G5_mel

Global Summary

%DE = 0.24

genes with fdr < 0.2 = 3191 (1886 + / 1305 −)

genes with fdr < 0.1 = 2577 (1568 + / 1009 −)

genes with fdr < 0.05 = 2149 (1325 + / 824 −)

genes with fdr < 0.01 = 1466 (922 + / 544 −)

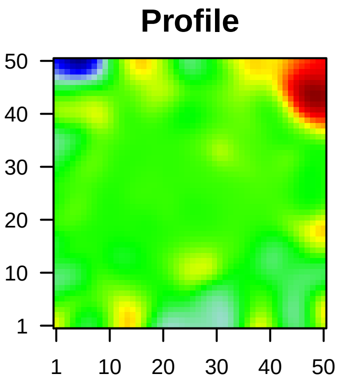
genes in genesets = 14839

<FC> = 0

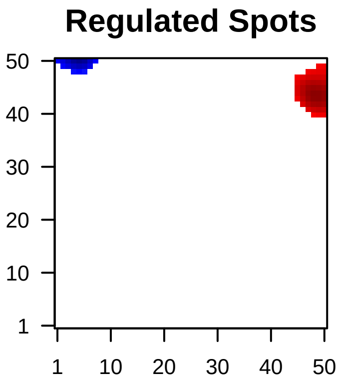
<shrinkage−t> = 0.07

<p−value> = 0.05

<fdr> = 0.76



Profile



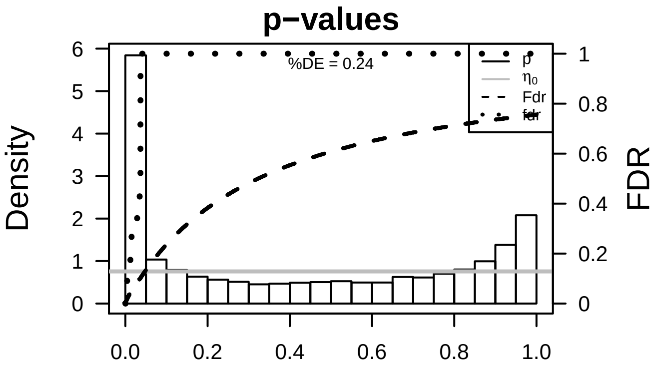
Regulated Spots

Global Genelist

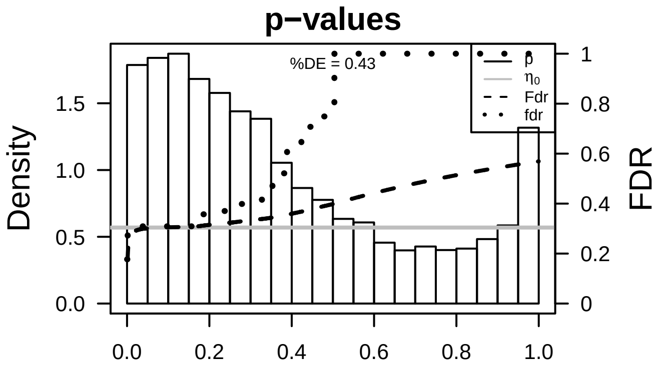
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ANXA7	−1.55	2e−16	1e−13	25 x 48	annexin A7 [Source:HGNC Symbol;Acc:HGNC:545]
2	ARHGAP8	−1.12	2e−16	1e−13	1 x 43	Rho GTPase activating protein 8 [Source:HGNC Symbol;Acc:
3	ARL8B	−1.41	2e−16	1e−13	1 x 33	ADP−ribosylation factor−like 8B [Source:HGNC Symbol;Acc:
4	BCAP29	−1.13	2e−16	1e−13	41 x 47	B−cell receptor−associated protein 29 [Source:HGNC Symbo
5	BLVRA	−1.44	2e−16	1e−13	2 x 14	biliverdin reductase A [Source:HGNC Symbol;Acc:HGNC:10
6	CA14	−1.53	2e−16	1e−13	1 x 46	carbonic anhydrase XIV [Source:HGNC Symbol;Acc:HGNC:1
7	CDKN3	−1.65	2e−16	1e−13	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
8	GLB1	−1.46	2e−16	1e−13	40 x 50	galactosidase, beta 1 [Source:HGNC Symbol;Acc:HGNC:429
9	HINFP	1.76	2e−16	1e−13	16 x 25	histone H4 transcription factor [Source:HGNC Symbol;Acc:H
10	LUZP6	1.73	2e−16	1e−13	50 x 49	leucine zipper protein 6 [Source:HGNC Symbol;Acc:HGNC:3
11	NNT	−1.13	2e−16	1e−13	6 x 47	nicotinamide nucleotide transhydrogenase [Source:HGNC Sy
12	PABPC4	−1.64	2e−16	1e−13	50 x 7	poly(A) binding protein, cytoplasmic 4 (inducible form) [Sourc
13	PSG4	1.67	2e−16	1e−13	12 x 6	pregnancy specific beta−1−glycoprotein 4 [Source:HGNC Sy
14	RAB27A	−1.43	2e−16	1e−13	1 x 11	RAB27A, member RAS oncogene family [Source:HGNC Sym
15	RAB34	−1.44	2e−16	1e−13	13 x 50	RAB34, member RAS oncogene family [Source:HGNC Symb
16	RFXANK	−1.45	2e−16	1e−13	38 x 50	regulatory factor X−associated ankyrin−containing protein [Sc
17	TCEAL8	−1.46	2e−16	1e−13	26 x 50	transcription elongation factor A (SII)−like 8 [Source:HGNC S
18	TK1	−1.55	2e−16	1e−13	4 x 50	thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:HGN
19	TXNDC12	−1.36	2e−16	1e−13	34 x 10	thioredoxin domain containing 12 (endoplasmic reticulum) [Sc
20	UCP2	−1.49	2e−16	1e−13	2 x 46	uncoupling protein 2 (mitochondrial, proton carrier) [Source:H

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	5.99	0.002	8580	Colon Cancer	TxWk_Colon
2	5.56	0.002	9027	Colon Cancer	Tx_Colon
3	5.11	0.003	1365	MF	RNA binding
4	4.81	0.004	21	CC	mitochondrial small ribosomal subunit
5	4.8	0.004	10	BP	histone mRNA catabolic process
6	4.69	0.004	162	BP	ribosome biogenesis
7	4.65	0.005	5184	Lymphoma	HOPP_Txn_transition
8	4.64	0.005	9482	Colon Cancer	TcgaA_Colon
9	4.59	0.005	756	GSEA C2	WEI_MYCN_TARGETS_WITH_E_BOX
10	4.45	0.005	213	GSEA C2	WONG_MITOCHONDRIA_GENE_MODULE
11	4.35	0.006	9330	Brain	Overlap_fetal_midbrain_ReprPC
12	4.3	0.006	1007	MF	poly(A) RNA binding
13	4.19	0.006	5940	Brain	Overlap_fetal_midbrain_HetRpts
14	4.11	0.007	277	BP	translation
15	4.09	0.007	748	Colon Cancer	Pentrack_CRC_TCGA_corr_R_normal_DN
16	4.02	0.007	71	MF	structural constituent of ribosome
17	4.01	0.007	72	GSEA C2	LEE_AGING_NEOCORTEX_UP
18	3.74	0.009	9013	Brain	Overlap_fetal_midbrain_K9K27me3
19	3.74	0.009	338	GSEA C2	BASAKI_YBX1_TARGETS_DN
20	3.73	0.009	10	GSEA C2	REACTOME_IRAK1_RECRUITS_IKK_COMPLEX
Underexpressed					
1	−12.26	1e−04	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
2	−10.53	2e−04	145	GSEA C2	CHANG_CYCLING_GENES
3	−9.98	3e−04	305	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
4	−9.67	3e−04	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
5	−9.46	3e−04	54	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
6	−9.44	1e−02	16	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
7	−9.12	4e−04	242	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
8	−9.05	4e−04	96	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
9	−8.93	4e−04	81	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
10	−8.81	4e−04	99	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
11	−8.47	5e−04	116	GSEA C2	MISSIAGLIA_REGULATED_BY_METHYLATION_DN
12	−8.46	5e−04	99	GSEA C2	BURTON_ADIPOGENESIS_3
13	−8.19	6e−04	52	GSEA C2	TANG_SENESCENCE_TP53_TARGETS_DN
14	−8.15	6e−04	327	GSEA C2	BLUM_RESPONSE_TO_SALIRASIB_DN
15	−8.14	6e−04	162	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
16	−7.98	6e−04	197	HM	HALLMARK_E2F_TARGETS
17	−7.82	7e−04	110	GSEA C2	WHITEFORD_PEDIATRIC_CANCER_MARKERS
18	−7.78	7e−04	155	GSEA C2	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
19	−7.75	7e−04	291	GSEA C2	HORIUCHI_WTAP_TARGETS_DN
20	−7.72	7e−04	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP



p−values



p−values

G5_mel

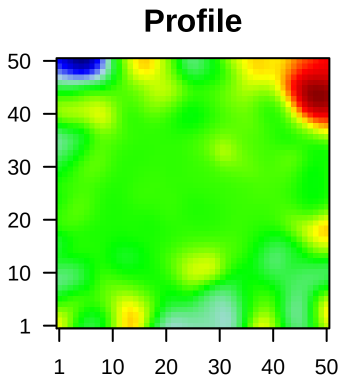
Local Summary

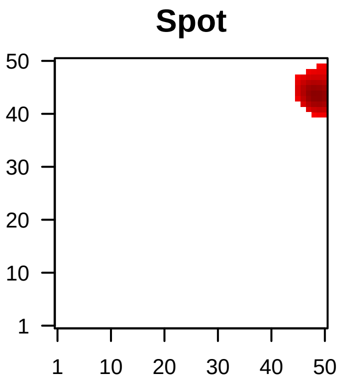
%DE = 0.72
metagenes = 48
genes = 428
genes in genesets = 427

genes with fdr < 0.1 = 240 (192 + / 48 −)
genes with fdr < 0.05 = 199 (162 + / 37 −)
genes with fdr < 0.01 = 155 (131 + / 24 −)

<r> metagenes = 0.8
<r> genes = 0.06

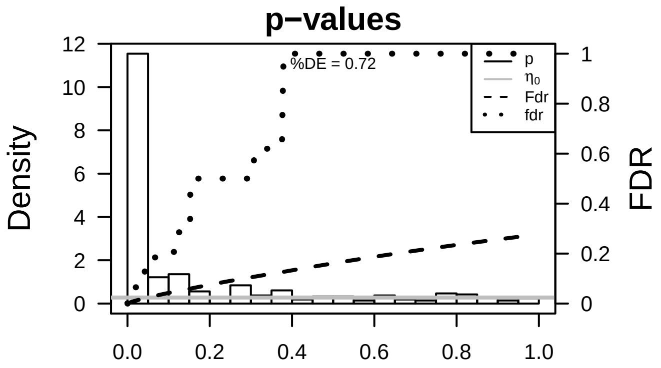
<FC> = 0.26
<shrinkage−t> = 4.27
<p−value> = 0
<fdr> = 0.5





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	LUZP6	1.73	2e−16	3e−14	50 x 49	leucine zipper protein 6 [Source:HGNC Symbol;Acc:HGNC:
2	IL18R1	1.59	6e−15	2e−11	46 x 44	interleukin 18 receptor 1 [Source:HGNC Symbol;Acc:HGNC:
3	LRRC23	1.5	2e−13	2e−11	50 x 43	leucine rich repeat containing 23 [Source:HGNC Symbol;Acc
4	CDAN1	1.49	3e−13	9e−11	49 x 44	codanin 1 [Source:HGNC Symbol;Acc:HGNC:1713]
5	PACRGL	1.45	1e−12	1e−10	47 x 44	PARK2 co−regulated−like [Source:HGNC Symbol;Acc:HGNC
6	C1S	1.43	2e−12	3e−09	49 x 45	complement component 1, s subcomponent [Source:HGNC
7	SPG7	1.35	3e−11	3e−09	50 x 40	spastic paraplegia 7 (pure and complicated autosomal recess
8	TOMM40L	1.34	5e−11	3e−09	47 x 45	translocase of outer mitochondrial membrane 40 homolog (y
9	PXYLP1	1.33	7e−11	7e−09	46 x 44	2−phosphoxylose phosphatase 1 [Source:HGNC Symbol;Acc
10	CTSK	1.31	1e−10	2e−08	49 x 41	cathepsin K [Source:HGNC Symbol;Acc:HGNC:2536]
11	EGFL7	1.29	3e−10	6e−08	49 x 42	EGF−like−domain, multiple 7 [Source:HGNC Symbol;Acc:HG
12	MFSD10	1.25	7e−10	1e−07	47 x 45	major facilitator superfamily domain containing 10 [Source:H
13	ZUFSP	1.23	2e−09	3e−07	50 x 46	zinc finger with UFM1−specific peptidase domain [Source:HG
14	ING4	1.2	4e−09	5e−07	47 x 43	inhibitor of growth family, member 4 [Source:HGNC Symbol;
15	HELB	1.17	9e−09	5e−07	47 x 42	helicase (DNA) B [Source:HGNC Symbol;Acc:HGNC:17196]
16	RNF146	1.16	1e−08	5e−07	48 x 42	ring finger protein 146 [Source:HGNC Symbol;Acc:HGNC:21
17	ABCF3	1.15	2e−08	5e−07	50 x 47	ATP−binding cassette, sub−family F (GCN20), member 3 [So
18	COQ10B	−1.08	2e−08	7e−07	50 x 49	coenzyme Q10 homolog B (S. cerevisiae) [Source:HGNC Sy
19	ABCD4	1.1	3e−08	7e−07	50 x 45	ATP−binding cassette, sub−family D (ALD), member 4 [Sourc
20	ATG101	1.12	4e−08	7e−07	50 x 48	autophagy related 101 [Source:HGNC Symbol;Acc:HGNC:25



G5_mel

Local Summary

%DE = 0.77

metagenes = 17

genes = 280

genes in genesets = 280

genes with fdr < 0.1 = 174 (26 + / 148 −)

genes with fdr < 0.05 = 171 (26 + / 145 −)

genes with fdr < 0.01 = 129 (17 + / 112 −)

<r> metagenes = 0.94

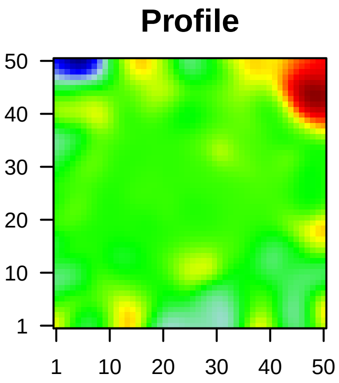
<r> genes = 0.34

<FC> = −0.37

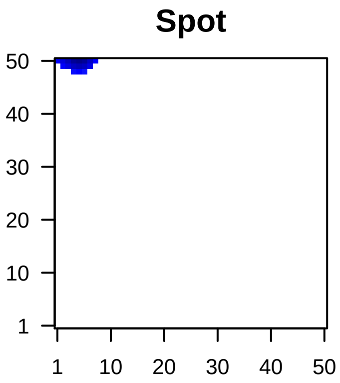
<shrinkage−t> = −5.84

<p−value> = 0

<fdr> = 0.43



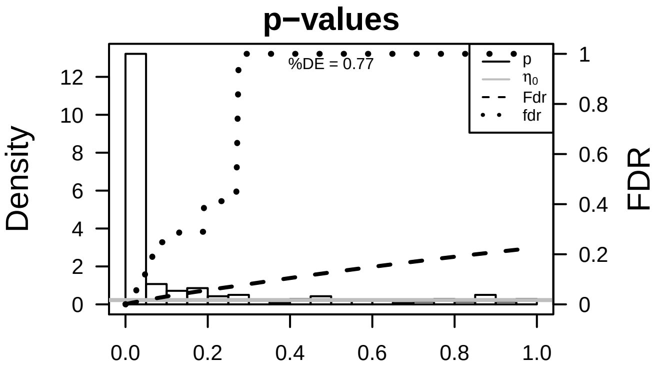
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CDKN3	−1.65	2e−16	7e−15	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
2	TK1	−1.55	2e−16	7e−15	4 x 50	thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:HGN
3	SMC4	−1.35	1e−15	3e−12	5 x 50	structural maintenance of chromosomes 4 [Source:HGNC Sy
4	MAD2L1	−1.35	9e−14	3e−12	5 x 50	MAD2 mitotic arrest deficient−like 1 (yeast) [Source:HGNC S
5	TUBA1B	−0.62	1e−13	4e−11	6 x 48	tubulin, alpha 1b [Source:HGNC Symbol;Acc:HGNC:18809]
6	TYMS	−1.29	7e−13	1e−10	3 x 50	thymidylate synthetase [Source:HGNC Symbol;Acc:HGNC:1
7	BIRC5	−1.28	3e−12	1e−09	6 x 50	baculoviral IAP repeat containing 5 [Source:HGNC Symbol;A
8	KIAA0101	−1.24	3e−11	9e−09	3 x 50	KIAA0101 [Source:HGNC Symbol;Acc:HGNC:28961]
9	CENPN	−1.21	2e−10	9e−09	4 x 50	centromere protein N [Source:HGNC Symbol;Acc:HGNC:308
10	TRIP13	−1.2	4e−10	9e−09	5 x 50	thyroid hormone receptor interactor 13 [Source:HGNC Symb
11	CKAP2	−1.19	4e−10	2e−08	6 x 50	cytoskeleton associated protein 2 [Source:HGNC Symbol;Ac
12	HELLS	−1.15	1e−09	2e−08	1 x 50	helicase, lymphoid−specific [Source:HGNC Symbol;Acc:HGN
13	CCNB1	1.22	1e−09	2e−08	7 x 50	cyclin B1 [Source:HGNC Symbol;Acc:HGNC:1579]
14	HMGN2	−0.61	2e−09	1e−07	8 x 50	high mobility group nucleosomal binding domain 2 [Source:H
15	NUSAP1	−1.17	3e−09	1e−07	6 x 50	nucleolar and spindle associated protein 1 [Source:HGNC Sy
16	H2AFV	−1.02	6e−09	4e−07	8 x 50	H2A histone family, member V [Source:HGNC Symbol;Acc:H
17	MCM4	−0.92	1e−08	1e−06	1 x 50	minichromosome maintenance complex component 4 [Sourc
18	CDK1	−1.11	4e−08	1e−06	5 x 50	cyclin−dependent kinase 1 [Source:HGNC Symbol;Acc:HGN
19	GAS2L3	−1.09	6e−08	1e−06	8 x 50	growth arrest−specific 2 like 3 [Source:HGNC Symbol;Acc:H
20	BARD1	−1.09	6e−08	1e−06	2 x 50	BRCA1 associated RING domain 1 [Source:HGNC Symbol;A



p−values