D10_mel

Global Summary

%DE = 0.2

genes with fdr < 0.2 = 2700 (1661 + / 1039 −)

genes with fdr < 0.1 = 1941 (1238 + / 703 −)

genes with fdr < 0.05 = 1632 (1062 + / 570 −)

genes with fdr < 0.01 = 1021 (660 + / 361 −)

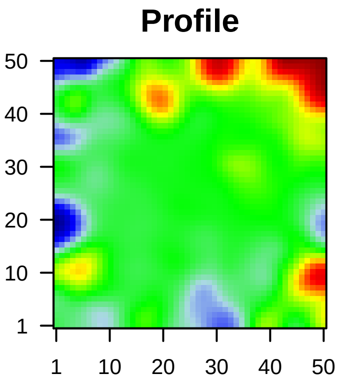
genes in genesets = 14839

<FC> = 0

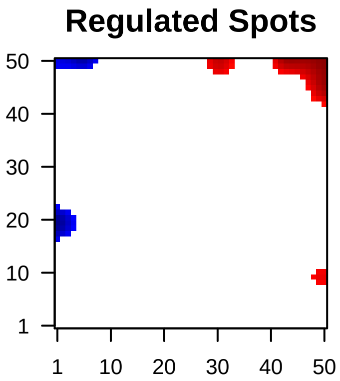
<shrinkage−t> = 0.05

<p−value> = 0.09

<fdr> = 0.8



Profile



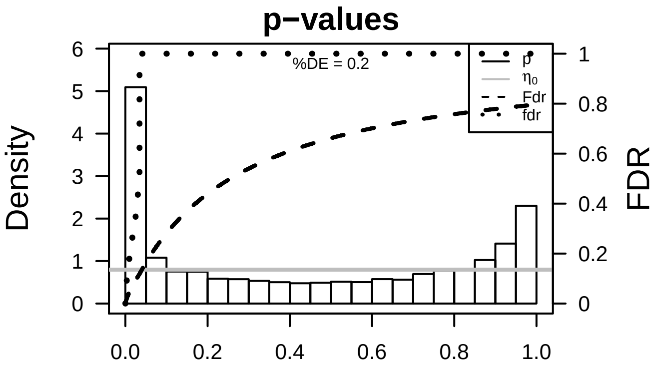
Regulated Spots

Global Genelist

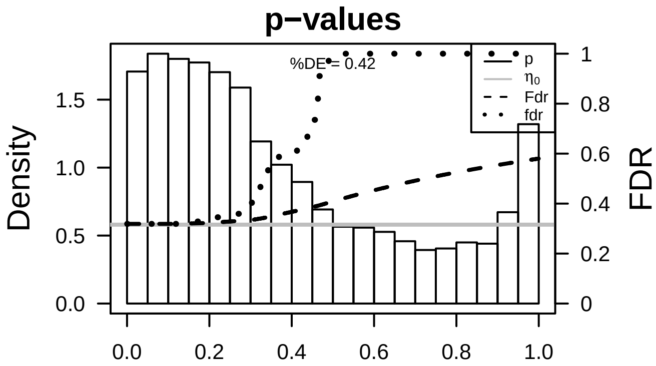
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	COX5A	−1.26	2e−16	3e−13	1 x 21	cytochrome c oxidase subunit Va [Source:HGNC Symbol;Acc
2	FDFT1	−1.75	2e−16	3e−13	1 x 38	farnesyl−diphosphate farnesyltransferase 1 [Source:HGNC S
3	HSD17B4	−1.63	2e−16	3e−13	11 x 50	hydroxysteroid (17−beta) dehydrogenase 4 [Source:HGNC S
4	ID3	−1.64	2e−16	3e−13	11 x 50	inhibitor of DNA binding 3, dominant negative helix−loop−heli
5	NELFCD	−1.25	2e−16	3e−13	6 x 38	negative elongation factor complex member C/D [Source:HG
6	PIGY	−1.02	2e−16	3e−13	1 x 20	phosphatidylinositol glycan anchor biosynthesis, class Y [Sou
7	PYURF	−1.53	2e−16	3e−13	1 x 19	PIGY upstream reading frame [Source:HGNC Symbol;Acc:H
8	RRM1	−1.58	2e−16	3e−13	2 x 50	ribonucleotide reductase M1 [Source:HGNC Symbol;Acc:HG
9	SLC25A27	1.92	2e−16	3e−13	6 x 40	solute carrier family 25, member 27 [Source:HGNC Symbol;A
10	SND1	−1.52	7e−16	2e−11	39 x 9	staphylococcal nuclease and tudor domain containing 1 [Sou
11	GLUL	−1.44	4e−15	2e−11	36 x 1	glutamate−ammonia ligase [Source:HGNC Symbol;Acc:HGN
12	CHCHD6	−0.96	7e−15	2e−11	1 x 43	coiled−coil−helix−coiled−coil−helix domain containing 6 [Sou
13	TSEN15	−1.49	7e−15	2e−11	14 x 39	TSEN15 tRNA splicing endonuclease subunit [Source:HGNC
14	ZNF77	1.79	7e−15	2e−11	12 x 1	zinc finger protein 77 [Source:HGNC Symbol;Acc:HGNC:131
15	C16orf13	−1.48	8e−15	2e−11	1 x 21	chromosome 16 open reading frame 13 [Source:HGNC Sym
16	KRTAP19−1	1.78	1e−14	4e−11	1 x 8	keratin associated protein 19−1 [Source:HGNC Symbol;Acc:
17	AZI2	−1.43	2e−14	4e−11	1 x 13	5−azacytidine induced 2 [Source:HGNC Symbol;Acc:HGNC:
18	NTPCR	−1.4	2e−14	1e−10	2 x 35	nucleoside−triphosphatase, cancer−related [Source:HGNC S
19	SH3BGRL	−1.47	2e−14	3e−10	48 x 37	SH3 domain binding glutamate−rich protein like [Source:HGN
20	UCP2	−1.31	7e−14	3e−10	2 x 46	uncoupling protein 2 (mitochondrial, proton carrier) [Source:H

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	5.98	0.002	9330	Brain	Overlap_fetal_midbrain_ReprPC
2	5.18	0.003	136	GSEA C2	PODAR_RESPONSE_TO_ADAPHOSTIN_UP
3	5.16	0.003	26	GSEA C2	KRIGE_AMINO_ACID_DEPRIVATION
4	5.11	0.003	120	GSEA C2	KARLSSON_TGFB1_TARGETS_UP
5	4.97	0.004	5184	Lymphoma	HOPP_Txn_transition
6	4.91	0.004	35	MF	aminoacyl−tRNA ligase activity
7	4.86	0.004	235	GSEA C2	BLUM_RESPONSE_TO_SALIRASIB_UP
8	4.86	0.004	162	BP	ribosome biogenesis
9	4.84	0.004	36	MF	tRNA binding
10	4.8	0.004	24	GSEA C2	REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION
11	4.75	0.004	42	GSEA C2	REACTOME_TRNA_AMINOACYLATION
12	4.7	0.004	2136	TF	ICGC_GabpPcr2_targets
13	4.65	0.005	44	BP	tRNA aminoacylation for protein translation
14	4.54	0.005	6929	Lymphoma	HOPP_Txn_elongation
15	4.52	0.005	784	GSEA C2	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
16	4.51	0.005	315	Glio	WILLSCHER_GBM_Verhaak−PNwt & CL_up
17	4.51	0.005	9027	Colon Cancer	Tx_Colon
18	4.45	0.005	1365	MF	RNA binding
19	4.41	0.005	393	GSEA C2	MITSIADES_RESPONSE_TO_APLIDIN_UP
20	4.36	0.006	8580	Colon Cancer	TxWk_Colon
Underexpressed					
1	−9.05	4e−04	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
2	−7.66	7e−04	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
3	−7.52	8e−04	305	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
4	−7.05	1e−03	267	GSEA C2	ZHANG_TLX_TARGETS_60HR_DN
5	−7.02	1e−03	124	GSEA C2	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
6	−6.98	1e−03	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
7	−6.9	1e−03	291	GSEA C2	HORIUCHI_WTAP_TARGETS_DN
8	−6.87	1e−02	16	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
9	−6.6	1e−03	50	GSEA C2	ISHIDA_E2F_TARGETS
10	−6.4	1e−03	118	GSEA C2	ODONNELL_TFRC_TARGETS_DN
11	−6.07	2e−03	327	GSEA C2	BLUM_RESPONSE_TO_SALIRASIB_DN
12	−6.04	2e−03	81	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
13	−5.86	2e−03	39	GSEA C2	KAMMINGA_EZH2_TARGETS
14	−5.83	2e−03	196	HM	HALLMARK_G2M_CHECKPOINT
15	−5.78	2e−03	93	GSEA C2	KONG_E2F3_TARGETS
16	−5.78	2e−03	96	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
17	−5.72	2e−03	145	GSEA C2	CHANG_CYCLING_GENES
18	−5.56	2e−03	265	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_UP
19	−5.55	2e−03	99	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
20	−5.51	3e−03	54	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP



p−values



p−values

D10_mel

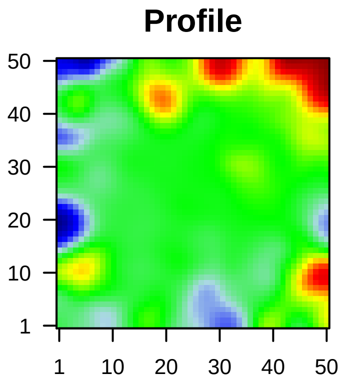
Local Summary

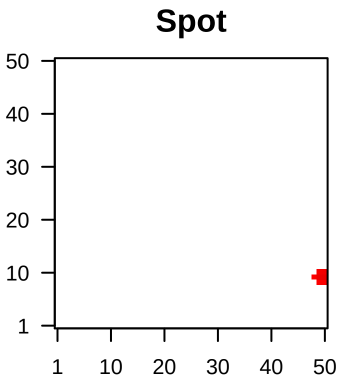
%DE = 0.83
metagenes = 7
genes = 65
genes in genesets = 65

genes with fdr < 0.1 = 43 (32 + / 11 −)
genes with fdr < 0.05 = 32 (26 + / 6 −)
genes with fdr < 0.01 = 20 (18 + / 2 −)

<r> metagenes = 0.98
<r> genes = 0.1

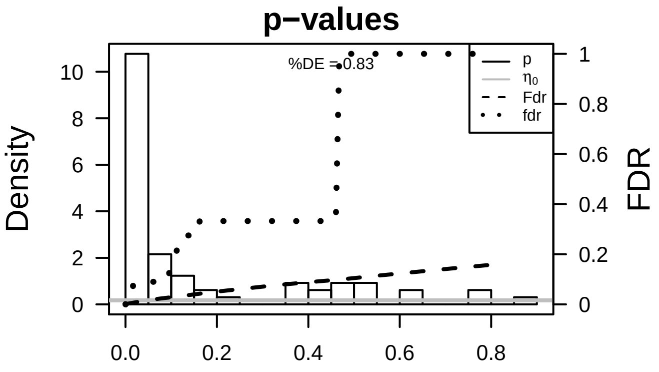
<FC> = 0.25
<shrinkage−t> = 4.07
<p−value> = 0.01
<fdr> = 0.54





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ATAD3A	1.28	3e−08	4e−06	50 x 11	ATPase family, AAA domain containing 3A [Source:HGNC Sy
2	RABL2B	1.17	4e−07	6e−05	50 x 11	RAB, member of RAS oncogene family−like 2B [Source:HGN
3	PRPSAP1	1	1e−05	6e−05	50 x 11	phosphoribosyl pyrophosphate synthetase−associated protei
4	ZNF76	1	1e−05	6e−05	50 x 11	zinc finger protein 76 [Source:HGNC Symbol;Acc:HGNC:131
5	ALG1	0.98	2e−05	6e−05	50 x 10	ALG1, chitobiosyldiphosphodolichol beta−mannosyltransfera
6	FBXO46	0.96	3e−05	6e−05	50 x 9	F−box protein 46 [Source:HGNC Symbol;Acc:HGNC:25069]
7	C11orf49	0.96	3e−05	6e−05	48 x 10	chromosome 11 open reading frame 49 [Source:HGNC Sym
8	SLC38A2	0.62	3e−05	8e−04	50 x 9	solute carrier family 38, member 2 [Source:HGNC Symbol;Ac
9	PRKAG1	0.88	1e−04	8e−04	50 x 11	protein kinase, AMP−activated, gamma 1 non−catalytic subu
10	PRR14	0.86	2e−04	8e−04	50 x 11	proline rich 14 [Source:HGNC Symbol;Acc:HGNC:28458]
11	FAM200B	0.76	3e−04	8e−04	50 x 11	family with sequence similarity 200, member B [Source:HGN
12	STK38L	0.83	3e−04	1e−03	49 x 10	serine/threonine kinase 38 like [Source:HGNC Symbol;Acc:H
13	FLRT2	0.81	4e−04	2e−03	50 x 10	fibronectin leucine rich transmembrane protein 2 [Source:HG
14	UBAC2	−0.78	7e−04	2e−03	50 x 11	UBA domain containing 2 [Source:HGNC Symbol;Acc:HGNC
15	SLC2A3	0.77	8e−04	4e−03	49 x 11	solute carrier family 2 (facilitated glucose transporter), memb
16	TRAPPC2	0.75	1e−03	4e−03	50 x 11	trafficking protein particle complex 2 [Source:HGNC Symbol;
17	EIF4A2	0.34	2e−03	4e−03	50 x 11	eukaryotic translation initiation factor 4A2 [Source:HGNC Syn
18	GALE	−0.71	2e−03	4e−03	50 x 10	UDP−galactose−4−epimerase [Source:HGNC Symbol;Acc:H
19	OLFML2A	0.7	2e−03	4e−03	48 x 10	olfactomedin−like 2A [Source:HGNC Symbol;Acc:HGNC:272
20	CCDC57	0.67	2e−03	4e−03	50 x 11	coiled−coil domain containing 57 [Source:HGNC Symbol;Acc



D10_mel

Local Summary

%DE = 0.69

metagenes = 49

genes = 607

genes in genesets = 606

genes with fdr < 0.1 = 255 (202 + / 53 −)

genes with fdr < 0.05 = 236 (189 + / 47 −)

genes with fdr < 0.01 = 177 (143 + / 34 −)

<r> metagenes = 0.74

<r> genes = 0.06

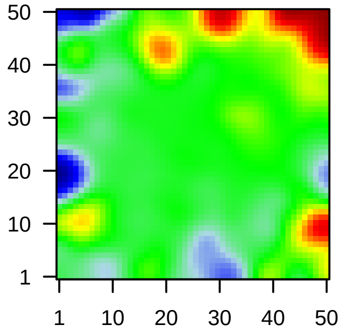
<FC> = 0.23

<shrinkage−t> = 3.83

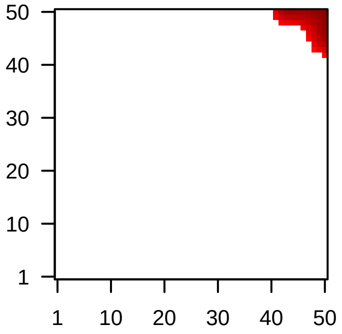
<p−value> = 0.01

<fdr> = 0.58

Profile



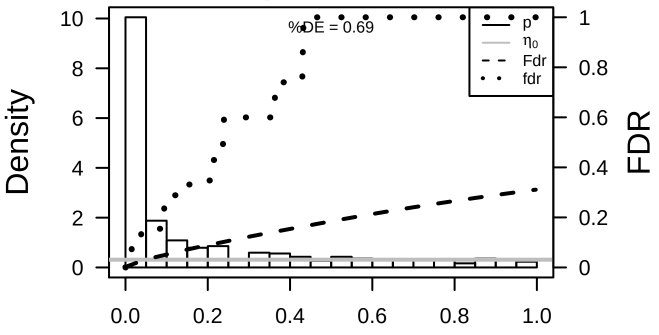
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	SC5D	−1.43	1e−12	2e−10	43 x 48	sterol−C5−desaturase [Source:HGNC Symbol;Acc:HGNC:10
2	ITIH3	1.62	2e−12	3e−09	50 x 50	inter−alpha−trypsin inhibitor heavy chain 3 [Source:HGNC Sy
3	TSC2	1.55	2e−11	1e−08	50 x 46	tuberous sclerosis 2 [Source:HGNC Symbol;Acc:HGNC:1236
4	CFH	1.5	7e−11	2e−08	43 x 50	complement factor H [Source:HGNC Symbol;Acc:HGNC:488
5	SELL	1.47	2e−10	8e−08	41 x 50	selectin L [Source:HGNC Symbol;Acc:HGNC:10720]
6	PGBD2	1.4	1e−09	8e−08	42 x 50	piggyBac transposable element derived 2 [Source:HGNC Sy
7	UGP2	0.99	1e−09	8e−08	50 x 50	UDP−glucose pyrophosphorylase 2 [Source:HGNC Symbol;A
8	SLC27A5	1.39	2e−09	8e−08	50 x 47	solute carrier family 27 (fatty acid transporter), member 5 [So
9	STK11IP	1.39	2e−09	4e−06	43 x 50	serine/threonine kinase 11 interacting protein [Source:HGNC
10	MYO1E	1.28	3e−08	4e−06	43 x 50	myosin IE [Source:HGNC Symbol;Acc:HGNC:7599]
11	HERPUD1	0.61	4e−08	4e−06	50 x 42	homocysteine−inducible, endoplasmic reticulum stress−induc
12	C1S	1.24	7e−08	4e−06	49 x 45	complement component 1, s subcomponent [Source:HGNC
13	PDE7A	1.23	9e−08	8e−06	49 x 45	phosphodiesterase 7A [Source:HGNC Symbol;Acc:HGNC:87
14	GMPR	1.21	1e−07	8e−06	50 x 43	guanosine monophosphate reductase [Source:HGNC Symbo
15	EHBP1	1.2	2e−07	8e−06	50 x 42	EH domain binding protein 1 [Source:HGNC Symbol;Acc:HG
16	POLR1B	1.19	2e−07	8e−06	47 x 45	polymerase (RNA) I polypeptide B, 128kDa [Source:HGNC S
17	DPH7	1.18	3e−07	8e−06	49 x 46	diphthamide biosynthesis 7 [Source:HGNC Symbol;Acc:HGN
18	CC2D2A	1.18	3e−07	8e−06	50 x 46	coiled−coil and C2 domain containing 2A [Source:HGNC Sy
19	LONP1	1.17	4e−07	8e−06	50 x 47	lon peptidase 1, mitochondrial [Source:HGNC Symbol;Acc:H
20	EARS2	1.17	4e−07	9e−06	43 x 48	glutamyl−tRNA synthetase 2, mitochondrial [Source:HGNC S

p−values



D10_mel

Local Summary

%DE = 0.75

metagenes = 13

genes = 140

genes in genesets = 140

genes with fdr < 0.1 = 78 (65 + / 13 −)

genes with fdr < 0.05 = 60 (51 + / 9 −)

genes with fdr < 0.01 = 48 (41 + / 7 −)

<r> metagenes = 0.94

<r> genes = 0.08

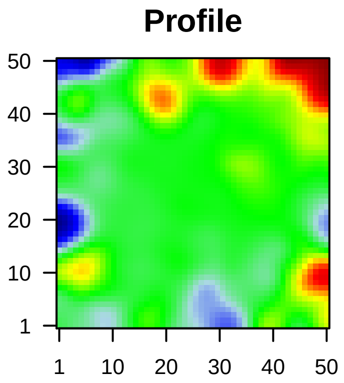
<FC> = 0.29

<shrinkage−t> = 4.59

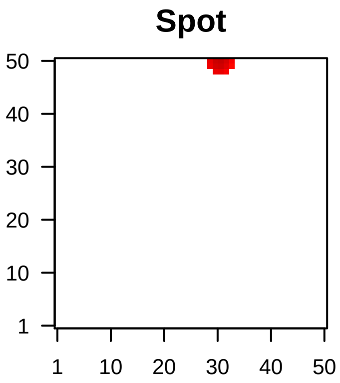
<p−value> = 0.01

<fdr> = 0.52

Profile



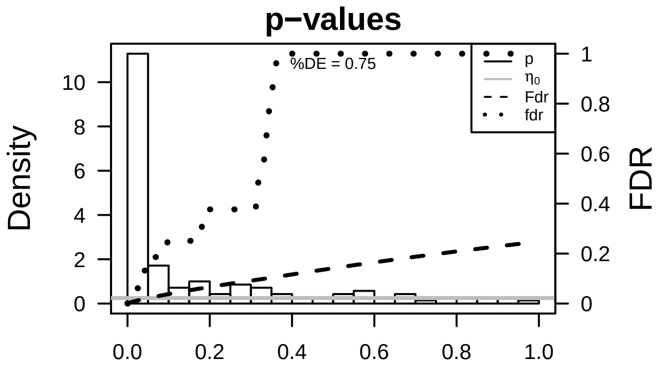
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	BAAT	1.62	2e−12	6e−11	32 x 50	bile acid CoA:amino acid N−acyltransferase [Source:HGNC S
2	FBXW4	1.6	3e−12	4e−08	33 x 49	F−box and WD repeat domain containing 4 [Source:HGNC Sy
3	PLCG1	1.38	2e−09	4e−08	31 x 50	phospholipase C, gamma 1 [Source:HGNC Symbol;Acc:HGN
4	UBE3D	1.38	2e−09	7e−08	33 x 50	ubiquitin protein ligase E3D [Source:HGNC Symbol;Acc:HGN
5	CD36	1.36	4e−09	1e−06	29 x 50	CD36 molecule (thrombospondin receptor) [Source:HGNC Sy
6	CHID1	−1	4e−08	5e−06	33 x 50	chitinase domain containing 1 [Source:HGNC Symbol;Acc:H
7	FKTN	1.18	3e−07	5e−06	30 x 50	fukutin [Source:HGNC Symbol;Acc:HGNC:3622]
8	RAD51B	1.18	3e−07	1e−05	33 x 50	RAD51 paralog B [Source:HGNC Symbol;Acc:HGNC:9822]
9	RCAN1	0.76	7e−07	1e−05	29 x 50	regulator of calcineurin 1 [Source:HGNC Symbol;Acc:HGNC:
10	HSPB9	1.12	1e−06	1e−05	30 x 50	heat shock protein, alpha−crystallin−related, B9 [Source:HGN
11	ILVBL	1.11	2e−06	1e−05	33 x 49	ilvB (bacterial acetolactate synthase)−like [Source:HGNC Sy
12	BPHL	−1.09	2e−06	1e−05	32 x 50	biphenyl hydrolase−like (serine hydrolase) [Source:HGNC Sy
13	TYK2	1.09	2e−06	6e−05	32 x 50	tyrosine kinase 2 [Source:HGNC Symbol;Acc:HGNC:12440]
14	NCK1	1.06	4e−06	6e−05	33 x 50	NCK adaptor protein 1 [Source:HGNC Symbol;Acc:HGNC:76
15	ELF2	1.05	5e−06	9e−05	30 x 50	E74−like factor 2 (ets domain transcription factor) [Source:HG
16	U2AF2	1.02	1e−05	9e−05	30 x 49	U2 small nuclear RNA auxiliary factor 2 [Source:HGNC Symb
17	CCNH	0.94	1e−05	9e−05	31 x 50	cyclin H [Source:HGNC Symbol;Acc:HGNC:1594]
18	ZNF384	1	1e−05	2e−04	31 x 48	zinc finger protein 384 [Source:HGNC Symbol;Acc:HGNC:11
19	CARKD	0.98	2e−05	5e−04	31 x 50	carbohydrate kinase domain containing [Source:HGNC Symb
20	TFIP11	0.95	4e−05	5e−04	32 x 50	tuftelin interacting protein 11 [Source:HGNC Symbol;Acc:HG

p−values



D10_mel

Local Summary

%DE = 0.64

metagenes = 20

genes = 282

genes in genesets = 281

genes with fdr < 0.1 = 104 (15 + / 89 −)

genes with fdr < 0.05 = 91 (12 + / 79 −)

genes with fdr < 0.01 = 50 (6 + / 44 −)

<r> metagenes = 0.96

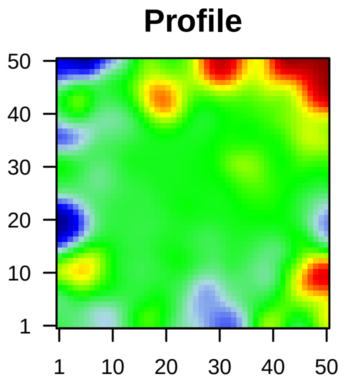
<r> genes = 0.14

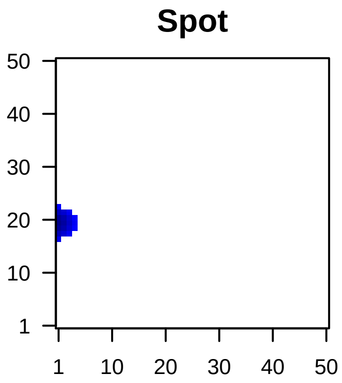
<FC> = −0.26

<shrinkage−t> = −4.53

<p−value> = 0.01

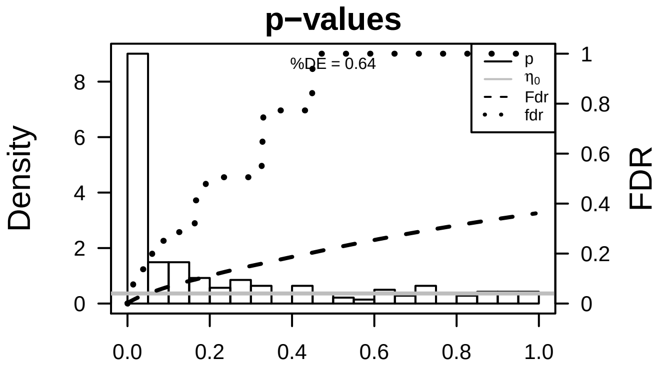
<fdr> = 0.64





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	COX5A	−1.26	2e−16	8e−15	1 x 21	cytochrome c oxidase subunit Va [Source:HGNC Symbol;Acc
2	PIGY	−1.02	2e−16	8e−15	1 x 20	phosphatidylinositol glycan anchor biosynthesis, class Y [Sou
3	PYURF	−1.53	2e−16	8e−15	1 x 19	PIGY upstream reading frame [Source:HGNC Symbol;Acc:H
4	C16orf13	−1.48	8e−15	3e−10	1 x 21	chromosome 16 open reading frame 13 [Source:HGNC Sym
5	TCF25	−1.26	3e−12	2e−09	1 x 23	transcription factor 25 (basic helix−loop−helix) [Source:HGN
6	PTPN2	−1.35	2e−11	4e−08	1 x 20	protein tyrosine phosphatase, non−receptor type 2 [Source:H
7	ATP1B3	−0.77	4e−10	6e−08	1 x 21	ATPase, Na+/K+ transporting, beta 3 polypeptide [Source:HG
8	P4HB	−0.57	1e−09	2e−07	1 x 20	prolyl 4−hydroxylase, beta polypeptide [Source:HGNC Symb
9	RCN1	−0.68	3e−09	6e−07	1 x 23	reticulocalbin 1, EF−hand calcium binding domain [Source:H
10	CLTA	−0.94	8e−09	2e−06	1 x 20	clathrin, light chain A [Source:HGNC Symbol;Acc:HGNC:209
11	MZT2B	−1.13	3e−08	4e−05	1 x 21	mitotic spindle organizing protein 2B [Source:HGNC Symbol;
12	PDIA3	−0.68	4e−07	1e−04	1 x 20	protein disulfide isomerase family A, member 3 [Source:HGN
13	ARF5	−1.08	2e−06	1e−04	1 x 20	ADP−ribosylation factor 5 [Source:HGNC Symbol;Acc:HGNC
14	PTP4A1	−0.86	3e−06	1e−04	1 x 21	protein tyrosine phosphatase type IVA, member 1 [Source:H
15	STUB1	−1.06	4e−06	2e−04	1 x 20	STIP1 homology and U−box containing protein 1, E3 ubiquiti
16	PPP2CA	−0.75	6e−06	2e−04	1 x 21	protein phosphatase 2, catalytic subunit, alpha isozyme [Sou
17	PIK3R4	1.01	1e−05	2e−04	1 x 18	phosphoinositide−3−kinase, regulatory subunit 4 [Source:HG
18	FTH1	−0.41	1e−05	3e−04	1 x 21	ferritin, heavy polypeptide 1 [Source:HGNC Symbol;Acc:HGN
19	ADPGK	1	2e−05	3e−04	1 x 21	ADP−dependent glucokinase [Source:HGNC Symbol;Acc:HG
20	TMEM192	0.92	2e−05	3e−04	1 x 18	transmembrane protein 192 [Source:HGNC Symbol;Acc:HGN



D10_mel

Local Summary

%DE = 0.79

metagenes = 15

genes = 278

genes in genesets = 278

genes with fdr < 0.1 = 146 (33 + / 113 −)

genes with fdr < 0.05 = 112 (27 + / 85 −)

genes with fdr < 0.01 = 65 (20 + / 45 −)

<r> metagenes = 0.93

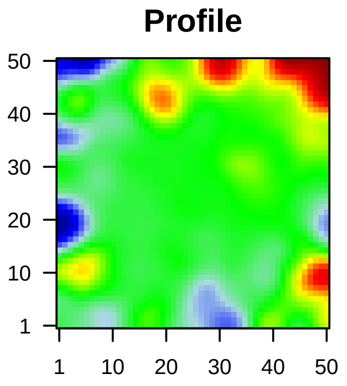
<r> genes = 0.34

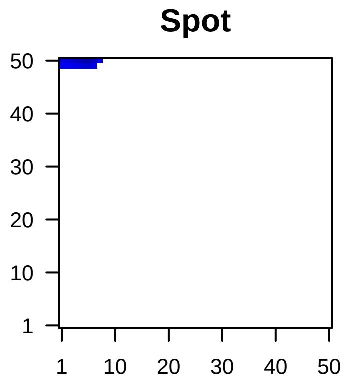
<FC> = −0.24

<shrinkage−t> = −3.79

<p−value> = 0.01

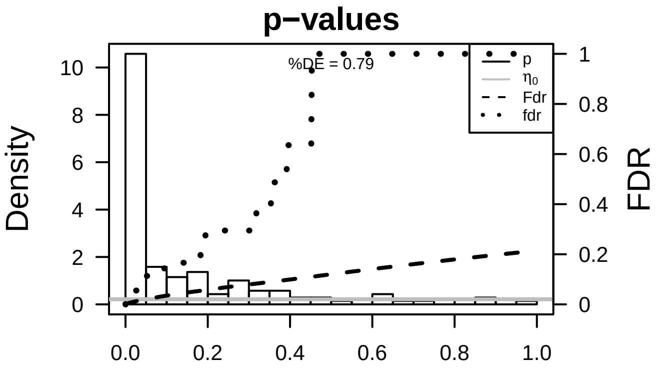
<fdr> = 0.6


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	RRM1	−1.58	2e−16	1e−14	2 x 50	ribonucleotide reductase M1 [Source:HGNC Symbol;Acc:HG
2	LBR	−1.39	8e−12	1e−08	7 x 50	lamin B receptor [Source:HGNC Symbol;Acc:HGNC:6518]
3	BIRC5	−1.33	2e−10	4e−08	6 x 50	baculoviral IAP repeat containing 5 [Source:HGNC Symbol;A
4	HMGB2	−1.28	1e−09	4e−08	5 x 50	high mobility group box 2 [Source:HGNC Symbol;Acc:HGNC:
5	GMNN	−1.19	2e−09	3e−07	2 x 50	geminin, DNA replication inhibitor [Source:HGNC Symbol;Acc
6	KPNA2	−0.55	1e−08	3e−07	7 x 50	karyopherin alpha 2 (RAG cohort 1, importin alpha 1) [Source
7	CENPF	−1.23	1e−08	3e−07	6 x 50	centromere protein F, 350/400kDa [Source:HGNC Symbol;Ac
8	ZNF143	1.31	1e−08	3e−06	5 x 50	zinc finger protein 143 [Source:HGNC Symbol;Acc:HGNC:12
9	SHCBP1	1.24	7e−08	3e−06	5 x 50	SHC SH2−domain binding protein 1 [Source:HGNC Symbol;
10	RFC2	−1.17	2e−07	3e−06	1 x 50	replication factor C (activator 1) 2, 40kDa [Source:HGNC Sym
11	NUSAP1	−1.17	2e−07	1e−05	6 x 50	nucleolar and spindle associated protein 1 [Source:HGNC Sy
12	CDCA7L	−1.15	4e−07	1e−05	1 x 50	cell division cycle associated 7−like [Source:HGNC Symbol;A
13	ZWINT	−1.13	6e−07	1e−05	5 x 50	ZW10 interacting kinetochore protein [Source:HGNC Symbol
14	FANCA	1.14	8e−07	5e−05	1 x 50	Fanconi anemia, complementation group A [Source:HGNC S
15	CENPW	−1.08	2e−06	5e−05	6 x 50	centromere protein W [Source:HGNC Symbol;Acc:HGNC:21
16	ZDHHC6	−1.07	3e−06	5e−05	1 x 49	zinc finger, DHHC−type containing 6 [Source:HGNC Symbol;
17	FANCI	1.06	3e−06	1e−04	3 x 50	Fanconi anemia, complementation group I [Source:HGNC Sy
18	PRC1	−0.98	8e−06	1e−04	5 x 50	protein regulator of cytokinesis 1 [Source:HGNC Symbol;Acc
19	ASF1B	−1.02	9e−06	1e−04	4 x 50	anti−silencing function 1B histone chaperone [Source:HGNC
20	SKP2	−1	1e−05	3e−04	3 x 50	S−phase kinase−associated protein 2, E3 ubiquitin protein lig


p−values