E6_mel

Global Summary

%DE = 0.22

genes with fdr < 0.2 = 2838 (1710 + / 1128 −)

genes with fdr < 0.1 = 2366 (1449 + / 917 −)

genes with fdr < 0.05 = 2086 (1283 + / 803 −)

genes with fdr < 0.01 = 1226 (770 + / 456 −)

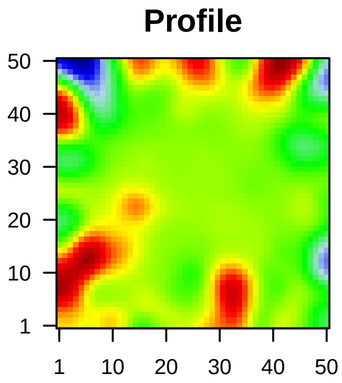
genes in genesets = 14839

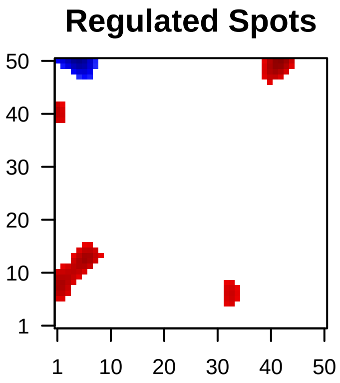
<FC> = 0

<shrinkage−t> = −0.01

<p−value> = 0.07

<fdr> = 0.78



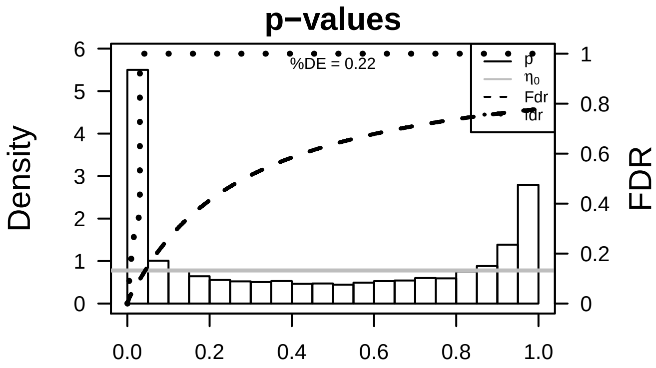


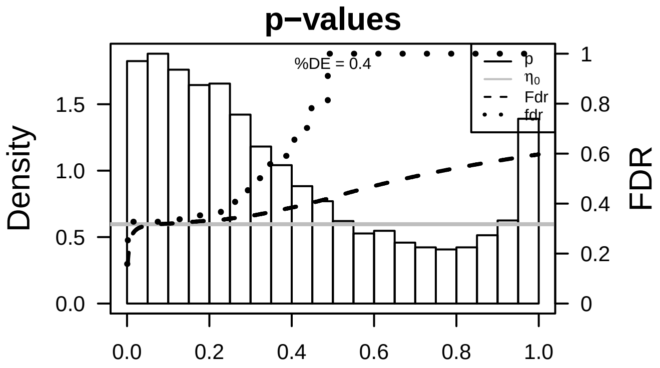
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ACTL6A	−1.27	2e−16	8e−14	4 x 50	actin−like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
2	AHSA1	−1.85	2e−16	8e−14	46 x 35	AHA1, activator of heat shock 90kDa protein ATPase homolo
3	ASPSCR1	−1.62	2e−16	8e−14	49 x 29	alveolar soft part sarcoma chromosome region, candidate 1 [
4	ATP1B3	−1.66	2e−16	8e−14	1 x 21	ATPase, Na+/K+ transporting, beta 3 polypeptide [Source:HG
5	ATPIF1	−1.45	2e−16	8e−14	50 x 47	ATPase inhibitory factor 1 [Source:HGNC Symbol;Acc:HGNC
6	AVPI1	−1.55	2e−16	8e−14	49 x 50	arginine vasopressin−induced 1 [Source:HGNC Symbol;Acc:
7	BLVRB	−1.37	2e−16	8e−14	1 x 6	biliverdin reductase B [Source:HGNC Symbol;Acc:HGNC:10
8	CCNG1	−1.6	2e−16	8e−14	12 x 48	cyclin G1 [Source:HGNC Symbol;Acc:HGNC:1592]
9	CKS2	−1.65	2e−16	8e−14	5 x 50	CDC28 protein kinase regulatory subunit 2 [Source:HGNC S
10	COPS3	−2.25	2e−16	8e−14	8 x 43	COP9 signalosome subunit 3 [Source:HGNC Symbol;Acc:HG
11	DKC1	−1.67	2e−16	8e−14	7 x 43	dyskeratosis congenita 1, dyskerin [Source:HGNC Symbol;A
12	ERGIC2	−1.87	2e−16	8e−14	6 x 44	ERGIC and golgi 2 [Source:HGNC Symbol;Acc:HGNC:30208
13	HAT1	−1.6	2e−16	8e−14	1 x 50	histone acetyltransferase 1 [Source:HGNC Symbol;Acc:HGN
14	HERPUD1	−1.3	2e−16	8e−14	50 x 42	homocysteine−inducible, endoplasmic reticulum stress−induc
15	HSD17B4	−1.63	2e−16	8e−14	11 x 50	hydroxysteroid (17−beta) dehydrogenase 4 [Source:HGNC S
16	IFT81	−1.69	2e−16	8e−14	6 x 43	intraflagellar transport 81 [Source:HGNC Symbol;Acc:HGNC:
17	MAPRE1	−1.61	2e−16	8e−14	7 x 45	microtubule−associated protein, RP/EB family, member 1 [So
18	MRPL13	−1.86	2e−16	8e−14	34 x 50	mitochondrial ribosomal protein L13 [Source:HGNC Symbol;
19	NUP85	−1.56	2e−16	8e−14	1 x 50	nucleoporin 85kDa [Source:HGNC Symbol;Acc:HGNC:8734]
20	PGM3	−1.31	2e−16	8e−14	5 x 45	phosphoglucomutase 3 [Source:HGNC Symbol;Acc:HGNC:8

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	5.61	0.002	63	Glio	Stuehler_Proteins_up_in_STS
2	4.64	0.005	198	HM	HALLMARK_OXIDATIVE_PHOSPHORYLATION
3	4.5	0.005	30	BP	cholesterol biosynthetic process
4	4.09	0.007	114	GSEA C2	REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_T
5	4.09	0.007	19	GSEA C2	KEGG_GALACTOSE_METABOLISM
6	4.07	0.007	14	BP	acyl−CoA metabolic process
7	3.91	0.008	94	BP	respiratory electron transport chain
8	3.85	0.008	135	BP	cellular metabolic process
9	3.8	0.009	85	GSEA C2	MOOTHA_VOXPHOS
10	3.73	0.009	44	GSEA C2	PID_HES_HEY_PATHWAY
11	3.7	0.010	18	BP	melanocyte differentiation
12	3.65	0.010	22	GSEA C2	REACTOME_CHOLESTEROL_BIOSYNTHESIS
13	3.58	0.011	28	BP	tricarboxylic acid cycle
14	3.58	0.011	303	miRNA target	hsa−miR−18b
15	3.54	0.011	19	GSEA C2	REACTOME_CITRIC_ACID_CYCLE_TCA_CYCLE
16	3.52	0.011	22	GSEA C2	BIOCARTA_GLEEVEC_PATHWAY
17	3.5	0.011	28	GSEA C2	KEGG_CITRATE_CYCLE_TCA_CYCLE
18	3.47	0.012	99	GSEA C2	PID_ERBB1_DOWNSTREAM_PATHWAY
19	3.41	0.012	145	miRNA target	hsa−miR−491−5p
20	3.36	0.013	136	GSEA C2	PODAR_RESPONSE_TO_ADAPHOSTIN_UP
Underexpressed					
1	−11.62	1e−04	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
2	−10.39	2e−04	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
3	−9.55	3e−04	390	GSEA C2	PUJANA_BRCA2_PCC_NETWORK
4	−9.4	3e−04	242	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
5	−9.31	3e−04	145	GSEA C2	CHANG_CYCLING_GENES
6	−8.88	4e−04	267	GSEA C2	ZHANG_TLX_TARGETS_60HR_DN
7	−8.49	5e−04	87	GSEA C2	ZHANG_TLX_TARGETS_UP
8	−8.44	5e−04	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
9	−8.35	1e−02	16	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
10	−8.32	5e−04	700	GSEA C2	MARSON_BOUND_BY_E2F4_UNSTIMULATED
11	−8.26	6e−04	305	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
12	−8.2	6e−04	1110	BP	cell cycle
13	−8.18	6e−04	944	GSEA C2	NUYTTEN_EZH2_TARGETS_DN
14	−8.15	6e−04	183	GSEA C2	ZHANG_TLX_TARGETS_36HR_DN
15	−8.09	6e−04	412	BP	mitotic cell cycle
16	−7.87	7e−04	160	GSEA C2	PUJANA_XPRSS_INT_NETWORK
17	−7.79	7e−04	162	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
18	−7.6	8e−04	110	GSEA C2	WHITEFORD_PEDIATRIC_CANCER_MARKERS
19	−7.47	8e−04	54	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
20	−7.43	8e−04	99	GSEA C2	BURTON_ADIPOGENESIS_3





E6_mel

Local Summary

%DE = 0.82

metagenes = 13

genes = 66

genes in genesets = 66

genes with fdr < 0.1 = 43 (40 + / 3 −)

genes with fdr < 0.05 = 39 (37 + / 2 −)

genes with fdr < 0.01 = 25 (24 + / 1 −)

<r> metagenes = 0.92

<r> genes = 0.12

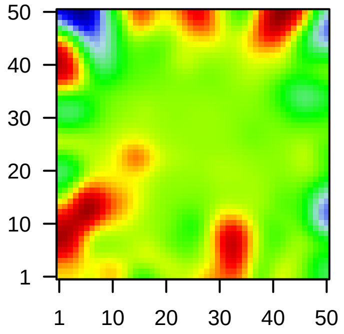
<FC> = 0.48

<shrinkage−t> = 7.37

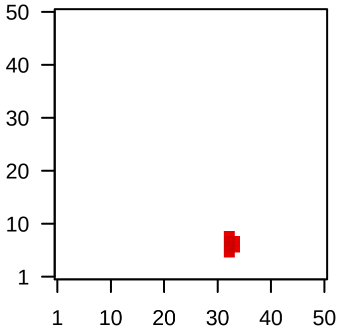
<p−value> = 0

<fdr> = 0.47

Profile



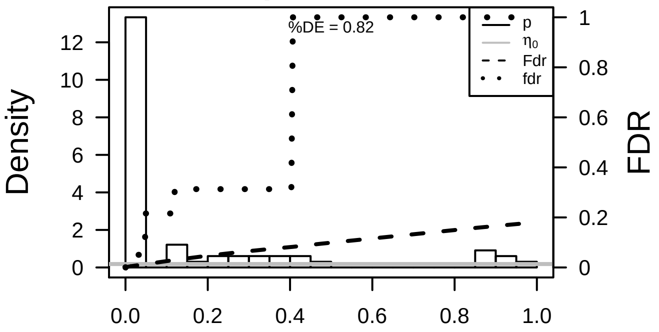
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CPD	1.3	5e−08	3e−07	34 x 7	carboxypeptidase D [Source:HGNC Symbol;Acc:HGNC:2301
2	MMP14	1.29	6e−08	2e−06	33 x 6	matrix metallopeptidase 14 (membrane−inserted) [Source:HG
3	ANXA2R	1.23	2e−07	8e−06	32 x 6	annexin A2 receptor [Source:HGNC Symbol;Acc:HGNC:3346
4	ARHGEF11	1.14	2e−06	8e−06	32 x 9	Rho guanine nucleotide exchange factor (GEF) 11 [Source:H
5	ARAP2	1.13	2e−06	8e−06	32 x 7	ArfGAP with RhoGAP domain, ankyrin repeat and PH domai
6	ABLIM1	1.12	2e−06	1e−05	32 x 5	actin binding LIM protein 1 [Source:HGNC Symbol;Acc:HGN
7	KLHDC10	1.1	3e−06	3e−05	33 x 9	kelch domain containing 10 [Source:HGNC Symbol;Acc:HGN
8	NUFIP1	1.06	8e−06	3e−05	34 x 6	nuclear fragile X mental retardation protein interacting protein
9	ZNF335	1.05	1e−05	3e−05	34 x 7	zinc finger protein 335 [Source:HGNC Symbol;Acc:HGNC:15
10	SRGAP1	1.04	1e−05	3e−05	32 x 8	SLIT−ROBO Rho GTPase activating protein 1 [Source:HGNC
11	ATP4A	1.03	1e−05	3e−05	32 x 6	ATPase, H+/K+ exchanging, alpha polypeptide [Source:HGN
12	APITD1−COR	1.03	1e−05	6e−05	34 x 7	APITD1−CORT readthrough [Source:HGNC Symbol;Acc:HG
13	BCL7A	1.01	2e−05	1e−04	33 x 5	B−cell CLL/lymphoma 7A [Source:HGNC Symbol;Acc:HGNC
14	ZBED5	−0.99	3e−05	1e−04	33 x 8	zinc finger, BED−type containing 5 [Source:HGNC Symbol;A
15	C6orf203	0.98	4e−05	3e−04	34 x 7	chromosome 6 open reading frame 203 [Source:HGNC Sym
16	PLCB4	0.95	6e−05	1e−03	33 x 9	phospholipase C, beta 4 [Source:HGNC Symbol;Acc:HGNC:
17	CEP135	0.88	2e−04	1e−03	33 x 9	centrosomal protein 135kDa [Source:HGNC Symbol;Acc:HG
18	S100PBP	0.86	3e−04	1e−03	33 x 8	S100P binding protein [Source:HGNC Symbol;Acc:HGNC:25
19	PHC2	0.85	3e−04	3e−03	34 x 6	polyhomeotic homolog 2 (Drosophila) [Source:HGNC Symbol
20	DDX51	0.81	6e−04	3e−03	32 x 8	DEAD (Asp−Glu−Ala−Asp) box polypeptide 51 [Source:HGN

p−values



E6_mel

Local Summary

%DE = 0.7

metagenes = 46

genes = 433

genes in genesets = 431

genes with fdr < 0.1 = 211 (181 + / 30 −)

genes with fdr < 0.05 = 181 (154 + / 27 −)

genes with fdr < 0.01 = 131 (111 + / 20 −)

<r> metagenes = 0.8

<r> genes = 0.08

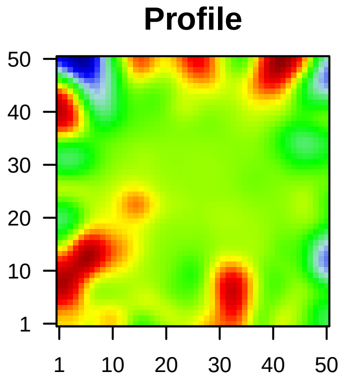
<FC> = 0.32

<shrinkage−t> = 5.07

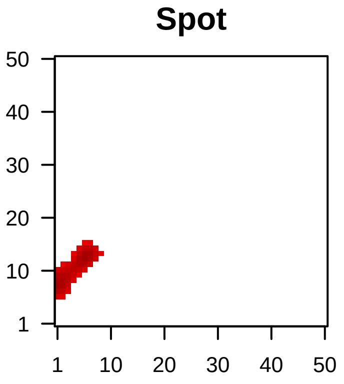
<p−value> = 0.01

<fdr> = 0.55

Profile



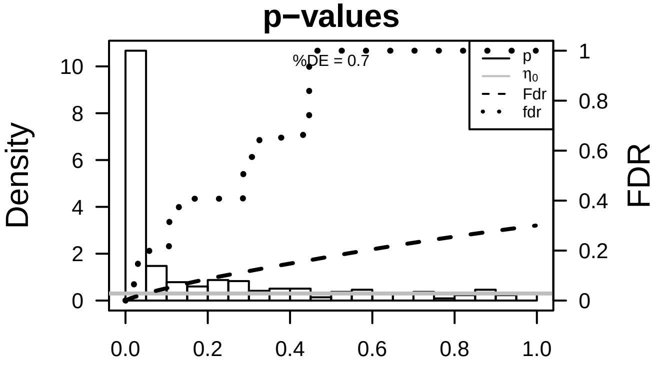
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	BLVRB	−1.37	2e−16	3e−14	1 x 6	biliverdin reductase B [Source:HGNC Symbol;Acc:HGNC:10
2	TRDMT1	1.73	3e−13	3e−10	7 x 14	tRNA aspartic acid methyltransferase 1 [Source:HGNC Symb
3	FUBP3	1.66	3e−12	1e−09	1 x 8	far upstream element (FUSE) binding protein 3 [Source:HGN
4	USP54	1.61	1e−11	1e−09	4 x 11	ubiquitin specific peptidase 54 [Source:HGNC Symbol;Acc:H
5	CTC−534A2.2	1.57	4e−11	1e−09	3 x 8	
6	DGKI	1.57	4e−11	1e−09	1 x 11	diacylglycerol kinase, iota [Source:HGNC Symbol;Acc:HGNC
7	SCRN2	1.57	4e−11	2e−08	5 x 15	secernin 2 [Source:HGNC Symbol;Acc:HGNC:30381]
8	TMEM150A	1.5	2e−10	2e−08	4 x 11	transmembrane protein 150A [Source:HGNC Symbol;Acc:HG
9	CCSER1	1.48	5e−10	2e−08	8 x 13	coiled−coil serine−rich protein 1 [Source:HGNC Symbol;Acc:
10	ERCC6L2	1.47	5e−10	2e−08	1 x 7	excision repair cross−complementation group 6−like 2 [Sourc
11	PEX1	1.46	7e−10	6e−08	1 x 7	peroxisomal biogenesis factor 1 [Source:HGNC Symbol;Acc:
12	ZZZ3	−1.13	1e−09	6e−08	1 x 11	zinc finger, ZZ−type containing 3 [Source:HGNC Symbol;Acc
13	SLC5A10	1.43	2e−09	9e−08	2 x 10	solute carrier family 5 (sodium/sugar cotransporter), member
14	GEMIN8	1.42	2e−09	2e−07	1 x 7	gem (nuclear organelle) associated protein 8 [Source:HGNC
15	SLC33A1	1.4	3e−09	7e−07	5 x 12	solute carrier family 33 (acetyl−CoA transporter), member 1 [
16	C1orf145	1.34	2e−08	7e−07	1 x 6	chromosome 1 open reading frame 145 [Source:HGNC Sym
17	CLYBL	1.34	2e−08	7e−07	5 x 15	citrate lyase beta like [Source:HGNC Symbol;Acc:HGNC:183
18	ATP6V0A1	0.99	2e−08	1e−06	1 x 10	ATPase, H+ transporting, lysosomal V0 subunit a1 [Source:H
19	PPARGC1A	−1.15	5e−08	1e−06	1 x 10	peroxisome proliferator−activated receptor gamma, coactivat
20	TACR2	1.29	6e−08	1e−06	7 x 13	tachykinin receptor 2 [Source:HGNC Symbol;Acc:HGNC:115

p−values



E6_mel

Local Summary

%DE = 0.88

metagenes = 8

genes = 142

genes in genesets = 141

genes with fdr < 0.1 = 107 (86 + / 21 −)

genes with fdr < 0.05 = 97 (77 + / 20 −)

genes with fdr < 0.01 = 69 (56 + / 13 −)

<r> metagenes = 0.99

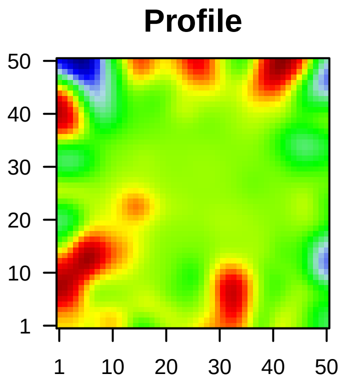
<r> genes = 0.19

<FC> = 0.3

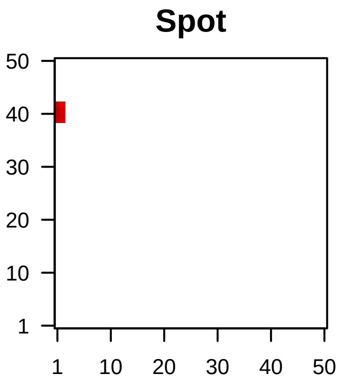
<shrinkage−t> = 5.73

<p−value> = 0

<fdr> = 0.44



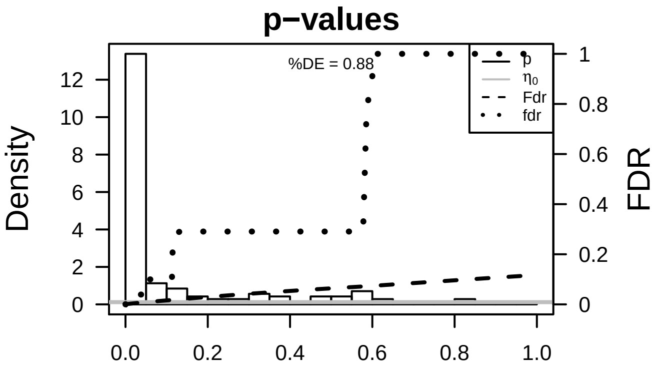
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ZNF577	1.94	2e−16	4e−15	2 x 39	zinc finger protein 577 [Source:HGNC Symbol;Acc:HGNC:28
2	MBP	0.57	3e−09	3e−08	1 x 42	myelin basic protein [Source:HGNC Symbol;Acc:HGNC:6925
3	MARS2	1.4	4e−09	1e−06	1 x 39	methionyl−tRNA synthetase 2, mitochondrial [Source:HGNC
4	EXOC3	0.52	8e−08	1e−06	1 x 42	exocyst complex component 3 [Source:HGNC Symbol;Acc:H
5	PLP1	0.5	2e−07	1e−05	1 x 42	proteolipid protein 1 [Source:HGNC Symbol;Acc:HGNC:9086
6	HDAC3	−1.14	1e−06	3e−05	1 x 41	histone deacetylase 3 [Source:HGNC Symbol;Acc:HGNC:48
7	SNAP29	1.1	4e−06	3e−05	1 x 40	synaptosomal−associated protein, 29kDa [Source:HGNC Sy
8	MITF	0.49	6e−06	3e−05	1 x 41	microphthalmia−associated transcription factor [Source:HGN
9	EPT1	1.07	6e−06	3e−05	1 x 39	ethanolaminephosphotransferase 1 [Source:HGNC Symbol;A
10	CITED1	0.6	8e−06	6e−05	1 x 41	Cbp/p300−interacting transactivator, with Glu/Asp−rich carbo
11	WIPF3	1.02	2e−05	6e−05	1 x 41	WAS/WASL interacting protein family, member 3 [Source:HG
12	FASTK	−1.01	2e−05	6e−05	1 x 39	Fas−activated serine/threonine kinase [Source:HGNC Symbo
13	SPG21	0.99	2e−05	6e−05	1 x 39	spastic paraplegia 21 (autosomal recessive, Mast syndrome)
14	MTAP	1	2e−05	6e−05	1 x 40	methylthioadenosine phosphorylase [Source:HGNC Symbol;
15	RBPMS2	1	2e−05	6e−05	1 x 42	RNA binding protein with multiple splicing 2 [Source:HGNC S
16	SMIM8	−0.99	3e−05	6e−05	1 x 39	small integral membrane protein 8 [Source:HGNC Symbol;Ac
17	PTDSS1	0.97	4e−05	6e−05	1 x 39	phosphatidylserine synthase 1 [Source:HGNC Symbol;Acc:H
18	MRPL40	0.98	4e−05	6e−05	1 x 40	mitochondrial ribosomal protein L40 [Source:HGNC Symbol;
19	TMC6	0.95	4e−05	6e−05	1 x 42	transmembrane channel−like 6 [Source:HGNC Symbol;Acc:H
20	STX7	0.66	5e−05	6e−05	1 x 42	syntaxin 7 [Source:HGNC Symbol;Acc:HGNC:11442]



p−values

E6_mel

Local Summary

%DE = 0.73

metagenes = 22

genes = 202

genes in genesets = 202

genes with fdr < 0.1 = 115 (95 + / 20 −)

genes with fdr < 0.05 = 113 (94 + / 19 −)

genes with fdr < 0.01 = 75 (65 + / 10 −)

<r> metagenes = 0.92

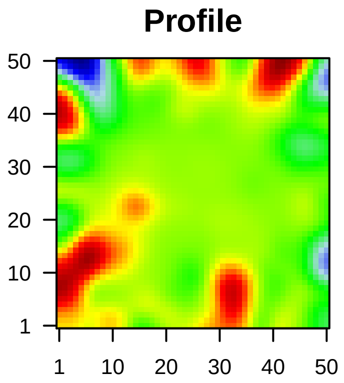
<r> genes = 0.09

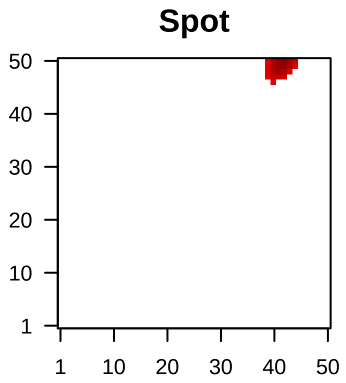
<FC> = 0.35

<shrinkage−t> = 5.68

<p−value> = 0

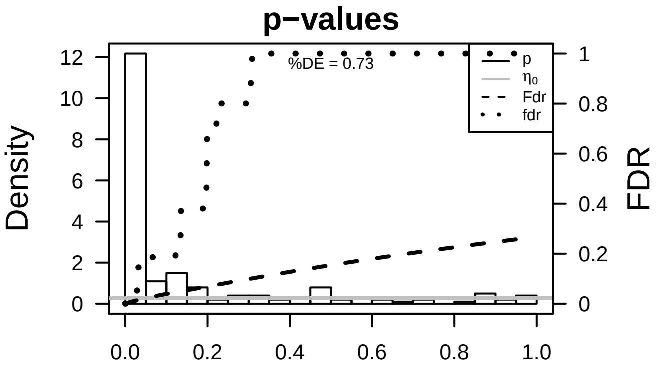
<fdr> = 0.48


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ITLN2	1.83	2e−14	2e−10	39 x 48	intelectin 2 [Source:HGNC Symbol;Acc:HGNC:20599]
2	GULP1	1.65	4e−12	1e−09	42 x 50	GULP, engulfment adaptor PTB domain containing 1 [Source:
3	AP4M1	1.57	4e−11	1e−09	44 x 50	adaptor−related protein complex 4, mu 1 subunit [Source:HG
4	FAM114A2	1.56	5e−11	7e−09	41 x 50	family with sequence similarity 114, member A2 [Source:HG
5	PDLIM2	1.51	2e−10	2e−07	42 x 50	PDZ and LIM domain 2 (mystique) [Source:HGNC Symbol;A
6	MRPL2	−1.28	4e−09	2e−07	40 x 50	mitochondrial ribosomal protein L2 [Source:HGNC Symbol;A
7	FUCA1	1.37	7e−09	1e−06	41 x 50	fucosidase, alpha−L− 1, tissue [Source:HGNC Symbol;Acc:H
8	SNAPC2	1.32	3e−08	1e−06	41 x 48	small nuclear RNA activating complex, polypeptide 2, 45kDa
9	CCDC93	1.29	6e−08	1e−06	42 x 50	coiled−coil domain containing 93 [Source:HGNC Symbol;Acc
10	SPA17	1.27	9e−08	1e−06	42 x 47	sperm autoantigenic protein 17 [Source:HGNC Symbol;Acc:
11	TSGA10	1.27	1e−07	4e−06	41 x 50	testis specific, 10 [Source:HGNC Symbol;Acc:HGNC:14927]
12	EMC1	1.23	2e−07	4e−06	41 x 50	ER membrane protein complex subunit 1 [Source:HGNC Sy
13	C1orf131	−1.17	3e−07	5e−06	40 x 50	chromosome 1 open reading frame 131 [Source:HGNC Sym
14	PARP11	1.2	5e−07	5e−06	43 x 50	poly (ADP−ribose) polymerase family, member 11 [Source:H
15	SDR39U1	1.19	5e−07	5e−06	43 x 50	short chain dehydrogenase/reductase family 39U, member 1
16	TRAF5	1.19	5e−07	4e−05	39 x 50	TNF receptor−associated factor 5 [Source:HGNC Symbol;Ac
17	SIL1	1.14	2e−06	4e−05	43 x 50	SIL1 nucleotide exchange factor [Source:HGNC Symbol;Acc:
18	SNAI1	1.13	2e−06	4e−05	39 x 50	snail family zinc finger 1 [Source:HGNC Symbol;Acc:HGNC:1
19	TRMT61B	1.1	3e−06	4e−05	41 x 50	tRNA methyltransferase 61B [Source:HGNC Symbol;Acc:HG
20	PEX6	1.09	4e−06	4e−05	41 x 47	peroxisomal biogenesis factor 6 [Source:HGNC Symbol;Acc:


p−values

E6_mel

Local Summary

%DE = 0.82

metagenes = 22

genes = 318

genes in genesets = 318

genes with fdr < 0.1 = 187 (13 + / 174 −)

genes with fdr < 0.05 = 183 (13 + / 170 −)

genes with fdr < 0.01 = 109 (9 + / 100 −)

<r> metagenes = 0.95

<r> genes = 0.33

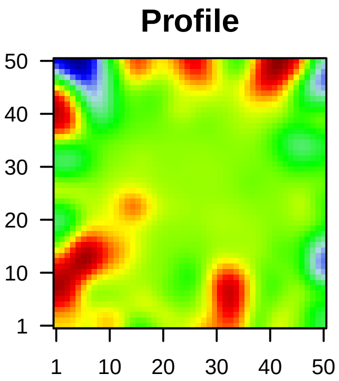
<FC> = −0.44

<shrinkage−t> = −7.11

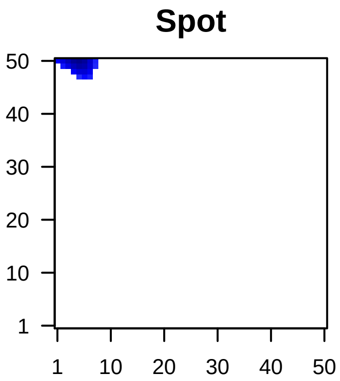
<p−value> = 0.01

<fdr> = 0.55

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ACTL6A	−1.27	2e−16	3e−15	4 x 50	actin−like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
2	CKS2	−1.65	2e−16	3e−15	5 x 50	CDC28 protein kinase regulatory subunit 2 [Source:HGNC Sy
3	HAT1	−1.6	2e−16	3e−15	1 x 50	histone acetyltransferase 1 [Source:HGNC Symbol;Acc:HGN
4	NUP85	−1.56	2e−16	3e−15	1 x 50	nucleoporin 85kDa [Source:HGNC Symbol;Acc:HGNC:8734]
5	TMEM106C	−2.07	2e−16	3e−15	5 x 48	transmembrane protein 106C [Source:HGNC Symbol;Acc:HG
6	SMC4	−1.49	4e−14	5e−10	5 x 50	structural maintenance of chromosomes 4 [Source:HGNC Sy
7	NUP54	−1.41	1e−11	5e−10	1 x 50	nucleoporin 54kDa [Source:HGNC Symbol;Acc:HGNC:17359
8	SKA2	−1.12	2e−11	2e−09	7 x 47	spindle and kinetochore associated complex subunit 2 [Sourc
9	TYMS	−1.37	5e−11	9e−08	3 x 50	thymidylate synthetase [Source:HGNC Symbol;Acc:HGNC:1
10	EMP2	−1.31	2e−09	1e−07	2 x 50	epithelial membrane protein 2 [Source:HGNC Symbol;Acc:H
11	HMGB2	−1.28	3e−09	1e−06	5 x 50	high mobility group box 2 [Source:HGNC Symbol;Acc:HGNC:
12	C19orf48	−1.22	3e−08	1e−06	1 x 50	chromosome 19 open reading frame 48 [Source:HGNC Sym
13	CENPN	−1.21	6e−08	1e−06	4 x 50	centromere protein N [Source:HGNC Symbol;Acc:HGNC:308
14	TUBA1B	−0.52	9e−08	1e−06	6 x 48	tubulin, alpha 1b [Source:HGNC Symbol;Acc:HGNC:18809]
15	PRC1	−1.2	1e−07	1e−06	5 x 50	protein regulator of cytokinesis 1 [Source:HGNC Symbol;Acc:
16	RFC4	−1.2	1e−07	2e−06	1 x 50	replication factor C (activator 1) 4, 37kDa [Source:HGNC Sy
17	MCM4	0.99	1e−07	1e−05	1 x 50	minichromosome maintenance complex component 4 [Sourc
18	SEPT10	−1.18	3e−07	2e−05	7 x 48	septin 10 [Source:HGNC Symbol;Acc:HGNC:14349]
19	STIL	1.17	8e−07	2e−05	5 x 47	SCL/TAL1 interrupting locus [Source:HGNC Symbol;Acc:HGN
20	VRK1	−1.13	1e−06	2e−05	3 x 50	vaccinia related kinase 1 [Source:HGNC Symbol;Acc:HGNC:

p−values