3601P

Global Summary

%DE = 0.06

genes with fdr < 0.2 = 1446 (796 + / 650 −)

genes with fdr < 0.1 = 983 (569 + / 414 −)

genes with fdr < 0.05 = 710 (431 + / 279 −)

genes with fdr < 0.01 = 364 (216 + / 148 −)

genes in genesets = 16360

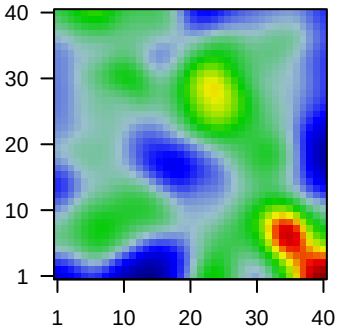
<FC> = 0

<t−score> = 0.13

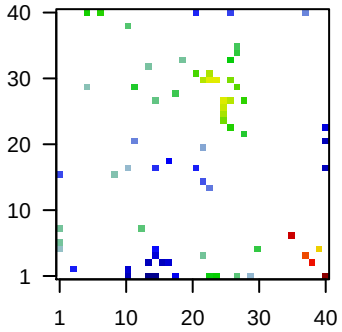
<p−value> = 0.26

<fdr> = 0.94

Portrait



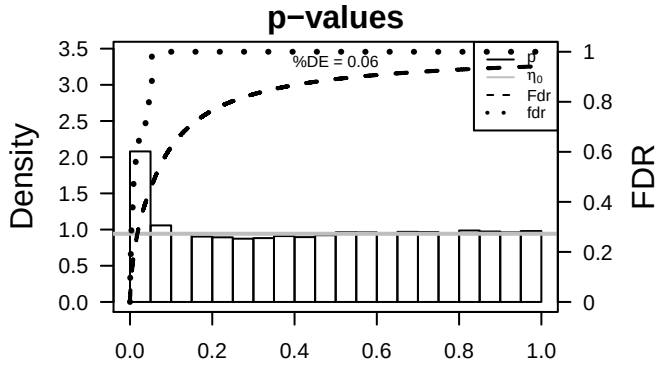
Top 100 DE genes



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	200672_x_at	−1.1	2e−16	1e−12	28 x 22	spectrin beta, non−erythrocytic 1 [Source:HGNC Symbol;Acc
2	201123_s_at	−1.9	2e−16	1e−12	11 x 2	eukaryotic translation initiation factor 5A [Source:HGNC Syml
3	201367_s_at	−1.42	2e−16	1e−12	21 x 40	ZFP36 ring finger protein like 2 [Source:HGNC Symbol;Acc:H
4	206640_x_at	1.97	2e−16	1e−12	26 x 33	G antigen 12J [Source:HGNC Symbol;Acc:HGNC:17778]
5	207086_x_at	1.94	2e−16	1e−12	27 x 35	G antigen 12J [Source:HGNC Symbol;Acc:HGNC:17778]
6	207739_s_at	2.11	2e−16	1e−12	37 x 40	G antigen 12J [Source:HGNC Symbol;Acc:HGNC:17778]
7	210055_at	1.92	2e−16	1e−12	1 x 6	thyroid stimulating hormone receptor [Source:HGNC Symbol;
8	215442_s_at	2.02	2e−16	1e−12	1 x 5	thyroid stimulating hormone receptor [Source:HGNC Symbol;
9	215443_at	2.15	2e−16	1e−12	26 x 30	thyroid stimulating hormone receptor [Source:HGNC Symbol;
10	215606_s_at	−1.54	2e−16	1e−12	11 x 38	ELKS/RAB6−interacting/CAST family member 1 [Source:HGI
11	221974_at	−1	2e−16	1e−12	27 x 29	small nucleolar RNA host gene 14 [Source:HGNC Symbol;Ac
12	227952_at	2.12	2e−16	1e−12	12 x 29	
13	208155_x_at	1.79	9e−16	1e−11	27 x 35	G antigen 12J [Source:HGNC Symbol;Acc:HGNC:17778]
14	207659_s_at	1.1	1e−15	1e−11	35 x 7	myelin−associated oligodendrocyte basic protein [Source:HG
15	203668_at	−1.2	1e−15	1e−11	40 x 21	mannosidase alpha class 2C member 1 [Source:HGNC Symt
16	208235_x_at	1.78	1e−15	1e−11	27 x 34	G antigen 12J [Source:HGNC Symbol;Acc:HGNC:17778]
17	239481_at	−1.36	2e−15	4e−10	24 x 1	family with sequence similarity 133 member A [Source:HGNC
18	201909_at	1.18	1e−14	8e−10	18 x 1	ribosomal protein S4 Y−linked 1 [Source:HGNC Symbol;Acc:I
19	210186_s_at	−1.29	3e−14	2e−09	14 x 1	FKBP prolyl isomerase 1A [Source:HGNC Symbol;Acc:HGNC
20	208334_at	1.67	7e−14	2e−09	23 x 1	N−deacetylase and N−sulfotransferase 4 [Source:HGNC Sym

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	4.93	NULL	27	BP	gamma−aminobutyric acid signaling pathway
2	4.75	NULL	236	BP	chemical synaptic transmission
3	4.63	NULL	13	BP	central nervous system myelination
4	4.29	NULL	657	BP	calcium ion binding
5	4.22	NULL	13	BP	synaptic transmission, GABAergic
6	4.15	NULL	10	BP	negative regulation of ryanodine−sensitive calcium−release channe
7	4.05	NULL	52	BP	myelination
8	3.89	NULL	31	BP	regulation of sensory perception of pain
9	3.75	NULL	19	BP	regulation of cardiac muscle contraction by regulation of the releas
10	3.69	NULL	24	BP	digestion
11	3.69	NULL	16	BP	positive regulation of calcium−mediated signaling
12	3.68	NULL	11	BP	cyclooxygenase pathway
13	3.64	NULL	61	BP	negative regulation of signal transduction
14	3.62	NULL	15	BP	axon development
15	3.61	NULL	12	BP	negative regulation by host of viral transcription
16	3.6	NULL	13	BP	positive regulation of chemokine secretion
17	3.6	NULL	19	BP	regulation of release of sequestered calcium ion into cytosol by sar
18	3.56	NULL	13	BP	protein polymerization
19	3.55	NULL	19	BP	lipid biosynthetic process
20	3.53	NULL	98	BP	cellular calcium ion homeostasis
Underexpressed					
1	−5.83	NULL	43	BP	antigen processing and presentation
2	−5.36	NULL	17	BP	antigen processing and presentation of peptide or polysaccharide a
3	−4.69	NULL	484	BP	cellular response to DNA damage stimulus
4	−4.68	NULL	342	BP	chromatin organization
5	−4.64	NULL	53	BP	IRE1−mediated unfolded protein response
6	−4.51	NULL	459	BP	viral process
7	−4.17	NULL	29	BP	beta−catenin−TCF complex assembly
8	−4.17	NULL	1086	BP	positive regulation of transcription by RNA polymerase II
9	−4.11	NULL	564	BP	immune system process
10	−3.69	NULL	158	BP	DNA replication
11	−3.68	NULL	74	BP	retrograde transport, endosome to Golgi
12	−3.68	NULL	400	BP	chromatin binding
13	−3.62	NULL	366	BP	DNA repair
14	−3.57	NULL	229	BP	mRNA splicing, via spliceosome
15	−3.53	NULL	19	BP	intracellular estrogen receptor signaling pathway
16	−3.45	NULL	231	BP	extracellular matrix organization
17	−3.38	NULL	99	BP	mRNA export from nucleus
18	−3.38	NULL	53	BP	cellular response to amino acid stimulus
19	−3.31	NULL	11	BP	pre−mRNA cleavage required for polyadenylation
20	−3.31	NULL	23	BP	cellular zinc ion homeostasis