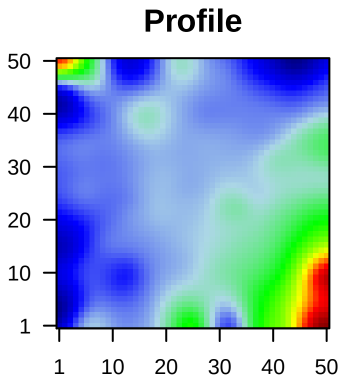
# GW_040

## Global Summary

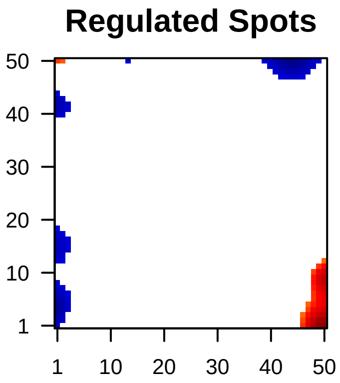
%DE = 0.13
# genes with fdr < 0.2  = 1753  ( 1036 + / 717  − )
# genes with fdr < 0.1  = 1372  ( 854 + / 518  − )
# genes with fdr < 0.05  = 1081  ( 717 + / 364  − )
# genes with fdr < 0.01 = 800  ( 569 + / 231  − )

# genes in genesets = 16332

<FC> = 0
<shrinkage−t> = 0
<p−value> = 0.1
<fdr> = 0.87



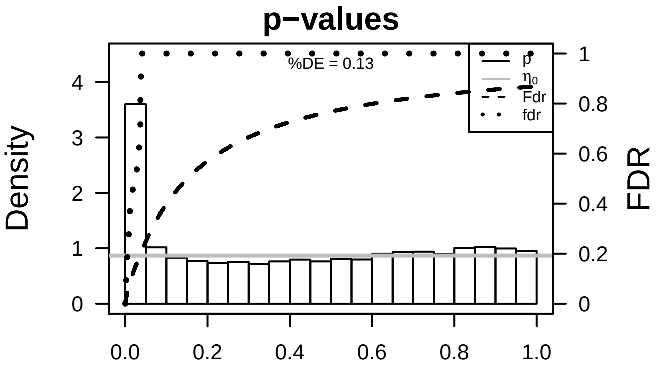
**Profile**



**Regulated Spots**

## Global Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 58 | 2.67 | 2e−16 | 3e−14 | 25 x 1 | actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12 |
| 2 | 72 | 1.5 | 2e−16 | 3e−14 | 4 x 1 | actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml |
| 3 | 10551 | 2.31 | 2e−16 | 3e−14 | 50 x 10 | anterior gradient 2 [Source:HGNC Symbol;Acc:328] |
| 4 | 347 | 2.18 | 2e−16 | 3e−14 | 50 x 7 | apolipoprotein D [Source:HGNC Symbol;Acc:612] |
| 5 | 563 | 1.3 | 2e−16 | 3e−14 | 50 x 10 | alpha−2−glycoprotein 1, zinc−binding [Source:HGNC Symbol |
| 6 | 80341 | 2.65 | 2e−16 | 3e−14 | 50 x 10 | BPI fold containing family B, member 2 [Source:HGNC Symb |
| 7 | 92747 | 3.28 | 2e−16 | 3e−14 | 50 x 10 | BPI fold containing family B, member 1 [Source:HGNC Symb |
| 8 | 260436 | 1.38 | 2e−16 | 3e−14 | 50 x 1 | follicular dendritic cell secreted protein [Source:HGNC Symbo |
| 9 | 375791 | 1.54 | 2e−16 | 3e−14 | 1 x 50 | chromosome 9 open reading frame 169 [Source:HGNC Symb |
| 10 | 57172 | 2.07 | 2e−16 | 3e−14 | 49 x 1 | calcium/calmodulin−dependent protein kinase IG [Source:HG |
| 11 | 6363 | 2.11 | 2e−16 | 3e−14 | 50 x 1 | chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc |
| 12 | 6366 | 1.74 | 2e−16 | 3e−14 | 50 x 2 | chemokine (C−C motif) ligand 21 [Source:HGNC Symbol;Acc |
| 13 | 1236 | 1.41 | 2e−16 | 3e−14 | 50 x 1 | chemokine (C−C motif) receptor 7 [Source:HGNC Symbol;Ac |
| 14 | 930 | 1.89 | 2e−16 | 3e−14 | 49 x 1 | CD19 molecule [Source:HGNC Symbol;Acc:1633] |
| 15 | 919 | 1.33 | 2e−16 | 3e−14 | 50 x 1 | CD247 molecule [Source:HGNC Symbol;Acc:1677] |
| 16 | 962 | 1.49 | 2e−16 | 3e−14 | 50 x 1 | CD48 molecule [Source:HGNC Symbol;Acc:1683] |
| 17 | 1043 | 1.37 | 2e−16 | 3e−14 | 50 x 1 | CD52 molecule [Source:HGNC Symbol;Acc:1804] |
| 18 | 1048 | 1.57 | 2e−16 | 3e−14 | 2 x 50 | carcinoembryonic antigen−related cell adhesion molecule 5 [S |
| 19 | 4680 | 1.39 | 2e−16 | 3e−14 | 1 x 50 | carcinoembryonic antigen−related cell adhesion molecule 6 (r |
| 20 | 1675 | 1.48 | 2e−16 | 3e−14 | 50 x 9 | complement factor D (adipsin) [Source:HGNC Symbol;Acc:27 |



**p−values**

## Global Geneset Analysis

| Rank | GSZ | p−value | #all | Geneset | |
|---|---|---|---|---|---|
| *Overexpressed* | | | | | |
| 1 | 20.44 | NULL | 16 | GSEA C2 | RICKMAN_HEAD_AND_NECK_CANCER_D |
| 2 | 17.93 | NULL | 417 | H.Tiss | WIRTH_Immune system |
| 3 | 14.76 | NULL | 135 | H.Tiss | WIRTH_Mucosa |
| 4 | 13.8 | NULL | 553 | Cancer | Lembcke_Colonic Inflammation |
| 5 | 13.48 | NULL | 16 | GSEA C2 | CROMER_TUMORIGENESIS_DN |
| 6 | 10.48 | NULL | 15 | CC | MHC class II protein complex |
| 7 | 9.98 | NULL | 312 | BP | immune response |
| 8 | 9.7 | NULL | 21 | CC | cornified envelope |
| 9 | 9.6 | NULL | 36 | BP | muscle filament sliding |
| 10 | 8.77 | NULL | 9 | GSEA C2 | MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN |
| 11 | 8.72 | NULL | 16 | H.Tiss | WIRTH_Hippocampus |
| 12 | 8.53 | NULL | 127 | H.Tiss | WIRTH_Muscle |
| 13 | 8.52 | NULL | 16 | GSEA C2 | RICKMAN_HEAD_AND_NECK_CANCER_F |
| 14 | 8.01 | NULL | 14 | GSEA C2 | SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D |
| 15 | 7.83 | NULL | 375 | Disease | GUDJ_psoriasis down |
| 16 | 7.69 | NULL | 16 | GSEA C2 | ROY_WOUND_BLOOD_VESSEL_DN |
| 17 | 7.68 | NULL | 28 | BP | B cell receptor signaling pathway |
| 18 | 7.67 | NULL | 60 | BP | T cell costimulation |
| 19 | 7.66 | NULL | 84 | BP | T cell receptor signaling pathway |
| 20 | 7.63 | NULL | 16 | GSEA C2 | TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_N |
| *Underexpressed* | | | | | |
| 1 | −13.97 | NULL | 142 | Glio | willscher_GBM_Verhaak−CL_expression_C_up |
| 2 | −13.97 | NULL | 142 | Glio | willscher_GBM_Verhaak−PNmut_expression_C_down |
| 3 | −11.54 | NULL | 530 | Cancer | Lembcke_Normal vs Adenoma |
| 4 | −9.13 | NULL | 370 | BP | mitotic cell cycle |
| 5 | −7.4 | NULL | 242 | BP | extracellular matrix organization |
| 6 | −7.36 | NULL | 15 | GSEA C2 | CROMER_TUMORIGENESIS_UP |
| 7 | −7.3 | NULL | 16 | GSEA C2 | EINAV_INTERFERON_SIGNATURE_IN_CANCER |
| 8 | −7 | NULL | 16 | GSEA C2 | MOSERLE_IFNA_RESPONSE |
| 9 | −6.87 | NULL | 64 | BP | collagen catabolic process |
| 10 | −6.84 | NULL | 69 | BP | extracellular matrix disassembly |
| 11 | −6.81 | NULL | 11 | GSEA C2 | BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS |
| 12 | −6.75 | NULL | 1233 | TF | KIM_MYC targets |
| 13 | −6.67 | NULL | 232 | BP | mitosis |
| 14 | −6.37 | NULL | 949 | CC | nucleoplasm |
| 15 | −6.26 | NULL | 148 | BP | G1/S transition of mitotic cell cycle |
| 16 | −6.12 | NULL | 13 | GSEA C2 | BOWIE_RESPONSE_TO_TAMOXIFEN |
| 17 | −6.02 | NULL | 10 | GSEA C2 | BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX |
| 18 | −5.82 | NULL | 8 | GSEA C2 | ROETH_TERT_TARGETS_UP |
| 19 | −5.81 | NULL | 16 | GSEA C2 | FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL |
| 20 | −5.64 | NULL | 74 | BP | anaphase−promoting complex−dependent proteasomal ubiquitin−c |

# GW_040

## Local Summary

%DE = 0.87

# metagenes = 44

# genes = 597

# genes in genesets = 594

# genes with fdr < 0.1 = 473 ( 466 + / 7 − )

# genes with fdr < 0.05 = 424 ( 420 + / 4 − )

# genes with fdr < 0.01 = 395 ( 391 + / 4 − )

<r> metagenes = 0.81

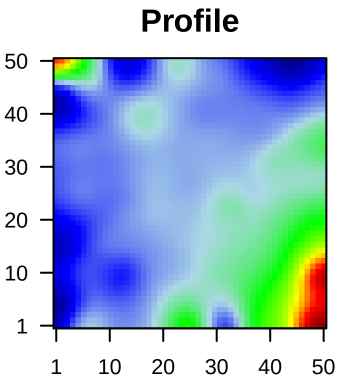
<r> genes = 0.32

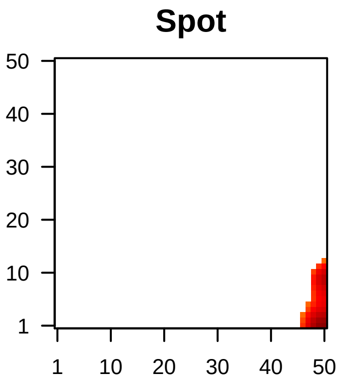
<FC> = 0.68

<shrinkage−t> = 23.69

<p−value> = 0

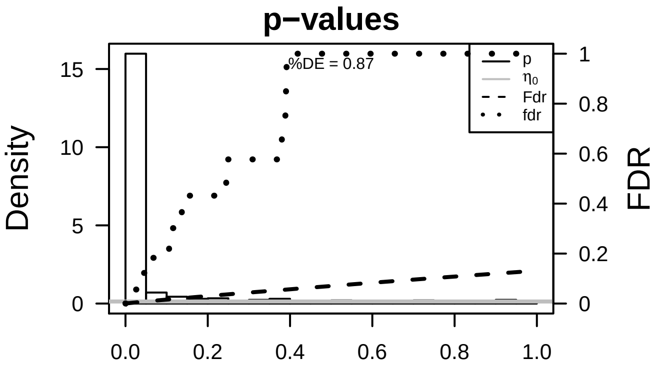
<fdr> = 0.28





## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 10551 | 2.31 | 2e−16 | 3e−16 | 50 x 10 | anterior gradient 2 [Source:HGNC Symbol;Acc:328] |
| 2 | 347 | 2.18 | 2e−16 | 3e−16 | 50 x 7 | apolipoprotein D [Source:HGNC Symbol;Acc:612] |
| 3 | 563 | 1.3 | 2e−16 | 3e−16 | 50 x 10 | alpha−2−glycoprotein 1, zinc−binding [Source:HGNC Symbol |
| 4 | 80341 | 2.65 | 2e−16 | 3e−16 | 50 x 10 | BPI fold containing family B, member 2 [Source:HGNC Symb |
| 5 | 92747 | 3.28 | 2e−16 | 3e−16 | 50 x 10 | BPI fold containing family B, member 1 [Source:HGNC Symb |
| 6 | 260436 | 1.38 | 2e−16 | 3e−16 | 50 x 1 | follicular dendritic cell secreted protein [Source:HGNC Symbo |
| 7 | 57172 | 2.07 | 2e−16 | 3e−16 | 49 x 1 | calcium/calmodulin−dependent protein kinase IG [Source:HG |
| 8 | 6363 | 2.11 | 2e−16 | 3e−16 | 50 x 1 | chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc |
| 9 | 6366 | 1.74 | 2e−16 | 3e−16 | 50 x 2 | chemokine (C−C motif) ligand 21 [Source:HGNC Symbol;Acc |
| 10 | 1236 | 1.41 | 2e−16 | 3e−16 | 50 x 1 | chemokine (C−C motif) receptor 7 [Source:HGNC Symbol;Ac |
| 11 | 930 | 1.89 | 2e−16 | 3e−16 | 49 x 1 | CD19 molecule [Source:HGNC Symbol;Acc:1633] |
| 12 | 919 | 1.33 | 2e−16 | 3e−16 | 50 x 1 | CD247 molecule [Source:HGNC Symbol;Acc:1677] |
| 13 | 962 | 1.49 | 2e−16 | 3e−16 | 50 x 1 | CD48 molecule [Source:HGNC Symbol;Acc:1683] |
| 14 | 1043 | 1.37 | 2e−16 | 3e−16 | 50 x 1 | CD52 molecule [Source:HGNC Symbol;Acc:1804] |
| 15 | 1675 | 1.48 | 2e−16 | 3e−16 | 50 x 9 | complement factor D (adipsin) [Source:HGNC Symbol;Acc:27 |
| 16 | 84952 | 1.49 | 2e−16 | 3e−16 | 50 x 10 | cingulin−like 1 [Source:HGNC Symbol;Acc:25931] |
| 17 | 9071 | 1.3 | 2e−16 | 3e−16 | 50 x 12 | claudin 10 [Source:HGNC Symbol;Acc:2033] |
| 18 | 10321 | 1.69 | 2e−16 | 3e−16 | 50 x 10 | cysteine−rich secretory protein 3 [Source:HGNC Symbol;Acc |
| 19 | 51755 | 1.73 | 2e−16 | 3e−16 | 49 x 1 | cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242 |
| 20 | 2532 | 1.41 | 2e−16 | 3e−16 | 50 x 5 | Duffy blood group, atypical chemokine receptor [Source:HGN |



## Local Geneset Analysis

*Overexpression*

| Rank | GSZ | p−value | #in/all | Geneset | |
|---|---|---|---|---|---|
| 1 | 35.77 | NULL | 14 / 16 | GSEA C2 | RICKMAN_HEAD_AND_NECK_CANCER_D |
| 2 | 22.92 | NULL | 103 / 417 | H.Tiss | WIRTH_Immune system |
| 3 | 22.49 | NULL | 129 / 553 | Cancer | Lembcke_Colonic Inflammation |
| 4 | 18.1 | NULL | 12 / 15 | CC | MHC class II protein complex |
| 5 | 16.13 | NULL | 4 / 7 | GSEA C2 | GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN |
| 6 | 15.58 | NULL | 9 / 16 | GSEA C2 | FARMER_BREAST_CANCER_CLUSTER_1 |
| 7 | 15.33 | NULL | 66 / 312 | BP | immune response |
| 8 | 15.31 | NULL | 5 / 9 | GSEA C2 | MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN |
| 9 | 13.71 | NULL | 7 / 8 | Glio | Donson−migration tethering and rolling−associated with LTS in HG |
| 10 | 12.78 | NULL | 5 / 14 | GSEA C2 | SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D |
| 11 | 12.08 | NULL | 3 / 5 | GSEA C2 | WONG_ENDOMETRIAL_CANCER_LATE |
| 12 | 12.07 | NULL | 18 / 60 | BP | T cell costimulation |
| 13 | 12.03 | NULL | 7 / 15 | GSEA C2 | FINAK_BREAST_CANCER_SDPP_SIGNATURE |
| 14 | 12.03 | NULL | 7 / 11 | GSEA C2 | BIOCARTA_TCYTOTOXIC_PATHWAY |
| 15 | 11.54 | NULL | 7 / 11 | GSEA C2 | BIOCARTA_THELPER_PATHWAY |
| 16 | 11.43 | NULL | 108 / 1182 | CC | extracellular region |
| 17 | 11.13 | NULL | 2 / 5 | GSEA C2 | FERRARI_RESPONSE_TO_FENRETINIDE_DN |
| 18 | 11.1 | NULL | 16 / 47 | BP | antigen processing and presentation |
| 19 | 10.89 | NULL | 5 / 12 | BP | dendritic cell chemotaxis |
| 20 | 10.73 | NULL | 12 / 28 | BP | B cell receptor signaling pathway |
| 21 | 10.68 | NULL | 37 / 162 | CC | external side of plasma membrane |
| 22 | 10.49 | NULL | 5 / 17 | BP | positive regulation of neutrophil chemotaxis |
| 23 | 10.48 | NULL | 77 / 683 | CC | extracellular space |
| 24 | 10.45 | NULL | 4 / 16 | GSEA C2 | TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_ |
| 25 | 10.12 | NULL | 3 / 10 | GSEA C2 | LUI_THYROID_CANCER_CLUSTER_5 |
| 26 | 10.11 | NULL | 8 / 13 | Cancer | GENTLES_modul18 |
| 27 | 10.08 | NULL | 3 / 13 | GSEA C2 | WONG_ENDMETRIUM_CANCER_UP |
| 28 | 9.89 | NULL | 7 / 12 | GSEA C2 | BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_D |
| 29 | 9.86 | NULL | 5 / 16 | GSEA C2 | TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR |
| 30 | 9.82 | NULL | 20 / 74 | BP | regulation of immune response |
| 31 | 9.77 | NULL | 7 / 13 | GSEA C2 | BIOCARTA_IL17_PATHWAY |
| 32 | 9.74 | NULL | 5 / 10 | GSEA C2 | FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_ |
| 33 | 9.59 | NULL | 4 / 8 | GSEA C2 | GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN |
| 34 | 9.54 | NULL | 18 / 84 | BP | T cell receptor signaling pathway |
| 35 | 9.45 | NULL | 5 / 8 | GSEA C2 | BIOCARTA_TCRA_PATHWAY |
| 36 | 9.44 | NULL | 3 / 9 | GSEA C2 | GOUYER_TATI_TARGETS_UP |
| 37 | 9.4 | NULL | 8 / 27 | MF | antigen binding |
| 38 | 9.35 | NULL | 61 / 265 | Glio | willscher_GBM_Verhaak−CL_expression_B_up |
| 39 | 9.35 | NULL | 61 / 265 | Glio | willscher_GBM_Verhaak−MES_expression_B_up |
| 40 | 9.35 | NULL | 61 / 265 | Glio | willscher_GBM_Verhaak−PNwt_expression_B_down |

# GW_040

## Local Summary

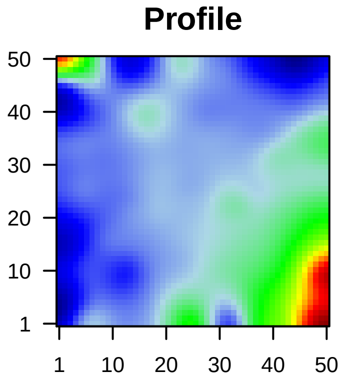
%DE = 0.96
# metagenes = 2
# genes = 71
# genes in genesets = 70

# genes with fdr < 0.1 = 64 ( 61 + / 3 − )
# genes with fdr < 0.05 = 63 ( 60 + / 3 − )
# genes with fdr < 0.01 = 62 ( 60 + / 2 − )

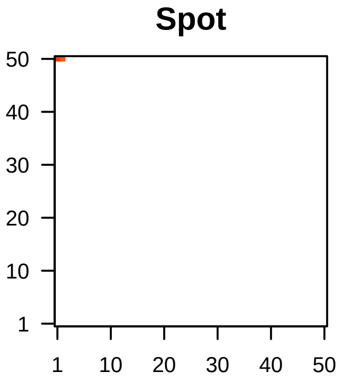
<r> metagenes = 1
<r> genes = 0.58

<FC> = 1.1
<shrinkage−t> = 38.95
<p−value> = 0
<fdr> = 0.11

**Profile**



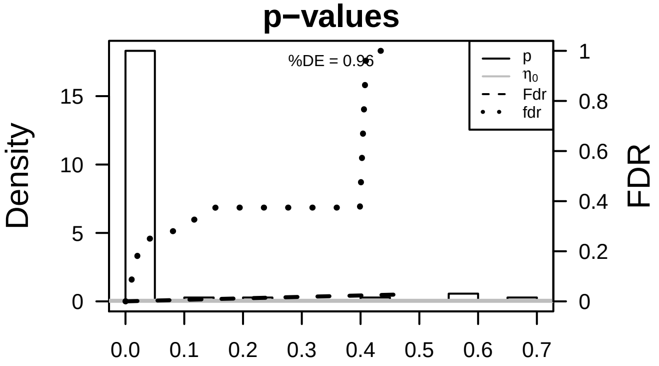
**Spot**



## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 375791 | 1.54 | 2e−16 | 2e−17 | 1 x 50 | chromosome 9 open reading frame 169 [Source:HGNC Symb |
| 2 | 1048 | 1.57 | 2e−16 | 2e−17 | 2 x 50 | carcinoembryonic antigen−related cell adhesion molecule 5 [ |
| 3 | 4680 | 1.39 | 2e−16 | 2e−17 | 1 x 50 | carcinoembryonic antigen−related cell adhesion molecule 6 ( |
| 4 | 22802 | 2.57 | 2e−16 | 2e−17 | 1 x 50 | chloride channel accessory 4 [Source:HGNC Symbol;Acc:20 |
| 5 | 84518 | 1.34 | 2e−16 | 2e−17 | 1 x 50 | cornifelin [Source:HGNC Symbol;Acc:30183] |
| 6 | 54544 | 1.36 | 2e−16 | 2e−17 | 1 x 50 | cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987 |
| 7 | 49860 | 2.99 | 2e−16 | 2e−17 | 1 x 50 | cornulin [Source:HGNC Symbol;Acc:1230] |
| 8 | 1475 | 1.61 | 2e−16 | 2e−17 | 1 x 50 | cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481] |
| 9 | 26085 | 1.37 | 2e−16 | 2e−17 | 1 x 50 | kallikrein−related peptidase 13 [Source:HGNC Symbol;Acc:6 |
| 10 | 5653 | 1.75 | 2e−16 | 2e−17 | 1 x 50 | kallikrein−related peptidase 6 [Source:HGNC Symbol;Acc:63 |
| 11 | 192666 | 2.38 | 2e−16 | 2e−17 | 1 x 50 | keratin 24 [Source:HGNC Symbol;Acc:18527] |
| 12 | 3851 | 2.61 | 2e−16 | 2e−17 | 1 x 50 | keratin 4 [Source:HGNC Symbol;Acc:6441] |
| 13 | 196374 | 2.43 | 2e−16 | 2e−17 | 1 x 50 | keratin 78 [Source:HGNC Symbol;Acc:28926] |
| 14 | 4118 | 2.62 | 2e−16 | 2e−17 | 1 x 50 | mal, T−cell differentiation protein [Source:HGNC Symbol;Acc |
| 15 | 342897 | 1.39 | 2e−16 | 2e−17 | 1 x 50 | non−specific cytotoxic cell receptor protein 1 homolog (zebraf |
| 16 | 5493 | 1.44 | 2e−16 | 2e−17 | 1 x 50 | periplakin [Source:HGNC Symbol;Acc:9273] |
| 17 | 83886 | 1.64 | 2e−16 | 2e−17 | 1 x 50 | protease, serine 27 [Source:HGNC Symbol;Acc:15475] |
| 18 | 51458 | 2.24 | 2e−16 | 2e−17 | 1 x 50 | Rh family, C glycoprotein [Source:HGNC Symbol;Acc:18140] |
| 19 | 8796 | 1.38 | 2e−16 | 2e−17 | 1 x 50 | sciellin [Source:HGNC Symbol;Acc:10573] |
| 20 | 11005 | 1.47 | 2e−16 | 2e−17 | 1 x 50 | serine peptidase inhibitor, Kazal type 5 [Source:HGNC Symb |

**p−values**



## Local Geneset Analysis

*Overexpression*

| Rank | GSZ | p−value | #in/all | Geneset | |
|---|---|---|---|---|---|
| 1 | 44.37 | NULL | 39 / 135 | H.Tiss | WIRTH_Mucosa |
| 2 | 36.4 | NULL | 10 / 21 | CC | cornified envelope |
| 3 | 28.72 | NULL | 11 / 42 | BP | keratinization |
| 4 | 28.62 | NULL | 7 / 19 | BP | peptide cross−linking |
| 5 | 24.8 | NULL | 12 / 53 | BP | keratinocyte differentiation |
| 6 | 22.68 | NULL | 4 / 16 | GSEA C2 | CROMER_TUMORIGENESIS_DN |
| 7 | 18.98 | NULL | 4 / 15 | GSEA C2 | HINATA_NFKB_TARGETS_KERATINOCYTE_DN |
| 8 | 14 | NULL | 9 / 76 | BP | epidermis development |
| 9 | 13.73 | NULL | 29 / 572 | Disease | GUDJ_psoriasis up |
| 10 | 13.54 | NULL | 3 / 13 | BP | negative regulation of peptidase activity |
| 11 | 13.37 | NULL | 3 / 16 | GSEA C2 | WANG_BARRETTS_ESOPHAGUS_DN |
| 12 | 13.2 | NULL | 10 / 186 | MF | structural molecule activity |
| 13 | 12.76 | NULL | 2 / 15 | GSEA C2 | RICKMAN_HEAD_AND_NECK_CANCER_E |
| 14 | 12.51 | NULL | 3 / 38 | BP | epithelial cell differentiation |
| 15 | 12.27 | NULL | 3 / 15 | GSEA C2 | WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE |
| 16 | 11.83 | NULL | 9 / 122 | MF | serine−type endopeptidase activity |
| 17 | 11.19 | NULL | 3 / 44 | CC | keratin filament |
| 18 | 10.94 | NULL | 4 / 82 | CC | intermediate filament |
| 19 | 10.8 | NULL | 1 / 11 | Glio | VERHAAK_Brain |
| 20 | 10.71 | NULL | 3 / 15 | GSEA C2 | LEE_LIVER_CANCER_MYC_E2F1_UP |
| 21 | 10.2 | NULL | 1 / 12 | MF | channel activity |
| 22 | 10.16 | NULL | 2 / 16 | BP | cobalamin metabolic process |
| 23 | 10.09 | NULL | 1 / 11 | GSEA C2 | ROME_INSULIN_TARGETS_IN_MUSCLE_DN |
| 24 | 9.83 | NULL | 1 / 10 | BP | homeostatic process |
| 25 | 9.69 | NULL | 1 / 13 | GSEA C2 | HASLINGER_B_CLL_WITH_MUTATED_VH_GENES |
| 26 | 9.54 | NULL | 1 / 12 | GSEA C2 | ODONNELL_METASTASIS_DN |
| 27 | 9.54 | NULL | 1 / 12 | GSEA C2 | SYED_ESTRADIOL_RESPONSE |
| 28 | 9.15 | NULL | 2 / 15 | GSEA C2 | CHANG_IMMORTALIZED_BY_HPV31_DN |
| 29 | 8.85 | NULL | 1 / 15 | BP | positive regulation of extrinsic apoptotic signaling pathway via deat |
| 30 | 8.85 | NULL | 1 / 15 | GSEA C2 | ALONSO_METASTASIS_NEURAL_UP |
| 31 | 8.85 | NULL | 1 / 15 | GSEA C2 | BIOCARTA_MAL_PATHWAY |
| 32 | 8.51 | NULL | 2 / 38 | BP | myelination |
| 33 | 8.5 | NULL | 1 / 16 | Cancer | GENTLES_modul11 |
| 34 | 8.34 | NULL | 1 / 16 | GSEA C2 | RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL |
| 35 | 8.3 | NULL | 2 / 16 | GSEA C2 | ONDER_CDH1_TARGETS_3_DN |
| 36 | 8.3 | NULL | 2 / 16 | GSEA C2 | CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_ |
| 37 | 8.14 | NULL | 1 / 8 | GSEA C2 | GRAHAM_CML_QUIESCENT_VS_CML_DIVIDING_DN |
| 38 | 7.9 | NULL | 1 / 14 | MF | ankyrin binding |
| 39 | 7.8 | NULL | 2 / 13 | H.Tiss | WIRTH_Tonsil |
| 40 | 7.22 | NULL | 6 / 79 | MF | serine−type endopeptidase inhibitor activity |

# GW_040

## Local Summary

%DE = 0.83

# metagenes = 20

# genes = 313

# genes in genesets = 310

# genes with fdr < 0.1  = 191  ( 10 + / 181  − )

# genes with fdr < 0.05  = 186  ( 9 + / 177  − )

# genes with fdr < 0.01 = 124  ( 7 + / 117  − )

<r> metagenes = 0.94

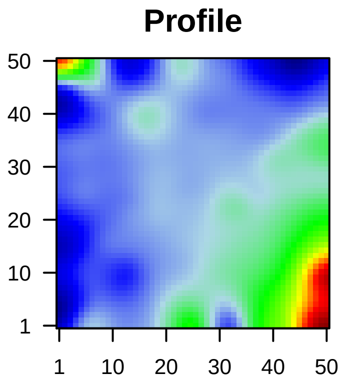
<r> genes = 0.32

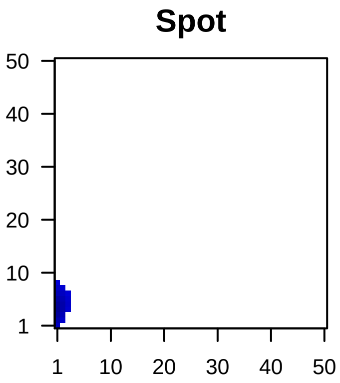
<FC> = −0.37

<shrinkage−t> = −13.01

<p−value> = 0

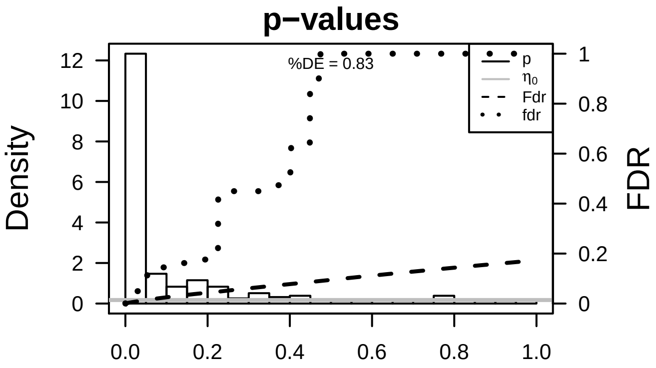
<fdr> = 0.5





## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 3569 | 1.6 | 2e−16 | 2e−15 | 1 x 1 | interleukin 6 (interferon, beta 2) [Source:HGNC Symbol;Acc:6 |
| 2 | 3918 | −1.45 | 2e−16 | 2e−15 | 1 x 4 | laminin, gamma 2 [Source:HGNC Symbol;Acc:6493] |
| 3 | 4312 | −1.75 | 2e−16 | 2e−15 | 1 x 1 | matrix metallopeptidase 1 (interstitial collagenase) [Source:H |
| 4 | 4319 | −1.93 | 2e−16 | 2e−15 | 1 x 3 | matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy |
| 5 | 4314 | −1.86 | 2e−16 | 2e−15 | 1 x 1 | matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou |
| 6 | 5328 | −1.5 | 2e−16 | 2e−15 | 1 x 3 | plasminogen activator, urokinase [Source:HGNC Symbol;Acc |
| 7 | 7045 | −1.18 | 2e−16 | 2e−15 | 1 x 2 | transforming growth factor, beta−induced, 68kDa [Source:HG |
| 8 | 3956 | −1.25 | 1e−15 | 2e−13 | 1 x 1 | lectin, galactoside−binding, soluble, 1 [Source:HGNC Symbol |
| 9 | 12 | 1.23 | 4e−15 | 2e−12 | 1 x 1 | |
| 10 | 10630 | −1.18 | 5e−14 | 5e−12 | 1 x 2 | podoplanin [Source:HGNC Symbol;Acc:29602] |
| 11 | 55107 | −1.16 | 1e−13 | 2e−11 | 1 x 5 | anoctamin 1, calcium activated chloride channel [Source:HGN |
| 12 | 2920 | 1.13 | 4e−13 | 2e−10 | 1 x 1 | chemokine (C−X−C motif) ligand 2 [Source:HGNC Symbol;Ac |
| 13 | 51330 | −1.09 | 4e−12 | 5e−10 | 1 x 4 | tumor necrosis factor receptor superfamily, member 12A [Sou |
| 14 | 768 | −1.05 | 2e−11 | 5e−10 | 1 x 6 | carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383] |
| 15 | 10381 | −1.05 | 2e−11 | 1e−09 | 1 x 4 | tubulin, beta 3 class III [Source:HGNC Symbol;Acc:20772] |
| 16 | 4322 | −1.03 | 4e−11 | 2e−08 | 1 x 2 | matrix metallopeptidase 13 (collagenase 3) [Source:HGNC S |
| 17 | 1464 | −0.96 | 1e−09 | 2e−08 | 1 x 3 | chondroitin sulfate proteoglycan 4 [Source:HGNC Symbol;Ac |
| 18 | 1294 | −0.96 | 1e−09 | 2e−08 | 1 x 5 | collagen, type VII, alpha 1 [Source:HGNC Symbol;Acc:2214] |
| 19 | 5054 | −0.95 | 1e−09 | 1e−07 | 1 x 2 | serpin peptidase inhibitor, clade E (nexin, plasminogen activa |
| 20 | 7130 | −0.92 | 4e−09 | 1e−07 | 1 x 1 | tumor necrosis factor, alpha−induced protein 6 [Source:HGN |



## Local Geneset Analysis

*Underexpression*

| Rank | GSZ | p−value | #in/all | Geneset | |
|---|---|---|---|---|---|
| 1 | −25.61 | NULL | 8 / 15 | GSEA C2 | CROMER_TUMORIGENESIS_UP |
| 2 | −20.04 | NULL | 43 / 242 | BP | extracellular matrix organization |
| 3 | −16.54 | NULL | 12 / 64 | BP | collagen catabolic process |
| 4 | −15.86 | NULL | 12 / 69 | BP | extracellular matrix disassembly |
| 5 | −15.46 | NULL | 18 / 183 | CC | proteinaceous extracellular matrix |
| 6 | −14.54 | NULL | 5 / 12 | BP | hemidesmosome assembly |
| 7 | −14.47 | NULL | 9 / 35 | Glio | Colman_survival_associated |
| 8 | −13.58 | NULL | 2 / 7 | GSEA C2 | FREDERICK_PRKCI_TARGETS |
| 9 | −13.33 | NULL | 5 / 11 | Glio | Phillips MES up vs Prolif & PN |
| 10 | −13.16 | NULL | 2 / 12 | GSEA C2 | GEISS_RESPONSE_TO_DSRNA_DN |
| 11 | −12.71 | NULL | 46 / 403 | BP | cell adhesion |
| 12 | −12.7 | NULL | 5 / 13 | GSEA C2 | MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH |
| 13 | −12.5 | NULL | 17 / 190 | CC | extracellular matrix |
| 14 | −12.18 | NULL | 8 / 51 | BP | regulation of cell migration |
| 15 | −11.92 | NULL | 29 / 250 | Lymphoma | LENZ_Stromal signature 1 |
| 16 | −11.54 | NULL | 7 / 73 | MF | metallopeptidase activity |
| 17 | −11.46 | NULL | 3 / 12 | GSEA C2 | SHI_SPARC_TARGETS_UP |
| 18 | −11.43 | NULL | 1 / 5 | GSEA C2 | OXFORD_RALA_AND_RALB_TARGETS_UP |
| 19 | −11.43 | NULL | 86 / 1182 | CC | extracellular region |
| 20 | −11.42 | NULL | 7 / 81 | MF | metalloendopeptidase activity |
| 21 | −11.41 | NULL | 4 / 10 | GSEA C2 | VERRECCHIA_RESPONSE_TO_TGFB1_C4 |
| 22 | −11.38 | NULL | 5 / 15 | GSEA C2 | ONDER_CDH1_SIGNALING_VIA_CTNNB1 |
| 23 | −11.04 | NULL | 2 / 14 | GSEA C2 | DAZARD_UV_RESPONSE_CLUSTER_G4 |
| 24 | −10.91 | NULL | 2 / 10 | BP | regulation of receptor activity |
| 25 | −10.91 | NULL | 2 / 10 | GSEA C2 | BIOCARTA_FIBRINOLYSIS_PATHWAY |
| 26 | −10.82 | NULL | 4 / 13 | GSEA C2 | REACTOME_REGULATION_OF_INSULIN_LIKE_GROWTH_FACT |
| 27 | −10.8 | NULL | 3 / 15 | BP | fibrinolysis |
| 28 | −10.74 | NULL | 3 / 11 | GSEA C2 | BIOCARTA_PLATELETAPP_PATHWAY |
| 29 | −10.72 | NULL | 10 / 83 | CC | basement membrane |
| 30 | −10.1 | NULL | 3 / 16 | GSEA C2 | MURATA_VIRULENCE_OF_H_PILORI |
| 31 | −10.03 | NULL | 4 / 16 | GSEA C2 | KERLEY_RESPONSE_TO_CISPLATIN_UP |
| 32 | −9.95 | NULL | 53 / 683 | CC | extracellular space |
| 33 | −9.87 | NULL | 3 / 16 | CC | lamellipodium membrane |
| 34 | −9.63 | NULL | 2 / 13 | GSEA C2 | XU_HGF_TARGETS_INDUCED_BY_AKT1_48HR_UP |
| 35 | −9.63 | NULL | 24 / 265 | Glio | willscher_GBM_Verhaak−CL_expression_B_up |
| 36 | −9.63 | NULL | 24 / 265 | Glio | willscher_GBM_Verhaak−MES_expression_B_up |
| 37 | −9.63 | NULL | 24 / 265 | Glio | willscher_GBM_Verhaak−PNwt_expression_B_down |
| 38 | −9.63 | NULL | 24 / 265 | Glio | willscher_GBM_Verhaak−PNmut_expression_B_down |
| 39 | −9.59 | NULL | 2 / 10 | GSEA C2 | VETTER_TARGETS_OF_PRKCA_AND_ETS1_DN |
| 40 | −9.39 | NULL | 4 / 15 | GSEA C2 | KANG_FLUOROURACIL_RESISTANCE_DN |

# GW_040

## Local Summary

%DE = 0.78

# metagenes = 16

# genes = 203

# genes in genesets = 202

# genes with fdr < 0.1  = 137  ( 2 + / 135  − )

# genes with fdr < 0.05  = 96  ( 1 + / 95  − )

# genes with fdr < 0.01 = 32  ( 0 + / 32  − )

<r> metagenes = 0.96

<r> genes = 0.29

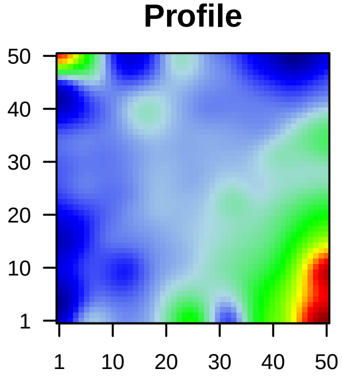
<FC> = −0.3

<shrinkage−t> = −10.59

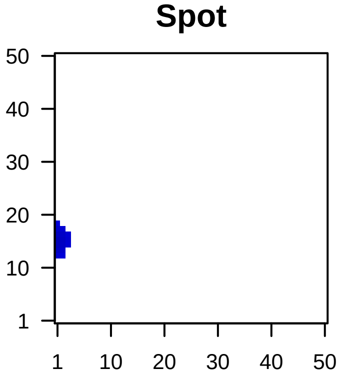
<p−value> = 0.03

<fdr> = 0.69

**Profile**



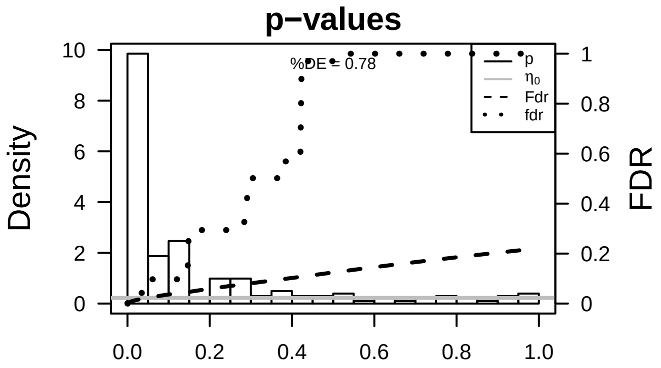
**Spot**



## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 10428 | −1.1 | 2e−12 | 8e−07 | 1 x 15 | craniofacial development protein 1 [Source:HGNC Symbol;Ac |
| 2 | 8772 | −0.86 | 3e−08 | 8e−07 | 1 x 14 | Fas (TNFRSF6)−associated via death domain [Source:HGNC |
| 3 | 991 | −0.86 | 4e−08 | 5e−05 | 1 x 16 | cell division cycle 20 [Source:HGNC Symbol;Acc:1723] |
| 4 | 3217 | −0.76 | 1e−06 | 5e−05 | 1 x 15 | homeobox B7 [Source:HGNC Symbol;Acc:5118] |
| 5 | 5708 | −0.74 | 2e−06 | 5e−05 | 1 x 14 | proteasome (prosome, macropain) 26S subunit, non−ATPase |
| 6 | 4282 | −0.66 | 4e−06 | 5e−05 | 2 x 15 | macrophage migration inhibitory factor (glycosylation−inhibitir |
| 7 | 2050 | −0.71 | 5e−06 | 5e−05 | 1 x 15 | EPH receptor B4 [Source:HGNC Symbol;Acc:3395] |
| 8 | 3237 | −0.71 | 5e−06 | 1e−04 | 1 x 16 | homeobox D11 [Source:HGNC Symbol;Acc:5134] |
| 9 | 283869 | −0.7 | 8e−06 | 3e−04 | 1 x 17 | neuropeptide W [Source:HGNC Symbol;Acc:30509] |
| 10 | 2932 | −0.67 | 2e−05 | 3e−04 | 1 x 17 | glycogen synthase kinase 3 beta [Source:HGNC Symbol;Acc |
| 11 | 6535 | −0.67 | 2e−05 | 7e−04 | 1 x 16 | solute carrier family 6 (neurotransmitter transporter), member |
| 12 | 10467 | −0.65 | 4e−05 | 8e−04 | 2 x 18 | zinc finger, HIT−type containing 1 [Source:HGNC Symbol;Acc |
| 13 | 23246 | −0.63 | 6e−05 | 1e−03 | 1 x 16 | block of proliferation 1 [Source:HGNC Symbol;Acc:15519] |
| 14 | 51367 | −0.62 | 8e−05 | 2e−03 | 1 x 17 | processing of precursor 5, ribonuclease P/MRP subunit (S. ce |
| 15 | 8563 | −0.57 | 2e−04 | 2e−03 | 1 x 16 | THO complex 5 [Source:HGNC Symbol;Acc:19074] |
| 16 | 55257 | −0.57 | 3e−04 | 2e−03 | 1 x 15 | MRG/MORF4L binding protein [Source:HGNC Symbol;Acc:1 |
| 17 | 84916 | −0.56 | 3e−04 | 2e−03 | 1 x 16 | cirrhosis, autosomal recessive 1A (cirhin) [Source:HGNC Syn |
| 18 | 2023 | −0.51 | 3e−04 | 2e−03 | 1 x 14 | enolase 1, (alpha) [Source:HGNC Symbol;Acc:3350] |
| 19 | 79080 | −0.55 | 4e−04 | 2e−03 | 1 x 14 | coiled−coil domain containing 86 [Source:HGNC Symbol;Acc |
| 20 | 26873 | −0.55 | 4e−04 | 2e−03 | 1 x 17 | 5−oxoprolinase (ATP−hydrolysing) [Source:HGNC Symbol;Ac |

**p−values**



## Local Geneset Analysis

*Underexpression*

| Rank | GSZ | p−value | #in/all | Geneset | |
|---|---|---|---|---|---|
| 1 | −12.14 | NULL | 4 / 13 | GSEA C2 | REACTOME_GLYCOLYSIS |
| 2 | −11.13 | NULL | 2 / 13 | GSEA C2 | NADERI_BREAST_CANCER_PROGNOSIS_UP |
| 3 | −10.88 | NULL | 3 / 9 | GSEA C2 | BIOCARTA_GLYCOLYSIS_PATHWAY |
| 4 | −10.79 | NULL | 3 / 10 | GSEA C2 | TOMIDA_METASTASIS_UP |
| 5 | −10.79 | NULL | 2 / 9 | GSEA C2 | KUMAMOTO_RESPONSE_TO_NUTLIN_3A_DN |
| 6 | −10.63 | NULL | 3 / 15 | GSEA C2 | LY_AGING_MIDDLE_DN |
| 7 | −10.12 | NULL | 7 / 66 | BP | positive regulation of ubiquitin−protein ligase activity involved in mit |
| 8 | −9.78 | NULL | 7 / 70 | BP | regulation of ubiquitin−protein ligase activity involved in mitotic cell |
| 9 | −9.55 | NULL | 3 / 16 | Cancer | RHODES_UNDIFFERENTIATED_CANCER |
| 10 | −9.47 | NULL | 7 / 74 | BP | anaphase−promoting complex−dependent proteasomal ubiquitin− |
| 11 | −9.29 | NULL | 6 / 62 | BP | negative regulation of ubiquitin−protein ligase activity involved in m |
| 12 | −9.09 | NULL | 2 / 10 | BP | creatine metabolic process |
| 13 | −8.98 | NULL | 1 / 6 | GSEA C2 | GALI_TP53_TARGETS_APOPTOTIC_DN |
| 14 | −8.97 | NULL | 12 / 96 | BP | rRNA processing |
| 15 | −8.95 | NULL | 1 / 6 | GSEA C2 | WAESCH_ANAPHASE_PROMOTING_COMPLEX |
| 16 | −8.86 | NULL | 2 / 7 | GSEA C2 | REACTOME_SIGNALING_BY_WNT |
| 17 | −8.83 | NULL | 2 / 15 | GSEA C2 | KEGG_AXON_GUIDANCE |
| 18 | −8.76 | NULL | 2 / 11 | BP | positive regulation of protein complex assembly |
| 19 | −8.66 | NULL | 2 / 10 | BP | negative regulation of DNA damage response, signal transduction |
| 20 | −8.55 | NULL | 2 / 9 | GSEA C2 | DACOSTA_UV_RESPONSE_VIA_ERCC3_UP |
| 21 | −8.51 | NULL | 5 / 39 | BP | glycolysis |
| 22 | −8.31 | NULL | 3 / 14 | GSEA C2 | KEGG_COLORECTAL_CANCER |
| 23 | −8.29 | NULL | 2 / 13 | BP | cell migration involved in sprouting angiogenesis |
| 24 | −8.21 | NULL | 3 / 15 | GSEA C2 | REACTOME_GLUCONEOGENESIS |
| 25 | −8.16 | NULL | 1 / 5 | GSEA C2 | VERRECCHIA_RESPONSE_TO_TGFB1_C6 |
| 26 | −8.14 | NULL | 6 / 55 | CC | proteasome complex |
| 27 | −8.12 | NULL | 3 / 16 | BP | monocyte differentiation |
| 28 | −7.96 | NULL | 2 / 15 | BP | positive regulation of branching involved in ureteric bud morphogen |
| 29 | −7.96 | NULL | 4 / 18 | MF | ribonucleoprotein complex binding |
| 30 | −7.88 | NULL | 3 / 17 | CC | proteasome accessory complex |
| 31 | −7.82 | NULL | 2 / 12 | BP | negative regulation of intrinsic apoptotic signaling pathway in respo |
| 32 | −7.64 | NULL | 2 / 7 | GSEA C2 | CAFFAREL_RESPONSE_TO_THC_24HR_5_UP |
| 33 | −7.59 | NULL | 5 / 48 | BP | regulation of cellular amino acid metabolic process |
| 34 | −7.46 | NULL | 2 / 12 | BP | positive regulation of peptidyl−threonine phosphorylation |
| 35 | −7.36 | NULL | 5 / 39 | BP | gluconeogenesis |
| 36 | −7.36 | NULL | 2 / 14 | GSEA C2 | REACTOME_PI3K_AKT_SIGNALLING |
| 37 | −7.18 | NULL | 1 / 9 | GSEA C2 | BIOCARTA_RELA_PATHWAY |
| 38 | −7.18 | NULL | 1 / 9 | GSEA C2 | BIOCARTA_NFKB_PATHWAY |
| 39 | −7.18 | NULL | 1 / 9 | GSEA C2 | BIOCARTA_SODD_PATHWAY |
| 40 | −7.18 | NULL | 1 / 9 | GSEA C2 | REACTOME_DEATH_RECEPTOR_SIGNALLING |

# GW_040

## Local Summary

%DE = 0.97

# metagenes = 11

# genes = 159

# genes in genesets = 156

# genes with fdr < 0.1  = 149  ( 11 + / 138  − )

# genes with fdr < 0.05  = 126  ( 4 + / 122  − )

# genes with fdr < 0.01 = 116  ( 4 + / 112  − )

<r> metagenes = 0.99

<r> genes = 0.36

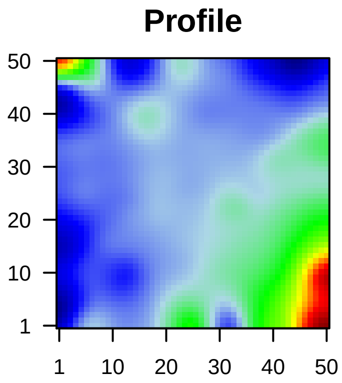
<FC> = −0.42

<shrinkage−t> = −14.75

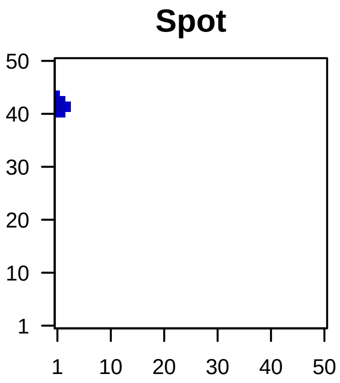
<p−value> = 0

<fdr> = 0.4

### Profile



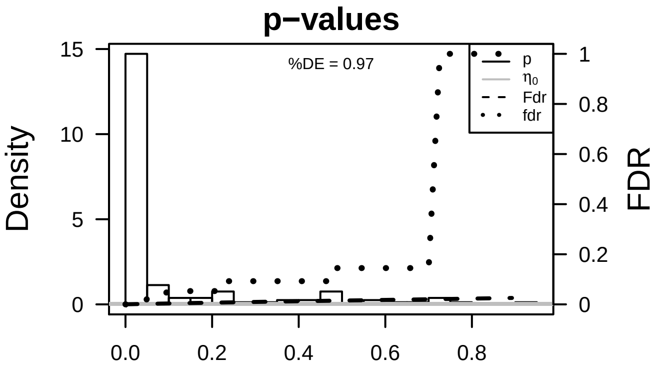
### Spot



## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 55214 | −1.82 | 2e−16 | 5e−16 | 1 x 42 | leprecan−like 1 [Source:HGNC Symbol;Acc:19317] |
| 2 | 5744 | −1.48 | 2e−16 | 5e−16 | 1 x 43 | parathyroid hormone−like hormone [Source:HGNC Symbol;A |
| 3 | 2697 | −1.13 | 4e−13 | 2e−12 | 1 x 44 | gap junction protein, alpha 1, 43kDa [Source:HGNC Symbol; |
| 4 | 6513 | −1.12 | 9e−13 | 2e−12 | 1 x 43 | solute carrier family 2 (facilitated glucose transporter), membe |
| 5 | 144406 | −1.11 | 1e−12 | 8e−12 | 1 x 42 | WD repeat domain 66 [Source:HGNC Symbol;Acc:28506] |
| 6 | 1001 | −1.09 | 3e−12 | 2e−09 | 1 x 43 | cadherin 3, type 1, P−cadherin (placental) [Source:HGNC Sy |
| 7 | 56901 | −0.98 | 4e−10 | 5e−09 | 1 x 44 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4−li |
| 8 | 3429 | −0.87 | 2e−09 | 1e−08 | 1 x 42 | interferon, alpha−inducible protein 27 [Source:HGNC Symbol |
| 9 | 5947 | −0.91 | 7e−09 | 1e−08 | 1 x 43 | retinol binding protein 1, cellular [Source:HGNC Symbol;Acc: |
| 10 | 10397 | −0.83 | 8e−09 | 9e−08 | 1 x 42 | N−myc downstream regulated 1 [Source:HGNC Symbol;Acc: |
| 11 | 50805 | −0.86 | 3e−08 | 9e−08 | 1 x 43 | iroquois homeobox 4 [Source:HGNC Symbol;Acc:6129] |
| 12 | 4015 | −0.85 | 5e−08 | 1e−07 | 1 x 41 | lysyl oxidase [Source:HGNC Symbol;Acc:6664] |
| 13 | 1288 | −0.84 | 9e−08 | 1e−07 | 1 x 43 | collagen, type IV, alpha 6 [Source:HGNC Symbol;Acc:2208] |
| 14 | 387882 | −0.82 | 1e−07 | 1e−07 | 2 x 41 | chromosome 12 open reading frame 75 [Source:HGNC Symb |
| 15 | 3664 | −0.82 | 1e−07 | 1e−06 | 1 x 41 | interferon regulatory factor 6 [Source:HGNC Symbol;Acc:612 |
| 16 | 3552 | 0.79 | 4e−07 | 2e−06 | 1 x 43 | interleukin 1, alpha [Source:HGNC Symbol;Acc:5991] |
| 17 | 4233 | −0.76 | 1e−06 | 2e−06 | 1 x 41 | met proto−oncogene [Source:HGNC Symbol;Acc:7029] |
| 18 | 1952 | −0.75 | 1e−06 | 2e−06 | 1 x 40 | cadherin, EGF LAG seven−pass G−type receptor 2 [Source:H |
| 19 | 81706 | −0.74 | 2e−06 | 2e−06 | 1 x 43 | protein phosphatase 1, regulatory (inhibitor) subunit 14C [Sou |
| 20 | 116211 | −0.73 | 3e−06 | 2e−06 | 1 x 43 | Transmembrane 4 L6 family member 19  [Source:UniProtKB/ |

### p−values



## Local Geneset Analysis

*Underexpression*

| Rank | GSZ | p−value | #in/all | Geneset | |
|---|---|---|---|---|---|
| 1 | −23.56 | NULL | 2 / 2 | miRNA target | miR−199a* |
| 2 | −15.35 | NULL | 4 / 16 | GSEA C2 | ELVIDGE_HIF1A_TARGETS_DN |
| 3 | −14.77 | NULL | 2 / 6 | GSEA C2 | WALLACE_PROSTATE_CANCER_DN |
| 4 | −14.71 | NULL | 4 / 16 | GSEA C2 | ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN |
| 5 | −12.31 | NULL | 2 / 15 | GSEA C2 | NGUYEN_NOTCH1_TARGETS_UP |
| 6 | −11.97 | NULL | 2 / 11 | GSEA C2 | BIOCARTA_VITCB_PATHWAY |
| 7 | −11.87 | NULL | 4 / 16 | GSEA C2 | HUPER_BREAST_BASAL_VS_LUMINAL_UP |
| 8 | −11.68 | NULL | 1 / 7 | GSEA C2 | BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_AND_PAX3 |
| 9 | −11.5 | NULL | 2 / 8 | GSEA C2 | MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_UP |
| 10 | −11.49 | NULL | 2 / 10 | MF | gap junction channel activity |
| 11 | −11.19 | NULL | 2 / 16 | GSEA C2 | WILLERT_WNT_SIGNALING |
| 12 | −11.03 | NULL | 3 / 16 | GSEA C2 | ELVIDGE_HYPOXIA_BY_DMOG_UP |
| 13 | −10.78 | NULL | 2 / 8 | GSEA C2 | SIMBULAN_UV_RESPONSE_NORMAL_UP |
| 14 | −10.72 | NULL | 1 / 5 | GSEA C2 | RODRIGUES_DCC_TARGETS_UP |
| 15 | −10.35 | NULL | 1 / 4 | MMML CGS | MACIEJ_MMML 47 |
| 16 | −10.26 | NULL | 4 / 32 | CC | cell−cell adherens junction |
| 17 | −10.12 | NULL | 2 / 16 | GSEA C2 | BECKER_TAMOXIFEN_RESISTANCE_DN |
| 18 | −9.91 | NULL | 3 / 15 | GSEA C2 | PRAMOONJAGO_SOX4_TARGETS_UP |
| 19 | −9.88 | NULL | 2 / 19 | MF | L−ascorbic acid binding |
| 20 | −9.83 | NULL | 2 / 12 | GSEA C2 | REACTOME_GAP_JUNCTION_ASSEMBLY |
| 21 | −9.81 | NULL | 7 / 76 | BP | epidermis development |
| 22 | −9.77 | NULL | 1 / 6 | GSEA C2 | SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP |
| 23 | −9.64 | NULL | 2 / 14 | GSEA C2 | VANHARANTA_UTERINE_FIBROID_DN |
| 24 | −9.57 | NULL | 7 / 85 | Glio | laffaire_hypermeth_LGG_vs_control |
| 25 | −9.49 | NULL | 1 / 10 | BP | surfactant homeostasis |
| 26 | −9.25 | NULL | 4 / 12 | BP | hemidesmosome assembly |
| 27 | −9.2 | NULL | 2 / 11 | GSEA C2 | GAUSSMANN_MLL_AF4_FUSION_TARGETS_G_UP |
| 28 | −8.96 | NULL | 3 / 26 | BP | positive regulation of vasodilation |
| 29 | −8.93 | NULL | 8 / 112 | Glio | Christensen_hypermethylated_in_grade2_oligoastrocytoma |
| 30 | −8.9 | NULL | 3 / 20 | MF | scaffold protein binding |
| 31 | −8.76 | NULL | 3 / 15 | GSEA C2 | FARMER_BREAST_CANCER_CLUSTER_3 |
| 32 | −8.65 | NULL | 2 / 15 | CC | connexon complex |
| 33 | −8.62 | NULL | 1 / 5 | GSEA C2 | KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_4NQ |
| 34 | −8.58 | NULL | 6 / 83 | CC | basement membrane |
| 35 | −8.48 | NULL | 2 / 15 | GSEA C2 | AMIT_EGF_RESPONSE_240_MCF10A |
| 36 | −8.44 | NULL | 3 / 16 | GSEA C2 | FARMER_BREAST_CANCER_CLUSTER_4 |
| 37 | −8.4 | NULL | 1 / 2 | miRNA target | miR−346 |
| 38 | −8.34 | NULL | 1 / 4 | miRNA target | miR−206 |
| 39 | −8.33 | NULL | 2 / 10 | GSEA C2 | DAZARD_UV_RESPONSE_CLUSTER_G3 |
| 40 | −8.32 | NULL | 3 / 12 | GSEA C2 | MIZUKAMI_HYPOXIA_UP |

# GW_040

## Local Summary

%DE = 0.78

# metagenes = 32

# genes = 465

# genes in genesets = 462

# genes with fdr < 0.1 = 264 ( 3 + / 261 − )

# genes with fdr < 0.05 = 210 ( 1 + / 209 − )

# genes with fdr < 0.01 = 115 ( 1 + / 114 − )

<r> metagenes = 0.89

<r> genes = 0.34

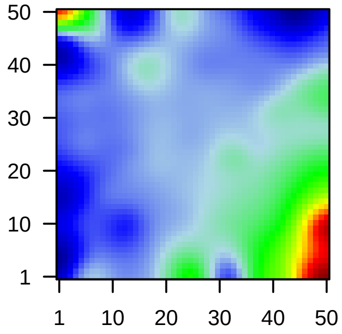
<FC> = −0.33

<shrinkage−t> = −11.58

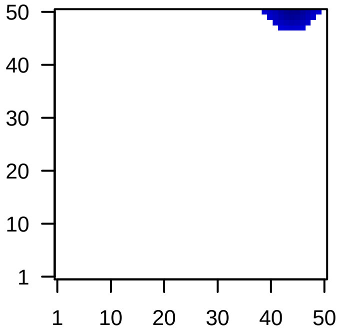
<p−value> = 0.01

<fdr> = 0.61

**Profile**



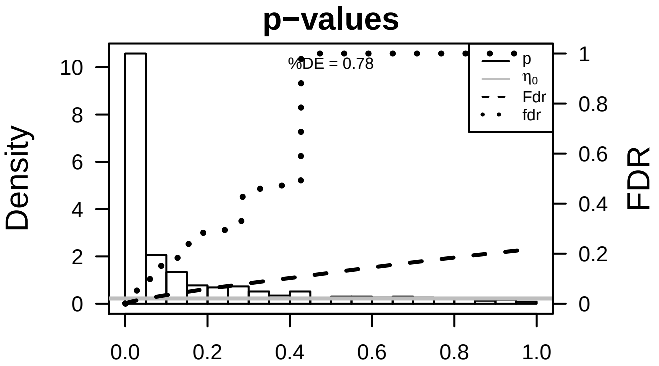
**Spot**



## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 51659 | −1.18 | 5e−14 | 1e−08 | 44 x 50 | GINS complex subunit 2 (Psf2 homolog) [Source:HGNC Sym |
| 2 | 7037 | −0.93 | 1e−10 | 3e−08 | 47 x 50 | transferrin receptor [Source:HGNC Symbol;Acc:11763] |
| 3 | 81831 | −0.98 | 4e−10 | 4e−08 | 42 x 50 | neuropilin (NRP) and tolloid (TLL)−like 2 [Source:HGNC Sym |
| 4 | 1894 | −0.96 | 8e−10 | 1e−06 | 45 x 50 | epithelial cell transforming sequence 2 oncogene [Source:HG |
| 5 | 152002 | −0.88 | 2e−08 | 1e−06 | 48 x 50 | xyloside xylosyltransferase 1 [Source:HGNC Symbol;Acc:266 |
| 6 | 55839 | −0.88 | 2e−08 | 3e−06 | 44 x 50 | centromere protein N [Source:HGNC Symbol;Acc:30873] |
| 7 | 55689 | −0.85 | 5e−08 | 4e−06 | 46 x 50 | YEATS domain containing 2 [Source:HGNC Symbol;Acc:254 |
| 8 | 8318 | −0.83 | 1e−07 | 4e−06 | 45 x 49 | cell division cycle 45 [Source:HGNC Symbol;Acc:1739] |
| 9 | 54443 | −0.82 | 1e−07 | 4e−06 | 43 x 50 | anillin, actin binding protein [Source:HGNC Symbol;Acc:1408 |
| 10 | 10643 | −0.82 | 2e−07 | 2e−05 | 48 x 50 | insulin−like growth factor 2 mRNA binding protein 3 [Source: |
| 11 | 86 | −0.78 | 6e−07 | 2e−05 | 46 x 50 | actin−like 6A [Source:HGNC Symbol;Acc:24124] |
| 12 | 200810 | −0.78 | 7e−07 | 2e−05 | 49 x 50 | ALG1, chitobiosyldiphosphodolichol beta−mannosyltransfera |
| 13 | 9319 | −0.77 | 8e−07 | 2e−05 | 43 x 50 | thyroid hormone receptor interactor 13 [Source:HGNC Symb |
| 14 | 9787 | −0.77 | 9e−07 | 2e−05 | 43 x 50 | discs, large (Drosophila) homolog−associated protein 5 [Sour |
| 15 | 55165 | −0.77 | 9e−07 | 3e−05 | 44 x 50 | centrosomal protein 55kDa [Source:HGNC Symbol;Acc:1161 |
| 16 | 116832 | −0.76 | 1e−06 | 6e−05 | 46 x 50 | ribosomal protein L39−like [Source:HGNC Symbol;Acc:1709 |
| 17 | 28978 | −0.74 | 2e−06 | 6e−05 | 49 x 50 | transmembrane protein 14A [Source:HGNC Symbol;Acc:210 |
| 18 | 3992 | −0.73 | 3e−06 | 6e−05 | 45 x 50 | fatty acid desaturase 1 [Source:HGNC Symbol;Acc:3574] |
| 19 | 1033 | −0.72 | 4e−06 | 6e−05 | 43 x 50 | cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A |
| 20 | 51319 | −0.72 | 4e−06 | 6e−05 | 43 x 50 | arginine/serine−rich coiled−coil 1 [Source:HGNC Symbol;Acc |

**p−values**



## Local Geneset Analysis

*Underexpression*

| Rank | GSZ | p−value | #in/all | Geneset | |
|---|---|---|---|---|---|
| 1 | −51 | NULL | 87 / 142 | Glio | willscher_GBM_Verhaak−CL_expression_C_up |
| 2 | −51 | NULL | 87 / 142 | Glio | willscher_GBM_Verhaak−PNmut_expression_C_down |
| 3 | −25.49 | NULL | 15 / 16 | GSEA C2 | FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL |
| 4 | −24.27 | NULL | 97 / 370 | BP | mitotic cell cycle |
| 5 | −24.07 | NULL | 11 / 13 | GSEA C2 | CROONQUIST_IL6_DEPRIVATION_DN |
| 6 | −23.98 | NULL | 23 / 57 | Glio | developing astrocytes |
| 7 | −23.58 | NULL | 14 / 15 | GSEA C2 | FINETTI_BREAST_CANCER_KINOME_RED |
| 8 | −22.64 | NULL | 12 / 14 | MMML CGS | MACIEJ_MMML 4 |
| 9 | −22.45 | NULL | 92 / 530 | Cancer | Lembcke_Normal vs Adenoma |
| 10 | −21.14 | NULL | 13 / 16 | GSEA C2 | FARMER_BREAST_CANCER_CLUSTER_2 |
| 11 | −19.85 | NULL | 8 / 10 | GSEA C2 | MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP |
| 12 | −19.55 | NULL | 12 / 18 | BP | spindle organization |
| 13 | −19.46 | NULL | 9 / 15 | GSEA C2 | SMID_BREAST_CANCER_LUMINAL_A_DN |
| 14 | −19.35 | NULL | 10 / 14 | GSEA C2 | ZHAN_MULTIPLE_MYELOMA_PR_UP |
| 15 | −18.79 | NULL | 11 / 15 | Cancer | SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP |
| 16 | −18.69 | NULL | 8 / 14 | GSEA C2 | AMUNDSON_GAMMA_RADIATION_RESPONSE |
| 17 | −18.56 | NULL | 9 / 14 | GSEA C2 | ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER |
| 18 | −18.53 | NULL | 69 / 572 | Disease | GUDJ_psoriasis up |
| 19 | −18.42 | NULL | 9 / 15 | GSEA C2 | LEE_EARLY_T_LYMPHOCYTE_UP |
| 20 | −18.15 | NULL | 10 / 16 | GSEA C2 | KANG_DOXORUBICIN_RESISTANCE_UP |
| 21 | −17.94 | NULL | 10 / 16 | GSEA C2 | CROONQUIST_NRAS_SIGNALING_DN |
| 22 | −17.8 | NULL | 11 / 15 | Cancer | SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP |
| 23 | −17.63 | NULL | 12 / 16 | GSEA C2 | EGUCHI_CELL_CYCLE_RB1_TARGETS |
| 24 | −17.37 | NULL | 10 / 16 | GSEA C2 | REACTOME_G2_M_CHECKPOINTS |
| 25 | −16.81 | NULL | 8 / 15 | GSEA C2 | WU_APOPTOSIS_BY_CDKN1A_VIA_TP53 |
| 26 | −16.79 | NULL | 9 / 15 | GSEA C2 | FOURNIER_ACINAR_DEVELOPMENT_LATE_DN |
| 27 | −16.7 | NULL | 48 / 232 | BP | mitosis |
| 28 | −16.62 | NULL | 11 / 16 | Cancer | WOLFER_overlap genes |
| 29 | −16.41 | NULL | 7 / 11 | GSEA C2 | ODONNELL_TFRC_TARGETS_DN |
| 30 | −16.07 | NULL | 8 / 16 | GSEA C2 | REACTOME_DNA_STRAND_ELONGATION |
| 31 | −16 | NULL | 38 / 149 | BP | DNA replication |
| 32 | −15.8 | NULL | 8 / 15 | GSEA C2 | CHANG_CYCLING_GENES |
| 33 | −15.47 | NULL | 36 / 148 | BP | G1/S transition of mitotic cell cycle |
| 34 | −15.46 | NULL | 6 / 9 | GSEA C2 | REACTOME_CELL_CYCLE_CHECKPOINTS |
| 35 | −15.4 | NULL | 9 / 16 | GSEA C2 | GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN |
| 36 | −15.38 | NULL | 20 / 56 | CC | chromosome, centromeric region |
| 37 | −15.2 | NULL | 8 / 15 | GSEA C2 | ODONNELL_TARGETS_OF_MYC_AND_TFRC_DN |
| 38 | −15.03 | NULL | 7 / 16 | GSEA C2 | FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN |
| 39 | −14.81 | NULL | 8 / 15 | GSEA C2 | BOYAULT_LIVER_CANCER_SUBCLASS_G23_UP |
| 40 | −14.53 | NULL | 7 / 16 | GSEA C2 | BENPORATH_PROLIFERATION |

# GW_040

## Local Summary

%DE = 0.85

# metagenes = 1

# genes = 28

# genes in genesets = 28

# genes with fdr < 0.1  = 18  ( 1 + / 17  − )

# genes with fdr < 0.05  = 18  ( 1 + / 17  − )

# genes with fdr < 0.01 = 10  ( 1 + / 9  − )

<r> metagenes = NA

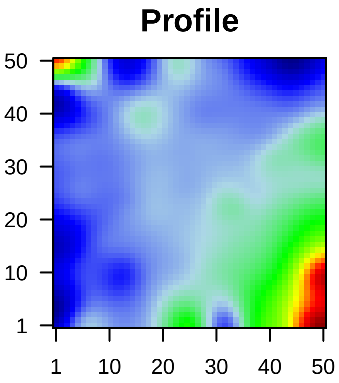
<r> genes = 0.31

<FC> = −0.33

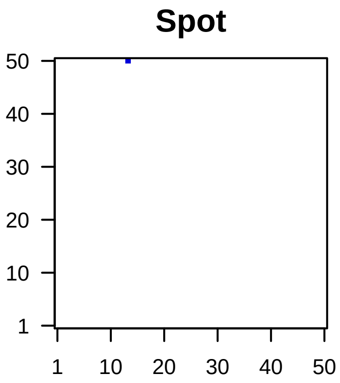
<shrinkage−t> = −11.59

<p−value> = 0.01

<fdr> = 0.58



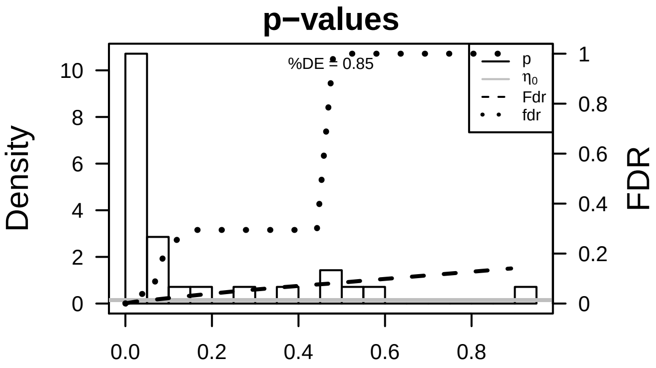
**Profile**



**Spot**

## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 5217 | −0.89 | 1e−08 | 1e−06 | 14 x 50 | profilin 2 [Source:HGNC Symbol;Acc:8882] |
| 2 | 57007 | −0.8 | 3e−07 | 1e−06 | 14 x 50 | atypical chemokine receptor 3 [Source:HGNC Symbol;Acc:23 |
| 3 | 100288413 | −0.78 | 5e−07 | 9e−05 | 14 x 50 | endogenous retrovirus group MER34, member 1 [Source:HG |
| 4 | 56666 | −0.66 | 2e−05 | 9e−05 | 14 x 50 | pannexin 2 [Source:HGNC Symbol;Acc:8600] |
| 5 | 386757 | −0.64 | 4e−05 | 7e−04 | 14 x 50 | solute carrier family 6 (neurotransmitter transporter), member |
| 6 | 2817 | −0.58 | 2e−04 | 2e−03 | 14 x 50 | glypican 1 [Source:HGNC Symbol;Acc:4449] |
| 7 | 1399 | −0.54 | 6e−04 | 5e−03 | 14 x 50 | v−crk avian sarcoma virus CT10 oncogene homolog−like [So |
| 8 | 200933 | −0.47 | 2e−03 | 5e−03 | 14 x 50 | F−box protein 45 [Source:HGNC Symbol;Acc:29148] |
| 9 | 5909 | 0.45 | 4e−03 | 5e−03 | 14 x 50 | RAP1 GTPase activating protein [Source:HGNC Symbol;Acc: |
| 10 | 7296 | −0.45 | 4e−03 | 7e−03 | 14 x 50 | thioredoxin reductase 1 [Source:HGNC Symbol;Acc:12437] |
| 11 | 9048 | −0.43 | 6e−03 | 3e−02 | 14 x 50 | artemin [Source:HGNC Symbol;Acc:727] |
| 12 | 23428 | −0.35 | 2e−02 | 3e−02 | 14 x 50 | solute carrier family 7 (amino acid transporter light chain, L sy |
| 13 | 9069 | −0.35 | 2e−02 | 3e−02 | 14 x 50 | claudin 12 [Source:HGNC Symbol;Acc:2034] |
| 14 | 1981 | −0.34 | 3e−02 | 4e−02 | 14 x 50 | eukaryotic translation initiation factor 4 gamma, 1 [Source:HG |
| 15 | 3005 | −0.32 | 4e−02 | 4e−02 | 14 x 50 | H1 histone family, member 0 [Source:HGNC Symbol;Acc:471 |
| 16 | 493861 | −0.3 | 6e−02 | 4e−02 | 14 x 50 | EP300 interacting inhibitor of differentiation 3 [Source:HGNC |
| 17 | 131408 | −0.29 | 6e−02 | 4e−02 | 14 x 50 | family with sequence similarity 131, member A [Source:HGN |
| 18 | 8323 | −0.28 | 7e−02 | 4e−02 | 14 x 50 | frizzled family receptor 6 [Source:HGNC Symbol;Acc:4044] |
| 19 | 4055 | −0.28 | 7e−02 | 1e−01 | 14 x 50 | lymphotoxin beta receptor (TNFR superfamily, member 3) [Sc |
| 20 | 3836 | −0.26 | 1e−01 | 2e−01 | 14 x 50 | karyopherin alpha 1 (importin alpha 5) [Source:HGNC Symbo |



**p−values**

## Local Geneset Analysis

*Underexpression*

| Rank | GSZ | p−value | #in/all | Geneset | |
|---|---|---|---|---|---|
| 1 | −16.8 | NULL | 1 / 6 | GSEA C2 | GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN |
| 2 | −14.98 | NULL | 1 / 12 | BP | negative regulation of intrinsic apoptotic signaling pathway in respo |
| 3 | −14.44 | NULL | 2 / 15 | miRNA target−starBase | hsa−miR−220a |
| 4 | −12.3 | NULL | 1 / 12 | MF | channel activity |
| 5 | −12.1 | NULL | 1 / 10 | BP | negative regulation of fibroblast growth factor receptor signaling pa |
| 6 | −11.72 | NULL | 1 / 13 | BP | response to ischemia |
| 7 | −11.4 | NULL | 2 / 41 | miRNA target−starBase | hsa−miR−525−3p |
| 8 | −11.23 | NULL | 2 / 11 | GSEA C2 | REACTOME_APOPTOSIS_INDUCED_DNA_FRAGMENTATION |
| 9 | −11.21 | NULL | 1 / 14 | GSEA C2 | NIKOLSKY_BREAST_CANCER_22Q13_AMPLICON |
| 10 | −11.11 | NULL | 2 / 56 | miRNA target−starBase | hsa−miR−151−3p |
| 11 | −10.82 | NULL | 1 / 12 | MF | heparan sulfate proteoglycan binding |
| 12 | −10.75 | NULL | 1 / 21 | BP | chemokine−mediated signaling pathway |
| 13 | −10.46 | NULL | 1 / 22 | MF | coreceptor activity |
| 14 | −9.85 | NULL | 1 / 14 | GSEA C2 | REACTOME_ACTIVATION_OF_RAC |
| 15 | −9.76 | NULL | 1 / 30 | miRNA 3UTR | GTGCA−346 |
| 16 | −9.58 | NULL | 1 / 31 | BP | positive regulation of actin filament polymerization |
| 17 | −9.41 | NULL | 1 / 32 | CC | terminal bouton |
| 18 | −9.2 | NULL | 4 / 147 | CC | endosome |
| 19 | −9.12 | NULL | 1 / 14 | GSEA C2 | BIOCARTA_PYK2_PATHWAY |
| 20 | −9.12 | NULL | 1 / 14 | GSEA C2 | ST_DIFFERENTIATION_PATHWAY_IN_PC12_CELLS |
| 21 | −9.12 | NULL | 1 / 14 | miRNA target−starBase | hsa−miR−452* |
| 22 | −8.95 | NULL | 1 / 7 | miRNA target−starBase | hsa−miR−611 |
| 23 | −8.92 | NULL | 1 / 29 | BP | receptor internalization |
| 24 | −8.82 | NULL | 1 / 21 | CC | gap junction |
| 25 | −8.75 | NULL | 1 / 15 | GSEA C2 | BIOCARTA_IL2RB_PATHWAY |
| 26 | −8.53 | NULL | 2 / 45 | miRNA 3UTR | TATC−488 |
| 27 | −8.42 | NULL | 1 / 16 | GSEA C2 | BIOCARTA_GLEEVEC_PATHWAY |
| 28 | −8.42 | NULL | 1 / 16 | GSEA C2 | REACTOME_DOWN_STREAM_SIGNAL_TRANSDUCTION |
| 29 | −8.22 | NULL | 1 / 19 | MF | laminin binding |
| 30 | −8 | NULL | 1 / 14 | GSEA C2 | GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_UP |
| 31 | −7.97 | NULL | 1 / 20 | MF | fibroblast growth factor binding |
| 32 | −7.72 | NULL | 4 / 155 | miRNA target−starBase | hsa−miR−802 |
| 33 | −7.62 | NULL | 1 / 13 | BP | induction of positive chemotaxis |
| 34 | −7.61 | NULL | 1 / 9 | miRNA target−starBase | hsa−miR−202* |
| 35 | −7.34 | NULL | 1 / 23 | BP | glycosaminoglycan catabolic process |
| 36 | −7.33 | NULL | 1 / 10 | MF | neutral amino acid transmembrane transporter activity |
| 37 | −7.12 | NULL | 1 / 43 | MF | scavenger receptor activity |
| 38 | −7.09 | NULL | 2 / 17 | MF | amino acid transmembrane transporter activity |
| 39 | −7.07 | NULL | 4 / 150 | miRNA target−starBase | hsa−miR−633 |
| 40 | −6.99 | NULL | 1 / 15 | Pathw Act | GUSTAFSON_PI3K_DN |