

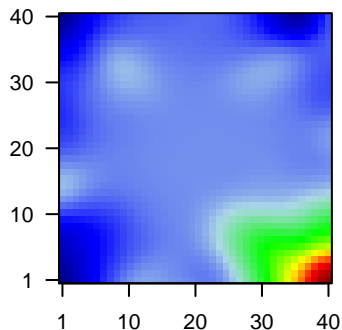
02.2351.003_cH

Global Summary

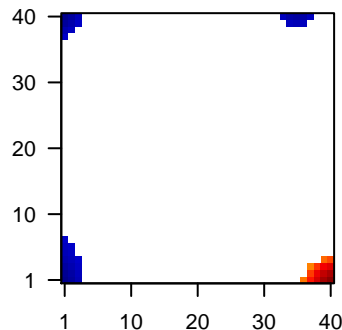
%DE = 0.27
 # genes with fdr < 0.2 = 4976 (2292 + / 2684 -)
 # genes with fdr < 0.1 = 4525 (2127 + / 2398 -)
 # genes with fdr < 0.05 = 4090 (1970 + / 2120 -)
 # genes with fdr < 0.01 = 3469 (1728 + / 1741 -)
 # genes in genesets = 18990

<FC> = 0
 <t-score> = 0
 <p-value> = 0
 <fdr> = 0.73

Profile



Regulated Spots

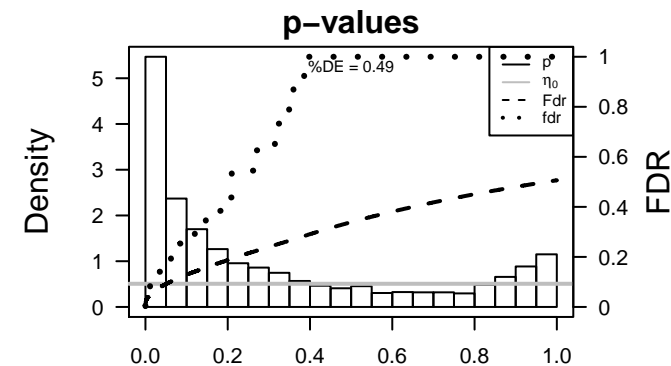
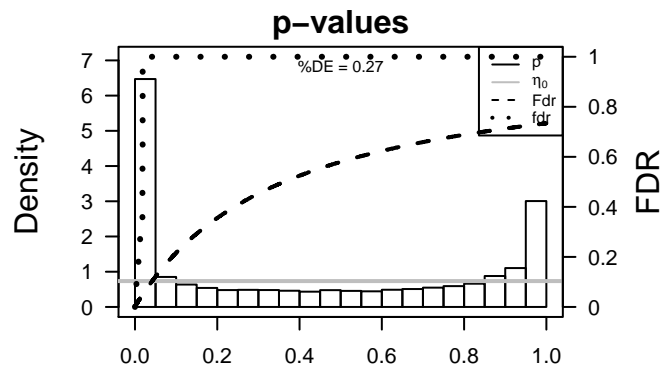


Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ENSG000000	-0.17	2e-16	3e-15	38 x 40 enolase 1, (alpha) [Source:HGNC Symbol;Acc:HGNC:3350]
2	ENSG000001	0.19	2e-16	3e-15	38 x 5 EF-hand domain family, member D2 [Source:HGNC Symbol;
3	ENSG000001	0.39	2e-16	3e-15	39 x 1 peptidyl arginine deiminase, type II [Source:HGNC Symbol;A
4	ENSG000001	0.27	2e-16	3e-15	25 x 1 ring finger protein 186 [Source:HGNC Symbol;Acc:HGNC:25
5	ENSG000001	1.33	2e-16	3e-15	40 x 40 phospholipase A2, group IIA (platelets, synovial fluid) [Source
6	ENSG000001	0.29	2e-16	3e-15	37 x 1 calcium/calmodulin-dependent protein kinase II inhibitor 1 [Si
7	ENSG000001	-0.24	2e-16	3e-15	1 x 3 complement component 1, q subcomponent, A chain [Source
8	ENSG000001	-0.17	2e-16	3e-15	1 x 4 complement component 1, q subcomponent, C chain [Source
9	ENSG000001	-0.15	2e-16	3e-15	5 x 5 complement component 1, q subcomponent, B chain [Source
10	ENSG000002	0.22	2e-16	3e-15	40 x 10 transcription elongation factor A (SII), 3 [Source:HGNC Symb
11	ENSG000001	0.15	2e-16	3e-15	33 x 1 inhibitor of DNA binding 3, dominant negative helix-loop-heli
12	ENSG000001	-0.2	2e-16	3e-15	34 x 40 ribosomal protein L11 [Source:HGNC Symbol;Acc:HGNC:10
13	ENSG000000	0.13	2e-16	3e-15	40 x 6 lysophospholipase II [Source:HGNC Symbol;Acc:HGNC:673
14	ENSG000001	0.2	2e-16	3e-15	40 x 7 UDP-galactose-4-epimerase [Source:HGNC Symbol;Acc:Hi
15	ENSG000001	0.38	2e-16	3e-15	38 x 1 fucosidase, alpha-L- 1, tissue [Source:HGNC Symbol;Acc:H
16	ENSG000001	-0.15	2e-16	3e-15	37 x 40 stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]
17	ENSG000001	0.15	2e-16	3e-15	32 x 5 platelet-activating factor acetylhydrolase 2, 40kDa [Source:Hi
18	ENSG000001	0.3	2e-16	3e-15	40 x 3 SH3 domain binding glutamate-rich protein like 3 [Source:HC
19	ENSG000001	-0.35	2e-16	3e-15	1 x 1 CD52 molecule [Source:HGNC Symbol;Acc:HGNC:1804]
20	ENSG000001	-0.2	2e-16	3e-15	35 x 40 high mobility group nucleosomal binding domain 2 [Source:Hi

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	32.29	0e+00	110	Colon Cancerisa_CRC-cluster-h
2	29.75	0e+00	104	Colon Cancerisa_CRC_TCGA_group.over_A_normal_UP
3	26.77	0e+00	507	Colon Cancerisa_CRC_TCGA_corr_C_normal_UP
4	21.91	8e-06	49	Colon Cancerisa_CRC-cluster-f
5	21.46	9e-06	688	Colon Cancerisa_CRC_TCGA-expr_kmeans_L_CIMP.H_UP_Cluster4_DN
6	19.78	2e-05	251	GSEA C2WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
7	19.64	2e-05	682	GSEA C2CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_3
8	18.17	2e-05	126	GSEA C2VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN
9	18.08	2e-05	132	GSEA C2WAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_UP
10	17.62	2e-05	429	GSEA C2CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_U
11	16.95	2e-05	55	Colon Cancerisa_CRC-cluster-e
12	16.91	2e-05	412	GSEA C2LIM_MAMMARY_STEM_CELL_DN
13	16.84	2e-05	1624	GSEA C2DODD_NASOPHARYNGEAL_CARCIOMA_UP
14	16.06	2e-05	616	Colon Cancerisa_CRC_TCGA-expr_kmeans_M_CIMP.H_DN
15	16.02	2e-05	222	GSEA C2COLDREN_GEFITINIB_RESISTANCE_DN
16	15.18	3e-05	643	Colon Cancerisa_CRC_TCGA_meth_kmeans_J_CIMP.H_DN
17	14.55	3e-05	144	LymphomaWIRTH_lymphoma937_spot G
18	13.85	4e-05	142	LymphomaWirth_June14_MMML937_tumors+controls_group.overexpression
19	13.38	4e-05	115	GSEA C2CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
20	13.32	4e-05	8	Colon Cancerisa_CRC_A_Surface crypt-like_UP
<i>Underexpressed</i>				
1	-21.77	9e-06	82	GSEA C2REACTOME_PEPTIDE_CHAIN_ELONGATION
2	-21.58	9e-06	88	BP translational termination
3	-21.4	9e-06	101	BP translational elongation
4	-20.98	1e-05	84	GSEA C2KEGG_RIBOSOME
5	-20.87	1e-05	102	GSEA C2REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATIO
6	-20.6	1e-05	109	BP viral transcription
7	-20.13	1e-05	98	GSEA C2REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND
8	-19.77	2e-05	102	GSEA C2REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY
9	-19.32	2e-05	108	BP SRP-dependent cotranslational protein targeting to membrane
10	-19.28	2e-05	117	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated
11	-18.82	2e-05	105	GSEA C2REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN
12	-18.8	2e-05	142	BP translational initiation
13	-18.71	2e-05	132	GSEA C2REACTOME_INFLUENZA_LIFE_CYCLE
14	-18.46	2e-05	142	GSEA C2REACTOME_TRANSLATION
15	-17.29	2e-05	574	Cancer Lembecke_Coloncic Inflammation
16	-16.96	2e-05	144	BP viral life cycle
17	-16.92	2e-05	162	MF structural constituent of ribosome
18	-16.83	2e-05	168	CC ribosome
19	-16.53	2e-05	844	Colon Cancerisa_CRC_TCGA-expr_kmeans_E_CIMP.H_UP_Cluster4_DN
20	-16.16	2e-05	1091	MF poly(A) RNA binding



02.2351.003_cH

Local Summary

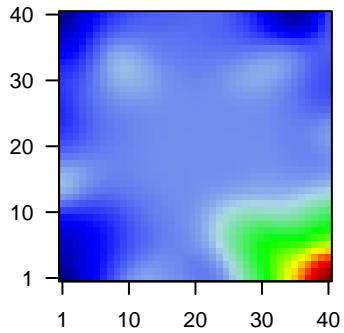
%DE = 0.99
 # metagenes = 15
 # genes = 288
 # genes in genesets = 282

 # genes with $fdr < 0.1$ = 285 (277 + / 8 -)
 # genes with $fdr < 0.05$ = 279 (271 + / 8 -)
 # genes with $fdr < 0.01$ = 277 (269 + / 8 -)

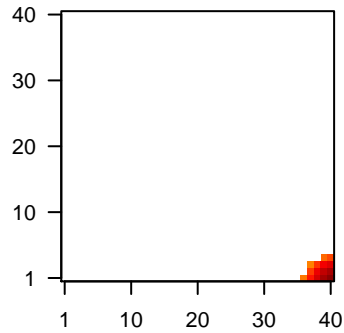
$\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.66

 $\langle FC \rangle$ = 0.29
 $\langle t\text{-score} \rangle$ = 5.97
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.04

Profile



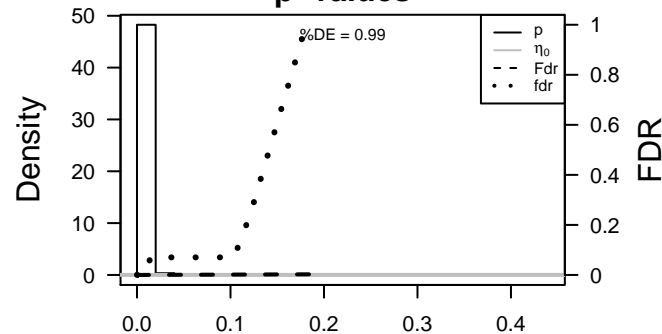
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ENSG0000001	0.39	2e-16	2e-18	39 x 1 peptidyl arginine deiminase, type II [Source:HGNC Symbol;Acc:HGNC:10773]
2	ENSG0000001	0.29	2e-16	2e-18	37 x 1 calcium/calmodulin-dependent protein kinase II inhibitor 1 [Source:HGNC Symbol;Acc:HGNC:10773]
3	ENSG0000001	0.38	2e-16	2e-18	38 x 1 fucosidase, alpha-L-1, tissue [Source:HGNC Symbol;Acc:HGNC:10773]
4	ENSG0000001	0.3	2e-16	2e-18	40 x 3 SH3 domain binding glutamate-rich protein like 3 [Source:HGNC Symbol;Acc:HGNC:10773]
5	ENSG0000001	0.18	2e-16	2e-18	40 x 1 stratifin [Source:HGNC Symbol;Acc:HGNC:10773]
6	ENSG0000001	0.3	2e-16	2e-18	40 x 1 serine incorporator 2 [Source:HGNC Symbol;Acc:HGNC:2322]
7	ENSG0000001	0.32	2e-16	2e-18	40 x 1 transmembrane protein 54 [Source:HGNC Symbol;Acc:HGNC:10773]
8	ENSG0000000	0.44	2e-16	2e-18	40 x 1 guanylate cyclase activator 2B (uroguanylin) [Source:HGNC Symbol;Acc:HGNC:10773]
9	ENSG0000001	0.77	2e-16	2e-18	40 x 1 guanylate cyclase activator 2A (guanylin) [Source:HGNC Symbol;Acc:HGNC:10773]
10	ENSG0000002	0.26	2e-16	2e-18	38 x 2 chromosome 1 open reading frame 210 [Source:HGNC Symbol;Acc:HGNC:10773]
11	ENSG0000001	0.34	2e-16	2e-18	36 x 1 bestrophin 4 [Source:HGNC Symbol;Acc:HGNC:17106]
12	ENSG0000001	0.61	2e-16	2e-18	40 x 1 tetraspanin 1 [Source:HGNC Symbol;Acc:HGNC:20657]
13	ENSG0000000	0.23	2e-16	2e-18	40 x 1 chloride channel accessory 4 [Source:HGNC Symbol;Acc:HGNC:10773]
14	ENSG0000001	0.19	2e-16	2e-18	40 x 3 EPS8-like 3 [Source:HGNC Symbol;Acc:HGNC:21297]
15	ENSG0000001	0.27	2e-16	2e-18	37 x 1 ras homolog family member C [Source:HGNC Symbol;Acc:HGNC:10773]
16	ENSG0000002	0.3	2e-16	2e-18	36 x 1 Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:U31061]
17	ENSG0000001	0.51	2e-16	2e-18	40 x 4 ATPase, Na+/K+ transporting, alpha 1 polypeptide [Source:HGNC Symbol;Acc:HGNC:10773]
18	ENSG0000001	0.69	2e-16	2e-18	40 x 1 3-hydroxy-3-methylglutaryl-CoA synthase 2 (mitochondrial) [Source:HGNC Symbol;Acc:HGNC:10773]
19	ENSG0000001	0.36	2e-16	2e-18	38 x 1 cathepsin S [Source:HGNC Symbol;Acc:HGNC:2545]
20	ENSG0000001	0.52	2e-16	2e-18	40 x 1 selenium binding protein 1 [Source:HGNC Symbol;Acc:HGNC:10773]

p-values



02.2351.003_cH

Local Summary

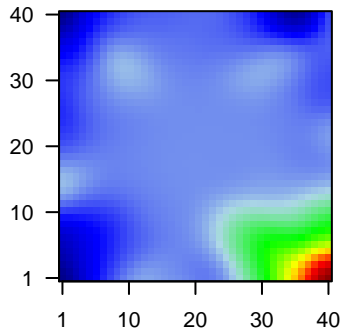
%DE = 0.99
 # metagenes = 17
 # genes = 344
 # genes in genesets = 326

 # genes with $fdr < 0.1$ = 333 (18 + / 315 -)
 # genes with $fdr < 0.05$ = 328 (16 + / 312 -)
 # genes with $fdr < 0.01$ = 318 (16 + / 302 -)

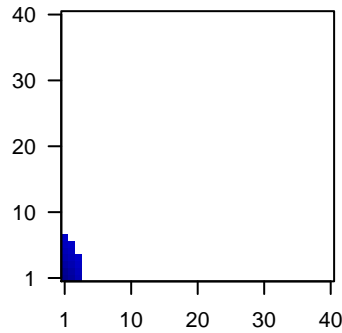
$\langle r \rangle$ metagenes = 0.95
 $\langle r \rangle$ genes = 0.68

 $\langle FC \rangle$ = -0.11
 $\langle t\text{-score} \rangle$ = -2.33
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.08

Profile



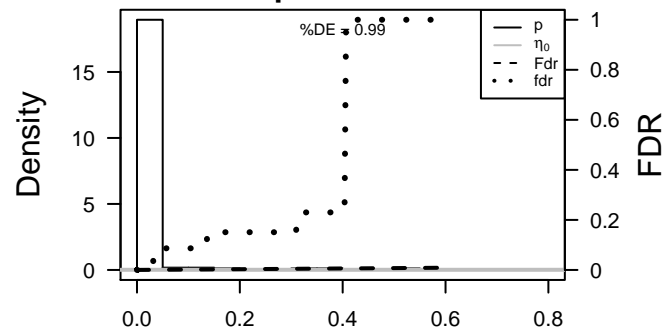
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ENSG0000001	-0.24	2e-16	7e-18	1 x 3 complement component 1, q subcomponent, A chain [Source:HGNC Symbol;Acc:HGNC:1804]
2	ENSG0000001	-0.17	2e-16	7e-18	1 x 4 complement component 1, q subcomponent, C chain [Source:HGNC Symbol;Acc:HGNC:1805]
3	ENSG0000001	-0.35	2e-16	7e-18	1 x 1 CD52 molecule [Source:HGNC Symbol;Acc:HGNC:1804]
4	ENSG0000001	-0.31	2e-16	7e-18	1 x 1 lysosomal protein transmembrane 5 [Source:HGNC Symbol;Acc:HGNC:1639]
5	ENSG0000001	-0.25	2e-16	7e-18	1 x 1 CD53 molecule [Source:HGNC Symbol;Acc:HGNC:1686]
6	ENSG0000001	-0.16	2e-16	7e-18	1 x 1 CD2 molecule [Source:HGNC Symbol;Acc:HGNC:1639]
7	ENSG0000001	-0.16	2e-16	7e-18	1 x 6
8	ENSG0000002	-0.17	2e-16	7e-18	1 x 6
9	ENSG0000002	-0.18	2e-16	7e-18	1 x 6
10	ENSG0000001	-0.13	2e-16	7e-18	1 x 1 CD1c molecule [Source:HGNC Symbol;Acc:HGNC:1636]
11	ENSG0000001	-0.18	2e-16	7e-18	1 x 1 CD48 molecule [Source:HGNC Symbol;Acc:HGNC:1683]
12	ENSG0000001	-0.21	2e-16	7e-18	1 x 1 selectin L [Source:HGNC Symbol;Acc:HGNC:10720]
13	ENSG0000000	-0.17	2e-16	7e-18	1 x 1 protein tyrosine phosphatase, receptor type, C [Source:HGNC Symbol;Acc:HGNC:1636]
14	ENSG0000001	-0.21	2e-16	7e-18	1 x 1 Fc fragment of IgM receptor [Source:HGNC Symbol;Acc:HGNC:1636]
15	ENSG0000001	-0.22	2e-16	7e-18	1 x 1 complement component (3d/Epstein Barr virus) receptor 2 [Source:HGNC Symbol;Acc:HGNC:1636]
16	ENSG0000000	-0.13	2e-16	7e-18	1 x 5 tribbles pseudokinase 2 [Source:HGNC Symbol;Acc:HGNC:1636]
17	ENSG0000002	-0.15	2e-16	7e-18	1 x 1 limb bud and heart development [Source:HGNC Symbol;Acc:HGNC:1636]
18	ENSG0000001	0.29	2e-16	7e-18	1 x 4 ZFP36 ring finger protein-like 2 [Source:HGNC Symbol;Acc:HGNC:1636]
19	ENSG0000001	-0.14	2e-16	7e-18	2 x 1 pleckstrin [Source:HGNC Symbol;Acc:HGNC:9070]
20	ENSG0000001	-0.25	2e-16	7e-18	1 x 1 chemokine (C-X-C motif) receptor 4 [Source:HGNC Symbol;Acc:HGNC:1636]

p-values



02.2351.003_cH

Local Summary

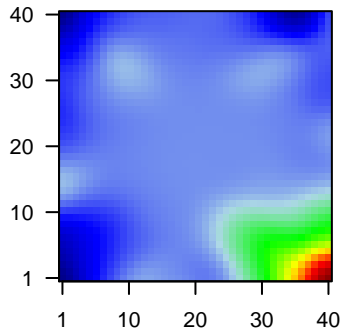
%DE = 0.96
 # metagenes = 9
 # genes = 206
 # genes in genesets = 205

 # genes with fdr < 0.1 = 195 (9 + / 186 -)
 # genes with fdr < 0.05 = 194 (9 + / 185 -)
 # genes with fdr < 0.01 = 188 (9 + / 179 -)

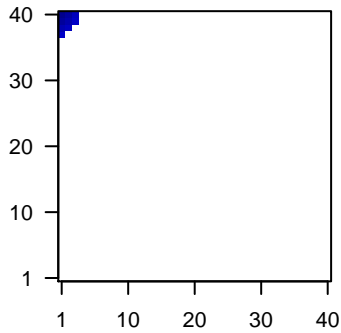
<r> metagenes = 1
 <r> genes = 0.81

 <FC> = -0.13
 <t-score> = -2.67
 <p-value> = 0
 <fdr> = 0.06

Profile



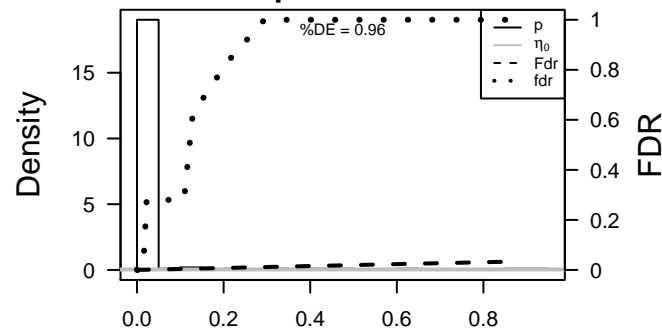
Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ENSG00000000	-0.19	2e-16	2e-17	1 x 39 pleckstrin homology domain containing, family O member 1 [S
2	ENSG00000001	-0.16	2e-16	2e-17	1 x 38 pre-B-cell leukemia homeobox interacting protein 1 [Source:
3	ENSG00000001	-0.14	2e-16	2e-17	1 x 38 phosphoprotein enriched in astrocytes 15 [Source:HGNC Syr
4	ENSG00000001	-0.16	2e-16	2e-17	1 x 40 regulator of G-protein signaling 5 [Source:HGNC Symbol;Acc
5	ENSG00000001	-0.3	2e-16	2e-17	1 x 40 dermatopontin [Source:HGNC Symbol;Acc:HGNC:3011]
6	ENSG00000001	-0.13	2e-16	2e-17	1 x 37 laminin, gamma 1 (formerly LAMB2) [Source:HGNC Symbol;A
7	ENSG00000001	-0.21	2e-16	2e-17	1 x 40 cysteine and glycine-rich protein 1 [Source:HGNC Symbol;A
8	ENSG00000001	-0.24	2e-16	2e-17	1 x 40 leiomodulin (smooth muscle) [Source:HGNC Symbol;Acc:HG
9	ENSG00000001	0.18	2e-16	2e-17	1 x 40 BTG family, member 2 [Source:HGNC Symbol;Acc:HGNC:11
10	ENSG00000000	-0.21	2e-16	2e-17	1 x 40 ATPase, Ca++ transporting, plasma membrane 4 [Source:HG
11	ENSG00000001	0.14	2e-16	2e-17	3 x 40 inhibitor of DNA binding 2, dominant negative helix-loop-heli
12	ENSG00000001	-0.38	2e-16	2e-17	1 x 40 actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
13	ENSG00000001	-0.25	2e-16	2e-17	1 x 40 collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:HGNC:
14	ENSG00000001	-0.27	2e-16	2e-17	1 x 40 fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
15	ENSG00000001	-0.26	2e-16	2e-17	1 x 40 insulin-like growth factor binding protein 5 [Source:HGNC Sy
16	ENSG00000000	-0.19	2e-16	2e-17	1 x 40 tensin 1 [Source:HGNC Symbol;Acc:HGNC:11973]
17	ENSG00000001	-0.31	2e-16	2e-17	1 x 40 desmin [Source:HGNC Symbol;Acc:HGNC:2770]
18	ENSG00000001	-0.13	2e-16	2e-17	1 x 38 collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:HGNC
19	ENSG00000001	-0.18	2e-16	2e-17	1 x 40 receptor (G protein-coupled) activity modifying protein 1 [Sou
20	ENSG00000001	-0.13	2e-16	2e-17	1 x 37 laminin, beta 2 (laminin S) [Source:HGNC Symbol;Acc:HGNC

p-values



02.2351.003_cH

Local Summary

%DE = 0.97
 # metagenes = 8
 # genes = 201
 # genes in genesets = 197

 # genes with fdr < 0.1 = 194 (0 + / 194 -)
 # genes with fdr < 0.05 = 194 (0 + / 194 -)
 # genes with fdr < 0.01 = 187 (0 + / 187 -)

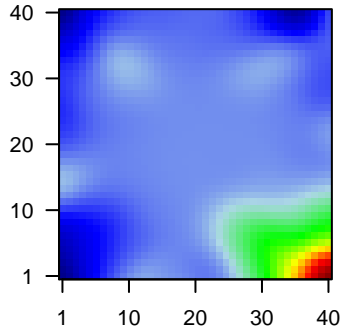
<r> metagenes = 0.98
 <r> genes = 0.63

 <FC> = -0.15
 <t-score> = -3.07
 <p-value> = 0
 <fdr> = 0.05

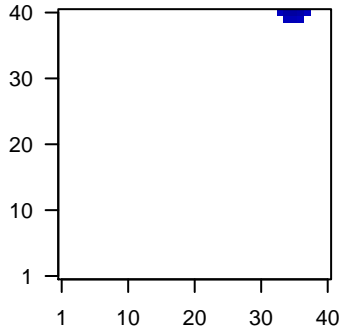
Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ENSG0000001	-0.2	2e-16	1e-17	34 x 40 ribosomal protein L11 [Source:HGNC Symbol;Acc:HGNC:100
2	ENSG0000001	-0.15	2e-16	1e-17	37 x 40 stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]
3	ENSG0000001	-0.2	2e-16	1e-17	35 x 40 high mobility group nucleosomal binding domain 2 [Source:HG
4	ENSG0000001	-0.21	2e-16	1e-17	35 x 40 ribosomal protein S8 [Source:HGNC Symbol;Acc:HGNC:104
5	ENSG0000001	-0.19	2e-16	1e-17	34 x 40 chaperonin containing TCP1, subunit 3 (gamma) [Source:HG
6	ENSG0000001	-0.13	2e-16	1e-17	36 x 40 EDAR-associated death domain [Source:HGNC Symbol;Acc
7	ENSG0000001	-0.19	2e-16	1e-17	34 x 40 ribosomal protein S7 [Source:HGNC Symbol;Acc:HGNC:104
8	ENSG0000002	-0.26	2e-16	1e-17	34 x 40 tRNA methyltransferase 11-2 homolog (S. cerevisiae) pseud
9	ENSG0000001	-0.18	2e-16	1e-17	34 x 40 ribosomal protein S27a [Source:HGNC Symbol;Acc:HGNC:11
10	ENSG0000001	-0.16	2e-16	1e-17	33 x 40 chaperonin containing TCP1, subunit 4 (delta) [Source:HGNC
11	ENSG0000000	-0.16	2e-16	1e-17	34 x 40 ribosomal protein L31 [Source:HGNC Symbol;Acc:HGNC:100
12	ENSG0000001	-0.13	2e-16	1e-17	35 x 40 neurobeachin-like 1 [Source:HGNC Symbol;Acc:HGNC:2068
13	ENSG0000001	-0.19	2e-16	1e-17	35 x 40 eukaryotic translation elongation factor 1 beta 2 [Source:HG
14	ENSG0000001	-0.24	2e-16	1e-17	35 x 40 ribosomal protein L37a [Source:HGNC Symbol;Acc:HGNC:100
15	ENSG0000001	-0.15	2e-16	1e-17	34 x 40 nucleolin [Source:HGNC Symbol;Acc:HGNC:7667]
16	ENSG0000001	-0.26	2e-16	1e-17	35 x 40 ribosomal protein L32 [Source:HGNC Symbol;Acc:HGNC:100
17	ENSG0000001	-0.24	2e-16	1e-17	36 x 40 ribosomal protein SA [Source:HGNC Symbol;Acc:HGNC:650
18	ENSG0000001	-0.24	2e-16	1e-17	36 x 40 ribosomal protein L14 [Source:HGNC Symbol;Acc:HGNC:100
19	ENSG0000001	-0.16	2e-16	1e-17	37 x 40 IMP (inosine 5'-monophosphate) dehydrogenase 2 [Source:HG
20	ENSG0000001	-0.2	2e-16	1e-17	37 x 40 ribosomal protein L29 [Source:HGNC Symbol;Acc:HGNC:100

Profile



Spot



p-values

