

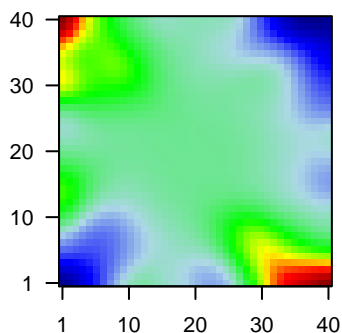
02.2351.003_nH

Global Summary

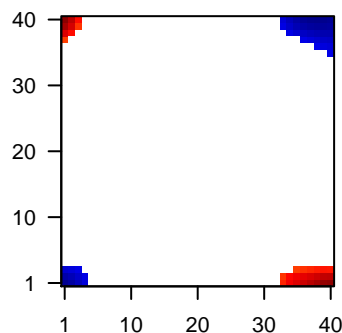
%DE = 0.26
 # genes with fdr < 0.2 = 4788 (2207 + / 2581 -)
 # genes with fdr < 0.1 = 4303 (2029 + / 2274 -)
 # genes with fdr < 0.05 = 4001 (1909 + / 2092 -)
 # genes with fdr < 0.01 = 3337 (1661 + / 1676 -)
 # genes in genesets = 18990

<FC> = 0
 <t-score> = 0
 <p-value> = 0.01
 <fdr> = 0.74

Profile



Regulated Spots



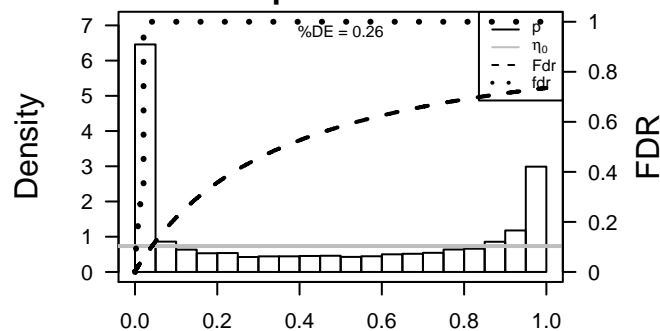
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ENSG00000001	0.2	2e-16	3e-15	31 x 8 G protein-coupled receptor 153 [Source:HGNC Symbol;Acc:ENSG00000001]
2	ENSG00000000	0.18	2e-16	3e-15	8 x 33 vesicle-associated membrane protein 3 [Source:HGNC Syml]
3	ENSG00000001	0.16	2e-16	3e-15	3 x 32 ERBB receptor feedback inhibitor 1 [Source:HGNC Symbol;A]
4	ENSG00000000	-0.22	2e-16	3e-15	38 x 40 enolase 1, (alpha) [Source:HGNC Symbol;Acc:HGNC:3350]
5	ENSG00000001	0.22	2e-16	3e-15	1 x 30 retinol binding protein 7, cellular [Source:HGNC Symbol;Acc:1]
6	ENSG00000000	-0.19	2e-16	3e-15	2 x 1 tumor necrosis factor receptor superfamily, member 1B [Sour]
7	ENSG00000001	0.17	2e-16	3e-15	38 x 5 EF-hand domain family, member D2 [Source:HGNC Symbol;]
8	ENSG00000001	0.41	2e-16	3e-15	39 x 1 peptidyl arginine deiminase, type II [Source:HGNC Symbol;A]
9	ENSG00000001	-0.15	2e-16	3e-15	36 x 40 regulator of chromosome condensation 2 [Source:HGNC Syn]
10	ENSG00000000	-0.15	2e-16	3e-15	37 x 39 MRT4 homolog, ribosome maturation factor [Source:HGNC S]
11	ENSG00000001	0.46	2e-16	3e-15	37 x 1 calcium/calmodulin-dependent protein kinase II inhibitor 1 [Si]
12	ENSG00000001	0.25	2e-16	3e-15	38 x 1 cytidine deaminase [Source:HGNC Symbol;Acc:HGNC:1712]
13	ENSG00000001	0.2	2e-16	3e-15	31 x 3 PTEN induced putative kinase 1 [Source:HGNC Symbol;Acc:1]
14	ENSG00000002	-0.26	2e-16	3e-15	38 x 40 dolichyl--diphosphooligosaccharide--protein glycosyltransfer:
15	ENSG00000000	0.23	2e-16	3e-15	29 x 8 RAP1 GTPase activating protein [Source:HGNC Symbol;Acc:1]
16	ENSG00000001	-0.15	2e-16	3e-15	40 x 40 EPH receptor B2 [Source:HGNC Symbol;Acc:HGNC:3393]
17	ENSG00000002	0.27	2e-16	3e-15	40 x 10 transcription elongation factor A (SII), 3 [Source:HGNC Symb]
18	ENSG00000001	0.18	2e-16	3e-15	9 x 1 proline-rich nuclear receptor coactivator 2 [Source:HGNC Sy]
19	ENSG00000001	0.33	2e-16	3e-15	1 x 40 chloride intracellular channel 4 [Source:HGNC Symbol;Acc:H]
20	ENSG00000001	0.31	2e-16	3e-15	40 x 3 SH3 domain binding glutamate-rich protein like 3 [Source:HC]

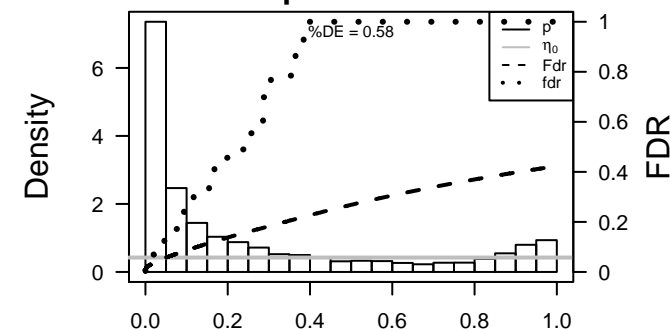
Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	29.27	0e+00	104	Colon CaReTrack_CRC_TCGA_group.over_A_normal_UP
2	26.56	0e+00	507	Colon CaReTrack_CRC_TCGA_corr_C_normal_UP
3	21.2	1e-05	110	Colon CaMarrisa_CRC-cluster-h
4	19.97	1e-05	101	GSEA C2CHEN_LVAD_SUPPORT_OF_FAILING_HEART_UP
5	17.1	2e-05	22	GSEA C2REACTOME_SMOOTH_MUSCLE_CONTRACTION
6	16.71	2e-05	37	GSEA C2JZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
7	15.05	3e-05	132	Colon CaMarrisa_CRC-cluster-b
8	15.02	3e-05	399	Disease GUDJ_poriasis down
9	14.93	3e-05	83	GSEA C2SMID_BREAST_CANCER_LUMINAL_A_UP
10	14.68	3e-05	78	GSEA C2NAKAYAMA_SOFT_TISSUE_TUMORS_PCA2_DN
11	14.62	3e-05	33	BP bicarbonate transport
12	14.49	3e-05	262	GSEA C2SABATES_COLORECTAL_ADENOMA_DN
13	14.39	3e-05	44	GSEA C2REACTOME_MUSCLE_CONTRACTION
14	14.02	4e-05	294	GSEA C2ACEVEDO_FGFR1_TARGETS_IN_PROSTATE_CANCER_MODE
15	13.77	4e-05	692	GSEA C2WONG_ADULT_TISSUE_STEM_MODULE
16	13.7	4e-05	18	GSEA C2NIELSEN_LEIOMYOSARCOMA_CNN1_UP
17	13.61	4e-05	303	GSEA C2PASINI_SUZ12_TARGETS_DN
18	13.55	4e-05	49	Colon CaMarrisa_CRC-cluster-f
19	13.42	2e-03	16	Cancer LIU_PROSTATE_CANCER_DN
20	13.18	4e-05	254	GSEA C2U_AGING_BRAIN_UP
<i>Underexpressed</i>				
1	-15.79	3e-05	108	BP SRP-dependent cotranslational protein targeting to membrane
2	-15.55	3e-05	105	GSEA C2REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN
3	-14.57	3e-05	88	BP translational termination
4	-14.46	3e-05	109	BP viral transcription
5	-14.38	3e-05	713	Colon CaReTrack_CRC_TCGA_group.over_C_normal_DN
6	-14.28	4e-05	84	GSEA C2KEGG_RIBOSOME
7	-14	4e-05	82	GSEA C2REACTOME_PEPTIDE_CHAIN_ELONGATION
8	-13.92	4e-05	98	GSEA C2REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND
9	-13.87	4e-05	101	BP translational elongation
10	-13.79	4e-05	132	GSEA C2REACTOME_INFLUENZA_LIFE_CYCLE
11	-13.71	4e-05	4052	CC integral component of membrane
12	-13.6	4e-05	5643	LymphomaMOPP_Txn_transition
13	-13.57	4e-05	844	Colon CaReTrack_CRC_TCGA-expr_kmeans_E_CIMP_H_UP_Cluster4_DN
14	-13.37	4e-05	813	GSEA C2GRADE_COLON_CANCER_UP
15	-13.28	4e-05	142	GSEA C2REACTOME_TRANSLATION
16	-13.05	4e-05	162	MF structural constituent of ribosome
17	-13.01	4e-05	102	GSEA C2REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATIO
18	-12.94	5e-05	830	Colon CaReTrack_CRC_TCGA_corr_R_normal_DN
19	-12.9	5e-05	22	CC integral component of luminal side of endoplasmic reticulum membr
20	-12.66	6e-05	102	GSEA C2REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY

p-values



p-values



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Local Summary

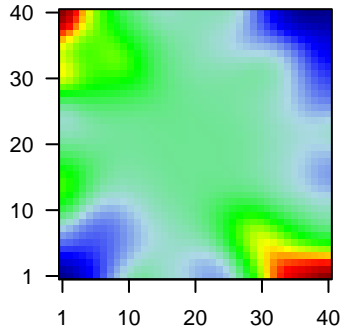
%DE = 0.89
 # metagenes = 22
 # genes = 399
 # genes in genesets = 389

 # genes with $fdr < 0.1$ = 345 (301 + / 44 -)
 # genes with $fdr < 0.05$ = 326 (288 + / 38 -)
 # genes with $fdr < 0.01$ = 325 (287 + / 38 -)

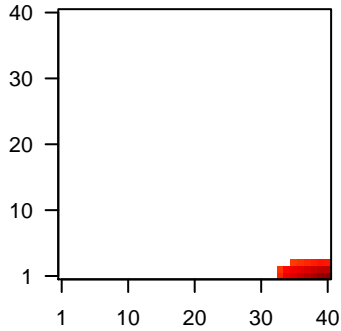
$\langle r \rangle$ metagenes = 0.97
 $\langle r \rangle$ genes = 0.62

 $\langle FC \rangle$ = 0.16
 $\langle t\text{-score} \rangle$ = 3.25
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.16

Profile



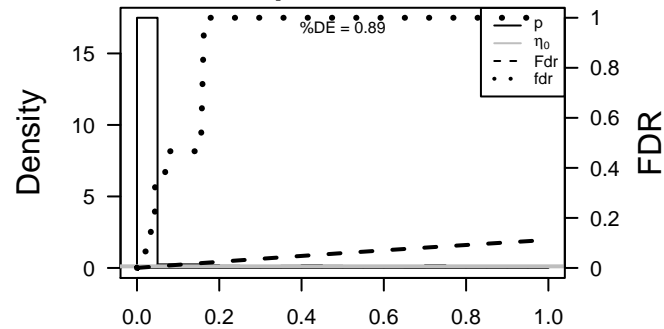
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ENSG0000001	0.41	2e-16	5e-17	39 x 1 peptidyl arginine deiminase, type II [Source:HGNC Symbol;Acc:HGNC:17112]
2	ENSG0000001	0.46	2e-16	5e-17	37 x 1 calcium/calmodulin-dependent protein kinase II inhibitor 1 [Source:HGNC Symbol;Acc:HGNC:17113]
3	ENSG0000001	0.25	2e-16	5e-17	38 x 1 cytidine deaminase [Source:HGNC Symbol;Acc:HGNC:17112]
4	ENSG0000001	0.31	2e-16	5e-17	40 x 3 SH3 domain binding glutamate-rich protein like 3 [Source:HGNC Symbol;Acc:HGNC:17114]
5	ENSG0000001	0.21	2e-16	5e-17	40 x 1 transmembrane protein 54 [Source:HGNC Symbol;Acc:HGNC:17115]
6	ENSG0000000	0.23	2e-16	5e-17	40 x 1 guanylate cyclase activator 2B (uroguanylin) [Source:HGNC Symbol;Acc:HGNC:17116]
7	ENSG0000001	0.64	2e-16	5e-17	40 x 1 guanylate cyclase activator 2A (guanylin) [Source:HGNC Symbol;Acc:HGNC:17117]
8	ENSG0000001	0.25	2e-16	5e-17	36 x 1 bestrophin 4 [Source:HGNC Symbol;Acc:HGNC:17106]
9	ENSG0000001	0.24	2e-16	5e-17	40 x 1 tetraspanin 1 [Source:HGNC Symbol;Acc:HGNC:20657]
10	ENSG0000001	0.35	2e-16	5e-17	33 x 2 cytidine monophosphate (UMP-CMP) kinase 1, cytosolic [Source:HGNC Symbol;Acc:HGNC:17118]
11	ENSG0000001	0.3	2e-16	5e-17	35 x 2 insulin-like 5 [Source:HGNC Symbol;Acc:HGNC:6088]
12	ENSG0000001	0.16	2e-16	5e-17	33 x 1 growth arrest and DNA-damage-inducible, alpha [Source:HGNC Symbol;Acc:HGNC:17119]
13	ENSG0000001	0.32	2e-16	5e-17	34 x 1 guanine nucleotide binding protein (G protein), gamma 12 [Source:HGNC Symbol;Acc:HGNC:17120]
14	ENSG0000001	0.15	2e-16	5e-17	35 x 3 B-cell CLL/lymphoma 10 [Source:HGNC Symbol;Acc:HGNC:17121]
15	ENSG0000000	0.48	2e-16	5e-17	40 x 1 chloride channel accessory 4 [Source:HGNC Symbol;Acc:HGNC:17122]
16	ENSG0000001	0.2	2e-16	5e-17	37 x 1 ras homolog family member C [Source:HGNC Symbol;Acc:HGNC:17123]
17	ENSG0000002	0.28	2e-16	5e-17	36 x 1 Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:U31112]
18	ENSG0000002	0.19	2e-16	5e-17	33 x 1 Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:U31113]
19	ENSG0000001	0.9	2e-16	5e-17	40 x 1 3-hydroxy-3-methylglutaryl-CoA synthase 2 (mitochondrial) [Source:HGNC Symbol;Acc:HGNC:17124]
20	ENSG0000001	-0.14	2e-16	5e-17	38 x 1 cathepsin S [Source:HGNC Symbol;Acc:HGNC:2545]

p-values



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Local Summary

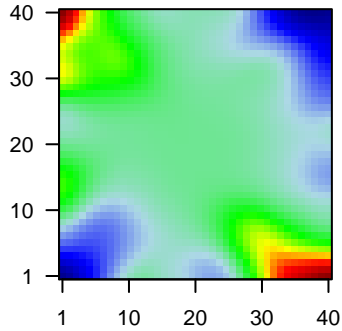
%DE = 0.94
 # metagenes = 9
 # genes = 206
 # genes in genesets = 205

 # genes with $fdr < 0.1$ = 182 (176 + / 6 -)
 # genes with $fdr < 0.05$ = 182 (176 + / 6 -)
 # genes with $fdr < 0.01$ = 176 (173 + / 3 -)

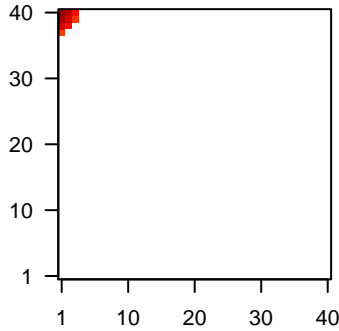
<r> metagenes = 1
 <r> genes = 0.81

 <FC> = 0.19
 <t-score> = 3.92
 <p-value> = 0
 <fdr> = 0.12

Profile



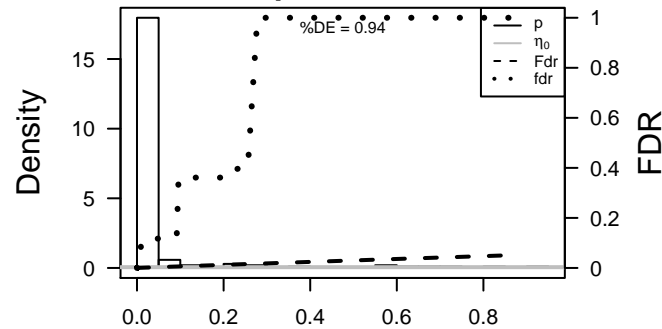
Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ENSG0000001	0.33	2e-16	3e-17	1 x 40 chloride intracellular channel 4 [Source:HGNC Symbol;Acc:H
2	ENSG0000001	0.38	2e-16	3e-17	1 x 38 cysteine-rich, angiogenic inducer, 61 [Source:HGNC Symbol
3	ENSG0000000	0.28	2e-16	3e-17	2 x 38 cold shock domain containing E1, RNA-binding [Source:HGNC
4	ENSG0000001	0.19	2e-16	3e-17	1 x 40 calsequestrin 2 (cardiac muscle) [Source:HGNC Symbol;Acc:
5	ENSG0000001	0.37	2e-16	3e-17	1 x 38
6	ENSG0000001	0.19	2e-16	3e-17	1 x 40 regulator of G-protein signaling 5 [Source:HGNC Symbol;Acc:
7	ENSG0000001	0.26	2e-16	3e-17	1 x 40 dermatopontin [Source:HGNC Symbol;Acc:HGNC:3011]
8	ENSG0000001	0.22	2e-16	3e-17	1 x 40 family with sequence similarity 129, member A [Source:HGNC
9	ENSG0000001	0.25	2e-16	3e-17	1 x 40 regulator of G-protein signaling 2 [Source:HGNC Symbol;Acc:
10	ENSG0000001	0.35	2e-16	3e-17	1 x 40 cysteine and glycine-rich protein 1 [Source:HGNC Symbol;A
11	ENSG0000001	0.46	2e-16	3e-17	1 x 40 leiomodulin 1 (smooth muscle) [Source:HGNC Symbol;Acc:HG
12	ENSG0000000	0.21	2e-16	3e-17	1 x 40 protein phosphatase 1, regulatory subunit 12B [Source:HGNC
13	ENSG0000001	0.46	2e-16	3e-17	1 x 40 BTG family, member 2 [Source:HGNC Symbol;Acc:HGNC:11
14	ENSG0000001	0.17	2e-16	3e-17	2 x 39 proline/arginine-rich end leucine-rich repeat protein [Source:
15	ENSG0000000	0.17	2e-16	3e-17	1 x 40 ATPase, Ca++ transporting, plasma membrane 4 [Source:HG
16	ENSG0000001	0.17	2e-16	3e-17	1 x 39 nidogen 1 [Source:HGNC Symbol;Acc:HGNC:7821]
17	ENSG0000001	0.41	2e-16	3e-17	1 x 40 ras homolog family member B [Source:HGNC Symbol;Acc:H
18	ENSG0000001	0.92	2e-16	3e-17	1 x 40 actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
19	ENSG0000002	0.18	2e-16	3e-17	2 x 38 POTE ankyrin domain family, member J [Source:HGNC Syml
20	ENSG0000001	0.15	2e-16	3e-17	2 x 38 POTE ankyrin domain family, member E [Source:HGNC Syml

p-values



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Local Summary

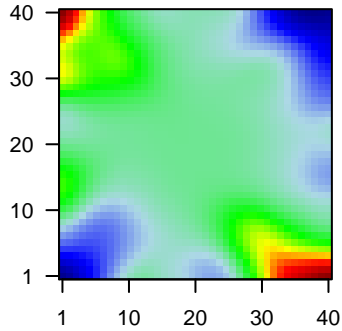
%DE = 0.99
 # metagenes = 11
 # genes = 238
 # genes in genesets = 233

 # genes with $fdr < 0.1$ = 233 (16 + / 217 -)
 # genes with $fdr < 0.05$ = 232 (15 + / 217 -)
 # genes with $fdr < 0.01$ = 226 (14 + / 212 -)

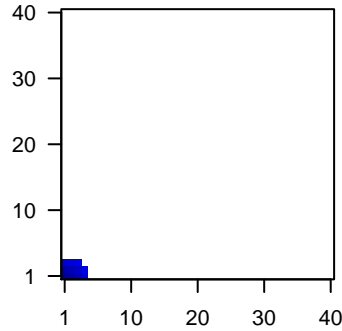
<r> metagenes = 1
 <r> genes = 0.8

 <FC> = -0.11
 <t-score> = -2.25
 <p-value> = 0
 <fdr> = 0.07

Profile



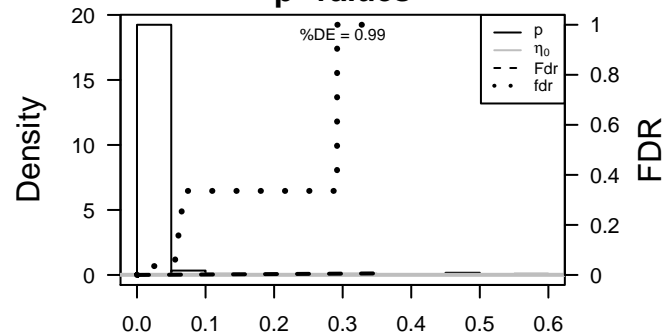
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ENSG00000000	-0.19	2e-16	7e-18	2 x 1 tumor necrosis factor receptor superfamily, member 1B [Soun
2	ENSG00000001	-0.33	2e-16	7e-18	1 x 1 CD52 molecule [Source:HGNC Symbol;Acc:HGNC:1804]
3	ENSG00000001	-0.32	2e-16	7e-18	1 x 1 lysosomal protein transmembrane 5 [Source:HGNC Symbol;f
4	ENSG00000001	-0.28	2e-16	7e-18	1 x 1 CD53 molecule [Source:HGNC Symbol;Acc:HGNC:1686]
5	ENSG00000001	-0.2	2e-16	7e-18	1 x 1 CD2 molecule [Source:HGNC Symbol;Acc:HGNC:1639]
6	ENSG00000001	-0.2	2e-16	7e-18	1 x 1 CD48 molecule [Source:HGNC Symbol;Acc:HGNC:1683]
7	ENSG00000001	-0.23	2e-16	7e-18	1 x 1 selectin L [Source:HGNC Symbol;Acc:HGNC:10720]
8	ENSG00000000	-0.19	2e-16	7e-18	1 x 1 protein tyrosine phosphatase, receptor type, C [Source:HGNC
9	ENSG00000001	-0.22	2e-16	7e-18	1 x 1 Fc fragment of IgM receptor [Source:HGNC Symbol;Acc:HGNC
10	ENSG00000001	-0.25	2e-16	7e-18	1 x 1 complement component (3d/Epstein Barr virus) receptor 2 [Si
11	ENSG00000002	-0.15	2e-16	7e-18	1 x 1 limb bud and heart development [Source:HGNC Symbol;Acc:
12	ENSG00000001	-0.31	2e-16	7e-18	1 x 1 chemokine (C-X-C motif) receptor 4 [Source:HGNC Symbol;
13	ENSG00000002	0.67	2e-16	7e-18	1 x 1 MT-RNR2-like 12 [Source:HGNC Symbol;Acc:HGNC:37169]
14	ENSG00000001	-0.52	2e-16	7e-18	1 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
15	ENSG00000001	-0.22	2e-16	7e-18	1 x 3 chemokine (C-X-C motif) ligand 9 [Source:HGNC Symbol;Ac
16	ENSG00000001	-0.52	2e-16	7e-18	1 x 1 chemokine (C-X-C motif) ligand 13 [Source:HGNC Symbol;f
17	ENSG00000002	0.69	2e-16	7e-18	1 x 1 MT-RNR2-like 2 [Source:HGNC Symbol;Acc:HGNC:37156]
18	ENSG00000001	0.29	2e-16	7e-18	1 x 1 chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;f
19	ENSG00000000	-0.44	2e-16	7e-18	1 x 1 CD74 molecule, major histocompatibility complex, class II inv
20	ENSG00000001	-0.14	2e-16	7e-18	2 x 1 lymphocyte antigen 86 [Source:HGNC Symbol;Acc:HGNC:16

p-values



02.2351.003_nH

Local Summary

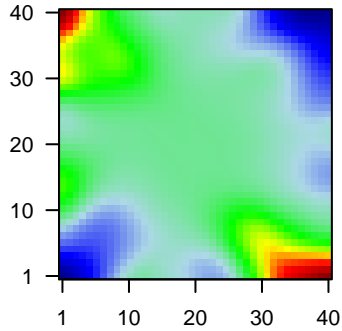
%DE = 0.93
 # metagenes = 32
 # genes = 636
 # genes in genesets = 626

 # genes with $fdr < 0.1$ = 558 (35 + / 523 -)
 # genes with $fdr < 0.05$ = 547 (32 + / 515 -)
 # genes with $fdr < 0.01$ = 525 (29 + / 496 -)

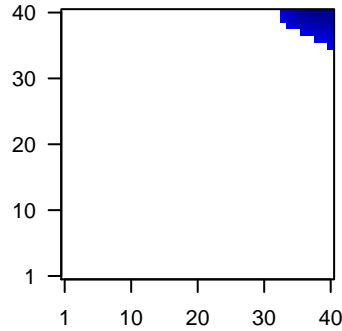
$\langle r \rangle$ metagenes = 0.93
 $\langle r \rangle$ genes = 0.53

 $\langle FC \rangle = -0.1$
 $\langle t\text{-score} \rangle = -1.94$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.14$

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ENSG00000000	-0.22	2e-16	6e-17	38 x 40 enolase 1, (alpha) [Source:HGNC Symbol;Acc:HGNC:3350]
2	ENSG00000001	-0.15	2e-16	6e-17	36 x 40 regulator of chromosome condensation 2 [Source:HGNC Syn
3	ENSG00000000	-0.15	2e-16	6e-17	37 x 39 MRT4 homolog, ribosome maturation factor [Source:HGNC S
4	ENSG00000002	-0.26	2e-16	6e-17	38 x 40 dolichyl--diphosphooligosaccharide--protein glycosyltransfer
5	ENSG00000001	-0.15	2e-16	6e-17	40 x 40 EPH receptor B2 [Source:HGNC Symbol;Acc:HGNC:3393]
6	ENSG00000001	-0.14	2e-16	6e-17	38 x 39 peroxiredoxin 1 [Source:HGNC Symbol;Acc:HGNC:9352]
7	ENSG00000001	-0.14	2e-16	6e-17	40 x 40 PDZK1 interacting protein 1 [Source:HGNC Symbol;Acc:HGNC
8	ENSG00000001	-0.16	2e-16	6e-17	38 x 37 thioredoxin domain containing 12 (endoplasmic reticulum) [Sc
9	ENSG00000001	-0.2	2e-16	6e-17	40 x 40 regenerating islet--derived family, member 4 [Source:HGNC S
10	ENSG00000001	-0.19	2e-16	6e-17	40 x 40 S100 calcium binding protein A11 [Source:HGNC Symbol;Acc
11	ENSG00000002	-0.17	2e-16	6e-17	40 x 35 Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:V9Q
12	ENSG00000001	-0.17	2e-16	6e-17	40 x 40 mucin 1, cell surface associated [Source:HGNC Symbol;Acc:HG
13	ENSG00000001	-0.19	2e-16	6e-17	34 x 40 chaperonin containing TCP1, subunit 3 (gamma) [Source:HG
14	ENSG00000001	0.23	2e-16	6e-17	40 x 40 intelectin 1 (galactofuranose binding) [Source:HGNC Symbol;
15	ENSG00000000	-0.14	2e-16	6e-17	39 x 39 ubiquitin--conjugating enzyme E2T [Source:HGNC Symbol;Acc
16	ENSG00000001	-0.18	2e-16	6e-17	40 x 37 CD55 molecule, decay accelerating factor for complement (C
17	ENSG00000001	-0.17	2e-16	6e-17	40 x 35 neudesin neurotrophic factor [Source:HGNC Symbol;Acc:HGNC
18	ENSG00000001	-0.14	2e-16	6e-17	36 x 40 EDAR--associated death domain [Source:HGNC Symbol;Acc
19	ENSG00000001	-0.26	2e-16	6e-17	39 x 40 ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C2 [S
20	ENSG00000001	-0.25	2e-16	6e-17	37 x 40 protein disulfide isomerase family A, member 6 [Source:HGNC

p-values

