

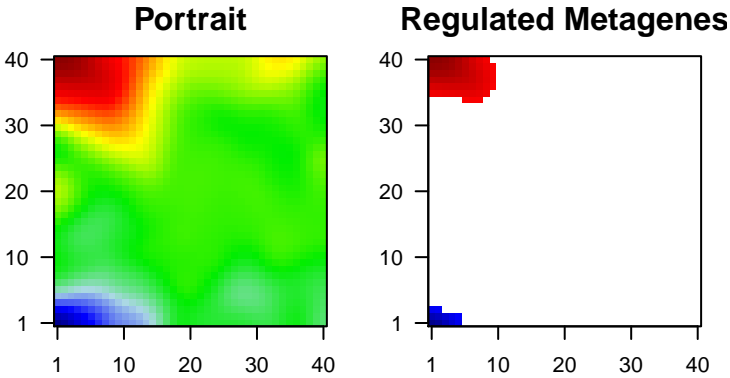
72hpf_neg_hand2

Global Summary

%DE = 0.16
genes with $\text{fdr} < 0.2$ = 3594 (2026 + / 1568 -)
genes with $\text{fdr} < 0.1$ = 3032 (1727 + / 1305 -)
genes with $\text{fdr} < 0.05$ = 2428 (1399 + / 1029 -)
genes with $\text{fdr} < 0.01$ = 1763 (1012 + / 751 -)

genes in genesets = 21072

<FC> = 0
<t-score> = -0.01
<p-value> = 0.09
<fdr> = 0.84



Global Genelist

Rank	ID	log(FC)	p-value	fdr	Description	
					Metagene	
1	ENSDARG0000000001	3.15	2e-16	5e-14	1 x 40	syntaxin 1B [Source:ZFIN;Acc:ZDB-GENE-000330-4]
2	ENSDARG0000000002	-3.27	2e-16	5e-14	3 x 1	microphthalmia-associated transcription factor a [Source:ZFIN;Acc:ZDB-GENE-000330-4]
3	ENSDARG0000000003	-4.51	2e-16	5e-14	2 x 1	phosphoribosylformylglycinamide synthase [Source:ZFIN;Acc:ZDB-GENE-000330-4]
4	ENSDARG0000000004	-3.27	2e-16	5e-14	4 x 1	phosphoribosyl pyrophosphate amidotransferase [Source:ZFIN;Acc:ZDB-GENE-000330-4]
5	ENSDARG0000000005	-2.97	2e-16	5e-14	1 x 1	aldo-keto reductase family 1, member B1 (aldose reductase) [Source:ZFIN;Acc:ZDB-GENE-000330-4]
6	ENSDARG0000000006	-2.9	2e-16	5e-14	3 x 1	RAB3A interacting protein (rabin3)-like 1 [Source:ZFIN;Acc:ZDB-GENE-000330-4]
7	ENSDARG0000000007	-5.05	2e-16	5e-14	29 x 7	heart and neural crest derivatives expressed 2 [Source:ZFIN;Acc:ZDB-GENE-000330-4]
8	ENSDARG0000000008	-3.87	2e-16	5e-14	6 x 1	zgc:63831 [Source:ZFIN;Acc:ZDB-GENE-030131-8690]
9	ENSDARG0000000009	-2.83	2e-16	5e-14	1 x 1	RAB34, member RAS oncogene family b [Source:ZFIN;Acc:ZDB-GENE-000330-4]
10	ENSDARG0000000010	-4.17	2e-16	5e-14	4 x 1	troponin C type 1a (slow) [Source:ZFIN;Acc:ZDB-GENE-030131-7741]
11	ENSDARG0000000011	-3.37	2e-16	5e-14	7 x 1	myosin binding protein C, cardiac [Source:ZFIN;Acc:ZDB-GENE-030131-7741]
12	ENSDARG0000000012	-3.71	2e-16	5e-14	2 x 1	phosphoribosyl transferase domain containing 1 [Source:ZFIN;Acc:ZDB-GENE-030131-7741]
13	ENSDARG0000000013	-4.98	2e-16	5e-14	6 x 1	solute carrier family 8 (sodium/calcium exchanger), member 1 [Source:ZFIN;Acc:ZDB-GENE-030131-7741]
14	ENSDARG0000000014	3.22	2e-16	5e-14	1 x 40	zgc:65894 [Source:ZFIN;Acc:ZDB-GENE-030131-7741]
15	ENSDARG0000000015	-3.91	2e-16	5e-14	3 x 1	solute carrier organic anion transporter family, member 1C1 [Source:ZFIN;Acc:ZDB-GENE-030131-7741]
16	ENSDARG0000000016	-2.97	2e-16	5e-14	12 x 1	GATA binding protein 5 [Source:ZFIN;Acc:ZDB-GENE-030131-7741]
17	ENSDARG0000000017	-3.27	2e-16	5e-14	6 x 1	myosin, light chain 7, regulatory [Source:ZFIN;Acc:ZDB-GENE-030131-7741]
18	ENSDARG0000000018	3.22	2e-16	5e-14	1 x 40	synaptosomal-associated protein, 25a [Source:ZFIN;Acc:ZDB-GENE-030131-7741]
19	ENSDARG0000000019	-3.71	2e-16	5e-14	4 x 1	troponin T type 2a (cardiac) [Source:ZFIN;Acc:ZDB-GENE-030131-7741]
20	ENSDARG0000000020	-3.34	2e-16	5e-14	1 x 1	formin 2a [Source:ZFIN;Acc:ZDB-GENE-101107-1]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	17.07	NULL	168	CC nucleosome
2	14.76	NULL	1484	MF DNA binding
3	14.64	NULL	229	CC chromosome
4	14.63	NULL	333	BP cell adhesion
5	13.83	NULL	172	BP homophilic cell adhesion via plasma membrane adhesion molecule
6	13.29	NULL	117	BP nucleosome assembly
7	13.17	NULL	155	CC synapse
8	12.8	NULL	175	BP nervous system development
9	12.56	NULL	2716	CC nucleus
10	12.48	NULL	270	MF ion channel activity
11	11.96	NULL	1162	CC plasma membrane
12	11.59	NULL	232	MF protein heterodimerization activity
13	11.47	NULL	49	MF extracellular matrix structural constituent
14	11.35	NULL	717	MF calcium ion binding
15	11.21	NULL	153	CC proteinaceous extracellular matrix
16	11.17	NULL	537	MF sequence-specific DNA binding
17	10.83	NULL	1239	BP regulation of transcription, DNA-templated
18	10.82	NULL	32	MF extracellular-glutamate-gated ion channel activity
19	10.82	NULL	32	MF ionotropic glutamate receptor activity
20	10.82	NULL	32	BP ionotropic glutamate receptor signaling pathway
<i>Underexpressed</i>				
1	-14.07	NULL	712	BP oxidation-reduction process
2	-13.43	NULL	522	MF oxidoreductase activity
3	-10.96	NULL	414	BP metabolic process
4	-9.89	NULL	96	CC lysosome
5	-7.89	NULL	43	MF iron-sulfur cluster binding
6	-7.45	NULL	480	MF catalytic activity
7	-7.43	NULL	30	BP pigmentation
8	-7.17	NULL	24	BP nucleoside metabolic process
9	-7.11	NULL	11	BP purine nucleotide biosynthetic process
10	-7.06	NULL	410	CC mitochondrion
11	-6.97	NULL	57	MF flavin adenine dinucleotide binding
12	-6.51	NULL	969	MF hydrolase activity
13	-6.49	NULL	67	BP lipid transport
14	-6.19	NULL	164	BP carbohydrate metabolic process
15	-6.18	NULL	1580	CC cellular_component
16	-6.05	NULL	25	MF glutathione transferase activity
17	-5.97	NULL	28	MF 2 iron, 2 sulfur cluster binding
18	-5.9	NULL	35	BP sarcomere organization
19	-5.76	NULL	23	BP lipoprotein metabolic process
20	-5.7	NULL	12	BP cardiac muscle tissue development

