E8_mel

Global Summary

%DE = 0.21

genes with fdr < 0.2 = 2687 (1664 + / 1023 −)

genes with fdr < 0.1 = 2061 (1311 + / 750 −)

genes with fdr < 0.05 = 1639 (1062 + / 577 −)

genes with fdr < 0.01 = 1060 (722 + / 338 −)

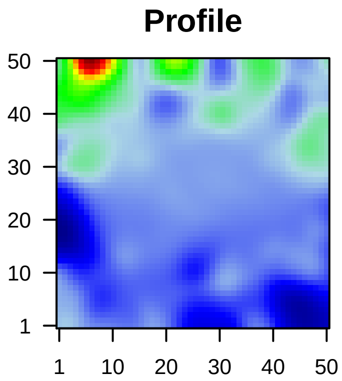
genes in genesets = 14839

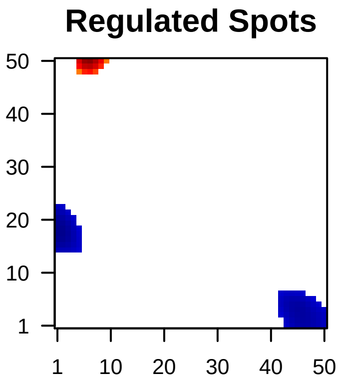
<FC> = 0

<shrinkage−t> = 0.06

<p−value> = 0.08

<fdr> = 0.79


Profile

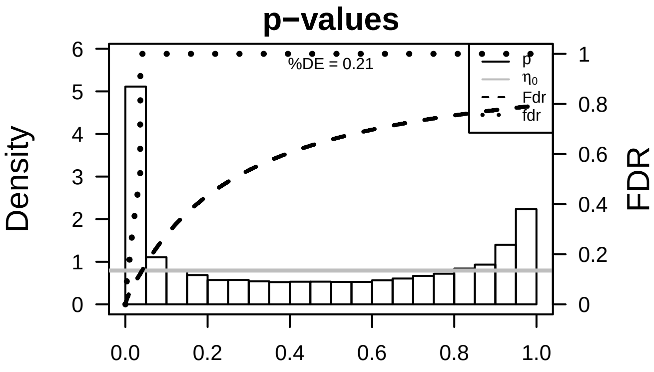

Regulated Spots

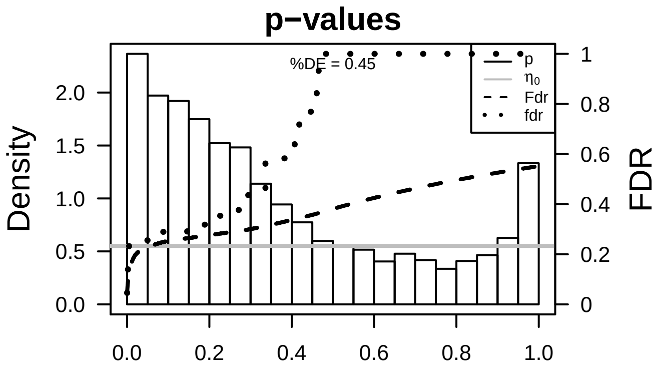
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ATP6AP2	−1.35	2e−16	3e−13	44 x 45	ATPase, H+ transporting, lysosomal accessory protein 2 [Sou
2	CCNB1	1.99	2e−16	3e−13	7 x 50	cyclin B1 [Source:HGNC Symbol;Acc:HGNC:1579]
3	CDC123	−1.56	2e−16	3e−13	46 x 50	cell division cycle 123 [Source:HGNC Symbol;Acc:HGNC:16
4	CNOT2	−0.87	2e−16	3e−13	39 x 1	CCR4−NOT transcription complex, subunit 2 [Source:HGNC
5	HIST1H2BB	2.23	2e−16	3e−13	21 x 50	histone cluster 1, H2bb [Source:HGNC Symbol;Acc:HGNC:4
6	HIST1H4E	1.9	2e−16	3e−13	7 x 50	histone cluster 1, H4e [Source:HGNC Symbol;Acc:HGNC:47
7	IMMP1L	1.8	2e−16	3e−13	10 x 50	IMP1 inner mitochondrial membrane peptidase−like (S. cerev
8	MARS	−1.49	2e−16	3e−13	43 x 47	methionyl−tRNA synthetase [Source:HGNC Symbol;Acc:HG
9	PAPOLA	−1.11	2e−16	3e−13	30 x 12	poly(A) polymerase alpha [Source:HGNC Symbol;Acc:HGNC
10	TXNRD1	−1.06	2e−16	3e−13	48 x 4	thioredoxin reductase 1 [Source:HGNC Symbol;Acc:HGNC:1
11	PPP2CA	−1.32	4e−16	2e−12	1 x 21	protein phosphatase 2, catalytic subunit, alpha isozyme [Sou
12	MSC	−1.39	7e−16	5e−12	32 x 1	musculin [Source:HGNC Symbol;Acc:HGNC:7321]
13	ZNF571	1.81	7e−16	5e−12	21 x 50	zinc finger protein 571 [Source:HGNC Symbol;Acc:HGNC:25
14	PLK1	1.8	1e−15	8e−12	8 x 50	polo−like kinase 1 [Source:HGNC Symbol;Acc:HGNC:9077]
15	RACGAP1	1.78	2e−15	8e−12	7 x 50	Rac GTPase activating protein 1 [Source:HGNC Symbol;Acc:
16	POLR2H	−1.48	2e−15	1e−11	1 x 27	polymerase (RNA) II (DNA directed) polypeptide H [Source:H
17	ATXN2	−1.47	4e−15	1e−11	28 x 11	ataxin 2 [Source:HGNC Symbol;Acc:HGNC:10555]
18	MPZL1	−1.44	6e−15	1e−11	1 x 19	myelin protein zero−like 1 [Source:HGNC Symbol;Acc:HGNC
19	PITPNB	−1.39	6e−15	1e−11	1 x 27	phosphatidylinositol transfer protein, beta [Source:HGNC Syn
20	TMEM194B	1.74	7e−15	3e−11	28 x 39	transmembrane protein 194B [Source:HGNC Symbol;Acc:HG

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	14.75	6e−05	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
2	13.43	8e−05	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
3	12.35	2e−03	16	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
4	12.28	1e−04	99	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
5	12.26	1e−04	700	GSEA C2	MARSON_BOUND_BY_E2F4_UNSTIMULATED
6	11.96	1e−04	124	GSEA C2	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
7	11.88	1e−04	93	GSEA C2	KONG_E2F3_TARGETS
8	11.69	1e−04	291	GSEA C2	HORIUCHI_WTAP_TARGETS_DN
9	11.61	1e−04	45	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
10	11.49	2e−04	145	GSEA C2	CHANG_CYCLING_GENES
11	11.07	2e−04	54	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
12	10.95	2e−04	155	GSEA C2	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
13	10.86	2e−04	40	GSEA C2	AMUNDSON_GAMMA_RADIATION_RESPONSE
14	10.66	2e−04	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
15	10.66	2e−04	42	GSEA C2	YU_MYC_TARGETS_UP
16	10.62	2e−04	81	GSEA C2	GAVIN_FOXP3_TARGETS_CLUSTER_P6
17	10.48	2e−04	52	GSEA C2	TANG_SENESCENCE_TP53_TARGETS_DN
18	10.31	2e−04	165	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
19	10.27	2e−04	616	GSEA C2	BENPORATH_CYCLING_GENES
20	10.25	2e−04	84	GSEA C2	MORI_LARGE_PRE_BII_LYMPHOCYTE_UP
Underexpressed					
1	−4.83	0.004	154	GSEA C2	AMUNDSON_POOR_SURVIVAL_AFTER_GAMMA_RADIATION_
2	−4.82	0.004	2185	Brain	Fetal_TssA
3	−4.64	0.005	833	GSEA C2	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
4	−4.57	0.470	14	Cancer	LIU_PROSTATE_CANCER_DN
5	−4.5	0.005	3897	Colon Cancer	Quies1_Colon
6	−4.42	0.005	72	GSEA C2	WNT_SIGNALING
7	−4.39	0.005	3396	Lymphoma	HOPP_Repressed
8	−4.36	0.006	182	miRNA target	hsa−miR−573
9	−4.35	0.006	3682	Toxic	LU_BPDE 0.005 DN
10	−4.33	0.006	22	GSEA C2	REACTOME_MYOGENESIS
11	−4.27	0.006	2188	Lymphoma	HOPP_Poised_promoter
12	−4.19	0.006	147	miRNA target	hsa−miR−506
13	−4.17	0.007	2159	Colon Cancer	TssP_Colon
14	−4.01	0.007	392	GSEA C2	HAN_SATB1_TARGETS_DN
15	−4	0.008	410	GSEA C2	LIM_MAMMARY_STEM_CELL_UP
16	−3.99	0.008	26	BP	positive regulation of Wnt signaling pathway
17	−3.94	0.008	278	GSEA C2	GABRIELY_MIR21_TARGETS
18	−3.92	0.008	447	miRNA target	hsa−miR−130b
19	−3.89	0.008	3383	Colon Cancer	EnhWk2_Colon
20	−3.86	0.008	85	GSEA C2	ELVIDGE_HIF1A_TARGETS_DN


p−values


p−values

E8_mel

Local Summary

%DE = 0.85

metagenes = 15

genes = 205

genes in genesets = 205

genes with fdr < 0.1 = 157 (148 + / 9 −)

genes with fdr < 0.05 = 141 (137 + / 4 −)

genes with fdr < 0.01 = 118 (116 + / 2 −)

<r> metagenes = 0.98

<r> genes = 0.36

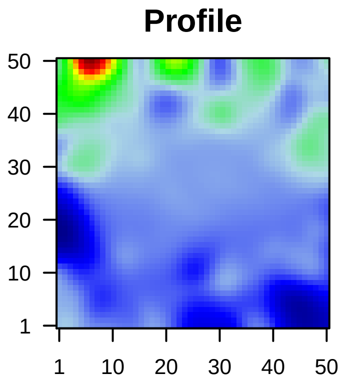
<FC> = 0.69

<shrinkage−t> = 11.04

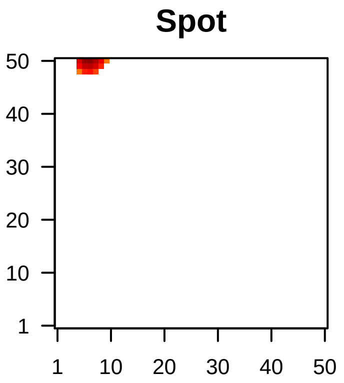
<p−value> = 0

<fdr> = 0.31

Profile



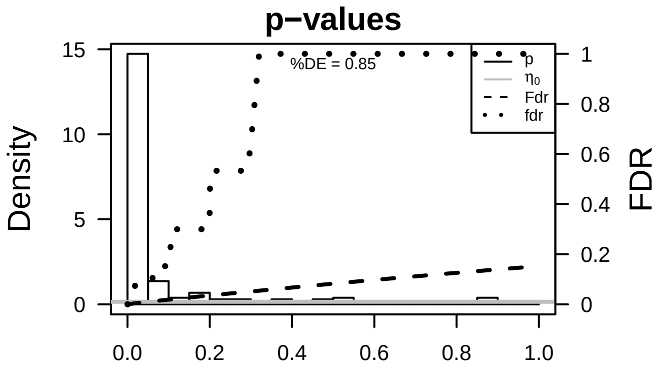
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CCNB1	1.99	2e−16	2e−15	7 x 50	cyclin B1 [Source:HGNC Symbol;Acc:HGNC:1579]
2	HIST1H4E	1.9	2e−16	2e−15	7 x 50	histone cluster 1, H4e [Source:HGNC Symbol;Acc:HGNC:47
3	IMMP1L	1.8	2e−16	2e−15	10 x 50	IMP1 inner mitochondrial membrane peptidase−like (S. cerev
4	PLK1	1.8	1e−15	2e−14	8 x 50	polo−like kinase 1 [Source:HGNC Symbol;Acc:HGNC:9077]
5	RACGAP1	1.78	2e−15	3e−13	7 x 50	Rac GTPase activating protein 1 [Source:HGNC Symbol;Acc:
6	KIF20A	1.73	1e−14	2e−12	7 x 50	kinesin family member 20A [Source:HGNC Symbol;Acc:HGN
7	CDKN3	1.25	7e−14	4e−12	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
8	CDCA3	1.65	2e−13	7e−12	6 x 50	cell division cycle associated 3 [Source:HGNC Symbol;Acc:H
9	HIST1H2AM	1.62	5e−13	7e−12	9 x 50	histone cluster 1, H2am [Source:HGNC Symbol;Acc:HGNC:4
10	HYLS1	1.61	7e−13	2e−11	8 x 50	hydrolethalus syndrome 1 [Source:HGNC Symbol;Acc:HGNC
11	CDC20	1.59	1e−12	2e−11	6 x 50	cell division cycle 20 [Source:HGNC Symbol;Acc:HGNC:172
12	ESPL1	1.58	2e−12	1e−10	7 x 49	extra spindle pole bodies homolog 1 (S. cerevisiae) [Source:
13	DLGAP5	1.53	8e−12	1e−10	7 x 50	discs, large (Drosophila) homolog−associated protein 5 [Sour
14	KIAA1524	1.53	8e−12	1e−10	6 x 50	KIAA1524 [Source:HGNC Symbol;Acc:HGNC:29302]
15	HMGB2	1.38	1e−11	1e−10	5 x 50	high mobility group box 2 [Source:HGNC Symbol;Acc:HGNC:
16	ECT2	1.51	2e−11	2e−10	6 x 50	epithelial cell transforming 2 [Source:HGNC Symbol;Acc:HG
17	KPNA2	0.62	3e−11	2e−10	7 x 50	karyopherin alpha 2 (RAG cohort 1, importin alpha 1) [Sourc
18	KIF2C	1.49	3e−11	4e−10	6 x 50	kinesin family member 2C [Source:HGNC Symbol;Acc:HGNC
19	CCNA2	1.47	5e−11	4e−10	6 x 50	cyclin A2 [Source:HGNC Symbol;Acc:HGNC:1578]
20	HMMR	1.47	6e−11	4e−10	7 x 50	hyaluronan−mediated motility receptor (RHAMM) [Source:HG

p−values



E8_mel

Local Summary

%DE = 0.65

metagenes = 54

genes = 565

genes in genesets = 565

genes with fdr < 0.1 = 173 (44 + / 129 −)

genes with fdr < 0.05 = 119 (34 + / 85 −)

genes with fdr < 0.01 = 63 (20 + / 43 −)

<r> metagenes = 0.89

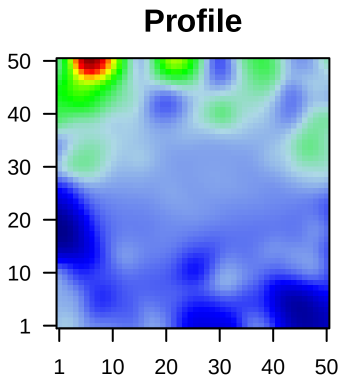
<r> genes = 0.15

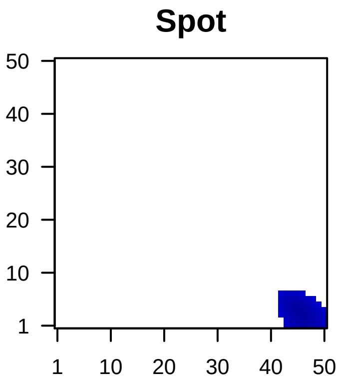
<FC> = −0.2

<shrinkage−t> = −3.06

<p−value> = 0.04

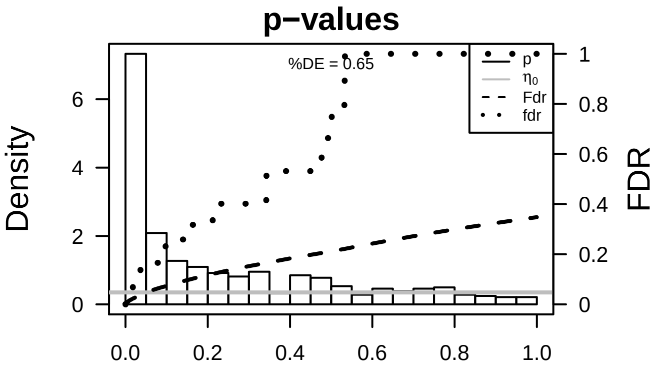
<fdr> = 0.71





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	TXNRD1	−1.06	2e−16	4e−14	48 x 4	thioredoxin reductase 1 [Source:HGNC Symbol;Acc:HGNC:1
2	HIST1H3D	1.59	1e−12	3e−10	50 x 1	histone cluster 1, H3d [Source:HGNC Symbol;Acc:HGNC:47
3	RGS2	1.56	3e−12	1e−09	49 x 1	regulator of G−protein signaling 2 [Source:HGNC Symbol;Ac
4	PLOD2	−1.36	1e−11	8e−09	49 x 3	procollagen−lysine, 2−oxoglutarate 5−dioxygenase 2 [Source
5	SHOC2	−1.21	5e−11	5e−07	42 x 6	soc−2 suppressor of clear homolog (C. elegans) [Source:HG
6	ACOT9	−1.24	3e−09	5e−07	47 x 1	acyl−CoA thioesterase 9 [Source:HGNC Symbol;Acc:HGNC:
7	ITFG1	−1.23	5e−09	5e−07	50 x 4	integrin alpha FG−GAP repeat containing 1 [Source:HGNC S
8	HHIP	1.3	7e−09	1e−05	48 x 4	hedgehog interacting protein [Source:HGNC Symbol;Acc:HG
9	ITSN1	−1.15	1e−07	1e−05	46 x 6	intersectin 1 (SH3 domain protein) [Source:HGNC Symbol;Ac
10	YPEL5	−1.15	2e−07	1e−05	50 x 1	yippee−like 5 (Drosophila) [Source:HGNC Symbol;Acc:HGNC
11	ABCC10	1.17	2e−07	8e−05	43 x 1	ATP−binding cassette, sub−family C (CFTR/MRP), member 1
12	EDIL3	−1.08	1e−06	8e−05	50 x 1	EGF−like repeats and discoidin I−like domains 3 [Source:HG
13	CD55	−1.04	1e−06	8e−05	50 x 1	CD55 molecule, decay accelerating factor for complement (C
14	ZNF608	1.07	2e−06	8e−05	46 x 4	zinc finger protein 608 [Source:HGNC Symbol;Acc:HGNC:29
15	HIST1H2AC	1.07	2e−06	1e−04	50 x 1	histone cluster 1, H2ac [Source:HGNC Symbol;Acc:HGNC:47
16	PLK2	0.78	3e−06	1e−04	50 x 1	polo−like kinase 2 [Source:HGNC Symbol;Acc:HGNC:19699]
17	ADK	−1.03	3e−06	3e−04	49 x 5	adenosine kinase [Source:HGNC Symbol;Acc:HGNC:257]
18	MYO9A	1.02	5e−06	3e−04	45 x 1	myosin IXA [Source:HGNC Symbol;Acc:HGNC:7608]
19	PDGFA	−1.01	7e−06	3e−04	49 x 1	platelet−derived growth factor alpha polypeptide [Source:HG
20	MPP5	1	8e−06	3e−04	50 x 1	membrane protein, palmitoylated 5 (MAGUK p55 subfamily m



E8_mel

Local Summary

%DE = 0.69

metagenes = 38

genes = 406

genes in genesets = 404

genes with fdr < 0.1 = 134 (25 + / 109 −)

genes with fdr < 0.05 = 113 (20 + / 93 −)

genes with fdr < 0.01 = 78 (13 + / 65 −)

<r> metagenes = 0.79

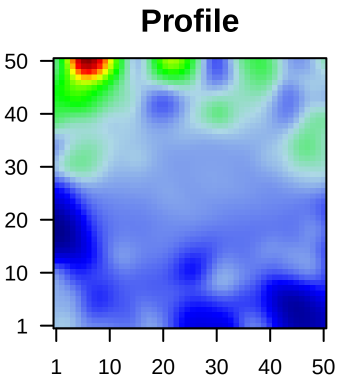
<r> genes = 0.09

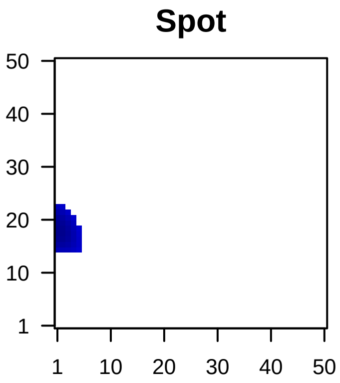
<FC> = −0.23

<shrinkage−t> = −3.81

<p−value> = 0.02

<fdr> = 0.68





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	PPP2CA	−1.32	4e−16	7e−13	1 x 21	protein phosphatase 2, catalytic subunit, alpha isozyme [Sour
2	MPZL1	−1.44	6e−15	3e−10	1 x 19	myelin protein zero−like 1 [Source:HGNC Symbol;Acc:HGNC
3	CLTA	−1.11	3e−12	3e−10	1 x 20	clathrin, light chain A [Source:HGNC Symbol;Acc:HGNC:209
4	RDX	−1.37	4e−12	3e−09	1 x 22	radixin [Source:HGNC Symbol;Acc:HGNC:9944]
5	CCNDBP1	−1.08	3e−11	7e−09	1 x 21	cyclin D−type binding−protein 1 [Source:HGNC Symbol;Acc:
6	MEF2C	−1.32	8e−11	1e−07	5 x 15	myocyte enhancer factor 2C [Source:HGNC Symbol;Acc:HG
7	APPL1	−1.24	1e−09	5e−07	1 x 21	adaptor protein, phosphotyrosine interaction, PH domain and
8	MYC	−1.22	6e−09	2e−05	5 x 15	v−myc avian myelocytomatosis viral oncogene homolog [Sou
9	HSPB1	−1.09	2e−07	2e−05	1 x 20	heat shock 27kDa protein 1 [Source:HGNC Symbol;Acc:HGN
10	SMAD1	1.13	5e−07	2e−05	4 x 16	SMAD family member 1 [Source:HGNC Symbol;Acc:HGNC:6
11	UBA1	−1.11	5e−07	2e−05	1 x 15	ubiquitin−like modifier activating enzyme 1 [Source:HGNC Sy
12	GOSR2	−1.05	6e−07	4e−05	5 x 15	golgi SNAP receptor complex member 2 [Source:HGNC Sym
13	RIOK2	1.09	1e−06	4e−05	1 x 20	RIO kinase 2 [Source:HGNC Symbol;Acc:HGNC:18999]
14	TMEM134	−1.07	1e−06	1e−04	1 x 19	transmembrane protein 134 [Source:HGNC Symbol;Acc:HGN
15	SLC9A3R1	−1.02	2e−06	1e−04	1 x 21	solute carrier family 9, subfamily A (NHE3, cation proton anti
16	PIK3R4	1.04	3e−06	1e−04	1 x 18	phosphoinositide−3−kinase, regulatory subunit 4 [Source:HG
17	MYO1B	−1.02	5e−06	1e−04	2 x 19	myosin IB [Source:HGNC Symbol;Acc:HGNC:7596]
18	KIAA0368	−1.02	5e−06	2e−04	3 x 16	KIAA0368 [Source:HGNC Symbol;Acc:HGNC:29020]
19	CDK9	1.01	7e−06	2e−04	2 x 21	cyclin−dependent kinase 9 [Source:HGNC Symbol;Acc:HGN
20	FBXO9	−0.79	9e−06	2e−04	2 x 21	F−box protein 9 [Source:HGNC Symbol;Acc:HGNC:13588]