

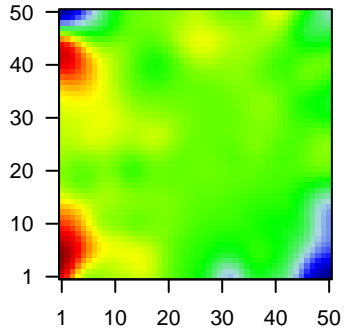
GW_200

Global Summary

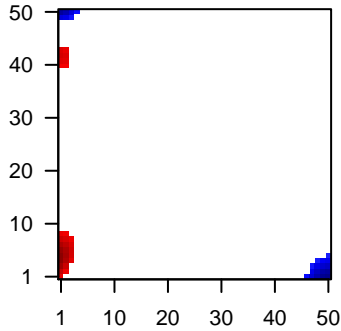
%DE = 0.14
 # genes with $fdr < 0.2$ = 1879 (968 + / 911 -)
 # genes with $fdr < 0.1$ = 1421 (733 + / 688 -)
 # genes with $fdr < 0.05$ = 1197 (612 + / 585 -)
 # genes with $fdr < 0.01$ = 833 (428 + / 405 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.11
 <fdr> = 0.86

Profile



Regulated Spots



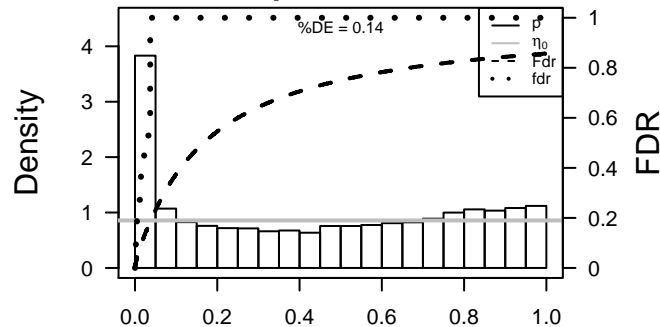
Global Genelist

| Rank | ID | log(FC) | fdr | p-value | Description |
|------|--------|---------|-------|---------|---|
| 1 | 9510 | 1.93 | 2e-16 | 5e-14 | 6 x 1 ADAM metallopeptidase with thrombospondin type 1 motif, 1 |
| 2 | 131 | -2.46 | 2e-16 | 5e-14 | 1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide |
| 3 | 8644 | -1.88 | 2e-16 | 5e-14 | 1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Sy |
| 4 | 1109 | -1.78 | 2e-16 | 5e-14 | 13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Sy |
| 5 | 216 | -1.92 | 2e-16 | 5e-14 | 50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC |
| 6 | 218 | -2.6 | 2e-16 | 5e-14 | 1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC |
| 7 | 684 | -1.78 | 2e-16 | 5e-14 | 32 x 1 bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A |
| 8 | 375791 | -1.84 | 2e-16 | 5e-14 | 1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Synt |
| 9 | 768 | 2.11 | 2e-16 | 5e-14 | 1 x 6 carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383] |
| 10 | 810 | -2.46 | 2e-16 | 5e-14 | 1 x 50 calmodulin-like 3 [Source:HGNC Symbol;Acc:1452] |
| 11 | 51806 | -1.79 | 2e-16 | 5e-14 | 4 x 50 calmodulin-like 5 [Source:HGNC Symbol;Acc:18180] |
| 12 | 4680 | -2.35 | 2e-16 | 5e-14 | 1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (i |
| 13 | 22802 | -2.22 | 2e-16 | 5e-14 | 1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20 |
| 14 | 1288 | 1.83 | 2e-16 | 5e-14 | 1 x 43 collagen, type IV, alpha 6 [Source:HGNC Symbol;Acc:2208] |
| 15 | 1289 | 1.81 | 2e-16 | 5e-14 | 2 x 1 collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209] |
| 16 | 51200 | 2.07 | 2e-16 | 5e-14 | 1 x 44 carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740] |
| 17 | 49860 | -2.48 | 2e-16 | 5e-14 | 1 x 50 cornulin [Source:HGNC Symbol;Acc:1230] |
| 18 | 1464 | 1.84 | 2e-16 | 5e-14 | 1 x 3 chondroitin sulfate proteoglycan 4 [Source:HGNC Symbol;Acc |
| 19 | 92196 | -1.95 | 2e-16 | 5e-14 | 3 x 50 death associated protein-like 1 [Source:HGNC Symbol;Acc:2 |
| 20 | 2634 | -1.84 | 2e-16 | 5e-14 | 47 x 1 guanylate binding protein 2, interferon-inducible [Source:HG |

Global Geneset Analysis

| Rank | GSZ | p-value | #all | Geneset |
|-----------------------|--------|---------|------|--|
| <i>Overexpressed</i> | | | | |
| 1 | 11.2 | NULL | 449 | Chr Chr 20 |
| 2 | 9.67 | NULL | 534 | Chr Chr 8 |
| 3 | 8.53 | NULL | 83 | CC basement membrane |
| 4 | 8.18 | NULL | 242 | BP extracellular matrix organization |
| 5 | 8.1 | NULL | 630 | Chr Chr X |
| 6 | 8.03 | NULL | 16 | GSEA C2BEGUM_TARGETS_OF_PAX3_FOXP01_FUSION_DN |
| 7 | 7.78 | NULL | 12 | BP hemidesmosome assembly |
| 8 | 6.97 | NULL | 15 | GSEA C2CROMER_TUMORIGENESIS_UP |
| 9 | 6.8 | NULL | 6 | GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP |
| 10 | 6.77 | NULL | 1135 | Chr Chr 19 |
| 11 | 6.39 | NULL | 35 | Glio Colman_survival_associated |
| 12 | 6.25 | NULL | 69 | BP extracellular matrix disassembly |
| 13 | 5.74 | NULL | 14 | GSEA C2AZARD_UV_RESPONSE_CLUSTER_G4 |
| 14 | 5.58 | NULL | 11 | GSEA C2BIOCARTA_PLATELETAPP_PATHWAY |
| 15 | 5.56 | NULL | 64 | BP collagen catabolic process |
| 16 | 5.49 | NULL | 519 | Chr Chr 14 |
| 17 | 5.42 | NULL | 299 | BP axon guidance |
| 18 | 5.24 | NULL | 10 | GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C4 |
| 19 | 5.22 | NULL | 13 | GSEA C2XU_HGF_TARGETS_INDUCED_BY_AKT1_48HR_UP |
| 20 | 5.19 | NULL | 11 | GSEA C2LIU_SOX4_TARGETS_UP |
| <i>Underexpressed</i> | | | | |
| 1 | -15.14 | NULL | 572 | Disease GUDJ_poriasis_up |
| 2 | -14.23 | NULL | 135 | H.Tiss WIRTH_Mucosa |
| 3 | -11.86 | NULL | 417 | H.Tiss WIRTH_Immune system |
| 4 | -10.99 | NULL | 553 | Cancer Lembcke_Colonc Inflammation |
| 5 | -9.74 | NULL | 312 | BP immune response |
| 6 | -9.53 | NULL | 21 | CC cornified envelope |
| 7 | -9.34 | NULL | 42 | BP keratinization |
| 8 | -8.98 | NULL | 51 | BP type I interferon signaling pathway |
| 9 | -8.07 | NULL | 12 | GSEA C2ZHAN_MULTIPLE_MYELOMA_DN |
| 10 | -8.04 | NULL | 16 | GSEA C2WANG_BARRETTS_ESOPHAGUS_DN |
| 11 | -7.81 | NULL | 16 | GSEA C2JROSEVIC_RESPONSE_TO_IMIQUIMOD |
| 12 | -7.44 | NULL | 74 | BP regulation of immune response |
| 13 | -7.42 | NULL | 10 | MF RAGE receptor binding |
| 14 | -7.33 | NULL | 123 | BP defense response to virus |
| 15 | -7.29 | NULL | 204 | BP cytokine-mediated signaling pathway |
| 16 | -7.24 | NULL | 16 | GSEA C2FARMER_BREAST_CANCER_CLUSTER_1 |
| 17 | -7.13 | NULL | 6 | GSEA C2SANA_RESPONSE_TO_IFNG_UP |
| 18 | -7.11 | NULL | 53 | BP keratinocyte differentiation |
| 19 | -6.73 | NULL | 16 | GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_D |
| 20 | -6.65 | NULL | 13 | GSEA C2WONG_ENDMETRIUM_CANCER_UP |

p-values



GW_200

Local Summary

%DE = 0.79
 # metagenes = 22
 # genes = 324
 # genes in genesets = 321

genes with $fdr < 0.1 = 202$ (196 + / 6 -)
 # genes with $fdr < 0.05 = 167$ (162 + / 5 -)
 # genes with $fdr < 0.01 = 134$ (131 + / 3 -)

$\langle r \rangle$ metagenes = 0.94
 $\langle r \rangle$ genes = 0.32

$\langle FC \rangle = 0.61$
 $\langle \text{shrinkage-t} \rangle = 21.4$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.47$

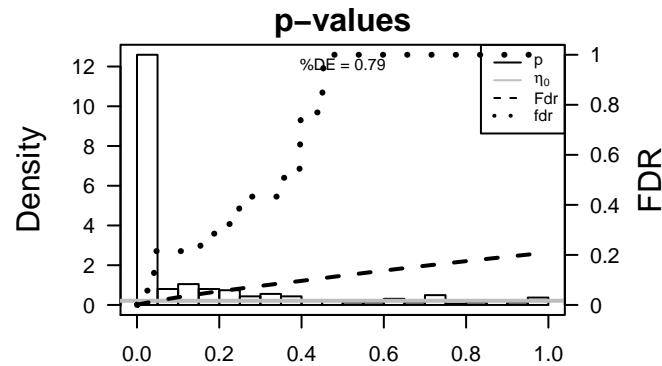
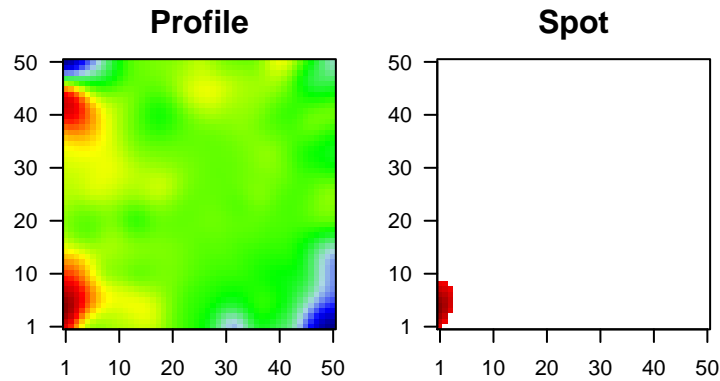
Local Genelist

| Rank | ID | log(FC) | fdr | p-value | Description |
|------|--------|---------|-------|---------|--|
| 1 | 768 | 2.11 | 2e-16 | 2e-15 | 1 x 6 carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383] |
| 2 | 1464 | 1.84 | 2e-16 | 2e-15 | 1 x 3 chondroitin sulfate proteoglycan 4 [Source:HGNC Symbol;Acc:11785] |
| 3 | 4319 | 3.04 | 2e-16 | 2e-15 | 1 x 3 matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Symbol;Acc:11785] |
| 4 | 4322 | 3.17 | 2e-16 | 2e-15 | 1 x 2 matrix metallopeptidase 13 (collagenase 3) [Source:HGNC Symbol;Acc:11785] |
| 5 | 4973 | 2.09 | 2e-16 | 2e-15 | 1 x 1 oxidized low density lipoprotein (lectin-like) receptor 1 [Source:HGNC Symbol;Acc:11785] |
| 6 | 5270 | 1.8 | 2e-16 | 2e-15 | 1 x 3 serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1) [Source:HGNC Symbol;Acc:11785] |
| 7 | 7057 | 1.91 | 2e-16 | 2e-15 | 1 x 1 thrombospondin 1 [Source:HGNC Symbol;Acc:11785] |
| 8 | 3371 | 2.22 | 2e-16 | 2e-15 | 1 x 3 tenascin C [Source:HGNC Symbol;Acc:5318] |
| 9 | 79783 | 1.71 | 2e-15 | 9e-14 | 1 x 5 succinyl-CoA:glutamate-CoA transferase [Source:HGNC Symbol;Acc:11785] |
| 10 | 56937 | 1.69 | 3e-15 | 2e-13 | 1 x 1 prostate transmembrane protein, androgen induced 1 [Source:HGNC Symbol;Acc:11785] |
| 11 | 163782 | 1.68 | 6e-15 | 8e-13 | 1 x 2 KN motif and ankyrin repeat domains 4 [Source:HGNC Symbol;Acc:11785] |
| 12 | 87 | 1.64 | 2e-14 | 8e-13 | 1 x 3 actinin, alpha 1 [Source:HGNC Symbol;Acc:163] |
| 13 | 1012 | 1.63 | 3e-14 | 1e-12 | 1 x 5 cadherin 13 [Source:HGNC Symbol;Acc:1753] |
| 14 | 4318 | 1.62 | 4e-14 | 2e-12 | 1 x 1 matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, matrilysin) [Source:HGNC Symbol;Acc:11785] |
| 15 | 1294 | 1.6 | 7e-14 | 4e-12 | 1 x 5 collagen, type VII, alpha 1 [Source:HGNC Symbol;Acc:2214] |
| 16 | 7424 | 1.58 | 2e-13 | 4e-12 | 1 x 3 vascular endothelial growth factor C [Source:HGNC Symbol;Acc:11785] |
| 17 | 3918 | 1.58 | 2e-13 | 5e-12 | 1 x 4 laminin, gamma 2 [Source:HGNC Symbol;Acc:6493] |
| 18 | 164284 | 1.57 | 3e-13 | 6e-12 | 1 x 3 adenomatous polyposis coli down-regulated 1-like [Source:HGNC Symbol;Acc:11785] |
| 19 | 650 | 1.56 | 4e-13 | 6e-12 | 1 x 4 bone morphogenetic protein 2 [Source:HGNC Symbol;Acc:11785] |
| 20 | 7045 | 1.43 | 4e-13 | 2e-11 | 1 x 2 transforming growth factor, beta-induced, 68kDa [Source:HGNC Symbol;Acc:11785] |

Local Geneset Analysis

Overexpression

| Rank | GSZ | p-value | #in/all | Geneset |
|------|-------|---------|-----------|---|
| 1 | 22.38 | NULL | 8 / 15 | GSEA C2CROMER_TUMORIGENESIS_UP |
| 2 | 19.93 | NULL | 44 / 242 | BP extracellular matrix organization |
| 3 | 17.93 | NULL | 4 / 10 | GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C4 |
| 4 | 14.37 | NULL | 47 / 403 | BP cell adhesion |
| 5 | 14.09 | NULL | 12 / 64 | BP collagen catabolic process |
| 6 | 14.08 | NULL | 86 / 1182 | CC extracellular region |
| 7 | 14.05 | NULL | 17 / 190 | CC extracellular matrix |
| 8 | 13.65 | NULL | 10 / 35 | Glio Colman_survival_associated |
| 9 | 13.5 | NULL | 12 / 69 | BP extracellular matrix disassembly |
| 10 | 13.25 | NULL | 54 / 683 | CC extracellular space |
| 11 | 13.11 | NULL | 7 / 16 | MF fibronectin binding |
| 12 | 13.01 | NULL | 5 / 16 | GSEA C2BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN |
| 13 | 12.85 | NULL | 3 / 6 | GSEA C2FOURNIER_ACINAR_DEVELOPMENT_EARLY_DN |
| 14 | 12.5 | NULL | 29 / 250 | LymphomaTENZ_Stromal signature 1 |
| 15 | 11.72 | NULL | 5 / 12 | BP hemidesmosome assembly |
| 16 | 11.59 | NULL | 18 / 183 | CC proteinaceous extracellular matrix |
| 17 | 11.54 | NULL | 3 / 11 | GSEA C2LIU_SOX4_TARGETS_UP |
| 18 | 11.49 | NULL | 4 / 13 | GSEA C2FRIDMAN_SENESCENCE_UP |
| 19 | 11.32 | NULL | 3 / 9 | GSEA C2REACTOME_SIGNALING_BY_VEGF |
| 20 | 11.14 | NULL | 12 / 72 | CC extracellular vesicular exosome |
| 21 | 11.12 | NULL | 6 / 15 | GSEA C2LEE_LIVER_CANCER_HEPATOBLAST |
| 22 | 10.9 | NULL | 4 / 16 | GSEA C2KEGG_BLADDER_CANCER |
| 23 | 10.89 | NULL | 3 / 16 | GSEA C2MURATA_VIRULENCE_OF_H_PILORI |
| 24 | 10.49 | NULL | 2 / 7 | GSEA C2FREDERICK_PRKCI_TARGETS |
| 25 | 10.45 | NULL | 3 / 10 | GSEA C2JEON_SMAD6_TARGETS_UP |
| 26 | 10.42 | NULL | 2 / 12 | GSEA C2Y_AGING_MIDDLE_UP |
| 27 | 10.33 | NULL | 3 / 14 | GSEA C2TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP |
| 28 | 10.16 | NULL | 1 / 8 | miRNA target-9 |
| 29 | 10.11 | NULL | 8 / 51 | BP regulation of cell migration |
| 30 | 10.09 | NULL | 4 / 10 | GSEA C2BIOCARTA_CELL2CELL_PATHWAY |
| 31 | 10.09 | NULL | 7 / 73 | MF metallopeptidase activity |
| 32 | 10.08 | NULL | 6 / 19 | MF laminin binding |
| 33 | 10.08 | NULL | 2 / 15 | GSEA C2MUELLER_METHYLATED_IN_GLIOMASTOMA |
| 34 | 9.97 | NULL | 4 / 15 | GSEA C2KANG_FLUOROURACIL_RESISTANCE_DN |
| 35 | 9.96 | NULL | 2 / 6 | Glio Martinez_Glio_hypometh |
| 36 | 9.9 | NULL | 7 / 81 | MF metalloendopeptidase activity |
| 37 | 9.88 | NULL | 3 / 11 | GSEA C2VERRECCHIA_DELAYED_RESPONSE_TO_TGFB1 |
| 38 | 9.81 | NULL | 12 / 70 | BP cell junction assembly |
| 39 | 9.66 | NULL | 2 / 8 | GSEA C2NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP |
| 40 | 9.62 | NULL | 3 / 16 | GSEA C2SU_PDEF_TARGETS_DN |



GW_200

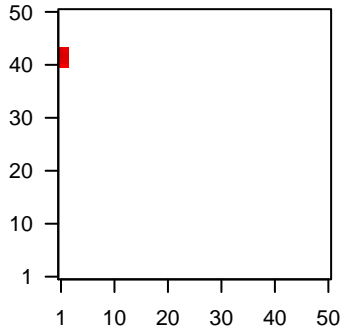
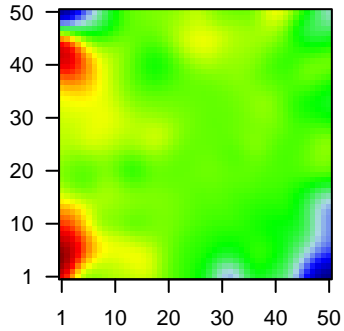
Local Summary

%DE = 0.83
 # metagenes = 8
 # genes = 116
 # genes in genesets = 114
 # genes with fdr < 0.1 = 76 (68 + / 8 -)
 # genes with fdr < 0.05 = 76 (68 + / 8 -)
 # genes with fdr < 0.01 = 66 (60 + / 6 -)

<r> metagenes = 0.99
 <r> genes = 0.36
 <FC> = 0.56
 <shrinkage-t> = 19.76
 <p-value> = 0
 <fdr> = 0.38

Profile

Spot



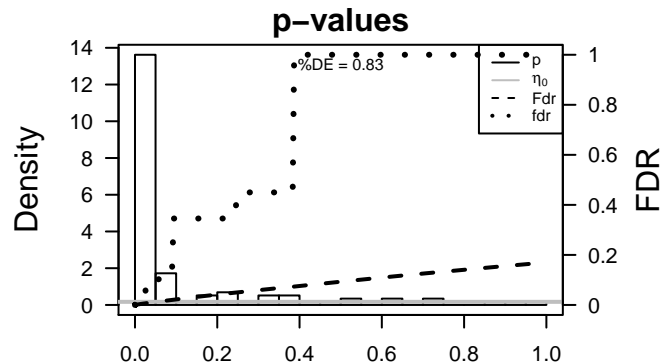
Local Genelist

| Rank | ID | log(FC) | fdr | p-value | Description |
|------|--------|---------|-------|---------|--|
| 1 | 1288 | 1.83 | 2e-16 | 7e-16 | 1 x 43 collagen, type IV, alpha 6 [Source:HGNC Symbol;Acc:2208] |
| 2 | 3306 | 2.21 | 2e-16 | 7e-16 | 1 x 42 heat shock 70kDa protein 2 [Source:HGNC Symbol;Acc:5235] |
| 3 | 3429 | -1.78 | 2e-16 | 7e-16 | 1 x 42 interferon, alpha-inducible protein 27 [Source:HGNC Symbol] |
| 4 | 147920 | 2.07 | 2e-16 | 7e-16 | 2 x 43 IGF-like family member 2 [Source:HGNC Symbol;Acc:32929] |
| 5 | 26499 | 1.88 | 2e-16 | 7e-16 | 1 x 42 pleckstrin 2 [Source:HGNC Symbol;Acc:19238] |
| 6 | 5744 | 2.2 | 2e-16 | 7e-16 | 1 x 43 parathyroid hormone-like hormone [Source:HGNC Symbol;A] |
| 7 | 8942 | -1.68 | 4e-15 | 6e-13 | 1 x 40 kynureninase [Source:HGNC Symbol;Acc:6469] |
| 8 | 1308 | 1.63 | 3e-14 | 1e-11 | 1 x 43 collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194] |
| 9 | 2352 | 1.54 | 7e-13 | 1e-08 | 1 x 42 folate receptor 3 (gamma) [Source:HGNC Symbol;Acc:3795] |
| 10 | 6513 | 1.3 | 1e-09 | 1e-08 | 1 x 43 solute carrier family 2 (facilitated glucose transporter), memb |
| 11 | 9124 | 1.28 | 2e-09 | 1e-08 | 1 x 40 PDZ and LIM domain 1 [Source:HGNC Symbol;Acc:2067] |
| 12 | 347735 | 1.28 | 2e-09 | 1e-08 | 1 x 43 serine incorporator 2 [Source:HGNC Symbol;Acc:23231] |
| 13 | 664 | 1.27 | 3e-09 | 1e-08 | 2 x 43 BCL2/adenovirus E1B 19kDa interacting protein 3 [Source:HK] |
| 14 | 2152 | 1.27 | 3e-09 | 6e-08 | 1 x 43 coagulation factor III (thromboplastin, tissue factor) [Source:H] |
| 15 | 133 | 1.14 | 8e-09 | 6e-08 | 1 x 42 adrenomedullin [Source:HGNC Symbol;Acc:259] |
| 16 | 3229 | 1.23 | 9e-09 | 1e-07 | 1 x 42 homeobox C13 [Source:HGNC Symbol;Acc:5125] |
| 17 | 4330 | 1.21 | 2e-08 | 2e-07 | 1 x 42 meningioma (disrupted in balanced translocation) 1 [Source:t] |
| 18 | 10397 | 1.08 | 5e-08 | 2e-07 | 1 x 42 N-myc downstream regulated 1 [Source:HGNC Symbol;Acc:1] |
| 19 | 5099 | 1.17 | 5e-08 | 2e-07 | 2 x 41 protocadherin 7 [Source:HGNC Symbol;Acc:8659] |
| 20 | 50805 | 1.16 | 6e-08 | 2e-07 | 1 x 43 iroquois homeobox 4 [Source:HGNC Symbol;Acc:6129] |

Local Geneset Analysis

Overexpression

| Rank | GSZ | p-value | #in/all | Geneset |
|------|-------|---------|---------|---|
| 1 | 19.11 | NULL | 2 / 2 | miRNA target-199a* |
| 2 | 14.88 | NULL | 2 / 5 | GSEA C2FERRARI_RESPONSE_TO_FENRETINIDE_DN |
| 3 | 14.51 | NULL | 2 / 11 | GSEA C2BIOCARTA_VITCB_PATHWAY |
| 4 | 13.29 | NULL | 1 / 7 | GSEA C2BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_AND_PAX3 |
| 5 | 12.37 | NULL | 3 / 15 | GSEA C2PRAMOONJAGO_SOX4_TARGETS_UP |
| 6 | 12.29 | NULL | 3 / 16 | GSEA C2LEONARD_HYPOXIA |
| 7 | 11.99 | NULL | 2 / 15 | GSEA C2NGUYEN_NOTCH1_TARGETS_UP |
| 8 | 11.92 | NULL | 3 / 16 | GSEA C2ELVIDGE_HIF1A_TARGETS_DN |
| 9 | 11.34 | NULL | 2 / 18 | BP male meiosis I |
| 10 | 11.14 | NULL | 2 / 10 | GSEA C2AZARD_UV_RESPONSE_CLUSTER_G3 |
| 11 | 10.99 | NULL | 1 / 4 | GSEA C2TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINI |
| 12 | 10.77 | NULL | 1 / 10 | GSEA C2CAFFAREL_RESPONSE_TO_THC_8HR_5_DN |
| 13 | 10.72 | NULL | 1 / 10 | BP surfactant homeostasis |
| 14 | 10.49 | NULL | 2 / 15 | GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN |
| 15 | 10.48 | NULL | 2 / 13 | GSEA C2HASINA_NOL7_TARGETS_UP |
| 16 | 10.36 | NULL | 1 / 4 | GSEA C2NIELSEN_LEIOMYOSARCOMA_DN |
| 17 | 10.26 | NULL | 2 / 12 | BP hemidesmosome assembly |
| 18 | 10.18 | NULL | 2 / 14 | GSEA C2MAINA_VHL_TARGETS_DN |
| 19 | 9.71 | NULL | 2 / 26 | BP positive regulation of cAMP biosynthetic process |
| 20 | 9.64 | NULL | 1 / 5 | GSEA C2RODRIGUES_DCC_TARGETS_UP |
| 21 | 9.41 | NULL | 2 / 16 | GSEA C2HARRIS_HYPOXIA |
| 22 | 9.17 | NULL | 1 / 13 | H.Tiss WIRTH_Thalamus |
| 23 | 9.05 | NULL | 2 / 16 | GSEA C2ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN |
| 24 | 9.04 | NULL | 2 / 16 | GSEA C2JZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN |
| 25 | 8.91 | NULL | 5 / 76 | BP epidermis development |
| 26 | 8.89 | NULL | 1 / 10 | GSEA C2BIOCARTA_ACE2_PATHWAY |
| 27 | 8.78 | NULL | 1 / 14 | BP negative regulation of chondrocyte differentiation |
| 28 | 8.66 | NULL | 1 / 5 | GSEA C2KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_4NC |
| 29 | 8.55 | NULL | 2 / 12 | GSEA C2MIZUKAMI_HYPOXIA_UP |
| 30 | 8.52 | NULL | 3 / 25 | BP brown fat cell differentiation |
| 31 | 8.51 | NULL | 2 / 16 | GSEA C2GALLUZZI_PERMEABILIZE_MITOCHONDRIA |
| 32 | 8.5 | NULL | 2 / 8 | GSEA C2MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_UP |
| 33 | 8.47 | NULL | 1 / 15 | GSEA C2FRIDMAN_IMMORTALIZATION_DN |
| 34 | 8.43 | NULL | 1 / 15 | GSEA C2AMIT_EGF_RESPONSE_240_MCF10A |
| 35 | 8.39 | NULL | 1 / 11 | GSEA C2BIOCARTA_PLATELETAPP_PATHWAY |
| 36 | 8.36 | NULL | 1 / 6 | GSEA C2MAINA_HYPOXIA_VHL_TARGETS_UP |
| 37 | 8.27 | NULL | 2 / 14 | GSEA C2VANHARANTA_UTERINE_FIBROID_DN |
| 38 | 8.17 | NULL | 2 / 14 | MF actin monomer binding |
| 39 | 8.16 | NULL | 1 / 16 | CC male germ cell nucleus |
| 40 | 8.11 | NULL | 1 / 6 | GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_21 |



GW_200

Local Summary

%DE = 0.89
 # metagenes = 17
 # genes = 291
 # genes in genesets = 289

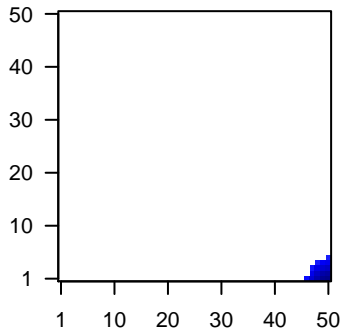
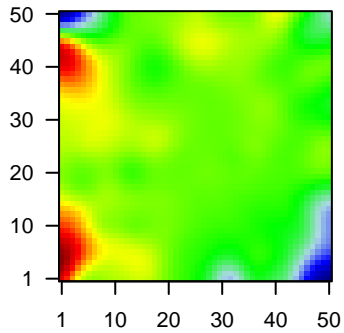
genes with $fdr < 0.1 = 250$ (8 + / 242 -)
 # genes with $fdr < 0.05 = 228$ (5 + / 223 -)
 # genes with $fdr < 0.01 = 186$ (1 + / 185 -)

$\langle r \rangle$ metagenes = 0.98
 $\langle r \rangle$ genes = 0.56

$\langle FC \rangle = -0.68$
 $\langle \text{shrinkage-t} \rangle = -23.83$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.32$

Profile

Spot



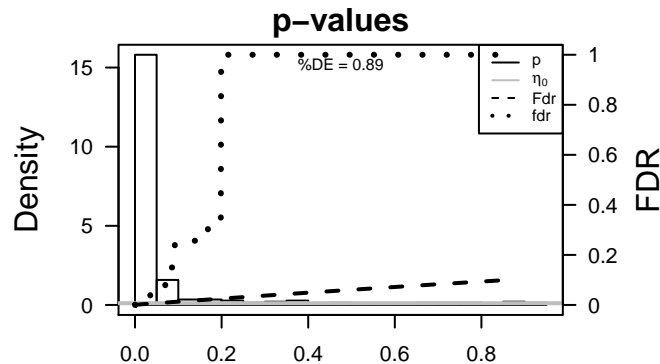
Local Genelist

| Rank | ID | log(FC) | fdr | p-value | Description |
|------|--------|---------|-------|---------|--|
| 1 | 2634 | -1.84 | 2e-16 | 1e-15 | 47 x 1 guanylate binding protein 2, interferon-inducible [Source:HGNC] |
| 2 | 3512 | -2.09 | 2e-16 | 1e-15 | 50 x 1 immunoglobulin J polypeptide, linker protein for immunoglobulin |
| 3 | 3543 | -2.69 | 2e-16 | 1e-15 | 49 x 1 immunoglobulin lambda-like polypeptide 1 [Source:HGNC] |
| 4 | 5920 | -2.11 | 2e-16 | 1e-15 | 48 x 1 retinoic acid receptor responder (tazarotene induced) 3 [Source:HGNC] |
| 5 | 10537 | -1.78 | 2e-16 | 1e-15 | 50 x 1 ubiquitin D [Source:HGNC Symbol;Acc:18795] |
| 6 | 3122 | -1.63 | 4e-16 | 2e-13 | 50 x 1 major histocompatibility complex, class II, DR alpha [Source:HGNC] |
| 7 | 3001 | -1.65 | 1e-14 | 2e-13 | 48 x 1 granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated protein 10) |
| 8 | 57172 | -1.65 | 1e-14 | 2e-13 | 49 x 1 calcium/calmodulin-dependent protein kinase IG [Source:HGNC] |
| 9 | 54855 | -1.64 | 2e-14 | 3e-12 | 49 x 1 family with sequence similarity 46, member C [Source:HGNC] |
| 10 | 3002 | -1.59 | 1e-13 | 1e-11 | 49 x 1 granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated protein 10) |
| 11 | 115361 | -1.54 | 7e-13 | 1e-11 | 48 x 1 guanylate binding protein 4 [Source:HGNC Symbol;Acc:2048] |
| 12 | 915 | -1.53 | 8e-13 | 5e-11 | 49 x 1 CD3d molecule, delta (CD3-TCR complex) [Source:HGNC] |
| 13 | 3108 | -1.48 | 5e-12 | 5e-11 | 50 x 1 major histocompatibility complex, class II, DM alpha [Source:HGNC] |
| 14 | 924 | -1.48 | 5e-12 | 5e-11 | 49 x 1 CD7 molecule [Source:HGNC Symbol;Acc:1695] |
| 15 | 3113 | -1.48 | 5e-12 | 6e-11 | 50 x 1 major histocompatibility complex, class II, DP alpha 1 [Source:HGNC] |
| 16 | 51755 | -1.47 | 7e-12 | 3e-10 | 49 x 1 cyclin-dependent kinase 12 [Source:HGNC Symbol;Acc:242] |
| 17 | 919 | -1.44 | 2e-11 | 3e-09 | 50 x 1 CD247 molecule [Source:HGNC Symbol;Acc:1677] |
| 18 | 260436 | -1.39 | 1e-10 | 7e-09 | 50 x 1 follicular dendritic cell secreted protein [Source:HGNC] |
| 19 | 3936 | -1.34 | 4e-10 | 7e-09 | 50 x 1 lymphocyte cytosolic protein 1 (L-plastin) [Source:HGNC] |
| 20 | 7318 | -1.32 | 8e-10 | 7e-09 | 48 x 1 ubiquitin-like modifier activating enzyme 7 [Source:HGNC] |

Local Geneset Analysis

Underexpression

| Rank | GSZ | p-value | #in/all | Geneset |
|------|--------|---------|----------|--|
| 1 | -27.68 | NULL | 91 / 417 | H.Tiss WIRTH_Immune system |
| 2 | -25.01 | NULL | 12 / 15 | CC MHC class II protein complex |
| 3 | -21.96 | NULL | 96 / 553 | Cancer Lembcke_Colonc Inflammation |
| 4 | -21.57 | NULL | 3 / 5 | GSEA C2WONG_ENDOMETRIAL_CANCER_LATE |
| 5 | -20.86 | NULL | 3 / 6 | GSEA C2SANA_RESPONSE_TO_IFNG_UP |
| 6 | -20.3 | NULL | 53 / 312 | BP immune response |
| 7 | -20.15 | NULL | 2 / 4 | MMML C6SCIEJ_MMML 2 |
| 8 | -19.17 | NULL | 9 / 16 | GSEA C2FARMER_BREAST_CANCER_CLUSTER_1 |
| 9 | -18.72 | NULL | 4 / 8 | GSEA C2GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN |
| 10 | -18.56 | NULL | 6 / 11 | GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY |
| 11 | -17.9 | NULL | 4 / 7 | Glio Donson-cytotoxic effectors-associated with LTS in HGA |
| 12 | -17.43 | NULL | 3 / 7 | GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN |
| 13 | -17.41 | NULL | 5 / 12 | GSEA C2BIOCARTA_CTL_PATHWAY |
| 14 | -15.87 | NULL | 5 / 11 | GSEA C2BIOCARTA_THELPER_PATHWAY |
| 15 | -15.72 | NULL | 2 / 3 | GSEA C2KEGG_VIRAL_MYOCARDITIS |
| 16 | -15.71 | NULL | 44 / 265 | Glio willscher_GBM_Verhaak-CL_expression_B_up |
| 17 | -15.71 | NULL | 44 / 265 | Glio willscher_GBM_Verhaak-MES_expression_B_up |
| 18 | -15.71 | NULL | 44 / 265 | Glio willscher_GBM_Verhaak-PNwt_expression_B_down |
| 19 | -15.71 | NULL | 44 / 265 | Glio willscher_GBM_Verhaak-PNmut_expression_B_down |
| 20 | -15.35 | NULL | 17 / 74 | BP regulation of immune response |
| 21 | -15.14 | NULL | 15 / 47 | BP antigen processing and presentation |
| 22 | -14.88 | NULL | 6 / 8 | BP Donson-migration tethering and rolling-associated with LTS in HGA |
| 23 | -14.37 | NULL | 15 / 60 | BP T cell costimulation |
| 24 | -14.26 | NULL | 7 / 15 | GSEA C2FINAK_BREAST_CANCER_SDPP_SIGNATURE |
| 25 | -14.12 | NULL | 5 / 13 | GSEA C2HAHTOLA_CTCL_PATHOGENESIS |
| 26 | -14.05 | NULL | 4 / 8 | GSEA C2NIELSEN_SYNOVIAL_SARCOMA_DN |
| 27 | -13.94 | NULL | 6 / 12 | GSEA C2ZHAN_MULTIPLE_MYELOMA_DN |
| 28 | -13.66 | NULL | 5 / 10 | GSEA C2FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_ |
| 29 | -13.37 | NULL | 2 / 5 | GSEA C2WEST_ADRENOCORTICAL_CARCINOMA_VS_ADENOMA_DN |
| 30 | -13.24 | NULL | 2 / 4 | GSEA C2KEGG_LEISHMANIA_INFECTIO |
| 31 | -13.12 | NULL | 6 / 13 | Cancer GENTLES_modul18 |
| 32 | -12.81 | NULL | 6 / 15 | Glio Donson-chemokines/cytokines-associated with LTS in HGA |
| 33 | -12.66 | NULL | 4 / 16 | BP cytolysis |
| 34 | -12.46 | NULL | 5 / 12 | BP immunoglobulin mediated immune response |
| 35 | -12.39 | NULL | 5 / 10 | GSEA C2LEE_DIFFERENTIATING_T_LYMPHOCYTE |
| 36 | -12.33 | NULL | 4 / 13 | GSEA C2BIOCARTA_IL17_PATHWAY |
| 37 | -12.27 | NULL | 4 / 9 | GSEA C2MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN |
| 38 | -12.05 | NULL | 25 / 162 | CC external side of plasma membrane |
| 39 | -11.94 | NULL | 1 / 6 | H.Tiss WIRTH_Bone marrow |
| 40 | -11.77 | NULL | 24 / 204 | BP cell surface receptor signaling pathway |



GW_200

Local Summary

%DE = 0.96
 # metagenes = 7
 # genes = 135
 # genes in genesets = 132

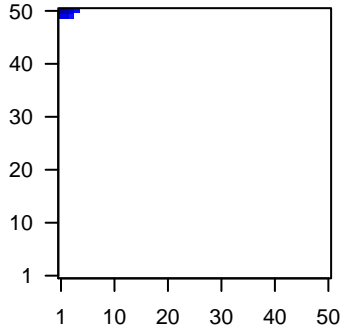
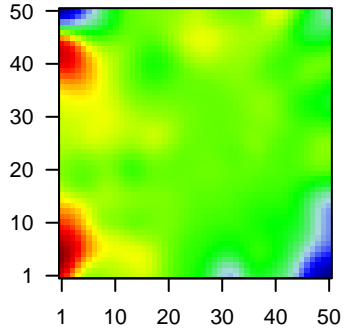
 # genes with $fdr < 0.1 = 117$ (6 + / 111 -)
 # genes with $fdr < 0.05 = 117$ (6 + / 111 -)
 # genes with $fdr < 0.01 = 113$ (6 + / 107 -)

<r> metagenes = 0.99
 <r> genes = 0.51

 <FC> = -1.04
 <shrinkage-t> = -36.86
 <p-value> = 0
 <fdr> = 0.17

Profile

Spot



Local Genelist

| Rank | ID | log(FC) | fdr | p-value | Description |
|------|--------|---------|-------|---------|--|
| 1 | 131 | -2.46 | 2e-16 | 5e-17 | 1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide |
| 2 | 8644 | -1.88 | 2e-16 | 5e-17 | 1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Sy] |
| 3 | 218 | -2.6 | 2e-16 | 5e-17 | 1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC] |
| 4 | 375791 | -1.84 | 2e-16 | 5e-17 | 1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Symt |
| 5 | 810 | -2.46 | 2e-16 | 5e-17 | 1 x 50 calmodulin-like 3 [Source:HGNC Symbol;Acc:1452] |
| 6 | 51806 | -1.79 | 2e-16 | 5e-17 | 4 x 50 calmodulin-like 5 [Source:HGNC Symbol;Acc:18180] |
| 7 | 4680 | -2.35 | 2e-16 | 5e-17 | 1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (i |
| 8 | 22802 | -2.22 | 2e-16 | 5e-17 | 1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20 |
| 9 | 49860 | -2.48 | 2e-16 | 5e-17 | 1 x 50 cornulin [Source:HGNC Symbol;Acc:1230] |
| 10 | 92196 | -1.95 | 2e-16 | 5e-17 | 3 x 50 death associated protein-like 1 [Source:HGNC Symbol;Acc:2 |
| 11 | 163351 | -1.92 | 2e-16 | 5e-17 | 1 x 50 guanylate binding protein family, member 6 [Source:HGNC S] |
| 12 | 3860 | -3.24 | 2e-16 | 5e-17 | 1 x 50 keratin 13 [Source:HGNC Symbol;Acc:6415] |
| 13 | 192666 | -1.77 | 2e-16 | 5e-17 | 1 x 50 keratin 24 [Source:HGNC Symbol;Acc:18527] |
| 14 | 3851 | -2.83 | 2e-16 | 5e-17 | 1 x 50 keratin 4 [Source:HGNC Symbol;Acc:6441] |
| 15 | 3934 | -2.58 | 2e-16 | 5e-17 | 1 x 50 lipocalin 2 [Source:HGNC Symbol;Acc:6526] |
| 16 | 4118 | -2.33 | 2e-16 | 5e-17 | 1 x 50 mal, T-cell differentiation protein [Source:HGNC Symbol;Acc |
| 17 | 6280 | -1.64 | 2e-16 | 5e-17 | 1 x 49 S100 calcium binding protein A9 [Source:HGNC Symbol;Acc: |
| 18 | 5275 | -1.84 | 2e-16 | 5e-17 | 1 x 50 serpin peptidase inhibitor, clade B (ovalbumin), member 13 [E |
| 19 | 6698 | -1.65 | 2e-16 | 5e-17 | 1 x 50 small proline-rich protein 1A [Source:HGNC Symbol;Acc:112 |
| 20 | 6700 | -1.97 | 2e-16 | 5e-17 | 1 x 50 small proline-rich protein 2A [Source:HGNC Symbol;Acc:112 |

Local Geneset Analysis

Underexpression

| Rank | GSZ | p-value | #in/all | Geneset |
|------|--------|---------|-----------|--|
| 1 | -52.19 | NULL | 57 / 135 | H.Tiss WIRTH_Mucosa |
| 2 | -30.43 | NULL | 12 / 21 | CC cornified envelope |
| 3 | -27.76 | NULL | 13 / 42 | BP keratinization |
| 4 | -26.06 | NULL | 16 / 53 | BP keratinocyte differentiation |
| 5 | -21.82 | NULL | 16 / 76 | BP epidermis development |
| 6 | -21.52 | NULL | 55 / 572 | Disease GUDJ_psooriasis up |
| 7 | -20.54 | NULL | 7 / 19 | BP peptide cross-linking |
| 8 | -17.64 | NULL | 5 / 16 | GSEA C2WNDER_CDH1_TARGETS_3_DN |
| 9 | -17.45 | NULL | 4 / 10 | MF RAGE receptor binding |
| 10 | -17.06 | NULL | 4 / 16 | GSEA C2WANG_BARRETTS_ESOPHAGUS_DN |
| 11 | -16.53 | NULL | 6 / 16 | GSEA C2CROMER_TUMORIGENESIS_DN |
| 12 | -15.53 | NULL | 5 / 15 | GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN |
| 13 | -14.33 | NULL | 1 / 6 | GSEA C2SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN |
| 14 | -13.82 | NULL | 4 / 15 | MF retinol dehydrogenase activity |
| 15 | -13.71 | NULL | 3 / 16 | GSEA C2CHEOK_RESPONSE_TO_MERCAPTOPYRINE_AND_LD_MTX_1 |
| 16 | -12.58 | NULL | 3 / 12 | BP cellular aldehyde metabolic process |
| 17 | -11.67 | NULL | 2 / 12 | GSEA C2ZHAN_MULTIPLE_MYELOMA_DN |
| 18 | -11.18 | NULL | 12 / 186 | MF structural molecule activity |
| 19 | -10.98 | NULL | 3 / 15 | GSEA C2LEE_LIVER_CANCER_MYC_E2F1_UP |
| 20 | -10.96 | NULL | 1 / 8 | GSEA C2LIU_CDX2_TARGETS_DN |
| 21 | -10.96 | NULL | 3 / 15 | GSEA C2ZHANG_IMMORTALIZED_BY_HPV31_DN |
| 22 | -10.95 | NULL | 9 / 79 | MF serine-type endopeptidase inhibitor activity |
| 23 | -10.61 | NULL | 4 / 44 | CC keratin filament |
| 24 | -10.56 | NULL | 3 / 15 | GSEA C2CRICKMAN_HEAD_AND_NECK_CANCER_E |
| 25 | -10.54 | NULL | 6 / 38 | BP epithelial cell differentiation |
| 26 | -10.45 | NULL | 1 / 10 | GSEA C2MURAKAMI_UV_RESPONSE_1HR_UP |
| 27 | -10.21 | NULL | 4 / 29 | BP regulation of proteolysis |
| 28 | -10.03 | NULL | 6 / 16 | GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN |
| 29 | -9.92 | NULL | 1 / 6 | GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN |
| 30 | -9.86 | NULL | 1 / 11 | GSEA C2MURAKAMI_UV_RESPONSE_6HR_DN |
| 31 | -9.52 | NULL | 7 / 52 | BP negative regulation of endopeptidase activity |
| 32 | -9.49 | NULL | 3 / 27 | BP response to bacterium |
| 33 | -9.42 | NULL | 5 / 13 | BP negative regulation of peptidase activity |
| 34 | -9.41 | NULL | 4 / 10 | GSEA C2SMID_BREAST_CANCER_ERBB2_UP |
| 35 | -9.4 | NULL | 2 / 13 | GSEA C2WONG_ENDOMETRIUM_CANCER_UP |
| 36 | -9.29 | NULL | 2 / 16 | GSEA C2MURATA_VIRULENCE_OF_H_PILORI |
| 37 | -9.22 | NULL | 41 / 1182 | CC extracellular region |
| 38 | -8.96 | NULL | 2 / 14 | GSEA C2KEGG_PHENYLALANINE_METABOLISM |
| 39 | -8.9 | NULL | 6 / 82 | CC intermediate filament |
| 40 | -8.71 | NULL | 3 / 16 | GSEA C2LEE_LIVER_CANCER_ACOX1_UP |

p-values

