# GW_086

## Global Summary

%DE = 0.14

# genes with fdr < 0.2 = 1767 ( 929 + / 838 − )

# genes with fdr < 0.1 = 1466 ( 779 + / 687 − )

# genes with fdr < 0.05 = 1118 ( 608 + / 510 − )

# genes with fdr < 0.01 = 794 ( 450 + / 344 − )

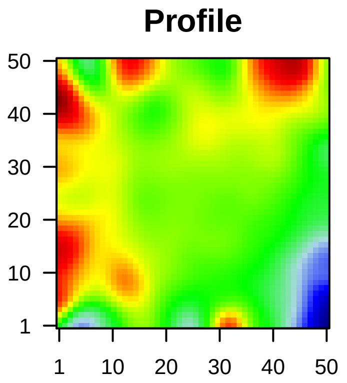
# genes in genesets = 16332

<FC> = 0

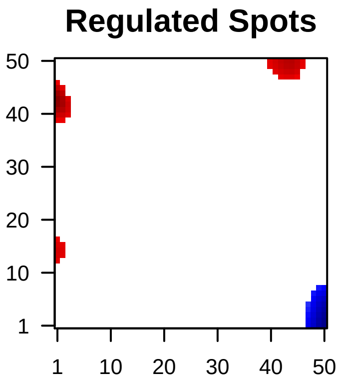
<shrinkage−t> = 0

<p−value> = 0.11

<fdr> = 0.86



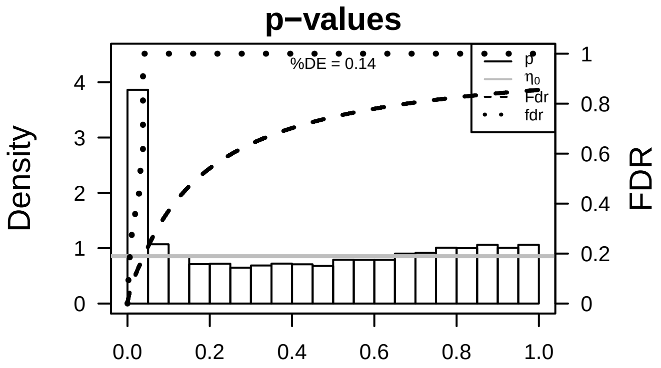
**Profile**



**Regulated Spots**

## Global Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 58 | −1.44 | 2e−16 | 6e−14 | 25 x 1 | actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12 |
| 2 | 131 | −1.78 | 2e−16 | 6e−14 | 1 x 50 | alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide |
| 3 | 113146 | 1.68 | 2e−16 | 6e−14 | 1 x 44 | AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125] |
| 4 | 230 | 1.64 | 2e−16 | 6e−14 | 2 x 17 | aldolase C, fructose−bisphosphate [Source:HGNC Symbol;A |
| 5 | 144193 | 1.73 | 2e−16 | 6e−14 | 15 x 50 | amidohydrolase domain containing 1 [Source:HGNC Symbol; |
| 6 | 55107 | 1.63 | 2e−16 | 6e−14 | 1 x 5 | anoctamin 1, calcium activated chloride channel [Source:HG |
| 7 | 10409 | −1.55 | 2e−16 | 6e−14 | 1 x 2 | brain abundant, membrane attached signal protein 1 [Source: |
| 8 | 64073 | 1.69 | 2e−16 | 6e−14 | 1 x 46 | chromosome 19 open reading frame 33 [Source:HGNC Sym |
| 9 | 339512 | 1.58 | 2e−16 | 6e−14 | 50 x 50 | chromosome 1 open reading frame 110 [Source:HGNC Sym |
| 10 | 79783 | 1.56 | 2e−16 | 6e−14 | 1 x 5 | succinylCoA:glutarate−CoA transferase [Source:HGNC Sym |
| 11 | 768 | 2.39 | 2e−16 | 6e−14 | 1 x 6 | carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383] |
| 12 | 793 | 1.66 | 2e−16 | 6e−14 | 39 x 50 | calbindin 1, 28kDa [Source:HGNC Symbol;Acc:1434] |
| 13 | 6352 | 1.42 | 2e−16 | 6e−14 | 48 x 1 | chemokine (C−C motif) ligand 5 [Source:HGNC Symbol;Acc: |
| 14 | 1308 | 1.7 | 2e−16 | 6e−14 | 1 x 43 | collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194 |
| 15 | 1288 | 1.57 | 2e−16 | 6e−14 | 1 x 43 | collagen, type IV, alpha 6 [Source:HGNC Symbol;Acc:2208] |
| 16 | 49860 | 2.06 | 2e−16 | 6e−14 | 1 x 50 | cornulin [Source:HGNC Symbol;Acc:1230] |
| 17 | 54541 | 1.4 | 2e−16 | 6e−14 | 1 x 4 | DNA−damage−inducible transcript 4 [Source:HGNC Symbol; |
| 18 | 2026 | 1.47 | 2e−16 | 6e−14 | 10 x 10 | enolase 2 (gamma, neuronal) [Source:HGNC Symbol;Acc:33 |
| 19 | 2167 | 1.85 | 2e−16 | 6e−14 | 1 x 44 | fatty acid binding protein 4, adipocyte [Source:HGNC Symbol |
| 20 | 8772 | 1.42 | 2e−16 | 6e−14 | 1 x 14 | Fas (TNFRSF6)−associated via death domain [Source:HGNC |



**p−values**

## Global Geneset Analysis

| Rank | GSZ | p−value | #all | Geneset | |
|---|---|---|---|---|---|
| *Overexpressed* | | | | | |
| 1 | 15.77 | NULL | 519 | Chr | Chr 14 |
| 2 | 13.57 | NULL | 918 | Chr | Chr 17 |
| 3 | 11.12 | NULL | 142 | Glio | willscher_GBM_Verhaak−CL_expression_C_up |
| 4 | 11.12 | NULL | 142 | Glio | willscher_GBM_Verhaak−PNmut_expression_C_down |
| 5 | 10.83 | NULL | 370 | BP | mitotic cell cycle |
| 6 | 9.15 | NULL | 13 | GSEA C2 | BOWIE_RESPONSE_TO_TAMOXIFEN |
| 7 | 8.07 | NULL | 12 | BP | hemidesmosome assembly |
| 8 | 7.97 | NULL | 135 | H.Tiss | WIRTH_Mucosa |
| 9 | 7.6 | NULL | 572 | Disease | GUDJ_psoriasis up |
| 10 | 7.58 | NULL | 51 | BP | type I interferon signaling pathway |
| 11 | 7.18 | NULL | 48 | BP | regulation of cellular amino acid metabolic process |
| 12 | 7.16 | NULL | 74 | BP | anaphase−promoting complex−dependent proteasomal ubiquitin− |
| 13 | 7.15 | NULL | 123 | BP | defense response to virus |
| 14 | 7.15 | NULL | 148 | BP | G1/S transition of mitotic cell cycle |
| 15 | 7.09 | NULL | 10 | GSEA C2 | BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX |
| 16 | 7.08 | NULL | 949 | CC | nucleoplasm |
| 17 | 6.7 | NULL | 70 | BP | antigen processing and presentation of exogenous peptide antigen |
| 18 | 6.64 | NULL | 866 | Chr | Chr 12 |
| 19 | 6.55 | NULL | 16 | GSEA C2 | UROSEVIC_RESPONSE_TO_IMIQUIMOD |
| 20 | 6.5 | NULL | 66 | BP | positive regulation of ubiquitin−protein ligase activity involved in mi |
| *Underexpressed* | | | | | |
| 1 | −13.93 | NULL | 618 | Chr | Chr 4 |
| 2 | −11.44 | NULL | 553 | Cancer | Lembcke_Colonic Inflammation |
| 3 | −8.08 | NULL | 417 | H.Tiss | WIRTH_Immune system |
| 4 | −7.06 | NULL | 16 | GSEA C2 | RICKMAN_HEAD_AND_NECK_CANCER_F |
| 5 | −6.48 | NULL | 4 | MMML CGS | MACIEJ_MMML 23 |
| 6 | −6.33 | NULL | 250 | Lymphoma | LENZ_Stromal signature 1 |
| 7 | −6.12 | NULL | 280 | Chr | Chr 13 |
| 8 | −5.84 | NULL | 127 | H.Tiss | WIRTH_Muscle |
| 9 | −5.74 | NULL | 162 | CC | external side of plasma membrane |
| 10 | −5.68 | NULL | 312 | BP | immune response |
| 11 | −5.67 | NULL | 16 | H.Tiss | WIRTH_Hippocampus |
| 12 | −5.57 | NULL | 7 | GSEA C2 | TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE |
| 13 | −5.5 | NULL | 92 | BP | translational elongation |
| 14 | −5.49 | NULL | 232 | Chr | Chr 18 |
| 15 | −5.41 | NULL | 81 | BP | viral transcription |
| 16 | −5.12 | NULL | 87 | BP | translational termination |
| 17 | −5.11 | NULL | 269 | BP | inflammatory response |
| 18 | −5.08 | NULL | 11 | GSEA C2 | KEGG_ARACHIDONIC_ACID_METABOLISM |
| 19 | −5.02 | NULL | 24 | TF Tissue | VAQUERIZAS_Trachea |
| 20 | −5.02 | NULL | 11 | GSEA C2 | BIOCARTA_TCYTOTOXIC_PATHWAY |

# GW_086

## Local Summary

%DE = 0.5

# metagenes = 8

# genes = 132

# genes in genesets = 132

# genes with fdr < 0.1 = 49 ( 49 + / 0 − )

# genes with fdr < 0.05 = 35 ( 35 + / 0 − )

# genes with fdr < 0.01 = 24 ( 24 + / 0 − )

<r> metagenes = 0.98

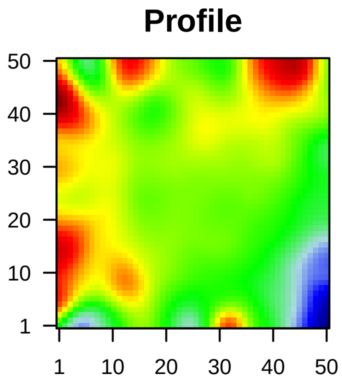
<r> genes = 0.31

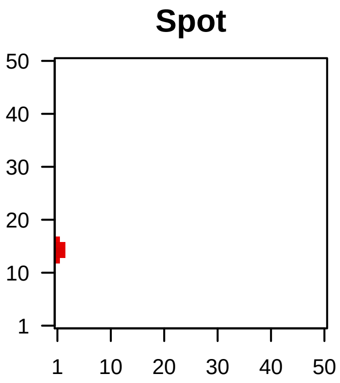
<FC> = 0.32

<shrinkage−t> = 11.15

<p−value> = 0.01

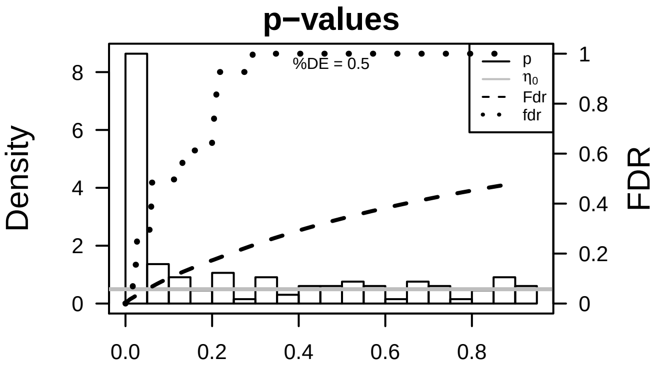
<fdr> = 0.64





## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 8772 | 1.42 | 2e−16 | 1e−14 | 1 x 14 | Fas (TNFRSF6)−associated via death domain [Source:HGNC |
| 2 | 220064 | 1.22 | 3e−13 | 3e−11 | 1 x 14 | oral cancer overexpressed 1 [Source:HGNC Symbol;Acc:175 |
| 3 | 2017 | 1.2 | 7e−13 | 4e−11 | 1 x 14 | cortactin [Source:HGNC Symbol;Acc:3338] |
| 4 | 131076 | 1.19 | 1e−12 | 8e−10 | 1 x 16 | coiled−coil domain containing 58 [Source:HGNC Symbol;Acc |
| 5 | 219927 | 1.13 | 1e−11 | 1e−09 | 1 x 15 | mitochondrial ribosomal protein L21 [Source:HGNC Symbol; |
| 6 | 219931 | 1.11 | 4e−11 | 1e−08 | 1 x 14 | two pore segment channel 2 [Source:HGNC Symbol;Acc:208 |
| 7 | 10428 | 1.06 | 2e−10 | 2e−07 | 1 x 15 | craniofacial development protein 1 [Source:HGNC Symbol;Ac |
| 8 | 51083 | 0.99 | 4e−09 | 2e−05 | 1 x 15 | galanin/GMAP prepropeptide [Source:HGNC Symbol;Acc:41 |
| 9 | 991 | 0.82 | 1e−06 | 2e−05 | 1 x 16 | cell division cycle 20 [Source:HGNC Symbol;Acc:1723] |
| 10 | 10598 | 0.81 | 1e−06 | 2e−05 | 1 x 14 | AHA1, activator of heat shock 90kDa protein ATPase homolo |
| 11 | 51367 | 0.81 | 1e−06 | 2e−05 | 1 x 17 | processing of precursor 5, ribonuclease P/MRP subunit (S. ce |
| 12 | 388581 | 0.81 | 1e−06 | 1e−04 | 1 x 15 | family with sequence similarity 132, member A [Source:HGN |
| 13 | 5214 | 0.77 | 4e−06 | 1e−04 | 1 x 13 | phosphofructokinase, platelet [Source:HGNC Symbol;Acc:88 |
| 14 | 23028 | 0.77 | 5e−06 | 3e−04 | 1 x 14 | lysine (K)−specific demethylase 1A [Source:HGNC Symbol;A |
| 15 | 1152 | 0.75 | 9e−06 | 4e−04 | 1 x 17 | creatine kinase, brain [Source:HGNC Symbol;Acc:1991] |
| 16 | 10419 | 0.73 | 1e−05 | 8e−04 | 1 x 17 | protein arginine methyltransferase 5 [Source:HGNC Symbol; |
| 17 | 283869 | 0.71 | 3e−05 | 2e−03 | 1 x 17 | neuropeptide W [Source:HGNC Symbol;Acc:30509] |
| 18 | 79929 | 0.67 | 6e−05 | 2e−03 | 1 x 16 | MAP6 domain containing 1 [Source:HGNC Symbol;Acc:2575 |
| 19 | 79080 | 0.66 | 8e−05 | 3e−03 | 1 x 14 | coiled−coil domain containing 86 [Source:HGNC Symbol;Acc |
| 20 | 55257 | 0.63 | 2e−04 | 3e−03 | 1 x 15 | MRG/MORF4L binding protein [Source:HGNC Symbol;Acc:1 |



## Local Geneset Analysis

*Overexpression*

| Rank | GSZ | p−value | #in/all | Geneset |
|---|---|---|---|---|
| 1 | 15.49 | NULL | 1 / 6 | GSEA C2 GALI_TP53_TARGETS_APOPTOTIC_DN |
| 2 | 13.33 | NULL | 2 / 13 | GSEA C2 NADERI_BREAST_CANCER_PROGNOSIS_UP |
| 3 | 12.46 | NULL | 2 / 18 | BP smooth muscle contraction |
| 4 | 12.3 | NULL | 1 / 9 | GSEA C2 BIOCARTA_RELA_PATHWAY |
| 5 | 12.3 | NULL | 1 / 9 | GSEA C2 BIOCARTA_NFKB_PATHWAY |
| 6 | 12.3 | NULL | 1 / 9 | GSEA C2 BIOCARTA_SODD_PATHWAY |
| 7 | 12.3 | NULL | 1 / 9 | GSEA C2 REACTOME_DEATH_RECEPTOR_SIGNALLING |
| 8 | 11.59 | NULL | 1 / 10 | MF death receptor binding |
| 9 | 11.59 | NULL | 1 / 10 | BP positive regulation of macrophage differentiation |
| 10 | 11.42 | NULL | 1 / 2 | GSEA C2 PELLICCIOTTA_HDAC_IN_ANTIGEN_PRESENTATION_DN |
| 11 | 11.42 | NULL | 1 / 2 | GSEA C2 REACTOME_DIABETES_PATHWAYS |
| 12 | 11.36 | NULL | 2 / 10 | GSEA C2 ZHU_CMV_24_HR_UP |
| 13 | 11.36 | NULL | 2 / 10 | GSEA C2 ZHU_CMV_ALL_UP |
| 14 | 11.17 | NULL | 2 / 10 | BP creatine metabolic process |
| 15 | 10.98 | NULL | 1 / 11 | BP regulation of extrinsic apoptotic signaling pathway in absence of lig |
| 16 | 10.98 | NULL | 1 / 11 | GSEA C2 HOFMANN_CELL_LYMPHOMA_DN |
| 17 | 10.98 | NULL | 1 / 11 | GSEA C2 ST_TUMOR_NECROSIS_FACTOR_PATHWAY |
| 18 | 10.77 | NULL | 1 / 6 | GSEA C2 REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTORS |
| 19 | 10.77 | NULL | 1 / 6 | GSEA C2 REACTOME_GPCR_LIGAND_BINDING |
| 20 | 10.57 | NULL | 2 / 13 | GSEA C2 RICKMAN_HEAD_AND_NECK_CANCER_C |
| 21 | 10.45 | NULL | 1 / 12 | GSEA C2 BIOCARTA_FAS_PATHWAY |
| 22 | 9.99 | NULL | 1 / 13 | BP lymph node development |
| 23 | 9.99 | NULL | 1 / 13 | GSEA C2 BIOCARTA_TNFR1_PATHWAY |
| 24 | 9.96 | NULL | 1 / 3 | GSEA C2 WEBER_METHYLATED_LCP_IN_SPERM_DN |
| 25 | 9.86 | NULL | 2 / 9 | GSEA C2 KUMAMOTO_RESPONSE_TO_NUTLIN_3A_DN |
| 26 | 9.85 | NULL | 1 / 7 | GSEA C2 CAFFAREL_RESPONSE_TO_THC_24HR_5_UP |
| 27 | 9.85 | NULL | 1 / 7 | GSEA C2 REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS |
| 28 | 9.64 | NULL | 2 / 8 | GSEA C2 MUELLER_PLURINET |
| 29 | 9.58 | NULL | 1 / 14 | GSEA C2 GENTILE_UV_RESPONSE_CLUSTER_D5 |
| 30 | 9.58 | NULL | 1 / 14 | GSEA C2 BIOCARTA_DEATH_PATHWAY |
| 31 | 9.5 | NULL | 2 / 10 | BP negative regulation of DNA damage response, signal transduction |
| 32 | 9.22 | NULL | 1 / 15 | BP positive regulation of extrinsic apoptotic signaling pathway via deat |
| 33 | 9.17 | NULL | 2 / 21 | BP feeding behavior |
| 34 | 9.13 | NULL | 1 / 8 | GSEA C2 SAMOLS_TARGETS_OF_KHSV_MIRNAS_UP |
| 35 | 9.13 | NULL | 1 / 8 | GSEA C2 REACTOME_G_ALPHA_I_SIGNALLING_EVENTS |
| 36 | 8.91 | NULL | 1 / 6 | GSEA C2 WAESCH_ANAPHASE_PROMOTING_COMPLEX |
| 37 | 8.89 | NULL | 1 / 16 | BP positive regulation of activated T cell proliferation |
| 38 | 8.89 | NULL | 1 / 16 | GSEA C2 LAU_APOPTOSIS_CDKN2A_UP |
| 39 | 8.89 | NULL | 1 / 16 | GSEA C2 BIOCARTA_CERAMIDE_PATHWAY |
| 40 | 8.67 | NULL | 2 / 30 | BP extrinsic apoptotic signaling pathway in absence of ligand |

# GW_086

## Local Summary

%DE = 0.63

# metagenes = 19

# genes = 249

# genes in genesets = 246

# genes with fdr < 0.1  = 133  ( 116 + / 17  − )

# genes with fdr < 0.05  = 123  ( 108 + / 15  − )

# genes with fdr < 0.01 = 109  ( 97 + / 12  − )

<r> metagenes = 0.96

<r> genes = 0.35

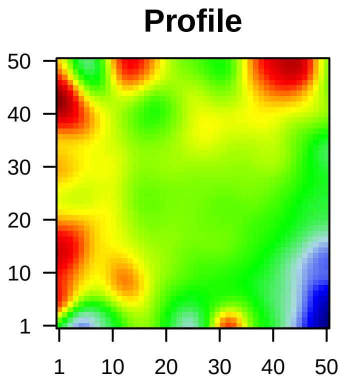
<FC> = 0.42

<shrinkage−t> = 14.62

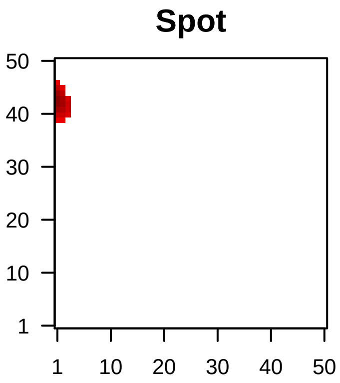
<p−value> = 0

<fdr> = 0.46

**Profile**



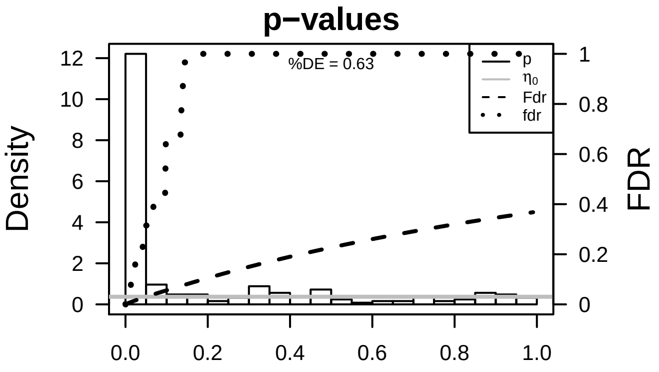
**Spot**



## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 113146 | 1.68 | 2e−16 | 1e−15 | 1 x 44 | AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125] |
| 2 | 64073 | 1.69 | 2e−16 | 1e−15 | 1 x 46 | chromosome 19 open reading frame 33 [Source:HGNC Symb |
| 3 | 1308 | 1.7 | 2e−16 | 1e−15 | 1 x 43 | collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194 |
| 4 | 1288 | 1.57 | 2e−16 | 1e−15 | 1 x 43 | collagen, type IV, alpha 6 [Source:HGNC Symbol;Acc:2208] |
| 5 | 2167 | 1.85 | 2e−16 | 1e−15 | 1 x 44 | fatty acid binding protein 4, adipocyte [Source:HGNC Symbol |
| 6 | 53836 | 1.38 | 2e−16 | 1e−15 | 2 x 42 | G protein−coupled receptor 87 [Source:HGNC Symbol;Acc:4 |
| 7 | 3306 | 1.4 | 2e−16 | 1e−15 | 1 x 42 | heat shock 70kDa protein 2 [Source:HGNC Symbol;Acc:5235 |
| 8 | 55214 | 1.83 | 2e−16 | 1e−15 | 1 x 42 | leprecan−like 1 [Source:HGNC Symbol;Acc:19317] |
| 9 | 4015 | 1.96 | 2e−16 | 1e−15 | 1 x 41 | lysyl oxidase [Source:HGNC Symbol;Acc:6664] |
| 10 | 4501 | 1.58 | 2e−16 | 1e−15 | 1 x 44 | metallothionein 1X [Source:HGNC Symbol;Acc:7405] |
| 11 | 56901 | 1.59 | 2e−16 | 1e−15 | 1 x 44 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4−li |
| 12 | 4747 | 1.73 | 2e−16 | 1e−15 | 1 x 43 |  |
| 13 | 4753 | 1.94 | 2e−16 | 1e−15 | 1 x 44 | NEL−like 2 (chicken) [Source:HGNC Symbol;Acc:7751] |
| 14 | 5744 | 2.49 | 2e−16 | 1e−15 | 1 x 43 | parathyroid hormone−like hormone [Source:HGNC Symbol;A |
| 15 | 5836 | 1.7 | 2e−16 | 1e−15 | 1 x 44 | phosphorylase, glycogen, liver [Source:HGNC Symbol;Acc:97 |
| 16 | 780851 | 2.12 | 2e−16 | 1e−15 | 2 x 39 | small nucleolar RNA, C/D box 3A [Source:HGNC Symbol;Acc |
| 17 | 780853 | 2.14 | 2e−16 | 1e−15 | 2 x 39 | small nucleolar RNA, C/D box 3C [Source:HGNC Symbol;Acc |
| 18 | 780854 | 2.3 | 2e−16 | 1e−15 | 2 x 39 | small nucleolar RNA, C/D box 3D [Source:HGNC Symbol;Acc |
| 19 | 112399 | 1.32 | 3e−15 | 1e−13 | 1 x 40 | egl−9 family hypoxia−inducible factor 3 [Source:HGNC Symb |
| 20 | 3861 | 1.21 | 4e−15 | 1e−13 | 1 x 45 | keratin 14 [Source:HGNC Symbol;Acc:6416] |

**p−values**



## Local Geneset Analysis

*Overexpression*

| Rank | GSZ | p−value | #in/all | Geneset |  |
|---|---|---|---|---|---|
| 1 | 18.85 | NULL | 7 / 16 | GSEA C2 | HUPER_BREAST_BASAL_VS_LUMINAL_UP |
| 2 | 17.09 | NULL | 5 / 12 | BP | hemidesmosome assembly |
| 3 | 12.83 | NULL | 12 / 76 | BP | epidermis development |
| 4 | 12.19 | NULL | 20 / 135 | H.Tiss | WIRTH_Mucosa |
| 5 | 11.83 | NULL | 4 / 16 | GSEA C2 | ELVIDGE_HIF1A_TARGETS_DN |
| 6 | 11.56 | NULL | 4 / 13 | BP | intermediate filament cytoskeleton organization |
| 7 | 11.55 | NULL | 1 / 7 | GSEA C2 | BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_AND_PAX3 |
| 8 | 11.06 | NULL | 1 / 5 | GSEA C2 | ELVIDGE_HIF2A_TARGETS_UP |
| 9 | 10.89 | NULL | 4 / 16 | GSEA C2 | ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN |
| 10 | 10.42 | NULL | 2 / 6 | GSEA C2 | SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP |
| 11 | 10.01 | NULL | 14 / 82 | CC | intermediate filament |
| 12 | 9.88 | NULL | 2 / 11 | GSEA C2 | BIOCARTA_VITCB_PATHWAY |
| 13 | 9.54 | NULL | 2 / 16 | Glio | VERHAAK_MES subtype |
| 14 | 9.42 | NULL | 2 / 8 | GSEA C2 | MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_UP |
| 15 | 9.4 | NULL | 1 / 10 | BP | surfactant homeostasis |
| 16 | 9.11 | NULL | 2 / 11 | BP | response to metal ion |
| 17 | 9.03 | NULL | 2 / 15 | GSEA C2 | KANG_CISPLATIN_RESISTANCE_UP |
| 18 | 8.93 | NULL | 2 / 12 | MF | fatty acid binding |
| 19 | 8.82 | NULL | 3 / 15 | GSEA C2 | PRAMOONJAGO_SOX4_TARGETS_UP |
| 20 | 8.75 | NULL | 2 / 10 | BP | skeletal muscle tissue regeneration |
| 21 | 8.69 | NULL | 3 / 38 | BP | epithelial cell differentiation |
| 22 | 8.37 | NULL | 2 / 15 | GSEA C2 | NGUYEN_NOTCH1_TARGETS_UP |
| 23 | 8.29 | NULL | 2 / 19 | MF | L−ascorbic acid binding |
| 24 | 8.23 | NULL | 9 / 44 | BP | skin development |
| 25 | 8.14 | NULL | 2 / 10 | GSEA C2 | NIELSEN_MALIGNAT_FIBROUS_HISTIOCYTOMA_UP |
| 26 | 8.09 | NULL | 1 / 13 | H.Tiss | WIRTH_Thalamus |
| 27 | 7.94 | NULL | 3 / 16 | GSEA C2 | ELVIDGE_HYPOXIA_BY_DMOG_UP |
| 28 | 7.84 | NULL | 1 / 7 | GSEA C2 | BIOCARTA_FEEDER_PATHWAY |
| 29 | 7.83 | NULL | 2 / 8 | GSEA C2 | LIU_CDX2_TARGETS_DN |
| 30 | 7.78 | NULL | 6 / 83 | CC | basement membrane |
| 31 | 7.75 | NULL | 1 / 14 | BP | negative regulation of chondrocyte differentiation |
| 32 | 7.71 | NULL | 10 / 82 | MF | structural constituent of cytoskeleton |
| 33 | 7.38 | NULL | 2 / 15 | GSEA C2 | AMIT_EGF_RESPONSE_240_MCF10A |
| 34 | 7.38 | NULL | 6 / 70 | BP | cell junction assembly |
| 35 | 7.34 | NULL | 1 / 5 | GSEA C2 | BUSA_SAM68_TARGETS_UP |
| 36 | 7.31 | NULL | 2 / 26 | BP | positive regulation of cAMP biosynthetic process |
| 37 | 7.29 | NULL | 2 / 15 | BP | response to osmotic stress |
| 38 | 7.27 | NULL | 1 / 10 | GSEA C2 | KIM_MYCL1_AMPLIFICATION_TARGETS_UP |
| 39 | 7.25 | NULL | 3 / 12 | CC | fascia adherens |
| 40 | 7.25 | NULL | 2 / 15 | GSEA C2 | HINATA_NFKB_TARGETS_KERATINOCYTE_DN |

# GW_086

## Local Summary

%DE = 0.63

# metagenes = 23

# genes = 334

# genes in genesets = 331

# genes with fdr < 0.1 = 144 ( 138 + / 6 − )

# genes with fdr < 0.05 = 108 ( 106 + / 2 − )

# genes with fdr < 0.01 = 63 ( 63 + / 0 − )

<r> metagenes = 0.95

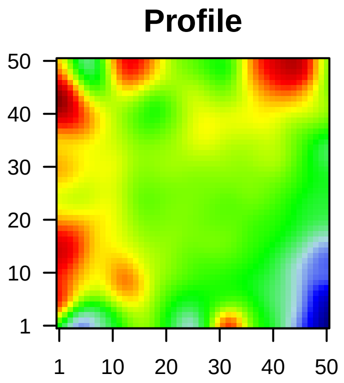
<r> genes = 0.38

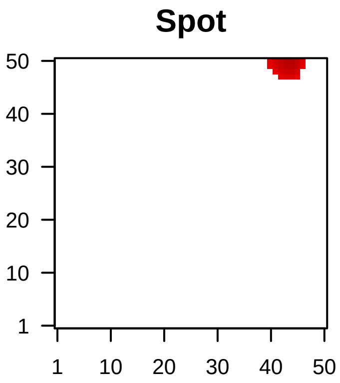
<FC> = 0.3

<shrinkage−t> = 10.55

<p−value> = 0.01

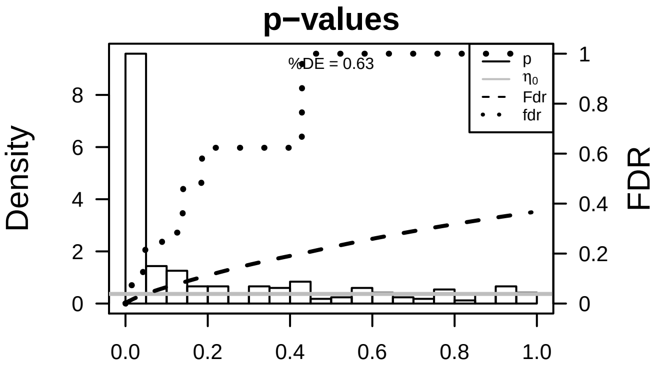
<fdr> = 0.63





## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 7083 | 1.28 | 3e−14 | 2e−11 | 45 x 49 | thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:1183 |
| 2 | 6596 | 1.23 | 3e−13 | 2e−11 | 46 x 50 | helicase−like transcription factor [Source:HGNC Symbol;Acc: |
| 3 | 8500 | 1.22 | 4e−13 | 2e−10 | 42 x 50 | protein tyrosine phosphatase, receptor type, f polypeptide (PT |
| 4 | 51122 | 1.18 | 2e−12 | 2e−10 | 42 x 50 | COMM domain containing 2 [Source:HGNC Symbol;Acc:249 |
| 5 | 23212 | 1.17 | 3e−12 | 3e−10 | 40 x 50 | RRS1 ribosome biogenesis regulator homolog (S. cerevisiae) |
| 6 | 51659 | 1.16 | 5e−12 | 3e−09 | 44 x 50 | GINS complex subunit 2 (Psf2 homolog) [Source:HGNC Sym |
| 7 | 10403 | 1.12 | 3e−11 | 8e−09 | 44 x 50 | NDC80 kinetochore complex component [Source:HGNC Sym |
| 8 | 5984 | 1.09 | 9e−11 | 1e−07 | 46 x 50 | replication factor C (activator 1) 4, 37kDa [Source:HGNC Syn |
| 9 | 116832 | 1.02 | 1e−09 | 2e−07 | 46 x 50 | ribosomal protein L39−like [Source:HGNC Symbol;Acc:1709 |
| 10 | 4173 | 1 | 2e−09 | 6e−07 | 44 x 50 | minichromosome maintenance complex component 4 [Source |
| 11 | 54443 | 0.96 | 9e−09 | 6e−07 | 43 x 50 | anillin, actin binding protein [Source:HGNC Symbol;Acc:1408 |
| 12 | 55689 | 0.96 | 1e−08 | 1e−06 | 46 x 50 | YEATS domain containing 2 [Source:HGNC Symbol;Acc:254 |
| 13 | 9650 | 0.94 | 2e−08 | 8e−06 | 40 x 50 | mitochondrial fission regulator 1 [Source:HGNC Symbol;Acc: |
| 14 | 3992 | 0.89 | 1e−07 | 8e−06 | 45 x 50 | fatty acid desaturase 1 [Source:HGNC Symbol;Acc:3574] |
| 15 | 6790 | 0.88 | 1e−07 | 3e−05 | 44 x 50 | aurora kinase A [Source:HGNC Symbol;Acc:11393] |
| 16 | 9787 | 0.85 | 4e−07 | 2e−04 | 43 x 50 | discs, large (Drosophila) homolog−associated protein 5 [Sour |
| 17 | 55157 | 0.8 | 2e−06 | 2e−04 | 43 x 50 | aspartyl−tRNA synthetase 2, mitochondrial [Source:HGNC S |
| 18 | 86 | 0.76 | 5e−06 | 2e−04 | 46 x 50 | actin−like 6A [Source:HGNC Symbol;Acc:24124] |
| 19 | 3838 | 0.76 | 6e−06 | 2e−04 | 43 x 50 | karyopherin alpha 2 (RAG cohort 1, importin alpha 1) [Source |
| 20 | 3833 | 0.75 | 8e−06 | 2e−04 | 45 x 48 | kinesin family member C1 [Source:HGNC Symbol;Acc:6389] |



## Local Geneset Analysis

*Overexpression*

| Rank | GSZ | p−value | #in/all | Geneset | |
|---|---|---|---|---|---|
| 1 | 39.57 | NULL | 80 / 142 | Glio | willscher_GBM_Verhaak−CL_expression_C_up |
| 2 | 39.57 | NULL | 80 / 142 | Glio | willscher_GBM_Verhaak−PNmut_expression_C_down |
| 3 | 22.3 | NULL | 85 / 370 | BP | mitotic cell cycle |
| 4 | 21.97 | NULL | 13 / 16 | GSEA C2 | FARMER_BREAST_CANCER_CLUSTER_2 |
| 5 | 20.56 | NULL | 10 / 13 | GSEA C2 | CROONQUIST_IL6_DEPRIVATION_DN |
| 6 | 20.53 | NULL | 9 / 15 | GSEA C2 | SMID_BREAST_CANCER_LUMINAL_A_DN |
| 7 | 17.79 | NULL | 10 / 14 | GSEA C2 | ZHAN_MULTIPLE_MYELOMA_PR_UP |
| 8 | 17.2 | NULL | 12 / 18 | BP | spindle organization |
| 9 | 17.06 | NULL | 9 / 30 | BP | DNA strand elongation involved in DNA replication |
| 10 | 17.02 | NULL | 8 / 16 | GSEA C2 | GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN |
| 11 | 16.73 | NULL | 82 / 530 | Cancer | Lembcke_Normal vs Adenoma |
| 12 | 16.32 | NULL | 8 / 10 | GSEA C2 | MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP |
| 13 | 16.22 | NULL | 6 / 16 | GSEA C2 | REACTOME_DNA_STRAND_ELONGATION |
| 14 | 16.1 | NULL | 10 / 16 | GSEA C2 | EGUCHI_CELL_CYCLE_RB1_TARGETS |
| 15 | 15.96 | NULL | 27 / 149 | BP | DNA replication |
| 16 | 15.87 | NULL | 15 / 16 | GSEA C2 | FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL |
| 17 | 15.59 | NULL | 14 / 15 | GSEA C2 | FINETTI_BREAST_CANCER_KINOME_RED |
| 18 | 15.41 | NULL | 9 / 16 | GSEA C2 | CROONQUIST_NRAS_SIGNALING_DN |
| 19 | 15.36 | NULL | 9 / 15 | GSEA C2 | FOURNIER_ACINAR_DEVELOPMENT_LATE_DN |
| 20 | 15.23 | NULL | 6 / 15 | GSEA C2 | TANG_SENESCENCE_TP53_TARGETS_DN |
| 21 | 14.87 | NULL | 5 / 9 | GSEA C2 | BIOCARTA_RANMS_PATHWAY |
| 22 | 14.81 | NULL | 44 / 232 | BP | mitosis |
| 23 | 14.58 | NULL | 6 / 14 | GSEA C2 | MISSIAGLIA_REGULATED_BY_METHYLATION_DN |
| 24 | 13.76 | NULL | 6 / 13 | GSEA C2 | REN_BOUND_BY_E2F |
| 25 | 13.47 | NULL | 9 / 16 | GSEA C2 | KANG_DOXORUBICIN_RESISTANCE_UP |
| 26 | 13.44 | NULL | 20 / 57 | Glio | developing astrocytes |
| 27 | 13.3 | NULL | 7 / 21 | BP | telomere maintenance via semi−conservative replication |
| 28 | 13.21 | NULL | 3 / 11 | GSEA C2 | REACTOME_UNWINDING_OF_DNA |
| 29 | 13.02 | NULL | 5 / 16 | GSEA C2 | CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN |
| 30 | 12.98 | NULL | 8 / 14 | GSEA C2 | ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER |
| 31 | 12.95 | NULL | 89 / 949 | CC | nucleoplasm |
| 32 | 12.79 | NULL | 6 / 16 | GSEA C2 | REACTOME_LAGGING_STRAND_SYNTHESIS |
| 33 | 12.74 | NULL | 30 / 148 | BP | G1/S transition of mitotic cell cycle |
| 34 | 12.56 | NULL | 4 / 12 | GSEA C2 | SHEPARD_BMYB_TARGETS |
| 35 | 12.55 | NULL | 63 / 572 | Disease | GUDJ_psoriasis up |
| 36 | 12.53 | NULL | 15 / 68 | Cancer | SHAUGHNESSY_MM high risk |
| 37 | 12.43 | NULL | 8 / 11 | BP | mitotic metaphase plate congression |
| 38 | 12.35 | NULL | 7 / 24 | BP | telomere maintenance via recombination |
| 39 | 12.23 | NULL | 11 / 15 | Cancer | SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP |
| 40 | 12.01 | NULL | 5 / 16 | GSEA C2 | FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN |

# GW_086

## Local Summary

%DE = 0.88

# metagenes = 28

# genes = 425

# genes in genesets = 423

# genes with fdr < 0.1 = 362 ( 16 + / 346 − )

# genes with fdr < 0.05 = 296 ( 10 + / 286 − )

# genes with fdr < 0.01 = 217 ( 9 + / 208 − )

<r> metagenes = 0.93

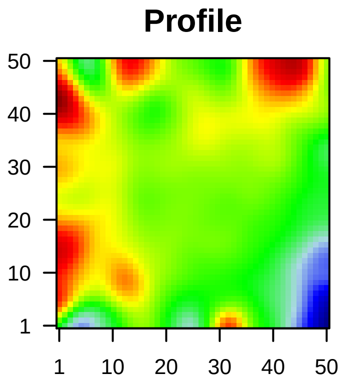
<r> genes = 0.45

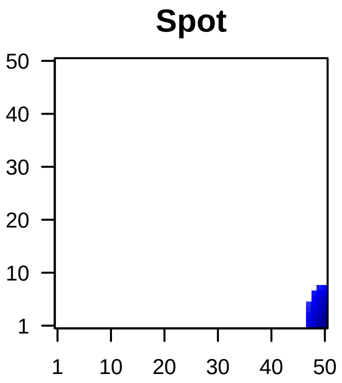
<FC> = −0.45

<shrinkage−t> = −15.76

<p−value> = 0

<fdr> = 0.4


Profile


Spot

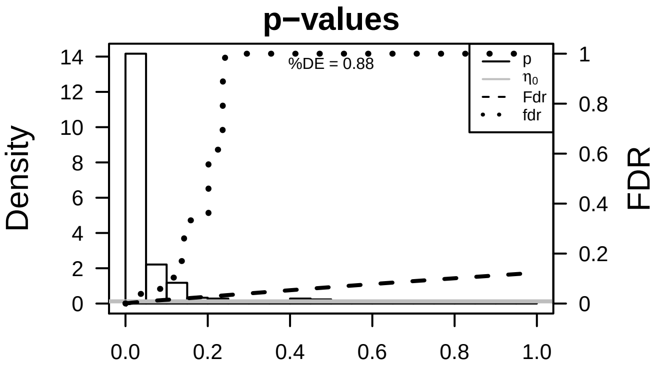
## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 6352 | 1.42 | 2e−16 | 2e−15 | 48 x 1 | chemokine (C−C motif) ligand 5 [Source:HGNC Symbol;Acc: |
| 2 | 3512 | −1.47 | 2e−16 | 2e−15 | 50 x 1 | immunoglobulin J polypeptide, linker protein for immunoglobu |
| 3 | 3543 | −1.46 | 2e−16 | 2e−15 | 49 x 1 | immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy |
| 4 | 10365 | −1.45 | 2e−16 | 2e−15 | 50 x 3 | Kruppel−like factor 2 [Source:HGNC Symbol;Acc:6347] |
| 5 | 6451 | −1.42 | 2e−16 | 2e−15 | 50 x 5 | SH3 domain binding glutamic acid−rich protein like [Source:H |
| 6 | 57172 | −1.3 | 9e−15 | 9e−13 | 49 x 1 | calcium/calmodulin−dependent protein kinase IG [Source:HG |
| 7 | 397 | −1.26 | 3e−14 | 1e−11 | 50 x 1 | Rho GDP dissociation inhibitor (GDI) beta [Source:HGNC Sy |
| 8 | 894 | −1.23 | 3e−13 | 1e−11 | 50 x 4 | cyclin D2 [Source:HGNC Symbol;Acc:1583] |
| 9 | 54855 | −1.22 | 4e−13 | 2e−10 | 49 x 1 | family with sequence similarity 46, member C [Source:HGNC |
| 10 | 29103 | −1.15 | 6e−12 | 2e−10 | 48 x 6 | DnaJ (Hsp40) homolog, subfamily C, member 15 [Source:HG |
| 11 | 25849 | −1.14 | 1e−11 | 2e−10 | 50 x 2 | prostate androgen−regulated mucin−like protein 1 [Source:H |
| 12 | 91607 | 1.14 | 1e−11 | 4e−10 | 48 x 4 | schlafen family member 11 [Source:HGNC Symbol;Acc:2663 |
| 13 | 83641 | −1.13 | 2e−11 | 4e−10 | 50 x 1 | family with sequence similarity 107, member B [Source:HGN |
| 14 | 241 | −1.12 | 2e−11 | 4e−10 | 50 x 1 | arachidonate 5−lipoxygenase−activating protein [Source:HG |
| 15 | 347 | −1.11 | 4e−11 | 4e−10 | 50 x 7 | apolipoprotein D [Source:HGNC Symbol;Acc:612] |
| 16 | 3059 | −1.11 | 4e−11 | 3e−09 | 50 x 1 | hematopoietic cell−specific Lyn substrate 1 [Source:HGNC S |
| 17 | 4256 | −1.08 | 1e−10 | 3e−09 | 50 x 6 | matrix Gla protein [Source:HGNC Symbol;Acc:7060] |
| 18 | 9806 | −1.07 | 2e−10 | 3e−09 | 50 x 1 | sparc/osteonectin, cwcv and kazal−like domains proteoglyca |
| 19 | 5730 | −1.06 | 2e−10 | 3e−09 | 50 x 1 | prostaglandin D2 synthase 21kDa (brain) [Source:HGNC Sy |
| 20 | 260436 | −1.05 | 3e−10 | 3e−09 | 50 x 1 | follicular dendritic cell secreted protein [Source:HGNC Symb |

## Local Geneset Analysis

*Underexpression*

| Rank | GSZ | p−value | #in/all | Geneset | |
|---|---|---|---|---|---|
| 1 | −22.28 | NULL | 95 / 417 | H.Tiss | WIRTH_Immune system |
| 2 | −21.88 | NULL | 119 / 553 | Cancer | Lembcke_Colonic Inflammation |
| 3 | −15.7 | NULL | 9 / 16 | GSEA C2 | FARMER_BREAST_CANCER_CLUSTER_1 |
| 4 | −15.37 | NULL | 7 / 8 | Glio | Donson−migration tethering and rolling−associated with LTS in HG |
| 5 | −13.44 | NULL | 6 / 15 | GSEA C2 | FINAK_BREAST_CANCER_SDPP_SIGNATURE |
| 6 | −12.59 | NULL | 54 / 265 | Glio | willscher_GBM_Verhaak−CL_expression_B_up |
| 7 | −12.59 | NULL | 54 / 265 | Glio | willscher_GBM_Verhaak−MES_expression_B_up |
| 8 | −12.59 | NULL | 54 / 265 | Glio | willscher_GBM_Verhaak−PNwt_expression_B_down |
| 9 | −12.59 | NULL | 54 / 265 | Glio | willscher_GBM_Verhaak−PNmut_expression_B_down |
| 10 | −12.09 | NULL | 58 / 312 | BP | immune response |
| 11 | −11.75 | NULL | 6 / 11 | GSEA C2 | BIOCARTA_TCYTOTOXIC_PATHWAY |
| 12 | −11.65 | NULL | 3 / 7 | GSEA C2 | GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN |
| 13 | −11.64 | NULL | 4 / 16 | GSEA C2 | KORKOLA_TERATOMA_UP |
| 14 | −11.3 | NULL | 4 / 8 | GSEA C2 | GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN |
| 15 | −10.84 | NULL | 19 / 74 | BP | regulation of immune response |
| 16 | −10.8 | NULL | 5 / 9 | GSEA C2 | MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN |
| 17 | −10.78 | NULL | 4 / 7 | GSEA C2 | TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE |
| 18 | −10.72 | NULL | 5 / 10 | GSEA C2 | FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_ |
| 19 | −10.06 | NULL | 5 / 11 | GSEA C2 | BIOCARTA_THELPER_PATHWAY |
| 20 | −9.99 | NULL | 5 / 12 | GSEA C2 | BIOCARTA_CTL_PATHWAY |
| 21 | −9.91 | NULL | 6 / 15 | Cancer | GENTLES_modul13 |
| 22 | −9.9 | NULL | 34 / 316 | Cancer | SPANG_BCL6−index2 |
| 23 | −9.89 | NULL | 6 / 16 | Lymphoma | WRIGHT_ABC UP |
| 24 | −9.81 | NULL | 2 / 3 | GSEA C2 | KEGG_VIRAL_MYOCARDITIS |
| 25 | −9.8 | NULL | 4 / 10 | GSEA C2 | FERRANDO_LYL1_NEIGHBORS |
| 26 | −9.72 | NULL | 4 / 7 | Glio | Donson−cytotoxic effectors−associated with LTS in HGA |
| 27 | −9.63 | NULL | 7 / 12 | GSEA C2 | ZHAN_MULTIPLE_MYELOMA_DN |
| 28 | −9.42 | NULL | 5 / 10 | GSEA C2 | LEE_DIFFERENTIATING_T_LYMPHOCYTE |
| 29 | −9.26 | NULL | 5 / 14 | BP | ruffle organization |
| 30 | −9.26 | NULL | 29 / 162 | CC | external side of plasma membrane |
| 31 | −9.2 | NULL | 3 / 5 | GSEA C2 | WONG_ENDOMETRIAL_CANCER_LATE |
| 32 | −9.18 | NULL | 6 / 15 | GSEA C2 | TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_GRANULO |
| 33 | −9.12 | NULL | 12 / 15 | CC | MHC class II protein complex |
| 34 | −9.02 | NULL | 4 / 16 | GSEA C2 | CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_UP |
| 35 | −9 | NULL | 5 / 9 | GSEA C2 | GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D |
| 36 | −8.92 | NULL | 2 / 7 | Cancer | ZHANG_MGUS up |
| 37 | −8.85 | NULL | 5 / 13 | GSEA C2 | BIOCARTA_IL17_PATHWAY |
| 38 | −8.83 | NULL | 8 / 16 | GSEA C2 | SU_THYMUS |
| 39 | −8.82 | NULL | 5 / 12 | GSEA C2 | BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_D |
| 40 | −8.79 | NULL | 14 / 60 | BP | T cell costimulation |


p−values