G11_mel

Global Summary

%DE = 0.22

genes with fdr < 0.2 = 3051 (1808 + / 1243 −)

genes with fdr < 0.1 = 2344 (1427 + / 917 −)

genes with fdr < 0.05 = 2066 (1266 + / 800 −)

genes with fdr < 0.01 = 1251 (780 + / 471 −)

genes in genesets = 14839

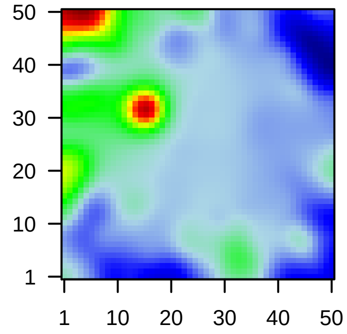
<FC> = 0

<shrinkage−t> = −0.02

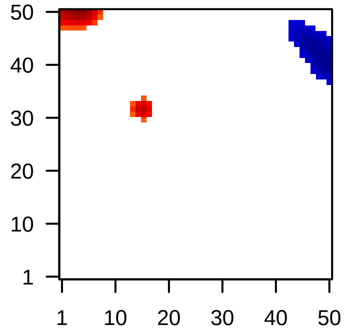
<p−value> = 0.07

<fdr> = 0.78

Profile



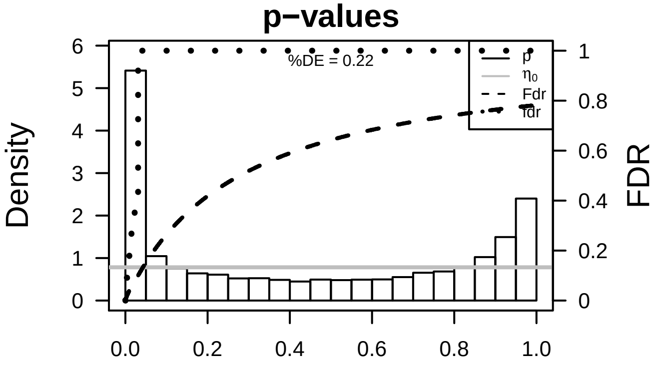
Regulated Spots



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	BECN1	−1.31	2e−16	1e−13	49 x 15	beclin 1, autophagy related [Source:HGNC Symbol;Acc:HGN
2	BSCL2	−1.37	2e−16	1e−13	50 x 50	Berardinelli−Seip congenital lipodystrophy 2 (seipin) [Source:
3	CACNA2D1	2.14	2e−16	1e−13	16 x 32	calcium channel, voltage−dependent, alpha 2/delta subunit 1
4	CNOT1	−1.31	2e−16	1e−13	15 x 50	CCR4−NOT transcription complex, subunit 1 [Source:HGNC
5	CRYZL1	−1.72	2e−16	1e−13	44 x 50	crystallin, zeta (quinone reductase)−like 1 [Source:HGNC Sy
6	DHX36	−1.46	2e−16	1e−13	30 x 12	DEAH (Asp−Glu−Ala−His) box polypeptide 36 [Source:HGNC
7	DLD	−1.74	2e−16	1e−13	1 x 7	dihydrolipoamide dehydrogenase [Source:HGNC Symbol;Acc
8	EIF2A	−1.64	2e−16	1e−13	50 x 12	eukaryotic translation initiation factor 2A, 65kDa [Source:HGN
9	GTF2A2	−2.44	2e−16	1e−13	45 x 49	general transcription factor IIA, 2, 12kDa [Source:HGNC Sym
10	HADHB	−1.66	2e−16	1e−13	1 x 39	hydroxyacyl−CoA dehydrogenase/3−ketoacyl−CoA thiolase/e
11	HIST1H4C	0.92	2e−16	1e−13	5 x 49	histone cluster 1, H4c [Source:HGNC Symbol;Acc:HGNC:47
12	HTN1	2.12	2e−16	1e−13	10 x 49	histatin 1 [Source:HGNC Symbol;Acc:HGNC:5283]
13	IMP4	−1.68	2e−16	1e−13	2 x 39	IMP4, U3 small nucleolar ribonucleoprotein [Source:HGNC S
14	LGALS1	−1.68	2e−16	1e−13	50 x 1	lectin, galactoside−binding, soluble, 1 [Source:HGNC Symbol
15	MARS	−1.72	2e−16	1e−13	43 x 47	methionyl−tRNA synthetase [Source:HGNC Symbol;Acc:HGN
16	MRPL47	−1.72	2e−16	1e−13	4 x 9	mitochondrial ribosomal protein L47 [Source:HGNC Symbol;
17	OTUB1	−1.75	2e−16	1e−13	47 x 46	OTU deubiquitinase, ubiquitin aldehyde binding 1 [Source:HG
18	RAB6A	−1.49	2e−16	1e−13	46 x 46	RAB6A, member RAS oncogene family [Source:HGNC Symb
19	RDH12	2.07	2e−16	1e−13	16 x 32	retinol dehydrogenase 12 (all−trans/9−cis/11−cis) [Source:HG
20	SLC39A9	−1.55	2e−16	1e−13	50 x 36	solute carrier family 39, member 9 [Source:HGNC Symbol;Ac

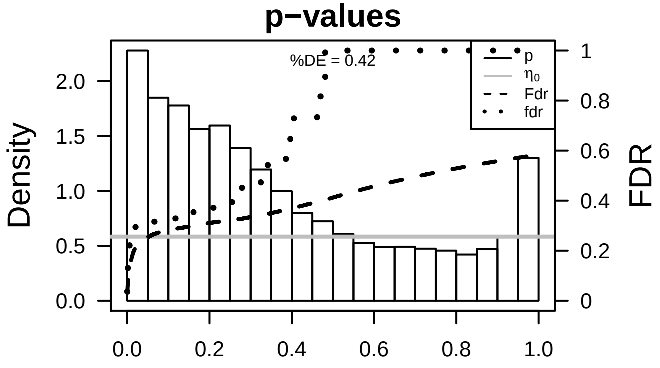
p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	15.73	4e−05	242	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
2	15.48	5e−05	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
3	14.92	5e−05	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
4	14.77	6e−05	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
5	14.76	6e−05	305	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
6	13.96	7e−05	197	HM	HALLMARK_E2F_TARGETS
7	13.55	3e−03	16	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
8	13.52	8e−05	96	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
9	13.44	8e−05	145	GSEA C2	CHANG_CYCLING_GENES
10	12.27	1e−04	124	GSEA C2	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
11	12.27	1e−04	50	GSEA C2	ISHIDA_E2F_TARGETS
12	12.19	1e−04	81	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
13	12.12	1e−04	110	GSEA C2	WHITEFORD_PEDIATRIC_CANCER_MARKERS
14	11.93	1e−04	72	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
15	11.92	1e−04	93	GSEA C2	KONG_E2F3_TARGETS
16	11.91	1e−04	436	GSEA C2	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
17	11.74	1e−04	390	GSEA C2	PUJANA_BRCA2_PCC_NETWORK
18	11.73	1e−04	162	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
19	11.48	2e−04	327	GSEA C2	BLUM_RESPONSE_TO_SALIRASIB_DN
20	11.39	2e−04	1192	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
Underexpressed					
1	−5.11	0.003	9027	Colon Cancer	Tx_Colon
2	−4.6	0.005	5940	Brain	Overlap_fetal_midbrain_HetRpts
3	−4.49	0.005	39	GSEA C2	REACTOME_RNA_POL_II_TRANSCRIPTION_PRE_INITIATION_
4	−4.46	0.005	13	GSEA C2	REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COU
5	−4.45	0.005	494	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
6	−4.45	0.005	8580	Colon Cancer	TxWk_Colon
7	−4.4	0.005	17	BP	mitochondrial ATP synthesis coupled proton transport
8	−4.35	0.006	140	GSEA C2	RAO_BOUND_BY_SALL4_ISOFORM_A
9	−4.28	0.006	94	BP	respiratory electron transport chain
10	−4.09	0.007	33	GSEA C2	KEGG_BASAL_TRANSCRIPTION_FACTORS
11	−4.09	0.007	233	GSEA C2	PENG_RAPAMYCIN_RESPONSE_DN
12	−4.06	0.007	69	BP	transcription elongation from RNA polymerase II promoter
13	−4.05	0.007	619	GSEA C2	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_C
14	−4.05	0.007	10	GSEA C2	REACTOME_COPI_MEDIATED_TRANSPORT
15	−4.01	0.007	1383	TF	ICGC_Six5_targets
16	−4.01	0.007	58	GSEA C2	REACTOME_RNA_POL_II_PRE_TRANSCRIPTION_EVENTS
17	−3.95	0.008	213	GSEA C2	WONG_MITOCHONDRIA_GENE_MODULE
18	−3.9	0.008	114	GSEA C2	REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_T
19	−3.89	0.008	8	GSEA C2	TURJANSKI_MAPK7_TARGETS
20	−3.88	0.008	78	GSEA C2	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_S

p−values



G11_mel

Local Summary

%DE = 0.99

metagenes = 14

genes = 108

genes in genesets = 106

genes with fdr < 0.1 = 106 (106 + / 0 −)

genes with fdr < 0.05 = 106 (106 + / 0 −)

genes with fdr < 0.01 = 103 (103 + / 0 −)

<r> metagenes = 0.99

<r> genes = 0.27

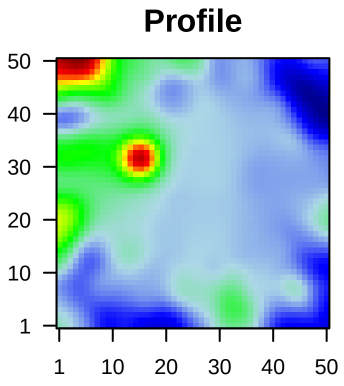
<FC> = 1.05

<shrinkage−t> = 15.99

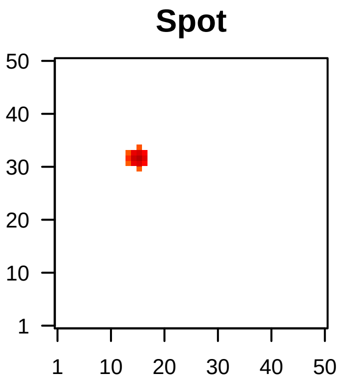
<p−value> = 0

<fdr> = 0.13

Profile



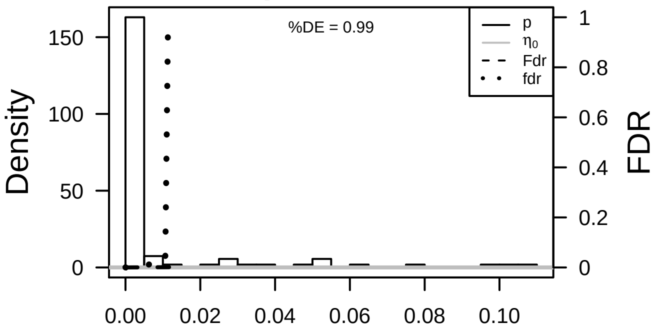
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CACNA2D1	2.14	2e−16	1e−16	16 x 32	calcium channel, voltage−dependent, alpha 2/delta subunit 1
2	RDH12	2.07	2e−16	1e−16	16 x 32	retinol dehydrogenase 12 (all−trans/9−cis/11−cis) [Source:HG
3	ZNF239	1.83	2e−14	3e−14	16 x 32	zinc finger protein 239 [Source:HGNC Symbol;Acc:HGNC:13
4	PCDH8	1.81	5e−14	2e−12	16 x 32	protocadherin 8 [Source:HGNC Symbol;Acc:HGNC:8660]
5	ARHGAP28	1.68	2e−12	2e−12	16 x 32	Rho GTPase activating protein 28 [Source:HGNC Symbol;Ac
6	CSNK1G2	1.66	5e−12	2e−12	16 x 32	casein kinase 1, gamma 2 [Source:HGNC Symbol;Acc:HGNC
7	KDM4C	1.65	6e−12	2e−12	16 x 32	lysine (K)−specific demethylase 4C [Source:HGNC Symbol;A
8	CTD−3214H1	1.64	8e−12	9e−12	16 x 32	
9	DDIT4L	1.61	2e−11	9e−12	16 x 32	DNA−damage−inducible transcript 4−like [Source:HGNC Sym
10	ZNF555	1.6	2e−11	2e−11	16 x 32	zinc finger protein 555 [Source:HGNC Symbol;Acc:HGNC:28
11	HOXA1	1.58	4e−11	2e−11	16 x 32	homeobox A1 [Source:HGNC Symbol;Acc:HGNC:5099]
12	ITGA9	1.56	7e−11	2e−11	16 x 32	integrin, alpha 9 [Source:HGNC Symbol;Acc:HGNC:6145]
13	SAMD13	1.56	8e−11	5e−11	16 x 32	sterile alpha motif domain containing 13 [Source:HGNC Sym
14	TGFA	1.54	1e−10	6e−11	16 x 32	transforming growth factor, alpha [Source:HGNC Symbol;Acc
15	N6AMT2	1.53	2e−10	4e−10	16 x 32	N−6 adenine−specific DNA methyltransferase 2 (putative) [Sc
16	ST3GAL5	1.49	6e−10	4e−10	16 x 32	ST3 beta−galactoside alpha−2,3−sialyltransferase 5 [Source:
17	ACP2	1.46	1e−09	4e−10	16 x 32	acid phosphatase 2, lysosomal [Source:HGNC Symbol;Acc:H
18	RIPK4	1.46	1e−09	1e−09	16 x 32	receptor−interacting serine−threonine kinase 4 [Source:HGN
19	FAM209B	1.43	3e−09	1e−09	16 x 32	family with sequence similarity 209, member B [Source:HGN
20	ELF4	1.41	4e−09	1e−09	16 x 32	E74−like factor 4 (ets domain transcription factor) [Source:HG

p−values



G11_mel

Local Summary

%DE = 0.86

metagenes = 28

genes = 411

genes in genesets = 410

genes with fdr < 0.1 = 285 (259 + / 26 −)

genes with fdr < 0.05 = 271 (247 + / 24 −)

genes with fdr < 0.01 = 211 (198 + / 13 −)

<r> metagenes = 0.92

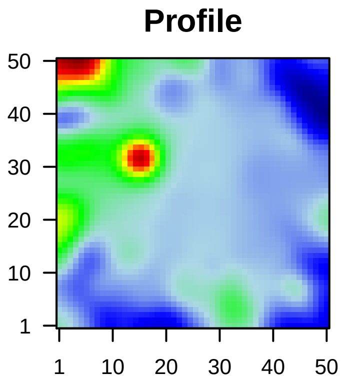
<r> genes = 0.27

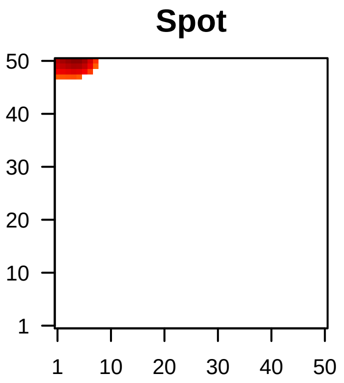
<FC> = 0.53

<shrinkage−t> = 8.47

<p−value> = 0

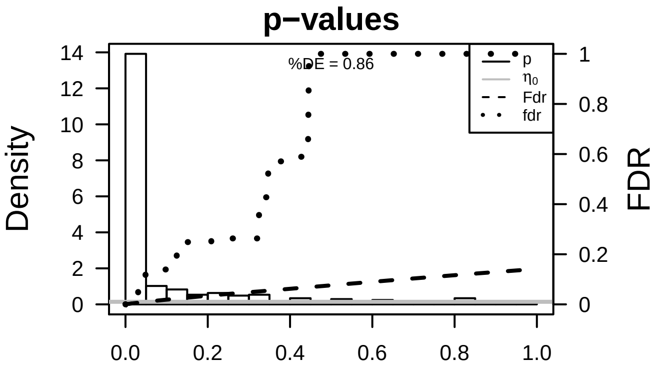
<fdr> = 0.39





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	HIST1H4C	0.92	2e−16	1e−14	5 x 49	histone cluster 1, H4c [Source:HGNC Symbol;Acc:HGNC:47
2	RAD51	1.81	4e−14	1e−11	1 x 50	RAD51 recombinase [Source:HGNC Symbol;Acc:HGNC:981
3	ZNF519	1.76	2e−13	2e−10	3 x 48	zinc finger protein 519 [Source:HGNC Symbol;Acc:HGNC:30
4	FBXO5	1.66	4e−12	4e−10	4 x 50	F−box protein 5 [Source:HGNC Symbol;Acc:HGNC:13584]
5	CDCA3	1.63	1e−11	3e−09	6 x 50	cell division cycle associated 3 [Source:HGNC Symbol;Acc:H
6	UBE2C	1.56	6e−11	1e−08	6 x 50	ubiquitin−conjugating enzyme E2C [Source:HGNC Symbol;A
7	DTL	1.51	3e−10	1e−08	1 x 50	denticleless E3 ubiquitin protein ligase homolog (Drosophila)
8	AURKB	1.5	4e−10	1e−08	6 x 50	aurora kinase B [Source:HGNC Symbol;Acc:HGNC:11390]
9	HMGB2	1.36	6e−10	1e−08	5 x 50	high mobility group box 2 [Source:HGNC Symbol;Acc:HGNC:
10	BRCA2	1.47	8e−10	2e−08	2 x 50	breast cancer 2, early onset [Source:HGNC Symbol;Acc:HG
11	NCAPH	1.45	1e−09	2e−08	5 x 50	non−SMC condensin I complex, subunit H [Source:HGNC Sy
12	G2E3	1.45	2e−09	2e−08	8 x 50	G2/M−phase specific E3 ubiquitin protein ligase [Source:HG
13	ASF1B	1.45	2e−09	4e−08	4 x 50	anti−silencing function 1B histone chaperone [Source:HGNC
14	EMP2	−1.31	2e−09	6e−08	2 x 50	epithelial membrane protein 2 [Source:HGNC Symbol;Acc:H
15	NUF2	1.41	4e−09	6e−08	6 x 50	NUF2, NDC80 kinetochore complex component [Source:HG
16	BUB1B	1.4	5e−09	6e−08	6 x 50	BUB1 mitotic checkpoint serine/threonine kinase B [Source:H
17	RFC3	1.4	5e−09	9e−08	2 x 50	replication factor C (activator 1) 3, 38kDa [Source:HGNC Sy
18	STMN1	0.56	7e−09	9e−08	5 x 50	stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]
19	CCDC138	1.38	9e−09	9e−08	7 x 48	coiled−coil domain containing 138 [Source:HGNC Symbol;Ac
20	NDC1	1.37	1e−08	9e−08	7 x 48	NDC1 transmembrane nucleoporin [Source:HGNC Symbol;A



G11_mel

Local Summary

%DE = 0.7

metagenes = 59

genes = 495

genes in genesets = 492

genes with fdr < 0.1 = 213 (37 + / 176 −)

genes with fdr < 0.05 = 196 (31 + / 165 −)

genes with fdr < 0.01 = 147 (22 + / 125 −)

<r> metagenes = 0.74

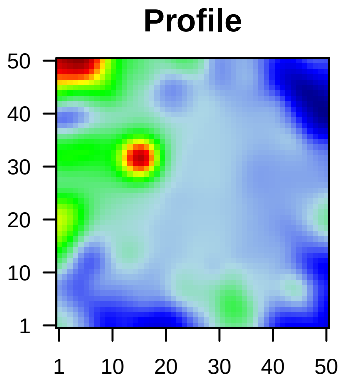
<r> genes = 0.06

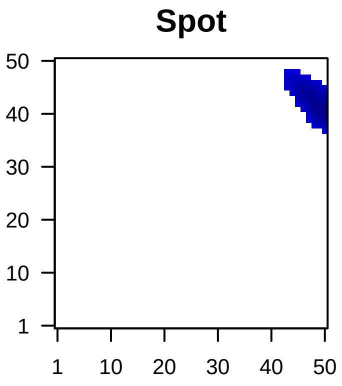
<FC> = −0.3

<shrinkage−t> = −5.19

<p−value> = 0.01

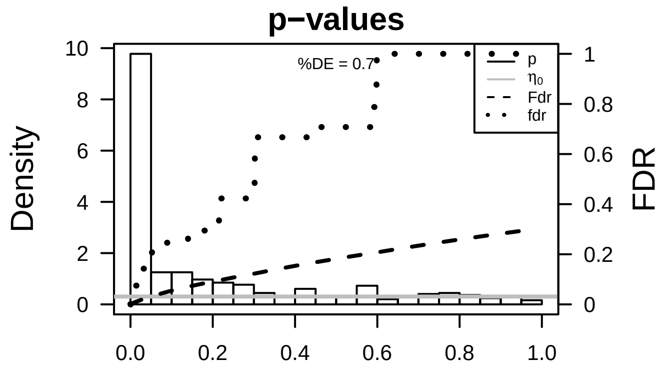
<fdr> = 0.59


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	MARS	−1.72	2e−16	7e−15	43 x 47	methionyl−tRNA synthetase [Source:HGNC Symbol;Acc:HG
2	OTUB1	−1.75	2e−16	7e−15	47 x 46	OTU deubiquitinase, ubiquitin aldehyde binding 1 [Source:HG
3	RAB6A	−1.49	2e−16	7e−15	46 x 46	RAB6A, member RAS oncogene family [Source:HGNC Symb
4	UQCRC2	−1.92	2e−16	7e−15	46 x 45	ubiquinol−cytochrome c reductase core protein II [Source:HG
5	WBSCR22	−1.39	2e−16	7e−15	45 x 48	Williams Beuren syndrome chromosome region 22 [Source:H
6	SH3BGRL3	−1.5	4e−14	6e−12	50 x 42	SH3 domain binding glutamate−rich protein like 3 [Source:HG
7	COPZ1	−1.3	8e−14	2e−11	46 x 45	coatomer protein complex, subunit zeta 1 [Source:HGNC Syn
8	RUVBL1	−1.47	4e−13	2e−11	50 x 40	RuvB−like AAA ATPase 1 [Source:HGNC Symbol;Acc:HGNC
9	BRD8	−1.17	4e−13	2e−11	50 x 39	bromodomain containing 8 [Source:HGNC Symbol;Acc:HGN
10	PHKB	−1.46	5e−13	1e−09	50 x 40	phosphorylase kinase, beta [Source:HGNC Symbol;Acc:HG
11	NMD3	−1.42	8e−12	4e−09	50 x 41	NMD3 ribosome export adaptor [Source:HGNC Symbol;Acc:
12	METTL5	−1.4	4e−11	4e−09	50 x 45	methyltransferase like 5 [Source:HGNC Symbol;Acc:HGNC:2
13	TRIB2	−1.38	7e−11	2e−08	44 x 46	tribbles pseudokinase 2 [Source:HGNC Symbol;Acc:HGNC:3
14	NARS	−0.73	2e−10	2e−08	43 x 45	asparaginyl−tRNA synthetase [Source:HGNC Symbol;Acc:H
15	ATP6V1A	−1.02	3e−10	1e−07	45 x 47	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A [So
16	TMEM50A	−0.93	9e−10	1e−07	50 x 37	transmembrane protein 50A [Source:HGNC Symbol;Acc:HG
17	ATP6V1E1	−1.3	2e−09	1e−07	48 x 44	ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E1 [S
18	DTD1	−1.31	2e−09	2e−07	49 x 46	D−tyrosyl−tRNA deacylase 1 [Source:HGNC Symbol;Acc:HG
19	CCDC53	−1.29	4e−09	3e−07	48 x 45	coiled−coil domain containing 53 [Source:HGNC Symbol;Acc
20	SEC31A	−0.77	6e−09	1e−06	50 x 38	SEC31 homolog A (S. cerevisiae) [Source:HGNC Symbol;Ac


p−values