

# F9\_mel

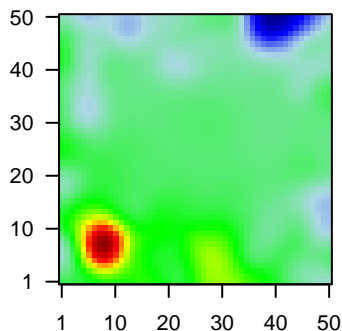
## Global Summary

%DE = 0.17  
 # genes with fdr < 0.2 = 2064 ( 1160 + / 904 - )  
 # genes with fdr < 0.1 = 1509 ( 852 + / 657 - )  
 # genes with fdr < 0.05 = 1151 ( 646 + / 505 - )  
 # genes with fdr < 0.01 = 622 ( 319 + / 303 - )

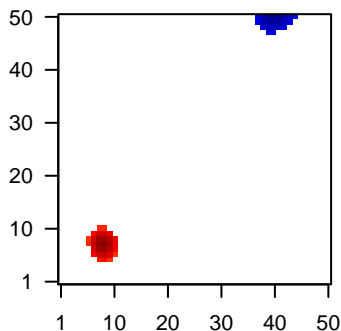
# genes in genesets = 14839

<FC> = 0  
 <shrinkage-t> = -0.05  
 <p-value> = 0.12  
 <fdr> = 0.83

Profile



Regulated Spots

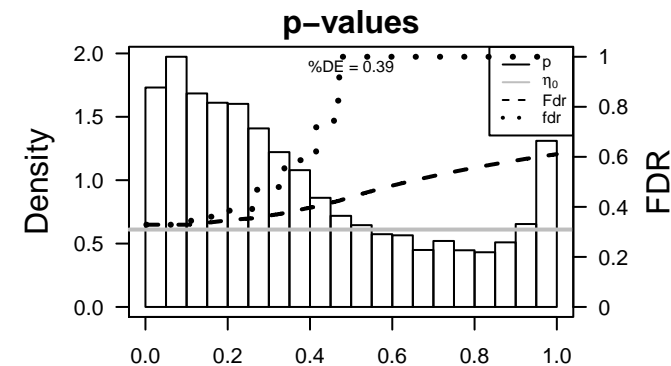
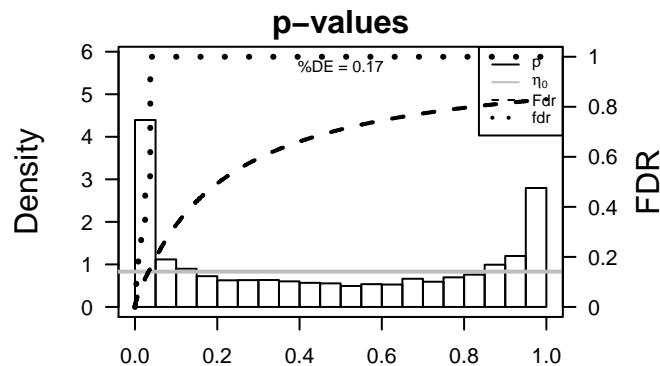


## Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	ACAT1	-1.77	2e-16 1e-13	41 x 50 acetyl-CoA acetyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:1000]
2	ARL2	-1.63	2e-16 1e-13	37 x 50 ADP-ribosylation factor-like 2 [Source:HGNC Symbol;Acc:HGNC:1000]
3	CCNL1	-1.87	2e-16 1e-13	38 x 47 cyclin L1 [Source:HGNC Symbol;Acc:HGNC:20569]
4	CHURC1	-2.07	2e-16 1e-13	39 x 50 churchill domain containing 1 [Source:HGNC Symbol;Acc:HGNC:1000]
5	COPS6	-2.19	2e-16 1e-13	39 x 50 COP9 signalosome subunit 6 [Source:HGNC Symbol;Acc:HGNC:1000]
6	CRYAB	-1.8	2e-16 1e-13	50 x 1 crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
7	EBP	-2.01	2e-16 1e-13	1 x 48 emopamil binding protein (sterol isomerase) [Source:HGNC Symbol;Acc:HGNC:1000]
8	GTF3A	-1.75	2e-16 1e-13	1 x 20 general transcription factor IIIA [Source:HGNC Symbol;Acc:HGNC:1000]
9	MOB1A	-1.81	2e-16 1e-13	38 x 50 MOB kinase activator 1A [Source:HGNC Symbol;Acc:HGNC:1000]
10	NDUFB1	-1.94	2e-16 1e-13	39 x 50 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7k [Source:HGNC Symbol;Acc:HGNC:1000]
11	NDUFB3	-2	2e-16 1e-13	40 x 48 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12 [Source:HGNC Symbol;Acc:HGNC:1000]
12	PET100	-2.07	2e-16 1e-13	6 x 34 PET100 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:1000]
13	PSMC2	-1.81	2e-16 1e-13	21 x 44 proteasome (prosome, macropain) 26S subunit, ATPase, 2 [Source:HGNC Symbol;Acc:HGNC:1000]
14	RAB11A	-1.89	2e-16 1e-13	36 x 50 RAB11A, member RAS oncogene family [Source:HGNC Symbol;Acc:HGNC:1000]
15	SAP30BP	-1.76	2e-16 1e-13	42 x 49 SAP30 binding protein [Source:HGNC Symbol;Acc:HGNC:30000]
16	SEC63	-1.99	2e-16 1e-13	38 x 50 SEC63 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:1000]
17	SEP15	-1.21	2e-16 1e-13	48 x 16
18	TIMM21	-1.79	2e-16 1e-13	14 x 50 translocase of inner mitochondrial membrane 21 homolog (yeast) [Source:HGNC Symbol;Acc:HGNC:1000]
19	TMEM230	-1.84	2e-16 1e-13	39 x 50 transmembrane protein 230 [Source:HGNC Symbol;Acc:HGNC:1000]
20	WBSCR22	-1.75	2e-16 1e-13	45 x 48 Williams Beuren syndrome chromosome region 22 [Source:HGNC Symbol;Acc:HGNC:1000]

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	4.46	0.005	310	miRNA target-miR-548l
2	4.38	0.006	1128	Lymphocyte PANG_BCR DN
3	4.37	0.006	3897	Colon Ca66es1_Colon
4	4.19	0.006	9020	Brain Overlap_fetal_midbrain_ReprPCWk
5	4.1	0.007	80	GSEA C2SEIDEN_ONCOGENESIS_BY_MET
6	3.96	0.008	11	GSEA C2REACTOME_SYNTHESES_OF_PE
7	3.89	0.008	102	miRNA target-miR-600
8	3.86	0.008	340	miRNA target-miR-142-5p
9	3.86	0.008	14	BP histone H4-K5 acetylation
10	3.86	0.008	14	BP histone H4-K8 acetylation
11	3.84	0.009	370	miRNA target-miR-144
12	3.74	0.009	344	miRNA target-miR-548d-5p
13	3.74	0.009	595	TF ICGC_NrstPcr2_targets
14	3.73	0.009	293	miRNA target-miR-548j
15	3.71	0.010	157	miRNA target-miR-450b-5p
16	3.71	0.010	328	miRNA target-miR-548a-5p
17	3.6	0.011	274	miRNA target-miR-548h
18	3.57	0.011	315	miRNA target-miR-559
19	3.51	0.011	251	miRNA target-miR-548l
20	3.51	0.011	145	miRNA target-miR-135a
<i>Underexpressed</i>				
1	-5.78	0.002	447	GSEA C2ENK_UV_RESPONSE_KERATINOCYTE_UP
2	-5.41	0.003	685	GSEA C2KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR
3	-5.34	0.003	368	GSEA C2STEIN_ESRRA_TARGETS_UP
4	-5.16	0.003	619	GSEA C2KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_C
5	-5.09	0.003	694	BP protein complex assembly
6	-5.08	0.003	500	GSEA C2STEIN_ESRRA_TARGETS
7	-4.8	0.004	62	Glio cultured astroglia vs. in vivo astrocytes
8	-4.72	0.004	24	GSEA C2KEGG_HOMOLOGOUS_RECOMBINATION
9	-4.56	0.005	48	GSEA C2REACTOME_DESTABILIZATION_OF_MRNA_BY_AUF1_HNRNP
10	-4.53	0.005	700	GSEA C2MARSON_BOUND_BY_E2F4_UNSTIMULATED
11	-4.51	0.005	7203	Colon Ca66es1_Colon
12	-4.47	0.005	101	GSEA C2REACTOME_S_PHASE
13	-4.44	0.005	181	GSEA C2ALONSO_METASTASIS_UP
14	-4.43	0.005	61	GSEA C2REACTOME_ASSEMBLY_OF_THE_PRE_REPLICATIVE_COMPL
15	-4.37	0.006	52	GSEA C2REACTOME_SCF5KP2_MEDIATED_DEGRADATION_OF_P27_P
16	-4.35	0.006	321	GSEA C2ACEVEDO_NORMAL_TISSUE_ADJACENT_TO_LIVER_TUMOR
17	-4.34	0.006	52	GSEA C2REACTOME_CDT1_ASSOCIATION_WITH_THE_CDC6_ORC_OF
18	-4.32	0.006	198	HM HALLMARK_OXIDATIVE_PHOSPHORYLATION
19	-4.3	0.006	85	GSEA C2REACTOME_SYNTHESES_OF_DNA
20	-4.3	0.006	167	GSEA C2YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER



# F9\_mel

## Local Summary

%DE = 0.99  
 # metagenes = 31  
 # genes = 228  
 # genes in genesets = 227  
  
 # genes with  $fdr < 0.1$  = 223 ( 223 + / 0 -)  
 # genes with  $fdr < 0.05$  = 223 ( 223 + / 0 -)  
 # genes with  $fdr < 0.01$  = 201 ( 201 + / 0 -)

<r> metagenes = 0.89

<r> genes = 0.15

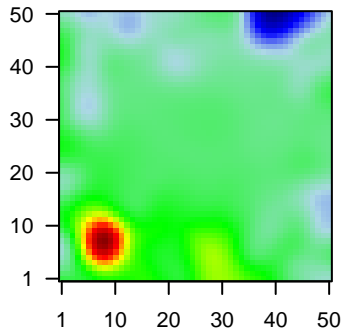
<FC> = 1.03

<shrinkage-t> = 16.04

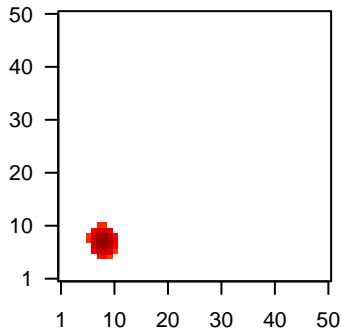
<p-value> = 0

<fdr> = 0.2

### Profile



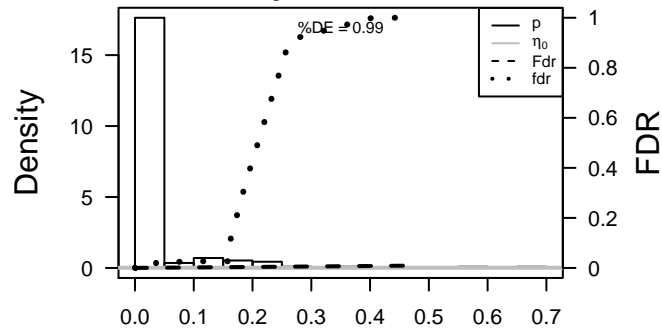
### Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	METAP1D	2.04	6e-12	1e-10	9 x 8 methionyl aminopeptidase type 1D (mitochondrial) [Source:H
2	SLC24A1	1.94	7e-11	1e-10	9 x 9 solute carrier family 24 (sodium/potassium/calcium exchange
3	GPR183	1.92	1e-10	1e-09	9 x 9 G protein-coupled receptor 183 [Source:HGNC Symbol;Acc:I
4	KCNIP4	1.84	7e-10	1e-09	9 x 8 Kv channel interacting protein 4 [Source:HGNC Symbol;Acc:I
5	JAM3	1.8	2e-09	1e-09	10 x 8 junctional adhesion molecule 3 [Source:HGNC Symbol;Acc:H
6	LYSMD2	1.8	2e-09	1e-09	8 x 5 LysM, putative peptidoglycan-binding, domain containing 2 [S
7	TMEM27	1.79	2e-09	1e-09	9 x 8 transmembrane protein 27 [Source:HGNC Symbol;Acc:HGNC
8	CHAMP1	1.78	2e-09	1e-09	9 x 9 chromosome alignment maintaining phosphoprotein 1 [Sourc
9	UGT3A2	1.78	2e-09	1e-09	9 x 8 UDP glycosyltransferase 3 family, polypeptide A2 [Source:HG
10	GPR171	1.78	2e-09	1e-08	9 x 8 G protein-coupled receptor 171 [Source:HGNC Symbol;Acc:I
11	CFAP46	1.73	6e-09	1e-08	9 x 9 cilia and flagella associated protein 46 [Source:HGNC Symbc
12	ADAM22	1.7	1e-08	1e-08	9 x 8 ADAM metallopeptidase domain 22 [Source:HGNC Symbol;A
13	DDX60L	1.69	1e-08	1e-08	7 x 9 DEAD (Asp-Glu-Ala-Asp) box polypeptide 60-like [Source:t
14	ACP6	1.68	1e-08	1e-08	9 x 8 acid phosphatase 6, lysophosphatidic [Source:HGNC Symbo
15	RD3L	1.67	2e-08	1e-08	9 x 9 retinal degeneration 3-like [Source:HGNC Symbol;Acc:HGNC
16	PDCD2L	1.66	2e-08	1e-08	9 x 7 programmed cell death 2-like [Source:HGNC Symbol;Acc:HC
17	ZNF546	1.65	3e-08	1e-08	8 x 8 zinc finger protein 546 [Source:HGNC Symbol;Acc:HGNC:2B
18	PGAP3	1.65	3e-08	9e-08	9 x 8 post-GPI attachment to proteins 3 [Source:HGNC Symbol;Ac
19	C11orf65	1.61	7e-08	9e-08	9 x 8 chromosome 11 open reading frame 65 [Source:HGNC Symt
20	PCSK6	1.59	9e-08	9e-08	9 x 8 proprotein convertase subtilisin/kexin type 6 [Source:HGNC S

### p-values



# F9\_mel

## Local Summary

%DE = 0.78  
 # metagenes = 22  
 # genes = 235  
 # genes in genesets = 235  
  
 # genes with  $fdr < 0.1$  = 137 ( 4 + / 133 -)  
 # genes with  $fdr < 0.05$  = 137 ( 4 + / 133 -)  
 # genes with  $fdr < 0.01$  = 99 ( 1 + / 98 -)

<r> metagenes = 0.89

<r> genes = 0.08

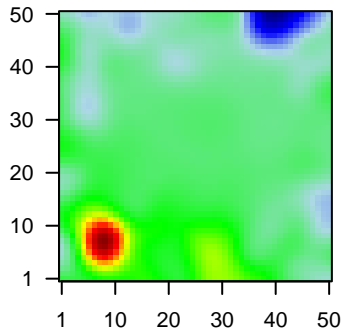
<FC> = -0.69

<shrinkage-t> = -12.46

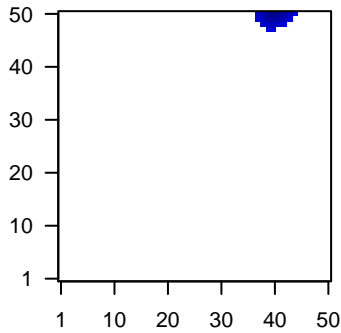
<p-value> = 0

<fdr> = 0.46

Profile



Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ACAT1	-1.77	2e-16	1e-15	41 x 50 acetyl-CoA acetyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:10000]
2	ARL2	-1.63	2e-16	1e-15	37 x 50 ADP-ribosylation factor-like 2 [Source:HGNC Symbol;Acc:HGNC:10000]
3	CHURC1	-2.07	2e-16	1e-15	39 x 50 churchill domain containing 1 [Source:HGNC Symbol;Acc:HGNC:10000]
4	COPS6	-2.19	2e-16	1e-15	39 x 50 COP9 signalosome subunit 6 [Source:HGNC Symbol;Acc:HGNC:10000]
5	MOB1A	-1.81	2e-16	1e-15	38 x 50 MOB kinase activator 1A [Source:HGNC Symbol;Acc:HGNC:10000]
6	NDUFB1	-1.94	2e-16	1e-15	39 x 50 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7k [Source:HGNC Symbol;Acc:HGNC:10000]
7	NDUFB3	-2	2e-16	1e-15	40 x 48 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12 [Source:HGNC Symbol;Acc:HGNC:10000]
8	SAP30BP	-1.76	2e-16	1e-15	42 x 49 SAP30 binding protein [Source:HGNC Symbol;Acc:HGNC:10000]
9	SEC63	-1.99	2e-16	1e-15	38 x 50 SEC63 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:10000]
10	TMEM230	-1.84	2e-16	1e-15	39 x 50 transmembrane protein 230 [Source:HGNC Symbol;Acc:HGNC:10000]
11	CRYZL1	-1.7	4e-16	3e-12	44 x 50 crystallin, zeta (quinone reductase)-like 1 [Source:HGNC Symbol;Acc:HGNC:10000]
12	RBM4	-1.66	6e-14	6e-11	38 x 50 RNA binding motif protein 4 [Source:HGNC Symbol;Acc:HGNC:10000]
13	JAGN1	-1.62	1e-12	2e-10	44 x 50 jagunal homolog 1 (Drosophila) [Source:HGNC Symbol;Acc:HGNC:10000]
14	C14orf119	-1.52	5e-12	1e-09	40 x 50 chromosome 14 open reading frame 119 [Source:HGNC Symbol;Acc:HGNC:10000]
15	ZFAND6	-1.57	3e-11	1e-09	43 x 50 zinc finger, AN1-type domain 6 [Source:HGNC Symbol;Acc:HGNC:10000]
16	DHRS7	-1.55	5e-11	1e-09	41 x 49 dehydrogenase/reductase (SDR family) member 7 [Source:HGNC Symbol;Acc:HGNC:10000]
17	CHURC1-FN	-1.54	7e-11	4e-09	39 x 50 CHURC1-FNTB readthrough [Source:HGNC Symbol;Acc:HGNC:10000]
18	PSMD10	-1.53	2e-10	4e-09	40 x 49 proteasome (prosome, macropain) 26S subunit, non-ATPase [Source:HGNC Symbol;Acc:HGNC:10000]
19	PPIE	-1.53	2e-10	4e-09	39 x 50 peptidylprolyl isomerase E (cyclophilin E) [Source:HGNC Symbol;Acc:HGNC:10000]
20	SPP1	-1.53	3e-10	2e-08	38 x 48 secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:HGNC:10000]

p-values

