

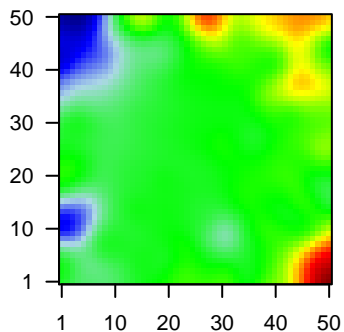
B4_mel

Global Summary

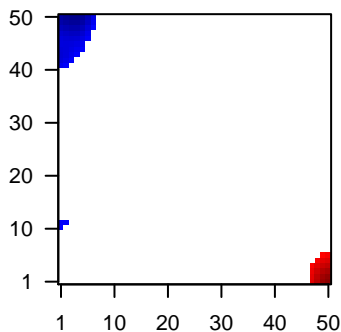
%DE = 0.21
 # genes with fdr < 0.2 = 2631 (1572 + / 1059 -)
 # genes with fdr < 0.1 = 2100 (1259 + / 841 -)
 # genes with fdr < 0.05 = 1653 (991 + / 662 -)
 # genes with fdr < 0.01 = 1049 (645 + / 404 -)
 # genes in genesets = 14839

<FC> = 0
 <shrinkage-t> = -0.01
 <p-value> = 0.08
 <fdr> = 0.79

Profile



Regulated Spots

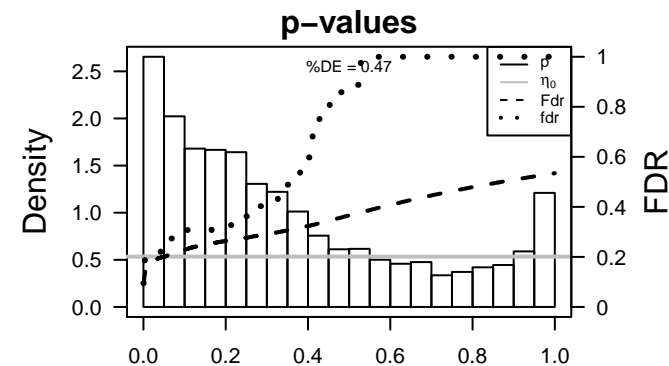
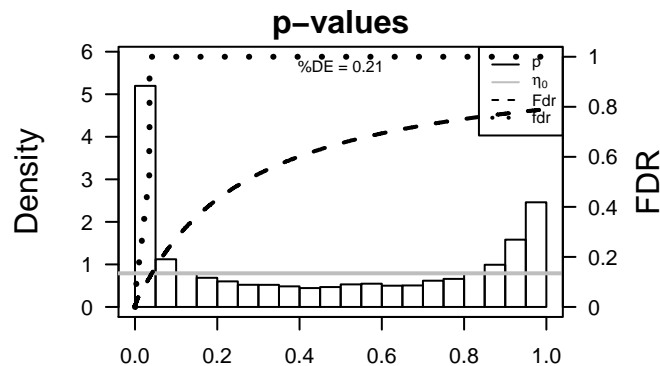


Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	ACADM	-1.6	2e-16 9e-14	1 x 45 acyl-CoA dehydrogenase, C-4 to C-12 straight chain [Source:HGNC Symbol;Acc:HGNC:533]
2	AKR1B1	-1.45	2e-16 9e-14	12 x 40 aldo-keto reductase family 1, member B1 (aldose reductase)
3	ANXA1	2.28	2e-16 9e-14	50 x 1 annexin A1 [Source:HGNC Symbol;Acc:HGNC:533]
4	ARHGAP8	-1.74	2e-16 9e-14	1 x 43 Rho GTPase activating protein 8 [Source:HGNC Symbol;Acc:HGNC:533]
5	ARL8B	-1.94	2e-16 9e-14	1 x 33 ADP-ribosylation factor-like 8B [Source:HGNC Symbol;Acc:HGNC:533]
6	CDK4	-1.62	2e-16 9e-14	3 x 44 cyclin-dependent kinase 4 [Source:HGNC Symbol;Acc:HGNC:533]
7	DCT	-1.7	2e-16 9e-14	1 x 11 dopachrome tautomerase [Source:HGNC Symbol;Acc:HGNC:533]
8	DCTN2	-1.57	2e-16 9e-14	50 x 44 dynactin 2 (p50) [Source:HGNC Symbol;Acc:HGNC:2712]
9	DEGS1	-1.93	2e-16 9e-14	9 x 43 delta(4)-desaturase, sphingolipid 1 [Source:HGNC Symbol;Acc:HGNC:533]
10	DKK1	2.49	2e-16 9e-14	50 x 1 dickkopf WNT signaling pathway inhibitor 1 [Source:HGNC Symbol;Acc:HGNC:533]
11	FH	-1.6	2e-16 9e-14	5 x 39 fumarate hydratase [Source:HGNC Symbol;Acc:HGNC:3700]
12	FOS	-1.85	2e-16 9e-14	4 x 7 FBJ murine osteosarcoma viral oncogene homolog [Source:HGNC Symbol;Acc:HGNC:533]
13	GGCT	-2.06	2e-16 9e-14	1 x 47 gamma-glutamylcyclotransferase [Source:HGNC Symbol;Acc:HGNC:533]
14	GNAI1	-1.36	2e-16 9e-14	42 x 1 guanine nucleotide binding protein (G protein), alpha inhibiting 1 [Source:HGNC Symbol;Acc:HGNC:533]
15	HMGCR	-1.62	2e-16 9e-14	2 x 11 3-hydroxy-3-methylglutaryl-CoA reductase [Source:HGNC Symbol;Acc:HGNC:533]
16	ID2	-1.89	2e-16 9e-14	1 x 13 inhibitor of DNA binding 2, dominant negative helix-loop-helix protein 2 [Source:HGNC Symbol;Acc:HGNC:533]
17	LAMB2	-1.61	2e-16 9e-14	50 x 6 laminin, beta 2 (laminin S) [Source:HGNC Symbol;Acc:HGNC:533]
18	LGALS3BP	-1.31	2e-16 9e-14	47 x 17 lectin, galactoside-binding, soluble, 3 binding protein [Source:HGNC Symbol;Acc:HGNC:533]
19	MITF	-2.01	2e-16 9e-14	1 x 41 microphthalmia-associated transcription factor [Source:HGNC Symbol;Acc:HGNC:533]
20	NAV2	-1.58	2e-16 9e-14	1 x 12 neuron navigator 2 [Source:HGNC Symbol;Acc:HGNC:15997]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
Overexpressed				
1	7.21	9e-04	235	GSEA C2BLUM_RESPONSE_TO_SALIRASIB_UP
2	7.06	1e-03	222	GSEA C2CONCANNON_APOPTOSIS_BY_EPOXOMICIN_UP
3	6.47	1e-03	26	GSEA C2KRIGE_AMINO_ACID_DEPRIVATION
4	6.39	1e-03	176	GSEA C2TIEN_INTESTINE_PROBIOTICS_24HR_DN
5	5.84	2e-03	136	GSEA C2FODAR_RESPONSE_TO_ADAPHOSTIN_UP
6	5.51	3e-03	277	BP translation
7	5.43	3e-03	683	GSEA C2KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
8	5.38	3e-03	42	GSEA C2REACTOME_TRNA_AMINOACYLATION
9	5.31	3e-03	44	BP tRNA aminoacylation for protein translation
10	5.15	3e-03	1326	GSEA C2DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
11	5.13	3e-03	293	GSEA C2DOUGLAS_BMI1_TARGETS_DN
12	5.02	3e-03	245	GSEA C2FORTSCHEGGER_PHF8_TARGETS_UP
13	4.86	4e-03	34	GSEA C2HOUSTIS_ROS
14	4.84	4e-03	510	GSEA C2FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR
15	4.8	4e-03	13	GSEA C2ZHENG_RESPONSE_TO_ARSENITE_UP
16	4.74	4e-03	41	GSEA C2KEGG_AMINOACYL_TRNA_BIOSYNTHESIS
17	4.69	4e-03	472	GSEA C2DUTERTRE ESTRADIOL_RESPONSE_24HR_DN
18	4.69	4e-03	457	GSEA C2SENESE_HDAC3_TARGETS_UP
19	4.69	4e-03	35	MF aminoacyl-tRNA ligase activity
20	4.69	4e-03	24	GSEA C2REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION
Underexpressed				
1	-12.68	1e-04	142	Glio WILLSCHER_GBM_Verhaak-CL_up (C)
2	-12.65	1e-04	139	GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
3	-12.52	1e-04	242	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN
4	-12.4	1e-04	305	GSEA C2DUTERTRE ESTRADIOL_RESPONSE_24HR_UP
5	-11.79	1e-04	327	GSEA C2BLUM_RESPONSE_TO_SALIRASIB_DN
6	-11.27	2e-04	110	GSEA C2WHITEFORD_PEDIATRIC_CANCER_MARKERS
7	-11.17	2e-04	550	GSEA C2GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
8	-10.37	2e-04	197	HM HALLMARK_E2F_TARGETS
9	-10.12	2e-04	145	GSEA C2ZHANG_CYCLING_GENES
10	-9.89	3e-04	267	GSEA C2ZHANG_TLX_TARGETS_60HR_DN
11	-9.83	3e-04	96	GSEA C2CROONQUIST_IL6_DEPRIVATION_DN
12	-9.6	3e-04	50	GSEA C2SHIDA_E2F_TARGETS
13	-9.24	4e-04	84	GSEA C2ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_6HR
14	-9.19	4e-04	81	GSEA C2GRAHAM_NORMAL QUIESCENT_VS_NORMAL_DIVIDING_DN
15	-8.99	4e-04	116	GSEA C2MISSIAGLIA_REGULATED_BY_METHYLATION_DN
16	-8.84	4e-04	54	GSEA C2KANG_DOXORUBICIN_RESISTANCE_UP
17	-8.83	4e-04	390	GSEA C2PUJANA_BRCA2_PCC_NETWORK
18	-8.81	8e-03	16	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
19	-8.8	4e-04	99	GSEA C2BURTON_ADIPOGENESIS_3
20	-8.78	4e-04	87	GSEA C2ZHANG_TLX_TARGETS_UP



B4_mel

Local Summary

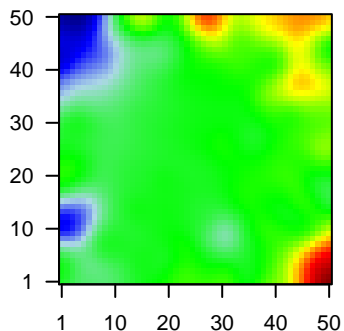
%DE = 0.77
 # metagenes = 21
 # genes = 320
 # genes in genesets = 319

 # genes with $fdr < 0.1$ = 199 (171 + / 28 -)
 # genes with $fdr < 0.05$ = 175 (155 + / 20 -)
 # genes with $fdr < 0.01$ = 131 (121 + / 10 -)

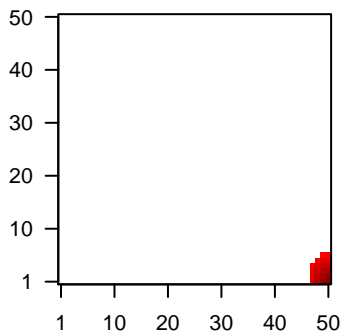
<r> metagenes = 0.97
 <r> genes = 0.19

<FC> = 0.45
 <shrinkage-t> = 7.23
 <p-value> = 0
 <fdr> = 0.44

Profile



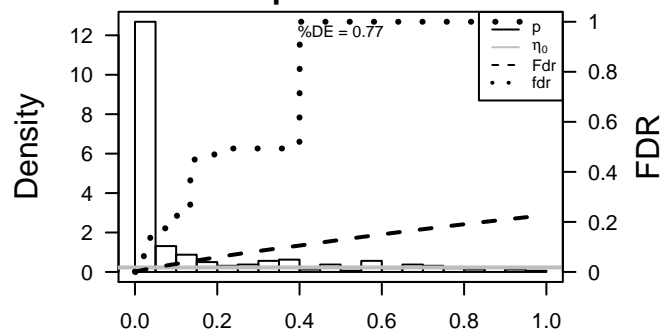
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ANXA1	2.28	2e-16	4e-15	50 x 1 annexin A1 [Source:HGNC Symbol;Acc:HGNC:533]
2	DKK1	2.49	2e-16	4e-15	50 x 1 dickkopf WNT signaling pathway inhibitor 1 [Source:HGNC S]
3	LAMB2	-1.61	2e-16	4e-15	50 x 6 laminin, beta 2 (laminin S) [Source:HGNC Symbol;Acc:HGNC
4	TXNRD1	0.9	2e-16	4e-15	48 x 4 thioredoxin reductase 1 [Source:HGNC Symbol;Acc:HGNC:1
5	MYEOV	1.89	8e-15	8e-12	47 x 4 myeloma overexpressed [Source:HGNC Symbol;Acc:HGNC:1
6	C10orf10	1.8	1e-13	8e-11	49 x 1 chromosome 10 open reading frame 10 [Source:HGNC Synt
7	CRYAB	1.13	1e-12	4e-10	50 x 1 crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
8	THBS1	1.65	1e-11	4e-10	50 x 1 thrombospondin 1 [Source:HGNC Symbol;Acc:HGNC:11785]
9	RND3	1.64	2e-11	4e-10	50 x 1 Rho family GTPase 3 [Source:HGNC Symbol;Acc:HGNC:671
10	PLK2	1.22	2e-11	1e-09	50 x 1 polo-like kinase 2 [Source:HGNC Symbol;Acc:HGNC:19699]
11	CDKN1A	1.61	4e-11	2e-09	50 x 1 cyclin-dependent kinase inhibitor 1A (p21, Cip1) [Source:HG
12	MYOF	1.59	6e-11	6e-09	50 x 1 myoferlin [Source:HGNC Symbol;Acc:HGNC:3656]
13	SLC7A11	1.55	2e-10	6e-09	49 x 4 solute carrier family 7 (anionic amino acid transporter light ch
14	DNAJC6	1.54	3e-10	6e-09	50 x 1 DnaJ (Hsp40) homolog, subfamily C, member 6 [Source:HGNC
15	LIMCH1	1.53	3e-10	1e-08	50 x 1 LIM and calponin homology domains 1 [Source:HGNC Symb
16	GLRX	1.51	5e-10	2e-08	50 x 2 glutaredoxin (thioltransferase) [Source:HGNC Symbol;Acc:HC
17	S100A10	1.49	8e-10	6e-08	50 x 4 S100 calcium binding protein A10 [Source:HGNC Symbol;Acc
18	ANXA2	0.59	2e-09	9e-08	50 x 3 annexin A2 [Source:HGNC Symbol;Acc:HGNC:537]
19	HBP1	1.44	3e-09	9e-08	50 x 4 HMG-box transcription factor 1 [Source:HGNC Symbol;Acc:1
20	BCL11A	1.42	6e-09	9e-08	47 x 1 B-cell CLL/lymphoma 11A (zinc finger protein) [Source:HGNC

p-values



B4_mel

Local Summary

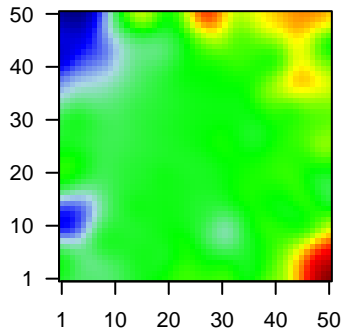
%DE = 0.8
 # metagenes = 3
 # genes = 92
 # genes in genesets = 91

 # genes with $fdr < 0.1$ = 57 (3 + / 54 -)
 # genes with $fdr < 0.05$ = 48 (3 + / 45 -)
 # genes with $fdr < 0.01$ = 36 (3 + / 33 -)

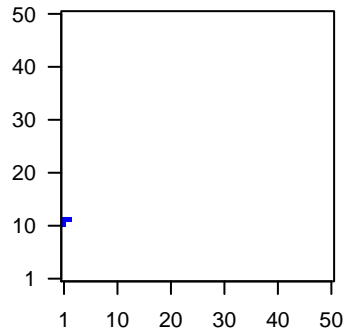
<r> metagenes = 1
 <r> genes = 0.2

 <FC> = -0.45
 <shrinkage-t> = -7.92
 <p-value> = 0
 <fdr> = 0.49

Profile



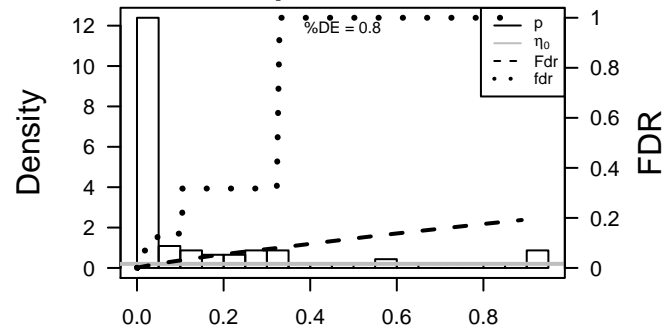
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	DCT	-1.7	2e-16	1e-15	1 x 11 dopachrome tautomerase [Source:HGNC Symbol;Acc:HGNC
2	NAV2	-1.58	2e-16	1e-15	1 x 12 neuron navigator 2 [Source:HGNC Symbol;Acc:HGNC:15997
3	TRAK2	-1.5	2e-16	1e-15	1 x 12 trafficking protein, kinesin binding 2 [Source:HGNC Symbol;A
4	ATP6V1D	-0.93	2e-15	6e-09	1 x 11 ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D [So
5	CCDC171	-1.21	3e-10	7e-09	1 x 11 coiled-coil domain containing 171 [Source:HGNC Symbol;Ac
6	SEMA6A	-0.78	8e-10	7e-09	1 x 11 sema domain, transmembrane domain (TM), and cytoplasmic
7	RAB27A	-1.22	1e-09	6e-08	1 x 11 RAB27A, member RAS oncogene family [Source:HGNC Sym
8	WDFY1	-1.26	5e-09	7e-07	1 x 12 WD repeat and FYVE domain containing 1 [Source:HGNC Sy
9	UGCG	-0.86	4e-08	4e-05	1 x 11 UDP-glucose ceramide glucosyltransferase [Source:HGNC E
10	VEPH1	-1.11	4e-06	4e-05	1 x 11 ventricular zone expressed PH domain-containing 1 [Source:
11	FNIP2	-1.11	4e-06	8e-05	1 x 11 folliculin interacting protein 2 [Source:HGNC Symbol;Acc:HGI
12	GPR19	-1.07	9e-06	5e-04	2 x 12 G protein-coupled receptor 19 [Source:HGNC Symbol;Acc:H
13	SEMA6D	-1	4e-05	5e-04	1 x 11 sema domain, transmembrane domain (TM), and cytoplasmic
14	ARAP1	-0.94	1e-04	5e-04	1 x 11 ArfGAP with RhoGAP domain, ankyrin repeat and PH domain
15	PDE3A	-0.94	1e-04	5e-04	2 x 12 phosphodiesterase 3A, cGMP-inhibited [Source:HGNC Synt
16	FAM69A	-0.92	1e-04	5e-04	1 x 12 family with sequence similarity 69, member A [Source:HGNC
17	DSTYK	-0.8	2e-04	6e-04	1 x 12 dual serine/threonine and tyrosine protein kinase [Source:HG
18	LONRF1	-0.9	2e-04	6e-04	1 x 12 LON peptidase N-terminal domain and ring finger 1 [Source:!
19	D4S234E	-0.9	2e-04	1e-03	1 x 11
20	ALDH1B1	-0.87	4e-04	1e-03	1 x 12 aldehyde dehydrogenase 1 family, member B1 [Source:HGNC

p-values



B4_mel

Local Summary

%DE = 0.81
 # metagenes = 52
 # genes = 704
 # genes in genesets = 702

 # genes with $fdr < 0.1$ = 432 (71 + / 361 -)
 # genes with $fdr < 0.05$ = 368 (58 + / 310 -)
 # genes with $fdr < 0.01$ = 253 (33 + / 220 -)

<r> metagenes = 0.79

<r> genes = 0.17

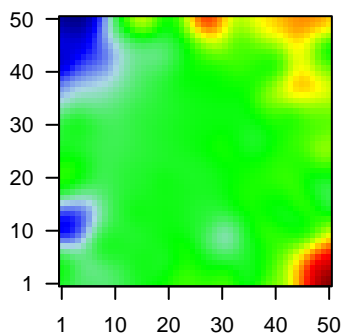
<FC> = -0.39

<shrinkage-t> = -6.81

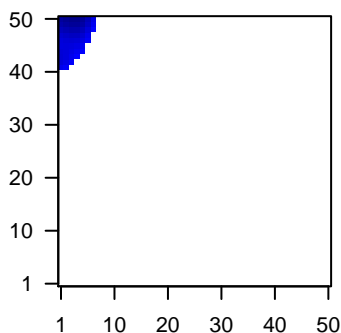
<p-value> = 0

<fdr> = 0.49

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ACADM	-1.6	2e-16	3e-15	1 x 45 acyl-CoA dehydrogenase, C-4 to C-12 straight chain [Source:HGNC Symbol;Acc:HGNC:10317]
2	ARHGAP8	-1.74	2e-16	3e-15	1 x 43 Rho GTPase activating protein 8 [Source:HGNC Symbol;Acc:HGNC:11442]
3	CDK4	-1.62	2e-16	3e-15	3 x 44 cyclin-dependent kinase 4 [Source:HGNC Symbol;Acc:HGNC:10317]
4	GGCT	-2.06	2e-16	3e-15	1 x 47 gamma-glutamylcyclotransferase [Source:HGNC Symbol;Acc:HGNC:10317]
5	MITF	-2.01	2e-16	3e-15	1 x 41 microphthalmia-associated transcription factor [Source:HGNC Symbol;Acc:HGNC:10317]
6	PEMT	-1.92	2e-16	3e-15	2 x 42 phosphatidylethanolamine N-methyltransferase [Source:HGNC Symbol;Acc:HGNC:10317]
7	SAE1	-1.49	2e-16	3e-15	4 x 47 SUMO1 activating enzyme subunit 1 [Source:HGNC Symbol;Acc:HGNC:11442]
8	STX7	-1.75	2e-16	3e-15	1 x 42 syntaxin 7 [Source:HGNC Symbol;Acc:HGNC:11442]
9	TRPM1	-1.66	2e-16	3e-15	1 x 42 transient receptor potential cation channel, subfamily M, member 1 [Source:HGNC Symbol;Acc:HGNC:11442]
10	TK1	-1.55	2e-15	1e-13	4 x 50 thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:HGNC:10317]
11	DNMT1	-1.29	2e-15	5e-13	2 x 48 DNA (cytosine-5)-methyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:10317]
12	DEK	-1.27	6e-15	5e-13	2 x 50 DEK proto-oncogene [Source:HGNC Symbol;Acc:HGNC:27643]
13	ST6GALNAC7	-1.46	9e-15	1e-12	1 x 44 ST6 (alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-transferase [Source:HGNC Symbol;Acc:HGNC:27643]
14	FANCL	-1.52	3e-14	1e-12	1 x 48 Fanconi anemia, complementation group L [Source:HGNC Symbol;Acc:HGNC:27643]
15	CKS2	-1.36	3e-14	1e-12	5 x 50 CDC28 protein kinase regulatory subunit 2 [Source:HGNC Symbol;Acc:HGNC:27643]
16	PLP1	-0.74	4e-14	1e-12	1 x 42 proteolipid protein 1 [Source:HGNC Symbol;Acc:HGNC:9086]
17	YIF1B	-1.51	4e-14	1e-12	4 x 45 Yip1 interacting factor homolog B (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:27643]
18	MBP	-0.74	5e-14	1e-11	1 x 42 myelin basic protein [Source:HGNC Symbol;Acc:HGNC:6925]
19	SMC4	-1.49	1e-13	2e-11	5 x 50 structural maintenance of chromosomes 4 [Source:HGNC Symbol;Acc:HGNC:27643]
20	MLPH	-1.48	3e-13	2e-10	1 x 43 melanophilin [Source:HGNC Symbol;Acc:HGNC:29643]

p-values

