

GW_253

Global Summary

%DE = 0.16
 # genes with fdr < 0.2 = 2024 (1188 + / 836 -)
 # genes with fdr < 0.1 = 1481 (902 + / 579 -)
 # genes with fdr < 0.05 = 1306 (801 + / 505 -)
 # genes with fdr < 0.01 = 888 (565 + / 323 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.09
 <fdr> = 0.84

Global Genelist

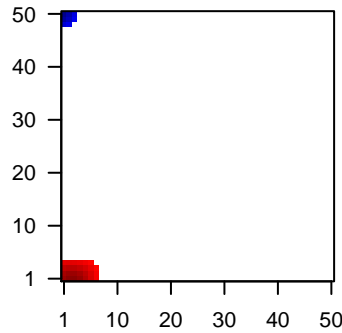
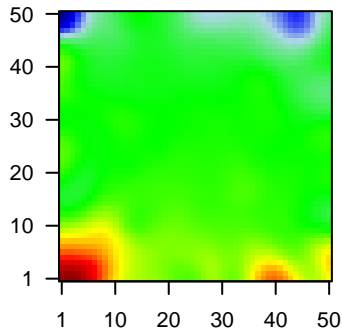
| Rank | ID | log(FC) | fdr | p-value | Description |
|------|--------|---------|-------|---------|--|
| 1 | 8728 | 1.65 | 2e-16 | 3e-14 | 50 x 3 ADAM metallopeptidase domain 19 [Source:HGNC Symbol;A |
| 2 | 131 | -1.92 | 2e-16 | 3e-14 | 1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide |
| 3 | 218 | -2.57 | 2e-16 | 3e-14 | 1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC |
| 4 | 401138 | 1.66 | 2e-16 | 3e-14 | 1 x 5 amelotin [Source:HGNC Symbol;Acc:33188] |
| 5 | 163782 | 2.06 | 2e-16 | 3e-14 | 1 x 2 KN motif and ankyrin repeat domains 4 [Source:HGNC Symb |
| 6 | 445328 | -1.78 | 2e-16 | 3e-14 | 4 x 46 Rho guanine nucleotide exchange factor (GEF) 35 [Source:H |
| 7 | 650 | 1.66 | 2e-16 | 3e-14 | 1 x 4 bone morphogenetic protein 2 [Source:HGNC Symbol;Acc:10 |
| 8 | 24141 | 1.48 | 2e-16 | 3e-14 | 7 x 1 lysosomal-associated membrane protein family, member 5 [S |
| 9 | 260436 | 1.7 | 2e-16 | 3e-14 | 50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc |
| 10 | 79783 | 1.57 | 2e-16 | 3e-14 | 1 x 5 succinylCoA:glutarate-CoA transferase [Source:HGNC Symbt |
| 11 | 375791 | -2.05 | 2e-16 | 3e-14 | 1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Symt |
| 12 | 51806 | -1.57 | 2e-16 | 3e-14 | 4 x 50 calmodulin-like 5 [Source:HGNC Symbol;Acc:18180] |
| 13 | 55450 | 1.47 | 2e-16 | 3e-14 | 1 x 4 calcium/calmodulin-dependent protein kinase II inhibitor 1 [S |
| 14 | 1000 | 2.05 | 2e-16 | 3e-14 | 4 x 1 cadherin 2, type 1, N-cadherin (neuronal) [Source:HGNC Syr |
| 15 | 84518 | -1.88 | 2e-16 | 3e-14 | 1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183] |
| 16 | 1307 | 1.5 | 2e-16 | 3e-14 | 1 x 2 collagen, type XVI, alpha 1 [Source:HGNC Symbol;Acc:2193] |
| 17 | 169044 | 2.41 | 2e-16 | 3e-14 | 45 x 1 collagen, type XXII, alpha 1 [Source:HGNC Symbol;Acc:2298 |
| 18 | 1289 | 1.61 | 2e-16 | 3e-14 | 2 x 1 collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209] |
| 19 | 1290 | 1.54 | 2e-16 | 3e-14 | 2 x 1 collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210] |
| 20 | 1311 | 1.93 | 2e-16 | 3e-14 | 7 x 1 cartilage oligomeric matrix protein [Source:HGNC Symbol;Ac |

Global Geneset Analysis

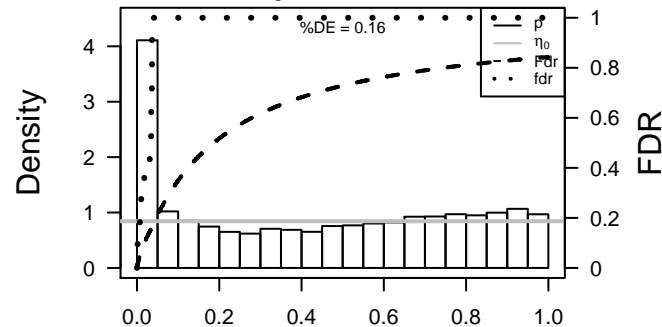
| Rank | GSZ | p-value | #all | Geneset |
|-----------------------|--------|---------|------|---|
| <i>Overexpressed</i> | | | | |
| 1 | 19.74 | NULL | 250 | LymphomaTENZ_Stromal signature 1 |
| 2 | 16.7 | NULL | 190 | CC extracellular matrix |
| 3 | 14.13 | NULL | 242 | BP extracellular matrix organization |
| 4 | 12.52 | NULL | 183 | CC proteinaceous extracellular matrix |
| 5 | 11.88 | NULL | 265 | Glio wilscher_GBM_Verhaak-CL_expression_B_up |
| 6 | 11.88 | NULL | 265 | Glio wilscher_GBM_Verhaak-MES_expression_B_up |
| 7 | 11.88 | NULL | 265 | Glio wilscher_GBM_Verhaak-PNwt_expression_B_down |
| 8 | 11.88 | NULL | 265 | Glio wilscher_GBM_Verhaak-PNmut_expression_B_down |
| 9 | 11.72 | NULL | 403 | BP cell adhesion |
| 10 | 10.37 | NULL | 16 | GSEA C2FARMER_BREAST_CANCER_CLUSTER_5 |
| 11 | 10.03 | NULL | 64 | BP collagen catabolic process |
| 12 | 9.84 | NULL | 69 | BP extracellular matrix disassembly |
| 13 | 9.7 | NULL | 16 | MMML C6CIEJ_MMML 1 |
| 14 | 9.61 | NULL | 683 | CC extracellular space |
| 15 | 9.42 | NULL | 57 | MF extracellular matrix structural constituent |
| 16 | 9.17 | NULL | 83 | CC basement membrane |
| 17 | 8.98 | NULL | 2659 | CC plasma membrane |
| 18 | 8.77 | NULL | 1135 | Chr 19 |
| 19 | 8.76 | NULL | 68 | CC collagen |
| 20 | 8.64 | NULL | 85 | MF integrin binding |
| <i>Underexpressed</i> | | | | |
| 1 | -18.86 | NULL | 572 | Disease GUDJ_poriasis up |
| 2 | -16.77 | NULL | 135 | H.Tiss WIRTH_Mucosa |
| 3 | -15.19 | NULL | 142 | Glio wilscher_GBM_Verhaak-CL_expression_C_up |
| 4 | -15.19 | NULL | 142 | Glio wilscher_GBM_Verhaak-PNmut_expression_C_down |
| 5 | -14.38 | NULL | 21 | CC cornified envelope |
| 6 | -11.55 | NULL | 42 | BP keratinization |
| 7 | -10.52 | NULL | 53 | BP keratinocyte differentiation |
| 8 | -10.47 | NULL | 370 | BP mitotic cell cycle |
| 9 | -9.97 | NULL | 10 | MF RAGE receptor binding |
| 10 | -9.61 | NULL | 10 | GSEA C2AUJLA_IL22_AND_IL17A_SIGNALING |
| 11 | -9.2 | NULL | 10 | GSEA C2NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON |
| 12 | -8.6 | NULL | 618 | Chr 4 |
| 13 | -8.25 | NULL | 11 | GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN |
| 14 | -8.19 | NULL | 16 | GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN |
| 15 | -7.65 | NULL | 949 | CC nucleoplasm |
| 16 | -7.45 | NULL | 1318 | CC mitochondrion |
| 17 | -7.4 | NULL | 232 | BP mitosis |
| 18 | -7.03 | NULL | 8 | GSEA C2MCLACHLAN_DENTAL_CARIES_UP |
| 19 | -6.84 | NULL | 10 | GSEA C2MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP |
| 20 | -6.77 | NULL | 16 | GSEA C2EGUCHI_CELL_CYCLE_RB1_TARGETS |

Profile

Regulated Spots



p-values



GW_253

Local Summary

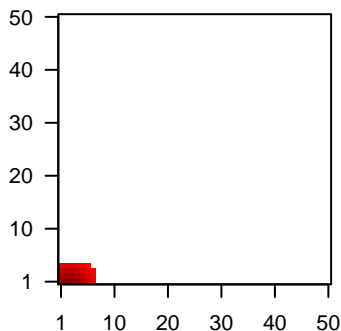
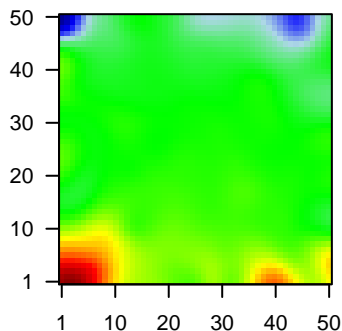
%DE = 0.83
 # metagenes = 27
 # genes = 387
 # genes in genesets = 383
 # genes with $fdr < 0.1$ = 280 (262 + / 18 -)
 # genes with $fdr < 0.05$ = 255 (238 + / 17 -)
 # genes with $fdr < 0.01$ = 224 (213 + / 11 -)

<r> metagenes = 0.94
 <r> genes = 0.37

<FC> = 0.63
 <shrinkage-t> = 21.95
 <p-value> = 0
 <fdr> = 0.33

Profile

Spot



Local Genelist

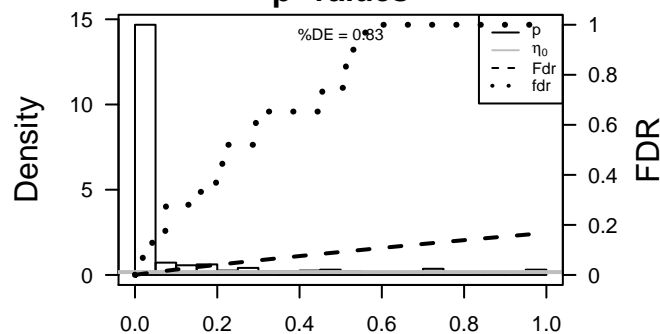
| Rank | ID | log(FC) | fdr | p-value | Description |
|------|--------|---------|-------|---------|---|
| 1 | 163782 | 2.06 | 2e-16 | 4e-16 | 1 x 2 KN motif and ankyrin repeat domains 4 [Source:HGNC Symb |
| 2 | 650 | 1.66 | 2e-16 | 4e-16 | 1 x 4 bone morphogenetic protein 2 [Source:HGNC Symbol;Acc:1C |
| 3 | 24141 | 1.48 | 2e-16 | 4e-16 | 7 x 1 lysosomal-associated membrane protein family, member 5 [S |
| 4 | 55450 | 1.47 | 2e-16 | 4e-16 | 1 x 4 calcium/calmodulin-dependent protein kinase II inhibitor 1 [S |
| 5 | 1000 | 2.05 | 2e-16 | 4e-16 | 4 x 1 cadherin 2, type 1, N-cadherin (neuronal) [Source:HGNC Syr |
| 6 | 1307 | 1.5 | 2e-16 | 4e-16 | 1 x 2 collagen, type XVI, alpha 1 [Source:HGNC Symbol;Acc:2193] |
| 7 | 1289 | 1.61 | 2e-16 | 4e-16 | 2 x 1 collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209] |
| 8 | 1290 | 1.54 | 2e-16 | 4e-16 | 2 x 1 collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210] |
| 9 | 1311 | 1.93 | 2e-16 | 4e-16 | 7 x 1 cartilage oligomeric matrix protein [Source:HGNC Symbol;Ac |
| 10 | 1464 | 2.18 | 2e-16 | 4e-16 | 1 x 3 chondroitin sulfate proteoglycan 4 [Source:HGNC Symbol;Ac |
| 11 | 285761 | 1.47 | 2e-16 | 4e-16 | 1 x 4 discoidin, CUB and LCCL domain containing 1 [Source:HGNC |
| 12 | 54541 | 1.49 | 2e-16 | 4e-16 | 1 x 4 DNA-damage-inducible transcript 4 [Source:HGNC Symbol; |
| 13 | 2191 | 1.52 | 2e-16 | 4e-16 | 1 x 1 fibroblast activation protein, alpha [Source:HGNC Symbol;Acc |
| 14 | 3043 | 1.56 | 2e-16 | 4e-16 | 5 x 1 hemoglobin, beta [Source:HGNC Symbol;Acc:4827] |
| 15 | 8988 | 2.29 | 2e-16 | 4e-16 | 1 x 4 heat shock 27kDa protein 3 [Source:HGNC Symbol;Acc:5248] |
| 16 | 3576 | -1.99 | 2e-16 | 4e-16 | 1 x 1 interleukin 8 [Source:HGNC Symbol;Acc:6025] |
| 17 | 4319 | 3.04 | 2e-16 | 4e-16 | 1 x 3 matrix metalloproteinase 10 (stromelysin 2) [Source:HGNC Sy |
| 18 | 4322 | 2.78 | 2e-16 | 4e-16 | 1 x 2 matrix metalloproteinase 13 (collagenase 3) [Source:HGNC S |
| 19 | 4316 | 2.58 | 2e-16 | 4e-16 | 2 x 1 matrix metalloproteinase 7 (matrilysin, uterine) [Source:HGNC |
| 20 | 25878 | 1.71 | 2e-16 | 4e-16 | 3 x 1 matrix-remodelling associated 5 [Source:HGNC Symbol;Acc: |

Local Geneset Analysis

Overexpression

| Rank | GSZ | p-value | #in/all | Geneset |
|------|-------|---------|------------|--|
| 1 | 33.46 | NULL | 70 / 190 | CC extracellular matrix |
| 2 | 32.84 | NULL | 89 / 250 | Lymphocyte ENZ_Stromal signature 1 |
| 3 | 27.91 | NULL | 72 / 242 | BP extracellular matrix organization |
| 4 | 27.34 | NULL | 15 / 16 | MMLL C63CIEJ_MMML 1 |
| 5 | 26.15 | NULL | 13 / 16 | GSEA C2FARMER_BREAST_CANCER_CLUSTER_5 |
| 6 | 24.76 | NULL | 33 / 69 | BP extracellular matrix disassembly |
| 7 | 24.52 | NULL | 11 / 15 | GSEA C2CROMER_TUMORIGENESIS_UP |
| 8 | 23.32 | NULL | 28 / 64 | BP collagen catabolic process |
| 9 | 20.89 | NULL | 44 / 183 | CC proteinaceous extracellular matrix |
| 10 | 18.22 | NULL | 22 / 57 | MF extracellular matrix structural constituent |
| 11 | 17.82 | NULL | 4 / 5 | GSEA C2COLLER_MYC_TARGETS_DN |
| 12 | 17.71 | NULL | 16 / 37 | BP collagen fibril organization |
| 13 | 17.58 | NULL | 11 / 19 | MF extracellular matrix binding |
| 14 | 16.74 | NULL | 8 / 16 | GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_L |
| 15 | 16.48 | NULL | 11 / 15 | GSEA C2ONDER_CDH1_TARGETS_2_UP |
| 16 | 16.25 | NULL | 8 / 11 | MF platelet-derived growth factor binding |
| 17 | 15.58 | NULL | 12 / 35 | Glio Colman_survival_associated |
| 18 | 15.5 | NULL | 50 / 265 | Glio willscher_GBM_Verhaak-CL_expression_B_up |
| 19 | 15.5 | NULL | 50 / 265 | Glio willscher_GBM_Verhaak-MES_expression_B_up |
| 20 | 15.5 | NULL | 50 / 265 | Glio willscher_GBM_Verhaak-PNwt_expression_B_down |
| 21 | 15.5 | NULL | 50 / 265 | Glio willscher_GBM_Verhaak-PNmut_expression_B_down |
| 22 | 15.46 | NULL | 4 / 7 | GSEA C2WANG_ESOPHAGUS_CANCER_PROGRESSION_UP |
| 23 | 15.33 | NULL | 7 / 16 | GSEA C2LIEN_BREAST_CARCINOMA_METAPLASTIC |
| 24 | 15.2 | NULL | 96 / 683 | CC extracellular space |
| 25 | 15.12 | NULL | 5 / 15 | GSEA C2ZHANG_POU5F1_TARGETS_UP |
| 26 | 14.78 | NULL | 9 / 25 | BP chondroitin sulfate biosynthetic process |
| 27 | 14.74 | NULL | 55 / 403 | BP cell adhesion |
| 28 | 14.67 | NULL | 20 / 68 | CC collagen |
| 29 | 14.57 | NULL | 5 / 11 | BP dermatan sulfate biosynthetic process |
| 30 | 14.38 | NULL | 7 / 11 | Glio Phillips MES up vs Prolif & PN |
| 31 | 14.32 | NULL | 6 / 10 | GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C4 |
| 32 | 14.04 | NULL | 127 / 1182 | CC extracellular region |
| 33 | 13.9 | NULL | 18 / 85 | MF integrin binding |
| 34 | 13.9 | NULL | 8 / 15 | GSEA C2DASU_IL6_SIGNALING_SCAR_DN |
| 35 | 13.84 | NULL | 6 / 13 | GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR |
| 36 | 13.79 | NULL | 9 / 16 | GSEA C2ROZANOV_MMP14_TARGETS_SUBSET |
| 37 | 13.66 | NULL | 8 / 12 | miRNA target-29c |
| 38 | 13.59 | NULL | 7 / 16 | GSEA C2CROONQUIST_STROMAL_STIMULATION_UP |
| 39 | 13.54 | NULL | 7 / 16 | GSEA C2U_TUMOR_VASCULATURE_UP |
| 40 | 13.44 | NULL | 9 / 15 | GSEA C2ONDER_CDH1_SIGNALING_VIA_CTNNB1 |

p-values



GW_253

Local Summary

%DE = 0.92
 # metagenes = 8
 # genes = 137
 # genes in genesets = 134

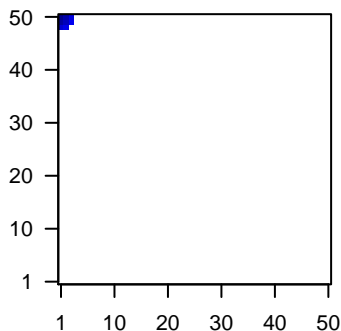
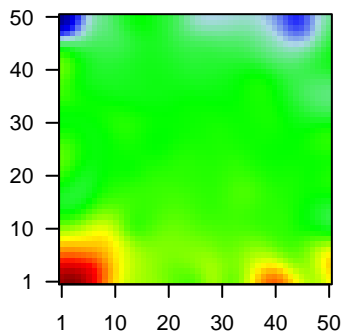
genes with $fdr < 0.1 = 119$ (9 + / 110 -)
 # genes with $fdr < 0.05 = 119$ (9 + / 110 -)
 # genes with $fdr < 0.01 = 107$ (9 + / 98 -)

<r> metagenes = 0.99
 <r> genes = 0.52

<FC> = -0.99
 <shrinkage-t> = -35.05
 <p-value> = 0
 <fdr> = 0.16

Profile

Spot



Local Genelist

| Rank | ID | log(FC) | fdr | p-value | Description |
|------|--------|---------|-------|---------|--|
| 1 | 131 | -1.92 | 2e-16 | 8e-17 | 1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide |
| 2 | 218 | -2.57 | 2e-16 | 8e-17 | 1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC] |
| 3 | 375791 | -2.05 | 2e-16 | 8e-17 | 1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Synt |
| 4 | 84518 | -1.88 | 2e-16 | 8e-17 | 1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183] |
| 5 | 49860 | -2.12 | 2e-16 | 8e-17 | 1 x 50 cornulin [Source:HGNC Symbol;Acc:1230] |
| 6 | 1475 | -2.23 | 2e-16 | 8e-17 | 1 x 50 cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481] |
| 7 | 1672 | -1.78 | 2e-16 | 8e-17 | 1 x 50 defensin, beta 1 [Source:HGNC Symbol;Acc:2766] |
| 8 | 414325 | -1.64 | 2e-16 | 8e-17 | 1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702] |
| 9 | 1673 | -2.18 | 2e-16 | 8e-17 | 1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193] |
| 10 | 128876 | -1.74 | 2e-16 | 8e-17 | 1 x 48 family with sequence similarity 83, member C [Source:HGNC] |
| 11 | 2877 | -1.64 | 2e-16 | 8e-17 | 1 x 50 glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Syr |
| 12 | 26085 | -1.65 | 2e-16 | 8e-17 | 1 x 50 kallikrein-related peptidase 13 [Source:HGNC Symbol;Acc:6: |
| 13 | 192666 | -1.6 | 2e-16 | 8e-17 | 1 x 50 keratin 24 [Source:HGNC Symbol;Acc:18527] |
| 14 | 3851 | -2.41 | 2e-16 | 8e-17 | 1 x 50 keratin 4 [Source:HGNC Symbol;Acc:6441] |
| 15 | 388533 | -3.12 | 2e-16 | 8e-17 | 1 x 49 keratinocyte differentiation-associated protein [Source:HGNC] |
| 16 | 84648 | -1.77 | 2e-16 | 8e-17 | 1 x 48 late cornified envelope 3D [Source:HGNC Symbol;Acc:16615] |
| 17 | 3934 | -1.68 | 2e-16 | 8e-17 | 1 x 50 lipocalin 2 [Source:HGNC Symbol;Acc:6526] |
| 18 | 8581 | -2.02 | 2e-16 | 8e-17 | 1 x 48 lymphocyte antigen 6 complex, locus D [Source:HGNC Symb |
| 19 | 5266 | -4.38 | 2e-16 | 8e-17 | 1 x 49 peptidase inhibitor 3, skin-derived [Source:HGNC Symbol;Ac |
| 20 | 6283 | -1.92 | 2e-16 | 8e-17 | 1 x 49 S100 calcium binding protein A12 [Source:HGNC Symbol;Ac |

Local Geneset Analysis

Underexpression

| Rank | GSZ | p-value | #in/all | Geneset |
|------|--------|---------|----------|---|
| 1 | -42.11 | NULL | 63 / 135 | H.Tiss WIRTH_Mucosa |
| 2 | -41.74 | NULL | 14 / 21 | CC cornified envelope |
| 3 | -31.91 | NULL | 16 / 42 | BP keratinization |
| 4 | -30.11 | NULL | 19 / 53 | BP keratinocyte differentiation |
| 5 | -26.48 | NULL | 4 / 10 | MF RAGE receptor binding |
| 6 | -25.06 | NULL | 65 / 572 | Disease GUDJ_psoriasis up |
| 7 | -23.99 | NULL | 2 / 8 | GSEA C2MCLACHLAN_DENTAL_CARIES_UP |
| 8 | -23.94 | NULL | 5 / 16 | GSEA C2ZONDER_CDH1_TARGETS_3_DN |
| 9 | -23.07 | NULL | 6 / 16 | GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN |
| 10 | -22.34 | NULL | 2 / 9 | GSEA C2MCLACHLAN_DENTAL_CARIES_DN |
| 11 | -21.55 | NULL | 8 / 19 | BP peptide cross-linking |
| 12 | -21.01 | NULL | 3 / 16 | GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP |
| 13 | -20.98 | NULL | 2 / 10 | GSEA C2NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON |
| 14 | -20.71 | NULL | 3 / 13 | GSEA C2FARMER_BREAST_CANCER_APOCRINE_VS_LUMINAL |
| 15 | -19.82 | NULL | 2 / 11 | GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN |
| 16 | -18.75 | NULL | 3 / 13 | GSEA C2HAN_SATB1_TARGETS_DN |
| 17 | -18.65 | NULL | 6 / 13 | BP negative regulation of peptidase activity |
| 18 | -18.5 | NULL | 16 / 76 | BP epidermis development |
| 19 | -18.36 | NULL | 3 / 16 | GSEA C2JAEGER_METASTASIS_DN |
| 20 | -17.96 | NULL | 2 / 13 | GSEA C2CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN |
| 21 | -17.18 | NULL | 2 / 10 | GSEA C2AUJLA_IL22_AND_IL17A_SIGNALING |
| 22 | -17.11 | NULL | 4 / 23 | MF peptidase inhibitor activity |
| 23 | -16.67 | NULL | 8 / 52 | BP negative regulation of endopeptidase activity |
| 24 | -16.52 | NULL | 2 / 15 | GSEA C2ZONDER_CDH1_TARGETS_2_DN |
| 25 | -16.52 | NULL | 2 / 15 | GSEA C2SMID_BREAST_CANCER_LUMINAL_B_DN |
| 26 | -16.41 | NULL | 3 / 16 | GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN |
| 27 | -15.74 | NULL | 3 / 15 | GSEA C2ZHANG_IMMORTALIZED_BY_HPV31_DN |
| 28 | -15.38 | NULL | 10 / 79 | MF serine-type endopeptidase inhibitor activity |
| 29 | -14.64 | NULL | 4 / 16 | GSEA C2LEE_LIVER_CANCER_MYC_TGFA_UP |
| 30 | -14.06 | NULL | 1 / 10 | GSEA C2THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_UP |
| 31 | -13.97 | NULL | 2 / 15 | GSEA C2JIN_SILENCED_BY_TUMOR_MICROENVIRONMENT |
| 32 | -13.71 | NULL | 4 / 15 | GSEA C2LEE_LIVER_CANCER_MYC_E2F1_UP |
| 33 | -13.43 | NULL | 4 / 34 | MF endopeptidase inhibitor activity |
| 34 | -13.34 | NULL | 2 / 15 | GSEA C2FERNANDEZ_BOUND_BY_MYC |
| 35 | -13.28 | NULL | 1 / 11 | GSEA C2LEI_MYB_TARGETS |
| 36 | -13.28 | NULL | 1 / 11 | GSEA C2HAN_SATB1_TARGETS_UP |
| 37 | -12.77 | NULL | 3 / 10 | GSEA C2SMID_BREAST_CANCER_ERBB2_UP |
| 38 | -12.14 | NULL | 3 / 12 | BP cellular aldehyde metabolic process |
| 39 | -12.02 | NULL | 1 / 13 | GSEA C2VECCHI_GASTRIC_CANCER_EARLY_UP |
| 40 | -12.02 | NULL | 1 / 13 | GSEA C2ZHANG_RESPONSE_TO_IKK_INHIBITOR_AND_TNF_UP |

p-values

