Heatschock Arrays

Elisabet Tintó, Lucas Michel Todó

February 5, 2019

Contents

1 Imputed FC

1.1 10E FC

s10E_T1_HS	s10E_T2_HS	s10E_T3_HS	Max_Dif	Gene	Annot
2.0489945	4.0265577	2.7637695	4.026558	PF3D7_0818900	heat shock prot. 70
-1.7218645	-3.8935602	0.2723678	-3.893560	PF3D7_1428000	cvd. Pl. memb. prot. ukwn. func.
1.2330183	3.6222511	2.8090811	3.622251	PF3D7_1000600	rifin
-2.6150582	-3.4433569	0.3468610	-3.443357	S2-type_28S:rRNA	NA
-1.9884922	-3.3929230	-0.6069939	-3.392923	PF3D7_0112600	unspecified product
-2.0439641	-3.3074306	0.3950818	-3.307431	PF3D7_1455900	polyprenol reductase put.
-1.3421985	-3.2800100	0.0124447	-3.280010	PF3D7_0717000	cvd. Pl. memb. prot. ukwn. func.
-1.6829756	-3.2617931	0.9056299	-3.261793	PF3D7_0622700	cvd. Pl. memb. prot. ukwn. func.
1.8267402	3.1565584	1.2542698	3.156558	PF3D7_1421800	cvd. Pl. prot. ukwn. func.
-1.6207045	-3.1124710	0.3854057	-3.112471	PF3D7_0911000	phosphatidylinositol N-acetylglucosaminyltransferase put.
NA	NA	-3.0633088	-3.063309	PF14TR007	NA
-1.3878045	-3.0022915	0.6412622	-3.002292	PF3D7_0929900	cvd. Pl. prot. ukwn. func.
-1.3984653	-2.8614779	0.0744639	-2.861478	PF3D7_0523500	dynein light chain Tctex-type put.
-1.5566419	-2.8224296	-0.1544318	-2.822430	PF3D7_0627200	myosin light chain put.
-0.9800127	-2.8060897	-0.0950306	-2.806090	PF3D7_0414200	calmodulin-like prot.
1.0834900	2.7624204	0.9954510	2.762420	PF3D7_0214300	cvd. Pl. prot. ukwn. func.
2.7529274	0.0941567	-0.1863445	2.752927	PF3D7_1314800	ubiquitin-like prot. put.
1.2478092	2.7240805	1.0579105	2.724080	PF3D7_0404600	cvd. Pl. memb. prot. ukwn. func.
-1.0022730	-2.6543406	1.0460634	-2.654341	PF3D7_1322800	cvd. Pl. prot. ukwn. func.
0.6521131	2.6276509	1.8115100	2.627651	PF3D7_0525000	zinc finger prot. put.
0.9531122	2.5804698	0.2909951	2.580470	PF3D7_1362700	cvd. Pl. prot. ukwn. func.
1.1187591	2.5662126	1.3217427	2.566213	PF3D7_0220300	Pl. xptd. prot. ukwn. func.
-1.3852968	-2.5657303	0.2571554	-2.565730	PF3D7_0613200	cvd. Pl. prot. ukwn. func.
-0.8289211	-2.5057559	0.2416806	-2.505759	PF3D7_1433600	signal peptidase complex subunit SPC1 put.
0.4870453	2.4677876	2.1483594	2.467788	PF3D7_1038700	Pl. xptd. prot. ukwn. func.
-0.4539304	0.8211792	2.4543858	2.454386	PF3D7_0324100	Pfmc-2TM Maurer's cleft two transmemb. prot.
0.6091590	2.4531509	1.6318496	2.453151	BSD	NA
-0.9269817	-2.4487225	0.0859541	-2.448723	PF3D7_1135000	PQ-loop repeat-containing prot. unspecified product
-0.9352453	-2.4359463	-0.2882011	-2.435946	PF3D7_0729200	1-cys peroxiredoxin
-0.7109644	-0.9582562	2.4359055	2.435906	PF3D7_0524200	cvd. Pl. memb. prot. ukwn. func.
-0.6880042	-2.4299811	-0.5552725	-2.429981	PF3D7_0323000	translation machinery-associated prot. 7 put.
0.8225018	1.8692184	2.4227689	2.422769	PF3D7_0800700	surface-associated interspersed prot. 8.3 (SURFIN 8.3)
-1.1773975	-2.4011238	0.1421178	-2.401124	PF3D7_1371500	probable prot. ukwn. func.
0.1143743	2.3856525	1.9254568	2.385652	PF3D7_1201100	RESA-like prot. with PHIST and DnaJ domains
-0.8600038	-2.3812869	0.3315026	-2.381287	PF3D7_0912700	cvd. Pl. prot. ukwn. func.
-0.5896510	-2.3785127	0.4246107	-2.378513	PF3D7_1413300	cvd. Pl. prot. ukwn. func.
-0.3469780	0.3254741	2.3646003	2.364600	PF3D7_1237300	cvd. Pl. prot. ukwn. func.
0.5498747	1.8887517	2.3534550	2.353455	PF3D7_0404500	6-cysteine prot.
-1.3798491	-2.3159824	1.8946139	-2.315982	PF3D7_0513700	secreted ookinete prot. put.
-0.5500801	-2.3145427	-0.3863081	-2.314543	PF3D7_1447700	cvd. Pl. prot. ukwn. func.
-0.7214122	-2.2885964	-0.6557671	-2.288596	PF3D7_1459300	OPA3-like prot. put.
-0.9626105	-2.2796311	-0.3062433	-2.279631	PF3D7_1463600	cvd. Pl. prot. ukwn. func.
-1.1915921	-2.2794752	-0.2588739	-2.279475	PF3D7_0112400	unspecified product
-0.9207716	-1.7445386	-2.2727826	-2.272783	PF3D7_1373000	rifin
-1.3589828	-2.2670347	0.8246955	-2.267035	PF3D7_0618600	rhomboid protease ROM10
-2.2648826	-2.0425870	-1.4067897	-2.264883	PF3D7_0800800	Pl. xptd. prot. (hyp7) ukwn. func.
0.6381268	2.2531239	1.1319811	2.253124	PF3D7_0113400	Pl. xptd. prot. ukwn. func.
-1.0199383	-2.2500155	0.3172939	-2.250015	PF3D7_0414300	Rab5-interacting prot. put.
0.9314392	2.2474121	1.0281318	2.247412	PF3D7_1236200	cvd. Pl. prot. ukwn. func.
-1.0373801	-2.2326496	-1.3494395	-2.232650	PF3D7_0936100	early transcribed memb. prot.

1.2   10G FC

| s10G_T1_HS	s10G_T2_HS	s10G_T3_HS	Max_Dif	Gene	Annot
2.1137451	4.2991723	4.9279716	4.927972	PF3D7_1201100	RESA-like prot. with PHIST and DnaJ domains
2.6347191	4.4548988	4.8855375	4.885537	PF3D7_0425900	rifin
-1.3298695	-4.5527720	-2.2619124	-4.552772	PF3D7_0211000	unspecified product
1.9378205	3.9765343	4.5024441	4.502444	Pfa_npcR_6502a	NA
3.0149005	3.8700142	4.0953486	4.095349	PF3D7_1000600	rifin
-0.0436569	1.5137139	4.0231735	4.023174	PF3D7_1479000	acyl-CoA synthetase
1.4033747	3.3103404	3.9649935	3.964993	PF3D7_1200200	rifin
1.1564351	2.7860372	3.8797703	3.879770	Pfa_raR_7295	NA
-0.4848050	1.5423599	3.8648579	3.864858	PF3D7_1478900	unspecified product
1.3015494	3.3485580	3.8227606	3.822761	PF3D7_0220500	Pl. xptd. prot. (hyp2) ukwn. func.
-1.8063928	-3.7768931	-2.9373609	-3.776893	PF3D7_0523500	dynein light chain Tctex-type put.
-1.4848834	-3.7246744	-2.8094441	-3.724674	PF3D7_1371500	probable prot. ukwn. func.
1.4217156	3.2457568	3.6716633	3.671663	BSD	NA
-1.7510847	-3.6173576	-2.4031305	-3.617358	PF3D7_1428000	cvd. Pl. memb. prot. ukwn. func.
-3.5057700	-3.2247349	0.0167300	-3.505770	S2-type_28S:rRNA	NA
0.0457444	2.1141881	3.4928105	3.492811	PF3D7_1104900	calcium/calmodulin-dependent prot. kinase put.
-0.5135120	-3.4531676	-2.3356841	-3.453168	PF3D7_0304800	cvd. Pl. memb. prot. ukwn. func.
1.1332030	3.0559121	3.3941579	3.394158	PF3D7_0830500	sporozoite and liver stage tryptophan-rich prot. put.
0.9869742	2.9827184	3.3563964	3.356396	PF3D7_1473700	nucleoporin NUP116/NSP116 put.
2.0091358	2.7803212	3.3537782	3.353778	PF3D7_0919200	PPPDE peptidase put.
0.9201151	2.9630996	3.3395569	3.339557	PF3D7_1455300	cvd. Pl. prot. ukwn. func.
1.3342481	3.1096949	3.3372747	3.337275	PF3D7_1461800	cvd. Pl. prot. ukwn. func.
0.9638254	2.7438073	3.3338683	3.333868	PF3D7_0115600	rifin
-0.9007556	-3.3322740	-2.7956473	-3.332274	PF3D7_1447700	cvd. Pl. prot. ukwn. func.
-2.1561557	-3.3289434	-2.8495299	-3.328943	PF3D7_0911500	cvd. Pl. prot. ukwn. func.
-2.0639038	-3.3133003	-2.4818534	-3.313300	PF3D7_1455900	polyprenol reductase put.
0.9461254	3.0010464	3.2978560	3.297856	PF3D7_1300200	rifin
-2.5060113	-3.2883457	-2.0785061	-3.288346	PF3D7_0622700	cvd. Pl. memb. prot. ukwn. func.
2.0435174	3.1597876	3.2399103	3.239910	PF3D7_1327300	cvd. Pl. prot. ukwn. func.
-1.0126413	-3.1831313	-2.4891014	-3.183131	PF3D7_1442800	cvd. Pl. prot. ukwn. func.
1.1244585	3.1824766	3.0773001	3.182477	PF3D7_0418600	regulator of chromosome condensation put.
-0.6657867	-3.1754078	-2.3003331	-3.175408	PF3D7_0612300	transmemb. prot. 234 put.
-1.6523152	-3.1702565	-2.4312476	-3.170256	PF3D7_1138900	unspecified product
-1.1460425	-3.1580070	-2.9965295	-3.158007	PF3D7_0414200	calmodulin-like prot.
-2.8134191	-3.1400926	-2.3479327	-3.140093	PF3D7_0112600	unspecified product
0.5806812	2.1703357	3.1307881	3.130788	Pfa_rasR_6152b	NA
1.0002653	3.1290953	3.1096016	3.129095	PF3D7_0424500	serine/threonine prot. kinase FIKK family
-0.7602257	0.3923218	3.1160955	3.116096	PF14TR011	NA
-0.0854555	3.0797745	2.4525542	3.079775	PF3D7_0425200	Pl. xptd. prot. (hyp15) ukwn. func.
-0.7019923	-3.0575793	-2.5612616	-3.057579	PF3D7_0531200	ribosomal prot. S16 mitochondrial put.
0.7540290	2.3200485	3.0542948	3.054295	PF3D7_0702100	Pl. xptd. prot. (PHISTb) ukwn. func. pseudo
1.1361720	2.4939047	3.0444175	3.044418	PF3D7_0401800	Pl. xptd. prot. (PHISTb) ukwn. func.
-2.1308832	-3.0369508	-2.3467176	-3.036951	PF3D7_0929900	cvd. Pl. prot. ukwn. func.
-1.2979217	-3.0258756	-2.6800888	-3.025876	PF3D7_0920300	cvd. Pl. prot. ukwn. func.
3.0036935	NA	0.5200563	3.003693	ETG10_13482	NA
0.2135770	2.1148377	2.9953831	2.995383	PF3D7_0931300	cvd. Pl. prot. ukwn. func.
-1.2072390	-2.9910360	-2.6865723	-2.991036	PF3D7_1415500	cvd. Pl. memb. prot. ukwn. func.
0.0233773	2.1999542	2.9807958	2.980796	PF3D7_0701900	Pl. xptd. prot. ukwn. func.
0.4493020	2.6346493	2.9774535	2.977454	Pfa_rasR_6152a	NA
0.9473589	2.5585782	2.9303477	2.930348	PF3D7_0902500	serine/threonine prot. kinase FIKK family

1.3 EK0 FC

| EK0_T1_HS	EK0_T2_HS	EK0_T3_HS	Max_Dif	Gene	Annot
3.8023938	4.8569453	4.692690	4.856945	PF3D7_1201100	RESA-like prot. with PHIST and DnaJ domains
-1.9416306	-4.2440483	-4.782000	-4.782000	PF3D7_0211000	unspecified product
1.9045315	2.5509136	4.638035	4.638035	Pfa_raR_7295	NA
-2.6191721	-4.5922710	-3.797023	-4.592271	PF3D7_0523500	dynein light chain Tctex-type put.
3.0829661	4.5840501	3.502010	4.584050	PF3D7_1301200	GBPH2 prot.
-1.7539348	-4.3045094	-3.829557	-4.304509	PF3D7_1442800	cvd. Pl. prot. ukwn. func.
-1.6471473	-2.9354249	-4.289994	-4.289994	PF3D7_0612300	transmemb. prot. 234 put.
-2.2993027	-4.2293721	-3.827649	-4.229372	PF3D7_0911500	cvd. Pl. prot. ukwn. func.
2.3895092	3.4186546	4.196898	4.196898	PF3D7_0220500	Pl. xptd. prot. (hyp2) ukwn. func.
-2.2256092	-3.9418175	-4.064436	-4.064436	PF3D7_1371500	probable prot. ukwn. func.
-1.4716560	-4.0427812	-3.727419	-4.042781	PF3D7_1243200	cvd. Pl. prot. ukwn. func.
-2.2013572	-2.2424364	-4.034055	-4.034055	PF3D7_1138900	unspecified product
2.9867359	3.1270593	3.965262	3.965262	Pfa_npcR_6502a	NA
2.7148473	3.6833436	3.914220	3.914220	BSD	NA
2.8828779	3.7149530	3.866368	3.866368	PF3D7_1200200	rifin
3.5422016	3.8330021	3.562946	3.833002	PF3D7_1000600	rifin
3.2599498	3.8277464	3.775691	3.827746	PF3D7_1300200	rifin
-2.3425589	-3.6534078	-3.422572	-3.653408	PF3D7_1415500	cvd. Pl. memb. prot. ukwn. func.
-1.1344729	-3.0483879	-3.621073	-3.621073	PF3D7_0715700	cvd. Pl. prot. ukwn. func.
2.3225763	3.1651720	3.608397	3.608397	PF3D7_1473700	nucleoporin NUP116/NSP116 put.
-1.5404627	-3.5764164	-2.827631	-3.576416	PF3D7_0531200	ribosomal prot. S16 mitochondrial put.
-1.7908769	-2.9899371	-3.427631	-3.427631	PF3D7_1428000	cvd. Pl. memb. prot. ukwn. func.
2.0581731	2.8904910	3.371153	3.371153	PF3D7_0830500	sporozoite and liver stage tryptophan-rich prot. put.
-1.7929202	-3.2893443	-3.314578	-3.314578	PF3D7_1447700	cvd. Pl. prot. ukwn. func.
-2.0022204	-3.2810434	-3.309032	-3.309032	PF3D7_1459300	OPA3-like prot. put.
0.6285579	0.9056818	3.289550	3.289550	PF3D7_0726200	serine/threonine prot. kinase FIKK family
-1.1327561	-3.2863665	-2.237896	-3.286367	PF3D7_0420500	cvd. Pl. prot. ukwn. func.
-1.4082491	-2.7197976	-3.284616	-3.284616	PF3D7_0111700	cvd. Pl. prot. ukwn. func.
-1.5023009	-2.4758748	-3.245238	-3.245238	PF3D7_1129800	cvd. Pl. prot. ukwn. func.
1.8234852	2.8196199	3.212838	3.212838	PF3D7_1016500	Pl. xptd. prot. (PHISTc) ukwn. func.
0.8527512	2.1333440	3.207891	3.207891	PF3D7_0726100	Pl. xptd. prot. ukwn. func.
1.7393624	2.8384464	3.186994	3.186994	PF3D7_1455300	cvd. Pl. prot. ukwn. func.
-2.5140261	-3.1742956	-3.117327	-3.174296	PF3D7_0622700	cvd. Pl. memb. prot. ukwn. func.
-1.3762392	-2.8846323	-3.172797	-3.172797	PF3D7_1322800	cvd. Pl. prot. ukwn. func.
1.6189063	2.5768360	3.122261	3.122261	PF3D7_1327500	cvd. Pl. prot. ukwn. func.
0.6551133	3.1165244	2.958353	3.116524	PF3D7_1000500	rifin
-2.2594348	-3.0964218	-2.469610	-3.096422	PF3D7_1474700	prot. kinase put.
-2.9305255	-2.9541177	-3.074790	-3.074790	PF3D7_1018400	cvd. Pl. prot. ukwn. func.
1.4200407	2.0950576	3.071462	3.071462	PF3D7_1362700	cvd. Pl. prot. ukwn. func.
-1.9342017	-3.0714373	-2.481436	-3.071437	PF3D7_0303600	plasmoredoxin
-1.7850804	-3.0144346	-2.845174	-3.014435	PF3D7_0612400	cvd. Pl. prot. ukwn. func.
1.9088095	3.0079359	2.782675	3.007936	PF3D7_1226100	haloacid dehalogenase-like hydrolase put.
1.3603219	2.3945868	2.996161	2.996161	PF3D7_1000300	rifin
1.3619715	2.3611783	2.987410	2.987410	PF3D7_0315600	zinc finger prot. put.
1.7961729	2.9766919	1.865438	2.976692	PF3D7_0832100	rifin pseudo
1.7493615	2.7702028	2.955449	2.955449	PF3D7_1461800	cvd. Pl. prot. ukwn. func.
1.1986903	2.6384073	2.948113	2.948113	PF3D7_0701900	Pl. xptd. prot. ukwn. func.
-1.1954013	-2.0072608	-2.932215	-2.932215	PF3D7_1346600	cvd. Pl. prot. ukwn. func.
-1.4459350	-2.6859144	-2.930878	-2.930878	PF3D7_0625700	cvd. Pl. prot. ukwn. func.
-1.4581395	-2.9126340	-2.493292	-2.912634	PF3D7_0920300	cvd. Pl. prot. ukwn. func.

4

2 Venn Diagrams

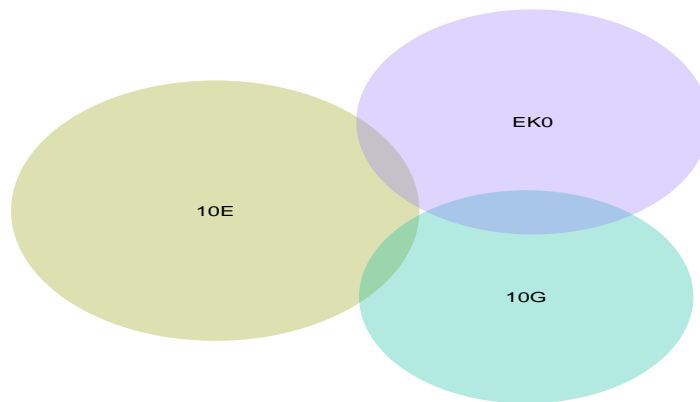## 2.1 Max.FC (any timepoint) > 4 FC
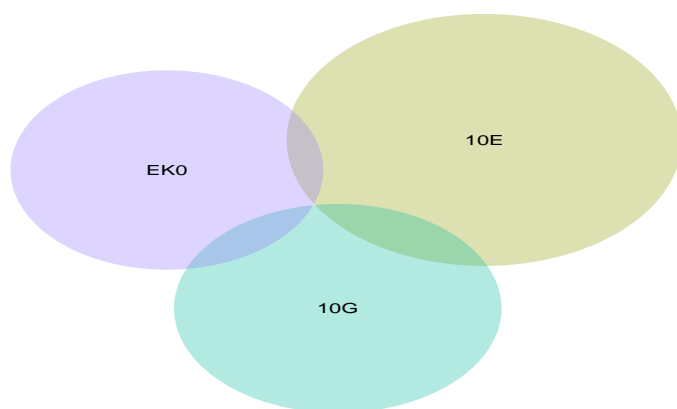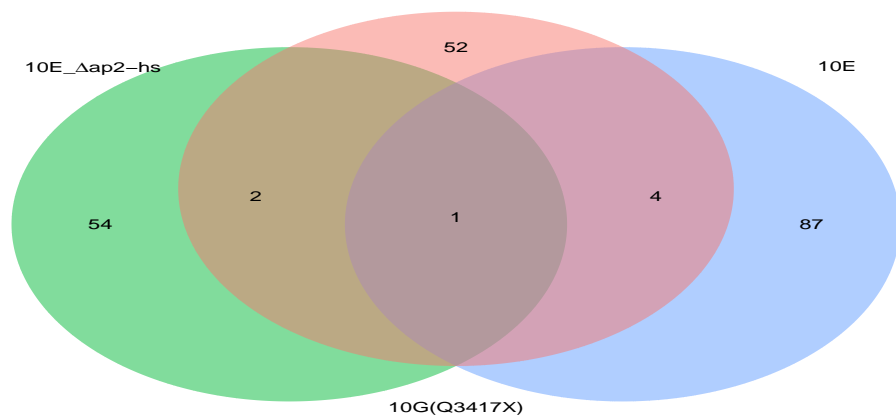
2.1.1 Up-regulated
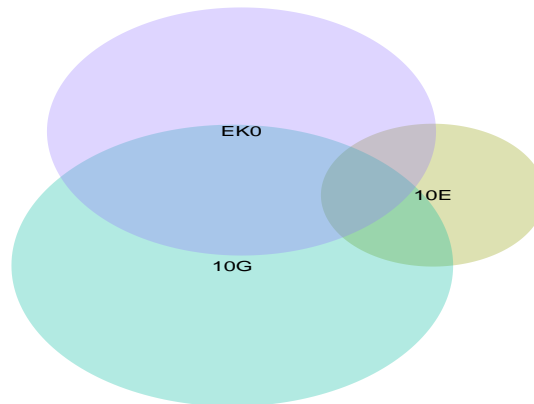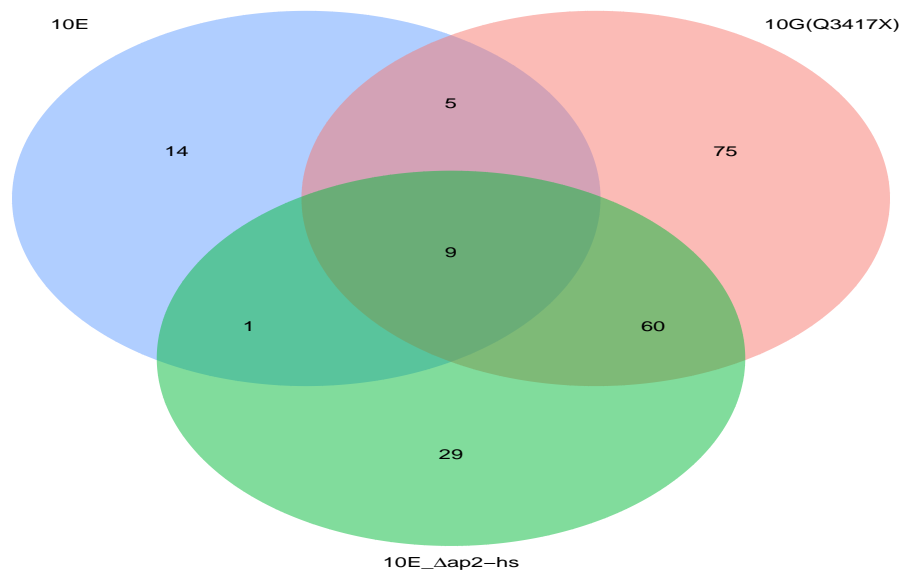
2.1.2 Down-regulated
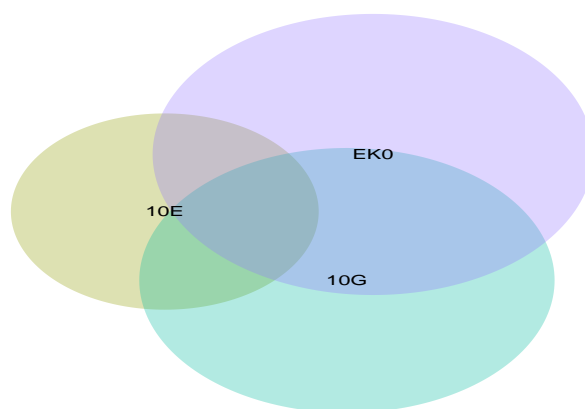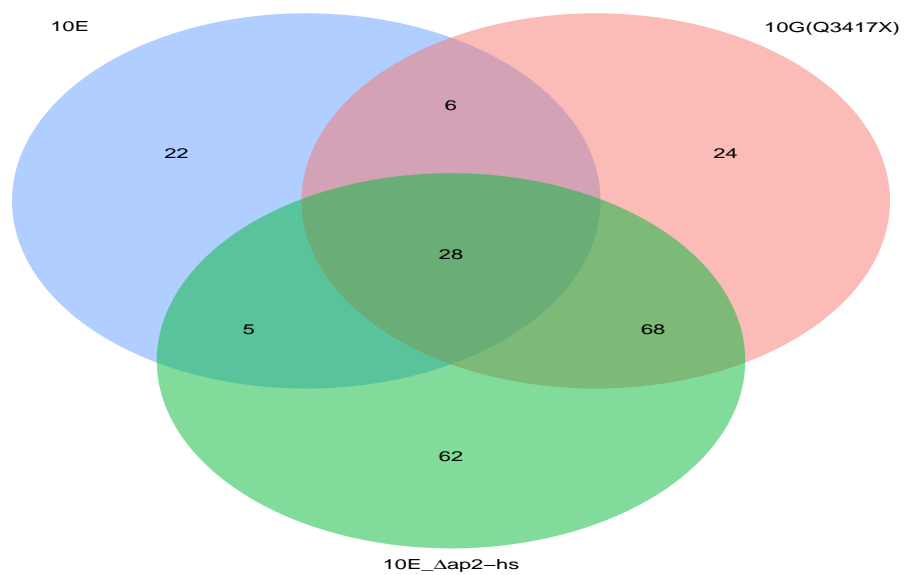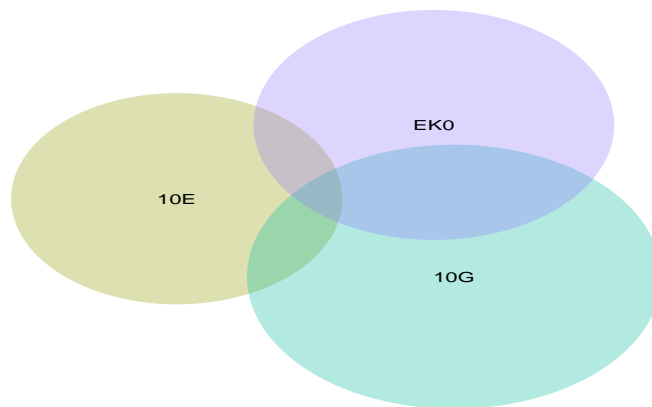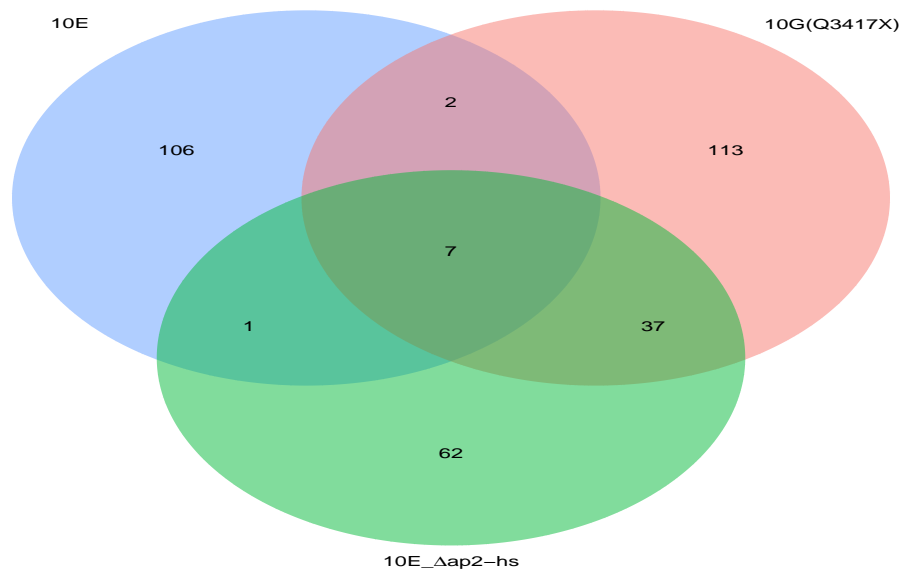
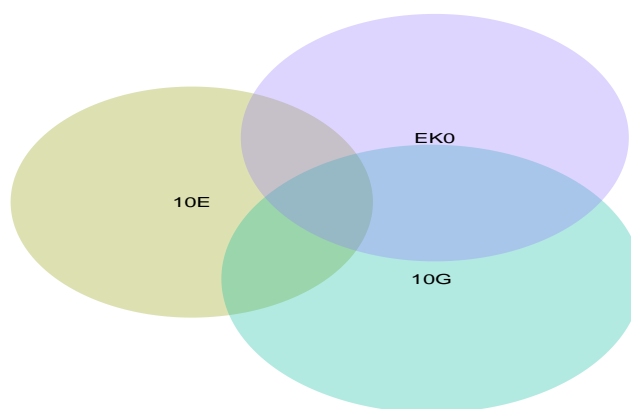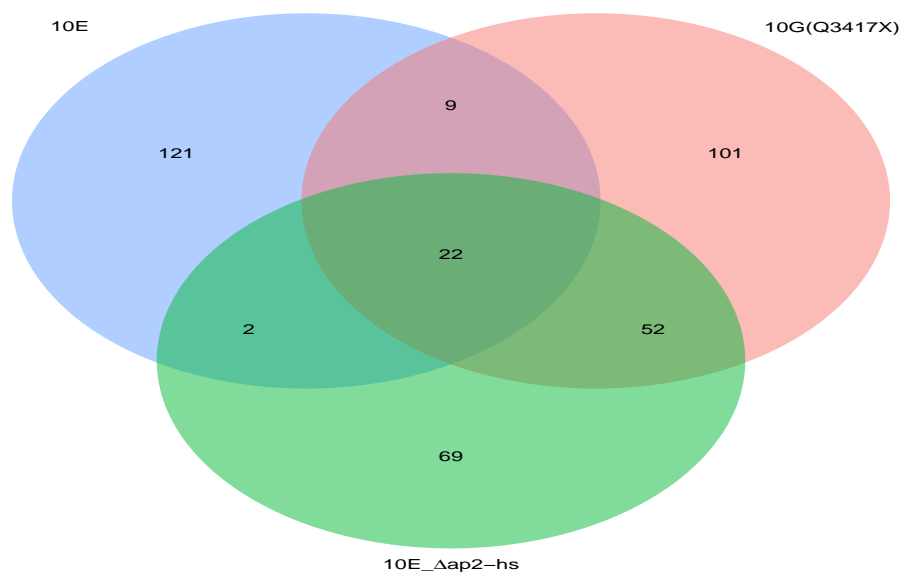## 2.2 Max.FC T1 > 4 FC

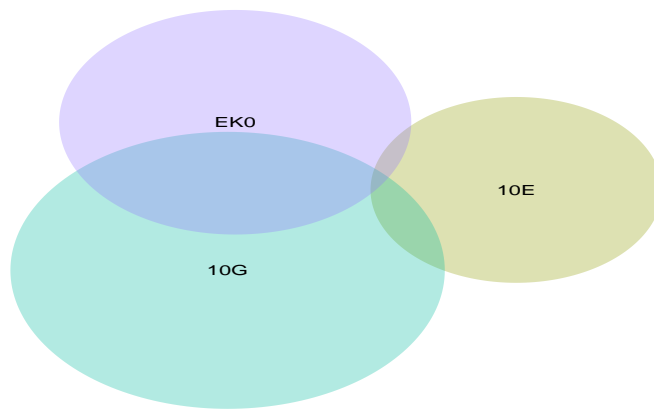### 2.2.1 Up-regulated

2.2.2 Down-regulated
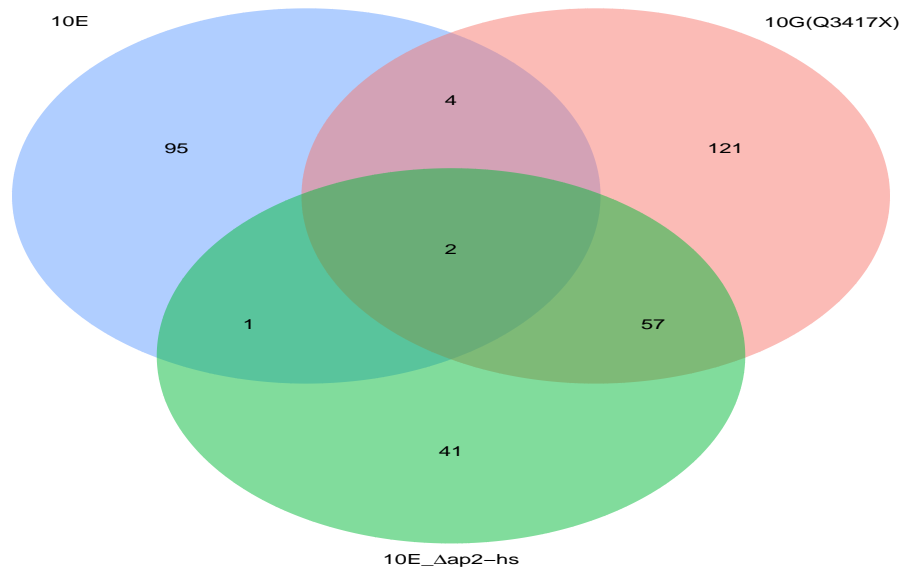
2.3 Max.FC T2 > 4 FC

2.3.1 Up-regulated
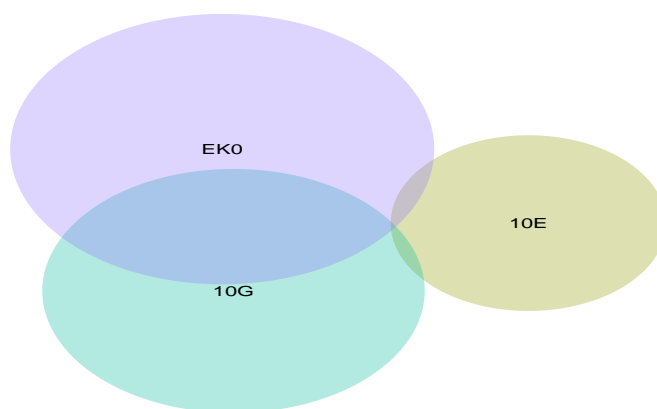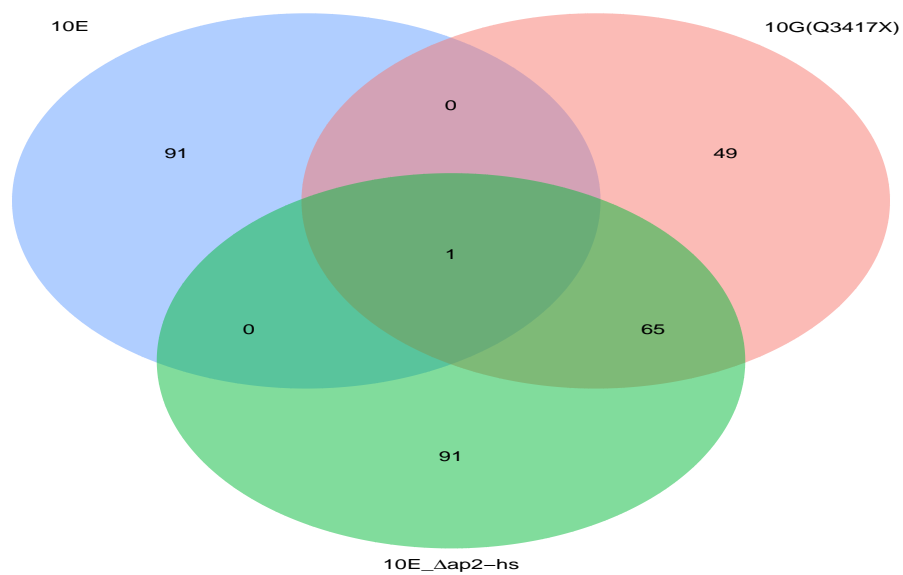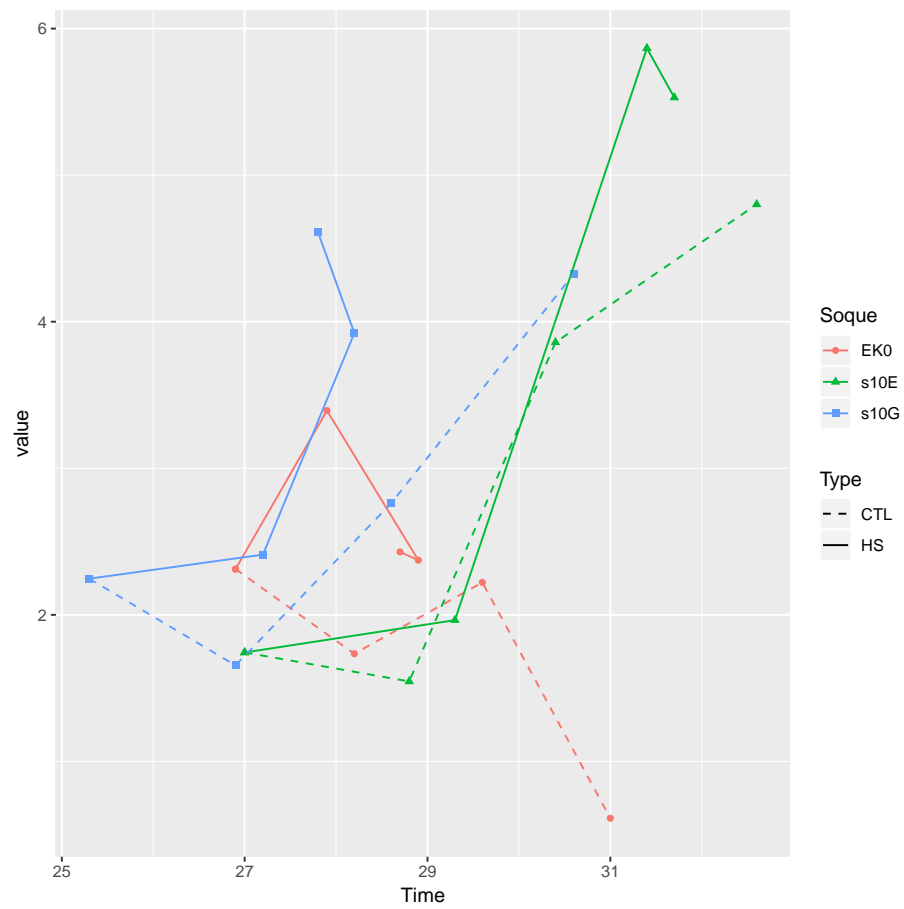
2.3.2 Down-Regulated

2.4 Max.FC T3 > 4 FC

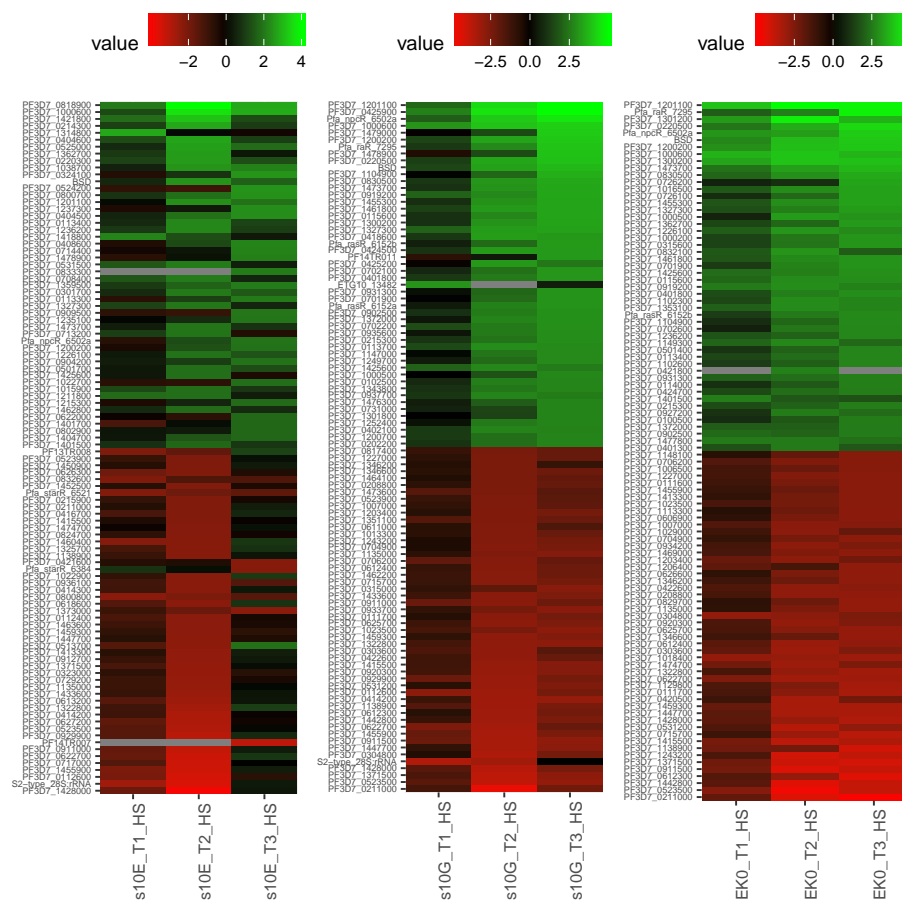### 2.4.1 Up-regulated

2.4.2 Down-Regulated
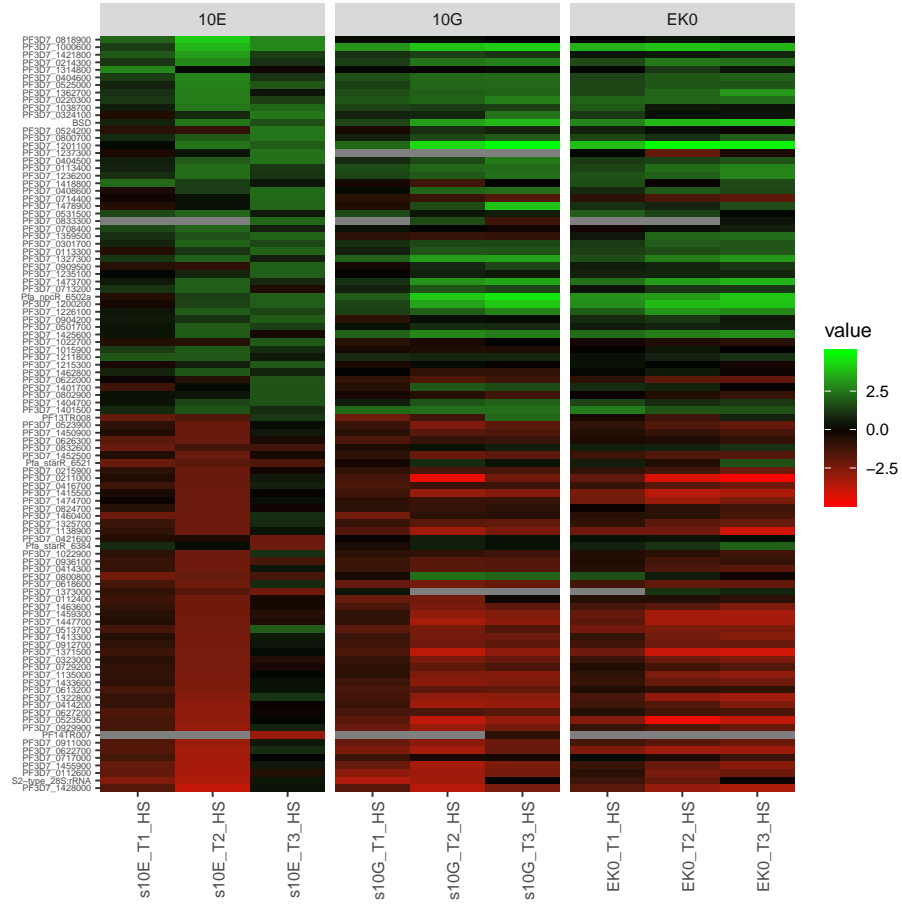
3   Example Custom Plot
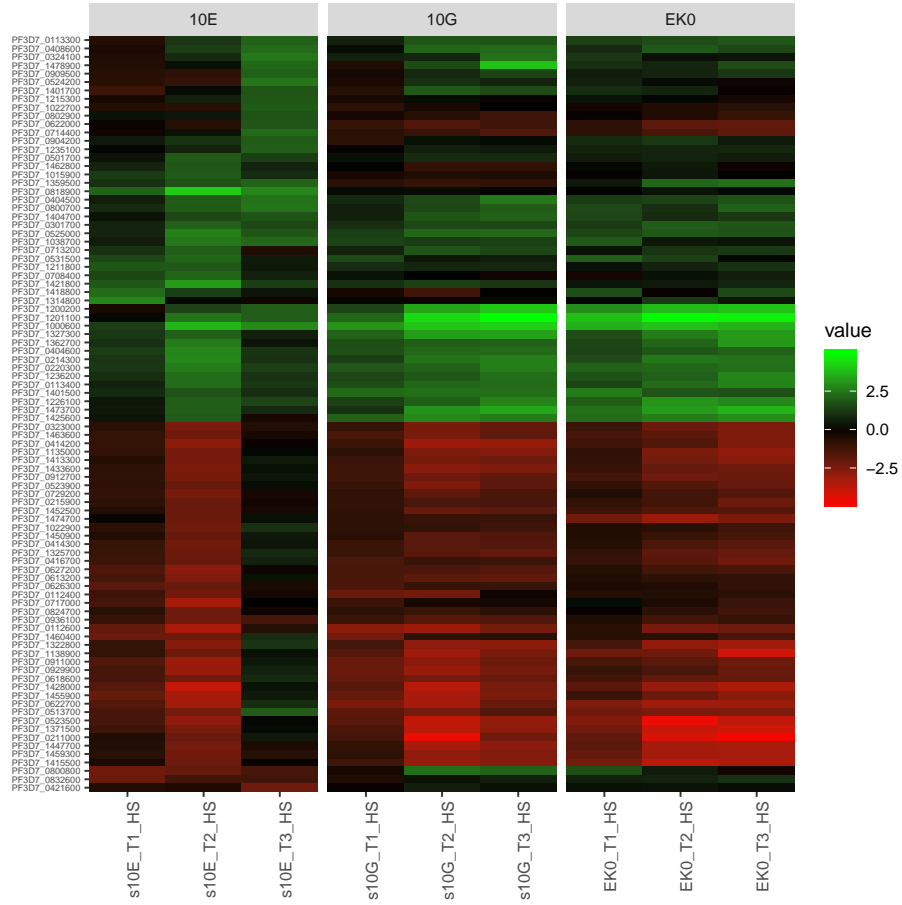
4 Heat maps
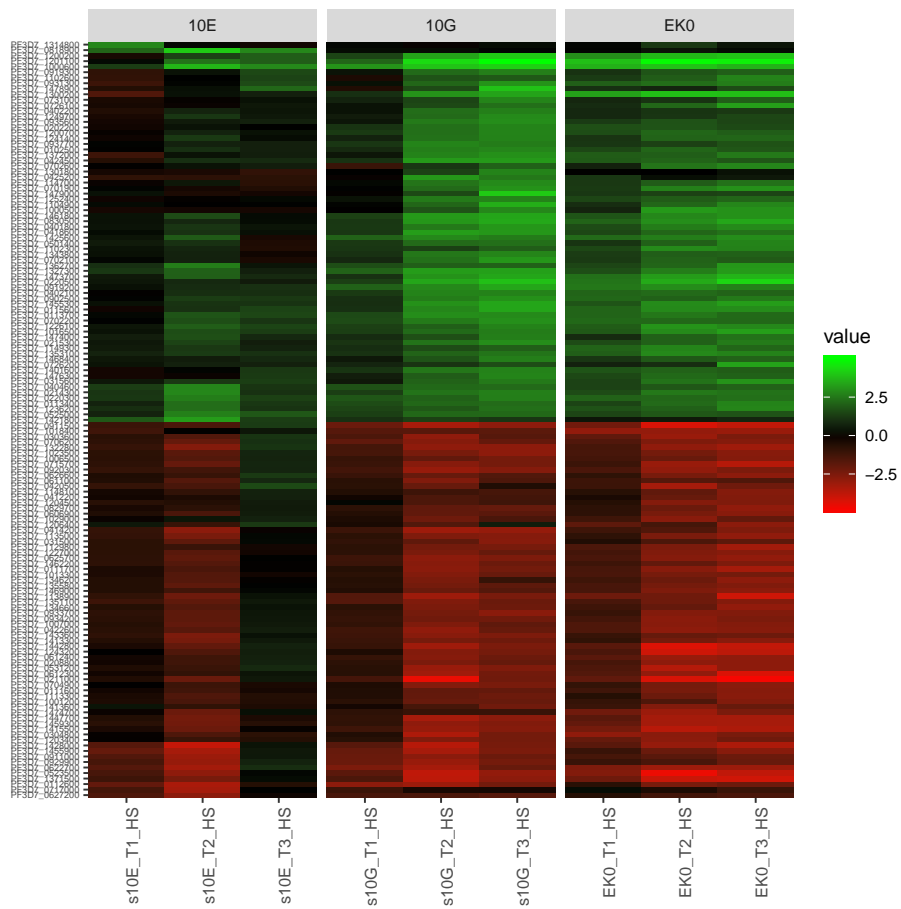
4.1 Top FC separated

4.2 Top FC in 10E, across strains, ordered

4.3 Top FC in 10E, across strains, clustered

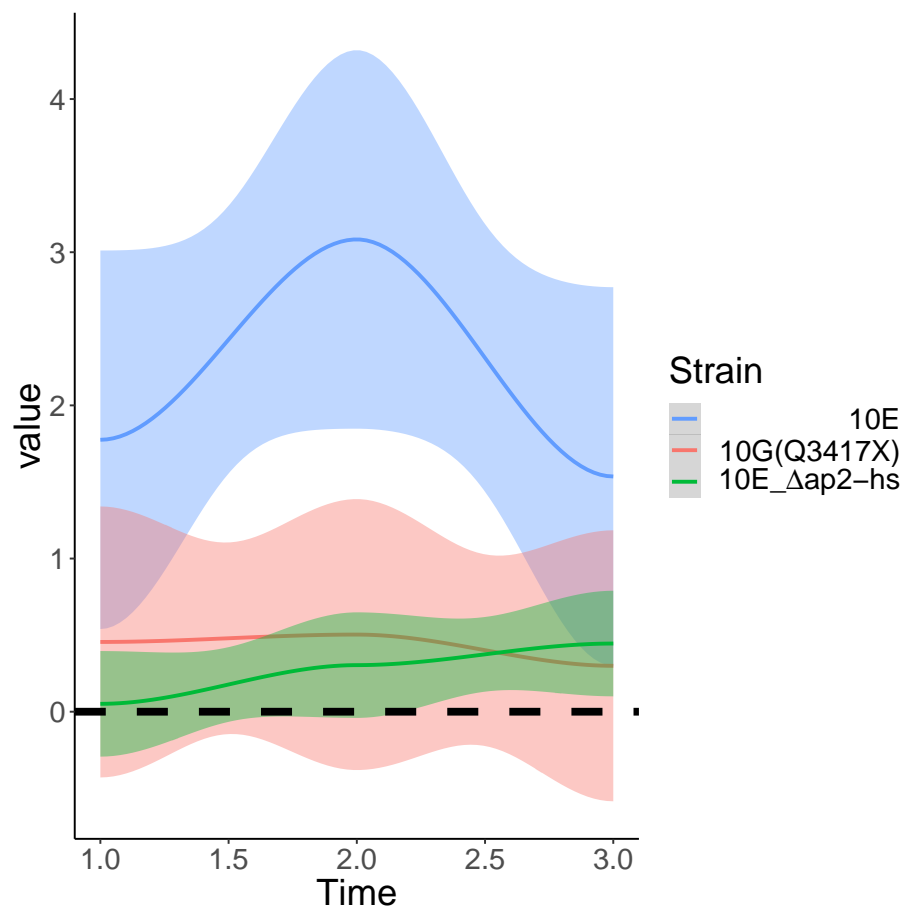## 4.4   FC >6 in all strains combined, clustered

5 Principal Component Analysis
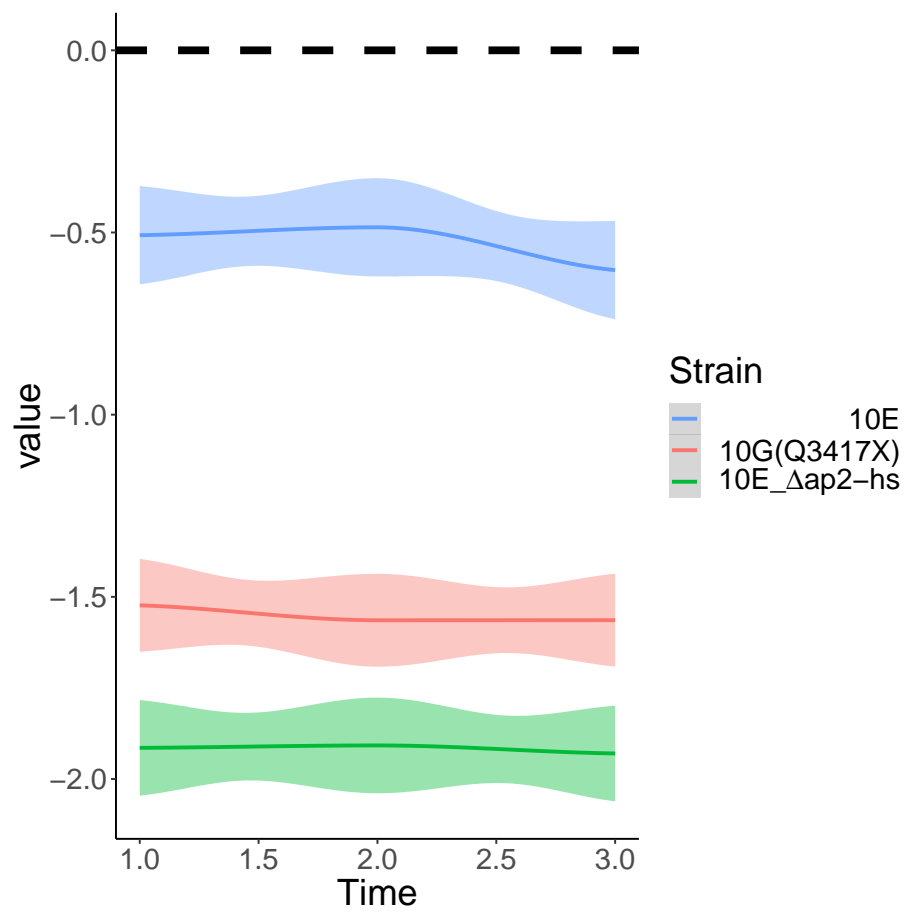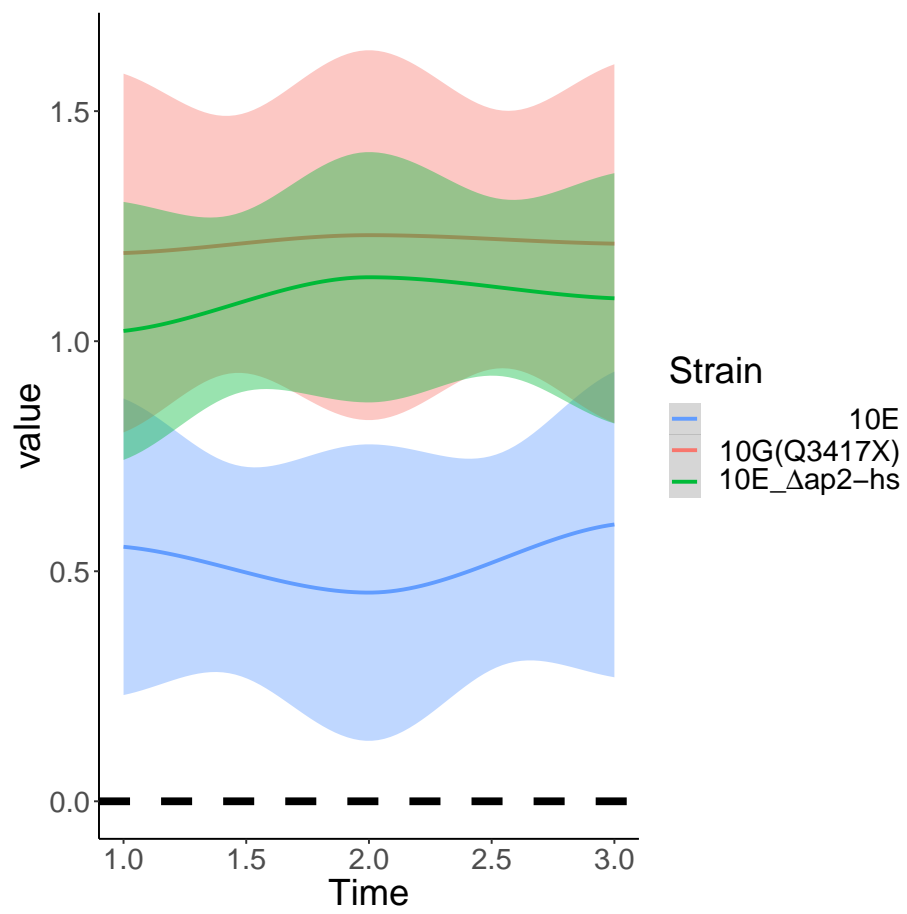
```
## Error:  Can't find shape name:
## * 'Status'
## Error in FUN(X[[i]], ...):  object 'Strain' not found
## Error in FUN(X[[i]], ...):  object 'Strain' not found
## Error in FUN(X[[i]], ...):  object 'Strain' not found
## Saving 7 x 7 in image
## Error in FUN(X[[i]], ...):  object 'Strain' not found
## Saving 7 x 7 in image
## Error in FUN(X[[i]], ...):  object 'Strain' not found
```
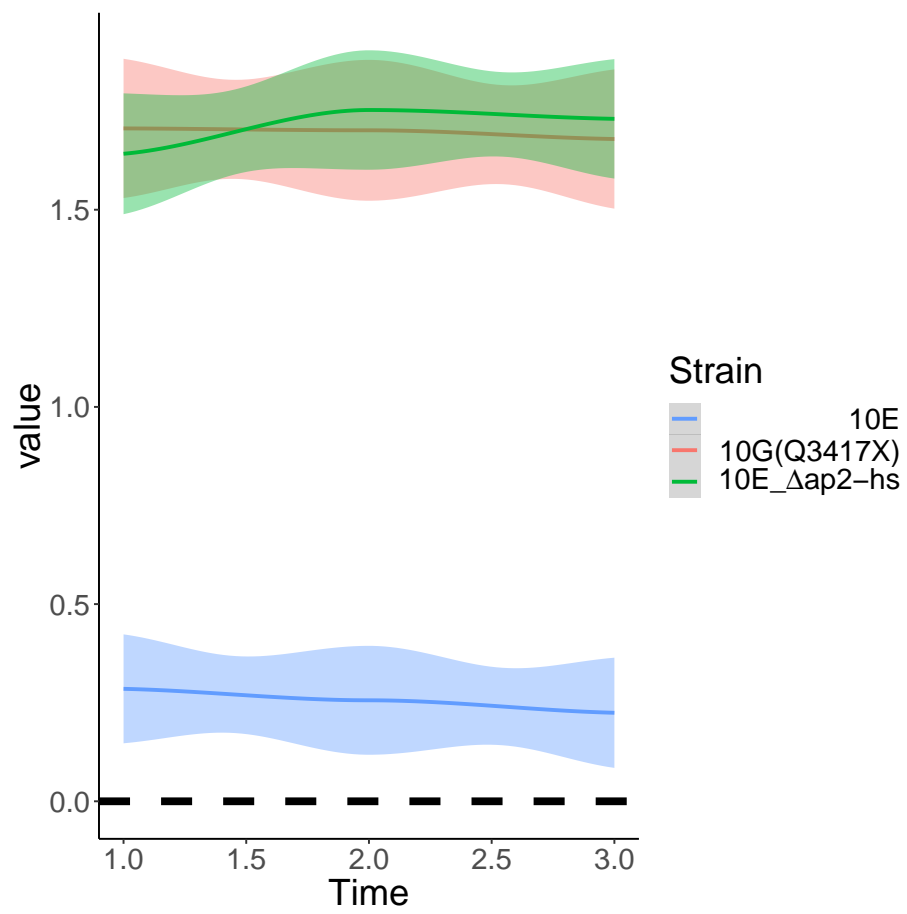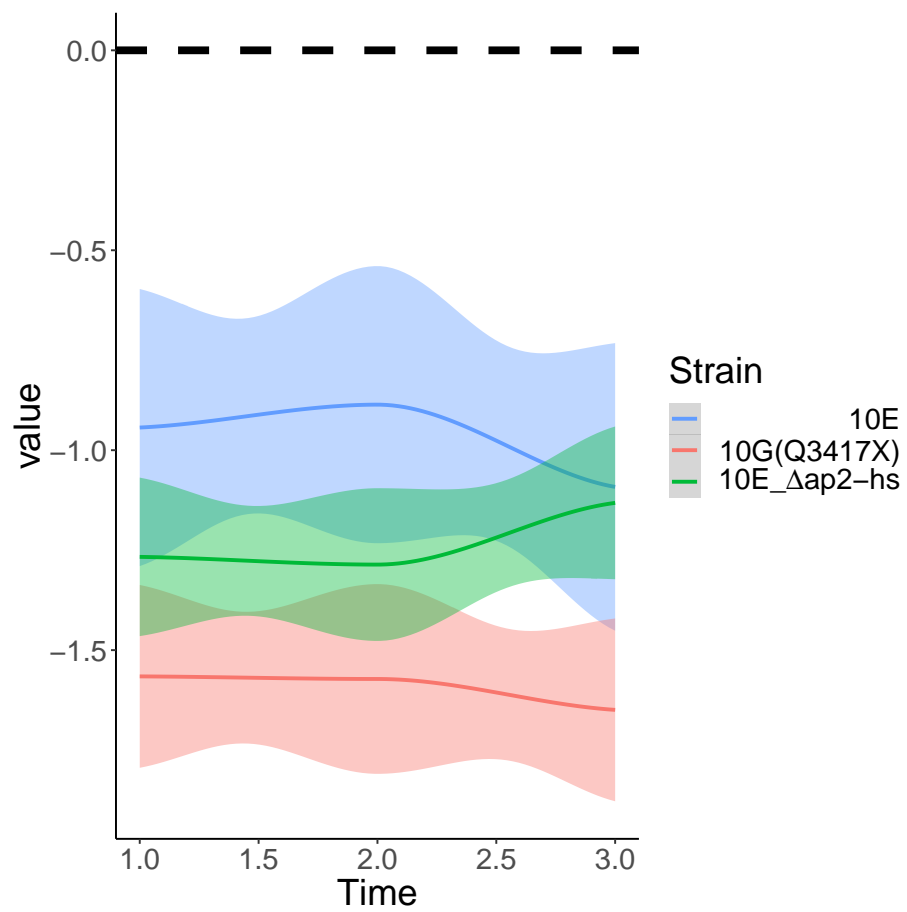
6 Cluster Expression Data

```
## Using Annot as id variables
## Saving 7 x 7 in image
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
## Using Annot as id variables
## Saving 7 x 7 in image
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
## Using Annot as id variables
## Saving 7 x 7 in image
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
## Using Annot as id variables
## Saving 7 x 7 in image
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
## Using Annot as id variables
## Saving 7 x 7 in image
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
## Using Annot as id variables
## Saving 7 x 7 in image
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```
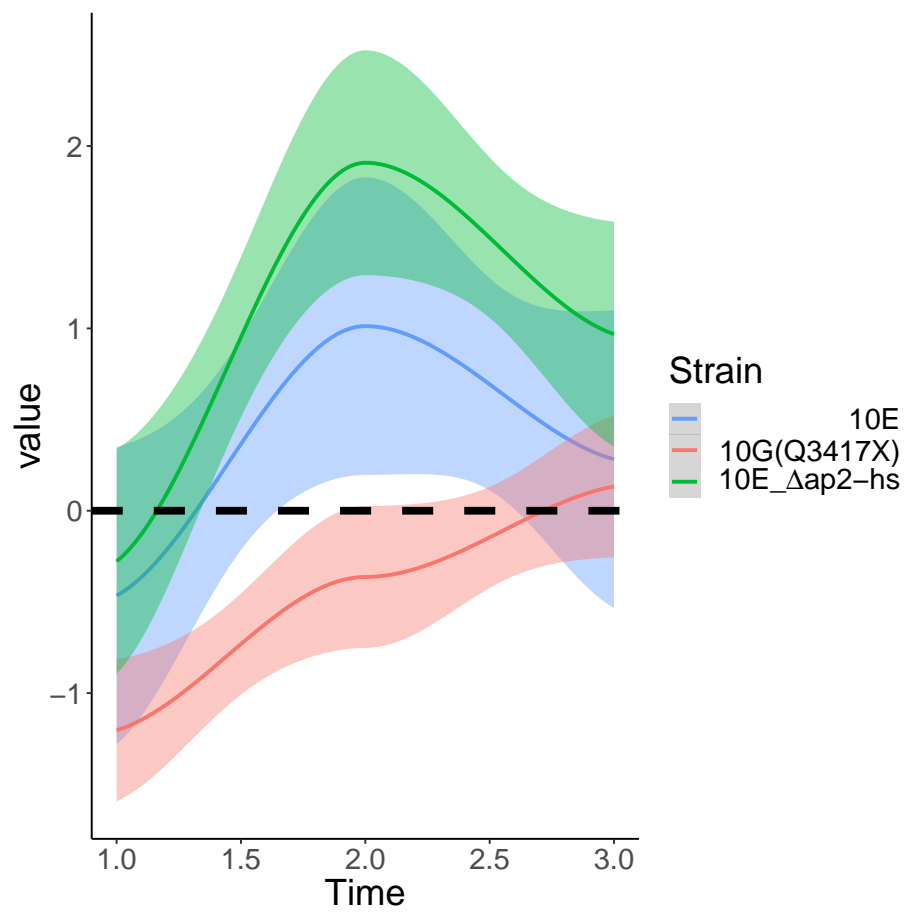
24

7 Functional Enrichment analysis

```
## Loading required package:  AnnotationDbi
## Loading required package:  stats4
## Loading required package:  IRanges
## Loading required package:  S4Vectors
##
## Attaching package:  'S4Vectors'
## The following object is masked from 'package:tidyr':
##
##     expand
## The following objects are masked from 'package:dplyr':
##
##     first, rename
## The following object is masked from 'package:gplots':
##
##     space
## The following object is masked from 'package:base':
##
##     expand.grid
##
## Attaching package:  'IRanges'
## The following objects are masked from 'package:dplyr':
##
##     collapse, desc, slice
##
## Attaching package:  'AnnotationDbi'
## The following object is masked from 'package:dplyr':
##
##     select
## Loading required package:  Category
## Loading required package:  Matrix
##
## Attaching package:  'Matrix'
## The following object is masked from 'package:S4Vectors':
##
##     expand
## The following object is masked from 'package:tidyr':
##
##     expand
## Loading required package:  graph
##
##
## Attaching package:  'GOstats'
```

```
## The following object is masked from 'package:AnnotationDbi':
##
##     makeGOGraph
##
## Loading required package:  XML
##
## Attaching package:  'XML'
## The following object is masked from 'package:graph':
##
##     addNode
##
## Attaching package:  'xtable'
## The following object is masked from 'package:ggdendro':
##
##     label
##
## Attaching package:  'Rgraphviz'
## The following object is masked from 'package:annotate':
##
##     toFile
## The following objects are masked from 'package:IRanges':
##
##     from, to
## The following objects are masked from 'package:S4Vectors':
##
##     from, to
## -- Attaching packages ---------------------------------------------------------
tidyverse 1.2.1 --
## v tibble  2.0.1     v purrr  0.3.0
## v readr   1.3.1     v stringr 1.3.1
## v tibble  2.0.1     v forcats 0.3.0
## -- Conflicts ------------------------------------------------------------------
tidyverse_conflicts() --
## x stringr::boundary()    masks graph::boundary()
## x IRanges::collapse()    masks dplyr::collapse()
## x gridExtra::combine()    masks dplyr::combine(), Biobase::combine(),
BiocGenerics::combine()
## x IRanges::desc()        masks dplyr::desc()
## x Matrix::expand()       masks S4Vectors::expand(), tidyr::expand()
## x dplyr::filter()        masks stats::filter()
## x S4Vectors::first()     masks dplyr::first()
## x dplyr::lag()           masks stats::lag()
## x ggplot2::Position()    masks BiocGenerics::Position(), base::Position()
## x purrr::reduce()        masks IRanges::reduce()
## x S4Vectors::rename()    masks dplyr::rename()
```

```
## x AnnotationDbi::select() masks dplyr::select()
## x IRanges::slice()      masks dplyr::slice()
## x readr::spec()         masks genefilter::spec()
```

f.plasmo.db"
f.plasmo_dbInfo"
f.plasmoENZYME2ORF"
f.plasmoGO2ALLORFS"
f.plasmoORGANISM"
f.plasmoSYMBOL"

value
2.i
OrgDb
AnnotationDbi
MALARIA_DB
Plasmodium falciparum
Malaria
23-Mar-2016
Plasmo DB
ase-28/Pfalciparum3D7/txt
ORF
36329
Gene Ontology
base/archive/latest-lite/
2018-Oct10
2018-Oct11
Entrez Gene
bi.nlm.nih.gov/gene/DATA
KEGG GENOME
enome.jp/pub/kegg/genomes
2011-Mar15

apped=4584)

858)

28

```
## 1 PF3D7_0100100 GO:0009405        IEA        BP
## 2 PF3D7_0100100 GO:0009405        IEA        BP
## 3 PF3D7_0100100 GO:0016337        TAS        BP
## 4 PF3D7_0100100 GO:0020013        TAS        BP
## 5 PF3D7_0100100 GO:0020033        TAS        BP
## 6 PF3D7_0100100 GO:0020035        TAS        BP
##          gene_id       go_id Evidence Ontology
## 1 PF3D7_0100100 GO:0009405        IEA        BP
## 2 PF3D7_0100100 GO:0009405        IEA        BP
## 3 PF3D7_0100100 GO:0016337        TAS        BP
## 4 PF3D7_0100100 GO:0020013        TAS        BP
## 5 PF3D7_0100100 GO:0020033        TAS        BP
## 6 PF3D7_0100100 GO:0020035        TAS        BP
```

Error: '.x' must be a list, not a 'Go3AnnDbBimap' object

```
## Gene to GO CC  test for over-representation
## 95 GO CC ids tested (4 have p < 0.05)
## Selected gene set size: 79
##     Gene universe size: 3540
##     Annotation package: org.Pf.plasmo
##       GOCCID      Pvalue OddsRatio  ExpCount Count Size                    Term
## 1 GO:0020036 0.008831129  2.641707 4.24011299    10  190         Maurer's cleft
## 2 GO:0005637 0.022316384       Inf 0.02231638     1    1 nuclear inner membrane
## 3 GO:0005638 0.022316384       Inf 0.02231638     1    1         lamin filament
## 4 GO:0005652 0.022316384       Inf 0.02231638     1    1         nuclear lamina
## $PF3D7_0209300
## $PF3D7_0209300$`GO:0016114`
## $PF3D7_0209300$`GO:0016114`$GOID
## [1] "GO:0016114"
##
## $PF3D7_0209300$`GO:0016114`$Evidence
## [1] "IEA"
##
## $PF3D7_0209300$`GO:0016114`$Ontology
## [1] "BP"
##
##
## $PF3D7_0209300$`GO:0016114`
## $PF3D7_0209300$`GO:0016114`$GOID
## [1] "GO:0016114"
##
## $PF3D7_0209300$`GO:0016114`$Evidence
## [1] "IEA"
##
## $PF3D7_0209300$`GO:0016114`$Ontology
```

```
## [1] "BP"
##
##
## $PF3D7_0209300$`GO:0016020`
## $PF3D7_0209300$`GO:0016020`$GOID
## [1] "GO:0016020"
##
## $PF3D7_0209300$`GO:0016020`$Evidence
## [1] "IEA"
##
## $PF3D7_0209300$`GO:0016020`$Ontology
## [1] "CC"
##
##
## $PF3D7_0209300$`GO:0020011`
## $PF3D7_0209300$`GO:0020011`$GOID
## [1] "GO:0020011"
##
## $PF3D7_0209300$`GO:0020011`$Evidence
## [1] "IDA"
##
## $PF3D7_0209300$`GO:0020011`$Ontology
## [1] "CC"
##
##
## $PF3D7_0209300$`GO:0008685`
## $PF3D7_0209300$`GO:0008685`$GOID
## [1] "GO:0008685"
##
## $PF3D7_0209300$`GO:0008685`$Evidence
## [1] "IEA"
##
## $PF3D7_0209300$`GO:0008685`$Ontology
## [1] "MF"
```