

# 02.4535.001\_cH

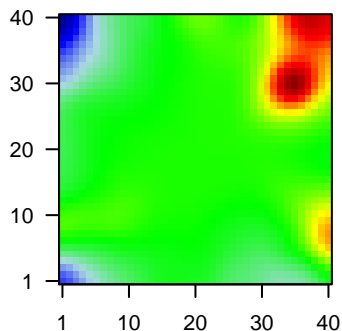
## Global Summary

%DE = 0.25  
 # genes with fdr < 0.2 = 4729 ( 2320 + / 2409 - )  
 # genes with fdr < 0.1 = 4274 ( 2120 + / 2154 - )  
 # genes with fdr < 0.05 = 3914 ( 1952 + / 1962 - )  
 # genes with fdr < 0.01 = 3342 ( 1714 + / 1628 - )

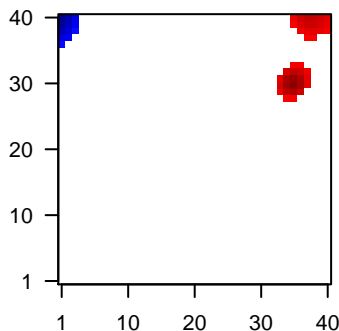
# genes in genesets = 18990

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

Profile



Regulated Spots



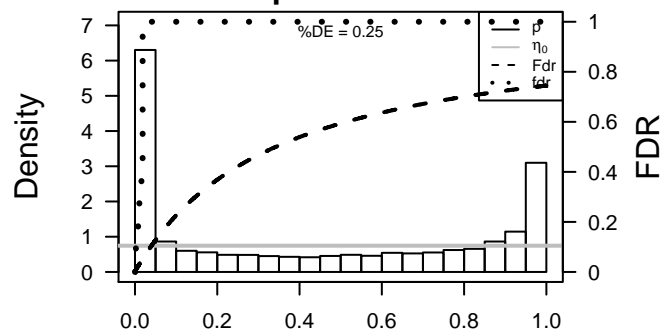
## Global Genelist

| Rank | ID           | log(FC) | fdr   | Description |  |
|------|--------------|---------|-------|-------------|--|
|      |              | p-value |       | Metagene    |  |
| 1    | ENSG00000001 | 0.19    | 2e-16 | 3e-15       | 40 x 36 family with sequence similarity 213, member B [Source:HGNC]                                      |
| 2    | ENSG00000001 | 0.17    | 2e-16 | 3e-15       | 28 x 1 dehydrogenase/reductase (SDR family) member 3 [Source:HGNC]                                       |
| 3    | ENSG00000001 | 0.19    | 2e-16 | 3e-15       | 37 x 34 agmatine ureohydrolase (agmatinase) [Source:HGNC Symbol;Acc:HGNC:24018]                          |
| 4    | ENSG00000001 | 0.16    | 2e-16 | 3e-15       | 39 x 1 peptidyl arginine deiminase, type II [Source:HGNC Symbol;Acc:HGNC:24018]                          |
| 5    | ENSG00000001 | 0.16    | 2e-16 | 3e-15       | 36 x 40 regulator of chromosome condensation 2 [Source:HGNC Symbol;Acc:HGNC:24018]                       |
| 6    | ENSG00000001 | 0.39    | 2e-16 | 3e-15       | 35 x 30 actin-like 8 [Source:HGNC Symbol;Acc:HGNC:24018]   |
| 7    | ENSG00000002 | -0.23   | 2e-16 | 3e-15       | 29 x 2 MINOS1-NBL1 readthrough [Source:HGNC Symbol;Acc:HGNC:24018]                                       |
| 8    | ENSG00000001 | -0.27   | 2e-16 | 3e-15       | 38 x 7 neuroblastoma 1, DAN family BMP antagonist [Source:HGNC Symbol;Acc:HGNC:24018]                    |
| 9    | ENSG00000001 | -0.4    | 2e-16 | 3e-15       | 37 x 1 calcium/calmodulin-dependent protein kinase II inhibitor 1 [Source:HGNC Symbol;Acc:HGNC:24018]    |
| 10   | ENSG00000001 | 0.19    | 2e-16 | 3e-15       | 40 x 40 EPH receptor B2 [Source:HGNC Symbol;Acc:HGNC:3393]   |
| 11   | ENSG00000002 | 0.15    | 2e-16 | 3e-15       | 40 x 10 transcription elongation factor A (SII), 3 [Source:HGNC Symbol;Acc:HGNC:3393]                    |
| 12   | ENSG00000001 | -0.22   | 2e-16 | 3e-15       | 33 x 1 inhibitor of DNA binding 3, dominant negative helix-loop-helix [Source:HGNC Symbol;Acc:HGNC:3393] |
| 13   | ENSG00000001 | 0.17    | 2e-16 | 3e-15       | 40 x 7 UDP-galactose-4-epimerase [Source:HGNC Symbol;Acc:HGNC:3393]                                      |
| 14   | ENSG00000001 | 0.27    | 2e-16 | 3e-15       | 38 x 1 fucosidase, alpha-L-1, tissue [Source:HGNC Symbol;Acc:HGNC:3393]                                  |
| 15   | ENSG00000001 | -0.17   | 2e-16 | 3e-15       | 1 x 40 chloride intracellular channel 4 [Source:HGNC Symbol;Acc:HGNC:3393]                               |
| 16   | ENSG00000001 | 0.29    | 2e-16 | 3e-15       | 37 x 40 stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]  |
| 17   | ENSG00000001 | -0.2    | 2e-16 | 3e-15       | 1 x 1 CD52 molecule [Source:HGNC Symbol;Acc:HGNC:1804]   |
| 18   | ENSG00000001 | 0.16    | 2e-16 | 3e-15       | 35 x 40 high mobility group nucleosomal binding domain 2 [Source:HGNC Symbol;Acc:HGNC:1804]              |
| 19   | ENSG00000001 | -0.36   | 2e-16 | 3e-15       | 29 x 40 interferon, alpha-inducible protein 6 [Source:HGNC Symbol;Acc:HGNC:1804]                         |
| 20   | ENSG00000001 | 0.17    | 2e-16 | 3e-15       | 38 x 40 regulator of chromosome condensation 1 [Source:HGNC Symbol;Acc:HGNC:1804]                        |

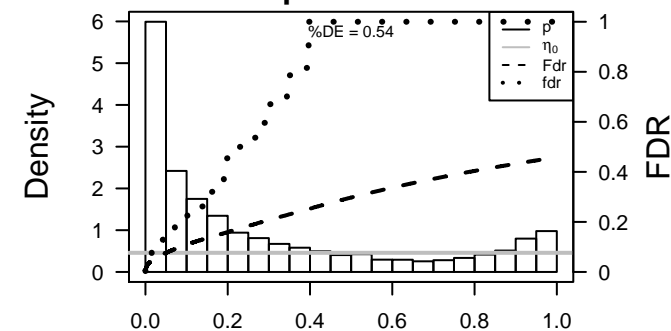
## Global Geneset Analysis

| Rank                  | GSZ    | p-value | #all | Geneset   |
|-----------------------|--------|---------|------|---|
| <i>Overexpressed</i>  |        |         |      |   |
| 1                     | 22.22  | 7e-06   | 713  | Colon Cancer TCGA_group.over_C_normal_DN                          |
| 2                     | 19.14  | 2e-05   | 830  | Colon Cancer TCGA_corr_R_normal_DN                                |
| 3                     | 19.09  | 2e-05   | 1425 | Chr Chr 19  |
| 4                     | 18.81  | 2e-05   | 582  | GSEA C2CAIRO_HEPATOBLASTOMA_CLASSES_UP                            |
| 5                     | 17.22  | 2e-05   | 807  | Lymphoma Topp_June14_MMML937_tumors+controls_group.overexpression |
| 6                     | 17.12  | 2e-05   | 811  | Lymphoma WIRTH_lymphoma937_spot D                                 |
| 7                     | 16.89  | 2e-05   | 327  | GSEA C2WONG_EMBRYONIC_STEM_CELL_CORE                              |
| 8                     | 16.77  | 2e-05   | 813  | GSEA C2GRADE_COLON_CANCER_UP                                      |
| 9                     | 16.72  | 2e-05   | 747  | GSEA C2PUJANA_CHEK2_PCC_NETWORK                                   |
| 10                    | 16.56  | 2e-05   | 1563 | GSEA C2PUJANA_BRCA1_PCC_NETWORK                                   |
| 11                    | 16.36  | 2e-05   | 1091 | MF poly(A) RNA binding  |
| 12                    | 16.31  | 2e-05   | 195  | HM HALLMARK_MYC_TARGETS_V1  |
| 13                    | 15.28  | 3e-05   | 162  | MF structural constituent of ribosome                             |
| 14                    | 15.16  | 3e-05   | 138  | GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER                |
| 15                    | 14.75  | 3e-05   | 754  | GSEA C2MARTENS_TRETINOIN_RESPONSE_DN                              |
| 16                    | 14.72  | 3e-05   | 400  | GSEA C2ECCH1_GASTRIC_CANCER_EARLY_UP                              |
| 17                    | 14.69  | 3e-03   | 16   | Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP                     |
| 18                    | 14.51  | 3e-05   | 102  | GSEA C2REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION           |
| 19                    | 14.48  | 3e-05   | 88   | BP translational termination                                      |
| 20                    | 14.47  | 3e-05   | 84   | GSEA C2KEGG_RIBOSOME  |
| <i>Underexpressed</i> |        |         |      |   |
| 1                     | -20.51 | 1e-05   | 368  | GSEA C2LINDGREN_BLADEDER_CANCER_CLUSTER_2B                        |
| 2                     | -18.71 | 2e-05   | 436  | GSEA C2SMID_BREAST_CANCER_NORMAL_LIKE_UP                          |
| 3                     | -16.82 | 2e-05   | 507  | Colon Cancer TCGA_corr_C_normal_UP                                |
| 4                     | -16.12 | 2e-05   | 132  | Colon Cancer TCGA_corr_C_normal_UP                                |
| 5                     | -15.62 | 3e-05   | 262  | GSEA C2SABATES_COLORECTAL_ADENOMA_DN                              |
| 6                     | -14.74 | 3e-05   | 196  | GSEA C2PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP                   |
| 7                     | -14.43 | 6e-03   | 16   | Cancer LIU_PROSTATE_CANCER_DN                                     |
| 8                     | -14.27 | 4e-05   | 314  | Lymphoma Topp_June14_MMML937_tumors+controls_group.overexpression |
| 9                     | -13.96 | 4e-05   | 263  | GSEA C2WALLACE_PROSTATE_CANCER_RACE_UP                            |
| 10                    | -13.78 | 4e-05   | 315  | Lymphoma WIRTH_lymphoma937_spot E                                 |
| 11                    | -13.73 | 4e-05   | 326  | GSEA C2SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP                   |
| 12                    | -13.59 | 4e-05   | 844  | Colon Cancer TCGA_expr_kmeans_E_CIMP_H_UP_Cluster4_DN             |
| 13                    | -13.11 | 4e-05   | 104  | Colon Cancer TCGA_group.over_A_normal_UP                          |
| 14                    | -12.92 | 5e-05   | 418  | GSEA C2SWEET_LUNG_CANCER_KRAS_DN                                  |
| 15                    | -12.64 | 6e-05   | 478  | GSEA C2JIM_MAMMARY_STEM_CELL_UP                                   |
| 16                    | -12.45 | 6e-05   | 692  | GSEA C2WONG_ADULT_TISSUE_STEM_MODULE                              |
| 17                    | -12.24 | 7e-05   | 6    | Lymphoma WAVE_MHC2I1 BL DN  |
| 18                    | -12.23 | 7e-05   | 73   | GSEA C2JIM_GLI2_TARGETS_UP  |
| 19                    | -12    | 7e-05   | 522  | GSEA C2SMID_BREAST_CANCER_LUMINAL_B_DN                            |
| 20                    | -11.93 | 8e-05   | 18   | GSEA C2NIELSEN_LEIOMYOSARCOMA_CNN1_UP                             |

p-values



p-values



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## Local Summary

%DE = 0.99  
 # metagenes = 22  
 # genes = 245  
 # genes in genesets = 230  
  
 # genes with  $fdr < 0.1$  = 240 ( 240 + / 0 -)  
 # genes with  $fdr < 0.05$  = 238 ( 238 + / 0 -)  
 # genes with  $fdr < 0.01$  = 238 ( 238 + / 0 -)

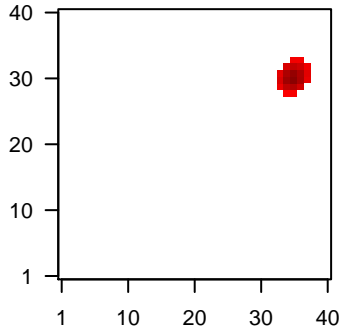
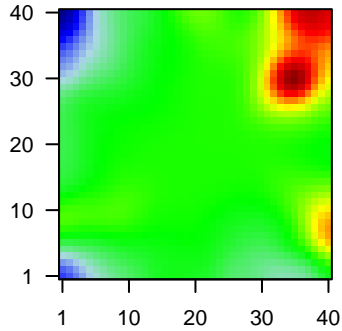
$\langle r \rangle$  metagenes = 0.94  
 $\langle r \rangle$  genes = 0.53  
  
 $\langle FC \rangle$  = 0.22  
 $\langle t\text{-score} \rangle$  = 4.49  
 $\langle p\text{-value} \rangle$  = 0  
 $\langle fdr \rangle$  = 0.03

## Local Genelist

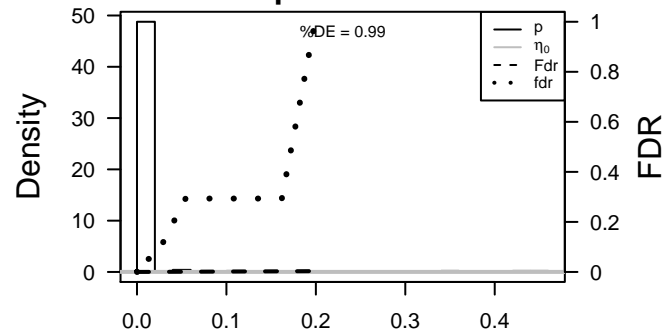
| Rank | ID          | log(FC) | fdr   | p-value | Description  |
|------|-------------|---------|-------|---------|--|
| 1    | ENSG0000001 | 0.39    | 2e-16 | 3e-18   | 35 x 30 actin-like 8 [Source:HGNC Symbol;Acc:HGNC:24018]                   |
| 2    | ENSG0000001 | 0.39    | 2e-16 | 3e-18   | 35 x 30 4-hydroxyphenylpyruvate dioxygenase-like [Source:HGNC S            |
| 3    | ENSG0000001 | 0.24    | 2e-16 | 3e-18   | 35 x 30 forkhead box D2 [Source:HGNC Symbol;Acc:HGNC:3803]                 |
| 4    | ENSG0000000 | 0.28    | 2e-16 | 3e-18   | 35 x 30 tetratricopeptide repeat domain 39A [Source:HGNC Symbol;/          |
| 5    | ENSG0000002 | 0.37    | 2e-16 | 3e-18   | 35 x 30  |
| 6    | ENSG0000001 | 0.42    | 2e-16 | 3e-18   | 35 x 30 apolipoprotein A-II [Source:HGNC Symbol;Acc:HGNC:601]              |
| 7    | ENSG0000001 | 0.16    | 2e-16 | 3e-18   | 34 x 30 tubulin folding cofactor E [Source:HGNC Symbol;Acc:HGNC::          |
| 8    | ENSG0000001 | 0.22    | 2e-16 | 3e-18   | 37 x 31 solute carrier family 5 (sodium/multivitamin and iodide cotrans    |
| 9    | ENSG0000001 | 0.22    | 2e-16 | 3e-18   | 34 x 30 formin-like 2 [Source:HGNC Symbol;Acc:HGNC:18267]                  |
| 10   | ENSG0000002 | 0.19    | 2e-16 | 3e-18   | 35 x 29  |
| 11   | ENSG0000001 | 0.28    | 2e-16 | 3e-18   | 35 x 30 myosin, light chain 3, alkali; ventricular, skeletal, slow [Source |
| 12   | ENSG0000001 | 0.26    | 2e-16 | 3e-18   | 34 x 31 epiregulin [Source:HGNC Symbol;Acc:HGNC:3443]                      |
| 13   | ENSG0000001 | 0.19    | 2e-16 | 3e-18   | 36 x 32 annexin A3 [Source:HGNC Symbol;Acc:HGNC:541]                       |
| 14   | ENSG0000001 | 0.73    | 2e-16 | 3e-18   | 34 x 30 exocyst complex component 3 [Source:HGNC Symbol;Acc:Hi             |
| 15   | ENSG0000001 | 0.17    | 2e-16 | 3e-18   | 35 x 33 H2A histone family, member Y [Source:HGNC Symbol;Acc:Hi            |
| 16   | ENSG0000001 | 0.17    | 2e-16 | 3e-18   | 34 x 29 CXXC finger protein 5 [Source:HGNC Symbol;Acc:HGNC:26              |
| 17   | ENSG0000001 | 0.22    | 2e-16 | 3e-18   | 34 x 30 glutamate receptor, ionotropic, AMPA 1 [Source:HGNC Symb           |
| 18   | ENSG0000001 | 0.3     | 2e-16 | 3e-18   | 35 x 30 sequestosome 1 [Source:HGNC Symbol;Acc:HGNC:11280]                 |
| 19   | ENSG0000001 | 0.27    | 2e-16 | 3e-18   | 35 x 29 chromosome 5 open reading frame 45 [Source:HGNC Symbc              |
| 20   | ENSG0000001 | 0.25    | 2e-16 | 3e-18   | 35 x 30  |

Profile

Spot



p-values



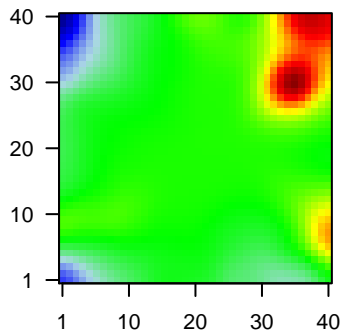
# 02.4535.001\_cH

## Local Summary

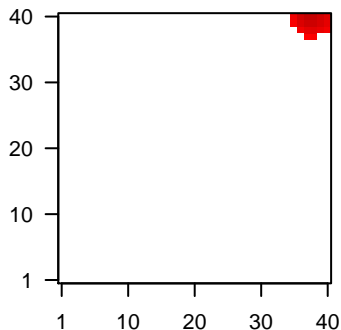
%DE = 0.92  
 # metagenes = 19  
 # genes = 385  
 # genes in genesets = 379  
  
 # genes with  $fdr < 0.1$  = 345 ( 303 + / 42 - )  
 # genes with  $fdr < 0.05$  = 335 ( 294 + / 41 - )  
 # genes with  $fdr < 0.01$  = 322 ( 281 + / 41 - )

$\langle r \rangle$  metagenes = 0.96  
 $\langle r \rangle$  genes = 0.58  
  
 $\langle FC \rangle$  = 0.13  
 $\langle t\text{-score} \rangle$  = 2.62  
 $\langle p\text{-value} \rangle$  = 0  
 $\langle fdr \rangle$  = 0.13

Profile



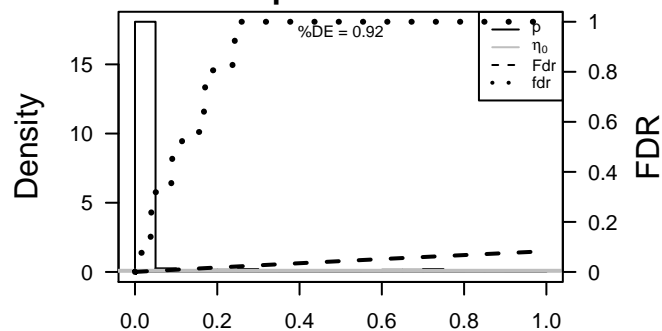
Spot



## Local Genelist

| Rank | ID          | log(FC) | p-value | fdr   | Description   |
|------|-------------|---------|---------|-------|---|
| 1    | ENSG0000001 | 0.16    | 2e-16   | 4e-17 | 36 x 40 regulator of chromosome condensation 2 [Source:HGNC Syn           |
| 2    | ENSG0000001 | 0.19    | 2e-16   | 4e-17 | 40 x 40 EPH receptor B2 [Source:HGNC Symbol;Acc:HGNC:3393]                |
| 3    | ENSG0000001 | 0.29    | 2e-16   | 4e-17 | 37 x 40 stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]                     |
| 4    | ENSG0000001 | 0.16    | 2e-16   | 4e-17 | 35 x 40 high mobility group nucleosomal binding domain 2 [Source:Hi       |
| 5    | ENSG0000001 | 0.17    | 2e-16   | 4e-17 | 38 x 40 regulator of chromosome condensation 1 [Source:HGNC Syn           |
| 6    | ENSG0000000 | 0.16    | 2e-16   | 4e-17 | 37 x 40 eukaryotic translation initiation factor 3, subunit I [Source:HGI |
| 7    | ENSG0000001 | 0.34    | 2e-16   | 4e-17 | 40 x 40 MARCKS-like 1 [Source:HGNC Symbol;Acc:HGNC:7142]                  |
| 8    | ENSG0000001 | 0.17    | 2e-16   | 4e-17 | 37 x 37 cell division cycle associated 8 [Source:HGNC Symbol;Acc:H        |
| 9    | ENSG0000001 | 0.21    | 2e-16   | 4e-17 | 40 x 39 cell division cycle 20 [Source:HGNC Symbol;Acc:HGNC:1722          |
| 10   | ENSG0000001 | 0.3     | 2e-16   | 4e-17 | 35 x 40 ribosomal protein S8 [Source:HGNC Symbol;Acc:HGNC:104             |
| 11   | ENSG0000001 | 0.36    | 2e-16   | 4e-17 | 38 x 39 peroxiredoxin 1 [Source:HGNC Symbol;Acc:HGNC:9352]                |
| 12   | ENSG0000001 | 0.21    | 2e-16   | 4e-17 | 40 x 40 PDZK1 interacting protein 1 [Source:HGNC Symbol;Acc:HGNC          |
| 13   | ENSG0000001 | 0.16    | 2e-16   | 4e-17 | 39 x 39 mitochondrial ribosomal protein L37 [Source:HGNC Symbol;#         |
| 14   | ENSG0000001 | 0.21    | 2e-16   | 4e-17 | 37 x 38 proprotein convertase subtilisin/kexin type 9 [Source:HGNC S      |
| 15   | ENSG0000000 | -0.32   | 2e-16   | 4e-17 | 40 x 40 chloride channel accessory 1 [Source:HGNC Symbol;Acc:HG           |
| 16   | ENSG0000001 | -0.26   | 2e-16   | 4e-17 | 40 x 40 regenerating islet-derived family, member 4 [Source:HGNC S        |
| 17   | ENSG0000001 | -0.21   | 2e-16   | 4e-17 | 40 x 40 intelectin 1 (galactofuranose binding) [Source:HGNC Symbol;       |
| 18   | ENSG0000002 | -0.24   | 2e-16   | 4e-17 | 40 x 40 left-right determination factor 1 [Source:HGNC Symbol;Acc:+       |
| 19   | ENSG0000001 | 0.21    | 2e-16   | 4e-17 | 40 x 40 keratinocyte associated protein 3 [Source:HGNC Symbol;Acc         |
| 20   | ENSG0000001 | -0.19   | 2e-16   | 4e-17 | 40 x 40 regenerating islet-derived 1 beta [Source:HGNC Symbol;Acc         |

p-values



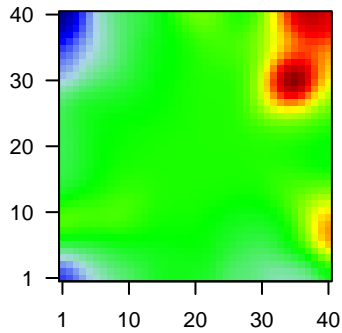
# 02.4535.001\_cH

## Local Summary

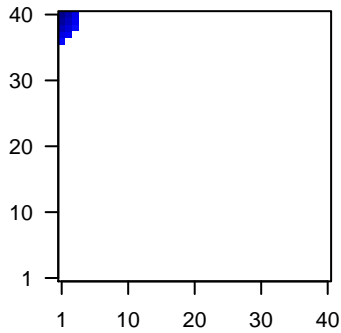
%DE = 0.97  
 # metagenes = 12  
 # genes = 228  
 # genes in genesets = 225  
  
 # genes with  $fdr < 0.1$  = 220 ( 8 + / 212 -)  
 # genes with  $fdr < 0.05$  = 220 ( 8 + / 212 -)  
 # genes with  $fdr < 0.01$  = 217 ( 8 + / 209 -)

$\langle r \rangle$  metagenes = 0.99  
 $\langle r \rangle$  genes = 0.79  
  
 $\langle FC \rangle$  = -0.18  
 $\langle t\text{-score} \rangle$  = -3.64  
 $\langle p\text{-value} \rangle$  = 0  
 $\langle fdr \rangle$  = 0.03

Profile



Spot



## Local Genelist

| Rank | ID          | log(FC) | p-value | fdr   | Description   |
|------|-------------|---------|---------|-------|---|
| 1    | ENSG0000001 | -0.17   | 2e-16   | 1e-17 | 1 x 40 chloride intracellular channel 4 [Source:HGNC Symbol;Acc:H   |
| 2    | ENSG0000001 | -0.22   | 2e-16   | 1e-17 | 1 x 38 cysteine-rich, angiogenic inducer, 61 [Source:HGNC Symbol    |
| 3    | ENSG0000001 | -0.16   | 2e-16   | 1e-17 | 2 x 40 olfactomedin-like 3 [Source:HGNC Symbol;Acc:HGNC:2495f       |
| 4    | ENSG0000001 | -0.34   | 2e-16   | 1e-17 | 1 x 38  |
| 5    | ENSG0000000 | -0.18   | 2e-16   | 1e-17 | 1 x 39 pleckstrin homology domain containing, family O member 1 [S  |
| 6    | ENSG0000001 | -0.27   | 2e-16   | 1e-17 | 1 x 38 pre-B-cell leukemia homeobox interacting protein 1 [Source:  |
| 7    | ENSG0000001 | -0.17   | 2e-16   | 1e-17 | 1 x 38 phosphoprotein enriched in astrocytes 15 [Source:HGNC Syr    |
| 8    | ENSG0000001 | -0.2    | 2e-16   | 1e-17 | 1 x 40 regulator of G-protein signaling 5 [Source:HGNC Symbol;Acc   |
| 9    | ENSG0000001 | -0.32   | 2e-16   | 1e-17 | 1 x 40 dermatopontin [Source:HGNC Symbol;Acc:HGNC:3011]             |
| 10   | ENSG0000001 | -0.37   | 2e-16   | 1e-17 | 1 x 40 regulator of G-protein signaling 2 [Source:HGNC Symbol;Acc   |
| 11   | ENSG0000001 | -0.37   | 2e-16   | 1e-17 | 1 x 40 cysteine and glycine-rich protein 1 [Source:HGNC Symbol;A    |
| 12   | ENSG0000001 | -0.35   | 2e-16   | 1e-17 | 1 x 40 leiomodulin 1 (smooth muscle) [Source:HGNC Symbol;Acc:HG     |
| 13   | ENSG0000000 | -0.2    | 2e-16   | 1e-17 | 1 x 40 protein phosphatase 1, regulatory subunit 12B [Source:HGNC   |
| 14   | ENSG0000001 | -0.32   | 2e-16   | 1e-17 | 1 x 40 BTG family, member 2 [Source:HGNC Symbol;Acc:HGNC:11         |
| 15   | ENSG0000000 | -0.23   | 2e-16   | 1e-17 | 1 x 40 ATPase, Ca++ transporting, plasma membrane 4 [Source:HG      |
| 16   | ENSG0000001 | -0.17   | 2e-16   | 1e-17 | 1 x 36 yippee-like 5 [Source:HGNC Symbol;Acc:HGNC:18329]            |
| 17   | ENSG0000001 | -0.62   | 2e-16   | 1e-17 | 1 x 40 actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml     |
| 18   | ENSG0000001 | -0.17   | 2e-16   | 1e-17 | 1 x 40 serum deprivation response [Source:HGNC Symbol;Acc:HG        |
| 19   | ENSG0000001 | -0.27   | 2e-16   | 1e-17 | 1 x 40 fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]             |
| 20   | ENSG0000001 | -0.33   | 2e-16   | 1e-17 | 1 x 40 insulin-like growth factor binding protein 5 [Source:HGNC Sy |

p-values

