

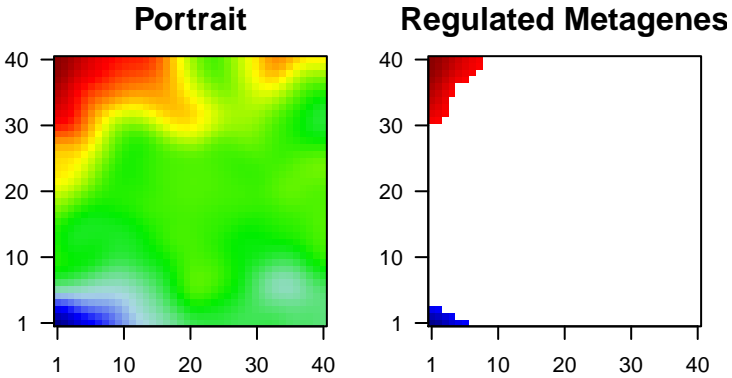
72hpf_neg_gata5

Global Summary

%DE = 0
genes with fdr < 0.2 = 0 (0 + / 0 -)
genes with fdr < 0.1 = 0 (0 + / 0 -)
genes with fdr < 0.05 = 0 (0 + / 0 -)
genes with fdr < 0.01 = 0 (0 + / 0 -)

genes in genesets = 21072

<FC> = 0
<t-score> = 0
<p-value> = 0.72
<fdr> = 1



Global Genelist

Rank	ID	log(FC)	p-value	fdr	Description
					Metagene
1	ENSDARG0000000001	-5.11	0.1	1	1 x 1 solute carrier family 2 (facilitated glucose transporter), memb
2	ENSDARG0000000002	-5.18	0.1	1	1 x 1 slc211-108c6.2 [Source:ZFIN;Acc:ZDB-GENE-040724-7]
3	ENSDARG0000000003	-4.94	0.1	1	1 x 1 cation/H+ exchanger protein 1 [Source:ZFIN;Acc:ZDB-GENE-
4	ENSDARG0000000004	-4.4	0.1	1	1 x 1 zgc:162150 [Source:ZFIN;Acc:ZDB-GENE-070410-23]
5	ENSDARG0000000005	-4.72	0.1	1	1 x 1 slc211-108c6.2 [Source:ZFIN;Acc:ZDB-GENE-131120-16]
6	ENSDARG0000000006	-4.41	0.1	1	1 x 1 solute carrier family 22 (organic anion transporter), member 7
7	ENSDARG0000000007	-4.41	0.1	1	1 x 1 transmembrane protein 130 [Source:ZFIN;Acc:ZDB-GENE-070410-23]
8	ENSDARG0000000008	-4.26	0.1	1	1 x 1 wu:fc46h12 [Source:ZFIN;Acc:ZDB-GENE-030131-3611]
9	ENSDARG0000000009	-4.47	0.1	1	1 x 1 melanophilin a [Source:ZFIN;Acc:ZDB-GENE-050208-724]
10	ENSDARG0000000010	-4.12	0.1	1	1 x 1 aldehyde oxidase 5 [Source:ZFIN;Acc:ZDB-GENE-001205-10]
11	ENSDARG0000000011	-4.21	0.1	1	3 x 1 cardiac myosin light chain-1 [Source:ZFIN;Acc:ZDB-GENE-001205-10]
12	ENSDARG0000000012	4.88	0.1	1	1 x 37 matrilin 1 [Source:ZFIN;Acc:ZDB-GENE-050307-3]
13	ENSDARG0000000013	-3.96	0.1	1	1 x 1 GTP cyclohydrolase 2 [Source:ZFIN;Acc:ZDB-GENE-001205-10]
14	ENSDARG0000000014	-4.17	0.1	1	1 x 1 O-acetyltransferase like [Source:ZFIN;Acc:ZDB-GENE-09071-1]
15	ENSDARG0000000015	-4.24	0.1	1	1 x 1 ops1n 5 [Source:ZFIN;Acc:ZDB-GENE-041001-179]
16	ENSDARG0000000016	-4	0.1	1	2 x 1 myosin, heavy chain 6, cardiac muscle, alpha [Source:ZFIN;Acc:ZDB-GENE-041001-179]
17	ENSDARG0000000017	-4.19	0.1	1	2 x 1 G protein-coupled receptor 143 [Source:ZFIN;Acc:ZDB-GENE-041001-179]
18	ENSDARG0000000018	-3.81	0.1	1	1 x 1 slc211-108c6.2 [Source:ZFIN;Acc:ZDB-GENE-141219-27]
19	ENSDARG0000000019	-3.73	0.1	1	1 x 1 RAS and EF-hand domain containing [Source:ZFIN;Acc:ZDB-GENE-041001-179]
20	ENSDARG0000000020	-3.56	0.1	1	1 x 1 slc211-108c6.2 [Source:ZFIN;Acc:ZDB-GENE-050506-10]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	16.18	NULL	49	MF extracellular matrix structural constituent
2	15.37	NULL	333	BP cell adhesion
3	14.81	NULL	537	MF sequence-specific DNA binding
4	13.66	NULL	172	BP homophilic cell adhesion via plasma membrane adhesion molecule
5	13.37	NULL	1239	BP regulation of transcription, DNA-templated
6	13.2	NULL	717	MF calcium ion binding
7	12.6	NULL	153	CC proteinaceous extracellular matrix
8	12.13	NULL	454	BP multicellular organism development
9	11.75	NULL	1162	CC plasma membrane
10	10.8	NULL	175	BP nervous system development
11	10.3	NULL	270	MF ion channel activity
12	10.25	NULL	1484	MF DNA binding
13	10.24	NULL	6248	CC integral component of membrane
14	9.97	NULL	633	MF transcription factor activity, sequence-specific DNA binding
15	9.46	NULL	6723	CC membrane
16	9.39	NULL	499	BP ion transport
17	9.23	NULL	155	CC synapse
18	8.76	NULL	78	BP axon guidance
19	8.09	NULL	2716	CC nucleus
20	7.75	NULL	176	BP ion transmembrane transport
<i>Underexpressed</i>				
1	-10.28	NULL	712	BP oxidation-reduction process
2	-9.99	NULL	522	MF oxidoreductase activity
3	-9	NULL	410	CC mitochondrion
4	-8.12	NULL	10	CC melanosome
5	-7.98	NULL	1580	CC cellular component
6	-7.79	NULL	11	BP melanosome organization
7	-7.68	NULL	480	MF catalytic activity
8	-7.64	NULL	30	BP pigmentation
9	-6.7	NULL	35	BP sarcomere organization
10	-6.68	NULL	96	CC lysosome
11	-6.65	NULL	561	MF GTP binding
12	-6.28	NULL	23	CC troponin complex
13	-6.15	NULL	62	BP proteolysis involved in cellular protein catabolic process
14	-5.97	NULL	34	MF electron carrier activity
15	-5.96	NULL	57	MF flavin adenine dinucleotide binding
16	-5.94	NULL	21	MF substrate-specific transmembrane transporter activity
17	-5.84	NULL	43	MF iron-sulfur cluster binding
18	-5.82	NULL	414	BP metabolic process
19	-5.77	NULL	11	BP purine nucleotide biosynthetic process
20	-5.76	NULL	54	BP heart contraction

