4627C

Global Summary

%DE = 0.05

genes with fdr < 0.2 = 1352 (639 + / 713 −)

genes with fdr < 0.1 = 893 (427 + / 466 −)

genes with fdr < 0.05 = 765 (363 + / 402 −)

genes with fdr < 0.01 = 401 (173 + / 228 −)

genes in genesets = 16360

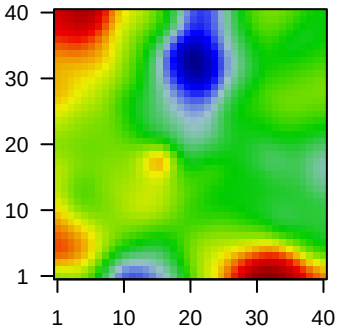
<FC> = 0

<t−score> = 0.09

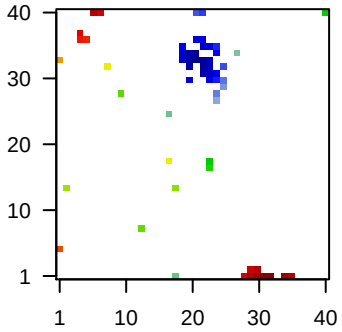
<p−value> = 0.26

<fdr> = 0.95

Portrait



Top 100 DE genes



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1553415_at	2.06	2e−16	7e−13	30 x 1	solute carrier family 17 member 8 [Source:HGNC Symbol;Acc
2	1567628_at	−1.45	2e−16	7e−13	20 x 33	CD74 molecule [Source:HGNC Symbol;Acc:HGNC:1697]
3	201909_at	−1.6	2e−16	7e−13	18 x 1	ribosomal protein S4 Y−linked 1 [Source:HGNC Symbol;Acc:I
4	203228_at	−1.57	2e−16	7e−13	10 x 28	platelet activating factor acetylhydrolase 1b catalytic subunit 3
5	203868_s_at	−1.87	2e−16	7e−13	23 x 31	vascular cell adhesion molecule 1 [Source:HGNC Symbol;Acc
6	204472_at	−1.26	2e−16	7e−13	22 x 31	GTP binding protein overexpressed in skeletal muscle [Sourc
7	208894_at	−1.23	2e−16	7e−13	20 x 33	major histocompatibility complex, class II, DR alpha [Source:H
8	209189_at	−1.15	2e−16	7e−13	20 x 30	Fos proto−oncogene, AP−1 transcription factor subunit [Sourc
9	210982_s_at	−1.23	2e−16	7e−13	20 x 33	major histocompatibility complex, class II, DR alpha [Source:H
10	211965_at	−1.58	2e−16	7e−13	25 x 32	ZFP36 ring finger protein like 1 [Source:HGNC Symbol;Acc:H
11	214218_s_at	2.3	2e−16	7e−13	17 x 18	X inactive specific transcript [Source:HGNC Symbol;Acc:HGN
12	215193_x_at	−1.06	2e−16	7e−13	19 x 33	major histocompatibility complex, class II, DR beta 3 [Source:
13	221728_x_at	2.19	2e−16	7e−13	17 x 18	X inactive specific transcript [Source:HGNC Symbol;Acc:HGN
14	224588_at	2.69	2e−16	7e−13	17 x 18	X inactive specific transcript [Source:HGNC Symbol;Acc:HGN
15	226192_at	−1.86	2e−16	7e−13	23 x 31	androgen receptor [Source:HGNC Symbol;Acc:HGNC:644]
16	227671_at	2.58	2e−16	7e−13	17 x 18	X inactive specific transcript [Source:HGNC Symbol;Acc:HGN
17	230781_at	−1.91	2e−16	7e−13	25 x 29	long intergenic non−protein coding RNA 1088 [Source:HGNC
18	201743_at	−1.16	4e−16	2e−11	21 x 33	CD14 molecule [Source:HGNC Symbol;Acc:HGNC:1628]
19	224590_at	1.96	4e−16	2e−11	17 x 18	X inactive specific transcript [Source:HGNC Symbol;Acc:HGN
20	201028_s_at	−0.92	9e−16	2e−11	23 x 30	CD99 molecule (Xg blood group) [Source:HGNC Symbol;Acc

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	5.66	NULL	394	BP	cell division
2	5.16	NULL	630	BP	cell cycle
3	4.55	NULL	236	BP	chemical synaptic transmission
4	3.94	NULL	505	BP	nervous system development
5	3.87	NULL	16	BP	L−glutamate transmembrane transport
6	3.71	NULL	12	BP	neural precursor cell proliferation
7	3.69	NULL	20	BP	axonal fasciculation
8	3.68	NULL	366	BP	DNA repair
9	3.66	NULL	158	BP	DNA replication
10	3.61	NULL	240	BP	postsynaptic membrane
11	3.52	NULL	27	BP	glutamate secretion
12	3.47	NULL	484	BP	cellular response to DNA damage stimulus
13	3.44	NULL	31	BP	adult behavior
14	3.39	NULL	28	BP	synaptic transmission, glutamatergic
15	3.39	NULL	16	BP	positive regulation of calcium ion−dependent exocytosis
16	3.37	NULL	22	BP	regulation of AMPA receptor activity
17	3.34	NULL	16	BP	dentate gyrus development
18	3.32	NULL	15	BP	isoprenoid biosynthetic process
19	3.27	NULL	13	BP	synaptic transmission, GABAergic
20	3.26	NULL	85	BP	chromosome segregation
Underexpressed					
1	−13.39	NULL	564	BP	immune system process
2	−13.26	NULL	17	BP	antigen processing and presentation of peptide or polysaccharide a
3	−12.91	NULL	388	BP	immune response
4	−12.29	NULL	460	BP	neutrophil degranulation
5	−12.16	NULL	43	BP	antigen processing and presentation
6	−10.61	NULL	7387	BP	membrane
7	−10.08	NULL	364	BP	inflammatory response
8	−9.65	NULL	289	BP	cytokine−mediated signaling pathway
9	−9.46	NULL	417	BP	innate immune response
10	−8.7	NULL	4278	BP	plasma membrane
11	−8.1	NULL	4740	BP	cytosol
12	−7.6	NULL	155	BP	regulation of immune response
13	−7.5	NULL	159	BP	response to lipopolysaccharide
14	−7.37	NULL	6202	BP	cytoplasm
15	−7.31	NULL	59	BP	response to cytokine
16	−7.15	NULL	59	BP	positive regulation of T cell proliferation
17	−7.08	NULL	231	BP	extracellular matrix organization
18	−7.06	NULL	172	BP	positive regulation of I−kappaB kinase/NF−kappaB signaling
19	−7.05	NULL	152	BP	leukocyte migration
20	−6.93	NULL	119	BP	cellular response to tumor necrosis factor

p−values