E1_mel

Global Summary

%DE = 0.25

\# genes with fdr < 0.2 = 3180 (1887 + / 1293 −)

\# genes with fdr < 0.1 = 2679 (1656 + / 1023 −)

\# genes with fdr < 0.05 = 2228 (1403 + / 825 −)

\# genes with fdr < 0.01 = 1497 (965 + / 532 −)

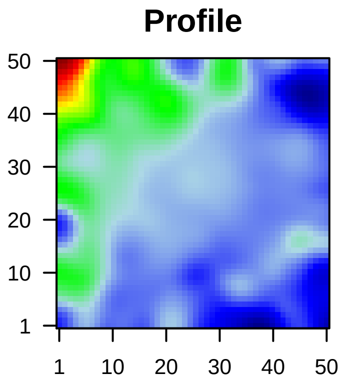
\# genes in genesets = 14839

<FC> = 0

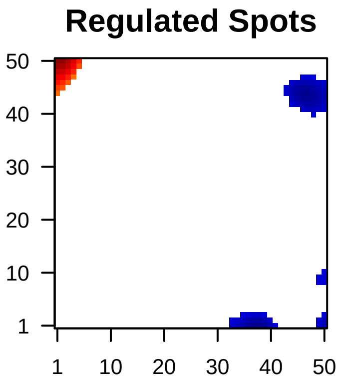
<shrinkage−t> = 0.04

<p−value> = 0.05

<fdr> = 0.75



Profile



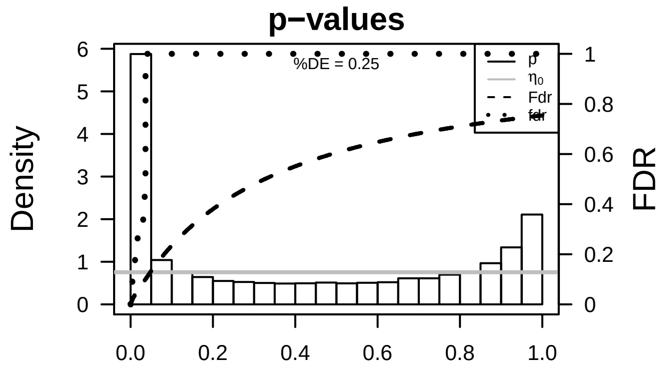
Regulated Spots

Global Genelist

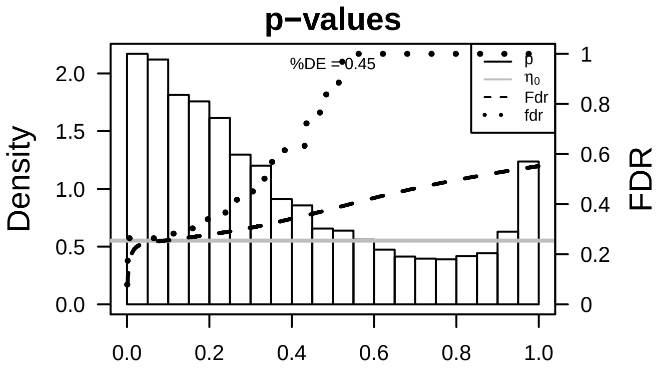
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ATP6AP2	−1.84	2e−16	9e−14	44 x 45	ATPase, H+ transporting, lysosomal accessory protein 2 [Sou
2	CALCOCO2	−1.34	2e−16	9e−14	26 x 50	calcium binding and coiled−coil domain 2 [Source:HGNC Syn
3	CCDC159	1.72	2e−16	9e−14	41 x 36	coiled−coil domain containing 159 [Source:HGNC Symbol;Ac
4	CCNDBP1	−1.41	2e−16	9e−14	1 x 21	cyclin D−type binding−protein 1 [Source:HGNC Symbol;Acc:
5	COMMD9	−1.46	2e−16	9e−14	31 x 1	COMM domain containing 9 [Source:HGNC Symbol;Acc:HGN
6	CRYAB	−1.82	2e−16	9e−14	50 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
7	DHRS7	−1.56	2e−16	9e−14	41 x 49	dehydrogenase/reductase (SDR family) member 7 [Source:H
8	ETNK1	−1.62	2e−16	9e−14	26 x 11	ethanolamine kinase 1 [Source:HGNC Symbol;Acc:HGNC:24
9	GLUL	−1.56	2e−16	9e−14	36 x 1	glutamate−ammonia ligase [Source:HGNC Symbol;Acc:HGN
10	HNRNPH2	−1.46	2e−16	9e−14	29 x 12	heterogeneous nuclear ribonucleoprotein H2 (H') [Source:HG
11	HSD17B4	−1.63	2e−16	9e−14	11 x 50	hydroxysteroid (17−beta) dehydrogenase 4 [Source:HGNC S
12	LIPG	1.72	2e−16	9e−14	38 x 50	lipase, endothelial [Source:HGNC Symbol;Acc:HGNC:6623]
13	MAD2L1BP	−1.79	2e−16	9e−14	37 x 49	MAD2L1 binding protein [Source:HGNC Symbol;Acc:HGNC:
14	MDM2	−0.72	2e−16	9e−14	46 x 37	MDM2 proto−oncogene, E3 ubiquitin protein ligase [Source:H
15	PHPT1	−1.79	2e−16	9e−14	50 x 35	phosphohistidine phosphatase 1 [Source:HGNC Symbol;Acc:
16	RAB11A	−1.82	2e−16	9e−14	36 x 50	RAB11A, member RAS oncogene family [Source:HGNC Sym
17	RAB34	−1.44	2e−16	9e−14	13 x 50	RAB34, member RAS oncogene family [Source:HGNC Symb
18	RFXANK	−1.45	2e−16	9e−14	38 x 50	regulatory factor X−associated ankyrin−containing protein [Sc
19	SERINC3	−1.21	2e−16	9e−14	50 x 41	serine incorporator 3 [Source:HGNC Symbol;Acc:HGNC:116
20	SF3B3	−1.49	2e−16	9e−14	12 x 49	splicing factor 3b, subunit 3, 130kDa [Source:HGNC Symbol;

Global Geneset Analysis

Rank	GSZ	p−value	#all		Geneset
Overexpressed					
1	12.87	9e−05	305	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
2	12.23	1e−04	197	HM	HALLMARK_E2F_TARGETS
3	11.86	1e−04	267	GSEA C2	ZHANG_TLX_TARGETS_60HR_DN
4	11.06	2e−04	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
5	10.96	2e−04	87	GSEA C2	ZHANG_TLX_TARGETS_UP
6	10.03	3e−04	81	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
7	9.92	3e−04	145	GSEA C2	CHANG_CYCLING_GENES
8	9.9	3e−04	1192	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
9	9.88	3e−04	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
10	9.87	3e−04	242	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
11	9.67	3e−04	700	GSEA C2	MARSON_BOUND_BY_E2F4_UNSTIMULATED
12	9.35	3e−04	436	GSEA C2	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
13	9.28	4e−04	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
14	9.28	4e−04	29	BP	DNA strand elongation involved in DNA replication
15	9.15	4e−04	58	GSEA C2	SONG_TARGETS_OF_IE86_CMV_PROTEIN
16	9.11	4e−04	388	GSEA C2	REACTOME_CELL_CYCLE
17	9.1	4e−04	27	GSEA C2	REACTOME_DNA_STRAND_ELONGATION
18	9.04	4e−04	155	GSEA C2	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
19	9.01	4e−04	68	GSEA C2	VERNELL_RETINOBLASTOMA_PATHWAY_UP
20	8.93	4e−04	301	GSEA C2	REACTOME_CELL_CYCLE_MITOTIC
Underexpressed					
1	−5.77	0.002	594	GSEA C2	WONG_ADULT_TISSUE_STEM_MODULE
2	−4.54	0.005	9	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
3	−4.48	0.005	88	GSEA C2	LIM_MAMMARY_LUMINAL_MATURE_DN
4	−4.36	0.006	221	GSEA C2	DANG_REGULATED_BY_MYC_DN
5	−4.3	0.006	12	CC	SMN complex
6	−4.18	0.006	12	BP	negative regulation of T cell receptor signaling pathway
7	−4.11	0.007	82	miRNA target	hsa−miR−630
8	−3.91	0.008	472	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
9	−3.79	0.009	35	GSEA C2	CHUNG_BLISTER_CYTOTOXICITY_DN
10	−3.79	0.009	27	GSEA C2	PID_IL8_CXCR2_PATHWAY
11	−3.77	0.009	87	HM	HALLMARK_INTERFERON_ALPHA_RESPONSE
12	−3.67	0.010	11	MF	structural constituent of eye lens
13	−3.65	0.010	171	GSEA C2	LI_WILMS_TUMOR_VS_FETAL_KIDNEY_1_UP
14	−3.64	0.010	130	BP	protein dephosphorylation
15	−3.64	0.010	126	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_ERYTHRO
16	−3.6	0.010	61	miRNA target	hsa−miR−219−5p
17	−3.6	0.011	14	BP	nucleotide metabolic process
18	−3.58	0.011	12	miRNA target	hsa−miR−639
19	−3.57	0.011	50	GSEA C2	LIU_SMARCA4_TARGETS
20	−3.55	0.011	59	MF	syntaxin binding



p−values



p−values

E1_mel

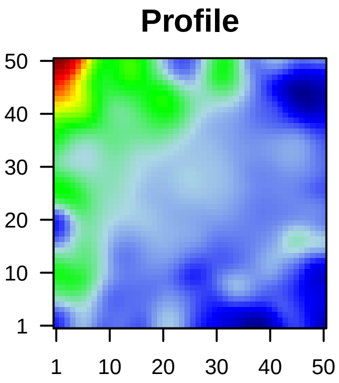
Local Summary

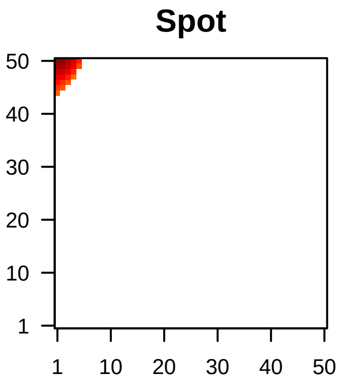
%DE = 0.86
metagenes = 24
genes = 377
genes in genesets = 375

genes with fdr < 0.1 = 273 (234 + / 39 −)
genes with fdr < 0.05 = 253 (217 + / 36 −)
genes with fdr < 0.01 = 199 (182 + / 17 −)

<r> metagenes = 0.9
<r> genes = 0.22

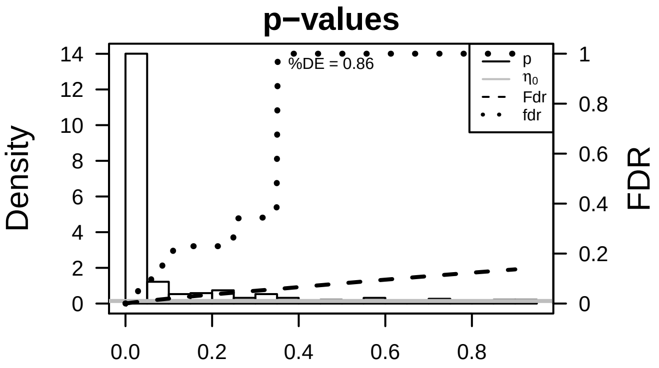
<FC> = 0.42
<shrinkage−t> = 6.79
<p−value> = 0
<fdr> = 0.36


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CHEK1	1.64	2e−15	2e−11	1 x 50	checkpoint kinase 1 [Source:HGNC Symbol;Acc:HGNC:1925
2	POLE	1.46	1e−12	2e−11	1 x 48	polymerase (DNA directed), epsilon, catalytic subunit [Source
3	DDX55	1.45	2e−12	2e−11	1 x 44	DEAD (Asp−Glu−Ala−Asp) box polypeptide 55 [Source:HGN
4	ZNF519	1.45	2e−12	2e−11	3 x 48	zinc finger protein 519 [Source:HGNC Symbol;Acc:HGNC:30
5	FIGNL1	1.45	2e−12	2e−10	2 x 50	fidgetin−like 1 [Source:HGNC Symbol;Acc:HGNC:13286]
6	GSTCD	1.41	6e−12	5e−10	1 x 49	glutathione S−transferase, C−terminal domain containing [So
7	PRIM1	1.39	2e−11	5e−10	1 x 50	primase, DNA, polypeptide 1 (49kDa) [Source:HGNC Symbol
8	NMRK2	1.3	2e−11	7e−10	1 x 44	nicotinamide riboside kinase 2 [Source:HGNC Symbol;Acc:H
9	CCDC150	1.36	4e−11	1e−09	5 x 50	coiled−coil domain containing 150 [Source:HGNC Symbol;Ac
10	TREX1	1.34	6e−11	3e−09	1 x 47	three prime repair exonuclease 1 [Source:HGNC Symbol;Acc
11	RRM2	1.32	1e−10	5e−09	5 x 50	ribonucleotide reductase M2 [Source:HGNC Symbol;Acc:HG
12	CKB	−1.22	3e−10	5e−09	2 x 47	creatine kinase, brain [Source:HGNC Symbol;Acc:HGNC:19
13	CEP97	1.22	3e−10	1e−08	2 x 47	centrosomal protein 97kDa [Source:HGNC Symbol;Acc:HGN
14	GSE1	1.27	7e−10	1e−08	1 x 47	Gse1 coiled−coil protein [Source:HGNC Symbol;Acc:HGNC:
15	POLA2	1.26	8e−10	1e−08	1 x 48	polymerase (DNA directed), alpha 2, accessory subunit [Sour
16	BRCA2	1.26	9e−10	1e−08	2 x 50	breast cancer 2, early onset [Source:HGNC Symbol;Acc:HGN
17	POLD3	1.15	1e−09	1e−08	2 x 50	polymerase (DNA−directed), delta 3, accessory subunit [Sour
18	SIN3A	1.25	1e−09	1e−08	1 x 49	SIN3 transcription regulator family member A [Source:HGNC
19	ANLN	1.24	2e−09	1e−08	5 x 50	anillin, actin binding protein [Source:HGNC Symbol;Acc:HGN
20	MYH10	0.61	3e−09	1e−08	1 x 44	myosin, heavy chain 10, non−muscle [Source:HGNC Symbol


p−values

E1_mel

Local Summary

%DE = 0.65

metagenes = 22

genes = 207

genes in genesets = 207

genes with fdr < 0.1 = 69 (11 + / 58 −)

genes with fdr < 0.05 = 66 (11 + / 55 −)

genes with fdr < 0.01 = 38 (6 + / 32 −)

<r> metagenes = 0.87

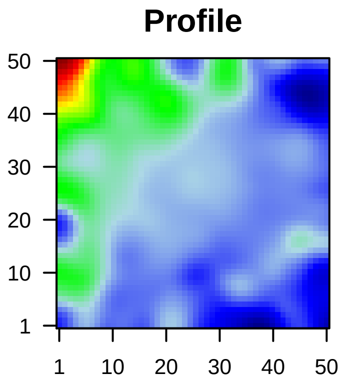
<r> genes = 0.08

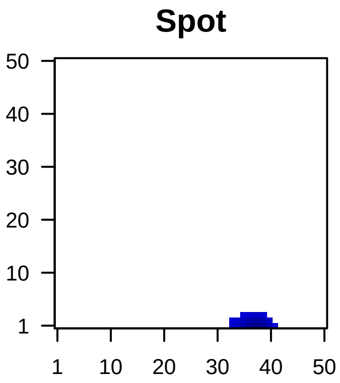
<FC> = −0.25

<shrinkage−t> = −3.94

<p−value> = 0.02

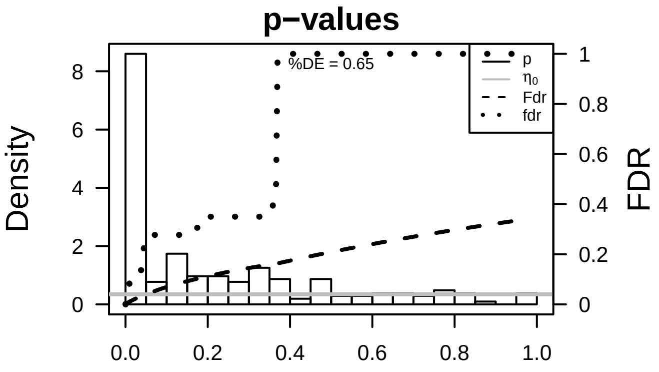
<fdr> = 0.64





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	GLUL	−1.56	2e−16	2e−14	36 x 1	glutamate−ammonia ligase [Source:HGNC Symbol;Acc:HGN
2	FAM127A	−1.27	4e−16	2e−13	37 x 1	family with sequence similarity 127, member A [Source:HGN
3	ITCH	−1.35	4e−15	2e−09	40 x 1	itchy E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:
4	UROD	−1.03	3e−11	2e−09	35 x 3	uroporphyrinogen decarboxylase [Source:HGNC Symbol;Acc
5	MSRB3	−1.23	6e−11	1e−07	37 x 1	methionine sulfoxide reductase B3 [Source:HGNC Symbol;Ac
6	CRK	−1.13	2e−09	1e−06	37 x 2	v−crk avian sarcoma virus CT10 oncogene homolog [Source:
7	BLCAP	−1.02	2e−08	2e−05	37 x 1	bladder cancer associated protein [Source:HGNC Symbol;Ac
8	MED31	−1.05	3e−07	5e−05	41 x 1	mediator complex subunit 31 [Source:HGNC Symbol;Acc:HG
9	ANXA11	−1	1e−06	5e−05	40 x 1	annexin A11 [Source:HGNC Symbol;Acc:HGNC:535]
10	OFD1	−0.98	2e−06	7e−05	38 x 1	oral−facial−digital syndrome 1 [Source:HGNC Symbol;Acc:H
11	SCARB2	−0.96	3e−06	1e−04	34 x 1	scavenger receptor class B, member 2 [Source:HGNC Symb
12	MAGED1	−0.86	5e−06	1e−04	39 x 1	melanoma antigen family D1 [Source:HGNC Symbol;Acc:HG
13	ACOT8	−0.91	7e−06	3e−04	34 x 1	acyl−CoA thioesterase 8 [Source:HGNC Symbol;Acc:HGNC:
14	PPFIBP1	0.9	1e−05	3e−04	40 x 2	PTPRF interacting protein, binding protein 1 (liprin beta 1) [S
15	CIR1	−0.89	1e−05	3e−04	41 x 1	corepressor interacting with RBPJ, 1 [Source:HGNC Symbol;
16	ST7L	−0.87	2e−05	3e−04	41 x 1	suppression of tumorigenicity 7 like [Source:HGNC Symbol;A
17	BAZ2B	−0.87	2e−05	7e−04	39 x 1	bromodomain adjacent to zinc finger domain, 2B [Source:HG
18	MAP3K7	−0.83	5e−05	7e−04	40 x 1	mitogen−activated protein kinase kinase kinase 7 [Source:HG
19	HSD17B12	−0.82	7e−05	7e−04	35 x 3	hydroxysteroid (17−beta) dehydrogenase 12 [Source:HGNC
20	BET1L	−0.81	8e−05	7e−04	37 x 1	Bet1 golgi vesicular membrane trafficking protein−like [Sourc



E1_mel

Local Summary

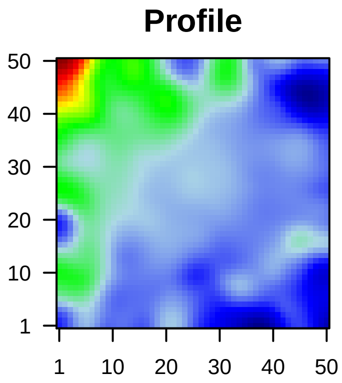
%DE = 0.73
metagenes = 5
genes = 147
genes in genesets = 147

genes with fdr < 0.1 = 71 (22 + / 49 −)
genes with fdr < 0.05 = 65 (20 + / 45 −)
genes with fdr < 0.01 = 41 (13 + / 28 −)

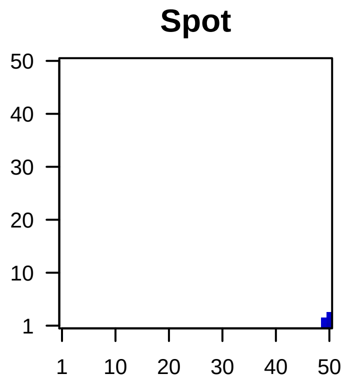
<r> metagenes = 1
<r> genes = 0.26

<FC> = −0.23
<shrinkage−t> = −3.88
<p−value> = 0
<fdr> = 0.56

Profile



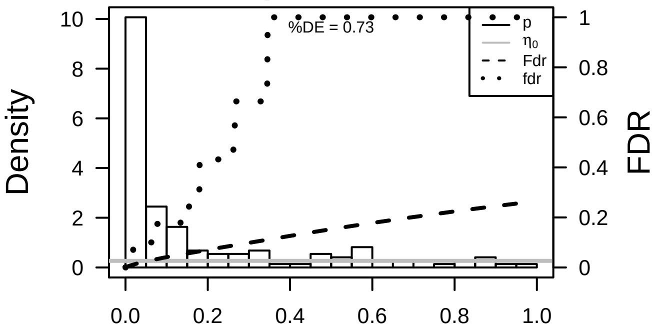
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CRYAB	−1.82	2e−16	3e−15	50 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
2	SNAP23	−1.58	2e−16	3e−15	50 x 1	synaptosomal−associated protein, 23kDa [Source:HGNC Sy
3	VIM	−1.63	2e−16	3e−15	50 x 2	vimentin [Source:HGNC Symbol;Acc:HGNC:12692]
4	STAM	−1.32	1e−12	1e−10	50 x 3	signal transducing adaptor molecule (SH3 domain and ITAM
5	LAMC1	−1.28	4e−12	3e−10	50 x 3	laminin, gamma 1 (formerly LAMB2) [Source:HGNC Symbol;
6	PLK2	−1.04	1e−11	2e−08	50 x 1	polo−like kinase 2 [Source:HGNC Symbol;Acc:HGNC:19699]
7	NOV	−1.2	5e−10	2e−07	50 x 1	nephroblastoma overexpressed [Source:HGNC Symbol;Acc:
8	CALD1	−0.77	5e−09	6e−07	50 x 1	caldesmon 1 [Source:HGNC Symbol;Acc:HGNC:1441]
9	UBE2E2	−1.12	3e−08	6e−07	50 x 1	ubiquitin−conjugating enzyme E2E 2 [Source:HGNC Symbol;
10	SRPX	−1.07	4e−08	3e−06	50 x 1	sushi−repeat containing protein, X−linked [Source:HGNC Sy
11	FN1	1.09	1e−07	2e−05	50 x 1	fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
12	EDIL3	−1.02	5e−07	3e−05	50 x 1	EGF−like repeats and discoidin I−like domains 3 [Source:HG
13	CDH19	−1	1e−06	2e−04	50 x 1	cadherin 19, type 2 [Source:HGNC Symbol;Acc:HGNC:1758]
14	FSTL1	−0.88	2e−05	2e−04	50 x 1	follistatin−like 1 [Source:HGNC Symbol;Acc:HGNC:3972]
15	RGS2	0.88	2e−05	2e−04	49 x 1	regulator of G−protein signaling 2 [Source:HGNC Symbol;Ac
16	KIAA0922	0.88	2e−05	3e−04	49 x 1	KIAA0922 [Source:HGNC Symbol;Acc:HGNC:29146]
17	PXDC1	0.86	3e−05	3e−04	50 x 1	PX domain containing 1 [Source:HGNC Symbol;Acc:HGNC:2
18	RHOBTB3	−0.85	4e−05	3e−04	50 x 1	Rho−related BTB domain containing 3 [Source:HGNC Symb
19	CAMK2D	−0.85	4e−05	1e−03	50 x 1	calcium/calmodulin−dependent protein kinase II delta [Sourc
20	PELO	−0.81	8e−05	1e−03	50 x 1	pelota homolog (Drosophila) [Source:HGNC Symbol;Acc:HG

p−values



E1_mel

Local Summary

%DE = 0.82

metagenes = 5

genes = 56

genes in genesets = 56

genes with fdr < 0.1 = 27 (6 + / 21 −)

genes with fdr < 0.05 = 23 (5 + / 18 −)

genes with fdr < 0.01 = 12 (4 + / 8 −)

<r> metagenes = 0.98

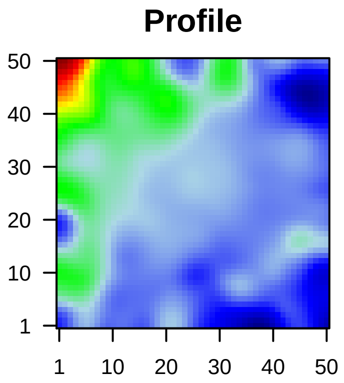
<r> genes = 0.1

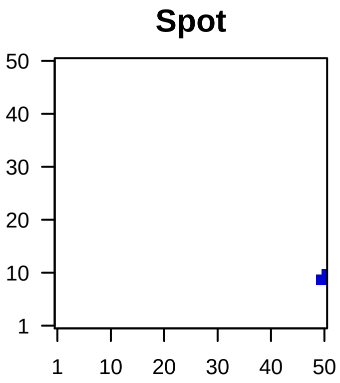
<FC> = −0.2

<shrinkage−t> = −3.13

<p−value> = 0.01

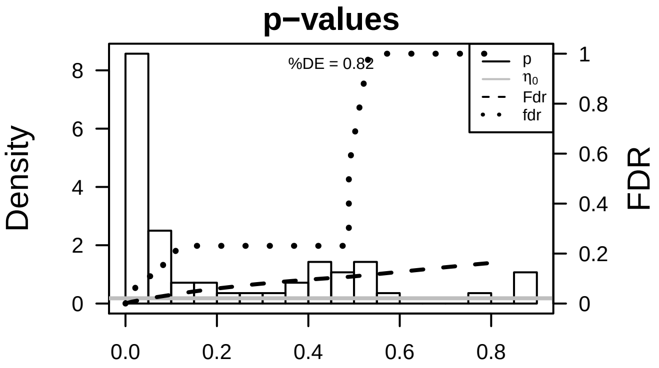
<fdr> = 0.61





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	SEC23B	−1.37	4e−14	9e−08	50 x 11	Sec23 homolog B (S. cerevisiae) [Source:HGNC Symbol;Acc
2	FBXO46	1.18	9e−09	6e−06	50 x 9	F−box protein 46 [Source:HGNC Symbol;Acc:HGNC:25069]
3	CORO1B	−1.02	7e−07	6e−06	50 x 10	coronin, actin binding protein, 1B [Source:HGNC Symbol;Acc
4	SOCS2	0.99	1e−06	6e−06	50 x 9	suppressor of cytokine signaling 2 [Source:HGNC Symbol;Ac
5	MRPL46	−0.98	2e−06	3e−05	50 x 11	mitochondrial ribosomal protein L46 [Source:HGNC Symbol;
6	CCDC57	0.91	4e−06	3e−05	50 x 11	coiled−coil domain containing 57 [Source:HGNC Symbol;Acc
7	RSL24D1	−0.88	7e−06	2e−04	50 x 11	ribosomal L24 domain containing 1 [Source:HGNC Symbol;A
8	EIF2B4	0.87	2e−05	1e−03	50 x 10	eukaryotic translation initiation factor 2B, subunit 4 delta, 67k
9	VPS8	−0.78	1e−04	1e−03	50 x 9	vacuolar protein sorting 8 homolog (S. cerevisiae) [Source:H
10	FLRT2	−0.73	3e−04	1e−03	50 x 10	fibronectin leucine rich transmembrane protein 2 [Source:HG
11	MYO18A	−0.73	4e−04	1e−03	50 x 10	myosin XVIIIA [Source:HGNC Symbol;Acc:HGNC:31104]
12	ZNF76	−0.72	5e−04	1e−03	50 x 11	zinc finger protein 76 [Source:HGNC Symbol;Acc:HGNC:131
13	GALE	−0.71	6e−04	1e−02	50 x 10	UDP−galactose−4−epimerase [Source:HGNC Symbol;Acc:H
14	TAF6	−0.6	4e−03	1e−02	50 x 11	TAF6 RNA polymerase II, TATA box binding protein (TBP)−as
15	ALG1	−0.59	4e−03	1e−02	50 x 10	ALG1, chitobiosyldiphosphodolichol beta−mannosyltransfera
16	MBD2	−0.58	4e−03	1e−02	50 x 10	methyl−CpG binding domain protein 2 [Source:HGNC Symbo
17	STK38L	−0.57	6e−03	1e−02	49 x 10	serine/threonine kinase 38 like [Source:HGNC Symbol;Acc:H
18	CLIC4	−0.52	6e−03	2e−02	50 x 9	chloride intracellular channel 4 [Source:HGNC Symbol;Acc:H
19	PRKAG1	−0.55	8e−03	3e−02	50 x 11	protein kinase, AMP−activated, gamma 1 non−catalytic subu
20	MAP4	−0.3	1e−02	3e−02	50 x 11	microtubule−associated protein 4 [Source:HGNC Symbol;Acc



E1_mel

Local Summary

%DE = 0.75

metagenes = 46

genes = 354

genes in genesets = 353

genes with fdr < 0.1 = 194 (49 + / 145 −)

genes with fdr < 0.05 = 154 (32 + / 122 −)

genes with fdr < 0.01 = 85 (17 + / 68 −)

<r> metagenes = 0.82

<r> genes = 0.07

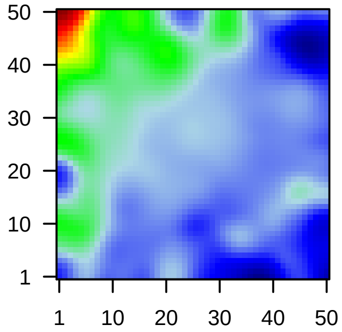
<FC> = −0.23

<shrinkage−t> = −3.83

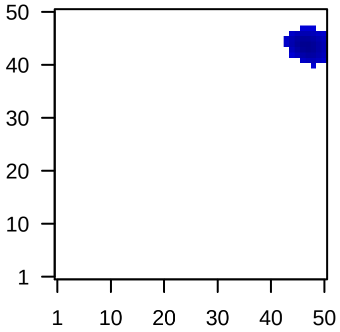
<p−value> = 0.01

<fdr> = 0.59

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ATP6AP2	−1.84	2e−16	1e−14	44 x 45	ATPase, H+ transporting, lysosomal accessory protein 2 [Sou
2	SERINC3	−1.21	2e−16	1e−14	50 x 41	serine incorporator 3 [Source:HGNC Symbol;Acc:HGNC:116
3	METTL5	−1.4	1e−14	1e−11	50 x 45	methyltransferase like 5 [Source:HGNC Symbol;Acc:HGNC:2
4	REXO2	−1.35	1e−13	5e−11	47 x 46	RNA exonuclease 2 [Source:HGNC Symbol;Acc:HGNC:1785
5	CNOT10	−1.27	1e−12	5e−11	46 x 45	CCR4−NOT transcription complex, subunit 10 [Source:HGNC
6	LARS	−0.94	1e−12	6e−11	46 x 44	leucyl−tRNA synthetase [Source:HGNC Symbol;Acc:HGNC:
7	LAMTOR4	−1.06	2e−12	2e−09	44 x 45	late endosomal/lysosomal adaptor, MAPK and MTOR activat
8	MRPS22	−1.26	2e−11	2e−09	47 x 43	mitochondrial ribosomal protein S22 [Source:HGNC Symbol;
9	TRIP12	−1.25	4e−11	2e−08	43 x 45	thyroid hormone receptor interactor 12 [Source:HGNC Symb
10	DNPH1	−1.18	2e−10	2e−08	50 x 43	2'−deoxynucleoside 5'−phosphate N−hydrolase 1 [Source:HG
11	DTD1	−1.16	5e−10	2e−08	49 x 46	D−tyrosyl−tRNA deacylase 1 [Source:HGNC Symbol;Acc:HG
12	NMD3	−1.11	6e−10	5e−08	50 x 41	NMD3 ribosome export adaptor [Source:HGNC Symbol;Acc:
13	PSMC4	−0.75	1e−09	2e−07	45 x 45	proteasome (prosome, macropain) 26S subunit, ATPase, 4 [S
14	ZNF146	−1.14	3e−09	5e−07	47 x 42	zinc finger protein 146 [Source:HGNC Symbol;Acc:HGNC:12
15	ABCD4	−1.15	9e−09	5e−07	50 x 45	ATP−binding cassette, sub−family D (ALD), member 4 [Sourc
16	IK	−1.03	2e−08	5e−07	50 x 41	IK cytokine, down−regulator of HLA II [Source:HGNC Symbol
17	UQCRC2	−0.69	2e−08	5e−06	46 x 45	ubiquinol−cytochrome c reductase core protein II [Source:HG
18	SECISBP2L	−1	9e−08	5e−06	47 x 41	SECIS binding protein 2−like [Source:HGNC Symbol;Acc:HG
19	C1orf52	−1.06	1e−07	1e−05	47 x 44	chromosome 1 open reading frame 52 [Source:HGNC Symb
20	CCDC53	−0.94	6e−07	1e−05	48 x 45	coiled−coil domain containing 53 [Source:HGNC Symbol;Acc

p−values