C8_mel

Global Summary

%DE = 0.2

genes with fdr < 0.2 = 2454 (1371 + / 1083 −)

genes with fdr < 0.1 = 2033 (1125 + / 908 −)

genes with fdr < 0.05 = 1532 (824 + / 708 −)

genes with fdr < 0.01 = 918 (438 + / 480 −)

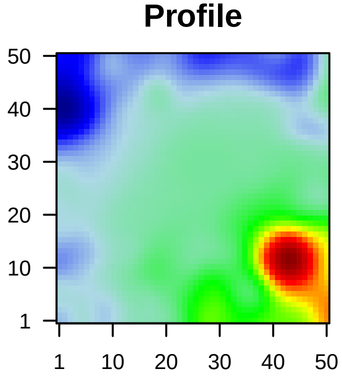
genes in genesets = 14839

<FC> = 0

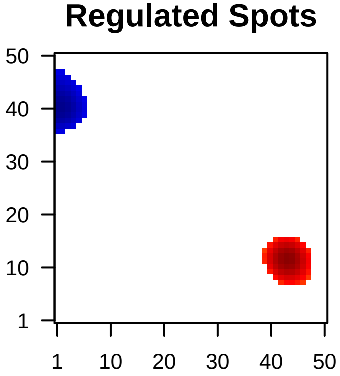
<shrinkage−t> = −0.29

<p−value> = 0.08

<fdr> = 0.8



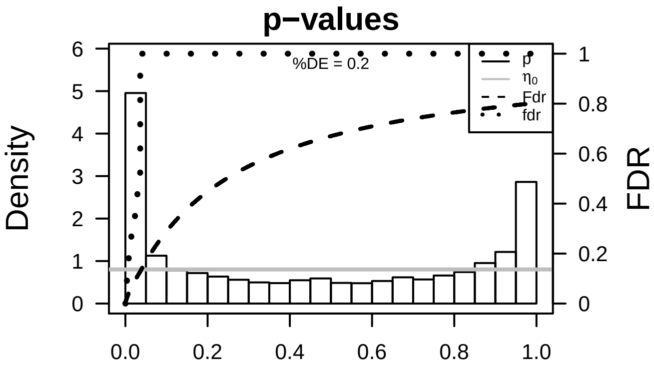
Profile



Regulated Spots

Global Genelist

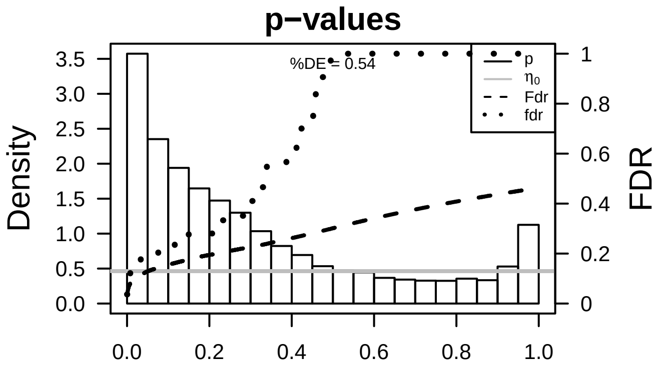
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	AAMDC	−1.28	2e−16	5e−14	41 x 46	adipogenesis associated, Mth938 domain containing [Source
2	AHSA1	−1.63	2e−16	5e−14	46 x 35	AHA1, activator of heat shock 90kDa protein ATPase homolo
3	ASAH1	−1.71	2e−16	5e−14	1 x 40	N−acylsphingosine amidohydrolase (acid ceramidase) 1 [Sou
4	ATP6V1C1	−1.7	2e−16	5e−14	4 x 40	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1 [S
5	BACE2	−1.84	2e−16	5e−14	1 x 42	beta−site APP−cleaving enzyme 2 [Source:HGNC Symbol;Ac
6	CCT6A	−1.3	2e−16	5e−14	6 x 41	chaperonin containing TCP1, subunit 6A (zeta 1) [Source:HG
7	CDK2	−1.42	2e−16	5e−14	1 x 43	cyclin−dependent kinase 2 [Source:HGNC Symbol;Acc:HGN
8	CHCHD6	−2.03	2e−16	5e−14	1 x 43	coiled−coil−helix−coiled−coil−helix domain containing 6 [Sour
9	CRYAB	1.97	2e−16	5e−14	50 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
10	DUS1L	−2.14	2e−16	5e−14	25 x 50	dihydrouridine synthase 1−like (S. cerevisiae) [Source:HGNC
11	ECHS1	−1.87	2e−16	5e−14	3 x 38	enoyl CoA hydratase, short chain, 1, mitochondrial [Source:H
12	EEF1E1	−1.83	2e−16	5e−14	3 x 40	eukaryotic translation elongation factor 1 epsilon 1 [Source:H
13	EIF4A3	−2.31	2e−16	5e−14	4 x 40	eukaryotic translation initiation factor 4A3 [Source:HGNC Syn
14	EMP3	−1.82	2e−16	5e−14	4 x 43	epithelial membrane protein 3 [Source:HGNC Symbol;Acc:H
15	ENY2	−1.86	2e−16	5e−14	12 x 47	enhancer of yellow 2 homolog (Drosophila) [Source:HGNC S
16	FDFT1	−1.86	2e−16	5e−14	1 x 38	farnesyl−diphosphate farnesyltransferase 1 [Source:HGNC S
17	GGH	−2.01	2e−16	5e−14	4 x 47	gamma−glutamyl hydrolase (conjugase, folylpolygammagluta
18	HSD17B10	−1.93	2e−16	5e−14	3 x 39	hydroxysteroid (17−beta) dehydrogenase 10 [Source:HGNC
19	HSPD1	−1.33	2e−16	5e−14	5 x 40	heat shock 60kDa protein 1 (chaperonin) [Source:HGNC Sym
20	IDH1	−1.9	2e−16	5e−14	3 x 41	isocitrate dehydrogenase 1 (NADP+), soluble [Source:HGNC



p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	8.88	4e−04	472	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
2	8.38	5e−04	1500	Chr	Chr 1
3	7.37	9e−04	3897	Colon Cancer	Quies1_Colon
4	7.25	9e−04	3396	Lymphoma	HOPP_Repressed
5	6.63	1e−03	2563	Lymphoma	HOPP_Heterochrom
6	6.38	1e−03	2188	Lymphoma	HOPP_Poised_promoter
7	6.19	2e−03	2159	Colon Cancer	TssP_Colon
8	6.01	2e−03	302	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
9	5.9	2e−03	616	GSEA C2	NABA_MATRISOME
10	5.67	2e−03	222	GSEA C2	UDAYAKUMAR_MED1_TARGETS_DN
11	5.62	2e−03	196	GSEA C2	CHANG_CORE_SERUM_RESPONSE_DN
12	5.44	3e−03	124	GSEA C2	ELVIDGE_HYPOXIA_BY_DMOG_UP
13	5.42	3e−03	2142	Colon Cancer	ReprPC_Colon
14	5.39	9e−01	14	Cancer	LIU_PROSTATE_CANCER_DN
15	5.28	3e−03	212	Lymphoma	LENZ_Stromal signature 1
16	5.26	3e−03	1889	Colon Cancer	ReprPCWk_Colon
17	5.26	3e−03	263	Colon Cancer	Rentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
18	5.25	3e−03	161	GSEA C2	ELVIDGE_HYPOXIA_UP
19	5.24	3e−03	833	GSEA C2	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
20	5.23	3e−03	95	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_UP
Underexpressed					
1	−14.24	6e−05	198	HM	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	−14.11	7e−05	1460	GSEA C2	PUJANA_BRCA1_PCC_NETWORK
3	−13.8	7e−05	1192	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
4	−13.34	8e−05	724	GSEA C2	PUJANA_CHEK2_PCC_NETWORK
5	−12.8	1e−04	562	GSEA C2	CAIRO_HEPATOBLASTOMA_CLASSES_UP
6	−12.73	1e−04	756	GSEA C2	WEI_MYCN_TARGETS_WITH_E_BOX
7	−12.71	1e−04	312	GSEA C2	WONG_EMBRYONIC_STEM_CELL_CORE
8	−11.96	1e−04	436	GSEA C2	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
9	−11.87	1e−04	1251	GSEA C2	DODD_NASOPHARYNGEAL_CARCINOMA_DN
10	−11.87	1e−04	405	GSEA C2	MOOTHA_HUMAN_MITODB_6_2002
11	−11.31	2e−04	401	CC	mitochondrial inner membrane
12	−10.82	2e−04	421	GSEA C2	MOOTHA_MITOCHONDRIA
13	−10.73	2e−04	278	GSEA C2	MANALO_HYPOXIA_DN
14	−10.52	2e−04	834	GSEA C2	LEE_BMP2_TARGETS_DN
15	−10.44	2e−04	213	GSEA C2	WONG_MITOCHONDRIA_GENE_MODULE
16	−10.41	2e−04	609	GSEA C2	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIA
17	−10.3	2e−04	242	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
18	−10.12	2e−04	1468	CC	mitochondrion
19	−10.09	2e−02	16	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
20	−9.85	3e−04	536	GSEA C2	TIEN_INTESTINE_PROBIOTICS_24HR_UP



p−values

C8_mel

Local Summary

%DE = 1

metagenes = 67

genes = 541

genes in genesets = 534

genes with fdr < 0.1 = 538 (538 + / 0 −)

genes with fdr < 0.05 = 535 (535 + / 0 −)

genes with fdr < 0.01 = 532 (532 + / 0 −)

<r> metagenes = 0.87

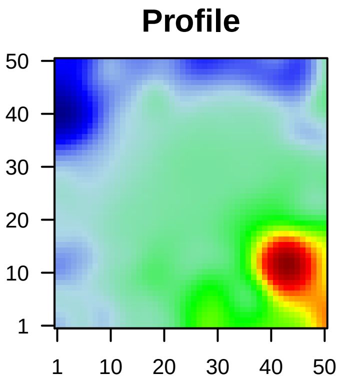
<r> genes = 0.15

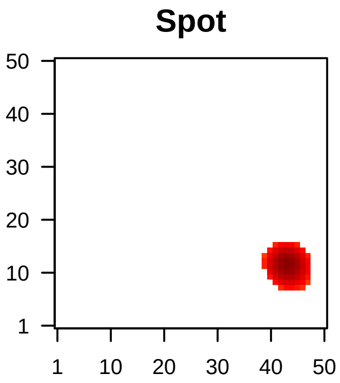
<FC> = 1.23

<shrinkage−t> = 18.68

<p−value> = 0

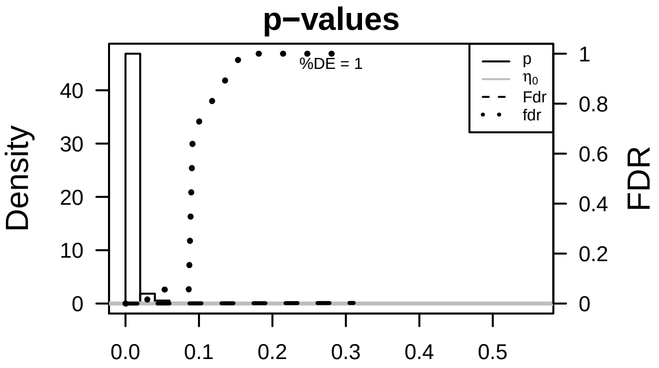
<fdr> = 0.08





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	PLA2G4C	2.46	1e−13	1e−12	41 x 10	phospholipase A2, group IVC (cytosolic, calcium−independen
2	FOLR3	2.37	9e−13	1e−12	41 x 9	folate receptor 3 (gamma) [Source:HGNC Symbol;Acc:HGNC
3	KRTAP21−2	2.37	1e−12	9e−11	44 x 13	keratin associated protein 21−2 [Source:HGNC Symbol;Acc:
4	GPR133	2.19	4e−11	9e−11	43 x 13	
5	HIST1H4H	2.16	8e−11	3e−10	41 x 10	histone cluster 1, H4h [Source:HGNC Symbol;Acc:HGNC:47
6	FBXL2	2.11	2e−10	4e−10	44 x 13	F−box and leucine−rich repeat protein 2 [Source:HGNC Sym
7	MNDA	2.08	4e−10	6e−10	43 x 13	myeloid cell nuclear differentiation antigen [Source:HGNC Sy
8	NREP	2.03	9e−10	6e−10	44 x 11	neuronal regeneration related protein [Source:HGNC Symbol
9	TUBA4A	2.01	1e−09	6e−10	42 x 13	tubulin, alpha 4a [Source:HGNC Symbol;Acc:HGNC:12407]
10	PHKA2	2.01	1e−09	6e−10	43 x 13	phosphorylase kinase, alpha 2 (liver) [Source:HGNC Symbol;
11	RTN1	2	2e−09	6e−10	45 x 11	reticulon 1 [Source:HGNC Symbol;Acc:HGNC:10467]
12	NCAM2	2	2e−09	6e−10	43 x 12	neural cell adhesion molecule 2 [Source:HGNC Symbol;Acc:
13	DCN	1.98	2e−09	6e−10	43 x 13	decorin [Source:HGNC Symbol;Acc:HGNC:2705]
14	SLC14A1	1.98	2e−09	7e−09	43 x 13	solute carrier family 14 (urea transporter), member 1 (Kidd bl
15	GAB1	1.9	1e−08	7e−09	44 x 11	GRB2−associated binding protein 1 [Source:HGNC Symbol;
16	CCDC149	1.89	1e−08	7e−09	44 x 14	coiled−coil domain containing 149 [Source:HGNC Symbol;Ac
17	FHIT	1.87	2e−08	7e−09	45 x 15	fragile histidine triad [Source:HGNC Symbol;Acc:HGNC:3701
18	SPAG4	1.86	2e−08	7e−09	43 x 13	sperm associated antigen 4 [Source:HGNC Symbol;Acc:HG
19	PCNXL2	1.86	2e−08	7e−09	43 x 11	pecanex−like 2 (Drosophila) [Source:HGNC Symbol;Acc:HG
20	ANXA10	1.85	2e−08	7e−09	43 x 12	annexin A10 [Source:HGNC Symbol;Acc:HGNC:534]



C8_mel

Local Summary

%DE = 0.86

metagenes = 54

genes = 623

genes in genesets = 620

genes with fdr < 0.1 = 438 (27 + / 411 −)

genes with fdr < 0.05 = 376 (21 + / 355 −)

genes with fdr < 0.01 = 298 (12 + / 286 −)

<r> metagenes = 0.88

<r> genes = 0.12

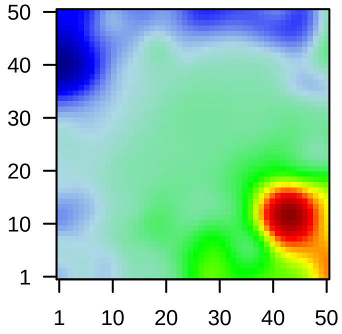
<FC> = −0.73

<shrinkage−t> = −14.71

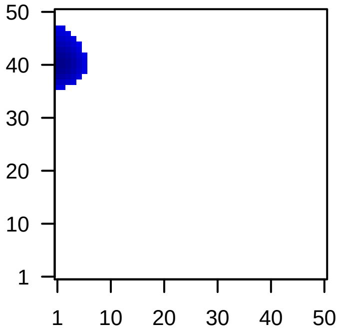
<p−value> = 0

<fdr> = 0.43

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ASAH1	−1.71	2e−16	5e−16	1 x 40	N−acylsphingosine amidohydrolase (acid ceramidase) 1 [Sou
2	ATP6V1C1	−1.7	2e−16	5e−16	4 x 40	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1 [S
3	BACE2	−1.84	2e−16	5e−16	1 x 42	beta−site APP−cleaving enzyme 2 [Source:HGNC Symbol;Ac
4	CCT6A	−1.3	2e−16	5e−16	6 x 41	chaperonin containing TCP1, subunit 6A (zeta 1) [Source:HG
5	CDK2	−1.42	2e−16	5e−16	1 x 43	cyclin−dependent kinase 2 [Source:HGNC Symbol;Acc:HGN
6	CHCHD6	−2.03	2e−16	5e−16	1 x 43	coiled−coil−helix−coiled−coil−helix domain containing 6 [Sour
7	ECHS1	−1.87	2e−16	5e−16	3 x 38	enoyl CoA hydratase, short chain, 1, mitochondrial [Source:H
8	EEF1E1	−1.83	2e−16	5e−16	3 x 40	eukaryotic translation elongation factor 1 epsilon 1 [Source:H
9	EIF4A3	−2.31	2e−16	5e−16	4 x 40	eukaryotic translation initiation factor 4A3 [Source:HGNC Syn
10	EMP3	−1.82	2e−16	5e−16	4 x 43	epithelial membrane protein 3 [Source:HGNC Symbol;Acc:H
11	FDFT1	−1.86	2e−16	5e−16	1 x 38	farnesyl−diphosphate farnesyltransferase 1 [Source:HGNC S
12	HSD17B10	−1.93	2e−16	5e−16	3 x 39	hydroxysteroid (17−beta) dehydrogenase 10 [Source:HGNC
13	HSPD1	−1.33	2e−16	5e−16	5 x 40	heat shock 60kDa protein 1 (chaperonin) [Source:HGNC Syn
14	IDH1	−1.9	2e−16	5e−16	3 x 41	isocitrate dehydrogenase 1 (NADP+), soluble [Source:HGNC
15	IDH3A	−2.24	2e−16	5e−16	1 x 42	isocitrate dehydrogenase 3 (NAD+) alpha [Source:HGNC Syr
16	ITGB1BP1	−1.77	2e−16	5e−16	1 x 44	integrin beta 1 binding protein 1 [Source:HGNC Symbol;Acc:
17	ITPA	−1.93	2e−16	5e−16	5 x 40	inosine triphosphatase (nucleoside triphosphate pyrophosph
18	M6PR	−1.45	2e−16	5e−16	3 x 41	mannose−6−phosphate receptor (cation dependent) [Source:
19	MLANA	−1.56	2e−16	5e−16	1 x 43	melan−A [Source:HGNC Symbol;Acc:HGNC:7124]
20	MRPL37	−1.87	2e−16	5e−16	4 x 37	mitochondrial ribosomal protein L37 [Source:HGNC Symbol;

p−values