H7_mel

Global Summary

%DE = 0.2

genes with fdr < 0.2 = 2508 (1541 + / 967 −)

genes with fdr < 0.1 = 2110 (1317 + / 793 −)

genes with fdr < 0.05 = 1729 (1088 + / 641 −)

genes with fdr < 0.01 = 989 (628 + / 361 −)

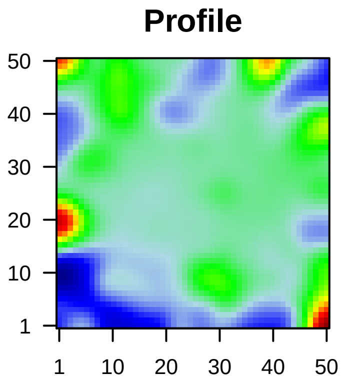
genes in genesets = 14839

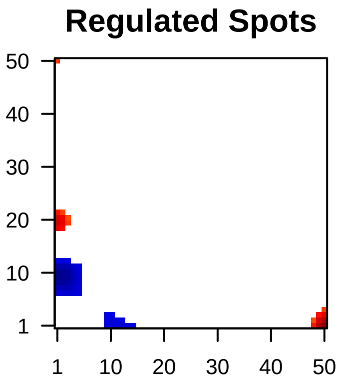
<FC> = 0

<shrinkage−t> = 0.04

<p−value> = 0.09

<fdr> = 0.8



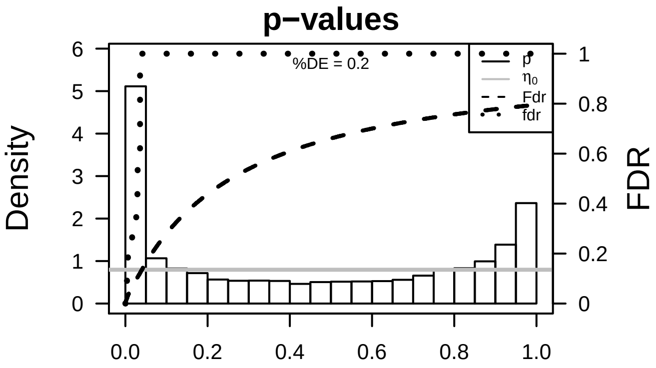


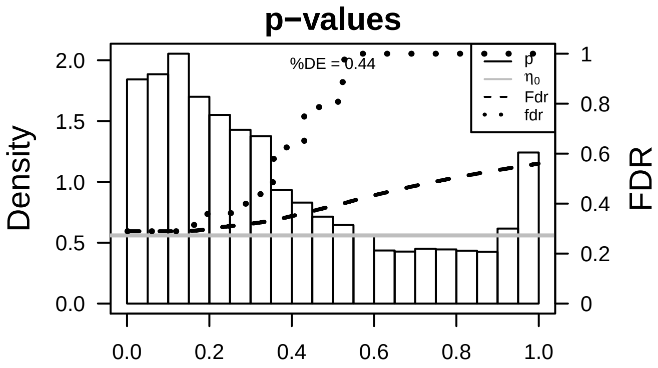
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ARHGAP8	−1.43	2e−16	2e−13	1 x 43	Rho GTPase activating protein 8 [Source:HGNC Symbol;Acc:
2	BSCL2	−1.65	2e−16	2e−13	50 x 50	Berardinelli−Seip congenital lipodystrophy 2 (seipin) [Source:
3	ECH1	−1.83	2e−16	2e−13	32 x 50	enoyl CoA hydratase 1, peroxisomal [Source:HGNC Symbol;
4	EIF4E2	−1.56	2e−16	2e−13	50 x 47	eukaryotic translation initiation factor 4E family member 2 [So
5	FOS	−1.76	2e−16	2e−13	4 x 7	FBJ murine osteosarcoma viral oncogene homolog [Source:
6	G6PC3	−1.49	2e−16	2e−13	48 x 49	glucose 6 phosphatase, catalytic, 3 [Source:HGNC Symbol;A
7	GNAI1	−1.71	2e−16	2e−13	42 x 1	guanine nucleotide binding protein (G protein), alpha inhibitin
8	GOLT1B	−1.48	2e−16	2e−13	47 x 15	golgi transport 1B [Source:HGNC Symbol;Acc:HGNC:20175]
9	HADHB	−1.47	2e−16	2e−13	1 x 39	hydroxyacyl−CoA dehydrogenase/3−ketoacyl−CoA thiolase/e
10	MLF2	−1.59	2e−16	2e−13	27 x 47	myeloid leukemia factor 2 [Source:HGNC Symbol;Acc:HGNC
11	NDUFAF3	−1.65	2e−16	2e−13	3 x 38	NADH dehydrogenase (ubiquinone) complex I, assembly fact
12	SHMT2	−1.57	2e−16	2e−13	31 x 50	serine hydroxymethyltransferase 2 (mitochondrial) [Source:H
13	TSN	−1.63	2e−16	2e−13	6 x 46	translin [Source:HGNC Symbol;Acc:HGNC:12379]
14	ZNF330	−1.69	2e−16	2e−13	2 x 13	zinc finger protein 330 [Source:HGNC Symbol;Acc:HGNC:15
15	GYPC	−1.53	9e−16	6e−11	1 x 38	glycophorin C (Gerbich blood group) [Source:HGNC Symbol;
16	COQ9	−1.51	6e−15	1e−10	1 x 38	coenzyme Q9 [Source:HGNC Symbol;Acc:HGNC:25302]
17	QPCT	−0.84	3e−14	1e−10	1 x 34	glutaminyl−peptide cyclotransferase [Source:HGNC Symbol;
18	USP41	1.78	4e−14	1e−10	20 x 46	ubiquitin specific peptidase 41 [Source:HGNC Symbol;Acc:H
19	FLII	−0.92	4e−14	3e−10	17 x 50	flightless I homolog (Drosophila) [Source:HGNC Symbol;Acc:
20	WDR43	−1.02	7e−14	3e−10	4 x 11	WD repeat domain 43 [Source:HGNC Symbol;Acc:HGNC:28

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset
Overexpressed				
1	7.19	9e−04	242	GSEA C2 KOBAYASHI_EGFR_SIGNALING_24HR_DN
2	7.11	1e−03	50	GSEA C2 ISHIDA_E2F_TARGETS
3	6.49	1e−03	81	GSEA C2 GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
4	5.88	2e−03	145	GSEA C2 CHANG_CYCLING_GENES
5	5.79	2e−03	270	GSEA C2 BASAKI_YBX1_TARGETS_UP
6	5.6	2e−03	89	GSEA C2 MORI_IMMATURE_B_LYMPHOCYTE_DN
7	5.5	3e−03	139	GSEA C2 ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
8	5.32	3e−03	124	GSEA C2 ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
9	5.27	3e−03	493	GSEA C2 MILI_PSEUDOPODIA_HAPTOTAXIS_UP
10	5.22	3e−03	862	GSEA C2 JOHNSTONE_PARVB_TARGETS_3_DN
11	5.17	3e−03	57	GSEA C2 REN_BOUND_BY_E2F
12	5.16	3e−03	29	GSEA C2 REACTOME_GLOBAL_GENOMIC_NER_GG_NER
13	5.09	3e−03	20	BP telomere maintenance via semi−conservative replication
14	5.09	3e−03	485	GSEA C2 CHICAS_RB1_TARGETS_SENESCENT
15	5.08	3e−03	136	GSEA C2 RUIZ_TNC_TARGETS_DN
16	5	4e−03	1008	GSEA C2 BRUINS_UVC_RESPONSE_LATE
17	4.96	4e−03	46	GSEA C2 MARIADASON_RESPONSE_TO_BUTYRATE_SULINDAC_6
18	4.92	4e−03	278	GSEA C2 MANALO_HYPOXIA_DN
19	4.91	4e−03	84	GSEA C2 MORI_LARGE_PRE_BII_LYMPHOCYTE_UP
20	4.9	4e−03	58	GSEA C2 SONG_TARGETS_OF_IE86_CMV_PROTEIN
Underexpressed				
1	−4.86	0.004	2698	Colon Cancer EnhA_Colon
2	−3.93	0.008	7	GSEA C2 KANG_CISPLATIN_RESISTANCE_DN
3	−3.91	0.008	37	BP gluconeogenesis
4	−3.9	0.008	2798	Colon Cancer TxEnhG1_Colon
5	−3.89	0.008	7	GSEA C2 HERNANDEZ_ABERRANT_MITOSIS_BY_DOCETACEL_4NM_DN
6	−3.75	0.009	12	MF GTPase activating protein binding
7	−3.71	0.010	32	GSEA C2 GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_Y
8	−3.58	0.011	318	miRNA target hsa−miR−98
9	−3.58	0.011	30	GSEA C2 CAFFAREL_RESPONSE_TO_THC_UP
10	−3.41	0.012	61	miRNA target hsa−miR−612
11	−3.37	0.013	35	GSEA C2 BIOCARTA_CARM_ER_PATHWAY
12	−3.34	0.013	13	GSEA C2 BIOCARTA_DREAM_PATHWAY
13	−3.31	0.014	361	MF binding
14	−3.17	0.015	22	GSEA C2 REACTOME_CIRCADIAN_REPRESSION_OF_EXPRESSION_BY
15	−3.17	0.015	2576	CC membrane
16	−3.17	0.015	42	GSEA C2 PID_RHOA_REG_PATHWAY
17	−3.17	0.015	26	GSEA C2 REACTOME_GLUCONEOGENESIS
18	−3.17	0.015	5880	Colon Cancer TssD2_Colon
19	−3.15	0.016	60	GSEA C2 PELLICCIOTTA_HDAC_IN_ANTIGEN_PRESENTATION_UP
20	−3.15	0.016	37	BP termination of G−protein coupled receptor signaling pathway





H7_mel

Local Summary

%DE = 0.81

metagenes = 9

genes = 192

genes in genesets = 192

genes with fdr < 0.1 = 112 (100 + / 12 −)

genes with fdr < 0.05 = 107 (97 + / 10 −)

genes with fdr < 0.01 = 75 (73 + / 2 −)

<r> metagenes = 0.99

<r> genes = 0.23

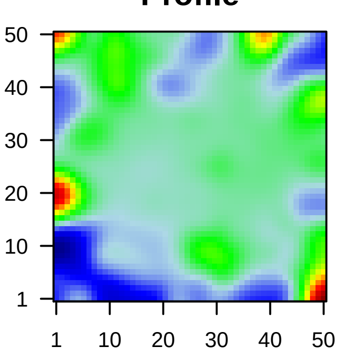
<FC> = 0.42

<shrinkage−t> = 6.67

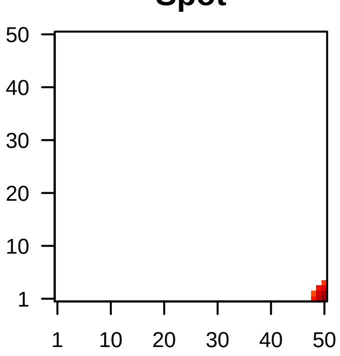
<p−value> = 0

<fdr> = 0.49

Profile



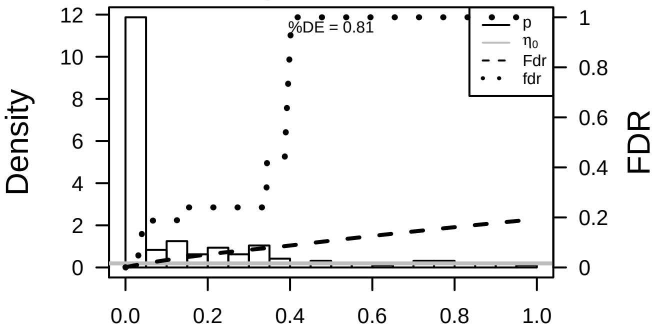
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CRYAB	1.11	6e−13	1e−10	50 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
2	HIST1H3D	1.6	9e−12	1e−10	50 x 1	histone cluster 1, H3d [Source:HGNC Symbol;Acc:HGNC:47
3	SORBS2	1.6	1e−11	1e−10	50 x 1	sorbin and SH3 domain containing 2 [Source:HGNC Symbol;
4	THBS1	1.59	1e−11	2e−09	50 x 1	thrombospondin 1 [Source:HGNC Symbol;Acc:HGNC:11785]
5	EFNA1	1.52	1e−10	2e−09	50 x 1	ephrin−A1 [Source:HGNC Symbol;Acc:HGNC:3221]
6	A2M	1.51	1e−10	6e−08	50 x 1	alpha−2−macroglobulin [Source:HGNC Symbol;Acc:HGNC:7
7	ITGB5	1.41	2e−09	6e−08	49 x 3	integrin, beta 5 [Source:HGNC Symbol;Acc:HGNC:6160]
8	PDLIM1	1.39	3e−09	1e−07	50 x 1	PDZ and LIM domain 1 [Source:HGNC Symbol;Acc:HGNC:2
9	KLF9	1.35	8e−09	1e−07	50 x 1	Kruppel−like factor 9 [Source:HGNC Symbol;Acc:HGNC:112
10	FN1	1.35	9e−09	2e−07	50 x 1	fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
11	TXNIP	1.33	2e−08	2e−07	50 x 1	thioredoxin interacting protein [Source:HGNC Symbol;Acc:H
12	HIST1H2BC	1.32	2e−08	6e−07	50 x 1	histone cluster 1, H2bc [Source:HGNC Symbol;Acc:HGNC:47
13	CTDSPL	1.29	4e−08	6e−07	49 x 1	CTD (carboxy−terminal domain, RNA polymerase II, polypept
14	CTGF	1.27	6e−08	6e−07	50 x 1	connective tissue growth factor [Source:HGNC Symbol;Acc:H
15	ITGA1	1.27	7e−08	2e−06	50 x 1	integrin, alpha 1 [Source:HGNC Symbol;Acc:HGNC:6134]
16	RSRP1	1.24	1e−07	2e−06	50 x 4	arginine/serine−rich protein 1 [Source:HGNC Symbol;Acc:H
17	ACTA2	1.23	2e−07	5e−06	50 x 1	actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;
18	CDH19	1.2	3e−07	8e−06	50 x 1	cadherin 19, type 2 [Source:HGNC Symbol;Acc:HGNC:1758]
19	DNAJC6	1.17	6e−07	8e−06	50 x 1	DnaJ (Hsp40) homolog, subfamily C, member 6 [Source:HGN
20	TMEM67	1.17	7e−07	9e−06	50 x 1	transmembrane protein 67 [Source:HGNC Symbol;Acc:HGN

p−values



H7_mel

Local Summary

%DE = 0.82

metagenes = 10

genes = 203

genes in genesets = 202

genes with fdr < 0.1 = 134 (120 + / 14 −)

genes with fdr < 0.05 = 98 (91 + / 7 −)

genes with fdr < 0.01 = 80 (74 + / 6 −)

<r> metagenes = 0.99

<r> genes = 0.17

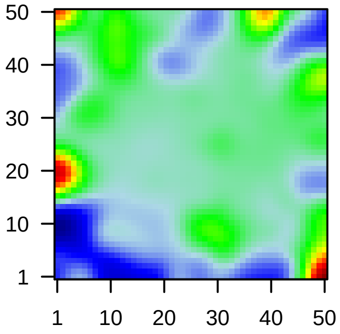
<FC> = 0.39

<shrinkage−t> = 6.46

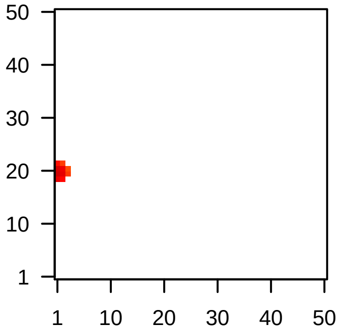
<p−value> = 0.01

<fdr> = 0.51

Profile



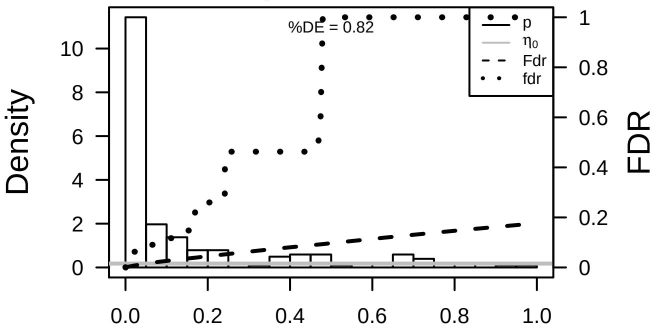
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	FAM120AOS	1.53	7e−11	1e−07	1 x 19	family with sequence similarity 120A opposite strand [Source:
2	NT5C	1.4	3e−09	1e−07	1 x 21	5', 3'−nucleotidase, cytosolic [Source:HGNC Symbol;Acc:HG
3	TMEM160	1.37	6e−09	8e−07	1 x 20	transmembrane protein 160 [Source:HGNC Symbol;Acc:HGN
4	SPRY2	1.29	4e−08	8e−07	1 x 21	sprouty homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:
5	RAB40B	1.28	5e−08	2e−06	1 x 20	RAB40B, member RAS oncogene family [Source:HGNC Sym
6	DBNDD2	1.25	1e−07	3e−06	1 x 22	dysbindin (dystrobrevin binding protein 1) domain containing
7	PUSL1	1.22	2e−07	3e−06	2 x 22	pseudouridylate synthase−like 1 [Source:HGNC Symbol;Acc:
8	PTP4A1	0.96	3e−07	3e−06	1 x 21	protein tyrosine phosphatase type IVA, member 1 [Source:HG
9	MPST	1.2	4e−07	2e−05	1 x 22	mercaptopyruvate sulfurtransferase [Source:HGNC Symbol;A
10	AKR7A2	1.16	8e−07	3e−05	1 x 21	aldo−keto reductase family 7, member A2 (aflatoxin aldehyde
11	YIPF4	1.12	2e−06	3e−05	1 x 21	Yip1 domain family, member 4 [Source:HGNC Symbol;Acc:H
12	ZNF511	1.1	3e−06	3e−05	1 x 21	zinc finger protein 511 [Source:HGNC Symbol;Acc:HGNC:28
13	C20orf24	1.03	3e−06	5e−05	1 x 21	chromosome 20 open reading frame 24 [Source:HGNC Sym
14	RRAGA	1.07	6e−06	5e−05	1 x 20	Ras−related GTP binding A [Source:HGNC Symbol;Acc:HGN
15	UBQLN1	−0.97	6e−06	5e−05	1 x 21	ubiquilin 1 [Source:HGNC Symbol;Acc:HGNC:12508]
16	CRTAP	0.91	1e−05	5e−05	1 x 19	cartilage associated protein [Source:HGNC Symbol;Acc:HGN
17	PPP2CA	0.75	1e−05	5e−05	1 x 21	protein phosphatase 2, catalytic subunit, alpha isozyme [Sou
18	TMEM256−PL	1.03	1e−05	5e−05	1 x 20	TMEM256−PLSCR3 readthrough (NMD candidate) [Source:
19	PACSIN2	1.03	1e−05	1e−04	1 x 22	protein kinase C and casein kinase substrate in neurons 2 [S
20	NT5C3B	−1	2e−05	1e−04	1 x 20	5'−nucleotidase, cytosolic IIIB [Source:HGNC Symbol;Acc:H

p−values



H7_mel

Local Summary

%DE = 0.84

metagenes = 1

genes = 58

genes in genesets = 58

genes with fdr < 0.1 = 41 (36 + / 5 −)

genes with fdr < 0.05 = 35 (33 + / 2 −)

genes with fdr < 0.01 = 29 (27 + / 2 −)

<r> metagenes = NA

<r> genes = 0.37

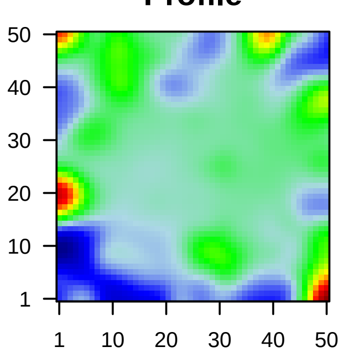
<FC> = 0.43

<shrinkage−t> = 6.82

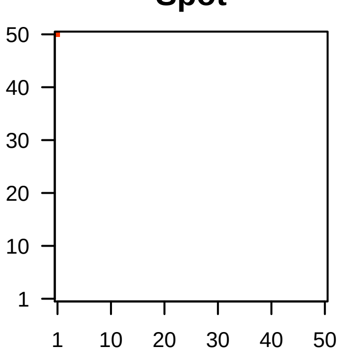
<p−value> = 0

<fdr> = 0.44

Profile



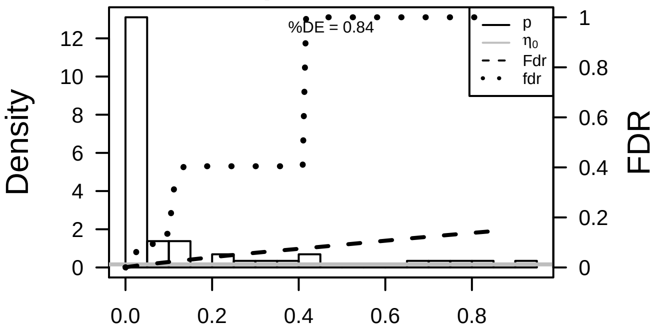
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	RFC2	1.22	9e−08	1e−06	1 x 50	replication factor C (activator 1) 2, 40kDa [Source:HGNC Sym
2	LMNB1	1.21	3e−07	7e−06	1 x 50	lamin B1 [Source:HGNC Symbol;Acc:HGNC:6637]
3	RFC4	1.08	1e−06	7e−06	1 x 50	replication factor C (activator 1) 4, 37kDa [Source:HGNC Sym
4	DSCC1	1.12	2e−06	3e−05	1 x 50	DNA replication and sister chromatid cohesion 1 [Source:HG
5	ANKRD32	1.07	5e−06	4e−05	1 x 50	ankyrin repeat domain 32 [Source:HGNC Symbol;Acc:HGNC
6	CDC6	1.03	1e−05	8e−05	1 x 50	cell division cycle 6 [Source:HGNC Symbol;Acc:HGNC:1744]
7	WDR76	1	2e−05	8e−05	1 x 50	WD repeat domain 76 [Source:HGNC Symbol;Acc:HGNC:25
8	MCM10	0.99	3e−05	2e−04	1 x 50	minichromosome maintenance complex component 10 [Sour
9	HELLS	0.89	6e−05	2e−04	1 x 50	helicase, lymphoid−specific [Source:HGNC Symbol;Acc:HGN
10	ZGRF1	0.93	8e−05	2e−04	1 x 50	zinc finger, GRF−type containing 1 [Source:HGNC Symbol;A
11	KNTC1	0.9	1e−04	2e−04	1 x 50	kinetochore associated 1 [Source:HGNC Symbol;Acc:HGNC:
12	PKMYT1	0.9	1e−04	7e−04	1 x 50	protein kinase, membrane associated tyrosine/threonine 1 [S
13	EXO1	0.86	2e−04	7e−04	1 x 50	exonuclease 1 [Source:HGNC Symbol;Acc:HGNC:3511]
14	NUP54	0.74	3e−04	2e−03	1 x 50	nucleoporin 54kDa [Source:HGNC Symbol;Acc:HGNC:17359
15	GINS2	0.81	5e−04	2e−03	1 x 50	GINS complex subunit 2 (Psf2 homolog) [Source:HGNC Sym
16	RAD51	0.8	7e−04	3e−03	1 x 50	RAD51 recombinase [Source:HGNC Symbol;Acc:HGNC:981
17	DTL	0.76	1e−03	3e−03	1 x 50	denticleless E3 ubiquitin protein ligase homolog (Drosophila)
18	PRIM1	0.73	2e−03	3e−03	1 x 50	primase, DNA, polypeptide 1 (49kDa) [Source:HGNC Symbol
19	UHRF1	0.73	2e−03	3e−03	1 x 50	ubiquitin−like with PHD and ring finger domains 1 [Source:HG
20	HAUS1	0.55	2e−03	3e−03	1 x 50	HAUS augmin−like complex, subunit 1 [Source:HGNC Symbo

p−values



H7_mel

Local Summary

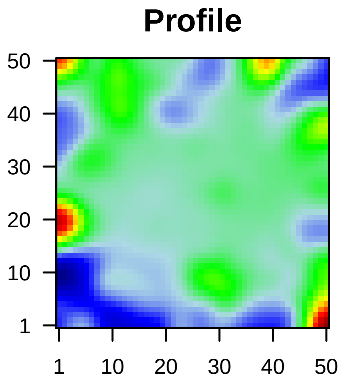
%DE = 0.19
metagenes = 12
genes = 222
genes in genesets = 220

genes with fdr < 0.1 = 21 (6 + / 15 −)
genes with fdr < 0.05 = 21 (6 + / 15 −)
genes with fdr < 0.01 = 8 (1 + / 7 −)

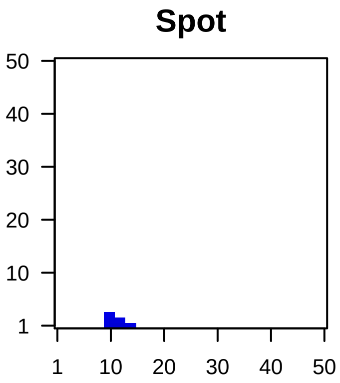
<r> metagenes = 0.92
<r> genes = 0.14

<FC> = −0.16
<shrinkage−t> = −2.5
<p−value> = 0.13
<fdr> = 0.86

Profile



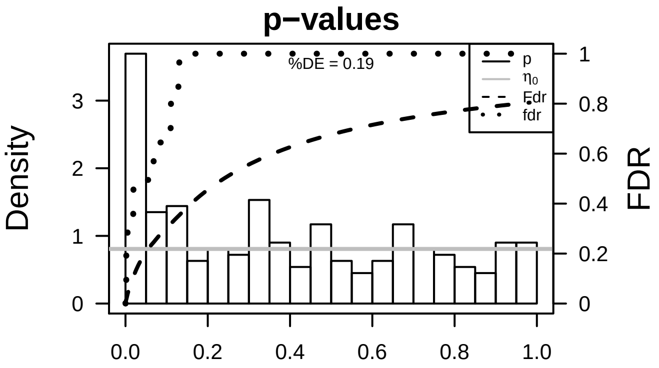
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	POLR2C	−1.08	2e−06	1e−04	10 x 2	polymerase (RNA) II (DNA directed) polypeptide C, 33kDa [
2	MLEC	−1.1	2e−06	1e−04	10 x 1	malectin [Source:HGNC Symbol;Acc:HGNC:28973]
3	DNAJC11	−1.1	2e−06	3e−04	13 x 1	DnaJ (Hsp40) homolog, subfamily C, member 11 [Source:HG
4	HSPA5	−0.62	5e−06	3e−04	11 x 1	heat shock 70kDa protein 5 (glucose−regulated protein, 78k
5	SERPINB1	−0.97	5e−06	1e−03	14 x 1	serpin peptidase inhibitor, clade B (ovalbumin), member 1 [S
6	MRPL28	−0.66	1e−05	1e−03	11 x 3	mitochondrial ribosomal protein L28 [Source:HGNC Symbol;
7	KIAA1429	−1.01	2e−05	4e−03	10 x 1	KIAA1429 [Source:HGNC Symbol;Acc:HGNC:24500]
8	MCAT	0.95	5e−05	4e−03	15 x 1	malonyl CoA:ACP acyltransferase (mitochondrial) [Source:H
9	L3MBTL4	0.94	7e−05	2e−02	10 x 2	l(3)mbt−like 4 (Drosophila) [Source:HGNC Symbol;Acc:HGN
10	RYK	−0.88	2e−04	2e−02	15 x 1	receptor−like tyrosine kinase [Source:HGNC Symbol;Acc:HG
11	ADARB1	−0.85	3e−04	2e−02	10 x 1	adenosine deaminase, RNA−specific, B1 [Source:HGNC Sy
12	TTI1	−0.83	4e−04	2e−02	14 x 1	TELO2 interacting protein 1 [Source:HGNC Symbol;Acc:HG
13	MYCBP	−0.83	4e−04	3e−02	11 x 2	MYC binding protein [Source:HGNC Symbol;Acc:HGNC:755
14	AARS	−0.78	8e−04	3e−02	10 x 1	alanyl−tRNA synthetase [Source:HGNC Symbol;Acc:HGNC:
15	BDH2	−0.77	1e−03	3e−02	10 x 3	3−hydroxybutyrate dehydrogenase, type 2 [Source:HGNC Sy
16	PTER	0.76	1e−03	3e−02	11 x 2	phosphotriesterase related [Source:HGNC Symbol;Acc:HGN
17	ZBTB8A	0.75	1e−03	3e−02	13 x 2	zinc finger and BTB domain containing 8A [Source:HGNC Sy
18	RBM33	0.74	2e−03	3e−02	10 x 1	RNA binding motif protein 33 [Source:HGNC Symbol;Acc:HG
19	MTERF4	−0.74	2e−03	3e−02	10 x 1	mitochondrial transcription termination factor 4 [Source:HGN
20	GRIK2	0.74	2e−03	3e−02	12 x 1	glutamate receptor, ionotropic, kainate 2 [Source:HGNC Sym

p−values



H7_mel

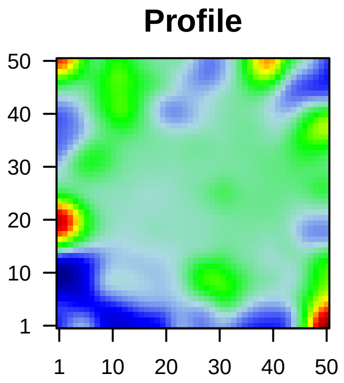
Local Summary

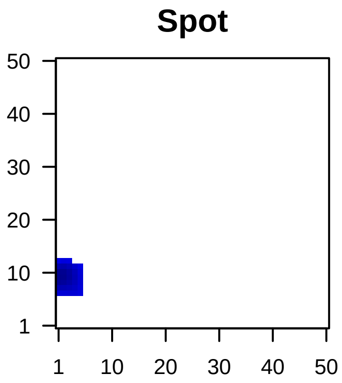
%DE = 0.72
metagenes = 33
genes = 376
genes in genesets = 373

genes with fdr < 0.1 = 185 (48 + / 137 −)
genes with fdr < 0.05 = 148 (37 + / 111 −)
genes with fdr < 0.01 = 83 (18 + / 65 −)

<r> metagenes = 0.89
<r> genes = 0.1

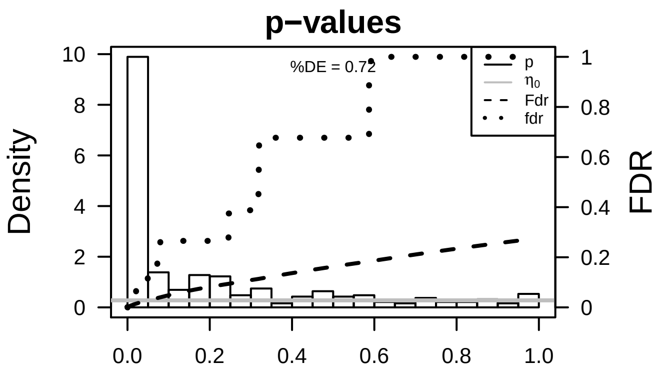
<FC> = −0.22
<shrinkage−t> = −3.56
<p−value> = 0.01
<fdr> = 0.61


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	FOS	−1.76	2e−16	1e−14	4 x 7	FBJ murine osteosarcoma viral oncogene homolog [Source:
2	ZNF330	−1.69	2e−16	1e−14	2 x 13	zinc finger protein 330 [Source:HGNC Symbol;Acc:HGNC:15
3	WDR43	−1.02	7e−14	2e−11	4 x 11	WD repeat domain 43 [Source:HGNC Symbol;Acc:HGNC:28
4	C21orf91	−1.29	3e−13	4e−10	1 x 9	chromosome 21 open reading frame 91 [Source:HGNC Sym
5	STAT3	−1.4	4e−12	1e−09	1 x 8	signal transducer and activator of transcription 3 (acute−phas
6	GBA	−1.4	2e−11	2e−09	4 x 12	glucosidase, beta, acid [Source:HGNC Symbol;Acc:HGNC:41
7	MET	−1.36	4e−11	4e−08	1 x 11	MET proto−oncogene, receptor tyrosine kinase [Source:HGN
8	PPARGC1A	−1.3	5e−10	4e−08	1 x 10	peroxisome proliferator−activated receptor gamma, coactivat
9	HSPB8	−1.29	8e−10	1e−07	1 x 11	heat shock 22kDa protein 8 [Source:HGNC Symbol;Acc:HGN
10	RAB27A	−1.13	4e−09	1e−07	1 x 11	RAB27A, member RAS oncogene family [Source:HGNC Sym
11	EXOC7	−1.26	6e−09	1e−07	1 x 8	exocyst complex component 7 [Source:HGNC Symbol;Acc:H
12	SAT1	0.55	6e−09	1e−07	1 x 11	spermidine/spermine N1−acetyltransferase 1 [Source:HGNC
13	ACO2	−1.21	7e−09	5e−07	2 x 10	aconitase 2, mitochondrial [Source:HGNC Symbol;Acc:HGN
14	UGCG	−0.87	1e−08	1e−06	1 x 11	UDP−glucose ceramide glucosyltransferase [Source:HGNC
15	APOL2	−1.18	3e−08	1e−06	1 x 9	apolipoprotein L, 2 [Source:HGNC Symbol;Acc:HGNC:619]
16	QRICH1	−0.87	4e−08	1e−06	1 x 8	glutamine−rich 1 [Source:HGNC Symbol;Acc:HGNC:24713]
17	SCIN	1.29	4e−08	4e−06	1 x 12	scinderin [Source:HGNC Symbol;Acc:HGNC:21695]
18	PCCB	−1.2	9e−08	1e−05	1 x 7	propionyl CoA carboxylase, beta polypeptide [Source:HGNC
19	MRPS2	−1.18	3e−07	1e−05	1 x 13	mitochondrial ribosomal protein S2 [Source:HGNC Symbol;A
20	ATP6V0A1	−0.9	3e−07	1e−05	1 x 10	ATPase, H+ transporting, lysosomal V0 subunit a1 [Source:H


p−values