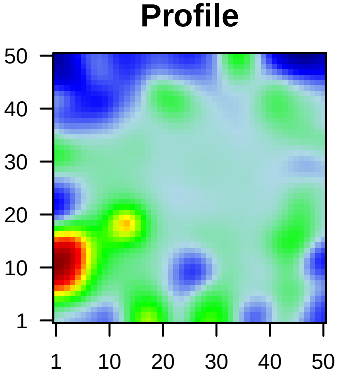
E5_mel

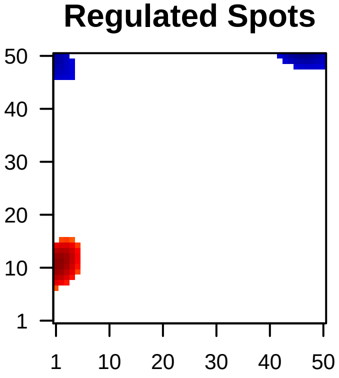
Global Summary

%DE = 0.22
genes with fdr < 0.2 = 2797 (1627 + / 1170 −)
genes with fdr < 0.1 = 2224 (1308 + / 916 −)
genes with fdr < 0.05 = 1947 (1145 + / 802 −)
genes with fdr < 0.01 = 1225 (723 + / 502 −)

genes in genesets = 14839

<FC> = 0
<shrinkage−t> = −0.05
<p−value> = 0.07
<fdr> = 0.78



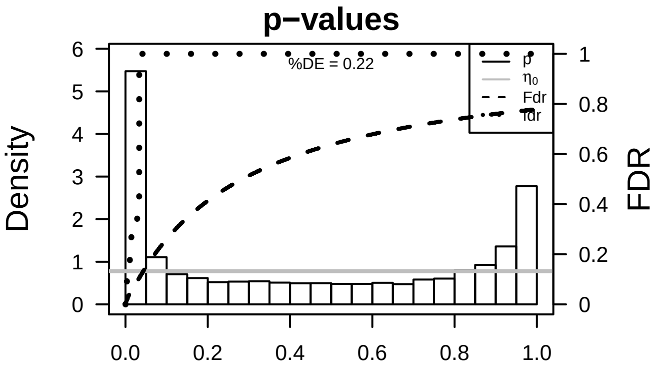


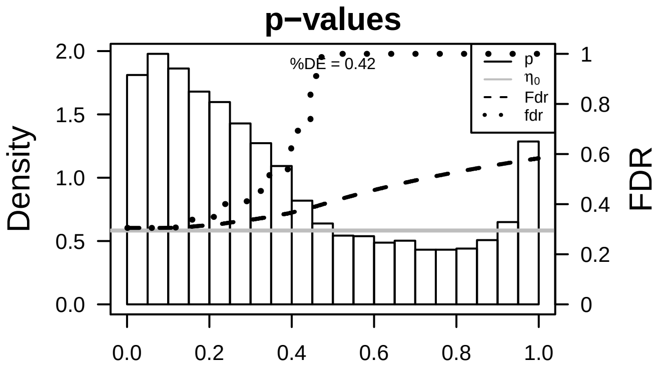
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ABCE1	−1.54	2e−16	6e−14	50 x 48	ATP−binding cassette, sub−family E (OABP), member 1 [Sou
2	ACTL6A	−1.79	2e−16	6e−14	4 x 50	actin−like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
3	ALG3	−1.63	2e−16	6e−14	48 x 50	ALG3, alpha−1,3− mannosyltransferase [Source:HGNC Symb
4	ARHGAP8	1.46	2e−16	6e−14	1 x 43	Rho GTPase activating protein 8 [Source:HGNC Symbol;Acc:
5	C11orf30	−1.35	2e−16	6e−14	16 x 50	chromosome 11 open reading frame 30 [Source:HGNC Symb
6	CDC42BPA	−1.21	2e−16	6e−14	50 x 38	CDC42 binding protein kinase alpha (DMPK−like) [Source:HC
7	CEP57	−1.34	2e−16	6e−14	5 x 46	centrosomal protein 57kDa [Source:HGNC Symbol;Acc:HGN
8	CEP97	1.96	2e−16	6e−14	2 x 47	centrosomal protein 97kDa [Source:HGNC Symbol;Acc:HGN
9	CLDND1	−1.82	2e−16	6e−14	28 x 50	claudin domain containing 1 [Source:HGNC Symbol;Acc:HGN
10	CRYZL1	−1.72	2e−16	6e−14	44 x 50	crystallin, zeta (quinone reductase)−like 1 [Source:HGNC Syr
11	DCUN1D5	−0.95	2e−16	6e−14	23 x 12	DCN1, defective in cullin neddylation 1, domain containing 5 [
12	FH	−1.6	2e−16	6e−14	5 x 39	fumarate hydratase [Source:HGNC Symbol;Acc:HGNC:3700]
13	HAUS1	−1.62	2e−16	6e−14	1 x 50	HAUS augmin−like complex, subunit 1 [Source:HGNC Symbo
14	HBS1L	−1.89	2e−16	6e−14	3 x 44	HBS1−like translational GTPase [Source:HGNC Symbol;Acc:
15	HERPUD1	−1.32	2e−16	6e−14	50 x 42	homocysteine−inducible, endoplasmic reticulum stress−induc
16	HNRNPR	−1.13	2e−16	6e−14	12 x 46	heterogeneous nuclear ribonucleoprotein R [Source:HGNC S
17	ICT1	−1.6	2e−16	6e−14	1 x 26	immature colon carcinoma transcript 1 [Source:HGNC Symbo
18	IMP4	−1.68	2e−16	6e−14	2 x 39	IMP4, U3 small nucleolar ribonucleoprotein [Source:HGNC S
19	MRPL3	−1.84	2e−16	6e−14	50 x 37	mitochondrial ribosomal protein L3 [Source:HGNC Symbol;Ac
20	MTRR	−1.64	2e−16	6e−14	1 x 26	5−methyltetrahydrofolate−homocysteine methyltransferase re

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset
Overexpressed				
1	4.14	0.007	2188	Lymphoma HOPP_Poised_promoter
2	4.08	0.007	3383	Colon Cancer EnhWk2_Colon
3	4.06	0.007	3396	Lymphoma HOPP_Repressed
4	3.96	0.008	393	GSEA C2 FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
5	3.85	0.008	376	GSEA C2 OSMAN_BLADDER_CANCER_UP
6	3.64	0.010	2984	CC integral component of membrane
7	3.57	0.011	301	GSEA C2 MULLIGHAN_NPM1_SIGNATURE_3_UP
8	3.54	0.011	232	GSEA C2 HUTTMANN_B_CLL_POOR_SURVIVAL_UP
9	3.53	0.011	57	GSEA C2 LANDIS_BREAST_CANCER_PROGRESSION_DN
10	3.51	0.011	995	GSEA C2 GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_DN
11	3.51	0.011	23	TF Tissue VAQUERIZAS_Trachea
12	3.5	0.011	4	GSEA C2 KERLEY_RESPONSE_TO_CISPLATIN_DN
13	3.5	0.011	112	GSEA C2 KEGG_LYSOSOME
14	3.46	0.012	238	GSEA C2 ZHOU_INFLAMMATORY_RESPONSE_FIMA_DN
15	3.45	0.012	3897	Colon Cancer Quies1_Colon
16	3.45	0.012	10	GSEA C2 CHASSOT_SKIN_WOUND
17	3.41	0.012	23	BP negative regulation of smooth muscle cell proliferation
18	3.38	0.013	76	CC cell projection
19	3.37	0.013	13	BP melanin biosynthetic process
20	3.34	0.013	16	BP nitrogen compound metabolic process
Underexpressed				
1	−7.43	8e−04	724	GSEA C2 PUJANA_CHEK2_PCC_NETWORK
2	−7.17	1e−03	1251	GSEA C2 DODD_NASOPHARYNGEAL_CARCINOMA_DN
3	−6.95	1e−03	1460	GSEA C2 PUJANA_BRCA1_PCC_NETWORK
4	−6.91	1e−03	1192	GSEA C2 KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
5	−6.44	1e−03	748	Colon Cancer Pentrack_CRC_TCGA_corr_R_normal_DN
6	−6.26	2e−03	834	GSEA C2 LEE_BMP2_TARGETS_DN
7	−6.18	2e−03	388	GSEA C2 REACTOME_CELL_CYCLE
8	−6.07	2e−03	562	GSEA C2 CAIRO_HEPATOBLASTOMA_CLASSES_UP
9	−6.01	2e−03	648	Colon Cancer Pentrack_CRC_TCGA_group.over_C_normal_DN
10	−5.95	2e−03	188	HM HALLMARK_MYC_TARGETS_V1
11	−5.91	2e−03	756	GSEA C2 WEI_MYCN_TARGETS_WITH_E_BOX
12	−5.86	2e−03	301	GSEA C2 REACTOME_CELL_CYCLE_MITOTIC
13	−5.78	2e−03	478	GSEA C2 STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
14	−5.57	2e−03	412	BP mitotic cell cycle
15	−5.49	3e−03	609	GSEA C2 RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIA
16	−5.34	3e−03	2577	CC nucleoplasm
17	−5.34	3e−03	181	GSEA C2 REACTOME_DNA_REPLICATION
18	−5.28	3e−03	183	GSEA C2 BOYAULT_LIVER_CANCER_SUBCLASS_G3_UP
19	−5.27	3e−03	408	GSEA C2 ZHANG_BREAST_CANCER_PROGENITORS_UP
20	−5.16	3e−03	312	GSEA C2 WONG_EMBRYONIC_STEM_CELL_CORE





E5_mel

Local Summary

%DE = 0.77

metagenes = 41

genes = 462

genes in genesets = 459

genes with fdr < 0.1 = 275 (256 + / 19 −)

genes with fdr < 0.05 = 243 (230 + / 13 −)

genes with fdr < 0.01 = 180 (173 + / 7 −)

<r> metagenes = 0.85

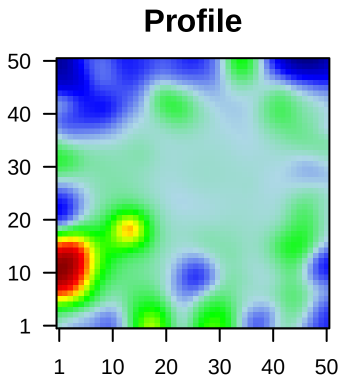
<r> genes = 0.09

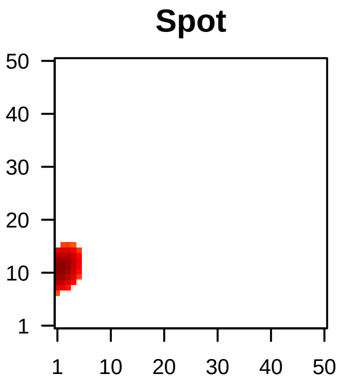
<FC> = 0.52

<shrinkage−t> = 8.25

<p−value> = 0

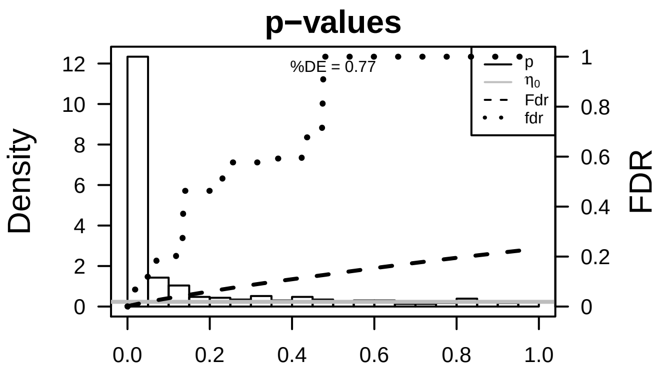
<fdr> = 0.46


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	SAT1	0.87	2e−16	2e−14	1 x 11	spermidine/spermine N1−acetyltransferase 1 [Source:HGNC
2	LYRM9	1.85	2e−13	2e−11	1 x 12	LYR motif containing 9 [Source:HGNC Symbol;Acc:HGNC:27
3	TAPBPL	1.83	4e−13	4e−11	3 x 13	TAP binding protein−like [Source:HGNC Symbol;Acc:HGNC:
4	SLC26A4	1.8	8e−13	2e−10	2 x 15	solute carrier family 26 (anion exchanger), member 4 [Source
5	LCMT2	1.75	3e−12	1e−09	3 x 13	leucine carboxyl methyltransferase 2 [Source:HGNC Symbol;
6	C1orf54	1.7	1e−11	1e−09	1 x 11	chromosome 1 open reading frame 54 [Source:HGNC Symbo
7	SCRN2	1.68	2e−11	1e−09	5 x 15	secernin 2 [Source:HGNC Symbol;Acc:HGNC:30381]
8	ATP6V1E2	1.67	3e−11	1e−09	5 x 12	ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E2 [S
9	SLC25A14	1.66	4e−11	3e−09	4 x 14	solute carrier family 25 (mitochondrial carrier, brain), member
10	ANGPTL2	1.64	7e−11	3e−09	3 x 13	angiopoietin−like 2 [Source:HGNC Symbol;Acc:HGNC:490]
11	FEZ1	1.62	1e−10	4e−09	1 x 7	fasciculation and elongation protein zeta 1 (zygin I) [Source:H
12	SMAD1	1.61	1e−10	3e−08	4 x 16	SMAD family member 1 [Source:HGNC Symbol;Acc:HGNC:6
13	ZNF18	1.57	4e−10	3e−08	2 x 8	zinc finger protein 18 [Source:HGNC Symbol;Acc:HGNC:129
14	PLA2G4B	1.55	8e−10	6e−08	3 x 9	phospholipase A2, group IVB (cytosolic) [Source:HGNC Sym
15	FZD3	1.52	1e−09	9e−08	4 x 13	frizzled class receptor 3 [Source:HGNC Symbol;Acc:HGNC:4
16	ERCC8	1.5	2e−09	2e−07	1 x 15	excision repair cross−complementation group 8 [Source:HGN
17	MTA3	1.48	4e−09	3e−07	1 x 8	metastasis associated 1 family, member 3 [Source:HGNC Sy
18	MSANTD3−TI	1.45	8e−09	3e−07	1 x 12	MSANTD3−TMEFF1 readthrough [Source:HGNC Symbol;Ac
19	TKTL1	1.44	1e−08	3e−07	4 x 15	transketolase−like 1 [Source:HGNC Symbol;Acc:HGNC:1183
20	BBS5	1.42	1e−08	3e−07	1 x 11	Bardet−Biedl syndrome 5 [Source:HGNC Symbol;Acc:HGNC


p−values

E5_mel

Local Summary

%DE = 0.72

metagenes = 19

genes = 278

genes in genesets = 277

genes with fdr < 0.1 = 147 (37 + / 110 −)

genes with fdr < 0.05 = 131 (33 + / 98 −)

genes with fdr < 0.01 = 80 (18 + / 62 −)

<r> metagenes = 0.96

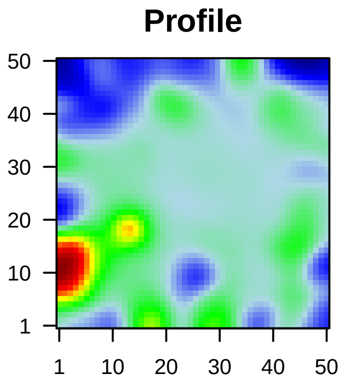
<r> genes = 0.23

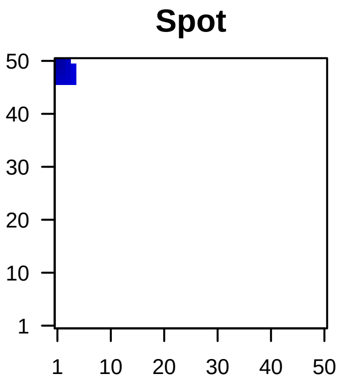
<FC> = −0.26

<shrinkage−t> = −4.17

<p−value> = 0.01

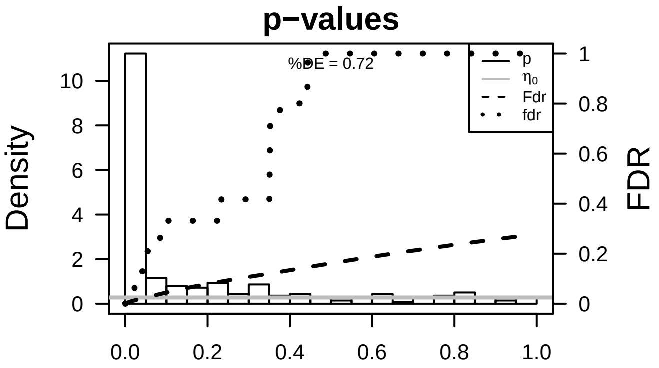
<fdr> = 0.55





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CEP97	1.96	2e−16	3e−15	2 x 47	centrosomal protein 97kDa [Source:HGNC Symbol;Acc:HGN
2	HAUS1	−1.62	2e−16	3e−15	1 x 50	HAUS augmin−like complex, subunit 1 [Source:HGNC Symbo
3	PAICS	−1.54	2e−16	3e−15	1 x 46	phosphoribosylaminoimidazole carboxylase, phosphoribosyla
4	TMEM97	−1.66	2e−16	3e−15	1 x 48	transmembrane protein 97 [Source:HGNC Symbol;Acc:HGN
5	UCP2	−1.62	2e−16	3e−15	2 x 46	uncoupling protein 2 (mitochondrial, proton carrier) [Source:H
6	POLR3K	−1.58	2e−15	2e−13	1 x 46	polymerase (RNA) III (DNA directed) polypeptide K, 12.3 kDa
7	SNX5	−1.45	4e−15	6e−08	4 x 46	sorting nexin 5 [Source:HGNC Symbol;Acc:HGNC:14969]
8	GMPS	−1.36	8e−10	3e−07	1 x 48	guanine monphosphate synthase [Source:HGNC Symbol;Acc
9	SMCHD1	−1.33	4e−09	3e−07	1 x 48	structural maintenance of chromosomes flexible hinge domai
10	CKLF	−1.3	1e−08	3e−07	3 x 49	chemokine−like factor [Source:HGNC Symbol;Acc:HGNC:13
11	NUP107	−0.86	1e−08	3e−07	2 x 48	nucleoporin 107kDa [Source:HGNC Symbol;Acc:HGNC:2991
12	GLA	1.41	2e−08	3e−07	4 x 46	galactosidase, alpha [Source:HGNC Symbol;Acc:HGNC:429
13	EXOSC9	−1.29	2e−08	4e−06	1 x 50	exosome component 9 [Source:HGNC Symbol;Acc:HGNC:91
14	HAT1	−1.02	2e−07	4e−06	1 x 50	histone acetyltransferase 1 [Source:HGNC Symbol;Acc:HGN
15	CENPK	−1.22	2e−07	4e−06	3 x 50	centromere protein K [Source:HGNC Symbol;Acc:HGNC:294
16	NUBP2	−1.22	2e−07	4e−06	1 x 46	nucleotide binding protein 2 [Source:HGNC Symbol;Acc:HGN
17	C19orf48	−1.21	2e−07	9e−06	1 x 50	chromosome 19 open reading frame 48 [Source:HGNC Symb
18	MTHFD2	−1.07	4e−07	9e−06	3 x 47	methylenetetrahydrofolate dehydrogenase (NADP+ depende
19	HAUS8	1.26	5e−07	6e−05	3 x 50	HAUS augmin−like complex, subunit 8 [Source:HGNC Symbo
20	RBBP8	−1.16	2e−06	6e−05	1 x 49	retinoblastoma binding protein 8 [Source:HGNC Symbol;Acc:



E5_mel

Local Summary

%DE = 0.77

metagenes = 23

genes = 350

genes in genesets = 349

genes with fdr < 0.1 = 186 (43 + / 143 −)

genes with fdr < 0.05 = 156 (33 + / 123 −)

genes with fdr < 0.01 = 85 (15 + / 70 −)

<r> metagenes = 0.85

<r> genes = 0.07

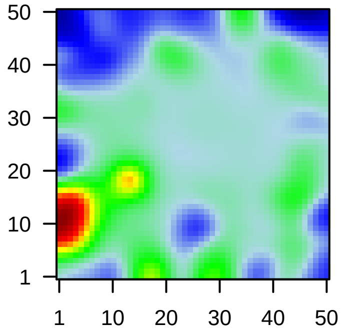
<FC> = −0.28

<shrinkage−t> = −4.82

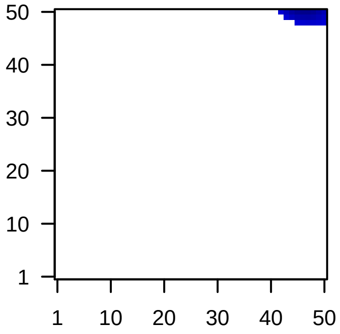
<p−value> = 0

<fdr> = 0.57

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ABCE1	−1.54	2e−16	4e−15	50 x 48	ATP−binding cassette, sub−family E (OABP), member 1 [Sou
2	ALG3	−1.63	2e−16	4e−15	48 x 50	ALG3, alpha−1,3− mannosyltransferase [Source:HGNC Sym
3	CRYZL1	−1.72	2e−16	4e−15	44 x 50	crystallin, zeta (quinone reductase)−like 1 [Source:HGNC Sy
4	RWDD2B	−1.8	2e−16	4e−15	46 x 50	RWD domain containing 2B [Source:HGNC Symbol;Acc:HGN
5	YIPF3	−1.33	2e−16	4e−15	45 x 50	Yip1 domain family, member 3 [Source:HGNC Symbol;Acc:H
6	ZFAND6	−1.57	4e−15	4e−13	43 x 50	zinc finger, AN1−type domain 6 [Source:HGNC Symbol;Acc:
7	CDC123	−1.55	9e−15	2e−11	46 x 50	cell division cycle 123 [Source:HGNC Symbol;Acc:HGNC:16
8	C19orf70	−1.5	3e−13	9e−11	48 x 50	chromosome 19 open reading frame 70 [Source:HGNC Sym
9	BLOC1S2	−1.47	2e−12	9e−11	48 x 50	biogenesis of lysosomal organelles complex−1, subunit 2 [So
10	DECR1	−1.47	3e−12	1e−09	47 x 50	2,4−dienoyl CoA reductase 1, mitochondrial [Source:HGNC
11	SMIM15	−1.44	2e−11	1e−09	42 x 50	small integral membrane protein 15 [Source:HGNC Symbol;A
12	CYSTM1	−1.09	4e−11	1e−09	47 x 50	cysteine−rich transmembrane module containing 1 [Source:H
13	UFM1	−1.43	6e−11	1e−09	50 x 49	ubiquitin−fold modifier 1 [Source:HGNC Symbol;Acc:HGNC:2
14	PAM16	−1.43	6e−11	3e−08	45 x 50	presequence translocase−associated motor 16 homolog (S.
15	KXD1	−1.36	1e−09	3e−08	44 x 50	KxDL motif containing 1 [Source:HGNC Symbol;Acc:HGNC:2
16	BSCL2	0.84	1e−09	3e−08	50 x 50	Berardinelli−Seip congenital lipodystrophy 2 (seipin) [Source:
17	NRD1	−1.36	1e−09	6e−08	50 x 50	nardilysin (N−arginine dibasic convertase) [Source:HGNC Sy
18	AARSD1	−1.29	2e−09	3e−07	44 x 50	alanyl−tRNA synthetase domain containing 1 [Source:HGNC
19	MRPS28	−1.32	8e−09	3e−07	45 x 50	mitochondrial ribosomal protein S28 [Source:HGNC Symbol;
20	WIPI1	−0.84	1e−08	3e−07	47 x 49	WD repeat domain, phosphoinositide interacting 1 [Source:H

p−values