C3_mel

Global Summary

%DE = 0.21

genes with fdr < 0.2 = 2676 (1618 + / 1058 −)

genes with fdr < 0.1 = 2216 (1359 + / 857 −)

genes with fdr < 0.05 = 1784 (1099 + / 685 −)

genes with fdr < 0.01 = 1204 (739 + / 465 −)

genes in genesets = 14839

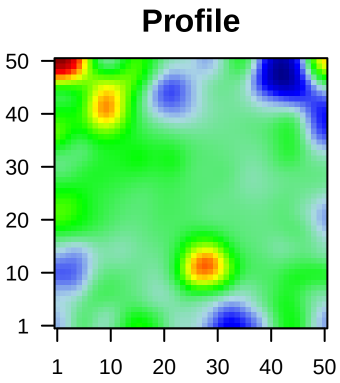
<FC> = 0

<shrinkage−t> = 0.01

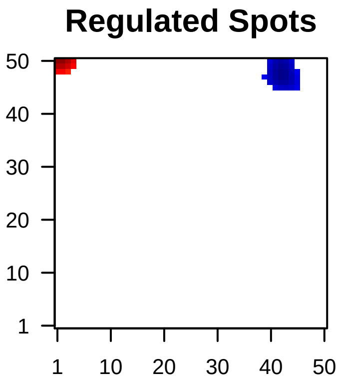
<p−value> = 0.08

<fdr> = 0.79

Profile



Regulated Spots



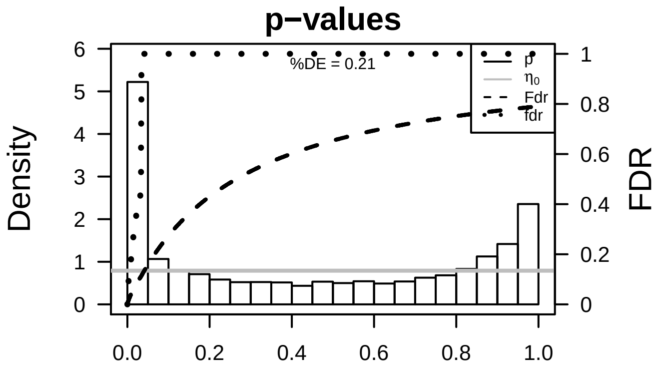
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	AMZ2	−1.52	2e−16	1e−13	48 x 42	archaelysin family metallopeptidase 2 [Source:HGNC Symbol
2	APEH	−1.64	2e−16	1e−13	1 x 42	acylaminoacyl−peptide hydrolase [Source:HGNC Symbol;Acc
3	BRD8	−1.76	2e−16	1e−13	50 x 39	bromodomain containing 8 [Source:HGNC Symbol;Acc:HGNC
4	CFAP20	−1.62	2e−16	1e−13	40 x 50	cilia and flagella associated protein 20 [Source:HGNC Symbo
5	CHD4	−1.77	2e−16	1e−13	21 x 43	chromodomain helicase DNA binding protein 4 [Source:HGNC
6	COPZ1	−1.68	2e−16	1e−13	46 x 45	coatomer protein complex, subunit zeta 1 [Source:HGNC Syn
7	CXCL1	2.09	2e−16	1e−13	42 x 36	chemokine (C−X−C motif) ligand 1 (melanoma growth stimula
8	EPS8	−1.98	2e−16	1e−13	49 x 13	epidermal growth factor receptor pathway substrate 8 [Source
9	GNPDA1	−1.52	2e−16	1e−13	1 x 42	glucosamine−6−phosphate deaminase 1 [Source:HGNC Sym
10	ID3	−1.73	2e−16	1e−13	11 x 50	inhibitor of DNA binding 3, dominant negative helix−loop−heli
11	ILK	−1.62	2e−16	1e−13	43 x 50	integrin−linked kinase [Source:HGNC Symbol;Acc:HGNC:60
12	LSM10	−1.56	2e−16	1e−13	46 x 50	LSM10, U7 small nuclear RNA associated [Source:HGNC Sy
13	MARS	−1.72	2e−16	1e−13	43 x 47	methionyl−tRNA synthetase [Source:HGNC Symbol;Acc:HGN
14	MSC	−1.62	2e−16	1e−13	32 x 1	musculin [Source:HGNC Symbol;Acc:HGNC:7321]
15	NDUFB3	−2	2e−16	1e−13	40 x 48	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12
16	NUF2	2.01	2e−16	1e−13	6 x 50	NUF2, NDC80 kinetochore complex component [Source:HGN
17	PIR	−1.48	2e−16	1e−13	1 x 42	pirin (iron−binding nuclear protein) [Source:HGNC Symbol;Ac
18	PSAT1	−1.72	2e−16	1e−13	14 x 50	phosphoserine aminotransferase 1 [Source:HGNC Symbol;Ac
19	RBM3	−1.58	2e−16	1e−13	5 x 15	RNA binding motif (RNP1, RRM) protein 3 [Source:HGNC Sy
20	RTCB	−1.65	2e−16	1e−13	50 x 39	RNA 2',3'−cyclic phosphate and 5'−OH ligase [Source:HGNC

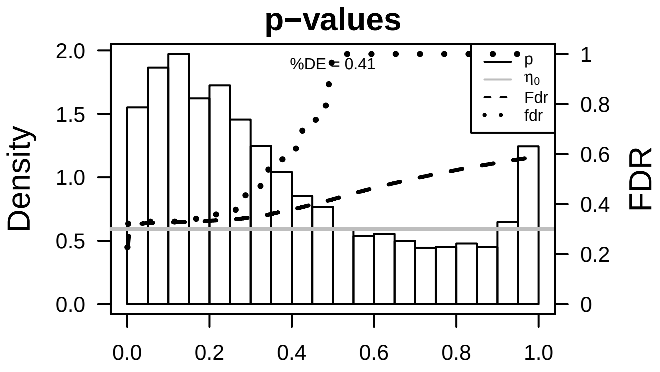
Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	10.49	2e−04	305	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
2	9.71	3e−04	267	GSEA C2	ZHANG_TLX_TARGETS_60HR_DN
3	9.34	3e−04	242	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
4	8.87	4e−04	145	GSEA C2	CHANG_CYCLING_GENES
5	8.77	4e−04	335	GSEA C2	WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_DN
6	8.76	4e−04	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
7	8.73	5e−04	81	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
8	8.52	5e−04	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
9	8.29	5e−04	136	GSEA C2	RUIZ_TNC_TARGETS_DN
10	8.26	6e−04	390	GSEA C2	PUJANA_BRCA2_PCC_NETWORK
11	8.23	6e−04	700	GSEA C2	MARSON_BOUND_BY_E2F4_UNSTIMULATED
12	7.66	7e−04	54	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
13	7.53	8e−04	59	GSEA C2	KAUFFMANN_MELANOMA_RELAPSE_UP
14	7.48	8e−04	99	GSEA C2	BURTON_ADIPOGENESIS_3
15	7.33	9e−04	198	GSEA C2	FUJII_YBX1_TARGETS_DN
16	7.31	9e−04	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
17	7.26	9e−04	197	HM	HALLMARK_E2F_TARGETS
18	7.03	1e−03	609	GSEA C2	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIA
19	7.03	1e−03	87	GSEA C2	ZHANG_TLX_TARGETS_UP
20	6.81	1e−03	327	GSEA C2	BLUM_RESPONSE_TO_SALIRASIB_DN
Underexpressed					
1	−4.29	0.006	132	GSEA C2	RAY_TUMORIGENESIS_BY_ERBB2_CDC25A_DN
2	−4.15	0.007	13	BP	COPI coating of Golgi vesicle
3	−4.02	0.007	147	BP	tRNA metabolic process
4	−3.9	0.008	421	GSEA C2	MOOTHA_MITOCHONDRIA
5	−3.87	0.008	40	Cancer	PanCan_HK_geneset_nanostring
6	−3.69	0.010	79	GSEA C2	MORI_SMALL_PRE_BII_LYMPHOCYTE_UP
7	−3.69	0.010	41	CC	mitochondrial nucleoid
8	−3.69	0.010	405	GSEA C2	MOOTHA_HUMAN_MITODB_6_2002
9	−3.68	0.010	9	TF	MYC_Targets DOWN
10	−3.67	0.010	1468	CC	mitochondrion
11	−3.65	0.010	27	Glio	Sturm_GBM_Meth_overexpression_H_K27_UP
12	−3.64	0.010	10	GSEA C2	REACTOME_COPI_MEDIATED_TRANSPORT
13	−3.6	0.010	26	GSEA C2	KRIGE_AMINO_ACID_DEPRIVATION
14	−3.58	0.011	8	GSEA C2	GAUTSCHI_SRC_SIGNALING
15	−3.54	0.011	15	CC	RNA polymerase II transcription factor complex
16	−3.46	0.012	18	CC	DNA−directed RNA polymerase III complex
17	−3.46	0.012	18	MF	RNA polymerase III activity
18	−3.46	0.012	18	BP	termination of RNA polymerase III transcription
19	−3.46	0.012	18	BP	transcription elongation from RNA polymerase III promoter
20	−3.46	0.012	17	GSEA C2	KIM_PTEN_TARGETS_UP

p−values



p−values



C3_mel

Local Summary

%DE = 0.86

metagenes = 11

genes = 187

genes in genesets = 186

genes with fdr < 0.1 = 139 (125 + / 14 −)

genes with fdr < 0.05 = 128 (116 + / 12 −)

genes with fdr < 0.01 = 98 (93 + / 5 −)

<r> metagenes = 0.98

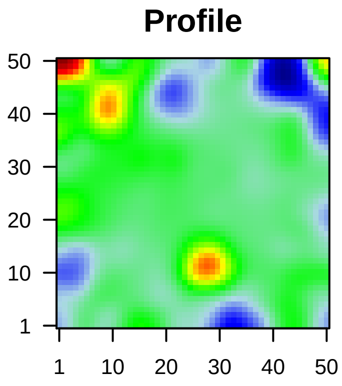
<r> genes = 0.31

<FC> = 0.54

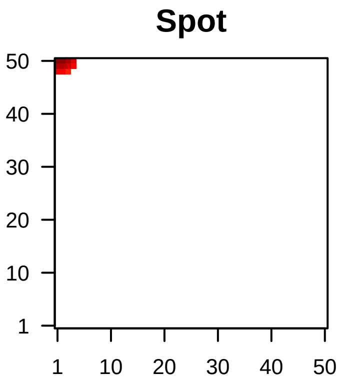
<shrinkage−t> = 8.54

<p−value> = 0

<fdr> = 0.39



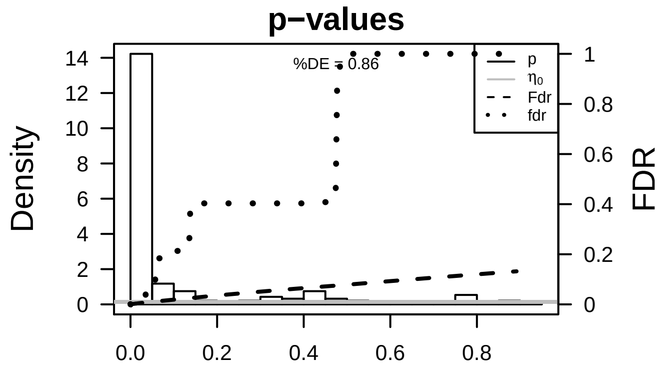
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	KNTC1	1.53	6e−11	8e−10	1 x 50	kinetochore associated 1 [Source:HGNC Symbol;Acc:HGNC:
2	EXO1	1.55	6e−11	1e−09	1 x 50	exonuclease 1 [Source:HGNC Symbol;Acc:HGNC:3511]
3	RNASEH2B	1.53	1e−10	5e−09	1 x 50	ribonuclease H2, subunit B [Source:HGNC Symbol;Acc:HGN
4	CENPQ	1.49	3e−10	8e−09	2 x 50	centromere protein Q [Source:HGNC Symbol;Acc:HGNC:213
5	MCM6	1.46	8e−10	8e−09	1 x 50	minichromosome maintenance complex component 6 [Source
6	CDC6	1.44	1e−09	8e−09	1 x 50	cell division cycle 6 [Source:HGNC Symbol;Acc:HGNC:1744]
7	TAF1A	1.44	1e−09	1e−08	1 x 48	TATA box binding protein (TBP)−associated factor, RNA polym
8	ZNF367	1.43	2e−09	9e−08	1 x 49	zinc finger protein 367 [Source:HGNC Symbol;Acc:HGNC:18
9	CDC45	1.38	6e−09	9e−08	1 x 50	cell division cycle 45 [Source:HGNC Symbol;Acc:HGNC:1739
10	SIN3A	1.36	1e−08	9e−08	1 x 49	SIN3 transcription regulator family member A [Source:HGNC
11	MND1	1.34	1e−08	9e−08	1 x 50	meiotic nuclear divisions 1 homolog (S. cerevisiae) [Source:H
12	ESCO2	1.34	2e−08	2e−07	4 x 50	establishment of sister chromatid cohesion N−acetyltransfera
13	HELLS	1.24	2e−08	8e−07	1 x 50	helicase, lymphoid−specific [Source:HGNC Symbol;Acc:HGN
14	OMD	1.27	8e−08	8e−07	1 x 49	osteomodulin [Source:HGNC Symbol;Acc:HGNC:8134]
15	ACTL6A	0.76	9e−08	9e−07	4 x 50	actin−like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
16	TUBGCP3	1.26	1e−07	1e−06	1 x 48	tubulin, gamma complex associated protein 3 [Source:HGNC
17	PSMC3IP	1.22	2e−07	1e−06	1 x 50	PSMC3 interacting protein [Source:HGNC Symbol;Acc:HGNC
18	ZGRF1	1.22	3e−07	1e−06	1 x 50	zinc finger, GRF−type containing 1 [Source:HGNC Symbol;Ac
19	TEN1	1.22	3e−07	3e−06	1 x 48	TEN1 CST complex subunit [Source:HGNC Symbol;Acc:HGN
20	ATAD2	1.2	4e−07	3e−06	2 x 50	ATPase family, AAA domain containing 2 [Source:HGNC Sym



p−values

C3_mel

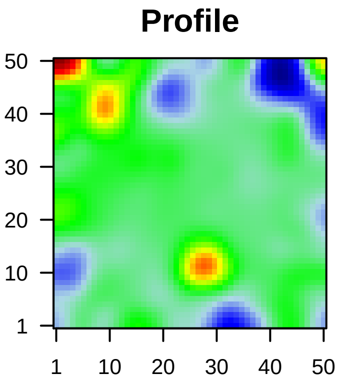
Local Summary

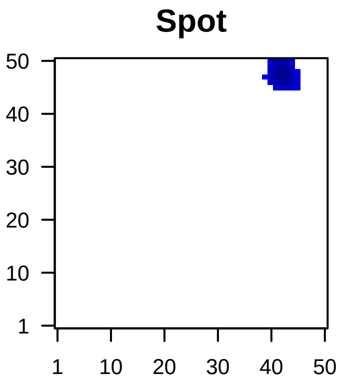
%DE = 0.72
metagenes = 34
genes = 261
genes in genesets = 261

genes with fdr < 0.1 = 138 (20 + / 118 −)
genes with fdr < 0.05 = 114 (13 + / 101 −)
genes with fdr < 0.01 = 83 (7 + / 76 −)

<r> metagenes = 0.87
<r> genes = 0.07

<FC> = −0.35
<shrinkage−t> = −6.02
<p−value> = 0
<fdr> = 0.51





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CFAP20	−1.62	2e−16	3e−15	40 x 50	cilia and flagella associated protein 20 [Source:HGNC Symbo
2	ILK	−1.62	2e−16	3e−15	43 x 50	integrin−linked kinase [Source:HGNC Symbol;Acc:HGNC:60
3	MARS	−1.72	2e−16	3e−15	43 x 47	methionyl−tRNA synthetase [Source:HGNC Symbol;Acc:HGN
4	NDUFB3	−2	2e−16	3e−15	40 x 48	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 1
5	VPS26A	−1.48	2e−16	3e−15	40 x 50	vacuolar protein sorting 26 homolog A (S. pombe) [Source:H
6	MLX	−1.36	3e−11	1e−09	44 x 49	MLX, MAX dimerization protein [Source:HGNC Symbol;Acc:H
7	FUNDC2	−1.38	4e−11	1e−09	45 x 45	FUN14 domain containing 2 [Source:HGNC Symbol;Acc:HGN
8	SGCE	−1.38	5e−11	1e−09	42 x 47	sarcoglycan, epsilon [Source:HGNC Symbol;Acc:HGNC:108
9	TMEM223	−1.37	6e−11	1e−08	41 x 50	transmembrane protein 223 [Source:HGNC Symbol;Acc:HGN
10	AKIP1	−1.33	2e−10	1e−07	44 x 46	A kinase (PRKA) interacting protein 1 [Source:HGNC Symbol
11	MAGEC1	−1.31	2e−09	2e−07	44 x 45	melanoma antigen family C1 [Source:HGNC Symbol;Acc:HG
12	DNAJA1	−1.08	5e−09	4e−07	41 x 47	DnaJ (Hsp40) homolog, subfamily A, member 1 [Source:HGN
13	GPN1	−1.25	1e−08	3e−06	44 x 48	GPN−loop GTPase 1 [Source:HGNC Symbol;Acc:HGNC:170
14	SMIM15	−1.11	5e−08	3e−06	42 x 50	small integral membrane protein 15 [Source:HGNC Symbol;A
15	APOBEC3C	−1.16	9e−08	3e−06	40 x 50	apolipoprotein B mRNA editing enzyme, catalytic polypeptide
16	DNAJC10	−1.19	1e−07	3e−06	40 x 48	DnaJ (Hsp40) homolog, subfamily C, member 10 [Source:HG
17	ORC5	−1.19	2e−07	3e−06	41 x 48	origin recognition complex, subunit 5 [Source:HGNC Symbol;
18	C1orf131	−1.18	2e−07	4e−06	40 x 50	chromosome 1 open reading frame 131 [Source:HGNC Symb
19	BCAP29	−0.82	2e−07	5e−06	41 x 47	B−cell receptor−associated protein 29 [Source:HGNC Symbo
20	AAR2	−1.14	3e−07	5e−06	43 x 46	AAR2 splicing factor homolog (S. cerevisiae) [Source:HGNC