

# B10\_mel

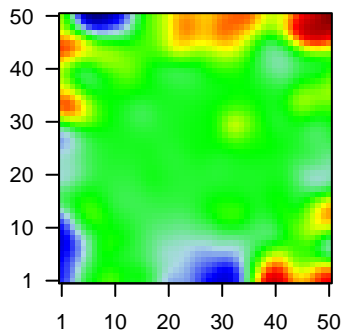
## Global Summary

%DE = 0.21  
 # genes with  $fdr < 0.2$  = 2545 ( 1573 + / 972 - )  
 # genes with  $fdr < 0.1$  = 2098 ( 1317 + / 781 - )  
 # genes with  $fdr < 0.05$  = 1751 ( 1121 + / 630 - )  
 # genes with  $fdr < 0.01$  = 1061 ( 706 + / 355 - )

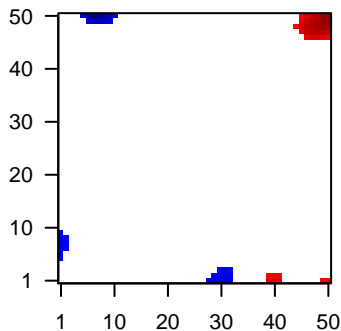
# genes in genesets = 14839

<FC> = 0  
 <shrinkage-t> = 0.05  
 <p-value> = 0.08  
 <fdr> = 0.79

Profile



Regulated Spots



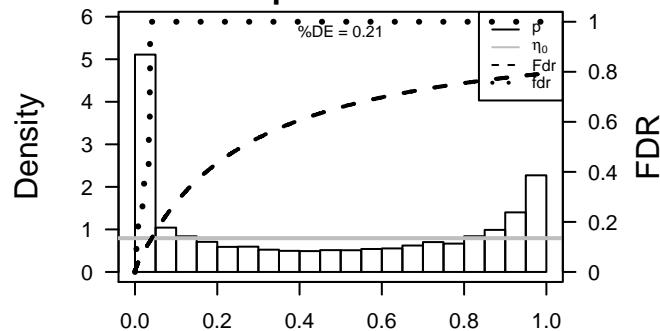
## Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ACTL6A	-1.18	2e-16	2e-13	4 x 50 actin-like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
2	CDKN3	-1.65	2e-16	2e-13	6 x 50 cyclin-dependent kinase inhibitor 3 [Source:HGNC Symbol;A
3	DCAF13	-1.73	2e-16	2e-13	1 x 1 DDB1 and CUL4 associated factor 13 [Source:HGNC Symbo
4	FAM210A	-1.39	2e-16	2e-13	4 x 40 family with sequence similarity 210, member A [Source:HGNC
5	FH	-1.46	2e-16	2e-13	5 x 39 fumarate hydratase [Source:HGNC Symbol;Acc:HGNC:3700]
6	HIST1H3D	2.16	2e-16	2e-13	50 x 1 histone cluster 1, H3d [Source:HGNC Symbol;Acc:HGNC:47f
7	HSPH1	-1.34	2e-16	2e-13	27 x 11 heat shock 105kDa/110kDa protein 1 [Source:HGNC Symbol
8	MPV17	-1.53	2e-16	2e-13	4 x 40 MpV17 mitochondrial inner membrane protein [Source:HGNC
9	SLC44A2	1.87	2e-16	2e-13	36 x 50 solute carrier family 44 (choline transporter), member 2 [Sour
10	SNRNP25	-1.58	2e-16	2e-13	1 x 46 small nuclear ribonucleoprotein 25kDa (U11/U12) [Source:HC
11	SWAP70	-1.48	2e-16	2e-13	21 x 7 SWAP switching B-cell complex 70kDa subunit [Source:HGNC
12	UROD	-1.48	2e-16	2e-13	35 x 3 uroporphyrinogen decarboxylase [Source:HGNC Symbol;Acc
13	ZZZ3	-1.59	2e-16	2e-13	1 x 11 zinc finger, ZZ-type containing 3 [Source:HGNC Symbol;Acc
14	DDB1	-1.43	4e-16	3e-12	33 x 50 damage-specific DNA binding protein 1, 127kDa [Source:HG
15	TCF12	-1.51	7e-16	7e-12	6 x 34 transcription factor 12 [Source:HGNC Symbol;Acc:HGNC:11f
16	FAM227A	1.81	1e-15	7e-12	41 x 16 family with sequence similarity 227, member A [Source:HGNC
17	SHQ1	1.79	3e-15	7e-12	18 x 43 SHQ1, H/ACA ribonucleoprotein assembly factor [Source:HG
18	UQCC1	-1.48	3e-15	7e-12	48 x 15 ubiquinol-cytochrome c reductase complex assembly factor 1
19	CSDE1	-0.94	3e-15	1e-11	36 x 47 cold shock domain containing E1, RNA-binding [Source:HGNC
20	FADS3	1.78	4e-15	1e-11	50 x 4 fatty acid desaturase 3 [Source:HGNC Symbol;Acc:HGNC:35

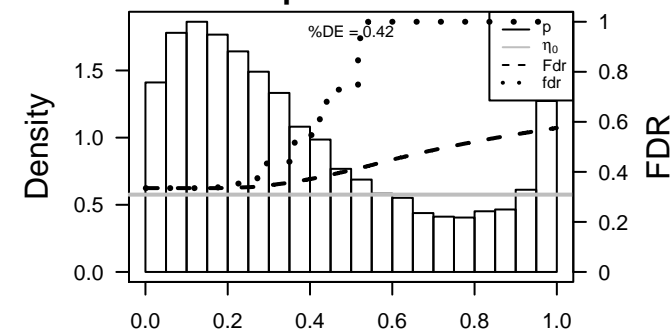
## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	5.28	0.003	30	BP cholesterol biosynthetic process
2	5.19	0.003	22	GSEA C2REACTOME_CHOLESTEROL_BIOSYNTHESIS
3	5.05	0.003	23	BP DNA methylation
4	4.59	0.005	24	GSEA C2SCHMIDT_POR_TARGETS_IN_LIMB_BUD_UP
5	4.5	0.005	11	GSEA C2REACTOME_ACTIVATION_OF_CHAPERONES_BY_ATF6_ALPH
6	4.4	0.005	9027	Colon Cancer Colon
7	4.4	0.005	9	GSEA C2REACTOME_ACTIVATION_OF_CHAPERONE_GENES_BY_ATF6
8	4.36	0.006	8580	Colon Cancer Colon
9	4.25	0.006	24	GSEA C2KEGG_SELENOAMINO_ACID_METABOLISM
10	3.98	0.008	12	BP sterol biosynthetic process
11	3.81	0.009	26	BP RNA phosphodiester bond hydrolysis, exonucleolytic
12	3.78	0.009	23	GSEA C2CHNG_MULTIPLE_MYELOMA_HYPERPLOID_UP
13	3.77	0.009	5940	Brain Overlap_fetal_midbrain_HetRpts
14	3.77	0.009	65	GSEA C2TCGA_GLIOMASTOMA_COPY_NUMBER_UP
15	3.74	0.009	36	MF tRNA binding
16	3.73	0.009	74	HM HALLMARK_CHOLESTEROL_HOMEOSTASIS
17	3.68	0.010	11	GSEA C2STEGMEIER_PRE-MITOTIC_CELL_CYCLE_REGULATORS
18	3.64	0.010	815	BP lipid metabolic process
19	3.61	0.010	12	MF protein methyltransferase activity
20	3.53	0.011	11	Glio WILLSCHEER_GBM_LTSwt_proteomics-C_UP
<i>Underexpressed</i>				
1	-7.7	7e-04	142	Glio WILLSCHEER_GBM_Verhaak-CL_up (C)
2	-6.9	1e-03	139	GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
3	-6.66	1e-03	242	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN
4	-6.4	1e-03	99	GSEA C2LEE_EARLY_T_LYMPHOCYTE_UP
5	-6.16	2e-03	81	GSEA C2GRAHAM_NORMAL QUIESCENT_VS_NORMAL_DIVIDING_DN
6	-6.13	2e-02	16	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
7	-5.86	2e-03	550	GSEA C2SOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
8	-5.54	2e-03	31	GSEA C2PID_AURORA_A_PATHWAY
9	-5.51	3e-03	54	GSEA C2KANG_DOXORUBICIN_RESISTANCE_UP
10	-5.48	3e-03	118	GSEA C2ODONNELL_TFRC_TARGETS_DN
11	-5.27	3e-03	42	GSEA C2YU_MYC_TARGETS_UP
12	-5.25	3e-03	155	GSEA C2HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
13	-5.06	3e-03	162	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL QUIESCENT_UP
14	-5.05	3e-03	270	GSEA C2BASAKI_YBX1_TARGETS_UP
15	-4.99	4e-03	75	GSEA C2SCIBETTA_KDMSB_TARGETS_DN
16	-4.98	4e-03	96	GSEA C2ORONQUIST_IL6_DEPRIVATION_DN
17	-4.96	4e-03	124	GSEA C2ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
18	-4.93	4e-03	84	GSEA C2MORI_LARGE_PRE_BII_LYMPHOCYTE_UP
19	-4.9	4e-03	44	GSEA C2WHITFIELD_CELL_CYCLE_LITERATURE
20	-4.85	4e-03	291	GSEA C2HORIUCHI_WTAP_TARGETS_DN

p-values



p-values

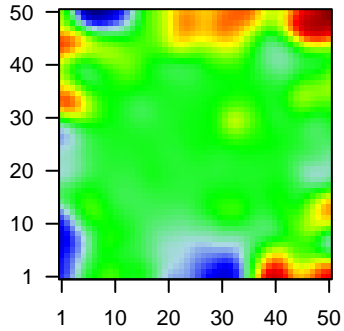


# B10\_mel

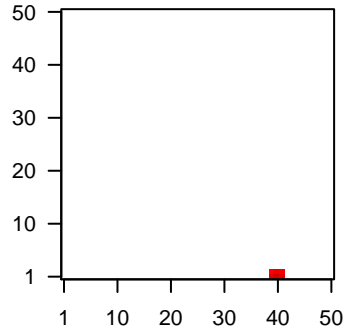
## Local Summary

%DE = 0.64  
 # metagenes = 6  
 # genes = 69  
 # genes in genesets = 69  
  
 # genes with  $fdr < 0.1$  = 31 ( 25 + / 6 - )  
 # genes with  $fdr < 0.05$  = 27 ( 22 + / 5 - )  
 # genes with  $fdr < 0.01$  = 20 ( 17 + / 3 - )  
  
 $\langle r \rangle$  metagenes = 0.98  
 $\langle r \rangle$  genes = 0.12  
  
 $\langle FC \rangle$  = 0.28  
 $\langle \text{shrinkage-t} \rangle$  = 4.55  
 $\langle p\text{-value} \rangle$  = 0.01  
 $\langle fdr \rangle$  = 0.57

Profile



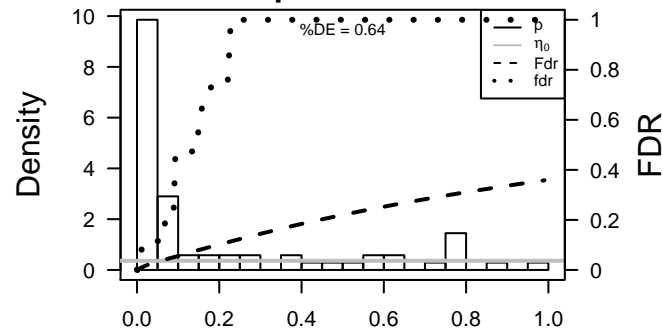
Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ALDH1A2	1.35	2e-09	9e-08	39 x 1 aldehyde dehydrogenase 1 family, member A2 [Source:HGNC
2	ADAMTSL3	1.31	7e-09	9e-08	40 x 1 ADAMTS-like 3 [Source:HGNC Symbol;Acc:HGNC:14633]
3	CHKB	1.3	1e-08	3e-06	39 x 1 choline kinase beta [Source:HGNC Symbol;Acc:HGNC:1938]
4	NBEA	1.19	1e-07	3e-06	41 x 1 neurobeachin [Source:HGNC Symbol;Acc:HGNC:7648]
5	MXD1	1.17	3e-07	2e-05	39 x 1 MAX dimerization protein 1 [Source:HGNC Symbol;Acc:HGNC
6	ACOT2	1.08	2e-06	2e-05	40 x 1 acyl-CoA thioesterase 2 [Source:HGNC Symbol;Acc:HGNC::
7	MAU2	1.08	2e-06	5e-05	40 x 1 MAU2 sister chromatid cohesion factor [Source:HGNC Symb
8	RHBDD3	1.05	4e-06	3e-04	39 x 2 rhomboid domain containing 3 [Source:HGNC Symbol;Acc:Hi
9	MINPP1	0.98	2e-05	3e-04	39 x 1 multiple inositol-polyphosphate phosphatase 1 [Source:HGNC
10	CCS	0.96	2e-05	5e-04	41 x 2 copper chaperone for superoxide dismutase [Source:HGNC S
11	FBXL4	0.9	7e-05	5e-04	40 x 1 F-box and leucine-rich repeat protein 4 [Source:HGNC Syml
12	CNOT2	0.42	8e-05	5e-04	39 x 1 CCR4-NOT transcription complex, subunit 2 [Source:HGNC :
13	ATP8B2	0.89	8e-05	1e-03	39 x 1 ATPase, aminophospholipid transporter, class I, type 8B, men
14	APC	0.84	1e-04	1e-03	41 x 2 adenomatous polyposis coli [Source:HGNC Symbol;Acc:HGNC
15	YAP1	0.67	2e-04	1e-03	39 x 1 Yes-associated protein 1 [Source:HGNC Symbol;Acc:HGNC:
16	MKLN1	0.72	3e-04	1e-03	40 x 1 muskelin 1, intracellular mediator containing kelch motifs [Sou
17	ACOT1	0.81	3e-04	1e-03	40 x 1 acyl-CoA thioesterase 1 [Source:HGNC Symbol;Acc:HGNC::
18	MAP3K7	-0.81	4e-04	1e-03	40 x 1 mitogen-activated protein kinase kinase kinase 7 [Source:HC
19	ATPAF2	-0.8	4e-04	1e-03	39 x 1 ATP synthase mitochondrial F1 complex assembly factor 2 [S
20	ARFIP1	-0.8	5e-04	3e-03	40 x 1 ADP-ribosylation factor interacting protein 1 [Source:HGNC S

p-values



# B10\_mel

## Local Summary

%DE = 0.86  
 # metagenes = 2  
 # genes = 111  
 # genes in genesets = 111  
  
 # genes with  $fdr < 0.1$  = 58 ( 45 + / 13 - )  
 # genes with  $fdr < 0.05$  = 57 ( 45 + / 12 - )  
 # genes with  $fdr < 0.01$  = 37 ( 34 + / 3 - )

<r> metagenes = 1

<r> genes = 0.27

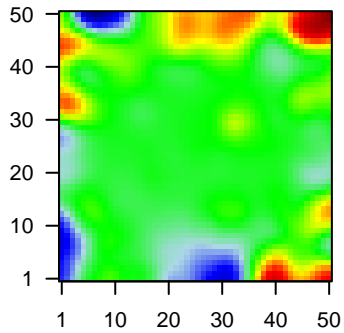
<FC> = 0.22

<shrinkage-t> = 3.63

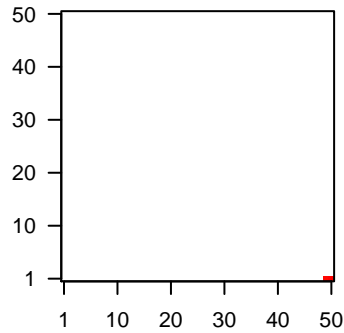
<p-value> = 0

<fdr> = 0.53

Profile



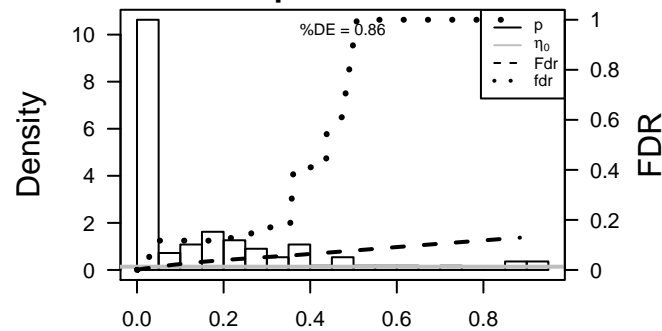
Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	HIST1H3D	2.16	2e-16	3e-15	50 x 1 histone cluster 1, H3d [Source:HGNC Symbol;Acc:HGNC:476]
2	CRYAB	1.05	2e-12	2e-10	50 x 1 crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
3	EFNA1	1.53	2e-11	4e-09	50 x 1 ephrin-A1 [Source:HGNC Symbol;Acc:HGNC:3221]
4	PTPRZ1	1.43	3e-10	1e-08	50 x 1 protein tyrosine phosphatase, receptor-type, Z polypeptide 1
5	ITGA1	1.39	9e-10	1e-07	50 x 1 integrin, alpha 1 [Source:HGNC Symbol;Acc:HGNC:6134]
6	SATB1	1.31	9e-09	3e-07	50 x 1 SATB homeobox 1 [Source:HGNC Symbol;Acc:HGNC:10541]
7	PLXNB2	1.26	3e-08	2e-06	50 x 1 plexin B2 [Source:HGNC Symbol;Acc:HGNC:9104]
8	KIAA0922	1.19	2e-07	2e-05	49 x 1 KIAA0922 [Source:HGNC Symbol;Acc:HGNC:29146]
9	MATN2	1.07	3e-06	2e-05	50 x 1 matrilin 2 [Source:HGNC Symbol;Acc:HGNC:6908]
10	HDAC9	1.06	3e-06	2e-05	50 x 1 histone deacetylase 9 [Source:HGNC Symbol;Acc:HGNC:146]
11	CALD1	0.67	4e-06	4e-05	50 x 1 caldesmon 1 [Source:HGNC Symbol;Acc:HGNC:1441]
12	VTN	1.02	6e-06	5e-05	50 x 1 vitronectin [Source:HGNC Symbol;Acc:HGNC:12724]
13	SORBS2	1	1e-05	5e-05	50 x 1 sorbin and SH3 domain containing 2 [Source:HGNC Symbol;Acc:HGNC:12724]
14	LGALS1	0.72	1e-05	6e-05	50 x 1 lectin, galactoside-binding, soluble, 1 [Source:HGNC Symbol;Acc:HGNC:12724]
15	LIMA1	0.96	2e-05	6e-05	49 x 1 LIM domain and actin binding 1 [Source:HGNC Symbol;Acc:HGNC:12724]
16	AMOTL2	0.95	3e-05	6e-05	49 x 1 angiomin like 2 [Source:HGNC Symbol;Acc:HGNC:17812]
17	TGIF1	0.81	3e-05	6e-05	50 x 1 TGFB-induced factor homeobox 1 [Source:HGNC Symbol;Acc:HGNC:12724]
18	HIST1H2AC	0.95	3e-05	8e-05	50 x 1 histone cluster 1, H2ac [Source:HGNC Symbol;Acc:HGNC:476]
19	FAM98A	0.91	4e-05	8e-05	49 x 1 family with sequence similarity 98, member A [Source:HGNC Symbol;Acc:HGNC:12724]
20	SLFN12	0.93	4e-05	2e-04	49 x 1 schlafen family member 12 [Source:HGNC Symbol;Acc:HGNC:12724]

p-values



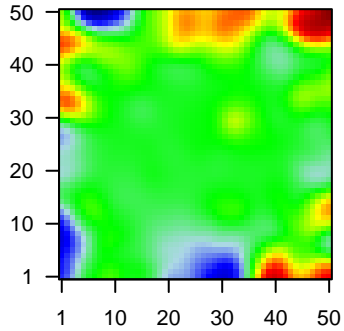
# B10\_mel

## Local Summary

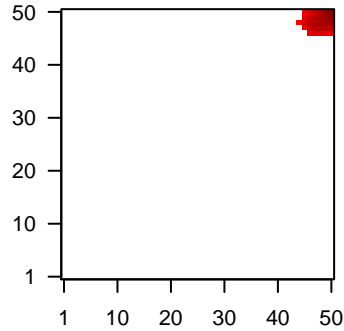
%DE = 0.69  
 # metagenes = 30  
 # genes = 379  
 # genes in genesets = 378  
  
 # genes with  $fdr < 0.1$  = 166 ( 128 + / 38 - )  
 # genes with  $fdr < 0.05$  = 115 ( 89 + / 26 - )  
 # genes with  $fdr < 0.01$  = 92 ( 71 + / 21 - )

$\langle r \rangle$  metagenes = 0.88  
 $\langle r \rangle$  genes = 0.08  
  
 $\langle FC \rangle$  = 0.22  
 $\langle \text{shrinkage-t} \rangle$  = 3.57  
 $\langle p\text{-value} \rangle$  = 0.01  
 $\langle fdr \rangle$  = 0.61

Profile



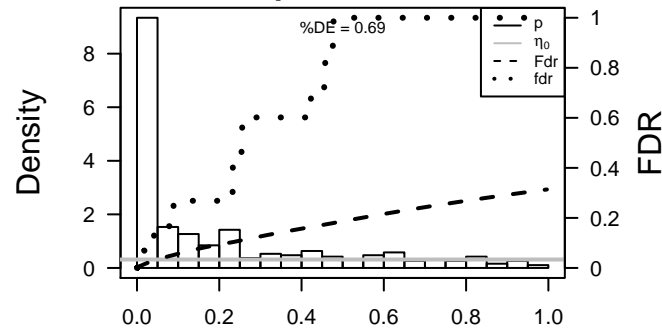
Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	TMEM53	1.71	5e-14	7e-12	50 x 47 transmembrane protein 53 [Source:HGNC Symbol;Acc:HGNC:10000]
2	SCFD1	-1.34	1e-13	1e-10	48 x 50 sec1 family domain containing 1 [Source:HGNC Symbol;Acc:HGNC:10000]
3	LUZP6	1.59	2e-12	1e-10	50 x 49 leucine zipper protein 6 [Source:HGNC Symbol;Acc:HGNC:30000]
4	GSDMB	1.59	3e-12	5e-09	50 x 47 gasdermin B [Source:HGNC Symbol;Acc:HGNC:23690]
5	GATSL3	1.49	5e-11	2e-08	46 x 48 GATS protein-like 3 [Source:HGNC Symbol;Acc:HGNC:3442]
6	PRPSAP2	-1.31	2e-10	2e-08	47 x 50 phosphoribosyl pyrophosphate synthetase-associated protein 2 [Source:HGNC Symbol;Acc:HGNC:10000]
7	PKN1	1.42	4e-10	7e-08	47 x 50 protein kinase N1 [Source:HGNC Symbol;Acc:HGNC:9405]
8	BNIP3L	-1.26	1e-09	7e-08	45 x 50 BCL2/adenovirus E1B 19kDa interacting protein 3-like [Source:HGNC Symbol;Acc:HGNC:10000]
9	WIP1	-0.8	2e-09	7e-08	47 x 49 WD repeat domain, phosphoinositide interacting 1 [Source:HGNC Symbol;Acc:HGNC:10000]
10	YIPF3	-0.77	2e-09	8e-08	45 x 50 Yip1 domain family, member 3 [Source:HGNC Symbol;Acc:HGNC:10000]
11	PHF8	1.35	3e-09	4e-07	50 x 47 PHD finger protein 8 [Source:HGNC Symbol;Acc:HGNC:2067]
12	NLRC5	1.32	6e-09	4e-07	50 x 50 NLR family, CARD domain containing 5 [Source:HGNC Symbol;Acc:HGNC:10000]
13	PDE8A	1.3	9e-09	1e-06	50 x 47 phosphodiesterase 8A [Source:HGNC Symbol;Acc:HGNC:87]
14	DPH7	1.26	3e-08	1e-06	49 x 46 diphthamide biosynthesis 7 [Source:HGNC Symbol;Acc:HGNC:10000]
15	ZMYM2	1.24	4e-08	1e-06	50 x 49 zinc finger, MYM-type 2 [Source:HGNC Symbol;Acc:HGNC:10000]
16	CDK16	1.24	4e-08	4e-06	50 x 50 cyclin-dependent kinase 16 [Source:HGNC Symbol;Acc:HGNC:10000]
17	CCND1	1.14	8e-08	5e-06	48 x 50 cyclin D1 [Source:HGNC Symbol;Acc:HGNC:1582]
18	SPHK2	1.19	2e-07	5e-06	47 x 46 sphingosine kinase 2 [Source:HGNC Symbol;Acc:HGNC:188]
19	TATDN3	1.18	2e-07	5e-06	46 x 47 TatD DNase domain containing 3 [Source:HGNC Symbol;Acc:HGNC:10000]
20	MED29	1.18	2e-07	6e-06	45 x 47 mediator complex subunit 29 [Source:HGNC Symbol;Acc:HGNC:10000]

p-values



# B10\_mel

## Local Summary

%DE = 0.38  
 # metagenes = 12  
 # genes = 153  
 # genes in genesets = 149  
  
 # genes with  $fdr < 0.1$  = 19 ( 7 + / 12 - )  
 # genes with  $fdr < 0.05$  = 15 ( 6 + / 9 - )  
 # genes with  $fdr < 0.01$  = 6 ( 2 + / 4 - )

<r> metagenes = 0.97

<r> genes = 0.18

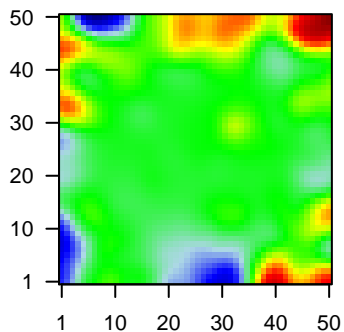
<FC> = -0.18

<shrinkage-t> = -2.82

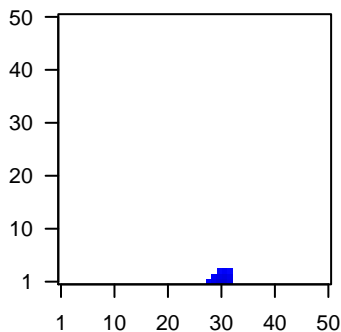
<p-value> = 0.1

<fdr> = 0.79

Profile



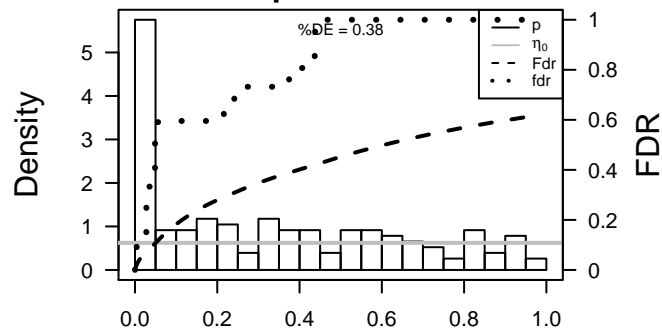
Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	TMEM98	-0.94	5e-06	4e-04	32 x 1 transmembrane protein 98 [Source:HGNC Symbol;Acc:HGNC:10811]
2	QSER1	-1.01	9e-06	1e-03	29 x 1 glutamine and serine rich 1 [Source:HGNC Symbol;Acc:HGNC:10812]
3	GGNBP2	-0.83	2e-05	4e-03	32 x 1 gametogenetin binding protein 2 [Source:HGNC Symbol;Acc:HGNC:10813]
4	YME1L1	-0.91	6e-05	4e-03	31 x 2 YME1-like 1 ATPase [Source:HGNC Symbol;Acc:HGNC:12814]
5	STYX	0.88	1e-04	4e-03	31 x 1 serine/threonine/tyrosine interacting protein [Source:HGNC Symbol;Acc:HGNC:10815]
6	BANP	0.85	2e-04	4e-03	29 x 1 BTG3 associated nuclear protein [Source:HGNC Symbol;Acc:HGNC:10816]
7	ARHGEF3	0.85	2e-04	2e-02	32 x 1 Rho guanine nucleotide exchange factor (GEF) 3 [Source:HGNC Symbol;Acc:HGNC:10817]
8	FASTKD5	0.79	5e-04	2e-02	32 x 1 FAST kinase domains 5 [Source:HGNC Symbol;Acc:HGNC:10818]
9	PIK3C2A	-0.71	1e-03	2e-02	32 x 1 phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 alpha [Source:HGNC Symbol;Acc:HGNC:10819]
10	ABHD13	0.73	1e-03	2e-02	28 x 1 abhydrolase domain containing 13 [Source:HGNC Symbol;Acc:HGNC:10820]
11	UHK1	-0.68	1e-03	2e-02	31 x 2 U2AF homology motif (UHM) kinase 1 [Source:HGNC Symbol;Acc:HGNC:10821]
12	TRIM2	-0.73	1e-03	2e-02	30 x 1 tripartite motif containing 2 [Source:HGNC Symbol;Acc:HGNC:10822]
13	GIT1	-0.72	1e-03	2e-02	31 x 1 G protein-coupled receptor kinase interacting ArfGAP 1 [Source:HGNC Symbol;Acc:HGNC:10823]
14	BTBD7	0.72	2e-03	2e-02	30 x 2 BTB (POZ) domain containing 7 [Source:HGNC Symbol;Acc:HGNC:10824]
15	ETS1	-0.72	2e-03	2e-02	28 x 1 v-ets avian erythroblastosis virus E26 oncogene homolog 1 [Source:HGNC Symbol;Acc:HGNC:10825]
16	VPS33A	-0.71	2e-03	6e-02	31 x 1 vacuolar protein sorting 33 homolog A (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:10826]
17	YWHAQ	-0.67	3e-03	6e-02	30 x 1 tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activating protein [Source:HGNC Symbol;Acc:HGNC:10827]
18	AP5S1	-0.66	3e-03	6e-02	32 x 1 adaptor-related protein complex 5, sigma 1 subunit [Source:HGNC Symbol;Acc:HGNC:10828]
19	APBB3	0.65	4e-03	6e-02	32 x 1 amyloid beta (A4) precursor protein-binding, family B, member 3 [Source:HGNC Symbol;Acc:HGNC:10829]
20	GBF1	0.65	4e-03	1e-01	30 x 1 golgi brefeldin A resistant guanine nucleotide exchange factor 1 [Source:HGNC Symbol;Acc:HGNC:10830]

p-values



# B10\_mel

## Local Summary

%DE = 0.52  
 # metagenes = 9  
 # genes = 211  
 # genes in genesets = 209  
  
 # genes with  $fdr < 0.1$  = 59 ( 18 + / 41 - )  
 # genes with  $fdr < 0.05$  = 41 ( 15 + / 26 - )  
 # genes with  $fdr < 0.01$  = 29 ( 11 + / 18 - )

<r> metagenes = 0.91

<r> genes = 0.1

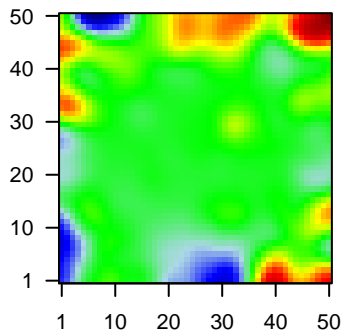
<FC> = -0.16

<shrinkage-t> = -2.59

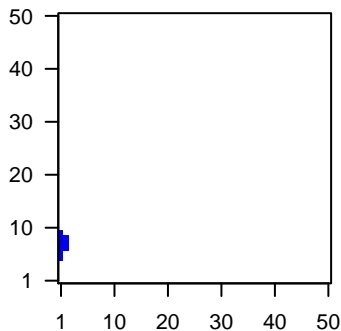
<p-value> = 0.03

<fdr> = 0.71

Profile



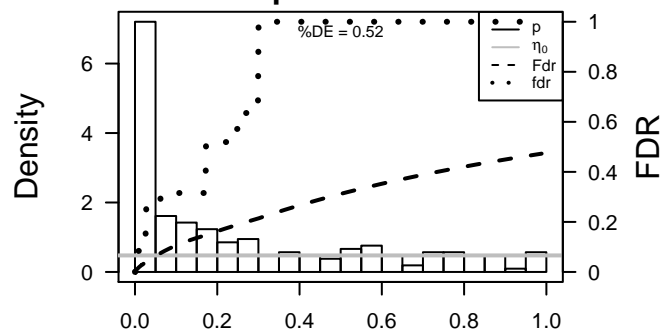
Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ATP6V0A1	-1.28	3e-14	2e-08	1 x 10 ATPase, H+ transporting, lysosomal V0 subunit a1 [Source:HGNC Symbol;Acc:HGNC:10240]
2	PEX19	-1.29	4e-10	2e-08	1 x 8 peroxisomal biogenesis factor 19 [Source:HGNC Symbol;Acc:HGNC:10240]
3	LPHN1	1.41	4e-10	5e-08	1 x 5
4	MGAT5	1.39	9e-10	1e-07	1 x 9 mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyl transferase 5 [Source:HGNC Symbol;Acc:HGNC:10240]
5	FUBP3	1.36	2e-09	3e-06	1 x 8 far upstream element (FUSE) binding protein 3 [Source:HGNC Symbol;Acc:HGNC:10240]
6	FEZ1	1.23	5e-08	3e-06	1 x 7 fasciculation and elongation protein zeta 1 (zyglin I) [Source:HGNC Symbol;Acc:HGNC:10240]
7	RHBDF2	1.23	6e-08	2e-05	1 x 5 rhomboid 5 homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:HGNC:10240]
8	NCOA4	-0.81	2e-07	7e-05	1 x 7 nuclear receptor coactivator 4 [Source:HGNC Symbol;Acc:HGNC:10240]
9	TRMT2A	1.11	1e-06	4e-04	1 x 6 tRNA methyltransferase 2 homolog A (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:10240]
10	COX11	-0.94	5e-06	1e-03	1 x 5 COX11 cytochrome c oxidase copper chaperone [Source:HGNC Symbol;Acc:HGNC:10240]
11	C12orf73	-0.98	2e-05	1e-03	1 x 10 chromosome 12 open reading frame 73 [Source:HGNC Symbol;Acc:HGNC:10240]
12	AGPAT6	-0.95	3e-05	1e-03	1 x 9 1-acylglycerol-3-phosphate O-acyltransferase 6 [Source:HGNC Symbol;Acc:HGNC:10240]
13	SLMAP	-0.92	5e-05	1e-03	1 x 10 sarcolemma associated protein [Source:HGNC Symbol;Acc:HGNC:10240]
14	WDR13	-0.91	6e-05	1e-03	1 x 8 WD repeat domain 13 [Source:HGNC Symbol;Acc:HGNC:10240]
15	SULT1C2	-0.91	6e-05	1e-03	1 x 9 sulfotransferase family, cytosolic, 1C, member 2 [Source:HGNC Symbol;Acc:HGNC:10240]
16	MFSD5	0.89	6e-05	2e-03	1 x 8 major facilitator superfamily domain containing 5 [Source:HGNC Symbol;Acc:HGNC:10240]
17	TBC1D16	-0.89	9e-05	3e-03	1 x 10 TBC1 domain family, member 16 [Source:HGNC Symbol;Acc:HGNC:10240]
18	ADD1	-0.77	1e-04	6e-03	1 x 8 adducin 1 (alpha) [Source:HGNC Symbol;Acc:HGNC:243]
19	OSBP19	-0.69	2e-04	6e-03	1 x 8 oxysterol binding protein-like 9 [Source:HGNC Symbol;Acc:HGNC:10240]
20	FUNDC1	-0.83	3e-04	6e-03	1 x 7 FUN14 domain containing 1 [Source:HGNC Symbol;Acc:HGNC:10240]

p-values



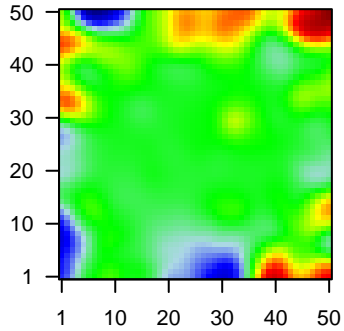
# B10\_mel

## Local Summary

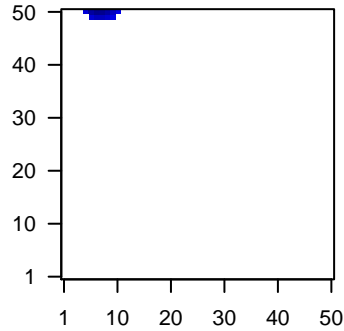
%DE = 0.88  
 # metagenes = 12  
 # genes = 213  
 # genes in genesets = 213  
  
 # genes with  $fdr < 0.1$  = 151 ( 30 + / 121 - )  
 # genes with  $fdr < 0.05$  = 123 ( 24 + / 99 - )  
 # genes with  $fdr < 0.01$  = 58 ( 11 + / 47 - )

$\langle r \rangle$  metagenes = 0.98  
 $\langle r \rangle$  genes = 0.31  
  
 $\langle FC \rangle$  = -0.29  
 $\langle \text{shrinkage-t} \rangle$  = -4.57  
 $\langle p\text{-value} \rangle$  = 0.01  
 $\langle fdr \rangle$  = 0.59

Profile



Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	CDKN3	-1.65	2e-16	6e-15	6 x 50 cyclin-dependent kinase inhibitor 3 [Source:HGNC Symbol;A
2	TUBB4B	-1.3	2e-13	4e-08	7 x 50 tubulin, beta 4B class IVb [Source:HGNC Symbol;Acc:HGNC
3	BIRC5	-1.24	1e-09	4e-07	6 x 50 baculoviral IAP repeat containing 5 [Source:HGNC Symbol;A
4	TRIP13	-1.2	2e-08	6e-07	5 x 50 thyroid hormone receptor interactor 13 [Source:HGNC Symb
5	NFYB	1.24	4e-08	3e-06	5 x 50 nuclear transcription factor Y, beta [Source:HGNC Symbol;Ac
6	HSD17B4	-0.9	1e-07	6e-06	11 x 50 hydroxysteroid (17-beta) dehydrogenase 4 [Source:HGNC S
7	COMMD4	-0.89	6e-07	6e-06	11 x 50 COMM domain containing 4 [Source:HGNC Symbol;Acc:HG
8	KANSL2	-1.11	8e-07	6e-06	9 x 50 KAT8 regulatory NSL complex subunit 2 [Source:HGNC Syml
9	CDC25B	-1.1	1e-06	6e-06	9 x 50 cell division cycle 25B [Source:HGNC Symbol;Acc:HGNC:17
10	CENPW	-1.08	1e-06	6e-06	6 x 50 centromere protein W [Source:HGNC Symbol;Acc:HGNC:214
11	DEPDC1B	1.09	1e-06	3e-05	7 x 50 DEP domain containing 1B [Source:HGNC Symbol;Acc:HGNC
12	KIF22	-1.05	4e-06	3e-05	6 x 50 kinesin family member 22 [Source:HGNC Symbol;Acc:HGNC
13	KIF23	-1.04	5e-06	3e-05	6 x 50 kinesin family member 23 [Source:HGNC Symbol;Acc:HGNC
14	GPR108	-1.04	5e-06	9e-05	11 x 50 G protein-coupled receptor 108 [Source:HGNC Symbol;Acc:I
15	C5orf34	1.01	8e-06	2e-04	6 x 50 chromosome 5 open reading frame 34 [Source:HGNC Symbc
16	METTL17	0.96	2e-05	2e-04	9 x 50 methyltransferase like 17 [Source:HGNC Symbol;Acc:HGNC:
17	CCDC150	0.94	3e-05	2e-04	5 x 50 coiled-coil domain containing 150 [Source:HGNC Symbol;Ac
18	HIST1H4E	0.94	4e-05	2e-04	7 x 50 histone cluster 1, H4e [Source:HGNC Symbol;Acc:HGNC:47
19	SPAG5	-0.93	4e-05	2e-04	6 x 50 sperm associated antigen 5 [Source:HGNC Symbol;Acc:HGNC
20	PPP2R5D	-0.93	4e-05	2e-04	10 x 50 protein phosphatase 2, regulatory subunit B', delta [Source:H

p-values

