

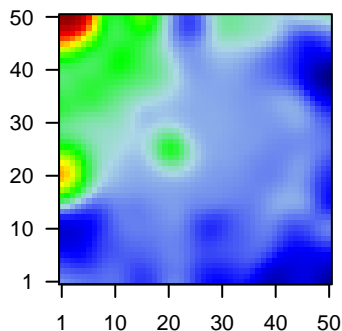
# A7\_mel

## Global Summary

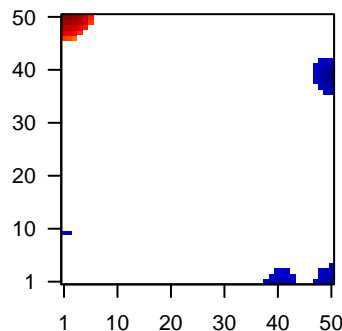
%DE = 0.25  
 # genes with fdr < 0.2 = 3229 ( 1919 + / 1310 - )  
 # genes with fdr < 0.1 = 2606 ( 1586 + / 1020 - )  
 # genes with fdr < 0.05 = 2291 ( 1421 + / 870 - )  
 # genes with fdr < 0.01 = 1574 ( 1002 + / 572 - )  
 # genes in genesets = 14839

<FC> = 0  
 <shrinkage-t> = 0.03  
 <p-value> = 0.05  
 <fdr> = 0.75

Profile



Regulated Spots



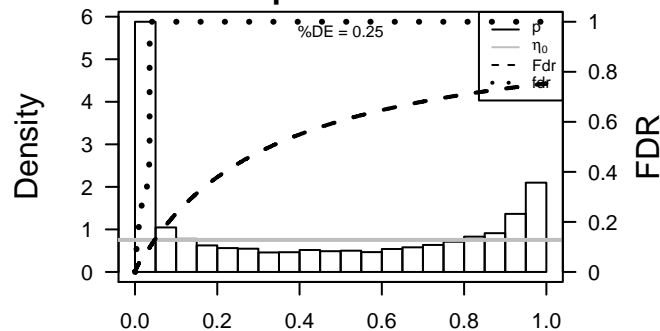
## Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	AK1	-1.59	2e-16 6e-14	2 x 40 adenylate kinase 1 [Source:HGNC Symbol;Acc:HGNC:361]
2	APEX1	-1.67	2e-16 6e-14	29 x 50 APEX nuclease (multifunctional DNA repair enzyme) 1 [Source:HGNC Symbol;Acc:HGNC:10000]
3	ARL1	-1.63	2e-16 6e-14	25 x 49 ADP-ribosylation factor-like 1 [Source:HGNC Symbol;Acc:HGNC:10000]
4	ATP6V0A1	-1.36	2e-16 6e-14	1 x 10 ATPase, H+ transporting, lysosomal V0 subunit a1 [Source:HGNC Symbol;Acc:HGNC:10000]
5	BBX	-1.53	2e-16 6e-14	50 x 7 bobby sox homolog (Drosophila) [Source:HGNC Symbol;Acc:HGNC:10000]
6	C5orf15	-1.42	2e-16 6e-14	48 x 5 chromosome 5 open reading frame 15 [Source:HGNC Symbol;Acc:HGNC:10000]
7	CD59	-1.02	2e-16 6e-14	49 x 12 CD59 molecule, complement regulatory protein [Source:HGNC Symbol;Acc:HGNC:10000]
8	CDH1	1.71	2e-16 6e-14	21 x 26 cadherin 1, type 1, E-cadherin (epithelial) [Source:HGNC Symbol;Acc:HGNC:10000]
9	CERS2	-1.87	2e-16 6e-14	3 x 34 ceramide synthase 2 [Source:HGNC Symbol;Acc:HGNC:10000]
10	CLK1	-1.54	2e-16 6e-14	50 x 40 CDC-like kinase 1 [Source:HGNC Symbol;Acc:HGNC:2068]
11	DNAJB4	-1.45	2e-16 6e-14	50 x 1 DnaJ (Hsp40) homolog, subfamily B, member 4 [Source:HGNC Symbol;Acc:HGNC:10000]
12	ERAL1	-1.73	2e-16 6e-14	46 x 44 Era-like 12S mitochondrial rRNA chaperone 1 [Source:HGNC Symbol;Acc:HGNC:10000]
13	FAM131A	1.72	2e-16 6e-14	1 x 22 family with sequence similarity 131, member A [Source:HGNC Symbol;Acc:HGNC:10000]
14	ITIH3	2.03	2e-16 6e-14	50 x 50 inter-alpha-trypsin inhibitor heavy chain 3 [Source:HGNC Symbol;Acc:HGNC:10000]
15	LGALS1	-1.68	2e-16 6e-14	50 x 1 lectin, galactoside-binding, soluble, 1 [Source:HGNC Symbol;Acc:HGNC:10000]
16	OCA2	-1.57	2e-16 6e-14	1 x 12 oculocutaneous albinism II [Source:HGNC Symbol;Acc:HGNC:10000]
17	OSER1	-1.54	2e-16 6e-14	45 x 6 oxidative stress responsive serine-rich 1 [Source:HGNC Symbol;Acc:HGNC:10000]
18	PHAX	-1.52	2e-16 6e-14	18 x 49 phosphorylated adaptor for RNA export [Source:HGNC Symbol;Acc:HGNC:10000]
19	PLK2	-1.65	2e-16 6e-14	50 x 1 polo-like kinase 2 [Source:HGNC Symbol;Acc:HGNC:19699]
20	POLR2K	-1.44	2e-16 6e-14	50 x 41 polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa [Source:HGNC Symbol;Acc:HGNC:10000]

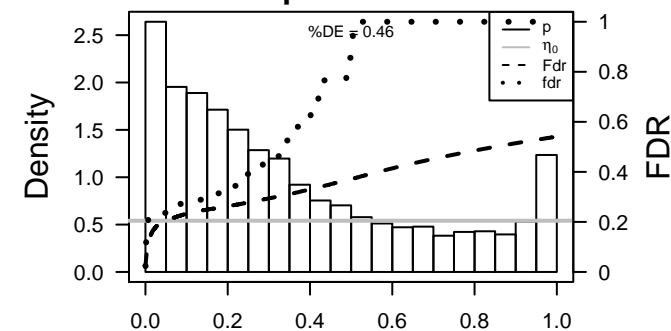
## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1		18.06	2e-05	305 GSEA C2DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
2		16.91	3e-05	550 GSEA C2SOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
3		16.12	4e-05	242 GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN
4		15.91	4e-05	142 Glio WILLSCHER_GBM_Verhaak-CL_up (C)
5		15.7	4e-05	267 GSEA C2ZHANG_TLX_TARGETS_60HR_DN
6		15.67	4e-05	197 HM HALLMARK_E2F_TARGETS
7		15.03	5e-05	139 GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
8		14.44	6e-05	1192 GSEA C2KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
9		13.91	7e-05	327 GSEA C2BLUM_RESPONSE_TO_SALIRASIB_DN
10		13.5	8e-03	16 Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
11		13.29	8e-05	171 GSEA C2SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP
12		13.23	8e-05	81 GSEA C2GRAHAM_NORMAL QUIESCENT_VS_NORMAL_DIVIDING_DN
13		13.13	9e-05	50 GSEA C2SHIDA_E2F_TARGETS
14		13.03	9e-05	335 GSEA C2WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_DN
15		12.96	9e-05	96 GSEA C2ROONQUIST_IL6_DEPRIVATION_DN
16		12.63	1e-04	390 GSEA C2PUJANA_BRCA2_PCC_NETWORK
17		12.54	1e-04	84 GSEA C2ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_6HR
18		12.5	1e-04	216 GSEA C2MARKEY_RB1_ACUTE_LOF_DN
19		12.48	1e-04	145 GSEA C2CHANG_CYCLING_GENES
20		12.44	1e-04	162 GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL QUIESCENT_UP
<i>Underexpressed</i>				
1		-6.53	0.001	5940 Brain Overlap_fetal_midbrain_HetRpts
2		-5.87	0.002	749 GSEA C2CUI_TCF21_TARGETS_2_DN
3		-5.64	0.002	472 GSEA C2DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
4		-5.38	0.003	139 GSEA C2RUIZ_TNC_TARGETS_UP
5		-5.22	0.003	298 Cancer SPANG_BCL6-index2
6		-5.02	0.003	200 GSEA C2KONDO_EZH2_TARGETS
7		-4.94	0.004	594 GSEA C2WONG_ADULT_TISSUE_STEM_MODULE
8		-4.83	0.004	126 GSEA C2LIU_SOX4_TARGETS_UP
9		-4.71	0.004	136 GSEA C2PODAR_RESPONSE_TO_ADAPHOSTIN_UP
10		-4.71	0.004	222 GSEA C2JDAYAKUMAR_MED1_TARGETS_DN
11		-4.57	0.005	50 GSEA C2LUI_THYROID_CANCER_CLUSTER_1
12		-4.36	0.006	11 Tissue WIRTH_Cortex_cerebri
13		-4.28	0.006	414 GSEA C2ZHENG_BOUND_BY_FOXP3
14		-4.24	0.006	8580 Colon Cancer_Kolon
15		-4.2	0.006	656 Brain Overlap_fetal_midbrain_EnhP
16		-4.18	0.006	84 miRNA target-miR-220c
17		-4.17	0.007	302 GSEA C2KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
18		-4.09	0.007	283 GSEA C2SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
19		-4.08	0.007	2984 CC integral component of membrane
20		-4.02	0.007	438 CC Golgi membrane

p-values



p-values



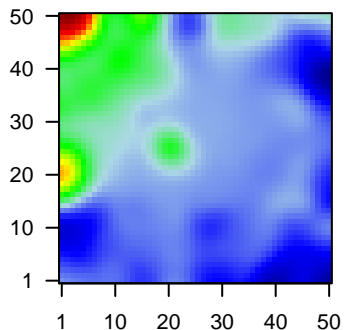
# A7\_mel

## Local Summary

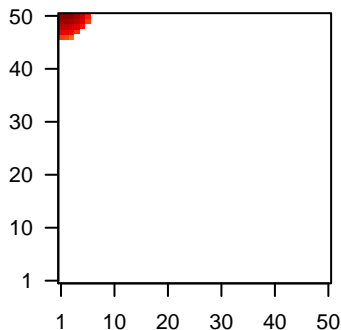
%DE = 0.89  
 # metagenes = 24  
 # genes = 378  
 # genes in genesets = 377  
  
 # genes with  $fdr < 0.1$  = 297 ( 278 + / 19 - )  
 # genes with  $fdr < 0.05$  = 297 ( 278 + / 19 - )  
 # genes with  $fdr < 0.01$  = 252 ( 239 + / 13 - )

$\langle r \rangle$  metagenes = 0.93  
 $\langle r \rangle$  genes = 0.26  
  
 $\langle FC \rangle$  = 0.62  
 $\langle \text{shrinkage-t} \rangle$  = 9.92  
 $\langle p\text{-value} \rangle$  = 0  
 $\langle fdr \rangle$  = 0.26

Profile



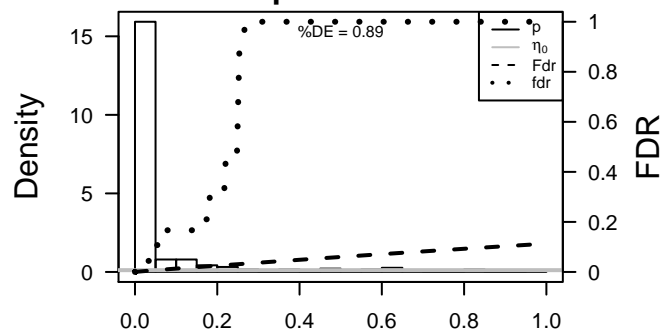
Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ORC1	1.67	9e-16	3e-14	1 x 49 origin recognition complex, subunit 1 [Source:HGNC Symbol;]
2	AURKB	1.66	1e-15	5e-14	6 x 50 aurora kinase B [Source:HGNC Symbol;Acc:HGNC:11390]
3	TK1	1.32	2e-15	1e-12	4 x 50 thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:HGNC:11390]
4	RAD51	1.56	5e-14	1e-12	1 x 50 RAD51 recombinase [Source:HGNC Symbol;Acc:HGNC:981]
5	DDIAS	1.54	1e-13	1e-12	4 x 48 DNA damage-induced apoptosis suppressor [Source:HGNC Symbol;Acc:HGNC:11390]
6	CENPH	1.54	1e-13	2e-12	1 x 47 centromere protein H [Source:HGNC Symbol;Acc:HGNC:172]
7	CCNE2	1.53	2e-13	2e-12	2 x 50 cyclin E2 [Source:HGNC Symbol;Acc:HGNC:1590]
8	NCAPG	1.52	2e-13	1e-11	6 x 50 non-SMC condensin I complex, subunit G [Source:HGNC Symbol;Acc:HGNC:11390]
9	DDX11	1.49	7e-13	1e-11	1 x 47 DEAD/H (Asp-Glu-Ala-Asp/His) box helicase 11 [Source:HGNC Symbol;Acc:HGNC:11390]
10	FBXO5	1.48	8e-13	2e-11	4 x 50 F-box protein 5 [Source:HGNC Symbol;Acc:HGNC:13584]
11	HIST1H4C	0.59	1e-12	4e-11	5 x 49 histone cluster 1, H4c [Source:HGNC Symbol;Acc:HGNC:478]
12	RRM2	1.45	3e-12	4e-11	5 x 50 ribonucleotide reductase M2 [Source:HGNC Symbol;Acc:HGNC:11390]
13	TRIP13	1.35	5e-12	4e-11	5 x 50 thyroid hormone receptor interactor 13 [Source:HGNC Symbol;Acc:HGNC:11390]
14	POLE	1.43	5e-12	4e-11	1 x 48 polymerase (DNA directed), epsilon, catalytic subunit [Source:HGNC Symbol;Acc:HGNC:11390]
15	CDC6	1.42	5e-12	3e-10	1 x 50 cell division cycle 6 [Source:HGNC Symbol;Acc:HGNC:1744]
16	RANBP17	1.4	2e-11	3e-10	1 x 50 RAN binding protein 17 [Source:HGNC Symbol;Acc:HGNC:11390]
17	HJURP	1.39	2e-11	3e-10	6 x 50 Holliday junction recognition protein [Source:HGNC Symbol;Acc:HGNC:11390]
18	NCAPD3	1.38	3e-11	3e-10	4 x 48 non-SMC condensin II complex, subunit D3 [Source:HGNC Symbol;Acc:HGNC:11390]
19	UBE2T	1.36	4e-11	3e-10	4 x 50 ubiquitin-conjugating enzyme E2T [Source:HGNC Symbol;Acc:HGNC:11390]
20	POC1A	1.37	5e-11	3e-10	4 x 48 POC1 centriolar protein A [Source:HGNC Symbol;Acc:HGNC:11390]

p-values



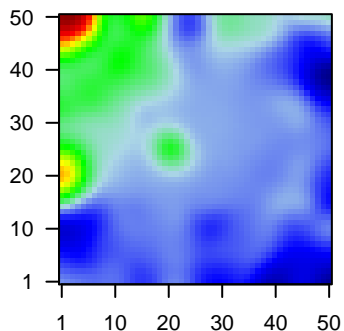
# A7\_mel

## Local Summary

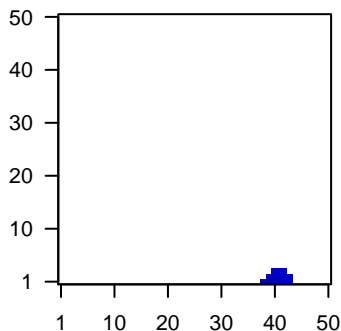
%DE = 0.8  
 # metagenes = 14  
 # genes = 140  
 # genes in genesets = 140  
  
 # genes with  $fdr < 0.1$  = 67 ( 9 + / 58 - )  
 # genes with  $fdr < 0.05$  = 50 ( 8 + / 42 - )  
 # genes with  $fdr < 0.01$  = 30 ( 3 + / 27 - )

$\langle r \rangle$  metagenes = 0.93  
 $\langle r \rangle$  genes = 0.11  
  
 $\langle FC \rangle$  = -0.28  
 $\langle \text{shrinkage-t} \rangle$  = -4.44  
 $\langle p\text{-value} \rangle$  = 0.01  
 $\langle fdr \rangle$  = 0.64

Profile



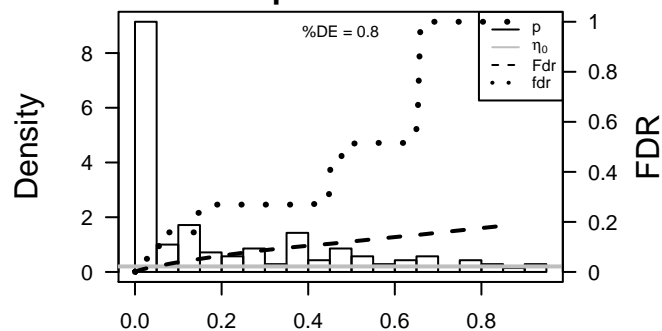
Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	SOX4	-0.94	2e-16	6e-15	41 x 1 SRY (sex determining region Y)-box 4 [Source:HGNC Symbol;Acc:HGNC:27111]
2	RFTN1	1.46	2e-12	2e-06	43 x 1 raftlin, lipid raft linker 1 [Source:HGNC Symbol;Acc:HGNC:30271]
3	DCTN1	-1.09	1e-07	2e-06	41 x 1 dynactin 1 [Source:HGNC Symbol;Acc:HGNC:27111]
4	MPRIIP	-1.08	1e-07	1e-05	42 x 2 myosin phosphatase Rho interacting protein [Source:HGNC Symbol;Acc:HGNC:27111]
5	CPEB4	-1.02	9e-07	1e-05	38 x 1 cytoplasmic polyadenylation element binding protein 4 [Source:HGNC Symbol;Acc:HGNC:27111]
6	STRN3	-0.87	1e-06	1e-05	39 x 1 striatin, calmodulin binding protein 3 [Source:HGNC Symbol;Acc:HGNC:27111]
7	ANXA11	-1	2e-06	1e-05	40 x 1 annexin A11 [Source:HGNC Symbol;Acc:HGNC:535]
8	RTCA	-0.99	2e-06	1e-05	42 x 3 RNA 3'-terminal phosphate cyclase [Source:HGNC Symbol;Acc:HGNC:27111]
9	MAGED1	-0.89	2e-06	2e-05	39 x 1 melanoma antigen family D1 [Source:HGNC Symbol;Acc:HGNC:27111]
10	ITCH	-0.81	3e-06	2e-05	40 x 1 itchy E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:HGNC:27111]
11	CCS	0.96	4e-06	2e-05	41 x 2 copper chaperone for superoxide dismutase [Source:HGNC Symbol;Acc:HGNC:27111]
12	USP9X	-0.86	5e-06	2e-05	38 x 1 ubiquitin specific peptidase 9, X-linked [Source:HGNC Symbol;Acc:HGNC:27111]
13	MFN1	-0.94	5e-06	2e-05	42 x 1 mitofusin 1 [Source:HGNC Symbol;Acc:HGNC:18262]
14	ABCF2	-0.94	6e-06	7e-05	40 x 1 ATP-binding cassette, sub-family F (GCN20), member 2 [Source:HGNC Symbol;Acc:HGNC:27111]
15	NOL10	-0.91	1e-05	7e-05	42 x 1 nucleolar protein 10 [Source:HGNC Symbol;Acc:HGNC:2586]
16	EVI5	-0.91	1e-05	7e-05	43 x 1 ecotropic viral integration site 5 [Source:HGNC Symbol;Acc:HGNC:27111]
17	CNOT2	-0.43	1e-05	3e-04	39 x 1 CCR4-NOT transcription complex, subunit 2 [Source:HGNC Symbol;Acc:HGNC:27111]
18	PPF1B1	-0.88	2e-05	3e-04	40 x 2 PTPRF interacting protein, binding protein 1 (liprin beta 1) [Source:HGNC Symbol;Acc:HGNC:27111]
19	ACBD3	-0.81	4e-05	3e-04	38 x 1 acyl-CoA binding domain containing 3 [Source:HGNC Symbol;Acc:HGNC:27111]
20	EXOC1	-0.85	4e-05	1e-03	39 x 1 exocyst complex component 1 [Source:HGNC Symbol;Acc:HGNC:27111]

p-values



# A7\_mel

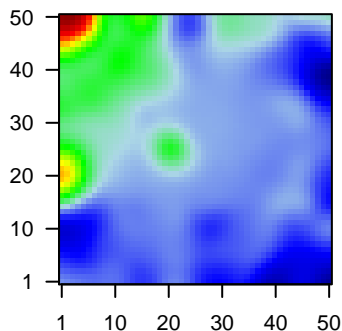
## Local Summary

%DE = 0.85  
 # metagenes = 11  
 # genes = 223  
 # genes in genesets = 223  
  
 # genes with fdr < 0.1 = 149 ( 31 + / 118 - )  
 # genes with fdr < 0.05 = 92 ( 21 + / 71 - )  
 # genes with fdr < 0.01 = 62 ( 17 + / 45 - )

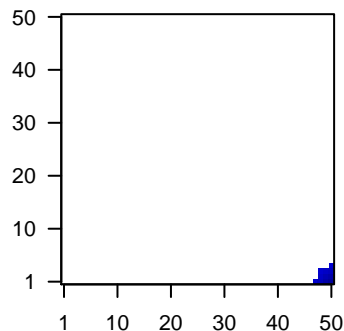
<r> metagenes = 0.99  
 <r> genes = 0.22

<FC> = -0.25  
 <shrinkage-t> = -4.08  
 <p-value> = 0.01  
 <fdr> = 0.6

Profile



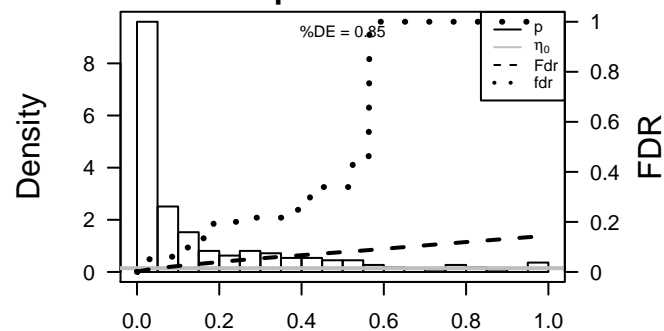
Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	DNAJB4	-1.45	2e-16	2e-15	50 x 1 DnaJ (Hsp40) homolog, subfamily B, member 4 [Source:HGNC]
2	LGALS1	-1.68	2e-16	2e-15	50 x 1 lectin, galactoside-binding, soluble, 1 [Source:HGNC Symbol]
3	PLK2	-1.65	2e-16	2e-15	50 x 1 polo-like kinase 2 [Source:HGNC Symbol;Acc:HGNC:19699]
4	FABP3	-1.44	7e-16	5e-13	50 x 1 fatty acid binding protein 3, muscle and heart [Source:HGNC]
5	EFNA1	1.59	2e-14	2e-11	50 x 1 ephrin-A1 [Source:HGNC Symbol;Acc:HGNC:3221]
6	CALD1	-0.95	6e-13	2e-11	50 x 1 caldesmon 1 [Source:HGNC Symbol;Acc:HGNC:1441]
7	TGIF1	-1.26	1e-12	1e-08	50 x 1 TGFB-induced factor homeobox 1 [Source:HGNC Symbol;Ac
8	GBE1	-1.18	5e-10	4e-08	50 x 3 glucan (1,4-alpha-), branching enzyme 1 [Source:HGNC Syr
9	CD55	-1.19	2e-09	2e-07	50 x 1 CD55 molecule, decay accelerating factor for complement (C
10	FAM98A	-1.16	9e-09	2e-07	49 x 1 family with sequence similarity 98, member A [Source:HGNC]
11	CTDSPL	1.18	1e-08	2e-07	49 x 1 CTD (carboxy-terminal domain, RNA polymerase II, polypept
12	YPEL5	-1.15	2e-08	4e-06	50 x 1 yippee-like 5 (Drosophila) [Source:HGNC Symbol;Acc:HGNC]
13	EDIL3	-1.07	2e-07	4e-06	50 x 1 EGF-like repeats and discoidin I-like domains 3 [Source:HGI
14	MBNL2	-1.04	4e-07	4e-06	50 x 1 muscleblind-like splicing regulator 2 [Source:HGNC Symbol;]
15	LMO7	1.05	4e-07	1e-05	50 x 2 LIM domain 7 [Source:HGNC Symbol;Acc:HGNC:6646]
16	SPTA1	1.02	1e-06	1e-05	50 x 1 spectrin, alpha, erythrocytic 1 [Source:HGNC Symbol;Acc:HC
17	NEK6	1	1e-06	1e-05	50 x 4 NIMA-related kinase 6 [Source:HGNC Symbol;Acc:HGNC:77
18	STK17B	-0.99	2e-06	1e-05	50 x 2 serine/threonine kinase 17b [Source:HGNC Symbol;Acc:HGNC]
19	ACOT9	-0.91	2e-06	1e-05	47 x 1 acyl-CoA thioesterase 9 [Source:HGNC Symbol;Acc:HGNC:]
20	SMAD3	0.97	3e-06	1e-05	47 x 1 SMAD family member 3 [Source:HGNC Symbol;Acc:HGNC:6

p-values



# A7\_mel

## Local Summary

%DE = 0.78  
 # metagenes = 2  
 # genes = 36  
 # genes in genesets = 36  
  
 # genes with  $fdr < 0.1$  = 16 ( 3 + / 13 - )  
 # genes with  $fdr < 0.05$  = 15 ( 2 + / 13 - )  
 # genes with  $fdr < 0.01$  = 10 ( 1 + / 9 - )

<r> metagenes = 1

<r> genes = 0.18

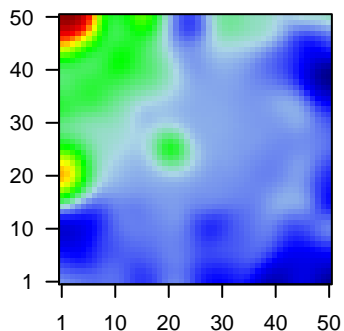
<FC> = -0.23

<shrinkage-t> = -3.67

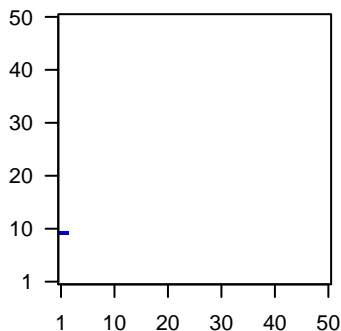
<p-value> = 0.01

<fdr> = 0.57

### Profile



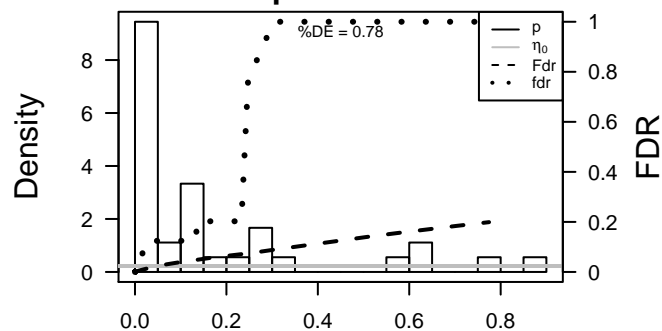
### Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ATP6V0A1	-1.36	2e-16	2e-15	1 x 10 ATPase, H+ transporting, lysosomal V0 subunit a1 [Source:HGNC Symbol;Acc:HGNC:10000]
2	MCC	-0.91	1e-05	6e-05	1 x 10 mutated in colorectal cancers [Source:HGNC Symbol;Acc:HGNC:10000]
3	PIP4K2C	-0.89	2e-05	4e-04	1 x 10 phosphatidylinositol-5-phosphate 4-kinase, type II, gamma [Source:HGNC Symbol;Acc:HGNC:10000]
4	KCNQ5	0.83	7e-05	4e-04	1 x 10 potassium channel, voltage gated KQT-like subfamily Q, member 5 [Source:HGNC Symbol;Acc:HGNC:10000]
5	MCF2L	-0.79	1e-04	4e-04	1 x 10 MCF2 cell line derived transforming sequence-like [Source:HGNC Symbol;Acc:HGNC:10000]
6	MSI2	-0.76	2e-04	4e-04	1 x 10 musashi RNA-binding protein 2 [Source:HGNC Symbol;Acc:HGNC:10000]
7	SS18L1	-0.76	2e-04	2e-03	1 x 10 synovial sarcoma translocation gene on chromosome 18-like [Source:HGNC Symbol;Acc:HGNC:10000]
8	NRP2	-0.71	6e-04	2e-03	1 x 10 neuropilin 2 [Source:HGNC Symbol;Acc:HGNC:8005]
9	RAPGEF6	-0.69	8e-04	5e-03	1 x 10 Rap guanine nucleotide exchange factor (GEF) 6 [Source:HGNC Symbol;Acc:HGNC:10000]
10	ROPN1B	-0.65	2e-03	5e-03	1 x 10 rhotropin associated tail protein 1B [Source:HGNC Symbol;Acc:HGNC:10000]
11	KCNAB2	-0.64	2e-03	1e-02	1 x 10 potassium channel, voltage gated subfamily A regulatory beta subunit 2 [Source:HGNC Symbol;Acc:HGNC:10000]
12	ADRBK2	-0.59	4e-03	1e-02	1 x 10 adrenergic, beta, receptor kinase 2 [Source:HGNC Symbol;Acc:HGNC:10000]
13	GAS8	-0.56	7e-03	1e-02	1 x 10 growth arrest-specific 8 [Source:HGNC Symbol;Acc:HGNC:10000]
14	ZNF284	-0.56	7e-03	4e-02	2 x 10 zinc finger protein 284 [Source:HGNC Symbol;Acc:HGNC:10000]
15	BEST1	0.48	1e-02	4e-02	1 x 10 bestrophin 1 [Source:HGNC Symbol;Acc:HGNC:12703]
16	NFU1	0.49	2e-02	7e-02	1 x 10 NFU1 iron-sulfur cluster scaffold [Source:HGNC Symbol;Acc:HGNC:10000]
17	PPARGC1A	0.41	3e-02	1e-01	1 x 10 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha [Source:HGNC Symbol;Acc:HGNC:10000]
18	BIN1	-0.38	7e-02	1e-01	1 x 10 bridging integrator 1 [Source:HGNC Symbol;Acc:HGNC:1052]
19	TOM1	0.37	7e-02	1e-01	2 x 10 target of myb1 (chicken) [Source:HGNC Symbol;Acc:HGNC:10000]
20	PCSK2	-0.32	1e-01	1e-01	1 x 10 proprotein convertase subtilisin/kexin type 2 [Source:HGNC Symbol;Acc:HGNC:10000]

### p-values



# A7\_mel

## Local Summary

%DE = 0.86  
 # metagenes = 24  
 # genes = 234  
 # genes in genesets = 232  
  
 # genes with  $fdr < 0.1$  = 172 ( 35 + / 137 - )  
 # genes with  $fdr < 0.05$  = 112 ( 23 + / 89 - )  
 # genes with  $fdr < 0.01$  = 94 ( 17 + / 77 - )

<r> metagenes = 0.92

<r> genes = 0.08

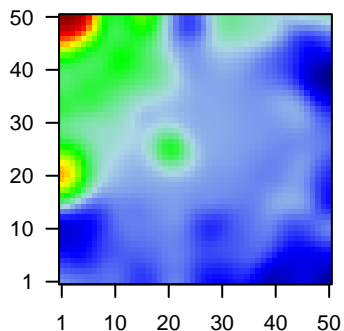
<FC> = -0.31

<shrinkage-t> = -5.44

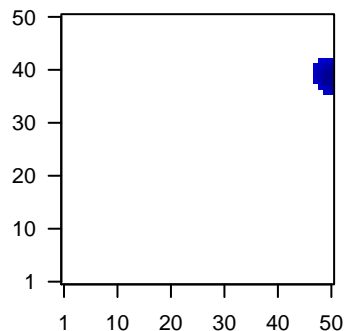
<p-value> = 0

<fdr> = 0.53

### Profile



### Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	CLK1	-1.54	2e-16	2e-15	50 x 40 CDC-like kinase 1 [Source:HGNC Symbol;Acc:HGNC:2068]
2	POLR2K	-1.44	2e-16	2e-15	50 x 41 polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa [S
3	SEC13	-1.75	2e-16	2e-15	50 x 40 SEC13 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:†
4	TBK1	-1.5	2e-16	2e-15	50 x 37 TANK-binding kinase 1 [Source:HGNC Symbol;Acc:HGNC:1
5	HERPUD1	-0.8	9e-16	1e-12	50 x 42 homocysteine-inducible, endoplasmic reticulum stress-induc
6	NMD3	-1.37	4e-14	1e-12	50 x 41 NMD3 ribosome export adaptor [Source:HGNC Symbol;Acc:†
7	WDR45	-1.37	7e-14	3e-10	50 x 39 WD repeat domain 45 [Source:HGNC Symbol;Acc:HGNC:28
8	BRD8	-0.95	1e-11	3e-10	50 x 39 bromodomain containing 8 [Source:HGNC Symbol;Acc:HGNC
9	DPH3	-1.27	2e-11	2e-09	49 x 39 diphthamide biosynthesis 3 [Source:HGNC Symbol;Acc:HGNC
10	SEC31A	-0.75	8e-11	2e-09	50 x 38 SEC31 homolog A (S. cerevisiae) [Source:HGNC Symbol;Acc
11	CFLAR	-1.23	1e-10	2e-08	50 x 39 CASP8 and FADD-like apoptosis regulator [Source:HGNC S
12	PFDN1	-0.85	1e-09	2e-08	50 x 40 prefoldin subunit 1 [Source:HGNC Symbol;Acc:HGNC:8866]
13	MPHOSPH10	-1.19	2e-09	3e-08	50 x 36 M-phase phosphoprotein 10 (U3 small nucleolar ribonucleop
14	GOSR1	-1.13	3e-09	3e-08	50 x 39 golgi SNAP receptor complex member 1 [Source:HGNC Sym
15	SLC39A9	-0.85	4e-09	3e-08	50 x 36 solute carrier family 39, member 9 [Source:HGNC Symbol;Ac
16	LTN1	-1.14	5e-09	3e-08	50 x 40 listerin E3 ubiquitin protein ligase 1 [Source:HGNC Symbol;A
17	SERINC3	-0.86	6e-09	8e-08	50 x 41 serine incorporator 3 [Source:HGNC Symbol;Acc:HGNC:116
18	ZNF195	-1.17	8e-09	8e-08	48 x 40 zinc finger protein 195 [Source:HGNC Symbol;Acc:HGNC:12
19	UBAP2L	-0.88	1e-08	2e-07	50 x 40 ubiquitin associated protein 2-like [Source:HGNC Symbol;Ac
20	RNFT1	-1.15	2e-08	2e-07	50 x 39 ring finger protein, transmembrane 1 [Source:HGNC Symbol;

### p-values

