H6_mel

Global Summary

%DE = 0.22

genes with fdr < 0.2 = 2748 (1612 + / 1136 −)

genes with fdr < 0.1 = 2236 (1333 + / 903 −)

genes with fdr < 0.05 = 1931 (1140 + / 791 −)

genes with fdr < 0.01 = 1206 (692 + / 514 −)

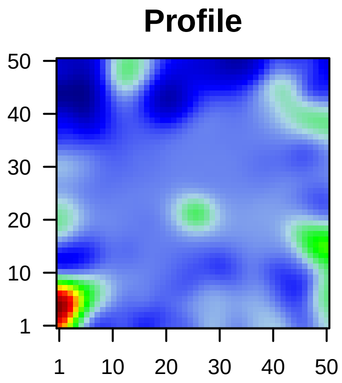
genes in genesets = 14839

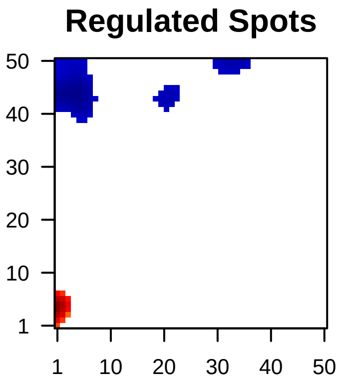
<FC> = 0

<shrinkage−t> = −0.11

<p−value> = 0.07

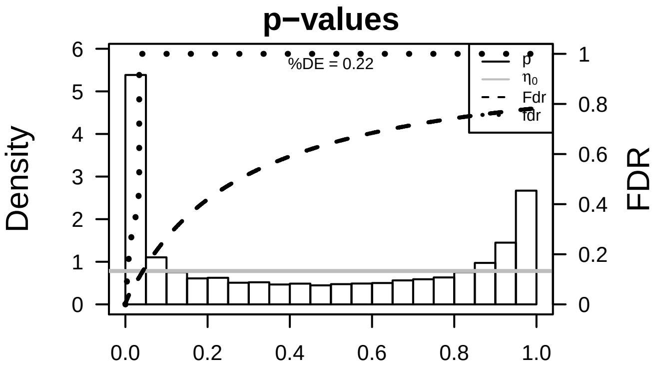
<fdr> = 0.78





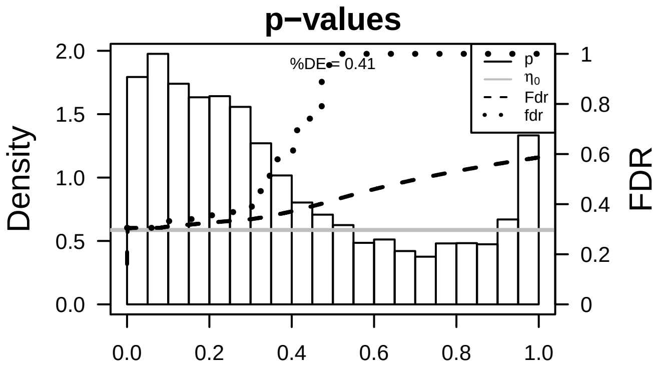
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ARL16	−1.64	2e−16	6e−14	50 x 50	ADP−ribosylation factor−like 16 [Source:HGNC Symbol;Acc:H
2	ARPC3	−1.79	2e−16	6e−14	6 x 42	actin related protein 2/3 complex, subunit 3, 21kDa [Source:H
3	C11orf31	−1.69	2e−16	6e−14	27 x 50	chromosome 11 open reading frame 31 [Source:HGNC Symb
4	C12orf57	−1.73	2e−16	6e−14	21 x 42	chromosome 12 open reading frame 57 [Source:HGNC Symb
5	CCDC167	−1.93	2e−16	6e−14	6 x 39	coiled−coil domain containing 167 [Source:HGNC Symbol;Ac
6	CDK2	−1.56	2e−16	6e−14	1 x 43	cyclin−dependent kinase 2 [Source:HGNC Symbol;Acc:HGN
7	CDKN3	−1.65	2e−16	6e−14	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
8	CEP57	−1.01	2e−16	6e−14	5 x 46	centrosomal protein 57kDa [Source:HGNC Symbol;Acc:HGN
9	CNIH1	−1.61	2e−16	6e−14	29 x 46	cornichon family AMPA receptor auxiliary protein 1 [Source:H
10	COPZ1	−1.68	2e−16	6e−14	46 x 45	coatomer protein complex, subunit zeta 1 [Source:HGNC Syn
11	CUTA	−1.32	2e−16	6e−14	36 x 47	cutA divalent cation tolerance homolog (E. coli) [Source:HGN
12	DCTN2	−1.81	2e−16	6e−14	50 x 44	dynactin 2 (p50) [Source:HGNC Symbol;Acc:HGNC:2712]
13	DUS1L	−1.13	2e−16	6e−14	25 x 50	dihydrouridine synthase 1−like (S. cerevisiae) [Source:HGNC
14	EDF1	−1.32	2e−16	6e−14	47 x 48	endothelial differentiation−related factor 1 [Source:HGNC Syr
15	ERGIC2	−1.87	2e−16	6e−14	6 x 44	ERGIC and golgi 2 [Source:HGNC Symbol;Acc:HGNC:30208
16	ETNK1	−1.61	2e−16	6e−14	26 x 11	ethanolamine kinase 1 [Source:HGNC Symbol;Acc:HGNC:24
17	EXOSC8	−1.71	2e−16	6e−14	1 x 50	exosome component 8 [Source:HGNC Symbol;Acc:HGNC:17
18	HDAC2	−1.48	2e−16	6e−14	1 x 45	histone deacetylase 2 [Source:HGNC Symbol;Acc:HGNC:48
19	HDDC2	−1.49	2e−16	6e−14	20 x 44	HD domain containing 2 [Source:HGNC Symbol;Acc:HGNC:
20	HERPUD1	1.05	2e−16	6e−14	50 x 42	homocysteine−inducible, endoplasmic reticulum stress−induc



Global Geneset Analysis

Rank	GSZ	p−value	#all		Geneset
Overexpressed					
1	6.32	0.002	155	GSEA C2	SMIRNOV_RESPONSE_TO_IR_6HR_UP
2	6.07	0.002	840	Chr	Chr 17
3	5.4	0.003	558	Chr	Chr 4
4	5.18	0.003	469	Chr	Chr 8
5	4.66	0.005	696	Chr	Chr 5
6	4.62	0.005	465	Chr	Chr 15
7	4.56	0.005	37	GSEA C2	KERLEY_RESPONSE_TO_CISPLATIN_UP
8	4.41	0.005	2563	Lymphoma	HOPP_Heterochrom
9	4.34	0.006	838	Chr	Chr 3
10	4.31	0.006	198	HM	HALLMARK_OXIDATIVE_PHOSPHORYLATION
11	4.29	0.006	20	GSEA C2	BRACHAT_RESPONSE_TO_CISPLATIN
12	4.24	0.006	1500	Chr	Chr 1
13	4.24	0.006	2391	TF	ICGC_Pbx3_targets
14	4.18	0.006	11	BP	macroautophagy
15	4.07	0.007	401	CC	mitochondrial inner membrane
16	4.03	0.007	16	CC	eukaryotic translation initiation factor 3 complex
17	4.01	0.007	181	HM	HALLMARK_P53_PATHWAY
18	3.94	0.008	3924	TF	ICGC_Zeb1_targets
19	3.92	0.008	15	CC	eukaryotic 48S preinitiation complex
20	3.89	0.008	132	miRNA target	hsa−miR−199b−5p
Underexpressed					
1	−17.13	3e−05	775	Chr	Chr 12
2	−13	9e−05	687	Chr	Chr 6
3	−6.04	2e−03	398	Chr	Chr 20
4	−5.97	2e−03	390	GSEA C2	PUJANA_BRCA2_PCC_NETWORK
5	−5.79	2e−03	38	GSEA C2	NIKOLSKY_BREAST_CANCER_12Q13_Q21_AMPLICON
6	−5.79	2e−03	242	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
7	−5.6	2e−03	301	GSEA C2	REACTOME_CELL_CYCLE_MITOTIC
8	−5.58	2e−03	305	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
9	−5.53	2e−03	267	GSEA C2	ZHANG_TLX_TARGETS_60HR_DN
10	−5.47	3e−03	7592	Lymphoma	HOPP_Active_promoter
11	−5.36	3e−03	724	GSEA C2	PUJANA_CHEK2_PCC_NETWORK
12	−5.35	3e−03	218	GSEA C2	CHICAS_RB1_TARGETS_GROWING
13	−5.21	3e−03	309	GSEA C2	GOLDRATH_ANTIGEN_RESPONSE
14	−5.19	3e−03	436	GSEA C2	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
15	−5.18	3e−03	193	GSEA C2	PAL_PRMT5_TARGETS_UP
16	−5.17	3e−03	36	GSEA C2	KORKOLA_EMBRYONAL_CARCINOMA_UP
17	−5.16	3e−03	275	GSEA C2	GRADE_COLON_AND_RECTAL_CANCER_UP
18	−5.09	3e−03	216	GSEA C2	MARKEY_RB1_ACUTE_LOF_DN
19	−5.06	3e−03	87	GSEA C2	ZHANG_TLX_TARGETS_UP
20	−5.02	3e−03	388	GSEA C2	REACTOME_CELL_CYCLE



H6_mel

Local Summary

%DE = 0.97

metagenes = 17

genes = 351

genes in genesets = 347

genes with fdr < 0.1 = 333 (331 + / 2 −)

genes with fdr < 0.05 = 321 (320 + / 1 −)

genes with fdr < 0.01 = 317 (317 + / 0 −)

<r> metagenes = 0.89

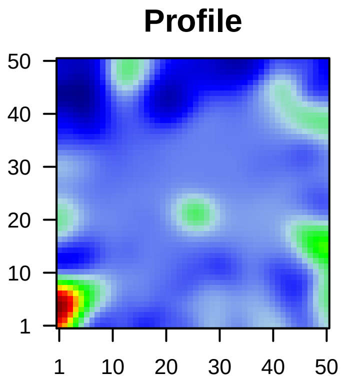
<r> genes = 0.12

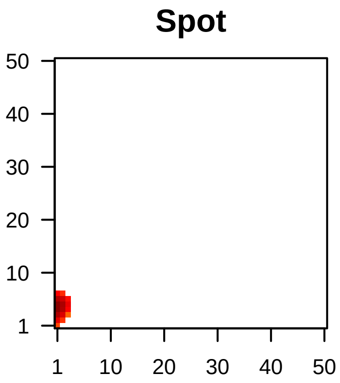
<FC> = 1.02

<shrinkage−t> = 15.6

<p−value> = 0

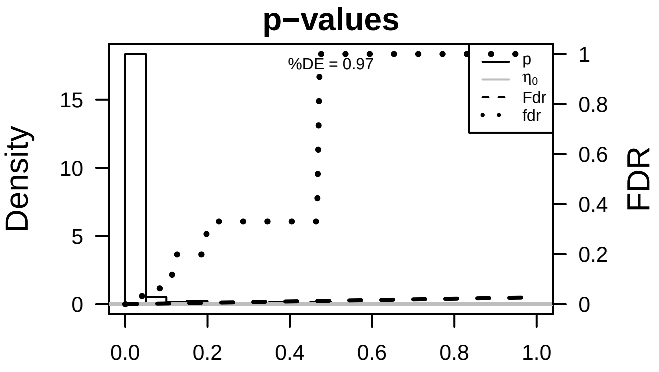
<fdr> = 0.14





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	SCHIP1	2.29	2e−16	2e−15	1 x 4	schwannomin interacting protein 1 [Source:HGNC Symbol;Ac
2	MAGEA1	2.11	2e−15	7e−13	1 x 5	melanoma antigen family A1 [Source:HGNC Symbol;Acc:HG
3	THNSL2	1.98	1e−13	7e−13	1 x 4	threonine synthase−like 2 (S. cerevisiae) [Source:HGNC Sym
4	RNF40	1.97	2e−13	5e−12	1 x 7	ring finger protein 40, E3 ubiquitin protein ligase [Source:HG
5	IFI44	1.9	1e−12	5e−12	1 x 5	interferon−induced protein 44 [Source:HGNC Symbol;Acc:HG
6	LPHN1	1.9	1e−12	7e−12	1 x 5	
7	PORCN	1.88	2e−12	3e−11	1 x 5	porcupine homolog (Drosophila) [Source:HGNC Symbol;Acc:
8	TP53I3	1.84	5e−12	6e−11	3 x 4	tumor protein p53 inducible protein 3 [Source:HGNC Symbol;
9	IKBKB	1.81	1e−11	8e−11	1 x 3	inhibitor of kappa light polypeptide gene enhancer in B−cells,
10	BMP1	1.79	2e−11	3e−10	1 x 4	bone morphogenetic protein 1 [Source:HGNC Symbol;Acc:H
11	CHRNA5	1.75	6e−11	3e−10	1 x 4	cholinergic receptor, nicotinic, alpha 5 (neuronal) [Source:HG
12	DNAH12	1.73	9e−11	4e−10	1 x 4	dynein, axonemal, heavy chain 12 [Source:HGNC Symbol;Ac
13	CD79B	1.71	2e−10	4e−10	1 x 4	CD79b molecule, immunoglobulin−associated beta [Source:
14	UBASH3B	1.7	2e−10	4e−10	1 x 4	ubiquitin associated and SH3 domain containing B [Source:
15	C1orf145	1.69	2e−10	4e−10	1 x 6	chromosome 1 open reading frame 145 [Source:HGNC Sym
16	IFIT1	1.69	3e−10	5e−10	1 x 4	interferon−induced protein with tetratricopeptide repeats 1 [S
17	ZNF14	1.68	3e−10	7e−10	1 x 4	zinc finger protein 14 [Source:HGNC Symbol;Acc:HGNC:129
18	ARMCX5	1.66	5e−10	7e−10	2 x 7	armadillo repeat containing, X−linked 5 [Source:HGNC Symb
19	TMED7−TICA	1.66	5e−10	7e−10	1 x 4	TMED7−TICAM2 readthrough [Source:HGNC Symbol;Acc:H
20	ADHFE1	1.66	5e−10	1e−09	1 x 5	alcohol dehydrogenase, iron containing, 1 [Source:HGNC Sy



H6_mel

Local Summary

%DE = 0.74

metagenes = 74

genes = 859

genes in genesets = 856

genes with fdr < 0.1 = 446 (99 + / 347 −)

genes with fdr < 0.05 = 339 (66 + / 273 −)

genes with fdr < 0.01 = 244 (40 + / 204 −)

<r> metagenes = 0.79

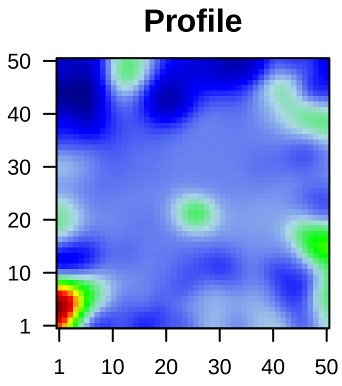
<r> genes = 0.14

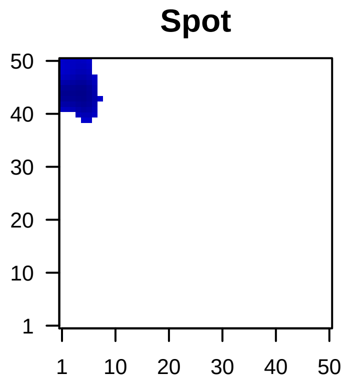
<FC> = −0.3

<shrinkage−t> = −5.64

<p−value> = 0

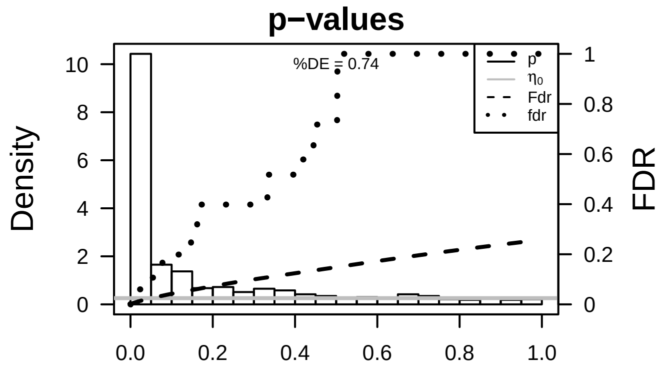
<fdr> = 0.57





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ARPC3	−1.79	2e−16	3e−15	6 x 42	actin related protein 2/3 complex, subunit 3, 21kDa [Source:H
2	CCDC167	−1.93	2e−16	3e−15	6 x 39	coiled−coil domain containing 167 [Source:HGNC Symbol;Ac
3	CDK2	−1.56	2e−16	3e−15	1 x 43	cyclin−dependent kinase 2 [Source:HGNC Symbol;Acc:HGN
4	CDKN3	−1.65	2e−16	3e−15	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;
5	CEP57	−1.01	2e−16	3e−15	5 x 46	centrosomal protein 57kDa [Source:HGNC Symbol;Acc:HGN
6	ERGIC2	−1.87	2e−16	3e−15	6 x 44	ERGIC and golgi 2 [Source:HGNC Symbol;Acc:HGNC:30208
7	EXOSC8	−1.71	2e−16	3e−15	1 x 50	exosome component 8 [Source:HGNC Symbol;Acc:HGNC:17
8	HDAC2	−1.48	2e−16	3e−15	1 x 45	histone deacetylase 2 [Source:HGNC Symbol;Acc:HGNC:48
9	MITF	−1.56	2e−16	3e−15	1 x 41	microphthalmia−associated transcription factor [Source:HGN
10	MRPL48	−2.19	2e−16	3e−15	5 x 41	mitochondrial ribosomal protein L48 [Source:HGNC Symbol;
11	MYH10	−1.35	2e−16	3e−15	1 x 44	myosin, heavy chain 10, non−muscle [Source:HGNC Symbol
12	NDUFA9	−1.17	2e−16	3e−15	4 x 42	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9,
13	PGM3	−1.8	2e−16	3e−15	5 x 45	phosphoglucomutase 3 [Source:HGNC Symbol;Acc:HGNC:8
14	PIR	−1.58	2e−16	3e−15	1 x 42	pirin (iron−binding nuclear protein) [Source:HGNC Symbol;Ac
15	POLR2I	−1.86	2e−16	3e−15	1 x 44	polymerase (RNA) II (DNA directed) polypeptide I, 14.5kDa [
16	SIVA1	−1.88	2e−16	3e−15	1 x 46	SIVA1, apoptosis−inducing factor [Source:HGNC Symbol;Acc
17	SNX3	−1.52	2e−16	3e−15	6 x 39	sorting nexin 3 [Source:HGNC Symbol;Acc:HGNC:11174]
18	TMEM106C	−1.82	2e−16	3e−15	5 x 48	transmembrane protein 106C [Source:HGNC Symbol;Acc:HG
19	TRPM1	−1.27	2e−16	3e−15	1 x 42	transient receptor potential cation channel, subfamily M, mem
20	NDUFAF4	−1.63	4e−16	2e−13	4 x 41	NADH dehydrogenase (ubiquinone) complex I, assembly fact



H6_mel

Local Summary

%DE = 0.81

metagenes = 16

genes = 110

genes in genesets = 110

genes with fdr < 0.1 = 49 (6 + / 43 −)

genes with fdr < 0.05 = 49 (6 + / 43 −)

genes with fdr < 0.01 = 36 (5 + / 31 −)

<r> metagenes = 0.97

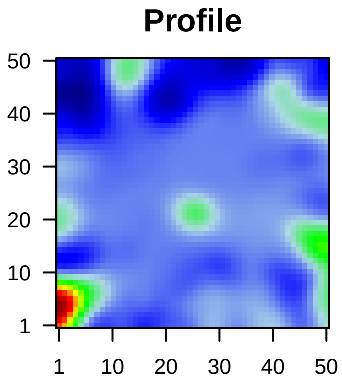
<r> genes = 0.1

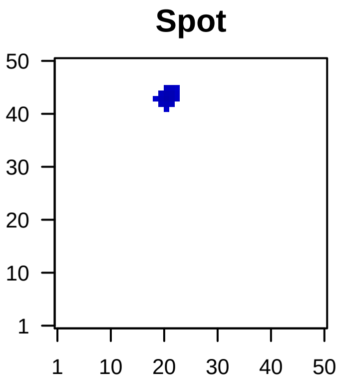
<FC> = −0.45

<shrinkage−t> = −8.24

<p−value> = 0

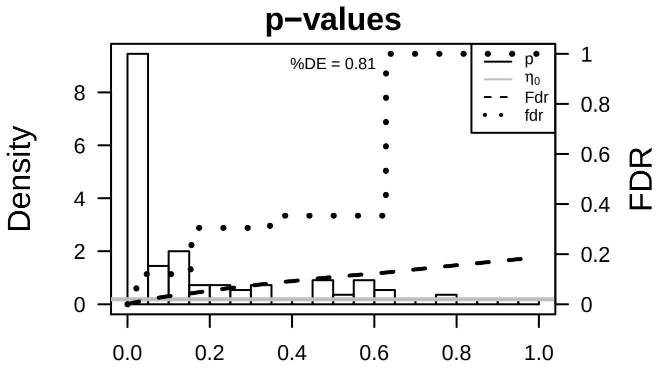
<fdr> = 0.58





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	C12orf57	−1.73	2e−16	2e−15	21 x 42	chromosome 12 open reading frame 57 [Source:HGNC Symb
2	HDDC2	−1.49	2e−16	2e−15	20 x 44	HD domain containing 2 [Source:HGNC Symbol;Acc:HGNC:
3	SRI	−1.52	2e−16	2e−15	20 x 43	sorcin [Source:HGNC Symbol;Acc:HGNC:11292]
4	CHD4	−1.4	8e−15	9e−14	21 x 43	chromodomain helicase DNA binding protein 4 [Source:HGN
5	ANAPC5	−1.58	9e−15	1e−12	20 x 42	anaphase promoting complex subunit 5 [Source:HGNC Symb
6	PLS3	−1.58	6e−14	3e−10	21 x 43	plastin 3 [Source:HGNC Symbol;Acc:HGNC:9091]
7	RARS2	−1.49	2e−11	7e−10	22 x 42	arginyl−tRNA synthetase 2, mitochondrial [Source:HGNC Sy
8	PRKD3	−1.26	5e−11	1e−09	21 x 43	protein kinase D3 [Source:HGNC Symbol;Acc:HGNC:9408]
9	IDH3B	−1.15	1e−10	5e−09	22 x 43	isocitrate dehydrogenase 3 (NAD+) beta [Source:HGNC Sym
10	NGDN	−1.44	5e−10	5e−09	22 x 45	neuroguidin, EIF4E binding protein [Source:HGNC Symbol;A
11	ARMC8	−1.42	5e−10	1e−07	21 x 43	armadillo repeat containing 8 [Source:HGNC Symbol;Acc:HG
12	ECI2	−0.95	5e−09	2e−05	20 x 42	enoyl−CoA delta isomerase 2 [Source:HGNC Symbol;Acc:HG
13	SAP130	1.29	1e−06	2e−05	20 x 43	Sin3A−associated protein, 130kDa [Source:HGNC Symbol;A
14	TAF11	−1.21	1e−06	2e−05	20 x 43	TAF11 RNA polymerase II, TATA box binding protein (TBP)−a
15	PSMC2	−0.83	2e−06	5e−05	21 x 44	proteasome (prosome, macropain) 26S subunit, ATPase, 2 [S
16	PIGC	−1	5e−06	8e−05	21 x 44	phosphatidylinositol glycan anchor biosynthesis, class C [Sou
17	PHF20	−0.67	1e−05	8e−05	22 x 43	PHD finger protein 20 [Source:HGNC Symbol;Acc:HGNC:16
18	BCLAF1	−0.72	1e−05	2e−04	19 x 43	BCL2−associated transcription factor 1 [Source:HGNC Symb
19	MRPS10	−0.85	2e−05	3e−04	21 x 44	mitochondrial ribosomal protein S10 [Source:HGNC Symbol;
20	ZC2HC1A	1.1	4e−05	1e−03	21 x 45	zinc finger, C2HC−type containing 1A [Source:HGNC Symbol



H6_mel

Local Summary

%DE = 0.73

metagenes = 18

genes = 202

genes in genesets = 202

genes with fdr < 0.1 = 83 (15 + / 68 −)

genes with fdr < 0.05 = 79 (14 + / 65 −)

genes with fdr < 0.01 = 50 (9 + / 41 −)

<r> metagenes = 0.89

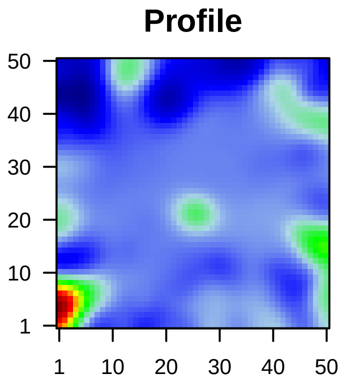
<r> genes = 0.07

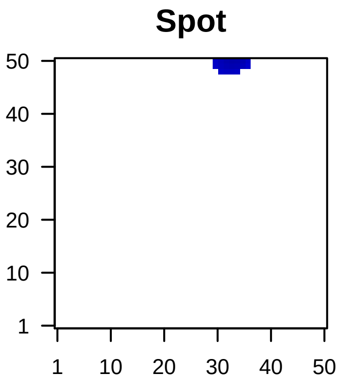
<FC> = −0.35

<shrinkage−t> = −5.88

<p−value> = 0.01

<fdr> = 0.62





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	RAB11A	−1.89	2e−16	6e−15	36 x 50	RAB11A, member RAS oncogene family [Source:HGNC Sym
2	SRPK1	−1.67	2e−16	6e−15	34 x 50	SRSF protein kinase 1 [Source:HGNC Symbol;Acc:HGNC:11
3	OS9	−1.59	4e−14	1e−11	34 x 50	osteosarcoma amplified 9, endoplasmic reticulum lectin [Sou
4	PMPCB	−1.43	3e−13	2e−08	33 x 50	peptidase (mitochondrial processing) beta [Source:HGNC Sy
5	DUSP6	−1.16	5e−10	2e−08	34 x 50	dual specificity phosphatase 6 [Source:HGNC Symbol;Acc:H
6	RWDD1	−1.42	9e−10	2e−08	32 x 50	RWD domain containing 1 [Source:HGNC Symbol;Acc:HGNC
7	TANK	−1.42	1e−09	1e−07	34 x 50	TRAF family member−associated NFKB activator [Source:HG
8	COA1	−1.39	3e−09	5e−07	32 x 50	cytochrome c oxidase assembly factor 1 homolog (S. cerevisi
9	MRPL18	−1.18	2e−08	5e−07	36 x 50	mitochondrial ribosomal protein L18 [Source:HGNC Symbol;
10	RBCK1	−1.34	2e−08	2e−06	30 x 50	RanBP−type and C3HC4−type zinc finger containing 1 [Sour
11	AP5M1	−1.31	5e−08	5e−06	34 x 50	adaptor−related protein complex 5, mu 1 subunit [Source:HG
12	NCKAP1	−1.27	2e−07	5e−06	32 x 50	NCK−associated protein 1 [Source:HGNC Symbol;Acc:HGNC
13	ALG6	−1.26	2e−07	9e−06	35 x 50	ALG6, alpha−1,3−glucosyltransferase [Source:HGNC Symbo
14	PIH1D1	−1.25	5e−07	9e−06	33 x 49	PIH1 domain containing 1 [Source:HGNC Symbol;Acc:HGNC
15	FAR1	−1.2	7e−07	9e−06	35 x 49	fatty acyl CoA reductase 1 [Source:HGNC Symbol;Acc:HGNC
16	TULP3	−1.24	8e−07	2e−05	35 x 50	tubby like protein 3 [Source:HGNC Symbol;Acc:HGNC:12425
17	NSUN2	−1.22	1e−06	1e−04	32 x 50	NOP2/Sun RNA methyltransferase family, member 2 [Source:
18	LTA4H	−1.16	8e−06	1e−04	35 x 50	leukotriene A4 hydrolase [Source:HGNC Symbol;Acc:HGNC:
19	ANAPC16	−1.04	8e−06	1e−04	36 x 50	anaphase promoting complex subunit 16 [Source:HGNC Sym
20	CIRBP	−1.16	8e−06	3e−04	32 x 50	cold inducible RNA binding protein [Source:HGNC Symbol;A