A11_mel

Global Summary

%DE = 0.23

genes with fdr < 0.2 = 2777 (1709 + / 1068 −)

genes with fdr < 0.1 = 2229 (1415 + / 814 −)

genes with fdr < 0.05 = 1787 (1167 + / 620 −)

genes with fdr < 0.01 = 1135 (743 + / 392 −)

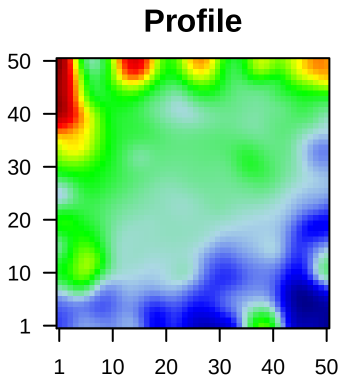
genes in genesets = 14839

<FC> = 0

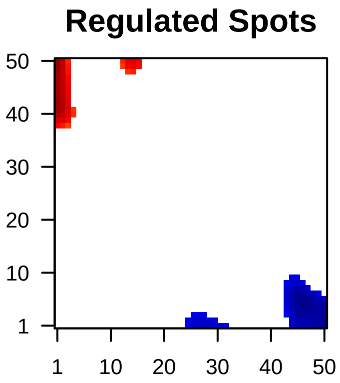
<shrinkage−t> = 0.1

<p−value> = 0.08

<fdr> = 0.77



Profile



Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ACAT2	−1.48	2e−16	6e−13	1 x 24	acetyl−CoA acetyltransferase 2 [Source:HGNC Symbol;Acc:
2	ANKHD1	−1.43	2e−16	6e−13	9 x 5	ankyrin repeat and KH domain containing 1 [Source:HGNC S
3	COL11A1	−1.12	2e−16	6e−13	45 x 1	collagen, type XI, alpha 1 [Source:HGNC Symbol;Acc:HGNC
4	TXNDC12	−1.51	2e−16	6e−13	34 x 10	thioredoxin domain containing 12 (endoplasmic reticulum) [S
5	ENDOV	−1.41	4e−16	9e−13	1 x 28	endonuclease V [Source:HGNC Symbol;Acc:HGNC:26640]
6	SRP54	−1.35	4e−16	9e−13	1 x 22	signal recognition particle 54kDa [Source:HGNC Symbol;Acc
7	TRIAP1	−1.41	4e−16	9e−13	50 x 22	TP53 regulated inhibitor of apoptosis 1 [Source:HGNC Symb
8	ACSF2	1.63	7e−16	3e−12	33 x 14	acyl−CoA synthetase family member 2 [Source:HGNC Symb
9	NFE2L2	−0.96	7e−16	3e−12	44 x 19	nuclear factor, erythroid 2−like 2 [Source:HGNC Symbol;Acc:
10	TKTL1	1.63	7e−16	3e−12	4 x 15	transketolase−like 1 [Source:HGNC Symbol;Acc:HGNC:1183
11	VDAC3	−1.08	9e−16	5e−12	4 x 43	voltage−dependent anion channel 3 [Source:HGNC Symbol;
12	ZCCHC17	−1.41	1e−15	1e−11	46 x 7	zinc finger, CCHC domain containing 17 [Source:HGNC Sym
13	ZFP62	1.6	2e−15	2e−11	50 x 50	ZFP62 zinc finger protein [Source:HGNC Symbol;Acc:HGNC:
14	MAP3K12	1.58	4e−15	2e−11	48 x 23	mitogen−activated protein kinase kinase kinase 12 [Source:
15	SLC25A36	−1.39	6e−15	2e−11	1 x 26	solute carrier family 25 (pyrimidine nucleotide carrier), memb
16	G3BP2	−1.1	7e−15	9e−11	50 x 49	GTPase activating protein (SH3 domain) binding protein 2 [S
17	CLU	1.55	1e−14	1e−10	37 x 5	clusterin [Source:HGNC Symbol;Acc:HGNC:2095]
18	WDR45	−1.35	3e−14	1e−10	50 x 39	WD repeat domain 45 [Source:HGNC Symbol;Acc:HGNC:28
19	MCU	1.51	6e−14	1e−10	14 x 14	mitochondrial calcium uniporter [Source:HGNC Symbol;Acc:
20	VPS41	−1.25	7e−14	1e−10	4 x 42	vacuolar protein sorting 41 homolog (S. cerevisiae) [Source:

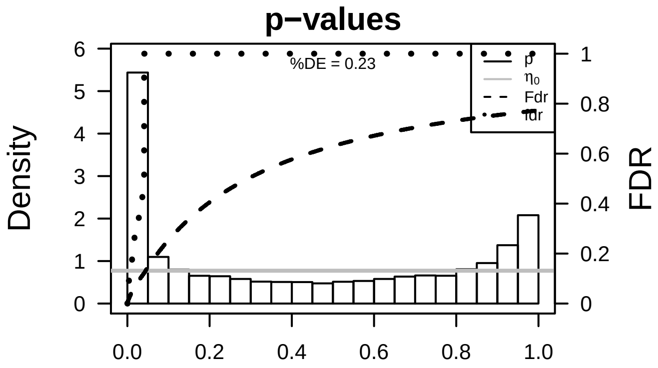
Global Geneset Analysis

Overexpressed

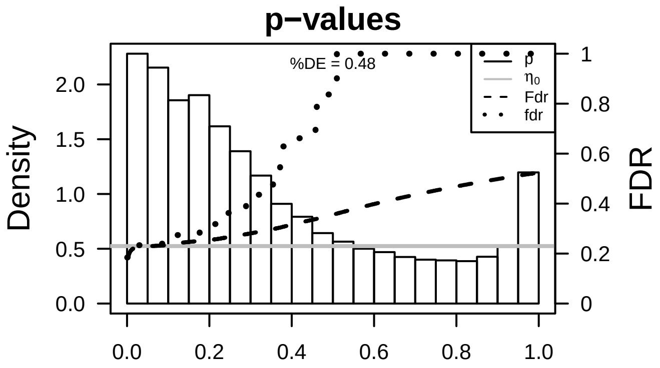
Rank	GSZ	p−value	#all	Geneset	
1	8.94	4e−04	562	GSEA C2	CAIRO_HEPATOBLASTOMA_CLASSES_UP
2	8.64	5e−04	401	CC	mitochondrial inner membrane
3	7.84	7e−04	233	GSEA C2	PENG_RAPAMYCIN_RESPONSE_DN
4	7.47	8e−04	505	GSEA C2	BERENJENO_TRANSFORMED_BY_RHOA_UP
5	7.33	9e−04	312	GSEA C2	WONG_EMBRYONIC_STEM_CELL_CORE
6	7.28	9e−04	405	GSEA C2	MOOTHA_HUMAN_MITODB_6_2002
7	7.21	9e−04	1460	GSEA C2	PUJANA_BRCA1_PCC_NETWORK
8	7.13	1e−03	198	HM	HALLMARK_OXIDATIVE_PHOSPHORYLATION
9	7.12	1e−03	32	GSEA C2	KEGG_DNA_REPLICATION
10	7.02	1e−03	24	BP	telomere maintenance via recombination
11	7	1e−03	267	GSEA C2	ZHANG_TLX_TARGETS_60HR_DN
12	6.93	1e−03	181	GSEA C2	PENG_LEUCINE_DEPRIVATION_DN
13	6.92	1e−03	478	GSEA C2	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
14	6.86	1e−03	341	GSEA C2	RHEIN_ALL_GLUCOCORTICOID_THERAPY_DN
15	6.85	1e−03	834	GSEA C2	LEE_BMP2_TARGETS_DN
16	6.83	1e−03	20	BP	telomere maintenance via semi−conservative replication
17	6.82	1e−03	29	BP	DNA strand elongation involved in DNA replication
18	6.81	1e−03	27	GSEA C2	REACTOME_DNA_STRAND_ELONGATION
19	6.79	1e−03	1468	CC	mitochondrion
20	6.76	1e−03	188	HM	HALLMARK_MYC_TARGETS_V1

Underexpressed

Rank	GSZ	p−value	#all	Geneset	
1	−4.38	0.006	3396	Lymphoma	HOPP_Repressed
2	−4.24	0.006	1139	TF	HEBENSTREIT_low expression TF
3	−4.12	0.007	3897	Colon Cancer	Quies1_Colon
4	−4.1	0.007	107	Lymphoma	SPANG_LPS 6hrs UP
5	−3.89	0.008	2159	Colon Cancer	TssP_Colon
6	−3.81	0.009	16	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_DN
7	−3.81	0.009	995	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_DN
8	−3.79	0.009	68	GSEA C2	REACTOME_L1CAM_INTERACTIONS
9	−3.77	0.009	1907	Brain	Fetal_TxTrans
10	−3.72	0.009	280	Lymphoma	SPANG_CD40 6hrs UP
11	−3.68	0.010	443	BP	anatomical structure formation involved in morphogenesis
12	−3.61	0.010	19	GSEA C2	REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPT
13	−3.55	0.011	15	MF	lysine−acetylated histone binding
14	−3.51	0.011	11	MF	insulin−like growth factor receptor binding
15	−3.5	0.011	2185	Brain	Fetal_TssA
16	−3.44	0.012	72	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN
17	−3.41	0.012	16	GSEA C2	REACTOME_ERK_MAPK_TARGETS
18	−3.4	0.013	1949	Brain	Fetal_TssF
19	−3.39	0.013	966	GSEA C2	PEREZ_TP53_TARGETS
20	−3.32	0.013	2188	Lymphoma	HOPP_Poised_promoter



p−values



p−values

A11_mel

Local Summary

%DE = 0.78

metagenes = 41

genes = 610

genes in genesets = 607

genes with fdr < 0.1 = 379 (317 + / 62 −)

genes with fdr < 0.05 = 354 (294 + / 60 −)

genes with fdr < 0.01 = 207 (173 + / 34 −)

<r> metagenes = 0.79

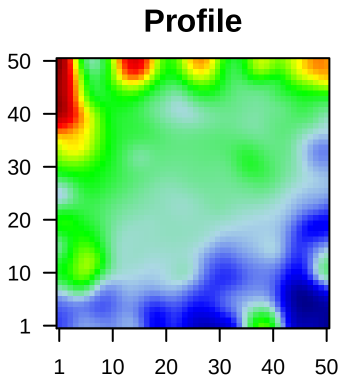
<r> genes = 0.14

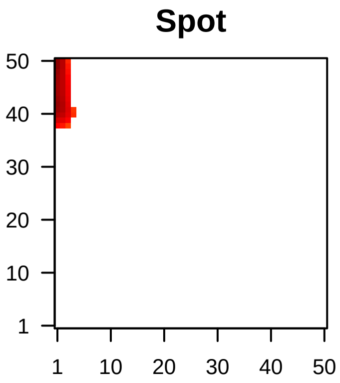
<FC> = 0.27

<shrinkage−t> = 4.82

<p−value> = 0

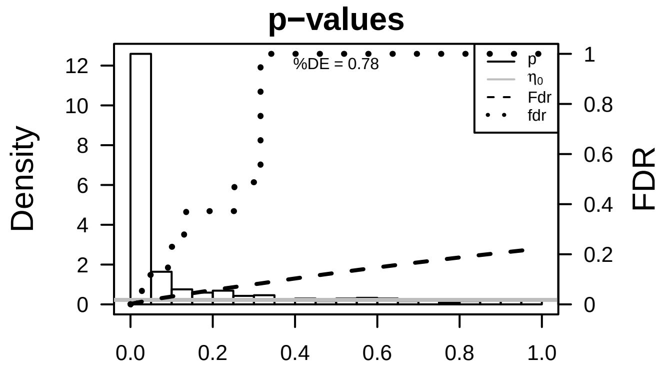
<fdr> = 0.45





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CHEK1	1.5	1e−13	3e−11	1 x 50	checkpoint kinase 1 [Source:HGNC Symbol;Acc:HGNC:1925
2	NCAPH2	1.47	3e−13	3e−11	1 x 50	non−SMC condensin II complex, subunit H2 [Source:HGNC S
3	MCCC1	1.46	5e−13	2e−10	2 x 45	methylcrotonoyl−CoA carboxylase 1 (alpha) [Source:HGNC S
4	POLD1	1.42	2e−12	4e−08	3 x 46	polymerase (DNA directed), delta 1, catalytic subunit [Source
5	ANO2	1.26	5e−10	4e−08	1 x 42	anoctamin 2, calcium activated chloride channel [Source:HG
6	DTL	1.25	5e−10	4e−08	1 x 50	denticleless E3 ubiquitin protein ligase homolog (Drosophila)
7	C19orf48	1.15	1e−09	4e−08	1 x 50	chromosome 19 open reading frame 48 [Source:HGNC Sym
8	MITF	0.56	1e−09	2e−07	1 x 41	microphthalmia−associated transcription factor [Source:HGN
9	RAD51	1.2	3e−09	2e−07	1 x 50	RAD51 recombinase [Source:HGNC Symbol;Acc:HGNC:981
10	IMPA2	1.18	6e−09	2e−07	1 x 48	inositol(myo)−1(or 4)−monophosphatase 2 [Source:HGNC Sy
11	DUS3L	1.17	7e−09	2e−07	1 x 40	dihydrouridine synthase 3−like (S. cerevisiae) [Source:HGNC
12	RBPMS2	1.17	7e−09	2e−07	1 x 42	RNA binding protein with multiple splicing 2 [Source:HGNC S
13	POLE2	1.16	9e−09	2e−07	1 x 47	polymerase (DNA directed), epsilon 2, accessory subunit [So
14	CYB5A	−1.01	1e−08	2e−07	1 x 45	cytochrome b5 type A (microsomal) [Source:HGNC Symbol;
15	ARHGAP8	0.78	1e−08	3e−07	1 x 43	Rho GTPase activating protein 8 [Source:HGNC Symbol;Acc
16	HIRIP3	1.14	1e−08	6e−07	2 x 50	HIRA interacting protein 3 [Source:HGNC Symbol;Acc:HGNC
17	CHCHD5	−1.12	2e−08	6e−07	4 x 41	coiled−coil−helix−coiled−coil−helix domain containing 5 [Sou
18	CDC6	1.12	2e−08	1e−06	1 x 50	cell division cycle 6 [Source:HGNC Symbol;Acc:HGNC:1744]
19	RNF138	−1.1	3e−08	1e−06	1 x 46	ring finger protein 138, E3 ubiquitin protein ligase [Source:HG
20	HAUS7	1.11	4e−08	2e−06	1 x 46	HAUS augmin−like complex, subunit 7 [Source:HGNC Symb



A11_mel

Local Summary

%DE = 0.76

metagenes = 10

genes = 114

genes in genesets = 114

genes with fdr < 0.1 = 66 (53 + / 13 −)

genes with fdr < 0.05 = 62 (50 + / 12 −)

genes with fdr < 0.01 = 46 (37 + / 9 −)

<r> metagenes = 0.97

<r> genes = 0.1

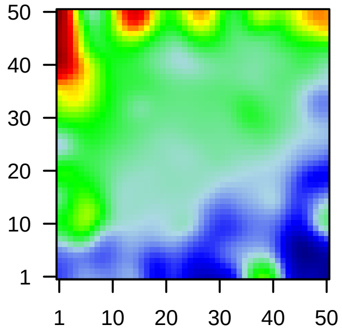
<FC> = 0.25

<shrinkage−t> = 4.22

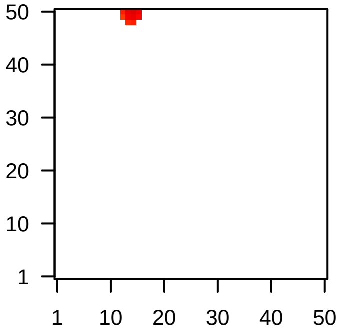
<p−value> = 0.01

<fdr> = 0.46

Profile



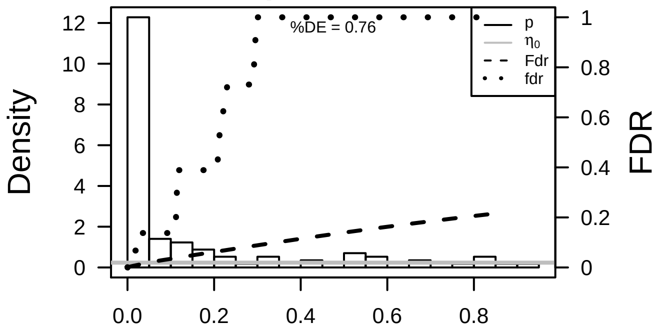
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CAAP1	1.17	7e−09	4e−06	15 x 50	caspase activity and apoptosis inhibitor 1 [Source:HGNC Syn
2	CASP4	1.06	2e−07	8e−06	15 x 50	caspase 4, apoptosis−related cysteine peptidase [Source:HG
3	GTF3C5	1.02	5e−07	9e−06	13 x 50	general transcription factor IIIC, polypeptide 5, 63kDa [Source
4	ZNF346	0.98	1e−06	9e−06	15 x 50	zinc finger protein 346 [Source:HGNC Symbol;Acc:HGNC:16
5	EMC2	0.9	1e−06	1e−05	14 x 50	ER membrane protein complex subunit 2 [Source:HGNC Syn
6	EIF1AD	−0.97	2e−06	4e−05	15 x 48	eukaryotic translation initiation factor 1A domain containing [S
7	C16orf59	0.93	5e−06	4e−05	14 x 48	chromosome 16 open reading frame 59 [Source:HGNC Symb
8	SLC41A3	0.92	5e−06	4e−05	15 x 50	solute carrier family 41, member 3 [Source:HGNC Symbol;Ac
9	ZDHHC3	0.91	7e−06	4e−05	16 x 50	zinc finger, DHHC−type containing 3 [Source:HGNC Symbol;
10	VPS16	0.9	9e−06	4e−05	16 x 50	vacuolar protein sorting 16 homolog (S. cerevisiae) [Source:
11	FNTB	0.89	1e−05	4e−05	14 x 50	farnesyltransferase, CAAX box, beta [Source:HGNC Symbol;
12	C9orf72	0.89	1e−05	8e−05	16 x 50	chromosome 9 open reading frame 72 [Source:HGNC Symbo
13	PRPF39	0.79	2e−05	8e−05	15 x 48	pre−mRNA processing factor 39 [Source:HGNC Symbol;Acc:
14	TMEM109	0.86	2e−05	8e−05	15 x 50	transmembrane protein 109 [Source:HGNC Symbol;Acc:HGN
15	THAP4	0.86	2e−05	8e−05	13 x 50	THAP domain containing 4 [Source:HGNC Symbol;Acc:HGN
16	LYRM1	0.86	2e−05	1e−04	16 x 50	LYR motif containing 1 [Source:HGNC Symbol;Acc:HGNC:25
17	INO80	0.85	3e−05	2e−04	16 x 50	INO80 complex subunit [Source:HGNC Symbol;Acc:HGNC:2
18	NDEL1	0.84	3e−05	6e−04	15 x 50	nudE neurodevelopment protein 1−like 1 [Source:HGNC Sym
19	STAG1	0.81	6e−05	9e−04	15 x 50	stromal antigen 1 [Source:HGNC Symbol;Acc:HGNC:11354]
20	PQBP1	−0.71	1e−04	9e−04	16 x 50	polyglutamine binding protein 1 [Source:HGNC Symbol;Acc:

p−values



A11_mel

Local Summary

%DE = 0.37

metagenes = 17

genes = 244

genes in genesets = 236

genes with fdr < 0.1 = 29 (6 + / 23 −)

genes with fdr < 0.05 = 19 (3 + / 16 −)

genes with fdr < 0.01 = 11 (2 + / 9 −)

<r> metagenes = 0.94

<r> genes = 0.21

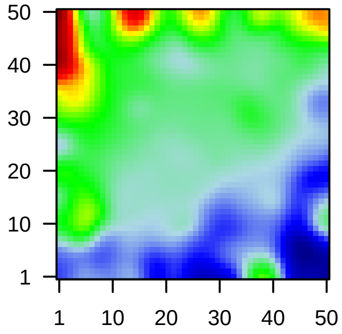
<FC> = −0.17

<shrinkage−t> = −2.65

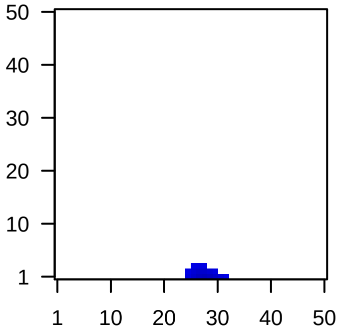
<p−value> = 0.11

<fdr> = 0.83

Profile



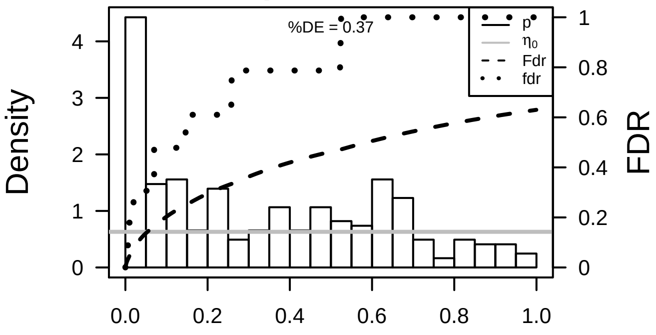
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	TMCO3	1.11	4e−08	4e−05	32 x 1	transmembrane and coiled−coil domains 3 [Source:HGNC Sy
2	LPP	−1.03	3e−07	2e−04	32 x 1	LIM domain containing preferred translocation partner in lipor
3	FNIP1	−0.86	2e−06	2e−04	29 x 1	folliculin interacting protein 1 [Source:HGNC Symbol;Acc:HG
4	FASTKD5	−0.91	6e−06	2e−04	32 x 1	FAST kinase domains 5 [Source:HGNC Symbol;Acc:HGNC:2
5	AP5S1	−0.91	6e−06	2e−04	32 x 1	adaptor−related protein complex 5, sigma 1 subunit [Source:
6	BOD1L1	−0.91	7e−06	4e−03	28 x 1	biorientation of chromosomes in cell division 1−like 1 [Source
7	MMS19	−0.84	3e−05	5e−03	28 x 1	MMS19 nucleotide excision repair homolog (S. cerevisiae) [S
8	RNF149	−0.78	1e−04	5e−03	29 x 1	ring finger protein 149 [Source:HGNC Symbol;Acc:HGNC:23
9	KIF3A	−0.76	1e−04	5e−03	25 x 2	kinesin family member 3A [Source:HGNC Symbol;Acc:HGNC
10	STXBP5	0.77	1e−04	8e−03	31 x 1	syntaxin binding protein 5 (tomosyn) [Source:HGNC Symbol;
11	ETS1	−0.74	2e−04	8e−03	28 x 1	v−ets avian erythroblastosis virus E26 oncogene homolog 1 [
12	SPAG9	−0.65	2e−04	1e−02	32 x 1	sperm associated antigen 9 [Source:HGNC Symbol;Acc:HGN
13	PRPF4B	−0.65	4e−04	1e−02	27 x 1	pre−mRNA processing factor 4B [Source:HGNC Symbol;Acc:
14	DCTN4	−0.7	5e−04	1e−02	26 x 1	dynactin 4 (p62) [Source:HGNC Symbol;Acc:HGNC:15518]
15	FOXO3	0.7	5e−04	1e−02	31 x 1	forkhead box O3 [Source:HGNC Symbol;Acc:HGNC:3821]
16	FLOT1	−0.69	6e−04	1e−02	31 x 1	flotillin 1 [Source:HGNC Symbol;Acc:HGNC:3757]
17	PKN2	−0.69	6e−04	4e−02	29 x 1	protein kinase N2 [Source:HGNC Symbol;Acc:HGNC:9406]
18	TRIM2	−0.66	1e−03	4e−02	30 x 1	tripartite motif containing 2 [Source:HGNC Symbol;Acc:HGN
19	MIB1	−0.65	1e−03	4e−02	29 x 1	mindbomb E3 ubiquitin protein ligase 1 [Source:HGNC Symb
20	FKBP14	−0.64	1e−03	8e−02	26 x 1	FK506 binding protein 14, 22 kDa [Source:HGNC Symbol;Ac

p−values



A11_mel

Local Summary

%DE = 0.7

metagenes = 64

genes = 654

genes in genesets = 653

genes with fdr < 0.1 = 241 (70 + / 171 −)

genes with fdr < 0.05 = 194 (60 + / 134 −)

genes with fdr < 0.01 = 107 (39 + / 68 −)

<r> metagenes = 0.86

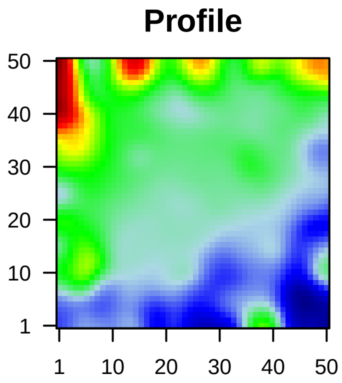
<r> genes = 0.14

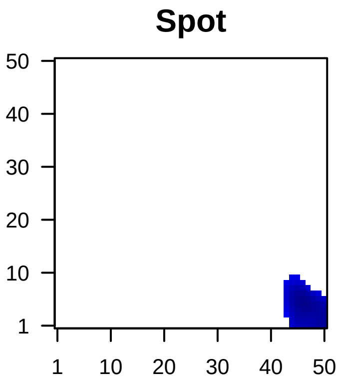
<FC> = −0.17

<shrinkage−t> = −2.61

<p−value> = 0.03

<fdr> = 0.67





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	COL11A1	−1.12	2e−16	4e−14	45 x 1	collagen, type XI, alpha 1 [Source:HGNC Symbol;Acc:HGNC
2	ZCCHC17	−1.41	1e−15	1e−11	46 x 7	zinc finger, CCHC domain containing 17 [Source:HGNC Sym
3	KITLG	1.51	7e−14	5e−09	48 x 1	KIT ligand [Source:HGNC Symbol;Acc:HGNC:6343]
4	SSBP2	1.35	3e−11	7e−08	50 x 3	single−stranded DNA binding protein 2 [Source:HGNC Symb
5	PHF20L1	−1.18	4e−10	7e−08	45 x 8	PHD finger protein 20−like 1 [Source:HGNC Symbol;Acc:HG
6	TCTN1	1.24	7e−10	1e−06	47 x 3	tectonic family member 1 [Source:HGNC Symbol;Acc:HGNC:
7	PVRL3	1.16	8e−09	1e−06	46 x 1	poliovirus receptor−related 3 [Source:HGNC Symbol;Acc:HG
8	TMEM179B	−0.77	1e−08	3e−06	49 x 7	transmembrane protein 179B [Source:HGNC Symbol;Acc:HG
9	CAV2	1.12	3e−08	3e−06	45 x 1	caveolin 2 [Source:HGNC Symbol;Acc:HGNC:1528]
10	STAT2	−0.81	4e−08	5e−06	49 x 5	signal transducer and activator of transcription 2, 113kDa [So
11	ORAOV1	−1.08	7e−08	1e−05	45 x 7	oral cancer overexpressed 1 [Source:HGNC Symbol;Acc:HG
12	DNAJC16	−1.05	1e−07	1e−05	50 x 5	DnaJ (Hsp40) homolog, subfamily C, member 16 [Source:HG
13	EXT2	1.05	2e−07	2e−05	47 x 1	exostosin glycosyltransferase 2 [Source:HGNC Symbol;Acc:
14	CCNL2	−0.94	3e−07	2e−05	45 x 4	cyclin L2 [Source:HGNC Symbol;Acc:HGNC:20570]
15	CDKN1A	−1.02	4e−07	2e−05	50 x 1	cyclin−dependent kinase inhibitor 1A (p21, Cip1) [Source:HG
16	TUBB2A	−0.91	6e−07	2e−05	49 x 6	tubulin, beta 2A class IIa [Source:HGNC Symbol;Acc:HGNC:
17	AASS	−1.01	6e−07	5e−05	50 x 3	aminoadipate−semialdehyde synthase [Source:HGNC Symb
18	ALCAM	−0.99	1e−06	5e−05	50 x 1	activated leukocyte cell adhesion molecule [Source:HGNC S
19	HIST1H3D	0.98	1e−06	7e−05	50 x 1	histone cluster 1, H3d [Source:HGNC Symbol;Acc:HGNC:47
20	UBE2E2	0.96	1e−06	7e−05	50 x 1	ubiquitin−conjugating enzyme E2E 2 [Source:HGNC Symbol;