D9_mel

Global Summary

%DE = 0.22

genes with fdr < 0.2 = 2813 (1627 + / 1186 −)

genes with fdr < 0.1 = 2416 (1414 + / 1002 −)

genes with fdr < 0.05 = 1952 (1140 + / 812 −)

genes with fdr < 0.01 = 1263 (721 + / 542 −)

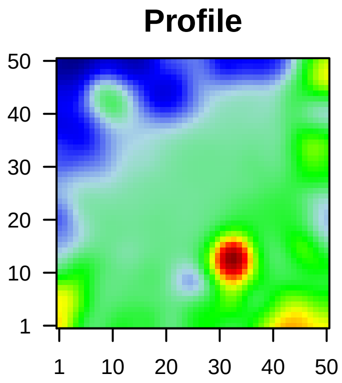
genes in genesets = 14839

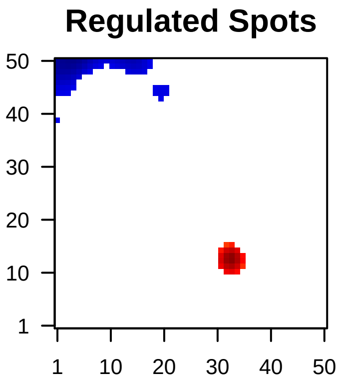
<FC> = 0

<shrinkage−t> = −0.09

<p−value> = 0.07

<fdr> = 0.78



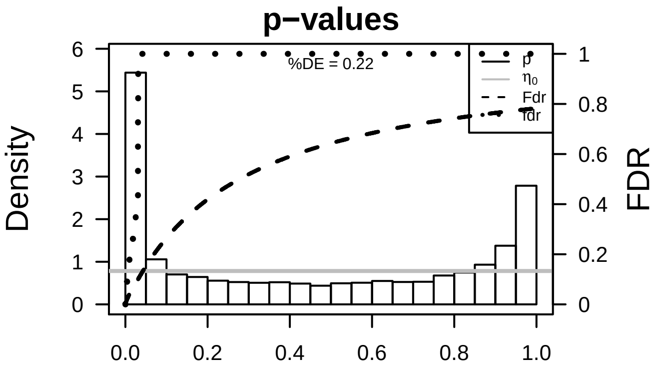


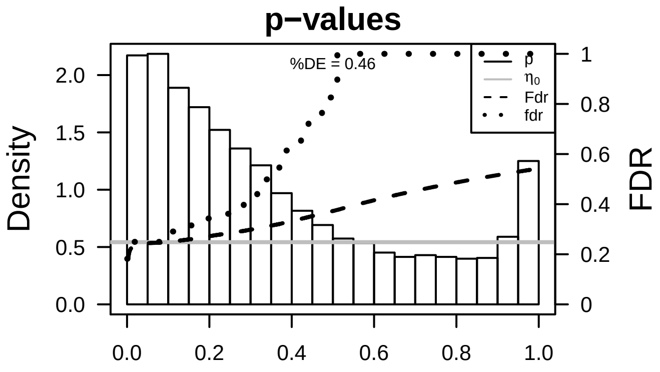
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	AIMP2	−1.56	2e−16	5e−14	5 x 34	aminoacyl tRNA synthetase complex−interacting multifunctior
2	AP3S1	−1.75	2e−16	5e−14	1 x 39	adaptor−related protein complex 3, sigma 1 subunit [Source:H
3	APOA1BP	−1.3	2e−16	5e−14	16 x 50	apolipoprotein A−I binding protein [Source:HGNC Symbol;Ac
4	AZIN1	−1.53	2e−16	5e−14	4 x 41	antizyme inhibitor 1 [Source:HGNC Symbol;Acc:HGNC:1643
5	BUD31	−1.77	2e−16	5e−14	14 x 50	BUD31 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:H
6	C12orf57	−1.7	2e−16	5e−14	21 x 42	chromosome 12 open reading frame 57 [Source:HGNC Symb
7	CAPN3	−1.51	2e−16	5e−14	1 x 43	calpain 3, (p94) [Source:HGNC Symbol;Acc:HGNC:1480]
8	CCNG1	−1.35	2e−16	5e−14	12 x 48	cyclin G1 [Source:HGNC Symbol;Acc:HGNC:1592]
9	CD164	−1.39	2e−16	5e−14	17 x 50	CD164 molecule, sialomucin [Source:HGNC Symbol;Acc:HG
10	CDKN3	−1.65	2e−16	5e−14	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
11	CFAP20	−1.62	2e−16	5e−14	40 x 50	cilia and flagella associated protein 20 [Source:HGNC Symbo
12	CHCHD6	−2.05	2e−16	5e−14	1 x 43	coiled−coil−helix−coiled−coil−helix domain containing 6 [Sour
13	COPZ1	−1.67	2e−16	5e−14	46 x 45	coatomer protein complex, subunit zeta 1 [Source:HGNC Syn
14	DDX47	−1.64	2e−16	5e−14	38 x 50	DEAD (Asp−Glu−Ala−Asp) box polypeptide 47 [Source:HGN
15	DERA	−1.78	2e−16	5e−14	1 x 43	deoxyribose−phosphate aldolase (putative) [Source:HGNC S
16	DPY30	−1.67	2e−16	5e−14	22 x 46	dpy−30 homolog (C. elegans) [Source:HGNC Symbol;Acc:HC
17	ETFA	−1.16	2e−16	5e−14	3 x 33	electron−transfer−flavoprotein, alpha polypeptide [Source:HG
18	GOT1	−1.62	2e−16	5e−14	1 x 39	glutamic−oxaloacetic transaminase 1, soluble [Source:HGNC
19	HBS1L	−1.89	2e−16	5e−14	3 x 44	HBS1−like translational GTPase [Source:HGNC Symbol;Acc:
20	HDAC2	−1.6	2e−16	5e−14	1 x 45	histone deacetylase 2 [Source:HGNC Symbol;Acc:HGNC:485

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	4.96	0.004	2698	Colon Cancer	EnhA_Colon
2	4.86	0.004	44	GSEA C2	REACTOME_INTERFERON_ALPHA_BETA_SIGNALING
3	4.75	0.004	2159	Colon Cancer	TssP_Colon
4	4.64	0.005	24	GSEA C2	HORTON_SREBF_TARGETS
5	4.59	0.005	157	GSEA C2	YAMAZAKI_TCEB3_TARGETS_UP
6	4.54	0.005	146	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
7	4.51	0.005	49	BP	type I interferon signaling pathway
8	4.46	0.005	157	GSEA C2	MCBRYAN_PUBERTAL_TGFB1_TARGETS_UP
9	4.42	0.005	175	GSEA C2	MCBRYAN_PUBERTAL_BREAST_6_7WK_UP
10	4.41	0.005	1028	GSEA C2	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_UP
11	4.39	0.005	24	GSEA C2	SCHMIDT_POR_TARGETS_IN_LIMB_BUD_UP
12	4.31	0.006	1889	Colon Cancer	ReprPCWk_Colon
13	4.21	0.006	2185	Brain	Fetal_TssA
14	4.18	0.006	2142	Colon Cancer	ReprPC_Colon
15	4.18	0.006	334	GSEA C2	YOSHIMURA_MAPK8_TARGETS_DN
16	4.17	0.007	3383	Colon Cancer	EnhWk2_Colon
17	4.15	0.007	1949	Brain	Fetal_TssF
18	4.13	0.007	3396	Lymphoma	HOPP_Repressed
19	4.05	0.007	256	Lymphoma	SPANG_IL21 DN
20	4	0.007	87	HM	HALLMARK_INTERFERON_ALPHA_RESPONSE
Underexpressed					
1	−8.85	4e−04	775	Chr	Chr 12
2	−8.44	5e−04	401	CC	mitochondrial inner membrane
3	−8.14	6e−04	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
4	−8.06	6e−04	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
5	−7.96	6e−04	144	GSEA C2	BENPORATH_PROLIFERATION
6	−7.95	6e−04	436	GSEA C2	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
7	−7.67	7e−04	308	GSEA C2	LINDGREN_BLADDER_CANCER_CLUSTER_3_UP
8	−7.66	7e−04	305	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
9	−7.37	3e−02	16	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
10	−7.29	9e−04	116	GSEA C2	MISSIAGLIA_REGULATED_BY_METHYLATION_DN
11	−7.22	9e−04	50	GSEA C2	ISHIDA_E2F_TARGETS
12	−7.11	1e−03	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
13	−7.04	1e−03	687	Chr	Chr 6
14	−6.99	1e−03	198	HM	HALLMARK_OXIDATIVE_PHOSPHORYLATION
15	−6.86	1e−03	700	GSEA C2	MARSON_BOUND_BY_E2F4_UNSTIMULATED
16	−6.82	1e−03	81	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
17	−6.78	1e−03	124	GSEA C2	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
18	−6.77	1e−03	211	GSEA C2	BIDUS_METASTASIS_UP
19	−6.66	1e−03	197	HM	HALLMARK_E2F_TARGETS
20	−6.62	1e−03	110	GSEA C2	WHITEFORD_PEDIATRIC_CANCER_MARKERS





D9_mel

Local Summary

%DE = 0.99

metagenes = 24

genes = 130

genes in genesets = 130

genes with fdr < 0.1 = 128 (128 + / 0 −)

genes with fdr < 0.05 = 126 (126 + / 0 −)

genes with fdr < 0.01 = 118 (118 + / 0 −)

<r> metagenes = 0.91

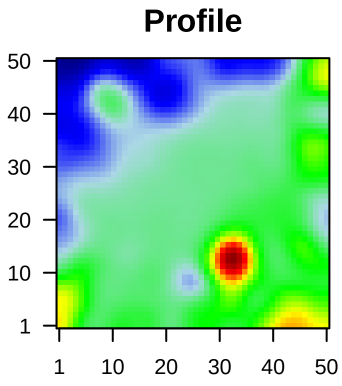
<r> genes = 0.22

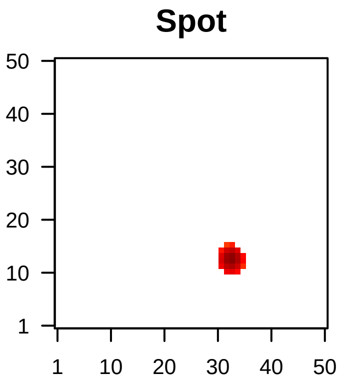
<FC> = 1.03

<shrinkage−t> = 15.82

<p−value> = 0

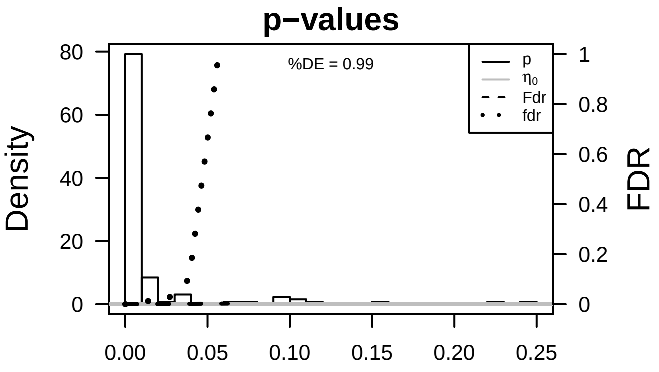
<fdr> = 0.15





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	IGF2BP2	2.5	2e−16	3e−16	33 x 14	insulin−like growth factor 2 mRNA binding protein 2 [Source:
2	ACSF2	2.1	7e−16	3e−15	33 x 14	acyl−CoA synthetase family member 2 [Source:HGNC Symb
3	CFAP44	2.06	3e−15	3e−14	33 x 14	cilia and flagella associated protein 44 [Source:HGNC Symb
4	KLF4	1.99	2e−14	5e−12	33 x 14	Kruppel−like factor 4 (gut) [Source:HGNC Symbol;Acc:HGNC
5	RNF125	1.77	1e−11	5e−12	34 x 14	ring finger protein 125, E3 ubiquitin protein ligase [Source:HG
6	EPGN	1.77	1e−11	5e−12	33 x 14	epithelial mitogen [Source:HGNC Symbol;Acc:HGNC:17470]
7	APLP1	1.75	2e−11	5e−12	32 x 13	amyloid beta (A4) precursor−like protein 1 [Source:HGNC Sy
8	PTHLH	1.75	2e−11	5e−12	33 x 14	parathyroid hormone−like hormone [Source:HGNC Symbol;A
9	NRCAM	1.74	2e−11	5e−12	33 x 14	neuronal cell adhesion molecule [Source:HGNC Symbol;Acc:
10	PLXDC1	1.74	2e−11	7e−11	33 x 14	plexin domain containing 1 [Source:HGNC Symbol;Acc:HGN
11	LRRC75A	1.68	1e−10	7e−11	34 x 12	leucine rich repeat containing 75A [Source:HGNC Symbol;Ac
12	RPUSD4	1.68	1e−10	2e−10	33 x 13	RNA pseudouridylate synthase domain containing 4 [Source:
13	GRB14	1.64	3e−10	7e−10	33 x 14	growth factor receptor−bound protein 14 [Source:HGNC Sym
14	ZNF782	1.58	1e−09	7e−10	33 x 14	zinc finger protein 782 [Source:HGNC Symbol;Acc:HGNC:33
15	ANKMY1	1.58	1e−09	1e−08	32 x 14	ankyrin repeat and MYND domain containing 1 [Source:HGN
16	TMEM241	1.47	2e−08	1e−08	32 x 13	transmembrane protein 241 [Source:HGNC Symbol;Acc:HGN
17	CA8	1.45	3e−08	1e−08	33 x 14	carbonic anhydrase VIII [Source:HGNC Symbol;Acc:HGNC:1
18	ALB	1.44	3e−08	3e−08	33 x 14	albumin [Source:HGNC Symbol;Acc:HGNC:399]
19	RNF169	1.41	6e−08	3e−08	33 x 13	ring finger protein 169 [Source:HGNC Symbol;Acc:HGNC:26
20	ARHGAP27	1.39	9e−08	3e−08	33 x 14	Rho GTPase activating protein 27 [Source:HGNC Symbol;Ac



D9_mel

Local Summary

%DE = 0.81

metagenes = 1

genes = 27

genes in genesets = 27

genes with fdr < 0.1 = 16 (3 + / 13 −)

genes with fdr < 0.05 = 14 (2 + / 12 −)

genes with fdr < 0.01 = 12 (1 + / 11 −)

<r> metagenes = NA

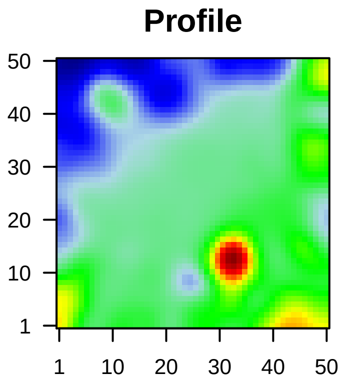
<r> genes = 0.17

<FC> = −0.49

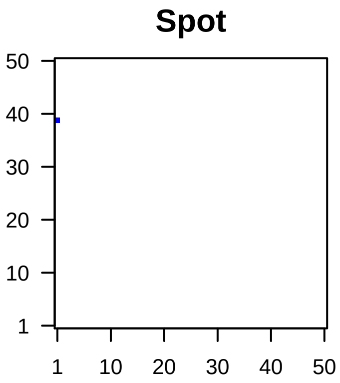
<shrinkage−t> = −8.91

<p−value> = 0

<fdr> = 0.44



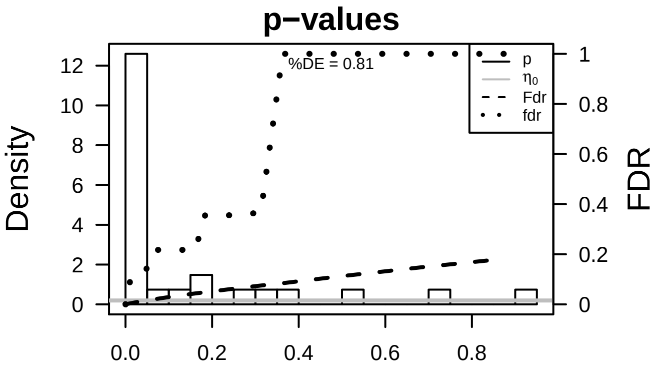
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	AP3S1	−1.75	2e−16	6e−16	1 x 39	adaptor−related protein complex 3, sigma 1 subunit [Source:
2	GOT1	−1.62	2e−16	6e−16	1 x 39	glutamic−oxaloacetic transaminase 1, soluble [Source:HGNC
3	DUSP23	−1.55	1e−13	9e−10	1 x 39	dual specificity phosphatase 23 [Source:HGNC Symbol;Acc:
4	UTP18	−1.44	2e−10	1e−09	1 x 39	UTP18 small subunit (SSU) processome component homolo
5	PARL	−1.42	4e−10	1e−08	1 x 39	presenilin associated, rhomboid−like [Source:HGNC Symbol;
6	SLC25A11	−1.37	3e−09	8e−07	1 x 39	solute carrier family 25 (mitochondrial carrier; oxoglutarate ca
7	NUDT5	−1.26	2e−07	2e−04	1 x 39	nudix (nucleoside diphosphate linked moiety X)−type motif 5
8	PTDSS1	−1.08	3e−05	2e−04	1 x 39	phosphatidylserine synthase 1 [Source:HGNC Symbol;Acc:
9	HADHB	0.76	9e−05	2e−04	1 x 39	hydroxyacyl−CoA dehydrogenase/3−ketoacyl−CoA thiolase/e
10	FASTK	−1.01	1e−04	2e−04	1 x 39	Fas−activated serine/threonine kinase [Source:HGNC Symbo
11	SMIM8	−0.99	1e−04	4e−03	1 x 39	small integral membrane protein 8 [Source:HGNC Symbol;Ac
12	ASUN	−0.86	1e−03	4e−03	1 x 39	asunder spermatogenesis regulator [Source:HGNC Symbol;
13	KIAA1191	−0.71	2e−03	2e−02	1 x 39	KIAA1191 [Source:HGNC Symbol;Acc:HGNC:29209]
14	FLOT2	0.64	6e−03	2e−02	1 x 39	flotillin 2 [Source:HGNC Symbol;Acc:HGNC:3758]
15	CLPB	0.66	1e−02	9e−02	1 x 39	ClpB caseinolytic peptidase B homolog (E. coli) [Source:HGN
16	OXA1L	−0.49	3e−02	9e−02	1 x 39	oxidase (cytochrome c) assembly 1−like [Source:HGNC Sym
17	MERTK	−0.52	5e−02	1e−01	1 x 39	MER proto−oncogene, tyrosine kinase [Source:HGNC Symb
18	EIF2B3	0.44	7e−02	2e−01	1 x 39	eukaryotic translation initiation factor 2B, subunit 3 gamma,
19	SPG21	0.39	1e−01	2e−01	1 x 39	spastic paraplegia 21 (autosomal recessive, Mast syndrome)
20	EPT1	−0.36	2e−01	2e−01	1 x 39	ethanolaminephosphotransferase 1 [Source:HGNC Symbol;



p−values

D9_mel

Local Summary

%DE = 0.48

metagenes = 7

genes = 35

genes in genesets = 35

genes with fdr < 0.1 = 9 (0 + / 9 −)

genes with fdr < 0.05 = 8 (0 + / 8 −)

genes with fdr < 0.01 = 4 (0 + / 4 −)

<r> metagenes = 0.98

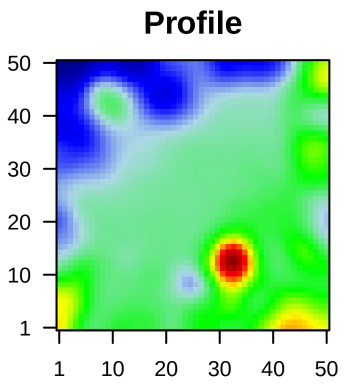
<r> genes = 0.13

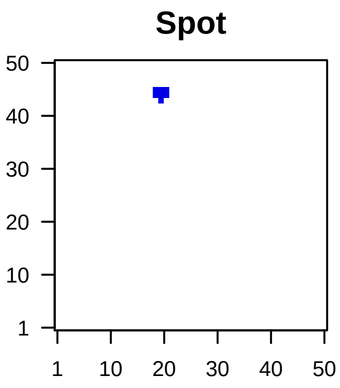
<FC> = −0.3

<shrinkage−t> = −5.44

<p−value> = 0.02

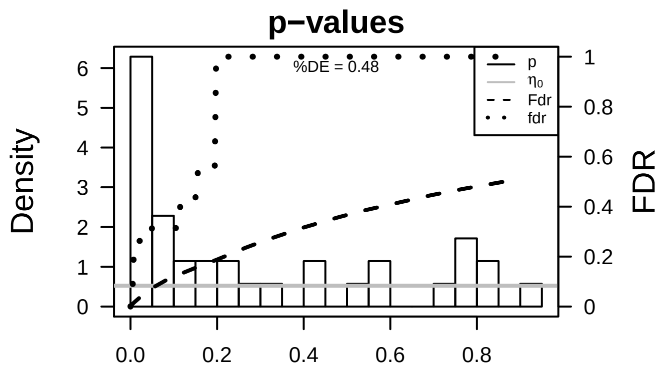
<fdr> = 0.73





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	HDDC2	−0.89	4e−11	7e−09	20 x 44	HD domain containing 2 [Source:HGNC Symbol;Acc:HGNC:2
2	NXF1	−1.11	4e−10	7e−07	20 x 43	nuclear RNA export factor 1 [Source:HGNC Symbol;Acc:HGN
3	MYL6B	−1.31	4e−08	1e−03	20 x 43	myosin, light chain 6B, alkali, smooth muscle and non−muscle
4	DPF2	−1.04	6e−05	6e−03	20 x 44	D4, zinc and double PHD fingers family 2 [Source:HGNC Syn
5	DIMT1	−0.89	4e−04	2e−02	21 x 44	DIM1 dimethyladenosine transferase 1 homolog (S. cerevisiae
6	TAF11	−0.77	2e−03	2e−02	20 x 43	TAF11 RNA polymerase II, TATA box binding protein (TBP)−a
7	CD2AP	−0.74	4e−03	2e−02	20 x 44	CD2−associated protein [Source:HGNC Symbol;Acc:HGNC:1
8	ZC2HC1A	−0.74	5e−03	2e−02	21 x 45	zinc finger, C2HC−type containing 1A [Source:HGNC Symbol
9	COMMD8	−0.66	5e−03	7e−02	19 x 44	COMM domain containing 8 [Source:HGNC Symbol;Acc:HGN
10	SCAF11	−0.46	9e−03	3e−01	19 x 44	SR−related CTD−associated factor 11 [Source:HGNC Symbo
11	SAP130	−0.54	4e−02	3e−01	20 x 43	Sin3A−associated protein, 130kDa [Source:HGNC Symbol;Ac
12	ZBTB17	−0.51	5e−02	3e−01	21 x 44	zinc finger and BTB domain containing 17 [Source:HGNC Sy
13	MTERF3	0.51	5e−02	3e−01	20 x 43	mitochondrial transcription termination factor 3 [Source:HGNC
14	TPRA1	0.44	9e−02	3e−01	21 x 44	transmembrane protein, adipocyte asscociated 1 [Source:HG
15	FANCM	−0.44	9e−02	3e−01	21 x 44	Fanconi anemia, complementation group M [Source:HGNC S
16	PIGC	0.34	1e−01	3e−01	21 x 44	phosphatidylinositol glycan anchor biosynthesis, class C [Sou
17	E2F6	−0.4	1e−01	4e−01	20 x 44	E2F transcription factor 6 [Source:HGNC Symbol;Acc:HGNC:
18	ERI2	−0.37	2e−01	4e−01	19 x 45	ERI1 exoribonuclease family member 2 [Source:HGNC Symb
19	SAMD9	−0.36	2e−01	5e−01	20 x 43	sterile alpha motif domain containing 9 [Source:HGNC Symb
20	C12orf29	0.33	2e−01	5e−01	21 x 44	chromosome 12 open reading frame 29 [Source:HGNC Symb



D9_mel

Local Summary

%DE = 0.78

metagenes = 62

genes = 796

genes in genesets = 793

genes with fdr < 0.1 = 454 (109 + / 345 −)

genes with fdr < 0.05 = 336 (78 + / 258 −)

genes with fdr < 0.01 = 227 (49 + / 178 −)

<r> metagenes = 0.77

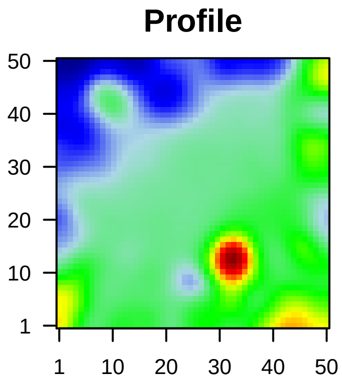
<r> genes = 0.14

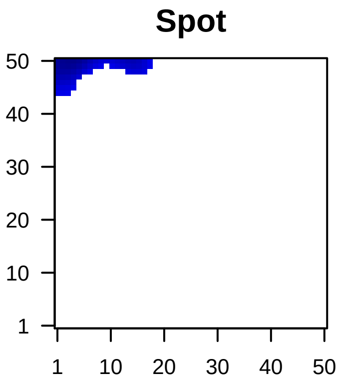
<FC> = −0.31

<shrinkage−t> = −5.21

<p−value> = 0.01

<fdr> = 0.58





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	APOA1BP	−1.3	2e−16	3e−15	16 x 50	apolipoprotein A−I binding protein [Source:HGNC Symbol;Ac
2	BUD31	−1.77	2e−16	3e−15	14 x 50	BUD31 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:
3	CD164	−1.39	2e−16	3e−15	17 x 50	CD164 molecule, sialomucin [Source:HGNC Symbol;Acc:HG
4	CDKN3	−1.65	2e−16	3e−15	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
5	HBS1L	−1.89	2e−16	3e−15	3 x 44	HBS1−like translational GTPase [Source:HGNC Symbol;Acc:
6	HDAC2	−1.6	2e−16	3e−15	1 x 45	histone deacetylase 2 [Source:HGNC Symbol;Acc:HGNC:48
7	ID3	−1.73	2e−16	3e−15	11 x 50	inhibitor of DNA binding 3, dominant negative helix−loop−heli
8	MRPL55	−1.38	2e−16	3e−15	17 x 50	mitochondrial ribosomal protein L55 [Source:HGNC Symbol;
9	NDUFS4	−1.9	2e−16	3e−15	17 x 50	NADH dehydrogenase (ubiquinone) Fe−S protein 4, 18kDa (
10	POP4	−1.63	2e−16	3e−15	15 x 50	processing of precursor 4, ribonuclease P/MRP subunit (S. c
11	TIMM21	−1.79	2e−16	3e−15	14 x 50	translocase of inner mitochondrial membrane 21 homolog (ye
12	LYRM4	−1.61	1e−15	5e−13	16 x 50	LYR motif containing 4 [Source:HGNC Symbol;Acc:HGNC:21
13	GUCD1	−1.59	4e−15	3e−12	1 x 47	guanylyl cyclase domain containing 1 [Source:HGNC Symbol
14	RRM1	−1.58	2e−14	2e−11	2 x 50	ribonucleotide reductase M1 [Source:HGNC Symbol;Acc:HG
15	TK1	−1.55	1e−13	3e−11	4 x 50	thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:HGN
16	ALDH9A1	−1.18	3e−13	1e−10	12 x 50	aldehyde dehydrogenase 9 family, member A1 [Source:HGN
17	SF3B3	−1.37	1e−12	2e−10	12 x 49	splicing factor 3b, subunit 3, 130kDa [Source:HGNC Symbol;
18	YIF1B	−1.51	2e−12	5e−10	4 x 45	Yip1 interacting factor homolog B (S. cerevisiae) [Source:HG
19	PLRG1	−1.49	5e−12	4e−09	12 x 49	pleiotropic regulator 1 [Source:HGNC Symbol;Acc:HGNC:90
20	MTHFD2	−1.46	3e−11	4e−09	3 x 47	methylenetetrahydrofolate dehydrogenase (NADP+ depende