

# 04.1195.001\_cH

## Global Summary

%DE = 0.25  
 # genes with  $fdr < 0.2$  = 4714 ( 2396 + / 2318 - )  
 # genes with  $fdr < 0.1$  = 4222 ( 2194 + / 2028 - )  
 # genes with  $fdr < 0.05$  = 3907 ( 2053 + / 1854 - )  
 # genes with  $fdr < 0.01$  = 3381 ( 1816 + / 1565 - )  
 # genes in genesets = 18990

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

## Global Genelist

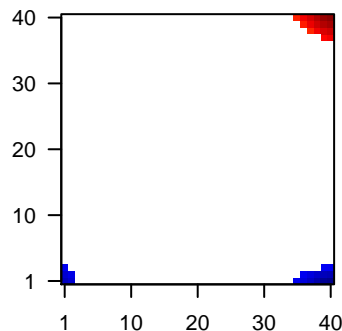
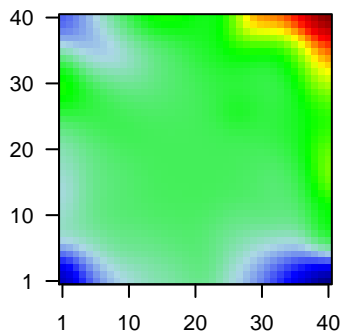
Rank	ID	log(FC)	fdr p-value	Description
1	ENSG000001	0.23	2e-16 3e-15	1 x 33 matrix-remodelling associated 8 [Source:HGNC Symbol;Acc:ENSG000001]
2	ENSG000001	0.17	2e-16 3e-15	40 x 8 aurora kinase A interacting protein 1 [Source:HGNC Symbol;Acc:ENSG000001]
3	ENSG000000	0.18	2e-16 3e-15	38 x 40 enolase 1, (alpha) [Source:HGNC Symbol;Acc:HGNC:3350]
4	ENSG000001	0.19	2e-16 3e-15	34 x 40 spermidine synthase [Source:HGNC Symbol;Acc:HGNC:112]
5	ENSG000001	0.17	2e-16 3e-15	36 x 37 angiotensin II receptor-associated protein [Source:HGNC Symbol;Acc:ENSG000001]
6	ENSG000000	0.2	2e-16 3e-15	31 x 40 procollagen-llysine, 2-oxoglutarate 5-dioxygenase 1 [Source:HGNC Symbol;Acc:ENSG000000]
7	ENSG000000	-0.17	2e-16 3e-15	2 x 1 tumor necrosis factor receptor superfamily, member 1B [Source:HGNC Symbol;Acc:ENSG000000]
8	ENSG000001	-0.18	2e-16 3e-15	28 x 1 dehydrogenase/reductase (SDR family) member 3 [Source:HGNC Symbol;Acc:ENSG000001]
9	ENSG000001	0.25	2e-16 3e-15	29 x 40 podoplanin [Source:HGNC Symbol;Acc:HGNC:29602]
10	ENSG000001	0.19	2e-16 3e-15	28 x 40 microfibrillar-associated protein 2 [Source:HGNC Symbol;Acc:ENSG000001]
11	ENSG000001	-0.28	2e-16 3e-15	39 x 1 peptidyl arginine deiminase, type II [Source:HGNC Symbol;Acc:ENSG000001]
12	ENSG000000	0.18	2e-16 3e-15	37 x 39 MRT4 homolog, ribosome maturation factor [Source:HGNC Symbol;Acc:ENSG000000]
13	ENSG000002	0.17	2e-16 3e-15	38 x 40 dolichyl-diphosphooligosaccharide--protein glycosyltransferase 1 [Source:HGNC Symbol;Acc:ENSG000002]
14	ENSG000001	0.16	2e-16 3e-15	1 x 33 low density lipoprotein receptor class A domain containing 2 [Source:HGNC Symbol;Acc:ENSG000001]
15	ENSG000001	-0.25	2e-16 3e-15	1 x 3 complement component 1, q subcomponent, A chain [Source:HGNC Symbol;Acc:ENSG000001]
16	ENSG000001	-0.2	2e-16 3e-15	1 x 4 complement component 1, q subcomponent, C chain [Source:HGNC Symbol;Acc:ENSG000001]
17	ENSG000001	-0.23	2e-16 3e-15	5 x 5 complement component 1, q subcomponent, B chain [Source:HGNC Symbol;Acc:ENSG000001]
18	ENSG000001	-0.19	2e-16 3e-15	38 x 1 fucosidase, alpha-L- 1, tissue [Source:HGNC Symbol;Acc:HGNC:6510]
19	ENSG000001	-0.23	2e-16 3e-15	9 x 1 proline-rich nuclear receptor coactivator 2 [Source:HGNC Symbol;Acc:ENSG000001]
20	ENSG000001	0.16	2e-16 3e-15	37 x 40 stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]

## Global Geneset Analysis

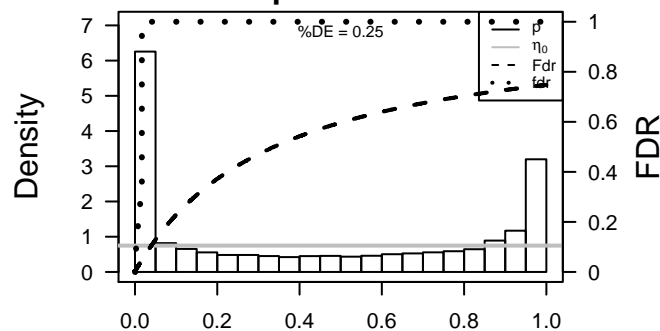
Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	23.87	6e-06	128	GSEA C2SABATES_COLORECTAL_ADENOMA_UP
2	21.94	8e-06	162	MF structural constituent of ribosome
3	21.61	9e-06	259	BP translation
4	21.6	9e-06	713	Colon Cancer Track_CRC_TCGA_group.over_C_normal_DN
5	21.31	9e-06	60	GSEA C2CROMER_TUMORIGENESIS_UP
6	20.89	1e-05	108	BP SRP-dependent cotranslational protein targeting to membrane
7	20.66	1e-05	550	Cancer Lembecke_Normal vs Adenoma
8	20.38	1e-05	105	GSEA C2REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE
9	20.2	1e-05	168	CC ribosome
10	19.87	2e-05	830	Colon Cancer Track_CRC_TCGA_corr_R_normal_DN
11	19.83	2e-05	813	GSEA C2GRADE_COLON_CANCER_UP
12	19.77	2e-05	142	GSEA C2REACTOME_TRANSLATION
13	19.11	2e-05	101	BP translational elongation
14	18.96	2e-05	84	GSEA C2KEGG_RIBOSOME
15	18.93	2e-05	88	BP translational termination
16	18.79	2e-05	400	GSEA C2ECCHI_GASTRIC_CANCER_EARLY_UP
17	18.66	2e-05	82	GSEA C2REACTOME_PEPTIDE_CHAIN_ELONGATION
18	18.32	2e-05	174	GSEA C2L1_AMPLIFIED_IN_LUNG_CANCER
19	18.13	2e-05	98	GSEA C2REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_TRANSLATION
20	17.84	2e-05	102	GSEA C2REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION
<i>Underexpressed</i>				
1	-29.96	0e+00	104	Colon Cancer Track_CRC_TCGA_group.over_A_normal_UP
2	-27.38	0e+00	507	Colon Cancer Track_CRC_TCGA_corr_C_normal_UP
3	-22.39	6e-06	110	Colon Cancer Track_CRC_TCGA_group.over_A_normal_UP
4	-20.96	1e-05	262	GSEA C2SABATES_COLORECTAL_ADENOMA_DN
5	-18.52	2e-05	436	GSEA C2SMID_BREAST_CANCER_NORMAL_LIKE_UP
6	-15.74	3e-05	16	CC MHC class II protein complex
7	-14.64	3e-05	616	Colon Cancer Track_CRC_TCGA-expr_kmeans_M_CIMP_H_DN
8	-13.03	4e-05	427	Tissue WIRTH_Immune system
9	-12.79	5e-05	11	BP antigen processing and presentation of peptide or polysaccharide antigen fragments
10	-12.71	5e-05	263	GSEA C2WALLACE_PROSTATE_CANCER_RACE_UP
11	-12.12	7e-05	73	GSEA C2WATANABE_COLON_CANCER_MS1_VS_MS2_DN
12	-11.51	1e-04	175	GSEA C2LEE_DIFFERENTIATING_T_LYMPHOCYTE
13	-11.27	1e-04	844	Colon Cancer Track_CRC_TCGA-expr_kmeans_E_CIMP_H_UP_Cluster4_DN
14	-10.7	1e-04	3507	CC plasma membrane
15	-10.6	2e-04	64	BP T cell costimulation
16	-10.13	2e-04	145	Lymphoma WIRTH_lymphoma937_spot F
17	-10.12	2e-04	145	Lymphoma WIRTH_lymphoma937_spot F
18	-10	2e-04	336	GSEA C2ECCHI_GASTRIC_CANCER_EARLY_DN
19	-9.56	3e-04	736	GSEA C2RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_TYROID_CARCINOMA
20	-9.55	3e-04	347	Lymphoma WIRTH_lymphoma937_spot H

Profile

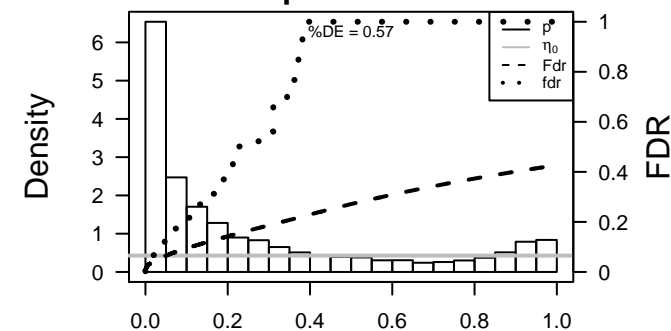
Regulated Spots



p-values



p-values



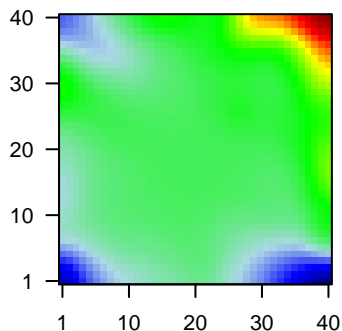
# 04.1195.001\_cH

## Local Summary

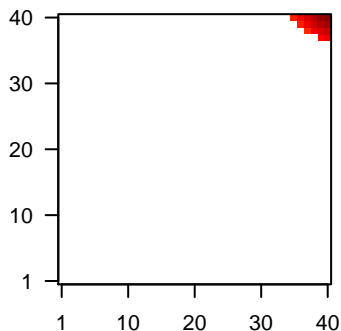
%DE = 0.98  
 # metagenes = 17  
 # genes = 391  
 # genes in genesets = 385  
  
 # genes with  $fdr < 0.1$  = 379 ( 365 + / 14 -)  
 # genes with  $fdr < 0.05$  = 374 ( 361 + / 13 -)  
 # genes with  $fdr < 0.01$  = 368 ( 356 + / 12 -)

$\langle r \rangle$  metagenes = 0.96  
 $\langle r \rangle$  genes = 0.58  
  
 $\langle FC \rangle$  = 0.21  
 $\langle t\text{-score} \rangle$  = 4.19  
 $\langle p\text{-value} \rangle$  = 0  
 $\langle fdr \rangle$  = 0.05

Profile



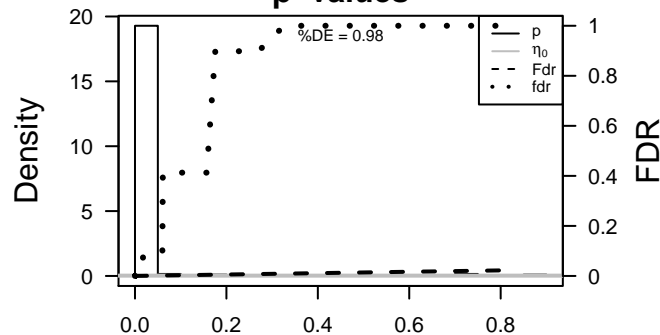
Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ENSG000000	0.18	2e-16	9e-18	38 x 40 enolase 1, (alpha) [Source:HGNC Symbol;Acc:HGNC:3350]
2	ENSG000000	0.18	2e-16	9e-18	37 x 39 MRT4 homolog, ribosome maturation factor [Source:HGNC S
3	ENSG000002	0.17	2e-16	9e-18	38 x 40 dolichyl--diphosphooligosaccharide--protein glycosyltransfer
4	ENSG000001	0.16	2e-16	9e-18	37 x 40 stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]
5	ENSG000001	0.25	2e-16	9e-18	38 x 40 regulator of chromosome condensation 1 [Source:HGNC Syn
6	ENSG000001	0.19	2e-16	9e-18	40 x 39 cell division cycle 20 [Source:HGNC Symbol;Acc:HGNC:1722
7	ENSG000001	0.17	2e-16	9e-18	35 x 40 ribosomal protein S8 [Source:HGNC Symbol;Acc:HGNC:104
8	ENSG000001	0.31	2e-16	9e-18	38 x 39 peroxiredoxin 1 [Source:HGNC Symbol;Acc:HGNC:9352]
9	ENSG000001	0.18	2e-16	9e-18	40 x 40 PDZK1 interacting protein 1 [Source:HGNC Symbol;Acc:HGNC
10	ENSG000001	0.19	2e-16	9e-18	39 x 39 mitochondrial ribosomal protein L37 [Source:HGNC Symbol;#
11	ENSG000000	-0.33	2e-16	9e-18	40 x 40 chloride channel accessory 1 [Source:HGNC Symbol;Acc:HG
12	ENSG000001	1.17	2e-16	9e-18	40 x 40 regenerating islet--derived family, member 4 [Source:HGNC S
13	ENSG000001	0.6	2e-16	9e-18	40 x 40 S100 calcium binding protein A11 [Source:HGNC Symbol;Ac
14	ENSG000001	0.33	2e-16	9e-18	38 x 40 S100 calcium binding protein A9 [Source:HGNC Symbol;Acc:
15	ENSG000001	0.18	2e-16	9e-18	37 x 40 interleukin enhancer binding factor 2 [Source:HGNC Symbol;
16	ENSG000001	0.24	2e-16	9e-18	40 x 37 CDC28 protein kinase regulatory subunit 1B [Source:HGNC S
17	ENSG000001	0.35	2e-16	9e-18	40 x 40 intelectin 1 (galactofuranose binding) [Source:HGNC Symbol;
18	ENSG000001	0.64	2e-16	9e-18	40 x 37 CD55 molecule, decay accelerating factor for complement (C
19	ENSG000002	-0.17	2e-16	9e-18	40 x 40 left--right determination factor 1 [Source:HGNC Symbol;Acc:+
20	ENSG000001	0.52	2e-16	9e-18	37 x 40 ornithine decarboxylase 1 [Source:HGNC Symbol;Acc:HGNC

p-values



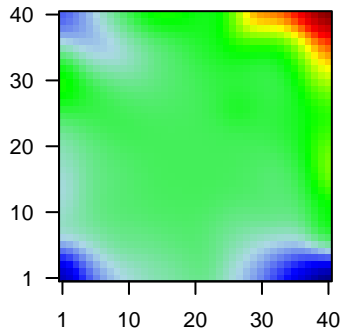
# 04.1195.001\_cH

## Local Summary

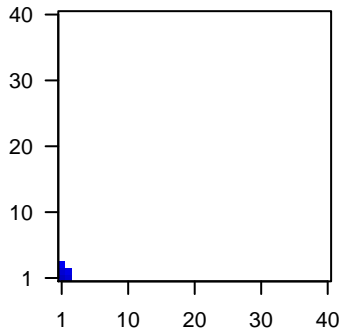
%DE = 0.98  
 # metagenes = 5  
 # genes = 152  
 # genes in genesets = 148  
  
 # genes with  $fdr < 0.1$  = 148 ( 2 + / 146 -)  
 # genes with  $fdr < 0.05$  = 148 ( 2 + / 146 -)  
 # genes with  $fdr < 0.01$  = 148 ( 2 + / 146 -)

<r> metagenes = 1  
 <r> genes = 0.8  
  
 <FC> = -0.19  
 <t-score> = -3.77  
 <p-value> = 0  
 <fdr> = 0.02

Profile



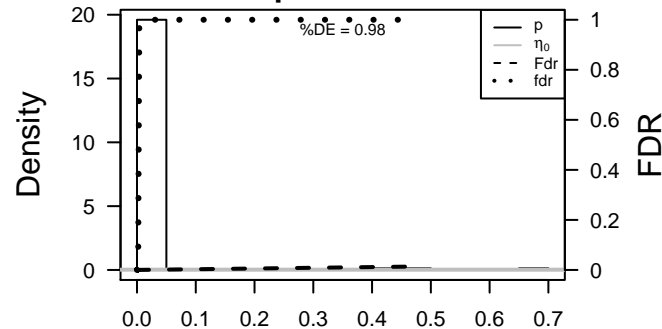
Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ENSG000000	-0.17	2e-16	9e-18	2 x 1 tumor necrosis factor receptor superfamily, member 1B [Soun
2	ENSG000001	-0.25	2e-16	9e-18	1 x 3 complement component 1, q subcomponent, A chain [Source
3	ENSG000001	-0.47	2e-16	9e-18	1 x 1 CD52 molecule [Source:HGNC Symbol;Acc:HGNC:1804]
4	ENSG000001	-0.31	2e-16	9e-18	1 x 1 lysosomal protein transmembrane 5 [Source:HGNC Symbol;/
5	ENSG000000	-0.16	2e-16	9e-18	1 x 1 small ArfGAP2 [Source:HGNC Symbol;Acc:HGNC:25082]
6	ENSG000001	-0.29	2e-16	9e-18	1 x 1 CD53 molecule [Source:HGNC Symbol;Acc:HGNC:1686]
7	ENSG000001	-0.23	2e-16	9e-18	1 x 1 CD2 molecule [Source:HGNC Symbol;Acc:HGNC:1639]
8	ENSG000001	-0.25	2e-16	9e-18	1 x 1 CD48 molecule [Source:HGNC Symbol;Acc:HGNC:1683]
9	ENSG000001	-0.22	2e-16	9e-18	1 x 1 selectin L [Source:HGNC Symbol;Acc:HGNC:10720]
10	ENSG000000	-0.19	2e-16	9e-18	1 x 1 protein tyrosine phosphatase, receptor type, C [Source:HGNC
11	ENSG000001	-0.21	2e-16	9e-18	1 x 1 Fc fragment of IgM receptor [Source:HGNC Symbol;Acc:HGNC
12	ENSG000001	-0.24	2e-16	9e-18	1 x 1 complement component (3d/Epstein Barr virus) receptor 2 [Si
13	ENSG000001	-0.27	2e-16	9e-18	1 x 1 chemokine (C-X-C motif) receptor 4 [Source:HGNC Symbol;
14	ENSG000002	-0.18	2e-16	9e-18	1 x 1 MT-RNR2-like 12 [Source:HGNC Symbol;Acc:HGNC:37169]
15	ENSG000001	-0.51	2e-16	9e-18	1 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
16	ENSG000001	-0.16	2e-16	9e-18	1 x 3 chemokine (C-X-C motif) ligand 9 [Source:HGNC Symbol;Ac
17	ENSG000001	-0.52	2e-16	9e-18	1 x 1 chemokine (C-X-C motif) ligand 13 [Source:HGNC Symbol;/
18	ENSG000002	-0.17	2e-16	9e-18	1 x 1
19	ENSG000002	-0.2	2e-16	9e-18	1 x 1 MT-RNR2-like 2 [Source:HGNC Symbol;Acc:HGNC:37156]
20	ENSG000001	-0.41	2e-16	9e-18	1 x 1 chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;/

p-values



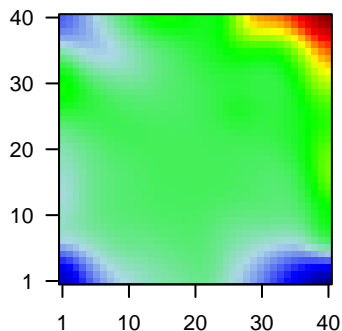
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## Local Summary

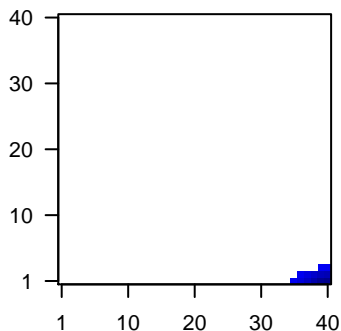
%DE = 0.95  
 # metagenes = 13  
 # genes = 272  
 # genes in genesets = 266  
  
 # genes with  $fdr < 0.1$  = 252 ( 23 + / 229 - )  
 # genes with  $fdr < 0.05$  = 252 ( 23 + / 229 - )  
 # genes with  $fdr < 0.01$  = 236 ( 19 + / 217 - )

$\langle r \rangle$  metagenes = 0.98  
 $\langle r \rangle$  genes = 0.65  
 $\langle FC \rangle$  = -0.19  
 $\langle t\text{-score} \rangle$  = -3.76  
 $\langle p\text{-value} \rangle$  = 0  
 $\langle fdr \rangle$  = 0.11

Profile



Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ENSG0000001	-0.28	2e-16	2e-17	39 x 1 peptidyl arginine deiminase, type II [Source:HGNC Symbol;Acc:HGNC:20657]
2	ENSG0000001	-0.19	2e-16	2e-17	38 x 1 fucosidase, alpha-L-1, tissue [Source:HGNC Symbol;Acc:HGNC:20657]
3	ENSG0000001	-0.18	2e-16	2e-17	40 x 1 transmembrane protein 54 [Source:HGNC Symbol;Acc:HGNC:20657]
4	ENSG0000000	-0.51	2e-16	2e-17	40 x 1 guanylate cyclase activator 2B (uroguanylin) [Source:HGNC Symbol;Acc:HGNC:20657]
5	ENSG0000001	-0.93	2e-16	2e-17	40 x 1 guanylate cyclase activator 2A (guanylin) [Source:HGNC Symbol;Acc:HGNC:20657]
6	ENSG0000002	-0.19	2e-16	2e-17	38 x 2 chromosome 1 open reading frame 210 [Source:HGNC Symbol;Acc:HGNC:20657]
7	ENSG0000001	-0.21	2e-16	2e-17	40 x 1 tetraspanin 1 [Source:HGNC Symbol;Acc:HGNC:20657]
8	ENSG0000000	-0.58	2e-16	2e-17	40 x 1 chloride channel accessory 4 [Source:HGNC Symbol;Acc:HGNC:20657]
9	ENSG0000001	-0.47	2e-16	2e-17	40 x 1 3-hydroxy-3-methylglutaryl-CoA synthase 2 (mitochondrial) [Source:HGNC Symbol;Acc:HGNC:20657]
10	ENSG0000001	-0.36	2e-16	2e-17	38 x 1 cathepsin S [Source:HGNC Symbol;Acc:HGNC:2545]
11	ENSG0000001	-0.72	2e-16	2e-17	40 x 1 selenium binding protein 1 [Source:HGNC Symbol;Acc:HGNC:20657]
12	ENSG0000001	-0.18	2e-16	2e-17	38 x 1 cingulin [Source:HGNC Symbol;Acc:HGNC:17429]
13	ENSG0000001	0.42	2e-16	2e-17	40 x 1 S100 calcium binding protein A14 [Source:HGNC Symbol;Acc:HGNC:20657]
14	ENSG0000001	-0.17	2e-16	2e-17	35 x 1 zinc finger and BTB domain containing 7B [Source:HGNC Symbol;Acc:HGNC:20657]
15	ENSG0000001	-0.53	2e-16	2e-17	40 x 1 glycoprotein A33 (transmembrane) [Source:HGNC Symbol;Acc:HGNC:20657]
16	ENSG0000001	-0.86	2e-16	2e-17	40 x 1 polymeric immunoglobulin receptor [Source:HGNC Symbol;Acc:HGNC:20657]
17	ENSG0000001	-0.19	2e-16	2e-17	36 x 1 chromosome 1 open reading frame 115 [Source:HGNC Symbol;Acc:HGNC:20657]
18	ENSG0000002	-0.6	2e-16	2e-17	40 x 1
19	ENSG0000001	-0.21	2e-16	2e-17	35 x 1 UDP-glucose pyrophosphorylase 2 [Source:HGNC Symbol;Acc:HGNC:20657]
20	ENSG0000001	-1.05	2e-16	2e-17	40 x 1 fatty acid binding protein 1, liver [Source:HGNC Symbol;Acc:HGNC:20657]

p-values

