

8453E

Global Summary

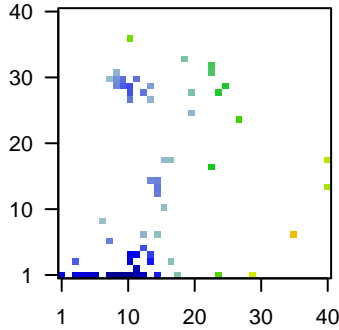
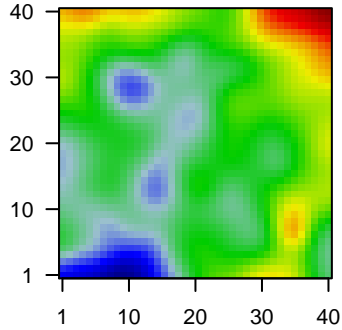
%DE = 0.04
 # genes with fdr < 0.2 = 619 (150 + / 469 -)
 # genes with fdr < 0.1 = 324 (66 + / 258 -)
 # genes with fdr < 0.05 = 230 (42 + / 188 -)
 # genes with fdr < 0.01 = 99 (13 + / 86 -)

 # genes in genesets = 16360

<FC> = 0
 <t-score> = -0.02
 <p-value> = 0.31
 <fdr> = 0.96

Portrait

Top 100 DE genes



Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	1557910_at	-1.37	2e-16	6e-12	11 x 1 heat shock protein 90 alpha family class B member 1 [Source:HGNC Symbol;Acc:HGNC:3350]
2	217294_s_at	-1.74	2e-16	6e-12	12 x 1 enolase 1 [Source:HGNC Symbol;Acc:HGNC:3350]
3	224588_at	2.7	4e-15	2e-09	17 x 18 X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:3350]
4	227671_at	2.65	4e-14	3e-09	17 x 18 X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:3350]
5	216570_x_at	-1.3	1e-13	1e-08	9 x 30 ribosomal protein L29 (RPL29) pseudogene
6	222406_s_at	-1.92	4e-13	1e-08	12 x 4 proline rich nuclear receptor coactivator 2 [Source:HGNC Symbol;Acc:HGNC:3350]
7	201274_at	-1.82	5e-13	1e-08	14 x 29 proteasome subunit alpha 5 [Source:HGNC Symbol;Acc:HGNC:3350]
8	200823_x_at	-1.19	7e-13	5e-08	9 x 30 ribosomal protein L29 [Source:HGNC Symbol;Acc:HGNC:3350]
9	229994_at	-1.63	2e-12	5e-08	12 x 1
10	1558214_s_at	-1.94	2e-12	1e-07	10 x 1 catenin alpha 1 [Source:HGNC Symbol;Acc:HGNC:2509]
11	213175_s_at	-1.28	5e-12	3e-06	13 x 28 small nuclear ribonucleoprotein polypeptides B and B1 [Source:HGNC Symbol;Acc:HGNC:2509]
12	203719_at	-1.49	1e-10	3e-06	13 x 28 ERCC excision repair 1, endonuclease non-catalytic subunit
13	234512_x_at	-1.05	2e-10	3e-06	9 x 31 ribosomal protein L7A (RPL7A) pseudogene
14	221728_x_at	2.18	2e-10	3e-06	17 x 18 X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:3350]
15	214527_s_at	-1.34	2e-10	7e-06	9 x 29 polyglutamine binding protein 1 [Source:HGNC Symbol;Acc:HGNC:3350]
16	214218_s_at	2.17	6e-10	7e-06	17 x 18 X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:3350]
17	216591_s_at	-1.71	7e-10	7e-06	11 x 3 succinate dehydrogenase complex, subunit C, integral membrane protein
18	234942_s_at	-1.56	7e-10	6e-05	15 x 13 deoxynucleotidyltransferase terminal interacting protein 1 [Source:HGNC Symbol;Acc:HGNC:3350]
19	218557_at	-1.62	2e-09	6e-05	15 x 14 nitrilase family member 2 [Source:HGNC Symbol;Acc:HGNC:3350]
20	217234_s_at	-1.34	4e-09	6e-05	12 x 1 ezrin [Source:HGNC Symbol;Acc:HGNC:12691]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	12.26	NULL	4278	BP plasma membrane
2	6.89	NULL	1500	BP signal transduction
3	6.58	NULL	887	BP cell differentiation
4	6.36	NULL	594	BP cell adhesion
5	6.21	NULL	777	BP G protein-coupled receptor signaling pathway
6	5.53	NULL	1080	BP multicellular organism development
7	5.48	NULL	1086	BP positive regulation of transcription by RNA polymerase II
8	4.89	NULL	505	BP nervous system development
9	4.86	NULL	148	BP chemotaxis
10	4.81	NULL	7387	BP membrane
11	4.78	NULL	231	BP extracellular matrix organization
12	4.77	NULL	627	BP ion transport
13	4.63	NULL	418	BP regulation of signaling receptor activity
14	4.42	NULL	30	BP oligodendrocyte differentiation
15	4.41	NULL	657	BP calcium ion binding
16	4.33	NULL	146	BP homophilic cell adhesion via plasma membrane adhesion molecules
17	4.25	NULL	175	BP regulation of cell population proliferation
18	4.18	NULL	20	BP response to corticosterone
19	4.12	NULL	455	BP intracellular signal transduction
20	4.06	NULL	43	BP chemokine activity
<i>Underexpressed</i>				
1	-16.78	NULL	276	BP translation
2	-15.12	NULL	1435	BP mitochondrion
3	-13.03	NULL	4740	BP cytosol
4	-12.58	NULL	85	BP mitochondrial translational termination
5	-12.27	NULL	83	BP mitochondrial translational elongation
6	-12.07	NULL	69	BP SRP-dependent cotranslational protein targeting to membrane
7	-11.63	NULL	120	BP translational initiation
8	-10.99	NULL	98	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
9	-10.91	NULL	90	BP viral transcription
10	-9.24	NULL	78	BP anaphase-promoting complex-dependent catabolic process
11	-9.01	NULL	78	BP regulation of mitotic cell cycle phase transition
12	-9	NULL	6202	BP cytoplasm
13	-8.99	NULL	152	BP rRNA processing
14	-8.7	NULL	279	BP RNA splicing
15	-8.66	NULL	366	BP DNA repair
16	-8.47	NULL	394	BP cell division
17	-8.47	NULL	229	BP mRNA splicing, via spliceosome
18	-8.37	NULL	48	BP regulation of cellular amino acid metabolic process
19	-8.28	NULL	93	BP ribosome biogenesis
20	-8.23	NULL	67	BP antigen processing and presentation of exogenous peptide antigen

p-values

