

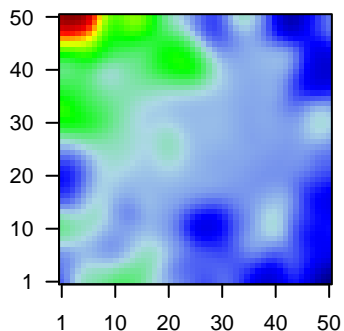
D12_mel

Global Summary

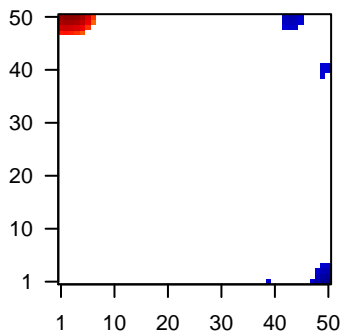
%DE = 0.21
 # genes with fdr < 0.2 = 2712 (1647 + / 1065 -)
 # genes with fdr < 0.1 = 2175 (1341 + / 834 -)
 # genes with fdr < 0.05 = 1849 (1155 + / 694 -)
 # genes with fdr < 0.01 = 1241 (787 + / 454 -)
 # genes in genesets = 14839

<FC> = 0
 <shrinkage-t> = 0.01
 <p-value> = 0.07
 <fdr> = 0.79

Profile



Regulated Spots

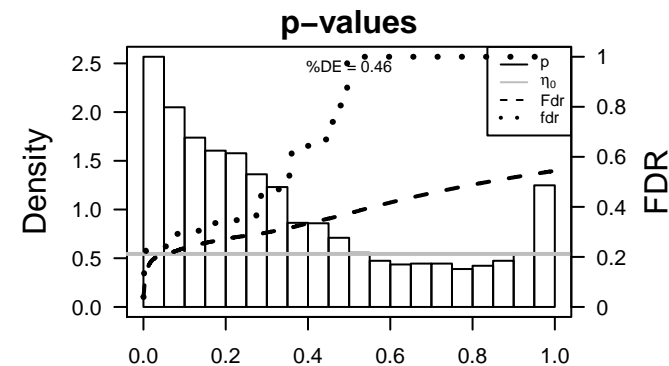
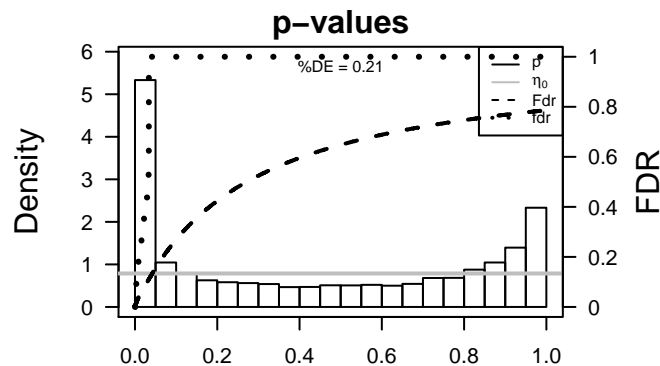


Global Genelist

| Rank | ID | log(FC) | fdr p-value | Description Metagene |
|------|---------|---------|-------------|--|
| 1 | ATIC | -1.73 | 2e-16 1e-13 | 44 x 50 5-aminoimidazole-4-carboxamide ribonucleotide formyltrans |
| 2 | CD46 | -1.32 | 2e-16 1e-13 | 46 x 37 CD46 molecule, complement regulatory protein [Source:HGNC |
| 3 | DHRS7 | -1.56 | 2e-16 1e-13 | 41 x 49 dehydrogenase/reductase (SDR family) member 7 [Source:HGNC |
| 4 | HECTD1 | -1.66 | 2e-16 1e-13 | 40 x 7 HECT domain containing E3 ubiquitin protein ligase 1 [Source:HGNC |
| 5 | ILK | -1.46 | 2e-16 1e-13 | 43 x 50 integrin-linked kinase [Source:HGNC Symbol;Acc:HGNC:604 |
| 6 | ING3 | -1.55 | 2e-16 1e-13 | 5 x 47 inhibitor of growth family, member 3 [Source:HGNC Symbol;Acc:HGNC:100 |
| 7 | LGALS1 | -1.68 | 2e-16 1e-13 | 50 x 1 lectin, galactoside-binding, soluble, 1 [Source:HGNC Symbol;Acc:HGNC:100 |
| 8 | MLIP | -1.89 | 2e-16 1e-13 | 3 x 44 muscular LMNA-interacting protein [Source:HGNC Symbol;Acc:HGNC:100 |
| 9 | MRPS23 | -1.27 | 2e-16 1e-13 | 2 x 26 mitochondrial ribosomal protein S23 [Source:HGNC Symbol;Acc:HGNC:100 |
| 10 | NOP16 | -1.81 | 2e-16 1e-13 | 1 x 38 NOP16 nucleolar protein [Source:HGNC Symbol;Acc:HGNC:100 |
| 11 | PGD | -1.56 | 2e-16 1e-13 | 42 x 50 phosphogluconate dehydrogenase [Source:HGNC Symbol;Acc:HGNC:100 |
| 12 | PLK2 | -1.65 | 2e-16 1e-13 | 50 x 1 polo-like kinase 2 [Source:HGNC Symbol;Acc:HGNC:19699] |
| 13 | RDH11 | -1.59 | 2e-16 1e-13 | 7 x 40 retinol dehydrogenase 11 (all-trans/9-cis/11-cis) [Source:HGNC |
| 14 | RER1 | -1.65 | 2e-16 1e-13 | 3 x 22 retention in endoplasmic reticulum sorting receptor 1 [Source:HGNC |
| 15 | SDAD1 | -1.75 | 2e-16 1e-13 | 50 x 44 SDA1 domain containing 1 [Source:HGNC Symbol;Acc:HGNC:100 |
| 16 | SEC13 | -1.42 | 2e-16 1e-13 | 50 x 40 SEC13 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:100 |
| 17 | SLC10A7 | 1.89 | 2e-16 1e-13 | 37 x 7 solute carrier family 10, member 7 [Source:HGNC Symbol;Acc:HGNC:100 |
| 18 | SLC44A2 | 1.9 | 2e-16 1e-13 | 36 x 50 solute carrier family 44 (choline transporter), member 2 [Source:HGNC |
| 19 | SLC6A15 | -1.31 | 2e-16 1e-13 | 48 x 45 solute carrier family 6 (neutral amino acid transporter), member 15 [Source:HGNC |
| 20 | SNRPN | -1.7 | 2e-16 1e-13 | 50 x 46 small nuclear ribonucleoprotein polypeptide N [Source:HGNC |

Global Geneset Analysis

| Rank | GSZ | p-value | #all | Geneset |
|-----------------------|-------|---------|------|--|
| <i>Overexpressed</i> | | | | |
| 1 | 16.7 | 3e-05 | 305 | GSEA C2DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP |
| 2 | 15.5 | 5e-05 | 550 | GSEA C2SOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP |
| 3 | 14.07 | 7e-05 | 242 | GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN |
| 4 | 13.43 | 8e-05 | 142 | Glio WILLSCHER_GBM_Verhaak-CL_up (C) |
| 5 | 13.3 | 8e-05 | 81 | GSEA C2GRAHAM_NORMAL QUIESCENT_VS_NORMAL_DIVIDING_DN |
| 6 | 12.96 | 9e-05 | 267 | GSEA C2ZHANG_TLX_TARGETS_60HR_DN |
| 7 | 12.88 | 9e-05 | 700 | GSEA C2MARSON_BOUND_BY_E2F4_UNSTIMULATED |
| 8 | 12.75 | 8e-03 | 16 | Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP |
| 9 | 12.74 | 1e-04 | 1192 | GSEA C2KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP |
| 10 | 12.56 | 1e-04 | 436 | GSEA C2SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6 |
| 11 | 12.3 | 1e-04 | 139 | GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER |
| 12 | 12.15 | 1e-04 | 54 | GSEA C2KANG_DOXORUBICIN_RESISTANCE_UP |
| 13 | 11.49 | 2e-04 | 96 | GSEA C2ROONQUIST_IL6_DEPRIVATION_DN |
| 14 | 11.32 | 2e-04 | 724 | GSEA C2PUJANA_CHEK2_PCC_NETWORK |
| 15 | 11.22 | 2e-04 | 327 | GSEA C2BLUM_RESPONSE_TO_SALIRASIB_DN |
| 16 | 11.13 | 2e-04 | 390 | GSEA C2PUJANA_BRCA2_PCC_NETWORK |
| 17 | 11.01 | 2e-04 | 145 | GSEA C2CHANG_CYCLING_GENES |
| 18 | 10.76 | 2e-04 | 197 | HM HALLMARK_E2F_TARGETS |
| 19 | 10.73 | 2e-04 | 93 | GSEA C2KONG_E2F3_TARGETS |
| 20 | 10.56 | 2e-04 | 50 | GSEA C2SHIDA_E2F_TARGETS |
| <i>Underexpressed</i> | | | | |
| 1 | -6.25 | 0.002 | 472 | GSEA C2DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN |
| 2 | -5.4 | 0.003 | 196 | GSEA C2CHANG_CORE_SERUM_RESPONSE_DN |
| 3 | -5.36 | 0.003 | 2 | TF MYC_ECM cell adhesion DOWN |
| 4 | -5.35 | 0.003 | 38 | GSEA C2AMIT_EGF_RESPONSE_60_MCF10A |
| 5 | -5.01 | 0.004 | 930 | GSEA C2NUYTEN_EZH2_TARGETS_UP |
| 6 | -4.96 | 0.004 | 594 | GSEA C2WONG_ADULT_TISSUE_UP_STEM_MODULE |
| 7 | -4.86 | 0.004 | 338 | GSEA C2BASAKI_YBX1_TARGETS_DN |
| 8 | -4.82 | 0.004 | 136 | GSEA C2PODAR_RESPONSE_TO_ADAPHOSTIN_UP |
| 9 | -4.67 | 0.004 | 510 | GSEA C2FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR |
| 10 | -4.66 | 0.005 | 10 | CC WASH complex |
| 11 | -4.57 | 0.005 | 385 | GSEA C2REN_ALVEOLAR_RHABDOMYOSARCOMA_DN |
| 12 | -4.54 | 0.005 | 3396 | LymphomaHOPP_Repressed |
| 13 | -4.42 | 0.005 | 64 | GSEA C2GRABARCZYK_BCL11B_TARGETS_UP |
| 14 | -4.38 | 0.006 | 166 | GSEA C2RODWELL_AGING_KIDNEY_NO_BLOOD_UP |
| 15 | -4.37 | 0.006 | 361 | GSEA C2BERENJENO_TRANSFORMED_BY_RHOA_DN |
| 16 | -4.35 | 0.006 | 784 | GSEA C2BUYTERT_PHOTOGENIC_DYNAMIC_THERAPY_STRESS_UP |
| 17 | -4.35 | 0.006 | 13 | Tissue WIRTH_B-cells |
| 18 | -4.29 | 0.006 | 139 | GSEA C2RUIZ_TNC_TARGETS_UP |
| 19 | -4.14 | 0.007 | 696 | GSEA C2NUYTEN_NIPPI1_TARGETS_UP |
| 20 | -4.09 | 0.007 | 176 | GSEA C2TIEN_INTESTINE_PROBIOTICS_24HR_DN |



D12_mel

Local Summary

%DE = 0.89
 # metagenes = 25
 # genes = 383
 # genes in genesets = 382

 # genes with $fdr < 0.1$ = 308 (275 + / 33 -)
 # genes with $fdr < 0.05$ = 281 (253 + / 28 -)
 # genes with $fdr < 0.01$ = 216 (205 + / 11 -)

<r> metagenes = 0.93

<r> genes = 0.28

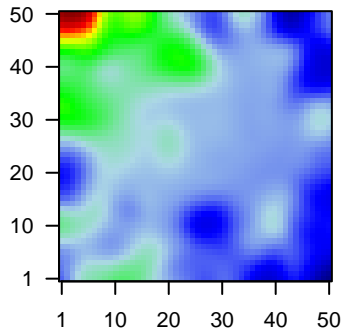
<FC> = 0.56

<shrinkage-t> = 8.94

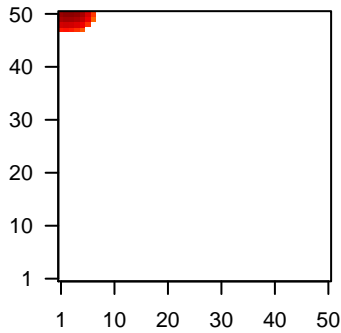
<p-value> = 0

<fdr> = 0.34

Profile



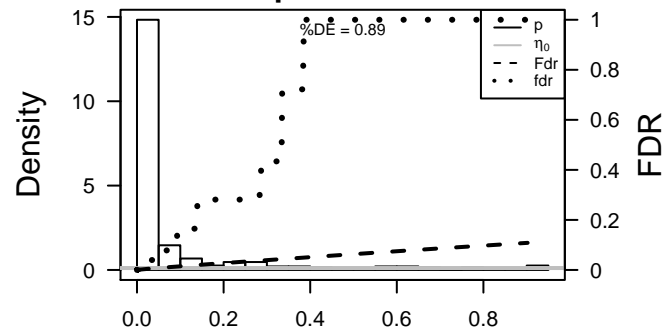
Spot



Local Genelist

| Rank | ID | log(FC) | p-value | fdr | Description |
|------|----------|---------|---------|-------|---|
| 1 | ING3 | -1.55 | 2e-16 | 1e-14 | 5 x 47 inhibitor of growth family, member 3 [Source:HGNC Symbol;A |
| 2 | CEP97 | 1.55 | 1e-12 | 4e-11 | 2 x 47 centrosomal protein 97kDa [Source:HGNC Symbol;Acc:HGNC:11390] |
| 3 | RRM2 | 1.62 | 2e-12 | 7e-11 | 5 x 50 ribonucleotide reductase M2 [Source:HGNC Symbol;Acc:HGNC:2468] |
| 4 | BUB1B | 1.6 | 3e-12 | 1e-10 | 6 x 50 BUB1 mitotic checkpoint serine/threonine kinase B [Source:HGNC Symbol;Acc:HGNC:11390] |
| 5 | FANCA | 1.58 | 6e-12 | 3e-10 | 1 x 50 Fanconi anemia, complementation group A [Source:HGNC Symbol;Acc:HGNC:2468] |
| 6 | POLE | 1.55 | 1e-11 | 4e-10 | 1 x 48 polymerase (DNA directed), epsilon, catalytic subunit [Source:HGNC Symbol;Acc:HGNC:2468] |
| 7 | NCAPG | 1.53 | 3e-11 | 4e-10 | 6 x 50 non-SMC condensin I complex, subunit G [Source:HGNC Symbol;Acc:HGNC:2468] |
| 8 | HIST1H4E | 1.53 | 3e-11 | 2e-09 | 7 x 50 histone cluster 1, H4e [Source:HGNC Symbol;Acc:HGNC:2468] |
| 9 | RAD51 | 1.5 | 7e-11 | 2e-09 | 1 x 50 RAD51 recombinase [Source:HGNC Symbol;Acc:HGNC:2468] |
| 10 | HJURP | 1.48 | 1e-10 | 2e-09 | 6 x 50 Holliday junction recognition protein [Source:HGNC Symbol;Acc:HGNC:2468] |
| 11 | HIST1H4C | 0.59 | 2e-10 | 4e-09 | 5 x 49 histone cluster 1, H4c [Source:HGNC Symbol;Acc:HGNC:2468] |
| 12 | PHF19 | 1.46 | 2e-10 | 4e-09 | 5 x 50 PHD finger protein 19 [Source:HGNC Symbol;Acc:HGNC:2468] |
| 13 | POLQ | 1.44 | 4e-10 | 4e-09 | 3 x 50 polymerase (DNA directed), theta [Source:HGNC Symbol;Acc:HGNC:2468] |
| 14 | AURKB | 1.44 | 4e-10 | 1e-08 | 6 x 50 aurora kinase B [Source:HGNC Symbol;Acc:HGNC:11390] |
| 15 | DCLRE1C | 1.41 | 8e-10 | 1e-08 | 3 x 49 DNA cross-link repair 1C [Source:HGNC Symbol;Acc:HGNC:2468] |
| 16 | SMCO4 | 1.4 | 1e-09 | 1e-08 | 1 x 47 single-pass membrane protein with coiled-coil domains 4 [Source:HGNC Symbol;Acc:HGNC:2468] |
| 17 | CDKN3 | 1.03 | 1e-09 | 3e-08 | 6 x 50 cyclin-dependent kinase inhibitor 3 [Source:HGNC Symbol;Acc:HGNC:2468] |
| 18 | EXO1 | 1.37 | 3e-09 | 3e-08 | 1 x 50 exonuclease 1 [Source:HGNC Symbol;Acc:HGNC:3511] |
| 19 | GTSE1 | 1.37 | 3e-09 | 3e-08 | 7 x 50 G-2 and S-phase expressed 1 [Source:HGNC Symbol;Acc:HGNC:2468] |
| 20 | ZWINT | 1.34 | 3e-09 | 4e-08 | 5 x 50 ZW10 interacting kinetochore protein [Source:HGNC Symbol;Acc:HGNC:2468] |

p-values



D12_mel

Local Summary

%DE = 0.6
 # metagenes = 1
 # genes = 22
 # genes in genesets = 22

 # genes with $fdr < 0.1 = 8$ (2 + / 6 -)
 # genes with $fdr < 0.05 = 8$ (2 + / 6 -)
 # genes with $fdr < 0.01 = 4$ (0 + / 4 -)

<r> metagenes = NA

<r> genes = 0.15

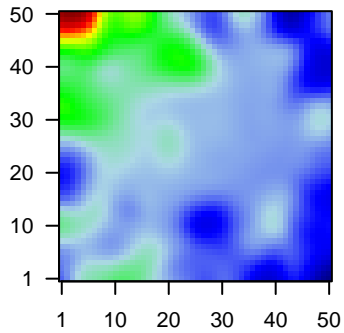
<FC> = -0.23

<shrinkage-t> = -3.51

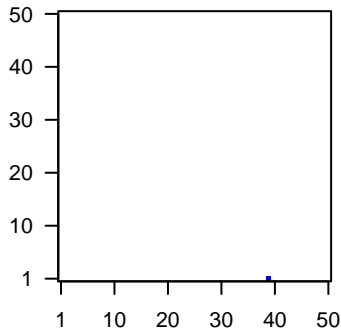
<p-value> = 0.01

<fdr> = 0.64

Profile



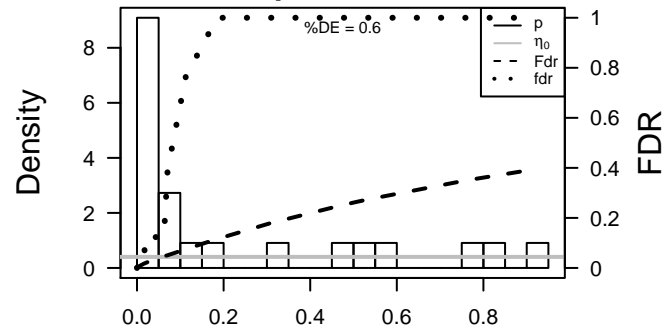
Spot



Local Genelist

| Rank | ID | log(FC) | p-value | fdr | Description |
|------|-------------|---------|---------|-------|---|
| 1 | ALG13 | -1.47 | 1e-14 | 8e-09 | 39 x 1 ALG13, UDP-N-acetylglucosaminyltransferase subunit [Sour |
| 2 | MAGED1 | -1.29 | 9e-10 | 6e-03 | 39 x 1 melanoma antigen family D1 [Source:HGNC Symbol;Acc:HG |
| 3 | CDC42SE1 | -0.77 | 9e-04 | 6e-03 | 39 x 1 CDC42 small effector 1 [Source:HGNC Symbol;Acc:HGNC:1 |
| 4 | EXOC1 | -0.71 | 2e-03 | 6e-03 | 39 x 1 exocyst complex component 1 [Source:HGNC Symbol;Acc:Hi |
| 5 | AFTPH | -0.71 | 2e-03 | 2e-02 | 39 x 1 aftiphilin [Source:HGNC Symbol;Acc:HGNC:25951] |
| 6 | MINPP1 | 0.66 | 4e-03 | 4e-02 | 39 x 1 multiple inositol-polyphosphate phosphatase 1 [Source:HG |
| 7 | TIA1 | 0.45 | 2e-02 | 4e-02 | 39 x 1 TIA1 cytotoxic granule-associated RNA binding protein [Sou |
| 8 | ZBTB44 | -0.54 | 2e-02 | 4e-02 | 39 x 1 zinc finger and BTB domain containing 44 [Source:HGNC Syr |
| 9 | ATP8B2 | -0.54 | 2e-02 | 1e-01 | 39 x 1 ATPase, aminophospholipid transporter, class 1, type 8B, men |
| 10 | RANBP2 | 0.45 | 5e-02 | 1e-01 | 39 x 1 RAN binding protein 2 [Source:HGNC Symbol;Acc:HGNC:98 |
| 11 | CNOT2 | 0.21 | 6e-02 | 1e-01 | 39 x 1 CCR4-NOT transcription complex, subunit 2 [Source:HGNC : |
| 12 | CHKB | -0.42 | 7e-02 | 1e-01 | 39 x 1 choline kinase beta [Source:HGNC Symbol;Acc:HGNC:1938] |
| 13 | YAP1 | 0.32 | 7e-02 | 4e-01 | 39 x 1 Yes-associated protein 1 [Source:HGNC Symbol;Acc:HGNC: |
| 14 | DHR SX | -0.36 | 1e-01 | 8e-01 | 39 x 1 dehydrogenase/reductase (SDR family) X-linked [Source:HG |
| 15 | BAZ2B | 0.3 | 2e-01 | 1e+00 | 39 x 1 bromodomain adjacent to zinc finger domain, 2B [Source:HG |
| 16 | ALDH1A2 | -0.23 | 3e-01 | 1e+00 | 39 x 1 aldehyde dehydrogenase 1 family, member A2 [Source:HGNC |
| 17 | ABCB1 | -0.16 | 5e-01 | 1e+00 | 39 x 1 ATP-binding cassette, sub-family B (MDR/TAP), member 1 [! |
| 18 | STRN3 | -0.12 | 5e-01 | 1e+00 | 39 x 1 striatin, calmodulin binding protein 3 [Source:HGNC Symbol;] |
| 19 | ATP5J2-PTCI | -0.13 | 6e-01 | 1e+00 | 39 x 1 ATP5J2-PTCD1 readthrough [Source:HGNC Symbol;Acc:HG |
| 20 | MXD1 | -0.06 | 8e-01 | 1e+00 | 39 x 1 MAX dimerization protein 1 [Source:HGNC Symbol;Acc:HG |

p-values



D12_mel

Local Summary

%DE = 0.7
 # metagenes = 12
 # genes = 228
 # genes in genesets = 228

 # genes with $fdr < 0.1$ = 79 (13 + / 66 -)
 # genes with $fdr < 0.05$ = 64 (9 + / 55 -)
 # genes with $fdr < 0.01$ = 45 (6 + / 39 -)

<r> metagenes = 0.99

<r> genes = 0.21

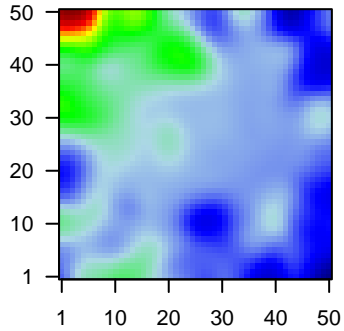
<FC> = -0.28

<shrinkage-t> = -4.41

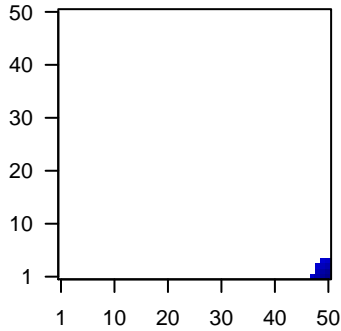
<p-value> = 0.02

<fdr> = 0.67

Profile



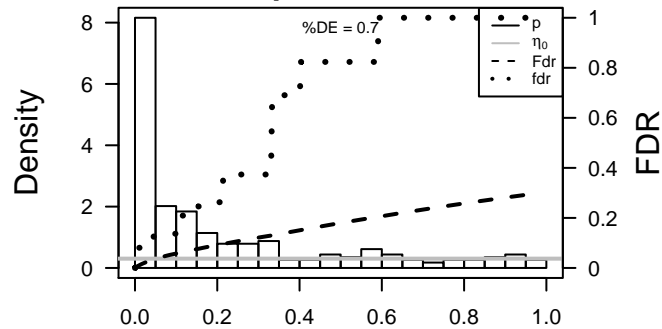
Spot



Local Genelist

| Rank | ID | log(FC) | p-value | fdr | Description |
|------|----------|---------|---------|-------|--|
| 1 | LGALS1 | -1.68 | 2e-16 | 8e-15 | 50 x 1 lectin, galactoside-binding, soluble, 1 [Source:HGNC Symbol] |
| 2 | PLK2 | -1.65 | 2e-16 | 8e-15 | 50 x 1 polo-like kinase 2 [Source:HGNC Symbol;Acc:HGNC:19699] |
| 3 | DNAJB4 | -1.14 | 4e-10 | 3e-08 | 50 x 1 DnaJ (Hsp40) homolog, subfamily B, member 4 [Source:HGNC] |
| 4 | GBE1 | -1.29 | 8e-10 | 1e-06 | 50 x 3 glucan (1,4-alpha-), branching enzyme 1 [Source:HGNC Symbol] |
| 5 | TGIF1 | -1.1 | 2e-08 | 1e-06 | 50 x 1 TGFB-induced factor homeobox 1 [Source:HGNC Symbol;Acc:HGNC:1441] |
| 6 | PPP1R15A | -1.12 | 3e-08 | 1e-06 | 49 x 4 protein phosphatase 1, regulatory subunit 15A [Source:HGNC Symbol] |
| 7 | CALD1 | -0.8 | 5e-08 | 2e-05 | 50 x 1 caldesmon 1 [Source:HGNC Symbol;Acc:HGNC:1441] |
| 8 | YPEL5 | -1.15 | 4e-07 | 2e-05 | 50 x 1 yippe-like 5 (Drosophila) [Source:HGNC Symbol;Acc:HGNC:1441] |
| 9 | STAM | -1.05 | 5e-07 | 2e-05 | 50 x 3 signal transducing adaptor molecule (SH3 domain and ITAM domain) |
| 10 | UBE2E2 | -1.12 | 8e-07 | 2e-05 | 50 x 1 ubiquitin-conjugating enzyme E2E 2 [Source:HGNC Symbol;Acc:HGNC:7095] |
| 11 | PVRL2 | 1.13 | 9e-07 | 4e-05 | 50 x 4 poliovirus receptor-related 2 (herpesvirus entry mediator B) [Source:HGNC Symbol] |
| 12 | RAB31 | -1.09 | 2e-06 | 4e-05 | 50 x 3 RAB31, member RAS oncogene family [Source:HGNC Symbol] |
| 13 | PTPRM | -1.08 | 2e-06 | 6e-05 | 50 x 1 protein tyrosine phosphatase, receptor type, M [Source:HGNC Symbol] |
| 14 | RHOBTB3 | 1.07 | 3e-06 | 6e-05 | 50 x 1 Rho-related BTB domain containing 3 [Source:HGNC Symbol] |
| 15 | MT2A | -1.06 | 4e-06 | 1e-04 | 50 x 3 metallothionein 2A [Source:HGNC Symbol;Acc:HGNC:7406] |
| 16 | MID1 | -1.04 | 6e-06 | 2e-04 | 50 x 3 midline 1 [Source:HGNC Symbol;Acc:HGNC:7095] |
| 17 | CDKN1A | -1.02 | 9e-06 | 2e-04 | 50 x 1 cyclin-dependent kinase inhibitor 1A (p21, Cip1) [Source:HGNC Symbol] |
| 18 | PITX2 | 1 | 1e-05 | 2e-04 | 50 x 4 paired-like homeodomain 2 [Source:HGNC Symbol;Acc:HGNC:7095] |
| 19 | ADRB2 | 1 | 1e-05 | 3e-04 | 47 x 1 adrenoceptor beta 2, surface [Source:HGNC Symbol;Acc:HGNC:7095] |
| 20 | EDIL3 | -0.97 | 2e-05 | 1e-03 | 50 x 1 EGF-like repeats and discoidin I-like domains 3 [Source:HGNC Symbol] |

p-values



D12_mel

Local Summary

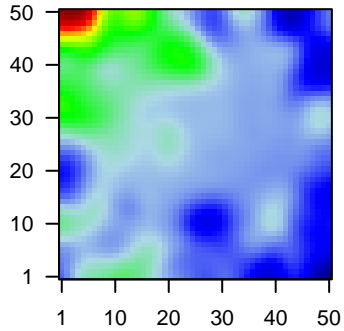
%DE = 0.73
 # metagenes = 5
 # genes = 63
 # genes in genesets = 63

 # genes with $fdr < 0.1$ = 36 (13 + / 23 -)
 # genes with $fdr < 0.05$ = 36 (13 + / 23 -)
 # genes with $fdr < 0.01$ = 23 (7 + / 16 -)

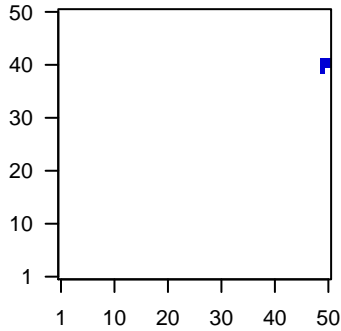
$\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.12

 $\langle FC \rangle$ = -0.18
 $\langle \text{shrinkage-t} \rangle$ = -3.15
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.48

Profile



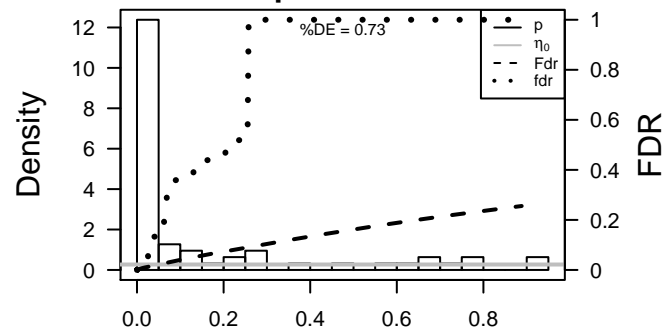
Spot



Local Genelist

| Rank | ID | log(FC) | p-value | fdr | Description |
|------|----------|---------|---------|-------|--|
| 1 | SEC13 | -1.42 | 2e-16 | 4e-15 | 50 x 40 SEC13 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:8866] |
| 2 | PFDN1 | -1.14 | 1e-13 | 2e-08 | 50 x 40 prefoldin subunit 1 [Source:HGNC Symbol;Acc:HGNC:8866] |
| 3 | FBXO42 | 1.4 | 1e-09 | 3e-07 | 50 x 41 F-box protein 42 [Source:HGNC Symbol;Acc:HGNC:29249] |
| 4 | PHKB | -1.09 | 2e-08 | 3e-06 | 50 x 40 phosphorylase kinase, beta [Source:HGNC Symbol;Acc:HGNC:8866] |
| 5 | DPH3 | -1.09 | 2e-07 | 3e-06 | 49 x 39 diphthamide biosynthesis 3 [Source:HGNC Symbol;Acc:HGNC:8866] |
| 6 | SPG7 | 1.17 | 3e-07 | 7e-06 | 50 x 40 spastic paraplegia 7 (pure and complicated autosomal recessive) [Source:HGNC Symbol;Acc:HGNC:8866] |
| 7 | EAPP | -1.12 | 8e-07 | 1e-05 | 50 x 40 E2F-associated phosphoprotein [Source:HGNC Symbol;Acc:HGNC:8866] |
| 8 | KDM5B | -1.08 | 2e-06 | 1e-05 | 50 x 40 lysine (K)-specific demethylase 5B [Source:HGNC Symbol;Acc:HGNC:8866] |
| 9 | PLIN3 | -1.07 | 2e-06 | 4e-05 | 49 x 40 perilipin 3 [Source:HGNC Symbol;Acc:HGNC:16893] |
| 10 | MARK3 | -1.05 | 5e-06 | 1e-04 | 50 x 41 MAP/microtubule affinity-regulating kinase 3 [Source:HGNC Symbol;Acc:HGNC:8866] |
| 11 | SMOX | 1 | 1e-05 | 1e-04 | 49 x 40 spermine oxidase [Source:HGNC Symbol;Acc:HGNC:15862] |
| 12 | C15orf57 | -0.99 | 2e-05 | 2e-04 | 50 x 41 chromosome 15 open reading frame 57 [Source:HGNC Symbol;Acc:HGNC:8866] |
| 13 | TIMM44 | -0.96 | 3e-05 | 6e-04 | 50 x 41 translocase of inner mitochondrial membrane 44 homolog (yeast) [Source:HGNC Symbol;Acc:HGNC:8866] |
| 14 | ZFP1 | 0.92 | 6e-05 | 2e-03 | 50 x 41 ZFP1 zinc finger protein [Source:HGNC Symbol;Acc:HGNC:8866] |
| 15 | TAF1D | 0.79 | 2e-04 | 2e-03 | 50 x 41 TATA box binding protein (TBP)-associated factor, RNA polymerase II [Source:HGNC Symbol;Acc:HGNC:8866] |
| 16 | IK | -0.74 | 3e-04 | 2e-03 | 50 x 41 IK cytokine, down-regulator of HLA II [Source:HGNC Symbol;Acc:HGNC:8866] |
| 17 | TRAPPC6A | -0.82 | 4e-04 | 2e-03 | 50 x 41 trafficking protein particle complex 6A [Source:HGNC Symbol;Acc:HGNC:8866] |
| 18 | CRYZ | -0.81 | 5e-04 | 6e-03 | 50 x 40 crystallin, zeta (quinone reductase) [Source:HGNC Symbol;Acc:HGNC:8866] |
| 19 | NDUFAF1 | -0.73 | 1e-03 | 6e-03 | 49 x 39 NADH dehydrogenase (ubiquinone) complex I, assembly factor 1 [Source:HGNC Symbol;Acc:HGNC:8866] |
| 20 | INTS12 | -0.73 | 1e-03 | 6e-03 | 50 x 40 integrator complex subunit 12 [Source:HGNC Symbol;Acc:HGNC:8866] |

p-values



D12_mel

Local Summary

%DE = 0.64
 # metagenes = 11
 # genes = 122
 # genes in genesets = 122

 # genes with $fdr < 0.1$ = 61 (13 + / 48 -)
 # genes with $fdr < 0.05$ = 61 (13 + / 48 -)
 # genes with $fdr < 0.01$ = 33 (4 + / 29 -)

<r> metagenes = 0.96

<r> genes = 0.1

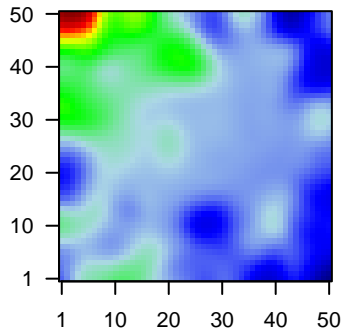
<FC> = -0.32

<shrinkage-t> = -5.37

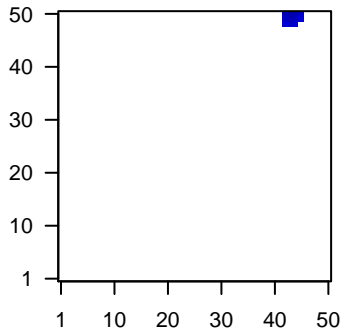
<p-value> = 0

<fdr> = 0.53

Profile



Spot



Local Genelist

| Rank | ID | log(FC) | p-value | fdr | Description |
|------|---------|---------|---------|-------|--|
| 1 | ATIC | -1.73 | 2e-16 | 2e-15 | 44 x 50 5-aminoimidazole-4-carboxamide ribonucleotide formyltrans |
| 2 | ILK | -1.46 | 2e-16 | 2e-15 | 43 x 50 integrin-linked kinase [Source:HGNC Symbol;Acc:HGNC:604 |
| 3 | PGD | -1.56 | 2e-16 | 2e-15 | 42 x 50 phosphogluconate dehydrogenase [Source:HGNC Symbol;Ac |
| 4 | SYPL1 | -1.98 | 2e-16 | 2e-15 | 42 x 48 synaptophysin-like 1 [Source:HGNC Symbol;Acc:HGNC:115 |
| 5 | SARAF | -1.51 | 2e-15 | 3e-11 | 44 x 48 store-operated calcium entry-associated regulatory factor [S |
| 6 | AARSD1 | -1.41 | 8e-13 | 7e-10 | 44 x 50 alanyl-tRNA synthetase domain containing 1 [Source:HGNC |
| 7 | ZFAND6 | -1.23 | 2e-11 | 1e-09 | 43 x 50 zinc finger, AN1-type domain 6 [Source:HGNC Symbol;Acc:t |
| 8 | INTS4 | -1.01 | 4e-11 | 5e-09 | 42 x 50 integrator complex subunit 4 [Source:HGNC Symbol;Acc:HG |
| 9 | KXD1 | -1.31 | 2e-10 | 5e-08 | 44 x 50 KxDL motif containing 1 [Source:HGNC Symbol;Acc:HGNC:2 |
| 10 | ZNF622 | -1.26 | 3e-09 | 5e-08 | 42 x 50 zinc finger protein 622 [Source:HGNC Symbol;Acc:HGNC:30 |
| 11 | SLC35B2 | -1.26 | 3e-09 | 5e-08 | 45 x 50 solute carrier family 35 (adenosine 3'-phospho 5'-phospho |
| 12 | ZNF706 | -0.77 | 4e-09 | 2e-06 | 45 x 50 zinc finger protein 706 [Source:HGNC Symbol;Acc:HGNC:24 |
| 13 | SLC35A4 | -1.2 | 4e-08 | 2e-06 | 44 x 50 solute carrier family 35, member A4 [Source:HGNC Symbol;A |
| 14 | BNIP3L | -1.13 | 9e-08 | 8e-05 | 45 x 50 BCL2/adenovirus E1B 19kDa interacting protein 3-like [Sourc |
| 15 | C12orf5 | -1.08 | 2e-06 | 8e-05 | 42 x 50 chromosome 12 open reading frame 5 [Source:HGNC Symbc |
| 16 | SDR39U1 | -1.06 | 4e-06 | 8e-04 | 43 x 50 short chain dehydrogenase/reductase family 39U, member 1 |
| 17 | POC5 | 0.93 | 5e-05 | 8e-04 | 45 x 50 POC5 centriolar protein [Source:HGNC Symbol;Acc:HGNC:2 |
| 18 | XBP1 | -0.92 | 7e-05 | 8e-04 | 44 x 48 X-box binding protein 1 [Source:HGNC Symbol;Acc:HGNC:1 |
| 19 | NAGK | -0.92 | 7e-05 | 8e-04 | 44 x 50 N-acetylglucosamine kinase [Source:HGNC Symbol;Acc:HG |
| 20 | PSEN1 | -0.9 | 1e-04 | 8e-04 | 43 x 50 presenilin 1 [Source:HGNC Symbol;Acc:HGNC:9508] |

p-values

