H2_mel

Global Summary

%DE = 0.2

genes with fdr < 0.2 = 2530 (1595 + / 935 −)

genes with fdr < 0.1 = 2066 (1316 + / 750 −)

genes with fdr < 0.05 = 1702 (1096 + / 606 −)

genes with fdr < 0.01 = 1066 (700 + / 366 −)

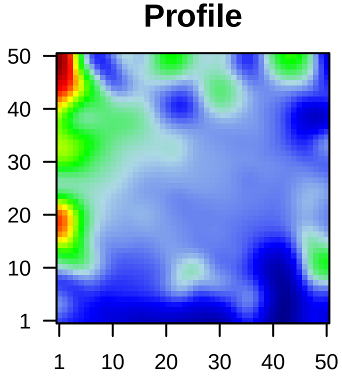
genes in genesets = 14839

<FC> = 0

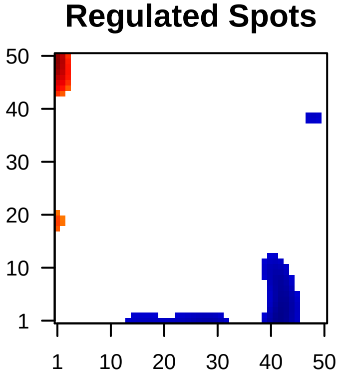
<shrinkage−t> = 0.07

<p−value> = 0.09

<fdr> = 0.8



Profile



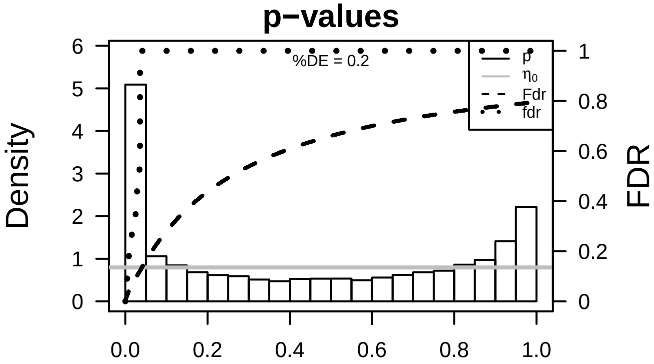
Regulated Spots

Global Genelist

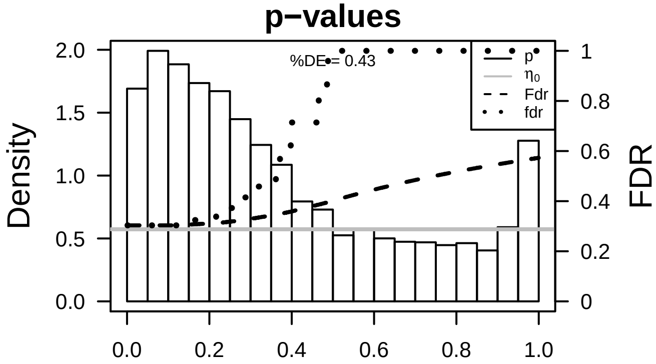
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	EXOSC7	−1.65	2e−16	7e−13	22 x 1	exosome component 7 [Source:HGNC Symbol;Acc:HGNC:2
2	PPP2R1A	−1.27	2e−16	7e−13	45 x 47	protein phosphatase 2, regulatory subunit A, alpha [Source:H
3	SMCO4	2.06	2e−16	7e−13	1 x 47	single−pass membrane protein with coiled−coil domains 4 [S
4	TXNDC17	−1.2	2e−16	7e−13	50 x 39	thioredoxin domain containing 17 [Source:HGNC Symbol;Acc
5	TIMMDC1	−1.14	4e−16	3e−12	4 x 4	translocase of inner mitochondrial membrane domain contain
6	PRKRA	−1.5	7e−16	5e−12	29 x 11	protein kinase, interferon−inducible double stranded RNA de
7	SCPEP1	−1.49	1e−15	1e−11	49 x 37	serine carboxypeptidase 1 [Source:HGNC Symbol;Acc:HGN
8	CEP97	1.67	3e−15	1e−11	2 x 47	centrosomal protein 97kDa [Source:HGNC Symbol;Acc:HGN
9	PRMT5	−1.48	3e−15	3e−10	34 x 50	protein arginine methyltransferase 5 [Source:HGNC Symbol;
10	CDC27	−1.44	4e−14	3e−10	9 x 49	cell division cycle 27 [Source:HGNC Symbol;Acc:HGNC:172
11	LMLN	1.68	6e−14	5e−10	1 x 20	leishmanolysin−like (metallopeptidase M8 family) [Source:HG
12	SLC26A4	1.66	1e−13	5e−10	2 x 15	solute carrier family 26 (anion exchanger), member 4 [Source
13	ETV1	1.65	2e−13	5e−10	48 x 4	ets variant 1 [Source:HGNC Symbol;Acc:HGNC:3490]
14	ISG20	1.65	2e−13	2e−09	17 x 50	interferon stimulated exonuclease gene 20kDa [Source:HGN
15	TXN2	−0.94	5e−13	2e−09	4 x 42	thioredoxin 2 [Source:HGNC Symbol;Acc:HGNC:17772]
16	AKAP9	−1.27	1e−12	2e−09	42 x 1	A kinase (PRKA) anchor protein 9 [Source:HGNC Symbol;Ac
17	MGAT4B	1.6	1e−12	2e−09	30 x 8	mannosyl (alpha−1,3−)−glycoprotein beta−1,4−N−acetylgluc
18	RCN1	0.79	1e−12	2e−09	1 x 23	reticulocalbin 1, EF−hand calcium binding domain [Source:H
19	CTD−2313N1	1.59	1e−12	6e−09	30 x 43	
20	DAK	1.58	2e−12	6e−09	31 x 50	dihydroxyacetone kinase 2 homolog (S. cerevisiae) [Source:

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	6.85	0.001	609	GSEA C2	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIA
2	6.6	0.001	1251	GSEA C2	DODD_NASOPHARYNGEAL_CARCINOMA_DN
3	6.27	0.002	485	GSEA C2	CHICAS_RB1_TARGETS_SENESCENT
4	6.26	0.002	1192	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
5	6.25	0.002	242	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
6	6.24	0.002	7592	Lymphoma	HOPP_Active_promoter
7	6.13	0.002	862	GSEA C2	JOHNSTONE_PARVB_TARGETS_3_DN
8	5.92	0.002	517	GSEA C2	FEVR_CTNNB1_TARGETS_DN
9	5.53	0.002	89	GSEA C2	PYEON_HPV_POSITIVE_TUMORS_UP
10	5.49	0.003	216	GSEA C2	MARKEY_RB1_ACUTE_LOF_DN
11	5.23	0.003	465	Chr	Chr 15
12	5.22	0.003	197	HM	HALLMARK_E2F_TARGETS
13	5.14	0.003	58	GSEA C2	SONG_TARGETS_OF_IE86_CMV_PROTEIN
14	5.13	0.003	12	GSEA C2	SA_REG_CASCADE_OF_CYCLIN_EXPR
15	5.13	0.003	32	GSEA C2	KEGG_DNA_REPLICATION
16	4.91	0.004	1326	GSEA C2	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
17	4.87	0.004	7209	Lymphoma	HOPP_Weak_promoter
18	4.84	0.004	834	GSEA C2	LEE_BMP2_TARGETS_DN
19	4.83	0.004	68	GSEA C2	VERNELL_RETINOBLASTOMA_PATHWAY_UP
20	4.83	0.004	136	GSEA C2	RUIZ_TNC_TARGETS_DN
Underexpressed					
1	−5.75	0.002	3081	Brain	Mid_Frontal_Lobe_ZNF
2	−4.7	0.004	2698	Colon Cancer	EnhA_Colon
3	−4.65	0.005	840	Chr	Chr 17
4	−4.64	0.005	2798	Colon Cancer	TxEnhG1_Colon
5	−4.15	0.007	270	GSEA C2	NIKOLSKY_BREAST_CANCER_17Q21_Q25_AMPLICON
6	−3.79	0.009	33	GSEA C2	APPIERTO_RESPONSE_TO_FENRETINIDE_UP
7	−3.73	0.009	304	GSEA C2	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
8	−3.63	0.010	77	GSEA C2	REACTOME_REGULATION_OF_MRNA_STABILITY_BY_PROTE
9	−3.49	0.012	649	Chr	Chr 16
10	−3.39	0.013	23	GSEA C2	REACTOME_ABORTIVE_ELONGATION_OF_HIV1_TRANSCRIP
11	−3.39	0.013	12	GSEA C2	BIOCARTA_ARENRF2_PATHWAY
12	−3.39	0.013	33	MF	RNA polymerase II transcription cofactor activity
13	−3.35	0.013	15	GSEA C2	BIOCARTA_CCR5_PATHWAY
14	−3.34	0.013	222	GSEA C2	CONCANNON_APOPTOSIS_BY_EPOXOMICIN_UP
15	−3.29	0.014	33	BP	regulation of mitotic cell cycle
16	−3.27	0.014	127	GSEA C2	REACTOME_METABOLISM_OF_MRNA
17	−3.27	0.014	35	CC	mediator complex
18	−3.26	0.014	5880	Colon Cancer	TssD2_Colon
19	−3.24	0.015	10	BP	protein deacetylation
20	−3.22	0.015	26	GSEA C2	BIOCARTA_PROTEASOME_PATHWAY



p−values



p−values

H2_mel

Local Summary

%DE = 0.78

metagenes = 6

genes = 180

genes in genesets = 180

genes with fdr < 0.1 = 107 (89 + / 18 −)

genes with fdr < 0.05 = 96 (82 + / 14 −)

genes with fdr < 0.01 = 60 (51 + / 9 −)

<r> metagenes = 0.98

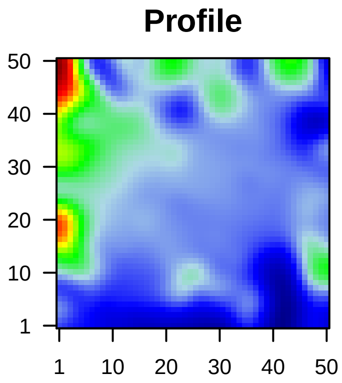
<r> genes = 0.18

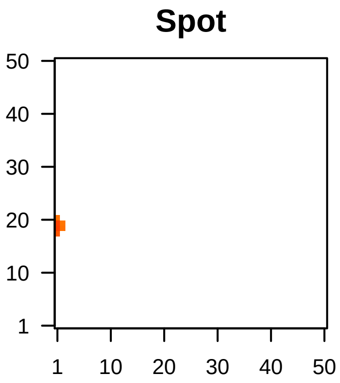
<FC> = 0.28

<shrinkage−t> = 4.96

<p−value> = 0.01

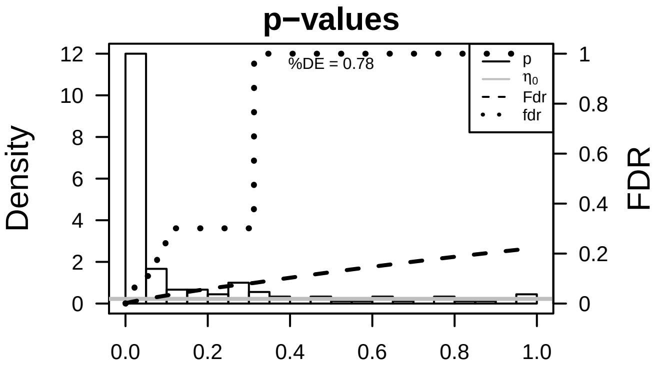
<fdr> = 0.49





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	LMLN	1.68	6e−14	1e−09	1 x 20	leishmanolysin−like (metallopeptidase M8 family) [Source:HG
2	PTP4A1	1.18	3e−11	1e−07	1 x 21	protein tyrosine phosphatase type IVA, member 1 [Source:HG
3	SDHAF1	1.33	3e−09	7e−07	2 x 19	succinate dehydrogenase complex assembly factor 1 [Source
4	HEXB	1.07	2e−08	2e−06	1 x 21	hexosaminidase B (beta polypeptide) [Source:HGNC Symbol
5	TMEM123	0.49	6e−08	3e−06	1 x 21	transmembrane protein 123 [Source:HGNC Symbol;Acc:HGN
6	MPZL1	0.96	2e−07	3e−06	1 x 19	myelin protein zero−like 1 [Source:HGNC Symbol;Acc:HGNC
7	COX5A	0.59	2e−07	4e−06	1 x 21	cytochrome c oxidase subunit Va [Source:HGNC Symbol;Acc
8	GTF3A	0.77	3e−07	2e−05	1 x 20	general transcription factor IIIA [Source:HGNC Symbol;Acc:H
9	HILPDA	1.11	7e−07	2e−05	1 x 18	hypoxia inducible lipid droplet−associated [Source:HGNC Sy
10	CYC1	0.95	1e−06	1e−04	1 x 20	cytochrome c−1 [Source:HGNC Symbol;Acc:HGNC:2579]
11	TOR2A	1.04	4e−06	2e−04	1 x 21	torsin family 2, member A [Source:HGNC Symbol;Acc:HGNC
12	INSIG1	0.98	1e−05	2e−04	1 x 20	insulin induced gene 1 [Source:HGNC Symbol;Acc:HGNC:60
13	SERPINE2	0.96	1e−05	2e−04	1 x 20	serpin peptidase inhibitor, clade E (nexin, plasminogen activa
14	DNAJC4	−0.96	2e−05	2e−04	1 x 19	DnaJ (Hsp40) homolog, subfamily C, member 4 [Source:HGN
15	PIGY	0.43	2e−05	2e−04	1 x 20	phosphatidylinositol glycan anchor biosynthesis, class Y [Sou
16	PGRMC1	0.95	2e−05	4e−04	1 x 20	progesterone receptor membrane component 1 [Source:HGN
17	YIPF4	0.91	5e−05	4e−04	1 x 21	Yip1 domain family, member 4 [Source:HGNC Symbol;Acc:HG
18	NT5C3B	0.89	5e−05	4e−04	1 x 20	5'−nucleotidase, cytosolic IIIB [Source:HGNC Symbol;Acc:HG
19	PRELID1	0.84	5e−05	5e−04	1 x 20	PRELI domain containing 1 [Source:HGNC Symbol;Acc:HGN
20	GAMT	0.89	7e−05	6e−04	1 x 20	guanidinoacetate N−methyltransferase [Source:HGNC Symb



H2_mel

Local Summary

%DE = 0.76

metagenes = 23

genes = 365

genes in genesets = 363

genes with fdr < 0.1 = 196 (172 + / 24 −)

genes with fdr < 0.05 = 196 (172 + / 24 −)

genes with fdr < 0.01 = 138 (123 + / 15 −)

<r> metagenes = 0.88

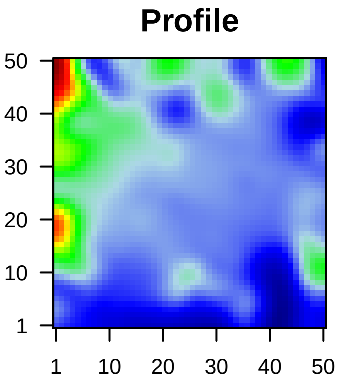
<r> genes = 0.19

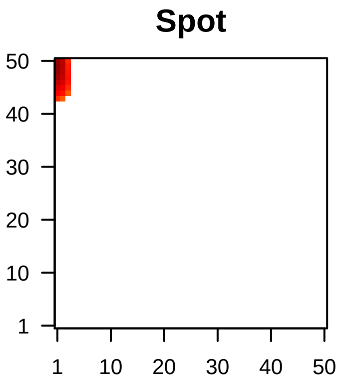
<FC> = 0.35

<shrinkage−t> = 5.81

<p−value> = 0.01

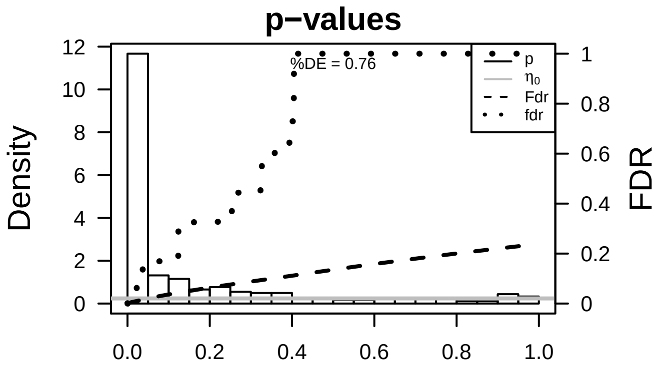
<fdr> = 0.49





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	SMCO4	2.06	2e−16	2e−14	1 x 47	single−pass membrane protein with coiled−coil domains 4 [S
2	CEP97	1.67	3e−15	2e−10	2 x 47	centrosomal protein 97kDa [Source:HGNC Symbol;Acc:HGN
3	MUC7	1.57	3e−12	3e−09	1 x 46	mucin 7, secreted [Source:HGNC Symbol;Acc:HGNC:7518]
4	RNASEH2B	1.48	3e−11	4e−08	1 x 50	ribonuclease H2, subunit B [Source:HGNC Symbol;Acc:HGN
5	EXO1	1.38	7e−10	4e−08	1 x 50	exonuclease 1 [Source:HGNC Symbol;Acc:HGNC:3511]
6	CEP76	1.37	1e−09	4e−08	1 x 43	centrosomal protein 76kDa [Source:HGNC Symbol;Acc:HGN
7	CAPG	1.36	1e−09	8e−08	1 x 43	capping protein (actin filament), gelsolin−like [Source:HGNC
8	PSMC3IP	1.33	3e−09	8e−08	1 x 50	PSMC3 interacting protein [Source:HGNC Symbol;Acc:HGN
9	ANKRD32	1.32	3e−09	3e−07	1 x 50	ankyrin repeat domain 32 [Source:HGNC Symbol;Acc:HGNC
10	MED21	−1.22	6e−09	1e−06	3 x 46	mediator complex subunit 21 [Source:HGNC Symbol;Acc:HG
11	NFKBIA	1.26	2e−08	2e−06	1 x 45	nuclear factor of kappa light polypeptide gene enhancer in B−
12	EXOSC8	0.85	1e−07	2e−06	1 x 50	exosome component 8 [Source:HGNC Symbol;Acc:HGNC:17
13	DOK5	1.15	1e−07	2e−06	1 x 44	docking protein 5 [Source:HGNC Symbol;Acc:HGNC:16173]
14	NUP205	1.18	1e−07	2e−06	1 x 47	nucleoporin 205kDa [Source:HGNC Symbol;Acc:HGNC:1865
15	RANBP17	1.17	2e−07	2e−06	1 x 50	RAN binding protein 17 [Source:HGNC Symbol;Acc:HGNC:1
16	DTL	1.17	2e−07	3e−06	1 x 50	denticleless E3 ubiquitin protein ligase homolog (Drosophila)
17	POLA1	1.16	2e−07	3e−06	1 x 47	polymerase (DNA directed), alpha 1, catalytic subunit [Sourc
18	TIMM8A	1.15	3e−07	3e−06	1 x 45	translocase of inner mitochondrial membrane 8 homolog A (y
19	ZDHHC6	1.14	3e−07	3e−06	1 x 49	zinc finger, DHHC−type containing 6 [Source:HGNC Symbol;
20	TUBGCP3	1.15	3e−07	3e−06	1 x 48	tubulin, gamma complex associated protein 3 [Source:HGNC



H2_mel

Local Summary

%DE = 0.71

metagenes = 33

genes = 490

genes in genesets = 477

genes with fdr < 0.1 = 125 (40 + / 85 −)

genes with fdr < 0.05 = 93 (30 + / 63 −)

genes with fdr < 0.01 = 40 (14 + / 26 −)

<r> metagenes = 0.73

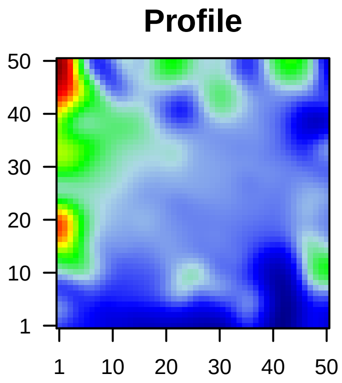
<r> genes = 0.11

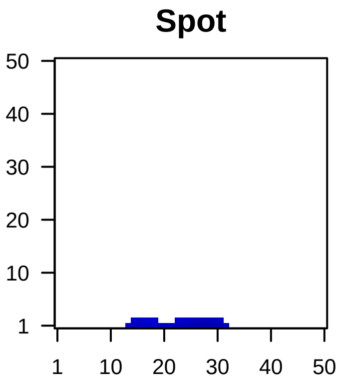
<FC> = −0.14

<shrinkage−t> = −2.17

<p−value> = 0.07

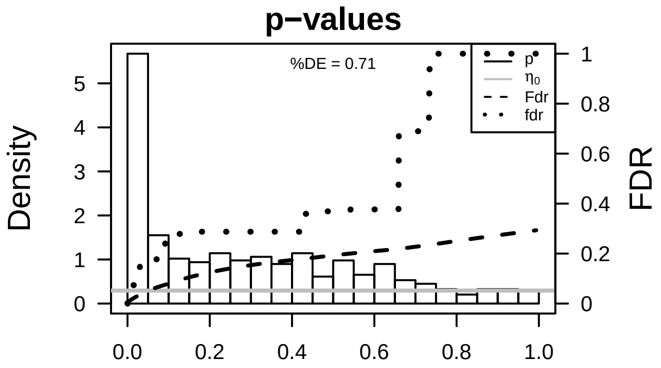
<fdr> = 0.78





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	EXOSC7	−1.65	2e−16	3e−14	22 x 1	exosome component 7 [Source:HGNC Symbol;Acc:HGNC:2
2	EML1	1.52	1e−11	7e−07	15 x 1	echinoderm microtubule associated protein like 1 [Source:HG
3	CNOT11	1.31	5e−09	1e−06	18 x 2	CCR4−NOT transcription complex, subunit 11 [Source:HGNC
4	WDR45B	−0.95	1e−08	8e−06	22 x 1	WD repeat domain 45B [Source:HGNC Symbol;Acc:HGNC:2
5	PRDM4	1.19	1e−07	8e−06	20 x 1	PR domain containing 4 [Source:HGNC Symbol;Acc:HGNC:
6	SPOP	−1.06	2e−07	8e−06	25 x 1	speckle−type POZ protein [Source:HGNC Symbol;Acc:HGNC
7	C2orf68	−1.07	2e−07	2e−05	17 x 1	chromosome 2 open reading frame 68 [Source:HGNC Symbo
8	TAF10	1.14	3e−07	3e−05	21 x 1	TAF10 RNA polymerase II, TATA box binding protein (TBP)−a
9	SLC30A9	−1	5e−07	3e−05	20 x 1	solute carrier family 30 (zinc transporter), member 9 [Source:
10	KIF3A	−1.1	7e−07	4e−05	25 x 2	kinesin family member 3A [Source:HGNC Symbol;Acc:HGNC
11	IL13RA1	1.1	1e−06	5e−05	17 x 1	interleukin 13 receptor, alpha 1 [Source:HGNC Symbol;Acc:H
12	SLC1A4	−1.07	1e−06	7e−04	32 x 1	solute carrier family 1 (glutamate/neutral amino acid transpor
13	QSER1	−0.99	1e−05	7e−04	29 x 1	glutamine and serine rich 1 [Source:HGNC Symbol;Acc:HGN
14	SERPINB1	−0.89	1e−05	7e−04	14 x 1	serpin peptidase inhibitor, clade B (ovalbumin), member 1 [S
15	MIPOL1	0.95	2e−05	7e−04	16 x 2	mirror−image polydactyly 1 [Source:HGNC Symbol;Acc:HGN
16	AP1G1	−0.93	3e−05	7e−04	19 x 1	adaptor−related protein complex 1, gamma 1 subunit [Source
17	GEMIN6	−0.94	3e−05	7e−04	22 x 1	gem (nuclear organelle) associated protein 6 [Source:HGNC
18	NFIC	−0.93	3e−05	7e−04	21 x 1	nuclear factor I/C (CCAAT−binding transcription factor) [Sour
19	MMS19	0.93	3e−05	1e−03	28 x 1	MMS19 nucleotide excision repair homolog (S. cerevisiae) [S
20	PSMD1	−0.5	5e−05	1e−03	16 x 1	proteasome (prosome, macropain) 26S subunit, non−ATPase



H2_mel

Local Summary

%DE = 0.72

metagenes = 70

genes = 532

genes in genesets = 530

genes with fdr < 0.1 = 122 (42 + / 80 −)

genes with fdr < 0.05 = 91 (33 + / 58 −)

genes with fdr < 0.01 = 46 (11 + / 35 −)

<r> metagenes = 0.75

<r> genes = 0.09

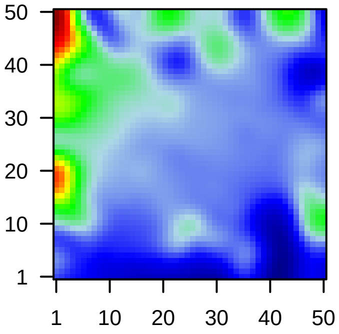
<FC> = −0.15

<shrinkage−t> = −2.35

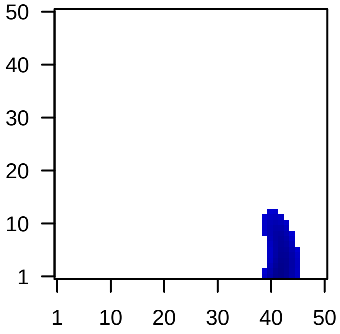
<p−value> = 0.07

<fdr> = 0.79

Profile



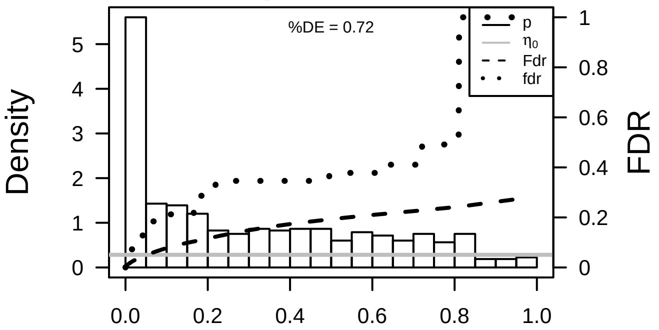
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	AKAP9	−1.27	1e−12	1e−08	42 x 1	A kinase (PRKA) anchor protein 9 [Source:HGNC Symbol;Ac
2	C9orf156	1.42	2e−10	1e−08	45 x 1	chromosome 9 open reading frame 156 [Source:HGNC Sym
3	ZBTB20	1.42	2e−10	1e−08	41 x 10	zinc finger and BTB domain containing 20 [Source:HGNC Sy
4	BBIP1	−1.29	3e−10	6e−07	42 x 4	BBSome interacting protein 1 [Source:HGNC Symbol;Acc:HG
5	ACOT13	−1.2	5e−09	9e−07	43 x 5	acyl−CoA thioesterase 13 [Source:HGNC Symbol;Acc:HGNC
6	CCNL2	−1.17	1e−08	7e−06	45 x 4	cyclin L2 [Source:HGNC Symbol;Acc:HGNC:20570]
7	CYB5R1	−1.18	6e−08	2e−05	41 x 2	cytochrome b5 reductase 1 [Source:HGNC Symbol;Acc:HGN
8	SUGT1	−1.13	3e−07	2e−05	43 x 2	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae) [Sour
9	SHOC2	−0.94	3e−07	9e−05	42 x 6	soc−2 suppressor of clear homolog (C. elegans) [Source:HG
10	DCTN1	−1.09	9e−07	2e−04	41 x 1	dynactin 1 [Source:HGNC Symbol;Acc:HGNC:2711]
11	PIGH	−1.05	2e−06	3e−04	40 x 11	phosphatidylinositol glycan anchor biosynthesis, class H [Sou
12	ABCF2	−1.01	7e−06	3e−04	40 x 1	ATP−binding cassette, sub−family F (GCN20), member 2 [So
13	ANXA11	−1	8e−06	3e−04	40 x 1	annexin A11 [Source:HGNC Symbol;Acc:HGNC:535]
14	CTSF	1	8e−06	4e−04	41 x 2	cathepsin F [Source:HGNC Symbol;Acc:HGNC:2531]
15	RTCA	−0.99	1e−05	1e−03	42 x 3	RNA 3'−terminal phosphate cyclase [Source:HGNC Symbol;
16	PIGM	0.95	2e−05	1e−03	40 x 1	phosphatidylinositol glycan anchor biosynthesis, class M [Sou
17	ANTXR1	0.94	3e−05	1e−03	45 x 5	anthrax toxin receptor 1 [Source:HGNC Symbol;Acc:HGNC:2
18	TNRC6A	−0.92	4e−05	1e−03	42 x 6	trinucleotide repeat containing 6A [Source:HGNC Symbol;Ac
19	TMEM43	−0.91	5e−05	1e−03	43 x 3	transmembrane protein 43 [Source:HGNC Symbol;Acc:HGN
20	PANK3	0.9	6e−05	3e−03	39 x 2	pantothenate kinase 3 [Source:HGNC Symbol;Acc:HGNC:19

p−values



H2_mel

Local Summary

%DE = 0.87

metagenes = 6

genes = 20

genes in genesets = 20

genes with fdr < 0.1 = 14 (0 + / 14 −)

genes with fdr < 0.05 = 11 (0 + / 11 −)

genes with fdr < 0.01 = 6 (0 + / 6 −)

<r> metagenes = 0.98

<r> genes = 0.16

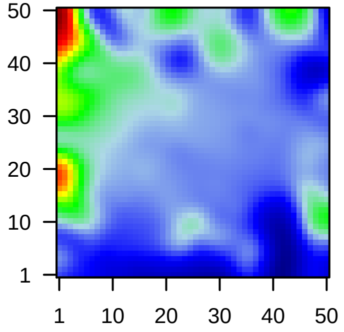
<FC> = −0.46

<shrinkage−t> = −7.39

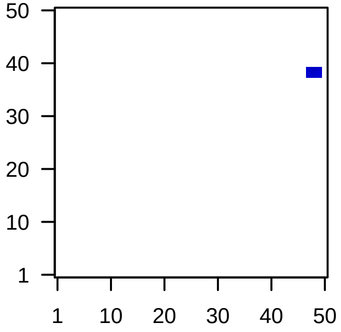
<p−value> = 0.01

<fdr> = 0.52

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	PSMC6	−1.04	3e−11	1e−04	49 x 38	proteasome (prosome, macropain) 26S subunit, ATPase, 6 [S
2	DPH3	−0.83	5e−05	2e−04	49 x 39	diphthamide biosynthesis 3 [Source:HGNC Symbol;Acc:HGN
3	LIPA	−0.85	1e−04	1e−03	48 x 39	lipase A, lysosomal acid, cholesterol esterase [Source:HGNC
4	WDR59	−0.74	1e−03	1e−03	48 x 39	WD repeat domain 59 [Source:HGNC Symbol;Acc:HGNC:25
5	NDUFAF1	−0.73	1e−03	4e−03	49 x 39	NADH dehydrogenase (ubiquinone) complex I, assembly fact
6	HN1	−0.5	3e−03	8e−03	47 x 39	hematological and neurological expressed 1 [Source:HGNC
7	PCGF3	−0.62	6e−03	1e−02	49 x 38	polycomb group ring finger 3 [Source:HGNC Symbol;Acc:HG
8	ELP3	−0.56	1e−02	1e−02	47 x 38	elongator acetyltransferase complex subunit 3 [Source:HGNC
9	SYNPR	−0.54	2e−02	1e−02	48 x 39	synaptoporin [Source:HGNC Symbol;Acc:HGNC:16507]
10	ATP8A1	−0.53	2e−02	3e−02	48 x 39	ATPase, aminophospholipid transporter (APLT), class I, type
11	SMEK2	−0.49	3e−02	3e−02	48 x 39	SMEK homolog 2, suppressor of mek1 (Dictyostelium) [Sourc
12	C11orf73	−0.46	4e−02	1e−01	48 x 39	chromosome 11 open reading frame 73 [Source:HGNC Symb
13	CES2	−0.36	1e−01	1e−01	49 x 39	carboxylesterase 2 [Source:HGNC Symbol;Acc:HGNC:1864]
14	TAMM41	−0.34	1e−01	1e−01	49 x 38	TAM41, mitochondrial translocator assembly and maintenanc
15	TSC1	−0.32	2e−01	2e−01	47 x 39	tuberous sclerosis 1 [Source:HGNC Symbol;Acc:HGNC:1236
16	EIF3G	0.18	3e−01	2e−01	47 x 39	eukaryotic translation initiation factor 3, subunit G [Source:HG
17	DECR2	−0.24	3e−01	4e−01	47 x 38	2,4−dienoyl CoA reductase 2, peroxisomal [Source:HGNC Sy
18	GLS2	−0.14	5e−01	4e−01	48 x 38	glutaminase 2 (liver, mitochondrial) [Source:HGNC Symbol;A
19	TTC3	0.08	6e−01	1e+00	47 x 39	tetratricopeptide repeat domain 3 [Source:HGNC Symbol;Acc
20	PTPRF	−0.11	6e−01	1e+00	48 x 38	protein tyrosine phosphatase, receptor type, F [Source:HGNC

p−values