C2_mel

Global Summary

%DE = 0.17

genes with fdr < 0.2 = 1882 (1013 + / 869 −)

genes with fdr < 0.1 = 1380 (716 + / 664 −)

genes with fdr < 0.05 = 1100 (548 + / 552 −)

genes with fdr < 0.01 = 579 (222 + / 357 −)

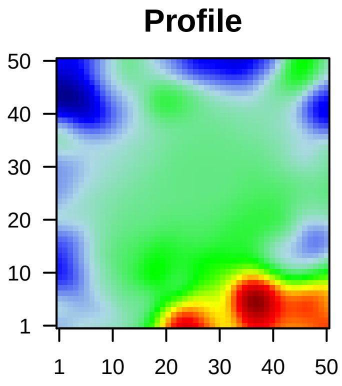
genes in genesets = 14839

<FC> = 0

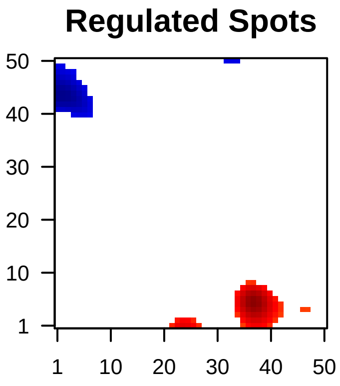
<shrinkage−t> = −0.24

<p−value> = 0.12

<fdr> = 0.83



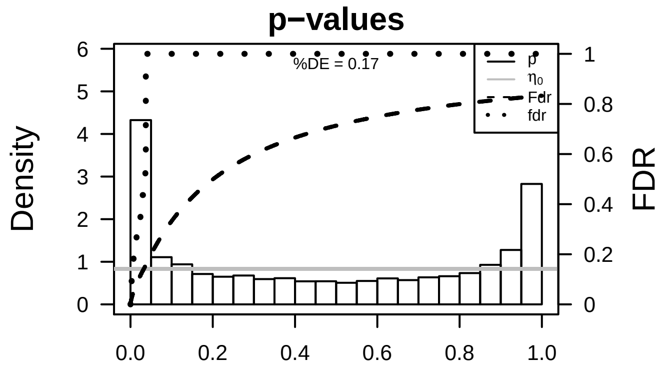
Profile



Regulated Spots

Global Genelist

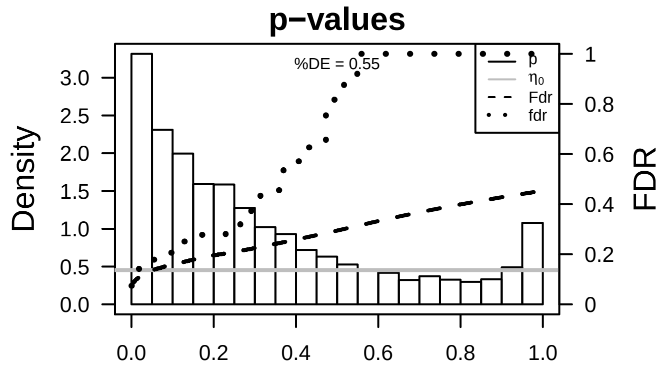
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ALG8	−1.48	2e−16	7e−14	5 x 43	ALG8, alpha−1,3−glucosyltransferase [Source:HGNC Symbo
2	APEX1	−1.67	2e−16	7e−14	29 x 50	APEX nuclease (multifunctional DNA repair enzyme) 1 [Sourc
3	C14orf166	−1.84	2e−16	7e−14	32 x 50	chromosome 14 open reading frame 166 [Source:HGNC Sym
4	CCT2	−2.31	2e−16	7e−14	31 x 50	chaperonin containing TCP1, subunit 2 (beta) [Source:HGNC
5	CCT6A	−2.41	2e−16	7e−14	6 x 41	chaperonin containing TCP1, subunit 6A (zeta 1) [Source:HG
6	CCT7	−2.15	2e−16	7e−14	1 x 17	chaperonin containing TCP1, subunit 7 (eta) [Source:HGNC
7	CITED1	−1.92	2e−16	7e−14	1 x 41	Cbp/p300−interacting transactivator, with Glu/Asp−rich carbo
8	CTSC	−1.99	2e−16	7e−14	1 x 42	cathepsin C [Source:HGNC Symbol;Acc:HGNC:2528]
9	DERL2	−1.85	2e−16	7e−14	6 x 41	derlin 2 [Source:HGNC Symbol;Acc:HGNC:17943]
10	EIF4A1	−1.43	2e−16	7e−14	1 x 27	eukaryotic translation initiation factor 4A1 [Source:HGNC Syn
11	EMC3	−1.92	2e−16	7e−14	5 x 43	ER membrane protein complex subunit 3 [Source:HGNC Sym
12	FAM96A	−2.09	2e−16	7e−14	1 x 11	family with sequence similarity 96, member A [Source:HGNC
13	GGH	−2.01	2e−16	7e−14	4 x 47	gamma−glutamyl hydrolase (conjugase, folylpolygammagluta
14	GNG5	−2.15	2e−16	7e−14	6 x 43	guanine nucleotide binding protein (G protein), gamma 5 [Sou
15	HSPA4	−1.88	2e−16	7e−14	6 x 8	heat shock 70kDa protein 4 [Source:HGNC Symbol;Acc:HGN
16	IDH3A	−2.24	2e−16	7e−14	1 x 42	isocitrate dehydrogenase 3 (NAD+) alpha [Source:HGNC Syr
17	ITGB1BP1	−2.17	2e−16	7e−14	1 x 44	integrin beta 1 binding protein 1 [Source:HGNC Symbol;Acc:
18	LGALS3BP	−1.88	2e−16	7e−14	47 x 17	lectin, galactoside−binding, soluble, 3 binding protein [Source
19	MBP	−1.47	2e−16	7e−14	1 x 42	myelin basic protein [Source:HGNC Symbol;Acc:HGNC:6925
20	MLANA	−1.47	2e−16	7e−14	1 x 43	melan−A [Source:HGNC Symbol;Acc:HGNC:7124]



p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	8.52	5e−04	3396	Lymphoma	HOPP_Repressed
2	7.57	8e−04	2188	Lymphoma	HOPP_Poised_promoter
3	7.04	1e−03	2185	Brain	Fetal_TssA
4	6.58	1e−03	3897	Colon Cancer	Quies1_Colon
5	6.23	2e−03	1949	Brain	Fetal_TssF
6	6.11	2e−03	1907	Brain	Fetal_TxTrans
7	5.82	2e−03	2159	Colon Cancer	TssP_Colon
8	5.52	3e−03	286	GSEA C2	PASINI_SUZ12_TARGETS_DN
9	5.12	3e−03	1013	Brain	Fetal_TssP
10	5.08	3e−03	2563	Lymphoma	HOPP_Heterochrom
11	5.07	3e−03	1139	TF	HEBENSTREIT_low expression TF
12	4.91	4e−03	195	GSEA C2	SENESE_HDAC1_AND_HDAC2_TARGETS_DN
13	4.89	4e−03	618	GSEA C2	GOZGIT_ESR1_TARGETS_DN
14	4.84	4e−03	1308	GSEA C2	DODD_NASOPHARYNGEAL_CARCINOMA_UP
15	4.8	4e−03	117	Colon Cancer	Marisa_CRC−cluster−b
16	4.76	4e−03	3088	CC	plasma membrane
17	4.73	4e−03	3383	Colon Cancer	EnhWk2_Colon
18	4.57	5e−03	616	GSEA C2	NABA_MATRISOME
19	4.51	5e−03	111	GSEA C2	ZHU_CMV_ALL_DN
20	4.38	6e−03	1394	GSEA C2	ZWANG_TRANSIENTLY_UP_BY_1ST_EGF_PULSE_ONLY
Underexpressed					
1	−12.33	1e−04	562	GSEA C2	CAIRO_HEPATOBLASTOMA_CLASSES_UP
2	−11.01	2e−04	341	GSEA C2	RHEIN_ALL_GLUCOCORTICOID_THERAPY_DN
3	−10.86	2e−04	724	GSEA C2	PUJANA_CHEK2_PCC_NETWORK
4	−10.83	2e−04	188	HM	HALLMARK_MYC_TARGETS_V1
5	−10.8	2e−04	1460	GSEA C2	PUJANA_BRCA1_PCC_NETWORK
6	−10.79	2e−04	13	GSEA C2	FU_INTERACT_WITH_ALKBH8
7	−10.29	2e−04	6929	Lymphoma	HOPP_Txn_elongation
8	−10	3e−04	1251	GSEA C2	DODD_NASOPHARYNGEAL_CARCINOMA_DN
9	−9.61	3e−04	756	GSEA C2	WEI_MYCN_TARGETS_WITH_E_BOX
10	−9.53	3e−04	298	GSEA C2	TARTE_PLASMA_CELL_VS_PLASMABLAST_DN
11	−9.32	3e−04	5184	Lymphoma	HOPP_Txn_transition
12	−9.3	3e−04	1192	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
13	−9.23	4e−04	1326	GSEA C2	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
14	−9.22	4e−04	9013	Brain	Overlap_fetal_midbrain_K9K27me3
15	−9.18	4e−04	294	Lymphoma	TARTE_Plasmablast signature
16	−8.96	4e−04	834	GSEA C2	LEE_BMP2_TARGETS_DN
17	−8.94	4e−04	312	GSEA C2	WONG_EMBRYONIC_STEM_CELL_CORE
18	−8.84	4e−04	327	GSEA C2	BLUM_RESPONSE_TO_SALIRASIB_DN
19	−8.7	5e−04	157	GSEA C2	SCHLOSSER_MYC_TARGETS_REPRESSED_BY_SERUM
20	−8.7	5e−04	9482	Colon Cancer	TssA_Colon



p−values

C2_mel

Local Summary

%DE = 0.99

metagenes = 10

genes = 153

genes in genesets = 149

genes with fdr < 0.1 = 151 (151 + / 0 −)

genes with fdr < 0.05 = 144 (144 + / 0 −)

genes with fdr < 0.01 = 133 (133 + / 0 −)

<r> metagenes = 0.96

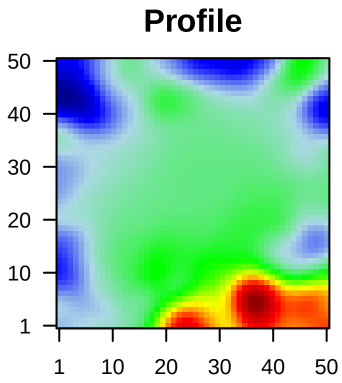
<r> genes = 0.16

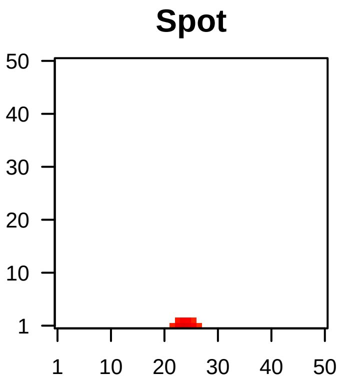
<FC> = 0.85

<shrinkage−t> = 13.01

<p−value> = 0.01

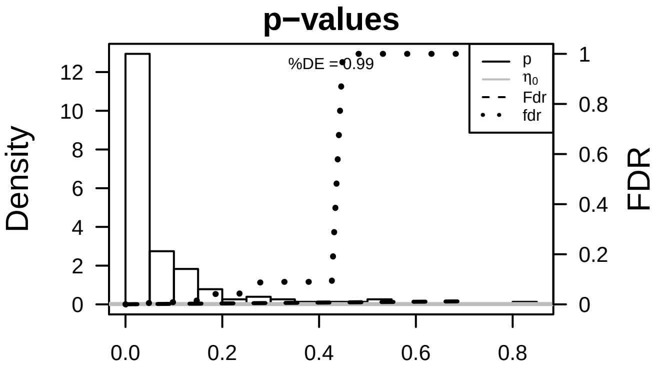
<fdr> = 0.5





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	PELP1	1.9	1e−07	2e−07	25 x 1	proline, glutamate and leucine rich protein 1 [Source:HGNC
2	BMP4	1.84	3e−07	2e−07	24 x 1	bone morphogenetic protein 4 [Source:HGNC Symbol;Acc:H
3	RCBTB2	1.84	3e−07	2e−06	24 x 1	regulator of chromosome condensation (RCC1) and BTB (P
4	BBS10	1.74	1e−06	3e−06	23 x 1	Bardet−Biedl syndrome 10 [Source:HGNC Symbol;Acc:HGN
5	ATG4A	1.64	5e−06	3e−06	22 x 1	autophagy related 4A, cysteine peptidase [Source:HGNC Sy
6	ITSN2	1.62	7e−06	3e−06	23 x 1	intersectin 2 [Source:HGNC Symbol;Acc:HGNC:6184]
7	IKBKE	1.62	7e−06	3e−06	22 x 1	inhibitor of kappa light polypeptide gene enhancer in B−cells,
8	TSPAN31	1.62	7e−06	4e−06	23 x 2	tetraspanin 31 [Source:HGNC Symbol;Acc:HGNC:10539]
9	AKR1C3	1.59	1e−05	4e−06	26 x 1	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
10	FBXO36	1.58	1e−05	1e−05	23 x 1	F−box protein 36 [Source:HGNC Symbol;Acc:HGNC:27020]
11	ADCY6	1.55	2e−05	5e−05	25 x 1	adenylate cyclase 6 [Source:HGNC Symbol;Acc:HGNC:237]
12	ARNT	1.44	6e−05	5e−05	27 x 1	aryl hydrocarbon receptor nuclear translocator [Source:HGN
13	BAG3	1.42	8e−05	5e−05	23 x 1	BCL2−associated athanogene 3 [Source:HGNC Symbol;Acc:
14	POLL	1.39	1e−04	5e−05	23 x 1	polymerase (DNA directed), lambda [Source:HGNC Symbol;
15	CTC−479C5.	1.39	1e−04	8e−05	25 x 1	
16	TLE1	1.36	1e−04	1e−04	26 x 1	transducin−like enhancer of split 1 (E(sp1) homolog, Drosoph
17	PRKCE	1.29	3e−04	1e−04	27 x 1	protein kinase C, epsilon [Source:HGNC Symbol;Acc:HGNC:
18	ADCK4	1.28	4e−04	1e−04	23 x 1	aarF domain containing kinase 4 [Source:HGNC Symbol;Acc
19	SH3BGRL2	1.27	4e−04	1e−04	24 x 1	SH3 domain binding glutamate−rich protein like 2 [Source:HG
20	PLEKHA4	1.26	4e−04	1e−04	25 x 1	pleckstrin homology domain containing, family A (phosphoino



C2_mel

Local Summary

%DE = 0.99

metagenes = 62

genes = 511

genes in genesets = 505

genes with fdr < 0.1 = 501 (500 + / 1 −)

genes with fdr < 0.05 = 475 (475 + / 0 −)

genes with fdr < 0.01 = 453 (453 + / 0 −)

<r> metagenes = 0.84

<r> genes = 0.15

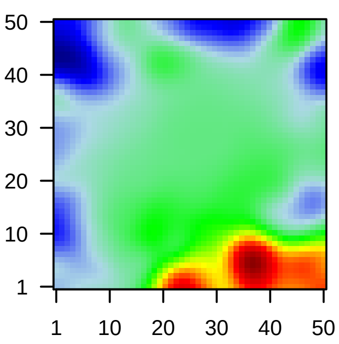
<FC> = 1

<shrinkage−t> = 15.35

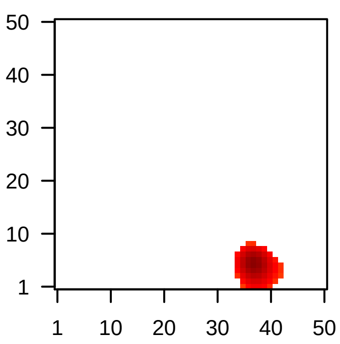
<p−value> = 0

<fdr> = 0.35

Profile



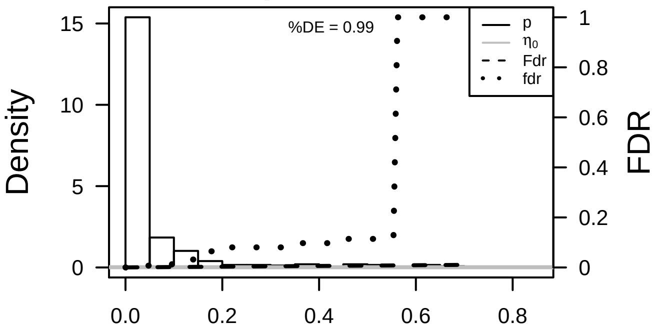
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	FAP	2.68	9e−14	4e−10	37 x 6	fibroblast activation protein, alpha [Source:HGNC Symbol;Acc
2	CLU	2.35	6e−11	1e−08	37 x 5	clusterin [Source:HGNC Symbol;Acc:HGNC:2095]
3	CPNE7	2.15	2e−09	3e−08	37 x 6	copine VII [Source:HGNC Symbol;Acc:HGNC:2320]
4	KLHDC8B	2.08	7e−09	3e−08	35 x 1	kelch domain containing 8B [Source:HGNC Symbol;Acc:HGN
5	WDR90	2.04	1e−08	3e−08	37 x 7	WD repeat domain 90 [Source:HGNC Symbol;Acc:HGNC:26
6	C2orf42	2.03	2e−08	1e−07	36 x 2	chromosome 2 open reading frame 42 [Source:HGNC Symbo
7	HSF4	1.98	4e−08	5e−07	37 x 5	heat shock transcription factor 4 [Source:HGNC Symbol;Acc:
8	CLDN15	1.9	1e−07	5e−07	37 x 6	claudin 15 [Source:HGNC Symbol;Acc:HGNC:2036]
9	STAMBPL1	1.85	3e−07	5e−07	35 x 5	STAM binding protein−like 1 [Source:HGNC Symbol;Acc:HGN
10	FHL3	1.83	4e−07	5e−07	36 x 6	four and a half LIM domains 3 [Source:HGNC Symbol;Acc:HG
11	PPP1R12B	1.81	4e−07	5e−07	37 x 7	protein phosphatase 1, regulatory subunit 12B [Source:HGNC
12	ARL6	1.79	6e−07	5e−07	35 x 7	ADP−ribosylation factor−like 6 [Source:HGNC Symbol;Acc:HG
13	C15orf65	1.79	7e−07	5e−07	37 x 5	chromosome 15 open reading frame 65 [Source:HGNC Symb
14	MRAS	1.78	7e−07	5e−07	37 x 6	muscle RAS oncogene homolog [Source:HGNC Symbol;Acc:
15	TMEM140	1.78	7e−07	7e−07	37 x 5	transmembrane protein 140 [Source:HGNC Symbol;Acc:HGN
16	ZNF350	1.76	9e−07	7e−07	37 x 6	zinc finger protein 350 [Source:HGNC Symbol;Acc:HGNC:16
17	TEP1	1.75	1e−06	7e−07	37 x 6	telomerase−associated protein 1 [Source:HGNC Symbol;Acc
18	AQPEP	1.75	1e−06	7e−07	37 x 5	
19	SOBP	1.74	1e−06	7e−07	37 x 6	sine oculis binding protein homolog (Drosophila) [Source:HG
20	DGKH	1.74	1e−06	7e−07	37 x 5	diacylglycerol kinase, eta [Source:HGNC Symbol;Acc:HGNC:

p−values



C2_mel

Local Summary

%DE = 0.85

metagenes = 2

genes = 26

genes in genesets = 26

genes with fdr < 0.1 = 15 (15 + / 0 −)

genes with fdr < 0.05 = 13 (13 + / 0 −)

genes with fdr < 0.01 = 13 (13 + / 0 −)

<r> metagenes = 1

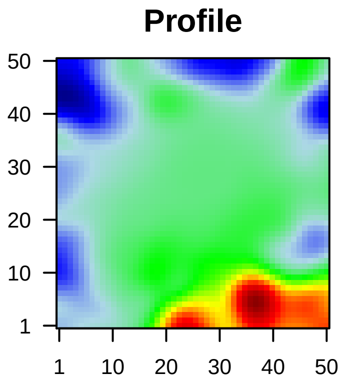
<r> genes = 0.24

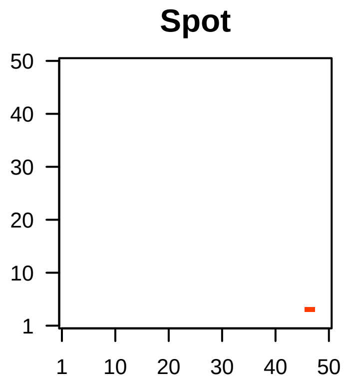
<FC> = 0.78

<shrinkage−t> = 12.46

<p−value> = 0.01

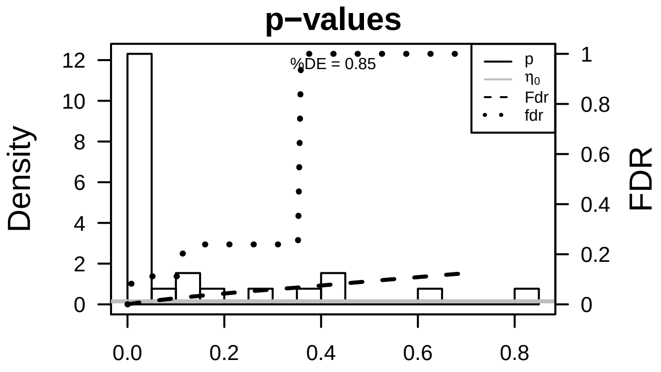
<fdr> = 0.46


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	HIST1H2BF	1.82	4e−07	1e−05	46 x 4	histone cluster 1, H2bf [Source:HGNC Symbol;Acc:HGNC:47
2	MYEOV	1.68	3e−06	2e−04	47 x 4	myeloma overexpressed [Source:HGNC Symbol;Acc:HGNC:
3	FOSL2	1.46	5e−05	2e−04	46 x 4	FOS−like antigen 2 [Source:HGNC Symbol;Acc:HGNC:3798]
4	GNG11	1.2	1e−04	3e−04	46 x 4	guanine nucleotide binding protein (G protein), gamma 11 [S
5	KLF5	1.34	2e−04	7e−04	46 x 4	Kruppel−like factor 5 (intestinal) [Source:HGNC Symbol;Acc:
6	ZNF608	1.24	6e−04	7e−04	46 x 4	zinc finger protein 608 [Source:HGNC Symbol;Acc:HGNC:29
7	CTNNA1	0.5	6e−04	1e−03	46 x 4	catenin (cadherin−associated protein), alpha 1, 102kDa [Sou
8	PPP3CA	1.05	1e−03	1e−03	46 x 4	protein phosphatase 3, catalytic subunit, alpha isozyme [Sou
9	CDKN2B	1.16	1e−03	1e−03	46 x 4	cyclin−dependent kinase inhibitor 2B (p15, inhibits CDK4) [S
10	PRKG1	1.14	1e−03	1e−03	47 x 4	protein kinase, cGMP−dependent, type I [Source:HGNC Sym
11	SGTB	1.12	2e−03	1e−03	46 x 4	small glutamine−rich tetratricopeptide repeat (TPR)−containi
12	CLEC2B	1.08	3e−03	1e−03	47 x 4	C−type lectin domain family 2, member B [Source:HGNC Sy
13	LCAT	1.08	3e−03	1e−03	46 x 4	lecithin−cholesterol acyltransferase [Source:HGNC Symbol;A
14	ITGB8	1.08	3e−03	8e−02	47 x 4	integrin, beta 8 [Source:HGNC Symbol;Acc:HGNC:6163]
15	ARHGEF10	0.79	3e−02	8e−02	46 x 4	Rho guanine nucleotide exchange factor (GEF) 10 [Source:H
16	PHACTR2	0.72	5e−02	1e−01	47 x 4	phosphatase and actin regulator 2 [Source:HGNC Symbol;Ac
17	TNFSF9	0.59	1e−01	1e−01	47 x 4	tumor necrosis factor (ligand) superfamily, member 9 [Source
18	ZNF217	0.56	1e−01	1e−01	47 x 4	zinc finger protein 217 [Source:HGNC Symbol;Acc:HGNC:13
19	CASC4	0.54	1e−01	2e−01	47 x 4	cancer susceptibility candidate 4 [Source:HGNC Symbol;Acc
20	PAWR	0.48	2e−01	2e−01	46 x 4	PRKC, apoptosis, WT1, regulator [Source:HGNC Symbol;Acc


p−values

C2_mel

Local Summary

%DE = 0.79

metagenes = 52

genes = 567

genes in genesets = 564

genes with fdr < 0.1 = 309 (12 + / 297 −)

genes with fdr < 0.05 = 272 (8 + / 264 −)

genes with fdr < 0.01 = 187 (2 + / 185 −)

<r> metagenes = 0.85

<r> genes = 0.13

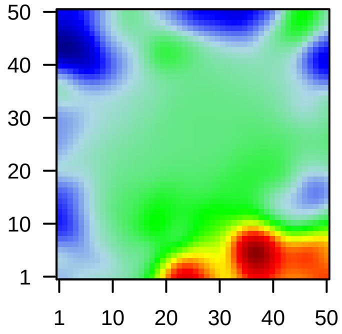
<FC> = −0.7

<shrinkage−t> = −13.81

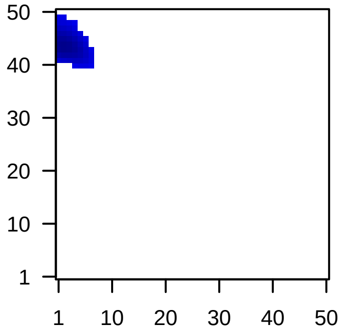
<p−value> = 0

<fdr> = 0.52

Profile



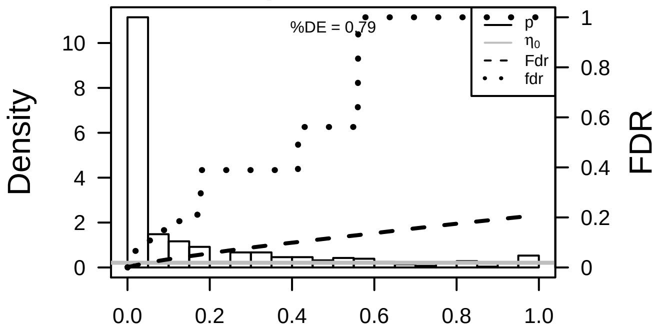
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ALG8	−1.48	2e−16	1e−15	5 x 43	ALG8, alpha−1,3−glucosyltransferase [Source:HGNC Symbo
2	CCT6A	−2.41	2e−16	1e−15	6 x 41	chaperonin containing TCP1, subunit 6A (zeta 1) [Source:HG
3	CITED1	−1.92	2e−16	1e−15	1 x 41	Cbp/p300−interacting transactivator, with Glu/Asp−rich carbo
4	CTSC	−1.99	2e−16	1e−15	1 x 42	cathepsin C [Source:HGNC Symbol;Acc:HGNC:2528]
5	DERL2	−1.85	2e−16	1e−15	6 x 41	derlin 2 [Source:HGNC Symbol;Acc:HGNC:17943]
6	EMC3	−1.92	2e−16	1e−15	5 x 43	ER membrane protein complex subunit 3 [Source:HGNC Sy
7	GGH	−2.01	2e−16	1e−15	4 x 47	gamma−glutamyl hydrolase (conjugase, folylpolygammagluta
8	GNG5	−2.15	2e−16	1e−15	6 x 43	guanine nucleotide binding protein (G protein), gamma 5 [So
9	IDH3A	−2.24	2e−16	1e−15	1 x 42	isocitrate dehydrogenase 3 (NAD+) alpha [Source:HGNC Sy
10	ITGB1BP1	−2.17	2e−16	1e−15	1 x 44	integrin beta 1 binding protein 1 [Source:HGNC Symbol;Acc:
11	MBP	−1.47	2e−16	1e−15	1 x 42	myelin basic protein [Source:HGNC Symbol;Acc:HGNC:6925
12	MLANA	−1.47	2e−16	1e−15	1 x 43	melan−A [Source:HGNC Symbol;Acc:HGNC:7124]
13	MLIP	−1.89	2e−16	1e−15	3 x 44	muscular LMNA−interacting protein [Source:HGNC Symbol;A
14	MTCH2	−1.95	2e−16	1e−15	2 x 42	mitochondrial carrier 2 [Source:HGNC Symbol;Acc:HGNC:17
15	NARS2	−1.47	2e−16	1e−15	1 x 42	asparaginyl−tRNA synthetase 2, mitochondrial (putative) [So
16	PEMT	−1.92	2e−16	1e−15	2 x 42	phosphatidylethanolamine N−methyltransferase [Source:HG
17	PEPD	−2.13	2e−16	1e−15	2 x 42	peptidase D [Source:HGNC Symbol;Acc:HGNC:8840]
18	PLP1	−1.43	2e−16	1e−15	1 x 42	proteolipid protein 1 [Source:HGNC Symbol;Acc:HGNC:9086
19	POLR2I	−1.86	2e−16	1e−15	1 x 44	polymerase (RNA) II (DNA directed) polypeptide I, 14.5kDa [
20	PON2	−2.24	2e−16	1e−15	7 x 41	paraoxonase 2 [Source:HGNC Symbol;Acc:HGNC:9205]

p−values



C2_mel

Local Summary

%DE = 0.81

metagenes = 3

genes = 73

genes in genesets = 73

genes with fdr < 0.1 = 43 (3 + / 40 −)

genes with fdr < 0.05 = 38 (1 + / 37 −)

genes with fdr < 0.01 = 21 (0 + / 21 −)

<r> metagenes = 0.98

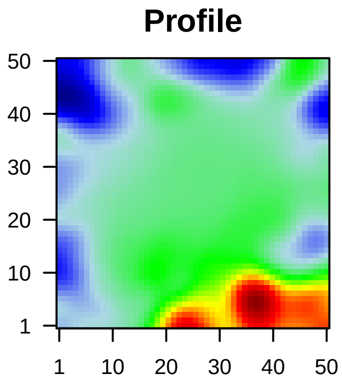
<r> genes = 0.11

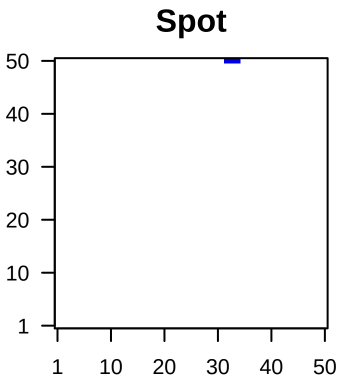
<FC> = −0.68

<shrinkage−t> = −11.95

<p−value> = 0

<fdr> = 0.6





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	C14orf166	−1.84	2e−16	3e−15	32 x 50	chromosome 14 open reading frame 166 [Source:HGNC Sym
2	ECH1	−1.82	5e−15	1e−12	32 x 50	enoyl CoA hydratase 1, peroxisomal [Source:HGNC Symbol;
3	WDR61	−1.79	1e−13	4e−09	33 x 50	WD repeat domain 61 [Source:HGNC Symbol;Acc:HGNC:30
4	PMPCB	−1.67	3e−10	1e−07	33 x 50	peptidase (mitochondrial processing) beta [Source:HGNC Sy
5	DDB1	−1.58	2e−08	1e−07	33 x 50	damage−specific DNA binding protein 1, 127kDa [Source:HG
6	OS9	−1.59	2e−08	2e−06	34 x 50	osteosarcoma amplified 9, endoplasmic reticulum lectin [Sou
7	CHID1	−1.5	1e−07	5e−06	33 x 50	chitinase domain containing 1 [Source:HGNC Symbol;Acc:H
8	DDX42	−1.47	7e−07	5e−06	33 x 50	DEAD (Asp−Glu−Ala−Asp) box helicase 42 [Source:HGNC S
9	PRMT5	−1.48	9e−07	6e−05	34 x 50	protein arginine methyltransferase 5 [Source:HGNC Symbol;
10	RWDD1	−1.42	5e−06	7e−05	32 x 50	RWD domain containing 1 [Source:HGNC Symbol;Acc:HGN
11	VCP	−1.39	1e−05	7e−05	32 x 50	valosin containing protein [Source:HGNC Symbol;Acc:HGNC
12	EIF2B1	−1.37	2e−05	1e−03	34 x 50	eukaryotic translation initiation factor 2B, subunit 1 alpha, 26k
13	STX8	−1.22	3e−04	1e−03	34 x 50	syntaxin 8 [Source:HGNC Symbol;Acc:HGNC:11443]
14	FAM204A	−1.22	3e−04	1e−03	34 x 50	family with sequence similarity 204, member A [Source:HGN
15	NSUN2	−1.22	3e−04	2e−03	32 x 50	NOP2/Sun RNA methyltransferase family, member 2 [Source:
16	ORMDL2	−1.2	5e−04	2e−03	34 x 50	ORMDL sphingolipid biosynthesis regulator 2 [Source:HGNC
17	SRPK1	−0.9	6e−04	6e−03	34 x 50	SRSF protein kinase 1 [Source:HGNC Symbol;Acc:HGNC:11
18	CIRBP	−1.09	2e−03	6e−03	32 x 50	cold inducible RNA binding protein [Source:HGNC Symbol;A
19	DUSP6	−0.76	2e−03	6e−03	34 x 50	dual specificity phosphatase 6 [Source:HGNC Symbol;Acc:H
20	WDR11	−1.08	2e−03	6e−03	33 x 50	WD repeat domain 11 [Source:HGNC Symbol;Acc:HGNC:13