D8_mel

Global Summary

%DE = 0.22

genes with fdr < 0.2 = 2727 (1606 + / 1121 −)

genes with fdr < 0.1 = 2286 (1367 + / 919 −)

genes with fdr < 0.05 = 1946 (1158 + / 788 −)

genes with fdr < 0.01 = 1292 (785 + / 507 −)

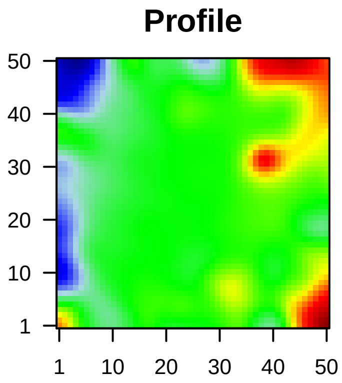
genes in genesets = 14839

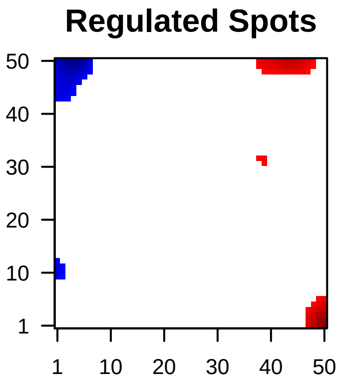
<FC> = 0

<shrinkage−t> = −0.03

<p−value> = 0.07

<fdr> = 0.78



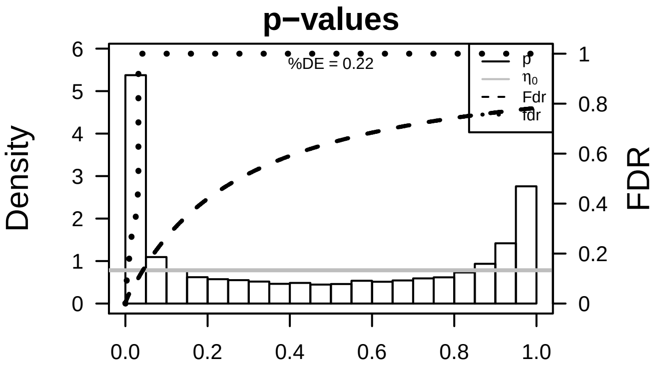


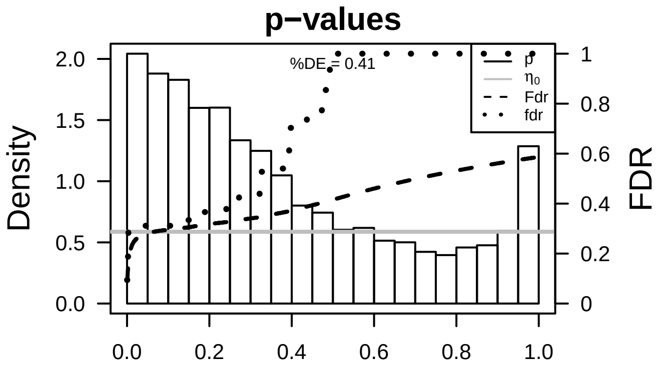
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CDKN3	−1.65	2e−16	8e−14	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
2	CERS2	−1.87	2e−16	8e−14	3 x 34	ceramide synthase 2 [Source:HGNC Symbol;Acc:HGNC:140
3	COMMD4	−1.59	2e−16	8e−14	11 x 50	COMM domain containing 4 [Source:HGNC Symbol;Acc:HGN
4	CRYAB	1.8	2e−16	8e−14	50 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
5	DAB2	−0.82	2e−16	8e−14	3 x 41	Dab, mitogen−responsive phosphoprotein, homolog 2 (Droso
6	DCT	−1.42	2e−16	8e−14	1 x 11	dopachrome tautomerase [Source:HGNC Symbol;Acc:HGNC
7	DDX39A	−1.8	2e−16	8e−14	5 x 46	DEAD (Asp−Glu−Ala−Asp) box polypeptide 39A [Source:HGN
8	DRG1	−1.9	2e−16	8e−14	48 x 19	developmentally regulated GTP binding protein 1 [Source:HG
9	EBP	−2.01	2e−16	8e−14	1 x 48	emopamil binding protein (sterol isomerase) [Source:HGNC
10	EMC6	−1.62	2e−16	8e−14	7 x 27	ER membrane protein complex subunit 6 [Source:HGNC Sym
11	FN1	2.12	2e−16	8e−14	50 x 1	fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
12	HAUS1	−1.62	2e−16	8e−14	1 x 50	HAUS augmin−like complex, subunit 1 [Source:HGNC Symbo
13	METTL9	−1.46	2e−16	8e−14	1 x 43	methyltransferase like 9 [Source:HGNC Symbol;Acc:HGNC:2
14	MRPL48	−1.17	2e−16	8e−14	5 x 41	mitochondrial ribosomal protein L48 [Source:HGNC Symbol;
15	MYH10	−2.15	2e−16	8e−14	1 x 44	myosin, heavy chain 10, non−muscle [Source:HGNC Symbol
16	NAA15	−1.61	2e−16	8e−14	48 x 19	N(alpha)−acetyltransferase 15, NatA auxiliary subunit [Source
17	NDUFAF4	−1.63	2e−16	8e−14	4 x 41	NADH dehydrogenase (ubiquinone) complex I, assembly fact
18	PRPF40A	−0.97	2e−16	8e−14	6 x 6	PRP40 pre−mRNA processing factor 40 homolog A (S. cerev
19	PTRHD1	−1.63	2e−16	8e−14	5 x 41	peptidyl−tRNA hydrolase domain containing 1 [Source:HGNC
20	RNF14	−1.67	2e−16	8e−14	1 x 43	ring finger protein 14 [Source:HGNC Symbol;Acc:HGNC:100

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	4.66	0.005	111	GSEA C2	ZHU_CMV_ALL_DN
2	4.59	0.005	5940	Brain	Overlap_fetal_midbrain_HetRpts
3	4.36	0.006	73	CC	basement membrane
4	4.34	0.006	37	CC	platelet alpha granule lumen
5	4.34	0.006	168	HM	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
6	4.29	0.006	594	GSEA C2	WONG_ADULT_TISSUE_STEM_MODULE
7	4.22	0.006	14	GSEA C2	GOUYER_TATI_TARGETS_DN
8	3.97	0.008	54	GSEA C2	VERRECCHIA_EARLY_RESPONSE_TO_TGFB1
9	3.92	0.008	22	CC	histone acetyltransferase complex
10	3.87	0.008	68	GSEA C2	FRIDMAN_SENESCENCE_UP
11	3.85	0.008	44	BP	post−Golgi vesicle−mediated transport
12	3.82	0.009	281	Colon Cancer	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
13	3.75	0.009	17	CC	basal lamina
14	3.74	0.009	11	BP	peptide cross−linking
15	3.74	0.009	86	MF	integrin binding
16	3.73	0.009	14	GSEA C2	CHANG_POU5F1_TARGETS_UP
17	3.67	0.010	59	GSEA C2	REACTOME_TRANS_GOLGI_NETWORK_VESICLE_BUDDING
18	3.66	0.010	157	GSEA C2	YAMAZAKI_TCEB3_TARGETS_UP
19	3.66	0.010	71	GSEA C2	RODRIGUES_THYROID_CARCINOMA_DN
20	3.64	0.010	75	GSEA C2	ZHU_CMV_24_HR_DN
Underexpressed					
1	−12.41	1e−04	305	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
2	−11.83	1e−04	81	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
3	−11.82	3e−03	16	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
4	−11.54	2e−04	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
5	−11.52	2e−04	327	GSEA C2	BLUM_RESPONSE_TO_SALIRASIB_DN
6	−11.37	2e−04	242	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
7	−11.1	2e−04	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
8	−10.95	2e−04	197	HM	HALLMARK_E2F_TARGETS
9	−10.48	2e−04	96	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
10	−10.22	2e−04	54	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
11	−10.17	2e−04	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
12	−9.58	3e−04	72	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
13	−9.45	3e−04	110	GSEA C2	WHITEFORD_PEDIATRIC_CANCER_MARKERS
14	−9.38	3e−04	216	GSEA C2	MARKEY_RB1_ACUTE_LOF_DN
15	−9.35	3e−04	162	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
16	−9.2	4e−04	84	GSEA C2	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_6HR
17	−8.9	4e−04	436	GSEA C2	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
18	−8.83	4e−04	116	GSEA C2	MISSIAGLIA_REGULATED_BY_METHYLATION_DN
19	−8.79	4e−04	99	GSEA C2	BURTON_ADIPOGENESIS_3
20	−8.77	4e−04	308	GSEA C2	LINDGREN_BLADDER_CANCER_CLUSTER_3_UP





D8_mel

Local Summary

%DE = 0.72

metagenes = 21

genes = 320

genes in genesets = 319

genes with fdr < 0.1 = 158 (140 + / 18 −)

genes with fdr < 0.05 = 156 (138 + / 18 −)

genes with fdr < 0.01 = 117 (105 + / 12 −)

<r> metagenes = 0.97

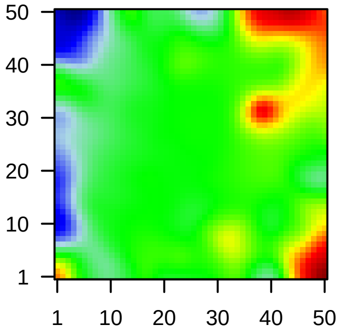
<r> genes = 0.19

<FC> = 0.41

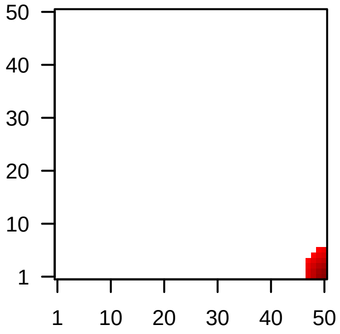
<shrinkage−t> = 6.55

<p−value> = 0

<fdr> = 0.5



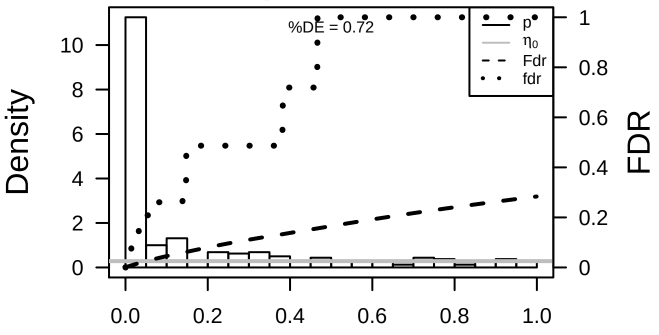
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CRYAB	1.8	2e−16	7e−15	50 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
2	FN1	2.12	2e−16	7e−15	50 x 1	fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
3	SERPINI1	2.21	2e−16	7e−15	50 x 1	serpin peptidase inhibitor, clade I (neuroserpin), member 1 [S
4	VTN	1.93	6e−15	6e−12	50 x 1	vitronectin [Source:HGNC Symbol;Acc:HGNC:12724]
5	SPTA1	1.85	7e−14	5e−11	50 x 1	spectrin, alpha, erythrocytic 1 [Source:HGNC Symbol;Acc:HG
6	SSBP2	1.76	9e−13	5e−11	50 x 3	single−stranded DNA binding protein 2 [Source:HGNC Symb
7	S100A4	1.74	2e−12	5e−11	50 x 1	S100 calcium binding protein A4 [Source:HGNC Symbol;Acc:
8	TAGLN	1.74	2e−12	8e−11	50 x 6	transgelin [Source:HGNC Symbol;Acc:HGNC:11553]
9	C10orf10	1.72	3e−12	8e−11	49 x 1	chromosome 10 open reading frame 10 [Source:HGNC Symb
10	PRKCI	1.72	3e−12	1e−10	47 x 3	protein kinase C, iota [Source:HGNC Symbol;Acc:HGNC:940
11	SPARC	0.85	5e−12	1e−10	50 x 2	secreted protein, acidic, cysteine−rich (osteonectin) [Source:
12	PPAP2A	1.69	7e−12	1e−10	50 x 4	phosphatidic acid phosphatase type 2A [Source:HGNC Symb
13	DNAJC6	1.69	7e−12	9e−09	50 x 1	DnaJ (Hsp40) homolog, subfamily C, member 6 [Source:HGN
14	MATN2	1.59	1e−10	3e−08	50 x 1	matrilin 2 [Source:HGNC Symbol;Acc:HGNC:6908]
15	IGFBP2	1.54	4e−10	5e−08	50 x 3	insulin−like growth factor binding protein 2, 36kDa [Source:H
16	MYOZ2	1.49	2e−09	5e−08	48 x 1	myozenin 2 [Source:HGNC Symbol;Acc:HGNC:1330]
17	TNFRSF12A	1.48	2e−09	5e−08	50 x 1	tumor necrosis factor receptor superfamily, member 12A [Sou
18	ITGB5	1.47	3e−09	5e−08	49 x 3	integrin, beta 5 [Source:HGNC Symbol;Acc:HGNC:6160]
19	COBLL1	1.47	3e−09	2e−07	50 x 6	cordon−bleu WH2 repeat protein−like 1 [Source:HGNC Symb
20	SULF2	1.43	6e−09	2e−07	50 x 3	sulfatase 2 [Source:HGNC Symbol;Acc:HGNC:20392]



p−values

D8_mel

Local Summary

%DE = 0.97

metagenes = 3

genes = 52

genes in genesets = 52

genes with fdr < 0.1 = 50 (50 + / 0 −)

genes with fdr < 0.05 = 49 (49 + / 0 −)

genes with fdr < 0.01 = 42 (42 + / 0 −)

<r> metagenes = 0.98

<r> genes = 0.48

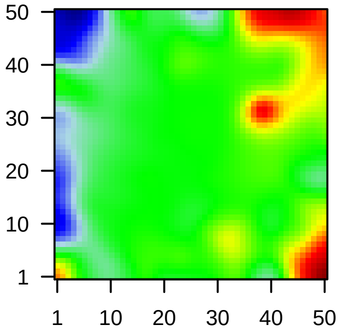
<FC> = 0.97

<shrinkage−t> = 14.77

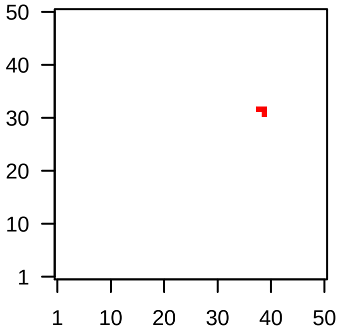
<p−value> = 0

<fdr> = 0.21

Profile



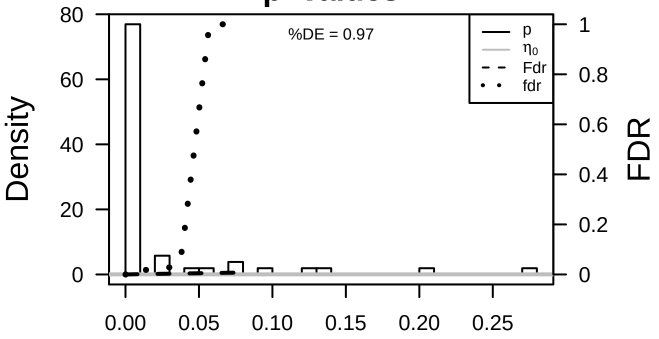
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	LRRIQ1	1.99	7e−16	6e−13	39 x 32	leucine−rich repeats and IQ motif containing 1 [Source:HGN
2	CDNF	1.79	4e−13	2e−12	38 x 32	cerebral dopamine neurotrophic factor [Source:HGNC Symb
3	ACOX2	1.74	2e−12	3e−12	39 x 32	acyl−CoA oxidase 2, branched chain [Source:HGNC Symbol;
4	DIRAS3	1.71	4e−12	4e−11	39 x 32	DIRAS family, GTP−binding RAS−like 3 [Source:HGNC Symb
5	ZNF547	1.62	5e−11	4e−11	39 x 32	zinc finger protein 547 [Source:HGNC Symbol;Acc:HGNC:26
6	WDR78	1.61	6e−11	3e−10	39 x 32	WD repeat domain 78 [Source:HGNC Symbol;Acc:HGNC:26
7	TDRP	1.55	3e−10	2e−09	38 x 32	testis development related protein [Source:HGNC Symbol;Ac
8	MGLL	1.47	3e−09	2e−09	39 x 32	monoglyceride lipase [Source:HGNC Symbol;Acc:HGNC:170
9	CD163L1	1.46	3e−09	3e−09	39 x 32	CD163 molecule−like 1 [Source:HGNC Symbol;Acc:HGNC:3
10	ZNF75D	1.44	5e−09	2e−08	39 x 32	zinc finger protein 75D [Source:HGNC Symbol;Acc:HGNC:13
11	COLEC11	1.39	2e−08	2e−07	39 x 32	collectin sub−family member 11 [Source:HGNC Symbol;Acc:
12	LXN	1.27	3e−07	2e−07	39 x 32	latexin [Source:HGNC Symbol;Acc:HGNC:13347]
13	GJB7	1.24	5e−07	2e−07	38 x 32	gap junction protein, beta 7, 25kDa [Source:HGNC Symbol;A
14	ZNF19	1.24	5e−07	6e−07	39 x 32	zinc finger protein 19 [Source:HGNC Symbol;Acc:HGNC:129
15	KIAA1257	1.21	1e−06	6e−07	38 x 32	KIAA1257 [Source:HGNC Symbol;Acc:HGNC:29231]
16	PAX9	1.19	1e−06	6e−07	38 x 32	paired box 9 [Source:HGNC Symbol;Acc:HGNC:8623]
17	SRGN	1.18	2e−06	2e−06	38 x 32	serglycin [Source:HGNC Symbol;Acc:HGNC:9361]
18	SLC9A9	1.15	3e−06	1e−05	39 x 32	solute carrier family 9, subfamily A (NHE9, cation proton anti
19	UFSP1	1.02	3e−05	1e−05	38 x 32	UFM1−specific peptidase 1 (non−functional) [Source:HGNC
20	CHIC1	1.02	4e−05	1e−05	38 x 32	cysteine−rich hydrophobic domain 1 [Source:HGNC Symbol;

p−values



D8_mel

Local Summary

%DE = 0.74

metagenes = 31

genes = 368

genes in genesets = 367

genes with fdr < 0.1 = 183 (157 + / 26 −)

genes with fdr < 0.05 = 161 (138 + / 23 −)

genes with fdr < 0.01 = 125 (108 + / 17 −)

<r> metagenes = 0.79

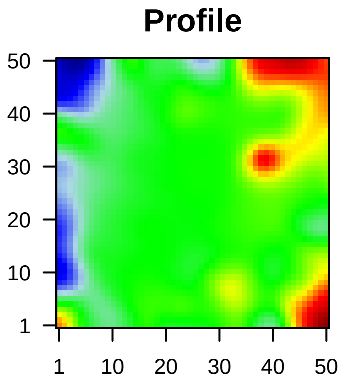
<r> genes = 0.07

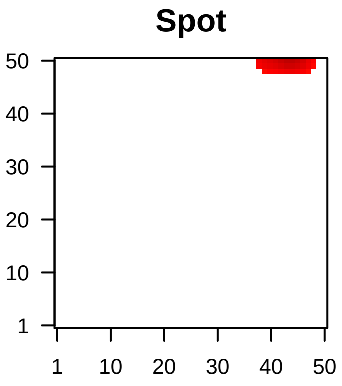
<FC> = 0.36

<shrinkage−t> = 5.99

<p−value> = 0.01

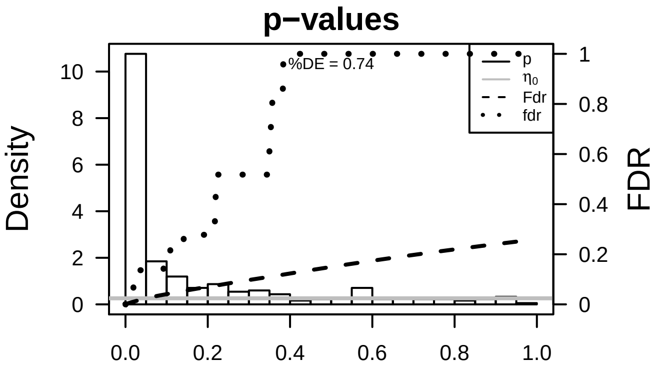
<fdr> = 0.54





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	BLOC1S2	−1.49	3e−13	3e−10	48 x 50	biogenesis of lysosomal organelles complex−1, subunit 2 [So
2	C14orf119	−1.27	3e−12	3e−09	40 x 50	chromosome 14 open reading frame 119 [Source:HGNC Sy
3	PGBD2	1.63	4e−11	4e−09	42 x 50	piggyBac transposable element derived 2 [Source:HGNC Sy
4	STK11IP	1.61	8e−11	1e−08	43 x 50	serine/threonine kinase 11 interacting protein [Source:HGNC
5	BBS4	1.56	2e−10	1e−08	46 x 50	Bardet−Biedl syndrome 4 [Source:HGNC Symbol;Acc:HGNC
6	ATG13	1.55	4e−10	1e−07	43 x 50	autophagy related 13 [Source:HGNC Symbol;Acc:HGNC:290
7	CFH	1.49	1e−09	1e−07	43 x 50	complement factor H [Source:HGNC Symbol;Acc:HGNC:488
8	MYO1E	1.47	2e−09	7e−07	43 x 50	myosin IE [Source:HGNC Symbol;Acc:HGNC:7599]
9	NMRK1	1.42	1e−08	3e−06	45 x 50	nicotinamide riboside kinase 1 [Source:HGNC Symbol;Acc:H
10	UBIAD1	1.34	6e−08	3e−06	45 x 50	UbiA prenyltransferase domain containing 1 [Source:HGNC
11	JMJD4	1.33	7e−08	6e−06	39 x 50	jumonji domain containing 4 [Source:HGNC Symbol;Acc:HG
12	HHLA3	1.3	1e−07	7e−06	45 x 50	HERV−H LTR−associating 3 [Source:HGNC Symbol;Acc:HG
13	PPCDC	1.27	3e−07	7e−06	47 x 50	phosphopantothenoylcysteine decarboxylase [Source:HGNC
14	SRD5A3	1.25	4e−07	7e−06	38 x 49	steroid 5 alpha−reductase 3 [Source:HGNC Symbol;Acc:HG
15	FAM89A	1.25	4e−07	7e−06	38 x 49	family with sequence similarity 89, member A [Source:HGNC
16	ZNF649	1.25	4e−07	7e−06	45 x 49	zinc finger protein 649 [Source:HGNC Symbol;Acc:HGNC:25
17	CRYZL1	0.87	5e−07	7e−06	44 x 50	crystallin, zeta (quinone reductase)−like 1 [Source:HGNC Sy
18	SLC25A20	1.24	6e−07	1e−05	38 x 50	solute carrier family 25 (carnitine/acylcarnitine translocase),
19	TTI2	1.23	7e−07	1e−05	48 x 50	TELO2 interacting protein 2 [Source:HGNC Symbol;Acc:HG
20	PLA2G4A	1.21	9e−07	1e−05	40 x 50	phospholipase A2, group IVA (cytosolic, calcium−dependent)



D8_mel

Local Summary

%DE = 0.7

metagenes = 7

genes = 147

genes in genesets = 146

genes with fdr < 0.1 = 81 (10 + / 71 −)

genes with fdr < 0.05 = 65 (6 + / 59 −)

genes with fdr < 0.01 = 50 (4 + / 46 −)

<r> metagenes = 0.98

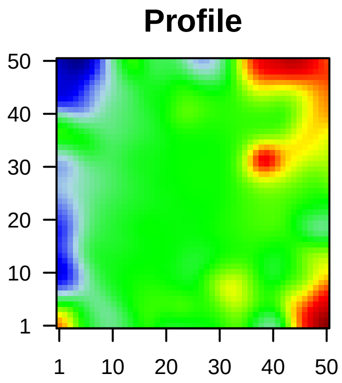
<r> genes = 0.17

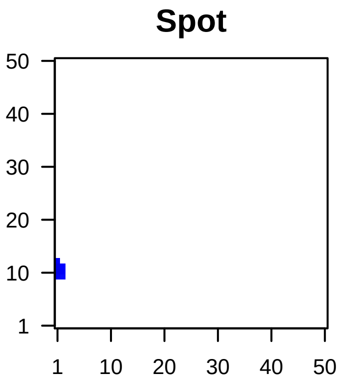
<FC> = −0.41

<shrinkage−t> = −6.79

<p−value> = 0

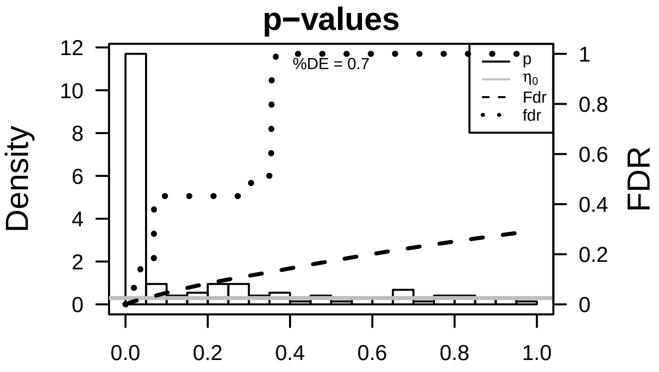
<fdr> = 0.51





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	DCT	−1.42	2e−16	1e−14	1 x 11	dopachrome tautomerase [Source:HGNC Symbol;Acc:HGNC
2	TTYH3	−1.48	8e−13	2e−09	1 x 12	tweety family member 3 [Source:HGNC Symbol;Acc:HGNC:2
3	CCDC171	−1.29	4e−11	3e−09	1 x 11	coiled−coil domain containing 171 [Source:HGNC Symbol;Ac
4	MET	−1.4	1e−10	2e−08	1 x 11	MET proto−oncogene, receptor tyrosine kinase [Source:HGN
5	OCA2	−1.2	9e−10	2e−08	1 x 12	oculocutaneous albinism II [Source:HGNC Symbol;Acc:HGN
6	HSPB8	−1.35	1e−09	2e−07	1 x 11	heat shock 22kDa protein 8 [Source:HGNC Symbol;Acc:HGN
7	SNAI2	−1.31	6e−09	2e−07	1 x 11	snail family zinc finger 2 [Source:HGNC Symbol;Acc:HGNC:1
8	KLHL24	−1.3	9e−09	2e−06	1 x 11	kelch−like family member 24 [Source:HGNC Symbol;Acc:HG
9	RAB27A	−1.1	5e−08	4e−05	1 x 11	RAB27A, member RAS oncogene family [Source:HGNC Sym
10	MRPS2	−1.18	1e−06	4e−05	1 x 13	mitochondrial ribosomal protein S2 [Source:HGNC Symbol;A
11	BAIAP2	−1.14	2e−06	4e−05	1 x 12	BAI1−associated protein 2 [Source:HGNC Symbol;Acc:HGN
12	PIK3CB	−0.99	2e−06	8e−05	1 x 11	phosphatidylinositol−4,5−bisphosphate 3−kinase, catalytic su
13	SLC7A5	−1.12	5e−06	8e−05	1 x 11	solute carrier family 7 (amino acid transporter light chain, L s
14	SCUBE3	−1.09	8e−06	8e−05	1 x 12	signal peptide, CUB domain, EGF−like 3 [Source:HGNC Sym
15	SEMA3C	−1.08	1e−05	8e−05	1 x 10	sema domain, immunoglobulin domain (Ig), short basic doma
16	SMEK1	−1.07	1e−05	8e−05	1 x 13	SMEK homolog 1, suppressor of mek1 (Dictyostelium) [Sour
17	GPR19	−1.07	1e−05	2e−04	2 x 12	G protein−coupled receptor 19 [Source:HGNC Symbol;Acc:H
18	CABLES1	−0.92	2e−05	3e−04	1 x 13	Cdk5 and Abl enzyme substrate 1 [Source:HGNC Symbol;Ac
19	MYO1D	1.05	2e−05	7e−04	1 x 12	myosin ID [Source:HGNC Symbol;Acc:HGNC:7598]
20	PIP4K2C	−0.99	6e−05	7e−04	1 x 10	phosphatidylinositol−5−phosphate 4−kinase, type II, gamma



D8_mel

Local Summary

%DE = 0.84

metagenes = 43

genes = 585

genes in genesets = 583

genes with fdr < 0.1 = 365 (60 + / 305 −)

genes with fdr < 0.05 = 315 (53 + / 262 −)

genes with fdr < 0.01 = 189 (27 + / 162 −)

<r> metagenes = 0.83

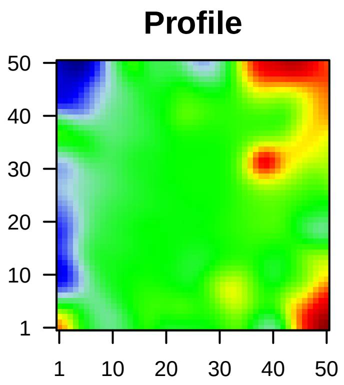
<r> genes = 0.2

<FC> = −0.39

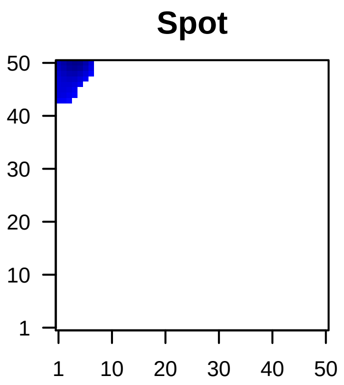
<shrinkage−t> = −6.6

<p−value> = 0

<fdr> = 0.52



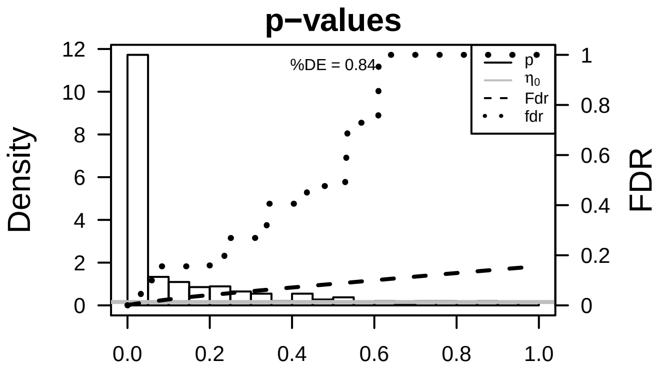
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CDKN3	−1.65	2e−16	2e−15	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
2	DDX39A	−1.8	2e−16	2e−15	5 x 46	DEAD (Asp−Glu−Ala−Asp) box polypeptide 39A [Source:HG
3	EBP	−2.01	2e−16	2e−15	1 x 48	emopamil binding protein (sterol isomerase) [Source:HGNC
4	HAUS1	−1.62	2e−16	2e−15	1 x 50	HAUS augmin−like complex, subunit 1 [Source:HGNC Symbo
5	METTL9	−1.46	2e−16	2e−15	1 x 43	methyltransferase like 9 [Source:HGNC Symbol;Acc:HGNC:2
6	MYH10	−2.15	2e−16	2e−15	1 x 44	myosin, heavy chain 10, non−muscle [Source:HGNC Symbol
7	RNF14	−1.67	2e−16	2e−15	1 x 43	ring finger protein 14 [Source:HGNC Symbol;Acc:HGNC:100
8	SAE1	−1.71	2e−16	2e−15	4 x 47	SUMO1 activating enzyme subunit 1 [Source:HGNC Symbol;
9	TTC39A	−1.57	2e−16	2e−15	1 x 43	tetratricopeptide repeat domain 39A [Source:HGNC Symbol;
10	UCP2	−1.62	2e−16	2e−15	2 x 46	uncoupling protein 2 (mitochondrial, proton carrier) [Source:H
11	MCM4	−1.58	9e−16	3e−13	1 x 50	minichromosome maintenance complex component 4 [Sourc
12	TK1	−1.55	6e−15	3e−13	4 x 50	thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:HGN
13	SMC1A	−1.41	7e−15	3e−11	3 x 48	structural maintenance of chromosomes 1A [Source:HGNC
14	SMC4	−1.49	3e−13	4e−10	5 x 50	structural maintenance of chromosomes 4 [Source:HGNC Sy
15	STMN1	−0.69	5e−12	1e−09	5 x 50	stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]
16	ILKAP	−1.44	2e−11	7e−09	2 x 44	integrin−linked kinase−associated serine/threonine phosphat
17	TYMS	−1.37	3e−10	7e−09	3 x 50	thymidylate synthetase [Source:HGNC Symbol;Acc:HGNC:1
18	RHOG	−1.37	3e−10	7e−09	1 x 46	ras homolog family member G [Source:HGNC Symbol;Acc:H
19	USP39	−1.37	3e−10	7e−09	2 x 45	ubiquitin specific peptidase 39 [Source:HGNC Symbol;Acc:H
20	ASRGL1	−1.37	3e−10	2e−08	1 x 50	asparaginase like 1 [Source:HGNC Symbol;Acc:HGNC:1644



p−values