E4_mel

Global Summary

%DE = 0.21

genes with fdr < 0.2 = 2486 (1479 + / 1007 −)

genes with fdr < 0.1 = 2026 (1215 + / 811 −)

genes with fdr < 0.05 = 1701 (1039 + / 662 −)

genes with fdr < 0.01 = 1042 (632 + / 410 −)

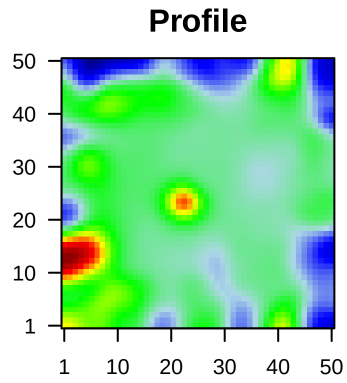
genes in genesets = 14839

<FC> = 0

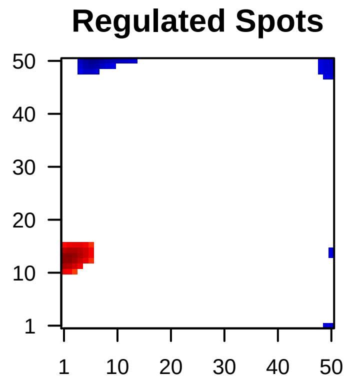
<shrinkage−t> = 0.01

<p−value> = 0.09

<fdr> = 0.79



Profile



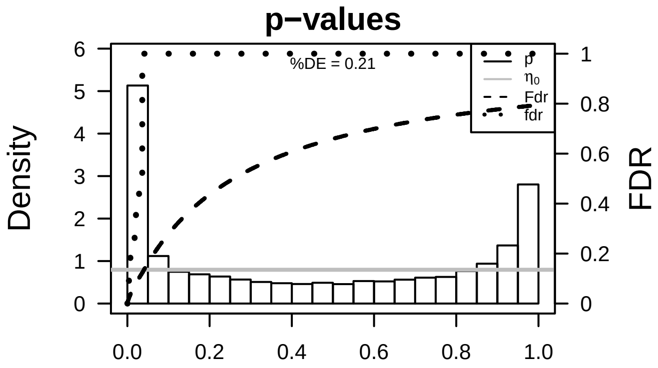
Regulated Spots

Global Genelist

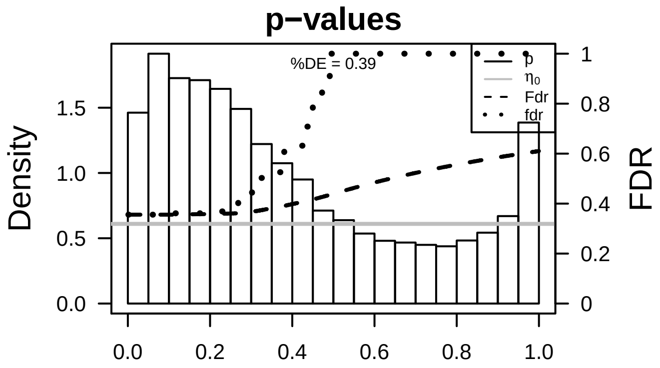
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	BECN1	−1.39	2e−16	1e−13	49 x 15	beclin 1, autophagy related [Source:HGNC Symbol;Acc:HGN
2	CRYAB	−1.82	2e−16	1e−13	50 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
3	DYNC1LI2	−1.82	2e−16	1e−13	27 x 50	dynein, cytoplasmic 1, light intermediate chain 2 [Source:HGI
4	G6PC3	−1.64	2e−16	1e−13	48 x 49	glucose 6 phosphatase, catalytic, 3 [Source:HGNC Symbol;A
5	GOLT1B	−1.61	2e−16	1e−13	47 x 15	golgi transport 1B [Source:HGNC Symbol;Acc:HGNC:20175]
6	HAUS1	−1.62	2e−16	1e−13	1 x 50	HAUS augmin−like complex, subunit 1 [Source:HGNC Symbo
7	HSD17B4	−1.63	2e−16	1e−13	11 x 50	hydroxysteroid (17−beta) dehydrogenase 4 [Source:HGNC S
8	IDH3A	−1.52	2e−16	1e−13	1 x 42	isocitrate dehydrogenase 3 (NAD+) alpha [Source:HGNC Syr
9	LSM4	−1.87	2e−16	1e−13	4 x 37	LSM4 homolog, U6 small nuclear RNA associated (S. cerevis
10	MRPS12	−1.6	2e−16	1e−13	48 x 50	mitochondrial ribosomal protein S12 [Source:HGNC Symbol;
11	NEMF	−1.78	2e−16	1e−13	47 x 13	nuclear export mediator factor [Source:HGNC Symbol;Acc:H
12	PCNA	−1.64	2e−16	1e−13	2 x 50	proliferating cell nuclear antigen [Source:HGNC Symbol;Acc:
13	PDCD10	−1.66	2e−16	1e−13	13 x 50	programmed cell death 10 [Source:HGNC Symbol;Acc:HGN
14	POP4	−1.63	2e−16	1e−13	15 x 50	processing of precursor 4, ribonuclease P/MRP subunit (S. c
15	PSMA5	−2.05	2e−16	1e−13	48 x 50	proteasome (prosome, macropain) subunit, alpha type, 5 [So
16	PSMD9	−1.64	2e−16	1e−13	50 x 14	proteasome (prosome, macropain) 26S subunit, non−ATPase
17	PTGES3	−1.42	2e−16	1e−13	21 x 48	prostaglandin E synthase 3 (cytosolic) [Source:HGNC Symbo
18	PTRHD1	−1.63	2e−16	1e−13	5 x 41	peptidyl−tRNA hydrolase domain containing 1 [Source:HGNC
19	PTTG1	−1.88	2e−16	1e−13	7 x 50	pituitary tumor−transforming 1 [Source:HGNC Symbol;Acc:H
20	RNF13	−1.79	2e−16	1e−13	50 x 7	ring finger protein 13 [Source:HGNC Symbol;Acc:HGNC:100

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	4.64	0.005	20	GSEA C2	BIOCARTA_ATM_PATHWAY
2	4.09	0.007	21	GSEA C2	REACTOME_MITOCHONDRIAL_TRNA_AMINOACYLATION
3	4.03	0.007	157	GSEA C2	KEGG_HUNTINGTONS_DISEASE
4	3.99	0.008	101	BP	RNA processing
5	3.96	0.008	42	GSEA C2	REACTOME_TRNA_AMINOACYLATION
6	3.88	0.008	157	GSEA C2	FERNANDEZ_BOUND_BY_MYC
7	3.88	0.008	15	BP	response to exogenous dsRNA
8	3.85	0.008	318	GSEA C2	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_UP
9	3.85	0.008	558	Chr	Chr 4
10	3.74	0.009	12	GSEA C2	ZEMBUTSU_SENSITIVITY_TO_MITOMYCIN
11	3.59	0.011	109	GSEA C2	NIKOLSKY_BREAST_CANCER_8Q12_Q22_AMPLICON
12	3.57	0.011	142	GSEA C2	KEGG_ALZHEIMERS_DISEASE
13	3.56	0.011	9	GSEA C2	DORN_ADENOVIRUS_INFECTION_24HR_UP
14	3.51	0.011	44	BP	tRNA aminoacylation for protein translation
15	3.49	0.012	41	GSEA C2	KEGG_AMINOACYL_TRNA_BIOSYNTHESIS
16	3.47	0.012	14	Colon Cancer	Hewish_dMMR−secondary−mutations_DNA−repair
17	3.33	0.013	78	GSEA C2	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_S
18	3.26	0.014	62	BP	canonical Wnt signaling pathway
19	3.24	0.015	281	GSEA C2	KEGG_PATHWAYS_IN_CANCER
20	3.17	0.015	140	GSEA C2	ONDER_CDH1_TARGETS_1_DN
Underexpressed					
1	−6.53	0.001	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
2	−6.24	0.002	145	GSEA C2	CHANG_CYCLING_GENES
3	−5.38	0.003	6	GSEA C2	CROSBY_E2F4_TARGETS
4	−5.34	0.003	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
5	−5.33	0.003	52	GSEA C2	REACTOME_CDT1_ASSOCIATION_WITH_THE_CDC6_ORC_OF
6	−5.08	0.003	18	CC	proteasome core complex
7	−5.07	0.003	78	BP	anaphase−promoting complex−dependent proteasomal ubiquitin−c
8	−5.03	0.003	39	GSEA C2	BURTON_ADIPOGENESIS_PEAK_AT_24HR
9	−5.03	0.003	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
10	−5.01	0.004	63	GSEA C2	REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_M
11	−4.97	0.004	45	GSEA C2	PID_PLK1_PATHWAY
12	−4.94	0.004	75	GSEA C2	REACTOME_REGULATION_OF_MITOTIC_CELL_CYCLE
13	−4.88	0.004	32	BP	proteolysis involved in cellular protein catabolic process
14	−4.86	0.004	18	MF	threonine−type endopeptidase activity
15	−4.84	0.004	388	GSEA C2	REACTOME_CELL_CYCLE
16	−4.74	0.004	412	BP	mitotic cell cycle
17	−4.71	0.004	170	GSEA C2	WHITFIELD_CELL_CYCLE_G2
18	−4.6	0.005	436	GSEA C2	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
19	−4.59	0.005	301	GSEA C2	REACTOME_CELL_CYCLE_MITOTIC
20	−4.55	0.005	62	GSEA C2	REACTOME_APC_C_CDH1_MEDIATED_DEGRADATION_OF_C



p−values



p−values

E4_mel

Local Summary

%DE = 0.73

metagenes = 31

genes = 324

genes in genesets = 322

genes with fdr < 0.1 = 134 (121 + / 13 −)

genes with fdr < 0.05 = 128 (116 + / 12 −)

genes with fdr < 0.01 = 99 (92 + / 7 −)

<r> metagenes = 0.89

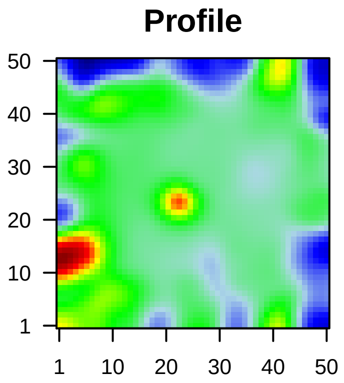
<r> genes = 0.1

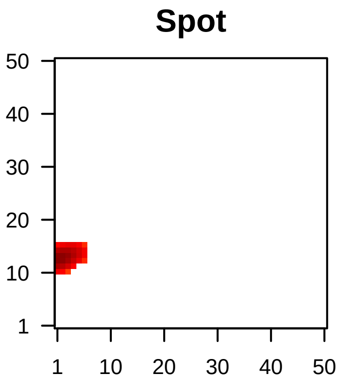
<FC> = 0.35

<shrinkage−t> = 5.74

<p−value> = 0.01

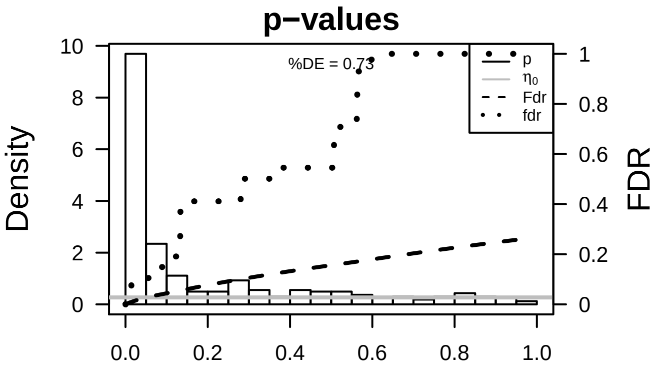
<fdr> = 0.59





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	SLC26A4	1.7	8e−12	5e−09	2 x 15	solute carrier family 26 (anion exchanger), member 4 [Source
2	PRKCH	1.63	6e−11	2e−07	1 x 12	protein kinase C, eta [Source:HGNC Symbol;Acc:HGNC:940
3	CYP7B1	1.48	3e−09	2e−07	2 x 14	cytochrome P450, family 7, subfamily B, polypeptide 1 [Sourc
4	PMF1−BGLA	1.46	4e−09	2e−07	3 x 16	PMF1−BGLAP readthrough [Source:HGNC Symbol;Acc:HG
5	ESRP1	1.45	6e−09	5e−07	1 x 12	epithelial splicing regulatory protein 1 [Source:HGNC Symbol
6	HMGCR	−1.06	2e−08	5e−07	2 x 11	3−hydroxy−3−methylglutaryl−CoA reductase [Source:HGNC
7	ZNF721	1.4	2e−08	8e−07	5 x 15	zinc finger protein 721 [Source:HGNC Symbol;Acc:HGNC:29
8	KIAA1551	1.38	3e−08	8e−07	2 x 13	KIAA1551 [Source:HGNC Symbol;Acc:HGNC:25559]
9	HDHD3	1.36	5e−08	8e−07	1 x 13	haloacid dehalogenase−like hydrolase domain containing 3 [
10	GDPD5	1.36	5e−08	8e−07	1 x 12	glycerophosphodiester phosphodiesterase domain containin
11	CNTLN	1.35	5e−08	2e−06	6 x 14	centlein, centrosomal protein [Source:HGNC Symbol;Acc:HG
12	STAT6	1.34	8e−08	5e−06	3 x 13	signal transducer and activator of transcription 6, interleukin−
13	CHST12	1.3	2e−07	5e−06	4 x 15	carbohydrate (chondroitin 4) sulfotransferase 12 [Source:HG
14	GOSR2	−1.22	2e−07	7e−06	5 x 15	golgi SNAP receptor complex member 2 [Source:HGNC Sym
15	ZNF527	1.28	3e−07	7e−06	4 x 14	zinc finger protein 527 [Source:HGNC Symbol;Acc:HGNC:29
16	SLC7A6	1.26	4e−07	7e−06	1 x 11	solute carrier family 7 (amino acid transporter light chain, y+L
17	RMDN3	1.26	4e−07	7e−06	3 x 11	regulator of microtubule dynamics 3 [Source:HGNC Symbol;
18	NFKB1	1.25	5e−07	5e−05	3 x 15	nuclear factor of kappa light polypeptide gene enhancer in B−
19	SMAD7	1.21	1e−06	6e−05	6 x 15	SMAD family member 7 [Source:HGNC Symbol;Acc:HGNC:6
20	BBS5	1.17	3e−06	6e−05	1 x 11	Bardet−Biedl syndrome 5 [Source:HGNC Symbol;Acc:HGNC



E4_mel

Local Summary

%DE = 0.92

metagenes = 2

genes = 111

genes in genesets = 111

genes with fdr < 0.1 = 88 (26 + / 62 −)

genes with fdr < 0.05 = 87 (26 + / 61 −)

genes with fdr < 0.01 = 20 (9 + / 11 −)

<r> metagenes = 1

<r> genes = 0.27

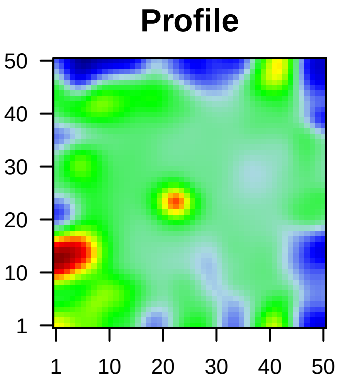
<FC> = −0.16

<shrinkage−t> = −2.49

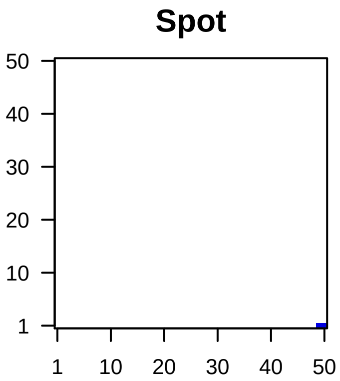
<p−value> = 0.02

<fdr> = 0.68

Profile



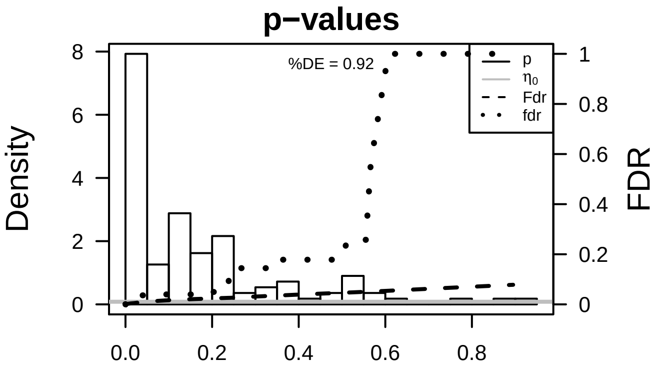
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CRYAB	−1.82	2e−16	2e−15	50 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
2	FABP3	−1.44	2e−11	6e−07	50 x 1	fatty acid binding protein 3, muscle and heart [Source:HGNC
3	FKBP7	1.34	7e−08	4e−06	50 x 1	FK506 binding protein 7 [Source:HGNC Symbol;Acc:HGNC:
4	CD55	−1.19	5e−07	4e−06	50 x 1	CD55 molecule, decay accelerating factor for complement (C
5	MATN2	1.22	9e−07	8e−06	50 x 1	matrilin 2 [Source:HGNC Symbol;Acc:HGNC:6908]
6	FAM98A	−1.16	2e−06	6e−05	49 x 1	family with sequence similarity 98, member A [Source:HGNC
7	RGS2	1.11	8e−06	1e−04	49 x 1	regulator of G−protein signaling 2 [Source:HGNC Symbol;Acc
8	LIMCH1	1.05	3e−05	1e−04	50 x 1	LIM and calponin homology domains 1 [Source:HGNC Symb
9	RND3	1.03	4e−05	1e−04	50 x 1	Rho family GTPase 3 [Source:HGNC Symbol;Acc:HGNC:671
10	RIN2	1.02	4e−05	1e−04	50 x 1	Ras and Rab interactor 2 [Source:HGNC Symbol;Acc:HGNC:
11	CTDSPL	1	5e−05	6e−04	49 x 1	CTD (carboxy−terminal domain, RNA polymerase II, polypept
12	LIMA1	−0.95	1e−04	6e−04	49 x 1	LIM domain and actin binding 1 [Source:HGNC Symbol;Acc:
13	DLGAP4	0.93	2e−04	2e−03	50 x 1	discs, large (Drosophila) homolog−associated protein 4 [Sour
14	TNFRSF12A	−0.89	4e−04	2e−03	50 x 1	tumor necrosis factor receptor superfamily, member 12A [Sou
15	PELO	−0.81	1e−03	2e−03	50 x 1	pelota homolog (Drosophila) [Source:HGNC Symbol;Acc:HG
16	A2M	−0.8	1e−03	2e−03	50 x 1	alpha−2−macroglobulin [Source:HGNC Symbol;Acc:HGNC:7
17	ABHD4	−0.8	1e−03	2e−03	49 x 1	abhydrolase domain containing 4 [Source:HGNC Symbol;Acc
18	P4HA1	−0.79	2e−03	2e−03	50 x 1	prolyl 4−hydroxylase, alpha polypeptide I [Source:HGNC Sym
19	ARID5B	0.69	2e−03	2e−03	50 x 1	AT rich interactive domain 5B (MRF1−like) [Source:HGNC Sy
20	PDLIM5	−0.77	2e−03	2e−03	50 x 1	PDZ and LIM domain 5 [Source:HGNC Symbol;Acc:HGNC:1

p−values



E4_mel

Local Summary

%DE = 0.73

metagenes = 2

genes = 38

genes in genesets = 38

genes with fdr < 0.1 = 21 (6 + / 15 −)

genes with fdr < 0.05 = 17 (6 + / 11 −)

genes with fdr < 0.01 = 13 (3 + / 10 −)

<r> metagenes = 0.99

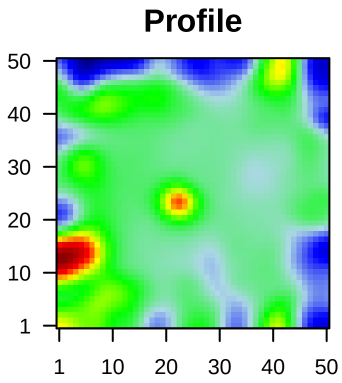
<r> genes = 0.12

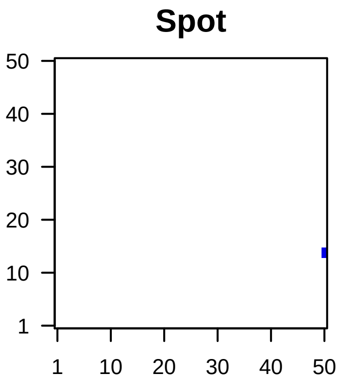
<FC> = −0.25

<shrinkage−t> = −4.29

<p−value> = 0

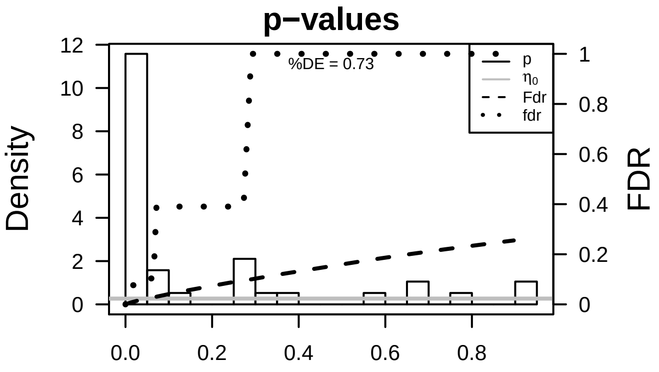
<fdr> = 0.52


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	PSMD9	−1.64	2e−16	2e−15	50 x 14	proteasome (prosome, macropain) 26S subunit, non−ATPase
2	NME7	−1.45	1e−11	9e−09	50 x 14	NME/NM23 family member 7 [Source:HGNC Symbol;Acc:HG
3	COMT	−1.36	9e−10	6e−08	50 x 15	catechol−O−methyltransferase [Source:HGNC Symbol;Acc:H
4	NADSYN1	−1.32	7e−09	2e−06	50 x 15	NAD synthetase 1 [Source:HGNC Symbol;Acc:HGNC:29832]
5	ZCCHC11	−1.22	2e−07	3e−05	50 x 15	zinc finger, CCHC domain containing 11 [Source:HGNC Sym
6	ZMYM1	1.16	3e−06	5e−05	50 x 15	zinc finger, MYM−type 1 [Source:HGNC Symbol;Acc:HGNC:
7	USP32	−1.02	8e−06	3e−04	50 x 15	ubiquitin specific peptidase 32 [Source:HGNC Symbol;Acc:H
8	GCLC	1.02	4e−05	6e−04	50 x 14	glutamate−cysteine ligase, catalytic subunit [Source:HGNC S
9	CHD7	0.96	1e−04	1e−03	50 x 14	chromodomain helicase DNA binding protein 7 [Source:HGN
10	RNF216	−0.88	2e−04	3e−03	50 x 14	ring finger protein 216 [Source:HGNC Symbol;Acc:HGNC:21
11	ZNF226	−0.83	9e−04	3e−03	50 x 14	zinc finger protein 226 [Source:HGNC Symbol;Acc:HGNC:13
12	TBC1D23	−0.81	1e−03	3e−03	50 x 15	TBC1 domain family, member 23 [Source:HGNC Symbol;Acc
13	STOM	−0.62	1e−03	3e−03	50 x 14	stomatin [Source:HGNC Symbol;Acc:HGNC:3383]
14	TTC33	−0.79	1e−03	2e−02	50 x 14	tetratricopeptide repeat domain 33 [Source:HGNC Symbol;A
15	RRM2B	0.74	3e−03	2e−02	50 x 15	ribonucleotide reductase M2 B (TP53 inducible) [Source:HG
16	CERS5	0.66	5e−03	5e−02	50 x 15	ceramide synthase 5 [Source:HGNC Symbol;Acc:HGNC:237
17	XPA	0.64	1e−02	5e−02	50 x 14	xeroderma pigmentosum, complementation group A [Source:
18	FAM103A1	−0.61	1e−02	8e−02	50 x 14	family with sequence similarity 103, member A1 [Source:HG
19	PAPOLG	−0.53	3e−02	8e−02	50 x 15	poly(A) polymerase gamma [Source:HGNC Symbol;Acc:HG
20	ARHGEF7	−0.53	3e−02	8e−02	50 x 15	Rho guanine nucleotide exchange factor (GEF) 7 [Source:HG


p−values

E4_mel

Local Summary

%DE = 0.72

metagenes = 11

genes = 191

genes in genesets = 191

genes with fdr < 0.1 = 94 (26 + / 68 −)

genes with fdr < 0.05 = 70 (19 + / 51 −)

genes with fdr < 0.01 = 60 (17 + / 43 −)

<r> metagenes = 0.97

<r> genes = 0.09

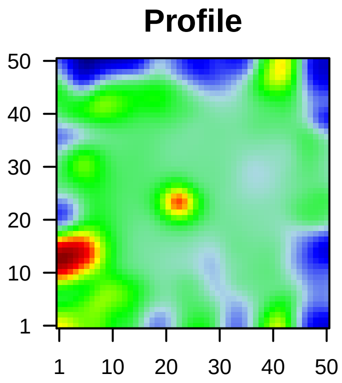
<FC> = −0.2

<shrinkage−t> = −3.59

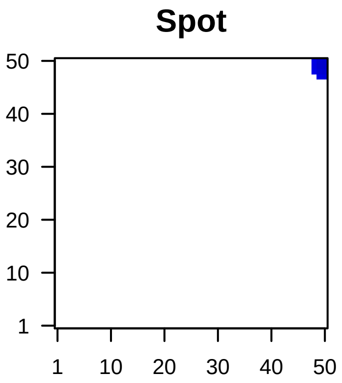
<p−value> = 0.01

<fdr> = 0.58

Profile



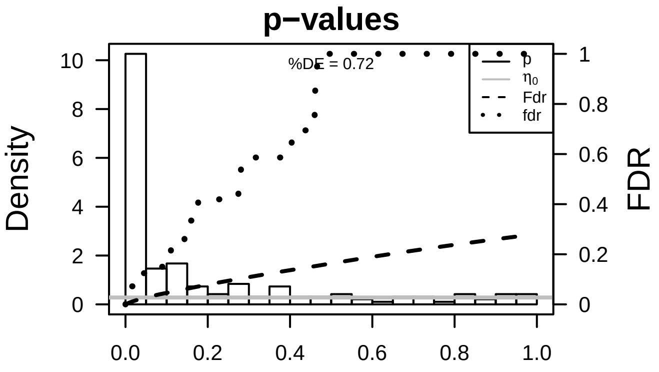
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	G6PC3	−1.64	2e−16	4e−15	48 x 49	glucose 6 phosphatase, catalytic, 3 [Source:HGNC Symbol;A
2	MRPS12	−1.6	2e−16	4e−15	48 x 50	mitochondrial ribosomal protein S12 [Source:HGNC Symbol;
3	PSMA5	−2.05	2e−16	4e−15	48 x 50	proteasome (prosome, macropain) subunit, alpha type, 5 [Sou
4	PIGP	−1.52	9e−14	3e−12	50 x 50	phosphatidylinositol glycan anchor biosynthesis, class P [Sou
5	LUZP6	1.84	1e−13	2e−10	50 x 49	leucine zipper protein 6 [Source:HGNC Symbol;Acc:HGNC:3
6	NIP7	−1.46	4e−12	2e−10	50 x 50	NIP7, nucleolar pre−rRNA processing protein [Source:HGNC
7	ITIH3	1.71	7e−12	2e−10	50 x 50	inter−alpha−trypsin inhibitor heavy chain 3 [Source:HGNC Sy
8	UGP2	−1.2	1e−11	1e−08	50 x 50	UDP−glucose pyrophosphorylase 2 [Source:HGNC Symbol;
9	SDF2	−1.16	2e−10	6e−08	48 x 50	stromal cell−derived factor 2 [Source:HGNC Symbol;Acc:HG
10	BSCL2	−0.83	1e−09	2e−07	50 x 50	Berardinelli−Seip congenital lipodystrophy 2 (seipin) [Source:
11	SCFD1	−1.15	6e−09	2e−07	48 x 50	sec1 family domain containing 1 [Source:HGNC Symbol;Acc:
12	IFT52	−1.31	8e−09	5e−06	50 x 47	intraflagellar transport 52 [Source:HGNC Symbol;Acc:HGNC:
13	LGMN	−1.23	2e−07	5e−06	50 x 50	legumain [Source:HGNC Symbol;Acc:HGNC:9472]
14	PROS1	−1.22	2e−07	1e−04	48 x 49	protein S (alpha) [Source:HGNC Symbol;Acc:HGNC:9456]
15	TCTN3	−1.12	5e−06	1e−04	50 x 50	tectonic family member 3 [Source:HGNC Symbol;Acc:HGNC:
16	CDC37	−0.99	7e−06	1e−04	50 x 47	cell division cycle 37 [Source:HGNC Symbol;Acc:HGNC:173
17	NQO1	−0.45	8e−06	2e−04	49 x 50	NAD(P)H dehydrogenase, quinone 1 [Source:HGNC Symbol;
18	CYB561A3	−1.08	1e−05	5e−04	48 x 50	cytochrome b561 family, member A3 [Source:HGNC Symbol;
19	ZBTB21	−1.03	3e−05	5e−04	50 x 50	zinc finger and BTB domain containing 21 [Source:HGNC Sy
20	TMED7	−1.02	4e−05	5e−04	50 x 47	transmembrane emp24 protein transport domain containing 7

p−values



E4_mel

Local Summary

%DE = 0.85

metagenes = 22

genes = 326

genes in genesets = 326

genes with fdr < 0.1 = 198 (50 + / 148 −)

genes with fdr < 0.05 = 178 (47 + / 131 −)

genes with fdr < 0.01 = 92 (27 + / 65 −)

<r> metagenes = 0.92

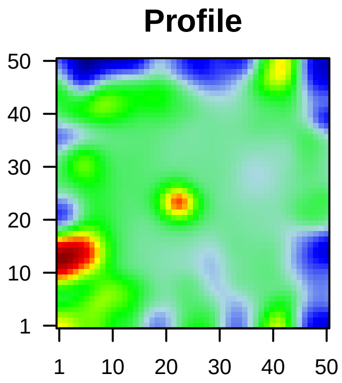
<r> genes = 0.24

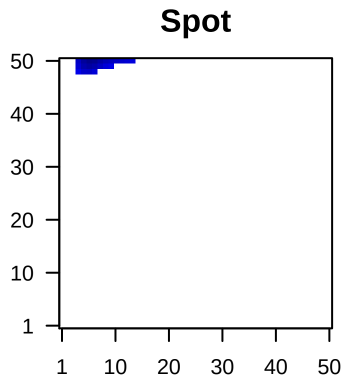
<FC> = −0.26

<shrinkage−t> = −4.02

<p−value> = 0.01

<fdr> = 0.59





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	HSD17B4	−1.63	2e−16	4e−15	11 x 50	hydroxysteroid (17−beta) dehydrogenase 4 [Source:HGNC S
2	PDCD10	−1.66	2e−16	4e−15	13 x 50	programmed cell death 10 [Source:HGNC Symbol;Acc:HGN
3	PTTG1	−1.88	2e−16	4e−15	7 x 50	pituitary tumor−transforming 1 [Source:HGNC Symbol;Acc:H
4	RAB34	−1.44	1e−11	2e−09	13 x 50	RAB34, member RAS oncogene family [Source:HGNC Symb
5	CCDC18	1.63	6e−11	8e−09	7 x 48	coiled−coil domain containing 18 [Source:HGNC Symbol;Acc
6	GPX4	−1.39	2e−10	4e−08	11 x 50	glutathione peroxidase 4 [Source:HGNC Symbol;Acc:HGNC:
7	SMARCC2	−1.36	1e−09	6e−08	11 x 50	SWI/SNF related, matrix associated, actin dependent regulat
8	CASP6	1.49	2e−09	4e−07	13 x 50	caspase 6, apoptosis−related cysteine peptidase [Source:HG
9	HMGB2	−1.28	2e−08	4e−07	5 x 50	high mobility group box 2 [Source:HGNC Symbol;Acc:HGNC:
10	CENPA	1.4	2e−08	9e−07	9 x 49	centromere protein A [Source:HGNC Symbol;Acc:HGNC:185
11	TUBB4B	−1.06	4e−08	2e−06	7 x 50	tubulin, beta 4B class IVb [Source:HGNC Symbol;Acc:HGNC
12	INCENP	1.31	1e−07	2e−06	8 x 50	inner centromere protein antigens 135/155kDa [Source:HGN
13	H2AFZ	0.53	2e−07	2e−06	7 x 48	H2A histone family, member Z [Source:HGNC Symbol;Acc:H
14	FBXL5	−1.22	2e−07	2e−06	11 x 50	F−box and leucine−rich repeat protein 5 [Source:HGNC Sym
15	MNS1	1.29	2e−07	4e−06	7 x 49	meiosis−specific nuclear structural 1 [Source:HGNC Symbol;
16	CAT	−1.19	4e−07	4e−06	14 x 50	catalase [Source:HGNC Symbol;Acc:HGNC:1516]
17	PRC1	−1.2	4e−07	4e−06	5 x 50	protein regulator of cytokinesis 1 [Source:HGNC Symbol;Acc:
18	IMMP1L	−1.19	5e−07	4e−06	10 x 50	IMP1 inner mitochondrial membrane peptidase−like (S. cerev
19	LRR1	1.19	5e−07	2e−05	4 x 49	leucine rich repeat protein 1 [Source:HGNC Symbol;Acc:HG
20	CDKN3	0.91	9e−07	8e−05	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A