H5_mel

Global Summary

%DE = 0.21

genes with fdr < 0.2 = 2775 (1599 + / 1176 −)

genes with fdr < 0.1 = 2263 (1324 + / 939 −)

genes with fdr < 0.05 = 1792 (1066 + / 726 −)

genes with fdr < 0.01 = 1127 (671 + / 456 −)

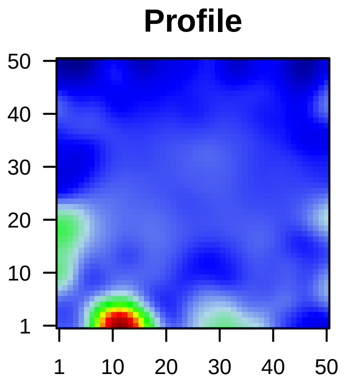
genes in genesets = 14839

<FC> = 0

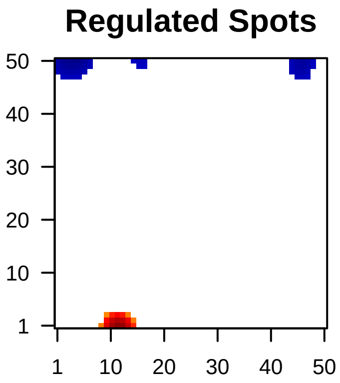
<shrinkage−t> = −0.05

<p−value> = 0.07

<fdr> = 0.79



Profile



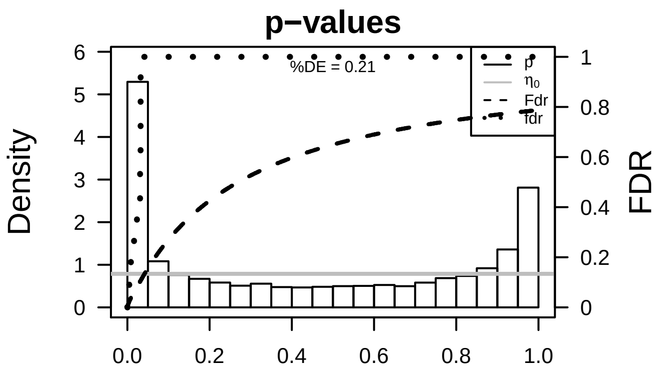
Regulated Spots

Global Genelist

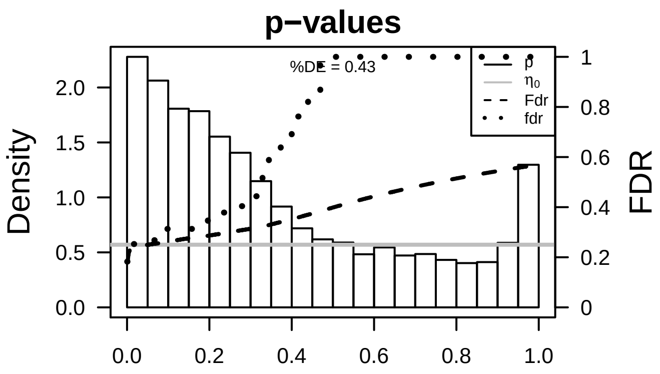
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ACTL6A	−1.47	2e−16	7e−14	4 x 50	actin−like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
2	APEH	−1.56	2e−16	7e−14	1 x 42	acylaminoacyl−peptide hydrolase [Source:HGNC Symbol;Acc
3	ATRX	−1.18	2e−16	7e−14	43 x 7	alpha thalassemia/mental retardation syndrome X−linked [So
4	BUB3	−1.17	2e−16	7e−14	7 x 48	BUB3 mitotic checkpoint protein [Source:HGNC Symbol;Acc:
5	C17orf62	−1.78	2e−16	7e−14	18 x 50	chromosome 17 open reading frame 62 [Source:HGNC Symb
6	C4orf3	−1.92	2e−16	7e−14	44 x 49	chromosome 4 open reading frame 3 [Source:HGNC Symbol
7	CFAP20	−1.62	2e−16	7e−14	40 x 50	cilia and flagella associated protein 20 [Source:HGNC Symbo
8	EIF4EBP1	−1.64	2e−16	7e−14	2 x 43	eukaryotic translation initiation factor 4E binding protein 1 [So
9	EIF5	−1.25	2e−16	7e−14	21 x 50	eukaryotic translation initiation factor 5 [Source:HGNC Symbo
10	EXOSC8	−1.71	2e−16	7e−14	1 x 50	exosome component 8 [Source:HGNC Symbol;Acc:HGNC:17
11	FDPS	−1.05	2e−16	7e−14	12 x 44	farnesyl diphosphate synthase [Source:HGNC Symbol;Acc:H
12	GNL3	−1.53	2e−16	7e−14	47 x 42	guanine nucleotide binding protein−like 3 (nucleolar) [Source:
13	HDAC2	−1.42	2e−16	7e−14	1 x 45	histone deacetylase 2 [Source:HGNC Symbol;Acc:HGNC:48
14	HECTD1	−1.66	2e−16	7e−14	40 x 7	HECT domain containing E3 ubiquitin protein ligase 1 [Sourc
15	HERPUD1	1.02	2e−16	7e−14	50 x 42	homocysteine−inducible, endoplasmic reticulum stress−induc
16	HSPA8	−0.88	2e−16	7e−14	49 x 50	heat shock 70kDa protein 8 [Source:HGNC Symbol;Acc:HGN
17	IARS	−1.81	2e−16	7e−14	16 x 50	isoleucyl−tRNA synthetase [Source:HGNC Symbol;Acc:HGN
18	MRPL17	−1.77	2e−16	7e−14	1 x 46	mitochondrial ribosomal protein L17 [Source:HGNC Symbol;
19	MRPL3	−1.84	2e−16	7e−14	50 x 37	mitochondrial ribosomal protein L3 [Source:HGNC Symbol;A
20	NOP16	−1.66	2e−16	7e−14	1 x 38	NOP16 nucleolar protein [Source:HGNC Symbol;Acc:HGNC:

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	4.58	0.005	205	GSEA C2	MCBRYAN_PUBERTAL_BREAST_4_5WK_UP
2	4.57	0.005	995	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_DN
3	4.47	0.005	3396	Lymphoma	HOPP_Repressed
4	4.31	0.006	148	HM	HALLMARK_KRAS_SIGNALING_UP
5	3.96	0.008	730	GSEA C2	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIA
6	3.95	0.008	11	BP	fatty acid beta−oxidation using acyl−CoA oxidase
7	3.9	0.008	622	GSEA C2	LEE_BMP2_TARGETS_UP
8	3.78	0.009	210	GSEA C2	WINTER_HYPOXIA_METAGENE
9	3.73	0.009	2188	Lymphoma	HOPP_Poised_promoter
10	3.71	0.010	356	GSEA C2	DELYS_THYROID_CANCER_UP
11	3.71	0.010	74	GSEA C2	SWEET_KRAS_ONCOGENIC_SIGNATURE
12	3.62	0.010	2142	Colon Cancer	ReprPC_Colon
13	3.61	0.010	15	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G56_DN
14	3.57	0.011	116	GSEA C2	RODRIGUES_DCC_TARGETS_DN
15	3.53	0.011	7	GSEA C2	REACTOME_ENDOSOMAL_VACUOLAR_PATHWAY
16	3.51	0.011	1889	Colon Cancer	ReprPCWk_Colon
17	3.51	0.011	280	GSEA C2	TORCHIA_TARGETS_OF_EWSR1_FLI1_FUSION_DN
18	3.51	0.011	79	GSEA C2	ST_INTEGRIN_SIGNALING_PATHWAY
19	3.38	0.013	8	GSEA C2	NADELLA_PRKAR1A_TARGETS_DN
20	3.38	0.013	7	GSEA C2	KANG_CISPLATIN_RESISTANCE_DN
Underexpressed					
1	−9.18	4e−04	242	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
2	−8.99	4e−04	724	GSEA C2	PUJANA_CHEK2_PCC_NETWORK
3	−8.35	5e−04	700	GSEA C2	MARSON_BOUND_BY_E2F4_UNSTIMULATED
4	−8.27	6e−04	1251	GSEA C2	DODD_NASOPHARYNGEAL_CARCINOMA_DN
5	−7.74	7e−04	834	GSEA C2	LEE_BMP2_TARGETS_DN
6	−7.63	8e−04	278	GSEA C2	MANALO_HYPOXIA_DN
7	−7.62	8e−04	197	HM	HALLMARK_E2F_TARGETS
8	−7.59	8e−04	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
9	−7.45	8e−04	267	GSEA C2	ZHANG_TLX_TARGETS_60HR_DN
10	−7.39	9e−04	188	HM	HALLMARK_MYC_TARGETS_V1
11	−7.38	9e−04	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
12	−7.35	9e−04	157	GSEA C2	SCHLOSSER_MYC_TARGETS_REPRESSED_BY_SERUM
13	−7.32	9e−04	305	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
14	−7.31	9e−04	756	GSEA C2	WEI_MYCN_TARGETS_WITH_E_BOX
15	−7.25	9e−04	85	GSEA C2	REACTOME_MITOTIC_PROMETAPHASE
16	−7.07	1e−03	124	GSEA C2	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
17	−6.98	1e−03	312	GSEA C2	WONG_EMBRYONIC_STEM_CELL_CORE
18	−6.96	1e−03	505	GSEA C2	BERENJENO_TRANSFORMED_BY_RHOA_UP
19	−6.8	1e−03	663	CC	chromosome
20	−6.75	1e−03	99	GSEA C2	BURTON_ADIPOGENESIS_3



p−values



p−values

H5_mel

Local Summary

%DE = 0.99

metagenes = 18

genes = 275

genes in genesets = 271

genes with fdr < 0.1 = 270 (270 + / 0 −)

genes with fdr < 0.05 = 270 (270 + / 0 −)

genes with fdr < 0.01 = 263 (263 + / 0 −)

<r> metagenes = 0.89

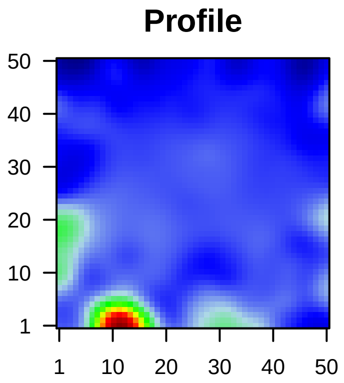
<r> genes = 0.12

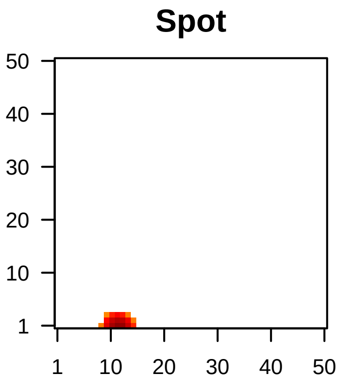
<FC> = 1.1

<shrinkage−t> = 16.74

<p−value> = 0

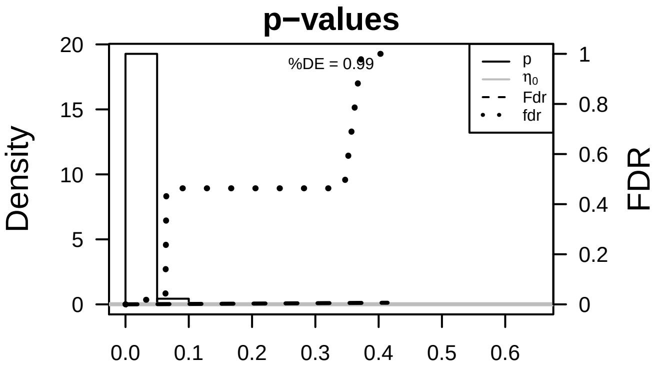
<fdr> = 0.08





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ZNF483	2.09	4e−16	1e−14	12 x 1	zinc finger protein 483 [Source:HGNC Symbol;Acc:HGNC:23
2	C1orf111	2.02	6e−15	7e−14	12 x 1	chromosome 1 open reading frame 111 [Source:HGNC Sym
3	MUTYH	1.96	3e−14	2e−13	15 x 1	mutY homolog [Source:HGNC Symbol;Acc:HGNC:7527]
4	SEPP1	1.92	1e−13	1e−12	12 x 1	selenoprotein P, plasma, 1 [Source:HGNC Symbol;Acc:HGN
5	PIGL	1.84	1e−12	1e−12	12 x 1	phosphatidylinositol glycan anchor biosynthesis, class L [Sou
6	FGFBP2	1.83	1e−12	1e−12	12 x 1	fibroblast growth factor binding protein 2 [Source:HGNC Sym
7	ZNF77	1.83	2e−12	4e−12	12 x 1	zinc finger protein 77 [Source:HGNC Symbol;Acc:HGNC:131
8	TENM3	1.79	4e−12	4e−12	11 x 1	teneurin transmembrane protein 3 [Source:HGNC Symbol;Ac
9	BAX	1.78	5e−12	8e−12	12 x 1	BCL2−associated X protein [Source:HGNC Symbol;Acc:HGN
10	ATP10B	1.76	8e−12	8e−12	14 x 1	ATPase, class V, type 10B [Source:HGNC Symbol;Acc:HGN
11	PTPRU	1.75	1e−11	8e−12	13 x 1	protein tyrosine phosphatase, receptor type, U [Source:HGN
12	DTNB	1.75	1e−11	1e−11	9 x 1	dystrobrevin, beta [Source:HGNC Symbol;Acc:HGNC:3058]
13	FPGS	1.74	2e−11	6e−11	9 x 1	folylpolyglutamate synthase [Source:HGNC Symbol;Acc:HGN
14	INTS1	1.69	6e−11	6e−11	13 x 1	integrator complex subunit 1 [Source:HGNC Symbol;Acc:HG
15	ANKH	1.68	8e−11	6e−11	12 x 1	ANKH inorganic pyrophosphate transport regulator [Source:H
16	C3orf67	1.67	9e−11	8e−11	12 x 1	chromosome 3 open reading frame 67 [Source:HGNC Symb
17	NICN1	1.66	1e−10	1e−10	13 x 1	nicolin 1 [Source:HGNC Symbol;Acc:HGNC:18317]
18	SLC9A8	1.64	2e−10	1e−10	10 x 1	solute carrier family 9, subfamily A (NHE8, cation proton anti
19	PLA2G16	1.64	2e−10	1e−10	12 x 1	phospholipase A2, group XVI [Source:HGNC Symbol;Acc:HG
20	YPEL2	1.63	2e−10	1e−10	15 x 1	yippee−like 2 (Drosophila) [Source:HGNC Symbol;Acc:HGN



H5_mel

Local Summary

%DE = 0.75

metagenes = 24

genes = 348

genes in genesets = 347

genes with fdr < 0.1 = 172 (35 + / 137 −)

genes with fdr < 0.05 = 159 (33 + / 126 −)

genes with fdr < 0.01 = 81 (20 + / 61 −)

<r> metagenes = 0.93

<r> genes = 0.3

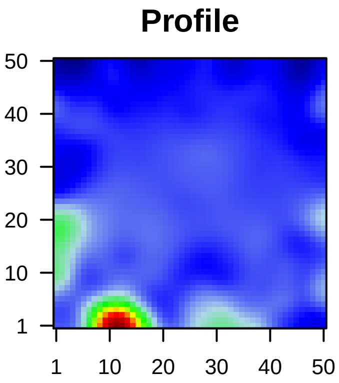
<FC> = −0.31

<shrinkage−t> = −4.96

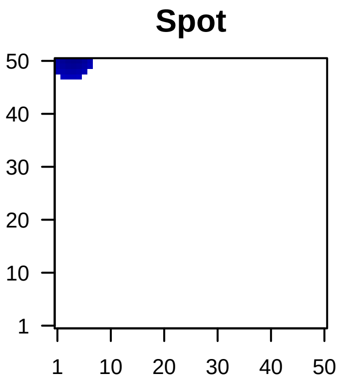
<p−value> = 0.01

<fdr> = 0.59

Profile



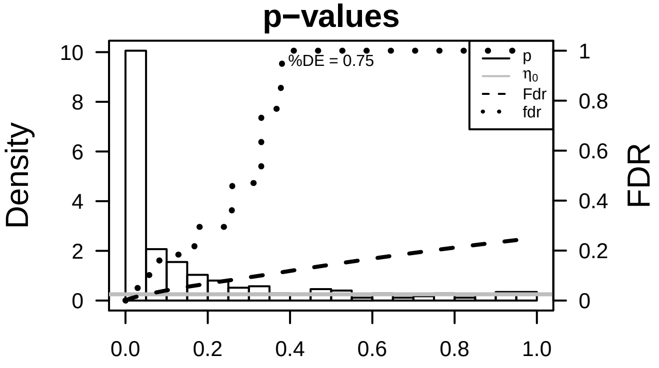
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ACTL6A	−1.47	2e−16	4e−15	4 x 50	actin−like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
2	EXOSC8	−1.71	2e−16	4e−15	1 x 50	exosome component 8 [Source:HGNC Symbol;Acc:HGNC:17
3	NUP107	−1.49	2e−16	4e−15	2 x 48	nucleoporin 107kDa [Source:HGNC Symbol;Acc:HGNC:2991
4	PCNA	−1.64	2e−16	4e−15	2 x 50	proliferating cell nuclear antigen [Source:HGNC Symbol;Acc:
5	PTTG1	−1.88	2e−16	4e−15	7 x 50	pituitary tumor−transforming 1 [Source:HGNC Symbol;Acc:H
6	SMC4	−1.49	3e−12	1e−09	5 x 50	structural maintenance of chromosomes 4 [Source:HGNC Sy
7	MTHFD2	−1.46	2e−11	3e−09	3 x 47	methylenetetrahydrofolate dehydrogenase (NADP+ dependen
8	HIST1H4C	−0.68	6e−11	3e−08	5 x 49	histone cluster 1, H4c [Source:HGNC Symbol;Acc:HGNC:47
9	CCP110	1.62	4e−10	4e−08	3 x 50	centriolar coiled coil protein 110kDa [Source:HGNC Symbol;
10	LBR	−1.39	1e−09	4e−08	7 x 50	lamin B receptor [Source:HGNC Symbol;Acc:HGNC:6518]
11	TYMS	−1.37	2e−09	4e−08	3 x 50	thymidylate synthetase [Source:HGNC Symbol;Acc:HGNC:12
12	HAT1	−1.2	2e−09	1e−07	1 x 50	histone acetyltransferase 1 [Source:HGNC Symbol;Acc:HGN
13	CEP112	1.53	3e−09	1e−07	1 x 48	centrosomal protein 112kDa [Source:HGNC Symbol;Acc:HG
14	MAD2L1	−1.35	4e−09	1e−06	5 x 50	MAD2 mitotic arrest deficient−like 1 (yeast) [Source:HGNC S
15	EMP2	−1.31	3e−08	1e−06	2 x 50	epithelial membrane protein 2 [Source:HGNC Symbol;Acc:H
16	MCM7	−1.29	4e−08	1e−06	2 x 50	minichromosome maintenance complex component 7 [Sourc
17	HMGB2	−1.28	5e−08	2e−05	5 x 50	high mobility group box 2 [Source:HGNC Symbol;Acc:HGNC:
18	CENPK	−1.22	5e−07	2e−05	3 x 50	centromere protein K [Source:HGNC Symbol;Acc:HGNC:294
19	CKB	−1.21	6e−07	2e−05	2 x 47	creatine kinase, brain [Source:HGNC Symbol;Acc:HGNC:199
20	CEP97	−1.2	7e−07	2e−05	2 x 47	centrosomal protein 97kDa [Source:HGNC Symbol;Acc:HGN

p−values



H5_mel

Local Summary

%DE = 0.7

metagenes = 17

genes = 189

genes in genesets = 188

genes with fdr < 0.1 = 99 (18 + / 81 −)

genes with fdr < 0.05 = 84 (15 + / 69 −)

genes with fdr < 0.01 = 52 (8 + / 44 −)

<r> metagenes = 0.93

<r> genes = 0.1

<FC> = −0.35

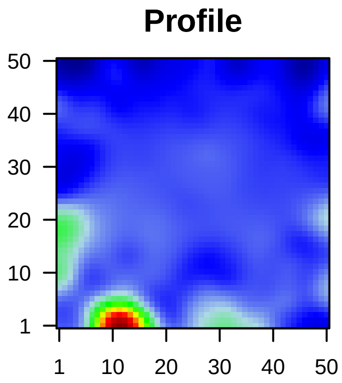
<shrinkage−t> = −6.01

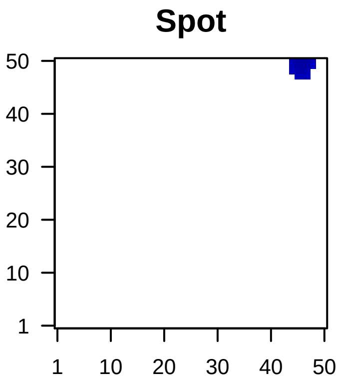
<p−value> = 0

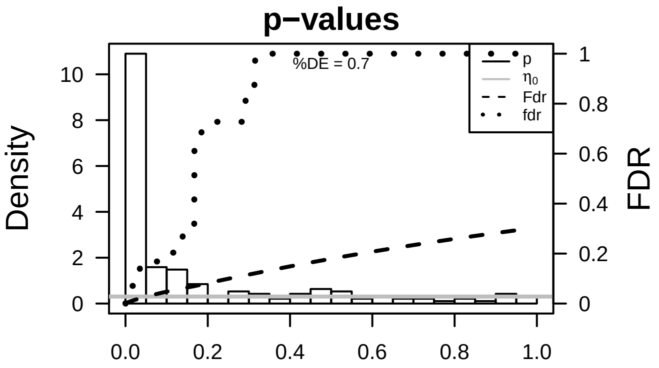
<fdr> = 0.55

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	C4orf3	−1.92	2e−16	6e−15	44 x 49	chromosome 4 open reading frame 3 [Source:HGNC Symbol
2	RHOC	−1.94	2e−16	6e−15	47 x 50	ras homolog family member C [Source:HGNC Symbol;Acc:H
3	GMFB	−1.61	4e−16	3e−12	46 x 49	glia maturation factor, beta [Source:HGNC Symbol;Acc:HGN
4	CDC123	−1.55	5e−14	7e−12	46 x 50	cell division cycle 123 [Source:HGNC Symbol;Acc:HGNC:16
5	TMEM219	−1.54	2e−13	8e−11	45 x 50	transmembrane protein 219 [Source:HGNC Symbol;Acc:HG
6	SARAF	−1.51	2e−12	2e−09	44 x 48	store−operated calcium entry−associated regulatory factor [S
7	PSMF1	−0.99	4e−11	9e−09	45 x 50	proteasome (prosome, macropain) inhibitor subunit 1 (PI31) [
8	PAM16	−1.43	2e−10	7e−07	45 x 50	presequence translocase−associated motor 16 homolog (S.
9	PRPSAP2	−1.32	2e−08	7e−07	47 x 50	phosphoribosyl pyrophosphate synthetase−associated protei
10	SKIV2L2	−1.31	3e−08	7e−07	46 x 49	superkiller viralicidic activity 2−like 2 (S. cerevisiae) [Source:
11	PDK4	−1.3	4e−08	3e−06	47 x 50	pyruvate dehydrogenase kinase, isozyme 4 [Source:HGNC S
12	MPHOSPH6	−1.26	9e−08	4e−05	47 x 50	M−phase phosphoprotein 6 [Source:HGNC Symbol;Acc:HGN
13	POP5	−1.19	1e−06	4e−05	46 x 49	processing of precursor 5, ribonuclease P/MRP subunit (S. c
14	NOP10	−0.59	2e−06	4e−05	48 x 50	NOP10 ribonucleoprotein [Source:HGNC Symbol;Acc:HGNC
15	XPO6	−1.17	3e−06	4e−05	46 x 50	exportin 6 [Source:HGNC Symbol;Acc:HGNC:19733]
16	SNAP47	−1.17	4e−06	4e−05	44 x 50	synaptosomal−associated protein, 47kDa [Source:HGNC Sy
17	RAB10	−1.02	4e−06	4e−05	45 x 48	RAB10, member RAS oncogene family [Source:HGNC Symb
18	EXOSC1	−1.16	5e−06	7e−05	46 x 50	exosome component 1 [Source:HGNC Symbol;Acc:HGNC:17
19	ARHGEF2	1.17	6e−06	1e−04	45 x 50	Rho/Rac guanine nucleotide exchange factor (GEF) 2 [Sourc
20	NDUFAF2	−1.12	1e−05	1e−04	48 x 50	NADH dehydrogenase (ubiquinone) complex I, assembly fact







H5_mel

Local Summary

%DE = 0.68

metagenes = 5

genes = 83

genes in genesets = 83

genes with fdr < 0.1 = 33 (6 + / 27 −)

genes with fdr < 0.05 = 32 (6 + / 26 −)

genes with fdr < 0.01 = 22 (4 + / 18 −)

<r> metagenes = 0.99

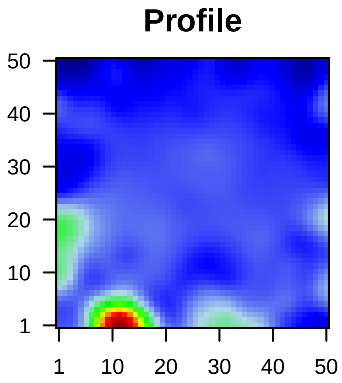
<r> genes = 0.11

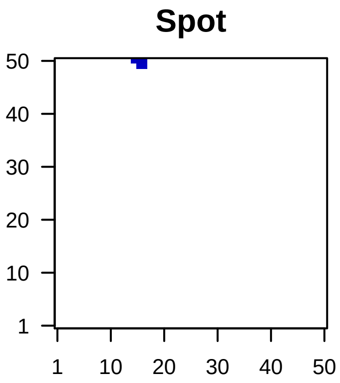
<FC> = −0.32

<shrinkage−t> = −5.65

<p−value> = 0.01

<fdr> = 0.59





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	IARS	−1.81	2e−16	6e−15	16 x 50	isoleucyl−tRNA synthetase [Source:HGNC Symbol;Acc:HGN
2	LYRM4	−1.61	7e−16	5e−08	16 x 50	LYR motif containing 4 [Source:HGNC Symbol;Acc:HGNC:21
3	IPO5	−1.37	2e−09	1e−07	16 x 49	importin 5 [Source:HGNC Symbol;Acc:HGNC:6402]
4	ZNF346	1.5	6e−09	3e−05	15 x 50	zinc finger protein 346 [Source:HGNC Symbol;Acc:HGNC:16
5	KCTD6	1.25	1e−06	8e−05	16 x 50	potassium channel tetramerization domain containing 6 [Sour
6	FASTKD3	−1.13	9e−06	8e−05	15 x 50	FAST kinase domains 3 [Source:HGNC Symbol;Acc:HGNC:2
7	FBXO22	−1.04	1e−05	8e−05	15 x 50	F−box protein 22 [Source:HGNC Symbol;Acc:HGNC:13593]
8	STT3A	−0.77	1e−05	8e−05	16 x 50	STT3A, subunit of the oligosaccharyltransferase complex (ca
9	DYM	−1.1	2e−05	8e−05	16 x 50	dymeclin [Source:HGNC Symbol;Acc:HGNC:21317]
10	PPM1G	−1.1	2e−05	2e−04	16 x 50	protein phosphatase, Mg2+/Mn2+ dependent, 1G [Source:H
11	RNF114	−0.84	3e−05	2e−04	16 x 50	ring finger protein 114 [Source:HGNC Symbol;Acc:HGNC:13
12	CNOT1	−0.65	3e−05	4e−04	15 x 50	CCR4−NOT transcription complex, subunit 1 [Source:HGNC
13	PANK2	−1.05	5e−05	2e−03	17 x 50	pantothenate kinase 2 [Source:HGNC Symbol;Acc:HGNC:15
14	NDEL1	−0.99	1e−04	8e−03	15 x 50	nudE neurodevelopment protein 1−like 1 [Source:HGNC Sym
15	ICE2	−0.88	7e−04	8e−03	15 x 50	interactor of little elongation complex ELL subunit 2 [Source:
16	COMMD5	−0.83	1e−03	8e−03	16 x 50	COMM domain containing 5 [Source:HGNC Symbol;Acc:HG
17	KLHL7	0.81	1e−03	8e−03	16 x 50	kelch−like family member 7 [Source:HGNC Symbol;Acc:HGN
18	ZNF292	−0.8	2e−03	8e−03	15 x 50	zinc finger protein 292 [Source:HGNC Symbol;Acc:HGNC:18
19	LYRM1	−0.81	2e−03	8e−03	16 x 50	LYR motif containing 1 [Source:HGNC Symbol;Acc:HGNC:25
20	GMDS	0.79	2e−03	8e−03	15 x 50	GDP−mannose 4,6−dehydratase [Source:HGNC Symbol;Acc