

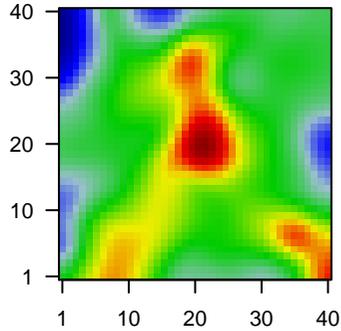
21129M

Global Summary

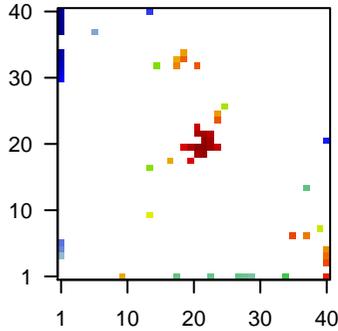
%DE = 0.09
 # genes with fdr < 0.2 = 2953 (1475 + / 1478 -)
 # genes with fdr < 0.1 = 1963 (981 + / 982 -)
 # genes with fdr < 0.05 = 1560 (778 + / 782 -)
 # genes with fdr < 0.01 = 842 (450 + / 392 -)
 # genes in genesets = 16360

<FC> = 0
 <t-score> = -0.08
 <p-value> = 0.21
 <fdr> = 0.91

Portrait



Top 100 DE genes



Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	1568780_at	-1.26	2e-16 4e-13	1 x 40 RNA binding protein, fox-1 homolog (C. elegans) 1 (RBFOX1)
2	201909_at	-2.05	2e-16 4e-13	18 x 1 ribosomal protein S4 Y-linked 1 [Source:HGNC Symbol;Acc:HGNC:2141]
3	202246_s_at	1.12	2e-16 4e-13	14 x 17 cyclin dependent kinase 4 [Source:HGNC Symbol;Acc:HGNC:2141]
4	202376_at	1.31	2e-16 4e-13	19 x 34 serpin family A member 3 [Source:HGNC Symbol;Acc:HGNC:2141]
5	203839_s_at	-1.27	2e-16 4e-13	29 x 1 tyrosine kinase non receptor 2 [Source:HGNC Symbol;Acc:HGNC:2141]
6	204850_s_at	-1.26	2e-16 4e-13	1 x 5 doublecortin [Source:HGNC Symbol;Acc:HGNC:2714]
7	205290_s_at	-1.53	2e-16 4e-13	1 x 5 bone morphogenetic protein 2 [Source:HGNC Symbol;Acc:HGNC:2714]
8	206172_at	2.35	2e-16 4e-13	21 x 19 interleukin 13 receptor subunit alpha 2 [Source:HGNC Symbol;Acc:HGNC:2714]
9	206201_s_at	2.46	2e-16 4e-13	21 x 20 mesenchyme homeobox 2 [Source:HGNC Symbol;Acc:HGNC:2714]
10	206382_s_at	2.31	2e-16 4e-13	40 x 5 brain derived neurotrophic factor [Source:HGNC Symbol;Acc:HGNC:2714]
11	206803_at	3.07	2e-16 4e-13	40 x 1 prodynorphin [Source:HGNC Symbol;Acc:HGNC:8820]
12	207542_s_at	1.52	2e-16 4e-13	22 x 22 aquaporin 1 (Colton blood group) [Source:HGNC Symbol;Acc:HGNC:1932]
13	209047_at	1.09	2e-16 4e-13	22 x 22 aquaporin 1 (Colton blood group) [Source:HGNC Symbol;Acc:HGNC:1932]
14	209395_at	1.4	2e-16 4e-13	21 x 19 chitinase 3 like 1 [Source:HGNC Symbol;Acc:HGNC:1932]
15	210135_s_at	2.53	2e-16 4e-13	20 x 20 short stature homeobox 2 [Source:HGNC Symbol;Acc:HGNC:16953]
16	210809_s_at	2.36	2e-16 4e-13	20 x 18 periostin [Source:HGNC Symbol;Acc:HGNC:16953]
17	213920_at	-1.92	2e-16 4e-13	34 x 1 cut like homeobox 2 [Source:HGNC Symbol;Acc:HGNC:1934]
18	219537_x_at	-1.53	2e-16 4e-13	1 x 5 delta like canonical Notch ligand 3 [Source:NCBI gene;Acc:16360]
19	219837_s_at	2.29	2e-16 4e-13	21 x 32 cytokine like 1 [Source:HGNC Symbol;Acc:HGNC:24435]
20	219867_at	2.36	2e-16 4e-13	20 x 20 chondrolectin [Source:HGNC Symbol;Acc:HGNC:17807]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	9.67	NULL	460	BP neutrophil degranulation
2	8.17	NULL	500	BP catalytic activity
3	8.17	NULL	17	BP antigen processing and presentation of peptide or polysaccharide antigen fragments
4	7.58	NULL	43	BP antigen processing and presentation
5	7.54	NULL	553	BP oxidoreductase activity
6	7.49	NULL	671	BP oxidation-reduction process
7	7.38	NULL	7387	BP membrane
8	6.96	NULL	1435	BP mitochondrion
9	6.29	NULL	388	BP immune response
10	5.64	NULL	180	BP cell projection organization
11	5.47	NULL	521	BP lipid metabolic process
12	5.44	NULL	364	BP inflammatory response
13	5.34	NULL	156	BP fatty acid metabolic process
14	5.29	NULL	21	BP motile cilium assembly
15	5.29	NULL	564	BP immune system process
16	5.27	NULL	46	BP fatty acid beta-oxidation
17	5.11	NULL	75	BP electron transfer activity
18	5.06	NULL	62	BP protein targeting to peroxisome
19	4.88	NULL	32	BP cilium movement
20	4.88	NULL	13	BP synaptic transmission, GABAergic
<i>Underexpressed</i>				
1	-7.66	NULL	342	BP chromatin organization
2	-7.09	NULL	98	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
3	-6.93	NULL	69	BP SRP-dependent cotranslational protein targeting to membrane
4	-6.92	NULL	783	BP negative regulation of transcription by RNA polymerase II
5	-6.33	NULL	400	BP chromatin binding
6	-6.14	NULL	541	BP negative regulation of transcription, DNA-templated
7	-6.02	NULL	90	BP viral transcription
8	-5.99	NULL	120	BP translational initiation
9	-5.8	NULL	613	BP positive regulation of transcription, DNA-templated
10	-5.61	NULL	1086	BP positive regulation of transcription by RNA polymerase II
11	-5.46	NULL	1416	BP DNA-binding transcription factor activity, RNA polymerase II-specific
12	-4.5	NULL	843	BP DNA-binding transcription factor activity
13	-4.26	NULL	25	BP cardiac muscle cell differentiation
14	-4.24	NULL	32	BP positive regulation of BMP signaling pathway
15	-4.15	NULL	11	BP positive regulation of endothelial cell differentiation
16	-3.99	NULL	1145	BP regulation of transcription by RNA polymerase II
17	-3.99	NULL	117	BP negative regulation of cell migration
18	-3.97	NULL	102	BP chromatin remodeling
19	-3.83	NULL	19	BP nucleosome disassembly
20	-3.82	NULL	1387	BP regulation of transcription, DNA-templated

p-values

