

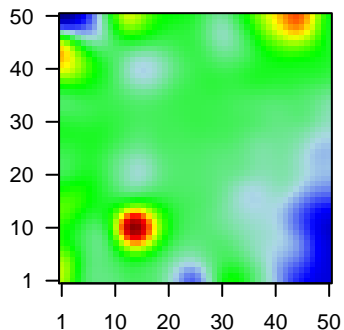
GW_104

Global Summary

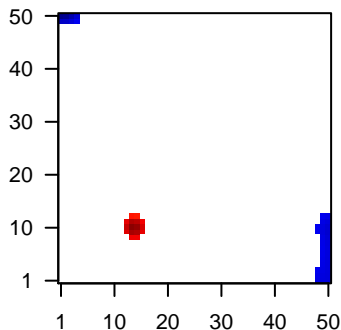
%DE = 0.15
 # genes with $fdr < 0.2$ = 1937 (1066 + / 871 -)
 # genes with $fdr < 0.1$ = 1573 (877 + / 696 -)
 # genes with $fdr < 0.05$ = 1275 (714 + / 561 -)
 # genes with $fdr < 0.01$ = 891 (510 + / 381 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.09
 <fdr> = 0.85

Profile



Regulated Spots



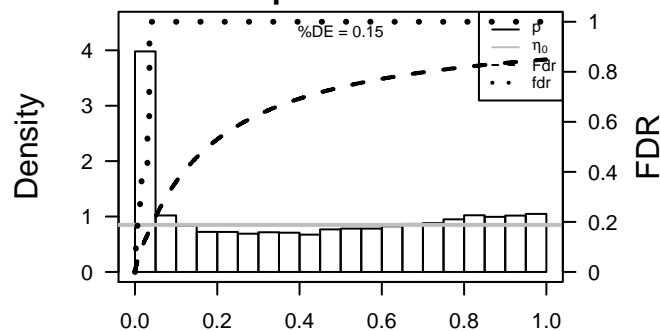
Global Genelist

| Rank | ID | log(FC) | fdr | p-value | Description |
|------|-----------|---------|-------|---------|---|
| 1 | 79852 | -1.42 | 2e-16 | 3e-14 | 3 x 50 epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760] |
| 2 | 57016 | 1.94 | 2e-16 | 3e-14 | 1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase) |
| 3 | 441282 | 1.34 | 2e-16 | 3e-14 | 1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S] |
| 4 | 8644 | 1.36 | 2e-16 | 3e-14 | 1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Syr] |
| 5 | 1109 | 1.42 | 2e-16 | 3e-14 | 13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Syr] |
| 6 | 501 | -2.17 | 2e-16 | 3e-14 | 6 x 46 aldehyde dehydrogenase 7 family, member A1 [Source:HGNC] |
| 7 | 55107 | 2.55 | 2e-16 | 3e-14 | 1 x 5 anoctamin 1, calcium activated chloride channel [Source:HGNC] |
| 8 | 25805 | 1.4 | 2e-16 | 3e-14 | 8 x 1 BMP and activin membrane-bound inhibitor [Source:HGNC S] |
| 9 | 260436 | 2.64 | 2e-16 | 3e-14 | 50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc] |
| 10 | 375791 | -1.66 | 2e-16 | 3e-14 | 1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Symt] |
| 11 | 51806 | -2.22 | 2e-16 | 3e-14 | 4 x 50 calmodulin-like 5 [Source:HGNC Symbol;Acc:18180] |
| 12 | 834 | 1.34 | 2e-16 | 3e-14 | 32 x 1 caspase 1, apoptosis-related cysteine peptidase [Source:HGNC] |
| 13 | 6363 | -1.64 | 2e-16 | 3e-14 | 50 x 1 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc] |
| 14 | 6364 | 1.81 | 2e-16 | 3e-14 | 46 x 1 chemokine (C-C motif) ligand 20 [Source:HGNC Symbol;Acc] |
| 15 | 894 | -1.55 | 2e-16 | 3e-14 | 50 x 4 cyclin D2 [Source:HGNC Symbol;Acc:1583] |
| 16 | 100133941 | -1.46 | 2e-16 | 3e-14 | 3 x 50 CD24 molecule [Source:HGNC Symbol;Acc:1645] |
| 17 | 948 | 2.41 | 2e-16 | 3e-14 | 6 x 44 CD36 molecule (thrombospondin receptor) [Source:HGNC S] |
| 18 | 1066 | 2.53 | 2e-16 | 3e-14 | 14 x 50 carboxylesterase 1 [Source:HGNC Symbol;Acc:1863] |
| 19 | 22802 | -2.76 | 2e-16 | 3e-14 | 1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20] |
| 20 | 9022 | -1.88 | 2e-16 | 3e-14 | 1 x 50 chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2] |

Global Geneset Analysis

| Rank | GSZ | p-value | #all | Geneset |
|-----------------------|-------|---------|------|--|
| <i>Overexpressed</i> | | | | |
| 1 | 12.97 | NULL | 142 | Glio wilscher_GBM_Verhaak-CL_expression_C_up |
| 2 | 12.97 | NULL | 142 | Glio wilscher_GBM_Verhaak-PNmut_expression_C_down |
| 3 | 7.26 | NULL | 12 | BP hemidesmosome assembly |
| 4 | 6.96 | NULL | 530 | Cancer Lembcke_Normal vs Adenoma |
| 5 | 6.73 | NULL | 1033 | Chr Chr 2 |
| 6 | 6.69 | NULL | 1720 | Chr Chr 1 |
| 7 | 6.3 | NULL | 16 | GSEA C2GRAHAM_NORMAL QUIESCENT_VS_NORMAL DIVIDING_DN |
| 8 | 6.29 | NULL | 68 | Glio cultured astroglia vs. in vivo astrocytes |
| 9 | 5.94 | NULL | 10 | GSEA C2MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP |
| 10 | 5.78 | NULL | 153 | CC endoplasmic reticulum lumen |
| 11 | 5.75 | NULL | 918 | Chr Chr 17 |
| 12 | 5.72 | NULL | 11 | MF glutathione binding |
| 13 | 5.66 | NULL | 16 | GSEA C2FARMER_BREAST_CANCER_CLUSTER_2 |
| 14 | 5.65 | NULL | 14 | GSEA C2ZHAN_MULTIPLE_MYELOMA_PR_UP |
| 15 | 5.65 | NULL | 370 | BP mitotic cell cycle |
| 16 | 5.65 | NULL | 14 | MMML C2CACIEJ_MMML_4 |
| 17 | 5.62 | NULL | 15 | GSEA C2SMID_BREAST_CANCER_LUMINAL_A_DN |
| 18 | 5.58 | NULL | 15 | GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL QUIESCENT_UP |
| 19 | 5.56 | NULL | 572 | Disease GUDJ_poriasis up |
| 20 | 5.5 | NULL | 57 | Glio developing astrocytes |
| <i>Underexpressed</i> | | | | |
| 1 | -7.39 | NULL | 602 | Chr Chr 10 |
| 2 | -7.33 | NULL | 16 | GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_D |
| 3 | -7.27 | NULL | 6 | GSEA C2SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP |
| 4 | -6.81 | NULL | 135 | H.Tiss WIRTH_Mucosa |
| 5 | -6.12 | NULL | 15 | GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E |
| 6 | -5.7 | NULL | 44 | MF structural constituent of muscle |
| 7 | -5.38 | NULL | 16 | GSEA C2CROMER_TUMORIGENESIS_DN |
| 8 | -5.28 | NULL | 15 | CC MHC class II protein complex |
| 9 | -5.22 | NULL | 92 | BP translational elongation |
| 10 | -4.78 | NULL | 81 | BP viral transcription |
| 11 | -4.66 | NULL | 519 | Chr Chr 14 |
| 12 | -4.6 | NULL | 21 | CC cornified envelope |
| 13 | -4.59 | NULL | 957 | Chr Chr 11 |
| 14 | -4.56 | NULL | 42 | BP keratinization |
| 15 | -4.56 | NULL | 8 | GSEA C2LIU_CDX2_TARGETS_DN |
| 16 | -4.55 | NULL | 16 | H.Tiss WIRTH_Hippocampus |
| 17 | -4.49 | NULL | 127 | H.Tiss WIRTH_Muscle |
| 18 | -4.45 | NULL | 15 | GSEA C2HOSHIDA_LIVER_CANCER_SUBCLASS_S3 |
| 19 | -4.44 | NULL | 417 | H.Tiss WIRTH_Immune system |
| 20 | -4.43 | NULL | 15 | GSEA C2E_SKI_TARGETS_UP |

p-values



GW_104

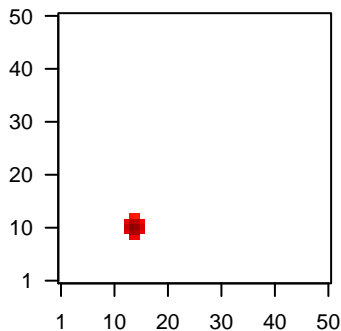
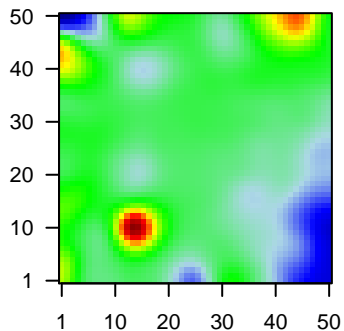
Local Summary

%DE = 0.67
 # metagenes = 16
 # genes = 81
 # genes in genesets = 57
 # genes with fdr < 0.1 = 53 (50 + / 3 -)
 # genes with fdr < 0.05 = 51 (48 + / 3 -)
 # genes with fdr < 0.01 = 49 (46 + / 3 -)

<r> metagenes = 0.98
 <r> genes = 0.34
 <FC> = 1.15
 <shrinkage-t> = 40.27
 <p-value> = 0
 <fdr> = 0.33

Profile

Spot



Local Genelist

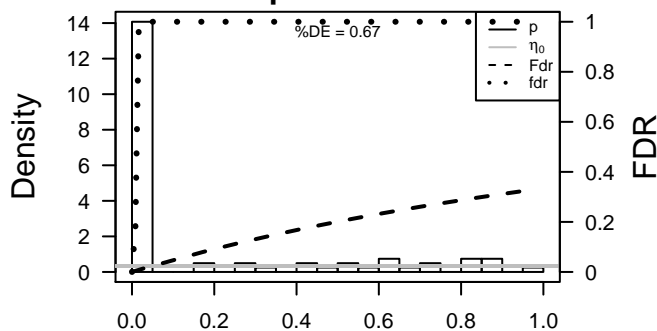
| Rank | ID | log(FC) | fdr | p-value | Description |
|------|-----------|---------|-------|---------|---|
| 1 | 170712 | 1.37 | 2e-16 | 2e-16 | 15 x 11 cytochrome c oxidase subunit VIIIb2 [Source:HGNC Symbol;Acc:21386] |
| 2 | 441520 | 2.94 | 2e-16 | 2e-16 | 14 x 11 cancer/testis antigen family 45, member A2 [Source:HGNC Symbol;Acc:21386] |
| 3 | 56884 | 1.82 | 2e-16 | 2e-16 | 16 x 11 follistatin-like 5 [Source:HGNC Symbol;Acc:21386] |
| 4 | 729428 | 3.81 | 2e-16 | 2e-16 | 14 x 11 G antigen 12C [Source:HGNC Symbol;Acc:28402] |
| 5 | 729422 | 3.93 | 2e-16 | 2e-16 | 14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778] |
| 6 | 100132399 | 2.05 | 2e-16 | 2e-16 | 14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778] |
| 7 | 729431 | 1.87 | 2e-16 | 2e-16 | 14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778] |
| 8 | 100008586 | 3.59 | 2e-16 | 2e-16 | 14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778] |
| 9 | 645073 | 3.74 | 2e-16 | 2e-16 | 14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778] |
| 10 | 729442 | 3.82 | 2e-16 | 2e-16 | 14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778] |
| 11 | 26748 | 3.49 | 2e-16 | 2e-16 | 14 x 11 G antigen 12I [Source:HGNC Symbol;Acc:4105] |
| 12 | 729396 | 3.12 | 2e-16 | 2e-16 | 14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778] |
| 13 | 729447 | 3.28 | 2e-16 | 2e-16 | 14 x 11 G antigen 2A [Source:HGNC Symbol;Acc:4099] |
| 14 | 645037 | 3.95 | 2e-16 | 2e-16 | 14 x 11 G antigen 2C [Source:HGNC Symbol;Acc:31958] |
| 15 | 26749 | 3.38 | 2e-16 | 2e-16 | 14 x 11 G antigen 2E [Source:HGNC Symbol;Acc:31960] |
| 16 | 2576 | 3.84 | 2e-16 | 2e-16 | 14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778] |
| 17 | 2577 | 3.62 | 2e-16 | 2e-16 | 14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778] |
| 18 | 2578 | 2.16 | 2e-16 | 2e-16 | 14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778] |
| 19 | 2579 | 2.51 | 2e-16 | 2e-16 | 14 x 11 G antigen 12I [Source:HGNC Symbol;Acc:4105] |
| 20 | 100101629 | 2.86 | 2e-16 | 2e-16 | 14 x 11 G antigen 2E [Source:HGNC Symbol;Acc:31960] |

Local Geneset Analysis

Overexpression

| Rank | GSZ | p-value | #in/all | Geneset |
|------|-------|---------|----------|--|
| 1 | 17.85 | NULL | 30 / 630 | Chr Chr X |
| 2 | 13.36 | NULL | 1 / 12 | GSEA C2RAY_TARGETS_OF_P210_BCR_ABL_FUSION_UP |
| 3 | 9.91 | NULL | 1 / 11 | GSEA C2SU_PLACENTA |
| 4 | 9.69 | NULL | 1 / 6 | GSEA C2NIELSEN_LEIOMYOSARCOMA_UP |
| 5 | 9.56 | NULL | 1 / 4 | GSEA C2WEBER_METHYLATED_ICP_IN_SPERM_DN |
| 6 | 8.46 | NULL | 1 / 14 | GSEA C2NIELSEN_GIST |
| 7 | 8.09 | NULL | 1 / 15 | GSEA C2BROWNE_HCMV_INFECTION_8HR_DN |
| 8 | 6.87 | NULL | 1 / 14 | GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_B |
| 9 | 6.79 | NULL | 1 / 6 | GSEA C2NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP |
| 10 | 6.42 | NULL | 1 / 17 | BP positive regulation of interleukin-1 beta secretion |
| 11 | 6.04 | NULL | 1 / 7 | GSEA C2NIELSEN_SYNOVIAL_SARCOMA_UP |
| 12 | 5.91 | NULL | 1 / 21 | BP negative regulation of Notch signaling pathway |
| 13 | 5.69 | NULL | 1 / 13 | CC mitochondrial respiratory chain |
| 14 | 5.48 | NULL | 1 / 8 | GSEA C2WEBER_METHYLATED_ICP_IN_FIBROBLAST |
| 15 | 4.96 | NULL | 1 / 11 | Glio willscher_GBM_Verhaak-CL_expression_M_down |
| 16 | 4.96 | NULL | 1 / 11 | Glio willscher_GBM_Verhaak-MES_expression_M_down |
| 17 | 4.96 | NULL | 1 / 11 | Glio willscher_GBM_Verhaak-PNmut_expression_M_up |
| 18 | 4.93 | NULL | 9 / 120 | H Tiss WIRTH_Testis |
| 19 | 4.76 | NULL | 6 / 419 | CC cellular_component |
| 20 | 4.73 | NULL | 8 / 481 | BP biological_process |
| 21 | 4.33 | NULL | 1 / 7 | GSEA C2REACTOME_AMINE_LIGAND_BINDING_RECEPTORS |
| 22 | 4.31 | NULL | 1 / 12 | GSEA C2HO_LIVER_CANCER_VASCULAR_INVASION |
| 23 | 4.29 | NULL | 9 / 549 | MF molecular_function |
| 24 | 4.1 | NULL | 1 / 7 | GSEA C2KONDO_PROSTATE_CANCER_WITH_H3K27ME3 |
| 25 | 3.95 | NULL | 1 / 37 | BP positive regulation of cysteine-type endopeptidase activity involved in |
| 26 | 3.91 | NULL | 1 / 13 | GSEA C2HATADA_METHYLATED_IN_LUNG_CANCER_DN |
| 27 | 3.91 | NULL | 1 / 13 | GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_BRAIN_UP |
| 28 | 3.72 | NULL | 1 / 14 | BP negative regulation of retinoic acid receptor signaling pathway |
| 29 | 3.72 | NULL | 1 / 14 | GSEA C2KORKOLA_EMBRYONIC_CARCINOMA_VS_SEMINOMA_DN |
| 30 | 3.64 | NULL | 1 / 26 | MF cytochrome-c oxidase activity |
| 31 | 3.55 | NULL | 1 / 15 | GSEA C2L_WILMS_TUMOR |
| 32 | 3.55 | NULL | 1 / 15 | GSEA C2REACTOME_ADHERENS_JUNCTIONS_INTERACTIONS |
| 33 | 3.4 | NULL | 1 / 16 | GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP |
| 34 | 3.16 | NULL | 1 / 10 | GSEA C2BOYERINAS_ONCOFETAL_TARGETS_OF_LET7A1 |
| 35 | 3.16 | NULL | 1 / 10 | GSEA C2CONRAD_STEM_CELL |
| 36 | 3.04 | NULL | 1 / 19 | MF retinoic acid receptor binding |
| 37 | 2.99 | NULL | 1 / 57 | Glio developing astrocytes |
| 38 | 2.96 | NULL | 1 / 11 | GSEA C2DODONNELL_TFRC_TARGETS_DN |
| 39 | 2.95 | NULL | 1 / 58 | Glio OPC |
| 40 | 2.92 | NULL | 1 / 13 | GSEA C2PIEOLI_LG11_TARGETS_DN |

p-values



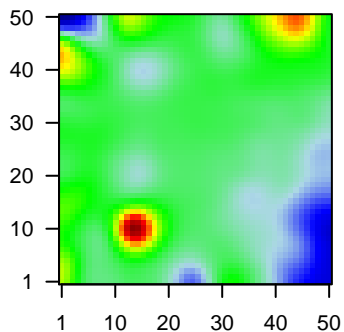
GW_104

Local Summary

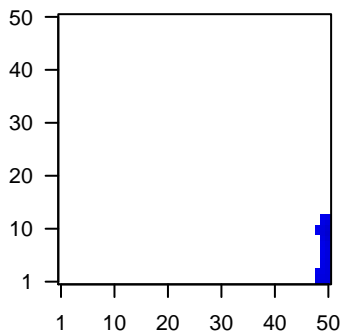
%DE = 0.7
 # metagenes = 31
 # genes = 491
 # genes in genesets = 488
 # genes with $fdr < 0.1 = 252$ (29 + / 223 -)
 # genes with $fdr < 0.05 = 205$ (23 + / 182 -)
 # genes with $fdr < 0.01 = 146$ (18 + / 128 -)

$\langle r \rangle$ metagenes = 0.79
 $\langle r \rangle$ genes = 0.3
 $\langle FC \rangle = -0.29$
 $\langle \text{shrinkage-t} \rangle = -10.01$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.55$

Profile



Spot



Local Genelist

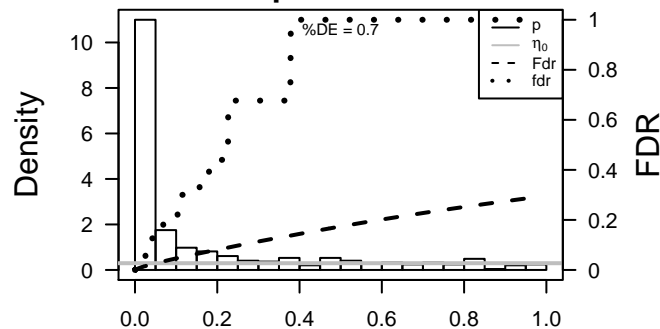
| Rank | ID | log(FC) | fdr | p-value | Description |
|------|--------|---------|-------|---------|--|
| 1 | 260436 | 2.64 | 2e-16 | 5e-15 | 50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc |
| 2 | 6363 | -1.64 | 2e-16 | 5e-15 | 50 x 1 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc |
| 3 | 894 | -1.55 | 2e-16 | 5e-15 | 50 x 4 cyclin D2 [Source:HGNC Symbol;Acc:1583] |
| 4 | 8857 | -1.84 | 2e-16 | 5e-15 | 50 x 13 Fc fragment of IgG binding protein [Source:HGNC Symbol;Ac |
| 5 | 6192 | -1.6 | 2e-16 | 5e-15 | 50 x 9 ribosomal protein S4, Y-linked 1 [Source:HGNC Symbol;Acc |
| 6 | 6422 | 2.46 | 2e-16 | 5e-15 | 50 x 8 secreted frizzled-related protein 1 [Source:HGNC Symbol;Ac |
| 7 | 7033 | -1.41 | 2e-16 | 5e-15 | 50 x 10 trefoil factor 3 (intestinal) [Source:HGNC Symbol;Acc:11757] |
| 8 | 10551 | -1.26 | 8e-15 | 6e-13 | 50 x 10 anterior gradient 2 [Source:HGNC Symbol;Acc:328] |
| 9 | 347 | -1.26 | 8e-15 | 1e-12 | 50 x 7 apolipoprotein D [Source:HGNC Symbol;Acc:612] |
| 10 | 2745 | 1.24 | 2e-14 | 2e-12 | 50 x 3 glutaredoxin (thioltransferase) [Source:HGNC Symbol;Acc:43 |
| 11 | 4256 | -1.23 | 3e-14 | 5e-12 | 50 x 6 matrix Gla protein [Source:HGNC Symbol;Acc:7060] |
| 12 | 51316 | -1.22 | 7e-14 | 2e-11 | 50 x 13 placenta-specific 8 [Source:HGNC Symbol;Acc:19254] |
| 13 | 6451 | -1.18 | 3e-13 | 2e-11 | 50 x 5 SH3 domain binding glutamic acid-rich protein like [Source:H |
| 14 | 2568 | -1.18 | 4e-13 | 1e-10 | 50 x 13 gamma-aminobutyric acid (GABA) A receptor, pi [Source:HG |
| 15 | 10232 | -1.14 | 2e-12 | 1e-10 | 50 x 11 mesothelin [Source:HGNC Symbol;Acc:7371] |
| 16 | 84952 | -1.14 | 2e-12 | 1e-10 | 50 x 10 cingulin-like 1 [Source:HGNC Symbol;Acc:25931] |
| 17 | 3488 | -1.13 | 3e-12 | 4e-10 | 50 x 7 insulin-like growth factor binding protein 5 [Source:HGNC Sy |
| 18 | 3128 | -1.12 | 6e-12 | 6e-10 | 50 x 1 major histocompatibility complex, class II, DR beta 6 (pseudo |
| 19 | 25840 | -1.1 | 1e-11 | 6e-10 | 50 x 11 methyltransferase like 7A [Source:HGNC Symbol;Acc:24550] |
| 20 | 347733 | -1.1 | 1e-11 | 9e-10 | 50 x 5 tubulin, beta 2B class IIb [Source:HGNC Symbol;Acc:30829] |

Local Geneset Analysis

Underexpression

| Rank | GSZ | p-value | #in/all | Geneset |
|------|--------|---------|----------|--|
| 1 | -23.38 | NULL | 14 / 16 | GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_D |
| 2 | -12.14 | NULL | 4 / 9 | GSEA C2MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN |
| 3 | -11.89 | NULL | 11 / 15 | CC MHC class II protein complex |
| 4 | -11.08 | NULL | 4 / 11 | GSEA C2TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN |
| 5 | -10.64 | NULL | 5 / 12 | BP dendritic cell chemotaxis |
| 6 | -10.52 | NULL | 3 / 14 | GSEA C2WANG_BARRETTES_ESOPHAGUS_UP |
| 7 | -10.47 | NULL | 97 / 553 | Cancer Lembecke_Colonc Inflammation |
| 8 | -10.39 | NULL | 9 / 16 | GSEA C2FARMER_BREAST_CANCER_CLUSTER_1 |
| 9 | -10.34 | NULL | 51 / 312 | BP immune response |
| 10 | -9.75 | NULL | 4 / 16 | GSEA C2KORKOLA_TERATOMA_UP |
| 11 | -9.7 | NULL | 3 / 10 | GSEA C2LUI_THYROID_CANCER_CLUSTER_5 |
| 12 | -9.3 | NULL | 5 / 16 | GSEA C2TURASHVIL_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR |
| 13 | -8.96 | NULL | 77 / 417 | H.Tiss WIRTH_Immune system |
| 14 | -8.65 | NULL | 4 / 10 | GSEA C2FERRANDO_LYL1_NEIGHBORS |
| 15 | -8.34 | NULL | 6 / 16 | TF TissuAQUERIZAS_Salivary gland |
| 16 | -8.27 | NULL | 1 / 2 | GSEA C2KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IQA_PRODUC |
| 17 | -8.27 | NULL | 1 / 2 | GSEA C2KEGG_AUTOIMMUNE_THYROID_DISEASE |
| 18 | -8.27 | NULL | 1 / 2 | GSEA C2KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS |
| 19 | -8.26 | NULL | 32 / 162 | CC external side of plasma membrane |
| 20 | -8.23 | NULL | 6 / 14 | GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LUNG_DN |
| 21 | -8.22 | NULL | 2 / 7 | GSEA C2LEE_NAIVE_T_LYMPHOCYTE |
| 22 | -8.16 | NULL | 4 / 13 | Cancer GENTLES_modul17 |
| 23 | -8.15 | NULL | 4 / 16 | GSEA C2TURASHVIL_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_L |
| 24 | -8.05 | NULL | 2 / 5 | GSEA C2FERRARI_RESPONSE_TO_FENRETINIDE_DN |
| 25 | -8.04 | NULL | 3 / 8 | LymphomaASCQUE_ABC UP |
| 26 | -8 | NULL | 1 / 5 | LymphomaRIGHT_custom ABC-DLBCL UP |
| 27 | -8 | NULL | 1 / 5 | miRNA target-15a |
| 28 | -7.94 | NULL | 3 / 7 | GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_DN |
| 29 | -7.81 | NULL | 4 / 15 | GSEA C2TANG_SENESCENCE_TP53_TARGETS_UP |
| 30 | -7.73 | NULL | 3 / 14 | GSEA C2WINPENNINGINCKX_MELANOMA_METASTASIS_DN |
| 31 | -7.61 | NULL | 5 / 17 | BP positive regulation of neutrophil chemotaxis |
| 32 | -7.48 | NULL | 4 / 9 | GSEA C2GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D |
| 33 | -7.47 | NULL | 4 / 14 | GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_E |
| 34 | -7.46 | NULL | 10 / 43 | MF chemokine activity |
| 35 | -7.46 | NULL | 14 / 47 | BP antigen processing and presentation |
| 36 | -7.28 | NULL | 3 / 14 | GSEA C2MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INH |
| 37 | -7.22 | NULL | 1 / 6 | GSEA C2HEIDENBLAD_AMPLIFIED_IN_BONE_CANCER |
| 38 | -7.22 | NULL | 1 / 6 | GSEA C2FUNG_IL2_TARGETS_WITH_STAT5_BINDING_SITES |
| 39 | -7.22 | NULL | 1 / 6 | miRNA target-26a |
| 40 | -7.14 | NULL | 5 / 21 | MF glycosaminoglycan binding |

p-values



GW_104

Local Summary

%DE = 0.95
 # metagenes = 8
 # genes = 140
 # genes in genesets = 137
 # genes with $fdr < 0.1$ = 128 (34 + / 94 -)
 # genes with $fdr < 0.05$ = 116 (28 + / 88 -)
 # genes with $fdr < 0.01$ = 111 (23 + / 88 -)

$\langle r \rangle$ metagenes = 0.99

$\langle r \rangle$ genes = 0.51

$\langle FC \rangle = -0.6$

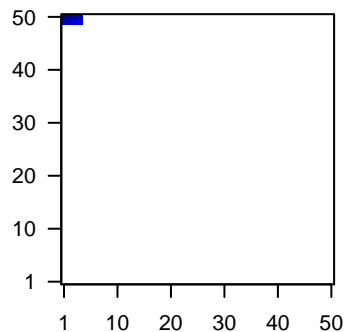
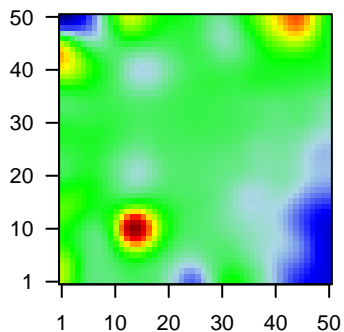
$\langle \text{shrinkage-t} \rangle = -21.08$

$\langle p\text{-value} \rangle = 0$

$\langle fdr \rangle = 0.21$

Profile

Spot



Local Genelist

| Rank | ID | log(FC) | fdr | p-value | Description |
|------|-----------|---------|-------|---------|---|
| 1 | 79852 | -1.42 | 2e-16 | 4e-17 | 3 x 50 epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760] |
| 2 | 57016 | 1.94 | 2e-16 | 4e-17 | 1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase) |
| 3 | 441282 | 1.34 | 2e-16 | 4e-17 | 1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC Symbol;Acc:23760] |
| 4 | 8644 | 1.36 | 2e-16 | 4e-17 | 1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Symbol;Acc:23760] |
| 5 | 375791 | -1.66 | 2e-16 | 4e-17 | 1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Symbol;Acc:23760] |
| 6 | 51806 | -2.22 | 2e-16 | 4e-17 | 4 x 50 calmodulin-like 5 [Source:HGNC Symbol;Acc:18180] |
| 7 | 100133941 | -1.46 | 2e-16 | 4e-17 | 3 x 50 CD24 molecule [Source:HGNC Symbol;Acc:1645] |
| 8 | 22802 | -2.76 | 2e-16 | 4e-17 | 1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20180] |
| 9 | 9022 | -1.88 | 2e-16 | 4e-17 | 1 x 50 chloride intracellular channel 3 [Source:HGNC Symbol;Acc:20180] |
| 10 | 84518 | -1.92 | 2e-16 | 4e-17 | 1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183] |
| 11 | 49860 | -3.1 | 2e-16 | 4e-17 | 1 x 50 cornulin [Source:HGNC Symbol;Acc:1230] |
| 12 | 92196 | 1.45 | 2e-16 | 4e-17 | 3 x 50 death associated protein-like 1 [Source:HGNC Symbol;Acc:20180] |
| 13 | 1672 | -1.66 | 2e-16 | 4e-17 | 1 x 50 defensin, beta 1 [Source:HGNC Symbol;Acc:2766] |
| 14 | 1673 | -2.71 | 2e-16 | 4e-17 | 1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193] |
| 15 | 5650 | -1.58 | 2e-16 | 4e-17 | 1 x 49 kallikrein-related peptidase 7 [Source:HGNC Symbol;Acc:63180] |
| 16 | 3860 | -4.77 | 2e-16 | 4e-17 | 1 x 50 keratin 13 [Source:HGNC Symbol;Acc:6415] |
| 17 | 3851 | -2.88 | 2e-16 | 4e-17 | 1 x 50 keratin 4 [Source:HGNC Symbol;Acc:6441] |
| 18 | 196374 | -1.44 | 2e-16 | 4e-17 | 1 x 50 keratin 78 [Source:HGNC Symbol;Acc:28926] |
| 19 | 388533 | -2.35 | 2e-16 | 4e-17 | 1 x 49 keratinocyte differentiation-associated protein [Source:HGNC Symbol;Acc:23760] |
| 20 | 137797 | -1.36 | 2e-16 | 4e-17 | 1 x 50 LY6/PLAUR domain containing 2 [Source:HGNC Symbol;Acc:23760] |

Local Geneset Analysis

Underexpression

| Rank | GSZ | p-value | #in/all | Geneset |
|------|--------|---------|----------|---|
| 1 | -32.27 | NULL | 60 / 135 | H.Tiss WIRTH_Mucosa |
| 2 | -22.94 | NULL | 1 / 6 | GSEA C2SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN |
| 3 | -16.82 | NULL | 1 / 10 | GSEA C2MURAKAMI_UV_RESPONSE_1HR_UP |
| 4 | -15.9 | NULL | 1 / 11 | GSEA C2MURAKAMI_UV_RESPONSE_6HR_DN |
| 5 | -15.77 | NULL | 5 / 15 | GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN |
| 6 | -14.55 | NULL | 4 / 44 | CC keratin filament |
| 7 | -13.67 | NULL | 7 / 19 | BP peptide cross-linking |
| 8 | -12.67 | NULL | 13 / 42 | BP keratinization |
| 9 | -12.25 | NULL | 3 / 15 | GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E |
| 10 | -11.94 | NULL | 2 / 11 | GSEA C2ROME_INSULIN_TARGETS_IN_MUSCLE_DN |
| 11 | -11.24 | NULL | 6 / 38 | BP epithelial cell differentiation |
| 12 | -10.94 | NULL | 2 / 15 | GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN |
| 13 | -10.58 | NULL | 4 / 16 | GSEA C2WANG_BARRETTS_ESOPHAGUS_DN |
| 14 | -10.14 | NULL | 6 / 16 | GSEA C2CROMER_TUMORIGENESIS_DN |
| 15 | -9.91 | NULL | 12 / 21 | CC cornified envelope |
| 16 | -9.47 | NULL | 1 / 27 | BP response to radiation |
| 17 | -9.45 | NULL | 6 / 82 | CC intermediate filament |
| 18 | -9.05 | NULL | 1 / 11 | Glo VERHAAK_Brain |
| 19 | -8.64 | NULL | 16 / 76 | BP epidermis development |
| 20 | -8.6 | NULL | 1 / 12 | MF channel activity |
| 21 | -8.21 | NULL | 1 / 6 | GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LIVER_UP |
| 22 | -8.2 | NULL | 1 / 13 | GSEA C2HASLINGER_B CLL_WITH_MUTATED_VH_GENES |
| 23 | -8.18 | NULL | 12 / 186 | MF structural molecule activity |
| 24 | -7.95 | NULL | 2 / 15 | GSEA C2ALONSO_METASTASIS_NEURAL_UP |
| 25 | -7.83 | NULL | 1 / 5 | GSEA C2FERRARI_RESPONSE_TO_FENRETINIDE_DN |
| 26 | -7.71 | NULL | 56 / 572 | Disease GUDJ_poriasis_up |
| 27 | -7.54 | NULL | 1 / 12 | GSEA C2ODONNELL_METASTASIS_DN |
| 28 | -7.54 | NULL | 1 / 12 | GSEA C2SYED_ESTRADIOL_RESPONSE |
| 29 | -7.53 | NULL | 1 / 15 | BP positive regulation of extrinsic apoptotic signaling pathway via death |
| 30 | -7.53 | NULL | 1 / 15 | GSEA C2BIOCARTA_MAL_PATHWAY |
| 31 | -7.29 | NULL | 3 / 16 | GSEA C2COLDREN_GEFITINIB_RESISTANCE_DN |
| 32 | -7.25 | NULL | 1 / 16 | Cancer GENTLES_modul11 |
| 33 | -7.02 | NULL | 2 / 14 | GSEA C2ZHAN_MULTIPLE_MYELOMA_MF_UP |
| 34 | -6.71 | NULL | 2 / 40 | MF chloride channel activity |
| 35 | -6.69 | NULL | 1 / 16 | GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATE |
| 36 | -6.5 | NULL | 1 / 8 | GSEA C2LIU_CDX2_TARGETS_DN |
| 37 | -6.5 | NULL | 1 / 52 | BP cellular response to retinoic acid |
| 38 | -6.46 | NULL | 2 / 16 | GSEA C2FRASOR_TAMOXIFEN_RESPONSE_UP |
| 39 | -6.46 | NULL | 3 / 15 | GSEA C2VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN |
| 40 | -6.43 | NULL | 3 / 16 | GSEA C2LEE_LIVER_CANCER_MYC_TGFA_UP |

p-values

