E10_mel

Global Summary

%DE = 0.21

genes with fdr < 0.2 = 2759 (1619 + / 1140 −)

genes with fdr < 0.1 = 2013 (1206 + / 807 −)

genes with fdr < 0.05 = 1551 (953 + / 598 −)

genes with fdr < 0.01 = 1000 (616 + / 384 −)

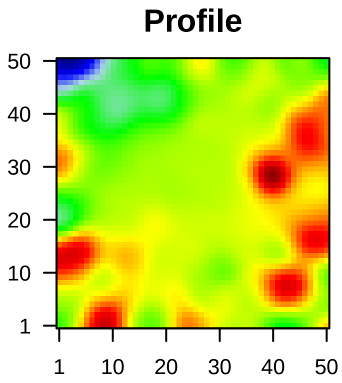
genes in genesets = 14839

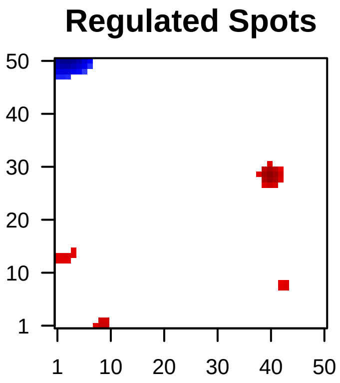
<FC> = 0

<shrinkage−t> = −0.04

<p−value> = 0.08

<fdr> = 0.79



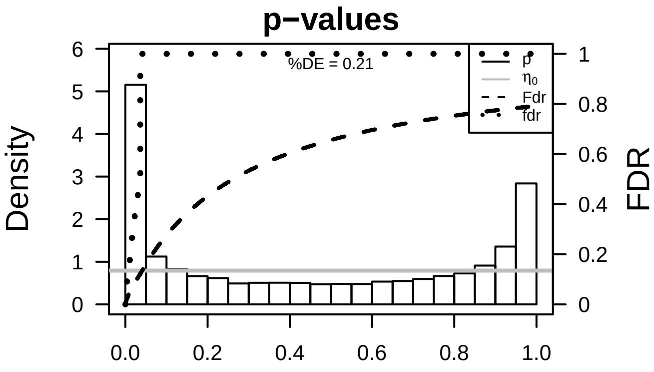


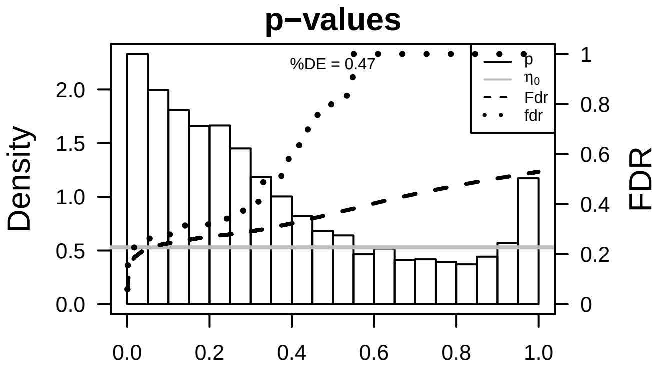
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	AKR1B1	−1.52	2e−16	8e−14	12 x 40	aldo−keto reductase family 1, member B1 (aldose reductase)
2	APOO	−1.69	2e−16	8e−14	2 x 46	apolipoprotein O [Source:HGNC Symbol;Acc:HGNC:28727]
3	ARL16	−1.63	2e−16	8e−14	50 x 50	ADP−ribosylation factor−like 16 [Source:HGNC Symbol;Acc:
4	ATIC	−1.71	2e−16	8e−14	44 x 50	5−aminoimidazole−4−carboxamide ribonucleotide formyltrans
5	AVPI1	−1.8	2e−16	8e−14	49 x 50	arginine vasopressin−induced 1 [Source:HGNC Symbol;Acc:
6	AZIN1	−1.8	2e−16	8e−14	4 x 41	antizyme inhibitor 1 [Source:HGNC Symbol;Acc:HGNC:1643
7	CACYBP	−1.26	2e−16	8e−14	8 x 44	calcyclin binding protein [Source:HGNC Symbol;Acc:HGNC:
8	CAMTA1	−1.85	2e−16	8e−14	3 x 45	calmodulin binding transcription activator 1 [Source:HGNC S
9	CCT6A	−1.03	2e−16	8e−14	6 x 41	chaperonin containing TCP1, subunit 6A (zeta 1) [Source:HG
10	CDKN3	−1.65	2e−16	8e−14	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
11	DEK	−1.53	2e−16	8e−14	2 x 50	DEK proto−oncogene [Source:HGNC Symbol;Acc:HGNC:27
12	EFTUD2	−1.92	2e−16	8e−14	13 x 42	elongation factor Tu GTP binding domain containing 2 [Sourc
13	FAM96B	−1.85	2e−16	8e−14	43 x 47	family with sequence similarity 96, member B [Source:HGNC
14	GLRX3	−1.72	2e−16	8e−14	4 x 42	glutaredoxin 3 [Source:HGNC Symbol;Acc:HGNC:15987]
15	GNAI1	−1.49	2e−16	8e−14	42 x 1	guanine nucleotide binding protein (G protein), alpha inhibitin
16	GTF3A	−1.76	2e−16	8e−14	1 x 20	general transcription factor IIIA [Source:HGNC Symbol;Acc:H
17	H2AFZ	−0.9	2e−16	8e−14	7 x 48	H2A histone family, member Z [Source:HGNC Symbol;Acc:H
18	HDDC2	−1.45	2e−16	8e−14	20 x 44	HD domain containing 2 [Source:HGNC Symbol;Acc:HGNC:
19	KTN1	−1.96	2e−16	8e−14	32 x 11	kinectin 1 (kinesin receptor) [Source:HGNC Symbol;Acc:HGN
20	MRPS6	−1.89	2e−16	8e−14	50 x 3	mitochondrial ribosomal protein S6 [Source:HGNC Symbol;A

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	4.29	0.006	85	BP	circadian rhythm
2	4.19	0.006	696	Chr	Chr 5
3	3.92	0.008	595	TF	ICGC_NrsfPcr2_targets
4	3.72	0.009	39	GSEA C2	CHANDRAN_METASTASIS_TOP50_DN
5	3.7	0.010	283	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
6	3.69	0.010	155	GSEA C2	MIKKELSEN_NPC_HCP_WITH_H3K4ME3_AND_H3K27ME3
7	3.62	0.010	15	GSEA C2	BIOCARTA_RARRXR_PATHWAY
8	3.61	0.010	930	GSEA C2	NUYTTEN_EZH2_TARGETS_UP
9	3.58	0.011	11	BP	macroautophagy
10	3.57	0.011	9653	Colon Cancer	Ecb_Colon
11	3.55	0.011	5155	Colon Cancer	EcbWk1_Colon
12	3.55	0.011	44	GSEA C2	REACTOME_CHONDROITIN_SULFATE_DERMATAN_SULFATE_
13	3.53	0.011	3396	Lymphoma	HOPP_Repressed
14	3.53	0.011	3081	Brain	Mid_Frontal_Lobe_ZNF
15	3.52	0.011	196	GSEA C2	CHANG_CORE_SERUM_RESPONSE_DN
16	3.51	0.011	42	CC	neuromuscular junction
17	3.46	0.012	422	GSEA C2	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_5
18	3.46	0.012	453	GSEA C2	WEST_ADRENOCORTICAL_TUMOR_DN
19	3.46	0.012	10	BP	mammary gland epithelial cell proliferation
20	3.45	0.012	24	GSEA C2	REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION
Underexpressed					
1	−11.69	1e−04	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
2	−11.41	2e−04	242	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
3	−10.94	2e−04	291	GSEA C2	HORIUCHI_WTAP_TARGETS_DN
4	−10.93	2e−04	197	HM	HALLMARK_E2F_TARGETS
5	−10.9	2e−02	16	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
6	−10.55	2e−04	724	GSEA C2	PUJANA_CHEK2_PCC_NETWORK
7	−10.44	2e−04	305	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
8	−10.32	2e−04	124	GSEA C2	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
9	−10.3	2e−04	81	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
10	−10.26	2e−04	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
11	−10.26	2e−04	436	GSEA C2	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
12	−10.26	2e−04	267	GSEA C2	ZHANG_TLX_TARGETS_60HR_DN
13	−10.17	2e−04	390	GSEA C2	PUJANA_BRCA2_PCC_NETWORK
14	−10.14	2e−04	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
15	−10.01	3e−04	1192	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
16	−9.91	3e−04	327	GSEA C2	BLUM_RESPONSE_TO_SALIRASIB_DN
17	−9.79	3e−04	216	GSEA C2	MARKEY_RB1_ACUTE_LOF_DN
18	−9.76	3e−04	72	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
19	−9.76	3e−04	162	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
20	−9.75	3e−04	99	GSEA C2	BURTON_ADIPOGENESIS_3





E10_mel

Local Summary

%DE = 0.61

metagenes = 5

genes = 94

genes in genesets = 93

genes with fdr < 0.1 = 36 (34 + / 2 −)

genes with fdr < 0.05 = 33 (31 + / 2 −)

genes with fdr < 0.01 = 22 (21 + / 1 −)

<r> metagenes = 0.97

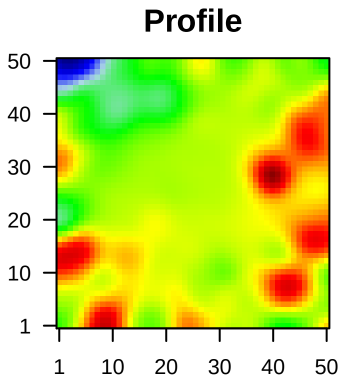
<r> genes = 0.11

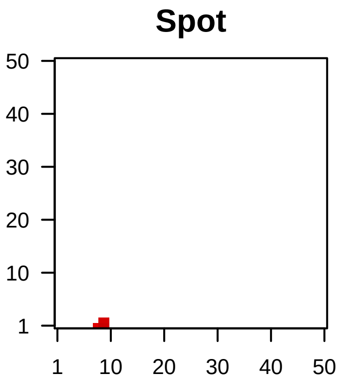
<FC> = 0.32

<shrinkage−t> = 5.03

<p−value> = 0.02

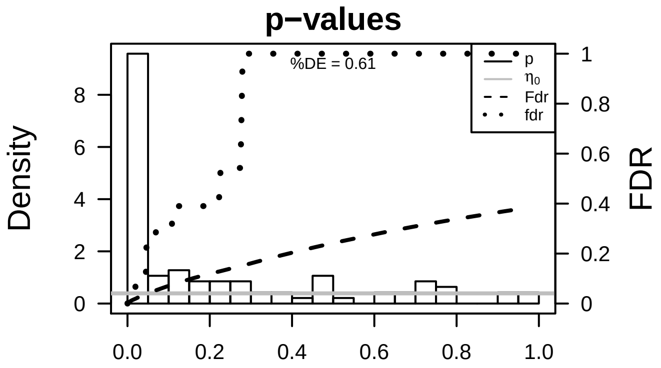
<fdr> = 0.62





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	IL16	1.56	5e−09	9e−06	10 x 1	interleukin 16 [Source:HGNC Symbol;Acc:HGNC:5980]
2	PDZRN3	1.38	3e−07	4e−05	9 x 1	PDZ domain containing ring finger 3 [Source:HGNC Symbol;
3	IRF9	1.29	1e−06	8e−05	10 x 2	interferon regulatory factor 9 [Source:HGNC Symbol;Acc:HG
4	IRGQ	1.21	6e−06	8e−05	8 x 1	immunity−related GTPase family, Q [Source:HGNC Symbol;A
5	TRIQK	1.2	7e−06	8e−05	10 x 1	triple QxxK/R motif containing [Source:HGNC Symbol;Acc:H
6	ERBB3	1.19	8e−06	1e−03	8 x 1	erb−b2 receptor tyrosine kinase 3 [Source:HGNC Symbol;Ac
7	MTERF4	1.08	5e−05	1e−03	10 x 1	mitochondrial transcription termination factor 4 [Source:HGN
8	NABP1	1.07	6e−05	1e−03	10 x 1	nucleic acid binding protein 1 [Source:HGNC Symbol;Acc:HG
9	ADARB1	1.02	1e−04	1e−03	10 x 1	adenosine deaminase, RNA−specific, B1 [Source:HGNC Sy
10	SIPA1L2	1.02	1e−04	3e−03	9 x 1	signal−induced proliferation−associated 1 like 2 [Source:HGN
11	ADNP2	0.96	3e−04	3e−03	8 x 1	ADNP homeobox 2 [Source:HGNC Symbol;Acc:HGNC:2380
12	POLR1C	0.9	3e−04	3e−03	9 x 1	polymerase (RNA) I polypeptide C, 30kDa [Source:HGNC Sy
13	MTHFR	0.96	3e−04	4e−03	8 x 1	methylenetetrahydrofolate reductase (NAD(P)H) [Source:HG
14	TECPR2	0.93	5e−04	4e−03	9 x 1	tectonin beta−propeller repeat containing 2 [Source:HGNC S
15	MTPAP	0.85	6e−04	4e−03	9 x 1	mitochondrial poly(A) polymerase [Source:HGNC Symbol;Ac
16	MSTO1	0.9	7e−04	4e−03	9 x 2	misato 1, mitochondrial distribution and morphology regulator
17	TMCO6	0.9	8e−04	8e−03	8 x 1	transmembrane and coiled−coil domains 6 [Source:HGNC Sy
18	UTP6	0.65	1e−03	8e−03	9 x 1	UTP6, small subunit (SSU) processome component, homolo
19	GPHN	0.86	1e−03	8e−03	9 x 1	gephyrin [Source:HGNC Symbol;Acc:HGNC:15465]
20	RBM33	0.84	2e−03	8e−03	10 x 1	RNA binding motif protein 33 [Source:HGNC Symbol;Acc:HG



E10_mel

Local Summary

%DE = 0.57

metagenes = 4

genes = 25

genes in genesets = 25

genes with fdr < 0.1 = 12 (12 + / 0 −)

genes with fdr < 0.05 = 12 (12 + / 0 −)

genes with fdr < 0.01 = 10 (10 + / 0 −)

<r> metagenes = 0.99

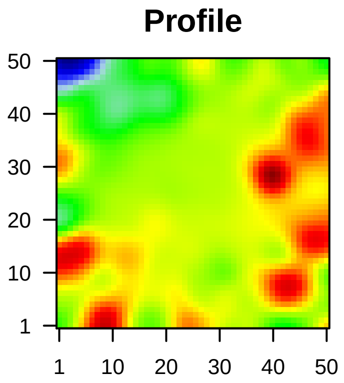
<r> genes = 0.19

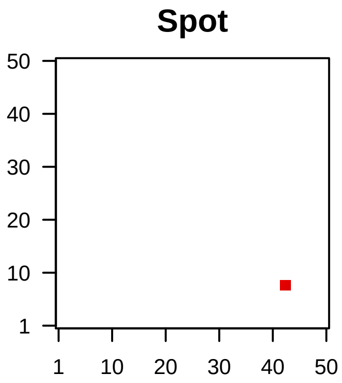
<FC> = 0.55

<shrinkage−t> = 8.4

<p−value> = 0.01

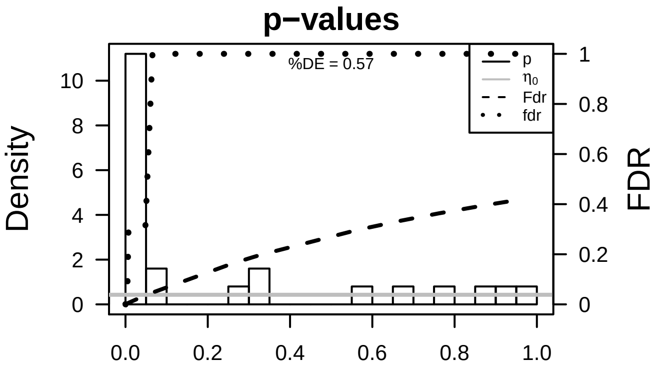
<fdr> = 0.5





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	GPR83	1.39	2e−07	2e−05	43 x 9	G protein−coupled receptor 83 [Source:HGNC Symbol;Acc:H
2	EPB41L5	1.27	2e−06	4e−05	43 x 8	erythrocyte membrane protein band 4.1 like 5 [Source:HGNC
3	CNTN4	1.21	5e−06	2e−04	43 x 8	contactin 4 [Source:HGNC Symbol;Acc:HGNC:2174]
4	ALS2	1.08	6e−05	2e−04	43 x 9	amyotrophic lateral sclerosis 2 (juvenile) [Source:HGNC Sym
5	MANBA	1.07	6e−05	2e−04	43 x 8	mannosidase, beta A, lysosomal [Source:HGNC Symbol;Acc
6	TNIP1	1.07	6e−05	7e−04	42 x 8	TNFAIP3 interacting protein 1 [Source:HGNC Symbol;Acc:H
7	TP53INP2	1.02	1e−04	8e−03	42 x 9	tumor protein p53 inducible nuclear protein 2 [Source:HGNC
8	FST	0.87	1e−03	8e−03	43 x 9	follistatin [Source:HGNC Symbol;Acc:HGNC:3971]
9	CNST	0.83	2e−03	8e−03	43 x 9	consortin, connexin sorting protein [Source:HGNC Symbol;A
10	BASP1	0.79	3e−03	8e−03	42 x 9	brain abundant, membrane attached signal protein 1 [Source
11	FBXL7	0.79	3e−03	1e−02	43 x 8	F−box and leucine−rich repeat protein 7 [Source:HGNC Sym
12	ANKS1A	0.76	4e−03	3e−02	43 x 9	ankyrin repeat and sterile alpha motif domain containing 1A [
13	TIGD6	0.72	7e−03	3e−01	42 x 8	tigger transposable element derived 6 [Source:HGNC Symbo
14	ERO1LB	0.53	5e−02	3e−01	42 x 9	ERO1−like beta (S. cerevisiae) [Source:HGNC Symbol;Acc:H
15	GNL3L	−0.49	7e−02	1e+00	42 x 8	guanine nucleotide binding protein−like 3 (nucleolar)−like [So
16	DCAF4	0.49	7e−02	1e+00	43 x 9	DDB1 and CUL4 associated factor 4 [Source:HGNC Symbol;
17	UBE4B	0.3	3e−01	1e+00	42 x 9	ubiquitination factor E4B [Source:HGNC Symbol;Acc:HGNC:
18	UBE4A	0.27	3e−01	1e+00	42 x 8	ubiquitination factor E4A [Source:HGNC Symbol;Acc:HGNC:
19	EPS15	0.26	3e−01	1e+00	43 x 8	epidermal growth factor receptor pathway substrate 15 [Sour
20	FAXDC2	−0.16	6e−01	1e+00	42 x 9	fatty acid hydroxylase domain containing 2 [Source:HGNC Sy



E10_mel

Local Summary

%DE = 0.8

metagenes = 8

genes = 77

genes in genesets = 77

genes with fdr < 0.1 = 33 (30 + / 3 −)

genes with fdr < 0.05 = 31 (28 + / 3 −)

genes with fdr < 0.01 = 18 (16 + / 2 −)

<r> metagenes = 0.97

<r> genes = 0.11

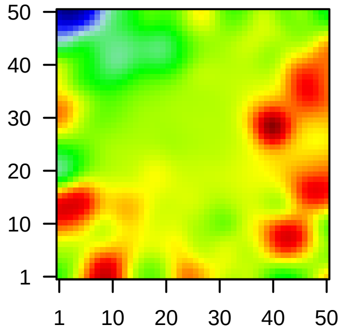
<FC> = 0.31

<shrinkage−t> = 5.25

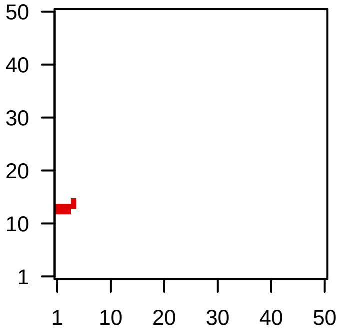
<p−value> = 0.01

<fdr> = 0.59

Profile



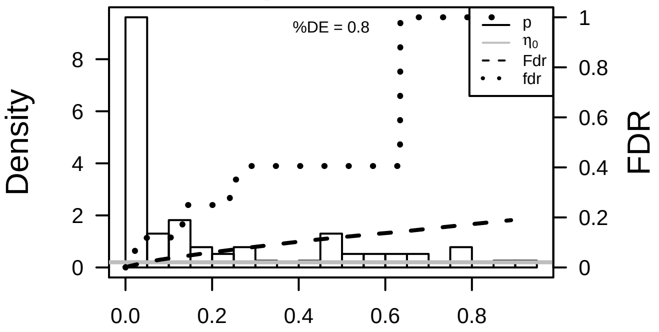
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	STAT6	1.71	2e−10	3e−08	3 x 13	signal transducer and activator of transcription 6, interleukin−
2	SLC25A14	1.6	2e−09	8e−07	4 x 14	solute carrier family 25 (mitochondrial carrier, brain), member
3	HMG20A	1.45	5e−08	2e−05	1 x 13	high mobility group 20A [Source:HGNC Symbol;Acc:HGNC:5
4	ECHDC2	1.27	2e−06	2e−05	1 x 14	enoyl CoA hydratase domain containing 2 [Source:HGNC Sy
5	BEAN1	1.27	2e−06	5e−05	3 x 14	brain expressed, associated with NEDD4, 1 [Source:HGNC S
6	MRPS2	−1.18	6e−06	5e−05	1 x 13	mitochondrial ribosomal protein S2 [Source:HGNC Symbol;A
7	ZNF589	1.17	1e−05	5e−05	1 x 14	zinc finger protein 589 [Source:HGNC Symbol;Acc:HGNC:16
8	ID2	0.47	1e−05	5e−05	1 x 13	inhibitor of DNA binding 2, dominant negative helix−loop−heli
9	VAV3	1.15	2e−05	3e−04	1 x 14	vav 3 guanine nucleotide exchange factor [Source:HGNC Sy
10	SMEK1	−1.07	5e−05	3e−04	1 x 13	SMEK homolog 1, suppressor of mek1 (Dictyostelium) [Sourc
11	HDHD3	1.07	6e−05	4e−04	1 x 13	haloacid dehalogenase−like hydrolase domain containing 3 [
12	PLEKHH1	1.05	8e−05	8e−04	2 x 13	pleckstrin homology domain containing, family H (with MyTH
13	KMT2C	1	1e−04	1e−03	4 x 15	lysine (K)−specific methyltransferase 2C [Source:HGNC Sym
14	CHST12	0.99	2e−04	1e−03	4 x 15	carbohydrate (chondroitin 4) sulfotransferase 12 [Source:HGN
15	GPR137B	0.97	3e−04	2e−03	3 x 13	G protein−coupled receptor 137B [Source:HGNC Symbol;Ac
16	KIAA1551	0.93	5e−04	2e−03	2 x 13	KIAA1551 [Source:HGNC Symbol;Acc:HGNC:25559]
17	LIN52	0.92	6e−04	2e−03	1 x 13	lin−52 DREAM MuvB core complex component [Source:HGN
18	RAB18	0.83	6e−04	4e−03	1 x 14	RAB18, member RAS oncogene family [Source:HGNC Symb
19	PFKFB2	0.54	9e−04	1e−02	2 x 13	6−phosphofructo−2−kinase/fructose−2,6−biphosphatase 2 [S
20	KIAA1456	0.82	2e−03	1e−02	2 x 14	KIAA1456 [Source:HGNC Symbol;Acc:HGNC:26725]

p−values



E10_mel

Local Summary

%DE = 0.97

metagenes = 17

genes = 106

genes in genesets = 105

genes with fdr < 0.1 = 102 (102 + / 0 −)

genes with fdr < 0.05 = 102 (102 + / 0 −)

genes with fdr < 0.01 = 84 (84 + / 0 −)

<r> metagenes = 0.9

<r> genes = 0.39

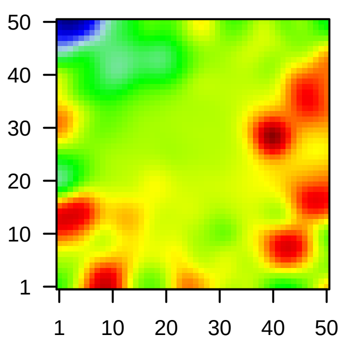
<FC> = 0.9

<shrinkage−t> = 14.29

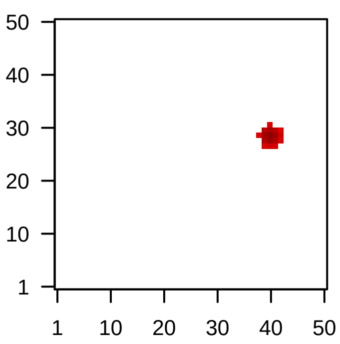
<p−value> = 0

<fdr> = 0.28

Profile



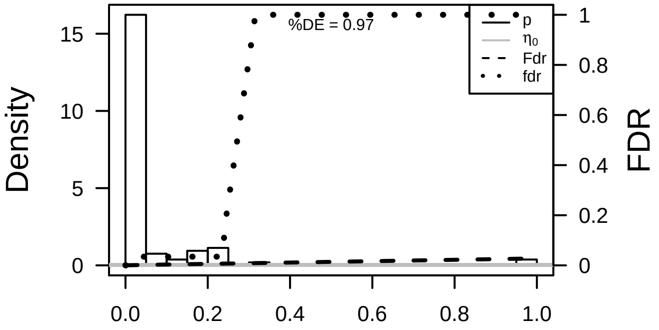
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ACTG1	0.76	2e−12	3e−12	39 x 29	actin gamma 1 [Source:HGNC Symbol;Acc:HGNC:144]
2	UBB	1.88	2e−12	6e−12	40 x 29	ubiquitin B [Source:HGNC Symbol;Acc:HGNC:12463]
3	IKZF4	1.85	4e−12	6e−12	40 x 29	IKAROS family zinc finger 4 (Eos) [Source:HGNC Symbol;Ac
4	MFSD2A	1.84	6e−12	2e−11	40 x 29	major facilitator superfamily domain containing 2A [Source:H
5	FGF9	1.81	1e−11	5e−11	40 x 29	fibroblast growth factor 9 [Source:HGNC Symbol;Acc:HGNC:
6	ZNF232	1.78	3e−11	2e−10	40 x 29	zinc finger protein 232 [Source:HGNC Symbol;Acc:HGNC:13
7	RAP1GAP2	1.73	8e−11	2e−09	40 x 29	RAP1 GTPase activating protein 2 [Source:HGNC Symbol;Ac
8	LMF1	1.65	6e−10	3e−09	40 x 29	lipase maturation factor 1 [Source:HGNC Symbol;Acc:HGNC
9	HOXA10	1.61	2e−09	7e−09	40 x 29	homeobox A10 [Source:HGNC Symbol;Acc:HGNC:5100]
10	WIF1	1.55	6e−09	7e−09	40 x 29	WNT inhibitory factor 1 [Source:HGNC Symbol;Acc:HGNC:1
11	BATF3	1.55	6e−09	1e−08	40 x 29	basic leucine zipper transcription factor, ATF−like 3 [Source:H
12	SDK1	1.53	1e−08	1e−08	40 x 29	sidekick cell adhesion molecule 1 [Source:HGNC Symbol;Ac
13	MLKL	1.52	1e−08	3e−08	40 x 29	mixed lineage kinase domain−like [Source:HGNC Symbol;Ac
14	C16orf45	1.49	2e−08	4e−08	40 x 29	chromosome 16 open reading frame 45 [Source:HGNC Sym
15	TTC24	1.45	5e−08	4e−08	40 x 29	tetratricopeptide repeat domain 24 [Source:HGNC Symbol;A
16	ZNF491	1.44	6e−08	4e−08	40 x 29	zinc finger protein 491 [Source:HGNC Symbol;Acc:HGNC:23
17	FAM72A	1.44	7e−08	4e−08	40 x 29	family with sequence similarity 72, member A [Source:HGNC
18	IL1R1	1.44	7e−08	2e−07	40 x 29	interleukin 1 receptor, type I [Source:HGNC Symbol;Acc:HG
19	TDRD15	1.4	1e−07	2e−07	40 x 29	tudor domain containing 15 [Source:HGNC Symbol;Acc:HGN
20	IL4R	1.39	2e−07	2e−07	40 x 29	interleukin 4 receptor [Source:HGNC Symbol;Acc:HGNC:601

p−values



E10_mel

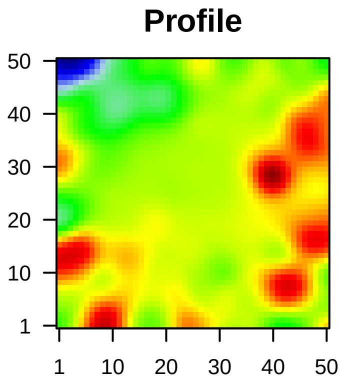
Local Summary

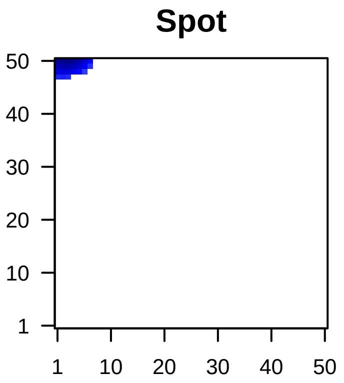
%DE = 0.9
metagenes = 23
genes = 367
genes in genesets = 366

genes with fdr < 0.1 = 269 (35 + / 234 −)
genes with fdr < 0.05 = 255 (31 + / 224 −)
genes with fdr < 0.01 = 139 (12 + / 127 −)

<r> metagenes = 0.92
<r> genes = 0.28

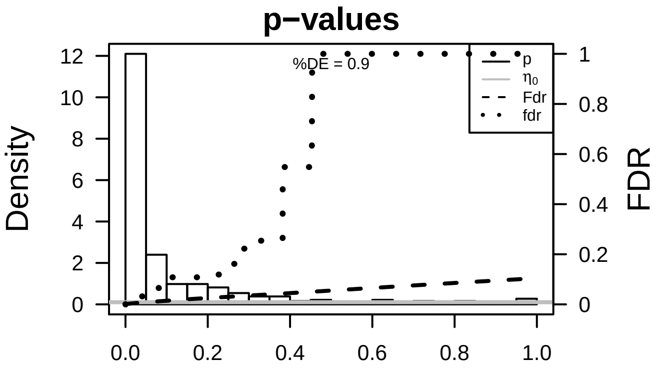
<FC> = −0.48
<shrinkage−t> = −7.83
<p−value> = 0
<fdr> = 0.52


Profile


Spot

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	DEK	−1.53	2e−16	2e−15	2 x 50	DEK proto−oncogene [Source:HGNC Symbol;Acc:HGNC:27
3	PCNA	−1.64	2e−16	2e−15	2 x 50	proliferating cell nuclear antigen [Source:HGNC Symbol;Acc:
4	TUBG1	−1.69	2e−16	2e−15	2 x 49	tubulin, gamma 1 [Source:HGNC Symbol;Acc:HGNC:12417]
5	NASP	−1.53	3e−15	4e−12	1 x 48	nuclear autoantigenic sperm protein (histone−binding) [Sourc
6	RRM1	−1.58	9e−14	8e−12	2 x 50	ribonucleotide reductase M1 [Source:HGNC Symbol;Acc:HG
7	CSE1L	−1.38	3e−13	8e−12	3 x 49	CSE1 chromosome segregation 1−like (yeast) [Source:HGN
8	TK1	−1.55	5e−13	3e−09	4 x 50	thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:HGN
9	HAT1	−1.34	1e−10	3e−09	1 x 50	histone acetyltransferase 1 [Source:HGNC Symbol;Acc:HGN
10	STMN1	−0.69	1e−10	1e−08	5 x 50	stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]
11	HLTF	−1.43	7e−10	1e−08	3 x 48	helicase−like transcription factor [Source:HGNC Symbol;Acc:
12	NUPL1	−1.43	8e−10	2e−08	1 x 48	nucleoporin like 1 [Source:HGNC Symbol;Acc:HGNC:20261]
13	NUP54	−1.41	1e−09	7e−08	1 x 50	nucleoporin 54kDa [Source:HGNC Symbol;Acc:HGNC:17359
14	CKS1B	−1.39	3e−09	2e−07	5 x 50	CDC28 protein kinase regulatory subunit 1B [Source:HGNC
15	GMPS	−1.36	7e−09	3e−07	1 x 48	guanine monphosphate synthase [Source:HGNC Symbol;Ac
16	SAAL1	−1.35	2e−08	3e−07	1 x 47	serum amyloid A−like 1 [Source:HGNC Symbol;Acc:HGNC:2
17	MCM3	−1.21	2e−08	3e−07	1 x 50	minichromosome maintenance complex component 3 [Sourc
18	FEN1	−1.34	3e−08	1e−06	1 x 50	flap structure−specific endonuclease 1 [Source:HGNC Symb
19	EMP2	−1.31	8e−08	1e−06	2 x 50	epithelial membrane protein 2 [Source:HGNC Symbol;Acc:H
20	CKLF	−1.31	9e−08	1e−06	3 x 49	chemokine−like factor [Source:HGNC Symbol;Acc:HGNC:13


p−values