C6_mel

Global Summary

%DE = 0.21

genes with fdr < 0.2 = 2737 (1621 + / 1116 −)

genes with fdr < 0.1 = 2182 (1318 + / 864 −)

genes with fdr < 0.05 = 1850 (1130 + / 720 −)

genes with fdr < 0.01 = 1231 (761 + / 470 −)

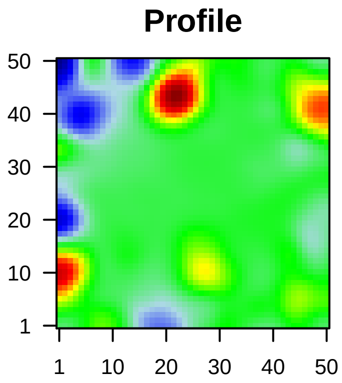
genes in genesets = 14839

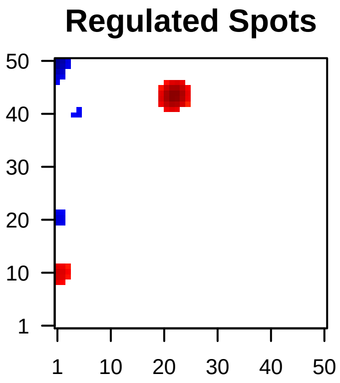
<FC> = 0

<shrinkage−t> = −0.02

<p−value> = 0.07

<fdr> = 0.79



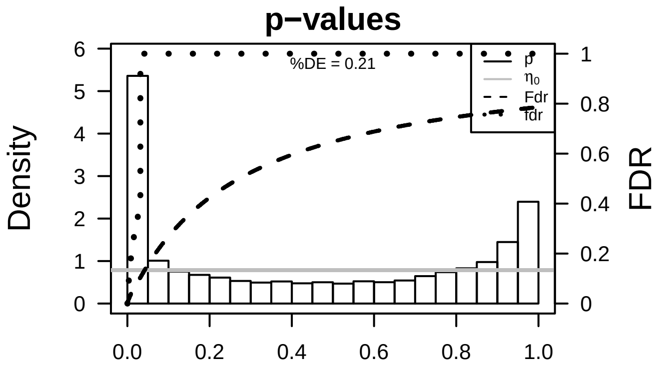


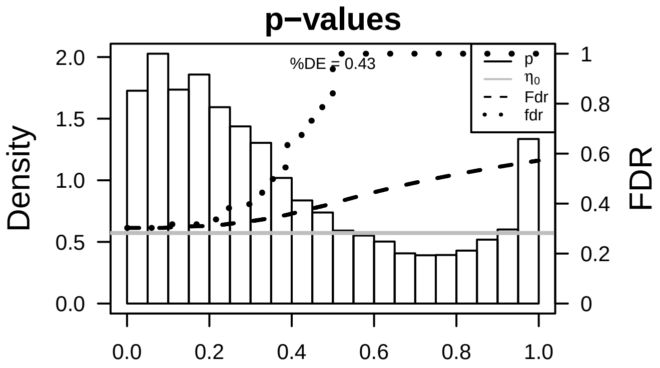
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ARF1	−0.86	2e−16	8e−14	46 x 35	ADP−ribosylation factor 1 [Source:HGNC Symbol;Acc:HGNC
2	ATP6V0D1	−1.3	2e−16	8e−14	23 x 50	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d1 [S
3	ATP6V1C1	−1.58	2e−16	8e−14	4 x 40	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1 [S
4	BAAT	1.99	2e−16	8e−14	32 x 50	bile acid CoA:amino acid N−acyltransferase [Source:HGNC S
5	BIRC2	−0.87	2e−16	8e−14	46 x 16	baculoviral IAP repeat containing 2 [Source:HGNC Symbol;A
6	BRIX1	−1.53	2e−16	8e−14	6 x 43	BRX1, biogenesis of ribosomes [Source:HGNC Symbol;Acc:H
7	BUD31	−1.48	2e−16	8e−14	14 x 50	BUD31 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:H
8	C11orf30	−1.7	2e−16	8e−14	16 x 50	chromosome 11 open reading frame 30 [Source:HGNC Symb
9	C9orf78	−1.57	2e−16	8e−14	6 x 40	chromosome 9 open reading frame 78 [Source:HGNC Symbo
10	CAPZB	−1.6	2e−16	8e−14	50 x 50	capping protein (actin filament) muscle Z−line, beta [Source:H
11	CEP97	1.89	2e−16	8e−14	2 x 47	centrosomal protein 97kDa [Source:HGNC Symbol;Acc:HGN
12	DCT	1.33	2e−16	8e−14	1 x 11	dopachrome tautomerase [Source:HGNC Symbol;Acc:HGNC
13	EXOC3	−0.94	2e−16	8e−14	1 x 42	exocyst complex component 3 [Source:HGNC Symbol;Acc:H
14	EXOSC8	−1.71	2e−16	8e−14	1 x 50	exosome component 8 [Source:HGNC Symbol;Acc:HGNC:17
15	GARS	−1.75	2e−16	8e−14	45 x 50	glycyl−tRNA synthetase [Source:HGNC Symbol;Acc:HGNC:4
16	GUCD1	−1.6	2e−16	8e−14	1 x 47	guanylyl cyclase domain containing 1 [Source:HGNC Symbol
17	HERPUD1	−1.94	2e−16	8e−14	50 x 42	homocysteine−inducible, endoplasmic reticulum stress−induc
18	ILF3	−1.32	2e−16	8e−14	11 x 44	interleukin enhancer binding factor 3, 90kDa [Source:HGNC
19	LARP4	−1.63	2e−16	8e−14	17 x 2	La ribonucleoprotein domain family, member 4 [Source:HGNC
20	MRPS25	−1.66	2e−16	8e−14	2 x 16	mitochondrial ribosomal protein S25 [Source:HGNC Symbol;

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	7.47	8e−04	993	Chr	Chr 2
2	5.21	3e−03	302	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
3	5.19	3e−03	2563	Lymphoma	HOPP_Heterochrom
4	4.69	4e−03	995	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_DN
5	4.31	6e−03	278	GSEA C2	GABRIELY_MIR21_TARGETS
6	4.21	6e−03	52	GSEA C2	IKEDA_MIR1_TARGETS_UP
7	3.9	8e−03	730	GSEA C2	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIA
8	3.75	9e−03	314	GSEA C2	RICKMAN_METASTASIS_UP
9	3.67	1e−02	20	CC	ciliary transition zone
10	3.58	1e−02	13	BP	head development
11	3.57	1e−02	1394	GSEA C2	ZWANG_TRANSIENTLY_UP_BY_1ST_EGF_PULSE_ONLY
12	3.55	1e−02	104	GSEA C2	LAIHO_COLORECTAL_CANCER_SERRATED_UP
13	3.47	1e−02	214	GSEA C2	HELLER_SILENCED_BY_METHYLATION_UP
14	3.38	1e−02	185	GSEA C2	WAMUNYOKOLI_OVARIAN_CANCER_LMP_DN
15	3.35	1e−02	1386	Colon Cancer	Het_Colon
16	3.35	1e−02	12	GSEA C2	BIOCARTA_IL10_PATHWAY
17	3.35	1e−02	141	GSEA C2	WHITFIELD_CELL_CYCLE_M_G1
18	3.32	1e−02	14	CC	Cul4−RING E3 ubiquitin ligase complex
19	3.32	1e−02	10	BP	Golgi vesicle transport
20	3.32	1e−02	416	GSEA C2	SHEN_SMARCA2_TARGETS_UP
Underexpressed					
1	−9.43	3e−04	278	GSEA C2	MANALO_HYPOXIA_DN
2	−7.11	1e−03	242	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
3	−7.1	1e−03	27	GSEA C2	REACTOME_DNA_STRAND_ELONGATION
4	−6.95	1e−03	801	Chr	Chr 11
5	−6.67	1e−03	29	BP	DNA strand elongation involved in DNA replication
6	−6.54	1e−03	32	GSEA C2	KEGG_DNA_REPLICATION
7	−6.48	1e−03	335	GSEA C2	WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_DN
8	−6.27	2e−03	68	GSEA C2	VERNELL_RETINOBLASTOMA_PATHWAY_UP
9	−6.18	2e−03	834	GSEA C2	LEE_BMP2_TARGETS_DN
10	−6.17	2e−03	505	GSEA C2	BERENJENO_TRANSFORMED_BY_RHOA_UP
11	−6.12	2e−03	756	GSEA C2	WEI_MYCN_TARGETS_WITH_E_BOX
12	−5.89	2e−03	136	GSEA C2	RUIZ_TNC_TARGETS_DN
13	−5.88	2e−03	157	GSEA C2	SCHLOSSER_MYC_TARGETS_REPRESSED_BY_SERUM
14	−5.86	2e−03	925	GSEA C2	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
15	−5.86	2e−03	171	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP
16	−5.72	2e−03	305	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
17	−5.69	2e−03	32	GSEA C2	REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLI
18	−5.67	2e−03	198	GSEA C2	FUJII_YBX1_TARGETS_DN
19	−5.66	2e−03	696	Chr	Chr 5
20	−5.62	2e−03	7203	Colon Cancer	TcF_Colon





C6_mel

Local Summary

%DE = 0.72

metagenes = 11

genes = 174

genes in genesets = 173

genes with fdr < 0.1 = 106 (91 + / 15 −)

genes with fdr < 0.05 = 82 (72 + / 10 −)

genes with fdr < 0.01 = 54 (49 + / 5 −)

<r> metagenes = 0.97

<r> genes = 0.16

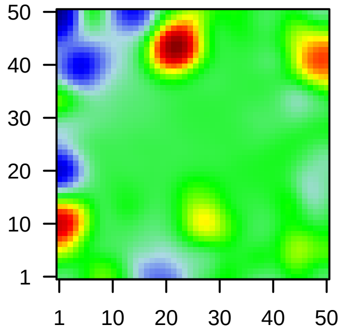
<FC> = 0.39

<shrinkage−t> = 6.46

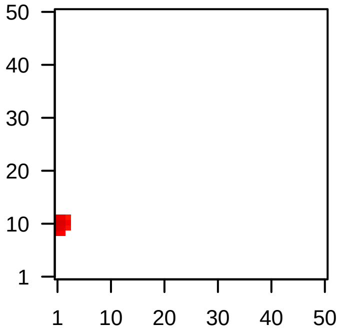
<p−value> = 0

<fdr> = 0.51

Profile



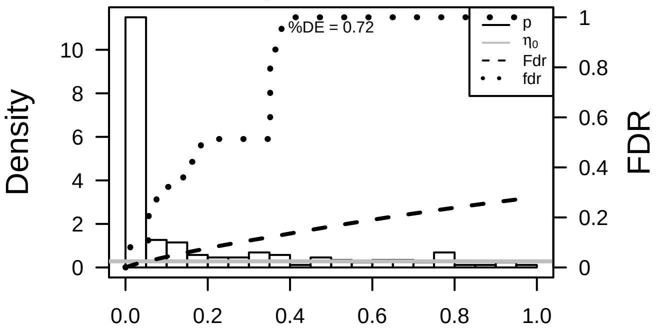
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	DCT	1.33	2e−16	1e−14	1 x 11	dopachrome tautomerase [Source:HGNC Symbol;Acc:HGNC
2	CC2D1B	1.66	7e−12	3e−07	1 x 9	coiled−coil and C2 domain containing 1B [Source:HGNC Sym
3	POPDC2	1.38	1e−08	3e−07	1 x 9	popeye domain containing 2 [Source:HGNC Symbol;Acc:HGN
4	C1orf54	1.38	1e−08	3e−07	1 x 11	chromosome 1 open reading frame 54 [Source:HGNC Symb
5	SLC5A10	1.35	2e−08	3e−07	2 x 10	solute carrier family 5 (sodium/sugar cotransporter), member
6	SULT1C2	1.35	2e−08	5e−06	1 x 9	sulfotransferase family, cytosolic, 1C, member 2 [Source:HGN
7	BCAT2	1.28	1e−07	8e−06	1 x 11	branched chain amino−acid transaminase 2, mitochondrial [S
8	LONRF1	1.23	3e−07	8e−06	1 x 12	LON peptidase N−terminal domain and ring finger 1 [Source:
9	TXNDC16	1.22	4e−07	1e−05	3 x 11	thioredoxin domain containing 16 [Source:HGNC Symbol;Acc
10	ESRP1	1.18	1e−06	1e−05	1 x 12	epithelial splicing regulatory protein 1 [Source:HGNC Symbol
11	HAS2	1.16	1e−06	1e−05	1 x 10	hyaluronan synthase 2 [Source:HGNC Symbol;Acc:HGNC:48
12	PPM1H	1.16	2e−06	1e−05	1 x 11	protein phosphatase, Mg2+/Mn2+ dependent, 1H [Source:HG
13	SCUBE3	1.15	2e−06	1e−05	1 x 12	signal peptide, CUB domain, EGF−like 3 [Source:HGNC Sym
14	TGDS	1.15	2e−06	5e−05	1 x 11	TDP−glucose 4,6−dehydratase [Source:HGNC Symbol;Acc:H
15	ENPP2	1.11	4e−06	5e−05	1 x 9	ectonucleotide pyrophosphatase/phosphodiesterase 2 [Sourc
16	EDNRB	0.88	5e−06	5e−05	1 x 11	endothelin receptor type B [Source:HGNC Symbol;Acc:HGNC
17	BHLHE41	1.09	5e−06	1e−04	1 x 12	basic helix−loop−helix family, member e41 [Source:HGNC Sy
18	TRIM63	1.08	8e−06	1e−04	1 x 12	tripartite motif containing 63, E3 ubiquitin protein ligase [Sour
19	XG	1.06	1e−05	1e−04	2 x 9	Xg blood group [Source:HGNC Symbol;Acc:HGNC:12806]
20	C21orf91	0.8	1e−05	1e−04	1 x 9	chromosome 21 open reading frame 91 [Source:HGNC Symb

p−values



C6_mel

Local Summary

%DE = 0.84

metagenes = 31

genes = 170

genes in genesets = 170

genes with fdr < 0.1 = 106 (105 + / 1 −)

genes with fdr < 0.05 = 104 (103 + / 1 −)

genes with fdr < 0.01 = 84 (83 + / 1 −)

<r> metagenes = 0.93

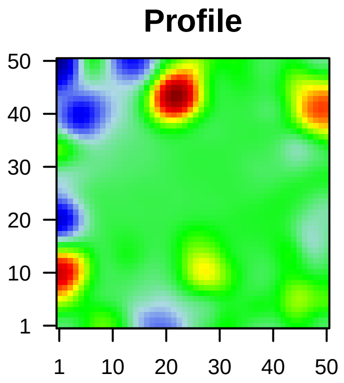
<r> genes = 0.09

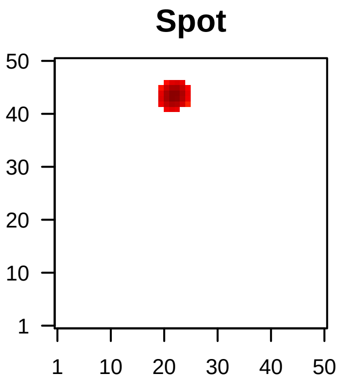
<FC> = 0.6

<shrinkage−t> = 9.56

<p−value> = 0

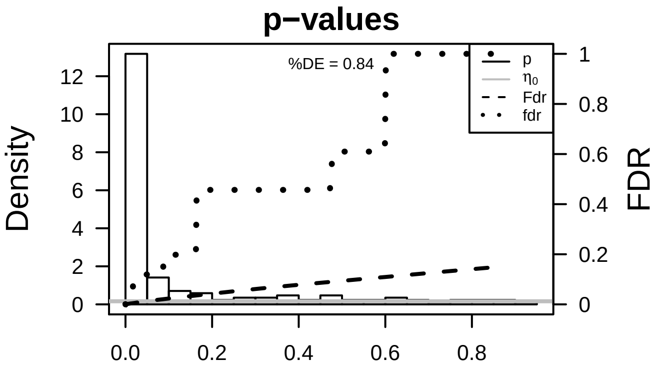
<fdr> = 0.4





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	GPRC5D	1.69	2e−12	3e−10	24 x 44	G protein−coupled receptor, class C, group 5, member D [So
2	DISP1	1.64	1e−11	2e−09	22 x 42	dispatched homolog 1 (Drosophila) [Source:HGNC Symbol;A
3	MPP3	1.57	8e−11	2e−08	23 x 45	membrane protein, palmitoylated 3 (MAGUK p55 subfamily m
4	CD3EAP	1.47	1e−09	2e−08	24 x 42	CD3e molecule, epsilon associated protein [Source:HGNC S
5	MTTP	1.45	2e−09	2e−08	25 x 43	microsomal triglyceride transfer protein [Source:HGNC Symb
6	AP3M2	1.44	2e−09	2e−08	22 x 43	adaptor−related protein complex 3, mu 2 subunit [Source:HG
7	CARD6	1.44	3e−09	1e−07	25 x 44	caspase recruitment domain family, member 6 [Source:HGN
8	GUCY1A2	1.4	7e−09	1e−07	25 x 44	guanylate cyclase 1, soluble, alpha 2 [Source:HGNC Symbol;
9	RGL3	1.37	1e−08	1e−07	25 x 44	ral guanine nucleotide dissociation stimulator−like 3 [Source:
10	FBXO8	1.37	1e−08	1e−07	22 x 45	F−box protein 8 [Source:HGNC Symbol;Acc:HGNC:13587]
11	PRKD1	1.36	2e−08	1e−07	21 x 44	protein kinase D1 [Source:HGNC Symbol;Acc:HGNC:9407]
12	CDADC1	1.35	2e−08	3e−07	23 x 42	cytidine and dCMP deaminase domain containing 1 [Source:
13	GOLGA1	1.33	3e−08	3e−07	23 x 46	golgin A1 [Source:HGNC Symbol;Acc:HGNC:4424]
14	ZNF324B	1.32	5e−08	3e−07	25 x 44	zinc finger protein 324B [Source:HGNC Symbol;Acc:HGNC:3
15	NDUFAF7	1.31	5e−08	5e−07	21 x 43	NADH dehydrogenase (ubiquinone) complex I, assembly fact
16	ZXDB	1.29	1e−07	5e−07	23 x 45	zinc finger, X−linked, duplicated B [Source:HGNC Symbol;Ac
17	RNF103	1.28	1e−07	5e−07	21 x 42	ring finger protein 103 [Source:HGNC Symbol;Acc:HGNC:12
18	PATZ1	1.28	1e−07	5e−07	21 x 44	POZ (BTB) and AT hook containing zinc finger 1 [Source:HG
19	SERPINB8	1.27	1e−07	5e−07	24 x 46	serpin peptidase inhibitor, clade B (ovalbumin), member 8 [S
20	FBXL3	1.27	2e−07	1e−06	22 x 44	F−box and leucine−rich repeat protein 3 [Source:HGNC Sym



C6_mel

Local Summary

%DE = 0.73

metagenes = 6

genes = 167

genes in genesets = 167

genes with fdr < 0.1 = 68 (8 + / 60 −)

genes with fdr < 0.05 = 68 (8 + / 60 −)

genes with fdr < 0.01 = 31 (1 + / 30 −)

<r> metagenes = 0.99

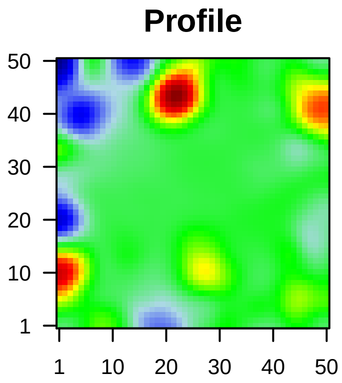
<r> genes = 0.19

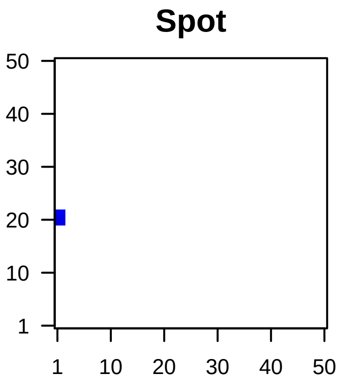
<FC> = −0.33

<shrinkage−t> = −5.6

<p−value> = 0.02

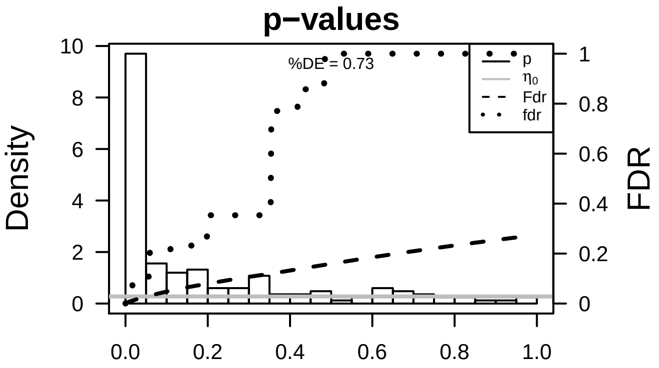
<fdr> = 0.61





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	HEXB	−1.46	1e−12	1e−09	1 x 21	hexosaminidase B (beta polypeptide) [Source:HGNC Symbol
2	UCK2	−1.34	3e−11	2e−08	1 x 21	uridine−cytidine kinase 2 [Source:HGNC Symbol;Acc:HGNC:
3	ERCC3	−1.35	4e−10	1e−07	2 x 22	excision repair cross−complementation group 3 [Source:HGN
4	PTPN2	−1.25	4e−09	2e−06	1 x 20	protein tyrosine phosphatase, non−receptor type 2 [Source:H
5	NXT1	−1.24	4e−08	9e−06	1 x 21	nuclear transport factor 2−like export factor 1 [Source:HGNC
6	GUK1	−0.6	3e−07	1e−05	1 x 21	guanylate kinase 1 [Source:HGNC Symbol;Acc:HGNC:4693]
7	SLC9A3R1	−1.18	5e−07	6e−05	1 x 21	solute carrier family 9, subfamily A (NHE3, cation proton anti
8	P4HB	−0.47	2e−06	2e−04	1 x 20	prolyl 4−hydroxylase, beta polypeptide [Source:HGNC Symb
9	ARF5	−1.08	7e−06	2e−04	1 x 20	ADP−ribosylation factor 5 [Source:HGNC Symbol;Acc:HGNC
10	STUB1	−1.06	1e−05	3e−04	1 x 20	STIP1 homology and U−box containing protein 1, E3 ubiquiti
11	SNF8	−0.76	2e−05	3e−04	1 x 21	SNF8, ESCRT−II complex subunit [Source:HGNC Symbol;Ac
12	PDIA3	−0.59	3e−05	3e−04	1 x 20	protein disulfide isomerase family A, member 3 [Source:HGN
13	FBXO7	−0.72	3e−05	4e−04	1 x 20	F−box protein 7 [Source:HGNC Symbol;Acc:HGNC:13586]
14	C17orf89	−0.99	4e−05	4e−04	1 x 21	chromosome 17 open reading frame 89 [Source:HGNC Symb
15	RIOK2	−0.98	5e−05	1e−03	1 x 20	RIO kinase 2 [Source:HGNC Symbol;Acc:HGNC:18999]
16	SIGMAR1	−0.96	7e−05	2e−03	1 x 21	sigma non−opioid intracellular receptor 1 [Source:HGNC Sym
17	MRPL41	−0.89	2e−04	2e−03	1 x 20	mitochondrial ribosomal protein L41 [Source:HGNC Symbol;
18	ADPGK	−0.88	2e−04	2e−03	1 x 21	ADP−dependent glucokinase [Source:HGNC Symbol;Acc:HG
19	VCL	−0.88	3e−04	2e−03	2 x 20	vinculin [Source:HGNC Symbol;Acc:HGNC:12665]
20	EIF2AK1	−0.82	3e−04	2e−03	1 x 20	eukaryotic translation initiation factor 2−alpha kinase 1 [Sourc



C6_mel

Local Summary

%DE = 0.81

metagenes = 3

genes = 22

genes in genesets = 22

genes with fdr < 0.1 = 13 (2 + / 11 −)

genes with fdr < 0.05 = 13 (2 + / 11 −)

genes with fdr < 0.01 = 6 (0 + / 6 −)

<r> metagenes = 0.99

<r> genes = 0.2

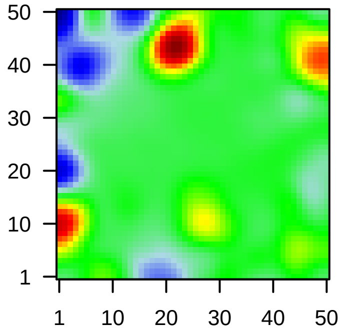
<FC> = −0.43

<shrinkage−t> = −8.05

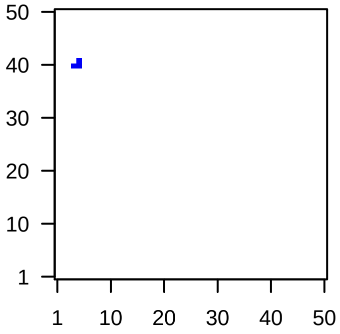
<p−value> = 0

<fdr> = 0.57

Profile



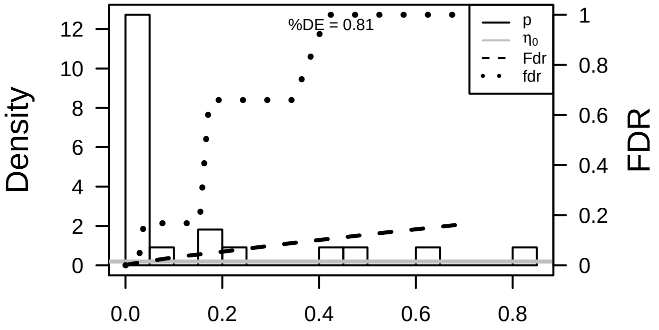
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ATP6V1C1	−1.58	2e−16	5e−16	4 x 40	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1 [S
2	ORMDL1	−1.84	2e−16	5e−16	5 x 40	ORMDL sphingolipid biosynthesis regulator 1 [Source:HGNC
3	HDHD2	−1.44	4e−12	5e−06	5 x 40	haloacid dehalogenase−like hydrolase domain containing 2 [
4	PIGU	−1.13	2e−06	5e−06	5 x 40	phosphatidylinositol glycan anchor biosynthesis, class U [Sou
5	ARMC6	−1.12	2e−06	2e−04	4 x 40	armadillo repeat containing 6 [Source:HGNC Symbol;Acc:HG
6	NTMT1	−0.93	8e−05	2e−04	4 x 40	N−terminal Xaa−Pro−Lys N−methyltransferase 1 [Source:HG
7	ATP5S	−0.95	8e−05	1e−02	5 x 40	ATP synthase, H+ transporting, mitochondrial Fo complex, su
8	MPV17	0.56	4e−03	1e−02	4 x 40	MpV17 mitochondrial inner membrane protein [Source:HGNC
9	NPRL2	−0.66	5e−03	2e−02	5 x 40	nitrogen permease regulator−like 2 (S. cerevisiae) [Source:H
10	FAM210A	−0.42	1e−02	3e−02	4 x 40	family with sequence similarity 210, member A [Source:HGN
11	TMEM199	0.47	3e−02	3e−02	4 x 40	transmembrane protein 199 [Source:HGNC Symbol;Acc:HGN
12	ITPA	−0.31	3e−02	3e−02	5 x 40	inosine triphosphatase (nucleoside triphosphate pyrophosph
13	MRPL48	−0.24	3e−02	5e−02	5 x 41	mitochondrial ribosomal protein L48 [Source:HGNC Symbol;
14	EIF4A3	0.2	4e−02	2e−01	4 x 40	eukaryotic translation initiation factor 4A3 [Source:HGNC Syn
15	COPS8	0.23	1e−01	2e−01	5 x 41	COP9 signalosome subunit 8 [Source:HGNC Symbol;Acc:HG
16	CTU2	−0.34	2e−01	2e−01	5 x 40	cytosolic thiouridylase subunit 2 homolog (S. pombe) [Source
17	HAGHL	−0.32	2e−01	2e−01	4 x 40	hydroxyacylglutathione hydrolase−like [Source:HGNC Symbo
18	UTP11L	0.23	2e−01	7e−01	5 x 41	UTP11−like, U3 small nucleolar ribonucleoprotein (yeast) [So
19	LYAR	−0.2	4e−01	7e−01	5 x 41	Ly1 antibody reactive [Source:HGNC Symbol;Acc:HGNC:260
20	PTRHD1	0.13	5e−01	1e+00	5 x 41	peptidyl−tRNA hydrolase domain containing 1 [Source:HGNC

p−values



C6_mel

Local Summary

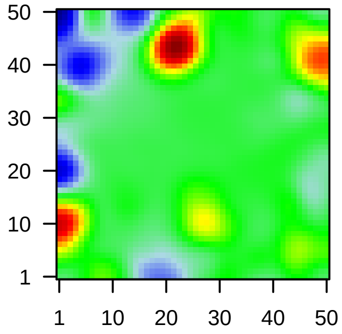
%DE = 0.79
metagenes = 11
genes = 229
genes in genesets = 228

genes with fdr < 0.1 = 147 (28 + / 119 −)
genes with fdr < 0.05 = 142 (27 + / 115 −)
genes with fdr < 0.01 = 79 (13 + / 66 −)

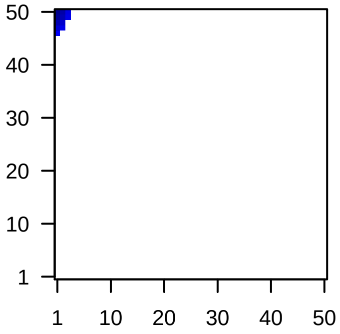
<r> metagenes = 0.97
<r> genes = 0.25

<FC> = −0.36
<shrinkage−t> = −5.88
<p−value> = 0
<fdr> = 0.49

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CEP97	1.89	2e−16	4e−15	2 x 47	centrosomal protein 97kDa [Source:HGNC Symbol;Acc:HGN
2	EXOSC8	−1.71	2e−16	4e−15	1 x 50	exosome component 8 [Source:HGNC Symbol;Acc:HGNC:17
3	GUCD1	−1.6	2e−16	4e−15	1 x 47	guanylyl cyclase domain containing 1 [Source:HGNC Symbol
4	MCM4	−1.36	1e−12	3e−09	1 x 50	minichromosome maintenance complex component 4 [Sourc
5	RFC5	−1.39	7e−11	3e−09	2 x 50	replication factor C (activator 1) 5, 36.5kDa [Source:HGNC S
6	RHOG	−1.37	1e−10	4e−09	1 x 46	ras homolog family member G [Source:HGNC Symbol;Acc:H
7	HADH	−1.33	3e−10	4e−09	1 x 48	hydroxyacyl−CoA dehydrogenase [Source:HGNC Symbol;Ac
8	RRM1	−1.21	3e−10	2e−08	2 x 50	ribonucleotide reductase M1 [Source:HGNC Symbol;Acc:HG
9	FEN1	−1.34	8e−10	2e−08	1 x 50	flap structure−specific endonuclease 1 [Source:HGNC Symb
10	TBCD	−1.33	1e−09	2e−08	1 x 46	tubulin folding cofactor D [Source:HGNC Symbol;Acc:HGNC:
11	GMPS	−1.29	1e−09	3e−08	1 x 48	guanine monphosphate synthase [Source:HGNC Symbol;Ac
12	TUBG1	−1.05	2e−09	5e−08	2 x 49	tubulin, gamma 1 [Source:HGNC Symbol;Acc:HGNC:12417]
13	CKLF	−1.31	3e−09	6e−08	3 x 49	chemokine−like factor [Source:HGNC Symbol;Acc:HGNC:13
14	MCM7	−1.29	4e−09	5e−07	2 x 50	minichromosome maintenance complex component 7 [Sourc
15	ORC6	−1.24	2e−08	5e−07	1 x 50	origin recognition complex, subunit 6 [Source:HGNC Symbol;
16	CENPQ	1.34	3e−08	5e−07	2 x 50	centromere protein Q [Source:HGNC Symbol;Acc:HGNC:213
17	UCK1	−1.24	4e−08	6e−07	1 x 46	uridine−cytidine kinase 1 [Source:HGNC Symbol;Acc:HGNC:
18	PDS5B	−1.21	5e−08	6e−07	1 x 50	PDS5 cohesin associated factor B [Source:HGNC Symbol;Ac
19	CENPK	−1.23	6e−08	1e−06	3 x 50	centromere protein K [Source:HGNC Symbol;Acc:HGNC:294
20	SMCHD1	−1.17	9e−08	7e−06	1 x 48	structural maintenance of chromosomes flexible hinge domai

p−values