

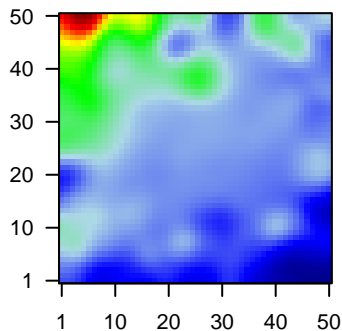
A4_mel

Global Summary

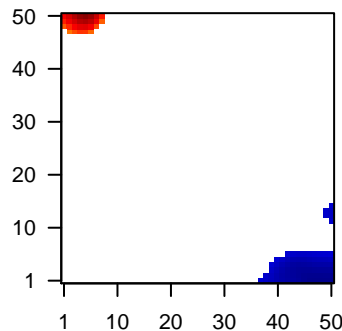
%DE = 0.2
 # genes with fdr < 0.2 = 2438 (1525 + / 913 -)
 # genes with fdr < 0.1 = 1982 (1270 + / 712 -)
 # genes with fdr < 0.05 = 1520 (988 + / 532 -)
 # genes with fdr < 0.01 = 973 (647 + / 326 -)
 # genes in genesets = 14839

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

Profile



Regulated Spots

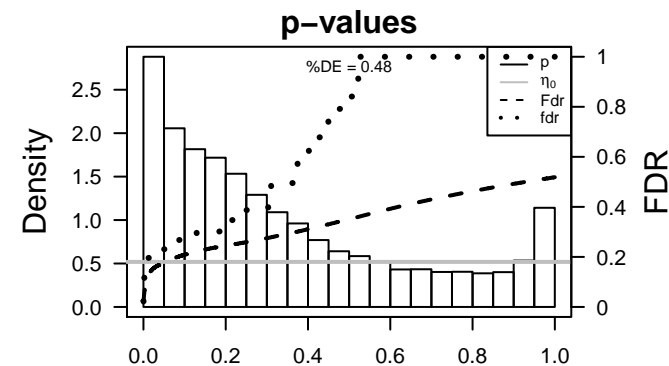
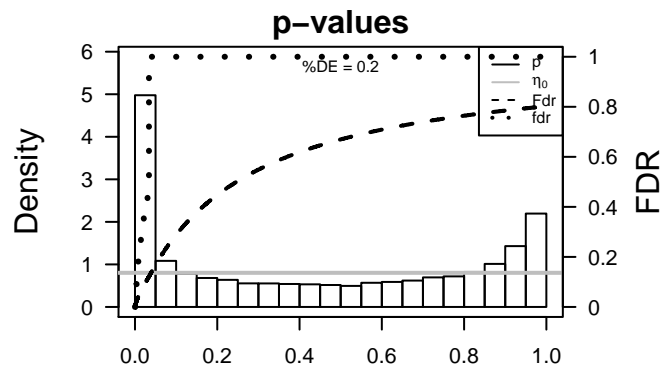


Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	BRD8	-1.55	2e-16 3e-13	50 x 39 bromodomain containing 8 [Source:HGNC Symbol;Acc:HGNC:10000]
2	CLTA	-1.35	2e-16 3e-13	1 x 20 clathrin, light chain A [Source:HGNC Symbol;Acc:HGNC:20910]
3	DPY30	-1.67	2e-16 3e-13	22 x 46 dpy-30 homolog (C. elegans) [Source:HGNC Symbol;Acc:HGNC:10000]
4	HIST1H4C	0.98	2e-16 3e-13	5 x 49 histone cluster 1, H4c [Source:HGNC Symbol;Acc:HGNC:47600]
5	MTRR	-1.61	2e-16 3e-13	1 x 26 5-methyltetrahydrofolate-homocysteine methyltransferase re [Source:HGNC Symbol;Acc:HGNC:10000]
6	OPHN1	1.99	2e-16 3e-13	36 x 28 oligophrenin 1 [Source:HGNC Symbol;Acc:HGNC:8148]
7	RNF10	-1.54	2e-16 3e-13	37 x 48 ring finger protein 10 [Source:HGNC Symbol;Acc:HGNC:10000]
8	SAT1	-0.74	2e-16 3e-13	1 x 11 spermidine/spermine N1-acetyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:10000]
9	SCFD1	-1.56	2e-16 3e-13	48 x 50 sec1 family domain containing 1 [Source:HGNC Symbol;Acc:HGNC:10000]
10	SNAP23	-1.54	2e-16 3e-13	50 x 1 synaptosomal-associated protein, 23kDa [Source:HGNC Symbol;Acc:HGNC:10000]
11	RARS2	-1.47	4e-16 2e-11	22 x 42 arginyl-tRNA synthetase 2, mitochondrial [Source:HGNC Symbol;Acc:HGNC:10000]
12	STAT2	-1.27	3e-15 2e-11	49 x 5 signal transducer and activator of transcription 2, 113kDa [Source:HGNC Symbol;Acc:HGNC:10000]
13	GLUL	-1.37	3e-15 4e-11	36 x 1 glutamate-ammonia ligase [Source:HGNC Symbol;Acc:HGNC:10000]
14	HMGN4	1.6	9e-15 4e-11	7 x 44 high mobility group nucleosomal binding domain 4 [Source:HGNC Symbol;Acc:HGNC:10000]
15	AARSD1	-1.45	1e-14 4e-11	44 x 50 alanyl-tRNA synthetase domain containing 1 [Source:HGNC Symbol;Acc:HGNC:10000]
16	EPS8	-0.97	1e-14 4e-11	49 x 13 epidermal growth factor receptor pathway substrate 8 [Source:HGNC Symbol;Acc:HGNC:10000]
17	FHIT	1.69	2e-14 2e-10	45 x 15 fragile histidine triad [Source:HGNC Symbol;Acc:HGNC:3701]
18	FAF2	-1.43	4e-14 2e-10	50 x 50 Fas associated factor family member 2 [Source:HGNC Symbol;Acc:HGNC:10000]
19	POC1A	1.66	4e-14 3e-10	4 x 48 POC1 centriolar protein A [Source:HGNC Symbol;Acc:HGNC:10000]
20	SC5D	-1.43	7e-14 3e-10	43 x 48 sterol-C5-desaturase [Source:HGNC Symbol;Acc:HGNC:10000]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	16.82	3e-05	242	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_UP
2	16.41	4e-05	142	Glio WILLSCHER_GBM_Verhaak-CL_up (C)
3	15.61	4e-05	550	GSEA C2GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
4	15.16	5e-05	305	GSEA C2DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
5	14.88	5e-05	197	HM HALLMARK_E2F_TARGETS
6	14.32	6e-05	139	GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
7	14.02	4e-03	16	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
8	13.38	8e-05	50	GSEA C2SHIDA_E2F_TARGETS
9	13.27	8e-05	124	GSEA C2ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
10	13.22	8e-05	96	GSEA C2CROONQUIST_IL6_DEPRIVATION_DN
11	13.13	9e-05	162	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
12	12.97	9e-05	412	BP mitotic cell cycle
13	12.81	1e-04	436	GSEA C2SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
14	12.8	1e-04	700	GSEA C2MARSON_BOUND_BY_E2F4_UNSTIMULATED
15	12.77	1e-04	110	GSEA C2WHITEFORD_PEDIATRIC_CANCER_MARKERS
16	12.74	1e-04	1192	GSEA C2KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
17	12.74	1e-04	724	GSEA C2PUJANA_CHEK2_PCC_NETWORK
18	12.56	1e-04	1460	GSEA C2PUJANA_BRCA1_PCC_NETWORK
19	12.4	1e-04	145	GSEA C2CHANG_CYCLING_GENES
20	12.16	1e-04	312	GSEA C2WONG_EMBRYONIC_STEM_CELL_CORE
<i>Underexpressed</i>				
1	-4.99	0.004	3897	Colon Ca639es1_Colon
2	-4.96	0.004	146	GSEA C2TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
3	-4.72	0.004	784	GSEA C2BUYTART_PHOTOGENOMIC_THERAPY_STRESS_UP
4	-4.63	0.005	3396	Lymphoma14OPP_Repressed
5	-4.52	0.005	302	GSEA C2KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
6	-4.4	0.005	3088	CC plasma membrane
7	-4.29	0.006	3383	Colon Ca639es1_Wk2_Colon
8	-4.29	0.006	594	GSEA C2WONG_ADULT_TISSUE_STEM_MODULE
9	-4.23	0.006	2984	CC integral component of membrane
10	-4.15	0.007	1949	Brain Fetal_TssF
11	-3.97	0.008	930	GSEA C2NUYTEN_EZH2_TARGETS_UP
12	-3.96	0.008	1386	Colon Ca639es1_Colon
13	-3.96	0.008	212	Lymphoma14ENZ_Stromal signature 1
14	-3.92	0.008	2188	Lymphoma14OPP_Poised_promoter
15	-3.91	0.008	10	BP histone mRNA catabolic process
16	-3.88	0.008	2185	Brain Fetal_TssA
17	-3.87	0.008	312	GSEA C2WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_UP
18	-3.81	0.009	426	GSEA C2ZWANG_CLASS_1_TRANSIENTLY_INDUCED_BY_EGF
19	-3.8	0.009	1065	Brain Overlap_fetal_midbrain_Enh
20	-3.75	0.009	683	GSEA C2GRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP



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Local Summary

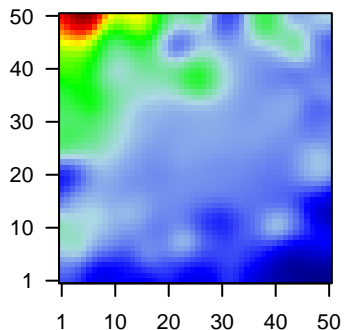
%DE = 0.82
 # metagenes = 28
 # genes = 383
 # genes in genesets = 382

 # genes with $fdr < 0.1$ = 259 (232 + / 27 -)
 # genes with $fdr < 0.05$ = 236 (215 + / 21 -)
 # genes with $fdr < 0.01$ = 200 (185 + / 15 -)

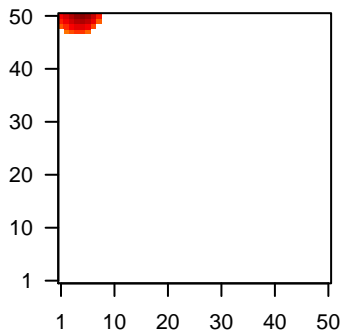
$\langle r \rangle$ metagenes = 0.92
 $\langle r \rangle$ genes = 0.29

 $\langle FC \rangle$ = 0.47
 $\langle \text{shrinkage-t} \rangle$ = 7.56
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.4

Profile



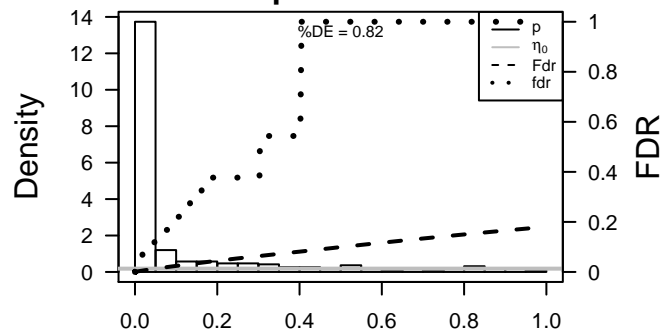
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	HIST1H4C	0.98	2e-16	2e-14	5 x 49 histone cluster 1, H4c [Source:HGNC Symbol;Acc:HGNC:476]
2	POC1A	1.66	4e-14	4e-10	4 x 48 POC1 centriolar protein A [Source:HGNC Symbol;Acc:HGNC:11390]
3	AURKB	1.51	6e-12	5e-10	6 x 50 aurora kinase B [Source:HGNC Symbol;Acc:HGNC:11390]
4	UBE2C	1.48	1e-11	7e-10	6 x 50 ubiquitin-conjugating enzyme E2C [Source:HGNC Symbol;Acc:HGNC:11390]
5	CDC45	1.47	2e-11	1e-09	1 x 50 cell division cycle 45 [Source:HGNC Symbol;Acc:HGNC:1736]
6	GEN1	1.45	4e-11	6e-09	5 x 50 GEN1 Holliday junction 5' flap endonuclease [Source:HGNC:11390]
7	CIT	1.4	2e-10	6e-09	7 x 50 citron rho-interacting serine/threonine kinase [Source:HGNC:11390]
8	PLK1	1.39	2e-10	1e-08	8 x 50 polo-like kinase 1 [Source:HGNC Symbol;Acc:HGNC:9077]
9	TRAIIP	1.37	4e-10	1e-08	5 x 50 TRAF interacting protein [Source:HGNC Symbol;Acc:HGNC:11390]
10	FBXO5	1.35	7e-10	1e-08	4 x 50 F-box protein 5 [Source:HGNC Symbol;Acc:HGNC:13584]
11	CDCA3	1.35	8e-10	1e-08	6 x 50 cell division cycle associated 3 [Source:HGNC Symbol;Acc:HGNC:11390]
12	RRM2	1.34	9e-10	2e-08	5 x 50 ribonucleotide reductase M2 [Source:HGNC Symbol;Acc:HGNC:11390]
13	ESCO2	1.32	2e-09	2e-08	4 x 50 establishment of sister chromatid cohesion N-acetyltransferase 2 [Source:HGNC Symbol;Acc:HGNC:11390]
14	HMGB2	1.21	2e-09	3e-08	5 x 50 high mobility group box 2 [Source:HGNC Symbol;Acc:HGNC:11390]
15	HAUS8	1.31	2e-09	3e-08	3 x 50 HAUS augmin-like complex, subunit 8 [Source:HGNC Symbol;Acc:HGNC:11390]
16	MTFR2	1.31	3e-09	3e-08	5 x 48 mitochondrial fission regulator 2 [Source:HGNC Symbol;Acc:HGNC:11390]
17	TK1	1.04	3e-09	3e-08	4 x 50 thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:HGNC:11390]
18	SPC25	1.3	3e-09	3e-08	6 x 50 SPC25, NDC80 kinetochore complex component [Source:HGNC:11390]
19	SPAG5	1.29	4e-09	3e-08	6 x 50 sperm associated antigen 5 [Source:HGNC Symbol;Acc:HGNC:11390]
20	BARD1	1.27	4e-09	3e-08	2 x 50 BRCA1 associated RING domain 1 [Source:HGNC Symbol;Acc:HGNC:11390]

p-values



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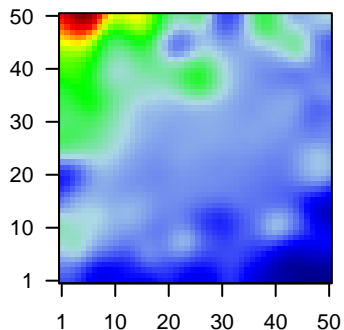
Local Summary

%DE = 0.7
 # metagenes = 71
 # genes = 750
 # genes in genesets = 749

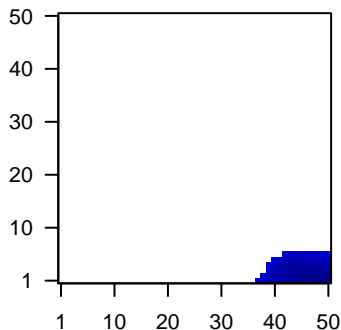
 # genes with $fdr < 0.1$ = 300 (73 + / 227 -)
 # genes with $fdr < 0.05$ = 177 (43 + / 134 -)
 # genes with $fdr < 0.01$ = 101 (18 + / 83 -)

$\langle r \rangle$ metagenes = 0.82
 $\langle r \rangle$ genes = 0.12
 $\langle FC \rangle$ = -0.2
 $\langle \text{shrinkage-t} \rangle$ = -3.23
 $\langle p\text{-value} \rangle$ = 0.03
 $\langle fdr \rangle$ = 0.71

Profile



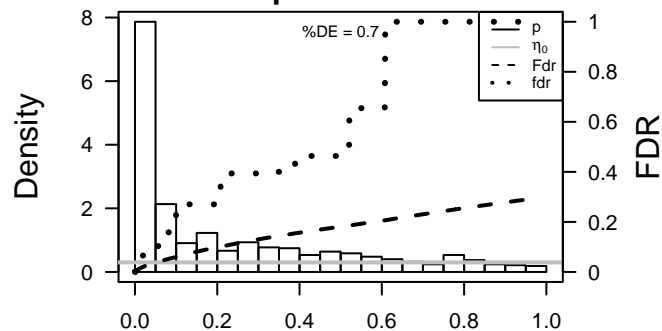
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	SNAP23	-1.54	2e-16	5e-14	50 x 1 synaptosomal-associated protein, 23kDa [Source:HGNC Syr
2	STAT2	-1.27	3e-15	3e-10	49 x 5 signal transducer and activator of transcription 2, 113kDa [So
3	DST	-1.06	1e-12	4e-10	46 x 1 dystonin [Source:HGNC Symbol;Acc:HGNC:1090]
4	PPP1R15A	-1.35	3e-12	5e-09	49 x 4 protein phosphatase 1, regulatory subunit 15A [Source:HGNC
5	STAM	-1.32	2e-11	7e-08	50 x 3 signal transducing adaptor molecule (SH3 domain and ITAM i
6	ABL2	-1.26	3e-10	7e-08	46 x 1 ABL proto-oncogene 2, non-receptor tyrosine kinase [Source
7	RAB3IP	1.36	6e-10	1e-07	50 x 3 RAB3A interacting protein [Source:HGNC Symbol;Acc:HGNC
8	MSRB3	-1.22	1e-09	3e-07	37 x 1 methionine sulfoxide reductase B3 [Source:HGNC Symbol;Ac
9	PLCD3	1.31	2e-09	1e-06	47 x 5 phospholipase C, delta 3 [Source:HGNC Symbol;Acc:HGNC:
10	SLFN12	1.24	2e-08	1e-06	49 x 1 schlafen family member 12 [Source:HGNC Symbol;Acc:HGNC
11	RND3	1.24	2e-08	1e-06	50 x 1 Rho family GTPase 3 [Source:HGNC Symbol;Acc:HGNC:671
12	LRPAP1	-0.9	2e-08	1e-06	42 x 1 low density lipoprotein receptor-related protein associated pr
13	DYNC1LI1	-1.1	2e-08	2e-05	47 x 1 dynein, cytoplasmic 1, light intermediate chain 1 [Source:HGI
14	ITCH	-0.98	9e-08	2e-05	40 x 1 itchy E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:-
15	FMN2	-1.11	2e-07	2e-05	48 x 1 formin 2 [Source:HGNC Symbol;Acc:HGNC:14074]
16	RNF141	-1.05	4e-07	2e-05	50 x 5 ring finger protein 141 [Source:HGNC Symbol;Acc:HGNC:21
17	UBR2	-1.1	4e-07	4e-05	40 x 1 ubiquitin protein ligase E3 component n-recognition 2 [Source:t
18	LGALS1	-0.8	6e-07	4e-05	50 x 1 lectin, galactoside-binding, soluble, 1 [Source:HGNC Symbol
19	MED31	-1.07	8e-07	4e-05	41 x 1 mediator complex subunit 31 [Source:HGNC Symbol;Acc:HG
20	VTN	1.08	9e-07	9e-05	50 x 1 vitronectin [Source:HGNC Symbol;Acc:HGNC:12724]

p-values



A4_mel

Local Summary

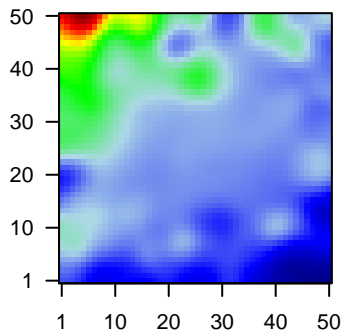
%DE = 0.83
 # metagenes = 6
 # genes = 73
 # genes in genesets = 73

 # genes with $fdr < 0.1$ = 44 (11 + / 33 -)
 # genes with $fdr < 0.05$ = 32 (6 + / 26 -)
 # genes with $fdr < 0.01$ = 23 (4 + / 19 -)

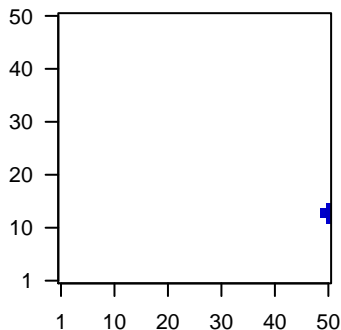
$\langle r \rangle$ metagenes = 0.97
 $\langle r \rangle$ genes = 0.1

$\langle FC \rangle = -0.28$
 $\langle \text{shrinkage-t} \rangle = -4.6$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.56$

Profile



Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	EPS8	-0.97	1e-14	2e-11	49 x 13 epidermal growth factor receptor pathway substrate 8 [Source:HGNC Symbol;Acc:HGNC:10117]
2	NME7	-1.33	2e-12	5e-11	50 x 14 NME/NM23 family member 7 [Source:HGNC Symbol;Acc:HGNC:10118]
3	SGCB	-1.34	6e-12	6e-09	50 x 13 sarcoglycan, beta (43kDa dystrophin-associated glycoprotein) [Source:HGNC Symbol;Acc:HGNC:10119]
4	USP32	-1.26	5e-10	2e-08	50 x 15 ubiquitin specific peptidase 32 [Source:HGNC Symbol;Acc:HGNC:10120]
5	EPB41L3	-1.2	2e-09	4e-07	50 x 15 erythrocyte membrane protein band 4.1-like 3 [Source:HGNC Symbol;Acc:HGNC:10121]
6	ZCCHC11	-1.14	4e-08	3e-06	50 x 15 zinc finger, CCHC domain containing 11 [Source:HGNC Symbol;Acc:HGNC:10122]
7	ARV1	-1.11	3e-07	3e-06	49 x 14 ARV1 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:10123]
8	CLIP1	-1.06	5e-07	1e-04	50 x 15 CAP-GLY domain containing linker protein 1 [Source:HGNC Symbol;Acc:HGNC:10124]
9	PSMD9	-0.72	1e-05	1e-04	50 x 14 proteasome (prosome, macropain) 26S subunit, non-ATPase [Source:HGNC Symbol;Acc:HGNC:10125]
10	CEP350	-0.82	2e-05	6e-04	50 x 14 centrosomal protein 350kDa [Source:HGNC Symbol;Acc:HGNC:10126]
11	STXBP6	0.85	1e-04	6e-04	50 x 13 syntaxin binding protein 6 (amisyn) [Source:HGNC Symbol;Acc:HGNC:10127]
12	ZNF226	-0.83	2e-04	6e-04	50 x 14 zinc finger protein 226 [Source:HGNC Symbol;Acc:HGNC:10128]
13	TBC1D23	-0.81	2e-04	6e-04	50 x 15 TBC1 domain family, member 23 [Source:HGNC Symbol;Acc:HGNC:10129]
14	TTC33	-0.79	3e-04	6e-04	50 x 14 tetratricopeptide repeat domain 33 [Source:HGNC Symbol;Acc:HGNC:10130]
15	RRM2B	-0.79	3e-04	6e-04	50 x 15 ribonucleotide reductase M2 B (TP53 inducible) [Source:HGNC Symbol;Acc:HGNC:10131]
16	LEO1	-0.79	3e-04	6e-04	50 x 13 Leo1, Paf1/RNA polymerase II complex component, homolog [Source:HGNC Symbol;Acc:HGNC:10132]
17	ACADVL	-0.79	3e-04	6e-04	49 x 13 acyl-CoA dehydrogenase, very long chain [Source:HGNC Symbol;Acc:HGNC:10133]
18	TRIM38	0.78	4e-04	6e-04	50 x 15 tripartite motif containing 38 [Source:HGNC Symbol;Acc:HGNC:10134]
19	ADAM9	-0.77	4e-04	2e-03	50 x 12 ADAM metallopeptidase domain 9 [Source:HGNC Symbol;Acc:HGNC:10135]
20	CHD7	-0.74	6e-04	2e-03	50 x 14 chromodomain helicase DNA binding protein 7 [Source:HGNC Symbol;Acc:HGNC:10136]

p-values

