

G12_mel

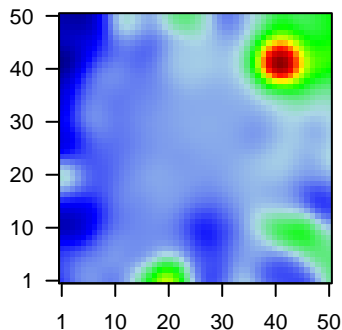
Global Summary

%DE = 0.24
 # genes with fdr < 0.2 = 3076 (1815 + / 1261 -)
 # genes with fdr < 0.1 = 2599 (1572 + / 1027 -)
 # genes with fdr < 0.05 = 2259 (1369 + / 890 -)
 # genes with fdr < 0.01 = 1426 (870 + / 556 -)

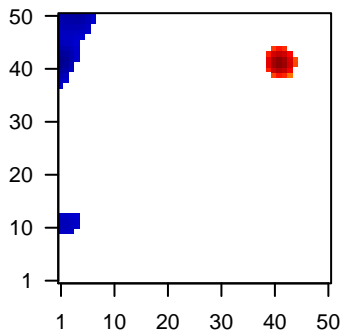
genes in genesets = 14839

<FC> = 0
 <shrinkage-t> = -0.07
 <p-value> = 0.05
 <fdr> = 0.76

Profile



Regulated Spots



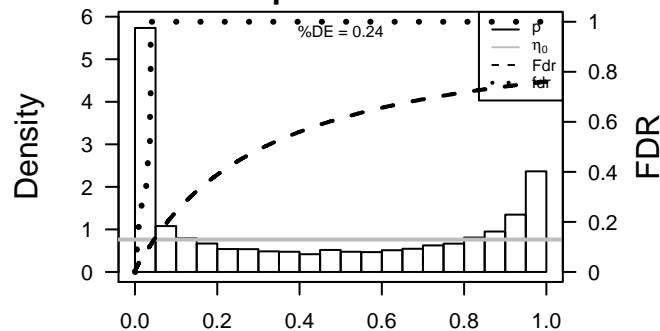
Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	ADSL	-1.61	2e-16 4e-14	28 x 50 adenylosuccinate lyase [Source:HGNC Symbol;Acc:HGNC:2]
2	ARHGAP8	-1.72	2e-16 4e-14	1 x 43 Rho GTPase activating protein 8 [Source:HGNC Symbol;Acc:
3	ATXN10	-1.76	2e-16 4e-14	46 x 17 ataxin 10 [Source:HGNC Symbol;Acc:HGNC:10549]
4	BZW2	-1.5	2e-16 4e-14	2 x 16 basic leucine zipper and W2 domains 2 [Source:HGNC Symb
5	C1orf198	-1.52	2e-16 4e-14	49 x 1 chromosome 1 open reading frame 198 [Source:HGNC Synt
6	CCDC171	-1.57	2e-16 4e-14	1 x 11 coiled-coil domain containing 171 [Source:HGNC Symbol;Ac
7	CDK2	-1.97	2e-16 4e-14	1 x 43 cyclin-dependent kinase 2 [Source:HGNC Symbol;Acc:HGNC
8	CDKL1	2.2	2e-16 4e-14	42 x 40 cyclin-dependent kinase-like 1 (CDC2-related kinase) [Sour
9	CEP97	1.87	2e-16 4e-14	2 x 47 centrosomal protein 97kDa [Source:HGNC Symbol;Acc:HGNC
10	CHCHD6	-1.78	2e-16 4e-14	1 x 43 coiled-coil-helix-coiled-coil-helix domain containing 6 [Sour
11	CHD1	-1.53	2e-16 4e-14	1 x 31 chromodomain helicase DNA binding protein 1 [Source:HGNC
12	CITED1	-1.99	2e-16 4e-14	1 x 41 Cbp/p300-interacting transactivator, with Glu/Asp-rich carbo
13	CKS2	-1.66	2e-16 4e-14	5 x 50 CDC28 protein kinase regulatory subunit 2 [Source:HGNC S
14	DAB2	-0.97	2e-16 4e-14	3 x 41 Dab, mitogen-responsive phosphoprotein, homolog 2 (Droso
15	DCAF13	-1.73	2e-16 4e-14	1 x 1 DDB1 and CUL4 associated factor 13 [Source:HGNC Symbo
16	DCT	-1.55	2e-16 4e-14	1 x 11 dopachrome tautomerase [Source:HGNC Symbol;Acc:HGNC
17	DERA	-1.57	2e-16 4e-14	1 x 43 deoxyribose-phosphate aldolase (putative) [Source:HGNC S
18	DHX15	-1.54	2e-16 4e-14	1 x 27 DEAH (Asp-Glu-Ala-His) box helicase 15 [Source:HGNC S
19	DUSP6	-1.73	2e-16 4e-14	34 x 50 dual specificity phosphatase 6 [Source:HGNC Symbol;Acc:Hi
20	EBP	-2.01	2e-16 4e-14	1 x 48 emopamil binding protein (sterol isomerase) [Source:HGNC S

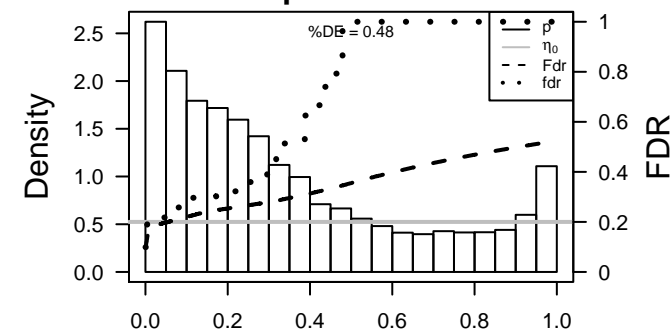
Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	5.68	0.002	30	GSEA C2FARDIN_HYPOXIA_11
2	4.87	0.004	25	GSEA C2REACTOME_GLYCOLYSIS
3	4.42	0.005	35	BP glycolytic process
4	4.39	0.006	129	BP autophagy
5	4.3	0.006	43	BP autophagic vacuole assembly
6	4.13	0.007	2698	Colon Cancer Colon
7	4.06	0.007	48	GSEA C2KEGG_GLYCOLYSIS_GLUconeogenesis
8	4.04	0.007	6	GSEA C2FARDIN_HYPOXIA_9
9	4.02	0.007	57	GSEA C2REACTOME_GLUcose_Metabolism
10	3.95	0.008	117	GSEA C2REACTOME_Membrane_Trafficking
11	3.89	0.008	39	CC autophagic vacuole
12	3.88	0.008	32	BP mitochondrion degradation
13	3.8	0.009	44	GSEA C2REACTOME_Packaging_of_Telomere_Ends
14	3.72	0.009	13	CC COPI vesicle coat
15	3.68	0.010	146	GSEA C2MARTORIATI_MDM4_TARGETS_Neuroepithelium_Up
16	3.67	0.010	91	GSEA C2MENSE_HYPOXIA_UP
17	3.6	0.010	293	GSEA C2DOUGLAS_BMI1_TARGETS_DN
18	3.57	0.011	30	GSEA C2KEGG_FRUCTOSE_AND_Mannose_Metabolism
19	3.57	0.011	1218	Lymphoma SPANG_BCR UP
20	3.55	0.011	1037	Chr Chr 19
<i>Underexpressed</i>				
1	-11.6	1e-04	1251	GSEA C2DODD_NASOPHARYNGEAL_Carcinoma_DN
2	-10.37	2e-04	13	BP melanin biosynthetic process
3	-10.29	2e-04	139	GSEA C2ROSTY_CERVICAL_Cancer_Proliferation_Cluster
4	-10.24	2e-04	1192	GSEA C2KINSEY_TARGETS_OF_EWSR1_FLII_Fusion_Up
5	-10.2	2e-04	242	GSEA C2OBAYASHI_EGFR_Signaling_24HR_DN
6	-10.19	2e-04	197	HM HALLMARK_E2F_TARGETS
7	-10.17	2e-04	550	GSEA C2GOBERT_OLIGODENDROCYTE_Differentiation_Up
8	-9.55	3e-04	267	GSEA C2ZHANG_TLX_TARGETS_60HR_DN
9	-9.48	3e-04	1460	GSEA C2PUJANA_BRCA1_PCC_NETWORK
10	-9.45	3e-04	724	GSEA C2PUJANA_CHEK2_PCC_NETWORK
11	-9.38	3e-04	834	GSEA C2LEE_BMP2_TARGETS_DN
12	-9.31	3e-04	18	BP melanocyte differentiation
13	-9.08	4e-04	50	GSEA C2SHIDA_E2F_TARGETS
14	-8.91	1e-01	16	Cancer SOTIRIOU_BREAST_Cancer_Grade_1_Vs_3_Up
15	-8.71	5e-04	505	GSEA C2BERENJENO_TRANSFORMED_BY_RHOA_UP
16	-8.61	5e-04	216	GSEA C2MARKEY_RB1_ACUTE_LOF_DN
17	-8.59	5e-04	268	GSEA C2FOURNIER_ACINAR_Development_Late_2
18	-8.37	5e-04	436	GSEA C2SHEDDEN_LUNG_Cancer_Poor_Survival_A6
19	-8.24	6e-04	142	Glio WILLSCHER_GBM_Verhaak-CL_up (C)
20	-8.19	6e-04	562	GSEA C2CAIRO_HEPATOBlastoma_Classes_Up

p-values



p-values



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Local Summary

%DE = 0.99
 # metagenes = 29
 # genes = 237
 # genes in genesets = 236

 # genes with $fdr < 0.1$ = 234 (234 + / 0 -)
 # genes with $fdr < 0.05$ = 234 (234 + / 0 -)
 # genes with $fdr < 0.01$ = 234 (234 + / 0 -)

<r> metagenes = 0.92

<r> genes = 0.21

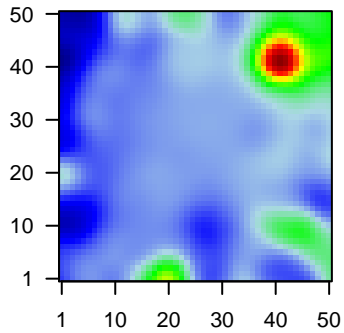
<FC> = 1.15

<shrinkage-t> = 17.51

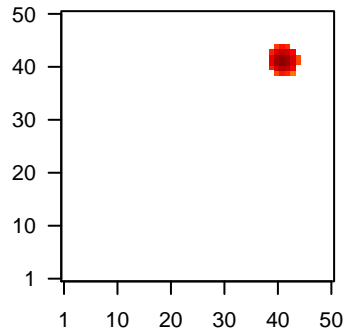
<p-value> = 0

<fdr> = 0.03

Profile



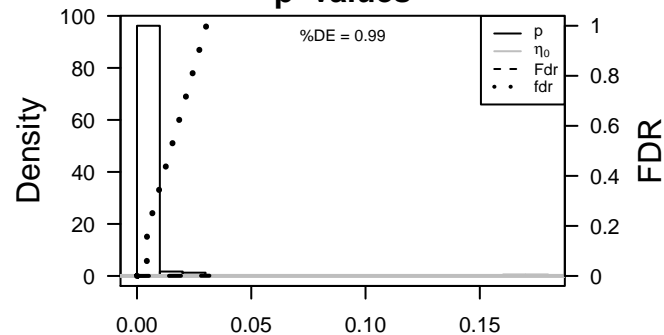
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	CDKL1	2.2	2e-16	3e-16	42 x 40 cyclin-dependent kinase-like 1 (CDC2-related kinase) [Sour
2	TMEM55B	1.81	1e-13	7e-14	42 x 43 transmembrane protein 55B [Source:HGNC Symbol;Acc:HGNC:11787]
3	SLC22A1	1.81	1e-13	1e-13	41 x 41 solute carrier family 22 (organic cation transporter), member 1
4	THBS3	1.78	2e-13	1e-13	41 x 41 thrombospondin 3 [Source:HGNC Symbol;Acc:HGNC:11787]
5	TBC1D19	1.77	3e-13	1e-13	42 x 41 TBC1 domain family, member 19 [Source:HGNC Symbol;Acc:HGNC:11787]
6	SPTLC3	1.76	5e-13	1e-13	41 x 41 serine palmitoyltransferase, long chain base subunit 3 [Source:HGNC Symbol;Acc:HGNC:11787]
7	SLC25A42	1.76	5e-13	3e-13	41 x 41 solute carrier family 25, member 42 [Source:HGNC Symbol;Acc:HGNC:11787]
8	PFKFB4	1.74	9e-13	3e-13	40 x 42 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 4 [Source:HGNC Symbol;Acc:HGNC:11787]
9	PFKP	1.73	1e-12	6e-13	42 x 41 phosphofructokinase, platelet [Source:HGNC Symbol;Acc:HGNC:11787]
10	RNASET2	1.72	2e-12	6e-13	41 x 41 ribonuclease T2 [Source:HGNC Symbol;Acc:HGNC:21686]
11	PAFAH2	1.7	3e-12	6e-13	43 x 42 platelet-activating factor acetylhydrolase 2, 40kDa [Source:HGNC Symbol;Acc:HGNC:11787]
12	ZACN	1.7	3e-12	6e-13	41 x 41 zinc activated ligand-gated ion channel [Source:HGNC Symbol;Acc:HGNC:11787]
13	STAP2	1.7	3e-12	9e-13	41 x 41 signal transducing adaptor family member 2 [Source:HGNC Symbol;Acc:HGNC:11787]
14	PLA2G1B	1.69	4e-12	2e-12	41 x 41 phospholipase A2, group IB (pancreas) [Source:HGNC Symbol;Acc:HGNC:11787]
15	GTF2A1L	1.67	7e-12	2e-12	41 x 41 general transcription factor IIA, 1-like [Source:HGNC Symbol;Acc:HGNC:11787]
16	SLC22A5	1.66	8e-12	2e-12	41 x 41 solute carrier family 22 (organic cation/carnitine transporter), member 5
17	KCNAB3	1.66	9e-12	2e-12	41 x 41 potassium channel, voltage gated subfamily A regulatory beta subunit 3
18	CREB3L4	1.65	1e-11	2e-12	40 x 42 cAMP responsive element binding protein 3-like 4 [Source:HGNC Symbol;Acc:HGNC:11787]
19	TLCD1	1.65	1e-11	4e-12	40 x 41 TLC domain containing 1 [Source:HGNC Symbol;Acc:HGNC:11787]
20	CXorf57	1.64	2e-11	4e-12	41 x 42 chromosome X open reading frame 57 [Source:HGNC Symbol;Acc:HGNC:11787]

p-values



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Local Summary

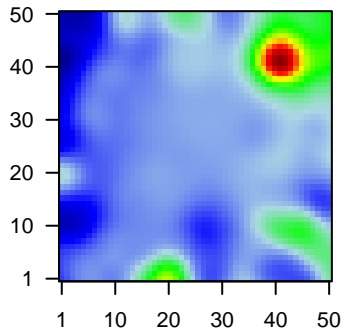
%DE = 0.74
 # metagenes = 15
 # genes = 202
 # genes in genesets = 201

 # genes with $fdr < 0.1$ = 104 (16 + / 88 -)
 # genes with $fdr < 0.05$ = 90 (14 + / 76 -)
 # genes with $fdr < 0.01$ = 61 (10 + / 51 -)

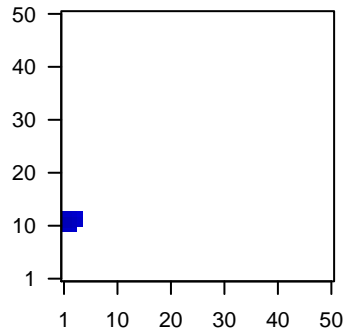
$\langle r \rangle$ metagenes = 0.97
 $\langle r \rangle$ genes = 0.15

 $\langle FC \rangle$ = -0.38
 $\langle \text{shrinkage-t} \rangle$ = -6.69
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.53

Profile



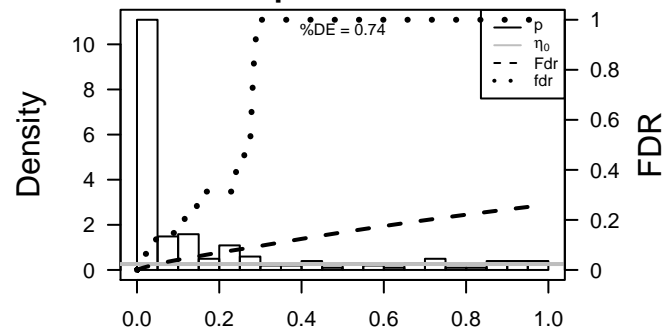
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	CCDC171	-1.57	2e-16	2e-15	1 x 11 coiled-coil domain containing 171 [Source:HGNC Symbol;Acc:HGNC:100000]
2	DCT	-1.55	2e-16	2e-15	1 x 11 dopachrome tautomerase [Source:HGNC Symbol;Acc:HGNC:100000]
3	HMGCR	-1.62	2e-16	2e-15	2 x 11 3-hydroxy-3-methylglutaryl-CoA reductase [Source:HGNC Symbol;Acc:HGNC:100000]
4	TYRP1	-1.7	2e-16	2e-15	2 x 13 tyrosinase-related protein 1 [Source:HGNC Symbol;Acc:HGNC:100000]
5	WDR43	-1.69	2e-16	2e-15	4 x 11 WD repeat domain 43 [Source:HGNC Symbol;Acc:HGNC:28000]
6	ZZZ3	-1.5	3e-15	4e-13	1 x 11 zinc finger, ZZ-type containing 3 [Source:HGNC Symbol;Acc:HGNC:100000]
7	EDNRB	-1.49	1e-14	6e-10	1 x 11 endothelin receptor type B [Source:HGNC Symbol;Acc:HGNC:100000]
8	NAV2	-1.3	1e-11	2e-09	1 x 12 neuron navigator 2 [Source:HGNC Symbol;Acc:HGNC:15997]
9	ADAM10	-1.08	4e-11	7e-09	4 x 11 ADAM metallopeptidase domain 10 [Source:HGNC Symbol;Acc:HGNC:100000]
10	SAT1	-0.62	2e-10	7e-09	1 x 11 spermidine/spermine N1-acetyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:100000]
11	MET	-1.34	3e-10	2e-08	1 x 11 MET proto-oncogene, receptor tyrosine kinase [Source:HGNC Symbol;Acc:HGNC:100000]
12	FARP1	-1.34	7e-10	2e-07	1 x 11 FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 [Source:HGNC Symbol;Acc:HGNC:100000]
13	MRS2	-1.29	6e-09	2e-07	1 x 13 MRS2 magnesium transporter [Source:HGNC Symbol;Acc:HGNC:100000]
14	DAAM1	-1.08	9e-09	1e-06	1 x 12 dishevelled associated activator of morphogenesis 1 [Source:HGNC Symbol;Acc:HGNC:100000]
15	DCTN5	-1.23	3e-08	2e-06	4 x 11 dynactin 5 (p25) [Source:HGNC Symbol;Acc:HGNC:24594]
16	RCHY1	-1.23	6e-08	3e-06	2 x 13 ring finger and CHY zinc finger domain containing 1, E3 ubiquitin-protein ligase [Source:HGNC Symbol;Acc:HGNC:100000]
17	GPRC5B	-1.22	1e-07	4e-05	1 x 12 G protein-coupled receptor, class C, group 5, member B [Source:HGNC Symbol;Acc:HGNC:100000]
18	SNAI2	-1.08	1e-06	4e-05	1 x 11 snail family zinc finger 2 [Source:HGNC Symbol;Acc:HGNC:100000]
19	PDE3A	1.15	2e-06	4e-05	2 x 12 phosphodiesterase 3A, cGMP-inhibited [Source:HGNC Symbol;Acc:HGNC:100000]
20	BHLHE41	-1.13	2e-06	4e-05	1 x 12 basic helix-loop-helix family, member e41 [Source:HGNC Symbol;Acc:HGNC:100000]

p-values



G12_mel

Local Summary

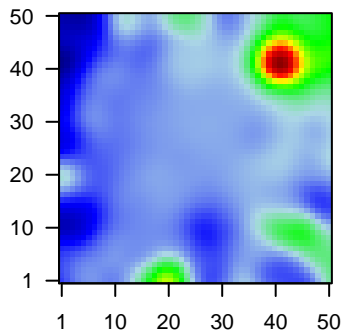
%DE = 0.75
 # metagenes = 58
 # genes = 822
 # genes in genesets = 819

 # genes with $fdr < 0.1$ = 471 (94 + / 377 -)
 # genes with $fdr < 0.05$ = 376 (68 + / 308 -)
 # genes with $fdr < 0.01$ = 274 (42 + / 232 -)

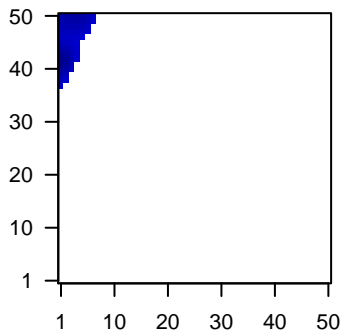
 $\langle r \rangle$ metagenes = 0.73
 $\langle r \rangle$ genes = 0.14

 $\langle FC \rangle$ = -0.35
 $\langle \text{shrinkage-t} \rangle$ = -6.56
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.5

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ARHGAP8	-1.72	2e-16	2e-15	1 x 43 Rho GTPase activating protein 8 [Source:HGNC Symbol;Acc:HGNC:10404]
2	CDK2	-1.97	2e-16	2e-15	1 x 43 cyclin-dependent kinase 2 [Source:HGNC Symbol;Acc:HGNC:10404]
3	CEP97	1.87	2e-16	2e-15	2 x 47 centrosomal protein 97kDa [Source:HGNC Symbol;Acc:HGNC:10404]
4	CHCHD6	-1.78	2e-16	2e-15	1 x 43 coiled-coil-helix-coiled-coil-helix domain containing 6 [Source:HGNC Symbol;Acc:HGNC:10404]
5	CITED1	-1.99	2e-16	2e-15	1 x 41 Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain 1 [Source:HGNC Symbol;Acc:HGNC:10404]
6	CKS2	-1.66	2e-16	2e-15	5 x 50 CDC28 protein kinase regulatory subunit 2 [Source:HGNC Symbol;Acc:HGNC:10404]
7	DAB2	-0.97	2e-16	2e-15	3 x 41 Dab, mitogen-responsive phosphoprotein, homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:HGNC:10404]
8	DERA	-1.57	2e-16	2e-15	1 x 43 deoxyribose-phosphate aldolase (putative) [Source:HGNC Symbol;Acc:HGNC:10404]
9	EBP	-2.01	2e-16	2e-15	1 x 48 emopamil binding protein (sterol isomerase) [Source:HGNC Symbol;Acc:HGNC:10404]
10	EXOC3	-1.2	2e-16	2e-15	1 x 42 exocyst complex component 3 [Source:HGNC Symbol;Acc:HGNC:10404]
11	FAM213A	-1.66	2e-16	2e-15	1 x 41 family with sequence similarity 213, member A [Source:HGNC Symbol;Acc:HGNC:10404]
12	GPM6B	-1.63	2e-16	2e-15	3 x 42 glycoprotein M6B [Source:HGNC Symbol;Acc:HGNC:4461]
13	GUCD1	-1.6	2e-16	2e-15	1 x 47 guanylyl cyclase domain containing 1 [Source:HGNC Symbol;Acc:HGNC:10404]
14	IDH3A	-0.97	2e-16	2e-15	1 x 42 isocitrate dehydrogenase 3 (NAD+) alpha [Source:HGNC Symbol;Acc:HGNC:10404]
15	IVNS1ABP	-1.36	2e-16	2e-15	4 x 44 influenza virus NS1A binding protein [Source:HGNC Symbol;Acc:HGNC:10404]
16	MBP	-1.55	2e-16	2e-15	1 x 42 myelin basic protein [Source:HGNC Symbol;Acc:HGNC:6925]
17	METTL9	-1.37	2e-16	2e-15	1 x 43 methyltransferase like 9 [Source:HGNC Symbol;Acc:HGNC:10404]
18	MITF	-1.93	2e-16	2e-15	1 x 41 microphthalmia-associated transcription factor [Source:HGNC Symbol;Acc:HGNC:10404]
19	MLANA	-1.46	2e-16	2e-15	1 x 43 melan-A [Source:HGNC Symbol;Acc:HGNC:7124]
20	MLIP	-1.52	2e-16	2e-15	3 x 44 muscular LMNA-interacting protein [Source:HGNC Symbol;Acc:HGNC:10404]

p-values

