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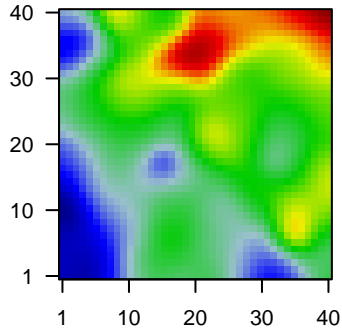
Global Summary

%DE = 0.04
 # genes with fdr < 0.2 = 727 (263 + / 464 -)
 # genes with fdr < 0.1 = 480 (173 + / 307 -)
 # genes with fdr < 0.05 = 263 (103 + / 160 -)
 # genes with fdr < 0.01 = 122 (49 + / 73 -)

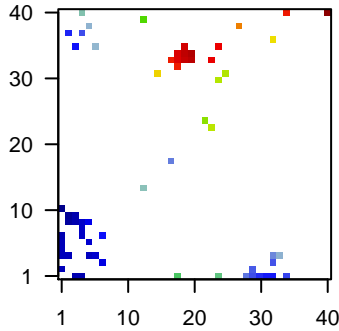
 # genes in genesets = 16360

<FC> = 0
 <t-score> = -0.03
 <p-value> = 0.3
 <fdr> = 0.96

Portrait



Top 100 DE genes



Global Genelist

Rank	ID	log(FC)	fdr p-value	Description
1	201295_s_at	-1.47	2e-16 1e-11 4 x 1	WD repeat and SOCS box containing 1 [Source:HGNC Symb
2	205374_at	2.72	5e-15 1e-09 19 x 33	sarcosin [Source:HGNC Symbol;Acc:HGNC:11089]
3	232028_at	-1.7	3e-14 1e-09 6 x 35	zinc finger protein 678 [Source:HGNC Symbol;Acc:HGNC:28
4	205523_at	-1.86	4e-14 4e-09 29 x 1	hyaluronan and proteoglycan link protein 1 [Source:HGNC Sy
5	244455_at	-1.66	1e-13 1e-07 4 x 7	potassium sodium-activated channel subfamily T member 2 [
6	234103_at	-1.72	5e-12 1e-07 5 x 38	
7	204850_s_at	-1.23	6e-12 1e-07 1 x 5	doublecortin [Source:HGNC Symbol;Acc:HGNC:2714]
8	206501_x_at	-1.33	7e-12 5e-07 1 x 2	ETS variant 1 [Source:HGNC Symbol;Acc:HGNC:3490]
9	211430_s_at	2.32	2e-11 5e-07 18 x 34	immunoglobulin heavy constant gamma 2 (G2m marker) [Sou
10	220405_at	-1.42	3e-11 5e-07 31 x 1	syntrophin gamma 1 [Source:HGNC Symbol;Acc:HGNC:1374
11	217022_s_at	2.29	4e-11 5e-07 18 x 33	immunoglobulin heavy constant alpha 2 (A2m marker) [Sourc
12	214677_x_at	2.29	4e-11 1e-06 18 x 33	immunoglobulin lambda constant 2 [Source:HGNC Symbol;Ac
13	202018_s_at	2.27	6e-11 1e-06 19 x 35	lactotransferrin [Source:HGNC Symbol;Acc:HGNC:6720]
14	215164_at	-1.62	8e-11 5e-06 2 x 37	
15	209138_x_at	2.19	3e-10 5e-06 18 x 33	immunoglobulin lambda constant 2 [Source:HGNC Symbol;Ac
16	203290_at	2.17	4e-10 5e-06 19 x 34	major histocompatibility complex, class II, DQ alpha 2 [Sourc
17	215121_x_at	2.14	6e-10 5e-06 18 x 33	immunoglobulin lambda constant 2 [Source:HGNC Symbol;Ac
18	228030_at	-1.07	6e-10 5e-06 4 x 9	
19	231380_at	2.14	7e-10 5e-06 22 x 24	chromosome 8 open reading frame 34 [Source:HGNC Symbc
20	224588_at	2.1	7e-10 5e-06 17 x 18	X inactive specific transcript [Source:HGNC Symbol;Acc:HGN

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	13.18	NULL	388	BP immune response
2	12.9	NULL	17	BP antigen processing and presentation of peptide or polysaccharide
3	12.75	NULL	564	BP immune system process
4	11.53	NULL	43	BP antigen processing and presentation
5	8.74	NULL	64	BP complement activation, classical pathway
6	8.72	NULL	222	BP adaptive immune response
7	8.7	NULL	460	BP neutrophil degranulation
8	8.55	NULL	364	BP inflammatory response
9	8.5	NULL	155	BP regulation of immune response
10	8.17	NULL	417	BP innate immune response
11	8.13	NULL	47	BP complement activation
12	7.67	NULL	152	BP leukocyte migration
13	7.51	NULL	64	BP regulation of complement activation
14	7.34	NULL	4278	BP plasma membrane
15	7.34	NULL	56	BP B cell receptor signaling pathway
16	7.27	NULL	89	BP Fc-gamma receptor signaling pathway involved in phagocytosis
17	6.9	NULL	148	BP chemotaxis
18	6.48	NULL	47	BP phagocytosis, engulfment
19	6.25	NULL	88	BP cellular response to interferon-gamma
20	6.09	NULL	65	BP chemokine-mediated signaling pathway
<i>Underexpressed</i>				
1	-10.14	NULL	1145	BP regulation of transcription by RNA polymerase II
2	-8.17	NULL	1416	BP DNA-binding transcription factor activity, RNA polymerase II-speci
3	-7.38	NULL	1387	BP regulation of transcription, DNA-templated
4	-7	NULL	630	BP cell cycle
5	-6.68	NULL	394	BP cell division
6	-6.5	NULL	366	BP DNA repair
7	-5.82	NULL	158	BP DNA replication
8	-5.33	NULL	484	BP cellular response to DNA damage stimulus
9	-4.7	NULL	358	BP mRNA processing
10	-4.61	NULL	31	BP mitotic sister chromatid segregation
11	-4.34	NULL	267	BP ubiquitin-protein transferase activity
12	-4.02	NULL	215	BP ubiquitin protein ligase activity
13	-3.95	NULL	164	BP mitotic cell cycle
14	-3.89	NULL	85	BP chromosome segregation
15	-3.88	NULL	22	BP mitotic spindle assembly checkpoint
16	-3.61	NULL	98	BP G1/S transition of mitotic cell cycle
17	-3.56	NULL	545	BP protein ubiquitination
18	-3.51	NULL	17	BP DNA replication origin binding
19	-3.5	NULL	279	BP RNA splicing
20	-3.47	NULL	37	BP negative regulation of G0 to G1 transition

p-values

