

# H10\_mel

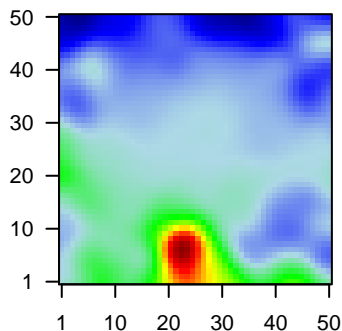
## Global Summary

%DE = 0.17  
 # genes with fdr < 0.2 = 1833 ( 1015 + / 818 - )  
 # genes with fdr < 0.1 = 1419 ( 794 + / 625 - )  
 # genes with fdr < 0.05 = 1040 ( 562 + / 478 - )  
 # genes with fdr < 0.01 = 531 ( 246 + / 285 - )

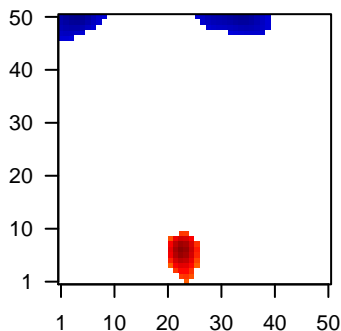
# genes in genesets = 14839

<FC> = 0  
 <shrinkage-t> = -0.12  
 <p-value> = 0.13  
 <fdr> = 0.83

Profile



Regulated Spots

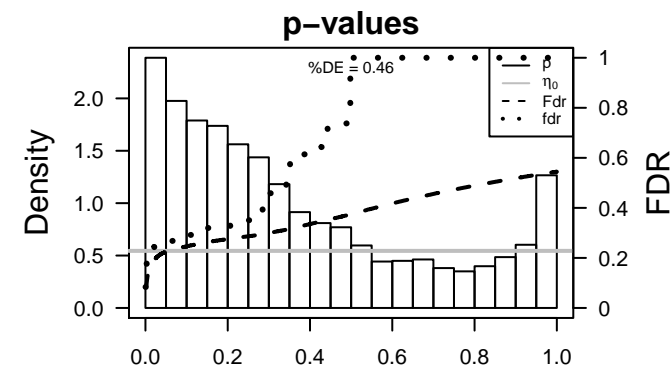
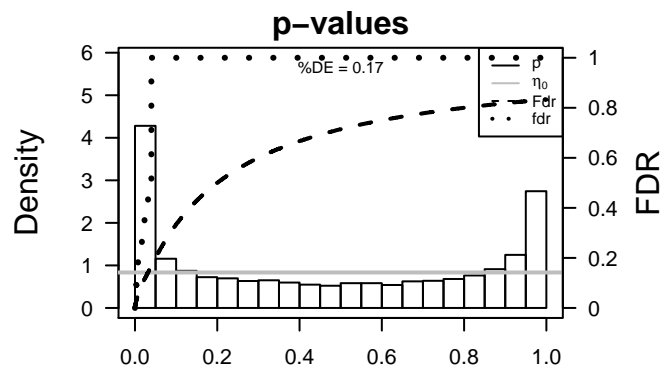


## Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	CAPN3	-2.11	2e-16	1e-13	1 x 43 calpain 3, (p94) [Source:HGNC Symbol;Acc:HGNC:1480]
2	CD46	-2.01	2e-16	1e-13	46 x 37 CD46 molecule, complement regulatory protein [Source:HGNC]
3	CLDN1	-1.77	2e-16	1e-13	28 x 50 claudin domain containing 1 [Source:HGNC Symbol;Acc:HGNC:1480]
4	EBP	-2.01	2e-16	1e-13	1 x 48 emopamil binding protein (sterol isomerase) [Source:HGNC]
5	EMP3	-1.82	2e-16	1e-13	4 x 43 epithelial membrane protein 3 [Source:HGNC Symbol;Acc:HGNC:1480]
6	ETFA	-2.1	2e-16	1e-13	3 x 33 electron-transfer-flavoprotein, alpha polypeptide [Source:HGNC]
7	JKAMP	-1.79	2e-16	1e-13	29 x 50 JNK1/MAPK8-associated membrane protein [Source:HGNC]
8	MARCH7	-1.79	2e-16	1e-13	50 x 41 membrane-associated ring finger (C3HC4) 7, E3 ubiquitin protein ligase [Source:HGNC]
9	MRPL13	-1.86	2e-16	1e-13	34 x 50 mitochondrial ribosomal protein L13 [Source:HGNC Symbol;Acc:HGNC:1480]
10	MRPL15	-1.93	2e-16	1e-13	5 x 33 mitochondrial ribosomal protein L15 [Source:HGNC Symbol;Acc:HGNC:1480]
11	MRPL55	-2.22	2e-16	1e-13	17 x 50 mitochondrial ribosomal protein L55 [Source:HGNC Symbol;Acc:HGNC:1480]
12	MYH10	-2.15	2e-16	1e-13	1 x 44 myosin, heavy chain 10, non-muscle [Source:HGNC Symbol;Acc:HGNC:1480]
13	NAE1	-1.87	2e-16	1e-13	10 x 45 NEDD8 activating enzyme E1 subunit 1 [Source:HGNC Symbol;Acc:HGNC:1480]
14	PSMA5	-1.32	2e-16	1e-13	48 x 50 proteasome (prosome, macropain) subunit, alpha type, 5 [Source:HGNC]
15	PSMD13	-1.96	2e-16	1e-13	29 x 50 proteasome (prosome, macropain) 26S subunit, non-ATPase [Source:HGNC]
16	STIP1	-2.13	2e-16	1e-13	30 x 47 stress-induced phosphoprotein 1 [Source:HGNC Symbol;Acc:HGNC:1480]
17	STMN1	-2.49	2e-16	1e-13	5 x 50 stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]
18	TECR	-2.04	2e-16	1e-13	28 x 50 trans-2,3-enoyl-CoA reductase [Source:HGNC Symbol;Acc:HGNC:1480]
19	TMEM106C	-2.07	2e-16	1e-13	5 x 48 transmembrane protein 106C [Source:HGNC Symbol;Acc:HGNC:1480]
20	VPS29	-2.06	2e-16	1e-13	33 x 50 vacuolar protein sorting 29 homolog (S. cerevisiae) [Source:HGNC]

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<b>Overexpressed</b>				
1	5.3	0.003	2159	Colon Cancer P_Colon
2	4.86	0.004	3396	Lymphoma OPP_Repressed
3	4.67	0.005	2188	Lymphoma OPP_Poised_promoter
4	4.53	0.005	182	miRNA target-miR-23a
5	4.5	0.005	176	miRNA target-miR-23b
6	4.04	0.007	16	GSEA C2NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
7	3.94	0.008	2972	Brain Mid_Frontal_Lobe_ReprPC
8	3.8	0.009	12	GSEA C2REACTOME_ADENYLATE_CYCLASE_INHIBITORY_PATHWAY
9	3.74	0.009	27	BP positive regulation of bone mineralization
10	3.71	0.010	172	GSEA C2STARK_PREFRONTAL_CORTEX_22Q11_DELETION_UP
11	3.69	0.010	47	BP positive regulation of osteoblast differentiation
12	3.67	0.010	1317	Colon Cancer P_Colon
13	3.51	0.011	55	BP BMP signaling pathway
14	3.38	0.013	14	GSEA C2SILIGAN_TARGETS_OF_EWS_FLI1_FUSION_UP
15	3.37	0.013	100	Aging HORVATH_aging_genes_meth_DOWN
16	3.31	0.014	66	miRNA target-miR-648
17	3.29	0.014	5	GSEA C2REACTOME_DIGESTION_OF_DIETARY_CARBOHYDRATE
18	3.26	0.014	170	miRNA target-miR-320b
19	3.26	0.014	36	MF G-protein beta/gamma-subunit complex binding
20	3.18	0.015	37	HM HALLMARK_APICAL_SURFACE
<b>Underexpressed</b>				
1	-10.63	2e-04	388	GSEA C2REACTOME_CELL_CYCLE
2	-10.6	2e-04	436	GSEA C2SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
3	-10.48	2e-04	412	BP mitotic cell cycle
4	-10.35	2e-04	305	GSEA C2DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
5	-10.32	2e-04	301	GSEA C2REACTOME_CELL_CYCLE_MITOTIC
6	-10.27	6e-02	16	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
7	-10.1	3e-04	197	HM HALLMARK_E2F_TARGETS
8	-10.06	3e-04	162	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
9	-9.91	3e-04	142	Glio WILLSCHER_GBM_Verhaak-CL_up (C)
10	-9.84	3e-04	550	GSEA C2GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
11	-9.68	3e-04	1110	BP cell cycle
12	-9.3	3e-04	390	GSEA C2PUJANA_BRCA2_PCC_NETWORK
13	-9.12	4e-04	96	GSEA C2CROONQUIST_IL6_DEPRIVATION_DN
14	-8.91	4e-04	242	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN
15	-8.71	5e-04	216	GSEA C2MARKEY_RB1_ACUTE_LOF_DN
16	-8.64	5e-04	72	GSEA C2CROONQUIST_NRAS_SIGNALING_DN
17	-8.49	5e-04	81	GSEA C2GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
18	-8.47	5e-04	181	GSEA C2REACTOME_DNA_REPLICATION
19	-8.46	5e-04	536	GSEA C2TIEN_INTENTINE_PROBIOTICS_24HR_UP
20	-8.43	5e-04	312	GSEA C2WONG_EMBRYONIC_STEM_CELL_CORE



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## Local Summary

%DE = 0.99  
 # metagenes = 45  
 # genes = 368  
 # genes in genesets = 365  
  
 # genes with  $fdr < 0.1$  = 365 ( 365 + / 0 -)  
 # genes with  $fdr < 0.05$  = 353 ( 353 + / 0 -)  
 # genes with  $fdr < 0.01$  = 348 ( 348 + / 0 -)

<r> metagenes = 0.87

<r> genes = 0.18

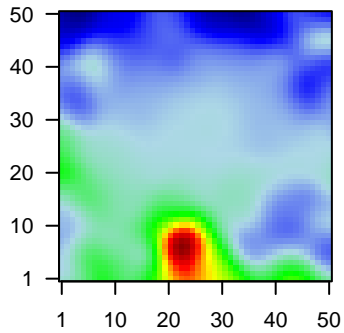
<FC> = 1

<shrinkage-t> = 15.28

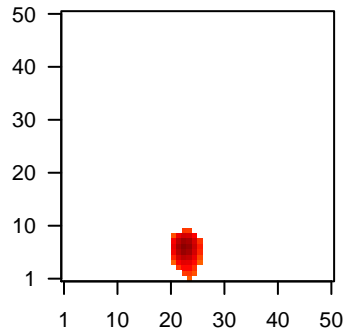
<p-value> = 0

<fdr> = 0.31

### Profile



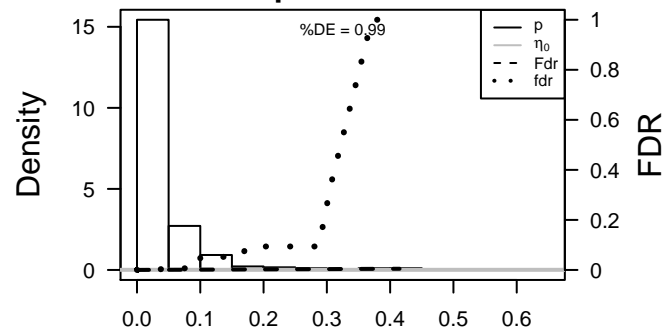
### Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	MDGA1	2.66	4e-16	3e-10	23 x 7 MAM domain containing glycosylphosphatidylinositol anchor
2	UCN	2.09	2e-10	3e-10	23 x 7 urocortin [Source:HGNC Symbol;Acc:HGNC:12516]
3	FAM214A	2.08	2e-10	4e-09	23 x 7 family with sequence similarity 214, member A [Source:HGNC
4	LACE1	1.9	6e-09	4e-09	24 x 8 lactation elevated 1 [Source:HGNC Symbol;Acc:HGNC:1641
5	BEND7	1.89	7e-09	4e-09	23 x 7 BEN domain containing 7 [Source:HGNC Symbol;Acc:HGNC
6	MFS09	1.89	7e-09	4e-09	24 x 8 major facilitator superfamily domain containing 9 [Source:HGI
7	PCOLCE	1.89	7e-09	4e-09	23 x 8 procollagen C-endopeptidase enhancer [Source:HGNC Sym
8	STAT5B	1.88	8e-09	4e-09	22 x 3 signal transducer and activator of transcription 5B [Source:HC
9	PPP1R3E	1.88	9e-09	4e-09	23 x 7 protein phosphatase 1, regulatory subunit 3E [Source:HGNC
10	ZNF625-ZNF	1.87	1e-08	1e-08	22 x 7 ZNF625-ZNF20 readthrough (NMD candidate) [Source:HGN
11	LAT	1.85	1e-08	4e-08	23 x 7 linker for activation of T cells [Source:HGNC Symbol;Acc:HGI
12	LRP5L	1.81	3e-08	4e-08	23 x 7 low density lipoprotein receptor-related protein 5-like [Source
13	SOX9	1.79	4e-08	4e-08	23 x 7 SRY (sex determining region Y)-box 9 [Source:HGNC Symb
14	ENGASE	1.77	6e-08	6e-08	22 x 7 endo-beta-N-acetylglucosaminidase [Source:HGNC Symbo
15	CHAC1	1.75	8e-08	6e-08	23 x 7 ChaC glutathione-specific gamma-glutamylcyclotransferase
16	MED17	1.72	1e-07	6e-08	26 x 8 mediator complex subunit 17 [Source:HGNC Symbol;Acc:HG
17	AGO2	1.72	1e-07	6e-08	23 x 7 argonaute RISC catalytic component 2 [Source:HGNC Symb
18	FAM227B	1.72	1e-07	6e-08	24 x 5 family with sequence similarity 227, member B [Source:HGNC
19	PBX3	1.71	2e-07	6e-08	23 x 7 pre-B-cell leukemia homeobox 3 [Source:HGNC Symbol;Acc
20	CDK3	1.7	2e-07	6e-08	23 x 7 cyclin-dependent kinase 3 [Source:HGNC Symbol;Acc:HGNC

### p-values



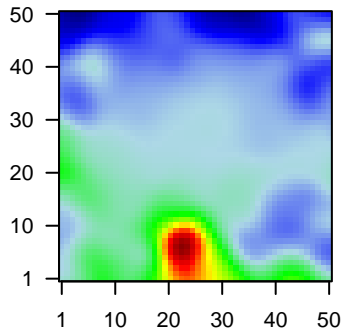
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## Local Summary

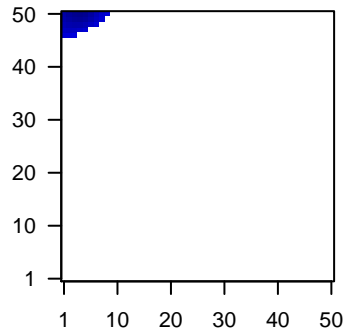
%DE = 0.78  
 # metagenes = 32  
 # genes = 469  
 # genes in genesets = 468  
  
 # genes with  $fdr < 0.1$  = 257 ( 42 + / 215 - )  
 # genes with  $fdr < 0.05$  = 159 ( 25 + / 134 - )  
 # genes with  $fdr < 0.01$  = 87 ( 7 + / 80 - )

$\langle r \rangle$  metagenes = 0.89  
 $\langle r \rangle$  genes = 0.24  
  
 $\langle FC \rangle$  = -0.42  
 $\langle \text{shrinkage-t} \rangle$  = -6.97  
 $\langle p\text{-value} \rangle$  = 0.02  
 $\langle fdr \rangle$  = 0.68

Profile



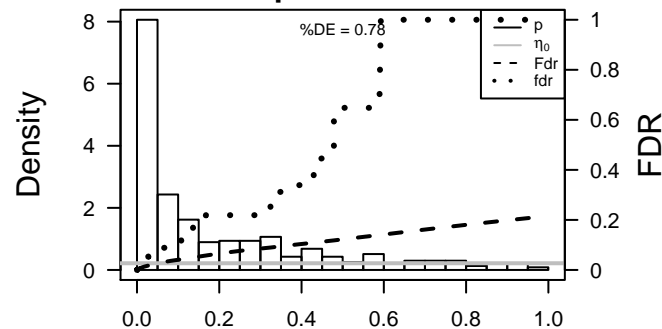
Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	EBP	-2.01	2e-16	7e-15	1 x 48 emopamil binding protein (sterol isomerase) [Source:HGNC S
2	STMN1	-2.49	2e-16	7e-15	5 x 50 stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]
3	TMEM106C	-2.07	2e-16	7e-15	5 x 48 transmembrane protein 106C [Source:HGNC Symbol;Acc:HG
4	MRPL17	-1.77	9e-16	5e-11	1 x 46 mitochondrial ribosomal protein L17 [Source:HGNC Symbol;#
5	CSE1L	-1.68	5e-13	3e-09	3 x 49 CSE1 chromosome segregation 1-like (yeast) [Source:HGNC
6	CKS2	-1.6	4e-11	3e-09	5 x 50 CDC28 protein kinase regulatory subunit 2 [Source:HGNC S]
7	UCP2	-1.62	5e-11	4e-09	2 x 46 uncoupling protein 2 (mitochondrial, proton carrier) [Source:H
8	CDKN3	-1.57	9e-11	3e-08	6 x 50 cyclin-dependent kinase inhibitor 3 [Source:HGNC Symbol;A
9	POLR3K	-1.58	9e-10	3e-08	1 x 46 polymerase (RNA) III (DNA directed) polypeptide K, 12.3 kDa
10	ACTL6A	1.19	9e-10	3e-08	4 x 50 actin-like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
11	SNRNP25	-1.58	1e-09	1e-07	1 x 46 small nuclear ribonucleoprotein 25kDa (U11/U12) [Source:HC
12	NUP85	-1.56	2e-09	1e-07	1 x 50 nucleoporin 85kDa [Source:HGNC Symbol;Acc:HGNC:8734]
13	TK1	-1.55	4e-09	2e-06	4 x 50 thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:HGNC
14	YEATS4	-1.52	2e-08	2e-06	1 x 47 YEATS domain containing 4 [Source:HGNC Symbol;Acc:HGNC
15	SMC4	-1.49	4e-08	8e-06	5 x 50 structural maintenance of chromosomes 4 [Source:HGNC Sy
16	MTHFD2	-1.46	1e-07	1e-05	3 x 47 methylenetetrahydrofolate dehydrogenase (NADP+ depend
17	GMNN	-1.45	2e-07	2e-05	2 x 50 geminin, DNA replication inhibitor [Source:HGNC Symbol;Acc
18	NUP107	-1	5e-07	2e-05	2 x 48 nucleoporin 107kDa [Source:HGNC Symbol;Acc:HGNC:2991
19	NUP54	-1.41	8e-07	2e-05	1 x 50 nucleoporin 54kDa [Source:HGNC Symbol;Acc:HGNC:17359
20	HADH	-1.41	8e-07	2e-05	1 x 48 hydroxyacyl-CoA dehydrogenase [Source:HGNC Symbol;Acc

p-values



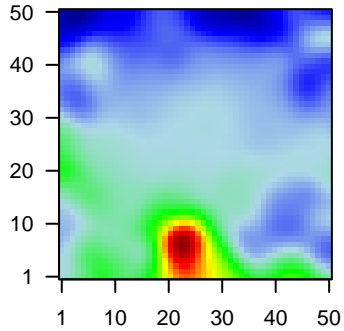
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## Local Summary

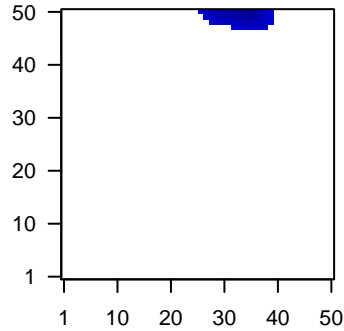
%DE = 0.69  
 # metagenes = 46  
 # genes = 452  
 # genes in genesets = 451  
  
 # genes with  $fdr < 0.1$  = 166 ( 15 + / 151 - )  
 # genes with  $fdr < 0.05$  = 127 ( 10 + / 117 - )  
 # genes with  $fdr < 0.01$  = 70 ( 3 + / 67 - )

$\langle r \rangle$  metagenes = 0.72  
 $\langle r \rangle$  genes = 0.05  
  
 $\langle FC \rangle = -0.44$   
 $\langle \text{shrinkage-t} \rangle = -7.7$   
 $\langle p\text{-value} \rangle = 0.02$   
 $\langle fdr \rangle = 0.67$

Profile



Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	CLDND1	-1.77	2e-16	5e-15	28 x 50 claudin domain containing 1 [Source:HGNC Symbol;Acc:HGNC:10000]
2	JKAMP	-1.79	2e-16	5e-15	29 x 50 JNK1/MAPK8-associated membrane protein [Source:HGNC Symbol;Acc:HGNC:10000]
3	MRPL13	-1.86	2e-16	5e-15	34 x 50 mitochondrial ribosomal protein L13 [Source:HGNC Symbol;Acc:HGNC:10000]
4	PSMD13	-1.96	2e-16	5e-15	29 x 50 proteasome (prosome, macropain) 26S subunit, non-ATPase [Source:HGNC Symbol;Acc:HGNC:10000]
5	TECR	-2.04	2e-16	5e-15	28 x 50 trans-2,3-enoyl-CoA reductase [Source:HGNC Symbol;Acc:HGNC:10000]
6	VPS29	-2.06	2e-16	5e-15	33 x 50 vacuolar protein sorting 29 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:10000]
7	PPA1	-1.76	2e-15	2e-10	36 x 50 pyrophosphatase (inorganic) 1 [Source:HGNC Symbol;Acc:HGNC:10000]
8	YARS	-1.68	1e-12	3e-10	30 x 50 tyrosyl-tRNA synthetase [Source:HGNC Symbol;Acc:HGNC:10000]
9	SRPK1	-1.67	3e-12	2e-09	34 x 50 SRSF protein kinase 1 [Source:HGNC Symbol;Acc:HGNC:10000]
10	MRPL52	-1.64	2e-11	2e-08	35 x 50 mitochondrial ribosomal protein L52 [Source:HGNC Symbol;Acc:HGNC:10000]
11	C11orf31	-1.48	3e-10	2e-08	27 x 50 chromosome 11 open reading frame 31 [Source:HGNC Symbol;Acc:HGNC:10000]
12	MRPL18	-1.6	4e-10	2e-08	36 x 50 mitochondrial ribosomal protein L18 [Source:HGNC Symbol;Acc:HGNC:10000]
13	HSBP1	-0.82	4e-10	4e-08	35 x 47 heat shock factor binding protein 1 [Source:HGNC Symbol;Acc:HGNC:10000]
14	OS9	-1.59	7e-10	7e-08	34 x 50 osteosarcoma amplified 9, endoplasmic reticulum lectin [Source:HGNC Symbol;Acc:HGNC:10000]
15	MRPS30	-1.58	1e-09	3e-07	38 x 47 mitochondrial ribosomal protein S30 [Source:HGNC Symbol;Acc:HGNC:10000]
16	RNF10	-1.54	6e-09	3e-07	37 x 48 ring finger protein 10 [Source:HGNC Symbol;Acc:HGNC:10000]
17	RABGGTB	-1.53	6e-09	6e-07	28 x 50 Rab geranylgeranyltransferase, beta subunit [Source:HGNC Symbol;Acc:HGNC:10000]
18	SPP1	-1.53	1e-08	7e-07	38 x 48 secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:HGNC:10000]
19	PDHB	-0.94	2e-08	2e-06	38 x 50 pyruvate dehydrogenase (lipoamide) beta [Source:HGNC Symbol;Acc:HGNC:10000]
20	DDX42	-1.48	5e-08	2e-06	33 x 50 DEAD (Asp-Glu-Ala-Asp) box helicase 42 [Source:HGNC Symbol;Acc:HGNC:10000]

p-values

