

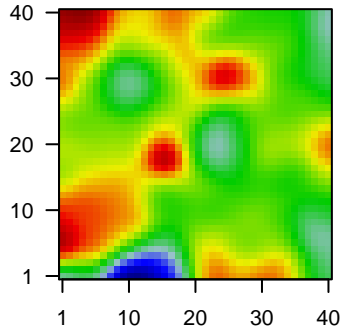
2730F

Global Summary

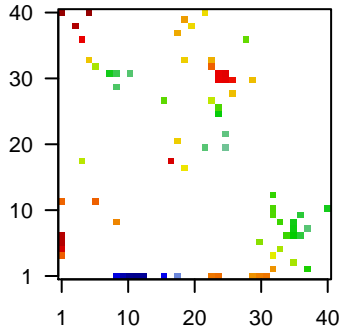
%DE = 0.06
 # genes with fdr < 0.2 = 1513 (834 + / 679 -)
 # genes with fdr < 0.1 = 1255 (676 + / 579 -)
 # genes with fdr < 0.05 = 870 (477 + / 393 -)
 # genes with fdr < 0.01 = 486 (263 + / 223 -)
 # genes in genesets = 16360

<FC> = 0
 <t-score> = 0.12
 <p-value> = 0.25
 <fdr> = 0.94

Portrait



Top 100 DE genes



Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	1552337_s_at	1.95	2e-16	8e-13	3 x 38 homeobox D4 [Source:NCBI gene;Acc:3233]
2	1554663_a_at	2.13	2e-16	8e-13	32 x 11 nuclear mitotic apparatus protein 1 [Source:HGNC Symbol;Acc:3233]
3	1556573_s_at	2.09	2e-16	8e-13	30 x 1 novel transcript
4	1565162_s_at	-1.04	2e-16	8e-13	23 x 27 microsomal glutathione S-transferase 1 [Source:HGNC Symbol;Acc:3233]
5	201909_at	-1.79	2e-16	8e-13	18 x 1 ribosomal protein S4 Y-linked 1 [Source:HGNC Symbol;Acc:3233]
6	204777_s_at	-1.28	2e-16	8e-13	35 x 7 mal, T cell differentiation protein [Source:HGNC Symbol;Acc:3233]
7	206785_s_at	-2.12	2e-16	8e-13	1 x 5 killer cell lectin like receptor C2 [Source:HGNC Symbol;Acc:3233]
8	211708_s_at	-1.85	2e-16	8e-13	10 x 1 stearyl-CoA desaturase [Source:HGNC Symbol;Acc:3233]
9	214079_at	2.24	2e-16	8e-13	1 x 5 dehydrogenase/reductase 2 [Source:HGNC Symbol;Acc:3233]
10	223122_s_at	-1.11	2e-16	8e-13	24 x 1 secreted frizzled related protein 2 [Source:HGNC Symbol;Acc:3233]
11	231155_at	2.44	2e-16	8e-13	26 x 30 defensin beta 119 [Source:HGNC Symbol;Acc:3233]
12	234830_at	2.34	2e-16	8e-13	29 x 30 FSHD region gene 2 family member E, pseudogene [Source:HGNC Symbol;Acc:3233]
13	237471_at	1.8	2e-16	8e-13	26 x 30
14	237898_at	2.37	2e-16	8e-13	25 x 30
15	205522_at	1.81	7e-16	2e-11	1 x 12
16	231828_at	-1.54	7e-16	2e-11	32 x 10 cutA divalent cation tolerance homolog-like, pseudogene [Source:HGNC Symbol;Acc:3233]
17	205000_at	-1.7	1e-15	3e-11	18 x 1 DEAD-box helicase 3 Y-linked [Source:HGNC Symbol;Acc:3233]
18	206460_at	1.78	2e-15	5e-11	30 x 6 adherens junctions associated protein 1 [Source:HGNC Symbol;Acc:3233]
19	205374_at	1.77	3e-15	5e-11	19 x 33 sarcolipin [Source:HGNC Symbol;Acc:3233]
20	205206_at	0.83	4e-15	5e-11	9 x 9 anosmin 1 [Source:HGNC Symbol;Acc:3233]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	9.31	NULL	1416	BP DNA-binding transcription factor activity, RNA polymerase II-specific
2	7.51	NULL	1387	BP regulation of transcription, DNA-templated
3	6.92	NULL	1145	BP regulation of transcription by RNA polymerase II
4	6.18	NULL	400	BP chromatin binding
5	6	NULL	541	BP negative regulation of transcription, DNA-templated
6	5.83	NULL	630	BP cell cycle
7	5.75	NULL	843	BP DNA-binding transcription factor activity
8	5.59	NULL	783	BP negative regulation of transcription by RNA polymerase II
9	5.36	NULL	394	BP cell division
10	5.31	NULL	13	BP eyelid development in camera-type eye
11	5.22	NULL	56	BP SMAD protein signal transduction
12	5.13	NULL	49	BP embryonic skeletal system morphogenesis
13	5.09	NULL	31	BP mitotic sister chromatid segregation
14	5.03	NULL	30	BP oligodendrocyte differentiation
15	5.01	NULL	46	BP positive regulation of pathway-restricted SMAD protein phosphorylation
16	4.83	NULL	12	BP dermatan sulfate biosynthetic process
17	4.56	NULL	26	BP chondroitin sulfate biosynthetic process
18	4.52	NULL	42	BP mitotic spindle organization
19	4.51	NULL	85	BP chromosome segregation
20	4.5	NULL	158	BP DNA replication
<i>Underexpressed</i>				
1	-6.59	NULL	1435	BP mitochondrion
2	-6.25	NULL	276	BP translation
3	-5.85	NULL	83	BP mitochondrial translational elongation
4	-5.84	NULL	85	BP mitochondrial translational termination
5	-5.14	NULL	48	BP regulation of cellular amino acid metabolic process
6	-5.1	NULL	460	BP neutrophil degranulation
7	-4.93	NULL	69	BP SRP-dependent cotranslational protein targeting to membrane
8	-4.89	NULL	671	BP oxidation-reduction process
9	-4.86	NULL	59	BP NIK/NF-kappaB signaling
10	-4.77	NULL	67	BP antigen processing and presentation of exogenous peptide antigen via MHC class II, invariant chain associated
11	-4.77	NULL	52	BP negative regulation of G2/M transition of mitotic cell cycle
12	-4.68	NULL	10	BP negative regulation of inclusion body assembly
13	-4.37	NULL	84	BP SCF-dependent proteasomal ubiquitin-dependent protein catabolic process
14	-4.25	NULL	67	BP regulation of transcription from RNA polymerase II promoter in response to hypoxia
15	-4.23	NULL	103	BP stimulatory C-type lectin receptor signaling pathway
16	-4.15	NULL	19	BP glutathione derivative biosynthetic process
17	-4	NULL	43	BP mitochondrial electron transport, NADH to ubiquinone
18	-3.96	NULL	18	BP glutathione peroxidase activity
19	-3.95	NULL	111	BP tumor necrosis factor-mediated signaling pathway
20	-3.92	NULL	41	BP negative regulation of viral genome replication

p-values

