

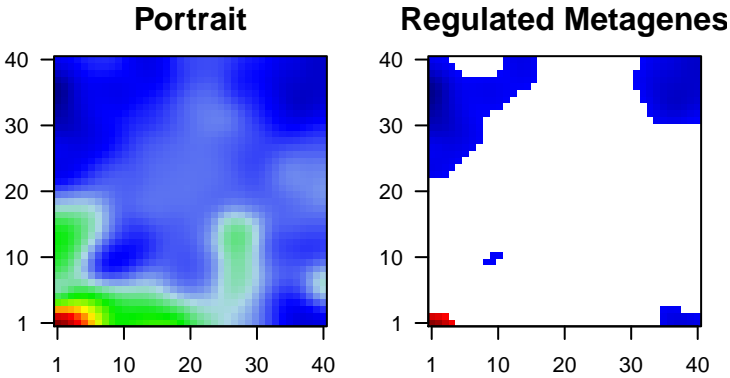
48hpf_pos

Global Summary

%DE = 0.13
genes with $\text{fdr} < 0.2$ = 2805 (1471 + / 1334 -)
genes with $\text{fdr} < 0.1$ = 2023 (1110 + / 913 -)
genes with $\text{fdr} < 0.05$ = 1743 (984 + / 759 -)
genes with $\text{fdr} < 0.01$ = 1199 (718 + / 481 -)

genes in genesets = 21072

<FC> = 0
<t-score> = 0.02
<p-value> = 0.12
<fdr> = 0.87



Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description	
					Metagene	
1	ENSDARG0001	-4.31	2e-16	4e-14	1 x 37	rhodopsin [Source:ZFIN;Acc:ZDB-GENE-990415-271]
2	ENSDARG0001	2.75	2e-16	4e-14	1 x 3	synaptogyrin 1a [Source:ZFIN;Acc:ZDB-GENE-041010-169]
3	ENSDARG0001	-3.67	2e-16	4e-14	1 x 36	guanine nucleotide binding protein (G protein), beta polypeptide 1 [Source:ZFIN;Acc:ZDB-GENE-041010-169]
4	ENSDARG0001	2.82	2e-16	4e-14	6 x 1	ryanodine receptor 2b (cardiac) [Source:ZFIN;Acc:ZDB-GENE-041010-169]
5	ENSDARG0001	2.79	2e-16	4e-14	3 x 1	microphthalmia-associated transcription factor a [Source:ZFIN;Acc:ZDB-GENE-041010-169]
6	ENSDARG0001	2.6	2e-16	4e-14	2 x 1	phosphoribosylformylglycinamide synthase [Source:ZFIN;Acc:ZDB-GENE-041010-169]
7	ENSDARG0001	2.39	2e-16	4e-14	4 x 1	phosphoribosyl pyrophosphate amidotransferase [Source:ZFIN;Acc:ZDB-GENE-041010-169]
8	ENSDARG0001	-2.79	2e-16	4e-14	1 x 35	upper zone of growth plate and cartilage matrix associated bone morphogenesis [Source:ZFIN;Acc:ZDB-GENE-041010-169]
9	ENSDARG0001	2.8	2e-16	4e-14	1 x 1	cyclin-dependent kinase 15 [Source:ZFIN;Acc:ZDB-GENE-041010-169]
10	ENSDARG0001	3.81	2e-16	4e-14	1 x 1	aldo-keto reductase family 1, member B1 (aldose reductase) [Source:ZFIN;Acc:ZDB-GENE-041010-169]
11	ENSDARG0001	-2.93	2e-16	4e-14	1 x 40	ATPase, Na+/K+ transporting, alpha 1a polypeptide, tandem c [Source:ZFIN;Acc:ZDB-GENE-041010-169]
12	ENSDARG0001	-3.34	2e-16	4e-14	5 x 29	protocadherin-related 15b [Source:ZFIN;Acc:ZDB-GENE-041010-169]
13	ENSDARG0001	3.2	2e-16	4e-14	1 x 1	RAB34, member RAS oncogene family b [Source:ZFIN;Acc:ZDB-GENE-041010-169]
14	ENSDARG0001	4.1	2e-16	4e-14	4 x 1	troponin C type 1a (slow) [Source:ZFIN;Acc:ZDB-GENE-041010-169]
15	ENSDARG0001	2.78	2e-16	4e-14	7 x 1	myosin binding protein C, cardiac [Source:ZFIN;Acc:ZDB-GENE-041010-169]
16	ENSDARG0001	2.38	2e-16	4e-14	2 x 1	phosphoribosyl transferase domain containing 1 [Source:ZFIN;Acc:ZDB-GENE-041010-169]
17	ENSDARG0001	2.66	2e-16	4e-14	6 x 1	solute carrier family 8 (sodium/calcium exchanger), member 1 [Source:ZFIN;Acc:ZDB-GENE-041010-169]
18	ENSDARG0001	3.06	2e-16	4e-14	2 x 1	cytochrome P450, family 2, subfamily AE, polypeptide 1 [Source:ZFIN;Acc:ZDB-GENE-041010-169]
19	ENSDARG0001	2.79	2e-16	4e-14	1 x 2	solute carrier family 24 (sodium/potassium/calcium exchanger) [Source:ZFIN;Acc:ZDB-GENE-041010-169]
20	ENSDARG0001	2.82	2e-16	4e-14	1 x 4	si:ch211-195b13.1 [Source:ZFIN;Acc:ZDB-GENE-030131-1]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	9.74	NULL	35	BP sarcomere organization
2	9.58	NULL	30	BP pigmentation
3	8.91	NULL	54	BP heart contraction
4	8.34	NULL	11	BP purine nucleotide biosynthetic process
5	8.03	NULL	712	BP oxidation-reduction process
6	7.3	NULL	522	MF oxidoreductase activity
7	7.17	NULL	12	BP cardiac muscle tissue development
8	7.17	NULL	10	CC melanosome
9	6.76	NULL	11	BP melanosome organization
10	6.68	NULL	24	BP nucleoside metabolic process
11	6.42	NULL	39	CC Z disc
12	6.38	NULL	11	BP striated muscle contraction
13	6.31	NULL	34	MF electron carrier activity
14	6.02	NULL	23	CC troponin complex
15	5.85	NULL	37	BP myofibril assembly
16	5.79	NULL	25	MF glutathione transferase activity
17	5.71	NULL	13	BP cardiac muscle cell proliferation
18	5.59	NULL	561	MF GTP binding
19	5.56	NULL	28	MF 2 iron, 2 sulfur cluster binding
20	5.45	NULL	43	MF iron-sulfur cluster binding
<i>Underexpressed</i>				
1	-8.04	NULL	49	MF extracellular matrix structural constituent
2	-7.66	NULL	117	BP nucleosome assembly
3	-7.54	NULL	2716	CC nucleus
4	-7.48	NULL	1484	MF DNA binding
5	-7.27	NULL	229	CC chromosome
6	-6.75	NULL	168	CC nucleosome
7	-6.18	NULL	83	BP visual perception
8	-5.6	NULL	28	BP phototransduction
9	-5.6	NULL	1787	MF ATP binding
10	-5.43	NULL	78	BP DNA replication
11	-5.19	NULL	42	MF histone binding
12	-5.13	NULL	153	CC proteinaceous extracellular matrix
13	-4.93	NULL	59	CC intracellular membrane-bounded organelle
14	-4.59	NULL	65	BP sodium ion transport
15	-4.58	NULL	32	BP DNA duplex unwinding
16	-4.5	NULL	500	CC extracellular space
17	-4.44	NULL	23	MF hyaluronic acid binding
18	-4.36	NULL	153	MF ATPase activity
19	-4.3	NULL	109	BP negative regulation of endopeptidase activity
20	-4.19	NULL	362	BP regulation of transcription from RNA polymerase II promoter

