

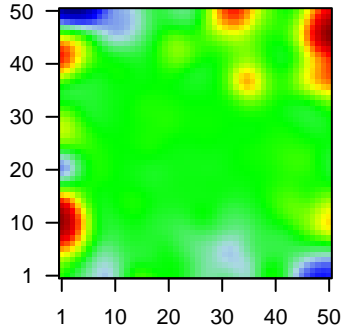
# D7\_mel

## Global Summary

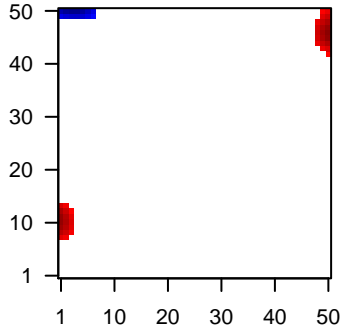
%DE = 0.2  
 # genes with fdr < 0.2 = 2529 ( 1556 + / 973 - )  
 # genes with fdr < 0.1 = 1909 ( 1205 + / 704 - )  
 # genes with fdr < 0.05 = 1696 ( 1078 + / 618 - )  
 # genes with fdr < 0.01 = 1052 ( 699 + / 353 - )  
  
 # genes in genesets = 14839

<FC> = 0  
 <shrinkage-t> = 0.06  
 <p-value> = 0.09  
 <fdr> = 0.8

Profile



Regulated Spots

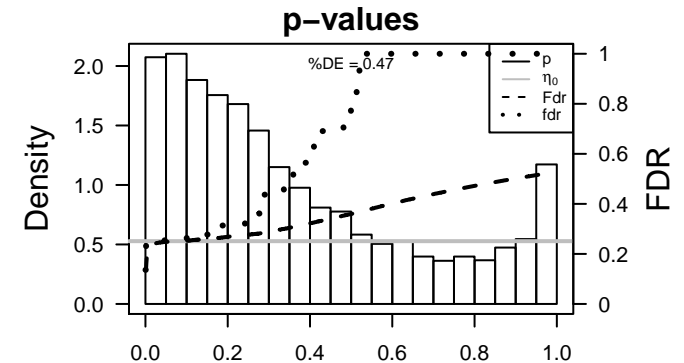
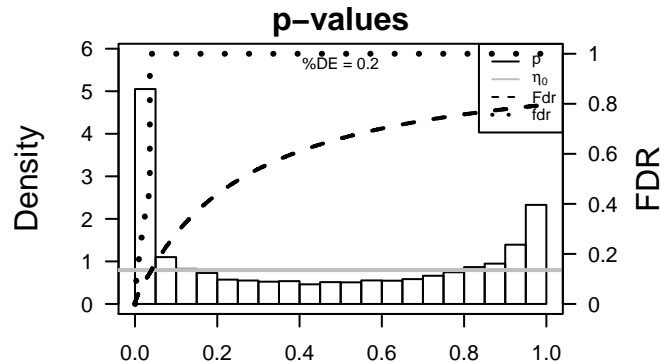


## Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ACTL6A	-1.91	2e-16	2e-13	4 x 50 actin-like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
2	AZI2	-1.5	2e-16	2e-13	1 x 13 5-azacytidine induced 2 [Source:HGNC Symbol;Acc:HGNC:24124]
3	BAAT	1.86	2e-16	2e-13	32 x 50 bile acid CoA:amino acid N-acyltransferase [Source:HGNC Symbol;Acc:HGNC:24124]
4	C9orf78	-1.57	2e-16	2e-13	6 x 40 chromosome 9 open reading frame 78 [Source:HGNC Symbol;Acc:HGNC:24124]
5	CEP97	2.34	2e-16	2e-13	2 x 47 centrosomal protein 97kDa [Source:HGNC Symbol;Acc:HGNC:24124]
6	EMP1	-1.53	2e-16	2e-13	25 x 48 epithelial membrane protein 1 [Source:HGNC Symbol;Acc:HGNC:24124]
7	EXOSC8	-1.33	2e-16	2e-13	1 x 50 exosome component 8 [Source:HGNC Symbol;Acc:HGNC:17]
8	GLB1	-1.64	2e-16	2e-13	40 x 50 galactosidase, beta 1 [Source:HGNC Symbol;Acc:HGNC:429]
9	HAUS1	-1.62	2e-16	2e-13	1 x 50 HAUS augmin-like complex, subunit 1 [Source:HGNC Symbol;Acc:HGNC:24124]
10	IFI16	-1.74	2e-16	2e-13	31 x 12 interferon, gamma-inducible protein 16 [Source:HGNC Symbol;Acc:HGNC:24124]
11	NAPA	-1.08	2e-16	2e-13	20 x 49 N-ethylmaleimide-sensitive factor attachment protein, alpha [Source:HGNC Symbol;Acc:HGNC:24124]
12	PABPC4	-1.64	2e-16	2e-13	50 x 7 poly(A) binding protein, cytoplasmic 4 (inducible form) [Source:HGNC Symbol;Acc:HGNC:24124]
13	PLK2	-1.65	2e-16	2e-13	50 x 1 polo-like kinase 2 [Source:HGNC Symbol;Acc:HGNC:19699]
14	PMP22	-1.44	2e-16	2e-13	48 x 1 peripheral myelin protein 22 [Source:HGNC Symbol;Acc:HGNC:24124]
15	POP4	-1.41	2e-16	2e-13	15 x 50 processing of precursor 4, ribonuclease P/MRP subunit (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:24124]
16	RDH12	1.87	2e-16	2e-13	16 x 32 retinol dehydrogenase 12 (all-trans/9-cis/11-cis) [Source:HGNC Symbol;Acc:HGNC:24124]
17	KMO	1.85	4e-16	3e-12	35 x 37 kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) [Source:HGNC Symbol;Acc:HGNC:24124]
18	TMX3	-1.52	7e-16	8e-11	44 x 1 thioredoxin-related transmembrane protein 3 [Source:HGNC Symbol;Acc:HGNC:24124]
19	TK1	-1.4	2e-14	8e-11	4 x 50 thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:HGNC:24124]
20	IFI44	1.74	2e-14	8e-11	1 x 5 interferon-induced protein 44 [Source:HGNC Symbol;Acc:HGNC:24124]

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<b>Overexpressed</b>				
1	5	0.004	19	GSEA C2REACTOME_INSULIN_SYNTHESIS_AND_PROCESSING
2	4.54	0.005	6929	Lymphoid_tissue_Txn_elongation
3	4.43	0.005	5940	Brain_Overlap_fetal_midbrain_HetRpts
4	4.42	0.005	8580	Colon_Cancer_Wk_Colon
5	4.32	0.006	2984	CC_integral_component_of_membrane
6	4.26	0.006	2136	TF_ICGC_GabpPcr2_targets
7	4.24	0.006	16	GSEA C2KEGG_STEROID_BIOSYNTHESIS
8	4.19	0.006	24	GSEA C2HORTON_SREBF_TARGETS
9	4.12	0.007	108	CC_late_endosome
10	4.07	0.007	9027	Colon_Cancer_Wk_Colon
11	4.06	0.007	24	GSEA C2SCHMIDT_POR_TARGETS_IN_LIMB_BUD_UP
12	4.04	0.007	94	CC_melanosome
13	4.02	0.007	198	HM_HALLMARK_OXIDATIVE_PHOSPHORYLATION
14	4	0.007	22	GSEA C2REACTOME_CHOLESTEROL_BIOSYNTHESIS
15	3.83	0.009	5184	Lymphoid_tissue_Txn_transition
16	3.82	0.009	37	MF_DNA-directed_RNA_polymerase_activity
17	3.55	0.011	4414	TF_ICGC_Bclaf101388_targets
18	3.52	0.011	1418	TF_ICGC_Ets1_targets
19	3.52	0.011	102	GSEA C2KEGG_PARKINSONS_DISEASE
20	3.49	0.012	368	GSEA C2STEIN_ESRRA_TARGETS_UP
<b>Underexpressed</b>				
1	-11.85	1e-04	305	GSEA C2DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
2	-11.62	1e-04	550	GSEA C2GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
3	-10.12	2e-04	242	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN
4	-9.84	3e-04	139	GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
5	-9.65	3e-04	50	GSEA C2SHIDA_E2F_TARGETS
6	-9.64	3e-04	142	Glio_WILLSCHER_GBM_Verhaak-CL_up (C)
7	-9.38	3e-04	136	GSEA C2RUIZ_TNC_TARGETS_DN
8	-8.71	5e-04	436	GSEA C2SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
9	-8.53	5e-04	218	GSEA C2CHICAS_RB1_TARGETS_GROWING
10	-8.38	5e-04	197	HM_HALLMARK_E2F_TARGETS
11	-8.35	5e-04	93	GSEA C2KONG_E2F3_TARGETS
12	-8.3	5e-04	171	GSEA C2SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP
13	-8.29	6e-04	110	GSEA C2WHITEFORD_PEDIATRIC_CANCER_MARKERS
14	-8.18	6e-04	162	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL QUIESCENT_UP
15	-8.12	6e-04	96	GSEA C2CROONQUIST_IL6_DEPRIVATION_DN
16	-8.1	6e-04	267	GSEA C2ZHANG_TLX_TARGETS_60HR_DN
17	-8.02	6e-04	99	GSEA C2BURTON_ADIPOGENESIS_3
18	-7.94	6e-04	155	GSEA C2HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
19	-7.89	7e-04	216	GSEA C2MARKEY_RB1_ACUTE_LOF_DN
20	-7.72	7e-04	72	GSEA C2CROONQUIST_NRAS_SIGNALING_DN



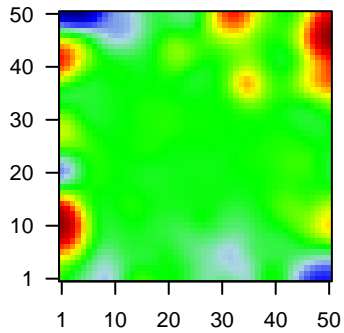
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## Local Summary

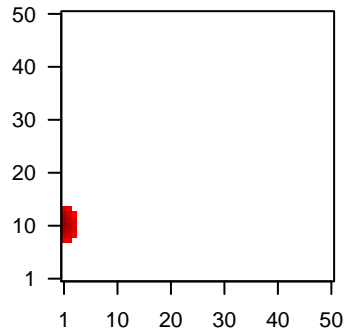
%DE = 0.76  
 # metagenes = 19  
 # genes = 266  
 # genes in genesets = 265  
  
 # genes with  $fdr < 0.1$  = 157 ( 138 + / 19 - )  
 # genes with  $fdr < 0.05$  = 123 ( 109 + / 14 - )  
 # genes with  $fdr < 0.01$  = 84 ( 74 + / 10 - )

$\langle r \rangle$  metagenes = 0.93  
 $\langle r \rangle$  genes = 0.13  
  
 $\langle FC \rangle$  = 0.33  
 $\langle \text{shrinkage-t} \rangle$  = 5.35  
 $\langle p\text{-value} \rangle$  = 0.01  
 $\langle fdr \rangle$  = 0.52

Profile



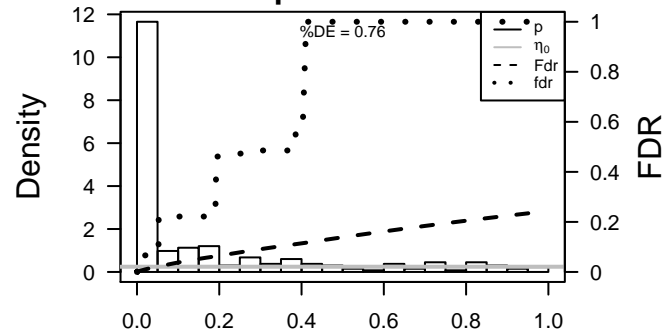
Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	AZI2	-1.5	2e-16	1e-14	1 x 13 5-azacytidine induced 2 [Source:HGNC Symbol;Acc:HGNC:]
2	FAM69C	1.4	8e-10	2e-08	1 x 14 family with sequence similarity 69, member C [Source:HGNC]
3	MADD	1.4	8e-10	2e-08	1 x 8 MAP-kinase activating death domain [Source:HGNC Symbol]
4	ECHDC2	1.39	1e-09	3e-07	1 x 14 enoyl CoA hydratase domain containing 2 [Source:HGNC Syr]
5	PIP5K1B	1.33	5e-09	5e-07	1 x 9 phosphatidylinositol-4-phosphate 5-kinase, type I, beta [Sou]
6	GREB1	1.29	2e-08	5e-07	1 x 9 growth regulation by estrogen in breast cancer 1 [Source:HGI]
7	CFAP61	1.28	2e-08	5e-07	1 x 12 cilia and flagella associated protein 61 [Source:HGNC Symbc]
8	SLC9A1	1.25	4e-08	5e-07	3 x 10 solute carrier family 9, subfamily A (NHE1, cation proton antiq
9	SNX1	-1.2	4e-08	2e-06	1 x 8 sorting nexin 1 [Source:HGNC Symbol;Acc:HGNC:11172]
10	MCF2L	1.23	6e-08	3e-06	1 x 10 MCF.2 cell line derived transforming sequence-like [Source:]-
11	METTL16	1.2	1e-07	3e-06	1 x 10 methyltransferase like 16 [Source:HGNC Symbol;Acc:HGNC:]
12	LCMT2	1.19	2e-07	3e-06	3 x 13 leucine carboxyl methyltransferase 2 [Source:HGNC Symbol];
13	RAPGEF6	1.19	2e-07	6e-06	1 x 10 Rap guanine nucleotide exchange factor (GEF) 6 [Source:HG]
14	MKS1	1.17	3e-07	8e-06	3 x 13 Meckel syndrome, type 1 [Source:HGNC Symbol;Acc:HGNC:]
15	MTA3	1.15	4e-07	8e-06	1 x 8 metastasis associated 1 family, member 3 [Source:HGNC Syr]
16	SUOX	1.14	6e-07	8e-06	1 x 12 sulfite oxidase [Source:HGNC Symbol;Acc:HGNC:11460]
17	LRCH1	1.13	7e-07	8e-06	3 x 11 leucine-rich repeats and calponin homology (CH) domain coi
18	HMG20A	1.13	7e-07	3e-05	1 x 13 high mobility group 20A [Source:HGNC Symbol;Acc:HGNC:5]
19	GDPD5	1.09	2e-06	3e-05	1 x 12 glycerophosphodiester phosphodiesterase domain containing
20	PPP2R1B	1.07	3e-06	3e-05	1 x 14 protein phosphatase 2, regulatory subunit A, beta [Source:HC]

p-values



# D7\_mel

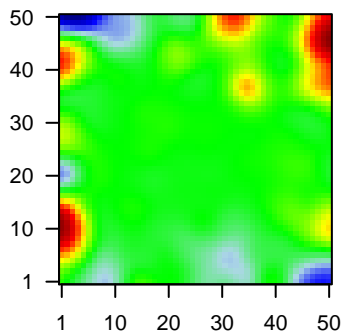
## Local Summary

%DE = 0.7  
 # metagenes = 22  
 # genes = 317  
 # genes in genesets = 317  
  
 # genes with  $fdr < 0.1$  = 166 ( 137 + / 29 - )  
 # genes with  $fdr < 0.05$  = 127 ( 110 + / 17 - )  
 # genes with  $fdr < 0.01$  = 91 ( 82 + / 9 - )

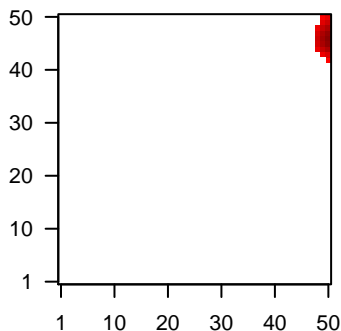
$\langle r \rangle$  metagenes = 0.87  
 $\langle r \rangle$  genes = 0.07

$\langle FC \rangle$  = 0.29  
 $\langle \text{shrinkage-t} \rangle$  = 4.66  
 $\langle p\text{-value} \rangle$  = 0.01  
 $\langle fdr \rangle$  = 0.56

Profile



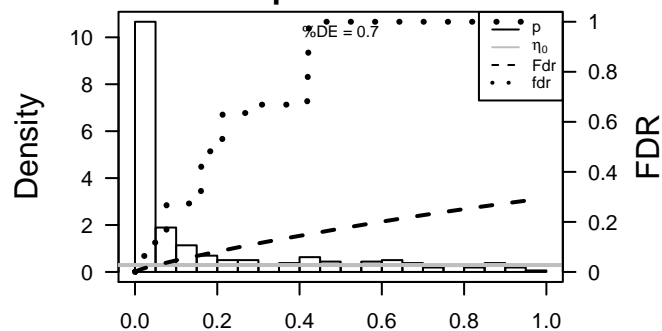
Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	UGP2	1.19	1e-13	2e-09	50 x 50 UDP-glucose pyrophosphorylase 2 [Source:HGNC Symbol;A
2	PHYKPL	1.52	2e-11	4e-08	50 x 45 5-phosphohydroxy-L-lysine phospho-lyase [Source:HGNC :
3	MFSD8	1.41	6e-10	4e-08	50 x 47 major facilitator superfamily domain containing 8 [Source:HGI
4	PRMT7	1.39	1e-09	4e-08	50 x 45 protein arginine methyltransferase 7 [Source:HGNC Symbol;/
5	CYP19A1	1.39	1e-09	5e-08	49 x 48 cytochrome P450, family 19, subfamily A, polypeptide 1 [Sou
6	NAA10	-1.26	2e-09	3e-07	50 x 50 N(alpha)-acetyltransferase 10, NatA catalytic subunit [Source
7	PIBF1	1.32	6e-09	3e-07	50 x 46 progesterone immunomodulatory binding factor 1 [Source:HG
8	SGK3	1.31	8e-09	3e-07	50 x 46 serum/glucocorticoid regulated kinase family, member 3 [Sou
9	UBE2Q2	1.29	1e-08	3e-07	50 x 50 ubiquitin-conjugating enzyme E2Q family member 2 [Source:
10	ZNF668	1.29	1e-08	4e-07	50 x 47 zinc finger protein 668 [Source:HGNC Symbol;Acc:HGNC:25
11	PHOSPHO2	1.28	2e-08	4e-07	50 x 46 phosphatase, orphan 2 [Source:HGNC Symbol;Acc:HGNC:2f
12	TSC2	1.27	2e-08	7e-07	50 x 46 tuberous sclerosis 2 [Source:HGNC Symbol;Acc:HGNC:1236
13	SIRT6	1.26	3e-08	2e-06	50 x 45 sirtuin 6 [Source:HGNC Symbol;Acc:HGNC:14934]
14	RAB4B	1.24	5e-08	6e-06	50 x 44 RAB4B, member RAS oncogene family [Source:HGNC Symb
15	ANKRA2	1.2	1e-07	6e-06	50 x 49 ankyrin repeat, family A (RFXANK-like), 2 [Source:HGNC Sy
16	VPS13B	1.19	2e-07	8e-06	50 x 45 vacuolar protein sorting 13 homolog B (yeast) [Source:HGNC
17	ICA1	1.17	3e-07	8e-06	50 x 50 islet cell autoantigen 1, 69kDa [Source:HGNC Symbol;Acc:Hf
18	ZNF10	1.16	4e-07	8e-06	50 x 43 zinc finger protein 10 [Source:HGNC Symbol;Acc:HGNC:128
19	BACH1	-1.12	5e-07	8e-06	50 x 50 BTB and CNC homology 1, basic leucine zipper transcription
20	ZNF189	1.14	5e-07	1e-05	50 x 44 zinc finger protein 189 [Source:HGNC Symbol;Acc:HGNC:12

p-values



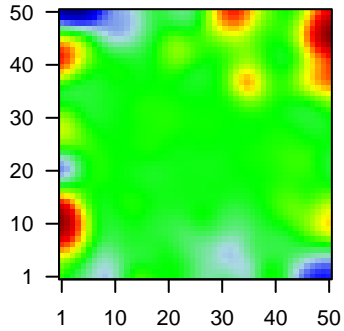
# D7\_mel

## Local Summary

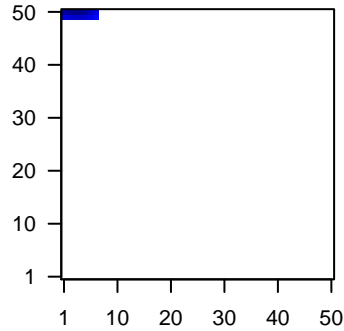
%DE = 0.84  
 # metagenes = 14  
 # genes = 262  
 # genes in genesets = 262  
  
 # genes with  $fdr < 0.1$  = 183 ( 29 + / 154 - )  
 # genes with  $fdr < 0.05$  = 164 ( 24 + / 140 - )  
 # genes with  $fdr < 0.01$  = 104 ( 14 + / 90 - )

$\langle r \rangle$  metagenes = 0.94  
 $\langle r \rangle$  genes = 0.35  
  
 $\langle FC \rangle = -0.4$   
 $\langle \text{shrinkage-t} \rangle = -6.37$   
 $\langle p\text{-value} \rangle = 0$   
 $\langle fdr \rangle = 0.45$

Profile



Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ACTL6A	-1.91	2e-16	3e-15	4 x 50 actin-like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
2	EXOSC8	-1.33	2e-16	3e-15	1 x 50 exosome component 8 [Source:HGNC Symbol;Acc:HGNC:17
3	HAUS1	-1.62	2e-16	3e-15	1 x 50 HAUS augmin-like complex, subunit 1 [Source:HGNC Symbc
4	TK1	-1.4	2e-14	3e-10	4 x 50 thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:HGN
5	TYMS	-1.37	8e-12	9e-10	3 x 50 thymidylate synthetase [Source:HGNC Symbol;Acc:HGNC:12
6	STMN1	-0.61	3e-11	7e-09	5 x 50 stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]
7	LBR	-1.26	3e-10	7e-09	7 x 50 lamin B receptor [Source:HGNC Symbol;Acc:HGNC:6518]
8	MIS18A	-1.3	4e-10	4e-08	3 x 49 MIS18 kinetochore protein A [Source:HGNC Symbol;Acc:HGI
9	POLD3	-1.27	1e-09	2e-07	2 x 50 polymerase (DNA-directed), delta 3, accessory subunit [Sour
10	CTNNA1	-1.23	7e-09	2e-07	1 x 50 catenin (cadherin-associated protein), alpha-like 1 [Source:t
11	CENPN	-1.21	1e-08	2e-07	4 x 50 centromere protein N [Source:HGNC Symbol;Acc:HGNC:308
12	TMPO	-1.21	2e-08	2e-07	5 x 50 thymopoietin [Source:HGNC Symbol;Acc:HGNC:11875]
13	TRIP13	-1.2	2e-08	2e-07	5 x 50 thyroid hormone receptor interactor 13 [Source:HGNC Symbc
14	HELLS	-1.18	3e-08	2e-07	1 x 50 helicase, lymphoid-specific [Source:HGNC Symbol;Acc:HGN
15	PRC1	-1.2	3e-08	9e-07	5 x 50 protein regulator of cytokinesis 1 [Source:HGNC Symbol;Acc:
16	C5orf34	1.23	7e-08	9e-07	6 x 50 chromosome 5 open reading frame 34 [Source:HGNC Symbc
17	MAD2L2	-1.18	8e-08	9e-07	2 x 50 MAD2 mitotic arrest deficient-like 2 (yeast) [Source:HGNC S;
18	BIRC5	-1.09	1e-07	3e-06	6 x 50 baculoviral IAP repeat containing 5 [Source:HGNC Symbol;A;
19	USP1	-1.16	2e-07	3e-06	2 x 50 ubiquitin specific peptidase 1 [Source:HGNC Symbol;Acc:HG
20	CDC47L	-1.15	3e-07	3e-06	1 x 50 cell division cycle associated 7-like [Source:HGNC Symbol;A

p-values

