

Heatschock Arrays

Elisabet Tintó, Lucas Michel Todó

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Contents

1	Imputed FC	2
1.1	10E FC	2
1.2	10G FC	3
1.3	EK0 FC	4
2	Venn Diagrams	5
2.1	Max.FC (any timepoint) > 3 FC	5
2.1.1	Up-regulated	5
2.1.2	Down-regulated	6
2.2	Max.FC T1 > 3 FC	7
2.2.1	Up-regulated	7
2.2.2	Down-regulated	8
2.3	Max.FC T2 > 3 FC	9
2.3.1	Up-regulated	9
2.3.2	Down-Regulated	10
2.4	Max.FC T3 > 3 FC	11
2.4.1	Up-regulated	11
2.4.2	Down-Regulated	12
3	Example Custom Plot	13
4	Heat maps	14
4.1	Top FC separated	14
4.2	Top FC in 10E, across strains, ordered	15
4.3	Top FC in 10E, across strains, clustered	16
4.4	FC >6 in all strains combined, clustered	17
5	Principal Component Analysis	18

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	rifu
-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 Tetex-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	-2.505756	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 transmembr. 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	l-cys peroxiredoxin
-0.7109644	-0.9582562	2.4359055	2.435906	PF3D7_0524200	cvd. Pl. memb. prot. ukwn. func.
-0.6880042	-2.4298111	-0.5552725	-2.429811	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	rifu
-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

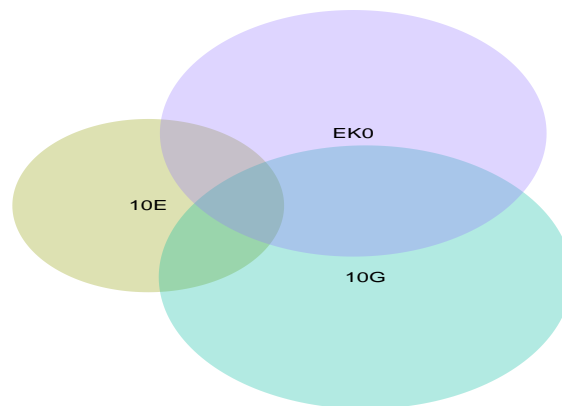
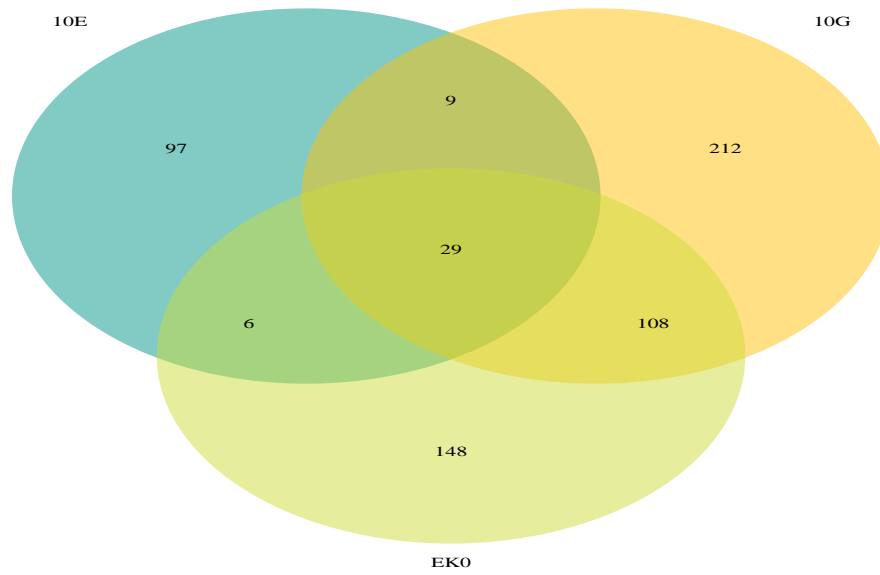
EK0_T1_HS	EK0_T2_HS	EK0_T3_HS	Max_Dif	Gene	Annot
3.8023938	4.8569453	4.692690	4.856945	PF3D7.1201100	RESA-like prot. with PHIST and DnaJ domains
-1.9416306	-4.2440483	-4.782000	-4.782000	PF3D7.0211000	unspecified product
1.9045315	2.5509136	4.638035	4.638035	Pfa.raR-7295	NA
-2.6191721	-4.5922710	-3.797023	-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.
-2.2266092	-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	PF3D7.1327300	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	PF3D7.1000200	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.

2 Venn Diagrams

2.1 Max.FC (any timepoint) > 3 FC

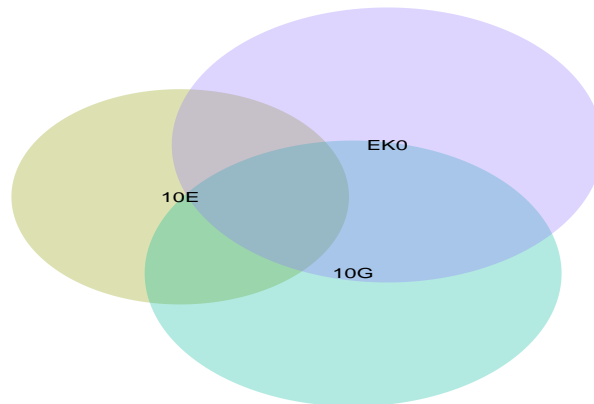
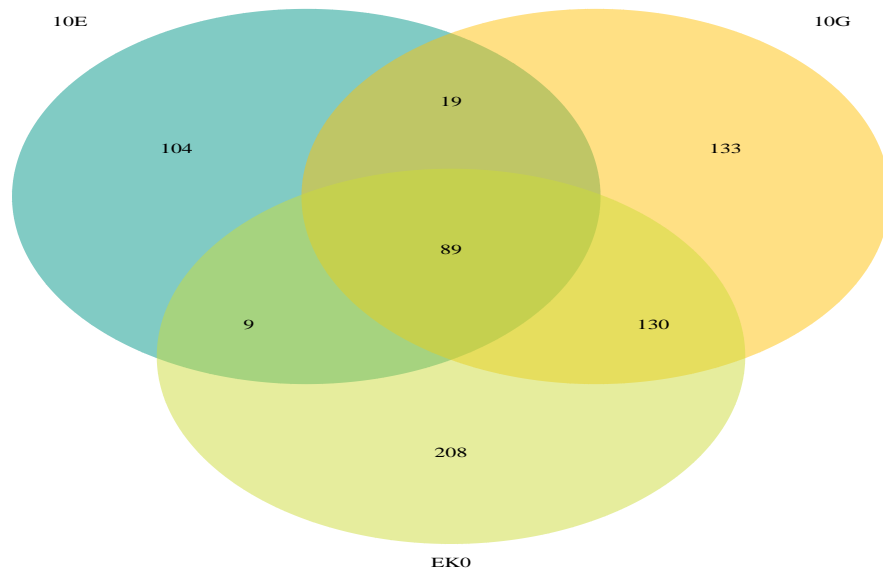
2.1.1 Up-regulated

```
## (polygon[GRID.polygon.1], polygon[GRID.polygon.2], polygon[GRID.polygon.3], polygon[GRID.polygon.4])
```



2.1.2 Down-regulated

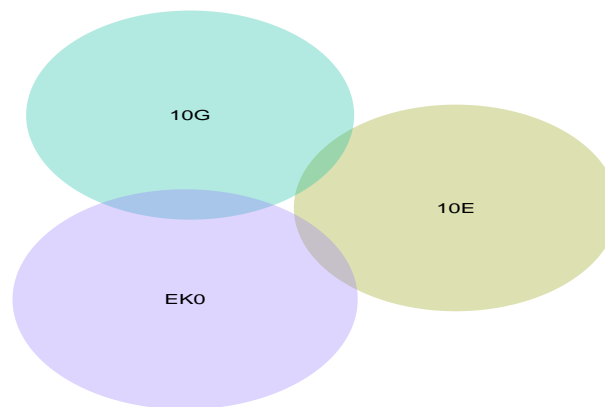
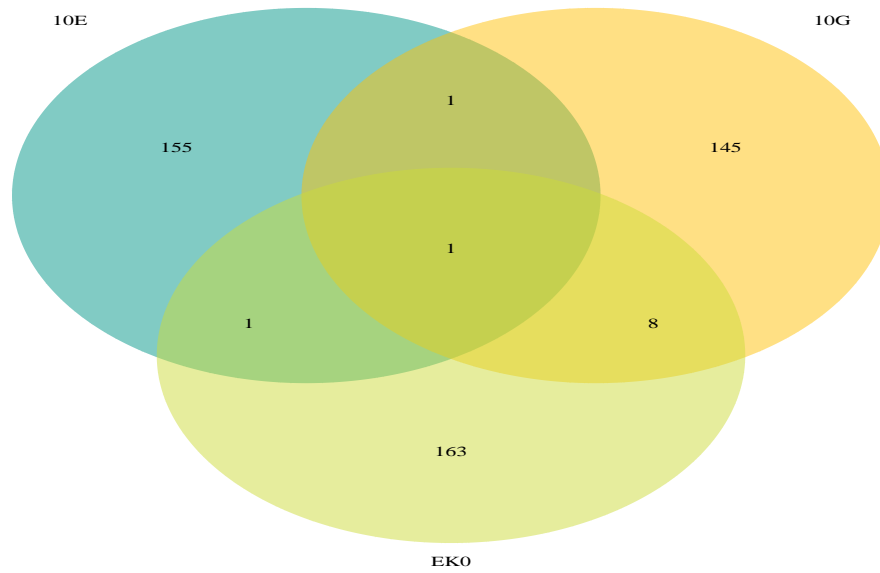
```
## (polygon[GRID.polygon.17], polygon[GRID.polygon.18], polygon[GRID.polygon.19], polygon[GRID.polygon.20])
```



2.2 Max.FC T1 > 3 FC

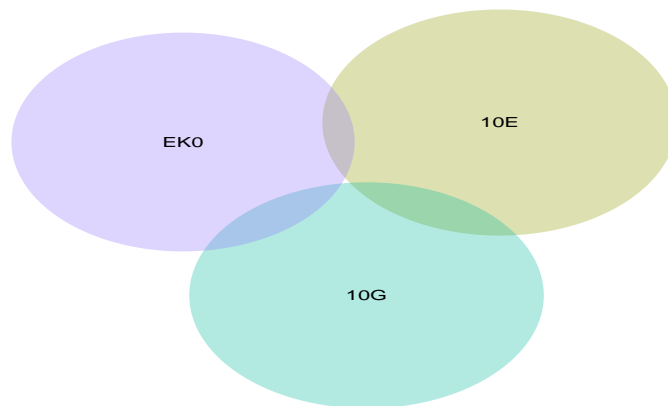
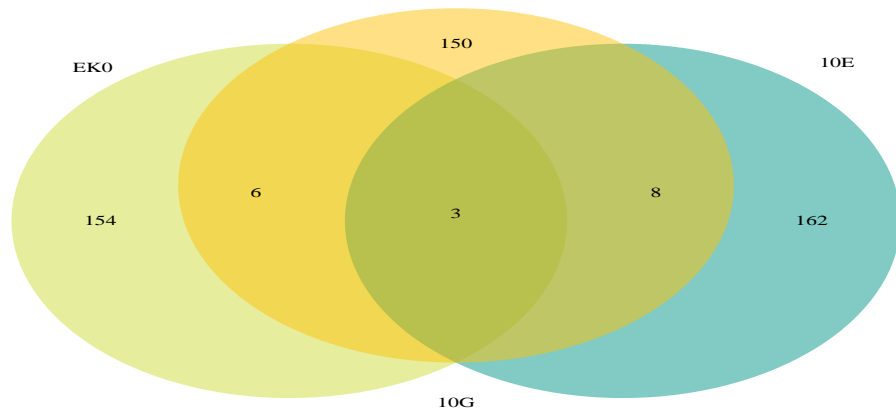
2.2.1 Up-regulated

```
## (polygon[GRID.polygon.33], polygon[GRID.polygon.34], polygon[GRID.polygon.35], polygon[GRID.polygon.36])
```



2.2.2 Down-regulated

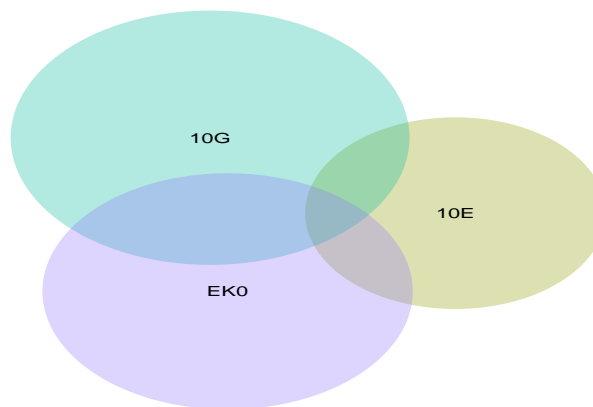
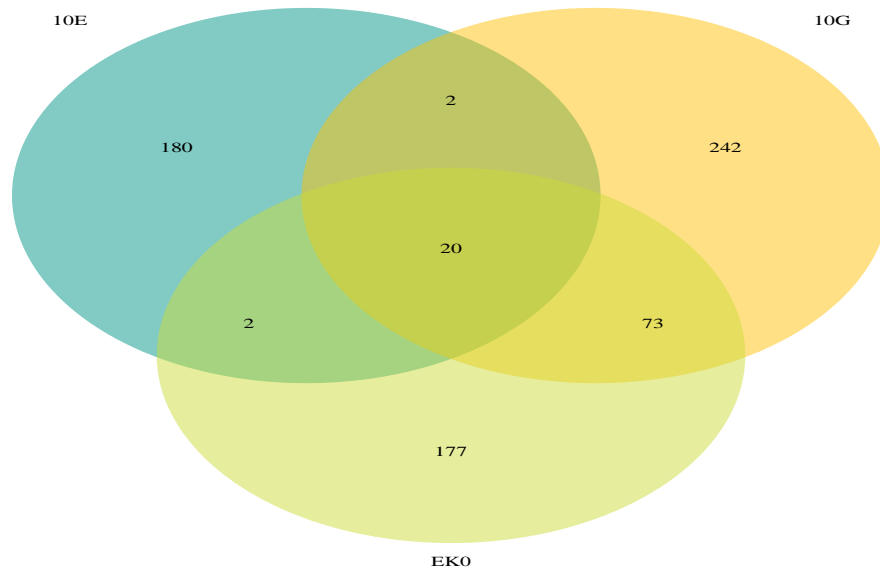
```
## (polygon[GRID.polygon.49], polygon[GRID.polygon.50], polygon[GRID.polygon.51], polygon[GRID.polygon.52])
```



2.3 Max.FC T2 > 3 FC

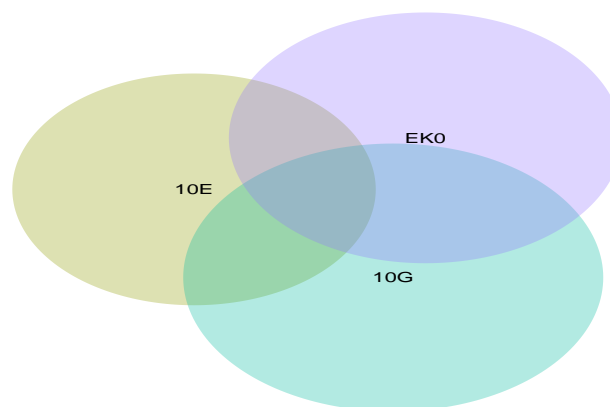
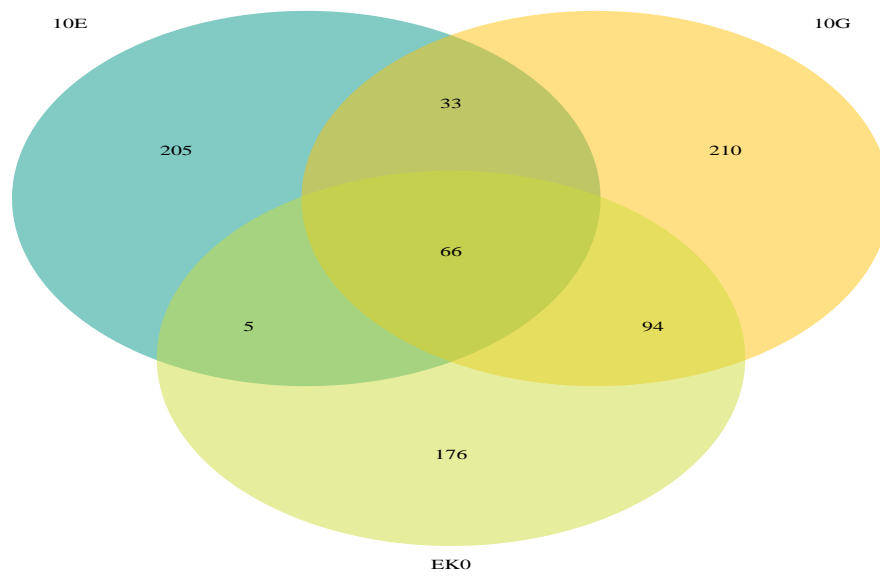
2.3.1 Up-regulated

```
## (polygon[GRID.polygon.64], polygon[GRID.polygon.65], polygon[GRID.polygon.66], polygon[GRID.polygon.67])
```



2.3.2 Down-Regulated

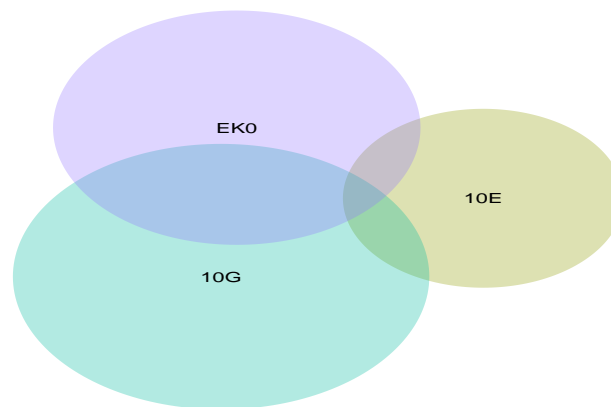
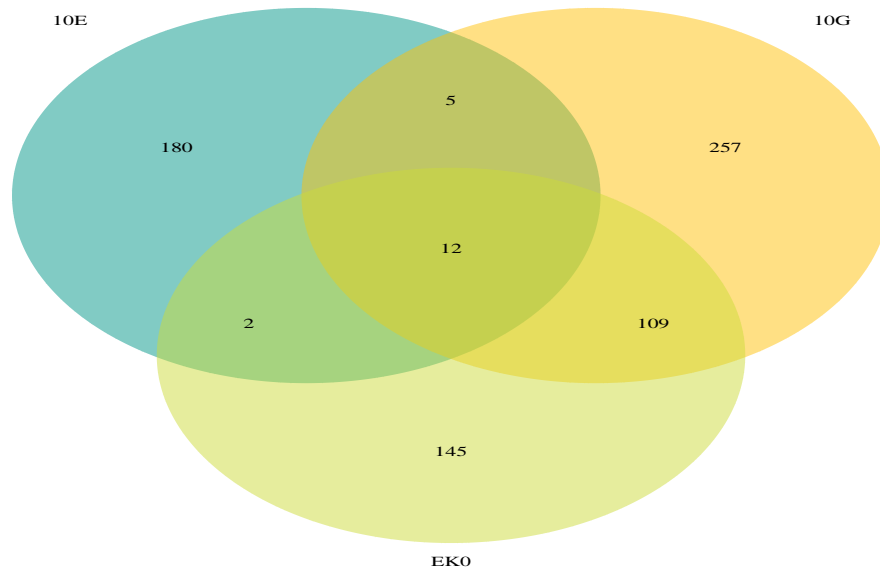
```
## (polygon[GRID.polygon.80], polygon[GRID.polygon.81], polygon[GRID.polygon.82], polygon[GRID.polygon.83])
```



2.4 Max.FC T3 > 3 FC

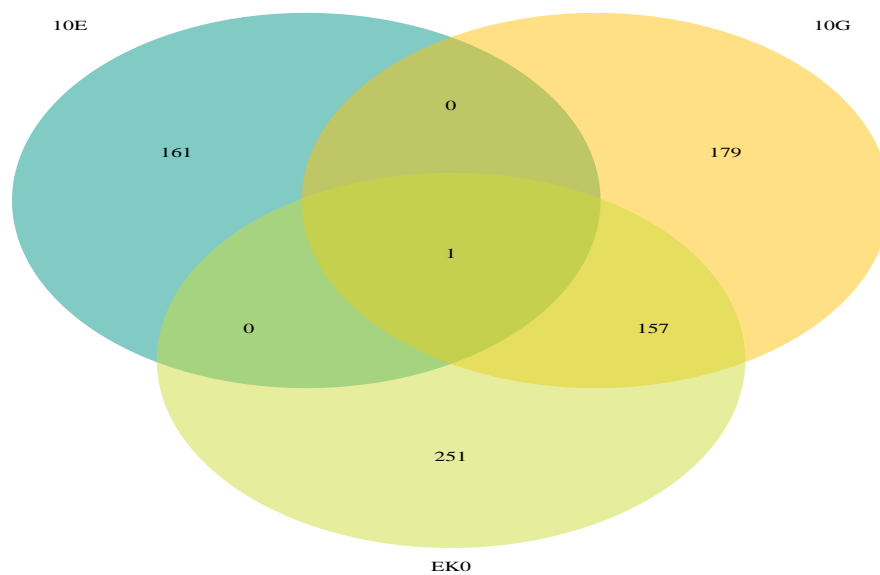
2.4.1 Up-regulated

```
## (polygon[GRID.polygon.96], polygon[GRID.polygon.97], polygon[GRID.polygon.98], polygon[GRID.polygon.99])
```

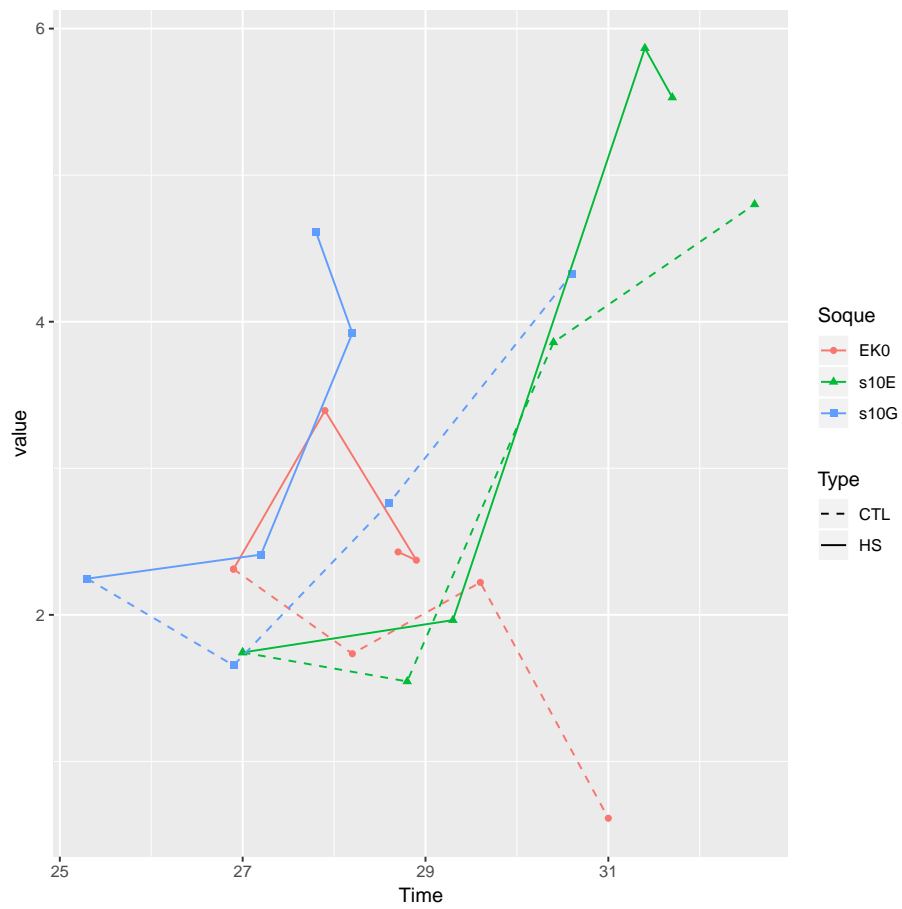


2.4.2 Down-Regulated

```
## (polygon[GRID.polygon.112], polygon[GRID.polygon.113], polygon[GRID.polygon.114], polygon[GRID.polygon.115])
```

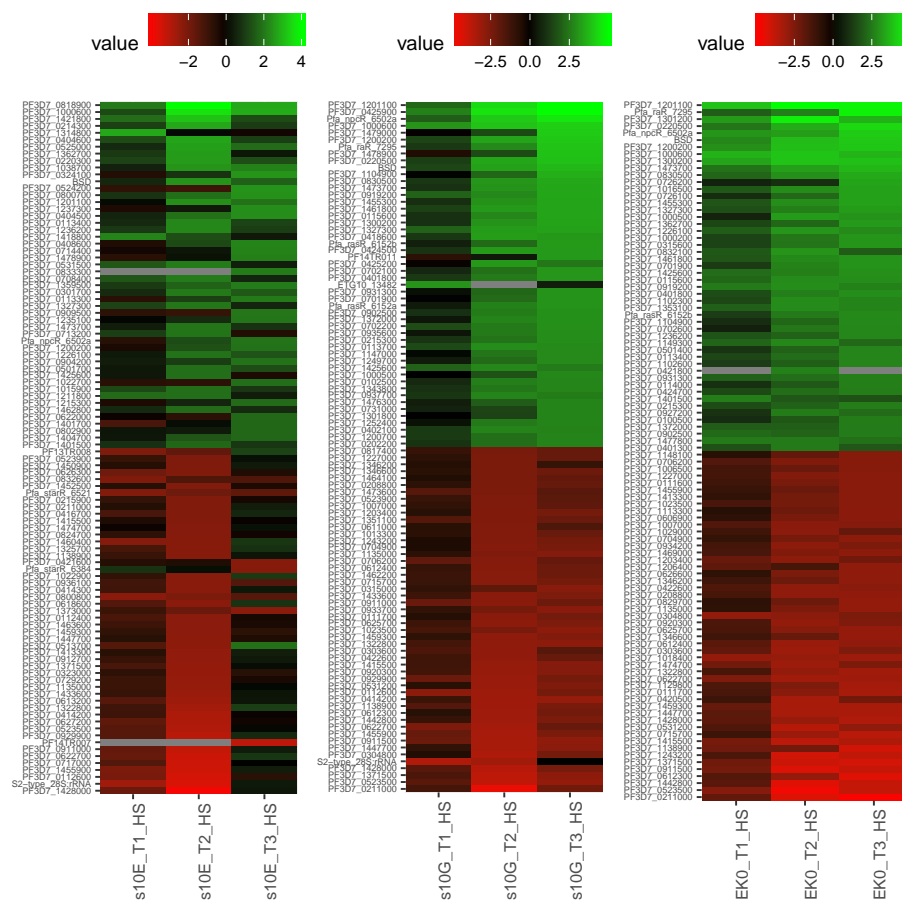


3 Example Custom Plot

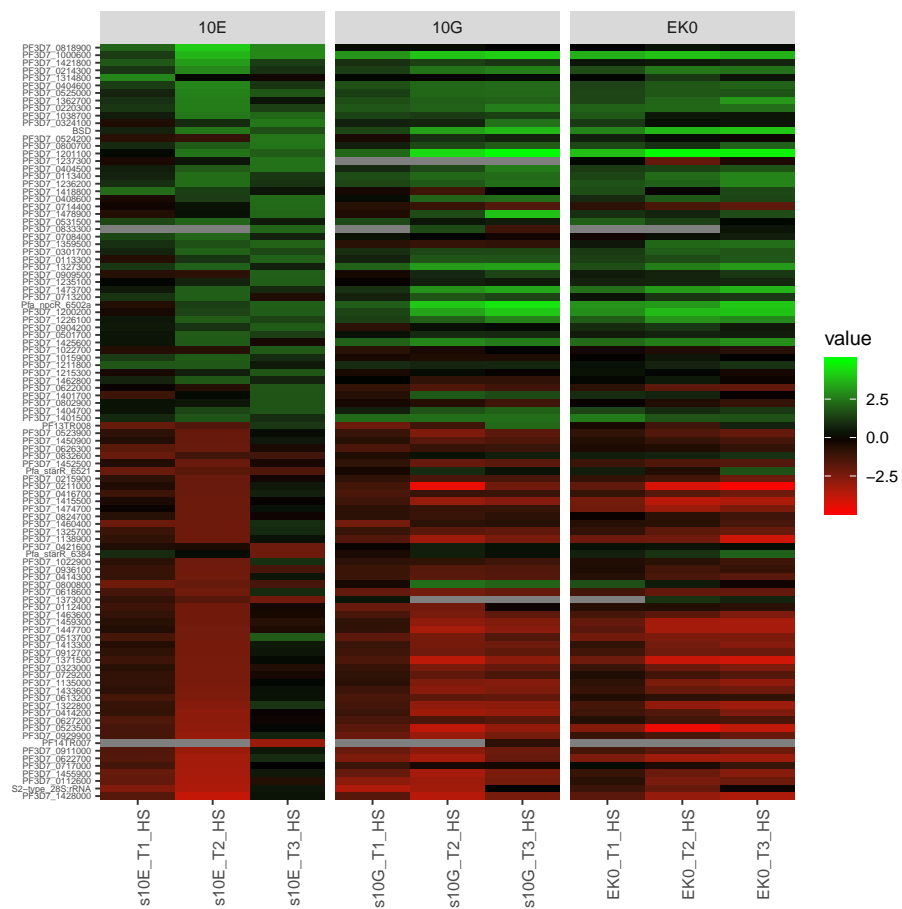


4 Heat maps

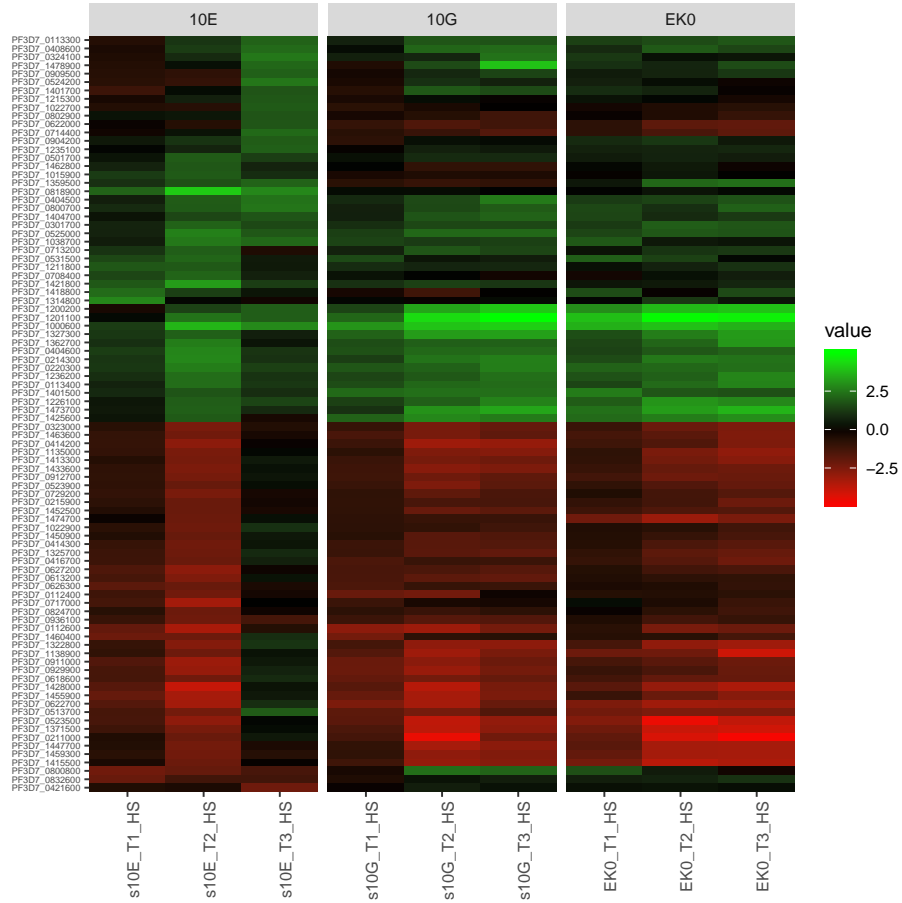
4.1 Top FC separated



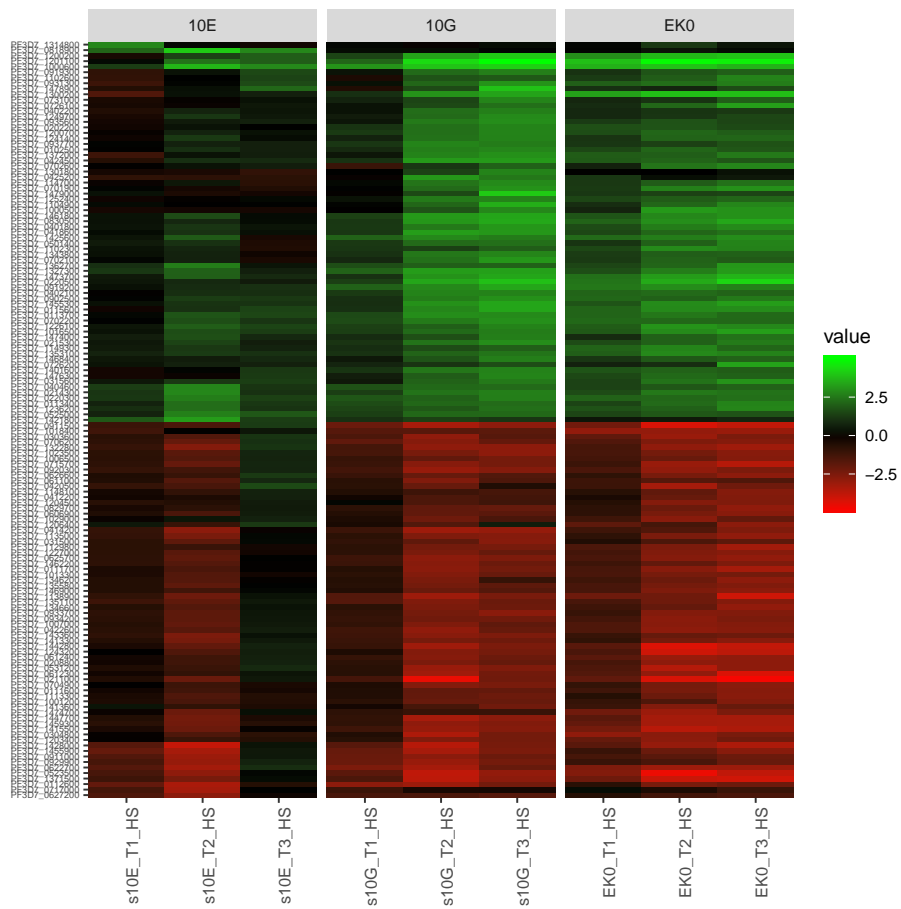
4.2 Top FC in 10E, across strains, ordered



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
```