A3_mel

Global Summary

%DE = 0.22

genes with fdr < 0.2 = 2748 (1672 + / 1076 −)

genes with fdr < 0.1 = 2401 (1476 + / 925 −)

genes with fdr < 0.05 = 1927 (1190 + / 737 −)

genes with fdr < 0.01 = 1278 (805 + / 473 −)

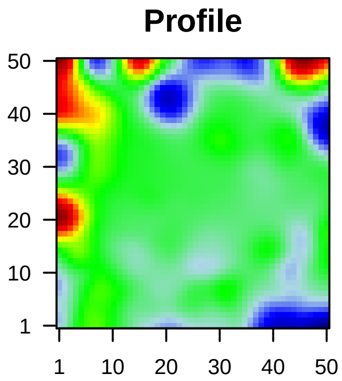
genes in genesets = 14839

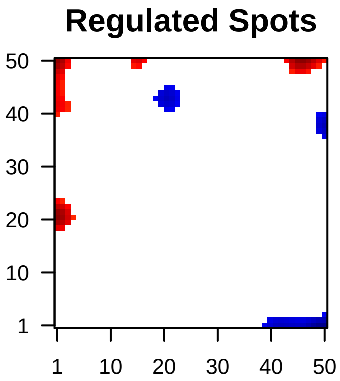
<FC> = 0

<shrinkage−t> = 0.01

<p−value> = 0.07

<fdr> = 0.78



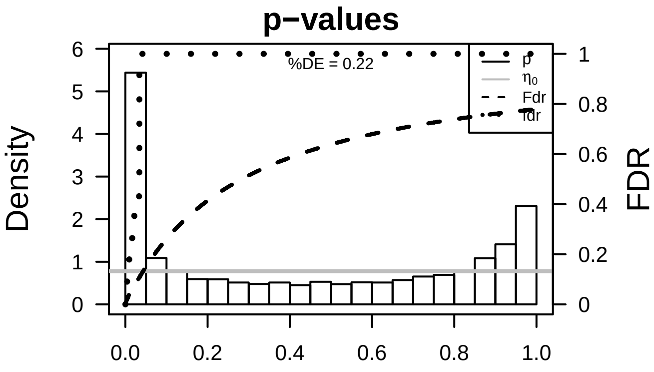


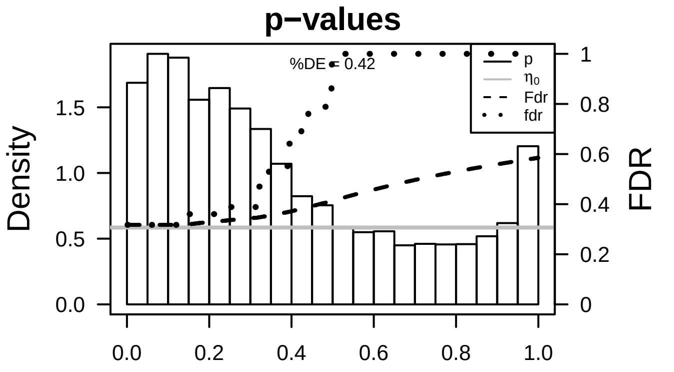
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	C14orf166	−1.15	2e−16	9e−14	32 x 50	chromosome 14 open reading frame 166 [Source:HGNC Syn
2	C1orf198	−1.31	2e−16	9e−14	49 x 1	chromosome 1 open reading frame 198 [Source:HGNC Symb
3	C21orf91	−1.5	2e−16	9e−14	1 x 9	chromosome 21 open reading frame 91 [Source:HGNC Symb
4	CCDC47	−1.64	2e−16	9e−14	3 x 18	coiled−coil domain containing 47 [Source:HGNC Symbol;Acc
5	CDC42BPA	−1.15	2e−16	9e−14	50 x 38	CDC42 binding protein kinase alpha (DMPK−like) [Source:HC
6	CDKN3	−1.65	2e−16	9e−14	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
7	CFL2	−1.33	2e−16	9e−14	50 x 7	cofilin 2 (muscle) [Source:HGNC Symbol;Acc:HGNC:1875]
8	CLDND1	−1.54	2e−16	9e−14	28 x 50	claudin domain containing 1 [Source:HGNC Symbol;Acc:HGN
9	COPZ1	−1.68	2e−16	9e−14	46 x 45	coatomer protein complex, subunit zeta 1 [Source:HGNC Syn
10	DCT	−1.55	2e−16	9e−14	1 x 11	dopachrome tautomerase [Source:HGNC Symbol;Acc:HGNC
11	GLB1	−1.63	2e−16	9e−14	40 x 50	galactosidase, beta 1 [Source:HGNC Symbol;Acc:HGNC:429
12	HERPUD1	−1.23	2e−16	9e−14	50 x 42	homocysteine−inducible, endoplasmic reticulum stress−induc
13	HSPA5	−1.75	2e−16	9e−14	11 x 1	heat shock 70kDa protein 5 (glucose−regulated protein, 78kD
14	ID3	−1.73	2e−16	9e−14	11 x 50	inhibitor of DNA binding 3, dominant negative helix−loop−heli
15	IDH3B	−1.48	2e−16	9e−14	22 x 43	isocitrate dehydrogenase 3 (NAD+) beta [Source:HGNC Sym
16	JKAMP	−1.49	2e−16	9e−14	29 x 50	JNK1/MAPK8−associated membrane protein [Source:HGNC
17	KRTCAP2	−1.78	2e−16	9e−14	26 x 50	keratinocyte associated protein 2 [Source:HGNC Symbol;Acc
18	LSM8	−1.59	2e−16	9e−14	12 x 44	LSM8 homolog, U6 small nuclear RNA associated (S. cerevis
19	MAGED2	−2.04	2e−16	9e−14	28 x 50	melanoma antigen family D2 [Source:HGNC Symbol;Acc:HGI
20	NEMF	−1.34	2e−16	9e−14	47 x 13	nuclear export mediator factor [Source:HGNC Symbol;Acc:HC

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset
Overexpressed				
1	6.41	0.001	27	GSEA C2 REACTOME_DNA_STRAND_ELONGATION
2	6.4	0.001	29	BP DNA strand elongation involved in DNA replication
3	6.38	0.001	32	GSEA C2 KEGG_DNA_REPLICATION
4	5.78	0.002	47	GSEA C2 SUNG_METASTASIS_STROMA_DN
5	5.66	0.002	215	GSEA C2 KAUFFMANN_DNA_REPAIR_GENES
6	5.63	0.002	278	GSEA C2 MANALO_HYPOXIA_DN
7	5.55	0.002	335	GSEA C2 WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_DN
8	5.38	0.003	68	GSEA C2 VERNELL_RETINOBLASTOMA_PATHWAY_UP
9	5.38	0.003	58	GSEA C2 SONG_TARGETS_OF_IE86_CMV_PROTEIN
10	5.35	0.003	139	BP DNA replication
11	5.35	0.003	59	GSEA C2 KAUFFMANN_MELANOMA_RELAPSE_UP
12	5.24	0.003	84	GSEA C2 ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_6HR
13	5.21	0.003	171	GSEA C2 SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP
14	5.11	0.003	212	GSEA C2 DUTERTRE_ESTRADIOL_RESPONSE_6HR_UP
15	5	0.004	235	GSEA C2 BLUM_RESPONSE_TO_SALIRASIB_UP
16	4.99	0.004	38	GSEA C2 BURTON_ADIPOGENESIS_PEAK_AT_16HR
17	4.98	0.004	20	BP telomere maintenance via semi−conservative replication
18	4.96	0.004	19	GSEA C2 KEGG_MISMATCH_REPAIR
19	4.9	0.004	16	GSEA C2 REACTOME_LAGGING_STRAND_SYNTHESIS
20	4.7	0.004	16	BP nucleotide−excision repair, DNA gap filling
Underexpressed				
1	−6.23	0.002	17	CC proteasome accessory complex
2	−5.66	0.002	60	GSEA C2 PELLICCIOTTA_HDAC_IN_ANTIGEN_PRESENTATION_UP
3	−4.96	0.004	286	GSEA C2 PASINI_SUZ12_TARGETS_DN
4	−4.92	0.004	8	GSEA C2 PASTURAL_RIZ1_TARGETS_UP
5	−4.84	0.004	13	CC proteasome regulatory particle
6	−4.63	0.005	62	GSEA C2 REACTOME_APC_C_CDH1_MEDIATED_DEGRADATION_OF_CI
7	−4.48	0.005	63	GSEA C2 REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_N
8	−4.4	0.005	11	Lymphoma Subero_T−ALL_hypo_meth
9	−4.34	0.006	425	GSEA C2 CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_
10	−4.33	0.006	104	GSEA C2 LAIHO_COLORECTAL_CANCER_SERRATED_UP
11	−4.31	0.006	85	GSEA C2 BURTON_ADIPOGENESIS_9
12	−4.29	0.006	41	GSEA C2 KEGG_PROTEASOME
13	−4.27	0.006	75	GSEA C2 REACTOME_REGULATION_OF_MITOTIC_CELL_CYCLE
14	−4.23	0.006	11	BP cellular aldehyde metabolic process
15	−4.2	0.006	90	GSEA C2 CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN
16	−4.2	0.006	78	BP anaphase−promoting complex−dependent proteasomal ubiquitin−c
17	−4.11	0.007	202	CC actin cytoskeleton
18	−4.04	0.007	45	GSEA C2 REACTOME_AUTODEGRADATION_OF_THE_E3_UBIQUITIN_LI
19	−4.03	0.007	68	BP positive regulation of ubiquitin−protein ligase activity involved in reg
20	−3.97	0.008	55	GSEA C2 REACTOME_AUTODEGRADATION_OF_CDH1_BY_CDH1_APC_





A3_mel

Local Summary

%DE = 0.78

metagenes = 17

genes = 244

genes in genesets = 243

genes with fdr < 0.1 = 128 (111 + / 17 −)

genes with fdr < 0.05 = 108 (97 + / 11 −)

genes with fdr < 0.01 = 61 (57 + / 4 −)

<r> metagenes = 0.96

<r> genes = 0.15

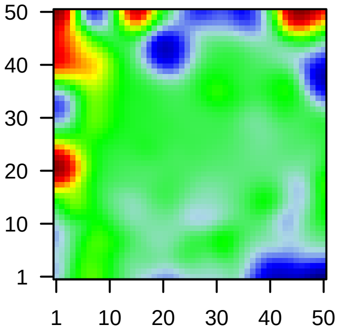
<FC> = 0.32

<shrinkage−t> = 5.38

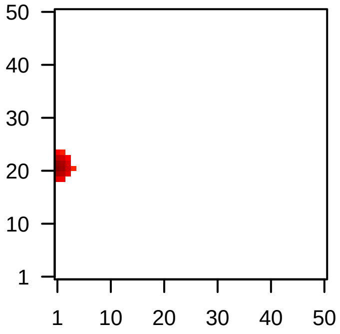
<p−value> = 0.01

<fdr> = 0.56

Profile



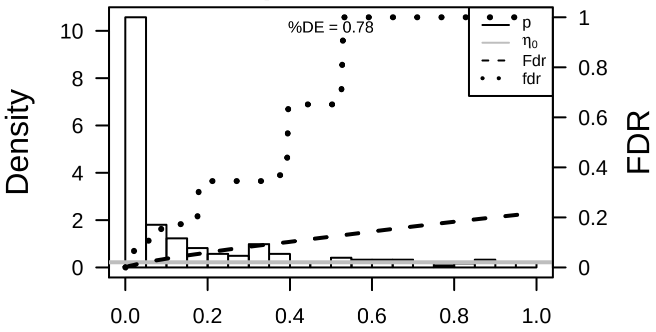
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	PIGY	0.75	1e−12	8e−10	1 x 20	phosphatidylinositol glycan anchor biosynthesis, class Y [Sou
2	RAD51D	1.55	2e−11	2e−08	1 x 23	RAD51 paralog D [Source:HGNC Symbol;Acc:HGNC:9823]
3	TMC8	1.45	3e−10	3e−08	1 x 24	transmembrane channel−like 8 [Source:HGNC Symbol;Acc:H
4	STXBP5L	1.41	9e−10	1e−07	4 x 21	syntaxin binding protein 5−like [Source:HGNC Symbol;Acc:H
5	EGLN2	1.35	4e−09	1e−07	1 x 23	egl−9 family hypoxia−inducible factor 2 [Source:HGNC Symb
6	RNF135	1.34	6e−09	6e−06	2 x 19	ring finger protein 135 [Source:HGNC Symbol;Acc:HGNC:21
7	SUMF1	1.2	2e−07	6e−06	2 x 22	sulfatase modifying factor 1 [Source:HGNC Symbol;Acc:HGN
8	MDM1	1.19	2e−07	1e−05	1 x 21	Mdm1 nuclear protein homolog (mouse) [Source:HGNC Sym
9	ADPGK	1.14	6e−07	1e−05	1 x 21	ADP−dependent glucokinase [Source:HGNC Symbol;Acc:HG
10	TNFRSF1A	1.14	8e−07	3e−05	1 x 24	tumor necrosis factor receptor superfamily, member 1A [Sour
11	TSEN54	1.11	1e−06	3e−05	1 x 22	TSEN54 tRNA splicing endonuclease subunit [Source:HGNC
12	PLA2G12A	1.1	2e−06	4e−05	1 x 21	phospholipase A2, group XIIA [Source:HGNC Symbol;Acc:H
13	C1orf86	1.06	4e−06	4e−05	2 x 21	chromosome 1 open reading frame 86 [Source:HGNC Symb
14	OGFOD3	1.05	6e−06	4e−05	1 x 21	2−oxoglutarate and iron−dependent oxygenase domain conta
15	NT5C	1.04	6e−06	4e−05	1 x 21	5', 3'−nucleotidase, cytosolic [Source:HGNC Symbol;Acc:HG
16	TMEM18	1.04	6e−06	4e−05	1 x 21	transmembrane protein 18 [Source:HGNC Symbol;Acc:HGN
17	DNAJC4	1.04	6e−06	4e−05	1 x 19	DnaJ (Hsp40) homolog, subfamily C, member 4 [Source:HG
18	C17orf89	1.04	7e−06	6e−05	1 x 21	chromosome 17 open reading frame 89 [Source:HGNC Sym
19	EPN2	1.02	9e−06	6e−05	1 x 21	epsin 2 [Source:HGNC Symbol;Acc:HGNC:18639]
20	PFN1	0.5	1e−05	6e−05	1 x 21	profilin 1 [Source:HGNC Symbol;Acc:HGNC:8881]

p−values



A3_mel

Local Summary

%DE = 0.79

metagenes = 25

genes = 453

genes in genesets = 450

genes with fdr < 0.1 = 258 (193 + / 65 −)

genes with fdr < 0.05 = 202 (157 + / 45 −)

genes with fdr < 0.01 = 167 (131 + / 36 −)

<r> metagenes = 0.8

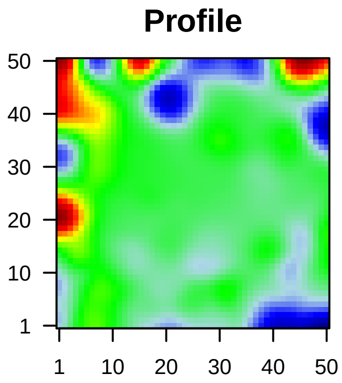
<r> genes = 0.16

<FC> = 0.25

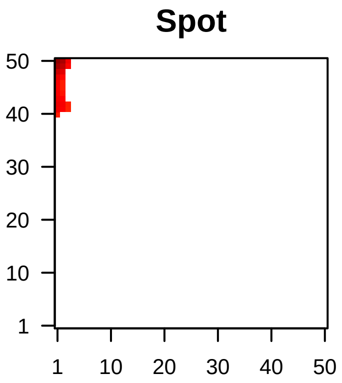
<shrinkage−t> = 4.23

<p−value> = 0

<fdr> = 0.52



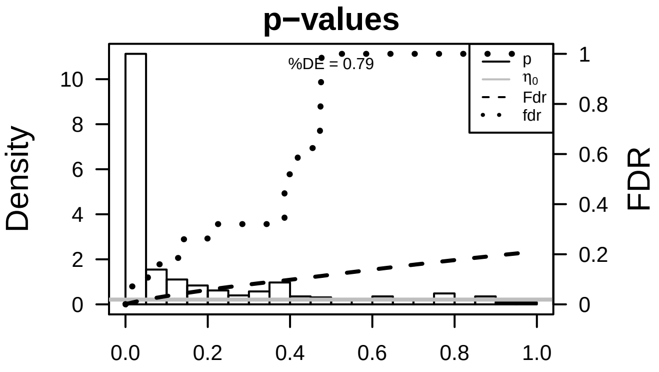
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	EXOC3	0.69	2e−13	2e−11	1 x 42	exocyst complex component 3 [Source:HGNC Symbol;Acc:H
2	NMRK2	1.57	6e−13	2e−11	1 x 44	nicotinamide riboside kinase 2 [Source:HGNC Symbol;Acc:H
3	SMCO4	1.66	6e−13	1e−09	1 x 47	single−pass membrane protein with coiled−coil domains 4 [S
4	RHOG	−1.37	1e−11	2e−09	1 x 46	ras homolog family member G [Source:HGNC Symbol;Acc:H
5	RNASEH2B	1.52	4e−11	3e−08	1 x 50	ribonuclease H2, subunit B [Source:HGNC Symbol;Acc:HGN
6	PDE6D	−1.3	6e−10	3e−08	1 x 44	phosphodiesterase 6D, cGMP−specific, rod, delta [Source:H
7	ZC3H13	0.85	6e−10	1e−07	3 x 42	zinc finger CCCH−type containing 13 [Source:HGNC Symbol
8	NCAPH2	1.37	2e−09	1e−07	1 x 50	non−SMC condensin II complex, subunit H2 [Source:HGNC
9	CENPH	1.37	3e−09	1e−07	1 x 47	centromere protein H [Source:HGNC Symbol;Acc:HGNC:172
10	MCM7	1.24	4e−09	5e−07	2 x 50	minichromosome maintenance complex component 7 [Sourc
11	PLP1	−0.53	1e−08	5e−07	1 x 42	proteolipid protein 1 [Source:HGNC Symbol;Acc:HGNC:9086
12	SNX8	1.3	1e−08	5e−07	1 x 42	sorting nexin 8 [Source:HGNC Symbol;Acc:HGNC:14972]
13	GINS1	1.29	2e−08	5e−07	2 x 49	GINS complex subunit 1 (Psf1 homolog) [Source:HGNC Sym
14	SLC5A6	1.29	2e−08	5e−07	1 x 45	solute carrier family 5 (sodium/multivitamin and iodide cotran
15	LIG1	1.28	3e−08	6e−07	2 x 50	ligase I, DNA, ATP−dependent [Source:HGNC Symbol;Acc:H
16	MCM10	1.26	4e−08	6e−07	1 x 50	minichromosome maintenance complex component 10 [Sour
17	FARSA	−1.09	4e−08	6e−07	3 x 41	phenylalanyl−tRNA synthetase, alpha subunit [Source:HGNC
18	MCM4	1	5e−08	6e−07	1 x 50	minichromosome maintenance complex component 4 [Sourc
19	ZNF367	1.25	6e−08	1e−06	1 x 49	zinc finger protein 367 [Source:HGNC Symbol;Acc:HGNC:18
20	YEATS4	1.03	7e−08	1e−06	1 x 47	YEATS domain containing 4 [Source:HGNC Symbol;Acc:HG



p−values

A3_mel

Local Summary

%DE = 0.83

metagenes = 18

genes = 282

genes in genesets = 281

genes with fdr < 0.1 = 157 (131 + / 26 −)

genes with fdr < 0.05 = 152 (126 + / 26 −)

genes with fdr < 0.01 = 91 (77 + / 14 −)

<r> metagenes = 0.89

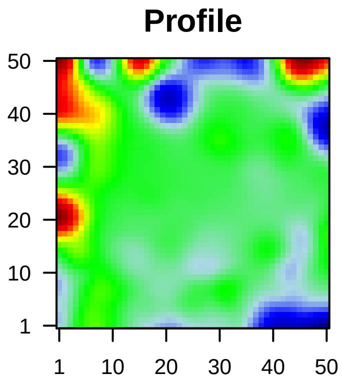
<r> genes = 0.08

<FC> = 0.3

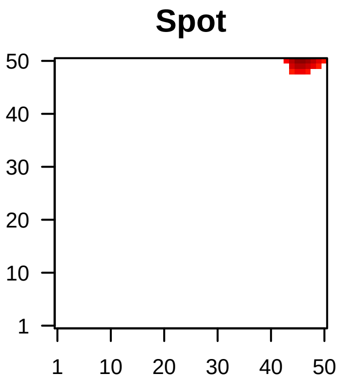
<shrinkage−t> = 5.11

<p−value> = 0.01

<fdr> = 0.55



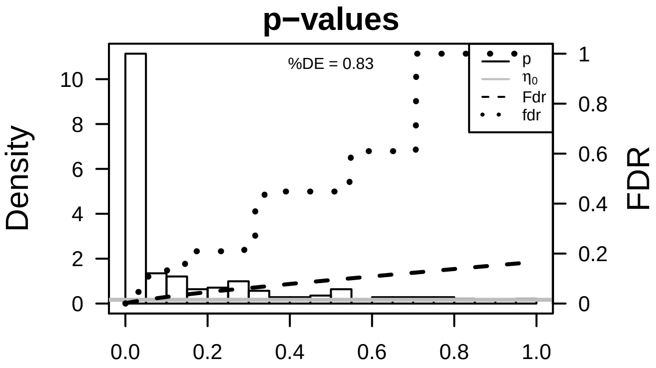
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	GDF15	1.75	9e−15	3e−11	47 x 50	growth differentiation factor 15 [Source:HGNC Symbol;Acc:H
2	SELT	−1.21	7e−13	5e−10	47 x 50	
3	ELOVL6	1.55	2e−11	5e−10	46 x 50	ELOVL fatty acid elongase 6 [Source:HGNC Symbol;Acc:HG
4	NLRC5	1.54	2e−11	8e−10	50 x 50	NLR family, CARD domain containing 5 [Source:HGNC Symb
5	TRIB3	1.52	4e−11	5e−09	45 x 50	tribbles pseudokinase 3 [Source:HGNC Symbol;Acc:HGNC:1
6	GATSL3	1.48	1e−10	2e−07	46 x 48	GATS protein−like 3 [Source:HGNC Symbol;Acc:HGNC:3442
7	PPCDC	1.36	4e−09	3e−07	47 x 50	phosphopantothenoylcysteine decarboxylase [Source:HGNC
8	AGTRAP	1.32	1e−08	3e−07	45 x 49	angiotensin II receptor−associated protein [Source:HGNC Sy
9	NAGK	1.3	2e−08	3e−07	44 x 50	N−acetylglucosamine kinase [Source:HGNC Symbol;Acc:HG
10	STK11IP	1.29	2e−08	4e−07	43 x 50	serine/threonine kinase 11 interacting protein [Source:HGNC
11	GABRA5	1.27	3e−08	4e−07	44 x 48	gamma−aminobutyric acid (GABA) A receptor, alpha 5 [Sour
12	CCDC51	1.27	4e−08	5e−07	47 x 50	coiled−coil domain containing 51 [Source:HGNC Symbol;Acc
13	TSEN2	1.25	5e−08	5e−07	45 x 50	TSEN2 tRNA splicing endonuclease subunit [Source:HGNC
14	COG5	1.24	7e−08	5e−07	45 x 48	component of oligomeric golgi complex 5 [Source:HGNC Sy
15	GSTZ1	1.24	7e−08	9e−07	48 x 50	glutathione S−transferase zeta 1 [Source:HGNC Symbol;Acc:
16	BBS4	1.23	9e−08	1e−06	46 x 50	Bardet−Biedl syndrome 4 [Source:HGNC Symbol;Acc:HGNC
17	GARS	0.83	1e−07	1e−06	45 x 50	glycyl−tRNA synthetase [Source:HGNC Symbol;Acc:HGNC:4
18	TBCB	−0.96	1e−07	2e−06	46 x 50	tubulin folding cofactor B [Source:HGNC Symbol;Acc:HGNC:
19	AVPI1	0.78	2e−07	5e−06	49 x 50	arginine vasopressin−induced 1 [Source:HGNC Symbol;Acc:
20	CCBL2	1.18	3e−07	5e−06	49 x 50	cysteine conjugate−beta lyase 2 [Source:HGNC Symbol;Acc:



p−values

A3_mel

Local Summary

%DE = 0.72

metagenes = 5

genes = 82

genes in genesets = 82

genes with fdr < 0.1 = 48 (44 + / 4 −)

genes with fdr < 0.05 = 46 (42 + / 4 −)

genes with fdr < 0.01 = 33 (32 + / 1 −)

<r> metagenes = 0.99

<r> genes = 0.11

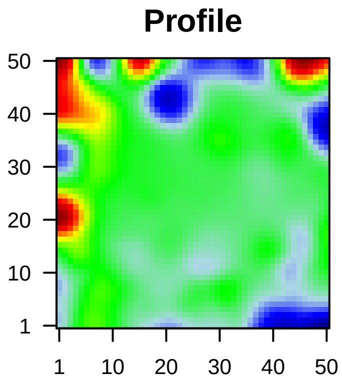
<FC> = 0.49

<shrinkage−t> = 8.01

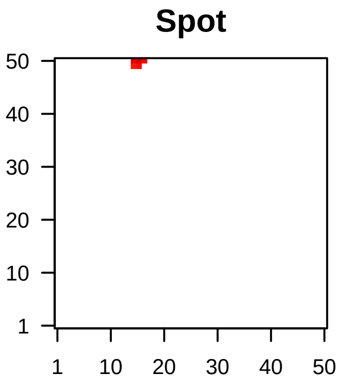
<p−value> = 0

<fdr> = 0.45

Profile



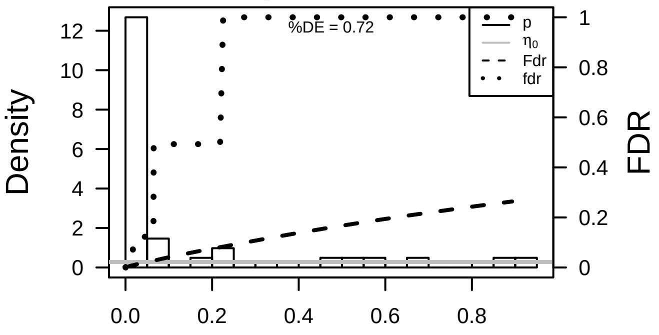
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	SLC41A3	1.6	4e−12	3e−08	15 x 50	solute carrier family 41, member 3 [Source:HGNC Symbol;Ac
2	APTX	1.39	2e−09	3e−08	15 x 50	aprataxin [Source:HGNC Symbol;Acc:HGNC:15984]
3	CASP4	1.36	4e−09	3e−08	15 x 50	caspase 4, apoptosis−related cysteine peptidase [Source:HG
4	NDEL1	1.35	4e−09	3e−08	15 x 50	nudE neurodevelopment protein 1−like 1 [Source:HGNC Sym
5	RHBDD1	1.34	6e−09	5e−08	16 x 50	rhomboid domain containing 1 [Source:HGNC Symbol;Acc:H
6	USP37	1.33	8e−09	3e−07	16 x 50	ubiquitin specific peptidase 37 [Source:HGNC Symbol;Acc:H
7	MAP2K5	1.29	2e−08	1e−06	17 x 50	mitogen−activated protein kinase kinase 5 [Source:HGNC Sy
8	SFMBT1	1.23	9e−08	1e−06	17 x 50	Scm−like with four mbt domains 1 [Source:HGNC Symbol;Ac
9	FBXO22	1.1	2e−07	1e−06	15 x 50	F−box protein 22 [Source:HGNC Symbol;Acc:HGNC:13593]
10	INO80	1.19	2e−07	2e−06	16 x 50	INO80 complex subunit [Source:HGNC Symbol;Acc:HGNC:2
11	LYRM1	1.17	4e−07	2e−06	16 x 50	LYR motif containing 1 [Source:HGNC Symbol;Acc:HGNC:25
12	GMDS	1.17	4e−07	2e−05	15 x 50	GDP−mannose 4,6−dehydratase [Source:HGNC Symbol;Acc
13	TUBD1	1.11	1e−06	4e−05	17 x 50	tubulin, delta 1 [Source:HGNC Symbol;Acc:HGNC:16811]
14	C9orf72	1.05	5e−06	4e−05	16 x 50	chromosome 9 open reading frame 72 [Source:HGNC Symb
15	ZNF346	1.05	5e−06	1e−04	15 x 50	zinc finger protein 346 [Source:HGNC Symbol;Acc:HGNC:16
16	KCTD6	1.01	1e−05	2e−04	16 x 50	potassium channel tetramerization domain containing 6 [Sour
17	IPO5	0.87	2e−05	2e−04	16 x 49	importin 5 [Source:HGNC Symbol;Acc:HGNC:6402]
18	DYM	0.96	3e−05	2e−04	16 x 50	dymeclin [Source:HGNC Symbol;Acc:HGNC:21317]
19	PANK2	0.95	4e−05	3e−04	17 x 50	pantothenate kinase 2 [Source:HGNC Symbol;Acc:HGNC:15
20	BCKDHA	0.93	5e−05	3e−04	15 x 50	branched chain keto acid dehydrogenase E1, alpha polypepti

p−values



A3_mel

Local Summary

%DE = 0.76

metagenes = 24

genes = 397

genes in genesets = 397

genes with fdr < 0.1 = 188 (44 + / 144 −)

genes with fdr < 0.05 = 119 (34 + / 85 −)

genes with fdr < 0.01 = 82 (25 + / 57 −)

<r> metagenes = 0.86

<r> genes = 0.15

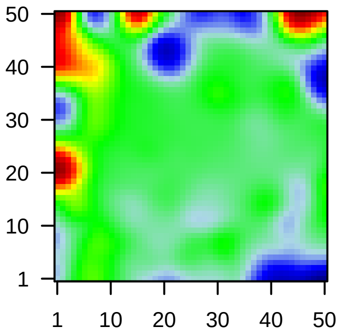
<FC> = −0.23

<shrinkage−t> = −3.8

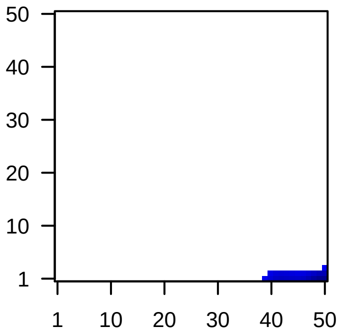
<p−value> = 0.01

<fdr> = 0.66

Profile



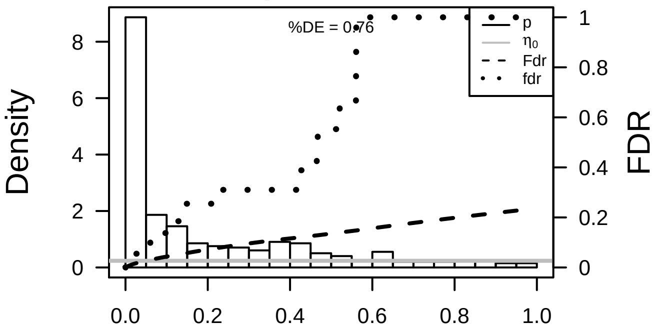
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	C1orf198	−1.31	2e−16	7e−15	49 x 1	chromosome 1 open reading frame 198 [Source:HGNC Symb
2	PMP22	−1.42	2e−16	7e−15	48 x 1	peripheral myelin protein 22 [Source:HGNC Symbol;Acc:HGN
3	SPARC	−2.13	2e−16	7e−15	50 x 2	secreted protein, acidic, cysteine−rich (osteonectin) [Source:H
4	DST	−1.21	2e−14	4e−08	46 x 1	dystonin [Source:HGNC Symbol;Acc:HGNC:1090]
5	MARCKS	−0.67	7e−10	4e−08	46 x 1	myristoylated alanine−rich protein kinase C substrate [Source
6	DKK1	1.4	1e−09	4e−08	50 x 1	dickkopf WNT signaling pathway inhibitor 1 [Source:HGNC S
7	AKAP9	−1.11	1e−09	9e−08	42 x 1	A kinase (PRKA) anchor protein 9 [Source:HGNC Symbol;Ac
8	RAB3IP	1.37	2e−09	2e−07	50 x 3	RAB3A interacting protein [Source:HGNC Symbol;Acc:HGNC
9	PLK2	−1	6e−09	2e−07	50 x 1	polo−like kinase 2 [Source:HGNC Symbol;Acc:HGNC:19699]
10	ANXA2	−0.54	8e−09	6e−07	50 x 3	annexin A2 [Source:HGNC Symbol;Acc:HGNC:537]
11	P2RX4	−1.22	1e−08	8e−07	43 x 1	purinergic receptor P2X, ligand gated ion channel, 4 [Source:
12	NOV	−1.2	3e−08	8e−07	50 x 1	nephroblastoma overexpressed [Source:HGNC Symbol;Acc:H
13	CDKN1A	1.27	4e−08	8e−07	50 x 1	cyclin−dependent kinase inhibitor 1A (p21, Cip1) [Source:HG
14	MYO9A	1.26	4e−08	2e−06	45 x 1	myosin IXA [Source:HGNC Symbol;Acc:HGNC:7608]
15	CD55	−1.19	6e−08	4e−06	50 x 1	CD55 molecule, decay accelerating factor for complement (C
16	ALKBH3	1.22	1e−07	4e−06	44 x 1	alkB, alkylation repair homolog 3 (E. coli) [Source:HGNC Sym
17	CYB5R1	−1.17	1e−07	4e−06	41 x 2	cytochrome b5 reductase 1 [Source:HGNC Symbol;Acc:HGN
18	CSRP2	−1.06	2e−07	4e−06	48 x 1	cysteine and glycine−rich protein 2 [Source:HGNC Symbol;A
19	FAM98A	−1.16	2e−07	2e−05	49 x 1	family with sequence similarity 98, member A [Source:HGNC
20	APC	−1.14	4e−07	3e−05	41 x 2	adenomatous polyposis coli [Source:HGNC Symbol;Acc:HGN

p−values



A3_mel

Local Summary

%DE = 0.68

metagenes = 9

genes = 136

genes in genesets = 135

genes with fdr < 0.1 = 65 (16 + / 49 −)

genes with fdr < 0.05 = 55 (14 + / 41 −)

genes with fdr < 0.01 = 40 (8 + / 32 −)

<r> metagenes = 0.96

<r> genes = 0.09

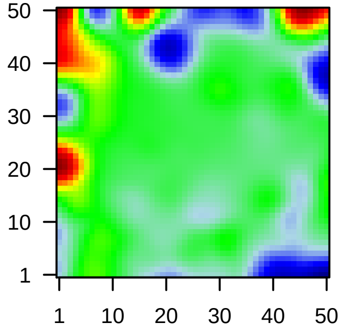
<FC> = −0.27

<shrinkage−t> = −4.37

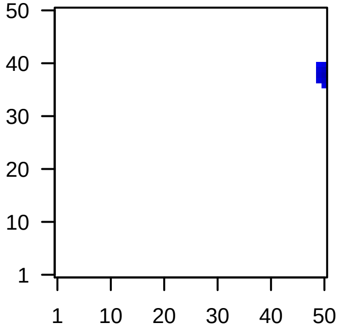
<p−value> = 0.01

<fdr> = 0.56

Profile



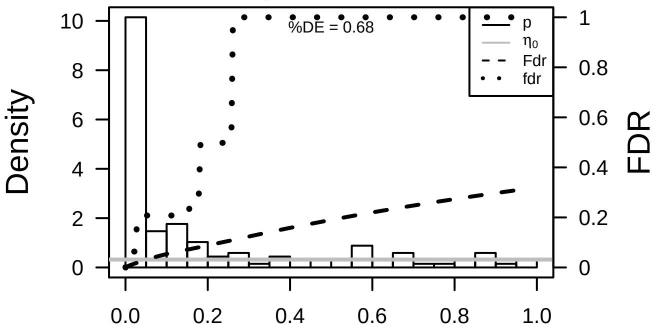
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CDC42BPA	−1.15	2e−16	1e−14	50 x 38	CDC42 binding protein kinase alpha (DMPK−like) [Source:H
2	SCPEP1	−1.49	6e−15	2e−08	49 x 37	serine carboxypeptidase 1 [Source:HGNC Symbol;Acc:HGN
3	RPUSD3	−1.31	4e−10	6e−07	50 x 39	RNA pseudouridylate synthase domain containing 3 [Source:
4	LTV1	−1.19	2e−08	6e−07	50 x 36	LTV1 ribosome biogenesis factor [Source:HGNC Symbol;Acc
5	PARN	1.26	4e−08	6e−07	50 x 39	poly(A)−specific ribonuclease [Source:HGNC Symbol;Acc:H
6	CFLAR	−1.16	4e−08	7e−06	50 x 39	CASP8 and FADD−like apoptosis regulator [Source:HGNC S
7	MGEA5	−1.05	2e−07	7e−06	50 x 40	meningioma expressed antigen 5 (hyaluronidase) [Source:H
8	RNFT1	−1.15	4e−07	1e−05	50 x 39	ring finger protein, transmembrane 1 [Source:HGNC Symbol;
9	USP11	−1.13	7e−07	1e−05	49 x 40	ubiquitin specific peptidase 11 [Source:HGNC Symbol;Acc:H
10	DNPEP	−1.11	1e−06	1e−05	50 x 38	aspartyl aminopeptidase [Source:HGNC Symbol;Acc:HGNC:
11	DEDD	−1.1	1e−06	1e−05	50 x 38	death effector domain containing [Source:HGNC Symbol;Acc
12	UXT	−0.86	2e−06	1e−05	50 x 38	ubiquitously−expressed, prefoldin−like chaperone [Source:H
13	HEATR1	−1.06	2e−06	1e−05	49 x 37	HEAT repeat containing 1 [Source:HGNC Symbol;Acc:HGNC
14	CLK1	−0.79	2e−06	2e−05	50 x 40	CDC−like kinase 1 [Source:HGNC Symbol;Acc:HGNC:2068]
15	SEC14L1	−0.96	2e−06	6e−05	50 x 40	SEC14−like 1 (S. cerevisiae) [Source:HGNC Symbol;Acc:HG
16	HPS5	−1.03	4e−06	1e−04	49 x 40	Hermansky−Pudlak syndrome 5 [Source:HGNC Symbol;Acc:
17	SLC25A46	−1.03	8e−06	1e−04	50 x 39	solute carrier family 25, member 46 [Source:HGNC Symbol;A
18	VPS45	−1.02	9e−06	3e−04	50 x 39	vacuolar protein sorting 45 homolog (S. cerevisiae) [Source:
19	USE1	−0.98	2e−05	3e−04	50 x 38	unconventional SNARE in the ER 1 homolog (S. cerevisiae) [
20	CRYZ	−0.98	2e−05	5e−04	50 x 40	crystallin, zeta (quinone reductase) [Source:HGNC Symbol;A

p−values



A3_mel

Local Summary

%DE = 0.78
metagenes = 17
genes = 116
genes in genesets = 116

genes with fdr < 0.1 = 55 (11 + / 44 −)
genes with fdr < 0.05 = 43 (9 + / 34 −)
genes with fdr < 0.01 = 33 (9 + / 24 −)

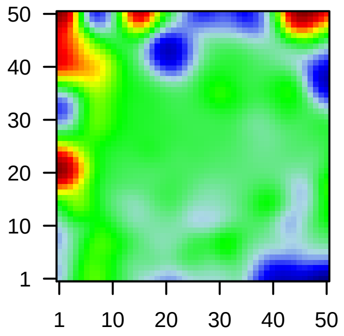
<r> metagenes = 0.97
<r> genes = 0.1

<FC> = −0.24
<shrinkage−t> = −4.09
<p−value> = 0.01
<fdr> = 0.6

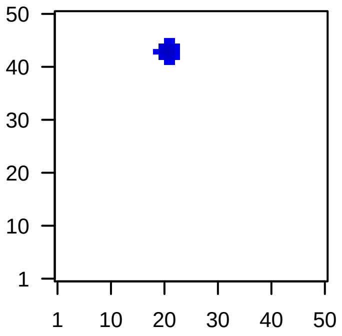
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	IDH3B	−1.48	2e−16	6e−15	22 x 43	isocitrate dehydrogenase 3 (NAD+) beta [Source:HGNC Sym
2	ARMC8	−1.43	4e−13	1e−07	21 x 43	armadillo repeat containing 8 [Source:HGNC Symbol;Acc:HG
3	SRI	−0.76	1e−08	1e−07	20 x 43	sorcin [Source:HGNC Symbol;Acc:HGNC:11292]
4	MRPS10	−0.99	1e−08	2e−06	21 x 44	mitochondrial ribosomal protein S10 [Source:HGNC Symbol;
5	DIMT1	−1.18	8e−08	7e−06	21 x 44	DIM1 dimethyladenosine transferase 1 homolog (S. cerevisia
6	PSMC2	−0.78	4e−07	2e−05	21 x 44	proteasome (prosome, macropain) 26S subunit, ATPase, 2 [S
7	NXF1	−0.77	1e−06	4e−05	20 x 43	nuclear RNA export factor 1 [Source:HGNC Symbol;Acc:HG
8	EXOC2	−1.07	2e−06	6e−05	23 x 43	exocyst complex component 2 [Source:HGNC Symbol;Acc:H
9	CDADC1	1.04	6e−06	6e−05	23 x 42	cytidine and dCMP deaminase domain containing 1 [Source:
10	TAF11	−0.97	8e−06	6e−05	20 x 43	TAF11 RNA polymerase II, TATA box binding protein (TBP)−a
11	RHOT1	−1	1e−05	1e−04	21 x 43	ras homolog family member T1 [Source:HGNC Symbol;Acc:
12	TSSC1	1	1e−05	5e−04	20 x 42	tumor suppressing subtransferable candidate 1 [Source:HGN
13	DDHD1	−0.95	3e−05	7e−04	21 x 43	DDHD domain containing 1 [Source:HGNC Symbol;Acc:HGN
14	PKNOX1	−0.9	1e−04	7e−04	20 x 43	PBX/knotted 1 homeobox 1 [Source:HGNC Symbol;Acc:HGN
15	COQ3	0.89	1e−04	7e−04	22 x 44	coenzyme Q3 methyltransferase [Source:HGNC Symbol;Acc:
16	NGDN	0.76	1e−04	7e−04	22 x 45	neuroguidin, EIF4E binding protein [Source:HGNC Symbol;A
17	CHD4	−0.59	1e−04	2e−03	21 x 43	chromodomain helicase DNA binding protein 4 [Source:HGN
18	WNK1	0.76	3e−04	2e−03	22 x 44	WNK lysine deficient protein kinase 1 [Source:HGNC Symbol
19	DHX8	0.76	3e−04	2e−03	22 x 41	DEAH (Asp−Glu−Ala−His) box polypeptide 8 [Source:HGNC
20	SUPT6H	−0.81	4e−04	2e−03	22 x 41	suppressor of Ty 6 homolog (S. cerevisiae) [Source:HGNC S

Profile



Spot



p−values