H3_mel

Global Summary

%DE = 0.22

genes with fdr < 0.2 = 2853 (1748 + / 1105 −)

genes with fdr < 0.1 = 2267 (1407 + / 860 −)

genes with fdr < 0.05 = 1892 (1194 + / 698 −)

genes with fdr < 0.01 = 1262 (821 + / 441 −)

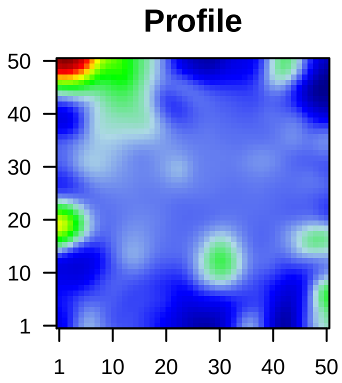
genes in genesets = 14839

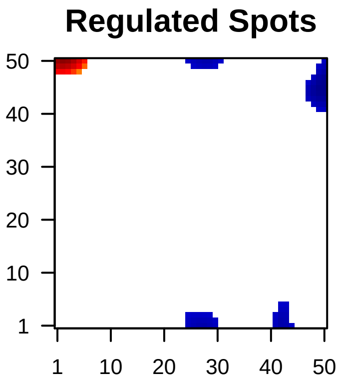
<FC> = 0

<shrinkage−t> = 0.01

<p−value> = 0.07

<fdr> = 0.78


Profile

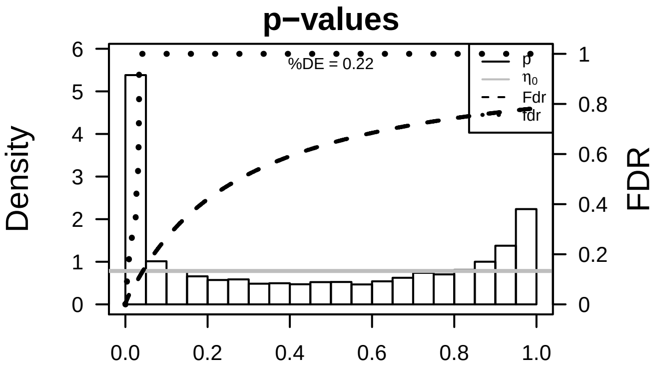

Regulated Spots

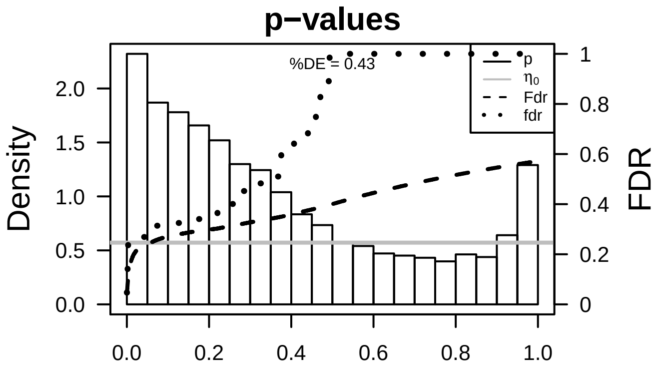
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ANKRD10	0.77	2e−16	7e−14	1 x 24	ankyrin repeat domain 10 [Source:HGNC Symbol;Acc:HGNC
2	AP3S1	−1.85	2e−16	7e−14	1 x 39	adaptor−related protein complex 3, sigma 1 subunit [Source:
3	ARL16	−1.46	2e−16	7e−14	50 x 50	ADP−ribosylation factor−like 16 [Source:HGNC Symbol;Acc:
4	ATP6V1F	−0.94	2e−16	7e−14	2 x 38	ATPase, H+ transporting, lysosomal 14kDa, V1 subunit F [So
5	ATRAID	−1.63	2e−16	7e−14	35 x 50	all−trans retinoic acid−induced differentiation factor [Source:
6	BUD31	−1.81	2e−16	7e−14	14 x 50	BUD31 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:
7	DERA	−1.26	2e−16	7e−14	1 x 43	deoxyribose−phosphate aldolase (putative) [Source:HGNC S
8	EIF4A1	−1.08	2e−16	7e−14	1 x 27	eukaryotic translation initiation factor 4A1 [Source:HGNC Syn
9	ERAL1	−1.74	2e−16	7e−14	46 x 44	Era−like 12S mitochondrial rRNA chaperone 1 [Source:HGN
10	EXOC3	−0.77	2e−16	7e−14	1 x 42	exocyst complex component 3 [Source:HGNC Symbol;Acc:H
11	FAM154B	1.99	2e−16	7e−14	6 x 1	
12	FH	−1.61	2e−16	7e−14	5 x 39	fumarate hydratase [Source:HGNC Symbol;Acc:HGNC:3700]
13	HDDC2	−0.97	2e−16	7e−14	20 x 44	HD domain containing 2 [Source:HGNC Symbol;Acc:HGNC:
14	HSD17B4	−1.63	2e−16	7e−14	11 x 50	hydroxysteroid (17−beta) dehydrogenase 4 [Source:HGNC S
15	KRTCAP2	−1.39	2e−16	7e−14	26 x 50	keratinocyte associated protein 2 [Source:HGNC Symbol;Acc
16	MRPL13	−1.86	2e−16	7e−14	34 x 50	mitochondrial ribosomal protein L13 [Source:HGNC Symbol;
17	MRPL48	−1.68	2e−16	7e−14	5 x 41	mitochondrial ribosomal protein L48 [Source:HGNC Symbol;
18	MRPL55	−0.98	2e−16	7e−14	17 x 50	mitochondrial ribosomal protein L55 [Source:HGNC Symbol;
19	MRPS15	−1.47	2e−16	7e−14	18 x 50	mitochondrial ribosomal protein S15 [Source:HGNC Symbol;
20	NAA20	−0.92	2e−16	7e−14	30 x 37	N(alpha)−acetyltransferase 20, NatB catalytic subunit [Source

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	15.18	5e−05	305	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
2	14.17	6e−05	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
3	13.18	9e−05	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
4	12.63	1e−04	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
5	12.52	1e−04	327	GSEA C2	BLUM_RESPONSE_TO_SALIRASIB_DN
6	12.5	1e−04	99	GSEA C2	BURTON_ADIPOGENESIS_3
7	12.49	1e−04	197	HM	HALLMARK_E2F_TARGETS
8	12.11	1e−04	390	GSEA C2	PUJANA_BRCA2_PCC_NETWORK
9	12.01	1e−04	242	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
10	11.94	1e−04	216	GSEA C2	MARKEY_RB1_ACUTE_LOF_DN
11	11.85	1e−04	81	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
12	11.45	2e−04	96	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
13	11.01	4e−02	16	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
14	10.91	2e−04	89	GSEA C2	MORI_IMMATURE_B_LYMPHOCYTE_DN
15	10.7	2e−04	155	GSEA C2	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
16	10.67	2e−04	267	GSEA C2	ZHANG_TLX_TARGETS_60HR_DN
17	10.66	2e−04	50	GSEA C2	ISHIDA_E2F_TARGETS
18	10.57	2e−04	485	GSEA C2	CHICAS_RB1_TARGETS_SENESCENT
19	10.3	2e−04	110	GSEA C2	WHITEFORD_PEDIATRIC_CANCER_MARKERS
20	10.15	2e−04	436	GSEA C2	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
Underexpressed					
1	−7.13	0.001	96	BP	mitochondrial translation
2	−7.05	0.001	83	BP	mitochondrial translational initiation
3	−7	0.001	83	BP	mitochondrial translational termination
4	−6.3	0.002	83	BP	mitochondrial translational elongation
5	−5.79	0.002	71	MF	structural constituent of ribosome
6	−5.75	0.002	277	BP	translation
7	−5.74	0.002	401	CC	mitochondrial inner membrane
8	−5.6	0.002	128	CC	ribosome
9	−4.98	0.004	24	CC	mitochondrial ribosome
10	−4.58	0.005	322	BP	mitochondrion organization
11	−4.44	0.005	1468	CC	mitochondrion
12	−4.4	0.005	198	HM	HALLMARK_OXIDATIVE_PHOSPHORYLATION
13	−4.08	0.007	107	GSEA C2	KEGG_OXIDATIVE_PHOSPHORYLATION
14	−4.01	0.007	58	BP	ER to Golgi vesicle−mediated transport
15	−3.94	0.008	285	BP	organelle organization
16	−3.74	0.009	393	GSEA C2	MITSIADES_RESPONSE_TO_APLIDIN_UP
17	−3.61	0.010	47	GSEA C2	TONG_INTERACT_WITH_PTTG1
18	−3.59	0.011	63	GSEA C2	KEGG_EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_P
19	−3.52	0.011	213	GSEA C2	WONG_MITOCHONDRIA_GENE_MODULE
20	−3.43	0.012	14	CC	Cul4−RING E3 ubiquitin ligase complex


p−values


p−values

H3_mel

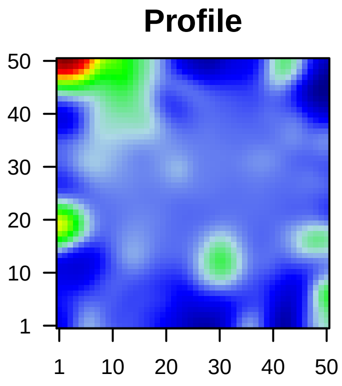
Local Summary

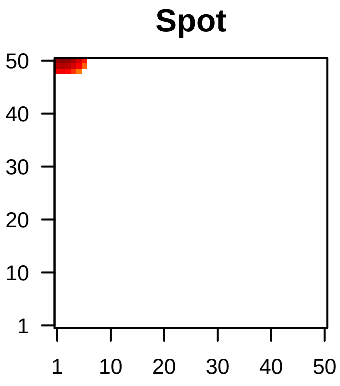
%DE = 0.85
metagenes = 17
genes = 287
genes in genesets = 286

genes with fdr < 0.1 = 213 (204 + / 9 −)
genes with fdr < 0.05 = 211 (204 + / 7 −)
genes with fdr < 0.01 = 174 (172 + / 2 −)

<r> metagenes = 0.95
<r> genes = 0.32

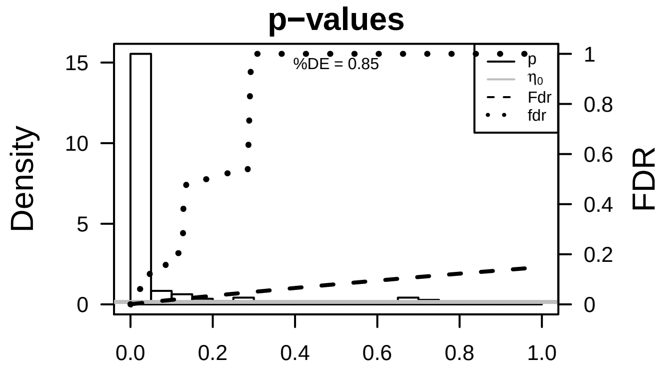
<FC> = 0.61
<shrinkage−t> = 9.77
<p−value> = 0
<fdr> = 0.29





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CCNE2	1.65	4e−13	1e−09	2 x 50	cyclin E2 [Source:HGNC Symbol;Acc:HGNC:1590]
2	ASF1B	1.48	7e−11	1e−09	4 x 50	anti−silencing function 1B histone chaperone [Source:HGNC
3	NCAPH2	1.48	7e−11	1e−09	1 x 50	non−SMC condensin II complex, subunit H2 [Source:HGNC
4	TRAIP	1.47	9e−11	1e−09	5 x 50	TRAF interacting protein [Source:HGNC Symbol;Acc:HGNC:
5	KIAA0101	1.34	1e−10	1e−08	3 x 50	KIAA0101 [Source:HGNC Symbol;Acc:HGNC:28961]
6	WDHD1	1.42	4e−10	1e−08	1 x 49	WD repeat and HMG−box DNA binding protein 1 [Source:HG
7	CKAP2L	1.4	8e−10	1e−08	6 x 50	cytoskeleton associated protein 2−like [Source:HGNC Symb
8	PCNA	1.05	8e−10	4e−08	2 x 50	proliferating cell nuclear antigen [Source:HGNC Symbol;Acc:
9	TK1	1.1	2e−09	1e−07	4 x 50	thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:HGN
10	CDK1	1.29	9e−09	1e−07	5 x 50	cyclin−dependent kinase 1 [Source:HGNC Symbol;Acc:HGN
11	MCM10	1.3	1e−08	1e−07	1 x 50	minichromosome maintenance complex component 10 [Sour
12	FANCB	1.29	1e−08	1e−07	2 x 50	Fanconi anemia, complementation group B [Source:HGNC S
13	STMN1	0.52	2e−08	1e−07	5 x 50	stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]
14	RAD1	−1.16	2e−08	1e−07	1 x 49	RAD1 checkpoint DNA exonuclease [Source:HGNC Symbol;
15	RFC5	1.12	2e−08	2e−07	2 x 50	replication factor C (activator 1) 5, 36.5kDa [Source:HGNC S
16	SPAG5	1.26	3e−08	2e−07	6 x 50	sperm associated antigen 5 [Source:HGNC Symbol;Acc:HG
17	HMGB2	1.13	4e−08	2e−07	5 x 50	high mobility group box 2 [Source:HGNC Symbol;Acc:HGNC:
18	E2F8	1.24	5e−08	2e−07	3 x 49	E2F transcription factor 8 [Source:HGNC Symbol;Acc:HGNC:
19	RRM2	1.24	5e−08	2e−07	5 x 50	ribonucleotide reductase M2 [Source:HGNC Symbol;Acc:HG
20	CEP250	1.24	5e−08	5e−07	4 x 48	centrosomal protein 250kDa [Source:HGNC Symbol;Acc:HG



H3_mel

Local Summary

%DE = 0.78

metagenes = 17

genes = 202

genes in genesets = 195

genes with fdr < 0.1 = 31 (7 + / 24 −)

genes with fdr < 0.05 = 18 (3 + / 15 −)

genes with fdr < 0.01 = 7 (1 + / 6 −)

<r> metagenes = 0.96

<r> genes = 0.25

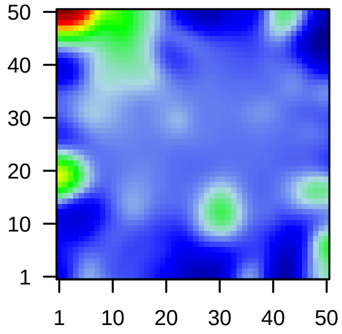
<FC> = −0.21

<shrinkage−t> = −3.18

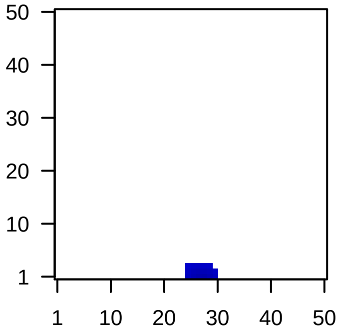
<p−value> = 0.13

<fdr> = 0.88

Profile



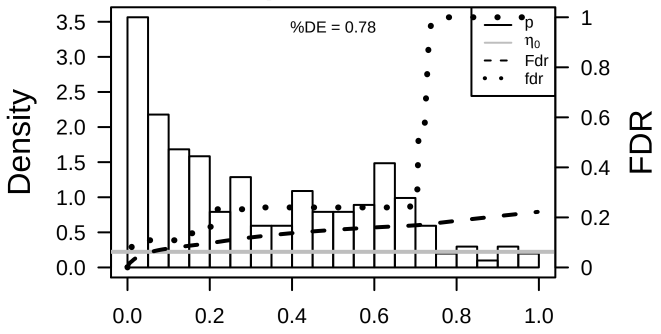
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	FKBP14	−1.03	4e−06	3e−04	26 x 1	FK506 binding protein 14, 22 kDa [Source:HGNC Symbol;Ac
2	PTPN14	−0.98	1e−05	3e−04	25 x 3	protein tyrosine phosphatase, non−receptor type 14 [Source:
3	DDX27	−0.95	2e−05	3e−04	27 x 1	DEAD (Asp−Glu−Ala−Asp) box polypeptide 27 [Source:HGN
4	FAM120A	−0.96	3e−05	3e−04	25 x 1	family with sequence similarity 120A [Source:HGNC Symbol;
5	SPOP	−0.85	3e−05	3e−04	25 x 1	speckle−type POZ protein [Source:HGNC Symbol;Acc:HGNC
6	ZNHIT6	0.94	4e−05	3e−04	30 x 1	zinc finger, HIT−type containing 6 [Source:HGNC Symbol;Ac
7	PKN2	−0.93	4e−05	3e−03	29 x 1	protein kinase N2 [Source:HGNC Symbol;Acc:HGNC:9406]
8	BMPR1A	0.88	1e−04	2e−02	29 x 3	bone morphogenetic protein receptor, type IA [Source:HGNC
9	RNF149	−0.8	4e−04	4e−02	29 x 1	ring finger protein 149 [Source:HGNC Symbol;Acc:HGNC:23
10	DNAJC24	−0.68	3e−03	4e−02	25 x 1	DnaJ (Hsp40) homolog, subfamily C, member 24 [Source:HG
11	FAM222B	−0.68	3e−03	4e−02	25 x 2	family with sequence similarity 222, member B [Source:HGN
12	NRAS	−0.65	4e−03	4e−02	27 x 1	neuroblastoma RAS viral (v−ras) oncogene homolog [Source
13	ZFYVE26	0.63	5e−03	4e−02	27 x 3	zinc finger, FYVE domain containing 26 [Source:HGNC Symb
14	ETS1	−0.62	6e−03	4e−02	28 x 1	v−ets avian erythroblastosis virus E26 oncogene homolog 1 [
15	UBE2E1	−0.61	7e−03	4e−02	27 x 1	ubiquitin−conjugating enzyme E2E 1 [Source:HGNC Symbol;
16	CDK11B	−0.6	9e−03	4e−02	26 x 3	cyclin−dependent kinase 11B [Source:HGNC Symbol;Acc:HG
17	GNAI3	−0.59	9e−03	4e−02	25 x 1	guanine nucleotide binding protein (G protein), alpha inhibitin
18	FAM73A	−0.58	1e−02	4e−02	25 x 2	family with sequence similarity 73, member A [Source:HGNC
19	FAHD2B	−0.58	1e−02	8e−02	25 x 2	fumarylacetoacetate hydrolase domain containing 2B [Source
20	ANP32A	−0.55	1e−02	8e−02	26 x 1	acidic (leucine−rich) nuclear phosphoprotein 32 family, memb

p−values



H3_mel

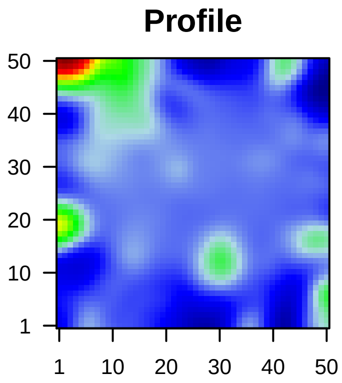
Local Summary

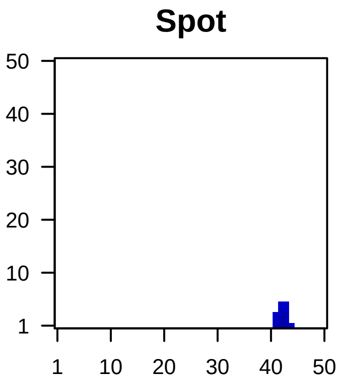
%DE = 0.71
metagenes = 14
genes = 131
genes in genesets = 131

genes with fdr < 0.1 = 51 (11 + / 40 −)
genes with fdr < 0.05 = 33 (5 + / 28 −)
genes with fdr < 0.01 = 17 (3 + / 14 −)

<r> metagenes = 0.96
<r> genes = 0.13

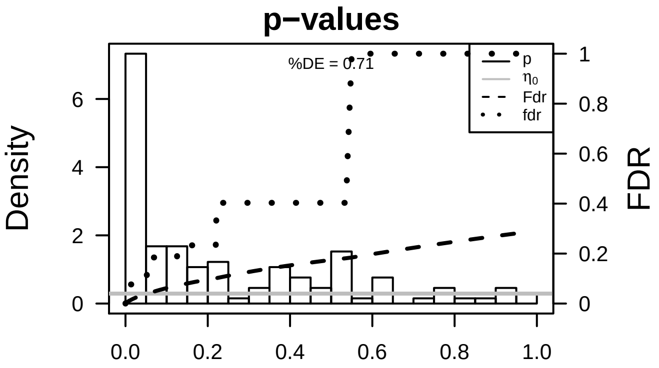
<FC> = −0.25
<shrinkage−t> = −3.87
<p−value> = 0.03
<fdr> = 0.73





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	RFTN1	1.58	3e−12	2e−09	43 x 1	raftlin, lipid raft linker 1 [Source:HGNC Symbol;Acc:HGNC:30
2	RAI14	−1.12	6e−11	2e−08	44 x 1	retinoic acid induced 14 [Source:HGNC Symbol;Acc:HGNC:1
3	BBIP1	−1.29	5e−10	1e−07	42 x 4	BBSome interacting protein 1 [Source:HGNC Symbol;Acc:HG
4	AKAP9	−1.07	3e−09	3e−06	42 x 1	A kinase (PRKA) anchor protein 9 [Source:HGNC Symbol;Ac
5	CYB5R1	−1.18	9e−08	1e−05	41 x 2	cytochrome b5 reductase 1 [Source:HGNC Symbol;Acc:HGN
6	ACTR1A	−1.13	5e−07	2e−04	42 x 1	ARP1 actin−related protein 1 homolog A, centractin alpha (ye
7	APOOL	−1.01	7e−06	2e−04	42 x 1	apolipoprotein O−like [Source:HGNC Symbol;Acc:HGNC:240
8	PLOD1	−1.01	9e−06	5e−04	44 x 1	procollagen−lysine, 2−oxoglutarate 5−dioxygenase 1 [Source
9	RTCA	−0.96	2e−05	7e−04	42 x 3	RNA 3'−terminal phosphate cyclase [Source:HGNC Symbol;
10	TMEM43	−0.93	4e−05	9e−04	43 x 3	transmembrane protein 43 [Source:HGNC Symbol;Acc:HGN
11	MED31	0.9	7e−05	9e−04	41 x 1	mediator complex subunit 31 [Source:HGNC Symbol;Acc:HG
12	CIR1	−0.89	9e−05	2e−03	41 x 1	corepressor interacting with RBPJ, 1 [Source:HGNC Symbol;
13	B9D1	−0.85	2e−04	2e−03	42 x 5	B9 protein domain 1 [Source:HGNC Symbol;Acc:HGNC:2412
14	EVI5	0.85	2e−04	4e−03	43 x 1	ecotropic viral integration site 5 [Source:HGNC Symbol;Acc:H
15	SLC16A6	−0.78	6e−04	4e−03	44 x 1	solute carrier family 16, member 6 [Source:HGNC Symbol;Ac
16	NOL10	−0.78	6e−04	4e−03	42 x 1	nucleolar protein 10 [Source:HGNC Symbol;Acc:HGNC:2586
17	RAB6C	−0.78	6e−04	4e−03	41 x 1	RAB6C, member RAS oncogene family [Source:HGNC Symb
18	ADRA2A	−0.78	6e−04	1e−02	42 x 1	adrenoceptor alpha 2A [Source:HGNC Symbol;Acc:HGNC:2
19	SERPINH1	−0.7	2e−03	1e−02	42 x 1	serpin peptidase inhibitor, clade H (heat shock protein 47), m
20	CCS	0.69	2e−03	1e−02	41 x 2	copper chaperone for superoxide dismutase [Source:HGNC



H3_mel

Local Summary

%DE = 0.79

metagenes = 29

genes = 357

genes in genesets = 357

genes with fdr < 0.1 = 184 (49 + / 135 −)

genes with fdr < 0.05 = 162 (45 + / 117 −)

genes with fdr < 0.01 = 81 (18 + / 63 −)

<r> metagenes = 0.84

<r> genes = 0.07

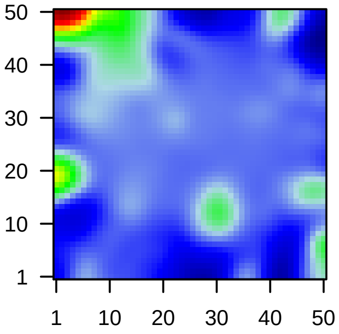
<FC> = −0.23

<shrinkage−t> = −3.66

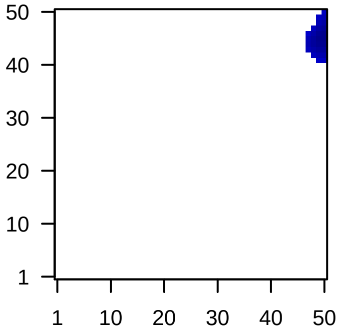
<p−value> = 0.01

<fdr> = 0.61

Profile



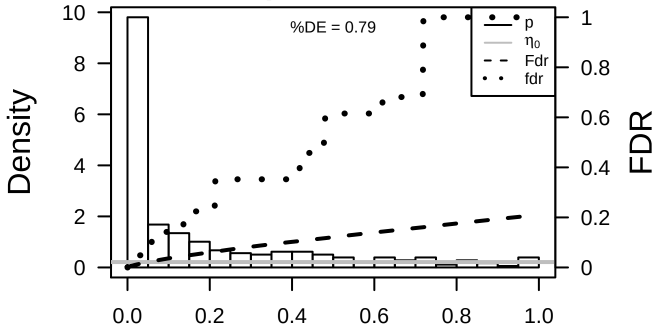
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ARL16	−1.46	2e−16	6e−15	50 x 50	ADP−ribosylation factor−like 16 [Source:HGNC Symbol;Acc:H
2	SNRPN	−1.36	2e−16	6e−15	50 x 46	small nuclear ribonucleoprotein polypeptide N [Source:HGNC
3	TMEM208	−1.47	2e−16	6e−15	48 x 46	transmembrane protein 208 [Source:HGNC Symbol;Acc:HGN
4	GABARAPL2	−1.02	8e−15	2e−09	49 x 48	GABA(A) receptor−associated protein−like 2 [Source:HGNC
5	XRN1	−1.33	5e−11	2e−09	47 x 45	5'−3' exoribonuclease 1 [Source:HGNC Symbol;Acc:HGNC:3
6	G3BP2	−1.03	9e−11	2e−09	50 x 49	GTPase activating protein (SH3 domain) binding protein 2 [S
7	SLC25A44	−1.33	9e−11	2e−09	50 x 44	solute carrier family 25, member 44 [Source:HGNC Symbol;A
8	CIAO1	−1.33	9e−11	3e−09	50 x 41	cytosolic iron−sulfur assembly component 1 [Source:HGNC S
9	ERCC1	−1.07	1e−10	3e−09	50 x 43	excision repair cross−complementation group 1 [Source:HGN
10	ATP6V1E1	−1.32	2e−10	1e−08	48 x 44	ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E1 [S
11	CTSK	1.43	3e−10	1e−08	49 x 41	cathepsin K [Source:HGNC Symbol;Acc:HGNC:2536]
12	LUZP6	1.41	5e−10	3e−07	50 x 49	leucine zipper protein 6 [Source:HGNC Symbol;Acc:HGNC:3
13	GOLGA7	−1.24	6e−09	3e−07	50 x 46	golgin A7 [Source:HGNC Symbol;Acc:HGNC:24876]
14	CHMP5	−1.22	9e−09	3e−07	50 x 47	charged multivesicular body protein 5 [Source:HGNC Symbol
15	KIAA1033	−1.17	1e−08	2e−06	50 x 49	KIAA1033 [Source:HGNC Symbol;Acc:HGNC:29174]
16	PRPF3	−1.18	3e−08	2e−06	50 x 42	pre−mRNA processing factor 3 [Source:HGNC Symbol;Acc:H
17	TRPT1	−1.17	1e−07	2e−06	50 x 49	tRNA phosphotransferase 1 [Source:HGNC Symbol;Acc:HGN
18	GMPR	1.2	1e−07	2e−06	50 x 43	guanosine monophosphate reductase [Source:HGNC Symbo
19	C1orf52	−1.16	2e−07	2e−06	47 x 44	chromosome 1 open reading frame 52 [Source:HGNC Symbo
20	PARP6	1.19	2e−07	2e−06	50 x 44	poly (ADP−ribose) polymerase family, member 6 [Source:HG

p−values



H3_mel

Local Summary

%DE = 0.74

metagenes = 12

genes = 180

genes in genesets = 180

genes with fdr < 0.1 = 90 (27 + / 63 −)

genes with fdr < 0.05 = 90 (27 + / 63 −)

genes with fdr < 0.01 = 61 (18 + / 43 −)

<r> metagenes = 0.9

<r> genes = 0.08

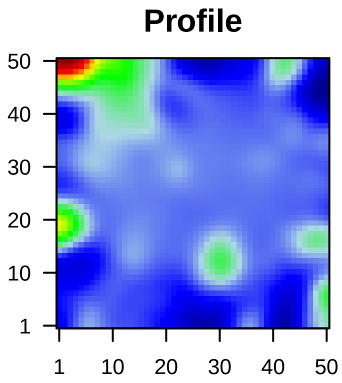
<FC> = −0.24

<shrinkage−t> = −4.03

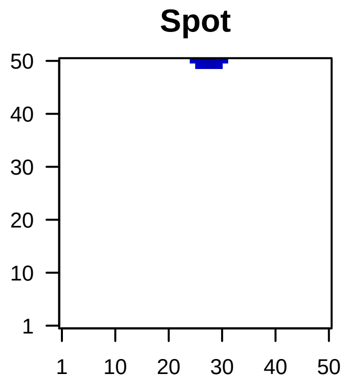
<p−value> = 0

<fdr> = 0.54

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	KRTCAP2	−1.39	2e−16	3e−15	26 x 50	keratinocyte associated protein 2 [Source:HGNC Symbol;Acc
2	RABGGTB	−1.53	2e−16	3e−15	28 x 50	Rab geranylgeranyltransferase, beta subunit [Source:HGNC
3	RCAN1	−1.26	2e−16	3e−15	29 x 50	regulator of calcineurin 1 [Source:HGNC Symbol;Acc:HGNC:
4	YARS	−1.45	2e−16	3e−15	30 x 50	tyrosyl−tRNA synthetase [Source:HGNC Symbol;Acc:HGNC:
5	PWP1	−0.93	3e−14	9e−12	25 x 50	PWP1 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:H
6	PAAF1	−1.44	2e−13	9e−12	27 x 50	proteasomal ATPase−associated factor 1 [Source:HGNC Sy
7	PTS	−1.43	4e−13	6e−11	26 x 50	6−pyruvoyltetrahydropterin synthase [Source:HGNC Symbol;
8	TOMM34	−1.4	2e−12	8e−11	29 x 50	translocase of outer mitochondrial membrane 34 [Source:HG
9	DDX49	−1.24	4e−12	5e−10	27 x 50	DEAD (Asp−Glu−Ala−Asp) box polypeptide 49 [Source:HGN
10	EXOSC3	−1.32	1e−11	5e−09	30 x 50	exosome component 3 [Source:HGNC Symbol;Acc:HGNC:17
11	NIPBL	−1.12	2e−10	5e−09	30 x 50	Nipped−B homolog (Drosophila) [Source:HGNC Symbol;Acc:
12	INTS10	−1.31	2e−10	7e−08	25 x 50	integrator complex subunit 10 [Source:HGNC Symbol;Acc:HG
13	APEX1	−0.74	2e−09	2e−06	29 x 50	APEX nuclease (multifunctional DNA repair enzyme) 1 [Sourc
14	SH3PXD2B	1.24	5e−08	3e−06	28 x 50	SH3 and PX domains 2B [Source:HGNC Symbol;Acc:HGNC:
15	LGALS8	−1.11	1e−07	5e−06	31 x 50	lectin, galactoside−binding, soluble, 8 [Source:HGNC Symbol
16	XPO5	1.1	2e−07	9e−06	30 x 50	exportin 5 [Source:HGNC Symbol;Acc:HGNC:17675]
17	TRUB2	−1.13	4e−07	1e−05	25 x 50	TruB pseudouridine (psi) synthase family member 2 [Source:
18	FAH	−1.12	6e−07	3e−05	29 x 50	fumarylacetoacetate hydrolase (fumarylacetoacetase) [Sourc
19	CHUK	1.1	1e−06	3e−05	27 x 50	conserved helix−loop−helix ubiquitous kinase [Source:HGNC
20	CHORDC1	−1.07	2e−06	4e−05	30 x 50	cysteine and histidine−rich domain (CHORD) containing 1 [S

p−values