C4_mel

Global Summary

%DE = 0.21

genes with fdr < 0.2 = 2579 (1584 + / 995 −)

genes with fdr < 0.1 = 1964 (1219 + / 745 −)

genes with fdr < 0.05 = 1663 (1033 + / 630 −)

genes with fdr < 0.01 = 1062 (700 + / 362 −)

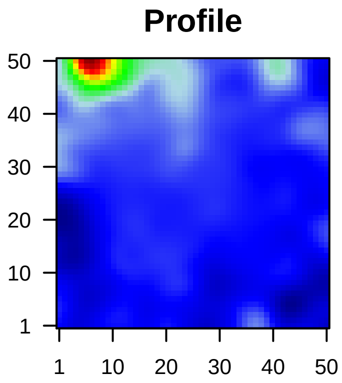
genes in genesets = 14839

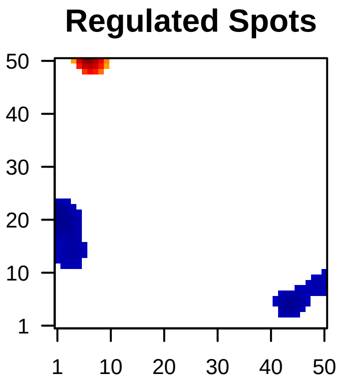
<FC> = 0

<shrinkage−t> = 0.04

<p−value> = 0.08

<fdr> = 0.79



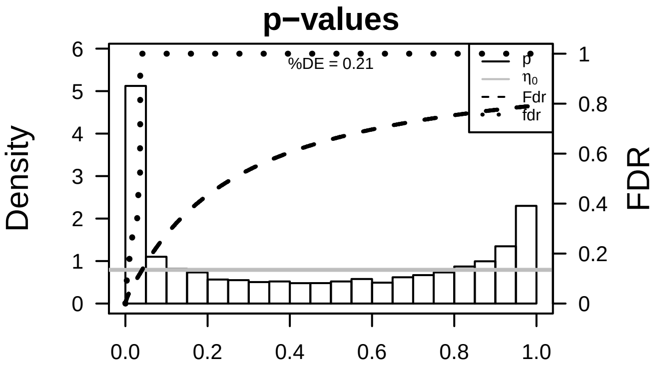


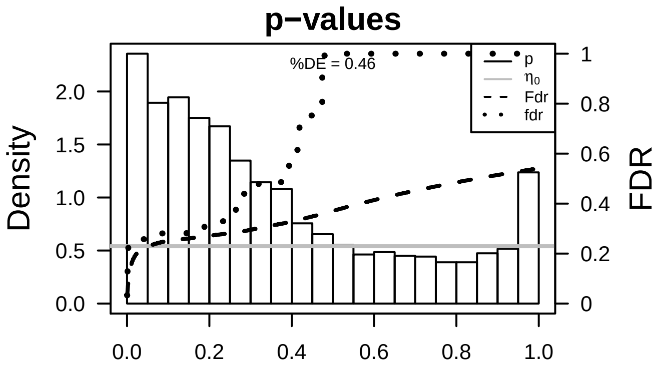
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CDCA3	1.88	2e−16	1e−13	6 x 50	cell division cycle associated 3 [Source:HGNC Symbol;Acc:H
2	CDKN3	1.8	2e−16	1e−13	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
3	CHD9	−1.48	2e−16	1e−13	31 x 10	chromodomain helicase DNA binding protein 9 [Source:HGN
4	CLK1	−1.7	2e−16	1e−13	50 x 40	CDC−like kinase 1 [Source:HGNC Symbol;Acc:HGNC:2068]
5	DCT	−1.84	2e−16	1e−13	1 x 11	dopachrome tautomerase [Source:HGNC Symbol;Acc:HGNC
6	DDOST	−1.85	2e−16	1e−13	45 x 18	dolichyl−diphosphooligosaccharide−−protein glycosyltransfera
7	DLGAP5	1.93	2e−16	1e−13	7 x 50	discs, large (Drosophila) homolog−associated protein 5 [Sour
8	GNL3	−1.54	2e−16	1e−13	47 x 42	guanine nucleotide binding protein−like 3 (nucleolar) [Source:
9	GTF3A	−1.36	2e−16	1e−13	1 x 20	general transcription factor IIIA [Source:HGNC Symbol;Acc:H
10	HORMAD1	2.38	2e−16	1e−13	1 x 4	HORMA domain containing 1 [Source:HGNC Symbol;Acc:HG
11	KIF20A	1.95	2e−16	1e−13	7 x 50	kinesin family member 20A [Source:HGNC Symbol;Acc:HGN
12	KPNA2	1.04	2e−16	1e−13	7 x 50	karyopherin alpha 2 (RAG cohort 1, importin alpha 1) [Source
13	MLIP	−1.17	2e−16	1e−13	3 x 44	muscular LMNA−interacting protein [Source:HGNC Symbol;A
14	NASP	−1.63	2e−16	1e−13	1 x 48	nuclear autoantigenic sperm protein (histone−binding) [Sourc
15	NEK2	2.02	2e−16	1e−13	8 x 50	NIMA−related kinase 2 [Source:HGNC Symbol;Acc:HGNC:77
16	PLK1	1.94	2e−16	1e−13	8 x 50	polo−like kinase 1 [Source:HGNC Symbol;Acc:HGNC:9077]
17	SEC63	−1.75	2e−16	1e−13	38 x 50	SEC63 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:H
18	SPCS1	−0.81	2e−16	1e−13	30 x 43	signal peptidase complex subunit 1 homolog (S. cerevisiae) [S
19	TCF25	−1.59	2e−16	1e−13	1 x 23	transcription factor 25 (basic helix−loop−helix) [Source:HGNC
20	TIMM21	−1.79	2e−16	1e−13	14 x 50	translocase of inner mitochondrial membrane 21 homolog (ye

Global Geneset Analysis

Rank	GSZ	p−value	#all		Geneset
Overexpressed					
1	16.13	4e−03	16	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
2	15.68	4e−05	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
3	15.58	4e−05	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
4	14.16	6e−05	124	GSEA C2	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
5	12.44	1e−04	291	GSEA C2	HORIUCHI_WTAP_TARGETS_DN
6	12.25	1e−04	409	BP	cell division
7	12.2	1e−04	45	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
8	12.15	1e−04	81	GSEA C2	GAVIN_FOXP3_TARGETS_CLUSTER_P6
9	12.11	1e−04	312	BP	mitotic nuclear division
10	12.08	1e−04	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
11	12.06	1e−04	165	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
12	12.06	1e−04	162	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
13	11.89	1e−04	196	HM	HALLMARK_G2M_CHECKPOINT
14	11.77	1e−04	216	GSEA C2	MARKEY_RB1_ACUTE_LOF_DN
15	11.72	1e−04	96	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
16	11.71	1e−04	99	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
17	11.64	1e−04	52	GSEA C2	TANG_SENESCENCE_TP53_TARGETS_DN
18	11.6	1e−04	270	GSEA C2	BASAKI_YBX1_TARGETS_UP
19	11.51	2e−04	40	GSEA C2	AMUNDSON_GAMMA_RADIATION_RESPONSE
20	11.46	2e−04	93	GSEA C2	KONG_E2F3_TARGETS
Underexpressed					
1	−5.55	0.002	884	Brain	Overlap_fetal_midbrain_EnhG
2	−5.19	0.003	1386	Colon Cancer	Het_Colon
3	−5.09	0.003	1065	Brain	Overlap_fetal_midbrain_Enh
4	−4.99	0.004	2188	Lymphoma	HOPP_Poised_promoter
5	−4.95	0.004	3897	Colon Cancer	Quies1_Colon
6	−4.8	0.004	730	GSEA C2	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIA
7	−4.68	0.004	3396	Lymphoma	HOPP_Repressed
8	−4.62	0.005	2185	Brain	Fetal_TssA
9	−4.54	0.005	1038	Colon Cancer	HetRpts_Colon
10	−4.41	0.005	2159	Colon Cancer	TssP_Colon
11	−4.4	0.005	435	GSEA C2	GARY_CD5_TARGETS_UP
12	−4.15	0.007	145	CC	endoplasmic reticulum lumen
13	−4.1	0.007	15	BP	developmental pigmentation
14	−4.04	0.007	338	GSEA C2	BASAKI_YBX1_TARGETS_DN
15	−3.99	0.008	594	GSEA C2	WONG_ADULT_TISSUE_STEM_MODULE
16	−3.89	0.008	10	GSEA C2	REACTOME_BASE_FREE_SUGAR_PHOSPHATE_REMOVAL_VI
17	−3.87	0.008	626	BP	cell adhesion
18	−3.79	0.009	11	GSEA C2	REACTOME_CALNEXIN_CALRETICULIN_CYCLE
19	−3.74	0.009	65	BP	telomere maintenance
20	−3.74	0.009	2211	Lymphoma	HOPP_Repetitive





C4_mel

Local Summary

%DE = 0.89

metagenes = 17

genes = 231

genes in genesets = 231

genes with fdr < 0.1 = 173 (155 + / 18 −)

genes with fdr < 0.05 = 172 (154 + / 18 −)

genes with fdr < 0.01 = 142 (137 + / 5 −)

<r> metagenes = 0.98

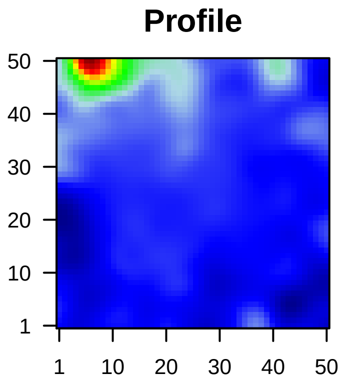
<r> genes = 0.35

<FC> = 0.64

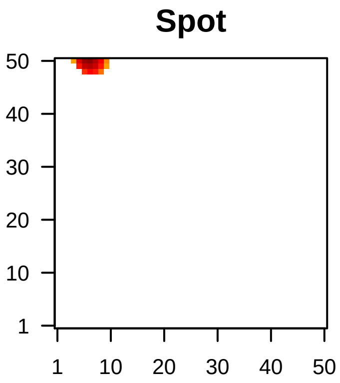
<shrinkage−t> = 10.45

<p−value> = 0

<fdr> = 0.32



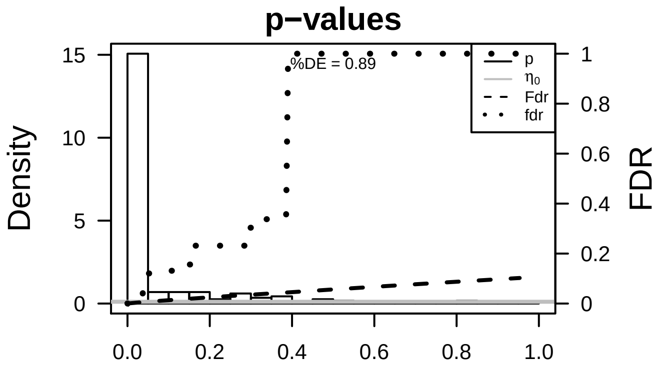
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CDCA3	1.88	2e−16	8e−16	6 x 50	cell division cycle associated 3 [Source:HGNC Symbol;Acc:H
2	CDKN3	1.8	2e−16	8e−16	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
3	DLGAP5	1.93	2e−16	8e−16	7 x 50	discs, large (Drosophila) homolog−associated protein 5 [Sour
4	KIF20A	1.95	2e−16	8e−16	7 x 50	kinesin family member 20A [Source:HGNC Symbol;Acc:HGN
5	KPNA2	1.04	2e−16	8e−16	7 x 50	karyopherin alpha 2 (RAG cohort 1, importin alpha 1) [Source
6	NEK2	2.02	2e−16	8e−16	8 x 50	NIMA−related kinase 2 [Source:HGNC Symbol;Acc:HGNC:77
7	PLK1	1.94	2e−16	8e−16	8 x 50	polo−like kinase 1 [Source:HGNC Symbol;Acc:HGNC:9077]
8	CCNB1	1.82	7e−16	1e−13	7 x 50	cyclin B1 [Source:HGNC Symbol;Acc:HGNC:1579]
9	H2AFZ	0.72	5e−15	5e−13	7 x 48	H2A histone family, member Z [Source:HGNC Symbol;Acc:H
10	DEPDC1	1.73	3e−14	3e−12	6 x 50	DEP domain containing 1 [Source:HGNC Symbol;Acc:HGNC
11	PBK	1.68	2e−13	3e−12	6 x 50	PDZ binding kinase [Source:HGNC Symbol;Acc:HGNC:1828
12	STMN1	0.67	3e−13	3e−12	5 x 50	stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]
13	SPC25	1.65	4e−13	5e−11	6 x 50	SPC25, NDC80 kinetochore complex component [Source:HG
14	CKAP2	1.49	3e−12	5e−11	6 x 50	cytoskeleton associated protein 2 [Source:HGNC Symbol;Ac
15	NDC80	1.58	5e−12	5e−11	6 x 50	NDC80 kinetochore complex component [Source:HGNC Sym
16	SPDL1	1.56	8e−12	5e−11	6 x 49	spindle apparatus coiled−coil protein 1 [Source:HGNC Symb
17	KIF11	1.56	8e−12	2e−10	6 x 50	kinesin family member 11 [Source:HGNC Symbol;Acc:HGNC
18	FAM64A	1.54	1e−11	2e−10	7 x 50	family with sequence similarity 64, member A [Source:HGNC
19	CDC20	1.52	3e−11	2e−10	6 x 50	cell division cycle 20 [Source:HGNC Symbol;Acc:HGNC:172
20	NEIL3	1.51	3e−11	4e−10	7 x 50	nei endonuclease VIII−like 3 (E. coli) [Source:HGNC Symbol;



p−values

C4_mel

Local Summary

%DE = 0.77

metagenes = 46

genes = 322

genes in genesets = 322

genes with fdr < 0.1 = 110 (32 + / 78 −)

genes with fdr < 0.05 = 93 (26 + / 67 −)

genes with fdr < 0.01 = 56 (17 + / 39 −)

<r> metagenes = 0.85

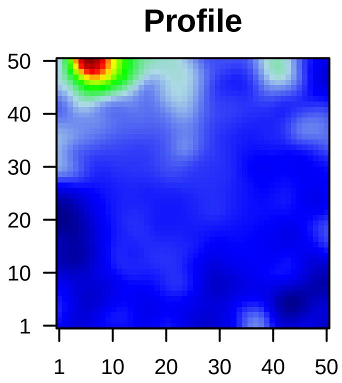
<r> genes = 0.1

<FC> = −0.17

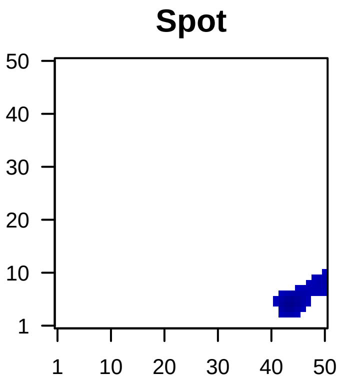
<shrinkage−t> = −2.62

<p−value> = 0.03

<fdr> = 0.69



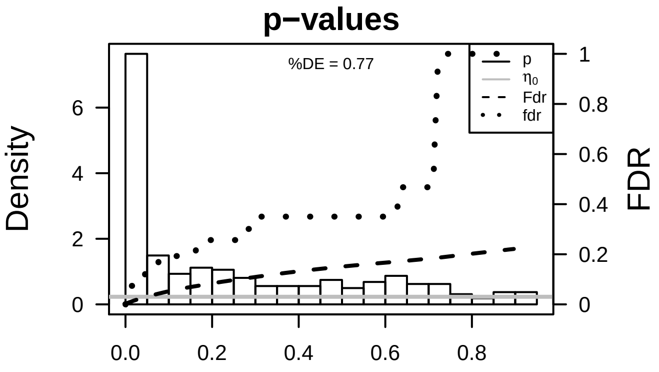
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	LEAP2	1.55	9e−12	2e−09	47 x 6	liver expressed antimicrobial peptide 2 [Source:HGNC Symbo
2	FAM129A	−1.19	4e−11	3e−09	50 x 11	family with sequence similarity 129, member A [Source:HGN
3	ORC3	−1.34	8e−11	2e−08	50 x 7	origin recognition complex, subunit 3 [Source:HGNC Symbol;
4	PABPC4	−1.07	3e−10	1e−06	50 x 7	poly(A) binding protein, cytoplasmic 4 (inducible form) [Sourc
5	S100A13	−1.21	2e−08	1e−06	50 x 7	S100 calcium binding protein A13 [Source:HGNC Symbol;Ac
6	MYO18A	1.26	3e−08	2e−06	50 x 10	myosin XVIIIA [Source:HGNC Symbol;Acc:HGNC:31104]
7	CCDC57	−1.18	7e−08	2e−06	50 x 11	coiled−coil domain containing 57 [Source:HGNC Symbol;Acc
8	UBLCP1	−1.14	9e−08	2e−05	50 x 8	ubiquitin−like domain containing CTD phosphatase 1 [Source
9	IP6K3	1.16	4e−07	1e−04	50 x 7	inositol hexakisphosphate kinase 3 [Source:HGNC Symbol;A
10	ORAOV1	−1.08	2e−06	2e−04	45 x 7	oral cancer overexpressed 1 [Source:HGNC Symbol;Acc:HG
11	SYF2	−0.97	4e−06	2e−04	45 x 5	SYF2 pre−mRNA−splicing factor [Source:HGNC Symbol;Acc
12	LEPROT	−1.02	6e−06	2e−04	49 x 7	leptin receptor overlapping transcript [Source:HGNC Symbol;
13	HIST1H2BK	−1	1e−05	2e−04	46 x 7	histone cluster 1, H2bk [Source:HGNC Symbol;Acc:HGNC:1
14	RASA1	0.99	1e−05	2e−04	45 x 7	RAS p21 protein activator (GTPase activating protein) 1 [Sou
15	SLC41A1	0.99	1e−05	4e−04	49 x 7	solute carrier family 41 (magnesium transporter), member 1 [
16	ABCB10	0.96	2e−05	4e−04	45 x 3	ATP−binding cassette, sub−family B (MDR/TAP), member 10
17	VGLL4	−0.95	3e−05	4e−04	47 x 9	vestigial−like family member 4 [Source:HGNC Symbol;Acc:H
18	FLRT2	−0.95	3e−05	7e−04	50 x 10	fibronectin leucine rich transmembrane protein 2 [Source:HG
19	UBAC2	−0.93	5e−05	7e−04	50 x 11	UBA domain containing 2 [Source:HGNC Symbol;Acc:HGNC
20	TP53	−0.92	5e−05	7e−04	43 x 5	tumor protein p53 [Source:HGNC Symbol;Acc:HGNC:11998]



p−values

C4_mel

Local Summary

%DE = 0.67

metagenes = 64

genes = 572

genes in genesets = 570

genes with fdr < 0.1 = 182 (62 + / 120 −)

genes with fdr < 0.05 = 145 (52 + / 93 −)

genes with fdr < 0.01 = 97 (36 + / 61 −)

<r> metagenes = 0.65

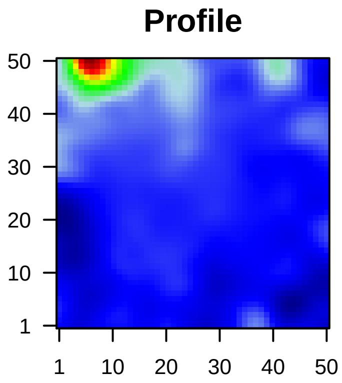
<r> genes = 0.06

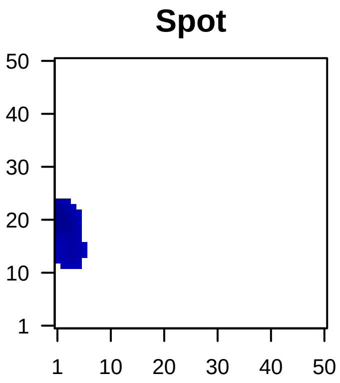
<FC> = −0.14

<shrinkage−t> = −2.35

<p−value> = 0.03

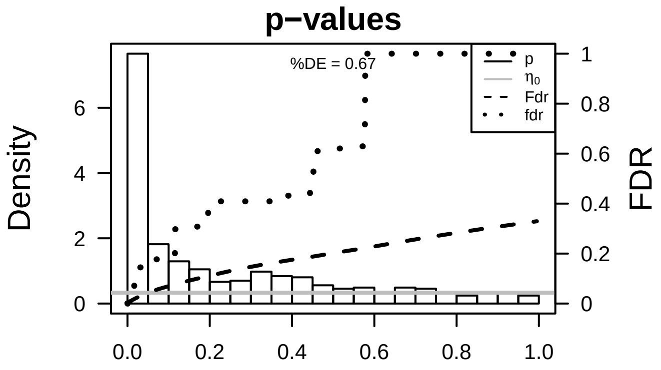
<fdr> = 0.69


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	GTF3A	−1.36	2e−16	2e−14	1 x 20	general transcription factor IIIA [Source:HGNC Symbol;Acc:H
2	TCF25	−1.59	2e−16	2e−14	1 x 23	transcription factor 25 (basic helix−loop−helix) [Source:HGNC
3	DFNA5	−1.3	2e−14	5e−11	3 x 18	deafness, autosomal dominant 5 [Source:HGNC Symbol;Acc
4	NOLC1	−1.24	3e−13	6e−09	1 x 16	nucleolar and coiled−body phosphoprotein 1 [Source:HGNC
5	EDRF1	1.51	4e−11	6e−09	3 x 20	erythroid differentiation regulatory factor 1 [Source:HGNC Sy
6	CANX	−0.63	6e−11	2e−08	5 x 17	calnexin [Source:HGNC Symbol;Acc:HGNC:1473]
7	C1QBP	−1.24	2e−10	6e−07	1 x 21	complement component 1, q subcomponent binding protein [
8	PHLDA1	−1.11	4e−09	6e−07	3 x 14	pleckstrin homology−like domain, family A, member 1 [Source
9	CCSER2	−1.21	6e−09	1e−06	2 x 18	coiled−coil serine−rich protein 2 [Source:HGNC Symbol;Acc:
10	HEXB	−1.09	2e−08	1e−06	1 x 21	hexosaminidase B (beta polypeptide) [Source:HGNC Symbol
11	ERCC3	−1.14	2e−08	1e−06	2 x 22	excision repair cross−complementation group 3 [Source:HGN
12	ID2	0.51	3e−08	5e−06	1 x 13	inhibitor of DNA binding 2, dominant negative helix−loop−heli
13	VPS36	−1.19	5e−08	5e−06	1 x 18	vacuolar protein sorting 36 homolog (S. cerevisiae) [Source:
14	MRPS2	−1.18	1e−07	5e−06	1 x 13	mitochondrial ribosomal protein S2 [Source:HGNC Symbol;A
15	CYC1	−1.05	1e−07	5e−06	1 x 20	cytochrome c−1 [Source:HGNC Symbol;Acc:HGNC:2579]
16	PTPN2	−1.04	2e−07	5e−06	1 x 20	protein tyrosine phosphatase, non−receptor type 2 [Source:H
17	GET4	1.18	2e−07	5e−06	1 x 19	golgi to ER traffic protein 4 homolog (S. cerevisiae) [Source:
18	DGUOK	−0.81	2e−07	5e−06	3 x 20	deoxyguanosine kinase [Source:HGNC Symbol;Acc:HGNC:2
19	GBA	−1.04	2e−07	2e−05	4 x 12	glucosidase, beta, acid [Source:HGNC Symbol;Acc:HGNC:41
20	ERCC8	1.16	3e−07	2e−05	1 x 15	excision repair cross−complementation group 8 [Source:HGN


p−values