

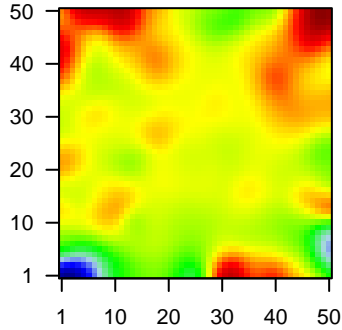
GW_035

Global Summary

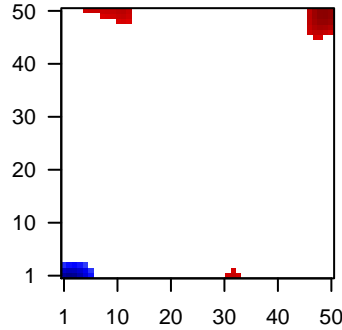
%DE = 0.14
 # genes with fdr < 0.2 = 1928 (1047 + / 881 -)
 # genes with fdr < 0.1 = 1547 (845 + / 702 -)
 # genes with fdr < 0.05 = 1372 (752 + / 620 -)
 # genes with fdr < 0.01 = 996 (570 + / 426 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.09
 <fdr> = 0.86

Profile



Regulated Spots



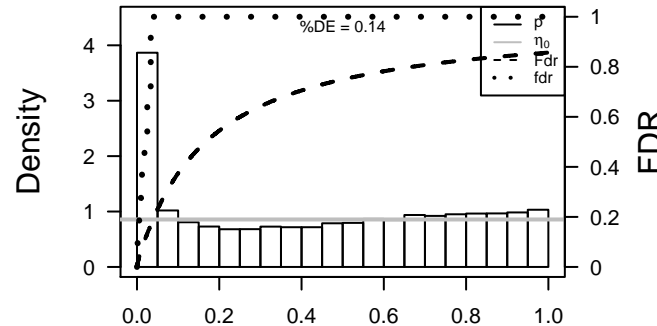
Global Genelist

| Rank | ID | log(FC) | fdr | p-value | Description |
|------|--------|---------|-------|---------|--|
| 1 | 59 | -1.37 | 2e-16 | 3e-14 | 3 x 1 actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;] |
| 2 | 131 | -2.5 | 2e-16 | 3e-14 | 1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide |
| 3 | 9447 | 1.4 | 2e-16 | 3e-14 | 32 x 1 absent in melanoma 2 [Source:HGNC Symbol;Acc:357] |
| 4 | 57016 | -1.67 | 2e-16 | 3e-14 | 1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase |
| 5 | 216 | -1.33 | 2e-16 | 3e-14 | 50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC] |
| 6 | 218 | -1.62 | 2e-16 | 3e-14 | 1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC] |
| 7 | 200810 | 1.3 | 2e-16 | 3e-14 | 49 x 50 ALG1, chitobiosylidiphosphodolichol beta--mannosyltransferas |
| 8 | 154796 | 1.25 | 2e-16 | 3e-14 | 50 x 12 angiomin [Source:HGNC Symbol;Acc:17810] |
| 9 | 200315 | 1.34 | 2e-16 | 3e-14 | 1 x 40 apolipoprotein B mRNA editing enzyme, catalytic polypeptide |
| 10 | 445 | 2.07 | 2e-16 | 3e-14 | 50 x 47 argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:756] |
| 11 | 84707 | 1.43 | 2e-16 | 3e-14 | 50 x 48 brain expressed X-linked 2 [Source:HGNC Symbol;Acc:3093] |
| 12 | 387695 | 1.27 | 2e-16 | 3e-14 | 1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Synt |
| 13 | 84419 | 1.38 | 2e-16 | 3e-14 | 5 x 50 chromosome 15 open reading frame 48 [Source:HGNC Synt |
| 14 | 339512 | 1.99 | 2e-16 | 3e-14 | 50 x 50 chromosome 1 open reading frame 110 [Source:HGNC Synt |
| 15 | 205428 | 1.55 | 2e-16 | 3e-14 | 50 x 50 chromosome 3 open reading frame 58 [Source:HGNC Synt |
| 16 | 387103 | 1.26 | 2e-16 | 3e-14 | 45 x 49 centromere protein W [Source:HGNC Symbol;Acc:21488] |
| 17 | 760 | 1.66 | 2e-16 | 3e-14 | 1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373] |
| 18 | 810 | 1.35 | 2e-16 | 3e-14 | 1 x 50 calmodulin-like 3 [Source:HGNC Symbol;Acc:1452] |
| 19 | 51806 | 1.92 | 2e-16 | 3e-14 | 4 x 50 calmodulin-like 5 [Source:HGNC Symbol;Acc:18180] |
| 20 | 595 | -1.92 | 2e-16 | 3e-14 | 1 x 6 cyclin D1 [Source:HGNC Symbol;Acc:1582] |

Global Geneset Analysis

| Rank | GSZ | p-value | #all | Geneset |
|-----------------------|--------|---------|------|--|
| <i>Overexpressed</i> | | | | |
| 1 | 21.47 | NULL | 914 | Chr Chr 3 |
| 2 | 10.35 | NULL | 135 | H.Tiss WIRTH_Mucosa |
| 3 | 7.87 | NULL | 572 | Disease GUDJ_pсориаз is up |
| 4 | 7.47 | NULL | 633 | Chr Chr 9 |
| 5 | 7.31 | NULL | 13 | H.Tiss WIRTH_Tonsil |
| 6 | 7.26 | NULL | 4 | MMML C63CIEJ_MMML 23 |
| 7 | 6.71 | NULL | 12 | BP hemidesmosome assembly |
| 8 | 6.58 | NULL | 13 | GSEA C2SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP |
| 9 | 6.54 | NULL | 16 | GSEA C2ELVIDGE_HIF1A_TARGETS_DN |
| 10 | 6.3 | NULL | 15 | GSEA C2AIGNER_ZEB1_TARGETS |
| 11 | 6.02 | NULL | 16 | GSEA C2ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN |
| 12 | 5.82 | NULL | 11 | GSEA C2BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS |
| 13 | 5.46 | NULL | 7 | MMML C63CIEJ_MMML 13 |
| 14 | 5.46 | NULL | 717 | Chr Chr 16 |
| 15 | 5.42 | NULL | 15 | GSEA C2PNDAR_RESPONSE_TO_ADAPHOSTIN_DN |
| 16 | 5.42 | NULL | 11 | GSEA C2BIOCARTA_AHSP_PATHWAY |
| 17 | 5.39 | NULL | 10 | BP cellular response to zinc ion |
| 18 | 5.31 | NULL | 12 | MF fatty acid binding |
| 19 | 5.19 | NULL | 51 | BP type I interferon signaling pathway |
| 20 | 5.18 | NULL | 13 | BP cellular response to lithium ion |
| <i>Underexpressed</i> | | | | |
| 1 | -14.47 | NULL | 190 | CC extracellular matrix |
| 2 | -11.9 | NULL | 250 | LymphomaL1ENZ_Stromal signature 1 |
| 3 | -9.77 | NULL | 957 | Chr Chr 11 |
| 4 | -9.51 | NULL | 16 | GSEA C2FARMER_BREAST_CANCER_CLUSTER_5 |
| 5 | -9.48 | NULL | 16 | GSEA C2CROONQUIST_STROMAL_STIMULATION_UP |
| 6 | -9.41 | NULL | 11 | MF platelet-derived growth factor binding |
| 7 | -9.16 | NULL | 683 | CC extracellular space |
| 8 | -9.06 | NULL | 183 | CC proteinaceous extracellular matrix |
| 9 | -8.86 | NULL | 69 | BP extracellular matrix disassembly |
| 10 | -8.5 | NULL | 64 | BP collagen catabolic process |
| 11 | -8.39 | NULL | 16 | MMML C63CIEJ_MMML 1 |
| 12 | -8.34 | NULL | 15 | GSEA C2MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INH |
| 13 | -8.16 | NULL | 242 | BP extracellular matrix organization |
| 14 | -8.13 | NULL | 57 | MF extracellular matrix structural constituent |
| 15 | -7.49 | NULL | 12 | miRNA target-29c |
| 16 | -7.43 | NULL | 92 | BP translational elongation |
| 17 | -7.3 | NULL | 1182 | CC extracellular region |
| 18 | -7.27 | NULL | 128 | BP translational initiation |
| 19 | -7.16 | NULL | 81 | BP viral transcription |
| 20 | -7.11 | NULL | 15 | GSEA C2AMIT_EGF_RESPONSE_40_HELA |

p-values



GW_035

Local Summary

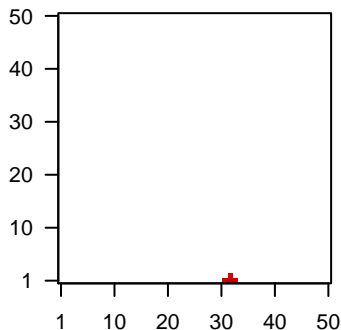
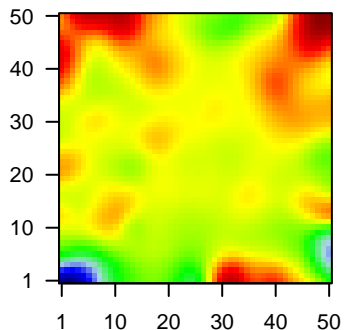
%DE = 0.7
 # metagenes = 4
 # genes = 109
 # genes in genesets = 107
 # genes with fdr < 0.1 = 57 (53 + / 4 -)
 # genes with fdr < 0.05 = 53 (49 + / 4 -)
 # genes with fdr < 0.01 = 39 (36 + / 3 -)

<r> metagenes = 1
 <r> genes = 0.49

<FC> = 0.33
 <shrinkage-t> = 11.74
 <p-value> = 0
 <fdr> = 0.52

Profile

Spot



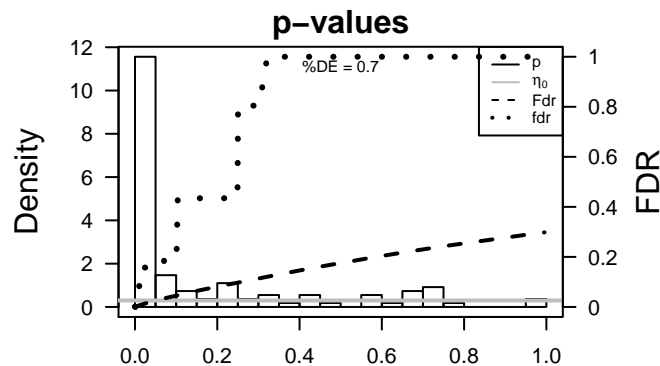
Local Genelist

| Rank | ID | log(FC) | fdr | p-value | Description |
|------|-------|---------|-------|---------|--|
| 1 | 9447 | 1.4 | 2e-16 | 2e-15 | 32 x 1 absent in melanoma 2 [Source:HGNC Symbol;Acc:357] |
| 2 | 27074 | 1.27 | 2e-16 | 2e-15 | 32 x 1 lysosomal-associated membrane protein 3 [Source:HGNC S |
| 3 | 83666 | 1.23 | 2e-16 | 2e-15 | 32 x 1 poly (ADP-ribose) polymerase family, member 9 [Source:HGI |
| 4 | 8743 | 1.45 | 2e-16 | 2e-15 | 32 x 1 tumor necrosis factor (ligand) superfamily, member 10 [Sourc |
| 5 | 629 | 1.22 | 7e-16 | 4e-10 | 32 x 1 complement factor B [Source:HGNC Symbol;Acc:1037] |
| 6 | 9997 | 1.03 | 1e-11 | 6e-10 | 32 x 1 SCO2 cytochrome c oxidase assembly protein [Source:HGNC |
| 7 | 23780 | 1 | 3e-11 | 9e-10 | 32 x 1 apolipoprotein L, 2 [Source:HGNC Symbol;Acc:619] |
| 8 | 54625 | 0.99 | 6e-11 | 9e-10 | 32 x 1 poly (ADP-ribose) polymerase family, member 14 [Source:HC |
| 9 | 3136 | 0.98 | 8e-11 | 1e-09 | 32 x 1 |
| 10 | 5699 | 0.97 | 1e-10 | 1e-08 | 32 x 1 proteasome (prosome, macropain) subunit, beta type, 10 [So |
| 11 | 4599 | 0.86 | 5e-10 | 1e-08 | 32 x 1 myxovirus (influenza virus) resistance 1, interferon-inducible |
| 12 | 55008 | 0.93 | 8e-10 | 3e-08 | 32 x 1 HECT and RLD domain containing E3 ubiquitin protein ligase |
| 13 | 3959 | 0.91 | 2e-09 | 2e-07 | 32 x 1 lectin, galactoside-binding, soluble, 3 binding protein [Source |
| 14 | 79156 | -0.87 | 9e-09 | 8e-07 | 31 x 1 pleckstrin homology domain containing, family F (with FYVE c |
| 15 | 64108 | 0.83 | 3e-08 | 8e-07 | 32 x 1 receptor (chemosensory) transporter protein 4 [Source:HGNC |
| 16 | 6355 | -0.82 | 6e-08 | 8e-07 | 32 x 1 chemokine (C-C motif) ligand 8 [Source:HGNC Symbol;Acc: |
| 17 | 94240 | 0.81 | 9e-08 | 8e-07 | 32 x 1 epithelial stromal interaction 1 (breast) [Source:HGNC Symbc |
| 18 | 5359 | 0.8 | 1e-07 | 1e-06 | 32 x 1 phospholipid scramblase 1 [Source:HGNC Symbol;Acc:9092] |
| 19 | 4940 | 0.79 | 2e-07 | 1e-06 | 32 x 1 2'-5'-oligoadenylate synthetase 3, 100kDa [Source:HGNC S |
| 20 | 3106 | 0.72 | 2e-07 | 1e-06 | 32 x 1 major histocompatibility complex, class I, B [Source:HGNC S |

Local Geneset Analysis

Overexpression

| Rank | GSZ | p-value | #in/all | Geneset |
|------|-------|---------|----------|--|
| 1 | 41.5 | NULL | 8 / 11 | GSEA C2BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS |
| 2 | 36.12 | NULL | 6 / 6 | Lymphoma_AVE_MHCII BL DN |
| 3 | 30.46 | NULL | 7 / 10 | CC MHC class I protein complex |
| 4 | 28.89 | NULL | 12 / 16 | GSEA C2MOSERLE_IFNA_RESPONSE |
| 5 | 27.31 | NULL | 29 / 51 | BP type I interferon signaling pathway |
| 6 | 26.51 | NULL | 6 / 14 | GSEA C2RADAIEVA_RESPONSE_TO_IFNA1_UP |
| 7 | 25.85 | NULL | 11 / 16 | GSEA C2ZHANG_INTERFERON_RESPONSE |
| 8 | 25.2 | NULL | 6 / 8 | GSEA C2ROETH_TERT_TARGETS_UP |
| 9 | 24.92 | NULL | 8 / 18 | BP positive regulation of T cell mediated cytotoxicity |
| 10 | 22.27 | NULL | 7 / 18 | MF peptide antigen binding |
| 11 | 21.75 | NULL | 11 / 16 | GSEA C2EINAV_INTERFERON_SIGNATURE_IN_CANCER |
| 12 | 21.5 | NULL | 31 / 123 | BP defense response to virus |
| 13 | 20.42 | NULL | 3 / 9 | GSEA C2FURUKAWA_DUSP6_TARGETS_PC135_UP |
| 14 | 19.92 | NULL | 7 / 16 | GSEA C2MAHADEVAN_RESPONSE_TO_MP470_UP |
| 15 | 19.56 | NULL | 46 / 572 | Disease GUDJ_poriasis up |
| 16 | 19.52 | NULL | 16 / 60 | BP interferon-gamma-mediated signaling pathway |
| 17 | 18.97 | NULL | 13 / 31 | BP negative regulation of viral genome replication |
| 18 | 18.77 | NULL | 2 / 2 | MMML C2SCIEJ_MMML_27 |
| 19 | 18.75 | NULL | 6 / 16 | GSEA C2XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR |
| 20 | 18.53 | NULL | 4 / 14 | GSEA C2SANA_TNF_SIGNALING_UP |
| 21 | 17.37 | NULL | 9 / 10 | GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX |
| 22 | 17.36 | NULL | 10 / 13 | GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN |
| 23 | 17.26 | NULL | 4 / 10 | GSEA C2DAUER_STAT3_TARGETS_DN |
| 24 | 17.01 | NULL | 12 / 70 | BP antigen processing and presentation of exogenous peptide antigen |
| 25 | 16.5 | NULL | 12 / 74 | BP antigen processing and presentation of exogenous peptide antigen |
| 26 | 15.6 | NULL | 1 / 6 | Glio Martinez_Glio_hypometh |
| 27 | 15.52 | NULL | 34 / 204 | BP cytokine-mediated signaling pathway |
| 28 | 15.12 | NULL | 3 / 15 | GSEA C2LIANG_SILENCED_BY_METHYLATION_2 |
| 29 | 14.98 | NULL | 5 / 23 | CC integral to luminal side of endoplasmic reticulum membrane |
| 30 | 14.79 | NULL | 8 / 52 | Chr HSCR6_MHC_QBL |
| 31 | 14.79 | NULL | 31 / 274 | Lymphoma_SPANG_IL21 DN |
| 32 | 14.73 | NULL | 12 / 91 | BP antigen processing and presentation of peptide antigen via MHC cl |
| 33 | 14.41 | NULL | 6 / 32 | CC ER to Golgi transport vesicle membrane |
| 34 | 14.39 | NULL | 2 / 16 | GSEA C2HAHTOLA_MYCOSIS_FUNGOIDES_SKIN_DN |
| 35 | 14.3 | NULL | 2 / 11 | GSEA C2LINDSTEDT_DENDRITIC_CELL_MATURATION_B |
| 36 | 13.49 | NULL | 1 / 2 | miRNA target-152 |
| 37 | 13.33 | NULL | 27 / 109 | BP response to virus |
| 38 | 13.32 | NULL | 4 / 22 | MF NAD+ ADP-ribosyltransferase activity |
| 39 | 12.51 | NULL | 3 / 5 | GSEA C2KIM_LRRC3B_TARGETS |
| 40 | 12.31 | NULL | 3 / 14 | GSEA C2XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_UP |



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Local Summary

%DE = 0.62
 # metagenes = 27
 # genes = 322
 # genes in genesets = 320

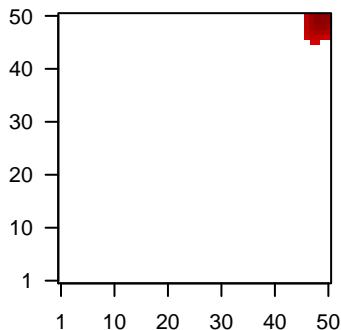
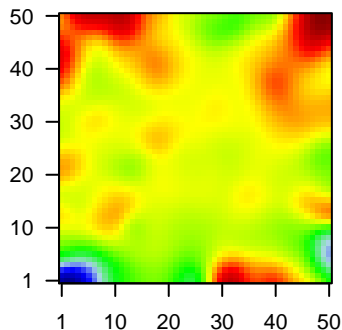
genes with $fdr < 0.1$ = 139 (117 + / 22 -)
 # genes with $fdr < 0.05$ = 137 (117 + / 20 -)
 # genes with $fdr < 0.01$ = 106 (93 + / 13 -)

<r> metagenes = 0.92
 <r> genes = 0.26

<FC> = 0.26
 <shrinkage-t> = 9.14
 <p-value> = 0
 <fdr> = 0.57

Profile

Spot



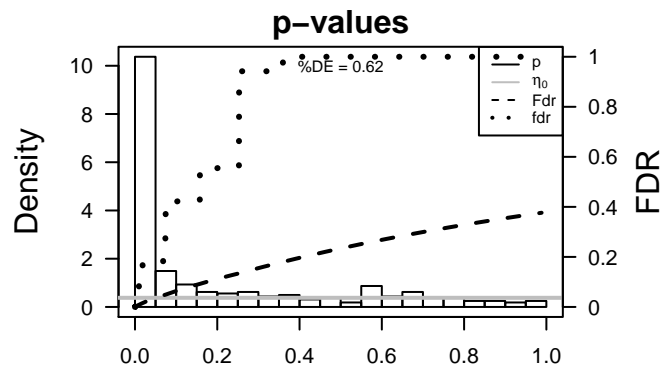
Local Genelist

| Rank | ID | log(FC) | fdr | p-value | Description |
|------|--------|---------|-------|---------|---|
| 1 | 216 | -1.33 | 2e-16 | 2e-15 | 50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC |
| 2 | 200810 | 1.3 | 2e-16 | 2e-15 | 49 x 50 ALG1, chitobiosyldiphosphodolichol beta-mannosyltransferas |
| 3 | 445 | 2.07 | 2e-16 | 2e-15 | 50 x 47 argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75f |
| 4 | 84707 | 1.43 | 2e-16 | 2e-15 | 50 x 48 brain expressed X-linked 2 [Source:HGNC Symbol;Acc:3093 |
| 5 | 339512 | 1.99 | 2e-16 | 2e-15 | 50 x 50 chromosome 1 open reading frame 110 [Source:HGNC Synt |
| 6 | 205428 | 1.55 | 2e-16 | 2e-15 | 50 x 50 chromosome 3 open reading frame 58 [Source:HGNC Symbc |
| 7 | 286676 | 1.33 | 2e-16 | 2e-15 | 50 x 49 immunoglobulin-like domain containing receptor 1 [Source:H |
| 8 | 3866 | 2.27 | 2e-16 | 2e-15 | 50 x 50 keratin 15 [Source:HGNC Symbol;Acc:6421] |
| 9 | 3880 | 1.83 | 2e-16 | 2e-15 | 50 x 49 keratin 19 [Source:HGNC Symbol;Acc:6436] |
| 10 | 3856 | 1.78 | 2e-16 | 2e-15 | 50 x 48 keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056] |
| 11 | 4171 | 1.24 | 2e-16 | 2e-15 | 46 x 48 minichromosome maintenance complex component 2 [Source |
| 12 | 84223 | 1.21 | 9e-16 | 7e-12 | 47 x 46 IQ motif containing G [Source:HGNC Symbol;Acc:25251] |
| 13 | 83959 | 1.21 | 9e-16 | 7e-12 | 50 x 50 solute carrier family 4, sodium borate transporter, member 11 |
| 14 | 80723 | 1.13 | 6e-14 | 6e-11 | 47 x 45 solute carrier family 35, member G2 [Source:HGNC Symbol;/ |
| 15 | 256764 | -1.07 | 1e-12 | 6e-11 | 50 x 50 WD repeat domain 72 [Source:HGNC Symbol;Acc:26790] |
| 16 | 10655 | 1.07 | 1e-12 | 6e-11 | 50 x 50 doublesex and mab-3 related transcription factor 2 [Source:H |
| 17 | 6565 | 1.07 | 2e-12 | 3e-10 | 50 x 50 solute carrier family 15 (oligopeptide transporter), member 2 |
| 18 | 56650 | 1.05 | 4e-12 | 2e-09 | 49 x 50 claudin domain containing 1 [Source:HGNC Symbol;Acc:132 |
| 19 | 80218 | 1.01 | 2e-11 | 2e-09 | 46 x 50 N(alpha)-acetyltransferase 50, NatE catalytic subunit [Source |
| 20 | 54800 | 1 | 4e-11 | 3e-09 | 50 x 48 kelch-like family member 24 [Source:HGNC Symbol;Acc:259 |

Local Geneset Analysis

Overexpression

| Rank | GSZ | p-value | #in/all | Geneset |
|------|-------|---------|----------|--|
| 1 | 21.63 | NULL | 3 / 8 | GSEA C2JUCDX2_TARGETS_DN |
| 2 | 18.62 | NULL | 75 / 914 | Chr Chr 3 |
| 3 | 13.16 | NULL | 1 / 5 | GSEA C2NIELSEN_SCHWANNOMA_DN |
| 4 | 11.45 | NULL | 5 / 13 | GSEA C2PUJANA_XPRSS_INT_NETWORK |
| 5 | 11.07 | NULL | 6 / 14 | GSEA C2PUJANA_BRCA_CENTERED_NETWORK |
| 6 | 11.01 | NULL | 4 / 15 | GSEA C2KIM_MYCN_AMPLIFICATION_TARGETS_DN |
| 7 | 10.58 | NULL | 4 / 11 | GSEA C2REACTOME_UNWINDING_OF_DNA |
| 8 | 10.26 | NULL | 3 / 16 | GSEA C2MOREAUX_MULTIPLE_MYELOMA_BY_TACI_DN |
| 9 | 9.86 | NULL | 4 / 16 | GSEA C2RODWELL_AGING_KIDNEY_DN |
| 10 | 9.85 | NULL | 3 / 13 | GSEA C2SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP |
| 11 | 9.54 | NULL | 4 / 11 | GSEA C2KALMA_E2F1_TARGETS |
| 12 | 9.34 | NULL | 3 / 15 | GSEA C2KAUFFMANN_DNA_REPLICATION_GENES |
| 13 | 8.97 | NULL | 3 / 13 | GSEA C2JAERVINEN_AMPLIFIED_IN_LARYNGEAL_CANCER |
| 14 | 8.92 | NULL | 1 / 10 | BP urea cycle |
| 15 | 8.87 | NULL | 3 / 15 | GSEA C2SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6 |
| 16 | 8.84 | NULL | 7 / 30 | BP DNA strand elongation involved in DNA replication |
| 17 | 8.71 | NULL | 3 / 16 | GSEA C2RODWELL_AGING_KIDNEY_NO_BLOOD_DN |
| 18 | 8.59 | NULL | 4 / 16 | GSEA C2PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP |
| 19 | 8.51 | NULL | 3 / 15 | GSEA C2TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_UP |
| 20 | 8.32 | NULL | 4 / 12 | GSEA C2J_WILMS_TUMOR_VS_FETAL_KIDNEY_1_DN |
| 21 | 7.95 | NULL | 2 / 7 | GSEA C2REACTOME_G1_S_TRANSITION |
| 22 | 7.85 | NULL | 3 / 16 | Cancer WOLFER_overlap genes |
| 23 | 7.83 | NULL | 1 / 15 | H.Tiss WIRTH_Cerebellum |
| 24 | 7.55 | NULL | 1 / 16 | GSEA C2ROY_WOUND_BLOOD_VESSEL_DN |
| 25 | 7.44 | NULL | 1 / 11 | GSEA C2WHITESIDE_CISPLATIN_RESISTANCE_DN |
| 26 | 7.43 | NULL | 4 / 16 | GSEA C2EGUCHI_CELL_CYCLE_RB1_TARGETS |
| 27 | 7.43 | NULL | 4 / 15 | GSEA C2JDAYAKUMAR_MED1_TARGETS_UP |
| 28 | 7.37 | NULL | 5 / 16 | GSEA C2SONG_TARGETS_OF_IE86_CMV_PROTEIN |
| 29 | 7.37 | NULL | 3 / 14 | GSEA C2KORKOLA_YOLK_SAC_TUMOR |
| 30 | 7.33 | NULL | 4 / 16 | GSEA C2BILD_E2F3_ONCOGENIC_SIGNATURE |
| 31 | 7.19 | NULL | 2 / 14 | GSEA C2BHATI_G2M_ARREST_BY_2METHOXYESTRADIOL_UP |
| 32 | 7.18 | NULL | 4 / 22 | BP DNA replication initiation |
| 33 | 7.02 | NULL | 3 / 14 | GSEA C2MITSIADES_RESPONSE_TO_APLIDIN_DN |
| 34 | 6.96 | NULL | 2 / 15 | GSEA C2RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP |
| 35 | 6.96 | NULL | 2 / 9 | GSEA C2REACTOME_MITOTIC_M_M_G1_PHASES |
| 36 | 6.96 | NULL | 3 / 16 | GSEA C2BIOCARTA_MCM_PATHWAY |
| 37 | 6.94 | NULL | 4 / 15 | GSEA C2KEGG_CELL_CYCLE |
| 38 | 6.83 | NULL | 4 / 24 | MF DNA helicase activity |
| 39 | 6.76 | NULL | 1 / 13 | GSEA C2CHEN_LUNG_CANCER_SURVIVAL |
| 40 | 6.73 | NULL | 2 / 7 | GSEA C2WALK_AML_CLUSTER_6 |



GW_035

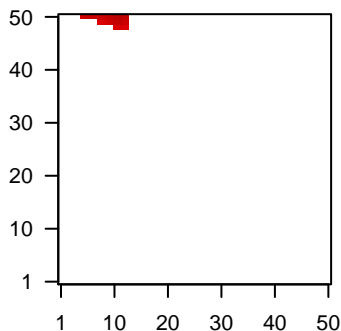
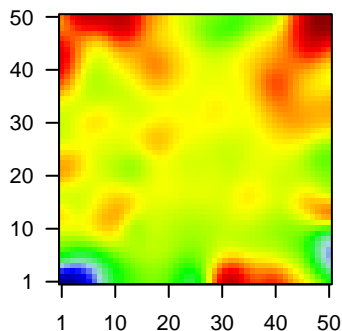
Local Summary

%DE = 0.68
 # metagenes = 18
 # genes = 272
 # genes in genesets = 271
 # genes with $fdr < 0.1$ = 138 (115 + / 23 -)
 # genes with $fdr < 0.05$ = 121 (102 + / 19 -)
 # genes with $fdr < 0.01$ = 82 (73 + / 9 -)

$\langle r \rangle$ metagenes = 0.87
 $\langle r \rangle$ genes = 0.25
 $\langle FC \rangle = 0.25$
 $\langle \text{shrinkage-t} \rangle = 8.93$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.54$

Profile

Spot



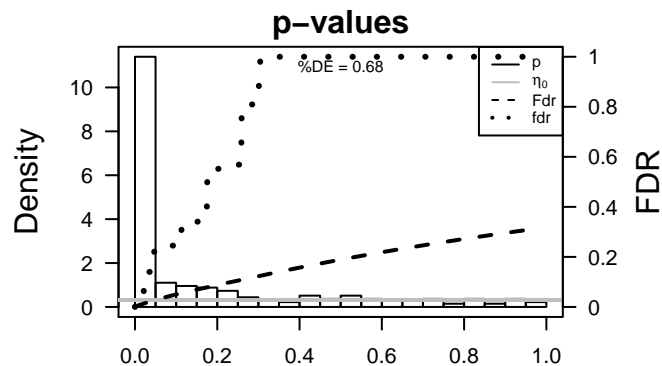
Local Genelist

| Rank | ID | log(FC) | fdr | p-value | Description |
|------|--------|---------|-------|---------|---|
| 1 | 84419 | 1.38 | 2e-16 | 2e-15 | 5 x 50 chromosome 15 open reading frame 48 [Source:HGNC Synt |
| 2 | 1717 | 1.36 | 2e-16 | 2e-15 | 13 x 50 7-dehydrocholesterol reductase [Source:HGNC Symbol;Acc: |
| 3 | 200958 | 1.5 | 2e-16 | 2e-15 | 6 x 50 mucin 20, cell surface associated [Source:HGNC Symbol;Acc: |
| 4 | 4828 | 1.4 | 2e-16 | 2e-15 | 13 x 50 neuromedin B [Source:HGNC Symbol;Acc:7842] |
| 5 | 5327 | 1.3 | 2e-16 | 2e-15 | 9 x 50 plasminogen activator, tissue [Source:HGNC Symbol;Acc:90f |
| 6 | 5627 | 1.6 | 2e-16 | 2e-15 | 7 x 50 protein S (alpha) [Source:HGNC Symbol;Acc:9456] |
| 7 | 7113 | 1.28 | 2e-16 | 2e-15 | 5 x 50 transmembrane protease, serine 2 [Source:HGNC Symbol;Ac |
| 8 | 25987 | 1.43 | 2e-16 | 2e-15 | 13 x 50 tsukushi, small leucine rich proteoglycan [Source:HGNC Sym |
| 9 | 9368 | 1.18 | 4e-15 | 5e-13 | 5 x 50 solute carrier family 9, subfamily A (NHE3, cation proton anti |
| 10 | 10610 | 1.16 | 1e-14 | 5e-13 | 12 x 50 ST6 (alpha-N-acetyl-neuraminy-2,3-beta-galactosyl-1,3)- |
| 11 | 10974 | 1.16 | 2e-14 | 4e-12 | 5 x 50 adipogenesis regulatory factor [Source:HGNC Symbol;Acc:24 |
| 12 | 483 | 1.13 | 6e-14 | 4e-10 | 13 x 50 ATPase, Na+/K+ transporting, beta 3 polypeptide [Source:HG |
| 13 | 84059 | 1.03 | 7e-12 | 4e-10 | 11 x 50 G protein-coupled receptor 98 [Source:HGNC Symbol;Acc:1 |
| 14 | 1366 | 1.02 | 1e-11 | 4e-10 | 6 x 50 claudin 7 [Source:HGNC Symbol;Acc:2049] |
| 15 | 157506 | 1.02 | 1e-11 | 3e-09 | 8 x 50 retinol dehydrogenase 10 (all-trans) [Source:HGNC Symbol;A |
| 16 | 2539 | -0.98 | 9e-11 | 3e-09 | 13 x 50 glucose-6-phosphate dehydrogenase [Source:HGNC Symb |
| 17 | 481 | 0.98 | 9e-11 | 9e-09 | 10 x 50 ATPase, Na+/K+ transporting, beta 1 polypeptide [Source:HG |
| 18 | 406988 | 0.96 | 2e-10 | 3e-08 | 12 x 50 MIR205 host gene (non-protein coding) [Source:HGNC Syml |
| 19 | 4071 | 0.86 | 5e-10 | 7e-08 | 12 x 50 transmembrane 4 L six family member 1 [Source:HGNC Sym |
| 20 | 1962 | 0.91 | 2e-09 | 7e-08 | 13 x 50 enoyl-CoA, hydratase/3-hydroxyacyl CoA dehydrogenase [S |

Local Geneset Analysis

Overexpression

| Rank | GSZ | p-value | #in/all | Geneset |
|------|-------|---------|---------|---|
| 1 | 15.71 | NULL | 6 / 13 | H.Tiss WIRTH_Tonsil |
| 2 | 11.72 | NULL | 2 / 15 | BP fibrinolysis |
| 3 | 11.61 | NULL | 5 / 15 | GSEA C2AIGNER_ZEB1_TARGETS |
| 4 | 11.02 | NULL | 2 / 10 | BP positive regulation of hormone secretion |
| 5 | 10.44 | NULL | 2 / 16 | CC microvillus membrane |
| 6 | 10.25 | NULL | 3 / 15 | GSEA C2PNDAR_RESPONSE_TO_ADAPHOSTIN_DN |
| 7 | 9.62 | NULL | 2 / 10 | GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_UP |
| 8 | 9.17 | NULL | 3 / 10 | GSEA C2REACTOME_TRANSFORMATION_OF_LANOSTEROL_TO_CHOL |
| 9 | 9.17 | NULL | 4 / 15 | GSEA C2REACTOME_CHOLESTEROL_BIOSYNTHESIS |
| 10 | 9.15 | NULL | 2 / 13 | GSEA C2KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION |
| 11 | 9.05 | NULL | 1 / 8 | GSEA C2REACTOME_GAMMA_CARBOXYLATION_TRANSPORT_AND_A |
| 12 | 8.76 | NULL | 3 / 15 | GSEA C2JEON_SMAD6_TARGETS_DN |
| 13 | 8.51 | NULL | 3 / 15 | GSEA C2KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTIO |
| 14 | 8.47 | NULL | 1 / 9 | GSEA C2REACTOME_COMMON_PATHWAY |
| 15 | 8.45 | NULL | 3 / 15 | GSEA C2IN_SILENCED_BY_TUMOR_MICROENVIRONMENT |
| 16 | 8.33 | NULL | 2 / 15 | GSEA C2MULLIGHAN_NPM1_MUTATED_SIGNATURE_2_DN |
| 17 | 8.32 | NULL | 4 / 45 | BP O-glycan processing |
| 18 | 8.2 | NULL | 4 / 15 | GSEA C2REACTOME_TIGHT_JUNCTION_INTERACTIONS |
| 19 | 8.19 | NULL | 3 / 16 | GSEA C2ELVIDGE_HYPOXIA_BY_DMOG_UP |
| 20 | 8.18 | NULL | 2 / 10 | miRNA 3UTR-325 |
| 21 | 8.15 | NULL | 5 / 63 | CC Golgi lumen |
| 22 | 8.15 | NULL | 2 / 16 | GSEA C2REACTOME_BASIGIN_INTERACTIONS |
| 23 | 7.67 | NULL | 2 / 15 | GSEA C2MASSARWEH_RESPONSE_TO ESTRADIOL |
| 24 | 7.57 | NULL | 1 / 11 | GSEA C2BIOCARTA_EXTRINSIC_PATHWAY |
| 25 | 7.57 | NULL | 1 / 5 | GSEA C2SHARMA_ASTROCYTOMA_WITH_NF1_SYNDROM |
| 26 | 7.55 | NULL | 6 / 106 | BP leukocyte migration |
| 27 | 7.25 | NULL | 2 / 14 | GSEA C2BOYALT_LIVER_CANCER_SUBCLASS_G12_DN |
| 28 | 7.08 | NULL | 1 / 10 | BP lateral ventricle development |
| 29 | 7.04 | NULL | 3 / 16 | GSEA C2KEGG_STEROID_BIOSYNTHESIS |
| 30 | 6.93 | NULL | 1 / 10 | BP arachidonic acid secretion |
| 31 | 6.89 | NULL | 1 / 13 | GSEA C2BIOCARTA_AMI_PATHWAY |
| 32 | 6.81 | NULL | 2 / 22 | BP metal ion transport |
| 33 | 6.65 | NULL | 2 / 12 | GSEA C2REACTOME_AMINO_ACID_SYNTHESIS_AND_INTERCONVERS |
| 34 | 6.64 | NULL | 2 / 9 | GSEA C2GHO_ATF5_TARGETS_UP |
| 35 | 6.57 | NULL | 1 / 11 | BP negative regulation of hormone secretion |
| 36 | 6.52 | NULL | 1 / 8 | GSEA C2IAZAG_TGFB1_SIGNALING_VIA_SMAD4_DN |
| 37 | 6.47 | NULL | 2 / 16 | GSEA C2MENSE_HYPOXIA_UP |
| 38 | 6.45 | NULL | 1 / 10 | GSEA C2BIOCARTA_FIBRINOLYSIS_PATHWAY |
| 39 | 6.44 | NULL | 2 / 14 | GSEA C2ZHAN_MULTIPLE_MYELOMA_CD2_DN |
| 40 | 6.38 | NULL | 1 / 11 | BP sterol biosynthetic process |



GW_035

Local Summary

%DE = 0.92
 # metagenes = 17
 # genes = 266
 # genes in genesets = 265

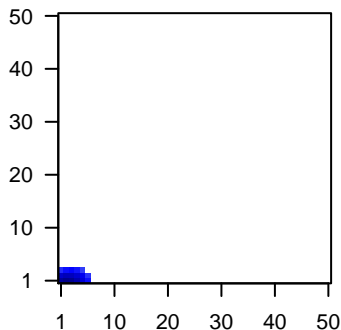
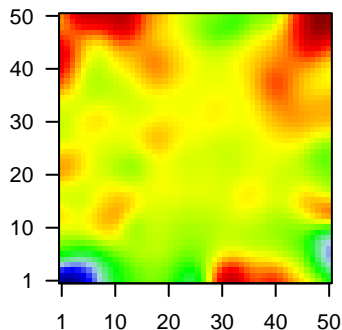
genes with $fdr < 0.1$ = 229 (12 + / 217 -)
 # genes with $fdr < 0.05$ = 216 (11 + / 205 -)
 # genes with $fdr < 0.01$ = 179 (9 + / 170 -)

$\langle r \rangle$ metagenes = 0.96
 $\langle r \rangle$ genes = 0.41

$\langle FC \rangle = -0.51$
 $\langle \text{shrinkage-t} \rangle = -18$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.29$

Profile

Spot



Local Genelist

| Rank | ID | log(FC) | fdr | p-value | Description |
|------|-------|---------|-------|---------|---|
| 1 | 59 | -1.37 | 2e-16 | 3e-16 | 3 x 1 actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;] |
| 2 | 1281 | -1.33 | 2e-16 | 3e-16 | 2 x 1 collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201] |
| 3 | 1291 | -1.33 | 2e-16 | 3e-16 | 2 x 1 collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211] |
| 4 | 1490 | -1.3 | 2e-16 | 3e-16 | 3 x 1 connective tissue growth factor [Source:HGNC Symbol;Acc:2] |
| 5 | 3039 | 2.17 | 2e-16 | 3e-16 | 5 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824] |
| 6 | 3040 | 2.19 | 2e-16 | 3e-16 | 4 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824] |
| 7 | 3043 | 1.98 | 2e-16 | 3e-16 | 5 x 1 hemoglobin, beta [Source:HGNC Symbol;Acc:4827] |
| 8 | 4312 | -1.67 | 2e-16 | 3e-16 | 1 x 1 matrix metalloproteinase 1 (interstitial collagenase) [Source:Hi] |
| 9 | 4319 | -1.33 | 2e-16 | 3e-16 | 1 x 3 matrix metalloproteinase 10 (stromelysin 2) [Source:HGNC Sy] |
| 10 | 4314 | -1.53 | 2e-16 | 3e-16 | 1 x 1 matrix metalloproteinase 3 (stromelysin 1, progelatinase) [Sou] |
| 11 | 4316 | -1.25 | 2e-16 | 3e-16 | 2 x 1 matrix metalloproteinase 7 (matrilysin, uterine) [Source:HGNC] |
| 12 | 55714 | -1.29 | 2e-16 | 3e-16 | 1 x 1 teneurin transmembrane protein 3 [Source:HGNC Symbol;Ac] |
| 13 | 10630 | -1.42 | 2e-16 | 3e-16 | 1 x 2 podoplanin [Source:HGNC Symbol;Acc:29602] |
| 14 | 5328 | 1.27 | 2e-16 | 3e-16 | 1 x 3 plasminogen activator, urokinase [Source:HGNC Symbol;Acc] |
| 15 | 7045 | -1.67 | 2e-16 | 3e-16 | 1 x 2 transforming growth factor, beta-induced, 68kDa [Source:HG] |
| 16 | 23452 | -1.22 | 7e-16 | 4e-14 | 3 x 1 angiotensin-like 2 [Source:HGNC Symbol;Acc:490] |
| 17 | 11098 | -1.19 | 2e-15 | 6e-14 | 1 x 1 protease, serine, 23 [Source:HGNC Symbol;Acc:14370] |
| 18 | 1277 | -1.17 | 8e-15 | 6e-14 | 2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197] |
| 19 | 7057 | -1.17 | 8e-15 | 6e-14 | 1 x 1 thrombospondin 1 [Source:HGNC Symbol;Acc:11785] |
| 20 | 7058 | -1.16 | 1e-14 | 6e-14 | 2 x 1 thrombospondin 2 [Source:HGNC Symbol;Acc:11786] |

Local Geneset Analysis

Underexpression

| Rank | GSZ | p-value | #in/all | Geneset |
|------|--------|---------|------------|--|
| 1 | -39.24 | NULL | 67 / 190 | CC extracellular matrix |
| 2 | -32.69 | NULL | 14 / 16 | MMML C63CIEJ_MMML 1 |
| 3 | -32.53 | NULL | 8 / 11 | MF platelet-derived growth factor binding |
| 4 | -32.38 | NULL | 31 / 69 | BP extracellular matrix disassembly |
| 5 | -31.32 | NULL | 77 / 250 | Lymphoma ENZ_Stromal signature 1 |
| 6 | -30.98 | NULL | 27 / 64 | BP collagen catabolic process |
| 7 | -30.67 | NULL | 12 / 16 | GSEA C27FARMER_BREAST_CANCER_CLUSTER_5 |
| 8 | -28.99 | NULL | 61 / 242 | BP extracellular matrix organization |
| 9 | -25.39 | NULL | 8 / 12 | miRNA target-29c |
| 10 | -23.84 | NULL | 11 / 15 | GSEA C27CROMER_TUMORIGENESIS_UP |
| 11 | -23.42 | NULL | 11 / 19 | MF extracellular matrix binding |
| 12 | -22.77 | NULL | 19 / 57 | MF extracellular matrix structural constituent |
| 13 | -22.56 | NULL | 10 / 15 | GSEA C27SONDER_CDH1_TARGETS_2_UP |
| 14 | -21.3 | NULL | 37 / 183 | CC proteinaceous extracellular matrix |
| 15 | -20.86 | NULL | 7 / 16 | GSEA C27CROONQUIST_STROMAL_STIMULATION_UP |
| 16 | -20.58 | NULL | 8 / 15 | GSEA C27DASU_IL6_SIGNALING_SCAR_DN |
| 17 | -19.95 | NULL | 12 / 35 | Glio Colman_survival_associated |
| 18 | -19.77 | NULL | 81 / 683 | CC extracellular space |
| 19 | -19.4 | NULL | 6 / 10 | GSEA C27VERRECCHIA_RESPONSE_TO_TGFB1_C4 |
| 20 | -19.28 | NULL | 5 / 10 | GSEA C27KEGG_ECM_RECEPTOR_INTERACTION |
| 21 | -19.13 | NULL | 6 / 12 | GSEA C27Y_AGING_MIDDLE_UP |
| 22 | -18.79 | NULL | 6 / 13 | GSEA C27FRIDMAN_SENESCENCE_UP |
| 23 | -18.79 | NULL | 6 / 13 | GSEA C27SAI_RESPONSE_TO_RADIATION_THERAPY |
| 24 | -18.5 | NULL | 5 / 10 | GSEA C27SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP |
| 25 | -17.23 | NULL | 6 / 11 | Glio Phillips MES up vs Prolif & PN |
| 26 | -17.18 | NULL | 107 / 1182 | CC extracellular region |
| 27 | -17.09 | NULL | 4 / 8 | GSEA C27AEGGERSTRAND_RESPONSE_TO_IMATINIB |
| 28 | -16.94 | NULL | 10 / 40 | BP cellular response to amino acid stimulus |
| 29 | -16.75 | NULL | 7 / 16 | GSEA C27SU_PDEF_TARGETS_UP |
| 30 | -16.68 | NULL | 6 / 11 | MMML C63CIEJ_MMML 31 |
| 31 | -16.59 | NULL | 68 / 553 | Cancer Lembcke_Colonc Inflammation |
| 32 | -16.23 | NULL | 7 / 16 | GSEA C27TURASHVIL_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_L |
| 33 | -16.21 | NULL | 2 / 3 | GSEA C27ONDO_HYPOXIA |
| 34 | -16.21 | NULL | 7 / 16 | GSEA C27ZHU_CMV_ALL_DN |
| 35 | -16.14 | NULL | 20 / 83 | CC basement membrane |
| 36 | -16.06 | NULL | 21 / 119 | Lymphoma OSOLOWSKI_green total |
| 37 | -15.96 | NULL | 17 / 85 | MF integrin binding |
| 38 | -15.92 | NULL | 4 / 12 | GSEA C27VERRECCHIA_RESPONSE_TO_TGFB1_C2 |
| 39 | -15.89 | NULL | 5 / 10 | BP negative regulation of fibroblast growth factor receptor signaling pa |
| 40 | -15.55 | NULL | 6 / 15 | GSEA C27MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INH |

p-values

