A6_mel

Global Summary

%DE = 0.2

genes with fdr < 0.2 = 2555 (1514 + / 1041 −)

genes with fdr < 0.1 = 2160 (1276 + / 884 −)

genes with fdr < 0.05 = 1684 (1016 + / 668 −)

genes with fdr < 0.01 = 1039 (632 + / 407 −)

genes in genesets = 14839

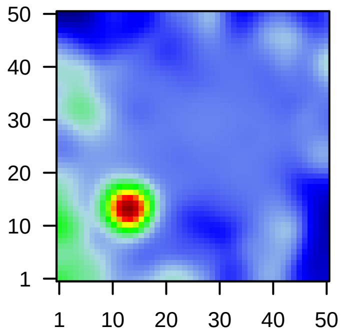
<FC> = 0

<shrinkage−t> = −0.01

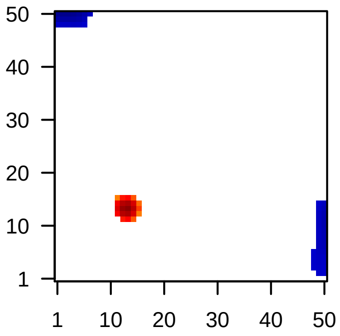
<p−value> = 0.08

<fdr> = 0.8

Profile



Regulated Spots



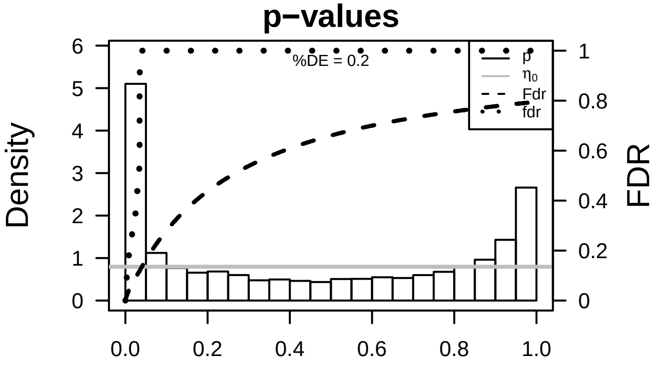
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ACTL6A	−1.86	2e−16	1e−13	4 x 50	actin−like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
2	C14orf119	−1.65	2e−16	1e−13	40 x 50	chromosome 14 open reading frame 119 [Source:HGNC Sym
3	DCTN2	−1.51	2e−16	1e−13	50 x 44	dynactin 2 (p50) [Source:HGNC Symbol;Acc:HGNC:2712]
4	EIF3D	−1.74	2e−16	1e−13	45 x 19	eukaryotic translation initiation factor 3, subunit D [Source:HG
5	EXOSC7	−1.64	2e−16	1e−13	22 x 1	exosome component 7 [Source:HGNC Symbol;Acc:HGNC:2
6	EXOSC8	−1.71	2e−16	1e−13	1 x 50	exosome component 8 [Source:HGNC Symbol;Acc:HGNC:17
7	HIF1A	−1.33	2e−16	1e−13	50 x 18	hypoxia inducible factor 1, alpha subunit (basic helix−loop−he
8	IFT81	−1.69	2e−16	1e−13	6 x 43	intraflagellar transport 81 [Source:HGNC Symbol;Acc:HGNC:
9	NAE1	−1.32	2e−16	1e−13	10 x 45	NEDD8 activating enzyme E1 subunit 1 [Source:HGNC Sym
10	POP4	−1.63	2e−16	1e−13	15 x 50	processing of precursor 4, ribonuclease P/MRP subunit (S. c
11	PTCD3	−1.65	2e−16	1e−13	48 x 50	pentatricopeptide repeat domain 3 [Source:HGNC Symbol;A
12	REEP5	−1.8	2e−16	1e−13	46 x 49	receptor accessory protein 5 [Source:HGNC Symbol;Acc:HG
13	RNF13	−1.79	2e−16	1e−13	50 x 7	ring finger protein 13 [Source:HGNC Symbol;Acc:HGNC:100
14	SEP15	−1.11	2e−16	1e−13	48 x 16	
15	SNRNP40	−1.64	2e−16	1e−13	12 x 48	small nuclear ribonucleoprotein 40kDa (U5) [Source:HGNC S
16	SRP72	−1.24	2e−16	1e−13	19 x 50	signal recognition particle 72kDa [Source:HGNC Symbol;Acc
17	STOM	−1.62	2e−16	1e−13	50 x 14	stomatin [Source:HGNC Symbol;Acc:HGNC:3383]
18	SYNE1	−1.59	2e−16	1e−13	49 x 1	spectrin repeat containing, nuclear envelope 1 [Source:HGN
19	TIMM21	−1.79	2e−16	1e−13	14 x 50	translocase of inner mitochondrial membrane 21 homolog (ye
20	LAMB2	−1.61	4e−16	2e−12	50 x 6	laminin, beta 2 (laminin S) [Source:HGNC Symbol;Acc:HGN

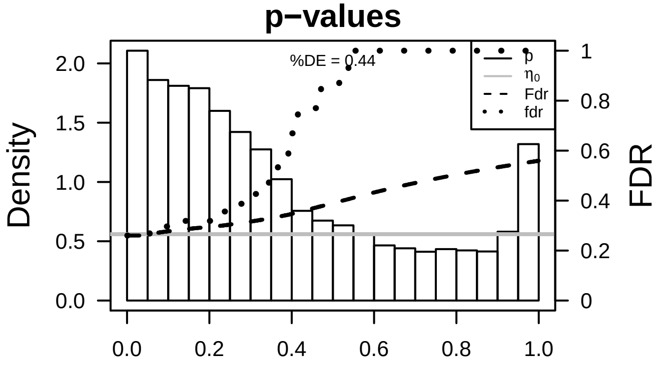
Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	4.54	0.005	167	GSEA C2	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTE
2	3.68	0.010	85	GSEA C2	MOOTHA_VOXPHOS
3	3.68	0.010	551	Chr	Chr X
4	3.65	0.010	94	BP	respiratory electron transport chain
5	3.64	0.010	37	miRNA target	hsa−miR−635
6	3.62	0.010	63	GSEA C2	LIN_MELANOMA_COPY_NUMBER_UP
7	3.56	0.011	14	BP	acyl−CoA metabolic process
8	3.54	0.011	10	CC	endoplasmic reticulum chaperone complex
9	3.48	0.012	16	BP	calcium ion−dependent exocytosis
10	3.43	0.012	16	GSEA C2	HAHTOLA_MYCOSIS_FUNGOIDES_UP
11	3.35	0.013	32	GSEA C2	ONGUSAHA_TP53_TARGETS
12	3.29	0.014	990	GSEA C2	DANG_BOUND_BY_MYC
13	3.21	0.015	3081	Brain	Mid_Frontal_Lobe_ZNF
14	3.19	0.015	84	GSEA C2	QI_PLASMACYTOMA_DN
15	3.18	0.015	8	GSEA C2	REACTOME_IONOTROPIC_ACTIVITY_OF_KAINATE_RECEPTO
16	3.18	0.015	294	GSEA C2	DACOSTA_UV_RESPONSE_VIA_ERCC3_UP
17	3.13	0.016	10	BP	nitrogen cycle metabolic process
18	3.13	0.016	12	BP	oxidative phosphorylation
19	3.12	0.016	6	GSEA C2	ZHAN_EARLY_DIFFERENTIATION_GENES_UP
20	3.12	0.016	19	GSEA C2	CAVARD_LIVER_CANCER_MALIGNANT_VS_BENIGN
Underexpressed					
1	−8.01	6e−04	242	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
2	−7.48	8e−04	93	GSEA C2	KONG_E2F3_TARGETS
3	−7.48	8e−04	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
4	−7.23	9e−04	609	GSEA C2	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIA
5	−7.19	9e−04	616	GSEA C2	BENPORATH_CYCLING_GENES
6	−7.19	1e−03	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
7	−7.16	1e−03	305	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
8	−7.07	1e−03	68	GSEA C2	VERNELL_RETINOBLASTOMA_PATHWAY_UP
9	−6.9	1e−03	171	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP
10	−6.6	1e−03	196	HM	HALLMARK_G2M_CHECKPOINT
11	−6.51	1e−03	50	GSEA C2	ISHIDA_E2F_TARGETS
12	−6.31	2e−03	19	GSEA C2	LI_WILMS_TUMOR_ANAPLASTIC_UP
13	−6.29	2e−03	862	GSEA C2	JOHNSTONE_PARVB_TARGETS_3_DN
14	−6.08	2e−03	81	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
15	−5.9	2e−03	110	GSEA C2	WHITEFORD_PEDIATRIC_CANCER_MARKERS
16	−5.89	2e−03	1192	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
17	−5.85	2e−03	6929	Lymphoma	HOPP_Txn_elongation
18	−5.84	2e−03	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
19	−5.78	2e−03	1110	BP	cell cycle
20	−5.65	2e−03	436	GSEA C2	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6

p−values



p−values



A6_mel

Local Summary

%DE = 0.99

metagenes = 22

genes = 189

genes in genesets = 189

genes with fdr < 0.1 = 187 (187 + / 0 −)

genes with fdr < 0.05 = 187 (187 + / 0 −)

genes with fdr < 0.01 = 187 (187 + / 0 −)

<r> metagenes = 0.98

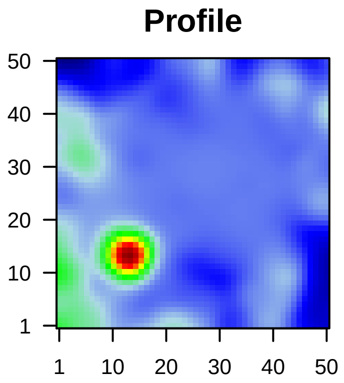
<r> genes = 0.25

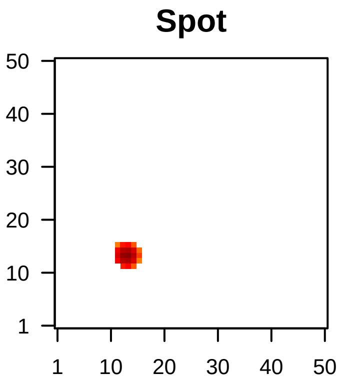
<FC> = 1.14

<shrinkage−t> = 17.23

<p−value> = 0

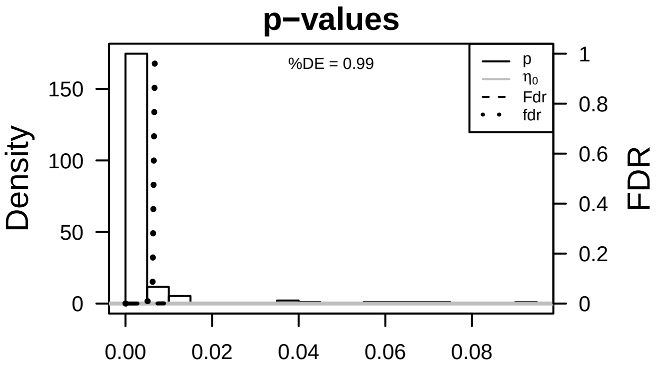
<fdr> = 0.07





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	MDK	2.02	3e−15	2e−15	14 x 14	midkine (neurite growth−promoting factor 2) [Source:HGNC S
2	TPRN	2.02	4e−15	6e−14	13 x 15	taperin [Source:HGNC Symbol;Acc:HGNC:26894]
3	C10orf107	1.93	6e−14	9e−14	14 x 14	chromosome 10 open reading frame 107 [Source:HGNC Sym
4	ANKS1B	1.88	2e−13	9e−14	14 x 14	ankyrin repeat and sterile alpha motif domain containing 1B [
5	MEGF10	1.88	2e−13	3e−13	14 x 14	multiple EGF−like−domains 10 [Source:HGNC Symbol;Acc:H
6	ZNF442	1.86	5e−13	3e−12	13 x 14	zinc finger protein 442 [Source:HGNC Symbol;Acc:HGNC:20
7	C9orf92	1.79	3e−12	3e−12	14 x 14	chromosome 9 open reading frame 92 [Source:HGNC Symbo
8	MDGA2	1.77	6e−12	3e−12	14 x 14	MAM domain containing glycosylphosphatidylinositol anchor
9	THAP9	1.76	8e−12	4e−12	14 x 14	THAP domain containing 9 [Source:HGNC Symbol;Acc:HGN
10	MCU	1.74	1e−11	7e−12	14 x 14	mitochondrial calcium uniporter [Source:HGNC Symbol;Acc:
11	SNAP25	1.72	2e−11	5e−11	14 x 14	synaptosomal−associated protein, 25kDa [Source:HGNC Sy
12	CTIF	1.67	8e−11	5e−11	14 x 14	CBP80/20−dependent translation initiation factor [Source:HG
13	ALDH1A1	1.65	1e−10	6e−11	14 x 14	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
14	PRKD2	1.64	2e−10	6e−11	14 x 14	protein kinase D2 [Source:HGNC Symbol;Acc:HGNC:17293]
15	ITIH4	1.62	3e−10	6e−11	14 x 14	inter−alpha−trypsin inhibitor heavy chain family, member 4 [S
16	PRDM15	1.62	3e−10	6e−11	13 x 14	PR domain containing 15 [Source:HGNC Symbol;Acc:HGNC:
17	RIMS3	1.61	3e−10	6e−11	14 x 14	regulating synaptic membrane exocytosis 3 [Source:HGNC S
18	GANC	1.59	5e−10	6e−11	13 x 15	glucosidase, alpha; neutral C [Source:HGNC Symbol;Acc:HG
19	NOM1	1.59	5e−10	6e−11	14 x 14	nucleolar protein with MIF4G domain 1 [Source:HGNC Symb
20	CHSY3	1.59	6e−10	6e−11	14 x 14	chondroitin sulfate synthase 3 [Source:HGNC Symbol;Acc:H



A6_mel

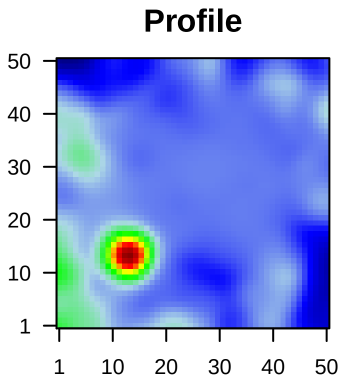
Local Summary

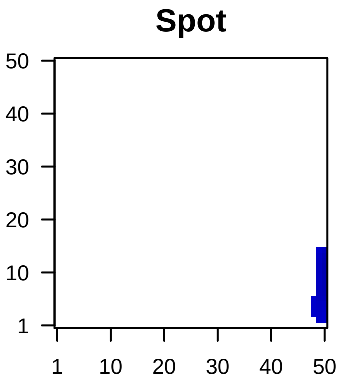
%DE = 0.82
metagenes = 32
genes = 345
genes in genesets = 344

genes with fdr < 0.1 = 167 (39 + / 128 −)
genes with fdr < 0.05 = 137 (35 + / 102 −)
genes with fdr < 0.01 = 92 (21 + / 71 −)

<r> metagenes = 0.84
<r> genes = 0.09

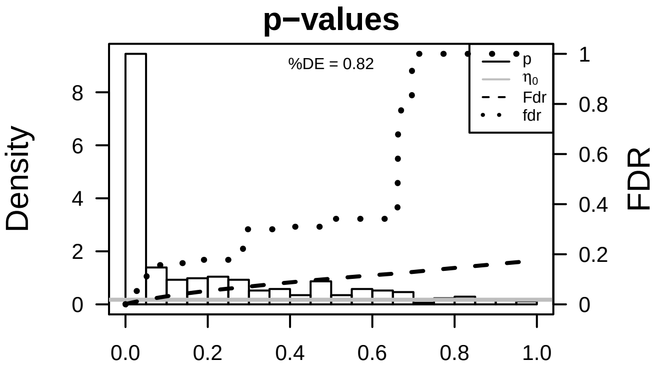
<FC> = −0.27
<shrinkage−t> = −4.45
<p−value> = 0.01
<fdr> = 0.61





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	RNF13	−1.79	2e−16	7e−15	50 x 7	ring finger protein 13 [Source:HGNC Symbol;Acc:HGNC:100
2	STOM	−1.62	2e−16	7e−15	50 x 14	stomatin [Source:HGNC Symbol;Acc:HGNC:3383]
3	LAMB2	−1.61	4e−16	3e−12	50 x 6	laminin, beta 2 (laminin S) [Source:HGNC Symbol;Acc:HGN
4	MYL12A	−0.78	6e−14	1e−08	48 x 3	myosin, light chain 12A, regulatory, non−sarcomeric [Source:
5	HUWE1	−1.41	3e−10	1e−08	49 x 14	HECT, UBA and WWE domain containing 1, E3 ubiquitin prot
6	FAM129A	−1.27	4e−10	1e−08	50 x 11	family with sequence similarity 129, member A [Source:HGN
7	S100A10	1.59	6e−10	3e−08	50 x 4	S100 calcium binding protein A10 [Source:HGNC Symbol;Ac
8	PPP1R15A	−1.38	1e−09	4e−08	49 x 4	protein phosphatase 1, regulatory subunit 15A [Source:HGN
9	SRPK2	−1.36	3e−09	4e−08	50 x 11	SRSF protein kinase 2 [Source:HGNC Symbol;Acc:HGNC:11
10	COMT	−1.36	3e−09	4e−08	50 x 15	catechol−O−methyltransferase [Source:HGNC Symbol;Acc:H
11	PLOD2	−1.36	3e−09	4e−07	49 x 3	procollagen−lysine, 2−oxoglutarate 5−dioxygenase 2 [Source
12	PABPC4	1.1	9e−09	3e−06	50 x 7	poly(A) binding protein, cytoplasmic 4 (inducible form) [Sourc
13	OSGIN1	−1.2	8e−08	3e−06	50 x 6	oxidative stress induced growth inhibitor 1 [Source:HGNC Sy
14	USP32	−1.26	1e−07	1e−05	50 x 15	ubiquitin specific peptidase 32 [Source:HGNC Symbol;Acc:H
15	AKR1A1	−1.2	3e−07	2e−05	50 x 7	aldo−keto reductase family 1, member A1 (aldehyde reductas
16	RNF141	−1.21	6e−07	2e−05	50 x 5	ring finger protein 141 [Source:HGNC Symbol;Acc:HGNC:21
17	SYTL2	1.25	1e−06	2e−05	50 x 4	synaptotagmin−like 2 [Source:HGNC Symbol;Acc:HGNC:155
18	SGCB	−1.1	1e−06	2e−05	50 x 13	sarcoglycan, beta (43kDa dystrophin−associated glycoprotei
19	CCDC57	−1.18	2e−06	5e−05	50 x 11	coiled−coil domain containing 57 [Source:HGNC Symbol;Acc
20	CAV1	1.19	3e−06	5e−05	50 x 3	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;



A6_mel

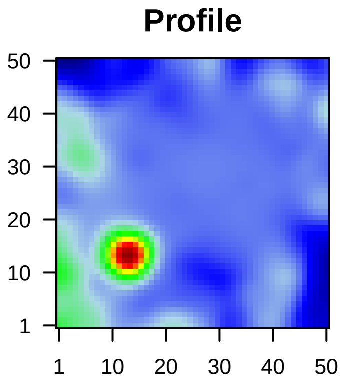
Local Summary

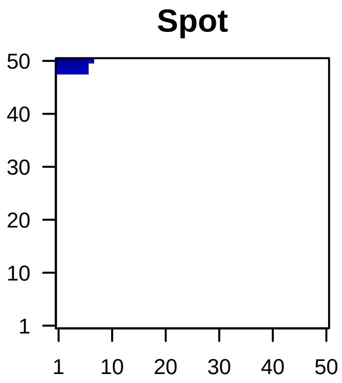
%DE = 0.86
metagenes = 19
genes = 320
genes in genesets = 319

genes with fdr < 0.1 = 216 (46 + / 170 −)
genes with fdr < 0.05 = 200 (42 + / 158 −)
genes with fdr < 0.01 = 100 (21 + / 79 −)

<r> metagenes = 0.94
<r> genes = 0.31

<FC> = −0.34
<shrinkage−t> = −5.41
<p−value> = 0.01
<fdr> = 0.53





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ACTL6A	−1.86	2e−16	5e−15	4 x 50	actin−like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
2	EXOSC8	−1.71	2e−16	5e−15	1 x 50	exosome component 8 [Source:HGNC Symbol;Acc:HGNC:17
3	HAT1	−1.61	7e−16	1e−11	1 x 50	histone acetyltransferase 1 [Source:HGNC Symbol;Acc:HGN
4	PCNA	−1.41	2e−13	5e−08	2 x 50	proliferating cell nuclear antigen [Source:HGNC Symbol;Acc:
5	ASRGL1	−1.37	1e−09	3e−07	1 x 50	asparaginase like 1 [Source:HGNC Symbol;Acc:HGNC:1644
6	SMCHD1	−1.33	9e−09	6e−07	1 x 48	structural maintenance of chromosomes flexible hinge domai
7	EMP2	−1.31	2e−08	6e−07	2 x 50	epithelial membrane protein 2 [Source:HGNC Symbol;Acc:H
8	EXOSC9	−1.29	4e−08	7e−07	1 x 50	exosome component 9 [Source:HGNC Symbol;Acc:HGNC:91
9	HAUS1	−1.06	5e−08	1e−06	1 x 50	HAUS augmin−like complex, subunit 1 [Source:HGNC Symb
10	POLD3	−1.27	8e−08	3e−06	2 x 50	polymerase (DNA−directed), delta 3, accessory subunit [Sou
11	LBR	−1.19	1e−07	5e−06	7 x 50	lamin B receptor [Source:HGNC Symbol;Acc:HGNC:6518]
12	C19orf48	−1.23	3e−07	5e−06	1 x 50	chromosome 19 open reading frame 48 [Source:HGNC Sym
13	CENPK	−1.23	3e−07	8e−06	3 x 50	centromere protein K [Source:HGNC Symbol;Acc:HGNC:294
14	TMPO	−1.21	5e−07	1e−05	5 x 50	thymopoietin [Source:HGNC Symbol;Acc:HGNC:11875]
15	ORC6	−1.14	1e−06	1e−05	1 x 50	origin recognition complex, subunit 6 [Source:HGNC Symbol;
16	ZNF519	1.25	1e−06	1e−05	3 x 48	zinc finger protein 519 [Source:HGNC Symbol;Acc:HGNC:30
17	TMEM237	1.23	2e−06	1e−05	4 x 48	transmembrane protein 237 [Source:HGNC Symbol;Acc:HGN
18	CDKN3	0.91	2e−06	1e−05	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
19	RFC2	−1.17	2e−06	1e−05	1 x 50	replication factor C (activator 1) 2, 40kDa [Source:HGNC Sym
20	NUSAP1	−1.17	3e−06	1e−05	6 x 50	nucleolar and spindle associated protein 1 [Source:HGNC Sy