

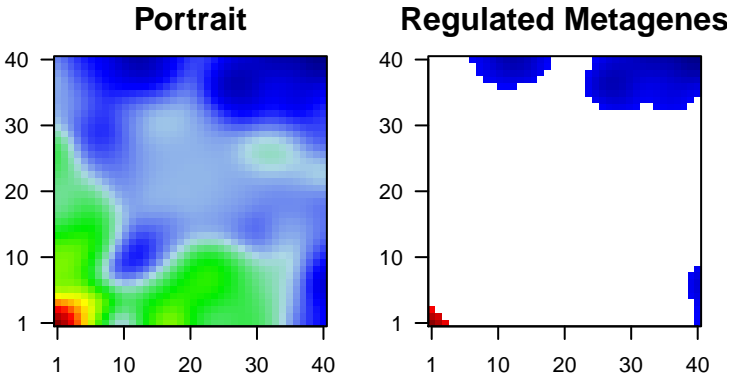
72hpf_pos_gata5.1

Global Summary

%DE = 0.13
genes with $\text{fdr} < 0.2$ = 2512 (1259 + / 1253 -)
genes with $\text{fdr} < 0.1$ = 1883 (952 + / 931 -)
genes with $\text{fdr} < 0.05$ = 1548 (785 + / 763 -)
genes with $\text{fdr} < 0.01$ = 945 (496 + / 449 -)

genes in genesets = 21072

<FC> = 0
<t-score> = 0.01
<p-value> = 0.15
<fdr> = 0.87



Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description	
					Metagene	
1	ENSDARG000	-3.49	2e-16	8e-14	27 x 36	unkempt family zinc finger [Source:ZFIN;Acc:ZDB-GENE-04
2	ENSDARG000	-4.29	2e-16	8e-14	11 x 1	obscurin-like 1a [Source:ZFIN;Acc:ZDB-GENE-060503-64
3	ENSDARG000	3.32	2e-16	8e-14	1 x 1	aldo-keto reductase family 1, member B1 (aldose reductase)
4	ENSDARG000	-4.5	2e-16	8e-14	40 x 40	myeloid/lymphoid or mixed-lineage leukemia (trithorax homol
5	ENSDARG000	3.67	2e-16	8e-14	1 x 40	ATPase, Na+/K+ transporting, alpha 1a polypeptide, tandem
6	ENSDARG000	3.01	2e-16	8e-14	1 x 1	RAB34, member RAS oncogene family b [Source:ZFIN;Acc:2
7	ENSDARG000	-4.08	2e-16	8e-14	4 x 1	troponin C type 1a (slow) [Source:ZFIN;Acc:ZDB-GENE-03
8	ENSDARG000	-3.56	2e-16	8e-14	37 x 39	DEP domain containing 1a [Source:ZFIN;Acc:ZDB-GENE-0
9	ENSDARG000	-3.46	2e-16	8e-14	40 x 7	filamin C, gamma a (actin binding protein 280) [Source:ZFIN;
10	ENSDARG000	-3.57	2e-16	8e-14	13 x 9	human immunodeficiency virus type I enhancer binding protei
11	ENSDARG000	3.28	2e-16	8e-14	1 x 3	alkylglycerol monooxygenase [Source:ZFIN;Acc:ZDB-GENE-
12	ENSDARG000	4.31	2e-16	8e-14	1 x 1	Bernardinelli-Seip congenital lipodystrophy 2, like [Source:ZF
13	ENSDARG000	3.72	2e-16	8e-14	1 x 1	cytochrome b561 family, member A3b [Source:ZFIN;Acc:ZDB
14	ENSDARG000	3.35	2e-16	8e-14	1 x 1	solute carrier family 2 (facilitated glucose transporter), membe
15	ENSDARG000	3.19	2e-16	8e-14	1 x 1	phytanoyl-CoA dioxygenase domain containing 1 [Source:ZF
16	ENSDARG000	3.42	2e-16	8e-14	1 x 3	neurogranin (protein kinase C substrate, RC3) a [Source:ZFIN
17	ENSDARG000	2.97	2e-16	8e-14	1 x 1	basic helix-loop-helix family, member e41 [Source:ZFIN;Acc:
18	ENSDARG000	3.62	2e-16	8e-14	1 x 1	zgc:113337 [Source:ZFIN;Acc:ZDB-GENE-050306-20]
19	ENSDARG000	3.37	2e-16	8e-14	1 x 1	tetraspanin 10 [Source:ZFIN;Acc:ZDB-GENE-041111-201]
20	ENSDARG000	3.2	2e-16	8e-14	1 x 1	6-pyruvoyltetrahydropterin synthase [Source:ZFIN;Acc:ZDB-

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	10.24	NULL	712	BP oxidation-reduction process
2	8.88	NULL	522	MF oxidoreductase activity
3	8.46	NULL	144	MF structural constituent of ribosome
4	7.68	NULL	147	CC ribosome
5	7.62	NULL	30	BP pigmentation
6	7.19	NULL	214	BP translation
7	7.11	NULL	25	MF glutathione transferase activity
8	6.83	NULL	561	MF GTP binding
9	6.57	NULL	67	BP lipid transport
10	6.44	NULL	1437	MF molecular_function
11	6.28	NULL	1580	CC cellular_component
12	6.27	NULL	23	BP lipoprotein metabolic process
13	6.21	NULL	96	CC lysosome
14	5.94	NULL	24	BP nucleoside metabolic process
15	5.78	NULL	31	BP autophagosome assembly
16	5.67	NULL	1066	CC intracellular
17	5.65	NULL	43	MF iron-sulfur cluster binding
18	5.64	NULL	1427	BP biological_process
19	5.57	NULL	414	BP metabolic process
20	5.54	NULL	321	MF GTPase activity
<i>Underexpressed</i>				
1	-12.09	NULL	1484	MF DNA binding
2	-11.53	NULL	1239	BP regulation of transcription, DNA-templated
3	-10.48	NULL	2716	CC nucleus
4	-9.61	NULL	2030	MF nucleic acid binding
5	-9.35	NULL	333	BP cell adhesion
6	-8.47	NULL	78	BP axon guidance
7	-8.09	NULL	537	MF sequence-specific DNA binding
8	-7.65	NULL	11	BP striated muscle contraction
9	-7.32	NULL	12	BP striated muscle myosin thick filament assembly
10	-7.24	NULL	454	BP multicellular organism development
11	-7.09	NULL	14	CC M band
12	-6.86	NULL	633	MF transcription factor activity, sequence-specific DNA binding
13	-6.59	NULL	65	CC extracellular matrix
14	-6.51	NULL	49	MF extracellular matrix structural constituent
15	-6.14	NULL	210	MF protein binding
16	-6	NULL	643	BP transcription, DNA-templated
17	-5.82	NULL	35	BP sarcomere organization
18	-5.74	NULL	91	BP heart looping
19	-5.7	NULL	15	CC basement membrane
20	-5.69	NULL	32	BP retinal ganglion cell axon guidance

