72hpf_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

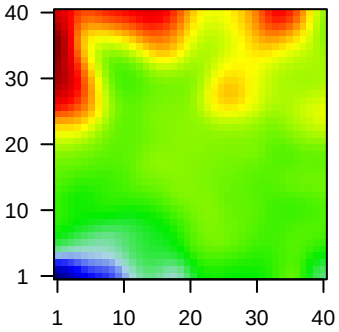
<FC> = 0

<t−score> = 0

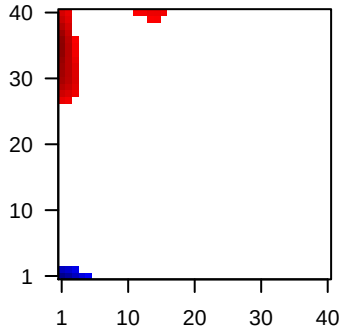
<p−value> = 0.75

<fdr> = 1

Portrait



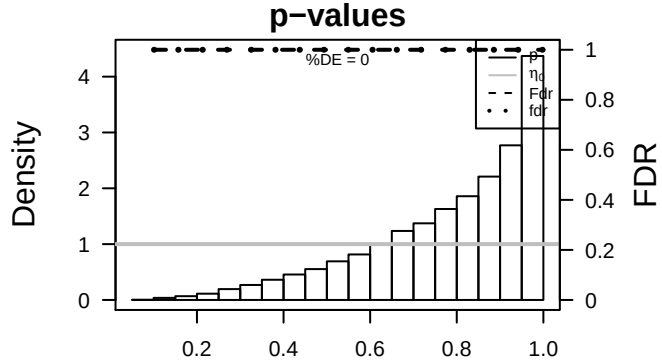
Regulated Metagenes



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ENSDARG00(	11.52	0.05	1	1 x 30	
2	ENSDARG00(	−6.44	0.08	1	1 x 1	GTP cyclohydrolase 2 [Source:ZFIN;Acc:ZDB−GENE−00120
3	ENSDARG00(	−6.18	0.08	1	1 x 1	solute carrier family 22 (organic anion transporter), member 7
4	ENSDARG00(	−5.71	0.09	1	1 x 1	wu:fc46h12 [Source:ZFIN;Acc:ZDB−GENE−030131−3611]
5	ENSDARG00(	6.48	0.10	1	35 x 1	
6	ENSDARG00(	−4.88	0.10	1	1 x 1	solute carrier family 2 (facilitated glucose transporter), membe
7	ENSDARG00(	−4.74	0.10	1	1 x 1	si:dkey−251i10.2 [Source:ZFIN;Acc:ZDB−GENE−050506−10
8	ENSDARG00(	−4.94	0.11	1	1 x 1	molybdenum cofactor sulfurase [Source:ZFIN;Acc:ZDB−GEN
9	ENSDARG00(	−4.34	0.11	1	1 x 1	zgc:162150 [Source:ZFIN;Acc:ZDB−GENE−070410−23]
10	ENSDARG00(	−4.4	0.11	1	1 x 1	Bernardinelli−Seip congenital lipodystrophy 2, like [Source:ZF
11	ENSDARG00(	−4.36	0.11	1	1 x 1	aldehyde oxidase 5 [Source:ZFIN;Acc:ZDB−GENE−001205−:
12	ENSDARG00(	−4.36	0.11	1	1 x 1	transmembrane protein 130 [Source:ZFIN;Acc:ZDB−GENE−(
13	ENSDARG00(	5.12	0.12	1	1 x 35	opsin 1 (cone pigments), short−wave−sensitive 2 [Source:ZFI
14	ENSDARG00(	4.78	0.12	1	1 x 40	mucin 5.1, oligomeric mucus/gel−forming [Source:ZFIN;Acc:Z
15	ENSDARG00(	−4.15	0.12	1	1 x 1	solute carrier family 2 (facilitated glucose transporter), membe
16	ENSDARG00(	5.04	0.12	1	1 x 35	opsin 1 (cone pigments), medium−wave−sensitive, 1 [Source:
17	ENSDARG00(	4.91	0.12	1	1 x 35	opsin 1 (cone pigments), short−wave−sensitive 1 [Source:ZFI
18	ENSDARG00(	4.65	0.12	1	1 x 37	rhodopsin [Source:ZFIN;Acc:ZDB−GENE−990415−271]
19	ENSDARG00(	4.72	0.12	1	1 x 37	actinodin2 [Source:ZFIN;Acc:ZDB−GENE−041105−2]
20	ENSDARG00(	−4.08	0.12	1	1 x 1	si:ch211−108c6.2 [Source:ZFIN;Acc:ZDB−GENE−040724−7]

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	18.24	NULL	49	MF	extracellular matrix structural constituent
2	13.25	NULL	153	CC	proteinaceous extracellular matrix
3	13.15	NULL	83	BP	visual perception
4	12.34	NULL	2716	CC	nucleus
5	12.12	NULL	1484	MF	DNA binding
6	11.4	NULL	537	MF	sequence−specific DNA binding
7	11.39	NULL	454	BP	multicellular organism development
8	11.31	NULL	333	BP	cell adhesion
9	10.79	NULL	717	MF	calcium ion binding
10	10.69	NULL	20	BP	fin development
11	10.68	NULL	1239	BP	regulation of transcription, DNA−templated
12	9.61	NULL	76	BP	cartilage development
13	9.51	NULL	634	CC	extracellular region
14	8.62	NULL	15	CC	basement membrane
15	8.55	NULL	28	BP	phototransduction
16	8.22	NULL	46	CC	collagen trimer
17	8.13	NULL	78	BP	axon guidance
18	7.46	NULL	93	BP	dorsal/ventral pattern formation
19	7.01	NULL	32	BP	retinal ganglion cell axon guidance
20	6.97	NULL	65	CC	extracellular matrix
Underexpressed					
1	−8.56	NULL	96	CC	lysosome
2	−8.24	NULL	30	BP	pigmentation
3	−7.87	NULL	11	BP	melanosome organization
4	−7.46	NULL	23	CC	troponin complex
5	−6.93	NULL	712	BP	oxidation−reduction process
6	−6.76	NULL	10	CC	melanosome
7	−6.47	NULL	522	MF	oxidoreductase activity
8	−6.34	NULL	480	MF	catalytic activity
9	−6.18	NULL	54	BP	heart contraction
10	−6.14	NULL	35	BP	sarcomere organization
11	−6.02	NULL	13	BP	regulation of muscle contraction
12	−5.78	NULL	62	BP	proteolysis involved in cellular protein catabolic process
13	−5.71	NULL	21	MF	substrate−specific transmembrane transporter activity
14	−5.68	NULL	51	CC	lysosomal membrane
15	−5.59	NULL	15	BP	cardiac muscle contraction
16	−5.51	NULL	15	BP	skeletal muscle contraction
17	−5.49	NULL	13	BP	response to cadmium ion
18	−5.42	NULL	414	BP	metabolic process
19	−5.31	NULL	11	BP	purine nucleotide biosynthetic process
20	−5.31	NULL	410	CC	mitochondrion