G10_mel

Global Summary

%DE = 0.22

genes with fdr < 0.2 = 2786 (1679 + / 1107 −)

genes with fdr < 0.1 = 2190 (1366 + / 824 −)

genes with fdr < 0.05 = 1863 (1179 + / 684 −)

genes with fdr < 0.01 = 1151 (768 + / 383 −)

genes in genesets = 14839

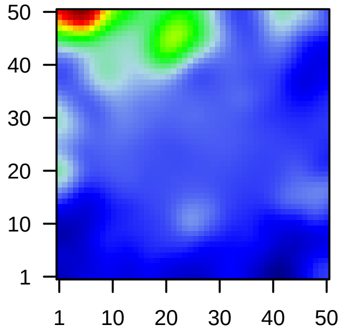
<FC> = 0

<shrinkage−t> = 0.05

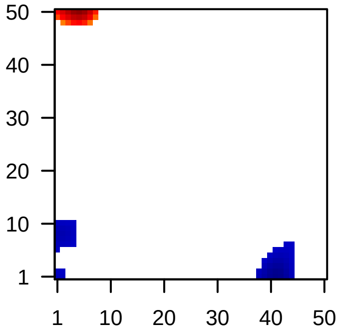
<p−value> = 0.07

<fdr> = 0.78

Profile



Regulated Spots



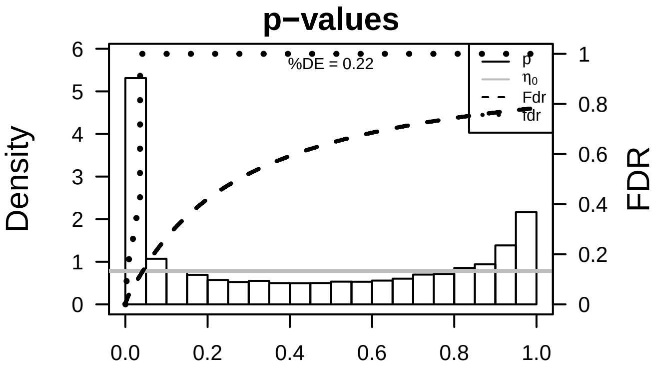
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ALG13	−1.49	2e−16	3e−13	39 x 1	ALG13, UDP−N−acetylglucosaminyltransferase subunit [Sour
2	ATRX	−1.41	2e−16	3e−13	43 x 7	alpha thalassemia/mental retardation syndrome X−linked [So
3	BSCL2	−2.04	2e−16	3e−13	50 x 50	Berardinelli−Seip congenital lipodystrophy 2 (seipin) [Source:
4	EIF3G	−1.3	2e−16	3e−13	47 x 39	eukaryotic translation initiation factor 3, subunit G [Source:HG
5	HIST1H4C	1.04	2e−16	3e−13	5 x 49	histone cluster 1, H4c [Source:HGNC Symbol;Acc:HGNC:47
6	IMP4	−1.36	2e−16	3e−13	2 x 39	IMP4, U3 small nucleolar ribonucleoprotein [Source:HGNC S
7	MRPL15	−1.23	2e−16	3e−13	5 x 33	mitochondrial ribosomal protein L15 [Source:HGNC Symbol;
8	RHEBL1	1.86	2e−16	3e−13	9 x 50	Ras homolog enriched in brain like 1 [Source:HGNC Symbol;
9	TSG101	−1.44	2e−16	3e−13	46 x 37	tumor susceptibility 101 [Source:HGNC Symbol;Acc:HGNC:1
10	RUVBL2	−1.46	4e−16	3e−12	6 x 13	RuvB−like AAA ATPase 2 [Source:HGNC Symbol;Acc:HGNC
11	PTP4A1	1.39	7e−16	3e−12	1 x 21	protein tyrosine phosphatase type IVA, member 1 [Source:HG
12	HJURP	1.74	9e−16	1e−11	6 x 50	Holliday junction recognition protein [Source:HGNC Symbol;
13	RRM2	1.72	2e−15	1e−11	5 x 50	ribonucleotide reductase M2 [Source:HGNC Symbol;Acc:HG
14	PDCD6IP	−1.15	4e−15	1e−11	33 x 50	programmed cell death 6 interacting protein [Source:HGNC S
15	SOX4	−0.91	5e−15	1e−11	41 x 1	SRY (sex determining region Y)−box 4 [Source:HGNC Symbo
16	IVNS1ABP	−1.16	5e−15	1e−11	4 x 44	influenza virus NS1A binding protein [Source:HGNC Symbol;
17	ACTL6A	1.01	6e−15	1e−11	4 x 50	actin−like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
18	ZEB2	−1.45	7e−15	1e−11	42 x 1	zinc finger E−box binding homeobox 2 [Source:HGNC Symbo
19	TRIP13	1.58	9e−15	1e−11	5 x 50	thyroid hormone receptor interactor 13 [Source:HGNC Symbo
20	CDKN3	1.25	1e−14	1e−11	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A

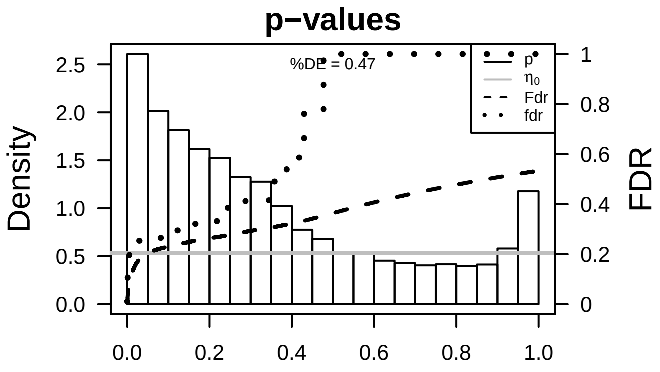
Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	22.37	9e−06	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
2	20.75	1e−05	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
3	20.45	1e−05	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
4	18.78	2e−05	305	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
5	18.69	2e−05	242	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
6	18.06	2e−05	145	GSEA C2	CHANG_CYCLING_GENES
7	17.9	6e−04	16	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
8	16.93	3e−05	1192	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
9	16.72	3e−05	197	HM	HALLMARK_E2F_TARGETS
10	16.55	4e−05	155	GSEA C2	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
11	16.41	4e−05	124	GSEA C2	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
12	16.25	4e−05	96	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
13	16.06	4e−05	72	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
14	15.92	4e−05	162	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
15	15.77	4e−05	436	GSEA C2	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
16	15.76	4e−05	54	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
17	15.39	5e−05	81	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
18	15.29	5e−05	700	GSEA C2	MARSON_BOUND_BY_E2F4_UNSTIMULATED
19	15.16	5e−05	110	GSEA C2	WHITEFORD_PEDIATRIC_CANCER_MARKERS
20	15.12	5e−05	390	GSEA C2	PUJANA_BRCA2_PCC_NETWORK
Underexpressed					
1	−4.82	0.004	1565	BP	regulation of transcription, DNA−templated
2	−4.64	0.005	168	GSEA C2	ZWANG_EGF_INTERVAL_DN
3	−4.51	0.005	2798	Colon Cancer	TxEnhG1_Colon
4	−4.37	0.006	5155	Colon Cancer	EnhWk1_Colon
5	−4.3	0.006	2698	Colon Cancer	EnhA_Colon
6	−4.1	0.007	57	HM	HALLMARK_MYC_TARGETS_V2
7	−4.07	0.007	1079	Colon Cancer	ZNF_Colon
8	−3.99	0.008	1308	GSEA C2	DODD_NASOPHARYNGEAL_CARCINOMA_UP
9	−3.86	0.008	143	TF Tissue	VAQUERIZAS_General
10	−3.83	0.009	325	GSEA C2	REACTOME_GENERIC_TRANSCRIPTION_PATHWAY
11	−3.75	0.009	1664	BP	transcription, DNA−templated
12	−3.74	0.009	830	MF	nucleic acid binding transcription factor activity
13	−3.64	0.010	11	GSEA C2	CLAUS_PGR_POSITIVE_MENINGIOMA_DN
14	−3.64	0.010	21	CC	immunological synapse
15	−3.63	0.010	19	GSEA C2	BIOCARTA_TGFB_PATHWAY
16	−3.62	0.010	148	GSEA C2	AMIT_EGF_RESPONSE_480_HELA
17	−3.58	0.011	77	GSEA C2	PID_MET_PATHWAY
18	−3.56	0.011	730	GSEA C2	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIA
19	−3.56	0.011	820	MF	sequence−specific DNA binding transcription factor activity
20	−3.51	0.011	3081	Brain	Mid_Frontal_Lobe_ZNF

p−values



p−values



G10_mel

Local Summary

%DE = 0.88

metagenes = 22

genes = 320

genes in genesets = 320

genes with fdr < 0.1 = 268 (259 + / 9 −)

genes with fdr < 0.05 = 253 (245 + / 8 −)

genes with fdr < 0.01 = 215 (212 + / 3 −)

<r> metagenes = 0.93

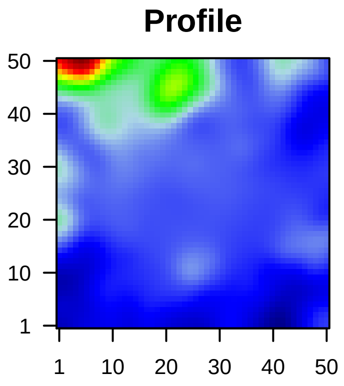
<r> genes = 0.32

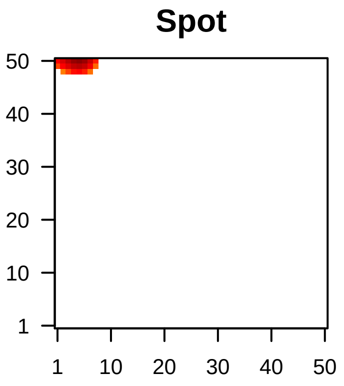
<FC> = 0.73

<shrinkage−t> = 11.67

<p−value> = 0

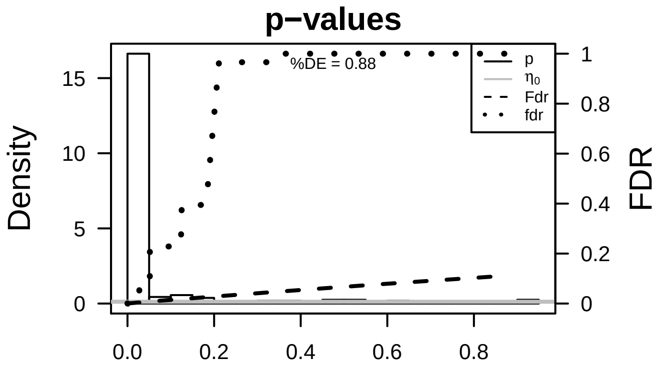
<fdr> = 0.23





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	HIST1H4C	1.04	2e−16	9e−15	5 x 49	histone cluster 1, H4c [Source:HGNC Symbol;Acc:HGNC:47
2	HJURP	1.74	9e−16	5e−14	6 x 50	Holliday junction recognition protein [Source:HGNC Symbol;
3	RRM2	1.72	2e−15	9e−14	5 x 50	ribonucleotide reductase M2 [Source:HGNC Symbol;Acc:HG
4	ACTL6A	1.01	6e−15	9e−14	4 x 50	actin−like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
5	TRIP13	1.58	9e−15	9e−14	5 x 50	thyroid hormone receptor interactor 13 [Source:HGNC Symb
6	CDKN3	1.25	1e−14	9e−14	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
7	AURKB	1.67	1e−14	6e−13	6 x 50	aurora kinase B [Source:HGNC Symbol;Acc:HGNC:11390]
8	CDK1	1.62	4e−14	6e−13	5 x 50	cyclin−dependent kinase 1 [Source:HGNC Symbol;Acc:HGN
9	BARD1	1.62	4e−14	1e−12	2 x 50	BRCA1 associated RING domain 1 [Source:HGNC Symbol;A
10	CKAP2L	1.61	1e−13	1e−12	6 x 50	cytoskeleton associated protein 2−like [Source:HGNC Symb
11	TOP2A	1.61	1e−13	3e−12	6 x 50	topoisomerase (DNA) II alpha 170kDa [Source:HGNC Symb
12	RNASEH2B	1.59	2e−13	3e−12	1 x 50	ribonuclease H2, subunit B [Source:HGNC Symbol;Acc:HGN
13	PBK	1.59	3e−13	3e−11	6 x 50	PDZ binding kinase [Source:HGNC Symbol;Acc:HGNC:1828
14	HMGB2	1.41	1e−12	4e−11	5 x 50	high mobility group box 2 [Source:HGNC Symbol;Acc:HGNC:
15	SKA3	1.51	3e−12	4e−11	5 x 50	spindle and kinetochore associated complex subunit 3 [Sourc
16	EXO1	1.51	3e−12	4e−11	1 x 50	exonuclease 1 [Source:HGNC Symbol;Acc:HGNC:3511]
17	SPC24	1.51	4e−12	5e−11	5 x 50	SPC24, NDC80 kinetochore complex component [Source:HG
18	NUF2	1.49	5e−12	5e−11	6 x 50	NUF2, NDC80 kinetochore complex component [Source:HGN
19	UBE2C	1.48	6e−12	2e−10	6 x 50	ubiquitin−conjugating enzyme E2C [Source:HGNC Symbol;A
20	HYLS1	1.47	1e−11	3e−10	8 x 50	hydrolethalus syndrome 1 [Source:HGNC Symbol;Acc:HGNC



G10_mel

Local Summary

%DE = 0.66

metagenes = 4

genes = 113

genes in genesets = 111

genes with fdr < 0.1 = 39 (14 + / 25 −)

genes with fdr < 0.05 = 34 (11 + / 23 −)

genes with fdr < 0.01 = 21 (7 + / 14 −)

<r> metagenes = 0.99

<r> genes = 0.12

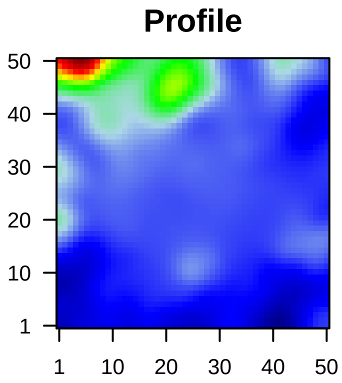
<FC> = −0.18

<shrinkage−t> = −2.67

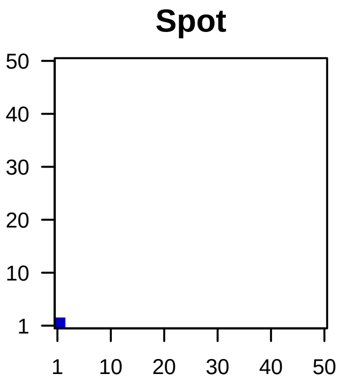
<p−value> = 0.03

<fdr> = 0.64

Profile



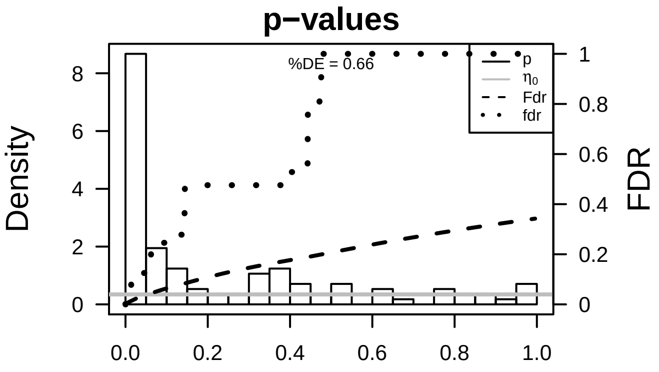
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	MED28	−1.2	6e−09	4e−06	1 x 1	mediator complex subunit 28 [Source:HGNC Symbol;Acc:HG
2	LARP7	−1.12	1e−07	1e−05	2 x 1	La ribonucleoprotein domain family, member 7 [Source:HGN
3	SLC30A5	1.1	4e−07	4e−05	2 x 2	solute carrier family 30 (zinc transporter), member 5 [Source:
4	ZNF32	−1.02	1e−06	8e−04	2 x 2	zinc finger protein 32 [Source:HGNC Symbol;Acc:HGNC:130
5	IREB2	−0.9	3e−05	8e−04	2 x 1	iron−responsive element binding protein 2 [Source:HGNC Sy
6	AASDHPPT	−0.89	4e−05	9e−04	1 x 1	aminoadipate−semialdehyde dehydrogenase−phosphopantet
7	PLOD3	−0.85	7e−05	9e−04	1 x 1	procollagen−lysine, 2−oxoglutarate 5−dioxygenase 3 [Source
8	FBL	0.84	1e−04	9e−04	1 x 2	fibrillarin [Source:HGNC Symbol;Acc:HGNC:3599]
9	PYGB	−0.84	1e−04	1e−03	1 x 1	phosphorylase, glycogen; brain [Source:HGNC Symbol;Acc:
10	CCDC126	0.82	2e−04	1e−03	1 x 1	coiled−coil domain containing 126 [Source:HGNC Symbol;Ac
11	AC009133.22	−0.81	2e−04	2e−03	2 x 1	
12	PSMD3	−0.8	2e−04	2e−03	1 x 1	proteasome (prosome, macropain) 26S subunit, non−ATPase
13	DHX29	−0.77	3e−04	2e−03	1 x 1	DEAH (Asp−Glu−Ala−His) box polypeptide 29 [Source:HGN
14	DHX33	−0.77	4e−04	2e−03	1 x 1	DEAH (Asp−Glu−Ala−His) box polypeptide 33 [Source:HGN
15	MTMR12	0.77	4e−04	3e−03	1 x 2	myotubularin related protein 12 [Source:HGNC Symbol;Acc:
16	LMAN2L	0.76	5e−04	3e−03	1 x 1	lectin, mannose−binding 2−like [Source:HGNC Symbol;Acc:
17	POFUT1	0.75	5e−04	3e−03	1 x 1	protein O−fucosyltransferase 1 [Source:HGNC Symbol;Acc:H
18	CTDSP2	−0.74	6e−04	3e−03	1 x 1	CTD (carboxy−terminal domain, RNA polymerase II, polypept
19	VPS4A	0.73	7e−04	3e−03	1 x 2	vacuolar protein sorting 4 homolog A (S. cerevisiae) [Source:
20	CHD3	−0.73	8e−04	3e−03	1 x 1	chromodomain helicase DNA binding protein 3 [Source:HGN

p−values



G10_mel

Local Summary

%DE = 0.58

metagenes = 37

genes = 296

genes in genesets = 296

genes with fdr < 0.1 = 83 (15 + / 68 −)

genes with fdr < 0.05 = 57 (9 + / 48 −)

genes with fdr < 0.01 = 37 (7 + / 30 −)

<r> metagenes = 0.88

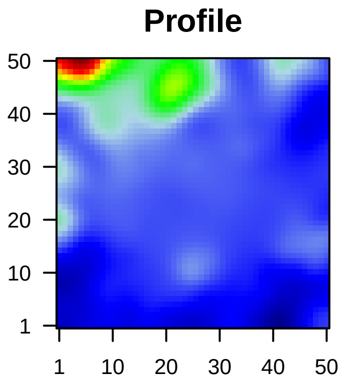
<r> genes = 0.1

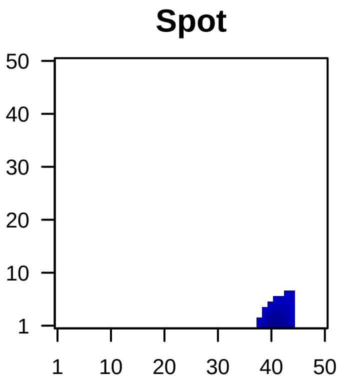
<FC> = −0.22

<shrinkage−t> = −3.6

<p−value> = 0.02

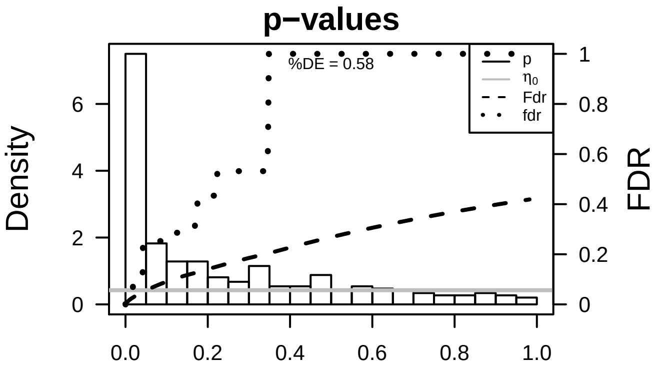
<fdr> = 0.71





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ALG13	−1.49	2e−16	1e−14	39 x 1	ALG13, UDP−N−acetylglucosaminyltransferase subunit [Sour
2	ATRX	−1.41	2e−16	1e−14	43 x 7	alpha thalassemia/mental retardation syndrome X−linked [So
3	SOX4	−0.91	5e−15	4e−13	41 x 1	SRY (sex determining region Y)−box 4 [Source:HGNC Symbo
4	ZEB2	−1.45	7e−15	7e−12	42 x 1	zinc finger E−box binding homeobox 2 [Source:HGNC Symbo
5	AKAP9	−1.3	6e−14	2e−07	42 x 1	A kinase (PRKA) anchor protein 9 [Source:HGNC Symbol;Ac
6	OGT	−1.23	1e−09	8e−06	40 x 5	O−linked N−acetylglucosamine (GlcNAc) transferase [Source
7	CDK8	1.15	1e−07	8e−06	38 x 1	cyclin−dependent kinase 8 [Source:HGNC Symbol;Acc:HGN
8	ACTR1A	−1.13	1e−07	1e−05	42 x 1	ARP1 actin−related protein 1 homolog A, centractin alpha (ye
9	APC	−1.09	3e−07	4e−05	41 x 2	adenomatous polyposis coli [Source:HGNC Symbol;Acc:HGN
10	CUL2	1.08	6e−07	1e−04	42 x 1	cullin 2 [Source:HGNC Symbol;Acc:HGNC:2552]
11	CWC27	−1.02	1e−06	2e−04	43 x 1	CWC27 spliceosome−associated protein homolog (S. cerevis
12	KIAA0195	1	4e−06	2e−04	43 x 7	KIAA0195 [Source:HGNC Symbol;Acc:HGNC:28983]
13	HIST2H2AC	0.99	5e−06	3e−04	43 x 5	histone cluster 2, H2ac [Source:HGNC Symbol;Acc:HGNC:47
14	DCTN1	−0.96	8e−06	3e−04	41 x 1	dynactin 1 [Source:HGNC Symbol;Acc:HGNC:2711]
15	BAZ2B	−0.96	9e−06	3e−04	39 x 1	bromodomain adjacent to zinc finger domain, 2B [Source:HG
16	FAM60A	−0.95	1e−05	3e−04	41 x 4	family with sequence similarity 60, member A [Source:HGNC
17	ABCF2	−0.94	1e−05	4e−04	40 x 1	ATP−binding cassette, sub−family F (GCN20), member 2 [So
18	MFN1	−0.93	2e−05	4e−04	42 x 1	mitofusin 1 [Source:HGNC Symbol;Acc:HGNC:18262]
19	VPS13C	−0.93	2e−05	8e−04	40 x 4	vacuolar protein sorting 13 homolog C (S. cerevisiae) [Source
20	RELN	0.9	3e−05	8e−04	44 x 2	reelin [Source:HGNC Symbol;Acc:HGNC:9957]



G10_mel

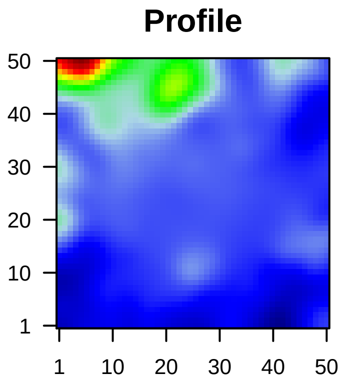
Local Summary

%DE = 0.73
metagenes = 21
genes = 284
genes in genesets = 281

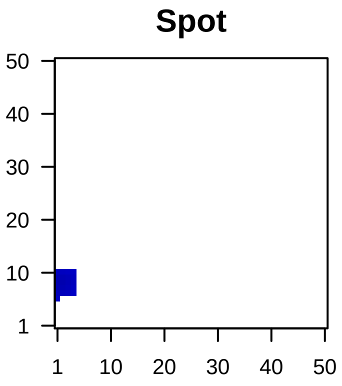
genes with fdr < 0.1 = 133 (33 + / 100 −)
genes with fdr < 0.05 = 98 (21 + / 77 −)
genes with fdr < 0.01 = 64 (13 + / 51 −)

<r> metagenes = 0.92
<r> genes = 0.11

<FC> = −0.2
<shrinkage−t> = −3.15
<p−value> = 0.02
<fdr> = 0.62



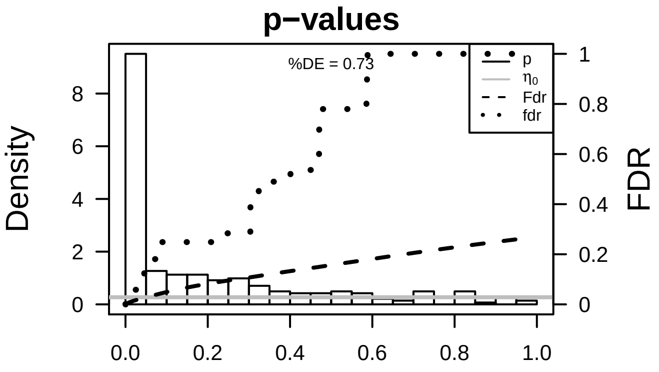
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	KLHL24	−1.3	6e−11	7e−09	1 x 11	kelch−like family member 24 [Source:HGNC Symbol;Acc:HG
2	ADD1	−1.23	2e−10	3e−08	1 x 8	adducin 1 (alpha) [Source:HGNC Symbol;Acc:HGNC:243]
3	SNAI2	−1.23	5e−10	8e−07	1 x 11	snail family zinc finger 2 [Source:HGNC Symbol;Acc:HGNC:1
4	WDR48	−1.15	1e−08	7e−06	1 x 9	WD repeat domain 48 [Source:HGNC Symbol;Acc:HGNC:30
5	CEACAM1	−1.05	1e−07	2e−05	1 x 10	carcinoembryonic antigen−related cell adhesion molecule 1 (
6	SNX1	−1.06	3e−07	3e−05	1 x 8	sorting nexin 1 [Source:HGNC Symbol;Acc:HGNC:11172]
7	GEMIN8	1.06	9e−07	3e−05	1 x 7	gem (nuclear organelle) associated protein 8 [Source:HGNC
8	TRIM69	1.05	1e−06	3e−05	1 x 7	tripartite motif containing 69 [Source:HGNC Symbol;Acc:HG
9	DRG2	−1.04	2e−06	5e−05	1 x 8	developmentally regulated GTP binding protein 2 [Source:HG
10	SEMA6A	−0.53	3e−06	5e−05	1 x 11	sema domain, transmembrane domain (TM), and cytoplasmi
11	ATP6V0A1	−0.76	3e−06	8e−05	1 x 10	ATPase, H+ transporting, lysosomal V0 subunit a1 [Source:H
12	RGS12	−0.99	5e−06	8e−05	1 x 9	regulator of G−protein signaling 12 [Source:HGNC Symbol;A
13	POMGNT1	−0.98	5e−06	8e−05	1 x 9	protein O−linked mannose N−acetylglucosaminyltransferase
14	SEMA6D	−0.98	6e−06	8e−05	1 x 11	sema domain, transmembrane domain (TM), and cytoplasmi
15	SH3BP4	−0.97	7e−06	1e−04	1 x 10	SH3−domain binding protein 4 [Source:HGNC Symbol;Acc:H
16	EXOC7	−0.88	1e−05	1e−04	1 x 8	exocyst complex component 7 [Source:HGNC Symbol;Acc:H
17	MTFMT	−0.95	1e−05	1e−04	3 x 9	mitochondrial methionyl−tRNA formyltransferase [Source:HG
18	CD109	0.94	2e−05	1e−04	1 x 8	CD109 molecule [Source:HGNC Symbol;Acc:HGNC:21685]
19	KCNAB2	−0.93	2e−05	1e−04	1 x 10	potassium channel, voltage gated subfamily A regulatory bet
20	PIP4K2C	−0.93	2e−05	1e−04	1 x 10	phosphatidylinositol−5−phosphate 4−kinase, type II, gamma [



p−values