H1_mel

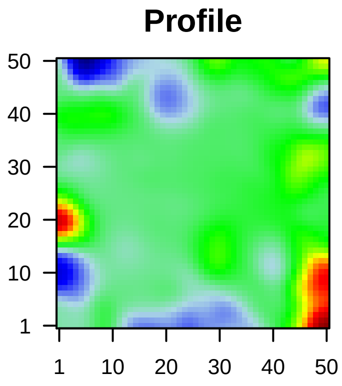
Global Summary

%DE = 0.21
genes with fdr < 0.2 = 2520 (1559 + / 961 −)
genes with fdr < 0.1 = 2037 (1284 + / 753 −)
genes with fdr < 0.05 = 1597 (1013 + / 584 −)
genes with fdr < 0.01 = 980 (636 + / 344 −)

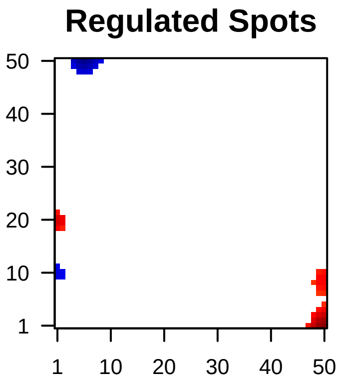
genes in genesets = 14839

<FC> = 0
<shrinkage−t> = 0.04
<p−value> = 0.09
<fdr> = 0.79

Profile



Regulated Spots



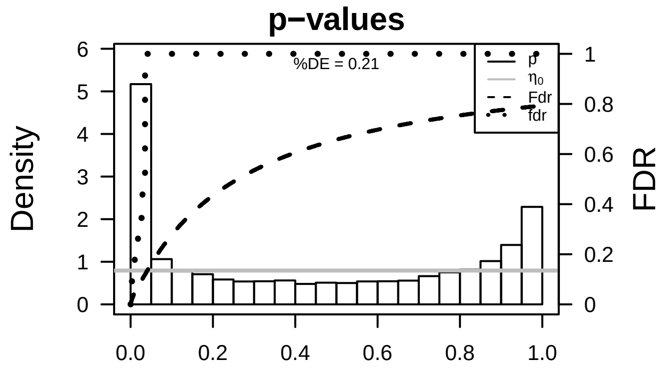
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	AMZ2	−1.26	2e−16	1e−13	48 x 42	archaelysin family metallopeptidase 2 [Source:HGNC Symbol
2	ARHGAP8	−1.34	2e−16	1e−13	1 x 43	Rho GTPase activating protein 8 [Source:HGNC Symbol;Acc:
3	ATP6V1H	−1.85	2e−16	1e−13	5 x 44	ATPase, H+ transporting, lysosomal 50/57kDa, V1 subunit H
4	CAPN3	−0.92	2e−16	1e−13	1 x 43	calpain 3, (p94) [Source:HGNC Symbol;Acc:HGNC:1480]
5	CDKN3	−1.65	2e−16	1e−13	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
6	CEP97	2.16	2e−16	1e−13	2 x 47	centrosomal protein 97kDa [Source:HGNC Symbol;Acc:HGN
7	CNOT1	−1.17	2e−16	1e−13	15 x 50	CCR4−NOT transcription complex, subunit 1 [Source:HGNC
8	CRYAB	1.37	2e−16	1e−13	50 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
9	CTGF	1.95	2e−16	1e−13	50 x 1	connective tissue growth factor [Source:HGNC Symbol;Acc:H
10	HBS1L	−1.22	2e−16	1e−13	3 x 44	HBS1−like translational GTPase [Source:HGNC Symbol;Acc:
11	MPC2	−1.06	2e−16	1e−13	3 x 32	mitochondrial pyruvate carrier 2 [Source:HGNC Symbol;Acc:
12	MRPL15	−1.58	2e−16	1e−13	5 x 33	mitochondrial ribosomal protein L15 [Source:HGNC Symbol;
13	NIT2	−1.57	2e−16	1e−13	50 x 42	nitrilase family, member 2 [Source:HGNC Symbol;Acc:HGNC
14	NNT	−1.8	2e−16	1e−13	6 x 47	nicotinamide nucleotide transhydrogenase [Source:HGNC Sy
15	RAB11A	−1.54	2e−16	1e−13	36 x 50	RAB11A, member RAS oncogene family [Source:HGNC Sym
16	RGS2	1.94	2e−16	1e−13	49 x 1	regulator of G−protein signaling 2 [Source:HGNC Symbol;Acc
17	RNF14	−1.67	2e−16	1e−13	1 x 43	ring finger protein 14 [Source:HGNC Symbol;Acc:HGNC:100
18	SIDT2	1.98	2e−16	1e−13	45 x 26	SID1 transmembrane family, member 2 [Source:HGNC Symb
19	STMN1	−0.92	2e−16	1e−13	5 x 50	stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]
20	TK1	−1.55	2e−16	1e−13	4 x 50	thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:HGN

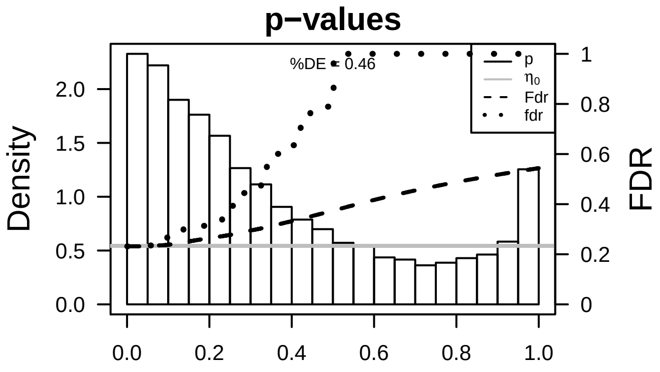
Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	5.86	0.002	385	GSEA C2	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
2	5.39	0.003	425	GSEA C2	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_
3	5.34	0.003	594	GSEA C2	WONG_ADULT_TISSUE_STEM_MODULE
4	5.07	0.003	135	GSEA C2	KAAB_FAILED_HEART_ATRIUM_DN
5	5.02	0.003	78	GSEA C2	SCHUHMACHER_MYC_TARGETS_UP
6	4.99	0.004	212	Lymphoma	LENZ_Stromal signature 1
7	4.79	0.004	410	GSEA C2	LIM_MAMMARY_STEM_CELL_UP
8	4.76	0.004	840	Chr	Chr 17
9	4.75	0.004	303	GSEA C2	LINDGREN_BLADDER_CANCER_CLUSTER_2B
10	4.74	0.004	55	GSEA C2	GERHOLD_ADIPOGENESIS_DN
11	4.73	0.004	831	GSEA C2	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
12	4.73	0.004	131	Colon Cancer	Marisa_CRC−cluster−a
13	4.7	0.004	925	GSEA C2	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
14	4.61	0.005	157	GSEA C2	HEDENFALK_BREAST_CANCER_BRCA1_VS_BRCA2
15	4.57	0.005	15	BP	cellular response to gamma radiation
16	4.56	0.005	283	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
17	4.54	0.005	426	GSEA C2	ZWANG_CLASS_1_TRANSIENTLY_INDUCED_BY_EGF
18	4.52	0.005	71	GSEA C2	RODRIGUES_THYROID_CARCINOMA_DN
19	4.48	0.005	166	GSEA C2	RODWELL_AGING_KIDNEY_NO_BLOOD_UP
20	4.44	0.005	1128	Lymphoma	SPANG_BCR DN
Underexpressed					
1	−8.24	6e−04	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
2	−7.69	2e−02	16	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
3	−7.5	8e−04	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
4	−7.23	9e−04	96	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
5	−7.07	1e−03	54	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
6	−6.94	1e−03	81	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
7	−6.59	1e−03	99	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
8	−6.34	2e−03	162	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
9	−6.33	2e−03	72	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
10	−6.2	2e−03	155	GSEA C2	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
11	−6.16	2e−03	165	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
12	−6.07	2e−03	33	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
13	−5.75	2e−03	93	GSEA C2	KONG_E2F3_TARGETS
14	−5.69	2e−03	110	GSEA C2	WHITEFORD_PEDIATRIC_CANCER_MARKERS
15	−5.59	2e−03	45	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
16	−5.56	2e−03	113	GSEA C2	VANTVEER_BREAST_CANCER_METASTASIS_DN
17	−5.21	3e−03	145	GSEA C2	CHANG_CYCLING_GENES
18	−5.19	3e−03	31	GSEA C2	GREENBAUM_E2A_TARGETS_UP
19	−5.09	3e−03	436	GSEA C2	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
20	−5.09	3e−03	10	GSEA C2	LIANG_SILENCED_BY_METHYLATION_DN

p−values



p−values



H1_mel

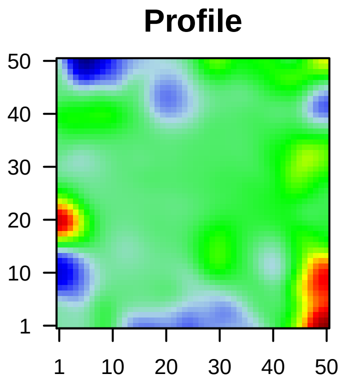
Local Summary

%DE = 0.89
metagenes = 13
genes = 256
genes in genesets = 256

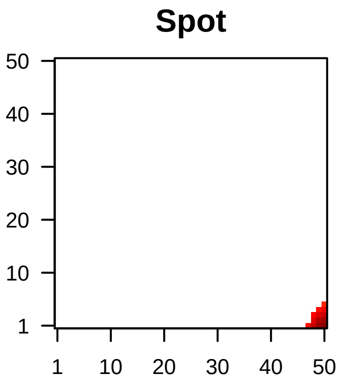
genes with fdr < 0.1 = 175 (144 + / 31 −)
genes with fdr < 0.05 = 153 (133 + / 20 −)
genes with fdr < 0.01 = 123 (111 + / 12 −)

<r> metagenes = 0.98
<r> genes = 0.2

<FC> = 0.41
<shrinkage−t> = 6.69
<p−value> = 0
<fdr> = 0.44



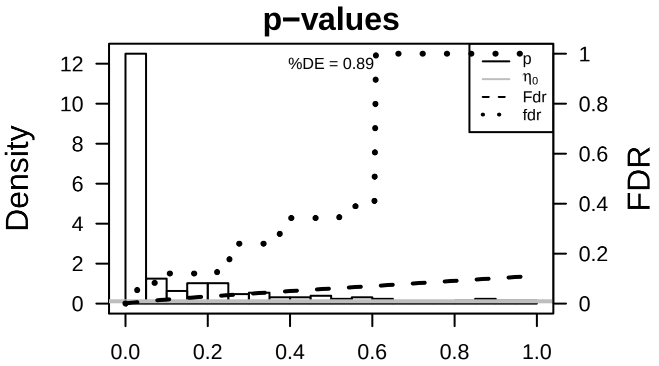
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CRYAB	1.37	2e−16	2e−15	50 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
2	CTGF	1.95	2e−16	2e−15	50 x 1	connective tissue growth factor [Source:HGNC Symbol;Acc:H
3	RGS2	1.94	2e−16	2e−15	49 x 1	regulator of G−protein signaling 2 [Source:HGNC Symbol;Acc
4	LMCD1	1.71	3e−13	2e−10	47 x 1	LIM and cysteine−rich domains 1 [Source:HGNC Symbol;Acc
5	A2M	1.58	2e−11	2e−10	50 x 1	alpha−2−macroglobulin [Source:HGNC Symbol;Acc:HGNC:7
6	TNFRSF12A	1.57	2e−11	2e−10	50 x 1	tumor necrosis factor receptor superfamily, member 12A [Sou
7	C10orf10	1.56	2e−11	2e−10	49 x 1	chromosome 10 open reading frame 10 [Source:HGNC Symb
8	ARMC9	−1.37	3e−11	6e−10	50 x 3	armadillo repeat containing 9 [Source:HGNC Symbol;Acc:HG
9	FOXO1	1.54	5e−11	1e−09	50 x 5	forkhead box O1 [Source:HGNC Symbol;Acc:HGNC:3819]
10	F2R	1.52	9e−11	9e−09	50 x 1	coagulation factor II (thrombin) receptor [Source:HGNC Symb
11	RGS4	1.47	4e−10	1e−08	50 x 1	regulator of G−protein signaling 4 [Source:HGNC Symbol;Acc
12	CREB5	1.42	1e−09	1e−08	49 x 1	cAMP responsive element binding protein 5 [Source:HGNC S
13	MAP2	1.42	1e−09	6e−08	50 x 2	microtubule−associated protein 2 [Source:HGNC Symbol;Acc
14	CALD1	0.88	5e−09	6e−08	50 x 1	caldesmon 1 [Source:HGNC Symbol;Acc:HGNC:1441]
15	KIAA0922	1.36	6e−09	6e−08	49 x 1	KIAA0922 [Source:HGNC Symbol;Acc:HGNC:29146]
16	HIST1H2BC	1.35	7e−09	7e−08	50 x 1	histone cluster 1, H2bc [Source:HGNC Symbol;Acc:HGNC:47
17	NRP1	1.34	1e−08	7e−08	50 x 5	neuropilin 1 [Source:HGNC Symbol;Acc:HGNC:8004]
18	TGIF1	1.14	1e−08	2e−07	50 x 1	TGFB−induced factor homeobox 1 [Source:HGNC Symbol;Ac
19	FAM98A	1.28	2e−08	2e−07	49 x 1	family with sequence similarity 98, member A [Source:HGNC
20	PLSCR4	1.3	3e−08	3e−07	49 x 1	phospholipid scramblase 4 [Source:HGNC Symbol;Acc:HGN



p−values

H1_mel

Local Summary

%DE = 0.8

metagenes = 11

genes = 113

genes in genesets = 113

genes with fdr < 0.1 = 64 (53 + / 11 −)

genes with fdr < 0.05 = 60 (50 + / 10 −)

genes with fdr < 0.01 = 43 (37 + / 6 −)

<r> metagenes = 0.95

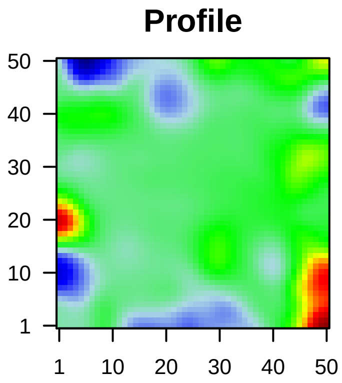
<r> genes = 0.09

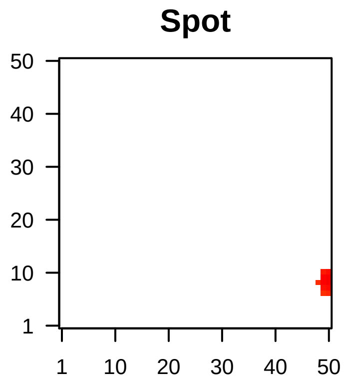
<FC> = 0.36

<shrinkage−t> = 5.76

<p−value> = 0

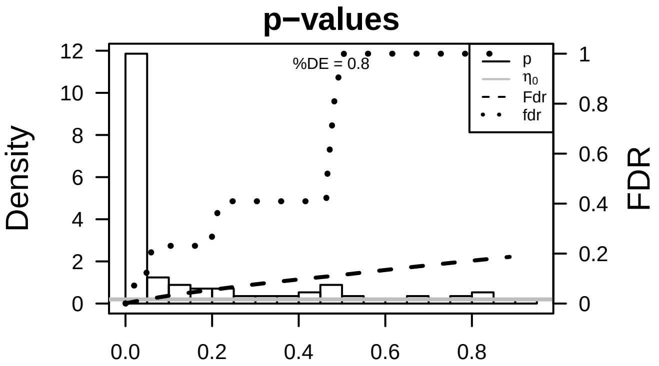
<fdr> = 0.47





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	C22orf29	1.32	2e−08	2e−07	50 x 10	chromosome 22 open reading frame 29 [Source:HGNC Symb
2	PRR14	1.31	2e−08	2e−07	50 x 11	proline rich 14 [Source:HGNC Symbol;Acc:HGNC:28458]
3	PRSS23	1.3	3e−08	2e−07	50 x 7	protease, serine, 23 [Source:HGNC Symbol;Acc:HGNC:1437
4	ACTN1	1.3	3e−08	2e−07	50 x 8	actinin, alpha 1 [Source:HGNC Symbol;Acc:HGNC:163]
5	ZNF621	1.29	4e−08	2e−07	49 x 8	zinc finger protein 621 [Source:HGNC Symbol;Acc:HGNC:24
6	S100A13	−1.21	4e−08	9e−07	50 x 7	S100 calcium binding protein A13 [Source:HGNC Symbol;Ac
7	SOCS2	1.25	9e−08	1e−06	50 x 9	suppressor of cytokine signaling 2 [Source:HGNC Symbol;Ac
8	ITM2B	0.89	1e−07	3e−06	50 x 10	integral membrane protein 2B [Source:HGNC Symbol;Acc:H
9	KCNE4	1.2	3e−07	3e−06	50 x 7	potassium channel, voltage gated subfamily E regulatory beta
10	FOXF2	1.18	4e−07	5e−06	50 x 11	forkhead box F2 [Source:HGNC Symbol;Acc:HGNC:3810]
11	IGF1R	1.16	8e−07	5e−06	50 x 7	insulin−like growth factor 1 receptor [Source:HGNC Symbol;A
12	DRAM2	1.04	9e−07	2e−05	50 x 8	DNA−damage regulated autophagy modulator 2 [Source:HG
13	PABPC4	0.84	2e−06	2e−05	50 x 7	poly(A) binding protein, cytoplasmic 4 (inducible form) [Sourc
14	PINK1	1.09	3e−06	2e−05	50 x 7	PTEN induced putative kinase 1 [Source:HGNC Symbol;Acc:
15	BAMBI	1.08	4e−06	2e−05	50 x 11	BMP and activin membrane−bound inhibitor [Source:HGNC
16	MBD2	1.08	4e−06	2e−05	50 x 10	methyl−CpG binding domain protein 2 [Source:HGNC Symbo
17	TOMM7	0.46	5e−06	3e−05	50 x 11	translocase of outer mitochondrial membrane 7 homolog (yea
18	HELQ	1.06	6e−06	6e−05	50 x 10	helicase, POLQ−like [Source:HGNC Symbol;Acc:HGNC:185
19	ORC3	−0.94	9e−06	2e−04	50 x 7	origin recognition complex, subunit 3 [Source:HGNC Symbol;
20	PRPSAP1	1	2e−05	2e−04	50 x 11	phosphoribosyl pyrophosphate synthetase−associated protei



H1_mel

Local Summary

%DE = 0.74

metagenes = 7

genes = 191

genes in genesets = 191

genes with fdr < 0.1 = 108 (102 + / 6 −)

genes with fdr < 0.05 = 108 (102 + / 6 −)

genes with fdr < 0.01 = 66 (63 + / 3 −)

<r> metagenes = 0.99

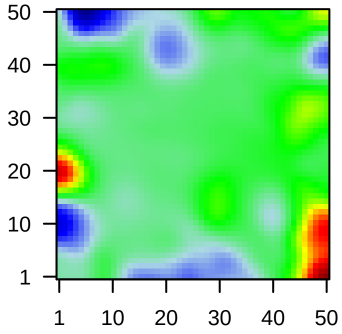
<r> genes = 0.18

<FC> = 0.43

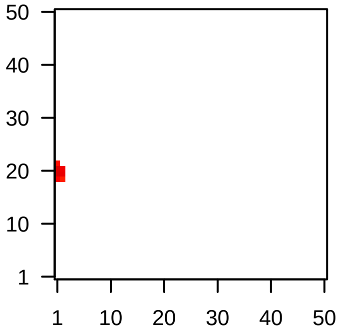
<shrinkage−t> = 7.28

<p−value> = 0

<fdr> = 0.47



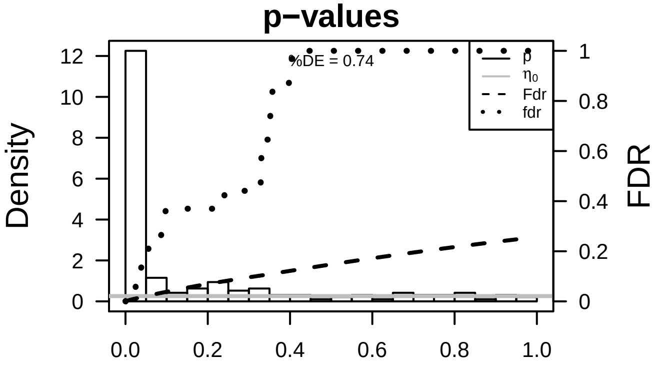
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	FAM131A	1.78	3e−14	5e−11	1 x 22	family with sequence similarity 131, member A [Source:HGN
2	LMLN	1.67	1e−12	4e−09	1 x 20	leishmanolysin−like (metallopeptidase M8 family) [Source:HG
3	RDX	−1.35	7e−11	9e−08	1 x 22	radixin [Source:HGNC Symbol;Acc:HGNC:9944]
4	CDK9	1.41	2e−09	3e−07	2 x 21	cyclin−dependent kinase 9 [Source:HGNC Symbol;Acc:HGN
5	ATP1B3	0.72	8e−09	3e−07	1 x 21	ATPase, Na+/K+ transporting, beta 3 polypeptide [Source:HG
6	RCE1	1.33	1e−08	4e−07	1 x 20	Ras converting CAAX endopeptidase 1 [Source:HGNC Symb
7	CCDC109B	1.31	2e−08	5e−07	1 x 20	coiled−coil domain containing 109B [Source:HGNC Symbol;
8	SPRY2	1.3	3e−08	5e−07	1 x 21	sprouty homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:
9	SQSTM1	0.59	4e−08	5e−06	1 x 21	sequestosome 1 [Source:HGNC Symbol;Acc:HGNC:11280]
10	SERPINE2	1.21	2e−07	5e−06	1 x 20	serpin peptidase inhibitor, clade E (nexin, plasminogen activa
11	ZCCHC9	1.21	2e−07	1e−05	1 x 20	zinc finger, CCHC domain containing 9 [Source:HGNC Symb
12	NUDT14	1.16	8e−07	1e−05	1 x 21	nudix (nucleoside diphosphate linked moiety X)−type motif 14
13	RAB32	0.55	9e−07	1e−05	1 x 20	RAB32, member RAS oncogene family [Source:HGNC Symb
14	C19orf60	1.14	1e−06	1e−05	1 x 21	chromosome 19 open reading frame 60 [Source:HGNC Sym
15	TMEM123	0.46	1e−06	2e−05	1 x 21	transmembrane protein 123 [Source:HGNC Symbol;Acc:HG
16	PFN1	0.55	2e−06	2e−05	1 x 21	profilin 1 [Source:HGNC Symbol;Acc:HGNC:8881]
17	OGFOD3	1.11	2e−06	4e−05	1 x 21	2−oxoglutarate and iron−dependent oxygenase domain conta
18	PEX10	1.08	4e−06	4e−05	1 x 20	peroxisomal biogenesis factor 10 [Source:HGNC Symbol;Acc
19	NT5C3B	1.06	4e−06	4e−05	1 x 20	5'−nucleotidase, cytosolic IIIB [Source:HGNC Symbol;Acc:H
20	PIGY	0.48	6e−06	4e−05	1 x 20	phosphatidylinositol glycan anchor biosynthesis, class Y [Sou



H1_mel

Local Summary

%DE = 0.71

metagenes = 5

genes = 125

genes in genesets = 124

genes with fdr < 0.1 = 71 (16 + / 55 −)

genes with fdr < 0.05 = 60 (13 + / 47 −)

genes with fdr < 0.01 = 27 (5 + / 22 −)

<r> metagenes = 0.99

<r> genes = 0.19

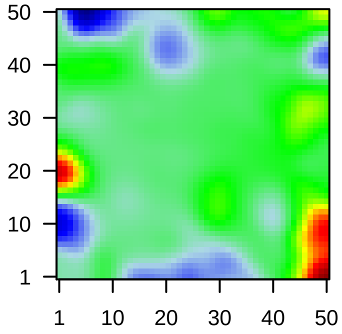
<FC> = −0.26

<shrinkage−t> = −3.99

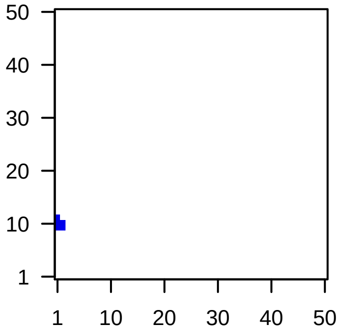
<p−value> = 0.01

<fdr> = 0.55

Profile



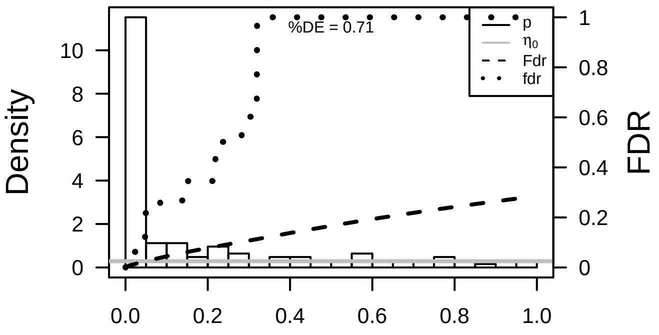
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	PPARGC1A	−1.35	1e−10	1e−07	1 x 10	peroxisome proliferator−activated receptor gamma, coactivat
2	SNAI2	−1.24	6e−09	1e−07	1 x 11	snail family zinc finger 2 [Source:HGNC Symbol;Acc:HGNC:1
3	PIK3CB	−1.16	7e−09	6e−07	1 x 11	phosphatidylinositol−4,5−bisphosphate 3−kinase, catalytic su
4	SOCS6	−1.2	2e−08	1e−05	1 x 11	suppressor of cytokine signaling 6 [Source:HGNC Symbol;Ac
5	BAIAP2	−1.16	4e−07	5e−05	1 x 12	BAI1−associated protein 2 [Source:HGNC Symbol;Acc:HGN
6	C4orf45	1.12	2e−06	1e−04	1 x 11	chromosome 4 open reading frame 45 [Source:HGNC Symb
7	SLC7A5	−1.05	6e−06	1e−04	1 x 11	solute carrier family 7 (amino acid transporter light chain, L s
8	SAT1	0.42	8e−06	4e−04	1 x 11	spermidine/spermine N1−acetyltransferase 1 [Source:HGNC
9	ATP6V0A1	0.73	3e−05	4e−04	1 x 10	ATPase, H+ transporting, lysosomal V0 subunit a1 [Source:H
10	GALNT3	−0.97	4e−05	4e−04	1 x 12	polypeptide N−acetylgalactosaminyltransferase 3 [Source:HG
11	ARAP1	−0.96	4e−05	4e−04	1 x 11	ArfGAP with RhoGAP domain, ankyrin repeat and PH domai
12	SORD	−0.93	7e−05	4e−04	1 x 11	sorbitol dehydrogenase [Source:HGNC Symbol;Acc:HGNC:1
13	SORBS1	−0.93	7e−05	4e−04	1 x 12	sorbin and SH3 domain containing 1 [Source:HGNC Symbol;
14	RINT1	−0.92	8e−05	4e−04	2 x 11	RAD50 interactor 1 [Source:HGNC Symbol;Acc:HGNC:2187
15	TOM1	−0.92	9e−05	1e−03	2 x 10	target of myb1 (chicken) [Source:HGNC Symbol;Acc:HGNC:1
16	DSTYK	−0.79	1e−04	3e−03	1 x 12	dual serine/threonine and tyrosine protein kinase [Source:HG
17	FAM63B	−0.84	3e−04	3e−03	1 x 11	family with sequence similarity 63, member B [Source:HGNC
18	TDRD7	−0.83	4e−04	3e−03	1 x 11	tudor domain containing 7 [Source:HGNC Symbol;Acc:HGNC
19	IRF4	−0.83	4e−04	3e−03	1 x 11	interferon regulatory factor 4 [Source:HGNC Symbol;Acc:HG
20	SIAH1	−0.83	4e−04	4e−03	1 x 12	siah E3 ubiquitin protein ligase 1 [Source:HGNC Symbol;Acc

p−values



H1_mel

Local Summary

%DE = 0.88

metagenes = 14

genes = 192

genes in genesets = 192

genes with fdr < 0.1 = 143 (18 + / 125 −)

genes with fdr < 0.05 = 121 (16 + / 105 −)

genes with fdr < 0.01 = 68 (10 + / 58 −)

<r> metagenes = 0.98

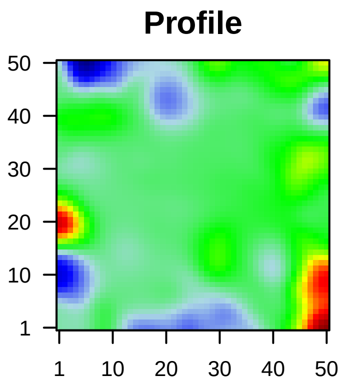
<r> genes = 0.4

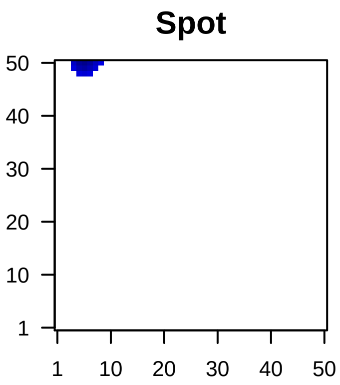
<FC> = −0.38

<shrinkage−t> = −6.22

<p−value> = 0.01

<fdr> = 0.55





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CDKN3	−1.65	2e−16	2e−15	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
2	STMN1	−0.92	2e−16	2e−15	5 x 50	stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]
3	TK1	−1.55	2e−16	2e−15	4 x 50	thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:HGN
4	TUBB4B	−1.37	6e−14	3e−07	7 x 50	tubulin, beta 4B class IVb [Source:HGNC Symbol;Acc:HGNC
5	MAD2L1	−1.18	1e−08	3e−07	5 x 50	MAD2 mitotic arrest deficient−like 1 (yeast) [Source:HGNC S
6	RAD21	−1.07	3e−08	3e−07	9 x 50	RAD21 homolog (S. pombe) [Source:HGNC Symbol;Acc:HG
7	CENPN	−1.22	3e−08	5e−07	4 x 50	centromere protein N [Source:HGNC Symbol;Acc:HGNC:308
8	PRC1	−1.2	8e−08	5e−07	5 x 50	protein regulator of cytokinesis 1 [Source:HGNC Symbol;Acc
9	TRIP13	−1.19	8e−08	5e−06	5 x 50	thyroid hormone receptor interactor 13 [Source:HGNC Symb
10	NUSAP1	−1.17	3e−07	5e−06	6 x 50	nucleolar and spindle associated protein 1 [Source:HGNC Sy
11	TMEM106C	−0.62	5e−07	9e−06	5 x 48	transmembrane protein 106C [Source:HGNC Symbol;Acc:HG
12	ZWINT	−1.13	9e−07	2e−05	5 x 50	ZW10 interacting kinetochore protein [Source:HGNC Symbol;
13	CDK1	−1.11	2e−06	2e−05	5 x 50	cyclin−dependent kinase 1 [Source:HGNC Symbol;Acc:HGN
14	ARL6IP1	−0.68	3e−06	2e−05	9 x 50	ADP−ribosylation factor−like 6 interacting protein 1 [Source:H
15	SMC2	−1.01	3e−06	8e−05	5 x 50	structural maintenance of chromosomes 2 [Source:HGNC Sy
16	KIF23	−1.04	9e−06	8e−05	6 x 50	kinesin family member 23 [Source:HGNC Symbol;Acc:HGNC
17	FAM111A	−1.02	1e−05	8e−05	4 x 50	family with sequence similarity 111, member A [Source:HGN
18	ASF1B	−1.02	1e−05	1e−04	4 x 50	anti−silencing function 1B histone chaperone [Source:HGNC
19	DEPDC1B	1	2e−05	1e−04	7 x 50	DEP domain containing 1B [Source:HGNC Symbol;Acc:HGN
20	WDR34	−0.99	2e−05	1e−04	5 x 50	WD repeat domain 34 [Source:HGNC Symbol;Acc:HGNC:28