F12_mel

Global Summary

%DE = 0.2

genes with fdr < 0.2 = 2491 (1494 + / 997 −)

genes with fdr < 0.1 = 2157 (1311 + / 846 −)

genes with fdr < 0.05 = 1724 (1063 + / 661 −)

genes with fdr < 0.01 = 1146 (688 + / 458 −)

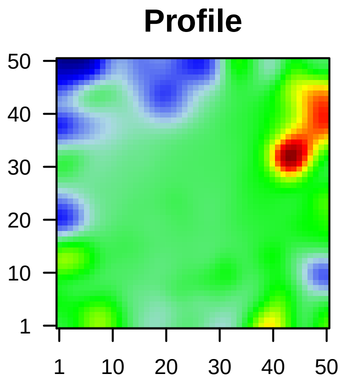
genes in genesets = 14839

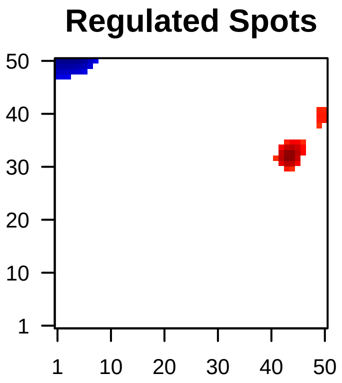
<FC> = 0

<shrinkage−t> = −0.03

<p−value> = 0.08

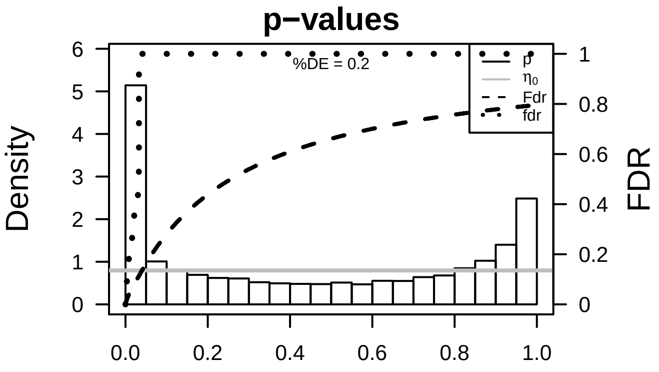
<fdr> = 0.8





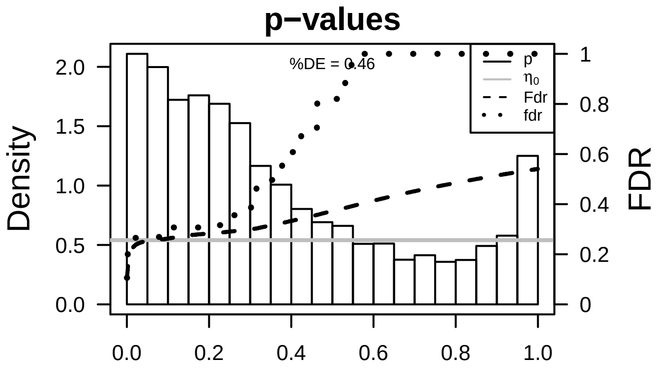
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	APOO	−1.73	2e−16	9e−14	2 x 46	apolipoprotein O [Source:HGNC Symbol;Acc:HGNC:28727]
2	ARHGAP8	−1.6	2e−16	9e−14	1 x 43	Rho GTPase activating protein 8 [Source:HGNC Symbol;Acc:
3	ARL6IP4	−1.42	2e−16	9e−14	5 x 36	ADP−ribosylation factor−like 6 interacting protein 4 [Source:H
4	ATP6V0A1	−1.65	2e−16	9e−14	1 x 10	ATPase, H+ transporting, lysosomal V0 subunit a1 [Source:H
5	CCL18	2.45	2e−16	9e−14	48 x 41	chemokine (C−C motif) ligand 18 (pulmonary and activation−
6	CDKN3	−1.65	2e−16	9e−14	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
7	CFAP20	−1.63	2e−16	9e−14	40 x 50	cilia and flagella associated protein 20 [Source:HGNC Symbo
8	CIAPIN1	−1.66	2e−16	9e−14	27 x 50	cytokine induced apoptosis inhibitor 1 [Source:HGNC Symbol
9	CMC2	−1.38	2e−16	9e−14	5 x 44	C−x(9)−C motif containing 2 [Source:HGNC Symbol;Acc:HGN
10	COLGALT1	−1.74	2e−16	9e−14	18 x 48	collagen beta(1−O)galactosyltransferase 1 [Source:HGNC Sy
11	DCAF13	−1.6	2e−16	9e−14	1 x 1	DDB1 and CUL4 associated factor 13 [Source:HGNC Symbol
12	DCT	1.33	2e−16	9e−14	1 x 11	dopachrome tautomerase [Source:HGNC Symbol;Acc:HGNC
13	DEK	−1.51	2e−16	9e−14	2 x 50	DEK proto−oncogene [Source:HGNC Symbol;Acc:HGNC:27
14	EXOSC8	−1.71	2e−16	9e−14	1 x 50	exosome component 8 [Source:HGNC Symbol;Acc:HGNC:17
15	GLRX3	−1.72	2e−16	9e−14	4 x 42	glutaredoxin 3 [Source:HGNC Symbol;Acc:HGNC:15987]
16	M6PR	−0.88	2e−16	9e−14	3 x 41	mannose−6−phosphate receptor (cation dependent) [Source:
17	METTL23	−1.79	2e−16	9e−14	4 x 21	methyltransferase like 23 [Source:HGNC Symbol;Acc:HGNC:
18	MRPL22	−1.71	2e−16	9e−14	40 x 47	mitochondrial ribosomal protein L22 [Source:HGNC Symbol;
19	NQO2	−1.53	2e−16	9e−14	50 x 50	NAD(P)H dehydrogenase, quinone 2 [Source:HGNC Symbol;
20	NSFL1C	−1.63	2e−16	9e−14	22 x 44	NSFL1 (p97) cofactor (p47) [Source:HGNC Symbol;Acc:HGN



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	4.95	0.004	3396	Lymphoma	HOPP_Repressed
2	4.41	0.005	245	GSEA C2	WANG_SMARCE1_TARGETS_UP
3	4.33	0.006	472	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
4	4.28	0.006	20	BP	carbohydrate phosphorylation
5	4.22	0.006	1907	Brain	Fetal_TxTrans
6	4.08	0.007	12	MF	NADPH binding
7	4.08	0.007	16	GSEA C2	NIELSEN_GIST_AND_SYNOVIAL_SARCOMA_UP
8	4.06	0.007	302	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
9	4.03	0.007	453	GSEA C2	WEST_ADRENOCORTICAL_TUMOR_DN
10	3.96	0.008	350	Tissue	WIRTH_Nervous System
11	3.93	0.008	10	GSEA C2	TERAMOTO_OPN_TARGETS_CLUSTER_1
12	3.82	0.009	60	GSEA C2	PELLICCIOTTA_HDAC_IN_ANTIGEN_PRESENTATION_UP
13	3.76	0.009	1139	TF	HEBENSTREIT_low expression TF
14	3.69	0.010	503	GSEA C2	MARTINEZ_RB1_AND_TP53_TARGETS_UP
15	3.67	0.010	622	GSEA C2	LEE_BMP2_TARGETS_UP
16	3.62	0.010	618	GSEA C2	GOZGIT_ESR1_TARGETS_DN
17	3.62	0.010	414	GSEA C2	ZHENG_BOUND_BY_FOXP3
18	3.59	0.011	2185	Brain	Fetal_TssA
19	3.55	0.011	54	miRNA target	hsa−miR−513a−5p
20	3.55	0.011	1949	Brain	Fetal_TssF
Underexpressed					
1	−11.38	2e−04	1192	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
2	−11.08	2e−02	16	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
3	−11.01	2e−04	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
4	−10.97	2e−04	305	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
5	−10.87	2e−04	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
6	−10.61	2e−04	242	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
7	−9.96	3e−04	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
8	−9.88	3e−04	436	GSEA C2	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
9	−9.79	3e−04	197	HM	HALLMARK_E2F_TARGETS
10	−9.77	3e−04	145	GSEA C2	CHANG_CYCLING_GENES
11	−9.61	3e−04	96	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
12	−9.36	3e−04	54	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
13	−9.07	4e−04	72	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
14	−8.89	4e−04	155	GSEA C2	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
15	−8.84	4e−04	116	GSEA C2	MISSIAGLIA_REGULATED_BY_METHYLATION_DN
16	−8.68	5e−04	84	GSEA C2	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_6HR
17	−8.66	5e−04	216	GSEA C2	MARKEY_RB1_ACUTE_LOF_DN
18	−8.6	5e−04	124	GSEA C2	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
19	−8.53	5e−04	724	GSEA C2	PUJANA_CHEK2_PCC_NETWORK
20	−8.52	5e−04	99	GSEA C2	BURTON_ADIPOGENESIS_3



F12_mel

Local Summary

%DE = 0.92

metagenes = 25

genes = 151

genes in genesets = 151

genes with fdr < 0.1 = 134 (133 + / 1 −)

genes with fdr < 0.05 = 129 (129 + / 0 −)

genes with fdr < 0.01 = 116 (116 + / 0 −)

<r> metagenes = 0.91

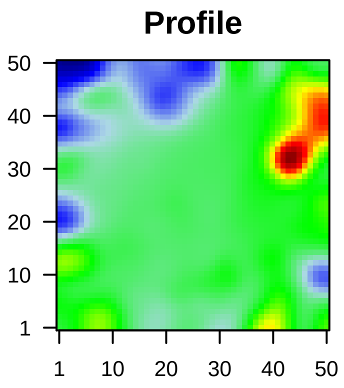
<r> genes = 0.22

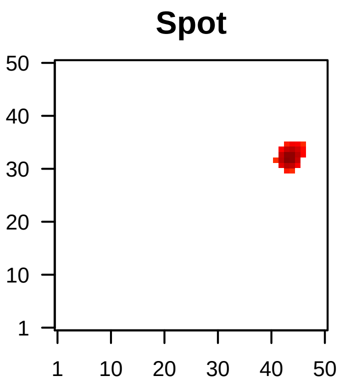
<FC> = 0.98

<shrinkage−t> = 15.2

<p−value> = 0

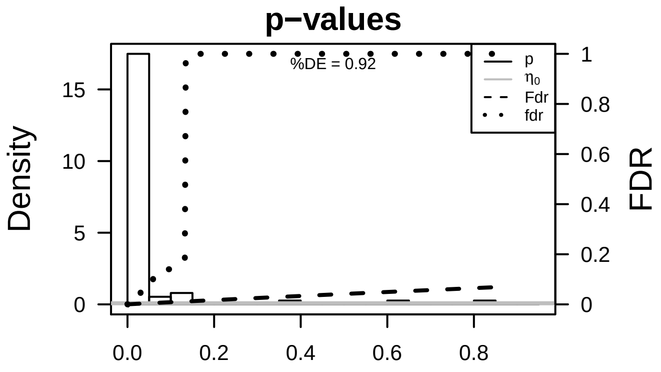
<fdr> = 0.18





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	GSG1L	1.94	5e−14	5e−12	43 x 32	GSG1−like [Source:HGNC Symbol;Acc:HGNC:28283]
2	OR10A2	1.85	7e−13	5e−12	43 x 32	olfactory receptor, family 10, subfamily A, member 2 [Source:
3	ALOX12B	1.84	1e−12	2e−11	43 x 32	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Sy
4	THSD7A	1.8	3e−12	5e−11	43 x 32	thrombospondin, type I, domain containing 7A [Source:HGNC
5	TOX	1.77	7e−12	5e−11	43 x 32	thymocyte selection−associated high mobility group box [Sou
6	CD33	1.74	1e−11	5e−11	44 x 32	CD33 molecule [Source:HGNC Symbol;Acc:HGNC:1659]
7	KLK6	1.74	2e−11	2e−10	43 x 32	kallikrein−related peptidase 6 [Source:HGNC Symbol;Acc:HG
8	SART1	1.71	3e−11	2e−10	43 x 33	squamous cell carcinoma antigen recognized by T cells [Sour
9	HIST1H4D	1.69	5e−11	3e−10	43 x 32	histone cluster 1, H4d [Source:HGNC Symbol;Acc:HGNC:47
10	LARGE	1.67	9e−11	3e−10	43 x 32	like−glycosyltransferase [Source:HGNC Symbol;Acc:HGNC:6
11	DNER	1.67	1e−10	3e−10	43 x 32	delta/notch−like EGF repeat containing [Source:HGNC Symb
12	KLRG1	1.66	1e−10	3e−10	44 x 32	killer cell lectin−like receptor subfamily G, member 1 [Source:
13	ZNF69	1.65	2e−10	3e−10	44 x 33	zinc finger protein 69 [Source:HGNC Symbol;Acc:HGNC:131
14	MX2	1.65	2e−10	3e−10	43 x 32	MX dynamin−like GTPase 2 [Source:HGNC Symbol;Acc:HG
15	MYBPHL	1.64	2e−10	2e−09	43 x 32	myosin binding protein H−like [Source:HGNC Symbol;Acc:HG
16	C1orf61	1.62	3e−10	5e−09	43 x 32	chromosome 1 open reading frame 61 [Source:HGNC Symb
17	LGI1	1.57	1e−09	5e−09	43 x 32	leucine−rich, glioma inactivated 1 [Source:HGNC Symbol;Ac
18	BRPF1	1.56	1e−09	5e−09	43 x 32	bromodomain and PHD finger containing, 1 [Source:HGNC S
19	TGFB2	1.55	2e−09	5e−09	43 x 32	transforming growth factor, beta 2 [Source:HGNC Symbol;Ac
20	DNASE1	1.54	2e−09	5e−09	43 x 34	deoxyribonuclease I [Source:HGNC Symbol;Acc:HGNC:2956



F12_mel

Local Summary

%DE = 0.7

metagenes = 7

genes = 97

genes in genesets = 97

genes with fdr < 0.1 = 57 (52 + / 5 −)

genes with fdr < 0.05 = 46 (42 + / 4 −)

genes with fdr < 0.01 = 30 (28 + / 2 −)

<r> metagenes = 0.98

<r> genes = 0.11

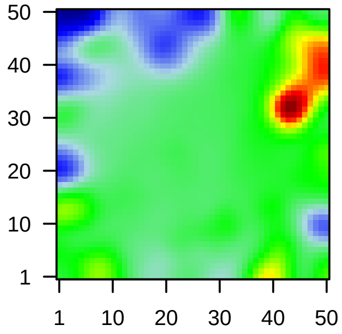
<FC> = 0.42

<shrinkage−t> = 6.97

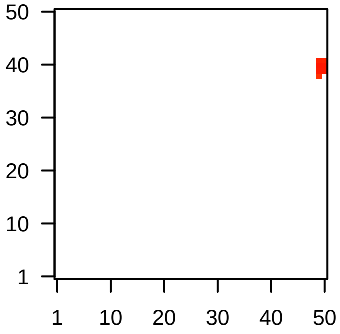
<p−value> = 0.01

<fdr> = 0.5

Profile



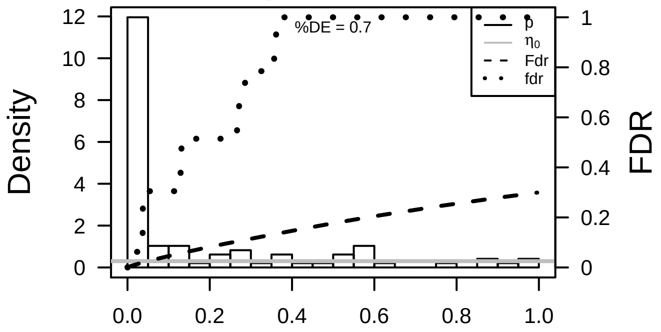
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CTSK	1.62	3e−10	7e−09	49 x 41	cathepsin K [Source:HGNC Symbol;Acc:HGNC:2536]
2	RNF217	1.6	5e−10	3e−06	50 x 39	ring finger protein 217 [Source:HGNC Symbol;Acc:HGNC:21
3	FBXO25	1.37	1e−07	1e−05	49 x 41	F−box protein 25 [Source:HGNC Symbol;Acc:HGNC:13596]
4	RUFY3	1.27	8e−07	1e−05	50 x 39	RUN and FYVE domain containing 3 [Source:HGNC Symbol;
5	BRD8	0.85	1e−06	2e−05	50 x 39	bromodomain containing 8 [Source:HGNC Symbol;Acc:HGN
6	PARN	1.23	2e−06	2e−05	50 x 39	poly(A)−specific ribonuclease [Source:HGNC Symbol;Acc:HG
7	SERPINB6	1.21	3e−06	2e−05	49 x 41	serpin peptidase inhibitor, clade B (ovalbumin), member 6 [S
8	TAF1D	1.1	4e−06	2e−05	50 x 41	TATA box binding protein (TBP)−associated factor, RNA poly
9	VAMP4	1.18	5e−06	2e−05	50 x 40	vesicle−associated membrane protein 4 [Source:HGNC Sym
10	SMIM10	1.17	5e−06	2e−05	50 x 39	small integral membrane protein 10 [Source:HGNC Symbol;A
11	MTO1	1.16	6e−06	2e−05	50 x 39	mitochondrial tRNA translation optimization 1 [Source:HGNC
12	C8orf88	1.16	7e−06	2e−04	50 x 39	chromosome 8 open reading frame 88 [Source:HGNC Symb
13	SMOX	1.11	2e−05	2e−04	49 x 40	spermine oxidase [Source:HGNC Symbol;Acc:HGNC:15862]
14	UBXN1	0.58	2e−05	2e−04	50 x 39	UBX domain protein 1 [Source:HGNC Symbol;Acc:HGNC:18
15	C15orf57	1.08	3e−05	1e−03	50 x 41	chromosome 15 open reading frame 57 [Source:HGNC Sym
16	CEP89	1.02	7e−05	1e−03	50 x 41	centrosomal protein 89kDa [Source:HGNC Symbol;Acc:HGN
17	CES2	0.99	1e−04	1e−03	49 x 39	carboxylesterase 2 [Source:HGNC Symbol;Acc:HGNC:1864]
18	NDUFAF1	0.96	2e−04	1e−03	49 x 39	NADH dehydrogenase (ubiquinone) complex I, assembly fact
19	TP53BP1	0.95	2e−04	2e−03	50 x 40	tumor protein p53 binding protein 1 [Source:HGNC Symbol;A
20	RNFT1	0.91	3e−04	2e−03	50 x 39	ring finger protein, transmembrane 1 [Source:HGNC Symbol;

p−values



F12_mel

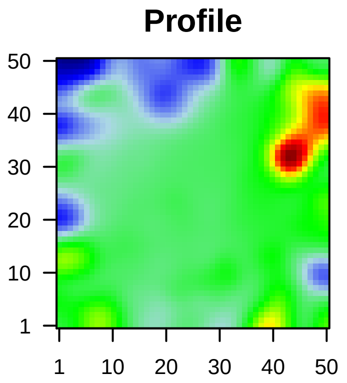
Local Summary

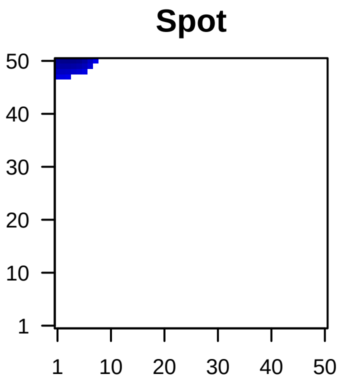
%DE = 0.81
metagenes = 24
genes = 383
genes in genesets = 382

genes with fdr < 0.1 = 222 (30 + / 192 −)
genes with fdr < 0.05 = 186 (27 + / 159 −)
genes with fdr < 0.01 = 105 (11 + / 94 −)

<r> metagenes = 0.92
<r> genes = 0.27

<FC> = −0.4
<shrinkage−t> = −6.46
<p−value> = 0.01
<fdr> = 0.56





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CDKN3	−1.65	2e−16	4e−15	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
2	DEK	−1.51	2e−16	4e−15	2 x 50	DEK proto−oncogene [Source:HGNC Symbol;Acc:HGNC:276
3	EXOSC8	−1.71	2e−16	4e−15	1 x 50	exosome component 8 [Source:HGNC Symbol;Acc:HGNC:17
4	PCNA	−1.64	2e−16	4e−15	2 x 50	proliferating cell nuclear antigen [Source:HGNC Symbol;Acc:
5	MCM4	−1.48	5e−13	2e−11	1 x 50	minichromosome maintenance complex component 4 [Sourc
6	FANCL	−1.52	7e−13	3e−11	1 x 48	Fanconi anemia, complementation group L [Source:HGNC S
7	YEATS4	−1.52	1e−12	3e−10	1 x 47	YEATS domain containing 4 [Source:HGNC Symbol;Acc:HG
8	MCM3	−1.43	6e−12	4e−09	1 x 50	minichromosome maintenance complex component 3 [Sourc
9	MAGOHB	−1.45	6e−11	3e−08	1 x 47	mago−nashi homolog B (Drosophila) [Source:HGNC Symbol;
10	HSD17B11	−1.4	4e−10	7e−08	8 x 50	hydroxysteroid (17−beta) dehydrogenase 11 [Source:HGNC
11	TYMS	−1.37	1e−09	5e−07	3 x 50	thymidylate synthetase [Source:HGNC Symbol;Acc:HGNC:12
12	FEN1	−1.34	9e−09	1e−06	1 x 50	flap structure−specific endonuclease 1 [Source:HGNC Symb
13	RAD1	−1.28	5e−08	1e−06	1 x 49	RAD1 checkpoint DNA exonuclease [Source:HGNC Symbol;
14	PLEKHJ1	−1.28	5e−08	1e−06	1 x 47	pleckstrin homology domain containing, family J member 1 [S
15	PRPS2	−1.28	6e−08	2e−06	2 x 48	phosphoribosyl pyrophosphate synthetase 2 [Source:HGNC
16	POLD3	−1.27	8e−08	4e−06	2 x 50	polymerase (DNA−directed), delta 3, accessory subunit [Sou
17	KIAA0101	−1.24	1e−07	4e−06	3 x 50	KIAA0101 [Source:HGNC Symbol;Acc:HGNC:28961]
18	MTFR2	1.34	2e−07	6e−06	5 x 48	mitochondrial fission regulator 2 [Source:HGNC Symbol;Acc:
19	C19orf48	−1.23	3e−07	6e−06	1 x 50	chromosome 19 open reading frame 48 [Source:HGNC Sym
20	CENPF	−1.23	4e−07	6e−06	6 x 50	centromere protein F, 350/400kDa [Source:HGNC Symbol;Ac