# GW_066

## Global Summary

%DE = 0.15

# genes with fdr < 0.2  = 1805  ( 1025 + / 780  − )

# genes with fdr < 0.1  = 1605  ( 917 + / 688  − )

# genes with fdr < 0.05  = 1312  ( 766 + / 546  − )

# genes with fdr < 0.01 = 894  ( 543 + / 351  − )

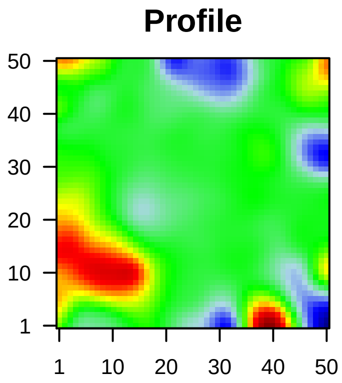
# genes in genesets = 16332

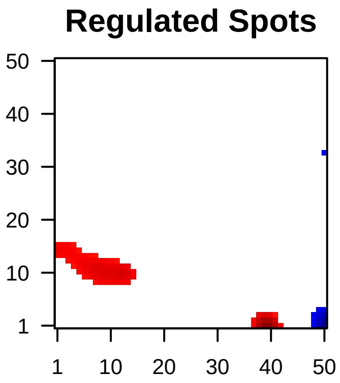
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.1

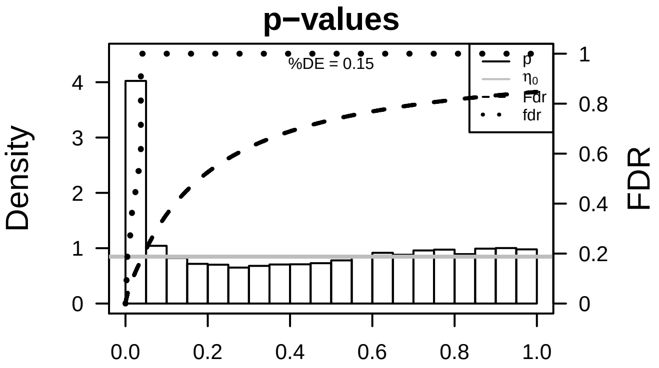
<fdr> = 0.85





## Global Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 124 | 2.57 | 2e−16 | 4e−14 | 50 x 11 | alcohol dehydrogenase 1A (class I), alpha polypeptide [Sourc |
| 2 | 126 | 2.19 | 2e−16 | 4e−14 | 50 x 12 | alcohol dehydrogenase 1C (class I), gamma polypeptide [Sou |
| 3 | 216 | 1.46 | 2e−16 | 4e−14 | 50 x 50 | aldehyde dehydrogenase 1 family, member A1 [Source:HGN |
| 4 | 220 | 1.55 | 2e−16 | 4e−14 | 4 x 46 | aldehyde dehydrogenase 1 family, member A3 [Source:HGN |
| 5 | 222 | 1.51 | 2e−16 | 4e−14 | 1 x 49 | aldehyde dehydrogenase 3 family, member B2 [Source:HGN |
| 6 | 55107 | 1.97 | 2e−16 | 4e−14 | 1 x 5 | anoctamin 1, calcium activated chloride channel [Source:HG |
| 7 | 344905 | 1.35 | 2e−16 | 4e−14 | 50 x 50 | ATPase type 13A5 [Source:HGNC Symbol;Acc:31789] |
| 8 | 25805 | −1.74 | 2e−16 | 4e−14 | 8 x 1 | BMP and activin membrane−bound inhibitor [Source:HGNC |
| 9 | 664 | −1.32 | 2e−16 | 4e−14 | 2 x 43 | BCL2/adenovirus E1B 19kDa interacting protein 3 [Source:H |
| 10 | 684 | −1.96 | 2e−16 | 4e−14 | 32 x 1 | bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A |
| 11 | 339512 | 1.7 | 2e−16 | 4e−14 | 50 x 50 | chromosome 1 open reading frame 110 [Source:HGNC Sym |
| 12 | 713 | −1.53 | 2e−16 | 4e−14 | 50 x 1 | complement component 1, q subcomponent, B chain [Source |
| 13 | 92747 | 1.67 | 2e−16 | 4e−14 | 50 x 10 | BPI fold containing family B, member 1 [Source:HGNC Symb |
| 14 | 140851 | −1.38 | 2e−16 | 4e−14 | 1 x 5 | |
| 15 | 6366 | 1.37 | 2e−16 | 4e−14 | 50 x 2 | chemokine (C−C motif) ligand 21 [Source:HGNC Symbol;Acc |
| 16 | 595 | 1.31 | 2e−16 | 4e−14 | 1 x 6 | cyclin D1 [Source:HGNC Symbol;Acc:1582] |
| 17 | 970 | 1.43 | 2e−16 | 4e−14 | 33 x 2 | CD70 molecule [Source:HGNC Symbol;Acc:11937] |
| 18 | 113130 | 1.39 | 2e−16 | 4e−14 | 44 x 49 | cell division cycle associated 5 [Source:HGNC Symbol;Acc:1 |
| 19 | 22802 | 1.87 | 2e−16 | 4e−14 | 1 x 50 | chloride channel accessory 4 [Source:HGNC Symbol;Acc:20 |
| 20 | 9073 | 1.66 | 2e−16 | 4e−14 | 8 x 50 | claudin 8 [Source:HGNC Symbol;Acc:2050] |



## Global Geneset Analysis

*Overexpressed*

| Rank | GSZ | p−value | #all | Geneset | |
|---|---|---|---|---|---|
| 1 | 13.13 | NULL | 42 | BP | keratinization |
| 2 | 8.62 | NULL | 21 | CC | cornified envelope |
| 3 | 7.59 | NULL | 9 | GSEA C2 | REACTOME_ETHANOL_OXIDATION |
| 4 | 7.45 | NULL | 504 | Chr | Chr 15 |
| 5 | 7.3 | NULL | 8 | GSEA C2 | LIU_CDX2_TARGETS_DN |
| 6 | 7.07 | NULL | 15 | GSEA C2 | RICKMAN_HEAD_AND_NECK_CANCER_E |
| 7 | 7.02 | NULL | 1135 | Chr | Chr 19 |
| 8 | 7.02 | NULL | 957 | Chr | Chr 11 |
| 9 | 6.39 | NULL | 15 | GSEA C2 | NIKOLSKY_BREAST_CANCER_8P12_P11_AMPLICON |
| 10 | 6.37 | NULL | 23 | Chr | Chr HSCHR6_MHC_DBB |
| 11 | 5.84 | NULL | 76 | BP | epidermis development |
| 12 | 5.82 | NULL | 135 | H.Tiss | WIRTH_Mucosa |
| 13 | 5.71 | NULL | 16 | GSEA C2 | KEGG_BLADDER_CANCER |
| 14 | 5.66 | NULL | 13 | GSEA C2 | REACTOME_REGULATION_OF_INSULIN_LIKE_GROWTH_FAC |
| 15 | 5.62 | NULL | 53 | BP | keratinocyte differentiation |
| 16 | 5.57 | NULL | 18 | BP | retinol metabolic process |
| 17 | 5.41 | NULL | 16 | GSEA C2 | GOUYER_TATI_TARGETS_DN |
| 18 | 5.38 | NULL | 15 | GSEA C2 | LY_AGING_MIDDLE_DN |
| 19 | 5.36 | NULL | 12 | GSEA C2 | LI_LUNG_CANCER |
| 20 | 5.33 | NULL | 186 | MF | structural molecule activity |

*Underexpressed*

| Rank | GSZ | p−value | #all | Geneset | |
|---|---|---|---|---|---|
| 1 | −17.13 | NULL | 633 | Chr | Chr 9 |
| 2 | −14.16 | NULL | 280 | Chr | Chr 13 |
| 3 | −10.54 | NULL | 699 | Chr | Chr 5 |
| 4 | −9.15 | NULL | 10 | GSEA C2 | CHASSOT_SKIN_WOUND |
| 5 | −8 | NULL | 16 | GSEA C2 | EINAV_INTERFERON_SIGNATURE_IN_CANCER |
| 6 | −7.28 | NULL | 123 | BP | defense response to virus |
| 7 | −7.15 | NULL | 16 | GSEA C2 | MOSERLE_IFNA_RESPONSE |
| 8 | −7.1 | NULL | 13 | GSEA C2 | BOWIE_RESPONSE_TO_TAMOXIFEN |
| 9 | −6.75 | NULL | 51 | BP | type I interferon signaling pathway |
| 10 | −6.69 | NULL | 16 | GSEA C2 | FARMER_BREAST_CANCER_CLUSTER_1 |
| 11 | −6.63 | NULL | 16 | GSEA C2 | ZHANG_INTERFERON_RESPONSE |
| 12 | −6.58 | NULL | 316 | Cancer | SPANG_BCL6−index2 |
| 13 | −6.5 | NULL | 265 | Glio | willscher_GBM_Verhaak−CL_expression_B_up |
| 14 | −6.5 | NULL | 265 | Glio | willscher_GBM_Verhaak−MES_expression_B_up |
| 15 | −6.5 | NULL | 265 | Glio | willscher_GBM_Verhaak−PNwt_expression_B_down |
| 16 | −6.5 | NULL | 265 | Glio | willscher_GBM_Verhaak−PNmut_expression_B_down |
| 17 | −6.24 | NULL | 31 | BP | negative regulation of viral genome replication |
| 18 | −6.15 | NULL | 16 | GSEA C2 | BILBAN_B_CLL_LPL_DN |
| 19 | −6.12 | NULL | 4 | GSEA C2 | REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEME |
| 20 | −6 | NULL | 10 | GSEA C2 | GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3 |

# GW_066

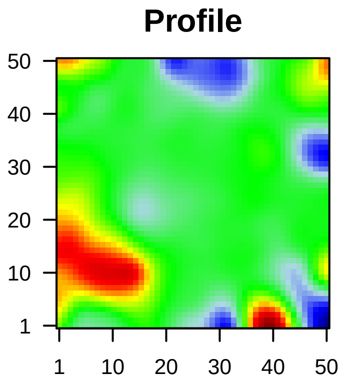
## Local Summary

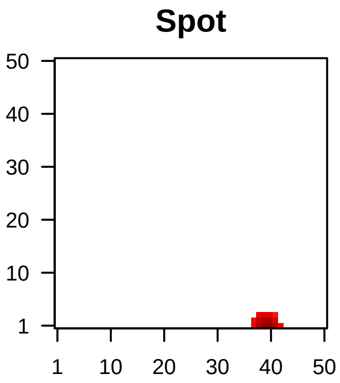
%DE = 0.8
# metagenes = 15
# genes = 251
# genes in genesets = 225

# genes with fdr < 0.1  = 154  ( 141 + / 13  − )
# genes with fdr < 0.05  = 115  ( 105 + / 10  − )
# genes with fdr < 0.01 = 79  ( 75 + / 4  − )

<r> metagenes = 0.98
<r> genes = 0.49

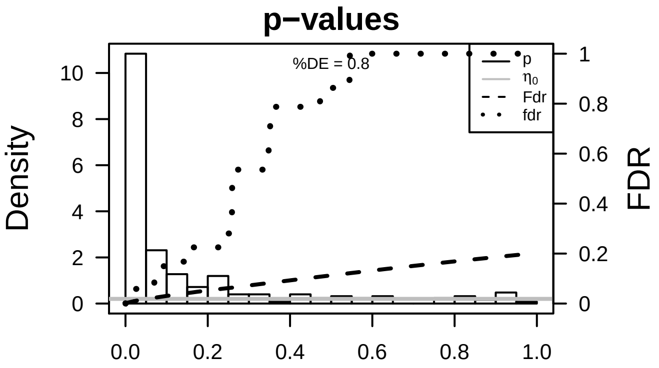
<FC> = 0.3
<shrinkage−t> = 10.69
<p−value> = 0.01
<fdr> = 0.58





## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 11180 | 1.2 | 8e−14 | 3e−08 | 42 x 1 | WD repeat domain 6 [Source:HGNC Symbol;Acc:12758] |
| 2 | 23466 | 0.98 | 1e−09 | 3e−08 | 41 x 1 | chromobox homolog 6 [Source:HGNC Symbol;Acc:1556] |
| 3 | 641737 | 0.91 | 1e−09 | 7e−06 | 40 x 1 | |
| 4 | 51326 | 0.84 | 2e−07 | 7e−06 | 42 x 1 | ADP−ribosylation factor−like 17B [Source:HGNC Symbol;Acc |
| 5 | 23162 | 0.82 | 3e−07 | 7e−06 | 39 x 1 | mitogen−activated protein kinase 8 interacting protein 3 [Sour |
| 6 | 9905 | 0.8 | 6e−07 | 7e−06 | 40 x 2 | small G protein signaling modulator 2 [Source:HGNC Symbol |
| 7 | 136051 | 0.79 | 9e−07 | 7e−06 | 40 x 1 | zinc finger protein 786 [Source:HGNC Symbol;Acc:21806] |
| 8 | 399761 | 0.79 | 9e−07 | 7e−06 | 39 x 1 | BMS1 pseudogene 5 [Source:HGNC Symbol;Acc:23653] |
| 9 | 51478 | 0.79 | 9e−07 | 2e−05 | 39 x 1 | hydroxysteroid (17−beta) dehydrogenase 7 [Source:HGNC S |
| 10 | 1375 | 0.77 | 2e−06 | 2e−05 | 42 x 1 | carnitine palmitoyltransferase 1B (muscle) [Source:HGNC Sy |
| 11 | 152485 | 0.77 | 2e−06 | 5e−05 | 41 x 1 | zinc finger protein 827 [Source:HGNC Symbol;Acc:27193] |
| 12 | 440275 | 0.75 | 3e−06 | 6e−05 | 40 x 1 | eukaryotic translation initiation factor 2 alpha kinase 4 [Sourc |
| 13 | 90586 | 0.74 | 4e−06 | 8e−05 | 39 x 1 | amine oxidase, copper containing 4, pseudogene [Source:HG |
| 14 | 8548 | 0.72 | 8e−06 | 8e−05 | 39 x 1 | basic leucine zipper nuclear factor 1 [Source:HGNC Symbol; |
| 15 | 256364 | 0.71 | 1e−05 | 8e−05 | 41 x 3 | echinoderm microtubule associated protein like 3 [Source:HG |
| 16 | 8930 | 0.71 | 1e−05 | 8e−05 | 39 x 1 | methyl−CpG binding domain protein 4 [Source:HGNC Symbo |
| 17 | 126205 | 0.71 | 1e−05 | 8e−05 | 40 x 1 | NLR family, pyrin domain containing 8 [Source:HGNC Symbo |
| 18 | 91368 | 0.64 | 1e−05 | 8e−05 | 39 x 1 | CDKN2A interacting protein N−terminal like [Source:HGNC S |
| 19 | 729603 | 0.64 | 1e−05 | 1e−04 | 40 x 1 | |
| 20 | 8566 | 0.69 | 2e−05 | 1e−04 | 41 x 2 | pyridoxal (pyridoxine, vitamin B6) kinase [Source:HGNC Sym |



## Local Geneset Analysis

*Overexpression*

| Rank | GSZ | p−value | #in/all | Geneset | |
|---|---|---|---|---|---|
| 1 | 8.14 | NULL | 2 / 13 | GSEA C2 | GAZDA_DIAMOND_BLACKFAN_ANEMIA_ERYTHROID_DN |
| 2 | 7.79 | NULL | 3 / 14 | MMML CGS | MACIEJ_MMML 8 |
| 3 | 6.98 | NULL | 2 / 4 | GSEA C2 | BIOCARTA_CYTOKINE_PATHWAY |
| 4 | 6.94 | NULL | 1 / 13 | MF | insulin receptor substrate binding |
| 5 | 6.72 | NULL | 2 / 19 | MF | mitogen−activated protein kinase kinase kinase binding |
| 6 | 6.59 | NULL | 3 / 13 | GSEA C2 | SPIRA_SMOKERS_LUNG_CANCER_DN |
| 7 | 6.4 | NULL | 1 / 15 | BP | negative regulation of autophagy |
| 8 | 6.38 | NULL | 1 / 7 | GSEA C2 | KEGG_STEROID_HORMONE_BIOSYNTHESIS |
| 9 | 5.79 | NULL | 1 / 4 | GSEA C2 | MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_5 |
| 10 | 5.63 | NULL | 2 / 22 | CC | heterochromatin |
| 11 | 5.4 | NULL | 1 / 10 | BP | lung morphogenesis |
| 12 | 5.25 | NULL | 2 / 29 | BP | positive regulation of JUN kinase activity |
| 13 | 5.2 | NULL | 1 / 10 | GSEA C2 | REACTOME_TRANSFORMATION_OF_LANOSTEROL_TO_CHOL |
| 14 | 5.11 | NULL | 1 / 11 | CC | axolemma |
| 15 | 5.04 | NULL | 2 / 15 | GSEA C2 | FIRESTEIN_PROLIFERATION |
| 16 | 5.01 | NULL | 1 / 11 | GSEA C2 | GARCIA_TARGETS_OF_FLI1_AND_DAX1_UP |
| 17 | 4.94 | NULL | 2 / 14 | BP | cellular response to estradiol stimulus |
| 18 | 4.93 | NULL | 1 / 4 | GSEA C2 | WEBER_METHYLATED_ICP_IN_SPERM_UP |
| 19 | 4.93 | NULL | 2 / 15 | GSEA C2 | ZHOU_INFLAMMATORY_RESPONSE_LIVE_DN |
| 20 | 4.93 | NULL | 2 / 15 | GSEA C2 | ZHOU_INFLAMMATORY_RESPONSE_LPS_DN |
| 21 | 4.92 | NULL | 1 / 9 | GSEA C2 | RODWELL_AGING_KIDNEY_UP |
| 22 | 4.89 | NULL | 4 / 44 | BP | meiosis |
| 23 | 4.81 | NULL | 1 / 9 | GSEA C2 | TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_UP |
| 24 | 4.81 | NULL | 1 / 9 | GSEA C2 | DER_IFN_ALPHA_RESPONSE_UP |
| 25 | 4.69 | NULL | 2 / 11 | GSEA C2 | STEIN_ESRRA_TARGETS_DN |
| 26 | 4.68 | NULL | 1 / 11 | GSEA C2 | BIOCARTA_EIF2_PATHWAY |
| 27 | 4.63 | NULL | 1 / 13 | BP | regulation of JNK cascade |
| 28 | 4.63 | NULL | 1 / 13 | CC | smooth endoplasmic reticulum |
| 29 | 4.63 | NULL | 2 / 23 | BP | G2 DNA damage checkpoint |
| 30 | 4.62 | NULL | 1 / 10 | MF | endodeoxyribonuclease activity |
| 31 | 4.62 | NULL | 1 / 10 | GSEA C2 | REACTOME_BASE_FREE_SUGAR_PHOSPHATE_REMOVAL_V |
| 32 | 4.51 | NULL | 3 / 16 | GSEA C2 | HAMAI_APOPTOSIS_VIA_TRAIL_UP |
| 33 | 4.5 | NULL | 3 / 15 | GSEA C2 | WANG_CLIM2_TARGETS_UP |
| 34 | 4.43 | NULL | 1 / 14 | MF | mitogen−activated protein kinase kinase binding |
| 35 | 4.43 | NULL | 1 / 14 | GSEA C2 | ST_DIFFERENTIATION_PATHWAY_IN_PC12_CELLS |
| 36 | 4.43 | NULL | 2 / 15 | GSEA C2 | REACTOME_SPHINGOLIPID_METABOLISM |
| 37 | 4.36 | NULL | 1 / 20 | miRNA target miRBase | hsa−miR−323−5p |
| 38 | 4.27 | NULL | 1 / 11 | GSEA C2 | DER_IFN_BETA_RESPONSE_UP |
| 39 | 4.26 | NULL | 1 / 15 | GSEA C2 | SA_B_CELL_RECEPTOR_COMPLEXES |
| 40 | 4.26 | NULL | 1 / 15 | GSEA C2 | SIG_CD40PATHWAYMAP |

# GW_066

## Local Summary

%DE = 0.56

# metagenes = 66

# genes = 536

# genes in genesets = 514

# genes with fdr < 0.1 = 175 ( 163 + / 12 − )

# genes with fdr < 0.05 = 138 ( 130 + / 8 − )

# genes with fdr < 0.01 = 99 ( 93 + / 6 − )

<r> metagenes = 0.78

<r> genes = 0.2

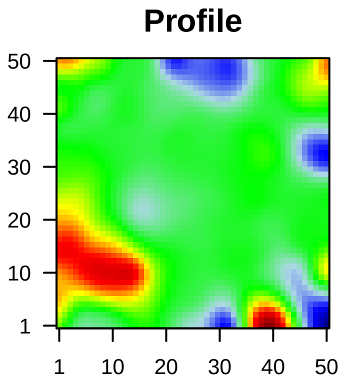
<FC> = 0.23

<shrinkage−t> = 8.17

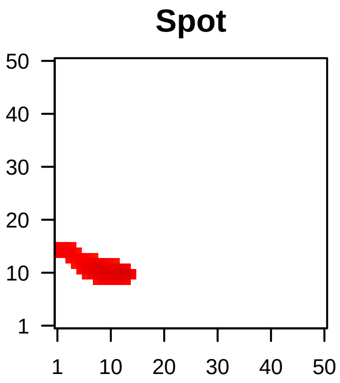
<p−value> = 0.01

<fdr> = 0.68

## Profile



## Spot



## Local Genelist

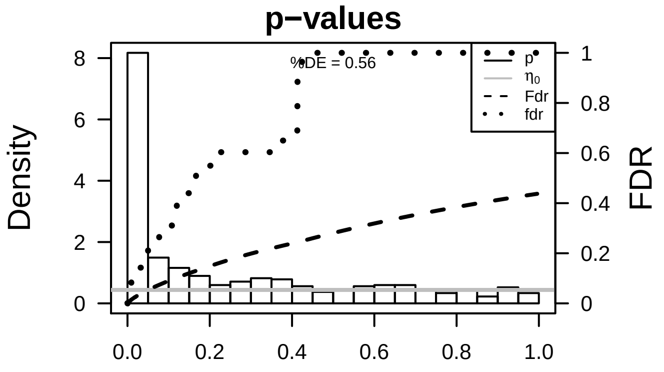
| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 10202 | 2.24 | 2e−16 | 3e−14 | 1 x 15 | dehydrogenase/reductase (SDR family) member 2 [Source:H |
| 2 | 121355 | 1.37 | 2e−16 | 3e−14 | 14 x 11 | gametocyte specific factor 1 [Source:HGNC Symbol;Acc:265 |
| 3 | 55655 | 1.23 | 2e−14 | 6e−12 | 15 x 11 | NLR family, pyrin domain containing 2 [Source:HGNC Symbo |
| 4 | 286499 | 1.21 | 4e−14 | 2e−10 | 15 x 11 | family with sequence similarity 133, member A [Source:HGN |
| 5 | 8772 | 1.15 | 9e−13 | 1e−09 | 1 x 14 | Fas (TNFRSF6)−associated via death domain [Source:HGNC |
| 6 | 219931 | 1.1 | 9e−12 | 1e−09 | 1 x 14 | two pore segment channel 2 [Source:HGNC Symbol;Acc:208 |
| 7 | 55291 | 1.08 | 1e−11 | 1e−09 | 6 x 11 | protein phosphatase 6, regulatory subunit 3 [Source:HGNC S |
| 8 | 219927 | 1.07 | 2e−11 | 1e−09 | 1 x 15 | mitochondrial ribosomal protein L21 [Source:HGNC Symbol; |
| 9 | 4109 | 1.07 | 3e−11 | 1e−09 | 14 x 11 | melanoma antigen family A, 10 [Source:HGNC Symbol;Acc:6 |
| 10 | 645037 | 1.07 | 3e−11 | 2e−07 | 14 x 11 | G antigen 2C [Source:HGNC Symbol;Acc:31958] |
| 11 | 26748 | 0.98 | 1e−09 | 2e−07 | 14 x 11 | G antigen 12I [Source:HGNC Symbol;Acc:4105] |
| 12 | 2577 | 0.97 | 2e−09 | 2e−07 | 14 x 11 | G antigen 12J [Source:HGNC Symbol;Acc:17778] |
| 13 | 402 | 0.96 | 2e−09 | 5e−07 | 8 x 10 | ADP−ribosylation factor−like 2 [Source:HGNC Symbol;Acc:6 |
| 14 | 55653 | 0.93 | 6e−09 | 5e−07 | 9 x 10 | breast carcinoma amplified sequence 4 [Source:HGNC Symb |
| 15 | 203068 | 0.92 | 1e−08 | 5e−07 | 3 x 15 | tubulin, beta class I [Source:HGNC Symbol;Acc:20778] |
| 16 | 4041 | 0.92 | 1e−08 | 5e−07 | 12 x 9 | low density lipoprotein receptor−related protein 5 [Source:HG |
| 17 | 3508 | 0.91 | 2e−08 | 5e−07 | 1 x 14 | immunoglobulin mu binding protein 2 [Source:HGNC Symbol; |
| 18 | 729442 | 0.91 | 2e−08 | 5e−07 | 14 x 11 | G antigen 12J [Source:HGNC Symbol;Acc:17778] |
| 19 | 55199 | 0.9 | 2e−08 | 5e−07 | 4 x 16 | family with sequence similarity 86, member C1 [Source:HGN |
| 20 | 23 | 0.9 | 2e−08 | 1e−06 | 7 x 12 | ATP−binding cassette, sub−family F (GCN20), member 1 [So |

## Local Geneset Analysis

*Overexpression*

| Rank | GSZ | p−value | #in/all | Geneset | |
|---|---|---|---|---|---|
| 1 | 8.07 | NULL | 4 / 23 | Chr | Chr HSCHR6_MHC_DBB |
| 2 | 7.76 | NULL | 1 / 15 | BP | myeloid dendritic cell differentiation |
| 3 | 7.76 | NULL | 1 / 15 | GSEA C2 | FARMER_BREAST_CANCER_CLUSTER_7 |
| 4 | 7.48 | NULL | 1 / 16 | GSEA C2 | TING_SILENCED_BY_DICER |
| 5 | 7.4 | NULL | 3 / 11 | GSEA C2 | MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_UP |
| 6 | 7.25 | NULL | 38 / 957 | Chr | Chr 11 |
| 7 | 7.02 | NULL | 11 / 45 | Glio | willscher_GBM_Verhaak−PNwt_expression_J_up |
| 8 | 6.99 | NULL | 3 / 15 | GSEA C2 | KAUFFMANN_DNA_REPLICATION_GENES |
| 9 | 6.8 | NULL | 3 / 14 | GSEA C2 | BONCI_TARGETS_OF_MIR15A_AND_MIR16_1 |
| 10 | 6.75 | NULL | 1 / 2 | miRNA target | miR−16−1 |
| 11 | 6.45 | NULL | 1 / 6 | GSEA C2 | GALI_TP53_TARGETS_APOPTOTIC_DN |
| 12 | 6.45 | NULL | 2 / 13 | GSEA C2 | NADERI_BREAST_CANCER_PROGNOSIS_UP |
| 13 | 6.44 | NULL | 4 / 28 | MF | ribosome binding |
| 14 | 6.43 | NULL | 1 / 4 | GSEA C2 | KRASNOSELSKAYA_ILF3_TARGETS_UP |
| 15 | 6.41 | NULL | 1 / 4 | GSEA C2 | NIELSEN_LEIOMYOSARCOMA_DN |
| 16 | 6.37 | NULL | 5 / 15 | GSEA C2 | MATTIOLI_MULTIPLE_MYELOMA_SUBGROUPS |
| 17 | 5.99 | NULL | 2 / 25 | BP | cellular response to oxidative stress |
| 18 | 5.97 | NULL | 3 / 12 | GSEA C2 | BROWNE_HCMV_INFECTION_14HR_UP |
| 19 | 5.93 | NULL | 3 / 10 | GSEA C2 | HOFMANN_MYELODYSPLASTIC_SYNDROM_LOW_RISK_DN |
| 20 | 5.78 | NULL | 3 / 10 | GSEA C2 | TOMIDA_METASTASIS_UP |
| 21 | 5.67 | NULL | 2 / 16 | GSEA C2 | SCHLOSSER_SERUM_RESPONSE_AUGMENTED_BY_MYC |
| 22 | 5.63 | NULL | 2 / 10 | GSEA C2 | CONRAD_STEM_CELL |
| 23 | 5.6 | NULL | 2 / 16 | GSEA C2 | TIEN_INTESTINE_PROBIOTICS_2HR_UP |
| 24 | 5.59 | NULL | 1 / 5 | GSEA C2 | GRASEMANN_RETINOBLASTOMA_WITH_6P_AMPLIFICATION |
| 25 | 5.57 | NULL | 3 / 16 | Cancer | RHODES_UNDIFFERENTIATED_CANCER |
| 26 | 5.52 | NULL | 2 / 12 | GSEA C2 | BACOLOD_RESISTANCE_TO_ALKYLATING_AGENTS_DN |
| 27 | 5.51 | NULL | 4 / 19 | MF | hydrolase activity, acting on acid anhydrides, in phosphorus−contai |
| 28 | 5.41 | NULL | 1 / 5 | GSEA C2 | REACTOME_ELECTRON_TRANSPORT_CHAIN |
| 29 | 5.34 | NULL | 2 / 15 | GSEA C2 | WNT_SIGNALING |
| 30 | 5.29 | NULL | 2 / 11 | Glio | willscher_GBM_Verhaak−CL_expression_M_down |
| 31 | 5.29 | NULL | 2 / 11 | Glio | willscher_GBM_Verhaak−MES_expression_M_down |
| 32 | 5.29 | NULL | 2 / 11 | Glio | willscher_GBM_Verhaak−PNmut_expression_M_up |
| 33 | 5.22 | NULL | 1 / 5 | GSEA C2 | NAGY_PCAF_COMPONENTS_HUMAN |
| 34 | 5.15 | NULL | 2 / 8 | GSEA C2 | KEGG_PRION_DISEASES |
| 35 | 5.13 | NULL | 2 / 15 | GSEA C2 | BROWNE_HCMV_INFECTION_8HR_DN |
| 36 | 5.13 | NULL | 1 / 9 | GSEA C2 | BIOCARTA_RELA_PATHWAY |
| 37 | 5.13 | NULL | 1 / 9 | GSEA C2 | BIOCARTA_NFKB_PATHWAY |
| 38 | 5.13 | NULL | 1 / 9 | GSEA C2 | BIOCARTA_SODD_PATHWAY |
| 39 | 5.13 | NULL | 1 / 9 | GSEA C2 | REACTOME_DEATH_RECEPTOR_SIGNALLING |
| 40 | 5.06 | NULL | 5 / 56 | BP | protein heterooligomerization |

## p−values



# GW_066

## Local Summary

%DE = 0.67

# metagenes = 11

# genes = 222

# genes in genesets = 220

# genes with fdr < 0.1  = 122  ( 19 + / 103  − )

# genes with fdr < 0.05  = 105  ( 16 + / 89  − )

# genes with fdr < 0.01 = 75  ( 14 + / 61  − )

<r> metagenes = 0.99

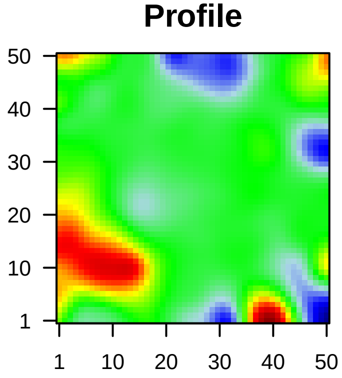
<r> genes = 0.61

<FC> = −0.26

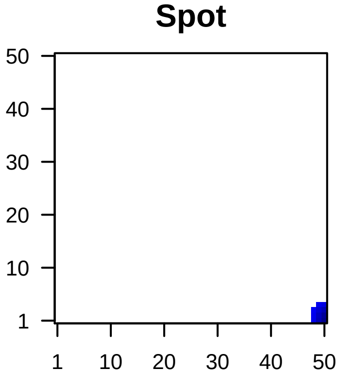
<shrinkage−t> = −8.99

<p−value> = 0

<fdr> = 0.52



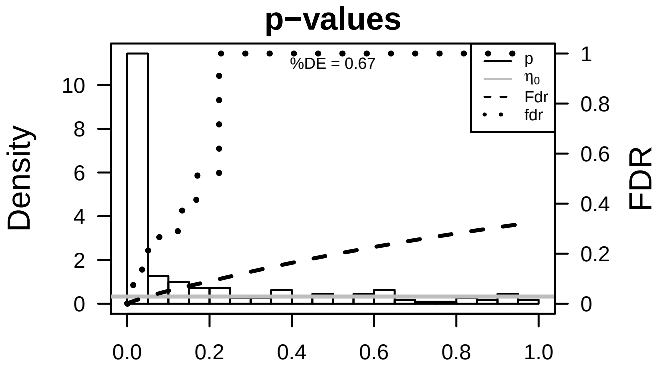
**Profile**



**Spot**

## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 713 | −1.53 | 2e−16 | 3e−15 | 50 x 1 | complement component 1, q subcomponent, B chain [Source |
| 2 | 6366 | 1.37 | 2e−16 | 3e−15 | 50 x 2 | chemokine (C−C motif) ligand 21 [Source:HGNC Symbol;Acc |
| 3 | 1545 | 1.69 | 2e−16 | 3e−15 | 50 x 4 | cytochrome P450, family 1, subfamily B, polypeptide 1 [Sourc |
| 4 | 3620 | 1.63 | 2e−16 | 3e−15 | 48 x 1 | indoleamine 2,3−dioxygenase 1 [Source:HGNC Symbol;Acc: |
| 5 | 3543 | 1.5 | 2e−16 | 3e−15 | 49 x 1 | immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy |
| 6 | 3128 | −1.25 | 7e−15 | 7e−13 | 50 x 1 | major histocompatibility complex, class II, DR beta 6 (pseudo |
| 7 | 5996 | −1.23 | 2e−14 | 9e−13 | 50 x 1 | regulator of G−protein signaling 1 [Source:HGNC Symbol;Acc |
| 8 | 5920 | 1.22 | 4e−14 | 9e−13 | 48 x 1 | retinoic acid receptor responder (tazarotene induced) 3 [Sour |
| 9 | 714 | −1.21 | 4e−14 | 1e−11 | 50 x 1 | complement component 1, q subcomponent, C chain [Source |
| 10 | 341 | −1.18 | 2e−13 | 2e−10 | 50 x 1 | apolipoprotein C−I [Source:HGNC Symbol;Acc:607] |
| 11 | 3122 | −1.05 | 3e−12 | 4e−09 | 50 x 1 | major histocompatibility complex, class II, DR alpha [Source: |
| 12 | 7305 | −1.05 | 5e−11 | 7e−09 | 50 x 1 | TYRO protein tyrosine kinase binding protein [Source:HGNC |
| 13 | 5552 | −1.02 | 2e−10 | 7e−09 | 50 x 1 | serglycin [Source:HGNC Symbol;Acc:9361] |
| 14 | 3113 | −1.01 | 3e−10 | 7e−09 | 50 x 1 | major histocompatibility complex, class II, DP alpha 1 [Source |
| 15 | 3109 | −1.01 | 3e−10 | 2e−08 | 50 x 1 | major histocompatibility complex, class II, DM beta [Source:H |
| 16 | 2207 | −0.99 | 6e−10 | 2e−07 | 50 x 1 | Fc fragment of IgE, high affinity I, receptor for; gamma polype |
| 17 | 57172 | 0.95 | 3e−09 | 7e−07 | 49 x 1 | calcium/calmodulin−dependent protein kinase IG [Source:HG |
| 18 | 84868 | −0.89 | 3e−08 | 7e−07 | 50 x 1 | hepatitis A virus cellular receptor 2 [Source:HGNC Symbol;A |
| 19 | 962 | −0.88 | 5e−08 | 7e−07 | 50 x 1 | CD48 molecule [Source:HGNC Symbol;Acc:1683] |
| 20 | 54855 | 0.87 | 5e−08 | 7e−07 | 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 | −27.67 | NULL | 11 / 15 | CC | MHC class II protein complex |
| 2 | −24.43 | NULL | 2 / 4 | GSEA C2 | REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN |
| 3 | −20.19 | NULL | 36 / 265 | Glio | willscher_GBM_Verhaak−CL_expression_B_up |
| 4 | −20.19 | NULL | 36 / 265 | Glio | willscher_GBM_Verhaak−MES_expression_B_up |
| 5 | −20.19 | NULL | 36 / 265 | Glio | willscher_GBM_Verhaak−PNwt_expression_B_down |
| 6 | −20.19 | NULL | 36 / 265 | Glio | willscher_GBM_Verhaak−PNmut_expression_B_down |
| 7 | −17.75 | NULL | 2 / 7 | GSEA C2 | BIOCARTA_COMP_PATHWAY |
| 8 | −16.64 | NULL | 2 / 3 | GSEA C2 | KEGG_VIRAL_MYOCARDITIS |
| 9 | −16.47 | NULL | 2 / 8 | GSEA C2 | BIOCARTA_CLASSIC_PATHWAY |
| 10 | −16.47 | NULL | 2 / 8 | GSEA C2 | REACTOME_COMPLEMENT_CASCADE |
| 11 | −16.47 | NULL | 2 / 8 | GSEA C2 | REACTOME_INITIAL_TRIGGERING_OF_COMPLEMENT |
| 12 | −15.42 | NULL | 13 / 47 | BP | antigen processing and presentation |
| 13 | −15.31 | NULL | 6 / 21 | CC | clathrin−coated endocytic vesicle membrane |
| 14 | −14.57 | NULL | 6 / 23 | CC | integral to lumenal side of endoplasmic reticulum membrane |
| 15 | −14.28 | NULL | 2 / 6 | GSEA C2 | BUDHU_LIVER_CANCER_METASTASIS_UP |
| 16 | −14.03 | NULL | 2 / 4 | GSEA C2 | KEGG_LEISHMANIA_INFECTION |
| 17 | −13.96 | NULL | 3 / 8 | GSEA C2 | LINDSTEDT_DENDRITIC_CELL_MATURATION_D |
| 18 | −13.93 | NULL | 76 / 417 | H.Tiss | WIRTH_Immune system |
| 19 | −13.49 | NULL | 3 / 16 | GSEA C2 | KAAB_FAILED_HEART_VENTRICLE_DN |
| 20 | −13.13 | NULL | 9 / 16 | GSEA C2 | FARMER_BREAST_CANCER_CLUSTER_1 |
| 21 | −13.11 | NULL | 15 / 74 | BP | regulation of immune response |
| 22 | −13.09 | NULL | 6 / 28 | CC | transport vesicle membrane |
| 23 | −12.98 | NULL | 5 / 12 | GSEA C2 | ZHAN_MULTIPLE_MYELOMA_DN |
| 24 | −12.74 | NULL | 80 / 553 | Cancer | Lembcke_Colonic Inflammation |
| 25 | −12.71 | NULL | 2 / 10 | GSEA C2 | AMUNDSON_GAMMA_RADIATION_RESISTANCE |
| 26 | −12.53 | NULL | 3 / 11 | GSEA C2 | KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY |
| 27 | −12.32 | NULL | 3 / 10 | GSEA C2 | HOSHIDA_LIVER_CANCER_SUBCLASS_S1 |
| 28 | −12.16 | NULL | 6 / 32 | CC | ER to Golgi transport vesicle membrane |
| 29 | −12.05 | NULL | 7 / 35 | CC | trans−Golgi network membrane |
| 30 | −11.96 | NULL | 11 / 87 | BP | antigen processing and presentation of exogenous peptide antigen |
| 31 | −11.86 | NULL | 4 / 10 | GSEA C2 | BIOCARTA_LYM_PATHWAY |
| 32 | −11.74 | NULL | 7 / 46 | CC | endocytic vesicle membrane |
| 33 | −11.72 | NULL | 6 / 11 | GSEA C2 | BIOCARTA_TCYTOTOXIC_PATHWAY |
| 34 | −11.55 | NULL | 2 / 6 | GSEA C2 | LUI_THYROID_CANCER_CLUSTER_4 |
| 35 | −11.21 | NULL | 3 / 11 | GSEA C2 | WILENSKY_RESPONSE_TO_DARAPLADIB |
| 36 | −11.07 | NULL | 4 / 11 | GSEA C2 | APPEL_IMATINIB_RESPONSE |
| 37 | −10.86 | NULL | 5 / 12 | BP | immunoglobulin mediated immune response |
| 38 | −10.79 | NULL | 5 / 10 | GSEA C2 | LEE_DIFFERENTIATING_T_LYMPHOCYTE |
| 39 | −10.68 | NULL | 6 / 15 | GSEA C2 | FINAK_BREAST_CANCER_SDPP_SIGNATURE |
| 40 | −10.32 | NULL | 3 / 13 | GSEA C2 | CAVARD_LIVER_CANCER_MALIGNANT_VS_BENIGN |

# GW_066

## Local Summary

%DE = 0.43

# metagenes = 1

# genes = 32

# genes in genesets = 32

# genes with fdr < 0.1 = 5 ( 0 + / 5 − )

# genes with fdr < 0.05 = 5 ( 0 + / 5 − )

# genes with fdr < 0.01 = 5 ( 0 + / 5 − )

<r> metagenes = NA

<r> genes = 0.37

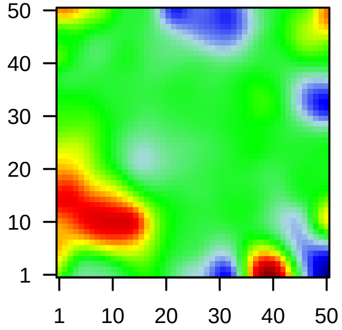
<FC> = −0.25

<shrinkage−t> = −8.64

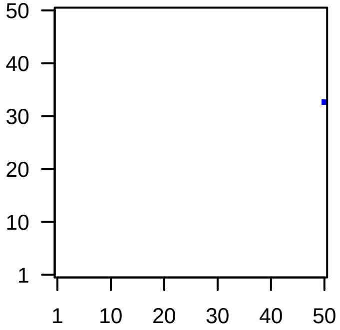
<p−value> = 0.02

<fdr> = 0.77

### Profile



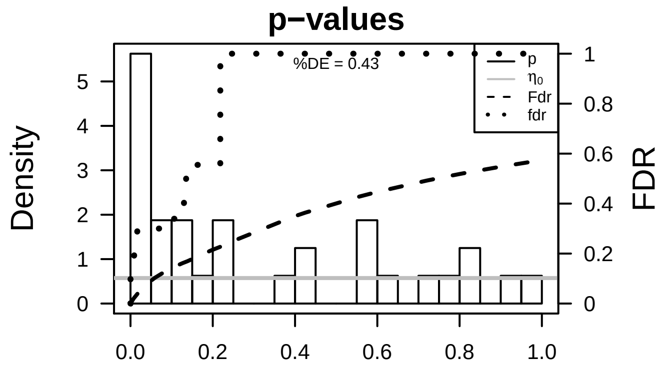
### Spot



## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 55958 | −1.04 | 1e−10 | 1e−05 | 50 x 33 | kelch−like family member 9 [Source:HGNC Symbol;Acc:1873 |
| 2 | 6139 | −0.8 | 7e−07 | 4e−05 | 50 x 33 | RPL17−C18orf32 readthrough [Source:HGNC Symbol;Acc:4 |
| 3 | 55074 | −0.75 | 3e−06 | 3e−04 | 50 x 33 | oxidation resistance 1 [Source:HGNC Symbol;Acc:15822] |
| 4 | 221154 | −0.69 | 2e−05 | 3e−04 | 50 x 33 | mitochondrial calcium uptake 2 [Source:HGNC Symbol;Acc:3 |
| 5 | 23484 | −0.67 | 3e−05 | 3e−04 | 50 x 33 | leptin receptor overlapping transcript−like 1 [Source:HGNC S |
| 6 | 51015 | −0.65 | 5e−05 | 1e−01 | 50 x 33 | isochorismatase domain containing 1 [Source:HGNC Symbol |
| 7 | 4677 | −0.43 | 8e−03 | 2e−01 | 50 x 33 | asparaginyl−tRNA synthetase [Source:HGNC Symbol;Acc:76 |
| 8 | 153364 | −0.38 | 2e−02 | 3e−01 | 50 x 33 | metallo−beta−lactamase domain containing 2 [Source:HGNC |
| 9 | 128338 | −0.32 | 5e−02 | 3e−01 | 50 x 33 | DNA−damage regulated autophagy modulator 2 [Source:HG |
| 10 | 115209 | −0.3 | 6e−02 | 3e−01 | 50 x 33 | OMA1 zinc metallopeptidase [Source:HGNC Symbol;Acc:29 |
| 11 | 317662 | −0.28 | 8e−02 | 3e−01 | 50 x 33 | family with sequence similarity 149, member B1 [Source:HG |
| 12 | 387921 | −0.28 | 8e−02 | 3e−01 | 50 x 33 | NHL repeat containing 3 [Source:HGNC Symbol;Acc:33751] |
| 13 | 221294 | −0.26 | 1e−01 | 3e−01 | 50 x 33 | 5'−nucleotidase domain containing 1 [Source:HGNC Symbol; |
| 14 | 120534 | −0.25 | 1e−01 | 3e−01 | 50 x 33 | ADP−ribosylation factor−like 14 effector protein [Source:HGN |
| 15 | 23588 | 0.24 | 1e−01 | 6e−01 | 50 x 33 | kelch domain containing 2 [Source:HGNC Symbol;Acc:20231 |
| 16 | 200845 | −0.21 | 2e−01 | 6e−01 | 50 x 33 | potassium channel tetramerization domain containing 6 [Sour |
| 17 | 7334 | −0.2 | 2e−01 | 6e−01 | 50 x 33 | ubiquitin−conjugating enzyme E2N [Source:HGNC Symbol;A |
| 18 | 10224 | −0.2 | 2e−01 | 1e+00 | 50 x 33 | zinc finger protein 443 [Source:HGNC Symbol;Acc:20878] |
| 19 | 8493 | −0.19 | 2e−01 | 1e+00 | 50 x 33 | protein phosphatase, Mg2+/Mn2+ dependent, 1D [Source:HG |
| 20 | 29929 | −0.14 | 4e−01 | 1e+00 | 50 x 33 | ALG6, alpha−1,3−glucosyltransferase [Source:HGNC Symbo |

### p−values



## Local Geneset Analysis

*Underexpression*

| Rank | GSZ | p−value | #in/all | Geneset | |
|---|---|---|---|---|---|
| 1 | −16.58 | NULL | 1 / 16 | GSEA C2 | BERNARD_PPAPDC1B_TARGETS_UP |
| 2 | −16.55 | NULL | 1 / 10 | CC | large ribosomal subunit |
| 3 | −15.63 | NULL | 3 / 89 | miRNA target starBase | hsa−miR−505 |
| 4 | −14.75 | NULL | 1 / 11 | BP | cell wall macromolecule catabolic process |
| 5 | −13.25 | NULL | 1 / 24 | CC | Cul3−RING ubiquitin ligase complex |
| 6 | −11.35 | NULL | 1 / 15 | GSEA C2 | DAIRKEE_TERT_TARGETS_DN |
| 7 | −10.95 | NULL | 1 / 16 | GSEA C2 | HAHTOLA_MYCOSIS_FUNGOIDES_SKIN_DN |
| 8 | −10.95 | NULL | 1 / 16 | GSEA C2 | ACEVEDO_NORMAL_TISSUE_ADJACENT_TO_LIVER_TUMOR_ |
| 9 | −10.64 | NULL | 1 / 16 | Cancer | GENTLES_modul11 |
| 10 | −9.95 | NULL | 1 / 19 | CC | calcium channel complex |
| 11 | −8.96 | NULL | 1 / 49 | miRNA target starBase | hsa−miR−1201 |
| 12 | −8.67 | NULL | 1 / 52 | miRNA target starBase | hsa−miR−191 |
| 13 | −8.67 | NULL | 3 / 61 | miRNA target starBase | hsa−miR−1200 |
| 14 | −8.58 | NULL | 1 / 29 | BP | adult walking behavior |
| 15 | −8.02 | NULL | 1 / 60 | BP | cytokinesis |
| 16 | −8.02 | NULL | 1 / 60 | miRNA target starBase | hsa−miR−643 |
| 17 | −8.02 | NULL | 1 / 60 | miRNA target starBase | hsa−miR−219−5p |
| 18 | −7.94 | NULL | 1 / 61 | miRNA target starBase | hsa−miR−659 |
| 19 | −7.8 | NULL | 1 / 63 | miRNA target starBase | hsa−miR−612 |
| 20 | −7.74 | NULL | 1 / 64 | miRNA target starBase | hsa−miR−873 |
| 21 | −7.31 | NULL | 1 / 71 | miRNA target starBase | hsa−miR−935 |
| 22 | −7.3 | NULL | 1 / 14 | GSEA C2 | REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION |
| 23 | −6.88 | NULL | 2 / 39 | miRNA target starBase | hsa−miR−1258 |
| 24 | −6.86 | NULL | 2 / 100 | miRNA target starBase | hsa−miR−377 |
| 25 | −6.83 | NULL | 1 / 34 | miRNA target starBase | hsa−miR−555 |
| 26 | −6.69 | NULL | 2 / 61 | miRNA target starBase | hsa−miR−514 |
| 27 | −6.68 | NULL | 1 / 51 | CC | cytosolic large ribosomal subunit |
| 28 | −6.48 | NULL | 1 / 88 | miRNA target starBase | hsa−miR−423−5p |
| 29 | −6.48 | NULL | 1 / 39 | miRNA target starBase | hsa−miR−593 |
| 30 | −6.46 | NULL | 3 / 113 | miRNA target starBase | hsa−miR−507 |
| 31 | −5.95 | NULL | 1 / 12 | BP | apoptotic nuclear changes |
| 32 | −5.91 | NULL | 1 / 46 | miRNA target starBase | hsa−miR−1322 |
| 33 | −5.9 | NULL | 1 / 104 | CC | midbody |
| 34 | −5.82 | NULL | 4 / 381 | miRNA target starBase | hsa−let−7c |
| 35 | −5.65 | NULL | 1 / 22 | miRNA target starBase | hsa−miR−596 |
| 36 | −5.59 | NULL | 3 / 109 | miRNA target starBase | hsa−miR−501−5p |
| 37 | −5.51 | NULL | 1 / 23 | miRNA target starBase | hsa−miR−609 |
| 38 | −5.48 | NULL | 4 / 421 | miRNA target starBase | hsa−let−7b |
| 39 | −5.43 | NULL | 3 / 315 | miRNA target starBase | hsa−miR−30e |
| 40 | −5.29 | NULL | 1 / 69 | miRNA target starBase | hsa−miR−651 |