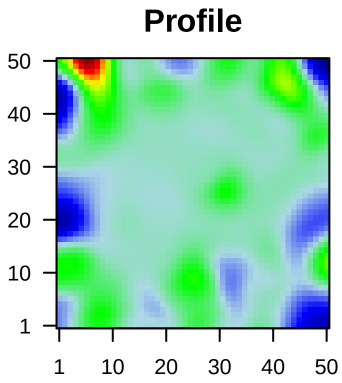
# F2_mel

## Global Summary

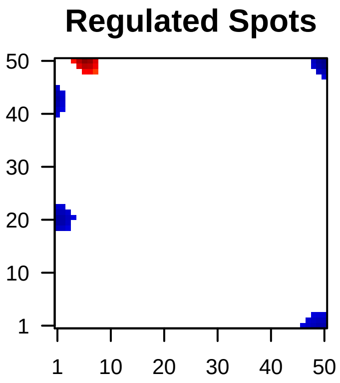
%DE = 0.2
# genes with fdr < 0.2  = 2682  ( 1589 + / 1093  −)
# genes with fdr < 0.1  = 2068  ( 1238 + / 830  −)
# genes with fdr < 0.05  = 1714  ( 1034 + / 680  −)
# genes with fdr < 0.01 = 1117  ( 662 + / 455  −)

# genes in genesets = 14839

<FC> = 0
<shrinkage−t> = −0.03
<p−value> = 0.08
<fdr> = 0.8



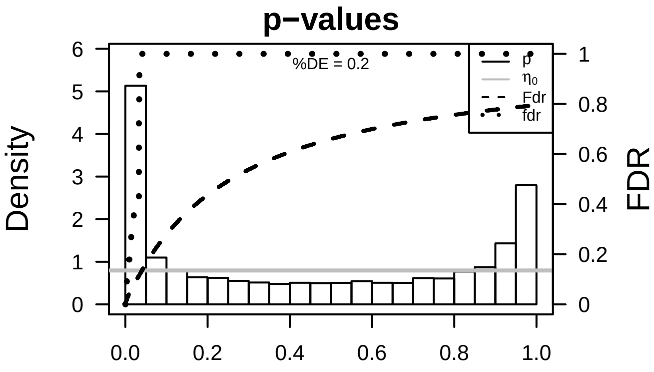
**Profile**



**Regulated Spots**

## Global Genelist

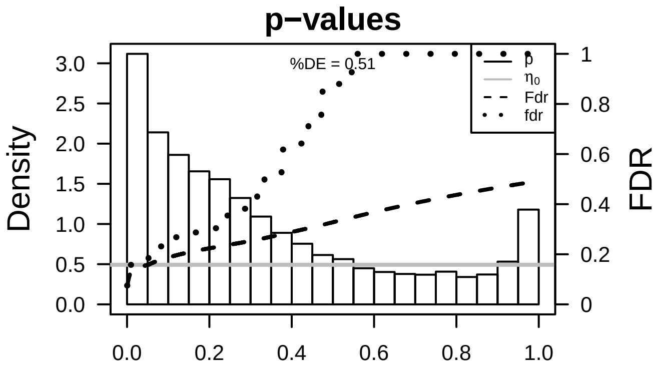
| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | APEH | −1.6 | 2e−16 | 7e−14 | 1 x 42 | acylaminoacyl−peptide hydrolase [Source:HGNC Symbol;Acc |
| 2 | ARHGAP8 | −1.71 | 2e−16 | 7e−14 | 1 x 43 | Rho GTPase activating protein 8 [Source:HGNC Symbol;Acc: |
| 3 | ARL2 | −1.81 | 2e−16 | 7e−14 | 37 x 50 | ADP−ribosylation factor−like 2 [Source:HGNC Symbol;Acc:H |
| 4 | CAPN3 | −0.93 | 2e−16 | 7e−14 | 1 x 43 | calpain 3, (p94) [Source:HGNC Symbol;Acc:HGNC:1480] |
| 5 | CCNDBP1 | −1.67 | 2e−16 | 7e−14 | 1 x 21 | cyclin D−type binding−protein 1 [Source:HGNC Symbol;Acc: |
| 6 | CD59 | −1.29 | 2e−16 | 7e−14 | 49 x 12 | CD59 molecule, complement regulatory protein [Source:HGN |
| 7 | CD99 | −0.96 | 2e−16 | 7e−14 | 43 x 18 | CD99 molecule [Source:HGNC Symbol;Acc:HGNC:7082] |
| 8 | CLK1 | −1.69 | 2e−16 | 7e−14 | 50 x 40 | CDC−like kinase 1 [Source:HGNC Symbol;Acc:HGNC:2068] |
| 9 | CUEDC2 | −1.63 | 2e−16 | 7e−14 | 1 x 38 | CUE domain containing 2 [Source:HGNC Symbol;Acc:HGNC |
| 10 | DCT | −1.39 | 2e−16 | 7e−14 | 1 x 11 | dopachrome tautomerase [Source:HGNC Symbol;Acc:HGNC |
| 11 | FAM213A | −1.65 | 2e−16 | 7e−14 | 1 x 41 | family with sequence similarity 213, member A [Source:HGN |
| 12 | FBXO7 | −1.45 | 2e−16 | 7e−14 | 1 x 20 | F−box protein 7 [Source:HGNC Symbol;Acc:HGNC:13586] |
| 13 | FOS | −1.49 | 2e−16 | 7e−14 | 4 x 7 | FBJ murine osteosarcoma viral oncogene homolog [Source: |
| 14 | GABARAPL2 | −1.96 | 2e−16 | 7e−14 | 49 x 48 | GABA(A) receptor−associated protein−like 2 [Source:HGNC |
| 15 | IFI16 | −1.42 | 2e−16 | 7e−14 | 31 x 12 | interferon, gamma−inducible protein 16 [Source:HGNC Symb |
| 16 | ITGB1BP1 | −2.17 | 2e−16 | 7e−14 | 1 x 44 | integrin beta 1 binding protein 1 [Source:HGNC Symbol;Acc: |
| 17 | LGALS3BP | −1.89 | 2e−16 | 7e−14 | 47 x 17 | lectin, galactoside−binding, soluble, 3 binding protein [Source |
| 18 | LITAF | −1.64 | 2e−16 | 7e−14 | 39 x 13 | lipopolysaccharide−induced TNF factor [Source:HGNC Symb |
| 19 | NDUFV1 | −0.81 | 2e−16 | 7e−14 | 6 x 42 | NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa [Sc |
| 20 | NGFRAP1 | −1.38 | 2e−16 | 7e−14 | 49 x 27 | nerve growth factor receptor (TNFRSF16) associated protein |



**p−values**

## Global Geneset Analysis

| Rank | GSZ | p−value | #all | | Geneset |
|---|---|---|---|---|---|
| *Overexpressed* | | | | | |
| 1 | 11.84 | 1e−04 | 1251 | GSEA C2 | DODD_NASOPHARYNGEAL_CARCINOMA_DN |
| 2 | 11.53 | 2e−04 | 142 | Glio | WILLSCHER_GBM_Verhaak−CL_up ( C) |
| 3 | 11.52 | 2e−03 | 16 | Cancer | SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP |
| 4 | 10.72 | 2e−04 | 550 | GSEA C2 | GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP |
| 5 | 9.84 | 3e−04 | 139 | GSEA C2 | ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER |
| 6 | 9.81 | 3e−04 | 50 | GSEA C2 | ISHIDA_E2F_TARGETS |
| 7 | 9.58 | 3e−04 | 118 | GSEA C2 | ODONNELL_TFRC_TARGETS_DN |
| 8 | 9.29 | 4e−04 | 72 | GSEA C2 | CROONQUIST_NRAS_SIGNALING_DN |
| 9 | 9.25 | 4e−04 | 1460 | GSEA C2 | PUJANA_BRCA1_PCC_NETWORK |
| 10 | 9.16 | 4e−04 | 1192 | GSEA C2 | KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP |
| 11 | 9.16 | 4e−04 | 96 | GSEA C2 | CROONQUIST_IL6_DEPRIVATION_DN |
| 12 | 9.14 | 4e−04 | 724 | GSEA C2 | PUJANA_CHEK2_PCC_NETWORK |
| 13 | 9.12 | 4e−04 | 700 | GSEA C2 | MARSON_BOUND_BY_E2F4_UNSTIMULATED |
| 14 | 8.98 | 4e−04 | 609 | GSEA C2 | RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIA |
| 15 | 8.94 | 4e−04 | 196 | HM | HALLMARK_G2M_CHECKPOINT |
| 16 | 8.93 | 4e−04 | 201 | GSEA C2 | WHITFIELD_CELL_CYCLE_G2_M |
| 17 | 8.78 | 4e−04 | 681 | GSEA C2 | RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP |
| 18 | 8.59 | 5e−04 | 155 | GSEA C2 | HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP |
| 19 | 8.48 | 5e−04 | 89 | GSEA C2 | MORI_IMMATURE_B_LYMPHOCYTE_DN |
| 20 | 8.46 | 5e−04 | 663 | CC | chromosome |
| *Underexpressed* | | | | | |
| 1 | −8.08 | 6e−04 | 2193 | CC | extracellular exosome |
| 2 | −8.05 | 6e−04 | 2798 | Colon Cancer | TxEnhG1_Colon |
| 3 | −7.53 | 8e−04 | 3132 | CC | extracellular region |
| 4 | −6.86 | 1e−03 | 9653 | Colon Cancer | Enh_Colon |
| 5 | −6.73 | 1e−03 | 447 | GSEA C2 | ENK_UV_RESPONSE_KERATINOCYTE_UP |
| 6 | −6.5 | 1e−03 | 998 | GSEA C2 | CHEN_METABOLIC_SYNDROM_NETWORK |
| 7 | −6.22 | 2e−03 | 2984 | CC | integral component of membrane |
| 8 | −6.12 | 2e−03 | 2972 | Brain | Mid_Frontal_Lobe_ReprPC |
| 9 | −5.89 | 2e−03 | 7203 | Colon Cancer | TssF_Colon |
| 10 | −5.81 | 2e−03 | 2698 | Colon Cancer | EnhA_Colon |
| 11 | −5.75 | 2e−03 | 3088 | CC | plasma membrane |
| 12 | −5.65 | 2e−03 | 385 | GSEA C2 | REN_ALVEOLAR_RHABDOMYOSARCOMA_DN |
| 13 | −5.55 | 2e−03 | 5155 | Colon Cancer | EnhWk1_Colon |
| 14 | −5.41 | 3e−03 | 897 | BP | vesicle−mediated transport |
| 15 | −5.39 | 3e−03 | 308 | CC | focal adhesion |
| 16 | −5.22 | 3e−03 | 9 | GSEA C2 | CHEN_HOXA5_TARGETS_6HR_UP |
| 17 | −5.11 | 3e−03 | 801 | Chr | Chr 11 |
| 18 | −5.05 | 3e−03 | 66 | Lymphoma | TARTE_Plasma cell signature |
| 19 | −5.04 | 3e−03 | 405 | GSEA C2 | REACTOME_METABOLISM_OF_LIPIDS_AND_LIPOPROTEINS |
| 20 | −4.95 | 4e−03 | 494 | GSEA C2 | CHICAS_RB1_TARGETS_CONFLUENT |



**p−values**

# F2_mel

## Local Summary

%DE = 0.9

# metagenes = 12

# genes = 174

# genes in genesets = 174

# genes with fdr < 0.1 = 136 ( 121 + / 15 −)

# genes with fdr < 0.05 = 121 ( 112 + / 9 −)

# genes with fdr < 0.01 = 102 ( 98 + / 4 −)

<r> metagenes = 0.98

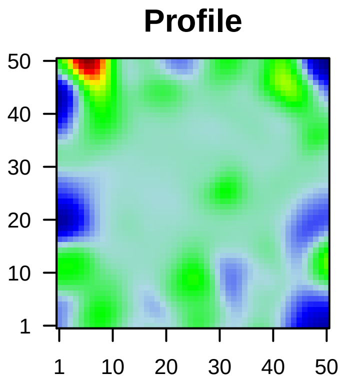
<r> genes = 0.43

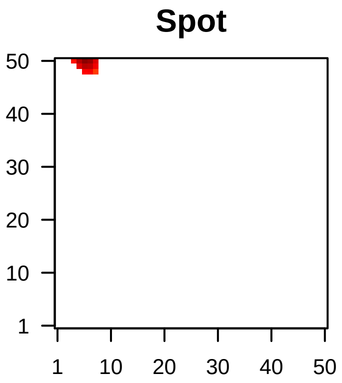
<FC> = 0.61

<shrinkage−t> = 10.04

<p−value> = 0

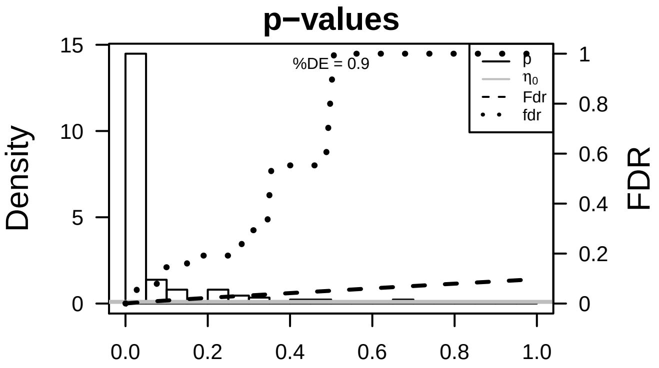
<fdr> = 0.35





## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | KPNA2 | 0.78 | 2e−14 | 1e−12 | 7 x 50 | karyopherin alpha 2 (RAG cohort 1, importin alpha 1) [Sourc |
| 2 | CDKN3 | 1.35 | 1e−13 | 1e−12 | 6 x 50 | cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A |
| 3 | CDK1 | 1.79 | 2e−13 | 1e−11 | 5 x 50 | cyclin−dependent kinase 1 [Source:HGNC Symbol;Acc:HGN |
| 4 | TOP2A | 1.76 | 9e−13 | 2e−11 | 6 x 50 | topoisomerase (DNA) II alpha 170kDa [Source:HGNC Symbo |
| 5 | STMN1 | 0.69 | 3e−12 | 2e−11 | 5 x 50 | stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510] |
| 6 | UBE2C | 1.7 | 4e−12 | 5e−11 | 6 x 50 | ubiquitin−conjugating enzyme E2C [Source:HGNC Symbol;A |
| 7 | PTTG1 | 1.05 | 7e−12 | 6e−10 | 7 x 50 | pituitary tumor−transforming 1 [Source:HGNC Symbol;Acc:H |
| 8 | CENPF | 1.51 | 6e−11 | 6e−10 | 6 x 50 | centromere protein F, 350/400kDa [Source:HGNC Symbol;Ac |
| 9 | H2AFZ | 0.65 | 8e−11 | 4e−09 | 7 x 48 | H2A histone family, member Z [Source:HGNC Symbol;Acc:H |
| 10 | PLK1 | 1.55 | 3e−10 | 1e−08 | 8 x 50 | polo−like kinase 1 [Source:HGNC Symbol;Acc:HGNC:9077] |
| 11 | AURKB | 1.48 | 2e−09 | 1e−08 | 6 x 50 | aurora kinase B [Source:HGNC Symbol;Acc:HGNC:11390] |
| 12 | CCNB1 | 1.46 | 2e−09 | 1e−08 | 7 x 50 | cyclin B1 [Source:HGNC Symbol;Acc:HGNC:1579] |
| 13 | KIF18A | 1.47 | 3e−09 | 2e−08 | 7 x 50 | kinesin family member 18A [Source:HGNC Symbol;Acc:HGN |
| 14 | CENPW | 1.43 | 4e−09 | 2e−08 | 6 x 50 | centromere protein W [Source:HGNC Symbol;Acc:HGNC:21 |
| 15 | KIF20A | 1.44 | 5e−09 | 2e−08 | 7 x 50 | kinesin family member 20A [Source:HGNC Symbol;Acc:HGN |
| 16 | TROAP | 1.43 | 6e−09 | 5e−08 | 6 x 50 | trophinin associated protein [Source:HGNC Symbol;Acc:HGN |
| 17 | NUF2 | 1.4 | 1e−08 | 5e−08 | 6 x 50 | NUF2, NDC80 kinetochore complex component [Source:HGN |
| 18 | HMMR | 1.4 | 1e−08 | 5e−08 | 7 x 50 | hyaluronan−mediated motility receptor (RHAMM) [Source:HG |
| 19 | DEPDC1 | 1.4 | 1e−08 | 1e−07 | 6 x 50 | DEP domain containing 1 [Source:HGNC Symbol;Acc:HGNC |
| 20 | NUSAP1 | 1.34 | 2e−08 | 6e−07 | 6 x 50 | nucleolar and spindle associated protein 1 [Source:HGNC Sy |



# F2_mel

## Local Summary

%DE = 0.75

# metagenes = 12

# genes = 230

# genes in genesets = 230

# genes with fdr < 0.1  = 103  ( 27 + / 76  −)

# genes with fdr < 0.05  = 71  ( 18 + / 53  −)

# genes with fdr < 0.01 = 49  ( 11 + / 38  −)

<r> metagenes = 0.98

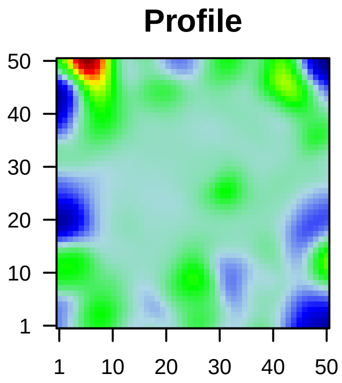
<r> genes = 0.22

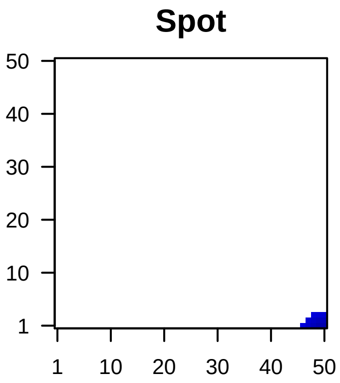
<FC> = −0.24

<shrinkage−t> = −3.85

<p−value> = 0.02

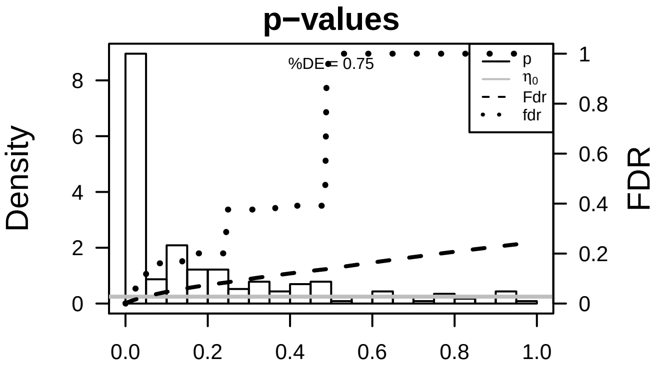
<fdr> = 0.65





## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | SPARC | −0.96 | 1e−14 | 3e−08 | 50 x 2 | secreted protein, acidic, cysteine−rich (osteonectin) [Source: |
| 2 | ARID5B | −1.35 | 5e−10 | 3e−08 | 50 x 1 | AT rich interactive domain 5B (MRF1−like) [Source:HGNC Sy |
| 3 | ARMC9 | −1.33 | 1e−09 | 3e−08 | 50 x 3 | armadillo repeat containing 9 [Source:HGNC Symbol;Acc:HG |
| 4 | FAT1 | 1.48 | 2e−09 | 3e−08 | 49 x 1 | FAT atypical cadherin 1 [Source:HGNC Symbol;Acc:HGNC:3 |
| 5 | MATN2 | 1.48 | 2e−09 | 5e−07 | 50 x 1 | matrilin 2 [Source:HGNC Symbol;Acc:HGNC:6908] |
| 6 | TAGLN2 | −1.16 | 1e−08 | 1e−06 | 50 x 2 | transgelin 2 [Source:HGNC Symbol;Acc:HGNC:11554] |
| 7 | DCBLD2 | −1.25 | 4e−08 | 3e−06 | 47 x 1 | discoidin, CUB and LCCL domain containing 2 [Source:HGN |
| 8 | CNN3 | −0.52 | 1e−07 | 3e−06 | 47 x 1 | calponin 3, acidic [Source:HGNC Symbol;Acc:HGNC:2157] |
| 9 | LAMC1 | −1.14 | 2e−07 | 3e−06 | 50 x 3 | laminin, gamma 1 (formerly LAMB2) [Source:HGNC Symbol; |
| 10 | NOV | −1.2 | 2e−07 | 3e−06 | 50 x 1 | nephroblastoma overexpressed [Source:HGNC Symbol;Acc: |
| 11 | SRPX | −1.2 | 3e−07 | 3e−06 | 50 x 1 | sushi−repeat containing protein, X−linked [Source:HGNC Sy |
| 12 | SNAP23 | −1 | 3e−07 | 7e−05 | 50 x 1 | synaptosomal−associated protein, 23kDa [Source:HGNC Sy |
| 13 | FMN2 | −1.16 | 2e−06 | 8e−05 | 48 x 1 | formin 2 [Source:HGNC Symbol;Acc:HGNC:14074] |
| 14 | UBE2E2 | −1.12 | 4e−06 | 8e−05 | 50 x 1 | ubiquitin−conjugating enzyme E2E 2 [Source:HGNC Symbol; |
| 15 | PALMD | 1.13 | 5e−06 | 8e−05 | 50 x 1 | palmdelphin [Source:HGNC Symbol;Acc:HGNC:15846] |
| 16 | ANXA2 | −0.45 | 6e−06 | 5e−04 | 50 x 3 | annexin A2 [Source:HGNC Symbol;Acc:HGNC:537] |
| 17 | MT2A | −1.06 | 2e−05 | 5e−04 | 50 x 3 | metallothionein 2A [Source:HGNC Symbol;Acc:HGNC:7406] |
| 18 | NEDD9 | −1.04 | 2e−05 | 5e−04 | 48 x 2 | neural precursor cell expressed, developmentally down−regul |
| 19 | SPTA1 | 1.02 | 4e−05 | 5e−04 | 50 x 1 | spectrin, alpha, erythrocytic 1 [Source:HGNC Symbol;Acc:H |
| 20 | PDGFA | −1.01 | 4e−05 | 5e−04 | 49 x 1 | platelet−derived growth factor alpha polypeptide [Source:HG |



# F2_mel

## Local Summary

%DE = 0.67

# metagenes = 15

# genes = 230

# genes in genesets = 229

# genes with fdr < 0.1 = 80 ( 17 + / 63 −)

# genes with fdr < 0.05 = 65 ( 12 + / 53 −)

# genes with fdr < 0.01 = 40 ( 3 + / 37 −)

<r> metagenes = 0.98

<r> genes = 0.16

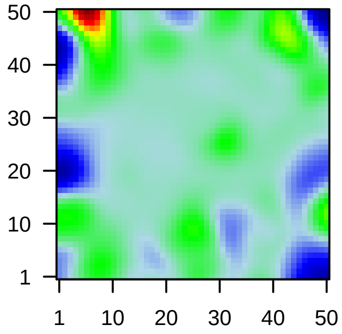
<FC> = −0.26

<shrinkage−t> = −4.59

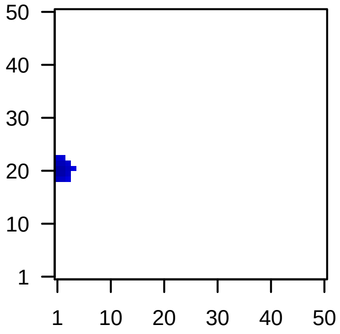
<p−value> = 0.01

<fdr> = 0.66

**Profile**



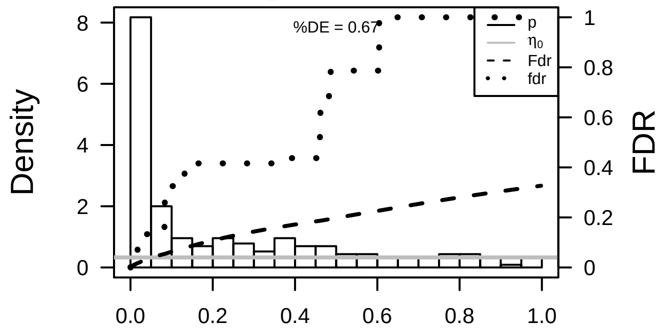
**Spot**



## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | CCNDBP1 | −1.67 | 2e−16 | 3e−15 | 1 x 21 | cyclin D−type binding−protein 1 [Source:HGNC Symbol;Acc: |
| 2 | FBXO7 | −1.45 | 2e−16 | 3e−15 | 1 x 20 | F−box protein 7 [Source:HGNC Symbol;Acc:HGNC:13586] |
| 3 | PIGY | −0.98 | 2e−16 | 3e−15 | 1 x 20 | phosphatidylinositol glycan anchor biosynthesis, class Y [Sou |
| 4 | RER1 | −1.28 | 2e−16 | 3e−15 | 3 x 22 | retention in endoplasmic reticulum sorting receptor 1 [Source |
| 5 | TCF25 | −1.59 | 2e−16 | 3e−15 | 1 x 23 | transcription factor 25 (basic helix−loop−helix) [Source:HGN |
| 6 | C16orf13 | −1.47 | 8e−13 | 3e−09 | 1 x 21 | chromosome 16 open reading frame 13 [Source:HGNC Sym |
| 7 | SYNGR2 | −1.42 | 4e−11 | 3e−07 | 1 x 21 | synaptogyrin 2 [Source:HGNC Symbol;Acc:HGNC:11499] |
| 8 | COX5A | −0.73 | 4e−09 | 5e−07 | 1 x 21 | cytochrome c oxidase subunit Va [Source:HGNC Symbol;Acc |
| 9 | JTB | −0.96 | 1e−08 | 2e−06 | 1 x 21 | jumping translocation breakpoint [Source:HGNC Symbol;Acc |
| 10 | HMGN1 | −0.85 | 3e−08 | 2e−06 | 1 x 21 | high mobility group nucleosome binding domain 1 [Source:H |
| 11 | RDX | −1.18 | 6e−08 | 4e−06 | 1 x 22 | radixin [Source:HGNC Symbol;Acc:HGNC:9944] |
| 12 | NRSN2 | −1.23 | 1e−07 | 5e−06 | 1 x 19 | neurensin 2 [Source:HGNC Symbol;Acc:HGNC:16229] |
| 13 | HERC3 | −0.9 | 2e−07 | 5e−06 | 1 x 20 | HECT and RLD domain containing E3 ubiquitin protein ligase |
| 14 | P4HB | −0.51 | 2e−07 | 5e−06 | 1 x 20 | prolyl 4−hydroxylase, beta polypeptide [Source:HGNC Symb |
| 15 | SCARB1 | −1.04 | 3e−07 | 6e−05 | 2 x 20 | scavenger receptor class B, member 1 [Source:HGNC Symb |
| 16 | USP14 | −0.94 | 1e−06 | 6e−05 | 1 x 22 | ubiquitin specific peptidase 14 (tRNA−guanine transglycosyla |
| 17 | CAMKK2 | 1.17 | 2e−06 | 2e−04 | 4 x 21 | calcium/calmodulin−dependent protein kinase kinase 2, beta |
| 18 | SQSTM1 | −0.5 | 7e−06 | 2e−04 | 1 x 21 | sequestosome 1 [Source:HGNC Symbol;Acc:HGNC:11280] |
| 19 | EMC8 | 1.1 | 8e−06 | 2e−04 | 1 x 19 | ER membrane protein complex subunit 8 [Source:HGNC Sy |
| 20 | TMEM134 | −1.08 | 9e−06 | 4e−04 | 1 x 19 | transmembrane protein 134 [Source:HGNC Symbol;Acc:HG |

**p−values**



# F2_mel

## Local Summary

%DE = 0.76

# metagenes = 10

# genes = 198

# genes in genesets = 196

# genes with fdr < 0.1  = 100  ( 19 + / 81  −)

# genes with fdr < 0.05  = 100  ( 19 + / 81  −)

# genes with fdr < 0.01 = 71  ( 13 + / 58  −)

<r> metagenes = 0.97

<r> genes = 0.2

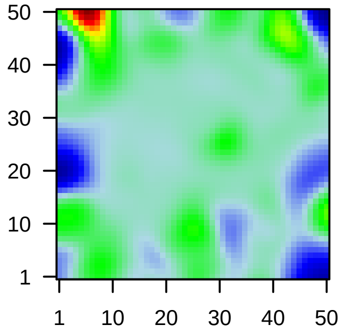
<FC> = −0.33

<shrinkage−t> = −5.76

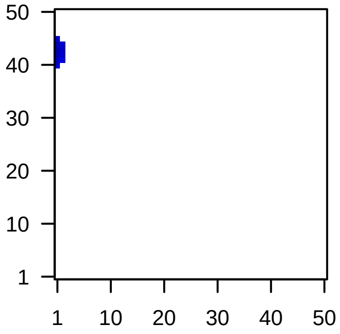
<p−value> = 0

<fdr> = 0.51

**Profile**



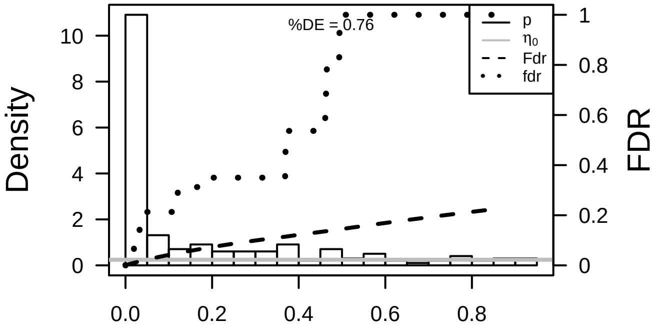
**Spot**



## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | APEH | −1.6 | 2e−16 | 2e−15 | 1 x 42 | acylaminoacyl−peptide hydrolase [Source:HGNC Symbol;Ac |
| 2 | ARHGAP8 | −1.71 | 2e−16 | 2e−15 | 1 x 43 | Rho GTPase activating protein 8 [Source:HGNC Symbol;Acc |
| 3 | CAPN3 | −0.93 | 2e−16 | 2e−15 | 1 x 43 | calpain 3, (p94) [Source:HGNC Symbol;Acc:HGNC:1480] |
| 4 | FAM213A | −1.65 | 2e−16 | 2e−15 | 1 x 41 | family with sequence similarity 213, member A [Source:HGN |
| 5 | ITGB1BP1 | −2.17 | 2e−16 | 2e−15 | 1 x 44 | integrin beta 1 binding protein 1 [Source:HGNC Symbol;Acc: |
| 6 | POLR2I | −1.86 | 2e−16 | 2e−15 | 1 x 44 | polymerase (RNA) II (DNA directed) polypeptide I, 14.5kDa [ |
| 7 | HIGD2A | −1.05 | 4e−15 | 2e−12 | 1 x 40 | HIG1 hypoxia inducible domain family, member 2A [Source:H |
| 8 | ABCB5 | −1.31 | 5e−14 | 2e−10 | 1 x 43 | ATP−binding cassette, sub−family B (MDR/TAP), member 5 [ |
| 9 | LIMS2 | −1.45 | 5e−12 | 2e−10 | 1 x 45 | LIM and senescent cell antigen−like domains 2 [Source:HGN |
| 10 | GSTM4 | −1.44 | 9e−12 | 1e−09 | 1 x 41 | glutathione S−transferase mu 4 [Source:HGNC Symbol;Acc: |
| 11 | PFKM | −1.42 | 4e−11 | 2e−09 | 1 x 41 | phosphofructokinase, muscle [Source:HGNC Symbol;Acc:HG |
| 12 | TRPM1 | 0.78 | 8e−11 | 6e−09 | 1 x 42 | transient receptor potential cation channel, subfamily M, mem |
| 13 | LGALS3 | −1.38 | 2e−10 | 8e−08 | 1 x 43 | lectin, galactoside−binding, soluble, 3 [Source:HGNC Symbol |
| 14 | SVIP | −1.05 | 4e−09 | 8e−08 | 1 x 44 | small VCP/p97−interacting protein [Source:HGNC Symbol;Ac |
| 15 | EXOC3 | −0.58 | 7e−09 | 8e−08 | 1 x 42 | exocyst complex component 3 [Source:HGNC Symbol;Acc:H |
| 16 | PDE6D | −1.3 | 7e−09 | 8e−08 | 1 x 44 | phosphodiesterase 6D, cGMP−specific, rod, delta [Source:H |
| 17 | SFXN4 | −1.3 | 8e−09 | 8e−08 | 1 x 41 | sideroflexin 4 [Source:HGNC Symbol;Acc:HGNC:16088] |
| 18 | AIFM1 | −1.26 | 9e−09 | 8e−08 | 1 x 42 | apoptosis−inducing factor, mitochondrion−associated, 1 [Sou |
| 19 | TUBB4A | −1.21 | 1e−08 | 2e−07 | 1 x 42 | tubulin, beta 4A class IVa [Source:HGNC Symbol;Acc:HGNC |
| 20 | CD58 | −1.27 | 2e−08 | 2e−07 | 1 x 43 | CD58 molecule [Source:HGNC Symbol;Acc:HGNC:1688] |

**p−values**



# F2_mel

## Local Summary

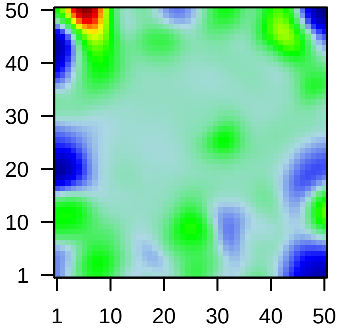
%DE = 0.77
# metagenes = 9
# genes = 181
# genes in genesets = 181

# genes with fdr < 0.1  = 108  ( 24 + / 84  −)
# genes with fdr < 0.05  = 68  ( 11 + / 57  −)
# genes with fdr < 0.01 = 65  ( 11 + / 54  −)

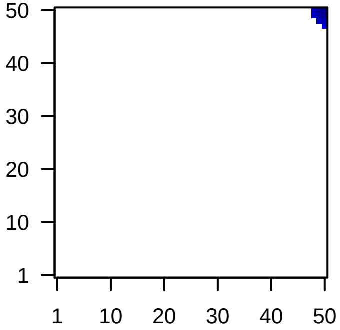
<r> metagenes = 0.97
<r> genes = 0.09

<FC> = −0.3
<shrinkage−t> = −4.86
<p−value> = 0
<fdr> = 0.57

**Profile**



**Spot**



## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | GABARAPL2 | −1.96 | 2e−16 | 5e−15 | 49 x 48 | GABA(A) receptor−associated protein−like 2 [Source:HGNC |
| 2 | PLEKHA5 | −1.63 | 2e−16 | 5e−15 | 50 x 50 | pleckstrin homology domain containing, family A member 5 [ |
| 3 | EIF4E2 | −1.42 | 5e−13 | 3e−11 | 50 x 47 | eukaryotic translation initiation factor 4E family member 2 [So |
| 4 | ARPC1B | −1.45 | 1e−12 | 1e−09 | 49 x 50 | actin related protein 2/3 complex, subunit 1B, 41kDa [Source: |
| 5 | LUZP6 | 1.63 | 3e−11 | 3e−09 | 50 x 49 | leucine zipper protein 6 [Source:HGNC Symbol;Acc:HGNC:3 |
| 6 | UGP2 | 1.13 | 9e−11 | 9e−08 | 50 x 50 | UDP−glucose pyrophosphorylase 2 [Source:HGNC Symbol; |
| 7 | KIAA1033 | −1.32 | 3e−09 | 9e−08 | 50 x 49 | KIAA1033 [Source:HGNC Symbol;Acc:HGNC:29174] |
| 8 | TAOK3 | −1.31 | 5e−09 | 9e−08 | 49 x 50 | TAO kinase 3 [Source:HGNC Symbol;Acc:HGNC:18133] |
| 9 | LYPLA2 | −1.3 | 7e−09 | 2e−07 | 50 x 49 | lysophospholipase II [Source:HGNC Symbol;Acc:HGNC:673 |
| 10 | APMAP | −1.27 | 1e−08 | 7e−07 | 50 x 49 | adipocyte plasma membrane associated protein [Source:HG |
| 11 | CAP2 | −1.26 | 3e−08 | 7e−06 | 50 x 50 | CAP, adenylate cyclase−associated protein, 2 (yeast) [Sourc |
| 12 | LMBRD1 | −1.2 | 3e−07 | 7e−06 | 50 x 49 | LMBR1 domain containing 1 [Source:HGNC Symbol;Acc:HG |
| 13 | OSTF1 | −1.2 | 4e−07 | 9e−06 | 50 x 49 | osteoclast stimulating factor 1 [Source:HGNC Symbol;Acc:H |
| 14 | NIP7 | −1.04 | 6e−07 | 9e−06 | 50 x 50 | NIP7, nucleolar pre−rRNA processing protein [Source:HGNC |
| 15 | GNL2 | −1.17 | 9e−07 | 9e−06 | 50 x 47 | guanine nucleotide binding protein−like 2 (nucleolar) [Source: |
| 16 | TRPT1 | −1.17 | 1e−06 | 9e−06 | 50 x 49 | tRNA phosphotransferase 1 [Source:HGNC Symbol;Acc:HG |
| 17 | LETMD1 | 1.2 | 1e−06 | 1e−05 | 50 x 50 | LETM1 domain containing 1 [Source:HGNC Symbol;Acc:HG |
| 18 | PCID2 | −1.16 | 1e−06 | 3e−05 | 48 x 50 | PCI domain containing 2 [Source:HGNC Symbol;Acc:HGNC: |
| 19 | BACH1 | −1.13 | 2e−06 | 3e−05 | 50 x 50 | BTB and CNC homology 1, basic leucine zipper transcription |
| 20 | UPP1 | −1.14 | 3e−06 | 1e−04 | 50 x 50 | uridine phosphorylase 1 [Source:HGNC Symbol;Acc:HGNC:1 |

**p−values**