A8_mel

Global Summary

%DE = 0.22

genes with fdr < 0.2 = 2754 (1685 + / 1069 −)

genes with fdr < 0.1 = 2308 (1431 + / 877 −)

genes with fdr < 0.05 = 1877 (1173 + / 704 −)

genes with fdr < 0.01 = 1115 (717 + / 398 −)

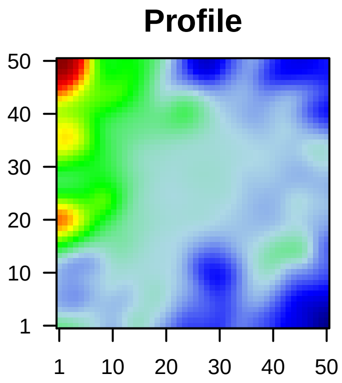
genes in genesets = 14839

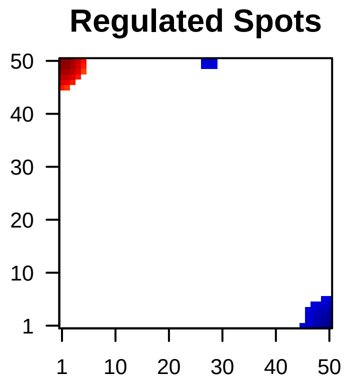
<FC> = 0

<shrinkage−t> = 0.03

<p−value> = 0.07

<fdr> = 0.78



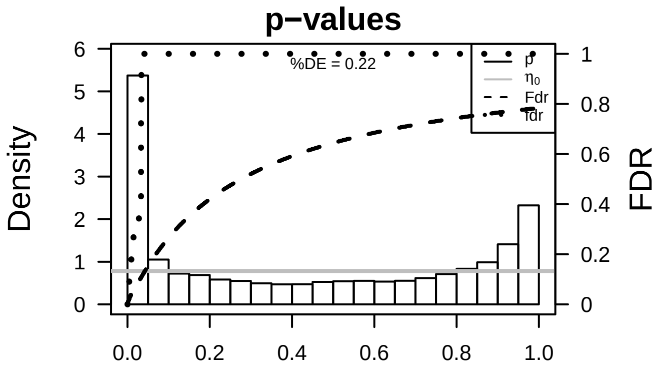


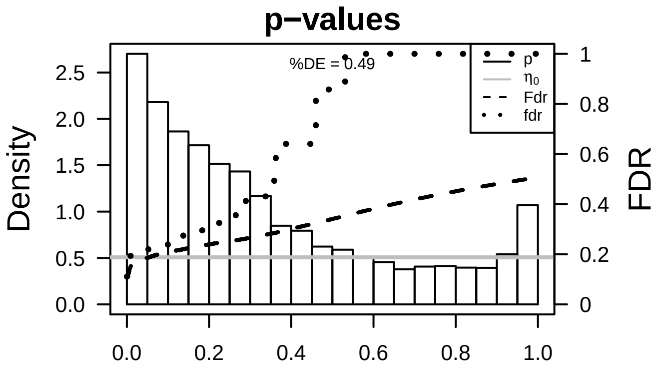
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	AMZ2	−1.18	2e−16	1e−13	48 x 42	archaelysin family metallopeptidase 2 [Source:HGNC Symbol
2	C12orf10	−1.53	2e−16	1e−13	29 x 50	chromosome 12 open reading frame 10 [Source:HGNC Symb
3	CALCOCO2	−1.46	2e−16	1e−13	26 x 50	calcium binding and coiled−coil domain 2 [Source:HGNC Syn
4	CDC42BPA	−1.8	2e−16	1e−13	50 x 38	CDC42 binding protein kinase alpha (DMPK−like) [Source:HC
5	CEP97	2.41	2e−16	1e−13	2 x 47	centrosomal protein 97kDa [Source:HGNC Symbol;Acc:HGN
6	CHD9	−1.59	2e−16	1e−13	31 x 10	chromodomain helicase DNA binding protein 9 [Source:HGN
7	CLDND1	−1.83	2e−16	1e−13	28 x 50	claudin domain containing 1 [Source:HGNC Symbol;Acc:HGN
8	CLK1	−1.55	2e−16	1e−13	50 x 40	CDC−like kinase 1 [Source:HGNC Symbol;Acc:HGNC:2068]
9	IFI16	−1.4	2e−16	1e−13	31 x 12	interferon, gamma−inducible protein 16 [Source:HGNC Symb
10	JKAMP	−1.79	2e−16	1e−13	29 x 50	JNK1/MAPK8−associated membrane protein [Source:HGNC
11	LINC00493	−1.61	2e−16	1e−13	36 x 39	long intergenic non−protein coding RNA 493 [Source:HGNC
12	MAGED2	−2.04	2e−16	1e−13	28 x 50	melanoma antigen family D2 [Source:HGNC Symbol;Acc:HG
13	MARCH7	−1.58	2e−16	1e−13	50 x 41	membrane−associated ring finger (C3HC4) 7, E3 ubiquitin pr
14	MRPL15	−1.16	2e−16	1e−13	5 x 33	mitochondrial ribosomal protein L15 [Source:HGNC Symbol;
15	OS9	−1.59	2e−16	1e−13	34 x 50	osteosarcoma amplified 9, endoplasmic reticulum lectin [Sour
16	PLS3	−1.58	2e−16	1e−13	21 x 43	plastin 3 [Source:HGNC Symbol;Acc:HGNC:9091]
17	POLR2K	−1.59	2e−16	1e−13	50 x 41	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa [S
18	PPIP5K2	−1.69	2e−16	1e−13	27 x 12	diphosphoinositol pentakisphosphate kinase 2 [Source:HGN
19	SAT1	−0.83	2e−16	1e−13	1 x 11	spermidine/spermine N1−acetyltransferase 1 [Source:HGNC
20	SPP1	−1.53	2e−16	1e−13	38 x 48	secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:HGN

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	13.85	7e−05	305	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
2	11.44	2e−04	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
3	11.32	2e−04	197	HM	HALLMARK_E2F_TARGETS
4	11	2e−04	242	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
5	10.45	2e−04	267	GSEA C2	ZHANG_TLX_TARGETS_60HR_DN
6	9.92	3e−04	81	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
7	9.85	3e−04	278	GSEA C2	MANALO_HYPOXIA_DN
8	9.58	3e−04	390	GSEA C2	PUJANA_BRCA2_PCC_NETWORK
9	9.54	3e−04	436	GSEA C2	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
10	9.37	3e−04	327	GSEA C2	BLUM_RESPONSE_TO_SALIRASIB_DN
11	9.13	4e−04	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
12	9.02	4e−04	1192	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
13	9.01	4e−04	87	GSEA C2	ZHANG_TLX_TARGETS_UP
14	8.95	4e−04	68	GSEA C2	VERNELL_RETINOBLASTOMA_PATHWAY_UP
15	8.66	5e−04	27	GSEA C2	REACTOME_DNA_STRAND_ELONGATION
16	8.5	5e−04	700	GSEA C2	MARSON_BOUND_BY_E2F4_UNSTIMULATED
17	8.36	5e−04	59	GSEA C2	KAUFFMANN_MELANOMA_RELAPSE_UP
18	8.16	6e−04	32	GSEA C2	KEGG_DNA_REPLICATION
19	8.03	6e−04	58	GSEA C2	SONG_TARGETS_OF_IE86_CMV_PROTEIN
20	7.86	7e−04	145	GSEA C2	CHANG_CYCLING_GENES
Underexpressed					
1	−5.95	0.002	268	miRNA target	hsa−miR−363
2	−5.67	0.002	472	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
3	−5.44	0.003	327	miRNA target	hsa−miR−367
4	−5.4	0.003	286	GSEA C2	PASINI_SUZ12_TARGETS_DN
5	−5.31	0.003	39	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAIND
6	−5.29	0.003	321	miRNA target	hsa−miR−32
7	−5.27	0.003	784	GSEA C2	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
8	−5.25	0.003	296	miRNA target	hsa−miR−25
9	−5.17	0.003	136	GSEA C2	PODAR_RESPONSE_TO_ADAPHOSTIN_UP
10	−5.08	0.003	64	GSEA C2	DELPUECH_FOXO3_TARGETS_UP
11	−5.05	0.003	302	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
12	−4.98	0.004	164	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_UP
13	−4.92	0.004	166	miRNA target	hsa−miR−548g
14	−4.91	0.004	263	miRNA target	hsa−miR−92b
15	−4.9	0.004	268	Lymphoma	SPANG_IL21 UP
16	−4.89	0.004	55	GSEA C2	AMIT_SERUM_RESPONSE_60_MCF10A
17	−4.86	0.004	271	miRNA target	hsa−miR−92a
18	−4.83	0.004	113	miRNA target	hsa−miR−507
19	−4.81	0.004	426	GSEA C2	ZWANG_CLASS_1_TRANSIENTLY_INDUCED_BY_EGF
20	−4.76	0.004	594	GSEA C2	WONG_ADULT_TISSUE_STEM_MODULE





A8_mel

Local Summary

%DE = 0.81

metagenes = 24

genes = 351

genes in genesets = 349

genes with fdr < 0.1 = 240 (224 + / 16 −)

genes with fdr < 0.05 = 213 (201 + / 12 −)

genes with fdr < 0.01 = 182 (174 + / 8 −)

<r> metagenes = 0.92

<r> genes = 0.24

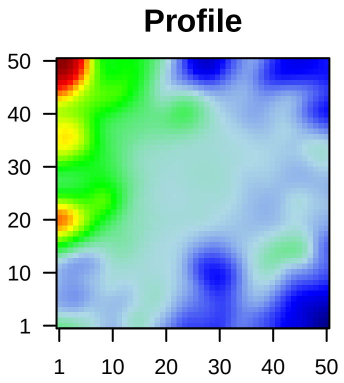
<FC> = 0.54

<shrinkage−t> = 8.71

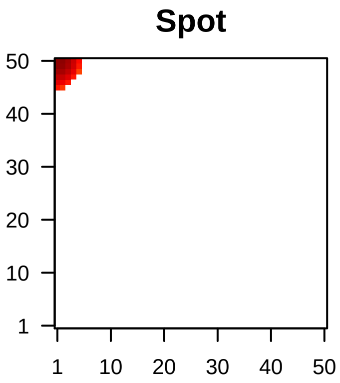
<p−value> = 0

<fdr> = 0.37

Profile



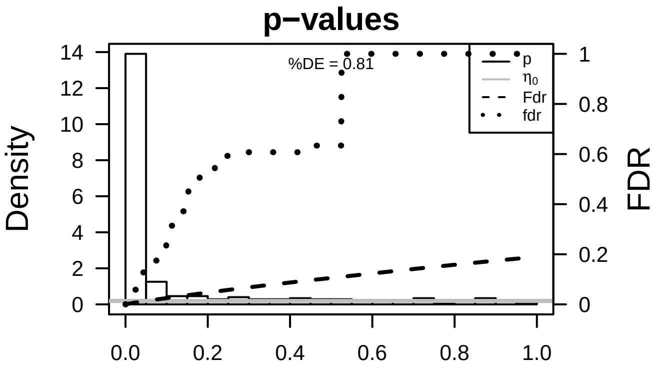
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CEP97	2.41	2e−16	1e−14	2 x 47	centrosomal protein 97kDa [Source:HGNC Symbol;Acc:HGN
2	SMCO4	1.8	3e−15	2e−12	1 x 47	single−pass membrane protein with coiled−coil domains 4 [S
3	POLE	1.73	3e−14	2e−11	1 x 48	polymerase (DNA directed), epsilon, catalytic subunit [Source
4	NCAPH2	1.66	3e−13	4e−11	1 x 50	non−SMC condensin II complex, subunit H2 [Source:HGNC
5	DTL	1.63	9e−13	2e−09	1 x 50	denticleless E3 ubiquitin protein ligase homolog (Drosophila)
6	CCNE2	1.49	7e−11	2e−09	2 x 50	cyclin E2 [Source:HGNC Symbol;Acc:HGNC:1590]
7	TEN1	1.48	7e−11	3e−09	1 x 48	TEN1 CST complex subunit [Source:HGNC Symbol;Acc:HG
8	FANCA	1.46	1e−10	3e−09	1 x 50	Fanconi anemia, complementation group A [Source:HGNC S
9	MCCC1	1.45	2e−10	3e−09	2 x 45	methylcrotonoyl−CoA carboxylase 1 (alpha) [Source:HGNC
10	MELK	1.45	2e−10	4e−08	5 x 50	maternal embryonic leucine zipper kinase [Source:HGNC Sy
11	RFC4	1.33	8e−10	4e−08	1 x 50	replication factor C (activator 1) 4, 37kDa [Source:HGNC Sy
12	HMGB2	1.25	2e−09	4e−08	5 x 50	high mobility group box 2 [Source:HGNC Symbol;Acc:HGNC:
13	NFYB	1.36	2e−09	4e−08	5 x 50	nuclear transcription factor Y, beta [Source:HGNC Symbol;Ac
14	C19orf48	1.26	3e−09	4e−08	1 x 50	chromosome 19 open reading frame 48 [Source:HGNC Sym
15	ACTL6A	−0.81	3e−09	7e−08	4 x 50	actin−like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
16	PKMYT1	1.33	5e−09	7e−08	1 x 50	protein kinase, membrane associated tyrosine/threonine 1 [S
17	TIFA	1.32	7e−09	7e−08	3 x 47	TRAF−interacting protein with forkhead−associated domain [
18	ZGRF1	1.32	7e−09	7e−08	1 x 50	zinc finger, GRF−type containing 1 [Source:HGNC Symbol;A
19	ASF1B	1.31	7e−09	7e−08	4 x 50	anti−silencing function 1B histone chaperone [Source:HGNC
20	RBM10	1.31	8e−09	2e−07	2 x 45	RNA binding motif protein 10 [Source:HGNC Symbol;Acc:HG

p−values



A8_mel

Local Summary

%DE = 0.79

metagenes = 27

genes = 407

genes in genesets = 406

genes with fdr < 0.1 = 187 (44 + / 143 −)

genes with fdr < 0.05 = 161 (40 + / 121 −)

genes with fdr < 0.01 = 100 (28 + / 72 −)

<r> metagenes = 0.96

<r> genes = 0.17

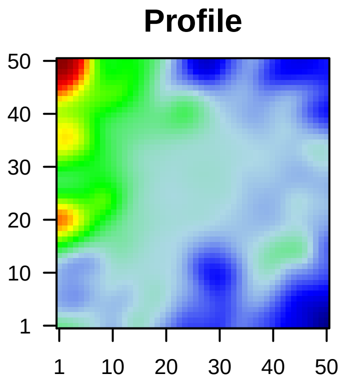
<FC> = −0.22

<shrinkage−t> = −3.66

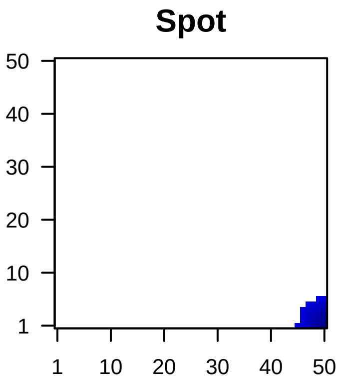
<p−value> = 0.02

<fdr> = 0.64

Profile



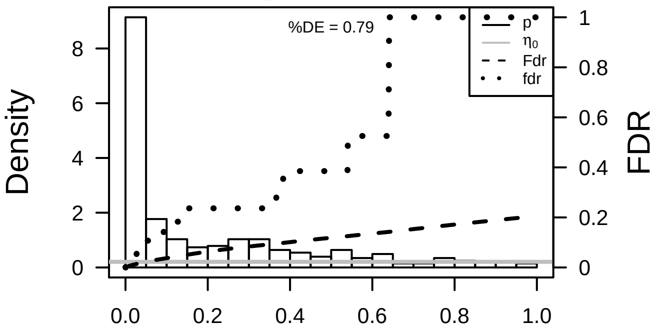
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	SYNE1	−1.4	2e−16	2e−14	49 x 1	spectrin repeat containing, nuclear envelope 1 [Source:HGN
2	C5orf15	−1.49	2e−15	5e−12	48 x 5	chromosome 5 open reading frame 15 [Source:HGNC Symb
3	TGIF1	−1.46	6e−14	2e−11	50 x 1	TGFB−induced factor homeobox 1 [Source:HGNC Symbol;A
4	PLK2	−1.24	3e−13	7e−10	50 x 1	polo−like kinase 2 [Source:HGNC Symbol;Acc:HGNC:19699]
5	ARMC9	−1.37	9e−12	9e−10	50 x 3	armadillo repeat containing 9 [Source:HGNC Symbol;Acc:HG
6	PLOD2	−1.36	2e−11	1e−09	49 x 3	procollagen−lysine, 2−oxoglutarate 5−dioxygenase 2 [Source
7	SPARC	−0.76	4e−11	2e−08	50 x 2	secreted protein, acidic, cysteine−rich (osteonectin) [Source:
8	TXNIP	1.44	3e−10	4e−07	50 x 1	thioredoxin interacting protein [Source:HGNC Symbol;Acc:H
9	GPBP1L1	−1.24	5e−09	1e−06	50 x 4	GC−rich promoter binding protein 1−like 1 [Source:HGNC Sy
10	NOV	−1.2	2e−08	8e−06	50 x 1	nephroblastoma overexpressed [Source:HGNC Symbol;Acc:
11	SERPINI1	1.18	2e−07	8e−06	50 x 1	serpin peptidase inhibitor, clade I (neuroserpin), member 1 [S
12	FMN2	−1.16	2e−07	1e−05	48 x 1	formin 2 [Source:HGNC Symbol;Acc:HGNC:14074]
13	EXT2	1.15	4e−07	1e−05	47 x 1	exostosin glycosyltransferase 2 [Source:HGNC Symbol;Acc:
14	LAMC1	1.01	6e−07	1e−05	50 x 3	laminin, gamma 1 (formerly LAMB2) [Source:HGNC Symbol;
15	FAM104A	−1.11	7e−07	2e−05	50 x 6	family with sequence similarity 104, member A [Source:HGN
16	CLOCK	−1.1	1e−06	4e−05	47 x 1	clock circadian regulator [Source:HGNC Symbol;Acc:HGNC:
17	THOC5	1.08	2e−06	4e−05	46 x 1	THO complex 5 [Source:HGNC Symbol;Acc:HGNC:19074]
18	DNAJC6	1.08	2e−06	4e−05	50 x 1	DnaJ (Hsp40) homolog, subfamily C, member 6 [Source:HG
19	PDLIM1	1.07	3e−06	4e−05	50 x 1	PDZ and LIM domain 1 [Source:HGNC Symbol;Acc:HGNC:2
20	MT2A	−1.06	3e−06	5e−05	50 x 3	metallothionein 2A [Source:HGNC Symbol;Acc:HGNC:7406]

p−values



A8_mel

Local Summary

%DE = 0.93

metagenes = 6

genes = 82

genes in genesets = 82

genes with fdr < 0.1 = 67 (17 + / 50 −)

genes with fdr < 0.05 = 54 (12 + / 42 −)

genes with fdr < 0.01 = 33 (6 + / 27 −)

<r> metagenes = 0.97

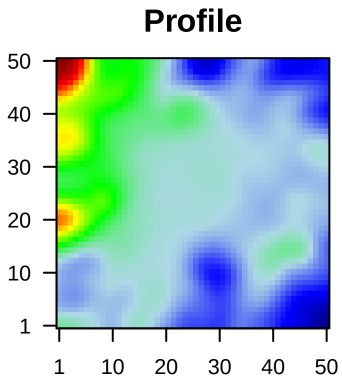
<r> genes = 0.11

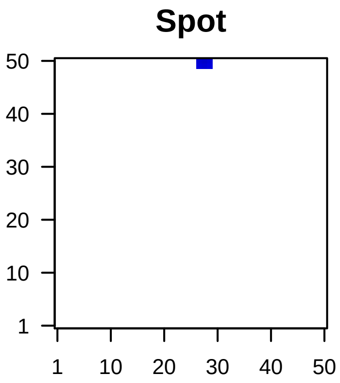
<FC> = −0.36

<shrinkage−t> = −6.56

<p−value> = 0

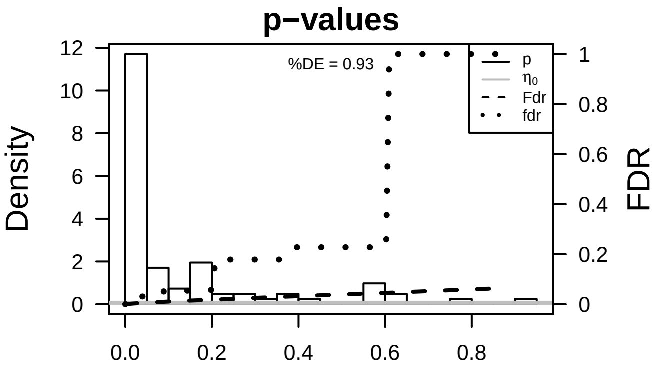
<fdr> = 0.52


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	C12orf10	−1.53	2e−16	3e−16	29 x 50	chromosome 12 open reading frame 10 [Source:HGNC Symb
2	CLDND1	−1.83	2e−16	3e−16	28 x 50	claudin domain containing 1 [Source:HGNC Symbol;Acc:HGN
3	JKAMP	−1.79	2e−16	3e−16	29 x 50	JNK1/MAPK8−associated membrane protein [Source:HGNC
4	MAGED2	−2.04	2e−16	3e−16	28 x 50	melanoma antigen family D2 [Source:HGNC Symbol;Acc:HG
5	RABGGTB	−1.39	4e−14	1e−09	28 x 50	Rab geranylgeranyltransferase, beta subunit [Source:HGNC
6	APEX1	−0.78	2e−10	5e−09	29 x 50	APEX nuclease (multifunctional DNA repair enzyme) 1 [Sour
7	MFSD1	−1.26	1e−09	5e−09	27 x 50	major facilitator superfamily domain containing 1 [Source:HG
8	OPA1	−1.13	2e−09	8e−08	28 x 50	optic atrophy 1 (autosomal dominant) [Source:HGNC Symbol
9	TAF2	−1.21	2e−08	4e−07	28 x 50	TAF2 RNA polymerase II, TATA box binding protein (TBP)−as
10	TRIP11	−1.1	1e−07	4e−07	27 x 50	thyroid hormone receptor interactor 11 [Source:HGNC Symb
11	DDX49	−0.94	2e−07	4e−06	27 x 50	DEAD (Asp−Glu−Ala−Asp) box polypeptide 49 [Source:HGN
12	RCAN1	−0.75	9e−07	1e−05	29 x 50	regulator of calcineurin 1 [Source:HGNC Symbol;Acc:HGNC:
13	CARS	−1.06	3e−06	2e−05	28 x 50	cysteinyl−tRNA synthetase [Source:HGNC Symbol;Acc:HGN
14	DNAJB14	−1	7e−06	2e−05	27 x 50	DnaJ (Hsp40) homolog, subfamily B, member 14 [Source:HG
15	TMEM126A	−1.01	9e−06	2e−05	29 x 50	transmembrane protein 126A [Source:HGNC Symbol;Acc:HG
16	DSCR3	−0.69	1e−05	2e−05	27 x 50	Down syndrome critical region 3 [Source:HGNC Symbol;Acc:
17	DDX43	−0.98	1e−05	1e−04	27 x 50	DEAD (Asp−Glu−Ala−Asp) box polypeptide 43 [Source:HGN
18	NUBP1	−0.92	6e−05	1e−04	29 x 50	nucleotide binding protein 1 [Source:HGNC Symbol;Acc:HGN
19	ARMCX6	−0.9	8e−05	1e−04	27 x 50	armadillo repeat containing, X−linked 6 [Source:HGNC Symb
20	VWA9	−0.89	9e−05	1e−04	27 x 50	von Willebrand factor A domain containing 9 [Source:HGNC


p−values