G6_mel

Global Summary

%DE = 0.2

genes with fdr < 0.2 = 2394 (1509 + / 885 −)

genes with fdr < 0.1 = 1987 (1278 + / 709 −)

genes with fdr < 0.05 = 1571 (1034 + / 537 −)

genes with fdr < 0.01 = 997 (686 + / 311 −)

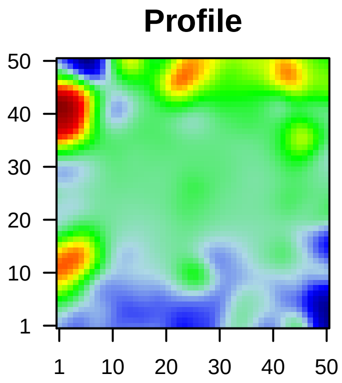
genes in genesets = 14839

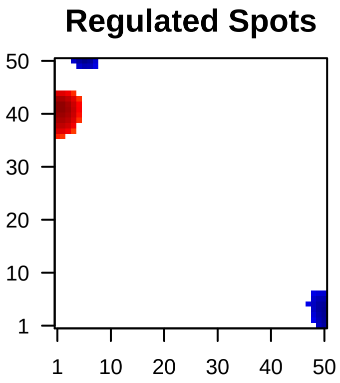
<FC> = 0

<shrinkage−t> = 0.09

<p−value> = 0.09

<fdr> = 0.8



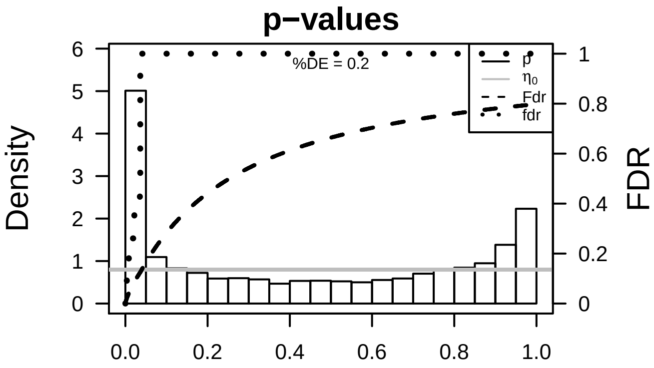


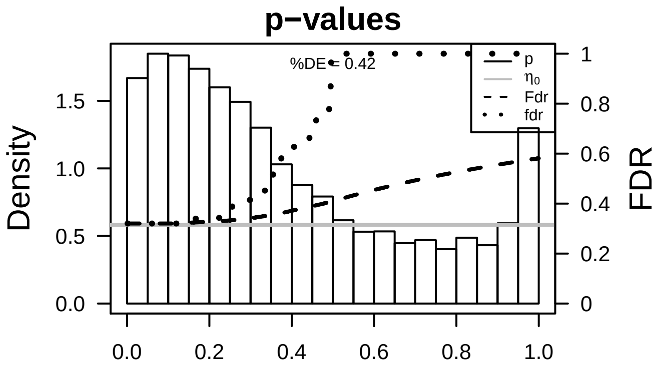
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CHMP3	−1.5	2e−16	4e−13	12 x 41	charged multivesicular body protein 3 [Source:HGNC Symbol
2	EIF3J	−1.51	2e−16	4e−13	30 x 50	eukaryotic translation initiation factor 3, subunit J [Source:HG
3	KDELR2	−1.44	2e−16	4e−13	1 x 19	KDEL (Lys−Asp−Glu−Leu) endoplasmic reticulum protein ret
4	LAMB2	−1.38	2e−16	4e−13	50 x 6	laminin, beta 2 (laminin S) [Source:HGNC Symbol;Acc:HGN
5	MRPL32	−1.64	2e−16	4e−13	50 x 38	mitochondrial ribosomal protein L32 [Source:HGNC Symbol;
6	MRPS15	−1.8	2e−16	4e−13	18 x 50	mitochondrial ribosomal protein S15 [Source:HGNC Symbol;
7	RAD51C	−1.4	2e−16	4e−13	12 x 48	RAD51 paralog C [Source:HGNC Symbol;Acc:HGNC:9820]
8	MRPS5	−1.42	1e−15	2e−11	3 x 7	mitochondrial ribosomal protein S5 [Source:HGNC Symbol;A
9	UBXN4	−1.08	1e−15	2e−11	45 x 17	UBX domain protein 4 [Source:HGNC Symbol;Acc:HGNC:14
10	ALG3	−1.2	2e−15	3e−11	48 x 50	ALG3, alpha−1,3− mannosyltransferase [Source:HGNC Sym
11	ZNF345	1.71	5e−15	1e−10	48 x 22	zinc finger protein 345 [Source:HGNC Symbol;Acc:HGNC:16
12	THOC1	−1.33	2e−14	1e−10	9 x 48	THO complex 1 [Source:HGNC Symbol;Acc:HGNC:19070]
13	CHD1	−1.16	2e−14	2e−10	1 x 31	chromodomain helicase DNA binding protein 1 [Source:HGN
14	BIRC6	−1.42	7e−14	2e−10	50 x 17	baculoviral IAP repeat containing 6 [Source:HGNC Symbol;A
15	PMF1	−1.42	8e−14	2e−10	7 x 47	polyamine−modulated factor 1 [Source:HGNC Symbol;Acc:H
16	NLE1	1.63	8e−14	2e−10	26 x 50	notchless homolog 1 (Drosophila) [Source:HGNC Symbol;Ac
17	EPB41L4A	1.62	9e−14	2e−10	14 x 1	erythrocyte membrane protein band 4.1 like 4A [Source:HGN
18	C9orf114	1.62	9e−14	2e−10	44 x 44	chromosome 9 open reading frame 114 [Source:HGNC Sym
19	SOX5	1.62	1e−13	2e−10	49 x 25	SRY (sex determining region Y)−box 5 [Source:HGNC Symb
20	RAE1	−1.21	1e−13	3e−10	7 x 46	ribonucleic acid export 1 [Source:HGNC Symbol;Acc:HGNC:

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	6.13	0.002	9330	Brain	Overlap_fetal_midbrain_ReprPC
2	5.6	0.002	1326	GSEA C2	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
3	5.3	0.003	9482	Colon Cancer	TCGA_Colon
4	5.19	0.003	478	GSEA C2	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
5	4.87	0.004	7592	Lymphoma	HOPP_Active_promoter
6	4.84	0.004	475	GSEA C2	ONKEN_UVEAL_MELANOMA_DN
7	4.64	0.005	94	CC	melanosome
8	4.59	0.005	47	BP	proton transport
9	4.44	0.005	63	GSEA C2	ELVIDGE_HIF1A_TARGETS_UP
10	4.4	0.005	1468	CC	mitochondrion
11	4.37	0.006	198	HM	HALLMARK_OXIDATIVE_PHOSPHORYLATION
12	4.27	0.006	21	GSEA C2	REACTOME_MITOCHONDRIAL_TRNA_AMINOACYLATION
13	4.26	0.006	8	GSEA C2	RAMJAUN_APOPTOSIS_BY_TGFB1_VIA_MAPK1_DN
14	4.19	0.006	401	CC	mitochondrial inner membrane
15	4.19	0.006	7209	Lymphoma	HOPP_Weak_promoter
16	4.04	0.007	23	GSEA C2	REACTOME_TRANSFERRIN_ENDOCYTOSIS_AND_RECYCLIN
17	4.03	0.007	20	BP	response to cadmium ion
18	4.03	0.007	107	GSEA C2	KEGG_OXIDATIVE_PHOSPHORYLATION
19	4.02	0.007	16	BP	porphyrin−containing compound metabolic process
20	4.01	0.007	20	GSEA C2	REACTOME_INSULIN_RECEPTOR_RECYCLING
Underexpressed					
1	−6.75	0.001	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
2	−6.51	0.001	242	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
3	−6.43	0.001	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
4	−5.8	0.002	93	GSEA C2	KONG_E2F3_TARGETS
5	−5.28	0.003	201	GSEA C2	WHITFIELD_CELL_CYCLE_G2_M
6	−5.27	0.003	412	BP	mitotic cell cycle
7	−5.26	0.003	145	GSEA C2	CHANG_CYCLING_GENES
8	−5.09	0.003	616	GSEA C2	BENPORATH_CYCLING_GENES
9	−4.97	0.004	53	GSEA C2	WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
10	−4.97	0.004	700	GSEA C2	MARSON_BOUND_BY_E2F4_UNSTIMULATED
11	−4.92	0.004	124	GSEA C2	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
12	−4.87	0.004	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
13	−4.86	0.004	99	GSEA C2	BURTON_ADIPOGENESIS_3
14	−4.82	0.004	118	GSEA C2	ODONNELL_TFRC_TARGETS_DN
15	−4.82	0.004	28	GSEA C2	REICHERT_MITOSIS_LIN9_TARGETS
16	−4.78	0.004	57	GSEA C2	MOLENAAR_TARGETS_OF_CCND1_AND_CDK4_DN
17	−4.65	0.005	72	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
18	−4.49	0.005	87	GSEA C2	ZHANG_TLX_TARGETS_UP
19	−4.39	0.006	89	GSEA C2	MORI_IMMATURE_B_LYMPHOCYTE_DN
20	−4.36	0.006	84	GSEA C2	MORI_LARGE_PRE_BII_LYMPHOCYTE_UP





G6_mel

Local Summary

%DE = 0.71

metagenes = 39

genes = 456

genes in genesets = 455

genes with fdr < 0.1 = 245 (198 + / 47 −)

genes with fdr < 0.05 = 209 (169 + / 40 −)

genes with fdr < 0.01 = 132 (108 + / 24 −)

<r> metagenes = 0.93

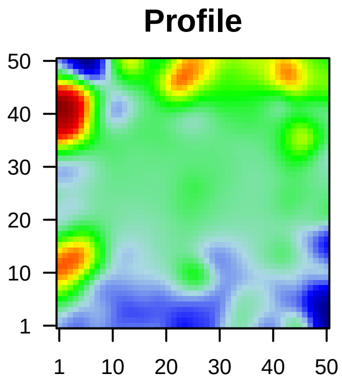
<r> genes = 0.14

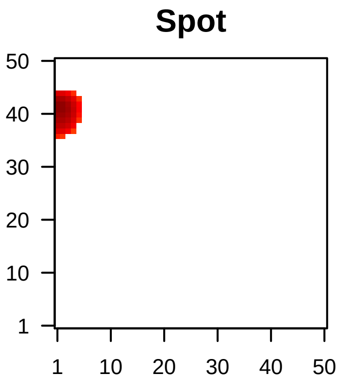
<FC> = 0.24

<shrinkage−t> = 4.72

<p−value> = 0.01

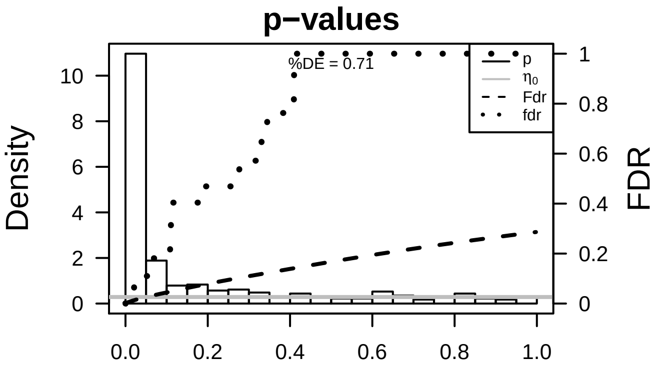
<fdr> = 0.54





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ZNF30	1.46	2e−11	8e−09	4 x 37	zinc finger protein 30 [Source:HGNC Symbol;Acc:HGNC:130
2	PDE4DIP	0.85	1e−10	8e−09	1 x 43	phosphodiesterase 4D interacting protein [Source:HGNC Sy
3	CD58	−1.28	1e−10	1e−08	1 x 43	CD58 molecule [Source:HGNC Symbol;Acc:HGNC:1688]
4	BTK	1.38	3e−10	1e−08	3 x 43	Bruton agammaglobulinemia tyrosine kinase [Source:HGNC
5	UHRF2	1.37	4e−10	1e−08	1 x 36	ubiquitin−like with PHD and ring finger domains 2, E3 ubiquiti
6	GAPDHS	1.32	4e−10	1e−08	1 x 43	glyceraldehyde−3−phosphate dehydrogenase, spermatogeni
7	TOM1L1	−1.25	5e−10	8e−08	1 x 38	target of myb1 (chicken)−like 1 [Source:HGNC Symbol;Acc:H
8	ISY1	1.3	2e−09	8e−08	1 x 40	ISY1 splicing factor homolog (S. cerevisiae) [Source:HGNC S
9	PLA2G15	1.3	3e−09	8e−08	1 x 36	phospholipase A2, group XV [Source:HGNC Symbol;Acc:HG
10	LINS	1.29	3e−09	8e−08	4 x 39	lines homolog (Drosophila) [Source:HGNC Symbol;Acc:HGN
11	ZNF141	1.29	3e−09	2e−06	1 x 36	zinc finger protein 141 [Source:HGNC Symbol;Acc:HGNC:12
12	GCFC2	1.23	2e−08	2e−06	3 x 38	GC−rich sequence DNA−binding factor 2 [Source:HGNC Sy
13	UBE3B	1.19	5e−08	2e−06	1 x 36	ubiquitin protein ligase E3B [Source:HGNC Symbol;Acc:HGN
14	M6PR	0.47	8e−08	2e−06	3 x 41	mannose−6−phosphate receptor (cation dependent) [Source:
15	RTN4R	1.17	8e−08	2e−06	4 x 42	reticulon 4 receptor [Source:HGNC Symbol;Acc:HGNC:1860
16	SLC6A8	1.16	9e−08	2e−06	3 x 37	solute carrier family 6 (neurotransmitter transporter), member
17	AIP	−1.14	1e−07	6e−06	1 x 40	aryl hydrocarbon receptor interacting protein [Source:HGNC
18	ZFYVE21	1.15	1e−07	6e−06	1 x 38	zinc finger, FYVE domain containing 21 [Source:HGNC Sym
19	ATP6V1C1	0.7	2e−07	6e−06	4 x 40	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1 [S
20	MLANA	0.45	4e−07	6e−06	1 x 43	melan−A [Source:HGNC Symbol;Acc:HGNC:7124]



G6_mel

Local Summary

%DE = 0.76

metagenes = 21

genes = 301

genes in genesets = 300

genes with fdr < 0.1 = 144 (37 + / 107 −)

genes with fdr < 0.05 = 96 (24 + / 72 −)

genes with fdr < 0.01 = 52 (10 + / 42 −)

<r> metagenes = 0.96

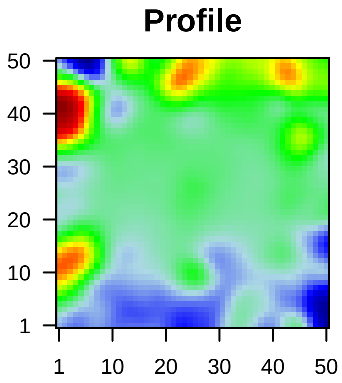
<r> genes = 0.18

<FC> = −0.22

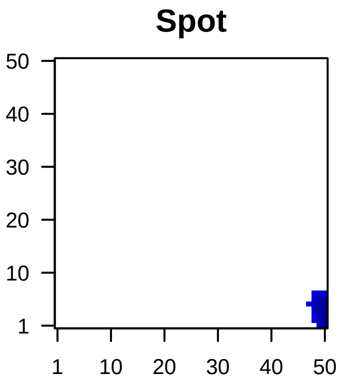
<shrinkage−t> = −3.36

<p−value> = 0.02

<fdr> = 0.66



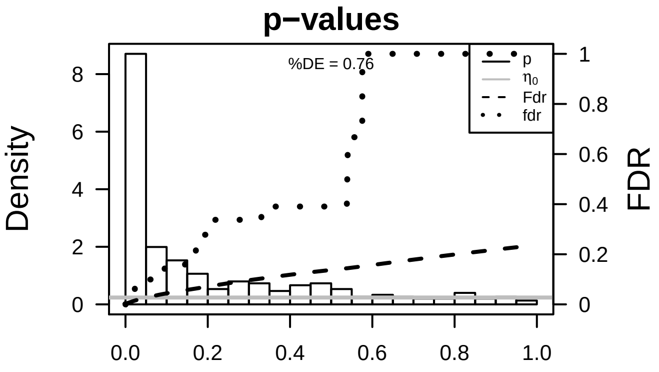
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	LAMB2	−1.38	2e−16	2e−14	50 x 6	laminin, beta 2 (laminin S) [Source:HGNC Symbol;Acc:HGNC
2	CRYAB	−1	3e−12	1e−08	50 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
3	LRRFIP2	−1.22	2e−10	6e−07	50 x 4	leucine rich repeat (in FLII) interacting protein 2 [Source:HGN
4	STAM	−1.13	8e−09	3e−06	50 x 3	signal transducing adaptor molecule (SH3 domain and ITAM
5	MACF1	−1.07	8e−08	3e−06	49 x 6	microtubule−actin crosslinking factor 1 [Source:HGNC Symb
6	ARRDC3	1.16	1e−07	3e−06	50 x 1	arrestin domain containing 3 [Source:HGNC Symbol;Acc:HG
7	MMGT1	1.14	2e−07	3e−06	50 x 3	membrane magnesium transporter 1 [Source:HGNC Symbol;
8	PDLIM5	−1.12	2e−07	1e−05	50 x 1	PDZ and LIM domain 5 [Source:HGNC Symbol;Acc:HGNC:1
9	AKAP13	−1.1	3e−07	7e−05	50 x 6	A kinase (PRKA) anchor protein 13 [Source:HGNC Symbol;A
10	FN1	−1.04	2e−06	7e−05	50 x 1	fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
11	CDKN1A	−1.02	3e−06	7e−05	50 x 1	cyclin−dependent kinase inhibitor 1A (p21, Cip1) [Source:HG
12	PDGFA	−1.01	4e−06	7e−05	49 x 1	platelet−derived growth factor alpha polypeptide [Source:HG
13	SLC5A3	−1	4e−06	1e−04	50 x 2	solute carrier family 5 (sodium/myo−inositol cotransporter), m
14	ALCAM	−0.98	6e−06	1e−04	50 x 1	activated leukocyte cell adhesion molecule [Source:HGNC S
15	UBE2E2	−0.94	1e−05	1e−04	50 x 1	ubiquitin−conjugating enzyme E2E 2 [Source:HGNC Symbol;
16	PEA15	−0.95	1e−05	1e−04	50 x 1	phosphoprotein enriched in astrocytes 15 [Source:HGNC Sy
17	TM7SF3	−0.95	1e−05	1e−04	50 x 5	transmembrane 7 superfamily member 3 [Source:HGNC Sym
18	SSSCA1	−0.95	1e−05	1e−04	50 x 7	Sjogren syndrome/scleroderma autoantigen 1 [Source:HGNC
19	CWF19L1	−0.94	2e−05	4e−04	49 x 4	CWF19−like 1, cell cycle control (S. pombe) [Source:HGNC
20	MBNL2	−0.92	2e−05	4e−04	50 x 1	muscleblind−like splicing regulator 2 [Source:HGNC Symbol;



p−values

G6_mel

Local Summary

%DE = 0.97

metagenes = 9

genes = 154

genes in genesets = 154

genes with fdr < 0.1 = 139 (29 + / 110 −)

genes with fdr < 0.05 = 139 (29 + / 110 −)

genes with fdr < 0.01 = 91 (21 + / 70 −)

<r> metagenes = 0.98

<r> genes = 0.46

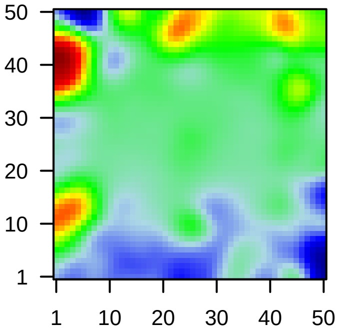
<FC> = −0.27

<shrinkage−t> = −4.04

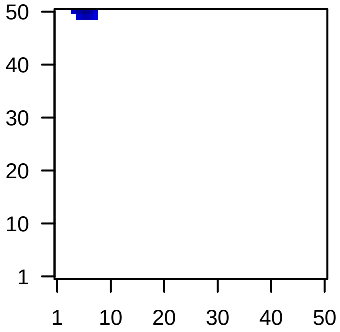
<p−value> = 0.01

<fdr> = 0.55

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	SMC2	−1.25	5e−10	5e−06	5 x 50	structural maintenance of chromosomes 2 [Source:HGNC Sy
2	HMGB2	−0.97	1e−06	7e−06	5 x 50	high mobility group box 2 [Source:HGNC Symbol;Acc:HGNC:
3	MPHOSPH9	1	2e−06	1e−05	7 x 49	M−phase phosphoprotein 9 [Source:HGNC Symbol;Acc:HGN
4	KIF23	−0.99	5e−06	2e−05	6 x 50	kinesin family member 23 [Source:HGNC Symbol;Acc:HGNC
5	ASF1B	−0.95	1e−05	2e−05	4 x 50	anti−silencing function 1B histone chaperone [Source:HGNC
6	FAM111A	−0.94	1e−05	2e−05	4 x 50	family with sequence similarity 111, member A [Source:HGN
7	ACTL6A	0.55	2e−05	2e−05	4 x 50	actin−like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
8	KIF22	−0.91	3e−05	2e−05	6 x 50	kinesin family member 22 [Source:HGNC Symbol;Acc:HGNC
9	APOBEC3B	0.9	3e−05	2e−05	6 x 50	apolipoprotein B mRNA editing enzyme, catalytic polypeptide
10	CDKN3	0.67	4e−05	2e−05	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
11	UBE2C	−0.89	4e−05	2e−05	6 x 50	ubiquitin−conjugating enzyme E2C [Source:HGNC Symbol;A
12	SMC4	−0.73	5e−05	2e−05	5 x 50	structural maintenance of chromosomes 4 [Source:HGNC Sy
13	WDR34	−0.88	5e−05	2e−05	5 x 50	WD repeat domain 34 [Source:HGNC Symbol;Acc:HGNC:28
14	GEN1	−0.88	5e−05	5e−05	5 x 50	GEN1 Holliday junction 5' flap endonuclease [Source:HGNC
15	KNSTRN	−0.86	7e−05	5e−05	8 x 50	kinetochore−localized astrin/SPAG5 binding protein [Source:
16	CDK1	−0.85	8e−05	1e−04	5 x 50	cyclin−dependent kinase 1 [Source:HGNC Symbol;Acc:HGN
17	RAD51AP1	−0.85	1e−04	1e−04	4 x 50	RAD51 associated protein 1 [Source:HGNC Symbol;Acc:HG
18	WHSC1	−0.82	2e−04	1e−04	4 x 50	Wolf−Hirschhorn syndrome candidate 1 [Source:HGNC Sym
19	NCAPG	−0.82	2e−04	2e−04	6 x 50	non−SMC condensin I complex, subunit G [Source:HGNC Sy
20	PARPBP	0.81	2e−04	2e−04	6 x 50	PARP1 binding protein [Source:HGNC Symbol;Acc:HGNC:26

p−values