

F4_mel

Global Summary

%DE = 0.21
 # genes with $fdr < 0.2 = 2665$ (1597 + / 1068 -)
 # genes with $fdr < 0.1 = 2205$ (1339 + / 866 -)
 # genes with $fdr < 0.05 = 1677$ (1046 + / 631 -)
 # genes with $fdr < 0.01 = 1059$ (676 + / 383 -)
 # genes in genesets = 14839

<FC> = 0
 <shrinkage-t> = 0.04
 <p-value> = 0.08
 <fdr> = 0.79

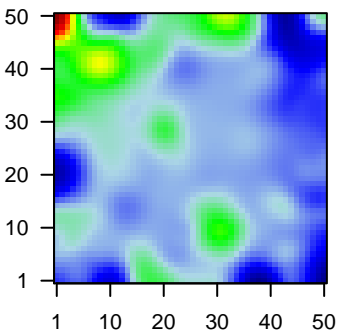
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	AMZ2	-1.3	2e-16	2e-13	48 x 42 archaeysin family metallopeptidase 2 [Source:HGNC Symbol]
2	ANKRD28	-1.57	2e-16	2e-13	50 x 5 ankyrin repeat domain 28 [Source:HGNC Symbol;Acc:HGNC]
3	CEP97	2.06	2e-16	2e-13	2 x 47 centrosomal protein 97kDa [Source:HGNC Symbol;Acc:HGNC]
4	DCT	-1.27	2e-16	2e-13	1 x 11 dopachrome tautomerase [Source:HGNC Symbol;Acc:HGNC]
5	IDH3B	-1.78	2e-16	2e-13	22 x 43 isocitrate dehydrogenase 3 (NAD+) beta [Source:HGNC Sym]
6	NUP214	-1.46	2e-16	2e-13	7 x 44 nucleoporin 214kDa [Source:HGNC Symbol;Acc:HGNC:8064]
7	OC1AD1	-1.45	2e-16	2e-13	39 x 34 OC1A domain containing 1 [Source:HGNC Symbol;Acc:HGNC]
8	PIGY	-2.23	2e-16	2e-13	1 x 20 phosphatidylinositol glycan anchor biosynthesis, class Y [Sou]
9	RSRC2	-1.53	2e-16	2e-13	25 x 7 arginine/serine-rich coiled-coil 2 [Source:HGNC Symbol;Acc]
10	SARS	-1.2	2e-16	2e-13	45 x 50 seryl-tRNA synthetase [Source:HGNC Symbol;Acc:HGNC:11]
11	SLC25A14	2.08	2e-16	2e-13	4 x 14 solute carrier family 25 (mitochondrial carrier, brain), member
12	TDRD12	-1.32	2e-16	2e-13	45 x 46 tudor domain containing 12 [Source:HGNC Symbol;Acc:HGNC]
13	THUMP3	-1.56	2e-16	2e-13	9 x 47 THUMP domain containing 3 [Source:HGNC Symbol;Acc:HGNC]
14	CA14	-1.52	4e-16	1e-11	1 x 46 carbonic anhydrase XIV [Source:HGNC Symbol;Acc:HGNC:11]
15	MALSU1	-1.53	4e-16	1e-11	49 x 15 mitochondrial assembly of ribosomal large subunit 1 [Source:HGNC]
16	MPZL1	-1.52	2e-15	1e-11	1 x 19 myelin protein zero-like 1 [Source:HGNC Symbol;Acc:HGNC]
17	BABAM1	-1.5	3e-15	1e-11	43 x 47 BRISC and BRCA1 A complex member 1 [Source:HGNC Syr]
18	DMPK	1.83	3e-15	1e-11	46 x 12 dystrophin myotonic-protein kinase [Source:HGNC Symbol;Acc:HGNC]
19	SARAF	-1.51	4e-15	3e-11	44 x 48 store-operated calcium entry-associated regulatory factor [S]
20	BLOC1S2	-1.5	7e-15	4e-11	48 x 50 biogenesis of lysosomal organelles complex-1, subunit 2 [So]

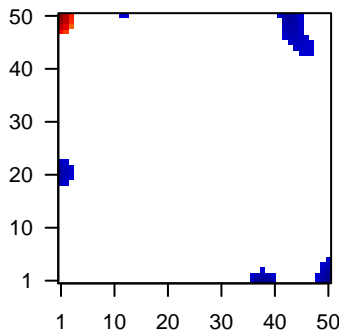
Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1		7.29	9e-04	135 GSEA C2WHITFIELD_CELL_CYCLE_G1_S
2		7.03	1e-03	305 GSEA C2DUTERTRE ESTRADIOL_RESPONSE_24HR_UP
3		7.02	1e-03	139 BP DNA replication
4		6.9	1e-03	59 GSEA C2KAUFFMANN_MELANOMA_RELAPSE_UP
5		6.63	1e-03	215 GSEA C2KAUFFMANN_DNA_REPAIR_GENES
6		6.57	1e-03	68 GSEA C2VERNELL_RETINOBLASTOMA_PATHWAY_UP
7		6.39	1e-03	94 BP respiratory electron transport chain
8		6.38	1e-03	38 GSEA C2BURTON_ADIPOGENESIS_PEAK_AT_16HR
9		6.27	2e-03	43 GSEA C2PID_FANCONI_PATHWAY
10		5.99	2e-03	26 GSEA C2REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMPLEX
11		5.98	2e-03	1192 GSEA C2KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
12		5.87	2e-03	32 GSEA C2KEGG_DNA_REPLICATION
13		5.75	2e-03	768 BP DNA metabolic process
14		5.74	2e-03	138 GSEA C2KAUFFMANN_DNA_REPLICATION_GENES
15		5.71	2e-03	78 GSEA C2REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_S
16		5.68	2e-03	198 GSEA C2FUJII_YBX1_TARGETS_DN
17		5.59	2e-03	11 GSEA C2MATHEW_FANCONI_ANEMIA_GENES
18		5.47	3e-03	267 GSEA C2ZHANG_TLX_TARGETS_60HR_DN
19		5.39	3e-03	85 GSEA C2REACTOME_SYNTHESIS_OF_DNA
20		5.34	3e-03	1251 GSEA C2DODD_NASOPHARYNGEAL_CARCINOMA_DN
<i>Underexpressed</i>				
1		-4.73	0.004	6 GSEA C2ZERBINI_RESPONSE_TO_SULINDAC_DN
2		-3.99	0.008	26 GSEA C2KRIGE_AMINO_ACID_DEPRIVATION
3		-3.91	0.008	472 GSEA C2DUTERTRE ESTRADIOL_RESPONSE_24HR_DN
4		-3.77	0.009	2798 Colon Cancer hG1_Colon
5		-3.65	0.010	838 Chr Chr 3
6		-3.59	0.011	208 GSEA C2ZHANG_TLX_TARGETS_36HR_UP
7		-3.56	0.011	475 GSEA C2ONKEN_UVEAL_MELANOMA_DN
8		-3.48	0.012	19 GSEA C2HEDENFALK_BREAST_CANCER_BRACX_DN
9		-3.48	0.012	101 GSEA C2ZHANG_TLX_TARGETS_DN
10		-3.46	0.012	43 GSEA C2KEGG_N_GLYCAN_BIOSYNTHESIS
11		-3.4	0.013	66 GSEA C2TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_UP
12		-3.4	0.013	256 GSEA C2PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_UP
13		-3.39	0.013	16 BP nitrogen compound metabolic process
14		-3.34	0.013	76 GSEA C2REACTOME_ASPARAGINE_N_LINKED_GLYCOSYLATION
15		-3.34	0.013	66 Lymphoma Tarte_Plasma cell signature
16		-3.26	0.014	17 GSEA C2KEGG_NITROGEN_METABOLISM
17		-3.25	0.014	26 GSEA C2KEGG_PRION_DISEASES
18		-3.16	0.016	42 miRNA target-miR-129-3p
19		-3.16	0.016	72 GSEA C2SAFFORD_T_LYMPHOCYTE_ANGRY
20		-3.15	0.016	271 GSEA C2ZHANG_TLX_TARGETS_60HR_UP

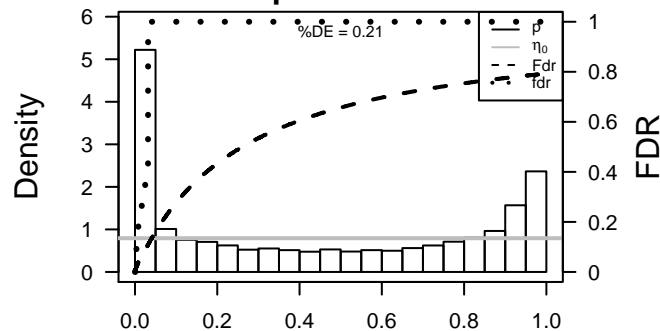
Profile



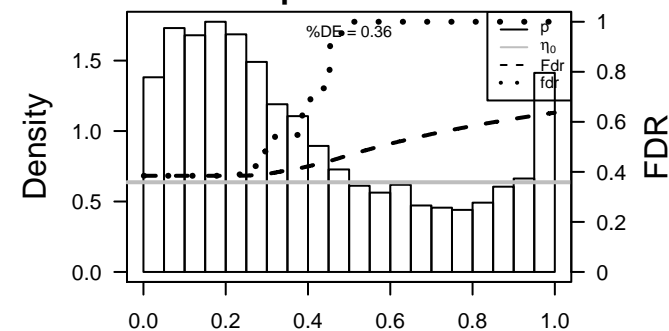
Regulated Spots



p-values



p-values



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Local Summary

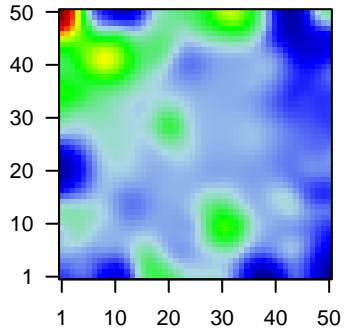
%DE = 0.87
 # metagenes = 11
 # genes = 206
 # genes in genesets = 205

 # genes with $fdr < 0.1$ = 135 (124 + / 11 -)
 # genes with $fdr < 0.05$ = 135 (124 + / 11 -)
 # genes with $fdr < 0.01$ = 97 (92 + / 5 -)

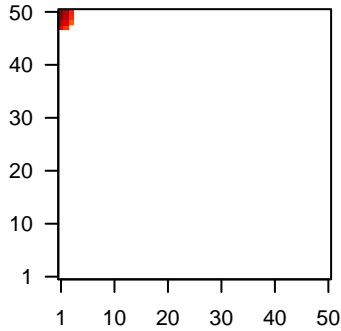
$\langle r \rangle$ metagenes = 0.98
 $\langle r \rangle$ genes = 0.27

 $\langle FC \rangle$ = 0.49
 $\langle \text{shrinkage-t} \rangle$ = 7.79
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.43

Profile



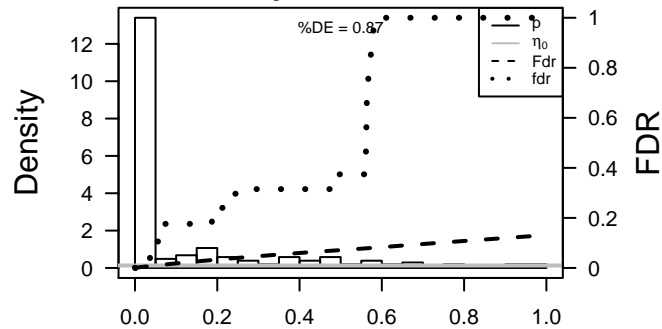
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	CEP97	2.06	2e-16	6e-15	2 x 47 centrosomal protein 97kDa [Source:HGNC Symbol;Acc:HGNC:10000]
2	MAGOHB	-1.45	4e-13	2e-08	1 x 47 mago-nashi homolog B (Drosophila) [Source:HGNC Symbol;Acc:HGNC:10000]
3	CENPH	1.44	6e-10	2e-08	1 x 47 centromere protein H [Source:HGNC Symbol;Acc:HGNC:172]
4	BRCA2	1.42	1e-09	2e-07	2 x 50 breast cancer 2, early onset [Source:HGNC Symbol;Acc:HGNC:10000]
5	POLA2	1.34	7e-09	3e-07	1 x 48 polymerase (DNA directed), alpha 2, accessory subunit [Source:HGNC Symbol;Acc:HGNC:10000]
6	POLE2	1.31	2e-08	6e-07	1 x 47 polymerase (DNA directed), epsilon 2, accessory subunit [Source:HGNC Symbol;Acc:HGNC:10000]
7	ZGRF1	1.24	1e-07	6e-07	1 x 50 zinc finger, GRF-type containing 1 [Source:HGNC Symbol;Acc:HGNC:10000]
8	TAF1A	1.24	1e-07	6e-07	1 x 48 TATA box binding protein (TBP)-associated factor, RNA polymerase II [Source:HGNC Symbol;Acc:HGNC:10000]
9	RAD51	1.23	1e-07	6e-07	1 x 50 RAD51 recombinase [Source:HGNC Symbol;Acc:HGNC:981]
10	CDC47	1.22	1e-07	6e-07	1 x 49 cell division cycle associated 7 [Source:HGNC Symbol;Acc:HGNC:10000]
11	FANCB	1.22	2e-07	6e-07	2 x 50 Fanconi anemia, complementation group B [Source:HGNC Symbol;Acc:HGNC:10000]
12	TUBGCP3	1.22	2e-07	6e-07	1 x 48 tubulin, gamma complex associated protein 3 [Source:HGNC Symbol;Acc:HGNC:10000]
13	CHEK1	1.22	2e-07	1e-06	1 x 50 checkpoint kinase 1 [Source:HGNC Symbol;Acc:HGNC:1925]
14	ZFYVE19	1.19	3e-07	1e-06	1 x 47 zinc finger, FYVE domain containing 19 [Source:HGNC Symbol;Acc:HGNC:10000]
15	C1GALT1	1.19	3e-07	1e-06	1 x 48 core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase [Source:HGNC Symbol;Acc:HGNC:10000]
16	CHEK2	1.18	4e-07	1e-06	3 x 50 checkpoint kinase 2 [Source:HGNC Symbol;Acc:HGNC:1662]
17	KIAA0101	1.07	4e-07	1e-06	3 x 50 KIAA0101 [Source:HGNC Symbol;Acc:HGNC:28961]
18	EXO1	1.18	4e-07	2e-06	1 x 50 exonuclease 1 [Source:HGNC Symbol;Acc:HGNC:3511]
19	RMI1	1.17	5e-07	1e-05	1 x 50 RecQ mediated genome instability 1 [Source:HGNC Symbol;Acc:HGNC:10000]
20	MCM4	0.9	1e-06	1e-05	1 x 50 minichromosome maintenance complex component 4 [Source:HGNC Symbol;Acc:HGNC:10000]

p-values



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Local Summary

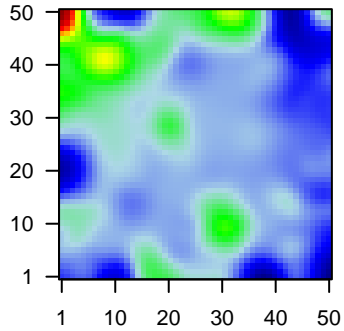
%DE = 0.6
 # metagenes = 11
 # genes = 112
 # genes in genesets = 112

 # genes with $fdr < 0.1$ = 49 (9 + / 40 -)
 # genes with $fdr < 0.05$ = 33 (6 + / 27 -)
 # genes with $fdr < 0.01$ = 27 (4 + / 23 -)

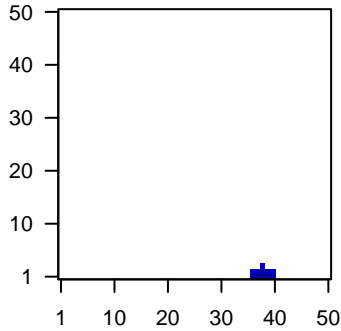
$\langle r \rangle$ metagenes = 0.95
 $\langle r \rangle$ genes = 0.1

 $\langle FC \rangle$ = -0.29
 $\langle \text{shrinkage-t} \rangle$ = -4.63
 $\langle p\text{-value} \rangle$ = 0.02
 $\langle fdr \rangle$ = 0.62

Profile



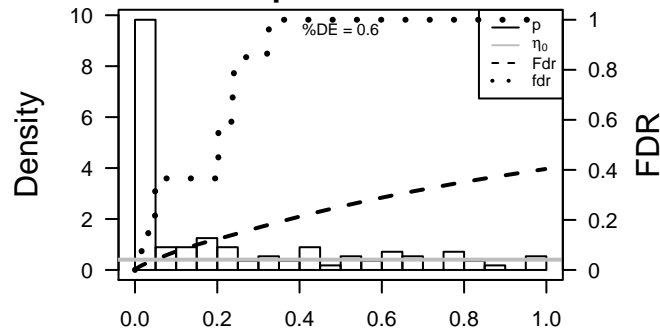
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ALG13	-1.45	5e-14	6e-10	39 x 1 ALG13, UDP-N-acetylglucosaminyltransferase subunit [Source:HGNC Symbol;Acc:HGNC:10000]
2	DPM1	-1.37	2e-11	6e-10	37 x 1 dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit [Source:HGNC Symbol;Acc:HGNC:10000]
3	GLUL	-1.23	3e-11	6e-10	36 x 1 glutamate-ammonia ligase [Source:HGNC Symbol;Acc:HGNC:10000]
4	BLCAP	-1.36	4e-11	1e-07	37 x 1 bladder cancer associated protein [Source:HGNC Symbol;Acc:HGNC:10000]
5	LAPTM4A	-1.04	2e-09	2e-04	36 x 1 lysosomal protein transmembrane 4 alpha [Source:HGNC Symbol;Acc:HGNC:10000]
6	TIMM10B	-1.04	4e-06	2e-04	36 x 1 translocase of inner mitochondrial membrane 10 homolog B (human) [Source:HGNC Symbol;Acc:HGNC:10000]
7	OFD1	-1.03	8e-06	1e-03	38 x 1 oral-facial-digital syndrome 1 [Source:HGNC Symbol;Acc:HGNC:10000]
8	ARFIP1	-0.96	4e-05	3e-03	40 x 1 ADP-ribosylation factor interacting protein 1 [Source:HGNC Symbol;Acc:HGNC:10000]
9	MAGED1	-0.81	1e-04	3e-03	39 x 1 melanoma antigen family D1 [Source:HGNC Symbol;Acc:HGNC:10000]
10	UBR2	-0.85	2e-04	3e-03	40 x 1 ubiquitin protein ligase E3 component n-recognin 2 [Source:HGNC Symbol;Acc:HGNC:10000]
11	DDX52	-0.85	3e-04	3e-03	37 x 1 DEAD (Asp-Glu-Ala-Asp) box polypeptide 52 [Source:HGNC Symbol;Acc:HGNC:10000]
12	HERC4	-0.84	3e-04	3e-03	37 x 1 HECT and RLD domain containing E3 ubiquitin protein ligase 4 [Source:HGNC Symbol;Acc:HGNC:10000]
13	PTGES3L-AA	0.82	4e-04	3e-03	39 x 2 PTGES3L-AARSD1 readthrough [Source:HGNC Symbol;Acc:HGNC:10000]
14	DHR SX	-0.81	5e-04	7e-03	39 x 1 dehydrogenase/reductase (SDR family) X-linked [Source:HGNC Symbol;Acc:HGNC:10000]
15	CPEB4	0.79	7e-04	7e-03	38 x 1 cytoplasmic polyadenylation element binding protein 4 [Source:HGNC Symbol;Acc:HGNC:10000]
16	ALG11	-0.77	9e-04	7e-03	38 x 1 ALG11, alpha-1,2-mannosyltransferase [Source:HGNC Symbol;Acc:HGNC:10000]
17	UBXN7	-0.77	9e-04	7e-03	39 x 2 UBX domain protein 7 [Source:HGNC Symbol;Acc:HGNC:10000]
18	KIAA0226	-0.76	1e-03	7e-03	38 x 1 KIAA0226 [Source:HGNC Symbol;Acc:HGNC:28991]
19	MAD1L1	0.75	1e-03	7e-03	37 x 1 MAD1 mitotic arrest deficient-like 1 (yeast) [Source:HGNC Symbol;Acc:HGNC:10000]
20	USP9X	-0.68	1e-03	7e-03	38 x 1 ubiquitin specific peptidase 9, X-linked [Source:HGNC Symbol;Acc:HGNC:10000]

p-values



F4_mel

Local Summary

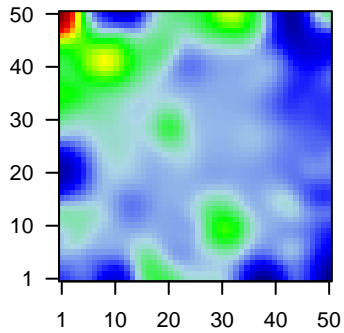
%DE = 0.81
 # metagenes = 11
 # genes = 225
 # genes in genesets = 225

 # genes with $fdr < 0.1$ = 141 (41 + / 100 -)
 # genes with $fdr < 0.05$ = 100 (32 + / 68 -)
 # genes with $fdr < 0.01$ = 56 (20 + / 36 -)

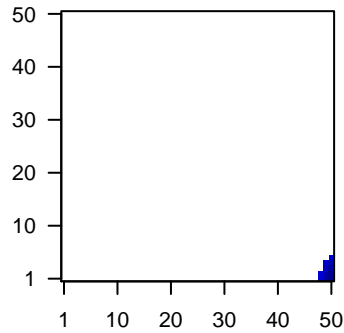
$\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.21

 $\langle FC \rangle$ = -0.19
 $\langle \text{shrinkage-t} \rangle$ = -3.05
 $\langle p\text{-value} \rangle$ = 0.01
 $\langle fdr \rangle$ = 0.61

Profile



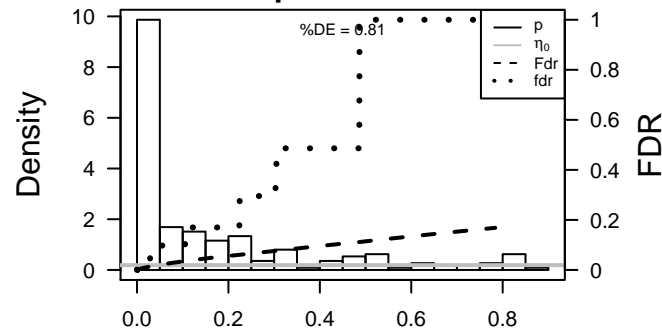
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ANKRD28	-1.57	2e-16	9e-15	ankyrin repeat domain 28 [Source:HGNC Symbol;Acc:HGNC]
2	ARMC9	-1.35	4e-11	2e-09	armadillo repeat containing 9 [Source:HGNC Symbol;Acc:HGNC]
3	RAB3IP	1.51	8e-11	2e-07	RAB3A interacting protein [Source:HGNC Symbol;Acc:HGNC]
4	LAMC1	-1.22	5e-09	7e-07	laminin, gamma 1 (formerly LAMB2) [Source:HGNC Symbol;Acc:HGNC]
5	STAM	1.16	3e-08	7e-07	signal transducing adaptor molecule (SH3 domain and ITAM domain) [Source:HGNC Symbol;Acc:HGNC]
6	RNF141	-1.21	4e-08	6e-06	ring finger protein 141 [Source:HGNC Symbol;Acc:HGNC:21411]
7	FAM98A	-1.16	3e-07	6e-06	family with sequence similarity 98, member A [Source:HGNC Symbol;Acc:HGNC:14411]
8	RAB30	1.19	3e-07	6e-06	RAB30, member RAS oncogene family [Source:HGNC Symbol;Acc:HGNC:14411]
9	YPEL5	-1.15	5e-07	6e-06	yippee-like 5 (Drosophila) [Source:HGNC Symbol;Acc:HGNC:14411]
10	ESYT1	1.15	7e-07	6e-06	extended synaptotagmin-like protein 1 [Source:HGNC Symbol;Acc:HGNC:14411]
11	CSRP2	1.02	7e-07	1e-05	cysteine and glycine-rich protein 2 [Source:HGNC Symbol;Acc:HGNC:14411]
12	DNAJC16	-1.12	1e-06	1e-05	DnaJ (Hsp40) homolog, subfamily C, member 16 [Source:HGNC Symbol;Acc:HGNC:14411]
13	EDIL3	-1.11	1e-06	2e-05	EGF-like repeats and discoidin I-like domains 3 [Source:HGNC Symbol;Acc:HGNC:14411]
14	PDLIM5	1.08	2e-06	2e-05	PDZ and LIM domain 5 [Source:HGNC Symbol;Acc:HGNC:14411]
15	PTPRM	-1.08	3e-06	2e-05	protein tyrosine phosphatase, receptor type, M [Source:HGNC Symbol;Acc:HGNC:14411]
16	TFPI	1.09	3e-06	2e-05	tissue factor pathway inhibitor (lipoprotein-associated coagulation pathway inhibitor) [Source:HGNC Symbol;Acc:HGNC:14411]
17	NRP1	1.08	3e-06	6e-05	neuropilin 1 [Source:HGNC Symbol;Acc:HGNC:8004]
18	KRTAP7-1	1.05	7e-06	6e-05	keratin associated protein 7-1 (gene/pseudogene) [Source:HGNC Symbol;Acc:HGNC:14411]
19	MID1	-1.04	7e-06	6e-05	midline 1 [Source:HGNC Symbol;Acc:HGNC:7095]
20	CALD1	-0.66	8e-06	1e-04	caldesmon 1 [Source:HGNC Symbol;Acc:HGNC:14411]

p-values



F4_mel

Local Summary

%DE = 0.63
 # metagenes = 13
 # genes = 222
 # genes in genesets = 221

 # genes with $fdr < 0.1$ = 67 (21 + / 46 -)
 # genes with $fdr < 0.05$ = 61 (19 + / 42 -)
 # genes with $fdr < 0.01$ = 31 (8 + / 23 -)

<r> metagenes = 0.98

<r> genes = 0.16

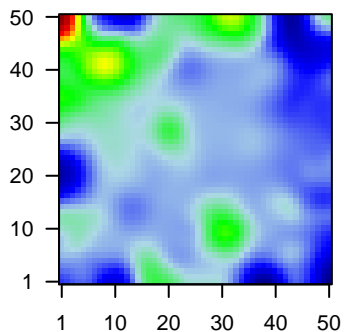
<FC> = -0.16

<shrinkage-t> = -2.87

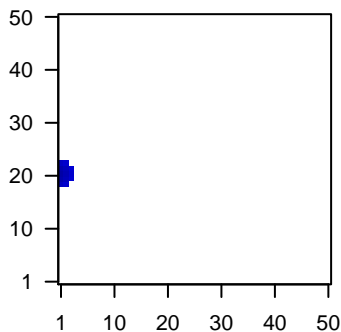
<p-value> = 0.03

<fdr> = 0.7

Profile



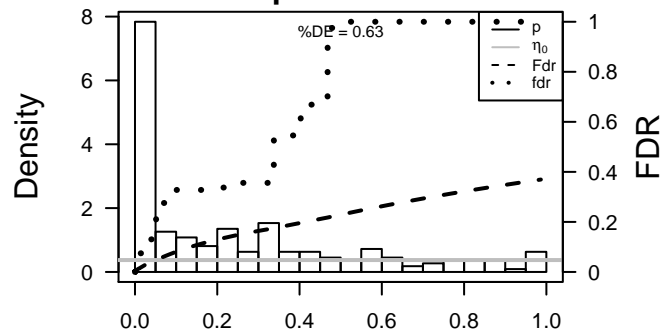
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	PIGY	-2.23	2e-16	2e-14	1 x 20 phosphatidylinositol glycan anchor biosynthesis, class Y [Sou
2	MPZL1	-1.52	2e-15	7e-07	1 x 19 myelin protein zero-like 1 [Source:HGNC Symbol;Acc:HGNC
3	P4HB	-0.54	8e-09	6e-05	1 x 20 prolyl 4-hydroxylase, beta polypeptide [Source:HGNC Symb
4	LAGE3	-1.14	7e-07	6e-05	1 x 21 L antigen family, member 3 [Source:HGNC Symbol;Acc:HGNC
5	PPP5C	-1.11	1e-06	9e-05	1 x 23 protein phosphatase 5, catalytic subunit [Source:HGNC Synt
6	KDEL2	-0.88	2e-06	3e-04	1 x 19 KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein ret
7	AKR7A2	1.01	1e-05	3e-04	1 x 21 aldo-keto reductase family 7, member A2 (aflatoxin aldehyde
8	RIOK2	1.01	1e-05	3e-04	1 x 20 RIO kinase 2 [Source:HGNC Symbol;Acc:HGNC:18999]
9	MRPS34	-1	2e-05	3e-04	1 x 21 mitochondrial ribosomal protein S34 [Source:HGNC Symbol;]
10	ARRDC1	0.99	2e-05	3e-04	2 x 22 arrestin domain containing 1 [Source:HGNC Symbol;Acc:HGI
11	PUM1	0.98	2e-05	3e-04	2 x 19 pumilio RNA-binding family member 1 [Source:HGNC Symb
12	C17orf89	-0.98	2e-05	3e-04	1 x 21 chromosome 17 open reading frame 89 [Source:HGNC Synt
13	SQSTM1	-0.44	3e-05	3e-04	1 x 21 sequestosome 1 [Source:HGNC Symbol;Acc:HGNC:11280]
14	AGPAT2	-0.96	3e-05	3e-04	1 x 21 1-acylglycerol-3-phosphate O-acyltransferase 2 [Source:HC
15	CD47	-0.87	4e-05	3e-04	1 x 22 CD47 molecule [Source:HGNC Symbol;Acc:HGNC:1682]
16	CDKN2A	-0.96	4e-05	3e-04	1 x 21 cyclin-dependent kinase inhibitor 2A [Source:HGNC Symbol;
17	DNAJC4	-0.95	4e-05	1e-03	1 x 19 DnaJ (Hsp40) homolog, subfamily C, member 4 [Source:HGNC
18	TRAPPC5	-0.94	6e-05	1e-03	1 x 20 trafficking protein particle complex 5 [Source:HGNC Symbol;]
19	RER1	0.57	7e-05	1e-03	3 x 22 retention in endoplasmic reticulum sorting receptor 1 [Source
20	MZT2A	-0.88	8e-05	4e-03	1 x 20 mitotic spindle organizing protein 2A [Source:HGNC Symbol;]

p-values



F4_mel

Local Summary

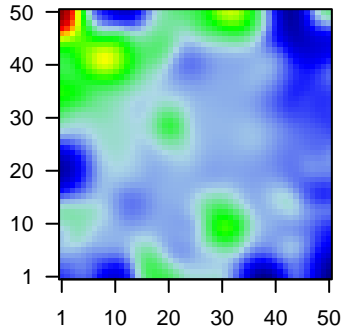
%DE = 0.64
 # metagenes = 34
 # genes = 285
 # genes in genesets = 284

 # genes with $fdr < 0.1$ = 118 (33 + / 85 -)
 # genes with $fdr < 0.05$ = 106 (30 + / 76 -)
 # genes with $fdr < 0.01$ = 63 (18 + / 45 -)

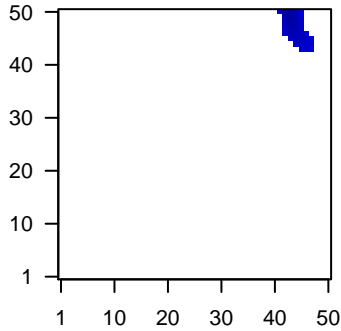
$\langle r \rangle$ metagenes = 0.83
 $\langle r \rangle$ genes = 0.07

 $\langle FC \rangle$ = -0.21
 $\langle \text{shrinkage-t} \rangle$ = -3.28
 $\langle p\text{-value} \rangle$ = 0.01
 $\langle fdr \rangle$ = 0.6

Profile



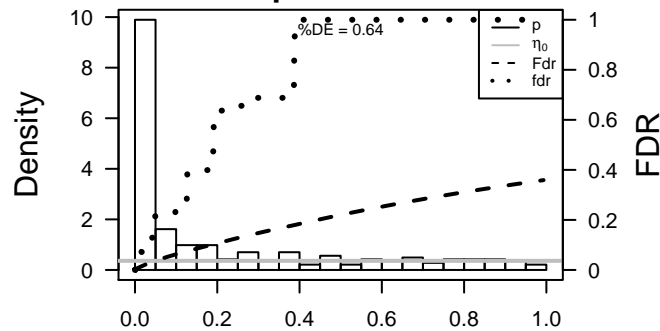
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	SARS	-1.2	2e-16	1e-14	45 x 50 seryl-tRNA synthetase [Source:HGNC Symbol;Acc:HGNC:10
2	TDRD12	-1.32	2e-16	1e-14	45 x 46 tudor domain containing 12 [Source:HGNC Symbol;Acc:HGNC
3	BABAM1	-1.5	3e-15	2e-13	43 x 47 BRISC and BRCA1 A complex member 1 [Source:HGNC Syr
4	SARAF	-1.51	4e-15	6e-11	44 x 48 store-operated calcium entry-associated regulatory factor [S
5	SMIM15	-1.44	6e-13	4e-09	42 x 50 small integral membrane protein 15 [Source:HGNC Symbol;A
6	ECHDC1	-1.05	4e-11	6e-07	42 x 46 ethylmalonyl-CoA decarboxylase 1 [Source:HGNC Symbol;A
7	PGD	-1.08	6e-09	2e-06	42 x 50 phosphogluconate dehydrogenase [Source:HGNC Symbol;Ar
8	GCC2	-1.19	2e-08	2e-06	44 x 50 GRIP and coiled-coil domain containing 2 [Source:HGNC Sy
9	TYW3	-1.2	4e-08	2e-06	44 x 44 tRNA-yW synthesizing protein 3 homolog (S. cerevisiae) [So
10	ATM	-1.16	5e-08	3e-06	45 x 50 ATM serine/threonine kinase [Source:HGNC Symbol;Acc:HGI
11	ISCU	-1.19	8e-08	3e-06	45 x 44 iron-sulfur cluster assembly enzyme [Source:HGNC Symbol;
12	ZNF706	0.7	1e-07	4e-06	45 x 50 zinc finger protein 706 [Source:HGNC Symbol;Acc:HGNC:24
13	TRIM21	1.23	1e-07	7e-06	45 x 47 tripartite motif containing 21 [Source:HGNC Symbol;Acc:HGNC
14	TMEM254	1.21	2e-07	2e-05	43 x 48 transmembrane protein 254 [Source:HGNC Symbol;Acc:HGNC
15	C1orf52	-1.15	4e-07	2e-05	47 x 44 chromosome 1 open reading frame 52 [Source:HGNC Symbc
16	MOCOS2	-1.15	6e-07	2e-05	41 x 50 molybdenum cofactor synthesis 2 [Source:HGNC Symbol;Acc
17	SC5D	0.99	1e-06	2e-05	43 x 48 sterol-C5-desaturase [Source:HGNC Symbol;Acc:HGNC:10
18	SIRT5	1.13	1e-06	2e-05	47 x 44 sirtuin 5 [Source:HGNC Symbol;Acc:HGNC:14933]
19	C9orf114	1.13	1e-06	4e-05	44 x 44 chromosome 9 open reading frame 114 [Source:HGNC Symt
20	RIT1	-1.02	2e-06	4e-05	42 x 47 Ras-like without CAAX 1 [Source:HGNC Symbol;Acc:HGNC:

p-values



F4_mel

Local Summary

%DE = 0.77
 # metagenes = 2
 # genes = 45
 # genes in genesets = 45

 # genes with $fdr < 0.1$ = 27 (4 + / 23 -)
 # genes with $fdr < 0.05$ = 24 (3 + / 21 -)
 # genes with $fdr < 0.01$ = 13 (0 + / 13 -)

<r> metagenes = 0.99

<r> genes = 0.12

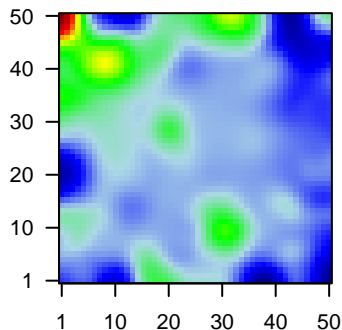
<FC> = -0.38

<shrinkage-t> = -5.97

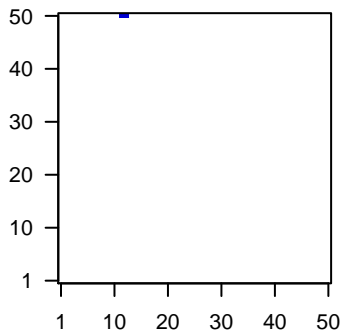
<p-value> = 0.01

<fdr> = 0.54

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	RAB34	-1.44	5e-13	4e-11	13 x 50 RAB34, member RAS oncogene family [Source:HGNC Symb
2	PIGK	-1.41	4e-12	8e-06	13 x 50 phosphatidylinositol glycan anchor biosynthesis, class K [Sou
3	SMIM20	-1.13	8e-07	1e-05	13 x 50 small integral membrane protein 20 [Source:HGNC Symbol;A
4	PEF1	-1.09	2e-06	4e-05	12 x 50 penta-EF-hand domain containing 1 [Source:HGNC Symbol
5	PDE4B	-1.05	7e-06	2e-04	12 x 50 phosphodiesterase 4B, cAMP-specific [Source:HGNC Symb
6	PGM2	-0.99	2e-05	4e-04	13 x 50 phosphoglucomutase 2 [Source:HGNC Symbol;Acc:HGNC:8
7	SMYD2	-0.9	7e-05	4e-04	12 x 50 SET and MYND domain containing 2 [Source:HGNC Symbol;
8	NUP35	-0.9	1e-04	2e-03	13 x 50 nucleoporin 35kDa [Source:HGNC Symbol;Acc:HGNC:29797
9	THAP4	-0.83	4e-04	2e-03	13 x 50 THAP domain containing 4 [Source:HGNC Symbol;Acc:HGNC
10	CCL28	-0.78	8e-04	2e-03	12 x 50 chemokine (C-C motif) ligand 28 [Source:HGNC Symbol;Acc
11	ALDH9A1	-0.48	9e-04	2e-03	12 x 50 aldehyde dehydrogenase 9 family, member A1 [Source:HGNC
12	SCAMP1	-0.76	1e-03	6e-03	13 x 50 secretory carrier membrane protein 1 [Source:HGNC Symbol
13	GMPPA	-0.71	2e-03	6e-03	13 x 50 GDP-mannose pyrophosphorylase A [Source:HGNC Symbol
14	TXNDC15	-0.71	2e-03	1e-02	12 x 50 thioredoxin domain containing 15 [Source:HGNC Symbol;Acc
15	PDCD10	0.5	3e-03	2e-02	13 x 50 programmed cell death 10 [Source:HGNC Symbol;Acc:HGNC
16	RAB8A	0.55	6e-03	3e-02	13 x 50 RAB8A, member RAS oncogene family [Source:HGNC Symb
17	CASP6	-0.59	1e-02	3e-02	13 x 50 caspase 6, apoptosis-related cysteine peptidase [Source:HG
18	SURF2	0.59	1e-02	3e-02	12 x 50 surfactant 2 [Source:HGNC Symbol;Acc:HGNC:11475]
19	RTN4IP1	-0.53	2e-02	3e-02	12 x 50 reticulon 4 interacting protein 1 [Source:HGNC Symbol;Acc:H
20	GTF3C5	-0.53	2e-02	3e-02	13 x 50 general transcription factor IIIc, polypeptide 5, 63kDa [Source

p-values

