A1_mel

Global Summary

%DE = 0.21

genes with fdr < 0.2 = 2658 (1674 + / 984 −)

genes with fdr < 0.1 = 2131 (1373 + / 758 −)

genes with fdr < 0.05 = 1767 (1158 + / 609 −)

genes with fdr < 0.01 = 1062 (713 + / 349 −)

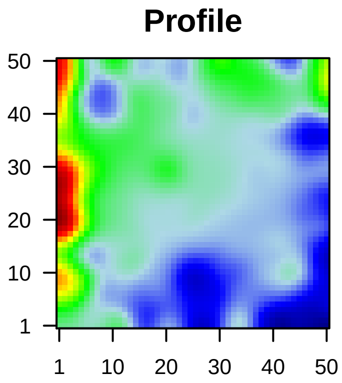
genes in genesets = 14839

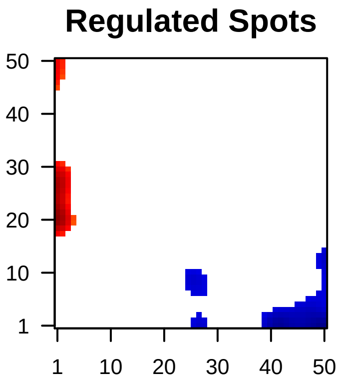
<FC> = 0

<shrinkage−t> = 0.06

<p−value> = 0.08

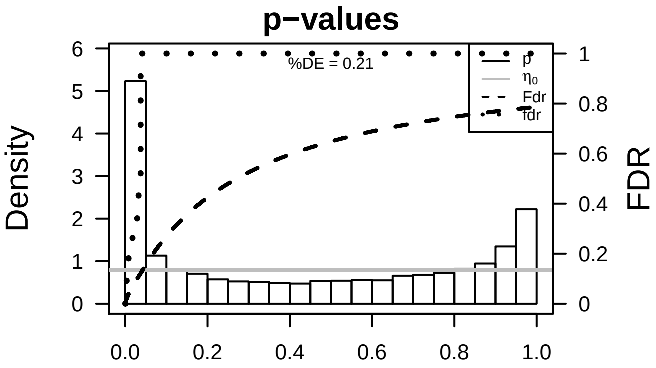
<fdr> = 0.79





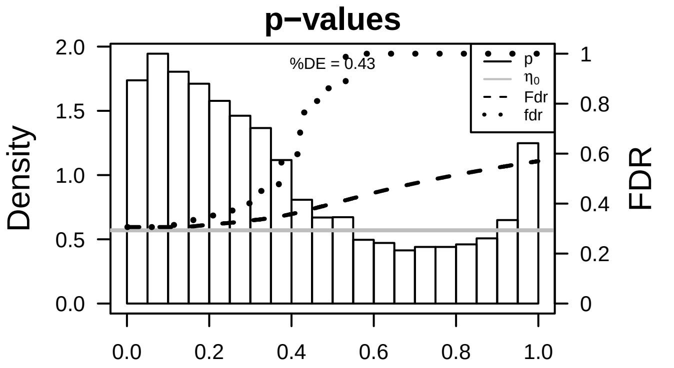
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	AHSA1	−1.92	2e−16	2e−13	46 x 35	AHA1, activator of heat shock 90kDa protein ATPase homolo
2	AZIN1	−1.75	2e−16	2e−13	4 x 41	antizyme inhibitor 1 [Source:HGNC Symbol;Acc:HGNC:1643
3	CALCOCO2	−1.4	2e−16	2e−13	26 x 50	calcium binding and coiled−coil domain 2 [Source:HGNC Syn
4	LAMB2	−1.61	2e−16	2e−13	50 x 6	laminin, beta 2 (laminin S) [Source:HGNC Symbol;Acc:HGNC
5	PCBP1	−1.44	2e−16	2e−13	10 x 44	poly(rC) binding protein 1 [Source:HGNC Symbol;Acc:HGNC
6	PGM3	−1.8	2e−16	2e−13	5 x 45	phosphoglucomutase 3 [Source:HGNC Symbol;Acc:HGNC:8
7	POR	−1.51	2e−16	2e−13	36 x 50	P450 (cytochrome) oxidoreductase [Source:HGNC Symbol;A
8	PTP4A1	−1.47	2e−16	2e−13	1 x 21	protein tyrosine phosphatase type IVA, member 1 [Source:HG
9	SAP30BP	−1.42	2e−16	2e−13	42 x 49	SAP30 binding protein [Source:HGNC Symbol;Acc:HGNC:30
10	SF3B3	−1.52	2e−16	2e−13	12 x 49	splicing factor 3b, subunit 3, 130kDa [Source:HGNC Symbol;
11	SMIM7	−1.7	2e−16	2e−13	44 x 33	small integral membrane protein 7 [Source:HGNC Symbol;Ac
12	SSR1	−1.06	2e−16	2e−13	50 x 35	signal sequence receptor, alpha [Source:HGNC Symbol;Acc:
13	WDR12	−1.8	2e−16	2e−13	5 x 43	WD repeat domain 12 [Source:HGNC Symbol;Acc:HGNC:14
14	MRPS35	−1.5	4e−16	1e−12	37 x 50	mitochondrial ribosomal protein S35 [Source:HGNC Symbol;
15	PPP1R13L	1.82	4e−16	1e−12	1 x 28	protein phosphatase 1, regulatory subunit 13 like [Source:HG
16	HARS	−1.49	7e−16	5e−12	42 x 50	histidyl−tRNA synthetase [Source:HGNC Symbol;Acc:HGNC:
17	SPP1	1.48	7e−16	5e−12	38 x 48	secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:HGN
18	UAP1	1.79	1e−15	2e−11	9 x 48	UDP−N−acetylglucosamine pyrophosphorylase 1 [Source:HG
19	NUP98	−1.4	3e−15	2e−11	34 x 50	nucleoporin 98kDa [Source:HGNC Symbol;Acc:HGNC:8068]
20	SIPA1L3	1.74	6e−15	2e−11	1 x 27	signal−induced proliferation−associated 1 like 3 [Source:HGN



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	7.09	0.001	198	HM	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	6.38	0.001	305	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
3	5.94	0.002	368	GSEA C2	STEIN_ESRRA_TARGETS_UP
4	5.49	0.003	99	GSEA C2	BURTON_ADIPOGENESIS_3
5	5.48	0.003	171	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP
6	5.46	0.003	298	BP	DNA repair
7	5.43	0.003	116	GSEA C2	MISSIAGLIA_REGULATED_BY_METHYLATION_DN
8	5.38	0.003	202	GSEA C2	CHANG_CORE_SERUM_RESPONSE_UP
9	5.29	0.003	1468	CC	mitochondrion
10	5.25	0.003	321	GSEA C2	ACEVEDO_NORMAL_TISSUE_ADJACENT_TO_LIVER_TUMOR_
11	5.24	0.003	139	BP	DNA replication
12	5.24	0.003	500	GSEA C2	STEIN_ESRRA_TARGETS
13	5.21	0.003	335	GSEA C2	WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_DN
14	5.18	0.003	135	BP	cellular metabolic process
15	5.14	0.003	401	CC	mitochondrial inner membrane
16	5.12	0.003	58	GSEA C2	SONG_TARGETS_OF_IE86_CMV_PROTEIN
17	5.05	0.003	212	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_6HR_UP
18	5.04	0.003	32	GSEA C2	KEGG_DNA_REPLICATION
19	4.99	0.004	768	BP	DNA metabolic process
20	4.99	0.004	724	GSEA C2	PUJANA_CHEK2_PCC_NETWORK
Underexpressed					
1	−4.09	0.007	278	GSEA C2	GABRIELY_MIR21_TARGETS
2	−4.07	0.007	23	miRNA target	hsa−miR−943
3	−4.02	0.007	749	GSEA C2	CUI_TCF21_TARGETS_2_DN
4	−3.89	0.008	121	GSEA C2	ONDER_CDH1_TARGETS_1_UP
5	−3.87	0.008	175	miRNA target	hsa−miR−548k
6	−3.84	0.009	32	GSEA C2	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_
7	−3.79	0.009	833	GSEA C2	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
8	−3.71	0.010	107	miRNA target	hsa−miR−190b
9	−3.7	0.010	33	BP	regulation of mitotic cell cycle
10	−3.69	0.010	95	miRNA target	hsa−miR−888
11	−3.68	0.010	993	Chr	Chr 2
12	−3.68	0.010	5538	Lymphoma	HOPP_Weak_txn
13	−3.68	0.010	268	miRNA target	hsa−miR−363
14	−3.66	0.010	340	miRNA target	hsa−miR−142−5p
15	−3.65	0.010	209	GSEA C2	IVANOVA_HEMATOPOIESIS_STEM_CELL
16	−3.52	0.011	14	GSEA C2	REACTOME_SYNTHESIS_OF_SUBSTRATES_IN_N_GLYCAN_B
17	−3.51	0.011	5693	Lymphoma	HOPP_Weak_enhancer
18	−3.5	0.011	45	miRNA target	hsa−miR−411
19	−3.47	0.012	659	GSEA C2	SCHLOSSER_SERUM_RESPONSE_DN
20	−3.44	0.012	10	BP	Schwann cell development



A1_mel

Local Summary

%DE = 0.75

metagenes = 42

genes = 399

genes in genesets = 395

genes with fdr < 0.1 = 210 (189 + / 21 −)

genes with fdr < 0.05 = 200 (180 + / 20 −)

genes with fdr < 0.01 = 121 (115 + / 6 −)

<r> metagenes = 0.68

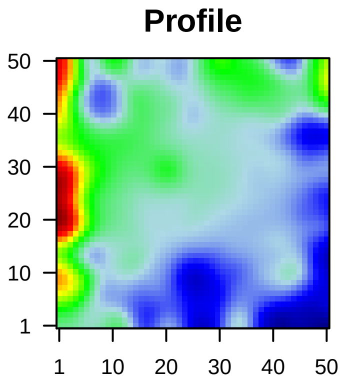
<r> genes = 0.08

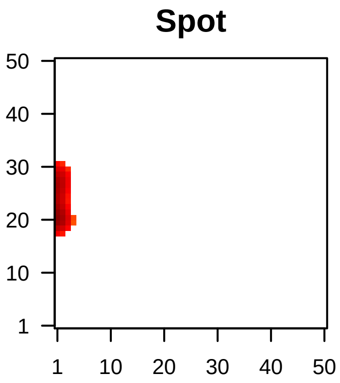
<FC> = 0.36

<shrinkage−t> = 5.96

<p−value> = 0

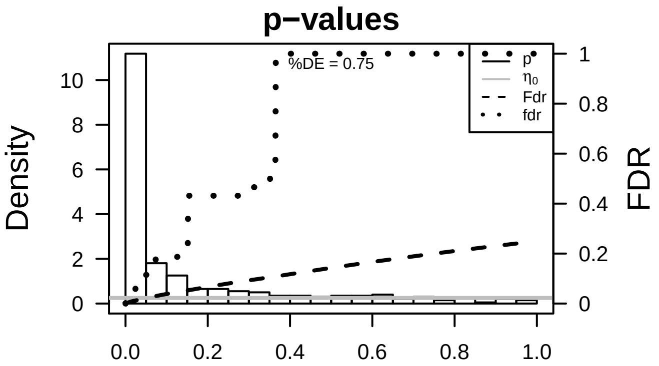
<fdr> = 0.52





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	PTP4A1	−1.47	2e−16	2e−14	1 x 21	protein tyrosine phosphatase type IVA, member 1 [Source:H
2	PPP1R13L	1.82	4e−16	5e−13	1 x 28	protein phosphatase 1, regulatory subunit 13 like [Source:HG
3	SIPA1L3	1.74	6e−15	5e−13	1 x 27	signal−induced proliferation−associated 1 like 3 [Source:HGN
4	SPATS1	1.73	1e−14	9e−12	2 x 30	spermatogenesis associated, serine−rich 1 [Source:HGNC S
5	ITGB1BP2	1.65	2e−13	9e−12	1 x 27	integrin beta 1 binding protein (melusin) 2 [Source:HGNC Sy
6	TFEB	1.64	2e−13	6e−10	1 x 26	transcription factor EB [Source:HGNC Symbol;Acc:HGNC:11
7	PEX16	1.54	6e−12	2e−08	1 x 29	peroxisomal biogenesis factor 16 [Source:HGNC Symbol;Acc
8	DCAKD	1.4	3e−10	2e−08	3 x 19	dephospho−CoA kinase domain containing [Source:HGNC S
9	CASKIN2	1.4	4e−10	9e−08	1 x 28	CASK interacting protein 2 [Source:HGNC Symbol;Acc:HGN
10	SCLY	1.35	1e−09	2e−07	1 x 25	selenocysteine lyase [Source:HGNC Symbol;Acc:HGNC:181
11	MIOS	1.3	6e−09	2e−07	1 x 21	missing oocyte, meiosis regulator, homolog (Drosophila) [Sou
12	IFNAR2	1.29	7e−09	2e−07	1 x 20	interferon (alpha, beta and omega) receptor 2 [Source:HGNC
13	FHL2	1.29	8e−09	2e−07	1 x 29	four and a half LIM domains 2 [Source:HGNC Symbol;Acc:H
14	GET4	1.28	9e−09	4e−07	1 x 19	golgi to ER traffic protein 4 homolog (S. cerevisiae) [Source:
15	FAM195A	1.27	1e−08	8e−07	1 x 18	family with sequence similarity 195, member A [Source:HGN
16	CHN1	1.25	2e−08	8e−07	1 x 26	chimerin 1 [Source:HGNC Symbol;Acc:HGNC:1943]
17	KLHL5	1.23	4e−08	8e−07	1 x 28	kelch−like family member 5 [Source:HGNC Symbol;Acc:HGN
18	ZNF511	1.23	4e−08	5e−06	1 x 21	zinc finger protein 511 [Source:HGNC Symbol;Acc:HGNC:28
19	COX5A	0.6	9e−08	8e−06	1 x 21	cytochrome c oxidase subunit Va [Source:HGNC Symbol;Acc
20	HILPDA	1.16	2e−07	8e−06	1 x 18	hypoxia inducible lipid droplet−associated [Source:HGNC Sy



A1_mel

Local Summary

%DE = 0.75

metagenes = 10

genes = 230

genes in genesets = 228

genes with fdr < 0.1 = 129 (108 + / 21 −)

genes with fdr < 0.05 = 108 (94 + / 14 −)

genes with fdr < 0.01 = 69 (63 + / 6 −)

<r> metagenes = 0.95

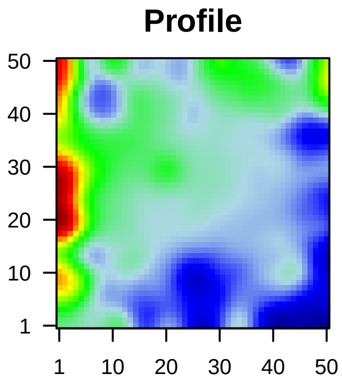
<r> genes = 0.23

<FC> = 0.3

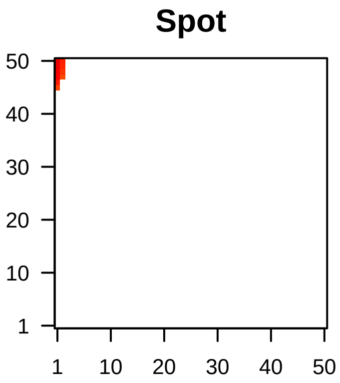
<shrinkage−t> = 4.81

<p−value> = 0.01

<fdr> = 0.52



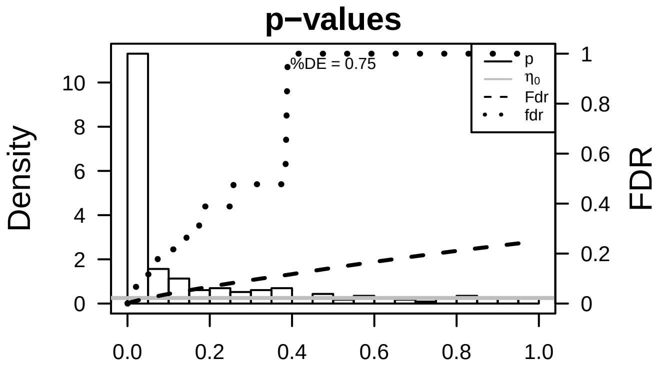
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	FANCA	1.41	3e−10	9e−09	1 x 50	Fanconi anemia, complementation group A [Source:HGNC S
2	HAT1	−1.09	3e−10	1e−07	1 x 50	histone acetyltransferase 1 [Source:HGNC Symbol;Acc:HGN
3	CCNE2	1.33	3e−09	2e−07	2 x 50	cyclin E2 [Source:HGNC Symbol;Acc:HGNC:1590]
4	CENPH	1.29	7e−09	2e−07	1 x 47	centromere protein H [Source:HGNC Symbol;Acc:HGNC:172
5	CEP97	−1.2	1e−08	2e−07	2 x 47	centrosomal protein 97kDa [Source:HGNC Symbol;Acc:HGN
6	GSE1	1.27	1e−08	2e−06	1 x 47	Gse1 coiled−coil protein [Source:HGNC Symbol;Acc:HGNC:
7	CKB	1.14	5e−08	5e−06	2 x 47	creatine kinase, brain [Source:HGNC Symbol;Acc:HGNC:199
8	RAD51	1.18	1e−07	5e−06	1 x 50	RAD51 recombinase [Source:HGNC Symbol;Acc:HGNC:981
9	FIGNL1	1.14	3e−07	5e−06	2 x 50	fidgetin−like 1 [Source:HGNC Symbol;Acc:HGNC:13286]
10	MCM7	1.04	3e−07	5e−06	2 x 50	minichromosome maintenance complex component 7 [Sourc
11	CENPU	1.12	5e−07	5e−06	2 x 50	centromere protein U [Source:HGNC Symbol;Acc:HGNC:213
12	MCM5	1.12	5e−07	2e−05	1 x 49	minichromosome maintenance complex component 5 [Sourc
13	TIPIN	1.1	8e−07	3e−05	1 x 47	TIMELESS interacting protein [Source:HGNC Symbol;Acc:H
14	NCAPH2	1.07	2e−06	3e−05	1 x 50	non−SMC condensin II complex, subunit H2 [Source:HGNC
15	PRIM1	1.06	2e−06	3e−05	1 x 50	primase, DNA, polypeptide 1 (49kDa) [Source:HGNC Symbol
16	DTL	1.05	2e−06	3e−05	1 x 50	denticleless E3 ubiquitin protein ligase homolog (Drosophila)
17	TIMM8A	1.04	3e−06	3e−05	1 x 45	translocase of inner mitochondrial membrane 8 homolog A (
18	MMS22L	1.03	4e−06	4e−05	2 x 50	MMS22−like, DNA repair protein [Source:HGNC Symbol;Acc:
19	EXO1	1.03	4e−06	4e−05	1 x 50	exonuclease 1 [Source:HGNC Symbol;Acc:HGNC:3511]
20	C19orf48	0.95	5e−06	1e−04	1 x 50	chromosome 19 open reading frame 48 [Source:HGNC Sym



p−values

A1_mel

Local Summary

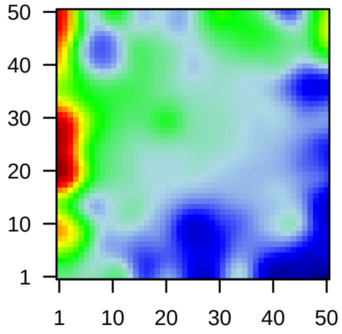
%DE = 0.66
metagenes = 7
genes = 105
genes in genesets = 103

genes with fdr < 0.1 = 15 (1 + / 14 −)
genes with fdr < 0.05 = 5 (0 + / 5 −)
genes with fdr < 0.01 = 1 (0 + / 1 −)

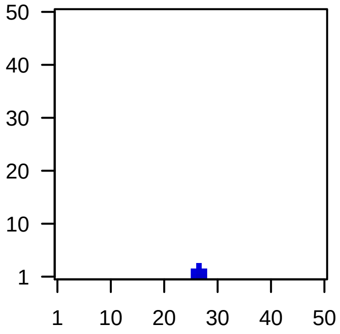
<r> metagenes = 0.99
<r> genes = 0.28

<FC> = −0.23
<shrinkage−t> = −3.51
<p−value> = 0.16
<fdr> = 0.87

Profile



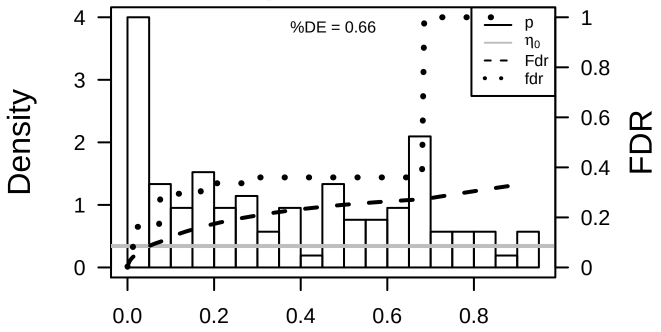
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ARIH1	−0.87	9e−05	0.003	26 x 1	ariadne RBR E3 ubiquitin protein ligase 1 [Source:HGNC Sy
2	MMS19	−0.84	2e−04	0.014	28 x 1	MMS19 nucleotide excision repair homolog (S. cerevisiae) [S
3	ANP32A	−0.77	5e−04	0.026	26 x 1	acidic (leucine−rich) nuclear phosphoprotein 32 family, memb
4	PRKCSH	−0.69	2e−03	0.026	27 x 1	protein kinase C substrate 80K−H [Source:HGNC Symbol;Ac
5	KLF6	−0.6	2e−03	0.026	27 x 1	Kruppel−like factor 6 [Source:HGNC Symbol;Acc:HGNC:223
6	DDX27	−0.66	3e−03	0.063	27 x 1	DEAD (Asp−Glu−Ala−Asp) box polypeptide 27 [Source:HGN
7	UBE2E1	−0.61	6e−03	0.063	27 x 1	ubiquitin−conjugating enzyme E2E 1 [Source:HGNC Symbol;
8	PRPF4B	−0.55	7e−03	0.063	27 x 1	pre−mRNA processing factor 4B [Source:HGNC Symbol;Acc:
9	ZNF286B	−0.59	8e−03	0.078	28 x 1	zinc finger protein 286B [Source:HGNC Symbol;Acc:HGNC:3
10	MAF	−0.56	1e−02	0.078	26 x 1	v−maf avian musculoaponeurotic fibrosarcoma oncogene ho
11	ZNF543	0.56	1e−02	0.078	27 x 1	zinc finger protein 543 [Source:HGNC Symbol;Acc:HGNC:25
12	AKIRIN1	−0.55	1e−02	0.089	28 x 1	akirin 1 [Source:HGNC Symbol;Acc:HGNC:25744]
13	PACS2	−0.52	2e−02	0.089	28 x 1	phosphofurin acidic cluster sorting protein 2 [Source:HGNC
14	ETS1	−0.51	2e−02	0.089	28 x 1	v−ets avian erythroblastosis virus E26 oncogene homolog 1 [
15	TLE1	−0.5	2e−02	0.089	26 x 1	transducin−like enhancer of split 1 (E(sp1) homolog, Drosoph
16	BOD1L1	−0.5	2e−02	0.162	28 x 1	biorientation of chromosomes in cell division 1−like 1 [Source
17	SERF1A	−0.47	4e−02	0.162	27 x 1	small EDRK−rich factor 1A (telomeric) [Source:HGNC Symb
18	C20orf194	−0.46	4e−02	0.162	26 x 1	chromosome 20 open reading frame 194 [Source:HGNC Sy
19	RGPD6	−0.46	4e−02	0.168	27 x 1	RANBP2−like and GRIP domain containing 6 [Source:HGNC
20	SERF1B	−0.44	5e−02	0.168	27 x 1	small EDRK−rich factor 1B (centromeric) [Source:HGNC Sy

p−values



A1_mel

Local Summary

%DE = 0.8

metagenes = 69

genes = 811

genes in genesets = 810

genes with fdr < 0.1 = 331 (101 + / 230 −)

genes with fdr < 0.05 = 262 (84 + / 178 −)

genes with fdr < 0.01 = 144 (49 + / 95 −)

<r> metagenes = 0.78

<r> genes = 0.1

<FC> = −0.16

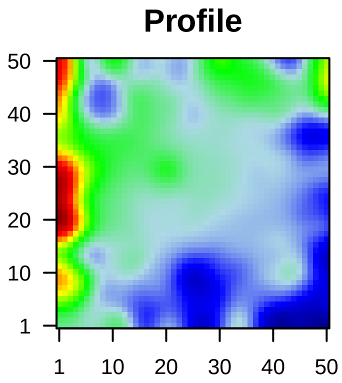
<shrinkage−t> = −2.53

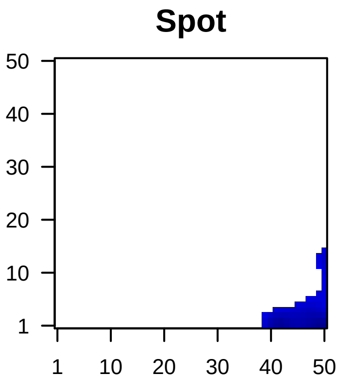
<p−value> = 0.03

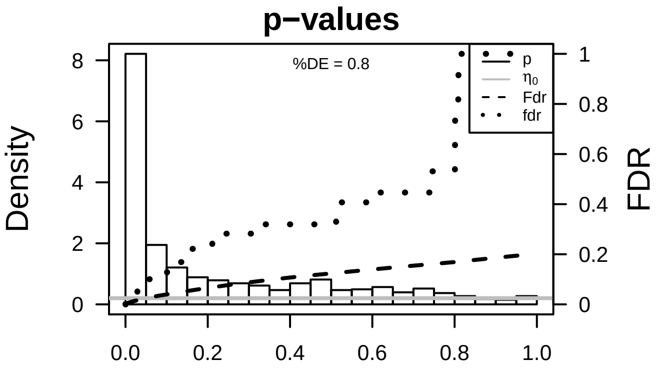
<fdr> = 0.67

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	LAMB2	−1.61	2e−16	4e−14	50 x 6	laminin, beta 2 (laminin S) [Source:HGNC Symbol;Acc:HGNC
2	PIEZO2	1.6	9e−13	1e−10	50 x 4	piezo−type mechanosensitive ion channel component 2 [Sour
3	AKAP9	−1.26	1e−12	2e−10	42 x 1	A kinase (PRKA) anchor protein 9 [Source:HGNC Symbol;Ac
4	OSGIN1	−1.37	3e−12	2e−10	50 x 6	oxidative stress induced growth inhibitor 1 [Source:HGNC Sy
5	TGIF1	−1.32	4e−12	4e−08	50 x 1	TGFB−induced factor homeobox 1 [Source:HGNC Symbol;Ac
6	BBIP1	−1.29	2e−10	2e−07	42 x 4	BBSome interacting protein 1 [Source:HGNC Symbol;Acc:HG
7	ARHGAP5	−1.08	2e−09	2e−07	50 x 14	Rho GTPase activating protein 5 [Source:HGNC Symbol;Acc:
8	UBLCP1	−1.24	3e−09	3e−07	50 x 8	ubiquitin−like domain containing CTD phosphatase 1 [Source
9	CERS5	−1.22	6e−09	3e−07	50 x 15	ceramide synthase 5 [Source:HGNC Symbol;Acc:HGNC:237
10	RALGPS2	1.29	7e−09	1e−06	50 x 5	Ral GEF with PH domain and SH3 binding motif 2 [Source:H
11	GBE1	−1.16	1e−08	2e−06	50 x 3	glucan (1,4−alpha−), branching enzyme 1 [Source:HGNC Sy
12	CBLB	−1.19	3e−08	2e−06	50 x 2	Cbl proto−oncogene B, E3 ubiquitin protein ligase [Source:H
13	CCDC57	−1.18	4e−08	6e−06	50 x 11	coiled−coil domain containing 57 [Source:HGNC Symbol;Acc
14	NRP1	1.19	9e−08	6e−06	50 x 5	neuropilin 1 [Source:HGNC Symbol;Acc:HGNC:8004]
15	PPAP2A	1.18	1e−07	6e−06	50 x 4	phosphatidic acid phosphatase type 2A [Source:HGNC Symb
16	WDR18	−1.15	2e−07	6e−06	50 x 12	WD repeat domain 18 [Source:HGNC Symbol;Acc:HGNC:17
17	WDR25	1.16	2e−07	6e−06	43 x 3	WD repeat domain 25 [Source:HGNC Symbol;Acc:HGNC:21
18	FAM104A	−1.14	2e−07	6e−06	50 x 6	family with sequence similarity 104, member A [Source:HGN
19	MARCKS	−0.55	2e−07	6e−06	46 x 1	myristoylated alanine−rich protein kinase C substrate [Source
20	EFCAB14	1.15	3e−07	6e−06	50 x 7	EF−hand calcium binding domain 14 [Source:HGNC Symbol;







A1_mel

Local Summary

%DE = 0.52

metagenes = 18

genes = 136

genes in genesets = 133

genes with fdr < 0.1 = 46 (11 + / 35 −)

genes with fdr < 0.05 = 23 (6 + / 17 −)

genes with fdr < 0.01 = 19 (3 + / 16 −)

<r> metagenes = 0.92

<r> genes = 0.11

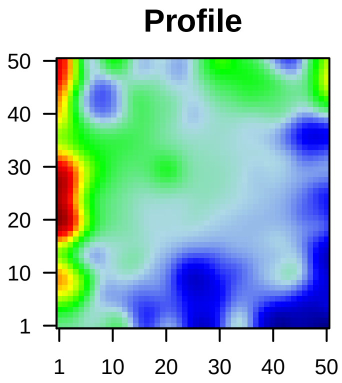
<FC> = −0.19

<shrinkage−t> = −3.09

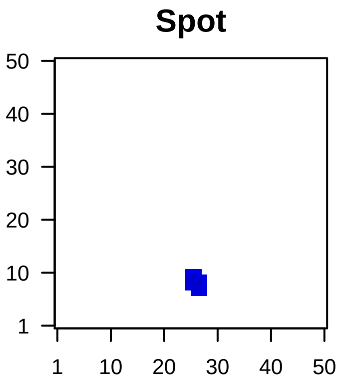
<p−value> = 0.04

<fdr> = 0.69

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	PTPLA	1.42	2e−10	4e−05	26 x 10	
2	ZNF638	−0.67	6e−07	6e−05	26 x 9	zinc finger protein 638 [Source:HGNC Symbol;Acc:HGNC:17
3	ZNF124	−1.06	2e−06	3e−04	27 x 9	zinc finger protein 124 [Source:HGNC Symbol;Acc:HGNC:12
4	GOLGA4	−0.89	1e−05	3e−04	26 x 10	golgin A4 [Source:HGNC Symbol;Acc:HGNC:4427]
5	C12orf45	−0.98	1e−05	4e−04	26 x 8	chromosome 12 open reading frame 45 [Source:HGNC Symb
6	TFB2M	−0.95	2e−05	4e−04	26 x 9	transcription factor B2, mitochondrial [Source:HGNC Symbol;
7	GTF3C3	−0.93	2e−05	1e−03	26 x 10	general transcription factor IIIC, polypeptide 3, 102kDa [Sour
8	RRP15	−0.83	4e−05	2e−03	26 x 11	ribosomal RNA processing 15 homolog (S. cerevisiae) [Sour
9	PPP6C	−0.76	8e−05	2e−03	25 x 11	protein phosphatase 6, catalytic subunit [Source:HGNC Symb
10	SRGAP2	−0.86	1e−04	2e−03	28 x 9	SLIT−ROBO Rho GTPase activating protein 2 [Source:HGNC
11	TMEM30A	0.81	1e−04	6e−03	26 x 11	transmembrane protein 30A [Source:HGNC Symbol;Acc:HGN
12	MKRN2	−0.8	4e−04	6e−03	25 x 9	makorin ring finger protein 2 [Source:HGNC Symbol;Acc:HGN
13	NFS1	−0.79	4e−04	6e−03	28 x 9	NFS1 cysteine desulfurase [Source:HGNC Symbol;Acc:HGN
14	CAMSAP2	−0.78	5e−04	6e−03	26 x 10	calmodulin regulated spectrin−associated protein family, mem
15	TMEM206	−0.77	6e−04	6e−03	26 x 10	transmembrane protein 206 [Source:HGNC Symbol;Acc:HGN
16	PAPD4	0.73	6e−04	6e−03	27 x 9	PAP associated domain containing 4 [Source:HGNC Symbol;
17	SPRYD7	−0.75	7e−04	6e−03	26 x 7	SPRY domain containing 7 [Source:HGNC Symbol;Acc:HGN
18	PBRM1	−0.63	7e−04	9e−03	25 x 11	polybromo 1 [Source:HGNC Symbol;Acc:HGNC:30064]
19	BLZF1	−0.74	1e−03	9e−03	26 x 11	basic leucine zipper nuclear factor 1 [Source:HGNC Symbol;
20	NAA25	0.67	1e−03	1e−02	25 x 9	N(alpha)−acetyltransferase 25, NatB auxiliary subunit [Source

p−values