C9_mel

Global Summary

%DE = 0.2

genes with fdr < 0.2 = 2459 (1375 + / 1084 −)

genes with fdr < 0.1 = 1913 (1040 + / 873 −)

genes with fdr < 0.05 = 1514 (791 + / 723 −)

genes with fdr < 0.01 = 932 (451 + / 481 −)

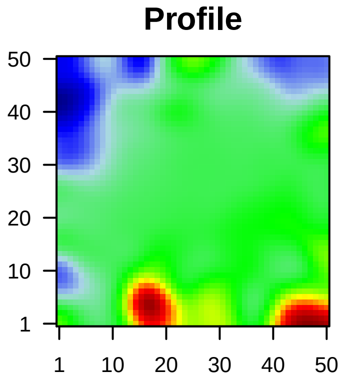
genes in genesets = 14839

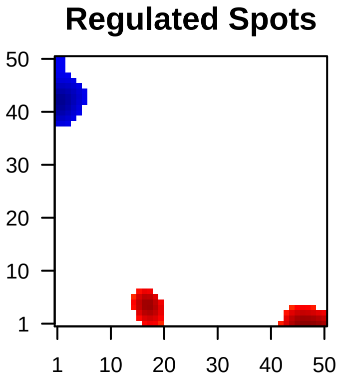
<FC> = 0

<shrinkage−t> = −0.17

<p−value> = 0.09

<fdr> = 0.8



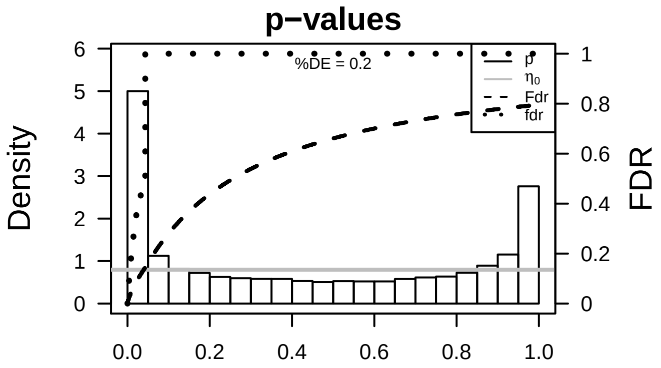


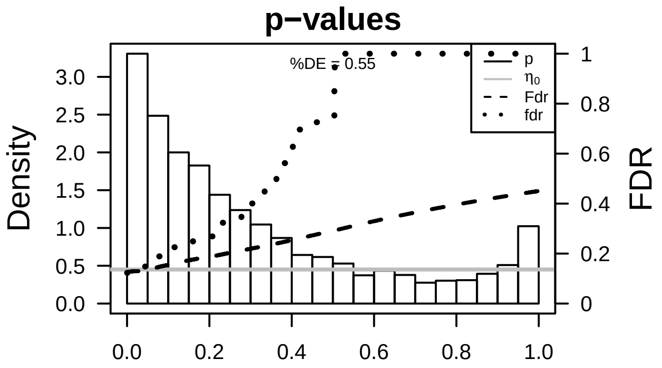
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ACAT1	−1.72	2e−16	5e−14	41 x 50	acetyl−CoA acetyltransferase 1 [Source:HGNC Symbol;Acc:
2	ACTL6A	−1.51	2e−16	5e−14	4 x 50	actin−like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
3	ALG8	−1.42	2e−16	5e−14	5 x 43	ALG8, alpha−1,3−glucosyltransferase [Source:HGNC Symbo
4	APOA1BP	−1.31	2e−16	5e−14	16 x 50	apolipoprotein A−I binding protein [Source:HGNC Symbol;Ac
5	CDK2	−2.19	2e−16	5e−14	1 x 43	cyclin−dependent kinase 2 [Source:HGNC Symbol;Acc:HGN
6	CHCHD6	−2.01	2e−16	5e−14	1 x 43	coiled−coil−helix−coiled−coil−helix domain containing 6 [Sour
7	CHD4	−1.72	2e−16	5e−14	21 x 43	chromodomain helicase DNA binding protein 4 [Source:HGN
8	CITED1	−1.94	2e−16	5e−14	1 x 41	Cbp/p300−interacting transactivator, with Glu/Asp−rich carbo
9	CMC2	−1.96	2e−16	5e−14	5 x 44	C−x(9)−C motif containing 2 [Source:HGNC Symbol;Acc:HG
10	CNDP2	−1.88	2e−16	5e−14	3 x 40	CNDP dipeptidase 2 (metallopeptidase M20 family) [Source:
11	COX14	−1.83	2e−16	5e−14	5 x 39	COX14 cytochrome c oxidase assembly factor [Source:HGN
12	DAB2	−1.4	2e−16	5e−14	3 x 41	Dab, mitogen−responsive phosphoprotein, homolog 2 (Droso
13	DERA	−1.78	2e−16	5e−14	1 x 43	deoxyribose−phosphate aldolase (putative) [Source:HGNC S
14	DERL2	−1.85	2e−16	5e−14	6 x 41	derlin 2 [Source:HGNC Symbol;Acc:HGNC:17943]
15	ECHDC1	−1.74	2e−16	5e−14	42 x 46	ethylmalonyl−CoA decarboxylase 1 [Source:HGNC Symbol;A
16	EMP3	−1.82	2e−16	5e−14	4 x 43	epithelial membrane protein 3 [Source:HGNC Symbol;Acc:H
17	ETFA	−2.1	2e−16	5e−14	3 x 33	electron−transfer−flavoprotein, alpha polypeptide [Source:HG
18	EXOC3	−1.33	2e−16	5e−14	1 x 42	exocyst complex component 3 [Source:HGNC Symbol;Acc:H
19	FAM96B	−1.85	2e−16	5e−14	43 x 47	family with sequence similarity 96, member B [Source:HGNC
20	FKBP3	−1.77	2e−16	5e−14	41 x 46	FK506 binding protein 3, 25kDa [Source:HGNC Symbol;Acc:

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	7.05	0.001	3396	Lymphoma	HOPP_Repressed
2	7.01	0.001	2188	Lymphoma	HOPP_Poised_promoter
3	6.4	0.001	472	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
4	6.38	0.001	36	GSEA C2	UZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
5	5.9	0.002	286	GSEA C2	PASINI_SUZ12_TARGETS_DN
6	5.86	0.002	594	GSEA C2	WONG_ADULT_TISSUE_STEM_MODULE
7	5.23	0.003	200	GSEA C2	ZWANG_CLASS_3_TRANSIENTLY_INDUCED_BY_EGF
8	5.2	0.003	177	HM	HALLMARK_TNFA_SIGNALING_VIA_NFKB
9	5.18	0.003	302	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
10	5.09	0.003	55	GSEA C2	AMIT_SERUM_RESPONSE_60_MCF10A
11	4.75	0.004	749	GSEA C2	CUI_TCF21_TARGETS_2_DN
12	4.69	0.004	377	GSEA C2	SMID_BREAST_CANCER_LUMINAL_B_DN
13	4.68	0.004	3088	CC	plasma membrane
14	4.66	0.005	3068	BP	signal transduction
15	4.61	0.005	64	GSEA C2	LEE_METASTASIS_AND_ALTERNATIVE_SPLICING_UP
16	4.59	0.005	2159	Colon Cancer	TssP_Colon
17	4.5	0.005	833	GSEA C2	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
18	4.43	0.005	2185	Brain	Fetal_TssA
19	4.39	0.006	61	GSEA C2	RHEIN_ALL_GLUCOCORTICOID_THERAPY_UP
20	4.39	0.006	120	GSEA C2	REACTOME_NGF_SIGNALLING_VIA_TRKA_FROM_THE_PLAS
Underexpressed					
1	−11.64	1e−04	198	HM	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	−10.49	2e−04	135	BP	cellular metabolic process
3	−9.91	3e−04	1468	CC	mitochondrion
4	−9.3	4e−04	401	CC	mitochondrial inner membrane
5	−9.02	4e−04	114	GSEA C2	REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_T
6	−8.74	4e−04	368	GSEA C2	STEIN_ESRRA_TARGETS_UP
7	−8.72	5e−04	405	GSEA C2	MOOTHA_HUMAN_MITODB_6_2002
8	−8.54	5e−04	213	GSEA C2	WONG_MITOCHONDRIA_GENE_MODULE
9	−8.43	5e−04	421	GSEA C2	MOOTHA_MITOCHONDRIA
10	−8.41	5e−04	94	BP	respiratory electron transport chain
11	−8.33	5e−04	700	GSEA C2	MARSON_BOUND_BY_E2F4_UNSTIMULATED
12	−8.26	6e−04	63	Glio	Stuehler_Proteins_up_in_STS
13	−8.25	6e−04	242	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
14	−8.13	6e−04	305	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
15	−8.05	6e−04	7	Lymphoma	CARO_OxPhos_vs_BCR_UP
16	−8.04	6e−04	500	GSEA C2	STEIN_ESRRA_TARGETS
17	−7.86	7e−04	1460	GSEA C2	PUJANA_BRCA1_PCC_NETWORK
18	−7.84	7e−04	78	GSEA C2	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_S
19	−7.54	8e−04	6929	Lymphoma	HOPP_Txn_elongation
20	−7.51	8e−04	724	GSEA C2	PUJANA_CHEK2_PCC_NETWORK





C9_mel

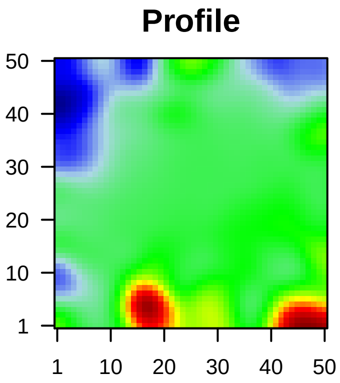
Local Summary

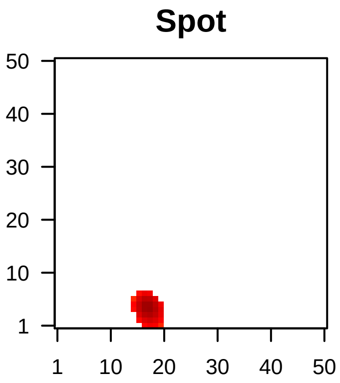
%DE = 0.95
metagenes = 34
genes = 339
genes in genesets = 336

genes with fdr < 0.1 = 303 (303 + / 0 −)
genes with fdr < 0.05 = 300 (300 + / 0 −)
genes with fdr < 0.01 = 227 (227 + / 0 −)

<r> metagenes = 0.89
<r> genes = 0.15

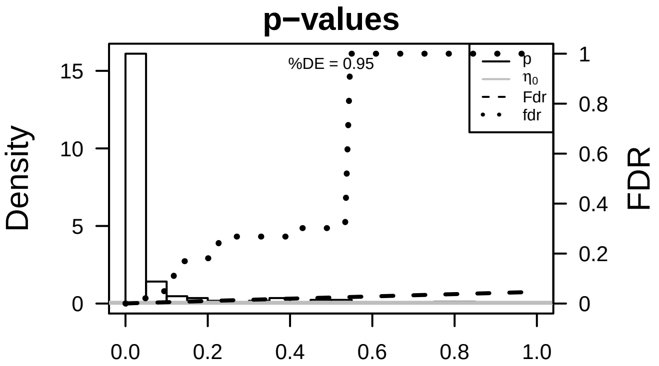
<FC> = 0.92
<shrinkage−t> = 14.07
<p−value> = 0
<fdr> = 0.3





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	LRRC27	2.04	3e−11	2e−09	17 x 5	leucine rich repeat containing 27 [Source:HGNC Symbol;Acc
2	CLCN5	1.98	1e−10	3e−09	18 x 5	chloride channel, voltage−sensitive 5 [Source:HGNC Symbol
3	SLC25A53	1.94	3e−10	3e−08	17 x 5	solute carrier family 25, member 53 [Source:HGNC Symbol;A
4	OSR2	1.84	2e−09	5e−08	17 x 5	odd−skipped related transciption factor 2 [Source:HGNC Sy
5	WDR54	1.78	8e−09	5e−08	18 x 4	WD repeat domain 54 [Source:HGNC Symbol;Acc:HGNC:25
6	HDGFRP2	1.77	9e−09	5e−08	17 x 5	
7	SPATA25	1.76	1e−08	6e−08	18 x 4	spermatogenesis associated 25 [Source:HGNC Symbol;Acc:
8	STAC	1.74	1e−08	2e−07	19 x 3	SH3 and cysteine rich domain [Source:HGNC Symbol;Acc:H
9	RELL1	1.69	4e−08	2e−07	18 x 4	RELT−like 1 [Source:HGNC Symbol;Acc:HGNC:27379]
10	DNAJB2	1.67	5e−08	2e−07	17 x 5	DnaJ (Hsp40) homolog, subfamily B, member 2 [Source:HG
11	CDC34	1.67	6e−08	2e−07	17 x 3	cell division cycle 34 [Source:HGNC Symbol;Acc:HGNC:173
12	BMF	1.66	7e−08	2e−07	18 x 4	Bcl2 modifying factor [Source:HGNC Symbol;Acc:HGNC:241
13	ZNF487	1.65	8e−08	2e−07	17 x 3	zinc finger protein 487 [Source:HGNC Symbol;Acc:HGNC:23
14	CTTNBP2	1.65	8e−08	2e−07	18 x 5	cortactin binding protein 2 [Source:HGNC Symbol;Acc:HGN
15	IFT46	1.64	1e−07	2e−07	18 x 4	intraflagellar transport 46 [Source:HGNC Symbol;Acc:HGNC
16	ZNF558	1.63	1e−07	2e−07	20 x 4	zinc finger protein 558 [Source:HGNC Symbol;Acc:HGNC:26
17	YPEL3	1.63	1e−07	2e−07	16 x 6	yippee−like 3 (Drosophila) [Source:HGNC Symbol;Acc:HGN
18	RHOV	1.62	1e−07	2e−07	17 x 5	ras homolog family member V [Source:HGNC Symbol;Acc:H
19	DUSP5	1.62	1e−07	8e−07	17 x 5	dual specificity phosphatase 5 [Source:HGNC Symbol;Acc:H
20	LONRF2	1.6	2e−07	8e−07	19 x 4	LON peptidase N−terminal domain and ring finger 2 [Source:



C9_mel

Local Summary

%DE = 0.89

metagenes = 30

genes = 420

genes in genesets = 420

genes with fdr < 0.1 = 325 (320 + / 5 −)

genes with fdr < 0.05 = 303 (301 + / 2 −)

genes with fdr < 0.01 = 240 (240 + / 0 −)

<r> metagenes = 0.93

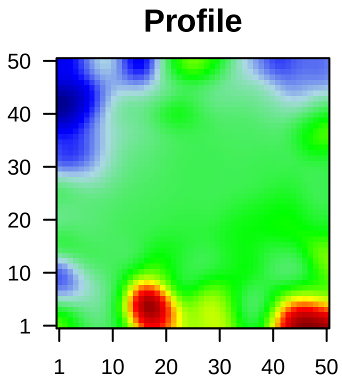
<r> genes = 0.17

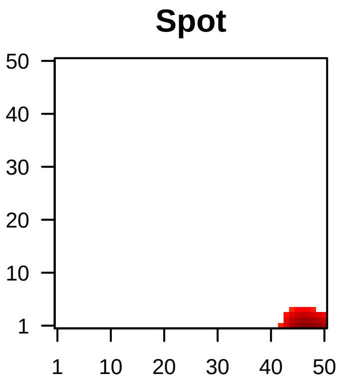
<FC> = 0.85

<shrinkage−t> = 13.42

<p−value> = 0

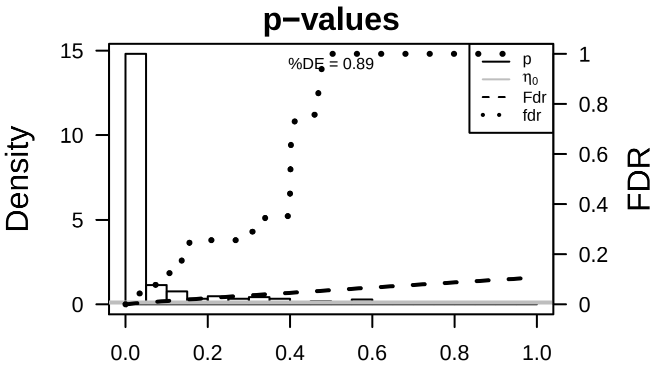
<fdr> = 0.33


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	PLK2	1.69	2e−13	4e−12	50 x 1	polo−like kinase 2 [Source:HGNC Symbol;Acc:HGNC:19699]
2	RGS2	2.26	2e−13	9e−10	49 x 1	regulator of G−protein signaling 2 [Source:HGNC Symbol;Ac
3	METTL8	2.02	5e−11	9e−10	45 x 1	methyltransferase like 8 [Source:HGNC Symbol;Acc:HGNC:2
4	TXNRD1	0.82	6e−11	9e−10	48 x 4	thioredoxin reductase 1 [Source:HGNC Symbol;Acc:HGNC:1
5	C10orf10	2.01	6e−11	6e−09	49 x 1	chromosome 10 open reading frame 10 [Source:HGNC Sym
6	CNN3	0.79	2e−10	1e−08	47 x 1	calponin 3, acidic [Source:HGNC Symbol;Acc:HGNC:2157]
7	PRICKLE2	1.91	5e−10	1e−08	44 x 3	prickle homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:H
8	MARCKS	0.89	9e−10	1e−08	46 x 1	myristoylated alanine−rich protein kinase C substrate [Source
9	TMEM45A	1.88	1e−09	2e−08	50 x 1	transmembrane protein 45A [Source:HGNC Symbol;Acc:HG
10	F2R	1.86	2e−09	3e−08	50 x 1	coagulation factor II (thrombin) receptor [Source:HGNC Sym
11	SORBS2	1.84	2e−09	3e−08	50 x 1	sorbin and SH3 domain containing 2 [Source:HGNC Symbol;
12	CDH6	1.82	3e−09	3e−08	45 x 1	cadherin 6, type 2, K−cadherin (fetal kidney) [Source:HGNC
13	MYOZ2	1.81	4e−09	3e−08	48 x 1	myozenin 2 [Source:HGNC Symbol;Acc:HGNC:1330]
14	AMOTL2	1.81	4e−09	1e−07	49 x 1	angiomotin like 2 [Source:HGNC Symbol;Acc:HGNC:17812]
15	AFAP1	1.75	1e−08	1e−07	44 x 1	actin filament associated protein 1 [Source:HGNC Symbol;Ac
16	HBEGF	1.74	2e−08	1e−07	48 x 1	heparin−binding EGF−like growth factor [Source:HGNC Sym
17	PRRG1	1.74	2e−08	1e−07	46 x 1	proline rich Gla (G−carboxyglutamic acid) 1 [Source:HGNC S
18	FRMD6	1.74	2e−08	1e−07	50 x 1	FERM domain containing 6 [Source:HGNC Symbol;Acc:HGN
19	RHOBTB3	1.73	2e−08	1e−07	50 x 1	Rho−related BTB domain containing 3 [Source:HGNC Symb
20	NTN4	1.72	2e−08	1e−07	46 x 2	netrin 4 [Source:HGNC Symbol;Acc:HGNC:13658]


p−values

C9_mel

Local Summary

%DE = 0.83

metagenes = 53

genes = 715

genes in genesets = 711

genes with fdr < 0.1 = 439 (46 + / 393 −)

genes with fdr < 0.05 = 363 (27 + / 336 −)

genes with fdr < 0.01 = 281 (15 + / 266 −)

<r> metagenes = 0.83

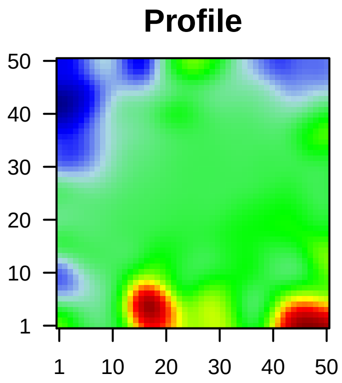
<r> genes = 0.13

<FC> = −0.56

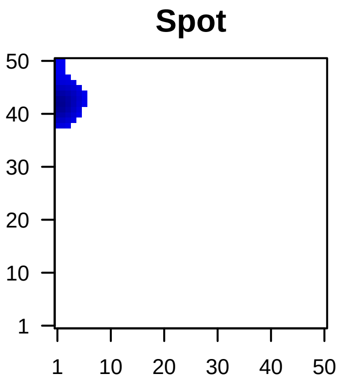
<shrinkage−t> = −10.45

<p−value> = 0

<fdr> = 0.51



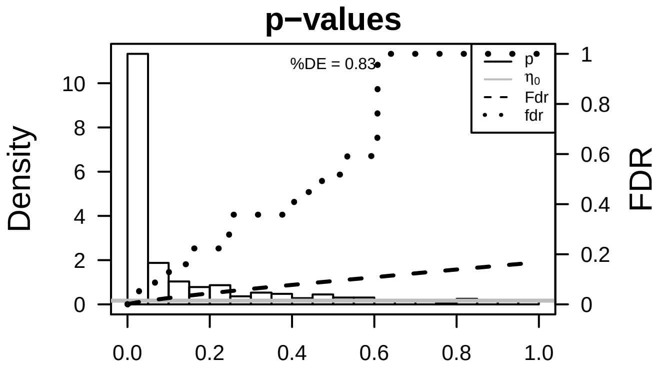
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ALG8	−1.42	2e−16	1e−15	5 x 43	ALG8, alpha−1,3−glucosyltransferase [Source:HGNC Symbo
2	CDK2	−2.19	2e−16	1e−15	1 x 43	cyclin−dependent kinase 2 [Source:HGNC Symbol;Acc:HGN
3	CHCHD6	−2.01	2e−16	1e−15	1 x 43	coiled−coil−helix−coiled−coil−helix domain containing 6 [Sour
4	CITED1	−1.94	2e−16	1e−15	1 x 41	Cbp/p300−interacting transactivator, with Glu/Asp−rich carbo
5	CMC2	−1.96	2e−16	1e−15	5 x 44	C−x(9)−C motif containing 2 [Source:HGNC Symbol;Acc:HG
6	CNDP2	−1.88	2e−16	1e−15	3 x 40	CNDP dipeptidase 2 (metallopeptidase M20 family) [Source:
7	DAB2	−1.4	2e−16	1e−15	3 x 41	Dab, mitogen−responsive phosphoprotein, homolog 2 (Droso
8	DERA	−1.78	2e−16	1e−15	1 x 43	deoxyribose−phosphate aldolase (putative) [Source:HGNC S
9	EMP3	−1.82	2e−16	1e−15	4 x 43	epithelial membrane protein 3 [Source:HGNC Symbol;Acc:H
10	EXOC3	−1.33	2e−16	1e−15	1 x 42	exocyst complex component 3 [Source:HGNC Symbol;Acc:H
11	GNPDA1	−1.77	2e−16	1e−15	1 x 42	glucosamine−6−phosphate deaminase 1 [Source:HGNC Sym
12	HBS1L	−1.89	2e−16	1e−15	3 x 44	HBS1−like translational GTPase [Source:HGNC Symbol;Acc:
13	IDH3A	−1.41	2e−16	1e−15	1 x 42	isocitrate dehydrogenase 3 (NAD+) alpha [Source:HGNC Sy
14	LSM7	−1.76	2e−16	1e−15	2 x 38	LSM7 homolog, U6 small nuclear RNA associated (S. cerevis
15	MITF	−1.31	2e−16	1e−15	1 x 41	microphthalmia−associated transcription factor [Source:HGN
16	MLANA	−1.87	2e−16	1e−15	1 x 43	melan−A [Source:HGNC Symbol;Acc:HGNC:7124]
17	MRPL34	−2.05	2e−16	1e−15	1 x 40	mitochondrial ribosomal protein L34 [Source:HGNC Symbol;
18	MTCH2	−1.95	2e−16	1e−15	2 x 42	mitochondrial carrier 2 [Source:HGNC Symbol;Acc:HGNC:17
19	MTX2	−1.91	2e−16	1e−15	1 x 42	metaxin 2 [Source:HGNC Symbol;Acc:HGNC:7506]
20	ORMDL1	−1.84	2e−16	1e−15	5 x 40	ORMDL sphingolipid biosynthesis regulator 1 [Source:HGNC



p−values