# GW_017

## Global Summary

%DE = 0.14

# genes with fdr < 0.2 = 1671 ( 1010 + / 661 − )

# genes with fdr < 0.1 = 1258 ( 795 + / 463 − )

# genes with fdr < 0.05 = 1060 ( 693 + / 367 − )

# genes with fdr < 0.01 = 713 ( 506 + / 207 − )

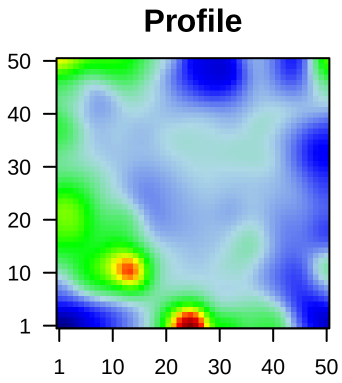
# genes in genesets = 16332

<FC> = 0

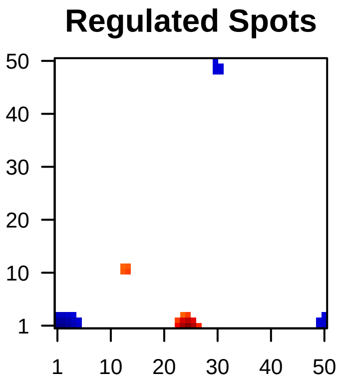
<shrinkage−t> = 0

<p−value> = 0.11

<fdr> = 0.86



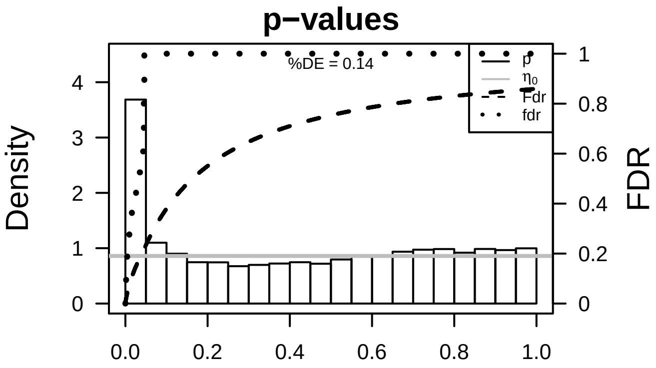
**Profile**



**Regulated Spots**

## Global Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 79852 | 1.47 | 2e−16 | 3e−14 | 3 x 50 | epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760] |
| 2 | 58 | 4.42 | 2e−16 | 3e−14 | 25 x 1 | actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12 |
| 3 | 70 | 2.84 | 2e−16 | 3e−14 | 25 x 1 | actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14 |
| 4 | 124 | 1.32 | 2e−16 | 3e−14 | 50 x 11 | alcohol dehydrogenase 1A (class I), alpha polypeptide [Sourc |
| 5 | 57016 | 2.09 | 2e−16 | 3e−14 | 1 x 50 | aldo−keto reductase family 1, member B10 (aldose reductase |
| 6 | 441282 | 2.14 | 2e−16 | 3e−14 | 1 x 49 | aldo−keto reductase family 1, member B15 [Source:HGNC S |
| 7 | 8644 | 1.67 | 2e−16 | 3e−14 | 1 x 50 | aldo−keto reductase family 1, member C3 [Source:HGNC Sy |
| 8 | 1109 | 2.25 | 2e−16 | 3e−14 | 13 x 50 | aldo−keto reductase family 1, member C4 [Source:HGNC Sy |
| 9 | 218 | 2.41 | 2e−16 | 3e−14 | 1 x 50 | aldehyde dehydrogenase 3 family, member A1 [Source:HGN |
| 10 | 655 | 1.36 | 2e−16 | 3e−14 | 50 x 50 | bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:1 |
| 11 | 664 | −1.35 | 2e−16 | 3e−14 | 2 x 43 | BCL2/adenovirus E1B 19kDa interacting protein 3 [Source:H |
| 12 | 10974 | 1.63 | 2e−16 | 3e−14 | 5 x 50 | adipogenesis regulatory factor [Source:HGNC Symbol;Acc:2 |
| 13 | 387695 | 2.01 | 2e−16 | 3e−14 | 1 x 49 | chromosome 10 open reading frame 99 [Source:HGNC Sym |
| 14 | 339512 | 2.25 | 2e−16 | 3e−14 | 50 x 50 | chromosome 1 open reading frame 110 [Source:HGNC Sym |
| 15 | 92747 | 1.65 | 2e−16 | 3e−14 | 50 x 10 | BPI fold containing family B, member 1 [Source:HGNC Symb |
| 16 | 260436 | −1.48 | 2e−16 | 3e−14 | 50 x 1 | follicular dendritic cell secreted protein [Source:HGNC Symb |
| 17 | 810 | 1.33 | 2e−16 | 3e−14 | 1 x 50 | calmodulin−like 3 [Source:HGNC Symbol;Acc:1452] |
| 18 | 51806 | 1.52 | 2e−16 | 3e−14 | 4 x 50 | calmodulin−like 5 [Source:HGNC Symbol;Acc:18180] |
| 19 | 6364 | −1.48 | 2e−16 | 3e−14 | 46 x 1 | chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc |
| 20 | 948 | 1.81 | 2e−16 | 3e−14 | 6 x 44 | CD36 molecule (thrombospondin receptor) [Source:HGNC Sy |



**p−values**

## Global Geneset Analysis

| Rank | GSZ | p−value | #all | Geneset | |
|---|---|---|---|---|---|
| *Overexpressed* | | | | | |
| 1 | 23.64 | NULL | 127 | H.Tiss | WIRTH_Muscle |
| 2 | 20.28 | NULL | 36 | BP | muscle filament sliding |
| 3 | 19.14 | NULL | 16 | GSEA C2 | RICKMAN_HEAD_AND_NECK_CANCER_F |
| 4 | 18.99 | NULL | 16 | H.Tiss | WIRTH_Hippocampus |
| 5 | 16.13 | NULL | 44 | MF | structural constituent of muscle |
| 6 | 12.73 | NULL | 12 | CC | myosin filament |
| 7 | 12.38 | NULL | 918 | Chr | Chr 17 |
| 8 | 12.1 | NULL | 135 | H.Tiss | WIRTH_Mucosa |
| 9 | 10.87 | NULL | 84 | BP | muscle contraction |
| 10 | 10.46 | NULL | 37 | CC | sarcomere |
| 11 | 10.3 | NULL | 13 | CC | muscle myosin complex |
| 12 | 9.98 | NULL | 34 | CC | myofibril |
| 13 | 9.32 | NULL | 37 | BP | cardiac muscle contraction |
| 14 | 9.26 | NULL | 14 | CC | contractile fiber |
| 15 | 8.26 | NULL | 88 | CC | Z disc |
| 16 | 8.03 | NULL | 11 | MF | glutathione binding |
| 17 | 7.97 | NULL | 16 | CC | M band |
| 18 | 7.69 | NULL | 8 | GSEA C2 | LIU_CDX2_TARGETS_DN |
| 19 | 7.68 | NULL | 12 | BP | skeletal muscle contraction |
| 20 | 7.54 | NULL | 20 | CC | I band |
| *Underexpressed* | | | | | |
| 1 | −8.65 | NULL | 633 | Chr | Chr 9 |
| 2 | −7.82 | NULL | 699 | Chr | Chr 5 |
| 3 | −7.29 | NULL | 250 | Lymphoma | LENZ_Stromal signature 1 |
| 4 | −7.22 | NULL | 280 | Chr | Chr 13 |
| 5 | −6.99 | NULL | 87 | BP | translational termination |
| 6 | −6.87 | NULL | 115 | BP | nuclear−transcribed mRNA catabolic process, nonsense−mediated |
| 7 | −6.83 | NULL | 81 | BP | viral transcription |
| 8 | −6.79 | NULL | 109 | BP | SRP−dependent cotranslational protein targeting to membrane |
| 9 | −6.73 | NULL | 265 | Glio | willscher_GBM_Verhaak−CL_expression_B_up |
| 10 | −6.73 | NULL | 265 | Glio | willscher_GBM_Verhaak−MES_expression_B_up |
| 11 | −6.73 | NULL | 265 | Glio | willscher_GBM_Verhaak−PNwt_expression_B_down |
| 12 | −6.73 | NULL | 265 | Glio | willscher_GBM_Verhaak−PNmut_expression_B_down |
| 13 | −6.58 | NULL | 8 | GSEA C2 | RUNNE_GENDER_EFFECT_UP |
| 14 | −6.36 | NULL | 92 | BP | viral life cycle |
| 15 | −6.26 | NULL | 321 | miRNA target−starBase | hsa−miR−548a−5p |
| 16 | −6.23 | NULL | 302 | miRNA target−starBase | hsa−miR−548i |
| 17 | −6.18 | NULL | 7 | MMML CGS | MACIEJ_MMML 5 |
| 18 | −6.18 | NULL | 336 | miRNA target−starBase | hsa−miR−548b−5p |
| 19 | −6.17 | NULL | 436 | miRNA target−starBase | hsa−miR−548n |
| 20 | −6.17 | NULL | 553 | Cancer | Lembcke_Colonic Inflammation |

# GW_017

## Local Summary

%DE = 0.94

# metagenes = 11

# genes = 104

# genes in genesets = 104

# genes with fdr < 0.1  = 89  ( 89 + / 0  − )

# genes with fdr < 0.05  = 86  ( 86 + / 0  − )

# genes with fdr < 0.01 = 83  ( 83 + / 0  − )

<r> metagenes = 0.99

<r> genes = 0.64

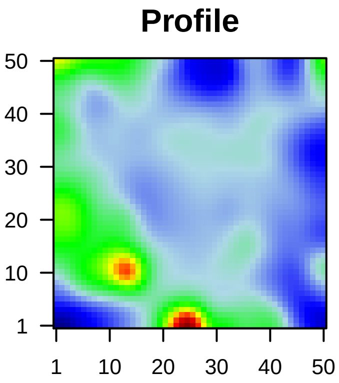
<FC> = 1

<shrinkage−t> = 35.08

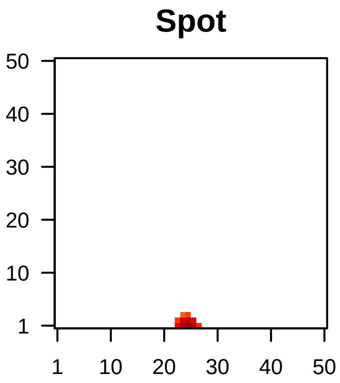
<p−value> = 0

<fdr> = 0.22

### Profile



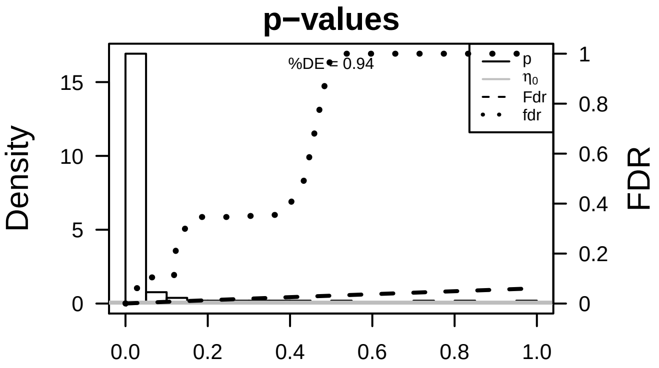
### Spot



## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 58 | 4.42 | 2e−16 | 5e−17 | 25 x 1 | actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12 |
| 2 | 70 | 2.84 | 2e−16 | 5e−17 | 25 x 1 | actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14 |
| 3 | 1158 | 2.93 | 2e−16 | 5e−17 | 25 x 1 | creatine kinase, muscle [Source:HGNC Symbol;Acc:1994] |
| 4 | 202333 | 1.53 | 2e−16 | 5e−17 | 25 x 1 | cardiomyopathy associated 5 [Source:HGNC Symbol;Acc:14 |
| 5 | 23109 | 1.32 | 2e−16 | 5e−17 | 25 x 1 | dendrin [Source:HGNC Symbol;Acc:24458] |
| 6 | 2027 | 1.46 | 2e−16 | 5e−17 | 25 x 1 | enolase 3 (beta, muscle) [Source:HGNC Symbol;Acc:3354] |
| 7 | 2273 | 1.45 | 2e−16 | 5e−17 | 25 x 1 | four and a half LIM domains 1 [Source:HGNC Symbol;Acc:37 |
| 8 | 2318 | 1.6 | 2e−16 | 5e−17 | 25 x 1 | filamin C, gamma [Source:HGNC Symbol;Acc:3756] |
| 9 | 283120 | 2.56 | 2e−16 | 5e−17 | 25 x 1 | H19, imprinted maternally expressed transcript (non−protein |
| 10 | 10324 | 2.24 | 2e−16 | 5e−17 | 25 x 1 | kelch−like family member 41 [Source:HGNC Symbol;Acc:169 |
| 11 | 4151 | 2.39 | 2e−16 | 5e−17 | 25 x 1 | myoglobin [Source:HGNC Symbol;Acc:6915] |
| 12 | 4604 | 1.4 | 2e−16 | 5e−17 | 25 x 1 | myosin binding protein C, slow type [Source:HGNC Symbol;A |
| 13 | 4606 | 1.6 | 2e−16 | 5e−17 | 25 x 1 | myosin binding protein C, fast type [Source:HGNC Symbol;A |
| 14 | 4608 | 1.61 | 2e−16 | 5e−17 | 25 x 1 | myosin binding protein H [Source:HGNC Symbol;Acc:7552] |
| 15 | 4619 | 1.6 | 2e−16 | 5e−17 | 25 x 1 | myosin, heavy chain 1, skeletal muscle, adult [Source:HGNC |
| 16 | 4620 | 3.18 | 2e−16 | 5e−17 | 25 x 1 | myosin, heavy chain 2, skeletal muscle, adult [Source:HGNC |
| 17 | 4625 | 1.57 | 2e−16 | 5e−17 | 25 x 1 | myosin, heavy chain 7, cardiac muscle, beta [Source:HGNC |
| 18 | 4632 | 1.86 | 2e−16 | 5e−17 | 25 x 1 | myosin, light chain 1, alkali; skeletal, fast [Source:HGNC Sym |
| 19 | 4633 | 2.11 | 2e−16 | 5e−17 | 25 x 1 | myosin, light chain 2, regulatory, cardiac, slow [Source:HGNC |
| 20 | 29895 | 1.67 | 2e−16 | 5e−17 | 25 x 1 | myosin light chain, phosphorylatable, fast skeletal muscle [So |

### p−values



## Local Geneset Analysis

*Overexpression*

| Rank | GSZ | p−value | #in/all | Geneset | |
|---|---|---|---|---|---|
| 1 | 63.9 | NULL | 23 / 36 | BP | muscle filament sliding |
| 2 | 63.27 | NULL | 57 / 127 | H.Tiss | WIRTH_Muscle |
| 3 | 60.34 | NULL | 11 / 16 | H.Tiss | WIRTH_Hippocampus |
| 4 | 59.49 | NULL | 11 / 16 | GSEA C2 | RICKMAN_HEAD_AND_NECK_CANCER_F |
| 5 | 46.11 | NULL | 22 / 44 | MF | structural constituent of muscle |
| 6 | 43.94 | NULL | 10 / 12 | CC | myosin filament |
| 7 | 35.55 | NULL | 8 / 13 | CC | muscle myosin complex |
| 8 | 35.13 | NULL | 12 / 37 | CC | sarcomere |
| 9 | 31.04 | NULL | 23 / 84 | BP | muscle contraction |
| 10 | 31.03 | NULL | 8 / 14 | CC | contractile fiber |
| 11 | 29.39 | NULL | 15 / 34 | CC | myofibril |
| 12 | 25.94 | NULL | 5 / 11 | BP | cardiac muscle tissue morphogenesis |
| 13 | 25.46 | NULL | 6 / 12 | BP | skeletal muscle contraction |
| 14 | 24.98 | NULL | 9 / 37 | BP | cardiac muscle contraction |
| 15 | 24.79 | NULL | 9 / 20 | CC | I band |
| 16 | 23.4 | NULL | 8 / 16 | CC | M band |
| 17 | 23.1 | NULL | 2 / 6 | GSEA C2 | BIOCARTA_HSP27_PATHWAY |
| 18 | 22.71 | NULL | 7 / 12 | MF | titin binding |
| 19 | 22.43 | NULL | 21 / 88 | CC | Z disc |
| 20 | 21.69 | NULL | 3 / 15 | Cancer | BEN−PORATH_UP |
| 21 | 20.64 | NULL | 4 / 11 | CC | A band |
| 22 | 19.34 | NULL | 7 / 15 | GSEA C2 | REACTOME_STRIATED_MUSCLE_CONTRACTION |
| 23 | 18.1 | NULL | 6 / 18 | BP | regulation of muscle contraction |
| 24 | 17.71 | NULL | 2 / 10 | BP | heart contraction |
| 25 | 17.7 | NULL | 8 / 42 | CC | myosin complex |
| 26 | 17.27 | NULL | 2 / 20 | MF | myosin binding |
| 27 | 17.15 | NULL | 7 / 15 | BP | striated muscle contraction |
| 28 | 16.87 | NULL | 1 / 9 | GSEA C2 | PENG_GLUCOSE_DEPRIVATION_UP |
| 29 | 16.87 | NULL | 1 / 9 | GSEA C2 | PENG_GLUCOSE_DEPRIVATION_DN |
| 30 | 16.41 | NULL | 4 / 16 | MF | microfilament motor activity |
| 31 | 15.8 | NULL | 1 / 5 | GSEA C2 | LIU_VAV3_PROSTATE_CARCINOGENESIS_UP |
| 32 | 15.8 | NULL | 1 / 10 | GSEA C2 | BIOCARTA_EPHA4_PATHWAY |
| 33 | 15.54 | NULL | 2 / 14 | GSEA C2 | BIOCARTA_UCALPAIN_PATHWAY |
| 34 | 15.11 | NULL | 25 / 297 | MF | actin binding |
| 35 | 14.91 | NULL | 2 / 15 | GSEA C2 | BIOCARTA_INTEGRIN_PATHWAY |
| 36 | 14.77 | NULL | 3 / 13 | CC | pseudopodium |
| 37 | 14.42 | NULL | 2 / 16 | GSEA C2 | SASSON_RESPONSE_TO_GONADOTROPHINS_DN |
| 38 | 14.42 | NULL | 2 / 16 | GSEA C2 | SASSON_RESPONSE_TO_FORSKOLIN_DN |
| 39 | 14.13 | NULL | 1 / 12 | GSEA C2 | BIOCARTA_NO1_PATHWAY |
| 40 | 14.13 | NULL | 1 / 12 | GSEA C2 | BIOCARTA_RAB_PATHWAY |

# GW_017

## Local Summary

%DE = 0.93

# metagenes = 4

# genes = 35

# genes in genesets = 20

# genes with fdr < 0.1 = 25 ( 24 + / 1 − )

# genes with fdr < 0.05 = 25 ( 24 + / 1 − )

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

<r> metagenes = 0.99

<r> genes = 0.57

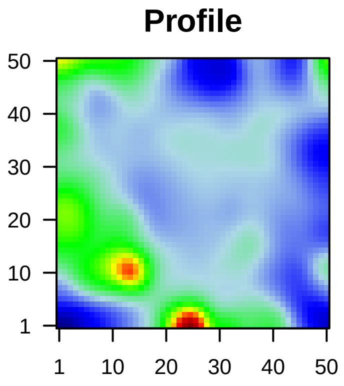
<FC> = 1.39

<shrinkage−t> = 48.68

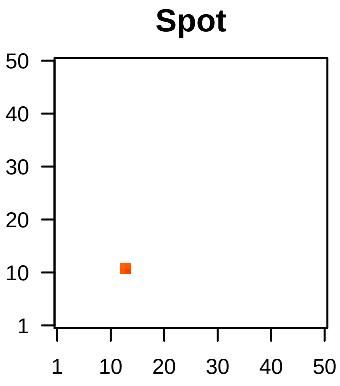
<p−value> = 0

<fdr> = 0.27

**Profile**



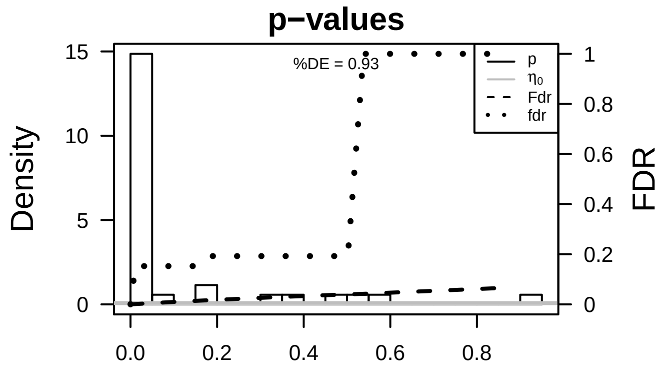
**Spot**



## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 729428 | 3.01 | 2e−16 | 3e−17 | 14 x 11 | G antigen 12C [Source:HGNC Symbol;Acc:28402] |
| 2 | 729422 | 3.2 | 2e−16 | 3e−17 | 14 x 11 | G antigen 12J [Source:HGNC Symbol;Acc:17778] |
| 3 | 100132399 | 1.35 | 2e−16 | 3e−17 | 14 x 11 | G antigen 12J [Source:HGNC Symbol;Acc:17778] |
| 4 | 100008586 | 2.64 | 2e−16 | 3e−17 | 14 x 11 | G antigen 12J [Source:HGNC Symbol;Acc:17778] |
| 5 | 645073 | 2.55 | 2e−16 | 3e−17 | 14 x 11 | G antigen 12J [Source:HGNC Symbol;Acc:17778] |
| 6 | 729442 | 3 | 2e−16 | 3e−17 | 14 x 11 | G antigen 12J [Source:HGNC Symbol;Acc:17778] |
| 7 | 26748 | 3.17 | 2e−16 | 3e−17 | 14 x 11 | G antigen 12I [Source:HGNC Symbol;Acc:4105] |
| 8 | 729396 | 1.81 | 2e−16 | 3e−17 | 14 x 11 | G antigen 12J [Source:HGNC Symbol;Acc:17778] |
| 9 | 729447 | 2.24 | 2e−16 | 3e−17 | 14 x 11 | G antigen 2A [Source:HGNC Symbol;Acc:4099] |
| 10 | 645037 | 3.13 | 2e−16 | 3e−17 | 14 x 11 | G antigen 2C [Source:HGNC Symbol;Acc:31958] |
| 11 | 26749 | 2.4 | 2e−16 | 3e−17 | 14 x 11 | G antigen 2E [Source:HGNC Symbol;Acc:31960] |
| 12 | 2576 | 2.69 | 2e−16 | 3e−17 | 14 x 11 | G antigen 12J [Source:HGNC Symbol;Acc:17778] |
| 13 | 2577 | 3.1 | 2e−16 | 3e−17 | 14 x 11 | G antigen 12J [Source:HGNC Symbol;Acc:17778] |
| 14 | 2578 | 1.6 | 2e−16 | 3e−17 | 14 x 11 | G antigen 12J [Source:HGNC Symbol;Acc:17778] |
| 15 | 2579 | 3.05 | 2e−16 | 3e−17 | 14 x 11 | G antigen 12I [Source:HGNC Symbol;Acc:4105] |
| 16 | 100101629 | 1.83 | 2e−16 | 3e−17 | 14 x 11 | G antigen 2E [Source:HGNC Symbol;Acc:31960] |
| 17 | 121355 | 1.61 | 2e−16 | 3e−17 | 14 x 11 | gametocyte specific factor 1 [Source:HGNC Symbol;Acc:265 |
| 18 | 24150 | 1.24 | 6e−15 | 7e−13 | 14 x 11 | TP53 target 3D [Source:HGNC Symbol;Acc:44657] |
| 19 | 729431 | 1.16 | 3e−13 | 2e−10 | 14 x 11 | G antigen 12J [Source:HGNC Symbol;Acc:17778] |
| 20 | 26609 | 1.04 | 7e−11 | 3e−09 | 13 x 11 | variable charge, X−linked [Source:HGNC Symbol;Acc:12667] |

**p−values**



## Local Geneset Analysis

*Overexpression*

| Rank | GSZ | p−value | #in/all | Geneset | |
|---|---|---|---|---|---|
| 1 | 27.42 | NULL | 1 / 12 | GSEA C2 | RAY_TARGETS_OF_P210_BCR_ABL_FUSION_UP |
| 2 | 17.14 | NULL | 1 / 5 | GSEA C2 | CHOI_ATL_ACUTE_STAGE |
| 3 | 13.66 | NULL | 16 / 630 | Chr | Chr X |
| 4 | 6.4 | NULL | 1 / 16 | GSEA C2 | ROZANOV_MMP14_TARGETS_DN |
| 5 | 5.74 | NULL | 1 / 21 | BP | chromatin organization |
| 6 | 4.89 | NULL | 3 / 419 | CC | cellular_component |
| 7 | 4.48 | NULL | 3 / 481 | BP | biological_process |
| 8 | 4.4 | NULL | 2 / 15 | GSEA C2 | MATTIOLI_MULTIPLE_MYELOMA_SUBGROUPS |
| 9 | 4.21 | NULL | 1 / 10 | GSEA C2 | TSUNODA_CISPLATIN_RESISTANCE_DN |
| 10 | 4.11 | NULL | 3 / 549 | MF | molecular_function |
| 11 | 2.87 | NULL | 1 / 15 | GSEA C2 | LOPEZ_MBD_TARGETS_IMPRINTED_AND_X_LINKED |
| 12 | 2.87 | NULL | 1 / 15 | GSEA C2 | ALONSO_METASTASIS_NEURAL_UP |
| 13 | 2.81 | NULL | 1 / 120 | H.Tiss | WIRTH_Testis |
| 14 | 2.72 | NULL | 1 / 16 | GSEA C2 | JAEGER_METASTASIS_UP |
| 15 | 2.35 | NULL | 1 / 68 | CC | collagen |
| 16 | 2.12 | NULL | 1 / 79 | MF | serine−type endopeptidase inhibitor activity |
| 17 | 2.05 | NULL | 1 / 83 | CC | basement membrane |
| 18 | 1.84 | NULL | 2 / 48 | Cancer | KUIPER_MM poor survival |
| 19 | 1.8 | NULL | 3 / 579 | CC | nucleolus |
| 20 | 1.3 | NULL | 1 / 16 | GSEA C2 | SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN |
| 21 | 1.3 | NULL | 1 / 153 | CC | endoplasmic reticulum lumen |
| 22 | 1.05 | NULL | 1 / 188 | BP | brain development |
| 23 | 0.86 | NULL | 1 / 242 | BP | extracellular matrix organization |
| 24 | 0.83 | NULL | 1 / 11 | GSEA C2 | SU_PLACENTA |
| 25 | 0.71 | NULL | 1 / 318 | MF | chromatin binding |
| 26 | 0.64 | NULL | 1 / 14 | GSEA C2 | NIELSEN_GIST |
| 27 | 0.59 | NULL | 1 / 15 | GSEA C2 | BROWNE_HCMV_INFECTION_8HR_DN |
| 28 | 0.55 | NULL | 2 / 259 | BP | spermatogenesis |
| 29 | 0.45 | NULL | 1 / 403 | BP | cell adhesion |
| 30 | 0.33 | NULL | 1 / 866 | Chr | Chr 12 |
| 31 | 0.23 | NULL | 1 / 717 | Chr | Chr 16 |
| 32 | 0 | NULL | 1 / 743 | Chr | Chr 7 |
| 33 | −0.14 | NULL | 0 / 10 | MF | 1−acylglycerol−3−phosphate O−acyltransferase activity |
| 34 | −0.14 | NULL | 0 / 10 | MF | 3−beta−hydroxy−delta5−steroid dehydrogenase activity |
| 35 | −0.14 | NULL | 0 / 10 | MF | acetyltransferase activity |
| 36 | −0.14 | NULL | 0 / 10 | MF | acid phosphatase activity |
| 37 | −0.14 | NULL | 0 / 10 | CC | acrosomal membrane |
| 38 | −0.14 | NULL | 0 / 10 | BP | acrosome reaction |
| 39 | −0.14 | NULL | 0 / 10 | BP | actin polymerization or depolymerization |
| 40 | −0.14 | NULL | 0 / 10 | MF | adenylate cyclase activity |

# GW_017

## Local Summary

%DE = 0.75

# metagenes = 14

# genes = 220

# genes in genesets = 219

# genes with fdr < 0.1 = 148 ( 21 + / 127 − )

# genes with fdr < 0.05 = 105 ( 15 + / 90 − )

# genes with fdr < 0.01 = 87 ( 12 + / 75 − )

<r> metagenes = 0.97

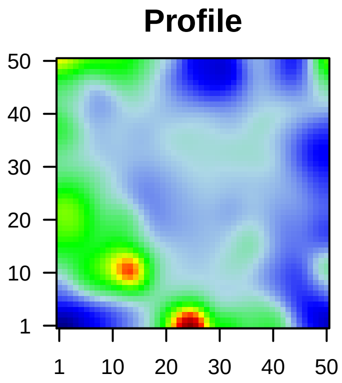
<r> genes = 0.43

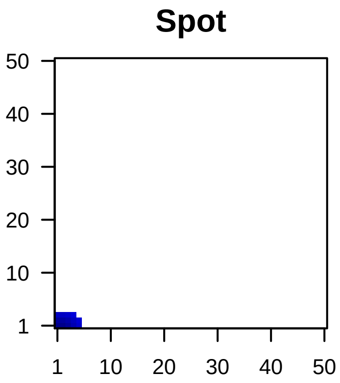
<FC> = −0.3

<shrinkage−t> = −10.43

<p−value> = 0

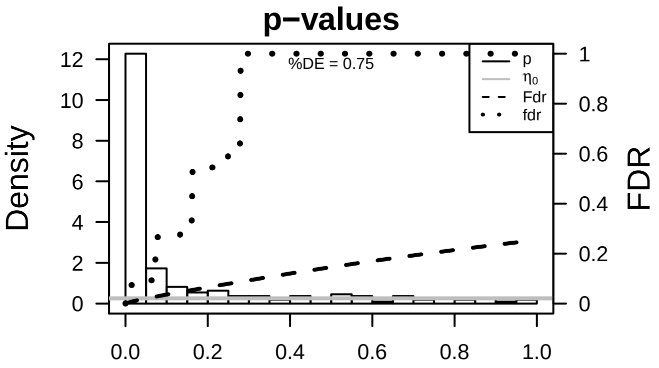
<fdr> = 0.48





## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 4060 | 2.02 | 2e−16 | 4e−15 | 2 x 1 | lumican [Source:HGNC Symbol;Acc:6724] |
| 2 | 10630 | −1.6 | 2e−16 | 4e−15 | 1 x 2 | podoplanin [Source:HGNC Symbol;Acc:29602] |
| 3 | 6696 | −1.31 | 2e−16 | 4e−15 | 2 x 1 | secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:1125 |
| 4 | 3956 | −1.26 | 3e−15 | 9e−13 | 1 x 1 | lectin, galactoside−binding, soluble, 1 [Source:HGNC Symbol |
| 5 | 1289 | −1.22 | 2e−14 | 2e−12 | 2 x 1 | collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209] |
| 6 | 1634 | 1.19 | 8e−14 | 2e−12 | 4 x 1 | decorin [Source:HGNC Symbol;Acc:2705] |
| 7 | 55714 | −1.19 | 8e−14 | 9e−12 | 1 x 1 | teneurin transmembrane protein 3 [Source:HGNC Symbol;Ac |
| 8 | 25878 | −1.17 | 2e−13 | 2e−11 | 3 x 1 | matrix−remodelling associated 5 [Source:HGNC Symbol;Acc: |
| 9 | 1009 | −1.15 | 6e−13 | 1e−09 | 3 x 1 | cadherin 11, type 2, OB−cadherin (osteoblast) [Source:HGN |
| 10 | 7057 | −1.07 | 2e−11 | 2e−09 | 1 x 1 | thrombospondin 1 [Source:HGNC Symbol;Acc:11785] |
| 11 | 633 | −0.96 | 7e−11 | 2e−09 | 3 x 1 | biglycan [Source:HGNC Symbol;Acc:1044] |
| 12 | 10409 | −1.04 | 8e−11 | 6e−09 | 1 x 2 | brain abundant, membrane attached signal protein 1 [Source: |
| 13 | 91663 | −1.02 | 2e−10 | 3e−08 | 2 x 1 | myeloid−associated differentiation marker [Source:HGNC Sy |
| 14 | 6423 | −0.97 | 1e−09 | 3e−08 | 3 x 1 | secreted frizzled−related protein 2 [Source:HGNC Symbol;Ac |
| 15 | 4320 | −0.97 | 1e−09 | 3e−08 | 3 x 1 | matrix metallopeptidase 11 (stromelysin 3) [Source:HGNC Sy |
| 16 | 6515 | −0.96 | 2e−09 | 3e−08 | 3 x 1 | solute carrier family 2 (facilitated glucose transporter), membe |
| 17 | 1293 | −0.95 | 2e−09 | 7e−08 | 2 x 1 | collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213] |
| 18 | 388 | 0.94 | 4e−09 | 2e−07 | 2 x 3 | ras homolog family member B [Source:HGNC Symbol;Acc:66 |
| 19 | 11031 | 0.93 | 6e−09 | 3e−07 | 1 x 3 | RAB31, member RAS oncogene family [Source:HGNC Symb |
| 20 | 1278 | −0.91 | 1e−08 | 9e−07 | 2 x 1 | collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198] |



## Local Geneset Analysis

*Underexpression*

| Rank | GSZ | p−value | #in/all | Geneset | |
|---|---|---|---|---|---|
| 1 | −27.51 | NULL | 12 / 16 | GSEA C2 | FARMER_BREAST_CANCER_CLUSTER_5 |
| 2 | −22.84 | NULL | 8 / 11 | MF | platelet−derived growth factor binding |
| 3 | −22.69 | NULL | 67 / 250 | Lymphoma | LENZ_Stromal signature 1 |
| 4 | −21 | NULL | 5 / 11 | MMML CGS | MACIEJ_MMML 31 |
| 5 | −20.93 | NULL | 62 / 190 | CC | extracellular matrix |
| 6 | −19.65 | NULL | 6 / 13 | GSEA C2 | TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR |
| 7 | −19.63 | NULL | 5 / 10 | GSEA C2 | KEGG_ECM_RECEPTOR_INTERACTION |
| 8 | −19.44 | NULL | 60 / 242 | BP | extracellular matrix organization |
| 9 | −19.43 | NULL | 11 / 19 | MF | extracellular matrix binding |
| 10 | −19.17 | NULL | 30 / 69 | BP | extracellular matrix disassembly |
| 11 | −18.53 | NULL | 7 / 16 | GSEA C2 | TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_ |
| 12 | −17.97 | NULL | 27 / 64 | BP | collagen catabolic process |
| 13 | −16.86 | NULL | 5 / 16 | GSEA C2 | LU_TUMOR_VASCULATURE_UP |
| 14 | −16.03 | NULL | 6 / 15 | GSEA C2 | VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP |
| 15 | −15.91 | NULL | 4 / 11 | GSEA C2 | ITO_PTTG1_TARGETS_UP |
| 16 | −15.72 | NULL | 11 / 15 | GSEA C2 | CROMER_TUMORIGENESIS_UP |
| 17 | −15.43 | NULL | 10 / 15 | GSEA C2 | ONDER_CDH1_TARGETS_2_UP |
| 18 | −15.22 | NULL | 12 / 68 | Glio | cultured astroglia vs. in vivo astrocytes |
| 19 | −15.14 | NULL | 5 / 16 | GSEA C2 | REACTOME_SIGNALING_BY_PDGF |
| 20 | −14.88 | NULL | 5 / 16 | GSEA C2 | URS_ADIPOCYTE_DIFFERENTIATION_DN |
| 21 | −14.85 | NULL | 37 / 265 | Glio | willscher_GBM_Verhaak−CL_expression_B_up |
| 22 | −14.85 | NULL | 37 / 265 | Glio | willscher_GBM_Verhaak−MES_expression_B_up |
| 23 | −14.85 | NULL | 37 / 265 | Glio | willscher_GBM_Verhaak−PNwt_expression_B_down |
| 24 | −14.85 | NULL | 37 / 265 | Glio | willscher_GBM_Verhaak−PNmut_expression_B_down |
| 25 | −14.33 | NULL | 6 / 16 | GSEA C2 | LIEN_BREAST_CARCINOMA_METAPLASTIC |
| 26 | −14.3 | NULL | 5 / 15 | GSEA C2 | TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_NO |
| 27 | −14.26 | NULL | 4 / 13 | GSEA C2 | BRUECKNER_TARGETS_OF_MIRLET7A3_DN |
| 28 | −14.11 | NULL | 3 / 6 | GSEA C2 | NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP |
| 29 | −14.09 | NULL | 8 / 12 | miRNA target | miR−29c |
| 30 | −14 | NULL | 12 / 35 | Glio | Colman_survival_associated |
| 31 | −13.75 | NULL | 5 / 10 | GSEA C2 | SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP |
| 32 | −13.48 | NULL | 6 / 15 | GSEA C2 | MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INH |
| 33 | −13.27 | NULL | 4 / 15 | GSEA C2 | WANG_SMARCE1_TARGETS_UP |
| 34 | −13.08 | NULL | 5 / 15 | GSEA C2 | CHANG_POU5F1_TARGETS_UP |
| 35 | −12.99 | NULL | 14 / 16 | MMML CGS | MACIEJ_MMML 1 |
| 36 | −12.71 | NULL | 4 / 15 | GSEA C2 | KIM_WT1_TARGETS_12HR_DN |
| 37 | −12.65 | NULL | 7 / 16 | GSEA C2 | ROZANOV_MMP14_TARGETS_SUBSET |
| 38 | −12.36 | NULL | 19 / 57 | MF | extracellular matrix structural constituent |
| 39 | −12.27 | NULL | 7 / 31 | BP | positive regulation of cell−substrate adhesion |
| 40 | −12.27 | NULL | 7 / 28 | BP | odontogenesis |

# GW_017

## Local Summary

%DE = 0.76

# metagenes = 5

# genes = 153

# genes in genesets = 152

# genes with fdr < 0.1 = 76 ( 8 + / 68 − )

# genes with fdr < 0.05 = 62 ( 7 + / 55 − )

# genes with fdr < 0.01 = 37 ( 4 + / 33 − )

<r> metagenes = 1

<r> genes = 0.65

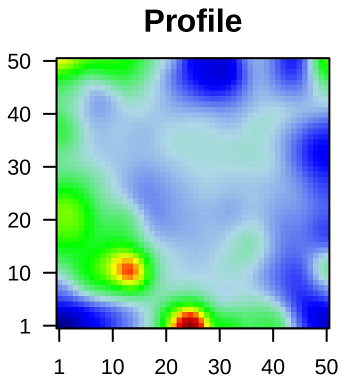
<FC> = −0.27

<shrinkage−t> = −9.5

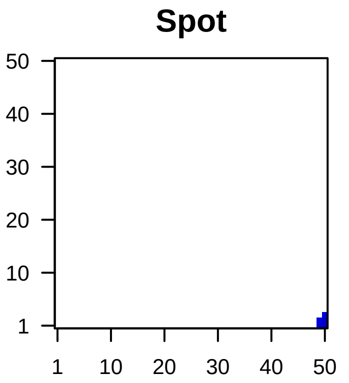
<p−value> = 0.01

<fdr> = 0.61

**Profile**



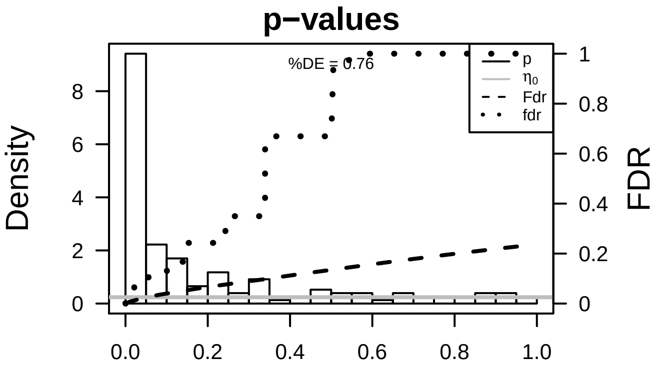
**Spot**



## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 260436 | −1.48 | 2e−16 | 8e−15 | 50 x 1 | follicular dendritic cell secreted protein [Source:HGNC Symbo |
| 2 | 3128 | −1.05 | 4e−11 | 3e−09 | 50 x 1 | major histocompatibility complex, class II, DR beta 6 (pseudo |
| 3 | 3543 | 0.94 | 1e−10 | 1e−06 | 49 x 1 | immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy |
| 4 | 5341 | −0.87 | 4e−08 | 1e−06 | 50 x 1 | pleckstrin [Source:HGNC Symbol;Acc:9070] |
| 5 | 9308 | −0.86 | 7e−08 | 2e−06 | 50 x 3 | CD83 molecule [Source:HGNC Symbol;Acc:1703] |
| 6 | 348 | −0.84 | 1e−07 | 3e−06 | 50 x 1 | apolipoprotein E [Source:HGNC Symbol;Acc:613] |
| 7 | 23180 | −0.83 | 2e−07 | 5e−05 | 50 x 1 | raftlin, lipid raft linker 1 [Source:HGNC Symbol;Acc:30278] |
| 8 | 3575 | −0.76 | 2e−06 | 5e−05 | 50 x 2 | interleukin 7 receptor [Source:HGNC Symbol;Acc:6024] |
| 9 | 5880 | −0.75 | 3e−06 | 6e−05 | 50 x 1 | ras−related C3 botulinum toxin substrate 2 (rho family, small |
| 10 | 6363 | −0.73 | 4e−06 | 8e−05 | 50 x 1 | chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc |
| 11 | 341 | −0.72 | 7e−06 | 1e−04 | 50 x 1 | apolipoprotein C−I [Source:HGNC Symbol;Acc:607] |
| 12 | 51755 | 0.69 | 2e−05 | 1e−04 | 49 x 1 | cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242 |
| 13 | 2113 | −0.68 | 2e−05 | 1e−04 | 50 x 3 | v−ets avian erythroblastosis virus E26 oncogene homolog 1 [ |
| 14 | 81704 | −0.67 | 2e−05 | 1e−04 | 50 x 1 | dedicator of cytokinesis 8 [Source:HGNC Symbol;Acc:19191] |
| 15 | 10019 | −0.67 | 2e−05 | 1e−04 | 50 x 3 | SH2B adaptor protein 3 [Source:HGNC Symbol;Acc:29605] |
| 16 | 241 | −0.67 | 3e−05 | 7e−04 | 50 x 1 | arachidonate 5−lipoxygenase−activating protein [Source:HG |
| 17 | 51762 | −0.65 | 5e−05 | 7e−04 | 50 x 3 | RAB8B, member RAS oncogene family [Source:HGNC Symb |
| 18 | 55619 | −0.64 | 6e−05 | 8e−04 | 50 x 1 | dedicator of cytokinesis 10 [Source:HGNC Symbol;Acc:2347 |
| 19 | 57484 | −0.62 | 1e−04 | 8e−04 | 50 x 2 | ring finger protein 150 [Source:HGNC Symbol;Acc:23138] |
| 20 | 930 | −0.62 | 1e−04 | 8e−04 | 49 x 1 | CD19 molecule [Source:HGNC Symbol;Acc:1633] |

**p−values**



## Local Geneset Analysis

*Underexpression*

| Rank | GSZ | p−value | #in/all | Geneset | |
|---|---|---|---|---|---|
| 1 | −19.11 | NULL | 56 / 553 | Cancer | Lembcke_Colonic Inflammation |
| 2 | −17.48 | NULL | 5 / 12 | GSEA C2 | ZHAN_MULTIPLE_MYELOMA_DN |
| 3 | −16.44 | NULL | 58 / 417 | H.Tiss | WIRTH_Immune system |
| 4 | −15.45 | NULL | 3 / 9 | GSEA C2 | MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN |
| 5 | −15.26 | NULL | 29 / 265 | Glio | willscher_GBM_Verhaak−CL_expression_B_up |
| 6 | −15.26 | NULL | 29 / 265 | Glio | willscher_GBM_Verhaak−MES_expression_B_up |
| 7 | −15.26 | NULL | 29 / 265 | Glio | willscher_GBM_Verhaak−PNwt_expression_B_down |
| 8 | −15.26 | NULL | 29 / 265 | Glio | willscher_GBM_Verhaak−PNmut_expression_B_down |
| 9 | −14.78 | NULL | 4 / 14 | BP | ruffle organization |
| 10 | −14.65 | NULL | 6 / 15 | GSEA C2 | FINAK_BREAST_CANCER_SDPP_SIGNATURE |
| 11 | −12.98 | NULL | 4 / 10 | GSEA C2 | BIOCARTA_LYM_PATHWAY |
| 12 | −12.33 | NULL | 2 / 3 | MMML CGS | MACIEJ_MMML 7 |
| 13 | −12.03 | NULL | 2 / 11 | BP | high−density lipoprotein particle remodeling |
| 14 | −12.03 | NULL | 2 / 11 | GSEA C2 | APPEL_IMATINIB_RESPONSE |
| 15 | −11.99 | NULL | 3 / 12 | BP | dendritic cell chemotaxis |
| 16 | −11.71 | NULL | 5 / 17 | BP | positive regulation of neutrophil chemotaxis |
| 17 | −11.55 | NULL | 4 / 13 | BP | lymph node development |
| 18 | −11.21 | NULL | 4 / 16 | GSEA C2 | SU_THYMUS |
| 19 | −11.16 | NULL | 7 / 16 | GSEA C2 | FARMER_BREAST_CANCER_CLUSTER_1 |
| 20 | −10.76 | NULL | 3 / 11 | GSEA C2 | KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY |
| 21 | −10.6 | NULL | 12 / 74 | BP | regulation of immune response |
| 22 | −10.53 | NULL | 2 / 14 | CC | very−low−density lipoprotein particle |
| 23 | −10.16 | NULL | 2 / 4 | GSEA C2 | REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN |
| 24 | −10.13 | NULL | 2 / 15 | BP | cholesterol efflux |
| 25 | −10.13 | NULL | 2 / 15 | CC | high−density lipoprotein particle |
| 26 | −10.04 | NULL | 2 / 10 | BP | positive regulation of chemotaxis |
| 27 | −10.03 | NULL | 3 / 15 | GSEA C2 | JAATINEN_HEMATOPOIETIC_STEM_CELL_DN |
| 28 | −9.83 | NULL | 2 / 13 | MMML CGS | MACIEJ_MMML 6 |
| 29 | −9.82 | NULL | 1 / 5 | GSEA C2 | NAKAMURA_ALVEOLAR_EPITHELIUM |
| 30 | −9.8 | NULL | 7 / 43 | BP | positive regulation of T cell proliferation |
| 31 | −9.65 | NULL | 3 / 16 | GSEA C2 | GRAHAM_CML_QUIESCENT_VS_CML_DIVIDING_UP |
| 32 | −9.64 | NULL | 2 / 9 | GSEA C2 | BIOCARTA_LAIR_PATHWAY |
| 33 | −9.5 | NULL | 2 / 12 | MF | fatty acid binding |
| 34 | −9.4 | NULL | 3 / 8 | GSEA C2 | BIOCARTA_GRANULOCYTES_PATHWAY |
| 35 | −9.31 | NULL | 6 / 45 | BP | cellular defense response |
| 36 | −9.3 | NULL | 16 / 162 | CC | external side of plasma membrane |
| 37 | −9.3 | NULL | 5 / 16 | GSEA C2 | FERRANDO_TAL1_NEIGHBORS |
| 38 | −9.07 | NULL | 2 / 12 | BP | positive regulation of receptor−mediated endocytosis |
| 39 | −9.01 | NULL | 2 / 10 | BP | chronic inflammatory response |
| 40 | −8.99 | NULL | 3 / 27 | MF | antigen binding |

# GW_017

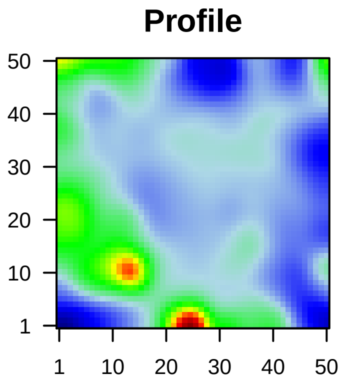
## Local Summary

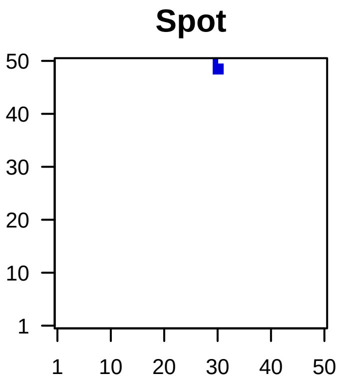
%DE = 0.64
# metagenes = 5
# genes = 57
# genes in genesets = 56

# genes with fdr < 0.1  = 20  ( 0 + / 20  − )
# genes with fdr < 0.05  = 8  ( 0 + / 8  − )
# genes with fdr < 0.01 = 4  ( 0 + / 4  − )

<r> metagenes = 0.99
<r> genes = 0.33

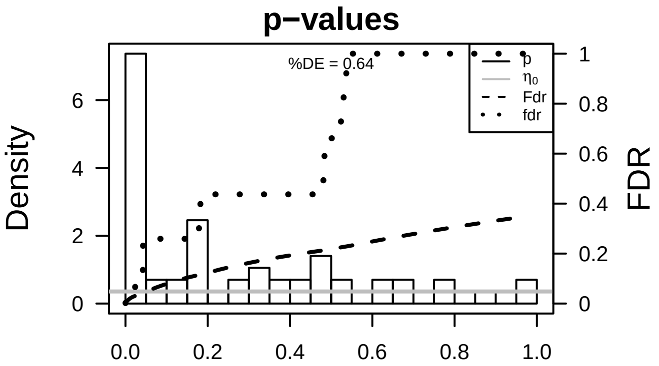
<FC> = −0.23
<shrinkage−t> = −8.18
<p−value> = 0.07
<fdr> = 0.74


Profile


Spot

## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 10412 | −0.64 | 6e−05 | 0.002 | 31 x 49 | NSA2 ribosome biogenesis homolog (S. cerevisiae) [Source:H |
| 2 | 10694 | −0.61 | 1e−04 | 0.004 | 30 x 48 | chaperonin containing TCP1, subunit 8 (theta) [Source:HGNC |
| 3 | 6166 | −0.57 | 4e−04 | 0.005 | 31 x 48 | ribosomal protein L36a−like [Source:HGNC Symbol;Acc:1034 |
| 4 | 84233 | −0.55 | 6e−04 | 0.005 | 31 x 49 | transmembrane protein 126A [Source:HGNC Symbol;Acc:253 |
| 5 | 152518 | −0.53 | 8e−04 | 0.012 | 30 x 49 | nuclear transcription factor, X−box binding−like 1 [Source:HG |
| 6 | 515 | −0.51 | 1e−03 | 0.031 | 30 x 50 | ATP synthase, H+ transporting, mitochondrial Fo complex, su |
| 7 | 9519 | −0.45 | 5e−03 | 0.031 | 30 x 49 | TBP−like 1 [Source:HGNC Symbol;Acc:11589] |
| 8 | 390284 | −0.45 | 5e−03 | 0.031 | 30 x 49 | |
| 9 | 55863 | −0.44 | 6e−03 | 0.053 | 31 x 49 | transmembrane protein 126B [Source:HGNC Symbol;Acc:308 |
| 10 | 6880 | −0.41 | 9e−03 | 0.053 | 30 x 50 | TAF9 RNA polymerase II, TATA box binding protein (TBP)−as |
| 11 | 5805 | −0.4 | 1e−02 | 0.053 | 30 x 50 | 6−pyruvoyltetrahydropterin synthase [Source:HGNC Symbol; |
| 12 | 23517 | −0.38 | 2e−02 | 0.053 | 30 x 50 | superkiller viralicidic activity 2−like 2 (S. cerevisiae) [Source:H |
| 13 | 153339 | −0.38 | 2e−02 | 0.053 | 30 x 50 | transmembrane protein 167A [Source:HGNC Symbol;Acc:283 |
| 14 | 6207 | −0.34 | 2e−02 | 0.053 | 31 x 48 | ribosomal protein S13 [Source:HGNC Symbol;Acc:10386] |
| 15 | 23609 | −0.37 | 2e−02 | 0.053 | 30 x 50 | makorin ring finger protein 2 [Source:HGNC Symbol;Acc:711 |
| 16 | 902 | −0.36 | 2e−02 | 0.074 | 31 x 48 | cyclin H [Source:HGNC Symbol;Acc:1594] |
| 17 | 60492 | −0.35 | 3e−02 | 0.074 | 31 x 48 | coiled−coil domain containing 90B [Source:HGNC Symbol;Ac |
| 18 | 51074 | −0.34 | 3e−02 | 0.074 | 31 x 49 | APAF1 interacting protein [Source:HGNC Symbol;Acc:17581] |
| 19 | 55781 | −0.33 | 4e−02 | 0.074 | 30 x 50 | RIO kinase 2 [Source:HGNC Symbol;Acc:18999] |
| 20 | 54148 | −0.32 | 4e−02 | 0.074 | 30 x 50 | mitochondrial ribosomal protein L39 [Source:HGNC Symbol; |


p−values

## Local Geneset Analysis

*Underexpression*

| Rank | GSZ | p−value | #in/all | Geneset | |
|---|---|---|---|---|---|
| 1 | −16.36 | NULL | 5 / 27 | BP | DNA−dependent transcription, initiation |
| 2 | −14.53 | NULL | 2 / 5 | GSEA C2 | NAGY_PCAF_COMPONENTS_HUMAN |
| 3 | −14.24 | NULL | 2 / 15 | GSEA C2 | SEIDEN_MET_SIGNALING |
| 4 | −13.31 | NULL | 2 / 11 | GSEA C2 | KEGG_BASAL_TRANSCRIPTION_FACTORS |
| 5 | −11.49 | NULL | 2 / 8 | GSEA C2 | NAGY_STAGA_COMPONENTS_HUMAN |
| 6 | −11.25 | NULL | 3 / 13 | GSEA C2 | NAGY_TFTC_COMPONENTS_HUMAN |
| 7 | −10.92 | NULL | 1 / 10 | MF | ATPase activity, coupled |
| 8 | −10.92 | NULL | 1 / 10 | CC | zona pellucida receptor complex |
| 9 | −10.83 | NULL | 3 / 14 | CC | transcription factor TFTC complex |
| 10 | −9.95 | NULL | 1 / 12 | GSEA C2 | NEBEN_AML_WITH_FLT3_OR_NRAS_DN |
| 11 | −9.95 | NULL | 1 / 12 | GSEA C2 | REACTOME_PREFOLDIN_MEDIATED_TRANSFER_OF_SUBST |
| 12 | −9.09 | NULL | 2 / 12 | BP | negative regulation of intrinsic apoptotic signaling pathway in respo |
| 13 | −8.99 | NULL | 2 / 13 | CC | STAGA complex |
| 14 | −8.97 | NULL | 3 / 11 | MMML CGS | MACIEJ_MMML 49 |
| 15 | −8.88 | NULL | 1 / 15 | GSEA C2 | REACTOME_FORMATION_OF_TUBULIN_FOLDING_INTERMED |
| 16 | −8.88 | NULL | 1 / 15 | GSEA C2 | REACTOME_ASSOCIATION_OF_TRIC_CCT_WITH_TARGET_P |
| 17 | −8.8 | NULL | 3 / 21 | CC | transcription factor TFIID complex |
| 18 | −8.62 | NULL | 4 / 66 | BP | transcription elongation from RNA polymerase II promoter |
| 19 | −8.07 | NULL | 1 / 10 | GSEA C2 | SAMOLS_TARGETS_OF_KHSV_MIRNAS_DN |
| 20 | −8.07 | NULL | 1 / 10 | GSEA C2 | KEGG_HUNTINGTONS_DISEASE |
| 21 | −7.98 | NULL | 1 / 13 | GSEA C2 | REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COU |
| 22 | −7.86 | NULL | 1 / 19 | CC | aggresome |
| 23 | −7.68 | NULL | 1 / 14 | BP | mitochondrial ATP synthesis coupled proton transport |
| 24 | −7.68 | NULL | 1 / 14 | GSEA C2 | SWEET_KRAS_ONCOGENIC_SIGNATURE |
| 25 | −7.67 | NULL | 1 / 7 | GSEA C2 | REACTOME_RNA_POLYMERASE_I_TRANSCRIPTION_INITIATI |
| 26 | −7.41 | NULL | 1 / 15 | BP | ATP synthesis coupled proton transport |
| 27 | −7.41 | NULL | 1 / 15 | GSEA C2 | ASTON_MAJOR_DEPRESSIVE_DISORDER_UP |
| 28 | −7.4 | NULL | 1 / 10 | BP | negative regulation of proteasomal ubiquitin−dependent protein cat |
| 29 | −7.17 | NULL | 1 / 16 | GSEA C2 | SWEET_KRAS_TARGETS_UP |
| 30 | −7.17 | NULL | 1 / 16 | GSEA C2 | SANA_RESPONSE_TO_IFNG_DN |
| 31 | −7.12 | NULL | 1 / 23 | BP | binding of sperm to zona pellucida |
| 32 | −7.06 | NULL | 1 / 13 | GSEA C2 | TONG_INTERACT_WITH_PTTG1 |
| 33 | −7.06 | NULL | 1 / 13 | GSEA C2 | BENPORATH_ES_CORE_NINE_CORRELATED |
| 34 | −7.06 | NULL | 1 / 13 | GSEA C2 | SAKAI_TUMOR_INFILTRATING_MONOCYTES_DN |
| 35 | −7.04 | NULL | 1 / 11 | MF | C2H2 zinc finger domain binding |
| 36 | −6.83 | NULL | 1 / 11 | GSEA C2 | KEGG_FOLATE_BIOSYNTHESIS |
| 37 | −6.75 | NULL | 1 / 9 | GSEA C2 | REACTOME_RNA_POLYMERASE_I_CHAIN_ELONGATION |
| 38 | −6.56 | NULL | 1 / 19 | CC | mitochondrial proton−transporting ATP synthase complex |
| 39 | −6.55 | NULL | 1 / 15 | MMML CGS | MACIEJ_MMML 22 |
| 40 | −6.55 | NULL | 1 / 15 | GSEA C2 | VANHARANTA_UTERINE_FIBROID_WITH_7Q_DELETION_UP |