E3_mel

Global Summary

%DE = 0.2

genes with fdr < 0.2 = 2689 (1544 + / 1145 −)

genes with fdr < 0.1 = 2038 (1186 + / 852 −)

genes with fdr < 0.05 = 1650 (969 + / 681 −)

genes with fdr < 0.01 = 999 (586 + / 413 −)

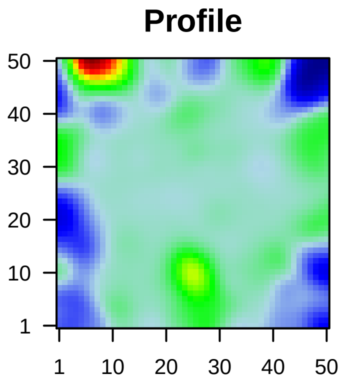
genes in genesets = 14839

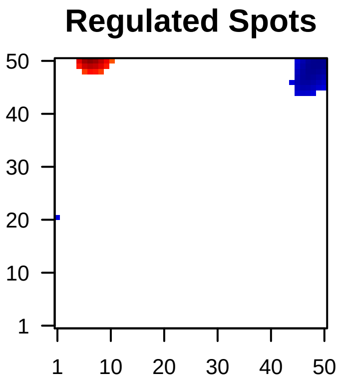
<FC> = 0

<shrinkage−t> = −0.03

<p−value> = 0.08

<fdr> = 0.8


Profile

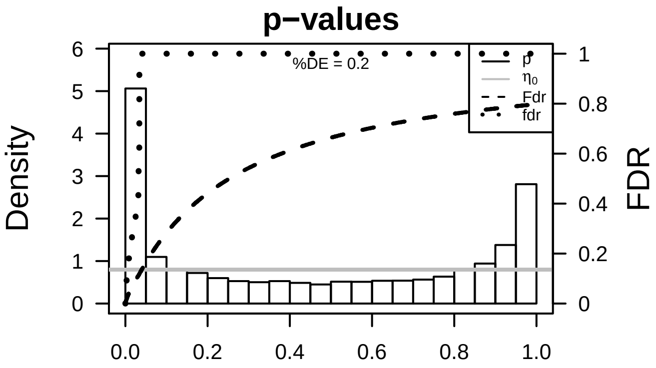

Regulated Spots

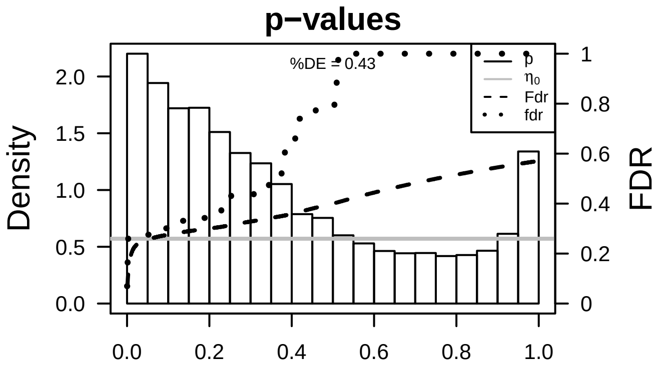
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	AP3S1	−1.41	2e−16	8e−14	1 x 39	adaptor−related protein complex 3, sigma 1 subunit [Source:H
2	ARHGAP8	−1.69	2e−16	8e−14	1 x 43	Rho GTPase activating protein 8 [Source:HGNC Symbol;Acc:
3	ATIC	−1.68	2e−16	8e−14	44 x 50	5−aminoimidazole−4−carboxamide ribonucleotide formyltrans
4	ATP1B3	−1.23	2e−16	8e−14	1 x 21	ATPase, Na+/K+ transporting, beta 3 polypeptide [Source:HG
5	BECN1	−1.79	2e−16	8e−14	49 x 15	beclin 1, autophagy related [Source:HGNC Symbol;Acc:HGN
6	BLVRB	−1.73	2e−16	8e−14	1 x 6	biliverdin reductase B [Source:HGNC Symbol;Acc:HGNC:106
7	C3orf14	2.29	2e−16	8e−14	14 x 14	chromosome 3 open reading frame 14 [Source:HGNC Symbo
8	CDKN3	1.57	2e−16	8e−14	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
9	CLK1	−1.69	2e−16	8e−14	50 x 40	CDC−like kinase 1 [Source:HGNC Symbol;Acc:HGNC:2068]
10	CMC1	−1.93	2e−16	8e−14	50 x 50	C−x(9)−C motif containing 1 [Source:HGNC Symbol;Acc:HGN
11	CRYAB	−1.82	2e−16	8e−14	50 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
12	CTSA	−0.97	2e−16	8e−14	7 x 19	cathepsin A [Source:HGNC Symbol;Acc:HGNC:9251]
13	DGUOK	−1.73	2e−16	8e−14	3 x 20	deoxyguanosine kinase [Source:HGNC Symbol;Acc:HGNC:2
14	EIF3H	−1.25	2e−16	8e−14	33 x 16	eukaryotic translation initiation factor 3, subunit H [Source:HG
15	EIF4A2	−1.63	2e−16	8e−14	50 x 11	eukaryotic translation initiation factor 4A2 [Source:HGNC Syn
16	FOS	−1.85	2e−16	8e−14	4 x 7	FBJ murine osteosarcoma viral oncogene homolog [Source:H
17	GRN	−1.3	2e−16	8e−14	46 x 48	granulin [Source:HGNC Symbol;Acc:HGNC:4601]
18	HSPA4	−1.38	2e−16	8e−14	6 x 8	heat shock 70kDa protein 4 [Source:HGNC Symbol;Acc:HGN
19	HTN1	2.15	2e−16	8e−14	10 x 49	histatin 1 [Source:HGNC Symbol;Acc:HGNC:5283]
20	MRPL12	−1.35	2e−16	8e−14	1 x 40	mitochondrial ribosomal protein L12 [Source:HGNC Symbol;A

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	16.04	4e−05	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
2	13.63	1e−03	16	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
3	13.56	8e−05	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
4	12.3	1e−04	165	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
5	12.24	1e−04	145	GSEA C2	CHANG_CYCLING_GENES
6	11.65	1e−04	45	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
7	11.27	2e−04	291	GSEA C2	HORIUCHI_WTAP_TARGETS_DN
8	11.21	2e−04	54	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
9	11.07	2e−04	99	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
10	10.81	2e−04	201	GSEA C2	WHITFIELD_CELL_CYCLE_G2_M
11	10.64	2e−04	118	GSEA C2	ODONNELL_TFRC_TARGETS_DN
12	10.59	2e−04	72	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
13	10.56	2e−04	96	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
14	10.43	2e−04	162	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
15	10.42	2e−04	124	GSEA C2	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
16	10.12	2e−04	110	GSEA C2	WHITEFORD_PEDIATRIC_CANCER_MARKERS
17	9.92	3e−04	270	GSEA C2	BASAKI_YBX1_TARGETS_UP
18	9.88	3e−04	82	GSEA C2	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA2_UP
19	9.69	3e−04	155	GSEA C2	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
20	9.61	3e−04	93	GSEA C2	KONG_E2F3_TARGETS
Underexpressed					
1	−5.75	0.002	68	GSEA C2	REACTOME_METABOLISM_OF_NUCLEOTIDES
2	−5.71	0.002	840	Chr	Chr 17
3	−5.41	0.003	32	BP	purine nucleobase metabolic process
4	−5.34	0.003	31	GSEA C2	REACTOME_PURINE_METABOLISM
5	−5.15	0.003	15	BP	purine nucleotide biosynthetic process
6	−5.08	0.003	221	Chr	Chr 18
7	−4.93	0.004	142	GSEA C2	KEGG_PURINE_METABOLISM
8	−4.79	0.004	6	GSEA C2	ISHIDA_TARGETS_OF_SYT_SSX_FUSIONS
9	−4.65	0.005	74	BP	nucleobase−containing small molecule metabolic process
10	−4.51	0.005	12	BP	purine ribonucleoside monophosphate biosynthetic process
11	−4.49	0.005	11	GSEA C2	REACTOME_PURINE_RIBONUCLEOSIDE_MONOPHOSPHATE_
12	−4.46	0.005	11	GSEA C2	TURJANSKI_MAPK1_AND_MAPK2_TARGETS
13	−4.35	0.006	340	GSEA C2	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
14	−4.31	0.006	729	GSEA C2	GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_DN
15	−4.25	0.006	15	BP	nucleoside metabolic process
16	−4.25	0.006	9653	Colon Cancer	Ecb_Colon
17	−4.21	0.006	38	GSEA C2	IRITANI_MAD1_TARGETS_DN
18	−4.2	0.006	277	BP	translation
19	−4.1	0.007	25	GSEA C2	REACTOME_PERK_REGULATED_GENE_EXPRESSION
20	−4.08	0.007	147	BP	tRNA metabolic process


p−values


p−values

E3_mel

Local Summary

%DE = 0.94

metagenes = 17

genes = 245

genes in genesets = 245

genes with fdr < 0.1 = 219 (192 + / 27 −)

genes with fdr < 0.05 = 191 (175 + / 16 −)

genes with fdr < 0.01 = 153 (148 + / 5 −)

<r> metagenes = 0.97

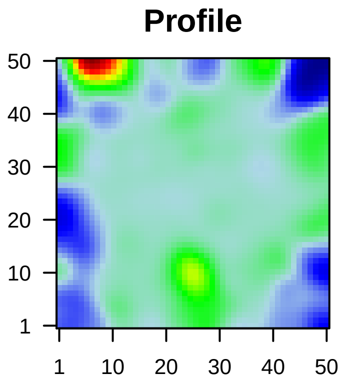
<r> genes = 0.3

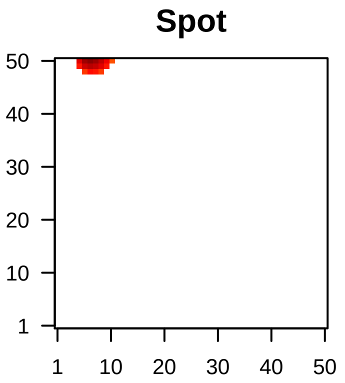
<FC> = 0.71

<shrinkage−t> = 11.44

<p−value> = 0

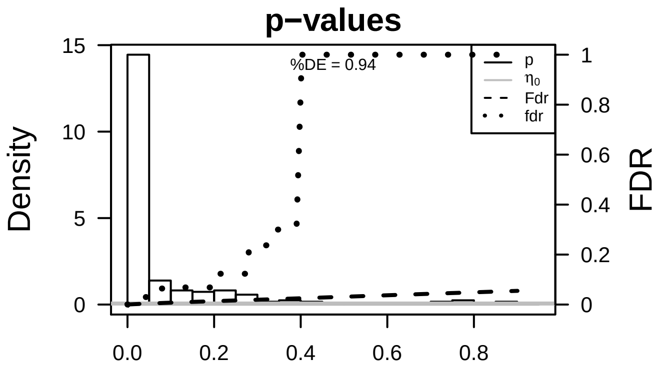
<fdr> = 0.33





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CDKN3	1.57	2e−16	2e−15	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;
2	HTN1	2.15	2e−16	2e−15	10 x 49	histatin 1 [Source:HGNC Symbol;Acc:HGNC:5283]
3	CCNB1	2.05	7e−16	6e−15	7 x 50	cyclin B1 [Source:HGNC Symbol;Acc:HGNC:1579]
4	PLK1	2.05	1e−15	9e−15	8 x 50	polo−like kinase 1 [Source:HGNC Symbol;Acc:HGNC:9077]
5	NEK2	2.04	2e−15	1e−13	8 x 50	NIMA−related kinase 2 [Source:HGNC Symbol;Acc:HGNC:77
6	KIF20A	1.98	1e−14	7e−12	7 x 50	kinesin family member 20A [Source:HGNC Symbol;Acc:HGN
7	SMTN	1.85	5e−13	3e−11	9 x 50	smoothelin [Source:HGNC Symbol;Acc:HGNC:11126]
8	PTTG1	1.11	3e−12	8e−11	7 x 50	pituitary tumor−transforming 1 [Source:HGNC Symbol;Acc:H
9	OIP5	1.75	9e−12	8e−11	7 x 50	Opa interacting protein 5 [Source:HGNC Symbol;Acc:HGNC:
10	FAM64A	1.73	1e−11	1e−10	7 x 50	family with sequence similarity 64, member A [Source:HGNC
11	CDC20	1.7	3e−11	1e−10	6 x 50	cell division cycle 20 [Source:HGNC Symbol;Acc:HGNC:172
12	KIAA1524	1.7	3e−11	9e−10	6 x 50	KIAA1524 [Source:HGNC Symbol;Acc:HGNC:29302]
13	DLGAP5	1.66	1e−10	2e−09	7 x 50	discs, large (Drosophila) homolog−associated protein 5 [Sour
14	HJURP	1.61	3e−10	2e−09	6 x 50	Holliday junction recognition protein [Source:HGNC Symbol;
15	ECT2	1.59	5e−10	2e−09	6 x 50	epithelial cell transforming 2 [Source:HGNC Symbol;Acc:HG
16	CENPF	1.49	5e−10	2e−09	6 x 50	centromere protein F, 350/400kDa [Source:HGNC Symbol;Ac
17	SPC24	1.57	8e−10	2e−09	5 x 50	SPC24, NDC80 kinetochore complex component [Source:HG
18	STMN1	0.63	9e−10	2e−09	5 x 50	stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]
19	NCAPG	1.57	9e−10	2e−09	6 x 50	non−SMC condensin I complex, subunit G [Source:HGNC Sy
20	CDCA3	1.57	9e−10	2e−09	6 x 50	cell division cycle associated 3 [Source:HGNC Symbol;Acc:H



E3_mel

Local Summary

%DE = 0.94

metagenes = 1

genes = 66

genes in genesets = 66

genes with fdr < 0.1 = 50 (11 + / 39 −)

genes with fdr < 0.05 = 40 (6 + / 34 −)

genes with fdr < 0.01 = 29 (3 + / 26 −)

<r> metagenes = NA

<r> genes = 0.24

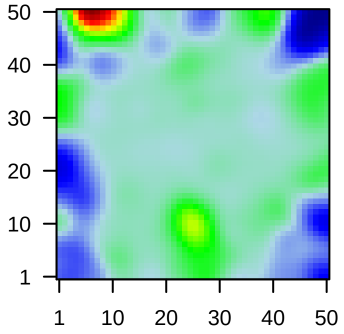
<FC> = −0.34

<shrinkage−t> = −6.63

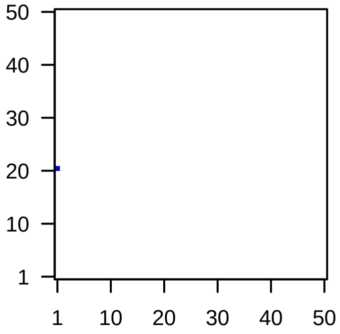
<p−value> = 0.01

<fdr> = 0.53

Profile



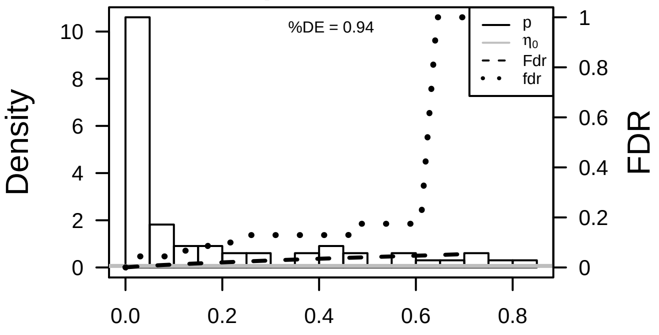
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ATP1B3	−1.23	2e−16	9e−16	1 x 21	ATPase, Na+/K+ transporting, beta 3 polypeptide [Source:HG
2	MOK	−1.31	2e−08	8e−08	1 x 21	MOK protein kinase [Source:HGNC Symbol;Acc:HGNC:9833
3	SQSTM1	−0.64	4e−08	4e−07	1 x 21	sequestosome 1 [Source:HGNC Symbol;Acc:HGNC:11280]
4	MAP1LC3B2	−1.24	2e−07	4e−07	1 x 21	microtubule−associated protein 1 light chain 3 beta 2 [Source
5	NXT1	−1.24	2e−07	7e−07	1 x 21	nuclear transport factor 2−like export factor 1 [Source:HGNC
6	FTH1	−0.52	4e−07	7e−06	1 x 21	ferritin, heavy polypeptide 1 [Source:HGNC Symbol;Acc:HGN
7	SLC9A3R1	−1.18	2e−06	2e−05	1 x 21	solute carrier family 9, subfamily A (NHE3, cation proton anti
8	SYNGR2	−1	7e−06	3e−05	1 x 21	synaptogyrin 2 [Source:HGNC Symbol;Acc:HGNC:11499]
9	MAP1LC3B	−0.89	2e−05	3e−05	1 x 21	microtubule−associated protein 1 light chain 3 beta [Source:
10	TMEM123	−0.44	2e−05	8e−05	1 x 21	transmembrane protein 123 [Source:HGNC Symbol;Acc:HGN
11	UCK2	−0.87	4e−05	4e−04	1 x 21	uridine−cytidine kinase 2 [Source:HGNC Symbol;Acc:HGNC:
12	UBQLN1	−0.9	1e−04	4e−04	1 x 21	ubiquilin 1 [Source:HGNC Symbol;Acc:HGNC:12508]
13	VAPA	−0.62	2e−04	6e−04	1 x 21	VAMP (vesicle−associated membrane protein)−associated pr
14	GUK1	−0.43	4e−04	6e−04	1 x 21	guanylate kinase 1 [Source:HGNC Symbol;Acc:HGNC:4693]
15	SURF4	−0.75	7e−04	6e−04	1 x 21	surfeit 4 [Source:HGNC Symbol;Acc:HGNC:11476]
16	TMEM18	−0.87	7e−04	6e−04	1 x 21	transmembrane protein 18 [Source:HGNC Symbol;Acc:HGN
17	COX5A	−0.43	8e−04	2e−03	1 x 21	cytochrome c oxidase subunit Va [Source:HGNC Symbol;Acc
18	APPL1	0.73	2e−03	2e−03	1 x 21	adaptor protein, phosphotyrosine interaction, PH domain and
19	UNC119	−0.8	2e−03	2e−03	1 x 21	unc−119 homolog (C. elegans) [Source:HGNC Symbol;Acc:
20	PFN1	−0.39	2e−03	3e−03	1 x 21	profilin 1 [Source:HGNC Symbol;Acc:HGNC:8881]

p−values



E3_mel

Local Summary

%DE = 0.74

metagenes = 41

genes = 481

genes in genesets = 479

genes with fdr < 0.1 = 211 (37 + / 174 −)

genes with fdr < 0.05 = 177 (28 + / 149 −)

genes with fdr < 0.01 = 127 (14 + / 113 −)

<r> metagenes = 0.85

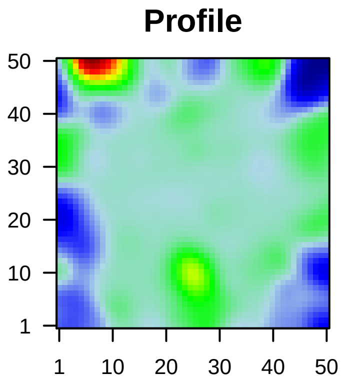
<r> genes = 0.07

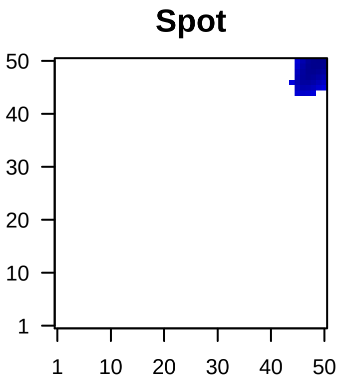
<FC> = −0.33

<shrinkage−t> = −5.6

<p−value> = 0.01

<fdr> = 0.6





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CMC1	−1.93	2e−16	6e−15	50 x 50	C−x(9)−C motif containing 1 [Source:HGNC Symbol;Acc:HGN
2	GRN	−1.3	2e−16	6e−15	46 x 48	granulin [Source:HGNC Symbol;Acc:HGNC:4601]
3	PSMC4	−1.41	2e−16	6e−15	45 x 45	proteasome (prosome, macropain) 26S subunit, ATPase, 4 [S
4	TDRD12	−1.86	2e−16	6e−15	45 x 46	tudor domain containing 12 [Source:HGNC Symbol;Acc:HGN
5	TPGS2	−1.88	2e−16	6e−15	47 x 50	tubulin polyglutamylase complex subunit 2 [Source:HGNC Sy
6	NHP2L1	−1.12	3e−15	2e−13	48 x 48	NHP2 non−histone chromosome protein 2−like 1 (S. cerevisi
7	NUPR1	−1.58	4e−15	7e−12	45 x 50	nuclear protein, transcriptional regulator, 1 [Source:HGNC Sy
8	AUP1	−1.51	9e−14	7e−12	46 x 47	ancient ubiquitous protein 1 [Source:HGNC Symbol;Acc:HGN
9	TMEM219	−1.54	1e−13	8e−11	45 x 50	transmembrane protein 219 [Source:HGNC Symbol;Acc:HGN
10	C19orf70	−1.5	8e−13	1e−10	48 x 50	chromosome 19 open reading frame 70 [Source:HGNC Symb
11	CTSB	−1.2	3e−12	1e−10	46 x 46	cathepsin B [Source:HGNC Symbol;Acc:HGNC:2527]
12	PPP2R1A	−1.17	3e−12	7e−10	45 x 47	protein phosphatase 2, regulatory subunit A, alpha [Source:H
13	CNPY2	−0.95	9e−12	4e−09	45 x 48	canopy FGF signaling regulator 2 [Source:HGNC Symbol;Acc
14	GMFB	−1.29	5e−11	4e−09	46 x 49	glia maturation factor, beta [Source:HGNC Symbol;Acc:HGN
15	DDIT3	−1.44	7e−11	8e−09	50 x 50	DNA−damage−inducible transcript 3 [Source:HGNC Symbol;
16	TMEM205	−1.43	1e−10	8e−09	45 x 48	transmembrane protein 205 [Source:HGNC Symbol;Acc:HGN
17	CNOT10	−1.42	2e−10	7e−08	46 x 45	CCR4−NOT transcription complex, subunit 10 [Source:HGNC
18	FUNDC2	−1.38	1e−09	7e−08	45 x 45	FUN14 domain containing 2 [Source:HGNC Symbol;Acc:HGN
19	FRYL	−1.37	1e−09	7e−07	50 x 50	FRY−like [Source:HGNC Symbol;Acc:HGNC:29127]
20	RIOK3	−1.31	2e−08	7e−07	47 x 49	RIO kinase 3 [Source:HGNC Symbol;Acc:HGNC:11451]