

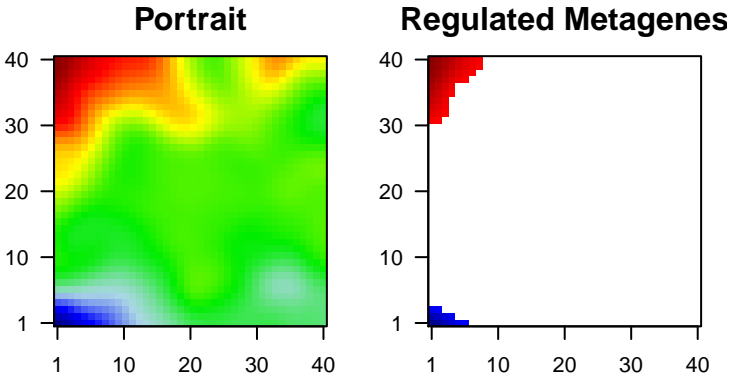
72hpf_neg_gata5

Global Summary

%DE = 0.14
genes with $\text{fdr} < 0.2$ = 2791 (1521 + / 1270 -)
genes with $\text{fdr} < 0.1$ = 2196 (1203 + / 993 -)
genes with $\text{fdr} < 0.05$ = 1682 (902 + / 780 -)
genes with $\text{fdr} < 0.01$ = 1190 (608 + / 582 -)

genes in genesets = 21072

<FC> = 0
<t-score> = 0
<p-value> = 0.13
<fdr> = 0.86



Global Genelist

Rank	ID	log(FC)	p-value	fdr	Description	
					Metagene	
1	ENSDARG000	-3.98	2e-16	7e-14	6 x 1	ryanodine receptor 2b (cardiac) [Source:ZFIN;Acc:ZDB-GENE-000000000]
2	ENSDARG000	-3.37	2e-16	7e-14	2 x 1	phosphoribosylformylglycinamide synthase [Source:ZFIN;Acc:ZDB-GENE-000000000]
3	ENSDARG000	-4.25	2e-16	7e-14	4 x 1	RAB20, member RAS oncogene family [Source:ZFIN;Acc:ZDB-GENE-000000000]
4	ENSDARG000	-4.37	2e-16	7e-14	1 x 1	aldo-keto reductase family 1, member B1 (aldose reductase) [Source:ZFIN;Acc:ZDB-GENE-000000000]
5	ENSDARG000	-3.85	2e-16	7e-14	1 x 1	RAB34, member RAS oncogene family b [Source:ZFIN;Acc:ZDB-GENE-000000000]
6	ENSDARG000	-4.03	2e-16	7e-14	4 x 1	troponin C type 1a (slow) [Source:ZFIN;Acc:ZDB-GENE-000000000]
7	ENSDARG000	-3.63	2e-16	7e-14	3 x 1	cysteine and glycine-rich protein 2 [Source:ZFIN;Acc:ZDB-GENE-000000000]
8	ENSDARG000	4.72	2e-16	7e-14	1 x 39	collagen, type XI, alpha 2 [Source:ZFIN;Acc:ZDB-GENE-000000000]
9	ENSDARG000	3.25	2e-16	7e-14	1 x 37	procollagen, type IX, alpha 2 [Source:ZFIN;Acc:ZDB-GENE-000000000]
10	ENSDARG000	-4.05	2e-16	7e-14	1 x 1	Bernardinelli-Seip congenital lipodystrophy 2, like [Source:ZFIN;Acc:ZDB-GENE-000000000]
11	ENSDARG000	3.41	2e-16	7e-14	1 x 38	collagen, type XI, alpha 1a [Source:ZFIN;Acc:ZDB-GENE-000000000]
12	ENSDARG000	-3.65	2e-16	7e-14	6 x 1	tripartite motif containing 63a [Source:ZFIN;Acc:ZDB-GENE-000000000]
13	ENSDARG000	-4.42	2e-16	7e-14	1 x 1	RAB32a, member RAS oncogene family [Source:ZFIN;Acc:ZDB-GENE-000000000]
14	ENSDARG000	-3.07	2e-16	7e-14	4 x 1	IMP (inosine 5'-monophosphate) dehydrogenase 1b [Source:ZFIN;Acc:ZDB-GENE-000000000]
15	ENSDARG000	-6.34	2e-16	7e-14	1 x 1	solute carrier family 2 (facilitated glucose transporter), member 2 [Source:ZFIN;Acc:ZDB-GENE-000000000]
16	ENSDARG000	-3.22	2e-16	7e-14	1 x 1	phytanoyl-CoA dioxygenase domain containing 1 [Source:ZFIN;Acc:ZDB-GENE-000000000]
17	ENSDARG000	5.34	2e-16	7e-14	1 x 37	matrilin 1 [Source:ZFIN;Acc:ZDB-GENE-050307-3]
18	ENSDARG000	-5.39	2e-16	7e-14	3 x 1	cardiac myosin light chain-1 [Source:ZFIN;Acc:ZDB-GENE-000000000]
19	ENSDARG000	-4.96	2e-16	7e-14	2 x 1	G protein-coupled receptor 143 [Source:ZFIN;Acc:ZDB-GENE-000000000]
20	ENSDARG000	3.82	2e-16	7e-14	1 x 37	aggrecan a [Source:ZFIN;Acc:ZDB-GENE-050208-221]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
Overexpressed				
1	17.25	NULL	49	MF extracellular matrix structural constituent
2	15.63	NULL	333	BP cell adhesion
3	14.7	NULL	537	MF sequence-specific DNA binding
4	13.58	NULL	172	BP homophilic cell adhesion via plasma membrane adhesion molecule
5	13.53	NULL	1239	BP regulation of transcription, DNA-templated
6	13.06	NULL	717	MF calcium ion binding
7	12.83	NULL	153	CC proteinaceous extracellular matrix
8	12.16	NULL	454	BP multicellular organism development
9	11.2	NULL	1162	CC plasma membrane
10	10.8	NULL	175	BP nervous system development
11	10.5	NULL	1484	MF DNA binding
12	10.21	NULL	633	MF transcription factor activity, sequence-specific DNA binding
13	9.75	NULL	6248	CC integral component of membrane
14	9.49	NULL	270	MF ion channel activity
15	9.13	NULL	78	BP axon guidance
16	8.9	NULL	6723	CC membrane
17	8.69	NULL	155	CC synapse
18	8.66	NULL	499	BP ion transport
19	8.32	NULL	2716	CC nucleus
20	7.62	NULL	23	MF hyaluronic acid binding
Underexpressed				
1	-10.62	NULL	712	BP oxidation-reduction process
2	-10.29	NULL	522	MF oxidoreductase activity
3	-9	NULL	410	CC mitochondrion
4	-8.49	NULL	10	CC melanosome
5	-8.19	NULL	30	BP pigmentation
6	-8.12	NULL	11	BP melanosome organization
7	-7.98	NULL	1580	CC cellular_component
8	-7.94	NULL	480	MF catalytic activity
9	-7.09	NULL	561	MF GTP binding
10	-6.9	NULL	35	BP sarcomere organization
11	-6.88	NULL	96	CC lysosome
12	-6.51	NULL	11	BP purine nucleotide biosynthetic process
13	-6.5	NULL	34	MF electron carrier activity
14	-6.4	NULL	62	BP proteolysis involved in cellular protein catabolic process
15	-6.35	NULL	21	MF substrate-specific transmembrane transporter activity
16	-6.27	NULL	57	MF flavin adenine dinucleotide binding
17	-6.27	NULL	43	MF iron-sulfur cluster binding
18	-6.12	NULL	414	BP metabolic process
19	-6.07	NULL	321	MF GTPase activity
20	-6.04	NULL	23	CC troponin complex

