B12_mel

Global Summary

%DE = 0.21

genes with fdr < 0.2 = 2690 (1612 + / 1078 −)

genes with fdr < 0.1 = 2245 (1360 + / 885 −)

genes with fdr < 0.05 = 1900 (1173 + / 727 −)

genes with fdr < 0.01 = 1201 (780 + / 421 −)

genes in genesets = 14839

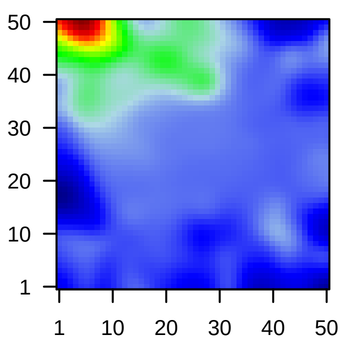
<FC> = 0

<shrinkage−t> = 0.01

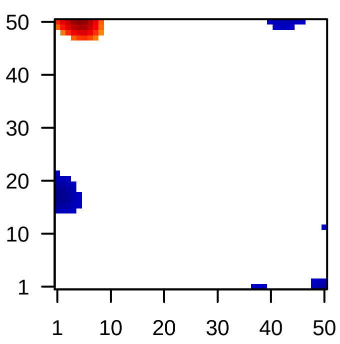
<p−value> = 0.07

<fdr> = 0.79

Profile



Regulated Spots



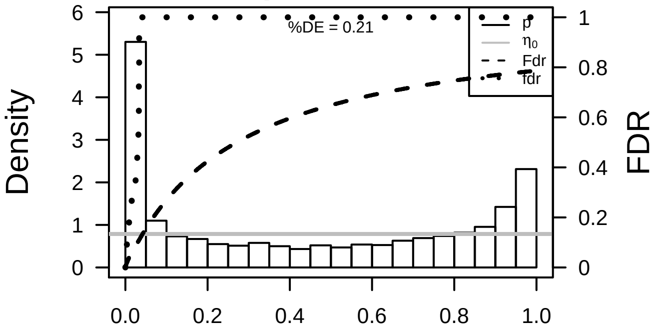
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	BCCIP	−1.55	2e−16	1e−13	2 x 15	BRCA2 and CDKN1A interacting protein [Source:HGNC Sym
2	CDC123	−1.56	2e−16	1e−13	46 x 50	cell division cycle 123 [Source:HGNC Symbol;Acc:HGNC:16
3	CEP97	2.41	2e−16	1e−13	2 x 47	centrosomal protein 97kDa [Source:HGNC Symbol;Acc:HGN
4	CITED1	−1.4	2e−16	1e−13	1 x 41	Cbp/p300−interacting transactivator, with Glu/Asp−rich carbo
5	CRYAB	−1.82	2e−16	1e−13	50 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
6	GTF3A	−1.55	2e−16	1e−13	1 x 20	general transcription factor IIIA [Source:HGNC Symbol;Acc:H
7	HIST1H4C	0.98	2e−16	1e−13	5 x 49	histone cluster 1, H4c [Source:HGNC Symbol;Acc:HGNC:47
8	JKAMP	−1.47	2e−16	1e−13	29 x 50	JNK1/MAPK8−associated membrane protein [Source:HGNC
9	MAP4	−1.85	2e−16	1e−13	50 x 11	microtubule−associated protein 4 [Source:HGNC Symbol;Acc
10	MRPS12	−1.6	2e−16	1e−13	48 x 50	mitochondrial ribosomal protein S12 [Source:HGNC Symbol;
11	MYO10	−1.21	2e−16	1e−13	5 x 16	myosin X [Source:HGNC Symbol;Acc:HGNC:7593]
12	NOL11	−1.82	2e−16	1e−13	14 x 10	nucleolar protein 11 [Source:HGNC Symbol;Acc:HGNC:2455
13	NOLC1	−1.53	2e−16	1e−13	1 x 16	nucleolar and coiled−body phosphoprotein 1 [Source:HGNC
14	PDCD5	−1.05	2e−16	1e−13	1 x 37	programmed cell death 5 [Source:HGNC Symbol;Acc:HGNC:
15	PDHA1	−1.93	2e−16	1e−13	16 x 50	pyruvate dehydrogenase (lipoamide) alpha 1 [Source:HGNC
16	PYCR1	−1.1	2e−16	1e−13	46 x 50	pyrroline−5−carboxylate reductase 1 [Source:HGNC Symbol;
17	RARRES1	2.09	2e−16	1e−13	5 x 36	retinoic acid receptor responder (tazarotene induced) 1 [Sour
18	SLC25A4	−1.79	2e−16	1e−13	41 x 47	solute carrier family 25 (mitochondrial carrier; adenine nucleo
19	SOX4	−1.25	2e−16	1e−13	41 x 1	SRY (sex determining region Y)−box 4 [Source:HGNC Symbo
20	VPS28	−1.49	2e−16	1e−13	47 x 50	vacuolar protein sorting 28 homolog (S. cerevisiae) [Source:H

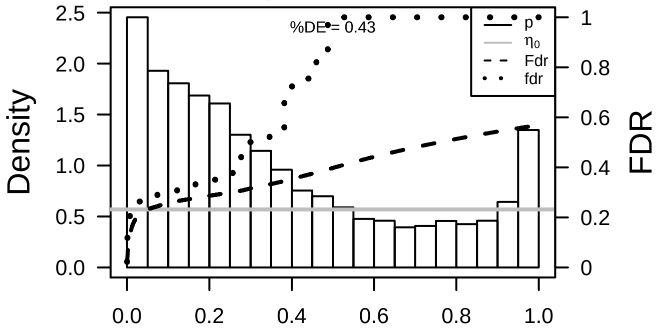
Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	18.06	2e−05	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
2	18.01	2e−05	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
3	17.46	3e−05	305	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
4	16.67	3e−05	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
5	15.47	4e−03	16	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
6	15	5e−05	242	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
7	14.78	6e−05	197	HM	HALLMARK_E2F_TARGETS
8	14.48	6e−05	96	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
9	14.44	6e−05	124	GSEA C2	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
10	14.24	6e−05	700	GSEA C2	MARSON_BOUND_BY_E2F4_UNSTIMULATED
11	14.17	6e−05	50	GSEA C2	ISHIDA_E2F_TARGETS
12	13.91	7e−05	72	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
13	13.77	7e−05	155	GSEA C2	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
14	13.71	7e−05	145	GSEA C2	CHANG_CYCLING_GENES
15	13.59	8e−05	93	GSEA C2	KONG_E2F3_TARGETS
16	13.53	8e−05	436	GSEA C2	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
17	13.34	8e−05	1192	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
18	13.33	8e−05	110	GSEA C2	WHITEFORD_PEDIATRIC_CANCER_MARKERS
19	13.32	8e−05	54	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
20	12.98	9e−05	81	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
Underexpressed					
1	−5.18	0.003	594	GSEA C2	WONG_ADULT_TISSUE_STEM_MODULE
2	−4.98	0.004	749	GSEA C2	CUI_TCF21_TARGETS_2_DN
3	−4.74	0.004	94	HM	HALLMARK_ANDROGEN_RESPONSE
4	−4.66	0.005	136	GSEA C2	PODAR_RESPONSE_TO_ADAPHOSTIN_UP
5	−4.52	0.005	9	GSEA C2	KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_BIOSYNTHESIS
6	−4.42	0.005	16	GSEA C2	LOPEZ_MBD_TARGETS_IMPRINTED_AND_X_LINKED
7	−4.32	0.006	2	Glio	WILLSCHER_GBM_LTSmut_proteomics−E_UP
8	−4.29	0.006	12	GSEA C2	GERHOLD_RESPONSE_TO_TZD_DN
9	−4.23	0.006	30	GSEA C2	GAZDA_DIAMOND_BLACKFAN_ANEMIA_MYELOID_DN
10	−4.19	0.006	79	GSEA C2	NELSON_RESPONSE_TO_ANDROGEN_UP
11	−4.12	0.007	367	GSEA C2	MONNIER_POSTRADIATION_TUMOR_ESCAPE_UP
12	−4.11	0.007	9	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
13	−4.1	0.007	472	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
14	−4.01	0.007	223	GSEA C2	HIRSCH_CELLULAR_TRANSFORMATION_SIGNATURE_UP
15	−3.99	0.008	26	GSEA C2	AKL_HTLV1_INFECTION_UP
16	−3.94	0.008	11	BP	positive regulation of endoplasmic reticulum stress−induced intrins
17	−3.91	0.008	35	GSEA C2	LOPEZ_TRANSLATION_VIA_FN1_SIGNALING
18	−3.9	0.008	91	GSEA C2	MARZEC_IL2_SIGNALING_UP
19	−3.86	0.008	120	miRNA target	hsa−miR−105
20	−3.81	0.009	34	GSEA C2	SPIRA_SMOKERS_LUNG_CANCER_UP

p−values



p−values



B12_mel

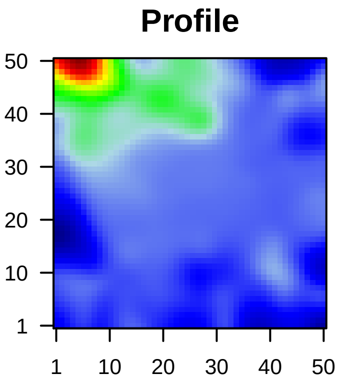
Local Summary

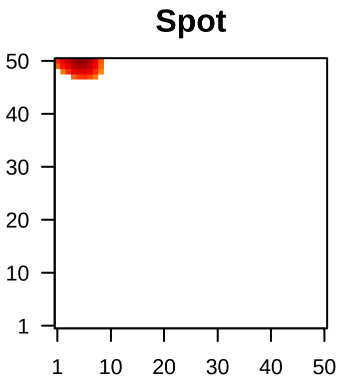
%DE = 0.87
metagenes = 31
genes = 398
genes in genesets = 398

genes with fdr < 0.1 = 305 (289 + / 16 −)
genes with fdr < 0.05 = 280 (266 + / 14 −)
genes with fdr < 0.01 = 246 (234 + / 12 −)

<r> metagenes = 0.93
<r> genes = 0.29

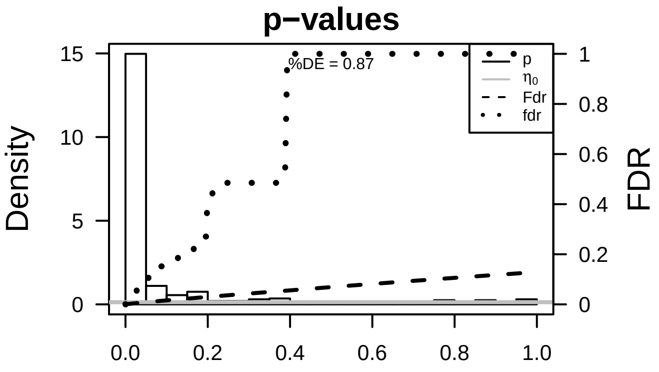
<FC> = 0.63
<shrinkage−t> = 10.2
<p−value> = 0
<fdr> = 0.32





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	HIST1H4C	0.98	2e−16	1e−14	5 x 49	histone cluster 1, H4c [Source:HGNC Symbol;Acc:HGNC:47
2	RRM2	1.8	1e−14	2e−12	5 x 50	ribonucleotide reductase M2 [Source:HGNC Symbol;Acc:HG
3	UBE2C	1.74	5e−14	3e−11	6 x 50	ubiquitin−conjugating enzyme E2C [Source:HGNC Symbol;A
4	CDK1	1.65	7e−13	5e−11	5 x 50	cyclin−dependent kinase 1 [Source:HGNC Symbol;Acc:HGN
5	CEP250	1.64	2e−12	5e−11	4 x 48	centrosomal protein 250kDa [Source:HGNC Symbol;Acc:HG
6	CDKN3	1.21	3e−12	8e−11	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
7	AURKB	1.61	4e−12	2e−10	6 x 50	aurora kinase B [Source:HGNC Symbol;Acc:HGNC:11390]
8	APOBEC3B	1.59	9e−12	2e−10	6 x 50	apolipoprotein B mRNA editing enzyme, catalytic polypeptide
9	SPC25	1.58	1e−11	3e−10	6 x 50	SPC25, NDC80 kinetochore complex component [Source:HG
10	GEN1	1.56	2e−11	3e−10	5 x 50	GEN1 Holliday junction 5' flap endonuclease [Source:HGNC
11	NUSAP1	1.51	2e−11	6e−10	6 x 50	nucleolar and spindle associated protein 1 [Source:HGNC Sy
12	SPC24	1.53	4e−11	6e−10	5 x 50	SPC24, NDC80 kinetochore complex component [Source:HG
13	POC1A	1.53	5e−11	6e−10	4 x 48	POC1 centriolar protein A [Source:HGNC Symbol;Acc:HGNC
14	HMGB2	1.39	6e−11	3e−09	5 x 50	high mobility group box 2 [Source:HGNC Symbol;Acc:HGNC
15	NUF2	1.5	1e−10	3e−09	6 x 50	NUF2, NDC80 kinetochore complex component [Source:HG
16	TK1	1.19	2e−10	3e−09	4 x 50	thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:HGN
17	MELK	1.48	2e−10	5e−08	5 x 50	maternal embryonic leucine zipper kinase [Source:HGNC Sy
18	ESCO2	1.42	1e−09	6e−08	4 x 50	establishment of sister chromatid cohesion N−acetyltransfera
19	POLQ	1.39	3e−09	6e−08	3 x 50	polymerase (DNA directed), theta [Source:HGNC Symbol;Acc
20	UBE2T	1.36	3e−09	6e−08	4 x 50	ubiquitin−conjugating enzyme E2T [Source:HGNC Symbol;A



B12_mel

Local Summary

%DE = 0.56

metagenes = 3

genes = 53

genes in genesets = 53

genes with fdr < 0.1 = 25 (6 + / 19 −)

genes with fdr < 0.05 = 21 (4 + / 17 −)

genes with fdr < 0.01 = 14 (2 + / 12 −)

<r> metagenes = 0.98

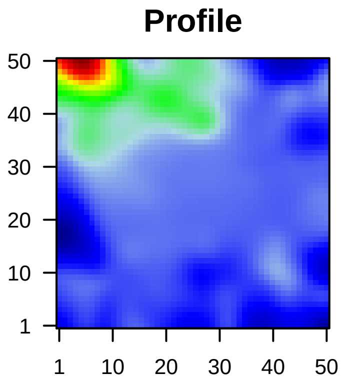
<r> genes = 0.13

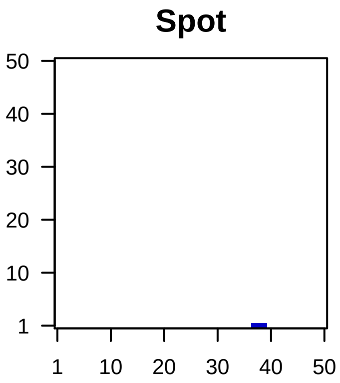
<FC> = −0.29

<shrinkage−t> = −4.69

<p−value> = 0.01

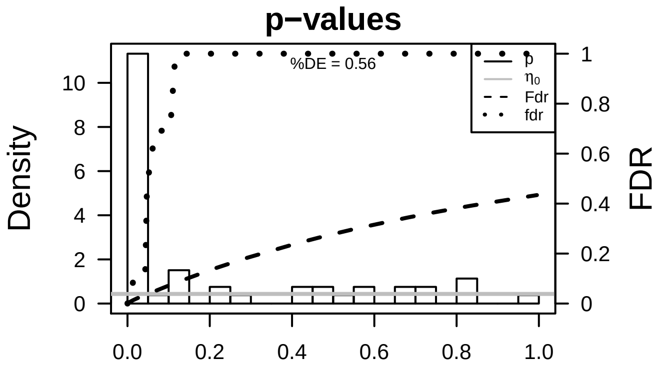
<fdr> = 0.55


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	MAGED1	−1.29	1e−09	2e−07	39 x 1	melanoma antigen family D1 [Source:HGNC Symbol;Acc:HG
2	CNOT2	−0.63	1e−08	6e−05	39 x 1	CCR4−NOT transcription complex, subunit 2 [Source:HGNC
3	ODF2L	−1.08	2e−06	1e−04	38 x 1	outer dense fiber of sperm tails 2−like [Source:HGNC Symbo
4	DDX52	−1.04	8e−06	2e−04	37 x 1	DEAD (Asp−Glu−Ala−Asp) box polypeptide 52 [Source:HGN
5	ARCN1	−1	1e−05	1e−03	38 x 1	archain 1 [Source:HGNC Symbol;Acc:HGNC:649]
6	TRAPPC6B	0.89	1e−04	1e−03	38 x 1	trafficking protein particle complex 6B [Source:HGNC Symbol
7	USP9X	−0.77	3e−04	1e−03	38 x 1	ubiquitin specific peptidase 9, X−linked [Source:HGNC Symb
8	ZBTB44	0.84	3e−04	1e−03	39 x 1	zinc finger and BTB domain containing 44 [Source:HGNC Sy
9	MAD1L1	−0.82	4e−04	1e−03	37 x 1	MAD1 mitotic arrest deficient−like 1 (yeast) [Source:HGNC S
10	PRUNE2	−0.75	4e−04	1e−03	38 x 1	prune homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:H
11	ALG11	−0.81	5e−04	1e−03	38 x 1	ALG11, alpha−1,2−mannosyltransferase [Source:HGNC Sym
12	BET1L	−0.81	5e−04	1e−03	37 x 1	Bet1 golgi vesicular membrane trafficking protein−like [Sourc
13	YAP1	−0.63	5e−04	1e−03	39 x 1	Yes−associated protein 1 [Source:HGNC Symbol;Acc:HGNC
14	ATPAF2	−0.8	6e−04	4e−03	39 x 1	ATP synthase mitochondrial F1 complex assembly factor 2 [S
15	HERC4	−0.79	7e−04	2e−02	37 x 1	HECT and RLD domain containing E3 ubiquitin protein ligase
16	KIAA0226	−0.73	2e−03	2e−02	38 x 1	KIAA0226 [Source:HGNC Symbol;Acc:HGNC:28991]
17	MSRB3	−0.64	3e−03	2e−02	37 x 1	methionine sulfoxide reductase B3 [Source:HGNC Symbol;A
18	BAZ2B	0.68	3e−03	3e−02	39 x 1	bromodomain adjacent to zinc finger domain, 2B [Source:HG
19	ZMAT3	−0.65	5e−03	3e−02	37 x 1	zinc finger, matrin−type 3 [Source:HGNC Symbol;Acc:HGNC
20	ACSL1	−0.64	6e−03	3e−02	37 x 1	acyl−CoA synthetase long−chain family member 1 [Source:H


p−values

B12_mel

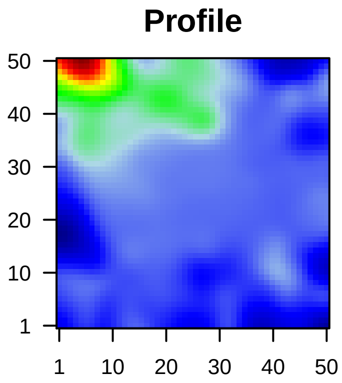
Local Summary

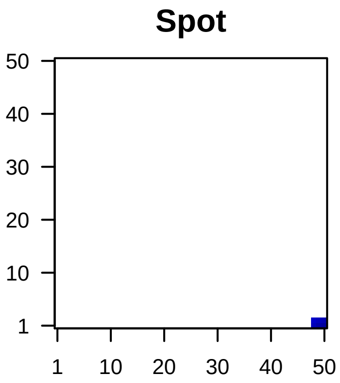
%DE = 0.74
metagenes = 6
genes = 142
genes in genesets = 142

genes with fdr < 0.1 = 69 (13 + / 56 −)
genes with fdr < 0.05 = 52 (11 + / 41 −)
genes with fdr < 0.01 = 35 (6 + / 29 −)

<r> metagenes = 1
<r> genes = 0.26

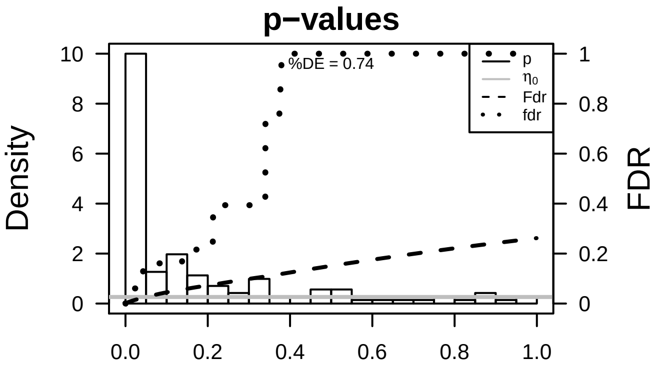
<FC> = −0.31
<shrinkage−t> = −4.99
<p−value> = 0.01
<fdr> = 0.6


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CRYAB	−1.82	2e−16	8e−15	50 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
2	ARID5B	−1.33	9e−11	3e−09	50 x 1	AT rich interactive domain 5B (MRF1−like) [Source:HGNC Sy
3	VIM	−1.02	1e−10	3e−09	50 x 2	vimentin [Source:HGNC Symbol;Acc:HGNC:12692]
4	TGIF1	−1.26	2e−10	1e−06	50 x 1	TGFB−induced factor homeobox 1 [Source:HGNC Symbol;A
5	SNAP23	−1.02	4e−08	5e−06	50 x 1	synaptosomal−associated protein, 23kDa [Source:HGNC Sy
6	BCL6	1.21	2e−07	5e−06	50 x 1	B−cell CLL/lymphoma 6 [Source:HGNC Symbol;Acc:HGNC:1
7	FAM98A	−1.16	3e−07	3e−05	49 x 1	family with sequence similarity 98, member A [Source:HGNC
8	FMN2	−1.11	1e−06	5e−05	48 x 1	formin 2 [Source:HGNC Symbol;Acc:HGNC:14074]
9	C1orf198	−0.73	3e−06	5e−05	49 x 1	chromosome 1 open reading frame 198 [Source:HGNC Sym
10	PTPRM	1.06	4e−06	2e−04	50 x 1	protein tyrosine phosphatase, receptor type, M [Source:HGN
11	PDGFA	−1.01	2e−05	2e−04	49 x 1	platelet−derived growth factor alpha polypeptide [Source:HG
12	CD55	−0.96	2e−05	2e−04	50 x 1	CD55 molecule, decay accelerating factor for complement (C
13	NEDD9	−0.99	2e−05	1e−03	48 x 2	neural precursor cell expressed, developmentally down−regul
14	CAMK2D	−0.9	1e−04	1e−03	50 x 1	calcium/calmodulin−dependent protein kinase II delta [Source
15	LMO7	0.9	1e−04	1e−03	50 x 2	LIM domain 7 [Source:HGNC Symbol;Acc:HGNC:6646]
16	A2M	−0.9	1e−04	2e−03	50 x 1	alpha−2−macroglobulin [Source:HGNC Symbol;Acc:HGNC:7
17	DNAJB4	−0.69	2e−04	2e−03	50 x 1	DnaJ (Hsp40) homolog, subfamily B, member 4 [Source:HG
18	DRAM1	0.86	2e−04	2e−03	50 x 2	DNA−damage regulated autophagy modulator 1 [Source:HG
19	DLGAP4	−0.84	3e−04	2e−03	50 x 1	discs, large (Drosophila) homolog−associated protein 4 [Sour
20	LIMCH1	−0.83	4e−04	2e−03	50 x 1	LIM and calponin homology domains 1 [Source:HGNC Symb


p−values

B12_mel

Local Summary

%DE = 0.78

metagenes = 1

genes = 13

genes in genesets = 13

genes with fdr < 0.1 = 8 (2 + / 6 −)

genes with fdr < 0.05 = 2 (0 + / 2 −)

genes with fdr < 0.01 = 2 (0 + / 2 −)

<r> metagenes = NA

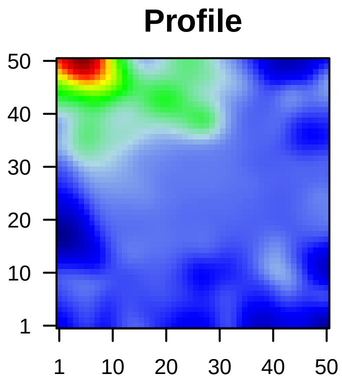
<r> genes = 0.16

<FC> = −0.33

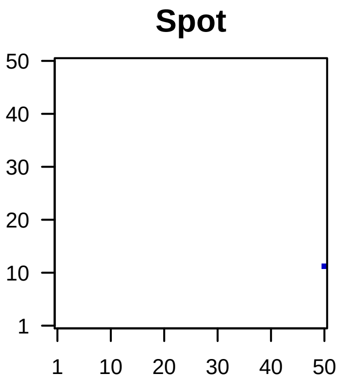
<shrinkage−t> = −5.53

<p−value> = 0.01

<fdr> = 0.72



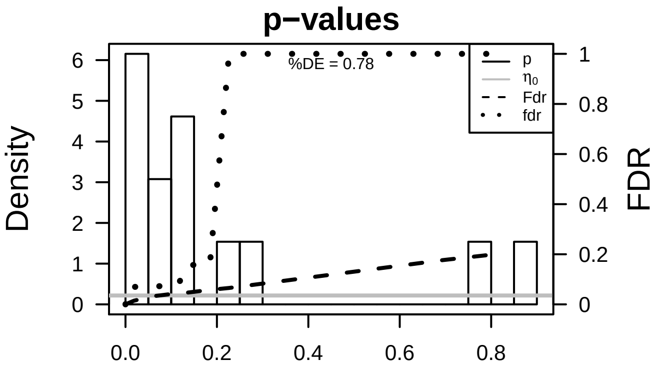
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	EIF5B	−1.3	3e−10	4e−06	50 x 12	eukaryotic translation initiation factor 5B [Source:HGNC Syml
2	TMED5	−1.11	2e−06	1e−03	50 x 12	transmembrane emp24 protein transport domain containing 5
3	TTC1	−0.67	4e−04	6e−02	50 x 12	tetratricopeptide repeat domain 1 [Source:HGNC Symbol;Acc
4	EXOC6	−0.54	2e−02	7e−02	50 x 12	exocyst complex component 6 [Source:HGNC Symbol;Acc:H
5	RBM28	0.43	6e−02	7e−02	50 x 12	RNA binding motif protein 28 [Source:HGNC Symbol;Acc:HG
6	CDKAL1	−0.42	7e−02	7e−02	50 x 12	CDK5 regulatory subunit associated protein 1−like 1 [Source:
7	DUS4L	−0.37	1e−01	7e−02	50 x 12	dihydrouridine synthase 4−like (S. cerevisiae) [Source:HGNC
8	WDR18	0.35	1e−01	7e−02	50 x 12	WD repeat domain 18 [Source:HGNC Symbol;Acc:HGNC:17
9	AK3	−0.34	1e−01	2e−01	50 x 12	adenylate kinase 3 [Source:HGNC Symbol;Acc:HGNC:17376
10	SRSF11	−0.18	2e−01	2e−01	50 x 12	serine/arginine−rich splicing factor 11 [Source:HGNC Symbol
11	ADAM9	−0.27	3e−01	1e+00	50 x 12	ADAM metallopeptidase domain 9 [Source:HGNC Symbol;Ac
12	EIF2A	0.05	8e−01	1e+00	50 x 12	eukaryotic translation initiation factor 2A, 65kDa [Source:HGN
13	EFNA4	0.03	9e−01	1e+00	50 x 12	ephrin−A4 [Source:HGNC Symbol;Acc:HGNC:3224]



p−values

B12_mel

Local Summary

%DE = 0.7

metagenes = 31

genes = 357

genes in genesets = 355

genes with fdr < 0.1 = 128 (25 + / 103 −)

genes with fdr < 0.05 = 124 (25 + / 99 −)

genes with fdr < 0.01 = 76 (15 + / 61 −)

<r> metagenes = 0.81

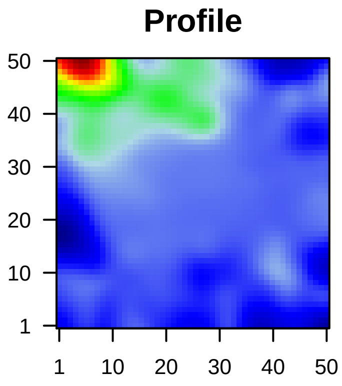
<r> genes = 0.1

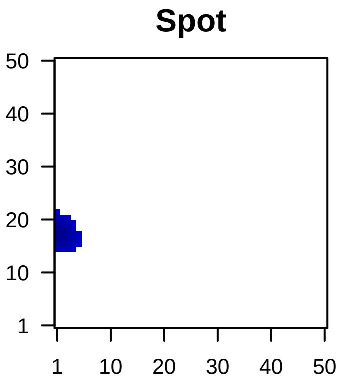
<FC> = −0.26

<shrinkage−t> = −4.38

<p−value> = 0.01

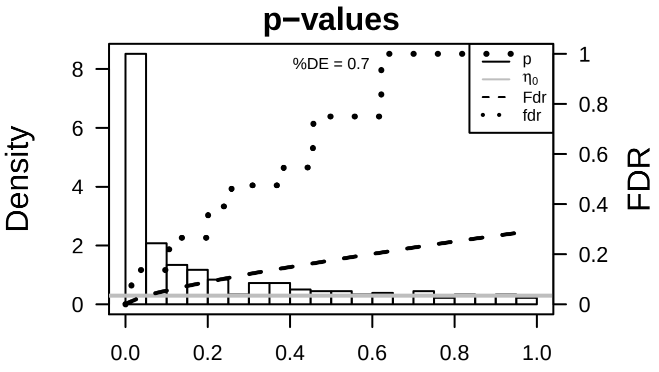
<fdr> = 0.65





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	BCCIP	−1.55	2e−16	6e−15	2 x 15	BRCA2 and CDKN1A interacting protein [Source:HGNC Sym
2	GTF3A	−1.55	2e−16	6e−15	1 x 20	general transcription factor IIIA [Source:HGNC Symbol;Acc:H
3	MYO10	−1.21	2e−16	6e−15	5 x 16	myosin X [Source:HGNC Symbol;Acc:HGNC:7593]
4	NOLC1	−1.53	2e−16	6e−15	1 x 16	nucleolar and coiled−body phosphoprotein 1 [Source:HGNC
5	BZW2	−1.21	5e−15	5e−11	2 x 16	basic leucine zipper and W2 domains 2 [Source:HGNC Symb
6	KDELR2	−1.35	5e−13	5e−08	1 x 19	KDEL (Lys−Asp−Glu−Leu) endoplasmic reticulum protein ret
7	JTB	−0.99	4e−10	4e−07	1 x 21	jumping translocation breakpoint [Source:HGNC Symbol;Acc
8	TXNL4A	−1.26	4e−09	1e−06	1 x 19	thioredoxin−like 4A [Source:HGNC Symbol;Acc:HGNC:30551
9	TMEM192	−1.21	2e−08	1e−06	1 x 18	transmembrane protein 192 [Source:HGNC Symbol;Acc:HGN
10	COMMD7	−1.21	4e−08	1e−06	4 x 17	COMM domain containing 7 [Source:HGNC Symbol;Acc:HGN
11	ZNF559	1.28	4e−08	2e−06	3 x 15	zinc finger protein 559 [Source:HGNC Symbol;Acc:HGNC:28
12	SLC7A8	−1.2	6e−08	2e−06	2 x 15	solute carrier family 7 (amino acid transporter light chain, L sy
13	PEX10	1.25	8e−08	2e−05	1 x 20	peroxisomal biogenesis factor 10 [Source:HGNC Symbol;Acc
14	EIF2AK1	−1.12	2e−07	2e−05	1 x 20	eukaryotic translation initiation factor 2−alpha kinase 1 [Sourc
15	NT5C3B	−1.15	5e−07	2e−05	1 x 20	5'−nucleotidase, cytosolic IIIB [Source:HGNC Symbol;Acc:HG
16	NCALD	−1.13	8e−07	2e−05	1 x 15	neurocalcin delta [Source:HGNC Symbol;Acc:HGNC:7655]
17	CYB5R3	−0.9	9e−07	4e−05	4 x 20	cytochrome b5 reductase 3 [Source:HGNC Symbol;Acc:HGN
18	MDM1	1.13	1e−06	4e−05	1 x 21	Mdm1 nuclear protein homolog (mouse) [Source:HGNC Sym
19	SLC25A32	−1.09	2e−06	4e−05	1 x 15	solute carrier family 25 (mitochondrial folate carrier), member
20	TMEM134	−1.08	3e−06	4e−05	1 x 19	transmembrane protein 134 [Source:HGNC Symbol;Acc:HGN



B12_mel

Local Summary

%DE = 0.69

metagenes = 11

genes = 171

genes in genesets = 171

genes with fdr < 0.1 = 77 (15 + / 62 −)

genes with fdr < 0.05 = 67 (14 + / 53 −)

genes with fdr < 0.01 = 50 (8 + / 42 −)

<r> metagenes = 0.91

<r> genes = 0.09

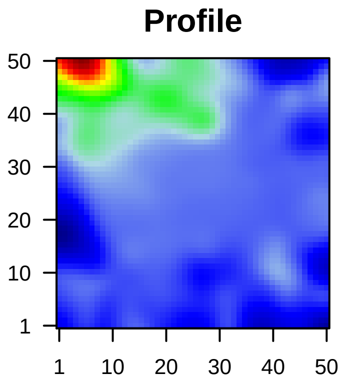
<FC> = −0.26

<shrinkage−t> = −4.29

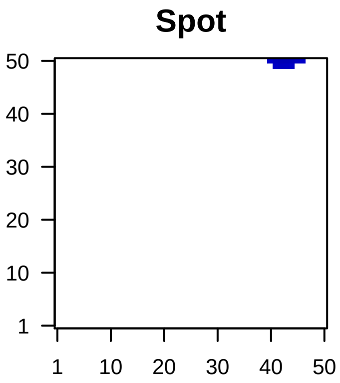
<p−value> = 0.01

<fdr> = 0.58

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CDC123	−1.56	2e−16	3e−15	46 x 50	cell division cycle 123 [Source:HGNC Symbol;Acc:HGNC:16
2	PYCR1	−1.1	2e−16	3e−15	46 x 50	pyrroline−5−carboxylate reductase 1 [Source:HGNC Symbol;
3	WARS	−1.41	2e−16	3e−15	46 x 50	tryptophanyl−tRNA synthetase [Source:HGNC Symbol;Acc:H
4	YIPF3	−1.5	2e−16	3e−15	45 x 50	Yip1 domain family, member 3 [Source:HGNC Symbol;Acc:H
5	PAM16	−1.43	2e−12	8e−08	45 x 50	presequence translocase−associated motor 16 homolog (S.
6	MRPL2	−1.28	2e−09	8e−08	40 x 50	mitochondrial ribosomal protein L2 [Source:HGNC Symbol;A
7	SCAMP2	−1.26	3e−09	3e−06	46 x 50	secretory carrier membrane protein 2 [Source:HGNC Symbol
8	CCDC132	1.26	6e−08	1e−05	42 x 50	coiled−coil domain containing 132 [Source:HGNC Symbol;Ac
9	PTGR1	−1.14	4e−07	1e−05	40 x 50	prostaglandin reductase 1 [Source:HGNC Symbol;Acc:HGNC
10	MOCS2	−1.15	6e−07	7e−05	41 x 50	molybdenum cofactor synthesis 2 [Source:HGNC Symbol;Ac
11	XPO6	−1.06	3e−06	7e−05	46 x 50	exportin 6 [Source:HGNC Symbol;Acc:HGNC:19733]
12	SNAP47	−1.05	4e−06	7e−05	44 x 50	synaptosomal−associated protein, 47kDa [Source:HGNC Sy
13	SDR39U1	−1.06	5e−06	2e−04	43 x 50	short chain dehydrogenase/reductase family 39U, member 1
14	TBCB	−0.82	1e−05	2e−04	46 x 50	tubulin folding cofactor B [Source:HGNC Symbol;Acc:HGNC:
15	CDC40	−1.01	1e−05	6e−04	40 x 50	cell division cycle 40 [Source:HGNC Symbol;Acc:HGNC:173
16	HHLA3	0.97	3e−05	6e−04	45 x 50	HERV−H LTR−associating 3 [Source:HGNC Symbol;Acc:HG
17	TRMT61B	−0.96	4e−05	6e−04	41 x 50	tRNA methyltransferase 61B [Source:HGNC Symbol;Acc:HG
18	ALX1	−0.93	6e−05	6e−04	43 x 50	ALX homeobox 1 [Source:HGNC Symbol;Acc:HGNC:1494]
19	C4orf3	0.54	8e−05	6e−04	44 x 49	chromosome 4 open reading frame 3 [Source:HGNC Symbol
20	ACTR6	−0.91	9e−05	6e−04	42 x 50	ARP6 actin−related protein 6 homolog (yeast) [Source:HGNC

p−values