

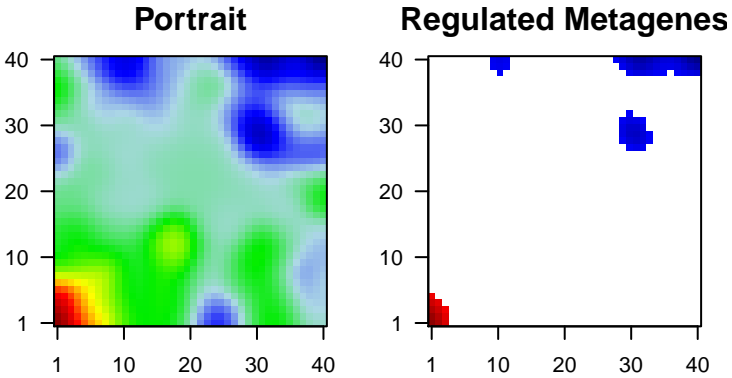
72hpf_pos

Global Summary

%DE = 0.16
genes with $\text{fdr} < 0.2$ = 3129 (1526 + / 1603 -)
genes with $\text{fdr} < 0.1$ = 2406 (1120 + / 1286 -)
genes with $\text{fdr} < 0.05$ = 1879 (857 + / 1022 -)
genes with $\text{fdr} < 0.01$ = 1220 (545 + / 675 -)

genes in genesets = 21072

<FC> = 0
<t-score> = 0.01
<p-value> = 0.11
<fdr> = 0.84



Global Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ENSDARG000	-3.69	2e-16	5e-14	32 x 40 FERM domain containing 6 [Source:ZFIN;Acc:ZDB-GENE-0
2	ENSDARG000	3.39	2e-16	5e-14	1 x 36 guanine nucleotide binding protein (G protein), beta polypepti
3	ENSDARG000	-4.48	2e-16	5e-14	40 x 40 hematopoietic death receptor [Source:ZFIN;Acc:ZDB-GENE-
4	ENSDARG000	2.91	2e-16	5e-14	1 x 1 aldo-keto reductase family 1, member B1 (aldose reductase)
5	ENSDARG000	-3.93	2e-16	5e-14	11 x 40 transmembrane protein 178B [Source:ZFIN;Acc:ZDB-GENE-
6	ENSDARG000	-3.36	2e-16	5e-14	1 x 40 ATPase, Na+/K+ transporting, alpha 1a polypeptide, tandem
7	ENSDARG000	-3.46	2e-16	5e-14	1 x 11 endothelial PAS domain protein 1a [Source:ZFIN;Acc:ZDB-G
8	ENSDARG000	2.93	2e-16	5e-14	1 x 1 RAB34, member RAS oncogene family b [Source:ZFIN;Acc:Z
9	ENSDARG000	3.21	2e-16	5e-14	4 x 1 troponin C type 1a (slow) [Source:ZFIN;Acc:ZDB-GENE-03C
10	ENSDARG000	3.34	2e-16	5e-14	1 x 3 tumor necrosis factor b (TNF superfamily, member 2) [Source
11	ENSDARG000	-3.58	2e-16	5e-14	38 x 38 bone morphogenetic protein 6 [Source:ZFIN;Acc:ZDB-GENE
12	ENSDARG000	3.08	2e-16	5e-14	1 x 4 apolipoprotein A-II [Source:ZFIN;Acc:ZDB-GENE-030131-1
13	ENSDARG000	2.92	2e-16	5e-14	1 x 4 transferrin-a [Source:ZFIN;Acc:ZDB-GENE-980526-35]
14	ENSDARG000	3.06	2e-16	5e-14	1 x 1 RAS, dexamethasone-induced 1 [Source:ZFIN;Acc:ZDB-GE
15	ENSDARG000	-3.75	2e-16	5e-14	1 x 27 ATP-binding cassette, sub-family B (MDR/TAP), member 5 [
16	ENSDARG000	3.16	2e-16	5e-14	1 x 3 alkylglycerol monooxygenase [Source:ZFIN;Acc:ZDB-GENE-
17	ENSDARG000	4.34	2e-16	5e-14	1 x 1 Bernardinelli-Seip congenital lipodystrophy 2, like [Source:Zf
18	ENSDARG000	-3.92	2e-16	5e-14	40 x 40 uroporphyrinogen III synthase [Source:ZFIN;Acc:ZDB-GENE
19	ENSDARG000	-3.15	2e-16	5e-14	30 x 29 ankyrin repeat domain 6b [Source:ZFIN;Acc:ZDB-GENE-03C
20	ENSDARG000	3.24	2e-16	5e-14	1 x 1 solute carrier family 2 (facilitated glucose transporter), mem

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	11.29	NULL	522	MF oxidoreductase activity
2	10.6	NULL	712	BP oxidation-reduction process
3	8.4	NULL	23	BP lipoprotein metabolic process
4	7.28	NULL	10	CC chylomicron
5	7.18	NULL	67	BP lipid transport
6	7.15	NULL	10	BP triglyceride catabolic process
7	6.83	NULL	11	BP cholesterol homeostasis
8	6.82	NULL	10	CC high-density lipoprotein particle
9	6.77	NULL	109	BP negative regulation of endopeptidase activity
10	6.76	NULL	33	MF endopeptidase inhibitor activity
11	6.22	NULL	30	BP pigmentation
12	5.99	NULL	33	MF photoreceptor activity
13	5.96	NULL	17	CC blood microparticle
14	5.89	NULL	35	BP sarcomere organization
15	5.76	NULL	1580	CC cellular_component
16	5.67	NULL	13	BP cholesterol efflux
17	5.67	NULL	31	BP protein-chromophore linkage
18	5.48	NULL	229	MF transporter activity
19	5.37	NULL	414	BP metabolic process
20	5.3	NULL	12	BP cholesterol biosynthetic process
<i>Underexpressed</i>				
1	-12.43	NULL	1484	MF DNA binding
2	-11.41	NULL	2716	CC nucleus
3	-10.91	NULL	168	CC nucleosome
4	-10	NULL	229	CC chromosome
5	-8.75	NULL	1239	BP regulation of transcription, DNA-templated
6	-8.36	NULL	537	MF sequence-specific DNA binding
7	-8.21	NULL	14	CC hemoglobin complex
8	-8.11	NULL	232	MF protein heterodimerization activity
9	-7.6	NULL	117	BP nucleosome assembly
10	-7.57	NULL	454	BP multicellular organism development
11	-6.8	NULL	19	MF oxygen binding
12	-6.8	NULL	19	BP oxygen transport
13	-6.8	NULL	19	MF oxygen transporter activity
14	-6.41	NULL	2030	MF nucleic acid binding
15	-6.15	NULL	333	BP cell adhesion
16	-6.08	NULL	172	BP homophilic cell adhesion via plasma membrane adhesion molecule
17	-5.53	NULL	43	BP DNA-templated transcription, initiation
18	-5.49	NULL	40	BP erythrocyte differentiation
19	-5.45	NULL	633	MF transcription factor activity, sequence-specific DNA binding
20	-5.44	NULL	38	BP vasculogenesis

