D1_mel

Global Summary

%DE = 0.21

\# genes with fdr < 0.2 = 2852 (1699 + / 1153 −)

\# genes with fdr < 0.1 = 2224 (1337 + / 887 −)

\# genes with fdr < 0.05 = 1812 (1084 + / 728 −)

\# genes with fdr < 0.01 = 1184 (717 + / 467 −)

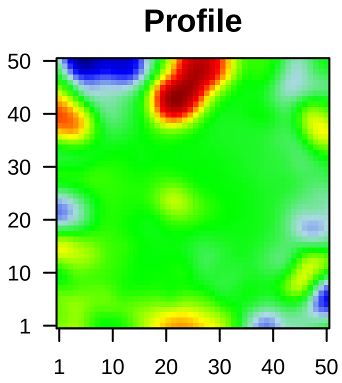
\# genes in genesets = 14839

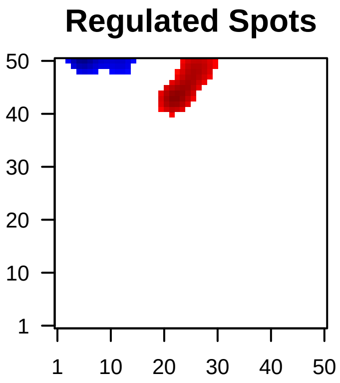
<FC> = 0

<shrinkage−t> = 0.03

<p−value> = 0.07

<fdr> = 0.79



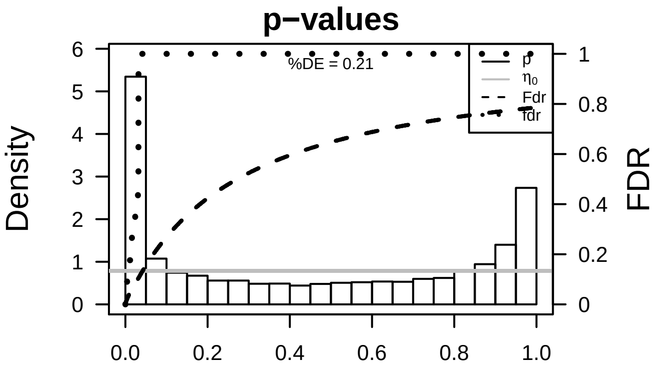


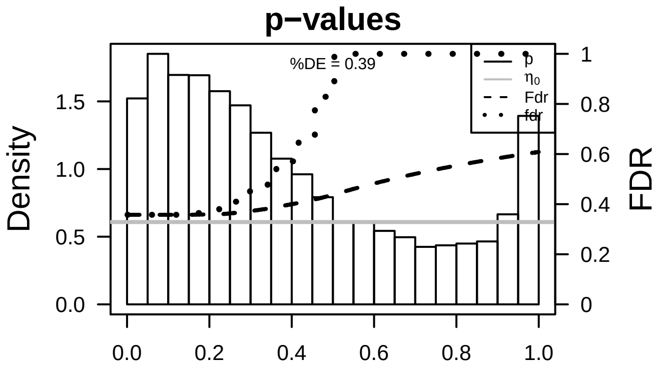
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ABCB5	−1.58	2e−16	1e−13	1 x 43	ATP−binding cassette, sub−family B (MDR/TAP), member 5 [
2	ATP6V1H	−1.81	2e−16	1e−13	5 x 44	ATPase, H+ transporting, lysosomal 50/57kDa, V1 subunit H
3	CCDC167	−1.45	2e−16	1e−13	6 x 39	coiled−coil domain containing 167 [Source:HGNC Symbol;Ac
4	CDC123	−1.55	2e−16	1e−13	46 x 50	cell division cycle 123 [Source:HGNC Symbol;Acc:HGNC:16
5	CEP97	2.09	2e−16	1e−13	2 x 47	centrosomal protein 97kDa [Source:HGNC Symbol;Acc:HGN
6	CNOT1	−1.2	2e−16	1e−13	15 x 50	CCR4−NOT transcription complex, subunit 1 [Source:HGNC
7	DDOST	−1.57	2e−16	1e−13	45 x 18	dolichyl−diphosphooligosaccharide−−protein glycosyltransfer
8	FAM126A	−1.7	2e−16	1e−13	45 x 35	family with sequence similarity 126, member A [Source:HGN
9	GPR107	2.16	2e−16	1e−13	1 x 1	G protein−coupled receptor 107 [Source:HGNC Symbol;Acc:
10	HSD17B4	−1.63	2e−16	1e−13	11 x 50	hydroxysteroid (17−beta) dehydrogenase 4 [Source:HGNC S
11	LAPTM4A	−1.63	2e−16	1e−13	36 x 1	lysosomal protein transmembrane 4 alpha [Source:HGNC Sy
12	NUPR1	−1.58	2e−16	1e−13	45 x 50	nuclear protein, transcriptional regulator, 1 [Source:HGNC Sy
13	PPM1K	−1.16	2e−16	1e−13	40 x 3	protein phosphatase, Mg2+/Mn2+ dependent, 1K [Source:HG
14	PSAT1	−1.72	2e−16	1e−13	14 x 50	phosphoserine aminotransferase 1 [Source:HGNC Symbol;A
15	RAB32	−0.91	2e−16	1e−13	1 x 20	RAB32, member RAS oncogene family [Source:HGNC Symb
16	RAE1	−1.64	2e−16	1e−13	7 x 46	ribonucleic acid export 1 [Source:HGNC Symbol;Acc:HGNC:
17	RBM5	−1.42	2e−16	1e−13	19 x 1	RNA binding motif protein 5 [Source:HGNC Symbol;Acc:HGN
18	RDH11	−1.68	2e−16	1e−13	7 x 40	retinol dehydrogenase 11 (all−trans/9−cis/11−cis) [Source:HG
19	SHMT2	−1.57	2e−16	1e−13	31 x 50	serine hydroxymethyltransferase 2 (mitochondrial) [Source:H
20	SPAG7	−1.65	2e−16	1e−13	2 x 44	sperm associated antigen 7 [Source:HGNC Symbol;Acc:HGN

Global Geneset Analysis

Rank	GSZ	p−value	#all		Geneset
Overexpressed					
1	5.08	0.003	925	GSEA C2	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
2	4.92	0.004	335	Chr	Chr 22
3	4.83	0.004	157	GSEA C2	SCHLOSSER_MYC_TARGETS_REPRESSED_BY_SERUM
4	4.38	0.006	15	BP	lipid biosynthetic process
5	4.33	0.006	834	GSEA C2	LEE_BMP2_TARGETS_DN
6	4.31	0.006	198	HM	HALLMARK_OXIDATIVE_PHOSPHORYLATION
7	4.11	0.007	61	GSEA C2	GOTTWEIN_TARGETS_OF_KSHV_MIR_K12_11
8	4.09	0.007	29	BP	spliceosomal snRNP assembly
9	4.04	0.007	4	GSEA C2	CHESLER_BRAIN_D6MIT150_QTL_CIS
10	4.01	0.007	26	GSEA C2	BIOCARTA_PROTEASOME_PATHWAY
11	3.97	0.008	48	GSEA C2	HOWLIN_PUBERTAL_MAMMARY_GLAND
12	3.96	0.008	23	BP	ncRNA metabolic process
13	3.91	0.008	71	MF	structural constituent of ribosome
14	3.87	0.008	233	GSEA C2	PENG_RAPAMYCIN_RESPONSE_DN
15	3.83	0.009	83	BP	mitochondrial translational initiation
16	3.79	0.009	212	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_6HR_UP
17	3.77	0.009	275	GSEA C2	GRADE_COLON_AND_RECTAL_CANCER_UP
18	3.76	0.009	83	BP	mitochondrial translational elongation
19	3.73	0.009	831	GSEA C2	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
20	3.71	0.010	41	BP	DNA catabolic process, endonucleolytic
Underexpressed					
1	−6.85	0.069	16	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
2	−6.71	0.001	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
3	−6.36	0.002	45	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
4	−6.18	0.002	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
5	−5.98	0.002	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
6	−5.71	0.002	99	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
7	−5.65	0.002	201	GSEA C2	WHITFIELD_CELL_CYCLE_G2_M
8	−5.59	0.002	312	BP	mitotic nuclear division
9	−5.48	0.003	40	GSEA C2	AMUNDSON_GAMMA_RADIATION_RESPONSE
10	−5.42	0.003	409	BP	cell division
11	−5.41	0.003	18	GSEA C2	REACTOME_INHIBITION_OF_THE_PROTEOLYTIC_ACTIVITY_
12	−5.39	0.003	11	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
13	−5.37	0.003	20	GSEA C2	REACTOME_APC_CDC20_MEDIATED_DEGRADATION_OF_NE
14	−5.36	0.003	52	GSEA C2	TANG_SENESCENCE_TP53_TARGETS_DN
15	−5.28	0.003	110	GSEA C2	WHITEFORD_PEDIATRIC_CANCER_MARKERS
16	−4.99	0.004	162	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
17	−4.91	0.004	96	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
18	−4.86	0.004	32	BP	mitotic spindle assembly checkpoint
19	−4.8	0.004	124	GSEA C2	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
20	−4.79	0.004	72	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN





D1_mel

Local Summary

%DE = 0.65

metagenes = 68

genes = 427

genes in genesets = 427

genes with fdr < 0.1 = 204 (171 + / 33 −)

genes with fdr < 0.05 = 153 (136 + / 17 −)

genes with fdr < 0.01 = 111 (98 + / 13 −)

<r> metagenes = 0.69

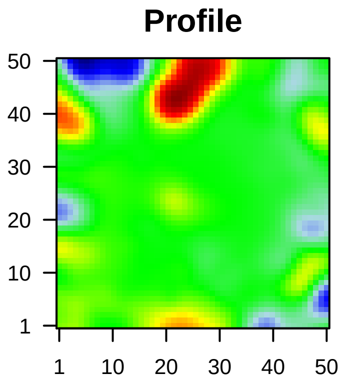
<r> genes = 0.05

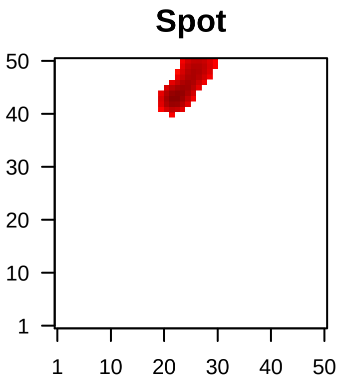
<FC> = 0.33

<shrinkage−t> = 5.24

<p−value> = 0.01

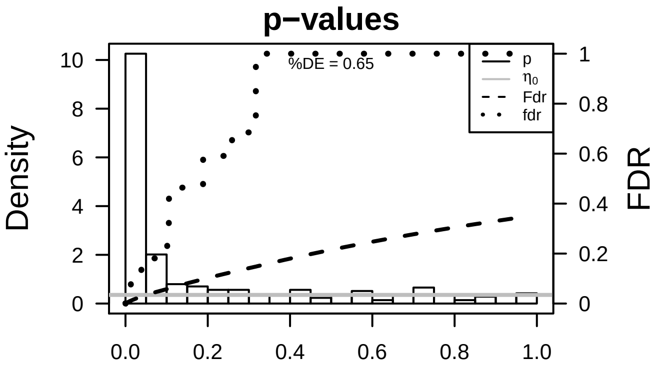
<fdr> = 0.56





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	C12orf10	−1.5	1e−15	1e−10	29 x 50	chromosome 12 open reading frame 10 [Source:HGNC Sym
2	LPAR2	1.66	9e−13	1e−10	21 x 41	lysophosphatidic acid receptor 2 [Source:HGNC Symbol;Acc:
3	ZNF438	1.65	1e−12	1e−10	26 x 45	zinc finger protein 438 [Source:HGNC Symbol;Acc:HGNC:21
4	TXNRD3	1.63	2e−12	1e−10	25 x 44	thioredoxin reductase 3 [Source:HGNC Symbol;Acc:HGNC:2
5	RFPL3S	1.62	3e−12	4e−10	26 x 45	RFPL3 antisense [Source:HGNC Symbol;Acc:HGNC:9981]
6	EDC3	1.59	7e−12	4e−10	26 x 50	enhancer of mRNA decapping 3 [Source:HGNC Symbol;Acc:
7	ZNF699	1.59	9e−12	2e−09	25 x 45	zinc finger protein 699 [Source:HGNC Symbol;Acc:HGNC:24
8	DUS2	1.56	2e−11	1e−08	28 x 49	dihydrouridine synthase 2 [Source:HGNC Symbol;Acc:HGNC
9	PROSER3	1.5	1e−10	5e−08	28 x 47	proline and serine rich 3 [Source:HGNC Symbol;Acc:HGNC:
10	USF1	1.45	4e−10	1e−07	28 x 50	upstream transcription factor 1 [Source:HGNC Symbol;Acc:H
11	ZBED8	1.38	3e−09	1e−07	24 x 50	zinc finger, BED−type containing 8 [Source:HGNC Symbol;A
12	SLC39A4	1.37	4e−09	1e−07	24 x 50	solute carrier family 39 (zinc transporter), member 4 [Source:
13	CDADC1	1.37	4e−09	1e−07	23 x 42	cytidine and dCMP deaminase domain containing 1 [Source:
14	LRIG1	1.37	4e−09	1e−07	22 x 43	leucine−rich repeats and immunoglobulin−like domains 1 [So
15	FRA10AC1	1.36	5e−09	1e−07	26 x 49	fragile site, folic acid type, rare, fra(10)(q23.3) or fra(10)(q24.
16	TMEM231	1.35	6e−09	1e−07	25 x 49	transmembrane protein 231 [Source:HGNC Symbol;Acc:HG
17	INPP4A	1.35	6e−09	7e−07	25 x 45	inositol polyphosphate−4−phosphatase, type I, 107kDa [Sour
18	PPP1R3F	1.33	1e−08	7e−07	26 x 46	protein phosphatase 1, regulatory subunit 3F [Source:HGNC
19	CCDC146	1.31	2e−08	7e−07	25 x 46	coiled−coil domain containing 146 [Source:HGNC Symbol;Ac
20	INTS8	1.3	2e−08	7e−07	25 x 48	integrator complex subunit 8 [Source:HGNC Symbol;Acc:HG



D1_mel

Local Summary

%DE = 0.77

metagenes = 32

genes = 401

genes in genesets = 400

genes with fdr < 0.1 = 240 (48 + / 192 −)

genes with fdr < 0.05 = 198 (41 + / 157 −)

genes with fdr < 0.01 = 119 (27 + / 92 −)

<r> metagenes = 0.89

<r> genes = 0.2

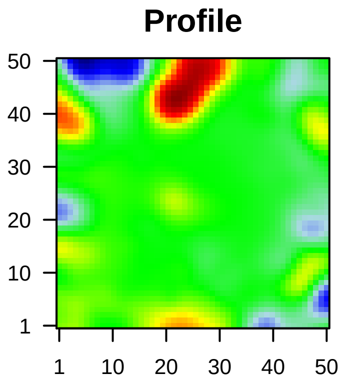
<FC> = −0.31

<shrinkage−t> = −5.11

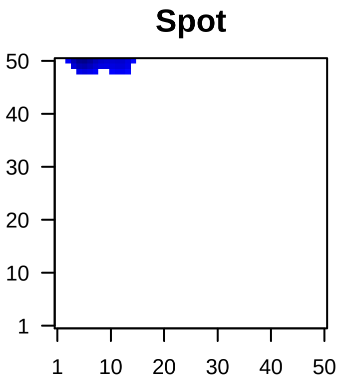
<p−value> = 0.01

<fdr> = 0.54

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CNOT1	−1.2	2e−16	4e−15	15 x 50	CCR4−NOT transcription complex, subunit 1 [Source:HGNC
2	HSD17B4	−1.63	2e−16	4e−15	11 x 50	hydroxysteroid (17−beta) dehydrogenase 4 [Source:HGNC S
3	PSAT1	−1.72	2e−16	4e−15	14 x 50	phosphoserine aminotransferase 1 [Source:HGNC Symbol;A
4	TIMM21	−1.37	2e−16	4e−15	14 x 50	translocase of inner mitochondrial membrane 21 homolog (ye
5	TMEM106C	−2.07	2e−16	4e−15	5 x 48	transmembrane protein 106C [Source:HGNC Symbol;Acc:HG
6	BUB3	−0.8	5e−11	3e−09	7 x 48	BUB3 mitotic checkpoint protein [Source:HGNC Symbol;Acc:
7	MAD2L1	−1.35	7e−11	3e−09	5 x 50	MAD2 mitotic arrest deficient−like 1 (yeast) [Source:HGNC S
8	CCNG1	−0.78	1e−10	9e−09	12 x 48	cyclin G1 [Source:HGNC Symbol;Acc:HGNC:1592]
9	PCM1	−1.33	2e−10	3e−08	11 x 50	pericentriolar material 1 [Source:HGNC Symbol;Acc:HGNC:8
10	STMN1	−0.58	5e−10	4e−08	5 x 50	stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]
11	RAP1GDS1	−1.29	1e−09	4e−08	14 x 50	RAP1, GTP−GDP dissociation stimulator 1 [Source:HGNC S
12	KIAA0101	−1.29	1e−09	7e−07	3 x 50	KIAA0101 [Source:HGNC Symbol;Acc:HGNC:28961]
13	TK1	−1.06	1e−08	7e−07	4 x 50	thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:HGN
14	PIGK	−1.14	2e−08	7e−07	13 x 50	phosphatidylinositol glycan anchor biosynthesis, class K [Sou
15	PDCD4	−0.78	3e−08	7e−07	12 x 48	programmed cell death 4 (neoplastic transformation inhibitor)
16	CENPN	−1.21	3e−08	1e−06	4 x 50	centromere protein N [Source:HGNC Symbol;Acc:HGNC:308
17	PRC1	−1.2	6e−08	1e−06	5 x 50	protein regulator of cytokinesis 1 [Source:HGNC Symbol;Acc:
18	CAT	−1.19	6e−08	1e−06	14 x 50	catalase [Source:HGNC Symbol;Acc:HGNC:1516]
19	IMMP1L	−1.19	8e−08	1e−06	10 x 50	IMP1 inner mitochondrial membrane peptidase−like (S. cerev
20	LRR1	−1.19	8e−08	1e−06	4 x 49	leucine rich repeat protein 1 [Source:HGNC Symbol;Acc:HGN

p−values