D11_mel

Global Summary

%DE = 0.21

genes with fdr < 0.2 = 2719 (1610 + / 1109 −)

genes with fdr < 0.1 = 2281 (1360 + / 921 −)

genes with fdr < 0.05 = 1712 (1045 + / 667 −)

genes with fdr < 0.01 = 1136 (700 + / 436 −)

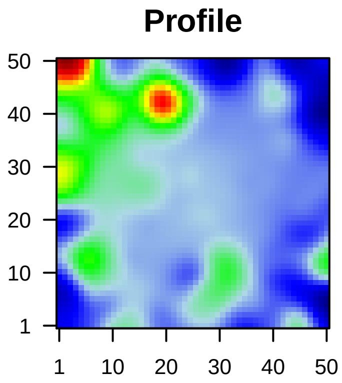
genes in genesets = 14839

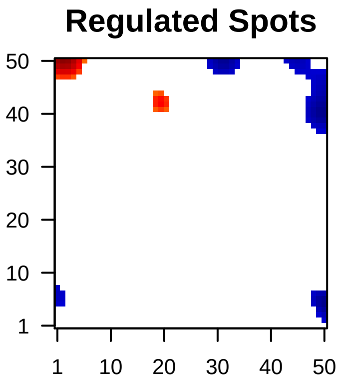
<FC> = 0

<shrinkage−t> = 0.01

<p−value> = 0.08

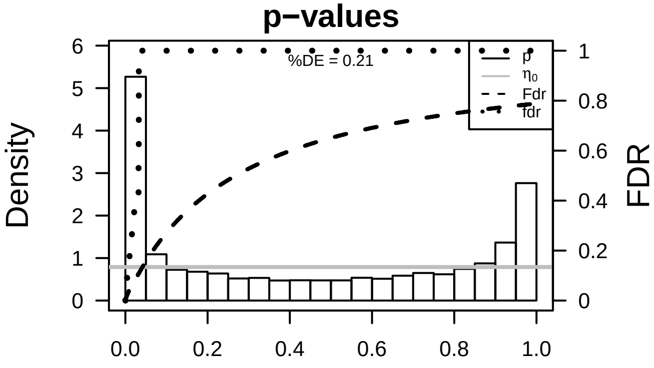
<fdr> = 0.79





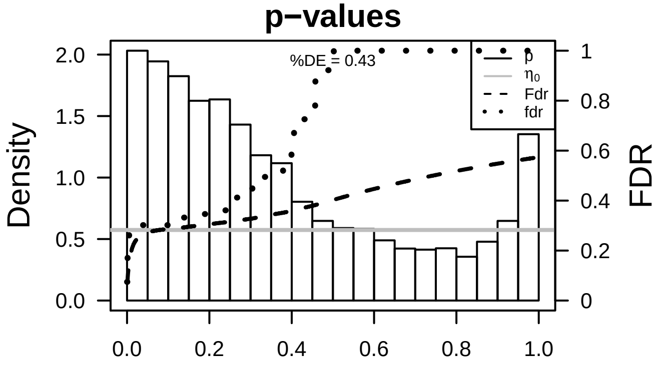
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ANKRD28	−1.43	2e−16	1e−13	50 x 5	ankyrin repeat domain 28 [Source:HGNC Symbol;Acc:HGNC
2	ARF1	−0.81	2e−16	1e−13	46 x 35	ADP−ribosylation factor 1 [Source:HGNC Symbol;Acc:HGNC
3	ARL16	−1.62	2e−16	1e−13	50 x 50	ADP−ribosylation factor−like 16 [Source:HGNC Symbol;Acc:
4	BRD8	−1.74	2e−16	1e−13	50 x 39	bromodomain containing 8 [Source:HGNC Symbol;Acc:HGN
5	C17orf62	−1.68	2e−16	1e−13	18 x 50	chromosome 17 open reading frame 62 [Source:HGNC Sym
6	DCTN2	−1.81	2e−16	1e−13	50 x 44	dynactin 2 (p50) [Source:HGNC Symbol;Acc:HGNC:2712]
7	DHRS7	−1.56	2e−16	1e−13	41 x 49	dehydrogenase/reductase (SDR family) member 7 [Source:H
8	EIF1B	−1.67	2e−16	1e−13	4 x 43	eukaryotic translation initiation factor 1B [Source:HGNC Sym
9	GARS	−1.74	2e−16	1e−13	45 x 50	glycyl−tRNA synthetase [Source:HGNC Symbol;Acc:HGNC:4
10	GRN	−1.44	2e−16	1e−13	46 x 48	granulin [Source:HGNC Symbol;Acc:HGNC:4601]
11	HERC3	−1.41	2e−16	1e−13	1 x 20	HECT and RLD domain containing E3 ubiquitin protein ligase
12	ID3	−1.73	2e−16	1e−13	11 x 50	inhibitor of DNA binding 3, dominant negative helix−loop−hel
13	NFE2L2	−1.62	2e−16	1e−13	44 x 19	nuclear factor, erythroid 2−like 2 [Source:HGNC Symbol;Acc:
14	NUDT19	−1.45	2e−16	1e−13	23 x 12	nudix (nucleoside diphosphate linked moiety X)−type motif 1
15	PABPC4	−1.64	2e−16	1e−13	50 x 7	poly(A) binding protein, cytoplasmic 4 (inducible form) [Sourc
16	PDE4D	−1.71	2e−16	1e−13	3 x 8	phosphodiesterase 4D, cAMP−specific [Source:HGNC Symb
17	RAB11A	−1.89	2e−16	1e−13	36 x 50	RAB11A, member RAS oncogene family [Source:HGNC Sym
18	SDF2	−1.67	2e−16	1e−13	48 x 50	stromal cell−derived factor 2 [Source:HGNC Symbol;Acc:HG
19	SHMT2	−1.57	2e−16	1e−13	31 x 50	serine hydroxymethyltransferase 2 (mitochondrial) [Source:H
20	TAF9	−1.59	2e−16	1e−13	1 x 38	TAF9 RNA polymerase II, TATA box binding protein (TBP)−as



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset
Overexpressed				
1	13.8	7e−05	242	GSEA C2 KOBAYASHI_EGFR_SIGNALING_24HR_DN
2	12.81	1e−04	305	GSEA C2 DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
3	12.23	1e−04	267	GSEA C2 ZHANG_TLX_TARGETS_60HR_DN
4	11.94	1e−04	700	GSEA C2 MARSON_BOUND_BY_E2F4_UNSTIMULATED
5	11.87	1e−04	197	HM HALLMARK_E2F_TARGETS
6	11.79	1e−04	550	GSEA C2 GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
7	11.7	1e−04	142	Glio WILLSCHER_GBM_Verhaak−CL_up (C)
8	11.05	2e−04	1192	GSEA C2 KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
9	10.94	2e−04	171	GSEA C2 SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP
10	10.6	2e−04	145	GSEA C2 CHANG_CYCLING_GENES
11	10.36	2e−04	93	GSEA C2 KONG_E2F3_TARGETS
12	9.96	3e−04	139	GSEA C2 ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
13	9.78	3e−04	81	GSEA C2 GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
14	9.65	3e−04	505	GSEA C2 BERENJENO_TRANSFORMED_BY_RHOA_UP
15	9.58	3e−04	159	GSEA C2 WINNEPENNINCKX_MELANOMA_METASTASIS_UP
16	9.44	3e−04	110	GSEA C2 WHITEFORD_PEDIATRIC_CANCER_MARKERS
17	9.43	3e−04	327	GSEA C2 BLUM_RESPONSE_TO_SALIRASIB_DN
18	9.39	3e−04	436	GSEA C2 SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
19	9.38	3e−04	216	GSEA C2 MARKEY_RB1_ACUTE_LOF_DN
20	9.19	4e−04	136	GSEA C2 RUIZ_TNC_TARGETS_DN
Underexpressed				
1	−5.6	0.002	361	GSEA C2 BERENJENO_TRANSFORMED_BY_RHOA_DN
2	−4.88	0.004	19	GSEA C2 KANG_CISPLATIN_RESISTANCE_UP
3	−4.22	0.006	42	Lymphoma CARO_OxPhos_in_DLBCL_UP
4	−3.98	0.008	14	GSEA C2 YANG_MUC2_TARGETS_DUODENUM_6MO_DN
5	−3.93	0.008	12	BP negative regulation of oxidative stress−induced intrinsic apoptotic s
6	−3.92	0.008	17	GSEA C2 YANG_MUC2_TARGETS_DUODENUM_3MO_DN
7	−3.91	0.008	683	GSEA C2 KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
8	−3.79	0.009	8	GSEA C2 GAUTSCHI_SRC_SIGNALING
9	−3.73	0.009	26	GSEA C2 MAYBURD_RESPONSE_TO_L663536_UP
10	−3.6	0.011	86	GSEA C2 KIM_MYC_AMPLIFICATION_TARGETS_DN
11	−3.54	0.011	1394	GSEA C2 ZWANG_TRANSIENTLY_UP_BY_1ST_EGF_PULSE_ONLY
12	−3.49	0.012	10	GSEA C2 REACTOME_DOWNREGULATION_OF_ERBB2_ERBB3_SIGNAL
13	−3.42	0.012	22	GSEA C2 SCHLINGEMANN_SKIN_CARCINOGENESIS_TPA_DN
14	−3.42	0.012	149	MF protein dimerization activity
15	−3.4	0.012	147	BP tRNA metabolic process
16	−3.33	0.013	472	GSEA C2 DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
17	−3.31	0.014	453	GSEA C2 WEST_ADRENOCORTICAL_TUMOR_DN
18	−3.3	0.014	196	GSEA C2 CHANG_CORE_SERUM_RESPONSE_DN
19	−3.3	0.014	23	BP positive regulation of glucose import
20	−3.29	0.014	11	GSEA C2 WU_HBX_TARGETS_3_DN



D11_mel

Local Summary

%DE = 0.96

metagenes = 11

genes = 64

genes in genesets = 64

genes with fdr < 0.1 = 60 (56 + / 4 −)

genes with fdr < 0.05 = 55 (51 + / 4 −)

genes with fdr < 0.01 = 41 (41 + / 0 −)

<r> metagenes = 0.98

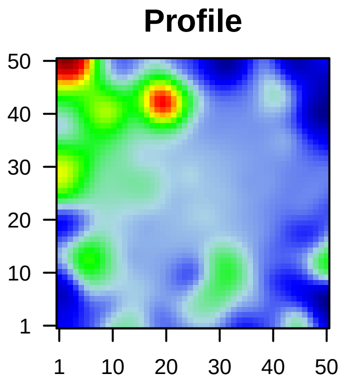
<r> genes = 0.12

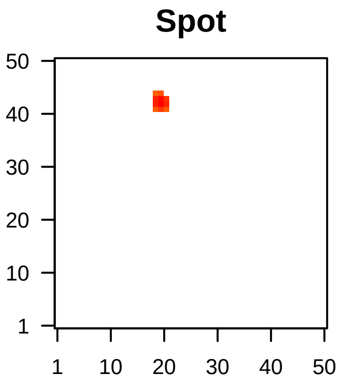
<FC> = 0.65

<shrinkage−t> = 10.25

<p−value> = 0

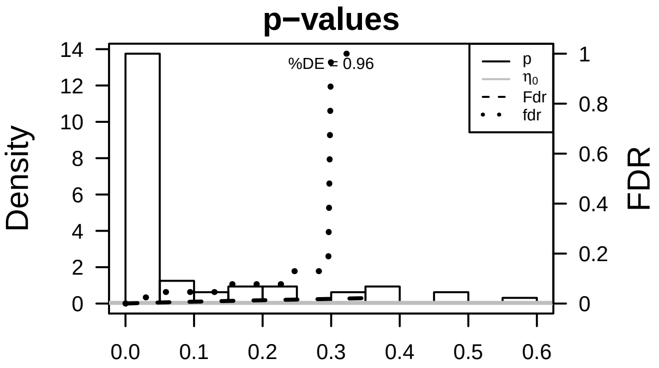
<fdr> = 0.37





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	MGAT1	1.62	1e−11	5e−09	19 x 41	mannosyl (alpha−1,3−)−glycoprotein beta−1,2−N−acetylgluc
2	RFX2	1.42	4e−09	5e−09	21 x 42	regulatory factor X, 2 (influences HLA class II expression) [S
3	LPAR2	1.41	4e−09	1e−08	21 x 41	lysophosphatidic acid receptor 2 [Source:HGNC Symbol;Acc:
4	NDUFAF7	1.38	9e−09	2e−07	21 x 43	NADH dehydrogenase (ubiquinone) complex I, assembly fac
5	ATF1	1.28	1e−07	2e−07	21 x 43	activating transcription factor 1 [Source:HGNC Symbol;Acc:H
6	HDX	1.23	3e−07	2e−07	21 x 41	highly divergent homeobox [Source:HGNC Symbol;Acc:HGN
7	FAXC	1.23	3e−07	2e−06	21 x 43	failed axon connections homolog (Drosophila) [Source:HGNC
8	RNF103	1.16	1e−06	2e−06	21 x 42	ring finger protein 103 [Source:HGNC Symbol;Acc:HGNC:12
9	TSPAN15	1.15	2e−06	2e−06	21 x 43	tetraspanin 15 [Source:HGNC Symbol;Acc:HGNC:23298]
10	RTEL1	1.11	4e−06	2e−06	21 x 42	regulator of telomere elongation helicase 1 [Source:HGNC S
11	ARMC8	0.96	4e−06	3e−06	21 x 43	armadillo repeat containing 8 [Source:HGNC Symbol;Acc:HG
12	ZFYVE27	1.08	7e−06	3e−06	21 x 43	zinc finger, FYVE domain containing 27 [Source:HGNC Sym
13	SPG11	1.08	7e−06	3e−06	19 x 43	spastic paraplegia 11 (autosomal recessive) [Source:HGNC
14	CPOX	1.07	8e−06	3e−06	19 x 43	coproporphyrinogen oxidase [Source:HGNC Symbol;Acc:HG
15	SAP130	1.07	8e−06	4e−05	20 x 43	Sin3A−associated protein, 130kDa [Source:HGNC Symbol;A
16	CDC42EP4	0.97	6e−05	4e−05	20 x 44	CDC42 effector protein (Rho GTPase binding) 4 [Source:HG
17	DPF2	0.95	7e−05	4e−05	20 x 44	D4, zinc and double PHD fingers family 2 [Source:HGNC Sy
18	CARHSP1	0.95	8e−05	4e−05	19 x 43	calcium regulated heat stable protein 1, 24kDa [Source:HGN
19	GRPEL2	0.95	8e−05	4e−05	20 x 42	GrpE−like 2, mitochondrial (E. coli) [Source:HGNC Symbol;A
20	HIST1H2AJ	0.92	1e−04	4e−05	19 x 43	histone cluster 1, H2aj [Source:HGNC Symbol;Acc:HGNC:47



D11_mel

Local Summary

%DE = 0.81

metagenes = 20

genes = 336

genes in genesets = 335

genes with fdr < 0.1 = 232 (200 + / 32 −)

genes with fdr < 0.05 = 202 (181 + / 21 −)

genes with fdr < 0.01 = 162 (150 + / 12 −)

<r> metagenes = 0.95

<r> genes = 0.28

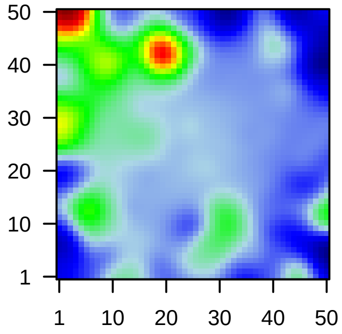
<FC> = 0.47

<shrinkage−t> = 7.6

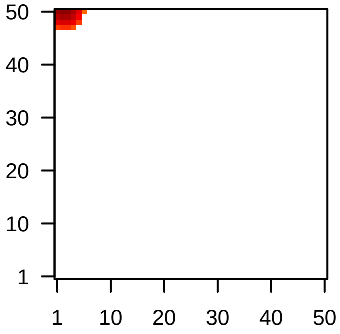
<p−value> = 0

<fdr> = 0.42

Profile



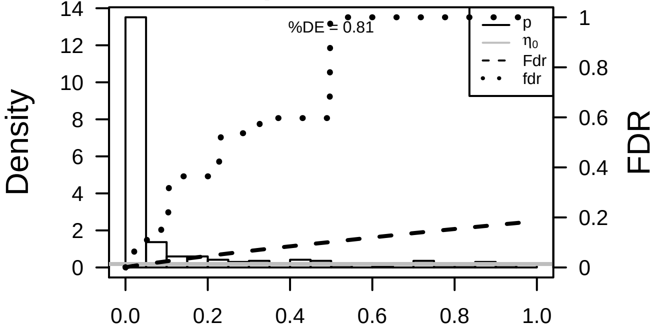
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CASC5	1.61	2e−11	2e−09	6 x 50	cancer susceptibility candidate 5 [Source:HGNC Symbol;Acc
2	RRM2	1.58	5e−11	7e−09	5 x 50	ribonucleotide reductase M2 [Source:HGNC Symbol;Acc:HG
3	BUB1B	1.53	2e−10	2e−08	6 x 50	BUB1 mitotic checkpoint serine/threonine kinase B [Source:H
4	GPD2	1.46	1e−09	2e−08	1 x 50	glycerol−3−phosphate dehydrogenase 2 (mitochondrial) [Sou
5	CCNE2	1.46	1e−09	2e−08	2 x 50	cyclin E2 [Source:HGNC Symbol;Acc:HGNC:1590]
6	BLM	1.46	1e−09	2e−08	4 x 50	Bloom syndrome, RecQ helicase−like [Source:HGNC Symbo
7	MCM10	1.46	1e−09	1e−07	1 x 50	minichromosome maintenance complex component 10 [Sour
8	GMNN	1.21	4e−09	1e−07	2 x 50	geminin, DNA replication inhibitor [Source:HGNC Symbol;Ac
9	DCK	1.41	4e−09	2e−07	2 x 50	deoxycytidine kinase [Source:HGNC Symbol;Acc:HGNC:270
10	FIGNL1	1.38	1e−08	2e−07	2 x 50	fidgetin−like 1 [Source:HGNC Symbol;Acc:HGNC:13286]
11	KIAA0101	1.25	1e−08	3e−07	3 x 50	KIAA0101 [Source:HGNC Symbol;Acc:HGNC:28961]
12	PHF19	1.36	2e−08	4e−07	5 x 50	PHD finger protein 19 [Source:HGNC Symbol;Acc:HGNC:24
13	CDK1	1.33	2e−08	4e−07	5 x 50	cyclin−dependent kinase 1 [Source:HGNC Symbol;Acc:HGN
14	PRIMPOL	1.33	3e−08	9e−07	1 x 48	primase and polymerase (DNA−directed) [Source:HGNC Sy
15	POLE2	1.32	4e−08	9e−07	1 x 47	polymerase (DNA directed), epsilon 2, accessory subunit [So
16	NUP107	0.79	7e−08	9e−07	2 x 48	nucleoporin 107kDa [Source:HGNC Symbol;Acc:HGNC:2991
17	DCLRE1C	1.28	1e−07	9e−07	3 x 49	DNA cross−link repair 1C [Source:HGNC Symbol;Acc:HGNC
18	MCM6	1.27	1e−07	9e−07	1 x 50	minichromosome maintenance complex component 6 [Sourc
19	NCAPH	1.27	1e−07	9e−07	5 x 50	non−SMC condensin I complex, subunit H [Source:HGNC Sy
20	ACTL6A	0.75	1e−07	9e−07	4 x 50	actin−like 6A [Source:HGNC Symbol;Acc:HGNC:24124]

p−values



D11_mel

Local Summary

%DE = 0.67

metagenes = 14

genes = 176

genes in genesets = 175

genes with fdr < 0.1 = 84 (14 + / 70 −)

genes with fdr < 0.05 = 69 (10 + / 59 −)

genes with fdr < 0.01 = 43 (8 + / 35 −)

<r> metagenes = 0.97

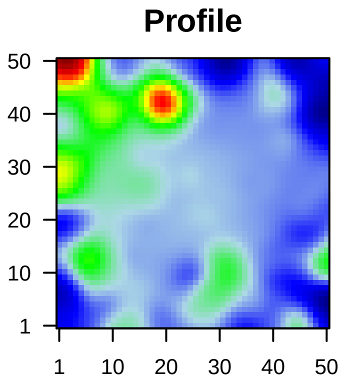
<r> genes = 0.15

<FC> = −0.31

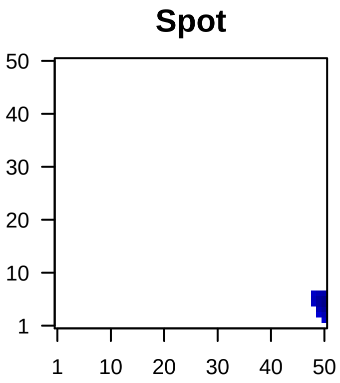
<shrinkage−t> = −5.22

<p−value> = 0.01

<fdr> = 0.56



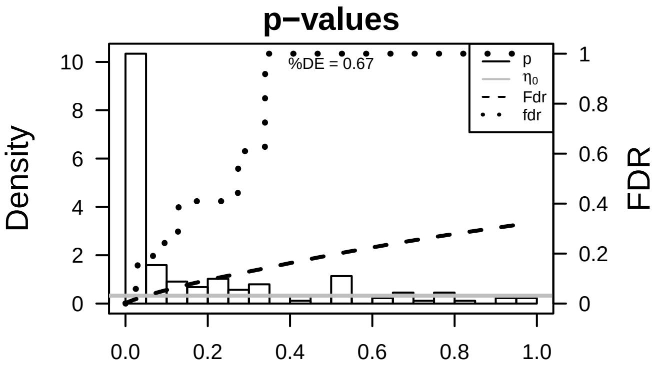
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ANKRD28	−1.43	2e−16	6e−15	50 x 5	ankyrin repeat domain 28 [Source:HGNC Symbol;Acc:HGNC
2	PABPC4	−1.64	2e−16	6e−15	50 x 7	poly(A) binding protein, cytoplasmic 4 (inducible form) [Sourc
3	TAGLN2	−1.51	2e−14	6e−09	50 x 2	transgelin 2 [Source:HGNC Symbol;Acc:HGNC:11554]
4	PLOD2	−1.36	2e−10	6e−09	49 x 3	procollagen−lysine, 2−oxoglutarate 5−dioxygenase 2 [Source
5	C11orf54	1.51	3e−10	6e−09	48 x 5	chromosome 11 open reading frame 54 [Source:HGNC Symb
6	ARMC9	−1.33	3e−10	3e−07	50 x 3	armadillo repeat containing 9 [Source:HGNC Symbol;Acc:HG
7	TLN1	−1.28	6e−09	8e−07	50 x 7	talin 1 [Source:HGNC Symbol;Acc:HGNC:11845]
8	LRRFIP2	−1.16	3e−08	8e−07	50 x 4	leucine rich repeat (in FLII) interacting protein 2 [Source:HGN
9	ALDH3A2	−1.21	4e−08	1e−06	50 x 5	aldehyde dehydrogenase 3 family, member A2 [Source:HGN
10	GLG1	−1.15	6e−08	1e−06	48 x 5	golgi glycoprotein 1 [Source:HGNC Symbol;Acc:HGNC:4316]
11	S100A13	−1.21	9e−08	1e−06	50 x 7	S100 calcium binding protein A13 [Source:HGNC Symbol;Ac
12	AKR1A1	−1.18	1e−07	6e−06	50 x 7	aldo−keto reductase family 1, member A1 (aldehyde reductas
13	IFT20	−1.13	2e−07	6e−06	50 x 6	intraflagellar transport 20 [Source:HGNC Symbol;Acc:HGNC:
14	AFF4	−1.08	3e−07	3e−05	50 x 6	AF4/FMR2 family, member 4 [Source:HGNC Symbol;Acc:HG
15	VIM	−0.79	1e−06	3e−05	50 x 2	vimentin [Source:HGNC Symbol;Acc:HGNC:12692]
16	PPP4R1	−1.14	2e−06	3e−05	50 x 7	protein phosphatase 4, regulatory subunit 1 [Source:HGNC S
17	DNAJC16	−1.12	2e−06	3e−04	50 x 5	DnaJ (Hsp40) homolog, subfamily C, member 16 [Source:HG
18	REV3L	−0.96	1e−05	3e−04	50 x 4	REV3−like, polymerase (DNA directed), zeta, catalytic subuni
19	ST5	1.04	1e−05	5e−04	50 x 5	suppression of tumorigenicity 5 [Source:HGNC Symbol;Acc:H
20	PCYOX1	0.99	2e−05	1e−03	49 x 4	prenylcysteine oxidase 1 [Source:HGNC Symbol;Acc:HGNC:



p−values

D11_mel

Local Summary

%DE = 0.44

metagenes = 7

genes = 153

genes in genesets = 151

genes with fdr < 0.1 = 31 (6 + / 25 −)

genes with fdr < 0.05 = 27 (5 + / 22 −)

genes with fdr < 0.01 = 12 (4 + / 8 −)

<r> metagenes = 0.95

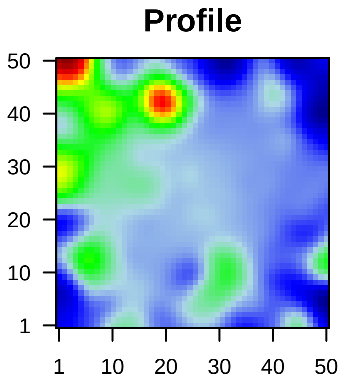
<r> genes = 0.11

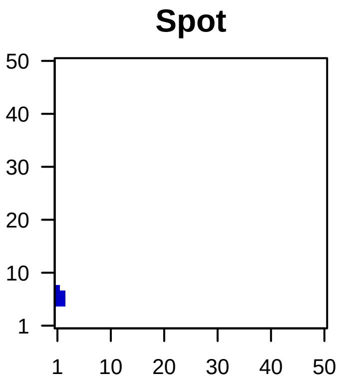
<FC> = −0.22

<shrinkage−t> = −3.5

<p−value> = 0.06

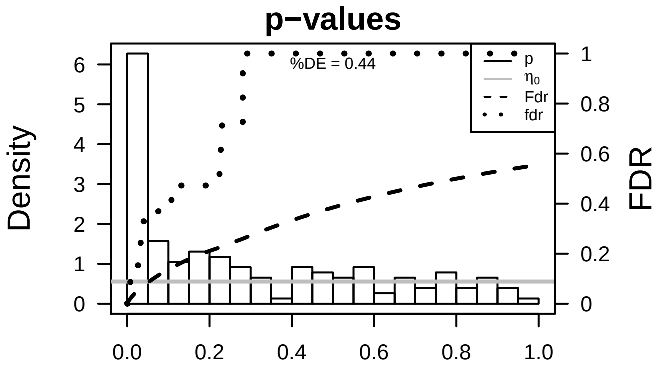
<fdr> = 0.74


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	XXYLT1	1.17	1e−06	7e−05	1 x 5	xyloside xylosyltransferase 1 [Source:HGNC Symbol;Acc:HG
2	QRICH1	−0.77	2e−06	2e−04	1 x 8	glutamine−rich 1 [Source:HGNC Symbol;Acc:HGNC:24713]
3	PANX1	1.11	4e−06	2e−04	1 x 5	pannexin 1 [Source:HGNC Symbol;Acc:HGNC:8599]
4	FECH	−1.08	6e−06	7e−04	1 x 8	ferrochelatase [Source:HGNC Symbol;Acc:HGNC:3647]
5	LPIN1	−0.95	2e−05	7e−04	1 x 8	lipin 1 [Source:HGNC Symbol;Acc:HGNC:13345]
6	TANGO2	−1.01	2e−05	2e−03	1 x 6	transport and golgi organization 2 homolog (Drosophila) [Sou
7	STAT3	−0.83	5e−05	2e−03	1 x 8	signal transducer and activator of transcription 3 (acute−phas
8	WDR13	−0.95	8e−05	3e−03	1 x 8	WD repeat domain 13 [Source:HGNC Symbol;Acc:HGNC:14
9	MCM3AP	−0.92	1e−04	3e−03	2 x 6	minichromosome maintenance complex component 3 associa
10	ADD1	−0.8	2e−04	8e−03	1 x 8	adducin 1 (alpha) [Source:HGNC Symbol;Acc:HGNC:243]
11	ANGEL2	0.88	2e−04	9e−03	1 x 7	angel homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:H
12	ST20	0.85	4e−04	9e−03	1 x 8	suppressor of tumorigenicity 20 [Source:HGNC Symbol;Acc:
13	OSBPL9	−0.69	5e−04	1e−02	1 x 8	oxysterol binding protein−like 9 [Source:HGNC Symbol;Acc:
14	MVB12A	−0.81	7e−04	1e−02	1 x 6	multivesicular body subunit 12A [Source:HGNC Symbol;Acc:
15	TRAPPC3	−0.81	8e−04	1e−02	1 x 8	trafficking protein particle complex 3 [Source:HGNC Symbol;
16	PCCB	−0.76	9e−04	1e−02	1 x 7	propionyl CoA carboxylase, beta polypeptide [Source:HGNC
17	GRINA	−0.79	1e−03	2e−02	1 x 6	glutamate receptor, ionotropic, N−methyl D−aspartate−associ
18	KRTAP19−1	−0.78	1e−03	3e−02	1 x 8	keratin associated protein 19−1 [Source:HGNC Symbol;Acc:
19	SDHC	−0.75	2e−03	3e−02	1 x 5	succinate dehydrogenase complex, subunit C, integral memb
20	ATXN3	−0.75	2e−03	3e−02	1 x 8	ataxin 3 [Source:HGNC Symbol;Acc:HGNC:7106]


p−values

D11_mel

Local Summary

%DE = 0.68

metagenes = 53

genes = 582

genes in genesets = 579

genes with fdr < 0.1 = 246 (73 + / 173 −)

genes with fdr < 0.05 = 196 (56 + / 140 −)

genes with fdr < 0.01 = 116 (30 + / 86 −)

<r> metagenes = 0.69

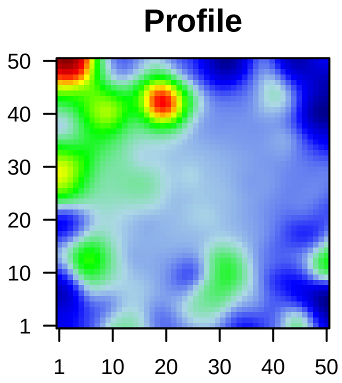
<r> genes = 0.05

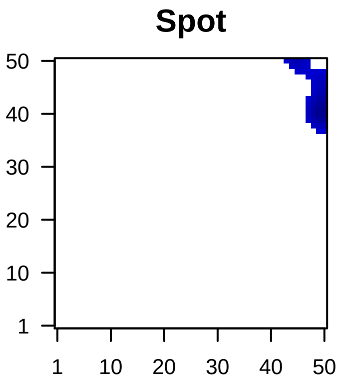
<FC> = −0.21

<shrinkage−t> = −3.57

<p−value> = 0.01

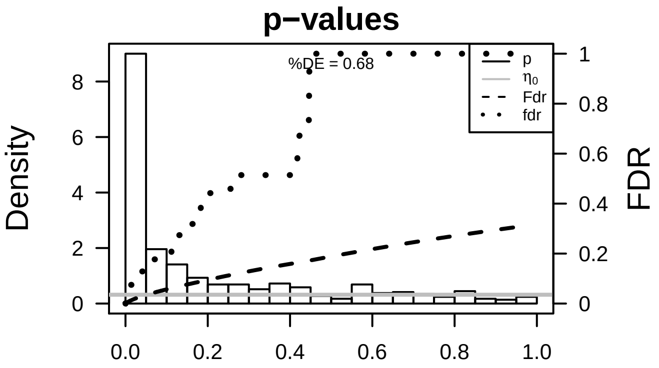
<fdr> = 0.63


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	BRD8	−1.74	2e−16	8e−15	50 x 39	bromodomain containing 8 [Source:HGNC Symbol;Acc:HGN
2	DCTN2	−1.81	2e−16	8e−15	50 x 44	dynactin 2 (p50) [Source:HGNC Symbol;Acc:HGNC:2712]
3	GARS	−1.74	2e−16	8e−15	45 x 50	glycyl−tRNA synthetase [Source:HGNC Symbol;Acc:HGNC:4
4	GRN	−1.44	2e−16	8e−15	46 x 48	granulin [Source:HGNC Symbol;Acc:HGNC:4601]
5	TMEM208	−1.63	2e−16	8e−15	48 x 46	transmembrane protein 208 [Source:HGNC Symbol;Acc:HG
6	TMEM219	−1.54	2e−15	7e−12	45 x 50	transmembrane protein 219 [Source:HGNC Symbol;Acc:HG
7	SCPEP1	−1.49	7e−14	7e−12	49 x 37	serine carboxypeptidase 1 [Source:HGNC Symbol;Acc:HGN
8	TFAP2A	−1.2	7e−14	2e−11	50 x 40	transcription factor AP−2 alpha (activating enhancer binding
9	CDC42BPA	−0.94	2e−13	7e−11	50 x 38	CDC42 binding protein kinase alpha (DMPK−like) [Source:H
10	PHKB	−1.46	6e−13	9e−11	50 x 40	phosphorylase kinase, beta [Source:HGNC Symbol;Acc:HG
11	MIA3	−1.46	1e−12	2e−09	50 x 44	melanoma inhibitory activity family, member 3 [Source:HGNC
12	SCP2	−1.2	2e−11	2e−09	50 x 40	sterol carrier protein 2 [Source:HGNC Symbol;Acc:HGNC:10
13	MGEA5	−1.4	3e−11	5e−08	50 x 40	meningioma expressed antigen 5 (hyaluronidase) [Source:H
14	MNAT1	−1.35	3e−10	5e−08	43 x 50	MNAT CDK−activating kinase assembly factor 1 [Source:HG
15	PJA2	−1.34	5e−10	2e−07	49 x 41	praja ring finger 2, E3 ubiquitin protein ligase [Source:HGNC
16	MRPS36	−1.18	2e−09	2e−07	45 x 50	mitochondrial ribosomal protein S36 [Source:HGNC Symbol;
17	PRMT7	1.42	3e−09	1e−06	50 x 45	protein arginine methyltransferase 7 [Source:HGNC Symbol;
18	NUPR1	−1.08	1e−08	1e−06	45 x 50	nuclear protein, transcriptional regulator, 1 [Source:HGNC Sy
19	PLD3	−1.25	2e−08	1e−06	49 x 48	phospholipase D family, member 3 [Source:HGNC Symbol;A
20	UNC50	−1.24	3e−08	1e−06	50 x 45	unc−50 homolog (C. elegans) [Source:HGNC Symbol;Acc:H


p−values

D11_mel

Local Summary

%DE = 0.88

metagenes = 16

genes = 170

genes in genesets = 170

genes with fdr < 0.1 = 101 (26 + / 75 −)

genes with fdr < 0.05 = 80 (19 + / 61 −)

genes with fdr < 0.01 = 57 (11 + / 46 −)

<r> metagenes = 0.91

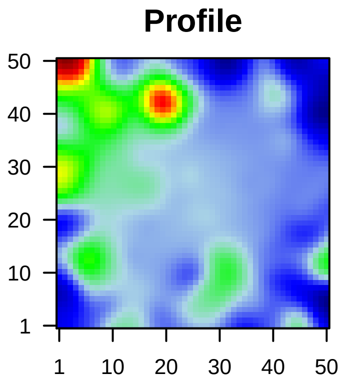
<r> genes = 0.08

<FC> = −0.28

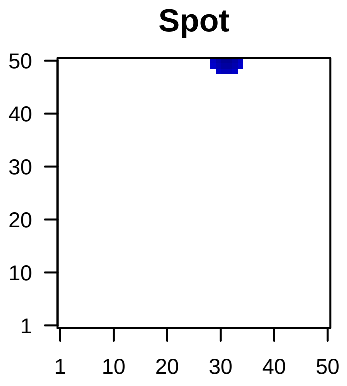
<shrinkage−t> = −4.59

<p−value> = 0

<fdr> = 0.59



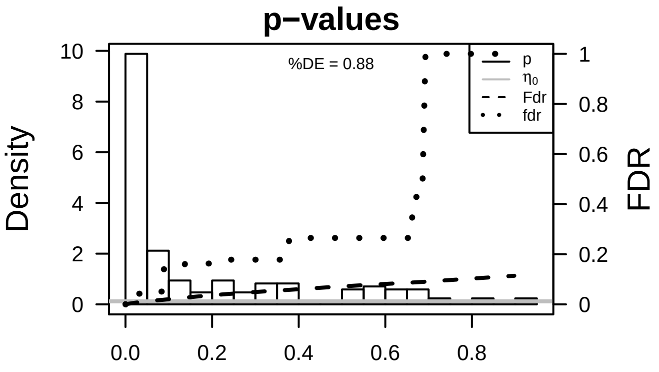
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	SHMT2	−1.57	2e−16	2e−15	31 x 50	serine hydroxymethyltransferase 2 (mitochondrial) [Source:H
2	YARS	−1.68	2e−16	2e−15	30 x 50	tyrosyl−tRNA synthetase [Source:HGNC Symbol;Acc:HGNC:
3	JKAMP	−1.3	7e−16	2e−14	29 x 50	JNK1/MAPK8−associated membrane protein [Source:HGNC
4	WDR61	−1.28	2e−15	3e−13	33 x 50	WD repeat domain 61 [Source:HGNC Symbol;Acc:HGNC:30
5	PDCD6IP	−1.24	1e−14	9e−09	33 x 50	programmed cell death 6 interacting protein [Source:HGNC S
6	RBCK1	−1.34	5e−10	4e−08	30 x 50	RanBP−type and C3HC4−type zinc finger containing 1 [Sour
7	TSFM	−1.29	4e−09	4e−08	33 x 49	Ts translation elongation factor, mitochondrial [Source:HGNC
8	PIGS	−1.29	4e−09	1e−07	29 x 50	phosphatidylinositol glycan anchor biosynthesis, class S [Sou
9	PIH1D1	−1.25	2e−08	1e−07	33 x 49	PIH1 domain containing 1 [Source:HGNC Symbol;Acc:HGNC
10	OS9	−1.05	3e−08	1e−07	34 x 50	osteosarcoma amplified 9, endoplasmic reticulum lectin [Sou
11	XPO5	−1.25	3e−08	1e−07	30 x 50	exportin 5 [Source:HGNC Symbol;Acc:HGNC:17675]
12	CCNH	−1.24	3e−08	3e−07	31 x 50	cyclin H [Source:HGNC Symbol;Acc:HGNC:1594]
13	UFC1	−0.88	5e−08	3e−06	33 x 48	ubiquitin−fold modifier conjugating enzyme 1 [Source:HGNC
14	ORMDL2	−1.2	2e−07	7e−06	34 x 50	ORMDL sphingolipid biosynthesis regulator 2 [Source:HGNC
15	ARSE	1.18	8e−07	7e−06	31 x 48	arylsulfatase E (chondrodysplasia punctata 1) [Source:HGNC
16	VCP	−1.03	1e−06	7e−06	32 x 50	valosin containing protein [Source:HGNC Symbol;Acc:HGNC
17	COA1	−1.03	1e−06	2e−05	32 x 50	cytochrome c oxidase assembly factor 1 homolog (S. cerevisi
18	CREB1	−1.12	2e−06	2e−05	32 x 50	cAMP responsive element binding protein 1 [Source:HGNC S
19	ASB8	−1.1	3e−06	9e−05	32 x 50	ankyrin repeat and SOCS box containing 8 [Source:HGNC S
20	SKAP2	1.04	1e−05	9e−05	31 x 50	src kinase associated phosphoprotein 2 [Source:HGNC Sym



p−values