

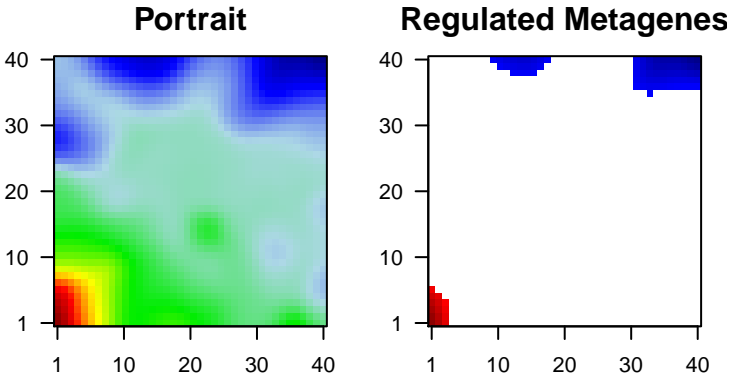
72hpf_pos_tbx5.1

Global Summary

%DE = 0.13
genes with $\text{fdr} < 0.2$ = 2651 (1338 + / 1313 -)
genes with $\text{fdr} < 0.1$ = 2072 (1047 + / 1025 -)
genes with $\text{fdr} < 0.05$ = 1678 (864 + / 814 -)
genes with $\text{fdr} < 0.01$ = 1137 (615 + / 522 -)

genes in genesets = 21072

<FC> = 0
<t-score> = 0.01
<p-value> = 0.13
<fdr> = 0.87



Global Genelist

Rank	ID	log(FC)	p-value	fdr	Description	
					Metagene	
1	ENSDARG000	3.1	2e-16	5e-14	1 x 1	aldo-keto reductase family 1, member B1 (aldose reductase)
2	ENSDARG000	3.8	2e-16	5e-14	1 x 5	fibrinogen beta chain [Source:ZFIN;Acc:ZDB-GENE-030131
3	ENSDARG000	-4.02	2e-16	5e-14	34 x 40	calpain 12 [Source:ZFIN;Acc:ZDB-GENE-050419-245]
4	ENSDARG000	2.8	2e-16	5e-14	1 x 1	RAB34, member RAS oncogene family b [Source:ZFIN;Acc:Z
5	ENSDARG000	3.04	2e-16	5e-14	1 x 3	apolipoprotein A-la [Source:ZFIN;Acc:ZDB-GENE-990415-
6	ENSDARG000	-4.79	2e-16	5e-14	40 x 40	solute carrier family 4 (anion exchanger), member 1a (Diego I
7	ENSDARG000	3.69	2e-16	5e-14	1 x 3	tumor necrosis factor b (TNF superfamily, member 2) [Source
8	ENSDARG000	5.99	2e-16	5e-14	3 x 8	si:ch211-220f21.2 [Source:ZFIN;Acc:ZDB-GENE-160113-1
9	ENSDARG000	-3.16	2e-16	5e-14	9 x 40	cAMP responsive element binding protein 3-like 1 [Source:ZF
10	ENSDARG000	3.71	2e-16	5e-14	1 x 4	apolipoprotein A-II [Source:ZFIN;Acc:ZDB-GENE-030131-1
11	ENSDARG000	2.95	2e-16	5e-14	1 x 4	transferrin-a [Source:ZFIN;Acc:ZDB-GENE-980526-35]
12	ENSDARG000	-3.49	2e-16	5e-14	40 x 40	Kruppel-like factor 1 (erythroid) [Source:ZFIN;Acc:ZDB-GEN
13	ENSDARG000	3.54	2e-16	5e-14	1 x 5	alanine-glyoxylate aminotransferase b [Source:ZFIN;Acc:ZDB
14	ENSDARG000	3.19	2e-16	5e-14	1 x 1	RAS, dexamethasone-induced 1 [Source:ZFIN;Acc:ZDB-GE
15	ENSDARG000	3.56	2e-16	5e-14	1 x 5	fibrinogen alpha chain [Source:ZFIN;Acc:ZDB-GENE-03101
16	ENSDARG000	3.01	2e-16	5e-14	1 x 5	apolipoprotein Bb, tandem duplicate 1 [Source:ZFIN;Acc:ZDB
17	ENSDARG000	3.62	2e-16	5e-14	1 x 5	plasminogen [Source:ZFIN;Acc:ZDB-GENE-030131-1411]
18	ENSDARG000	2.79	2e-16	5e-14	1 x 1	formin 2a [Source:ZFIN;Acc:ZDB-GENE-101107-1]
19	ENSDARG000	4.23	2e-16	5e-14	1 x 1	Bernardinelli-Seip congenital lipodystrophy 2, like [Source:ZF
20	ENSDARG000	3.4	2e-16	5e-14	1 x 1	cytochrome b561 family, member A3b [Source:ZFIN;Acc:ZDB

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	13.12	NULL	712	BP oxidation-reduction process
2	13.01	NULL	522	MF oxidoreductase activity
3	11	NULL	10	CC chylomicron
4	10.19	NULL	23	BP lipoprotein metabolic process
5	10.02	NULL	480	MF catalytic activity
6	9.93	NULL	33	MF endopeptidase inhibitor activity
7	9.86	NULL	10	BP triglyceride catabolic process
8	9.81	NULL	10	CC high-density lipoprotein particle
9	9.1	NULL	11	BP cholesterol homeostasis
10	8.91	NULL	67	BP lipid transport
11	8.87	NULL	12	BP cholesterol biosynthetic process
12	8.63	NULL	109	BP negative regulation of endopeptidase activity
13	8.53	NULL	414	BP metabolic process
14	8.42	NULL	13	BP cholesterol efflux
15	8.42	NULL	17	CC blood microparticle
16	8.28	NULL	17	MF cholesterol binding
17	7.57	NULL	17	MF cholesterol transporter activity
18	7.39	NULL	1580	CC cellular_component
19	7.24	NULL	30	BP pigmentation
20	7.15	NULL	105	MF lipid binding
<i>Underexpressed</i>				
1	-15.46	NULL	1484	MF DNA binding
2	-14.89	NULL	2716	CC nucleus
3	-12.42	NULL	1239	BP regulation of transcription, DNA-templated
4	-11.62	NULL	229	CC chromosome
5	-11.6	NULL	168	CC nucleosome
6	-11	NULL	14	CC hemoglobin complex
7	-10.38	NULL	537	MF sequence-specific DNA binding
8	-10.33	NULL	454	BP multicellular organism development
9	-9.66	NULL	333	BP cell adhesion
10	-9.47	NULL	117	BP nucleosome assembly
11	-9.34	NULL	19	MF oxygen binding
12	-9.34	NULL	19	BP oxygen transport
13	-9.34	NULL	19	MF oxygen transporter activity
14	-8.93	NULL	2030	MF nucleic acid binding
15	-8.58	NULL	232	MF protein heterodimerization activity
16	-8.52	NULL	37	MF nucleosomal DNA binding
17	-8.35	NULL	49	MF extracellular matrix structural constituent
18	-7.38	NULL	34	BP ephrin receptor signaling pathway
19	-7.13	NULL	153	CC proteinaceous extracellular matrix
20	-6.94	NULL	52	BP blood vessel development

