

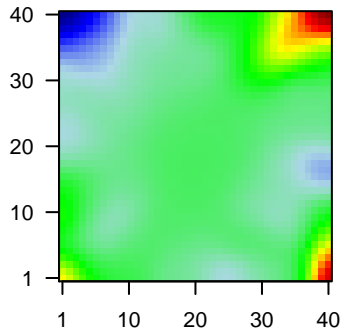
# 11\_cH

## Global Summary

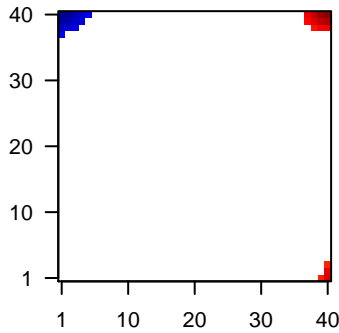
%DE = 0.27  
 # genes with  $fdr < 0.2$  = 4976 ( 2249 + / 2727 - )  
 # genes with  $fdr < 0.1$  = 4331 ( 2074 + / 2257 - )  
 # genes with  $fdr < 0.05$  = 3866 ( 1929 + / 1937 - )  
 # genes with  $fdr < 0.01$  = 3363 ( 1760 + / 1603 - )  
 # genes in genesets = 18990

<FC> = 0  
 <t-score> = 0  
 <p-value> = 0.01  
 <fdr> = 0.73

Profile



Regulated Spots



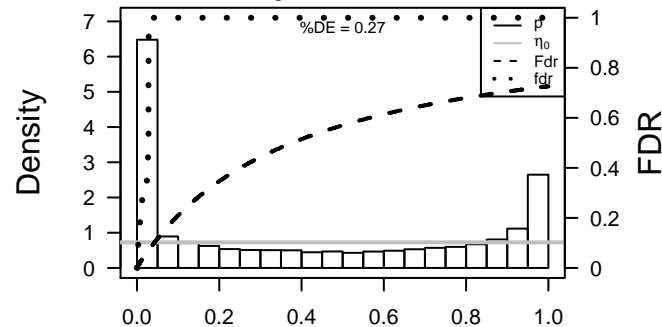
## Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	ENSG00000001	0.2	2e-16 3e-15	36 x 4 ISG15 ubiquitin-like modifier [Source:HGNC Symbol;Acc:HGNC:10000]
2	ENSG00000001	-0.15	2e-16 3e-15	3 x 32 ERBB receptor feedback inhibitor 1 [Source:HGNC Symbol;Acc:HGNC:10000]
3	ENSG00000000	0.22	2e-16 3e-15	38 x 40 enolase 1, (alpha) [Source:HGNC Symbol;Acc:HGNC:3350]
4	ENSG00000001	-0.1	2e-16 3e-15	3 x 40 heat shock 27kDa protein family, member 7 (cardiovascular) [Source:HGNC Symbol;Acc:HGNC:10000]
5	ENSG00000001	0.72	2e-16 3e-15	40 x 40 phospholipase A2, group IIA (platelets, synovial fluid) [Source:HGNC Symbol;Acc:HGNC:10000]
6	ENSG00000001	0.15	2e-16 3e-15	5 x 1 phospholipase A2, group IID [Source:HGNC Symbol;Acc:HGNC:10000]
7	ENSG00000001	-0.1	2e-16 3e-15	38 x 1 cytidine deaminase [Source:HGNC Symbol;Acc:HGNC:1712]
8	ENSG00000002	0.12	2e-16 3e-15	38 x 40 dolichyl-diphosphooligosaccharide--protein glycosyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:10000]
9	ENSG00000001	-0.11	2e-16 3e-15	1 x 33 low density lipoprotein receptor class A domain containing 2 [Source:HGNC Symbol;Acc:HGNC:10000]
10	ENSG00000001	0.21	2e-16 3e-15	1 x 3 complement component 1, q subcomponent, A chain [Source:HGNC Symbol;Acc:HGNC:10000]
11	ENSG00000001	0.19	2e-16 3e-15	1 x 4 complement component 1, q subcomponent, C chain [Source:HGNC Symbol;Acc:HGNC:10000]
12	ENSG00000001	0.17	2e-16 3e-15	5 x 5 complement component 1, q subcomponent, B chain [Source:HGNC Symbol;Acc:HGNC:10000]
13	ENSG00000001	0.27	2e-16 3e-15	40 x 40 EPH receptor B2 [Source:HGNC Symbol;Acc:HGNC:3393]
14	ENSG00000001	-0.13	2e-16 3e-15	33 x 1 inhibitor of DNA binding 3, dominant negative helix-loop-helix protein [Source:HGNC Symbol;Acc:HGNC:10000]
15	ENSG00000001	-0.11	2e-16 3e-15	1 x 40 chloride intracellular channel 4 [Source:HGNC Symbol;Acc:HGNC:10000]
16	ENSG00000001	0.17	2e-16 3e-15	1 x 1 CD52 molecule [Source:HGNC Symbol;Acc:HGNC:1804]
17	ENSG00000001	0.15	2e-16 3e-15	35 x 40 high mobility group nucleosomal binding domain 2 [Source:HGNC Symbol;Acc:HGNC:10000]
18	ENSG00000001	0.48	2e-16 3e-15	40 x 1 stratifin [Source:HGNC Symbol;Acc:HGNC:10773]
19	ENSG00000001	-0.1	2e-16 3e-15	29 x 40 interferon, alpha-inducible protein 6 [Source:HGNC Symbol;Acc:HGNC:10000]
20	ENSG00000002	-0.12	2e-16 3e-15	40 x 18

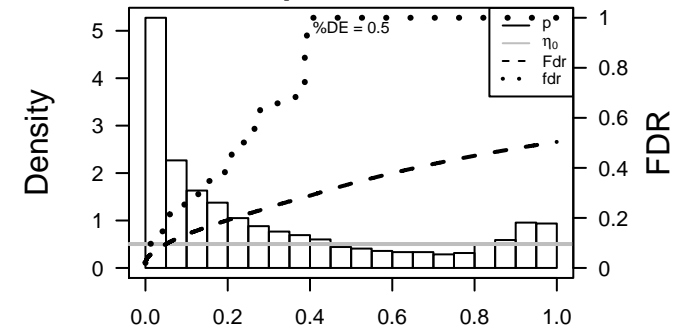
## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	14.99	3e-05	2638	CC extracellular exosome
2	13.99	4e-05	174	GSEA C2L1_AMPLIFIED_IN_LUNG_CANCER
3	13.37	4e-05	220	GSEA C2M1CLACHLAN_DENTAL_CARIES_UP
4	12.95	5e-05	259	GSEA C2P00LA_INVASIVE_BREAST_CANCER_UP
5	12.87	5e-05	210	GSEA C2M1CLACHLAN_DENTAL_CARIES_DN
6	12.77	5e-05	79	GSEA C2FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_ACCEPTED
7	12.75	5e-05	400	GSEA C2VECHI_GASTRIC_CANCER_EARLY_UP
8	12.7	5e-05	467	GSEA C2SWEET_LUNG_CANCER_KRAS_UP
9	12.68	5e-05	747	GSEA C2PUJANA_CHEK2_PCC_NETWORK
10	12.67	6e-05	1563	GSEA C2PUJANA_BRCA1_PCC_NETWORK
11	12.56	6e-05	713	Colon CaRectrack_CRC_TCGA_group.over_C_normal_DN
12	12.39	6e-05	608	Disease GUDJ_psooriasis up
13	12.3	6e-05	199	HM HALLMARK_MTORC1_SIGNALING
14	12.27	7e-05	813	GSEA C2GRADE_COLON_CANCER_UP
15	12.09	7e-05	455	GSEA C2ONDER_CDH1_TARGETS_2_DN
16	11.98	8e-05	275	GSEA C2GRADE_COLON_AND_RECTAL_CANCER_UP
17	11.97	8e-05	86	GSEA C2WIELAND_UP_BY_HBV_INFECTION
18	11.87	8e-05	195	HM HALLMARK_MYC_TARGETS_V1
19	11.42	1e-04	5	GSEA C2BIERIE_INFLAMMATORY_RESPONSE_TGFB1
20	11.28	1e-04	183	GSEA C2PENG_LEUCINE_DEPRIVATION_DN
<i>Underexpressed</i>				
1	-14.85	3e-05	132	Colon CaMisa_CRC-cluster-b
2	-11.61	4e-02	16	Cancer LIU_PROSTATE_CANCER_DN
3	-8.49	5e-04	40	GSEA C2TOMLINS_PROSTATE_CANCER_DN
4	-8.31	5e-04	22	GSEA C2REACTOME_SMOOTH_MUSCLE_CONTRACTION
5	-8.01	6e-04	160	GSEA C2BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_DN
6	-7.94	6e-04	478	GSEA C2L1M_MAMMARY_STEM_CELL_UP
7	-7.53	8e-04	40	GSEA C2PAPASPYRIDONOS_UNSTABLE_ATEROSCLEROTIC_PLAQUE_UP
8	-7.11	1e-03	294	GSEA C2ACEVEDO_FGFR1_TARGETS_IN_PROSTATE_CANCER_MODE
9	-7.03	1e-03	18	GSEA C2NIELSEN_LEIOMYOSARCOMA_CNN1_UP
10	-6.31	2e-03	3109	Colon CaRectrack_CRC
11	-6.3	2e-03	42	GSEA C2BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_D
12	-6.27	2e-03	10278	Brain Overlap_fetal_midbrain_ReprPCWk
13	-6.22	2e-03	105	BP muscle contraction
14	-6.18	2e-03	399	Disease GUDJ_psooriasis down
15	-6.07	2e-03	4879	Colon CaRectrack_CRC
16	-6.01	2e-03	5039	LymphomaOPP_Repressed
17	-5.98	2e-03	67	GSEA C2KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P
18	-5.92	2e-03	10800	Brain Overlap_fetal_midbrain_Quies
19	-5.91	2e-03	2838	LymphomaOPP_Poised_promoter
20	-5.83	2e-03	44	GSEA C2REACTOME_MUSCLE_CONTRACTION

p-values



p-values



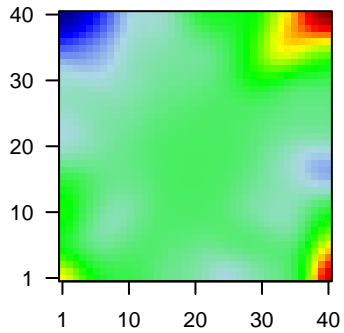
# 11\_cH

## Local Summary

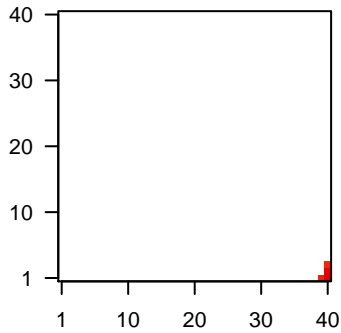
%DE = 0.92  
 # metagenes = 4  
 # genes = 146  
 # genes in genesets = 144  
  
 # genes with  $fdr < 0.1$  = 132 ( 108 + / 24 -)  
 # genes with  $fdr < 0.05$  = 128 ( 107 + / 21 -)  
 # genes with  $fdr < 0.01$  = 123 ( 103 + / 20 -)

$\langle r \rangle$  metagenes = 1  
 $\langle r \rangle$  genes = 0.68  
  
 $\langle FC \rangle$  = 0.14  
 $\langle t\text{-score} \rangle$  = 2.92  
 $\langle p\text{-value} \rangle$  = 0  
 $\langle fdr \rangle$  = 0.11

Profile



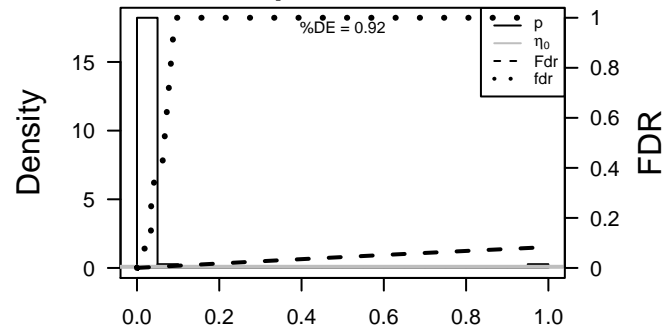
Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ENSG0000001	0.48	2e-16	3e-17	40 x 1 stratifin [Source:HGNC Symbol;Acc:HGNC:10773]
2	ENSG0000001	0.61	2e-16	3e-17	40 x 1 guanylate cyclase activator 2A (guanylin) [Source:HGNC Syn
3	ENSG0000001	0.36	2e-16	3e-17	40 x 1 tetraspanin 1 [Source:HGNC Symbol;Acc:HGNC:20657]
4	ENSG0000000	0.26	2e-16	3e-17	40 x 1 chloride channel accessory 4 [Source:HGNC Symbol;Acc:HG
5	ENSG0000001	-0.24	2e-16	3e-17	40 x 1 3-hydroxy-3-methylglutaryl-CoA synthase 2 (mitochondrial)
6	ENSG0000001	0.29	2e-16	3e-17	40 x 1 selenium binding protein 1 [Source:HGNC Symbol;Acc:HGNC
7	ENSG0000001	0.27	2e-16	3e-17	40 x 1 S100 calcium binding protein A14 [Source:HGNC Symbol;Ac
8	ENSG0000001	0.28	2e-16	3e-17	40 x 1 glycoprotein A33 (transmembrane) [Source:HGNC Symbol;A
9	ENSG0000001	0.13	2e-16	3e-17	40 x 3 ATPase, Na+/K+ transporting, beta 1 polypeptide [Source:HG
10	ENSG0000001	0.13	2e-16	3e-17	40 x 3 E74-like factor 3 (ets domain transcription factor, epithelial-s
11	ENSG0000001	0.88	2e-16	3e-17	40 x 1 polymeric immunoglobulin receptor [Source:HGNC Symbol;A
12	ENSG0000002	0.33	2e-16	3e-17	40 x 1
13	ENSG0000001	0.31	2e-16	3e-17	40 x 1 epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
14	ENSG0000001	0.14	2e-16	3e-17	40 x 1 vesicle-associated membrane protein 8 [Source:HGNC Syml
15	ENSG0000001	0.27	2e-16	3e-17	40 x 1 fatty acid binding protein 1, liver [Source:HGNC Symbol;Acc:f
16	ENSG0000001	0.18	2e-16	3e-17	40 x 1 mal, T-cell differentiation protein-like [Source:HGNC Symbol
17	ENSG0000000	-0.11	2e-16	3e-17	39 x 1 dehydrogenase/reductase (SDR family) member 9 [Source:Hi
18	ENSG0000001	0.46	2e-16	3e-17	40 x 1 integral membrane protein 2C [Source:HGNC Symbol;Acc:HC
19	ENSG0000002	-0.14	2e-16	3e-17	40 x 1 UDP glucuronosyltransferase 1 family, polypeptide A10 [Sour
20	ENSG0000002	-0.15	2e-16	3e-17	40 x 1 UDP glucuronosyltransferase 1 family, polypeptide A9 [Sourc

p-values



# 11\_cH

## Local Summary

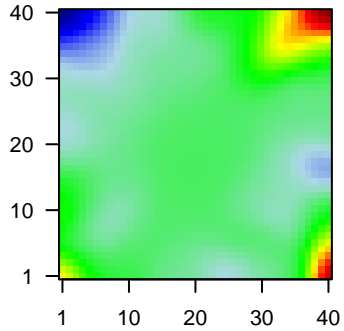
%DE = 0.97  
 # metagenes = 11  
 # genes = 248  
 # genes in genesets = 244

# genes with  $fdr < 0.1$  = 231 ( 209 + / 22 -)  
 # genes with  $fdr < 0.05$  = 230 ( 209 + / 21 -)  
 # genes with  $fdr < 0.01$  = 214 ( 198 + / 16 -)

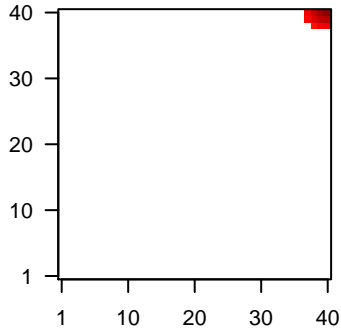
$\langle r \rangle$  metagenes = 0.99  
 $\langle r \rangle$  genes = 0.64

$\langle FC \rangle$  = 0.13  
 $\langle t\text{-score} \rangle$  = 2.54  
 $\langle p\text{-value} \rangle$  = 0  
 $\langle fdr \rangle$  = 0.11

Profile



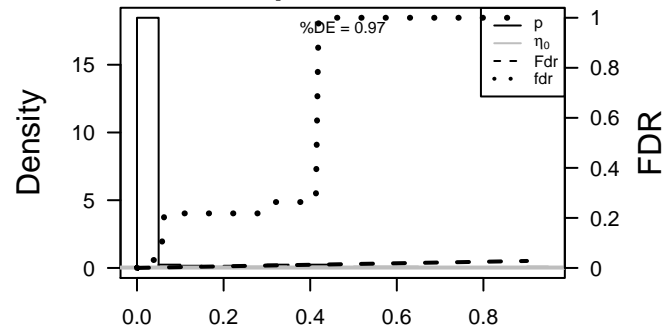
Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ENSG000000	0.22	2e-16	1e-17	38 x 40 enolase 1, (alpha) [Source:HGNC Symbol;Acc:HGNC:3350]
2	ENSG000001	0.72	2e-16	1e-17	40 x 40 phospholipase A2, group IIA (platelets, synovial fluid) [Source:HGNC Symbol;Acc:HGNC:3393]
3	ENSG000002	0.12	2e-16	1e-17	38 x 40 dolichyl--diphosphooligosaccharide--protein glycosyltransferase 2 [Source:HGNC Symbol;Acc:HGNC:3393]
4	ENSG000001	0.27	2e-16	1e-17	40 x 40 EPH receptor B2 [Source:HGNC Symbol;Acc:HGNC:3393]
5	ENSG000001	0.18	2e-16	1e-17	38 x 40 regulator of chromosome condensation 1 [Source:HGNC Symbol;Acc:HGNC:3393]
6	ENSG000001	0.18	2e-16	1e-17	40 x 40 MARCKS-like 1 [Source:HGNC Symbol;Acc:HGNC:7142]
7	ENSG000001	0.34	2e-16	1e-17	40 x 40 PDZK1 interacting protein 1 [Source:HGNC Symbol;Acc:HGNC:7142]
8	ENSG000001	0.11	2e-16	1e-17	39 x 39 mitochondrial ribosomal protein L37 [Source:HGNC Symbol;Acc:HGNC:7142]
9	ENSG000000	0.21	2e-16	1e-17	40 x 40 chloride channel accessory 1 [Source:HGNC Symbol;Acc:HGNC:7142]
10	ENSG000001	-0.2	2e-16	1e-17	40 x 40 regenerating islet--derived family, member 4 [Source:HGNC Symbol;Acc:HGNC:7142]
11	ENSG000001	0.31	2e-16	1e-17	38 x 40 S100 calcium binding protein A9 [Source:HGNC Symbol;Acc:HGNC:7142]
12	ENSG000001	0.37	2e-16	1e-17	40 x 40 mucin 1, cell surface associated [Source:HGNC Symbol;Acc:HGNC:7142]
13	ENSG000001	0.13	2e-16	1e-17	40 x 40 intelectin 1 (galactofuranose binding) [Source:HGNC Symbol;Acc:HGNC:7142]
14	ENSG000000	0.09	2e-16	1e-17	39 x 39 ubiquitin--conjugating enzyme E2T [Source:HGNC Symbol;Acc:HGNC:7142]
15	ENSG000002	0.1	2e-16	1e-17	40 x 40 left--right determination factor 1 [Source:HGNC Symbol;Acc:HGNC:7142]
16	ENSG000001	0.15	2e-16	1e-17	37 x 40 protein disulfide isomerase family A, member 6 [Source:HGNC Symbol;Acc:HGNC:7142]
17	ENSG000001	0.5	2e-16	1e-17	40 x 40 family with sequence similarity 84, member A [Source:HGNC Symbol;Acc:HGNC:7142]
18	ENSG000002	0.3	2e-16	1e-17	40 x 38
19	ENSG000001	-0.19	2e-16	1e-17	40 x 40 regenerating islet--derived 1 beta [Source:HGNC Symbol;Acc:HGNC:7142]
20	ENSG000001	-0.27	2e-16	1e-17	40 x 40 regenerating islet--derived 1 alpha [Source:HGNC Symbol;Acc:HGNC:7142]

p-values



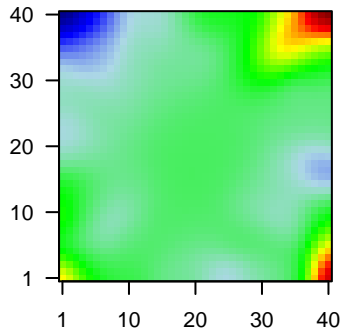
# 11\_cH

## Local Summary

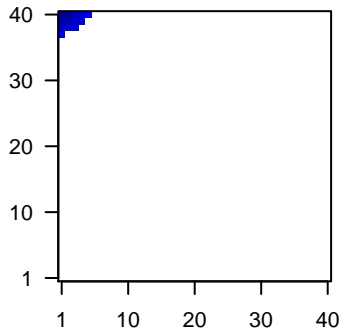
%DE = 0.97  
 # metagenes = 13  
 # genes = 298  
 # genes in genesets = 295  
  
 # genes with  $fdr < 0.1$  = 282 ( 21 + / 261 - )  
 # genes with  $fdr < 0.05$  = 281 ( 20 + / 261 - )  
 # genes with  $fdr < 0.01$  = 269 ( 16 + / 253 - )

$\langle r \rangle$  metagenes = 0.99  
 $\langle r \rangle$  genes = 0.81  
  
 $\langle FC \rangle$  = -0.08  
 $\langle t\text{-score} \rangle$  = -1.7  
 $\langle p\text{-value} \rangle$  = 0  
 $\langle fdr \rangle$  = 0.08

Profile



Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ENSG00000001	-0.1	2e-16	2e-17	3 x 40 heat shock 27kDa protein family, member 7 (cardiovascular) [
2	ENSG00000001	-0.11	2e-16	2e-17	1 x 40 chloride intracellular channel 4 [Source:HGNC Symbol;Acc:H
3	ENSG00000001	-0.1	2e-16	2e-17	2 x 40 olfactomedin-like 3 [Source:HGNC Symbol;Acc:HGNC:2495f
4	ENSG00000001	-0.11	2e-16	2e-17	1 x 40 tetraspanin 2 [Source:HGNC Symbol;Acc:HGNC:20659]
5	ENSG00000001	-0.11	2e-16	2e-17	1 x 40 calsequestrin 2 (cardiac muscle) [Source:HGNC Symbol;Acc:
6	ENSG00000001	-0.1	2e-16	2e-17	2 x 40 discoidin domain receptor tyrosine kinase 2 [Source:HGNC S
7	ENSG00000001	-0.11	2e-16	2e-17	1 x 40 regulator of G-protein signaling 5 [Source:HGNC Symbol;Acc
8	ENSG00000001	-0.16	2e-16	2e-17	1 x 40 dermatopontin [Source:HGNC Symbol;Acc:HGNC:3011]
9	ENSG00000001	-0.1	2e-16	2e-17	3 x 40 angiotensin-like 1 [Source:HGNC Symbol;Acc:HGNC:489]
10	ENSG00000001	-0.12	2e-16	2e-17	1 x 40 family with sequence similarity 129, member A [Source:HGNC
11	ENSG00000001	-0.15	2e-16	2e-17	1 x 40 regulator of G-protein signaling 2 [Source:HGNC Symbol;Acc
12	ENSG00000001	-0.21	2e-16	2e-17	1 x 40 cysteine and glycine-rich protein 1 [Source:HGNC Symbol;A
13	ENSG00000001	-0.27	2e-16	2e-17	1 x 40 leiomodulin 1 (smooth muscle) [Source:HGNC Symbol;Acc:HG
14	ENSG00000000	-0.13	2e-16	2e-17	1 x 40 protein phosphatase 1, regulatory subunit 12B [Source:HGNC
15	ENSG00000000	-0.14	2e-16	2e-17	1 x 40 ATPase, Ca++ transporting, plasma membrane 4 [Source:HG
16	ENSG00000001	-0.18	2e-16	2e-17	3 x 40 inhibitor of DNA binding 2, dominant negative helix-loop-heli
17	ENSG00000001	-0.1	2e-16	2e-17	1 x 40 actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
18	ENSG00000000	-0.1	2e-16	2e-17	3 x 40 LIM and senescent cell antigen-like domains 2 [Source:HGNC
19	ENSG00000001	0.17	2e-16	2e-17	1 x 40 collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:HGNC:
20	ENSG00000001	-0.14	2e-16	2e-17	1 x 40 serum deprivation response [Source:HGNC Symbol;Acc:HGNC

p-values

