D3_mel

Global Summary

%DE = 0.2

genes with fdr < 0.2 = 2526 (1482 + / 1044 −)

genes with fdr < 0.1 = 2099 (1234 + / 865 −)

genes with fdr < 0.05 = 1526 (904 + / 622 −)

genes with fdr < 0.01 = 1016 (606 + / 410 −)

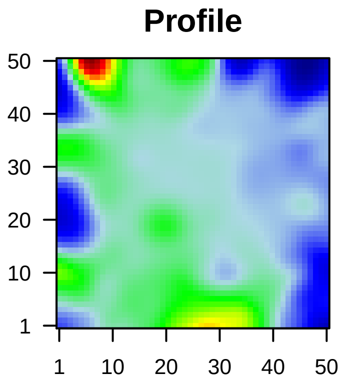
genes in genesets = 14839

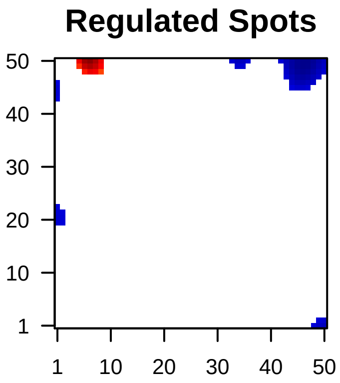
<FC> = 0

<shrinkage−t> = −0.01

<p−value> = 0.09

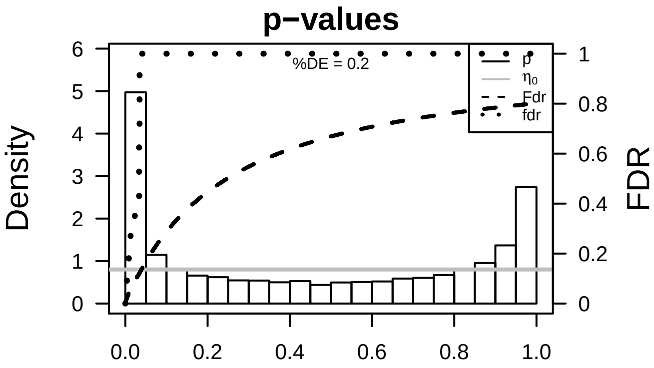
<fdr> = 0.8





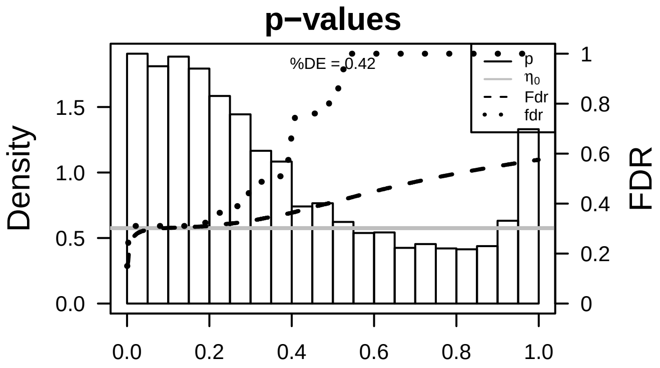
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ACTR3	−1.68	2e−16	1e−13	4 x 42	ARP3 actin−related protein 3 homolog (yeast) [Source:HGNC
2	ATP6V1H	−1.77	2e−16	1e−13	5 x 44	ATPase, H+ transporting, lysosomal 50/57kDa, V1 subunit H
3	CCNDBP1	−1.66	2e−16	1e−13	1 x 21	cyclin D−type binding−protein 1 [Source:HGNC Symbol;Acc:
4	CRYZL1	−1.72	2e−16	1e−13	44 x 50	crystallin, zeta (quinone reductase)−like 1 [Source:HGNC Sy
5	DFNA5	−1.63	2e−16	1e−13	3 x 18	deafness, autosomal dominant 5 [Source:HGNC Symbol;Acc
6	EIF4A1	−1.06	2e−16	1e−13	1 x 27	eukaryotic translation initiation factor 4A1 [Source:HGNC Syn
7	GMFB	−1.61	2e−16	1e−13	46 x 49	glia maturation factor, beta [Source:HGNC Symbol;Acc:HGN
8	GPATCH4	−1.7	2e−16	1e−13	46 x 45	G patch domain containing 4 [Source:HGNC Symbol;Acc:HG
9	LGALS3BP	−1.3	2e−16	1e−13	47 x 17	lectin, galactoside−binding, soluble, 3 binding protein [Source
10	MYH10	−1.09	2e−16	1e−13	1 x 44	myosin, heavy chain 10, non−muscle [Source:HGNC Symbol
11	NUP107	−1.27	2e−16	1e−13	2 x 48	nucleoporin 107kDa [Source:HGNC Symbol;Acc:HGNC:2991
12	PDCD6IP	−1.77	2e−16	1e−13	33 x 50	programmed cell death 6 interacting protein [Source:HGNC S
13	PDHA1	−1.47	2e−16	1e−13	16 x 50	pyruvate dehydrogenase (lipoamide) alpha 1 [Source:HGNC
14	PLEKHA5	−1.48	2e−16	1e−13	50 x 50	pleckstrin homology domain containing, family A member 5 [
15	QARS	−2.1	2e−16	1e−13	3 x 43	glutaminyl−tRNA synthetase [Source:HGNC Symbol;Acc:HG
16	STMN1	0.86	2e−16	1e−13	5 x 50	stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]
17	TOMM7	−0.93	2e−16	1e−13	50 x 11	translocase of outer mitochondrial membrane 7 homolog (yea
18	WIPI1	−1.95	2e−16	1e−13	47 x 49	WD repeat domain, phosphoinositide interacting 1 [Source:H
19	YIF1A	−1.7	2e−16	1e−13	47 x 50	Yip1 interacting factor homolog A (S. cerevisiae) [Source:HG
20	ZNF644	−1.65	2e−16	1e−13	36 x 50	zinc finger protein 644 [Source:HGNC Symbol;Acc:HGNC:29



Global Geneset Analysis

Rank	GSZ	p−value	#all		Geneset
Overexpressed					
1	11.94	1e−04	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
2	11.32	2e−04	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
3	9.49	3e−04	52	GSEA C2	TANG_SENESCENCE_TP53_TARGETS_DN
4	9.25	4e−04	312	BP	mitotic nuclear division
5	9.22	4e−04	54	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
6	9.17	4e−04	45	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
7	9.13	4e−04	155	GSEA C2	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
8	9.08	3e−02	16	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
9	8.99	4e−04	99	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
10	8.93	4e−04	96	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
11	8.56	5e−04	436	GSEA C2	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
12	8.56	5e−04	201	GSEA C2	WHITFIELD_CELL_CYCLE_G2_M
13	8.17	6e−04	33	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
14	8.01	6e−04	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
15	7.95	6e−04	72	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
16	7.81	7e−04	110	GSEA C2	WHITEFORD_PEDIATRIC_CANCER_MARKERS
17	7.8	7e−04	291	GSEA C2	HORIUCHI_WTAP_TARGETS_DN
18	7.8	7e−04	82	GSEA C2	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA2_UP
19	7.67	7e−04	165	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
20	7.61	8e−04	93	GSEA C2	KONG_E2F3_TARGETS
Underexpressed					
1	−5.33	0.003	31	GSEA C2	MA_MYELOID_DIFFERENTIATION_UP
2	−4.76	0.004	255	BP	cellular amino acid metabolic process
3	−4.74	0.004	136	GSEA C2	IVANOVA_HEMATOPOIESIS_INTERMEDIATE_PROGENITOR
4	−4.67	0.004	38	GSEA C2	IRITANI_MAD1_TARGETS_DN
5	−4.59	0.005	23	GSEA C2	CHNG_MULTIPLE_MYELOMA_HYPERPLOID_UP
6	−4.34	0.006	176	GSEA C2	TIEN_INTESTINE_PROBIOTICS_24HR_DN
7	−4.3	0.006	84	BP	endoplasmic reticulum unfolded protein response
8	−4.2	0.006	66	BP	activation of signaling protein activity involved in unfolded protein re
9	−4.16	0.007	27	GSEA C2	REACTOME_DNA_STRAND_ELONGATION
10	−4.15	0.007	10	MF	ligase activity, forming aminoacyl−tRNA and related compounds
11	−4.1	0.007	16	GSEA C2	BIOCARTA_P53_PATHWAY
12	−4.09	0.007	1008	GSEA C2	BRUINS_UVC_RESPONSE_LATE
13	−4.05	0.007	26	GSEA C2	YANG_BREAST_CANCER_ESR1_UP
14	−4.04	0.007	2137	TF	ICGC_SrfV0416101_targets
15	−4.03	0.007	74	BP	nucleobase−containing small molecule metabolic process
16	−3.97	0.008	246	CC	mitochondrial matrix
17	−3.97	0.008	12	GSEA C2	REACTOME_PROCESSIVE_SYNTHESIS_ON_THE_LAGGING_
18	−3.93	0.008	68	GSEA C2	REACTOME_METABOLISM_OF_NUCLEOTIDES
19	−3.92	0.008	7203	Colon Cancer	TcoF_Colon
20	−3.89	0.008	135	GSEA C2	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTE



D3_mel

Local Summary

%DE = 0.89

metagenes = 14

genes = 190

genes in genesets = 190

genes with fdr < 0.1 = 146 (129 + / 17 −)

genes with fdr < 0.05 = 136 (126 + / 10 −)

genes with fdr < 0.01 = 113 (108 + / 5 −)

<r> metagenes = 0.99

<r> genes = 0.39

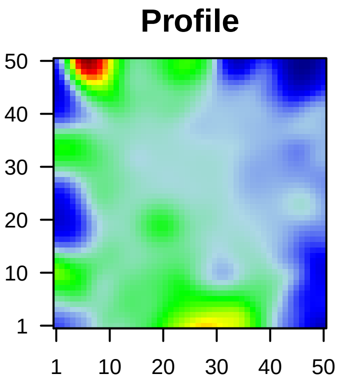
<FC> = 0.61

<shrinkage−t> = 10.04

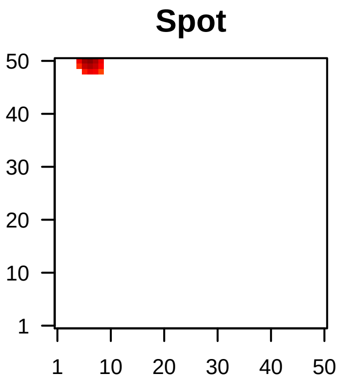
<p−value> = 0

<fdr> = 0.34

Profile



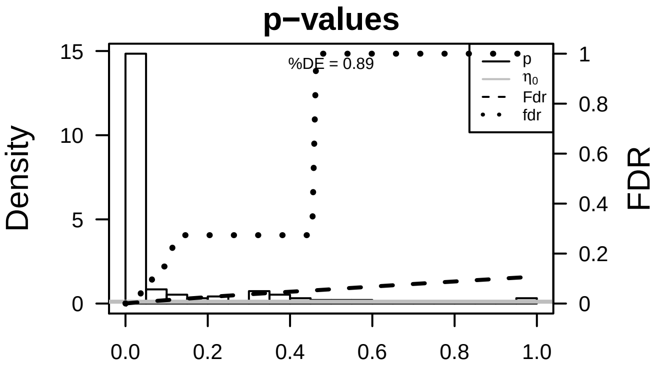
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	STMN1	0.86	2e−16	5e−15	5 x 50	stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]
2	CDKN3	1.54	4e−16	5e−14	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
3	H2AFZ	0.81	3e−15	1e−11	7 x 48	H2A histone family, member Z [Source:HGNC Symbol;Acc:H
4	PBK	1.85	5e−13	7e−11	6 x 50	PDZ binding kinase [Source:HGNC Symbol;Acc:HGNC:1828
5	PLK1	1.75	8e−12	7e−11	8 x 50	polo−like kinase 1 [Source:HGNC Symbol;Acc:HGNC:9077]
6	CDC20	1.75	9e−12	7e−11	6 x 50	cell division cycle 20 [Source:HGNC Symbol;Acc:HGNC:172
7	NCAPG	1.74	1e−11	2e−10	6 x 50	non−SMC condensin I complex, subunit G [Source:HGNC Sy
8	RACGAP1	1.71	3e−11	2e−10	7 x 50	Rac GTPase activating protein 1 [Source:HGNC Symbol;Acc:
9	PTTG1	1.05	3e−11	8e−10	7 x 50	pituitary tumor−transforming 1 [Source:HGNC Symbol;Acc:H
10	DLGAP5	1.66	1e−10	8e−10	7 x 50	discs, large (Drosophila) homolog−associated protein 5 [Sour
11	PLK4	1.65	1e−10	2e−09	5 x 50	polo−like kinase 4 [Source:HGNC Symbol;Acc:HGNC:11397]
12	CCNB1	1.6	2e−10	2e−09	7 x 50	cyclin B1 [Source:HGNC Symbol;Acc:HGNC:1579]
13	ANP32E	0.77	3e−10	2e−09	8 x 50	acidic (leucine−rich) nuclear phosphoprotein 32 family, memb
14	NEK2	1.61	4e−10	1e−08	8 x 50	NIMA−related kinase 2 [Source:HGNC Symbol;Acc:HGNC:77
15	FAM64A	1.55	1e−09	1e−08	7 x 50	family with sequence similarity 64, member A [Source:HGNC
16	ARL6IP1	0.95	2e−09	2e−08	9 x 50	ADP−ribosylation factor−like 6 interacting protein 1 [Source:H
17	CCNB2	1.52	3e−09	3e−08	6 x 50	cyclin B2 [Source:HGNC Symbol;Acc:HGNC:1580]
18	NCAPD2	1.49	6e−09	3e−08	7 x 50	non−SMC condensin I complex, subunit D2 [Source:HGNC S
19	CENPE	1.48	8e−09	3e−08	7 x 50	centromere protein E, 312kDa [Source:HGNC Symbol;Acc:H
20	SHCBP1	1.48	8e−09	1e−07	5 x 50	SHC SH2−domain binding protein 1 [Source:HGNC Symbol;

p−values



D3_mel

Local Summary

%DE = 0.97

metagenes = 5

genes = 140

genes in genesets = 140

genes with fdr < 0.1 = 138 (34 + / 104 −)

genes with fdr < 0.05 = 114 (24 + / 90 −)

genes with fdr < 0.01 = 65 (17 + / 48 −)

<r> metagenes = 1

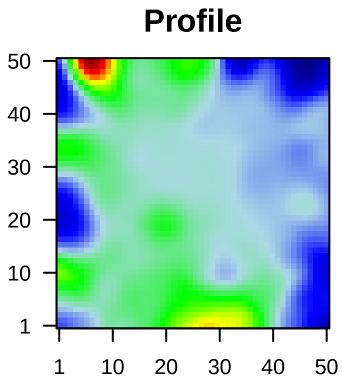
<r> genes = 0.26

<FC> = −0.27

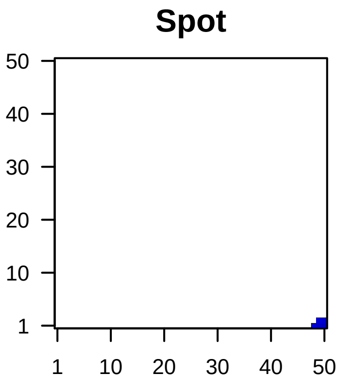
<shrinkage−t> = −4.25

<p−value> = 0.01

<fdr> = 0.62



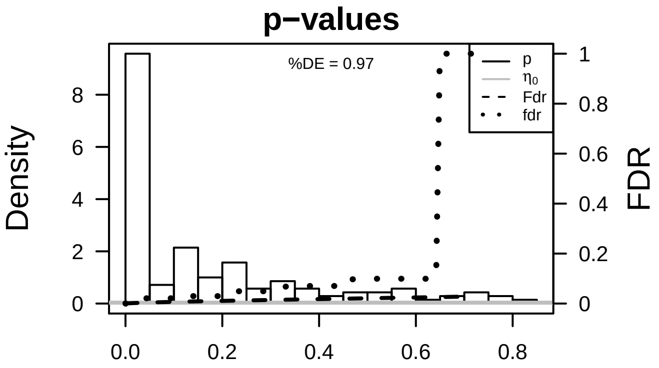
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	TGIF1	−1.46	3e−11	2e−10	50 x 1	TGFB−induced factor homeobox 1 [Source:HGNC Symbol;Ac
2	FABP3	−1.44	6e−11	3e−09	50 x 1	fatty acid binding protein 3, muscle and heart [Source:HGNC
3	TXNIP	1.58	6e−10	1e−08	50 x 1	thioredoxin interacting protein [Source:HGNC Symbol;Acc:HG
4	DNAJB4	−1.21	3e−09	5e−07	50 x 1	DnaJ (Hsp40) homolog, subfamily B, member 4 [Source:HGN
5	CRYAB	−0.89	1e−07	6e−06	50 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
6	CD55	−1.18	1e−06	6e−06	50 x 1	CD55 molecule, decay accelerating factor for complement (Cr
7	FMN2	−1.16	4e−06	6e−06	48 x 1	formin 2 [Source:HGNC Symbol;Acc:HGNC:14074]
8	TMEM45A	1.17	5e−06	6e−06	50 x 1	transmembrane protein 45A [Source:HGNC Symbol;Acc:HGN
9	YPEL5	−1.15	5e−06	1e−05	50 x 1	yippee−like 5 (Drosophila) [Source:HGNC Symbol;Acc:HGNC
10	UBE2E2	−1.12	9e−06	1e−05	50 x 1	ubiquitin−conjugating enzyme E2E 2 [Source:HGNC Symbol;
11	PDLIM5	−1.12	1e−05	2e−05	50 x 1	PDZ and LIM domain 5 [Source:HGNC Symbol;Acc:HGNC:1
12	ECM1	1.1	2e−05	2e−05	49 x 1	extracellular matrix protein 1 [Source:HGNC Symbol;Acc:HG
13	PTPRM	−1.08	2e−05	3e−05	50 x 1	protein tyrosine phosphatase, receptor type, M [Source:HGN
14	FAT1	1.07	3e−05	8e−05	49 x 1	FAT atypical cadherin 1 [Source:HGNC Symbol;Acc:HGNC:3
15	ABHD4	1.04	5e−05	8e−05	49 x 1	abhydrolase domain containing 4 [Source:HGNC Symbol;Acc
16	VIM	−0.69	7e−05	8e−05	50 x 2	vimentin [Source:HGNC Symbol;Acc:HGNC:12692]
17	PDGFA	−1.01	9e−05	8e−05	49 x 1	platelet−derived growth factor alpha polypeptide [Source:HGN
18	P4HA1	−0.99	1e−04	8e−05	50 x 1	prolyl 4−hydroxylase, alpha polypeptide I [Source:HGNC Sym
19	CDH19	−0.98	1e−04	8e−05	50 x 1	cadherin 19, type 2 [Source:HGNC Symbol;Acc:HGNC:1758]
20	PLK2	0.73	1e−04	2e−04	50 x 1	polo−like kinase 2 [Source:HGNC Symbol;Acc:HGNC:19699]



p−values

D3_mel

Local Summary

%DE = 0.53

metagenes = 7

genes = 179

genes in genesets = 179

genes with fdr < 0.1 = 69 (15 + / 54 −)

genes with fdr < 0.05 = 51 (9 + / 42 −)

genes with fdr < 0.01 = 27 (3 + / 24 −)

<r> metagenes = 0.99

<r> genes = 0.18

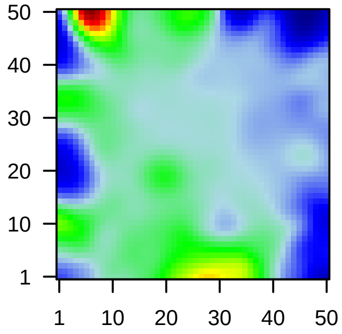
<FC> = −0.2

<shrinkage−t> = −3.65

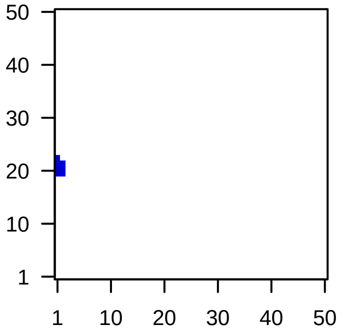
<p−value> = 0.02

<fdr> = 0.65

Profile



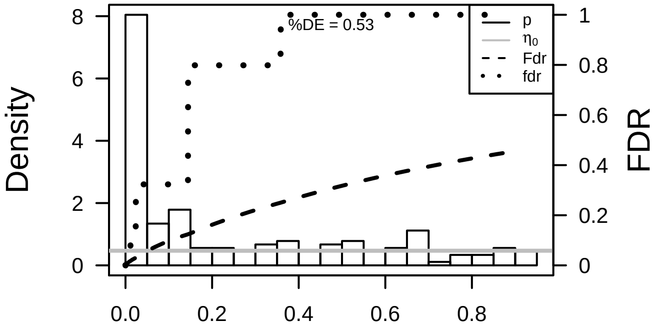
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CCNDBP1	−1.66	2e−16	2e−14	1 x 21	cyclin D−type binding−protein 1 [Source:HGNC Symbol;Acc:
2	P4HB	−0.56	5e−08	3e−06	1 x 20	prolyl 4−hydroxylase, beta polypeptide [Source:HGNC Symb
3	ATP1B3	−0.74	7e−08	1e−05	1 x 21	ATPase, Na+/K+ transporting, beta 3 polypeptide [Source:HG
4	NXT1	−1.24	2e−07	3e−05	1 x 21	nuclear transport factor 2−like export factor 1 [Source:HGNC
5	C20orf24	−1.18	9e−07	3e−05	1 x 21	chromosome 20 open reading frame 24 [Source:HGNC Symb
6	PFN1	−0.62	1e−06	5e−05	1 x 21	profilin 1 [Source:HGNC Symbol;Acc:HGNC:8881]
7	RCN1	−0.6	2e−06	5e−05	1 x 23	reticulocalbin 1, EF−hand calcium binding domain [Source:H
8	PTPN2	−1.06	2e−06	5e−05	1 x 20	protein tyrosine phosphatase, non−receptor type 2 [Source:H
9	IMP3	−1.08	3e−06	2e−04	1 x 22	IMP3, U3 small nucleolar ribonucleoprotein [Source:HGNC S
10	LAGE3	−1.13	7e−06	2e−04	1 x 21	L antigen family, member 3 [Source:HGNC Symbol;Acc:HGN
11	SYNGR2	−1	7e−06	2e−04	1 x 21	synaptogyrin 2 [Source:HGNC Symbol;Acc:HGNC:11499]
12	AKR7A2	1.14	9e−06	4e−04	1 x 21	aldo−keto reductase family 7, member A2 (aflatoxin aldehyde
13	TMEM123	−0.45	1e−05	4e−04	1 x 21	transmembrane protein 123 [Source:HGNC Symbol;Acc:HG
14	SNF8	−0.82	2e−05	1e−03	1 x 21	SNF8, ESCRT−II complex subunit [Source:HGNC Symbol;Ac
15	TMEM147	−0.49	5e−05	1e−03	1 x 22	transmembrane protein 147 [Source:HGNC Symbol;Acc:HG
16	SQSTM1	−0.47	6e−05	1e−03	1 x 21	sequestosome 1 [Source:HGNC Symbol;Acc:HGNC:11280]
17	UBE2J2	1.02	7e−05	1e−03	1 x 20	ubiquitin−conjugating enzyme E2, J2 [Source:HGNC Symbol;
18	MRPS34	−1	1e−04	1e−03	1 x 21	mitochondrial ribosomal protein S34 [Source:HGNC Symbol;
19	CST3	−0.79	1e−04	1e−03	1 x 20	cystatin C [Source:HGNC Symbol;Acc:HGNC:2475]
20	RIOK2	−0.98	1e−04	1e−03	1 x 20	RIO kinase 2 [Source:HGNC Symbol;Acc:HGNC:18999]

p−values



D3_mel

Local Summary

%DE = 0.73

metagenes = 4

genes = 116

genes in genesets = 115

genes with fdr < 0.1 = 61 (18 + / 43 −)

genes with fdr < 0.05 = 45 (10 + / 35 −)

genes with fdr < 0.01 = 32 (7 + / 25 −)

<r> metagenes = 0.96

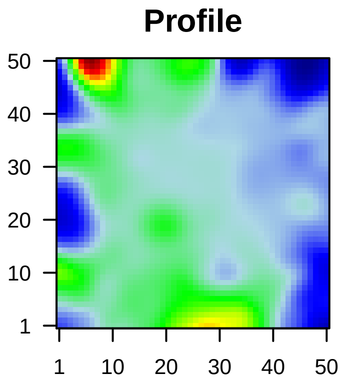
<r> genes = 0.19

<FC> = −0.23

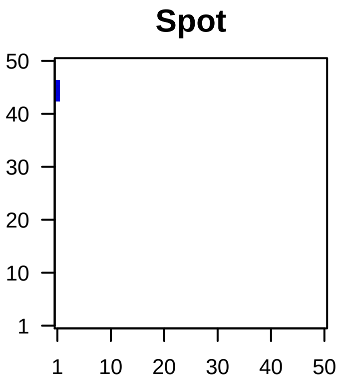
<shrinkage−t> = −3.77

<p−value> = 0.01

<fdr> = 0.58



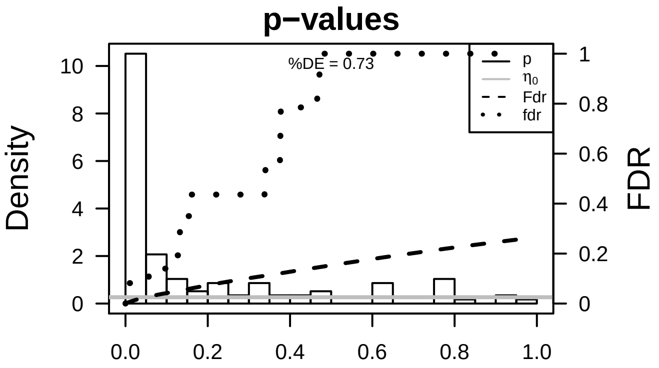
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	MYH10	−1.09	2e−16	7e−15	1 x 44	myosin, heavy chain 10, non−muscle [Source:HGNC Symbol
2	VPS25	−1.58	5e−15	1e−10	1 x 45	vacuolar protein sorting 25 homolog (S. cerevisiae) [Source:
3	MLPH	−1.48	4e−12	4e−09	1 x 43	melanophilin [Source:HGNC Symbol;Acc:HGNC:29643]
4	MTHFD1	−1.42	2e−10	4e−09	1 x 45	methylenetetrahydrofolate dehydrogenase (NADP+ depender
5	CYB5A	−1.41	3e−10	2e−08	1 x 45	cytochrome b5 type A (microsomal) [Source:HGNC Symbol;
6	LGALS3	−1.38	1e−09	1e−07	1 x 43	lectin, galactoside−binding, soluble, 3 [Source:HGNC Symbol
7	C6orf211	−1.33	5e−09	2e−06	1 x 45	
8	CD58	−1.26	7e−08	3e−05	1 x 43	CD58 molecule [Source:HGNC Symbol;Acc:HGNC:1688]
9	MTFP1	−1.2	1e−06	4e−05	1 x 45	mitochondrial fission process 1 [Source:HGNC Symbol;Acc:
10	BCKDK	−1.13	3e−06	4e−05	1 x 43	branched chain ketoacid dehydrogenase kinase [Source:HG
11	DHCR7	−1.15	5e−06	4e−05	1 x 44	7−dehydrocholesterol reductase [Source:HGNC Symbol;Acc:
12	CAPN3	0.52	6e−06	4e−05	1 x 43	calpain 3, (p94) [Source:HGNC Symbol;Acc:HGNC:1480]
13	KLHDC3	−1.14	7e−06	2e−04	1 x 46	kelch domain containing 3 [Source:HGNC Symbol;Acc:HGN
14	RNF138	−1.1	1e−05	8e−04	1 x 46	ring finger protein 138, E3 ubiquitin protein ligase [Source:H
15	MYO19	−1.05	4e−05	1e−03	1 x 46	myosin XIX [Source:HGNC Symbol;Acc:HGNC:26234]
16	HAUS7	−1.01	7e−05	1e−03	1 x 46	HAUS augmin−like complex, subunit 7 [Source:HGNC Symb
17	NT5DC2	−0.98	1e−04	2e−03	1 x 46	5'−nucleotidase domain containing 2 [Source:HGNC Symbol;
18	DERA	−0.62	3e−04	2e−03	1 x 43	deoxyribose−phosphate aldolase (putative) [Source:HGNC S
19	SLC25A37	−0.92	3e−04	2e−03	1 x 44	solute carrier family 25 (mitochondrial iron transporter), mem
20	PPWD1	−0.92	3e−04	2e−03	1 x 44	peptidylprolyl isomerase domain and WD repeat containing 1



p−values

D3_mel

Local Summary

%DE = 0.82

metagenes = 41

genes = 466

genes in genesets = 464

genes with fdr < 0.1 = 267 (78 + / 189 −)

genes with fdr < 0.05 = 190 (52 + / 138 −)

genes with fdr < 0.01 = 115 (21 + / 94 −)

<r> metagenes = 0.83

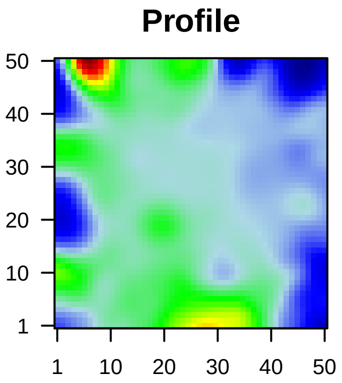
<r> genes = 0.07

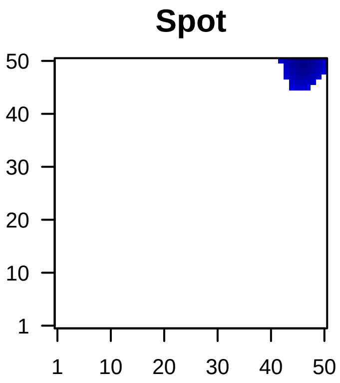
<FC> = −0.23

<shrinkage−t> = −4.02

<p−value> = 0.01

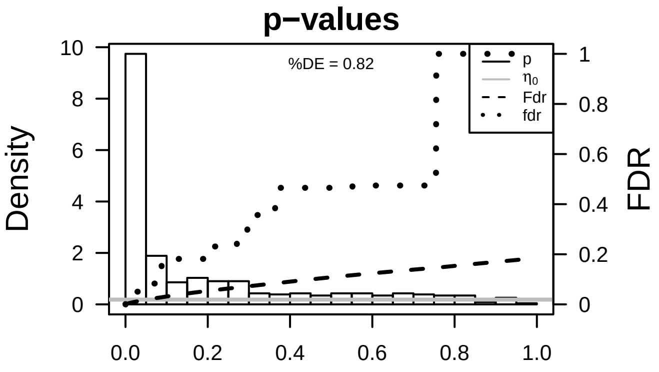
<fdr> = 0.6





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CRYZL1	−1.72	2e−16	3e−15	44 x 50	crystallin, zeta (quinone reductase)−like 1 [Source:HGNC Sy
2	GMFB	−1.61	2e−16	3e−15	46 x 49	glia maturation factor, beta [Source:HGNC Symbol;Acc:HGN
3	GPATCH4	−1.7	2e−16	3e−15	46 x 45	G patch domain containing 4 [Source:HGNC Symbol;Acc:HG
4	PLEKHA5	−1.48	2e−16	3e−15	50 x 50	pleckstrin homology domain containing, family A member 5 [
5	WIPI1	−1.95	2e−16	3e−15	47 x 49	WD repeat domain, phosphoinositide interacting 1 [Source:H
6	YIF1A	−1.7	2e−16	3e−15	47 x 50	Yip1 interacting factor homolog A (S. cerevisiae) [Source:HG
7	BABAM1	−1.44	7e−12	4e−10	43 x 47	BRISC and BRCA1 A complex member 1 [Source:HGNC Sy
8	BLOC1S2	−1.44	9e−12	6e−10	48 x 50	biogenesis of lysosomal organelles complex−1, subunit 2 [So
9	GARS	−1.18	2e−11	2e−09	45 x 50	glycyl−tRNA synthetase [Source:HGNC Symbol;Acc:HGNC:4
10	MLX	−1.45	4e−11	2e−09	44 x 49	MLX, MAX dimerization protein [Source:HGNC Symbol;Acc:
11	FYTTD1	−1.44	6e−11	6e−09	45 x 50	forty−two−three domain containing 1 [Source:HGNC Symbol;
12	SC5D	−1.43	1e−10	6e−09	43 x 48	sterol−C5−desaturase [Source:HGNC Symbol;Acc:HGNC:10
13	PYCR1	−0.93	2e−10	6e−09	46 x 50	pyrroline−5−carboxylate reductase 1 [Source:HGNC Symbol;
14	APRT	−0.82	3e−10	9e−09	49 x 50	adenine phosphoribosyltransferase [Source:HGNC Symbol;A
15	DNAJB1	−1.4	5e−10	9e−09	46 x 49	DnaJ (Hsp40) homolog, subfamily B, member 1 [Source:HG
16	EEF2	−0.97	5e−10	2e−07	45 x 46	eukaryotic translation elongation factor 2 [Source:HGNC Sym
17	XRN1	−1.36	3e−09	2e−07	47 x 45	5'−3' exoribonuclease 1 [Source:HGNC Symbol;Acc:HGNC:3
18	RFT1	1.5	5e−09	3e−07	50 x 50	RFT1 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:H
19	MRPS28	−1.32	2e−08	3e−07	45 x 50	mitochondrial ribosomal protein S28 [Source:HGNC Symbol;
20	AARSD1	−1.23	2e−08	3e−07	44 x 50	alanyl−tRNA synthetase domain containing 1 [Source:HGNC



D3_mel

Local Summary

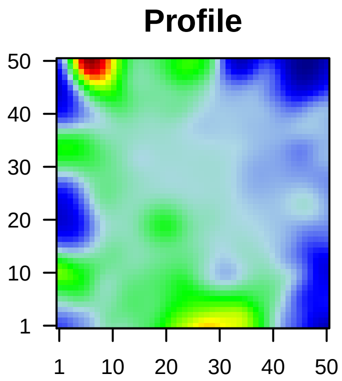
%DE = 0.85
metagenes = 6
genes = 108
genes in genesets = 108

genes with fdr < 0.1 = 69 (14 + / 55 −)
genes with fdr < 0.05 = 49 (8 + / 41 −)
genes with fdr < 0.01 = 32 (5 + / 27 −)

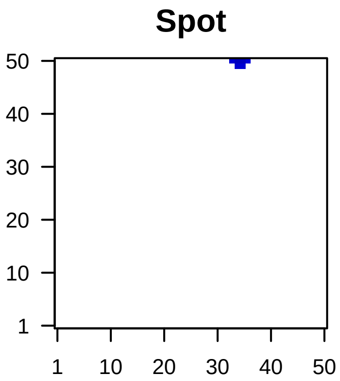
<r> metagenes = 0.97
<r> genes = 0.1

<FC> = −0.38
<shrinkage−t> = −6.38
<p−value> = 0
<fdr> = 0.58

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	PDCD6IP	−1.77	2e−16	2e−15	33 x 50	programmed cell death 6 interacting protein [Source:HGNC S
2	ZNF644	−1.65	2e−16	2e−15	36 x 50	zinc finger protein 644 [Source:HGNC Symbol;Acc:HGNC:29
3	NUP98	−1.57	1e−14	1e−13	34 x 50	nucleoporin 98kDa [Source:HGNC Symbol;Acc:HGNC:8068]
4	CHID1	−1.56	2e−14	2e−11	33 x 50	chitinase domain containing 1 [Source:HGNC Symbol;Acc:H
5	SRPK1	−1.34	9e−13	2e−11	34 x 50	SRSF protein kinase 1 [Source:HGNC Symbol;Acc:HGNC:11
6	DUSP6	−1.26	2e−12	5e−11	34 x 50	dual specificity phosphatase 6 [Source:HGNC Symbol;Acc:H
7	PRMT5	−1.48	6e−12	3e−10	34 x 50	protein arginine methyltransferase 5 [Source:HGNC Symbol;
8	TAF7	−1.46	2e−11	1e−09	35 x 50	TAF7 RNA polymerase II, TATA box binding protein (TBP)−as
9	PMPCB	−1.21	1e−10	1e−09	33 x 50	peptidase (mitochondrial processing) beta [Source:HGNC Sy
10	TANK	−1.42	2e−10	8e−06	34 x 50	TRAF family member−associated NFKB activator [Source:HG
11	ALG6	−1.15	8e−07	8e−06	35 x 50	ALG6, alpha−1,3−glucosyltransferase [Source:HGNC Symbo
12	ORMDL2	−1.2	1e−06	2e−05	34 x 50	ORMDL sphingolipid biosynthesis regulator 2 [Source:HGNC
13	PIGN	−1.17	3e−06	2e−05	36 x 50	phosphatidylinositol glycan anchor biosynthesis, class N [Sou
14	C1orf27	−1.14	4e−06	3e−05	34 x 50	chromosome 1 open reading frame 27 [Source:HGNC Symb
15	TMEM126B	−1.15	5e−06	3e−05	35 x 50	transmembrane protein 126B [Source:HGNC Symbol;Acc:HG
16	RBM22	−1.13	7e−06	1e−03	34 x 49	RNA binding motif protein 22 [Source:HGNC Symbol;Acc:HG
17	TULP3	0.92	1e−04	1e−03	35 x 50	tubby like protein 3 [Source:HGNC Symbol;Acc:HGNC:12425
18	PRRC1	−0.95	2e−04	1e−03	35 x 50	proline−rich coiled−coil 1 [Source:HGNC Symbol;Acc:HGNC:
19	WDR11	0.93	3e−04	1e−03	33 x 50	WD repeat domain 11 [Source:HGNC Symbol;Acc:HGNC:13
20	DHDDS	−0.91	4e−04	1e−03	34 x 50	dehydrodolichyl diphosphate synthase [Source:HGNC Symb

p−values