

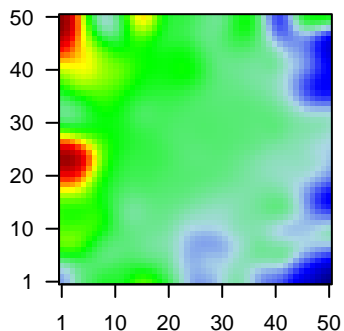
# B1\_mel

## Global Summary

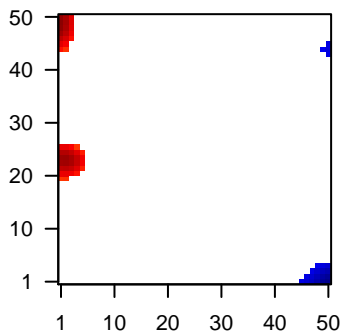
%DE = 0.21  
 # genes with  $fdr < 0.2 = 2775$  ( 1693 + / 1082 -)  
 # genes with  $fdr < 0.1 = 2093$  ( 1306 + / 787 -)  
 # genes with  $fdr < 0.05 = 1815$  ( 1134 + / 681 -)  
 # genes with  $fdr < 0.01 = 1144$  ( 716 + / 428 -)  
 # genes in genesets = 14839

<FC> = 0  
 <shrinkage-t> = 0.02  
 <p-value> = 0.08  
 <fdr> = 0.79

Profile



Regulated Spots



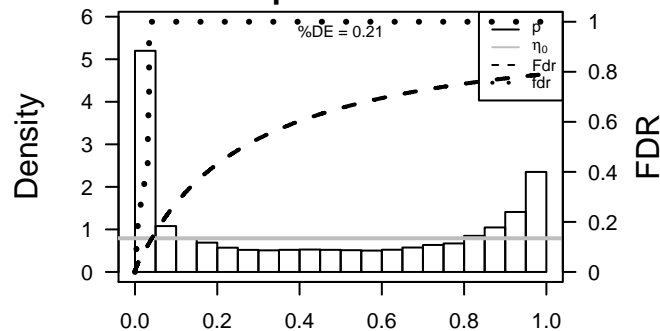
## Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	ACTR10	-1.81	2e-16 1e-13	50 x 45 actin-related protein 10 homolog (S. cerevisiae) [Source:HGNC]
2	CDC42BPA	-1.95	2e-16 1e-13	50 x 38 CDC42 binding protein kinase alpha (DMPK-like) [Source:HGNC]
3	CDKN3	-1.65	2e-16 1e-13	6 x 50 cyclin-dependent kinase inhibitor 3 [Source:HGNC Symbol;Acc:HGNC:2712]
4	CEP97	2.34	2e-16 1e-13	2 x 47 centrosomal protein 97kDa [Source:HGNC Symbol;Acc:HGNC:2712]
5	DCTN2	-1.81	2e-16 1e-13	50 x 44 dynactin 2 (p50) [Source:HGNC Symbol;Acc:HGNC:2712]
6	DYNC1L1L2	-1.43	2e-16 1e-13	27 x 50 dynein, cytoplasmic 1, light intermediate chain 2 [Source:HGNC]
7	EIF3H	-1.57	2e-16 1e-13	33 x 16 eukaryotic translation initiation factor 3, subunit H [Source:HGNC]
8	GTF2H1	-1.62	2e-16 1e-13	50 x 46 general transcription factor IIH, polypeptide 1, 62kDa [Source:HGNC]
9	MARCKS	-1.43	2e-16 1e-13	46 x 1 myristoylated alanine-rich protein kinase C substrate [Source:HGNC]
10	MDM2	-0.86	2e-16 1e-13	46 x 37 MDM2 proto-oncogene, E3 ubiquitin protein ligase [Source:HGNC]
11	NAMPT	-1.58	2e-16 1e-13	4 x 42 nicotinamide phosphoribosyltransferase [Source:HGNC Symbol;Acc:HGNC:19699]
12	NSA2	-1.55	2e-16 1e-13	45 x 46 NSA2 ribosome biogenesis homolog (S. cerevisiae) [Source:HGNC]
13	PLK2	-1.54	2e-16 1e-13	50 x 1 polo-like kinase 2 [Source:HGNC Symbol;Acc:HGNC:19699]
14	PMP22	-1.79	2e-16 1e-13	48 x 1 peripheral myelin protein 22 [Source:HGNC Symbol;Acc:HGNC:19699]
15	PMPCB	-1.46	2e-16 1e-13	33 x 50 peptidase (mitochondrial processing) beta [Source:HGNC Symbol;Acc:HGNC:19699]
16	PNRC2	-1.62	2e-16 1e-13	9 x 46 proline-rich nuclear receptor coactivator 2 [Source:HGNC Symbol;Acc:HGNC:19699]
17	RWDD2B	-1.8	2e-16 1e-13	46 x 50 RWD domain containing 2B [Source:HGNC Symbol;Acc:HGNC:19699]
18	SAP30BP	-1.76	2e-16 1e-13	42 x 49 SAP30 binding protein [Source:HGNC Symbol;Acc:HGNC:19699]
19	SCAMP3	-1.74	2e-16 1e-13	45 x 38 secretory carrier membrane protein 3 [Source:HGNC Symbol;Acc:HGNC:19699]
20	SF3B1	-1.67	2e-16 1e-13	50 x 36 splicing factor 3b, subunit 1, 155kDa [Source:HGNC Symbol;Acc:HGNC:19699]

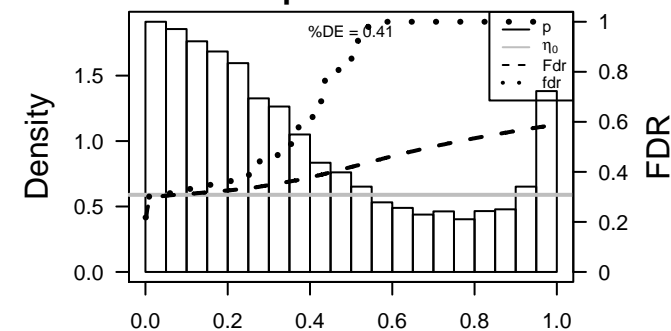
## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	10.07	3e-04	305	GSEA C2DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
2	9.46	3e-04	242	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN
3	9.27	4e-04	29	BP DNA strand elongation involved in DNA replication
4	9.26	4e-04	267	GSEA C2ZHANG_TLX_TARGETS_60HR_DN
5	9.24	4e-04	27	GSEA C2REACTOME_DNA_STRAND_ELONGATION
6	9.09	4e-04	278	GSEA C2MANALO_HYPOXIA_DN
7	8.49	5e-04	32	GSEA C2KEGG_DNA_REPLICATION
8	7.86	7e-04	20	BP telomere maintenance via semi-conservative replication
9	7.64	7e-04	24	BP telomere maintenance via recombination
10	7.5	8e-04	562	GSEA C2CAIRO_HEPATOBLASTOMA_CLASSES_UP
11	7.28	9e-04	68	GSEA C2VERNELL_RETINOBLASTOMA_PATHWAY_UP
12	7.26	9e-04	38	GSEA C2BURTON_ADIPOGENESIS_PEAK_AT_16HR
13	7.26	9e-04	139	BP DNA replication
14	7.24	9e-04	197	HM HALLMARK_E2F_TARGETS
15	7.22	9e-04	33	GSEA C2REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICATION
16	7.22	9e-04	38	GSEA C2REACTOME_G2_M_CHECKPOINTS
17	7.21	9e-04	26	GSEA C2REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMPLEX
18	7.1	1e-03	24	GSEA C2REACTOME_EXTENSION_OF_TELOMERES
19	7.06	1e-03	139	GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
20	7.04	1e-03	81	GSEA C2GRAHAM_NORMAL QUIESCENT_VS_NORMAL_DIVIDING_DN
<i>Underexpressed</i>				
1	-5.32	0.003	472	GSEA C2DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
2	-5.14	0.003	2	Colon Cancerish_dMMR-secondary-mutations_Cell-motility
3	-4.67	0.005	13	GSEA C2DAVICIONI_RHABDOMYOSARCOMA_PAX_FOXP1_FUSION_DN
4	-4.6	0.005	136	GSEA C2PODAR_RESPONSE_TO_ADAPHOSTIN_UP
5	-4.55	0.005	784	GSEA C2BUYTERT_PHOTO_DYNAMICAL_THERAPY_STRESS_UP
6	-4.5	0.005	696	Chr 5
7	-4.35	0.006	26	MF oxidoreductase activity, acting on paired donors, with incorporation
8	-4.34	0.006	393	GSEA C2MITSIADES_RESPONSE_TO_APLIDIN_UP
9	-4.32	0.006	1394	GSEA C2ZWANG_TRANSIENTLY_UP_BY_1ST_EGF_PULSE_ONLY
10	-4.23	0.006	178	GSEA C2ZHENG_FOXP3_TARGETS_IN_THYMUS_UP
11	-4.15	0.007	378	miRNA target-miR-454
12	-4.15	0.007	123	GSEA C2PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_DN
13	-4.13	0.007	447	miRNA target-miR-130b
14	-4.12	0.007	467	miRNA target-miR-301a
15	-4.07	0.007	286	GSEA C2PASINI_SUZ12_TARGETS_DN
16	-4	0.008	426	GSEA C2ZWANG_CLASS_1_TRANSIENTLY_INDUCED_BY_EGF
17	-3.97	0.008	343	GSEA C2THUM_SYSTOLIC_HEART_FAILURE_UP
18	-3.86	0.008	11	GSEA C2WANG_RESPONSE_TO_PACLITAXEL_VIA_MAPK8_UP
19	-3.85	0.008	222	GSEA C2JUDAYAKUMAR_MED1_TARGETS_DN
20	-3.83	0.009	17	BP actomyosin structure organization

p-values



p-values



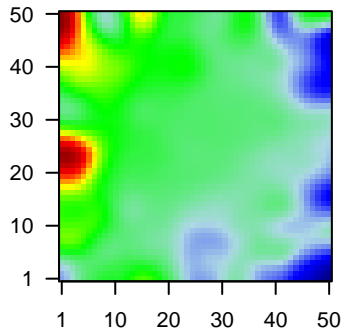
# B1\_mel

## Local Summary

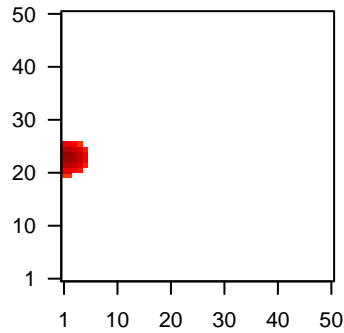
%DE = 0.75  
 # metagenes = 30  
 # genes = 301  
 # genes in genesets = 298  
  
 # genes with  $fdr < 0.1$  = 167 ( 155 + / 12 - )  
 # genes with  $fdr < 0.05$  = 151 ( 141 + / 10 - )  
 # genes with  $fdr < 0.01$  = 100 ( 93 + / 7 - )

$\langle r \rangle$  metagenes = 0.89  
 $\langle r \rangle$  genes = 0.11  
  
 $\langle FC \rangle$  = 0.42  
 $\langle \text{shrinkage-t} \rangle$  = 6.87  
 $\langle p\text{-value} \rangle$  = 0  
 $\langle fdr \rangle$  = 0.49

Profile



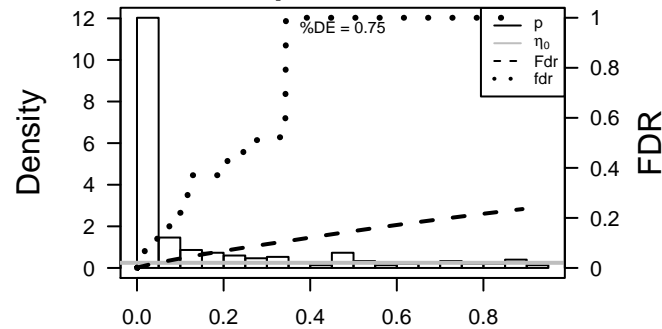
Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	IFT140	1.62	6e-12	3e-09	4 x 24 intraflagellar transport 140 [Source:HGNC Symbol;Acc:HGNC
2	IL11RA	1.55	6e-11	3e-09	4 x 24 interleukin 11 receptor, alpha [Source:HGNC Symbol;Acc:HG
3	FBXL6	1.53	1e-10	1e-08	2 x 26 F-box and leucine-rich repeat protein 6 [Source:HGNC Syml
4	RAB2A	-1.24	2e-10	2e-08	1 x 20 RAB2A, member RAS oncogene family [Source:HGNC Symb
5	FANCD2OS	1.47	5e-10	2e-07	5 x 24 FANCD2 opposite strand [Source:HGNC Symbol;Acc:HGNC:
6	HPDL	1.4	3e-09	2e-07	3 x 26 4-hydroxyphenylpyruvate dioxygenase-like [Source:HGNC S
7	SNAP91	1.38	6e-09	7e-07	5 x 24 synaptosomal-associated protein, 91kDa [Source:HGNC Syr
8	BCL7B	1.33	2e-08	7e-07	1 x 25 B-cell CLL/lymphoma 7B [Source:HGNC Symbol;Acc:HGNC
9	KIF13B	1.3	4e-08	7e-07	1 x 24 kinesin family member 13B [Source:HGNC Symbol;Acc:HGN
10	PQLC3	1.29	5e-08	7e-07	2 x 22 PQ loop repeat containing 3 [Source:HGNC Symbol;Acc:HGT
11	NSUN6	1.29	5e-08	7e-07	5 x 24 NOP2/Sun domain family, member 6 [Source:HGNC Symbol;
12	CUL4A	1.28	6e-08	7e-07	1 x 23 cullin 4A [Source:HGNC Symbol;Acc:HGNC:2554]
13	MTMR1	1.28	6e-08	7e-07	2 x 24 myotubularin related protein 1 [Source:HGNC Symbol;Acc:HK
14	ATR	1.27	7e-08	9e-07	1 x 22 ATR serine/threonine kinase [Source:HGNC Symbol;Acc:HGT
15	C9orf89	1.27	8e-08	2e-06	1 x 23 chromosome 9 open reading frame 89 [Source:HGNC Symbc
16	COG1	1.25	1e-07	2e-06	1 x 21 component of oligomeric golgi complex 1 [Source:HGNC Syr
17	CHRNA3	1.23	2e-07	2e-06	5 x 24 cholinergic receptor, nicotinic, alpha 3 (neuronal) [Source:HG
18	LRRC45	1.23	2e-07	2e-06	1 x 25 leucine rich repeat containing 45 [Source:HGNC Symbol;Acc:
19	CDK9	1.23	2e-07	3e-06	2 x 21 cyclin-dependent kinase 9 [Source:HGNC Symbol;Acc:HGN
20	PTP4A1	0.97	2e-07	1e-05	1 x 21 protein tyrosine phosphatase type IVA, member 1 [Source:HC

p-values



# B1\_mel

## Local Summary

%DE = 0.88  
 # metagenes = 19  
 # genes = 313  
 # genes in genesets = 311  
  
 # genes with  $fdr < 0.1$  = 218 ( 190 + / 28 - )  
 # genes with  $fdr < 0.05$  = 216 ( 188 + / 28 - )  
 # genes with  $fdr < 0.01$  = 156 ( 144 + / 12 - )

<r> metagenes = 0.91

<r> genes = 0.21

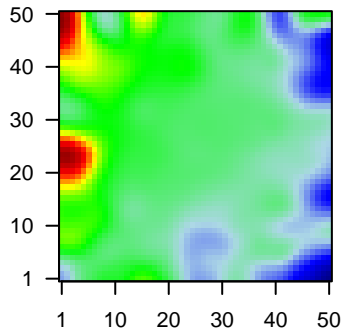
<FC> = 0.46

<shrinkage-t> = 7.49

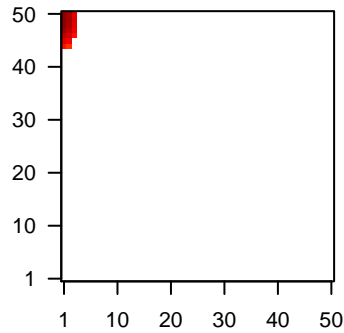
<p-value> = 0

<fdr> = 0.41

Profile



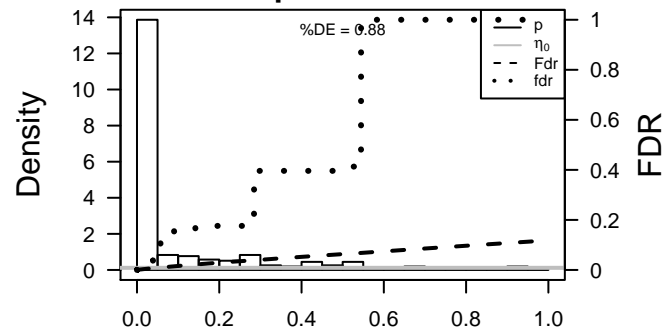
Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	CEP97	2.34	2e-16	8e-15	2 x 47 centrosomal protein 97kDa [Source:HGNC Symbol;Acc:HGNC:10000]
2	MUC7	1.61	1e-11	1e-08	1 x 46 mucin 7, secreted [Source:HGNC Symbol;Acc:HGNC:7518]
3	TREX1	1.47	5e-10	1e-08	1 x 47 three prime repair exonuclease 1 [Source:HGNC Symbol;Acc:HGNC:10000]
4	MCM5	1.46	7e-10	1e-08	1 x 49 minichromosome maintenance complex component 5 [Source:HGNC Symbol;Acc:HGNC:10000]
5	FRMD5	1.44	1e-09	1e-08	1 x 49 FERM domain containing 5 [Source:HGNC Symbol;Acc:HGNC:10000]
6	POLE2	1.44	1e-09	1e-08	1 x 47 polymerase (DNA directed), epsilon 2, accessory subunit [Source:HGNC Symbol;Acc:HGNC:10000]
7	POLA2	1.43	1e-09	1e-08	1 x 48 polymerase (DNA directed), alpha 2, accessory subunit [Source:HGNC Symbol;Acc:HGNC:10000]
8	PDE6D	-1.3	2e-09	2e-08	1 x 44 phosphodiesterase 6D, cGMP-specific, rod, delta [Source:HGNC Symbol;Acc:HGNC:10000]
9	ADAT1	1.41	2e-09	2e-08	1 x 44 adenosine deaminase, tRNA-specific 1 [Source:HGNC Symbol;Acc:HGNC:10000]
10	WDR91	1.41	3e-09	6e-08	1 x 44 WD repeat domain 91 [Source:HGNC Symbol;Acc:HGNC:24000]
11	NMRK2	1.3	7e-09	6e-08	1 x 44 nicotinamide riboside kinase 2 [Source:HGNC Symbol;Acc:HGNC:10000]
12	CEP128	1.37	8e-09	6e-08	3 x 48 centrosomal protein 128kDa [Source:HGNC Symbol;Acc:HGNC:10000]
13	ST6GALNAC7	1.06	8e-09	6e-08	1 x 44 ST6 (alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-transferase [Source:HGNC Symbol;Acc:HGNC:10000]
14	MCM6	1.36	9e-09	6e-08	1 x 50 minichromosome maintenance complex component 6 [Source:HGNC Symbol;Acc:HGNC:10000]
15	C4orf46	1.35	1e-08	6e-07	1 x 48 chromosome 4 open reading frame 46 [Source:HGNC Symbol;Acc:HGNC:10000]
16	POLE	1.29	4e-08	6e-07	1 x 48 polymerase (DNA directed), epsilon, catalytic subunit [Source:HGNC Symbol;Acc:HGNC:10000]
17	RFWD3	1.29	4e-08	1e-06	1 x 49 ring finger and WD repeat domain 3 [Source:HGNC Symbol;Acc:HGNC:10000]
18	PRIM1	1.27	7e-08	1e-06	1 x 50 primase, DNA, polypeptide 1 (49kDa) [Source:HGNC Symbol;Acc:HGNC:10000]
19	SGSH	1.25	1e-07	1e-06	1 x 44 N-sulfoglucosamine sulfohydrolase [Source:HGNC Symbol;Acc:HGNC:10000]
20	POLD1	1.23	2e-07	1e-06	3 x 46 polymerase (DNA directed), delta 1, catalytic subunit [Source:HGNC Symbol;Acc:HGNC:10000]

p-values



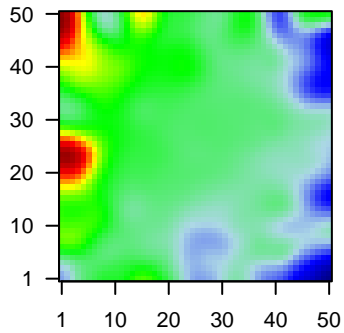
# B1\_mel

## Local Summary

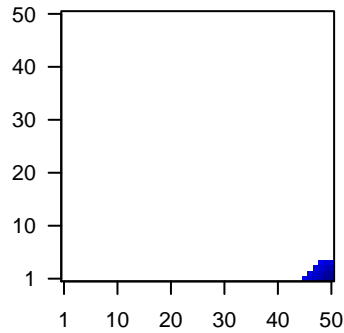
%DE = 0.78  
 # metagenes = 18  
 # genes = 305  
 # genes in genesets = 305  
 # genes with  $fdr < 0.1$  = 155 ( 32 + / 123 - )  
 # genes with  $fdr < 0.05$  = 116 ( 23 + / 93 - )  
 # genes with  $fdr < 0.01$  = 59 ( 11 + / 48 - )

$\langle r \rangle$  metagenes = 0.97  
 $\langle r \rangle$  genes = 0.19  
 $\langle FC \rangle = -0.29$   
 $\langle \text{shrinkage-t} \rangle = -4.78$   
 $\langle p\text{-value} \rangle = 0.02$   
 $\langle fdr \rangle = 0.63$

Profile



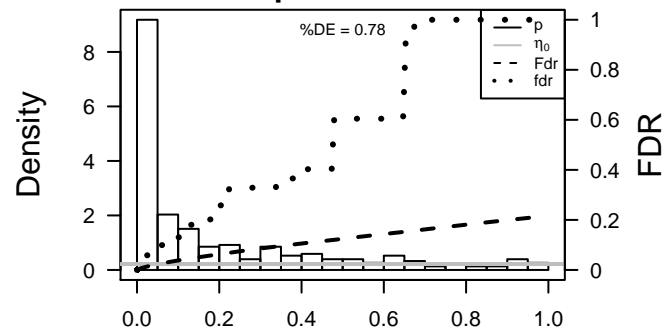
Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	MARCKS	-1.43	2e-16	5e-15	46 x 1 myristoylated alanine-rich protein kinase C substrate [Source:HGNC Symbol;Acc:HGNC:19699]
2	PLK2	-1.54	2e-16	5e-15	50 x 1 polo-like kinase 2 [Source:HGNC Symbol;Acc:HGNC:19699]
3	PMP22	-1.79	2e-16	5e-15	48 x 1 peripheral myelin protein 22 [Source:HGNC Symbol;Acc:HGNC:19699]
4	PRKCI	1.65	3e-12	3e-09	47 x 3 protein kinase C, iota [Source:HGNC Symbol;Acc:HGNC:940]
5	ARMC9	-1.37	6e-11	3e-09	50 x 3 armadillo repeat containing 9 [Source:HGNC Symbol;Acc:HGNC:19699]
6	PLOD2	-1.36	1e-10	3e-07	49 x 3 procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2 [Source:HGNC Symbol;Acc:HGNC:19699]
7	MRPS6	-0.86	4e-09	8e-07	50 x 3 mitochondrial ribosomal protein S6 [Source:HGNC Symbol;Acc:HGNC:19699]
8	GPBP1L1	-1.24	2e-08	1e-05	50 x 4 GC-rich promoter binding protein 1-like 1 [Source:HGNC Symbol;Acc:HGNC:19699]
9	PVRL2	1.22	2e-07	2e-05	50 x 4 poliovirus receptor-related 2 (herpesvirus entry mediator B) [Source:HGNC Symbol;Acc:HGNC:19699]
10	ITFG1	-1.11	5e-07	2e-05	50 x 4 integrin alpha FG-GAP repeat containing 1 [Source:HGNC Symbol;Acc:HGNC:19699]
11	YPEL5	-1.15	7e-07	3e-05	50 x 1 yippee-like 5 (Drosophila) [Source:HGNC Symbol;Acc:HGNC:19699]
12	EDIL3	-1.11	2e-06	3e-05	50 x 1 EGF-like repeats and discoidin I-like domains 3 [Source:HGNC Symbol;Acc:HGNC:19699]
13	CBLB	-1.07	2e-06	3e-05	50 x 2 Cbl proto-oncogene B, E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:HGNC:19699]
14	DSTN	-0.46	3e-06	3e-05	48 x 3 destrin (actin depolymerizing factor) [Source:HGNC Symbol;Acc:HGNC:19699]
15	COL11A1	-0.56	3e-06	3e-05	45 x 1 collagen, type XI, alpha 1 [Source:HGNC Symbol;Acc:HGNC:19699]
16	RAB31	1.09	3e-06	1e-04	50 x 3 RAB31, member RAS oncogene family [Source:HGNC Symbol;Acc:HGNC:19699]
17	CD55	-1.02	6e-06	1e-04	50 x 1 CD55 molecule, decay accelerating factor for complement (CD55) [Source:HGNC Symbol;Acc:HGNC:19699]
18	UGGT2	-1.05	8e-06	2e-04	48 x 3 UDP-glucose glycoprotein glucosyltransferase 2 [Source:HGNC Symbol;Acc:HGNC:19699]
19	MID1	-1.04	1e-05	2e-04	50 x 3 midline 1 [Source:HGNC Symbol;Acc:HGNC:7095]
20	SLC5A3	-1.03	1e-05	2e-04	50 x 2 solute carrier family 5 (sodium/myo-inositol cotransporter), member 3 [Source:HGNC Symbol;Acc:HGNC:19699]

p-values



# B1\_mel

## Local Summary

%DE = 0.76  
 # metagenes = 4  
 # genes = 71  
 # genes in genesets = 71  
  
 # genes with  $fdr < 0.1$  = 33 ( 3 + / 30 - )  
 # genes with  $fdr < 0.05$  = 24 ( 1 + / 23 - )  
 # genes with  $fdr < 0.01$  = 17 ( 1 + / 16 - )

<r> metagenes = 0.98

<r> genes = 0.11

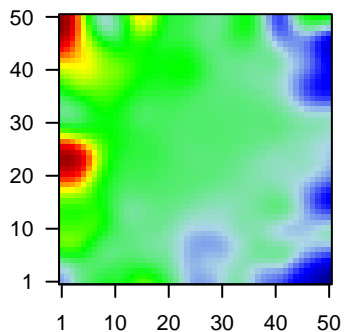
<FC> = -0.38

<shrinkage-t> = -6.47

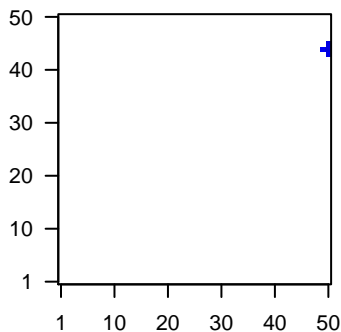
<p-value> = 0.01

<fdr> = 0.65

### Profile



### Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ACTR10	-1.81	2e-16	2e-15	50 x 45 actin-related protein 10 homolog (S. cerevisiae) [Source:HGNC]
2	DCTN2	-1.81	2e-16	2e-15	50 x 44 dynactin 2 (p50) [Source:HGNC Symbol;Acc:HGNC:2712]
3	PNISR	-1.37	3e-13	4e-10	50 x 44 PNN-interacting serine/arginine-rich protein [Source:HGNC]
4	METTL5	-1.4	2e-11	1e-05	50 x 45 methyltransferase like 5 [Source:HGNC Symbol;Acc:HGNC:2]
5	MOSPD1	-1.06	1e-06	1e-05	50 x 43 motile sperm domain containing 1 [Source:HGNC Symbol;Ac]
6	ERCC1	-0.84	1e-06	3e-05	50 x 43 excision repair cross-complementation group 1 [Source:HGNC]
7	MIA3	-0.92	4e-06	3e-05	50 x 44 melanoma inhibitory activity family, member 3 [Source:HGNC]
8	COPS7A	-1.06	5e-06	3e-05	50 x 45 COP9 signalosome subunit 7A [Source:HGNC Symbol;Acc:H]
9	SLC25A44	-0.97	6e-06	5e-04	50 x 44 solute carrier family 25, member 44 [Source:HGNC Symbol;A]
10	SLC25A26	0.96	5e-05	5e-04	50 x 45 solute carrier family 25 (S-adenosylmethionine carrier), mem
11	SLC50A1	-0.94	7e-05	3e-03	50 x 43 solute carrier family 50 (sugar efflux transporter), member 1 [:
12	CLCN3	-0.79	7e-04	3e-03	50 x 45 chloride channel, voltage-sensitive 3 [Source:HGNC Symbol;
13	MUL1	-0.8	8e-04	3e-03	50 x 43 mitochondrial E3 ubiquitin protein ligase 1 [Source:HGNC Sym]
14	ZMYM5	-0.79	8e-04	3e-03	50 x 43 zinc finger, MYM-type 5 [Source:HGNC Symbol;Acc:HGNC:1]
15	VPS13B	-0.79	8e-04	3e-03	50 x 45 vacuolar protein sorting 13 homolog B (yeast) [Source:HGNC]
16	EIF4G3	-0.75	1e-03	9e-03	50 x 45 eukaryotic translation initiation factor 4 gamma, 3 [Source:HG]
17	C16orf91	-0.74	2e-03	9e-03	50 x 45 chromosome 16 open reading frame 91 [Source:HGNC Synt]
18	ASCC1	-0.73	2e-03	3e-02	50 x 45 activating signal cointegrator 1 complex subunit 1 [Source:HC]
19	HEXDC	-0.64	6e-03	3e-02	50 x 43 hexosaminidase (glycosyl hydrolase family 20, catalytic doma
20	COMMD3-B1	-0.62	8e-03	3e-02	50 x 45 COMMD3-BMI1 readthrough [Source:HGNC Symbol;Acc:HC]

### p-values

