

# F7\_mel

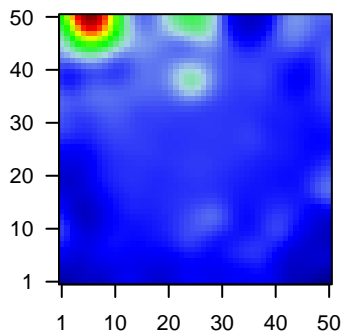
## Global Summary

%DE = 0.22  
 # genes with fdr < 0.2 = 2808 ( 1699 + / 1109 - )  
 # genes with fdr < 0.1 = 2375 ( 1464 + / 911 - )  
 # genes with fdr < 0.05 = 1971 ( 1233 + / 738 - )  
 # genes with fdr < 0.01 = 1378 ( 883 + / 495 - )

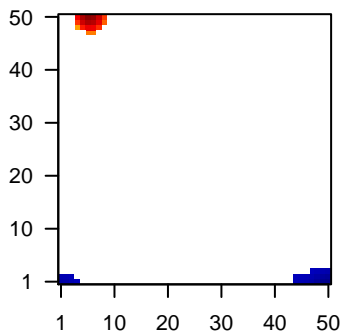
# genes in genesets = 14839

<FC> = 0  
 <shrinkage-t> = 0.01  
 <p-value> = 0.06  
 <fdr> = 0.78

Profile



Regulated Spots



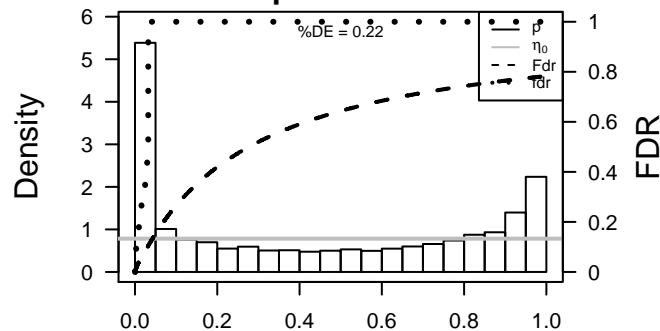
## Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	ANP32E	0.87	2e-16 7e-14	8 x 50 acidic (leucine-rich) nuclear phosphoprotein 32 family, memb
2	CEP97	2.29	2e-16 7e-14	2 x 47 centrosomal protein 97kDa [Source:HGNC Symbol;Acc:HGNC]
3	CHURC1-FN	-1.57	2e-16 7e-14	39 x 50 CHURC1-FNTB readthrough [Source:HGNC Symbol;Acc:HGNC]
4	CKAP2L	2.01	2e-16 7e-14	6 x 50 cytoskeleton associated protein 2-like [Source:HGNC Symbol;Acc:HGNC]
5	DAP3	-2	2e-16 7e-14	7 x 11 death associated protein 3 [Source:HGNC Symbol;Acc:HGNC]
6	DGKA	1.96	2e-16 7e-14	41 x 13 diacylglycerol kinase, alpha 80kDa [Source:HGNC Symbol;Acc:HGNC]
7	DLGAP5	1.82	2e-16 7e-14	7 x 50 discs, large (Drosophila) homolog-associated protein 5 [Source:HGNC]
8	EIF2A	-1.57	2e-16 7e-14	50 x 12 eukaryotic translation initiation factor 2A, 65kDa [Source:HGNC]
9	EIF3D	-1.74	2e-16 7e-14	45 x 19 eukaryotic translation initiation factor 3, subunit D [Source:HGNC]
10	EIF4E2	-1.56	2e-16 7e-14	50 x 47 eukaryotic translation initiation factor 4E family member 2 [Source:HGNC]
11	FAM127B	-1.51	2e-16 7e-14	47 x 50 family with sequence similarity 127, member B [Source:HGNC]
12	GPATCH4	-1.71	2e-16 7e-14	46 x 45 G patch domain containing 4 [Source:HGNC Symbol;Acc:HGNC]
13	GRPEL1	-1.47	2e-16 7e-14	1 x 3 GrpE-like 1, mitochondrial (E. coli) [Source:HGNC Symbol;Acc:HGNC]
14	HIST1H4C	1.04	2e-16 7e-14	5 x 49 histone cluster 1, H4c [Source:HGNC Symbol;Acc:HGNC]
15	HNRNPF	-1.29	2e-16 7e-14	1 x 46 heterogeneous nuclear ribonucleoprotein F [Source:HGNC Symbol;Acc:HGNC]
16	IMP4	-1.68	2e-16 7e-14	2 x 39 IMP4, U3 small nucleolar ribonucleoprotein [Source:HGNC Symbol;Acc:HGNC]
17	ITM2B	-1.57	2e-16 7e-14	50 x 10 integral membrane protein 2B [Source:HGNC Symbol;Acc:HGNC]
18	KIF20A	1.86	2e-16 7e-14	7 x 50 kinesin family member 20A [Source:HGNC Symbol;Acc:HGNC]
19	KPNA2	0.97	2e-16 7e-14	7 x 50 karyopherin alpha 2 (RAG cohort 1, importin alpha 1) [Source:HGNC]
20	LARP4	-1.4	2e-16 7e-14	17 x 2 La ribonucleoprotein domain family, member 4 [Source:HGNC]

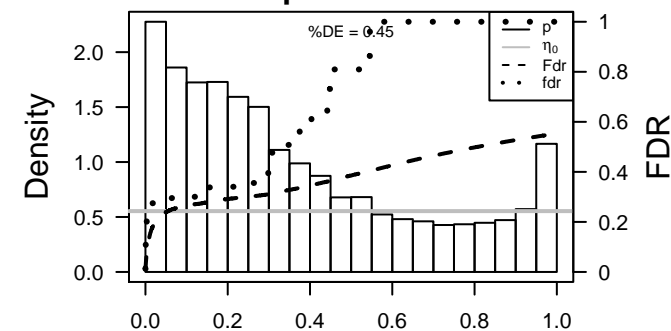
## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	23.12	8e-06	142	Glio WILLSCHER_GBM_Verhaak-CL_up ( C )
2	20.1	1e-05	139	GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
3	19.39	1e-03	16	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
4	18.29	2e-05	550	GSEA C2BOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
5	17.89	2e-05	145	GSEA C2ZHANG_CYCLING_GENES
6	17.13	3e-05	124	GSEA C2ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
7	16.57	3e-05	305	GSEA C2DUTERTRE ESTRADIOL_RESPONSE_24HR_UP
8	15.94	4e-05	242	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN
9	15.28	5e-05	155	GSEA C2HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
10	15.2	5e-05	291	GSEA C2HORIUCHI_WTAP_TARGETS_DN
11	14.92	5e-05	99	GSEA C2LEE_EARLY_T_LYMPHOCYTE_UP
12	14.9	5e-05	54	GSEA C2KANG_DOXORUBICIN_RESISTANCE_UP
13	14.84	5e-05	93	GSEA C2KONG_E2F3_TARGETS
14	14.79	6e-05	616	GSEA C2BENPORATH_CYCLING_GENES
15	14.77	6e-05	312	BP mitotic nuclear division
16	14.61	6e-05	165	GSEA C2CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
17	14.6	6e-05	170	GSEA C2WHITFIELD_CELL_CYCLE_G2
18	14.52	6e-05	110	GSEA C2WHITFIELD_PEDIATRIC_CANCER_MARKERS
19	14.51	6e-05	700	GSEA C2MARSON_BOUND_BY_E2F4_UNSTIMULATED
20	14.39	6e-05	96	GSEA C2CROONQUIST_IL6_DEPRIVATION_DN
<i>Underexpressed</i>				
1	-8.92	4e-04	925	GSEA C2KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
2	-7.24	9e-04	831	GSEA C2KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
3	-5.93	2e-03	57	HM HALLMARK_MYC_TARGETS_V2
4	-5.84	2e-03	101	BP RNA processing
5	-5.39	3e-03	1007	MF poly(A) RNA binding
6	-5.25	3e-03	1365	MF RNA binding
7	-5.23	3e-03	91	GSEA C2MARZEC_IL2_SIGNALING_UP
8	-4.87	4e-03	120	GSEA C2KARLSSON_TGFB1_TARGETS_UP
9	-4.74	4e-03	78	GSEA C2SCHUHMACHER_MYC_TARGETS_UP
10	-4.61	5e-03	162	BP ribosome biogenesis
11	-4.61	5e-03	2698	Colon Ca562hA_Colon
12	-4.41	5e-03	3132	CC extracellular region
13	-4.37	6e-03	233	GSEA C2PENG_RAPAMYCIN_RESPONSE_DN
14	-4.33	6e-03	62	GSEA C2REACTOME_TRANSLATION
15	-4.28	6e-03	47	GSEA C2SCHLOSSER_MYC_TARGETS_AND_SERUM_RESPONSE_UP
16	-4.24	6e-03	1468	CC mitochondrion
17	-4.2	6e-03	2798	Colon Ca562hG1_Colon
18	-4.17	7e-03	51	GSEA C2MENSSEN_MYC_TARGETS
19	-4.1	7e-03	367	GSEA C2MONNIER_POSTRADIATION_TUMOR_ESCAPE_UP
20	-4.09	7e-03	56	BP translational initiation

p-values



p-values



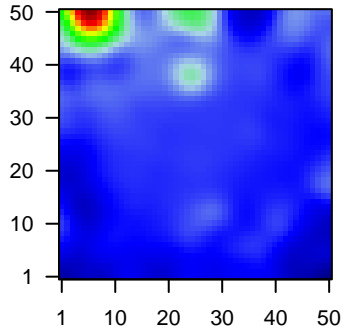
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## Local Summary

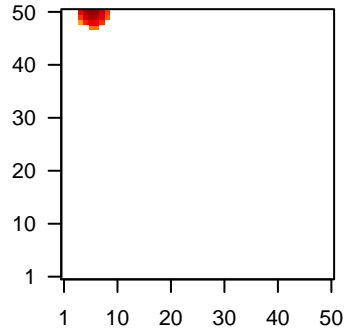
%DE = 0.97  
 # metagenes = 19  
 # genes = 232  
 # genes in genesets = 232  
  
 # genes with  $fdr < 0.1$  = 213 ( 208 + / 5 -)  
 # genes with  $fdr < 0.05$  = 213 ( 208 + / 5 -)  
 # genes with  $fdr < 0.01$  = 189 ( 187 + / 2 -)

$\langle r \rangle$  metagenes = 0.97  
 $\langle r \rangle$  genes = 0.36  
  
 $\langle FC \rangle$  = 0.96  
 $\langle \text{shrinkage-t} \rangle$  = 15.63  
 $\langle p\text{-value} \rangle$  = 0  
 $\langle fdr \rangle$  = 0.15

Profile



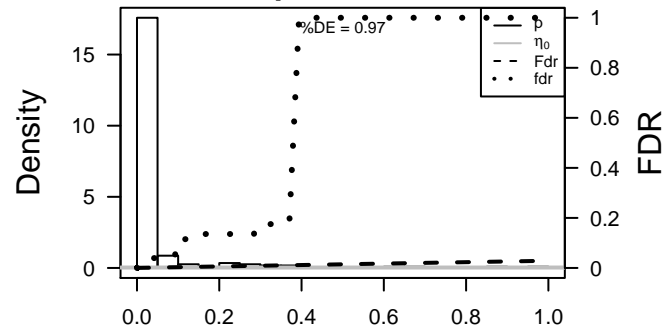
Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ANP32E	0.87	2e-16	2e-16	8 x 50 acidic (leucine-rich) nuclear phosphoprotein 32 family, memb
2	CKAP2L	2.01	2e-16	2e-16	6 x 50 cytoskeleton associated protein 2-like [Source:HGNC Symbc
3	DLGAP5	1.82	2e-16	2e-16	7 x 50 discs, large (Drosophila) homolog-associated protein 5 [Sour
4	HIST1H4C	1.04	2e-16	2e-16	5 x 49 histone cluster 1, H4c [Source:HGNC Symbol;Acc:HGNC:476
5	KIF20A	1.86	2e-16	2e-16	7 x 50 kinesin family member 20A [Source:HGNC Symbol;Acc:HGNC
6	KPNA2	0.97	2e-16	2e-16	7 x 50 karyopherin alpha 2 (RAG cohort 1, importin alpha 1) [Source
7	PLK1	1.88	2e-16	2e-16	8 x 50 polo-like kinase 1 [Source:HGNC Symbol;Acc:HGNC:9077]
8	UBE2C	1.9	2e-16	2e-16	6 x 50 ubiquitin-conjugating enzyme E2C [Source:HGNC Symbol;Acc
9	NUSAP1	1.75	4e-16	3e-15	6 x 50 nucleolar and spindle associated protein 1 [Source:HGNC Sy
10	CDKN3	1.33	9e-16	7e-15	6 x 50 cyclin-dependent kinase inhibitor 3 [Source:HGNC Symbol;Acc
11	CDK1	1.74	2e-15	7e-15	5 x 50 cyclin-dependent kinase 1 [Source:HGNC Symbol;Acc:HGNC
12	AURKB	1.74	4e-15	5e-14	6 x 50 aurora kinase B [Source:HGNC Symbol;Acc:HGNC:11390]
13	CDCA3	1.74	4e-15	5e-14	6 x 50 cell division cycle associated 3 [Source:HGNC Symbol;Acc:H
14	HJURP	1.7	2e-14	5e-14	6 x 50 Holliday junction recognition protein [Source:HGNC Symbol;Acc
15	CCNB1	1.68	2e-14	5e-14	7 x 50 cyclin B1 [Source:HGNC Symbol;Acc:HGNC:1579]
16	TOP2A	1.68	3e-14	5e-14	6 x 50 topoisomerase (DNA) II alpha 170kDa [Source:HGNC Symbc
17	PRR11	1.68	4e-14	5e-14	7 x 50 proline rich 11 [Source:HGNC Symbol;Acc:HGNC:25619]
18	CDCA5	1.68	4e-14	2e-13	4 x 50 cell division cycle associated 5 [Source:HGNC Symbol;Acc:H
19	CENPE	1.66	9e-14	2e-13	7 x 50 centromere protein E, 312kDa [Source:HGNC Symbol;Acc:H
20	TROAP	1.66	9e-14	2e-13	6 x 50 trophinin associated protein [Source:HGNC Symbol;Acc:HGNC

p-values



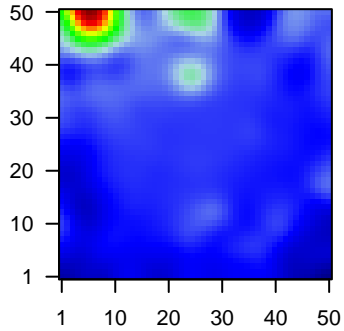
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## Local Summary

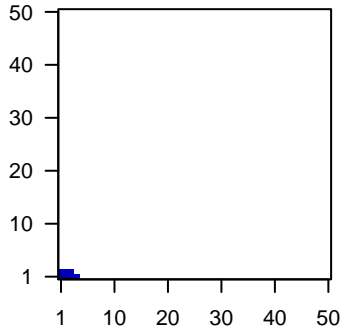
%DE = 0.62  
 # metagenes = 7  
 # genes = 154  
 # genes in genesets = 152  
  
 # genes with  $fdr < 0.1$  = 45 ( 15 + / 30 -)  
 # genes with  $fdr < 0.05$  = 30 ( 9 + / 21 -)  
 # genes with  $fdr < 0.01$  = 22 ( 7 + / 15 -)

$\langle r \rangle$  metagenes = 0.96  
 $\langle r \rangle$  genes = 0.11  
  
 $\langle FC \rangle = -0.19$   
 $\langle \text{shrinkage-t} \rangle = -2.92$   
 $\langle p\text{-value} \rangle = 0.05$   
 $\langle fdr \rangle = 0.73$

Profile



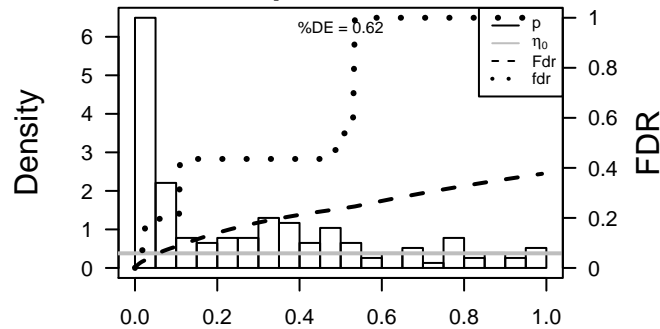
Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	CSTF3	-1.22	6e-10	9e-06	2 x 2 cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa [Sc
2	DHX29	-1.14	2e-07	3e-05	1 x 1 DEAH (Asp-Glu-Ala-His) box polypeptide 29 [Source:HGNC
3	LARP7	-1.07	7e-07	1e-04	2 x 1 La ribonucleoprotein domain family, member 7 [Source:HGNC
4	ANKRD17	-0.95	5e-06	1e-04	1 x 1 ankyrin repeat domain 17 [Source:HGNC Symbol;Acc:HGNC
5	POGLUT1	-1.01	5e-06	1e-03	1 x 1 protein O-glucosyltransferase 1 [Source:HGNC Symbol;Acc:HGNC
6	DOCK7	-0.91	3e-05	1e-03	1 x 1 dedicator of cytokinesis 7 [Source:HGNC Symbol;Acc:HGNC
7	ZNF32	-0.85	9e-05	1e-03	2 x 2 zinc finger protein 32 [Source:HGNC Symbol;Acc:HGNC:130
8	DEF8	0.73	1e-04	1e-03	4 x 1 differentially expressed in FDCP 8 homolog (mouse) [Source:HGNC
9	NBAS	-0.86	1e-04	1e-03	1 x 1 neuroblastoma amplified sequence [Source:HGNC Symbol;Acc:HGNC
10	TGIF2	-0.86	1e-04	1e-03	1 x 1 TGFB-induced factor homeobox 2 [Source:HGNC Symbol;Acc:HGNC
11	MAPKAPK3	-0.85	1e-04	2e-03	1 x 1 mitogen-activated protein kinase-activated protein kinase 3 [
12	WASF1	0.83	2e-04	2e-03	1 x 1 WAS protein family, member 1 [Source:HGNC Symbol;Acc:HGNC
13	DUSP11	-0.83	2e-04	2e-03	1 x 1 dual specificity phosphatase 11 (RNA/RNP complex 1-interacti
14	MTMR12	-0.81	3e-04	2e-03	1 x 2 myotubularin related protein 12 [Source:HGNC Symbol;Acc:HGNC
15	AC009133.22	-0.8	3e-04	2e-03	2 x 1
16	SLC30A5	-0.8	3e-04	2e-03	2 x 2 solute carrier family 30 (zinc transporter), member 5 [Source:HGNC
17	TMA16	-0.79	3e-04	5e-03	2 x 1 translation machinery associated 16 homolog (S. cerevisiae)
18	FAM206A	0.78	4e-04	5e-03	1 x 2 family with sequence similarity 206, member A [Source:HGNC
19	GLE1	0.77	5e-04	5e-03	3 x 1 GLE1 RNA export mediator [Source:HGNC Symbol;Acc:HGNC
20	MED28	0.72	7e-04	5e-03	1 x 1 mediator complex subunit 28 [Source:HGNC Symbol;Acc:HGNC

p-values



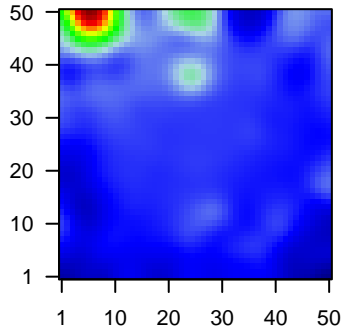
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## Local Summary

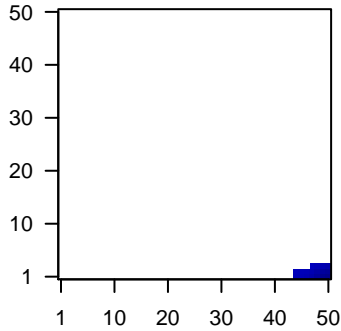
%DE = 0.77  
 # metagenes = 18  
 # genes = 301  
 # genes in genesets = 301  
  
 # genes with  $fdr < 0.1$  = 126 ( 33 + / 93 -)  
 # genes with  $fdr < 0.05$  = 114 ( 30 + / 84 -)  
 # genes with  $fdr < 0.01$  = 58 ( 16 + / 42 -)

$\langle r \rangle$  metagenes = 0.96  
 $\langle r \rangle$  genes = 0.19  
  
 $\langle FC \rangle$  = -0.23  
 $\langle \text{shrinkage-t} \rangle$  = -3.77  
 $\langle p\text{-value} \rangle$  = 0.02  
 $\langle fdr \rangle$  = 0.65

Profile



Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	TAGLN2	-1.51	2e-16	2e-14	50 x 2 transgelin 2 [Source:HGNC Symbol;Acc:HGNC:11554]
2	TMX3	-1.4	2e-14	4e-10	44 x 1 thioredoxin-related transmembrane protein 3 [Source:HGNC
3	SYNE1	-1.02	5e-12	5e-10	49 x 1 spectrin repeat containing, nuclear envelope 1 [Source:HGNC
4	LAMC1	-1.35	1e-11	1e-08	50 x 3 laminin, gamma 1 (formerly LAMB2) [Source:HGNC Symbol;]
5	LMO7	1.41	2e-10	8e-08	50 x 2 LIM domain 7 [Source:HGNC Symbol;Acc:HGNC:6646]
6	SATB1	1.34	2e-09	8e-08	50 x 1 SATB homeobox 1 [Source:HGNC Symbol;Acc:HGNC:10541]
7	PLK2	-0.99	3e-09	1e-06	50 x 1 polo-like kinase 2 [Source:HGNC Symbol;Acc:HGNC:19699]
8	CD55	-1.19	2e-08	5e-06	50 x 1 CD55 molecule, decay accelerating factor for complement (Ci
9	FMN2	-1.16	1e-07	5e-06	48 x 1 formin 2 [Source:HGNC Symbol;Acc:HGNC:14074]
10	SNAP23	-0.92	2e-07	1e-05	50 x 1 synaptosomal-associated protein, 23kDa [Source:HGNC Syr
11	PDLIM5	-1.12	3e-07	2e-05	50 x 1 PDZ and LIM domain 5 [Source:HGNC Symbol;Acc:HGNC:1:
12	RAB31	-1.09	7e-07	1e-04	50 x 3 RAB31, member RAS oncogene family [Source:HGNC Symb
13	FLNB	1.03	3e-06	1e-04	45 x 1 filamin B, beta [Source:HGNC Symbol;Acc:HGNC:3755]
14	CDKN1A	-1.02	4e-06	1e-04	50 x 1 cyclin-dependent kinase inhibitor 1A (p21, Cip1) [Source:HG
15	PDGFA	-1.01	6e-06	1e-04	49 x 1 platelet-derived growth factor alpha polypeptide [Source:HG†
16	DCBLD2	0.92	7e-06	1e-04	47 x 1 discoidin, CUB and LCCL domain containing 2 [Source:HGNC
17	PLOD1	-0.98	9e-06	1e-04	44 x 1 procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1 [Source
18	DOLK	0.97	1e-05	1e-04	46 x 1 dolichol kinase [Source:HGNC Symbol;Acc:HGNC:23406]
19	MBNL2	-0.96	1e-05	4e-04	50 x 1 muscleblind-like splicing regulator 2 [Source:HGNC Symbol;]
20	LIMA1	-0.95	2e-05	4e-04	49 x 1 LIM domain and actin binding 1 [Source:HGNC Symbol;Acc:†

p-values

