

04.1045.021_aH

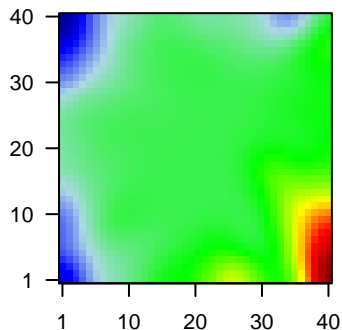
Global Summary

%DE = 0.25
 # genes with fdr < 0.2 = 4540 (2194 + / 2346 -)
 # genes with fdr < 0.1 = 4270 (2081 + / 2189 -)
 # genes with fdr < 0.05 = 3764 (1864 + / 1900 -)
 # genes with fdr < 0.01 = 3144 (1593 + / 1551 -)

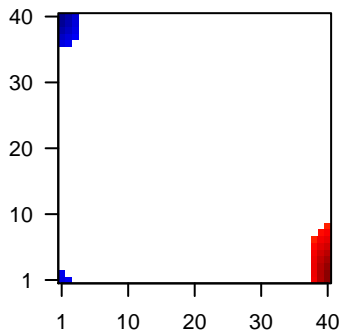
genes in genesets = 18990

<FC> = 0
 <t-score> = 0
 <p-value> = 0.01
 <fdr> = 0.75

Profile



Regulated Spots

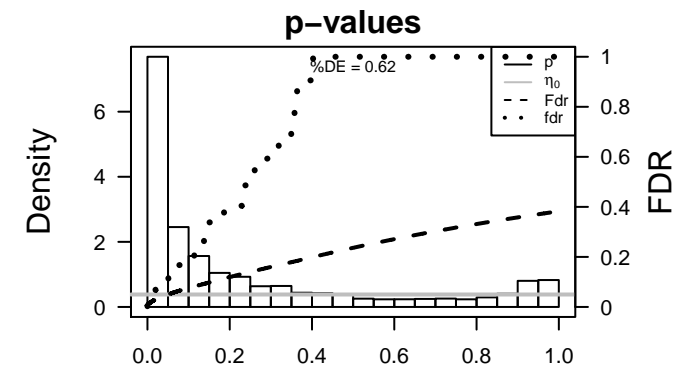
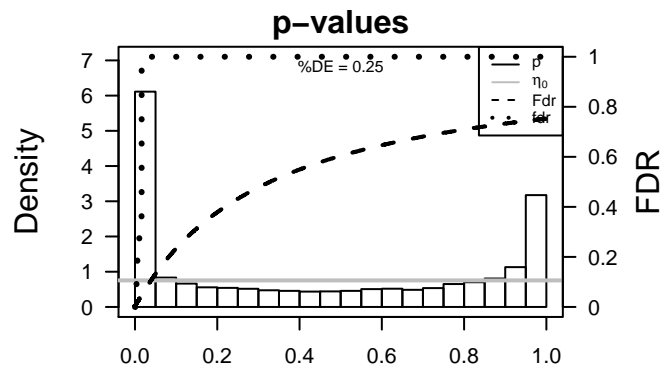


Global Genelist

Rank	ID	log(FC)	fdr p-value	Description
1	ENSG0000001	0.21	2e-16 3e-15	40 x 8 aurora kinase A interacting protein 1 [Source:HGNC Symbol;Acc:HGNC:1101]
2	ENSG0000001	0.21	2e-16 3e-15	16 x 1 tumor necrosis factor receptor superfamily, member 14 [Source:HGNC Symbol;Acc:HGNC:1102]
3	ENSG0000001	0.24	2e-16 3e-15	40 x 36 family with sequence similarity 213, member B [Source:HGNC Symbol;Acc:HGNC:1103]
4	ENSG0000001	0.17	2e-16 3e-15	38 x 5 EF-hand domain family, member D2 [Source:HGNC Symbol;Acc:HGNC:1104]
5	ENSG0000001	0.45	2e-16 3e-15	38 x 6 EPH receptor A2 [Source:HGNC Symbol;Acc:HGNC:3386]
6	ENSG0000001	0.32	2e-16 3e-15	39 x 1 peptidyl arginine deiminase, type II [Source:HGNC Symbol;Acc:HGNC:1105]
7	ENSG0000000	0.19	2e-16 3e-15	39 x 11 Rho guanine nucleotide exchange factor (GEF) 10-like [Source:HGNC Symbol;Acc:HGNC:1106]
8	ENSG0000001	0.55	2e-16 3e-15	25 x 1 aldo-keto reductase family 7, member A3 (afatoxin aldehyde reductase) [Source:HGNC Symbol;Acc:HGNC:1107]
9	ENSG0000000	0.22	2e-16 3e-15	26 x 3 aldo-keto reductase family 7, member A2 [Source:HGNC Symbol;Acc:HGNC:1108]
10	ENSG0000002	0.24	2e-16 3e-15	29 x 2 MINOS1-NBL1 readthrough [Source:HGNC Symbol;Acc:HGNC:1109]
11	ENSG0000001	0.28	2e-16 3e-15	38 x 7 neuroblastoma 1, DAN family BMP antagonist [Source:HGNC Symbol;Acc:HGNC:1110]
12	ENSG0000001	-0.39	2e-16 3e-15	40 x 40 phospholipase A2, group IIA (platelets, synovial fluid) [Source:HGNC Symbol;Acc:HGNC:1111]
13	ENSG0000001	0.29	2e-16 3e-15	37 x 1 calcium/calmodulin-dependent protein kinase II inhibitor 1 [Source:HGNC Symbol;Acc:HGNC:1112]
14	ENSG0000001	0.17	2e-16 3e-15	38 x 1 cytidine deaminase [Source:HGNC Symbol;Acc:HGNC:1712]
15	ENSG0000001	-0.37	2e-16 3e-15	1 x 3 complement component 1, q subcomponent, A chain [Source:HGNC Symbol;Acc:HGNC:1113]
16	ENSG0000001	-0.26	2e-16 3e-15	1 x 4 complement component 1, q subcomponent, C chain [Source:HGNC Symbol;Acc:HGNC:1114]
17	ENSG0000001	-0.26	2e-16 3e-15	5 x 5 complement component 1, q subcomponent, B chain [Source:HGNC Symbol;Acc:HGNC:1115]
18	ENSG0000001	0.28	2e-16 3e-15	33 x 1 inhibitor of DNA binding 3, dominant negative helix-loop-helix [Source:HGNC Symbol;Acc:HGNC:1116]
19	ENSG0000000	0.19	2e-16 3e-15	40 x 6 lysophospholipase II [Source:HGNC Symbol;Acc:HGNC:6736]
20	ENSG0000001	0.17	2e-16 3e-15	40 x 7 UDP-galactose-4-epimerase [Source:HGNC Symbol;Acc:HGNC:1117]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	18.74	2e-05	429	GSEA C2CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL
2	16.22	2e-05	3122	Colon Cancer G1_Colon
3	15.46	3e-05	251	GSEA C2WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
4	15.32	3e-05	126	GSEA C2VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN
5	14.7	3e-05	643	Colon Cancer TCGA_meth_kmeans_J_CIMP_H_DN
6	14.45	3e-05	412	GSEA C2LIM_MAMMARY_STEM_CELL_DN
7	14.09	4e-05	425	CC mitochondrial inner membrane
8	13.83	4e-05	198	HM HALLMARK_OXIDATIVE_PHOSPHORYLATION
9	13.79	4e-05	76	GSEA C2REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_S
10	13.75	4e-05	8123	Colon Cancer F_Colon
11	13.7	4e-05	96	BP respiratory electron transport chain
12	13.28	4e-05	3112	Colon Cancer A_Colon
13	13.05	4e-05	60	GSEA C2REACTOME_RESPIRATORY_ELECTRON_TRANSPORT
14	13	4e-05	222	GSEA C2COLDREN_GEFITINIB_RESISTANCE_DN
15	12.69	5e-05	1418	BP small molecule metabolic process
16	12.65	6e-05	877	Colon Cancer G2_Colon
17	12.6	6e-05	207	GSEA C2WONG_MITOCHONDRIA_GENE_MODULE
18	12.54	6e-05	23	BP flavonoid biosynthetic process
19	12.54	6e-05	23	BP flavonoid glucuronidation
20	12.53	6e-05	27	GSEA C2KEGG_PENTOSE_AND_GLUCURONATE_INTERCONVERSION
<i>Underexpressed</i>				
1	-22.94	6e-06	368	GSEA C2INDGREN_BLADDER_CANCER_CLUSTER_2B
2	-20.99	1e-05	326	GSEA C2SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
3	-20.46	1e-05	436	GSEA C2SMID_BREAST_CANCER_NORMAL_LIKE_UP
4	-20.21	1e-05	314	Lymphoma Topp_June14_MMML937_tumors+controls_group.overexpression
5	-20.07	1e-05	315	Lymphoma TIRTH_lymphoma937_spot E
6	-19.76	2e-05	196	GSEA C2PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
7	-18.8	2e-05	844	Colon Cancer TCGA-expr_kmeans_E_CIMP_H_UP_Cluster4_DN
8	-18.06	2e-05	574	Cancer Lembecke_Colonc Inflammation
9	-17.67	2e-05	332	Colon Cancer track_CRC_TCGA_corr_J_msi-h_UP_mss_DN
10	-16.66	2e-05	263	GSEA C2WALLACE_PROSTATE_CANCER_RACE_UP
11	-16.51	2e-05	539	GSEA C2FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR
12	-16.31	2e-05	144	GSEA C2GLESIAS_E2F_TARGETS_UP
13	-16.15	2e-05	1340	GSEA C2PUJANA_ATM_PCC_NETWORK
14	-16.03	2e-05	445	GSEA C2CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL
15	-15.99	2e-05	198	HM HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
16	-15.88	3e-05	132	Colon Cancer TCGA-cluster-b
17	-15.8	3e-05	148	Colon Cancer TCGA-cluster-a
18	-15.3	3e-05	522	GSEA C2SMID_BREAST_CANCER_LUMINAL_B_DN
19	-15.19	3e-05	1914	GSEA C2PILON_KLF1_TARGETS_DN
20	-15.13	3e-05	220	GSEA C2MCLAHLAN_DENTAL_CARIES_UP



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Local Summary

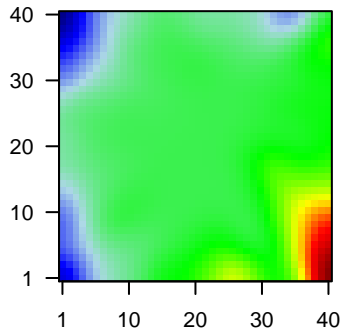
%DE = 0.96
 # metagenes = 24
 # genes = 462
 # genes in genesets = 455

 # genes with $fdr < 0.1$ = 428 (408 + / 20 -)
 # genes with $fdr < 0.05$ = 425 (406 + / 19 -)
 # genes with $fdr < 0.01$ = 418 (399 + / 19 -)

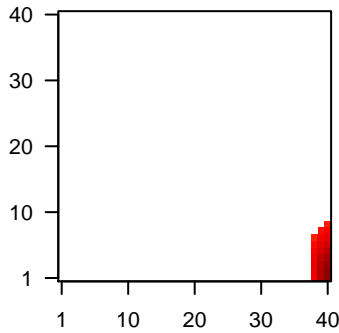
$\langle r \rangle$ metagenes = 0.94
 $\langle r \rangle$ genes = 0.58

 $\langle FC \rangle$ = 0.23
 $\langle t\text{-score} \rangle$ = 4.64
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.08

Profile



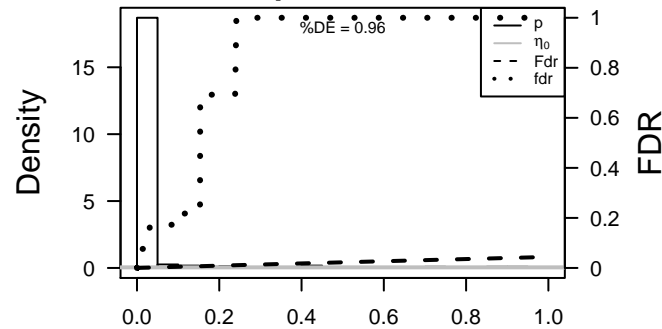
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ENSG0000001	0.21	2e-16	1e-17	40 x 8 aurora kinase A interacting protein 1 [Source:HGNC Symbol;]
2	ENSG0000001	0.17	2e-16	1e-17	38 x 5 EF-hand domain family, member D2 [Source:HGNC Symbol;]
3	ENSG0000001	0.45	2e-16	1e-17	38 x 6 EPH receptor A2 [Source:HGNC Symbol;Acc:HGNC:3386]
4	ENSG0000001	0.32	2e-16	1e-17	39 x 1 peptidyl arginine deiminase, type II [Source:HGNC Symbol;A]
5	ENSG0000001	0.28	2e-16	1e-17	38 x 7 neuroblastoma 1, DAN family BMP antagonist [Source:HGNC
6	ENSG0000001	0.17	2e-16	1e-17	38 x 1 cytidine deaminase [Source:HGNC Symbol;Acc:HGNC:1712]
7	ENSG0000000	0.19	2e-16	1e-17	40 x 6 lysophospholipase II [Source:HGNC Symbol;Acc:HGNC:6736]
8	ENSG0000001	0.17	2e-16	1e-17	40 x 7 UDP-galactose-4-epimerase [Source:HGNC Symbol;Acc:HGNC:10773]
9	ENSG0000001	0.28	2e-16	1e-17	40 x 3 SH3 domain binding glutamate-rich protein like 3 [Source:HGNC
10	ENSG0000001	0.21	2e-16	1e-17	39 x 4 ribosomal protein S6 kinase, 90kDa, polypeptide 1 [Source:H
11	ENSG0000001	0.21	2e-16	1e-17	40 x 1 stratifin [Source:HGNC Symbol;Acc:HGNC:10773]
12	ENSG0000001	0.19	2e-16	1e-17	40 x 7 ATPase inhibitory factor 1 [Source:HGNC Symbol;Acc:HGNC
13	ENSG0000001	0.35	2e-16	1e-17	40 x 1 serine incorporator 2 [Source:HGNC Symbol;Acc:HGNC:232]
14	ENSG0000001	0.19	2e-16	1e-17	40 x 5 KIAA1522 [Source:HGNC Symbol;Acc:HGNC:29301]
15	ENSG0000001	0.51	2e-16	1e-17	40 x 1 transmembrane protein 54 [Source:HGNC Symbol;Acc:HGNC:10773]
16	ENSG0000000	-0.21	2e-16	1e-17	40 x 1 guanylate cyclase activator 2B (uroguanylin) [Source:HGNC S
17	ENSG0000001	0.33	2e-16	1e-17	40 x 1 guanylate cyclase activator 2A (guanylin) [Source:HGNC Sym
18	ENSG0000001	0.17	2e-16	1e-17	40 x 6 transmembrane protein 125 [Source:HGNC Symbol;Acc:HGNC:10773]
19	ENSG0000002	0.18	2e-16	1e-17	38 x 2 chromosome 1 open reading frame 210 [Source:HGNC Symt
20	ENSG0000000	0.32	2e-16	1e-17	38 x 7 ELOVL fatty acid elongase 1 [Source:HGNC Symbol;Acc:HGNC:10773]

p-values



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Local Summary

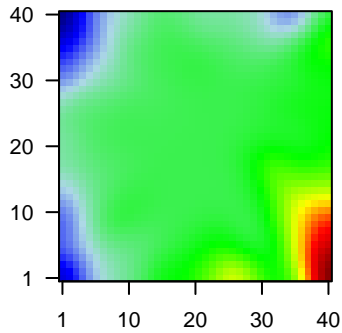
%DE = 0.98
 # metagenes = 3
 # genes = 126
 # genes in genesets = 122

 # genes with fdr < 0.1 = 122 (5 + / 117 -)
 # genes with fdr < 0.05 = 122 (5 + / 117 -)
 # genes with fdr < 0.01 = 122 (5 + / 117 -)

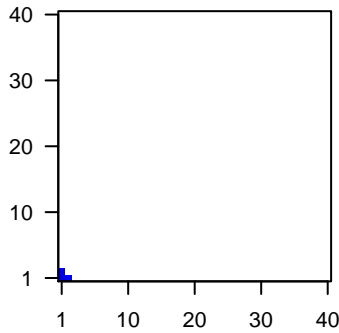
<r> metagenes = 1
 <r> genes = 0.81

 <FC> = -0.19
 <t-score> = -3.83
 <p-value> = 0
 <fdr> = 0.03

Profile



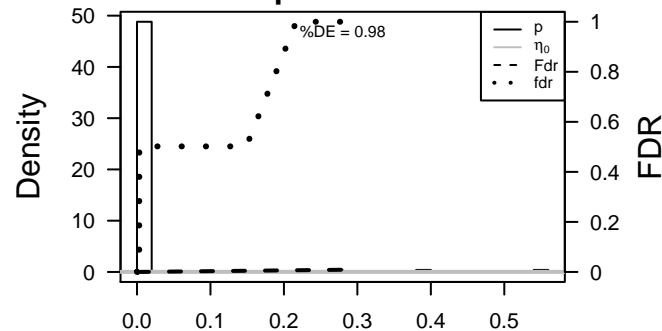
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description	
1	ENSG0000001	-0.46	2e-16	7e-18	1 x 1	CD52 molecule [Source:HGNC Symbol;Acc:HGNC:1804]
2	ENSG0000001	-0.45	2e-16	7e-18	1 x 1	lysosomal protein transmembrane 5 [Source:HGNC Symbol;]
3	ENSG0000001	-0.35	2e-16	7e-18	1 x 1	CD53 molecule [Source:HGNC Symbol;Acc:HGNC:1686]
4	ENSG0000001	-0.18	2e-16	7e-18	1 x 1	CD2 molecule [Source:HGNC Symbol;Acc:HGNC:1639]
5	ENSG0000001	-0.24	2e-16	7e-18	1 x 1	CD48 molecule [Source:HGNC Symbol;Acc:HGNC:1683]
6	ENSG0000001	-0.24	2e-16	7e-18	1 x 1	selectin L [Source:HGNC Symbol;Acc:HGNC:10720]
7	ENSG0000000	-0.2	2e-16	7e-18	1 x 1	protein tyrosine phosphatase, receptor type, C [Source:HGNC]
8	ENSG0000001	-0.25	2e-16	7e-18	1 x 1	complement component (3d/Epstein Barr virus) receptor 2 [S]
9	ENSG0000002	-0.19	2e-16	7e-18	1 x 1	limb bud and heart development [Source:HGNC Symbol;Acc:
10	ENSG0000001	-0.17	2e-16	7e-18	2 x 1	pleckstrin [Source:HGNC Symbol;Acc:HGNC:9070]
11	ENSG0000001	-0.51	2e-16	7e-18	1 x 1	chemokine (C-X-C motif) receptor 4 [Source:HGNC Symbol;
12	ENSG0000002	0.49	2e-16	7e-18	1 x 1	MT-RNR2-like 12 [Source:HGNC Symbol;Acc:HGNC:37169]
13	ENSG0000001	-0.17	2e-16	7e-18	1 x 1	hematopoietic cell-specific Lyn substrate 1 [Source:HGNC S]
14	ENSG0000001	-0.52	2e-16	7e-18	1 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbc
15	ENSG0000001	-0.52	2e-16	7e-18	1 x 1	chemokine (C-X-C motif) ligand 13 [Source:HGNC Symbol;]
16	ENSG0000002	-0.19	2e-16	7e-18	1 x 1	
17	ENSG0000002	0.54	2e-16	7e-18	1 x 1	MT-RNR2-like 2 [Source:HGNC Symbol;Acc:HGNC:37156]
18	ENSG0000000	-0.48	2e-16	7e-18	1 x 1	CD74 molecule, major histocompatibility complex, class II inv
19	ENSG0000002	-0.45	2e-16	7e-18	1 x 1	ubiquitin D [Source:HGNC Symbol;Acc:HGNC:18795]
20	ENSG0000002	0.18	2e-16	7e-18	1 x 1	major histocompatibility complex, class I, E [Source:HGNC S]

p-values



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Local Summary

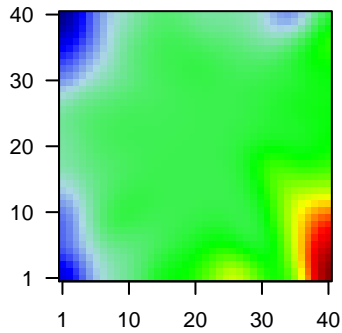
%DE = 0.99
 # metagenes = 14
 # genes = 245
 # genes in genesets = 242

 # genes with $fdr < 0.1$ = 240 (3 + / 237 -)
 # genes with $fdr < 0.05$ = 240 (3 + / 237 -)
 # genes with $fdr < 0.01$ = 235 (2 + / 233 -)

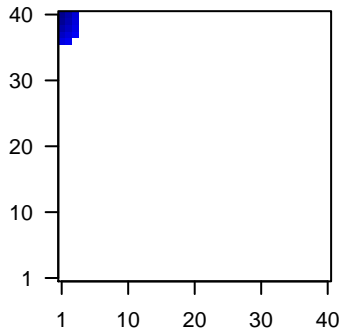
$\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.79

 $\langle FC \rangle$ = -0.21
 $\langle t\text{-score} \rangle$ = -4.18
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.04

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ENSG0000001	-0.35	2e-16	3e-18	1 x 40 chloride intracellular channel 4 [Source:HGNC Symbol;Acc:H
2	ENSG0000001	-0.38	2e-16	3e-18	1 x 38 cysteine-rich, angiogenic inducer, 61 [Source:HGNC Symbol
3	ENSG0000001	-0.17	2e-16	3e-18	3 x 37 RAP1A, member of RAS oncogene family [Source:HGNC Syr
4	ENSG0000001	-0.17	2e-16	3e-18	2 x 40 olfactomedin-like 3 [Source:HGNC Symbol;Acc:HGNC:2495f
5	ENSG0000000	-0.23	2e-16	3e-18	2 x 38 cold shock domain containing E1, RNA-binding [Source:HGNC
6	ENSG0000001	-0.21	2e-16	3e-18	1 x 38
7	ENSG0000000	-0.2	2e-16	3e-18	1 x 39 pleckstrin homology domain containing, family O member 1 [f
8	ENSG0000001	-0.31	2e-16	3e-18	1 x 38 phosphoprotein enriched in astrocytes 15 [Source:HGNC Syr
9	ENSG0000001	-0.33	2e-16	3e-18	1 x 40 dermatopontin [Source:HGNC Symbol;Acc:HGNC:3011]
10	ENSG0000001	-0.2	2e-16	3e-18	1 x 40 regulator of G-protein signaling 2 [Source:HGNC Symbol;Acc
11	ENSG0000001	-0.37	2e-16	3e-18	1 x 40 cysteine and glycine-rich protein 1 [Source:HGNC Symbol;Acc
12	ENSG0000001	-0.34	2e-16	3e-18	1 x 40 leiomodulin 1 (smooth muscle) [Source:HGNC Symbol;Acc:HG
13	ENSG0000000	-0.2	2e-16	3e-18	1 x 40 protein phosphatase 1, regulatory subunit 12B [Source:HGNC
14	ENSG0000001	-0.22	2e-16	3e-18	1 x 40 BTG family, member 2 [Source:HGNC Symbol;Acc:HGNC:11
15	ENSG0000000	-0.2	2e-16	3e-18	1 x 40 ATPase, Ca++ transporting, plasma membrane 4 [Source:HG
16	ENSG0000002	-0.26	2e-16	3e-18	2 x 37
17	ENSG0000001	-0.24	2e-16	3e-18	1 x 36 delta(4)-desaturase, sphingolipid 1 [Source:HGNC Symbol;A
18	ENSG0000001	-0.32	2e-16	3e-18	1 x 40 ras homolog family member B [Source:HGNC Symbol;Acc:HC
19	ENSG0000001	-0.63	2e-16	3e-18	1 x 40 actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
20	ENSG0000002	-0.18	2e-16	3e-18	2 x 38 POTE ankyrin domain family, member J [Source:HGNC Synt

p-values

