

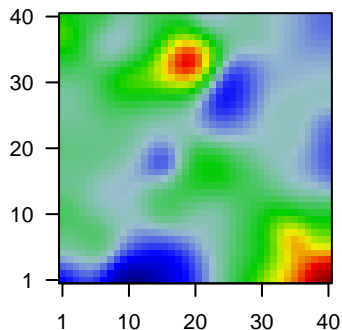
3114H

Global Summary

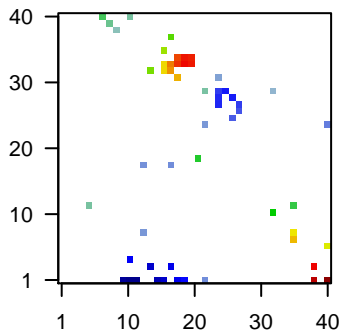
%DE = 0.07
 # genes with fdr < 0.2 = 2324 (1448 + / 876 -)
 # genes with fdr < 0.1 = 1730 (1111 + / 619 -)
 # genes with fdr < 0.05 = 1222 (789 + / 433 -)
 # genes with fdr < 0.01 = 767 (507 + / 260 -)
 # genes in genesets = 16360

<FC> = 0
 <t-score> = 0.1
 <p-value> = 0.23
 <fdr> = 0.93

Portrait



Top 100 DE genes



Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	1405_i_at	2	2e-16 5e-13	18 x 33 C-C motif chemokine ligand 5 [Source:HGNC Symbol;Acc:HGNC:1405]
2	1554663_a_at	1.93	2e-16 5e-13	32 x 11 nuclear mitotic apparatus protein 1 [Source:HGNC Symbol;Acc:HGNC:1554663]
3	202203_s_at	-1.79	2e-16 5e-13	13 x 8 autocrine motility factor receptor [Source:HGNC Symbol;Acc:HGNC:202203]
4	202376_at	1.12	2e-16 5e-13	19 x 34 serpin family A member 3 [Source:HGNC Symbol;Acc:HGNC:202376]
5	203290_at	1.93	2e-16 5e-13	19 x 34 major histocompatibility complex, class II, DQ alpha 2 [Source:HGNC Symbol;Acc:HGNC:203290]
6	203915_at	1.81	2e-16 5e-13	17 x 33 C-X-C motif chemokine ligand 9 [Source:HGNC Symbol;Acc:HGNC:203915]
7	204655_at	2.06	2e-16 5e-13	19 x 34 C-C motif chemokine ligand 5 [Source:HGNC Symbol;Acc:HGNC:204655]
8	205856_at	-1.28	2e-16 5e-13	24 x 27 solute carrier family 14 member 1 (Kidd blood group) [Source:HGNC Symbol;Acc:HGNC:205856]
9	206803_at	1.76	2e-16 5e-13	40 x 1 prodynorphin [Source:HGNC Symbol;Acc:HGNC:206803]
10	209101_at	-1.78	2e-16 5e-13	11 x 4 cellular communication network factor 2 [Source:HGNC Symbol;Acc:HGNC:209101]
11	209138_x_at	1.76	2e-16 5e-13	18 x 33 immunoglobulin lambda constant 2 [Source:HGNC Symbol;Acc:HGNC:209138]
12	209395_at	1.7	2e-16 5e-13	21 x 19 chitinase 3 like 1 [Source:HGNC Symbol;Acc:HGNC:1932]
13	209396_s_at	1.89	2e-16 5e-13	21 x 19 chitinase 3 like 1 [Source:HGNC Symbol;Acc:HGNC:1932]
14	210756_s_at	-1.27	2e-16 5e-13	14 x 3 notch 2 [Source:HGNC Symbol;Acc:HGNC:7882]
15	210944_s_at	0.95	2e-16 5e-13	35 x 8 novel transcript
16	211990_at	0.85	2e-16 5e-13	19 x 34 major histocompatibility complex, class II, DP alpha 1 [Source:HGNC Symbol;Acc:HGNC:211990]
17	217022_s_at	1.91	2e-16 5e-13	18 x 33 immunoglobulin heavy constant alpha 2 (A2m marker) [Source:HGNC Symbol;Acc:HGNC:217022]
18	224522_s_at	-1.88	2e-16 5e-13	27 x 27 dephospho-CoA kinase domain containing [Source:HGNC Symbol;Acc:HGNC:224522]
19	224588_at	-1.73	2e-16 5e-13	17 x 18 X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:224588]
20	227722_at	-1.34	2e-16 5e-13	19 x 1 ribosomal protein S23 [Source:HGNC Symbol;Acc:HGNC:10722]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	17	NULL	17	BP antigen processing and presentation of peptide or polysaccharide antigen fragments
2	16.5	NULL	388	BP immune response
3	15.28	NULL	564	BP immune system process
4	14.56	NULL	43	BP antigen processing and presentation
5	11.12	NULL	7387	BP membrane
6	11.01	NULL	155	BP regulation of immune response
7	10.46	NULL	364	BP inflammatory response
8	10.08	NULL	4278	BP plasma membrane
9	8.79	NULL	417	BP innate immune response
10	8.54	NULL	160	BP T cell receptor signaling pathway
11	8.24	NULL	236	BP chemical synaptic transmission
12	7.94	NULL	65	BP chemokine-mediated signaling pathway
13	7.45	NULL	43	BP chemokine activity
14	7.4	NULL	23	BP positive regulation of T cell activation
15	7.35	NULL	460	BP neutrophil degranulation
16	7.23	NULL	59	BP positive regulation of T cell proliferation
17	7.08	NULL	18	BP positive regulation of monocyte chemotaxis
18	6.94	NULL	17	BP positive regulation of T cell migration
19	6.71	NULL	148	BP chemotaxis
20	6.69	NULL	67	BP antigen processing and presentation of exogenous peptide antigen fragments
<i>Underexpressed</i>				
1	-11.59	NULL	1416	BP DNA-binding transcription factor activity, RNA polymerase II-specific
2	-10.53	NULL	1387	BP regulation of transcription, DNA-templated
3	-10.37	NULL	1145	BP regulation of transcription by RNA polymerase II
4	-8.98	NULL	843	BP DNA-binding transcription factor activity
5	-8.34	NULL	1086	BP positive regulation of transcription by RNA polymerase II
6	-7.9	NULL	400	BP chromatin binding
7	-7.8	NULL	630	BP cell cycle
8	-6.77	NULL	541	BP negative regulation of transcription, DNA-templated
9	-6.73	NULL	158	BP DNA replication
10	-6.6	NULL	783	BP negative regulation of transcription by RNA polymerase II
11	-6.35	NULL	342	BP chromatin organization
12	-5.89	NULL	613	BP positive regulation of transcription, DNA-templated
13	-5.88	NULL	11	BP chondrocyte proliferation
14	-5.85	NULL	394	BP cell division
15	-5.65	NULL	484	BP cellular response to DNA damage stimulus
16	-5.46	NULL	130	BP regulation of signal transduction by p53 class mediator
17	-5.34	NULL	366	BP DNA repair
18	-5.18	NULL	129	BP rhythmic process
19	-5.07	NULL	95	BP anterior/posterior pattern specification
20	-4.97	NULL	21	BP tissue homeostasis

p-values

