

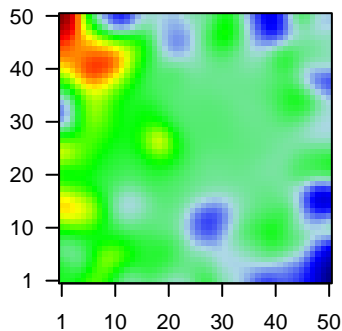
A12_mel

Global Summary

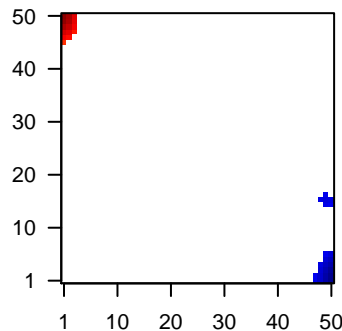
%DE = 0.21
 # genes with $fdr < 0.2$ = 2633 (1581 + / 1052 -)
 # genes with $fdr < 0.1$ = 2067 (1254 + / 813 -)
 # genes with $fdr < 0.05$ = 1733 (1045 + / 688 -)
 # genes with $fdr < 0.01$ = 1072 (660 + / 412 -)
 # genes in genesets = 14839

<FC> = 0
 <shrinkage-t> = 0.02
 <p-value> = 0.08
 <fdr> = 0.79

Profile



Regulated Spots



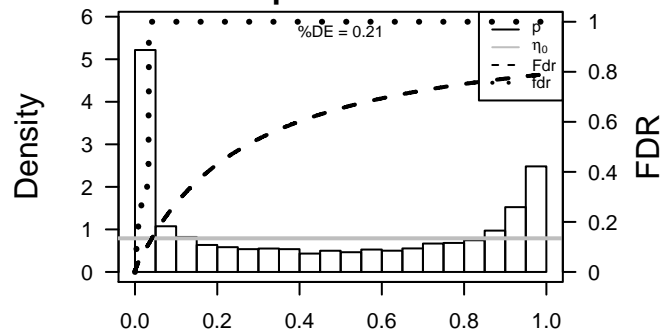
Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	ALDH9A1	-1.22	2e-16 1e-13	12 x 50 aldehyde dehydrogenase 9 family, member A1 [Source:HGNC]
2	BCAP29	-1.78	2e-16 1e-13	41 x 47 B-cell receptor-associated protein 29 [Source:HGNC Symbol]
3	C1orf198	-1.39	2e-16 1e-13	49 x 1 chromosome 1 open reading frame 198 [Source:HGNC Synt]
4	CNOT2	-0.98	2e-16 1e-13	39 x 1 CCR4-NOT transcription complex, subunit 2 [Source:HGNC]
5	DRG1	-1.21	2e-16 1e-13	48 x 19 developmentally regulated GTP binding protein 1 [Source:HG]
6	HN1	-1.67	2e-16 1e-13	47 x 39 hematological and neurological expressed 1 [Source:HGNC]
7	MRPL32	-1.64	2e-16 1e-13	50 x 38 mitochondrial ribosomal protein L32 [Source:HGNC Symbol]
8	PAN2	2.19	2e-16 1e-13	7 x 1 PAN2 poly(A) specific ribonuclease subunit [Source:HGNC Sy]
9	PDHA1	-2.18	2e-16 1e-13	16 x 50 pyruvate dehydrogenase (lipoamide) alpha 1 [Source:HGNC]
10	PNKD	-1.64	2e-16 1e-13	14 x 17 paroxysmal nonkinetogenic dyskinesia [Source:HGNC Symbc]
11	PPIP5K2	-1.42	2e-16 1e-13	27 x 12 diphosphoinositol pentakisphosphate kinase 2 [Source:HGNC]
12	PSMG2	-1.69	2e-16 1e-13	4 x 43 proteasome (prosome, macropain) assembly chaperone 2 [S]
13	QPCT	-1.58	2e-16 1e-13	1 x 34 glutaminyl-peptide cyclotransferase [Source:HGNC Symbol]
14	RARS	-1.6	2e-16 1e-13	50 x 43 arginyl-tRNA synthetase [Source:HGNC Symbol;Acc:HGNC]
15	SEC11A	-1.76	2e-16 1e-13	19 x 48 SEC11 homolog A (S. cerevisiae) [Source:HGNC Symbol;Acc:
16	SPARC	-1.83	2e-16 1e-13	50 x 2 secreted protein, acidic, cysteine-rich (osteonectin) [Source:]
17	SRP19	-1.11	2e-16 1e-13	40 x 46 signal recognition particle 19kDa [Source:HGNC Symbol;Acc
18	TMEM138	-1.6	2e-16 1e-13	1 x 33 transmembrane protein 138 [Source:HGNC Symbol;Acc:HG]
19	TMEM179B	-1.81	2e-16 1e-13	49 x 7 transmembrane protein 179B [Source:HGNC Symbol;Acc:HG]
20	TMEM50A	-1.27	2e-16 1e-13	50 x 37 transmembrane protein 50A [Source:HGNC Symbol;Acc:HG]

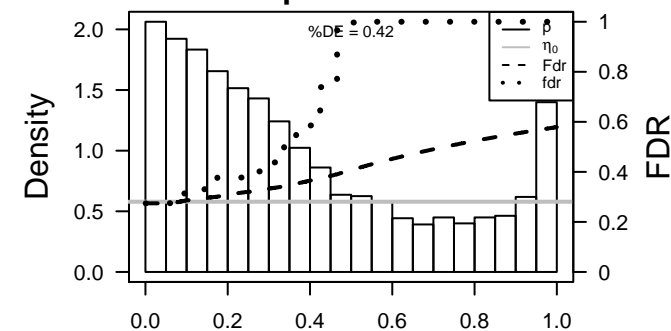
Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	7.65	7e-04	197	HM HALLMARK_E2F_TARGETS
2	7.37	9e-04	242	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN
3	7.31	9e-04	68	GSEA C2VERNELL_RETINOBLASTOMA_PATHWAY_UP
4	7.27	9e-04	278	GSEA C2MUELLER_PLURINET
5	7.11	1e-03	58	GSEA C2SONG_TARGETS_OF_IE86_CMV_PROTEIN
6	7.04	1e-03	278	GSEA C2MANALO_HYPOXIA_DN
7	6.96	1e-03	267	GSEA C2ZHANG_TLX_TARGETS_60HR_DN
8	6.93	1e-03	834	GSEA C2LEE_BMP2_TARGETS_DN
9	6.9	1e-03	335	GSEA C2WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_DN
10	6.76	1e-03	59	GSEA C2KAUFFMANN_MELANOMA_RELAPSE_UP
11	6.75	1e-03	188	HM HALLMARK_MYC_TARGETS_V1
12	6.58	1e-03	32	GSEA C2KEGG_DNA_REPLICATION
13	6.38	1e-03	312	GSEA C2WONG_EMBRYONIC_STEM_CELL_CORE
14	6.3	2e-03	29	BP DNA strand elongation involved in DNA replication
15	6.29	2e-03	27	GSEA C2REACTOME_DNA_STRAND_ELONGATION
16	6.16	2e-03	26	GSEA C2REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COM
17	6.09	2e-03	301	GSEA C2REACTOME_CELL_CYCLE_MITOTIC
18	6.05	2e-03	517	GSEA C2FEVR_CTNNB1_TARGETS_DN
19	6.04	2e-03	305	GSEA C2DUTERTRE ESTRADIOL_RESPONSE_24HR_UP
20	5.84	2e-03	562	GSEA C2CAIRO_HEPATOBLASTOMA_CLASSES_UP
<i>Underexpressed</i>				
1	-8.25	6e-04	2	Glio WILLSCHER_GBM_LTSmut_proteomics-E_UP
2	-4.86	4e-03	57	GSEA C2BRUNO_HEMATOPOIESIS
3	-4.63	5e-03	234	GSEA C2LU_AGING_BRAIN_UP
4	-4.5	5e-03	107	HM HALLMARK_COAGULATION
5	-4.31	6e-03	385	GSEA C2REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
6	-4.28	6e-03	16	MF extracellular matrix binding
7	-4.2	6e-03	63	GSEA C2RAGHAVACHARI_PLATELET_SPECIFIC_GENES
8	-4.2	6e-03	749	GSEA C2CUI_TCF21_TARGETS_2_DN
9	-4.17	7e-03	286	GSEA C2PASINI_SUZ12_TARGETS_DN
10	-4.14	7e-03	11	Tissue WIRTH_Sec_lymphoid organs
11	-4.09	7e-03	221	GSEA C2DANG_REGULATED_BY_MYC_DN
12	-4.03	7e-03	2563	LymphomaMOPP_Heterochrom
13	-3.97	8e-03	212	LymphomaENZ_Stromal signature 1
14	-3.94	8e-03	28	BP SRP-dependent cotranslational protein targeting to membrane
15	-3.92	8e-03	54	GSEA C2VERRECCHIA_EARLY_RESPONSE_TO_TGFB1
16	-3.91	8e-03	139	GSEA C2RUIZ_TNC_TARGETS_UP
17	-3.9	8e-03	302	GSEA C2KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
18	-3.8	1e-01	14	Cancer LIU_PROSTATE_CANCER_DN
19	-3.8	9e-03	401	GSEA C2CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
20	-3.79	9e-03	69	GSEA C2ROSS_LEUKEMIA_WITH_MLL_FUSIONS

p-values



p-values



A12_mel

Local Summary

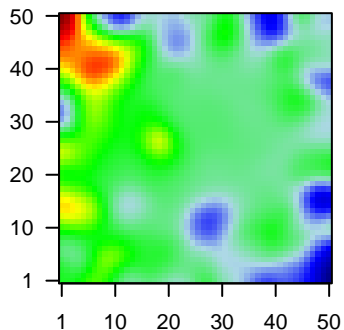
%DE = 0.82
 # metagenes = 15
 # genes = 266
 # genes in genesets = 264

 # genes with $fdr < 0.1$ = 167 (137 + / 30 -)
 # genes with $fdr < 0.05$ = 142 (120 + / 22 -)
 # genes with $fdr < 0.01$ = 98 (86 + / 12 -)

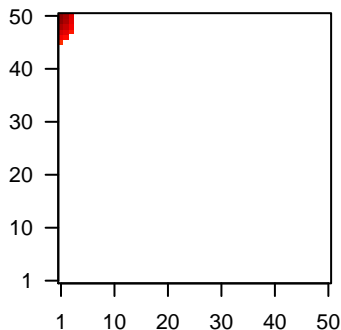
$\langle r \rangle$ metagenes = 0.95
 $\langle r \rangle$ genes = 0.23

 $\langle FC \rangle$ = 0.33
 $\langle \text{shrinkage-t} \rangle$ = 5.47
 $\langle p\text{-value} \rangle$ = 0.01
 $\langle fdr \rangle$ = 0.5

Profile



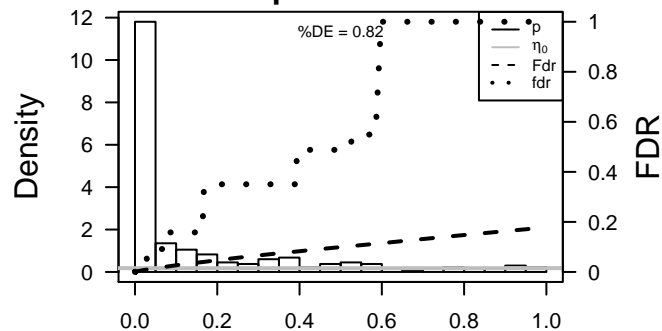
Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	POLE	1.58	5e-11	2e-09	1 x 48 polymerase (DNA directed), epsilon, catalytic subunit [Source:HGNC Symbol;Acc:HGNC:1735]
2	RHOG	-1.37	1e-10	1e-07	1 x 46 ras homolog family member G [Source:HGNC Symbol;Acc:HGNC:1735]
3	CDC45	1.43	3e-09	1e-07	1 x 50 cell division cycle 45 [Source:HGNC Symbol;Acc:HGNC:1735]
4	DTL	1.4	5e-09	1e-07	1 x 50 denticleless E3 ubiquitin protein ligase homolog (Drosophila)
5	KNTC1	1.37	7e-09	2e-07	1 x 50 kinetochore associated 1 [Source:HGNC Symbol;Acc:HGNC:1735]
6	MCM7	1.25	1e-08	3e-06	2 x 50 minichromosome maintenance complex component 7 [Source:HGNC Symbol;Acc:HGNC:1735]
7	CKB	-1.22	7e-08	3e-06	2 x 47 creatine kinase, brain [Source:HGNC Symbol;Acc:HGNC:199]
8	CDC44	1.24	2e-07	3e-06	1 x 47 cell division cycle associated 4 [Source:HGNC Symbol;Acc:HGNC:1735]
9	GSE1	1.24	3e-07	3e-06	1 x 47 Gse1 coiled-coil protein [Source:HGNC Symbol;Acc:HGNC:1735]
10	FRMD5	1.23	3e-07	3e-06	1 x 49 FERM domain containing 5 [Source:HGNC Symbol;Acc:HGNC:1735]
11	ORC1	1.23	3e-07	3e-06	1 x 49 origin recognition complex, subunit 1 [Source:HGNC Symbol;Acc:HGNC:1735]
12	ZNF519	1.23	3e-07	3e-06	3 x 48 zinc finger protein 519 [Source:HGNC Symbol;Acc:HGNC:30]
13	PKMYT1	1.21	4e-07	3e-06	1 x 50 protein kinase, membrane associated tyrosine/threonine 1 [Source:HGNC Symbol;Acc:HGNC:1735]
14	ORC6	1.1	5e-07	4e-06	1 x 50 origin recognition complex, subunit 6 [Source:HGNC Symbol;Acc:HGNC:1735]
15	CHST9	1.2	6e-07	4e-06	1 x 46 carbohydrate (N-acetylgalactosamine 4-O) sulfotransferase 9 [Source:HGNC Symbol;Acc:HGNC:1735]
16	HAUS8	1.2	7e-07	6e-06	3 x 50 HAUS augmin-like complex, subunit 8 [Source:HGNC Symbol;Acc:HGNC:1735]
17	MCM6	1.18	9e-07	6e-06	1 x 50 minichromosome maintenance complex component 6 [Source:HGNC Symbol;Acc:HGNC:1735]
18	EXO1	1.18	1e-06	6e-06	1 x 50 exonuclease 1 [Source:HGNC Symbol;Acc:HGNC:3511]
19	MCM5	1.17	1e-06	6e-06	1 x 49 minichromosome maintenance complex component 5 [Source:HGNC Symbol;Acc:HGNC:1735]
20	EBP	0.66	1e-06	6e-06	1 x 48 emopamil binding protein (sterol isomerase) [Source:HGNC Symbol;Acc:HGNC:1735]

p-values



A12_mel

Local Summary

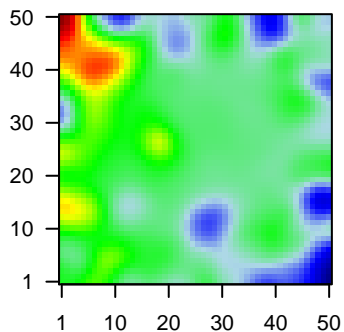
%DE = 0.69
 # metagenes = 18
 # genes = 298
 # genes in genesets = 297

 # genes with $fdr < 0.1$ = 103 (30 + / 73 -)
 # genes with $fdr < 0.05$ = 96 (28 + / 68 -)
 # genes with $fdr < 0.01$ = 56 (14 + / 42 -)

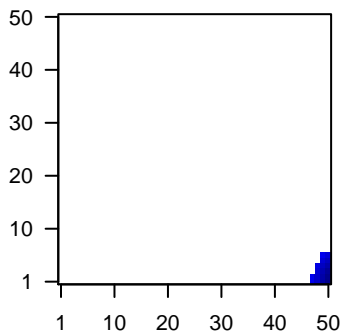
$\langle r \rangle$ metagenes = 0.97
 $\langle r \rangle$ genes = 0.19

 $\langle FC \rangle = -0.2$
 $\langle \text{shrinkage-t} \rangle = -3.3$
 $\langle p\text{-value} \rangle = 0.02$
 $\langle fdr \rangle = 0.67$

Profile



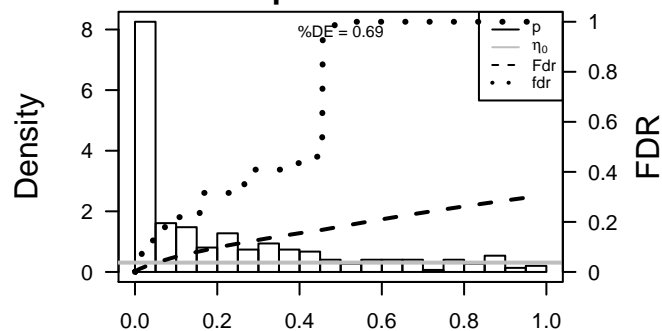
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	C1orf198	-1.39	2e-16	1e-14	49 x 1 chromosome 1 open reading frame 198 [Source:HGNC Symt
2	SPARC	-1.83	2e-16	1e-14	50 x 2 secreted protein, acidic, cysteine-rich (osteonectin) [Source:t
3	ANKRD28	-1.32	3e-14	1e-07	50 x 5 ankyrin repeat domain 28 [Source:HGNC Symbol;Acc:HGNC
4	STAM	-1.32	1e-09	5e-07	50 x 3 signal transducing adaptor molecule (SH3 domain and ITAM i
5	LGALS1	-1.02	6e-09	2e-06	50 x 1 lectin, galactoside-binding, soluble, 1 [Source:HGNC Symbol
6	UBE2E2	1.29	6e-08	2e-06	50 x 1 ubiquitin-conjugating enzyme E2E 2 [Source:HGNC Symbol;
7	APBB2	1.29	8e-08	2e-06	47 x 1 amyloid beta (A4) precursor protein-binding, family B, membr
8	FABP3	-1.1	1e-07	2e-06	50 x 1 fatty acid binding protein 3, muscle and heart [Source:HGNC
9	NOV	-1.2	1e-07	3e-06	50 x 1 nephroblastoma overexpressed [Source:HGNC Symbol;Acc:t
10	CALD1	-0.81	1e-07	3e-05	50 x 1 caldesmon 1 [Source:HGNC Symbol;Acc:HGNC:1441]
11	FAM98A	-1.16	7e-07	3e-05	49 x 1 family with sequence similarity 98, member A [Source:HGNC
12	YPEL5	-1.15	1e-06	3e-05	50 x 1 yippee-like 5 (Drosophila) [Source:HGNC Symbol;Acc:HGNC
13	PLK2	-0.87	1e-06	3e-05	50 x 1 polo-like kinase 2 [Source:HGNC Symbol;Acc:HGNC:19699]
14	FPGT	1.16	1e-06	1e-04	50 x 6 fucose-1-phosphate guanylyltransferase [Source:HGNC Syn
15	ANXA2	-0.45	3e-06	1e-04	50 x 3 annexin A2 [Source:HGNC Symbol;Acc:HGNC:537]
16	RAB31	-1.09	5e-06	1e-04	50 x 3 RAB31, member RAS oncogene family [Source:HGNC Symb
17	ARID5B	-0.96	5e-06	2e-04	50 x 1 AT rich interactive domain 5B (MRF1-like) [Source:HGNC Sy
18	AKAP13	-1.06	9e-06	2e-04	50 x 6 A kinase (PRKA) anchor protein 13 [Source:HGNC Symbol;A
19	TOB1	-0.5	1e-05	2e-04	50 x 5 transducer of ERBB2, 1 [Source:HGNC Symbol;Acc:HGNC:1
20	MID1	-1.04	1e-05	2e-04	50 x 3 midline 1 [Source:HGNC Symbol;Acc:HGNC:7095]

p-values



A12_mel

Local Summary

%DE = 0.95
 # metagenes = 6
 # genes = 61
 # genes in genesets = 60

 # genes with $fdr < 0.1$ = 52 (9 + / 43 -)
 # genes with $fdr < 0.05$ = 46 (8 + / 38 -)
 # genes with $fdr < 0.01$ = 30 (3 + / 27 -)

<r> metagenes = 0.98

<r> genes = 0.11

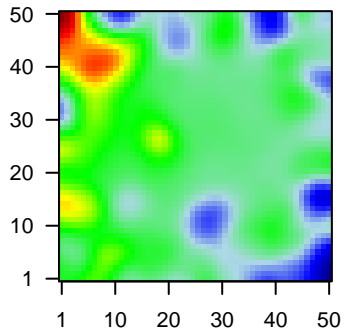
<FC> = -0.35

<shrinkage-t> = -5.72

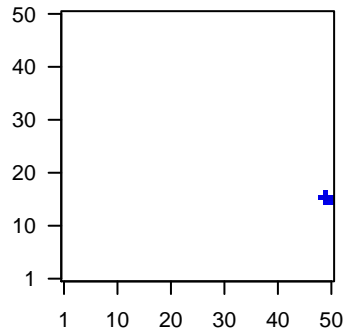
<p-value> = 0.01

<fdr> = 0.59

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	NADSYN1	-1.32	2e-09	9e-09	50 x 15 NAD synthetase 1 [Source:HGNC Symbol;Acc:HGNC:29832]
2	ATP2B1	-1.28	5e-09	3e-08	49 x 16 ATPase, Ca++ transporting, plasma membrane 1 [Source:HGNC Symbol;Acc:HGNC:29832]
3	KMT2E	-0.91	2e-08	1e-06	49 x 17 lysine (K)-specific methyltransferase 2E [Source:HGNC Symbol;Acc:HGNC:29832]
4	PAPOLG	1.2	6e-07	1e-06	50 x 15 poly(A) polymerase gamma [Source:HGNC Symbol;Acc:HGNC:29832]
5	ZCCHC11	-1.11	1e-06	1e-06	50 x 15 zinc finger, CCHC domain containing 11 [Source:HGNC Symbol;Acc:HGNC:29832]
6	N4BP2L2	-0.68	1e-06	1e-06	50 x 15 NEDD4 binding protein 2-like 2 [Source:HGNC Symbol;Acc:HGNC:29832]
7	TAX1BP3	-1.14	1e-06	7e-04	48 x 16 Tax1 (human T-cell leukemia virus type I) binding protein 3 [Source:HGNC Symbol;Acc:HGNC:29832]
8	ATF6	-0.88	2e-04	7e-04	50 x 15 activating transcription factor 6 [Source:HGNC Symbol;Acc:HGNC:29832]
9	TBC1D23	-0.81	8e-04	7e-04	50 x 15 TBC1 domain family, member 23 [Source:HGNC Symbol;Acc:HGNC:29832]
10	VRK3	-0.8	9e-04	7e-04	49 x 17 vaccinia related kinase 3 [Source:HGNC Symbol;Acc:HGNC:29832]
11	RRM2B	-0.79	1e-03	7e-04	50 x 15 ribonucleotide reductase M2 B (TP53 inducible) [Source:HGNC Symbol;Acc:HGNC:29832]
12	FNTA	-0.67	1e-03	7e-04	48 x 16 farnesyltransferase, CAAX box, alpha [Source:HGNC Symbol;Acc:HGNC:29832]
13	USP32	-0.7	2e-03	7e-04	50 x 15 ubiquitin specific peptidase 32 [Source:HGNC Symbol;Acc:HGNC:29832]
14	ZMYM1	-0.76	2e-03	1e-03	50 x 15 zinc finger, MYM-type 1 [Source:HGNC Symbol;Acc:HGNC:29832]
15	AKAP8L	-0.74	2e-03	3e-03	50 x 16 A kinase (PRKA) anchor protein 8-like [Source:HGNC Symbol;Acc:HGNC:29832]
16	RBM34	0.57	3e-03	3e-03	50 x 16 RNA binding motif protein 34 [Source:HGNC Symbol;Acc:HGNC:29832]
17	SLC25A17	-0.66	5e-03	3e-03	49 x 15 solute carrier family 25 (mitochondrial carrier; peroxisomal membrane protein) member 17 [Source:HGNC Symbol;Acc:HGNC:29832]
18	MAP4K5	-0.67	5e-03	3e-03	48 x 16 mitogen-activated protein kinase kinase kinase kinase 5 [Source:HGNC Symbol;Acc:HGNC:29832]
19	CERS5	-0.61	7e-03	3e-03	50 x 15 ceramide synthase 5 [Source:HGNC Symbol;Acc:HGNC:29832]
20	GALK1	-0.65	7e-03	4e-03	49 x 16 galactokinase 1 [Source:HGNC Symbol;Acc:HGNC:4118]

p-values

