B8_mel

Global Summary

%DE = 0.21

genes with fdr < 0.2 = 2648 (1588 + / 1060 −)

genes with fdr < 0.1 = 2083 (1266 + / 817 −)

genes with fdr < 0.05 = 1697 (1042 + / 655 −)

genes with fdr < 0.01 = 1074 (661 + / 413 −)

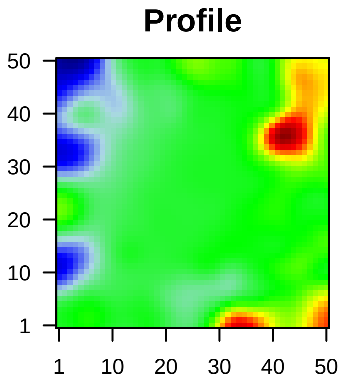
genes in genesets = 14839

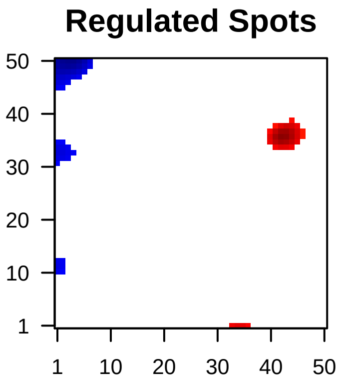
<FC> = 0

<shrinkage−t> = −0.01

<p−value> = 0.08

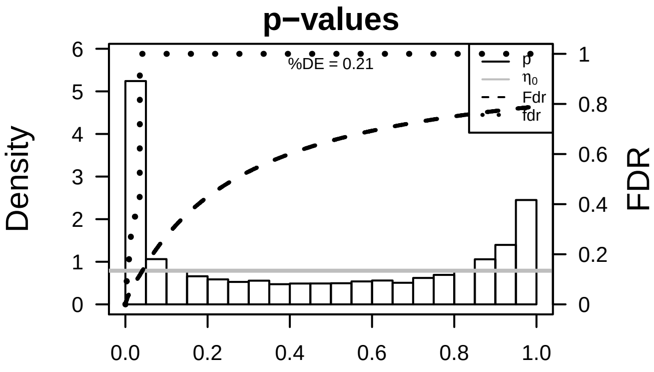
<fdr> = 0.79





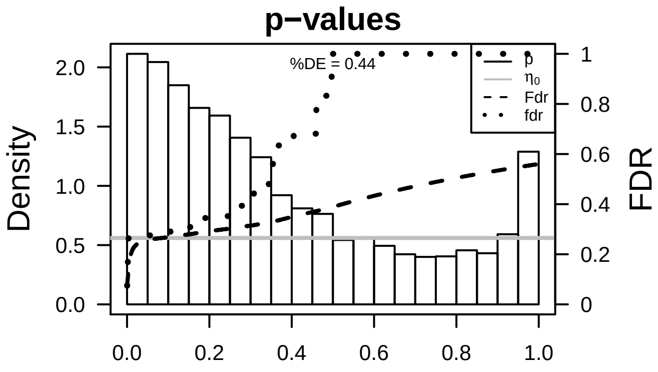
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	APOO	−1.72	2e−16	8e−14	2 x 46	apolipoprotein O [Source:HGNC Symbol;Acc:HGNC:28727]
2	ARHGAP8	−1.74	2e−16	8e−14	1 x 43	Rho GTPase activating protein 8 [Source:HGNC Symbol;Acc:
3	ARL8B	−1.57	2e−16	8e−14	1 x 33	ADP−ribosylation factor−like 8B [Source:HGNC Symbol;Acc:
4	ATRAID	−1.73	2e−16	8e−14	35 x 50	all−trans retinoic acid−induced differentiation factor [Source:
5	CHCHD6	−2.06	2e−16	8e−14	1 x 43	coiled−coil−helix−coiled−coil−helix domain containing 6 [Sour
6	CRBN	−1.31	2e−16	8e−14	1 x 8	cereblon [Source:HGNC Symbol;Acc:HGNC:30185]
7	CSE1L	−1.57	2e−16	8e−14	3 x 49	CSE1 chromosome segregation 1−like (yeast) [Source:HGNC
8	CTSC	−1.26	2e−16	8e−14	1 x 42	cathepsin C [Source:HGNC Symbol;Acc:HGNC:2528]
9	DCT	−1.8	2e−16	8e−14	1 x 11	dopachrome tautomerase [Source:HGNC Symbol;Acc:HGNC
10	DNMT1	−1.78	2e−16	8e−14	2 x 48	DNA (cytosine−5−)−methyltransferase 1 [Source:HGNC Sym
11	DYNLT1	−2.01	2e−16	8e−14	5 x 33	dynein, light chain, Tctex−type 1 [Source:HGNC Symbol;Acc:
12	IMPDH2	−1.46	2e−16	8e−14	5 x 15	IMP (inosine 5'−monophosphate) dehydrogenase 2 [Source:
13	MARS	−1.72	2e−16	8e−14	43 x 47	methionyl−tRNA synthetase [Source:HGNC Symbol;Acc:HG
14	MBP	−0.92	2e−16	8e−14	1 x 42	myelin basic protein [Source:HGNC Symbol;Acc:HGNC:6925
15	MLIP	−1.63	2e−16	8e−14	3 x 44	muscular LMNA−interacting protein [Source:HGNC Symbol;A
16	MYO5B	2.19	2e−16	8e−14	35 x 1	myosin VB [Source:HGNC Symbol;Acc:HGNC:7603]
17	NASP	−1.7	2e−16	8e−14	1 x 48	nuclear autoantigenic sperm protein (histone−binding) [Sourc
18	PDE4DIP	−1.37	2e−16	8e−14	1 x 43	phosphodiesterase 4D interacting protein [Source:HGNC Sy
19	PHACTR1	−0.84	2e−16	8e−14	4 x 14	phosphatase and actin regulator 1 [Source:HGNC Symbol;Ac
20	PSMC5	−2.14	2e−16	8e−14	28 x 50	proteasome (prosome, macropain) 26S subunit, ATPase, 5 [S



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	6.15	0.002	222	GSEA C2	CONCANNON_APOPTOSIS_BY_EPOXOMICIN_UP
2	5.5	0.003	620	GSEA C2	MILI_PSEUDOPODIA_HAPTOTAXIS_DN
3	4.57	0.005	22	BP	regulation of angiogenesis
4	4.43	0.005	13	GSEA C2	AMUNDSON_DNA_DAMAGE_RESPONSE_TP53
5	4.19	0.006	2698	Colon Cancer	EcbA_Colon
6	4.19	0.006	46	miRNA target	hsa−miR−1322
7	4.18	0.006	155	GSEA C2	SMIRNOV_RESPONSE_TO_IR_6HR_UP
8	4.12	0.007	447	GSEA C2	ENK_UV_RESPONSE_KERATINOCYTE_UP
9	4.11	0.007	193	BP	protein folding
10	3.99	0.008	101	BP	response to oxidative stress
11	3.97	0.008	683	GSEA C2	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
12	3.87	0.008	87	MF	unfolded protein binding
13	3.85	0.008	12	MF	NAD−dependent histone deacetylase activity (H3−K18 specific)
14	3.84	0.009	424	GSEA C2	MILI_PSEUDOPODIA_CHEMOTAXIS_DN
15	3.81	0.009	39	GSEA C2	WARTERS_IR_RESPONSE_5GY
16	3.73	0.009	235	GSEA C2	BLUM_RESPONSE_TO_SALIRASIB_UP
17	3.7	0.010	85	GSEA C2	KEEN_RESPONSE_TO_ROSIGLITAZONE_DN
18	3.69	0.010	274	GSEA C2	DEBIASI_APOPTOSIS_BY_REOVIRUS_INFECTION_DN
19	3.68	0.010	57	GSEA C2	WOO_LIVER_CANCER_RECURRENCE_DN
20	3.58	0.011	20	GSEA C2	MANN_RESPONSE_TO_AMIFOSTINE_UP
Underexpressed					
1	−12.34	1e−04	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
2	−12.21	1e−04	305	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
3	−12.17	1e−04	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
4	−11.09	2e−04	162	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
5	−11.01	2e−04	242	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
6	−10.93	2e−04	700	GSEA C2	MARSON_BOUND_BY_E2F4_UNSTIMULATED
7	−10.91	2e−04	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
8	−10.8	2e−04	197	HM	HALLMARK_E2F_TARGETS
9	−10.7	2e−04	99	GSEA C2	BURTON_ADIPOGENESIS_3
10	−10.62	2e−04	110	GSEA C2	WHITEFORD_PEDIATRIC_CANCER_MARKERS
11	−10.07	3e−03	16	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
12	−10.07	3e−04	93	GSEA C2	KONG_E2F3_TARGETS
13	−10.05	3e−04	1192	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
14	−10.02	3e−04	72	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
15	−9.84	3e−04	390	GSEA C2	PUJANA_BRCA2_PCC_NETWORK
16	−9.62	3e−04	50	GSEA C2	ISHIDA_E2F_TARGETS
17	−9.44	3e−04	436	GSEA C2	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
18	−9.36	3e−04	216	GSEA C2	MARKEY_RB1_ACUTE_LOF_DN
19	−9.34	3e−04	96	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
20	−9.24	4e−04	81	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN



B8_mel

Local Summary

%DE = 0.71

metagenes = 4

genes = 60

genes in genesets = 60

genes with fdr < 0.1 = 36 (36 + / 0 −)

genes with fdr < 0.05 = 36 (36 + / 0 −)

genes with fdr < 0.01 = 33 (33 + / 0 −)

<r> metagenes = 0.95

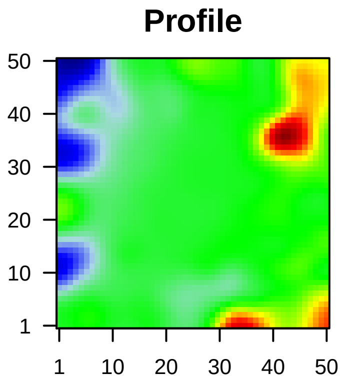
<r> genes = 0.15

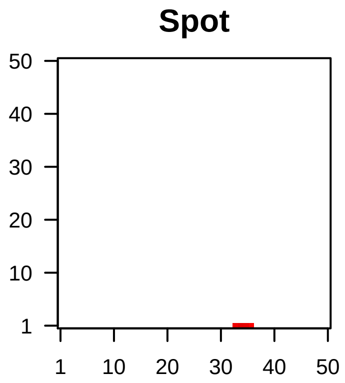
<FC> = 0.72

<shrinkage−t> = 10.95

<p−value> = 0

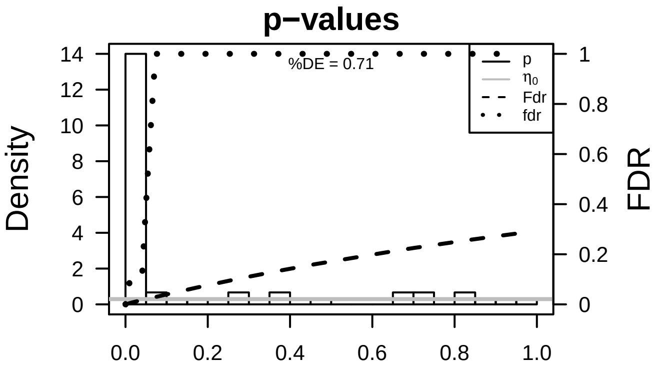
<fdr> = 0.37


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	MYO5B	2.19	2e−16	4e−15	35 x 1	myosin VB [Source:HGNC Symbol;Acc:HGNC:7603]
2	RFX3	1.8	7e−13	9e−08	34 x 1	regulatory factor X, 3 (influences HLA class II expression) [S
3	AVIL	1.47	5e−09	6e−07	36 x 1	advillin [Source:HGNC Symbol;Acc:HGNC:14188]
4	L3HYPDH	1.37	4e−08	6e−07	33 x 1	L−3−hydroxyproline dehydratase (trans−) [Source:HGNC Sy
5	ADH6	1.35	7e−08	7e−07	33 x 1	alcohol dehydrogenase 6 (class V) [Source:HGNC Symbol;A
6	PIGB	1.33	1e−07	2e−06	33 x 1	phosphatidylinositol glycan anchor biosynthesis, class B [Sou
7	CETN3	1.3	2e−07	2e−06	35 x 1	centrin, EF−hand protein, 3 [Source:HGNC Symbol;Acc:HGN
8	ABCA9	1.28	3e−07	2e−06	33 x 1	ATP−binding cassette, sub−family A (ABC1), member 9 [Sou
9	AKAP7	1.27	4e−07	4e−06	33 x 1	A kinase (PRKA) anchor protein 7 [Source:HGNC Symbol;Ac
10	ZNF701	1.25	6e−07	5e−06	33 x 1	zinc finger protein 701 [Source:HGNC Symbol;Acc:HGNC:25
11	ASAP3	1.22	1e−06	5e−06	35 x 1	ArfGAP with SH3 domain, ankyrin repeat and PH domain 3 [
12	ACTR8	1.22	1e−06	2e−05	33 x 1	ARP8 actin−related protein 8 homolog (yeast) [Source:HGNC
13	AFAP1L2	1.17	3e−06	2e−05	34 x 1	actin filament associated protein 1−like 2 [Source:HGNC Sy
14	ZNF138	1.15	4e−06	2e−05	34 x 1	zinc finger protein 138 [Source:HGNC Symbol;Acc:HGNC:12
15	TSPAN13	1.15	5e−06	2e−05	36 x 1	tetraspanin 13 [Source:HGNC Symbol;Acc:HGNC:21643]
16	C7orf25	1.14	5e−06	5e−05	35 x 1	chromosome 7 open reading frame 25 [Source:HGNC Symb
17	RC3H2	1.11	1e−05	5e−05	36 x 1	ring finger and CCCH−type domains 2 [Source:HGNC Symb
18	MTF1	1.1	1e−05	5e−05	36 x 1	metal−regulatory transcription factor 1 [Source:HGNC Symb
19	LYPLAL1	1.02	2e−05	5e−05	35 x 1	lysophospholipase−like 1 [Source:HGNC Symbol;Acc:HGNC:
20	ABHD14A	1.07	2e−05	5e−05	34 x 1	abhydrolase domain containing 14A [Source:HGNC Symbol;


p−values

B8_mel

Local Summary

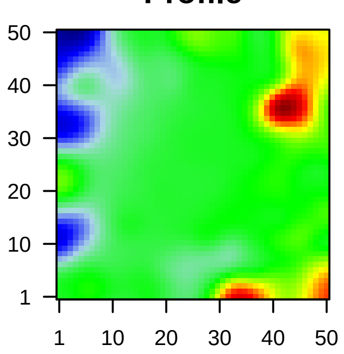
%DE = 0.94
metagenes = 30
genes = 153
genes in genesets = 152

genes with fdr < 0.1 = 134 (134 + / 0 −)
genes with fdr < 0.05 = 131 (131 + / 0 −)
genes with fdr < 0.01 = 116 (116 + / 0 −)

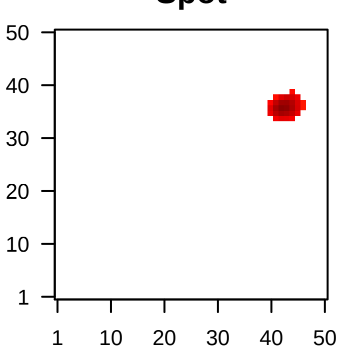
<r> metagenes = 0.88
<r> genes = 0.18

<FC> = 0.89
<shrinkage−t> = 13.98
<p−value> = 0
<fdr> = 0.21

Profile



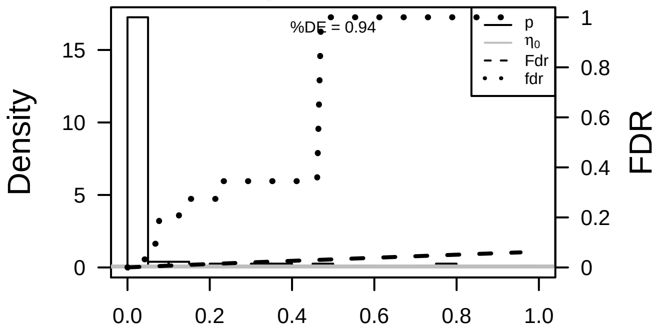
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	NR0B1	1.71	9e−12	6e−11	42 x 36	nuclear receptor subfamily 0, group B, member 1 [Source:HG
2	DNAJC22	1.7	1e−11	9e−11	41 x 36	DnaJ (Hsp40) homolog, subfamily C, member 22 [Source:HG
3	EDC4	1.67	3e−11	9e−11	43 x 37	enhancer of mRNA decapping 4 [Source:HGNC Symbol;Acc:
4	SCGB1D2	1.66	3e−11	9e−11	42 x 36	secretoglobin, family 1D, member 2 [Source:HGNC Symbol;A
5	COL4A2	1.65	5e−11	9e−11	42 x 37	collagen, type IV, alpha 2 [Source:HGNC Symbol;Acc:HGNC:
6	CARD10	1.65	5e−11	3e−09	41 x 36	caspase recruitment domain family, member 10 [Source:HGN
7	GDPD1	1.57	4e−10	4e−09	41 x 36	glycerophosphodiester phosphodiesterase domain containing
8	NRG1	1.54	8e−10	4e−09	42 x 36	neuregulin 1 [Source:HGNC Symbol;Acc:HGNC:7997]
9	CSRNP2	1.53	1e−09	9e−09	42 x 36	cysteine−serine−rich nuclear protein 2 [Source:HGNC Symbo
10	TMEM184B	1.49	3e−09	9e−09	41 x 36	transmembrane protein 184B [Source:HGNC Symbol;Acc:HG
11	CCDC159	1.49	3e−09	1e−08	41 x 36	coiled−coil domain containing 159 [Source:HGNC Symbol;Ac
12	PIGO	1.46	6e−09	1e−08	41 x 36	phosphatidylinositol glycan anchor biosynthesis, class O [Sou
13	SOSTDC1	1.45	8e−09	1e−08	42 x 36	sclerostin domain containing 1 [Source:HGNC Symbol;Acc:
14	KHNYN	1.44	9e−09	1e−08	42 x 36	KH and NYN domain containing [Source:HGNC Symbol;Acc:
15	IGSF6	1.44	9e−09	1e−08	41 x 36	immunoglobulin superfamily, member 6 [Source:HGNC Symb
16	FAM217A	1.43	1e−08	2e−08	41 x 36	family with sequence similarity 217, member A [Source:HGN
17	ZNF786	1.42	1e−08	2e−08	42 x 36	zinc finger protein 786 [Source:HGNC Symbol;Acc:HGNC:21
18	NEK11	1.42	2e−08	2e−08	41 x 38	NIMA−related kinase 11 [Source:HGNC Symbol;Acc:HGNC:1
19	DNM3	1.41	2e−08	2e−08	42 x 36	dynamin 3 [Source:HGNC Symbol;Acc:HGNC:29125]
20	IPP	1.41	2e−08	7e−08	45 x 38	intracisternal A particle−promoted polypeptide [Source:HGN

p−values



B8_mel

Local Summary

%DE = 0.84

metagenes = 6

genes = 119

genes in genesets = 118

genes with fdr < 0.1 = 83 (9 + / 74 −)

genes with fdr < 0.05 = 73 (9 + / 64 −)

genes with fdr < 0.01 = 52 (5 + / 47 −)

<r> metagenes = 0.99

<r> genes = 0.18

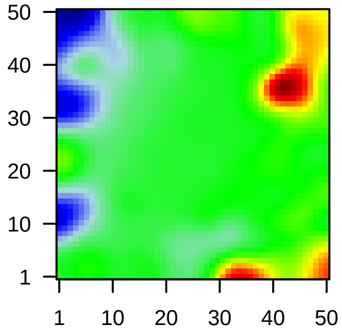
<FC> = −0.5

<shrinkage−t> = −8.86

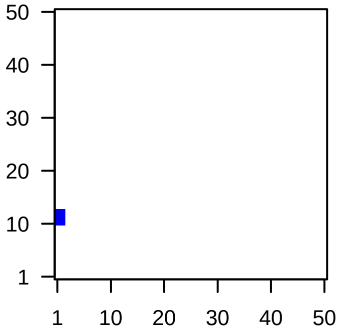
<p−value> = 0

<fdr> = 0.43

Profile



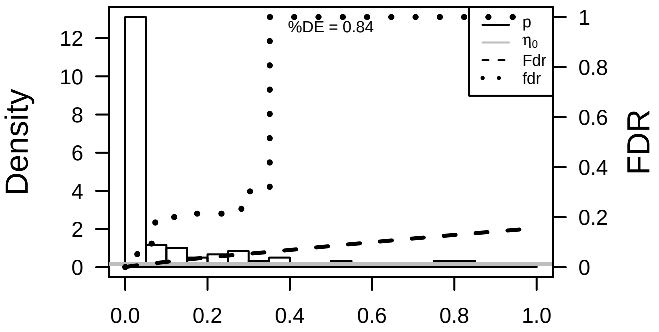
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	DCT	−1.8	2e−16	2e−15	1 x 11	dopachrome tautomerase [Source:HGNC Symbol;Acc:HGNC
2	TRAK2	−1.68	2e−16	2e−15	1 x 12	trafficking protein, kinesin binding 2 [Source:HGNC Symbol;A
3	ZZZ3	−1.59	4e−16	2e−14	1 x 11	zinc finger, ZZ−type containing 3 [Source:HGNC Symbol;Acc
4	SAT1	−0.8	2e−15	2e−14	1 x 11	spermidine/spermine N1−acetyltransferase 1 [Source:HGNC
5	ZNF330	−1.44	2e−15	5e−11	2 x 13	zinc finger protein 330 [Source:HGNC Symbol;Acc:HGNC:15
6	ID2	−0.71	3e−12	2e−09	1 x 13	inhibitor of DNA binding 2, dominant negative helix−loop−heli
7	SGK1	−0.66	1e−10	9e−09	1 x 13	serum/glucocorticoid regulated kinase 1 [Source:HGNC Sym
8	SNX27	−1.37	6e−10	3e−08	1 x 12	sorting nexin family member 27 [Source:HGNC Symbol;Acc:
9	FARP1	−1.34	2e−09	1e−07	1 x 11	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1
10	SNAI2	−1.31	1e−08	6e−07	1 x 11	snail family zinc finger 2 [Source:HGNC Symbol;Acc:HGNC:1
11	SOCS6	−1.26	4e−08	2e−06	1 x 11	suppressor of cytokine signaling 6 [Source:HGNC Symbol;Ac
12	GPRC5B	−1.22	3e−07	2e−06	1 x 12	G protein−coupled receptor, class C, group 5, member B [So
13	PFKFB2	−0.78	3e−07	2e−06	2 x 13	6−phosphofructo−2−kinase/fructose−2,6−biphosphatase 2 [S
14	NAV2	−0.99	5e−07	2e−06	1 x 12	neuron navigator 2 [Source:HGNC Symbol;Acc:HGNC:15997
15	TNFRSF14	−1.15	6e−07	2e−06	1 x 11	tumor necrosis factor receptor superfamily, member 14 [Sour
16	AZI2	−1	7e−07	4e−06	1 x 13	5−azacytidine induced 2 [Source:HGNC Symbol;Acc:HGNC:
17	C5orf22	−0.78	9e−07	3e−05	2 x 12	chromosome 5 open reading frame 22 [Source:HGNC Symb
18	BAIAP2	−1.15	2e−06	3e−05	1 x 12	BAI1−associated protein 2 [Source:HGNC Symbol;Acc:HGN
19	BHLHE41	−1.12	5e−06	3e−05	1 x 12	basic helix−loop−helix family, member e41 [Source:HGNC Sy
20	VEPH1	−1.11	7e−06	3e−05	1 x 11	ventricular zone expressed PH domain−containing 1 [Source:

p−values



B8_mel

Local Summary

%DE = 0.88

metagenes = 13

genes = 99

genes in genesets = 99

genes with fdr < 0.1 = 80 (9 + / 71 −)

genes with fdr < 0.05 = 46 (5 + / 41 −)

genes with fdr < 0.01 = 34 (3 + / 31 −)

<r> metagenes = 0.96

<r> genes = 0.09

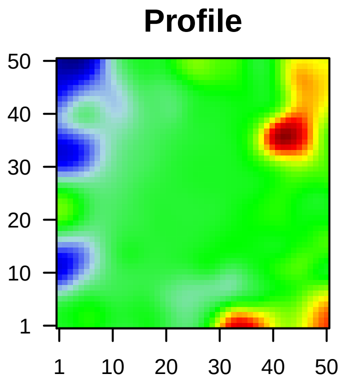
<FC> = −0.46

<shrinkage−t> = −7.68

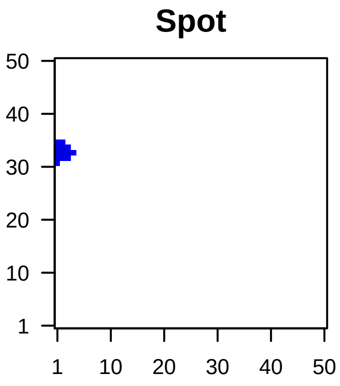
<p−value> = 0

<fdr> = 0.57

Profile



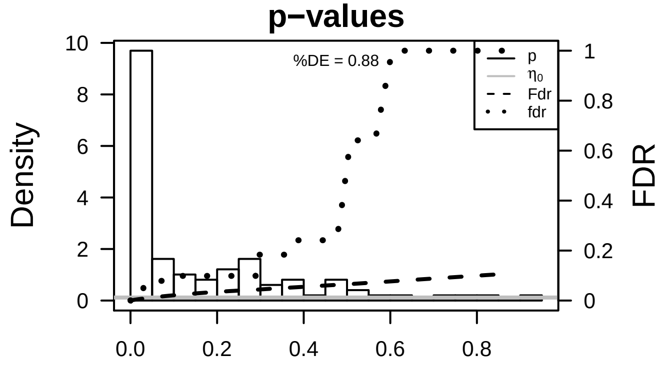
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ARL8B	−1.57	2e−16	1e−15	1 x 33	ADP−ribosylation factor−like 8B [Source:HGNC Symbol;Acc:
2	TIMM50	−1.9	2e−16	1e−15	1 x 33	translocase of inner mitochondrial membrane 50 homolog (S.
3	NDUFS3	−1.57	4e−15	4e−11	1 x 32	NADH dehydrogenase (ubiquinone) Fe−S protein 3, 30kDa (
4	TMEM138	−1.53	4e−15	4e−11	1 x 33	transmembrane protein 138 [Source:HGNC Symbol;Acc:HG
5	THOC2	−1.07	4e−12	4e−11	1 x 33	THO complex 2 [Source:HGNC Symbol;Acc:HGNC:19073]
6	NUCB2	−1.07	7e−12	2e−07	1 x 35	nucleobindin 2 [Source:HGNC Symbol;Acc:HGNC:8044]
7	PPP1R7	−1.28	2e−08	7e−06	1 x 35	protein phosphatase 1, regulatory subunit 7 [Source:HGNC S
8	MRPL11	−1.07	1e−06	7e−06	4 x 33	mitochondrial ribosomal protein L11 [Source:HGNC Symbol;
9	SMYD3	−1.17	1e−06	7e−06	4 x 33	SET and MYND domain containing 3 [Source:HGNC Symbol
10	USB1	−1.1	2e−06	4e−05	1 x 35	U6 snRNA biogenesis 1 [Source:HGNC Symbol;Acc:HGNC:2
11	GNPAT	−1.12	6e−06	4e−05	3 x 32	glyceronephosphate O−acyltransferase [Source:HGNC Symb
12	CHD1	−0.77	9e−06	7e−05	1 x 31	chromodomain helicase DNA binding protein 1 [Source:HGN
13	CDKN2AIPNL	−1.02	2e−05	7e−05	1 x 32	CDKN2A interacting protein N−terminal like [Source:HGNC S
14	KANK2	−1.04	3e−05	7e−05	1 x 31	KN motif and ankyrin repeat domains 2 [Source:HGNC Symb
15	BTBD10	−1.04	3e−05	4e−04	1 x 31	BTB (POZ) domain containing 10 [Source:HGNC Symbol;Ac
16	AHCTF1	−0.98	6e−05	7e−04	1 x 35	AT hook containing transcription factor 1 [Source:HGNC Sym
17	AP3B1	−0.93	2e−04	7e−04	1 x 32	adaptor−related protein complex 3, beta 1 subunit [Source:H
18	JMJD6	−0.93	2e−04	7e−04	1 x 33	jumonji domain containing 6 [Source:HGNC Symbol;Acc:HG
19	CERS2	0.58	2e−04	1e−03	3 x 34	ceramide synthase 2 [Source:HGNC Symbol;Acc:HGNC:140
20	AATF	−0.86	6e−04	1e−03	1 x 35	apoptosis antagonizing transcription factor [Source:HGNC Sy

p−values



B8_mel

Local Summary

%DE = 0.82

metagenes = 30

genes = 448

genes in genesets = 446

genes with fdr < 0.1 = 277 (37 + / 240 −)

genes with fdr < 0.05 = 233 (33 + / 200 −)

genes with fdr < 0.01 = 141 (17 + / 124 −)

<r> metagenes = 0.89

<r> genes = 0.24

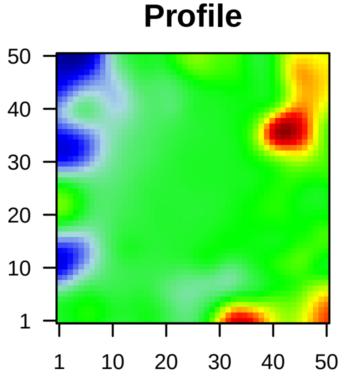
<FC> = −0.43

<shrinkage−t> = −7.11

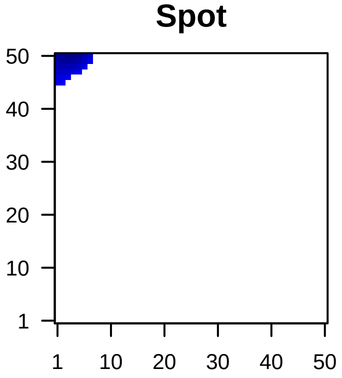
<p−value> = 0

<fdr> = 0.53

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	APOO	−1.72	2e−16	3e−15	2 x 46	apolipoprotein O [Source:HGNC Symbol;Acc:HGNC:28727]
2	CSE1L	−1.57	2e−16	3e−15	3 x 49	CSE1 chromosome segregation 1−like (yeast) [Source:HGNC
3	DNMT1	−1.78	2e−16	3e−15	2 x 48	DNA (cytosine−5−)−methyltransferase 1 [Source:HGNC Sym
4	NASP	−1.7	2e−16	3e−15	1 x 48	nuclear autoantigenic sperm protein (histone−binding) [Sourc
5	SIVA1	−1.88	2e−16	3e−15	1 x 46	SIVA1, apoptosis−inducing factor [Source:HGNC Symbol;Acc
6	STMN1	−2.49	2e−16	3e−15	5 x 50	stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]
7	TMEM106C	−1.48	2e−16	3e−15	5 x 48	transmembrane protein 106C [Source:HGNC Symbol;Acc:HG
8	MCM4	−1.58	2e−15	5e−13	1 x 50	minichromosome maintenance complex component 4 [Source
9	POLE3	−1.55	1e−14	5e−13	3 x 46	polymerase (DNA directed), epsilon 3, accessory subunit [So
10	TK1	−1.55	1e−14	2e−11	4 x 50	thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:HGN
11	YEATS4	−1.52	2e−13	2e−10	1 x 47	YEATS domain containing 4 [Source:HGNC Symbol;Acc:HG
12	SNRNP25	−1.39	3e−12	7e−10	1 x 46	small nuclear ribonucleoprotein 25kDa (U11/U12) [Source:H
13	CA14	−1.37	1e−11	7e−10	1 x 46	carbonic anhydrase XIV [Source:HGNC Symbol;Acc:HGNC:1
14	CTPS1	−1.44	2e−11	1e−09	1 x 47	CTP synthase 1 [Source:HGNC Symbol;Acc:HGNC:2519]
15	GGCT	−0.88	5e−11	1e−09	1 x 47	gamma−glutamylcyclotransferase [Source:HGNC Symbol;Ac
16	HLTF	−1.43	5e−11	2e−08	3 x 48	helicase−like transcription factor [Source:HGNC Symbol;Acc:
17	RFC5	−1.39	3e−10	2e−08	2 x 50	replication factor C (activator 1) 5, 36.5kDa [Source:HGNC S
18	TYMS	−1.37	5e−10	2e−08	3 x 50	thymidylate synthetase [Source:HGNC Symbol;Acc:HGNC:1
19	RANBP1	−1.36	7e−10	2e−08	1 x 48	RAN binding protein 1 [Source:HGNC Symbol;Acc:HGNC:98
20	C6orf211	−1.36	8e−10	2e−07	1 x 45	

p−values