72hpf_pos.1

Global Summary

%DE = 0.18

genes with fdr < 0.2 = 3787 (1924 + / 1863 −)

genes with fdr < 0.1 = 2734 (1279 + / 1455 −)

genes with fdr < 0.05 = 2304 (1032 + / 1272 −)

genes with fdr < 0.01 = 1401 (564 + / 837 −)

genes in genesets = 21072

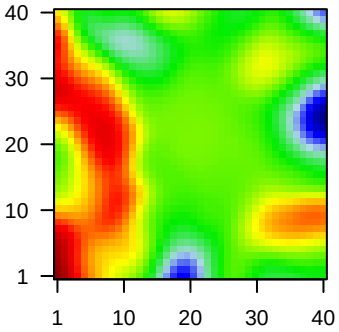
<FC> = 0

<t−score> = 0

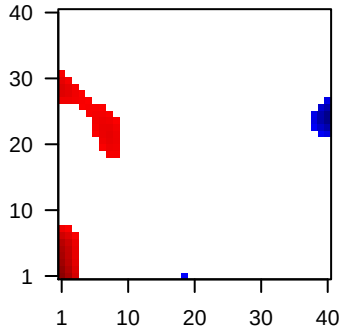
<p−value> = 0.09

<fdr> = 0.82

Portrait



Regulated Metagenes



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ENSDARG00(	3.69	2e−16	4e−14	1 x 36	myosin, heavy chain b [Source:ZFIN;Acc:ZDB−GENE−08112
2	ENSDARG00(	3.42	2e−16	4e−14	1 x 37	rhodopsin [Source:ZFIN;Acc:ZDB−GENE−990415−271]
3	ENSDARG00(	−3.89	2e−16	4e−14	40 x 40	Rh blood group, D antigen [Source:ZFIN;Acc:ZDB−GENE−05
4	ENSDARG00(	4.24	2e−16	4e−14	1 x 36	guanine nucleotide binding protein (G protein), beta polypepti
5	ENSDARG00(	2.89	2e−16	4e−14	1 x 6	parvalbumin 2 [Source:ZFIN;Acc:ZDB−GENE−000322−4]
6	ENSDARG00(	−4.56	2e−16	4e−14	39 x 40	myeloid ecotropic viral integration site 3 [Source:ZFIN;Acc:ZD
7	ENSDARG00(	−4.1	2e−16	4e−14	40 x 24	dachshund c [Source:ZFIN;Acc:ZDB−GENE−020402−5]
8	ENSDARG00(	−2.93	2e−16	4e−14	40 x 25	tetraspanin 2a [Source:ZFIN;Acc:ZDB−GENE−050522−511]
9	ENSDARG00(	−3.9	2e−16	4e−14	40 x 24	RAB23, member RAS oncogene family [Source:ZFIN;Acc:ZD
10	ENSDARG00(	−4.85	2e−16	4e−14	40 x 40	hematopoietic death receptor [Source:ZFIN;Acc:ZDB−GENE−
11	ENSDARG00(	−3.39	2e−16	4e−14	40 x 23	5'−nucleotidase domain containing 1 [Source:ZFIN;Acc:ZDB−
12	ENSDARG00(	−3.9	2e−16	4e−14	3 x 40	calcium channel, voltage−dependent, P/Q type, alpha 1A sub
13	ENSDARG00(	−4.29	2e−16	4e−14	4 x 40	cugbp, Elav−like family member 3b [Source:ZFIN;Acc:ZDB−G
14	ENSDARG00(	−3.04	2e−16	4e−14	40 x 24	interferon regulatory factor 2a [Source:ZFIN;Acc:ZDB−GENE
15	ENSDARG00(	−3.95	2e−16	4e−14	40 x 40	zinc finger−like gene 2a [Source:ZFIN;Acc:ZDB−GENE−0308
16	ENSDARG00(	−4.44	2e−16	4e−14	40 x 40	glucocorticoid induced 1 [Source:ZFIN;Acc:ZDB−GENE−031(
17	ENSDARG00(	−3.59	2e−16	4e−14	3 x 38	N−myc downstream regulated 1b [Source:ZFIN;Acc:ZDB−GE
18	ENSDARG00(	−3.75	2e−16	4e−14	6 x 37	cadherin 13, H−cadherin (heart) [Source:ZFIN;Acc:ZDB−GEI
19	ENSDARG00(	3.05	2e−16	4e−14	1 x 4	apolipoprotein A−II [Source:ZFIN;Acc:ZDB−GENE−030131−1
20	ENSDARG00(	−4.5	2e−16	4e−14	40 x 25	phosphatidylinositol glycan anchor biosynthesis, class S [Sou

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	10.05	NULL	62	CC	intermediate filament
2	9.26	NULL	159	MF	structural molecule activity
3	9.03	NULL	23	CC	troponin complex
4	9.02	NULL	70	CC	myosin complex
5	7.93	NULL	522	MF	oxidoreductase activity
6	7.49	NULL	83	BP	visual perception
7	7.36	NULL	717	MF	calcium ion binding
8	7.1	NULL	712	BP	oxidation−reduction process
9	7.08	NULL	33	MF	photoreceptor activity
10	7.07	NULL	109	BP	negative regulation of endopeptidase activity
11	6.8	NULL	634	CC	extracellular region
12	6.78	NULL	15	BP	cardiac muscle contraction
13	6.74	NULL	13	BP	regulation of muscle contraction
14	6.74	NULL	120	MF	motor activity
15	6.63	NULL	15	BP	skeletal muscle contraction
16	6.56	NULL	229	MF	transporter activity
17	6.56	NULL	35	BP	sarcomere organization
18	6.37	NULL	31	BP	protein−chromophore linkage
19	6.29	NULL	108	MF	actin filament binding
20	6.29	NULL	231	MF	actin binding
Underexpressed					
1	−16.66	NULL	168	CC	nucleosome
2	−15.98	NULL	229	CC	chromosome
3	−14.21	NULL	232	MF	protein heterodimerization activity
4	−12.54	NULL	2030	MF	nucleic acid binding
5	−10.84	NULL	2716	CC	nucleus
6	−10.03	NULL	117	BP	nucleosome assembly
7	−9.44	NULL	43	BP	DNA−templated transcription, initiation
8	−9.25	NULL	1484	MF	DNA binding
9	−8.02	NULL	14	CC	hemoglobin complex
10	−7.13	NULL	25	BP	membrane disruption in other organism
11	−6.49	NULL	608	MF	RNA binding
12	−6.03	NULL	30	BP	defense response to Gram−positive bacterium
13	−5.88	NULL	34	BP	chromatin silencing
14	−5.64	NULL	37	MF	nucleosomal DNA binding
15	−5.26	NULL	40	BP	erythrocyte differentiation
16	−5.23	NULL	19	MF	oxygen binding
17	−5.23	NULL	19	BP	oxygen transport
18	−5.23	NULL	19	MF	oxygen transporter activity
19	−5.22	NULL	214	BP	translation
20	−5.18	NULL	33	CC	cytosolic small ribosomal subunit

p−values