C1_mel

Global Summary

%DE = 0.2

genes with fdr < 0.2 = 2509 (1584 + / 925 −)

genes with fdr < 0.1 = 2018 (1307 + / 711 −)

genes with fdr < 0.05 = 1476 (991 + / 485 −)

genes with fdr < 0.01 = 903 (634 + / 269 −)

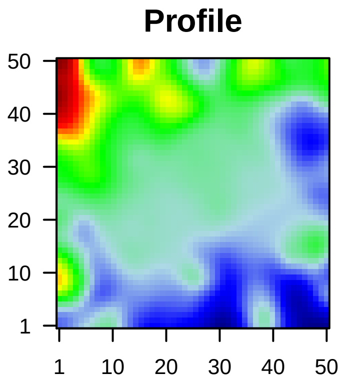
genes in genesets = 14839

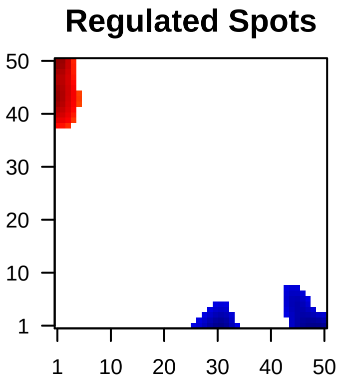
<FC> = 0

<shrinkage−t> = 0.1

<p−value> = 0.1

<fdr> = 0.8



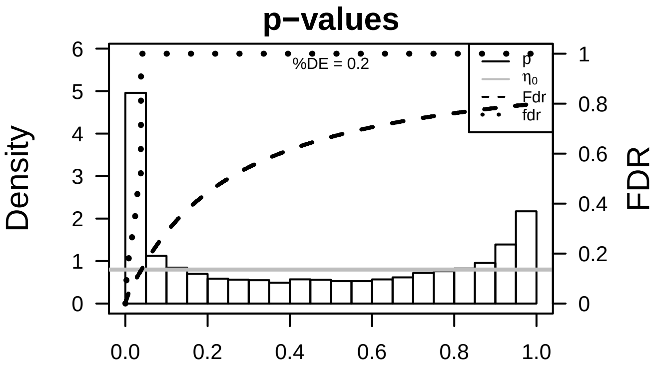


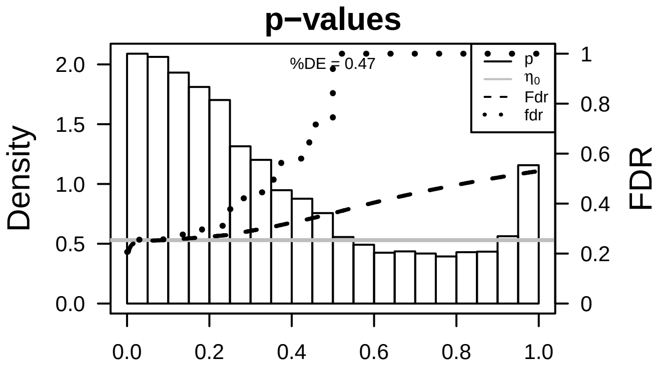
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CEP97	2.16	2e−16	2e−13	2 x 47	centrosomal protein 97kDa [Source:HGNC Symbol;Acc:HGN
2	CHURC1	−0.95	2e−16	2e−13	39 x 50	churchill domain containing 1 [Source:HGNC Symbol;Acc:HG
3	HMGCR	−1.6	2e−16	2e−13	2 x 11	3−hydroxy−3−methylglutaryl−CoA reductase [Source:HGNC
4	PDCD6IP	−1.73	2e−16	2e−13	33 x 50	programmed cell death 6 interacting protein [Source:HGNC S
5	PLK2	−1.65	2e−16	2e−13	50 x 1	polo−like kinase 2 [Source:HGNC Symbol;Acc:HGNC:19699]
6	PLRG1	−1.49	2e−16	2e−13	12 x 49	pleiotropic regulator 1 [Source:HGNC Symbol;Acc:HGNC:90
7	PMPCB	−1.47	2e−16	2e−13	33 x 50	peptidase (mitochondrial processing) beta [Source:HGNC Sy
8	PSMD9	−1.64	2e−16	2e−13	50 x 14	proteasome (prosome, macropain) 26S subunit, non−ATPase
9	PTRHD1	−1.36	2e−16	2e−13	5 x 41	peptidyl−tRNA hydrolase domain containing 1 [Source:HGNC
10	SACM1L	−1.51	2e−16	2e−13	9 x 7	SAC1 suppressor of actin mutations 1−like (yeast) [Source:H
11	STOM	−1.46	2e−16	2e−13	50 x 14	stomatin [Source:HGNC Symbol;Acc:HGNC:3383]
12	TPRN	2.07	2e−16	2e−13	13 x 15	taperin [Source:HGNC Symbol;Acc:HGNC:26894]
13	RUVBL1	−1.47	9e−16	4e−11	50 x 40	RuvB−like AAA ATPase 1 [Source:HGNC Symbol;Acc:HGNC
14	VAMP7	−1.44	9e−15	4e−11	42 x 37	vesicle−associated membrane protein 7 [Source:HGNC Sym
15	C1orf43	−0.67	1e−14	4e−11	46 x 42	chromosome 1 open reading frame 43 [Source:HGNC Symb
16	SMIM4	−1.25	1e−14	4e−11	4 x 14	small integral membrane protein 4 [Source:HGNC Symbol;Ac
17	ATG5	−1.43	1e−14	1e−10	50 x 38	autophagy related 5 [Source:HGNC Symbol;Acc:HGNC:589]
18	IQCH	1.65	2e−14	1e−10	50 x 32	IQ motif containing H [Source:HGNC Symbol;Acc:HGNC:257
19	NDRG2	1.65	3e−14	9e−10	43 x 15	NDRG family member 2 [Source:HGNC Symbol;Acc:HGNC:1
20	CAPN3	0.72	1e−13	9e−10	1 x 43	calpain 3, (p94) [Source:HGNC Symbol;Acc:HGNC:1480]

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	10.22	2e−04	198	HM	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	8.69	5e−04	405	GSEA C2	MOOTHA_HUMAN_MITODB_6_2002
3	8.36	5e−04	135	BP	cellular metabolic process
4	8.09	6e−04	85	GSEA C2	MOOTHA_VOXPHOS
5	8.01	6e−04	114	GSEA C2	REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_T
6	7.93	7e−04	99	GSEA C2	BURTON_ADIPOGENESIS_3
7	7.84	7e−04	78	GSEA C2	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_S
8	7.83	7e−04	107	GSEA C2	KEGG_OXIDATIVE_PHOSPHORYLATION
9	7.78	7e−04	421	GSEA C2	MOOTHA_MITOCHONDRIA
10	7.65	7e−04	81	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
11	7.65	7e−04	1468	CC	mitochondrion
12	7.59	8e−04	401	CC	mitochondrial inner membrane
13	7.55	8e−04	94	BP	respiratory electron transport chain
14	7.51	8e−04	368	GSEA C2	STEIN_ESRRA_TARGETS_UP
15	7.44	8e−04	213	GSEA C2	WONG_MITOCHONDRIA_GENE_MODULE
16	7.16	1e−03	278	GSEA C2	MANALO_HYPOXIA_DN
17	7.16	1e−03	500	GSEA C2	STEIN_ESRRA_TARGETS
18	7.04	1e−03	102	GSEA C2	KEGG_PARKINSONS_DISEASE
19	6.99	1e−03	32	GSEA C2	REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLI
20	6.9	1e−03	62	GSEA C2	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT
Underexpressed					
1	−4.74	0.004	626	BP	cell adhesion
2	−4.4	0.005	3068	BP	signal transduction
3	−4.31	0.006	3396	Lymphoma	HOPP_Repressed
4	−4.13	0.007	185	GSEA C2	WAMUNYOKOLI_OVARIAN_CANCER_LMP_DN
5	−4.13	0.007	79	CC	nucleosome
6	−4.03	0.007	64	GSEA C2	LEE_METASTASIS_AND_ALTERNATIVE_SPLICING_UP
7	−3.98	0.008	2159	Colon Cancer	TseP_Colon
8	−3.95	0.008	749	GSEA C2	CUI_TCF21_TARGETS_2_DN
9	−3.8	0.009	286	GSEA C2	PASINI_SUZ12_TARGETS_DN
10	−3.77	0.009	461	MF	transferase activity, transferring phosphorus−containing groups
11	−3.66	0.010	11	Tissue	WIRTH_Cortex cerebri
12	−3.61	0.010	53	HM	HALLMARK_TGF_BETA_SIGNALING
13	−3.54	0.011	68	GSEA C2	FRIDMAN_SENESCENCE_UP
14	−3.52	0.011	1128	Lymphoma	SPANG_BCR DN
15	−3.51	0.011	303	GSEA C2	LINDGREN_BLADDER_CANCER_CLUSTER_2B
16	−3.49	0.012	50	GSEA C2	HENDRICKS_SMARCA4_TARGETS_UP
17	−3.48	0.012	311	GSEA C2	SATO_SILENCED_BY_METHYLATION_IN_PANCREATIC_CANC
18	−3.48	0.012	866	MF	signal transducer activity
19	−3.47	0.012	398	MF	protein tyrosine kinase activity
20	−3.46	0.012	185	GSEA C2	DELYS_THYROID_CANCER_DN





C1_mel

Local Summary

%DE = 0.77

metagenes = 54

genes = 721

genes in genesets = 718

genes with fdr < 0.1 = 398 (323 + / 75 −)

genes with fdr < 0.05 = 365 (296 + / 69 −)

genes with fdr < 0.01 = 230 (189 + / 41 −)

<r> metagenes = 0.79

<r> genes = 0.13

<FC> = 0.27

<shrinkage−t> = 4.75

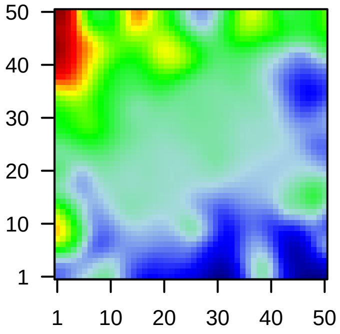
<p−value> = 0.01

<fdr> = 0.5

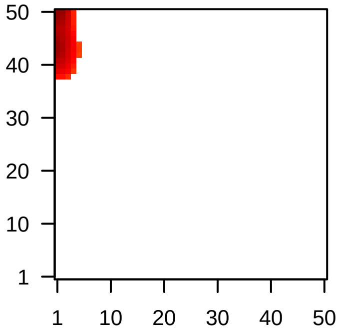
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CEP97	2.16	2e−16	4e−14	2 x 47	centrosomal protein 97kDa [Source:HGNC Symbol;Acc:HGN
2	CAPN3	0.72	1e−13	2e−10	1 x 43	calpain 3, (p94) [Source:HGNC Symbol;Acc:HGNC:1480]
3	ARHGAP8	1.04	1e−12	5e−09	1 x 43	Rho GTPase activating protein 8 [Source:HGNC Symbol;Acc
4	ST6GALNAC	1.12	3e−11	3e−08	1 x 44	ST6 (alpha−N−acetyl−neuraminyl−2,3−beta−galactosyl−1,3)−
5	FANCA	1.36	3e−10	3e−08	1 x 50	Fanconi anemia, complementation group A [Source:HGNC S
6	MIS18A	−1.24	4e−10	4e−08	3 x 49	MIS18 kinetochore protein A [Source:HGNC Symbol;Acc:HG
7	TRPM1	0.66	6e−10	8e−08	1 x 42	transient receptor potential cation channel, subfamily M, mem
8	MCM5	1.32	1e−09	8e−08	1 x 49	minichromosome maintenance complex component 5 [Sourc
9	BCS1L	1.31	2e−09	2e−07	1 x 38	BC1 (ubiquinol−cytochrome c reductase) synthesis−like [Sou
10	CEP128	1.29	3e−09	4e−07	3 x 48	centrosomal protein 128kDa [Source:HGNC Symbol;Acc:HG
11	FAM193B	1.26	6e−09	4e−07	3 x 39	family with sequence similarity 193, member B [Source:HGN
12	EXOC3	0.5	1e−08	4e−07	1 x 42	exocyst complex component 3 [Source:HGNC Symbol;Acc:H
13	DDX55	1.23	1e−08	4e−07	1 x 44	DEAD (Asp−Glu−Ala−Asp) box polypeptide 55 [Source:HGN
14	RBM10	1.23	1e−08	7e−07	2 x 45	RNA binding motif protein 10 [Source:HGNC Symbol;Acc:HG
15	EXOSC8	−0.86	2e−08	7e−07	1 x 50	exosome component 8 [Source:HGNC Symbol;Acc:HGNC:17
16	NMRK2	1.14	3e−08	7e−07	1 x 44	nicotinamide riboside kinase 2 [Source:HGNC Symbol;Acc:H
17	HPGD	1.19	3e−08	8e−07	1 x 44	hydroxyprostaglandin dehydrogenase 15−(NAD) [Source:HG
18	TEN1	1.19	3e−08	8e−07	1 x 48	TEN1 CST complex subunit [Source:HGNC Symbol;Acc:HGN
19	ANO2	1.19	4e−08	8e−07	1 x 42	anoctamin 2, calcium activated chloride channel [Source:HG
20	NTMT1	−1.16	4e−08	8e−07	4 x 40	N−terminal Xaa−Pro−Lys N−methyltransferase 1 [Source:HG

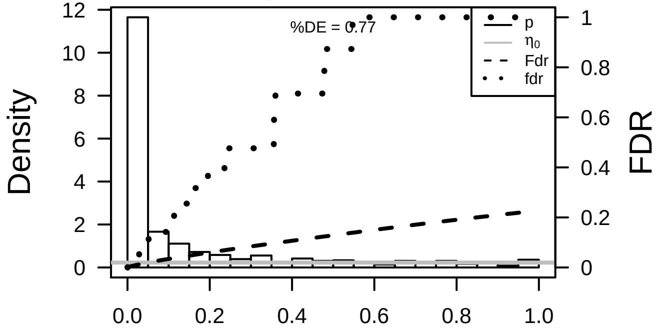
Profile



Spot



p−values



C1_mel

Local Summary

%DE = 0.54

metagenes = 29

genes = 310

genes in genesets = 298

genes with fdr < 0.1 = 33 (8 + / 25 −)

genes with fdr < 0.05 = 16 (5 + / 11 −)

genes with fdr < 0.01 = 4 (2 + / 2 −)

<r> metagenes = 0.92

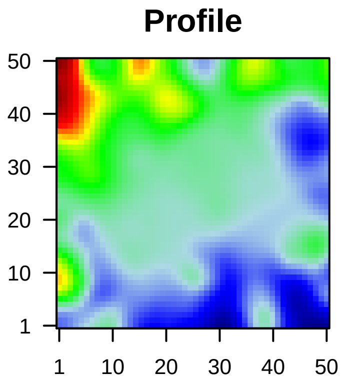
<r> genes = 0.18

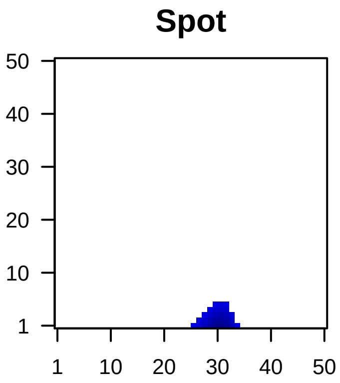
<FC> = −0.17

<shrinkage−t> = −2.62

<p−value> = 0.15

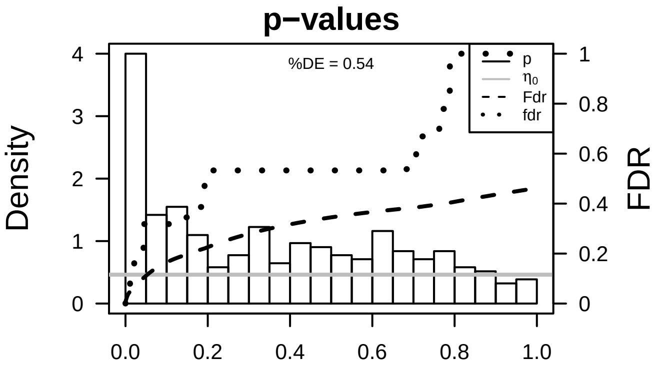
<fdr> = 0.87





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	VPRBP	1.04	2e−06	1e−04	31 x 1	Vpr (HIV−1) binding protein [Source:HGNC Symbol;Acc:HGN
2	MAF1	1.02	3e−06	1e−04	27 x 1	MAF1 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:H
3	FKBP14	−0.99	4e−06	1e−04	26 x 1	FK506 binding protein 14, 22 kDa [Source:HGNC Symbol;Ac
4	AIMP1	−0.79	4e−06	3e−04	31 x 1	aminoacyl tRNA synthetase complex−interacting multifunctio
5	SPAG9	−0.86	6e−06	2e−02	32 x 1	sperm associated antigen 9 [Source:HGNC Symbol;Acc:HGN
6	AAK1	−0.78	3e−04	2e−02	30 x 1	AP2 associated kinase 1 [Source:HGNC Symbol;Acc:HGNC:
7	AKIRIN1	−0.77	4e−04	2e−02	28 x 1	akirin 1 [Source:HGNC Symbol;Acc:HGNC:25744]
8	ZNF281	−0.74	7e−04	2e−02	30 x 5	zinc finger protein 281 [Source:HGNC Symbol;Acc:HGNC:13
9	SREBF2	0.74	7e−04	2e−02	28 x 1	sterol regulatory element binding transcription factor 2 [Sourc
10	GATC	−0.72	9e−04	2e−02	32 x 1	glutamyl−tRNA(Gln) amidotransferase, subunit C [Source:HG
11	TMCO3	−0.71	1e−03	2e−02	32 x 1	transmembrane and coiled−coil domains 3 [Source:HGNC Sy
12	ACTR8	−0.7	1e−03	2e−02	33 x 1	ARP8 actin−related protein 8 homolog (yeast) [Source:HGNC
13	ATG2B	0.7	1e−03	4e−02	26 x 1	autophagy related 2B [Source:HGNC Symbol;Acc:HGNC:201
14	MIB1	−0.69	2e−03	4e−02	29 x 1	mindbomb E3 ubiquitin protein ligase 1 [Source:HGNC Symb
15	UTP20	0.66	2e−03	4e−02	31 x 2	UTP20, small subunit (SSU) processome component, homolo
16	GIT1	−0.66	2e−03	4e−02	31 x 1	G protein−coupled receptor kinase interacting ArfGAP 1 [Sou
17	ZNF701	0.66	2e−03	8e−02	33 x 1	zinc finger protein 701 [Source:HGNC Symbol;Acc:HGNC:25
18	YTHDF1	−0.64	3e−03	8e−02	30 x 1	YTH N(6)−methyladenosine RNA binding protein 1 [Source:H
19	AGPS	−0.63	3e−03	8e−02	31 x 1	alkylglycerone phosphate synthase [Source:HGNC Symbol;A
20	CLEC16A	−0.62	4e−03	8e−02	29 x 1	C−type lectin domain family 16, member A [Source:HGNC Sy



C1_mel

Local Summary

%DE = 0.78

metagenes = 45

genes = 494

genes in genesets = 494

genes with fdr < 0.1 = 208 (54 + / 154 −)

genes with fdr < 0.05 = 152 (44 + / 108 −)

genes with fdr < 0.01 = 64 (22 + / 42 −)

<r> metagenes = 0.89

<r> genes = 0.16

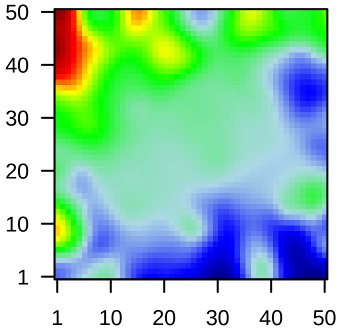
<FC> = −0.19

<shrinkage−t> = −3.04

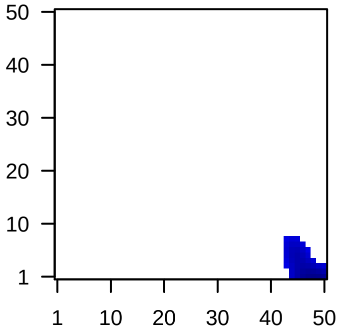
<p−value> = 0.03

<fdr> = 0.69

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	PLK2	−1.65	2e−16	2e−14	50 x 1	polo−like kinase 2 [Source:HGNC Symbol;Acc:HGNC:19699]
2	SATB1	1.53	1e−12	3e−10	50 x 1	SATB homeobox 1 [Source:HGNC Symbol;Acc:HGNC:10541
3	SSBP2	1.5	4e−12	1e−08	50 x 3	single−stranded DNA binding protein 2 [Source:HGNC Symb
4	HIST1H1C	−1.28	1e−10	4e−07	48 x 4	histone cluster 1, H1c [Source:HGNC Symbol;Acc:HGNC:471
5	ACOT13	−1.16	4e−09	1e−06	43 x 5	acyl−CoA thioesterase 13 [Source:HGNC Symbol;Acc:HGNC
6	STAM	−1.09	2e−08	1e−06	50 x 3	signal transducing adaptor molecule (SH3 domain and ITAM
7	RNF7	−0.86	2e−08	1e−06	47 x 6	ring finger protein 7 [Source:HGNC Symbol;Acc:HGNC:1007
8	TNFRSF12A	1.19	4e−08	1e−06	50 x 1	tumor necrosis factor receptor superfamily, member 12A [Sou
9	SLC38A9	1.18	5e−08	1e−06	43 x 8	solute carrier family 38, member 9 [Source:HGNC Symbol;Ac
10	PRNP	−1.1	6e−08	1e−06	47 x 2	prion protein [Source:HGNC Symbol;Acc:HGNC:9449]
11	PVRL3	1.17	6e−08	2e−06	46 x 1	poliovirus receptor−related 3 [Source:HGNC Symbol;Acc:HG
12	DRAM1	1.16	8e−08	4e−06	50 x 2	DNA−damage regulated autophagy modulator 1 [Source:HG
13	SUPT20H	−1.13	1e−07	4e−06	45 x 8	suppressor of Ty 20 homolog (S. cerevisiae) [Source:HGNC
14	SRPX	−1.07	2e−07	4e−06	50 x 1	sushi−repeat containing protein, X−linked [Source:HGNC Sy
15	EDIL3	−1.11	2e−07	7e−06	50 x 1	EGF−like repeats and discoidin I−like domains 3 [Source:HG
16	CLOCK	−1.1	3e−07	1e−05	47 x 1	clock circadian regulator [Source:HGNC Symbol;Acc:HGNC:
17	CRYAB	−0.72	4e−07	1e−05	50 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
18	RAB31	−1.08	5e−07	4e−05	50 x 3	RAB31, member RAS oncogene family [Source:HGNC Symb
19	KLF5	1.07	8e−07	7e−05	46 x 4	Kruppel−like factor 5 (intestinal) [Source:HGNC Symbol;Acc:
20	FN1	−1.04	1e−06	8e−05	50 x 1	fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]

p−values