72hpf_pos_gata5

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 2574 (1433 + / 1141 −)

genes with fdr < 0.1 = 1938 (1131 + / 807 −)

genes with fdr < 0.05 = 1516 (918 + / 598 −)

genes with fdr < 0.01 = 968 (615 + / 353 −)

genes in genesets = 21072

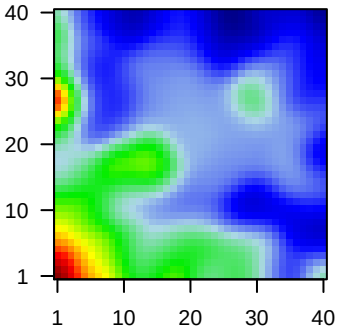
<FC> = 0

<t−score> = 0.01

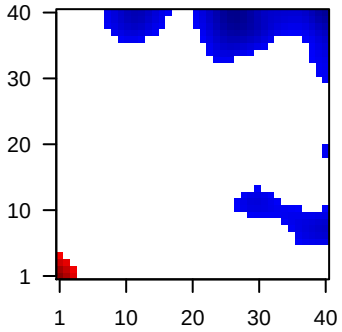
<p−value> = 0.14

<fdr> = 0.86

Portrait



Regulated Metagenes



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ENSDARG00(	−3.95	2e−16	8e−14	39 x 40	myeloid ecotropic viral integration site 3 [Source:ZFIN;Acc:ZD
2	ENSDARG00(	3.81	2e−16	8e−14	1 x 28	zgc:100868 [Source:ZFIN;Acc:ZDB−GENE−040801−33]
3	ENSDARG00(	4.58	2e−16	8e−14	3 x 8	zgc:111983 [Source:ZFIN;Acc:ZDB−GENE−050417−335]
4	ENSDARG00(	5.19	2e−16	8e−14	1 x 40	ATPase, Na+/K+ transporting, alpha 1a polypeptide, tandem
5	ENSDARG00(	−3.92	2e−16	8e−14	40 x 35	E2F transcription factor 7 [Source:ZFIN;Acc:ZDB−GENE−030
6	ENSDARG00(	3.38	2e−16	8e−14	1 x 28	keratin 4 [Source:ZFIN;Acc:ZDB−GENE−000607−83]
7	ENSDARG00(	3.09	2e−16	8e−14	1 x 27	envoplakin a [Source:ZFIN;Acc:ZDB−GENE−030829−19]
8	ENSDARG00(	3.24	2e−16	8e−14	1 x 27	ATP−binding cassette, sub−family B (MDR/TAP), member 5 [S
9	ENSDARG00(	3.7	2e−16	8e−14	1 x 1	Bernardinelli−Seip congenital lipodystrophy 2, like [Source:ZF
10	ENSDARG00(	2.75	2e−16	8e−14	5 x 1	heme oxygenase 1a [Source:ZFIN;Acc:ZDB−GENE−030131-
11	ENSDARG00(	2.8	2e−16	8e−14	1 x 1	solute carrier family 2 (facilitated glucose transporter), membe
12	ENSDARG00(	3.77	2e−16	8e−14	1 x 37	matrilin 1 [Source:ZFIN;Acc:ZDB−GENE−050307−3]
13	ENSDARG00(	4.25	2e−16	8e−14	3 x 11	si:dkey−239b22.1 [Source:ZFIN;Acc:ZDB−GENE−131119−12
14	ENSDARG00(	3.03	2e−16	8e−14	1 x 39	keratin 17 [Source:ZFIN;Acc:ZDB−GENE−060503−86]
15	ENSDARG00(	3.71	2e−16	8e−14	1 x 28	type I cytokeratin, enveloping layer, like [Source:ZFIN;Acc:ZD
16	ENSDARG00(	3.18	2e−16	8e−14	1 x 1	zgc:113142 [Source:ZFIN;Acc:ZDB−GENE−050220−2]
17	ENSDARG00(	2.89	2e−16	8e−14	1 x 11	aerolysin−like protein [Source:ZFIN;Acc:ZDB−GENE−050306
18	ENSDARG00(	2.91	2e−16	8e−14	1 x 1	zgc:113337 [Source:ZFIN;Acc:ZDB−GENE−050306−20]
19	ENSDARG00(	−2.99	2e−16	8e−14	40 x 8	tRNA methyltransferase 6 homolog (S. cerevisiae) [Source:ZF
20	ENSDARG00(	−3.59	2e−16	8e−14	40 x 40	bloody fingers [Source:ZFIN;Acc:ZDB−GENE−050721−1]

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	11.82	NULL	712	BP	oxidation−reduction process
2	10.5	NULL	522	MF	oxidoreductase activity
3	9.4	NULL	62	CC	intermediate filament
4	7.97	NULL	159	MF	structural molecule activity
5	7.42	NULL	96	CC	lysosome
6	7.35	NULL	29	BP	cellular response to xenobiotic stimulus
7	7.18	NULL	13	MF	ATP−activated inward rectifier potassium channel activity
8	6.46	NULL	480	MF	catalytic activity
9	6.44	NULL	414	BP	metabolic process
10	6.23	NULL	194	BP	lipid metabolic process
11	6.02	NULL	1580	CC	cellular_component
12	5.97	NULL	25	MF	glutathione transferase activity
13	5.82	NULL	27	BP	response to bacterium
14	5.54	NULL	1084	BP	transport
15	5.52	NULL	6248	CC	integral component of membrane
16	5.45	NULL	13	BP	iron ion transport
17	5.38	NULL	10	MF	transition metal ion binding
18	5.35	NULL	6723	CC	membrane
19	5.31	NULL	57	MF	flavin adenine dinucleotide binding
20	5.29	NULL	11	MF	ferric iron binding
Underexpressed					
1	−19.37	NULL	2030	MF	nucleic acid binding
2	−10.87	NULL	2716	CC	nucleus
3	−9.58	NULL	1484	MF	DNA binding
4	−9.04	NULL	454	BP	multicellular organism development
5	−8.98	NULL	1239	BP	regulation of transcription, DNA−templated
6	−7.69	NULL	608	MF	RNA binding
7	−7.04	NULL	78	BP	axon guidance
8	−6.66	NULL	34	BP	ephrin receptor signaling pathway
9	−6.6	NULL	537	MF	sequence−specific DNA binding
10	−6.2	NULL	172	BP	homophilic cell adhesion via plasma membrane adhesion molecule
11	−5.83	NULL	175	BP	nervous system development
12	−5.76	NULL	117	BP	Wnt signaling pathway
13	−5.71	NULL	333	BP	cell adhesion
14	−5.25	NULL	72	MF	helicase activity
15	−5.05	NULL	52	BP	blood vessel development
16	−4.96	NULL	210	MF	protein binding
17	−4.94	NULL	78	BP	DNA replication
18	−4.92	NULL	19	MF	ephrin receptor activity
19	−4.86	NULL	32	BP	retinal ganglion cell axon guidance
20	−4.81	NULL	140	CC	nucleolus

p−values