# G9_mel

## Global Summary

%DE = 0.17

# genes with fdr < 0.2 = 1947 ( 1071 + / 876 −)

# genes with fdr < 0.1 = 1527 ( 825 + / 702 −)

# genes with fdr < 0.05 = 1031 ( 513 + / 518 −)

# genes with fdr < 0.01 = 524 ( 216 + / 308 −)

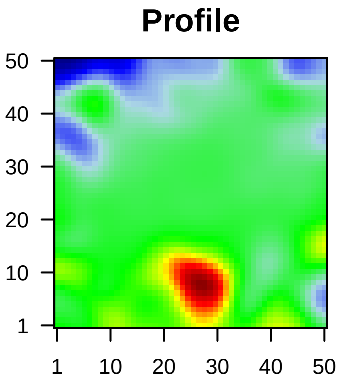
# genes in genesets = 14839

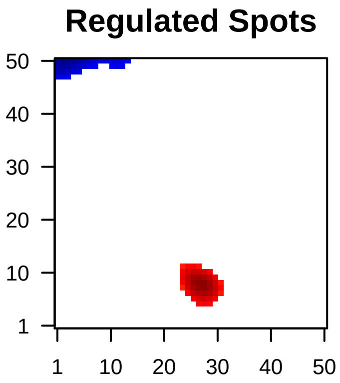
<FC> = 0

<shrinkage−t> = −0.11

<p−value> = 0.13

<fdr> = 0.83



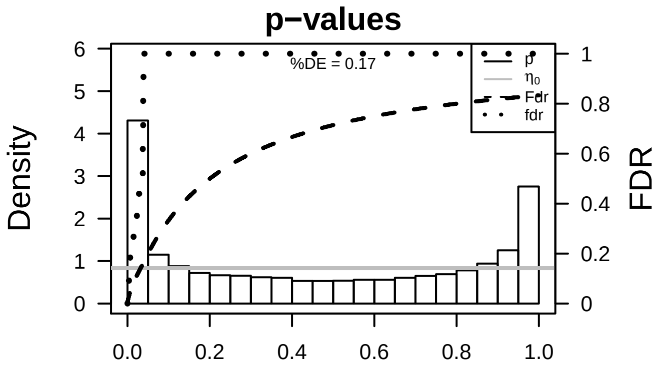


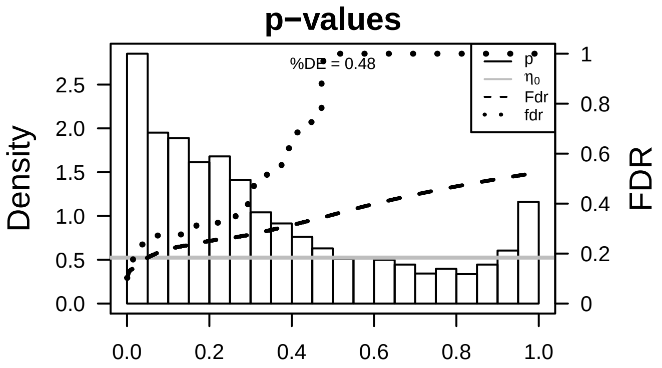
## Global Genelist

| Rank | log(FC) | fdr | | Description |
|---|---|---|---|---|
| ID | | p−value | Metagene | |
| 1 ARL6IP1 | −1.61 | 2e−16 1e−13 | 9 x 50 | ADP−ribosylation factor−like 6 interacting protein 1 [Source:H |
| 2 ATPIF1 | −1.69 | 2e−16 1e−13 | 50 x 47 | ATPase inhibitory factor 1 [Source:HGNC Symbol;Acc:HGNC |
| 3 BSCL2 | −1.85 | 2e−16 1e−13 | 50 x 50 | Berardinelli−Seip congenital lipodystrophy 2 (seipin) [Source: |
| 4 CALM1 | −2.18 | 2e−16 1e−13 | 12 x 50 | calmodulin 1 (phosphorylase kinase, delta) [Source:HGNC Sy |
| 5 CERS2 | −1.81 | 2e−16 1e−13 | 3 x 34 | ceramide synthase 2 [Source:HGNC Symbol;Acc:HGNC:140 |
| 6 ECI2 | −1.9 | 2e−16 1e−13 | 20 x 42 | enoyl−CoA delta isomerase 2 [Source:HGNC Symbol;Acc:HG |
| 7 EFTUD2 | −1.92 | 2e−16 1e−13 | 13 x 42 | elongation factor Tu GTP binding domain containing 2 [Sourc |
| 8 FAM195B | −1.92 | 2e−16 1e−13 | 50 x 45 | family with sequence similarity 195, member B [Source:HGN |
| 9 GTF2A2 | −2.44 | 2e−16 1e−13 | 45 x 49 | general transcription factor IIA, 2, 12kDa [Source:HGNC Sym |
| 10 JKAMP | −1.79 | 2e−16 1e−13 | 29 x 50 | JNK1/MAPK8−associated membrane protein [Source:HGNC |
| 11 LMAN2 | −1.83 | 2e−16 1e−13 | 13 x 50 | lectin, mannose−binding 2 [Source:HGNC Symbol;Acc:HGN |
| 12 LSM7 | −1.76 | 2e−16 1e−13 | 2 x 38 | LSM7 homolog, U6 small nuclear RNA associated (S. cerevis |
| 13 MORN2 | −1.78 | 2e−16 1e−13 | 47 x 37 | MORN repeat containing 2 [Source:HGNC Symbol;Acc:HGN |
| 14 MRPL20 | −1.88 | 2e−16 1e−13 | 3 x 36 | mitochondrial ribosomal protein L20 [Source:HGNC Symbol; |
| 15 MRPL27 | −2.04 | 2e−16 1e−13 | 4 x 38 | mitochondrial ribosomal protein L27 [Source:HGNC Symbol; |
| 16 NAPA | −1.99 | 2e−16 1e−13 | 20 x 49 | N−ethylmaleimide−sensitive factor attachment protein, alpha |
| 17 NDUFB7 | −2.18 | 2e−16 1e−13 | 5 x 36 | NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 1 |
| 18 NUCB2 | −1.88 | 2e−16 1e−13 | 1 x 35 | nucleobindin 2 [Source:HGNC Symbol;Acc:HGNC:8044] |
| 19 PET100 | −2.07 | 2e−16 1e−13 | 6 x 34 | PET100 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc: |
| 20 POLD2 | −2.06 | 2e−16 1e−13 | 3 x 37 | polymerase (DNA directed), delta 2, accessory subunit [Sour |

## Global Geneset Analysis

| Rank | GSZ | p−value | #all | Geneset |
|---|---|---|---|---|
| *Overexpressed* | | | | |
| 1 | 5.57 | 0.002 | 833 | GSEA C2 DACOSTA_UV_RESPONSE_VIA_ERCC3_DN |
| 2 | 5.49 | 0.003 | 9020 | Brain Overlap_fetal_midbrain_ReprPCWk |
| 3 | 5.43 | 0.003 | 5940 | Brain Overlap_fetal_midbrain_HetRpts |
| 4 | 5.17 | 0.003 | 784 | GSEA C2 BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP |
| 5 | 4.91 | 0.004 | 447 | miRNA target hsa−miR−130b |
| 6 | 4.86 | 0.004 | 3897 | Colon Cancer Quies1_Colon |
| 7 | 4.84 | 0.004 | 473 | GSEA C2 DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN |
| 8 | 4.8 | 0.004 | 2211 | Lymphoma HOPP_Repetitive |
| 9 | 4.78 | 0.004 | 214 | GSEA C2 CHEN_HOXA5_TARGETS_9HR_UP |
| 10 | 4.75 | 0.004 | 138 | miRNA target hsa−miR−136 |
| 11 | 4.69 | 0.004 | 50 | miRNA target hsa−miR−487a |
| 12 | 4.68 | 0.004 | 214 | miRNA target hsa−miR−548m |
| 13 | 4.66 | 0.005 | 488 | miRNA target hsa−miR−107 |
| 14 | 4.47 | 0.005 | 367 | GSEA C2 MONNIER_POSTRADIATION_TUMOR_ESCAPE_UP |
| 15 | 4.47 | 0.005 | 471 | GSEA C2 ENK_UV_RESPONSE_KERATINOCYTE_DN |
| 16 | 4.41 | 0.005 | 493 | GSEA C2 MILI_PSEUDOPODIA_HAPTOTAXIS_UP |
| 17 | 4.38 | 0.006 | 749 | GSEA C2 CUI_TCF21_TARGETS_2_DN |
| 18 | 4.34 | 0.006 | 456 | miRNA target hsa−miR−130a |
| 19 | 4.28 | 0.006 | 443 | miRNA target hsa−miR−19a |
| 20 | 4.27 | 0.006 | 120 | GSEA C2 KARLSSON_TGFB1_TARGETS_UP |
| *Underexpressed* | | | | |
| 1 | −11.99 | 1e−04 | 142 | Glio WILLSCHER_GBM_Verhaak−CL_up ( C) |
| 2 | −11.22 | 2e−04 | 550 | GSEA C2 GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP |
| 3 | −10.58 | 2e−04 | 305 | GSEA C2 DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP |
| 4 | −10.09 | 3e−04 | 96 | GSEA C2 CROONQUIST_IL6_DEPRIVATION_DN |
| 5 | −9.99 | 3e−04 | 309 | GSEA C2 GOLDRATH_ANTIGEN_RESPONSE |
| 6 | −9.93 | 3e−04 | 139 | GSEA C2 ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER |
| 7 | −9.88 | 3e−04 | 110 | GSEA C2 WHITEFORD_PEDIATRIC_CANCER_MARKERS |
| 8 | −9.84 | 3e−04 | 99 | GSEA C2 BURTON_ADIPOGENESIS_3 |
| 9 | −9.8 | 3e−04 | 72 | GSEA C2 CROONQUIST_NRAS_SIGNALING_DN |
| 10 | −9.65 | 3e−04 | 116 | GSEA C2 MISSIAGLIA_REGULATED_BY_METHYLATION_DN |
| 11 | −9.53 | 3e−04 | 242 | GSEA C2 KOBAYASHI_EGFR_SIGNALING_24HR_DN |
| 12 | −9.29 | 4e−04 | 54 | GSEA C2 KANG_DOXORUBICIN_RESISTANCE_UP |
| 13 | −9.18 | 1e−02 | 16 | Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP |
| 14 | −9.03 | 4e−04 | 171 | GSEA C2 SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP |
| 15 | −8.99 | 4e−04 | 162 | GSEA C2 GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP |
| 16 | −8.98 | 4e−04 | 700 | GSEA C2 MARSON_BOUND_BY_E2F4_UNSTIMULATED |
| 17 | −8.6 | 5e−04 | 144 | GSEA C2 BENPORATH_PROLIFERATION |
| 18 | −8.59 | 5e−04 | 197 | HM HALLMARK_E2F_TARGETS |
| 19 | −8.43 | 5e−04 | 327 | GSEA C2 BLUM_RESPONSE_TO_SALIRASIB_DN |
| 20 | −8.32 | 5e−04 | 145 | GSEA C2 CHANG_CYCLING_GENES |





# G9_mel

## Local Summary

%DE = 0.86

# metagenes = 48

# genes = 388

# genes in genesets = 381

# genes with fdr < 0.1  = 207  ( 204 + / 3  −)

# genes with fdr < 0.05  = 171  ( 168 + / 3  −)

# genes with fdr < 0.01 = 124  ( 123 + / 1  −)

<r> metagenes = 0.81

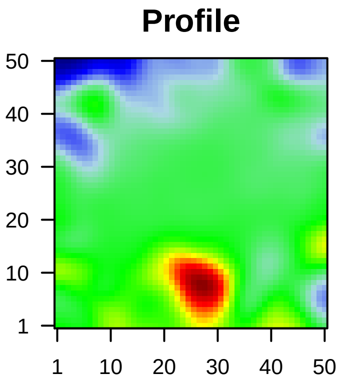
<r> genes = 0.15

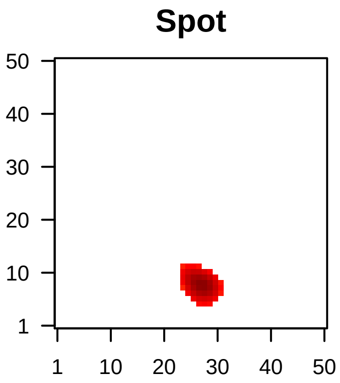
<FC> = 0.64

<shrinkage−t> = 9.89

<p−value> = 0.01

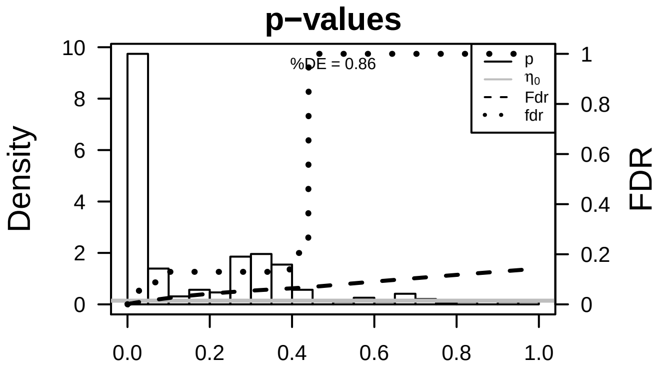
<fdr> = 0.59





## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | CTNNB1 | 0.95 | 9e−14 | 3e−08 | 26 x 9 | catenin (cadherin−associated protein), beta 1, 88kDa [Sourc |
| 2 | GPR82 | 1.95 | 6e−10 | 5e−08 | 24 x 9 | G protein−coupled receptor 82 [Source:HGNC Symbol;Acc:H |
| 3 | TRIM52 | 1.9 | 2e−09 | 1e−06 | 28 x 6 | tripartite motif containing 52 [Source:HGNC Symbol;Acc:HG |
| 4 | CRYBA1 | 1.75 | 3e−08 | 1e−06 | 27 x 9 | crystallin, beta A1 [Source:HGNC Symbol;Acc:HGNC:2394] |
| 5 | PIGA | 1.73 | 4e−08 | 3e−06 | 25 x 10 | phosphatidylinositol glycan anchor biosynthesis, class A [Sou |
| 6 | ZNF436 | 1.67 | 1e−07 | 3e−06 | 28 x 9 | zinc finger protein 436 [Source:HGNC Symbol;Acc:HGNC:20 |
| 7 | STON1−GTF | 1.64 | 2e−07 | 3e−06 | 29 x 8 | STON1−GTF2A1L readthrough [Source:HGNC Symbol;Acc: |
| 8 | AC004076.9 | 1.62 | 3e−07 | 3e−06 | 25 x 10 |  |
| 9 | TIAM2 | 1.62 | 3e−07 | 3e−06 | 26 x 10 | T−cell lymphoma invasion and metastasis 2 [Source:HGNC |
| 10 | OGN | 1.59 | 4e−07 | 3e−06 | 29 x 9 | osteoglycin [Source:HGNC Symbol;Acc:HGNC:8126] |
| 11 | C10orf131 | 1.59 | 5e−07 | 3e−06 | 28 x 7 | chromosome 10 open reading frame 131 [Source:HGNC Sy |
| 12 | PMP2 | 1.57 | 7e−07 | 3e−06 | 27 x 9 | peripheral myelin protein 2 [Source:HGNC Symbol;Acc:HGN |
| 13 | SPPL2A | 1.56 | 7e−07 | 3e−06 | 26 x 10 | signal peptide peptidase like 2A [Source:HGNC Symbol;Acc: |
| 14 | BTBD18 | 1.56 | 7e−07 | 3e−06 | 29 x 7 | BTB (POZ) domain containing 18 [Source:HGNC Symbol;Ac |
| 15 | ZNF235 | 1.56 | 8e−07 | 3e−06 | 31 x 8 | zinc finger protein 235 [Source:HGNC Symbol;Acc:HGNC:12 |
| 16 | KIF7 | 1.56 | 8e−07 | 3e−06 | 29 x 7 | kinesin family member 7 [Source:HGNC Symbol;Acc:HGNC: |
| 17 | RGS5 | 1.55 | 8e−07 | 3e−06 | 26 x 6 | regulator of G−protein signaling 5 [Source:HGNC Symbol;Ac |
| 18 | STX19 | 1.55 | 8e−07 | 7e−06 | 27 x 10 | syntaxin 19 [Source:HGNC Symbol;Acc:HGNC:19300] |
| 19 | KCNJ13 | 1.54 | 1e−06 | 7e−06 | 24 x 12 | potassium channel, inwardly rectifying subfamily J, member 1 |
| 20 | WDR19 | 1.54 | 1e−06 | 2e−05 | 27 x 10 | WD repeat domain 19 [Source:HGNC Symbol;Acc:HGNC:18 |



# G9_mel

## Local Summary

%DE = 0.83

# metagenes = 33

# genes = 527

# genes in genesets = 525

# genes with fdr < 0.1 = 326 ( 47 + / 279 −)

# genes with fdr < 0.05 = 232 ( 32 + / 200 −)

# genes with fdr < 0.01 = 124 ( 13 + / 111 −)

<r> metagenes = 0.86

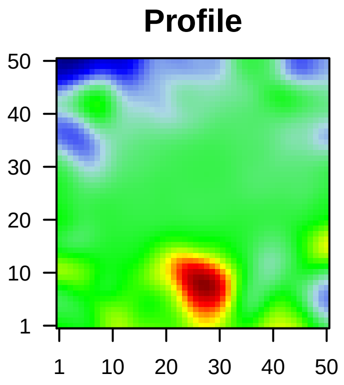
<r> genes = 0.2

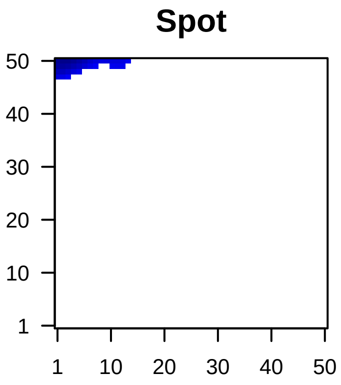
<FC> = −0.47

<shrinkage−t> = −7.76

<p−value> = 0.01

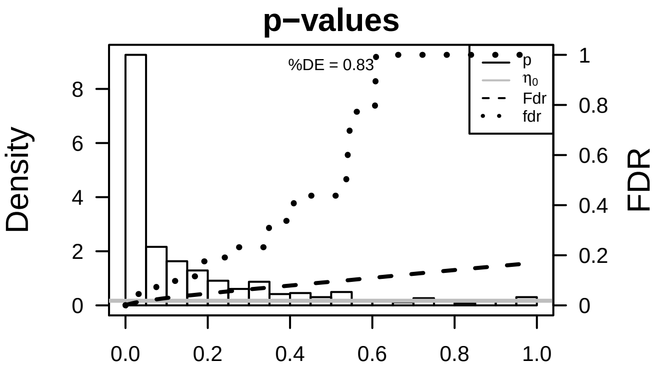
<fdr> = 0.64


Profile


Spot

## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | ARL6IP1 | −1.61 | 2e−16 | 5e−15 | 9 x 50 | ADP−ribosylation factor−like 6 interacting protein 1 [Source:H |
| 2 | CALM1 | −2.18 | 2e−16 | 5e−15 | 12 x 50 | calmodulin 1 (phosphorylase kinase, delta) [Source:HGNC Sy |
| 3 | LMAN2 | −1.83 | 2e−16 | 5e−15 | 13 x 50 | lectin, mannose−binding 2 [Source:HGNC Symbol;Acc:HGN |
| 4 | TIMM21 | −1.79 | 2e−16 | 5e−15 | 14 x 50 | translocase of inner mitochondrial membrane 21 homolog (ye |
| 5 | NASP | −1.7 | 1e−13 | 6e−12 | 1 x 48 | nuclear autoantigenic sperm protein (histone−binding) [Sourc |
| 6 | TUBG1 | −1.69 | 1e−13 | 2e−11 | 2 x 49 | tubulin, gamma 1 [Source:HGNC Symbol;Acc:HGNC:12417] |
| 7 | STMN1 | −0.92 | 6e−13 | 2e−11 | 5 x 50 | stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510] |
| 8 | PDCD10 | −1.66 | 8e−13 | 2e−11 | 13 x 50 | programmed cell death 10 [Source:HGNC Symbol;Acc:HGN |
| 9 | TMEM97 | −1.66 | 9e−13 | 3e−10 | 1 x 48 | transmembrane protein 97 [Source:HGNC Symbol;Acc:HGN |
| 10 | PCNA | −1.64 | 4e−12 | 8e−10 | 2 x 50 | proliferating cell nuclear antigen [Source:HGNC Symbol;Acc: |
| 11 | CDKN3 | −1.59 | 1e−11 | 5e−09 | 6 x 50 | cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A |
| 12 | GUCD1 | −1.59 | 9e−11 | 5e−09 | 1 x 47 | guanylyl cyclase domain containing 1 [Source:HGNC Symbol |
| 13 | HMGN2 | −0.99 | 2e−10 | 5e−09 | 8 x 50 | high mobility group nucleosomal binding domain 2 [Source:H |
| 14 | COMMD4 | −1.56 | 3e−10 | 5e−09 | 11 x 50 | COMM domain containing 4 [Source:HGNC Symbol;Acc:HGN |
| 15 | RRM1 | −1.58 | 3e−10 | 5e−09 | 2 x 50 | ribonucleotide reductase M1 [Source:HGNC Symbol;Acc:HG |
| 16 | MCM4 | −1.58 | 3e−10 | 6e−08 | 1 x 50 | minichromosome maintenance complex component 4 [Source |
| 17 | TK1 | −1.55 | 1e−09 | 4e−07 | 4 x 50 | thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:HGN |
| 18 | YEATS4 | −1.52 | 6e−09 | 4e−06 | 1 x 47 | YEATS domain containing 4 [Source:HGNC Symbol;Acc:HGN |
| 19 | RAB34 | −1.44 | 1e−07 | 4e−06 | 13 x 50 | RAB34, member RAS oncogene family [Source:HGNC Symb |
| 20 | H2AFV | −1.44 | 1e−07 | 4e−06 | 8 x 50 | H2A histone family, member V [Source:HGNC Symbol;Acc:H |


p−values