

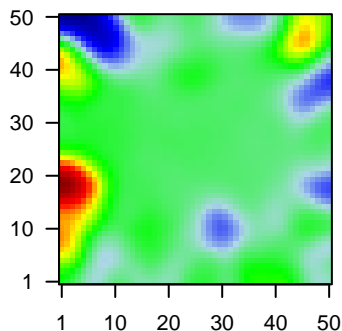
A9_mel

Global Summary

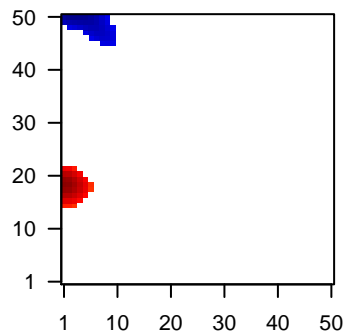
%DE = 0.21
 # genes with $fdr < 0.2$ = 2696 (1636 + / 1060 -)
 # genes with $fdr < 0.1$ = 2387 (1446 + / 941 -)
 # genes with $fdr < 0.05$ = 1826 (1099 + / 727 -)
 # genes with $fdr < 0.01$ = 1166 (697 + / 469 -)
 # genes in genesets = 14839

<FC> = 0
 <shrinkage-t> = -0.01
 <p-value> = 0.07
 <fdr> = 0.79

Profile



Regulated Spots



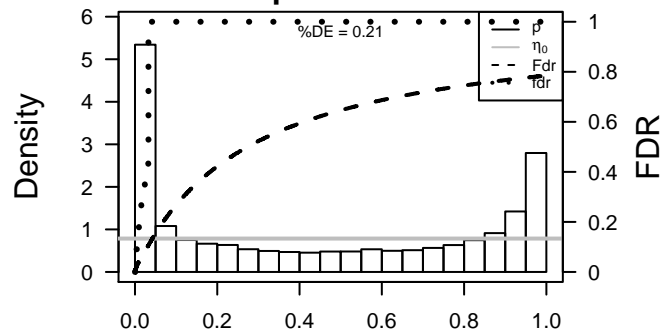
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ABCE1	-1.58	2e-16	8e-14	50 x 48 ATP-binding cassette, sub-family E (OABP), member 1 [Sou
2	ACTL6A	-1.82	2e-16	8e-14	4 x 50 actin-like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
3	AHSA1	-1.83	2e-16	8e-14	46 x 35 AHA1, activator of heat shock 90kDa protein ATPase homolo
4	ANKHD1	-1.63	2e-16	8e-14	9 x 5 ankryin repeat and KH domain containing 1 [Source:HGNC S
5	ANP32E	-1.28	2e-16	8e-14	8 x 50 acidic (leucine-rich) nuclear phosphoprotein 32 family, memb
6	APOO	-1.68	2e-16	8e-14	2 x 46 apolipoprotein O [Source:HGNC Symbol;Acc:HGNC:28727]
7	BNIP2	-1.5	2e-16	8e-14	46 x 37 BCL2/adenovirus E1B 19kDa interacting protein 2 [Source:HK
8	CDC42BPA	-1.64	2e-16	8e-14	50 x 38 CDC42 binding protein kinase alpha (DMPK-like) [Source:HC
9	CLDND1	-1.42	2e-16	8e-14	28 x 50 claudin domain containing 1 [Source:HGNC Symbol;Acc:HGNC
10	DEGS1	-1.93	2e-16	8e-14	9 x 43 delta(4)-desaturase, sphingolipid 1 [Source:HGNC Symbol;A
11	HAUS1	-1.62	2e-16	8e-14	1 x 50 HAUS augmin-like complex, subunit 1 [Source:HGNC Symbc
12	IWS1	-1.62	2e-16	8e-14	34 x 48 IWS1 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:HC
13	KPNB1	-1.52	2e-16	8e-14	8 x 43 karyopherin (importin) beta 1 [Source:HGNC Symbol;Acc:HG
14	MCM4	-1.58	2e-16	8e-14	1 x 50 minichromosome maintenance complex component 4 [Source
15	MMADHC	-1.45	2e-16	8e-14	50 x 37 methylmalonic aciduria (cobalamin deficiency) cblD type, with
16	MORN2	-1.79	2e-16	8e-14	47 x 37 MORN repeat containing 2 [Source:HGNC Symbol;Acc:HGNC
17	NOP16	-1.73	2e-16	8e-14	1 x 38 NOP16 nucleolar protein [Source:HGNC Symbol;Acc:HGNC:
18	NOP56	-1.52	2e-16	8e-14	11 x 42 NOP56 ribonucleoprotein [Source:HGNC Symbol;Acc:HGNC
19	POP4	-1.63	2e-16	8e-14	15 x 50 processing of precursor 4, ribonuclease P/MRP subunit (S. ce
20	SAT1	-1.33	2e-16	8e-14	1 x 11 spermidine/spermine N1-acetyltransferase 1 [Source:HGNC

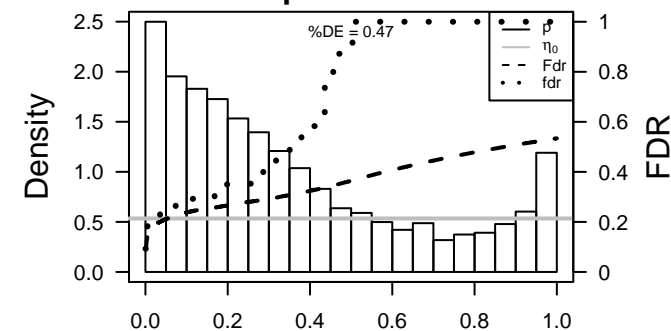
Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	6.14	0.002	198	HM HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	5.14	0.003	206	GSEA C2SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM4
3	4.96	0.004	3081	Brain Mid_Frontal_Lobe_ZNF
4	4.92	0.004	401	CC mitochondrial inner membrane
5	4.59	0.005	107	GSEA C2KEGG_OXIDATIVE_PHOSPHORYLATION
6	4.54	0.005	94	BP respiratory electron transport chain
7	4.48	0.005	78	GSEA C2REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_S
8	4.44	0.005	1468	CC mitochondrion
9	4.43	0.005	412	CC lysosome
10	4.37	0.006	102	GSEA C2KEGG_PARKINSONS_DISEASE
11	4.17	0.007	685	GSEA C2KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR
12	4.16	0.007	2984	CC integral component of membrane
13	4.13	0.007	85	GSEA C2MOOHA_VOXPPOS
14	4.09	0.007	18	BP melanocyte differentiation
15	4	0.007	2798	Colon Cancer hG1_Colon
16	3.97	0.008	1730	BP small molecule metabolic process
17	3.96	0.008	62	GSEA C2REACTOME_RESPIRATORY_ELECTRON_TRANSPORT
18	3.96	0.008	592	MF oxidoreductase activity
19	3.93	0.008	114	GSEA C2REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_T
20	3.93	0.008	10	BP protein autoprocessing
<i>Underexpressed</i>				
1	-11.94	1e-04	242	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN
2	-10.15	2e-04	197	HM HALLMARK_E2F_TARGETS
3	-10.03	3e-04	724	GSEA C2PUJANA_CHEK2_PCC_NETWORK
4	-9.7	3e-04	550	GSEA C2SOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
5	-9.6	3e-04	505	GSEA C2BERENJENO_TRANSFORMED_BY_RHOA_UP
6	-9.49	3e-04	1251	GSEA C2DODD_NASOPHARYNGEAL_CARCINOMA_DN
7	-9.39	3e-04	145	GSEA C2ZHANG_CYCLING_GENES
8	-8.94	4e-04	700	GSEA C2MARSON_BOUND_BY_E2F4_UNSTIMULATED
9	-8.89	4e-04	1192	GSEA C2KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
10	-8.73	5e-04	139	GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
11	-8.7	5e-04	517	GSEA C2FEVR_CTNNB1_TARGETS_DN
12	-8.68	5e-04	270	GSEA C2BASAKI_YBX1_TARGETS_UP
13	-8.59	5e-04	216	GSEA C2MARKEY_RB1_ACUTE_LOF_DN
14	-8.56	5e-04	159	GSEA C2WINPENNINGCKX_MELANOMA_METASTASIS_UP
15	-8.56	5e-04	834	GSEA C2LEE_BMP2_TARGETS_DN
16	-8.51	5e-04	59	GSEA C2KAUFFMANN_MELANOMA_RELAPSE_UP
17	-8.46	5e-04	305	GSEA C2DUTERTRE ESTRADIOL_RESPONSE_24HR_UP
18	-8.45	5e-04	267	GSEA C2ZHANG_TLX_TARGETS_60HR_DN
19	-8.44	5e-04	412	BP mitotic cell cycle
20	-8.38	5e-04	278	GSEA C2MANALO_HYPOXIA_DN

p-values



p-values



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Local Summary

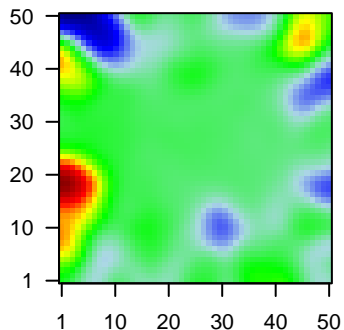
%DE = 0.86
 # metagenes = 36
 # genes = 378
 # genes in genesets = 376

 # genes with $fdr < 0.1$ = 252 (231 + / 21 -)
 # genes with $fdr < 0.05$ = 238 (222 + / 16 -)
 # genes with $fdr < 0.01$ = 170 (164 + / 6 -)

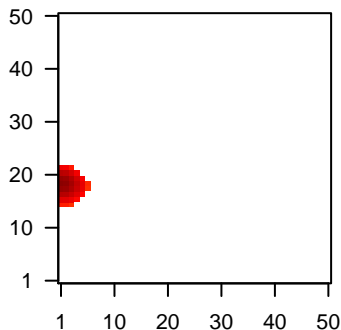
$\langle r \rangle$ metagenes = 0.84
 $\langle r \rangle$ genes = 0.1

 $\langle FC \rangle$ = 0.46
 $\langle \text{shrinkage-t} \rangle$ = 7.58
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.46

Profile



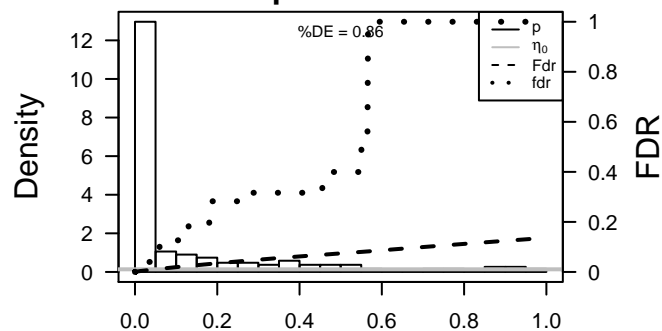
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	KCNU1	1.78	2e-13	1e-09	6 x 19 potassium channel, subfamily U, member 1 [Source:HGNC S
2	PXMP4	1.59	4e-11	1e-09	3 x 22 peroxisomal membrane protein 4, 24kDa [Source:HGNC Syrr
3	DTNA	1.59	4e-11	6e-09	1 x 17 dystrobrevin, alpha [Source:HGNC Symbol;Acc:HGNC:3057]
4	L2HGDH	1.52	3e-10	6e-09	5 x 18 L-2-hydroxyglutarate dehydrogenase [Source:HGNC Symbo
5	DNAJC18	1.52	3e-10	6e-09	1 x 17 DnaJ (Hsp40) homolog, subfamily C, member 18 [Source:HG
6	ZNF691	1.51	4e-10	1e-08	5 x 17 zinc finger protein 691 [Source:HGNC Symbol;Acc:HGNC:28
7	IRX6	1.49	6e-10	9e-08	1 x 17 iroquois homeobox 6 [Source:HGNC Symbol;Acc:HGNC:146
8	EML3	1.44	2e-09	1e-07	5 x 19 echinoderm microtubule associated protein like 3 [Source:HG
9	SLC44A5	1.4	6e-09	1e-07	4 x 16 solute carrier family 44, member 5 [Source:HGNC Symbol;Ac
10	ZNF559	1.38	1e-08	1e-07	3 x 15 zinc finger protein 559 [Source:HGNC Symbol;Acc:HGNC:28
11	STARD3	1.38	1e-08	3e-07	1 x 15 STAR-related lipid transfer (START) domain containing 3 [So
12	SERPINE2	1.34	2e-08	3e-07	1 x 20 serpin peptidase inhibitor, clade E (nexin, plasminogen activa
13	EDRF1	1.34	2e-08	3e-07	3 x 20 erythroid differentiation regulatory factor 1 [Source:HGNC Syi
14	YKT6	1.34	3e-08	6e-07	1 x 18 YKT6 v-SNARE homolog (S. cerevisiae) [Source:HGNC Syrr
15	RAB32	0.63	4e-08	6e-07	1 x 20 RAB32, member RAS oncogene family [Source:HGNC Symb
16	PTDSS2	1.31	5e-08	6e-07	1 x 19 phosphatidylserine synthase 2 [Source:HGNC Symbol;Acc:H
17	E2F4	1.3	6e-08	3e-06	1 x 20 E2F transcription factor 4, p107/p130-binding [Source:HGNC
18	TIRAP	1.27	1e-07	3e-06	5 x 19 toll-interleukin 1 receptor (TIR) domain containing adaptor pr
19	DPYSL4	1.25	2e-07	3e-06	3 x 19 dihydropyrimidinase-like 4 [Source:HGNC Symbol;Acc:HGNC
20	IER2	1.24	3e-07	3e-06	1 x 21 immediate early response 2 [Source:HGNC Symbol;Acc:HGNC

p-values



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Local Summary

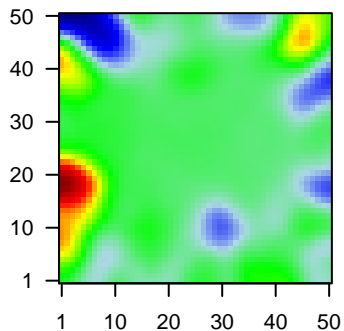
%DE = 0.8
 # metagenes = 41
 # genes = 478
 # genes in genesets = 477

 # genes with $fdr < 0.1$ = 277 (51 + / 226 -)
 # genes with $fdr < 0.05$ = 233 (42 + / 191 -)
 # genes with $fdr < 0.01$ = 121 (19 + / 102 -)

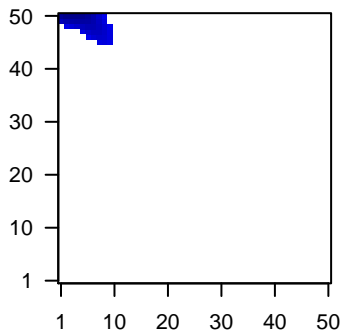
$\langle r \rangle$ metagenes = 0.93
 $\langle r \rangle$ genes = 0.24

$\langle FC \rangle$ = -0.35
 $\langle \text{shrinkage-t} \rangle$ = -5.83
 $\langle p\text{-value} \rangle$ = 0.01
 $\langle fdr \rangle$ = 0.56

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ACTL6A	-1.82	2e-16	4e-15	4 x 50 actin-like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
2	ANP32E	-1.28	2e-16	4e-15	8 x 50 acidic (leucine-rich) nuclear phosphoprotein 32 family, memb
3	HAUS1	-1.62	2e-16	4e-15	1 x 50 HAUS augmin-like complex, subunit 1 [Source:HGNC Symbc
4	MCM4	-1.58	2e-16	4e-15	1 x 50 minichromosome maintenance complex component 4 [Source
5	TUBG1	-1.69	2e-16	4e-15	2 x 49 tubulin, gamma 1 [Source:HGNC Symbol;Acc:HGNC:12417]
6	XPO1	-1.36	2e-16	4e-15	8 x 46 exportin 1 [Source:HGNC Symbol;Acc:HGNC:12825]
7	THUMP3	-1.56	4e-16	3e-13	9 x 47 THUMP domain containing 3 [Source:HGNC Symbol;Acc:HG
8	MCM3	-1.53	3e-15	2e-10	1 x 50 minichromosome maintenance complex component 3 [Source
9	GMNN	-1.45	2e-12	2e-10	2 x 50 geminin, DNA replication inhibitor [Source:HGNC Symbol;Acc
10	H2AFV	-1.44	4e-12	3e-09	8 x 50 H2A histone family, member V [Source:HGNC Symbol;Acc:Hi
11	RFC5	-1.39	6e-11	3e-09	2 x 50 replication factor C (activator 1) 5, 36.5kDa [Source:HGNC S]
12	PTTG1	-0.97	8e-11	3e-09	7 x 50 pituitary tumor-transforming 1 [Source:HGNC Symbol;Acc:Hi
13	ZC3H14	-1.38	9e-11	3e-09	9 x 45 zinc finger CCCH-type containing 14 [Source:HGNC Symbol
14	LSM5	-0.88	1e-10	2e-08	10 x 46 LSM5 homolog, U6 small nuclear RNA associated (S. cerevis
15	MAD2L1	-1.35	3e-10	4e-08	5 x 50 MAD2 mitotic arrest deficient-like 1 (yeast) [Source:HGNC S]
16	FEN1	-1.34	8e-10	5e-08	1 x 50 flap structure-specific endonuclease 1 [Source:HGNC Symbc
17	CBX5	-1.32	1e-09	1e-07	9 x 46 chromobox homolog 5 [Source:HGNC Symbol;Acc:HGNC:15
18	LCMT1	-1.3	4e-09	1e-07	6 x 46 leucine carboxyl methyltransferase 1 [Source:HGNC Symbol];
19	MCM7	-1.29	4e-09	1e-07	2 x 50 minichromosome maintenance complex component 7 [Source
20	KIAA0101	-1.29	5e-09	3e-07	3 x 50 KIAA0101 [Source:HGNC Symbol;Acc:HGNC:28961]

p-values

