

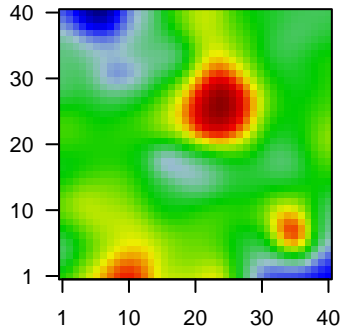
22190L

Global Summary

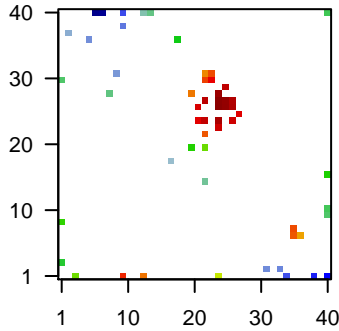
%DE = 0.08
 # genes with fdr < 0.2 = 2802 (1460 + / 1342 -)
 # genes with fdr < 0.1 = 1836 (987 + / 849 -)
 # genes with fdr < 0.05 = 1566 (836 + / 730 -)
 # genes with fdr < 0.01 = 832 (458 + / 374 -)
 # genes in genesets = 16360

<FC> = 0
 <t-score> = 0.08
 <p-value> = 0.22
 <fdr> = 0.92

Portrait



Top 100 DE genes



Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	1558678_s_at	-1.01	2e-16 3e-13	7 x 40 metastasis associated lung adenocarcinoma transcript 1 [Source:HGNC Symbol;Acc:HGNC:1582]
2	1559402_a_at	-1.12	2e-16 3e-13	10 x 40
3	201551_s_at	-1.84	2e-16 3e-13	13 x 1 lysosomal associated membrane protein 1 [Source:HGNC Symbol;Acc:HGNC:1582]
4	203815_at	-1.91	2e-16 3e-13	22 x 15 glutathione S-transferase theta 1 [Source:HGNC Symbol;Acc:HGNC:1582]
5	204103_at	-1.53	2e-16 3e-13	22 x 30 C-C motif chemokine ligand 4 [Source:HGNC Symbol;Acc:HGNC:1582]
6	205114_s_at	-1.8	2e-16 3e-13	23 x 30 C-C motif chemokine ligand 3 [Source:HGNC Symbol;Acc:HGNC:1582]
7	205856_at	1.23	2e-16 3e-13	24 x 27 solute carrier family 14 member 1 (Kidd blood group) [Source:HGNC Symbol;Acc:HGNC:1582]
8	206899_at	1.46	2e-16 3e-13	36 x 7 neurotensin receptor 2 [Source:HGNC Symbol;Acc:HGNC:1582]
9	207542_s_at	1.38	2e-16 3e-13	22 x 22 aquaporin 1 (Colton blood group) [Source:HGNC Symbol;Acc:HGNC:1582]
10	207695_s_at	1.94	2e-16 3e-13	25 x 26 immunoglobulin superfamily member 1 [Source:HGNC Symbol;Acc:HGNC:1582]
11	208711_s_at	-1.38	2e-16 3e-13	6 x 40 cyclin D1 [Source:HGNC Symbol;Acc:HGNC:1582]
12	208712_at	-0.98	2e-16 3e-13	1 x 30 cyclin D1 [Source:HGNC Symbol;Acc:HGNC:1582]
13	208859_s_at	-1.23	2e-16 3e-13	7 x 40 ATRX, chromatin remodeler [Source:HGNC Symbol;Acc:HGNC:1582]
14	209047_at	1.03	2e-16 3e-13	22 x 22 aquaporin 1 (Colton blood group) [Source:HGNC Symbol;Acc:HGNC:1582]
15	209116_x_at	-1.29	2e-16 3e-13	40 x 40 hemoglobin subunit beta [Source:HGNC Symbol;Acc:HGNC:1582]
16	211696_x_at	-1.07	2e-16 3e-13	40 x 40 hemoglobin subunit beta [Source:HGNC Symbol;Acc:HGNC:1582]
17	211699_x_at	-0.86	2e-16 3e-13	40 x 40 hemoglobin subunit alpha 2 [Source:HGNC Symbol;Acc:HGNC:1582]
18	213824_at	-1.45	2e-16 3e-13	1 x 3 oligodendrocyte transcription factor 2 [Source:HGNC Symbol;Acc:HGNC:1582]
19	214464_at	-1.65	2e-16 3e-13	7 x 40 CDC42 binding protein kinase alpha [Source:HGNC Symbol;Acc:HGNC:1582]
20	215123_at	-1.24	2e-16 3e-13	2 x 37 nuclear pore complex interacting protein family member B3 [Source:HGNC Symbol;Acc:HGNC:1582]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	7.72	NULL	521	BP lipid metabolic process
2	7.69	NULL	500	BP catalytic activity
3	6.75	NULL	553	BP oxidoreductase activity
4	5.61	NULL	6202	BP cytoplasm
5	5.5	NULL	1242	BP Golgi apparatus
6	4.64	NULL	25	BP cellular response to unfolded protein
7	4.63	NULL	671	BP oxidation-reduction process
8	4.53	NULL	13	BP central nervous system myelination
9	4.53	NULL	11	BP response to pH
10	4.3	NULL	11	BP amyloid precursor protein metabolic process
11	4.18	NULL	173	BP cilium assembly
12	4.14	NULL	16	BP linoleic acid metabolic process
13	4.13	NULL	216	BP carbohydrate metabolic process
14	4.08	NULL	156	BP fatty acid metabolic process
15	3.95	NULL	4740	BP cytosol
16	3.91	NULL	16	BP negative regulation of intrinsic apoptotic signaling pathway in response to hypoxia
17	3.91	NULL	25	BP positive regulation of blood vessel diameter
18	3.84	NULL	34	BP glycolytic process
19	3.84	NULL	15	BP water transport
20	3.8	NULL	163	BP autophagy
<i>Underexpressed</i>				
1	-9.99	NULL	69	BP SRP-dependent cotranslational protein targeting to membrane
2	-8.93	NULL	276	BP translation
3	-7.99	NULL	120	BP translational initiation
4	-7.69	NULL	90	BP viral transcription
5	-7.67	NULL	98	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
6	-7.37	NULL	236	BP chemical synaptic transmission
7	-6.27	NULL	43	BP mitochondrial electron transport, NADH to ubiquinone
8	-6.14	NULL	17	BP antigen processing and presentation of peptide or polysaccharide antigen fragments
9	-5.87	NULL	574	BP synapse
10	-5.77	NULL	18	BP eosinophil chemotaxis
11	-5.55	NULL	59	BP mitochondrial respiratory chain complex I assembly
12	-5.54	NULL	16	BP positive regulation of calcium-mediated signaling
13	-5.52	NULL	83	BP mitochondrial translational elongation
14	-5.51	NULL	29	BP cytoplasmic translation
15	-5.5	NULL	85	BP mitochondrial translational termination
16	-5.4	NULL	20	BP response to corticosterone
17	-5.23	NULL	84	BP nucleosome assembly
18	-5	NULL	12	BP negative regulation by host of viral transcription
19	-4.93	NULL	36	BP monocyte chemotaxis
20	-4.79	NULL	51	BP regulation of synaptic vesicle exocytosis

p-values

