B7_mel

Global Summary

%DE = 0.19

genes with fdr < 0.2 = 2401 (1544 + / 857 −)

genes with fdr < 0.1 = 1789 (1176 + / 613 −)

genes with fdr < 0.05 = 1392 (915 + / 477 −)

genes with fdr < 0.01 = 867 (583 + / 284 −)

genes in genesets = 14839

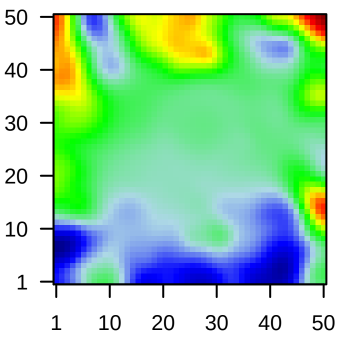
<FC> = 0

<shrinkage−t> = 0.1

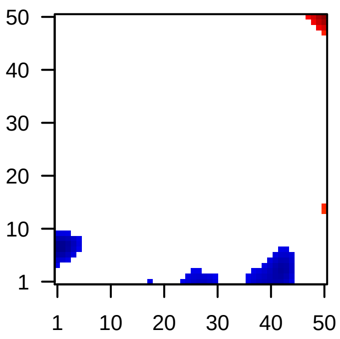
<p−value> = 0.1

<fdr> = 0.81

Profile

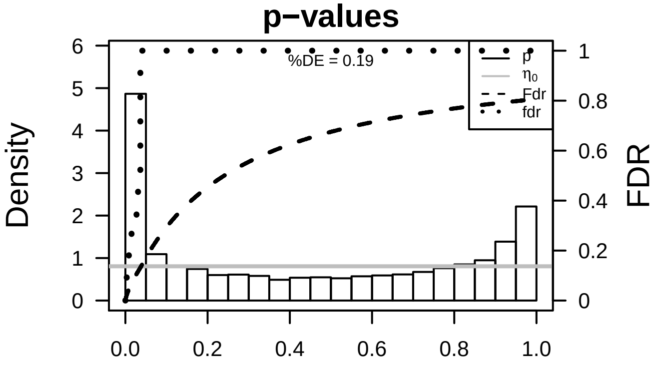


Regulated Spots



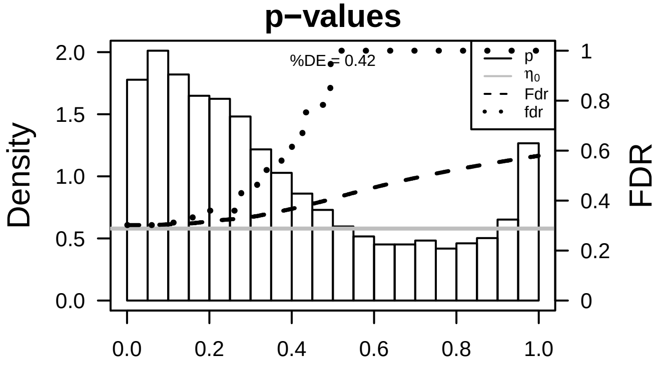
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CHURC1−FN	−1.57	2e−16	2e−13	39 x 50	CHURC1−FNTB readthrough [Source:HGNC Symbol;Acc:HG
2	GPBP1	−1.59	2e−16	2e−13	22 x 7	GC−rich promoter binding protein 1 [Source:HGNC Symbol;A
3	LAPTM4A	−1.35	2e−16	2e−13	36 x 1	lysosomal protein transmembrane 4 alpha [Source:HGNC Sy
4	LITAF	−1.37	2e−16	2e−13	39 x 13	lipopolysaccharide−induced TNF factor [Source:HGNC Symb
5	NNT	−1.31	2e−16	2e−13	6 x 47	nicotinamide nucleotide transhydrogenase [Source:HGNC Sy
6	NUP93	−1.49	2e−16	2e−13	5 x 43	nucleoporin 93kDa [Source:HGNC Symbol;Acc:HGNC:28958
7	OSBPL9	−1.46	2e−16	2e−13	1 x 8	oxysterol binding protein−like 9 [Source:HGNC Symbol;Acc:H
8	PDCD10	−1.62	2e−16	2e−13	13 x 50	programmed cell death 10 [Source:HGNC Symbol;Acc:HGNC
9	PGM3	−1.49	2e−16	2e−13	5 x 45	phosphoglucomutase 3 [Source:HGNC Symbol;Acc:HGNC:8
10	SERINC3	−1.67	2e−16	2e−13	50 x 41	serine incorporator 3 [Source:HGNC Symbol;Acc:HGNC:116
11	TGFB3	1.9	2e−16	2e−13	28 x 43	transforming growth factor, beta 3 [Source:HGNC Symbol;Ac
12	TPRN	1.84	2e−16	2e−13	13 x 15	taperin [Source:HGNC Symbol;Acc:HGNC:26894]
13	TXLNA	−1.31	2e−16	2e−13	12 x 43	taxilin alpha [Source:HGNC Symbol;Acc:HGNC:30685]
14	CYB5R3	−1.39	7e−16	4e−11	4 x 20	cytochrome b5 reductase 3 [Source:HGNC Symbol;Acc:HGN
15	DDB1	−1.33	6e−15	4e−11	33 x 50	damage−specific DNA binding protein 1, 127kDa [Source:HG
16	RNF157	1.7	8e−15	4e−11	5 x 35	ring finger protein 157 [Source:HGNC Symbol;Acc:HGNC:29
17	LMNA	−1.1	1e−14	4e−11	2 x 19	lamin A/C [Source:HGNC Symbol;Acc:HGNC:6636]
18	GRB14	1.68	2e−14	3e−10	33 x 14	growth factor receptor−bound protein 14 [Source:HGNC Sym
19	SEMA3A	1.65	4e−14	3e−10	7 x 12	sema domain, immunoglobulin domain (Ig), short basic doma
20	ICA1	1.64	7e−14	7e−10	50 x 50	islet cell autoantigen 1, 69kDa [Source:HGNC Symbol;Acc:H



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	8.38	5e−04	834	GSEA C2	LEE_BMP2_TARGETS_DN
2	7.25	9e−04	9330	Brain	Overlap_fetal_midbrain_ReprPC
3	6.9	1e−03	7592	Lymphoma	HOPP_Active_promoter
4	6.32	2e−03	162	BP	ribosome biogenesis
5	6.12	2e−03	1365	MF	RNA binding
6	6.07	2e−03	9482	Colon Cancer	TssA_Colon
7	6.02	2e−03	278	GSEA C2	MANALO_HYPOXIA_DN
8	6.02	2e−03	756	GSEA C2	WEI_MYCN_TARGETS_WITH_E_BOX
9	5.91	2e−03	7209	Lymphoma	HOPP_Weak_promoter
10	5.81	2e−03	1126	GSEA C2	BLALOCK_ALZHEIMERS_DISEASE_DN
11	5.65	2e−03	1171	TF	KIM_MYC targets
12	5.61	2e−03	1251	GSEA C2	DODD_NASOPHARYNGEAL_CARCINOMA_DN
13	5.41	3e−03	925	GSEA C2	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
14	5.34	3e−03	471	GSEA C2	ENK_UV_RESPONSE_KERATINOCYTE_DN
15	5.32	3e−03	800	GSEA C2	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_
16	5.28	3e−03	6929	Lymphoma	HOPP_Txn_elongation
17	5.18	3e−03	505	GSEA C2	BERENJENO_TRANSFORMED_BY_RHOA_UP
18	5.14	3e−03	1007	MF	poly(A) RNA binding
19	5.12	3e−03	10290	Colon Cancer	TssWk_Colon
20	5.06	3e−03	862	GSEA C2	JOHNSTONE_PARVB_TARGETS_3_DN
Underexpressed					
1	−5.34	0.003	81	GSEA C2	GAVIN_FOXP3_TARGETS_CLUSTER_P6
2	−4.92	0.004	11	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
3	−4.57	0.005	16	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
4	−4.39	0.006	73	GSEA C2	LIN_APC_TARGETS
5	−4.31	0.006	30	CC	endoplasmic reticulum−Golgi intermediate compartment membran
6	−4.3	0.006	17	GSEA C2	PID_SMAD2_3PATHWAY
7	−4.29	0.006	2798	Colon Cancer	TxEnhG1_Colon
8	−4.25	0.006	16	GSEA C2	LY_AGING_MIDDLE_DN
9	−4.17	0.007	28	GSEA C2	REICHERT_MITOSIS_LIN9_TARGETS
10	−4.11	0.007	80	GSEA C2	BHAT_ESR1_TARGETS_NOT_VIA_AKT1_DN
11	−3.94	0.008	17	GSEA C2	SESTO_RESPONSE_TO_UV_C4
12	−3.84	0.009	232	GSEA C2	HUTTMANN_B_CLL_POOR_SURVIVAL_UP
13	−3.79	0.009	99	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
14	−3.77	0.009	22	CC	histone acetyltransferase complex
15	−3.71	0.010	622	GSEA C2	LEE_BMP2_TARGETS_UP
16	−3.58	0.011	40	GSEA C2	AMUNDSON_GAMMA_RADIATION_RESPONSE
17	−3.56	0.011	2698	Colon Cancer	EnhA_Colon
18	−3.55	0.011	115	CC	midbody
19	−3.52	0.011	995	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_DN
20	−3.48	0.012	11	GSEA C2	MARKS_HDAC_TARGETS_DN



B7_mel

Local Summary

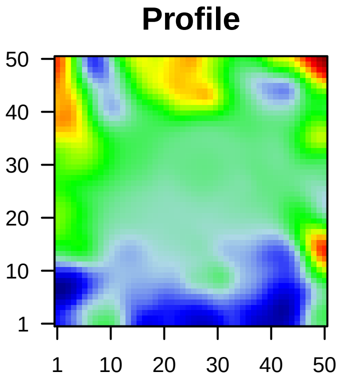
%DE = 0.86
metagenes = 2
genes = 38
genes in genesets = 38

genes with fdr < 0.1 = 19 (17 + / 2 −)
genes with fdr < 0.05 = 19 (17 + / 2 −)
genes with fdr < 0.01 = 12 (12 + / 0 −)

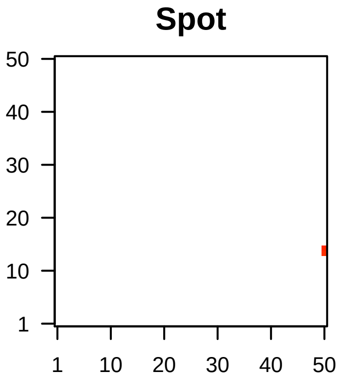
<r> metagenes = 0.99
<r> genes = 0.12

<FC> = 0.24
<shrinkage−t> = 3.93
<p−value> = 0.02
<fdr> = 0.6

Profile



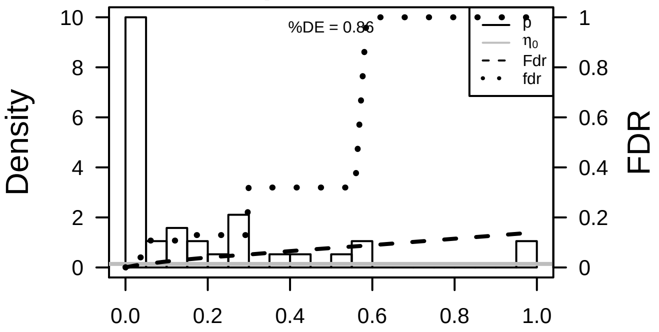
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	XPA	1.27	5e−09	2e−05	50 x 14	xeroderma pigmentosum, complementation group A [Source:
2	ARSK	1	5e−06	2e−04	50 x 15	arylsulfatase family, member K [Source:HGNC Symbol;Acc:H
3	EPB41L3	0.81	5e−05	3e−04	50 x 15	erythrocyte membrane protein band 4.1−like 3 [Source:HGN
4	ZNF529	0.85	1e−04	5e−04	50 x 15	zinc finger protein 529 [Source:HGNC Symbol;Acc:HGNC:29
5	LMBRD2	0.81	2e−04	6e−04	50 x 14	LMBR1 domain containing 2 [Source:HGNC Symbol;Acc:HG
6	CHD7	0.76	4e−04	6e−04	50 x 14	chromodomain helicase DNA binding protein 7 [Source:HGN
7	PAPOLG	0.77	4e−04	1e−03	50 x 15	poly(A) polymerase gamma [Source:HGNC Symbol;Acc:HG
8	NME7	0.61	1e−03	1e−03	50 x 14	NME/NM23 family member 7 [Source:HGNC Symbol;Acc:HG
9	ARHGAP5	0.57	1e−03	1e−03	50 x 14	Rho GTPase activating protein 5 [Source:HGNC Symbol;Acc:
10	NADSYN1	0.64	1e−03	3e−03	50 x 15	NAD synthetase 1 [Source:HGNC Symbol;Acc:HGNC:29832]
11	CERS5	0.63	2e−03	3e−03	50 x 15	ceramide synthase 5 [Source:HGNC Symbol;Acc:HGNC:237
12	FAM103A1	0.65	3e−03	3e−03	50 x 14	family with sequence similarity 103, member A1 [Source:HG
13	N4BP2L2	0.38	3e−03	4e−02	50 x 15	NEDD4 binding protein 2−like 2 [Source:HGNC Symbol;Acc:
14	ARHGEF7	0.49	2e−02	4e−02	50 x 15	Rho guanine nucleotide exchange factor (GEF) 7 [Source:HG
15	ZMYM1	0.49	2e−02	4e−02	50 x 15	zinc finger, MYM−type 1 [Source:HGNC Symbol;Acc:HGNC:
16	RRM2B	−0.48	3e−02	4e−02	50 x 15	ribonucleotide reductase M2 B (TP53 inducible) [Source:HG
17	DYNC2H1	0.3	3e−02	4e−02	50 x 14	dynein, cytoplasmic 2, heavy chain 1 [Source:HGNC Symbol;
18	RNF216	−0.43	4e−02	4e−02	50 x 14	ring finger protein 216 [Source:HGNC Symbol;Acc:HGNC:21
19	ZFP36L2	0.43	5e−02	4e−02	50 x 14	ZFP36 ring finger protein−like 2 [Source:HGNC Symbol;Acc:
20	GCLC	−0.42	5e−02	1e−01	50 x 14	glutamate−cysteine ligase, catalytic subunit [Source:HGNC S

p−values



B7_mel

Local Summary

%DE = 0.71

metagenes = 10

genes = 208

genes in genesets = 207

genes with fdr < 0.1 = 101 (81 + / 20 −)

genes with fdr < 0.05 = 93 (75 + / 18 −)

genes with fdr < 0.01 = 54 (41 + / 13 −)

<r> metagenes = 0.96

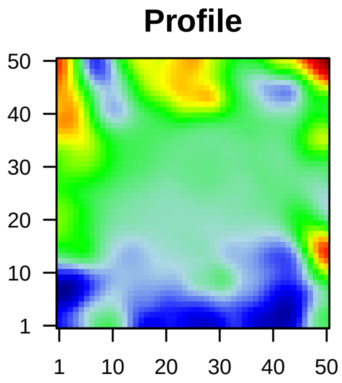
<r> genes = 0.09

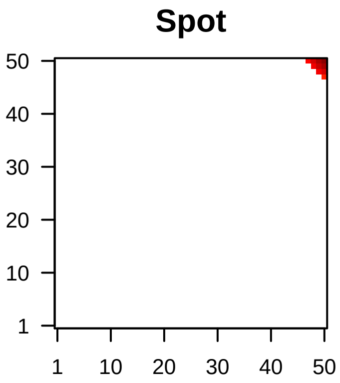
<FC> = 0.25

<shrinkage−t> = 4.21

<p−value> = 0.01

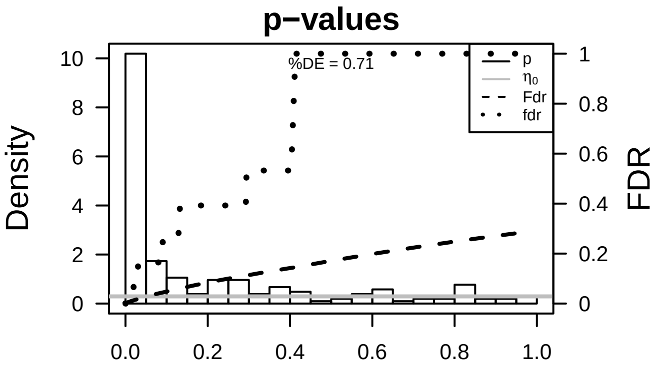
<fdr> = 0.56





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ICA1	1.64	7e−14	6e−09	50 x 50	islet cell autoantigen 1, 69kDa [Source:HGNC Symbol;Acc:H
2	PDK4	−1.29	1e−10	2e−08	47 x 50	pyruvate dehydrogenase kinase, isozyme 4 [Source:HGNC S
3	PKN1	1.36	4e−10	6e−08	47 x 50	protein kinase N1 [Source:HGNC Symbol;Acc:HGNC:9405]
4	OXLD1	−1.24	1e−09	6e−07	47 x 50	oxidoreductase−like domain containing 1 [Source:HGNC Sym
5	LUZP6	1.25	1e−08	6e−07	50 x 49	leucine zipper protein 6 [Source:HGNC Symbol;Acc:HGNC:3
6	PDE8A	1.22	2e−08	7e−07	50 x 47	phosphodiesterase 8A [Source:HGNC Symbol;Acc:HGNC:87
7	NLRC5	1.21	3e−08	5e−06	50 x 50	NLR family, CARD domain containing 5 [Source:HGNC Symb
8	TMEM53	1.15	1e−07	5e−06	50 x 47	transmembrane protein 53 [Source:HGNC Symbol;Acc:HGN
9	CYP19A1	1.13	2e−07	6e−06	49 x 48	cytochrome P450, family 19, subfamily A, polypeptide 1 [Sou
10	GUSB	−1.1	3e−07	9e−06	47 x 50	glucuronidase, beta [Source:HGNC Symbol;Acc:HGNC:4696
11	ITIH3	1.1	5e−07	1e−05	50 x 50	inter−alpha−trypsin inhibitor heavy chain 3 [Source:HGNC Sy
12	ZNF184	1.09	6e−07	3e−05	50 x 50	zinc finger protein 184 [Source:HGNC Symbol;Acc:HGNC:12
13	IL1RAP	1.06	1e−06	3e−05	50 x 50	interleukin 1 receptor accessory protein [Source:HGNC Symb
14	GDAP1	1.04	2e−06	8e−05	50 x 50	ganglioside induced differentiation associated protein 1 [Sour
15	FAM192A	−0.92	3e−06	8e−05	50 x 47	family with sequence similarity 192, member A [Source:HGN
16	UBE2Q2	1	5e−06	8e−05	50 x 50	ubiquitin−conjugating enzyme E2Q family member 2 [Source:
17	TRAPPC8	−0.98	6e−06	8e−05	50 x 49	trafficking protein particle complex 8 [Source:HGNC Symbol;
18	CCDC51	0.98	7e−06	3e−04	47 x 50	coiled−coil domain containing 51 [Source:HGNC Symbol;Acc
19	RFT1	0.95	1e−05	3e−04	50 x 50	RFT1 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:H
20	NTAN1	−0.94	2e−05	4e−04	50 x 48	N−terminal asparagine amidase [Source:HGNC Symbol;Acc:



B7_mel

Local Summary

%DE = 0.56

metagenes = 1

genes = 15

genes in genesets = 15

genes with fdr < 0.1 = 2 (0 + / 2 −)

genes with fdr < 0.05 = 1 (0 + / 1 −)

genes with fdr < 0.01 = 0 (0 + / 0 −)

<r> metagenes = NA

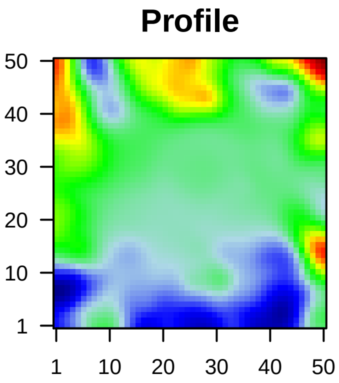
<r> genes = 0.2

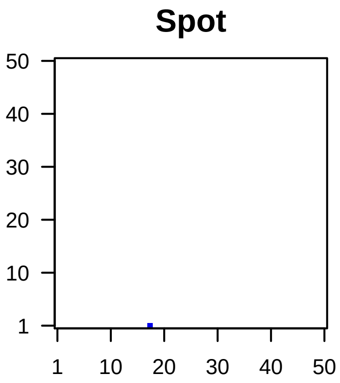
<FC> = −0.2

<shrinkage−t> = −3.02

<p−value> = 0.15

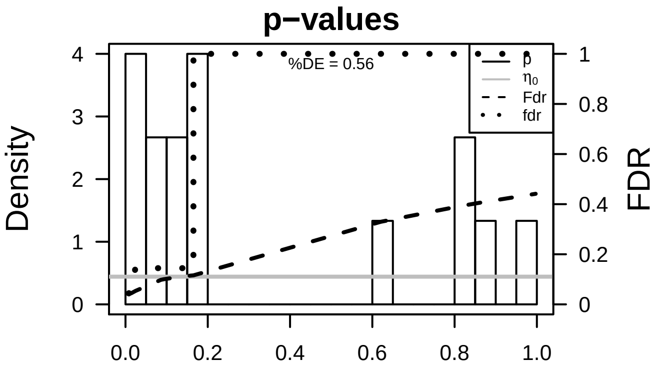
<fdr> = 0.85





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	RRP8	−0.58	0.008	0.04	18 x 1	ribosomal RNA processing 8, methyltransferase, homolog (ye
2	KIAA0586	−0.54	0.013	0.07	18 x 1	KIAA0586 [Source:HGNC Symbol;Acc:HGNC:19960]
3	AGPAT1	−0.49	0.024	0.14	18 x 1	1−acylglycerol−3−phosphate O−acyltransferase 1 [Source:H
4	GDAP2	0.37	0.086	0.14	18 x 1	ganglioside induced differentiation associated protein 2 [Sour
5	SLC30A6	−0.37	0.092	0.14	18 x 1	solute carrier family 30 (zinc transporter), member 6 [Source:
6	NFIX	−0.33	0.136	0.14	18 x 1	nuclear factor I/X (CCAAT−binding transcription factor) [Sourc
7	SLC39A3	−0.31	0.149	0.14	18 x 1	solute carrier family 39 (zinc transporter), member 3 [Source:
8	NEU1	−0.31	0.160	0.14	18 x 1	sialidase 1 (lysosomal sialidase) [Source:HGNC Symbol;Acc:
9	PRMT9	−0.3	0.165	0.14	18 x 1	protein arginine methyltransferase 9 [Source:HGNC Symbol;
10	TMEM63B	−0.3	0.165	1.00	18 x 1	transmembrane protein 63B [Source:HGNC Symbol;Acc:HG
11	TET2	0.11	0.621	1.00	18 x 1	tet methylcytosine dioxygenase 2 [Source:HGNC Symbol;Acc
12	FXR1	0.05	0.809	1.00	18 x 1	fragile X mental retardation, autosomal homolog 1 [Source:H
13	PPID	0.04	0.841	1.00	18 x 1	peptidylprolyl isomerase D [Source:HGNC Symbol;Acc:HGN
14	RORB	−0.04	0.865	1.00	18 x 1	RAR−related orphan receptor B [Source:HGNC Symbol;Acc:
15	DAG1	0	0.997	1.00	18 x 1	dystroglycan 1 (dystrophin−associated glycoprotein 1) [Sourc



B7_mel

Local Summary

%DE = 0.72

metagenes = 15

genes = 208

genes in genesets = 201

genes with fdr < 0.1 = 15 (2 + / 13 −)

genes with fdr < 0.05 = 11 (2 + / 9 −)

genes with fdr < 0.01 = 3 (2 + / 1 −)

<r> metagenes = 0.96

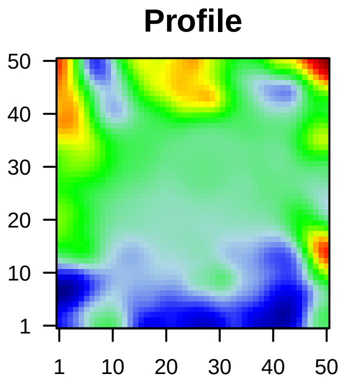
<r> genes = 0.22

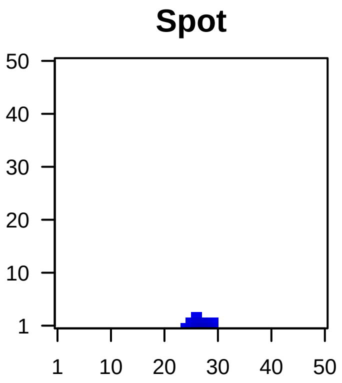
<FC> = −0.19

<shrinkage−t> = −2.85

<p−value> = 0.15

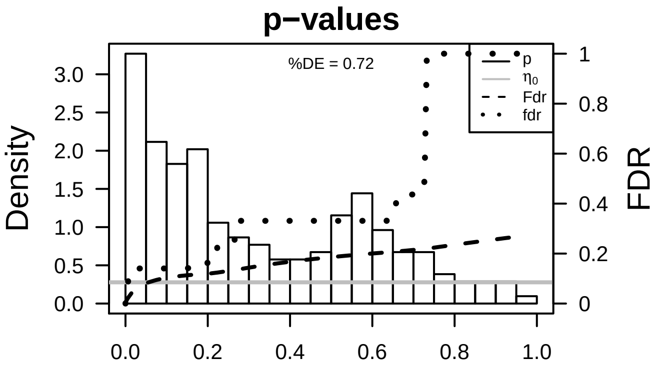
<fdr> = 0.89





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	BMP4	1.2	4e−08	1e−05	24 x 1	bone morphogenetic protein 4 [Source:HGNC Symbol;Acc:H
2	KIF3A	−1.11	2e−07	4e−03	25 x 2	kinesin family member 3A [Source:HGNC Symbol;Acc:HGNC
3	KLF6	0.73	1e−04	4e−03	27 x 1	Kruppel−like factor 6 [Source:HGNC Symbol;Acc:HGNC:2235
4	PKN2	−0.83	2e−04	1e−02	29 x 1	protein kinase N2 [Source:HGNC Symbol;Acc:HGNC:9406]
5	TRIM2	−0.76	5e−04	1e−02	30 x 1	tripartite motif containing 2 [Source:HGNC Symbol;Acc:HGN
6	YTHDF1	−0.74	7e−04	1e−02	30 x 1	YTH N(6)−methyladenosine RNA binding protein 1 [Source:H
7	C14orf39	−0.71	1e−03	1e−02	30 x 2	chromosome 14 open reading frame 39 [Source:HGNC Symb
8	LRP8	−0.7	1e−03	1e−02	24 x 1	low density lipoprotein receptor−related protein 8, apolipoprot
9	CLN5	−0.69	2e−03	1e−02	24 x 1	ceroid−lipofuscinosis, neuronal 5 [Source:HGNC Symbol;Acc
10	FAM222B	−0.69	2e−03	1e−02	25 x 2	family with sequence similarity 222, member B [Source:HGN
11	PPRC1	−0.68	2e−03	4e−02	24 x 1	peroxisome proliferator−activated receptor gamma, coactivat
12	NRAS	−0.66	3e−03	6e−02	27 x 1	neuroblastoma RAS viral (v−ras) oncogene homolog [Source
13	RRP12	−0.6	6e−03	6e−02	25 x 1	ribosomal RNA processing 12 homolog (S. cerevisiae) [Sourc
14	MAF1	−0.6	6e−03	6e−02	27 x 1	MAF1 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:H
15	CLEC16A	−0.6	6e−03	6e−02	29 x 1	C−type lectin domain family 16, member A [Source:HGNC Sy
16	ADCK3	−0.6	6e−03	1e−01	24 x 1	aarF domain containing kinase 3 [Source:HGNC Symbol;Acc
17	AKT3	0.53	2e−02	1e−01	24 x 1	v−akt murine thymoma viral oncogene homolog 3 [Source:HG
18	ZNF557	−0.5	2e−02	1e−01	26 x 1	zinc finger protein 557 [Source:HGNC Symbol;Acc:HGNC:28
19	KRT10	−0.5	2e−02	1e−01	26 x 1	keratin 10, type I [Source:HGNC Symbol;Acc:HGNC:6413]
20	ARRB1	−0.5	2e−02	1e−01	24 x 1	arrestin, beta 1 [Source:HGNC Symbol;Acc:HGNC:711]



B7_mel

Local Summary

%DE = 0.61

metagenes = 43

genes = 339

genes in genesets = 339

genes with fdr < 0.1 = 75 (23 + / 52 −)

genes with fdr < 0.05 = 43 (12 + / 31 −)

genes with fdr < 0.01 = 41 (11 + / 30 −)

<r> metagenes = 0.85

<r> genes = 0.09

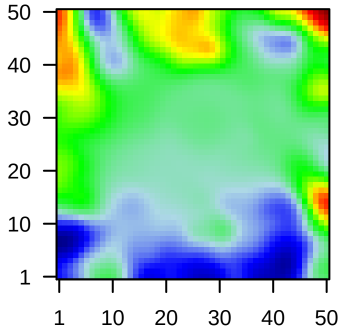
<FC> = −0.16

<shrinkage−t> = −2.41

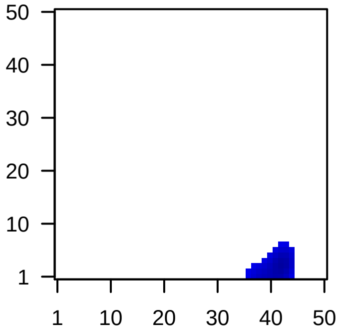
<p−value> = 0.05

<fdr> = 0.75

Profile



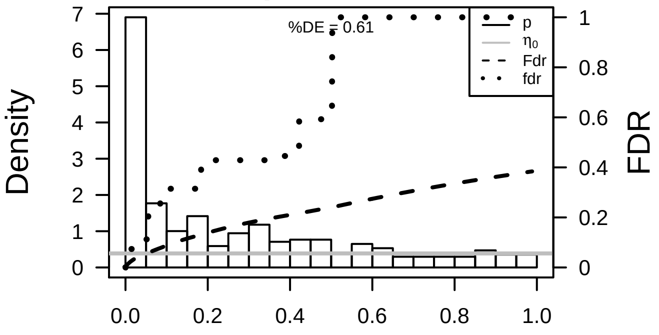
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	LAPTM4A	−1.35	2e−16	3e−14	36 x 1	lysosomal protein transmembrane 4 alpha [Source:HGNC Sy
2	BBIP1	−1.29	9e−11	7e−05	42 x 4	BBSome interacting protein 1 [Source:HGNC Symbol;Acc:HG
3	ODF2L	−1.08	5e−07	2e−04	38 x 1	outer dense fiber of sperm tails 2−like [Source:HGNC Symbo
4	TTC27	1.03	3e−06	2e−04	38 x 3	tetratricopeptide repeat domain 27 [Source:HGNC Symbol;Ac
5	TNRC6A	−1	4e−06	2e−04	42 x 6	trinucleotide repeat containing 6A [Source:HGNC Symbol;Ac
6	ANXA11	−1	4e−06	3e−04	40 x 1	annexin A11 [Source:HGNC Symbol;Acc:HGNC:535]
7	ACTR1A	−0.96	7e−06	3e−04	42 x 1	ARP1 actin−related protein 1 homolog A, centractin alpha (ye
8	DPM1	−0.85	1e−05	3e−04	37 x 1	dolichyl−phosphate mannosyltransferase polypeptide 1, catal
9	TMEM43	−0.96	1e−05	7e−04	43 x 3	transmembrane protein 43 [Source:HGNC Symbol;Acc:HGN
10	MCL1	0.94	2e−05	1e−03	44 x 1	myeloid cell leukemia 1 [Source:HGNC Symbol;Acc:HGNC:6
11	NOL10	−0.91	3e−05	1e−03	42 x 1	nucleolar protein 10 [Source:HGNC Symbol;Acc:HGNC:2586
12	ZNF33A	0.9	3e−05	1e−03	38 x 2	zinc finger protein 33A [Source:HGNC Symbol;Acc:HGNC:13
13	TSC22D2	−0.79	4e−05	1e−03	44 x 1	TSC22 domain family, member 2 [Source:HGNC Symbol;Acc
14	ZKSCAN1	−0.87	6e−05	1e−03	44 x 6	zinc finger with KRAB and SCAN domains 1 [Source:HGNC
15	TOMM70A	−0.87	7e−05	1e−03	43 x 5	translocase of outer mitochondrial membrane 70 homolog A (
16	TRAPPC6B	0.86	8e−05	1e−03	38 x 1	trafficking protein particle complex 6B [Source:HGNC Symbol
17	B9D1	−0.85	9e−05	1e−03	42 x 5	B9 protein domain 1 [Source:HGNC Symbol;Acc:HGNC:2412
18	FAM60A	−0.85	9e−05	1e−03	41 x 4	family with sequence similarity 60, member A [Source:HGNC
19	C9orf85	−0.85	1e−04	1e−03	43 x 3	chromosome 9 open reading frame 85 [Source:HGNC Symbo
20	MED31	0.84	1e−04	3e−03	41 x 1	mediator complex subunit 31 [Source:HGNC Symbol;Acc:HG

p−values



B7_mel

Local Summary

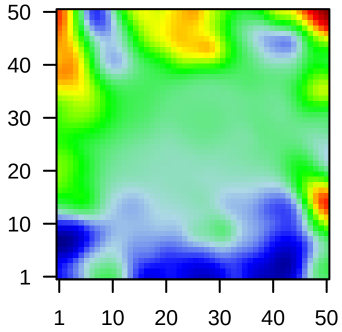
%DE = 0.34
metagenes = 26
genes = 365
genes in genesets = 361

genes with fdr < 0.1 = 55 (16 + / 39 −)
genes with fdr < 0.05 = 55 (16 + / 39 −)
genes with fdr < 0.01 = 36 (11 + / 25 −)

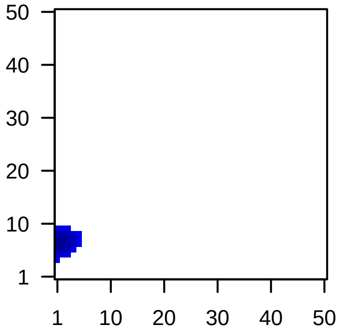
<r> metagenes = 0.87
<r> genes = 0.11

<FC> = −0.17
<shrinkage−t> = −2.61
<p−value> = 0.06
<fdr> = 0.75

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	OSBPL9	−1.46	2e−16	5e−14	1 x 8	oxysterol binding protein−like 9 [Source:HGNC Symbol;Acc:H
2	CEACAM1	−1.27	2e−10	1e−07	1 x 10	carcinoembryonic antigen−related cell adhesion molecule 1 (
3	QRICH1	−0.9	6e−10	2e−07	1 x 8	glutamine−rich 1 [Source:HGNC Symbol;Acc:HGNC:24713]
4	PEX19	−1.2	1e−09	2e−07	1 x 8	peroxisomal biogenesis factor 19 [Source:HGNC Symbol;Acc
5	PDHX	−1.22	2e−09	1e−05	1 x 7	pyruvate dehydrogenase complex, component X [Source:HG
6	ADPRHL1	1.18	6e−08	6e−05	1 x 4	ADP−ribosylhydrolase like 1 [Source:HGNC Symbol;Acc:HG
7	CNTROB	1.08	7e−07	6e−05	1 x 6	centrobin, centrosomal BRCA2 interacting protein [Source:H
8	ZNF776	1.08	7e−07	6e−05	1 x 5	zinc finger protein 776 [Source:HGNC Symbol;Acc:HGNC:26
9	TMEM55A	−1.07	8e−07	1e−04	4 x 9	transmembrane protein 55A [Source:HGNC Symbol;Acc:HG
10	COPG1	−1.02	2e−06	1e−04	1 x 9	coatomer protein complex, subunit gamma 1 [Source:HGNC
11	ADSS	−1.01	2e−06	2e−04	1 x 9	adenylosuccinate synthase [Source:HGNC Symbol;Acc:HGN
12	GAK	1.01	3e−06	2e−04	1 x 5	cyclin G associated kinase [Source:HGNC Symbol;Acc:HGN
13	ACOX1	−0.98	4e−06	2e−04	1 x 7	acyl−CoA oxidase 1, palmitoyl [Source:HGNC Symbol;Acc:H
14	SULT1C2	−1	5e−06	2e−04	1 x 9	sulfotransferase family, cytosolic, 1C, member 2 [Source:HG
15	SH3BP4	−0.99	5e−06	2e−03	1 x 10	SH3−domain binding protein 4 [Source:HGNC Symbol;Acc:H
16	CRBN	0.58	2e−05	2e−03	1 x 8	cereblon [Source:HGNC Symbol;Acc:HGNC:30185]
17	SGPL1	−0.92	2e−05	2e−03	4 x 6	sphingosine−1−phosphate lyase 1 [Source:HGNC Symbol;Ac
18	MSI2	−0.89	3e−05	2e−03	1 x 10	musashi RNA−binding protein 2 [Source:HGNC Symbol;Acc:
19	TRAPPC3	0.88	6e−05	2e−03	1 x 8	trafficking protein particle complex 3 [Source:HGNC Symbol;
20	MTIF3	0.8	6e−05	2e−03	1 x 9	mitochondrial translational initiation factor 3 [Source:HGNC S

p−values