

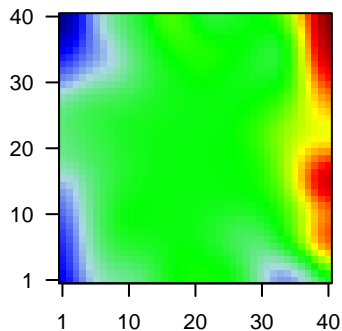
# 02.0015.002\_aH

## Global Summary

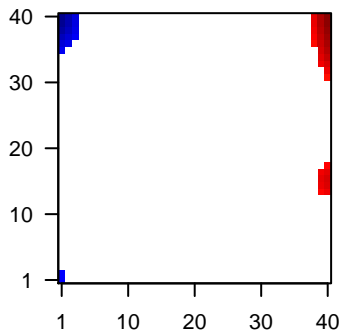
%DE = 0.24  
 # genes with fdr < 0.2 = 4533 ( 2290 + / 2243 - )  
 # genes with fdr < 0.1 = 4004 ( 2066 + / 1938 - )  
 # genes with fdr < 0.05 = 3618 ( 1885 + / 1733 - )  
 # genes with fdr < 0.01 = 2998 ( 1616 + / 1382 - )  
 # genes in genesets = 18990

<FC> = 0  
 <t-score> = 0  
 <p-value> = 0.01  
 <fdr> = 0.76

Profile



Regulated Spots



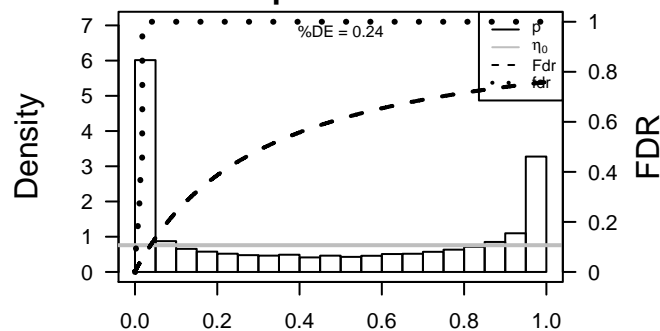
## Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	ENSG000001	0.26	2e-16 4e-15	40 x 16 sterile alpha motif domain containing 11 [Source:HGNC Syml
2	ENSG000001	0.36	2e-16 4e-15	40 x 8 aurora kinase A interacting protein 1 [Source:HGNC Symbol;]
3	ENSG000002	0.28	2e-16 4e-15	40 x 34 mitochondrial ribosomal protein L20 [Source:HGNC Symbol;]
4	ENSG000000	-0.22	2e-16 4e-15	1 x 12 guanine nucleotide binding protein (G protein), beta polypepti
5	ENSG000001	-0.21	2e-16 4e-15	3 x 32 ERBB receptor feedback inhibitor 1 [Source:HGNC Symbol;A
6	ENSG000000	0.22	2e-16 4e-15	37 x 39 MRT4 homolog, ribosome maturation factor [Source:HGNC S
7	ENSG000000	-0.21	2e-16 4e-15	7 x 35 capping protein (actin filament) muscle Z-line, beta [Source:+
8	ENSG000001	0.22	2e-16 4e-15	40 x 16 mitochondrial inner membrane organizing system 1 [Source:+
9	ENSG000001	0.33	2e-16 4e-15	40 x 40 phospholipase A2, group IIA (platelets, synovial fluid) [Source
10	ENSG000001	-0.22	2e-16 4e-15	38 x 1 cytidine deaminase [Source:HGNC Symbol;Acc:HGNC:1712]
11	ENSG000000	-0.23	2e-16 4e-15	1 x 15 cell division cycle 42 [Source:HGNC Symbol;Acc:HGNC:1736]
12	ENSG000001	-0.21	2e-16 4e-15	1 x 4 complement component 1, q subcomponent, C chain [Source
13	ENSG000001	0.29	2e-16 4e-15	40 x 40 EPH receptor B2 [Source:HGNC Symbol;Acc:HGNC:3393]
14	ENSG000000	0.22	2e-16 4e-15	40 x 6 lysophospholipase II [Source:HGNC Symbol;Acc:HGNC:6736]
15	ENSG000001	-0.23	2e-16 4e-15	9 x 1 proline-rich nuclear receptor coactivator 2 [Source:HGNC Sy
16	ENSG000001	-0.32	2e-16 4e-15	1 x 40 chloride intracellular channel 4 [Source:HGNC Symbol;Acc:H
17	ENSG000001	0.46	2e-16 4e-15	40 x 36 zinc finger protein 593 [Source:HGNC Symbol;Acc:HGNC:30
18	ENSG000001	0.33	2e-16 4e-15	38 x 7 UBX domain protein 11 [Source:HGNC Symbol;Acc:HGNC:31
19	ENSG000000	0.22	2e-16 4e-15	40 x 33 nudC nuclear distribution protein [Source:HGNC Symbol;Acc:
20	ENSG000002	-0.25	2e-16 4e-15	1 x 11

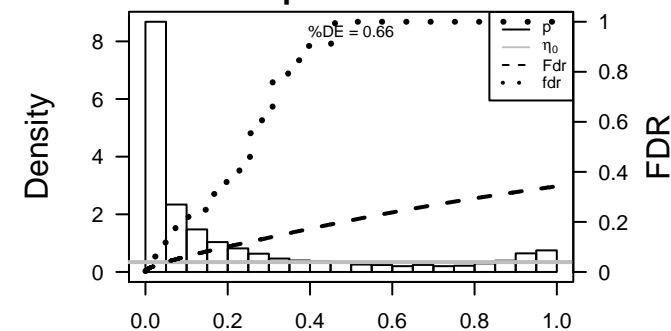
## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	17.05	2e-05	162	MF structural constituent of ribosome
2	16.14	2e-05	813	GSEA C2GRADE_COLON_CANCER_UP
3	15.94	3e-05	8123	Colon CaHNSecF_Colon
4	15.46	3e-05	168	CC ribosome
5	15.03	3e-05	807	LymphomHNSecF_June14_MMML937_tumors+controls_group.overexpression_
6	14.88	3e-05	550	Cancer Lembecke_Normal vs Adenoma
7	14.58	3e-05	811	LymphomHNSecF_IRTH_lymphoma937_spot D
8	14.49	3e-05	84	GSEA C2KEGG_RIBOSOME
9	13.89	4e-05	259	BP translation
10	13.66	4e-05	98	GSEA C2REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND
11	13.63	4e-05	944	GSEA C2KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
12	13.61	4e-05	400	GSEA C2VECCI_GASTRIC_CANCER_EARLY_UP
13	13.45	4e-05	88	BP translational termination
14	13.19	4e-05	82	GSEA C2REACTOME_PEPTIDE_CHAIN_ELONGATION
15	13.16	4e-05	105	GSEA C2REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN
16	12.91	5e-05	108	BP SRP-dependent cotranslational protein targeting to membrane
17	12.76	5e-05	754	GSEA C2MARTENS_TRETINOIN_RESPONSE_DN
18	12.72	5e-05	101	BP translational elongation
19	12.4	6e-05	499	GSEA C2STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
20	12.34	6e-05	128	GSEA C2SABATES_COLORECTAL_ADENOMA_UP
<i>Underexpressed</i>				
1	-20.52	1e-05	368	GSEA C2INDGREN_BLADDER_CANCER_CLUSTER_2B
2	-19.52	2e-05	507	Colon CaHNSecF_track_CRC_TCGA_corr_C_normal_UP
3	-18.62	2e-05	539	GSEA C2FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR
4	-18.48	2e-05	196	GSEA C2PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
5	-18.29	2e-05	326	GSEA C2SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
6	-17.54	2e-05	303	GSEA C2PASINI_SUZ12_TARGETS_DN
7	-17.07	2e-05	332	Colon CaHNSecF_track_CRC_TCGA_corr_J_msi-h_UP_mss_DN
8	-16.73	2e-05	262	GSEA C2SABATES_COLORECTAL_ADENOMA_DN
9	-16.73	2e-05	104	Colon CaHNSecF_track_CRC_TCGA_group.over_A_normal_UP
10	-16.72	2e-05	314	LymphomHNSecF_June14_MMML937_tumors+controls_group.overexpression_
11	-16.57	2e-05	315	LymphomHNSecF_IRTH_lymphoma937_spot E
12	-16.36	2e-05	436	GSEA C2SMID_BREAST_CANCER_NORMAL_LIKE_UP
13	-16	2e-05	198	HM HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
14	-15.93	3e-05	692	GSEA C2WONG_ADULT_TISSUE_STEM_MODULE
15	-15.73	3e-05	419	GSEA C2BAELDE_DIABETIC_NEPHROPATHY_DN
16	-15.02	3e-05	804	GSEA C2CUI_TCF21_TARGETS_2_DN
17	-14.99	3e-05	418	GSEA C2SWEET_LUNG_CANCER_KRAS_DN
18	-14.6	3e-05	192	HM HALLMARK_TNFA_SIGNALING_VIA_NFKB
19	-14.39	3e-05	261	LymphomHNSecF_ENZ_Stromal signature 1
20	-14.26	4e-05	386	GSEA C2THUM_SYSTOLIC_HEART_FAILURE_UP

p-values



p-values



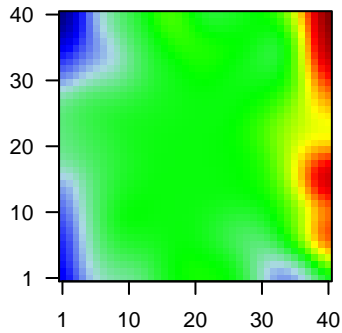
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## Local Summary

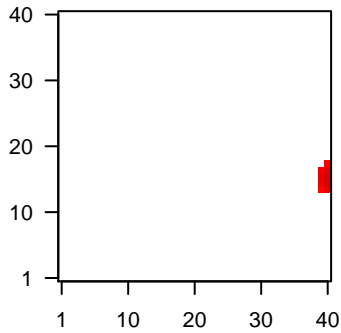
%DE = 0.99  
 # metagenes = 9  
 # genes = 185  
 # genes in genesets = 182  
  
 # genes with  $fdr < 0.1$  = 182 ( 182 + / 0 -)  
 # genes with  $fdr < 0.05$  = 182 ( 182 + / 0 -)  
 # genes with  $fdr < 0.01$  = 177 ( 177 + / 0 -)

$\langle r \rangle$  metagenes = 0.98  
 $\langle r \rangle$  genes = 0.64  
  
 $\langle FC \rangle$  = 0.21  
 $\langle t\text{-score} \rangle$  = 4.35  
 $\langle p\text{-value} \rangle$  = 0  
 $\langle fdr \rangle$  = 0.04

Profile



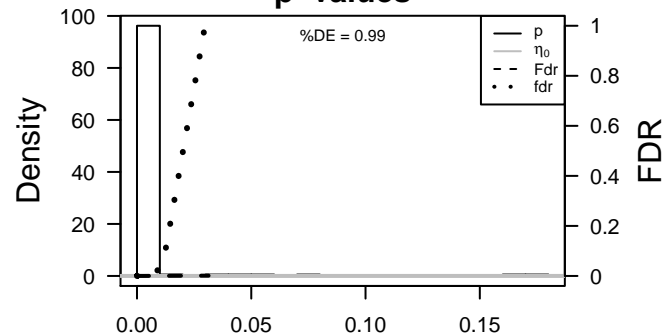
Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ENSG0000001	0.26	2e-16	3e-18	40 x 16 sterile alpha motif domain containing 11 [Source:HGNC Syml
2	ENSG0000001	0.22	2e-16	3e-18	40 x 16 mitochondrial inner membrane organizing system 1 [Source:t
3	ENSG0000001	0.28	2e-16	3e-18	40 x 17 chromosome 1 open reading frame 122 [Source:HGNC Synt
4	ENSG0000001	0.29	2e-16	3e-18	40 x 15 late endosomal/lysosomal adaptor, MAPK and MTOR activat
5	ENSG0000001	0.37	2e-16	3e-18	40 x 14 dual specificity phosphatase 23 [Source:HGNC Symbol;Acc:t
6	ENSG0000001	0.24	2e-16	3e-18	40 x 16 polymerase (DNA-directed), epsilon 4, accessory subunit [Sc
7	ENSG0000001	0.28	2e-16	3e-18	40 x 17 myeloma overexpressed 2 [Source:HGNC Symbol;Acc:HGNC
8	ENSG0000001	0.4	2e-16	3e-18	40 x 16 NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (f
9	ENSG0000002	0.24	2e-16	3e-18	40 x 15 MAX dimerization protein 3 [Source:HGNC Symbol;Acc:HGNC
10	ENSG0000001	0.26	2e-16	3e-18	40 x 16 serpin peptidase inhibitor, clade B (ovalbumin), member 6 [Sc
11	ENSG0000002	0.23	2e-16	3e-18	39 x 14 coiled-coil alpha-helical rod protein 1 [Source:HGNC Symbo
12	ENSG0000001	0.27	2e-16	3e-18	40 x 16 radial spoke head 9 homolog (Chlamydomonas) [Source:HGf
13	ENSG0000001	0.3	2e-16	3e-18	40 x 16 general transcription factor IIIC, polypeptide 6, alpha 35kDa [f
14	ENSG0000001	0.22	2e-16	3e-18	40 x 14 serine/threonine/tyrosine interacting-like 1 [Source:HGNC Sy
15	ENSG0000001	0.22	2e-16	3e-18	40 x 16 split hand/foot malformation (ectrodactyly) type 1 [Source:HG
16	ENSG0000001	0.22	2e-16	3e-18	40 x 16 BUD31 homolog [Source:HGNC Symbol;Acc:HGNC:29629]
17	ENSG0000002	0.33	2e-16	3e-18	40 x 15 ATP synthase, H+ transporting, mitochondrial Fo complex, su
18	ENSG0000001	0.22	2e-16	3e-18	40 x 15 protein phosphatase 1, regulatory subunit 35 [Source:HGNC
19	ENSG0000001	0.3	2e-16	3e-18	40 x 15 zinc finger, HIT-type containing 1 [Source:HGNC Symbol;Acc
20	ENSG0000002	0.36	2e-16	3e-18	40 x 17 fission, mitochondrial 1 [Source:HGNC Symbol;Acc:HGNC:21

p-values



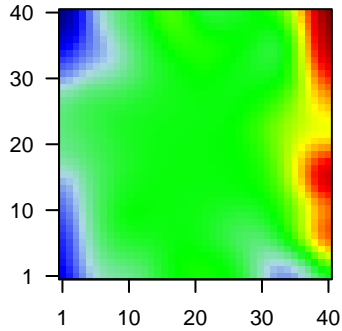
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## Local Summary

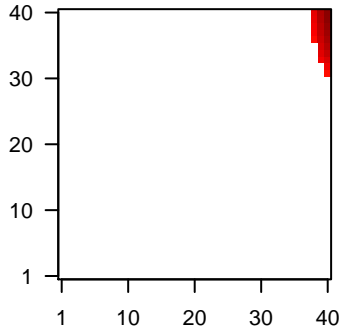
%DE = 0.95  
 # metagenes = 23  
 # genes = 548  
 # genes in genesets = 539  
  
 # genes with  $fdr < 0.1$  = 503 ( 496 + / 7 -)  
 # genes with  $fdr < 0.05$  = 503 ( 496 + / 7 -)  
 # genes with  $fdr < 0.01$  = 487 ( 481 + / 6 -)

$\langle r \rangle$  metagenes = 0.97  
 $\langle r \rangle$  genes = 0.61  
  
 $\langle FC \rangle$  = 0.22  
 $\langle t\text{-score} \rangle$  = 4.37  
 $\langle p\text{-value} \rangle$  = 0  
 $\langle fdr \rangle$  = 0.09

Profile



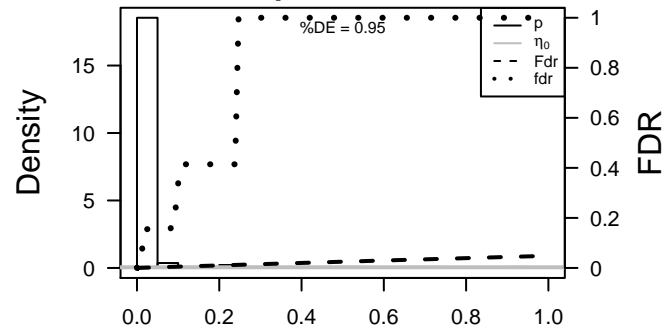
Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ENSG000002	0.28	2e-16	2e-17	40 x 34 mitochondrial ribosomal protein L20 [Source:HGNC Symbol;]
2	ENSG000001	0.33	2e-16	2e-17	40 x 40 phospholipase A2, group IIA (platelets, synovial fluid) [Source:
3	ENSG000001	0.29	2e-16	2e-17	40 x 40 EPH receptor B2 [Source:HGNC Symbol;Acc:HGNC:3393]
4	ENSG000001	0.46	2e-16	2e-17	40 x 36 zinc finger protein 593 [Source:HGNC Symbol;Acc:HGNC:30]
5	ENSG000000	0.22	2e-16	2e-17	40 x 33 nudC nuclear distribution protein [Source:HGNC Symbol;Acc:
6	ENSG000001	0.23	2e-16	2e-17	40 x 39 cell division cycle 20 [Source:HGNC Symbol;Acc:HGNC:172]
7	ENSG000001	0.57	2e-16	2e-17	40 x 40 PDZK1 interacting protein 1 [Source:HGNC Symbol;Acc:HGNC:
8	ENSG000001	0.21	2e-16	2e-17	39 x 39 mitochondrial ribosomal protein L37 [Source:HGNC Symbol;]
9	ENSG000000	0.22	2e-16	2e-17	40 x 40 chloride channel accessory 1 [Source:HGNC Symbol;Acc:HGNC:
10	ENSG000001	0.4	2e-16	2e-17	40 x 40 S100 calcium binding protein A11 [Source:HGNC Symbol;Acc:
11	ENSG000001	0.26	2e-16	2e-17	40 x 36 jumping translocation breakpoint [Source:HGNC Symbol;Acc:
12	ENSG000001	0.25	2e-16	2e-17	40 x 37 CDC28 protein kinase regulatory subunit 1B [Source:HGNC S]
13	ENSG000002	0.29	2e-16	2e-17	40 x 35 Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:V9K
14	ENSG000001	0.21	2e-16	2e-17	40 x 32 ubiquitin 4 [Source:HGNC Symbol;Acc:HGNC:1237]
15	ENSG000001	0.24	2e-16	2e-17	40 x 34 apolipoprotein A-I binding protein [Source:HGNC Symbol;Ac
16	ENSG000001	-0.24	2e-16	2e-17	40 x 40 intelectin 1 (galactofuranose binding) [Source:HGNC Symbol;
17	ENSG000001	0.26	2e-16	2e-17	40 x 36 small nuclear ribonucleoprotein polypeptide E [Source:HGNC
18	ENSG000001	0.51	2e-16	2e-17	40 x 35 neudesin neurotrophic factor [Source:HGNC Symbol;Acc:HGNC:
19	ENSG000001	0.21	2e-16	2e-17	39 x 40 ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C2 [S
20	ENSG000001	0.41	2e-16	2e-17	40 x 40 keratinocyte associated protein 3 [Source:HGNC Symbol;Acc

p-values



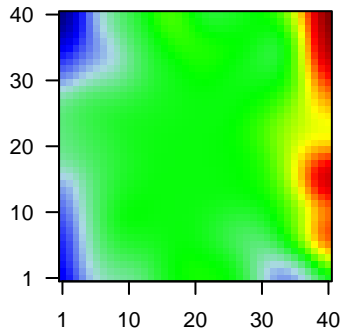
# 02.0015.002\_aH

## Local Summary

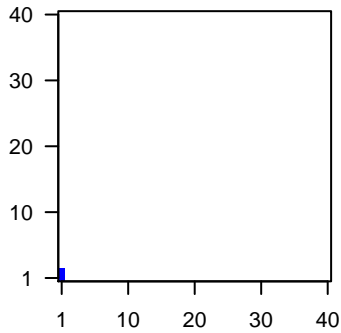
%DE = 0.92  
 # metagenes = 2  
 # genes = 113  
 # genes in genesets = 110  
  
 # genes with  $fdr < 0.1$  = 100 ( 2 + / 98 -)  
 # genes with  $fdr < 0.05$  = 97 ( 2 + / 95 -)  
 # genes with  $fdr < 0.01$  = 95 ( 2 + / 93 -)

$\langle r \rangle$  metagenes = 1  
 $\langle r \rangle$  genes = 0.82  
  
 $\langle FC \rangle$  = -0.18  
 $\langle t\text{-score} \rangle$  = -3.75  
 $\langle p\text{-value} \rangle$  = 0  
 $\langle fdr \rangle$  = 0.13

Profile



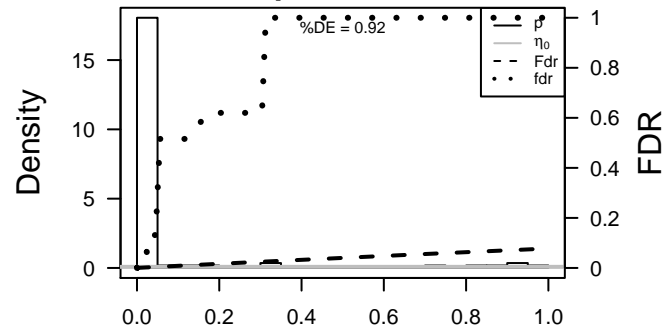
Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ENSG0000001	-0.28	2e-16	5e-17	1 x 1 lysosomal protein transmembrane 5 [Source:HGNC Symbol;]
2	ENSG0000001	-0.3	2e-16	5e-17	1 x 1 CD53 molecule [Source:HGNC Symbol;Acc:HGNC:1686]
3	ENSG0000001	-0.24	2e-16	5e-17	1 x 1 selectin L [Source:HGNC Symbol;Acc:HGNC:10720]
4	ENSG0000001	-0.22	2e-16	5e-17	1 x 1 Fc fragment of IgM receptor [Source:HGNC Symbol;Acc:HGNC:1686]
5	ENSG0000001	-0.25	2e-16	5e-17	1 x 1 complement component (3d/Epstein Barr virus) receptor 2 [Source:HGNC Symbol;Acc:HGNC:1686]
6	ENSG0000001	-0.44	2e-16	5e-17	1 x 1 chemokine (C-X-C motif) receptor 4 [Source:HGNC Symbol;Acc:HGNC:1686]
7	ENSG0000002	-0.64	2e-16	5e-17	1 x 1 MT-RNR2-like 12 [Source:HGNC Symbol;Acc:HGNC:37169]
8	ENSG0000001	-0.48	2e-16	5e-17	1 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbol;Acc:HGNC:1686]
9	ENSG0000001	-0.48	2e-16	5e-17	1 x 1 chemokine (C-X-C motif) ligand 13 [Source:HGNC Symbol;Acc:HGNC:1686]
10	ENSG0000002	-0.61	2e-16	5e-17	1 x 1 MT-RNR2-like 2 [Source:HGNC Symbol;Acc:HGNC:37156]
11	ENSG0000001	-0.23	2e-16	5e-17	1 x 1 chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;Acc:HGNC:1686]
12	ENSG0000002	-0.31	2e-16	5e-17	1 x 1 major histocompatibility complex, class I, E [Source:HGNC Symbol;Acc:HGNC:1686]
13	ENSG0000002	-0.49	2e-16	5e-17	1 x 1 major histocompatibility complex, class II, DR alpha [Source:HGNC Symbol;Acc:HGNC:1686]
14	ENSG0000002	-0.25	2e-16	5e-17	1 x 1 major histocompatibility complex, class II, DQ alpha 2 [Source:HGNC Symbol;Acc:HGNC:1686]
15	ENSG0000002	-0.25	2e-16	5e-17	1 x 1 Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:FGS0000002]
16	ENSG0000002	-0.31	2e-16	5e-17	1 x 1 major histocompatibility complex, class II, DP alpha 1 [Source:HGNC Symbol;Acc:HGNC:1686]
17	ENSG0000002	-0.32	2e-16	5e-17	1 x 1 major histocompatibility complex, class II, DP beta 1 [Source:HGNC Symbol;Acc:HGNC:1686]
18	ENSG0000002	-0.37	2e-16	5e-17	1 x 1 MT-RNR2-like 9 [Source:HGNC Symbol;Acc:HGNC:37166]
19	ENSG0000001	-0.25	2e-16	5e-17	1 x 1 GTPase, IMAP family member 7 [Source:HGNC Symbol;Acc:HGNC:1686]
20	ENSG0000001	-0.22	2e-16	5e-17	1 x 1 ADAM-like, decysin 1 [Source:HGNC Symbol;Acc:HGNC:1686]

p-values



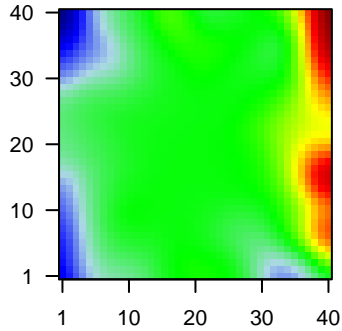
# 02.0015.002\_aH

## Local Summary

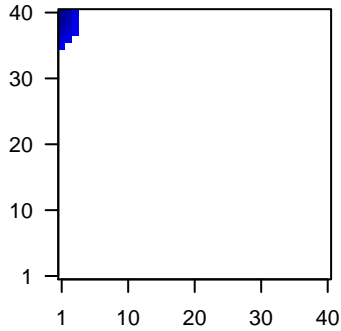
%DE = 0.99  
 # metagenes = 15  
 # genes = 258  
 # genes in genesets = 255  
  
 # genes with  $fdr < 0.1$  = 254 ( 3 + / 251 - )  
 # genes with  $fdr < 0.05$  = 253 ( 3 + / 250 - )  
 # genes with  $fdr < 0.01$  = 250 ( 3 + / 247 - )

$\langle r \rangle$  metagenes = 0.99  
 $\langle r \rangle$  genes = 0.77  
  
 $\langle FC \rangle$  = -0.22  
 $\langle t\text{-score} \rangle$  = -4.55  
 $\langle p\text{-value} \rangle$  = 0  
 $\langle fdr \rangle$  = 0.02

Profile



Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ENSG0000001	-0.32	2e-16	4e-18	1 x 40 chloride intracellular channel 4 [Source:HGNC Symbol;Acc:H
2	ENSG0000001	-0.24	2e-16	4e-18	2 x 36 ring finger protein 11 [Source:HGNC Symbol;Acc:HGNC:100
3	ENSG0000001	-0.38	2e-16	4e-18	1 x 38 cysteine-rich, angiogenic inducer, 61 [Source:HGNC Symbol
4	ENSG0000000	-0.25	2e-16	4e-18	2 x 38 cold shock domain containing E1, RNA-binding [Source:HGNC
5	ENSG0000001	-0.77	2e-16	4e-18	1 x 38
6	ENSG0000001	-0.25	2e-16	4e-18	1 x 38 phosphoprotein enriched in astrocytes 15 [Source:HGNC Syr
7	ENSG0000001	-0.25	2e-16	4e-18	1 x 40 regulator of G-protein signaling 5 [Source:HGNC Symbol;Acc
8	ENSG0000001	-0.33	2e-16	4e-18	1 x 40 dermatopontin [Source:HGNC Symbol;Acc:HGNC:3011]
9	ENSG0000001	-0.4	2e-16	4e-18	1 x 40 regulator of G-protein signaling 2 [Source:HGNC Symbol;Acc
10	ENSG0000001	-0.35	2e-16	4e-18	1 x 40 cysteine and glycine-rich protein 1 [Source:HGNC Symbol;A
11	ENSG0000001	-0.35	2e-16	4e-18	1 x 40 leiomodulin 1 (smooth muscle) [Source:HGNC Symbol;Acc:HG
12	ENSG0000001	-0.4	2e-16	4e-18	1 x 40 BTG family, member 2 [Source:HGNC Symbol;Acc:HGNC:11
13	ENSG0000002	-0.33	2e-16	4e-18	2 x 37
14	ENSG0000001	-0.38	2e-16	4e-18	3 x 40 inhibitor of DNA binding 2, dominant negative helix-loop-heli
15	ENSG0000001	-0.57	2e-16	4e-18	1 x 40 ras homolog family member B [Source:HGNC Symbol;Acc:H
16	ENSG0000001	-0.23	2e-16	4e-18	1 x 36 yippee-like 5 [Source:HGNC Symbol;Acc:HGNC:18329]
17	ENSG0000001	-0.64	2e-16	4e-18	1 x 40 actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
18	ENSG0000002	-0.41	2e-16	4e-18	2 x 38 POTE ankyrin domain family, member J [Source:HGNC Syml
19	ENSG0000001	-0.42	2e-16	4e-18	2 x 38 POTE ankyrin domain family, member E [Source:HGNC Syml
20	ENSG0000000	-0.24	2e-16	4e-18	1 x 35 cytochrome b reductase 1 [Source:HGNC Symbol;Acc:HGNC

p-values

