B9_mel

Global Summary

%DE = 0.22

genes with fdr < 0.2 = 2933 (1681 + / 1252 −)

genes with fdr < 0.1 = 2342 (1347 + / 995 −)

genes with fdr < 0.05 = 1954 (1122 + / 832 −)

genes with fdr < 0.01 = 1285 (719 + / 566 −)

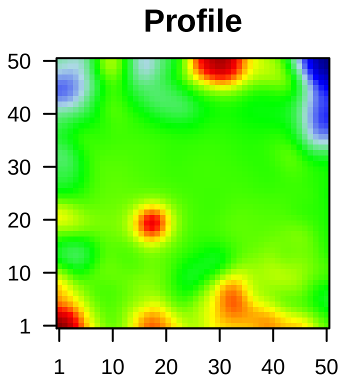
genes in genesets = 14839

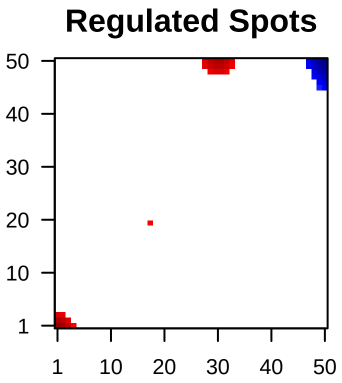
<FC> = 0

<shrinkage−t> = −0.1

<p−value> = 0.07

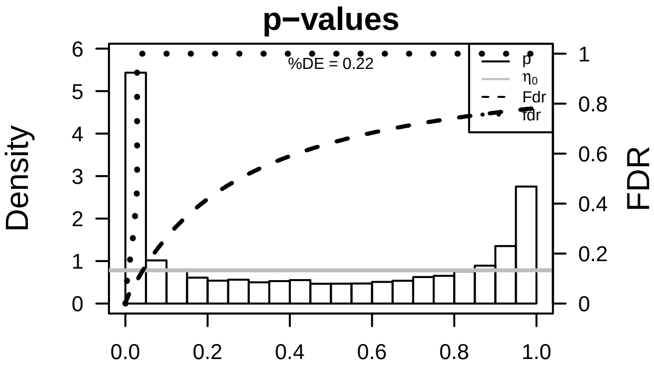
<fdr> = 0.78


Profile


Regulated Spots

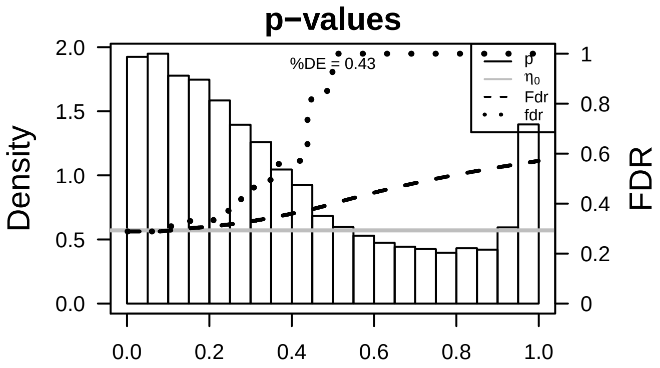
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ACTL6A	−1.74	2e−16	5e−14	4 x 50	actin−like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
2	ALG3	−1.59	2e−16	5e−14	48 x 50	ALG3, alpha−1,3− mannosyltransferase [Source:HGNC Syml
3	AMZ2	−1.75	2e−16	5e−14	48 x 42	archaelysin family metallopeptidase 2 [Source:HGNC Symbol
4	ARHGAP8	−1.65	2e−16	5e−14	1 x 43	Rho GTPase activating protein 8 [Source:HGNC Symbol;Acc:
5	ARL8B	−1.86	2e−16	5e−14	1 x 33	ADP−ribosylation factor−like 8B [Source:HGNC Symbol;Acc:I
6	ATP1B3	−1.24	2e−16	5e−14	1 x 21	ATPase, Na+/K+ transporting, beta 3 polypeptide [Source:HG
7	ATP6V1H	−1.77	2e−16	5e−14	5 x 44	ATPase, H+ transporting, lysosomal 50/57kDa, V1 subunit H [
8	BCLAF1	−1.82	2e−16	5e−14	19 x 43	BCL2−associated transcription factor 1 [Source:HGNC Symb
9	CAPZB	−1.85	2e−16	5e−14	50 x 50	capping protein (actin filament) muscle Z−line, beta [Source:H
10	CEP95	−2.01	2e−16	5e−14	48 x 36	centrosomal protein 95kDa [Source:HGNC Symbol;Acc:HGN
11	CFL2	−1.76	2e−16	5e−14	50 x 7	cofilin 2 (muscle) [Source:HGNC Symbol;Acc:HGNC:1875]
12	CHURC1	−1.13	2e−16	5e−14	39 x 50	churchill domain containing 1 [Source:HGNC Symbol;Acc:HG
13	CMC1	−1.93	2e−16	5e−14	50 x 50	C−x(9)−C motif containing 1 [Source:HGNC Symbol;Acc:HGN
14	COA6	−1.74	2e−16	5e−14	48 x 36	cytochrome c oxidase assembly factor 6 [Source:HGNC Syml
15	CRYAB	−1.82	2e−16	5e−14	50 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
16	CRYZL1	−1.72	2e−16	5e−14	44 x 50	crystallin, zeta (quinone reductase)−like 1 [Source:HGNC Syr
17	CYB5B	−1.69	2e−16	5e−14	15 x 50	cytochrome b5 type B (outer mitochondrial membrane) [Sourc
18	DCXR	0.97	2e−16	5e−14	5 x 37	dicarbonyl/L−xylulose reductase [Source:HGNC Symbol;Acc:
19	EIF1B	−1.67	2e−16	5e−14	4 x 43	eukaryotic translation initiation factor 1B [Source:HGNC Syml
20	G3BP2	−1.72	2e−16	5e−14	50 x 49	GTPase activating protein (SH3 domain) binding protein 2 [Sc


p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	4.74	0.004	2972	Brain	Mid_Frontal_Lobe_ReprPC
2	4.63	0.005	2798	Colon Cancer	TxEnhG1_Colon
3	4.56	0.005	620	GSEA C2	MILI_PSEUDOPODIA_HAPTOTAXIS_DN
4	4.4	0.005	483	GSEA C2	SCHAEFFER_PROSTATE_DEVELOPMENT_6HR_DN
5	4.38	0.006	3396	Lymphoma	HOPP_Repressed
6	4.31	0.006	3081	Brain	Mid_Frontal_Lobe_ZNF
7	4.21	0.006	43	GSEA C2	PID_A6B1_A6B4_INTEGRIN_PATHWAY
8	4.21	0.006	11	CC	Gemini of coiled bodies
9	4.15	0.007	2210	BP	anatomical structure development
10	4.12	0.007	115	BP	protein N−linked glycosylation via asparagine
11	4.08	0.007	90	GSEA C2	FIGUEROA_AML_METHYLATION_CLUSTER_4_UP
12	4.07	0.007	13	MF	mannosyltransferase activity
13	4.04	0.007	12	CC	SMN complex
14	4.02	0.007	143	GSEA C2	VANTVEER_BREAST_CANCER_ESR1_UP
15	3.94	0.008	15	GSEA C2	BIOCARTA_ERK5_PATHWAY
16	3.93	0.008	815	BP	lipid metabolic process
17	3.83	0.009	2984	CC	integral component of membrane
18	3.77	0.009	22	MF	RNA polymerase II transcription coactivator activity
19	3.66	0.010	2188	Lymphoma	HOPP_Poised_promoter
20	3.64	0.010	70	GSEA C2	VANLOO_SP3_TARGETS_DN
Underexpressed					
1	−6.78	0.001	213	GSEA C2	WONG_MITOCHONDRIA_GENE_MODULE
2	−5.93	0.002	6929	Lymphoma	HOPP_Txn_elongation
3	−5.9	0.002	401	CC	mitochondrial inner membrane
4	−5.84	0.002	388	GSEA C2	REACTOME_CELL_CYCLE
5	−5.78	0.002	242	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
6	−5.75	0.002	7592	Lymphoma	HOPP_Active_promoter
7	−5.58	0.002	7209	Lymphoma	HOPP_Weak_promoter
8	−5.38	0.003	609	GSEA C2	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIA
9	−5.34	0.003	277	BP	translation
10	−5.34	0.003	170	GSEA C2	WHITFIELD_CELL_CYCLE_G2
11	−5.15	0.003	312	GSEA C2	WONG_EMBRYONIC_STEM_CELL_CORE
12	−5.06	0.003	1126	GSEA C2	BLALOCK_ALZHEIMERS_DISEASE_DN
13	−5.03	0.003	478	GSEA C2	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
14	−4.97	0.004	616	GSEA C2	BENPORATH_CYCLING_GENES
15	−4.91	0.004	198	HM	HALLMARK_OXIDATIVE_PHOSPHORYLATION
16	−4.86	0.016	16	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
17	−4.83	0.004	12	BP	histone H2A acetylation
18	−4.83	0.004	700	GSEA C2	MARSON_BOUND_BY_E2F4_UNSTIMULATED
19	−4.82	0.004	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
20	−4.75	0.004	83	BP	mitochondrial translational termination


p−values

B9_mel

Local Summary

%DE = 0.84

metagenes = 9

genes = 180

genes in genesets = 177

genes with fdr < 0.1 = 122 (119 + / 3 −)

genes with fdr < 0.05 = 122 (119 + / 3 −)

genes with fdr < 0.01 = 97 (95 + / 2 −)

<r> metagenes = 0.94

<r> genes = 0.11

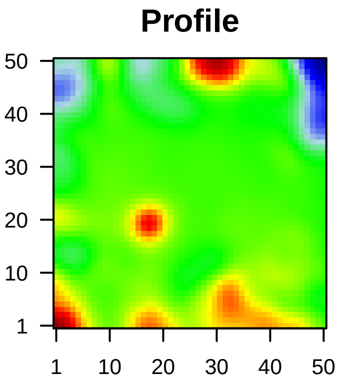
<FC> = 0.66

<shrinkage−t> = 10.02

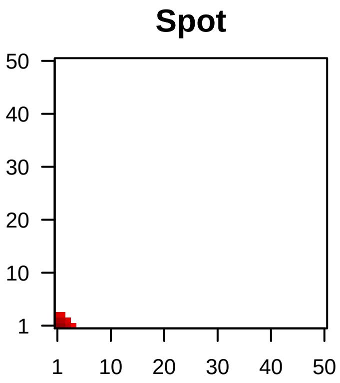
<p−value> = 0

<fdr> = 0.36

Profile



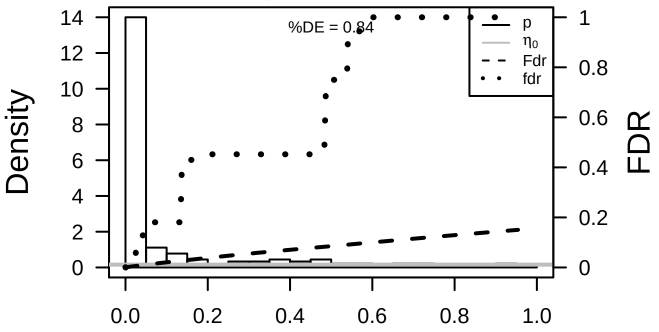
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	APBB1	1.74	5e−11	4e−08	1 x 1	amyloid beta (A4) precursor protein−binding, family B, membe
2	ZNF513	1.6	1e−09	8e−08	1 x 1	zinc finger protein 513 [Source:HGNC Symbol;Acc:HGNC:26
3	GRAMD1C	1.54	5e−09	8e−08	4 x 1	GRAM domain containing 1C [Source:HGNC Symbol;Acc:HG
4	CCDC126	1.52	9e−09	8e−08	1 x 1	coiled−coil domain containing 126 [Source:HGNC Symbol;Ac
5	RBM11	1.52	1e−08	3e−07	4 x 1	RNA binding motif protein 11 [Source:HGNC Symbol;Acc:HG
6	OSBPL5	1.48	2e−08	3e−07	3 x 1	oxysterol binding protein−like 5 [Source:HGNC Symbol;Acc:H
7	SPATA5L1	1.47	3e−08	7e−07	1 x 2	spermatogenesis associated 5−like 1 [Source:HGNC Symbol
8	PCNX	1.43	6e−08	7e−07	1 x 2	pecanex homolog (Drosophila) [Source:HGNC Symbol;Acc:H
9	CTD−2116N1	1.41	1e−07	7e−07	2 x 2	
10	POFUT1	1.4	1e−07	7e−07	1 x 1	protein O−fucosyltransferase 1 [Source:HGNC Symbol;Acc:H
11	RAB24	1.4	1e−07	8e−07	1 x 1	RAB24, member RAS oncogene family [Source:HGNC Symb
12	SLC30A5	1.38	2e−07	8e−07	2 x 2	solute carrier family 30 (zinc transporter), member 5 [Source:
13	LMAN2L	1.38	2e−07	8e−07	1 x 1	lectin, mannose−binding 2−like [Source:HGNC Symbol;Acc:H
14	AIF1L	1.37	2e−07	2e−06	1 x 1	allograft inflammatory factor 1−like [Source:HGNC Symbol;Ac
15	ALG2	1.35	4e−07	2e−06	1 x 3	ALG2, alpha−1,3/1,6−mannosyltransferase [Source:HGNC S
16	SLC46A3	1.35	4e−07	5e−06	1 x 3	solute carrier family 46, member 3 [Source:HGNC Symbol;Ac
17	CRELD1	1.33	6e−07	3e−05	1 x 1	cysteine−rich with EGF−like domains 1 [Source:HGNC Symb
18	HTATSF1	1.25	2e−06	3e−05	1 x 1	HIV−1 Tat specific factor 1 [Source:HGNC Symbol;Acc:HGNC
19	PHF2	1.23	4e−06	3e−05	1 x 1	PHD finger protein 2 [Source:HGNC Symbol;Acc:HGNC:892
20	CRKL	1.22	4e−06	4e−05	1 x 2	v−crk avian sarcoma virus CT10 oncogene homolog−like [So

p−values



B9_mel

Local Summary

%DE = 0.98

metagenes = 1

genes = 63

genes in genesets = 61

genes with fdr < 0.1 = 61 (61 + / 0 −)

genes with fdr < 0.05 = 61 (61 + / 0 −)

genes with fdr < 0.01 = 57 (57 + / 0 −)

<r> metagenes = NA

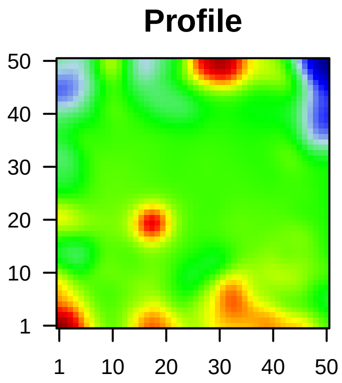
<r> genes = 0.39

<FC> = 0.99

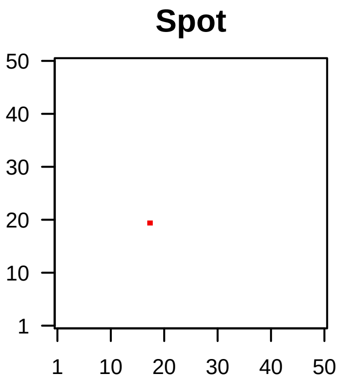
<shrinkage−t> = 15.14

<p−value> = 0

<fdr> = 0.2



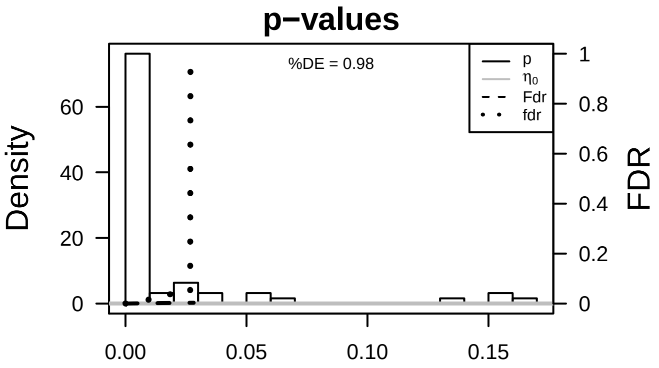
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	LAMA5	1.81	9e−12	1e−11	18 x 20	laminin, alpha 5 [Source:HGNC Symbol;Acc:HGNC:6485]
2	ESRP2	1.78	2e−11	8e−11	18 x 20	epithelial splicing regulatory protein 2 [Source:HGNC Symbol
3	PCDHB15	1.72	9e−11	2e−10	18 x 20	protocadherin beta 15 [Source:HGNC Symbol;Acc:HGNC:86
4	DPY19L2	1.68	2e−10	4e−10	18 x 20	dpy−19−like 2 (C. elegans) [Source:HGNC Symbol;Acc:HGN
5	DEPDC4	1.64	5e−10	1e−09	18 x 20	DEP domain containing 4 [Source:HGNC Symbol;Acc:HGNC
6	TNFSF13B	1.6	2e−09	6e−09	18 x 20	tumor necrosis factor (ligand) superfamily, member 13b [Sour
7	RGS14	1.54	6e−09	2e−08	18 x 20	regulator of G−protein signaling 14 [Source:HGNC Symbol;A
8	GJB2	1.48	2e−08	6e−08	18 x 20	gap junction protein, beta 2, 26kDa [Source:HGNC Symbol;A
9	SLC45A4	1.41	1e−07	6e−08	18 x 20	solute carrier family 45, member 4 [Source:HGNC Symbol;Ac
10	FITM2	1.4	1e−07	2e−07	18 x 20	fat storage−inducing transmembrane protein 2 [Source:HGN
11	MOCS1	1.32	6e−07	2e−07	18 x 20	molybdenum cofactor synthesis 1 [Source:HGNC Symbol;Ac
12	ZDHHC23	1.31	7e−07	2e−07	18 x 20	zinc finger, DHHC−type containing 23 [Source:HGNC Symbo
13	SSH3	1.3	9e−07	2e−07	18 x 20	slingshot protein phosphatase 3 [Source:HGNC Symbol;Acc:
14	SH3TC1	1.3	9e−07	3e−07	18 x 20	SH3 domain and tetratricopeptide repeats 1 [Source:HGNC
15	STOML1	1.29	1e−06	1e−06	18 x 20	stomatin (EPB72)−like 1 [Source:HGNC Symbol;Acc:HGNC:
16	BTNL9	1.25	2e−06	1e−06	18 x 20	butyrophilin−like 9 [Source:HGNC Symbol;Acc:HGNC:24176]
17	TBC1D22B	1.24	3e−06	1e−06	18 x 20	TBC1 domain family, member 22B [Source:HGNC Symbol;Ac
18	HIRA	1.23	4e−06	3e−06	18 x 20	histone cell cycle regulator [Source:HGNC Symbol;Acc:HGN
19	ZNF658	1.2	6e−06	3e−06	18 x 20	zinc finger protein 658 [Source:HGNC Symbol;Acc:HGNC:25
20	INPP5E	1.18	9e−06	3e−06	18 x 20	inositol polyphosphate−5−phosphatase, 72 kDa [Source:HGN



p−values

B9_mel

Local Summary

%DE = 0.83

metagenes = 16

genes = 168

genes in genesets = 168

genes with fdr < 0.1 = 113 (108 + / 5 −)

genes with fdr < 0.05 = 113 (108 + / 5 −)

genes with fdr < 0.01 = 82 (80 + / 2 −)

<r> metagenes = 0.91

<r> genes = 0.08

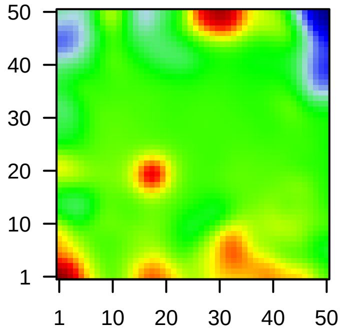
<FC> = 0.64

<shrinkage−t> = 10.13

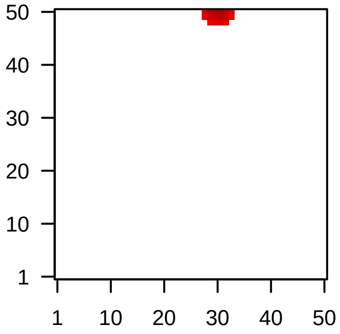
<p−value> = 0

<fdr> = 0.41

Profile



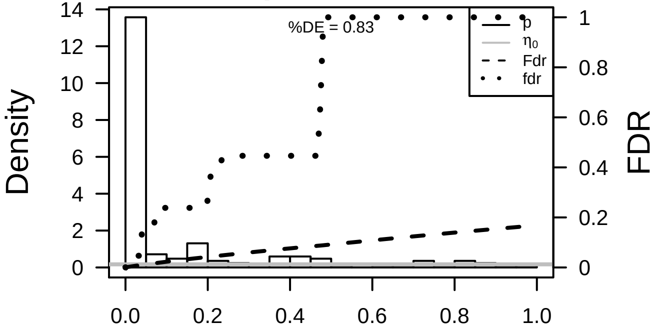
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	TYK2	2.15	4e−16	6e−11	32 x 50	tyrosine kinase 2 [Source:HGNC Symbol;Acc:HGNC:12440]
2	PLCG1	1.83	4e−12	6e−11	31 x 50	phospholipase C, gamma 1 [Source:HGNC Symbol;Acc:HGN
3	SLC25A35	1.83	4e−12	1e−09	32 x 48	solute carrier family 25, member 35 [Source:HGNC Symbol;A
4	C8orf46	1.75	4e−11	3e−09	31 x 48	chromosome 8 open reading frame 46 [Source:HGNC Symbo
5	DAK	1.69	2e−10	3e−09	31 x 50	dihydroxyacetone kinase 2 homolog (S. cerevisiae) [Source:H
6	POLI	1.67	3e−10	4e−08	30 x 50	polymerase (DNA directed) iota [Source:HGNC Symbol;Acc:H
7	CD36	1.58	2e−09	4e−08	29 x 50	CD36 molecule (thrombospondin receptor) [Source:HGNC Sy
8	ARSE	1.56	4e−09	4e−08	31 x 48	arylsulfatase E (chondrodysplasia punctata 1) [Source:HGNC
9	MPI	1.56	4e−09	1e−07	28 x 50	mannose phosphate isomerase [Source:HGNC Symbol;Acc:H
10	APPL2	1.52	1e−08	1e−07	32 x 50	adaptor protein, phosphotyrosine interaction, PH domain and
11	TXNDC11	1.5	2e−08	1e−07	28 x 50	thioredoxin domain containing 11 [Source:HGNC Symbol;Acc
12	TRIM68	1.49	2e−08	2e−07	30 x 50	tripartite motif containing 68 [Source:HGNC Symbol;Acc:HGN
13	DHRS12	1.47	3e−08	2e−07	33 x 50	dehydrogenase/reductase (SDR family) member 12 [Source:H
14	DPY19L3	1.46	3e−08	5e−07	32 x 50	dpy−19−like 3 (C. elegans) [Source:HGNC Symbol;Acc:HGN
15	POMT2	1.43	7e−08	5e−07	28 x 49	protein−O−mannosyltransferase 2 [Source:HGNC Symbol;Ac
16	CDPF1	1.42	8e−08	5e−07	28 x 50	cysteine−rich, DPF motif domain containing 1 [Source:HGNC
17	POLR3F	1.41	9e−08	5e−07	31 x 50	polymerase (RNA) III (DNA directed) polypeptide F, 39 kDa [S
18	CREB1	1.39	1e−07	1e−06	32 x 50	cAMP responsive element binding protein 1 [Source:HGNC S
19	U2AF2	1.38	2e−07	1e−06	30 x 49	U2 small nuclear RNA auxiliary factor 2 [Source:HGNC Symb
20	CD9	1.38	2e−07	1e−06	30 x 50	CD9 molecule [Source:HGNC Symbol;Acc:HGNC:1709]

p−values



B9_mel

Local Summary

%DE = 0.76

metagenes = 18

genes = 289

genes in genesets = 288

genes with fdr < 0.1 = 156 (3 + / 153 −)

genes with fdr < 0.05 = 150 (2 + / 148 −)

genes with fdr < 0.01 = 114 (0 + / 114 −)

<r> metagenes = 0.92

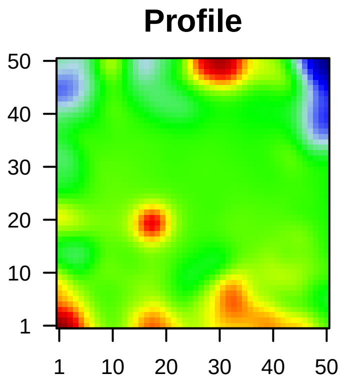
<r> genes = 0.08

<FC> = −0.62

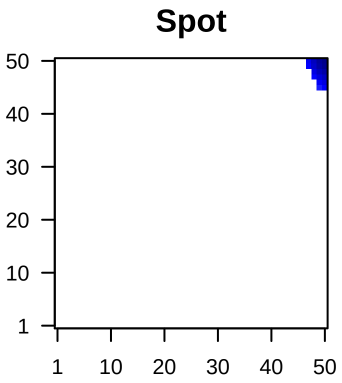
<shrinkage−t> = −11.05

<p−value> = 0

<fdr> = 0.48



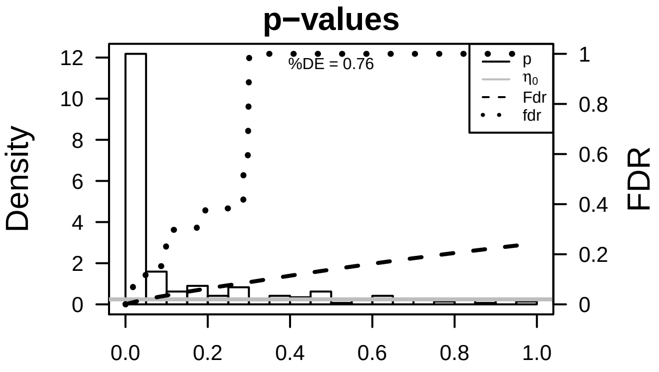
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ALG3	−1.59	2e−16	1e−15	48 x 50	ALG3, alpha−1,3− mannosyltransferase [Source:HGNC Sym
2	CAPZB	−1.85	2e−16	1e−15	50 x 50	capping protein (actin filament) muscle Z−line, beta [Source:
3	CMC1	−1.93	2e−16	1e−15	50 x 50	C−x(9)−C motif containing 1 [Source:HGNC Symbol;Acc:HG
4	G3BP2	−1.72	2e−16	1e−15	50 x 49	GTPase activating protein (SH3 domain) binding protein 2 [S
5	MRPS18A	−1.98	2e−16	1e−15	50 x 50	mitochondrial ribosomal protein S18A [Source:HGNC Symbo
6	NQO2	−1.76	2e−16	1e−15	50 x 50	NAD(P)H dehydrogenase, quinone 2 [Source:HGNC Symbol;
7	PTCD3	−1.65	2e−16	1e−15	48 x 50	pentatricopeptide repeat domain 3 [Source:HGNC Symbol;A
8	SDF2	−1.67	2e−16	1e−15	48 x 50	stromal cell−derived factor 2 [Source:HGNC Symbol;Acc:HG
9	SEC61G	−2.03	2e−16	1e−15	49 x 48	Sec61 gamma subunit [Source:HGNC Symbol;Acc:HGNC:18
10	SELT	−1.67	2e−16	1e−15	47 x 50	
11	SFT2D1	−1.8	2e−16	1e−15	49 x 49	SFT2 domain containing 1 [Source:HGNC Symbol;Acc:HGN
12	SNRPN	−1.53	2e−16	1e−15	50 x 46	small nuclear ribonucleoprotein polypeptide N [Source:HGNC
13	VPS28	−1.66	2e−16	1e−15	47 x 50	vacuolar protein sorting 28 homolog (S. cerevisiae) [Source:
14	WDR83OS	−1.32	2e−16	1e−15	50 x 47	WD repeat domain 83 opposite strand [Source:HGNC Symb
15	GTF2H1	−1.62	4e−16	2e−13	50 x 46	general transcription factor IIH, polypeptide 1, 62kDa [Source
16	ABCE1	−1.5	3e−15	2e−10	50 x 48	ATP−binding cassette, sub−family E (OABP), member 1 [Sou
17	PIGP	−1.52	2e−12	3e−10	50 x 50	phosphatidylinositol glycan anchor biosynthesis, class P [Sou
18	UGP2	−1.28	8e−12	3e−10	50 x 50	UDP−glucose pyrophosphorylase 2 [Source:HGNC Symbol;A
19	CYSTM1	−1.19	1e−11	6e−10	47 x 50	cysteine−rich transmembrane module containing 1 [Source:H
20	TPGS2	−1.09	4e−11	6e−10	47 x 50	tubulin polyglutamylase complex subunit 2 [Source:HGNC Sy



p−values