

4462H

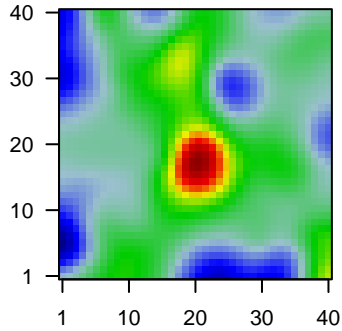
Global Summary

%DE = 0.09
 # genes with fdr < 0.2 = 3093 (1694 + / 1399 -)
 # genes with fdr < 0.1 = 2392 (1324 + / 1068 -)
 # genes with fdr < 0.05 = 1933 (1085 + / 848 -)
 # genes with fdr < 0.01 = 1280 (712 + / 568 -)

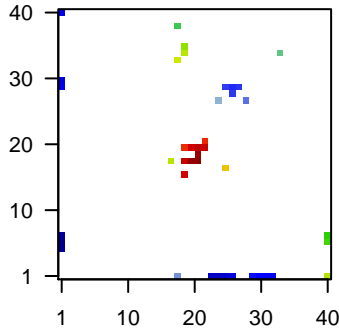
 # genes in genesets = 16360

<FC> = 0
 <t-score> = -0.02
 <p-value> = 0.19
 <fdr> = 0.91

Portrait



Top 100 DE genes



Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	1554281_at	-1.96	2e-16	1e-13	1 x 5 novel transcript
2	1554474_a_a	1.94	2e-16	1e-13	22 x 20 monooxygenase DBH like 1 [Source:HGNC Symbol;Acc:HGNC:16953]
3	1555778_a_a	2.91	2e-16	1e-13	20 x 18 periostin [Source:HGNC Symbol;Acc:HGNC:16953]
4	1568780_at	-1.68	2e-16	1e-13	1 x 40 RNA binding protein, fox-1 homolog (C. elegans) 1 (RBFOX1)
5	201852_x_at	2.04	2e-16	1e-13	19 x 16 collagen type III alpha 1 chain [Source:HGNC Symbol;Acc:HGNC:16953]
6	201909_at	-1.62	2e-16	1e-13	18 x 1 ribosomal protein S4 Y-linked 1 [Source:HGNC Symbol;Acc:HGNC:16953]
7	202376_at	1.28	2e-16	1e-13	19 x 34 serpin family A member 3 [Source:HGNC Symbol;Acc:HGNC:16953]
8	203131_at	-0.91	2e-16	1e-13	24 x 1 platelet derived growth factor receptor alpha [Source:HGNC Symbol;Acc:HGNC:16953]
9	204529_s_at	-0.97	2e-16	1e-13	23 x 1 thymocyte selection associated high mobility group box [Source:HGNC Symbol;Acc:HGNC:16953]
10	204850_s_at	-1.91	2e-16	1e-13	1 x 5 doublecortin [Source:HGNC Symbol;Acc:HGNC:2714]
11	204851_s_at	-1.7	2e-16	1e-13	1 x 5 doublecortin [Source:HGNC Symbol;Acc:HGNC:2714]
12	204913_s_at	-0.98	2e-16	1e-13	1 x 40 SRY-box 11 [Source:HGNC Symbol;Acc:HGNC:11191]
13	204914_s_at	-1.26	2e-16	1e-13	1 x 7 SRY-box 11 [Source:HGNC Symbol;Acc:HGNC:11191]
14	204915_s_at	-1.32	2e-16	1e-13	1 x 6 SRY-box 11 [Source:HGNC Symbol;Acc:HGNC:11191]
15	205000_at	-1.85	2e-16	1e-13	18 x 1 DEAD-box helicase 3 Y-linked [Source:HGNC Symbol;Acc:HGNC:11191]
16	205289_at	-1.86	2e-16	1e-13	1 x 5 bone morphogenetic protein 2 [Source:HGNC Symbol;Acc:HGNC:11191]
17	205290_s_at	-2.34	2e-16	1e-13	1 x 5 bone morphogenetic protein 2 [Source:HGNC Symbol;Acc:HGNC:11191]
18	205453_at	1.97	2e-16	1e-13	18 x 33 homeobox B2 [Source:HGNC Symbol;Acc:HGNC:5113]
19	205493_s_at	-1.28	2e-16	1e-13	25 x 1 dihydropyrimidinase like 4 [Source:HGNC Symbol;Acc:HGNC:5113]
20	205575_at	-1.11	2e-16	1e-13	1 x 30 complement C1q like 1 [Source:HGNC Symbol;Acc:HGNC:2714]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	13.74	NULL	7387	BP membrane
2	11.9	NULL	254	BP angiogenesis
3	11.18	NULL	231	BP extracellular matrix organization
4	10.26	NULL	4278	BP plasma membrane
5	8.61	NULL	460	BP neutrophil degranulation
6	8.37	NULL	1435	BP mitochondrion
7	8.1	NULL	44	BP collagen fibril organization
8	7.33	NULL	118	BP platelet degranulation
9	7.24	NULL	1242	BP Golgi apparatus
10	6.85	NULL	594	BP cell adhesion
11	6.73	NULL	131	BP positive regulation of angiogenesis
12	6.49	NULL	671	BP oxidation-reduction process
13	6.23	NULL	141	BP regulation of cell shape
14	6.15	NULL	152	BP leukocyte migration
15	6.15	NULL	43	BP antigen processing and presentation
16	6.07	NULL	84	BP negative regulation of angiogenesis
17	6.01	NULL	17	BP antigen processing and presentation of peptide or polysaccharide
18	5.96	NULL	13	BP supramolecular fiber organization
19	5.9	NULL	500	BP catalytic activity
20	5.79	NULL	12	BP keratan sulfate catabolic process
<i>Underexpressed</i>				
1	-6.51	NULL	1416	BP DNA-binding transcription factor activity, RNA polymerase II-specific
2	-6.36	NULL	342	BP chromatin organization
3	-5.32	NULL	1145	BP regulation of transcription by RNA polymerase II
4	-5.13	NULL	1387	BP regulation of transcription, DNA-templated
5	-4.74	NULL	783	BP negative regulation of transcription by RNA polymerase II
6	-4.62	NULL	15	BP positive regulation of cartilage development
7	-4.27	NULL	55	BP somitogenesis
8	-4.18	NULL	400	BP chromatin binding
9	-4.14	NULL	14	BP positive regulation of cell adhesion mediated by integrin
10	-4.03	NULL	16	BP positive regulation of ossification
11	-4.01	NULL	358	BP mRNA processing
12	-3.88	NULL	11	BP neural tube formation
13	-3.77	NULL	30	BP oligodendrocyte differentiation
14	-3.68	NULL	229	BP mRNA splicing, via spliceosome
15	-3.64	NULL	17	BP urogenital system development
16	-3.59	NULL	61	BP regulation of MAPK cascade
17	-3.57	NULL	82	BP BMP signaling pathway
18	-3.52	NULL	10	BP positive regulation of osteoblast proliferation
19	-3.51	NULL	16	BP sympathetic nervous system development
20	-3.51	NULL	12	BP establishment of epithelial cell polarity

p-values

