

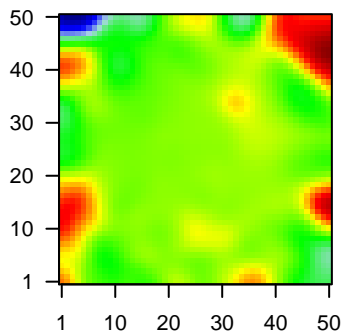
# G4\_mel

## Global Summary

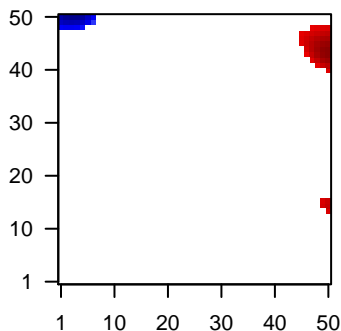
%DE = 0.21  
 # genes with  $fdr < 0.2$  = 2743 ( 1667 + / 1076 - )  
 # genes with  $fdr < 0.1$  = 2133 ( 1326 + / 807 - )  
 # genes with  $fdr < 0.05$  = 1729 ( 1079 + / 650 - )  
 # genes with  $fdr < 0.01$  = 1149 ( 722 + / 427 - )  
 # genes in genesets = 14839

<FC> = 0  
 <shrinkage-t> = 0.04  
 <p-value> = 0.08  
 <fdr> = 0.79

Profile



Regulated Spots

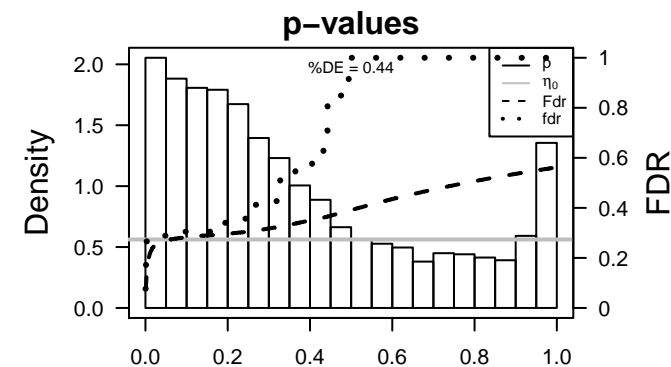
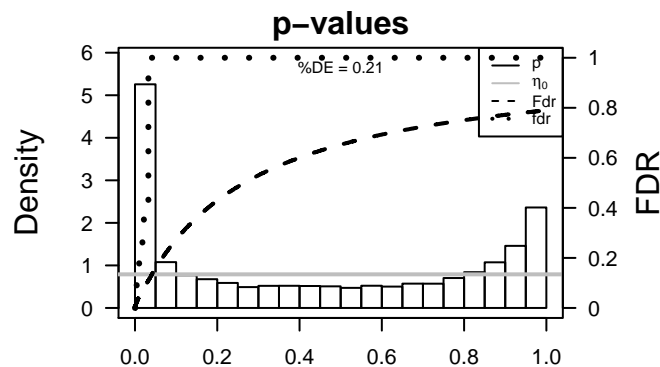


## Global Genelist

| Rank | ID     | log(FC) | fdr   | p-value | Description   |
|------|--------|---------|-------|---------|---|
| 1    | ANKHD1 | -1.59   | 2e-16 | 1e-13   | 9 x 5 ankryin repeat and KH domain containing 1 [Source:HGNC S        |
| 2    | CALU   | -0.92   | 2e-16 | 1e-13   | 45 x 36 calumenin [Source:HGNC Symbol;Acc:HGNC:1458]                  |
| 3    | FLII   | -1.1    | 2e-16 | 1e-13   | 17 x 50 flightless I homolog (Drosophila) [Source:HGNC Symbol;Acc:    |
| 4    | GGH    | -2.02   | 2e-16 | 1e-13   | 4 x 47 gamma-glutamyl hydrolase (conjugase, folypolygamagluta         |
| 5    | HMG2   | -1.17   | 2e-16 | 1e-13   | 8 x 50 high mobility group nucleosomal binding domain 2 [Source:Hi    |
| 6    | ING3   | -1.55   | 2e-16 | 1e-13   | 5 x 47 inhibitor of growth family, member 3 [Source:HGNC Symbol;A     |
| 7    | LGALS1 | -1.68   | 2e-16 | 1e-13   | 50 x 1 lectin, galactoside-binding, soluble, 1 [Source:HGNC Symbol    |
| 8    | MRPL28 | -1.31   | 2e-16 | 1e-13   | 11 x 3 mitochondrial ribosomal protein L28 [Source:HGNC Symbol;f      |
| 9    | MRPL52 | -1.45   | 2e-16 | 1e-13   | 35 x 50 mitochondrial ribosomal protein L52 [Source:HGNC Symbol;f     |
| 10   | NASP   | -1.43   | 2e-16 | 1e-13   | 1 x 48 nuclear autoantigenic sperm protein (histone-binding) [Sourc   |
| 11   | NDUFS3 | -1.57   | 2e-16 | 1e-13   | 1 x 32 NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (f       |
| 12   | NUPR1  | -1.58   | 2e-16 | 1e-13   | 45 x 50 nuclear protein, transcriptional regulator, 1 [Source:HGNC Sy |
| 13   | PABPC4 | -1.54   | 2e-16 | 1e-13   | 50 x 7 poly(A) binding protein, cytoplasmic 4 (inducible form) [Sourc |
| 14   | RRM1   | -1.58   | 2e-16 | 1e-13   | 2 x 50 ribonucleotide reductase M1 [Source:HGNC Symbol;Acc:HGI        |
| 15   | SF3A3  | -1.72   | 2e-16 | 1e-13   | 12 x 50 splicing factor 3a, subunit 3, 60kDa [Source:HGNC Symbol;A    |
| 16   | TCF25  | -1.59   | 2e-16 | 1e-13   | 1 x 23 transcription factor 25 (basic helix-loop-helix) [Source:HGNC  |
| 17   | TIMM50 | -1.56   | 2e-16 | 1e-13   | 1 x 33 translocase of inner mitochondrial membrane 50 homolog (S.     |
| 18   | TSG101 | -1.36   | 2e-16 | 1e-13   | 46 x 37 tumor susceptibility 101 [Source:HGNC Symbol;Acc:HGNC:1       |
| 19   | TXNDC9 | -1.6    | 2e-16 | 1e-13   | 48 x 36 thioredoxin domain containing 9 [Source:HGNC Symbol;Acc:l     |
| 20   | VPS25  | -1.58   | 2e-16 | 1e-13   | 1 x 45 vacuolar protein sorting 25 homolog (S. cerevisiae) [Source:l  |

## Global Geneset Analysis

| Rank                  | GSZ    | p-value | #all | Geneset   |
|-----------------------|--------|---------|------|---|
| <i>Overexpressed</i>  |        |         |      |   |
| 1                     | 4.1    | 0.007   | 20   | BP cellular response to fibroblast growth factor stimulus |
| 2                     | 4.09   | 0.007   | 18   | GSEA C2BIOCARTA_IL2_PATHWAY                               |
| 3                     | 4.01   | 0.007   | 426  | GSEA C2ZWANG_CLASS_1_TRANSIENTLY_INDUCED_BY_EGF           |
| 4                     | 3.96   | 0.008   | 65   | miRNA target-miR-9*                                       |
| 5                     | 3.89   | 0.008   | 56   | GSEA C2BURTON_ADIPOGENESIS_11                             |
| 6                     | 3.79   | 0.009   | 5    | GSEA C2M_SREBF1A_TARGETS                                  |
| 7                     | 3.74   | 0.009   | 26   | MF protein kinase inhibitor activity                      |
| 8                     | 3.69   | 0.010   | 195  | miRNA target-miR-206                                      |
| 9                     | 3.67   | 0.010   | 723  | GSEA C2REACTOME_IMMUNE_SYSTEM                             |
| 10                    | 3.61   | 0.010   | 21   | miRNA target-miR-554                                      |
| 11                    | 3.58   | 0.011   | 7    | GSEA C2HESSON_TUMOR_SUPPRESSOR_CLUSTER_3P21_3             |
| 12                    | 3.54   | 0.011   | 34   | GSEA C2SPIRA_SMOKERS_LUNG_CANCER_UP                       |
| 13                    | 3.46   | 0.012   | 33   | GSEA C2BIOCARTA_AT1R_PATHWAY                              |
| 14                    | 3.45   | 0.012   | 16   | GSEA C2REACTOME_ERK_MAPK_TARGETS                          |
| 15                    | 3.44   | 0.012   | 43   | GSEA C2PAPASPYRIDONOS_UNSTABLE_ATEROSCLEROTIC_PLAQUE_     |
| 16                    | 3.39   | 0.013   | 32   | GSEA C2BIOCARTA_IL2R2B_PATHWAY                            |
| 17                    | 3.39   | 0.013   | 79   | GSEA C2NELSON_RESPONSE_TO_ANDROGEN_UP                     |
| 18                    | 3.37   | 0.013   | 80   | GSEA C2KEGG_ERBB_SIGNALING_PATHWAY                        |
| 19                    | 3.32   | 0.014   | 11   | BP positive regulation of protein sumoylation             |
| 20                    | 3.3    | 0.014   | 19   | GSEA C2MIZUSHIMA_AUTOPHAGOSOME_FORMATION                  |
| <i>Underexpressed</i> |        |         |      |   |
| 1                     | -13.92 | 7e-05   | 305  | GSEA C2DUTERTRE ESTRADIOL_RESPONSE_24HR_UP                |
| 2                     | -13.67 | 7e-05   | 142  | Glio WILLSCHER_GBM_Verhaak-CL_up ( C                      |
| 3                     | -12.09 | 1e-04   | 96   | GSEA C2CROONQUIST_IL6_DEPRIVATION_DN                      |
| 4                     | -11.9  | 1e-04   | 550  | GSEA C2SOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP          |
| 5                     | -11.35 | 2e-04   | 197  | HM HALLMARK_E2F_TARGETS                                   |
| 6                     | -11.35 | 2e-04   | 81   | GSEA C2GRAHAM_NORMAL QUIESCENT_VS_NORMAL_DIVIDING_DN      |
| 7                     | -10.74 | 2e-04   | 139  | GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER        |
| 8                     | -10.64 | 2e-04   | 99   | GSEA C2BURTON_ADIPOGENESIS_3                              |
| 9                     | -10.23 | 2e-04   | 242  | GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN                   |
| 10                    | -10.22 | 2e-04   | 89   | GSEA C2MORI_IMMATURE_B_LYMPHOCYTE_DN                      |
| 11                    | -10.14 | 2e-04   | 155  | GSEA C2HOFFMANN_LARGE_TO_SMALL_PRE_BIL_LYMPHOCYTE_UP      |
| 12                    | -10.1  | 3e-04   | 72   | GSEA C2CROONQUIST_NRAS_SIGNALING_DN                       |
| 13                    | -10.07 | 3e-04   | 50   | GSEA C2SHIDA_E2F_TARGETS                                  |
| 14                    | -9.82  | 3e-04   | 162  | GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL QUIESCENT_UP         |
| 15                    | -9.82  | 3e-04   | 54   | GSEA C2KANG_DOXORUBICIN_RESISTANCE_UP                     |
| 16                    | -9.79  | 3e-04   | 110  | GSEA C2WHITEFORD_PEDIATRIC_CANCER_MARKERS                 |
| 17                    | -9.68  | 3e-04   | 124  | GSEA C2ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR          |
| 18                    | -9.19  | 4e-04   | 93   | GSEA C2KONG_E2F3_TARGETS                                  |
| 19                    | -9.06  | 4e-04   | 390  | GSEA C2PUJANA_BRCA2_PCC_NETWORK                           |
| 20                    | -9.01  | 2e-02   | 16   | Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP             |



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## Local Summary

%DE = 0.62  
 # metagenes = 5  
 # genes = 68  
 # genes in genesets = 68  
  
 # genes with  $fdr < 0.1$  = 39 ( 38 + / 1 - )  
 # genes with  $fdr < 0.05$  = 35 ( 34 + / 1 - )  
 # genes with  $fdr < 0.01$  = 27 ( 26 + / 1 - )

<r> metagenes = 0.98

<r> genes = 0.11

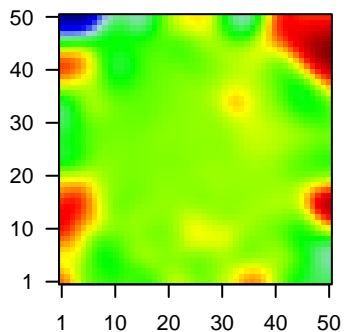
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<shrinkage-t> = 8.55

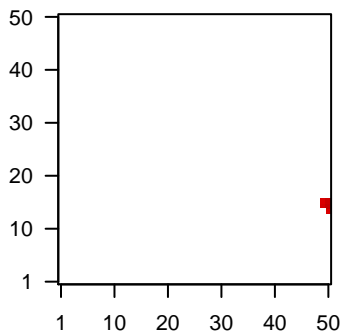
<p-value> = 0

<fdr> = 0.46

Profile



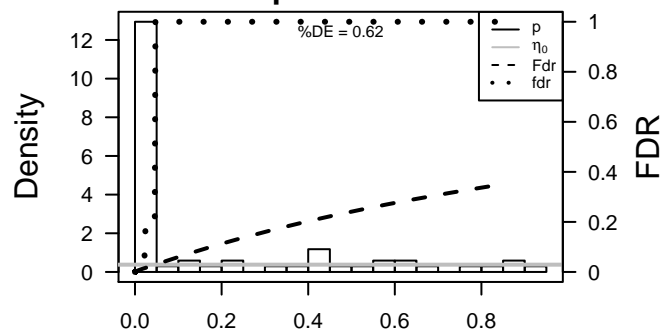
Spot



## Local Genelist

| Rank | ID        | log(FC) | p-value | fdr   | Description  |
|------|-----------|---------|---------|-------|--|
| 1    | RASA2     | 1.59    | 1e-11   | 3e-10 | 50 x 14 RAS p21 protein activator 2 [Source:HGNC Symbol;Acc:HGNC:10000]                        |
| 2    | HYAL2     | 1.56    | 2e-11   | 2e-08 | 50 x 16 hyaluronoglucosaminidase 2 [Source:HGNC Symbol;Acc:HGNC:10000]                         |
| 3    | SLC16A4   | 1.43    | 8e-10   | 1e-06 | 50 x 16 solute carrier family 16, member 4 [Source:HGNC Symbol;Acc:HGNC:10000]                 |
| 4    | AP4B1     | 1.26    | 6e-08   | 5e-06 | 50 x 16 adaptor-related protein complex 4, beta 1 subunit [Source:HGNC Symbol;Acc:HGNC:10000]  |
| 5    | ZNF211    | 1.2     | 3e-07   | 2e-05 | 50 x 16 zinc finger protein 211 [Source:HGNC Symbol;Acc:HGNC:10000]                            |
| 6    | BICD1     | 1.12    | 2e-06   | 2e-05 | 50 x 16 bicaudal D homolog 1 (Drosophila) [Source:HGNC Symbol;Acc:HGNC:10000]                  |
| 7    | AKAP8L    | 1.09    | 3e-06   | 2e-05 | 50 x 16 A kinase (PRKA) anchor protein 8-like [Source:HGNC Symbol;Acc:HGNC:10000]              |
| 8    | PRELID2   | 1.08    | 3e-06   | 2e-05 | 50 x 16 PRELI domain containing 2 [Source:HGNC Symbol;Acc:HGNC:10000]                          |
| 9    | XPA       | 1.08    | 3e-06   | 1e-04 | 50 x 14 xeroderma pigmentosum, complementation group A [Source:HGNC Symbol;Acc:HGNC:10000]     |
| 10   | GALK1     | 1.03    | 1e-05   | 1e-04 | 49 x 16 galactokinase 1 [Source:HGNC Symbol;Acc:HGNC:4118]                                     |
| 11   | TBC1D23   | 0.98    | 2e-05   | 1e-04 | 50 x 15 TBC1 domain family, member 23 [Source:HGNC Symbol;Acc:HGNC:10000]                      |
| 12   | ARHGEF1   | 0.98    | 3e-05   | 1e-04 | 50 x 16 Rho guanine nucleotide exchange factor (GEF) 1 [Source:HGNC Symbol;Acc:HGNC:10000]     |
| 13   | FAM134C   | 0.98    | 3e-05   | 1e-04 | 49 x 15 family with sequence similarity 134, member C [Source:HGNC Symbol;Acc:HGNC:10000]      |
| 14   | PPP2R2A   | 0.98    | 3e-05   | 3e-04 | 50 x 15 protein phosphatase 2, regulatory subunit B, alpha [Source:HGNC Symbol;Acc:HGNC:10000] |
| 15   | RRM2B     | 0.95    | 5e-05   | 3e-04 | 50 x 15 ribonucleotide reductase M2 B (TP53 inducible) [Source:HGNC Symbol;Acc:HGNC:10000]     |
| 16   | HIST2H2BE | 0.94    | 5e-05   | 3e-04 | 49 x 15 histone cluster 2, H2be [Source:HGNC Symbol;Acc:HGNC:4118]                             |
| 17   | FAM32A    | 0.82    | 6e-05   | 8e-04 | 49 x 16 family with sequence similarity 32, member A [Source:HGNC Symbol;Acc:HGNC:10000]       |
| 18   | PAPOLG    | 0.9     | 1e-04   | 8e-04 | 50 x 15 poly(A) polymerase gamma [Source:HGNC Symbol;Acc:HGNC:10000]                           |
| 19   | CDC37L1   | 0.88    | 2e-04   | 8e-04 | 50 x 15 cell division cycle 37-like 1 [Source:HGNC Symbol;Acc:HGNC:10000]                      |
| 20   | RBM34     | 0.69    | 2e-04   | 8e-04 | 50 x 16 RNA binding motif protein 34 [Source:HGNC Symbol;Acc:HGNC:10000]                       |

p-values



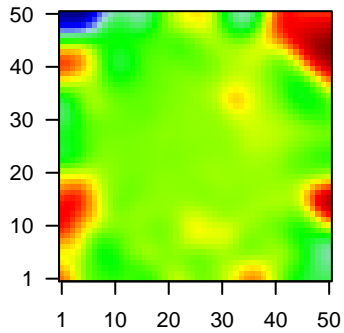
# G4\_mel

## Local Summary

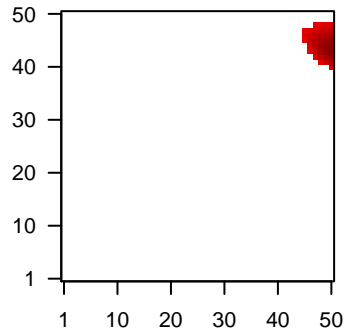
%DE = 0.82  
 # metagenes = 40  
 # genes = 379  
 # genes in genesets = 378  
  
 # genes with  $fdr < 0.1$  = 221 ( 185 + / 36 - )  
 # genes with  $fdr < 0.05$  = 204 ( 173 + / 31 - )  
 # genes with  $fdr < 0.01$  = 143 ( 126 + / 17 - )

$\langle r \rangle$  metagenes = 0.82  
 $\langle r \rangle$  genes = 0.07  
  
 $\langle FC \rangle$  = 0.3  
 $\langle \text{shrinkage-t} \rangle$  = 4.89  
 $\langle p\text{-value} \rangle$  = 0.01  
 $\langle fdr \rangle$  = 0.53

Profile



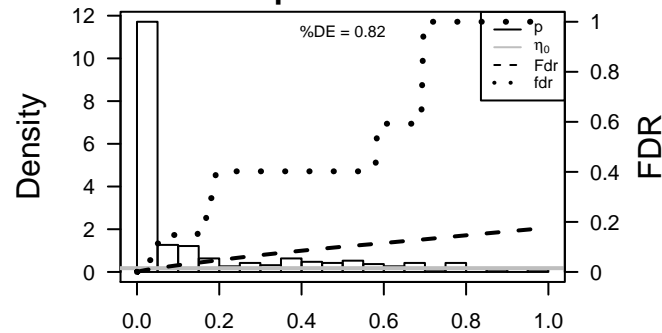
Spot



## Local Genelist

| Rank | ID      | log(FC) | p-value | fdr   | Description   |
|------|---------|---------|---------|-------|---|
| 1    | GSDMB   | 1.66    | 1e-12   | 2e-09 | 50 x 47 gasdermin B [Source:HGNC Symbol;Acc:HGNC:23690]   |
| 2    | DENND2D | 1.53    | 5e-11   | 2e-09 | 46 x 45 DENN/MADD domain containing 2D [Source:HGNC Symbol;Acc:HGNC:23690]                          |
| 3    | XRN1    | -1.36   | 6e-11   | 2e-09 | 47 x 45 5'-3' exoribonuclease 1 [Source:HGNC Symbol;Acc:HGNC:30829]                                 |
| 4    | CCT6B   | 1.51    | 1e-10   | 4e-08 | 50 x 44 chaperonin containing TCP1, subunit 6B (zeta 2) [Source:HGNC Symbol;Acc:HGNC:23690]         |
| 5    | KARS    | -1.07   | 7e-10   | 1e-06 | 45 x 46 lysyl-tRNA synthetase [Source:HGNC Symbol;Acc:HGNC:62092]                                   |
| 6    | VASP    | 1.3     | 2e-08   | 1e-06 | 48 x 45 vasodilator-stimulated phosphoprotein [Source:HGNC Symbol;Acc:HGNC:23690]                   |
| 7    | PXYLP1  | 1.29    | 3e-08   | 2e-06 | 46 x 44 2-phosphoxylose phosphatase 1 [Source:HGNC Symbol;Acc:HGNC:23690]                           |
| 8    | STYXL1  | 1.26    | 7e-08   | 2e-06 | 49 x 43 serine/threonine/tyrosine interacting-like 1 [Source:HGNC Symbol;Acc:HGNC:23690]            |
| 9    | GTF2H3  | 1.24    | 9e-08   | 2e-06 | 48 x 43 general transcription factor IIH, polypeptide 3, 34kDa [Source:HGNC Symbol;Acc:HGNC:23690]  |
| 10   | MIB2    | 1.22    | 2e-07   | 2e-06 | 50 x 41 mindbomb E3 ubiquitin protein ligase 2 [Source:HGNC Symbol;Acc:HGNC:23690]                  |
| 11   | ZFP1    | 1.21    | 2e-07   | 2e-06 | 50 x 41 ZFP1 zinc finger protein [Source:HGNC Symbol;Acc:HGNC:23690]                                |
| 12   | HMGCL   | 1.21    | 2e-07   | 2e-06 | 50 x 42 3-hydroxymethyl-3-methylglutaryl-CoA lyase [Source:HGNC Symbol;Acc:HGNC:23690]              |
| 13   | DEPDC5  | 1.21    | 2e-07   | 6e-06 | 50 x 41 DEP domain containing 5 [Source:HGNC Symbol;Acc:HGNC:23690]                                 |
| 14   | NRDE2   | 1.19    | 4e-07   | 6e-06 | 50 x 44 NRDE-2, necessary for RNA interference, domain containing                                   |
| 15   | ACER3   | 1.17    | 5e-07   | 6e-06 | 50 x 45 alkaline ceramidase 3 [Source:HGNC Symbol;Acc:HGNC:16092]                                   |
| 16   | RNF170  | 1.16    | 6e-07   | 6e-06 | 47 x 48 ring finger protein 170 [Source:HGNC Symbol;Acc:HGNC:25092]                                 |
| 17   | DAPP1   | 1.16    | 6e-07   | 6e-06 | 48 x 44 dual adaptor of phosphotyrosine and 3-phosphoinositides [Source:HGNC Symbol;Acc:HGNC:23690] |
| 18   | CTNS    | 1.16    | 6e-07   | 6e-06 | 46 x 47 cystinosis, lysosomal cystine transporter [Source:HGNC Symbol;Acc:HGNC:23690]               |
| 19   | KANK1   | 1.15    | 8e-07   | 6e-06 | 50 x 41 KN motif and ankyrin repeat domains 1 [Source:HGNC Symbol;Acc:HGNC:23690]                   |
| 20   | CEP68   | 1.15    | 9e-07   | 6e-06 | 50 x 42 centrosomal protein 68kDa [Source:HGNC Symbol;Acc:HGNC:23690]                               |

p-values



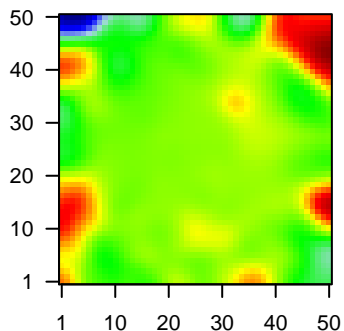
# G4\_mel

## Local Summary

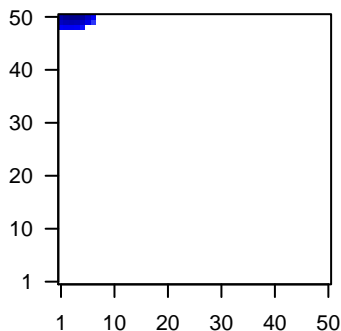
%DE = 0.89  
 # metagenes = 19  
 # genes = 318  
 # genes in genesets = 317  
  
 # genes with  $fdr < 0.1$  = 244 ( 22 + / 222 - )  
 # genes with  $fdr < 0.05$  = 208 ( 13 + / 195 - )  
 # genes with  $fdr < 0.01$  = 138 ( 8 + / 130 - )

$\langle r \rangle$  metagenes = 0.94  
 $\langle r \rangle$  genes = 0.31  
  
 $\langle FC \rangle$  = -0.5  
 $\langle \text{shrinkage-t} \rangle$  = -8.01  
 $\langle p\text{-value} \rangle$  = 0  
 $\langle fdr \rangle$  = 0.46

Profile



Spot



## Local Genelist

| Rank | ID       | log(FC) | p-value | fdr   | Description  |
|------|----------|---------|---------|-------|--|
| 1    | NASP     | -1.43   | 2e-16   | 4e-15 | 1 x 48 nuclear autoantigenic sperm protein (histone-binding) [Source:HGNC Symbol;Acc:HGNC:17359] |
| 2    | RRM1     | -1.58   | 2e-16   | 4e-15 | 2 x 50 ribonucleotide reductase M1 [Source:HGNC Symbol;Acc:HGNC:17359]                           |
| 3    | CDKN3    | -1.39   | 1e-15   | 3e-14 | 6 x 50 cyclin-dependent kinase inhibitor 3 [Source:HGNC Symbol;Acc:HGNC:17359]                   |
| 4    | FANCL    | -1.52   | 2e-15   | 8e-13 | 1 x 48 Fanconi anemia, complementation group L [Source:HGNC Symbol;Acc:HGNC:17359]               |
| 5    | STMN1    | -0.72   | 2e-14   | 7e-11 | 5 x 50 stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]   |
| 6    | NUP54    | -1.41   | 4e-12   | 7e-11 | 1 x 50 nucleoporin 54kDa [Source:HGNC Symbol;Acc:HGNC:17359]                                     |
| 7    | HADH     | -1.41   | 4e-12   | 3e-10 | 1 x 48 hydroxyacyl-CoA dehydrogenase [Source:HGNC Symbol;Acc:HGNC:17359]                         |
| 8    | RFC5     | -1.39   | 1e-11   | 1e-08 | 2 x 50 replication factor C (activator 1) 5, 36.5kDa [Source:HGNC Symbol;Acc:HGNC:17359]         |
| 9    | TK1      | -1.18   | 3e-10   | 1e-08 | 4 x 50 thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:HGNC:17359]                           |
| 10   | MCM7     | -1.29   | 1e-09   | 1e-08 | 2 x 50 minichromosome maintenance complex component 7 [Source:HGNC Symbol;Acc:HGNC:17359]        |
| 11   | PCNA     | -1.06   | 1e-09   | 1e-08 | 2 x 50 proliferating cell nuclear antigen [Source:HGNC Symbol;Acc:HGNC:17359]                    |
| 12   | EXOSC9   | -1.29   | 1e-09   | 1e-08 | 1 x 50 exosome component 9 [Source:HGNC Symbol;Acc:HGNC:91]                                      |
| 13   | KIAA0101 | -1.29   | 1e-09   | 8e-08 | 3 x 50 KIAA0101 [Source:HGNC Symbol;Acc:HGNC:28961]  |
| 14   | BIRC5    | -1.23   | 5e-09   | 8e-08 | 6 x 50 baculoviral IAP repeat containing 5 [Source:HGNC Symbol;Acc:HGNC:17359]                   |
| 15   | SMC2     | -1.25   | 6e-09   | 2e-07 | 5 x 50 structural maintenance of chromosomes 2 [Source:HGNC Symbol;Acc:HGNC:17359]               |
| 16   | C19orf48 | -1.23   | 1e-08   | 2e-07 | 1 x 50 chromosome 19 open reading frame 48 [Source:HGNC Symbol;Acc:HGNC:17359]                   |
| 17   | HELLS    | -1.23   | 2e-08   | 2e-07 | 1 x 50 helicase, lymphoid-specific [Source:HGNC Symbol;Acc:HGNC:17359]                           |
| 18   | CENPK    | -1.23   | 2e-08   | 2e-07 | 3 x 50 centromere protein K [Source:HGNC Symbol;Acc:HGNC:294]                                    |
| 19   | ORC6     | -1.18   | 3e-08   | 2e-07 | 1 x 50 origin recognition complex, subunit 6 [Source:HGNC Symbol;Acc:HGNC:17359]                 |
| 20   | CENPN    | -1.21   | 3e-08   | 5e-07 | 4 x 50 centromere protein N [Source:HGNC Symbol;Acc:HGNC:308]                                    |

p-values

