

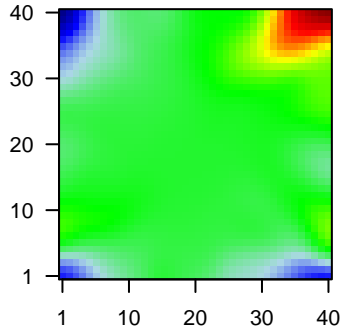
C31921_cH

Global Summary

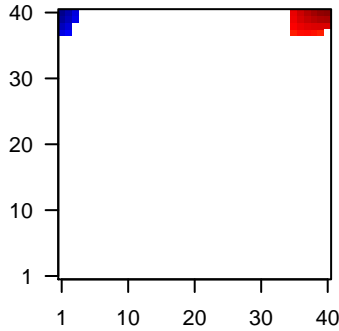
%DE = 0.25
 # genes with $fdr < 0.2$ = 4499 (2224 + / 2275 -)
 # genes with $fdr < 0.1$ = 4212 (2104 + / 2108 -)
 # genes with $fdr < 0.05$ = 3825 (1910 + / 1915 -)
 # genes with $fdr < 0.01$ = 3260 (1684 + / 1576 -)
 # genes in genesets = 18990

<FC> = 0
 <t-score> = 0
 <p-value> = 0.01
 <fdr> = 0.75

Profile



Regulated Spots

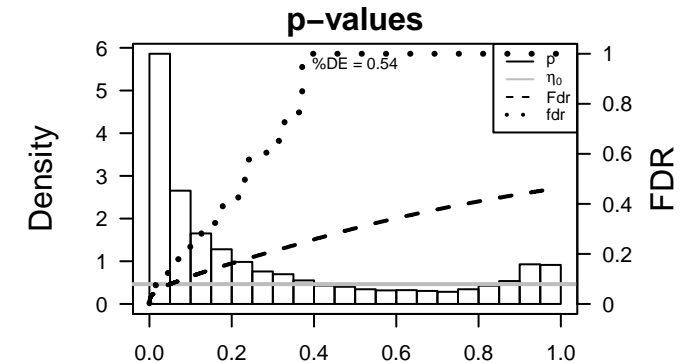
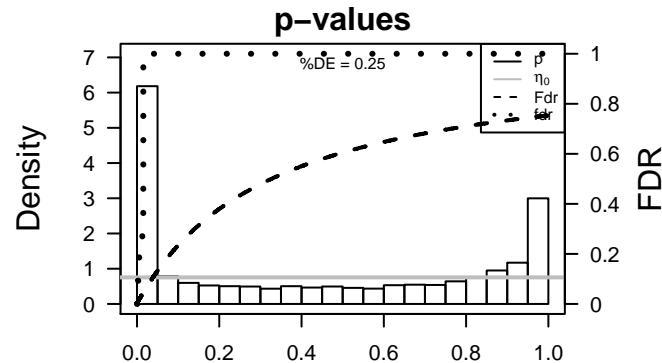


Global Genelist

Rank	ID	log(FC)	fdr	Description	
		p-value		Metagene	
1	ENSG000002	0.19	2e-16	3e-15	7 x 8
2	ENSG000001	-0.32	2e-16	3e-15	36 x 4 ISG15 ubiquitin-like modifier [Source:HGNC Symbol;Acc:HGNC:100]
3	ENSG000002	0.38	2e-16	3e-15	1 x 26 cyclin L2 [Source:HGNC Symbol;Acc:HGNC:20570]
4	ENSG000001	0.17	2e-16	3e-15	1 x 8 ribosomal protein L22 [Source:HGNC Symbol;Acc:HGNC:100]
5	ENSG000001	-0.19	2e-16	3e-15	3 x 32 ERBB receptor feedback inhibitor 1 [Source:HGNC Symbol;Acc:HGNC:100]
6	ENSG000000	0.34	2e-16	3e-15	38 x 40 enolase 1, (alpha) [Source:HGNC Symbol;Acc:HGNC:3350]
7	ENSG000001	0.18	2e-16	3e-15	36 x 37 angiotensin II receptor-associated protein [Source:HGNC Symbol;Acc:HGNC:100]
8	ENSG000001	-0.17	2e-16	3e-15	33 x 1 filamin binding LIM protein 1 [Source:HGNC Symbol;Acc:HGNC:100]
9	ENSG000001	-0.16	2e-16	3e-15	39 x 1 peptidyl arginine deiminase, type II [Source:HGNC Symbol;Acc:HGNC:100]
10	ENSG000001	0.19	2e-16	3e-15	36 x 40 regulator of chromosome condensation 2 [Source:HGNC Symbol;Acc:HGNC:100]
11	ENSG000000	0.21	2e-16	3e-15	39 x 11 Rho guanine nucleotide exchange factor (GEF) 10-like [Source:HGNC Symbol;Acc:HGNC:100]
12	ENSG000001	0.18	2e-16	3e-15	25 x 1 ring finger protein 186 [Source:HGNC Symbol;Acc:HGNC:250]
13	ENSG000001	-0.47	2e-16	3e-15	37 x 1 calcium/calmodulin-dependent protein kinase II inhibitor 1 [Source:HGNC Symbol;Acc:HGNC:100]
14	ENSG000001	-0.24	2e-16	3e-15	38 x 1 cytidine deaminase [Source:HGNC Symbol;Acc:HGNC:1712]
15	ENSG000002	0.2	2e-16	3e-15	38 x 40 dolichyl-diphosphooligosaccharide--protein glycosyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:100]
16	ENSG000001	-0.16	2e-16	3e-15	1 x 33 low density lipoprotein receptor class A domain containing 2 [Source:HGNC Symbol;Acc:HGNC:100]
17	ENSG000001	0.38	2e-16	3e-15	40 x 40 EPH receptor B2 [Source:HGNC Symbol;Acc:HGNC:3393]
18	ENSG000001	0.2	2e-16	3e-15	34 x 40 ribosomal protein L11 [Source:HGNC Symbol;Acc:HGNC:100]
19	ENSG000001	0.22	2e-16	3e-15	40 x 7 UDP-galactose-4-epimerase [Source:HGNC Symbol;Acc:HGNC:100]
20	ENSG000001	-0.3	2e-16	3e-15	1 x 40 chloride intracellular channel 4 [Source:HGNC Symbol;Acc:HGNC:100]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	22.78	6e-06	88	BP translational termination
2	22.76	6e-06	82	GSEA C2REACTOME_PEPTIDE_CHAIN_ELONGATION
3	22.51	6e-06	102	GSEA C2REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION
4	22.17	7e-06	101	BP translational elongation
5	22.11	8e-06	108	BP SRP-dependent cotranslational protein targeting to membrane
6	21.79	9e-06	142	GSEA C2REACTOME_TRANSLATION
7	21.75	9e-06	84	GSEA C2KEGG_RIBOSOME
8	21.32	9e-06	105	GSEA C2REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE
9	21.24	9e-06	109	BP viral transcription
10	21.14	1e-05	713	Colon CaReTrack_CRC_TCGA_group.over_C_normal_DN
11	20.77	1e-05	142	BP translational initiation
12	20.35	1e-05	102	GSEA C2REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_TRANSCRIPTION
13	20.33	1e-05	98	GSEA C2REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLICATION
14	20.32	1e-05	117	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
15	19.88	2e-05	259	BP translation
16	19.39	2e-05	132	GSEA C2REACTOME_INFLUENZA_LIFE_CYCLE
17	19.37	2e-05	162	MF structural constituent of ribosome
18	19.28	2e-05	168	CC ribosome
19	18.04	2e-05	582	GSEA C2CAIRO_HEPATOBLASTOMA_CLASSES_UP
20	17.7	2e-05	830	Colon CaReTrack_CRC_TCGA_corr_R_normal_DN
<i>Underexpressed</i>				
1	-20.71	1e-05	262	GSEA C2SABATES_COLORECTAL_ADENOMA_DN
2	-20.52	1e-05	104	Colon CaReTrack_CRC_TCGA_group.over_A_normal_UP
3	-20.49	1e-05	436	GSEA C2SMID_BREAST_CANCER_NORMAL_LIKE_UP
4	-20.02	1e-05	507	Colon CaReTrack_CRC_TCGA_corr_C_normal_UP
5	-19.75	2e-05	368	GSEA C2LINDGREN_BLADDER_CANCER_CLUSTER_2B
6	-17.53	2e-05	196	GSEA C2PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
7	-15.9	6e-04	16	Cancer LIU_PROSTATE_CANCER_DN
8	-15.88	3e-05	132	Colon CaReTrack_CRC-cluster-b
9	-15	3e-05	315	LymphomaWIRTH_lymphoma937_spot E
10	-14.88	3e-05	314	LymphomaLopp_June14_MMML937_tumors+controls_group.overexpression
11	-14.87	3e-05	522	GSEA C2SMID_BREAST_CANCER_LUMINAL_B_DN
12	-14.63	3e-05	261	LymphomaLuzStromal signature 1
13	-14.61	3e-05	326	GSEA C2SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
14	-14.46	3e-05	9	GSEA C2MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
15	-14.45	3e-05	22	GSEA C2REACTOME_SMOOTH_MUSCLE_CONTRACTION
16	-13.46	4e-05	110	Colon CaReTrack_CRC-cluster-h
17	-13.37	4e-05	478	GSEA C2JIM_MAMMARY_STEM_CELL_UP
18	-13.29	4e-05	535	GSEA C2CHICAS_RB1_TARGETS_CONFLUENT
19	-12.64	6e-05	44	GSEA C2REACTOME_MUSCLE_CONTRACTION
20	-12.48	6e-05	263	GSEA C2WALLACE_PROSTATE_CANCER_RACE_UP



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Local Summary

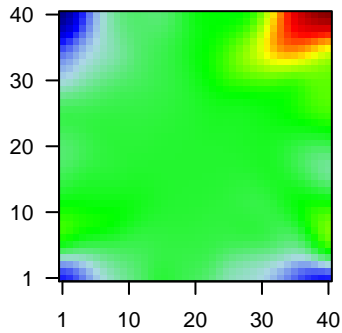
%DE = 0.97
 # metagenes = 23
 # genes = 425
 # genes in genesets = 419

 # genes with $fdr < 0.1$ = 391 (377 + / 14 -)
 # genes with $fdr < 0.05$ = 391 (377 + / 14 -)
 # genes with $fdr < 0.01$ = 385 (371 + / 14 -)

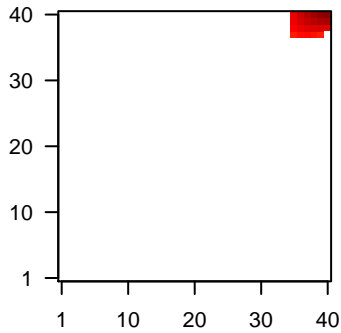
$\langle r \rangle$ metagenes = 0.96
 $\langle r \rangle$ genes = 0.59

 $\langle FC \rangle = 0.2$
 $\langle t\text{-score} \rangle = 3.99$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.09$

Profile



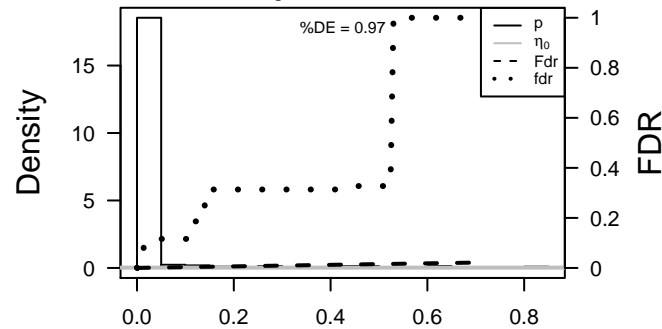
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ENSG00000000	0.34	2e-16	1e-17	38 x 40 enolase 1, (alpha) [Source:HGNC Symbol;Acc:HGNC:3350]
2	ENSG00000001	0.18	2e-16	1e-17	36 x 37 angiotensin II receptor-associated protein [Source:HGNC Sy
3	ENSG00000001	0.19	2e-16	1e-17	36 x 40 regulator of chromosome condensation 2 [Source:HGNC Syn
4	ENSG00000002	0.2	2e-16	1e-17	38 x 40 dolichyl--diphosphooligosaccharide--protein glycosyltransfer
5	ENSG00000001	0.38	2e-16	1e-17	40 x 40 EPH receptor B2 [Source:HGNC Symbol;Acc:HGNC:3393]
6	ENSG00000001	0.3	2e-16	1e-17	35 x 40 ribosomal protein S8 [Source:HGNC Symbol;Acc:HGNC:104
7	ENSG00000001	0.31	2e-16	1e-17	40 x 40 PDZK1 interacting protein 1 [Source:HGNC Symbol;Acc:HGN
8	ENSG00000001	0.32	2e-16	1e-17	37 x 38 proprotein convertase subtilisin/kexin type 9 [Source:HGNC S
9	ENSG00000000	1.11	2e-16	1e-17	40 x 40 chloride channel accessory 1 [Source:HGNC Symbol;Acc:HG
10	ENSG00000001	-0.29	2e-16	1e-17	40 x 40 regenerating islet--derived family, member 4 [Source:HGNC S
11	ENSG00000001	-0.22	2e-16	1e-17	40 x 40 S100 calcium binding protein A11 [Source:HGNC Symbol;Acc
12	ENSG00000001	0.76	2e-16	1e-17	40 x 40 mucin 1, cell surface associated [Source:HGNC Symbol;Acc:I
13	ENSG00000001	0.51	2e-16	1e-17	40 x 40 intelectin 1 (galactofuranose binding) [Source:HGNC Symbol;
14	ENSG00000002	0.67	2e-16	1e-17	40 x 40 left--right determination factor 1 [Source:HGNC Symbol;Acc:I
15	ENSG00000001	0.27	2e-16	1e-17	36 x 40 EDAR--associated death domain [Source:HGNC Symbol;Acc
16	ENSG00000001	0.28	2e-16	1e-17	39 x 40 ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C2 [S
17	ENSG00000001	0.26	2e-16	1e-17	37 x 40 protein disulfide isomerase family A, member 6 [Source:HGNC
18	ENSG00000001	0.3	2e-16	1e-17	40 x 40 family with sequence similarity 84, member A [Source:HGNC
19	ENSG00000002	0.25	2e-16	1e-17	40 x 38
20	ENSG00000001	0.32	2e-16	1e-17	40 x 40 keratinocyte associated protein 3 [Source:HGNC Symbol;Acc

p-values



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Local Summary

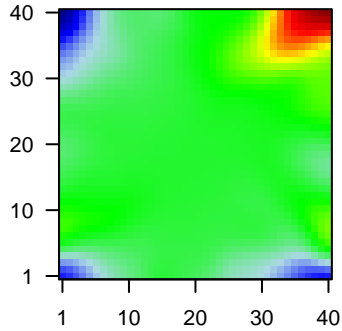
%DE = 0.98
 # metagenes = 10
 # genes = 208
 # genes in genesets = 206

 # genes with $fdr < 0.1$ = 201 (5 + / 196 -)
 # genes with $fdr < 0.05$ = 197 (2 + / 195 -)
 # genes with $fdr < 0.01$ = 197 (2 + / 195 -)

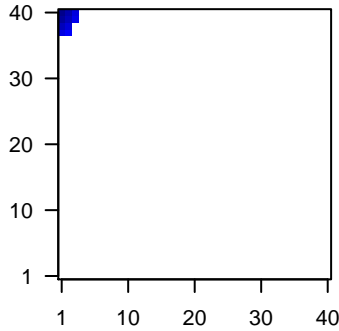
$\langle r \rangle$ metagenes = 1
 $\langle r \rangle$ genes = 0.81

 $\langle FC \rangle$ = -0.21
 $\langle t\text{-score} \rangle$ = -4.22
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.05

Profile



Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ENSG0000001	-0.3	2e-16	9e-18	1 x 40 chloride intracellular channel 4 [Source:HGNC Symbol;Acc:H
2	ENSG0000001	-0.33	2e-16	9e-18	1 x 38 cysteine-rich, angiogenic inducer, 61 [Source:HGNC Symbol
3	ENSG0000001	-0.17	2e-16	9e-18	2 x 40 olfactomedin-like 3 [Source:HGNC Symbol;Acc:HGNC:2495f
4	ENSG0000001	-0.23	2e-16	9e-18	1 x 38
5	ENSG0000000	-0.19	2e-16	9e-18	1 x 39 pleckstrin homology domain containing, family O member 1 [f
6	ENSG0000001	-0.29	2e-16	9e-18	1 x 38 pre-B-cell leukemia homeobox interacting protein 1 [Source:
7	ENSG0000001	-0.26	2e-16	9e-18	1 x 38 phosphoprotein enriched in astrocytes 15 [Source:HGNC Syr
8	ENSG0000001	-0.23	2e-16	9e-18	1 x 40 regulator of G-protein signaling 5 [Source:HGNC Symbol;Acc
9	ENSG0000001	-0.34	2e-16	9e-18	1 x 40 dermatopontin [Source:HGNC Symbol;Acc:HGNC:3011]
10	ENSG0000001	-0.36	2e-16	9e-18	1 x 40 regulator of G-protein signaling 2 [Source:HGNC Symbol;Acc
11	ENSG0000001	-0.36	2e-16	9e-18	1 x 40 cysteine and glycine-rich protein 1 [Source:HGNC Symbol;A
12	ENSG0000001	-0.36	2e-16	9e-18	1 x 40 leiomodulin 1 (smooth muscle) [Source:HGNC Symbol;Acc:HG
13	ENSG0000000	-0.24	2e-16	9e-18	1 x 40 ATPase, Ca++ transporting, plasma membrane 4 [Source:HG
14	ENSG0000001	-0.25	2e-16	9e-18	3 x 40 inhibitor of DNA binding 2, dominant negative helix-loop-heli
15	ENSG0000001	-0.16	2e-16	9e-18	3 x 40 elastin microfibril interlacer 1 [Source:HGNC Symbol;Acc:HG
16	ENSG0000001	-0.68	2e-16	9e-18	1 x 40 actin, gamma 2, smooth muscle, enteric [Source:HGNC Sym
17	ENSG0000002	-0.23	2e-16	9e-18	2 x 38 POTE ankyrin domain family, member J [Source:HGNC Symt
18	ENSG0000001	-0.25	2e-16	9e-18	2 x 38 POTE ankyrin domain family, member E [Source:HGNC Sym
19	ENSG0000001	-0.24	2e-16	9e-18	1 x 40 collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:HGNC:
20	ENSG0000001	-0.19	2e-16	9e-18	1 x 40 serum deprivation response [Source:HGNC Symbol;Acc:HG

p-values

