

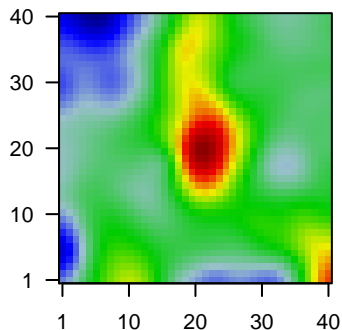
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Global Summary

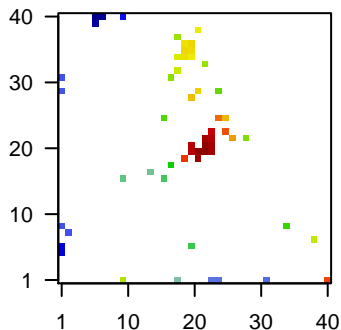
%DE = 0.1
 # genes with fdr < 0.2 = 3383 (1985 + / 1398 -)
 # genes with fdr < 0.1 = 2881 (1719 + / 1162 -)
 # genes with fdr < 0.05 = 2239 (1372 + / 867 -)
 # genes with fdr < 0.01 = 1433 (894 + / 539 -)
 # genes in genesets = 16360

<FC> = 0
 <t-score> = -0.04
 <p-value> = 0.17
 <fdr> = 0.9

Portrait



Top 100 DE genes



Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	1554474_a_a	2.06	2e-16	1e-13	22 x 20 monooxygenase DBH like 1 [Source:HGNC Symbol;Acc:HGNC:1554474]
2	1559402_a_a	-1.07	2e-16	1e-13	10 x 40
3	1569871_at	-0.99	2e-16	1e-13	1 x 6 novel transcript
4	201909_at	-1.79	2e-16	1e-13	18 x 1 ribosomal protein S4 Y-linked 1 [Source:HGNC Symbol;Acc:HGNC:201909]
5	202018_s_at	2.16	2e-16	1e-13	19 x 35 lactotransferrin [Source:HGNC Symbol;Acc:HGNC:6720]
6	202133_at	1.01	2e-16	1e-13	20 x 28 WW domain containing transcription regulator 1 [Source:HGNC Symbol;Acc:HGNC:202133]
7	202376_at	1.5	2e-16	1e-13	19 x 34 serpin family A member 3 [Source:HGNC Symbol;Acc:HGNC:202376]
8	203397_s_at	2	2e-16	1e-13	21 x 20 polypeptide N-acetylgalactosaminyltransferase 3 [Source:HGNC Symbol;Acc:HGNC:203397]
9	203484_at	1.09	2e-16	1e-13	19 x 19 Sec61 translocon gamma subunit [Source:HGNC Symbol;Acc:HGNC:203484]
10	204041_at	1.48	2e-16	1e-13	23 x 20 monoamine oxidase B [Source:HGNC Symbol;Acc:HGNC:6820]
11	204362_at	1.22	2e-16	1e-13	21 x 29 src kinase associated phosphoprotein 2 [Source:HGNC Symbol;Acc:HGNC:204362]
12	205577_at	2.07	2e-16	1e-13	38 x 7 glycogen phosphorylase, muscle associated [Source:HGNC Symbol;Acc:HGNC:205577]
13	205736_at	2.25	2e-16	1e-13	22 x 22 phosphoglycerate mutase 2 [Source:HGNC Symbol;Acc:HGNC:205736]
14	205901_at	2.32	2e-16	1e-13	40 x 1 prepronociceptin [Source:HGNC Symbol;Acc:HGNC:9163]
15	205967_at	-1.82	2e-16	1e-13	6 x 40 histone cluster 1 H4 family member c [Source:HGNC Symbol;Acc:HGNC:205967]
16	206067_s_at	2.36	2e-16	1e-13	20 x 21 Wilms tumor 1 [Source:HGNC Symbol;Acc:HGNC:12796]
17	206514_s_at	2.03	2e-16	1e-13	28 x 22 cytochrome P450 family 4 subfamily F member 2 [Source:HGNC Symbol;Acc:HGNC:206514]
18	206515_at	2.74	2e-16	1e-13	23 x 23 cytochrome P450 family 4 subfamily F member 3 [Source:HGNC Symbol;Acc:HGNC:206515]
19	206785_s_at	-2.03	2e-16	1e-13	1 x 5 killer cell lectin like receptor C2 [Source:HGNC Symbol;Acc:HGNC:206785]
20	206803_at	2.42	2e-16	1e-13	40 x 1 prodynorphin [Source:HGNC Symbol;Acc:HGNC:8820]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	15.11	NULL	4278	BP plasma membrane
2	14.3	NULL	7387	BP membrane
3	11.6	NULL	231	BP extracellular matrix organization
4	9.96	NULL	131	BP positive regulation of angiogenesis
5	9.21	NULL	254	BP angiogenesis
6	8.61	NULL	1242	BP Golgi apparatus
7	7.63	NULL	1500	BP signal transduction
8	7.6	NULL	94	BP cell-matrix adhesion
9	7.4	NULL	17	BP antigen processing and presentation of peptide or polysaccharide antigens on MHC class II
10	7.19	NULL	594	BP cell adhesion
11	7.13	NULL	159	BP response to lipopolysaccharide
12	6.82	NULL	6202	BP cytoplasm
13	6.67	NULL	141	BP regulation of cell shape
14	6.49	NULL	615	BP transmembrane transport
15	6.45	NULL	657	BP calcium ion binding
16	6.41	NULL	521	BP lipid metabolic process
17	6.29	NULL	289	BP cytokine-mediated signaling pathway
18	6.29	NULL	43	BP antigen processing and presentation
19	6.26	NULL	44	BP collagen fibril organization
20	6.25	NULL	460	BP neutrophil degranulation
<i>Underexpressed</i>				
1	-11.76	NULL	69	BP SRP-dependent cotranslational protein targeting to membrane
2	-11.33	NULL	120	BP translational initiation
3	-10.82	NULL	90	BP viral transcription
4	-10.54	NULL	276	BP translation
5	-10.07	NULL	98	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
6	-8.11	NULL	152	BP rRNA processing
7	-6.33	NULL	29	BP cytoplasmic translation
8	-6.19	NULL	342	BP chromatin organization
9	-5.92	NULL	358	BP mRNA processing
10	-5.7	NULL	630	BP cell cycle
11	-5.58	NULL	394	BP cell division
12	-5.49	NULL	279	BP RNA splicing
13	-5.47	NULL	84	BP nucleosome assembly
14	-5.38	NULL	366	BP DNA repair
15	-5.36	NULL	85	BP mitochondrial translational termination
16	-5.36	NULL	229	BP mRNA splicing, via spliceosome
17	-5.22	NULL	93	BP ribosome biogenesis
18	-5.12	NULL	83	BP mitochondrial translational elongation
19	-4.81	NULL	400	BP chromatin binding
20	-4.44	NULL	484	BP cellular response to DNA damage stimulus

p-values

