G1_mel

Global Summary

%DE = 0.21

genes with fdr < 0.2 = 2498 (1549 + / 949 −)

genes with fdr < 0.1 = 2017 (1290 + / 727 −)

genes with fdr < 0.05 = 1603 (1048 + / 555 −)

genes with fdr < 0.01 = 1041 (708 + / 333 −)

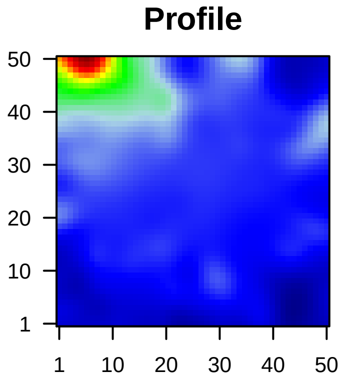
genes in genesets = 14839

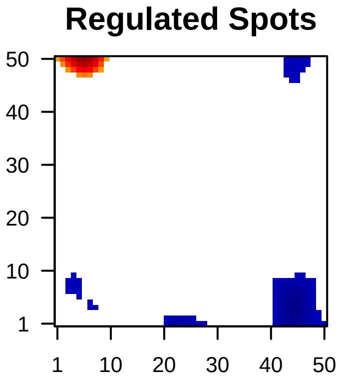
<FC> = 0

<shrinkage−t> = 0.07

<p−value> = 0.09

<fdr> = 0.79



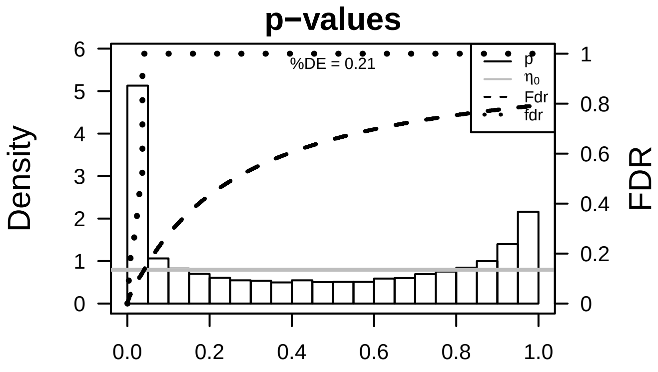


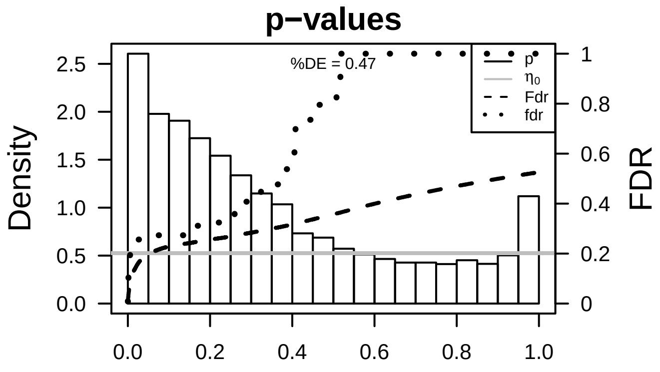
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	COL11A1	−0.92	2e−16	3e−13	45 x 1	collagen, type XI, alpha 1 [Source:HGNC Symbol;Acc:HGNC
2	CRYAB	−1.82	2e−16	3e−13	50 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
3	EIF4EBP1	−1.55	2e−16	3e−13	2 x 43	eukaryotic translation initiation factor 4E binding protein 1 [So
4	HTN1	2.69	2e−16	3e−13	10 x 49	histatin 1 [Source:HGNC Symbol;Acc:HGNC:5283]
5	SDF2	−1.65	2e−16	3e−13	48 x 50	stromal cell−derived factor 2 [Source:HGNC Symbol;Acc:HG
6	SGK1	−0.81	2e−16	3e−13	1 x 13	serum/glucocorticoid regulated kinase 1 [Source:HGNC Sym
7	UQCC1	−1.5	2e−16	3e−13	48 x 15	ubiquinol−cytochrome c reductase complex assembly factor 1
8	USP8	−1.33	2e−16	3e−13	8 x 5	ubiquitin specific peptidase 8 [Source:HGNC Symbol;Acc:HG
9	HSF4	1.8	4e−16	2e−12	37 x 5	heat shock transcription factor 4 [Source:HGNC Symbol;Acc:
10	CDC20	1.78	7e−16	3e−12	6 x 50	cell division cycle 20 [Source:HGNC Symbol;Acc:HGNC:172
11	PLK2	−1.33	7e−16	3e−12	50 x 1	polo−like kinase 2 [Source:HGNC Symbol;Acc:HGNC:19699]
12	TKTL1	1.78	9e−16	3e−12	4 x 15	transketolase−like 1 [Source:HGNC Symbol;Acc:HGNC:1183
13	CDKN3	1.31	1e−15	2e−11	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
14	RNF181	−1.46	1e−15	2e−11	43 x 45	ring finger protein 181 [Source:HGNC Symbol;Acc:HGNC:28
15	ARPC1B	−1.44	3e−15	1e−10	49 x 50	actin related protein 2/3 complex, subunit 1B, 41kDa [Source:
16	PSMD10	−1.37	1e−14	1e−10	40 x 49	proteasome (prosome, macropain) 26S subunit, non−ATPase
17	ZEB2	−1.44	3e−14	1e−10	42 x 1	zinc finger E−box binding homeobox 2 [Source:HGNC Symb
18	RAB3IP	1.67	4e−14	1e−10	50 x 3	RAB3A interacting protein [Source:HGNC Symbol;Acc:HGNC
19	ANAPC13	−1.43	5e−14	1e−10	44 x 36	anaphase promoting complex subunit 13 [Source:HGNC Sym
20	UBR4	−1.43	6e−14	2e−10	13 x 18	ubiquitin protein ligase E3 component n−recognin 4 [Source:

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	22.22	9e−06	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
2	20.22	4e−04	16	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
3	20.02	1e−05	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
4	19.5	2e−05	242	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
5	18.98	2e−05	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
6	18.87	2e−05	145	GSEA C2	CHANG_CYCLING_GENES
7	18.02	2e−05	436	GSEA C2	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
8	18.02	2e−05	305	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
9	16.98	3e−05	197	HM	HALLMARK_E2F_TARGETS
10	16.67	3e−05	124	GSEA C2	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
11	16.6	3e−05	155	GSEA C2	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
12	16.56	3e−05	700	GSEA C2	MARSON_BOUND_BY_E2F4_UNSTIMULATED
13	16.55	4e−05	327	GSEA C2	BLUM_RESPONSE_TO_SALIRASIB_DN
14	16.53	4e−05	616	GSEA C2	BENPORATH_CYCLING_GENES
15	16.32	4e−05	96	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
16	15.8	4e−05	50	GSEA C2	ISHIDA_E2F_TARGETS
17	15.62	4e−05	99	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
18	15.56	4e−05	99	GSEA C2	BURTON_ADIPOGENESIS_3
19	15.44	5e−05	1192	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
20	15.43	5e−05	162	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
Underexpressed					
1	−5.07	0.003	840	Chr	Chr 17
2	−4.41	0.005	15	BP	positive regulation of G1/S transition of mitotic cell cycle
3	−4.39	0.006	2798	Colon Cancer	TxEnhG1_Colon
4	−4.03	0.007	2984	CC	integral component of membrane
5	−3.96	0.008	20	MF	activating transcription factor binding
6	−3.94	0.008	13	GSEA C2	DAVICIONI_RHABDOMYOSARCOMA_PAX_FOXO1_FUSION_DN
7	−3.81	0.009	19	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_DN
8	−3.81	0.009	5155	Colon Cancer	EnhWk1_Colon
9	−3.68	0.010	208	GSEA C2	ZHANG_TLX_TARGETS_36HR_UP
10	−3.67	0.010	62	GSEA C2	NIKOLSKY_BREAST_CANCER_7Q21_Q22_AMPLICON
11	−3.6	0.011	47	BP	positive regulation of osteoblast differentiation
12	−3.46	0.012	54	miRNA target	hsa−miR−940
13	−3.44	0.012	49	GSEA C2	PRAMOONJAGO_SOX4_TARGETS_UP
14	−3.44	0.012	4	GSEA C2	LY_AGING_OLD_UP
15	−3.43	0.012	101	GSEA C2	ZHANG_TLX_TARGETS_DN
16	−3.4	0.013	293	GSEA C2	DOUGLAS_BMI1_TARGETS_DN
17	−3.36	0.013	995	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_DN
18	−3.35	0.013	166	GSEA C2	RODWELL_AGING_KIDNEY_NO_BLOOD_UP
19	−3.33	0.013	132	GSEA C2	SENGUPTA_EBNA1_ANTICORRELATED
20	−3.32	0.014	42	GSEA C2	PID_TNF_PATHWAY





G1_mel

Local Summary

%DE = 0.89

metagenes = 28

genes = 382

genes in genesets = 382

genes with fdr < 0.1 = 299 (287 + / 12 −)

genes with fdr < 0.05 = 280 (270 + / 10 −)

genes with fdr < 0.01 = 227 (224 + / 3 −)

<r> metagenes = 0.93

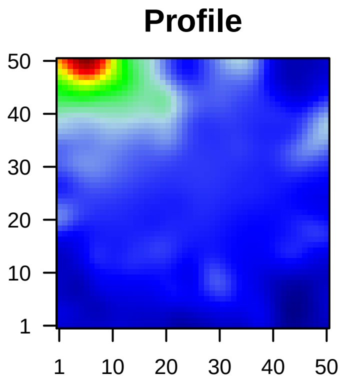
<r> genes = 0.29

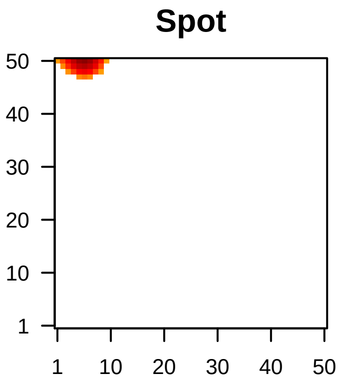
<FC> = 0.66

<shrinkage−t> = 10.7

<p−value> = 0

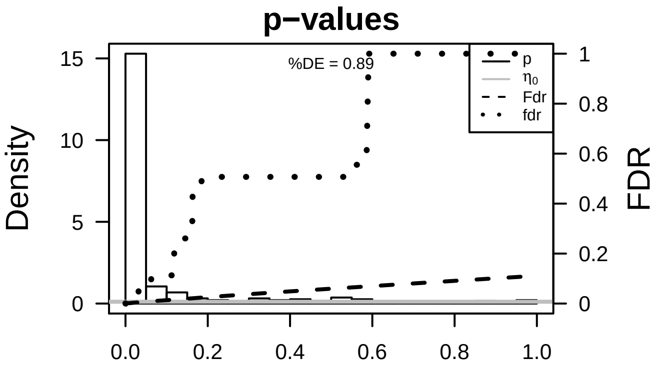
<fdr> = 0.3





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CDC20	1.78	7e−16	3e−14	6 x 50	cell division cycle 20 [Source:HGNC Symbol;Acc:HGNC:1723
2	CDKN3	1.31	1e−15	2e−12	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
3	HIST1H4C	0.67	7e−14	2e−12	5 x 49	histone cluster 1, H4c [Source:HGNC Symbol;Acc:HGNC:478
4	CDCA3	1.64	1e−13	2e−12	6 x 50	cell division cycle associated 3 [Source:HGNC Symbol;Acc:H
5	NDC80	1.63	1e−13	6e−12	6 x 50	NDC80 kinetochore complex component [Source:HGNC Sym
6	AURKB	1.6	5e−13	6e−12	6 x 50	aurora kinase B [Source:HGNC Symbol;Acc:HGNC:11390]
7	HMGB2	1.45	6e−13	6e−12	5 x 50	high mobility group box 2 [Source:HGNC Symbol;Acc:HGNC:
8	CCNB1	1.57	7e−13	6e−12	7 x 50	cyclin B1 [Source:HGNC Symbol;Acc:HGNC:1579]
9	NEK2	1.58	7e−13	6e−12	8 x 50	NIMA−related kinase 2 [Source:HGNC Symbol;Acc:HGNC:77
10	NCAPG	1.58	8e−13	4e−11	6 x 50	non−SMC condensin I complex, subunit G [Source:HGNC Sy
11	ANP32E	0.74	2e−12	4e−11	8 x 50	acidic (leucine−rich) nuclear phosphoprotein 32 family, memb
12	DLGAP5	1.54	3e−12	4e−11	7 x 50	discs, large (Drosophila) homolog−associated protein 5 [Sour
13	NUF2	1.53	4e−12	4e−11	6 x 50	NUF2, NDC80 kinetochore complex component [Source:HGN
14	PLK1	1.52	5e−12	4e−11	8 x 50	polo−like kinase 1 [Source:HGNC Symbol;Acc:HGNC:9077]
15	NUSAP1	1.48	5e−12	7e−11	6 x 50	nucleolar and spindle associated protein 1 [Source:HGNC Sy
16	FAM83D	1.51	7e−12	3e−10	7 x 50	family with sequence similarity 83, member D [Source:HGNC
17	UBE2S	1.47	3e−11	3e−10	10 x 50	ubiquitin−conjugating enzyme E2S [Source:HGNC Symbol;Ac
18	CKAP2L	1.47	3e−11	3e−10	6 x 50	cytoskeleton associated protein 2−like [Source:HGNC Symbo
19	SGOL1	1.46	3e−11	3e−10	5 x 50	shugoshin−like 1 (S. pombe) [Source:HGNC Symbol;Acc:HG
20	CCNB2	1.46	3e−11	3e−10	6 x 50	cyclin B2 [Source:HGNC Symbol;Acc:HGNC:1580]



G1_mel

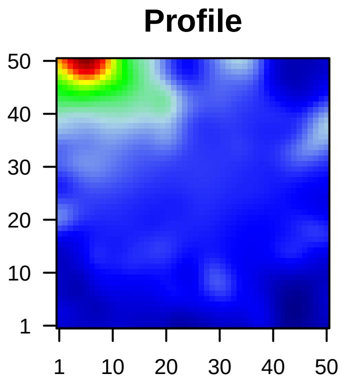
Local Summary

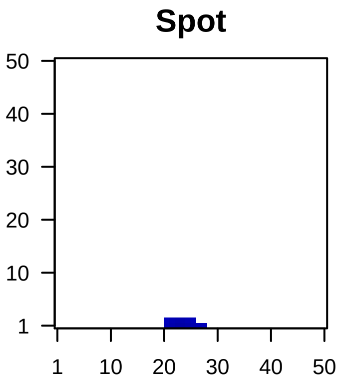
%DE = 0.82
metagenes = 14
genes = 225
genes in genesets = 219

genes with fdr < 0.1 = 70 (12 + / 58 −)
genes with fdr < 0.05 = 61 (10 + / 51 −)
genes with fdr < 0.01 = 10 (2 + / 8 −)

<r> metagenes = 0.93
<r> genes = 0.16

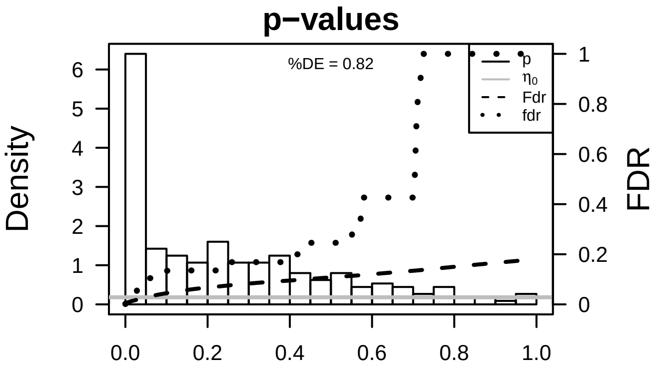
<FC> = −0.22
<shrinkage−t> = −3.41
<p−value> = 0.08
<fdr> = 0.76





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	SPOP	−1.32	4e−11	0.001	25 x 1	speckle−type POZ protein [Source:HGNC Symbol;Acc:HGNC
2	PRKCE	0.9	4e−05	0.001	27 x 1	protein kinase C, epsilon [Source:HGNC Symbol;Acc:HGNC:
3	C8orf33	−0.87	8e−05	0.001	21 x 1	chromosome 8 open reading frame 33 [Source:HGNC Symbo
4	MMS19	−0.84	1e−04	0.001	28 x 1	MMS19 nucleotide excision repair homolog (S. cerevisiae) [S
5	BTG1	−0.84	1e−04	0.001	25 x 1	B−cell translocation gene 1, anti−proliferative [Source:HGNC
6	ZNF652	−0.83	2e−04	0.001	21 x 1	zinc finger protein 652 [Source:HGNC Symbol;Acc:HGNC:29
7	WWP1	0.82	2e−04	0.003	21 x 1	WW domain containing E3 ubiquitin protein ligase 1 [Source:
8	FKBP14	−0.8	3e−04	0.004	26 x 1	FK506 binding protein 14, 22 kDa [Source:HGNC Symbol;Acc
9	VAPB	−0.78	4e−04	0.004	21 x 1	VAMP (vesicle−associated membrane protein)−associated pr
10	TSPAN31	−0.77	5e−04	0.004	23 x 2	tetraspanin 31 [Source:HGNC Symbol;Acc:HGNC:10539]
11	C17orf58	−0.76	5e−04	0.010	21 x 1	chromosome 17 open reading frame 58 [Source:HGNC Symb
12	PTPN1	−0.74	8e−04	0.010	23 x 2	protein tyrosine phosphatase, non−receptor type 1 [Source:H
13	STX16	−0.72	1e−03	0.010	22 x 1	syntaxin 16 [Source:HGNC Symbol;Acc:HGNC:11431]
14	PRPF6	−0.7	2e−03	0.010	23 x 1	pre−mRNA processing factor 6 [Source:HGNC Symbol;Acc:H
15	METTL4	−0.69	2e−03	0.010	23 x 1	methyltransferase like 4 [Source:HGNC Symbol;Acc:HGNC:2
16	STAM2	0.68	2e−03	0.010	24 x 1	signal transducing adaptor molecule (SH3 domain and ITAM
17	DDX27	0.66	2e−03	0.010	27 x 1	DEAD (Asp−Glu−Ala−Asp) box polypeptide 27 [Source:HGN
18	RIOK1	−0.62	3e−03	0.010	21 x 2	RIO kinase 1 [Source:HGNC Symbol;Acc:HGNC:18656]
19	LRP8	−0.66	3e−03	0.010	24 x 1	low density lipoprotein receptor−related protein 8, apolipoprot
20	XRRA1	−0.49	3e−03	0.010	22 x 1	X−ray radiation resistance associated 1 [Source:HGNC Symb



G1_mel

Local Summary

%DE = 0.69

metagenes = 78

genes = 665

genes in genesets = 665

genes with fdr < 0.1 = 187 (53 + / 134 −)

genes with fdr < 0.05 = 148 (47 + / 101 −)

genes with fdr < 0.01 = 67 (24 + / 43 −)

<r> metagenes = 0.82

<r> genes = 0.13

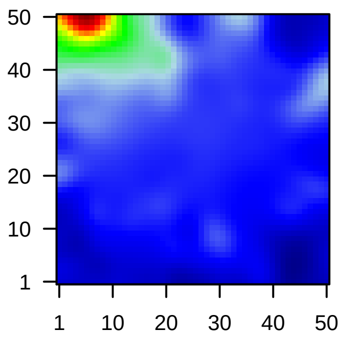
<FC> = −0.18

<shrinkage−t> = −2.9

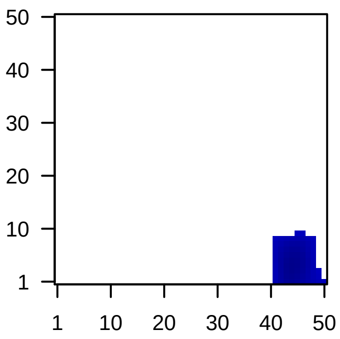
<p−value> = 0.05

<fdr> = 0.74

Profile



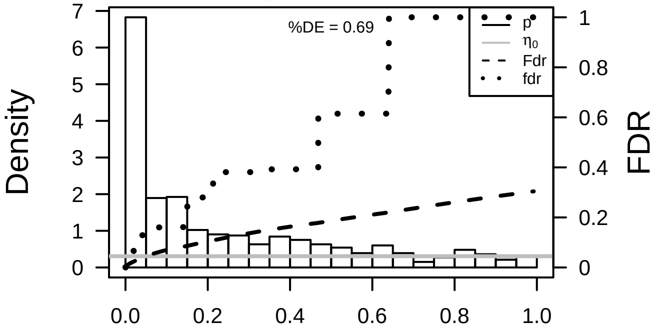
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	COL11A1	−0.92	2e−16	2e−14	45 x 1	collagen, type XI, alpha 1 [Source:HGNC Symbol;Acc:HGNC
2	CRYAB	−1.82	2e−16	2e−14	50 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
3	PLK2	−1.33	7e−16	5e−12	50 x 1	polo−like kinase 2 [Source:HGNC Symbol;Acc:HGNC:19699]
4	ZEB2	−1.44	3e−14	3e−08	42 x 1	zinc finger E−box binding homeobox 2 [Source:HGNC Symb
5	SNAP23	−1.12	1e−10	4e−06	50 x 1	synaptosomal−associated protein, 23kDa [Source:HGNC Sy
6	CTSF	1.23	2e−08	4e−06	41 x 2	cathepsin F [Source:HGNC Symbol;Acc:HGNC:2531]
7	CYB5R1	−1.18	4e−08	2e−05	41 x 2	cytochrome b5 reductase 1 [Source:HGNC Symbol;Acc:HGN
8	CSRP2	−1.03	2e−07	2e−05	48 x 1	cysteine and glycine−rich protein 2 [Source:HGNC Symbol;A
9	UBE2E2	−1.12	3e−07	2e−05	50 x 1	ubiquitin−conjugating enzyme E2E 2 [Source:HGNC Symbol;
10	FAM98A	−1.09	4e−07	4e−05	49 x 1	family with sequence similarity 98, member A [Source:HGNC
11	PDE5A	1.1	6e−07	6e−05	46 x 10	phosphodiesterase 5A, cGMP−specific [Source:HGNC Symb
12	MED31	−1.07	1e−06	6e−05	41 x 1	mediator complex subunit 31 [Source:HGNC Symbol;Acc:HG
13	MBOAT2	1.07	1e−06	6e−05	50 x 1	membrane bound O−acyltransferase domain containing 2 [S
14	PTPN12	1.06	1e−06	1e−04	46 x 1	protein tyrosine phosphatase, non−receptor type 12 [Source:
15	PNRC1	1.05	2e−06	3e−04	50 x 1	proline−rich nuclear receptor coactivator 1 [Source:HGNC Sy
16	CNN3	−0.4	6e−06	3e−04	47 x 1	calponin 3, acidic [Source:HGNC Symbol;Acc:HGNC:2157]
17	TM2D1	−0.87	6e−06	3e−04	42 x 1	TM2 domain containing 1 [Source:HGNC Symbol;Acc:HGNC
18	BCL11A	0.99	7e−06	3e−04	47 x 1	B−cell CLL/lymphoma 11A (zinc finger protein) [Source:HGN
19	RAD52	−0.98	8e−06	3e−04	41 x 1	RAD52 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:
20	CNTN4	0.98	8e−06	6e−04	43 x 8	contactin 4 [Source:HGNC Symbol;Acc:HGNC:2174]

p−values



G1_mel

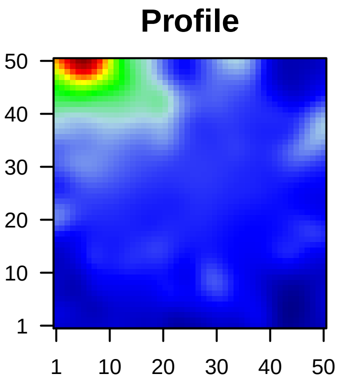
Local Summary

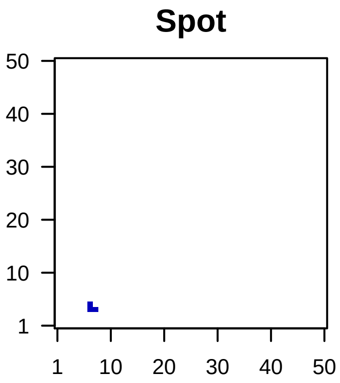
%DE = 0.84
metagenes = 3
genes = 19
genes in genesets = 19

genes with fdr < 0.1 = 11 (2 + / 9 −)
genes with fdr < 0.05 = 2 (0 + / 2 −)
genes with fdr < 0.01 = 2 (0 + / 2 −)

<r> metagenes = 0.98
<r> genes = 0.18

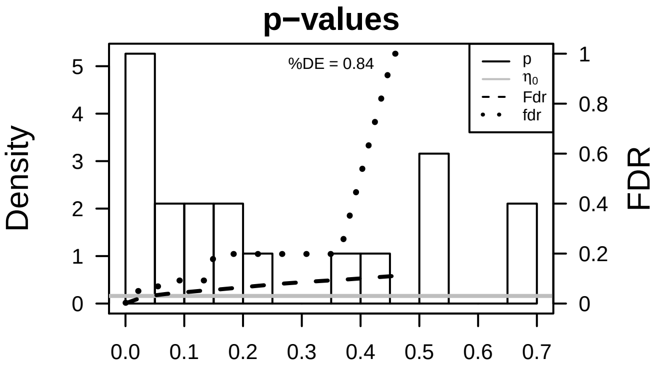
<FC> = −0.21
<shrinkage−t> = −3.19
<p−value> = 0.09
<fdr> = 0.79





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	MAP3K2	−0.82	2e−04	0.003	8 x 4	mitogen−activated protein kinase kinase kinase 2 [Source:HG
2	TMEM128	−0.69	2e−03	0.003	8 x 4	transmembrane protein 128 [Source:HGNC Symbol;Acc:HG
3	PDAP1	−0.68	2e−03	0.050	8 x 4	PDGFA associated protein 1 [Source:HGNC Symbol;Acc:HG
4	ANKRD36B	0.47	4e−02	0.050	7 x 4	ankyrin repeat domain 36B [Source:HGNC Symbol;Acc:HGN
5	PIAS2	0.47	4e−02	0.069	7 x 5	protein inhibitor of activated STAT, 2 [Source:HGNC Symbol;
6	RAP1A	−0.4	7e−02	0.069	7 x 4	RAP1A, member of RAS oncogene family [Source:HGNC Sy
7	PHF1	−0.37	1e−01	0.069	8 x 4	PHD finger protein 1 [Source:HGNC Symbol;Acc:HGNC:891
8	HES1	−0.35	1e−01	0.069	8 x 4	hes family bHLH transcription factor 1 [Source:HGNC Symbol
9	NADK2	−0.34	1e−01	0.092	7 x 5	NAD kinase 2, mitochondrial [Source:HGNC Symbol;Acc:HG
10	ASAH2B	−0.29	2e−01	0.092	7 x 4	N−acylsphingosine amidohydrolase (non−lysosomal ceramid
11	SLC2A10	−0.29	2e−01	0.092	7 x 5	solute carrier family 2 (facilitated glucose transporter), memb
12	SMARCB1	0.27	2e−01	0.198	7 x 4	SWI/SNF related, matrix associated, actin dependent regulat
13	SARM1	−0.2	4e−01	0.198	7 x 5	sterile alpha and TIR motif containing 1 [Source:HGNC Symb
14	ZSCAN2	−0.17	4e−01	0.198	7 x 5	zinc finger and SCAN domain containing 2 [Source:HGNC Sy
15	MTR	−0.13	5e−01	0.198	7 x 5	5−methyltetrahydrofolate−homocysteine methyltransferase [S
16	MEGF8	−0.14	5e−01	0.198	7 x 4	multiple EGF−like−domains 8 [Source:HGNC Symbol;Acc:HG
17	TBC1D2B	−0.13	5e−01	0.345	7 x 4	TBC1 domain family, member 2B [Source:HGNC Symbol;Acc
18	C5	−0.1	7e−01	1.000	7 x 4	complement component 5 [Source:HGNC Symbol;Acc:HGNC
19	TAF1L	−0.09	7e−01	1.000	7 x 4	TAF1 RNA polymerase II, TATA box binding protein (TBP)−as



G1_mel

Local Summary

%DE = 0.71

metagenes = 11

genes = 59

genes in genesets = 57

genes with fdr < 0.1 = 22 (2 + / 20 −)

genes with fdr < 0.05 = 17 (1 + / 16 −)

genes with fdr < 0.01 = 11 (0 + / 11 −)

<r> metagenes = 0.93

<r> genes = 0.11

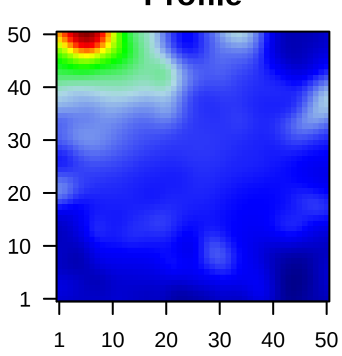
<FC> = −0.27

<shrinkage−t> = −4.37

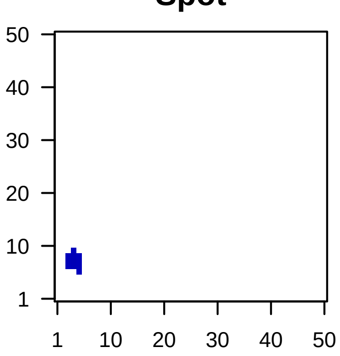
<p−value> = 0.03

<fdr> = 0.67

Profile



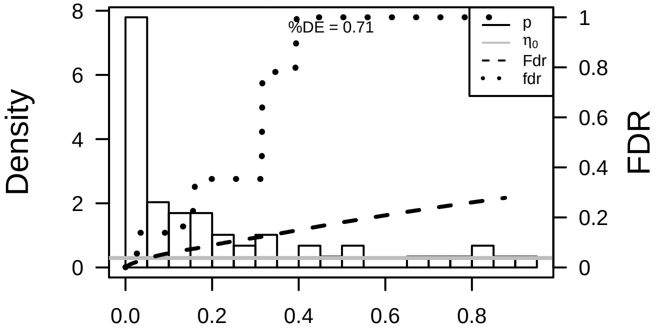
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ST3GAL6	−1.15	5e−09	5e−04	4 x 8	ST3 beta−galactoside alpha−2,3−sialyltransferase 6 [Source:
2	CH507−9B2.3	−0.8	6e−05	5e−04	4 x 7	
3	C21orf33	−0.82	9e−05	5e−04	4 x 7	chromosome 21 open reading frame 33 [Source:HGNC Symb
4	CAB39L	−0.86	1e−04	5e−04	3 x 8	calcium binding protein 39−like [Source:HGNC Symbol;Acc:H
5	PI4KB	−0.7	1e−04	2e−03	5 x 9	phosphatidylinositol 4−kinase, catalytic, beta [Source:HGNC
6	ATP5G1	−0.33	2e−04	2e−03	3 x 7	ATP synthase, H+ transporting, mitochondrial Fo complex, su
7	SMDT1	−0.78	4e−04	2e−03	4 x 7	single−pass membrane protein with aspartate−rich tail 1 [Sou
8	UBE3C	−0.77	5e−04	9e−03	4 x 8	ubiquitin protein ligase E3C [Source:HGNC Symbol;Acc:HGN
9	HEATR6	−0.72	1e−03	9e−03	4 x 10	HEAT repeat containing 6 [Source:HGNC Symbol;Acc:HGNC
10	RAB5B	−0.68	2e−03	9e−03	4 x 10	RAB5B, member RAS oncogene family [Source:HGNC Symb
11	TNKS2	−0.67	2e−03	9e−03	5 x 7	tankyrase, TRF1−interacting ankyrin−related ADP−ribose pol
12	FOS	−0.43	2e−03	4e−02	4 x 7	FBJ murine osteosarcoma viral oncogene homolog [Source:H
13	WDR55	−0.62	5e−03	4e−02	5 x 6	WD repeat domain 55 [Source:HGNC Symbol;Acc:HGNC:25
14	KCTD21	−0.57	9e−03	4e−02	3 x 9	potassium channel tetramerization domain containing 21 [Sou
15	ANKRD54	−0.57	1e−02	4e−02	4 x 10	ankyrin repeat domain 54 [Source:HGNC Symbol;Acc:HGNC
16	RAB13	0.54	1e−02	4e−02	4 x 8	RAB13, member RAS oncogene family [Source:HGNC Symb
17	CARD14	−0.54	1e−02	4e−02	3 x 7	caspase recruitment domain family, member 14 [Source:HGN
18	USP46	0.53	2e−02	6e−02	5 x 6	ubiquitin specific peptidase 46 [Source:HGNC Symbol;Acc:H
19	STX12	−0.51	2e−02	6e−02	5 x 7	syntaxin 12 [Source:HGNC Symbol;Acc:HGNC:11430]
20	CHST11	−0.49	3e−02	6e−02	4 x 10	carbohydrate (chondroitin 4) sulfotransferase 11 [Source:HGN

p−values



G1_mel

Local Summary

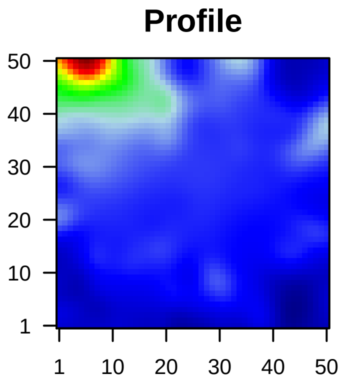
%DE = 0.61
metagenes = 19
genes = 204
genes in genesets = 203

genes with fdr < 0.1 = 65 (16 + / 49 −)
genes with fdr < 0.05 = 50 (10 + / 40 −)
genes with fdr < 0.01 = 35 (7 + / 28 −)

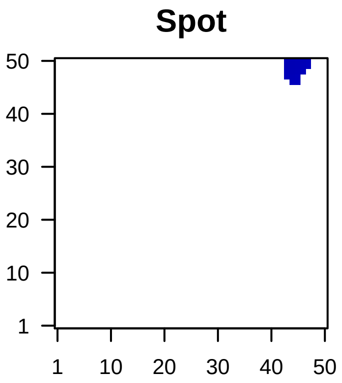
<r> metagenes = 0.92
<r> genes = 0.09

<FC> = −0.15
<shrinkage−t> = −2.42
<p−value> = 0.02
<fdr> = 0.68

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	SLC25A13	−1.4	3e−13	1e−08	47 x 50	solute carrier family 25 (aspartate/glutamate carrier), membe
2	LSM10	−1.12	2e−10	6e−07	46 x 50	LSM10, U7 small nuclear RNA associated [Source:HGNC Sy
3	CMSS1	−1.2	1e−08	6e−07	43 x 50	cms1 ribosomal small subunit homolog (yeast) [Source:HGN
4	SLC35A4	−1.19	2e−08	4e−06	44 x 50	solute carrier family 35, member A4 [Source:HGNC Symbol;
5	SCAMP2	−1.09	7e−08	2e−05	46 x 50	secretory carrier membrane protein 2 [Source:HGNC Symbol
6	KARS	−0.84	3e−07	4e−05	45 x 46	lysyl−tRNA synthetase [Source:HGNC Symbol;Acc:HGNC:62
7	ASNS	−1.06	1e−06	4e−05	44 x 50	asparagine synthetase (glutamine−hydrolyzing) [Source:HGN
8	PARP11	1.06	2e−06	4e−05	43 x 50	poly (ADP−ribose) polymerase family, member 11 [Source:H
9	ABHD14B	−1.05	2e−06	2e−04	43 x 50	abhydrolase domain containing 14B [Source:HGNC Symbol;
10	RAB10	−0.86	5e−06	2e−04	45 x 48	RAB10, member RAS oncogene family [Source:HGNC Symb
11	ENO3	0.99	7e−06	2e−04	44 x 46	enolase 3 (beta, muscle) [Source:HGNC Symbol;Acc:HGNC:
12	HSPE1−MOB	−0.98	1e−05	5e−04	43 x 50	HSPE1−MOB4 readthrough [Source:HGNC Symbol;Acc:HGN
13	CLN3	−0.92	3e−05	5e−04	44 x 47	ceroid−lipofuscinosis, neuronal 3 [Source:HGNC Symbol;Acc
14	MRPL54	−0.92	3e−05	5e−04	47 x 50	mitochondrial ribosomal protein L54 [Source:HGNC Symbol;
15	NAGK	−0.91	4e−05	5e−04	44 x 50	N−acetylglucosamine kinase [Source:HGNC Symbol;Acc:HG
16	ELP4	0.9	5e−05	5e−04	47 x 49	elongator acetyltransferase complex subunit 4 [Source:HGNC
17	UBIAD1	0.9	5e−05	5e−04	45 x 50	UbiA prenyltransferase domain containing 1 [Source:HGNC
18	DDX19B	−0.89	5e−05	5e−04	43 x 50	DEAD (Asp−Glu−Ala−Asp) box polypeptide 19B [Source:HGN
19	PSEN1	−0.89	6e−05	3e−03	43 x 50	presenilin 1 [Source:HGNC Symbol;Acc:HGNC:9508]
20	GSKIP	−0.85	1e−04	3e−03	45 x 50	GSK3B interacting protein [Source:HGNC Symbol;Acc:HGNC

p−values