24hpf_pos

Global Summary

%DE = 0.21

genes with fdr < 0.2 = 4535 (2078 + / 2457 −)

genes with fdr < 0.1 = 3519 (1449 + / 2070 −)

genes with fdr < 0.05 = 3036 (1164 + / 1872 −)

genes with fdr < 0.01 = 2397 (831 + / 1566 −)

genes in genesets = 21072

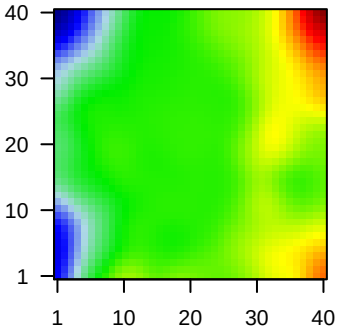
<FC> = 0

<t−score> = −0.03

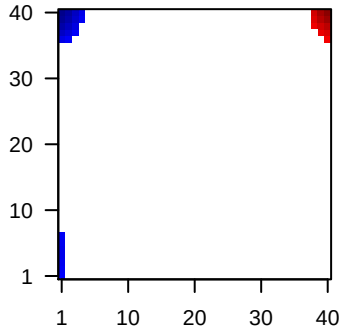
<p−value> = 0.05

<fdr> = 0.79

Portrait



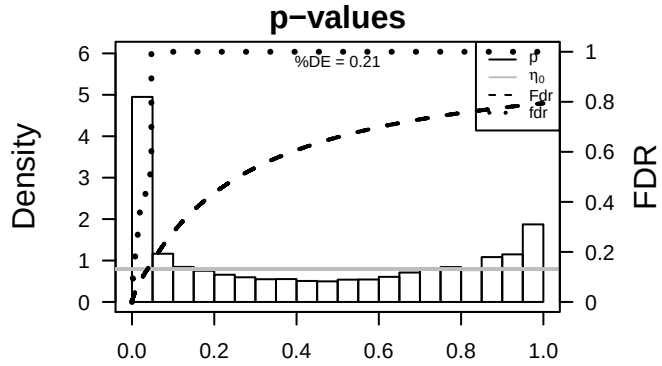
Regulated Metagenes



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ENSDARG00(	−5.21	2e−16	1e−14	1 x 40	syntaxin 1B [Source:ZFIN;Acc:ZDB−GENE−000330−4]
2	ENSDARG00(	−3.48	2e−16	1e−14	1 x 9	RAR−related orphan receptor A, paralog b [Source:ZFIN;Acc
3	ENSDARG00(	−4.31	2e−16	1e−14	1 x 37	rhodopsin [Source:ZFIN;Acc:ZDB−GENE−990415−271]
4	ENSDARG00(	3.83	2e−16	1e−14	40 x 40	Rh blood group, D antigen [Source:ZFIN;Acc:ZDB−GENE−05
5	ENSDARG00(	−3.59	2e−16	1e−14	1 x 38	synaptophysin b [Source:ZFIN;Acc:ZDB−GENE−040718−205
6	ENSDARG00(	−3.64	2e−16	1e−14	1 x 3	synaptogyrin 1a [Source:ZFIN;Acc:ZDB−GENE−041010−169
7	ENSDARG00(	−4.83	2e−16	1e−14	1 x 7	myosin light chain, phosphorylatable, fast skeletal muscle b [
8	ENSDARG00(	−3.67	2e−16	1e−14	1 x 36	guanine nucleotide binding protein (G protein), beta polypepti
9	ENSDARG00(	−6.37	2e−16	1e−14	1 x 6	parvalbumin 2 [Source:ZFIN;Acc:ZDB−GENE−000322−4]
10	ENSDARG00(	−3.84	2e−16	1e−14	1 x 6	apobec1 complementation factor [Source:ZFIN;Acc:ZDB−GE
11	ENSDARG00(	−3.89	2e−16	1e−14	1 x 6	annexin A2a [Source:ZFIN;Acc:ZDB−GENE−030131−4282]
12	ENSDARG00(	3.65	2e−16	1e−14	40 x 38	ferrochelatase [Source:ZFIN;Acc:ZDB−GENE−000928−1]
13	ENSDARG00(	−5.13	2e−16	1e−14	1 x 40	neuronal differentiation 4 [Source:ZFIN;Acc:ZDB−GENE−030
14	ENSDARG00(	−4.34	2e−16	1e−14	1 x 3	aquaporin 3a [Source:ZFIN;Acc:ZDB−GENE−040426−2826]
15	ENSDARG00(	−5.07	2e−16	1e−14	1 x 4	cathepsin L.1 [Source:ZFIN;Acc:ZDB−GENE−040718−61]
16	ENSDARG00(	3.39	2e−16	1e−14	40 x 36	tyrosine kinase with immunoglobulin−like and EGF−like doma
17	ENSDARG00(	−3.74	2e−16	1e−14	1 x 7	family with sequence similarity 169, member Ab [Source:ZFI
18	ENSDARG00(	−4.35	2e−16	1e−14	3 x 40	HECT, C2 and WW domain containing E3 ubiquitin protein lig
19	ENSDARG00(	−5.15	2e−16	1e−14	1 x 39	guanine nucleotide binding protein (G protein), beta polypepti
20	ENSDARG00(	5.37	2e−16	1e−14	40 x 40	hematopoietic death receptor [Source:ZFIN;Acc:ZDB−GENE−

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all		Geneset
Overexpressed					
1	18.02	NULL	229	CC	chromosome
2	17.42	NULL	168	CC	nucleosome
3	13.58	NULL	2030	MF	nucleic acid binding
4	13.49	NULL	117	BP	nucleosome assembly
5	13.43	NULL	232	MF	protein heterodimerization activity
6	11.54	NULL	14	CC	hemoglobin complex
7	11.33	NULL	28	BP	embryonic hemopoiesis
8	9.05	NULL	19	MF	oxygen binding
9	9.05	NULL	19	BP	oxygen transport
10	9.05	NULL	19	MF	oxygen transporter activity
11	9.01	NULL	43	BP	DNA−templated transcription, initiation
12	8.65	NULL	140	CC	nucleolus
13	8.55	NULL	37	MF	nucleosomal DNA binding
14	8.53	NULL	40	BP	erythrocyte differentiation
15	8.37	NULL	15	BP	heme biosynthetic process
16	8.2	NULL	78	BP	DNA replication
17	7.83	NULL	24	BP	myeloid cell differentiation
18	7.56	NULL	25	BP	membrane disruption in other organism
19	7.31	NULL	52	BP	blood vessel development
20	7.29	NULL	608	MF	RNA binding
Underexpressed					
1	−11.74	NULL	717	MF	calcium ion binding
2	−11.43	NULL	499	BP	ion transport
3	−9.74	NULL	49	MF	extracellular matrix structural constituent
4	−9.71	NULL	175	BP	nervous system development
5	−9.67	NULL	1162	CC	plasma membrane
6	−9.49	NULL	155	CC	synapse
7	−8.94	NULL	270	MF	ion channel activity
8	−8.74	NULL	32	MF	extracellular−glutamate−gated ion channel activity
9	−8.74	NULL	32	MF	ionotropic glutamate receptor activity
10	−8.74	NULL	32	BP	ionotropic glutamate receptor signaling pathway
11	−8.73	NULL	6723	CC	membrane
12	−8.66	NULL	172	BP	homophilic cell adhesion via plasma membrane adhesion molecule
13	−8.52	NULL	62	CC	intermediate filament
14	−8.21	NULL	1084	BP	transport
15	−7.97	NULL	74	CC	neuron projection
16	−7.72	NULL	6248	CC	integral component of membrane
17	−7.63	NULL	109	BP	negative regulation of endopeptidase activity
18	−7.51	NULL	158	MF	microtubule binding
19	−7.27	NULL	333	BP	cell adhesion
20	−7.09	NULL	23	BP	lipoprotein metabolic process