10g02300: * Type1.2

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

Vitvi10g02300

35.2

not assigned.unknown

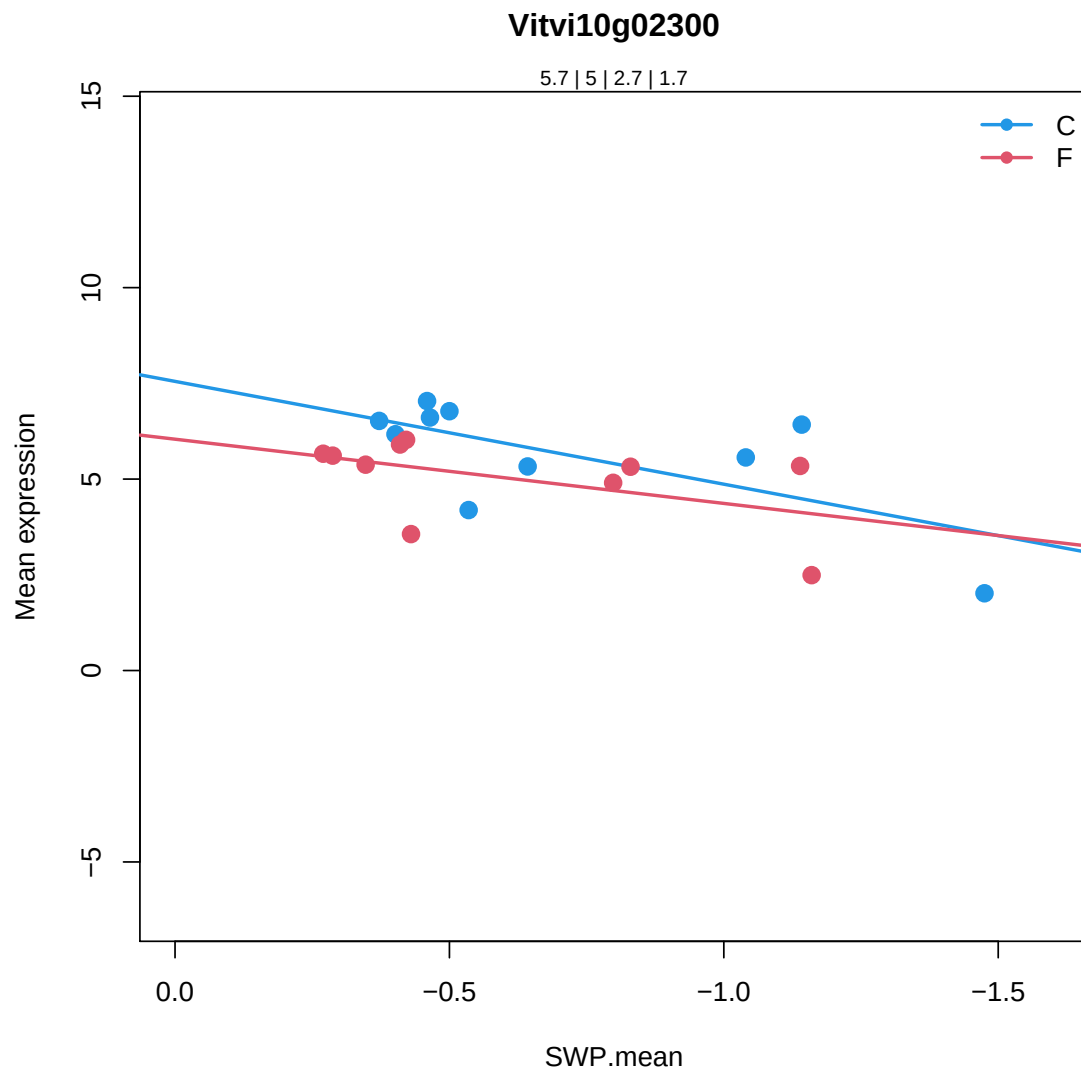
Subtilase family protein |

Chr5:24096895-24100387 REVERSE LENGTH=778 |

201606

Coefficients for Vitvi10g02300.

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



8.2.2 Vitvi14g01717: Type1.2

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

Vitvi14g01717

3.1.2.2

minor CHO metabolism.raffinose family.raffinose synthases.putative

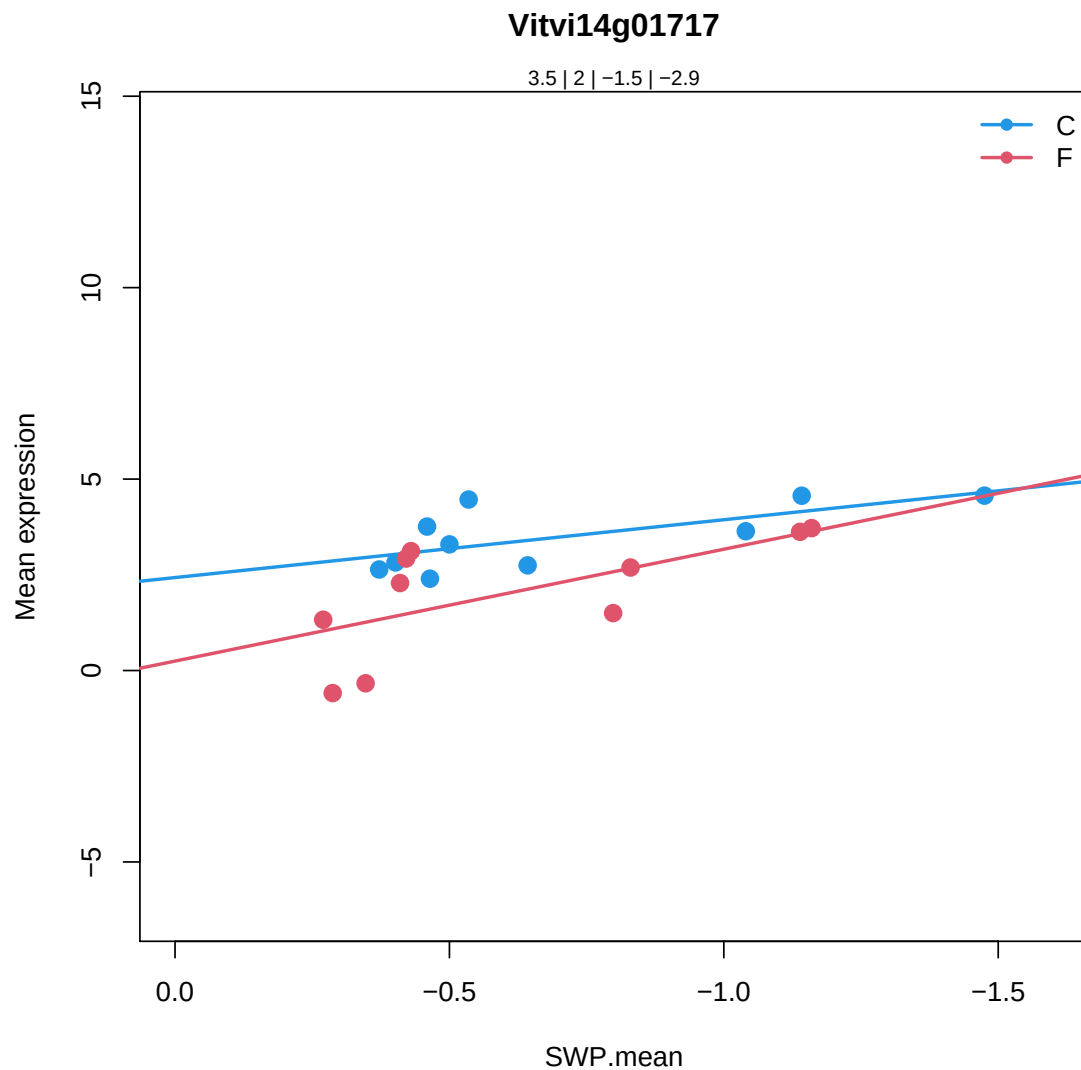
Raffinose synthase family protein |

Chr5:16161720-16165085 FORWARD LENGTH=783 |

201606

Coefficients for Vitvi14g01717.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.48977	2.551646e-11	***	3.423608e-11	***
SlopeC	-1.510356	0.06495838	.	0.5518928	
MeanF-MeanC	-1.463541	0.001266488	**	0.01523584	*
SlopeF-SlopeC	-1.411876	0.2350381		0.9999488	



8.2.3 Vitvi07g03083: Type1.2

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

Vitvi07g03083

16.2.1.10

secondary metabolism.phenylpropanoids.lignin biosynthesis.CAD

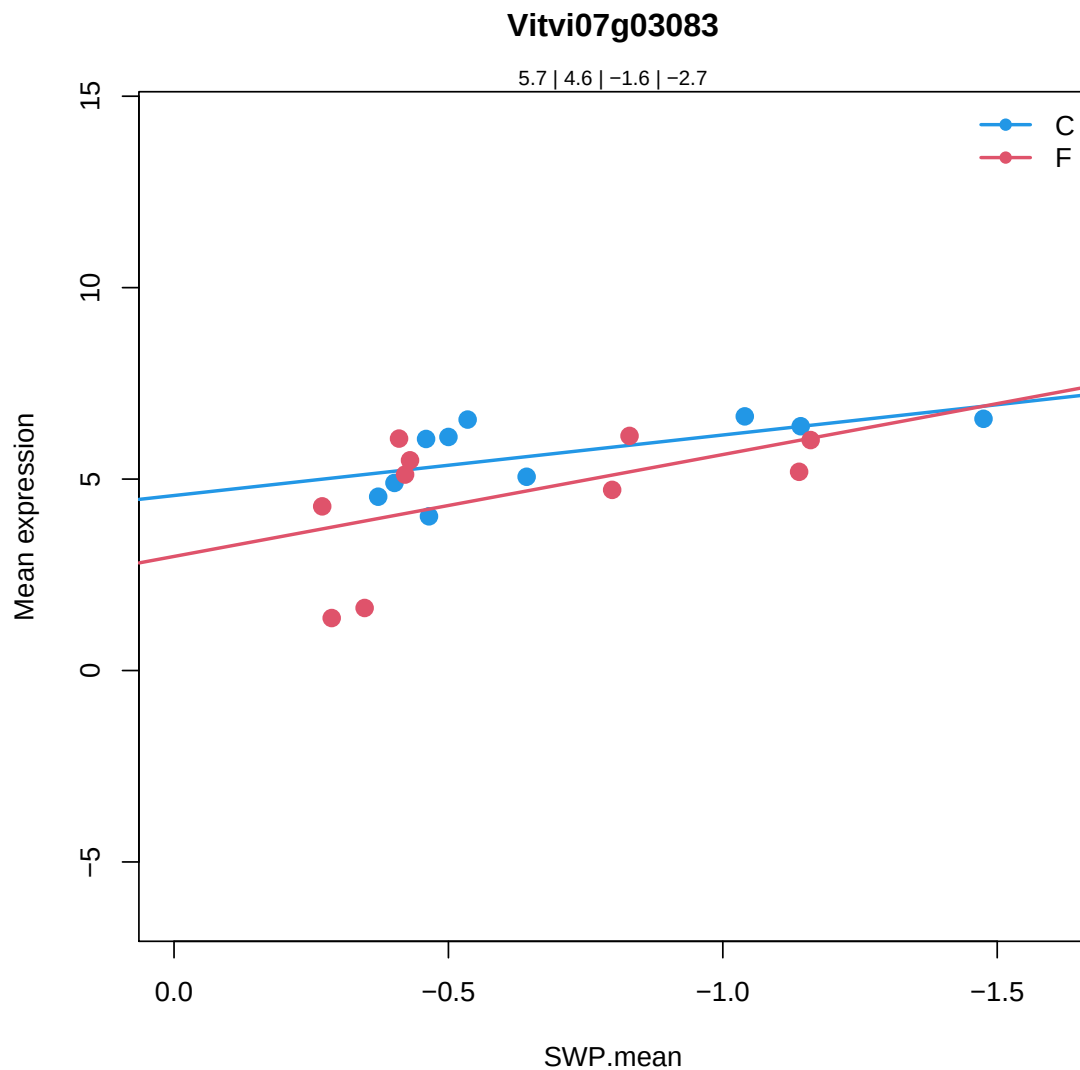
cinnamyl alcohol dehydrogenase 7 |

Chr4:17852670-17854302 FORWARD LENGTH=357 |

201606

Coefficients for Vitvi07g03083.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.681929	1.478938e-13	***	2.242536e-13	***
SlopeC	-1.581192	0.1177783		0.6341652	
MeanF-MeanC	-1.080877	0.03958276	*	0.204845	
SlopeF-SlopeC	-1.079921	0.4626984		0.9999488	



8.2.4 Vitvi04g01126: * Type1.2

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

Vitvi04g01126

35.2

not assigned.unknown

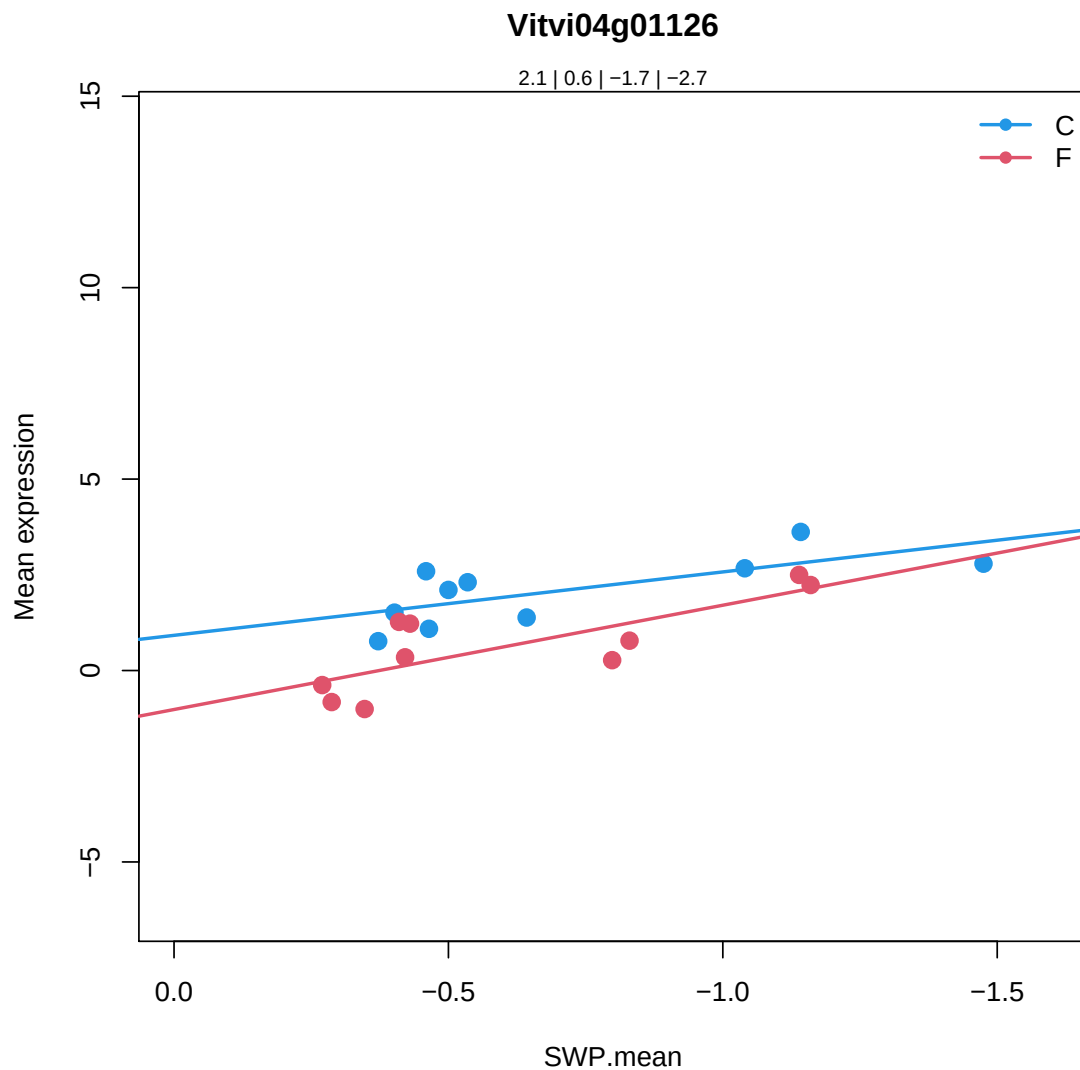
transmembrane protein |

Chr5:14191711-14193654 REVERSE LENGTH=295 |

201606

Coefficients for Vitvi04g01126.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.083353	2.456297e-09	***	3.058482e-09	***
SlopeC	-1.656076	0.01093921	*	0.3141738	
MeanF-MeanC	-1.442417	9.732007e-05	***	0.001768001	**
SlopeF-SlopeC	-1.068136	0.2404919		0.9999488	



8.2.5 Vitvi05g00681: * Type1.2

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

Vitvi05g00681

10.2.1

cell wall.cellulose synthesis.cellulose synthase

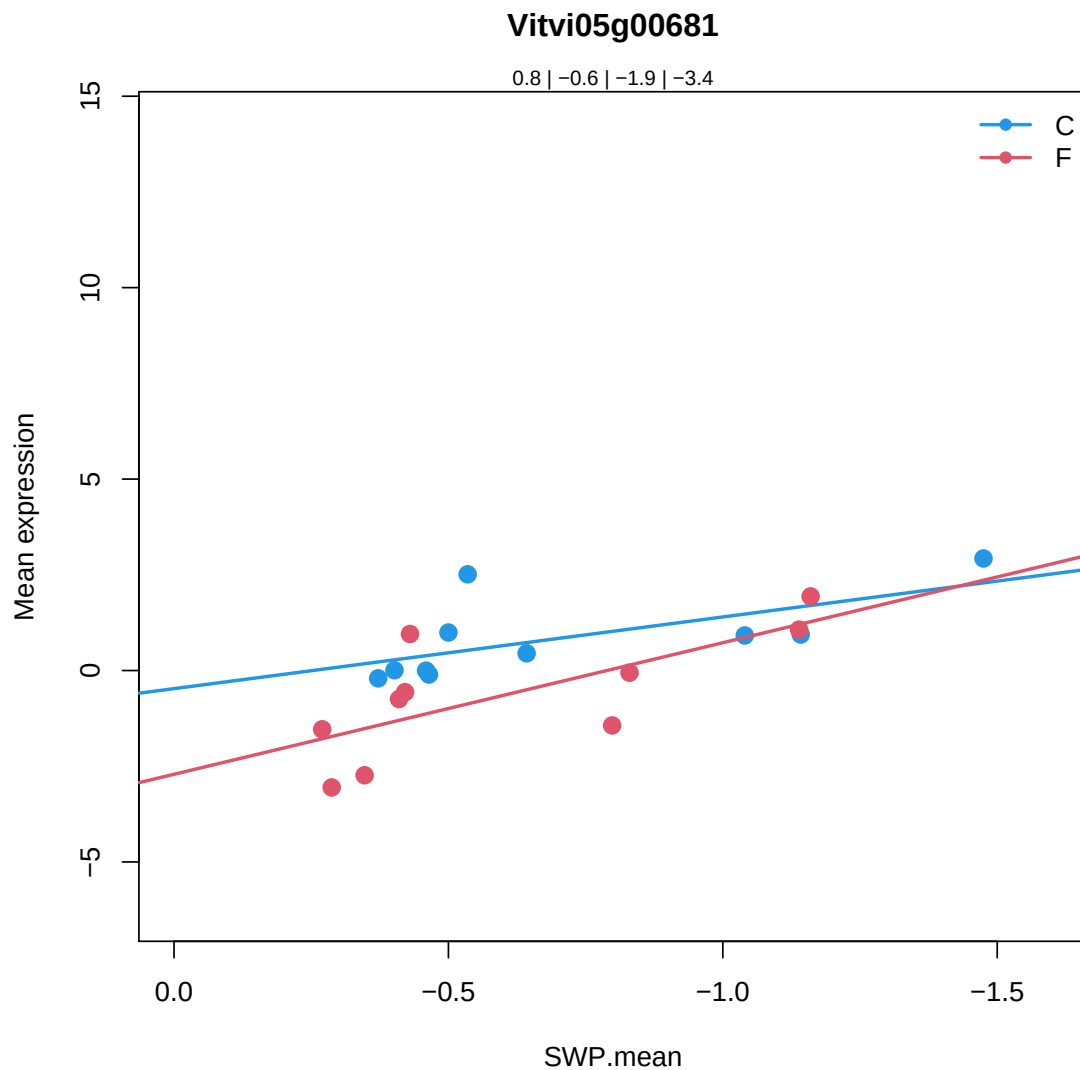
cysteine-rich RECEPTOR-like kinase |

Chr4:12129485-12133157 FORWARD LENGTH=1043 |

201606

Coefficients for Vitvi05g00681.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8430558	0.009925451	**	0.01051311	*
SlopeC	-1.872315	0.03446689	*	0.444078	
MeanF-MeanC	-1.460116	0.002266089	**	0.02434089	*
SlopeF-SlopeC	-1.563097	0.218861		0.9999488	



8.2.6 Vitvi13g00451: * Type1.2

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

Vitvi13g00451

20.2.1

stress.abiotic.heat

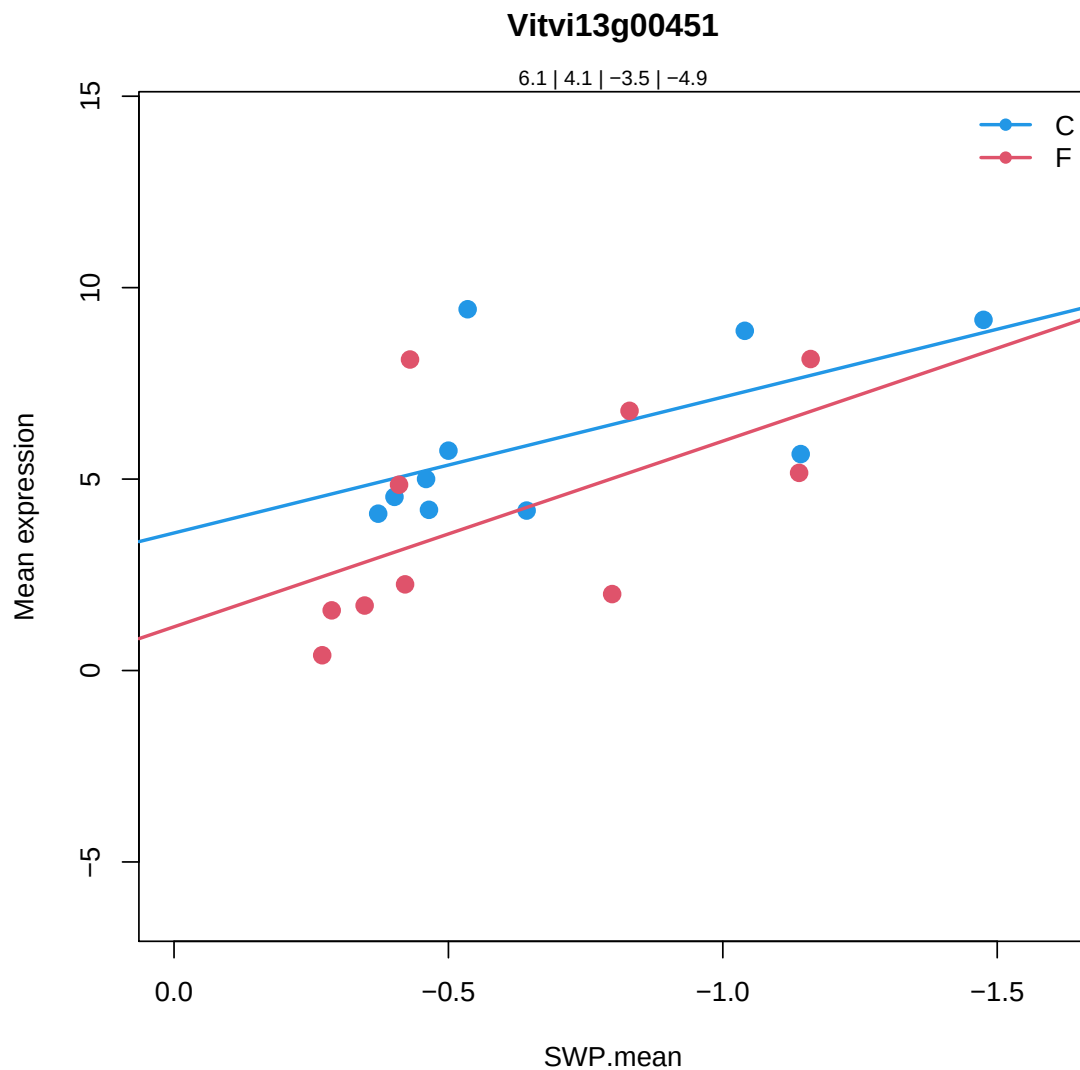
heat shock protein 18.2 |

Chr5:24062632-24063117 FORWARD LENGTH=161 |

201606

Coefficients for Vitvi13g00451.

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



8.2.7 Vitvi13g00278: * Type1.2

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

Vitvi13g00278

20.2.1

stress.abiotic.heat

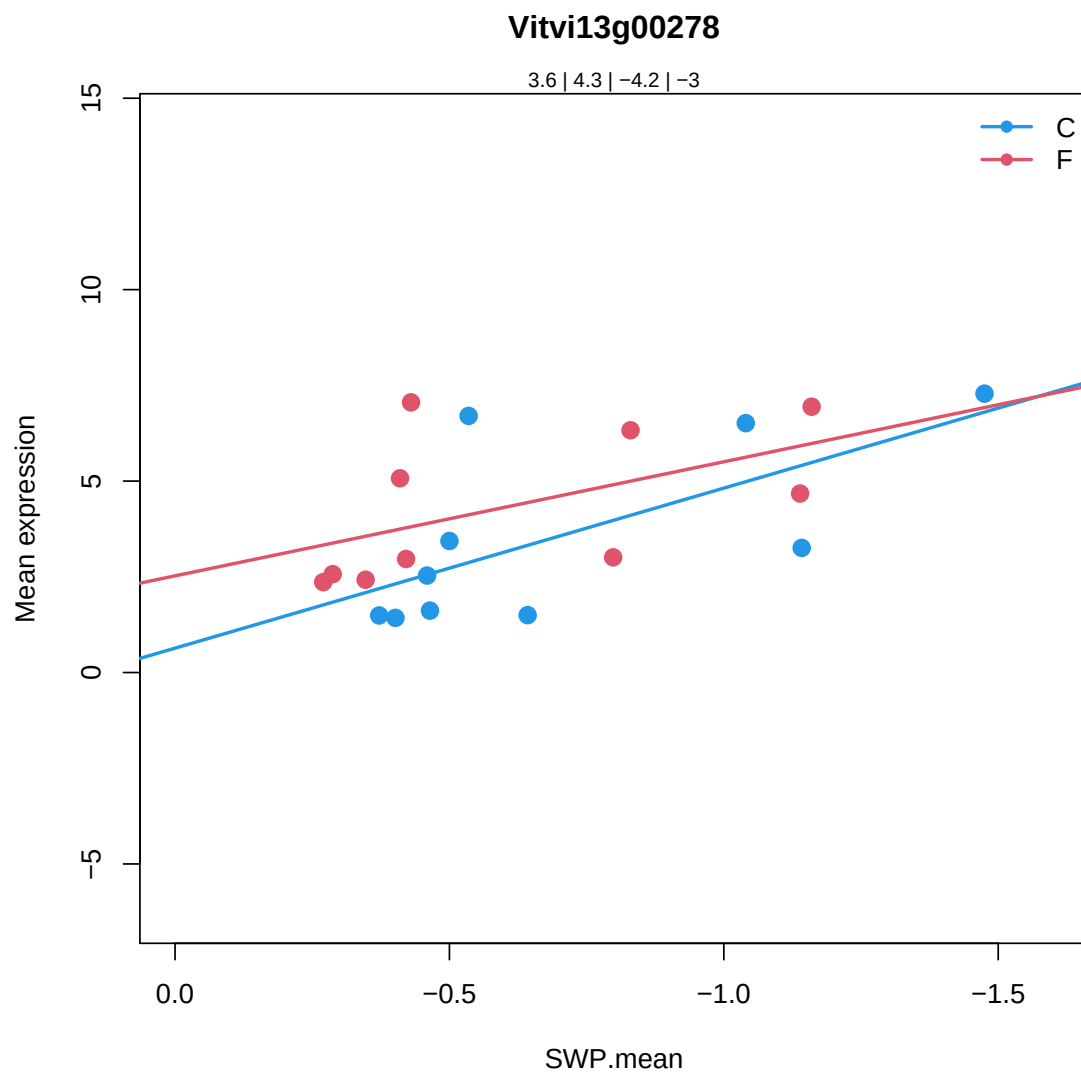
HSP20-like chaperones superfamily protein |

Chr5:14969035-14969448 FORWARD LENGTH=137 |

201606

Coefficients for Vitvi13g00278.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.575152	3.806346e-07	***	4.441951e-07	***
SlopeC	-4.180072	0.006354519	**	0.2661465	
MeanF-MeanC	0.7647119	0.2885058		0.6536088	
SlopeF-SlopeC	1.200427	0.565639		0.9999488	



8.2.8 Vitvi07g00457: * Type1.2

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

Vitvi07g00457

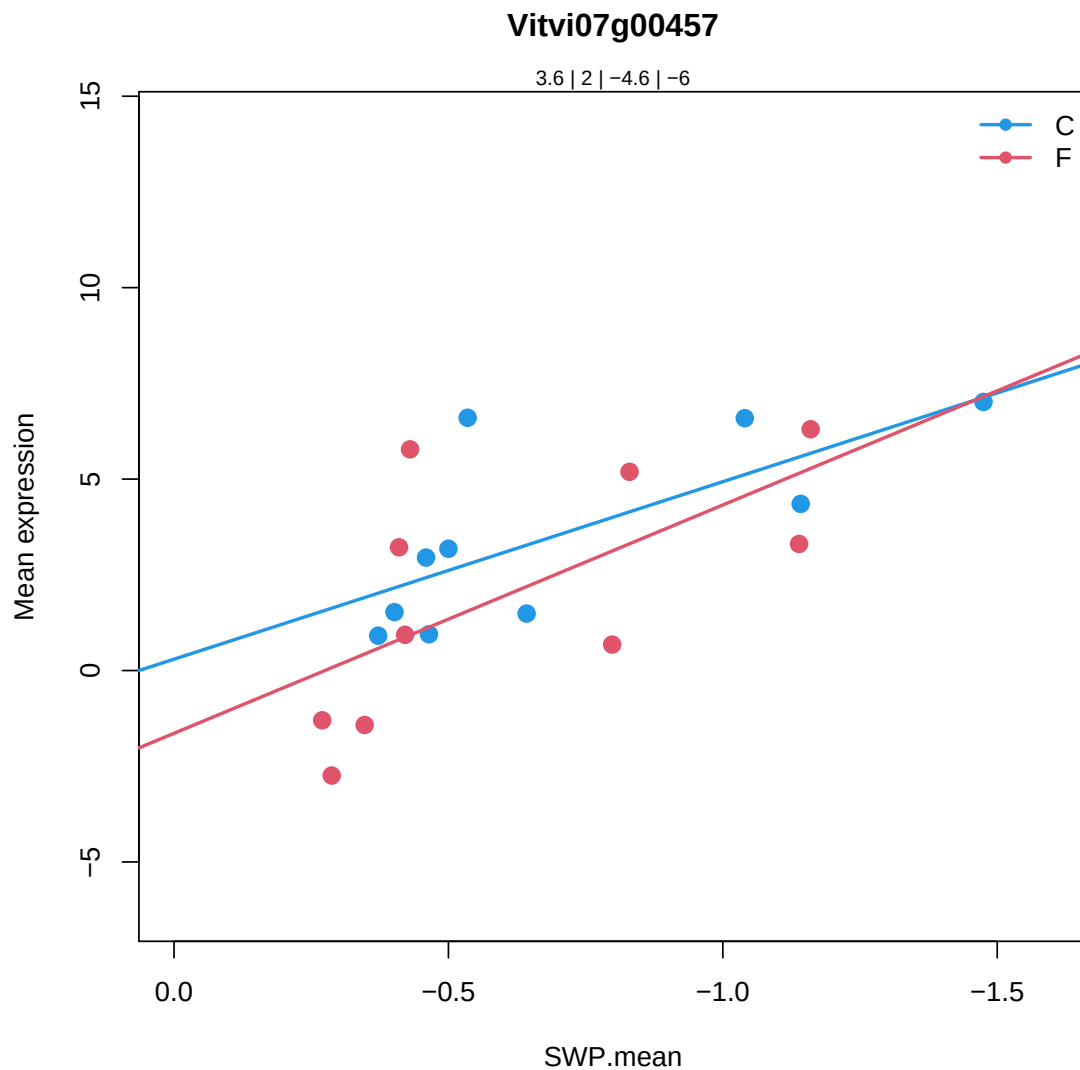
3.1.1.1

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

Chr2:19369049-19370372 REVERSE LENGTH=344 |
201606

Coefficients for Vitvi07g00457.

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



8.3 Type1.4

8.3.1 Vitvi13g02005: Type1.4

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

Vitvi13g02005

29.5.1

protein.degradation.subtilases

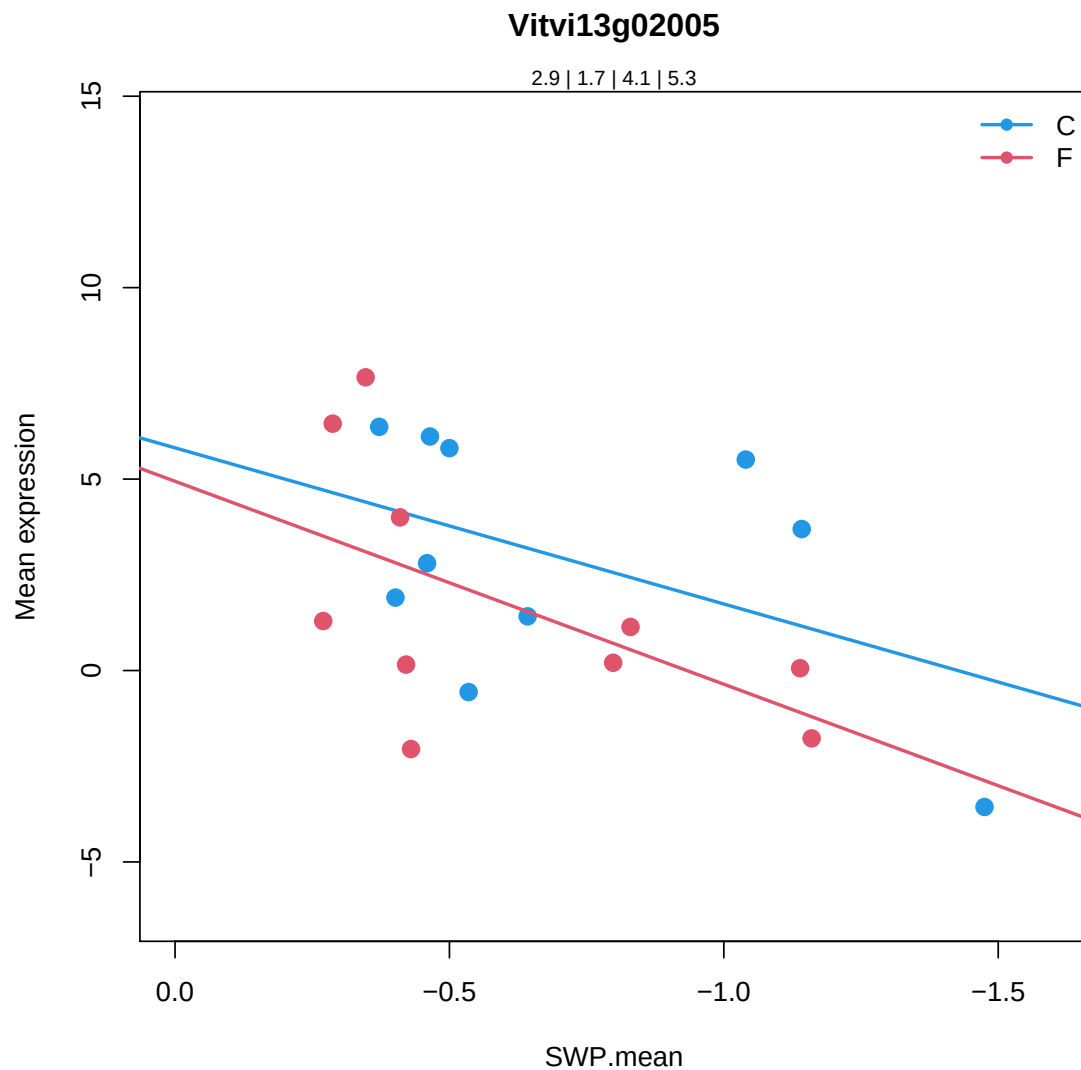
Subtilisin-like serine endopeptidase family protein |

Chr5:23755787-23758600 FORWARD LENGTH=710 |

201606

Coefficients for Vitvi13g02005.

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

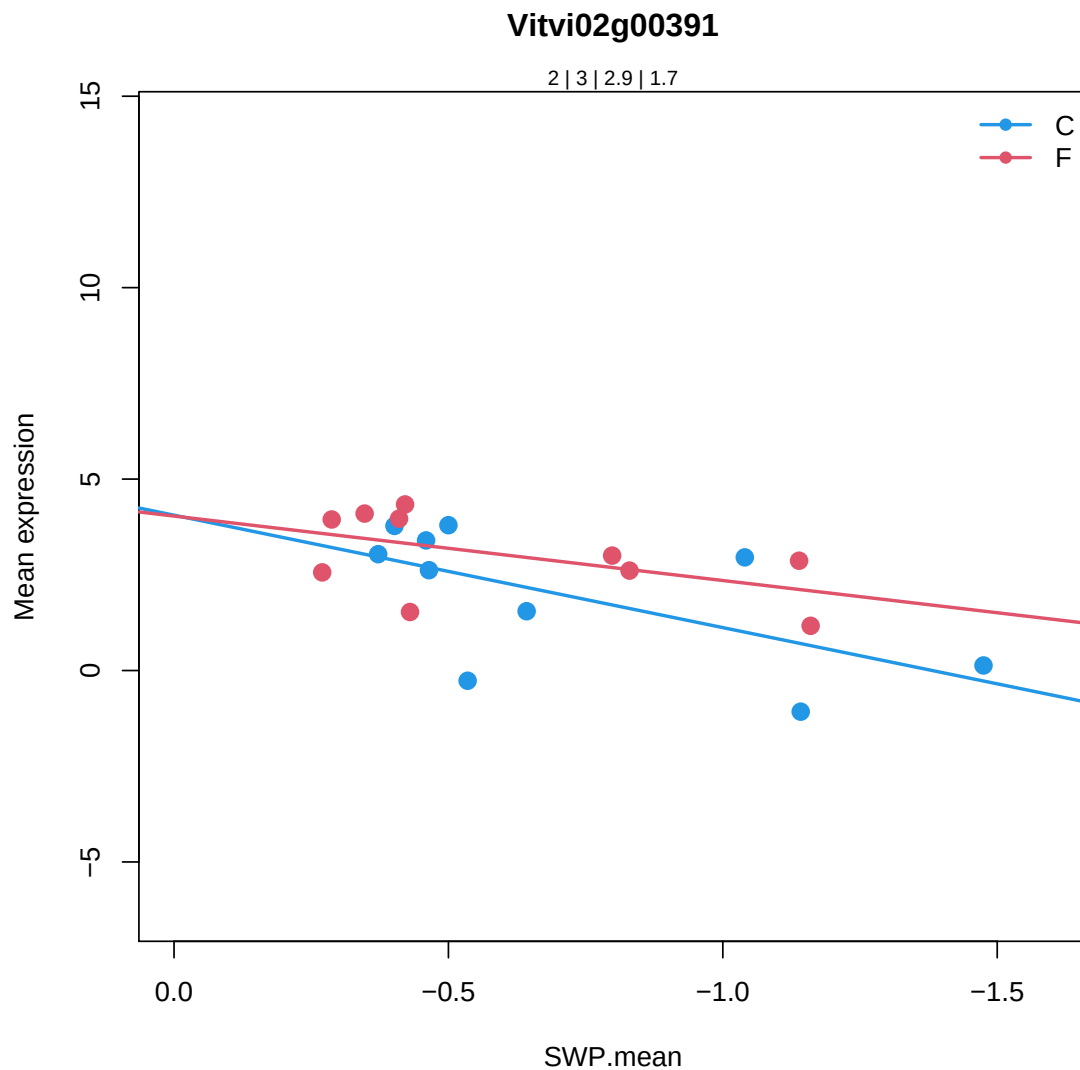


8.3.2 Vitvi02g00391: * Type1.4

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

Coefficients for Vitvi02g00391.

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

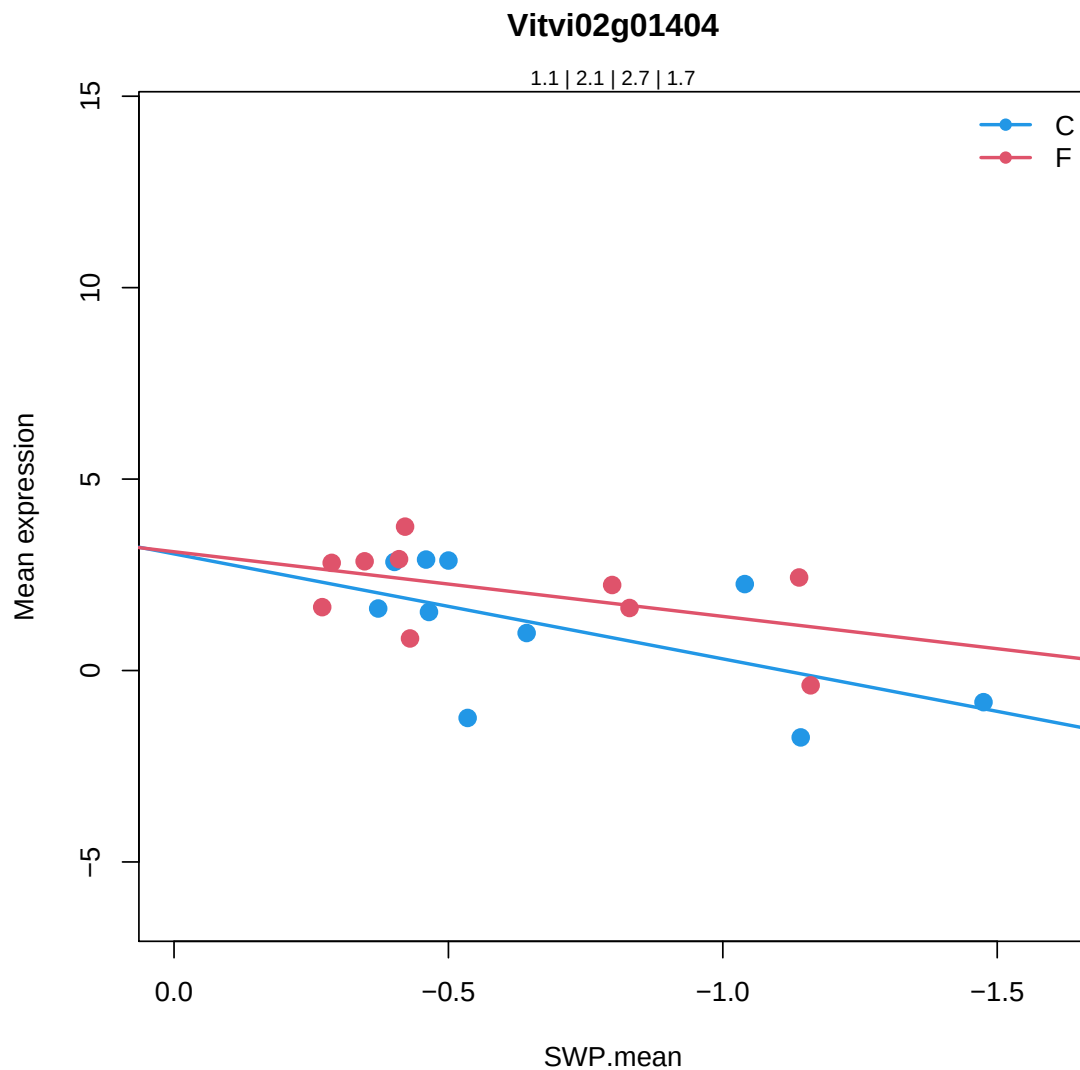


8.3.3 Vitvi02g01404: * Type1.4

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

Coefficients for Vitvi02g01404.

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



8.3.4 Vitvi12g02414: * Type1.4

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

Vitvi12g02414

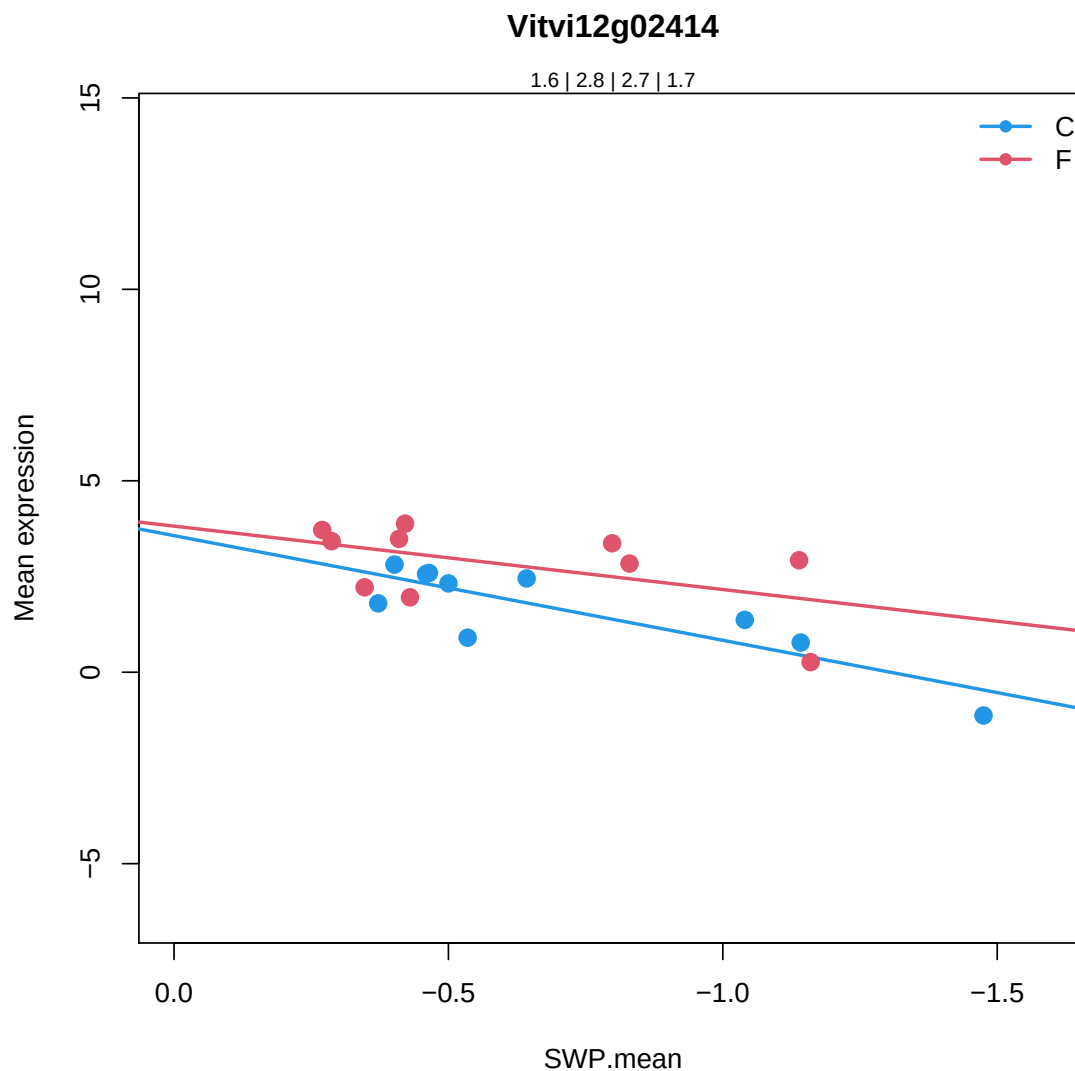
35.2

not assigned.unknown

Genomic DNA chromosome 3 P1 clone MSD21

Coefficients for Vitvi12g02414.

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



8.3.5 Vitvi13g00490: * Type1.4

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

Vitvi13g00490

20.2.1

stress.abiotic.heat

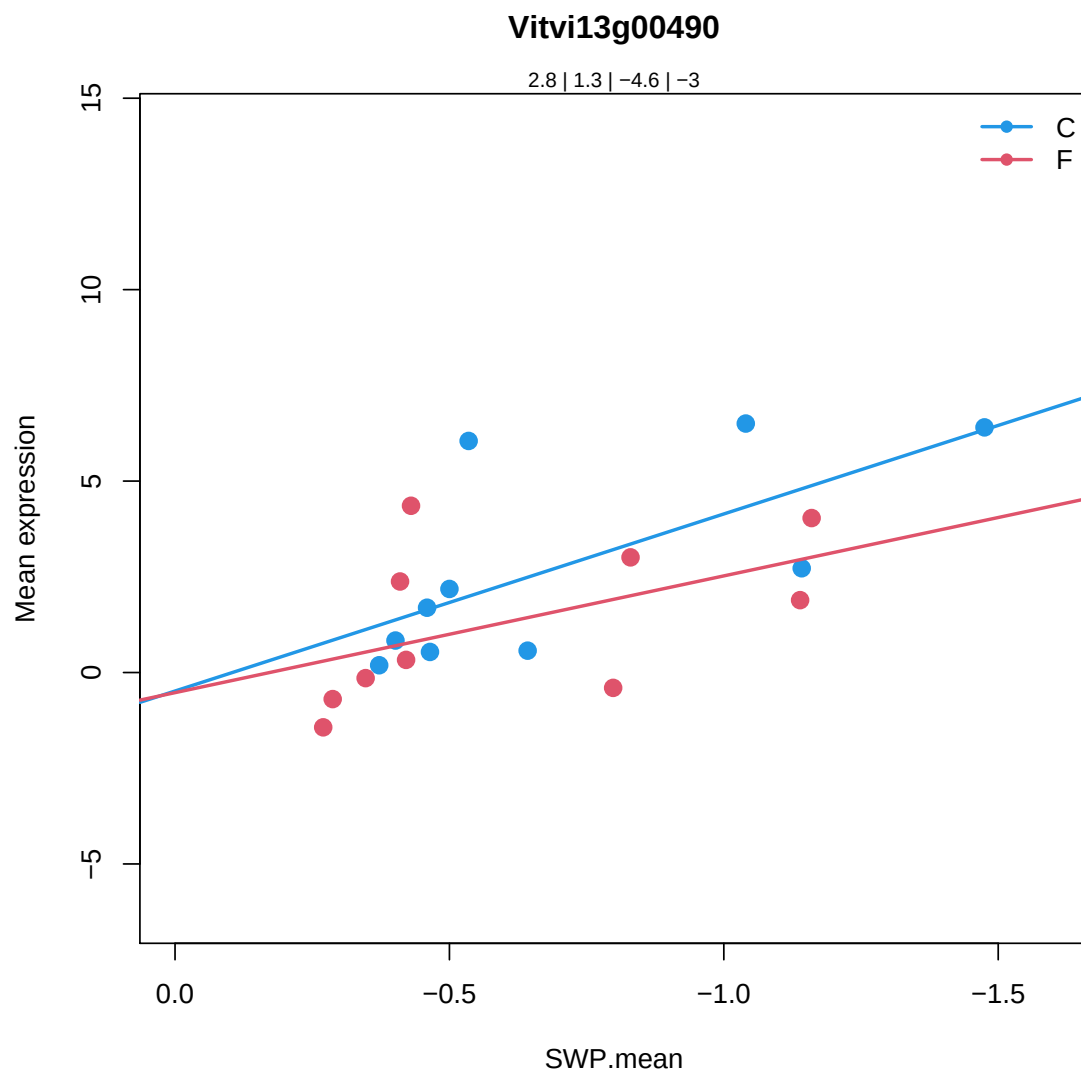
heat shock protein 18.2 |

Chr5:24062632-24063117 FORWARD LENGTH=161 |

201606

Coefficients for Vitvi13g00490.

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



8.3.6 Vitvi04g01802: * Type1.4

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

Vitvi04g01802

20.2.1

stress.abiotic.heat

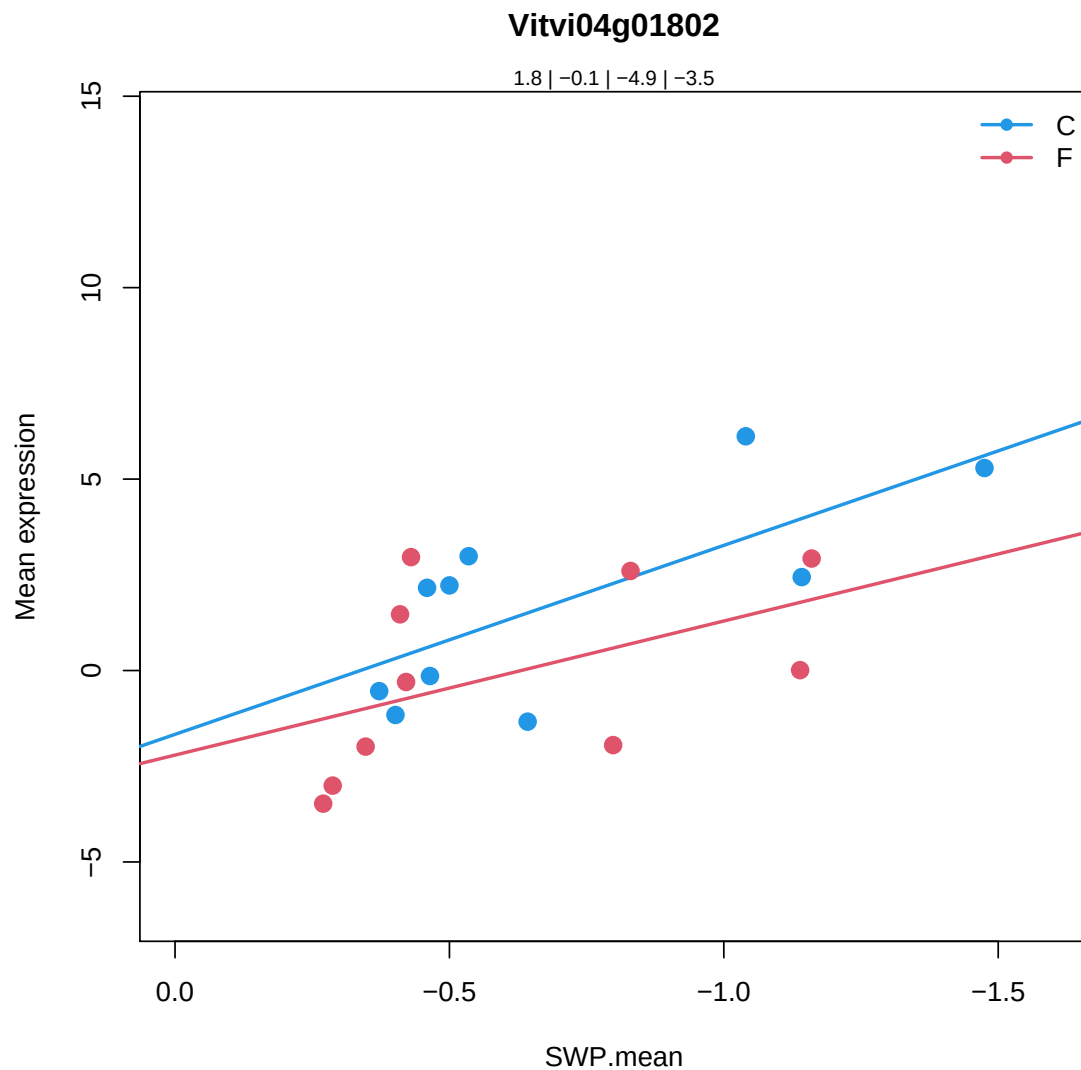
17.6 kDa class II heat shock protein |

Chr5:3882409-3882876 REVERSE LENGTH=155 |

201606

Coefficients for Vitvi04g01802.

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



8.3.7 Vitvi04g01801: * Type1.4

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

Vitvi04g01801

20.2.1

stress.abiotic.heat

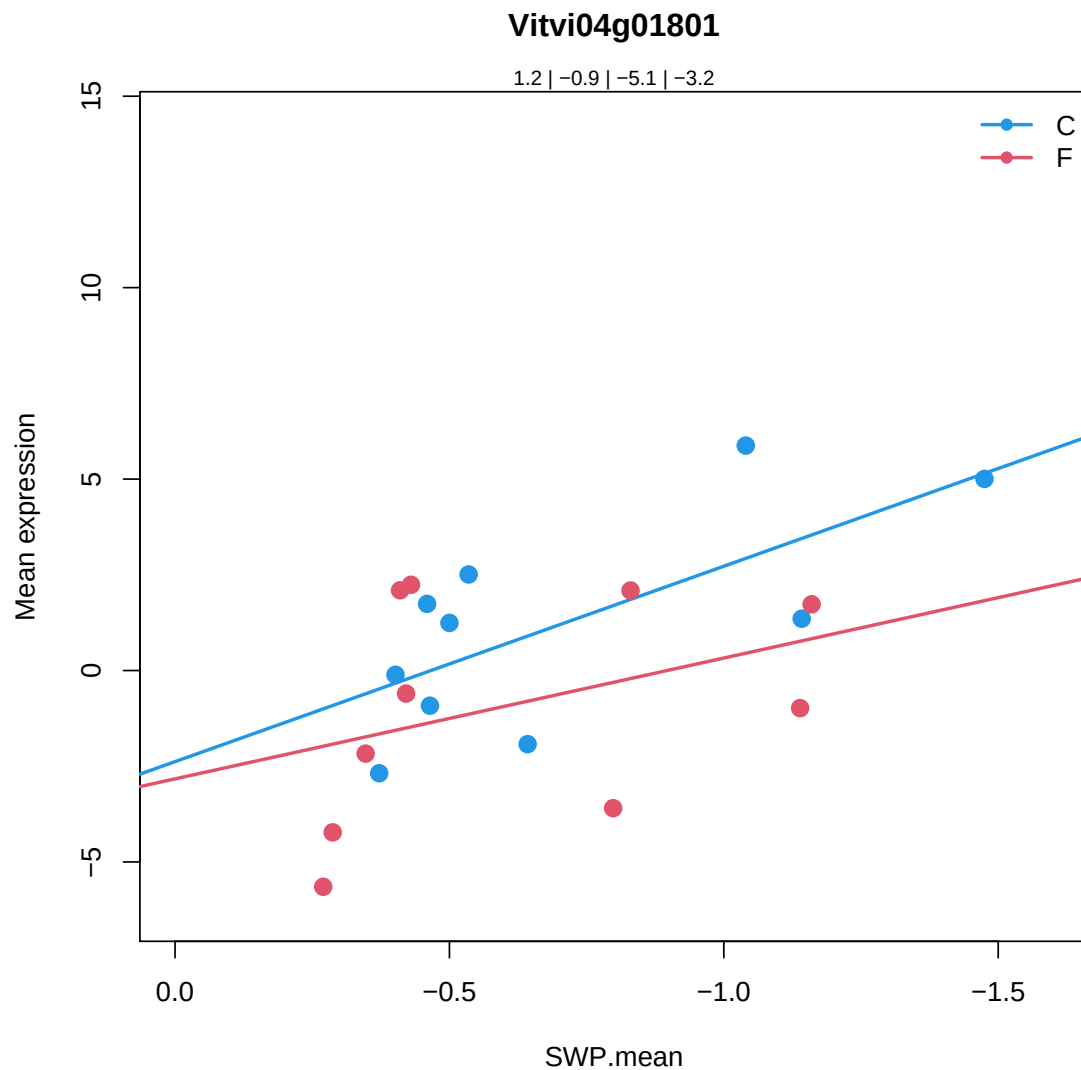
17.6 kDa class II heat shock protein |

Chr5:3882409-3882876 REVERSE LENGTH=155 |

201606

Coefficients for Vitvi04g01801.

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



8.3.8 Vitvi02g00025: * Type1.4

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

Vitvi02g00025

20.2.1

stress.abiotic.heat

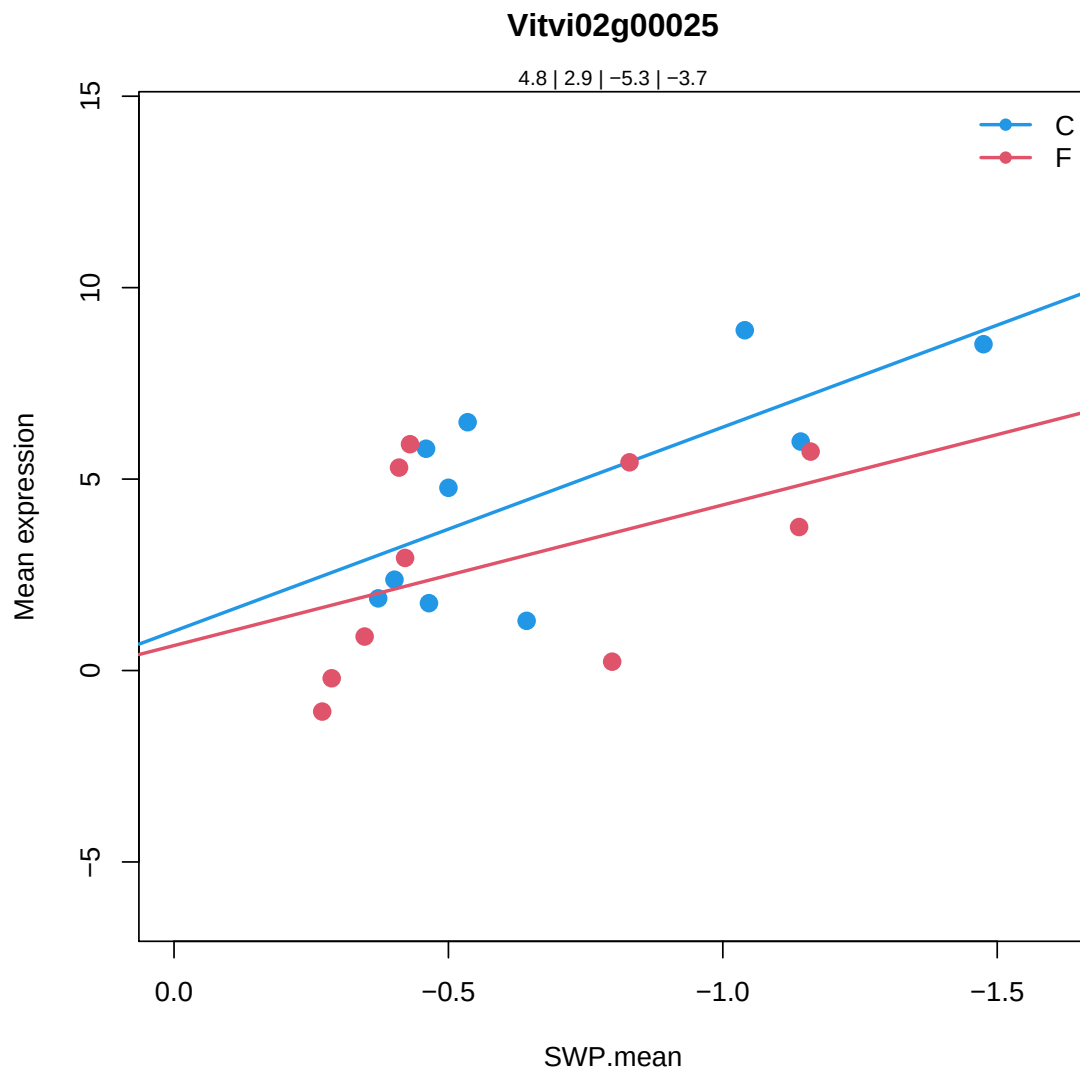
heat shock-like protein |

Chr5:21352557-21355147 FORWARD LENGTH=700 |

201606

Coefficients for Vitvi02g00025.

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



8.3.9 Vitvi04g01799: * Type1.4

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

Vitvi04g01799

20.2.1

stress.abiotic.heat

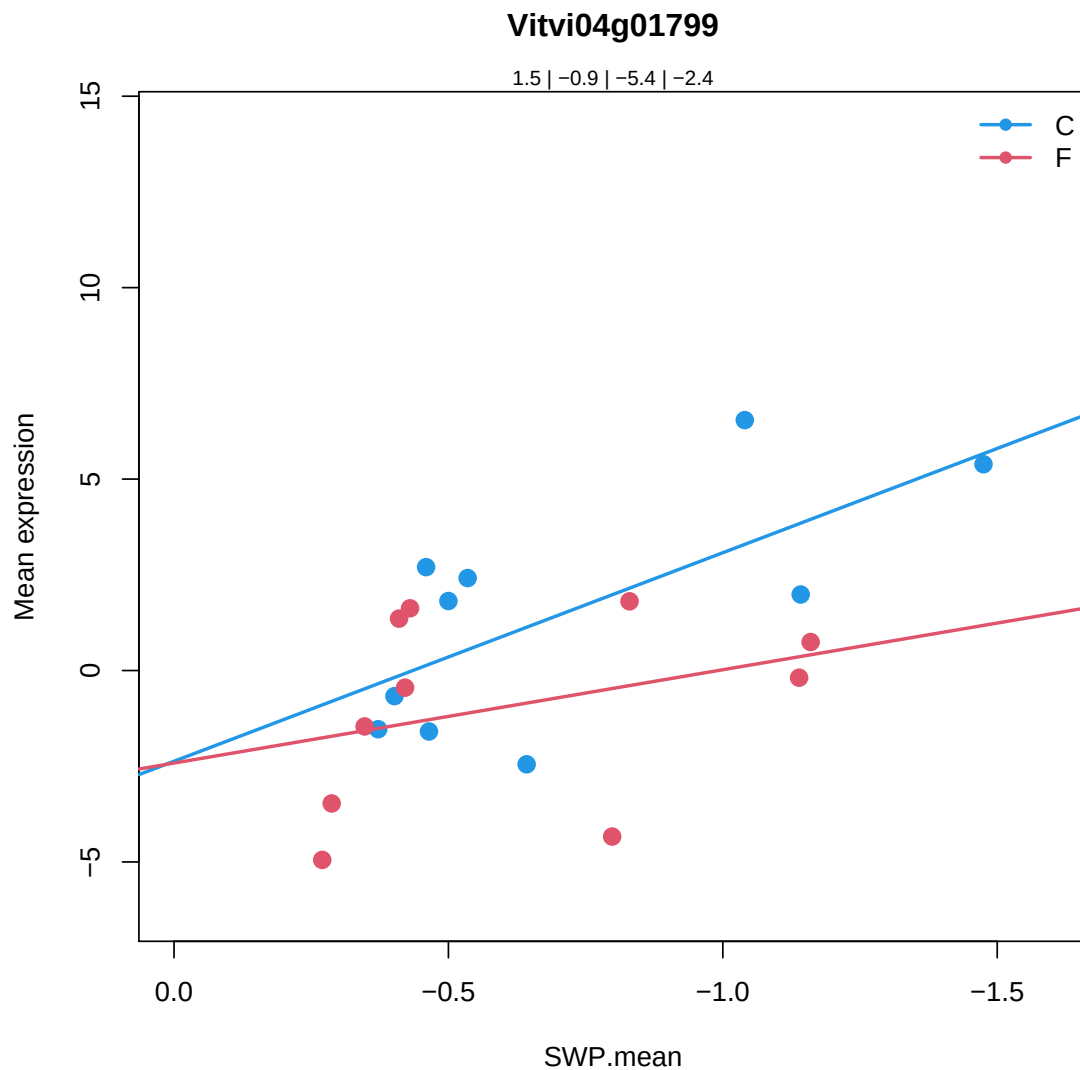
17.6 kDa class II heat shock protein |

Chr5:3882409-3882876 REVERSE LENGTH=155 |

201606

Coefficients for Vitvi04g01799.

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



8.3.10 Vitvi04g01794: * Type1.4

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

Vitvi04g01794

20.2.1

stress.abiotic.heat

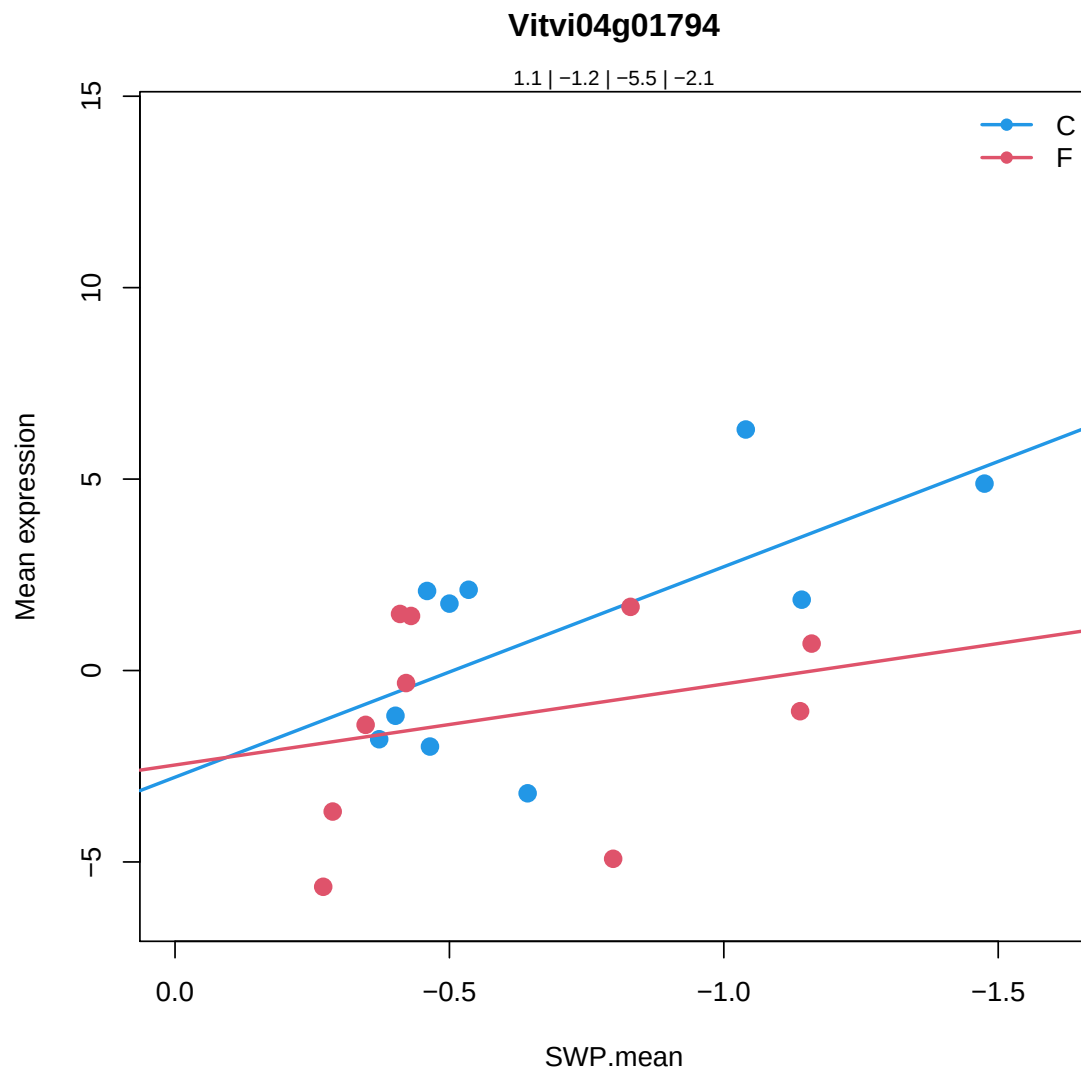
17.6 kDa class II heat shock protein |

Chr5:3882409-3882876 REVERSE LENGTH=155 |

201606

Coefficients for Vitvi04g01794.

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



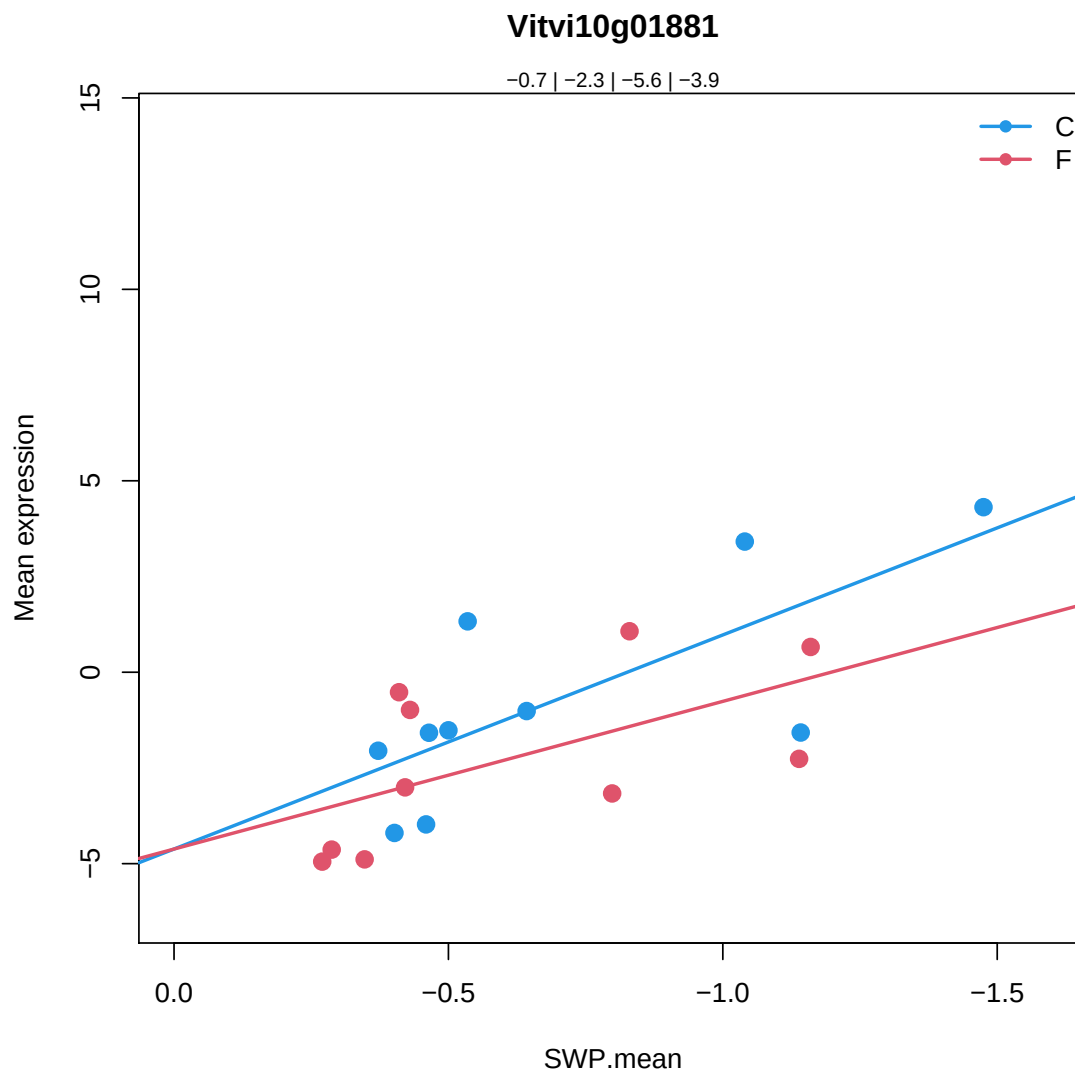
8.3.11 Vitvi10g01881: * Type1.4

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

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

Coefficients for Vitvi10g01881.

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



8.3.12 Vitvi06g00561: * Type1.4

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

Vitvi06g00561

35.2

not assigned.unknown

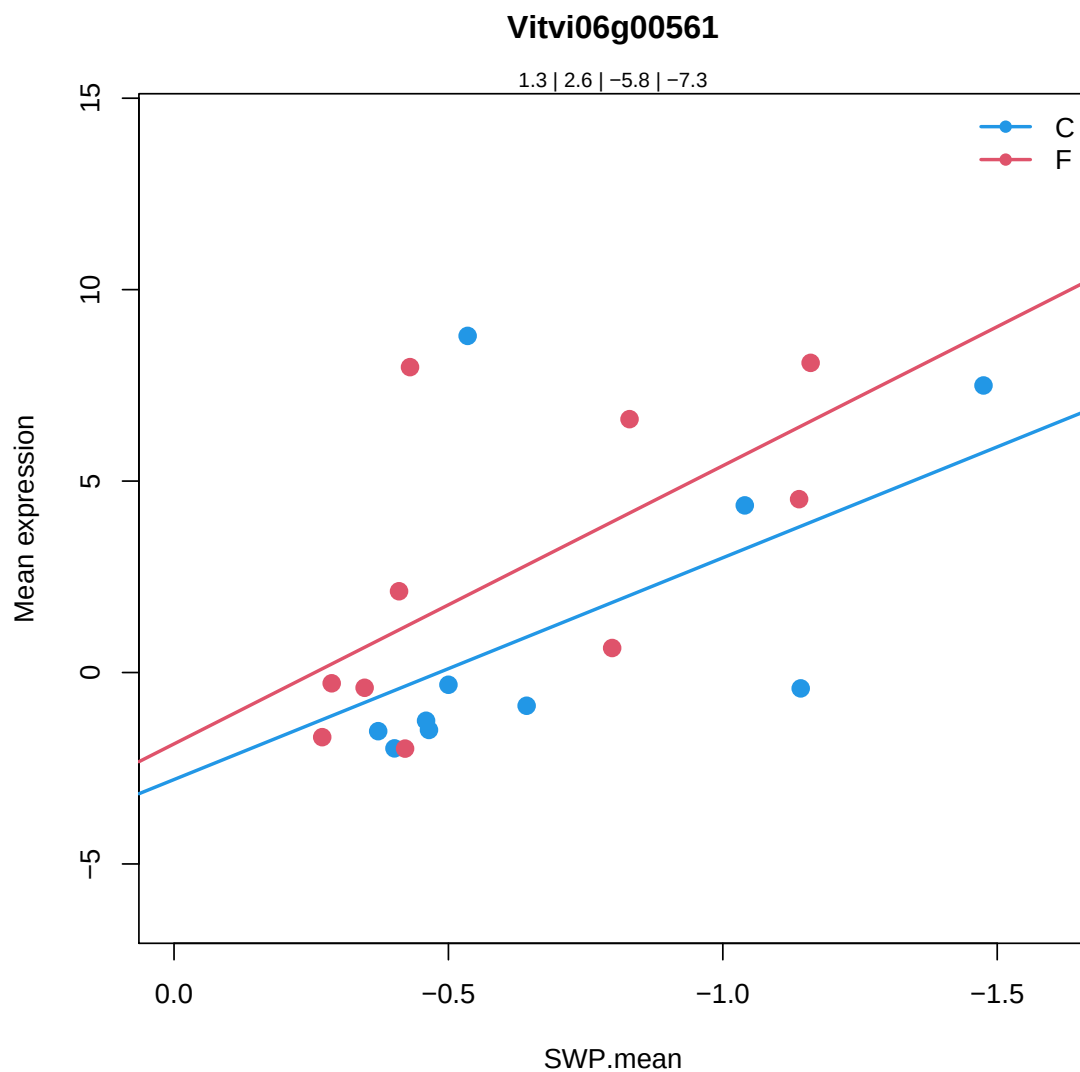
HSP20-like chaperones superfamily protein |

Chr2:12633279-12633740 REVERSE LENGTH=153 |

201606

Coefficients for Vitvi06g00561.

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



8.3.13 Vitvi16g01352: * Type1.4

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

Vitvi16g01352

20.2.1

stress.abiotic.heat

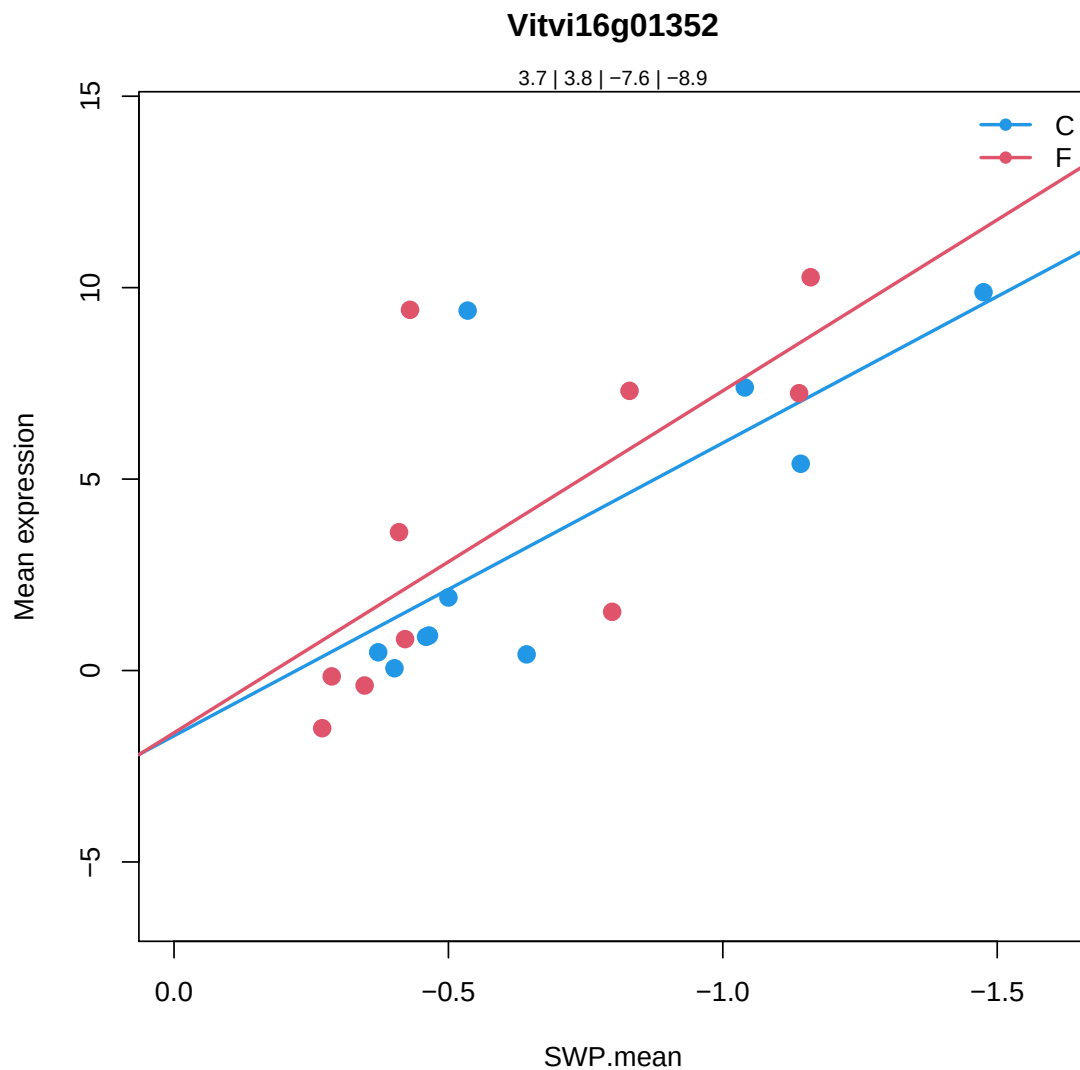
heat shock protein 21 |

Chr4:13819048-13819895 REVERSE LENGTH=227 |

201606

Coefficients for Vitvi16g01352.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.673182	0.0002848136	***	0.0003116389	***
SlopeC	-7.649088	0.00385391	**	0.2269459	
MeanF-MeanC	0.1420623	0.9068882		0.9757034	
SlopeF-SlopeC	-1.282333	0.7187855		0.9999488	



8.4 Type3.C

8.4.1 Vitvi09g01874: * Type3.C

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

```
Vitvi09g01874
```

```
35.2
```

```
not assigned.unknown
```

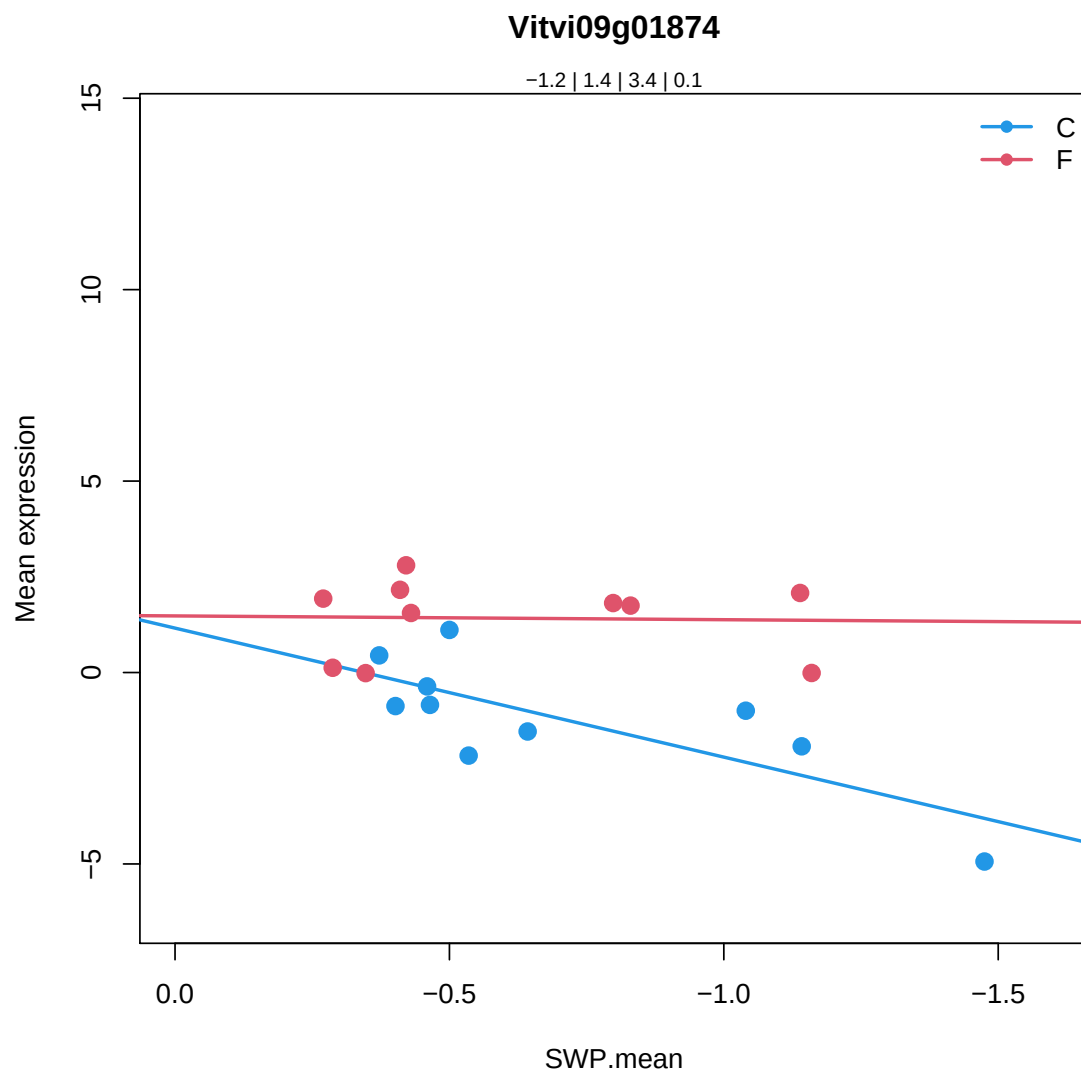
```
disease resistance family protein / LRR family protein |
```

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

```
201606
```

Coefficients for Vitvi09g01874.

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



8.4.2 Vitvi10g00663: * Type3.C

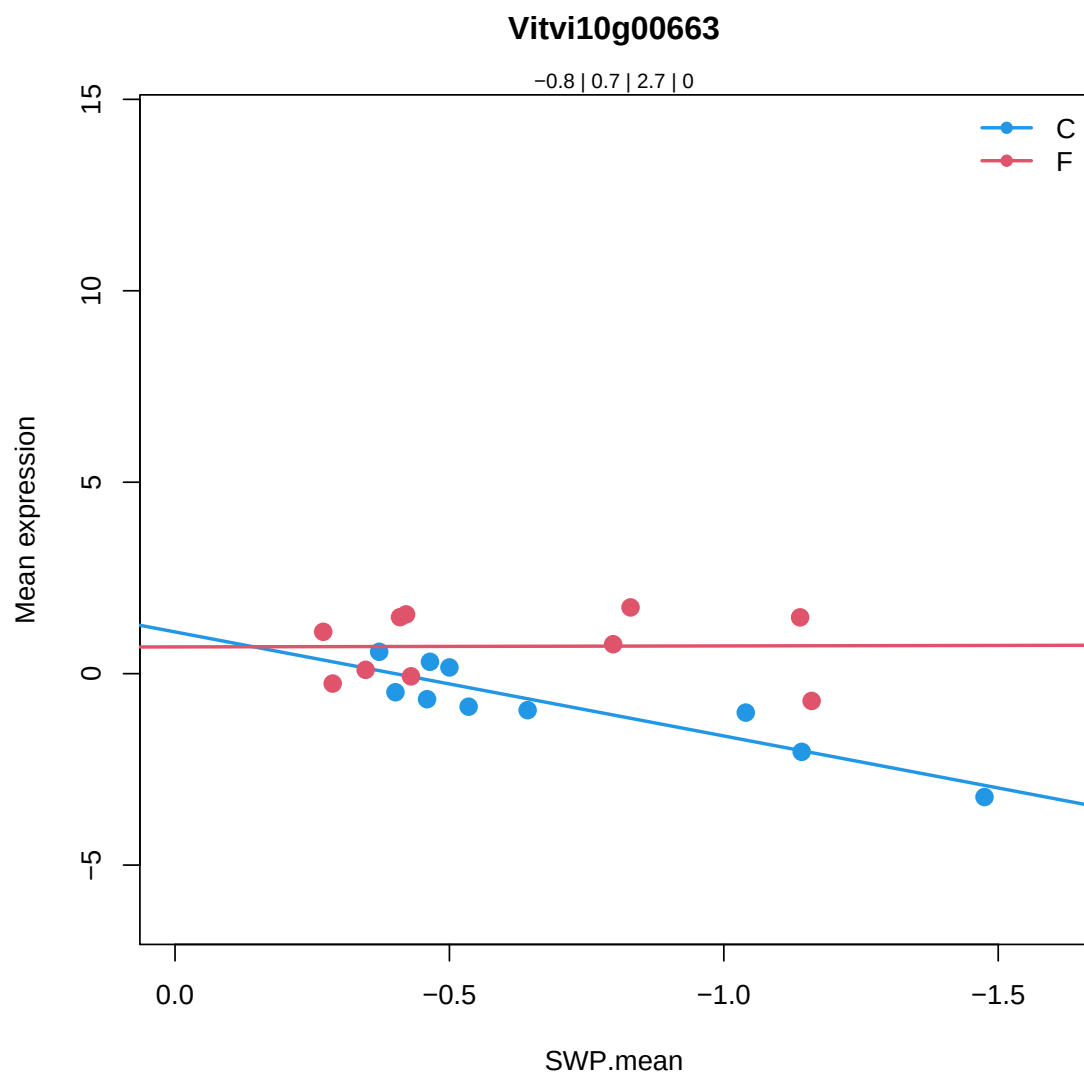
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi10g00663
33.99
development.unspecified
K-box region and MADS-box transcription factor family protein |
Chr3:21739150-21741766 FORWARD LENGTH=241 |
201606

Vitvi10g00663
27.3.24
RNA.regulation of transcription.MADS box transcription factor family
K-box region and MADS-box transcription factor family protein |
Chr3:21739150-21741766 FORWARD LENGTH=241 |
201606
```

Coefficients for Vitvi10g00663.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.8209171	0.001213348	**	0.001311992	**
SlopeC	2.716708	0.0002212026	***	0.08109226	.
MeanF-MeanC	1.534975	6.737202e-05	***	0.001277494	**
SlopeF-SlopeC	-2.742007	0.00662921	**	0.9999488	



8.4.3 Vitvi18g03250: * Type3.C

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

Vitvi18g03250

26.10

misc.cytochrome P450

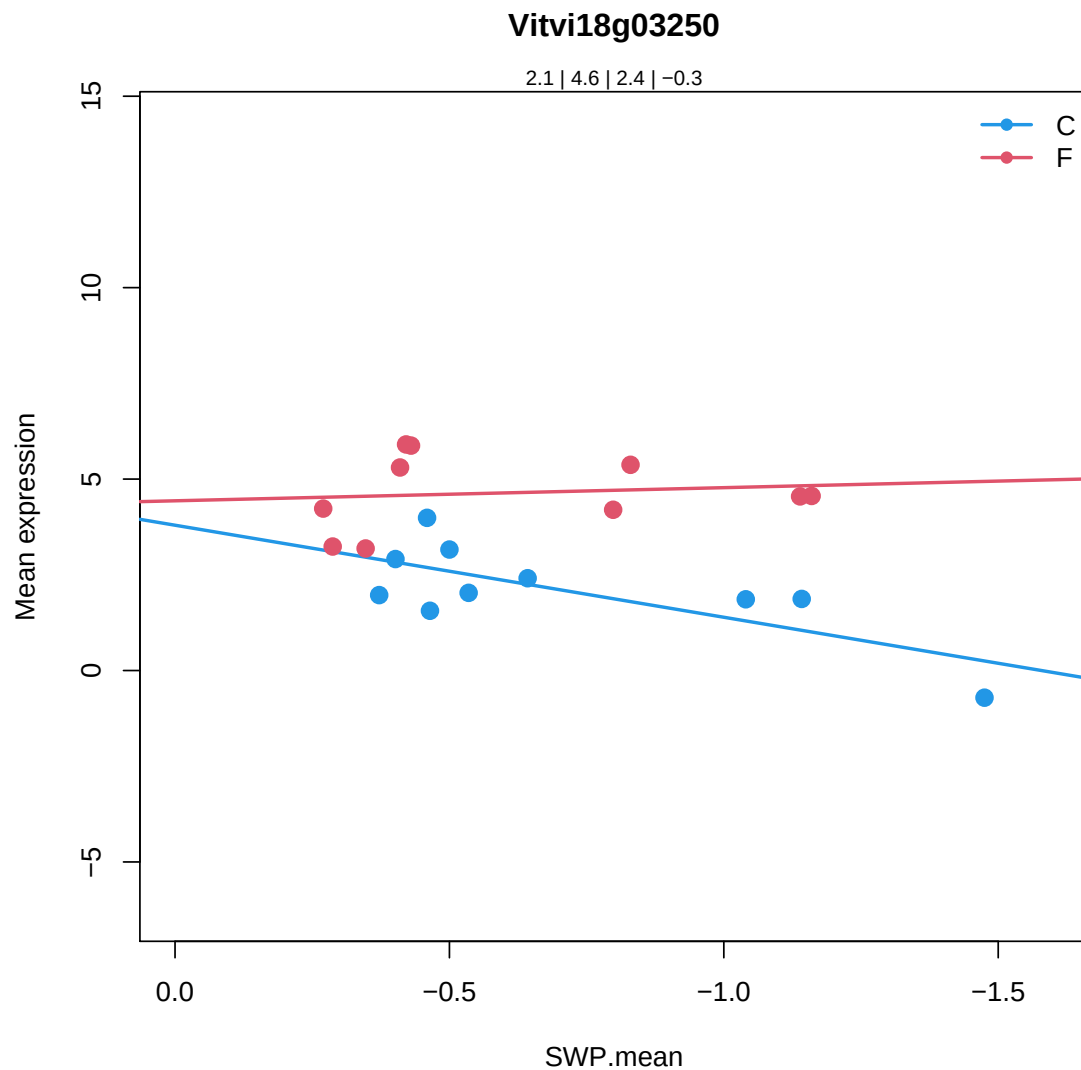
cytochrome P450%2C family 714%2C subfamily A%2C polypeptide 1 |

Chr5:8567674-8570260 REVERSE LENGTH=532 |

201606

Coefficients for Vitvi18g03250.

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



8.4.4 Vitvi05g01758: Type3.C

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

Vitvi05g01758

35.2

not assigned.unknown

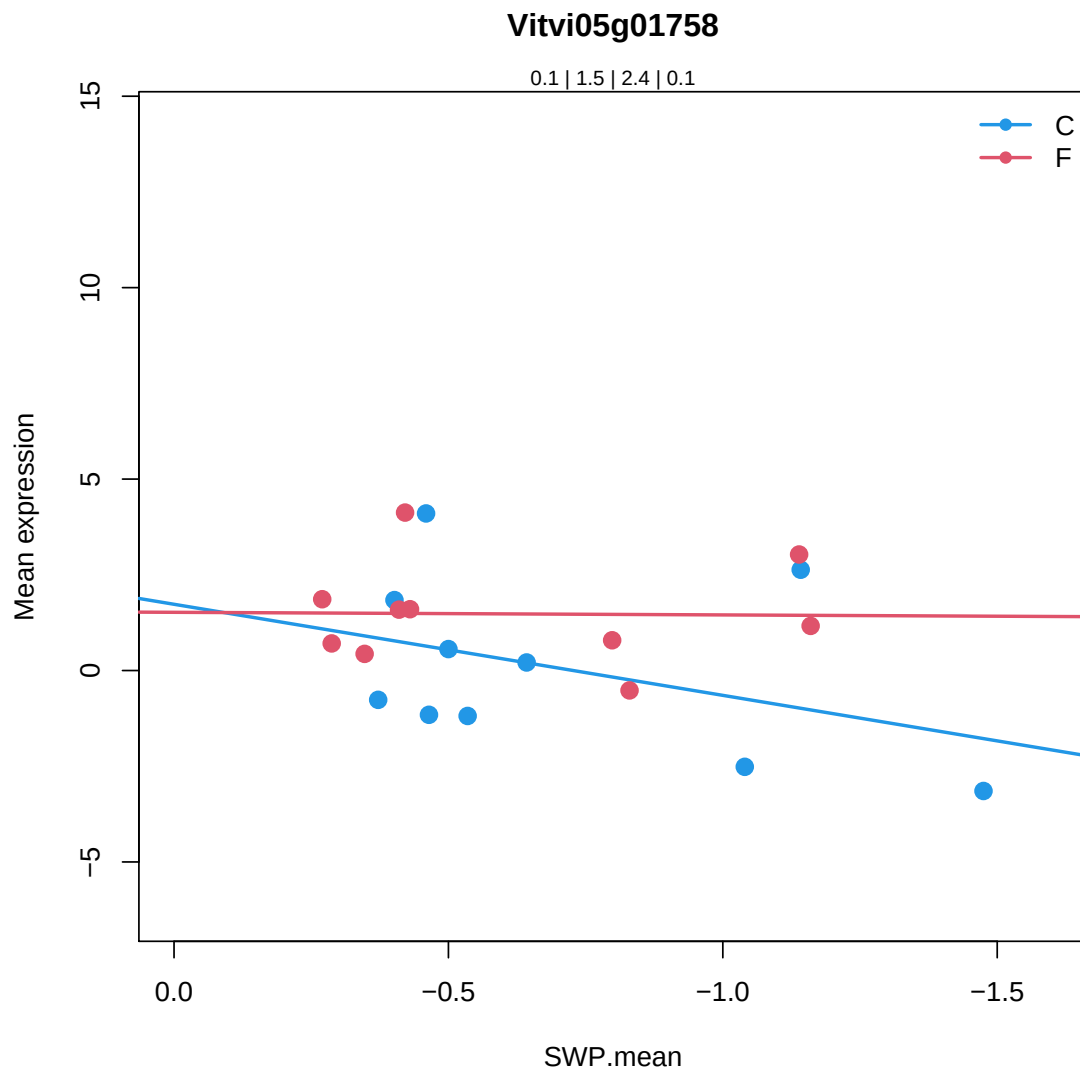
MLP-like protein 423 |

Chr1:8500653-8501458 REVERSE LENGTH=155 |

201606

Coefficients for Vitvi05g01758.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.0573489	0.9123565		0.914276	
SlopeC	2.378762	0.1113767		0.6258604	
MeanF-MeanC	1.421246	0.06415951	.	0.2806081	
SlopeF-SlopeC	-2.310635	0.2905474		0.9999488	



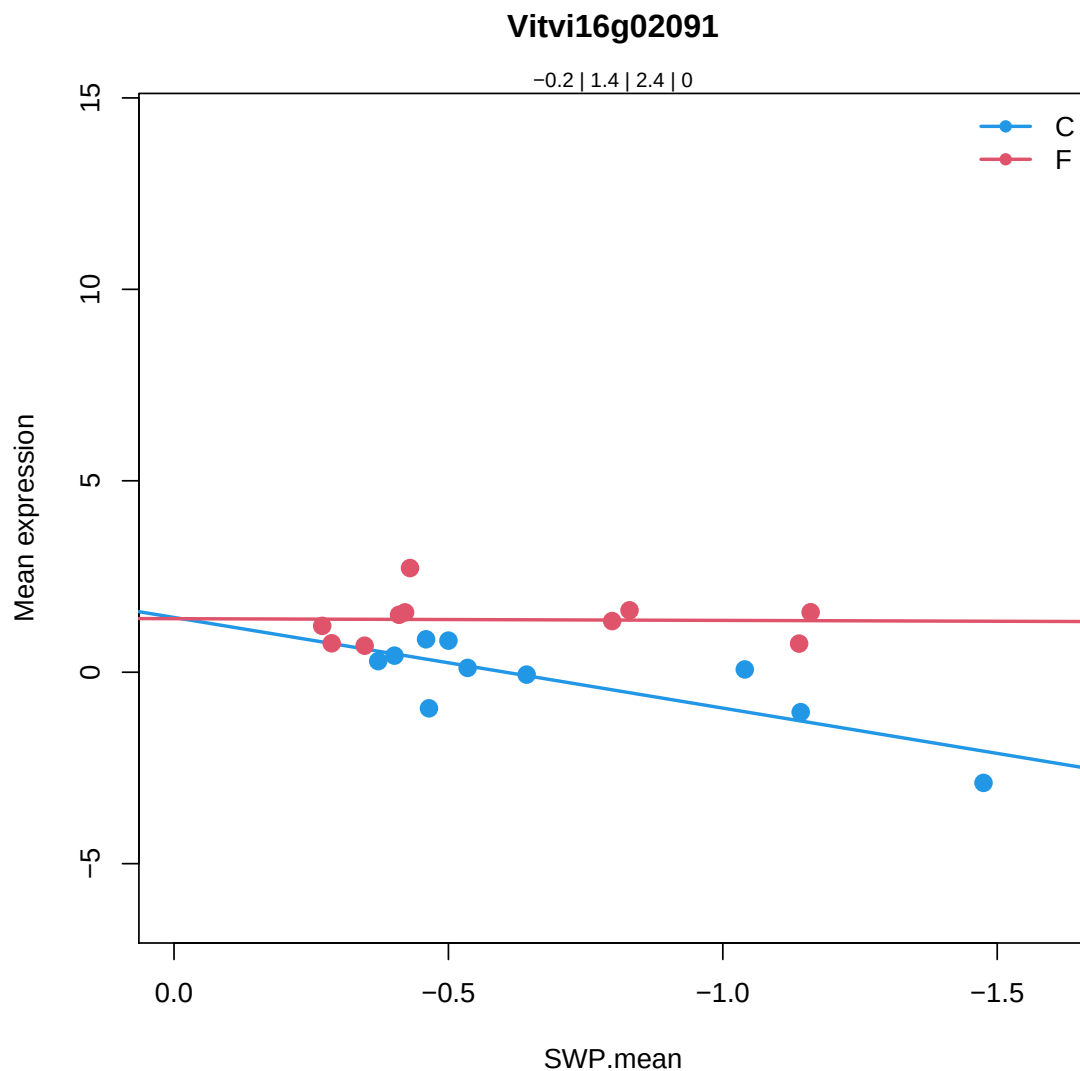
8.4.5 Vitvi16g02091: * Type3.C

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

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

Coefficients for Vitvi16g02091.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.2346616	0.2592422		0.2646775	
SlopeC	2.366765	0.0003865785	***	0.09467692	.
MeanF-MeanC	1.605684	1.346083e-05	***	0.0003309194	***
SlopeF-SlopeC	-2.321945	0.01135478	*	0.9999488	



8.4.6 Vitvi16g02098: * Type3.C

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

Vitvi16g02098

35.2

not assigned.unknown

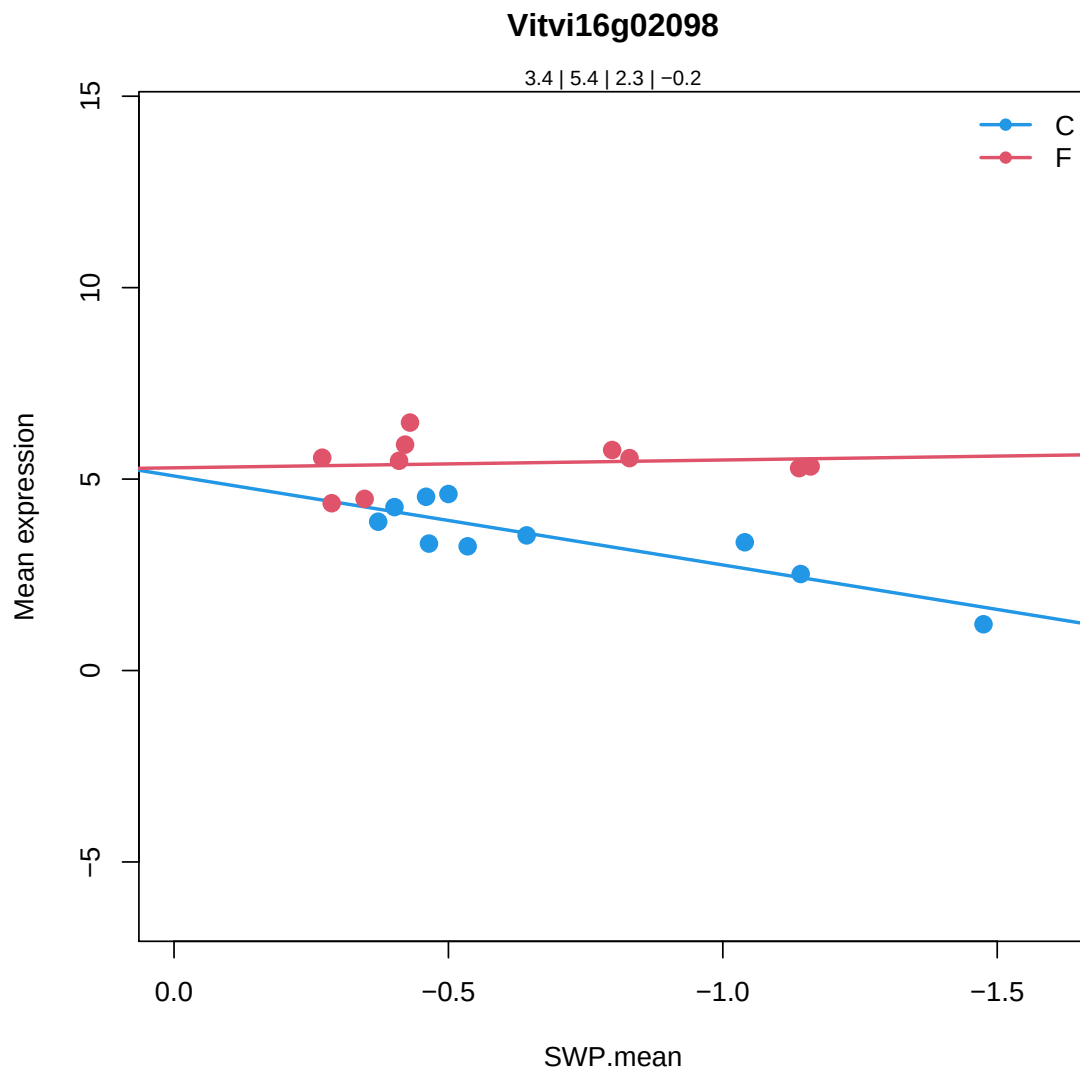
PR5-like receptor kinase |

Chr5:15293325-15295838 REVERSE LENGTH=665 |

201606

Coefficients for Vitvi16g02098.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.446831	7.658968e-15	***	1.295793e-14	***
SlopeC	2.32385	0.000156973	***	0.07644173	.
MeanF-MeanC	1.97166	1.502738e-07	***	5.828175e-06	***
SlopeF-SlopeC	-2.527587	0.003019792	**	0.9999488	



8.4.7 Vitvi00g02226: * Type3.C

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

Vitvi00g02226

35.2

not assigned.unknown

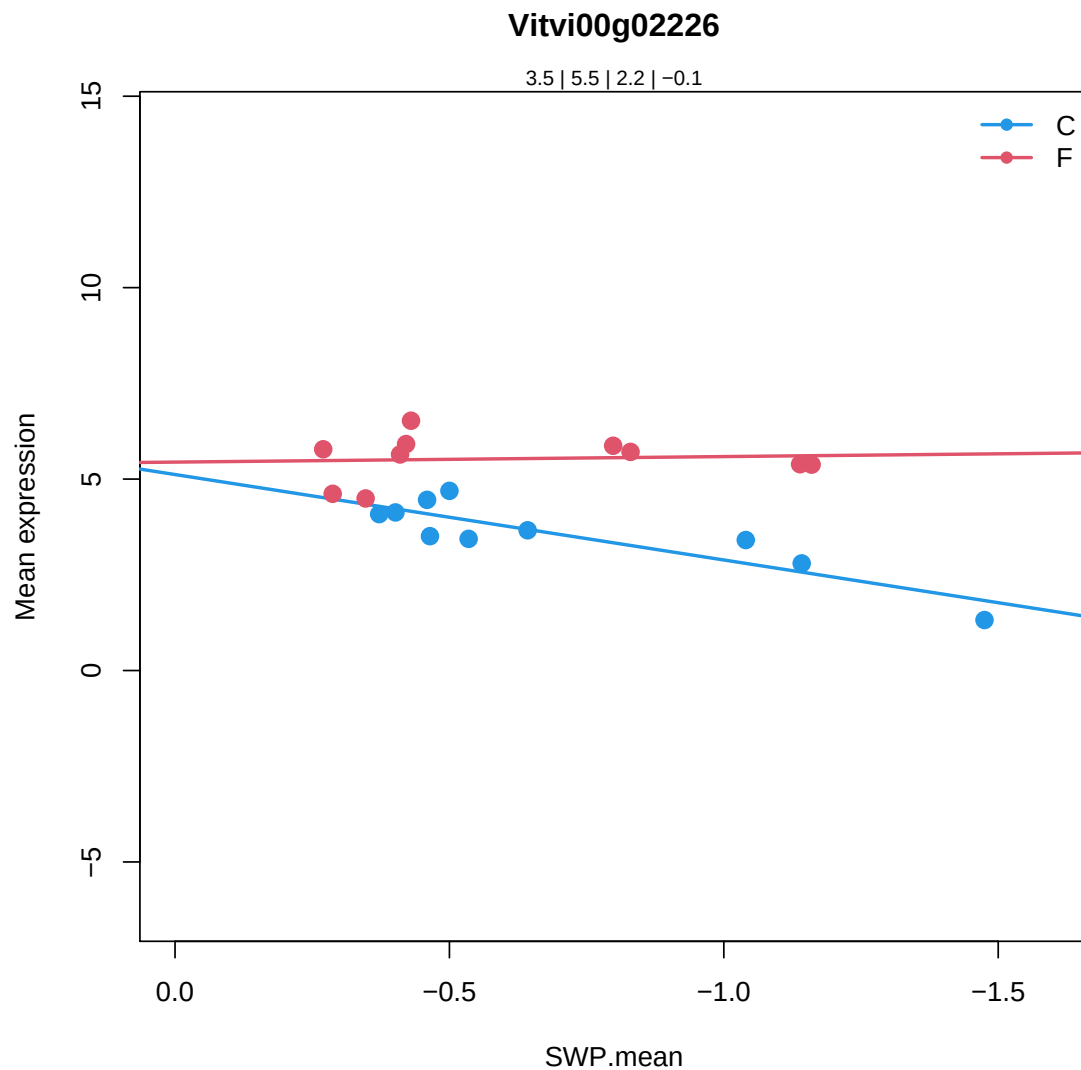
PR5-like receptor kinase |

Chr5:15293325-15295838 REVERSE LENGTH=665 |

201606

Coefficients for Vitvi00g02226.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.549584	1.613386e-15	***	2.94647e-15	***
SlopeC	2.231859	0.0001456927	***	0.07644173	.
MeanF-MeanC	1.981757	6.472083e-08	***	2.794547e-06	***
SlopeF-SlopeC	-2.375927	0.003388446	**	0.9999488	



8.4.8 Vitvi09g01948: * Type3.C

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

Vitvi09g01948

35.2

not assigned.unknown

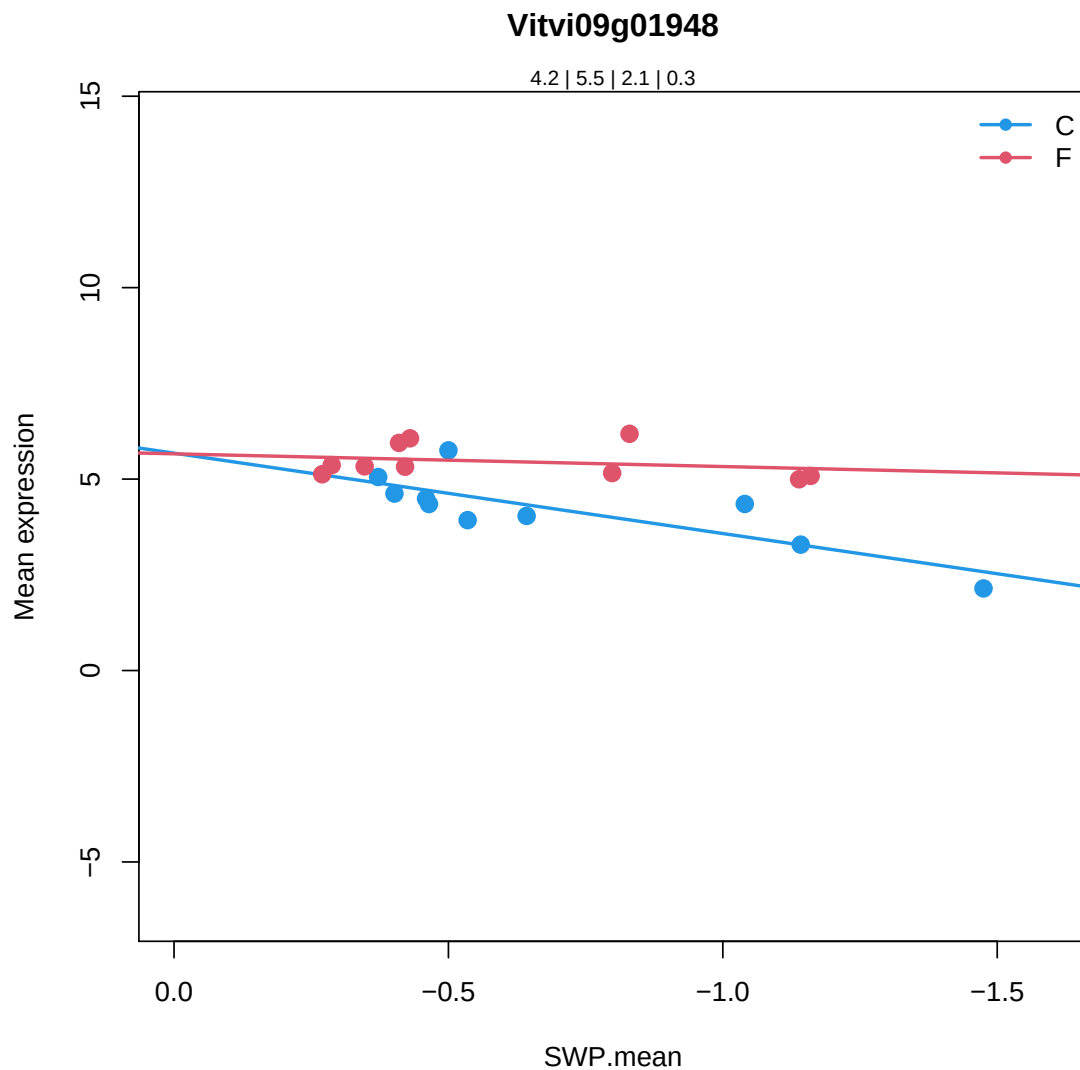
disease resistance family protein / LRR family protein |

Chr2:14737169-14739886 REVERSE LENGTH=905 |

201606

Coefficients for Vitvi09g01948.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.200998	1.598364e-17	***	4.037499e-17	***
SlopeC	2.099137	0.0001557553	***	0.07644173	.
MeanF-MeanC	1.256068	2.246776e-05	***	0.0005036082	***
SlopeF-SlopeC	-1.766936	0.01695143	*	0.9999488	



8.4.9 Vitvi09g01335: * Type3.C

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

Vitvi09g01335

35.2

not assigned.unknown

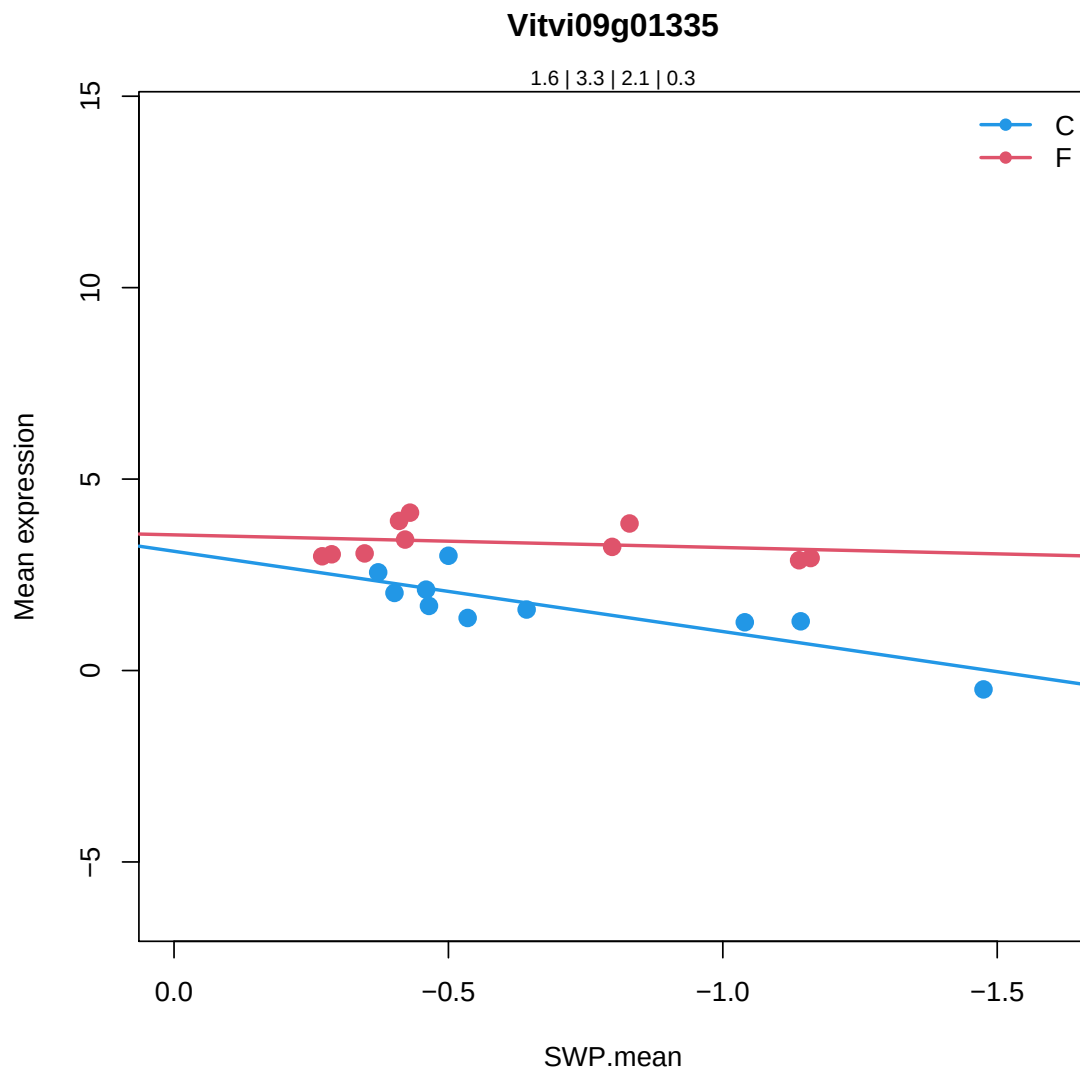
disease resistance family protein / LRR family protein |

Chr2:14737169-14739886 REVERSE LENGTH=905 |

201606

Coefficients for Vitvi09g01335.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.640402	8.137972e-10	***	1.029284e-09	***
SlopeC	2.095882	9.96398e-05	***	0.07644173	.
MeanF-MeanC	1.701105	1.598465e-07	***	6.152474e-06	***
SlopeF-SlopeC	-1.765299	0.01338604	*	0.9999488	



8.4.10 Vitvi16g01549: * Type3.C

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

Vitvi16g01549

35.2

not assigned.unknown

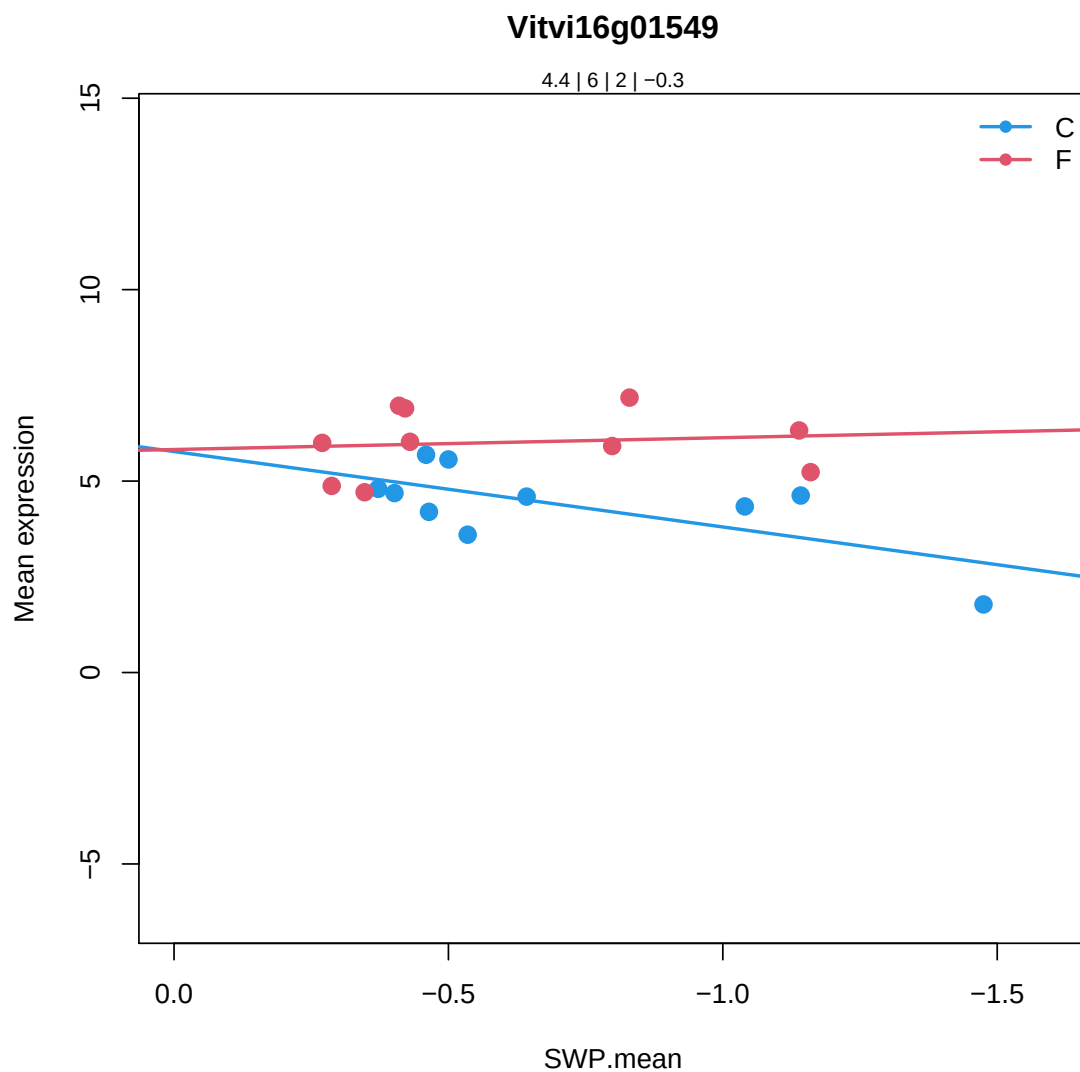
receptor like protein 34 |

Chr3:3450988-3453672 REVERSE LENGTH=894 |

201606

Coefficients for Vitvi16g01549.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.386477	4.739072e-14	***	7.467481e-14	***
SlopeC	1.969869	0.01098639	*	0.3141738	
MeanF-MeanC	1.62591	0.0001789125	***	0.002941731	**
SlopeF-SlopeC	-2.278492	0.0419335	*	0.9999488	



8.4.11 Vitvi16g01995: * Type3.C

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

Vitvi16g01995

35.2

not assigned.unknown

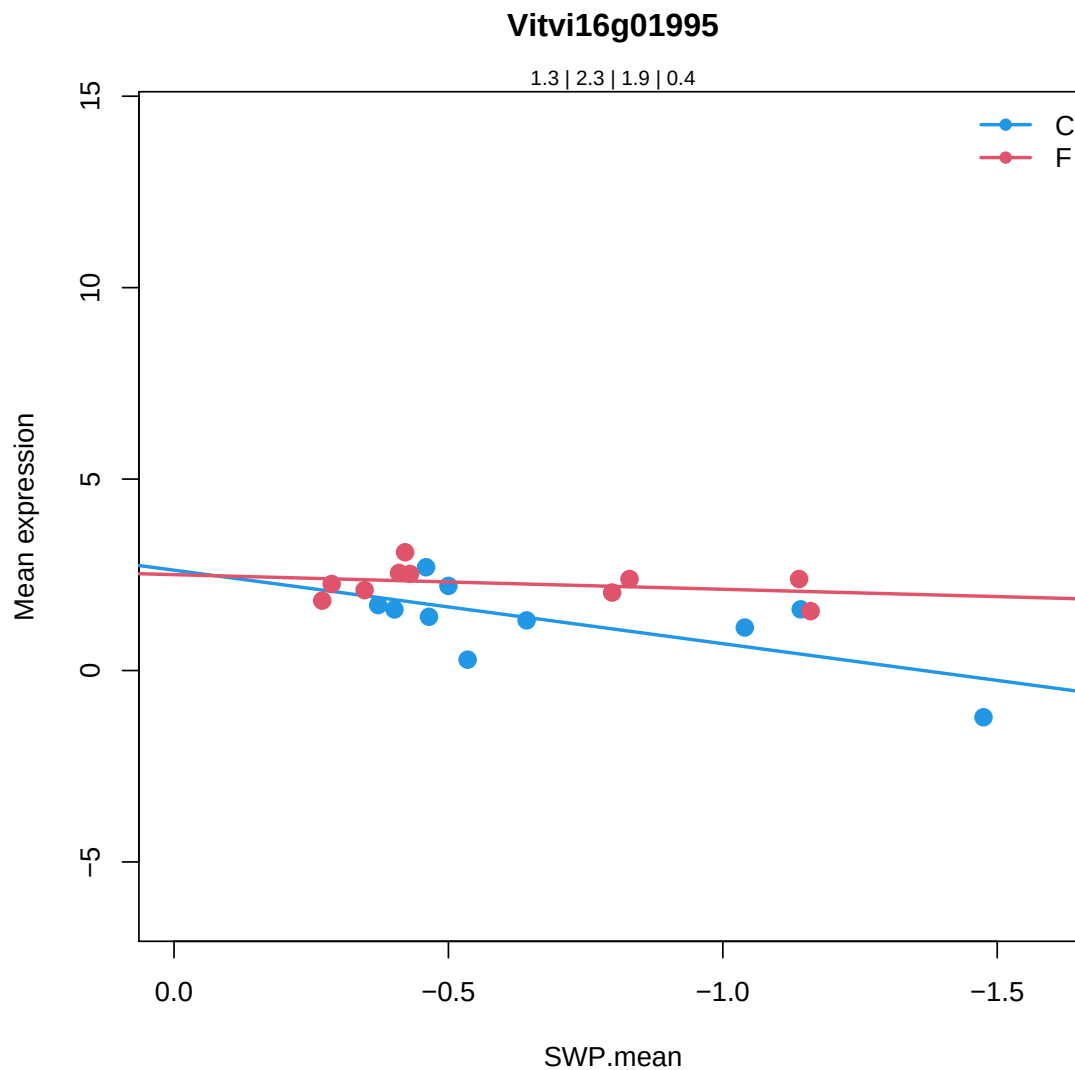
PR5-like receptor kinase |

Chr5:15293325-15295838 REVERSE LENGTH=665 |

201606

Coefficients for Vitvi16g01995.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.270518	2.436594e-06	***	2.787971e-06	***
SlopeC	1.918908	0.002355775	**	0.1841371	
MeanF-MeanC	1.000552	0.001907489	**	0.02124687	*
SlopeF-SlopeC	-1.536769	0.07734706	.	0.9999488	



8.4.12 Vitvi14g03032: * Type3.C

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

Vitvi14g03032

35.2

not assigned.unknown

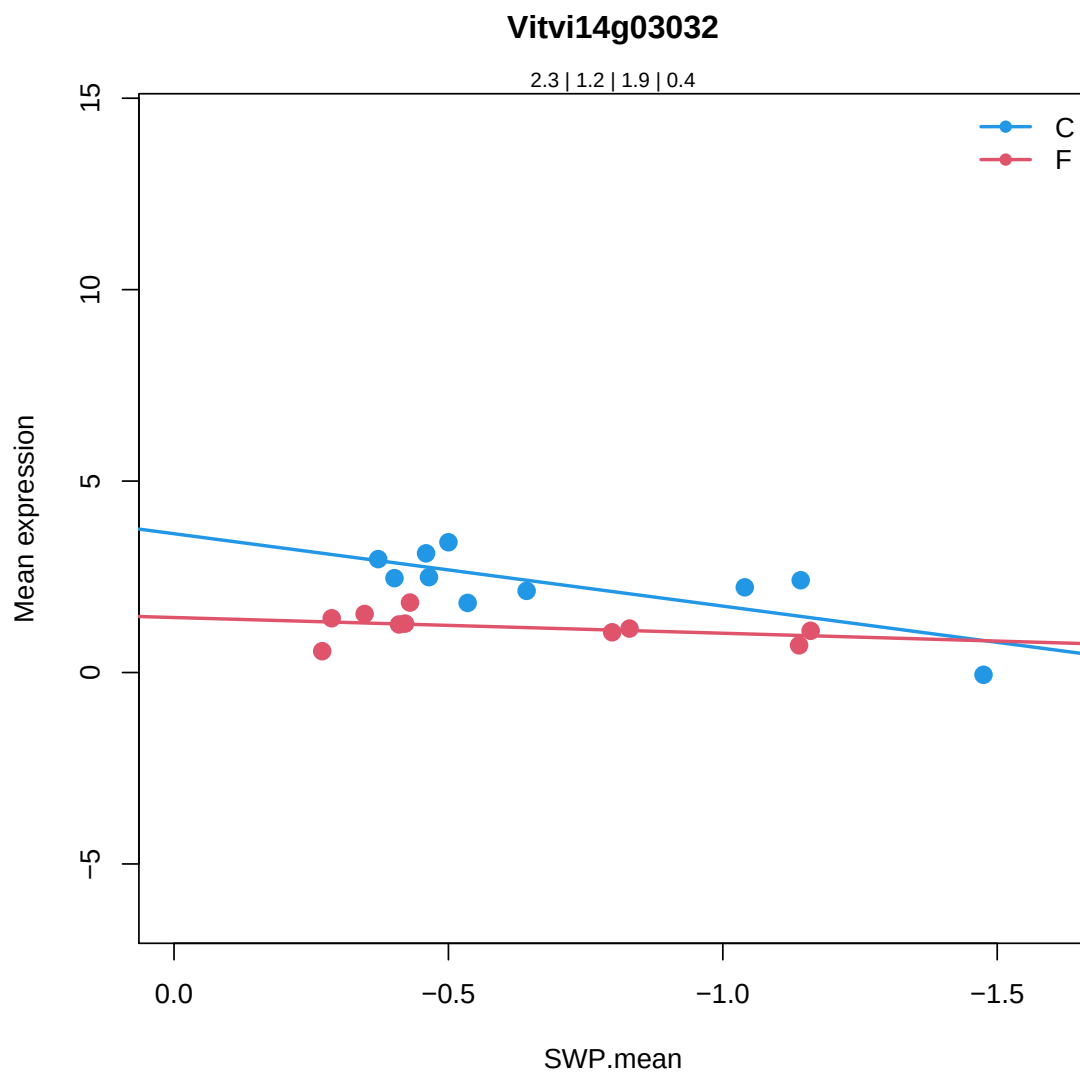
senescence-associated gene 101 |

Chr5:4828754-4830769 FORWARD LENGTH=537 |

201606

Coefficients for Vitvi14g03032.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.295758	4.137197e-12	***	5.741001e-12	***
SlopeC	1.890992	0.0005292593	***	0.1005065	
MeanF-MeanC	-1.109618	0.00011621	***	0.002052459	**
SlopeF-SlopeC	-1.481025	0.04379561	*	0.9999488	



8.4.13 Vitvi05g01285: * Type3.C

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

Vitvi05g01285

35.2

not assigned.unknown

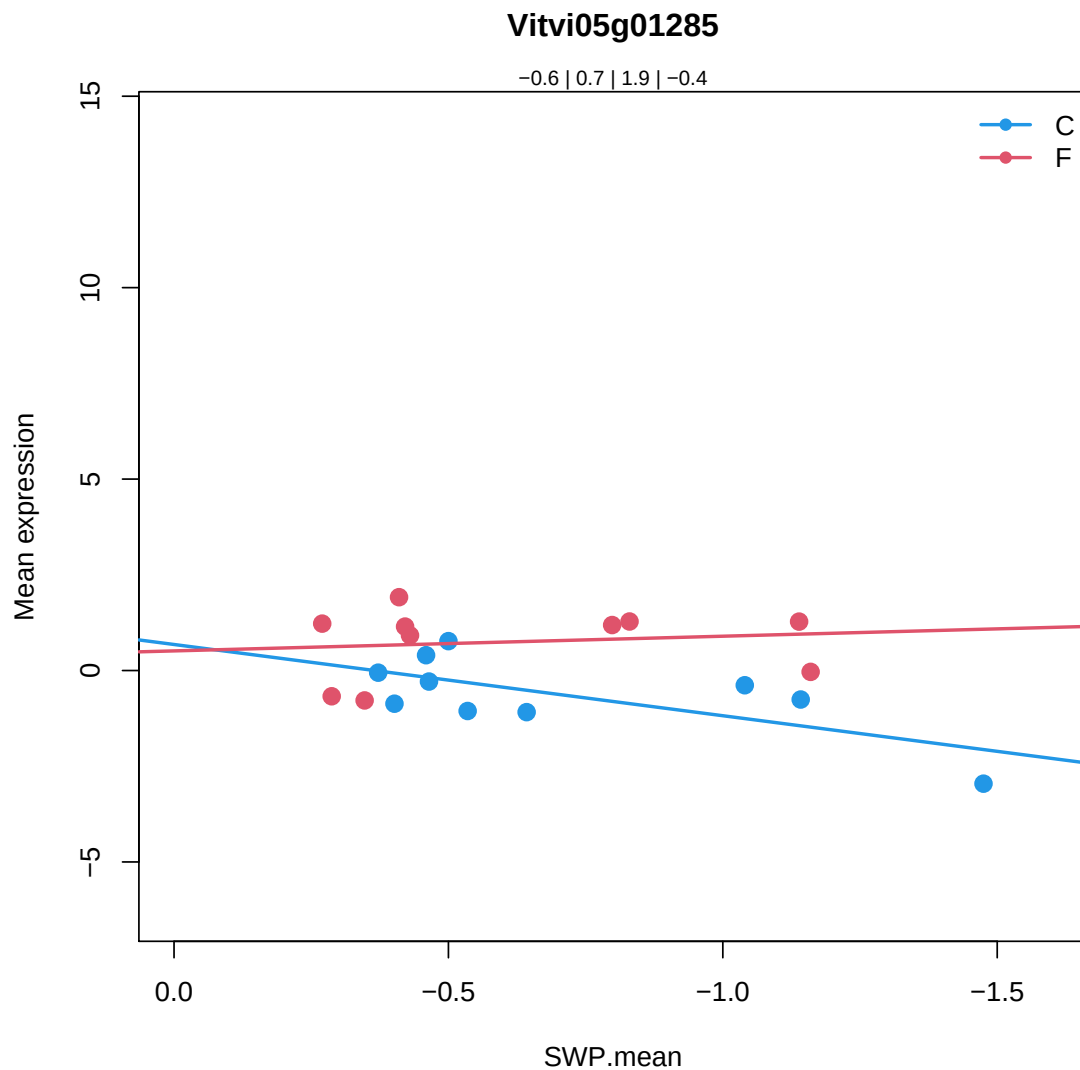
indole-3-acetate beta-D-glucosyltransferase |

Chr4:8877877-8879301 REVERSE LENGTH=474 |

201606

Coefficients for Vitvi05g01285.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.6285472	0.02067477	*	0.02173275	*
SlopeC	1.860691	0.01455316	*	0.3359386	
MeanF-MeanC	1.374557	0.0008738596	***	0.01117397	*
SlopeF-SlopeC	-2.244205	0.04275548	*	0.9999488	



8.4.14 Vitvi14g03057: * Type3.C

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

Vitvi14g03057

35.2

not assigned.unknown

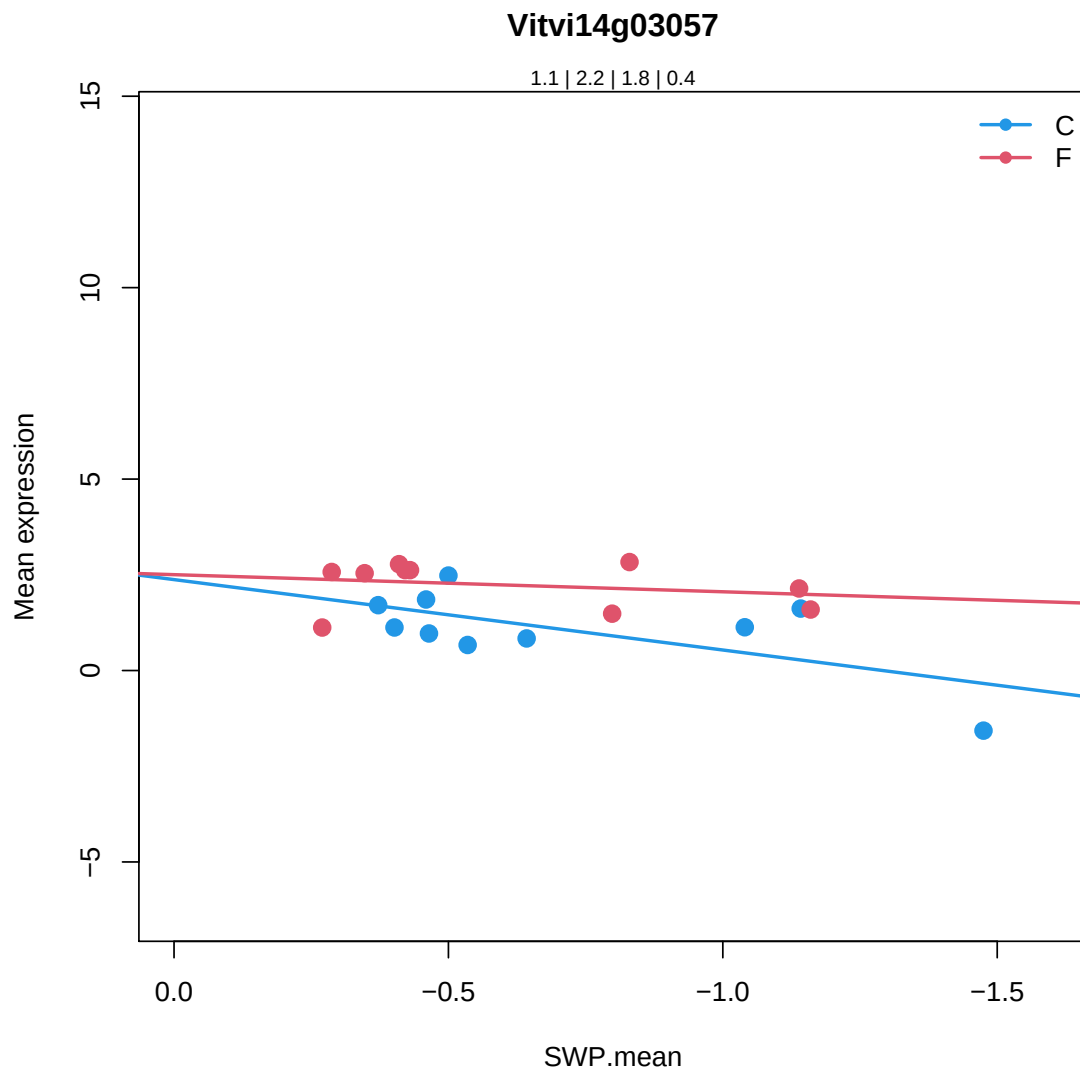
Leucine-rich repeat receptor-like protein kinase family protein |

Chr4:5637467-5640496 REVERSE LENGTH=1009 |

201606

Coefficients for Vitvi14g03057.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.081444	7.919614e-05	***	8.76176e-05	***
SlopeC	1.839061	0.007193766	**	0.2775469	
MeanF-MeanC	1.149688	0.001446577	**	0.01693451	*
SlopeF-SlopeC	-1.391957	0.1455251		0.9999488	



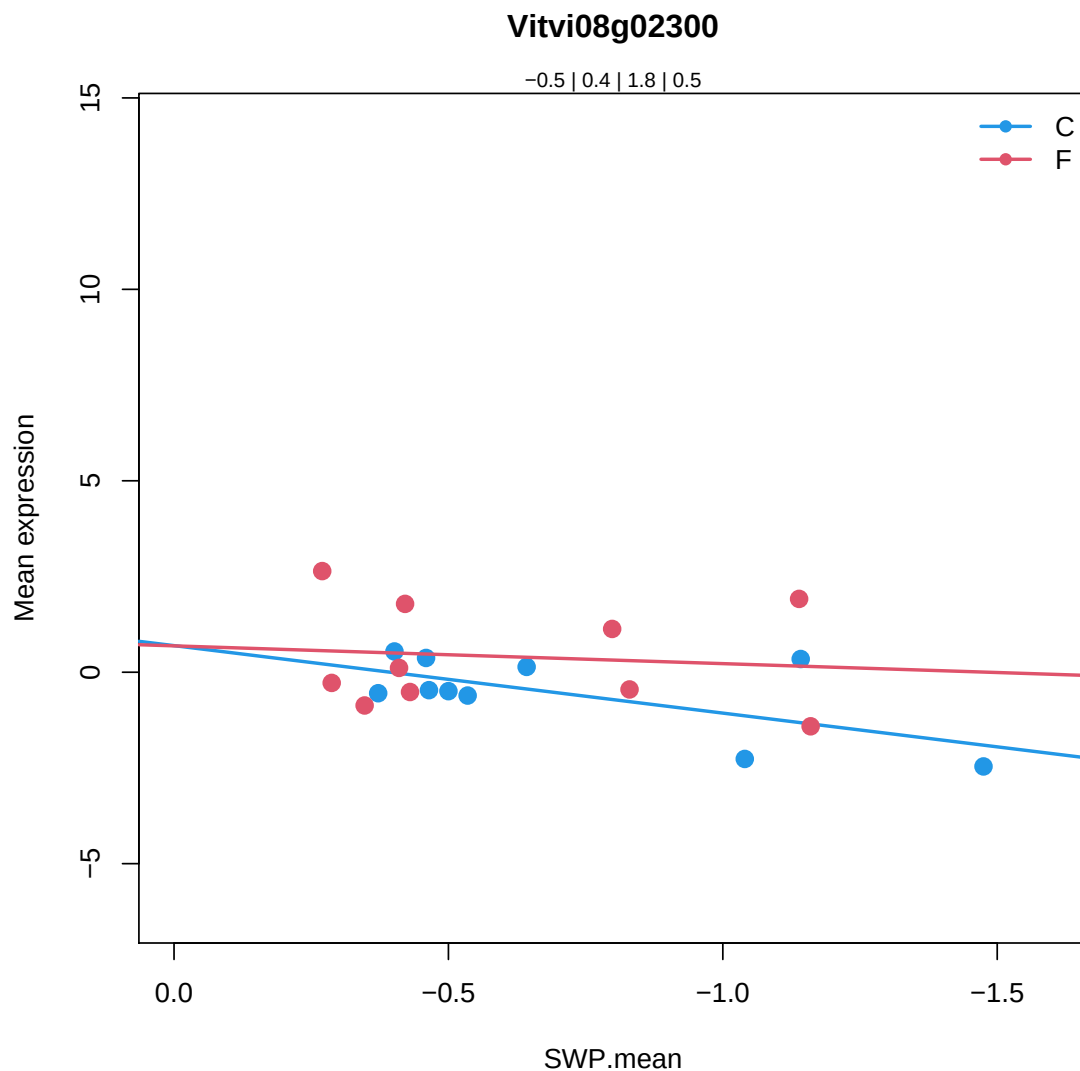
8.4.15 Vitvi08g02300: Type3.C

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

```
Vitvi08g02300
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi08g02300.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.5448287	0.1162978		0.1200712	
SlopeC	1.762531	0.07054354	.	0.5607758	
MeanF-MeanC	0.9504926	0.05616735	.	0.25794	
SlopeF-SlopeC	-1.298304	0.3567596		0.9999488	



8.4.16 Vitvi18g00973: * Type3.C

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

Vitvi18g00973

27.3.25

RNA.regulation of transcription.MYB domain transcription factor family

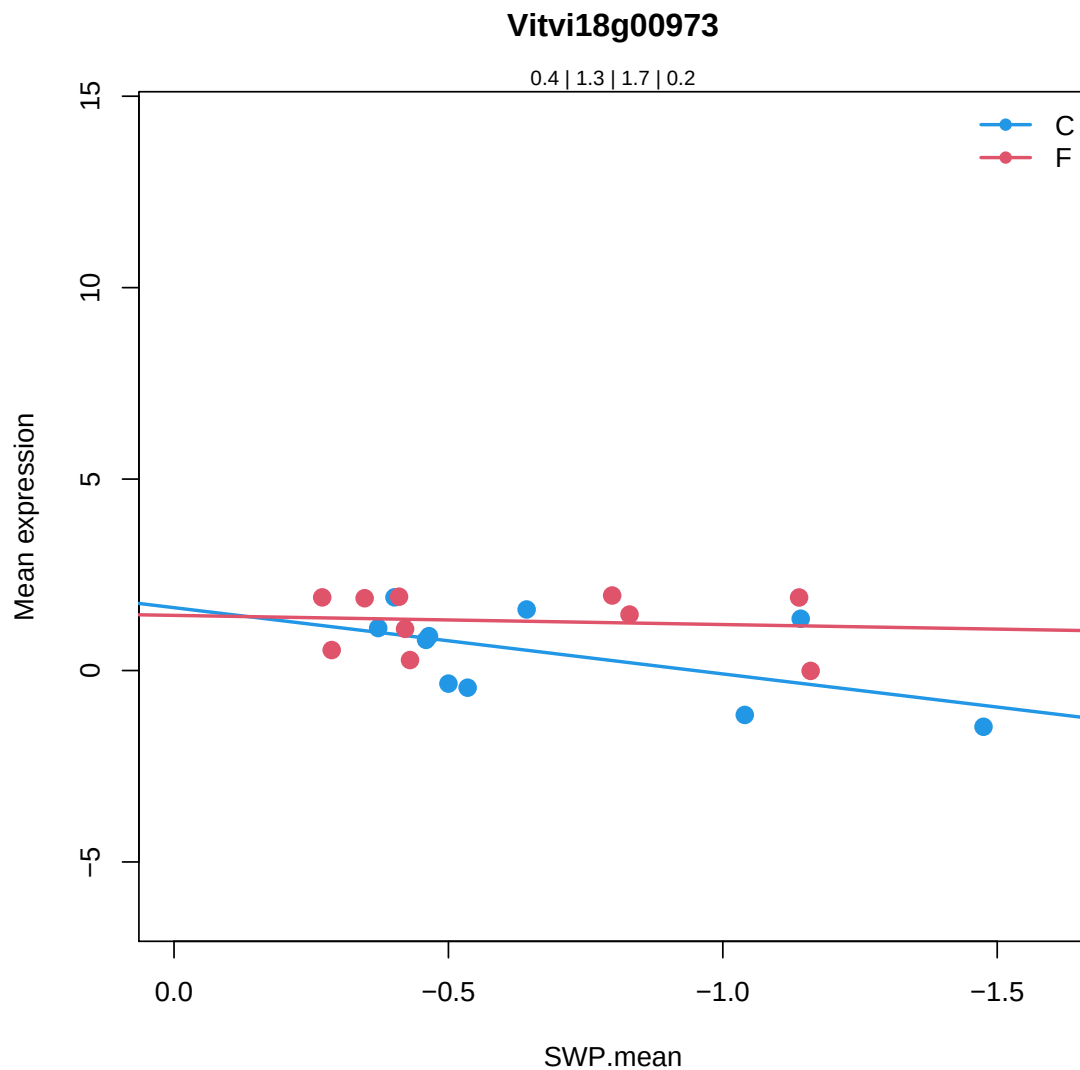
RAD-like 1 |

Chr4:18271457-18271857 REVERSE LENGTH=100 |

201606

Coefficients for Vitvi18g00973.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4243761	0.1283994		0.1324309	
SlopeC	1.730751	0.03038041	*	0.4320841	
MeanF-MeanC	0.8696495	0.03213576	*	0.1776605	
SlopeF-SlopeC	-1.491567	0.1935135		0.9999488	



8.4.17 Vitvi16g01960: * Type3.C

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

Vitvi16g01960

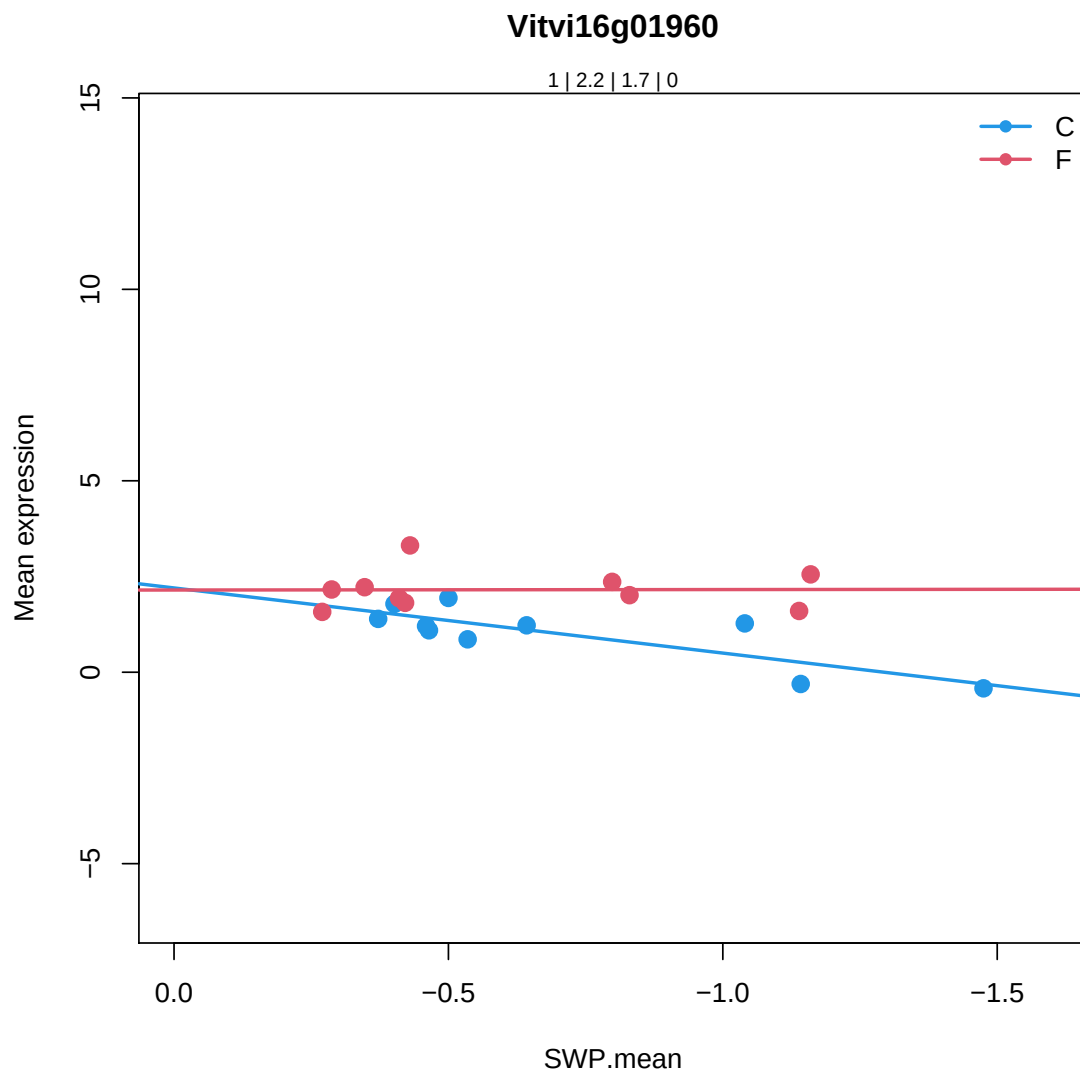
30.2.24

signalling.receptor kinases.S-locus glycoprotein like

NA

Coefficients for Vitvi16g01960.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.004778	2.984788e-06	***	3.408056e-06	***
SlopeC	1.701228	0.0009907854	***	0.1271346	
MeanF-MeanC	1.149623	4.831542e-05	***	0.0009563943	***
SlopeF-SlopeC	-1.713058	0.0173612	*	0.9999488	



8.4.18 Vitvi18g01262: * Type3.C

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

Vitvi18g01262

30.2.12

signalling.receptor kinases.leucine rich repeat XII

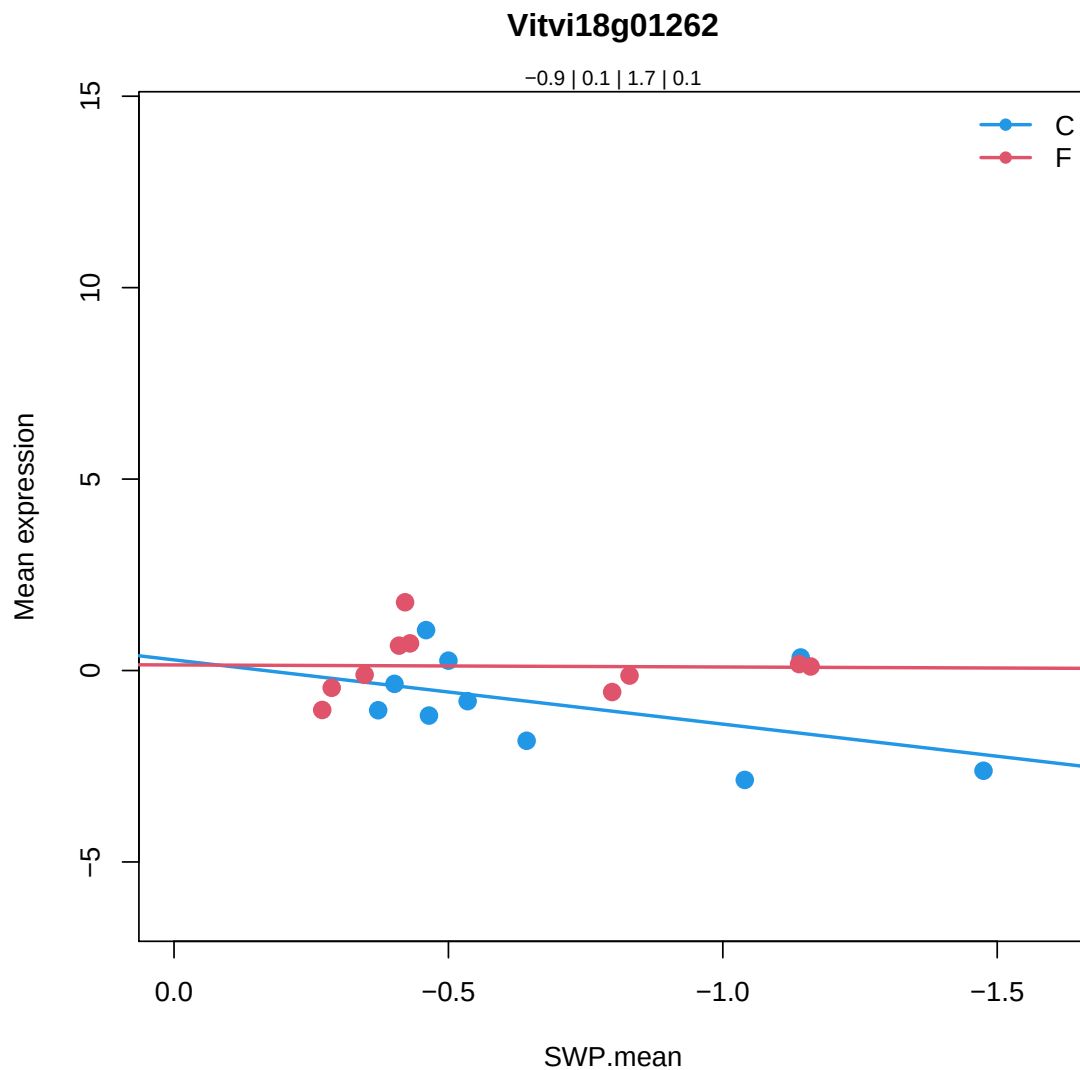
Leucine-rich repeat protein kinase family protein |

Chr3:17527611-17530748 FORWARD LENGTH=1010 |

201606

Coefficients for Vitvi18g01262.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.902123	0.005227458	**	0.005572202	**
SlopeC	1.678005	0.04986674	*	0.5091026	
MeanF-MeanC	1.014862	0.02184095	*	0.1343421	
SlopeF-SlopeC	-1.624447	0.1905261		0.9999488	



8.4.19 Vitvi11g00766: * Type3.C

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

Vitvi11g00766

30.2.12

signalling.receptor kinases.leucine rich repeat XII

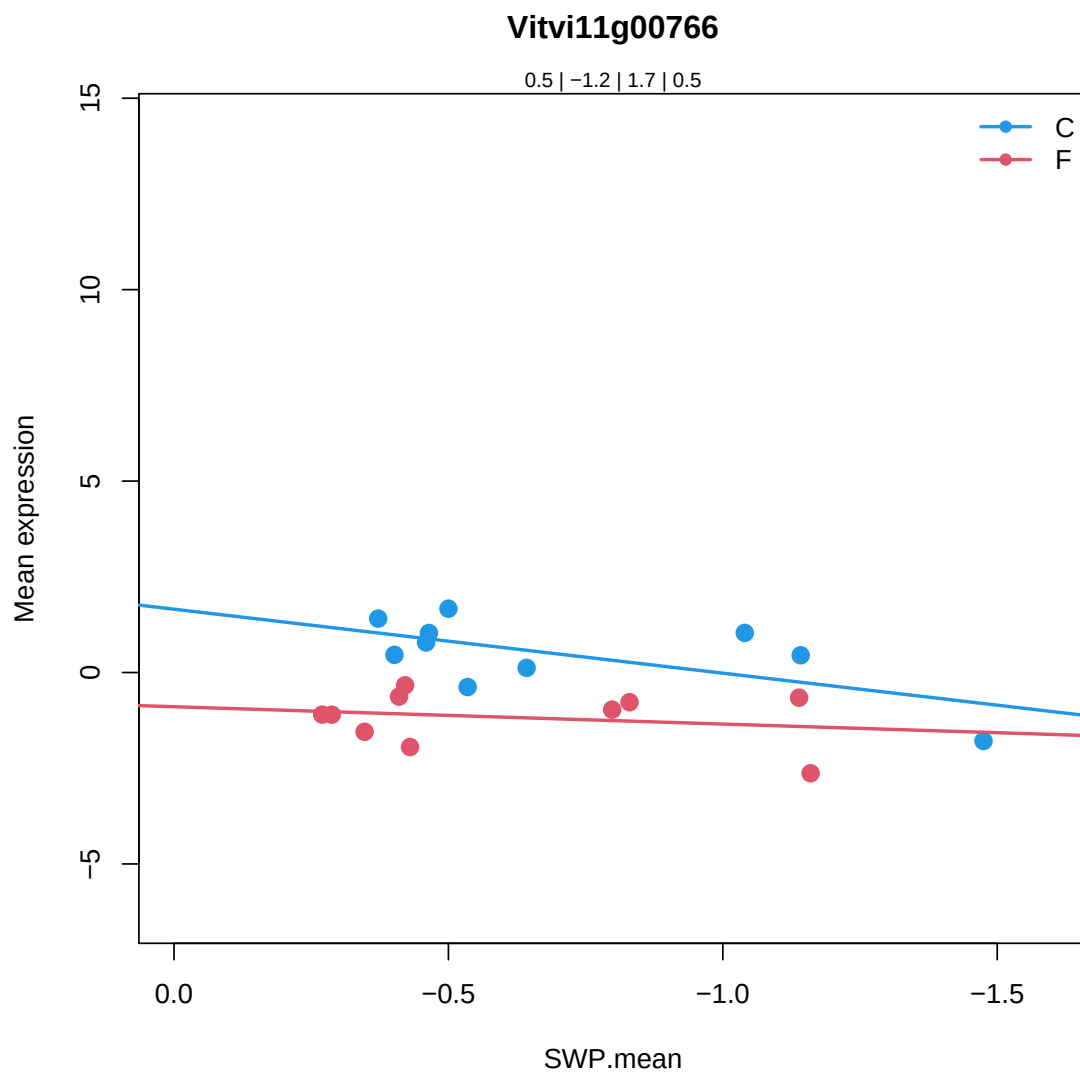
kinase family with leucine-rich repeat domain-containing protein |

Chr1:13220940-13224386 FORWARD LENGTH=1120 |

201606

Coefficients for Vitvi11g00766.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.479062	0.04456731	*	0.04647612	*
SlopeC	1.67106	0.01401099	*	0.3359386	
MeanF-MeanC	-1.648529	3.581314e-05	***	0.000745199	***
SlopeF-SlopeC	-1.219236	0.2035843		0.9999488	



8.4.20 Vitvi08g00630: * Type3.C

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

Vitvi08g00630

35.2

not assigned.unknown

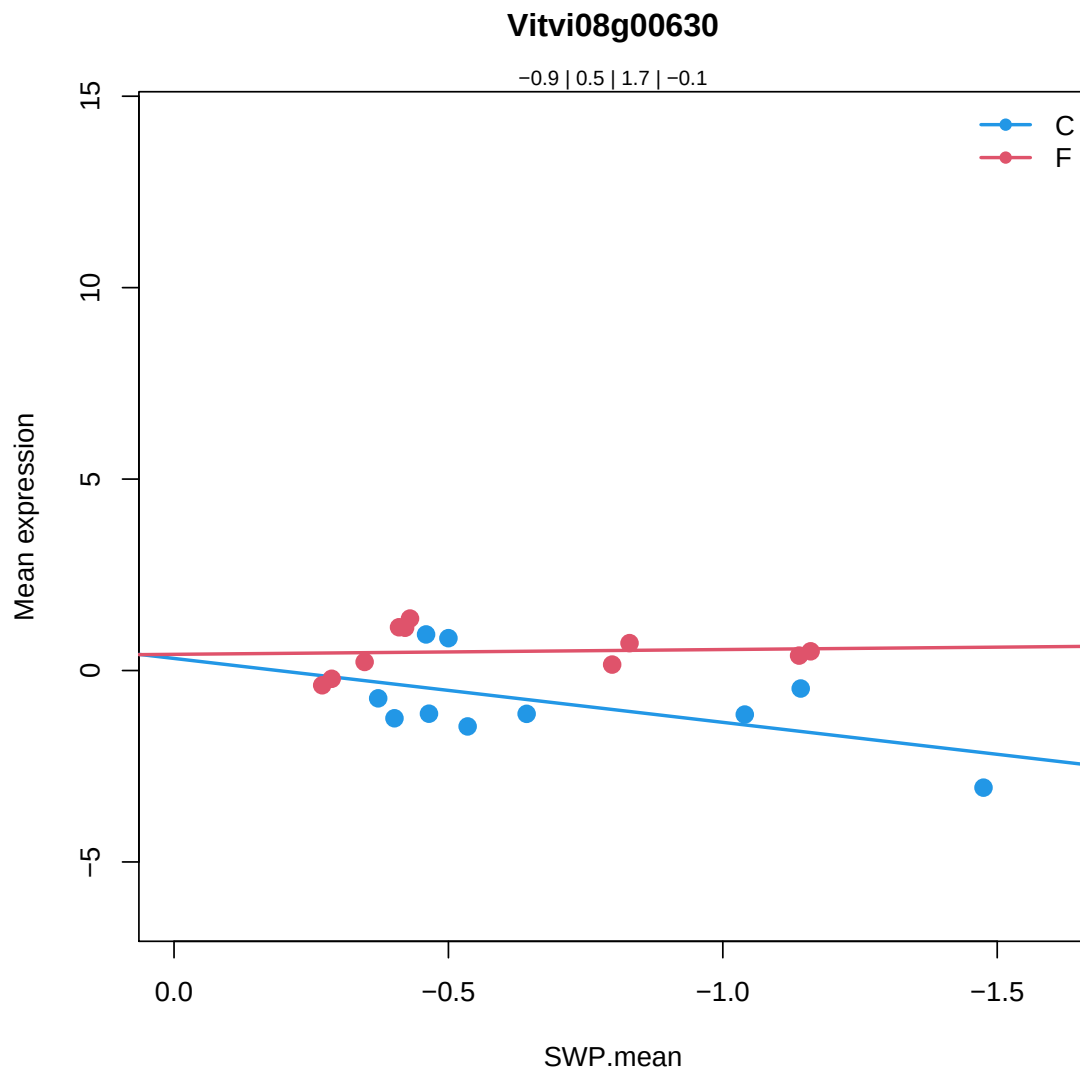
E3 ubiquitin-protein ligase PUB24-like protein |

Chr3:3736578-3738208 REVERSE LENGTH=456 |

201606

Coefficients for Vitvi08g00630.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.8585846	0.001922776	**	0.002068677	**
SlopeC	1.668838	0.0220346	*	0.3914352	
MeanF-MeanC	1.357437	0.0007080838	***	0.009384875	**
SlopeF-SlopeC	-1.793805	0.08877097	.	0.9999488	



8.4.21 Vitvi16g02010: * Type3.C

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

Vitvi16g02010

29.5.11.4.2

protein.degradation.ubiquitin.E3.RING

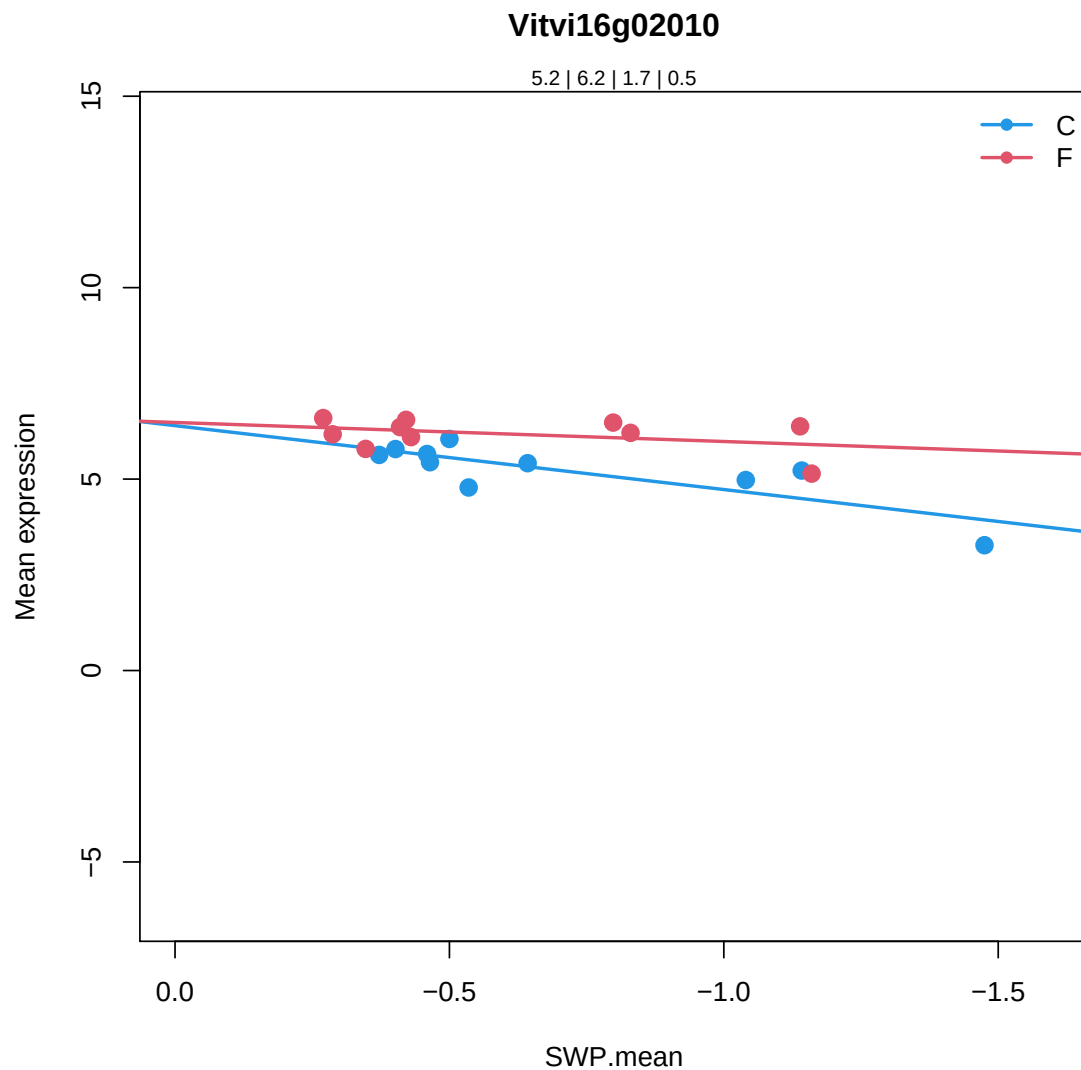
Protein kinase superfamily protein |

Chr1:24965410-24967432 REVERSE LENGTH=609 |

201606

Coefficients for Vitvi16g02010.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.222345	1.552625e-20	***	1.013495e-19	***
SlopeC	1.668473	0.0005237736	***	0.1005065	
MeanF-MeanC	0.9532332	0.0001547785	***	0.002583936	**
SlopeF-SlopeC	-1.171397	0.06793874	.	0.9999488	



8.4.22 Vitvi01g02251: * Type3.C

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

```
Vitvi01g02251
```

```
35.2
```

```
not assigned.unknown
```

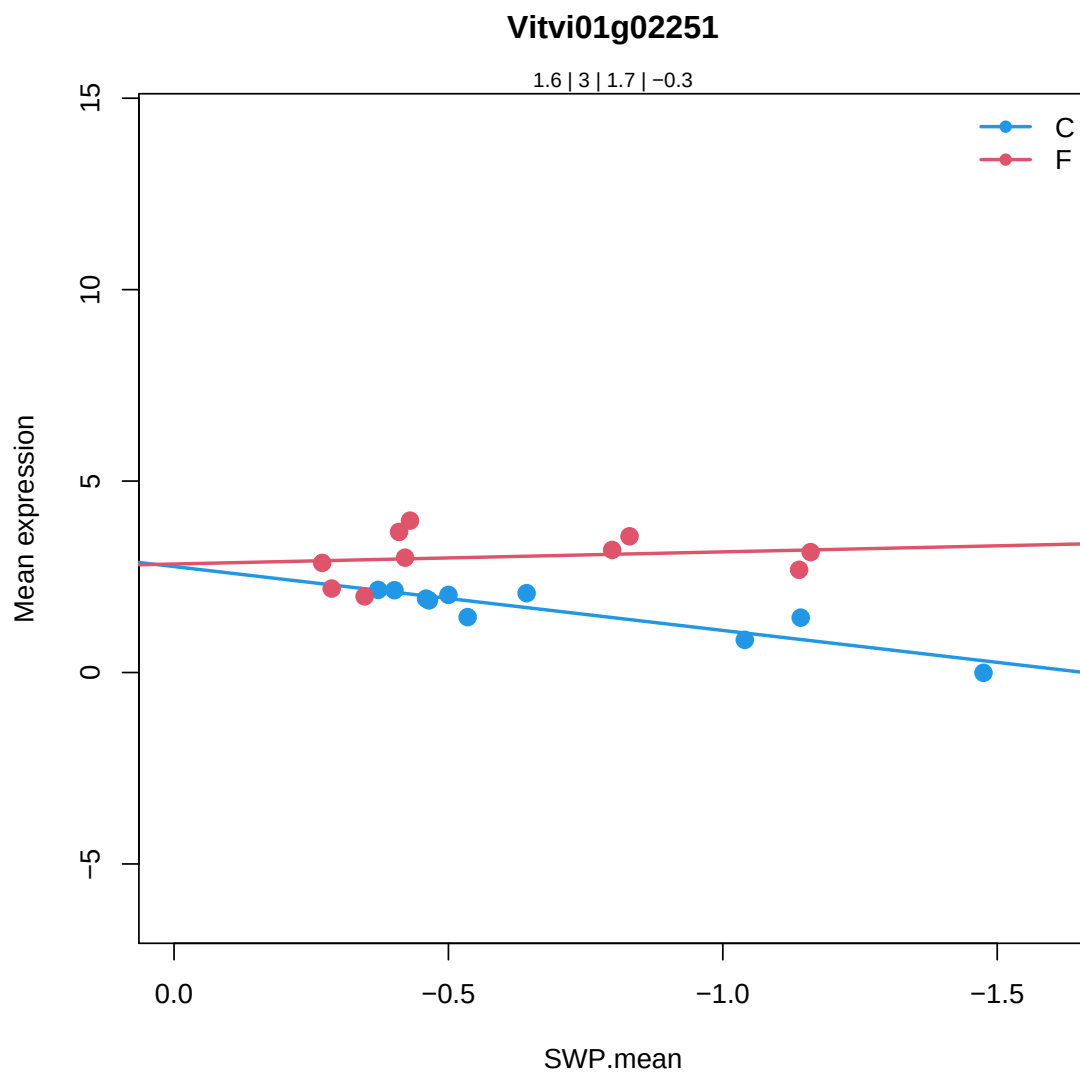
```
disease resistance family protein / LRR family protein |
```

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

```
201606
```

Coefficients for Vitvi01g02251.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.594571	1.864711e-09	***	2.33043e-09	***
SlopeC	1.66785	0.001222641	**	0.1365704	
MeanF-MeanC	1.432543	2.793651e-06	***	8.079855e-05	***
SlopeF-SlopeC	-1.98467	0.007088398	**	0.9999488	



8.4.23 Vitvi18g01321: * Type3.C

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

Vitvi18g01321

33.99

development.unspecified

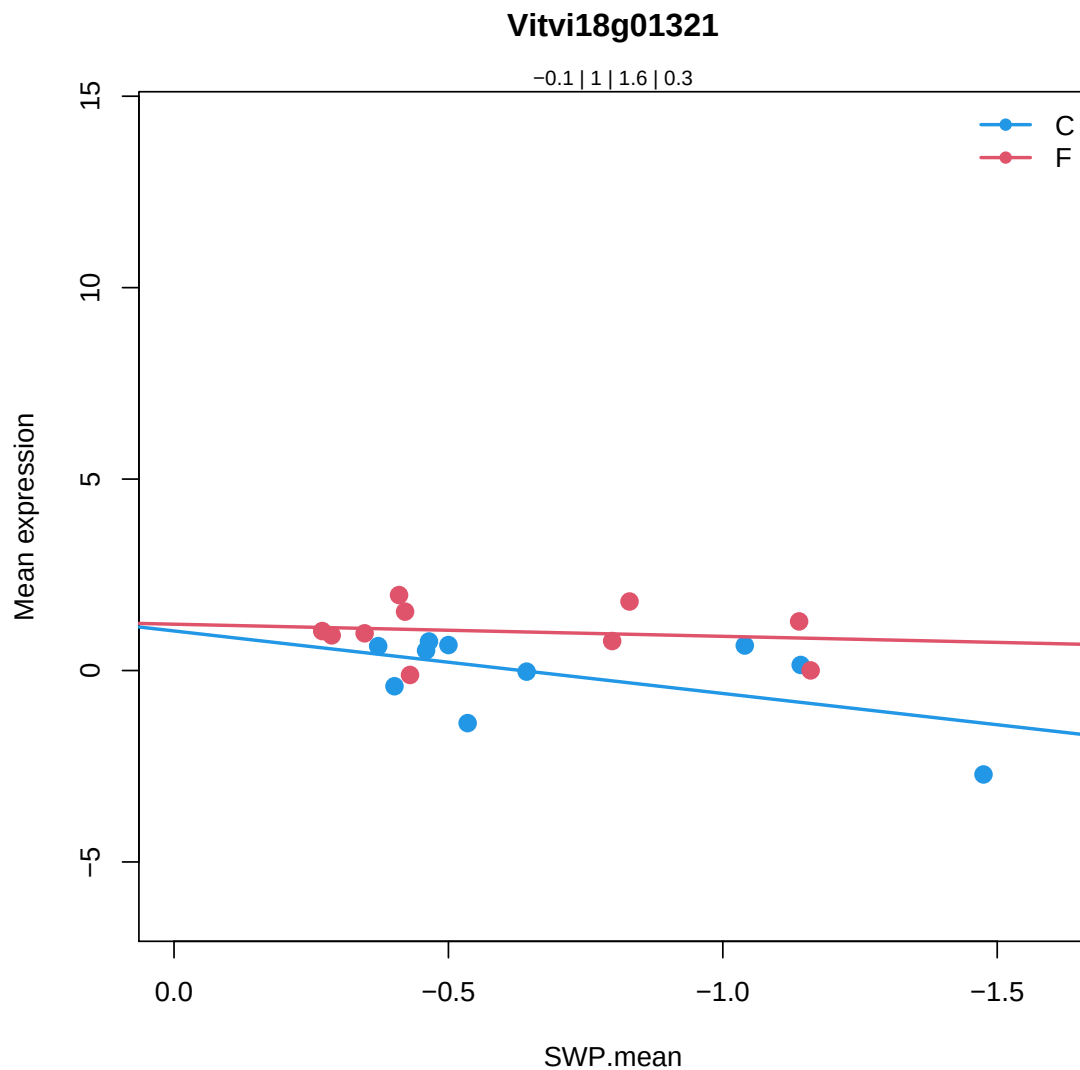
cysteine-rich RECEPTOR-like kinase |

Chr4:12129485-12133157 FORWARD LENGTH=1043 |

201606

Coefficients for Vitvi18g01321.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.1149328	0.650885		0.6558333	
SlopeC	1.632696	0.02881099	*	0.4275443	
MeanF-MeanC	1.131846	0.004265536	**	0.04015769	*
SlopeF-SlopeC	-1.315766	0.2180917		0.9999488	



8.4.24 Vitvi01g01520: * Type3.C

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

Vitvi01g01520

35.2

not assigned.unknown

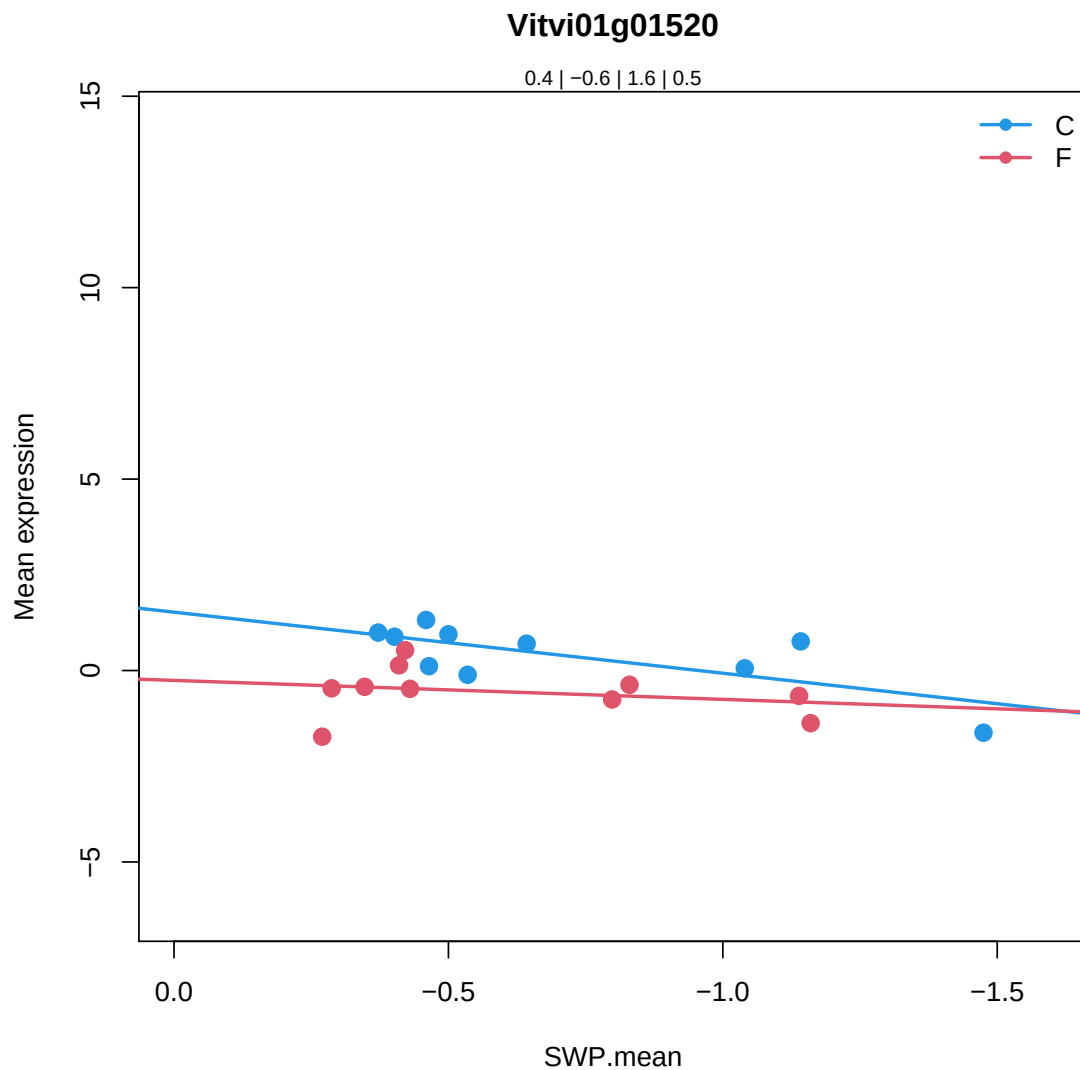
HXXXD-type acyl-transferase family protein |

Chr3:9519741-9521069 FORWARD LENGTH=442 |

201606

Coefficients for Vitvi01g01520.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4033867	0.04994232	*	0.05200662	.
SlopeC	1.5941	0.007517301	**	0.2777732	
MeanF-MeanC	-0.9633581	0.002041678	**	0.02237186	*
SlopeF-SlopeC	-1.09904	0.1857964		0.9999488	



8.4.25 Vitvi14g01615: * Type3.C

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

Vitvi14g01615

27.3.25

RNA.regulation of transcription.MYB domain transcription factor family

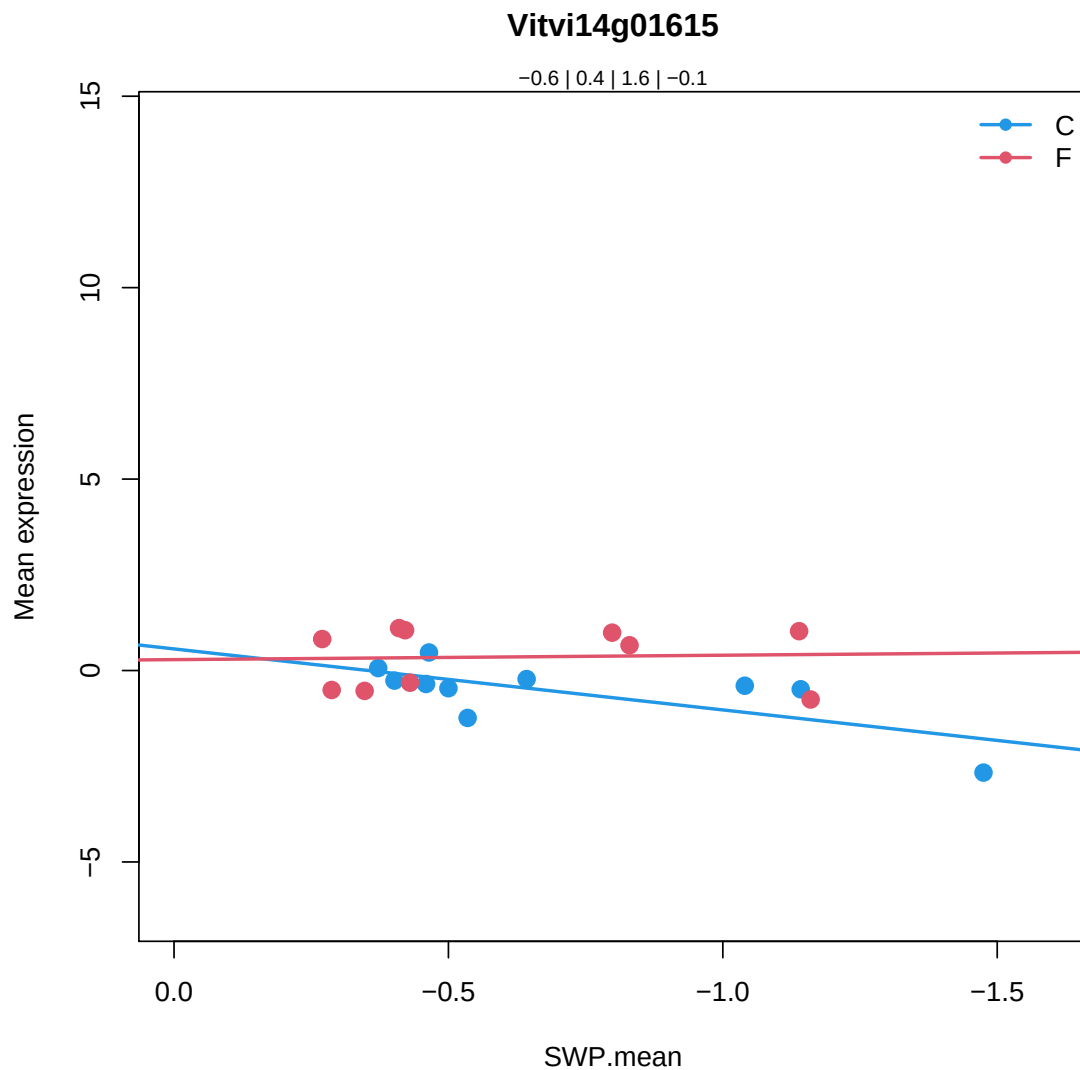
myb domain protein 63 |

Chr1:29786509-29787589 FORWARD LENGTH=327 |

201606

Coefficients for Vitvi14g01615.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.5559626	0.01792939	*	0.01887161	*
SlopeC	1.593458	0.01512027	*	0.3384188	
MeanF-MeanC	0.9101389	0.007240515	**	0.0599131	.
SlopeF-SlopeC	-1.708661	0.07060673	.	0.9999488	



8.4.26 Vitvi02g00514: * Type3.C

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

Vitvi02g00514

3.2.2

minor CHO metabolism.trehalose.TPP

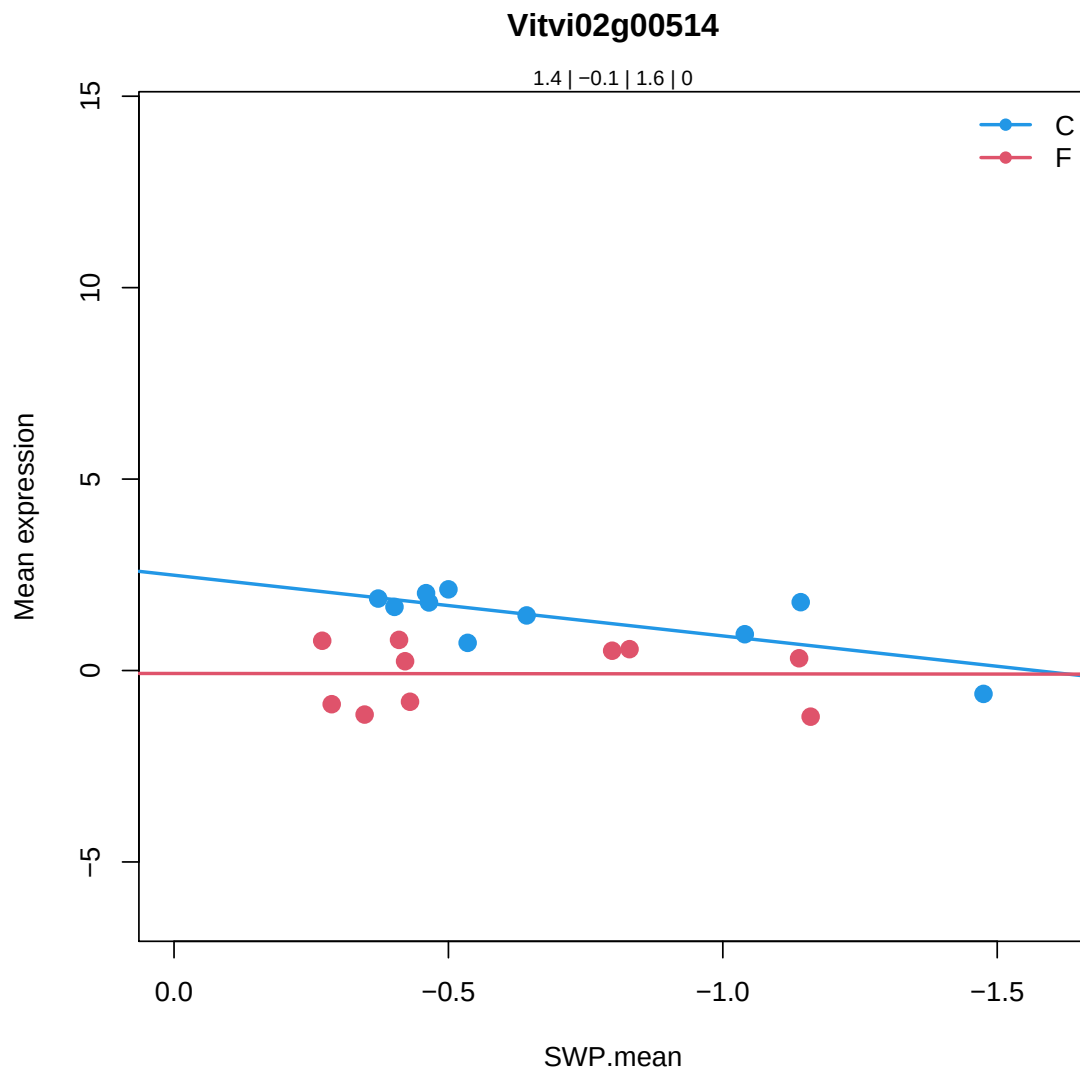
Haloacid dehalogenase-like hydrolase (HAD) superfamily protein |

Chr4:7365480-7367346 REVERSE LENGTH=368 |

201606

Coefficients for Vitvi02g00514.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.374201	3.098048e-06	***	3.536053e-06	***
SlopeC	1.585843	0.01689594	*	0.3532619	
MeanF-MeanC	-1.458001	0.0001202433	***	0.002114546	**
SlopeF-SlopeC	-1.575343	0.0981852	.	0.9999488	



8.4.27 Vitvi18g03246: * Type3.C

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

Vitvi18g03246

30.2.12

signalling.receptor kinases.leucine rich repeat XII

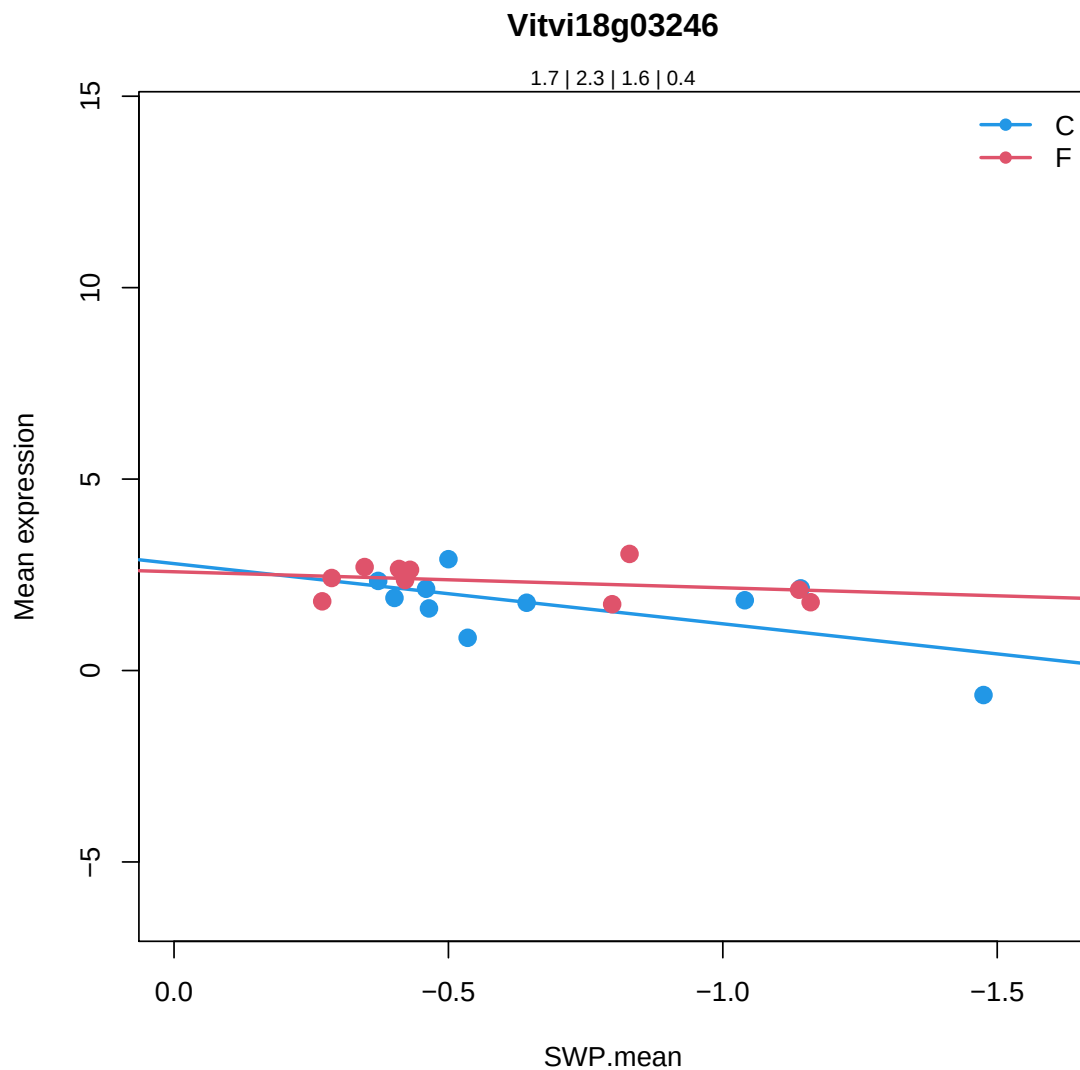
receptor like protein 6 |

Chr1:17183550-17186534 REVERSE LENGTH=994 |

201606

Coefficients for Vitvi18g03246.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.686416	2.199991e-08	***	2.657283e-08	***
SlopeC	1.572368	0.008889031	**	0.2903326	
MeanF-MeanC	0.6376899	0.03185468	*	0.176556	
SlopeF-SlopeC	-1.153825	0.1703506		0.9999488	



8.4.28 Vitvi13g00085: Type3.C

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

Vitvi13g00085

27.3.37

RNA.regulation of transcription.lateral organ boundaries gene family (

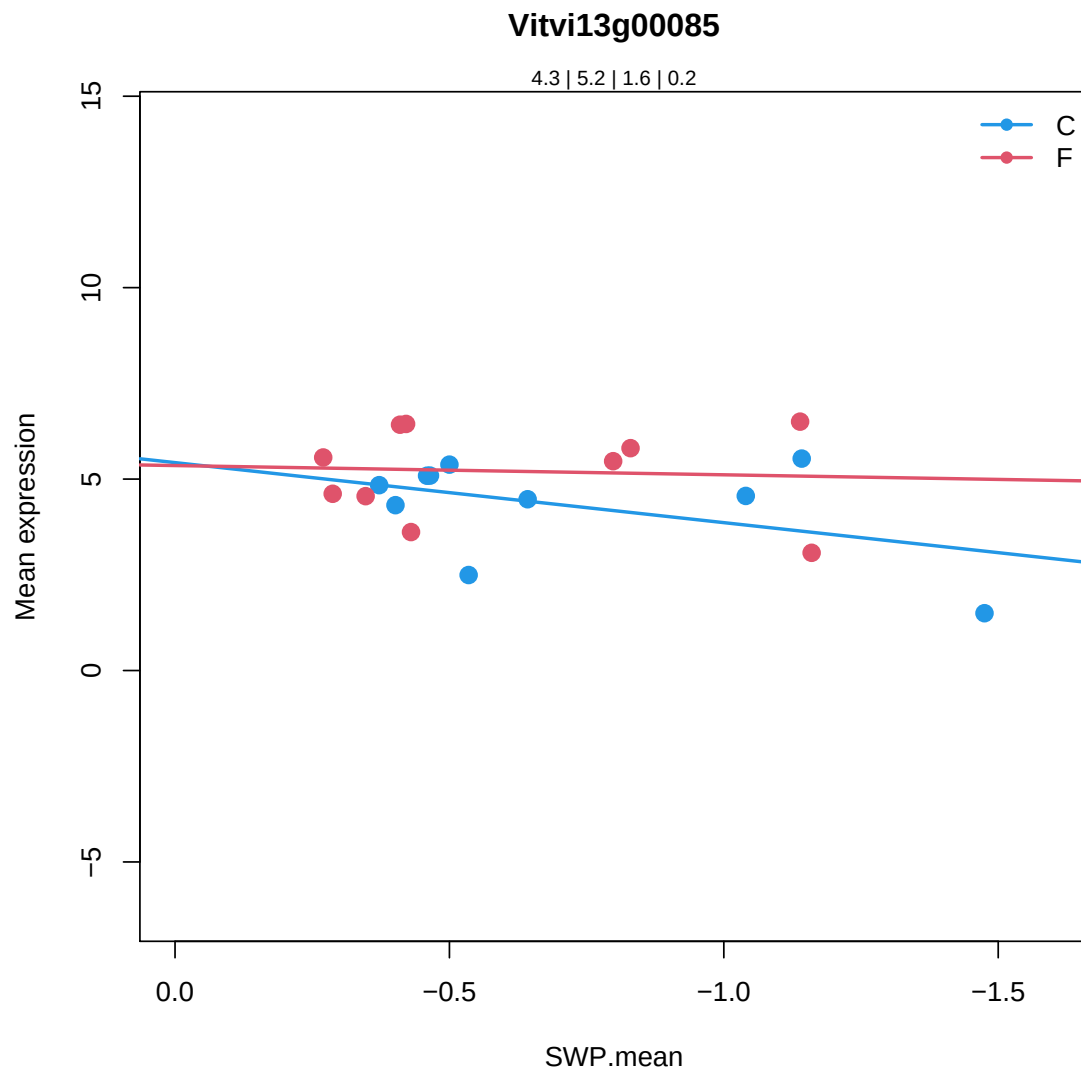
LOB domain-containing protein 21 |

Chr3:3475036-3475533 FORWARD LENGTH=165 |

201606

Coefficients for Vitvi13g00085.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.327386	3.542528e-11	***	4.720273e-11	***
SlopeC	1.567726	0.1241348		0.6455347	
MeanF-MeanC	0.8784706	0.09193566	.	0.3472821	
SlopeF-SlopeC	-1.32646	0.3730393		0.9999488	



8.4.29 Vitvi16g02015: * Type3.C

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

Vitvi16g02015

35.2

not assigned.unknown

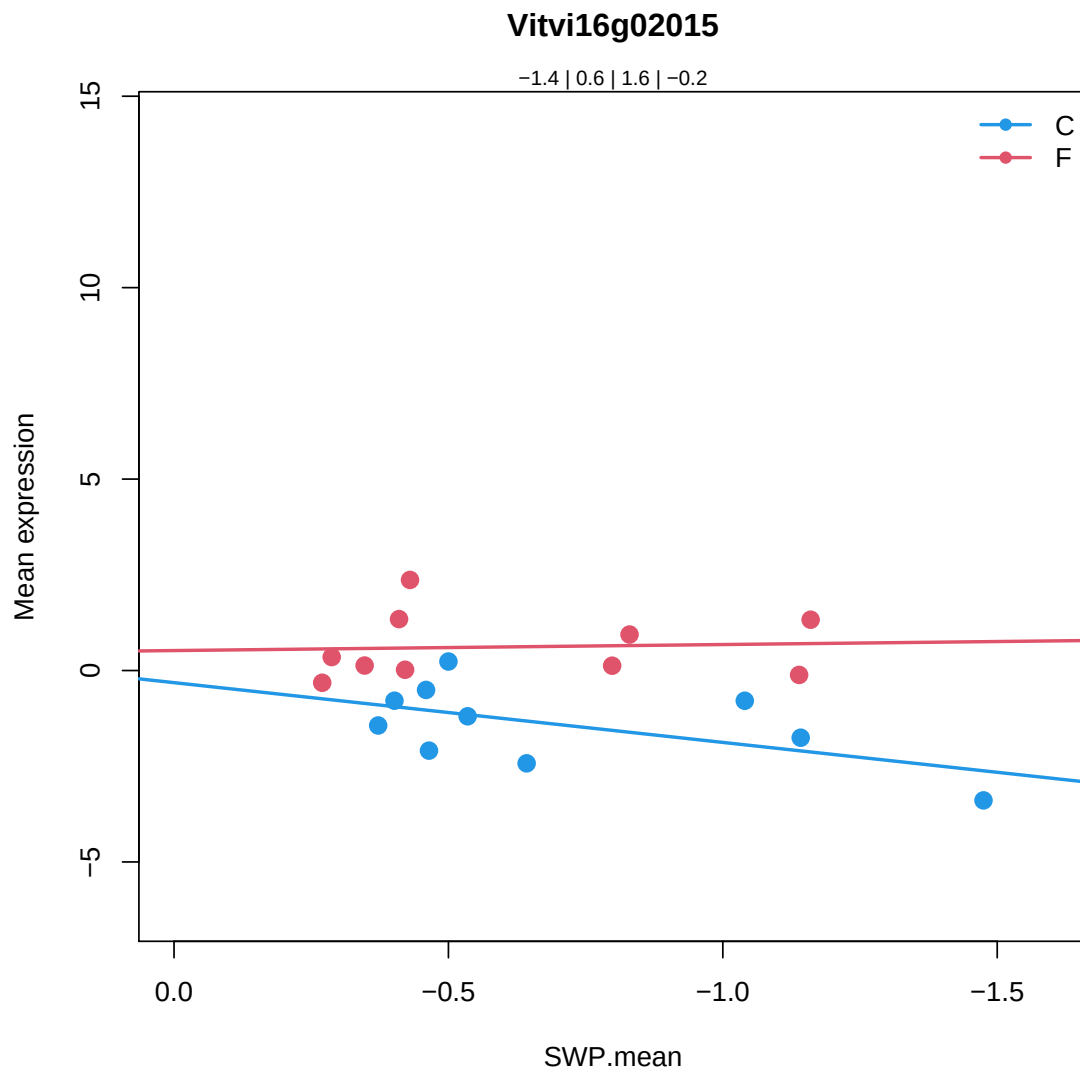
PR5-like receptor kinase |

Chr5:15293325-15295838 REVERSE LENGTH=665 |

201606

Coefficients for Vitvi16g02015.

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



8.4.30 Vitvi16g02019: * Type3.C

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

Vitvi16g02019

35.2

not assigned.unknown

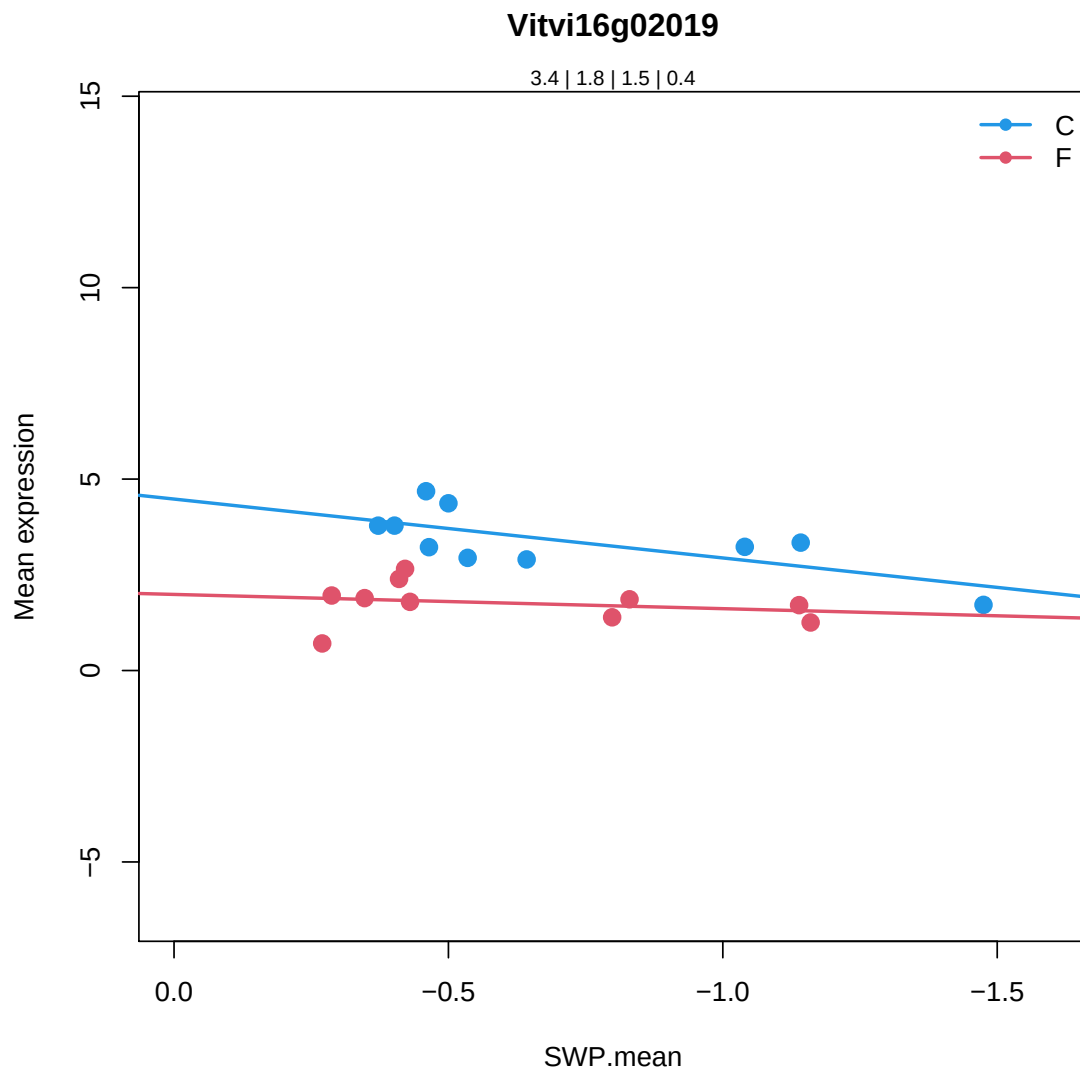
PR5-like receptor kinase |

Chr5:15293325-15295838 REVERSE LENGTH=665 |

201606

Coefficients for Vitvi16g02019.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.39667	9.859704e-15	***	1.649633e-14	***
SlopeC	1.537975	0.006208008	**	0.2647742	
MeanF-MeanC	-1.635778	2.45203e-06	***	7.201126e-05	***
SlopeF-SlopeC	-1.165723	0.1369239		0.9999488	



8.4.31 Vitvi17g00400: * Type3.C

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

Vitvi17g00400

30.2.25

signalling.receptor kinases.wall associated kinase

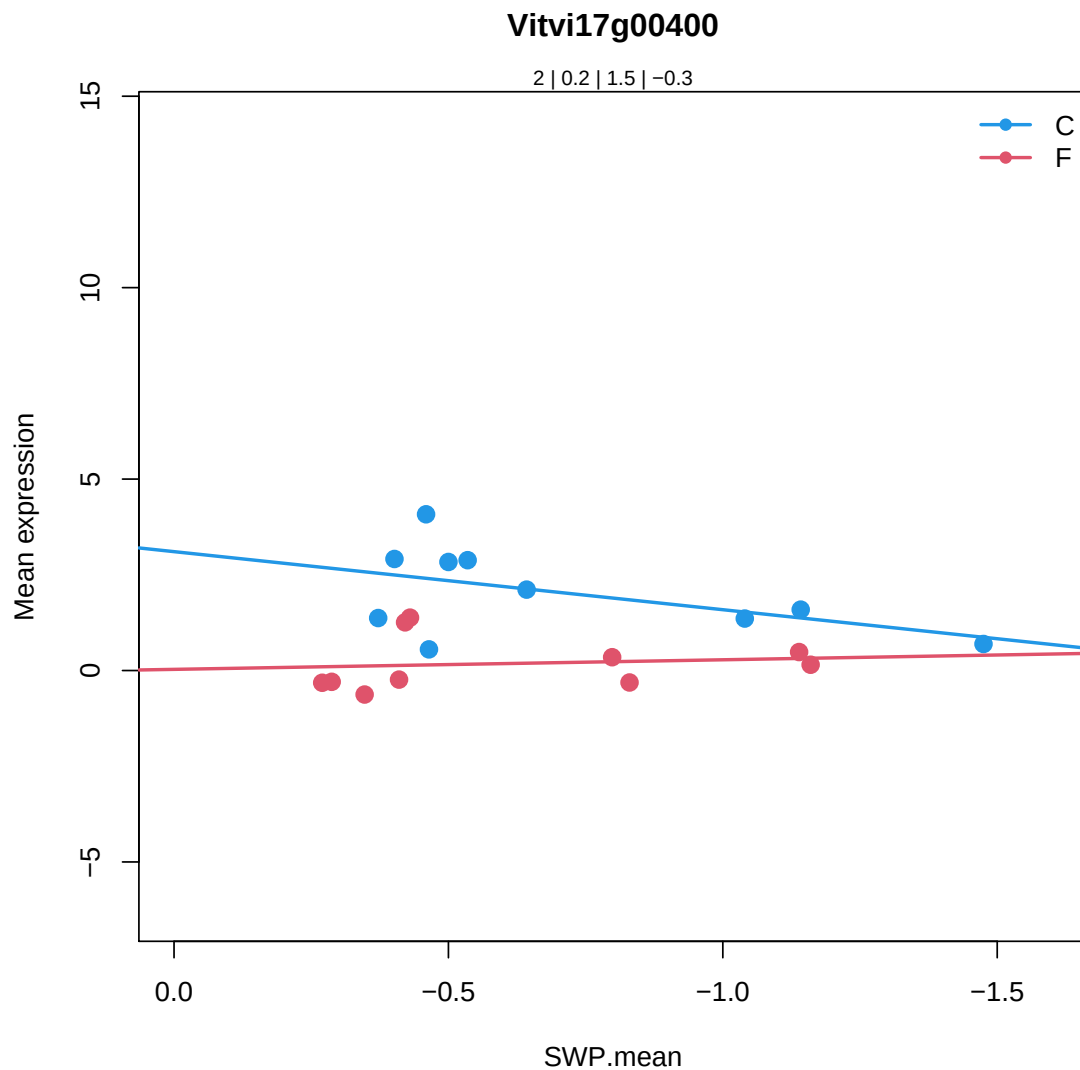
Wall-associated kinase family protein |

Chr1:26228703-26231339 REVERSE LENGTH=792 |

201606

Coefficients for Vitvi17g00400.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.038537	7.219069e-08	***	8.594317e-08	***
SlopeC	1.516381	0.04429824	*	0.4885628	
MeanF-MeanC	-1.855852	4.008841e-05	***	0.000815791	***
SlopeF-SlopeC	-1.766717	0.108939		0.9999488	



8.4.32 Vitvi13g02359: * Type3.C

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

Vitvi13g02359

27.2

RNA.transcription

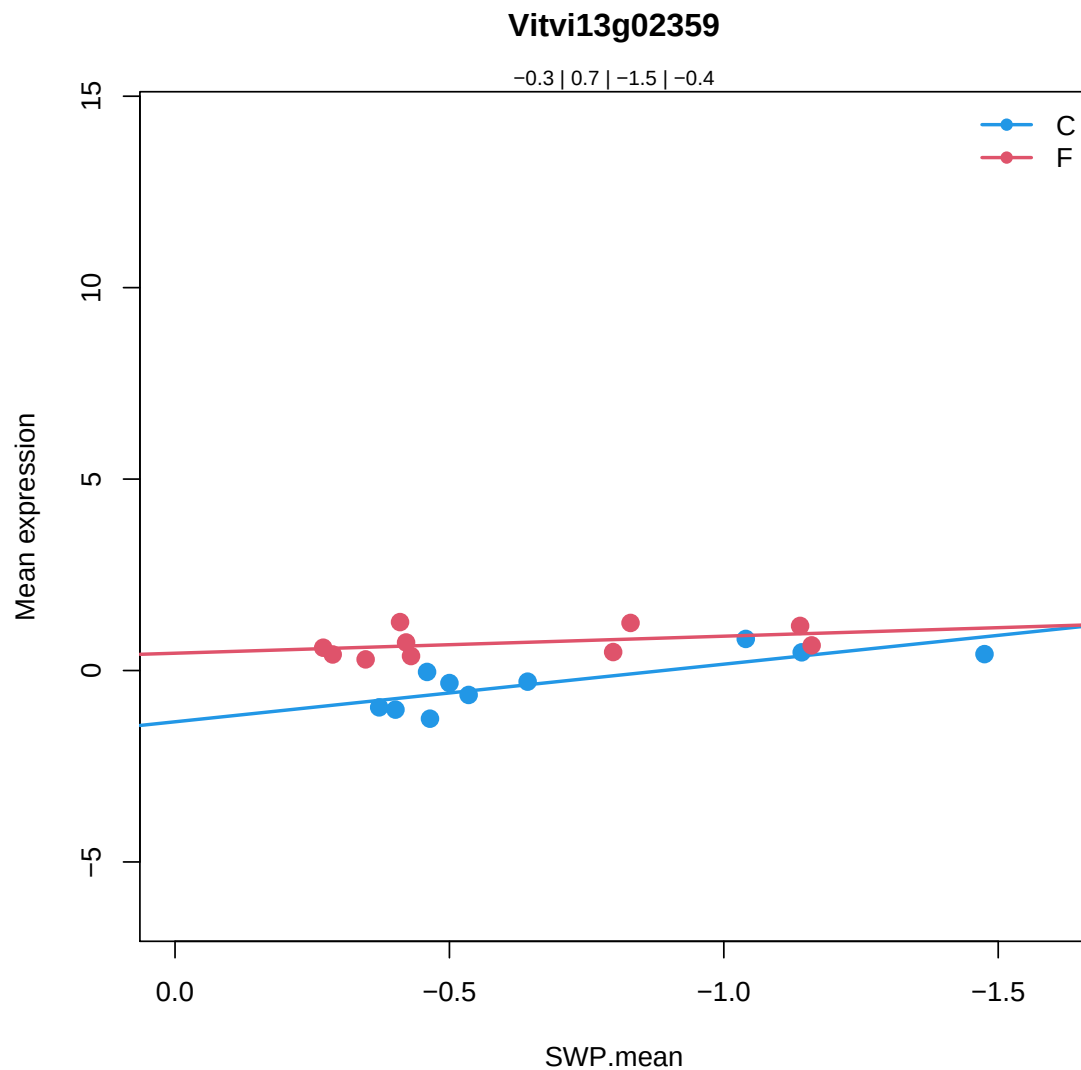
RNA polymerase II fifth largest subunit%2C E |

Chr3:20173673-20175297 FORWARD LENGTH=233 |

201606

Coefficients for Vitvi13g02359.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.28085	0.04842468	*	0.05043659	.
SlopeC	-1.504967	0.0005830364	***	0.1005065	
MeanF-MeanC	1.003501	2.853815e-05	***	0.0006213979	***
SlopeF-SlopeC	1.060049	0.06991798	.	0.9999488	



8.4.33 Vitvi07g01329: * Type3.C

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

Vitvi07g01329

29.2.1.1.3.2

protein.synthesis.ribosomal protein.prokaryotic.unknown organellar.50S

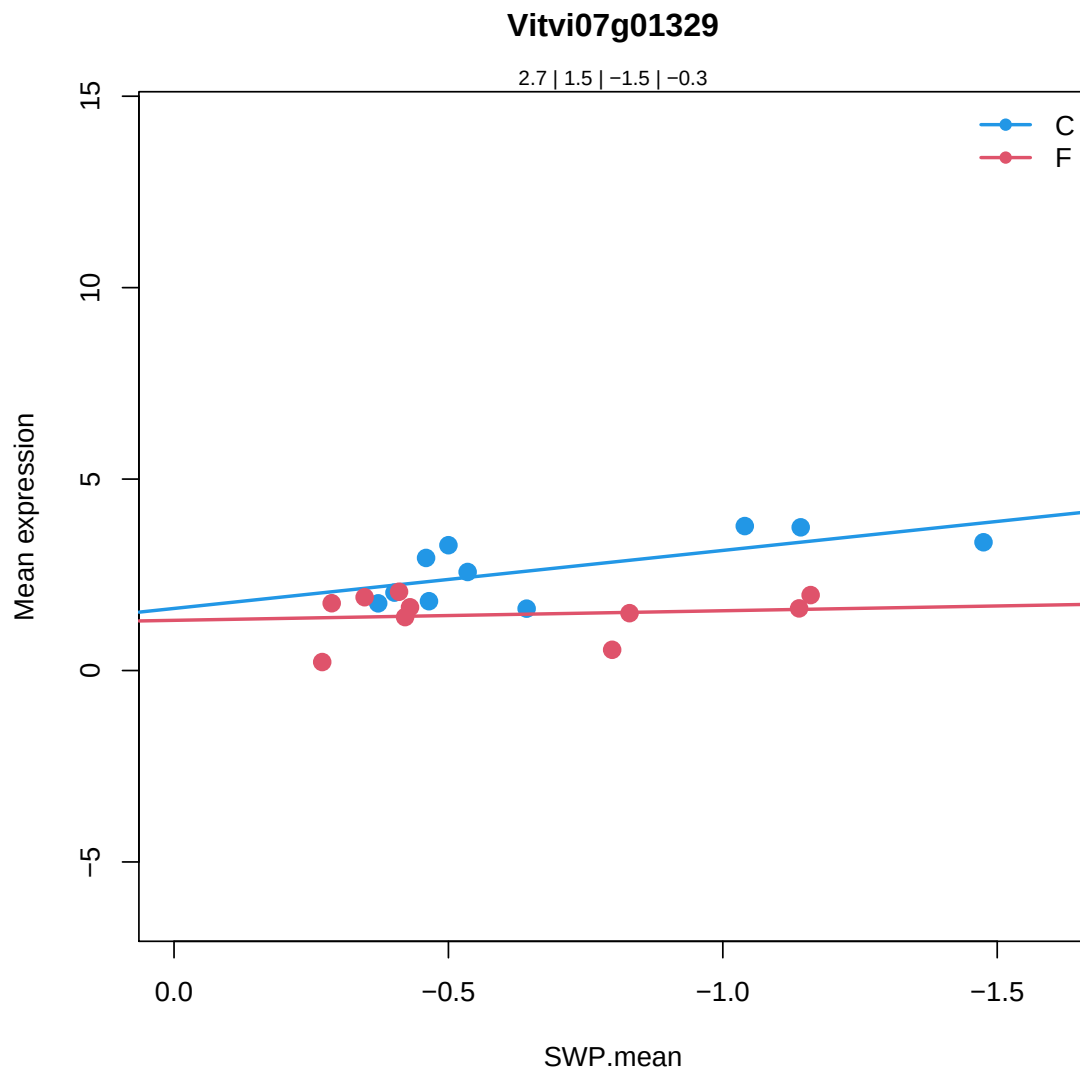
Ribosomal protein L25/Gln-tRNA synthetase%2C anti-codon-binding domain

Chr5:26701233-26702531 REVERSE LENGTH=249 |

201606

Coefficients for Vitvi07g01329.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.686338	3.285794e-12	***	4.584172e-12	***
SlopeC	-1.5151	0.01010604	*	0.3042563	
MeanF-MeanC	-1.22352	0.0001964968	***	0.00321008	**
SlopeF-SlopeC	1.26484	0.1282284		0.9999488	



8.4.34 Vitvi06g00668: Type3.C

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

```
Vitvi06g00668
```

```
30.6
```

```
signalling.MAP kinases
```

```
mitogen-activated protein kinase kinase kinase 13 |
```

```
Chr1:2194279-2195778 REVERSE LENGTH=499 |
```

```
201606
```

```
Vitvi06g00668
```

```
29.4
```

```
protein.postranslational modification
```

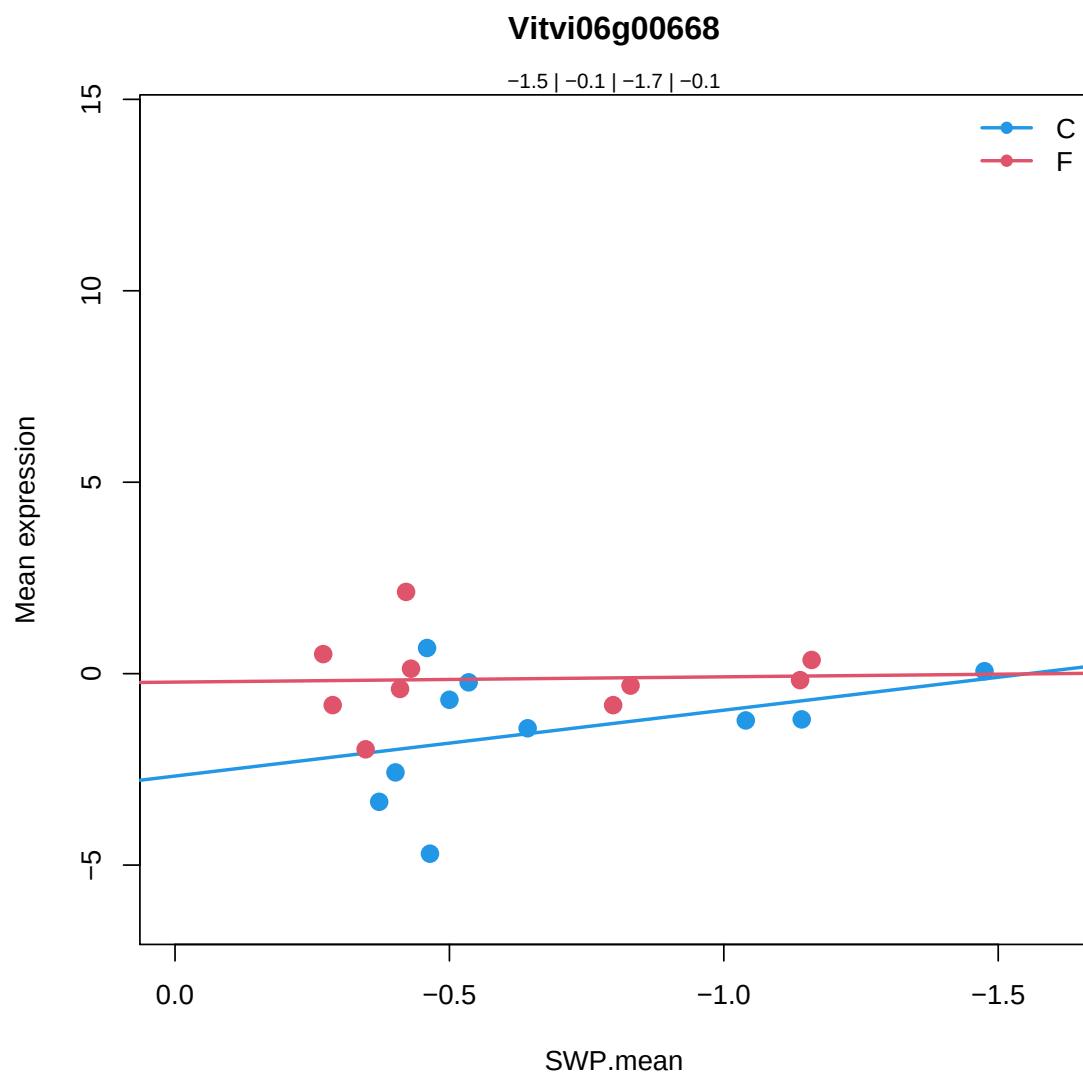
```
mitogen-activated protein kinase kinase kinase 13 |
```

```
Chr1:2194279-2195778 REVERSE LENGTH=499 |
```

```
201606
```

Coefficients for Vitvi06g00668.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.464965	0.001070088	**	0.001158071	**
SlopeC	-1.720059	0.1254121		0.6460361	
MeanF-MeanC	1.328022	0.02435779	*	0.1456157	
SlopeF-SlopeC	1.582692	0.3351886		0.9999488	



8.4.35 Vitvi14g01560: * Type3.C

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

Vitvi14g01560

34.18

transport.unspecified anions

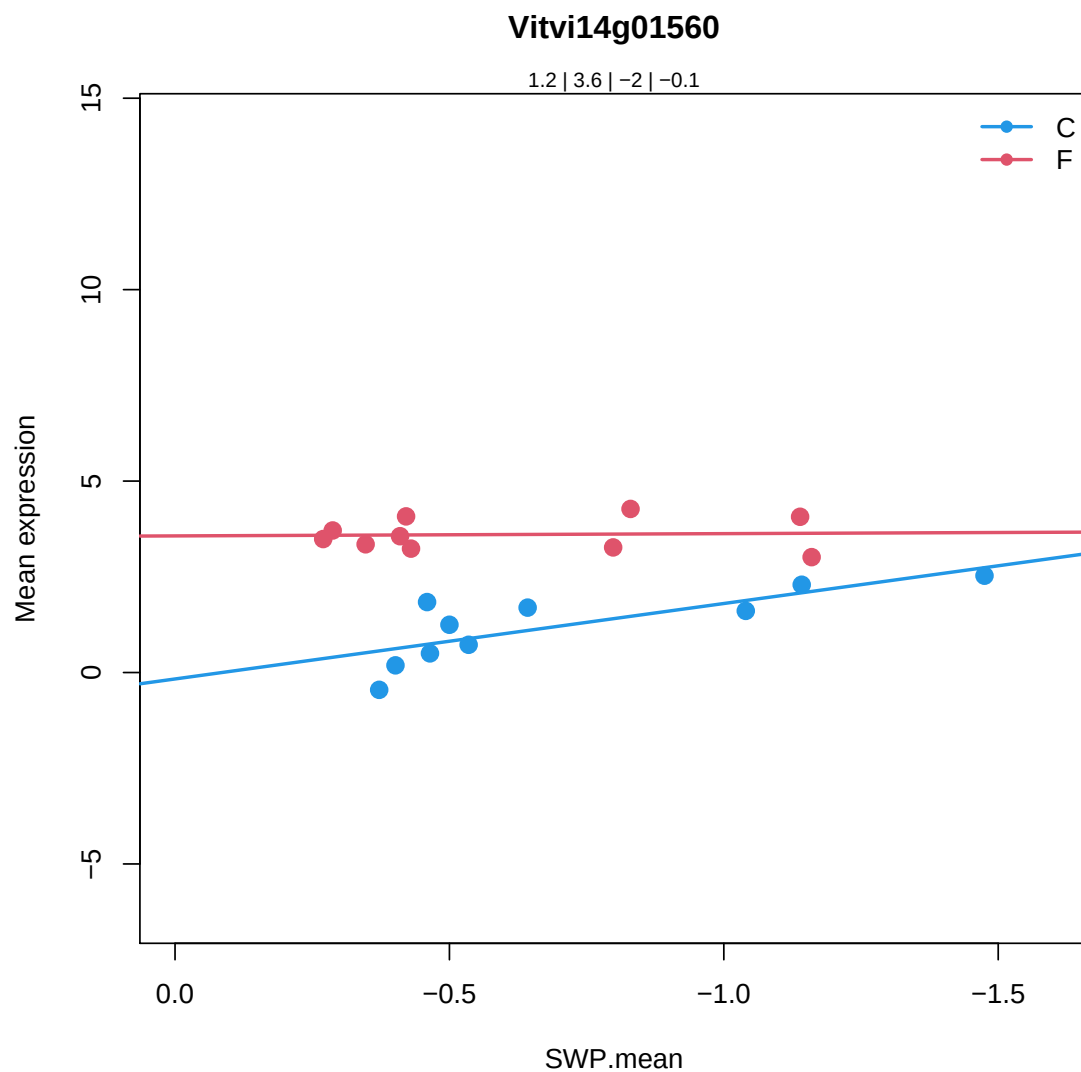
chloride channel B |

Chr3:10024147-10026921 FORWARD LENGTH=780 |

201606

Coefficients for Vitvi14g01560.

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



8.4.36 Vitvi05g01789: * Type3.C

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

Vitvi05g01789

35.2

not assigned.unknown

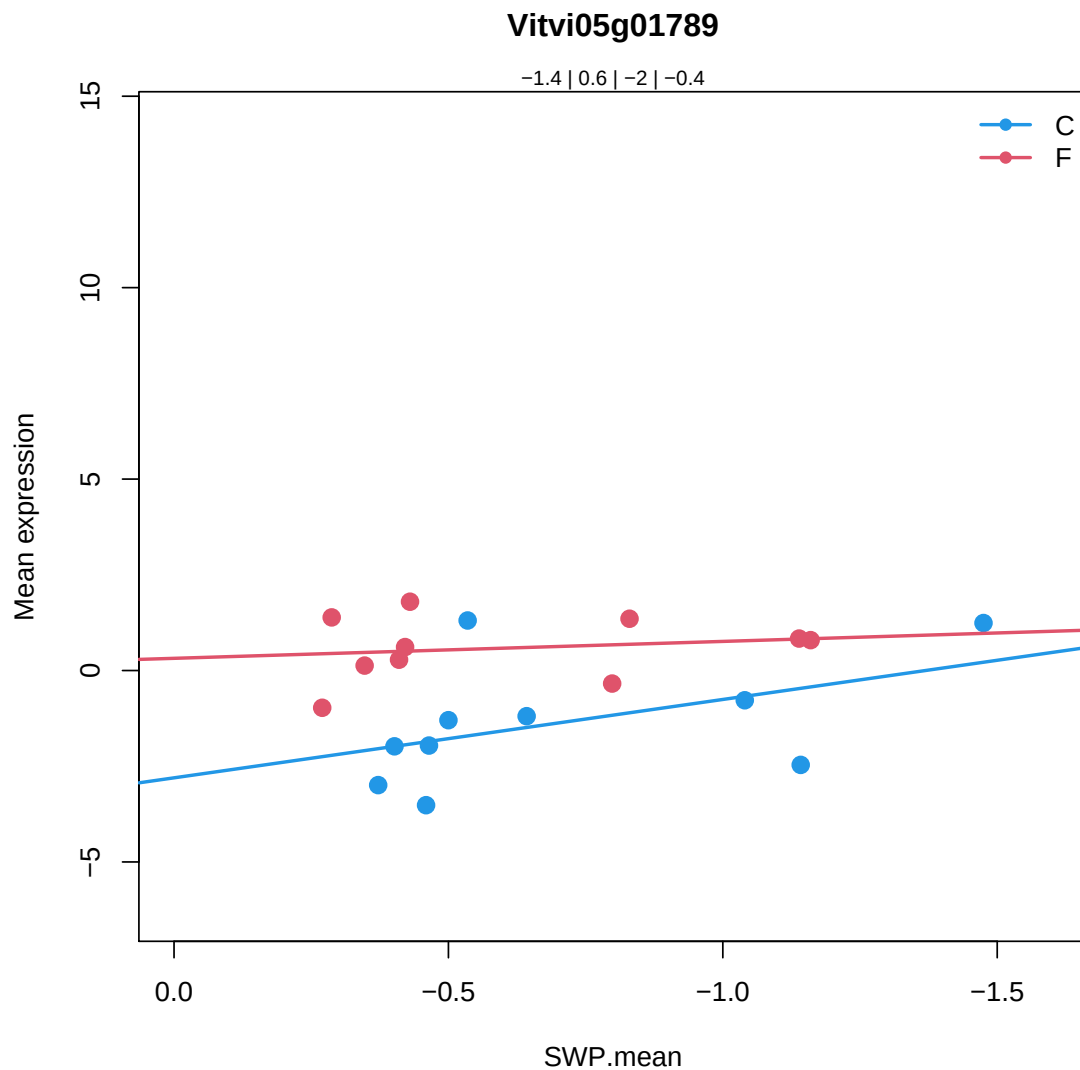
hAT dimerization domain-containing protein |

Chr3:5972793-5975684 REVERSE LENGTH=877 |

201606

Coefficients for Vitvi05g01789.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.363668	0.0007159484	***	0.0007777411	***
SlopeC	-2.046809	0.04501978	*	0.4904752	
MeanF-MeanC	1.951171	0.0006402893	***	0.008670318	**
SlopeF-SlopeC	1.605349	0.2743618		0.9999488	



8.5 Type3.F

8.5.1 Vitvi06g01743: Type3.F

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

Vitvi06g01743

35.2

not assigned.unknown

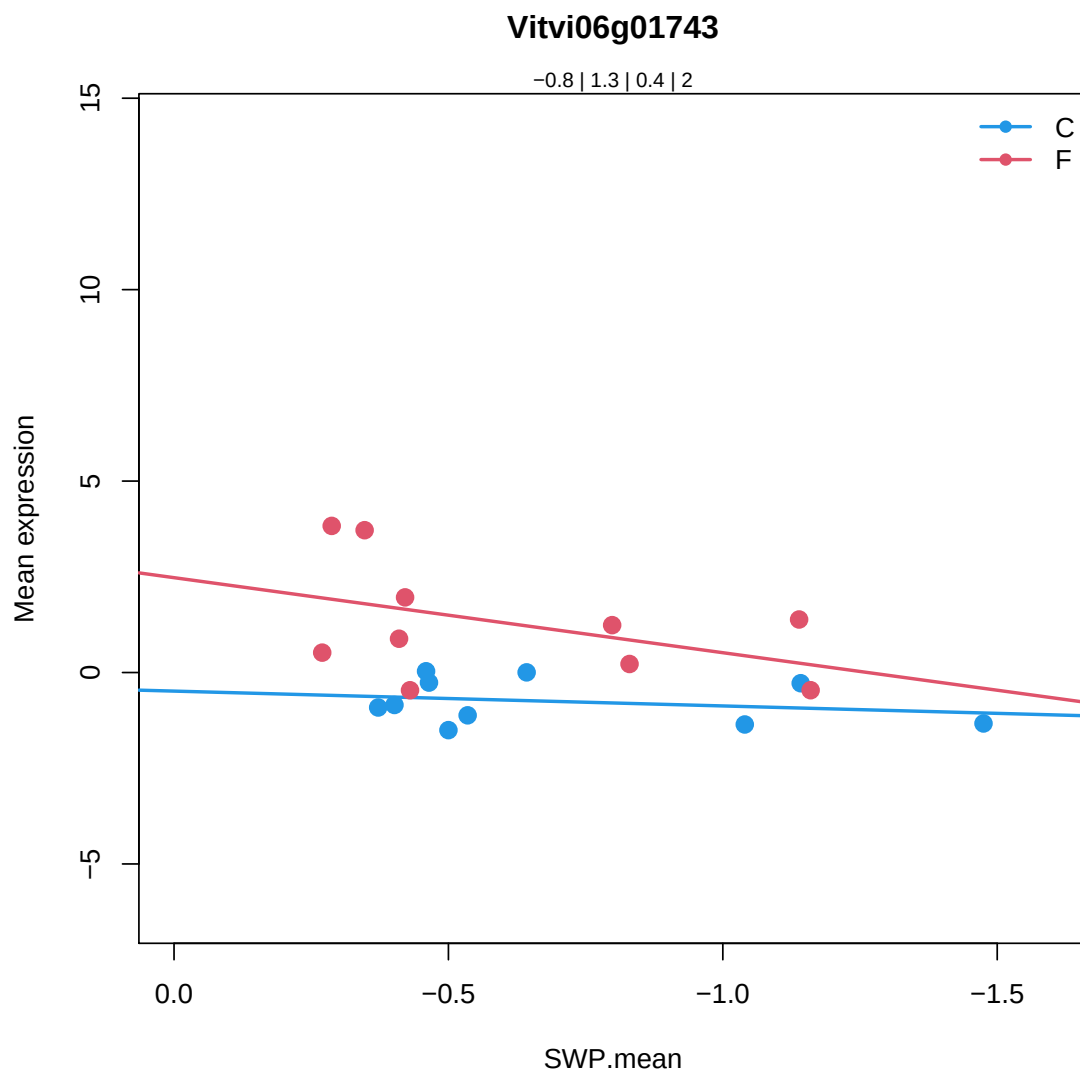
UDP-glucosyl transferase 71C4 |

Chr1:2225963-2227402 FORWARD LENGTH=479 |

201606

Coefficients for Vitvi06g01743.

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



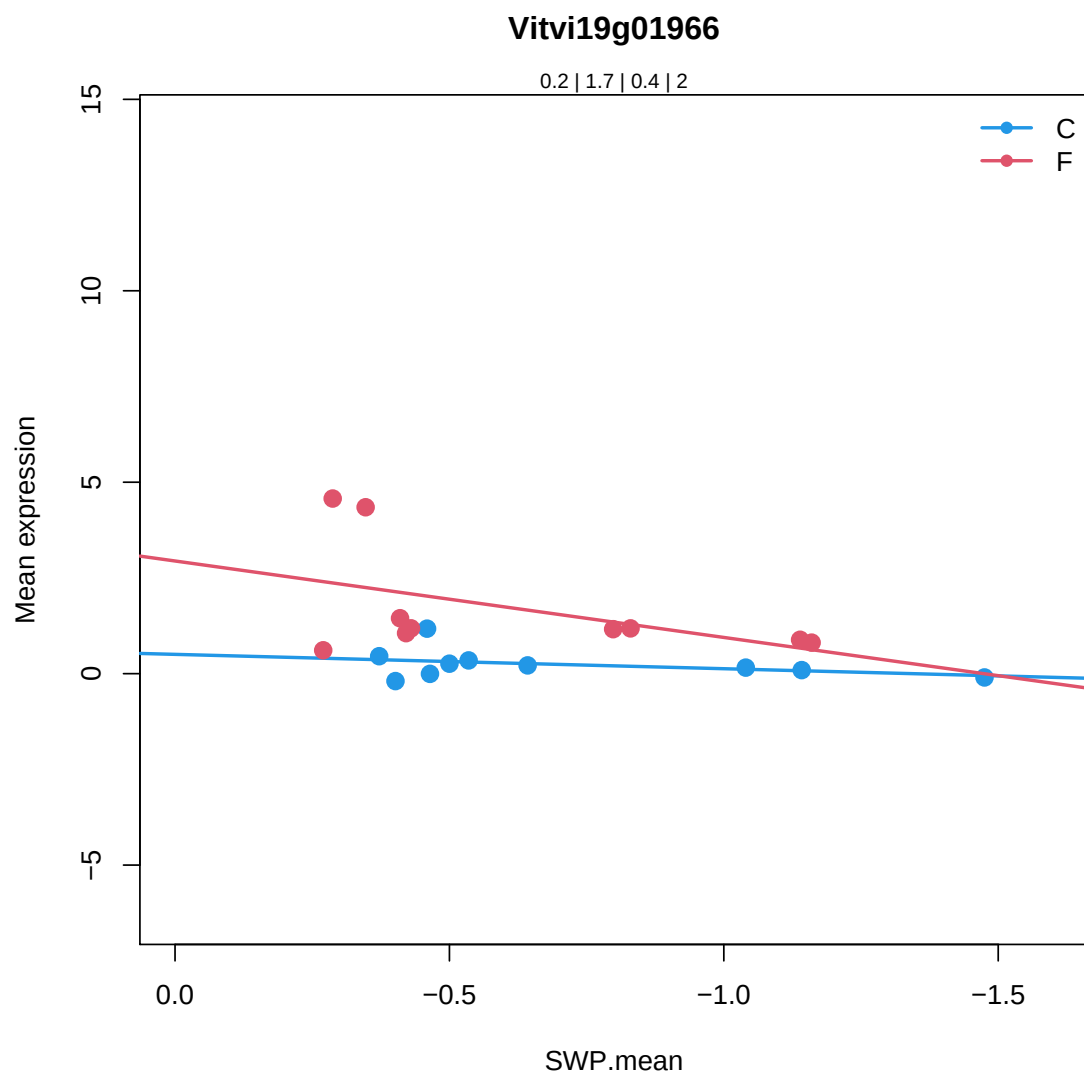
8.5.2 Vitvi19g01966: Type3.F

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
Vitvi19g01966
  30.2.24
  signalling.receptor kinases.S-locus glycoprotein like
  S-locus lectin protein kinase family protein |
  Chr4:13666281-13669202 FORWARD LENGTH=783 |
  201606

Vitvi19g01966
  29.4
  protein.postranslational modification
  S-locus lectin protein kinase family protein |
  Chr4:13666281-13669202 FORWARD LENGTH=783 |
  201606
```

Coefficients for Vitvi19g01966.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.2401875	0.4085668		0.4146608	
SlopeC	0.3750725	0.6408989		0.9150039	
MeanF-MeanC	1.485613	0.001334182	**	0.01587478	*
SlopeF-SlopeC	1.621511	0.183549		0.9999488	



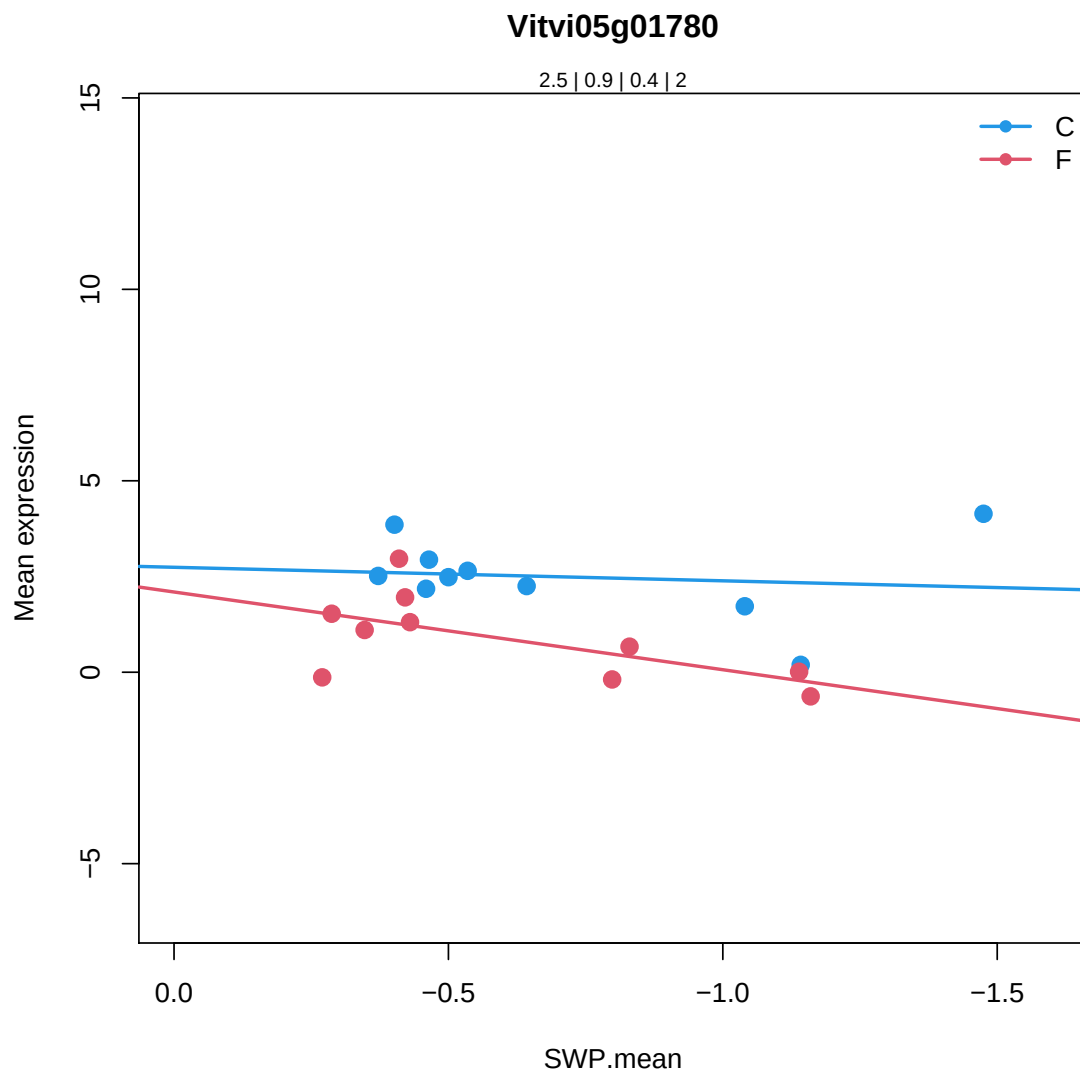
8.5.3 Vitvi05g01780: Type3.F

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

```
Vitvi05g01780
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi05g01780.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.492285	3.342069e-08	***	4.017336e-08	***
SlopeC	0.3531567	0.6739755		0.9246326	
MeanF-MeanC	-1.633824	0.0008349926	***	0.01076731	*
SlopeF-SlopeC	1.677069	0.1876866		0.9999488	



8.5.4 Vitvi19g00391: Type3.F

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

Vitvi19g00391

16.1.5

secondary metabolism.isoprenoids.terpenoids

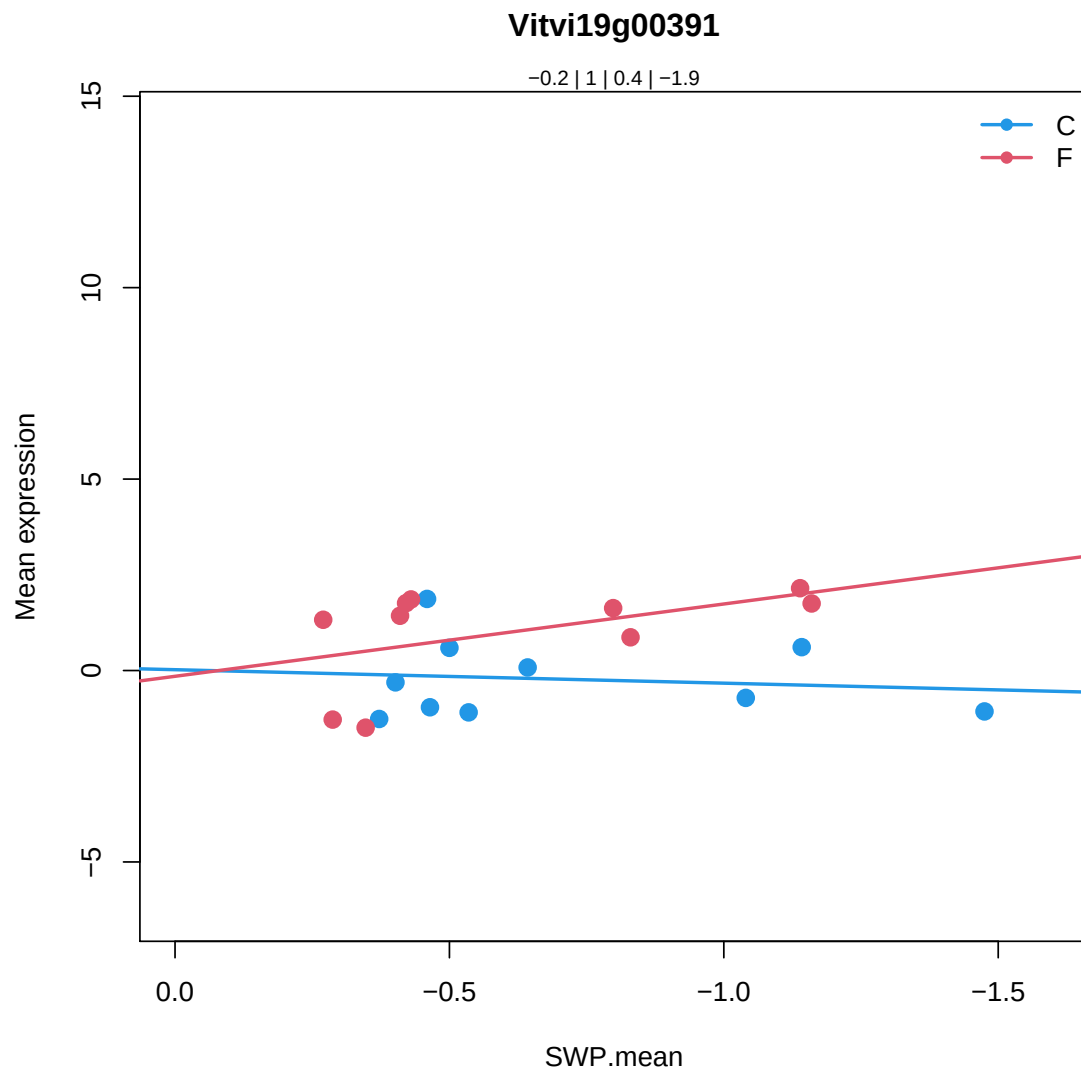
terpene synthase 21 |

Chr5:8092969-8095128 FORWARD LENGTH=545 |

201606

Coefficients for Vitvi19g00391.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.2259877	0.4867558		0.4929328	
SlopeC	0.3515541	0.6962291		0.9317974	
MeanF-MeanC	1.225536	0.01285799	*	0.09162296	.
SlopeF-SlopeC	-2.240139	0.1047179		0.9999488	



8.5.5 Vitvi05g01675: + Type3.F

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

Vitvi05g01675

26.11.1

misc.alcohol dehydrogenases.cinnamyl alcohol dehydrogenase

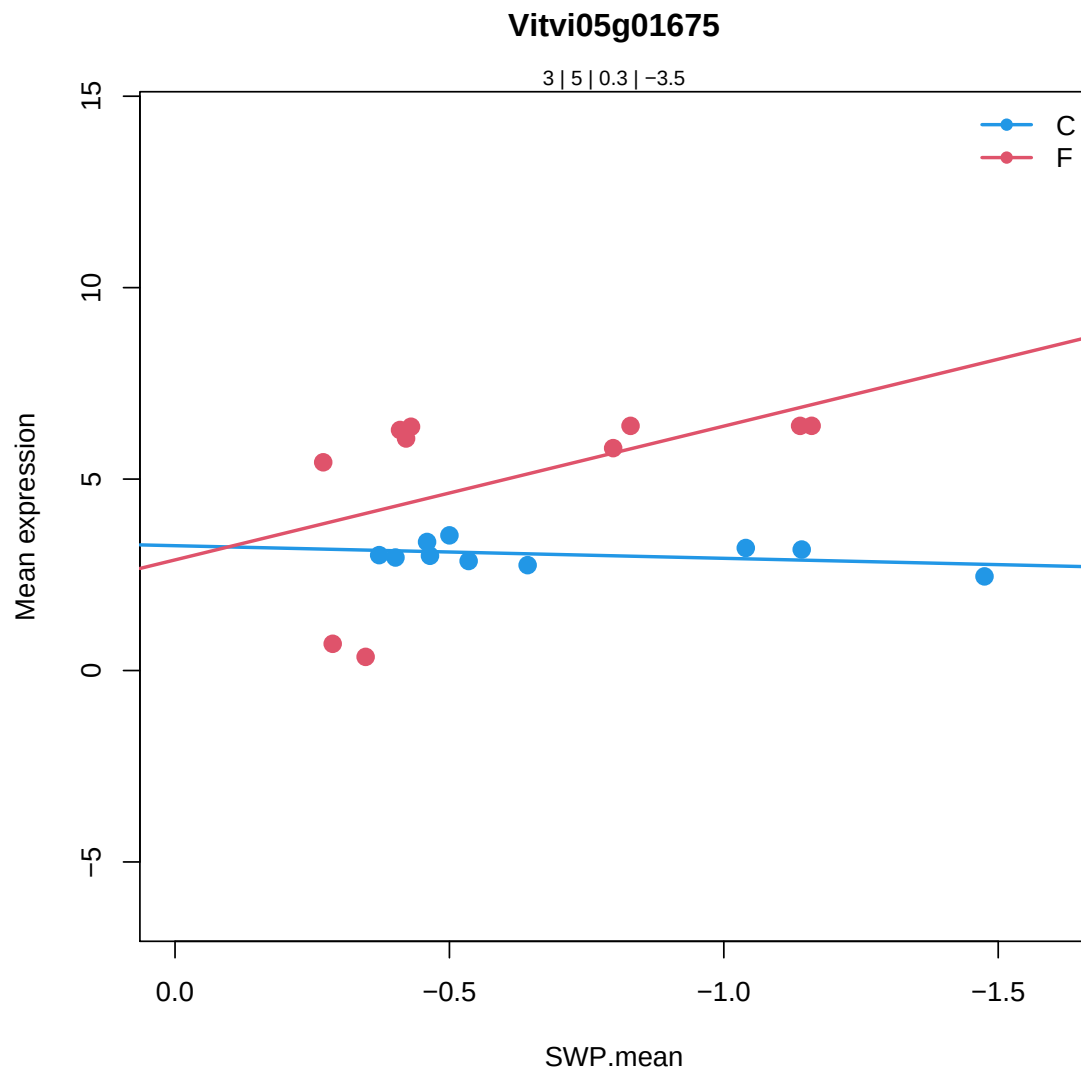
Zinc-binding dehydrogenase family protein |

Chr5:5584983-5586991 REVERSE LENGTH=345 |

201606

Coefficients for Vitvi05g01675.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.027901	6.100684e-07	***	7.084695e-07	***
SlopeC	0.3297008	0.7874006		0.9533712	
MeanF-MeanC	1.9902	0.003821472	**	0.03702916	*
SlopeF-SlopeC	-3.824121	0.04507823	*	0.9999488	



8.5.6 Vitvi14g03071: + Type3.F

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

Vitvi14g03071

35.2

not assigned.unknown

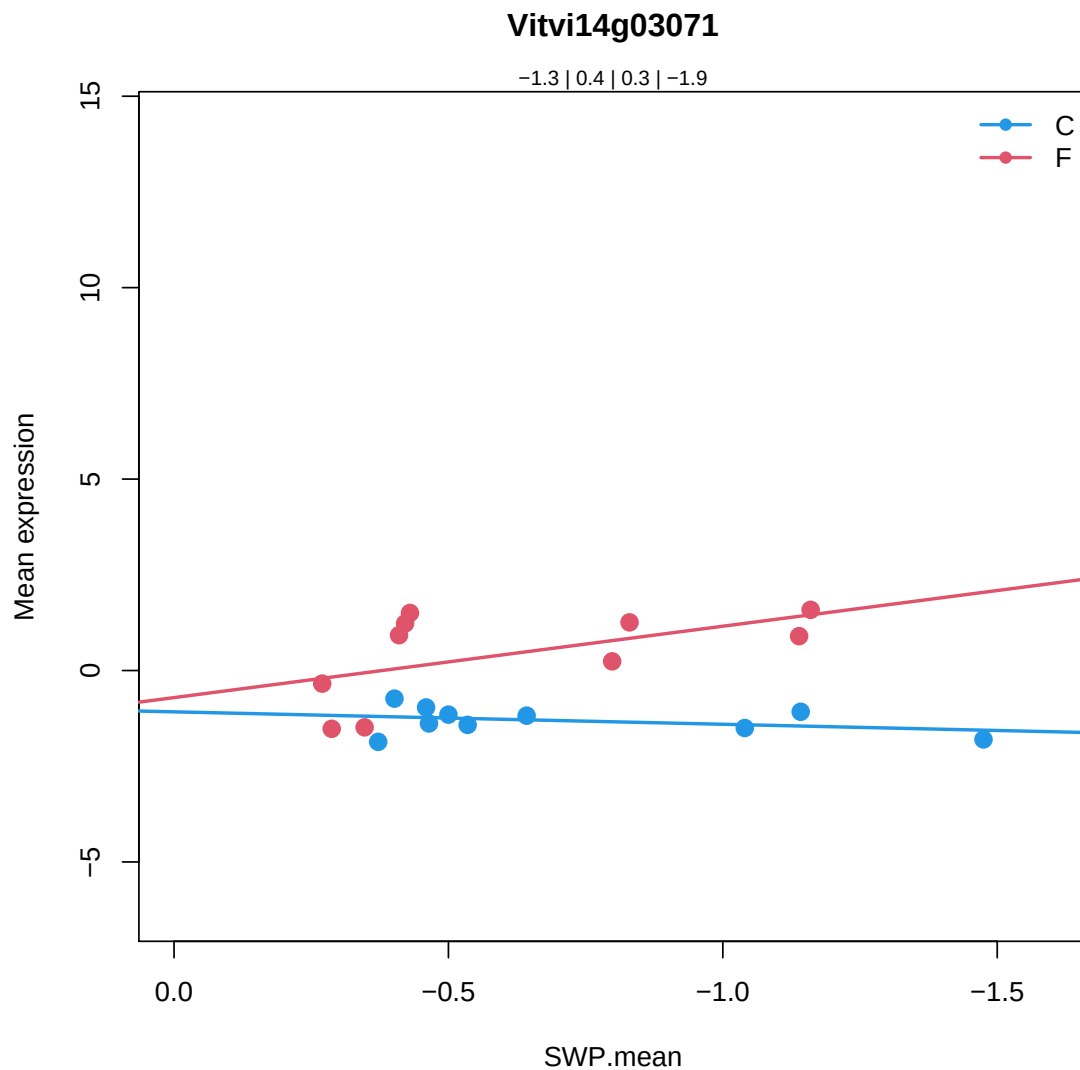
kinase family with leucine-rich repeat domain-containing protein |

Chr1:13220940-13224386 FORWARD LENGTH=1120 |

201606

Coefficients for Vitvi14g03071.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.307629	9.148178e-06	***	1.034165e-05	***
SlopeC	0.3246997	0.6116398		0.9065647	
MeanF-MeanC	1.736141	2.088562e-05	***	0.0004765548	***
SlopeF-SlopeC	-2.188816	0.02941108	*	0.9999488	



8.5.7 Vitvi01g02299: Type3.F

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

Vitvi01g02299

35.2

not assigned.unknown

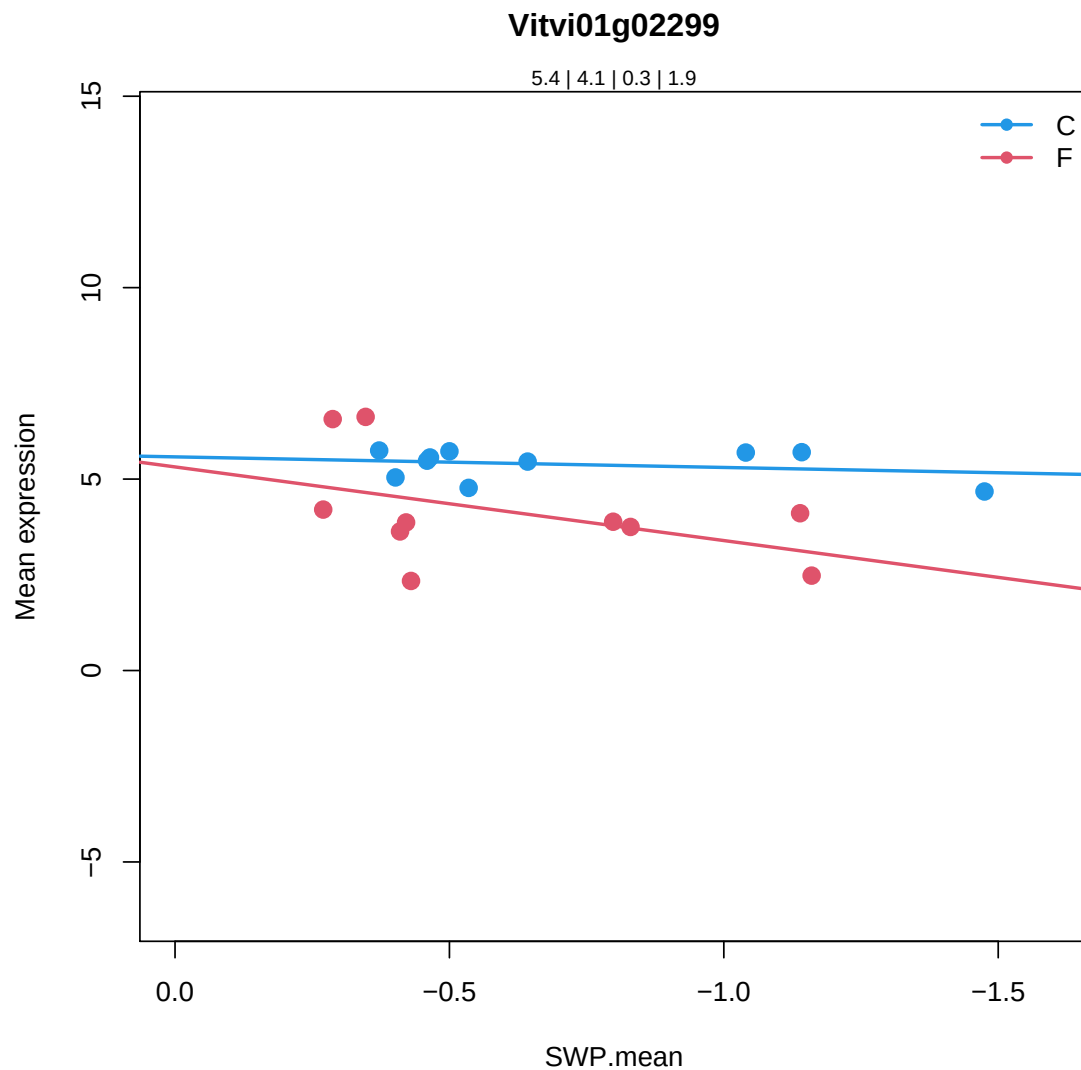
Major facilitator superfamily protein |

Chr5:4296854-4299079 REVERSE LENGTH=624 |

201606

Coefficients for Vitvi01g02299.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.38558	7.345511e-15	***	1.245248e-14	***
SlopeC	0.2763339	0.7305845		0.9406676	
MeanF-MeanC	-1.240036	0.005587167	**	0.04964575	*
SlopeF-SlopeC	1.64721	0.1766302		0.9999488	



8.5.8 Vitvi13g00600: Type3.F

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

Vitvi13g00600

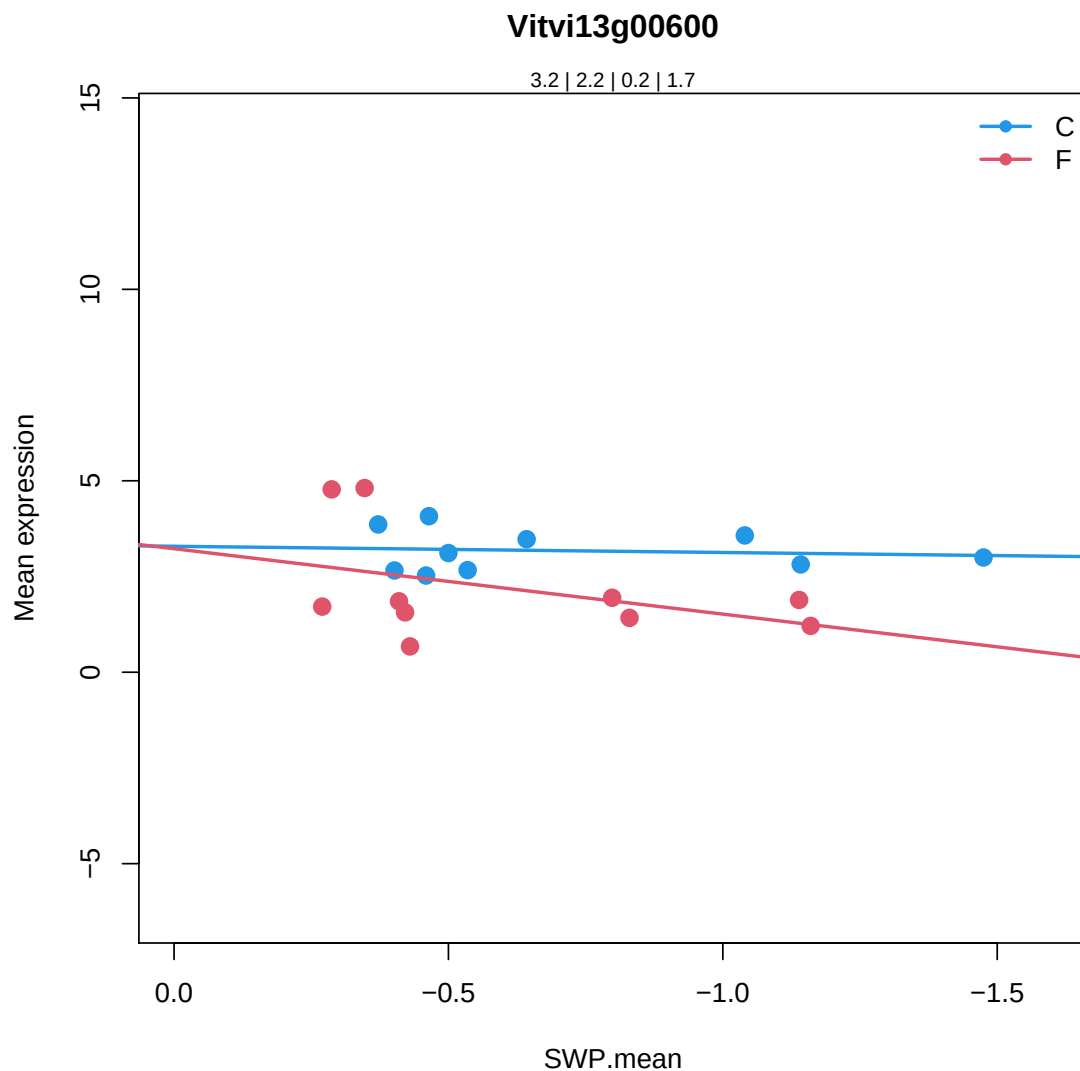
34.3

transport.amino acids

Tyrosine-specific transport protein IPR018227 Tryptophan_tyrosine perm

Coefficients for Vitvi13g00600.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.175325	5.143251e-10	***	6.550253e-10	***
SlopeC	0.1619251	0.8472215		0.9711946	
MeanF-MeanC	-0.990095	0.02867047	*	0.1640545	
SlopeF-SlopeC	1.546758	0.2242124		0.9999488	



8.5.9 Vitvi07g01779: Type3.F

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

Vitvi07g01779

34.6

transport.sulphate

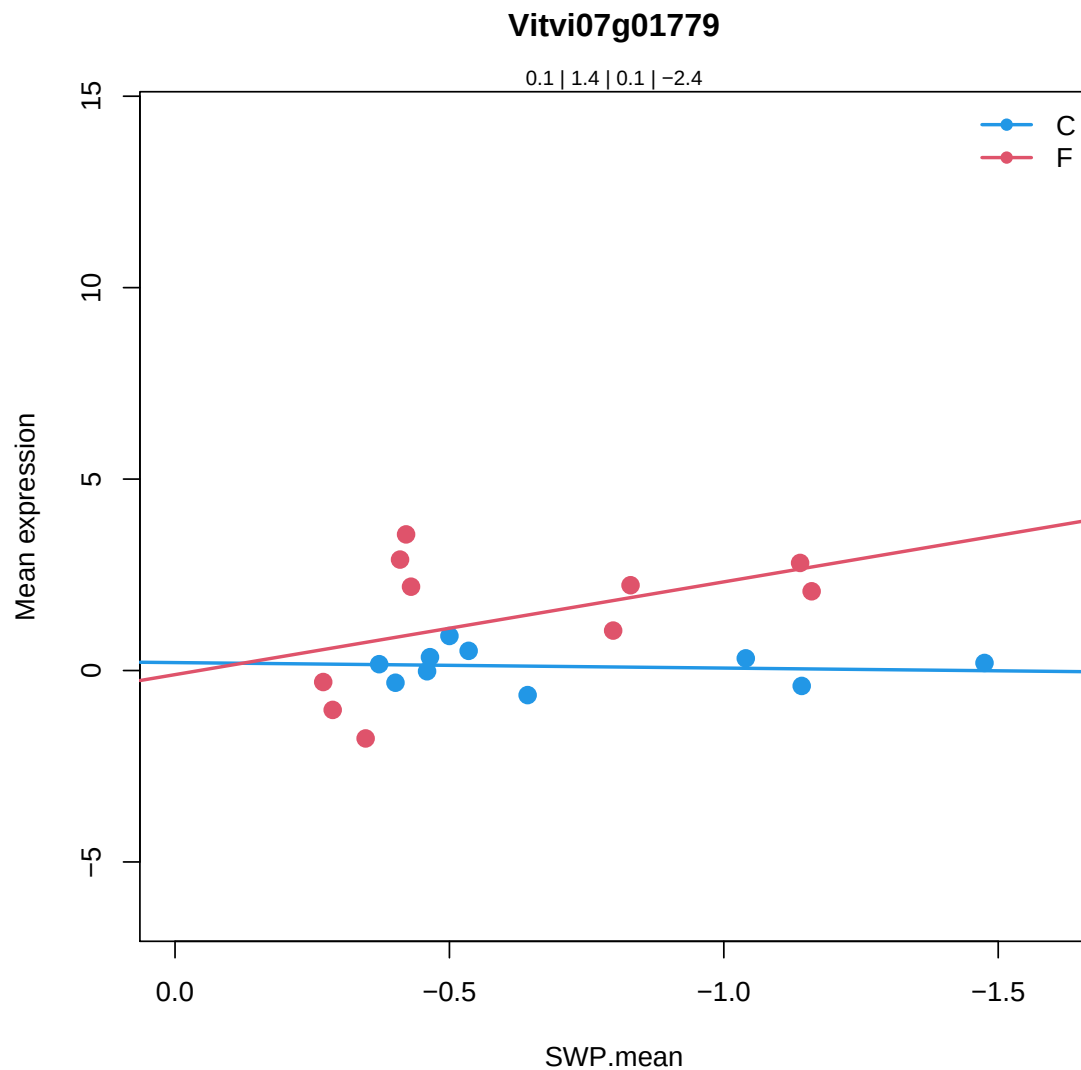
STAS domain / Sulfate transporter family |

Chr1:29317965-29323249 REVERSE LENGTH=677 |

201606

Coefficients for Vitvi07g01779.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1061768	0.7659189		0.7703158	
SlopeC	0.1430805	0.8852476		0.9789972	
MeanF-MeanC	1.262582	0.01906637	*	0.1219474	
SlopeF-SlopeC	-2.565898	0.09271658	.	0.9999488	



8.5.10 Vitvi15g00727: Type3.F

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

Vitvi15g00727

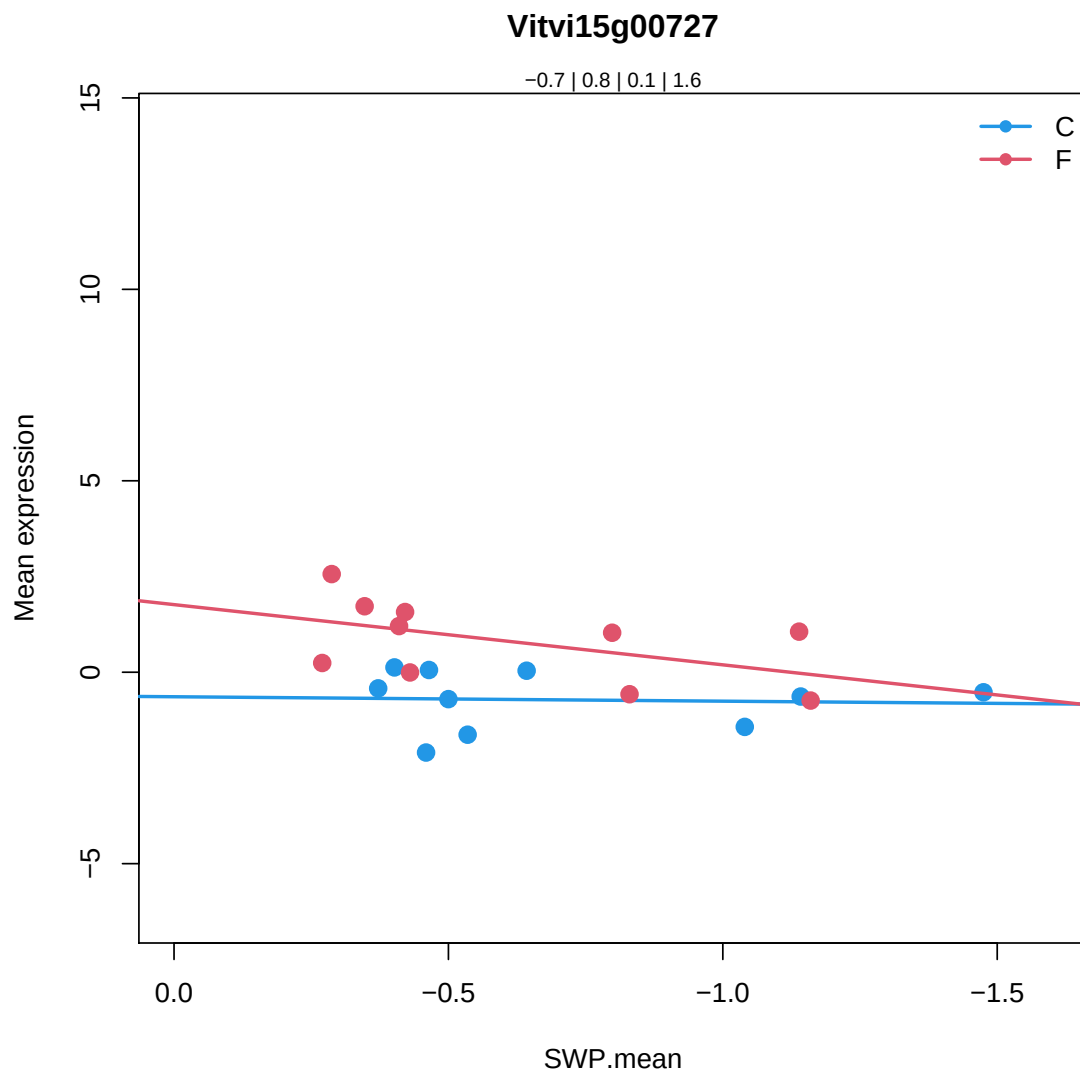
35.2

not assigned.unknown

Unknown Protein

Coefficients for Vitvi15g00727.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.7217807	0.009994891	**	0.01058593	*
SlopeC	0.1155023	0.8724035		0.9762394	
MeanF-MeanC	1.529218	0.0003576357	***	0.005333741	**
SlopeF-SlopeC	1.457204	0.1824867		0.9999488	



8.5.11 Vitvi15g01075: Type3.F

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

Vitvi15g01075

16.8.1.12

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

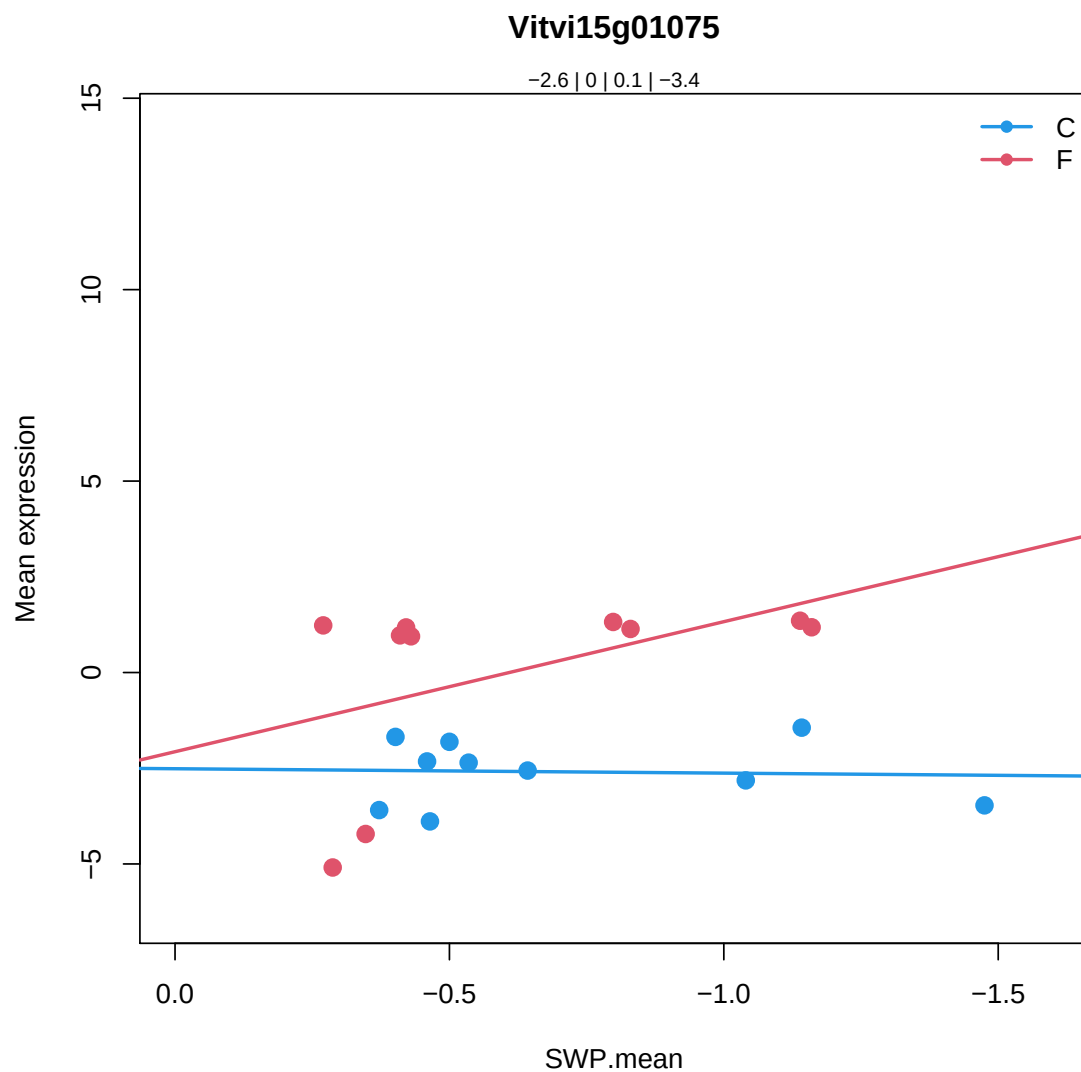
UDP-Glycosyltransferase superfamily protein |

Chr2:9593012-9594424 FORWARD LENGTH=470 |

201606

Coefficients for Vitvi15g01075.

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



8.5.12 Vitvi18g02012: Type3.F

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

Vitvi18g02012

26.2

misc.UDP glucosyl and glucoronyl transferases

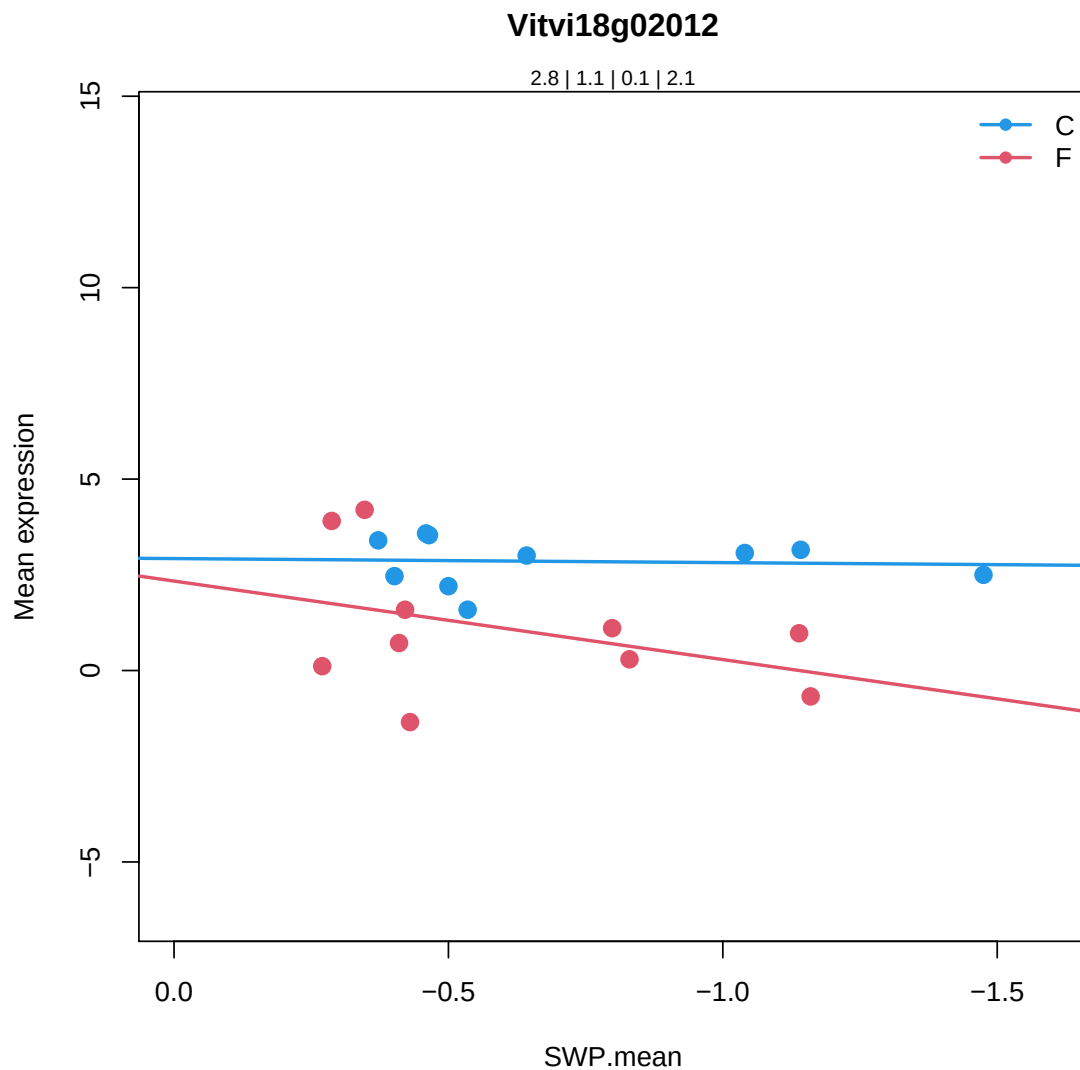
UDP-glucosyl transferase 88A1 |

Chr3:5618847-5620833 REVERSE LENGTH=446 |

201606

Coefficients for Vitvi18g02012.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.849471	1.2602e-07	***	1.491301e-07	***
SlopeC	0.1057251	0.9189502		0.9851716	
MeanF-MeanC	-1.76252	0.002789493	**	0.02898258	*
SlopeF-SlopeC	1.945201	0.2167274		0.9999488	



8.5.13 Vitvi04g01421: Type3.F

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

Vitvi04g01421

1.3.6

PS.calvin cycle.aldolase

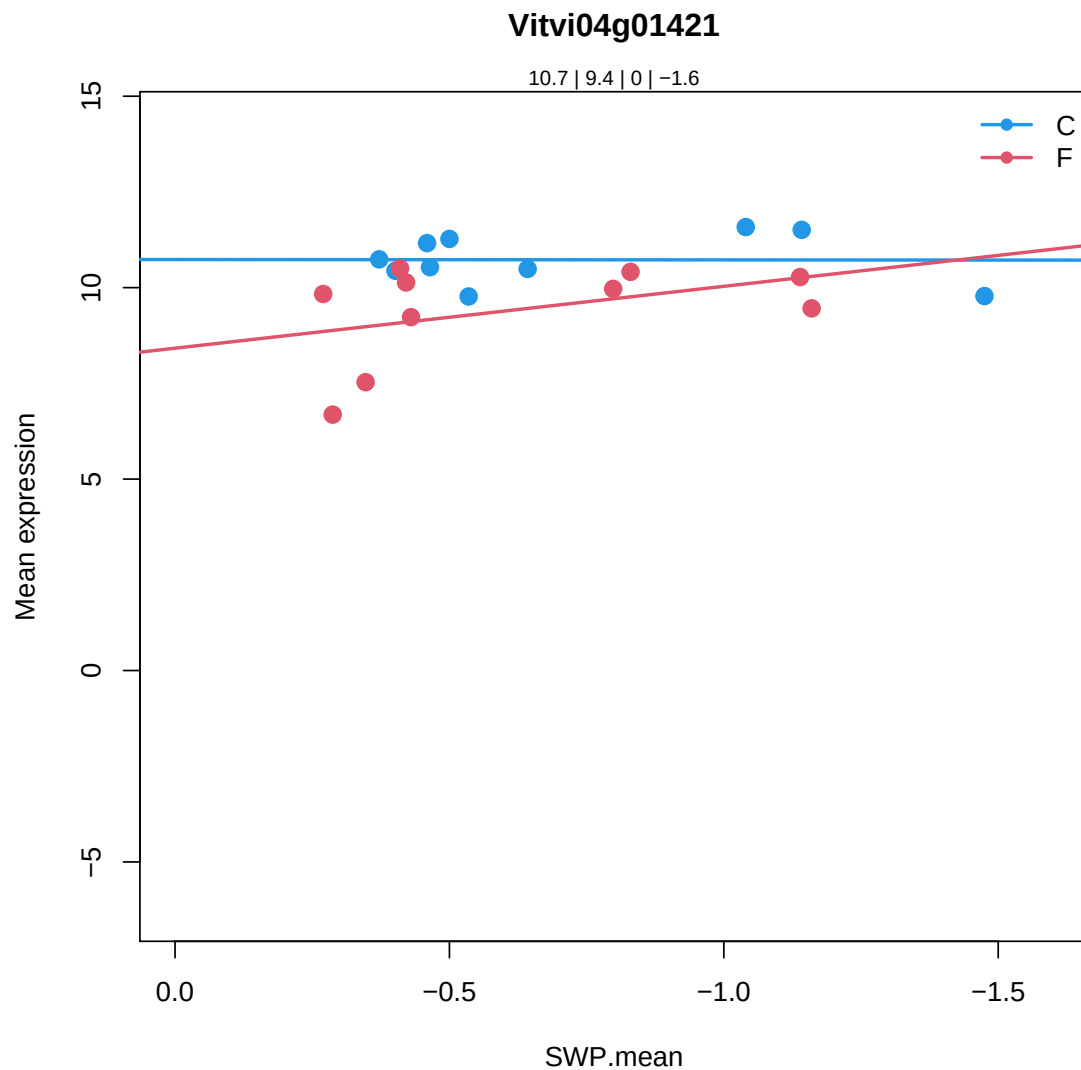
fructose-bisphosphate aldolase 1 |

Chr2:9128416-9130152 REVERSE LENGTH=399 |

201606

Coefficients for Vitvi04g01421.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	10.72777	4.215446e-21	***	3.550678e-20	***
SlopeC	0.009195738	0.9908277		0.9983274	
MeanF-MeanC	-1.324901	0.003368974	**	0.03362796	*
SlopeF-SlopeC	-1.625479	0.1814085		0.9999488	



8.5.14 Vitvi01g00064: Type3.F

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

Vitvi01g00064

2.2.2.2

major CHO metabolism.degradation.starch.starch phosphorylase

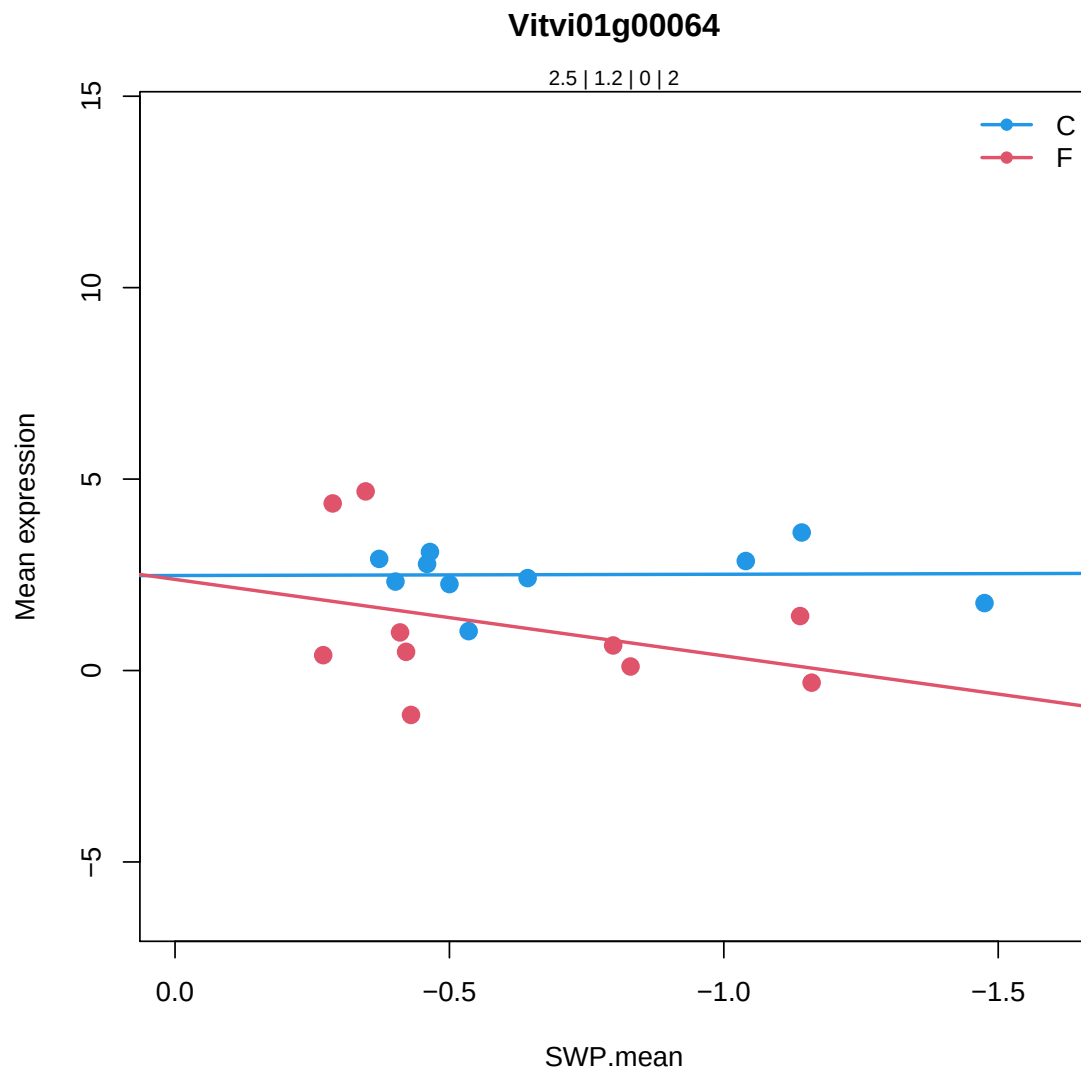
Glycosyl transferase%2C family 35 |

Chr3:11252871-11257587 FORWARD LENGTH=962 |

201606

Coefficients for Vitvi01g00064.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.50421	3.137274e-06	***	3.580556e-06	***
SlopeC	-0.03291293	0.9767566		0.9965809	
MeanF-MeanC	-1.341287	0.02762602	*	0.1599574	
SlopeF-SlopeC	2.030061	0.2351312		0.9999488	



8.5.15 Vitvi18g00154: Type3.F

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

Vitvi18g00154

29.4

protein.postranslational modification

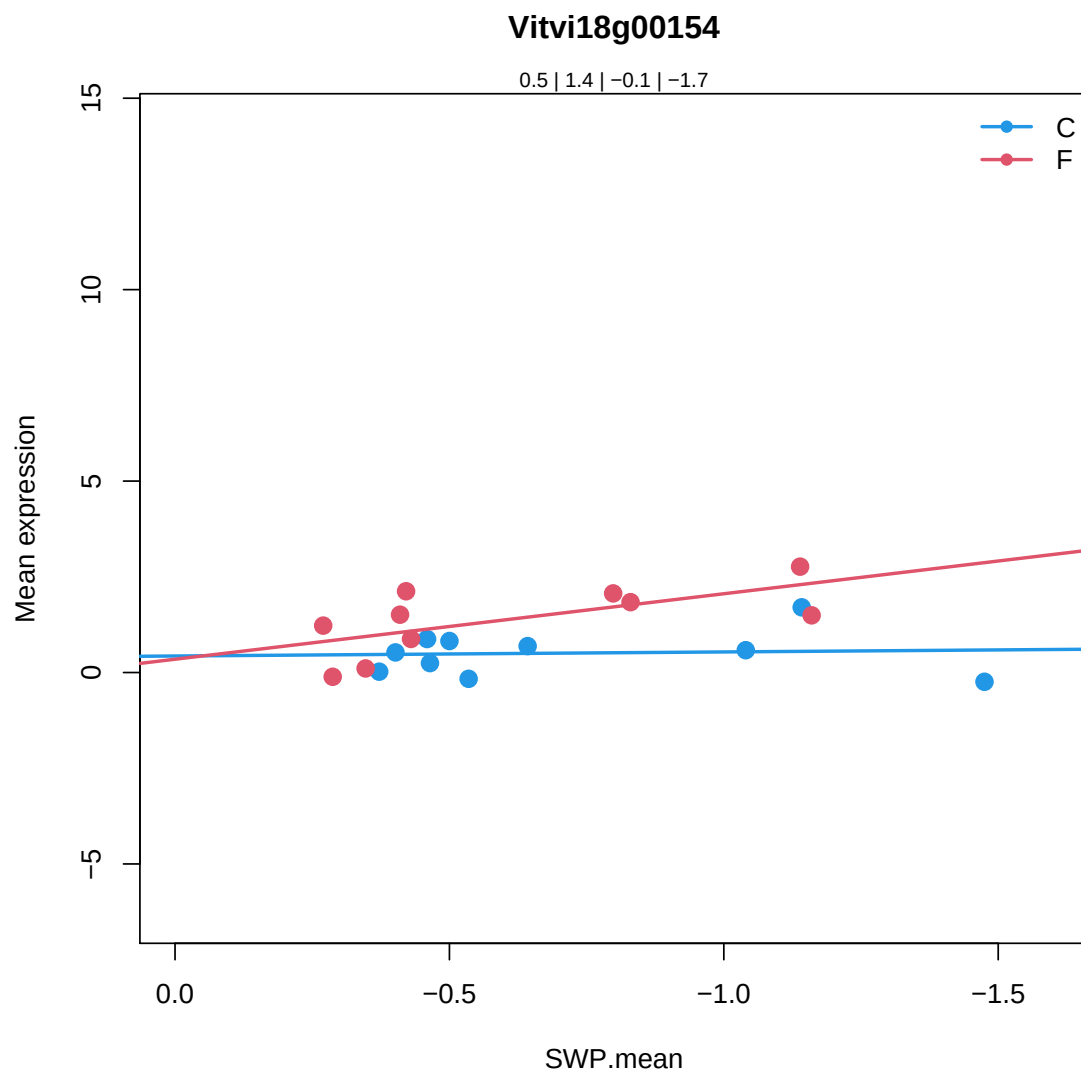
ACT-like protein tyrosine kinase family protein |

Chr4:17999432-18003193 FORWARD LENGTH=508 |

201606

Coefficients for Vitvi18g00154.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.5058717	0.01887407	*	0.01985496	*
SlopeC	-0.1060377	0.8500358		0.9719233	
MeanF-MeanC	0.8832002	0.004908278	**	0.04506746	*
SlopeF-SlopeC	-1.604135	0.06499196	.	0.9999488	



8.5.16 Vitvi08g00662: Type3.F

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

Vitvi08g00662

11.2.3

lipid metabolism.FA desaturation.omega 3 desaturase

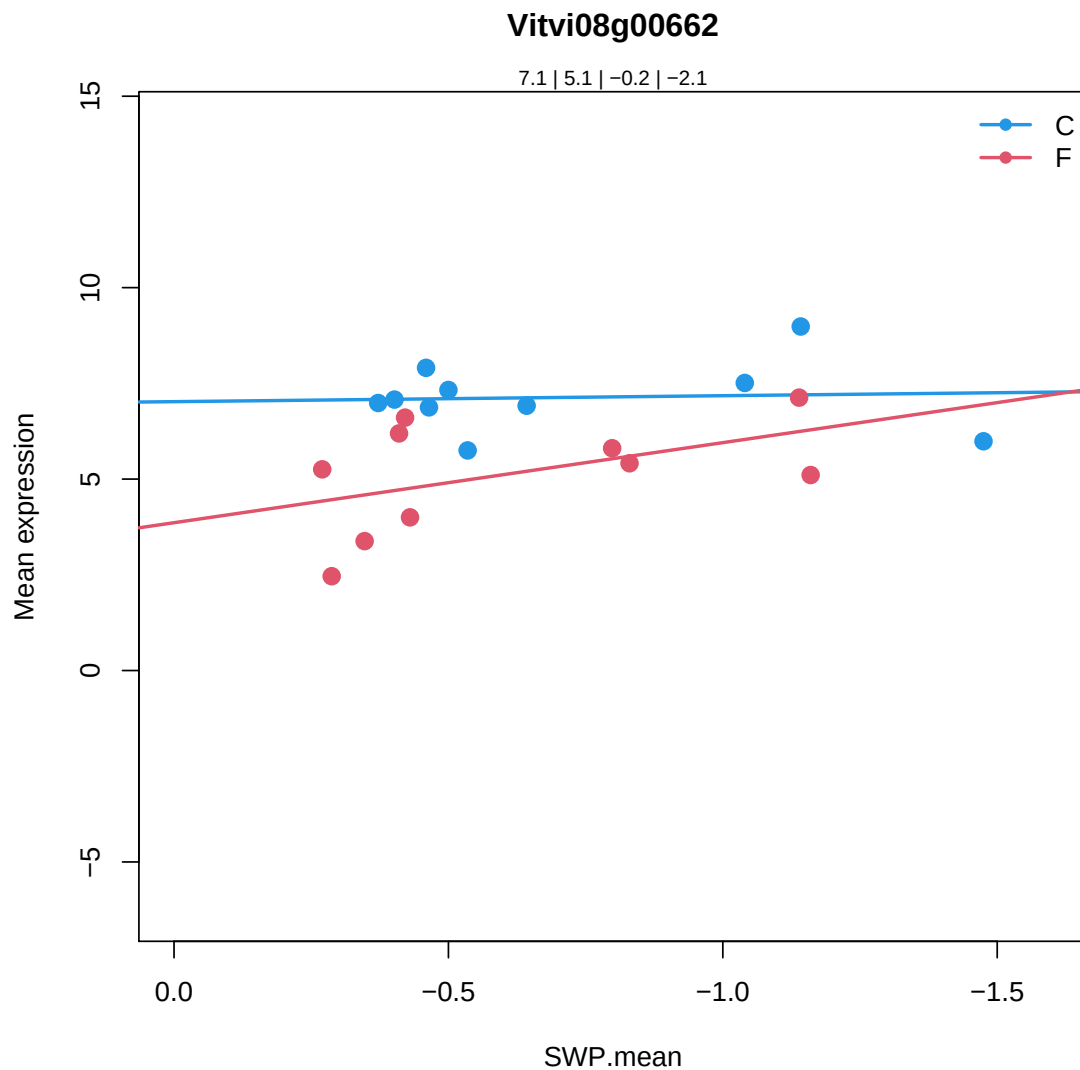
fatty acid desaturase 7 |

Chr3:3499959-3502126 FORWARD LENGTH=446 |

201606

Coefficients for Vitvi08g00662.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.131549	5.18266e-16	***	1.007321e-15	***
SlopeC	-0.1554342	0.867576		0.975839	
MeanF-MeanC	-1.997009	0.0003312959	***	0.005009536	**
SlopeF-SlopeC	-1.935515	0.1723518		0.9999488	



8.5.17 Vitvi15g00795: Type3.F

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

Vitvi15g00795

26.10

misc.cytochrome P450

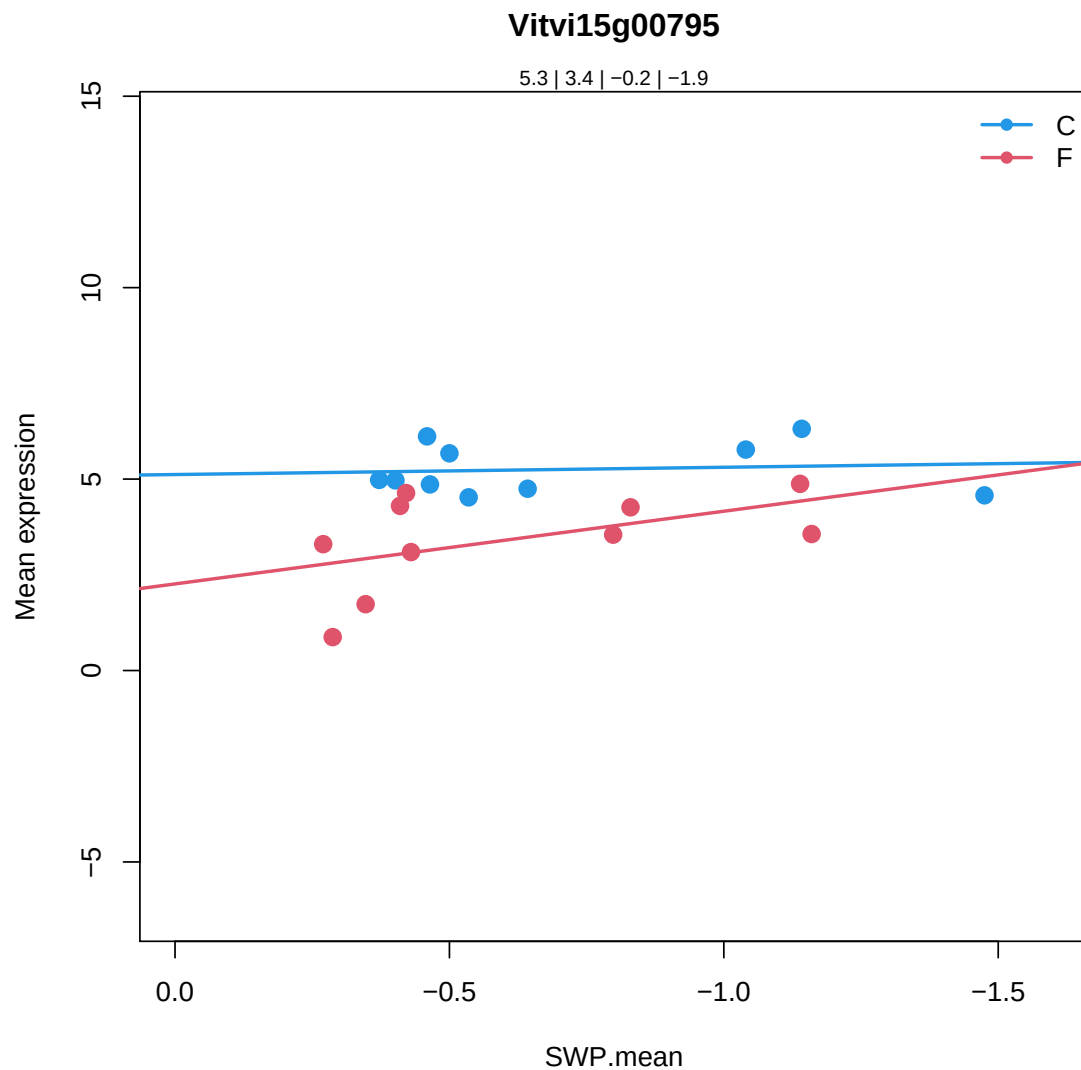
cytochrome P450%2C family 76%2C subfamily C%2C polypeptide 6 |

Chr1:12220957-12222171 REVERSE LENGTH=404 |

201606

Coefficients for Vitvi15g00795.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	5.252041	4.859016e-15	***	8.432326e-15	***
SlopeC	-0.1898245	0.8043535		0.9573096	
MeanF-MeanC	-1.833566	9.910431e-05	***	0.001796133	**
SlopeF-SlopeC	-1.708449	0.1439725		0.9999488	



8.5.18 Vitvi00g01320: Type3.F

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

```
Vitvi00g01320
```

```
29.5.11.4.2
```

```
protein.degradation.ubiquitin.E3.RING
```

```
plant U-box 8 |
```

```
Chr4:11356143-11357267 REVERSE LENGTH=374 |
```

```
201606
```

```
Vitvi00g01320
```

```
35.2
```

```
not assigned.unknown
```

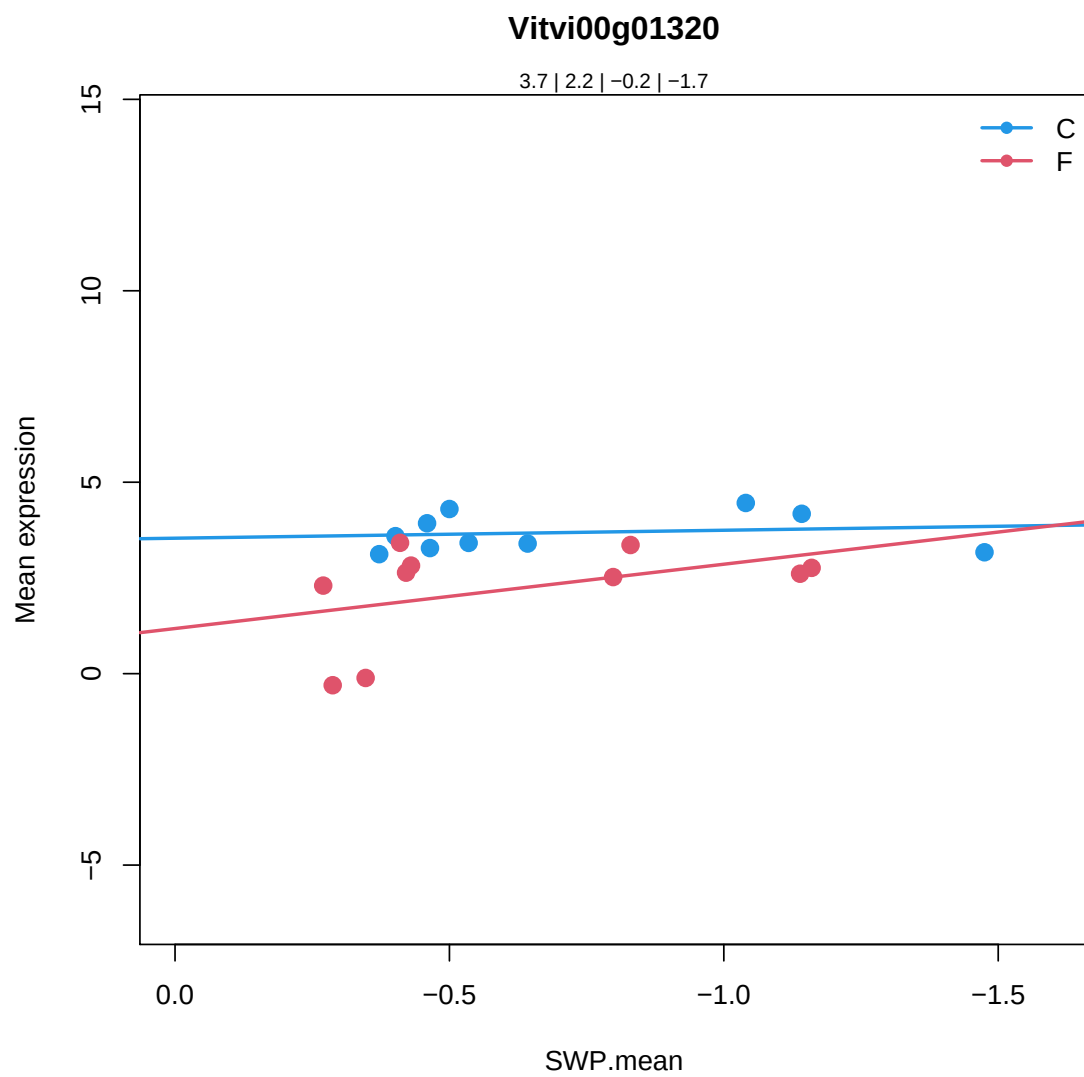
```
plant U-box 8 |
```

```
Chr4:11356143-11357267 REVERSE LENGTH=374 |
```

```
201606
```

Coefficients for Vitvi00g01320.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.683425	6.235563e-12	***	8.592574e-12	***
SlopeC	-0.2077702	0.7875161		0.9533712	
MeanF-MeanC	-1.481705	0.0009480829	***	0.01196248	*
SlopeF-SlopeC	-1.472132	0.2076405		0.9999488	



8.5.19 Vitvi19g01715: Type3.F

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

Vitvi19g01715

34.12

transport.metal

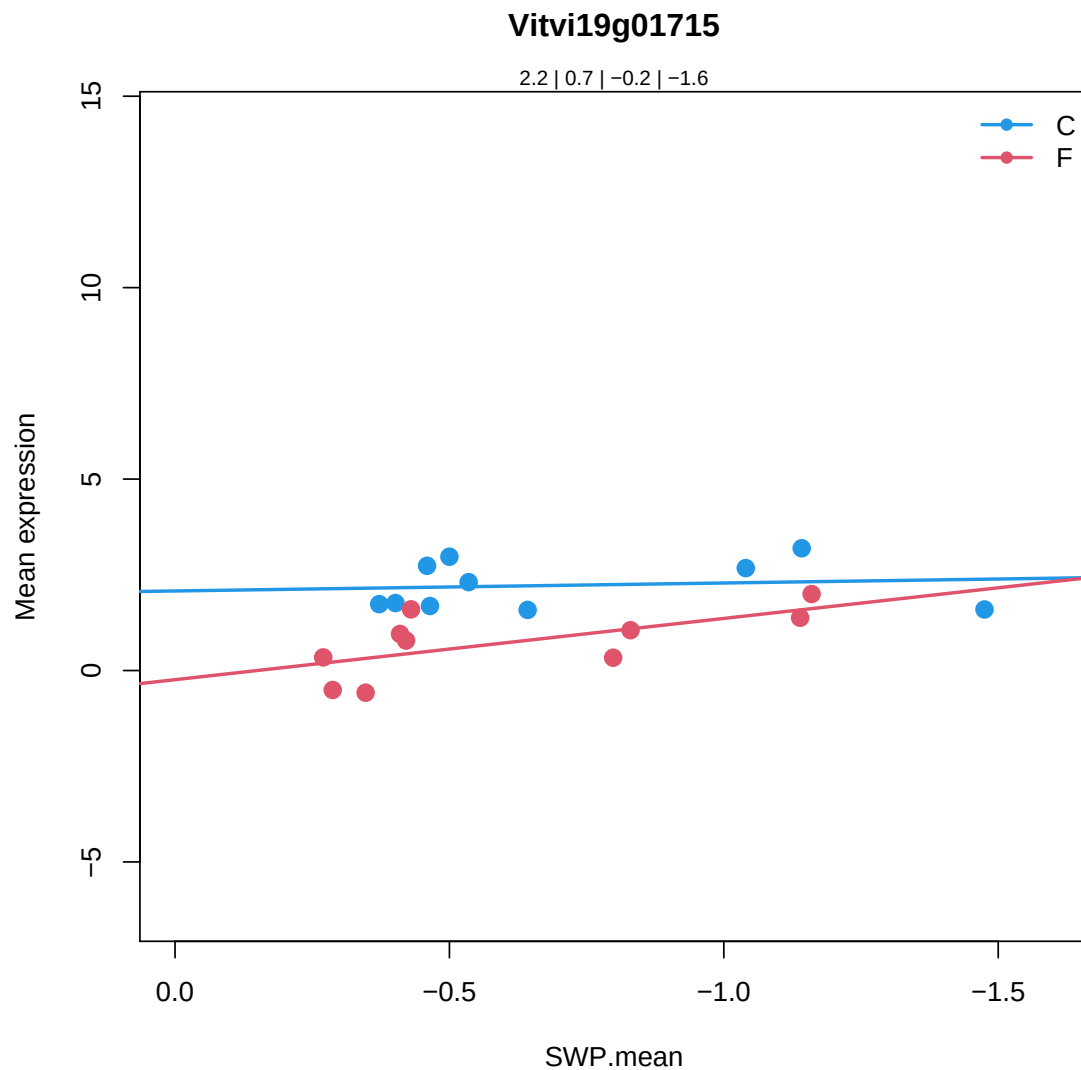
Cation efflux family protein |

Chr1:5579300-5580585 FORWARD LENGTH=315 |

201606

Coefficients for Vitvi19g01715.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.224069	2.212116e-10	***	2.855685e-10	***
SlopeC	-0.2082918	0.7113119		0.9350571	
MeanF-MeanC	-1.488937	2.947183e-05	***	0.0006389896	***
SlopeF-SlopeC	-1.391626	0.1067773		0.9999488	



8.5.20 Vitvi12g00574: + Type3.F

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

Vitvi12g00574

16.1.5

secondary metabolism.isoprenoids.terpenoids

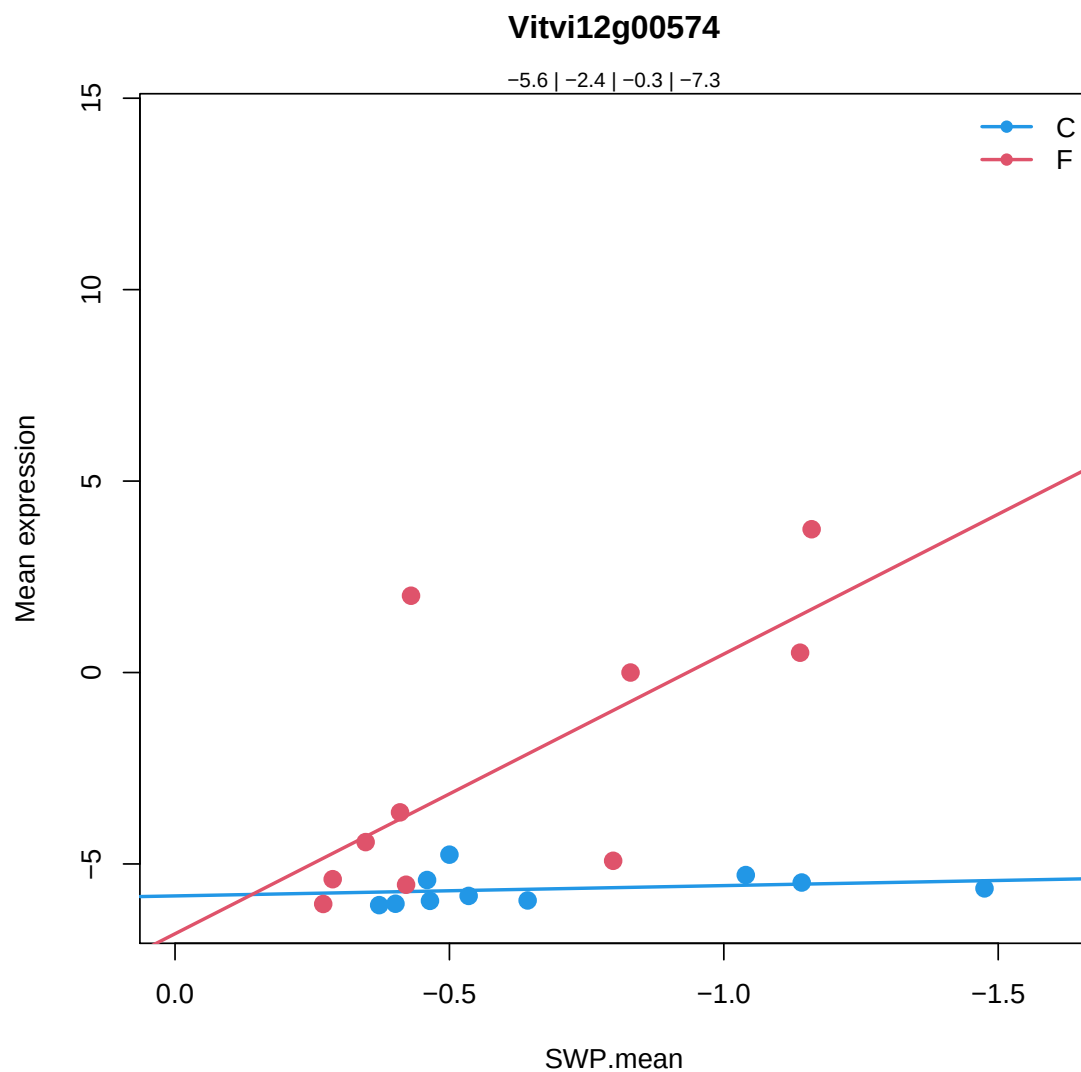
terpene synthase-like sequence-1%2C8-cineole |

Chr3:9447545-9450316 FORWARD LENGTH=600 |

201606

Coefficients for Vitvi12g00574.

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



8.5.21 Vitvi01g01284: Type3.F

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

Vitvi01g01284

26.2

misc.UDP glucosyl and glucoronyl transferases

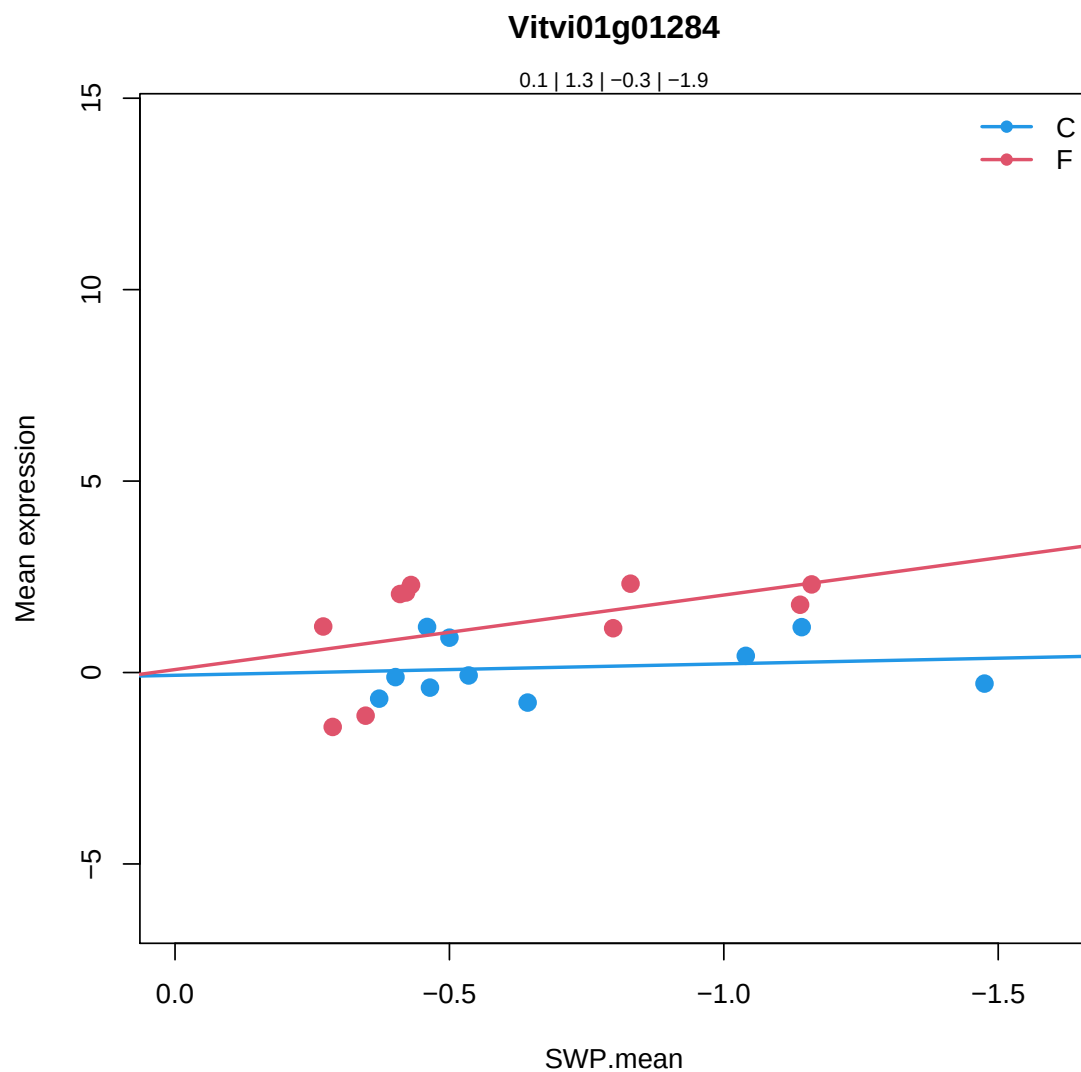
UDP-Glycosyltransferase superfamily protein |

Chr3:7867806-7870053 FORWARD LENGTH=461 |

201606

Coefficients for Vitvi01g01284.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1370866	0.6571859		0.6620507	
SlopeC	-0.297883	0.7286342		0.9401373	
MeanF-MeanC	1.125667	0.01607415	*	0.1069411	
SlopeF-SlopeC	-1.648302	0.2051119		0.9999488	



8.5.22 Vitvi19g02155: Type3.F

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

Vitvi19g02155

26.10

misc.cytochrome P450

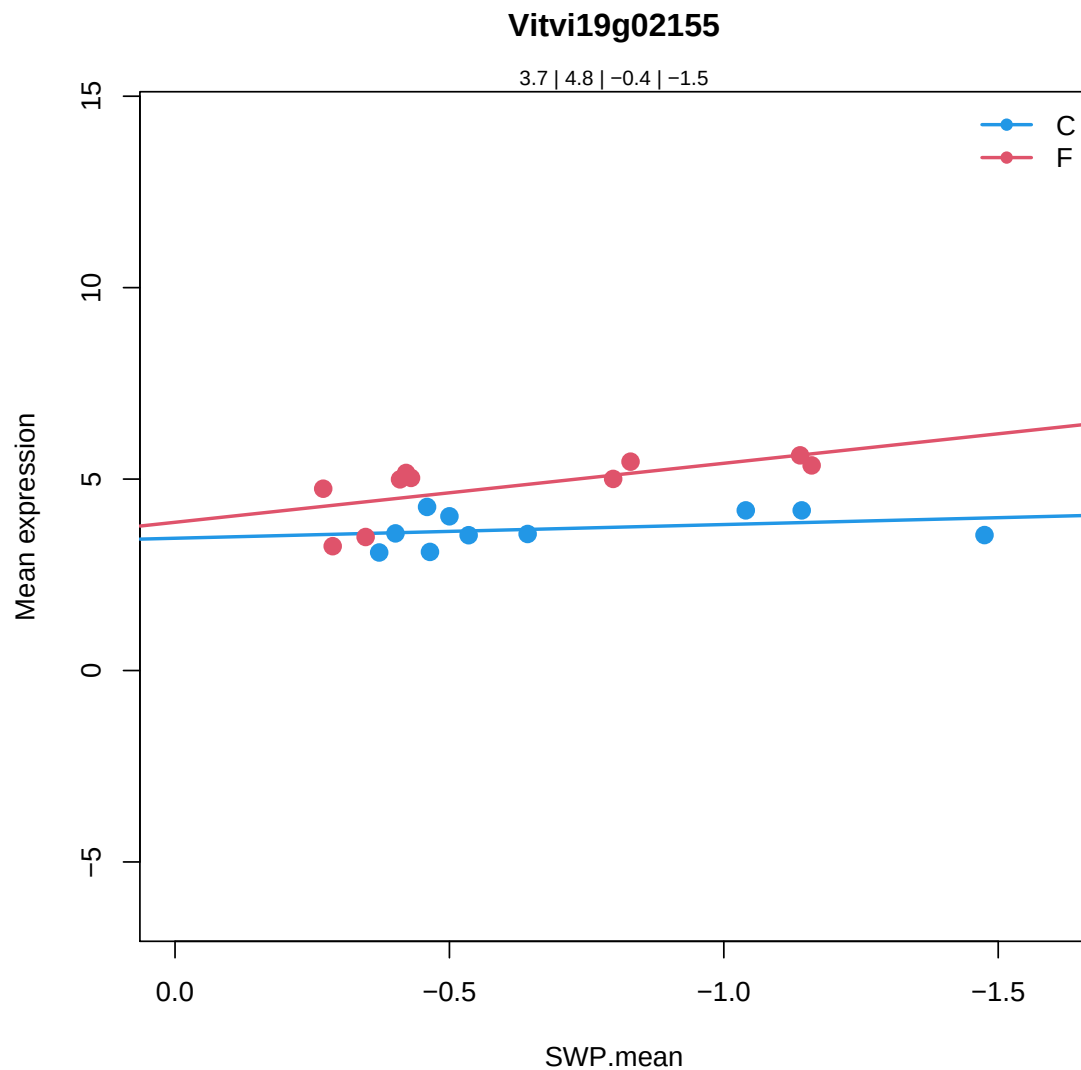
cytochrome P450%2C family 72%2C subfamily A%2C polypeptide 15 |

Chr3:4937410-4939310 FORWARD LENGTH=512 |

201606

Coefficients for Vitvi19g02155.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.70633	3.792541e-16	***	7.527791e-16	***
SlopeC	-0.3578616	0.4561085		0.8579805	
MeanF-MeanC	1.103896	0.0001455722	***	0.002468088	**
SlopeF-SlopeC	-1.183277	0.1062559		0.9999488	



8.5.23 Vitvi18g02446: Type3.F

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

Vitvi18g02446

16.1.5

secondary metabolism.isoprenoids.terpenoids

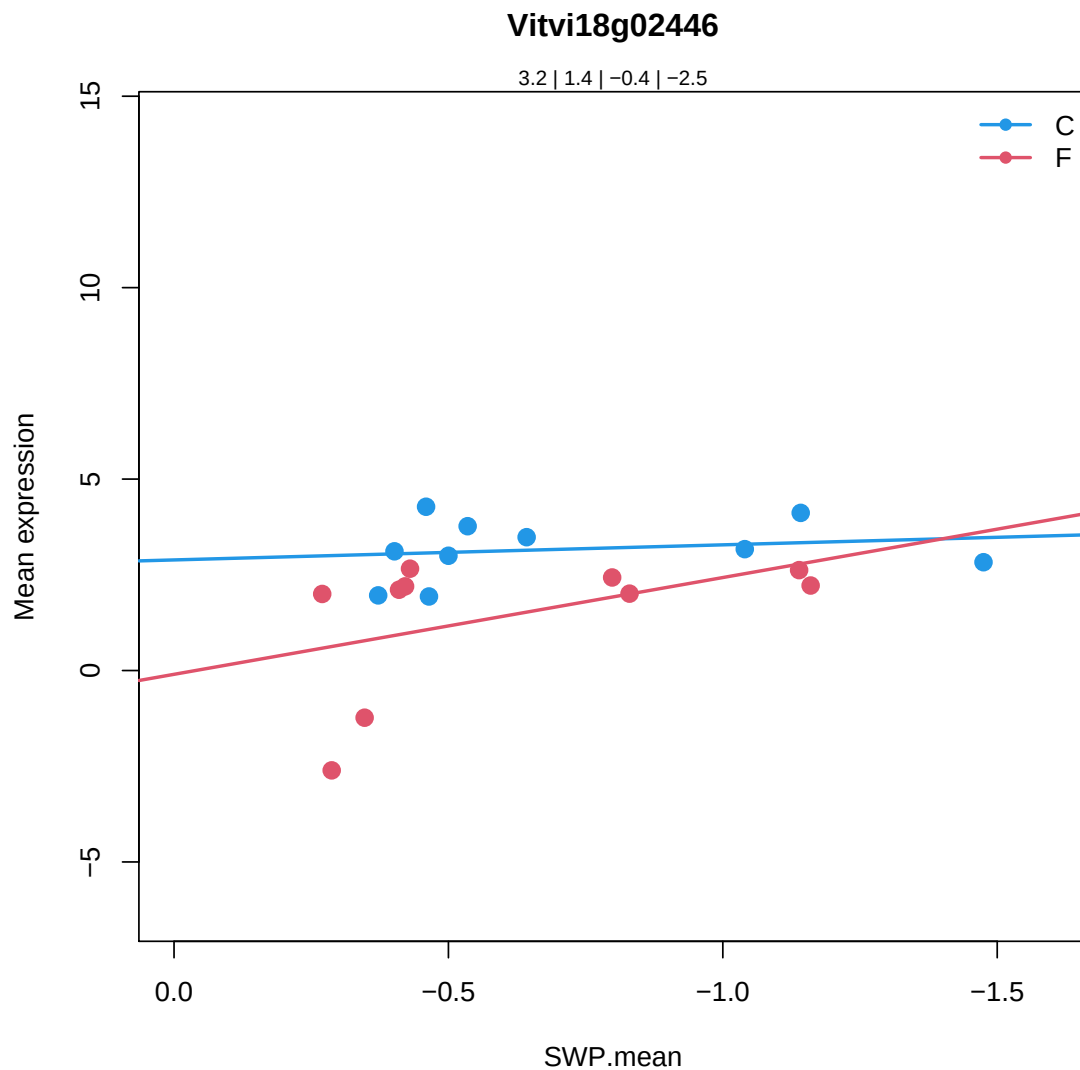
terpene synthase 21 |

Chr5:8092969-8095128 FORWARD LENGTH=547 |

201606

Coefficients for Vitvi18g02446.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.165086	2.576314e-08	***	3.106413e-08	***
SlopeC	-0.3940815	0.7071927		0.9346979	
MeanF-MeanC	-1.724404	0.003528654	**	0.03482595	*
SlopeF-SlopeC	-2.13365	0.1803668		0.9999488	



8.5.24 Vitvi09g00303: Type3.F

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

Vitvi09g00303

34.16

transport.ABC transporters and multidrug resistance systems

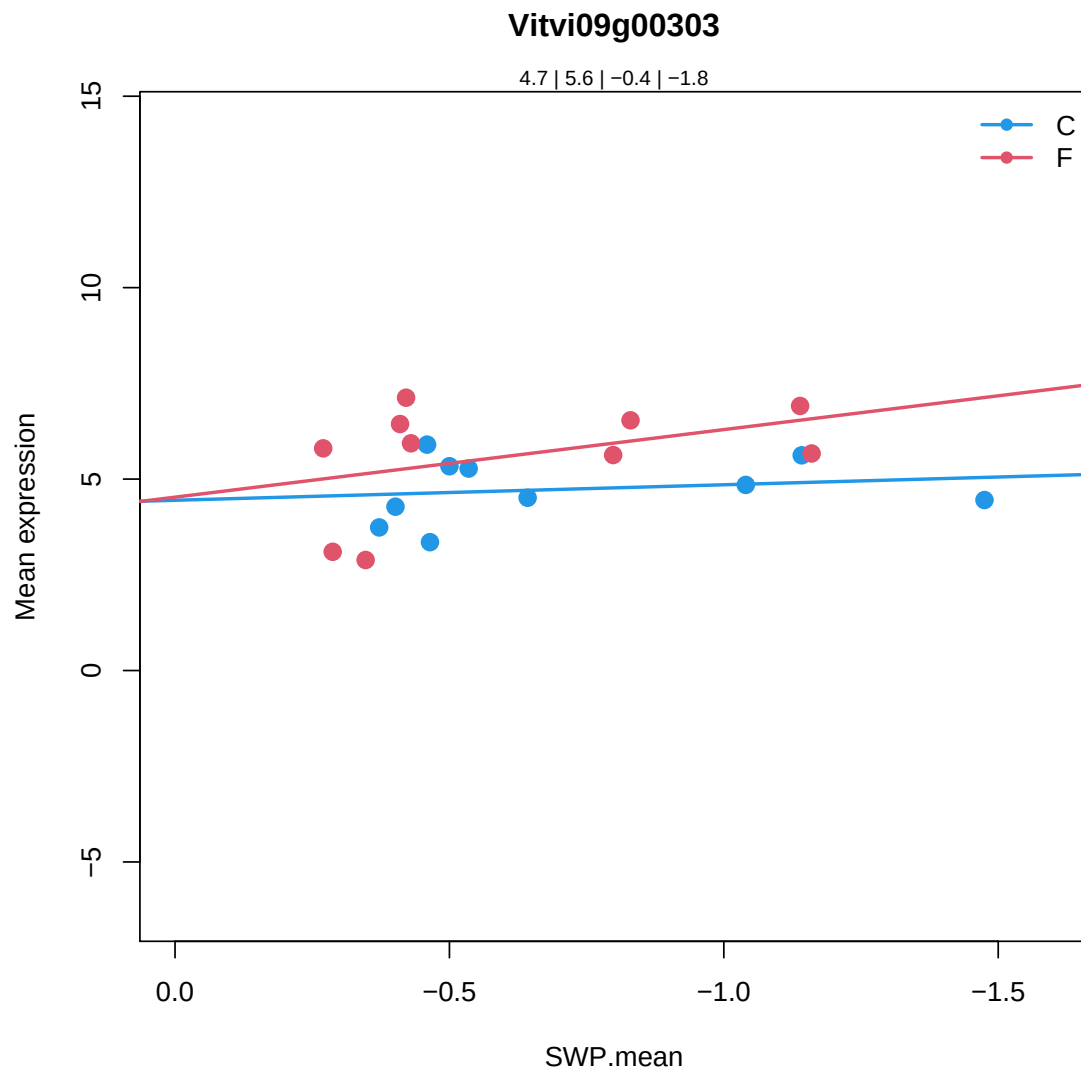
pleiotropic drug resistance 1 |

Chr3:5539897-5546263 FORWARD LENGTH=1411 |

201606

Coefficients for Vitvi09g00303.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.73112	1.740727e-12	***	2.463068e-12	***
SlopeC	-0.4047651	0.6628311		0.9225525	
MeanF-MeanC	0.8715695	0.07479004	.	0.3078422	
SlopeF-SlopeC	-1.360039	0.3293618		0.9999488	



8.5.25 Vitvi01g01021: Type3.F

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

Vitvi01g01021

27.1.19

RNA.processing.ribonucleases

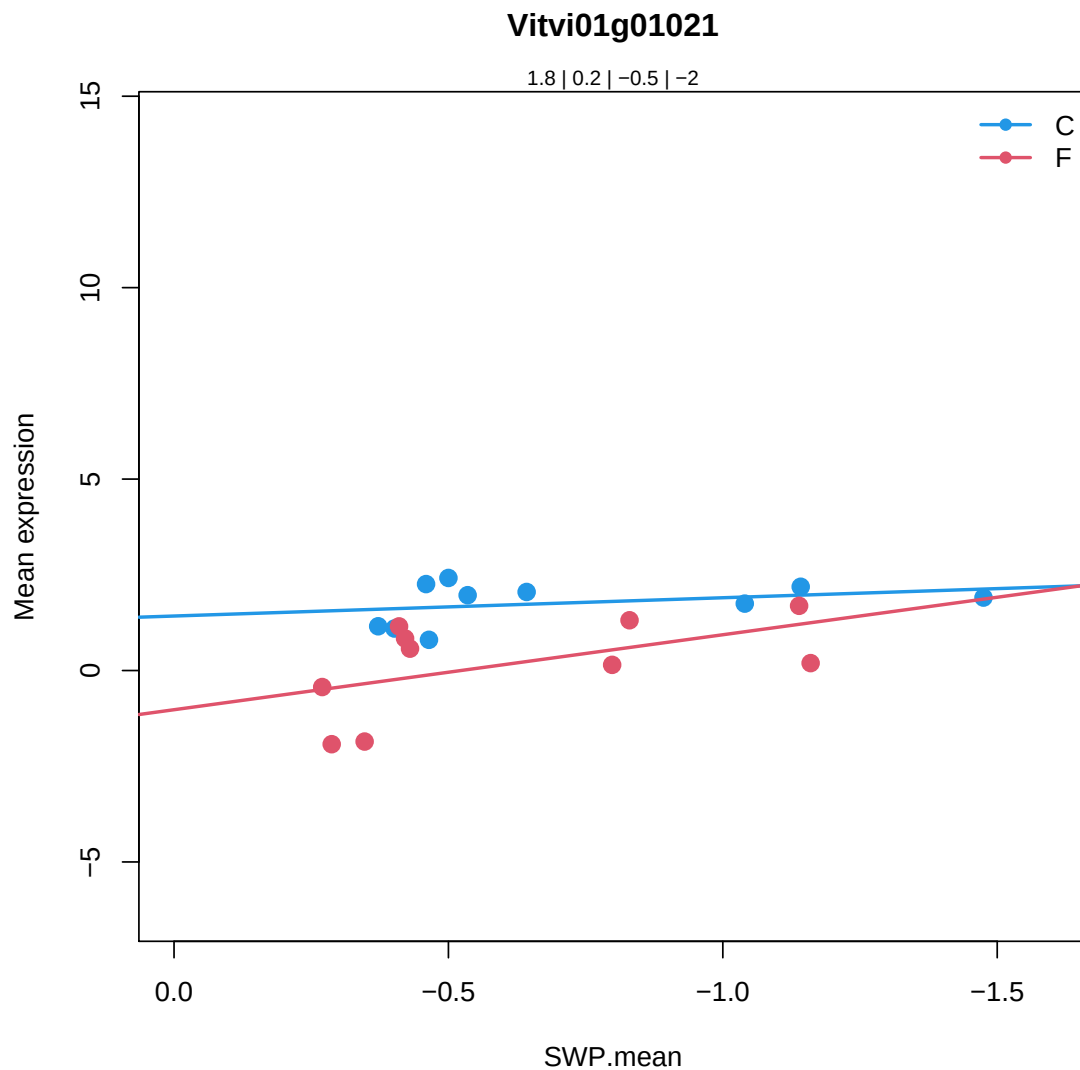
ribonuclease 1 |

Chr2:873714-874667 FORWARD LENGTH=230 |

201606

Coefficients for Vitvi01g01021.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.758743	6.402902e-07	***	7.427737e-07	***
SlopeC	-0.477187	0.5048389		0.8706312	
MeanF-MeanC	-1.589466	0.0002147614	***	0.003456592	**
SlopeF-SlopeC	-1.48126	0.1715283		0.9999488	



8.6 Type5

8.6.1 Vitvi03g00325: * Type5

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

Vitvi03g00325

27.3.25

RNA.regulation of transcription.MYB domain transcription factor family

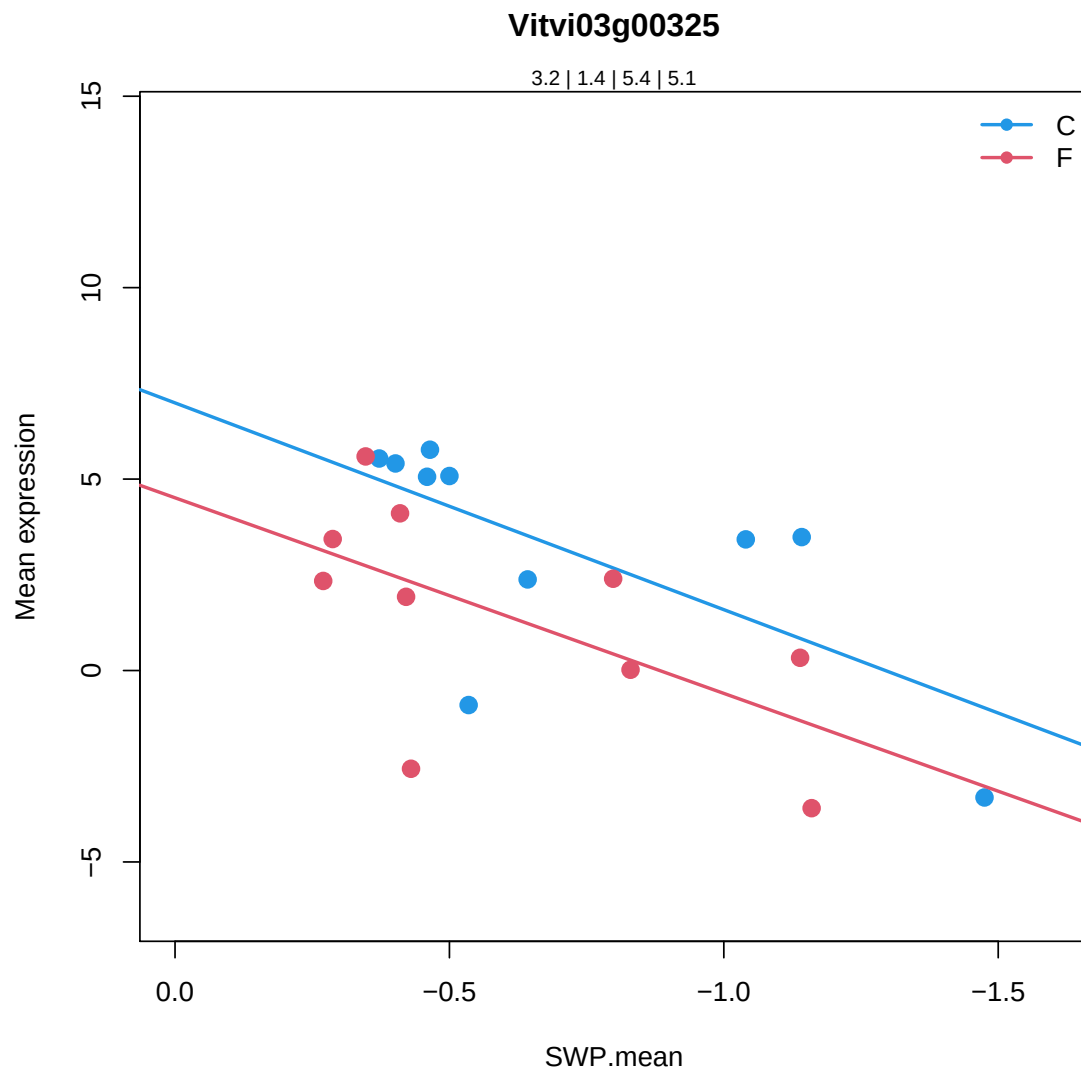
RAD-like 1 |

Chr4:18271457-18271857 REVERSE LENGTH=100 |

201606

Coefficients for Vitvi03g00325.

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



8.6.2 Vitvi17g00601: * Type5

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

Vitvi17g00601

17.6.3

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

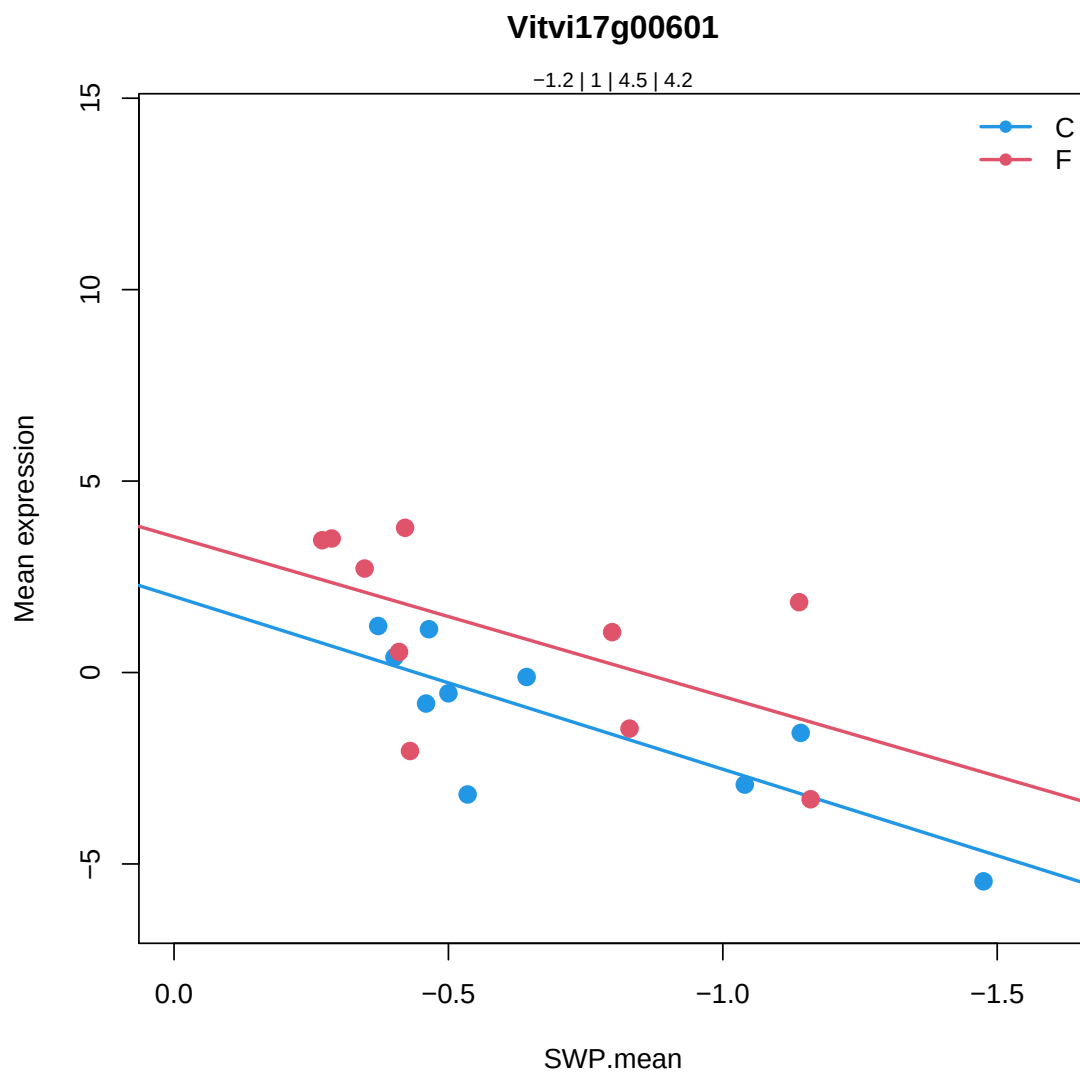
Gibberellin-regulated family protein |

Chr1:28053378-28053893 FORWARD LENGTH=101 |

201606

Coefficients for Vitvi17g00601.

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



8.6.3 Vitvi05g01577: * Type5

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

Vitvi05g01577

20.1.7.3

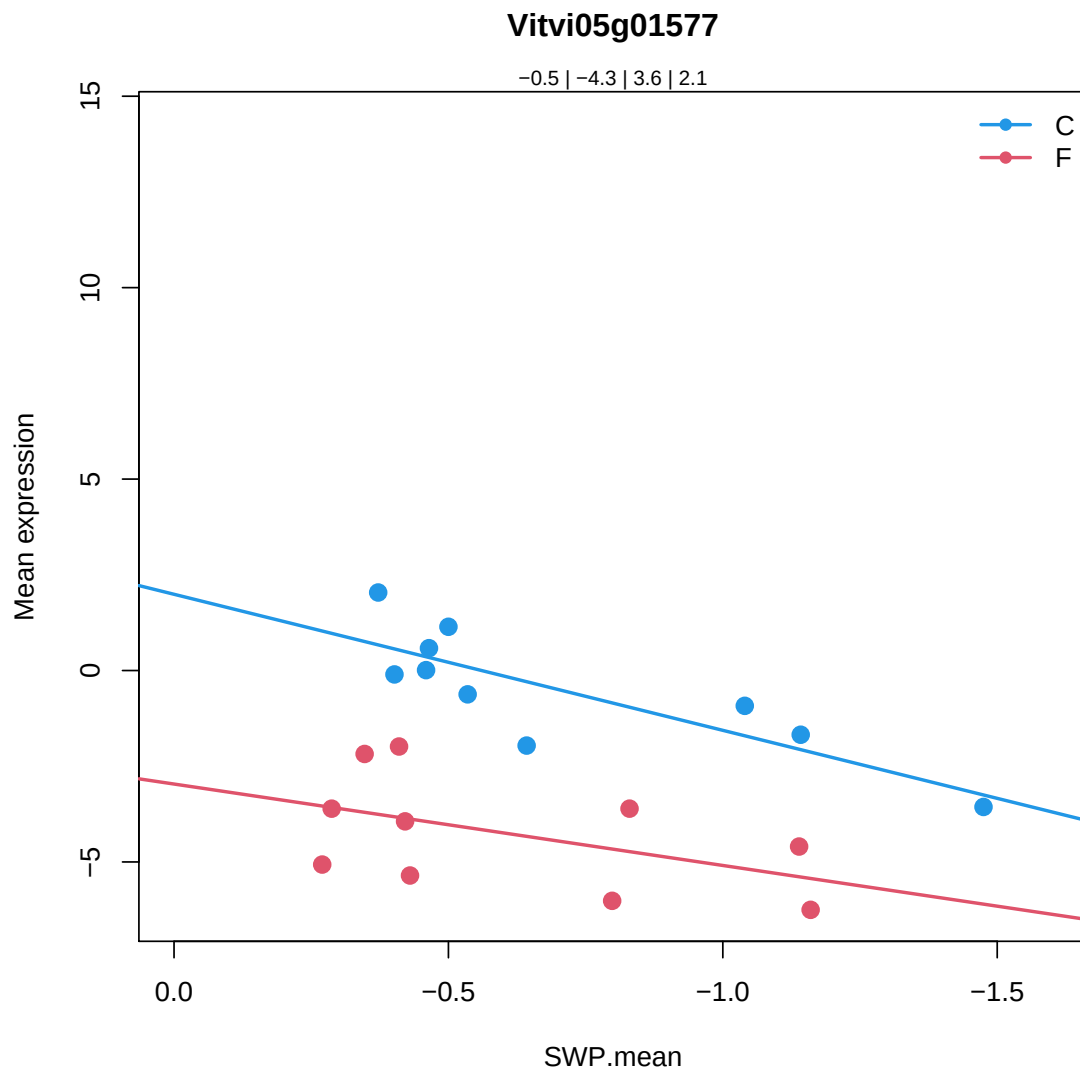
stress.biotic.PR-proteins.PR3/4/8/11 (chitinases and chitin binding pr
homolog of carrot EP3-3 chitinase |

Chr3:20145935-20147034 FORWARD LENGTH=273 |

201606

Coefficients for Vitvi05g01577.

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



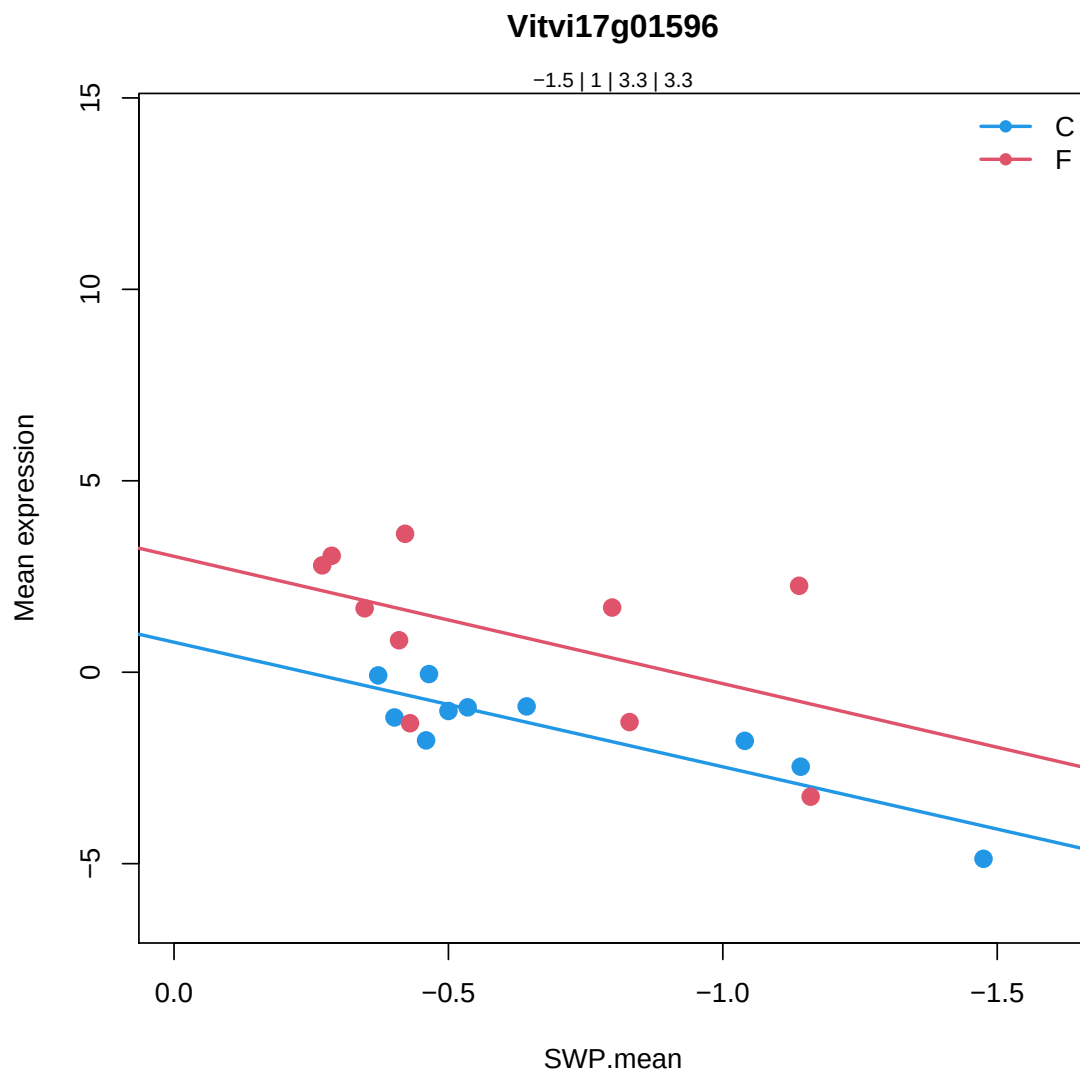
8.6.4 Vitvi17g01596: * Type5

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

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

Coefficients for Vitvi17g01596.

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



8.6.5 Vitvi07g00445: Type5

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

Vitvi07g00445

11.1.9

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

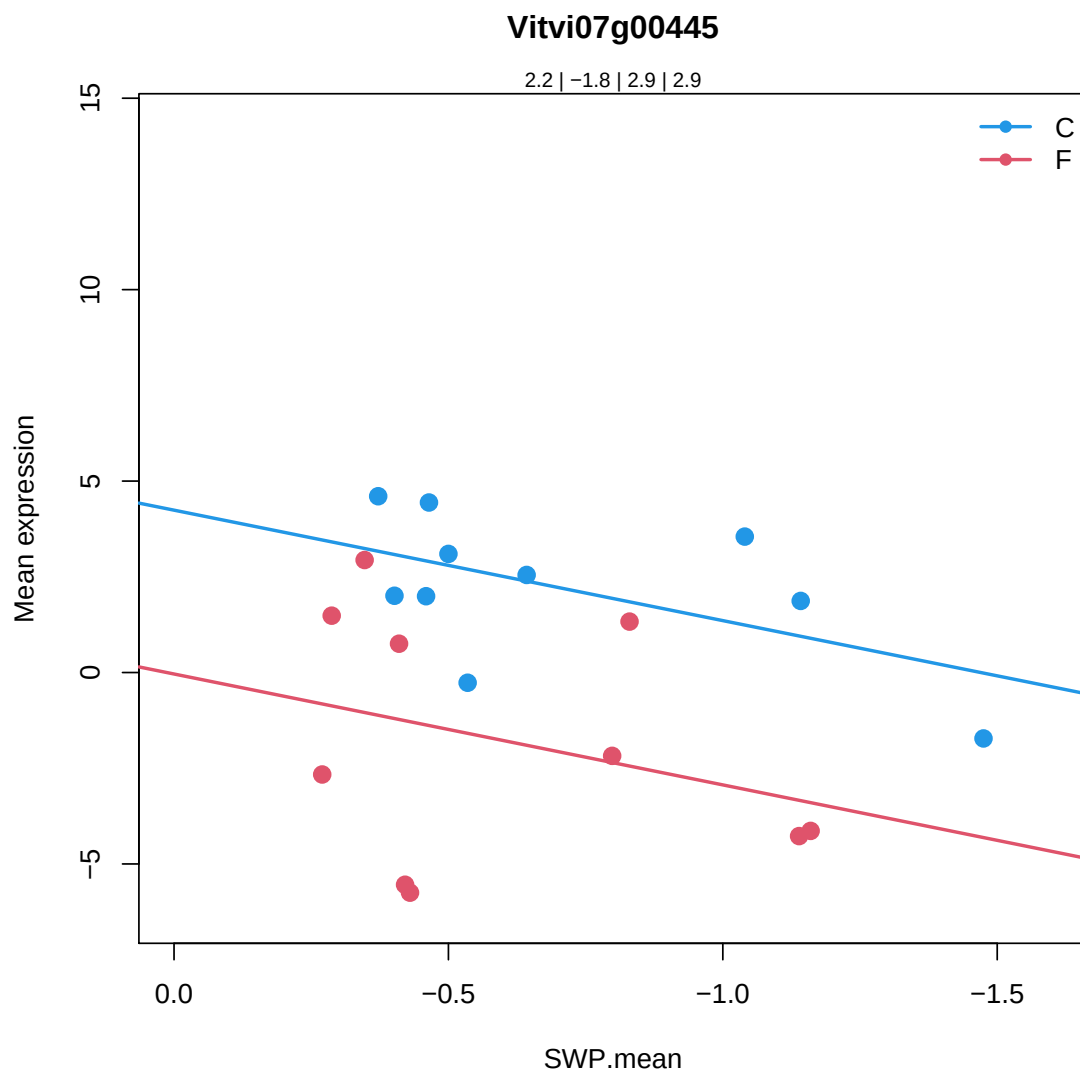
AMP-dependent synthetase and ligase family protein |

Chr2:19393835-19397616 FORWARD LENGTH=660 |

201606

Coefficients for Vitvi07g00445.

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



8.6.6 Vitvi07g00586: * Type5

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

Vitvi07g00586

29.5.4

protein.degradation.aspartate protease

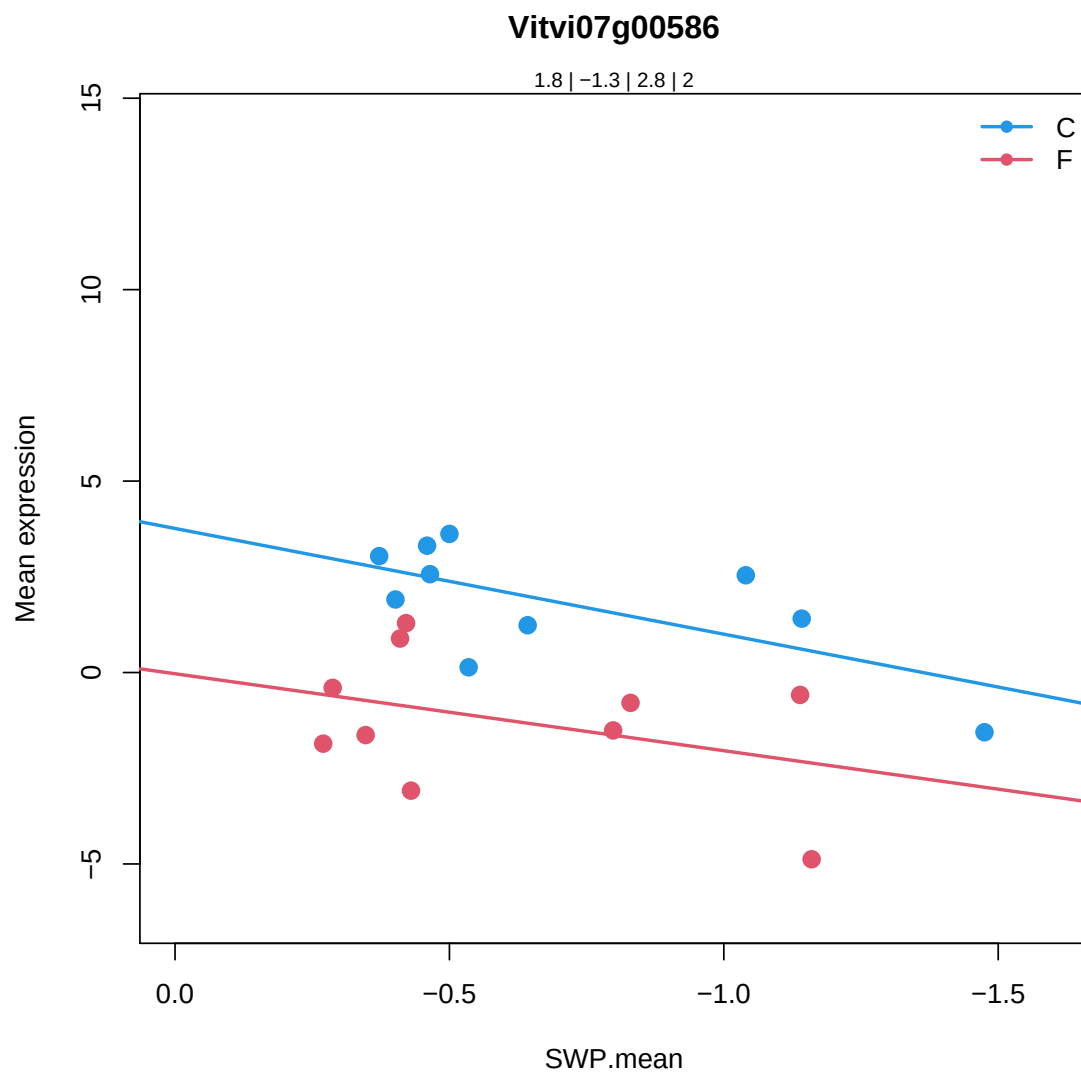
Eukaryotic aspartyl protease family protein |

Chr2:966506-967891 REVERSE LENGTH=461 |

201606

Coefficients for Vitvi07g00586.

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



8.6.7 Vitvi15g00714: Type5

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

Vitvi15g00714

26.21

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

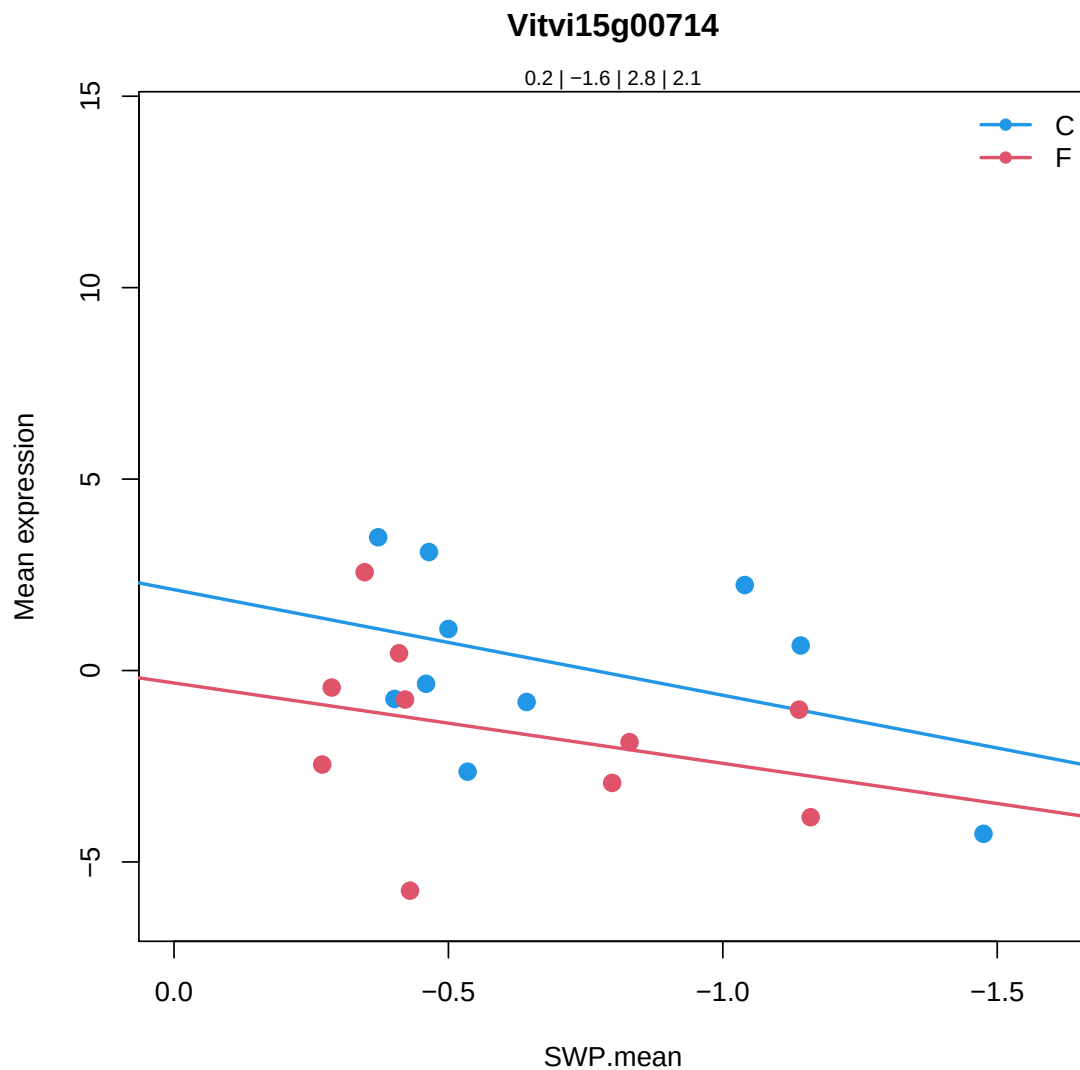
Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin

Chr4:69433-69819 REVERSE LENGTH=128 |

201606

Coefficients for Vitvi15g00714.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1724214	0.7927213		0.7967463	
SlopeC	2.757195	0.1407973		0.6676582	
MeanF-MeanC	-1.777328	0.06572122	.	0.2846357	
SlopeF-SlopeC	-0.6577505	0.8086901		0.9999488	



8.6.8 Vitvi01g00593: * Type5

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

Vitvi01g00593

10.6.3

cell wall.degradation.pectate lyases and polygalacturonases

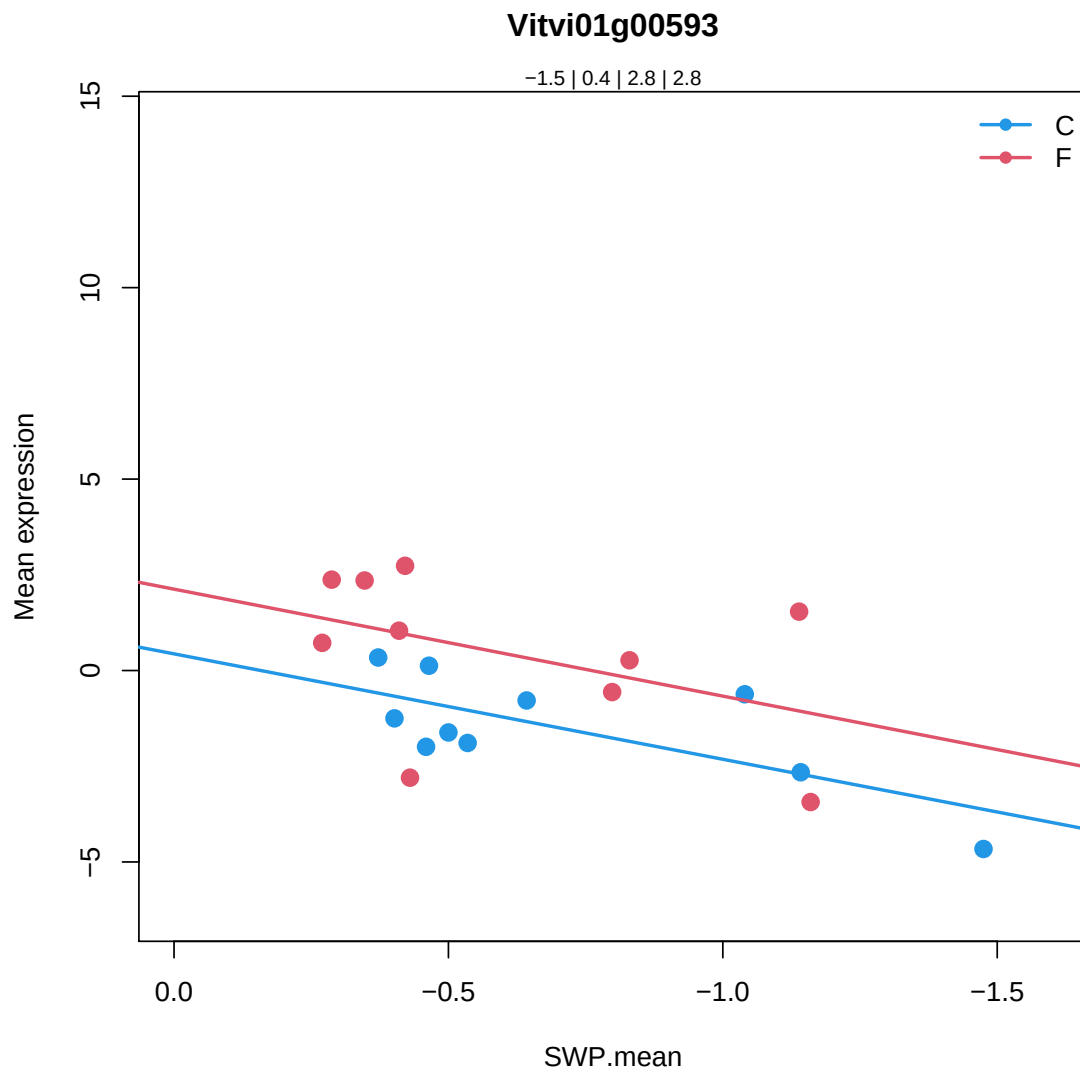
Pectate lyase family protein |

Chr1:25401660-25403165 FORWARD LENGTH=408 |

201606

Coefficients for Vitvi01g00593.

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



8.6.9 Vitvi18g02709: * Type5

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

Vitvi18g02709

35.1.40

not assigned.no ontology.glycine rich proteins

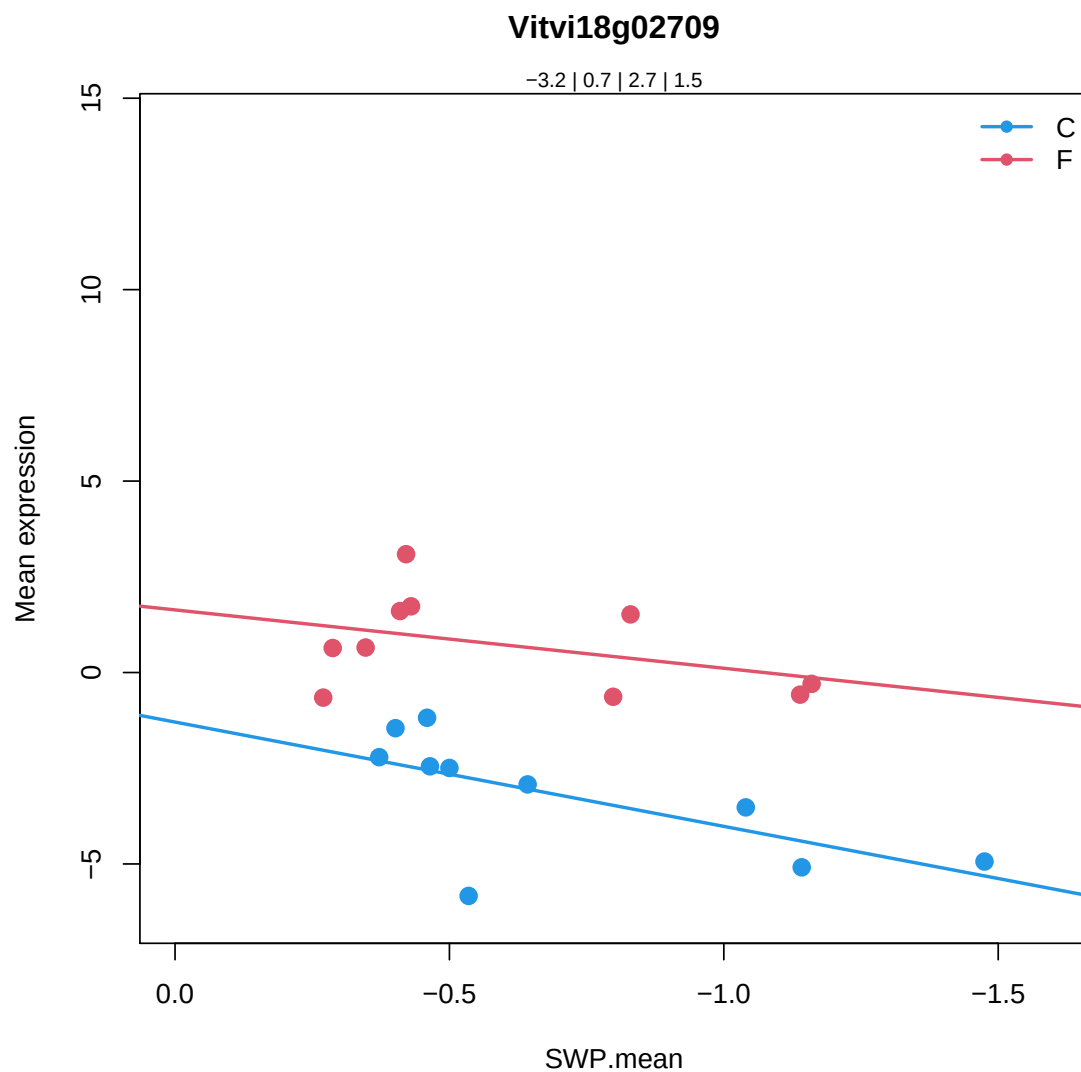
Cupredoxin superfamily protein |

Chr2:6873666-6874701 REVERSE LENGTH=257 |

201606

Coefficients for Vitvi18g02709.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-3.209467	8.027118e-09	***	9.824888e-09	***
SlopeC	2.724042	0.01110047	*	0.3143947	
MeanF-MeanC	3.91652	9.423432e-08	***	3.871481e-06	***
SlopeF-SlopeC	-1.199916	0.4198128		0.9999488	



8.6.10 Vitvi03g00318: * Type5

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

Vitvi03g00318

27.3.25

RNA.regulation of transcription.MYB domain transcription factor family

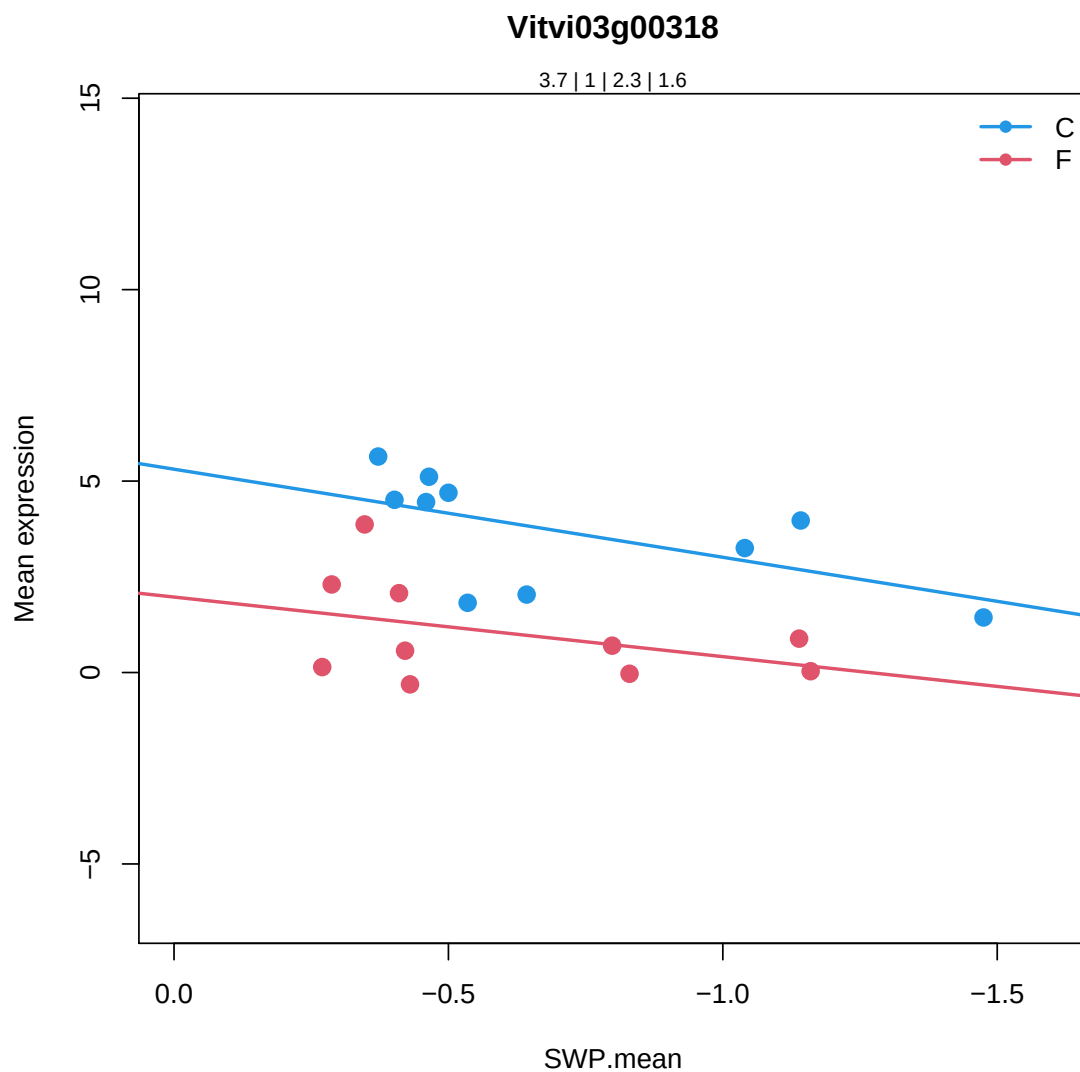
RAD-like 6 |

Chr1:28245073-28245453 REVERSE LENGTH=126 |

201606

Coefficients for Vitvi03g00318.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.692558	8.664173e-10	***	1.094475e-09	***
SlopeC	2.300824	0.03059091	*	0.4321285	
MeanF-MeanC	-2.669643	2.876014e-05	***	0.0006253381	***
SlopeF-SlopeC	-0.7449947	0.6196467		0.9999488	



8.6.11 Vitvi05g00094: Type5

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

Vitvi05g00094

20.1.7.3

stress.biotic.PR-proteins.PR3/4/8/11 (chitinases and chitin binding pr

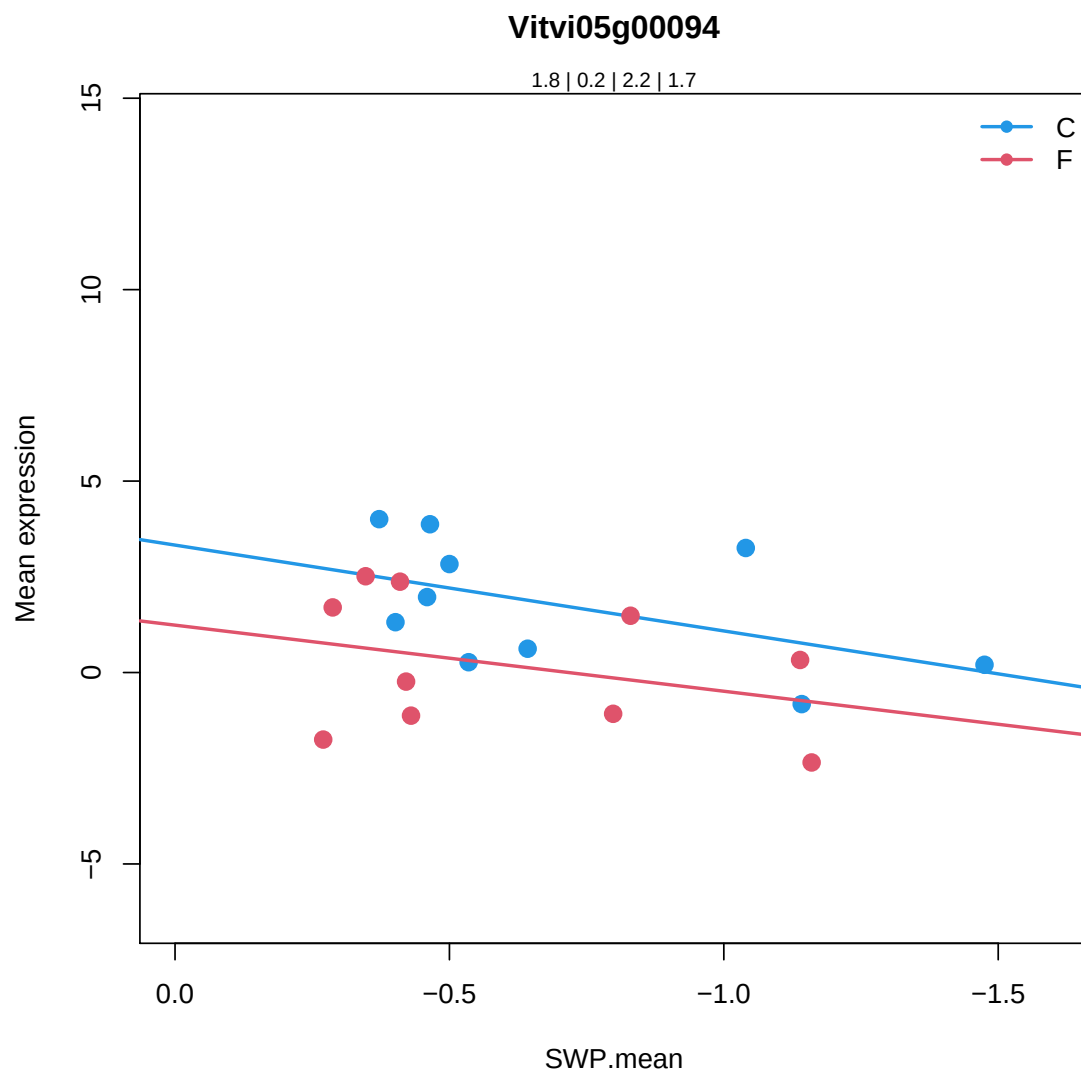
Chitinase family protein |

Chr1:1766833-1768117 REVERSE LENGTH=321 |

201606

Coefficients for Vitvi05g00094.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.75152	0.0009882148	***	0.001070151	**
SlopeC	2.242017	0.09374752	.	0.6028633	
MeanF-MeanC	-1.566073	0.02500179	*	0.1486222	
SlopeF-SlopeC	-0.5159695	0.7888473		0.9999488	



8.6.12 Vitvi07g00665: Type5

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

Vitvi07g00665

10.2.1

cell wall.cellulose synthesis.cellulose synthase

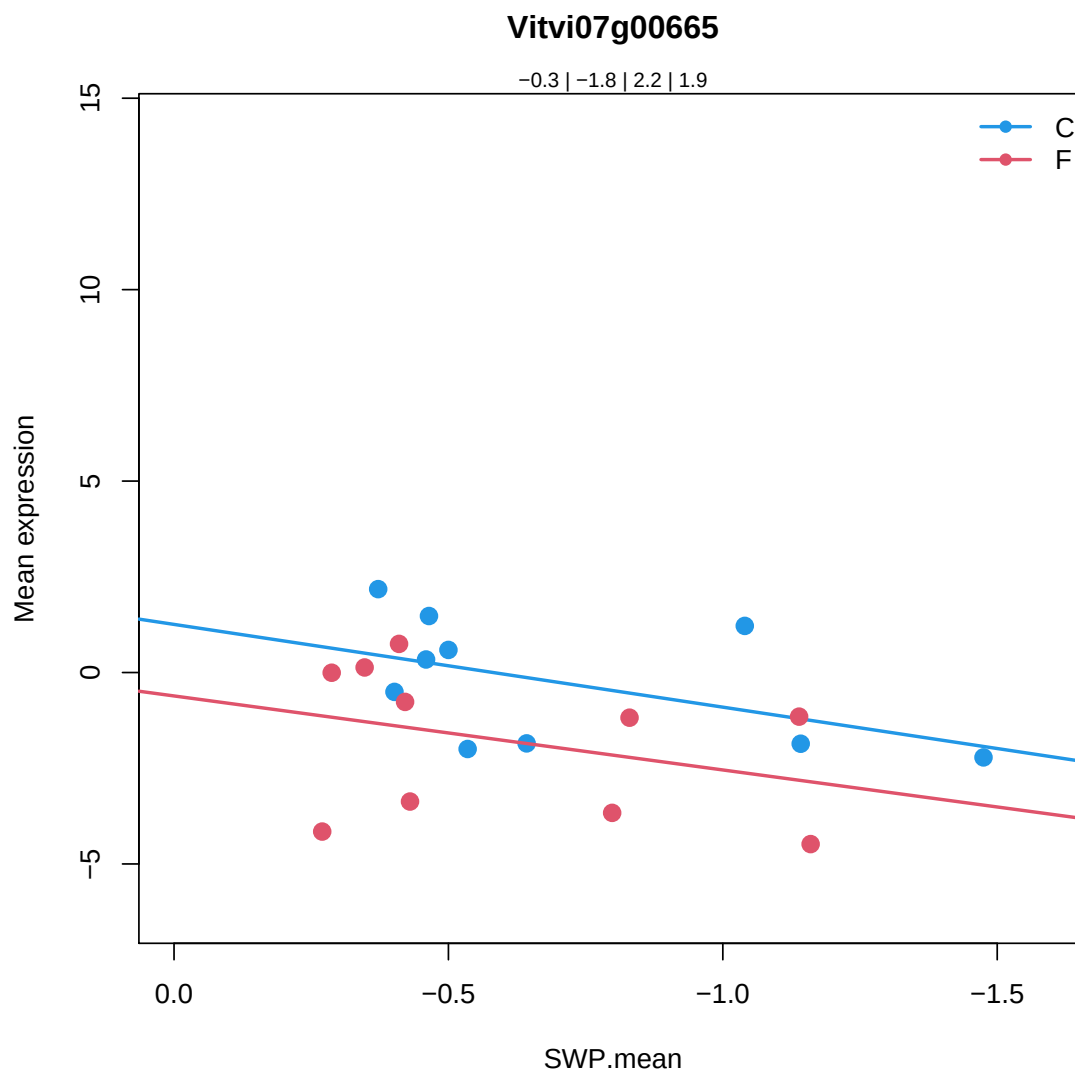
cellulose synthase A4 |

Chr5:17714713-17719564 FORWARD LENGTH=1078 |

201606

Coefficients for Vitvi07g00665.

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



8.6.13 Vitvi16g02137: * Type5

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

Vitvi16g02137

35.2

not assigned.unknown

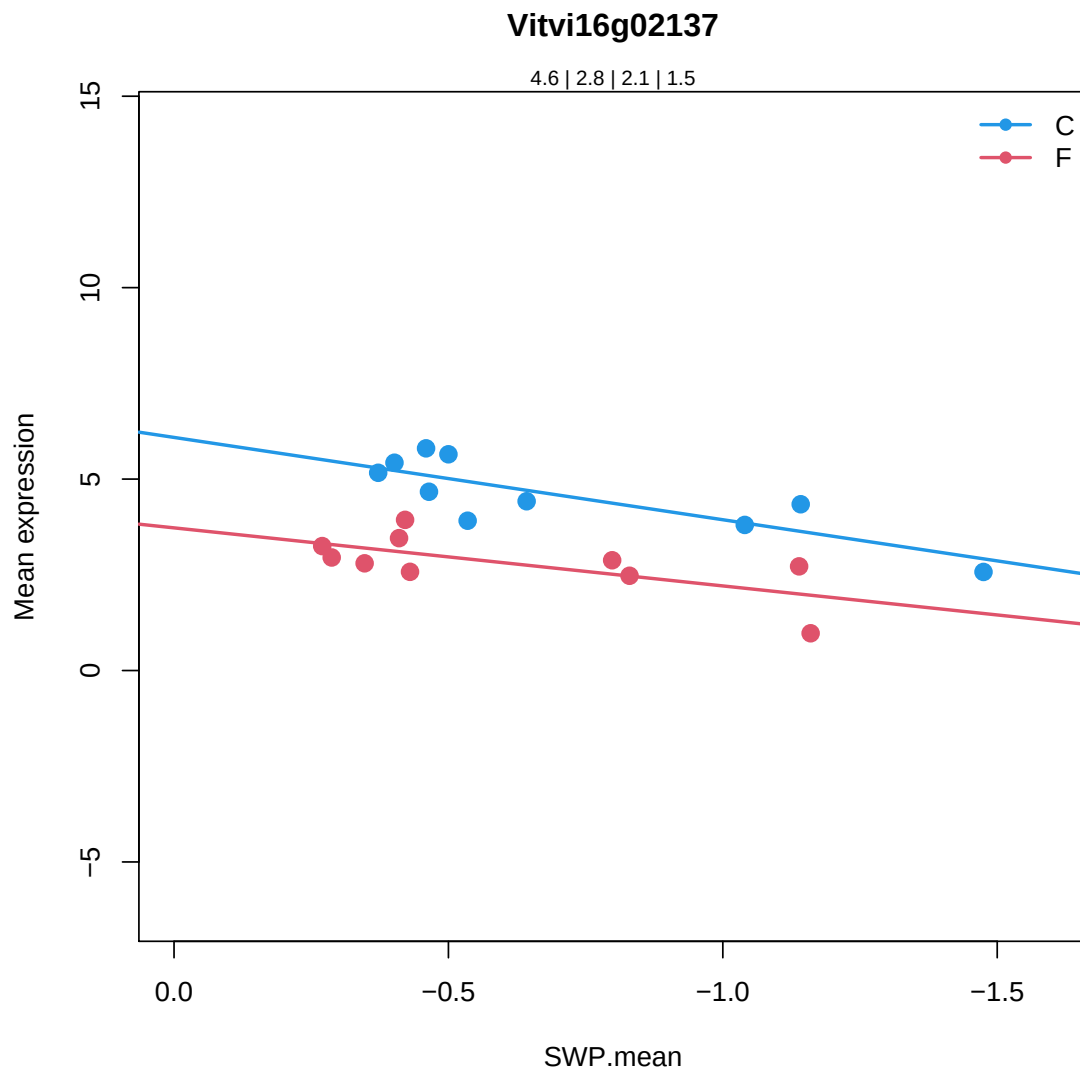
PR5-like receptor kinase |

Chr5:15293325-15295838 REVERSE LENGTH=665 |

201606

Coefficients for Vitvi16g02137.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.576307	2.446722e-17	***	5.954484e-17	***
SlopeC	2.149758	0.0003725907	***	0.09467692	.
MeanF-MeanC	-1.774357	8.117334e-07	***	2.701199e-05	***
SlopeF-SlopeC	-0.6336356	0.4129181		0.9999488	



8.6.14 Vitvi03g01503: Type5

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

Vitvi03g01503

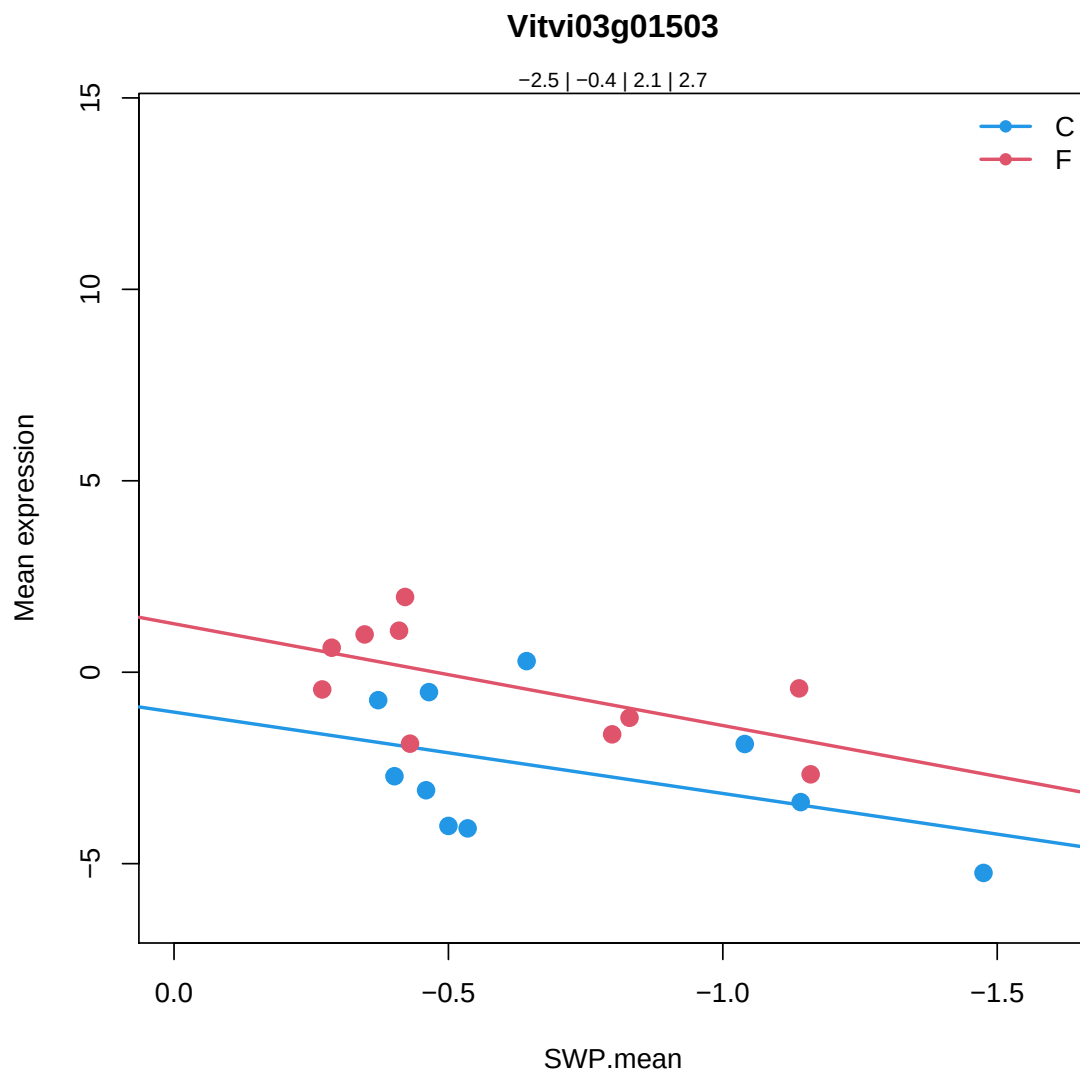
35.2

not assigned.unknown

Organ-specific protein S2

Coefficients for Vitvi03g01503.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-2.536121	4.151528e-06	***	4.725735e-06	***
SlopeC	2.124611	0.07938146	.	0.5748584	
MeanF-MeanC	2.181984	0.00122855	**	0.01484977	*
SlopeF-SlopeC	0.5331686	0.7591512		0.9999488	



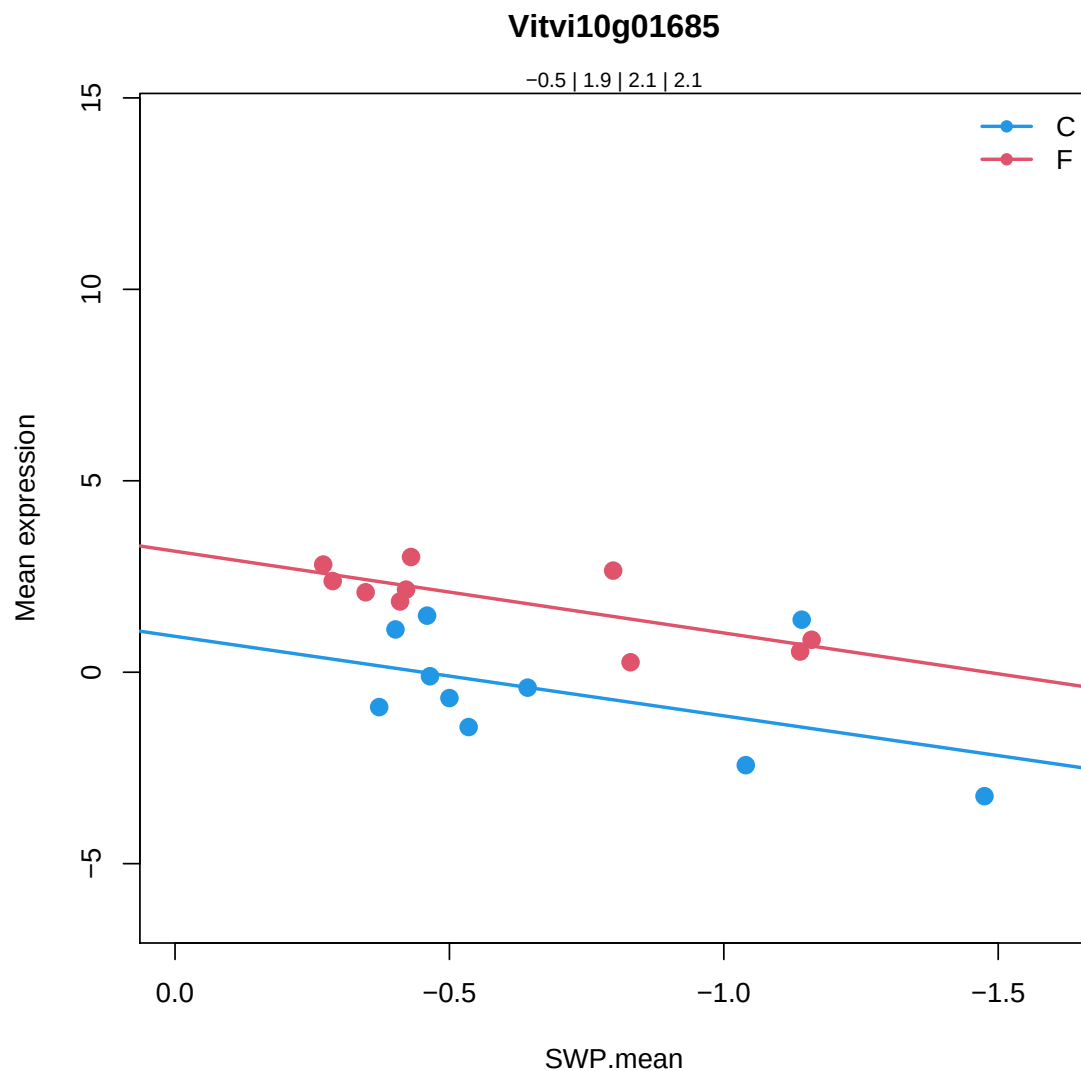
8.6.15 Vitvi10g01685: * Type5

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

```
Vitvi10g01685
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi10g01685.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.5224823	0.1171482		0.1209328	
SlopeC	2.076279	0.02951921	*	0.4299803	
MeanF-MeanC	2.382122	3.023132e-05	***	0.0006517479	***
SlopeF-SlopeC	0.05856843	0.9651568		0.9999488	



8.6.16 Vitvi11g00726: Type5

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

Vitvi11g00726

10.2.1

cell wall.cellulose synthesis.cellulose synthase

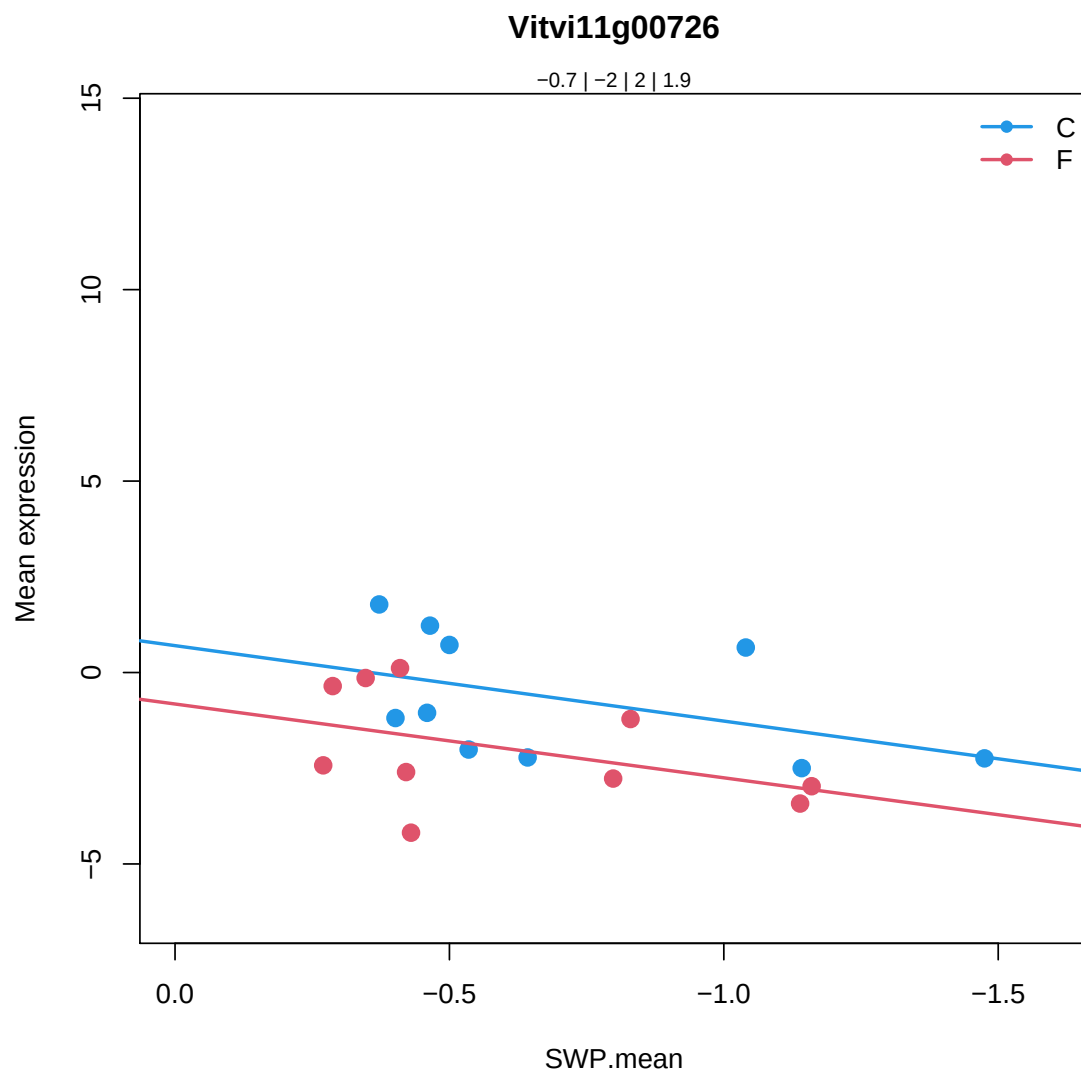
Cellulose synthase family protein |

Chr5:5736859-5741407 REVERSE LENGTH=1026 |

201606

Coefficients for Vitvi11g00726.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.6836656	0.1103692		0.114012	
SlopeC	1.970264	0.0988823	.	0.6110181	
MeanF-MeanC	-1.313174	0.03419632	*	0.1847644	
SlopeF-SlopeC	-0.04289516	0.9801009		0.9999488	



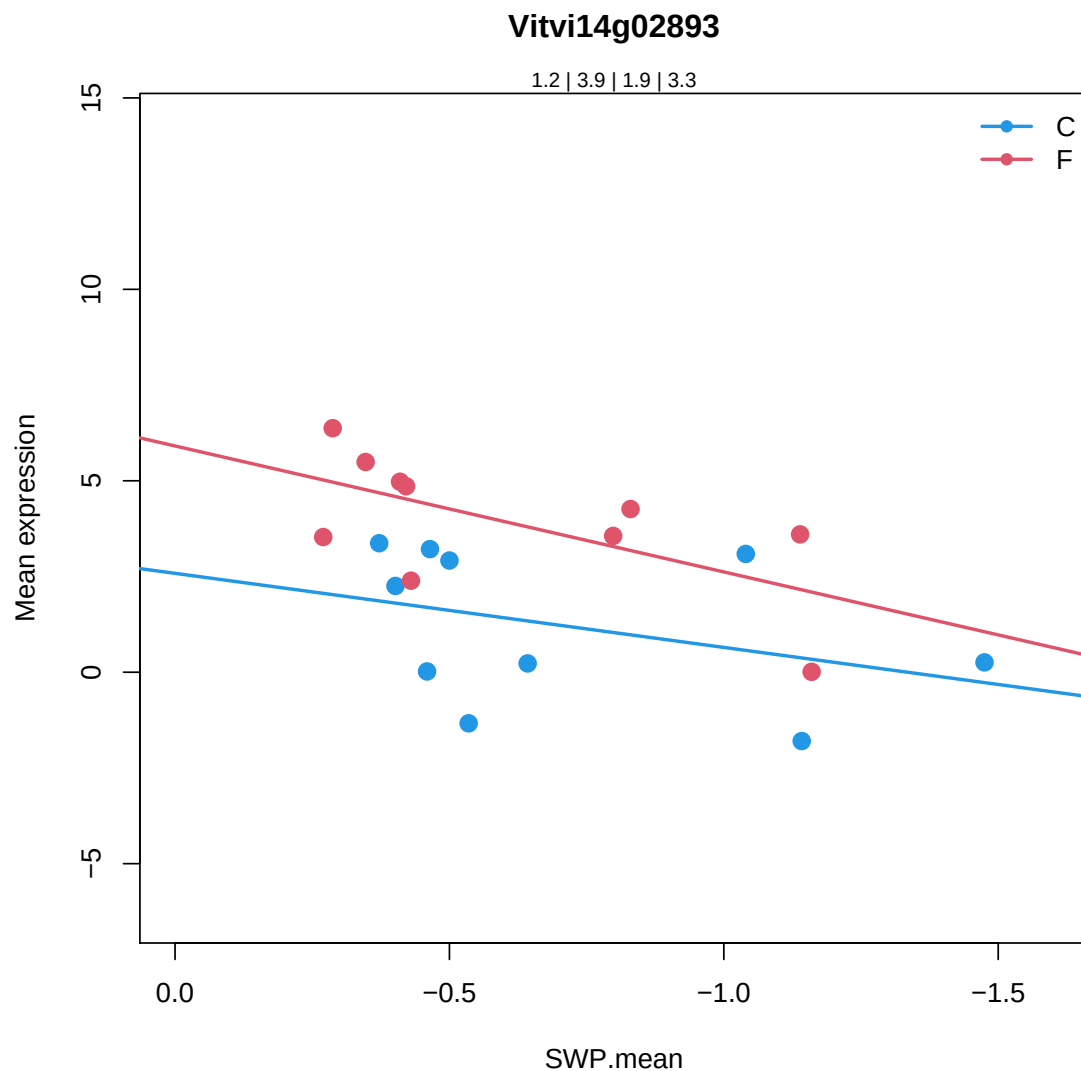
8.6.17 Vitvi14g02893: Type5

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

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

Coefficients for Vitvi14g02893.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.221987	0.017794	*	0.01873169	*
SlopeC	1.934911	0.1585324		0.6889929	
MeanF-MeanC	2.683206	0.0006505913	***	0.008798857	**
SlopeF-SlopeC	1.355003	0.4992098		0.9999488	



8.6.18 Vitvi01g00784: Type5

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

Vitvi01g00784

10.7

cell wall.modification

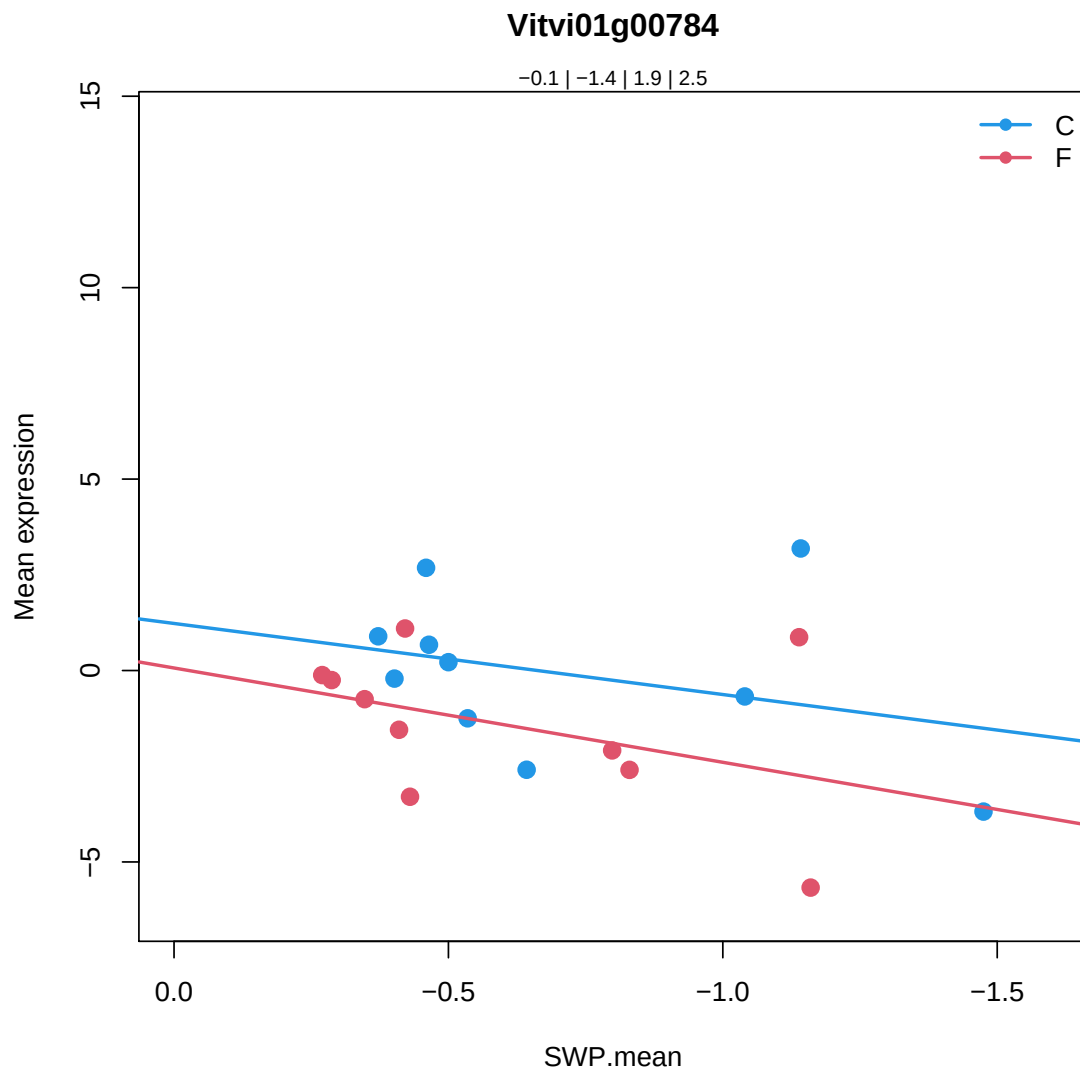
xyloglucan:xyloglucosyl transferase 33 |

Chr1:3479257-3480957 REVERSE LENGTH=310 |

201606

Coefficients for Vitvi01g00784.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.07603549	0.8952843		0.89764	
SlopeC	1.85592	0.2554205		0.7656086	
MeanF-MeanC	-1.358668	0.1069009		0.3801643	
SlopeF-SlopeC	0.6076206	0.7995979		0.9999488	



8.6.19 Vitvi18g01019: Type5

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

```
Vitvi18g01019
```

```
17.4.1
```

```
hormone metabolism.cytokinin.synthesis-degradation
```

```
cytokinin oxidase 5 |
```

```
Chr1:28315248-28318064 REVERSE LENGTH=540 |
```

```
201606
```

```
Vitvi18g01019
```

```
35.2
```

```
not assigned.unknown
```

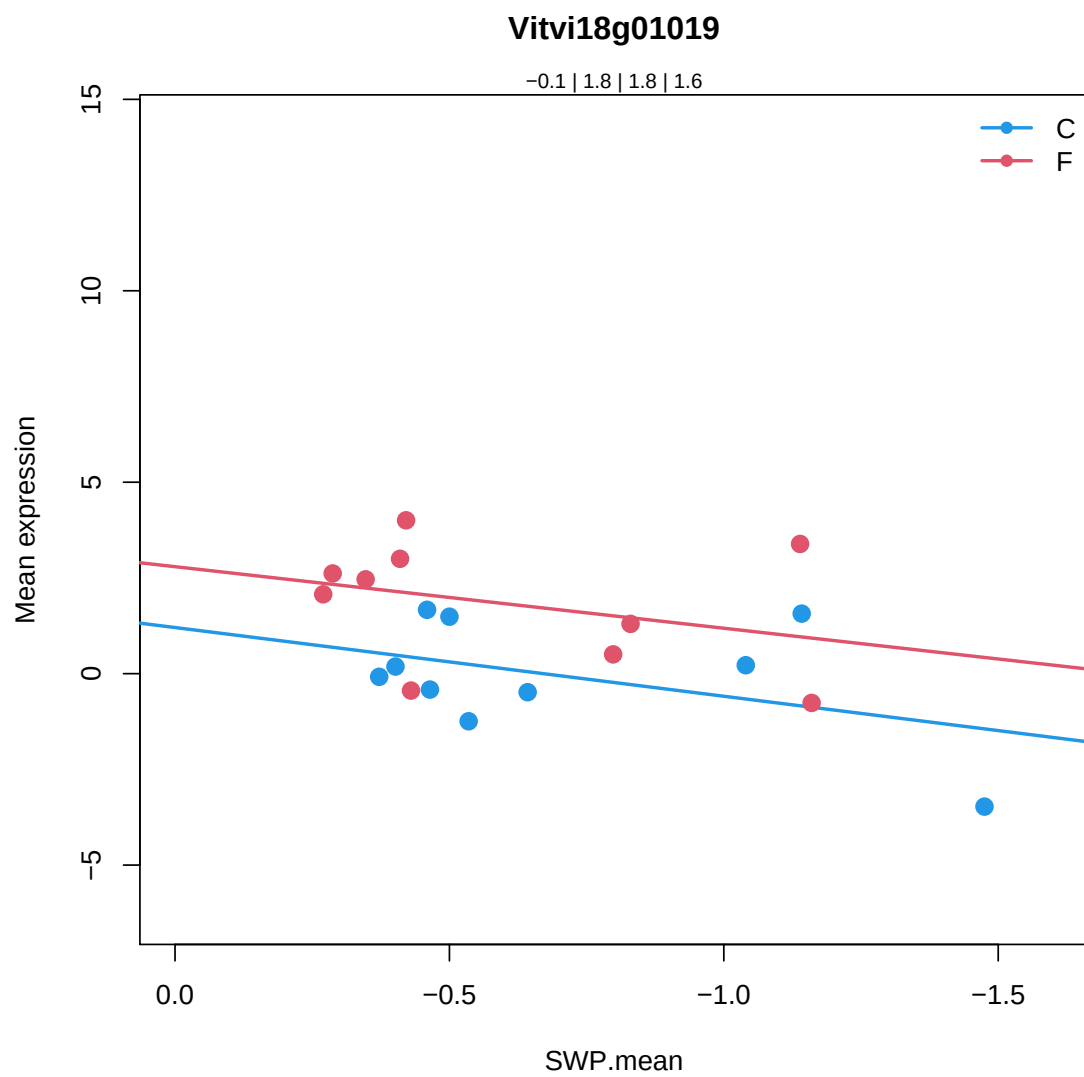
```
cytokinin oxidase 5 |
```

```
Chr1:28315248-28318064 REVERSE LENGTH=540 |
```

```
201606
```

Coefficients for Vitvi18g01019.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.05724541	0.8950899		0.8975041	
SlopeC	1.79425	0.1473439		0.6736918	
MeanF-MeanC	1.871392	0.005526883	**	0.04935017	*
SlopeF-SlopeC	-0.1871561	0.9170727		0.9999488	



8.6.20 Vitvi04g00644: * Type5

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

Vitvi04g00644

27.3.99

RNA.regulation of transcription.unclassified

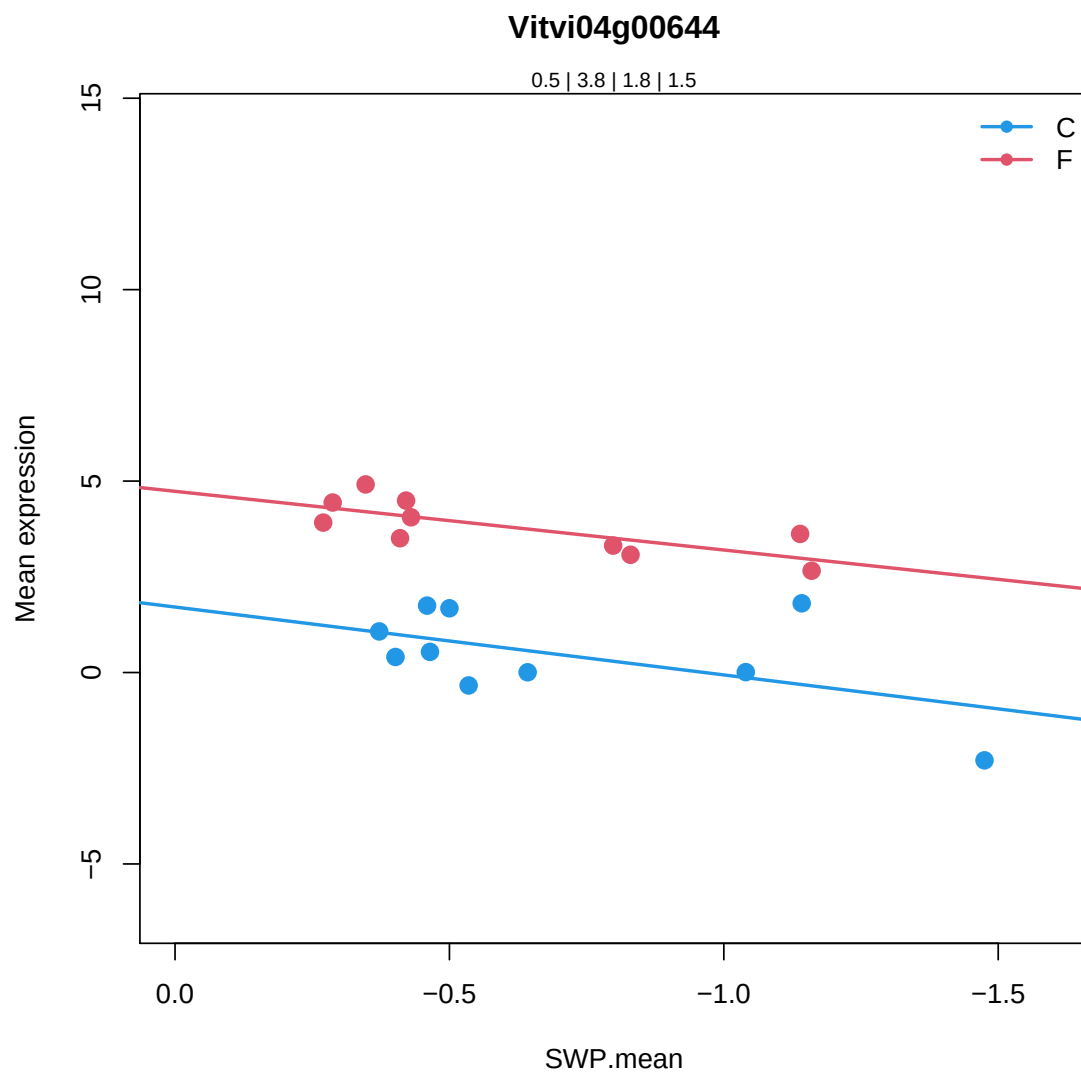
Eukaryotic aspartyl protease family protein |

Chr5:3403331-3405331 REVERSE LENGTH=474 |

201606

Coefficients for Vitvi04g00644.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.4634607	0.07445566	.	0.07723768	.
SlopeC	1.773287	0.01733481	*	0.3551322	
MeanF-MeanC	3.335309	3.590415e-09	***	1.887073e-07	***
SlopeF-SlopeC	-0.240009	0.8168131		0.9999488	



8.6.21 Vitvi16g01118: * Type5

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

Vitvi16g01118

31.1

cell.organisation

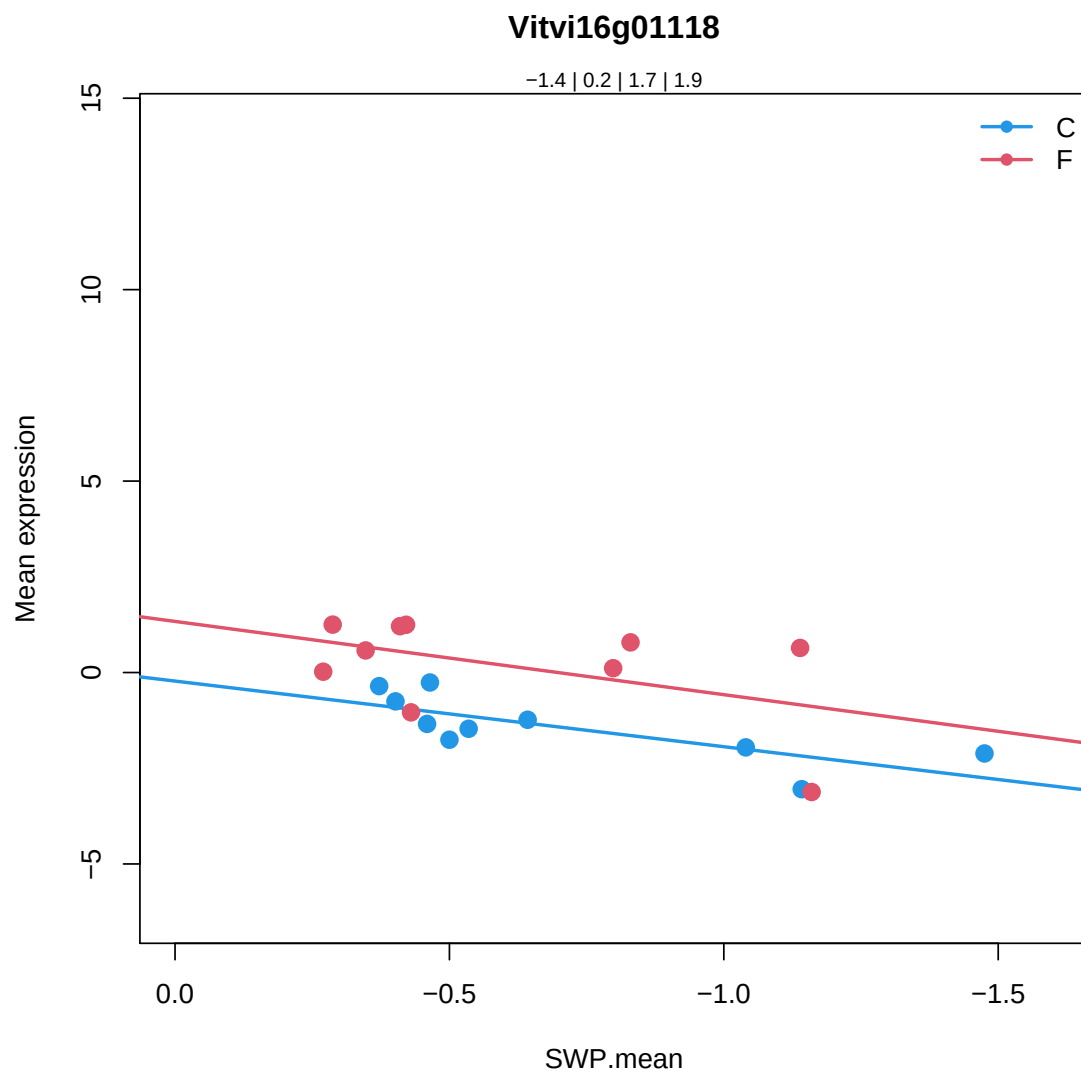
cysteine-rich RECEPTOR-like kinase |

Chr4:12129485-12133157 FORWARD LENGTH=1043 |

201606

Coefficients for Vitvi16g01118.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.428624	4.13253e-05	***	4.599681e-05	***
SlopeC	1.71423	0.03784566	*	0.4650681	
MeanF-MeanC	1.597388	0.0005472244	***	0.007561917	**
SlopeF-SlopeC	0.1988921	0.8646378		0.9999488	



8.6.22 Vitvi13g01760: Type5

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

Vitvi13g01760

35.2

not assigned.unknown

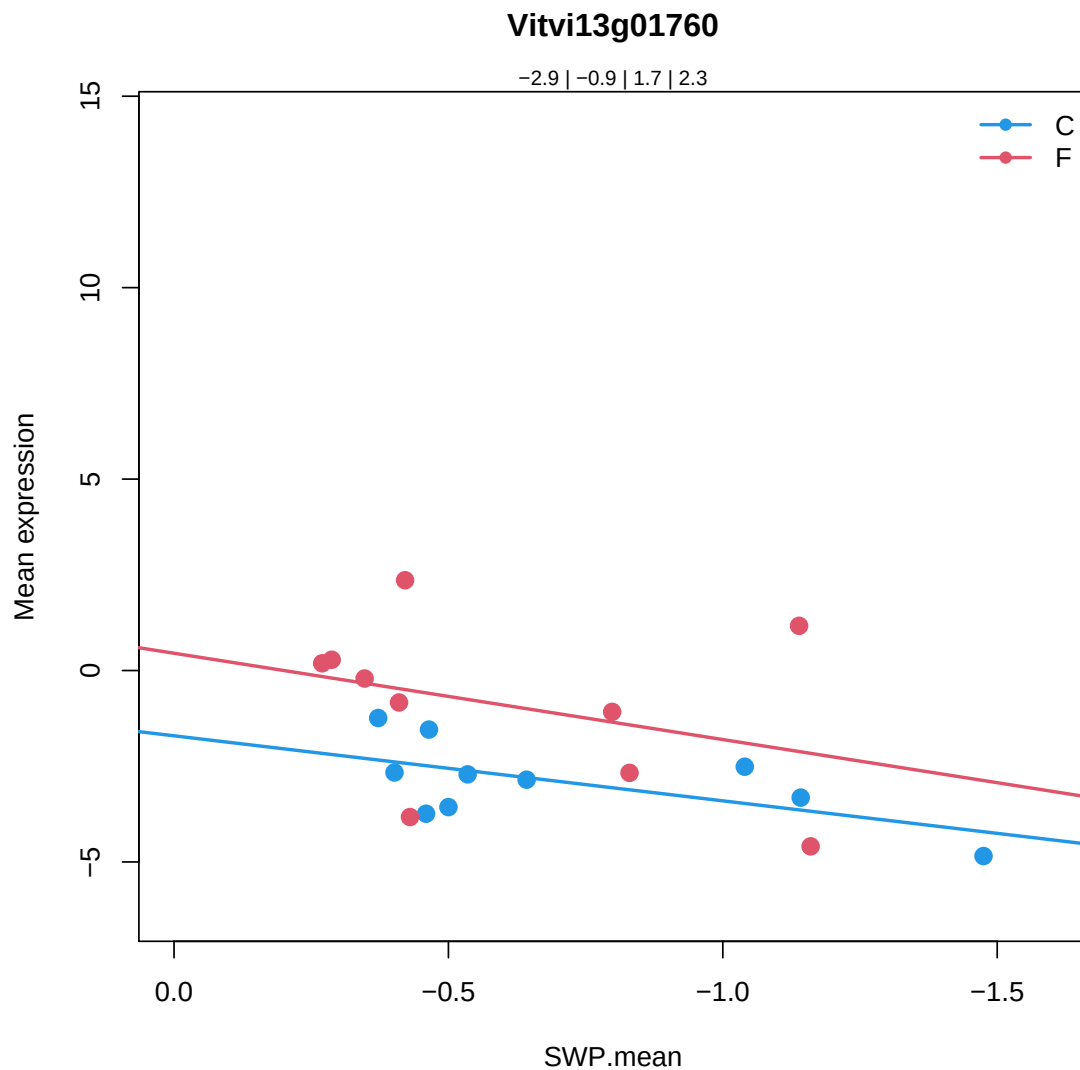
Leucine-rich repeat (LRR) family protein |

Chr3:7280930-7282027 FORWARD LENGTH=365 |

201606

Coefficients for Vitvi13g01760.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-2.899762	2.749233e-06	***	3.140979e-06	***
SlopeC	1.698164	0.1988836		0.7265417	
MeanF-MeanC	1.977597	0.00616659	**	0.05307237	.
SlopeF-SlopeC	0.5558194	0.7734422		0.9999488	



8.6.23 Vitvi10g00650: * Type5

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

Vitvi10g00650

30.2.8.2

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

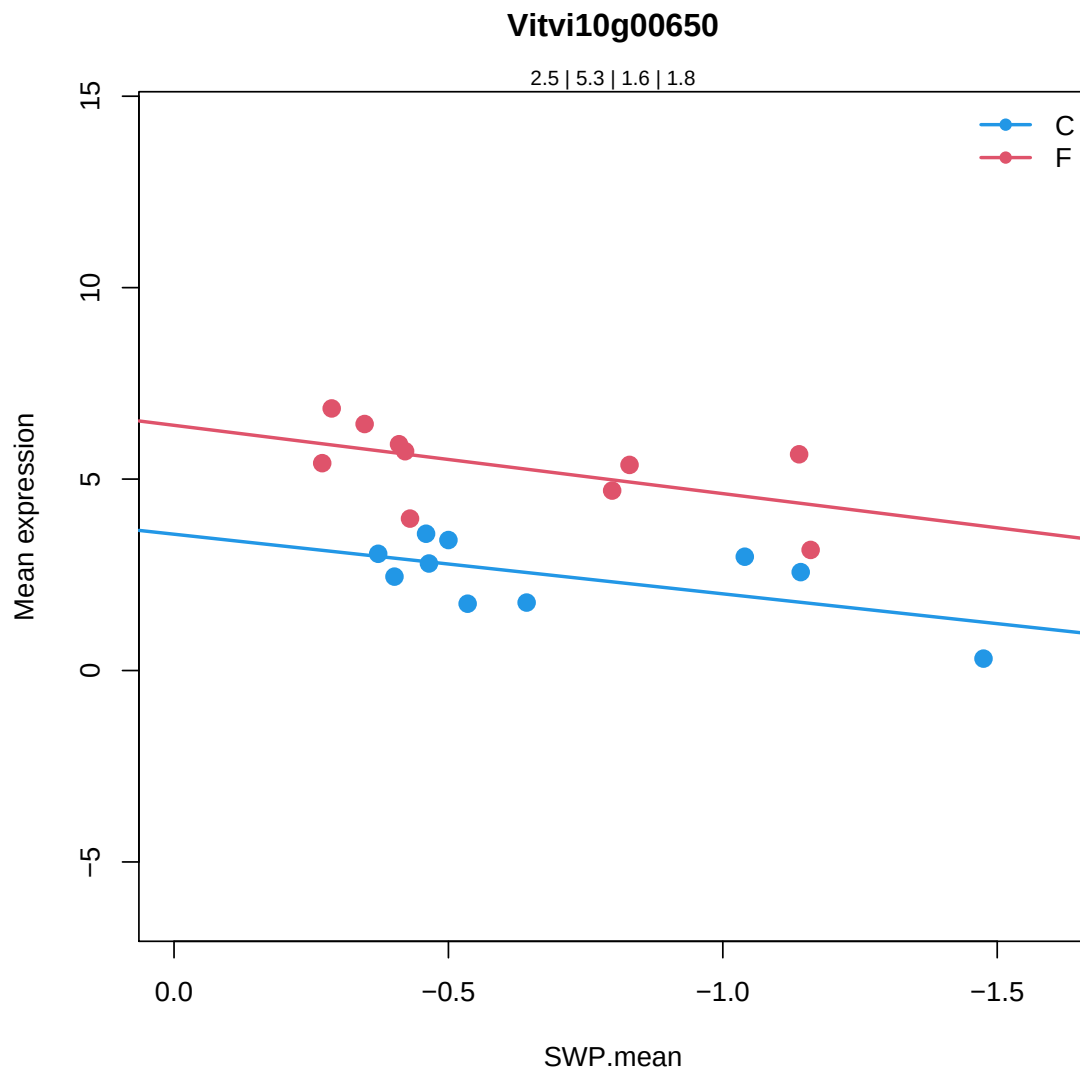
Leucine-rich repeat transmembrane protein kinase |

Chr1:2359817-2363859 REVERSE LENGTH=801 |

201606

Coefficients for Vitvi10g00650.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.464913	3.775848e-09	***	4.66987e-09	***
SlopeC	1.557723	0.04212555	*	0.4812642	
MeanF-MeanC	2.852172	1.1026e-07	***	4.434256e-06	***
SlopeF-SlopeC	0.2259447	0.835169		0.9999488	



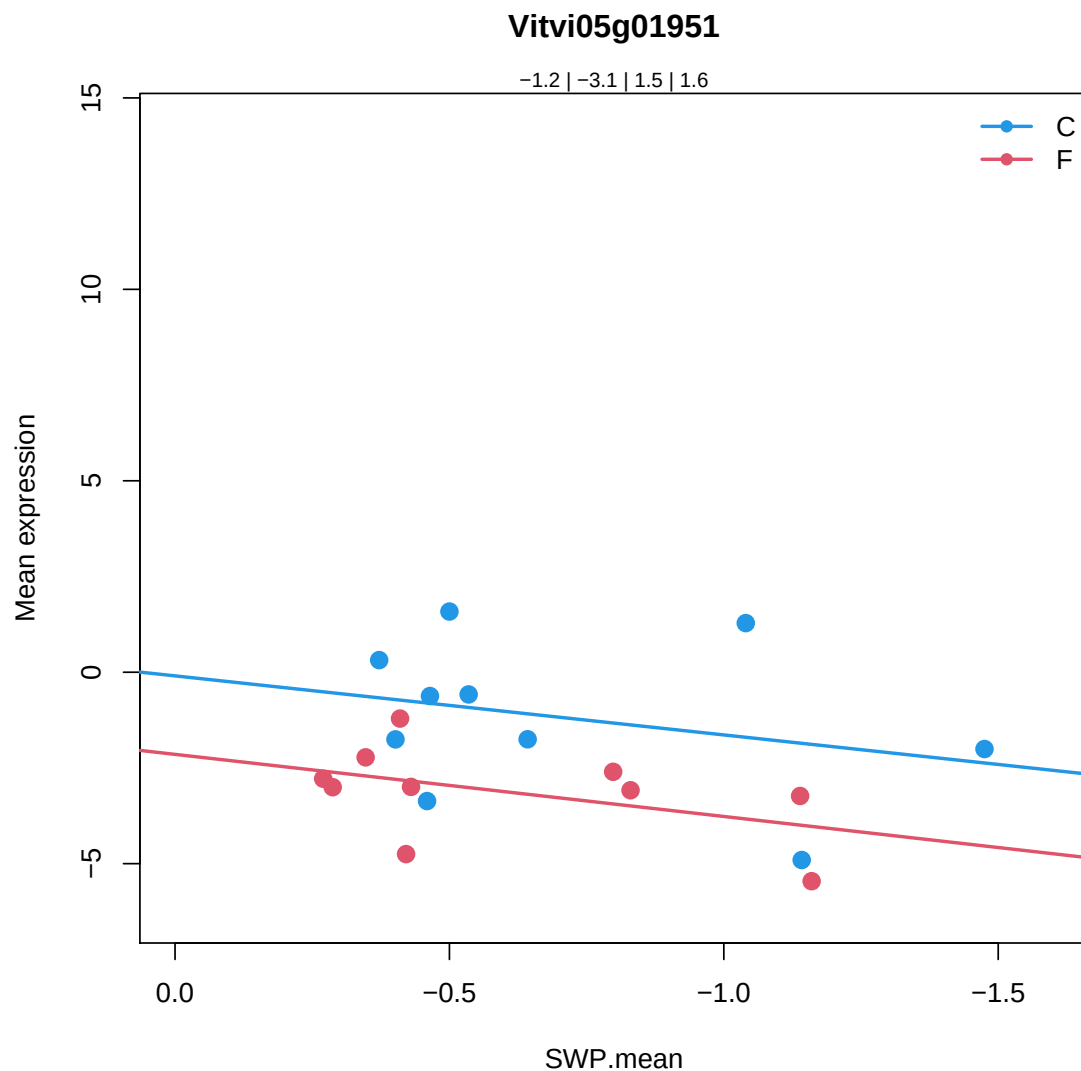
8.6.24 Vitvi05g01951: Type5

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

```
Vitvi05g01951
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi05g01951.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.180023	0.01749749	*	0.01842337	*
SlopeC	1.542255	0.2396463		0.7540013	
MeanF-MeanC	-1.953694	0.006503444	**	0.05528837	.
SlopeF-SlopeC	0.07982944	0.9668383		0.9999488	



8.6.25 Vitvi12g00036: Type5

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

Vitvi12g00036

11.3

lipid metabolism.phospholipid synthesis

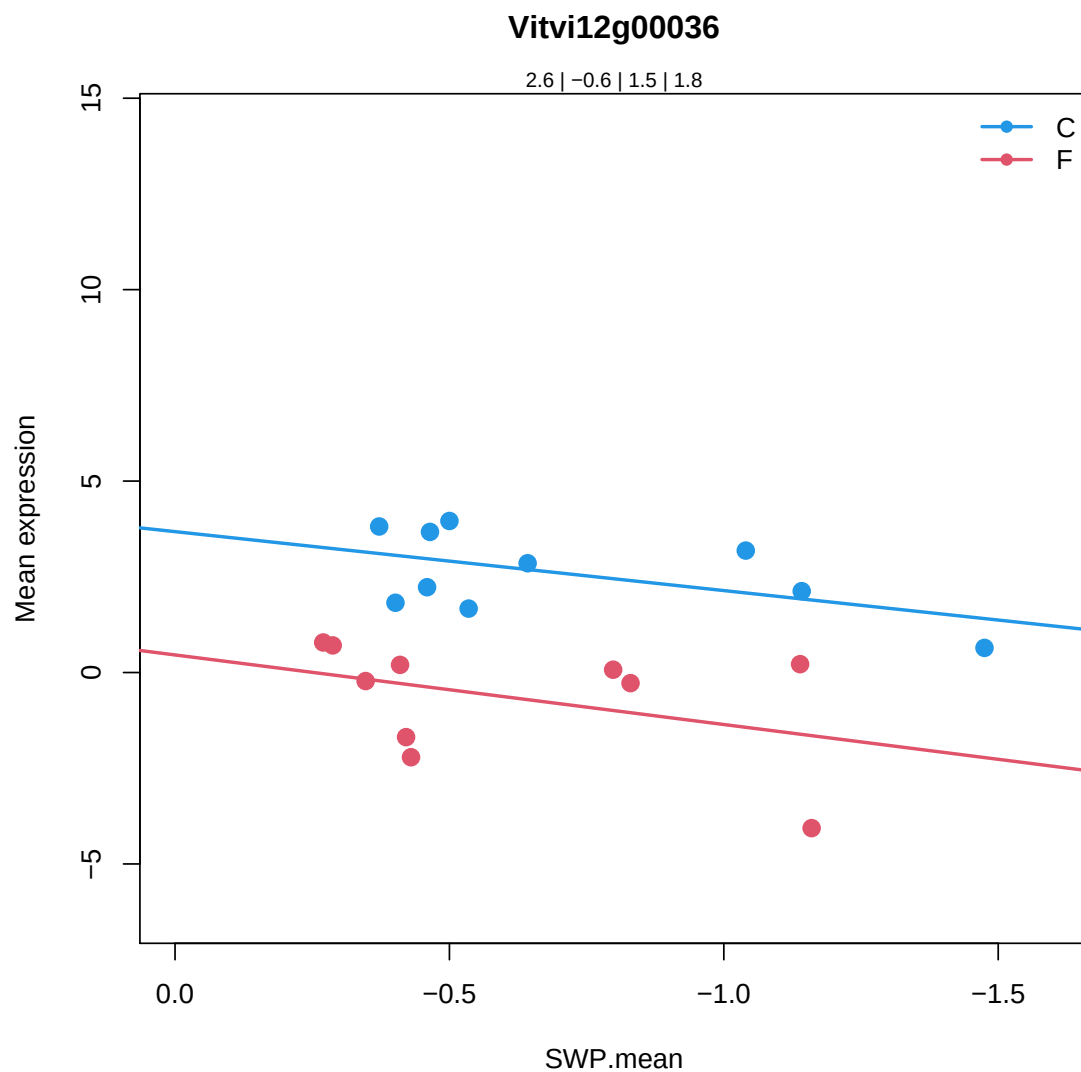
glycerol-3-phosphate acyltransferase 1 |

Chr1:1994170-1996067 REVERSE LENGTH=585 |

201606

Coefficients for Vitvi12g00036.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.596959	2.662307e-07	***	3.119533e-07	***
SlopeC	1.53938	0.1313064		0.6540431	
MeanF-MeanC	-3.245096	1.721806e-06	***	5.291083e-05	***
SlopeF-SlopeC	0.2776615	0.8509929		0.9999488	



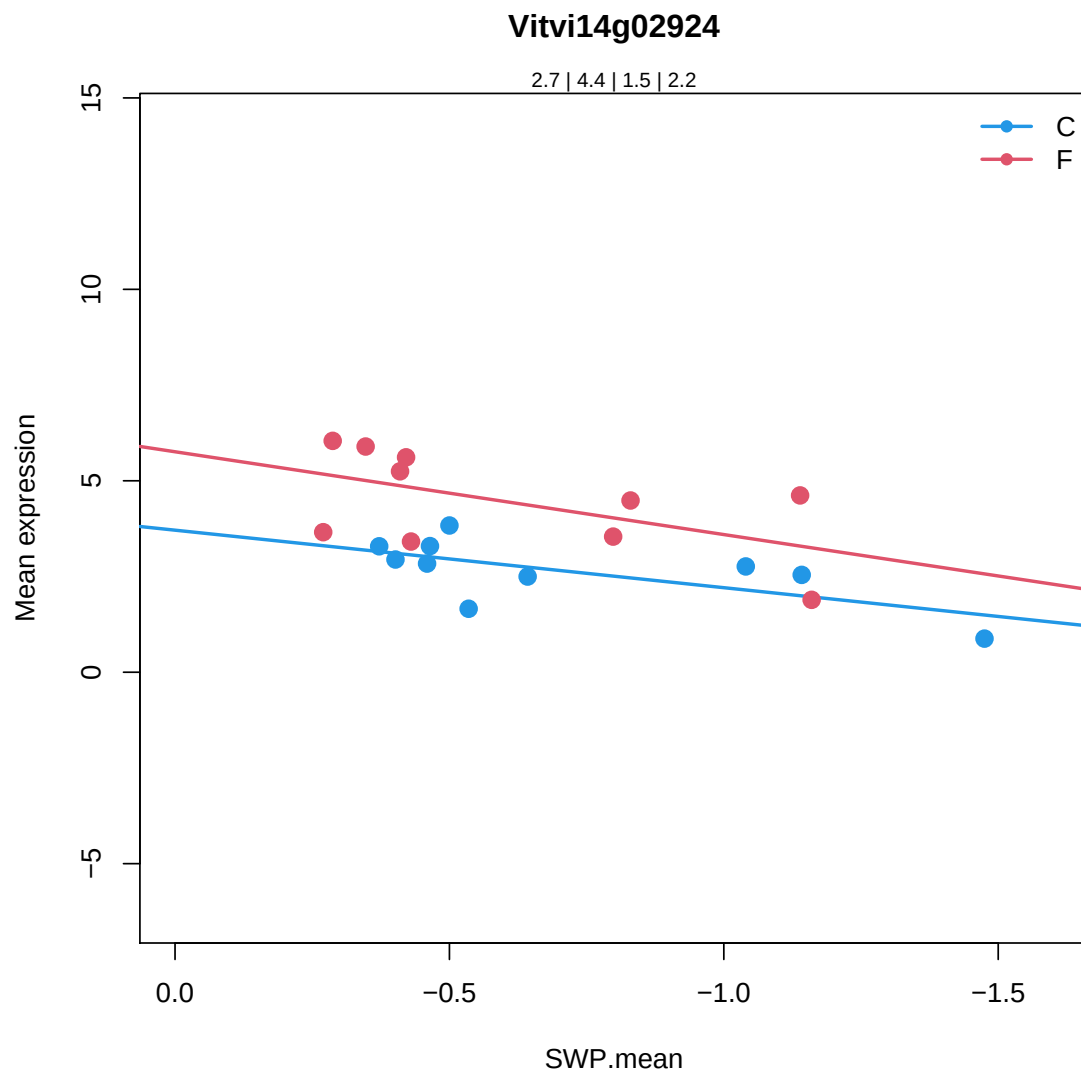
8.6.26 Vitvi14g02924: Type5

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

```
Vitvi14g02924
35.2
not assigned.unknown
NA
```

Coefficients for Vitvi14g02924.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.65358	2.158855e-09	***	2.692518e-09	***
SlopeC	1.502144	0.05850777	.	0.5384614	
MeanF-MeanC	1.786688	0.0001229555	***	0.002154124	**
SlopeF-SlopeC	0.660274	0.5612348		0.9999488	



8.6.27 Vitvi01g02061: * Type5

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

Vitvi01g02061

35.1.26

not assigned.no ontology.DC1 domain containing protein

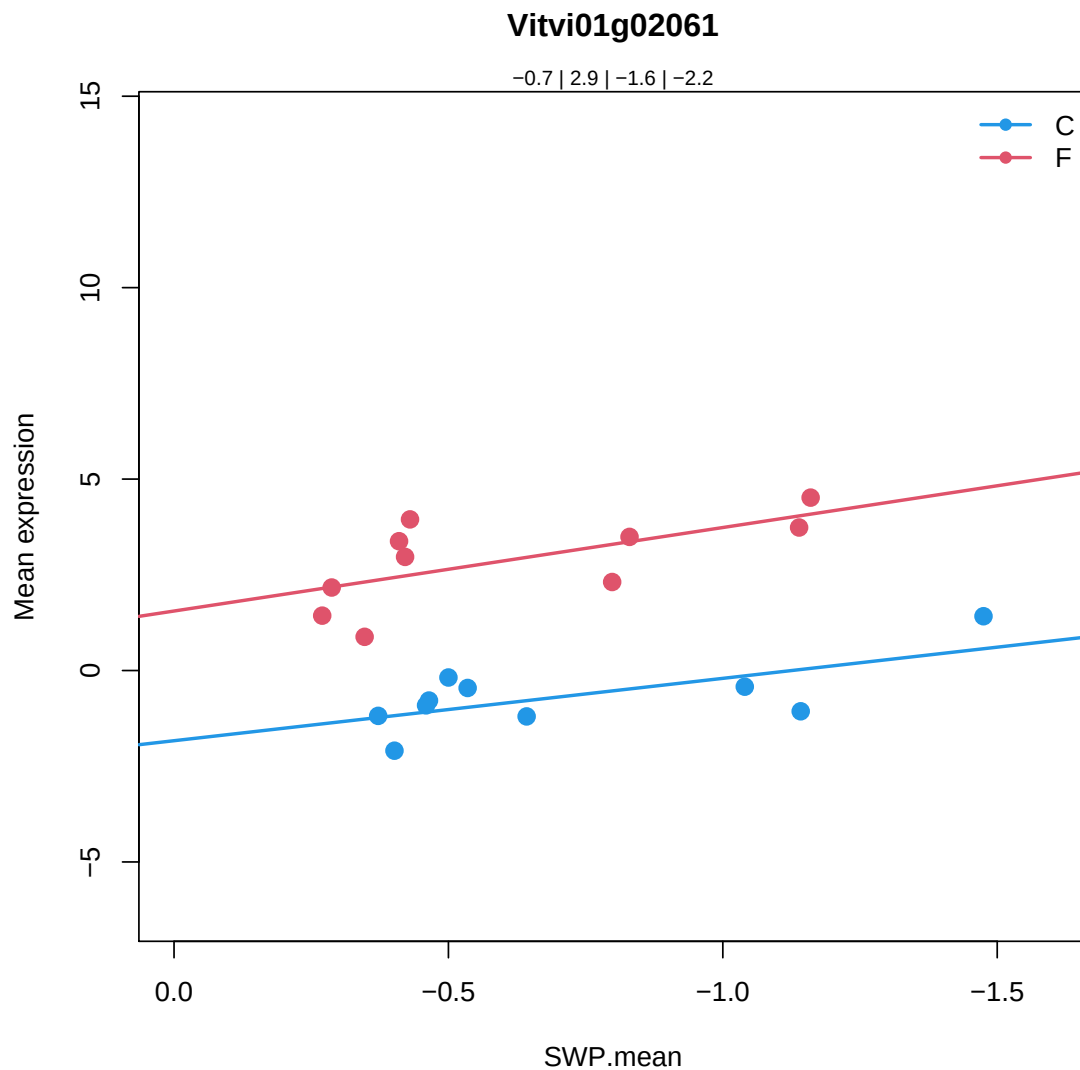
DC1 domain-containing protein |

Chr1:22261978-22264243 FORWARD LENGTH=578 |

201606

Coefficients for Vitvi01g02061.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.6880274	0.009278023	**	0.009836925	**
SlopeC	-1.628569	0.02384104	*	0.3984486	
MeanF-MeanC	3.570542	6.641649e-10	***	4.033148e-08	***
SlopeF-SlopeC	-0.5520575	0.5853545		0.9999488	



8.6.28 Vitvi05g01116: * Type5

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

Vitvi05g01116

11.1.11

lipid metabolism.FA synthesis and FA elongation.fatty acid elongase

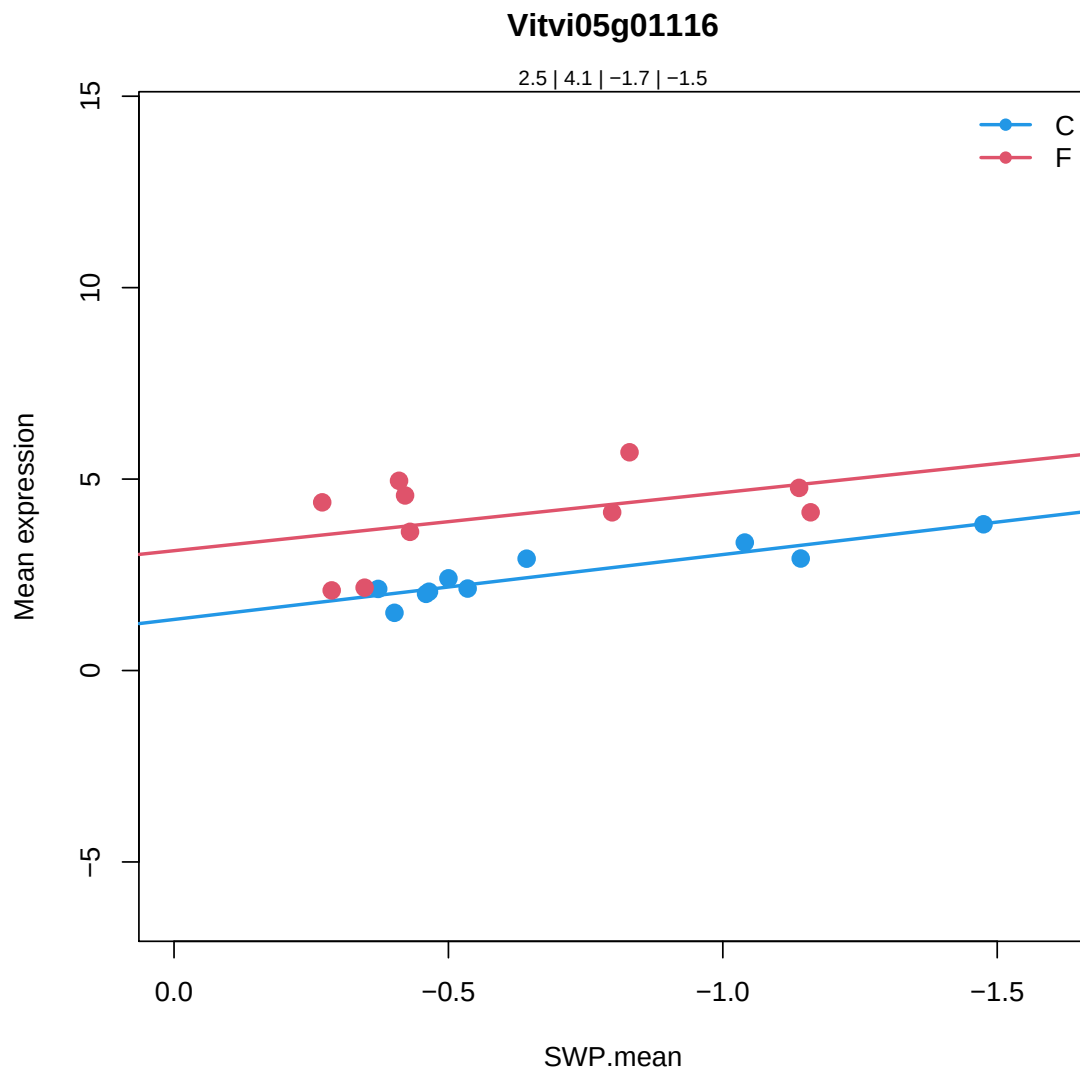
HXXXD-type acyl-transferase family protein |

Chr4:12660929-12662537 FORWARD LENGTH=421 |

201606

Coefficients for Vitvi05g01116.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.52539	3.801912e-10	***	4.865962e-10	***
SlopeC	-1.695659	0.01616485	*	0.3486596	
MeanF-MeanC	1.527811	0.0001382594	***	0.002365151	**
SlopeF-SlopeC	0.1786811	0.8550996		0.9999488	



8.6.29 Vitvi18g00508: * Type5

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

Vitvi18g00508

9.8

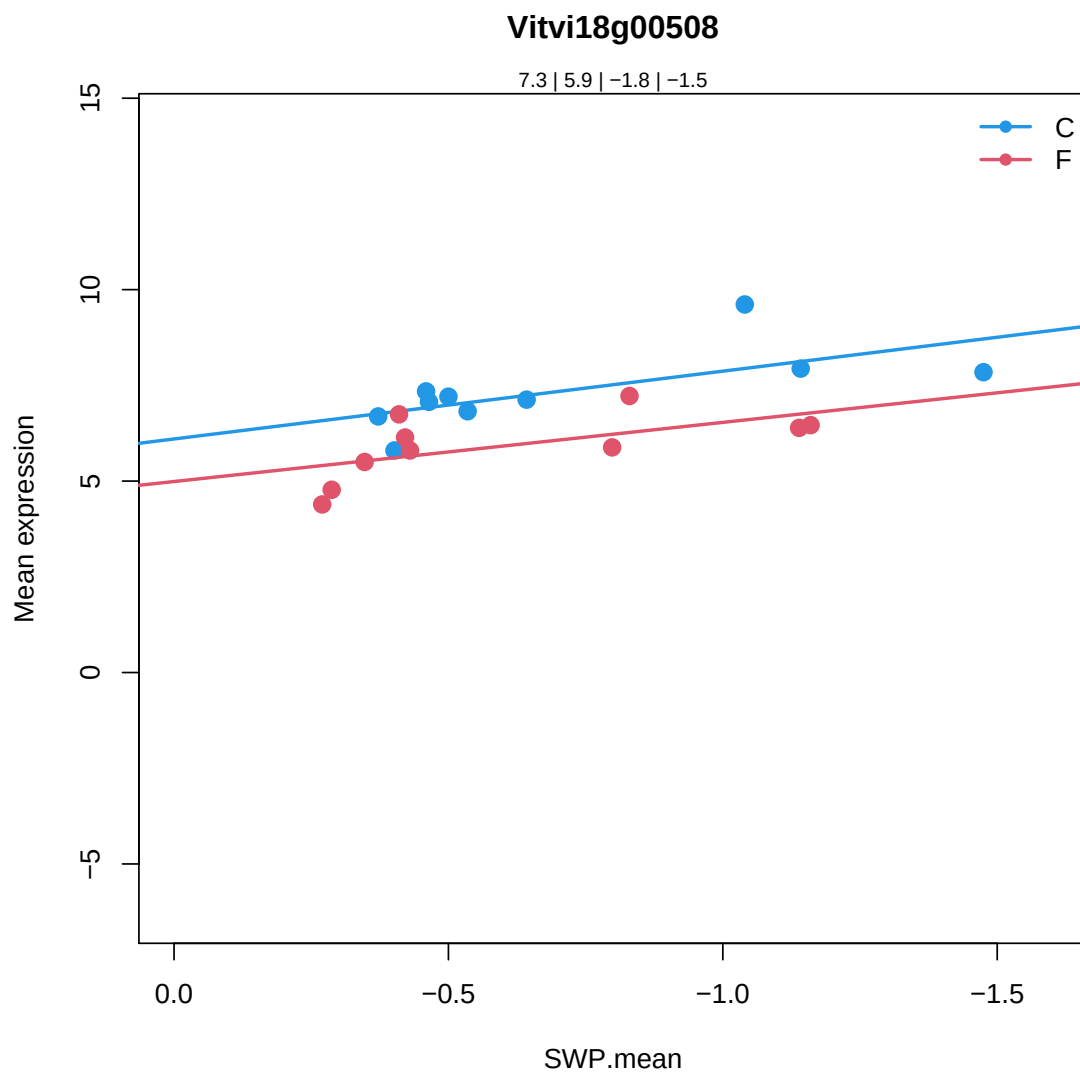
mitochondrial electron transport / ATP synthesis.uncoupling protein
uncoupling protein 5 |

Chr2:9563531-9564472 REVERSE LENGTH=313 |

201606

Coefficients for Vitvi18g00508.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	7.344885	6.22014e-20	***	3.185732e-19	***
SlopeC	-1.770808	0.008851147	**	0.2903326	
MeanF-MeanC	-1.415514	0.0001756439	***	0.002897364	**
SlopeF-SlopeC	0.2259134	0.8074009		0.9999488	



8.6.30 Vitvi07g02448: * Type5

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

Vitvi07g02448

26.2

misc.UDP glucosyl and glucoronyl transferases

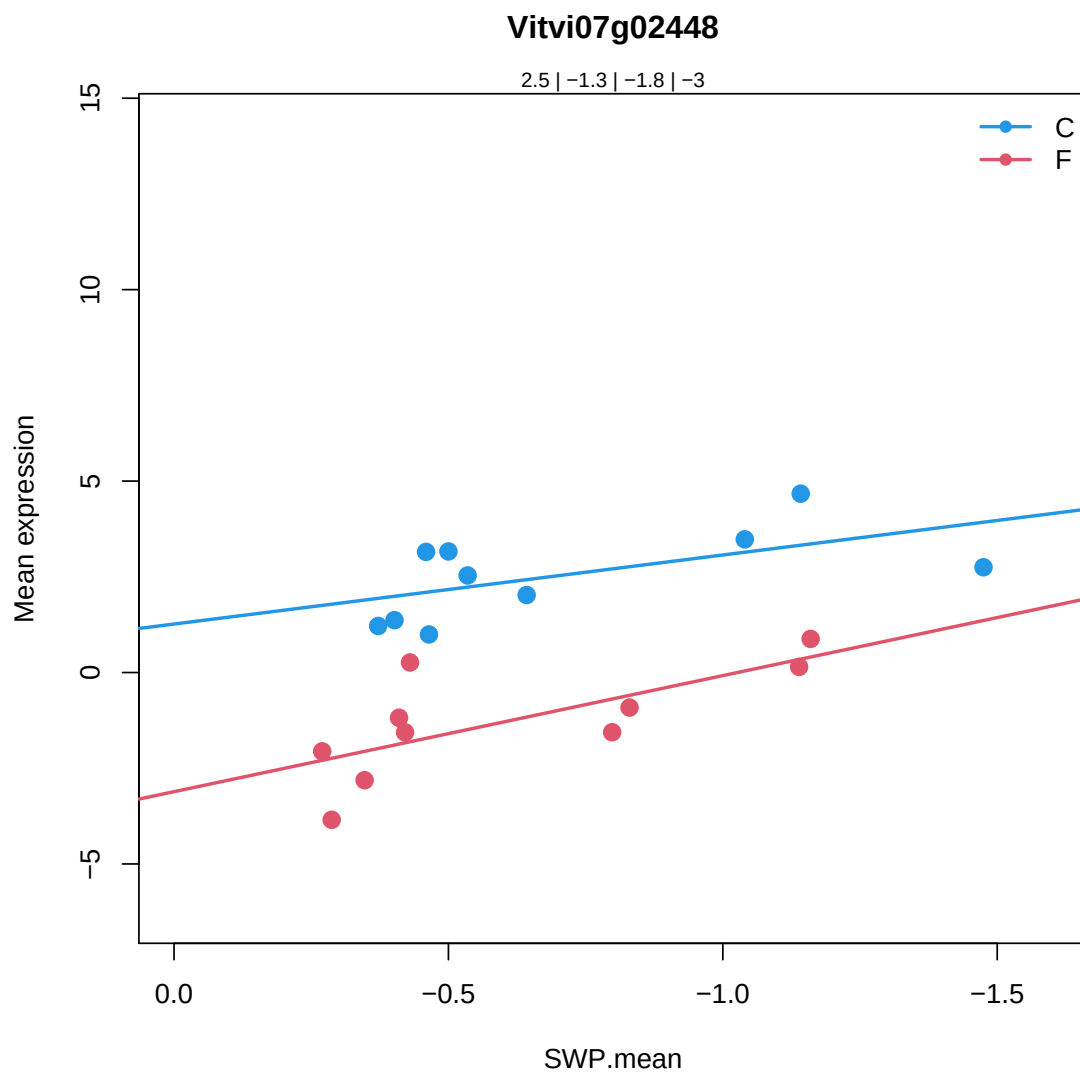
Uridine diphosphate glycosyltransferase 74E2 |

Chr1:1703196-1704639 REVERSE LENGTH=453 |

201606

Coefficients for Vitvi07g02448.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.534319	1.823511e-08	***	2.209025e-08	***
SlopeC	-1.803435	0.03725763	*	0.4620709	
MeanF-MeanC	-3.799573	6.720516e-09	***	3.41447e-07	***
SlopeF-SlopeC	-1.227884	0.3209972		0.9999488	



8.6.31 Vitvi19g01048: Type5

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

Vitvi19g01048

26.9

misc.glutathione S transferases

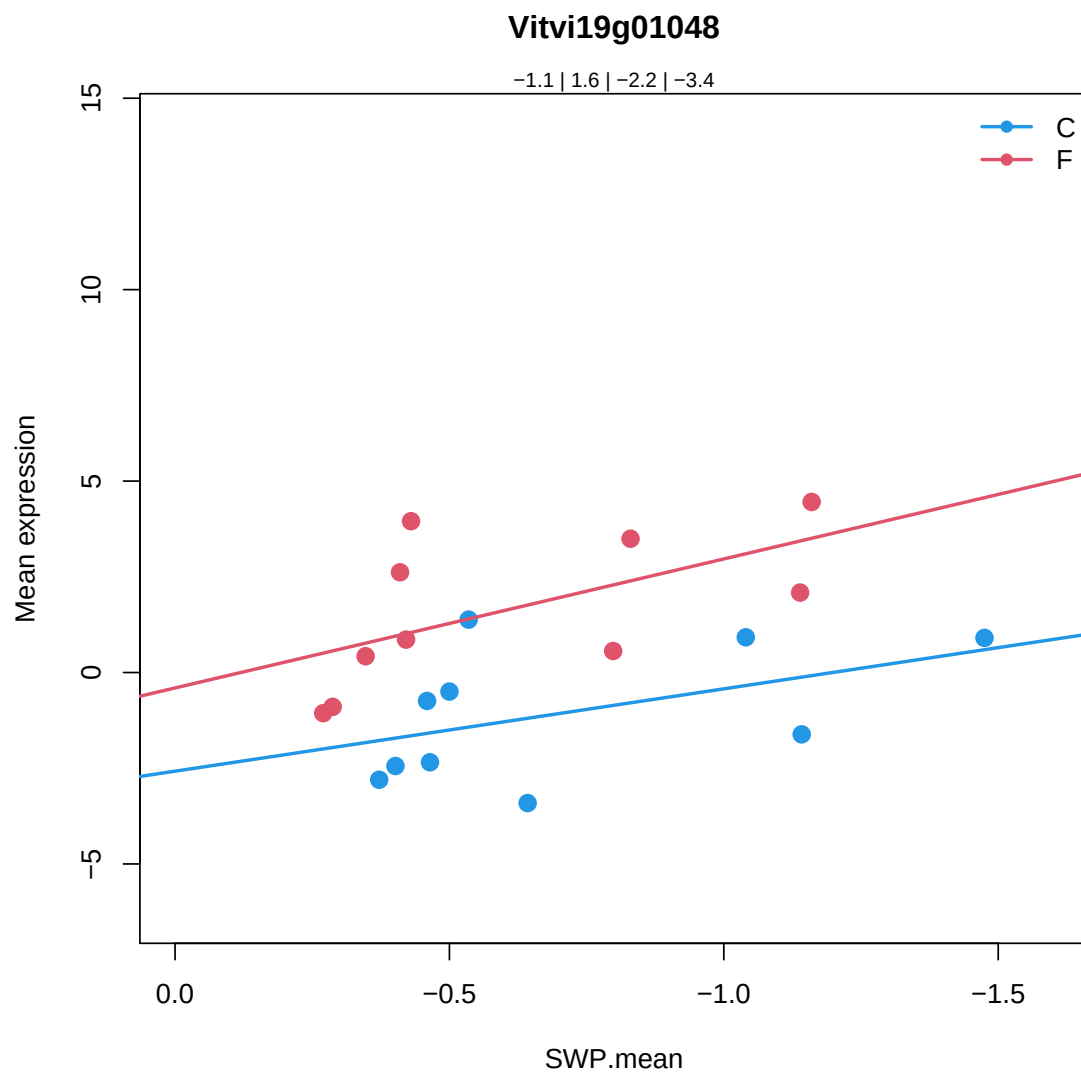
glutathione S-transferase TAU 25 |

Chr1:5872208-5872958 FORWARD LENGTH=221 |

201606

Coefficients for Vitvi19g01048.

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



8.6.32 Vitvi03g00443: * Type5

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

Vitvi03g00443

26.8

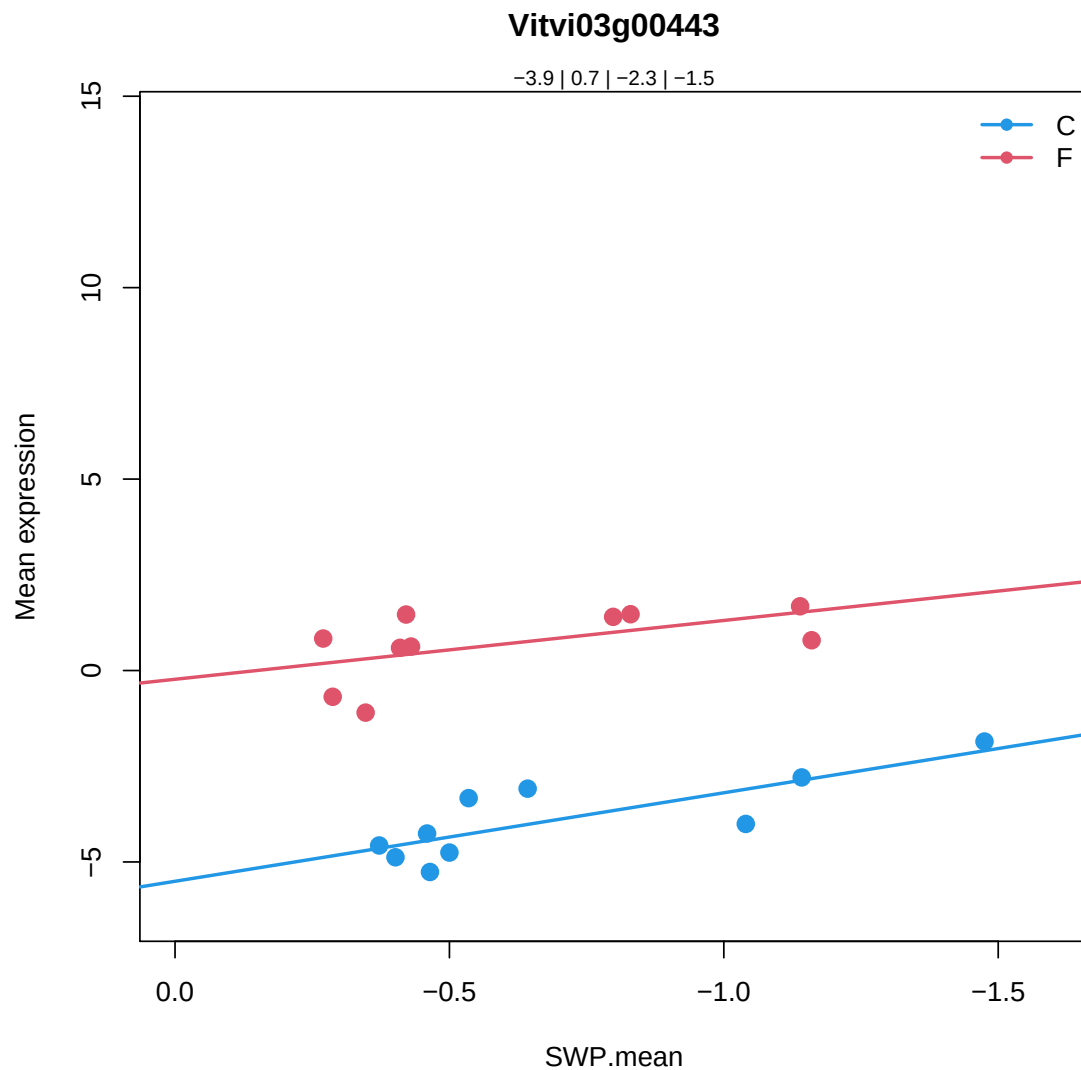
misc.nitrilases, nitrile lyases, berberine bridge enzymes, reticuline
acetone-cyanohydrin lyase |

Chr2:10042681-10043686 REVERSE LENGTH=187 |

201606

Coefficients for Vitvi03g00443.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-3.879575	2.657365e-14	***	4.276136e-14	***
SlopeC	-2.311521	0.001013174	**	0.1271346	
MeanF-MeanC	4.586549	9.379116e-13	***	8.360029e-11	***
SlopeF-SlopeC	0.7750986	0.401223		0.9999488	



8.6.33 Vitvi02g00263: Type5

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

Vitvi02g00263

26.6

misc.O-methyl transferases

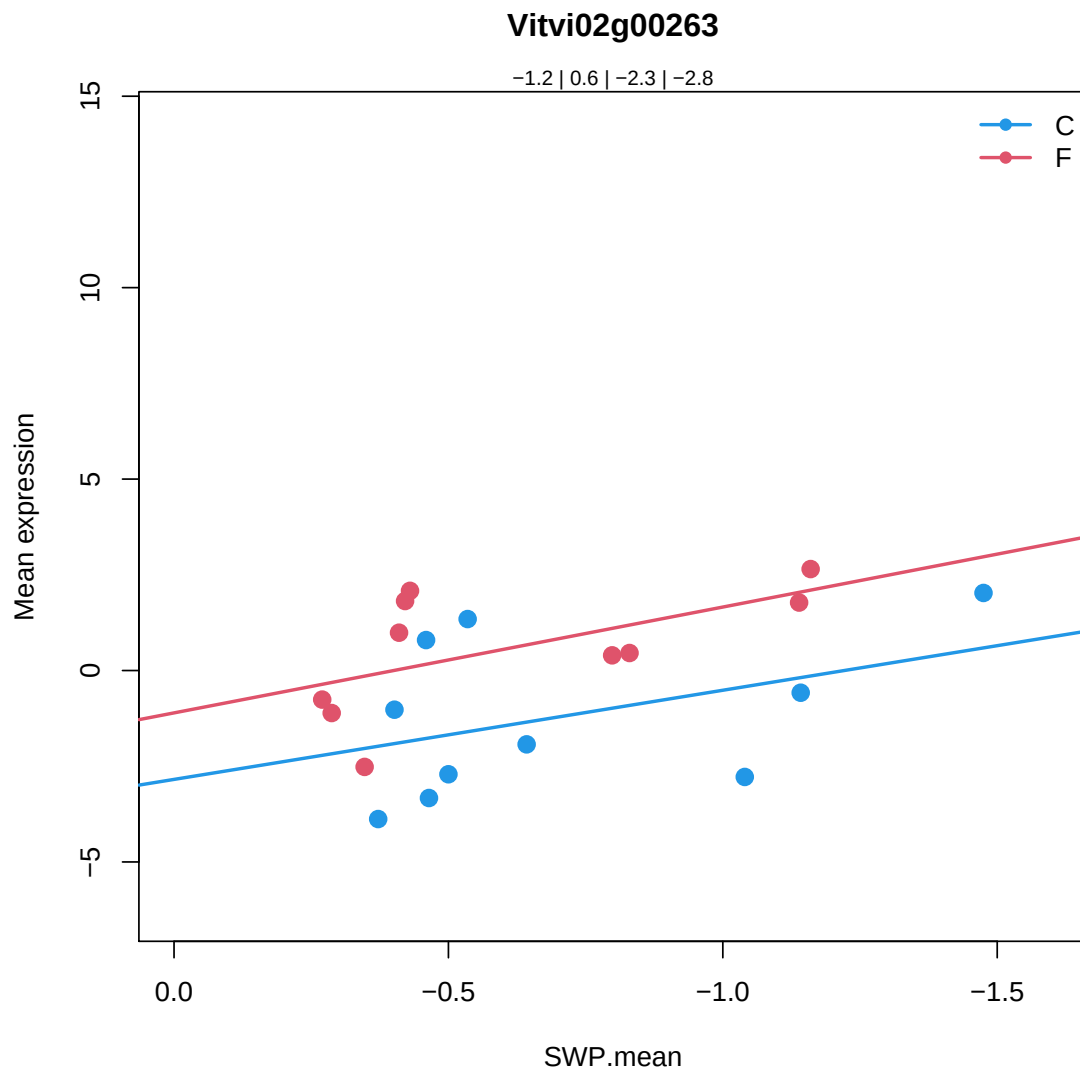
O-methyltransferase 1 |

Chr5:21982075-21984167 FORWARD LENGTH=363 |

201606

Coefficients for Vitvi02g00263.

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



8.6.34 Vitvi09g01282: Type5

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

Vitvi09g01282

26.13

misc.acid and other phosphatases

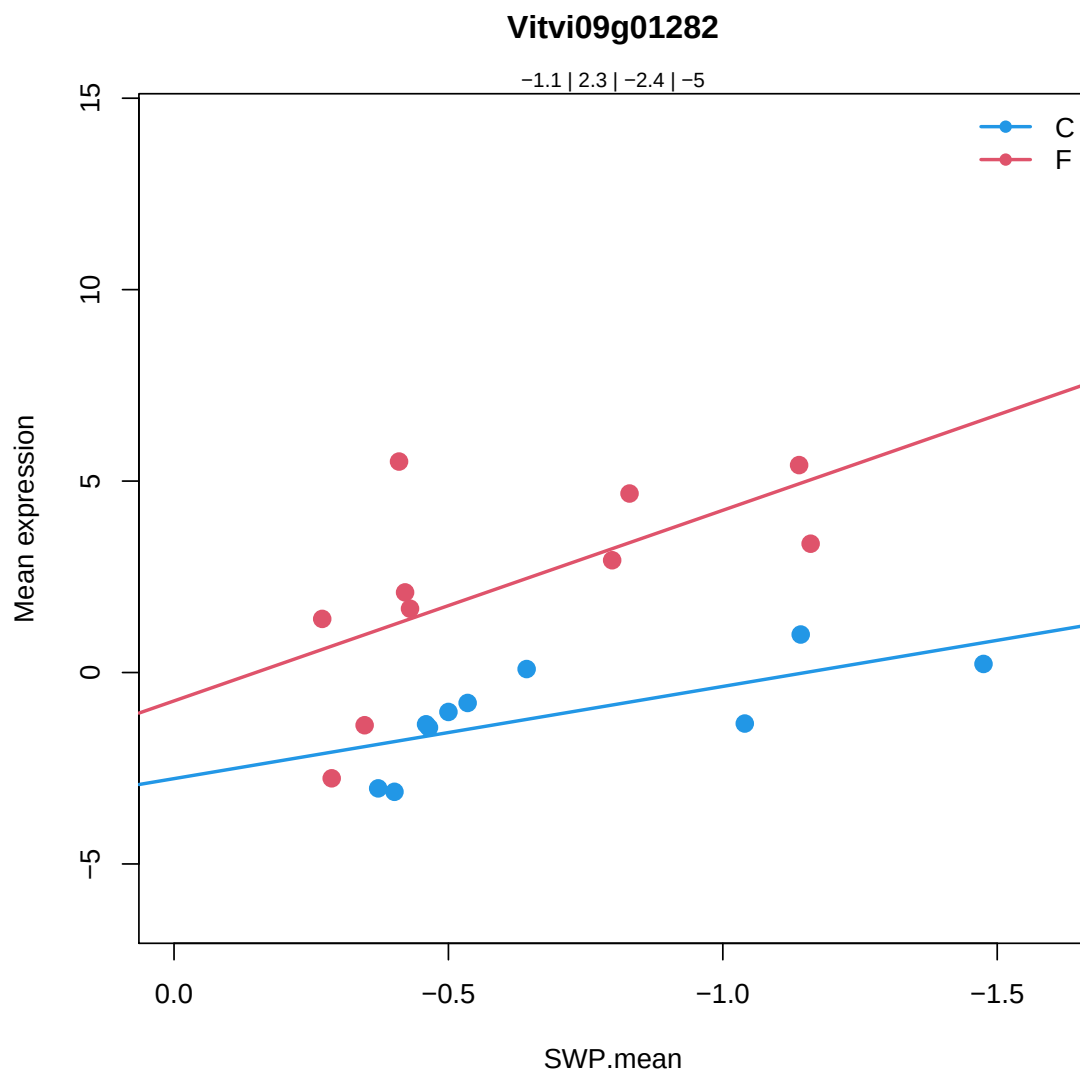
HAD superfamily%2C subfamily IIIB acid phosphatase |

Chr4:12901736-12902882 REVERSE LENGTH=260 |

201606

Coefficients for Vitvi09g01282.

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



8.6.35 Vitvi07g01552: * Type5

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

Vitvi07g01552

35.2

not assigned.unknown

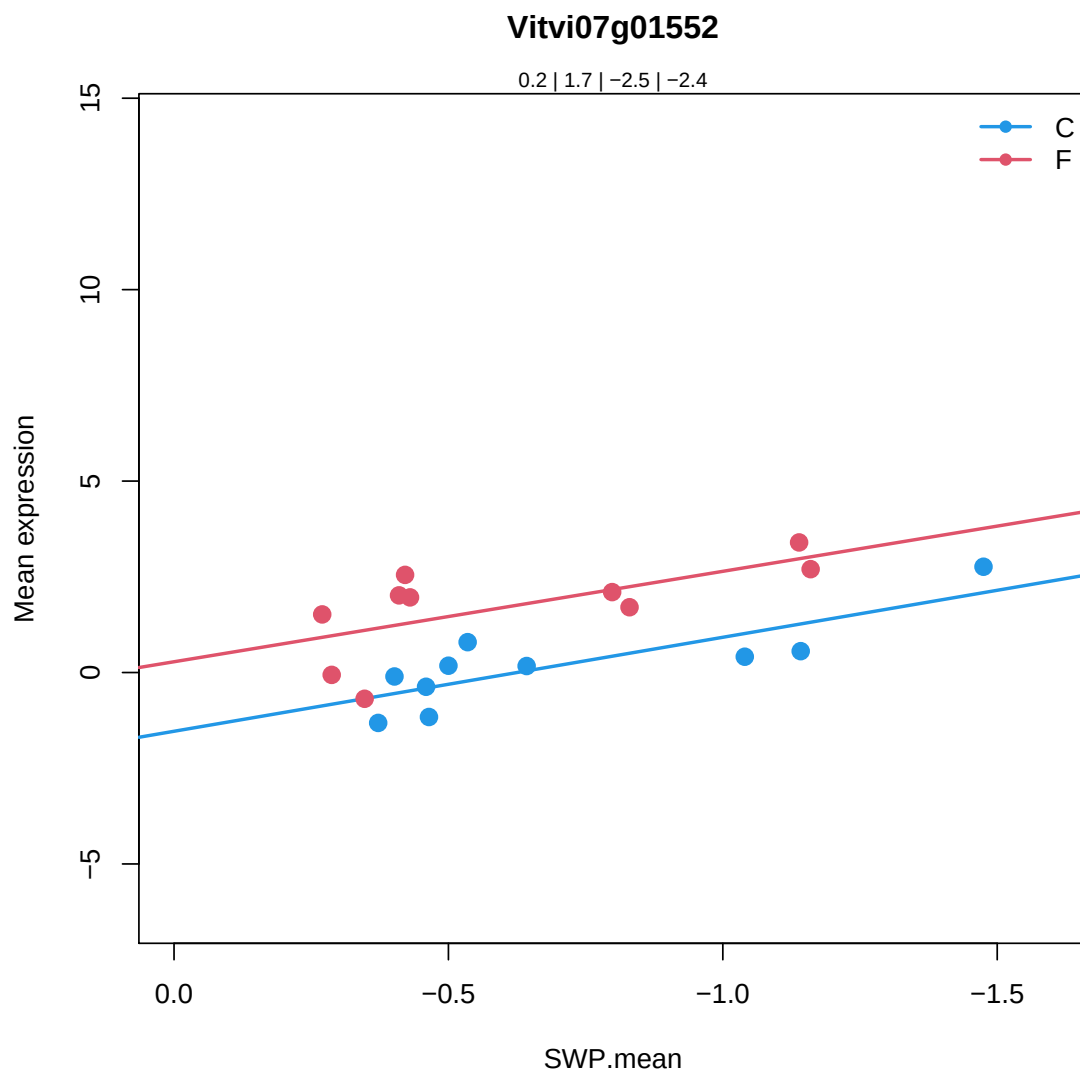
basic leucine-zipper 6 |

Chr2:9732601-9733284 REVERSE LENGTH=227 |

201606

Coefficients for Vitvi07g01552.

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



8.6.36 Vitvi07g01120: Type5

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

Vitvi07g01120

35.2

not assigned.unknown

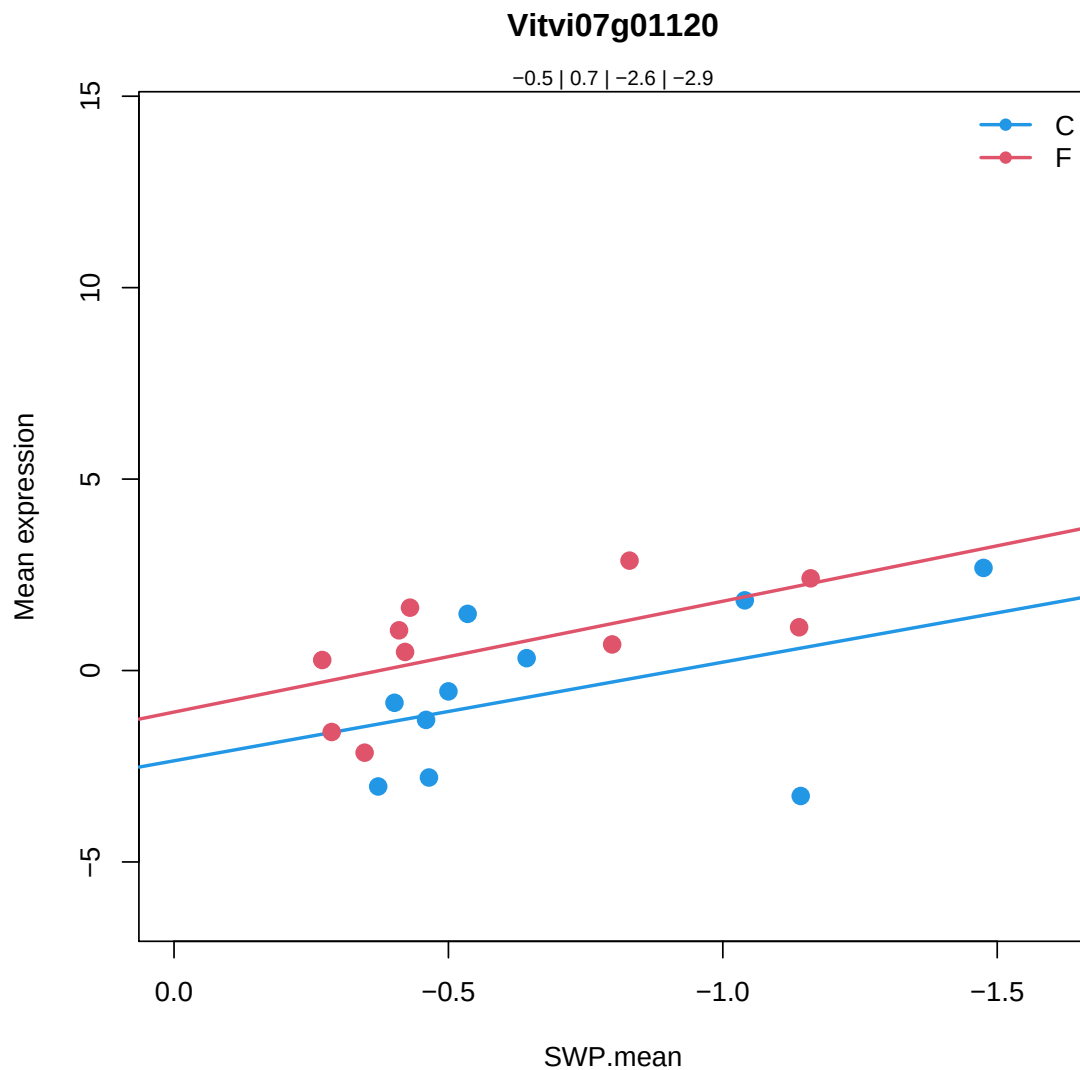
nuclear transport factor 2/RNA recognition motif protein |

Chr3:2307289-2308326 REVERSE LENGTH=293 |

201606

Coefficients for Vitvi07g01120.

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



8.6.37 Vitvi05g00421: * Type5

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

Vitvi05g00421

17.4.1

hormone metabolism.cytokinin.synthesis-degradation

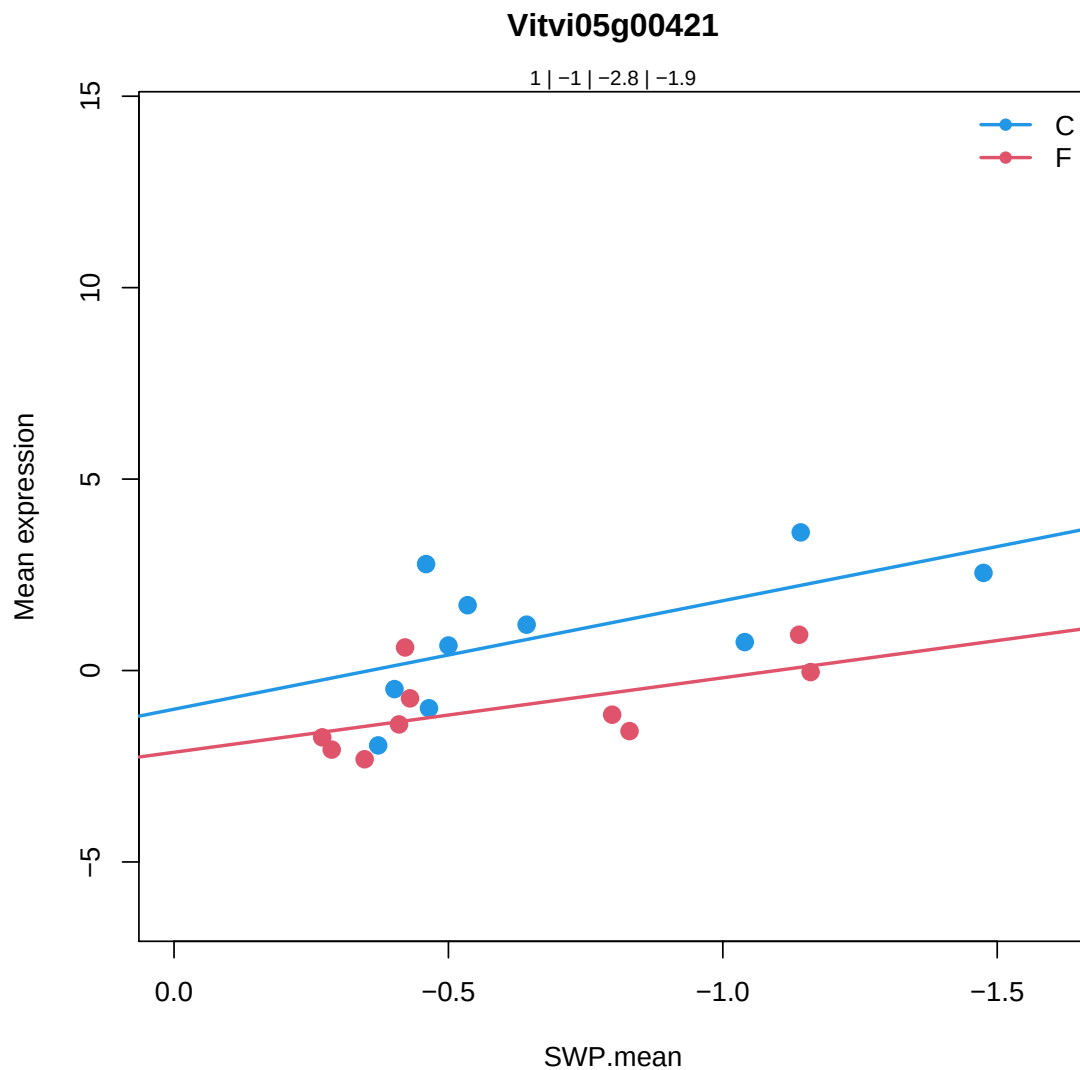
isopentenyltransferase 5 |

Chr5:6362389-6363381 REVERSE LENGTH=330 |

201606

Coefficients for Vitvi05g00421.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.9809172	0.01036541	*	0.01097607	*
SlopeC	-2.832505	0.008139059	**	0.2851324	
MeanF-MeanC	-1.931301	0.0007771899	***	0.01010745	*
SlopeF-SlopeC	0.8876307	0.5456677		0.9999488	



8.6.38 Vitvi01g01708: * Type5

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

Vitvi01g01708

20.2.1

stress.abiotic.heat

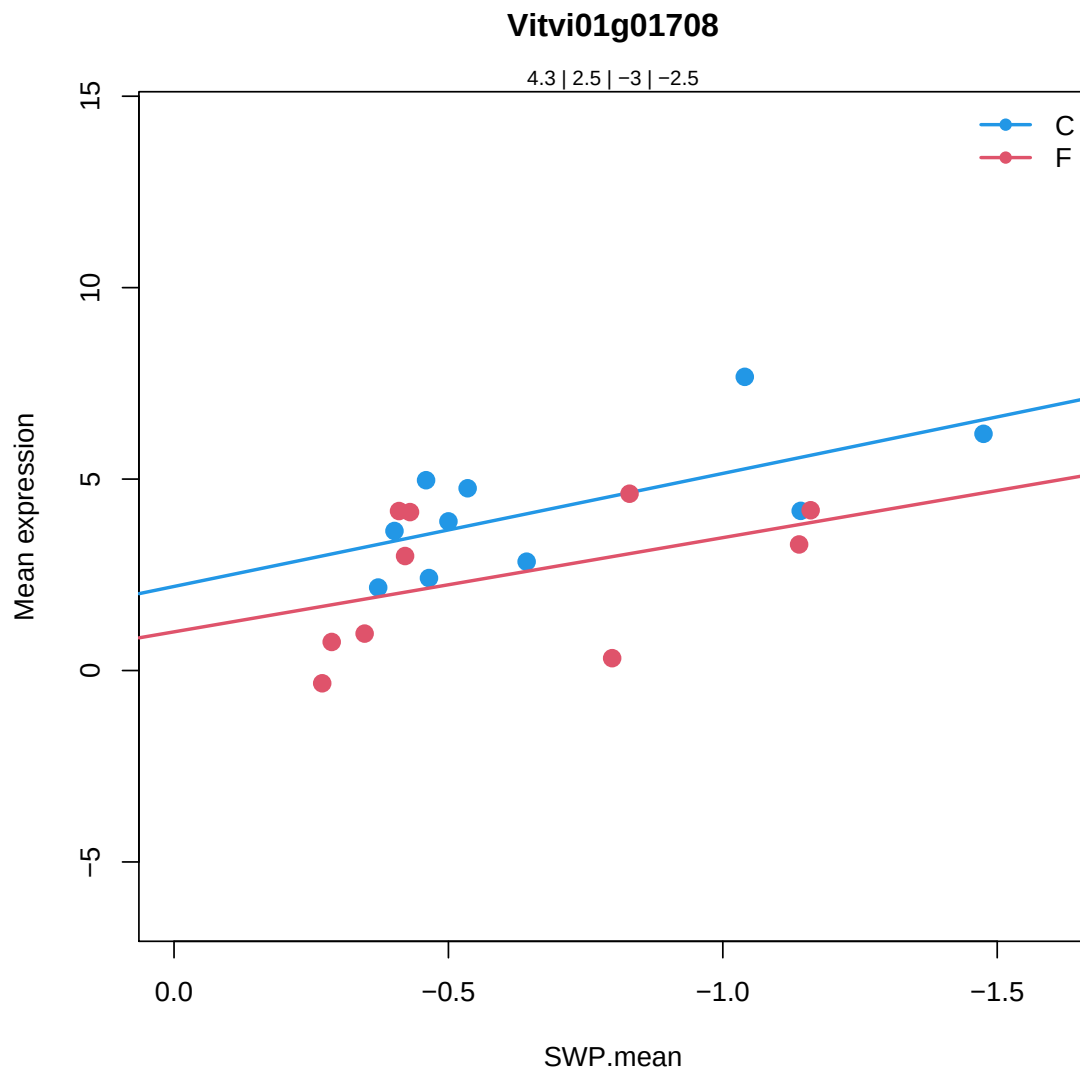
BCL-2-associated athanogene 5 |

Chr1:4076334-4076981 FORWARD LENGTH=215 |

201606

Coefficients for Vitvi01g01708.

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



8.6.39 Vitvi09g00045: * Type5

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

Vitvi09g00045

20.2.1

stress.abiotic.heat

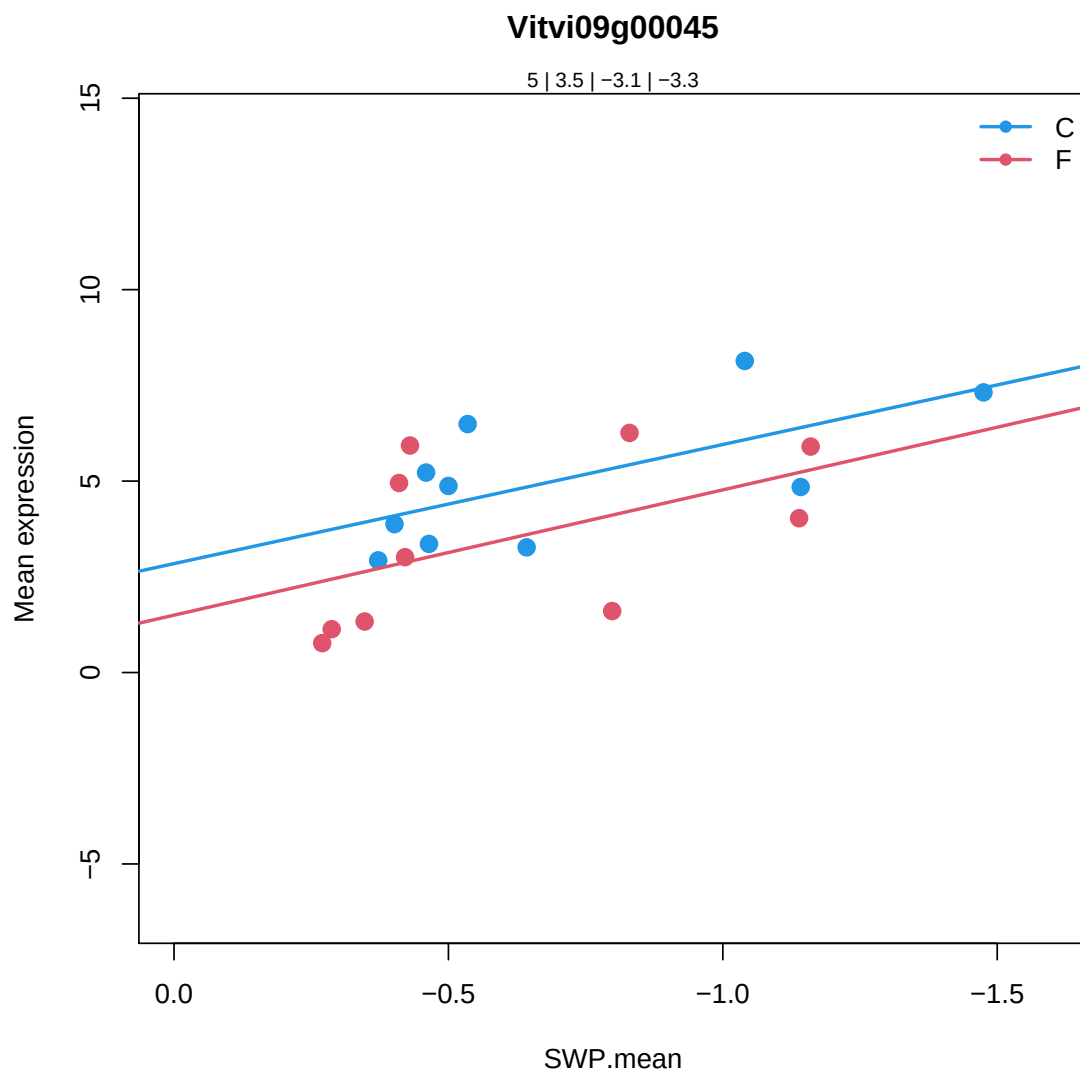
HSP20-like chaperones superfamily protein |

Chr1:20179558-20180122 REVERSE LENGTH=155 |

201606

Coefficients for Vitvi09g00045.

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



8.6.40 Vitvi19g02145: * Type5

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

Vitvi19g02145

26.9

misc.glutathione S transferases

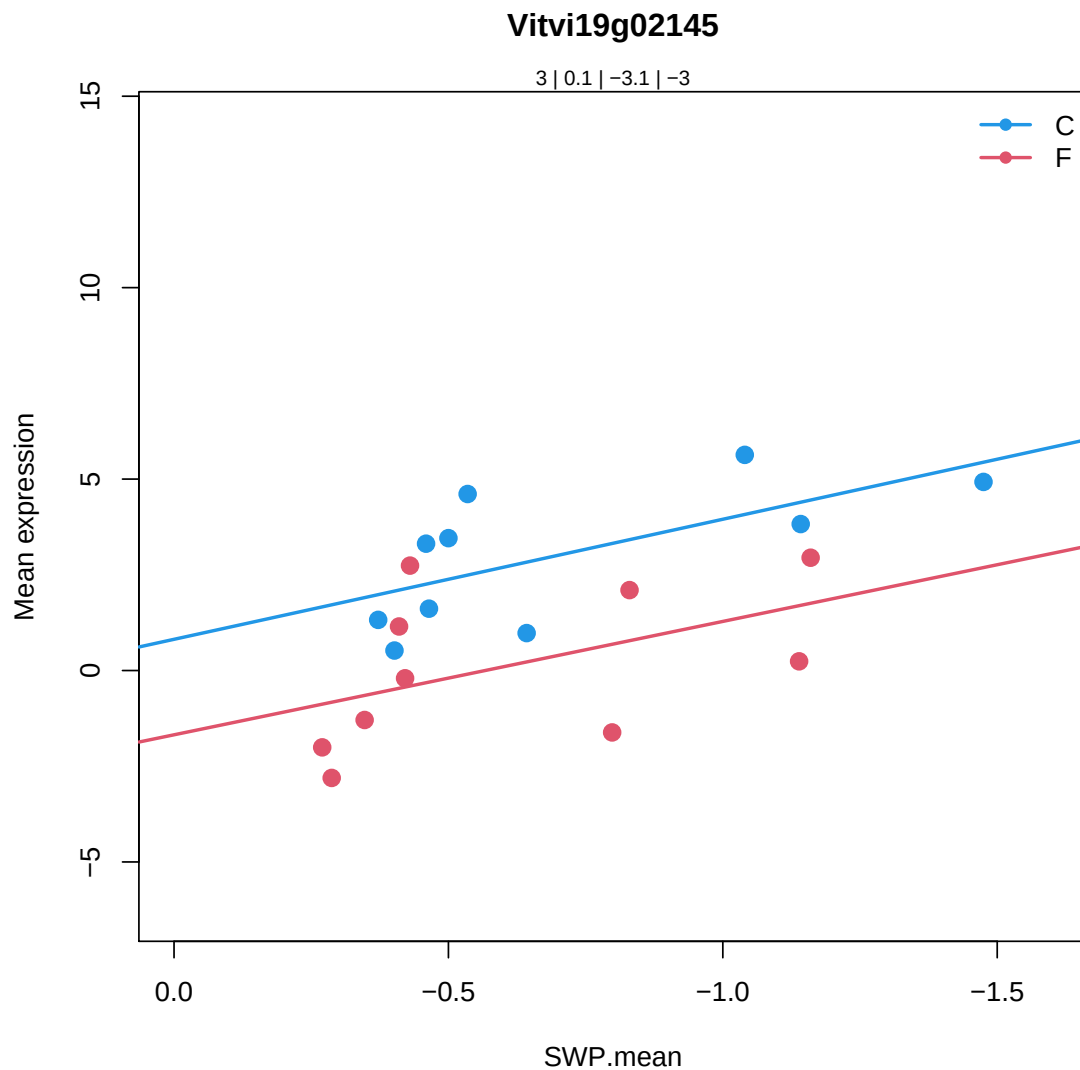
glutathione S-transferase TAU 25 |

Chr1:5872208-5872958 FORWARD LENGTH=221 |

201606

Coefficients for Vitvi19g02145.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	3.020018	1.808191e-06	***	2.075492e-06	***
SlopeC	-3.135408	0.02447993	*	0.4039715	
MeanF-MeanC	-2.894891	0.0002419684	***	0.003857827	**
SlopeF-SlopeC	0.1742035	0.9288624		0.9999488	



8.6.41 Vitvi11g01516: * Type5

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

Vitvi11g01516

29.5.5

protein.degradation.serine protease

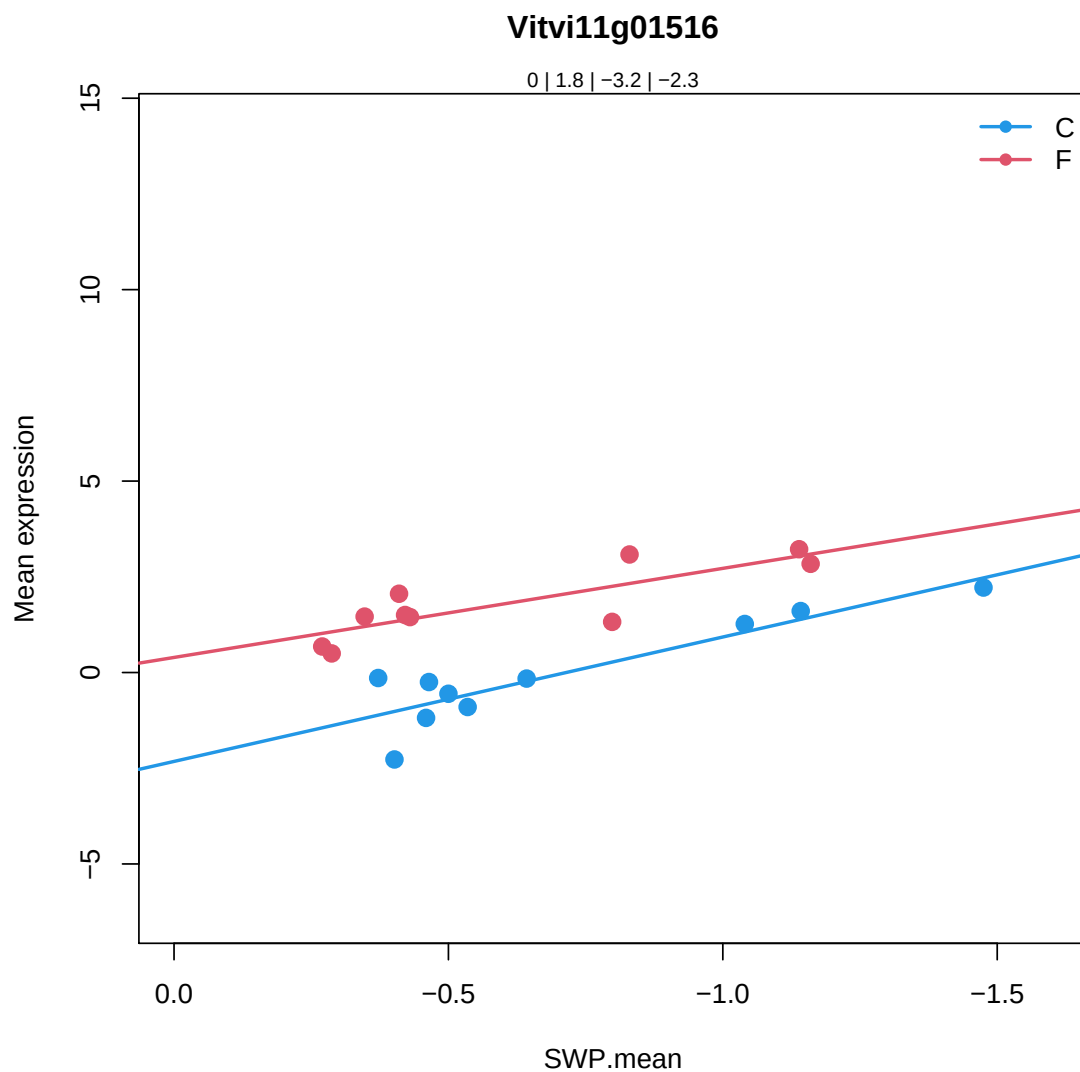
serine carboxypeptidase-like 29 |

Chr4:15003474-15006017 FORWARD LENGTH=479 |

201606

Coefficients for Vitvi11g01516.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.03709564	0.840428		0.8435271	
SlopeC	-3.24962	2.102715e-06	***	0.01365018	*
MeanF-MeanC	1.848123	3.942282e-07	***	1.417176e-05	***
SlopeF-SlopeC	0.9230391	0.2339817		0.9999488	



8.6.42 Vitvi05g00857: * Type5

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

Vitvi05g00857

34.99

transport.misc

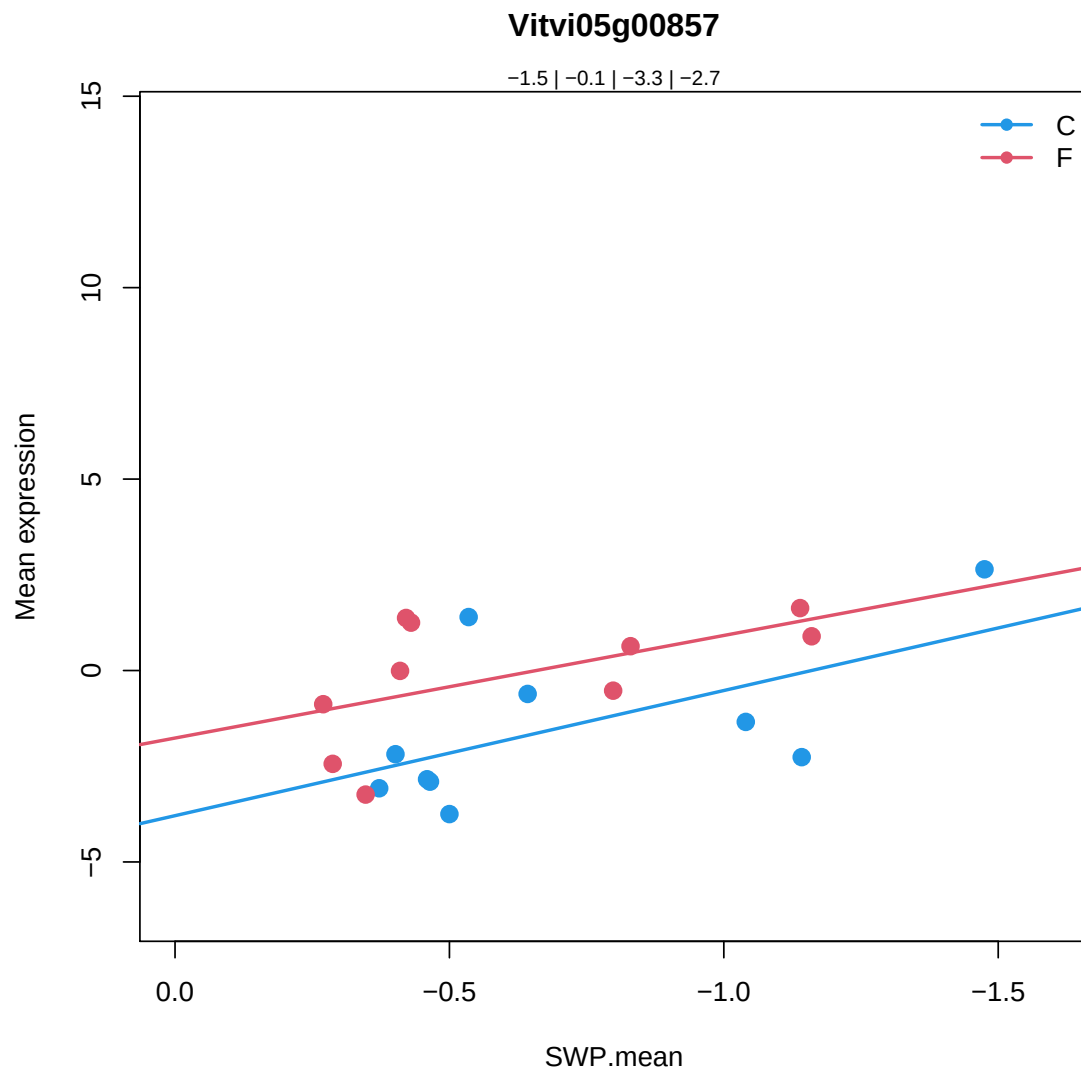
AWPM-19-like family protein |

Chr1:1245070-1245888 FORWARD LENGTH=186 |

201606

Coefficients for Vitvi05g00857.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.493231	0.003146049	**	0.003369788	**
SlopeC	-3.268603	0.01595194	*	0.3483374	
MeanF-MeanC	1.361971	0.04355944	*	0.2186479	
SlopeF-SlopeC	0.5892431	0.754362		0.9999488	



8.6.43 Vitvi13g02018: * Type5

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

Vitvi13g02018

20.2.1

stress.abiotic.heat

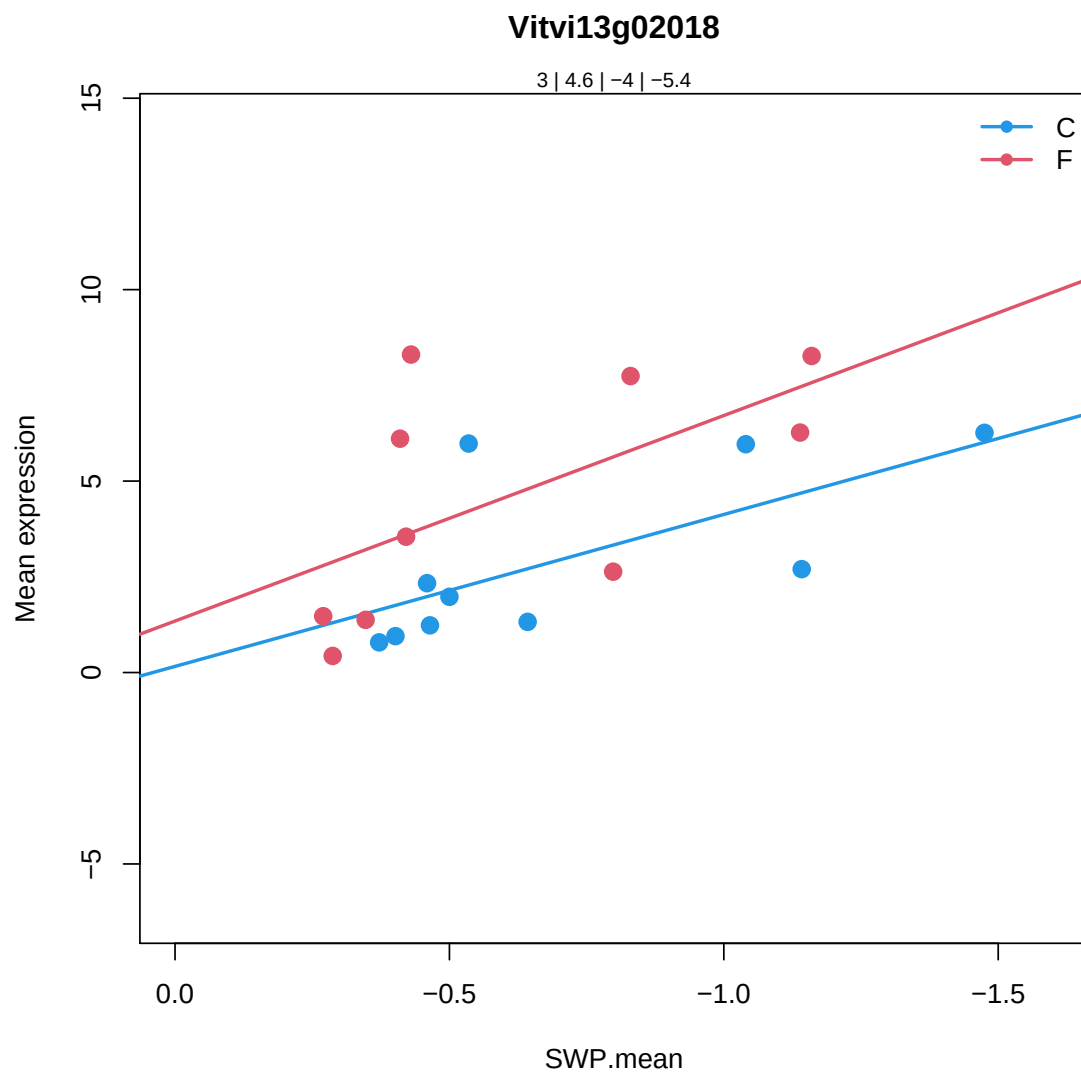
heat shock protein 18.2 |

Chr5:24062632-24063117 FORWARD LENGTH=161 |

201606

Coefficients for Vitvi13g02018.

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



8.6.44 Vitvi07g02242: * Type5

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

Vitvi07g02242

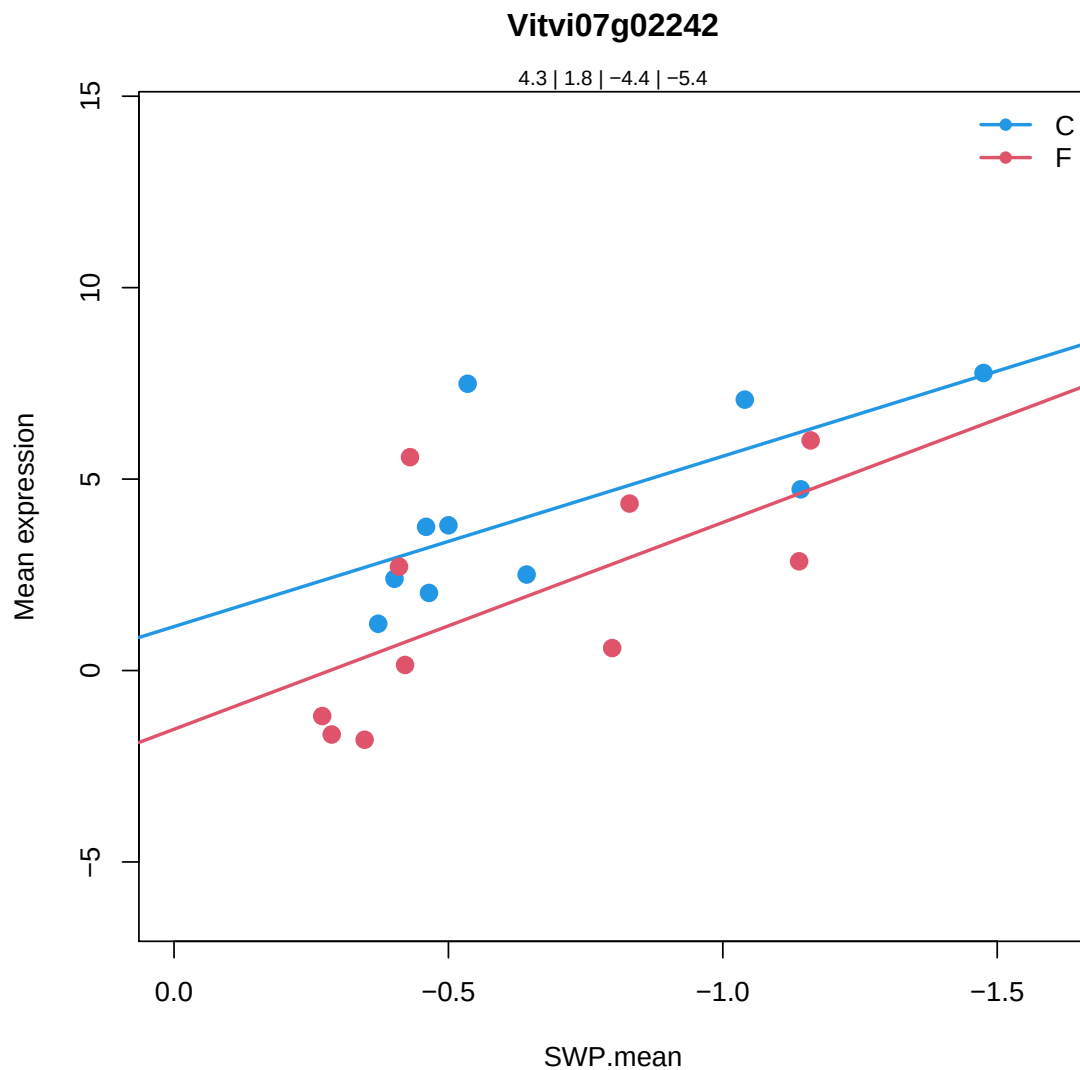
3.1.1.1

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

Chr2:19369049-19370372 REVERSE LENGTH=344 |
201606

Coefficients for Vitvi07g02242.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.276297	3.725657e-07	***	4.348787e-07	***
SlopeC	-4.449677	0.01340344	*	0.3305597	
MeanF-MeanC	-2.519255	0.00668982	**	0.05649099	.
SlopeF-SlopeC	-0.9519606	0.7022784		0.9999488	



8.6.45 Vitvi09g00599: * Type5

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

Vitvi09g00599

20.2.1

stress.abiotic.heat

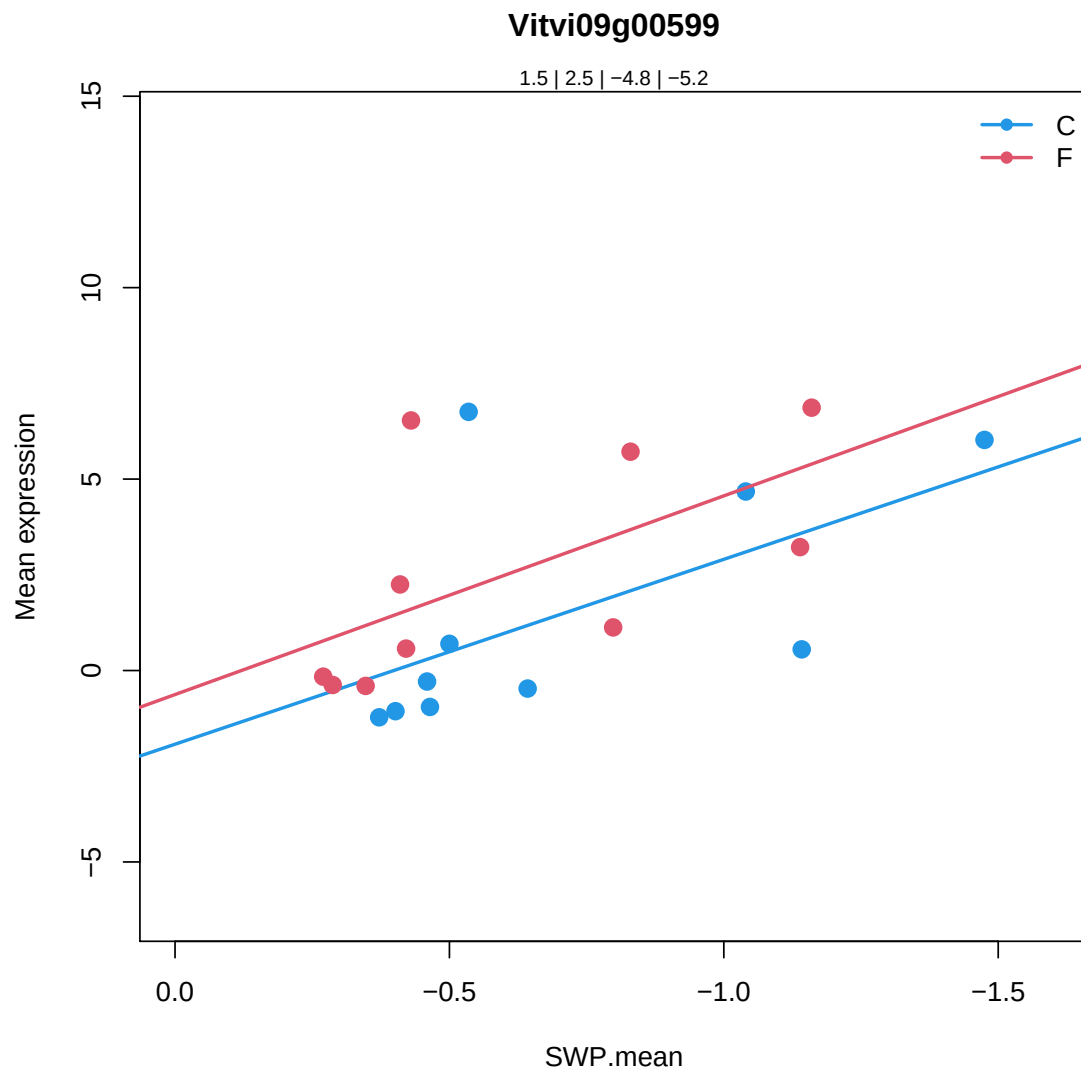
HSP20-like chaperones superfamily protein |

Chr1:19574783-19575766 REVERSE LENGTH=232 |

201606

Coefficients for Vitvi09g00599.

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



8.6.46 Vitvi16g01103: * Type5

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

Vitvi16g01103

20.2.1

stress.abiotic.heat

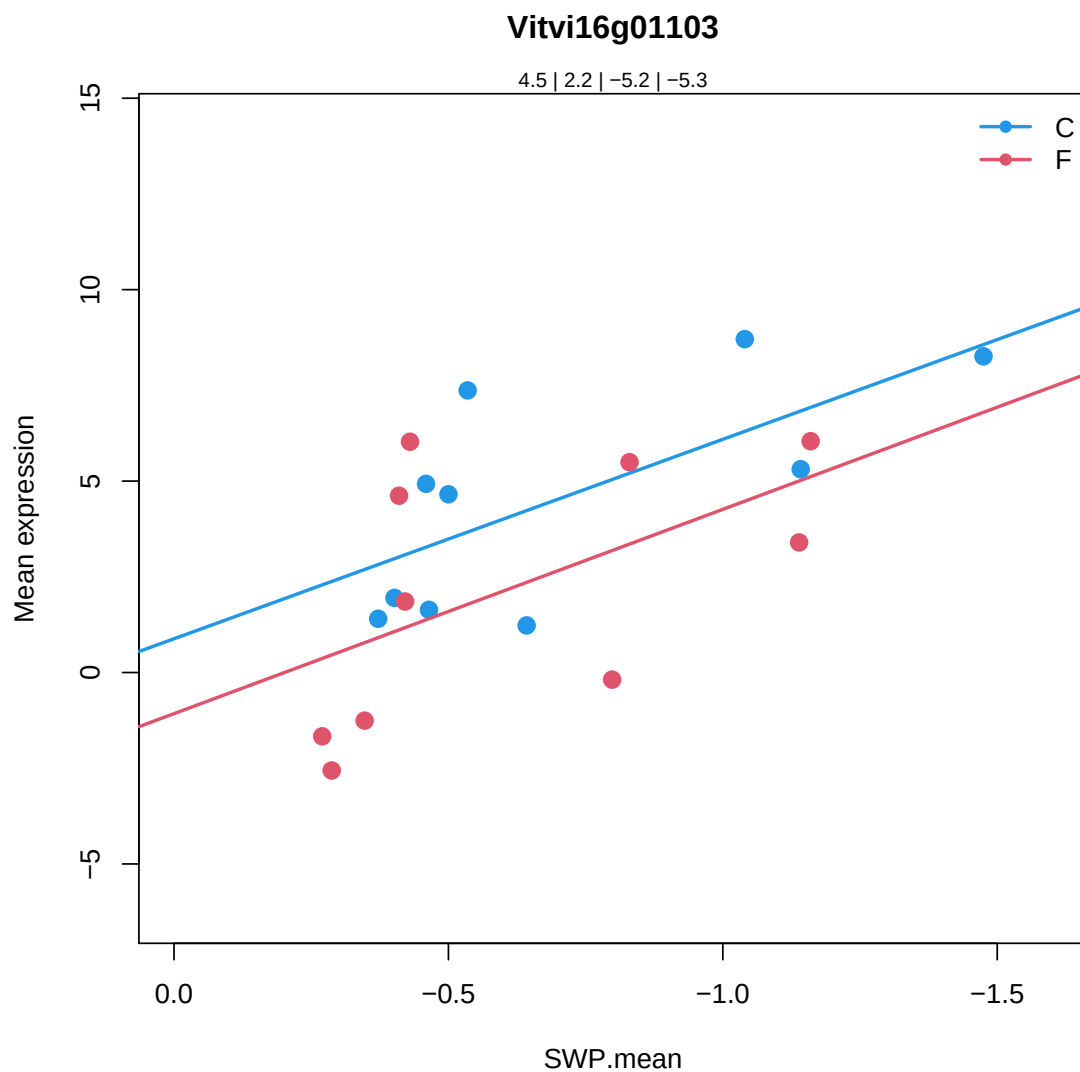
heat shock-like protein |

Chr5:21352557-21355147 FORWARD LENGTH=700 |

201606

Coefficients for Vitvi16g01103.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.544681	3.332247e-06	***	3.801939e-06	***
SlopeC	-5.209495	0.01806874	*	0.3612388	
MeanF-MeanC	-2.368196	0.03229181	*	0.1781367	
SlopeF-SlopeC	-0.1260899	0.9671792		0.9999488	



8.7 Type6.C

8.7.1 Vitvi18g03084: * Type6.C

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

Vitvi18g03084

30.2.25

signalling.receptor kinases.wall associated kinase

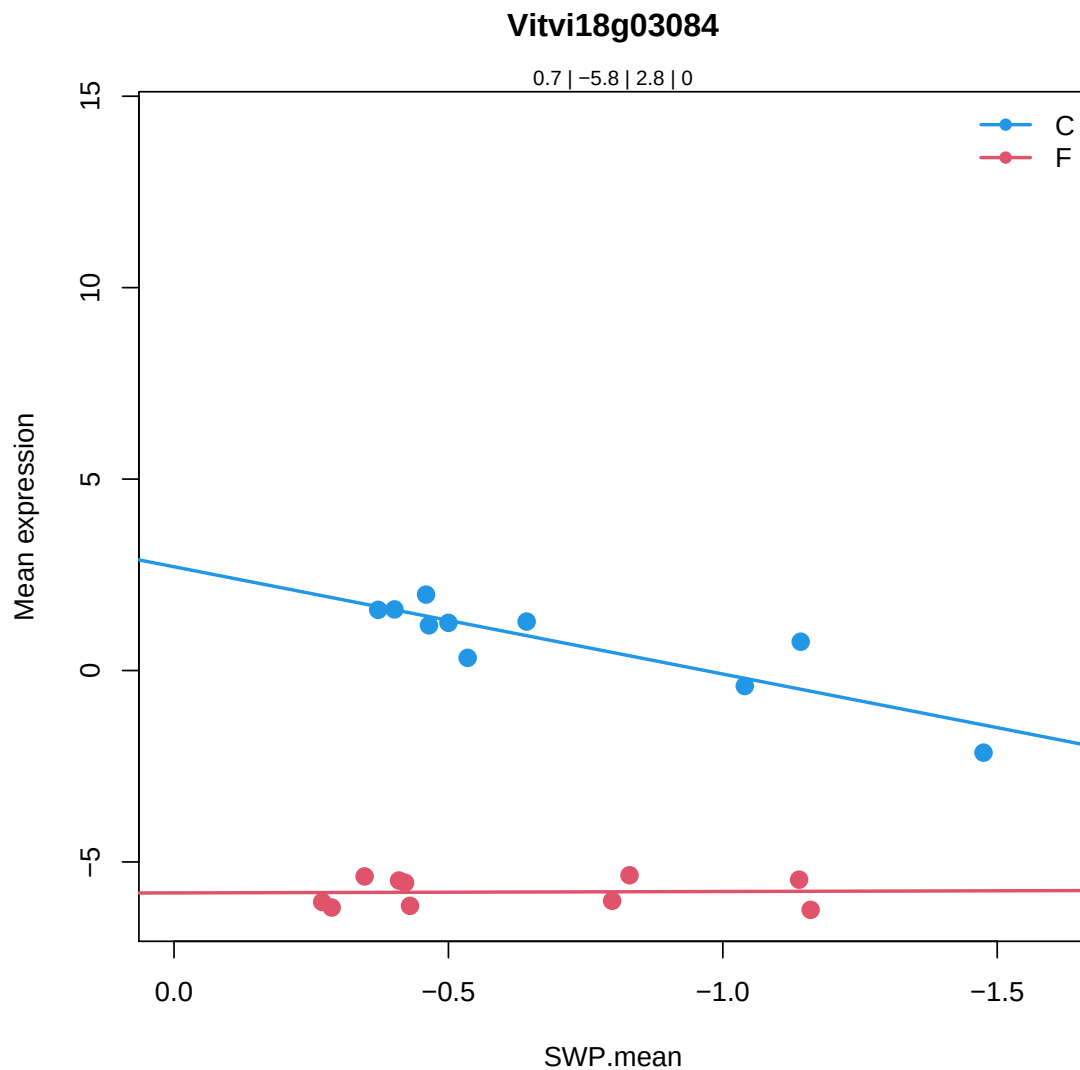
Protein kinase family protein |

Chr3:9241725-9243113 FORWARD LENGTH=433 |

201606

Coefficients for Vitvi18g03084.

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



8.7.2 Vitvi16g02090: * Type6.C

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

```
Vitvi16g02090
```

```
35.2
```

```
not assigned.unknown
```

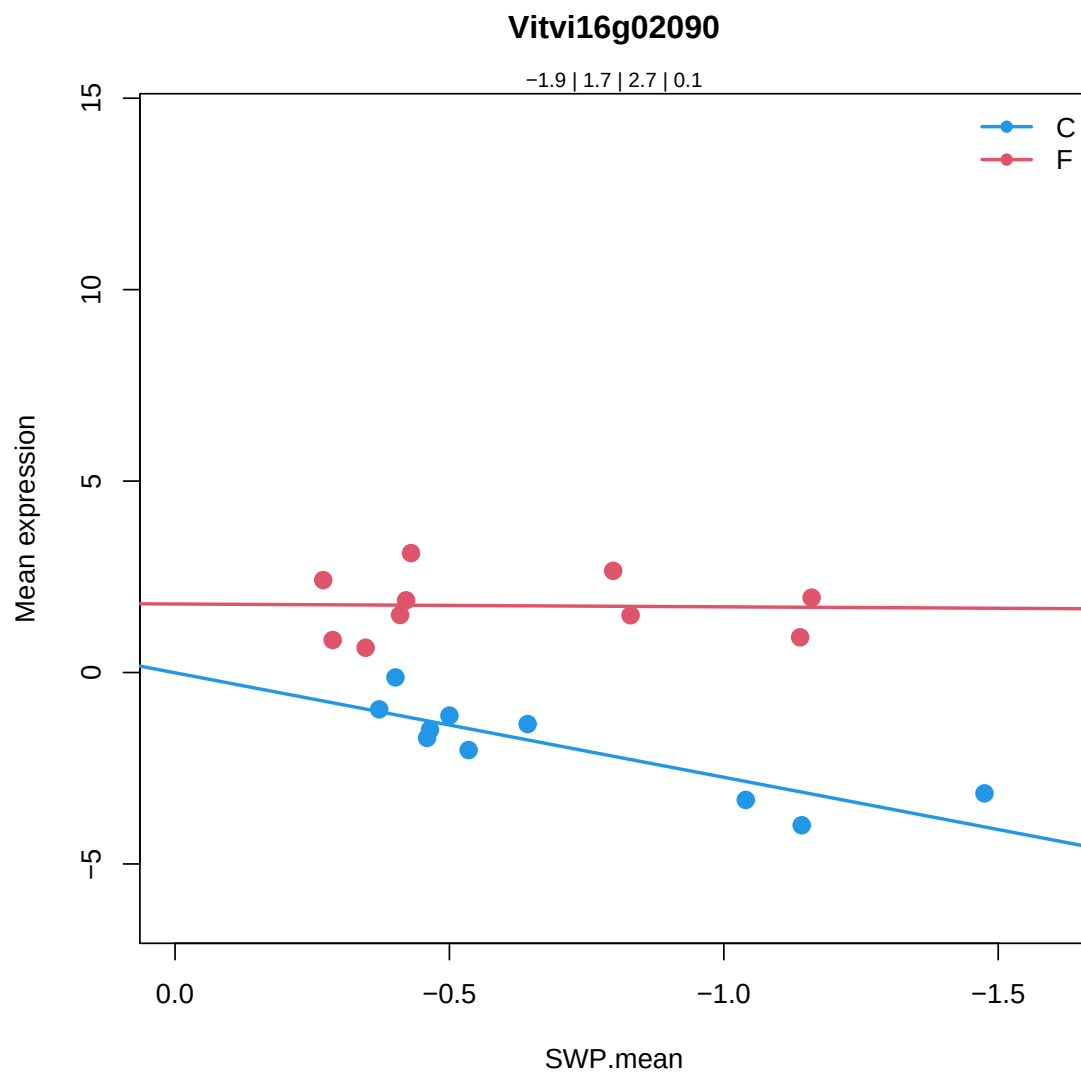
```
PR5-like receptor kinase |
```

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

```
201606
```

Coefficients for Vitvi16g02090.

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



8.7.3 Vitvi16g02003: * Type6.C

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

Vitvi16g02003

35.2

not assigned.unknown

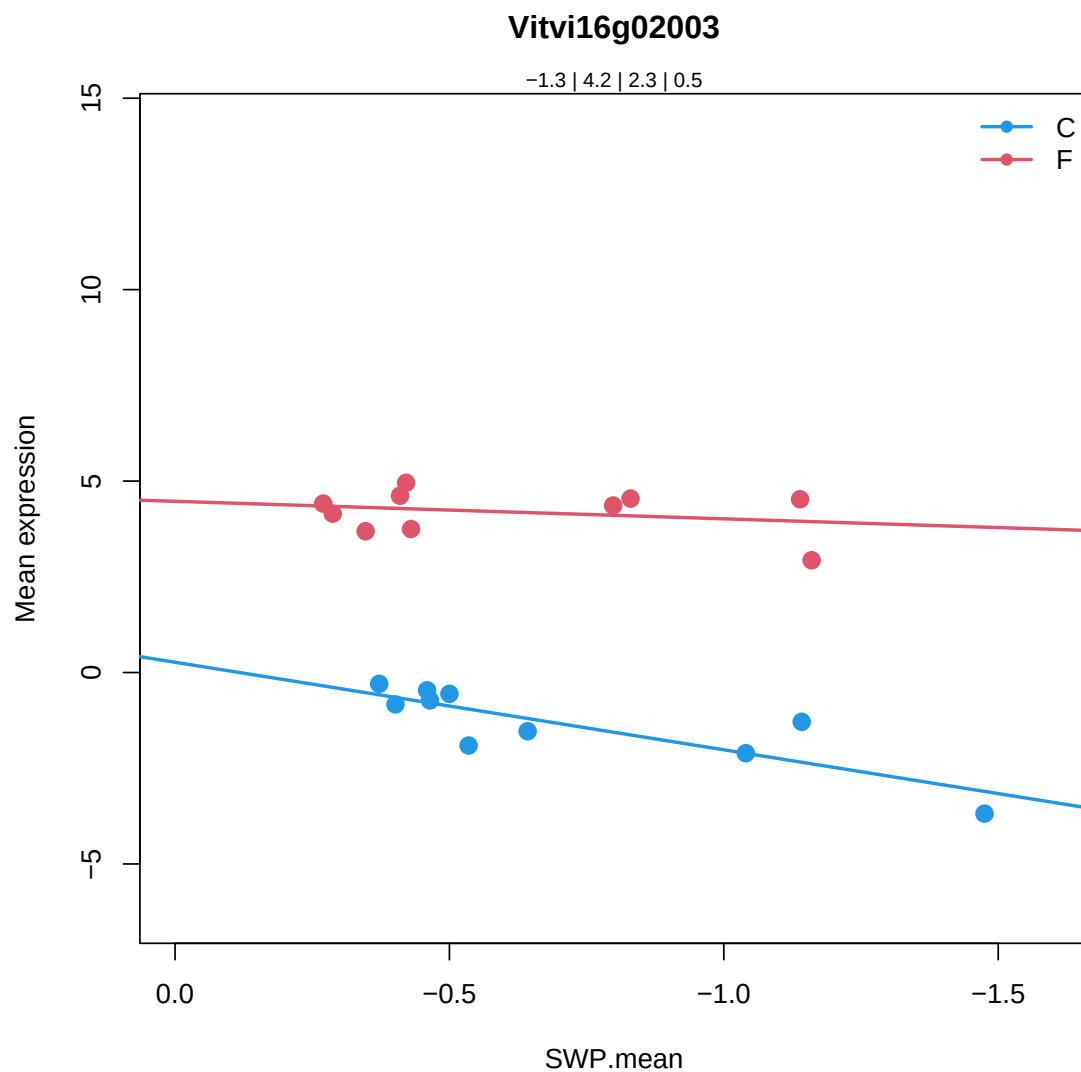
PR5-like receptor kinase |

Chr5:15293325-15295838 REVERSE LENGTH=665 |

201606

Coefficients for Vitvi16g02003.

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



8.7.4 Vitvi16g01548: * Type6.C

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

Vitvi16g01548

35.2

not assigned.unknown

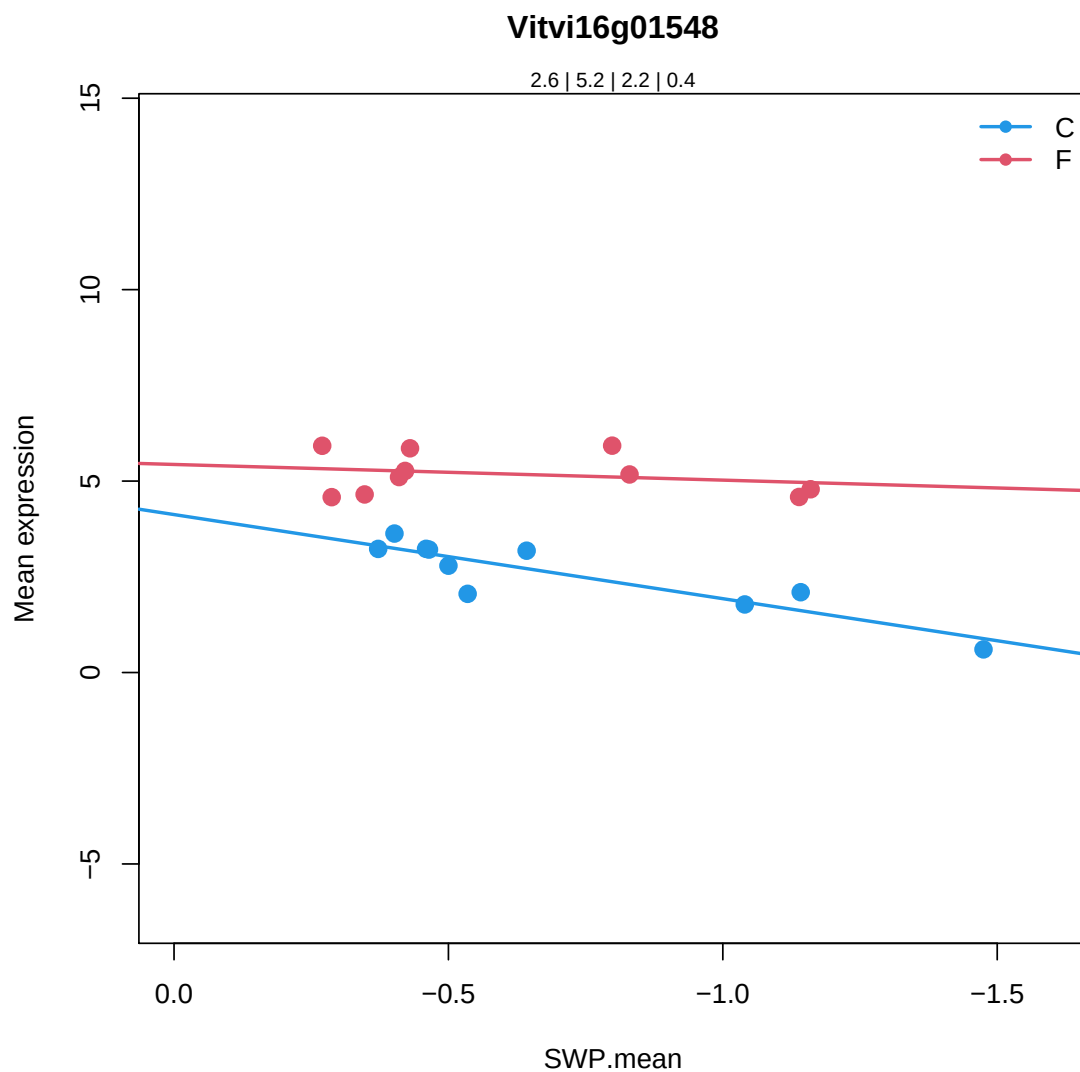
dihydroflavonol 4-reductase |

Chr5:17164296-17165864 REVERSE LENGTH=382 |

201606

Coefficients for Vitvi16g01548.

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



8.7.5 Vitvi09g00681: * Type6.C

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

Vitvi09g00681

20.1.2

stress.biotic.receptors

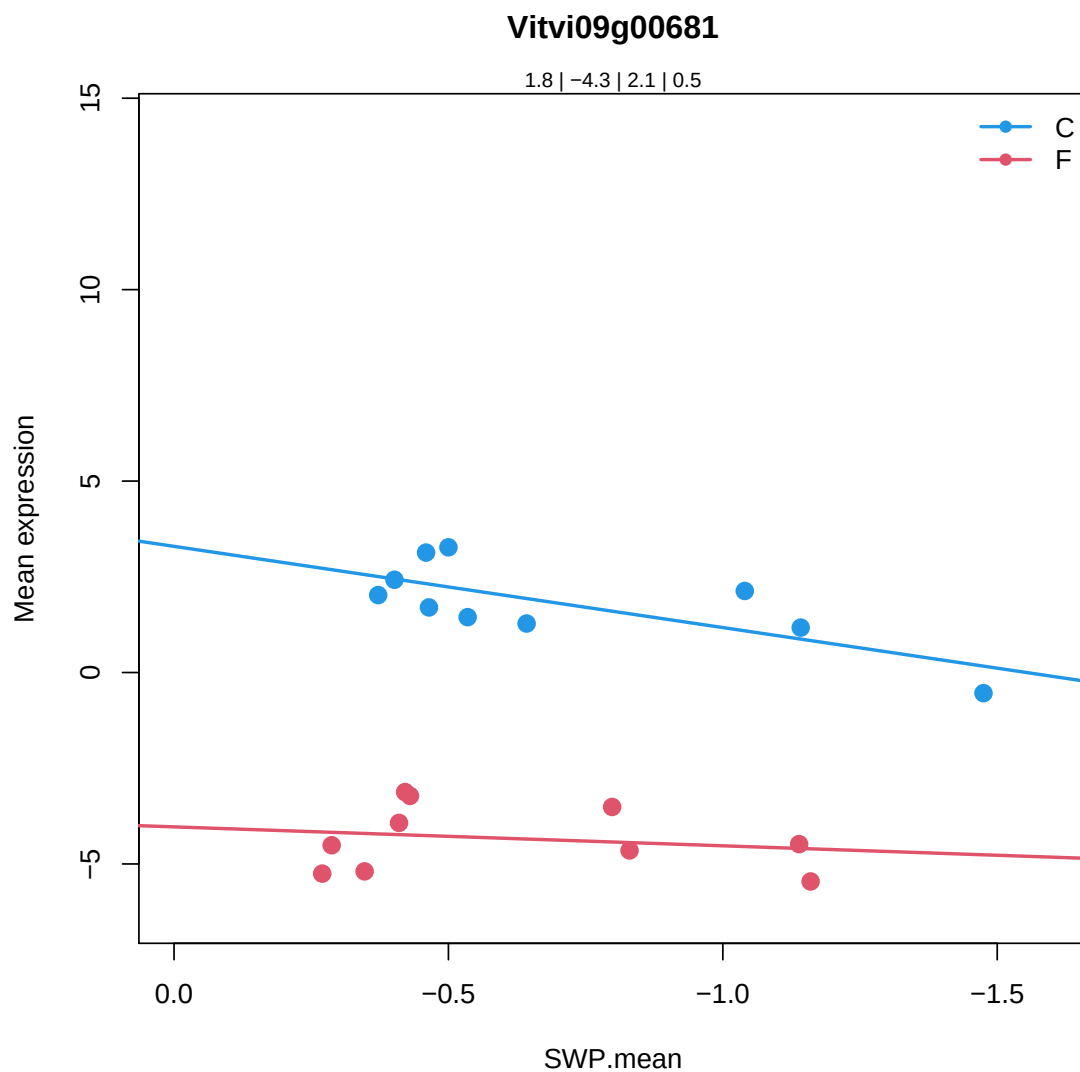
receptor like protein 1 |

Chr1:2270633-2274654 FORWARD LENGTH=913 |

201606

Coefficients for Vitvi09g00681.

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



8.7.6 Vitvi12g00606: * Type6.C

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

```
Vitvi12g00606
```

```
29.4
```

```
protein.postranslational modification
```

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

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

```
201606
```

```
Vitvi12g00606
```

```
30.2.24
```

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

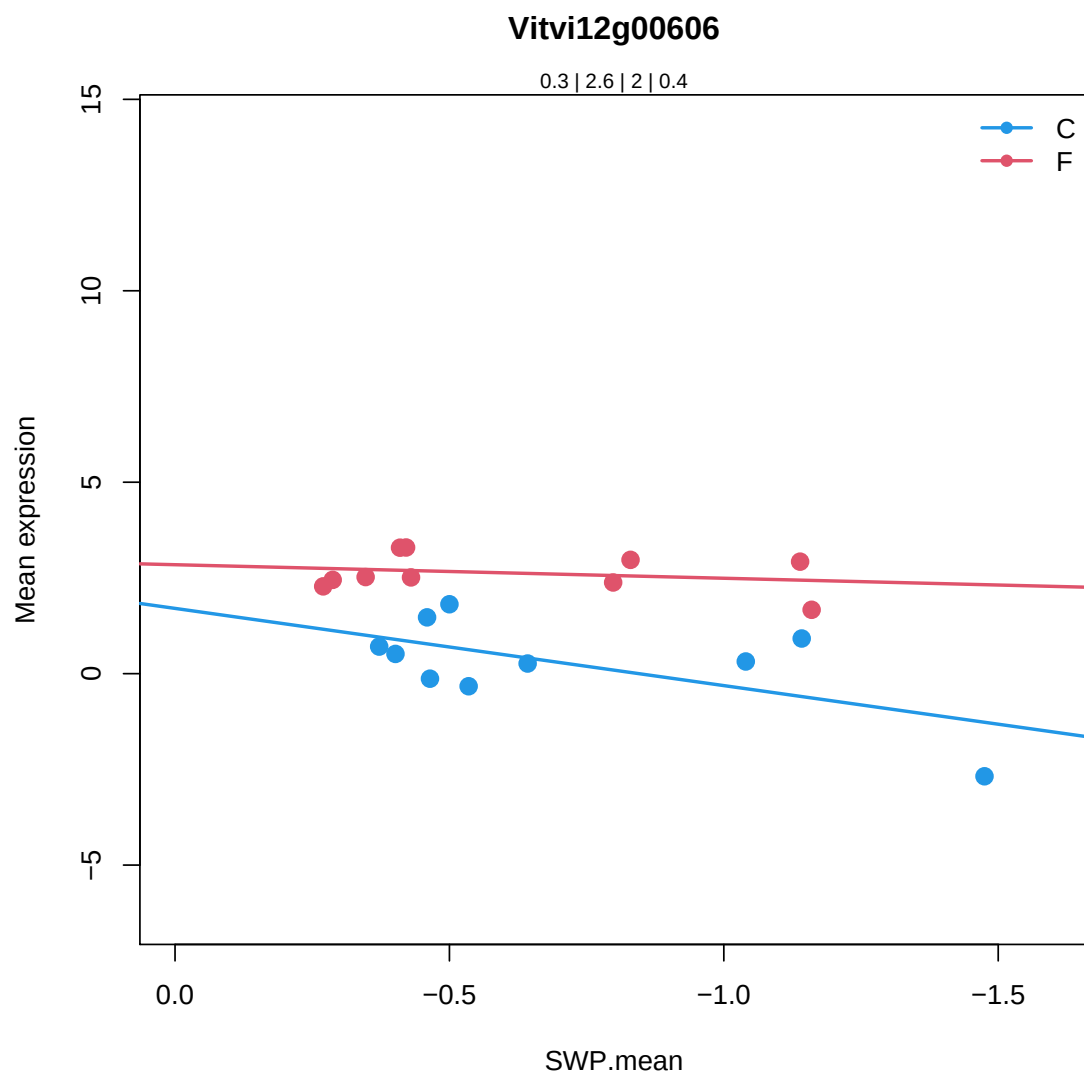
```
G-type lectin S-receptor-like Serine/Threonine-kinase |
```

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

```
201606
```

Coefficients for Vitvi12g00606.

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



8.7.7 Vitvi07g02459: * Type6.C

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

Vitvi07g02459

35.2

not assigned.unknown

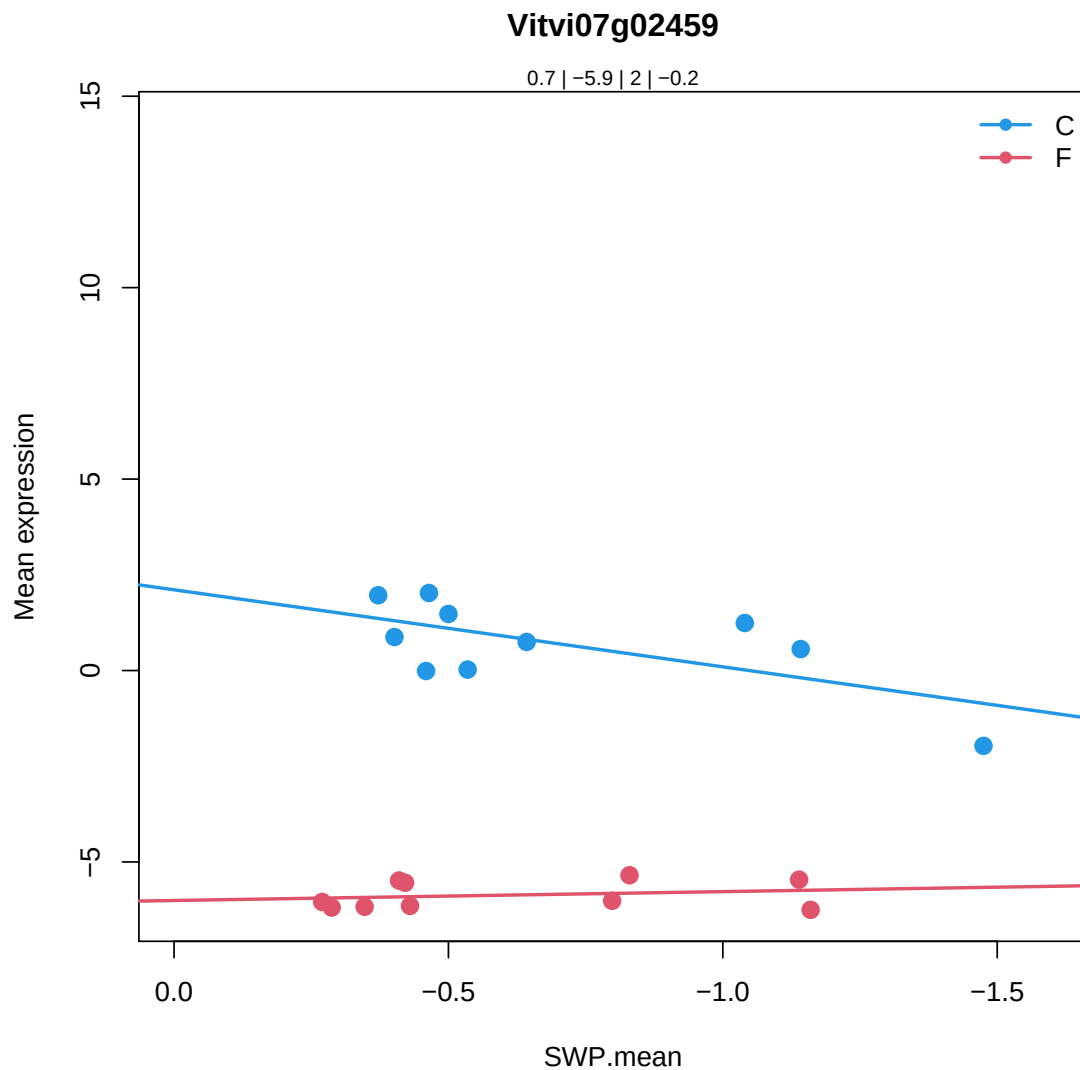
Ankyrin repeat family protein |

Chr5:1349781-1352525 REVERSE LENGTH=625 |

201606

Coefficients for Vitvi07g02459.

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



8.7.8 Vitvi08g00723: * Type6.C

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

Vitvi08g00723

34.5

transport.ammonium

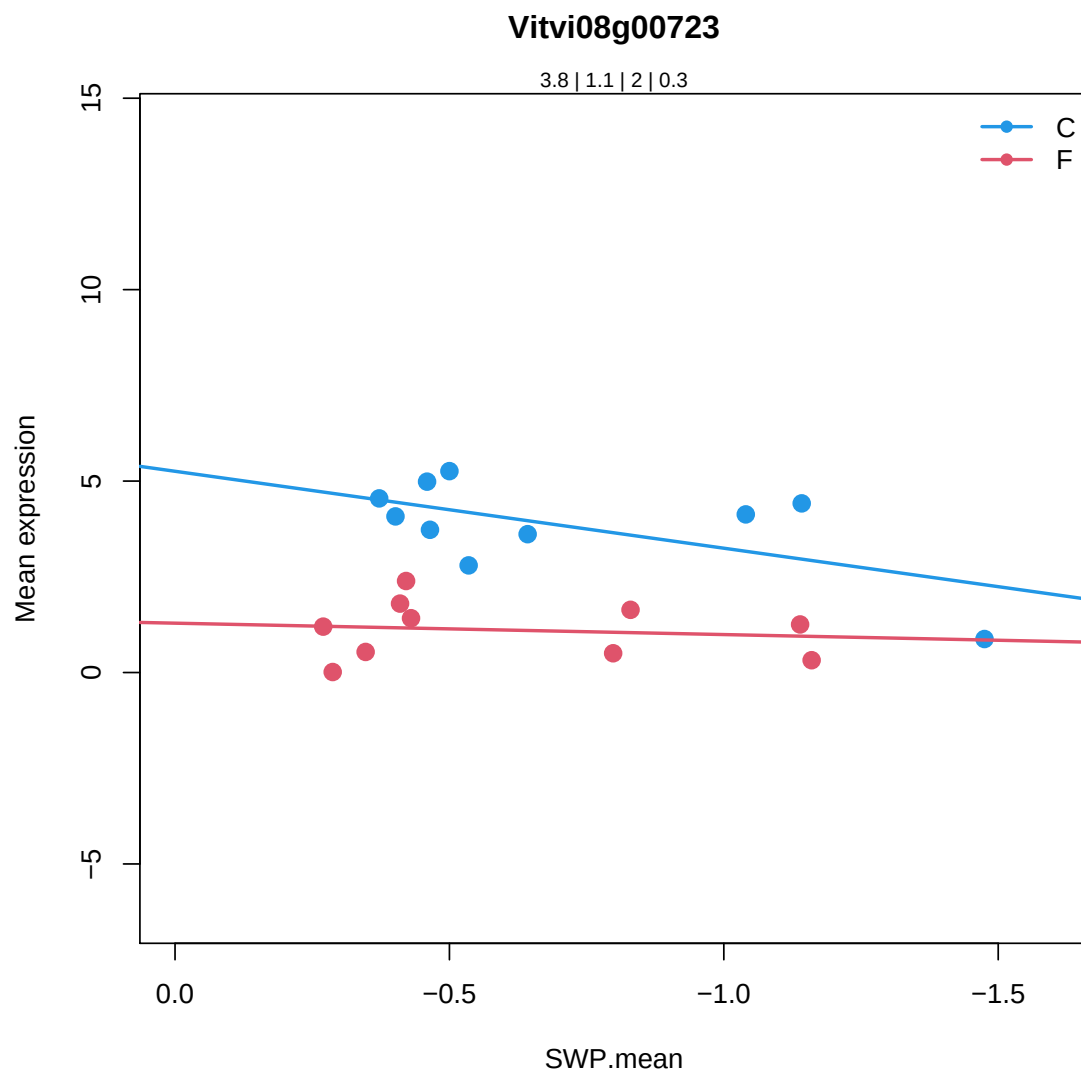
ammonium transporter 2 |

Chr2:16039672-16042291 REVERSE LENGTH=475 |

201606

Coefficients for Vitvi08g00723.

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



8.7.9 Vitvi16g01010: * Type6.C

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

Vitvi16g01010

35.2

not assigned.unknown

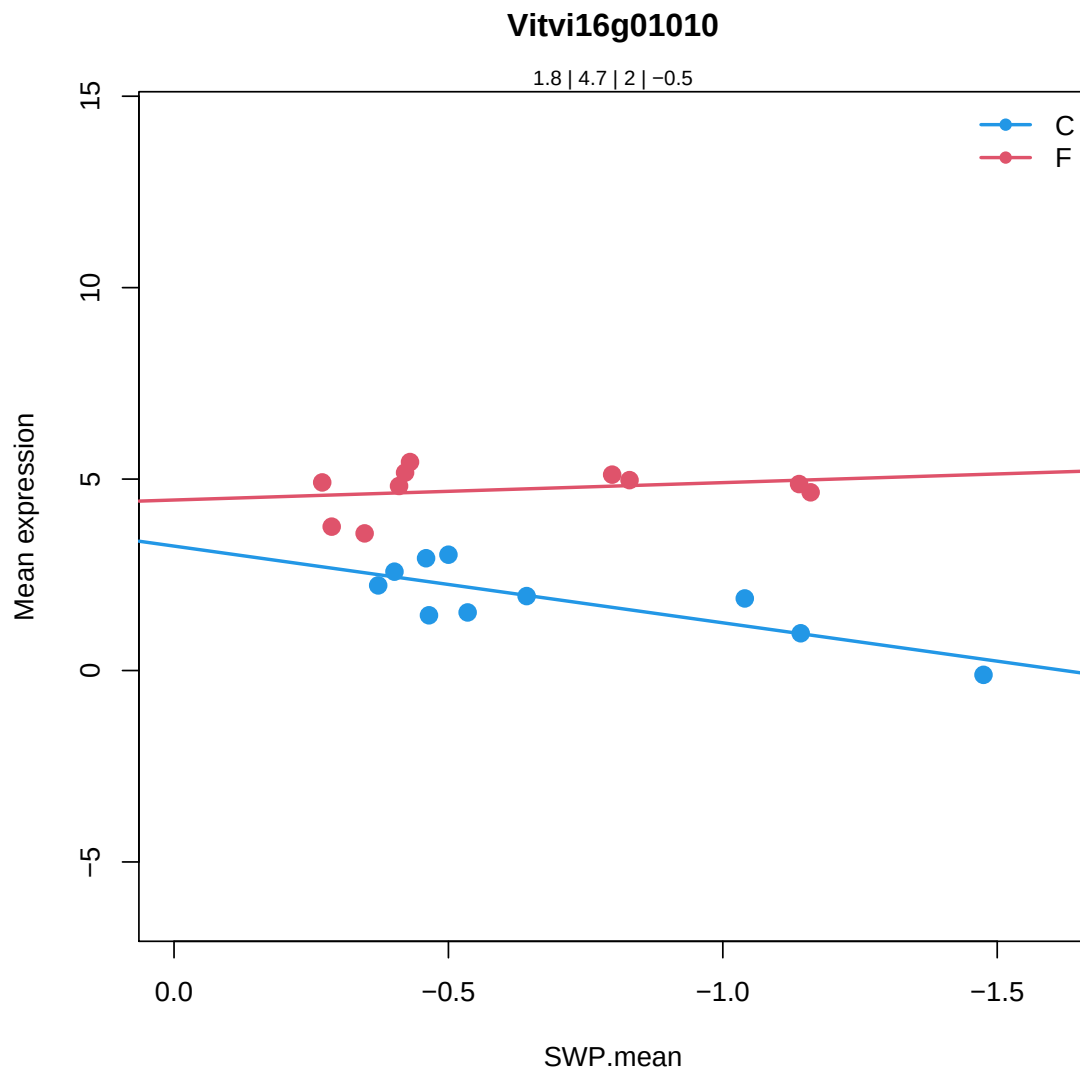
suppressor of npr1-1 constitutive 4 |

Chr1:24997491-25001961 REVERSE LENGTH=1101 |

201606

Coefficients for Vitvi16g01010.

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



8.7.10 Vitvi14g03027: * Type6.C

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

Vitvi14g03027

35.2

not assigned.unknown

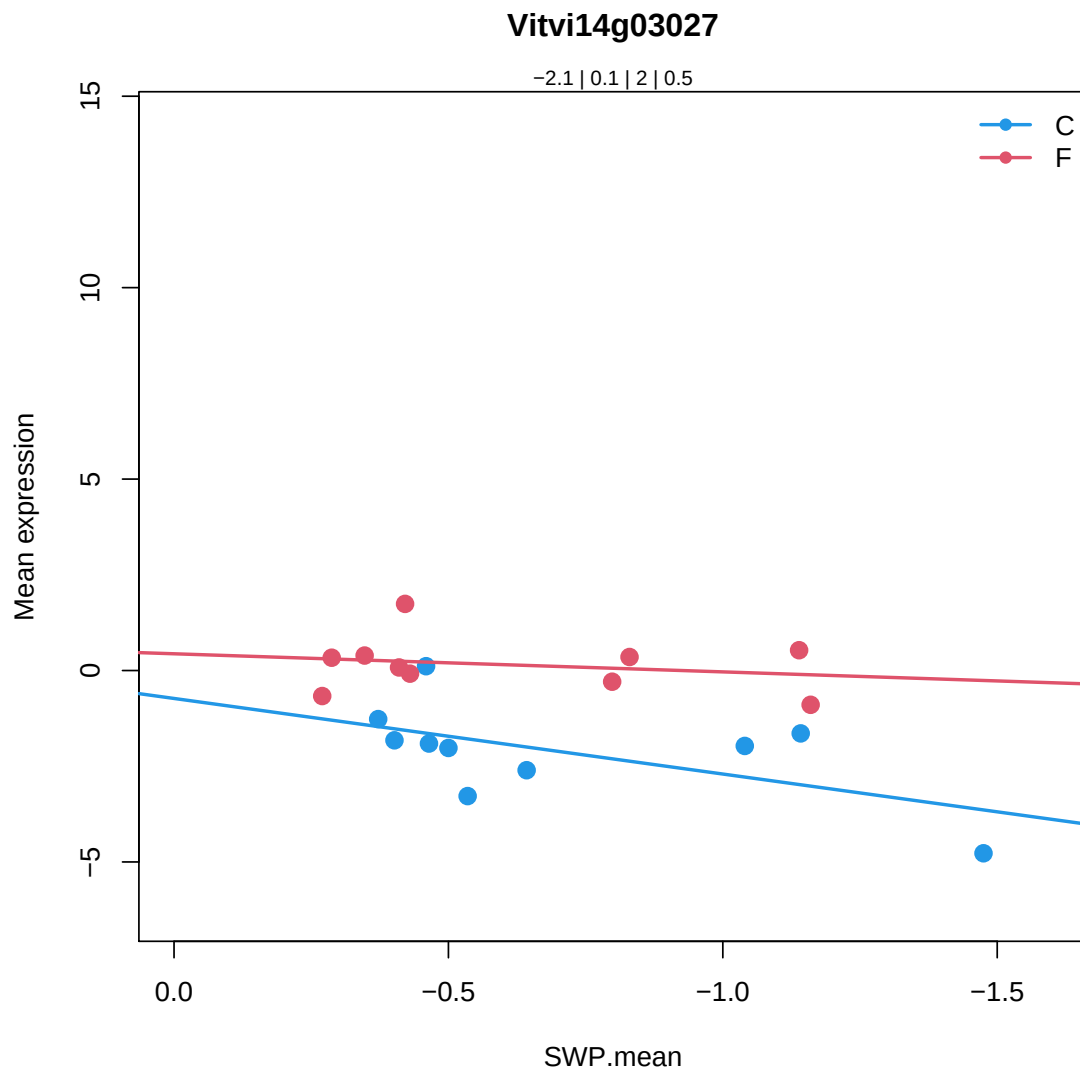
transmembrane protein |

Chr1:8425981-8427045 REVERSE LENGTH=354 |

201606

Coefficients for Vitvi14g03027.

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



8.7.11 Vitvi12g02241: * Type6.C

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

Vitvi12g02241

26.6

misc.O-methyl transferases

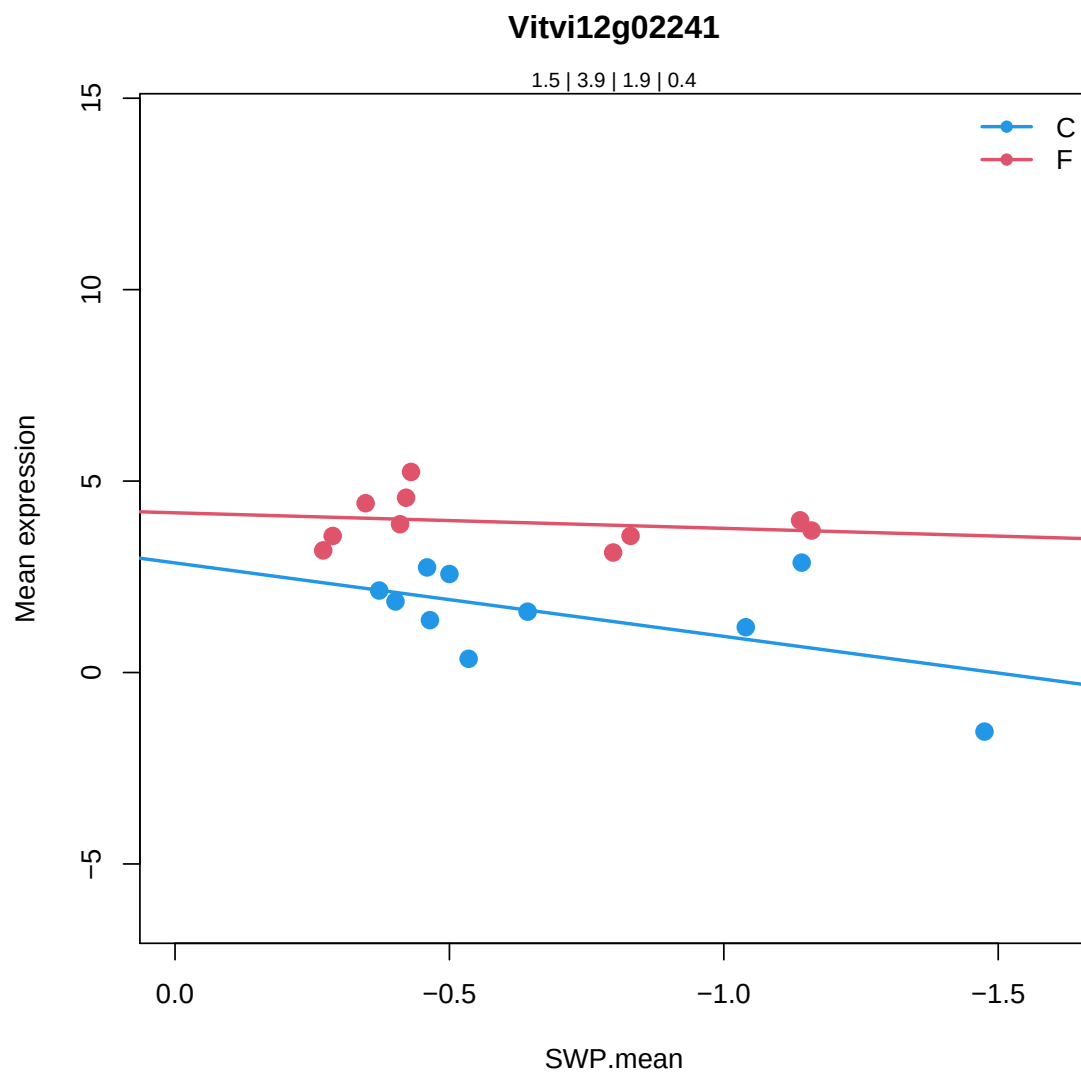
O-methyltransferase family protein |

Chr4:16730989-16732808 REVERSE LENGTH=382 |

201606

Coefficients for Vitvi12g02241.

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



8.7.12 Vitvi16g01695: * Type6.C

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

Vitvi16g01695

35.2

not assigned.unknown

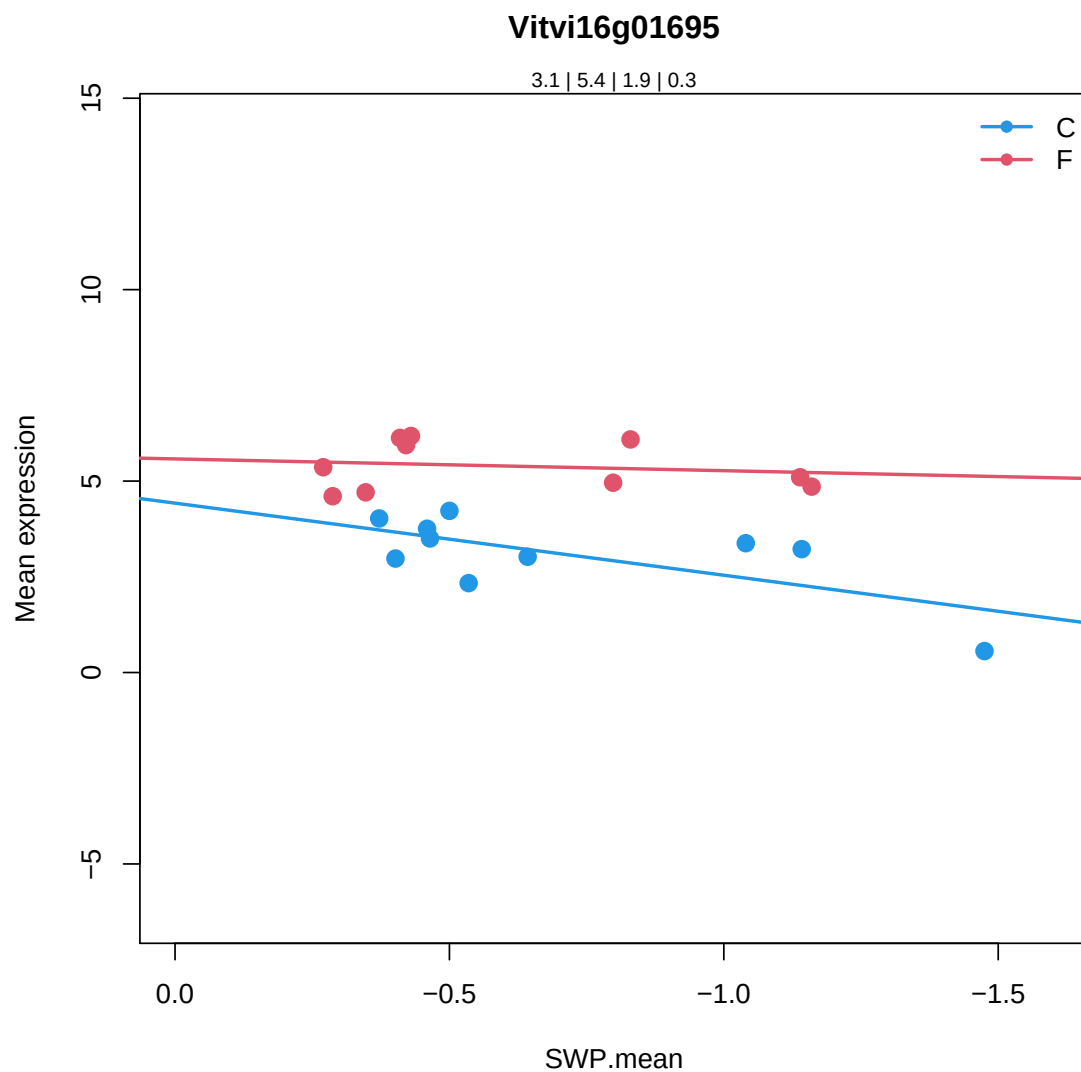
receptor like protein 6 |

Chr1:17183550-17186534 REVERSE LENGTH=994 |

201606

Coefficients for Vitvi16g01695.

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

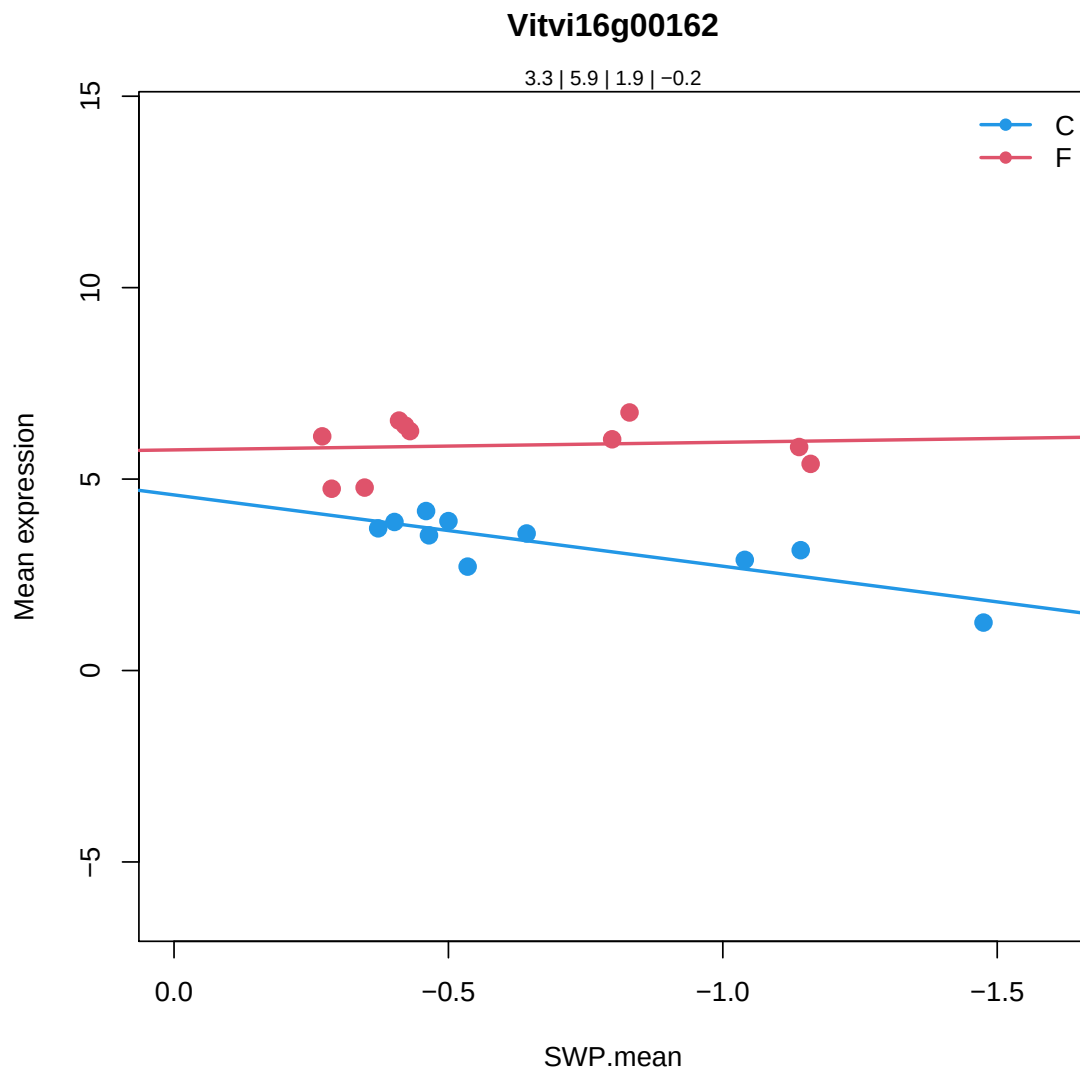


8.7.13 Vitvi16g00162: * Type6.C

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

Coefficients for Vitvi16g00162.

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



8.7.14 Vitvi07g01975: * Type6.C

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

Vitvi07g01975

35.2

not assigned.unknown

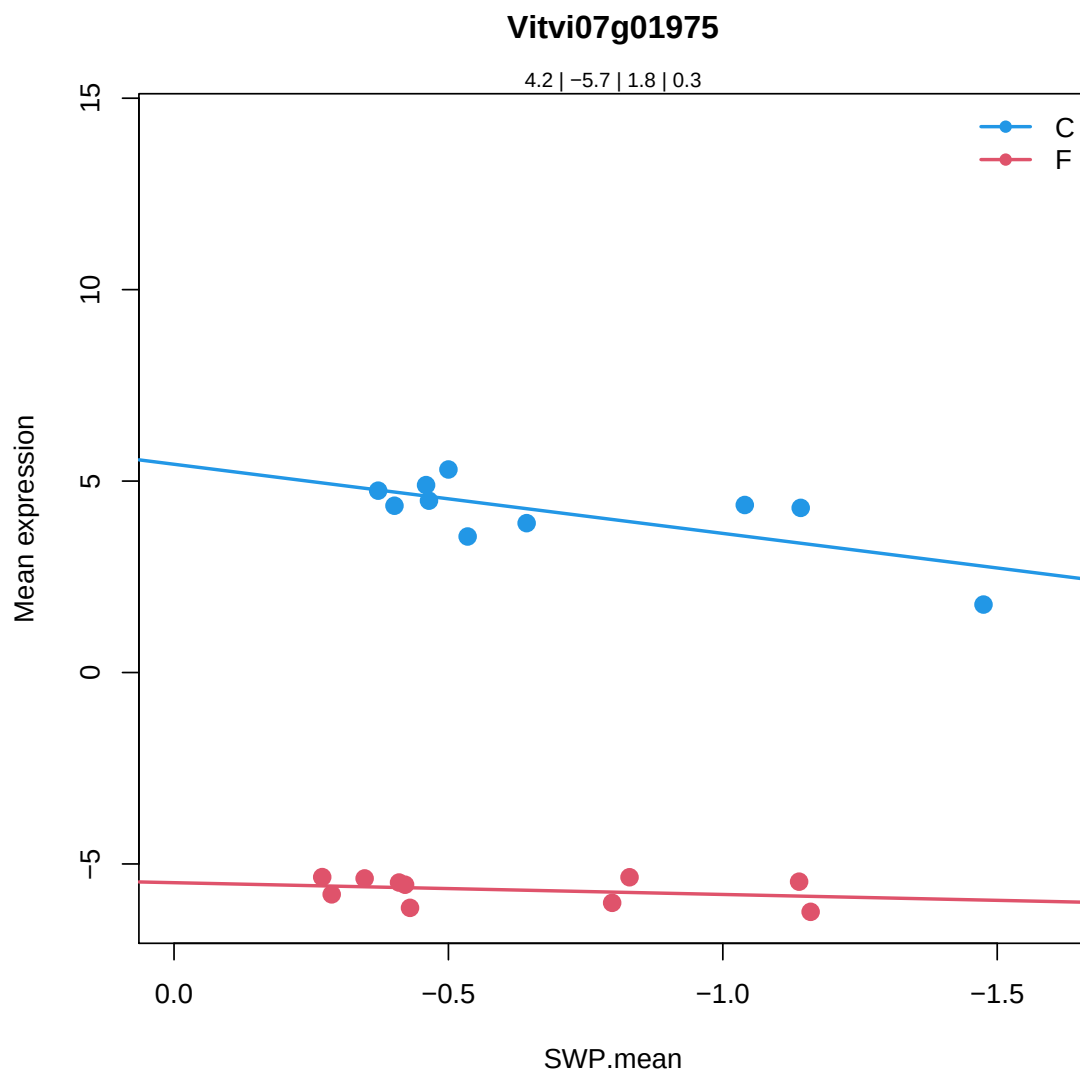
ammonium transporter 2 |

Chr2:16039672-16042291 REVERSE LENGTH=475 |

201606

Coefficients for Vitvi07g01975.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	4.169379	6.951417e-17	***	1.554254e-16	***
SlopeC	1.805957	0.001302019	**	0.1417527	
MeanF-MeanC	-9.845904	1.491184e-21	***	9.882012e-19	***
SlopeF-SlopeC	-1.498707	0.05160997	.	0.9999488	



8.7.15 Vitvi12g02434: * Type6.C

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi12g02434

29.4

protein.postranslational modification

G-type lectin S-receptor-like Serine/Threonine-kinase |

Chr4:1419278-1422828 REVERSE LENGTH=1010 |

201606

Vitvi12g02434

30.2.24

signalling.receptor kinases.S-locus glycoprotein like

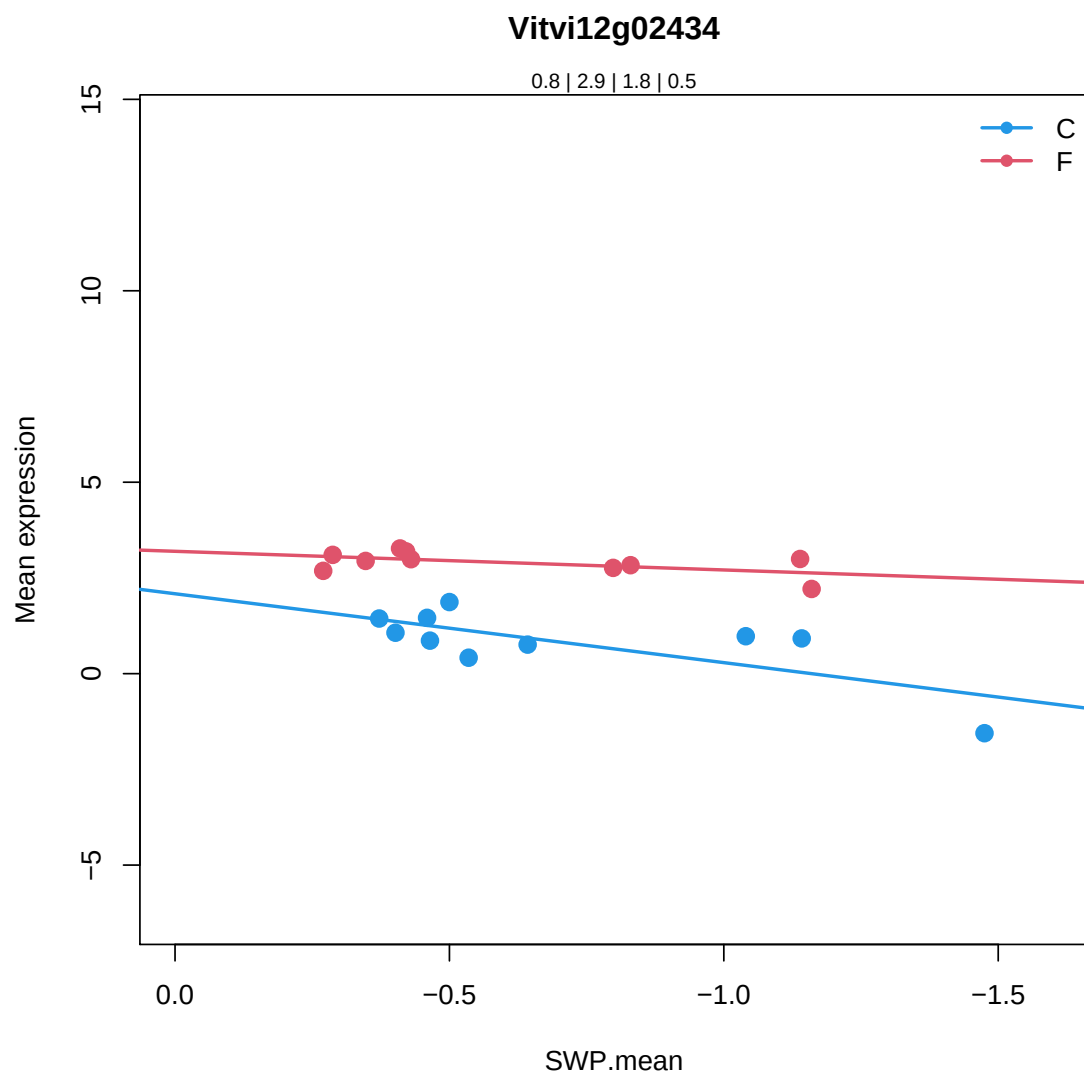
G-type lectin S-receptor-like Serine/Threonine-kinase |

Chr4:1419278-1422828 REVERSE LENGTH=1010 |

201606

Coefficients for Vitvi12g02434.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.8214444	4.165707e-05	***	4.635592e-05	***
SlopeC	1.798958	0.0005749267	***	0.1005065	
MeanF-MeanC	2.077066	7.184554e-09	***	3.638105e-07	***
SlopeF-SlopeC	-1.311562	0.06099283	.	0.9999488	



8.7.16 Vitvi17g01499: * Type6.C

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi17g01499

26.2

misc.UDP glucosyl and glucoronyl transferases

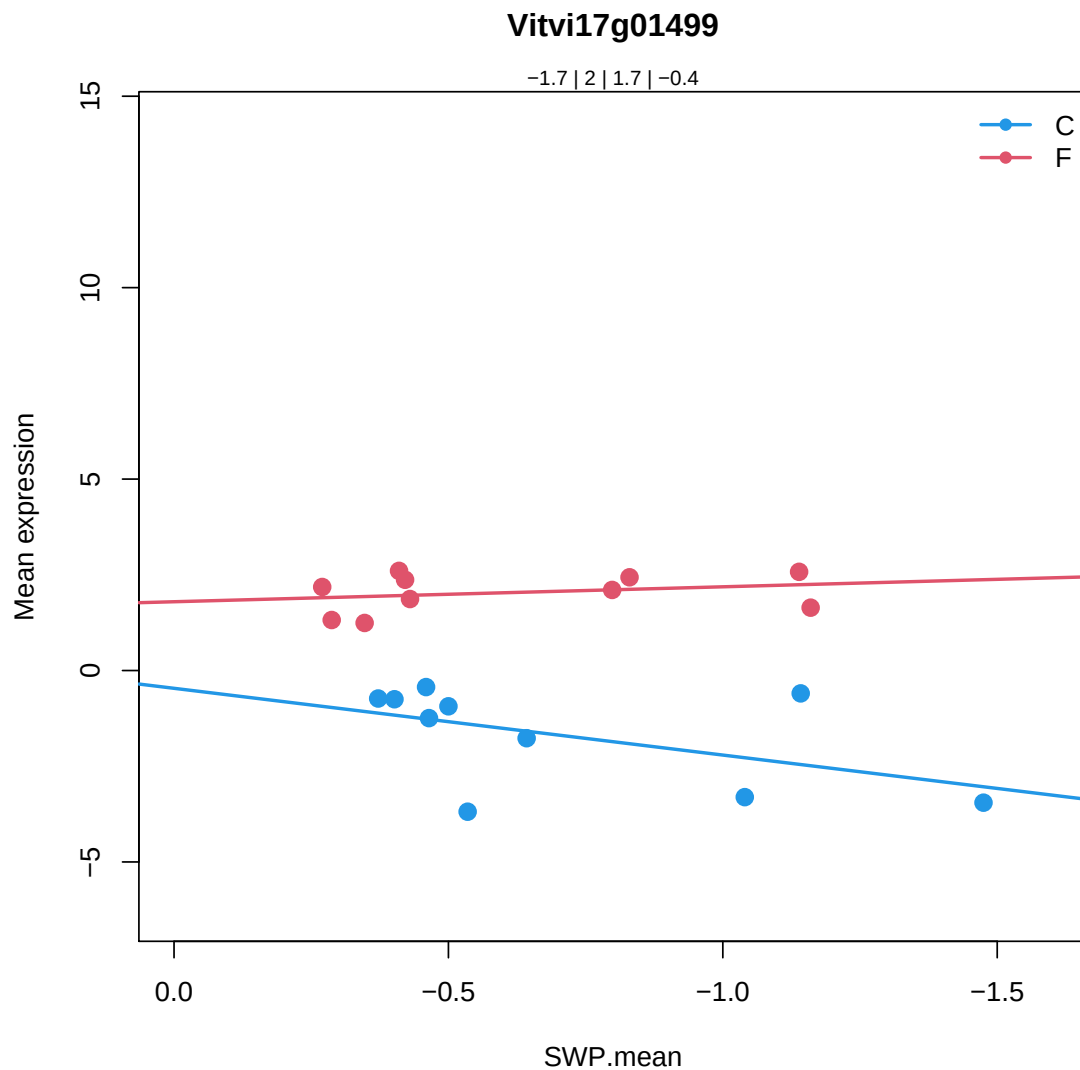
UDP-Glycosyltransferase superfamily protein |

Chr3:368840-370484 REVERSE LENGTH=464 |

201606

Coefficients for Vitvi17g01499.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.690499	1.763896e-06	***	2.024953e-06	***
SlopeC	1.743445	0.02511451	*	0.4079655	
MeanF-MeanC	3.724487	1.268641e-09	***	7.215157e-08	***
SlopeF-SlopeC	-2.133583	0.06070084	.	0.9999488	



8.7.17 Vitvi09g00253: * Type6.C

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi09g00253

29.4

protein.postranslational modification

Leucine-rich repeat transmembrane protein kinase protein |

Chr4:14665802-14669438 REVERSE LENGTH=876 |

201606

Vitvi09g00253

30.2.1

signalling.receptor kinases.leucine rich repeat I

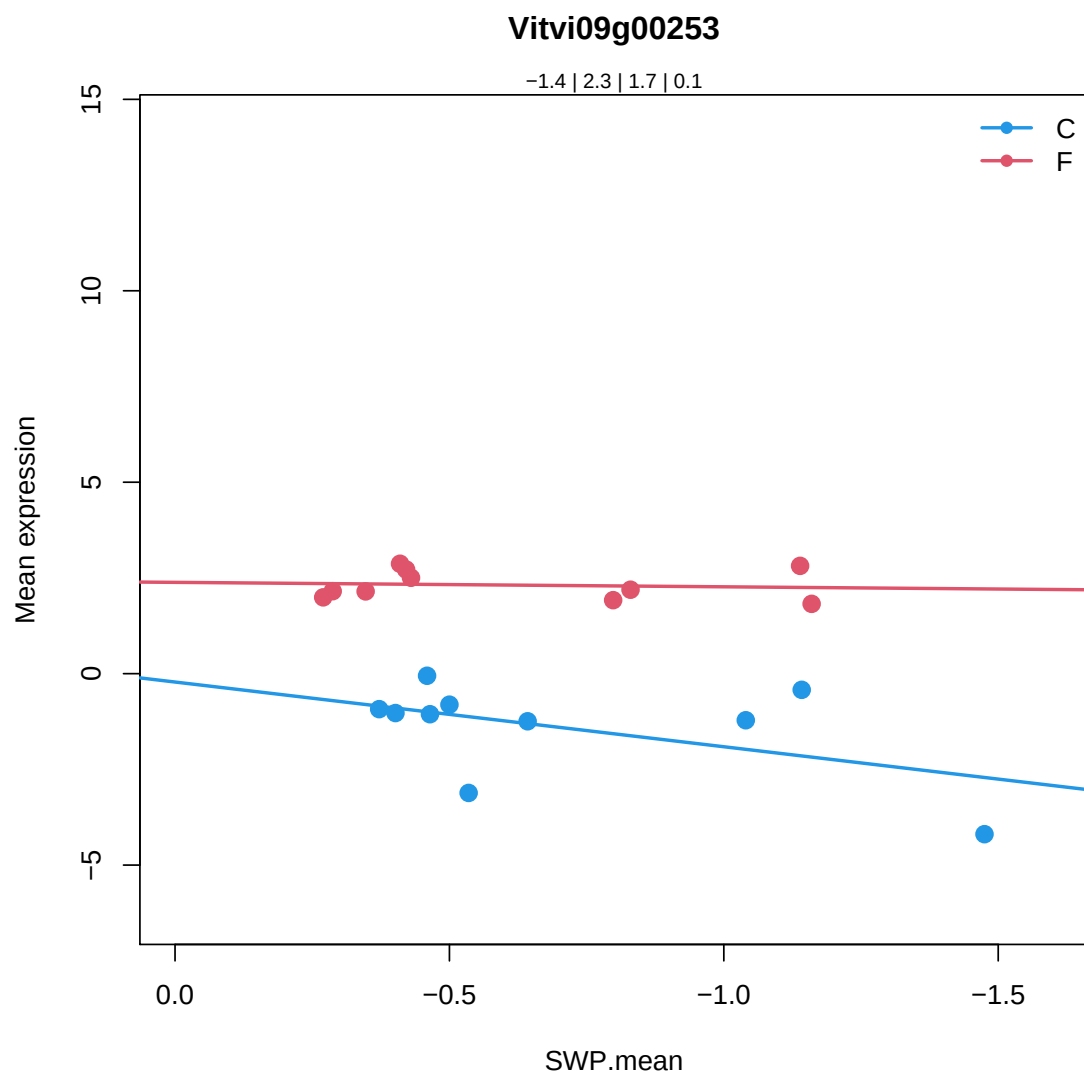
Leucine-rich repeat transmembrane protein kinase protein |

Chr4:14665802-14669438 REVERSE LENGTH=876 |

201606

Coefficients for Vitvi09g00253.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.407384	1.22789e-05	***	1.383771e-05	***
SlopeC	1.690283	0.02356607	*	0.3983963	
MeanF-MeanC	3.721139	5.921833e-10	***	3.639539e-08	***
SlopeF-SlopeC	-1.574086	0.1418375		0.9999488	



8.7.18 Vitvi07g02479: * Type6.C

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi07g02479

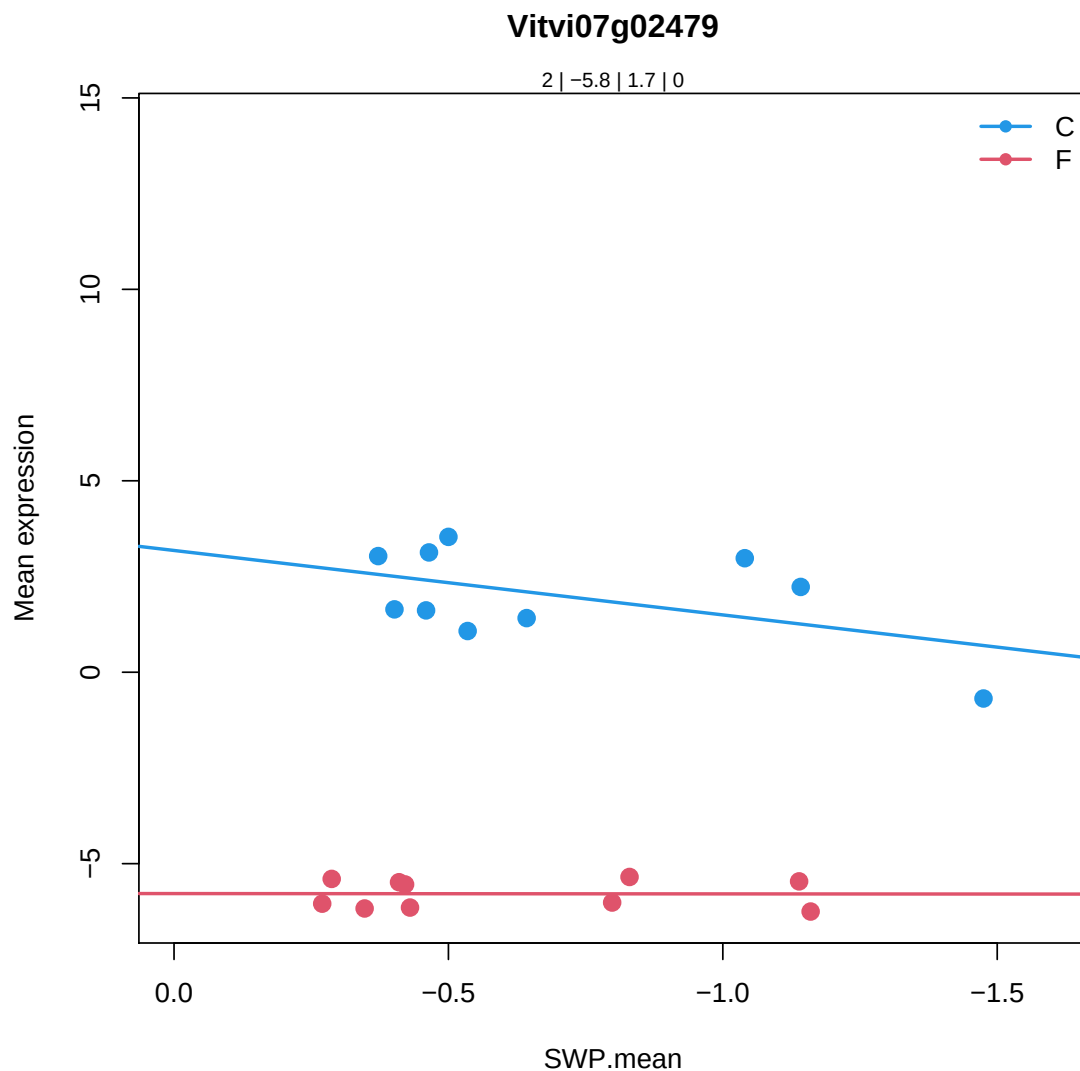
35.2

not assigned.unknown

Serine_threonine-protein phosphatase 6 regulatory ankyrin repeat subun

Coefficients for Vitvi07g02479.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.996167	6.687837e-08	***	7.966241e-08	***
SlopeC	1.683394	0.02375949	*	0.3983963	
MeanF-MeanC	-7.7825	2.962028e-16	***	4.961235e-14	***
SlopeF-SlopeC	-1.67543	0.1182497		0.9999488	



8.7.19 Vitvi07g03003: * Type6.C

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi07g03003

31.1

cell.organisation

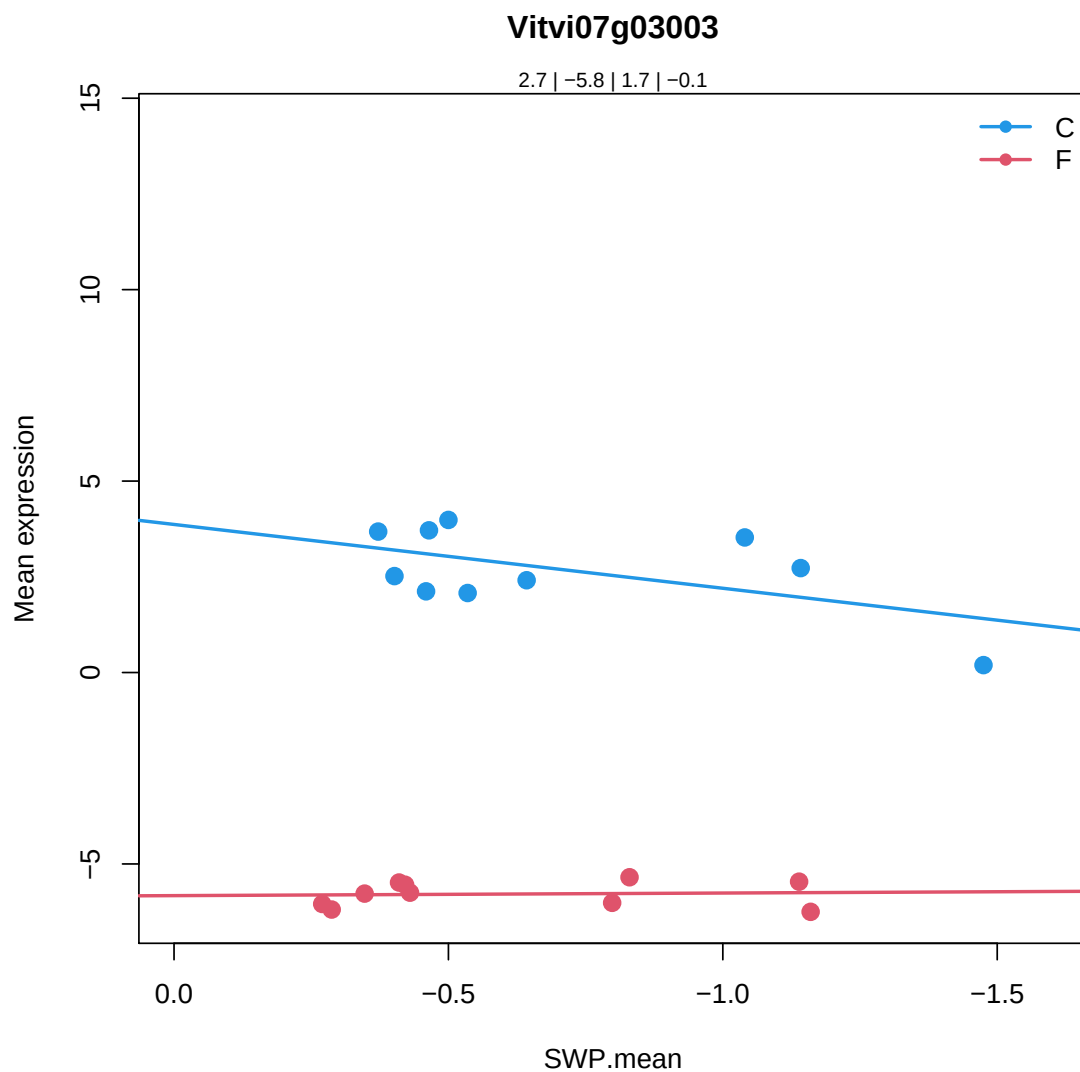
Ankyrin repeat family protein |

Chr3:6424135-6426471 REVERSE LENGTH=653 |

201606

Coefficients for Vitvi07g03003.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.695259	2.950611e-11	***	3.947789e-11	***
SlopeC	1.666543	0.01164374	*	0.318473	
MeanF-MeanC	-8.481592	3.014671e-18	***	7.411229e-16	***
SlopeF-SlopeC	-1.734139	0.0671711	.	0.9999488	



8.7.20 Vitvi11g00749: Type6.C

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi11g00749

30.2.12

signalling.receptor kinases.leucine rich repeat XII

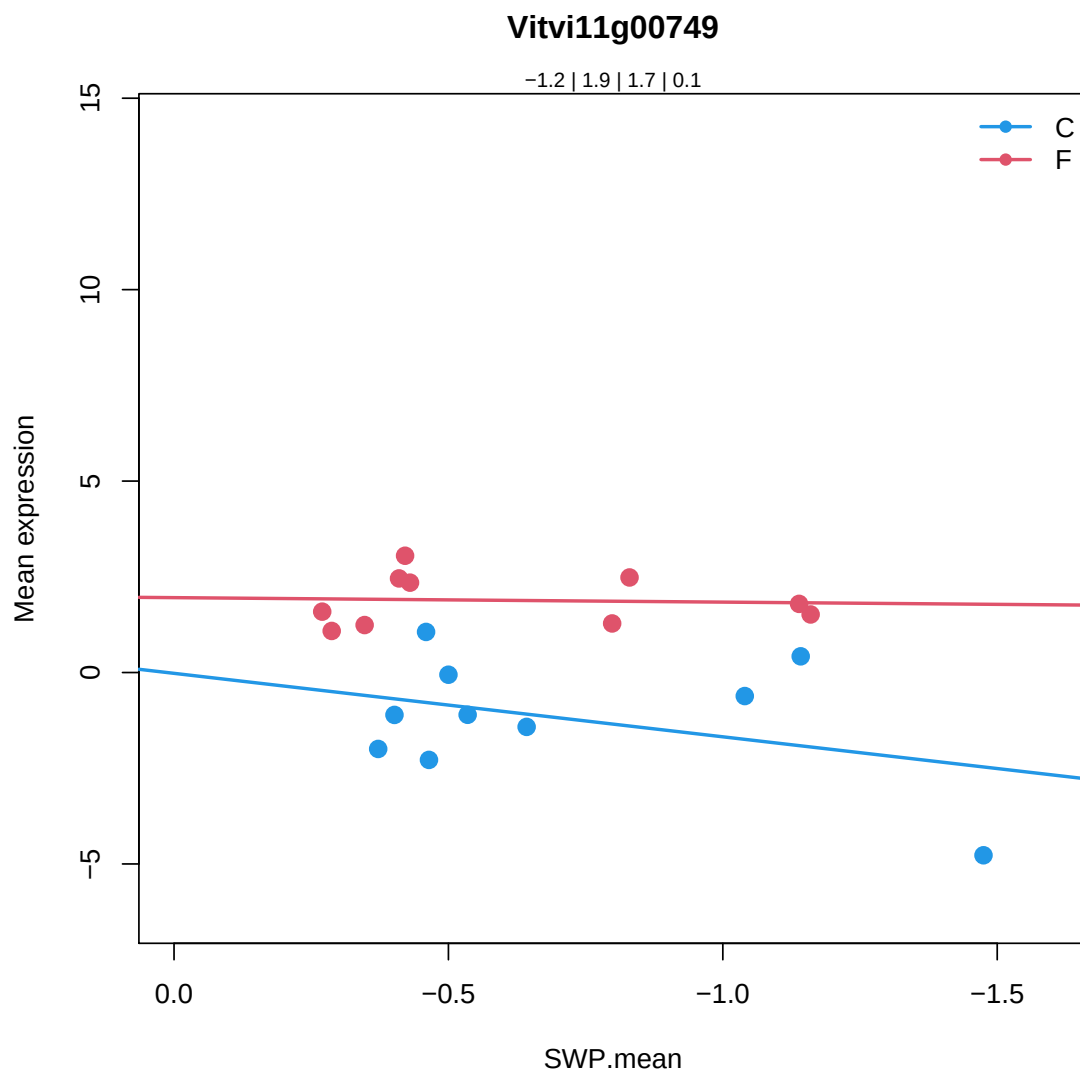
kinase family with leucine-rich repeat domain-containing protein |

Chr1:13220940-13224386 FORWARD LENGTH=1120 |

201606

Coefficients for Vitvi11g00749.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.187309	0.002453198	**	0.002632658	**
SlopeC	1.657462	0.09954394	.	0.6110181	
MeanF-MeanC	3.071475	2.889466e-06	***	8.264173e-05	***
SlopeF-SlopeC	-1.540859	0.2941879		0.9999488	



8.7.21 Vitvi16g02128: * Type6.C

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi16g02128

35.2

not assigned.unknown

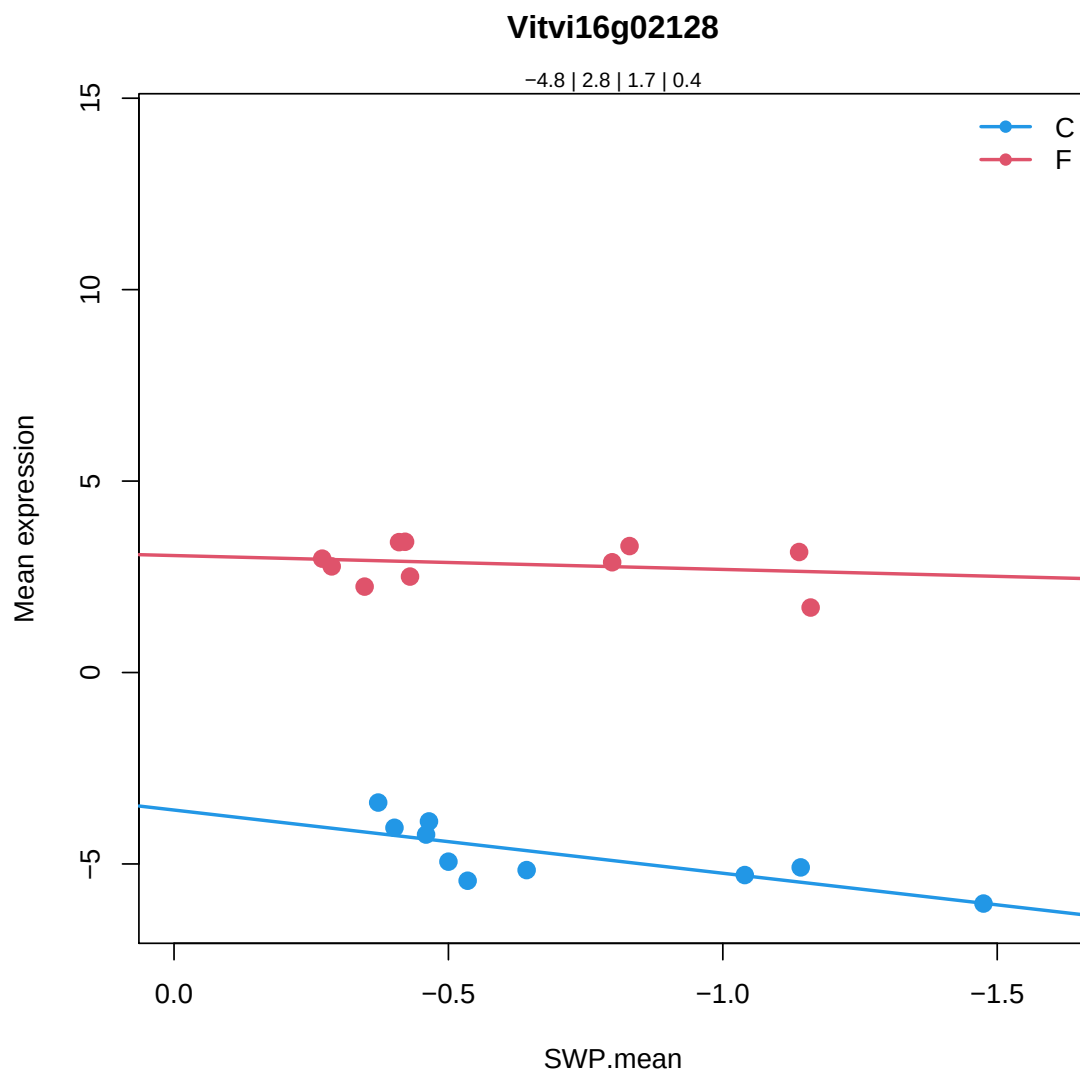
PR5-like receptor kinase |

Chr5:15293325-15295838 REVERSE LENGTH=665 |

201606

Coefficients for Vitvi16g02128.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-4.752626	3.621096e-18	***	1.065291e-17	***
SlopeC	1.650819	0.002533182	**	0.1902008	
MeanF-MeanC	7.586807	2.867599e-19	***	8.405375e-17	***
SlopeF-SlopeC	-1.288502	0.08722927	.	0.9999488	



8.7.22 Vitvi12g02492: * Type6.C

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi12g02492

30.2.12

signalling.receptor kinases.leucine rich repeat XII

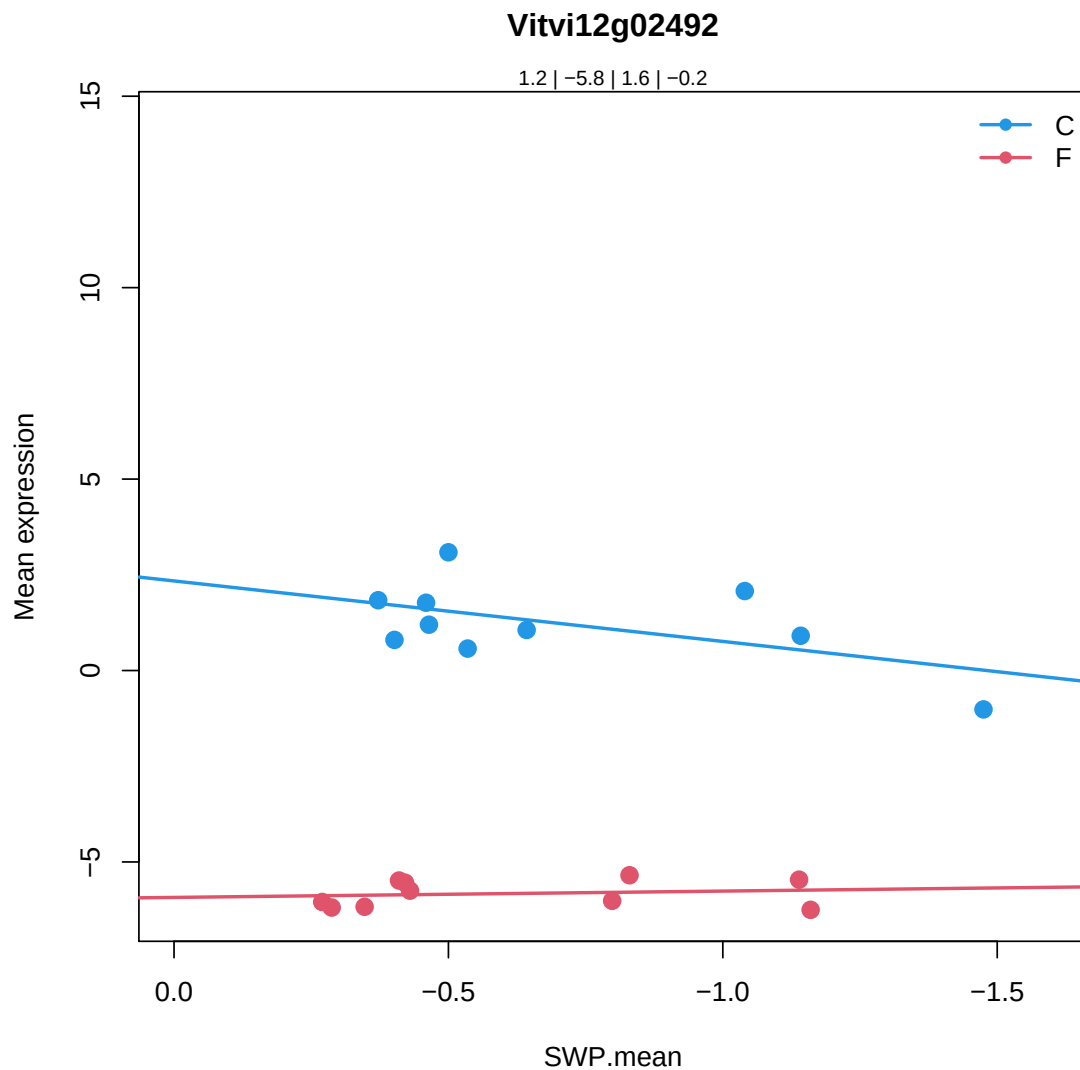
receptor like protein 22 |

Chr2:13853897-13855666 REVERSE LENGTH=589 |

201606

Coefficients for Vitvi12g02492.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.228831	9.368109e-06	***	1.058714e-05	***
SlopeC	1.579994	0.01438592	*	0.3359386	
MeanF-MeanC	-7.054787	9.455527e-17	***	1.736399e-14	***
SlopeF-SlopeC	-1.745248	0.06109156	.	0.9999488	



8.7.23 Vitvi07g01880: * Type6.C

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi07g01880

29.2.1.2.2.3

protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L3

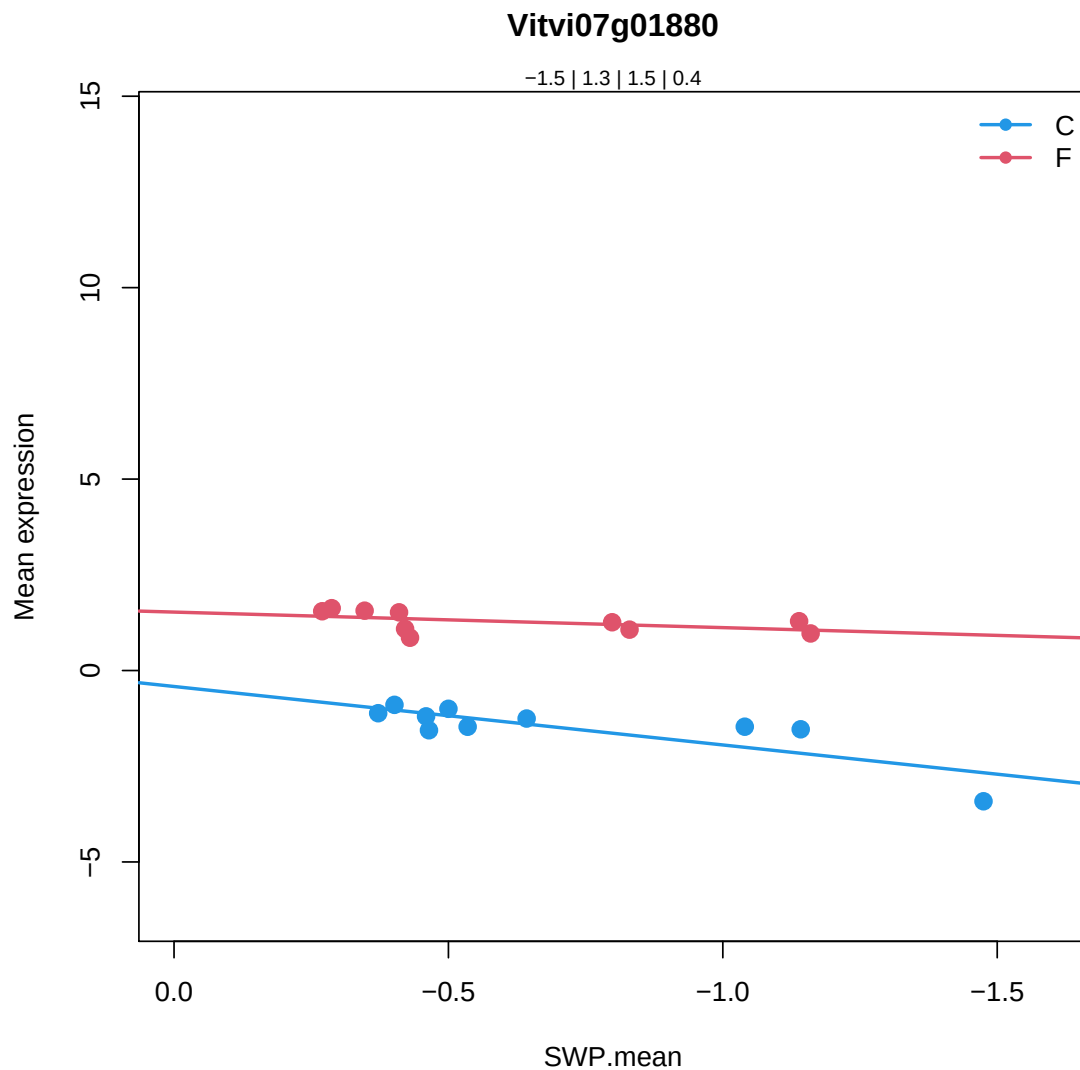
cysteine-rich RECEPTOR-like kinase |

Chr4:12129485-12133157 FORWARD LENGTH=1043 |

201606

Coefficients for Vitvi07g01880.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.491084	7.084737e-11	***	9.323568e-11	***
SlopeC	1.527266	0.0002627845	***	0.08298279	.
MeanF-MeanC	2.769697	3.688811e-13	***	3.627411e-11	***
SlopeF-SlopeC	-1.121594	0.04294883	*	0.9999488	



8.7.24 Vitvi09g00038: Type6.C

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi09g00038

26.28

misc.GDSL-motif lipase

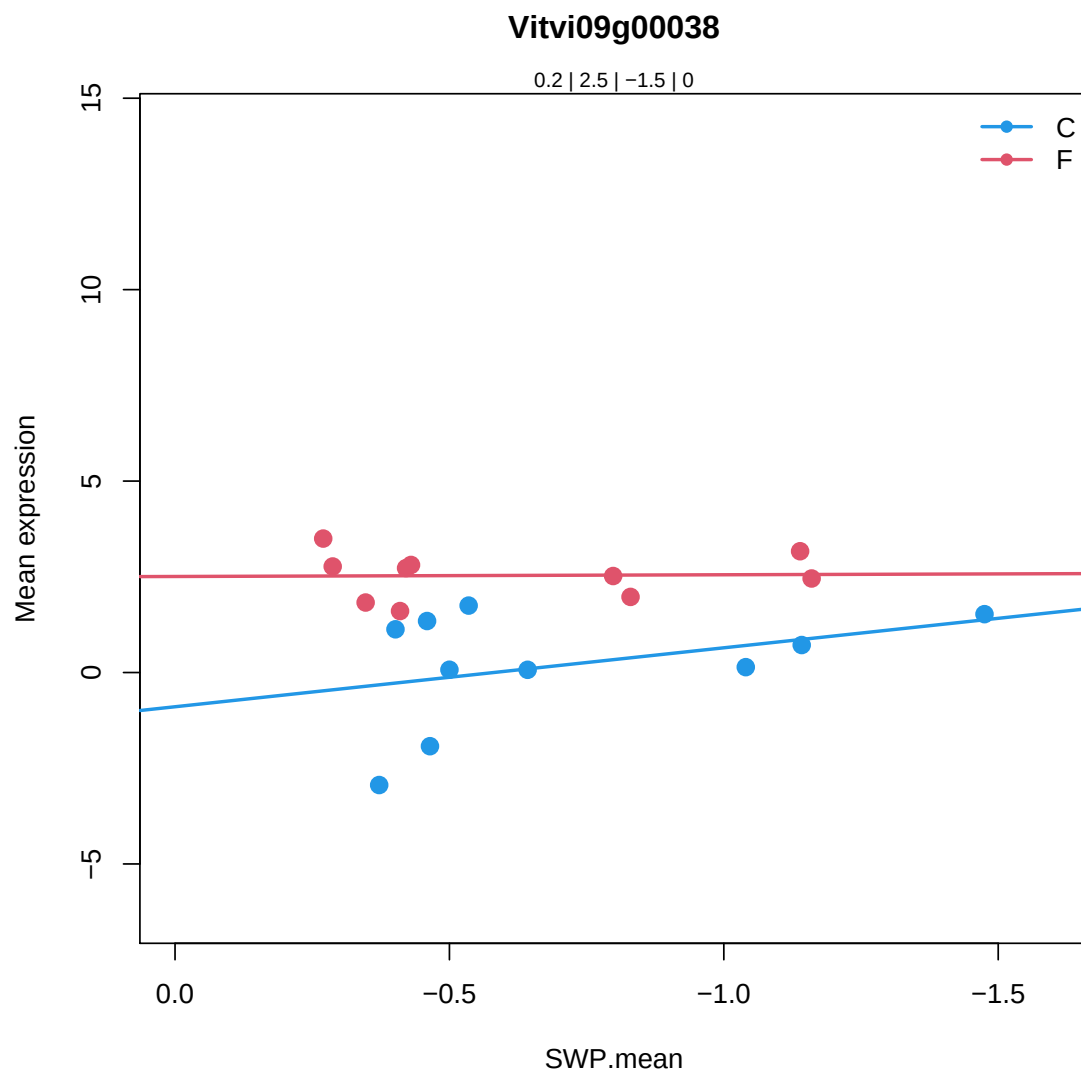
GDSL lipase 1 |

Chr5:16418920-16420400 FORWARD LENGTH=374 |

201606

Coefficients for Vitvi09g00038.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.1883609	0.5662382		0.5720935	
SlopeC	-1.539814	0.1013475		0.6135572	
MeanF-MeanC	2.347224	4.113761e-05	***	0.0008326951	***
SlopeF-SlopeC	1.494714	0.2765741		0.9999488	



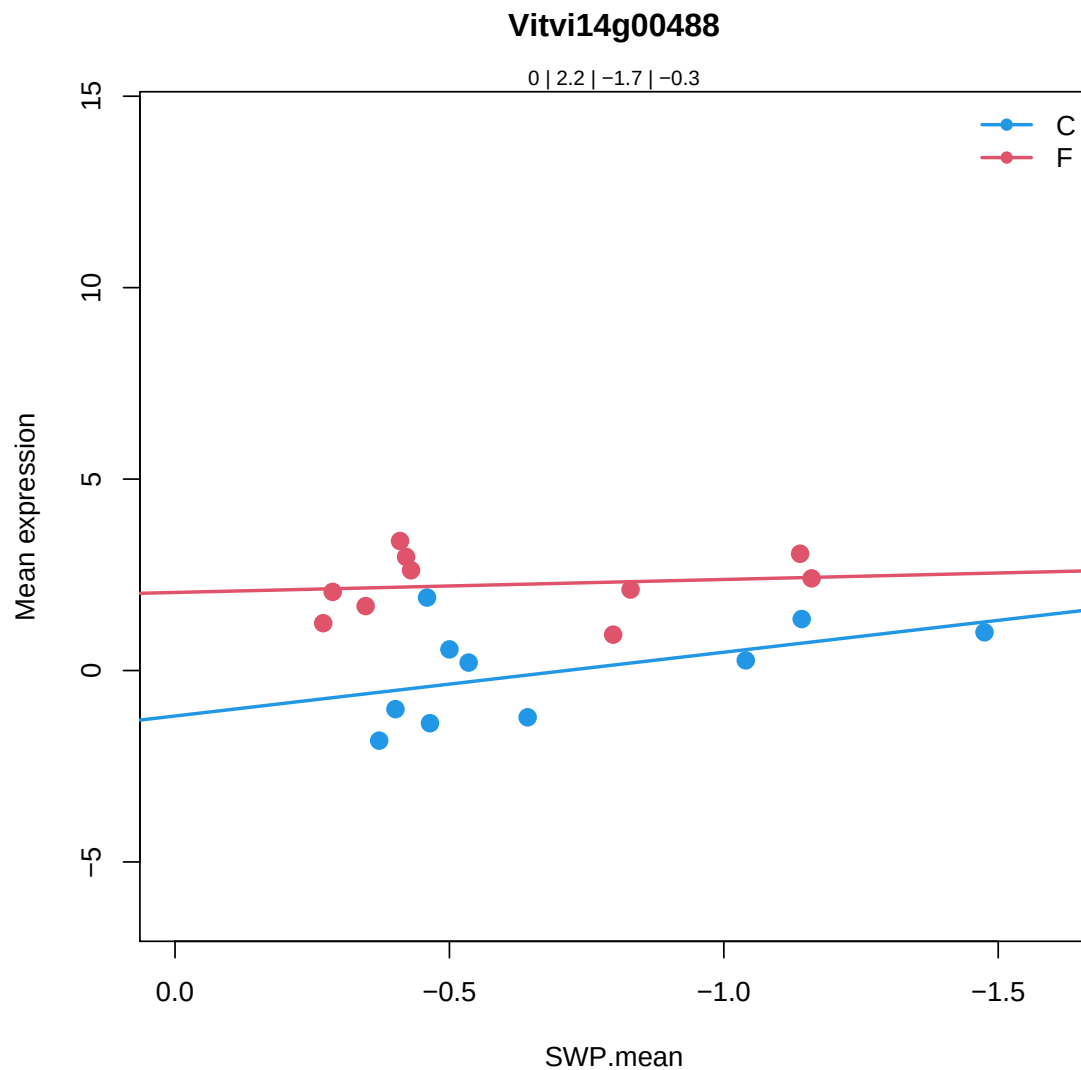
8.7.25 Vitvi14g00488: Type6.C

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi14g00488
20.1.7
stress.biotic.PR-proteins
pathogenesis-related 4 |
Chr3:1285691-1286531 REVERSE LENGTH=212 |
201606
```

Coefficients for Vitvi14g00488.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.01658827	0.954802		0.9555543	
SlopeC	-1.665567	0.0507581	.	0.5104439	
MeanF-MeanC	2.2616	1.619289e-05	***	0.0003838445	***
SlopeF-SlopeC	1.326057	0.2805442		0.9999488	



8.7.26 Vitvi01g01977: * Type6.C

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi01g01977

20.1

stress.biotic

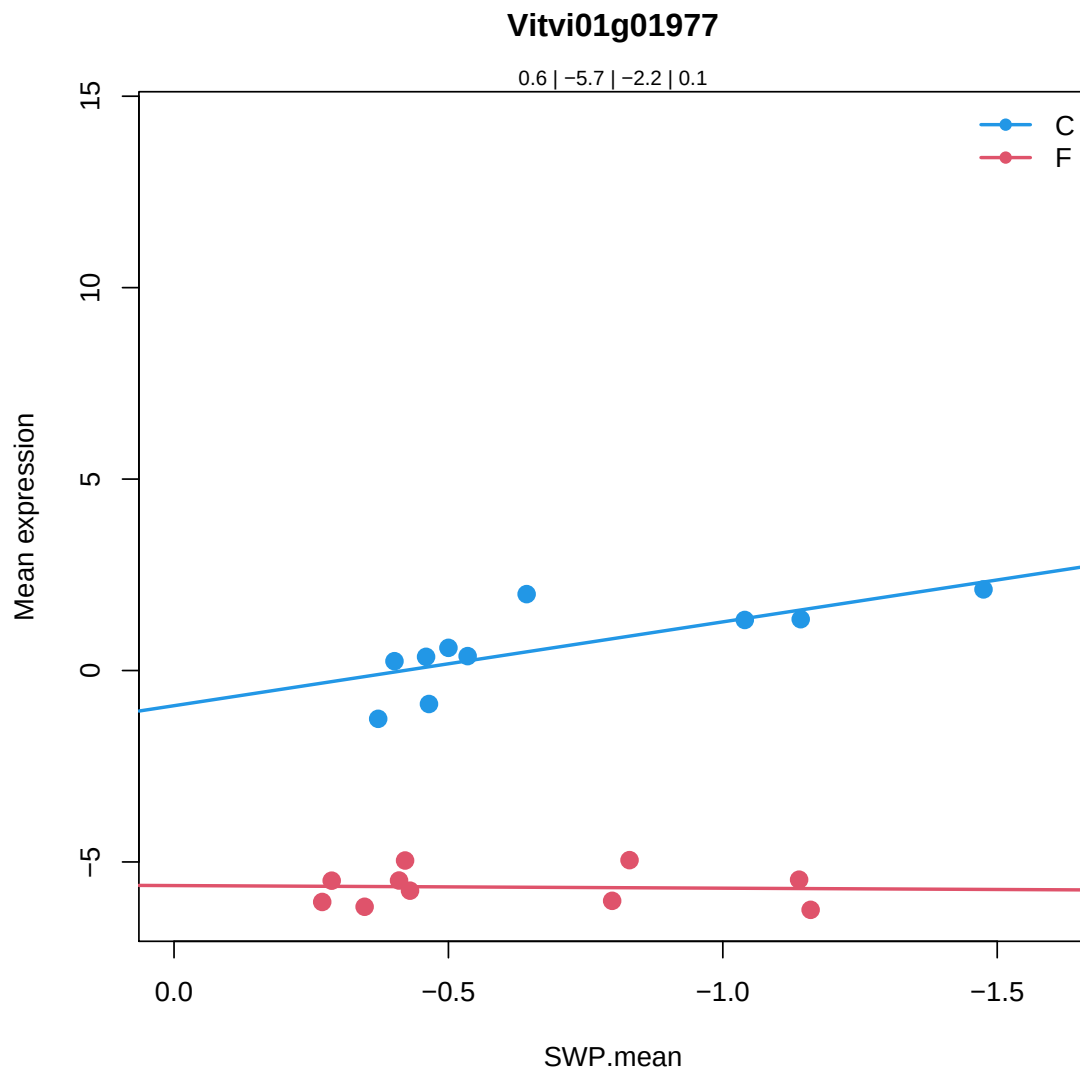
Polyketide cyclase/dehydrase and lipid transport superfamily protein |

Chr1:8198788-8199359 FORWARD LENGTH=148 |

201606

Coefficients for Vitvi01g01977.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.6206962	0.004645355	**	0.004958298	**
SlopeC	-2.189318	0.0006200866	***	0.1005065	
MeanF-MeanC	-6.278969	1.930905e-16	***	3.344415e-14	***
SlopeF-SlopeC	2.257369	0.01121402	*	0.9999488	



8.7.27 Vitvi03g01431: * Type6.C

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi03g01431

26.7

misc.oxidases - copper, flavone etc

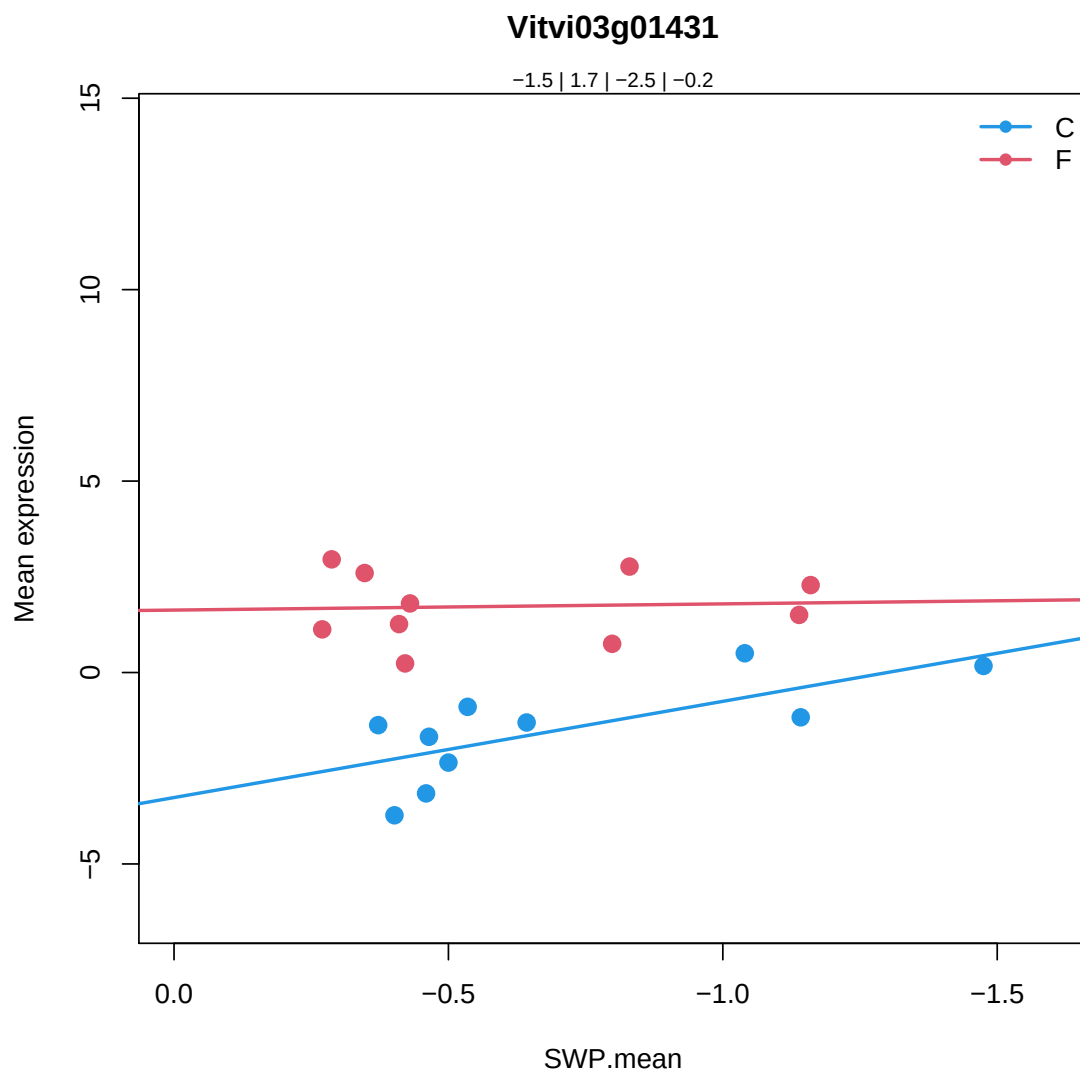
flavin-dependent monooxygenase 1 |

Chr1:6650656-6653053 REVERSE LENGTH=530 |

201606

Coefficients for Vitvi03g01431.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-1.498922	2.078617e-05	***	2.330265e-05	***
SlopeC	-2.513015	0.003608732	**	0.2248659	
MeanF-MeanC	3.228153	4.224193e-08	***	1.877118e-06	***
SlopeF-SlopeC	2.351136	0.05238461	.	0.9999488	



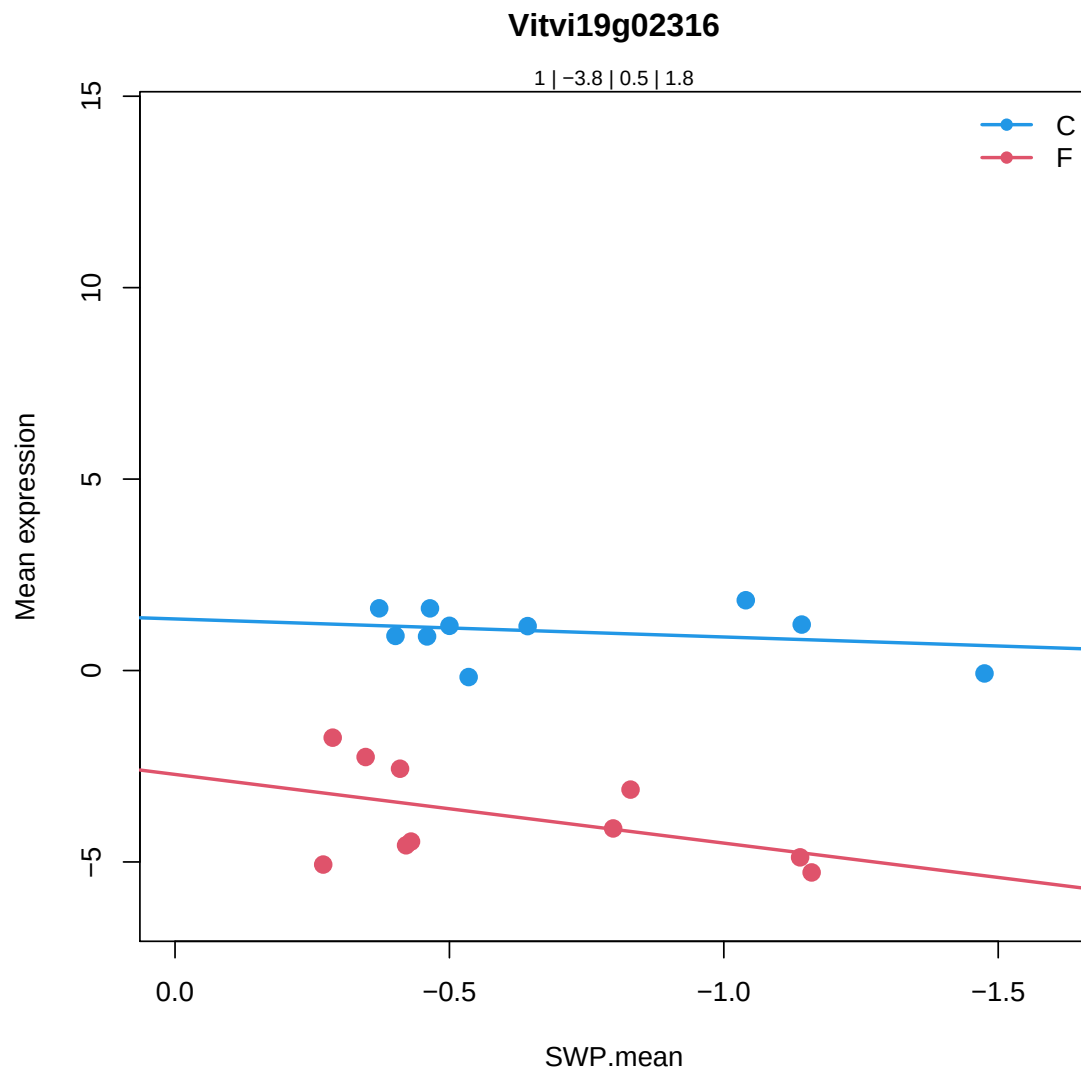
8.8 Type6.F

8.8.1 Vitvi19g02316: Type6.F

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
Vitvi19g02316
35.2
not assigned.unknown
Disease resistance protein (CC-NBS-LRR class) family |
Chr1:4145011-4147680 FORWARD LENGTH=889 |
201606
```

Coefficients for Vitvi19g02316.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.015579	0.001366712	**	0.001476046	**
SlopeC	0.4709163	0.5464691		0.8857058	
MeanF-MeanC	-4.822373	3.259702e-11	***	2.400211e-09	***
SlopeF-SlopeC	1.323198	0.2600661		0.9999488	



8.8.2 Vitvi17g00175: Type6.F

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi17g00175

30.2.25

signalling.receptor kinases.wall associated kinase

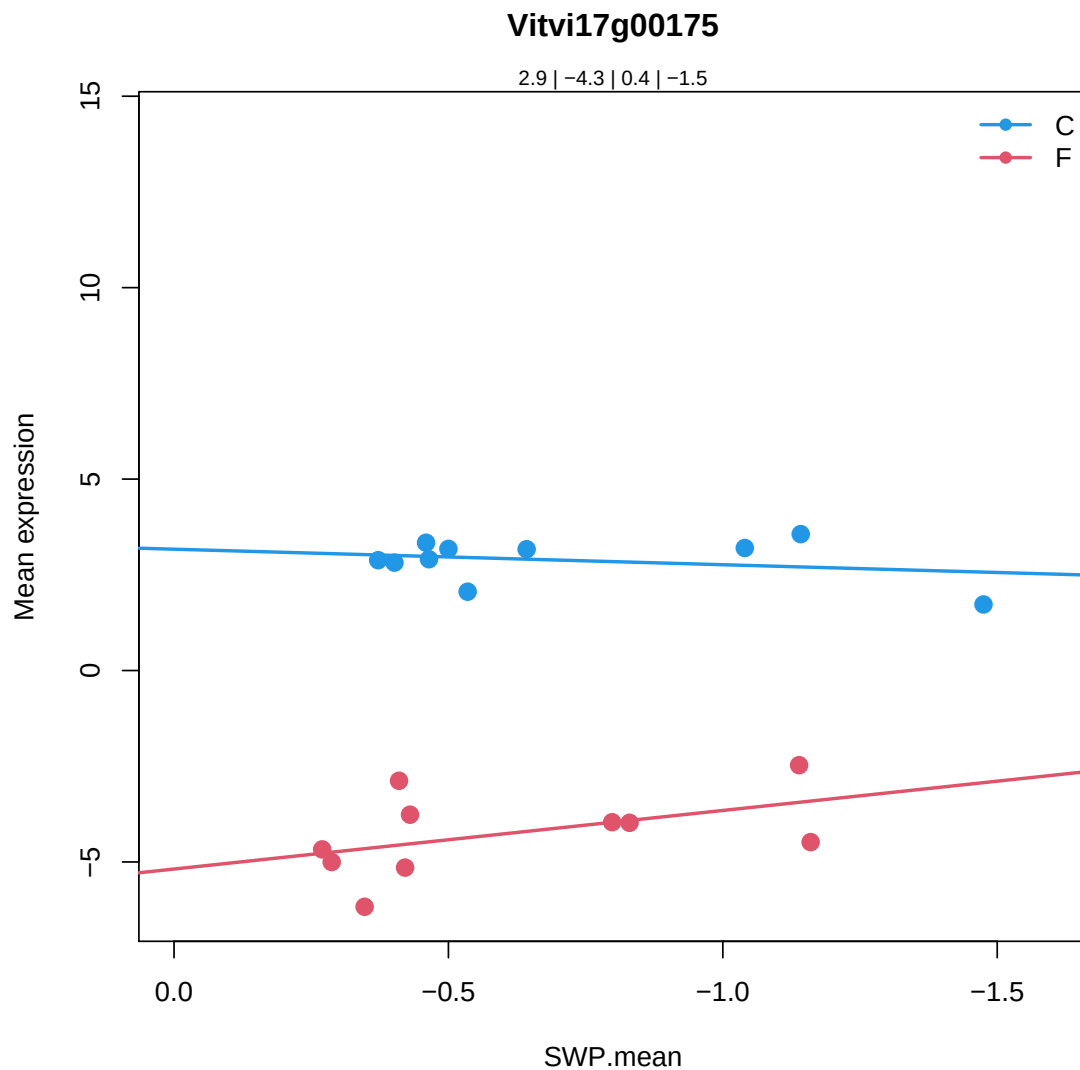
wall associated kinase 5 |

Chr1:7429980-7432346 FORWARD LENGTH=733 |

201606

Coefficients for Vitvi17g00175.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	2.883592	5.172864e-11	***	6.845355e-11	***
SlopeC	0.4052957	0.5492078		0.8871925	
MeanF-MeanC	-7.136685	8.065835e-16	***	1.193587e-13	***
SlopeF-SlopeC	-1.935313	0.06406735	.	0.9999488	



8.8.3 Vitvi05g00038: Type6.F

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi05g00038

26.3.5

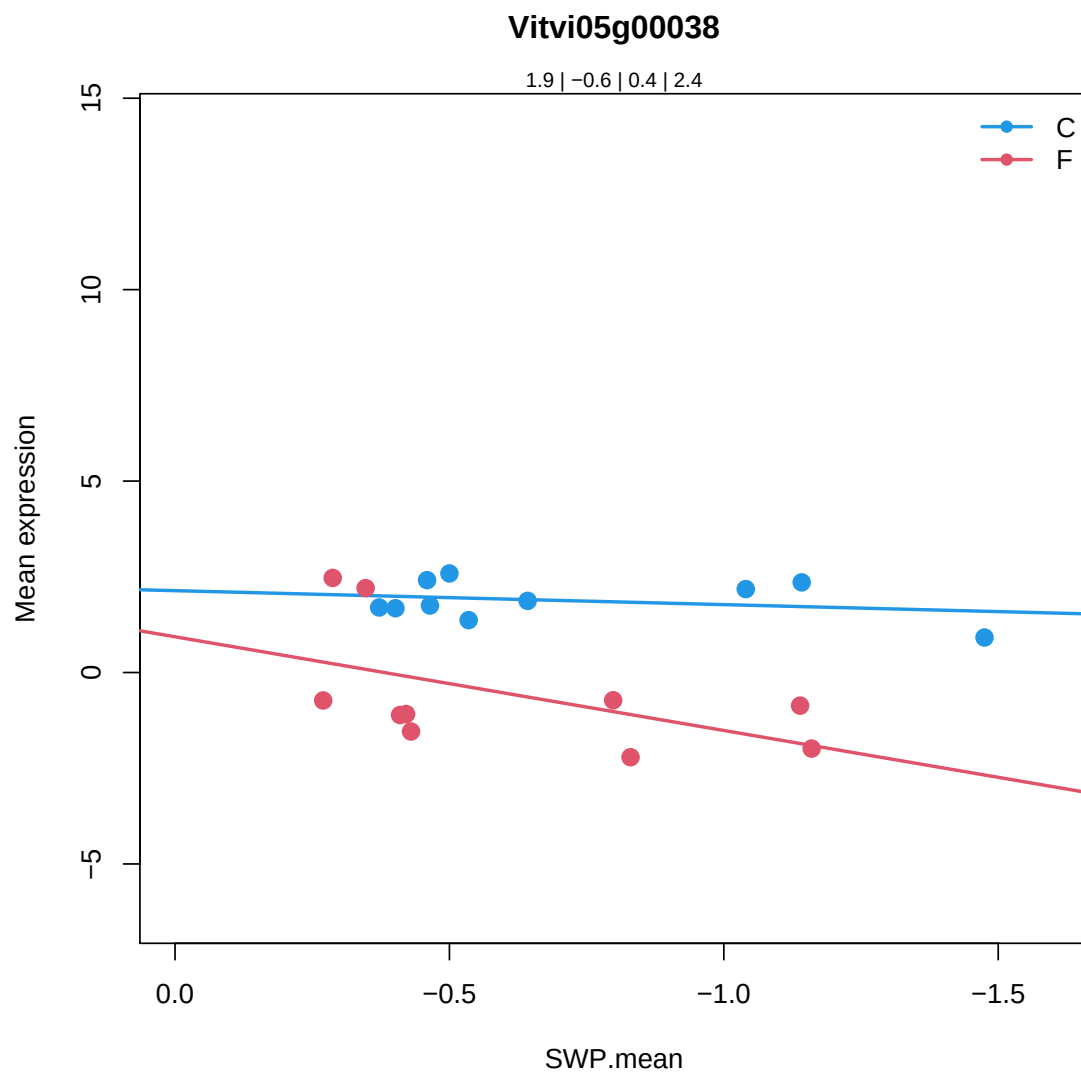
misc.gluco-, galacto- and mannosidases.glycosyl hydrolase family 5
alpha/beta-Hydrolases superfamily protein |

Chr4:1035722-1037403 FORWARD LENGTH=324 |

201606

Coefficients for Vitvi05g00038.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.881532	4.363251e-06	***	4.964146e-06	***
SlopeC	0.3647677	0.6752848		0.9252688	
MeanF-MeanC	-2.439425	1.40955e-05	***	0.0003437499	***
SlopeF-SlopeC	2.082283	0.1179377		0.9999488	



8.8.4 Vitvi15g01643: Type6.F

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi15g01643

16.8.1.12

secondary metabolism.flavonoids.anthocyanins.anthocyanidin 3-O-glucosyl

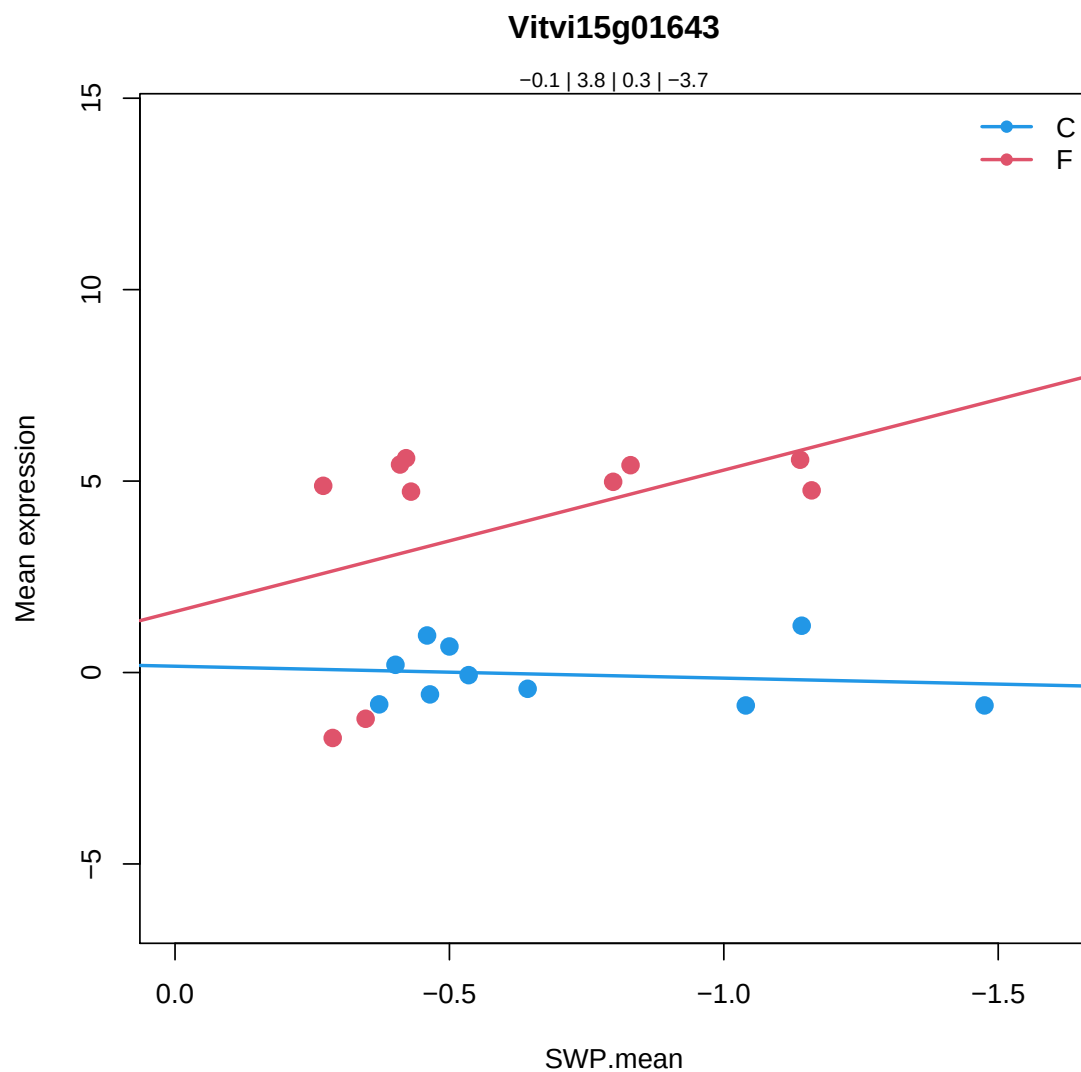
UDP-Glycosyltransferase superfamily protein |

Chr2:9593012-9594424 FORWARD LENGTH=470 |

201606

Coefficients for Vitvi15g01643.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-0.05461697	0.9210385		0.922673	
SlopeC	0.3115766	0.8389936		0.9693055	
MeanF-MeanC	3.897101	4.895259e-05	***	0.0009663134	***
SlopeF-SlopeC	-4.007713	0.08969632	.	0.9999488	



8.8.5 Vitvi05g01578: Type6.F

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi05g01578

35.2

not assigned.unknown

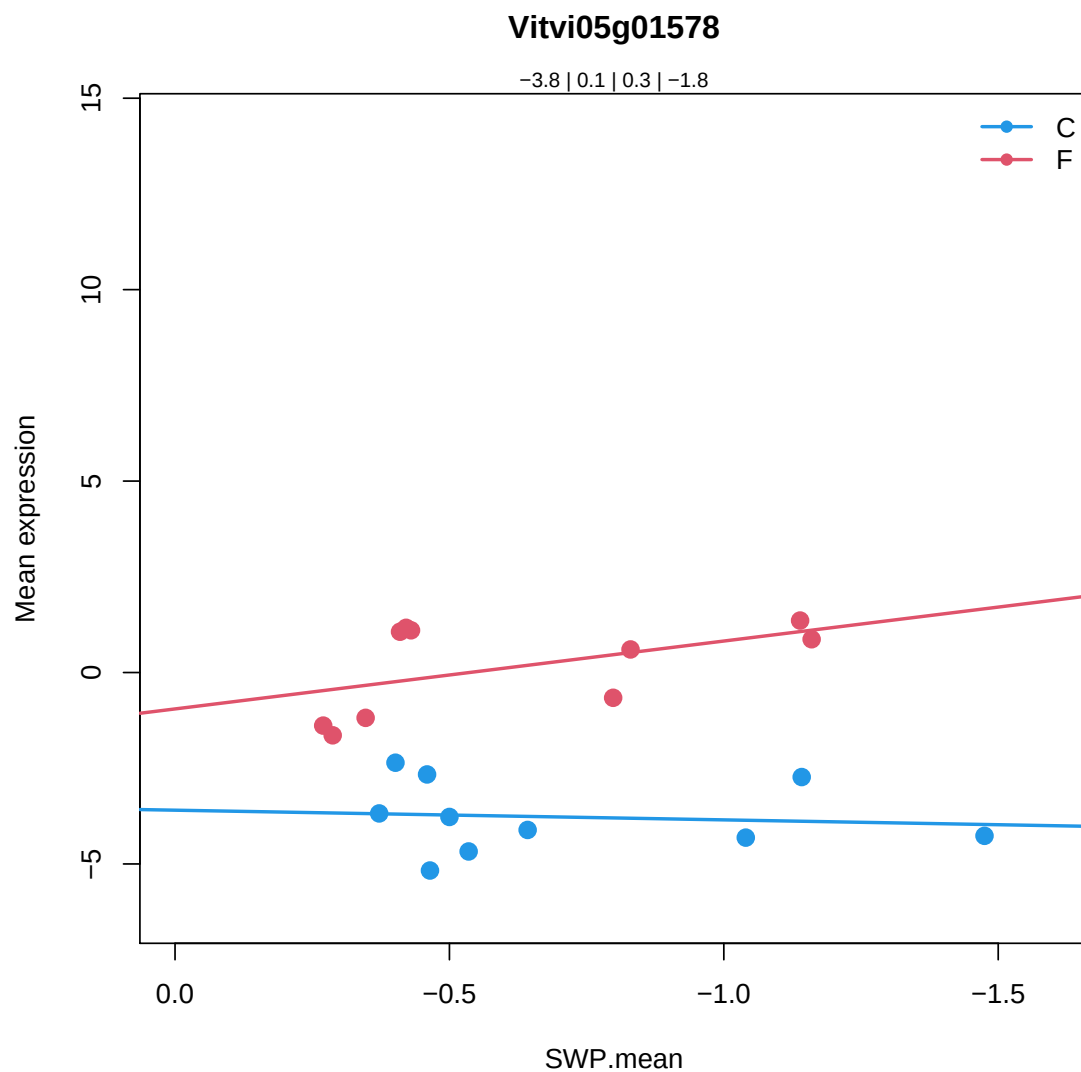
homolog of carrot EP3-3 chitinase |

Chr3:20145935-20147034 FORWARD LENGTH=273 |

201606

Coefficients for Vitvi05g01578.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-3.773614	1.602428e-11	***	2.168121e-11	***
SlopeC	0.2532287	0.7602289		0.9479775	
MeanF-MeanC	3.902919	4.915293e-09	***	2.531044e-07	***
SlopeF-SlopeC	-2.026263	0.1111117		0.9999488	



8.8.6 Vitvi11g00865: Type6.F

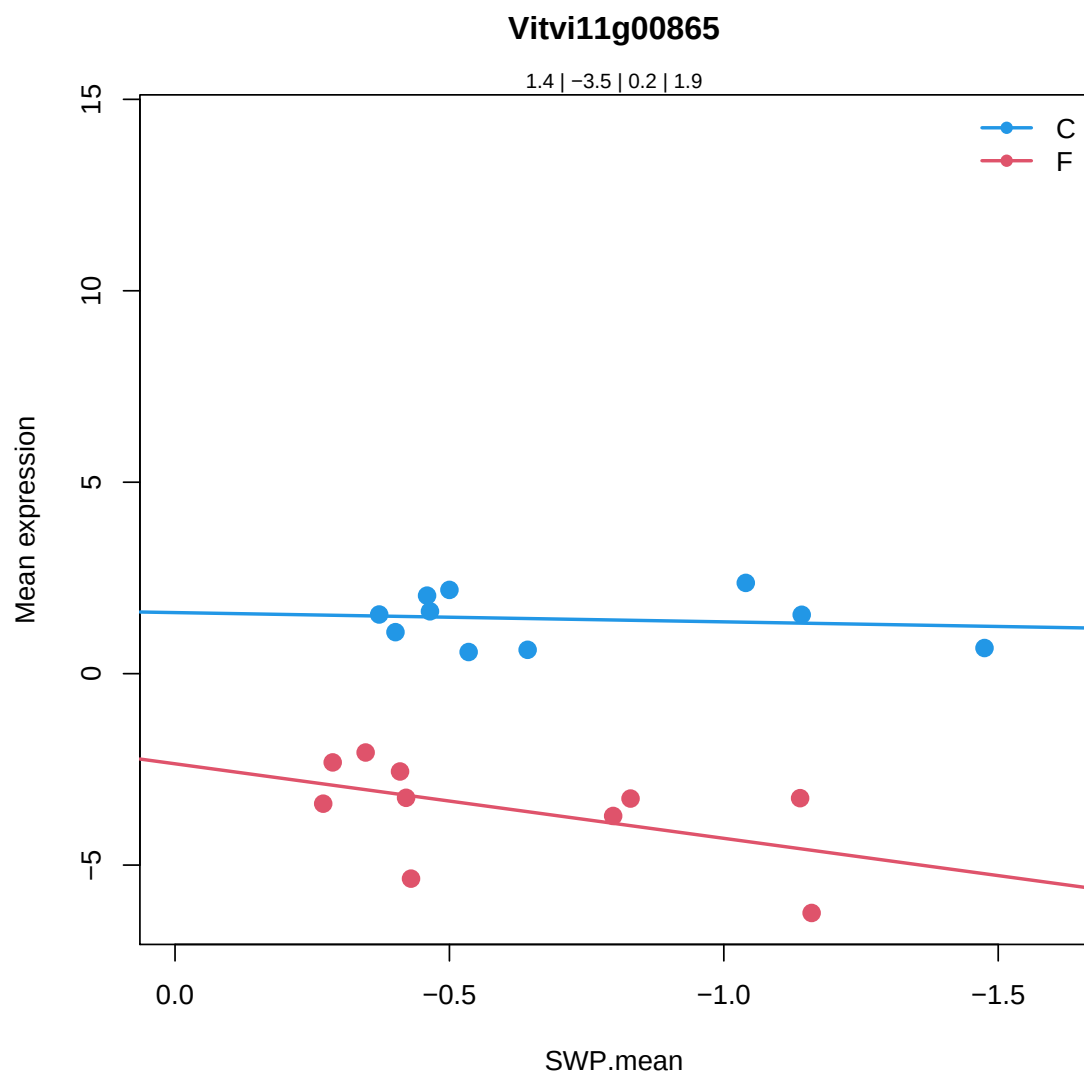
```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi11g00865
20
stress
Ankyrin repeat family protein |
Chr5:1354240-1356754 REVERSE LENGTH=669 |
201606
```

```
Vitvi11g00865
19.99
tetrapyrrole synthesis.unspecified
Ankyrin repeat family protein |
Chr5:1354240-1356754 REVERSE LENGTH=669 |
201606
```

Coefficients for Vitvi11g00865.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.424545	4.543505e-05	***	5.050843e-05	***
SlopeC	0.241433	0.7594168		0.9479775	
MeanF-MeanC	-4.965309	2.386458e-11	***	1.774361e-09	***
SlopeF-SlopeC	1.705682	0.1554573		0.9999488	



8.8.7 Vitvi10g00313: Type6.F

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi10g00313

29.5.11.4.2

protein.degradation.ubiquitin.E3.RING

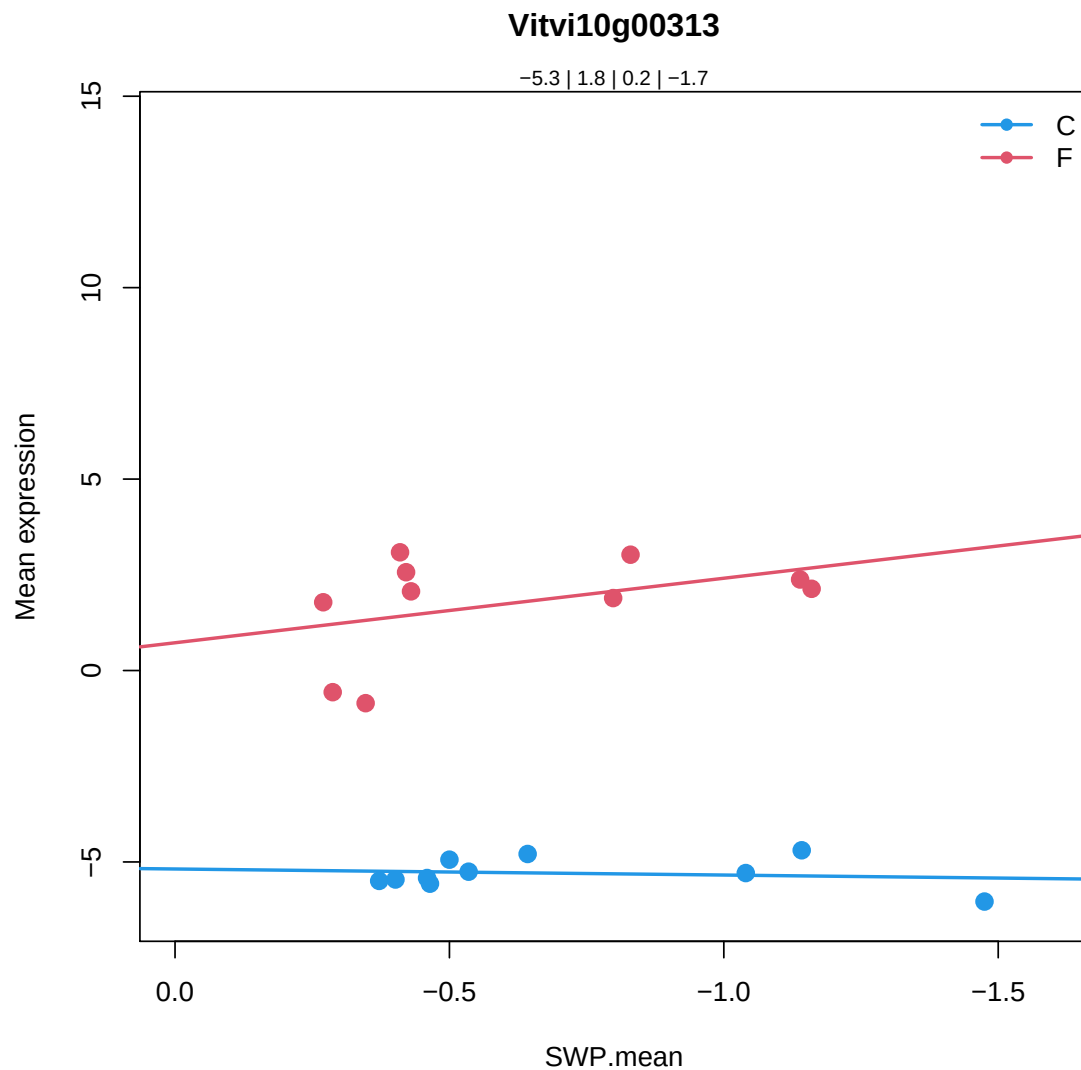
plant U-box 8 |

Chr4:11356143-11357267 REVERSE LENGTH=374 |

201606

Coefficients for Vitvi10g00313.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.2947	6.44878e-15	***	1.098975e-14	***
SlopeC	0.1580878	0.8400291		0.9694858	
MeanF-MeanC	7.046217	2.205385e-14	***	2.605774e-12	***
SlopeF-SlopeC	-1.843471	0.12405		0.9999488	



8.8.8 Vitvi12g02177: Type6.F

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi12g02177

16.1.5

secondary metabolism.isoprenoids.terpenoids

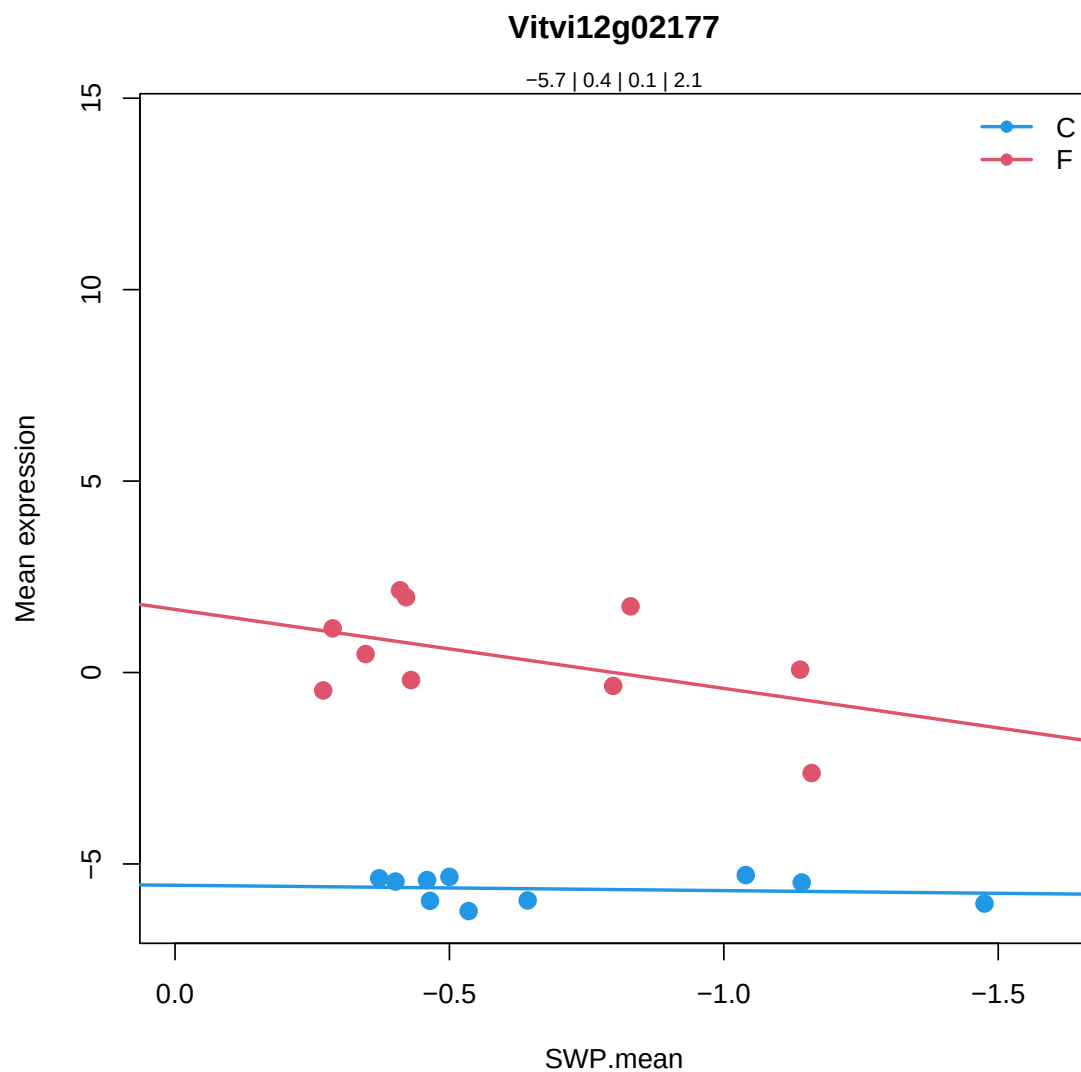
terpene synthase 21 |

Chr5:8092969-8095128 FORWARD LENGTH=545 |

201606

Coefficients for Vitvi12g02177.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.654707	1.734801e-15	***	3.157989e-15	***
SlopeC	0.1400847	0.8582087		0.9733541	
MeanF-MeanC	6.045631	4.807264e-13	***	4.608322e-11	***
SlopeF-SlopeC	1.922026	0.1100849		0.9999488	



8.8.9 Vitvi07g03123: Type6.F

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi07g03123

31.1

cell.organisation

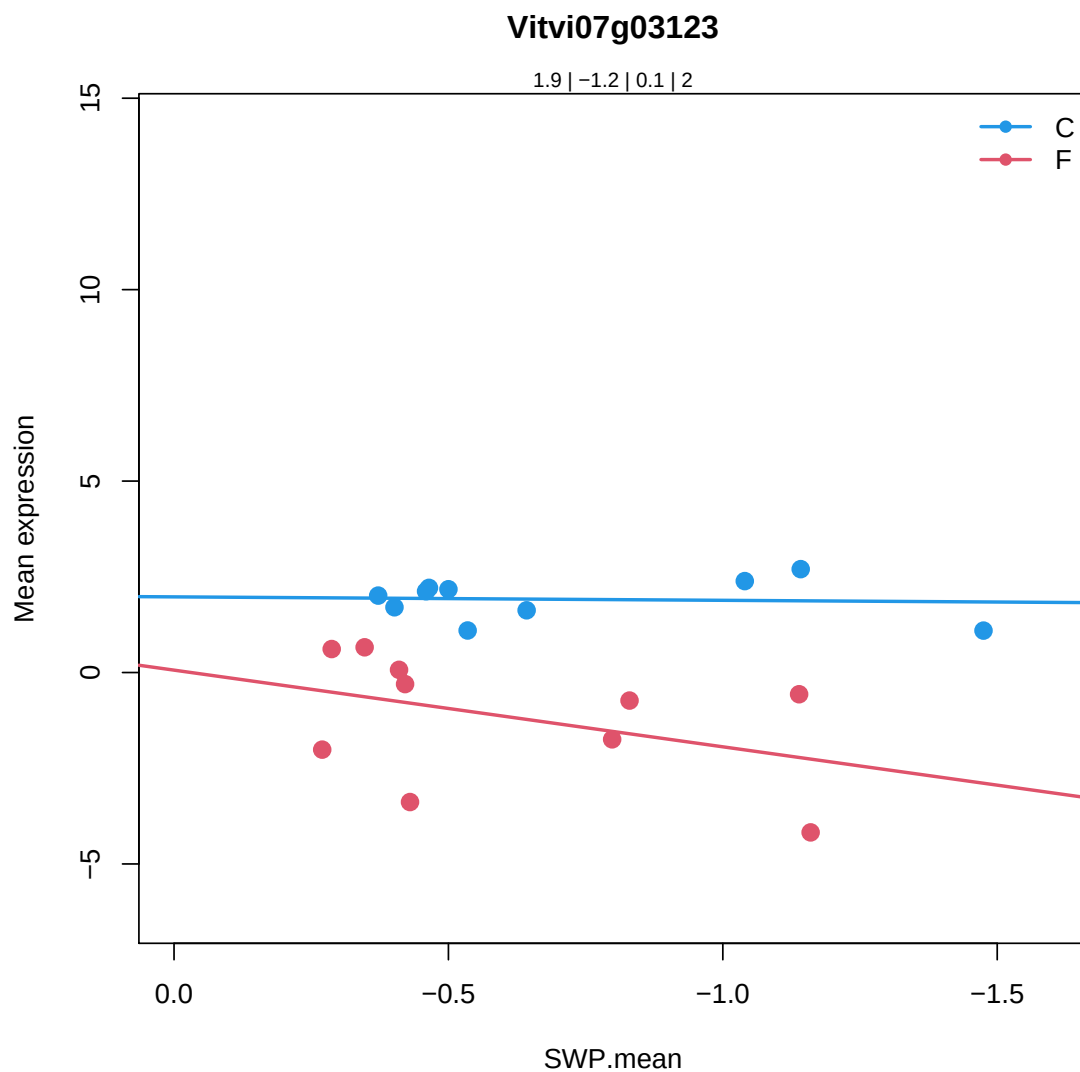
tubulin alpha-5 |

Chr5:6687212-6688926 FORWARD LENGTH=450 |

201606

Coefficients for Vitvi07g03123.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.912632	1.0113e-05	***	1.14188e-05	***
SlopeC	0.0898298	0.9238393		0.9860755	
MeanF-MeanC	-3.070558	1.72904e-06	***	5.302623e-05	***
SlopeF-SlopeC	1.912759	0.1806418		0.9999488	



8.8.10 Vitvi10g02396: Type6.F

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi10g02396

14.2

S-assimilation.APR

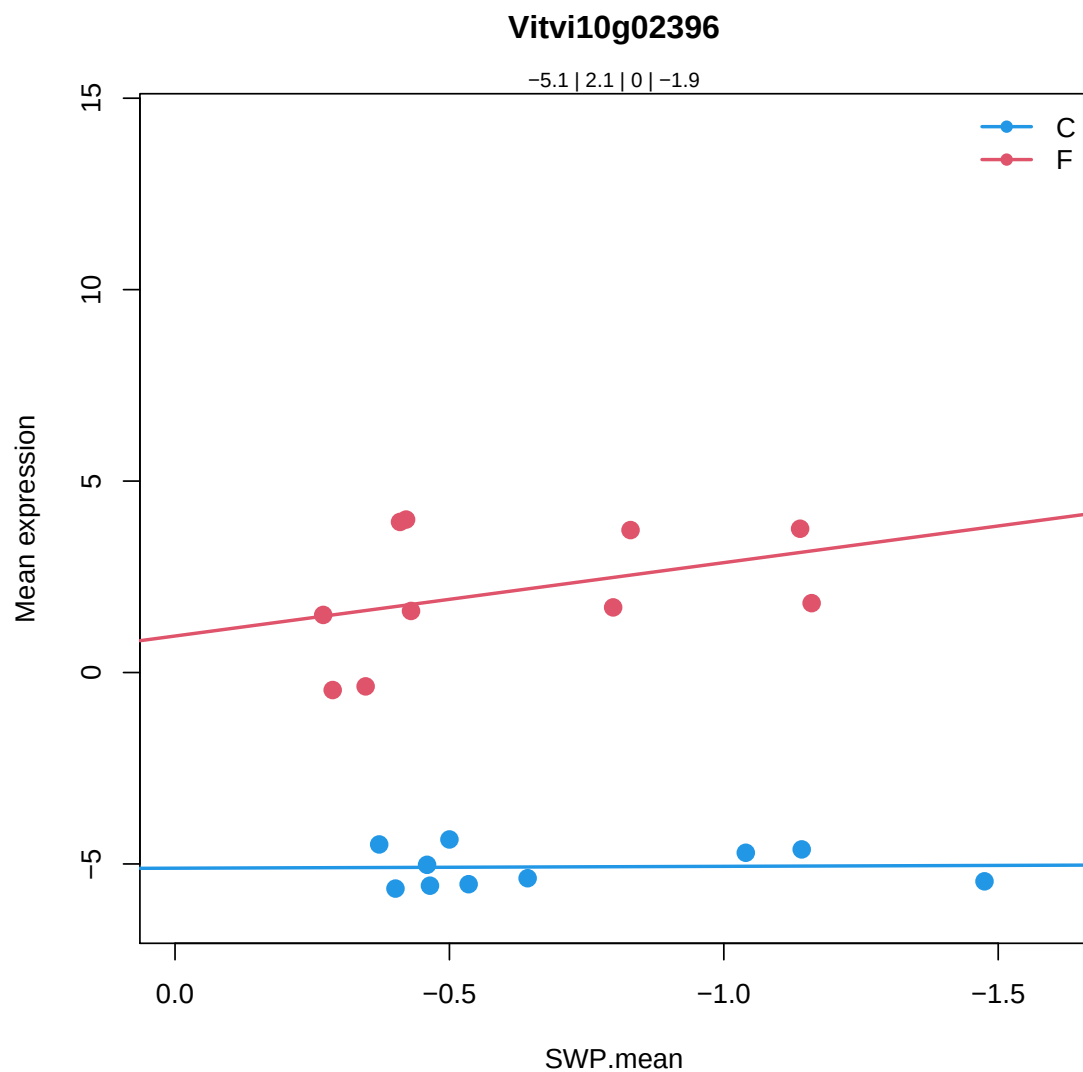
APS reductase 1 |

Chr4:2325069-2326718 FORWARD LENGTH=465 |

201606

Coefficients for Vitvi10g02396.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.076664	1.036555e-12	***	1.485024e-12	***
SlopeC	-0.04830116	0.9602008		0.9937458	
MeanF-MeanC	7.197329	9.873187e-13	***	8.749251e-11	***
SlopeF-SlopeC	-1.867763	0.2034859		0.9999488	



8.8.11 Vitvi07g03066: Type6.F

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi07g03066

35.2

not assigned.unknown

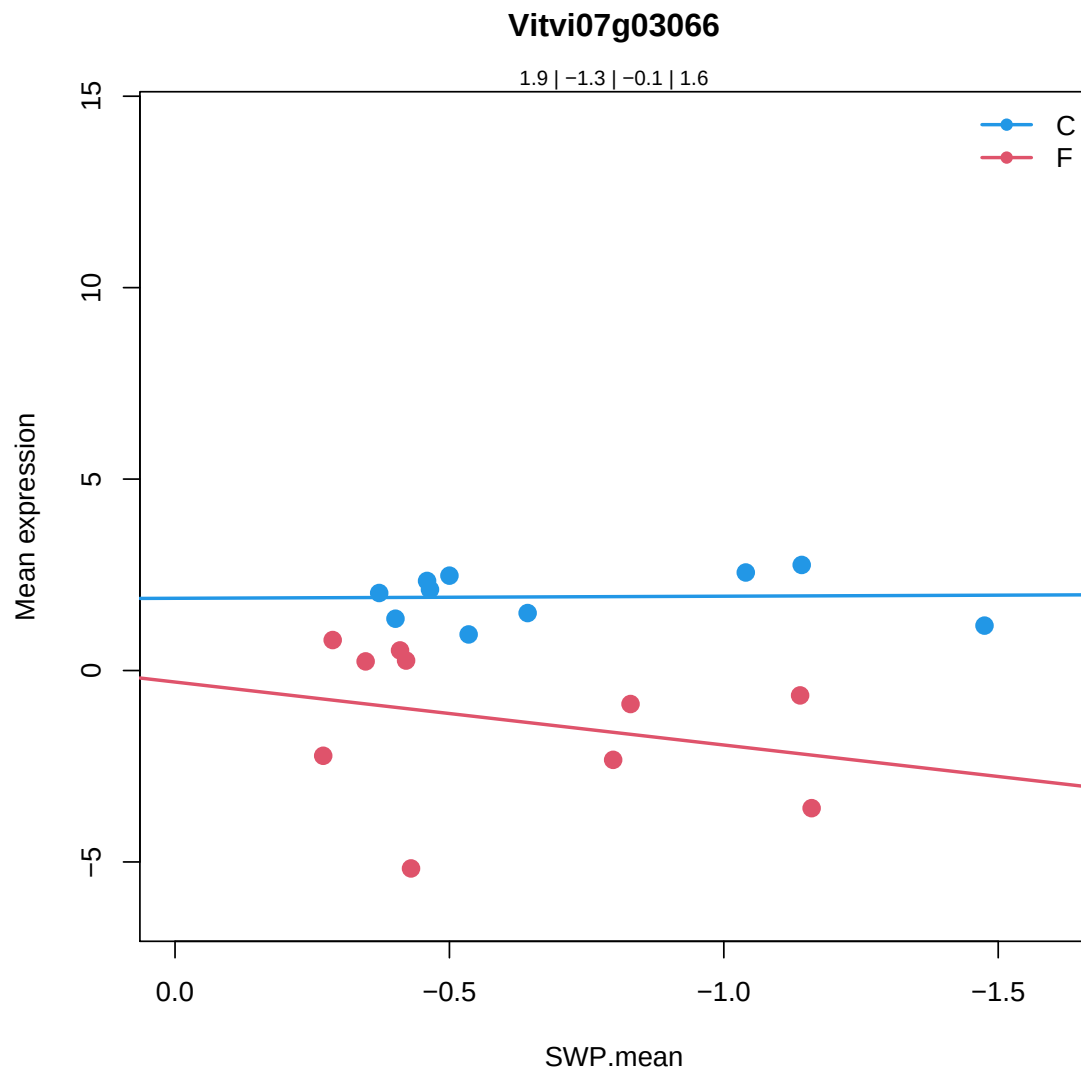
tubulin alpha-5 |

Chr5:6687212-6688926 FORWARD LENGTH=450 |

201606

Coefficients for Vitvi07g03066.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.924411	0.0001445351	***	0.0001590961	***
SlopeC	-0.0543839	0.9630928		0.9939741	
MeanF-MeanC	-3.22752	1.874679e-05	***	0.0004355772	***
SlopeF-SlopeC	1.698955	0.3367385		0.9999488	



8.8.12 Vitvi18g01877: Type6.F

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi18g01877

20.1.2.2

stress.biotic.receptors.TIR-NBS-LRR

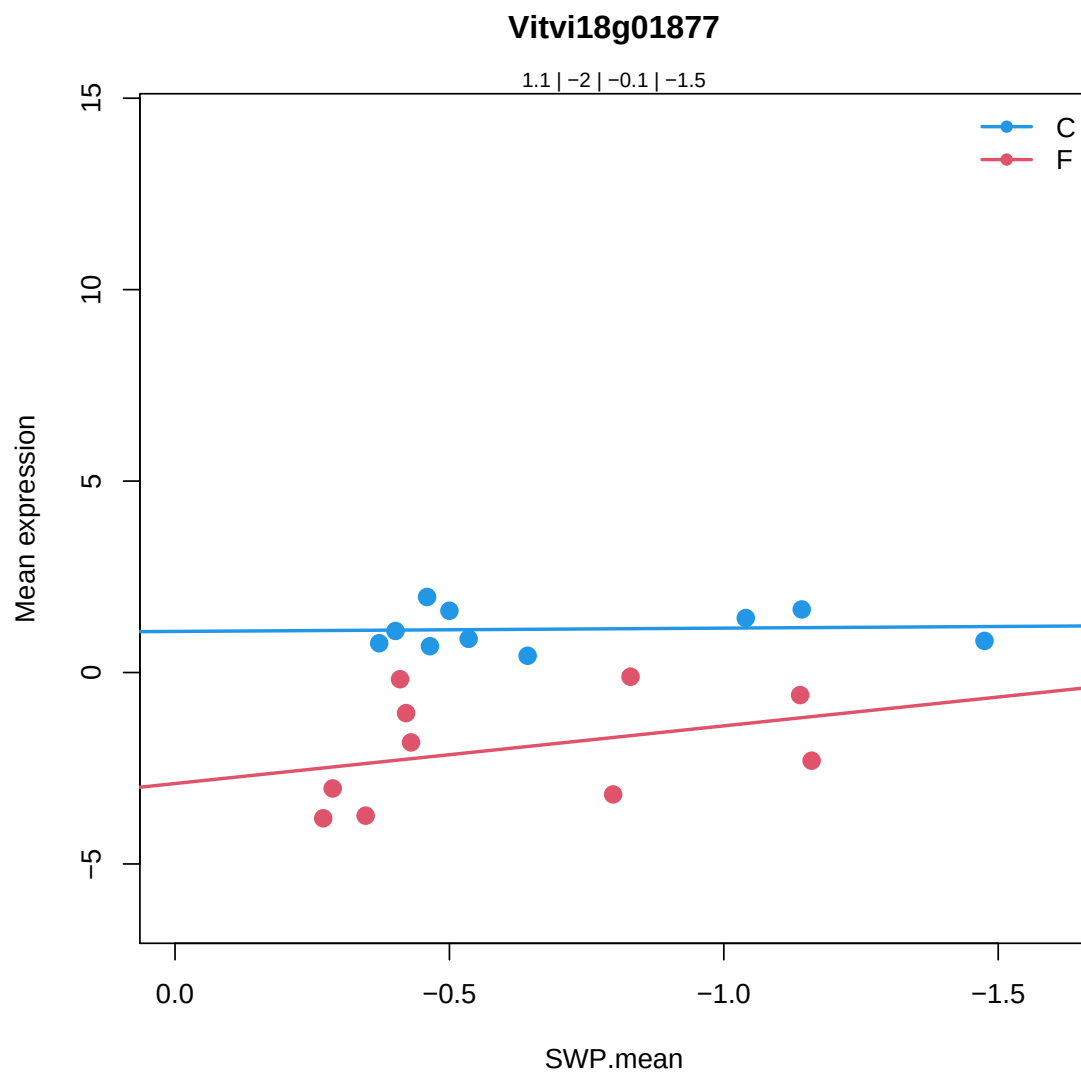
Disease resistance protein (TIR-NBS-LRR class) family |

Chr5:14568141-14571907 REVERSE LENGTH=1125 |

201606

Coefficients for Vitvi18g01877.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	1.133662	0.001197745	**	0.001295489	**
SlopeC	-0.08588147	0.9200083		0.9853314	
MeanF-MeanC	-3.115832	3.373809e-07	***	1.227294e-05	***
SlopeF-SlopeC	-1.420387	0.2713186		0.9999488	



8.8.13 Vitvi08g02249: Type6.F

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi08g02249
```

```
29.5
```

```
protein.degradation
```

```
Eukaryotic aspartyl protease family protein |
```

```
Chr3:19465644-19467053 REVERSE LENGTH=469 |
```

```
201606
```

```
Vitvi08g02249
```

```
35.2
```

```
not assigned.unknown
```

```
Eukaryotic aspartyl protease family protein |
```

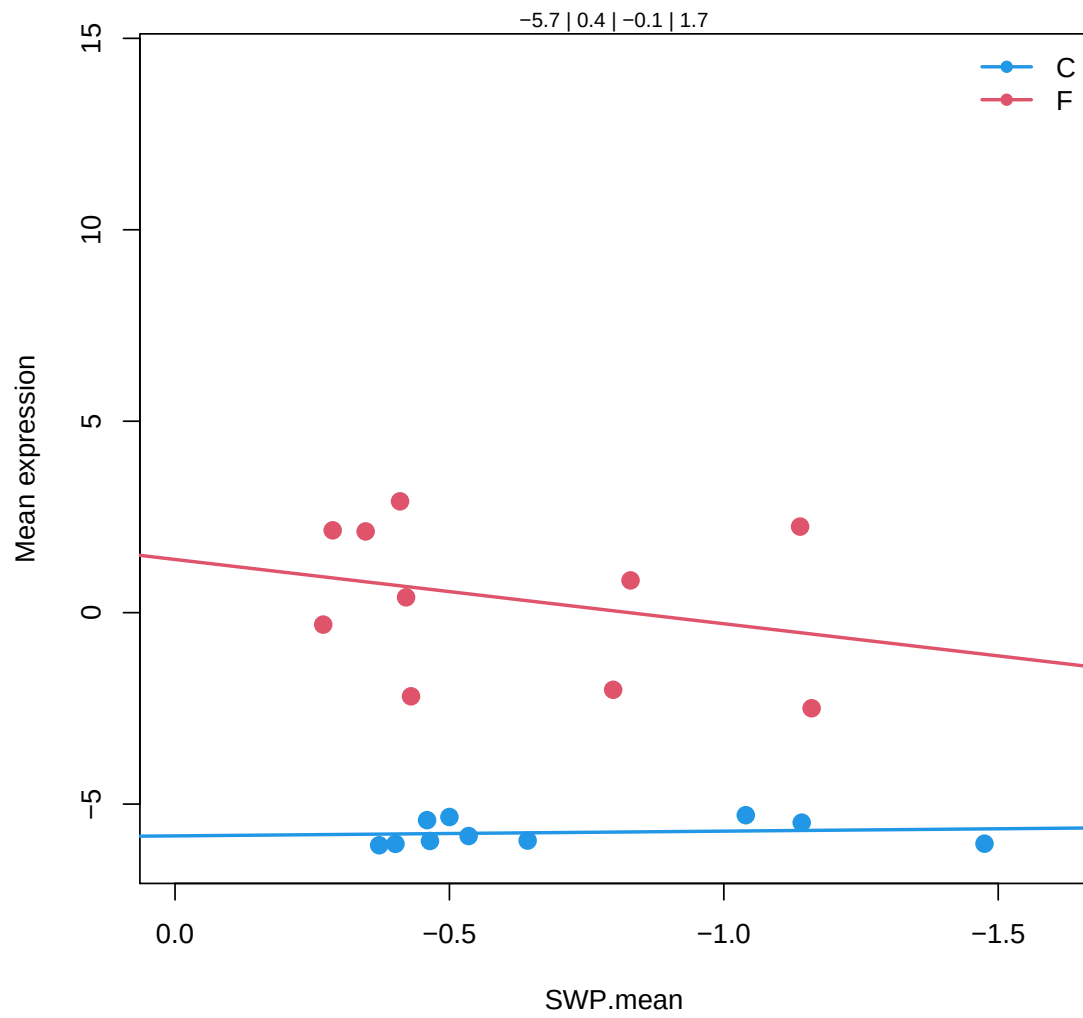
```
Chr3:19465644-19467053 REVERSE LENGTH=469 |
```

```
201606
```

Coefficients for Vitvi08g02249.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.743315	3.296028e-12	***	4.598028e-12	***
SlopeC	-0.1237221	0.9152126		0.9842726	
MeanF-MeanC	6.109273	6.937645e-10	***	4.179588e-08	***
SlopeF-SlopeC	1.802499	0.3033914		0.9999488	

Vitvi08g02249



8.8.14 Vitvi13g00261: + Type6.F

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

```
Vitvi13g00261
```

```
35.2
```

```
not assigned.unknown
```

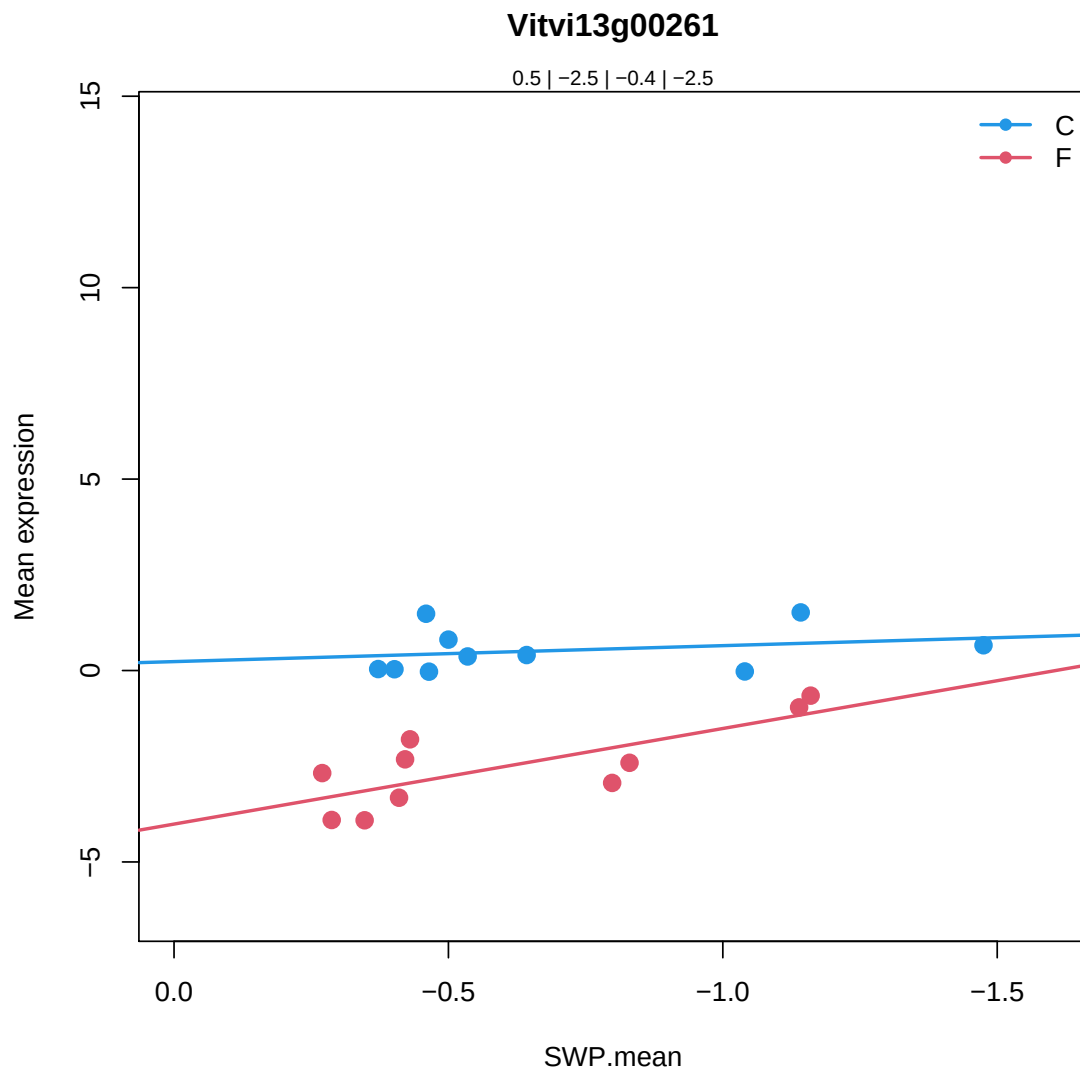
```
PIF / Ping-Pong family of plant transposase |
```

```
Chr3:20518518-20520690 FORWARD LENGTH=406 |
```

```
201606
```

Coefficients for Vitvi13g00261.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	0.5253927	0.0164883	*	0.01737758	*
SlopeC	-0.4169403	0.4660837		0.8618199	
MeanF-MeanC	-3.015297	5.911452e-10	***	3.639539e-08	***
SlopeF-SlopeC	-2.079326	0.02120173	*	0.9999488	



8.8.15 Vitvi00g02022: Type6.F

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi00g02022

17.1.2

hormone metabolism.abscisic acid.signal transduction

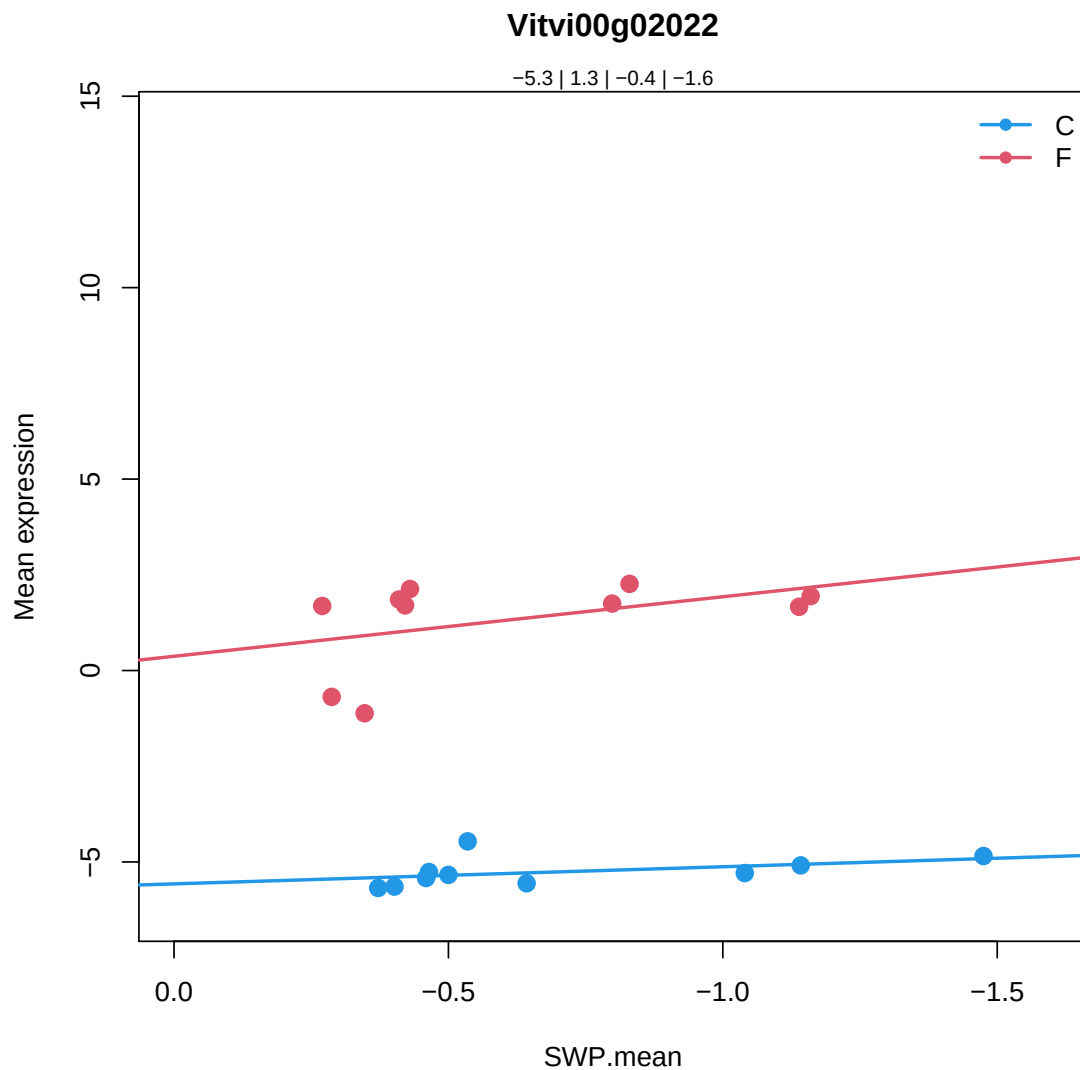
GCR2-like 1 |

Chr5:26086129-26087304 REVERSE LENGTH=311 |

201606

Coefficients for Vitvi00g02022.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-5.25859	4.249314e-16	***	8.367965e-16	***
SlopeC	-0.446971	0.5134631		0.8711742	
MeanF-MeanC	6.577033	5.234018e-15	***	6.818539e-13	***
SlopeF-SlopeC	-1.107401	0.2809345		0.9999488	



8.8.16 Vitvi17g01497: Type6.F

```
> cat.feature(fdata[fdata$geneID %in% varname,2:5])
```

Vitvi17g01497

26.2

misc.UDP glucosyl and glucoronyl transferases

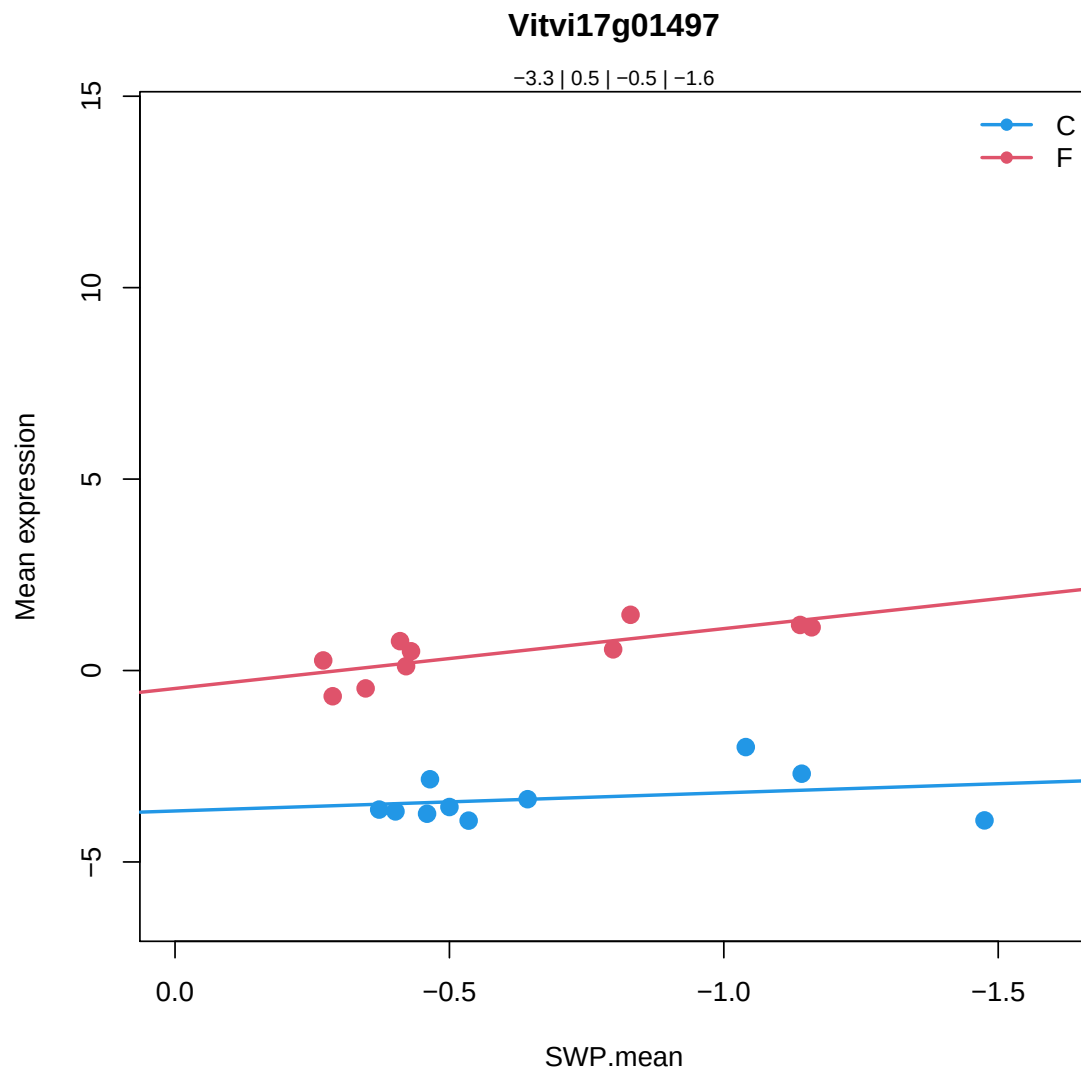
UDP-Glycosyltransferase superfamily protein |

Chr3:368840-370484 REVERSE LENGTH=464 |

201606

Coefficients for Vitvi17g01497.

	Value	P.value	sig	P.value.adj	sig.adj
MeanC	-3.334798	4.342005e-15	***	7.574779e-15	***
SlopeC	-0.4744792	0.331881		0.801141	
MeanF-MeanC	3.817918	3.025e-13	***	3.053447e-11	***
SlopeF-SlopeC	-1.089142	0.1403554		0.9999488	



```

> #
> fit2 <- eBayes(fit2)
> fit2[testvar,]$coefficients
              (Intercept)              swp  varietyF swp:varietyF
Vitvi01g01391    1.595041 -0.7685916  0.2722187    0.4814101
> head(fit2[1:6,]$coefficients)
              (Intercept)              swp  varietyF swp:varietyF
Vitvi15g01736    5.550751  1.593545190 -0.2500355  -0.31758915
Vitvi07g02832   -2.634115  0.508155686  5.4166972  -0.25109586
Vitvi07g02830   -1.750650  1.548036562  4.3321685  -0.90607176
Vitvi07g02812   -1.381363 -0.009794742  2.3030352   0.40349136
Vitvi07g02811    2.236177  0.566269561  1.2588734   0.02240192
Vitvi09g02033   -2.842837  0.419564483  4.1984533  -0.76028515

```

A Metadata files

A.1 Project metadata

Table 2: Project metadata

Item	Value
project:	_p_VinskaTrta
Short Name:	VinskaTrta
Title:	Vine related research
Description:	*
pISA projects path:	D:/DEJAVNOSTI/OMIKE/pISA-projects
Local pISA-tree organisation:	NIB
pISA project creation date:	2020-11-13
pISA project creator:	AB
Project funding code:	*
Project coordinator:	Marusa Pompe Novak
Project partners:	*
Project start date:	*
Project end date:	*
Principal investigator:	*
License:	CC BY 4.0
Sharing permission:	Private
Upload to FAIRDOMHub:	Yes

A.2 Investigation metadata

Table 3: Investigation metadata

Item	Value
Investigation:	_I_EnViRoS
Short Name:	EnViRoS
Title:	Integration of data from different platforms
Description:	*
Phenodata:	./phenodata_20201113.txt
pISA Investigation creation date:	2020-11-13
pISA Investigation creator:	AB
Principal investigator:	*
License:	CC BY 4.0
Sharing permission:	Private
Upload to FAIRDOMHub:	Yes

A.3 Study metadata

Table 4: Study metadata

Item	Value
Study:	_S_01_Integ
Short Name:	01_Integ
Title:	*
Description:	*
Raw Data:	
pISA Study creation date:	2020-11-13
pISA Study creator:	AB
Principal investigator:	*
License:	CC BY 4.0
Sharing permission:	Private
Upload to FAIRDOMHub:	Yes

A.4 Assay metadata

Table 5: Assay metadata

Item	Value
Assay:	_A_01_Desc-R
Short Name:	01_Desc-R
Assay Class:	DRY
Assay Type:	R
Title:	Data overview and descriptive statistical presentation
Description:	First we will organize the data and perform preliminary data analyses to overview what we have.
pISA Assay creation date:	2020-11-13
pISA Assay creator:	Andrej Blejec
Analyst:	Andrej Blejec
Phenodata:	Phenodata_20201109.txt
Featuredata:	Transcripts1819-02.txt
Featuredata metabolites:	Featuredata_metabolites_210127.txt
Transcript data 18:	/input/Transcripts 2018.txt
Transcript data 19:	/input/Transcripts 2019.txt
Metabolite data 18:	/input/Metabolites_2018_raw_-data.txt
Metabolite data 19:	/input/Metabolites_2019_raw_-data.txt
Water potential data:	/input/Stem water potential 2018 2019.txt
Interesting bins:	Bin_selection.txt
Transcript stats:	/output/50_Expression-water-stress-0.05-1.5-0.5-1-1/lm-fit-means-swpXvariety-statistics.txt

B SessionInfo

Windows 10 x64 (build 19041)

- R version 4.0.2 (2020-06-22), x86_64-w64-mingw32
- Locale: LC_COLLATE=Slovenian_Slovenia.1250, LC_CTYPE=Slovenian_Slovenia.1250, LC_NUMERIC=C, LC_TIME=Slovenian_Slovenia.1250
- Running under: Windows 10 x64 (build 19041)
- Matrix products: default
- Base packages: base, datasets, graphics, grDevices, grid, methods, parallel, stats, utils
- Other packages: amisc 0.1.0, Biobase 2.50.0, BiocGenerics 0.36.0, dotCall64 1.0-0, fields 11.6, Formula 1.2-4, ggplot2 3.3.3, Hmisc 4.4-1, knitr 1.30, lattice 0.20-41, limma 3.46.0, lubridate 1.7.9.2, MASS 7.3-51.6, reshape2 1.4.4, spam 2.6-0, survival 3.2-7, xtable 1.8-4
- Loaded via a namespace (and not attached): backports 1.2.0, base64enc 0.1-3, checkmate 2.0.0, cluster 2.1.0, colorspace 1.4-1, compiler 4.0.2, crayon 1.3.4, data.table 1.13.2, digest 0.6.27, dplyr 1.0.2, ellipsis 0.3.1, evaluate 0.14, foreign 0.8-80, generics 0.1.0, glue 1.4.2, gridExtra 2.3, gtable 0.3.0, highr 0.8, htmlTable 2.1.0, htmltools 0.5.0, htmlwidgets 1.5.3, jpeg 0.1-8.1, latticeExtra 0.6-29, lifecycle 0.2.0, magrittr 2.0.1, maps 3.3.0, Matrix 1.2-18, munsell 0.5.0, nnet 7.3-14, pillar 1.4.7, pkgconfig 2.0.3, plyr 1.8.6, png 0.1-7, purrr 0.3.4, R6 2.5.0, RColorBrewer 1.1-2, Rcpp 1.0.5, rlang 0.4.10, rpart 4.1-15, rstudioapi 0.13, scales 1.1.1, splines 4.0.2, stringi 1.5.3, stringr 1.4.0, tibble 3.0.4, tidyselect 1.1.0, tools 4.0.2, vctrs 0.3.6, withr 2.3.0, xfun 0.19

Analysis project path: [\[link\]](#)

Local

D:

DEJAVNOSTI

OMIKE

pISA-projects

_p_VinskaTrta

_I_EnViRoS

_S_01_Integ

_A_01_Desc-R

other

Network

O:

DEJAVNOSTI

OMIKE

pISA-projects

_p_VinskaTrta

_I_EnViRoS

_S_01_Integ

_A_01_Desc-R

other

Main file : [../doc/50_Expression-water-stress.Rnw](#)

Main file : [../scripts/50_Expression-water-stress.Rnw](#)

Project file: [\[link\]](#)

View as vignette

Source files can be viewed by pasting this code to R console:

```
projectName <-"other"
mainFile <-"50_Expression-water-stress"
commandArgs()
library(tkWidgets)
openPDF(file.path(dirname(getwd()),"doc",
paste(mainFile,"PDF",sep=".")
viewVignette("viewVignette", projectName,
file.path("../doc",paste(mainFile,"Rnw",sep=".")))
```