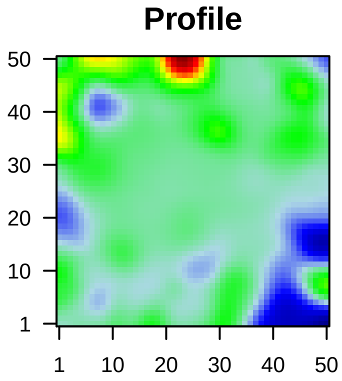
C7_mel

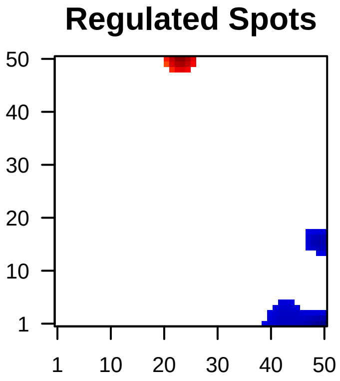
Global Summary

%DE = 0.21
genes with fdr < 0.2 = 2651 (1597 + / 1054 −)
genes with fdr < 0.1 = 2123 (1296 + / 827 −)
genes with fdr < 0.05 = 1762 (1091 + / 671 −)
genes with fdr < 0.01 = 1006 (670 + / 336 −)

genes in genesets = 14839

<FC> = 0
<shrinkage−t> = 0.04
<p−value> = 0.08
<fdr> = 0.79


Profile

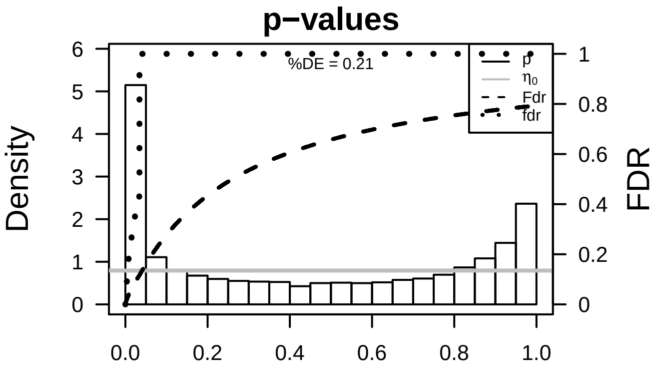

Regulated Spots

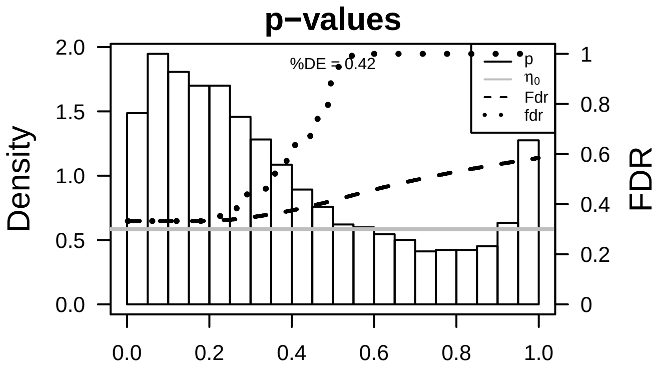
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CCDC47	−1.51	2e−16	1e−13	3 x 18	coiled−coil domain containing 47 [Source:HGNC Symbol;Acc
2	CEP97	1.98	2e−16	1e−13	2 x 47	centrosomal protein 97kDa [Source:HGNC Symbol;Acc:HGN
3	CRYAB	−1.5	2e−16	1e−13	50 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
4	DCTN2	−1.62	2e−16	1e−13	50 x 44	dynactin 2 (p50) [Source:HGNC Symbol;Acc:HGNC:2712]
5	GARS	−1.45	2e−16	1e−13	45 x 50	glycyl−tRNA synthetase [Source:HGNC Symbol;Acc:HGNC:4
6	GNAI1	−1.92	2e−16	1e−13	42 x 1	guanine nucleotide binding protein (G protein), alpha inhibitin
7	GUCD1	−1.6	2e−16	1e−13	1 x 47	guanylyl cyclase domain containing 1 [Source:HGNC Symbol
8	HSD17B4	−1.63	2e−16	1e−13	11 x 50	hydroxysteroid (17−beta) dehydrogenase 4 [Source:HGNC S
9	IMPDH2	−1.39	2e−16	1e−13	5 x 15	IMP (inosine 5'−monophosphate) dehydrogenase 2 [Source:
10	ITM2B	−1.4	2e−16	1e−13	50 x 10	integral membrane protein 2B [Source:HGNC Symbol;Acc:H
11	MTRR	−1.64	2e−16	1e−13	1 x 26	5−methyltetrahydrofolate−homocysteine methyltransferase re
12	NCOR1	−1.41	2e−16	1e−13	50 x 18	nuclear receptor corepressor 1 [Source:HGNC Symbol;Acc:H
13	NFE2L2	−1.24	2e−16	1e−13	44 x 19	nuclear factor, erythroid 2−like 2 [Source:HGNC Symbol;Acc:
14	PNRC2	−1.62	2e−16	1e−13	9 x 46	proline−rich nuclear receptor coactivator 2 [Source:HGNC Sy
15	PON2	−1.51	2e−16	1e−13	7 x 41	paraoxonase 2 [Source:HGNC Symbol;Acc:HGNC:9205]
16	SHMT2	−1.57	2e−16	1e−13	31 x 50	serine hydroxymethyltransferase 2 (mitochondrial) [Source:H
17	SIPA1L3	2.07	2e−16	1e−13	1 x 27	signal−induced proliferation−associated 1 like 3 [Source:HGN
18	SPARC	−1.13	2e−16	1e−13	50 x 2	secreted protein, acidic, cysteine−rich (osteonectin) [Source:
19	SRP19	−2.02	2e−16	1e−13	40 x 46	signal recognition particle 19kDa [Source:HGNC Symbol;Acc
20	STMN1	0.79	2e−16	1e−13	5 x 50	stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset
Overexpressed				
1	5.93	0.454	16	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
2	5.54	0.002	341	GSEA C2 RHEIN_ALL_GLUCOCORTICOID_THERAPY_DN
3	5.49	0.003	96	GSEA C2 CROONQUIST_IL6_DEPRIVATION_DN
4	5.32	0.003	139	GSEA C2 ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
5	5.29	0.003	110	GSEA C2 WHITEFORD_PEDIATRIC_CANCER_MARKERS
6	5.25	0.003	162	GSEA C2 GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
7	4.92	0.004	99	GSEA C2 LEE_EARLY_T_LYMPHOCYTE_UP
8	4.91	0.004	308	GSEA C2 LINDGREN_BLADDER_CANCER_CLUSTER_3_UP
9	4.88	0.004	291	GSEA C2 HORIUCHI_WTAP_TARGETS_DN
10	4.81	0.004	478	GSEA C2 STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
11	4.71	0.004	124	GSEA C2 ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
12	4.57	0.005	202	GSEA C2 CHANG_CORE_SERUM_RESPONSE_UP
13	4.55	0.005	436	GSEA C2 SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
14	4.52	0.005	41	GSEA C2 KEGG_PROTEASOME
15	4.44	0.005	81	GSEA C2 GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
16	4.41	0.005	48	BP regulation of cellular amino acid metabolic process
17	4.38	0.006	47	GSEA C2 REACTOME_VIF_MEDIATED_DEGRADATION_OF_APOBEC3G
18	4.34	0.006	58	GSEA C2 REACTOME_ACTIVATION_OF_NF_KAPPAB_IN_B_CELLS
19	4.3	0.006	54	GSEA C2 KANG_DOXORUBICIN_RESISTANCE_UP
20	4.28	0.006	47	GSEA C2 REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLAS
Underexpressed				
1	−5.41	0.003	11	BP mitotic G2 DNA damage checkpoint
2	−4.83	0.004	310	GSEA C2 DAZARD_RESPONSE_TO_UV_NHEK_DN
3	−4.18	0.006	327	miRNA target hsa−miR−367
4	−4.15	0.007	833	GSEA C2 DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
5	−4.12	0.007	20	GSEA C2 WILLERT_WNT_SIGNALING
6	−4.12	0.007	74	miRNA target hsa−miR−1827
7	−3.83	0.009	842	GSEA C2 KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP
8	−3.82	0.009	410	GSEA C2 LIM_MAMMARY_STEM_CELL_UP
9	−3.82	0.009	12	BP negative regulation of T cell receptor signaling pathway
10	−3.79	0.009	22	GSEA C2 DORSEY_GAB2_TARGETS
11	−3.78	0.009	33	GSEA C2 BIOCARTA_PAR1_PATHWAY
12	−3.77	0.009	1128	Lymphoma SPANG_BCR DN
13	−3.69	0.010	176	GSEA C2 TIEN_INTESTINE_PROBIOTICS_24HR_DN
14	−3.58	0.011	199	GSEA C2 CAIRO_HEPATOBLASTOMA_UP
15	−3.58	0.011	41	GSEA C2 JOHANSSON_BRAIN_CANCER_EARLY_VS_LATE_DN
16	−3.57	0.011	196	GSEA C2 CHANG_CORE_SERUM_RESPONSE_DN
17	−3.53	0.011	70	GSEA C2 SESTO_RESPONSE_TO_UV_C8
18	−3.51	0.011	26	BP GPI anchor biosynthetic process
19	−3.46	0.012	683	GSEA C2 KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
20	−3.45	0.012	6	GSEA C2 BUSA_SAM68_TARGETS_UP


p−values


p−values

C7_mel

Local Summary

%DE = 0.77

metagenes = 16

genes = 145

genes in genesets = 145

genes with fdr < 0.1 = 86 (77 + / 9 −)

genes with fdr < 0.05 = 79 (72 + / 7 −)

genes with fdr < 0.01 = 52 (49 + / 3 −)

<r> metagenes = 0.94

<r> genes = 0.08

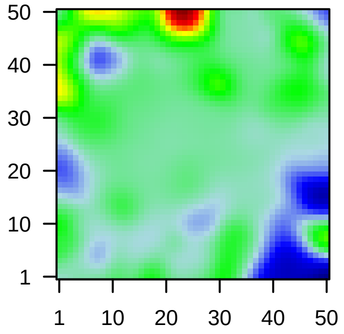
<FC> = 0.44

<shrinkage−t> = 6.9

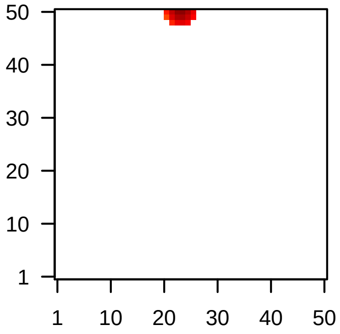
<p−value> = 0

<fdr> = 0.47

Profile



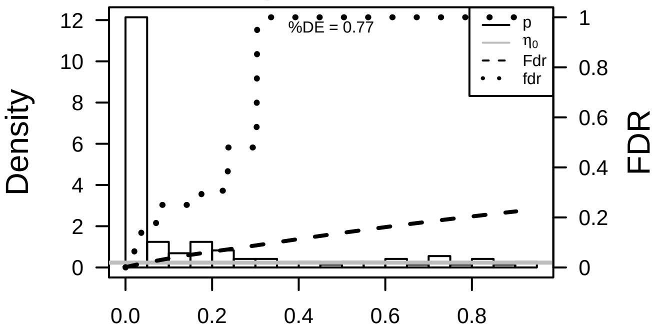
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	PLCD1	1.79	3e−14	6e−11	22 x 50	phospholipase C, delta 1 [Source:HGNC Symbol;Acc:HGNC:
2	MECOM	1.66	2e−12	8e−10	22 x 50	MDS1 and EVI1 complex locus [Source:HGNC Symbol;Acc:
3	EDC3	1.57	3e−11	8e−10	26 x 50	enhancer of mRNA decapping 3 [Source:HGNC Symbol;Acc:
4	MAP2K6	1.54	7e−11	8e−10	23 x 48	mitogen−activated protein kinase kinase 6 [Source:HGNC Sy
5	MFAP2	1.53	9e−11	8e−10	22 x 50	microfibrillar−associated protein 2 [Source:HGNC Symbol;Ac
6	DENND6A	1.52	1e−10	2e−09	24 x 50	DENN/MADD domain containing 6A [Source:HGNC Symbol;
7	SPINK2	1.5	2e−10	6e−09	22 x 50	serine peptidase inhibitor, Kazal type 2 (acrosin−trypsin inhibi
8	PLEKHF2	1.48	3e−10	2e−07	23 x 50	pleckstrin homology domain containing, family F (with FYVE
9	CLK4	1.37	5e−09	6e−07	25 x 50	CDC−like kinase 4 [Source:HGNC Symbol;Acc:HGNC:13659
10	RGS19	1.32	2e−08	5e−06	26 x 50	regulator of G−protein signaling 19 [Source:HGNC Symbol;A
11	NXT2	1.22	2e−07	5e−06	26 x 50	nuclear transport factor 2−like export factor 2 [Source:HGNC
12	CCDC15	1.2	4e−07	5e−06	21 x 50	coiled−coil domain containing 15 [Source:HGNC Symbol;Acc
13	UBE2U	1.18	5e−07	5e−06	22 x 50	ubiquitin−conjugating enzyme E2U (putative) [Source:HGNC
14	ALKBH8	1.18	6e−07	6e−06	24 x 50	alkB, alkylation repair homolog 8 (E. coli) [Source:HGNC Sy
15	WIBG	1.16	8e−07	6e−06	24 x 50	within bgcn homolog (Drosophila) [Source:HGNC Symbol;Ac
16	SLC39A4	1.15	1e−06	6e−06	24 x 50	solute carrier family 39 (zinc transporter), member 4 [Source:
17	RRNAD1	1.15	1e−06	7e−06	26 x 50	ribosomal RNA adenine dimethylase domain containing 1 [So
18	RBM48	1.14	1e−06	7e−06	23 x 50	RNA binding motif protein 48 [Source:HGNC Symbol;Acc:HG
19	DAAM2	1.13	2e−06	7e−06	23 x 50	dishevelled associated activator of morphogenesis 2 [Source:
20	OSGIN2	1.13	2e−06	1e−05	24 x 48	oxidative stress induced growth inhibitor family member 2 [So

p−values



C7_mel

Local Summary

%DE = 0.62

metagenes = 42

genes = 500

genes in genesets = 500

genes with fdr < 0.1 = 157 (40 + / 117 −)

genes with fdr < 0.05 = 130 (36 + / 94 −)

genes with fdr < 0.01 = 54 (15 + / 39 −)

<r> metagenes = 0.87

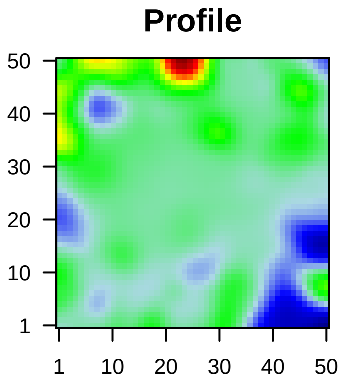
<r> genes = 0.14

<FC> = −0.22

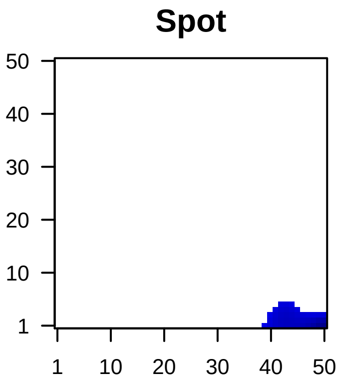
<shrinkage−t> = −3.45

<p−value> = 0.03

<fdr> = 0.69



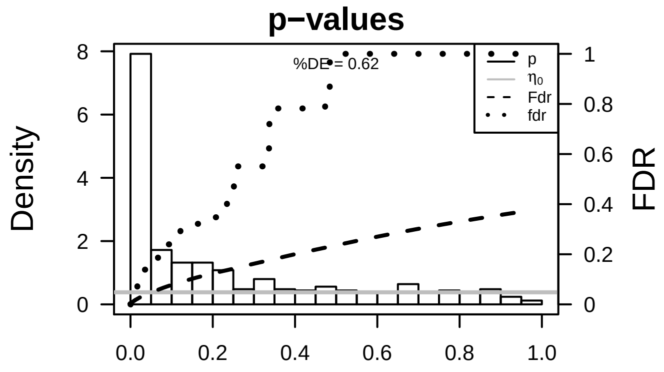
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CRYAB	−1.5	2e−16	1e−14	50 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
2	GNAI1	−1.92	2e−16	1e−14	42 x 1	guanine nucleotide binding protein (G protein), alpha inhibitin
3	SPARC	−1.13	2e−16	1e−14	50 x 2	secreted protein, acidic, cysteine−rich (osteonectin) [Source:
4	TMX3	−1.52	5e−15	6e−11	44 x 1	thioredoxin−related transmembrane protein 3 [Source:HGNC
5	TGIF1	−1.46	4e−13	6e−11	50 x 1	TGFB−induced factor homeobox 1 [Source:HGNC Symbol;A
6	TIA1	−1.41	6e−13	4e−06	39 x 1	TIA1 cytotoxic granule−associated RNA binding protein [Sour
7	P2RX4	−1.22	3e−08	4e−06	43 x 1	purinergic receptor P2X, ligand gated ion channel, 4 [Source:
8	MAGED1	−1.18	4e−08	6e−06	39 x 1	melanoma antigen family D1 [Source:HGNC Symbol;Acc:HG
9	SRPX	−1.2	8e−08	6e−06	50 x 1	sushi−repeat containing protein, X−linked [Source:HGNC Sy
10	LAMC1	−1.12	1e−07	6e−06	50 x 3	laminin, gamma 1 (formerly LAMB2) [Source:HGNC Symbol;
11	CBLB	−1.18	1e−07	3e−05	50 x 2	Cbl proto−oncogene B, E3 ubiquitin protein ligase [Source:H
12	FAM107B	1.2	4e−07	3e−05	46 x 3	family with sequence similarity 107, member B [Source:HGN
13	FAM98A	−1.16	4e−07	1e−04	49 x 1	family with sequence similarity 98, member A [Source:HGNC
14	AKAP9	−0.89	2e−06	1e−04	42 x 1	A kinase (PRKA) anchor protein 9 [Source:HGNC Symbol;Ac
15	LSS	−1.11	2e−06	2e−04	41 x 3	lanosterol synthase (2,3−oxidosqualene−lanosterol cyclase) [
16	MRPS6	−0.68	3e−06	2e−04	50 x 3	mitochondrial ribosomal protein S6 [Source:HGNC Symbol;A
17	KITLG	1.08	4e−06	2e−04	48 x 1	KIT ligand [Source:HGNC Symbol;Acc:HGNC:6343]
18	ZFHX4	1.08	5e−06	3e−04	41 x 1	zinc finger homeobox 4 [Source:HGNC Symbol;Acc:HGNC:3
19	CAV1	1.05	9e−06	3e−04	50 x 3	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;
20	FAM177A1	−1	9e−06	3e−04	45 x 1	family with sequence similarity 177, member A1 [Source:HG



p−values

C7_mel

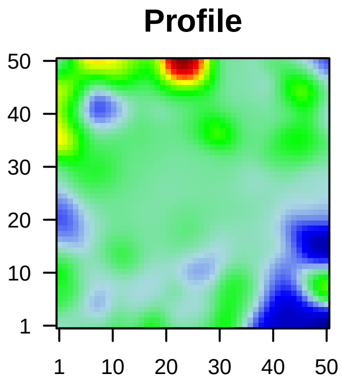
Local Summary

%DE = 0.66
metagenes = 18
genes = 158
genes in genesets = 157

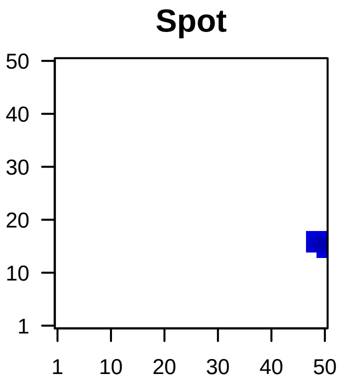
genes with fdr < 0.1 = 69 (15 + / 54 −)
genes with fdr < 0.05 = 46 (9 + / 37 −)
genes with fdr < 0.01 = 37 (6 + / 31 −)

<r> metagenes = 0.93
<r> genes = 0.09

<FC> = −0.27
<shrinkage−t> = −4.31
<p−value> = 0.01
<fdr> = 0.64



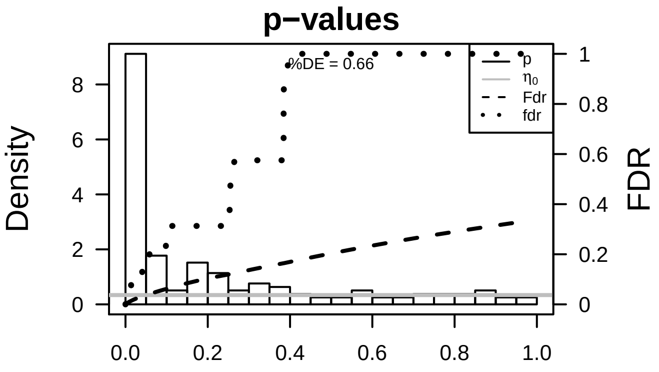
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	NCOR1	−1.41	2e−16	1e−14	50 x 18	nuclear receptor corepressor 1 [Source:HGNC Symbol;Acc:H
2	UQCC1	−1.5	1e−14	2e−09	48 x 15	ubiquinol−cytochrome c reductase complex assembly factor 1
3	SLU7	−1.37	4e−11	7e−08	50 x 16	SLU7 splicing factor homolog (S. cerevisiae) [Source:HGNC
4	EPB41L3	−1.3	1e−09	1e−06	50 x 15	erythrocyte membrane protein band 4.1−like 3 [Source:HGN
5	ATP2B1	−1.2	2e−08	3e−05	49 x 16	ATPase, Ca++ transporting, plasma membrane 1 [Source:HG
6	PAPOLG	1.18	6e−07	3e−05	50 x 15	poly(A) polymerase gamma [Source:HGNC Symbol;Acc:HG
7	FNTA	−0.98	2e−06	3e−05	48 x 16	farnesyltransferase, CAAX box, alpha [Source:HGNC Symbol
8	APLP2	−0.86	2e−06	3e−05	47 x 17	amyloid beta (A4) precursor−like protein 2 [Source:HGNC Sy
9	ZCCHC10	−1.09	3e−06	3e−05	48 x 18	zinc finger, CCHC domain containing 10 [Source:HGNC Sym
10	CYFIP1	−1.09	3e−06	1e−04	50 x 16	cytoplasmic FMR1 interacting protein 1 [Source:HGNC Symb
11	CERS5	−1	6e−06	1e−04	50 x 15	ceramide synthase 5 [Source:HGNC Symbol;Acc:HGNC:237
12	RBM34	−0.84	7e−06	6e−04	50 x 16	RNA binding motif protein 34 [Source:HGNC Symbol;Acc:HG
13	LGALS3BP	−0.62	2e−05	1e−03	47 x 17	lectin, galactoside−binding, soluble, 3 binding protein [Source
14	METTL2A	−0.94	7e−05	1e−03	50 x 18	methyltransferase like 2A [Source:HGNC Symbol;Acc:HGNC:
15	CCNT2	−0.93	8e−05	1e−03	47 x 18	cyclin T2 [Source:HGNC Symbol;Acc:HGNC:1600]
16	VRK3	−0.92	9e−05	1e−03	49 x 17	vaccinia related kinase 3 [Source:HGNC Symbol;Acc:HGNC:
17	CTNND1	0.87	1e−04	1e−03	48 x 18	catenin (cadherin−associated protein), delta 1 [Source:HGN
18	DICER1	−0.9	1e−04	1e−03	47 x 18	dicer 1, ribonuclease type III [Source:HGNC Symbol;Acc:HG
19	TTC39C	−0.88	2e−04	1e−03	50 x 17	tetratricopeptide repeat domain 39C [Source:HGNC Symbol;
20	POLR3E	−0.87	2e−04	1e−03	50 x 18	polymerase (RNA) III (DNA directed) polypeptide E (80kD) [S



p−values