

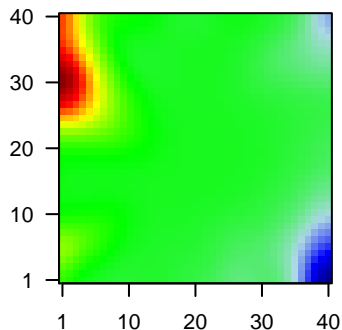
04.3047.001_cH

Global Summary

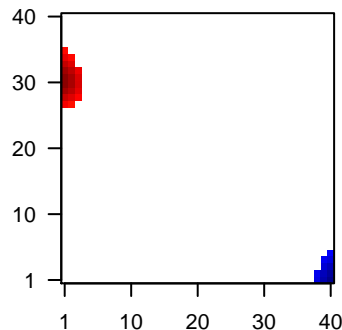
%DE = 0.26
 # genes with fdr < 0.2 = 5022 (2384 + / 2638 -)
 # genes with fdr < 0.1 = 4565 (2215 + / 2350 -)
 # genes with fdr < 0.05 = 4274 (2093 + / 2181 -)
 # genes with fdr < 0.01 = 3608 (1824 + / 1784 -)
 # genes in genesets = 18990

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

Profile



Regulated Spots



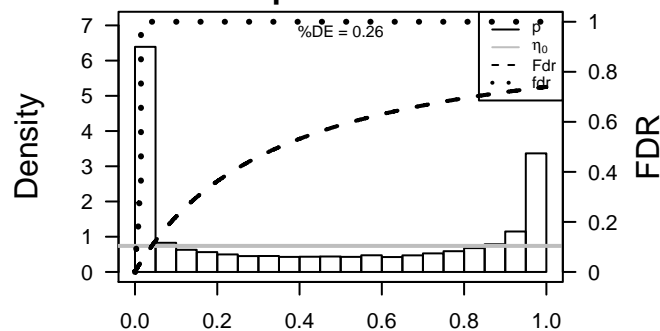
Global Genelist

| Rank | ID | log(FC) | fdr | p-value | Description |
|------|--------------|---------|-------|---------|--|
| 1 | ENSG00000001 | 0.34 | 2e-16 | 3e-15 | 1 x 33 matrix-remodelling associated 8 [Source:HGNC Symbol;Acc:ENSG00000000173] |
| 2 | ENSG00000001 | -0.21 | 2e-16 | 3e-15 | 40 x 8 aurora kinase A interacting protein 1 [Source:HGNC Symbol;Acc:ENSG00000000173] |
| 3 | ENSG00000002 | 0.38 | 2e-16 | 3e-15 | 1 x 26 cyclin L2 [Source:HGNC Symbol;Acc:HGNC:20570] |
| 4 | ENSG00000001 | 0.27 | 2e-16 | 3e-15 | 3 x 32 ERBB receptor feedback inhibitor 1 [Source:HGNC Symbol;Acc:ENSG00000000173] |
| 5 | ENSG00000000 | -0.2 | 2e-16 | 3e-15 | 38 x 40 enolase 1, (alpha) [Source:HGNC Symbol;Acc:HGNC:3350] |
| 6 | ENSG00000001 | 0.84 | 2e-16 | 3e-15 | 1 x 30 retinol binding protein 7, cellular [Source:HGNC Symbol;Acc:ENSG00000000173] |
| 7 | ENSG00000000 | 0.27 | 2e-16 | 3e-15 | 2 x 1 tumor necrosis factor receptor superfamily, member 1B [Source:HGNC Symbol;Acc:ENSG00000000173] |
| 8 | ENSG00000001 | -0.25 | 2e-16 | 3e-15 | 38 x 5 EF-hand domain family, member D2 [Source:HGNC Symbol;Acc:ENSG00000000173] |
| 9 | ENSG00000001 | -0.27 | 2e-16 | 3e-15 | 39 x 1 peptidyl arginine deiminase, type II [Source:HGNC Symbol;Acc:ENSG00000000173] |
| 10 | ENSG00000001 | -0.25 | 2e-16 | 3e-15 | 25 x 1 aldo-keto reductase family 7, member A3 (aflatoxin aldehyde reductase) [Source:HGNC Symbol;Acc:ENSG00000000173] |
| 11 | ENSG00000001 | -0.19 | 2e-16 | 3e-15 | 25 x 1 ring finger protein 186 [Source:HGNC Symbol;Acc:HGNC:25172] |
| 12 | ENSG00000001 | -0.32 | 2e-16 | 3e-15 | 37 x 1 calcium/calmodulin-dependent protein kinase II inhibitor 1 [Source:HGNC Symbol;Acc:ENSG00000000173] |
| 13 | ENSG00000001 | -0.19 | 2e-16 | 3e-15 | 38 x 1 cytidine deaminase [Source:HGNC Symbol;Acc:HGNC:1712] |
| 14 | ENSG00000001 | 0.63 | 2e-16 | 3e-15 | 1 x 33 low density lipoprotein receptor class A domain containing 2 [Source:HGNC Symbol;Acc:ENSG00000000173] |
| 15 | ENSG00000001 | 0.43 | 2e-16 | 3e-15 | 1 x 35 heparan sulfate proteoglycan 2 [Source:HGNC Symbol;Acc:ENSG00000000173] |
| 16 | ENSG00000001 | 0.28 | 2e-16 | 3e-15 | 1 x 3 complement component 1, q subcomponent, A chain [Source:HGNC Symbol;Acc:ENSG00000000173] |
| 17 | ENSG00000002 | -0.21 | 2e-16 | 3e-15 | 40 x 10 transcription elongation factor A (SII), 3 [Source:HGNC Symbol;Acc:ENSG00000000173] |
| 18 | ENSG00000001 | 0.39 | 2e-16 | 3e-15 | 33 x 1 inhibitor of DNA binding 3, dominant negative helix-loop-helix [Source:HGNC Symbol;Acc:ENSG00000000173] |
| 19 | ENSG00000001 | -0.24 | 2e-16 | 3e-15 | 40 x 7 UDP-galactose-4-epimerase [Source:HGNC Symbol;Acc:ENSG00000000173] |
| 20 | ENSG00000001 | -0.32 | 2e-16 | 3e-15 | 38 x 1 fucosidase, alpha-L-1, tissue [Source:HGNC Symbol;Acc:ENSG00000000173] |

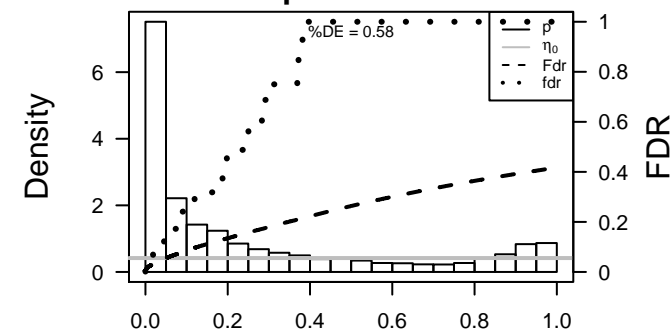
Global Geneset Analysis

| Rank | GSZ | p-value | #all | Geneset |
|-----------------------|--------|---------|------|---|
| <i>Overexpressed</i> | | | | |
| 1 | 30.36 | 0e+00 | 326 | GSEA C2SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP |
| 2 | 30.19 | 0e+00 | 196 | GSEA C2PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP |
| 3 | 28.65 | 0e+00 | 368 | GSEA C2LINDGREN_BLADDER_CANCER_CLUSTER_2B |
| 4 | 26.09 | 0e+00 | 198 | HM HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION |
| 5 | 24.7 | 1e-06 | 59 | LymphomaL1ENZ_Stromal signature 2 |
| 6 | 24.69 | 2e-06 | 478 | GSEA C2LIM_MAMMARY_STEM_CELL_UP |
| 7 | 24.28 | 5e-06 | 314 | LymphomaL1opp_June14_MMML937_tumors+controls_group.overexpression |
| 8 | 24.05 | 5e-06 | 315 | LymphomaL1WIRTH_lymphoma937_spot E |
| 9 | 23.73 | 6e-06 | 418 | GSEA C2SWEET_LUNG_CANCER_KRAS_DN |
| 10 | 22.48 | 6e-06 | 73 | GSEA C2KIM_GLIS2_TARGETS_UP |
| 11 | 22.24 | 6e-06 | 261 | LymphomaL1ENZ_Stromal signature 1 |
| 12 | 22.14 | 8e-06 | 202 | CC extracellular matrix |
| 13 | 21.9 | 8e-06 | 332 | Colon CancerTrack_CRC_TCGA_corr_J_msi-h_UP_mss_DN |
| 14 | 21.7 | 9e-06 | 692 | GSEA C2WONG_ADULT_TISSUE_STEM_MODULE |
| 15 | 21.68 | 9e-06 | 148 | Colon CancerCancerisa_CRC-cluster-a |
| 16 | 21.27 | 9e-06 | 55 | GSEA C2CROONQUIST_STROMAL_STIMULATION_UP |
| 17 | 20.68 | 1e-05 | 78 | GSEA C2NAKAYAMA_SOFT_TISSUE_TUMORS_PCA2_DN |
| 18 | 20.66 | 1e-05 | 248 | GSEA C2ZONDER_CDH1_TARGETS_2_UP |
| 19 | 20.43 | 1e-05 | 261 | GSEA C2NABA_CORE_MATRISOME |
| 20 | 20.36 | 1e-05 | 62 | GSEA C2ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGN |
| <i>Underexpressed</i> | | | | |
| 1 | -19.01 | 2e-05 | 251 | GSEA C2NAMUNYOKOLI_OVARIAN_CANCER_LMP_UP |
| 2 | -16.36 | 2e-05 | 126 | GSEA C2VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN |
| 3 | -16.3 | 2e-05 | 429 | GSEA C2CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL |
| 4 | -16.01 | 2e-05 | 412 | GSEA C2LIM_MAMMARY_STEM_CELL_DN |
| 5 | -15.72 | 3e-05 | 144 | LymphomaL1WIRTH_lymphoma937_spot G |
| 6 | -15.12 | 3e-05 | 222 | GSEA C2COLDREN_GEFITINIB_RESISTANCE_DN |
| 7 | -15.04 | 3e-05 | 142 | LymphomaL1opp_June14_MMML937_tumors+controls_group.overexpression |
| 8 | -14.66 | 3e-05 | 132 | GSEA C2NAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_UP |
| 9 | -13.69 | 4e-05 | 110 | Colon CancerCancerisa_CRC-cluster-h |
| 10 | -13.2 | 4e-05 | 643 | Colon CancerCancerbcke_TCGA_meth_kmeans_J_CIMP.H_DN |
| 11 | -13.16 | 4e-05 | 425 | CC mitochondrial inner membrane |
| 12 | -12.98 | 4e-05 | 104 | Colon CancerCancerTrack_CRC_TCGA_group.over_A_normal_UP |
| 13 | -12.03 | 7e-05 | 137 | Tissue WIRTH_Mucosa |
| 14 | -11.88 | 8e-05 | 400 | GSEA C2VECCHI_GASTRIC_CANCER_EARLY_UP |
| 15 | -11.37 | 1e-04 | 616 | Colon CancerCancerbcke_TCGA-expr_kmeans_M_CIMP.H_DN |
| 16 | -11.35 | 1e-04 | 455 | GSEA C2ZONDER_CDH1_TARGETS_2_DN |
| 17 | -11.27 | 1e-04 | 688 | Colon CancerCancerbcke_TCGA-expr_kmeans_L_CIMP.H_UP_Cluster4_DN |
| 18 | -11.16 | 1e-04 | 32 | GSEA C2AIGNER_ZEB1_TARGETS |
| 19 | -11.05 | 1e-04 | 326 | GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN |
| 20 | -11.03 | 1e-04 | 807 | LymphomaL1opp_June14_MMML937_tumors+controls_group.overexpression |

p-values



p-values



04.3047.001_cH

Local Summary

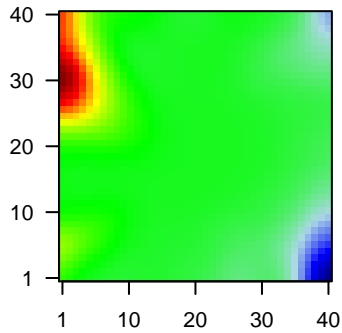
%DE = 1
 # metagenes = 22
 # genes = 309
 # genes in genesets = 308

 # genes with $fdr < 0.1$ = 307 (307 + / 0 -)
 # genes with $fdr < 0.05$ = 307 (307 + / 0 -)
 # genes with $fdr < 0.01$ = 307 (307 + / 0 -)

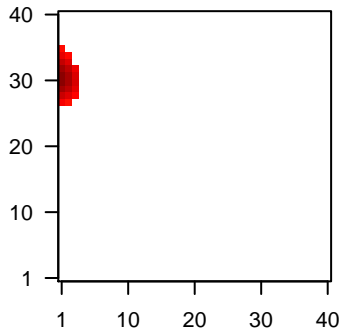
$\langle r \rangle$ metagenes = 0.93
 $\langle r \rangle$ genes = 0.62

 $\langle FC \rangle$ = 0.44
 $\langle t\text{-score} \rangle$ = 8.84
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0

Profile



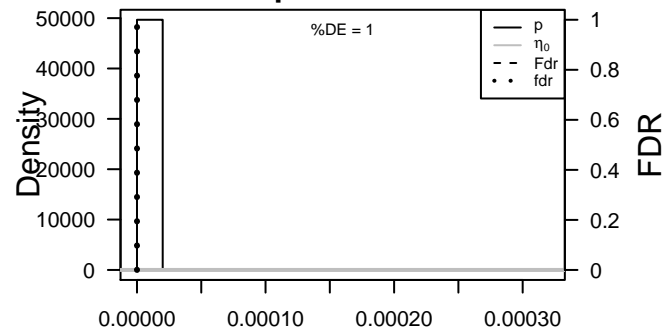
Spot



Local Genelist

| Rank | ID | log(FC) | fdr | p-value | Description |
|------|-------------|---------|-------|---------|---|
| 1 | ENSG0000001 | 0.34 | 2e-16 | 7e-19 | 1 x 33 matrix-remodelling associated 8 [Source:HGNC Symbol;Acc: |
| 2 | ENSG0000001 | 0.27 | 2e-16 | 7e-19 | 3 x 32 ERBB receptor feedback inhibitor 1 [Source:HGNC Symbol;A |
| 3 | ENSG0000001 | 0.84 | 2e-16 | 7e-19 | 1 x 30 retinol binding protein 7, cellular [Source:HGNC Symbol;Acc:I |
| 4 | ENSG0000001 | 0.63 | 2e-16 | 7e-19 | 1 x 33 low density lipoprotein receptor class A domain containing 2 [|
| 5 | ENSG0000001 | 0.43 | 2e-16 | 7e-19 | 1 x 35 heparan sulfate proteoglycan 2 [Source:HGNC Symbol;Acc:H |
| 6 | ENSG0000001 | 0.26 | 2e-16 | 7e-19 | 3 x 32 selenoprotein N, 1 [Source:HGNC Symbol;Acc:HGNC:15999] |
| 7 | ENSG0000001 | 0.5 | 2e-16 | 7e-19 | 1 x 30 gap junction protein, alpha 4, 37kDa [Source:HGNC Symbol;v |
| 8 | ENSG0000001 | 0.44 | 2e-16 | 7e-19 | 1 x 29 hes-related family bHLH transcription factor with YRPW moti |
| 9 | ENSG0000000 | 0.31 | 2e-16 | 7e-19 | 2 x 28 tyrosine kinase with immunoglobulin-like and EGF-like doma |
| 10 | ENSG0000001 | 0.19 | 2e-16 | 7e-19 | 2 x 33 jun proto-oncogene [Source:HGNC Symbol;Acc:HGNC:6204 |
| 11 | ENSG0000001 | 0.24 | 2e-16 | 7e-19 | 1 x 27 interferon-induced protein 44 [Source:HGNC Symbol;Acc:HC |
| 12 | ENSG0000001 | 0.55 | 2e-16 | 7e-19 | 1 x 30 adhesion G protein-coupled receptor L4 [Source:HGNC Sym |
| 13 | ENSG0000001 | 0.19 | 2e-16 | 7e-19 | 3 x 32 guanylate binding protein 1, interferon-inducible [Source:HG |
| 14 | ENSG0000001 | 0.34 | 2e-16 | 7e-19 | 2 x 29 coagulation factor III (thromboplastin, tissue factor) [Source:H |
| 15 | ENSG0000001 | 0.47 | 2e-16 | 7e-19 | 1 x 35 calponin 3, acidic [Source:HGNC Symbol;Acc:HGNC:2157] |
| 16 | ENSG0000000 | 0.48 | 2e-16 | 7e-19 | 1 x 29 palmdelphin [Source:HGNC Symbol;Acc:HGNC:15846] |
| 17 | ENSG0000001 | 0.73 | 2e-16 | 7e-19 | 1 x 30 |
| 18 | ENSG0000001 | 0.3 | 2e-16 | 7e-19 | 2 x 33 chromosome 1 open reading frame 54 [Source:HGNC Symbc |
| 19 | ENSG0000001 | 0.48 | 2e-16 | 7e-19 | 1 x 30 myeloid cell leukemia 1 [Source:HGNC Symbol;Acc:HGNC:6 |
| 20 | ENSG0000001 | 0.35 | 2e-16 | 7e-19 | 1 x 29 cathepsin K [Source:HGNC Symbol;Acc:HGNC:2536] |

p-values



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Local Summary

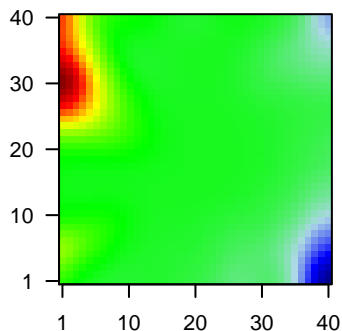
%DE = 0.99
 # metagenes = 11
 # genes = 236
 # genes in genesets = 233

 # genes with $fdr < 0.1$ = 233 (4 + / 229 -)
 # genes with $fdr < 0.05$ = 231 (2 + / 229 -)
 # genes with $fdr < 0.01$ = 231 (2 + / 229 -)

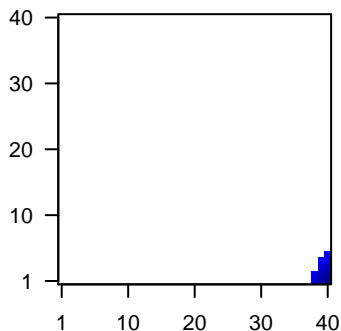
$\langle r \rangle$ metagenes = 0.98
 $\langle r \rangle$ genes = 0.66

 $\langle FC \rangle$ = -0.42
 $\langle t\text{-score} \rangle$ = -8.44
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.02

Profile



Spot



Local Genelist

| Rank | ID | log(FC) | p-value | fdr | Description |
|------|-------------|---------|---------|-------|--|
| 1 | ENSG0000001 | -0.27 | 2e-16 | 2e-18 | 39 x 1 peptidyl arginine deiminase, type II [Source:HGNC Symbol;Acc:HGNC:1712] |
| 2 | ENSG0000001 | -0.19 | 2e-16 | 2e-18 | 38 x 1 cytidine deaminase [Source:HGNC Symbol;Acc:HGNC:1712] |
| 3 | ENSG0000001 | -0.32 | 2e-16 | 2e-18 | 38 x 1 fucosidase, alpha-L- 1, tissue [Source:HGNC Symbol;Acc:HGNC:1712] |
| 4 | ENSG0000001 | -0.22 | 2e-16 | 2e-18 | 40 x 3 SH3 domain binding glutamate-rich protein like 3 [Source:HGNC Symbol;Acc:HGNC:1712] |
| 5 | ENSG0000001 | -0.29 | 2e-16 | 2e-18 | 39 x 4 ribosomal protein S6 kinase, 90kDa, polypeptide 1 [Source:HGNC Symbol;Acc:HGNC:1712] |
| 6 | ENSG0000001 | -0.85 | 2e-16 | 2e-18 | 40 x 1 stratifin [Source:HGNC Symbol;Acc:HGNC:10773] |
| 7 | ENSG0000001 | -0.42 | 2e-16 | 2e-18 | 40 x 1 serine incorporator 2 [Source:HGNC Symbol;Acc:HGNC:23201] |
| 8 | ENSG0000001 | -0.3 | 2e-16 | 2e-18 | 40 x 5 KIAA1522 [Source:HGNC Symbol;Acc:HGNC:29301] |
| 9 | ENSG0000001 | -0.78 | 2e-16 | 2e-18 | 40 x 1 transmembrane protein 54 [Source:HGNC Symbol;Acc:HGNC:20657] |
| 10 | ENSG0000000 | -0.52 | 2e-16 | 2e-18 | 40 x 1 guanylate cyclase activator 2B (uroguanylin) [Source:HGNC Symbol;Acc:HGNC:21297] |
| 11 | ENSG0000001 | -0.98 | 2e-16 | 2e-18 | 40 x 1 guanylate cyclase activator 2A (guanylin) [Source:HGNC Symbol;Acc:HGNC:21297] |
| 12 | ENSG0000002 | -0.27 | 2e-16 | 2e-18 | 38 x 2 chromosome 1 open reading frame 210 [Source:HGNC Symbol;Acc:HGNC:20657] |
| 13 | ENSG0000001 | -0.95 | 2e-16 | 2e-18 | 40 x 1 tetraspanin 1 [Source:HGNC Symbol;Acc:HGNC:20657] |
| 14 | ENSG0000001 | -0.38 | 2e-16 | 2e-18 | 40 x 5 24-dehydrocholesterol reductase [Source:HGNC Symbol;Acc:HGNC:21297] |
| 15 | ENSG0000000 | -0.59 | 2e-16 | 2e-18 | 40 x 1 chloride channel accessory 4 [Source:HGNC Symbol;Acc:HGNC:21297] |
| 16 | ENSG0000001 | -0.5 | 2e-16 | 2e-18 | 40 x 3 EPS8-like 3 [Source:HGNC Symbol;Acc:HGNC:21297] |
| 17 | ENSG0000001 | -0.27 | 2e-16 | 2e-18 | 40 x 4 ATPase, Na+/K+ transporting, alpha 1 polypeptide [Source:HGNC Symbol;Acc:HGNC:21297] |
| 18 | ENSG0000001 | -0.48 | 2e-16 | 2e-18 | 40 x 1 3-hydroxy-3-methylglutaryl-CoA synthase 2 (mitochondrial) [Source:HGNC Symbol;Acc:HGNC:21297] |
| 19 | ENSG0000001 | -0.35 | 2e-16 | 2e-18 | 38 x 1 cathepsin S [Source:HGNC Symbol;Acc:HGNC:2545] |
| 20 | ENSG0000001 | -0.34 | 2e-16 | 2e-18 | 40 x 1 selenium binding protein 1 [Source:HGNC Symbol;Acc:HGNC:2545] |

p-values

