

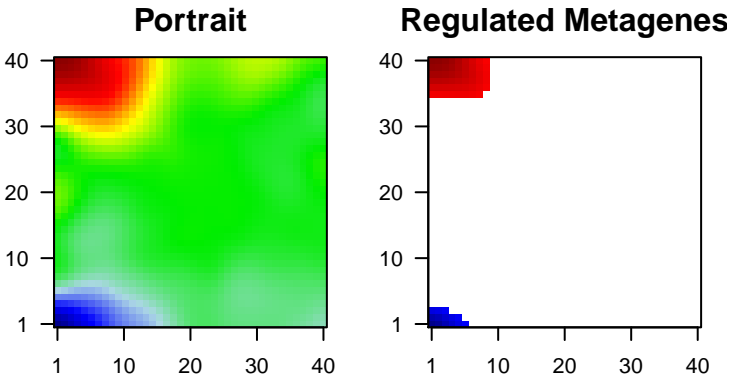
72hpf_neg_tbx5

Global Summary

%DE = 0.17
genes with $\text{fdr} < 0.2$ = 4153 (2478 + / 1675 -)
genes with $\text{fdr} < 0.1$ = 3491 (2139 + / 1352 -)
genes with $\text{fdr} < 0.05$ = 3117 (1939 + / 1178 -)
genes with $\text{fdr} < 0.01$ = 2237 (1468 + / 769 -)

genes in genesets = 21072

<FC> = 0
<t-score> = -0.01
<p-value> = 0.06
<fdr> = 0.83



Global Genelist

Rank	ID	log(FC)	p-value	fdr	Description	
					Metagene	
1	ENSDARG000	3.9	2e-16	3e-14	1 x 40	syntaxin 1B [Source:ZFIN;Acc:ZDB-GENE-000330-4]
2	ENSDARG000	3.13	2e-16	3e-14	6 x 37	CUB and Sushi multiple domains 2 [Source:ZFIN;Acc:ZDB-GENE-000330-4]
3	ENSDARG000	3.41	2e-16	3e-14	1 x 36	myosin, heavy chain b [Source:ZFIN;Acc:ZDB-GENE-08112-2]
4	ENSDARG000	2.92	2e-16	3e-14	4 x 40	syntaxin binding protein 1a [Source:ZFIN;Acc:ZDB-GENE-000330-4]
5	ENSDARG000	3.76	2e-16	3e-14	1 x 37	rhodopsin [Source:ZFIN;Acc:ZDB-GENE-990415-271]
6	ENSDARG000	3.48	2e-16	3e-14	1 x 36	guanine nucleotide binding protein (G protein), beta polypeptide [Source:ZFIN;Acc:ZDB-GENE-000330-4]
7	ENSDARG000	-3.98	2e-16	3e-14	6 x 1	ryanodine receptor 2b (cardiac) [Source:ZFIN;Acc:ZDB-GENE-000330-4]
8	ENSDARG000	-4.04	2e-16	3e-14	3 x 1	microphthalmia-associated transcription factor a [Source:ZFIN;Acc:ZDB-GENE-000330-4]
9	ENSDARG000	-3.84	2e-16	3e-14	2 x 1	phosphoribosylformylglycinamide synthase [Source:ZFIN;Acc:ZDB-GENE-000330-4]
10	ENSDARG000	-2.9	2e-16	3e-14	4 x 1	phosphoribosyl pyrophosphate amidotransferase [Source:ZFIN;Acc:ZDB-GENE-000330-4]
11	ENSDARG000	3.16	2e-16	3e-14	2 x 40	sodium channel, voltage gated, type VIII, alpha subunit a [Source:ZFIN;Acc:ZDB-GENE-000330-4]
12	ENSDARG000	-3.89	2e-16	3e-14	1 x 1	aldo-keto reductase family 1, member B1 (aldose reductase) [Source:ZFIN;Acc:ZDB-GENE-000330-4]
13	ENSDARG000	3.42	2e-16	3e-14	3 x 40	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit [Source:ZFIN;Acc:ZDB-GENE-000330-4]
14	ENSDARG000	2.81	2e-16	3e-14	4 x 40	neural adhesion molecule L1.2 [Source:ZFIN;Acc:ZDB-GENE-000330-4]
15	ENSDARG000	3.13	2e-16	3e-14	1 x 40	N-ethylmaleimide-sensitive factor a [Source:ZFIN;Acc:ZDB-GENE-000330-4]
16	ENSDARG000	-2.89	2e-16	3e-14	3 x 1	RAB3A interacting protein (rab3)-like 1 [Source:ZFIN;Acc:ZDB-GENE-000330-4]
17	ENSDARG000	2.92	2e-16	3e-14	1 x 40	calmodulin binding transcription activator 1b [Source:ZFIN;Acc:ZDB-GENE-000330-4]
18	ENSDARG000	2.8	2e-16	3e-14	4 x 38	dynamin 1a [Source:ZFIN;Acc:ZDB-GENE-081104-27]
19	ENSDARG000	-4.03	2e-16	3e-14	1 x 1	RAB34, member RAS oncogene family b [Source:ZFIN;Acc:ZDB-GENE-000330-4]
20	ENSDARG000	-4.7	2e-16	3e-14	4 x 1	troponin C type 1a (slow) [Source:ZFIN;Acc:ZDB-GENE-000330-4]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	17.56	NULL	172	BP homophilic cell adhesion via plasma membrane adhesion molecules
2	17.27	NULL	155	CC synapse
3	16.59	NULL	1162	CC plasma membrane
4	15.72	NULL	333	BP cell adhesion
5	15.55	NULL	175	BP nervous system development
6	15.36	NULL	270	MF ion channel activity
7	15.24	NULL	499	BP ion transport
8	13.13	NULL	32	MF extracellular-glutamate-gated ion channel activity
9	13.13	NULL	32	MF ionotropic glutamate receptor activity
10	13.13	NULL	32	BP ionotropic glutamate receptor signaling pathway
11	12.47	NULL	717	MF calcium ion binding
12	12.42	NULL	1239	BP regulation of transcription, DNA-templated
13	12.08	NULL	537	MF sequence-specific DNA binding
14	11.61	NULL	49	MF extracellular matrix structural constituent
15	11.27	NULL	79	BP excitatory postsynaptic potential
16	11.18	NULL	130	BP regulation of ion transmembrane transport
17	11.18	NULL	130	MF voltage-gated ion channel activity
18	11.02	NULL	80	CC postsynaptic membrane
19	11	NULL	1484	MF DNA binding
20	10.6	NULL	78	BP axon guidance
<i>Underexpressed</i>				
1	-15.74	NULL	712	BP oxidation-reduction process
2	-14.95	NULL	522	MF oxidoreductase activity
3	-9.92	NULL	410	CC mitochondrion
4	-9.31	NULL	214	BP translation
5	-9.29	NULL	414	BP metabolic process
6	-8.81	NULL	147	CC ribosome
7	-8.71	NULL	144	MF structural constituent of ribosome
8	-8.13	NULL	480	MF catalytic activity
9	-7.85	NULL	96	CC lysosome
10	-7.74	NULL	43	MF iron-sulfur cluster binding
11	-7.63	NULL	33	MF endopeptidase inhibitor activity
12	-7.21	NULL	30	BP pigmentation
13	-6.82	NULL	1580	CC cellular_component
14	-6.57	NULL	34	MF electron carrier activity
15	-6.55	NULL	164	BP carbohydrate metabolic process
16	-6.54	NULL	23	BP lipoprotein metabolic process
17	-6.5	NULL	57	MF flavin adenine dinucleotide binding
18	-6.43	NULL	62	BP proteolysis involved in cellular protein catabolic process
19	-6.34	NULL	11	BP purine nucleotide biosynthetic process
20	-6.13	NULL	47	CC cytosolic large ribosomal subunit

