48hpf_neg

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

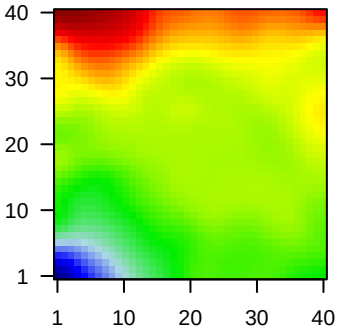
<FC> = 0

<t−score> = 0

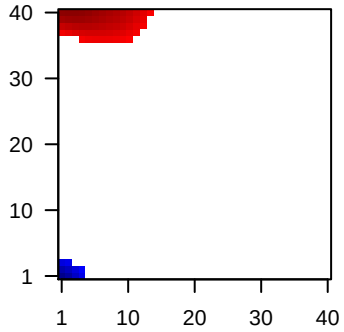
<p−value> = 0.73

<fdr> = 1

Portrait



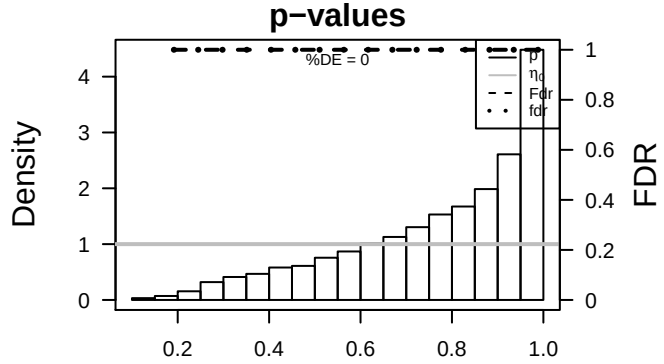
Regulated Metagenes



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ENSDARG00(	−5.46	0.1	1	1 x 1	basic helix−loop−helix family, member e41 [Source:ZFIN;Acc:
2	ENSDARG00(	−4.68	0.1	1	1 x 1	zgc:162150 [Source:ZFIN;Acc:ZDB−GENE−070410−23]
3	ENSDARG00(	−4.69	0.1	1	1 x 1	wu:fc46h12 [Source:ZFIN;Acc:ZDB−GENE−030131−3611]
4	ENSDARG00(	−4.91	0.1	1	1 x 1	RAS and EF−hand domain containing [Source:ZFIN;Acc:ZDE
5	ENSDARG00(	−4.69	0.1	1	1 x 1	transmembrane protein 130 [Source:ZFIN;Acc:ZDB−GENE−(
6	ENSDARG00(	−4.74	0.1	1	1 x 1	melanophilin a [Source:ZFIN;Acc:ZDB−GENE−050208−724]
7	ENSDARG00(	−4.47	0.1	1	1 x 1	si:dkey−251i10.2 [Source:ZFIN;Acc:ZDB−GENE−050506−10
8	ENSDARG00(	−4.68	0.1	1	1 x 1	solute carrier family 2 (facilitated glucose transporter), membe
9	ENSDARG00(	−4.98	0.1	1	6 x 1	solute carrier family 8 (sodium/calcium exchanger), member 1
10	ENSDARG00(	−4.43	0.1	1	1 x 1	aldehyde oxidase 5 [Source:ZFIN;Acc:ZDB−GENE−001205−1
11	ENSDARG00(	−4.48	0.1	1	3 x 1	cardiac myosin light chain−1 [Source:ZFIN;Acc:ZDB−GENE−
12	ENSDARG00(	−4.33	0.1	1	1 x 1	solute carrier family 2 (facilitated glucose transporter), membe
13	ENSDARG00(	−4.59	0.1	1	1 x 1	si:ch1073−281m9.1 [Source:ZFIN;Acc:ZDB−GENE−131127−
14	ENSDARG00(	−4.51	0.1	1	1 x 1	opsin 5 [Source:ZFIN;Acc:ZDB−GENE−041001−179]
15	ENSDARG00(	−4.4	0.1	1	1 x 1	6−pyruvoyltetrahydropterin synthase [Source:ZFIN;Acc:ZDB−
16	ENSDARG00(	−4.26	0.1	1	2 x 1	myosin, heavy chain 6, cardiac muscle, alpha [Source:ZFIN;A
17	ENSDARG00(	−4.31	0.1	1	4 x 1	ventricular myosin heavy chain−like [Source:ZFIN;Acc:ZDB−(
18	ENSDARG00(	−4.34	0.1	1	1 x 1	zgc:113337 [Source:ZFIN;Acc:ZDB−GENE−050306−20]
19	ENSDARG00(	−3.82	0.1	1	1 x 1	GTP cyclohydrolase 2 [Source:ZFIN;Acc:ZDB−GENE−00120
20	ENSDARG00(	−4.06	0.1	1	1 x 1	cation/H+ exchanger protein 1 [Source:ZFIN;Acc:ZDB−GENE

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	20.03	NULL	1484	MF	DNA binding
2	19.6	NULL	2716	CC	nucleus
3	18.64	NULL	1239	BP	regulation of transcription, DNA−templated
4	17.24	NULL	537	MF	sequence−specific DNA binding
5	13.53	NULL	172	BP	homophilic cell adhesion via plasma membrane adhesion molecule
6	13.07	NULL	175	BP	nervous system development
7	12.63	NULL	2030	MF	nucleic acid binding
8	12.44	NULL	454	BP	multicellular organism development
9	12.42	NULL	14	CC	hemoglobin complex
10	11.2	NULL	333	BP	cell adhesion
11	10.77	NULL	643	BP	transcription, DNA−templated
12	10.71	NULL	19	MF	oxygen binding
13	10.71	NULL	19	BP	oxygen transport
14	10.71	NULL	19	MF	oxygen transporter activity
15	9.71	NULL	633	MF	transcription factor activity, sequence−specific DNA binding
16	9.32	NULL	78	BP	axon guidance
17	9.16	NULL	158	MF	microtubule binding
18	8.05	NULL	155	CC	synapse
19	7.97	NULL	108	CC	microtubule
20	7.92	NULL	168	CC	nucleosome
Underexpressed					
1	−16.57	NULL	712	BP	oxidation−reduction process
2	−15.82	NULL	522	MF	oxidoreductase activity
3	−10.73	NULL	414	BP	metabolic process
4	−9.82	NULL	480	MF	catalytic activity
5	−9.42	NULL	30	BP	pigmentation
6	−9.09	NULL	35	BP	sarcomere organization
7	−9.08	NULL	54	BP	heart contraction
8	−8.08	NULL	33	MF	endopeptidase inhibitor activity
9	−7.72	NULL	23	BP	lipoprotein metabolic process
10	−7.57	NULL	410	CC	mitochondrion
11	−6.93	NULL	10	CC	melanosome
12	−6.91	NULL	96	CC	lysosome
13	−6.85	NULL	1580	CC	cellular_component
14	−6.8	NULL	67	BP	lipid transport
15	−6.79	NULL	164	BP	carbohydrate metabolic process
16	−6.77	NULL	109	BP	negative regulation of endopeptidase activity
17	−6.7	NULL	43	MF	iron−sulfur cluster binding
18	−6.53	NULL	27	BP	response to bacterium
19	−6.52	NULL	11	BP	melanosome organization
20	−6.48	NULL	147	CC	ribosome