B3_mel

Global Summary

%DE = 0.2

genes with fdr < 0.2 = 2640 (1600 + / 1040 −)

genes with fdr < 0.1 = 2016 (1206 + / 810 −)

genes with fdr < 0.05 = 1644 (983 + / 661 −)

genes with fdr < 0.01 = 967 (596 + / 371 −)

genes in genesets = 14839

<FC> = 0

<shrinkage−t> = 0.03

<p−value> = 0.09

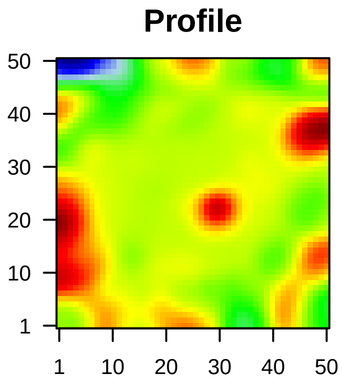
<fdr> = 0.8

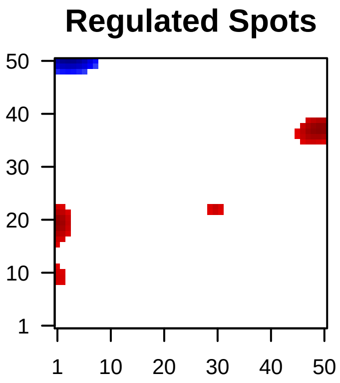
Global Genelist

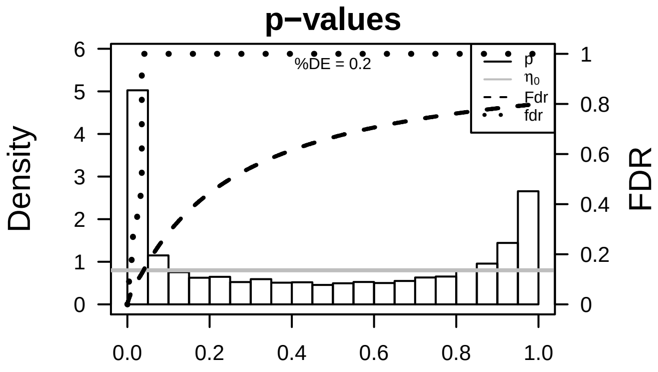
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ATIC	−1.72	2e−16	2e−13	44 x 50	5−aminoimidazole−4−carboxamide ribonucleotide formyltrans
2	CKS2	−1.65	2e−16	2e−13	5 x 50	CDC28 protein kinase regulatory subunit 2 [Source:HGNC Sy
3	DCT	−1.37	2e−16	2e−13	1 x 11	dopachrome tautomerase [Source:HGNC Symbol;Acc:HGNC
4	DNAJA1	−1.6	2e−16	2e−13	41 x 47	DnaJ (Hsp40) homolog, subfamily A, member 1 [Source:HGN
5	DNTTIP2	−1.35	2e−16	2e−13	12 x 47	deoxynucleotidyltransferase, terminal, interacting protein 2 [S
6	EBP	−2.01	2e−16	2e−13	1 x 48	emopamil binding protein (sterol isomerase) [Source:HGNC S
7	EIF3D	−1.74	2e−16	2e−13	45 x 19	eukaryotic translation initiation factor 3, subunit D [Source:HG
8	EXOSC8	−1.71	2e−16	2e−13	1 x 50	exosome component 8 [Source:HGNC Symbol;Acc:HGNC:17
9	HSD17B4	−1.63	2e−16	2e−13	11 x 50	hydroxysteroid (17−beta) dehydrogenase 4 [Source:HGNC Sy
10	IQGAP1	−1.53	2e−16	2e−13	9 x 32	IQ motif containing GTPase activating protein 1 [Source:HGN
11	MRPL9	−1.48	2e−16	2e−13	39 x 11	mitochondrial ribosomal protein L9 [Source:HGNC Symbol;Ac
12	NDUFA10	−1.72	2e−16	2e−13	37 x 50	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10,
13	PTTG1	−1.37	2e−16	2e−13	7 x 50	pituitary tumor−transforming 1 [Source:HGNC Symbol;Acc:H
14	ST6GALNAC1	−1.6	2e−16	2e−13	1 x 44	ST6 (alpha−N−acetyl−neuraminyl−2,3−beta−galactosyl−1,3)−
15	TIMM21	−1.79	2e−16	2e−13	14 x 50	translocase of inner mitochondrial membrane 21 homolog (ye
16	TUBG1	−1.69	2e−16	2e−13	2 x 49	tubulin, gamma 1 [Source:HGNC Symbol;Acc:HGNC:12417]
17	STMN1	−0.81	4e−16	3e−12	5 x 50	stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]
18	RRM1	−1.58	7e−16	8e−12	2 x 50	ribonucleotide reductase M1 [Source:HGNC Symbol;Acc:HG
19	DHRS7	−1.56	2e−15	8e−12	41 x 49	dehydrogenase/reductase (SDR family) member 7 [Source:H
20	NUP85	−1.56	2e−15	2e−11	1 x 50	nucleoporin 85kDa [Source:HGNC Symbol;Acc:HGNC:8734]

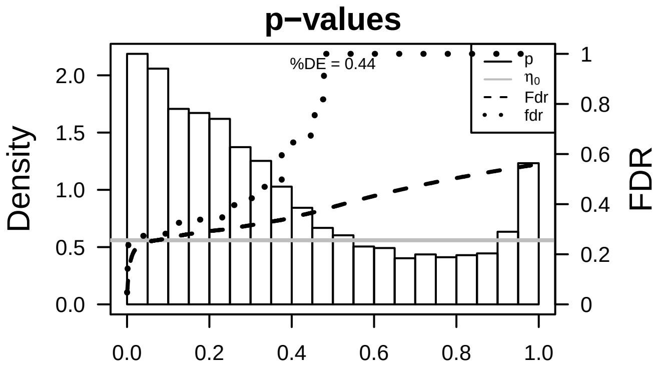
Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	4.32	0.006	12	BP	regulation of acetyl−CoA biosynthetic process from pyruvate
2	4.32	0.006	12	GSEA C2	REACTOME_REGULATION_OF_PYRUVATE_DEHYDROGENAS
3	4.24	0.006	19	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_DN
4	4.03	0.007	7	GSEA C2	MOOTHA_PYR
5	3.73	0.009	10	BP	ribosomal large subunit biogenesis
6	3.68	0.010	11	GSEA C2	SANCHEZ_MDM2_TARGETS
7	3.66	0.010	23	GSEA C2	GAZDA_DIAMOND_BLACKFAN_ANEMIA_ERYTHROID_UP
8	3.66	0.010	18	GSEA C2	PID_HIF1A_PATHWAY
9	3.66	0.010	162	BP	ribosome biogenesis
10	3.63	0.010	13	GSEA C2	CAIRO_PML_TARGETS_BOUND_BY_MYC_DN
11	3.63	0.010	7	GSEA C2	MARIADASON_RESPONSE_TO_BUTYRATE_CURCUMIN_SULI
12	3.58	0.011	60	GSEA C2	MOLENAAR_TARGETS_OF_CCND1_AND_CDK4_UP
13	3.49	0.012	22	BP	negative regulation of JNK cascade
14	3.48	0.012	22	BP	sarcomere organization
15	3.43	0.012	33	GSEA C2	PID_P38_ALPHA_BETA_DOWNSTREAM_PATHWAY
16	3.42	0.012	47	GSEA C2	PID_CERAMIDE_PATHWAY
17	3.41	0.012	41	GSEA C2	BIOCARTA_KERATINOCYTE_PATHWAY
18	3.39	0.013	30	GSEA C2	PID_MAPK_TRK_PATHWAY
19	3.37	0.013	25	GSEA C2	REACTOME_MAPK_TARGETS_NUCLEAR_EVENTS_MEDIATED
20	3.34	0.013	21	MF	R−SMAD binding
Underexpressed					
1	−14.93	5e−05	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
2	−13.66	7e−05	242	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
3	−13.59	8e−05	305	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
4	−13.28	8e−05	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
5	−13.02	9e−05	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
6	−12.91	9e−05	197	HM	HALLMARK_E2F_TARGETS
7	−12.43	1e−04	96	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
8	−11.98	3e−02	16	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
9	−11.89	1e−04	124	GSEA C2	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
10	−11.85	1e−04	99	GSEA C2	BURTON_ADIPOGENESIS_3
11	−11.36	2e−04	155	GSEA C2	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
12	−11.3	2e−04	110	GSEA C2	WHITEFORD_PEDIATRIC_CANCER_MARKERS
13	−11.22	2e−04	50	GSEA C2	ISHIDA_E2F_TARGETS
14	−11.11	2e−04	145	GSEA C2	CHANG_CYCLING_GENES
15	−11.05	2e−04	327	GSEA C2	BLUM_RESPONSE_TO_SALIRASIB_DN
16	−10.98	2e−04	81	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
17	−10.95	2e−04	72	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
18	−10.73	2e−04	116	GSEA C2	MISSIAGLIA_REGULATED_BY_METHYLATION_DN
19	−10.71	2e−04	58	GSEA C2	SONG_TARGETS_OF_IE86_CMV_PROTEIN
20	−10.69	2e−04	291	GSEA C2	HORIUCHI_WTAP_TARGETS_DN









B3_mel

Local Summary

%DE = 0.71

metagenes = 7

genes = 155

genes in genesets = 154

genes with fdr < 0.1 = 78 (61 + / 17 −)

genes with fdr < 0.05 = 65 (53 + / 12 −)

genes with fdr < 0.01 = 43 (36 + / 7 −)

<r> metagenes = 0.98

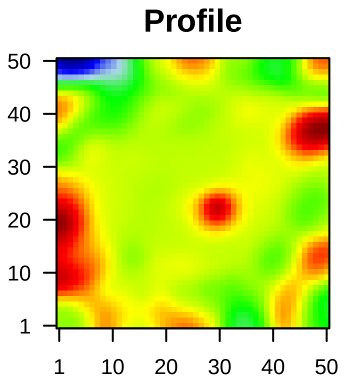
<r> genes = 0.17

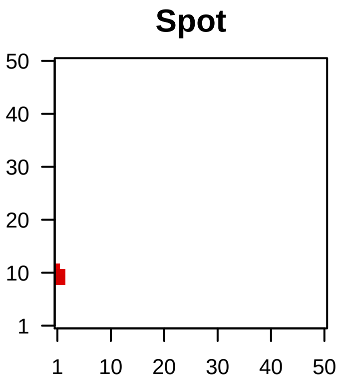
<FC> = 0.26

<shrinkage−t> = 4.18

<p−value> = 0.01

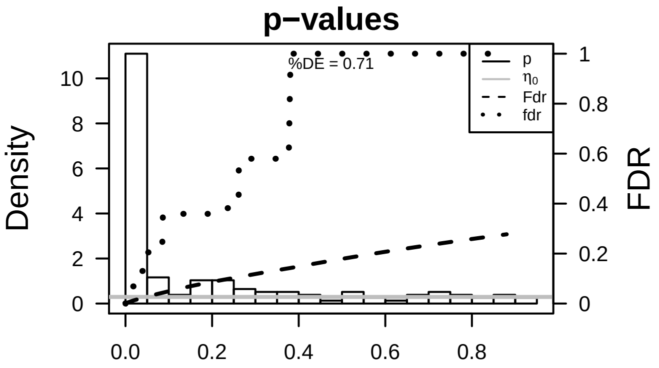
<fdr> = 0.54





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	DCT	−1.37	2e−16	1e−14	1 x 11	dopachrome tautomerase [Source:HGNC Symbol;Acc:HGNC
2	POPDC2	1.86	5e−14	2e−09	1 x 9	popeye domain containing 2 [Source:HGNC Symbol;Acc:HG
3	KCNQ5	1.62	4e−11	5e−08	1 x 10	potassium channel, voltage gated KQT−like subfamily Q, mer
4	XG	1.5	1e−09	2e−07	2 x 9	Xg blood group [Source:HGNC Symbol;Acc:HGNC:12806]
5	RAPGEF6	1.44	5e−09	7e−07	1 x 10	Rap guanine nucleotide exchange factor (GEF) 6 [Source:HG
6	MCF2L	1.35	4e−08	7e−07	1 x 10	MCF.2 cell line derived transforming sequence−like [Source:
7	C1orf54	1.34	5e−08	7e−07	1 x 11	chromosome 1 open reading frame 54 [Source:HGNC Symb
8	RGS12	1.33	6e−08	7e−07	1 x 9	regulator of G−protein signaling 12 [Source:HGNC Symbol;A
9	WDR3	1.33	7e−08	5e−06	1 x 12	WD repeat domain 3 [Source:HGNC Symbol;Acc:HGNC:127
10	SAT1	0.52	2e−07	9e−06	1 x 11	spermidine/spermine N1−acetyltransferase 1 [Source:HGNC
11	BCAT2	1.24	5e−07	9e−06	1 x 11	branched chain amino−acid transaminase 2, mitochondrial [S
12	PRKCH	1.23	6e−07	9e−06	1 x 12	protein kinase C, eta [Source:HGNC Symbol;Acc:HGNC:940
13	CXorf23	1.21	9e−07	9e−06	1 x 9	chromosome X open reading frame 23 [Source:HGNC Symb
14	C12orf73	1.2	1e−06	3e−05	1 x 10	chromosome 12 open reading frame 73 [Source:HGNC Symb
15	BBS5	1.17	2e−06	3e−05	1 x 11	Bardet−Biedl syndrome 5 [Source:HGNC Symbol;Acc:HGNC
16	GDPD5	1.17	2e−06	9e−05	1 x 12	glycerophosphodiester phosphodiesterase domain containing
17	GALNTL6	1.13	4e−06	2e−04	1 x 11	polypeptide N−acetylgalactosaminyltransferase−like 6 [Sourc
18	BIN1	1.07	1e−05	2e−04	1 x 10	bridging integrator 1 [Source:HGNC Symbol;Acc:HGNC:1052
19	WDR48	0.98	2e−05	2e−04	1 x 9	WD repeat domain 48 [Source:HGNC Symbol;Acc:HGNC:30
20	FAM69A	1.05	2e−05	2e−04	1 x 12	family with sequence similarity 69, member A [Source:HGNC



B3_mel

Local Summary

%DE = 0.85

metagenes = 20

genes = 294

genes in genesets = 293

genes with fdr < 0.1 = 182 (155 + / 27 −)

genes with fdr < 0.05 = 164 (142 + / 22 −)

genes with fdr < 0.01 = 111 (97 + / 14 −)

<r> metagenes = 0.92

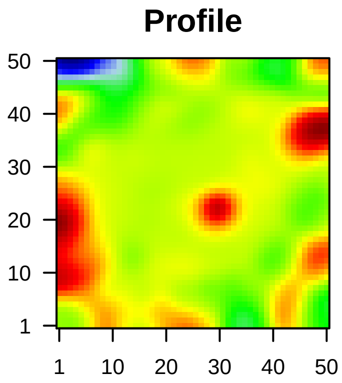
<r> genes = 0.13

<FC> = 0.32

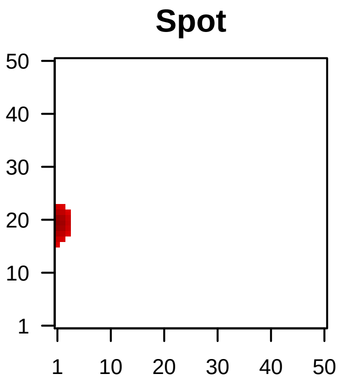
<shrinkage−t> = 5.28

<p−value> = 0.01

<fdr> = 0.55



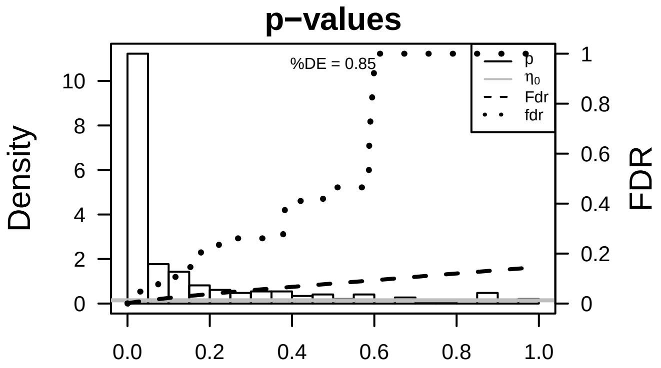
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	GPAA1	−1.42	4e−11	2e−09	1 x 22	glycosylphosphatidylinositol anchor attachment 1 [Source:HG
2	GET4	1.6	9e−11	1e−06	1 x 19	golgi to ER traffic protein 4 homolog (S. cerevisiae) [Source:
3	OGFOD3	1.36	3e−08	2e−06	1 x 21	2−oxoglutarate and iron−dependent oxygenase domain conta
4	NRSN2	−1.23	1e−07	2e−06	1 x 19	neurensin 2 [Source:HGNC Symbol;Acc:HGNC:16229]
5	RAB32	0.61	2e−07	2e−06	1 x 20	RAB32, member RAS oncogene family [Source:HGNC Symb
6	C9orf91	1.28	2e−07	6e−06	1 x 16	chromosome 9 open reading frame 91 [Source:HGNC Symb
7	SQSTM1	0.57	4e−07	6e−06	1 x 21	sequestosome 1 [Source:HGNC Symbol;Acc:HGNC:11280]
8	FAM120AOS	1.24	5e−07	1e−05	1 x 19	family with sequence similarity 120A opposite strand [Source:
9	BID	1.22	7e−07	1e−05	1 x 16	BH3 interacting domain death agonist [Source:HGNC Symbo
10	E2F4	1.2	1e−06	2e−05	1 x 20	E2F transcription factor 4, p107/p130−binding [Source:HGNC
11	PUSL1	1.18	2e−06	2e−05	2 x 22	pseudouridylate synthase−like 1 [Source:HGNC Symbol;Acc:
12	PIGY	0.54	2e−06	2e−05	1 x 20	phosphatidylinositol glycan anchor biosynthesis, class Y [Sou
13	UBE2J2	1.17	2e−06	4e−05	1 x 20	ubiquitin−conjugating enzyme E2, J2 [Source:HGNC Symbol;
14	SH3GLB1	1.15	3e−06	4e−05	1 x 20	SH3−domain GRB2−like endophilin B1 [Source:HGNC Symb
15	EDRF1	1.12	5e−06	4e−05	3 x 20	erythroid differentiation regulatory factor 1 [Source:HGNC Sy
16	RNF144A	1.11	6e−06	4e−05	1 x 17	ring finger protein 144A [Source:HGNC Symbol;Acc:HGNC:2
17	ATP2C1	−1.1	6e−06	4e−05	1 x 17	ATPase, Ca++ transporting, type 2C, member 1 [Source:HGN
18	PDIA3	0.65	7e−06	4e−05	1 x 20	protein disulfide isomerase family A, member 3 [Source:HGN
19	NUDT14	1.1	7e−06	4e−05	1 x 21	nudix (nucleoside diphosphate linked moiety X)−type motif 14
20	NR2C2AP	1.1	8e−06	5e−05	1 x 21	nuclear receptor 2C2−associated protein [Source:HGNC Sym



p−values

B3_mel

Local Summary

%DE = 0.97

metagenes = 6

genes = 62

genes in genesets = 61

genes with fdr < 0.1 = 60 (60 + / 0 −)

genes with fdr < 0.05 = 54 (54 + / 0 −)

genes with fdr < 0.01 = 45 (45 + / 0 −)

<r> metagenes = 0.97

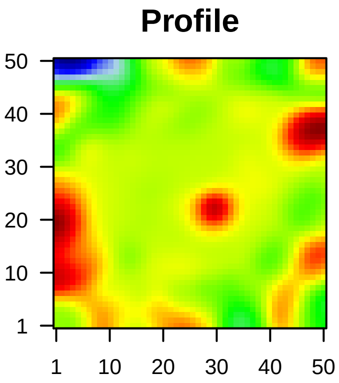
<r> genes = 0.51

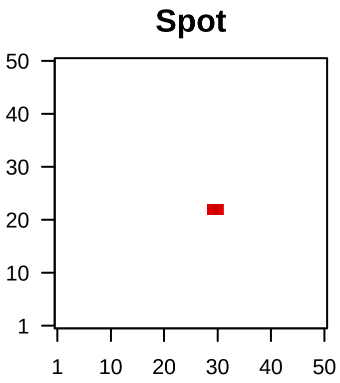
<FC> = 0.8

<shrinkage−t> = 12.08

<p−value> = 0

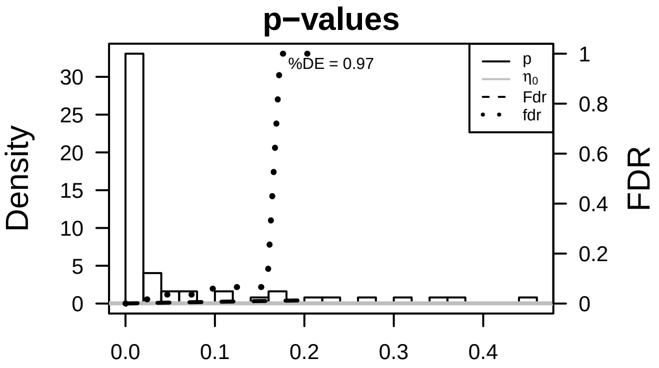
<fdr> = 0.33





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	NMU	1.69	8e−12	7e−12	30 x 23	neuromedin U [Source:HGNC Symbol;Acc:HGNC:7859]
2	D2HGDH	1.68	8e−12	1e−09	30 x 23	D−2−hydroxyglutarate dehydrogenase [Source:HGNC Symbo
3	PARP16	1.52	7e−10	2e−09	30 x 23	poly (ADP−ribose) polymerase family, member 16 [Source:H
4	ZNF177	1.48	2e−09	2e−09	30 x 23	zinc finger protein 177 [Source:HGNC Symbol;Acc:HGNC:12
5	GSAP	1.47	3e−09	3e−09	30 x 23	gamma−secretase activating protein [Source:HGNC Symbol;
6	HMSD	1.45	4e−09	6e−09	30 x 23	histocompatibility (minor) serpin domain containing [Source:H
7	TTR	1.42	7e−09	2e−08	30 x 23	transthyretin [Source:HGNC Symbol;Acc:HGNC:12405]
8	RBM24	1.39	2e−08	6e−08	30 x 23	RNA binding motif protein 24 [Source:HGNC Symbol;Acc:HG
9	XIRP2	1.33	7e−08	6e−08	30 x 23	xin actin−binding repeat containing 2 [Source:HGNC Symbol;
10	DIXDC1	1.32	9e−08	2e−07	30 x 23	DIX domain containing 1 [Source:HGNC Symbol;Acc:HGNC:
11	RMI2	1.27	3e−07	2e−07	30 x 23	RecQ mediated genome instability 2 [Source:HGNC Symbol;
12	LEKR1	1.27	3e−07	2e−06	30 x 23	leucine, glutamate and lysine rich 1 [Source:HGNC Symbol;A
13	ROM1	1.15	3e−06	2e−06	30 x 23	retinal outer segment membrane protein 1 [Source:HGNC Sy
14	TM7SF2	1.13	4e−06	2e−06	30 x 23	transmembrane 7 superfamily member 2 [Source:HGNC Sym
15	GRK5	1.12	5e−06	2e−06	30 x 23	G protein−coupled receptor kinase 5 [Source:HGNC Symbol;
16	C20orf144	1.12	5e−06	1e−05	30 x 23	chromosome 20 open reading frame 144 [Source:HGNC Sym
17	SLX4IP	1.08	1e−05	7e−05	30 x 23	SLX4 interacting protein [Source:HGNC Symbol;Acc:HGNC:1
18	ZNF584	0.97	9e−05	7e−05	29 x 22	zinc finger protein 584 [Source:HGNC Symbol;Acc:HGNC:27
19	FAM186B	0.94	1e−04	7e−05	30 x 23	family with sequence similarity 186, member B [Source:HGN
20	TMEM253	0.94	1e−04	7e−05	30 x 23	transmembrane protein 253 [Source:HGNC Symbol;Acc:HGN



B3_mel

Local Summary

%DE = 0.73

metagenes = 26

genes = 194

genes in genesets = 193

genes with fdr < 0.1 = 114 (101 + / 13 −)

genes with fdr < 0.05 = 72 (66 + / 6 −)

genes with fdr < 0.01 = 53 (47 + / 6 −)

<r> metagenes = 0.9

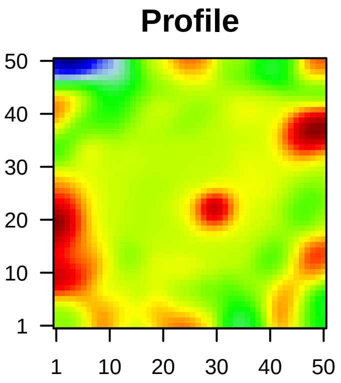
<r> genes = 0.08

<FC> = 0.38

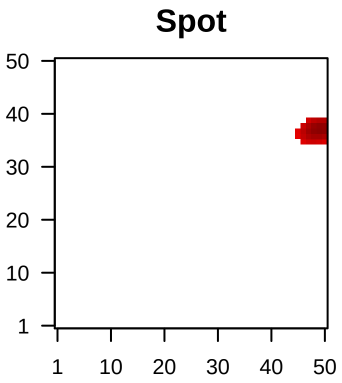
<shrinkage−t> = 6.31

<p−value> = 0.01

<fdr> = 0.6



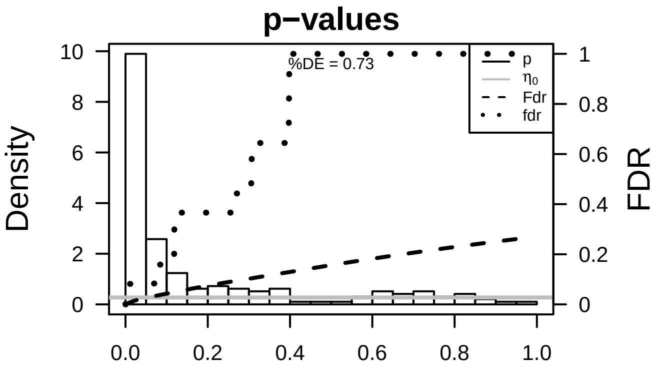
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	LHPP	1.6	8e−11	2e−07	46 x 36	phospholysine phosphohistidine inorganic pyrophosphate ph
2	KPNA5	1.45	4e−09	3e−07	50 x 38	karyopherin alpha 5 (importin alpha 6) [Source:HGNC Symb
3	TSG101	0.64	1e−08	3e−07	46 x 37	tumor susceptibility 101 [Source:HGNC Symbol;Acc:HGNC:1
4	SYNPR	1.38	2e−08	3e−07	48 x 39	synaptoporin [Source:HGNC Symbol;Acc:HGNC:16507]
5	ZNF678	1.37	2e−08	8e−07	50 x 37	zinc finger protein 678 [Source:HGNC Symbol;Acc:HGNC:28
6	KHDRBS3	1.35	5e−08	8e−07	47 x 37	KH domain containing, RNA binding, signal transduction ass
7	PGBD3	1.34	5e−08	2e−06	48 x 36	piggyBac transposable element derived 3 [Source:HGNC Sy
8	ELP3	1.31	9e−08	2e−06	47 x 38	elongator acetyltransferase complex subunit 3 [Source:HGNC
9	RNF139	1.3	1e−07	2e−05	50 x 37	ring finger protein 139 [Source:HGNC Symbol;Acc:HGNC:17
10	FAM13B	1.23	6e−07	2e−05	50 x 36	family with sequence similarity 13, member B [Source:HGNC
11	ZNF720	1.2	1e−06	2e−05	47 x 36	zinc finger protein 720 [Source:HGNC Symbol;Acc:HGNC:26
12	PROCR	1.2	1e−06	2e−05	50 x 36	protein C receptor, endothelial [Source:HGNC Symbol;Acc:H
13	CAPS2	1.19	1e−06	3e−05	50 x 37	calcyphosine 2 [Source:HGNC Symbol;Acc:HGNC:16471]
14	RNFT1	−1.15	2e−06	3e−05	50 x 39	ring finger protein, transmembrane 1 [Source:HGNC Symbol;
15	PIK3C3	1.02	2e−06	3e−05	46 x 38	phosphatidylinositol 3−kinase, catalytic subunit type 3 [Sourc
16	IKZF5	1.15	3e−06	5e−05	50 x 38	IKAROS family zinc finger 5 (Pegasus) [Source:HGNC Symb
17	HACL1	1.12	5e−06	5e−05	50 x 39	2−hydroxyacyl−CoA lyase 1 [Source:HGNC Symbol;Acc:HG
18	DEDD	−1.1	6e−06	5e−05	50 x 38	death effector domain containing [Source:HGNC Symbol;Acc
19	TMEM173	1.11	6e−06	5e−05	50 x 38	transmembrane protein 173 [Source:HGNC Symbol;Acc:HG
20	DNAAF2	1.11	7e−06	8e−05	50 x 38	dynein, axonemal, assembly factor 2 [Source:HGNC Symbol;



p−values

B3_mel

Local Summary

%DE = 0.88

metagenes = 22

genes = 345

genes in genesets = 344

genes with fdr < 0.1 = 234 (24 + / 210 −)

genes with fdr < 0.05 = 228 (23 + / 205 −)

genes with fdr < 0.01 = 145 (17 + / 128 −)

<r> metagenes = 0.92

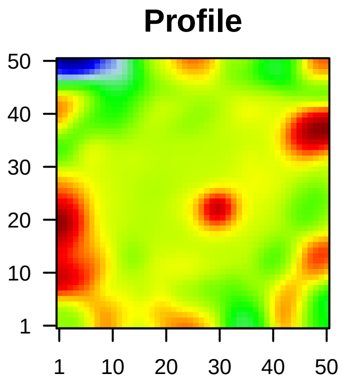
<r> genes = 0.3

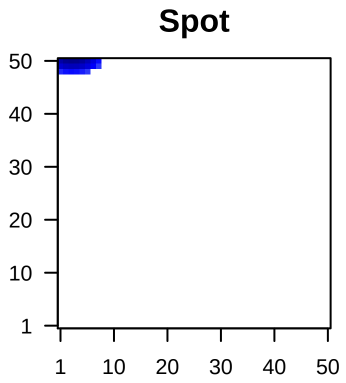
<FC> = −0.49

<shrinkage−t> = −8.04

<p−value> = 0

<fdr> = 0.48





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CKS2	−1.65	2e−16	2e−15	5 x 50	CDC28 protein kinase regulatory subunit 2 [Source:HGNC Sy
2	EBP	−2.01	2e−16	2e−15	1 x 48	emopamil binding protein (sterol isomerase) [Source:HGNC
3	EXOSC8	−1.71	2e−16	2e−15	1 x 50	exosome component 8 [Source:HGNC Symbol;Acc:HGNC:17
4	PTTG1	−1.37	2e−16	2e−15	7 x 50	pituitary tumor−transforming 1 [Source:HGNC Symbol;Acc:H
5	TUBG1	−1.69	2e−16	2e−15	2 x 49	tubulin, gamma 1 [Source:HGNC Symbol;Acc:HGNC:12417]
6	STMN1	−0.81	4e−16	9e−15	5 x 50	stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]
7	RRM1	−1.58	7e−16	6e−14	2 x 50	ribonucleotide reductase M1 [Source:HGNC Symbol;Acc:HG
8	NUP85	−1.56	2e−15	1e−13	1 x 50	nucleoporin 85kDa [Source:HGNC Symbol;Acc:HGNC:8734]
9	TK1	−1.55	5e−15	1e−10	4 x 50	thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:HGN
10	CDKN3	−1.27	3e−12	1e−10	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
11	GMNN	−1.45	6e−12	1e−09	2 x 50	geminin, DNA replication inhibitor [Source:HGNC Symbol;Acc
12	HSD17B11	−1.4	7e−11	1e−09	8 x 50	hydroxysteroid (17−beta) dehydrogenase 11 [Source:HGNC
13	SMC4	−1.33	7e−11	3e−09	5 x 50	structural maintenance of chromosomes 4 [Source:HGNC Sy
14	RFC5	−1.39	2e−10	1e−08	2 x 50	replication factor C (activator 1) 5, 36.5kDa [Source:HGNC S
15	MCM3	−1.24	4e−10	1e−08	1 x 50	minichromosome maintenance complex component 3 [Sourc
16	MAD2L1	−1.35	8e−10	6e−08	5 x 50	MAD2 mitotic arrest deficient−like 1 (yeast) [Source:HGNC S
17	SMCHD1	−1.33	2e−09	1e−07	1 x 48	structural maintenance of chromosomes flexible hinge domai
18	HLTF	−1.25	5e−09	1e−07	3 x 48	helicase−like transcription factor [Source:HGNC Symbol;Acc:
19	MCM4	−1.13	7e−09	1e−07	1 x 50	minichromosome maintenance complex component 4 [Sourc
20	KIAA0101	−1.29	1e−08	5e−07	3 x 50	KIAA0101 [Source:HGNC Symbol;Acc:HGNC:28961]