

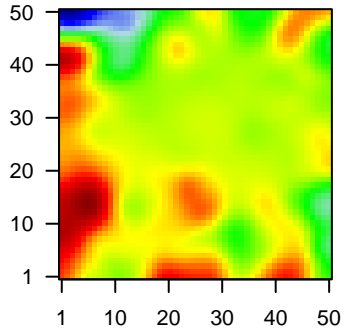
# B5\_mel

## Global Summary

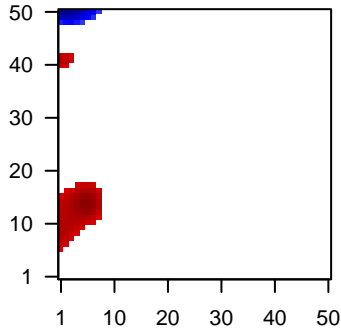
%DE = 0.2  
 # genes with fdr < 0.2 = 2452 ( 1453 + / 999 - )  
 # genes with fdr < 0.1 = 2017 ( 1197 + / 820 - )  
 # genes with fdr < 0.05 = 1535 ( 911 + / 624 - )  
 # genes with fdr < 0.01 = 991 ( 580 + / 411 - )  
 # genes in genesets = 14839

<FC> = 0  
 <shrinkage-t> = 0.01  
 <p-value> = 0.09  
 <fdr> = 0.8

Profile



Regulated Spots



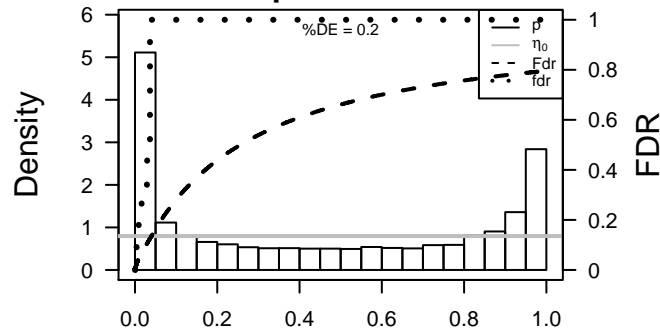
## Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	AKR1B1	-1.45	2e-16	1e-13	12 x 40 aldo-keto reductase family 1, member B1 (aldose reductase)
2	APEX1	-1.54	2e-16	1e-13	29 x 50 APEX nuclease (multifunctional DNA repair enzyme) 1 [Source:HGNC Symbol;Acc:HGNC:10000]
3	ATF4	-1.57	2e-16	1e-13	38 x 46 activating transcription factor 4 [Source:HGNC Symbol;Acc:HGNC:10000]
4	CDKN3	-1.65	2e-16	1e-13	6 x 50 cyclin-dependent kinase inhibitor 3 [Source:HGNC Symbol;Acc:HGNC:10000]
5	DCTN2	-1.4	2e-16	1e-13	50 x 44 dynactin 2 (p50) [Source:HGNC Symbol;Acc:HGNC:2712]
6	EBP	-2.01	2e-16	1e-13	1 x 48 empamil binding protein (sterol isomerase) [Source:HGNC Symbol;Acc:HGNC:10000]
7	EFTUD2	-1.39	2e-16	1e-13	13 x 42 elongation factor Tu GTP binding domain containing 2 [Source:HGNC Symbol;Acc:HGNC:10000]
8	EMC6	-1.62	2e-16	1e-13	7 x 27 ER membrane protein complex subunit 6 [Source:HGNC Symbol;Acc:HGNC:10000]
9	EPS8	-1.6	2e-16	1e-13	49 x 13 epidermal growth factor receptor pathway substrate 8 [Source:HGNC Symbol;Acc:HGNC:10000]
10	ERAL1	-1.73	2e-16	1e-13	46 x 44 Era-like 12S mitochondrial rRNA chaperone 1 [Source:HGNC Symbol;Acc:HGNC:10000]
11	FAM126A	-1.7	2e-16	1e-13	45 x 35 family with sequence similarity 126, member A [Source:HGNC Symbol;Acc:HGNC:10000]
12	HAT1	-1.6	2e-16	1e-13	1 x 50 histone acetyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:10000]
13	HAUS1	-1.62	2e-16	1e-13	1 x 50 HAUS augmin-like complex, subunit 1 [Source:HGNC Symbol;Acc:HGNC:10000]
14	HERPUD1	-1.81	2e-16	1e-13	50 x 42 homocysteine-inducible, endoplasmic reticulum stress-inducible protein 1 [Source:HGNC Symbol;Acc:HGNC:10000]
15	IARS	-1.81	2e-16	1e-13	16 x 50 isoleucyl-tRNA synthetase [Source:HGNC Symbol;Acc:HGNC:10000]
16	KPNA2	-0.92	2e-16	1e-13	7 x 50 karyopherin alpha 2 (RAG cohort 1, importin alpha 1) [Source:HGNC Symbol;Acc:HGNC:10000]
17	MLF2	-1.27	2e-16	1e-13	27 x 47 myeloid leukemia factor 2 [Source:HGNC Symbol;Acc:HGNC:10000]
18	MLIP	-1.41	2e-16	1e-13	3 x 44 muscular LMNA-interacting protein [Source:HGNC Symbol;Acc:HGNC:10000]
19	MYL6	-0.89	2e-16	1e-13	50 x 6 myosin, light chain 6, alkali, smooth muscle and non-muscle [Source:HGNC Symbol;Acc:HGNC:10000]
20	NUP214	-1.65	2e-16	1e-13	7 x 44 nucleoporin 214kDa [Source:HGNC Symbol;Acc:HGNC:8064]

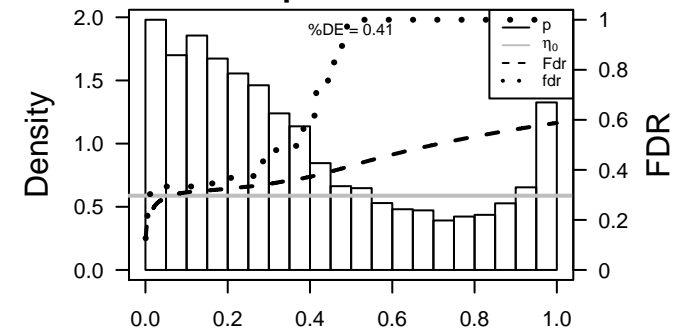
## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	5.27	0.003	26	GSEA C2REACTOME_PIP3_ACTIVATES_AKT_SIGNALING
2	5.05	0.003	33	GSEA C2REACTOME_PI3K_AKT_ACTIVATION
3	4.99	0.004	34	GSEA C2REACTOME_PI3K_EVENTS_IN_ERBB4_SIGNALING
4	4.81	0.004	35	GSEA C2REACTOME_GAB1_SIGNALOSOME
5	4.61	0.005	85	GSEA C2MOOTHA_VOXPHOS
6	4.4	0.005	10	BP DNA catabolic process
7	4.2	0.006	94	BP respiratory electron transport chain
8	4.18	0.006	685	GSEA C2KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR
9	4.06	0.007	31	BP lysosome organization
10	3.85	0.008	40	GSEA C2REACTOME_PI3K_EVENTS_IN_ERBB2_SIGNALING
11	3.83	0.009	18	BP phosphatidylinositol metabolic process
12	3.83	0.009	198	HM HALLMARK_OXIDATIVE_PHOSPHORYLATION
13	3.73	0.009	3682	Toxic LU_BPDE 0.005 DN
14	3.72	0.009	20	GSEA C2HERNANDEZ_ABERRANT_MITOSIS_BY_DOCETACEL_4NM_UP
15	3.69	0.010	50	Glio WILLSCHER_GBM_proteomics_wtOnly_SpotG
16	3.68	0.010	78	GSEA C2REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_S
17	3.65	0.010	44	GSEA C2REACTOME_PI3K_CASCADE
18	3.64	0.010	19	GSEA C2MAHADEVAN_RESPONSE_TO_MP470_DN
19	3.6	0.010	18	GSEA C2REACTOME_CD28_DEPENDENT_PI3K_AKT_SIGNALING
20	3.6	0.011	401	CC mitochondrial inner membrane
<i>Underexpressed</i>				
1	-11.45	2e-04	550	GSEA C2GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
2	-11.44	2e-04	305	GSEA C2DUTERTRE ESTRADIOL_RESPONSE_24HR_UP
3	-10.4	2e-04	462	Chr Chr 14
4	-10.4	2e-04	242	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN
5	-10.35	2e-04	267	GSEA C2ZHANG_TLX_TARGETS_60HR_DN
6	-9.75	3e-04	145	GSEA C2ZHANG_CYCLING_GENES
7	-9.39	3e-04	81	GSEA C2GRAHAM_NORMAL QUIESCENT_VS_NORMAL_DIVIDING_DN
8	-9.29	4e-04	1192	GSEA C2KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
9	-9.19	4e-04	412	BP mitotic cell cycle
10	-9.03	4e-04	162	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL QUIESCENT_UP
11	-8.97	4e-04	142	Glio WILLSCHER_GBM_Verhaak-CL_up (C)
12	-8.95	4e-04	99	GSEA C2BURTON_ADIPOGENESIS_3
13	-8.79	4e-04	87	GSEA C2ZHANG_TLX_TARGETS_UP
14	-8.58	5e-04	54	GSEA C2KANG_DOXORUBICIN_RESISTANCE_UP
15	-8.57	5e-04	215	GSEA C2KAUFFMANN_DNA_REPAIR_GENES
16	-8.52	5e-04	139	GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
17	-8.28	6e-04	301	GSEA C2REACTOME_CELL_CYCLE_MITOTIC
18	-8.07	6e-04	700	GSEA C2MARSON_BOUND_BY_E2F4_UNSTIMULATED
19	-7.92	7e-04	1110	BP cell cycle
20	-7.89	7e-04	388	GSEA C2REACTOME_CELL_CYCLE

p-values



p-values



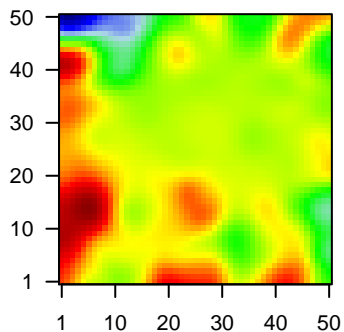
# B5\_mel

## Local Summary

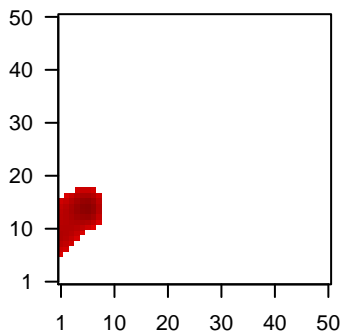
%DE = 0.77  
 # metagenes = 73  
 # genes = 643  
 # genes in genesets = 640  
  
 # genes with  $fdr < 0.1$  = 293 ( 227 + / 66 - )  
 # genes with  $fdr < 0.05$  = 217 ( 174 + / 43 - )  
 # genes with  $fdr < 0.01$  = 145 ( 120 + / 25 - )

$\langle r \rangle$  metagenes = 0.77  
 $\langle r \rangle$  genes = 0.07  
 $\langle FC \rangle$  = 0.22  
 $\langle \text{shrinkage-t} \rangle$  = 3.49  
 $\langle p\text{-value} \rangle$  = 0.02  
 $\langle fdr \rangle$  = 0.64

Profile



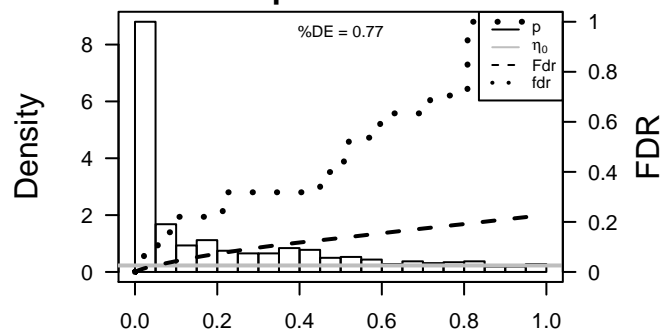
Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	RUVBL2	-1.49	1e-12	7e-10	6 x 13 RuvB-like AAA ATPase 2 [Source:HGNC Symbol;Acc:HGNC
2	CD53	1.74	6e-12	1e-09	8 x 17 CD53 molecule [Source:HGNC Symbol;Acc:HGNC:1686]
3	TRDMT1	1.71	1e-11	4e-09	7 x 14 tRNA aspartic acid methyltransferase 1 [Source:HGNC Symb
4	SLAIN1	1.67	4e-11	6e-09	6 x 14 SLAIN motif family, member 1 [Source:HGNC Symbol;Acc:HC
5	STARD3	1.63	1e-10	6e-09	1 x 15 StAR-related lipid transfer (START) domain containing 3 [Sou
6	AZI2	-1.31	1e-10	7e-09	1 x 13 5-azacytidine induced 2 [Source:HGNC Symbol;Acc:HGNC:2
7	TCEANC	1.62	2e-10	1e-08	6 x 18 transcription elongation factor A (SII) N-terminal and central r
8	SLC5A9	1.59	3e-10	1e-08	7 x 16 solute carrier family 5 (sodium/sugar cotransporter), member
9	ERCC6L2	1.59	3e-10	4e-08	1 x 7 excision repair cross-complementation group 6-like 2 [Sourc
10	CFAP61	1.56	6e-10	4e-07	1 x 12 cilia and flagella associated protein 61 [Source:HGNC Symbc
11	PIP5K1B	1.48	5e-09	4e-07	1 x 9 phosphatidylinositol-4-phosphate 5-kinase, type I, beta [Sou
12	SLC8A2	1.47	6e-09	7e-07	8 x 17 solute carrier family 8 (sodium/calcium exchanger), member 2
13	SLC25A14	1.45	1e-08	7e-07	4 x 14 solute carrier family 25 (mitochondrial carrier, brain), member
14	C1orf54	1.43	1e-08	3e-06	1 x 11 chromosome 1 open reading frame 54 [Source:HGNC Symbc
15	TANGO2	1.39	4e-08	3e-06	1 x 6 transport and golgi organization 2 homolog (Drosophila) [Sou
16	C20orf196	1.36	8e-08	3e-06	1 x 7 chromosome 20 open reading frame 196 [Source:HGNC Syrr
17	POPDC2	1.36	8e-08	7e-06	1 x 9 popeye domain containing 2 [Source:HGNC Symbol;Acc:HGNC
18	ENC1	1.31	2e-07	7e-06	3 x 14 ectodermal-neural cortex 1 (with BTB domain) [Source:HGNC
19	PMVK	1.29	4e-07	7e-06	4 x 10 phosphomevalonate kinase [Source:HGNC Symbol;Acc:HGNC
20	RUNX2	1.28	4e-07	7e-06	6 x 13 runt-related transcription factor 2 [Source:HGNC Symbol;Acc

p-values



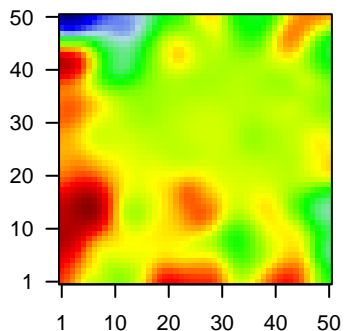
# B5\_mel

## Local Summary

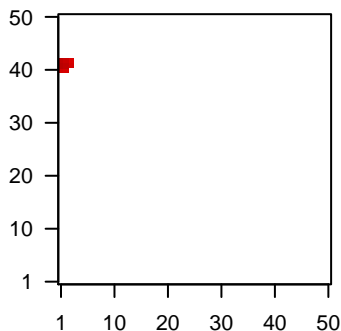
%DE = 0.79  
 # metagenes = 8  
 # genes = 126  
 # genes in genesets = 125  
  
 # genes with  $fdr < 0.1$  = 77 ( 62 + / 15 - )  
 # genes with  $fdr < 0.05$  = 62 ( 51 + / 11 - )  
 # genes with  $fdr < 0.01$  = 33 ( 28 + / 5 - )

$\langle r \rangle$  metagenes = 0.99  
 $\langle r \rangle$  genes = 0.22  
  
 $\langle FC \rangle$  = 0.31  
 $\langle \text{shrinkage-t} \rangle$  = 5.98  
 $\langle p\text{-value} \rangle$  = 0.01  
 $\langle fdr \rangle$  = 0.51

Profile



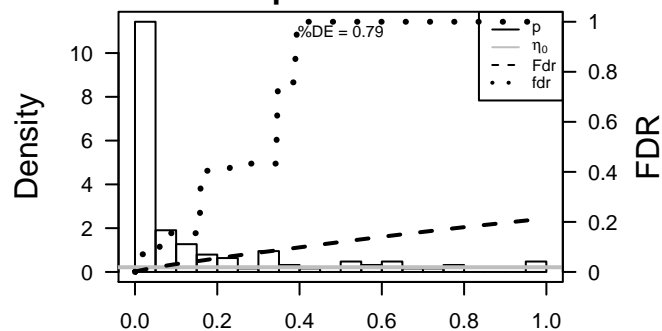
Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	EXOC3	0.82	2e-15	4e-09	1 x 42 exocyst complex component 3 [Source:HGNC Symbol;Acc:Hi
2	WIPF3	1.62	1e-10	8e-08	1 x 41 WAS/WASL interacting protein family, member 3 [Source:HGI
3	TBC1D7	0.6	3e-09	1e-05	1 x 42 TBC1 domain family, member 7 [Source:HGNC Symbol;Acc:†
4	SNX8	1.24	9e-07	1e-05	1 x 42 sorting nexin 8 [Source:HGNC Symbol;Acc:HGNC:14972]
5	ANO2	1.24	9e-07	1e-05	1 x 42 anoctamin 2, calcium activated chloride channel [Source:HGI
6	MITF	0.55	1e-06	3e-05	1 x 41 microphthalmia-associated transcription factor [Source:HGN
7	CTSL	0.51	3e-06	3e-05	2 x 40 cathepsin L [Source:HGNC Symbol;Acc:HGNC:2537]
8	IFI35	1.17	4e-06	1e-04	3 x 41 interferon-induced protein 35 [Source:HGNC Symbol;Acc:HC
9	PFKM	0.99	7e-06	2e-04	1 x 41 phosphofructokinase, muscle [Source:HGNC Symbol;Acc:HG
10	CCNB1IP1	-1.08	2e-05	2e-04	1 x 41 cyclin B1 interacting protein 1, E3 ubiquitin protein ligase [So
11	STARD10	1.06	3e-05	2e-04	1 x 40 STAR-related lipid transfer (START) domain containing 10 [Sc
12	ZC3H13	0.62	4e-05	2e-04	3 x 42 zinc finger CCCH-type containing 13 [Source:HGNC Symbol
13	NANS	-1.04	4e-05	2e-04	1 x 40 N-acetylneuraminic acid synthase [Source:HGNC Symbol;Ac
14	PPAP2C	1.03	4e-05	2e-04	1 x 40 phosphatidic acid phosphatase type 2C [Source:HGNC Synt
15	PLP1	0.41	6e-05	2e-04	1 x 42 proteolipid protein 1 [Source:HGNC Symbol;Acc:HGNC:9086
16	TUBB4A	0.86	7e-05	2e-04	1 x 42 tubulin, beta 4A class IVa [Source:HGNC Symbol;Acc:HGNC:
17	GABRB3	1	7e-05	2e-04	1 x 41 gamma-aminobutyric acid (GABA) A receptor, beta 3 [Source
18	ATP1A1	0.67	8e-05	2e-04	1 x 42 ATPase, Na+/K+ transporting, alpha 1 polypeptide [Source:Hi
19	COQ10A	0.99	8e-05	5e-04	1 x 41 coenzyme Q10 homolog A (S. cerevisiae) [Source:HGNC Syr
20	ITFG2	-0.98	1e-04	5e-04	1 x 41 integrin alpha FG-GAP repeat containing 2 [Source:HGNC S

p-values



# B5\_mel

## Local Summary

%DE = 0.87  
 # metagenes = 20  
 # genes = 334  
 # genes in genesets = 333  
  
 # genes with  $fdr < 0.1$  = 212 ( 30 + / 182 - )  
 # genes with  $fdr < 0.05$  = 195 ( 29 + / 166 - )  
 # genes with  $fdr < 0.01$  = 121 ( 13 + / 108 - )

<r> metagenes = 0.93

<r> genes = 0.3

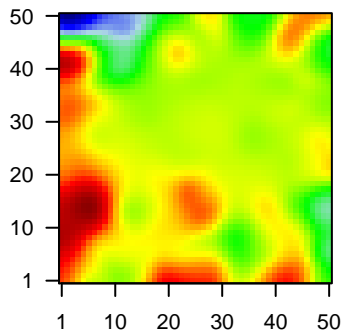
<FC> = -0.42

<shrinkage-t> = -6.81

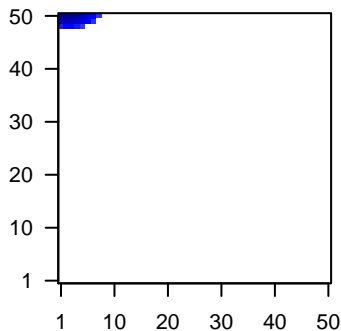
<p-value> = 0.01

<fdr> = 0.54

### Profile



### Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	CDKN3	-1.65	2e-16	2e-15	6 x 50 cyclin-dependent kinase inhibitor 3 [Source:HGNC Symbol;A
2	EBP	-2.01	2e-16	2e-15	1 x 48 emopamil binding protein (sterol isomerase) [Source:HGNC S
3	HAT1	-1.6	2e-16	2e-15	1 x 50 histone acetyltransferase 1 [Source:HGNC Symbol;Acc:HGNC
4	HAUS1	-1.62	2e-16	2e-15	1 x 50 HAUS augmin-like complex, subunit 1 [Source:HGNC Symbc
5	KPNA2	-0.92	2e-16	2e-15	7 x 50 karyopherin alpha 2 (RAG cohort 1, importin alpha 1) [Source
6	PCNA	-1.64	2e-16	2e-15	2 x 50 proliferating cell nuclear antigen [Source:HGNC Symbol;Acc:I
7	NUP85	-1.56	1e-14	9e-10	1 x 50 nucleoporin 85kDa [Source:HGNC Symbol;Acc:HGNC:8734]
8	GMNN	-1.45	2e-11	2e-09	2 x 50 geminin, DNA replication inhibitor [Source:HGNC Symbol;Acc
9	DNMT1	-1.1	7e-11	1e-08	2 x 48 DNA (cytosine-5-)-methyltransferase 1 [Source:HGNC Symb
10	SMC1A	-1.15	5e-10	1e-08	3 x 48 structural maintenance of chromosomes 1A [Source:HGNC S
11	TYMS	-1.37	7e-10	1e-08	3 x 50 thymidylate synthetase [Source:HGNC Symbol;Acc:HGNC:12
12	GMPS	-1.36	1e-09	4e-08	1 x 48 guanine monphosphate synthase [Source:HGNC Symbol;Acc
13	MAD2L1	-1.35	2e-09	1e-07	5 x 50 MAD2 mitotic arrest deficient-like 1 (yeast) [Source:HGNC S
14	FEN1	-1.34	5e-09	3e-07	1 x 50 flap structure-specific endonuclease 1 [Source:HGNC Symbc
15	EMP2	-1.31	1e-08	3e-07	2 x 50 epithelial membrane protein 2 [Source:HGNC Symbol;Acc:HC
16	MCM7	-1.29	2e-08	3e-07	2 x 50 minichromosome maintenance complex component 7 [Source
17	KIAA0101	-1.29	2e-08	1e-06	3 x 50 KIAA0101 [Source:HGNC Symbol;Acc:HGNC:28961]
18	POLD3	-1.27	5e-08	3e-06	2 x 50 polymerase (DNA-directed), delta 3, accessory subunit [Sour
19	HELLS	-1.23	2e-07	3e-06	1 x 50 helicase, lymphoid-specific [Source:HGNC Symbol;Acc:HGNC
20	CTNNA1	-1.23	2e-07	5e-06	1 x 50 catenin (cadherin-associated protein), alpha-like 1 [Source:HG

### p-values

