# G8_mel

## Global Summary

%DE = 0.19

# genes with fdr < 0.2  = 2450  ( 1530 + / 920  −)

# genes with fdr < 0.1  = 1835  ( 1195 + / 640  −)

# genes with fdr < 0.05  = 1507  ( 1000 + / 507  −)

# genes with fdr < 0.01 = 948  ( 622 + / 326  −)

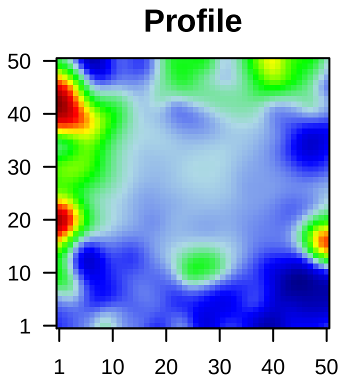
# genes in genesets = 14839

<FC> = 0

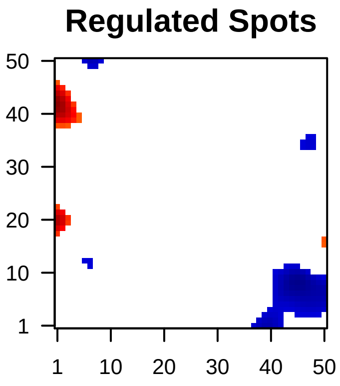
<shrinkage−t> = 0.09

<p−value> = 0.1

<fdr> = 0.81



**Profile**



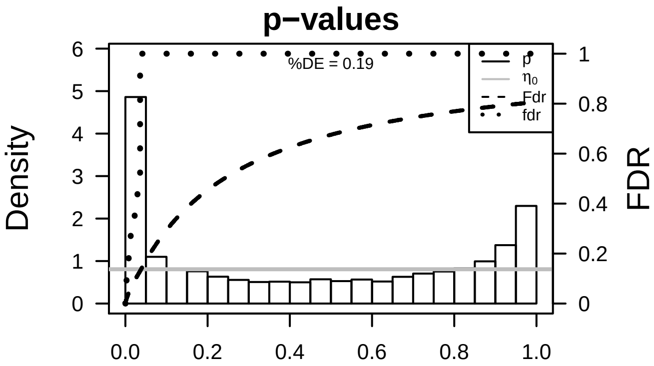
**Regulated Spots**

## Global Genelist

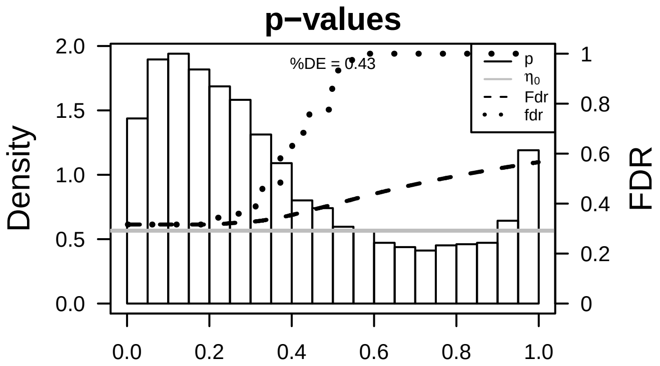
| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | ANKHD1 | −1.65 | 2e−16 | 3e−13 | 9 x 5 | ankyrin repeat and KH domain containing 1 [Source:HGNC S |
| 2 | CFL2 | −1.56 | 2e−16 | 3e−13 | 50 x 7 | cofilin 2 (muscle) [Source:HGNC Symbol;Acc:HGNC:1875] |
| 3 | COMMD4 | −1.48 | 2e−16 | 3e−13 | 11 x 50 | COMM domain containing 4 [Source:HGNC Symbol;Acc:HGN |
| 4 | CRBN | −1.79 | 2e−16 | 3e−13 | 1 x 8 | cereblon [Source:HGNC Symbol;Acc:HGNC:30185] |
| 5 | NDUFS3 | −1.57 | 2e−16 | 3e−13 | 1 x 32 | NADH dehydrogenase (ubiquinone) Fe−S protein 3, 30kDa ( |
| 6 | RNF114 | −1.44 | 2e−16 | 3e−13 | 16 x 50 | ring finger protein 114 [Source:HGNC Symbol;Acc:HGNC:13 |
| 7 | SMCO4 | 2.1 | 2e−16 | 3e−13 | 1 x 47 | single−pass membrane protein with coiled−coil domains 4 [S |
| 8 | THOC1 | −1.55 | 2e−16 | 3e−13 | 9 x 48 | THO complex 1 [Source:HGNC Symbol;Acc:HGNC:19070] |
| 9 | TMEM138 | −1.43 | 2e−16 | 3e−13 | 1 x 33 | transmembrane protein 138 [Source:HGNC Symbol;Acc:HGN |
| 10 | PDCD6IP | −1.23 | 4e−16 | 2e−11 | 33 x 50 | programmed cell death 6 interacting protein [Source:HGNC S |
| 11 | ASPA | 1.77 | 2e−15 | 9e−11 | 12 x 1 | aspartoacylase [Source:HGNC Symbol;Acc:HGNC:756] |
| 12 | POMT2 | 1.72 | 1e−14 | 9e−11 | 28 x 49 | protein−O−mannosyltransferase 2 [Source:HGNC Symbol;Ac |
| 13 | SACM1L | −1.24 | 2e−14 | 9e−11 | 9 x 7 | SAC1 suppressor of actin mutations 1−like (yeast) [Source:H |
| 14 | CARD10 | 1.7 | 3e−14 | 7e−10 | 41 x 36 | caspase recruitment domain family, member 10 [Source:HGN |
| 15 | PLA2G4B | 1.65 | 1e−13 | 7e−10 | 3 x 9 | phospholipase A2, group IVB (cytosolic) [Source:HGNC Sym |
| 16 | ZBTB8OS | −1.43 | 1e−13 | 2e−09 | 47 x 36 | zinc finger and BTB domain containing 8 opposite strand [Sou |
| 17 | TANK | −1.42 | 3e−13 | 3e−09 | 34 x 50 | TRAF family member−associated NFKB activator [Source:HG |
| 18 | RBM23 | −1.41 | 6e−13 | 5e−09 | 49 x 30 | RNA binding motif protein 23 [Source:HGNC Symbol;Acc:HG |
| 19 | MRPS33 | −1.4 | 1e−12 | 5e−09 | 5 x 17 | mitochondrial ribosomal protein S33 [Source:HGNC Symbol; |
| 20 | CELF4 | 1.57 | 2e−12 | 5e−09 | 27 x 15 | CUGBP, Elav−like family member 4 [Source:HGNC Symbol;A |

## Global Geneset Analysis

| Rank | GSZ | p−value | #all | | Geneset |
|---|---|---|---|---|---|
| *Overexpressed* | | | | | |
| 1 | 5.92 | 0.002 | 198 | HM | HALLMARK_OXIDATIVE_PHOSPHORYLATION |
| 2 | 5.54 | 0.002 | 1468 | CC | mitochondrion |
| 3 | 5.07 | 0.003 | 9482 | Colon Cancer | TCGA_Colon |
| 4 | 5.05 | 0.003 | 7592 | Lymphoma | HOPP_Active_promoter |
| 5 | 5.03 | 0.003 | 724 | GSEA C2 | PUJANA_CHEK2_PCC_NETWORK |
| 6 | 5.01 | 0.004 | 478 | GSEA C2 | STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN |
| 7 | 4.92 | 0.004 | 1460 | GSEA C2 | PUJANA_BRCA1_PCC_NETWORK |
| 8 | 4.88 | 0.004 | 1171 | TF | KIM_MYC targets |
| 9 | 4.58 | 0.005 | 401 | CC | mitochondrial inner membrane |
| 10 | 4.54 | 0.005 | 11 | GSEA C2 | REACTOME_UNWINDING_OF_DNA |
| 11 | 4.52 | 0.005 | 135 | BP | cellular metabolic process |
| 12 | 4.5 | 0.005 | 752 | GSEA C2 | GRADE_COLON_CANCER_UP |
| 13 | 4.48 | 0.005 | 113 | GSEA C2 | OUELLET_OVARIAN_CANCER_INVASIVE_VS_LMP_UP |
| 14 | 4.47 | 0.005 | 1126 | GSEA C2 | BLALOCK_ALZHEIMERS_DISEASE_DN |
| 15 | 4.45 | 0.005 | 683 | GSEA C2 | MARTENS_TRETINOIN_RESPONSE_DN |
| 16 | 4.43 | 0.005 | 398 | GSEA C2 | MOOTHA_PGC |
| 17 | 4.4 | 0.005 | 2193 | CC | extracellular exosome |
| 18 | 4.39 | 0.006 | 925 | GSEA C2 | KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN |
| 19 | 4.29 | 0.006 | 29 | BP | DNA strand elongation involved in DNA replication |
| 20 | 4.21 | 0.006 | 34 | GSEA C2 | YIH_RESPONSE_TO_ARSENITE_C3 |
| *Underexpressed* | | | | | |
| 1 | −4.17 | 0.007 | 187 | miRNA target | hsa−miR−382 |
| 2 | −4.11 | 0.007 | 118 | GSEA C2 | ODONNELL_TFRC_TARGETS_DN |
| 3 | −4.07 | 0.007 | 75 | GSEA C2 | SCIBETTA_KDM5B_TARGETS_DN |
| 4 | −3.93 | 0.008 | 222 | GSEA C2 | UDAYAKUMAR_MED1_TARGETS_DN |
| 5 | −3.82 | 0.009 | 2211 | Lymphoma | HOPP_Repetitive |
| 6 | −3.77 | 0.009 | 425 | GSEA C2 | TOYOTA_TARGETS_OF_MIR34B_AND_MIR34C |
| 7 | −3.7 | 0.010 | 3897 | Colon Cancer | Quies1_Colon |
| 8 | −3.68 | 0.010 | 5 | GSEA C2 | INAMURA_LUNG_CANCER_SCC_SUBTYPES_DN |
| 9 | −3.66 | 0.010 | 70 | miRNA target | hsa−miR−502−5p |
| 10 | −3.62 | 0.010 | 1394 | GSEA C2 | ZWANG_TRANSIENTLY_UP_BY_1ST_EGF_PULSE_ONLY |
| 11 | −3.61 | 0.010 | 310 | GSEA C2 | DAZARD_RESPONSE_TO_UV_NHEK_DN |
| 12 | −3.6 | 0.011 | 312 | BP | mitotic nuclear division |
| 13 | −3.6 | 0.011 | 40 | miRNA target | hsa−miR−758 |
| 14 | −3.59 | 0.011 | 44 | GSEA C2 | REACTOME_PI_METABOLISM |
| 15 | −3.58 | 0.011 | 81 | GSEA C2 | GAVIN_FOXP3_TARGETS_CLUSTER_P6 |
| 16 | −3.56 | 0.011 | 15 | GSEA C2 | REACTOME_SYNTHESIS_OF_PIPS_AT_THE_GOLGI_MEMBRA |
| 17 | −3.53 | 0.011 | 28 | GSEA C2 | REICHERT_MITOSIS_LIN9_TARGETS |
| 18 | −3.51 | 0.011 | 133 | BP | G2/M transition of mitotic cell cycle |
| 19 | −3.5 | 0.012 | 55 | miRNA target | hsa−miR−191 |
| 20 | −3.47 | 0.012 | 1050 | Brain | Fetal_EnhP |



**p−values**



**p−values**

# G8_mel

## Local Summary

%DE = 0.53

# metagenes = 2

# genes = 35

# genes in genesets = 35

# genes with fdr < 0.1 = 13 ( 12 + / 1 −)

# genes with fdr < 0.05 = 12 ( 11 + / 1 −)

# genes with fdr < 0.01 = 7 ( 7 + / 0 −)

<r> metagenes = 0.99

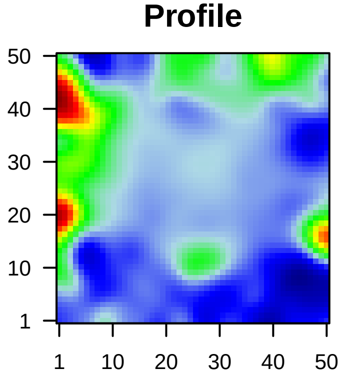
<r> genes = 0.12

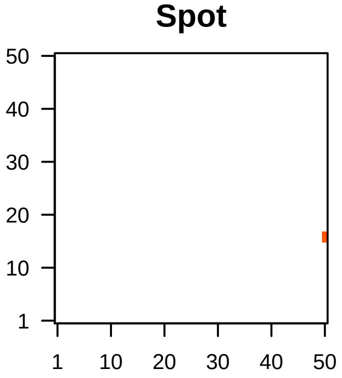
<FC> = 0.29

<shrinkage−t> = 4.39

<p−value> = 0.02

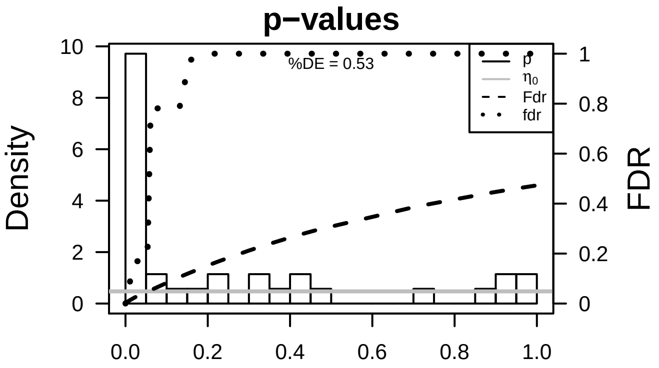
<fdr> = 0.61





## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | CCL2 | 1.34 | 2e−09 | 6e−05 | 50 x 17 | chemokine (C−C motif) ligand 2 [Source:HGNC Symbol;Acc: |
| 2 | SLC16A4 | 1.03 | 4e−06 | 3e−04 | 50 x 16 | solute carrier family 16, member 4 [Source:HGNC Symbol;Ac |
| 3 | SAP30L | 0.95 | 2e−05 | 1e−03 | 50 x 17 | SAP30−like [Source:HGNC Symbol;Acc:HGNC:25663] |
| 4 | HYAL2 | 0.87 | 1e−04 | 5e−03 | 50 x 16 | hyaluronoglucosaminidase 2 [Source:HGNC Symbol;Acc:HG |
| 5 | AKAP8L | 0.77 | 5e−04 | 5e−03 | 50 x 16 | A kinase (PRKA) anchor protein 8−like [Source:HGNC Symb |
| 6 | PARD6B | 0.75 | 8e−04 | 5e−03 | 50 x 17 | par−6 family cell polarity regulator beta [Source:HGNC Symb |
| 7 | CYP20A1 | 0.73 | 1e−03 | 5e−03 | 50 x 17 | cytochrome P450, family 20, subfamily A, polypeptide 1 [Sour |
| 8 | PARP9 | 0.72 | 1e−03 | 2e−02 | 50 x 17 | poly (ADP−ribose) polymerase family, member 9 [Source:HG |
| 9 | TGFBR1 | −0.57 | 4e−03 | 2e−02 | 50 x 17 | transforming growth factor, beta receptor 1 [Source:HGNC Sy |
| 10 | CLCN6 | 0.64 | 4e−03 | 2e−02 | 50 x 16 | chloride channel, voltage−sensitive 6 [Source:HGNC Symbol; |
| 11 | SLU7 | 0.55 | 6e−03 | 2e−02 | 50 x 16 | SLU7 splicing factor homolog (S. cerevisiae) [Source:HGNC |
| 12 | AP4B1 | 0.6 | 7e−03 | 4e−02 | 50 x 16 | adaptor−related protein complex 4, beta 1 subunit [Source:H |
| 13 | VEZF1 | 0.57 | 9e−03 | 7e−02 | 50 x 16 | vascular endothelial zinc finger 1 [Source:HGNC Symbol;Acc |
| 14 | RNF123 | −0.55 | 1e−02 | 1e−01 | 50 x 17 | ring finger protein 123 [Source:HGNC Symbol;Acc:HGNC:21 |
| 15 | EZH1 | 0.52 | 2e−02 | 2e−01 | 50 x 17 | enhancer of zeste 1 polycomb repressive complex 2 subunit [ |
| 16 | TTC39C | 0.46 | 4e−02 | 2e−01 | 50 x 17 | tetratricopeptide repeat domain 39C [Source:HGNC Symbol; |
| 17 | ARHGEF1 | −0.45 | 4e−02 | 2e−01 | 50 x 16 | Rho guanine nucleotide exchange factor (GEF) 1 [Source:HG |
| 18 | EDEM1 | 0.39 | 5e−02 | 2e−01 | 50 x 17 | ER degradation enhancer, mannosidase alpha−like 1 [Source |
| 19 | PRELID2 | 0.42 | 6e−02 | 8e−01 | 50 x 16 | PRELI domain containing 2 [Source:HGNC Symbol;Acc:HGN |
| 20 | BIRC6 | −0.29 | 1e−01 | 8e−01 | 50 x 17 | baculoviral IAP repeat containing 6 [Source:HGNC Symbol;A |



# G8_mel

## Local Summary

%DE = 0.74

# metagenes = 12

# genes = 231

# genes in genesets = 230

# genes with fdr < 0.1 = 129 ( 112 + / 17 −)

# genes with fdr < 0.05 = 101 ( 90 + / 11 −)

# genes with fdr < 0.01 = 80 ( 72 + / 8 −)

<r> metagenes = 0.98

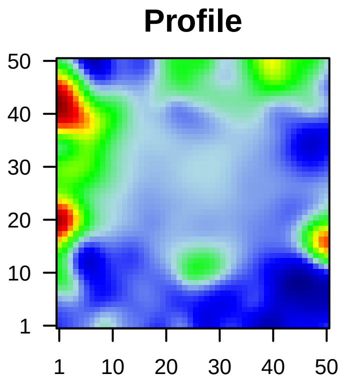
<r> genes = 0.16

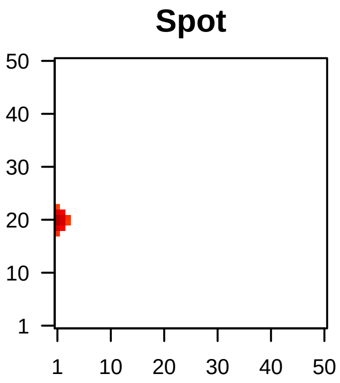
<FC> = 0.3

<shrinkage−t> = 5.16

<p−value> = 0.01

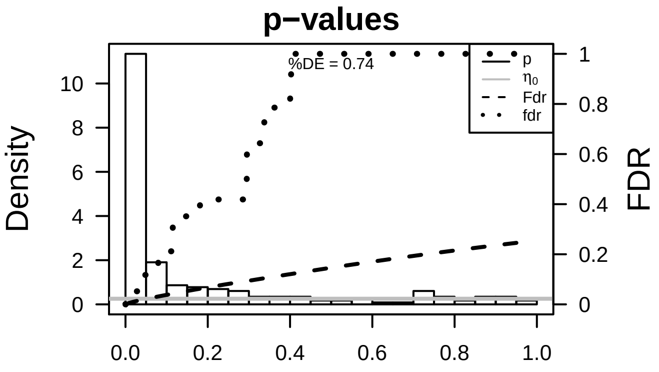
<fdr> = 0.51





## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | SPRY2 | 1.36 | 1e−09 | 8e−07 | 1 x 21 | sprouty homolog 2 (Drosophila) [Source:HGNC Symbol;Acc: |
| 2 | PIGY | 0.58 | 1e−08 | 2e−06 | 1 x 20 | phosphatidylinositol glycan anchor biosynthesis, class Y [Sou |
| 3 | ZNF511 | 1.21 | 5e−08 | 1e−05 | 1 x 21 | zinc finger protein 511 [Source:HGNC Symbol;Acc:HGNC:28 |
| 4 | CDKN2A | 1.14 | 3e−07 | 1e−05 | 1 x 21 | cyclin−dependent kinase inhibitor 2A [Source:HGNC Symbol; |
| 5 | PLEKHA1 | 1.13 | 4e−07 | 2e−05 | 2 x 21 | pleckstrin homology domain containing, family A (phosphoino |
| 6 | RCE1 | 1.1 | 8e−07 | 3e−05 | 1 x 20 | Ras converting CAAX endopeptidase 1 [Source:HGNC Symb |
| 7 | EI24 | 1.08 | 1e−06 | 3e−05 | 1 x 20 | etoposide induced 2.4 [Source:HGNC Symbol;Acc:HGNC:13 |
| 8 | FAM120AOS | 1.06 | 2e−06 | 7e−05 | 1 x 19 | family with sequence similarity 120A opposite strand [Source: |
| 9 | TMEM123 | 0.41 | 5e−06 | 7e−05 | 1 x 21 | transmembrane protein 123 [Source:HGNC Symbol;Acc:HGN |
| 10 | RAB32 | 0.48 | 5e−06 | 7e−05 | 1 x 20 | RAB32, member RAS oncogene family [Source:HGNC Symb |
| 11 | AGPAT2 | 1.01 | 5e−06 | 8e−05 | 1 x 21 | 1−acylglycerol−3−phosphate O−acyltransferase 2 [Source:H |
| 12 | SURF1 | 1 | 7e−06 | 2e−04 | 1 x 18 | surfeit 1 [Source:HGNC Symbol;Acc:HGNC:11474] |
| 13 | PFN1 | 0.48 | 1e−05 | 2e−04 | 1 x 21 | profilin 1 [Source:HGNC Symbol;Acc:HGNC:8881] |
| 14 | MICU2 | 0.97 | 1e−05 | 2e−04 | 1 x 21 | mitochondrial calcium uptake 2 [Source:HGNC Symbol;Acc:H |
| 15 | PRCP | −0.95 | 2e−05 | 2e−04 | 1 x 19 | prolylcarboxypeptidase (angiotensinase C) [Source:HGNC S |
| 16 | GTF3A | 0.63 | 3e−05 | 2e−04 | 1 x 20 | general transcription factor IIIA [Source:HGNC Symbol;Acc:H |
| 17 | COPRS | 0.93 | 3e−05 | 2e−04 | 1 x 20 | coordinator of PRMT5, differentiation stimulator [Source:HGN |
| 18 | FXN | 0.92 | 4e−05 | 2e−04 | 1 x 20 | frataxin [Source:HGNC Symbol;Acc:HGNC:3951] |
| 19 | FAM58A | 0.92 | 4e−05 | 2e−04 | 1 x 20 | family with sequence similarity 58, member A [Source:HGNC |
| 20 | PTPN2 | 0.81 | 4e−05 | 2e−04 | 1 x 20 | protein tyrosine phosphatase, non−receptor type 2 [Source:H |



# G8_mel

## Local Summary

%DE = 0.78
# metagenes = 30
# genes = 407
# genes in genesets = 405

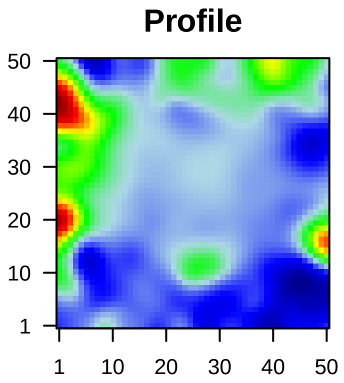
# genes with fdr < 0.1  = 219  ( 183 + / 36  −)
# genes with fdr < 0.05  = 160  ( 136 + / 24  −)
# genes with fdr < 0.01 = 116  ( 98 + / 18  −)

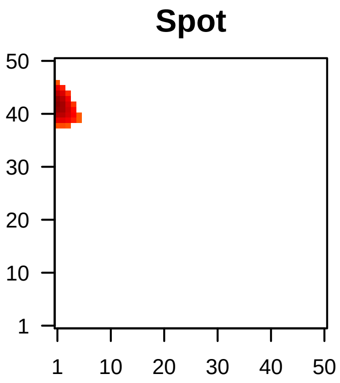
<r> metagenes = 0.94
<r> genes = 0.15

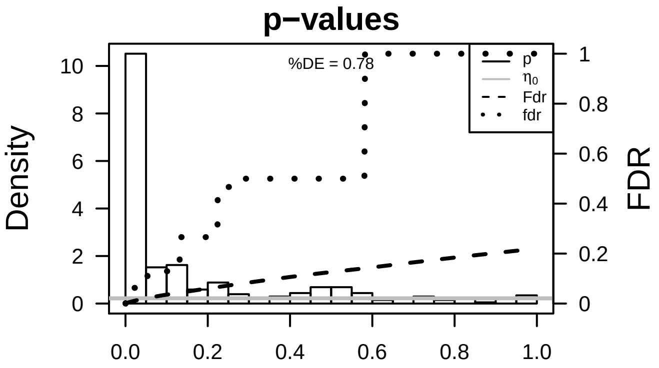
<FC> = 0.25
<shrinkage−t> = 4.66
<p−value> = 0.01
<fdr> = 0.57

## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | VPS41 | −1.27 | 6e−12 | 2e−08 | 4 x 42 | vacuolar protein sorting 41 homolog (S. cerevisiae) [Source:H |
| 2 | SFXN4 | −1.3 | 2e−10 | 2e−07 | 1 x 41 | sideroflexin 4 [Source:HGNC Symbol;Acc:HGNC:16088] |
| 3 | CAPN3 | 0.6 | 2e−09 | 6e−07 | 1 x 43 | calpain 3, (p94) [Source:HGNC Symbol;Acc:HGNC:1480] |
| 4 | ARHGAP8 | 0.87 | 9e−09 | 3e−06 | 1 x 43 | Rho GTPase activating protein 8 [Source:HGNC Symbol;Acc |
| 5 | CRYL1 | 1.21 | 6e−08 | 3e−06 | 1 x 41 | crystallin, lambda 1 [Source:HGNC Symbol;Acc:HGNC:1824 |
| 6 | ST6GALNAC1 | 0.93 | 7e−08 | 3e−06 | 1 x 44 | ST6 (alpha−N−acetyl−neuraminyl−2,3−beta−galactosyl−1,3)− |
| 7 | LGALS3 | 1.05 | 9e−08 | 4e−06 | 1 x 43 | lectin, galactoside−binding, soluble, 3 [Source:HGNC Symbol |
| 8 | ISY1 | 1.18 | 1e−07 | 6e−06 | 1 x 40 | ISY1 splicing factor homolog (S. cerevisiae) [Source:HGNC S |
| 9 | EIF4A3 | 0.49 | 2e−07 | 6e−06 | 4 x 40 | eukaryotic translation initiation factor 4A3 [Source:HGNC Syn |
| 10 | BTK | 1.15 | 3e−07 | 1e−05 | 3 x 43 | Bruton agammaglobulinemia tyrosine kinase [Source:HGNC |
| 11 | ATP6V0E2 | 1.12 | 5e−07 | 1e−05 | 1 x 44 | ATPase, H+ transporting V0 subunit e2 [Source:HGNC Symb |
| 12 | SOAT1 | −1.01 | 7e−07 | 1e−05 | 1 x 44 | sterol O−acyltransferase 1 [Source:HGNC Symbol;Acc:HGN |
| 13 | EIF5A2 | 1.05 | 9e−07 | 1e−05 | 3 x 41 | eukaryotic translation initiation factor 5A2 [Source:HGNC Syn |
| 14 | SLC16A7 | 1.1 | 9e−07 | 3e−05 | 4 x 39 | solute carrier family 16 (monocarboxylate transporter), memb |
| 15 | TEX30 | 1.08 | 1e−06 | 3e−05 | 1 x 46 | testis expressed 30 [Source:HGNC Symbol;Acc:HGNC:2518 |
| 16 | SNAP29 | 1.07 | 2e−06 | 3e−05 | 1 x 40 | synaptosomal−associated protein, 29kDa [Source:HGNC Sy |
| 17 | LINS | 1.06 | 2e−06 | 5e−05 | 4 x 39 | lines homolog (Drosophila) [Source:HGNC Symbol;Acc:HGN |
| 18 | AZIN1 | −0.69 | 3e−06 | 6e−05 | 4 x 41 | antizyme inhibitor 1 [Source:HGNC Symbol;Acc:HGNC:1643 |
| 19 | NARS2 | 0.42 | 4e−06 | 6e−05 | 1 x 42 | asparaginyl−tRNA synthetase 2, mitochondrial (putative) [Sou |
| 20 | FAM174B | 1.02 | 5e−06 | 6e−05 | 1 x 42 | family with sequence similarity 174, member B [Source:HGN |







# G8_mel

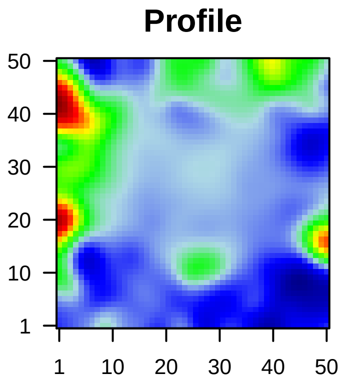
## Local Summary

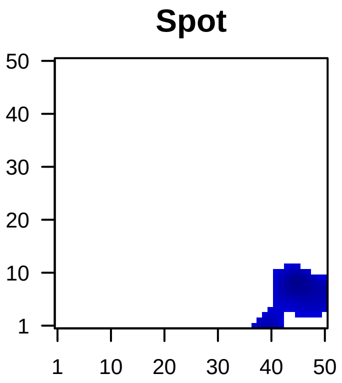
%DE = 0.43
# metagenes = 101
# genes = 772
# genes in genesets = 770

# genes with fdr < 0.1 = 170 ( 60 + / 110 −)
# genes with fdr < 0.05 = 110 ( 39 + / 71 −)
# genes with fdr < 0.01 = 76 ( 25 + / 51 −)

<r> metagenes = 0.74
<r> genes = 0.09

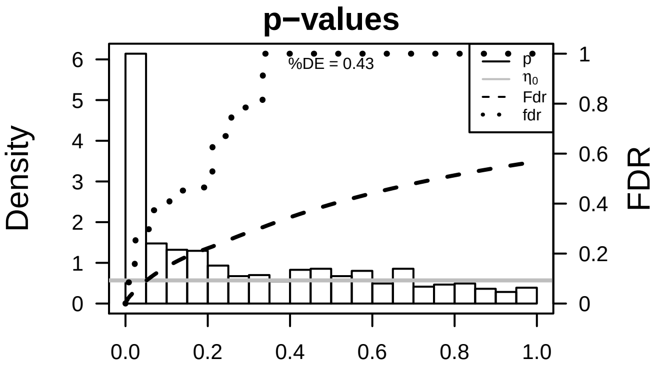
<FC> = −0.14
<shrinkage−t> = −2.14
<p−value> = 0.06
<fdr> = 0.76





## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | CFL2 | −1.56 | 2e−16 | 1e−13 | 50 x 7 | cofilin 2 (muscle) [Source:HGNC Symbol;Acc:HGNC:1875] |
| 2 | BBX | −1.25 | 4e−12 | 2e−07 | 50 x 7 | bobby sox homolog (Drosophila) [Source:HGNC Symbol;Acc: |
| 3 | MYCBP2 | −1.26 | 4e−10 | 2e−07 | 39 x 3 | MYC binding protein 2, E3 ubiquitin protein ligase [Source:H |
| 4 | SHOC2 | −1.13 | 7e−10 | 2e−07 | 42 x 6 | soc−2 suppressor of clear homolog (C. elegans) [Source:HG |
| 5 | AKR1A1 | −1.25 | 1e−09 | 2e−07 | 50 x 7 | aldo−keto reductase family 1, member A1 (aldehyde reductas |
| 6 | FAXDC2 | 1.35 | 2e−09 | 3e−06 | 42 x 9 | fatty acid hydroxylase domain containing 2 [Source:HGNC Sy |
| 7 | ERLEC1 | −1.21 | 8e−09 | 1e−05 | 38 x 1 | endoplasmic reticulum lectin 1 [Source:HGNC Symbol;Acc:H |
| 8 | ADAMTSL5 | 1.22 | 4e−08 | 1e−05 | 45 x 3 | ADAMTS−like 5 [Source:HGNC Symbol;Acc:HGNC:27912] |
| 9 | FAM76A | −1.17 | 8e−08 | 1e−05 | 50 x 7 | family with sequence similarity 76, member A [Source:HGNC |
| 10 | ITSN1 | −1.16 | 9e−08 | 3e−05 | 46 x 6 | intersectin 1 (SH3 domain protein) [Source:HGNC Symbol;Ac |
| 11 | LUM | 1.16 | 2e−07 | 3e−05 | 49 x 7 | lumican [Source:HGNC Symbol;Acc:HGNC:6724] |
| 12 | PPP4R1 | −1.14 | 2e−07 | 6e−05 | 50 x 7 | protein phosphatase 4, regulatory subunit 1 [Source:HGNC S |
| 13 | TMEM167B | 1.12 | 5e−07 | 6e−05 | 39 x 3 | transmembrane protein 167B [Source:HGNC Symbol;Acc:HG |
| 14 | ITGB1 | −0.81 | 6e−07 | 6e−05 | 50 x 5 | integrin, beta 1 (fibronectin receptor, beta polypeptide, antige |
| 15 | ACBD3 | −1.05 | 8e−07 | 6e−05 | 38 x 1 | acyl−CoA binding domain containing 3 [Source:HGNC Symb |
| 16 | INTS6 | 1.1 | 8e−07 | 1e−04 | 44 x 6 | integrator complex subunit 6 [Source:HGNC Symbol;Acc:HG |
| 17 | HNRNPLL | −1.05 | 1e−06 | 1e−04 | 41 x 10 | heterogeneous nuclear ribonucleoprotein L−like [Source:HG |
| 18 | MAD1L1 | −1.07 | 1e−06 | 5e−04 | 37 x 1 | MAD1 mitotic arrest deficient−like 1 (yeast) [Source:HGNC S |
| 19 | PPP1R15A | −0.91 | 4e−06 | 5e−04 | 49 x 4 | protein phosphatase 1, regulatory subunit 15A [Source:HGN |
| 20 | ZBTB20 | 1.02 | 5e−06 | 5e−04 | 41 x 10 | zinc finger and BTB domain containing 20 [Source:HGNC Sy |



# G8_mel

## Local Summary

%DE = 0.86

# metagenes = 3

# genes = 24

# genes in genesets = 24

# genes with fdr < 0.1 = 13 ( 3 + / 10 −)

# genes with fdr < 0.05 = 6 ( 0 + / 6 −)

# genes with fdr < 0.01 = 1 ( 0 + / 1 −)

<r> metagenes = 0.99

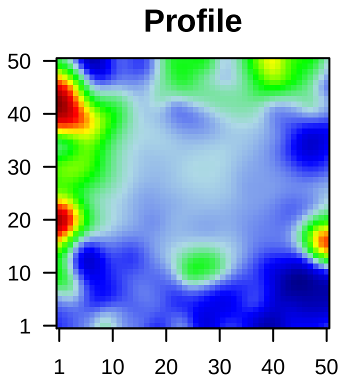
<r> genes = 0.15

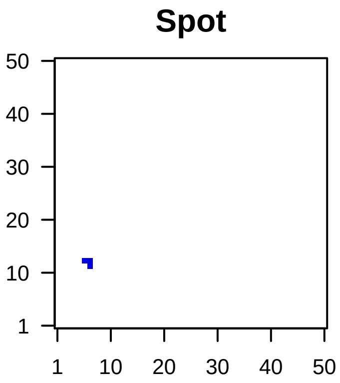
<FC> = −0.2

<shrinkage−t> = −3.05

<p−value> = 0.1

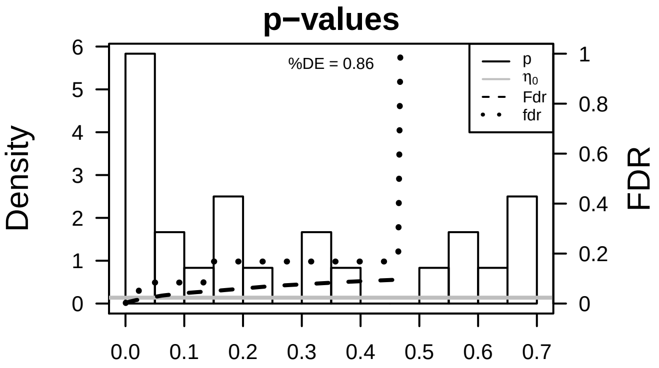
<fdr> = 0.78





## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | BMPR1B | −0.77 | 6e−04 | 0.002 | 6 x 13 | bone morphogenetic protein receptor, type IB [Source:HGNC |
| 2 | PPP2R3A | −0.72 | 1e−03 | 0.012 | 7 x 13 | protein phosphatase 2, regulatory subunit B", alpha [Source: |
| 3 | HLA−DPB1 | −0.6 | 7e−03 | 0.012 | 7 x 13 | major histocompatibility complex, class II, DP beta 1 [Source: |
| 4 | TSPAN4 | −0.59 | 9e−03 | 0.026 | 6 x 13 | tetraspanin 4 [Source:HGNC Symbol;Acc:HGNC:11859] |
| 5 | MBD3 | −0.5 | 3e−02 | 0.026 | 7 x 13 | methyl−CpG binding domain protein 3 [Source:HGNC Symbo |
| 6 | RCL1 | −0.48 | 3e−02 | 0.026 | 6 x 13 | RNA terminal phosphate cyclase−like 1 [Source:HGNC Sym |
| 7 | SEMA3A | −0.48 | 3e−02 | 0.084 | 7 x 12 | sema domain, immunoglobulin domain (Ig), short basic doma |
| 8 | CNOT6 | −0.38 | 9e−02 | 0.084 | 7 x 12 | CCR4−NOT transcription complex, subunit 6 [Source:HGNC |
| 9 | RUVBL2 | 0.31 | 9e−02 | 0.084 | 6 x 13 | RuvB−like AAA ATPase 2 [Source:HGNC Symbol;Acc:HGNC |
| 10 | MAFB | 0.32 | 1e−01 | 0.084 | 7 x 13 | v−maf avian musculoaponeurotic fibrosarcoma oncogene ho |
| 11 | C6orf136 | −0.31 | 2e−01 | 0.084 | 6 x 13 | chromosome 6 open reading frame 136 [Source:HGNC Sym |
| 12 | HECTD3 | −0.31 | 2e−01 | 0.084 | 7 x 13 | HECT domain containing E3 ubiquitin protein ligase 3 [Sourc |
| 13 | MRPS14 | 0.24 | 2e−01 | 0.084 | 6 x 13 | mitochondrial ribosomal protein S14 [Source:HGNC Symbol; |
| 14 | VCPIP1 | −0.28 | 2e−01 | 0.168 | 6 x 13 | valosin containing protein (p97)/p47 complex interacting prote |
| 15 | ARHGDIA | −0.15 | 3e−01 | 0.168 | 7 x 13 | Rho GDP dissociation inhibitor (GDI) alpha [Source:HGNC S |
| 16 | DUSP7 | −0.21 | 3e−01 | 0.168 | 7 x 12 | dual specificity phosphatase 7 [Source:HGNC Symbol;Acc:H |
| 17 | PDP2 | 0.19 | 4e−01 | 0.168 | 7 x 13 | pyruvate dehyrogenase phosphatase catalytic subunit 2 [Sou |
| 18 | TACR2 | −0.13 | 5e−01 | 0.168 | 7 x 13 | tachykinin receptor 2 [Source:HGNC Symbol;Acc:HGNC:115 |
| 19 | BCL2 | −0.12 | 6e−01 | 0.168 | 7 x 13 | B−cell CLL/lymphoma 2 [Source:HGNC Symbol;Acc:HGNC:9 |
| 20 | RUNX2 | −0.12 | 6e−01 | 0.168 | 6 x 13 | runt−related transcription factor 2 [Source:HGNC Symbol;Acc |



# G8_mel

## Local Summary

%DE = 0.73

# metagenes = 8

# genes = 36

# genes in genesets = 36

# genes with fdr < 0.1 = 17 ( 4 + / 13 −)

# genes with fdr < 0.05 = 16 ( 4 + / 12 −)

# genes with fdr < 0.01 = 14 ( 3 + / 11 −)

<r> metagenes = 0.96

<r> genes = 0.13

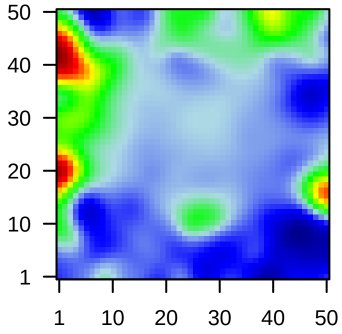
<FC> = −0.29

<shrinkage−t> = −4.81

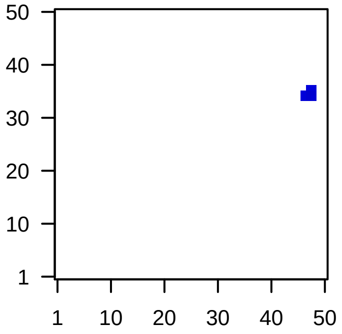
<p−value> = 0

<fdr> = 0.52

**Profile**



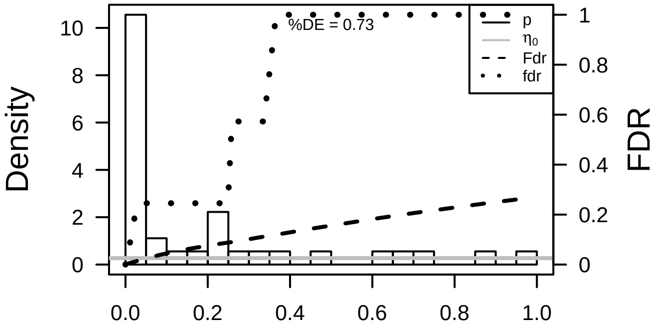
**Spot**



## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | ZBTB8OS | −1.43 | 1e−13 | 5e−11 | 47 x 36 | zinc finger and BTB domain containing 8 opposite strand [Sou |
| 2 | ANAPC7 | −1.36 | 5e−12 | 4e−05 | 46 x 34 | anaphase promoting complex subunit 7 [Source:HGNC Symb |
| 3 | BLOC1S3 | −1.03 | 4e−06 | 4e−05 | 48 x 36 | biogenesis of lysosomal organelles complex−1, subunit 3 [So |
| 4 | NR2C2 | 1 | 8e−06 | 2e−04 | 47 x 36 | nuclear receptor subfamily 2, group C, member 2 [Source:HG |
| 5 | GLUD1 | −0.94 | 2e−05 | 5e−04 | 46 x 34 | glutamate dehydrogenase 1 [Source:HGNC Symbol;Acc:HG |
| 6 | P4HA2 | −0.88 | 8e−05 | 7e−04 | 48 x 34 | prolyl 4−hydroxylase, alpha polypeptide II [Source:HGNC Sy |
| 7 | DPM3 | −0.69 | 2e−04 | 3e−03 | 46 x 34 | dolichyl−phosphate mannosyltransferase polypeptide 3 [Sour |
| 8 | KIAA0020 | 0.76 | 7e−04 | 3e−03 | 47 x 36 | KIAA0020 [Source:HGNC Symbol;Acc:HGNC:29676] |
| 9 | EXTL2 | −0.74 | 9e−04 | 3e−03 | 47 x 34 | exostosin−like glycosyltransferase 2 [Source:HGNC Symbol; |
| 10 | OGFOD1 | −0.65 | 1e−03 | 8e−03 | 47 x 34 | 2−oxoglutarate and iron−dependent oxygenase domain conta |
| 11 | WSB1 | −0.28 | 2e−03 | 8e−03 | 47 x 35 | WD repeat and SOCS box containing 1 [Source:HGNC Symb |
| 12 | XPNPEP3 | −0.66 | 3e−03 | 8e−03 | 48 x 36 | X−prolyl aminopeptidase 3, mitochondrial [Source:HGNC Sy |
| 13 | AHSA1 | 0.38 | 5e−03 | 8e−03 | 46 x 35 | AHA1, activator of heat shock 90kDa protein ATPase homolo |
| 14 | SYNJ2BP−C | −0.57 | 5e−03 | 8e−03 | 48 x 36 | SYNJ2BP−COX16 readthrough [Source:HGNC Symbol;Acc: |
| 15 | FTSJ3 | 0.63 | 5e−03 | 2e−02 | 47 x 34 | FtsJ homolog 3 (E. coli) [Source:HGNC Symbol;Acc:HGNC:1 |
| 16 | XIAP | −0.6 | 7e−03 | 2e−02 | 48 x 35 | X−linked inhibitor of apoptosis, E3 ubiquitin protein ligase [So |
| 17 | THUMPD1 | −0.48 | 9e−03 | 7e−02 | 46 x 35 | THUMP domain containing 1 [Source:HGNC Symbol;Acc:HG |
| 18 | DZIP1 | −0.54 | 2e−02 | 2e−01 | 47 x 34 | DAZ interacting zinc finger protein 1 [Source:HGNC Symbol; |
| 19 | SCFD2 | −0.48 | 3e−02 | 2e−01 | 46 x 35 | sec1 family domain containing 2 [Source:HGNC Symbol;Acc: |
| 20 | MAPK8 | −0.39 | 8e−02 | 2e−01 | 48 x 35 | mitogen−activated protein kinase 8 [Source:HGNC Symbol;A |

**p−values**



# G8_mel

## Local Summary

%DE = 0.83

# metagenes = 6

# genes = 120

# genes in genesets = 120

# genes with fdr < 0.1 = 73 ( 21 + / 52 −)

# genes with fdr < 0.05 = 63 ( 17 + / 46 −)

# genes with fdr < 0.01 = 26 ( 10 + / 16 −)

<r> metagenes = 0.99

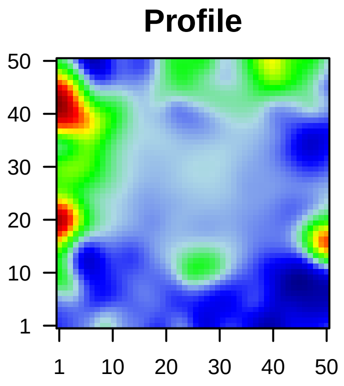
<r> genes = 0.43

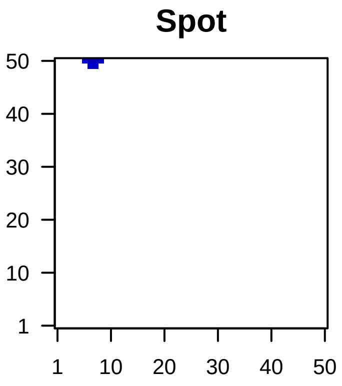
<FC> = −0.19

<shrinkage−t> = −2.78

<p−value> = 0.02

<fdr> = 0.59





## Local Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | CKAP2 | −1.22 | 6e−09 | 2e−05 | 6 x 50 | cytoskeleton associated protein 2 [Source:HGNC Symbol;Acc |
| 2 | NEDD1 | −1.09 | 8e−07 | 4e−05 | 8 x 49 | neural precursor cell expressed, developmentally down−regul |
| 3 | KIF23 | −1.04 | 3e−06 | 4e−05 | 6 x 50 | kinesin family member 23 [Source:HGNC Symbol;Acc:HGNC |
| 4 | CCNB1 | −0.99 | 7e−06 | 4e−05 | 7 x 50 | cyclin B1 [Source:HGNC Symbol;Acc:HGNC:1579] |
| 5 | TTF2 | 1 | 8e−06 | 2e−04 | 8 x 50 | transcription termination factor, RNA polymerase II [Source:H |
| 6 | CCNB2 | −0.95 | 2e−05 | 2e−04 | 6 x 50 | cyclin B2 [Source:HGNC Symbol;Acc:HGNC:1580] |
| 7 | CENPL | −0.94 | 3e−05 | 2e−04 | 6 x 50 | centromere protein L [Source:HGNC Symbol;Acc:HGNC:178 |
| 8 | CDC20 | 0.91 | 5e−05 | 2e−04 | 6 x 50 | cell division cycle 20 [Source:HGNC Symbol;Acc:HGNC:172 |
| 9 | UACA | 0.87 | 5e−05 | 2e−04 | 9 x 50 | uveal autoantigen with coiled−coil domains and ankyrin repe |
| 10 | APOBEC3B | 0.9 | 5e−05 | 2e−04 | 6 x 50 | apolipoprotein B mRNA editing enzyme, catalytic polypeptide |
| 11 | MIS18BP1 | −0.9 | 5e−05 | 2e−04 | 6 x 50 | MIS18 binding protein 1 [Source:HGNC Symbol;Acc:HGNC:2 |
| 12 | AURKA | −0.89 | 6e−05 | 1e−03 | 8 x 50 | aurora kinase A [Source:HGNC Symbol;Acc:HGNC:11393] |
| 13 | DEPDC1 | 0.85 | 2e−04 | 1e−03 | 6 x 50 | DEP domain containing 1 [Source:HGNC Symbol;Acc:HGNC |
| 14 | KIAA1524 | 0.84 | 2e−04 | 1e−03 | 6 x 50 | KIAA1524 [Source:HGNC Symbol;Acc:HGNC:29302] |
| 15 | NCAPG | −0.82 | 2e−04 | 4e−03 | 6 x 50 | non−SMC condensin I complex, subunit G [Source:HGNC Sy |
| 16 | ADD3 | 0.78 | 5e−04 | 4e−03 | 9 x 50 | adducin 3 (gamma) [Source:HGNC Symbol;Acc:HGNC:245] |
| 17 | TUBB4B | −0.59 | 7e−04 | 4e−03 | 7 x 50 | tubulin, beta 4B class IVb [Source:HGNC Symbol;Acc:HGNC |
| 18 | BUB1B | −0.75 | 8e−04 | 4e−03 | 6 x 50 | BUB1 mitotic checkpoint serine/threonine kinase B [Source:H |
| 19 | SYNE2 | −0.74 | 1e−03 | 4e−03 | 9 x 50 | spectrin repeat containing, nuclear envelope 2 [Source:HGN |
| 20 | UBE2C | 0.71 | 1e−03 | 4e−03 | 6 x 50 | ubiquitin−conjugating enzyme E2C [Source:HGNC Symbol;A |