# GW_269

## Global Summary

%DE = 0.12

# genes with fdr < 0.2 = 1465 ( 714 + / 751 − )

# genes with fdr < 0.1 = 1111 ( 536 + / 575 − )

# genes with fdr < 0.05 = 926 ( 441 + / 485 − )

# genes with fdr < 0.01 = 671 ( 333 + / 338 − )

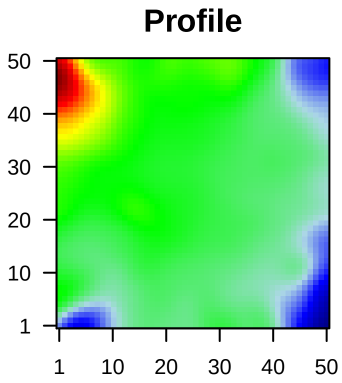
# genes in genesets = 16332

<FC> = 0

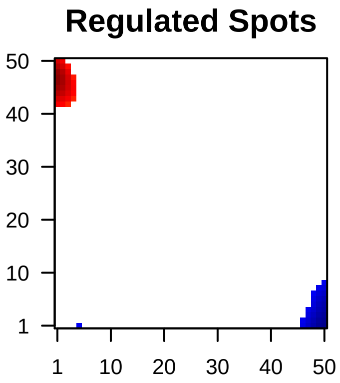
<shrinkage−t> = 0

<p−value> = 0.13

<fdr> = 0.88



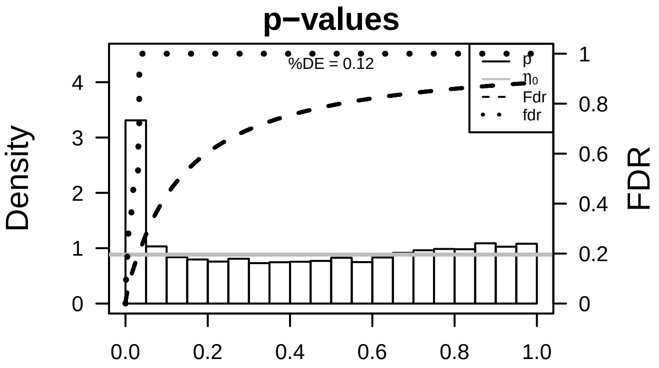
**Profile**



**Regulated Spots**

## Global Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 216 | −1.72 | 2e−16 | 6e−14 | 50 x 50 | aldehyde dehydrogenase 1 family, member A1 [Source:HGN |
| 2 | 387695 | 2.45 | 2e−16 | 6e−14 | 1 x 49 | chromosome 10 open reading frame 99 [Source:HGNC Sym |
| 3 | 760 | 1.89 | 2e−16 | 6e−14 | 1 x 44 | carbonic anhydrase II [Source:HGNC Symbol;Acc:1373] |
| 4 | 768 | 2.19 | 2e−16 | 6e−14 | 1 x 6 | carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383] |
| 5 | 595 | −1.65 | 2e−16 | 6e−14 | 1 x 6 | cyclin D1 [Source:HGNC Symbol;Acc:1582] |
| 6 | 894 | 1.72 | 2e−16 | 6e−14 | 50 x 4 | cyclin D2 [Source:HGNC Symbol;Acc:1583] |
| 7 | 1041 | 1.82 | 2e−16 | 6e−14 | 1 x 46 | corneodesmosin [Source:HGNC Symbol;Acc:1802] |
| 8 | 22802 | −1.74 | 2e−16 | 6e−14 | 1 x 50 | chloride channel accessory 4 [Source:HGNC Symbol;Acc:20 |
| 9 | 1278 | −2.04 | 2e−16 | 6e−14 | 2 x 1 | collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198] |
| 10 | 1281 | −1.82 | 2e−16 | 6e−14 | 2 x 1 | collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201] |
| 11 | 1293 | −1.85 | 2e−16 | 6e−14 | 2 x 1 | collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213] |
| 12 | 51200 | 2.68 | 2e−16 | 6e−14 | 1 x 44 | carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740] |
| 13 | 126410 | 1.78 | 2e−16 | 6e−14 | 1 x 49 | cytochrome P450, family 4, subfamily F, polypeptide 22 [Sour |
| 14 | 55894 | 2.66 | 2e−16 | 6e−14 | 1 x 47 | defensin, beta 103B [Source:HGNC Symbol;Acc:31702] |
| 15 | 414325 | 2.74 | 2e−16 | 6e−14 | 1 x 48 | defensin, beta 103B [Source:HGNC Symbol;Acc:31702] |
| 16 | 93099 | 1.77 | 2e−16 | 6e−14 | 1 x 47 | dermokine [Source:HGNC Symbol;Acc:25063] |
| 17 | 1809 | −1.94 | 2e−16 | 6e−14 | 6 x 1 | dihydropyrimidinase−like 3 [Source:HGNC Symbol;Acc:3015] |
| 18 | 1828 | 2.75 | 2e−16 | 6e−14 | 1 x 48 | desmoglein 1 [Source:HGNC Symbol;Acc:3048] |
| 19 | 2201 | 1.84 | 2e−16 | 6e−14 | 1 x 5 | fibrillin 2 [Source:HGNC Symbol;Acc:3604] |
| 20 | 80157 | 1.72 | 2e−16 | 6e−14 | 1 x 48 | cell wall biogenesis 43 C−terminal homolog (S. cerevisiae) [S |



## Global Geneset Analysis

| Rank | GSZ | p−value | #all | Geneset | |
|---|---|---|---|---|---|
| *Overexpressed* | | | | | |
| 1 | 21.08 | NULL | 135 | H.Tiss | WIRTH_Mucosa |
| 2 | 15.76 | NULL | 572 | Disease | GUDJ_psoriasis up |
| 3 | 11.97 | NULL | 21 | CC | cornified envelope |
| 4 | 10.29 | NULL | 76 | BP | epidermis development |
| 5 | 9.87 | NULL | 42 | BP | keratinization |
| 6 | 9.75 | NULL | 53 | BP | keratinocyte differentiation |
| 7 | 8.59 | NULL | 21 | CC | desmosome |
| 8 | 8.38 | NULL | 743 | Chr | Chr 7 |
| 9 | 7.92 | NULL | 16 | GSEA C2 | HUPER_BREAST_BASAL_VS_LUMINAL_UP |
| 10 | 7.3 | NULL | 16 | GSEA C2 | JAEGER_METASTASIS_DN |
| 11 | 7.13 | NULL | 10 | GSEA C2 | REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P |
| 12 | 6.82 | NULL | 15 | GSEA C2 | RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL |
| 13 | 6.64 | NULL | 15 | GSEA C2 | RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN |
| 14 | 6.25 | NULL | 15 | GSEA C2 | AIGNER_ZEB1_TARGETS |
| 15 | 6.2 | NULL | 16 | GSEA C2 | WANG_BARRETTS_ESOPHAGUS_DN |
| 16 | 5.86 | NULL | 15 | GSEA C2 | ONDER_CDH1_TARGETS_2_DN |
| 17 | 5.06 | NULL | 14 | GSEA C2 | CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U |
| 18 | 5.04 | NULL | 15 | MF | interleukin−1 receptor binding |
| 19 | 4.85 | NULL | 15 | GSEA C2 | WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE |
| 20 | 4.67 | NULL | 16 | GSEA C2 | COLDREN_GEFITINIB_RESISTANCE_DN |
| *Underexpressed* | | | | | |
| 1 | −13.82 | NULL | 553 | Cancer | Lembcke_Colonic Inflammation |
| 2 | −11.24 | NULL | 417 | H.Tiss | WIRTH_Immune system |
| 3 | −11.05 | NULL | 190 | CC | extracellular matrix |
| 4 | −10.57 | NULL | 142 | Glio | willscher_GBM_Verhaak−CL_expression_C_up |
| 5 | −10.57 | NULL | 142 | Glio | willscher_GBM_Verhaak−PNmut_expression_C_down |
| 6 | −10.53 | NULL | 11 | MF | platelet−derived growth factor binding |
| 7 | −10.28 | NULL | 250 | Lymphoma | LENZ_Stromal signature 1 |
| 8 | −8.57 | NULL | 12 | miRNA target | miR−29c |
| 9 | −8.57 | NULL | 375 | Disease | GUDJ_psoriasis down |
| 10 | −8.26 | NULL | 57 | Glio | developing astrocytes |
| 11 | −8.23 | NULL | 16 | GSEA C2 | FARMER_BREAST_CANCER_CLUSTER_5 |
| 12 | −7.54 | NULL | 8023 | MF | protein binding |
| 13 | −7.4 | NULL | 16 | MMML CGS | MACIEJ_MMML 1 |
| 14 | −7.37 | NULL | 8 | GSEA C2 | RUNNE_GENDER_EFFECT_UP |
| 15 | −7.17 | NULL | 7 | MMML CGS | MACIEJ_MMML 5 |
| 16 | −7.01 | NULL | 16 | GSEA C2 | CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN |
| 17 | −6.93 | NULL | 162 | CC | external side of plasma membrane |
| 18 | −6.72 | NULL | 37 | BP | collagen fibril organization |
| 19 | −6.71 | NULL | 312 | BP | immune response |
| 20 | −6.65 | NULL | 242 | BP | extracellular matrix organization |

# GW_269

## Local Summary

%DE = 0.89

# metagenes = 31

# genes = 385

# genes in genesets = 377

# genes with fdr < 0.1 = 313 ( 297 + / 16 − )

# genes with fdr < 0.05 = 293 ( 278 + / 15 − )

# genes with fdr < 0.01 = 252 ( 238 + / 14 − )

<r> metagenes = 0.89

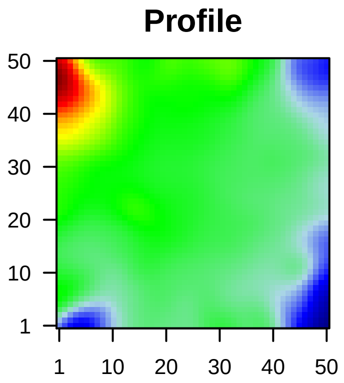
<r> genes = 0.36

<FC> = 0.74

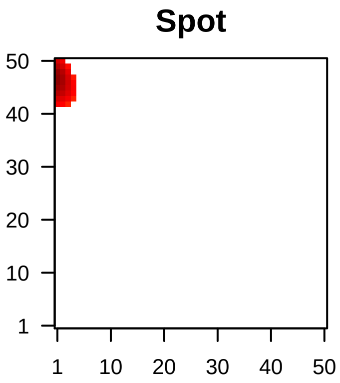
<shrinkage−t> = 25.95

<p−value> = 0

<fdr> = 0.29



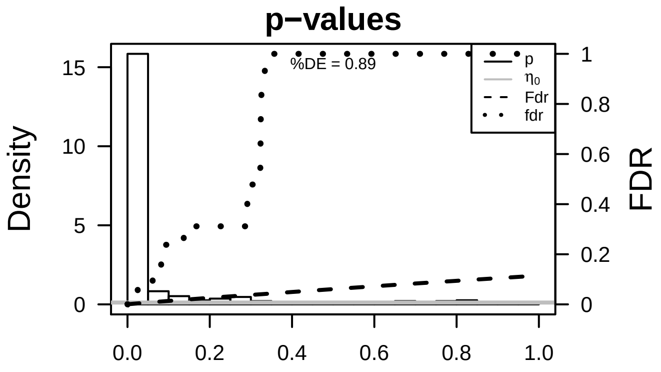
**Profile**



**Spot**

## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 387695 | 2.45 | 2e−16 | 3e−16 | 1 x 49 | chromosome 10 open reading frame 99 [Source:HGNC Symb |
| 2 | 760 | 1.89 | 2e−16 | 3e−16 | 1 x 44 | carbonic anhydrase II [Source:HGNC Symbol;Acc:1373] |
| 3 | 1041 | 1.82 | 2e−16 | 3e−16 | 1 x 46 | corneodesmosin [Source:HGNC Symbol;Acc:1802] |
| 4 | 22802 | −1.74 | 2e−16 | 3e−16 | 1 x 50 | chloride channel accessory 4 [Source:HGNC Symbol;Acc:20 |
| 5 | 51200 | 2.68 | 2e−16 | 3e−16 | 1 x 44 | carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740] |
| 6 | 126410 | 1.78 | 2e−16 | 3e−16 | 1 x 49 | cytochrome P450, family 4, subfamily F, polypeptide 22 [Sour |
| 7 | 55894 | 2.66 | 2e−16 | 3e−16 | 1 x 47 | defensin, beta 103B [Source:HGNC Symbol;Acc:31702] |
| 8 | 414325 | 2.74 | 2e−16 | 3e−16 | 1 x 48 | defensin, beta 103B [Source:HGNC Symbol;Acc:31702] |
| 9 | 93099 | 1.77 | 2e−16 | 3e−16 | 1 x 47 | dermokine [Source:HGNC Symbol;Acc:25063] |
| 10 | 1828 | 2.75 | 2e−16 | 3e−16 | 1 x 48 | desmoglein 1 [Source:HGNC Symbol;Acc:3048] |
| 11 | 80157 | 1.72 | 2e−16 | 3e−16 | 1 x 48 | cell wall biogenesis 43 C−terminal homolog (S. cerevisiae) [S |
| 12 | 10804 | 1.69 | 2e−16 | 3e−16 | 1 x 47 | gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A |
| 13 | 374918 | 2.35 | 2e−16 | 3e−16 | 1 x 45 | IGF−like family member 1 [Source:HGNC Symbol;Acc:24093 |
| 14 | 26525 | 1.71 | 2e−16 | 3e−16 | 1 x 49 | interleukin 36 receptor antagonist [Source:HGNC Symbol;Ac |
| 15 | 3868 | 1.69 | 2e−16 | 3e−16 | 1 x 46 | keratin 16 [Source:HGNC Symbol;Acc:6423] |
| 16 | 3851 | −1.93 | 2e−16 | 3e−16 | 1 x 50 | keratin 4 [Source:HGNC Symbol;Acc:6441] |
| 17 | 388533 | 2.82 | 2e−16 | 3e−16 | 1 x 49 | keratinocyte differentiation−associated protein [Source:HGNC |
| 18 | 3963 | 1.7 | 2e−16 | 3e−16 | 1 x 47 | lectin, galactoside−binding, soluble, 7 [Source:HGNC Symbol |
| 19 | 653499 | 1.85 | 2e−16 | 3e−16 | 1 x 47 | lectin, galactoside−binding, soluble, 7 [Source:HGNC Symbol |
| 20 | 643479 | 1.8 | 2e−16 | 3e−16 | 1 x 49 | |



**p−values**

## Local Geneset Analysis

*Overexpression*

| Rank | GSZ | p−value | #in/all | Geneset | |
|---|---|---|---|---|---|
| 1 | 41.26 | NULL | 88 / 135 | H.Tiss | WIRTH_Mucosa |
| 2 | 30.05 | NULL | 125 / 572 | Disease | GUDJ_psoriasis up |
| 3 | 28.33 | NULL | 18 / 21 | CC | cornified envelope |
| 4 | 24.12 | NULL | 31 / 76 | BP | epidermis development |
| 5 | 21.47 | NULL | 20 / 42 | BP | keratinization |
| 6 | 21.34 | NULL | 26 / 53 | BP | keratinocyte differentiation |
| 7 | 20.76 | NULL | 13 / 21 | CC | desmosome |
| 8 | 16.34 | NULL | 10 / 16 | GSEA C2 | HUPER_BREAST_BASAL_VS_LUMINAL_UP |
| 9 | 13.77 | NULL | 4 / 10 | GSEA C2 | REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P |
| 10 | 13.3 | NULL | 7 / 15 | GSEA C2 | AIGNER_ZEB1_TARGETS |
| 11 | 13.18 | NULL | 7 / 16 | GSEA C2 | WANG_BARRETTS_ESOPHAGUS_DN |
| 12 | 12.98 | NULL | 11 / 19 | BP | peptide cross−linking |
| 13 | 12.84 | NULL | 6 / 15 | GSEA C2 | RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL |
| 14 | 11.93 | NULL | 5 / 10 | MF | RAGE receptor binding |
| 15 | 11.54 | NULL | 7 / 15 | GSEA C2 | HINATA_NFKB_TARGETS_KERATINOCYTE_DN |
| 16 | 11.52 | NULL | 5 / 15 | GSEA C2 | RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN |
| 17 | 11.15 | NULL | 6 / 16 | GSEA C2 | JAEGER_METASTASIS_DN |
| 18 | 10.2 | NULL | 7 / 15 | GSEA C2 | WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE |
| 19 | 10.06 | NULL | 14 / 79 | MF | serine−type endopeptidase inhibitor activity |
| 20 | 9.97 | NULL | 6 / 16 | GSEA C2 | SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN |
| 21 | 9.54 | NULL | 4 / 13 | GSEA C2 | REACTOME_GAP_JUNCTION_TRAFFICKING |
| 22 | 9.25 | NULL | 4 / 15 | GSEA C2 | SENESE_HDAC1_AND_HDAC2_TARGETS_DN |
| 23 | 9.21 | NULL | 70 / 1182 | CC | extracellular region |
| 24 | 9.19 | NULL | 10 / 52 | BP | negative regulation of endopeptidase activity |
| 25 | 9.14 | NULL | 6 / 14 | GSEA C2 | CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U |
| 26 | 8.96 | NULL | 8 / 16 | GSEA C2 | ONDER_CDH1_TARGETS_3_DN |
| 27 | 8.85 | NULL | 3 / 10 | GSEA C2 | AUJLA_IL22_AND_IL17A_SIGNALING |
| 28 | 8.8 | NULL | 5 / 25 | BP | response to zinc ion |
| 29 | 8.74 | NULL | 4 / 8 | GSEA C2 | LIU_CDX2_TARGETS_DN |
| 30 | 8.74 | NULL | 7 / 29 | BP | regulation of proteolysis |
| 31 | 8.66 | NULL | 4 / 15 | GSEA C2 | ONDER_CDH1_TARGETS_2_DN |
| 32 | 8.6 | NULL | 32 / 186 | MF | structural molecule activity |
| 33 | 8.57 | NULL | 7 / 16 | GSEA C2 | COLDREN_GEFITINIB_RESISTANCE_DN |
| 34 | 8.47 | NULL | 3 / 12 | GSEA C2 | REACTOME_GAP_JUNCTION_ASSEMBLY |
| 35 | 8.43 | NULL | 3 / 10 | GSEA C2 | SMID_BREAST_CANCER_ERBB2_UP |
| 36 | 8.42 | NULL | 4 / 15 | GSEA C2 | CHANG_IMMORTALIZED_BY_HPV31_DN |
| 37 | 8.4 | NULL | 5 / 16 | GSEA C2 | SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN |
| 38 | 8.37 | NULL | 4 / 10 | GSEA C2 | FOURNIER_ACINAR_DEVELOPMENT_LATE_UP |
| 39 | 8.31 | NULL | 6 / 49 | Glio | Christensen_hypomethylated_in_primary_glioblastoma |
| 40 | 8.08 | NULL | 23 / 82 | CC | intermediate filament |

# GW_269

## Local Summary

%DE = 0.96

# metagenes = 1

# genes = 36

# genes in genesets = 36

# genes with fdr < 0.1 = 32 ( 3 + / 29 − )

# genes with fdr < 0.05 = 32 ( 3 + / 29 − )

# genes with fdr < 0.01 = 25 ( 3 + / 22 − )

<r> metagenes = NA

<r> genes = 0.44

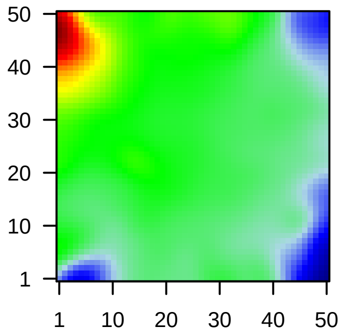
<FC> = −0.53

<shrinkage−t> = −18.67

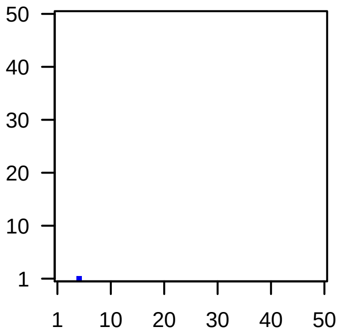
<p−value> = 0

<fdr> = 0.39

**Profile**



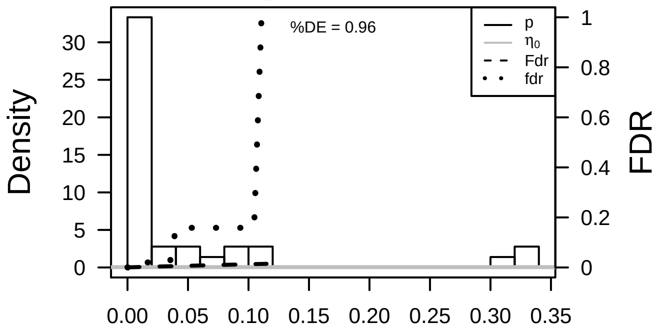
**Spot**



## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 3487 | −1.75 | 2e−16 | 3e−16 | 5 x 1 | insulin−like growth factor binding protein 4 [Source:HGNC Sy |
| 2 | 4692 | −1.24 | 3e−10 | 5e−09 | 5 x 1 | necdin, melanoma antigen (MAGE) family member [Source:H |
| 3 | 5156 | −1.16 | 3e−09 | 8e−08 | 5 x 1 | platelet−derived growth factor receptor, alpha polypeptide [Sc |
| 4 | 2791 | −1.05 | 9e−08 | 8e−08 | 5 x 1 | guanine nucleotide binding protein (G protein), gamma 11 [Sc |
| 5 | 83700 | −1.03 | 1e−07 | 8e−08 | 5 x 1 | junctional adhesion molecule 3 [Source:HGNC Symbol;Acc:1 |
| 6 | 81035 | −1.03 | 2e−07 | 5e−06 | 5 x 1 | collectin sub−family member 12 [Source:HGNC Symbol;Acc: |
| 7 | 10962 | −0.91 | 3e−06 | 1e−05 | 5 x 1 | myeloid/lymphoid or mixed−lineage leukemia (trithorax homol |
| 8 | 221395 | −0.85 | 2e−05 | 1e−05 | 5 x 1 | G protein−coupled receptor 116 [Source:HGNC Symbol;Acc: |
| 9 | 3043 | 0.83 | 2e−05 | 1e−05 | 5 x 1 | hemoglobin, beta [Source:HGNC Symbol;Acc:4827] |
| 10 | 2982 | −0.82 | 3e−05 | 1e−05 | 5 x 1 | guanylate cyclase 1, soluble, alpha 3 [Source:HGNC Symbol; |
| 11 | 29995 | −0.81 | 4e−05 | 6e−05 | 5 x 1 | LIM and cysteine−rich domains 1 [Source:HGNC Symbol;Acc |
| 12 | 5866 | −0.77 | 8e−05 | 2e−04 | 5 x 1 | RAB3A interacting protein (rabin3)−like 1 [Source:HGNC Sym |
| 13 | 5919 | −0.72 | 2e−04 | 2e−04 | 5 x 1 | retinoic acid receptor responder (tazarotene induced) 2 [Sour |
| 14 | 187 | −0.71 | 3e−04 | 8e−04 | 5 x 1 | apelin receptor [Source:HGNC Symbol;Acc:339] |
| 15 | 114757 | −0.66 | 8e−04 | 2e−03 | 5 x 1 | cytoglobin [Source:HGNC Symbol;Acc:16505] |
| 16 | 56944 | −0.59 | 2e−03 | 3e−03 | 5 x 1 | olfactomedin−like 3 [Source:HGNC Symbol;Acc:24956] |
| 17 | 54749 | −0.55 | 5e−03 | 3e−03 | 5 x 1 | ependymin related 1 [Source:HGNC Symbol;Acc:17572] |
| 18 | 9891 | −0.54 | 6e−03 | 3e−03 | 5 x 1 | NUAK family, SNF1−like kinase, 1 [Source:HGNC Symbol;Ac |
| 19 | 5997 | −0.51 | 9e−03 | 3e−03 | 5 x 1 | regulator of G−protein signaling 2, 24kDa [Source:HGNC Syn |
| 20 | 10395 | −0.49 | 1e−02 | 3e−03 | 5 x 1 | deleted in liver cancer 1 [Source:HGNC Symbol;Acc:2897] |

**p−values**



## Local Geneset Analysis

*Underexpression*

| Rank | GSZ | p−value | #in/all | Geneset | |
|---|---|---|---|---|---|
| 1 | −35.82 | NULL | 1 / 5 | GSEA C2 | VERRECCHIA_RESPONSE_TO_TGFB1_C6 |
| 2 | −23.62 | NULL | 1 / 5 | Glio | laffaire_hypometh_LGG_vs_control |
| 3 | −21.22 | NULL | 2 / 13 | GSEA C2 | REACTOME_HEMOSTASIS |
| 4 | −20.96 | NULL | 2 / 13 | GSEA C2 | LEE_INTRATHYMIC_T_PROGENITOR |
| 5 | −18.82 | NULL | 1 / 12 | BP | regulation of glucose metabolic process |
| 6 | −17.98 | NULL | 2 / 14 | GSEA C2 | TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_GRANULO |
| 7 | −17.86 | NULL | 1 / 13 | GSEA C2 | GAUSSMANN_MLL_AF4_FUSION_TARGETS_E_DN |
| 8 | −17.86 | NULL | 1 / 13 | GSEA C2 | IIZUKA_LIVER_CANCER_PROGRESSION_L1_G1_UP |
| 9 | −17.86 | NULL | 1 / 13 | GSEA C2 | REACTOME_REGULATION_OF_INSULIN_LIKE_GROWTH_FAC |
| 10 | −17.03 | NULL | 1 / 14 | GSEA C2 | STEIN_ESTROGEN_RESPONSE_NOT_VIA_ESRRA |
| 11 | −16.29 | NULL | 1 / 15 | GSEA C2 | WILLIAMS_ESR1_TARGETS_UP |
| 12 | −16.29 | NULL | 1 / 15 | GSEA C2 | GILDEA_METASTASIS |
| 13 | −15.64 | NULL | 1 / 16 | GSEA C2 | NOJIMA_SFRP2_TARGETS_DN |
| 14 | −15.64 | NULL | 1 / 16 | GSEA C2 | MACLACHLAN_BRCA1_TARGETS_UP |
| 15 | −15.28 | NULL | 2 / 15 | MF | platelet−derived growth factor receptor binding |
| 16 | −15.06 | NULL | 1 / 9 | GSEA C2 | KANG_GIST_WITH_PDGFRA_UP |
| 17 | −15.02 | NULL | 2 / 15 | GSEA C2 | CORRE_MULTIPLE_MYELOMA_DN |
| 18 | −14.91 | NULL | 2 / 10 | GSEA C2 | SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP |
| 19 | −14.79 | NULL | 1 / 8 | GSEA C2 | REACTOME_G_ALPHA_I_SIGNALLING_EVENTS |
| 20 | −14.65 | NULL | 1 / 5 | GSEA C2 | NAKAMURA_ALVEOLAR_EPITHELIUM |
| 21 | −14.6 | NULL | 1 / 8 | GSEA C2 | CASORELLI_APL_SECONDARY_VS_DE_NOVO_DN |
| 22 | −14.6 | NULL | 1 / 8 | GSEA C2 | KEGG_CELL_ADHESION_MOLECULES_CAMS |
| 23 | −14 | NULL | 1 / 10 | GSEA C2 | IIZUKA_RECURRENT_LIVER_CANCER |
| 24 | −13.67 | NULL | 2 / 15 | GSEA C2 | ONDER_CDH1_TARGETS_2_UP |
| 25 | −13.6 | NULL | 1 / 9 | GSEA C2 | JISON_SICKLE_CELL_DISEASE_UP |
| 26 | −13.6 | NULL | 1 / 9 | GSEA C2 | REACTOME_G_ALPHA_Q_SIGNALLING_EVENTS |
| 27 | −13.16 | NULL | 2 / 53 | BP | regulation of growth |
| 28 | −13.12 | NULL | 1 / 11 | BP | estrogen metabolic process |
| 29 | −13.12 | NULL | 1 / 11 | MF | platelet−derived growth factor binding |
| 30 | −12.84 | NULL | 1 / 22 | MF | insulin−like growth factor binding |
| 31 | −12.56 | NULL | 1 / 13 | BP | axon extension |
| 32 | −12.38 | NULL | 1 / 12 | BP | Leydig cell differentiation |
| 33 | −11.97 | NULL | 1 / 14 | BP | axonal fasciculation |
| 34 | −11.85 | NULL | 1 / 11 | GSEA C2 | REACTOME_G_ALPHA_S_SIGNALLING_EVENTS |
| 35 | −11.75 | NULL | 1 / 13 | Glio | Christensen_hypomethylated_in_grade2_oligodendroglioma |
| 36 | −11.75 | NULL | 1 / 13 | GSEA C2 | BIOCARTA_CBL_PATHWAY |
| 37 | −11.69 | NULL | 1 / 11 | CC | Schmidt−Lanterman incisure |
| 38 | −11.19 | NULL | 1 / 14 | Glio | Christensen_hypomethylated_in_grade2_oligoastrocytoma |
| 39 | −11.19 | NULL | 1 / 14 | Glio | Christensen_hypomethylated_in_grade3_oligoastrocytoma |
| 40 | −11.18 | NULL | 1 / 12 | GSEA C2 | REACTOME_G_PROTEIN_ACTIVATION |

# GW_269

## Local Summary

%DE = 0.85

# metagenes = 30

# genes = 448

# genes in genesets = 446

# genes with fdr < 0.1 = 326 ( 8 + / 318 − )

# genes with fdr < 0.05 = 314 ( 8 + / 306 − )

# genes with fdr < 0.01 = 214 ( 5 + / 209 − )

<r> metagenes = 0.91

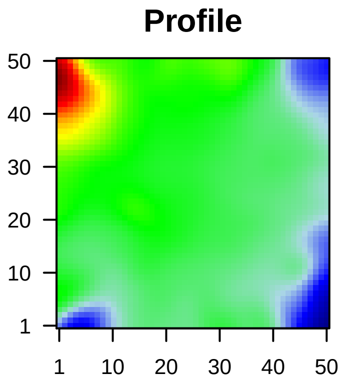
<r> genes = 0.43

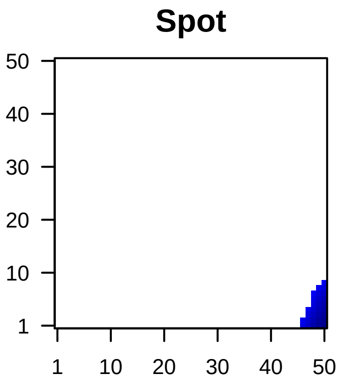
<FC> = −0.55

<shrinkage−t> = −19.25

<p−value> = 0

<fdr> = 0.44


**Profile**


**Spot**

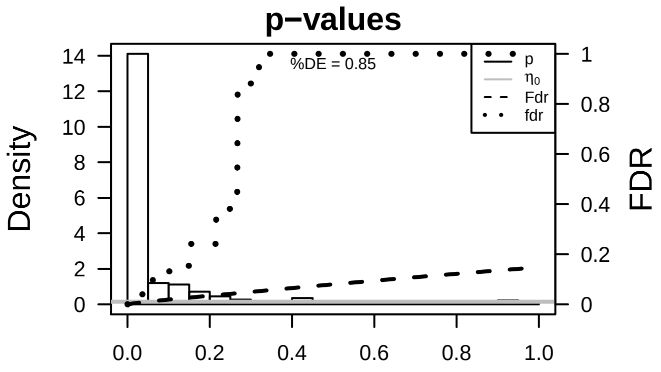
## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 894 | 1.72 | 2e−16 | 2e−15 | 50 x 4 | cyclin D2 [Source:HGNC Symbol;Acc:1583] |
| 2 | 3488 | −2.22 | 2e−16 | 2e−15 | 50 x 7 | insulin−like growth factor binding protein 5 [Source:HGNC Sy |
| 3 | 3512 | −1.83 | 2e−16 | 2e−15 | 50 x 1 | immunoglobulin J polypeptide, linker protein for immunoglobu |
| 4 | 3543 | −1.88 | 2e−16 | 2e−15 | 49 x 1 | immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy |
| 5 | 4256 | −1.6 | 2e−16 | 2e−15 | 50 x 6 | matrix Gla protein [Source:HGNC Symbol;Acc:7060] |
| 6 | 6192 | −3.1 | 2e−16 | 2e−15 | 50 x 9 | ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc |
| 7 | 5920 | −1.59 | 4e−16 | 4e−14 | 48 x 1 | retinoic acid receptor responder (tazarotene induced) 3 [Sour |
| 8 | 6578 | −1.57 | 1e−15 | 1e−12 | 50 x 4 | solute carrier organic anion transporter family, member 2A1 [ |
| 9 | 90865 | 1.49 | 3e−14 | 1e−12 | 50 x 7 | interleukin 33 [Source:HGNC Symbol;Acc:16028] |
| 10 | 54855 | −1.48 | 4e−14 | 5e−12 | 49 x 1 | family with sequence similarity 46, member C [Source:HGNC |
| 11 | 3936 | −1.45 | 1e−13 | 5e−12 | 50 x 1 | lymphocyte cytosolic protein 1 (L−plastin) [Source:HGNC Sy |
| 12 | 8404 | −1.43 | 2e−13 | 5e−12 | 50 x 6 | SPARC−like 1 (hevin) [Source:HGNC Symbol;Acc:11220] |
| 13 | 10537 | −1.43 | 3e−13 | 4e−11 | 50 x 1 | ubiquitin D [Source:HGNC Symbol;Acc:18795] |
| 14 | 57172 | −1.39 | 1e−12 | 4e−11 | 49 x 1 | calcium/calmodulin−dependent protein kinase IG [Source:HG |
| 15 | 25849 | −1.39 | 2e−12 | 1e−10 | 50 x 2 | prostate androgen−regulated mucin−like protein 1 [Source:H |
| 16 | 2532 | −1.36 | 4e−12 | 1e−10 | 50 x 5 | Duffy blood group, atypical chemokine receptor [Source:HGN |
| 17 | 1363 | −1.36 | 4e−12 | 1e−09 | 50 x 7 | carboxypeptidase E [Source:HGNC Symbol;Acc:2303] |
| 18 | 919 | −1.3 | 3e−11 | 1e−09 | 50 x 1 | CD247 molecule [Source:HGNC Symbol;Acc:1677] |
| 19 | 1396 | −1.29 | 5e−11 | 3e−09 | 50 x 5 | cysteine−rich protein 1 (intestinal) [Source:HGNC Symbol;Ac |
| 20 | 51176 | −1.27 | 9e−11 | 3e−09 | 50 x 5 | lymphoid enhancer−binding factor 1 [Source:HGNC Symbol; |

## Local Geneset Analysis

*Underexpression*

| Rank | GSZ | p−value | #in/all | Geneset | |
|---|---|---|---|---|---|
| 1 | −22.57 | NULL | 96 / 417 | H.Tiss | WIRTH_Immune system |
| 2 | −20.37 | NULL | 120 / 553 | Cancer | Lembcke_Colonic Inflammation |
| 3 | −17.17 | NULL | 63 / 312 | BP | immune response |
| 4 | −15.17 | NULL | 7 / 8 | Glio | Donson−migration tethering and rolling−associated with LTS in HG |
| 5 | −15.14 | NULL | 3 / 5 | GSEA C2 | WONG_ENDOMETRIAL_CANCER_LATE |
| 6 | −14.62 | NULL | 9 / 16 | GSEA C2 | FARMER_BREAST_CANCER_CLUSTER_1 |
| 7 | −14.31 | NULL | 2 / 4 | MMML CGS | MACIEJ_MMML 2 |
| 8 | −14.13 | NULL | 5 / 9 | GSEA C2 | MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN |
| 9 | −13.98 | NULL | 7 / 15 | GSEA C2 | FINAK_BREAST_CANCER_SDPP_SIGNATURE |
| 10 | −13.38 | NULL | 7 / 11 | GSEA C2 | BIOCARTA_TCYTOTOXIC_PATHWAY |
| 11 | −13.26 | NULL | 3 / 7 | GSEA C2 | GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN |
| 12 | −13.16 | NULL | 4 / 11 | GSEA C2 | TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN |
| 13 | −13.05 | NULL | 4 / 8 | GSEA C2 | GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN |
| 14 | −13.03 | NULL | 6 / 12 | GSEA C2 | BIOCARTA_CTL_PATHWAY |
| 15 | −12.87 | NULL | 12 / 15 | CC | MHC class II protein complex |
| 16 | −12.5 | NULL | 2 / 7 | GSEA C2 | LEE_NAIVE_T_LYMPHOCYTE |
| 17 | −12.23 | NULL | 3 / 6 | GSEA C2 | SANA_RESPONSE_TO_IFNG_UP |
| 18 | −11.97 | NULL | 4 / 7 | Glio | Donson−cytotoxic effectors−associated with LTS in HGA |
| 19 | −11.94 | NULL | 6 / 11 | GSEA C2 | BIOCARTA_THELPER_PATHWAY |
| 20 | −11.7 | NULL | 32 / 162 | CC | external side of plasma membrane |
| 21 | −11.66 | NULL | 3 / 13 | GSEA C2 | KANG_IMMORTALIZED_BY_TERT_UP |
| 22 | −11.32 | NULL | 6 / 13 | GSEA C2 | BIOCARTA_IL17_PATHWAY |
| 23 | −11.14 | NULL | 20 / 74 | BP | regulation of immune response |
| 24 | −10.79 | NULL | 17 / 60 | BP | T cell costimulation |
| 25 | −10.76 | NULL | 7 / 12 | GSEA C2 | ZHAN_MULTIPLE_MYELOMA_DN |
| 26 | −10.74 | NULL | 7 / 13 | Cancer | GENTLES_modul18 |
| 27 | −10.72 | NULL | 4 / 8 | GSEA C2 | BIOCARTA_TCRA_PATHWAY |
| 28 | −10.68 | NULL | 1 / 7 | MMML CGS | MACIEJ_MMML 5 |
| 29 | −10.65 | NULL | 5 / 8 | GSEA C2 | NIELSEN_SYNOVIAL_SARCOMA_DN |
| 30 | −10.61 | NULL | 6 / 14 | GSEA C2 | WU_SILENCED_BY_METHYLATION_IN_BLADDER_CANCER |
| 31 | −9.89 | NULL | 1 / 8 | GSEA C2 | RUNNE_GENDER_EFFECT_UP |
| 32 | −9.89 | NULL | 1 / 8 | GSEA C2 | REACTOME_REGULATION_OF_GENE_EXPRESSION_IN_BETA |
| 33 | −9.81 | NULL | 5 / 12 | BP | dendritic cell chemotaxis |
| 34 | −9.76 | NULL | 3 / 13 | GSEA C2 | ZIRN_TRETINOIN_RESPONSE_UP |
| 35 | −9.67 | NULL | 2 / 6 | GSEA C2 | TRAYNOR_RETT_SYNDROM_DN |
| 36 | −9.59 | NULL | 9 / 28 | Lymphoma | DAVE_Immune response 1 |
| 37 | −9.53 | NULL | 56 / 265 | Glio | willscher_GBM_Verhaak−CL_expression_B_up |
| 38 | −9.53 | NULL | 56 / 265 | Glio | willscher_GBM_Verhaak−MES_expression_B_up |
| 39 | −9.53 | NULL | 56 / 265 | Glio | willscher_GBM_Verhaak−PNwt_expression_B_down |
| 40 | −9.53 | NULL | 56 / 265 | Glio | willscher_GBM_Verhaak−PNmut_expression_B_down |


**p−values**