# GW_241

## Global Summary

%DE = 0.14

# genes with fdr < 0.2 = 1757 ( 964 + / 793 − )

# genes with fdr < 0.1 = 1350 ( 758 + / 592 − )

# genes with fdr < 0.05 = 1085 ( 625 + / 460 − )

# genes with fdr < 0.01 = 756 ( 448 + / 308 − )

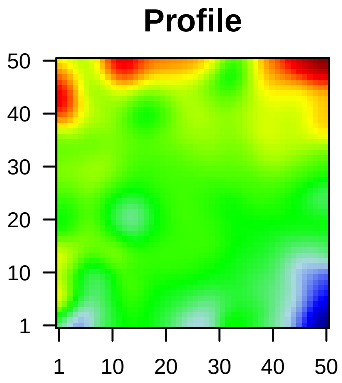
# genes in genesets = 16332

<FC> = 0

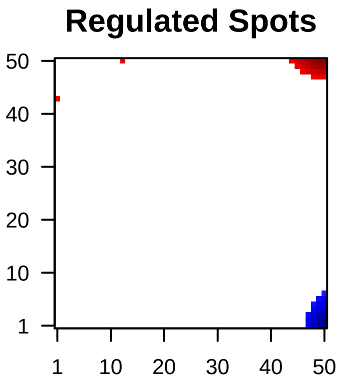
<shrinkage−t> = 0

<p−value> = 0.12

<fdr> = 0.86



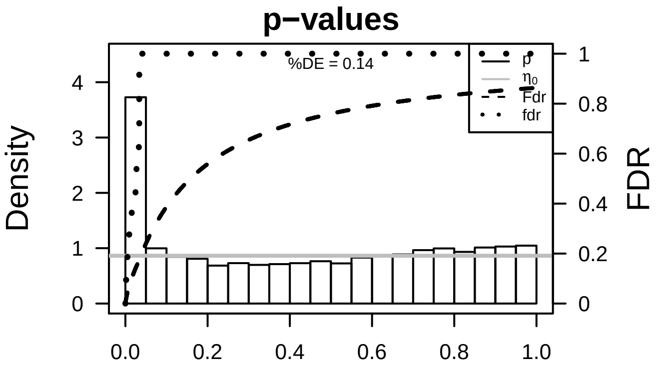
**Profile**



**Regulated Spots**

## Global Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 154664 | 1.83 | 2e−16 | 5e−14 | 50 x 50 | ATP−binding cassette, sub−family A (ABC1), member 13 [Sou |
| 2 | 242 | 1.84 | 2e−16 | 5e−14 | 1 x 48 | arachidonate 12−lipoxygenase, 12R type [Source:HGNC Sym |
| 3 | 55107 | 2.18 | 2e−16 | 5e−14 | 1 x 5 | anoctamin 1, calcium activated chloride channel [Source:HGN |
| 4 | 10409 | −1.47 | 2e−16 | 5e−14 | 1 x 2 | brain abundant, membrane attached signal protein 1 [Source: |
| 5 | 599 | 1.4 | 2e−16 | 5e−14 | 3 x 42 | BCL2−like 2 [Source:HGNC Symbol;Acc:995] |
| 6 | 148170 | −1.38 | 2e−16 | 5e−14 | 50 x 9 | CDC42 effector protein (Rho GTPase binding) 5 [Source:HGN |
| 7 | 9076 | 1.79 | 2e−16 | 5e−14 | 49 x 50 | claudin 1 [Source:HGNC Symbol;Acc:2032] |
| 8 | 54102 | 1.5 | 2e−16 | 5e−14 | 50 x 10 | chloride intracellular channel 6 [Source:HGNC Symbol;Acc:2 |
| 9 | 49860 | −2.37 | 2e−16 | 5e−14 | 1 x 50 | cornulin [Source:HGNC Symbol;Acc:1230] |
| 10 | 57007 | 2.05 | 2e−16 | 5e−14 | 14 x 50 | atypical chemokine receptor 3 [Source:HGNC Symbol;Acc:23 |
| 11 | 8632 | 1.52 | 2e−16 | 5e−14 | 1 x 8 | dynein, axonemal, heavy chain 17 [Source:HGNC Symbol;Ac |
| 12 | 8772 | 1.55 | 2e−16 | 5e−14 | 1 x 14 | Fas (TNFRSF6)−associated via death domain [Source:HGNC |
| 13 | 10457 | 1.71 | 2e−16 | 5e−14 | 13 x 50 | glycoprotein (transmembrane) nmb [Source:HGNC Symbol;A |
| 14 | 2877 | 1.42 | 2e−16 | 5e−14 | 1 x 50 | glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy |
| 15 | 2941 | 1.63 | 2e−16 | 5e−14 | 3 x 50 | glutathione S−transferase alpha 4 [Source:HGNC Symbol;Ac |
| 16 | 121355 | 1.96 | 2e−16 | 5e−14 | 14 x 11 | gametocyte specific factor 1 [Source:HGNC Symbol;Acc:265 |
| 17 | 283120 | −2.13 | 2e−16 | 5e−14 | 25 x 1 | H19, imprinted maternally expressed transcript (non−protein |
| 18 | 3040 | −2.05 | 2e−16 | 5e−14 | 4 x 1 | hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824] |
| 19 | 3043 | −2.12 | 2e−16 | 5e−14 | 5 x 1 | hemoglobin, beta [Source:HGNC Symbol;Acc:4827] |
| 20 | 8349 | 1.5 | 2e−16 | 5e−14 | 21 x 50 | histone cluster 2, H2be [Source:HGNC Symbol;Acc:4760] |



**p−values**

## Global Geneset Analysis

| Rank | GSZ | p−value | #all | Geneset | |
|---|---|---|---|---|---|
| *Overexpressed* | | | | | |
| 1 | 9.84 | NULL | 572 | Disease | GUDJ_psoriasis up |
| 2 | 9.56 | NULL | 142 | Glio | willscher_GBM_Verhaak−CL_expression_C_up |
| 3 | 9.56 | NULL | 142 | Glio | willscher_GBM_Verhaak−PNmut_expression_C_down |
| 4 | 8.66 | NULL | 135 | H.Tiss | WIRTH_Mucosa |
| 5 | 8.2 | NULL | 53 | BP | keratinocyte differentiation |
| 6 | 7.63 | NULL | 918 | Chr | Chr 17 |
| 7 | 7.55 | NULL | 603 | miRNA target−starBase | hsa−miR−20a |
| 8 | 7.51 | NULL | 1720 | Chr | Chr 1 |
| 9 | 7.08 | NULL | 545 | miRNA target−starBase | hsa−miR−93 |
| 10 | 7.02 | NULL | 76 | BP | epidermis development |
| 11 | 6.99 | NULL | 517 | miRNA target−starBase | hsa−miR−106a |
| 12 | 6.74 | NULL | 42 | BP | keratinization |
| 13 | 6.72 | NULL | 914 | Chr | Chr 3 |
| 14 | 6.54 | NULL | 511 | miRNA target−starBase | hsa−miR−106b |
| 15 | 6.39 | NULL | 494 | miRNA target−starBase | hsa−miR−107 |
| 16 | 6.37 | NULL | 495 | miRNA target−starBase | hsa−miR−103 |
| 17 | 6.35 | NULL | 538 | miRNA target−starBase | hsa−miR−17 |
| 18 | 6.33 | NULL | 565 | miRNA target−starBase | hsa−miR−20b |
| 19 | 6.28 | NULL | 335 | miRNA target−starBase | hsa−miR−520d−3p |
| 20 | 6.26 | NULL | 187 | Chr | Chr 21 |
| *Underexpressed* | | | | | |
| 1 | −10.09 | NULL | 957 | Chr | Chr 11 |
| 2 | −9.84 | NULL | 92 | BP | translational elongation |
| 3 | −9.8 | NULL | 81 | BP | viral transcription |
| 4 | −9.43 | NULL | 553 | Cancer | Lembcke_Colonic Inflammation |
| 5 | −9.03 | NULL | 1135 | Chr | Chr 19 |
| 6 | −8.82 | NULL | 87 | BP | translational termination |
| 7 | −8.76 | NULL | 128 | BP | translational initiation |
| 8 | −8.76 | NULL | 109 | BP | SRP−dependent cotranslational protein targeting to membrane |
| 9 | −8.62 | NULL | 92 | BP | viral life cycle |
| 10 | −8.27 | NULL | 265 | Glio | willscher_GBM_Verhaak−CL_expression_B_up |
| 11 | −8.27 | NULL | 265 | Glio | willscher_GBM_Verhaak−MES_expression_B_up |
| 12 | −8.27 | NULL | 265 | Glio | willscher_GBM_Verhaak−PNwt_expression_B_down |
| 13 | −8.27 | NULL | 265 | Glio | willscher_GBM_Verhaak−PNmut_expression_B_down |
| 14 | −7.95 | NULL | 37 | CC | cytosolic small ribosomal subunit |
| 15 | −7.49 | NULL | 115 | BP | nuclear−transcribed mRNA catabolic process, nonsense−mediated |
| 16 | −7.41 | NULL | 280 | Chr | Chr 13 |
| 17 | −7.36 | NULL | 683 | CC | extracellular space |
| 18 | −7.36 | NULL | 153 | MF | structural constituent of ribosome |
| 19 | −7.08 | NULL | 4 | MMML CGS | MACIEJ_MMML 23 |
| 20 | −7 | NULL | 417 | H.Tiss | WIRTH_Immune system |

# GW_241

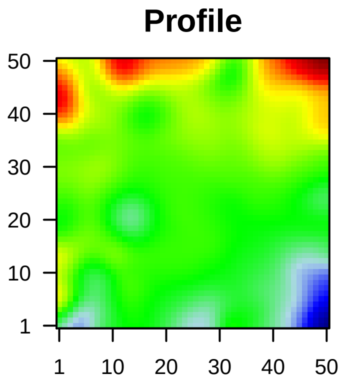
## Local Summary

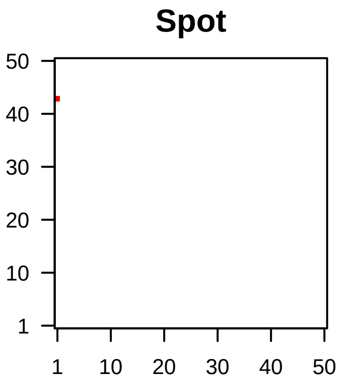
%DE = 0.91
# metagenes = 1
# genes = 29
# genes in genesets = 28

# genes with fdr < 0.1  = 22  ( 21 + / 1  − )
# genes with fdr < 0.05  = 22  ( 21 + / 1  − )
# genes with fdr < 0.01 = 21  ( 20 + / 1  − )

<r> metagenes = NA
<r> genes = 0.42

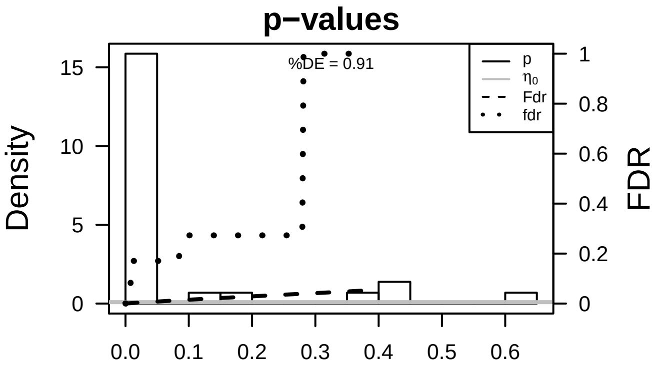
<FC> = 0.55
<shrinkage−t> = 19.35
<p−value> = 0
<fdr> = 0.25





## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 1288 | 1.06 | 8e−11 | 2e−10 | 1 x 43 | collagen, type IV, alpha 6 [Source:HGNC Symbol;Acc:2208] |
| 2 | 50805 | 1.05 | 1e−10 | 2e−09 | 1 x 43 | iroquois homeobox 4 [Source:HGNC Symbol;Acc:6129] |
| 3 | 116211 | 0.98 | 2e−09 | 2e−09 | 1 x 43 | Transmembrane 4 L6 family member 19  [Source:UniProtKB/ |
| 4 | 244 | 0.98 | 2e−09 | 9e−09 | 1 x 43 | annexin A8−like 2 [Source:HGNC Symbol;Acc:23335] |
| 5 | 3552 | 0.94 | 8e−09 | 9e−09 | 1 x 43 | interleukin 1, alpha [Source:HGNC Symbol;Acc:5991] |
| 6 | 6274 | 0.93 | 1e−08 | 9e−09 | 1 x 43 | S100 calcium binding protein A3 [Source:HGNC Symbol;Acc: |
| 7 | 6513 | 0.93 | 1e−08 | 2e−08 | 1 x 43 | solute carrier family 2 (facilitated glucose transporter), membe |
| 8 | 1308 | 0.92 | 2e−08 | 4e−08 | 1 x 43 | collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194 |
| 9 | 404203 | 0.9 | 4e−08 | 5e−07 | 1 x 43 | serine peptidase inhibitor, Kazal type 6 [Source:HGNC Symb |
| 10 | 3038 | 0.84 | 2e−07 | 6e−06 | 1 x 43 | hyaluronan synthase 3 [Source:HGNC Symbol;Acc:4820] |
| 11 | 81706 | 0.77 | 3e−06 | 6e−06 | 1 x 43 | protein phosphatase 1, regulatory (inhibitor) subunit 14C [Sou |
| 12 | 5358 | 0.75 | 5e−06 | 2e−05 | 1 x 43 | plastin 3 [Source:HGNC Symbol;Acc:9091] |
| 13 | 5947 | 0.69 | 2e−05 | 2e−05 | 1 x 43 | retinol binding protein 1, cellular [Source:HGNC Symbol;Acc: |
| 14 | 83882 | 0.69 | 2e−05 | 2e−05 | 1 x 43 | tetraspanin 10 [Source:HGNC Symbol;Acc:29942] |
| 15 | 5744 | 0.69 | 3e−05 | 7e−05 | 1 x 43 | parathyroid hormone−like hormone [Source:HGNC Symbol;A |
| 16 | 55612 | 0.66 | 5e−05 | 7e−04 | 1 x 43 | fermitin family member 1 [Source:HGNC Symbol;Acc:15889] |
| 17 | 163732 | 0.56 | 5e−04 | 7e−04 | 1 x 43 | Cbp/p300−interacting transactivator, with Glu/Asp−rich carbo |
| 18 | 2152 | −0.56 | 6e−04 | 2e−03 | 1 x 43 | coagulation factor III (thromboplastin, tissue factor) [Source:H |
| 19 | 375061 | 0.52 | 1e−03 | 8e−03 | 1 x 43 | family with sequence similarity 89, member A [Source:HGNC |
| 20 | 80115 | 0.45 | 6e−03 | 8e−03 | 1 x 43 | BAI1−associated protein 2−like 2 [Source:HGNC Symbol;Acc |



## Local Geneset Analysis

*Overexpression*

| Rank | GSZ | p−value | #in/all | Geneset | |
|---|---|---|---|---|---|
| 1 | 34.29 | NULL | 1 / 4 | GSEA C2 | BUDHU_LIVER_CANCER_METASTASIS_DN |
| 2 | 28.57 | NULL | 2 / 11 | GSEA C2 | BIOCARTA_VITCB_PATHWAY |
| 3 | 25.96 | NULL | 1 / 5 | GSEA C2 | RODRIGUES_DCC_TARGETS_UP |
| 4 | 21.95 | NULL | 1 / 6 | GSEA C2 | SEIKE_LUNG_CANCER_POOR_SURVIVAL |
| 5 | 19.1 | NULL | 1 / 8 | GSEA C2 | NIKOLSKY_BREAST_CANCER_5P15_AMPLICON |
| 6 | 16.9 | NULL | 1 / 8 | GSEA C2 | REACTOME_FACILITATIVE_NA_INDEPENDENT_GLUCOSE_TR |
| 7 | 16.28 | NULL | 1 / 10 | GSEA C2 | BIOCARTA_ACE2_PATHWAY |
| 8 | 16.2 | NULL | 1 / 6 | GSEA C2 | OHM_EMBRYONIC_CARCINOMA_DN |
| 9 | 15.96 | NULL | 2 / 15 | GSEA C2 | NGUYEN_NOTCH1_TARGETS_UP |
| 10 | 15.17 | NULL | 1 / 11 | GSEA C2 | BIOCARTA_PLATELETAPP_PATHWAY |
| 11 | 14.62 | NULL | 1 / 6 | GSEA C2 | SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN |
| 12 | 14.4 | NULL | 1 / 10 | GSEA C2 | BIOCARTA_LYM_PATHWAY |
| 13 | 14.25 | NULL | 1 / 12 | GSEA C2 | BIOCARTA_INTRINSIC_PATHWAY |
| 14 | 13.96 | NULL | 1 / 7 | GSEA C2 | BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_AND_PAX3 |
| 15 | 13.57 | NULL | 1 / 8 | GSEA C2 | GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN |
| 16 | 13.47 | NULL | 1 / 13 | GSEA C2 | BIOCARTA_AMI_PATHWAY |
| 17 | 13.24 | NULL | 1 / 11 | MF | substrate−specific transmembrane transporter activity |
| 18 | 12.6 | NULL | 1 / 12 | GSEA C2 | BIOCARTA_ERYTH_PATHWAY |
| 19 | 12.29 | NULL | 1 / 12 | BP | hemidesmosome assembly |
| 20 | 11.91 | NULL | 1 / 13 | BP | positive regulation of interleukin−2 biosynthetic process |
| 21 | 11.91 | NULL | 1 / 13 | BP | response to copper ion |
| 22 | 11.65 | NULL | 2 / 16 | GSEA C2 | LANDEMAINE_LUNG_METASTASIS |
| 23 | 11.5 | NULL | 1 / 9 | GSEA C2 | RODWELL_AGING_KIDNEY_UP |
| 24 | 11.29 | NULL | 1 / 12 | BP | extracellular polysaccharide biosynthetic process |
| 25 | 10.79 | NULL | 1 / 15 | MF | interleukin−1 receptor binding |
| 26 | 10.79 | NULL | 1 / 15 | BP | positive regulation vascular endothelial growth factor production |
| 27 | 10.74 | NULL | 1 / 15 | Pathw Act | GUSTAFSON_PI3K_DN |
| 28 | 10.65 | NULL | 1 / 15 | BP | response to osmotic stress |
| 29 | 10.65 | NULL | 1 / 15 | GSEA C2 | KANG_FLUOROURACIL_RESISTANCE_DN |
| 30 | 10.65 | NULL | 1 / 15 | GSEA C2 | GHO_ATF5_TARGETS_DN |
| 31 | 10.63 | NULL | 1 / 11 | MMML CGS | MACIEJ_MMML 31 |
| 32 | 10.61 | NULL | 1 / 10 | GSEA C2 | OUELLET_OVARIAN_CANCER_INVASIVE_VS_LMP_DN |
| 33 | 10.61 | NULL | 1 / 10 | GSEA C2 | LOPES_METHYLATED_IN_COLON_CANCER_DN |
| 34 | 10.49 | NULL | 1 / 10 | BP | surfactant homeostasis |
| 35 | 10.19 | NULL | 1 / 16 | GSEA C2 | WILLERT_WNT_SIGNALING |
| 36 | 10.07 | NULL | 1 / 16 | GSEA C2 | WATTEL_AUTONOMOUS_THYROID_ADENOMA_UP |
| 37 | 9.98 | NULL | 1 / 12 | GSEA C2 | PEPPER_CHRONIC_LYMPHOCYTIC_LEUKEMIA_UP |
| 38 | 9.89 | NULL | 1 / 11 | GSEA C2 | GAUSSMANN_MLL_AF4_FUSION_TARGETS_G_UP |
| 39 | 9.89 | NULL | 1 / 11 | GSEA C2 | SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN |
| 40 | 9.79 | NULL | 1 / 17 | BP | cellular response to glucose starvation |

# GW_241

## Local Summary

%DE = 0.74

# metagenes = 21

# genes = 304

# genes in genesets = 302

# genes with fdr < 0.1  = 200  ( 184 + / 16  − )

# genes with fdr < 0.05  = 178  ( 167 + / 11  − )

# genes with fdr < 0.01 = 135  ( 131 + / 4  − )

<r> metagenes = 0.91

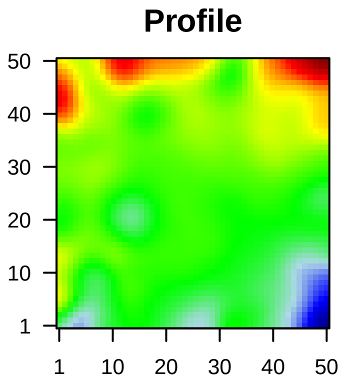
<r> genes = 0.27

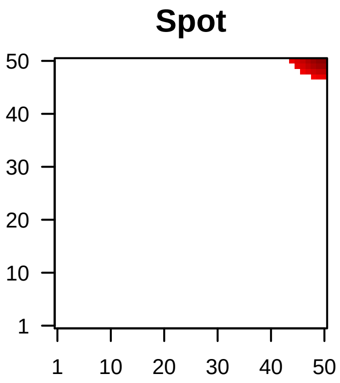
<FC> = 0.44

<shrinkage−t> = 15.44

<p−value> = 0

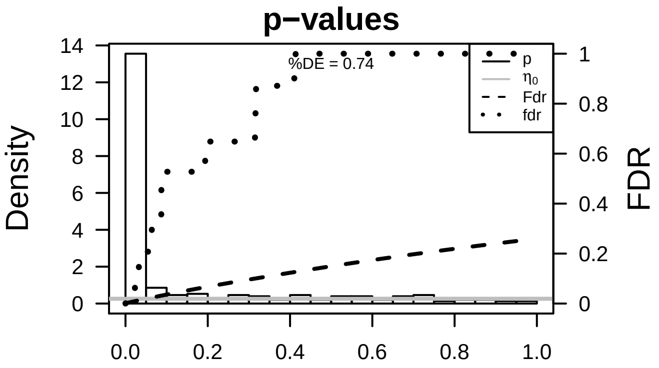
<fdr> = 0.41


**Profile**


**Spot**

## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 154664 | 1.83 | 2e−16 | 2e−15 | 50 x 50 | ATP−binding cassette, sub−family A (ABC1), member 13 [Sou |
| 2 | 9076 | 1.79 | 2e−16 | 2e−15 | 49 x 50 | claudin 1 [Source:HGNC Symbol;Acc:2032] |
| 3 | 56922 | 1.38 | 2e−16 | 2e−15 | 50 x 50 | methylcrotonoyl−CoA carboxylase 1 (alpha) [Source:HGNC S |
| 4 | 4922 | 2.4 | 2e−16 | 2e−15 | 50 x 50 | neurotensin [Source:HGNC Symbol;Acc:8038] |
| 5 | 116832 | 1.5 | 2e−16 | 2e−15 | 46 x 50 | ribosomal protein L39−like [Source:HGNC Symbol;Acc:17094 |
| 6 | 23321 | 1.48 | 2e−16 | 2e−15 | 50 x 50 | tripartite motif containing 2 [Source:HGNC Symbol;Acc:1597 |
| 7 | 79679 | 1.66 | 2e−16 | 2e−15 | 50 x 50 | V−set domain containing T cell activation inhibitor 1 [Source: |
| 8 | 256764 | 1.61 | 2e−16 | 2e−15 | 50 x 50 | WD repeat domain 72 [Source:HGNC Symbol;Acc:26790] |
| 9 | 4915 | 1.3 | 2e−15 | 4e−13 | 50 x 50 | neurotrophic tyrosine kinase, receptor, type 2 [Source:HGNC |
| 10 | 56548 | 1.27 | 7e−15 | 4e−13 | 50 x 50 | carbohydrate (N−acetylglucosamine 6−O) sulfotransferase 7 [ |
| 11 | 1894 | 1.26 | 1e−14 | 7e−13 | 45 x 50 | epithelial cell transforming sequence 2 oncogene [Source:HG |
| 12 | 10655 | 1.24 | 2e−14 | 7e−13 | 50 x 50 | doublesex and mab−3 related transcription factor 2 [Source:H |
| 13 | 216 | 1.24 | 3e−14 | 2e−12 | 50 x 50 | aldehyde dehydrogenase 1 family, member A1 [Source:HGN |
| 14 | 79718 | 1.22 | 7e−14 | 2e−12 | 48 x 50 | transducin (beta)−like 1 X−linked receptor 1 [Source:HGNC S |
| 15 | 10057 | 1.22 | 7e−14 | 2e−12 | 50 x 50 | ATP−binding cassette, sub−family C (CFTR/MRP), member 5 |
| 16 | 6657 | 1.21 | 9e−14 | 2e−12 | 50 x 50 | SRY (sex determining region Y)−box 2 [Source:HGNC Symb |
| 17 | 1857 | 1.21 | 1e−13 | 2e−12 | 49 x 50 | dishevelled segment polarity protein 3 [Source:HGNC Symbo |
| 18 | 205428 | 1.2 | 1e−13 | 7e−12 | 50 x 50 | chromosome 3 open reading frame 58 [Source:HGNC Symb |
| 19 | 3880 | 1.19 | 2e−13 | 2e−10 | 50 x 49 | keratin 19 [Source:HGNC Symbol;Acc:6436] |
| 20 | 57552 | 1.14 | 3e−12 | 2e−10 | 48 x 47 | neutral cholesterol ester hydrolase 1 [Source:HGNC Symbol; |


**p−values**

## Local Geneset Analysis

*Overexpression*

| Rank | GSZ | p−value | #in/all | Geneset | |
|---|---|---|---|---|---|
| 1 | 19.68 | NULL | 43 / 142 | Glio | willscher_GBM_Verhaak−CL_expression_C_up |
| 2 | 19.68 | NULL | 43 / 142 | Glio | willscher_GBM_Verhaak−PNmut_expression_C_down |
| 3 | 17.27 | NULL | 2 / 7 | GSEA C2 | MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN |
| 4 | 15.17 | NULL | 72 / 914 | Chr | Chr 3 |
| 5 | 14.03 | NULL | 17 / 57 | Glio | developing astrocytes |
| 6 | 13.12 | NULL | 4 / 9 | GSEA C2 | SEMBA_FHIT_TARGETS_DN |
| 7 | 12.96 | NULL | 4 / 13 | BP | regulation of blood vessel size |
| 8 | 11.95 | NULL | 4 / 8 | GSEA C2 | REACTOME_E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S |
| 9 | 11.52 | NULL | 5 / 14 | GSEA C2 | VANTVEER_BREAST_CANCER_METASTASIS_DN |
| 10 | 11.29 | NULL | 7 / 15 | GSEA C2 | WU_APOPTOSIS_BY_CDKN1A_VIA_TP53 |
| 11 | 10.89 | NULL | 8 / 16 | GSEA C2 | FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL |
| 12 | 10.25 | NULL | 6 / 16 | GSEA C2 | EGUCHI_CELL_CYCLE_RB1_TARGETS |
| 13 | 10.15 | NULL | 6 / 15 | GSEA C2 | ODONNELL_TARGETS_OF_MYC_AND_TFRC_DN |
| 14 | 9.97 | NULL | 6 / 26 | BP | cellular response to ionizing radiation |
| 15 | 9.96 | NULL | 4 / 11 | GSEA C2 | REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLIC |
| 16 | 9.84 | NULL | 7 / 15 | GSEA C2 | FINETTI_BREAST_CANCER_KINOME_RED |
| 17 | 9.8 | NULL | 3 / 6 | GSEA C2 | MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_7 |
| 18 | 9.73 | NULL | 5 / 16 | GSEA C2 | REACTOME_DNA_STRAND_ELONGATION |
| 19 | 9.7 | NULL | 7 / 15 | Cancer | SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP |
| 20 | 9.63 | NULL | 3 / 13 | GSEA C2 | JAERVINEN_AMPLIFIED_IN_LARYNGEAL_CANCER |
| 21 | 9.54 | NULL | 4 / 11 | GSEA C2 | KALMA_E2F1_TARGETS |
| 22 | 9.52 | NULL | 6 / 16 | GSEA C2 | PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP |
| 23 | 9.45 | NULL | 1 / 5 | GSEA C2 | TURASHVILI_BREAST_CARCINOMA_DUCTAL_VS_LOBULAR_ |
| 24 | 9.34 | NULL | 6 / 14 | MMML CGS | MACIEJ_MMML 4 |
| 25 | 9.33 | NULL | 8 / 16 | GSEA C2 | FARMER_BREAST_CANCER_CLUSTER_2 |
| 26 | 9.17 | NULL | 6 / 13 | GSEA C2 | CROONQUIST_IL6_DEPRIVATION_DN |
| 27 | 9.02 | NULL | 3 / 16 | GSEA C2 | BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN |
| 28 | 9.01 | NULL | 42 / 530 | Cancer | Lembcke_Normal vs Adenoma |
| 29 | 8.77 | NULL | 1 / 11 | Glio | neurons_glio |
| 30 | 8.68 | NULL | 5 / 16 | GSEA C2 | KANG_DOXORUBICIN_RESISTANCE_UP |
| 31 | 8.65 | NULL | 6 / 15 | GSEA C2 | LY_AGING_MIDDLE_DN |
| 32 | 8.49 | NULL | 6 / 14 | GSEA C2 | ZHAN_MULTIPLE_MYELOMA_PR_UP |
| 33 | 8.48 | NULL | 2 / 7 | GSEA C2 | FREDERICK_PRKCI_TARGETS |
| 34 | 8.47 | NULL | 7 / 14 | GSEA C2 | PUJANA_BRCA_CENTERED_NETWORK |
| 35 | 8.44 | NULL | 3 / 15 | GSEA C2 | YANG_BREAST_CANCER_ESR1_LASER_DN |
| 36 | 8.42 | NULL | 3 / 8 | GSEA C2 | LIU_CDX2_TARGETS_DN |
| 37 | 8.42 | NULL | 2 / 9 | GSEA C2 | REACTOME_METABOLISM_OF_AMINO_ACIDS |
| 38 | 8.4 | NULL | 7 / 14 | GSEA C2 | AMUNDSON_GAMMA_RADIATION_RESPONSE |
| 39 | 8.31 | NULL | 2 / 10 | GSEA C2 | CONRAD_STEM_CELL |
| 40 | 8.3 | NULL | 6 / 15 | GSEA C2 | SMID_BREAST_CANCER_LUMINAL_A_DN |

# GW_241

## Local Summary

%DE = 0.78

# metagenes = 1

# genes = 36

# genes in genesets = 36

# genes with fdr < 0.1 = 22 ( 19 + / 3 − )

# genes with fdr < 0.05 = 20 ( 17 + / 3 − )

# genes with fdr < 0.01 = 15 ( 15 + / 0 − )

<r> metagenes = NA

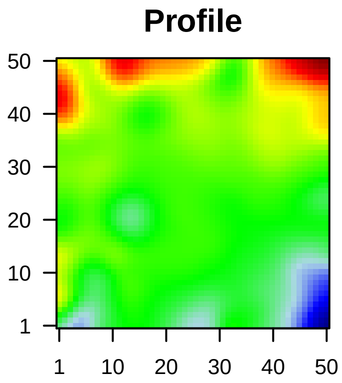
<r> genes = 0.33

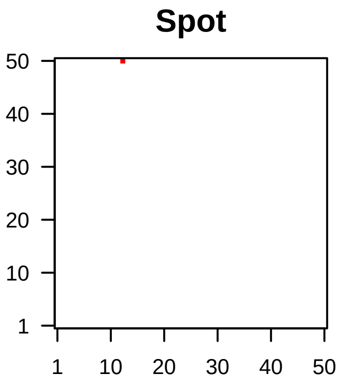
<FC> = 0.41

<shrinkage−t> = 14.19

<p−value> = 0

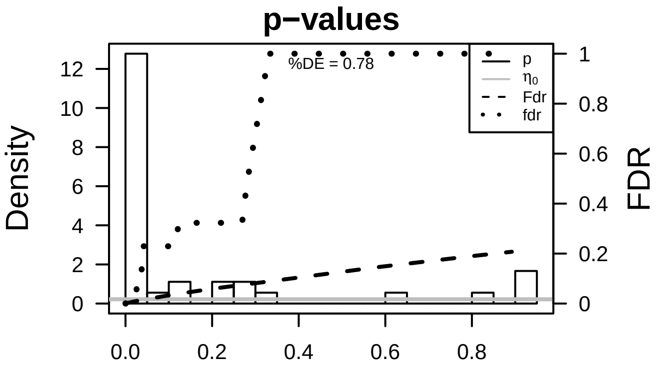
<fdr> = 0.48





## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 10457 | 1.71 | 2e−16 | 9e−16 | 13 x 50 | glycoprotein (transmembrane) nmb [Source:HGNC Symbol;A |
| 2 | 7062 | 1.9 | 2e−16 | 9e−16 | 13 x 50 | trichohyalin [Source:HGNC Symbol;Acc:11791] |
| 3 | 483 | 1.28 | 5e−15 | 2e−11 | 13 x 50 | ATPase, Na+/K+ transporting, beta 3 polypeptide [Source:HG |
| 4 | 1749 | 1.14 | 2e−12 | 3e−10 | 13 x 50 | distal−less homeobox 5 [Source:HGNC Symbol;Acc:2918] |
| 5 | 84002 | 1.07 | 4e−11 | 1e−08 | 13 x 50 | UDP−GlcNAc:betaGal beta−1,3−N−acetylglucosaminyltransfe |
| 6 | 8626 | 0.99 | 1e−09 | 2e−05 | 13 x 50 | tumor protein p63 [Source:HGNC Symbol;Acc:15979] |
| 7 | 1962 | 0.77 | 2e−06 | 6e−05 | 13 x 50 | enoyl−CoA, hydratase/3−hydroxyacyl CoA dehydrogenase [S |
| 8 | 144402 | 0.72 | 9e−06 | 4e−04 | 13 x 50 | copine VIII [Source:HGNC Symbol;Acc:23498] |
| 9 | 3321 | 0.64 | 9e−05 | 4e−04 | 13 x 50 | immunoglobulin superfamily, member 3 [Source:HGNC Symb |
| 10 | 57609 | 0.63 | 1e−04 | 5e−04 | 13 x 50 | DIP2 disco−interacting protein 2 homolog B (Drosophila) [Sou |
| 11 | 2564 | 0.61 | 2e−04 | 1e−03 | 13 x 50 | gamma−aminobutyric acid (GABA) A receptor, epsilon [Sourc |
| 12 | 9121 | 0.55 | 7e−04 | 1e−03 | 13 x 50 | solute carrier family 16 (monocarboxylate transporter), memb |
| 13 | 1728 | 0.55 | 7e−04 | 1e−03 | 13 x 50 | NAD(P)H dehydrogenase, quinone 1 [Source:HGNC Symbol; |
| 14 | 85236 | 0.54 | 9e−04 | 1e−03 | 13 x 50 | histone cluster 1, H2bk [Source:HGNC Symbol;Acc:13954] |
| 15 | 79850 | 0.54 | 9e−04 | 6e−03 | 13 x 50 | family with sequence similarity 57, member A [Source:HGNC |
| 16 | 7086 | −0.51 | 2e−03 | 1e−02 | 13 x 50 | transketolase [Source:HGNC Symbol;Acc:11834] |
| 17 | 51071 | 0.48 | 3e−03 | 5e−02 | 13 x 50 | deoxyribose−phosphate aldolase (putative) [Source:HGNC S |
| 18 | 1109 | 0.38 | 2e−02 | 5e−02 | 13 x 50 | aldo−keto reductase family 1, member C4 [Source:HGNC Sy |
| 19 | 10553 | −0.37 | 2e−02 | 5e−02 | 13 x 50 | HIV−1 Tat interactive protein 2, 30kDa [Source:HGNC Symbo |
| 20 | 1717 | −0.36 | 3e−02 | 5e−02 | 13 x 50 | 7−dehydrocholesterol reductase [Source:HGNC Symbol;Acc: |



## Local Geneset Analysis

*Overexpression*

| Rank | GSZ | p−value | #in/all | Geneset | |
|---|---|---|---|---|---|
| 1 | 24 | NULL | 1 / 9 | Glio | Colman_survival_robust |
| 2 | 22.56 | NULL | 2 / 15 | GSEA C2 | KANG_FLUOROURACIL_RESISTANCE_UP |
| 3 | 22.29 | NULL | 1 / 10 | GSEA C2 | FOURNIER_ACINAR_DEVELOPMENT_LATE_UP |
| 4 | 21.69 | NULL | 1 / 6 | GSEA C2 | ZAIDI_OSTEOBLAST_TRANSCRIPTION_FACTORS |
| 5 | 21.69 | NULL | 1 / 6 | GSEA C2 | NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP |
| 6 | 20.88 | NULL | 1 / 11 | GSEA C2 | ITO_PTTG1_TARGETS_UP |
| 7 | 18.88 | NULL | 1 / 15 | GSEA C2 | NAGASHIMA_NRG1_SIGNALING_DN |
| 8 | 18.68 | NULL | 1 / 13 | GSEA C2 | GAUSSMANN_MLL_AF4_FUSION_TARGETS_E_DN |
| 9 | 18.26 | NULL | 2 / 19 | BP | anatomical structure formation involved in morphogenesis |
| 10 | 16.56 | NULL | 1 / 10 | GSEA C2 | TARTE_PLASMA_CELL_VS_PLASMABLAST_DN |
| 11 | 16.56 | NULL | 1 / 10 | GSEA C2 | HOSHIDA_LIVER_CANCER_SUBCLASS_S1 |
| 12 | 15.03 | NULL | 1 / 8 | TF Tissue | VAQUERIZAS_Tongue |
| 13 | 14.63 | NULL | 1 / 12 | GSEA C2 | SCHLOSSER_MYC_TARGETS_AND_SERUM_RESPONSE_UP |
| 14 | 14.63 | NULL | 1 / 12 | GSEA C2 | KEGG_CARDIAC_MUSCLE_CONTRACTION |
| 15 | 13.95 | NULL | 3 / 38 | BP | epithelial cell differentiation |
| 16 | 13.88 | NULL | 1 / 11 | BP | ear development |
| 17 | 13.88 | NULL | 1 / 11 | GSEA C2 | SU_PLACENTA |
| 18 | 13.87 | NULL | 1 / 13 | GSEA C2 | CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN |
| 19 | 13.87 | NULL | 1 / 13 | GSEA C2 | TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_MONOCYT |
| 20 | 13.87 | NULL | 1 / 13 | GSEA C2 | SANA_TNF_SIGNALING_DN |
| 21 | 13.87 | NULL | 1 / 13 | GSEA C2 | SCHUHMACHER_MYC_TARGETS_UP |
| 22 | 13.87 | NULL | 1 / 13 | GSEA C2 | KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION |
| 23 | 13.87 | NULL | 1 / 13 | GSEA C2 | REACTOME_HEMOSTASIS |
| 24 | 13.68 | NULL | 2 / 51 | BP | osteoblast differentiation |
| 25 | 13.43 | NULL | 1 / 26 | Disease | BCHETNIA_EBM−DM up |
| 26 | 13.21 | NULL | 1 / 14 | GSEA C2 | OUELLET_OVARIAN_CANCER_INVASIVE_VS_LMP_UP |
| 27 | 13.21 | NULL | 1 / 14 | GSEA C2 | GRUETZMANN_PANCREATIC_CANCER_UP |
| 28 | 13.21 | NULL | 1 / 14 | GSEA C2 | RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_DN |
| 29 | 13.21 | NULL | 1 / 14 | GSEA C2 | REACTOME_CELL_SURFACE_INTERACTIONS_AT_THE_VASCU |
| 30 | 13.08 | NULL | 1 / 12 | BP | head development |
| 31 | 12.64 | NULL | 1 / 15 | GSEA C2 | DELYS_THYROID_CANCER_UP |
| 32 | 12.64 | NULL | 1 / 15 | GSEA C2 | ZHAN_V2_LATE_DIFFERENTIATION_GENES |
| 33 | 12.64 | NULL | 1 / 15 | GSEA C2 | RUTELLA_RESPONSE_TO_HGF_UP |
| 34 | 12.64 | NULL | 1 / 15 | GSEA C2 | JIANG_HYPOXIA_NORMAL |
| 35 | 12.64 | NULL | 1 / 15 | GSEA C2 | KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTIC |
| 36 | 12.41 | NULL | 1 / 13 | GSEA C2 | SMID_BREAST_CANCER_RELAPSE_IN_BRAIN_UP |
| 37 | 12.14 | NULL | 2 / 15 | GSEA C2 | WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP |
| 38 | 12.12 | NULL | 1 / 16 | GSEA C2 | WONG_MITOCHONDRIA_GENE_MODULE |
| 39 | 12.12 | NULL | 1 / 16 | GSEA C2 | BRUECKNER_TARGETS_OF_MIRLET7A3_UP |
| 40 | 12.12 | NULL | 1 / 16 | GSEA C2 | RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_UP |

# GW_241

## Local Summary

%DE = 0.92

# metagenes = 21

# genes = 366

# genes in genesets = 364

# genes with fdr < 0.1 = 329 ( 4 + / 325 − )

# genes with fdr < 0.05 = 297 ( 3 + / 294 − )

# genes with fdr < 0.01 = 220 ( 2 + / 218 − )

<r> metagenes = 0.95

<r> genes = 0.48

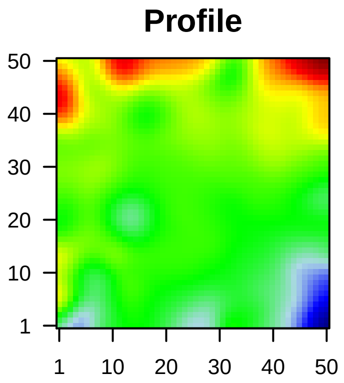
<FC> = −0.46

<shrinkage−t> = −16.24

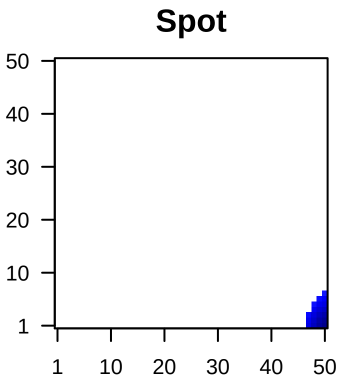
<p−value> = 0

<fdr> = 0.41

### Profile



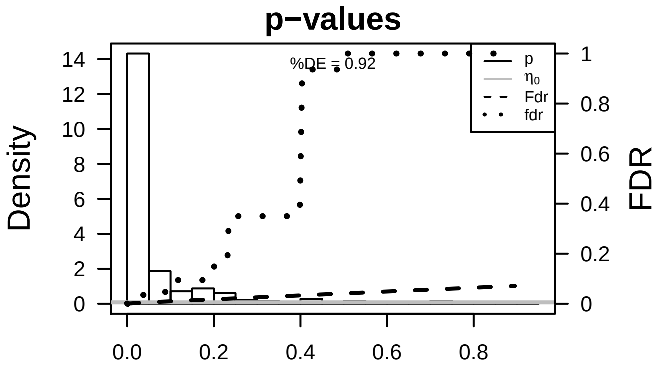
### Spot



## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 894 | −1.26 | 1e−14 | 4e−13 | 50 x 4 | cyclin D2 [Source:HGNC Symbol;Acc:1583] |
| 2 | 347733 | −1.24 | 2e−14 | 7e−11 | 50 x 5 | tubulin, beta 2B class IIb [Source:HGNC Symbol;Acc:30829] |
| 3 | 6363 | −1.14 | 3e−12 | 7e−11 | 50 x 1 | chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc |
| 4 | 10537 | −1.12 | 5e−12 | 1e−10 | 50 x 1 | ubiquitin D [Source:HGNC Symbol;Acc:18795] |
| 5 | 4069 | −1.11 | 1e−11 | 1e−10 | 50 x 2 | lysozyme [Source:HGNC Symbol;Acc:6740] |
| 6 | 3126 | −1.1 | 1e−11 | 7e−10 | 50 x 1 | major histocompatibility complex, class II, DR beta 4 [Source: |
| 7 | 83641 | −1.07 | 5e−11 | 7e−10 | 50 x 1 | family with sequence similarity 107, member B [Source:HGN |
| 8 | 23643 | −1.06 | 9e−11 | 7e−10 | 50 x 3 | lymphocyte antigen 96 [Source:HGNC Symbol;Acc:17156] |
| 9 | 348 | −1.05 | 1e−10 | 6e−09 | 50 x 1 | apolipoprotein E [Source:HGNC Symbol;Acc:613] |
| 10 | 3109 | −1.02 | 4e−10 | 6e−09 | 50 x 1 | major histocompatibility complex, class II, DM beta [Source:H |
| 11 | 3385 | −1 | 8e−10 | 6e−09 | 50 x 1 | intercellular adhesion molecule 3 [Source:HGNC Symbol;Acc |
| 12 | 260436 | −1 | 9e−10 | 6e−09 | 50 x 1 | follicular dendritic cell secreted protein [Source:HGNC Symbo |
| 13 | 51303 | −1 | 1e−09 | 1e−08 | 49 x 3 | FK506 binding protein 11, 19 kDa [Source:HGNC Symbol;Ac |
| 14 | 3119 | −0.98 | 2e−09 | 1e−08 | 49 x 1 | major histocompatibility complex, class II, DQ beta 1 [Source: |
| 15 | 57172 | −0.98 | 2e−09 | 2e−08 | 49 x 1 | calcium/calmodulin−dependent protein kinase IG [Source:HG |
| 16 | 3108 | −0.97 | 3e−09 | 2e−08 | 50 x 1 | major histocompatibility complex, class II, DM alpha [Source: |
| 17 | 6748 | −0.96 | 3e−09 | 5e−08 | 48 x 4 | signal sequence receptor, delta [Source:HGNC Symbol;Acc:1 |
| 18 | 6451 | −0.94 | 7e−09 | 5e−08 | 50 x 5 | SH3 domain binding glutamic acid−rich protein like [Source:H |
| 19 | 9535 | −0.93 | 1e−08 | 5e−08 | 50 x 1 | glia maturation factor, gamma [Source:HGNC Symbol;Acc:43 |
| 20 | 54855 | −0.93 | 1e−08 | 5e−08 | 49 x 1 | family with sequence similarity 46, member C [Source:HGNC |

### p−values



## Local Geneset Analysis

*Underexpression*

| Rank | GSZ | p−value | #in/all | Geneset | |
|---|---|---|---|---|---|
| 1 | −27.88 | NULL | 12 / 15 | CC | MHC class II protein complex |
| 2 | −24.03 | NULL | 104 / 553 | Cancer | Lembcke_Colonic Inflammation |
| 3 | −23.48 | NULL | 89 / 417 | H.Tiss | WIRTH_Immune system |
| 4 | −16.85 | NULL | 55 / 312 | BP | immune response |
| 5 | −16.12 | NULL | 7 / 12 | GSEA C2 | ZHAN_MULTIPLE_MYELOMA_DN |
| 6 | −16.12 | NULL | 9 / 16 | GSEA C2 | FARMER_BREAST_CANCER_CLUSTER_1 |
| 7 | −16.09 | NULL | 47 / 265 | Glio | willscher_GBM_Verhaak−CL_expression_B_up |
| 8 | −16.09 | NULL | 47 / 265 | Glio | willscher_GBM_Verhaak−MES_expression_B_up |
| 9 | −16.09 | NULL | 47 / 265 | Glio | willscher_GBM_Verhaak−PNwt_expression_B_down |
| 10 | −16.09 | NULL | 47 / 265 | Glio | willscher_GBM_Verhaak−PNmut_expression_B_down |
| 11 | −15.62 | NULL | 15 / 47 | BP | antigen processing and presentation |
| 12 | −15.2 | NULL | 7 / 8 | Glio | Donson−migration tethering and rolling−associated with LTS in HG |
| 13 | −14.64 | NULL | 5 / 12 | BP | immunoglobulin mediated immune response |
| 14 | −14.4 | NULL | 4 / 9 | GSEA C2 | MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN |
| 15 | −14.22 | NULL | 6 / 15 | GSEA C2 | FINAK_BREAST_CANCER_SDPP_SIGNATURE |
| 16 | −13.95 | NULL | 2 / 3 | GSEA C2 | KEGG_VIRAL_MYOCARDITIS |
| 17 | −12.8 | NULL | 18 / 74 | BP | regulation of immune response |
| 18 | −12.68 | NULL | 14 / 60 | BP | T cell costimulation |
| 19 | −12.27 | NULL | 3 / 6 | GSEA C2 | SANA_RESPONSE_TO_IFNG_UP |
| 20 | −12.12 | NULL | 5 / 10 | GSEA C2 | FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_ |
| 21 | −11.89 | NULL | 5 / 17 | BP | positive regulation of neutrophil chemotaxis |
| 22 | −11.8 | NULL | 2 / 4 | GSEA C2 | KEGG_LEISHMANIA_INFECTION |
| 23 | −11.75 | NULL | 7 / 21 | CC | clathrin−coated endocytic vesicle membrane |
| 24 | −11.49 | NULL | 3 / 11 | GSEA C2 | WILENSKY_RESPONSE_TO_DARAPLADIB |
| 25 | −11.43 | NULL | 5 / 10 | GSEA C2 | LEE_DIFFERENTIATING_T_LYMPHOCYTE |
| 26 | −11.26 | NULL | 6 / 16 | GSEA C2 | FERRANDO_TAL1_NEIGHBORS |
| 27 | −11.15 | NULL | 7 / 23 | CC | integral to lumenal side of endoplasmic reticulum membrane |
| 28 | −10.89 | NULL | 3 / 8 | Lymphoma | MASCQUE_ABC UP |
| 29 | −10.87 | NULL | 4 / 7 | GSEA C2 | TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE |
| 30 | −10.65 | NULL | 6 / 11 | GSEA C2 | BIOCARTA_TCYTOTOXIC_PATHWAY |
| 31 | −10.61 | NULL | 6 / 16 | Lymphoma | WRIGHT_ABC UP |
| 32 | −10.59 | NULL | 3 / 8 | GSEA C2 | LINDSTEDT_DENDRITIC_CELL_MATURATION_D |
| 33 | −10.37 | NULL | 5 / 15 | GSEA C2 | JAATINEN_HEMATOPOIETIC_STEM_CELL_DN |
| 34 | −10.36 | NULL | 8 / 28 | CC | transport vesicle membrane |
| 35 | −10.35 | NULL | 3 / 7 | GSEA C2 | BOYAULT_LIVER_CANCER_SUBCLASS_G5_DN |
| 36 | −10.35 | NULL | 4 / 13 | BP | positive regulation of endocytosis |
| 37 | −10.28 | NULL | 4 / 16 | GSEA C2 | KORKOLA_TERATOMA_UP |
| 38 | −10.26 | NULL | 27 / 162 | CC | external side of plasma membrane |
| 39 | −10.21 | NULL | 5 / 11 | BP | positive regulation of B cell differentiation |
| 40 | −10.18 | NULL | 4 / 10 | GSEA C2 | FERRANDO_LYL1_NEIGHBORS |