2213A

Global Summary

%DE = 0.06

genes with fdr < 0.2 = 1514 (950 + / 564 −)

genes with fdr < 0.1 = 979 (646 + / 333 −)

genes with fdr < 0.05 = 737 (495 + / 242 −)

genes with fdr < 0.01 = 370 (254 + / 116 −)

genes in genesets = 16360

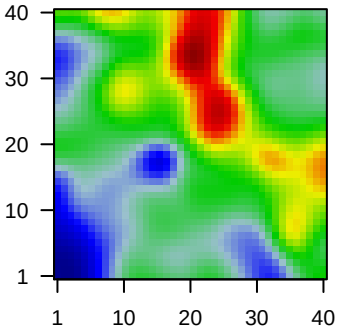
<FC> = 0

<t−score> = 0.11

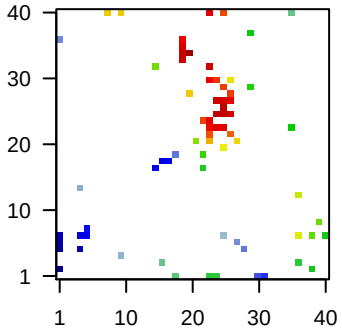
<p−value> = 0.26

<fdr> = 0.94

Portrait



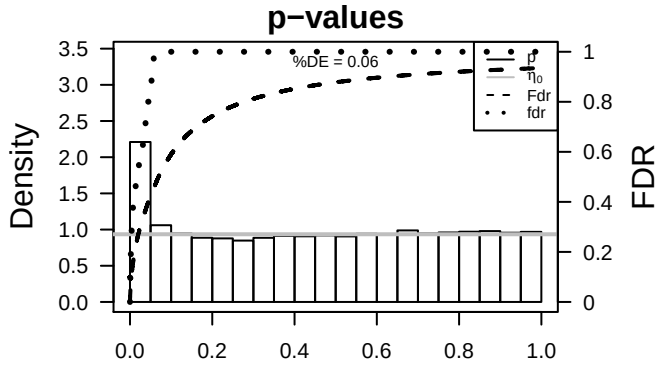
Top 100 DE genes



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	202018_s_at	1.98	2e−16	2e−12	19 x 35	lactotransferrin [Source:HGNC Symbol;Acc:HGNC:6720]
2	205856_at	1.01	2e−16	2e−12	24 x 27	solute carrier family 14 member 1 (Kidd blood group) [Source
3	206785_s_at	−2.08	2e−16	2e−12	1 x 5	killer cell lectin like receptor C2 [Source:HGNC Symbol;Acc:H
4	213592_at	1.05	2e−16	2e−12	19 x 36	apelin receptor [Source:HGNC Symbol;Acc:HGNC:339]
5	213707_s_at	2.08	2e−16	2e−12	28 x 5	distal−less homeobox 5 [Source:HGNC Symbol;Acc:HGNC:2
6	233369_at	−1.48	2e−16	2e−12	1 x 36	
7	243390_at	1.82	7e−16	8e−11	36 x 13	
8	204713_s_at	1.69	2e−15	9e−11	8 x 40	coagulation factor V [Source:HGNC Symbol;Acc:HGNC:3542
9	224588_at	−1.73	4e−15	9e−11	17 x 18	X inactive specific transcript [Source:HGNC Symbol;Acc:HGN
10	244455_at	−1.14	6e−15	1e−10	4 x 7	potassium sodium−activated channel subfamily T member 2 [
11	203290_at	1.75	8e−15	8e−10	19 x 34	major histocompatibility complex, class II, DQ alpha 2 [Source
12	238863_x_at	−1.65	3e−14	8e−10	35 x 40	component of oligomeric golgi complex 8 [Source:HGNC Sym
13	204151_x_at	1.22	4e−14	6e−09	23 x 1	aldo−keto reductase family 1 member C1 [Source:HGNC Syn
14	207695_s_at	1.56	3e−13	6e−09	25 x 26	immunoglobulin superfamily member 1 [Source:HGNC Symbo
15	229778_at	1.17	4e−13	6e−09	25 x 25	spexin hormone [Source:HGNC Symbol;Acc:HGNC:28139]
16	231628_s_at	1.63	4e−13	6e−09	29 x 37	
17	209368_at	1.63	5e−13	2e−08	23 x 24	epoxide hydrolase 2 [Source:HGNC Symbol;Acc:HGNC:3402
18	206899_at	1.1	1e−12	2e−08	36 x 7	neurotensin receptor 2 [Source:HGNC Symbol;Acc:HGNC:80
19	201909_at	1.1	1e−12	2e−08	18 x 1	ribosomal protein S4 Y−linked 1 [Source:HGNC Symbol;Acc:I
20	204803_s_at	1.58	2e−12	2e−08	23 x 22	RRAD, Ras related glycolysis inhibitor and calcium channel re

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all		Geneset
Overexpressed					
1	10.32	NULL	460	BP	neutrophil degranulation
2	10.27	NULL	671	BP	oxidation−reduction process
3	9.97	NULL	7387	BP	membrane
4	9.28	NULL	1435	BP	mitochondrion
5	8.58	NULL	553	BP	oxidoreductase activity
6	8.35	NULL	564	BP	immune system process
7	8.18	NULL	364	BP	inflammatory response
8	8.04	NULL	43	BP	antigen processing and presentation
9	7.84	NULL	17	BP	antigen processing and presentation of peptide or polysaccharide a
10	7.81	NULL	6202	BP	cytoplasm
11	7.52	NULL	4278	BP	plasma membrane
12	7.12	NULL	388	BP	immune response
13	6.37	NULL	4740	BP	cytosol
14	5.77	NULL	67	BP	antigen processing and presentation of exogenous peptide antigen
15	5.75	NULL	500	BP	catalytic activity
16	5.66	NULL	1500	BP	signal transduction
17	5.53	NULL	141	BP	regulation of cell shape
18	5.36	NULL	815	BP	protein homodimerization activity
19	5.26	NULL	83	BP	xenobiotic metabolic process
20	5.12	NULL	521	BP	lipid metabolic process
Underexpressed					
1	−8.65	NULL	1387	BP	regulation of transcription, DNA−templated
2	−8.65	NULL	1416	BP	DNA−binding transcription factor activity, RNA polymerase II−speci
3	−8.49	NULL	1145	BP	regulation of transcription by RNA polymerase II
4	−6.88	NULL	394	BP	cell division
5	−6.5	NULL	630	BP	cell cycle
6	−5.52	NULL	158	BP	DNA replication
7	−5.27	NULL	61	BP	positive regulation of synapse assembly
8	−5	NULL	85	BP	chromosome segregation
9	−4.46	NULL	10	BP	presynaptic membrane assembly
10	−4.19	NULL	366	BP	DNA repair
11	−4.11	NULL	42	BP	mitotic spindle organization
12	−4.09	NULL	16	BP	membrane depolarization during action potential
13	−3.94	NULL	10	BP	negative regulation of excitatory postsynaptic potential
14	−3.66	NULL	164	BP	mitotic cell cycle
15	−3.63	NULL	28	BP	neuronal action potential
16	−3.51	NULL	19	BP	protein localization to centrosome
17	−3.49	NULL	15	BP	neuron cell−cell adhesion
18	−3.48	NULL	110	BP	meiotic cell cycle
19	−3.48	NULL	98	BP	G1/S transition of mitotic cell cycle
20	−3.37	NULL	15	BP	DNA double−strand break processing