

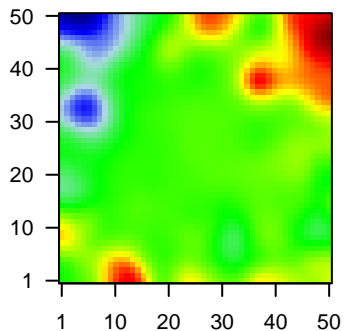
F8_mel

Global Summary

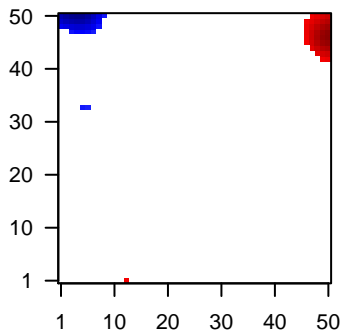
%DE = 0.22
 # genes with fdr < 0.2 = 2848 (1694 + / 1154 -)
 # genes with fdr < 0.1 = 2223 (1340 + / 883 -)
 # genes with fdr < 0.05 = 1899 (1146 + / 753 -)
 # genes with fdr < 0.01 = 1233 (747 + / 486 -)
 # genes in genesets = 14839

<FC> = 0
 <shrinkage-t> = -0.03
 <p-value> = 0.07
 <fdr> = 0.78

Profile



Regulated Spots

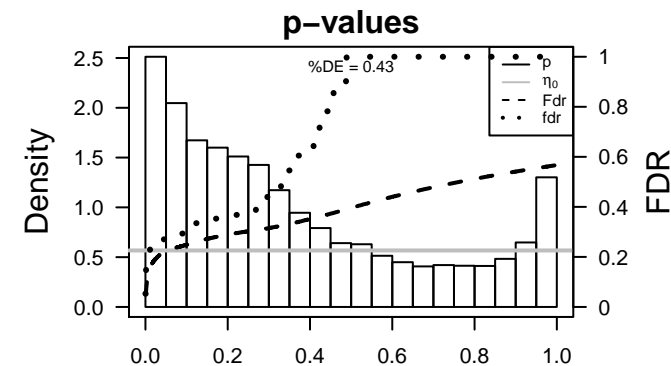
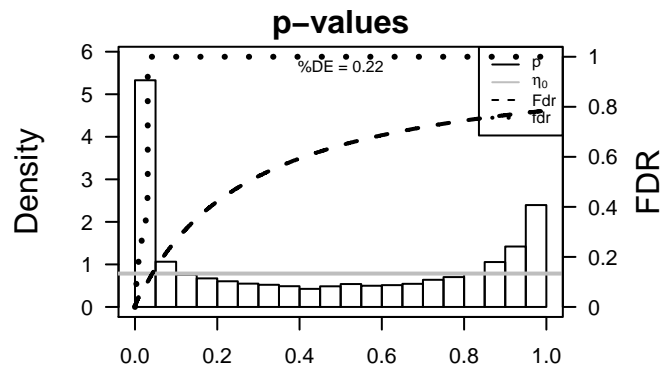


Global Genelist

Rank	ID	log(FC)	fdr p-value	Description
1	ADIPOR1	-1.66	2e-16 7e-14	6 x 32 adiponectin receptor 1 [Source:HGNC Symbol;Acc:HGNC:24
2	AIMP2	-1.73	2e-16 7e-14	5 x 34 aminoacyl tRNA synthetase complex-interacting multifunction
3	ANKRD28	-1.56	2e-16 7e-14	50 x 5 ankyrin repeat domain 28 [Source:HGNC Symbol;Acc:HGNC
4	APOO	-1.71	2e-16 7e-14	2 x 46 apolipoprotein O [Source:HGNC Symbol;Acc:HGNC:28727]
5	ARL6IP4	-1.74	2e-16 7e-14	5 x 36 ADP-ribosylation factor-like 6 interacting protein 4 [Source:H
6	ARL6IP5	-1.68	2e-16 7e-14	50 x 10 ADP-ribosylation factor-like 6 interacting protein 5 [Source:H
7	ARPC1A	-1.74	2e-16 7e-14	6 x 34 actin related protein 2/3 complex, subunit 1A, 41kDa [Source:
8	ATP1A1	-1.61	2e-16 7e-14	1 x 42 ATPase, Na+/K+ transporting, alpha 1 polypeptide [Source:Hi
9	AZIN1	-1.68	2e-16 7e-14	4 x 41 antizyme inhibitor 1 [Source:HGNC Symbol;Acc:HGNC:1643;
10	C19orf53	-1.3	2e-16 7e-14	7 x 32 chromosome 19 open reading frame 53 [Source:HGNC Synt
11	CD59	-2.06	2e-16 7e-14	49 x 12 CD59 molecule, complement regulatory protein [Source:HGNC
12	CSE1L	-1.71	2e-16 7e-14	3 x 49 CSE1 chromosome segregation 1-like (yeast) [Source:HGNC
13	CY5B	-1.7	2e-16 7e-14	15 x 50 cytochrome b5 type B (outer mitochondrial membrane) [Sour
14	DCAF13	-1.45	2e-16 7e-14	1 x 1 DDB1 and CUL4 associated factor 13 [Source:HGNC Symbo
15	EBP	-2.01	2e-16 7e-14	1 x 48 emopamil binding protein (sterol isomerase) [Source:HGNC S
16	ENY2	-1.86	2e-16 7e-14	12 x 47 enhancer of yellow 2 homolog (Drosophila) [Source:HGNC S
17	GPR161	-1.12	2e-16 7e-14	3 x 16 G protein-coupled receptor 161 [Source:HGNC Symbol;Acc:
18	HERPUD1	1.24	2e-16 7e-14	50 x 42 homocysteine-inducible, endoplasmic reticulum stress-induc
19	HMG2	-0.99	2e-16 7e-14	8 x 50 high mobility group nucleosomal binding domain 2 [Source:Hi
20	IQGAP1	-1.43	2e-16 7e-14	9 x 32 IQ motif containing GTPase activating protein 1 [Source:HGNC

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	9.69	3e-04	784	GSEA C2BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
2	9.08	4e-04	235	GSEA C2BLUM_RESPONSE_TO_SALIRASIB_UP
3	8.89	4e-04	176	GSEA C2TIEN_INTESTINE_PROBIOTICS_24HR_DN
4	7.7	7e-04	136	GSEA C2PODAR_RESPONSE_TO_ADAPHOSTIN_UP
5	6.6	1e-03	683	GSEA C2KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
6	6.54	1e-03	93	GSEA C2HELLER_SILENCED_BY_METHYLATION_DN
7	6.54	1e-03	84	BP endoplasmic reticulum unfolded protein response
8	6.53	1e-03	26	GSEA C2KRIGE_AMINO_ACID_DEPRIVATION
9	6.53	1e-03	66	BP activation of signaling protein activity involved in unfolded protein re
10	6.37	2e-03	109	HM HALLMARK_UNFOLDED_PROTEIN_RESPONSE
11	6.21	2e-03	60	GSEA C2PELLICCIOTTA_HDAC_IN_ANTIGEN_PRESENTATION_UP
12	5.97	2e-03	842	GSEA C2KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP
13	5.41	3e-03	66	LymphomaTARTE_Plasma cell signature
14	5.21	3e-03	74	GSEA C2REACTOME_UNFOLDED_PROTEIN_RESPONSE
15	5.19	3e-03	34	GSEA C2PACHER_TARGETS_OF_IGF1_AND_IGF2_UP
16	5.17	3e-03	1128	LymphomaTARTE_PANG_BCR_DN
17	4.84	4e-03	121	GSEA C2ONDER_CDH1_TARGETS_1_UP
18	4.82	4e-03	1132	CC Golgi apparatus
19	4.8	4e-03	66	GSEA C2TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_UP
20	4.77	4e-03	5940	Brain Overlap_fetal_midbrain_HetRpts
<i>Underexpressed</i>				
1	-14.14	6e-05	550	GSEA C2GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
2	-13.08	9e-05	116	GSEA C2MISSIAGLIA_REGULATED_BY_METHYLATION_DN
3	-12.91	9e-03	16	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
4	-12.87	9e-05	327	GSEA C2BLUM_RESPONSE_TO_SALIRASIB_DN
5	-12.63	1e-04	242	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN
6	-12.57	1e-04	197	HM HALLMARK_E2F_TARGETS
7	-12.02	1e-04	305	GSEA C2DUTERTRE ESTRADIOL_RESPONSE_24HR_UP
8	-11.86	1e-04	142	Glio WILLSCHER_GBM_Verhaak-CL_up (C)
9	-11.69	1e-04	267	GSEA C2ZHANG_TLX_TARGETS_60HR_DN
10	-11.61	1e-04	1192	GSEA C2KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
11	-11.23	2e-04	72	GSEA C2CROONQUIST_NRAS_SIGNALING_DN
12	-11.18	2e-04	373	GSEA C2VECCHI_GASTRIC_CANCER_EARLY_UP
13	-11.05	2e-04	724	GSEA C2PUJANA_CHEK2_PCC_NETWORK
14	-11.05	2e-04	390	GSEA C2PUJANA_BRCA2_PCC_NETWORK
15	-11	2e-04	139	GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
16	-10.67	2e-04	162	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
17	-10.42	2e-04	96	GSEA C2CROONQUIST_IL6_DEPRIVATION_DN
18	-10.27	2e-04	50	GSEA C2SHIDA_E2F_TARGETS
19	-10.16	2e-04	110	GSEA C2WHITEFORD_PEDIATRIC_CANCER_MARKERS
20	-10.04	3e-04	81	GSEA C2GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN



F8_mel

Local Summary

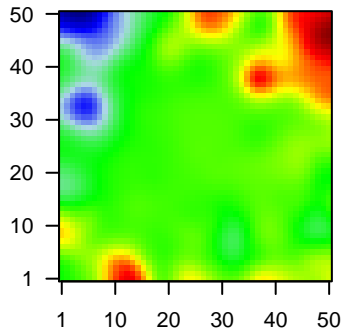
%DE = 0.29
 # metagenes = 1
 # genes = 50
 # genes in genesets = 50

 # genes with fdr < 0.1 = 12 (12 + / 0 -)
 # genes with fdr < 0.05 = 12 (12 + / 0 -)
 # genes with fdr < 0.01 = 12 (12 + / 0 -)

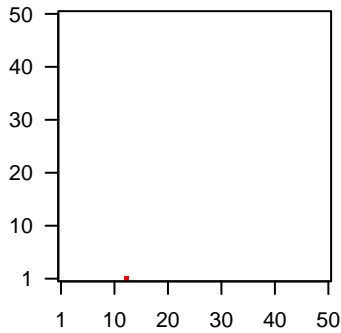
<r> metagenes = NA
 <r> genes = 0.24

 <FC> = 0.39
 <shrinkage-t> = 5.86
 <p-value> = 0.01
 <fdr> = 0.68

Profile



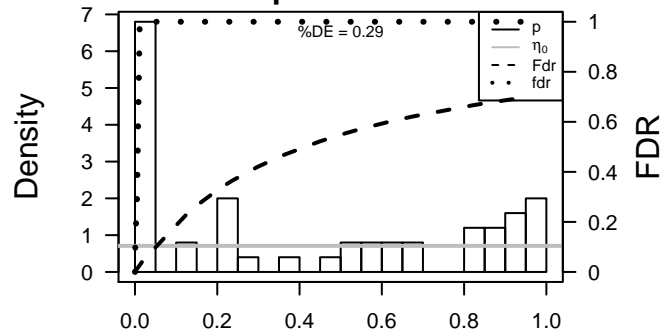
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	SERPINE3	1.75	6e-13	2e-10	13 x 1 serpin peptidase inhibitor, clade E (nexin, plasminogen activa
2	ZNF609	1.68	6e-12	1e-09	13 x 1 zinc finger protein 609 [Source:HGNC Symbol;Acc:HGNC:29
3	NICN1	1.61	4e-11	4e-09	13 x 1 nicolin 1 [Source:HGNC Symbol;Acc:HGNC:18317]
4	SH3BGR	1.56	1e-10	4e-07	13 x 1 SH3 domain binding glutamate-rich protein [Source:HGNC S
5	MAL	1.39	1e-08	4e-07	13 x 1 mal, T-cell differentiation protein [Source:HGNC Symbol;Acc
6	SESN2	1.36	2e-08	1e-06	13 x 1 sestrin 2 [Source:HGNC Symbol;Acc:HGNC:20746]
7	TYSND1	1.32	6e-08	2e-06	13 x 1 trypsin domain containing 1 [Source:HGNC Symbol;Acc:HGNC
8	TMEM131	1.29	1e-07	2e-05	13 x 1 transmembrane protein 131 [Source:HGNC Symbol;Acc:HGNC
9	SEC24A	1.2	8e-07	1e-03	13 x 1 SEC24 family member A [Source:HGNC Symbol;Acc:HGNC:
10	ENTPD7	1	4e-05	7e-03	13 x 1 ectonucleoside triphosphate diphosphohydrolase 7 [Source:H
11	C20orf96	0.89	3e-04	7e-03	13 x 1 chromosome 20 open reading frame 96 [Source:HGNC Synt
12	AKAP8	0.86	4e-04	9e-03	13 x 1 A kinase (PRKA) anchor protein 8 [Source:HGNC Symbol;Ac
13	BOC	0.83	7e-04	1e-01	13 x 1 BOC cell adhesion associated, oncogene regulated [Source:t
14	LRRC1	0.69	4e-03	3e-01	13 x 1 leucine rich repeat containing 1 [Source:HGNC Symbol;Acc:t
15	TCFL5	0.62	1e-02	1e+00	13 x 1 transcription factor-like 5 (basic helix-loop-helix) [Source:HC
16	TMEM144	0.6	1e-02	1e+00	13 x 1 transmembrane protein 144 [Source:HGNC Symbol;Acc:HGNC
17	FMNL2	0.56	2e-02	1e+00	13 x 1 formin-like 2 [Source:HGNC Symbol;Acc:HGNC:18267]
18	C16orf58	0.36	1e-01	1e+00	13 x 1 chromosome 16 open reading frame 58 [Source:HGNC Synt
19	MBOAT7	0.36	1e-01	1e+00	13 x 1 membrane bound O-acyltransferase domain containing 7 [Sc
20	MDN1	0.31	2e-01	1e+00	13 x 1 MDN1, midasin homolog (yeast) [Source:HGNC Symbol;Acc:

p-values



F8_mel

Local Summary

%DE = 0.76
 # metagenes = 38
 # genes = 457
 # genes in genesets = 455

 # genes with $fdr < 0.1$ = 244 (210 + / 34 -)
 # genes with $fdr < 0.05$ = 219 (191 + / 28 -)
 # genes with $fdr < 0.01$ = 166 (147 + / 19 -)

$\langle r \rangle$ metagenes = 0.83

$\langle r \rangle$ genes = 0.07

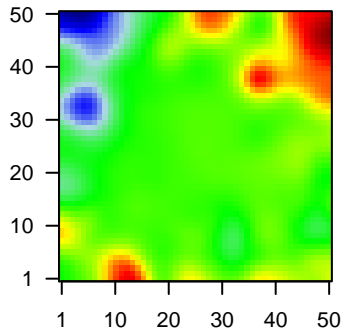
$\langle FC \rangle$ = 0.35

$\langle \text{shrinkage-t} \rangle$ = 5.75

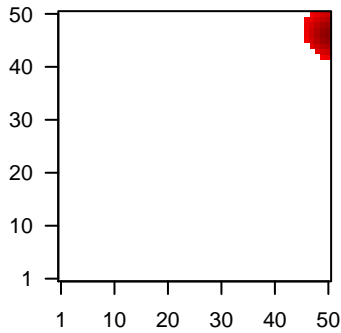
$\langle p\text{-value} \rangle$ = 0.01

$\langle fdr \rangle$ = 0.52

Profile



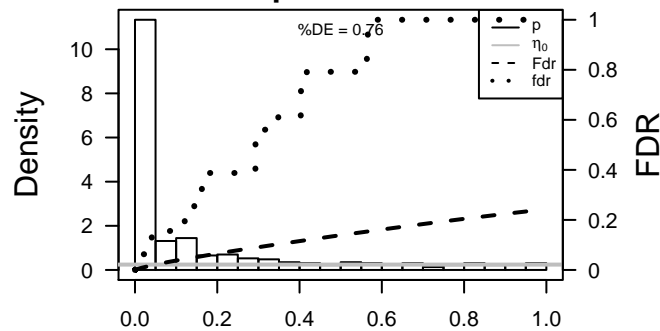
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	HERPUD1	1.24	2e-16	2e-14	50 x 42 homocysteine-inducible, endoplasmic reticulum stress-induc
2	MX11	1.66	1e-11	1e-08	47 x 47 MAX interactor 1, dimerization protein [Source:HGNC Symbo
3	DDIT3	1.35	1e-10	2e-08	50 x 50 DNA-damage-inducible transcript 3 [Source:HGNC Symbol];
4	WIP1	0.89	4e-10	2e-08	47 x 49 WD repeat domain, phosphoinositide interacting 1 [Source:HI
5	C1S	1.52	5e-10	9e-08	49 x 45 complement component 1, s subcomponent [Source:HGNC S
6	VASP	1.47	2e-09	9e-08	48 x 45 vasodilator-stimulated phosphoprotein [Source:HGNC Symb
7	ICA1	1.46	2e-09	2e-07	50 x 50 islet cell autoantigen 1, 69kDa [Source:HGNC Symbol;Acc:HI
8	NECAB2	1.43	4e-09	2e-07	47 x 44 N-terminal EF-hand calcium binding protein 2 [Source:HGNC
9	LIN37	1.41	6e-09	2e-07	50 x 43 lin-37 DREAM MuvB core complex component [Source:HGNC
10	CCDC53	-1.29	7e-09	5e-07	48 x 45 coiled-coil domain containing 53 [Source:HGNC Symbol;Acc
11	MFSB8	1.37	2e-08	5e-07	50 x 47 major facilitator superfamily domain containing 8 [Source:HGI
12	MAN2C1	1.36	2e-08	5e-07	50 x 50 mannosidase, alpha, class 2C, member 1 [Source:HGNC Syr
13	SGK3	1.35	3e-08	5e-07	50 x 46 serum/glucocorticoid regulated kinase family, member 3 [Sou
14	DPH7	1.35	3e-08	5e-07	49 x 46 diphthamide biosynthesis 7 [Source:HGNC Symbol;Acc:HGNC
15	HRK	1.35	3e-08	5e-07	50 x 44 harakiri, BCL2 interacting protein [Source:HGNC Symbol;Acc
16	AVP11	-0.88	4e-08	5e-07	49 x 50 arginine vasopressin-induced 1 [Source:HGNC Symbol;Acc:HI
17	MKRN1	1.34	4e-08	6e-07	50 x 49 makorin ring finger protein 1 [Source:HGNC Symbol;Acc:HGNC
18	IL1RAP	1.33	5e-08	6e-07	50 x 50 interleukin 1 receptor accessory protein [Source:HGNC Symt
19	USP19	1.33	5e-08	2e-06	49 x 43 ubiquitin specific peptidase 19 [Source:HGNC Symbol;Acc:HI
20	BSCL2	0.72	7e-08	2e-06	50 x 50 Berardinelli-Seip congenital lipodystrophy 2 (seipin) [Source:!

p-values



F8_mel

Local Summary

%DE = 0.67
 # metagenes = 2
 # genes = 12
 # genes in genesets = 12

 # genes with $fdr < 0.1 = 7$ (0 + / 7 -)
 # genes with $fdr < 0.05 = 7$ (0 + / 7 -)
 # genes with $fdr < 0.01 = 3$ (0 + / 3 -)

<r> metagenes = 1

<r> genes = 0.22

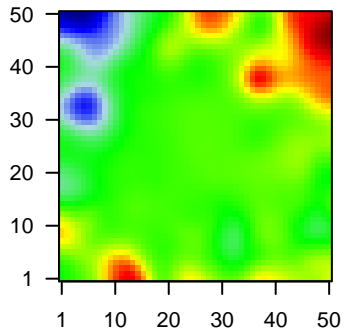
<FC> = -0.65

<shrinkage-t> = -15.78

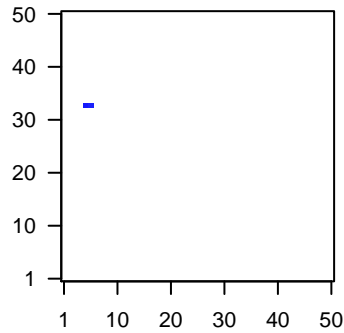
<p-value> = 0

<fdr> = 0.49

Profile



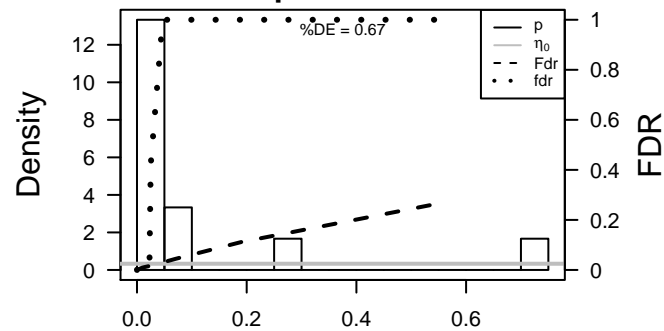
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ITGAE	-1.72	2e-16	4e-16	6 x 33 integrin, alpha E (antigen CD103, human mucosal lymphocyte)
2	MRPL15	-1.93	2e-16	4e-16	5 x 33 mitochondrial ribosomal protein L15 [Source:HGNC Symbol;A
3	THOC7	-1.03	2e-12	7e-11	6 x 33 THO complex 7 homolog (Drosophila) [Source:HGNC Symbo
4	NDUFB9	-0.66	2e-11	3e-02	5 x 33 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22
5	ATP5C1	-0.25	1e-02	3e-02	6 x 33 ATP synthase, H+ transporting, mitochondrial F1 complex, ga
6	MAP1S	-0.59	2e-02	3e-02	5 x 33 microtubule-associated protein 1S [Source:HGNC Symbol;A
7	TIMM8B	-0.48	3e-02	3e-02	5 x 33 translocase of inner mitochondrial membrane 8 homolog B (y
8	MIF	-0.21	3e-02	4e-01	6 x 33 macrophage migration inhibitory factor (glycosylation-inhibitir
9	SNAPIN	-0.3	6e-02	1e+00	5 x 33 SNAP-associated protein [Source:HGNC Symbol;Acc:HGNC
10	MOSPD3	-0.41	9e-02	1e+00	6 x 33 motile sperm domain containing 3 [Source:HGNC Symbol;Ac
11	DYNLT1	-0.16	3e-01	1e+00	5 x 33 dynein, light chain, Tctex-type 1 [Source:HGNC Symbol;Acc:
12	ALKBH7	-0.07	7e-01	1e+00	5 x 33 alkB, alkylation repair homolog 7 (E. coli) [Source:HGNC Syrr

p-values



F8_mel

Local Summary

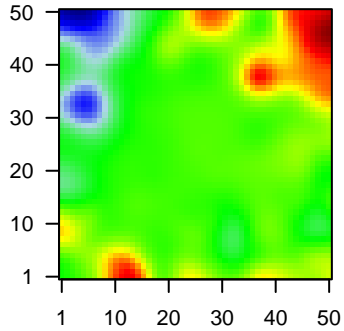
%DE = 0.89
 # metagenes = 30
 # genes = 417
 # genes in genesets = 416

 # genes with $fdr < 0.1$ = 292 (34 + / 258 -)
 # genes with $fdr < 0.05$ = 256 (25 + / 231 -)
 # genes with $fdr < 0.01$ = 170 (15 + / 155 -)

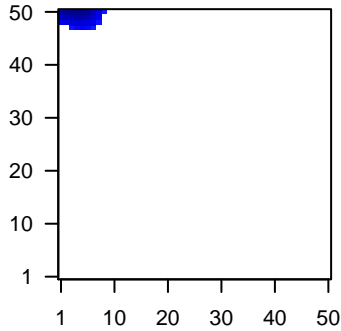
$\langle r \rangle$ metagenes = 0.92
 $\langle r \rangle$ genes = 0.27

 $\langle FC \rangle$ = -0.46
 $\langle \text{shrinkage-t} \rangle$ = -7.71
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.51

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	CSE1L	-1.71	2e-16	2e-15	3 x 49 CSE1 chromosome segregation 1-like (yeast) [Source:HGNC
2	EBP	-2.01	2e-16	2e-15	1 x 48 emopamil binding protein (sterol isomerase) [Source:HGNC
3	HMG2	-0.99	2e-16	2e-15	8 x 50 high mobility group nucleosomal binding domain 2 [Source:HGNC
4	SMC1A	-1.68	2e-16	2e-15	3 x 48 structural maintenance of chromosomes 1A [Source:HGNC
5	STMN1	-2.13	2e-16	2e-15	5 x 50 stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]
6	HMGB1	-0.99	2e-15	1e-12	7 x 47 high mobility group box 1 [Source:HGNC Symbol;Acc:HGNC:
7	MCM4	-1.47	2e-14	2e-12	1 x 50 minichromosome maintenance complex component 4 [Source:HGNC
8	CDKN3	-1.35	7e-14	1e-10	6 x 50 cyclin-dependent kinase inhibitor 3 [Source:HGNC Symbol;A
9	GMNN	-1.45	3e-12	1e-10	2 x 50 geminin, DNA replication inhibitor [Source:HGNC Symbol;Acc
10	CKAP5	-1.43	9e-12	1e-10	9 x 50 cytoskeleton associated protein 5 [Source:HGNC Symbol;Acc
11	DUT	-1.43	1e-11	1e-10	1 x 48 deoxyuridine triphosphatase [Source:HGNC Symbol;Acc:HGNC
12	RRM1	-1.31	1e-11	7e-10	2 x 50 ribonucleotide reductase M1 [Source:HGNC Symbol;Acc:HGNC
13	HADH	-1.41	3e-11	7e-10	1 x 48 hydroxyacyl-CoA dehydrogenase [Source:HGNC Symbol;Acc
14	HSD17B11	-1.4	4e-11	3e-09	8 x 50 hydroxysteroid (17-beta) dehydrogenase 11 [Source:HGNC
15	RFC5	-1.39	1e-10	4e-08	2 x 50 replication factor C (activator 1) 5, 36.5kDa [Source:HGNC
16	FEN1	-1.34	1e-09	4e-08	1 x 50 flap structure-specific endonuclease 1 [Source:HGNC
17	SKA2	-1.03	2e-09	5e-08	7 x 47 spindle and kinetochore associated complex subunit 2 [Source
18	ITGB3BP	-1.28	3e-09	2e-07	8 x 48 integrin beta 3 binding protein (beta3-endonexin) [Source:HGNC
19	HMGB2	-1.28	8e-09	2e-07	5 x 50 high mobility group box 2 [Source:HGNC Symbol;Acc:HGNC:
20	POLD3	-1.27	1e-08	2e-07	2 x 50 polymerase (DNA-directed), delta 3, accessory subunit [Source

p-values

