

GW_170

Global Summary

%DE = 0.13
 # genes with fdr < 0.2 = 1629 (932 + / 697 -)
 # genes with fdr < 0.1 = 1355 (799 + / 556 -)
 # genes with fdr < 0.05 = 1117 (672 + / 445 -)
 # genes with fdr < 0.01 = 798 (501 + / 297 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.1
 <fdr> = 0.87

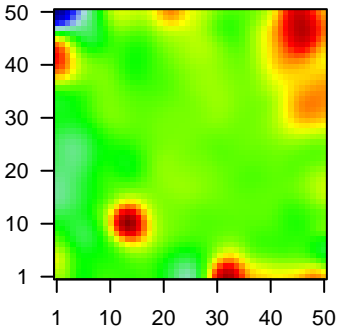
Global Genelist

| Rank | ID | log(FC) | fdr | p-value | Description |
|------|--------|---------|-------|---------|--|
| 1 | 9447 | 1.25 | 2e-16 | 3e-14 | 32 x 1 absent in melanoma 2 [Source:HGNC Symbol;Acc:357] |
| 2 | 216 | -1.28 | 2e-16 | 3e-14 | 50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC |
| 3 | 222 | -1.25 | 2e-16 | 3e-14 | 1 x 49 aldehyde dehydrogenase 3 family, member B2 [Source:HGNC |
| 4 | 401138 | 2.24 | 2e-16 | 3e-14 | 1 x 5 amelotin [Source:HGNC Symbol;Acc:33188] |
| 5 | 445 | 1.36 | 2e-16 | 3e-14 | 50 x 47 argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75f |
| 6 | 387695 | 1.3 | 2e-16 | 3e-14 | 1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Synt |
| 7 | 388115 | -1.24 | 2e-16 | 3e-14 | 26 x 2 chromosome 15 open reading frame 52 [Source:HGNC Synt |
| 8 | 92747 | 1.52 | 2e-16 | 3e-14 | 50 x 10 BPI fold containing family B, member 1 [Source:HGNC Symb |
| 9 | 343990 | 1.24 | 2e-16 | 3e-14 | 50 x 12 KIAA1211-like [Source:HGNC Symbol;Acc:33454] |
| 10 | 375791 | -1.2 | 2e-16 | 3e-14 | 1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Synt |
| 11 | 760 | 1.7 | 2e-16 | 3e-14 | 1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373] |
| 12 | 51806 | 1.48 | 2e-16 | 3e-14 | 4 x 50 calmodulin-like 5 [Source:HGNC Symbol;Acc:18180] |
| 13 | 131076 | -1.27 | 2e-16 | 3e-14 | 1 x 16 coiled-coil domain containing 58 [Source:HGNC Symbol;Acc |
| 14 | 595 | -1.55 | 2e-16 | 3e-14 | 1 x 6 cyclin D1 [Source:HGNC Symbol;Acc:1582] |
| 15 | 1675 | 1.24 | 2e-16 | 3e-14 | 50 x 9 complement factor D (adipsin) [Source:HGNC Symbol;Acc:27 |
| 16 | 84518 | -1.25 | 2e-16 | 3e-14 | 1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183] |
| 17 | 1308 | 1.21 | 2e-16 | 3e-14 | 1 x 43 collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194 |
| 18 | 1277 | 1.48 | 2e-16 | 3e-14 | 2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197] |
| 19 | 1278 | 1.33 | 2e-16 | 3e-14 | 2 x 1 collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198] |
| 20 | 1281 | 1.18 | 2e-16 | 3e-14 | 2 x 1 collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201] |

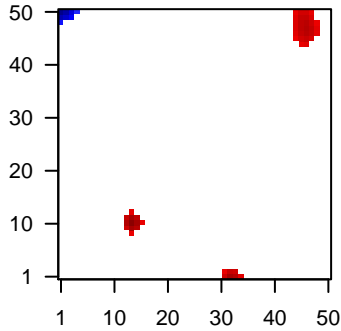
Global Geneset Analysis

| Rank | GSZ | p-value | #all | Geneset |
|-----------------------|-------|---------|------|---|
| <i>Overexpressed</i> | | | | |
| 1 | 10.04 | NULL | 123 | BP defense response to virus |
| 2 | 9.77 | NULL | 1720 | Chr Chr 1 |
| 3 | 9.68 | NULL | 13 | GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN |
| 4 | 9.62 | NULL | 15 | CC MHC class II protein complex |
| 5 | 9.45 | NULL | 16 | GSEA C2JROSEVIC_RESPONSE_TO_IMIQUMOD |
| 6 | 9.28 | NULL | 16 | GSEA C2MOSERLE_IFNA_RESPONSE |
| 7 | 8.72 | NULL | 51 | BP type I interferon signaling pathway |
| 8 | 8.71 | NULL | 10 | GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX |
| 9 | 8.59 | NULL | 8 | GSEA C2RUNNE_GENDER_EFFECT_UP |
| 10 | 8.42 | NULL | 13 | GSEA C2SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP |
| 11 | 8.24 | NULL | 14 | GSEA C2RADAEVA_RESPONSE_TO_IFNA1_UP |
| 12 | 7.89 | NULL | 13 | GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR |
| 13 | 7.87 | NULL | 16 | GSEA C2EINAV_INTERFERON_SIGNATURE_IN_CANCER |
| 14 | 7.79 | NULL | 7 | MMML C2SCIEJ_MMML_5 |
| 15 | 7.78 | NULL | 16 | GSEA C2ZHANG_INTERFERON_RESPONSE |
| 16 | 7.57 | NULL | 31 | BP negative regulation of viral genome replication |
| 17 | 7.5 | NULL | 204 | BP cytokine-mediated signaling pathway |
| 18 | 7.35 | NULL | 23 | CC integral to luminal side of endoplasmic reticulum membrane |
| 19 | 7.32 | NULL | 14 | GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_B |
| 20 | 7.23 | NULL | 47 | BP antigen processing and presentation |
| <i>Underexpressed</i> | | | | |
| 1 | -8.43 | NULL | 42 | BP keratinization |
| 2 | -7.89 | NULL | 21 | CC cornified envelope |
| 3 | -7.82 | NULL | 957 | Chr Chr 11 |
| 4 | -6.99 | NULL | 53 | BP keratinocyte differentiation |
| 5 | -6.82 | NULL | 16 | GSEA C2ONDER_CDH1_TARGETS_3_DN |
| 6 | -6.02 | NULL | 16 | GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN |
| 7 | -5.87 | NULL | 743 | Chr Chr 7 |
| 8 | -5.74 | NULL | 504 | Chr Chr 15 |
| 9 | -5.71 | NULL | 135 | H.Tiss WIRTH_Mucosa |
| 10 | -5.68 | NULL | 15 | GSEA C2JIN_SILENCED_BY_TUMOR_MICROENVIRONMENT |
| 11 | -5.41 | NULL | 15 | GSEA C2BILD_HRAS_ONCOGENIC_SIGNATURE |
| 12 | -5.41 | NULL | 16 | GSEA C2WANG_BARRETTES_ESOPHAGUS_DN |
| 13 | -5.4 | NULL | 15 | GSEA C2ONDER_CDH1_TARGETS_2_DN |
| 14 | -5.23 | NULL | 23 | MF peptidase inhibitor activity |
| 15 | -5.15 | NULL | 11 | GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN |
| 16 | -4.91 | NULL | 16 | GSEA C2CROMER_TUMORIGENESIS_DN |
| 17 | -4.82 | NULL | 5 | GSEA C2BUSA_SAM68_TARGETS_UP |
| 18 | -4.74 | NULL | 13 | GSEA C2ZHANG_RESPONSE_TO_IKK_INHIBITOR_AND_TNF_UP |
| 19 | -4.62 | NULL | 482 | BP cellular protein metabolic process |
| 20 | -4.56 | NULL | 15 | GSEA C2LUI_THYROID_CANCER_CLUSTER_2 |

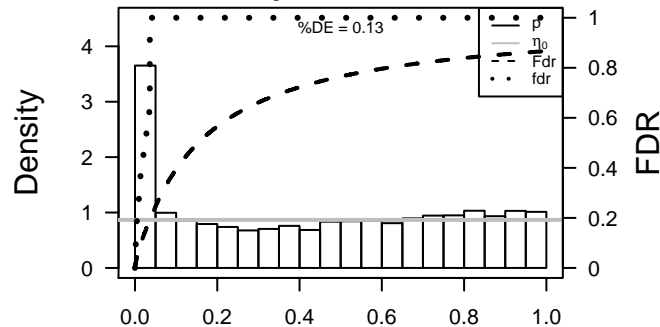
Profile



Regulated Spots



p-values



GW_170

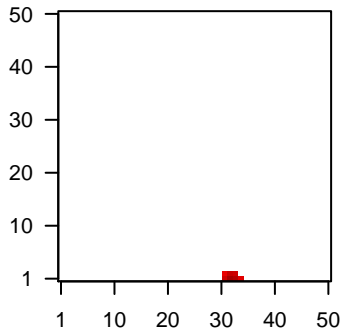
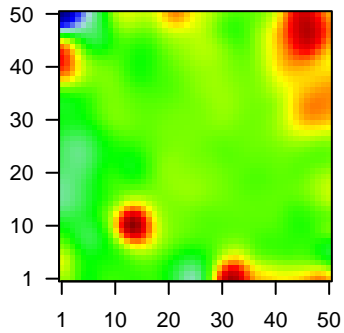
Local Summary

%DE = 0.8
 # metagenes = 7
 # genes = 119
 # genes in genesets = 117
 # genes with $fdr < 0.1 = 76$ (75 + / 1 -)
 # genes with $fdr < 0.05 = 72$ (71 + / 1 -)
 # genes with $fdr < 0.01 = 62$ (62 + / 0 -)

<r> metagenes = 0.99
 <r> genes = 0.46
 <FC> = 0.49
 <shrinkage-t> = 17.19
 <p-value> = 0
 <fdr> = 0.39

Profile

Spot



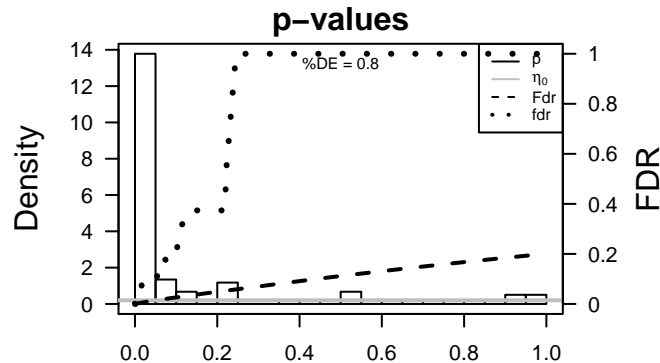
Local Genelist

| Rank | ID | log(FC) | fdr | p-value | Description |
|------|--------|---------|-------|---------|---|
| 1 | 9447 | 1.25 | 2e-16 | 8e-16 | 32 x 1 absent in melanoma 2 [Source:HGNC Symbol;Acc:357] |
| 2 | 3627 | 2.24 | 2e-16 | 8e-16 | 32 x 1 chemokine (C-X-C motif) ligand 10 [Source:HGNC Symbol;Acc:357] |
| 3 | 6373 | 1.8 | 2e-16 | 8e-16 | 32 x 1 chemokine (C-X-C motif) ligand 11 [Source:HGNC Symbol;Acc:357] |
| 4 | 115362 | 1.24 | 2e-16 | 8e-16 | 32 x 1 guanylate binding protein 5 [Source:HGNC Symbol;Acc:1989] |
| 5 | 10964 | 1.19 | 2e-16 | 8e-16 | 32 x 1 interferon-induced protein 44-like [Source:HGNC Symbol;Acc:357] |
| 6 | 2537 | 1.28 | 2e-16 | 8e-16 | 32 x 1 interferon, alpha-inducible protein 6 [Source:HGNC Symbol;Acc:357] |
| 7 | 9636 | 1.27 | 2e-16 | 8e-16 | 32 x 1 ISG15 ubiquitin-like modifier [Source:HGNC Symbol;Acc:405] |
| 8 | 4599 | 1.08 | 7e-16 | 1e-14 | 32 x 1 myxovirus (influenza virus) resistance 1, interferon-inducible |
| 9 | 23780 | 1.15 | 2e-15 | 3e-13 | 32 x 1 apolipoprotein L, 2 [Source:HGNC Symbol;Acc:619] |
| 10 | 6772 | 1.15 | 2e-15 | 3e-13 | 32 x 1 signal transducer and activator of transcription 1, 91kDa [Source:HGNC Symbol;Acc:357] |
| 11 | 2633 | 1.11 | 2e-14 | 3e-13 | 32 x 1 guanylate binding protein 1, interferon-inducible [Source:HGNC Symbol;Acc:357] |
| 12 | 54739 | 1.1 | 3e-14 | 2e-11 | 32 x 1 XIAP associated factor 1 [Source:HGNC Symbol;Acc:30932] |
| 13 | 6890 | 1.04 | 8e-13 | 6e-10 | 32 x 1 transporter 1, ATP-binding cassette, sub-family B (MDR/TAP) |
| 14 | 27074 | 0.95 | 5e-11 | 6e-10 | 32 x 1 lysosomal-associated membrane protein 3 [Source:HGNC Symbol;Acc:357] |
| 15 | 91543 | 0.95 | 6e-11 | 6e-10 | 32 x 1 radical S-adenosyl methionine domain containing 2 [Source:HGNC Symbol;Acc:357] |
| 16 | 9997 | 0.95 | 7e-11 | 8e-10 | 32 x 1 SCO2 cytochrome c oxidase assembly protein [Source:HGNC Symbol;Acc:357] |
| 17 | 10346 | 0.94 | 1e-10 | 2e-08 | 32 x 1 tripartite motif containing 22 [Source:HGNC Symbol;Acc:163] |
| 18 | 3458 | 0.87 | 2e-09 | 2e-08 | 32 x 1 interferon, gamma [Source:HGNC Symbol;Acc:5438] |
| 19 | 51191 | 0.87 | 2e-09 | 3e-08 | 32 x 1 HECT and RLD domain containing E3 ubiquitin protein ligase |
| 20 | 51296 | 0.86 | 4e-09 | 3e-08 | 32 x 1 solute carrier family 15 (oligopeptide transporter), member 3 [Source:HGNC Symbol;Acc:357] |

Local Geneset Analysis

Overexpression

| Rank | GSZ | p-value | #in/all | Geneset |
|------|-------|---------|----------|---|
| 1 | 50.16 | NULL | 12 / 16 | GSEA C2MOSERLE_IFNA_RESPONSE |
| 2 | 45.81 | NULL | 9 / 10 | GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX |
| 3 | 42.47 | NULL | 29 / 51 | BP type I interferon signaling pathway |
| 4 | 42.42 | NULL | 11 / 16 | GSEA C2EINAV_INTERFERON_SIGNATURE_IN_CANCER |
| 5 | 41.67 | NULL | 10 / 13 | GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN |
| 6 | 40.67 | NULL | 8 / 11 | GSEA C2BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS |
| 7 | 40.59 | NULL | 6 / 14 | GSEA C2RADAIEVA_RESPONSE_TO_IFNA1_UP |
| 8 | 40.15 | NULL | 10 / 16 | GSEA C2JROSEVIC_RESPONSE_TO_IMIQIMOD |
| 9 | 39.46 | NULL | 6 / 8 | GSEA C2ROETH_TERT_TARGETS_UP |
| 10 | 39.12 | NULL | 3 / 4 | GSEA C2KRASNOSELSKAYA_ILF3_TARGETS_UP |
| 11 | 38.71 | NULL | 11 / 16 | GSEA C2ZHANG_INTERFERON_RESPONSE |
| 12 | 37.02 | NULL | 31 / 123 | BP defense response to virus |
| 13 | 33.74 | NULL | 7 / 16 | GSEA C2MAHADEVAN_RESPONSE_TO_MP470_UP |
| 14 | 33.06 | NULL | 13 / 31 | BP negative regulation of viral genome replication |
| 15 | 32 | NULL | 8 / 10 | GSEA C2GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3 |
| 16 | 31.78 | NULL | 27 / 109 | BP response to virus |
| 17 | 31.48 | NULL | 4 / 12 | GSEA C2ZHU_CMV_8_HR_UP |
| 18 | 30.79 | NULL | 3 / 5 | GSEA C2KIM_LRRC3B_TARGETS |
| 19 | 29.52 | NULL | 6 / 12 | GSEA C2TSAI_DNAJB4_TARGETS_UP |
| 20 | 27.45 | NULL | 6 / 16 | GSEA C2XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR |
| 21 | 26.53 | NULL | 5 / 16 | GSEA C2FARMER_BREAST_CANCER_CLUSTER_1 |
| 22 | 26.38 | NULL | 2 / 10 | BP positive regulation of cAMP-mediated signaling |
| 23 | 26.03 | NULL | 6 / 14 | GSEA C2XU_AKT1_TARGETS_6HR |
| 24 | 24.97 | NULL | 34 / 204 | BP cytokine-mediated signaling pathway |
| 25 | 24.31 | NULL | 4 / 14 | GSEA C2TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP |
| 26 | 24.29 | NULL | 46 / 572 | Disease GUDJ_poriasis up |
| 27 | 23.72 | NULL | 3 / 9 | GSEA C2DER_IFN_ALPHA_RESPONSE_UP |
| 28 | 23.72 | NULL | 3 / 9 | GSEA C2DER_IFN_GAMMA_RESPONSE_UP |
| 29 | 23.72 | NULL | 2 / 12 | BP positive regulation of leukocyte chemotaxis |
| 30 | 23.48 | NULL | 6 / 14 | Glio Donson-immune cell intra signaling-associated with LTS in HGA |
| 31 | 23.43 | NULL | 3 / 4 | MMML C69CIEJ_MMML 47 |
| 32 | 23.1 | NULL | 2 / 2 | MMML C69CIEJ_MMML 27 |
| 33 | 21.97 | NULL | 31 / 274 | Lymphoma SPANG_IL21 DN |
| 34 | 21.77 | NULL | 4 / 16 | GSEA C2SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_UP |
| 35 | 20.05 | NULL | 5 / 16 | GSEA C2ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_UP |
| 36 | 19.42 | NULL | 2 / 17 | BP positive regulation of release of sequestered calcium ion into cytosol |
| 37 | 18.42 | NULL | 4 / 10 | GSEA C2DAUER_STAT3_TARGETS_DN |
| 38 | 18.02 | NULL | 4 / 10 | GSEA C2GRANDVAUX_IRF3_TARGETS_UP |
| 39 | 17.8 | NULL | 28 / 312 | BP immune response |
| 40 | 17.65 | NULL | 3 / 5 | GSEA C2BROWNE_INTERFERON_RESPONSIVE_GENES |



GW_170

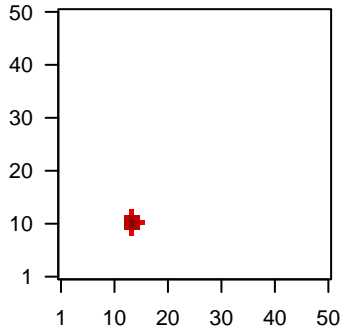
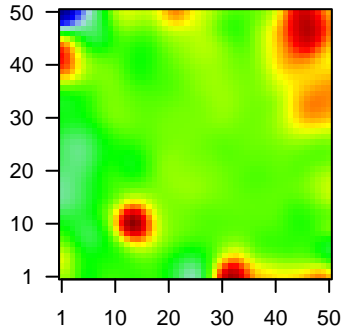
Local Summary

%DE = 0.61
 # metagenes = 12
 # genes = 73
 # genes in genesets = 54
 # genes with fdr < 0.1 = 35 (27 + / 8 -)
 # genes with fdr < 0.05 = 28 (26 + / 2 -)
 # genes with fdr < 0.01 = 28 (26 + / 2 -)

<r> metagenes = 0.99
 <r> genes = 0.35
 <FC> = 0.67
 <shrinkage-t> = 23.38
 <p-value> = 0
 <fdr> = 0.53

Profile

Spot



Local Genelist

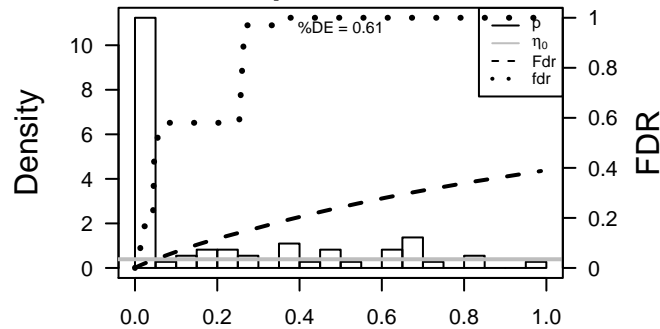
| Rank | ID | log(FC) | fdr | p-value | Description |
|------|-----------|---------|-------|---------|---|
| 1 | 729428 | 3.06 | 2e-16 | 4e-16 | 14 x 11 G antigen 12C [Source:HGNC Symbol;Acc:28402] |
| 2 | 729422 | 3.14 | 2e-16 | 4e-16 | 14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778] |
| 3 | 100132399 | 1.31 | 2e-16 | 4e-16 | 14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778] |
| 4 | 100008586 | 3.01 | 2e-16 | 4e-16 | 14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778] |
| 5 | 645073 | 2.82 | 2e-16 | 4e-16 | 14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778] |
| 6 | 729442 | 3.14 | 2e-16 | 4e-16 | 14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778] |
| 7 | 26748 | 3.25 | 2e-16 | 4e-16 | 14 x 11 G antigen 12I [Source:HGNC Symbol;Acc:4105] |
| 8 | 729396 | 1.99 | 2e-16 | 4e-16 | 14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778] |
| 9 | 729447 | 2.48 | 2e-16 | 4e-16 | 14 x 11 G antigen 2A [Source:HGNC Symbol;Acc:4099] |
| 10 | 645037 | 3.28 | 2e-16 | 4e-16 | 14 x 11 G antigen 2C [Source:HGNC Symbol;Acc:31958] |
| 11 | 26749 | 2.48 | 2e-16 | 4e-16 | 14 x 11 G antigen 2E [Source:HGNC Symbol;Acc:31960] |
| 12 | 2576 | 2.95 | 2e-16 | 4e-16 | 14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778] |
| 13 | 2577 | 3.24 | 2e-16 | 4e-16 | 14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778] |
| 14 | 2578 | 1.59 | 2e-16 | 4e-16 | 14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778] |
| 15 | 2579 | 3.1 | 2e-16 | 4e-16 | 14 x 11 G antigen 12I [Source:HGNC Symbol;Acc:4105] |
| 16 | 100101629 | 2.05 | 2e-16 | 4e-16 | 14 x 11 G antigen 2E [Source:HGNC Symbol;Acc:31960] |
| 17 | 4109 | 2.04 | 2e-16 | 4e-16 | 14 x 11 melanoma antigen family A, 10 [Source:HGNC Symbol;Acc:6 |
| 18 | 8277 | 3.46 | 2e-16 | 4e-16 | 14 x 10 transketolase-like 1 [Source:HGNC Symbol;Acc:11835] |
| 19 | 402381 | 1.17 | 7e-16 | 4e-14 | 13 x 11 spermatogenesis and oogenesis specific basic helix-loop-he |
| 20 | 4100 | 1.15 | 2e-15 | 4e-13 | 14 x 11 melanoma antigen family A, 1 (directs expression of antigen 1 |

Local Geneset Analysis

Overexpression

| Rank | GSZ | p-value | #in/all | Geneset |
|------|-------|---------|----------|---|
| 1 | 24.17 | NULL | 1 / 9 | GSEA C2ABE_VEGFA_TARGETS_30MIN |
| 2 | 21.12 | NULL | 1 / 11 | GSEA C2ABE_VEGFA_TARGETS_2HR |
| 3 | 18.29 | NULL | 1 / 12 | GSEA C2RAY_TARGETS_OF_P210_BCR_ABL_FUSION_UP |
| 4 | 18.07 | NULL | 1 / 14 | GSEA C2WALK_AML_WITH_11Q23_REARRANGED |
| 5 | 17.3 | NULL | 1 / 15 | GSEA C2WALK_AML_CLUSTER_16 |
| 6 | 17.3 | NULL | 1 / 15 | GSEA C2KEGG_PENTOSE_PHOSPHATE_PATHWAY |
| 7 | 13.63 | NULL | 29 / 630 | Chr Chr X |
| 8 | 12.38 | NULL | 1 / 11 | GSEA C2SU_PLACENTA |
| 9 | 10.59 | NULL | 1 / 14 | GSEA C2NIELSEN_GIST |
| 10 | 10.14 | NULL | 1 / 15 | GSEA C2BROWNE_HCMV_INFECTION_8HR_DN |
| 11 | 4.98 | NULL | 1 / 19 | BP oogenesis |
| 12 | 4.6 | NULL | 1 / 21 | BP negative regulation of Notch signaling pathway |
| 13 | 3.62 | NULL | 9 / 120 | H.Tiss WIRTH_Testis |
| 14 | 3.42 | NULL | 1 / 13 | CC axonemal dynein complex |
| 15 | 3.33 | NULL | 8 / 481 | BP biological_process |
| 16 | 3.31 | NULL | 1 / 37 | BP ovarian follicle development |
| 17 | 3.21 | NULL | 6 / 419 | CC cellular_component |
| 18 | 3.18 | NULL | 1 / 13 | GSEA C2PIPOLI_LG11_TARGETS_DN |
| 19 | 3.04 | NULL | 9 / 549 | MF molecular_function |
| 20 | 2.99 | NULL | 1 / 16 | BP ciliary or bacterial-type flagellar motility |
| 21 | 2.59 | NULL | 1 / 20 | CC dynein complex |
| 22 | 2.51 | NULL | 1 / 390 | BP metabolic process |
| 23 | 2.24 | NULL | 1 / 68 | MF histone deacetylase binding |
| 24 | 2.17 | NULL | 1 / 5 | GSEA C2CHOI_ATL_ACUTE_STAGE |
| 25 | 2.02 | NULL | 1 / 531 | MF catalytic activity |
| 26 | 1.35 | NULL | 1 / 7 | GSEA C2KONDO_PROSTATE_CANCER_WITH_H3K27ME3 |
| 27 | 1.32 | NULL | 1 / 156 | MF protein dimerization activity |
| 28 | 1.26 | NULL | 1 / 10 | GSEA C2TSUNODA_CISPLATIN_RESISTANCE_DN |
| 29 | 1.16 | NULL | 1 / 68 | BP microtubule-based movement |
| 30 | 1.13 | NULL | 1 / 71 | MF microtubule motor activity |
| 31 | 1.03 | NULL | 1 / 10 | GSEA C2BOYERINAS_ONCOFETAL_TARGETS_OF_LET7A1 |
| 32 | 1.03 | NULL | 1 / 10 | GSEA C2CONRAD_STEM_CELL |
| 33 | 1 | NULL | 1 / 10 | GSEA C2NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN |
| 34 | 0.96 | NULL | 1 / 11 | GSEA C2ODONNELL_TFRC_TARGETS_DN |
| 35 | 0.94 | NULL | 1 / 15 | GSEA C2LOPEZ_MBD_TARGETS_IMPRINTED_AND_X_LINKED |
| 36 | 0.94 | NULL | 1 / 15 | GSEA C2ALONSO_METASTASIS_NEURAL_UP |
| 37 | 0.93 | NULL | 1 / 11 | GSEA C2NIKOLSKY_BREAST_CANCER_7Q21_Q22_AMPLICON |
| 38 | 0.9 | NULL | 1 / 16 | GSEA C2JAEGER_METASTASIS_UP |
| 39 | 0.87 | NULL | 1 / 12 | GSEA C2HSIAO_LIVER_SPECIFIC_GENES |
| 40 | 0.82 | NULL | 1 / 13 | GSEA C2HOSHIDA_LIVER_CANCER_SURVIVAL_DN |

p-values



GW_170

Local Summary

%DE = 0.65
 # metagenes = 29
 # genes = 327
 # genes in genesets = 325
 # genes with $fdr < 0.1$ = 128 (120 + / 8 -)
 # genes with $fdr < 0.05$ = 100 (95 + / 5 -)
 # genes with $fdr < 0.01$ = 73 (71 + / 2 -)

<r> metagenes = 0.94

<r> genes = 0.36

<FC> = 0.26

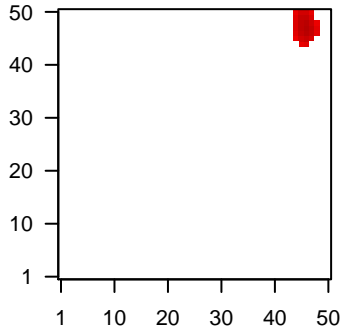
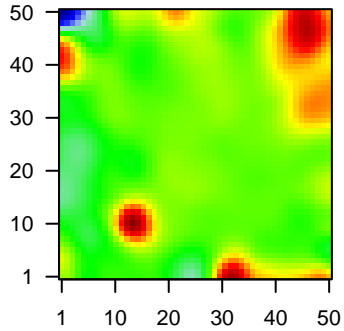
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<p-value> = 0.01

<fdr> = 0.63

Profile

Spot



Local Genelist

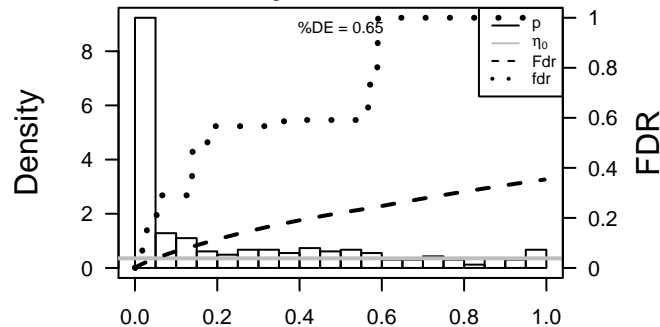
| Rank | ID | log(FC) | fdr | p-value | Description |
|------|--------|---------|-------|---------|--|
| 1 | 3787 | 2.11 | 2e-16 | 4e-15 | 46 x 45 potassium voltage-gated channel, delayed-rectifier, subfamil |
| 2 | 283212 | 1.29 | 2e-16 | 4e-15 | 46 x 44 kelch-like family member 35 [Source:HGNC Symbol;Acc:265 |
| 3 | 4744 | 1.53 | 2e-16 | 4e-15 | 45 x 44 neurofilament, heavy polypeptide [Source:HGNC Symbol;Acc |
| 4 | 10388 | 1.82 | 2e-16 | 4e-15 | 47 x 46 synaptonemal complex protein 2 [Source:HGNC Symbol;Acc: |
| 5 | 51087 | 1.33 | 2e-16 | 4e-15 | 47 x 46 Y box binding protein 2 [Source:HGNC Symbol;Acc:17948] |
| 6 | 84215 | 1.45 | 2e-16 | 4e-15 | 46 x 45 zinc finger protein 541 [Source:HGNC Symbol;Acc:25294] |
| 7 | 54457 | 1.18 | 4e-16 | 1e-12 | 46 x 44 TAF7-like RNA polymerase II, TATA box binding protein (TBP |
| 8 | 285498 | 1.11 | 2e-14 | 1e-12 | 46 x 44 ring finger protein 212 [Source:HGNC Symbol;Acc:27729] |
| 9 | 116028 | 1.11 | 2e-14 | 3e-11 | 46 x 47 RecQ mediated genome instability 2 [Source:HGNC Symbol; |
| 10 | 146771 | 1.06 | 3e-13 | 1e-09 | 46 x 45 testicular cell adhesion molecule 1, pseudogene [Source:HGI |
| 11 | 1029 | 0.99 | 9e-12 | 2e-08 | 45 x 45 cyclin-dependent kinase inhibitor 2A [Source:HGNC Symbol; |
| 12 | 9582 | 0.93 | 2e-10 | 2e-08 | 46 x 49 apolipoprotein B mRNA editing enzyme, catalytic polypeptide |
| 13 | 4175 | 0.91 | 3e-10 | 3e-08 | 46 x 47 minichromosome maintenance complex component 6 [Source |
| 14 | 54830 | 0.9 | 6e-10 | 3e-08 | 45 x 49 nucleoporin 62kDa C-terminal like [Source:HGNC Symbol;Ac |
| 15 | 79042 | 0.89 | 8e-10 | 1e-07 | 45 x 44 TSEN34 tRNA splicing endonuclease subunit [Source:HGNC |
| 16 | 3992 | 0.87 | 2e-09 | 3e-07 | 45 x 50 fatty acid desaturase 1 [Source:HGNC Symbol;Acc:3574] |
| 17 | 1163 | 0.85 | 5e-09 | 3e-07 | 44 x 50 CDC28 protein kinase regulatory subunit 1B [Source:HGNC |
| 18 | 84318 | 0.84 | 7e-09 | 1e-06 | 47 x 46 coiled-coil domain containing 77 [Source:HGNC Symbol;Acc |
| 19 | 80321 | 0.81 | 2e-08 | 1e-06 | 48 x 47 centrosomal protein 70kDa [Source:HGNC Symbol;Acc:2997. |
| 20 | 27127 | 0.8 | 4e-08 | 1e-06 | 46 x 44 structural maintenance of chromosomes 1B [Source:HGNC S |

Local Geneset Analysis

Overexpression

| Rank | GSZ | p-value | #in/all | Geneset |
|------|-------|---------|----------|---|
| 1 | 32.74 | NULL | 6 / 13 | GSEA C2SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP |
| 2 | 21.11 | NULL | 9 / 11 | GSEA C2KALMA_E2F1_TARGETS |
| 3 | 20.96 | NULL | 80 / 142 | Glio willscher_GBM_Verhaak-CL_expression_C_up |
| 4 | 20.96 | NULL | 80 / 142 | Glio willscher_GBM_Verhaak-PNmut_expression_C_down |
| 5 | 19.1 | NULL | 17 / 30 | BP DNA strand elongation involved in DNA replication |
| 6 | 18.39 | NULL | 86 / 370 | BP mitotic cell cycle |
| 7 | 18.27 | NULL | 15 / 16 | GSEA C2EGUCHI_CELL_CYCLE_RB1_TARGETS |
| 8 | 17.72 | NULL | 44 / 149 | BP DNA replication |
| 9 | 16.11 | NULL | 8 / 11 | GSEA C2REACTOME_UNWINDING_OF_DNA |
| 10 | 15.62 | NULL | 12 / 16 | GSEA C2FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL |
| 11 | 15.39 | NULL | 4 / 20 | CC synaptonemal complex |
| 12 | 15.09 | NULL | 6 / 14 | GSEA C2SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP |
| 13 | 14.84 | NULL | 11 / 16 | GSEA C2REACTOME_DNA_STRAND_ELONGATION |
| 14 | 14.5 | NULL | 12 / 22 | BP DNA replication initiation |
| 15 | 14.22 | NULL | 11 / 15 | GSEA C2FINETTI_BREAST_CANCER_KINOME_RED |
| 16 | 13.52 | NULL | 1 / 3 | GSEA C2KONDO_COLON_CANCER_HCP_WITH_H3K27ME3 |
| 17 | 13.3 | NULL | 11 / 21 | BP telomere maintenance via semi-conservative replication |
| 18 | 12.35 | NULL | 11 / 24 | BP telomere maintenance via recombination |
| 19 | 11.75 | NULL | 88 / 530 | Cancer Lembcke_Normal vs Adenoma |
| 20 | 11.31 | NULL | 8 / 18 | BP nucleotide-excision repair, DNA gap filling |
| 21 | 11.15 | NULL | 45 / 298 | BP DNA repair |
| 22 | 11.14 | NULL | 8 / 15 | GSEA C2WU_APOPTOSIS_BY_CDKN1A_VIA_TP53 |
| 23 | 11.08 | NULL | 8 / 16 | GSEA C2PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP |
| 24 | 11.03 | NULL | 1 / 10 | GSEA C2NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON |
| 25 | 10.91 | NULL | 4 / 10 | CC lateral element |
| 26 | 10.75 | NULL | 2 / 5 | GSEA C2NAKAMURA_LUNG_CANCER |
| 27 | 10.75 | NULL | 2 / 5 | GSEA C2NAKAMURA_LUNG_CANCER_MARKERS |
| 28 | 10.73 | NULL | 6 / 14 | GSEA C2REACTOME_POLYMERASE_SWITCHING |
| 29 | 10.71 | NULL | 27 / 148 | BP G1/S transition of mitotic cell cycle |
| 30 | 10.46 | NULL | 4 / 16 | BP cell cycle checkpoint |
| 31 | 10.08 | NULL | 10 / 16 | GSEA C2SONG_TARGETS_OF_IE86_CMV_PROTEIN |
| 32 | 10.05 | NULL | 8 / 16 | GSEA C2REACTOME_LAGGING_STRAND_SYNTHESIS |
| 33 | 9.85 | NULL | 7 / 16 | Cancer WOLFER_overlap genes |
| 34 | 9.85 | NULL | 9 / 15 | GSEA C2BOYVAULT_LIVER_CANCER_SUBCLASS_G23_UP |
| 35 | 9.81 | NULL | 2 / 14 | GSEA C2TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_GRANULO |
| 36 | 9.7 | NULL | 7 / 15 | GSEA C2REACTOME_REPAIR_SYNTHESIS_OF_PATCH_27_30_BASES |
| 37 | 9.61 | NULL | 11 / 68 | Cancer SHAUGHNESSY_MM high risk |
| 38 | 9.5 | NULL | 3 / 9 | GSEA C2BIOCARTA_AKAP95_PATHWAY |
| 39 | 9.22 | NULL | 4 / 13 | Pathw Ac:GUSTAFSON_PI3K_UP |
| 40 | 9.14 | NULL | 89 / 949 | CC nucleoplasm |

p-values



GW_170

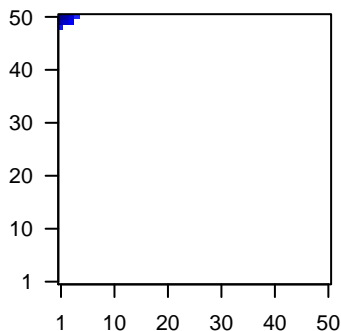
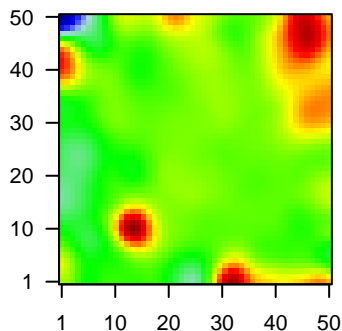
Local Summary

%DE = 0.79
 # metagenes = 8
 # genes = 154
 # genes in genesets = 151
 # genes with $fdr < 0.1 = 104$ (16 + / 88 -)
 # genes with $fdr < 0.05 = 104$ (16 + / 88 -)
 # genes with $fdr < 0.01 = 91$ (12 + / 79 -)

<r> metagenes = 0.99
 <r> genes = 0.5
 <FC> = -0.52
 <shrinkage-t> = -18.12
 <p-value> = 0
 <fdr> = 0.32

Profile

Spot



Local Genelist

| Rank | ID | log(FC) | fdr | p-value | Description |
|------|--------|---------|-------|---------|---|
| 1 | 222 | -1.25 | 2e-16 | 2e-16 | 1 x 49 aldehyde dehydrogenase 3 family, member B2 [Source:HGNC |
| 2 | 387695 | 1.3 | 2e-16 | 2e-16 | 1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Synt |
| 3 | 375791 | -1.2 | 2e-16 | 2e-16 | 1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Synt |
| 4 | 51806 | 1.48 | 2e-16 | 2e-16 | 4 x 50 calmodulin-like 5 [Source:HGNC Symbol;Acc:18180] |
| 5 | 84518 | -1.25 | 2e-16 | 2e-16 | 1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183] |
| 6 | 49860 | -1.82 | 2e-16 | 2e-16 | 1 x 50 cornulin [Source:HGNC Symbol;Acc:1230] |
| 7 | 1672 | -1.98 | 2e-16 | 2e-16 | 1 x 50 defensin, beta 1 [Source:HGNC Symbol;Acc:2766] |
| 8 | 1673 | -1.49 | 2e-16 | 2e-16 | 1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193] |
| 9 | 1828 | -1.26 | 2e-16 | 2e-16 | 1 x 48 desmoglein 1 [Source:HGNC Symbol;Acc:3048] |
| 10 | 128876 | -1.51 | 2e-16 | 2e-16 | 1 x 48 family with sequence similarity 83, member C [Source:HGNC |
| 11 | 9245 | -1.32 | 2e-16 | 2e-16 | 4 x 50 glucosaminyl (N-acetyl) transferase 3, mucin type [Source:H |
| 12 | 43849 | -1.22 | 2e-16 | 2e-16 | 1 x 50 kallikrein-related peptidase 12 [Source:HGNC Symbol;Acc:6: |
| 13 | 26085 | -1.58 | 2e-16 | 2e-16 | 1 x 50 kallikrein-related peptidase 13 [Source:HGNC Symbol;Acc:6: |
| 14 | 5653 | -2.01 | 2e-16 | 2e-16 | 1 x 50 kallikrein-related peptidase 6 [Source:HGNC Symbol;Acc:63: |
| 15 | 5650 | -1.47 | 2e-16 | 2e-16 | 1 x 49 kallikrein-related peptidase 7 [Source:HGNC Symbol;Acc:63: |
| 16 | 3851 | -2.36 | 2e-16 | 2e-16 | 1 x 50 keratin 4 [Source:HGNC Symbol;Acc:6441] |
| 17 | 388533 | -2.26 | 2e-16 | 2e-16 | 1 x 49 keratinocyte differentiation-associated protein [Source:HGNC |
| 18 | 5266 | -2.51 | 2e-16 | 2e-16 | 1 x 49 peptidase inhibitor 3, skin-derived [Source:HGNC Symbol;Ac |
| 19 | 57111 | -1.38 | 2e-16 | 2e-16 | 2 x 50 RAB25, member RAS oncogene family [Source:HGNC Symb |
| 20 | 6278 | -1.35 | 2e-16 | 2e-16 | 1 x 49 S100 calcium binding protein A7 [Source:HGNC Symbol;Acc: |

Local Geneset Analysis

Underexpression

| Rank | GSZ | p-value | #in/all | Geneset |
|------|--------|---------|----------|---------------------------------------|
| 1 | -29.83 | NULL | 66 / 135 | H.Tiss WIRTH_Mucosa |
| 2 | -25.6 | NULL | 13 / 21 | CC cornified envelope |
| 3 | -20.82 | NULL | 17 / 53 | BP keratinocyte differentiation |
| 4 | -20.19 | NULL | 15 / 42 | BP keratinization |
| 5 | -17.65 | NULL | 5 / 16 | GSEA C2WANG_BARRETTS_ESOPHAGUS_DN |
| 6 | -17.61 | NULL | 6 / 16 | GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCI |
| 7 | -17.33 | NULL | 5 / 16 | GSEA C2ONDER_CDH1_TARGETS_3_DN |
| 8 | -17.01 | NULL | 3 / 15 | GSEA C2LIN_SILENCED_BY_TUMOR_MICROENV |
| 9 | -15.85 | NULL | 4 / 16 | GSEA C2JAEGER_METASTASIS_DN |
| 10 | -15.72 | NULL | 3 / 13 | GSEA C2FARMER_BREAST_CANCER_APOCRINE |
| 11 | -14.85 | NULL | 2 / 8 | GSEA C2MCLACHLAN_DENTAL_CARIES_UP |
| 12 | -14.83 | NULL | 3 / 15 | GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS |
| 13 | -14.55 | NULL | 69 / 572 | Disease GUDJ_psooriasis up |
| 14 | -14.48 | NULL | 3 / 13 | GSEA C2HAN_SATB1_TARGETS_DN |
| 15 | -13.85 | NULL | 2 / 9 | GSEA C2MCLACHLAN_DENTAL_CARIES_DN |
| 16 | -13.01 | NULL | 2 / 10 | GSEA C2NIKOLSKY_BREAST_CANCER_20Q12 |
| 17 | -12.45 | NULL | 4 / 23 | MF peptidase inhibitor activity |
| 18 | -12.3 | NULL | 2 / 11 | GSEA C2SMID_BREAST_CANCER_RELAPSE_IN |
| 19 | -12.22 | NULL | 6 / 16 | GSEA C2CROMER_TUMORIGENESIS_DN |
| 20 | -12.03 | NULL | 2 / 15 | GSEA C2BILD_HRAS_ONCOGENIC_SIGNATURE |
| 21 | -11.85 | NULL | 3 / 16 | GSEA C2SMID_BREAST_CANCER_RELAPSE_IN |
| 22 | -11.51 | NULL | 3 / 16 | GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL |
| 23 | -11.38 | NULL | 1 / 10 | GSEA C2THEILGAARD_NEUTROPHIL_AT_SKIN |
| 24 | -11.21 | NULL | 3 / 15 | GSEA C2FERNANDEZ_BOUND_BY_MYC |
| 25 | -11.15 | NULL | 2 / 13 | GSEA C2CHARAFE_BREAST_CANCER_LUMINAL |
| 26 | -11.13 | NULL | 2 / 11 | GSEA C2ROME_INSULIN_TARGETS_IN_MUSCLE |
| 27 | -10.96 | NULL | 7 / 19 | BP peptide cross-linking |
| 28 | -10.75 | NULL | 1 / 11 | GSEA C2LEI_MYB_TARGETS |
| 29 | -10.75 | NULL | 1 / 11 | GSEA C2HAN_SATB1_TARGETS_UP |
| 30 | -10.65 | NULL | 18 / 76 | BP epidermis development |
| 31 | -10.63 | NULL | 2 / 17 | Disease BCHETNIA_EBM up |
| 32 | -10.27 | NULL | 6 / 15 | GSEA C2HINATA_NFKB_TARGETS_KERATINOC |
| 33 | -10.26 | NULL | 2 / 15 | GSEA C2ONDER_CDH1_TARGETS_2_DN |
| 34 | -10.26 | NULL | 2 / 15 | GSEA C2SMID_BREAST_CANCER_LUMINAL_B |
| 35 | -9.75 | NULL | 1 / 13 | GSEA C2VECCHI_GASTRIC_CANCER_EARLY_UP |
| 36 | -9.75 | NULL | 1 / 13 | GSEA C2ZHANG_RESPONSE_TO_IKK_INHIBIT |
| 37 | -9.75 | NULL | 1 / 13 | GSEA C2ST_GA13_PATHWAY |
| 38 | -9.75 | NULL | 1 / 13 | GSEA C2ST_INTERLEUKIN_4_PATHWAY |
| 39 | -9.6 | NULL | 4 / 10 | GSEA C2SMID_BREAST_CANCER_ERBB2_UP |
| 40 | -9.34 | NULL | 1 / 14 | GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCI |

