

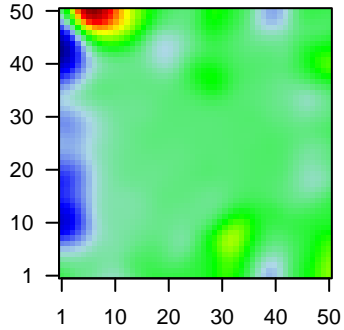
E9_mel

Global Summary

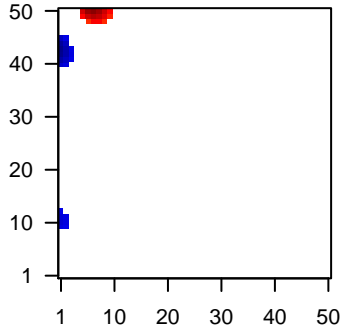
%DE = 0.22
 # genes with $fdr < 0.2$ = 2892 (1683 + / 1209 -)
 # genes with $fdr < 0.1$ = 2226 (1310 + / 916 -)
 # genes with $fdr < 0.05$ = 1910 (1117 + / 793 -)
 # genes with $fdr < 0.01$ = 1267 (750 + / 517 -)
 # genes in genesets = 14839

<FC> = 0
 <shrinkage-t> = -0.07
 <p-value> = 0.06
 <fdr> = 0.78

Profile



Regulated Spots



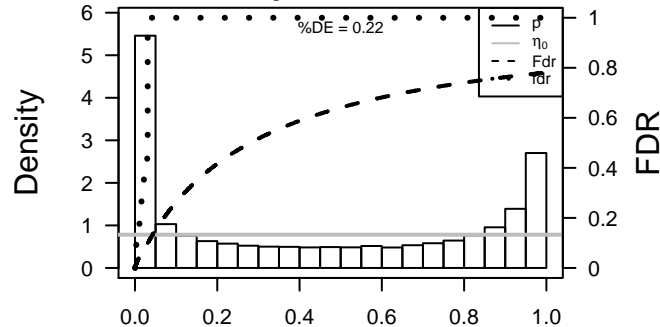
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	AHCY	-1.42	2e-16	5e-14	1 x 41 adenosylhomocysteinase [Source:HGNC Symbol;Acc:HGNC:10000]
2	AP3S1	-1.81	2e-16	5e-14	1 x 39 adaptor-related protein complex 3, sigma 1 subunit [Source:HGNC Symbol;Acc:HGNC:10000]
3	APEH	-1.62	2e-16	5e-14	1 x 42 acylaminoacyl-peptidase [Source:HGNC Symbol;Acc:HGNC:10000]
4	APOO	-1.69	2e-16	5e-14	2 x 46 apolipoprotein O [Source:HGNC Symbol;Acc:HGNC:28727]
5	ARHGAP8	-1.72	2e-16	5e-14	1 x 43 Rho GTPase activating protein 8 [Source:HGNC Symbol;Acc:HGNC:10000]
6	ATOX1	-1.27	2e-16	5e-14	4 x 38 antioxidant 1 copper chaperone [Source:HGNC Symbol;Acc:HGNC:10000]
7	ATP6V0A1	-1.62	2e-16	5e-14	1 x 10 ATPase, H+ transporting, lysosomal V0 subunit a1 [Source:HGNC Symbol;Acc:HGNC:10000]
8	ATP6V1D	-1.07	2e-16	5e-14	1 x 11 ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D [Source:HGNC Symbol;Acc:HGNC:10000]
9	BACE2	-1.65	2e-16	5e-14	1 x 42 beta-site APP-cleaving enzyme 2 [Source:HGNC Symbol;Acc:HGNC:10000]
10	CALM2	0.86	2e-16	5e-14	9 x 49 calmodulin 2 (phosphorylase kinase, delta) [Source:HGNC Symbol;Acc:HGNC:10000]
11	CAPN3	-1.99	2e-16	5e-14	1 x 43 calpain 3, (p94) [Source:HGNC Symbol;Acc:HGNC:1480]
12	CCNB1	2.14	2e-16	5e-14	7 x 50 cyclin B1 [Source:HGNC Symbol;Acc:HGNC:1579]
13	CCT7	-0.87	2e-16	5e-14	1 x 17 chaperonin containing TCP1, subunit 7 (eta) [Source:HGNC Symbol;Acc:HGNC:10000]
14	CD81	-1.33	2e-16	5e-14	3 x 9 CD81 molecule [Source:HGNC Symbol;Acc:HGNC:1701]
15	CDKN3	1.68	2e-16	5e-14	6 x 50 cyclin-dependent kinase inhibitor 3 [Source:HGNC Symbol;Acc:HGNC:10000]
16	CEP97	1.9	2e-16	5e-14	2 x 47 centrosomal protein 97kDa [Source:HGNC Symbol;Acc:HGNC:10000]
17	CITED1	-1.99	2e-16	5e-14	1 x 41 Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain 1 [Source:HGNC Symbol;Acc:HGNC:10000]
18	CTSC	-1.36	2e-16	5e-14	1 x 42 cathepsin C [Source:HGNC Symbol;Acc:HGNC:2528]
19	CTSL	-1.06	2e-16	5e-14	2 x 40 cathepsin L [Source:HGNC Symbol;Acc:HGNC:2537]
20	DERA	-1.79	2e-16	5e-14	1 x 43 deoxyribose-phosphate aldolase (putative) [Source:HGNC Symbol;Acc:HGNC:10000]

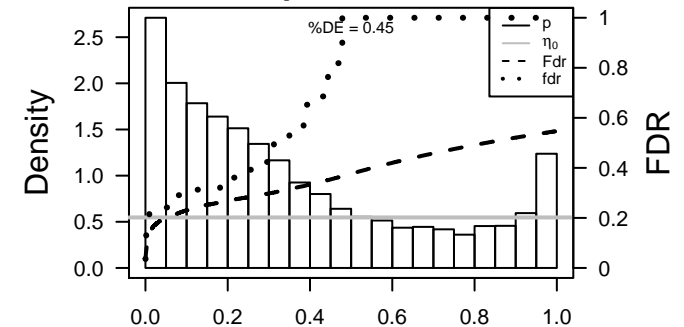
Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	17.4	3e-05	142	Glio WILLSCHER_GBM_Verhaak-CL_up (C)
2	14.85	5e-05	139	GSEA C2RSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
3	14.81	7e-04	16	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
4	13.88	7e-05	40	GSEA C2AMUNDSON_GAMMA_RADIATION_RESPONSE
5	13.86	7e-05	201	GSEA C2WHITFIELD_CELL_CYCLE_G2_M
6	13.31	8e-05	99	GSEA C2LEE_EARLY_T_LYMPHOCYTE_UP
7	13.06	9e-05	291	GSEA C2HORIUCHI_WTAP_TARGETS_DN
8	12.91	9e-05	550	GSEA C2SOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
9	12.68	1e-04	155	GSEA C2HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
10	12.62	1e-04	45	GSEA C2ZHAN_MULTIPLE_MYELOMA_PR_UP
11	12.44	1e-04	110	GSEA C2WHITEFORD_PEDIATRIC_CANCER_MARKERS
12	12.39	1e-04	124	GSEA C2ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
13	12.17	1e-04	312	BP mitotic nuclear division
14	12.06	1e-04	170	GSEA C2WHITFIELD_CELL_CYCLE_G2
15	11.48	2e-04	28	GSEA C2REICHERT_MITOSIS_LIN9_TARGETS
16	11.26	2e-04	72	GSEA C2CROONQUIST_NRAS_SIGNALING_DN
17	11.25	2e-04	54	GSEA C2KANG_DOXORUBICIN_RESISTANCE_UP
18	11.14	2e-04	145	GSEA C2CHANG_CYCLING_GENES
19	10.82	2e-04	196	HM HALLMARK_G2M_CHECKPOINT
20	10.72	2e-04	616	GSEA C2BENPORATH_CYCLING_GENES
<i>Underexpressed</i>				
1	-6.15	0.002	13	BP melanin biosynthetic process
2	-6.04	0.002	456	CC vacuole
3	-6.04	0.002	1468	CC mitochondrion
4	-6.03	0.002	107	GSEA C2KEGG_OXIDATIVE_PHOSPHORYLATION
5	-6.02	0.002	421	GSEA C2MOOHTA_MITOCHONDRIA
6	-5.99	0.002	198	HM HALLMARK_OXIDATIVE_PHOSPHORYLATION
7	-5.89	0.002	368	GSEA C2STEIN_ESRRA_TARGETS_UP
8	-5.88	0.002	412	CC lysosome
9	-5.81	0.002	94	BP respiratory electron transport chain
10	-5.73	0.002	94	CC melanosome
11	-5.6	0.002	405	GSEA C2MOOHTA_HUMAN_MITODB_6_2002
12	-5.59	0.002	398	GSEA C2MOOHTA_PGC
13	-5.51	0.003	1730	BP small molecule metabolic process
14	-5.47	0.003	114	GSEA C2REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT
15	-5.39	0.003	135	BP cellular metabolic process
16	-5.29	0.003	36	BP myelination
17	-5.26	0.003	78	GSEA C2REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_Synthase
18	-5.2	0.003	85	GSEA C2MOOHTA_VOXPPOS
19	-5.19	0.003	19	MF Hsp90 protein binding
20	-5.08	0.003	2984	CC integral component of membrane

p-values



p-values



E9_mel

Local Summary

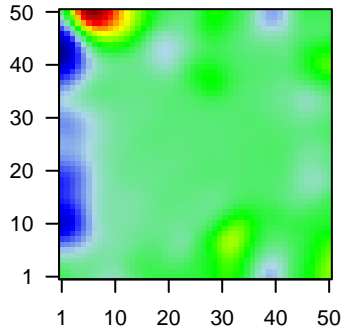
%DE = 0.9
 # metagenes = 16
 # genes = 214
 # genes in genesets = 214

 # genes with $fdr < 0.1$ = 181 (173 + / 8 -)
 # genes with $fdr < 0.05$ = 174 (169 + / 5 -)
 # genes with $fdr < 0.01$ = 159 (157 + / 2 -)

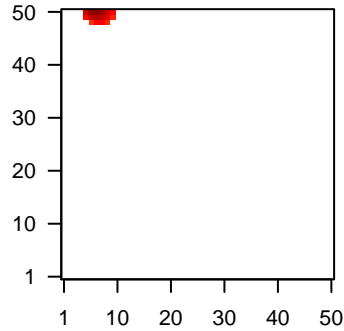
$\langle r \rangle$ metagenes = 0.98
 $\langle r \rangle$ genes = 0.35

 $\langle FC \rangle$ = 0.89
 $\langle \text{shrinkage-t} \rangle$ = 14.42
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.21

Profile



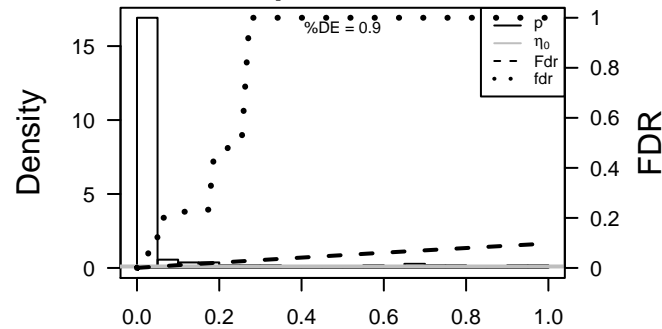
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	CALM2	0.86	2e-16	7e-16	9 x 49 calmodulin 2 (phosphorylase kinase, delta) [Source:HGNC S]
2	CCNB1	2.14	2e-16	7e-16	7 x 50 cyclin B1 [Source:HGNC Symbol;Acc:HGNC:1579]
3	CDKN3	1.68	2e-16	7e-16	6 x 50 cyclin-dependent kinase inhibitor 3 [Source:HGNC Symbol;A
4	KPNA2	1.04	2e-16	7e-16	7 x 50 karyopherin alpha 2 (RAG cohort 1, importin alpha 1) [Source
5	NEK2	2.14	2e-16	7e-16	8 x 50 NIMA-related kinase 2 [Source:HGNC Symbol;Acc:HGNC:77
6	PLK1	2.03	2e-16	7e-16	8 x 50 polo-like kinase 1 [Source:HGNC Symbol;Acc:HGNC:9077]
7	UBE2C	2.13	2e-16	7e-16	6 x 50 ubiquitin-conjugating enzyme E2C [Source:HGNC Symbol;A
8	CDK1	1.95	4e-16	3e-14	5 x 50 cyclin-dependent kinase 1 [Source:HGNC Symbol;Acc:HGNC
9	KIF20A	1.97	4e-16	3e-14	7 x 50 kinesin family member 20A [Source:HGNC Symbol;Acc:HGNC
10	PRR11	1.93	2e-15	5e-14	7 x 50 proline rich 11 [Source:HGNC Symbol;Acc:HGNC:25619]
11	CDC20	1.9	4e-15	8e-14	6 x 50 cell division cycle 20 [Source:HGNC Symbol;Acc:HGNC:1723
12	DLGAP5	1.88	8e-15	4e-13	7 x 50 discs, large (Drosophila) homolog-associated protein 5 [Sour
13	CDC25C	1.83	4e-14	4e-13	8 x 50 cell division cycle 25C [Source:HGNC Symbol;Acc:HGNC:17
14	ARL6IP1	1.13	5e-14	3e-12	9 x 50 ADP-ribosylation factor-like 6 interacting protein 1 [Source:H
15	TOP2A	1.78	2e-13	6e-12	6 x 50 topoisomerase (DNA) II alpha 170kDa [Source:HGNC Symbc
16	FAM64A	1.75	5e-13	6e-12	7 x 50 family with sequence similarity 64, member A [Source:HGNC
17	CCNB2	1.73	8e-13	2e-11	6 x 50 cyclin B2 [Source:HGNC Symbol;Acc:HGNC:1580]
18	NCAPG	1.69	3e-12	2e-11	6 x 50 non-SMC condensin I complex, subunit G [Source:HGNC Sy
19	PTTG1	1.05	3e-12	2e-11	7 x 50 pituitary tumor-transforming 1 [Source:HGNC Symbol;Acc:H
20	PRC1	1.61	3e-12	2e-11	5 x 50 protein regulator of cytokinesis 1 [Source:HGNC Symbol;Acc:

p-values



E9_mel

Local Summary

%DE = 0.89
 # metagenes = 7
 # genes = 147
 # genes in genesets = 146

 # genes with $fdr < 0.1$ = 114 (16 + / 98 -)
 # genes with $fdr < 0.05$ = 100 (11 + / 89 -)
 # genes with $fdr < 0.01$ = 73 (8 + / 65 -)

<r> metagenes = 0.98

<r> genes = 0.17

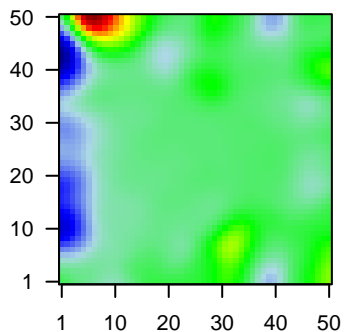
<FC> = -0.47

<shrinkage-t> = -8.43

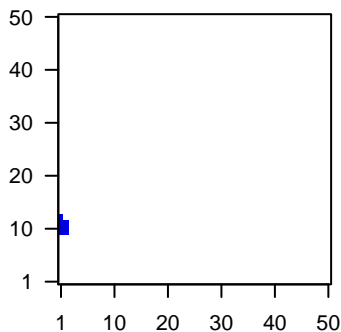
<p-value> = 0

<fdr> = 0.43

Profile



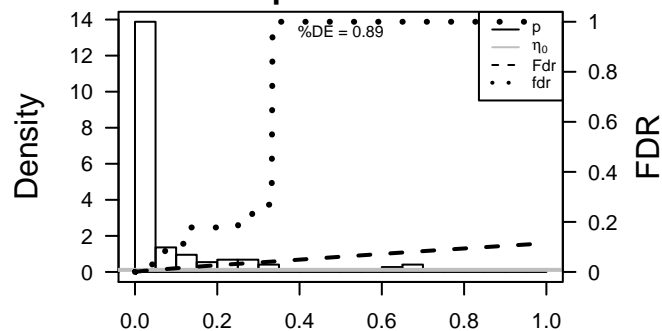
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ATP6V0A1	-1.62	2e-16	9e-16	1 x 10 ATPase, H+ transporting, lysosomal V0 subunit a1 [Source:HGNC Symbol;Acc:NCBI]
2	ATP6V1D	-1.07	2e-16	9e-16	1 x 11 ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D [Source:HGNC Symbol;Acc:NCBI]
3	GPR143	-1.78	2e-16	9e-16	1 x 11 G protein-coupled receptor 143 [Source:HGNC Symbol;Acc:NCBI]
4	SGK1	-2.35	2e-16	9e-16	1 x 13 serum/glucocorticoid regulated kinase 1 [Source:HGNC Symbol;Acc:NCBI]
5	ID2	-0.77	4e-15	9e-14	1 x 13 inhibitor of DNA binding 2, dominant negative helix-loop-helix [Source:HGNC Symbol;Acc:NCBI]
6	DAAM1	-1.45	9e-15	1e-10	1 x 12 dishevelled associated activator of morphogenesis 1 [Source:HGNC Symbol;Acc:NCBI]
7	CABLES1	-1.43	8e-12	6e-10	1 x 13 Cdk5 and Abl enzyme substrate 1 [Source:HGNC Symbol;Acc:NCBI]
8	MET	-1.4	4e-11	2e-09	1 x 11 MET proto-oncogene, receptor tyrosine kinase [Source:HGNC Symbol;Acc:NCBI]
9	LYRM9	1.54	2e-10	7e-08	1 x 12 LYR motif containing 9 [Source:HGNC Symbol;Acc:NCBI]
10	KLHL24	-1.3	4e-09	7e-08	1 x 11 kelch-like family member 24 [Source:HGNC Symbol;Acc:NCBI]
11	CEACAM1	-1.27	9e-09	2e-07	1 x 10 carcinoembryonic antigen-related cell adhesion molecule 1 [Source:HGNC Symbol;Acc:NCBI]
12	SEMA6A	-0.71	2e-08	2e-06	1 x 11 sema domain, transmembrane domain (TM), and cytoplasmic tail domain containing 6A [Source:HGNC Symbol;Acc:NCBI]
13	HSPB8	-1.14	1e-07	4e-06	1 x 11 heat shock 22kDa protein 8 [Source:HGNC Symbol;Acc:NCBI]
14	TULP4	-1.01	5e-07	4e-06	1 x 11 tubby like protein 4 [Source:HGNC Symbol;Acc:NCBI]
15	SNAI2	-1.1	6e-07	2e-05	1 x 11 snail family zinc finger 2 [Source:HGNC Symbol;Acc:NCBI]
16	BHLHE41	-1.11	3e-06	2e-05	1 x 12 basic helix-loop-helix family, member e41 [Source:HGNC Symbol;Acc:NCBI]
17	VEPH1	-1.11	3e-06	2e-05	1 x 11 ventricular zone expressed PH domain-containing 1 [Source:HGNC Symbol;Acc:NCBI]
18	FNIP2	-1.11	4e-06	2e-05	1 x 11 follistatin interacting protein 2 [Source:HGNC Symbol;Acc:NCBI]
19	SCUBE3	-1.09	5e-06	2e-05	1 x 12 signal peptide, CUB domain, EGF-like 3 [Source:HGNC Symbol;Acc:NCBI]
20	SEMA3C	-1.08	6e-06	2e-04	1 x 10 sema domain, immunoglobulin domain (Ig), short basic domain type 3 [Source:HGNC Symbol;Acc:NCBI]

p-values



E9_mel

Local Summary

%DE = 0.82
 # metagenes = 15
 # genes = 232
 # genes in genesets = 230

 # genes with $fdr < 0.1$ = 155 (8 + / 147 -)
 # genes with $fdr < 0.05$ = 143 (6 + / 137 -)
 # genes with $fdr < 0.01$ = 121 (5 + / 116 -)

<r> metagenes = 0.96

<r> genes = 0.19

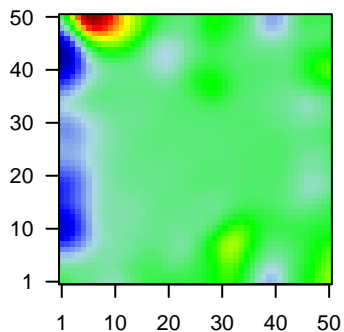
<FC> = -0.61

<shrinkage-t> = -12.37

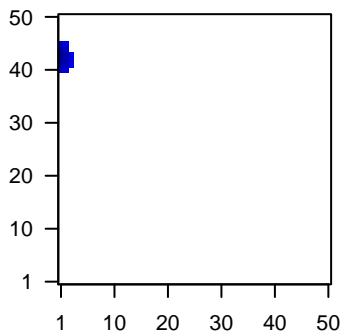
<p-value> = 0

<fdr> = 0.4

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	AHCY	-1.42	2e-16	4e-16	1 x 41 adenosylhomocysteinase [Source:HGNC Symbol;Acc:HGNC:10000]
2	APEH	-1.62	2e-16	4e-16	1 x 42 acylaminoacyl-peptidase [Source:HGNC Symbol;Acc:HGNC:10000]
3	ARHGAP8	-1.72	2e-16	4e-16	1 x 43 Rho GTPase activating protein 8 [Source:HGNC Symbol;Acc:HGNC:10000]
4	BACE2	-1.65	2e-16	4e-16	1 x 42 beta-site APP-cleaving enzyme 2 [Source:HGNC Symbol;Acc:HGNC:10000]
5	CAPN3	-1.99	2e-16	4e-16	1 x 43 calpain 3, (p94) [Source:HGNC Symbol;Acc:HGNC:1480]
6	CITED1	-1.99	2e-16	4e-16	1 x 41 Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain 1 [Source:HGNC Symbol;Acc:HGNC:10000]
7	CTSC	-1.36	2e-16	4e-16	1 x 42 cathepsin C [Source:HGNC Symbol;Acc:HGNC:2528]
8	CTSL	-1.06	2e-16	4e-16	2 x 40 cathepsin L [Source:HGNC Symbol;Acc:HGNC:2537]
9	DERA	-1.79	2e-16	4e-16	1 x 43 deoxyribose-phosphate aldolase (putative) [Source:HGNC Symbol;Acc:HGNC:10000]
10	EXOC3	-1.12	2e-16	4e-16	1 x 42 exocyst complex component 3 [Source:HGNC Symbol;Acc:HGNC:10000]
11	GNPDA1	-1.77	2e-16	4e-16	1 x 42 glucosamine-6-phosphate deaminase 1 [Source:HGNC Symbol;Acc:HGNC:10000]
12	HDAC2	-1.35	2e-16	4e-16	1 x 45 histone deacetylase 2 [Source:HGNC Symbol;Acc:HGNC:4800]
13	MBP	-2.22	2e-16	4e-16	1 x 42 myelin basic protein [Source:HGNC Symbol;Acc:HGNC:6925]
14	METTL9	-1.87	2e-16	4e-16	1 x 43 methyltransferase like 9 [Source:HGNC Symbol;Acc:HGNC:20000]
15	MLANA	-1.86	2e-16	4e-16	1 x 43 melan-A [Source:HGNC Symbol;Acc:HGNC:7124]
16	MYH10	-1.38	2e-16	4e-16	1 x 44 myosin, heavy chain 10, non-muscle [Source:HGNC Symbol;Acc:HGNC:10000]
17	PDE4DIP	-1.91	2e-16	4e-16	1 x 43 phosphodiesterase 4D interacting protein [Source:HGNC Symbol;Acc:HGNC:10000]
18	PLP1	-1.83	2e-16	4e-16	1 x 42 proteolipid protein 1 [Source:HGNC Symbol;Acc:HGNC:9086]
19	SLC39A6	-1.21	2e-16	4e-16	1 x 42 solute carrier family 39 (zinc transporter), member 6 [Source:HGNC Symbol;Acc:HGNC:10000]
20	ST6GALNAC1	-1.6	2e-16	4e-16	1 x 44 ST6 (alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-galactosyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:10000]

p-values

