42580K

Global Summary

%DE = 0.07

genes with fdr < 0.2 = 2226 (1241 + / 985 −)

genes with fdr < 0.1 = 1459 (847 + / 612 −)

genes with fdr < 0.05 = 1170 (678 + / 492 −)

genes with fdr < 0.01 = 640 (378 + / 262 −)

genes in genesets = 16360

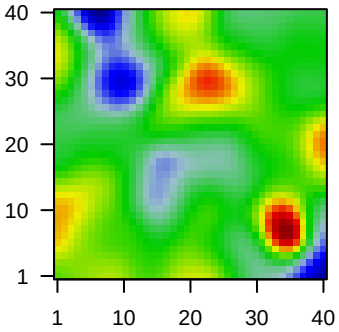
<FC> = 0

<t−score> = 0.12

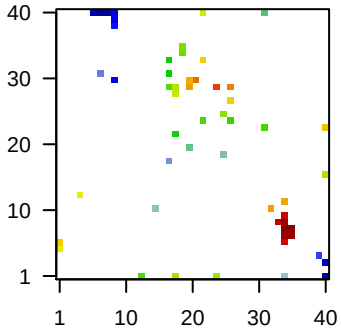
<p−value> = 0.23

<fdr> = 0.93

Portrait



Top 100 DE genes



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1554663_a_a	2.28	2e−16	9e−13	32 x 11	nuclear mitotic apparatus protein 1 [Source:HGNC Symbol;Ac
2	201551_s_at	−1.57	2e−16	9e−13	13 x 1	lysosomal associated membrane protein 1 [Source:HGNC Sy
3	206359_at	1.78	2e−16	9e−13	31 x 40	suppressor of cytokine signaling 3 [Source:HGNC Symbol;Ac
4	207323_s_at	0.88	2e−16	9e−13	35 x 7	myelin basic protein [Source:HGNC Symbol;Acc:HGNC:6925
5	208285_at	1.74	2e−16	9e−13	34 x 9	olfactory receptor family 7 subfamily A member 5 [Source:HG
6	208389_s_at	−0.97	2e−16	9e−13	8 x 40	solute carrier family 1 member 2 [Source:HGNC Symbol;Acc:
7	209072_at	0.79	2e−16	9e−13	35 x 7	myelin basic protein [Source:HGNC Symbol;Acc:HGNC:6925
8	210090_at	1.8	2e−16	9e−13	22 x 40	activity regulated cytoskeleton associated protein [Source:HG
9	216570_x_at	−0.94	2e−16	9e−13	9 x 30	ribosomal protein L29 (RPL29) pseudogene
10	223940_x_at	−0.81	2e−16	9e−13	6 x 40	metastasis associated lung adenocarcinoma transcript 1 [Sou
11	224568_x_at	−0.96	2e−16	9e−13	6 x 40	metastasis associated lung adenocarcinoma transcript 1 [Sou
12	227697_at	1.79	2e−16	9e−13	17 x 33	suppressor of cytokine signaling 3 [Source:HGNC Symbol;Ac
13	239624_at	−1.64	2e−16	9e−13	24 x 1	
14	201531_at	0.91	4e−16	1e−11	20 x 29	ZFP36 ring finger protein [Source:NCBI gene;Acc:7538]
15	242765_at	1.19	7e−16	2e−11	35 x 7	myelin−associated oligodendrocyte basic protein [Source:HG
16	209189_at	0.9	1e−15	2e−11	20 x 30	Fos proto−oncogene, AP−1 transcription factor subunit [Sourc
17	228984_at	1.22	2e−15	7e−11	35 x 7	carnosine synthase 1 [Source:HGNC Symbol;Acc:HGNC:292
18	239575_at	1.61	3e−15	7e−11	35 x 7	oligodendrocytic myelin paranodal and inner loop protein [Sou
19	209392_at	0.8	4e−15	1e−10	35 x 7	ectonucleotide pyrophosphatase/phosphodiesterase 2 [Sourc
20	208451_s_at	0.75	7e−15	2e−10	22 x 33	complement C4B (Chido blood group) [Source:HGNC Symbo

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	9.55	NULL	1086	BP	positive regulation of transcription by RNA polymerase II
2	8.87	NULL	1416	BP	DNA−binding transcription factor activity, RNA polymerase II−speci
3	8.48	NULL	13	BP	central nervous system myelination
4	8.31	NULL	4278	BP	plasma membrane
5	8.28	NULL	613	BP	positive regulation of transcription, DNA−templated
6	8.01	NULL	843	BP	DNA−binding transcription factor activity
7	7.57	NULL	398	BP	positive regulation of gene expression
8	7.43	NULL	289	BP	cytokine−mediated signaling pathway
9	7.38	NULL	783	BP	negative regulation of transcription by RNA polymerase II
10	7.1	NULL	623	BP	protein phosphorylation
11	7.04	NULL	1387	BP	regulation of transcription, DNA−templated
12	6.77	NULL	412	BP	negative regulation of cell population proliferation
13	6.63	NULL	131	BP	positive regulation of angiogenesis
14	6.4	NULL	159	BP	response to lipopolysaccharide
15	6.34	NULL	1500	BP	signal transduction
16	6.32	NULL	1145	BP	regulation of transcription by RNA polymerase II
17	6.25	NULL	541	BP	negative regulation of transcription, DNA−templated
18	5.92	NULL	513	BP	positive regulation of cell population proliferation
19	5.88	NULL	119	BP	cellular response to tumor necrosis factor
20	5.82	NULL	28	BP	cellular response to vascular endothelial growth factor stimulus
Underexpressed					
1	−13.85	NULL	1435	BP	mitochondrion
2	−11.83	NULL	83	BP	mitochondrial translational elongation
3	−11.75	NULL	85	BP	mitochondrial translational termination
4	−11.14	NULL	43	BP	mitochondrial electron transport, NADH to ubiquinone
5	−10.89	NULL	59	BP	mitochondrial respiratory chain complex I assembly
6	−10.46	NULL	276	BP	translation
7	−7.13	NULL	36	BP	mitochondrial translation
8	−6.72	NULL	69	BP	SRP−dependent cotranslational protein targeting to membrane
9	−6.59	NULL	20	BP	mitochondrial ATP synthesis coupled proton transport
10	−6.47	NULL	30	BP	cristae formation
11	−6.46	NULL	25	BP	cytochrome−c oxidase activity
12	−6.05	NULL	78	BP	anaphase−promoting complex−dependent catabolic process
13	−5.91	NULL	48	BP	regulation of cellular amino acid metabolic process
14	−5.9	NULL	17	BP	mitochondrial electron transport, cytochrome c to oxygen
15	−5.73	NULL	13	BP	synaptic transmission, GABAergic
16	−5.69	NULL	78	BP	regulation of mitotic cell cycle phase transition
17	−5.59	NULL	120	BP	translational initiation
18	−5.56	NULL	671	BP	oxidation−reduction process
19	−5.53	NULL	16	BP	ATP synthesis coupled proton transport
20	−5.5	NULL	52	BP	negative regulation of G2/M transition of mitotic cell cycle

p−values