B2_mel

Global Summary

%DE = 0.21

genes with fdr < 0.2 = 2549 (1562 + / 987 −)

genes with fdr < 0.1 = 2074 (1289 + / 785 −)

genes with fdr < 0.05 = 1700 (1056 + / 644 −)

genes with fdr < 0.01 = 1084 (687 + / 397 −)

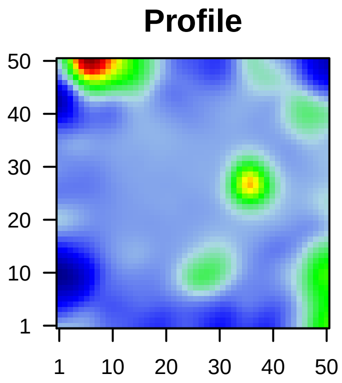
genes in genesets = 14839

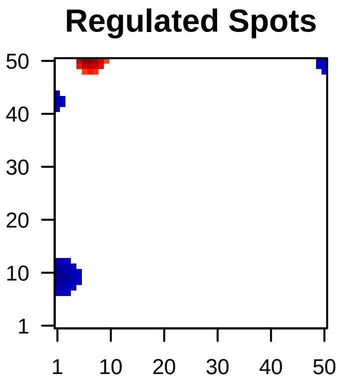
<FC> = 0

<shrinkage−t> = −0.01

<p−value> = 0.08

<fdr> = 0.79



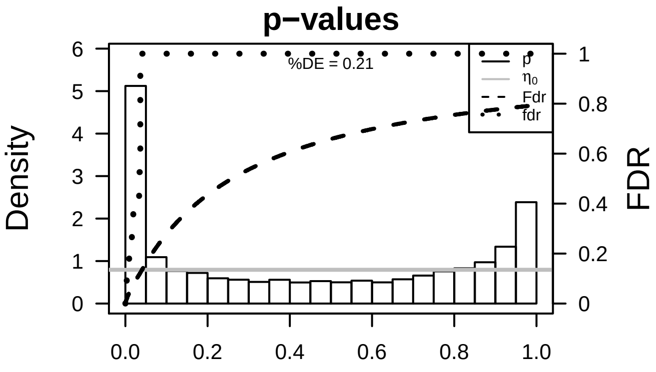


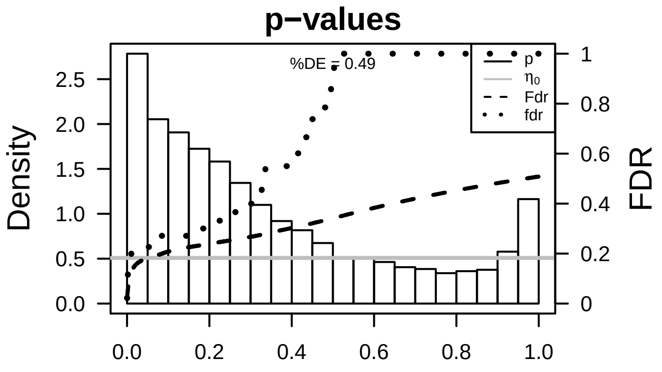
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	AHCY	−1.77	2e−16	7e−14	1 x 41	adenosylhomocysteinase [Source:HGNC Symbol;Acc:HGNC
2	AK2	−1.55	2e−16	7e−14	1 x 26	adenylate kinase 2 [Source:HGNC Symbol;Acc:HGNC:362]
3	ARHGAP8	−1.76	2e−16	7e−14	1 x 43	Rho GTPase activating protein 8 [Source:HGNC Symbol;Acc
4	ATP1A1	−1.32	2e−16	7e−14	1 x 42	ATPase, Na+/K+ transporting, alpha 1 polypeptide [Source:H
5	BSCL2	−1.14	2e−16	7e−14	50 x 50	Berardinelli−Seip congenital lipodystrophy 2 (seipin) [Source:
6	CADM1	2.03	2e−16	7e−14	44 x 10	cell adhesion molecule 1 [Source:HGNC Symbol;Acc:HGNC:
7	CCNB1	2.05	2e−16	7e−14	7 x 50	cyclin B1 [Source:HGNC Symbol;Acc:HGNC:1579]
8	CDC20	2	2e−16	7e−14	6 x 50	cell division cycle 20 [Source:HGNC Symbol;Acc:HGNC:172
9	CHID1	−1.57	2e−16	7e−14	33 x 50	chitinase domain containing 1 [Source:HGNC Symbol;Acc:H
10	CPNE3	−1.54	2e−16	7e−14	44 x 34	copine III [Source:HGNC Symbol;Acc:HGNC:2316]
11	CTSB	−1.39	2e−16	7e−14	46 x 46	cathepsin B [Source:HGNC Symbol;Acc:HGNC:2527]
12	DCXR	1.33	2e−16	7e−14	5 x 37	dicarbonyl/L−xylulose reductase [Source:HGNC Symbol;Acc:
13	DERA	−1.79	2e−16	7e−14	1 x 43	deoxyribose−phosphate aldolase (putative) [Source:HGNC S
14	EXOC3	−0.83	2e−16	7e−14	1 x 42	exocyst complex component 3 [Source:HGNC Symbol;Acc:H
15	FAHD1	−1.65	2e−16	7e−14	1 x 40	fumarylacetoacetate hydrolase domain containing 1 [Source:
16	FOS	−1.79	2e−16	7e−14	4 x 7	FBJ murine osteosarcoma viral oncogene homolog [Source:
17	KIF20A	1.96	2e−16	7e−14	7 x 50	kinesin family member 20A [Source:HGNC Symbol;Acc:HGN
18	KPNA2	1.46	2e−16	7e−14	7 x 50	karyopherin alpha 2 (RAG cohort 1, importin alpha 1) [Source
19	METTL9	−1.59	2e−16	7e−14	1 x 43	methyltransferase like 9 [Source:HGNC Symbol;Acc:HGNC:2
20	MTX2	−1.91	2e−16	7e−14	1 x 42	metaxin 2 [Source:HGNC Symbol;Acc:HGNC:7506]

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	19.8	2e−05	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
2	16.82	3e−05	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
3	16.74	5e−04	16	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
4	15.62	4e−05	291	GSEA C2	HORIUCHI_WTAP_TARGETS_DN
5	14.98	5e−05	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
6	14.59	6e−05	99	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
7	14.57	6e−05	201	GSEA C2	WHITFIELD_CELL_CYCLE_G2_M
8	13.84	7e−05	124	GSEA C2	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
9	13.81	7e−05	96	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
10	13.62	7e−05	155	GSEA C2	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
11	13.6	8e−05	40	GSEA C2	AMUNDSON_GAMMA_RADIATION_RESPONSE
12	13.59	8e−05	52	GSEA C2	TANG_SENESCENCE_TP53_TARGETS_DN
13	13.38	8e−05	45	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
14	13.31	8e−05	312	BP	mitotic nuclear division
15	13.27	8e−05	196	HM	HALLMARK_G2M_CHECKPOINT
16	13.25	8e−05	39	GSEA C2	BURTON_ADIPOGENESIS_PEAK_AT_24HR
17	13.24	8e−05	28	GSEA C2	REICHERT_MITOSIS_LIN9_TARGETS
18	13.1	9e−05	409	BP	cell division
19	12.75	1e−04	170	GSEA C2	WHITFIELD_CELL_CYCLE_G2
20	12.46	1e−04	145	GSEA C2	CHANG_CYCLING_GENES
Underexpressed					
1	−7.11	0.001	198	HM	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	−5.96	0.002	212	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_6HR_UP
3	−5.77	0.002	368	GSEA C2	STEIN_ESRRA_TARGETS_UP
4	−5.54	0.002	35	MF	aminoacyl−tRNA ligase activity
5	−5.44	0.003	500	GSEA C2	STEIN_ESRRA_TARGETS
6	−5.2	0.003	32	GSEA C2	KEGG_DNA_REPLICATION
7	−5.12	0.003	135	GSEA C2	WHITFIELD_CELL_CYCLE_G1_S
8	−5.07	0.003	401	CC	mitochondrial inner membrane
9	−5.06	0.003	1468	CC	mitochondrion
10	−5.03	0.003	29	BP	DNA strand elongation involved in DNA replication
11	−4.95	0.004	398	GSEA C2	MOOTHA_PGC
12	−4.89	0.004	213	GSEA C2	WONG_MITOCHONDRIA_GENE_MODULE
13	−4.81	0.004	6	GSEA C2	ISHIDA_TARGETS_OF_SYT_SSX_FUSIONS
14	−4.76	0.004	41	GSEA C2	KEGG_AMINOACYL_TRNA_BIOSYNTHESIS
15	−4.64	0.005	27	GSEA C2	REACTOME_DNA_STRAND_ELONGATION
16	−4.39	0.006	44	BP	tRNA aminoacylation for protein translation
17	−4.39	0.006	16	Cancer	GENTLES_modul7
18	−4.38	0.006	25	GSEA C2	MOOTHA_GLUCONEOGENESIS
19	−4.31	0.006	695	MF	transmembrane transporter activity
20	−4.31	0.006	107	GSEA C2	KEGG_OXIDATIVE_PHOSPHORYLATION





B2_mel

Local Summary

%DE = 0.96

metagenes = 14

genes = 199

genes in genesets = 199

genes with fdr < 0.1 = 176 (170 + / 6 −)

genes with fdr < 0.05 = 176 (170 + / 6 −)

genes with fdr < 0.01 = 165 (161 + / 4 −)

<r> metagenes = 0.98

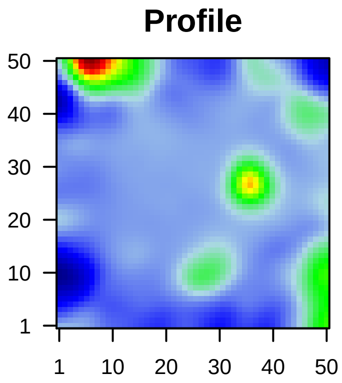
<r> genes = 0.36

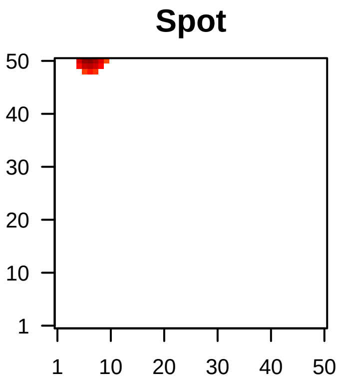
<FC> = 0.94

<shrinkage−t> = 15.17

<p−value> = 0

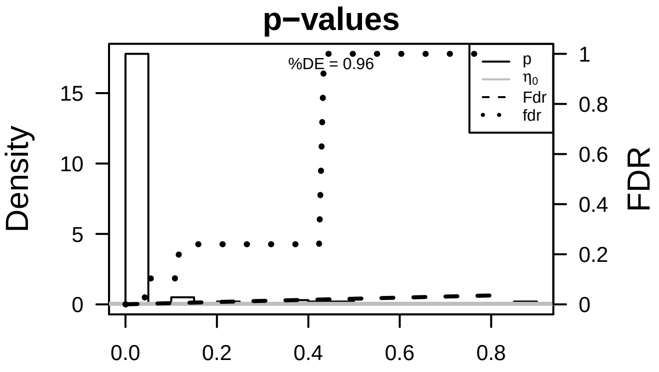
<fdr> = 0.17





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CCNB1	2.05	2e−16	2e−16	7 x 50	cyclin B1 [Source:HGNC Symbol;Acc:HGNC:1579]
2	CDC20	2	2e−16	2e−16	6 x 50	cell division cycle 20 [Source:HGNC Symbol;Acc:HGNC:1723
3	KIF20A	1.96	2e−16	2e−16	7 x 50	kinesin family member 20A [Source:HGNC Symbol;Acc:HGN
4	KPNA2	1.46	2e−16	2e−16	7 x 50	karyopherin alpha 2 (RAG cohort 1, importin alpha 1) [Source
5	NEK2	2	2e−16	2e−16	8 x 50	NIMA−related kinase 2 [Source:HGNC Symbol;Acc:HGNC:77
6	PLK1	2.09	2e−16	2e−16	8 x 50	polo−like kinase 1 [Source:HGNC Symbol;Acc:HGNC:9077]
7	PTTG1	1.28	2e−16	2e−16	7 x 50	pituitary tumor−transforming 1 [Source:HGNC Symbol;Acc:H
8	UBE2C	2.22	2e−16	2e−16	6 x 50	ubiquitin−conjugating enzyme E2C [Source:HGNC Symbol;A
9	FAM64A	1.85	8e−15	5e−14	7 x 50	family with sequence similarity 64, member A [Source:HGNC
10	PSRC1	1.84	1e−14	1e−13	8 x 50	proline/serine−rich coiled−coil 1 [Source:HGNC Symbol;Acc:
11	ARL6IP1	1.11	4e−14	1e−13	9 x 50	ADP−ribosylation factor−like 6 interacting protein 1 [Source:H
12	RACGAP1	1.79	5e−14	3e−13	7 x 50	Rac GTPase activating protein 1 [Source:HGNC Symbol;Acc:
13	HMGB2	1.61	1e−13	3e−13	5 x 50	high mobility group box 2 [Source:HGNC Symbol;Acc:HGNC:
14	CDK1	1.74	1e−13	3e−13	5 x 50	cyclin−dependent kinase 1 [Source:HGNC Symbol;Acc:HGN
15	TOP2A	1.75	2e−13	9e−13	6 x 50	topoisomerase (DNA) II alpha 170kDa [Source:HGNC Symbo
16	CKAP2L	1.74	3e−13	1e−12	6 x 50	cytoskeleton associated protein 2−like [Source:HGNC Symbo
17	AURKB	1.72	5e−13	1e−12	6 x 50	aurora kinase B [Source:HGNC Symbol;Acc:HGNC:11390]
18	STMN1	0.69	6e−13	1e−12	5 x 50	stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]
19	CDCA3	1.7	8e−13	1e−12	6 x 50	cell division cycle associated 3 [Source:HGNC Symbol;Acc:H
20	BIRC5	1.54	9e−13	1e−12	6 x 50	baculoviral IAP repeat containing 5 [Source:HGNC Symbol;A



B2_mel

Local Summary

%DE = 0.72

metagenes = 29

genes = 355

genes in genesets = 353

genes with fdr < 0.1 = 143 (22 + / 121 −)

genes with fdr < 0.05 = 122 (21 + / 101 −)

genes with fdr < 0.01 = 75 (13 + / 62 −)

<r> metagenes = 0.91

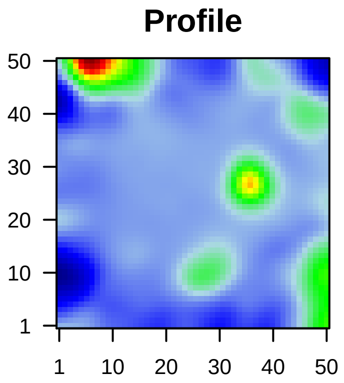
<r> genes = 0.11

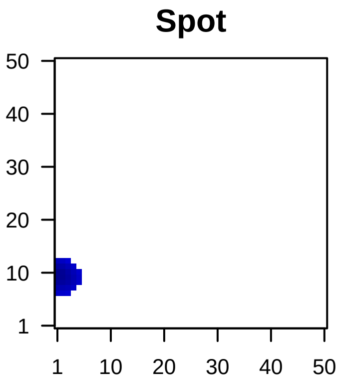
<FC> = −0.3

<shrinkage−t> = −4.85

<p−value> = 0.01

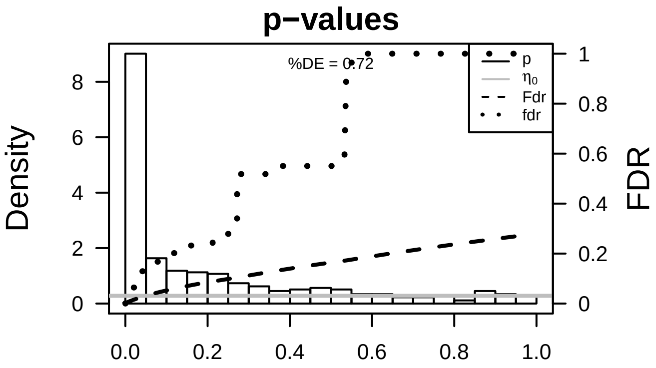
<fdr> = 0.63





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	WDR43	−1.4	2e−16	2e−14	4 x 11	WD repeat domain 43 [Source:HGNC Symbol;Acc:HGNC:28
2	ZZZ3	−1.52	4e−16	4e−14	1 x 11	zinc finger, ZZ−type containing 3 [Source:HGNC Symbol;Acc
3	CCDC171	−1.52	9e−16	6e−13	1 x 11	coiled−coil domain containing 171 [Source:HGNC Symbol;Ac
4	RAB27A	−1.52	6e−15	3e−10	1 x 11	RAB27A, member RAS oncogene family [Source:HGNC Sym
5	ADAM10	−1.11	4e−12	3e−10	4 x 11	ADAM metallopeptidase domain 10 [Source:HGNC Symbol;A
6	DCT	0.94	7e−12	1e−09	1 x 11	dopachrome tautomerase [Source:HGNC Symbol;Acc:HGNC
7	MET	−1.4	2e−11	1e−09	1 x 11	MET proto−oncogene, receptor tyrosine kinase [Source:HGN
8	SGK1	−0.65	3e−11	8e−09	1 x 13	serum/glucocorticoid regulated kinase 1 [Source:HGNC Sym
9	ST3GAL6	−1.36	1e−10	8e−09	4 x 8	ST3 beta−galactoside alpha−2,3−sialyltransferase 6 [Source:
10	PPARGC1A	−1.35	2e−10	1e−08	1 x 10	peroxisome proliferator−activated receptor gamma, coactivat
11	LRPPRC	−1.12	3e−10	2e−08	3 x 8	leucine−rich pentatricopeptide repeat containing [Source:HG
12	MRPS5	−1.21	4e−10	1e−07	3 x 7	mitochondrial ribosomal protein S5 [Source:HGNC Symbol;A
13	UGCG	−0.92	2e−09	1e−07	1 x 11	UDP−glucose ceramide glucosyltransferase [Source:HGNC
14	CEACAM1	−1.27	4e−09	1e−07	1 x 10	carcinoembryonic antigen−related cell adhesion molecule 1 (
15	MRS2	−1.27	5e−09	1e−07	1 x 13	MRS2 magnesium transporter [Source:HGNC Symbol;Acc:H
16	TNFRSF14	−1.27	6e−09	3e−07	1 x 11	tumor necrosis factor receptor superfamily, member 14 [Sour
17	SOCS6	−1.26	8e−09	1e−05	1 x 11	suppressor of cytokine signaling 6 [Source:HGNC Symbol;Ac
18	WDR3	1.2	4e−07	1e−05	1 x 12	WD repeat domain 3 [Source:HGNC Symbol;Acc:HGNC:127
19	SCIN	1.2	4e−07	1e−05	1 x 12	scinderin [Source:HGNC Symbol;Acc:HGNC:21695]
20	IRF4	1.2	5e−07	1e−05	1 x 11	interferon regulatory factor 4 [Source:HGNC Symbol;Acc:HG



B2_mel

Local Summary

%DE = 0.85

metagenes = 6

genes = 146

genes in genesets = 146

genes with fdr < 0.1 = 89 (10 + / 79 −)

genes with fdr < 0.05 = 84 (9 + / 75 −)

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

<r> metagenes = 0.99

<r> genes = 0.23

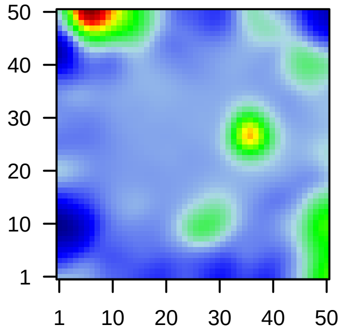
<FC> = −0.5

<shrinkage−t> = −9.44

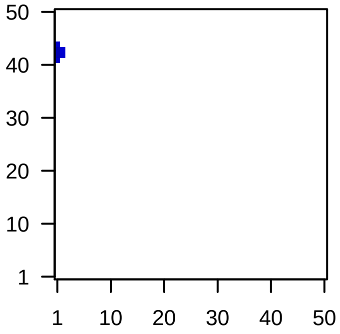
<p−value> = 0

<fdr> = 0.45

Profile



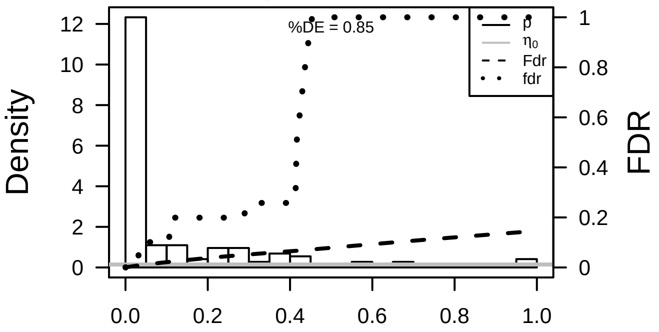
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	AHCY	−1.77	2e−16	5e−16	1 x 41	adenosylhomocysteinase [Source:HGNC Symbol;Acc:HGNC
2	ARHGAP8	−1.76	2e−16	5e−16	1 x 43	Rho GTPase activating protein 8 [Source:HGNC Symbol;Acc
3	ATP1A1	−1.32	2e−16	5e−16	1 x 42	ATPase, Na+/K+ transporting, alpha 1 polypeptide [Source:
4	DERA	−1.79	2e−16	5e−16	1 x 43	deoxyribose−phosphate aldolase (putative) [Source:HGNC S
5	EXOC3	−0.83	2e−16	5e−16	1 x 42	exocyst complex component 3 [Source:HGNC Symbol;Acc:
6	METTL9	−1.59	2e−16	5e−16	1 x 43	methyltransferase like 9 [Source:HGNC Symbol;Acc:HGNC:2
7	MTX2	−1.91	2e−16	5e−16	1 x 42	metaxin 2 [Source:HGNC Symbol;Acc:HGNC:7506]
8	NARS2	−2.48	2e−16	5e−16	1 x 42	asparaginyl−tRNA synthetase 2, mitochondrial (putative) [So
9	PDE4DIP	−1.79	2e−16	5e−16	1 x 43	phosphodiesterase 4D interacting protein [Source:HGNC Syn
10	RNF14	−1.67	2e−16	5e−16	1 x 43	ring finger protein 14 [Source:HGNC Symbol;Acc:HGNC:100
11	MLPH	−1.48	9e−14	7e−12	1 x 43	melanophilin [Source:HGNC Symbol;Acc:HGNC:29643]
12	ABCB5	−1.22	4e−13	2e−11	1 x 43	ATP−binding cassette, sub−family B (MDR/TAP), member 5 [
13	GSTM4	−1.45	2e−12	3e−11	1 x 41	glutathione S−transferase mu 4 [Source:HGNC Symbol;Acc:
14	MPC1	−1.37	3e−12	1e−10	1 x 43	mitochondrial pyruvate carrier 1 [Source:HGNC Symbol;Acc:
15	PSMB10	−1.42	8e−12	5e−10	1 x 42	proteasome (prosome, macropain) subunit, beta type, 10 [So
16	SAMM50	−1.39	4e−11	5e−10	1 x 42	SAMM50 sorting and assembly machinery component [Sourc
17	PAFAH1B3	−1.38	5e−11	1e−09	1 x 43	platelet−activating factor acetylhydrolase 1b, catalytic subunit
18	TUBB4A	−1.32	1e−10	1e−08	1 x 42	tubulin, beta 4A class IVa [Source:HGNC Symbol;Acc:HGNC
19	FASTKD2	−1.3	6e−10	1e−08	1 x 43	FAST kinase domains 2 [Source:HGNC Symbol;Acc:HGNC:2
20	AIFM1	−1.29	1e−09	1e−08	1 x 42	apoptosis−inducing factor, mitochondrion−associated, 1 [Sou

p−values



B2_mel

Local Summary

%DE = 0.74

metagenes = 5

genes = 115

genes in genesets = 115

genes with fdr < 0.1 = 60 (12 + / 48 −)

genes with fdr < 0.05 = 43 (6 + / 37 −)

genes with fdr < 0.01 = 41 (5 + / 36 −)

<r> metagenes = 0.99

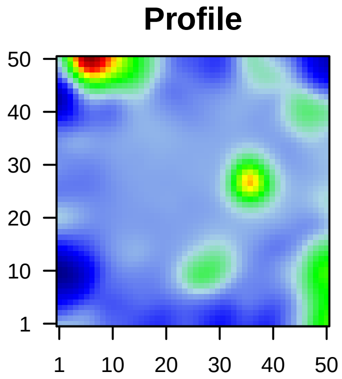
<r> genes = 0.1

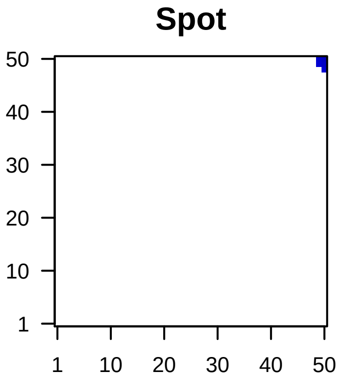
<FC> = −0.32

<shrinkage−t> = −5.51

<p−value> = 0

<fdr> = 0.54





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	BSCL2	−1.14	2e−16	3e−15	50 x 50	Berardinelli−Seip congenital lipodystrophy 2 (seipin) [Source:
2	PLEKHA5	−1.86	2e−16	3e−15	50 x 50	pleckstrin homology domain containing, family A member 5 [
3	G3BP2	−1.33	1e−15	5e−12	50 x 49	GTPase activating protein (SH3 domain) binding protein 2 [S
4	NQO2	−1.18	2e−13	7e−12	50 x 50	NAD(P)H dehydrogenase, quinone 2 [Source:HGNC Symbol;
5	NIP7	−1.46	4e−13	5e−11	50 x 50	NIP7, nucleolar pre−rRNA processing protein [Source:HGNC
6	DDIT3	−1.44	2e−12	1e−08	50 x 50	DNA−damage−inducible transcript 3 [Source:HGNC Symbol;
7	ALDOC	−1.34	4e−10	1e−07	50 x 50	aldolase C, fructose−bisphosphate [Source:HGNC Symbol;A
8	DARS	−1.27	4e−09	3e−06	50 x 50	aspartyl−tRNA synthetase [Source:HGNC Symbol;Acc:HGN
9	GSN	−1.2	1e−07	3e−06	50 x 50	gelsolin [Source:HGNC Symbol;Acc:HGNC:4620]
10	ENTPD6	−1.13	2e−07	3e−06	50 x 50	ectonucleoside triphosphate diphosphohydrolase 6 (putative)
11	WDR26	−1.1	3e−07	4e−06	50 x 50	WD repeat domain 26 [Source:HGNC Symbol;Acc:HGNC:21
12	TRPT1	−1.17	4e−07	8e−06	50 x 49	tRNA phosphotransferase 1 [Source:HGNC Symbol;Acc:HG
13	ERC2	−1.15	1e−06	8e−06	50 x 49	ELKS/RAB6−interacting/CAST family member 2 [Source:HG
14	CAP2	−1.06	1e−06	8e−06	50 x 50	CAP, adenylate cyclase−associated protein, 2 (yeast) [Sourc
15	UPP1	−1.14	1e−06	5e−05	50 x 50	uridine phosphorylase 1 [Source:HGNC Symbol;Acc:HGNC:1
16	NQO1	−0.45	3e−06	7e−05	49 x 50	NAD(P)H dehydrogenase, quinone 1 [Source:HGNC Symbol;
17	TM2D3	−1.06	7e−06	7e−05	50 x 49	TM2 domain containing 3 [Source:HGNC Symbol;Acc:HGNC
18	SRPR	−1.06	8e−06	1e−04	50 x 48	signal recognition particle receptor (docking protein) [Source:
19	LUZP6	−1.03	1e−05	1e−04	50 x 49	leucine zipper protein 6 [Source:HGNC Symbol;Acc:HGNC:
20	DUSP3	−0.91	2e−05	1e−04	50 x 49	dual specificity phosphatase 3 [Source:HGNC Symbol;Acc:H