Supplementary material

Supplementary Tables

Table S1. DEGs identified by the DESeq and edgeR package.

Table S2. DEMs identified by the DESeq and edgeR package.

Table S3. DELs identified by the DESeq and edgeR package.

Table S4. Clinical features of HCC patients who received RNA sequencing in TCGA cohort.

Table S5. Clinical features of HCC patients who received miRNA sequencing in TCGA cohort.

Table S6. The univariate survival analysis results of the differentially expressed RNAs in ceRNA network.

Table S7. GSEA results of c5 reference gene sets in high-risk groups

Table S8. GSEA results of c2 reference gene sets in high-risk groups

Supplementary Figures

Figure S1. Flow chart of ceRNA networks construction.

Figure S2. Heat map of overlapping DEGs in TCGA HCC cohort.

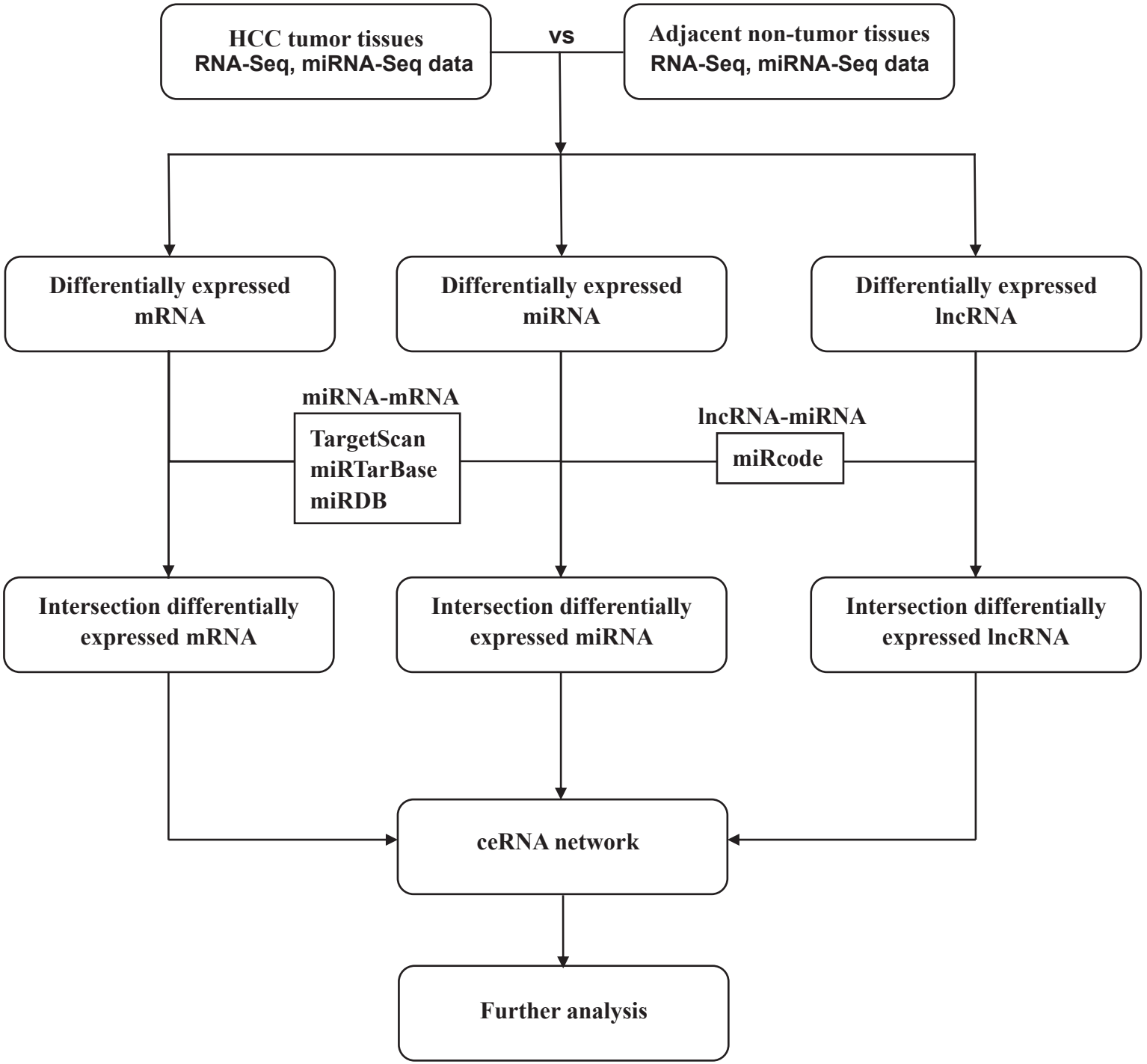
Figure S3. Heat map of overlapping DEMs in TCGA HCC cohort.

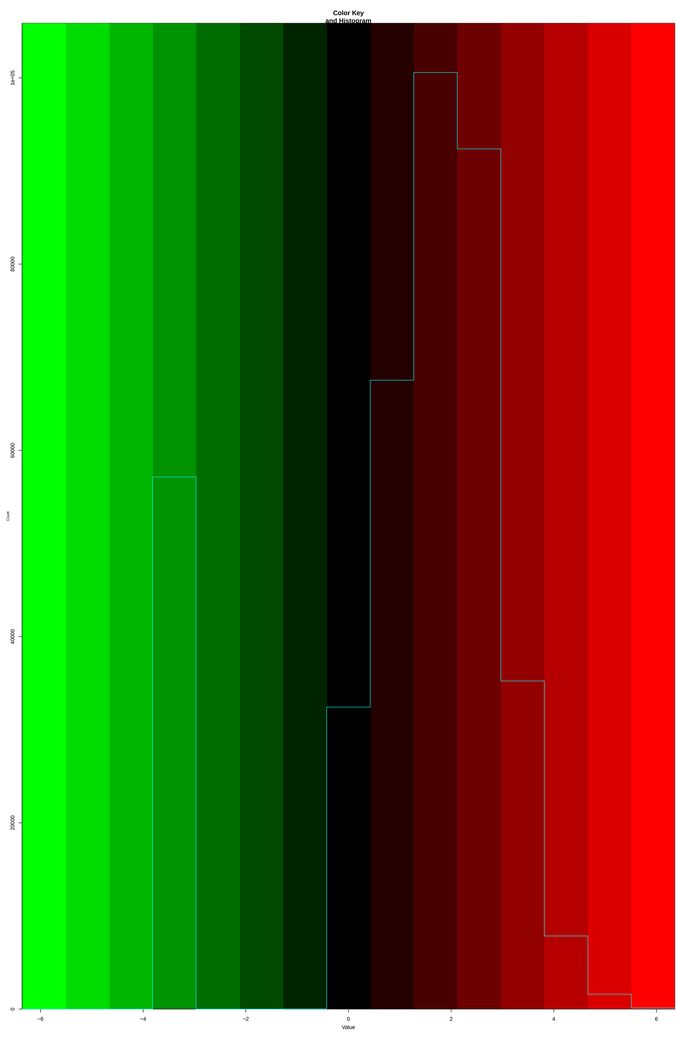
Figure S4. Heat map of overlapping DELs in TCGA HCC cohort.

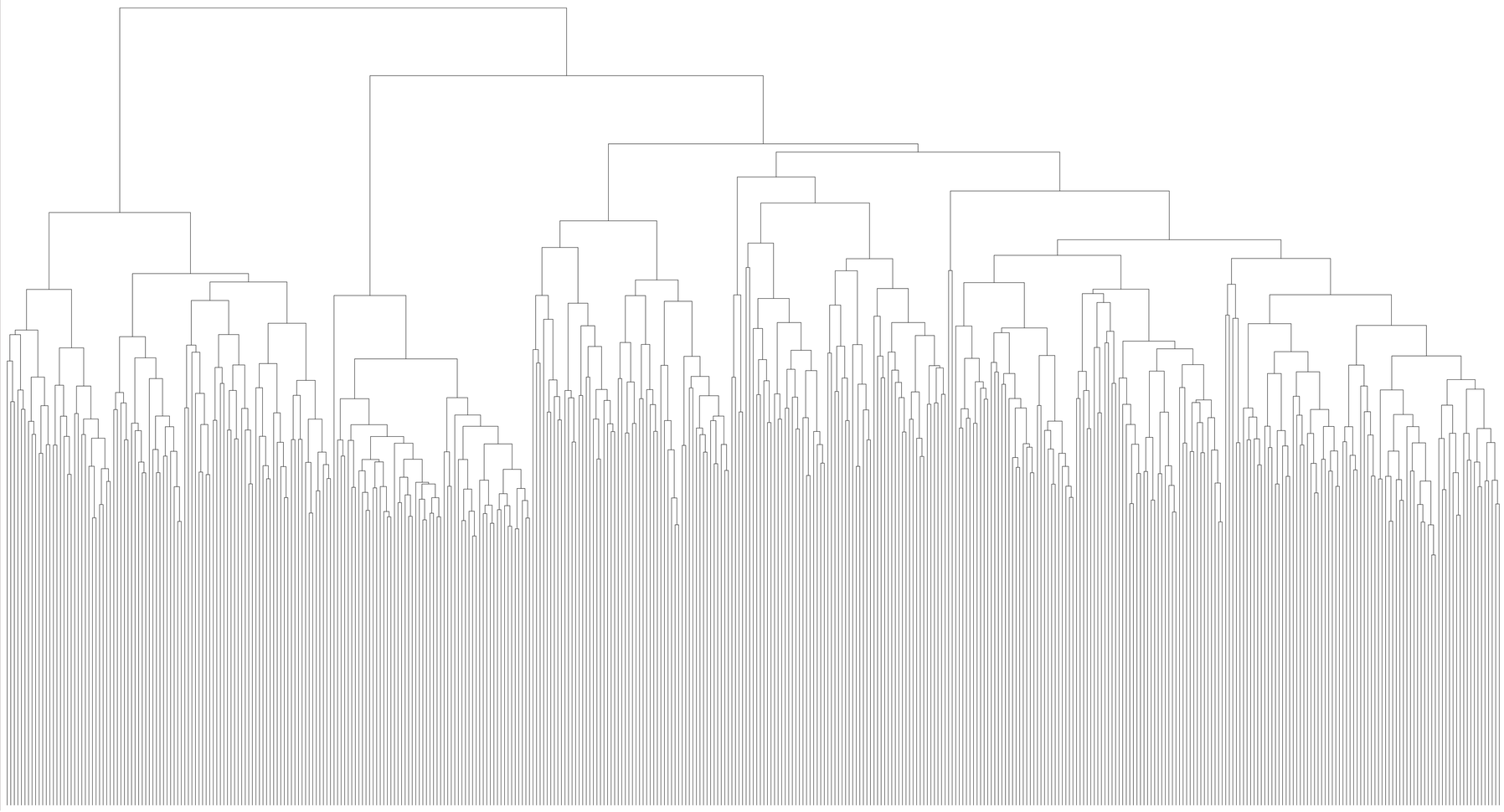
Figure S5. Directed acyclic graph of DEGs in ceRNA network.

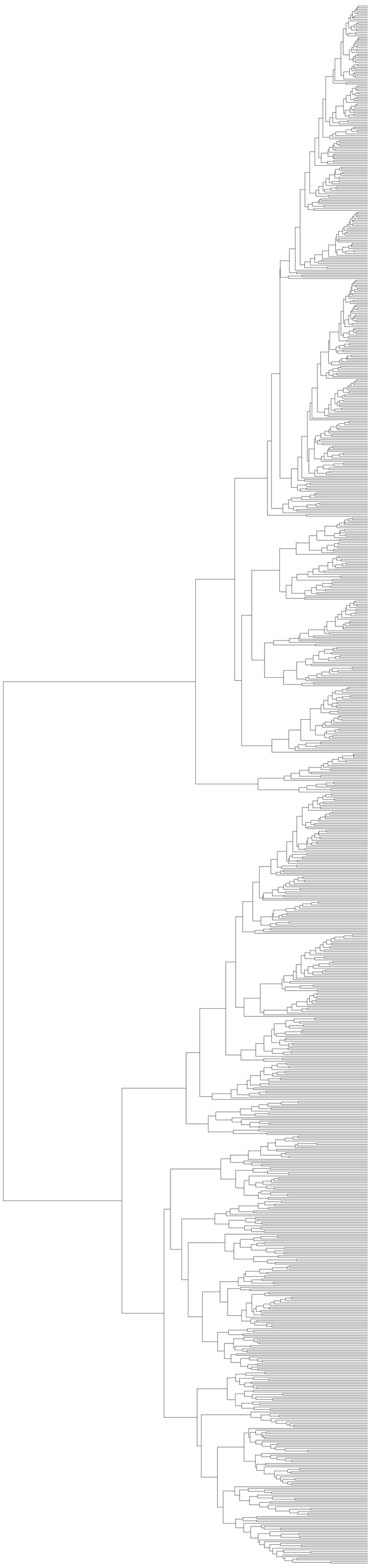
Figure S6. Protein-protein and gene-gene interaction networks of these DEGs in ceRNA network. (A) Protein–protein interaction networks; (B) GeneMANIA interaction networks.

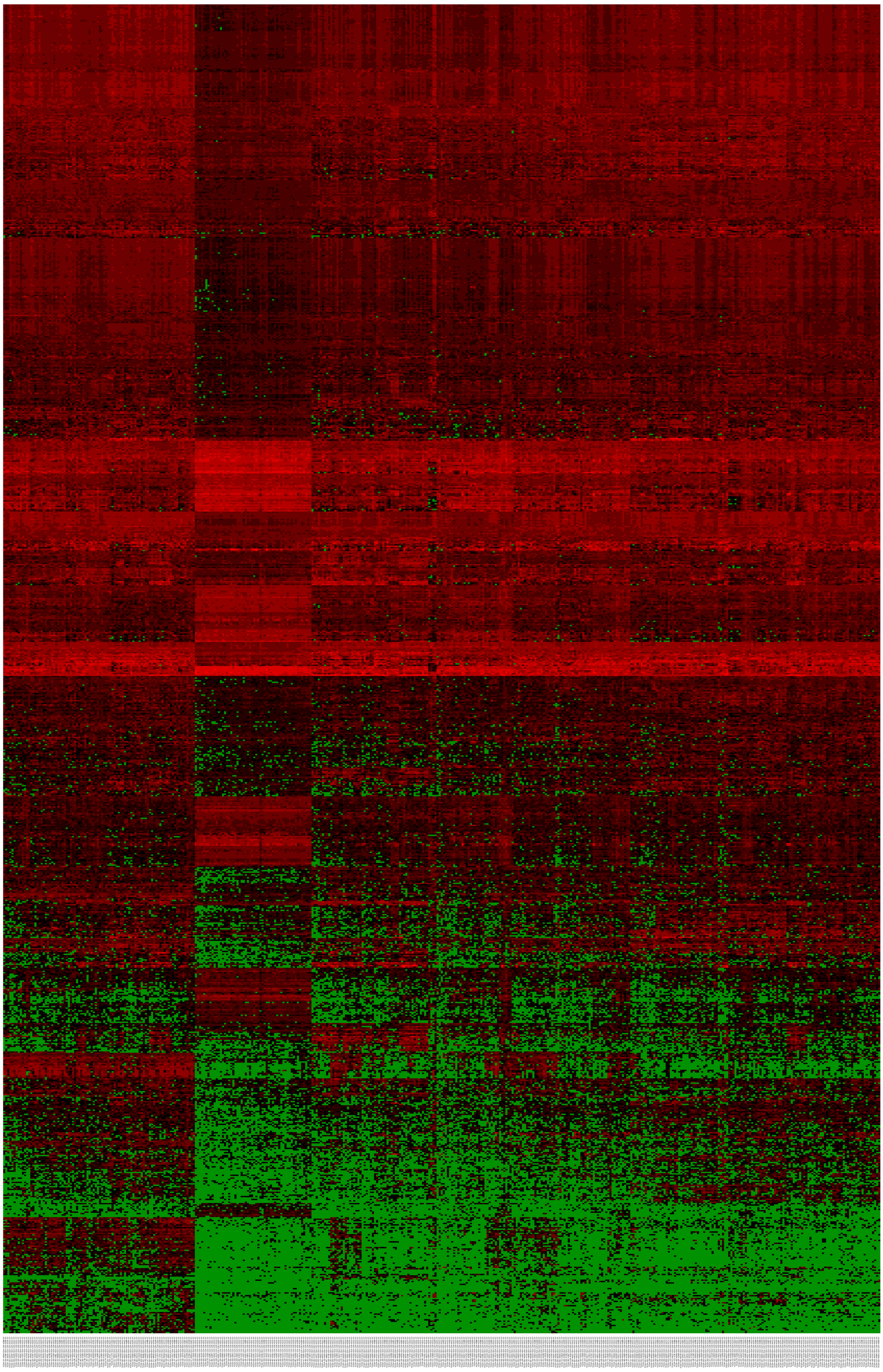
Figure S7. Co-expression matrix heatmap of the RNAs in the prognostic signature.

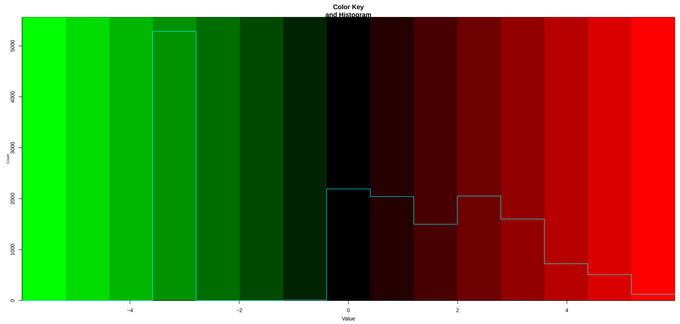

HCC tumor tissues
RNA-Seq, miRNA-Seq data
vs
Adjacent non-tumor tissues
RNA-Seq, miRNA-Seq data
Differentially expressed mRNA
Differentially expressed miRNA
Differentially expressed lncRNA
miRNA-mRNA
TargetScan
miRTarBase
miRDB
lncRNA-miRNA
miRcode
Intersection differentially expressed mRNA
Intersection differentially expressed miRNA
Intersection differentially expressed lncRNA
ceRNA network
Further analysis

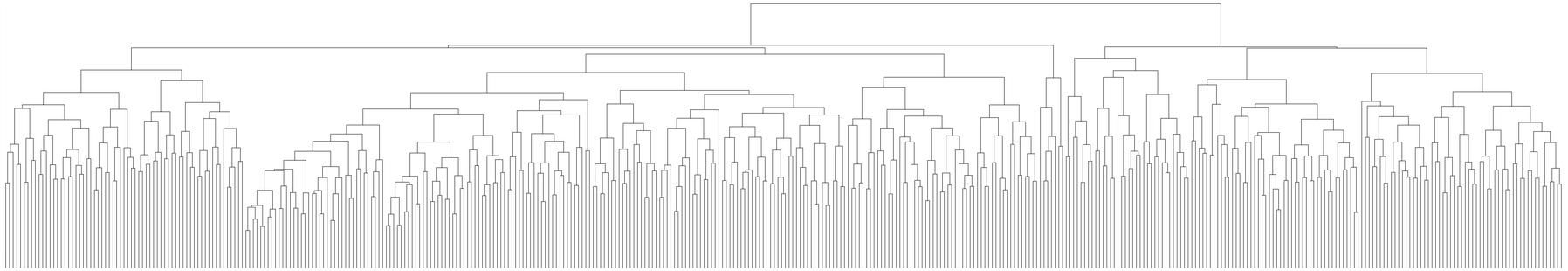

Color Key
and Histogram
Count
Value

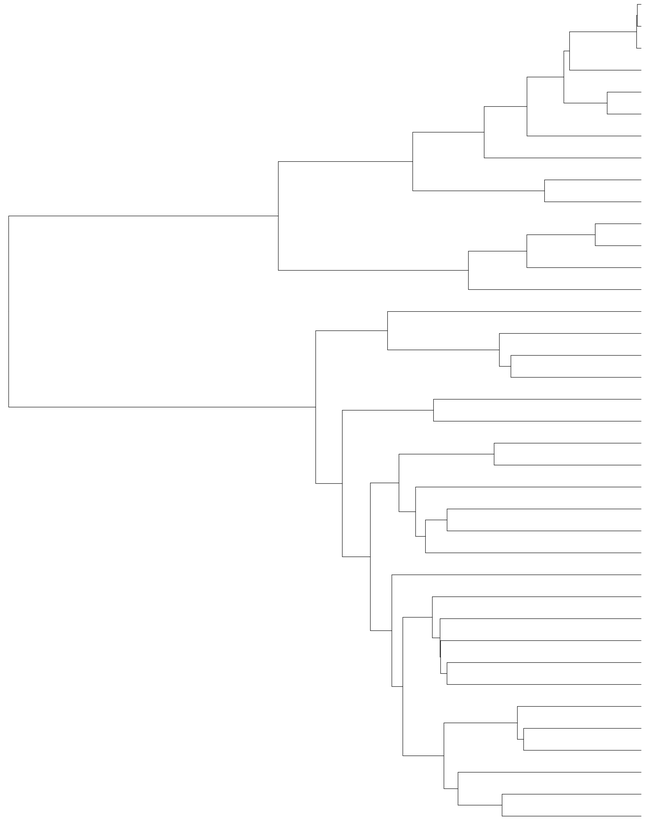


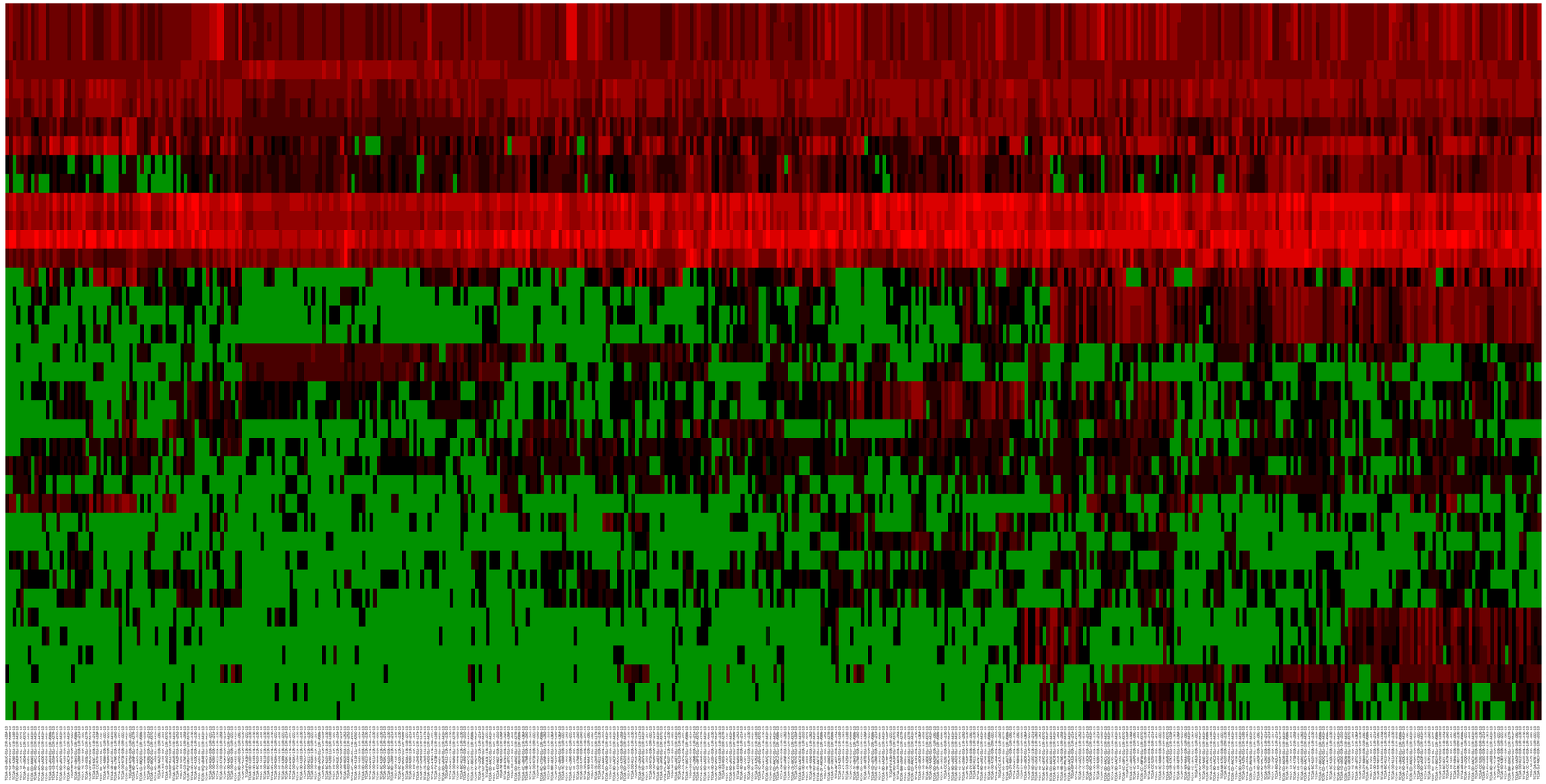


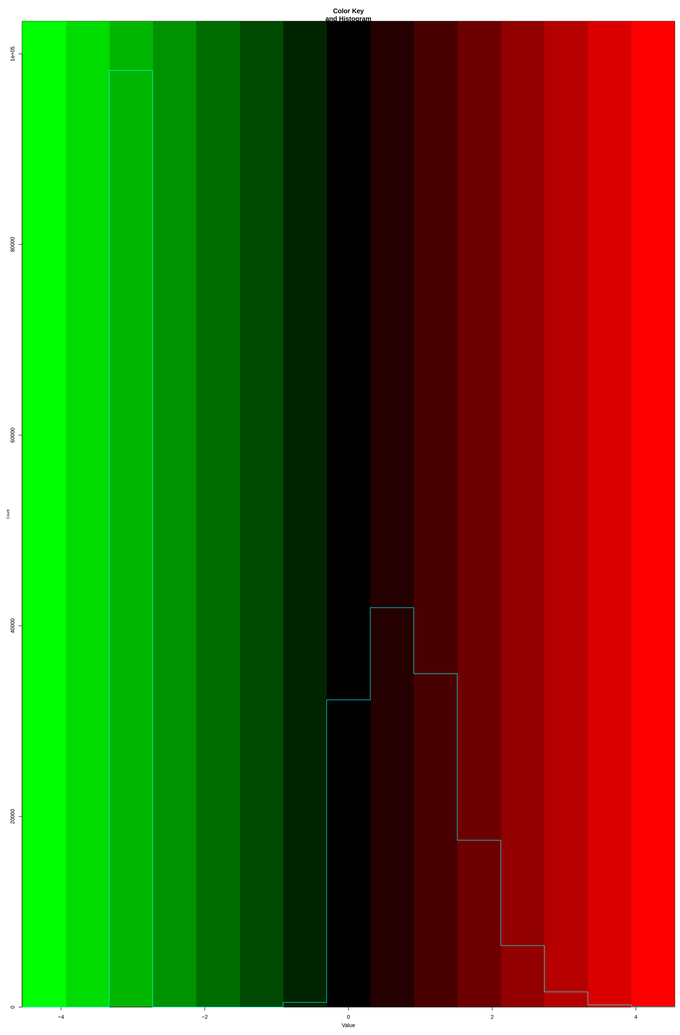


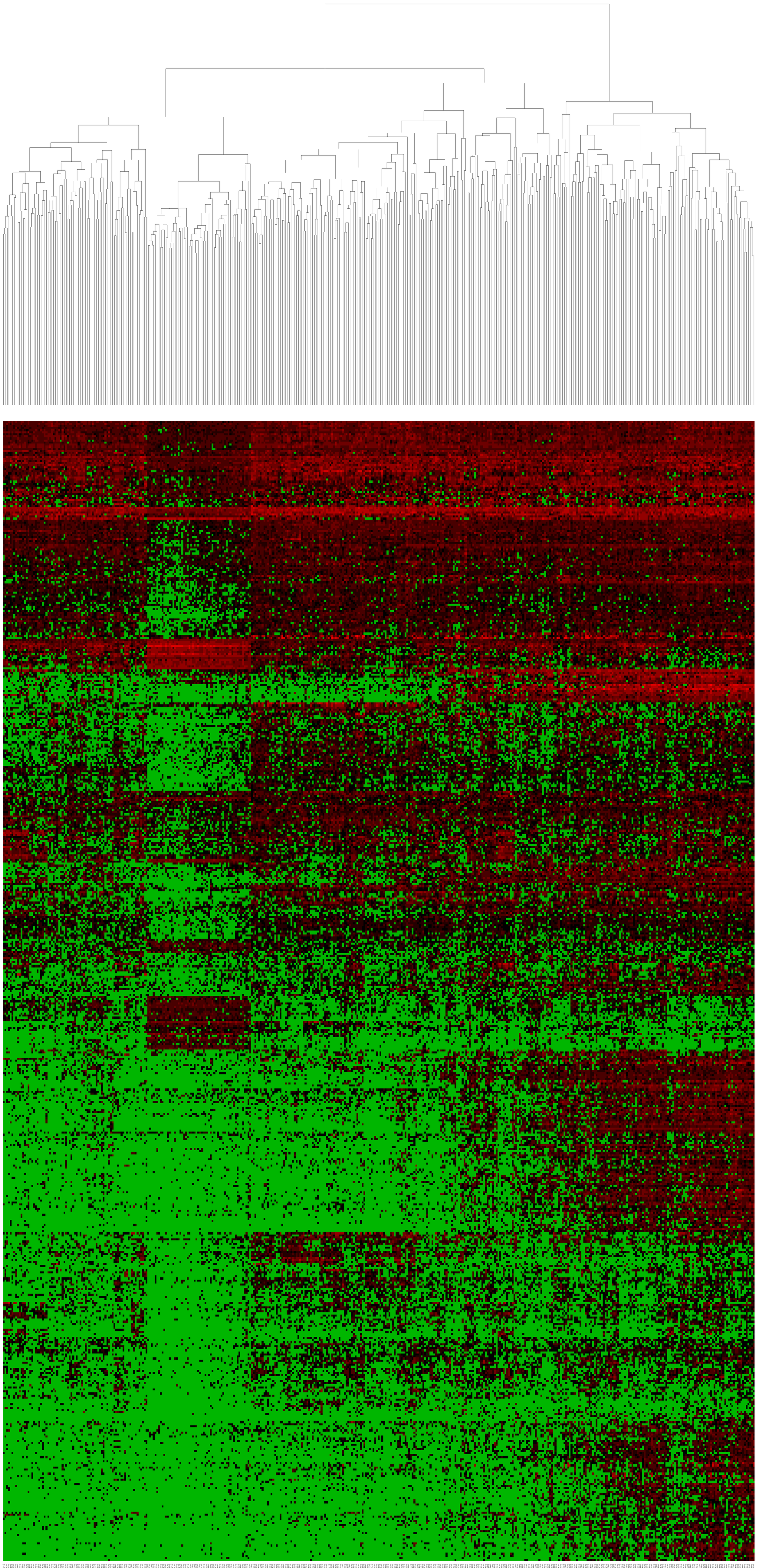

Color Key
and Histogram
Count
0
1000
2000
3000
4000
5000
−4
−2
0
2
4
Value

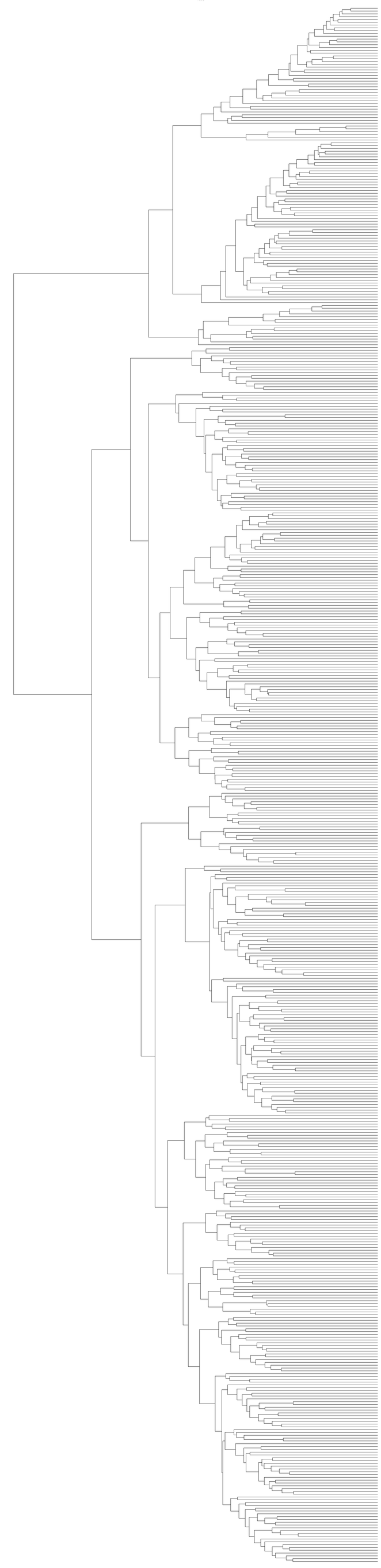


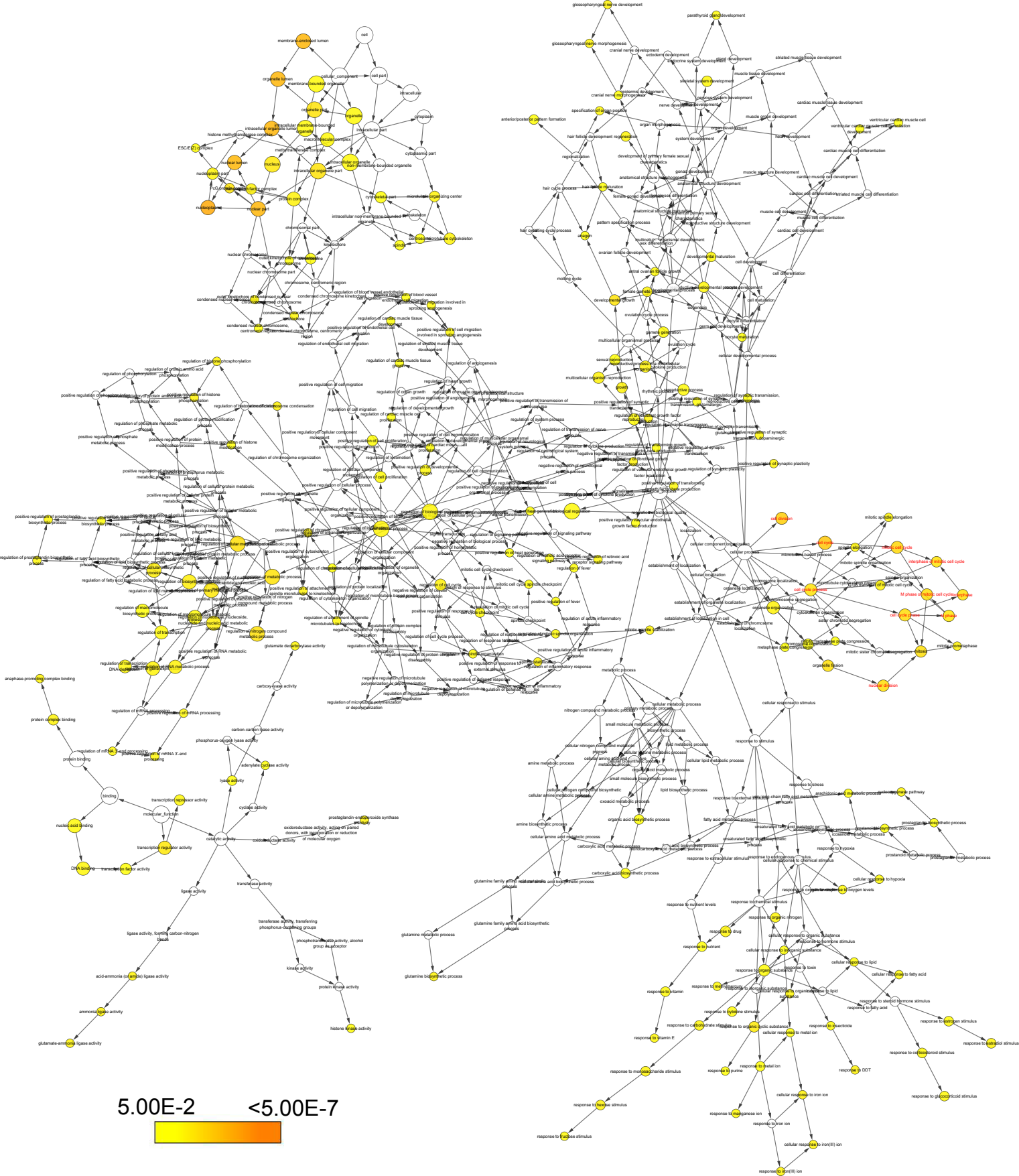


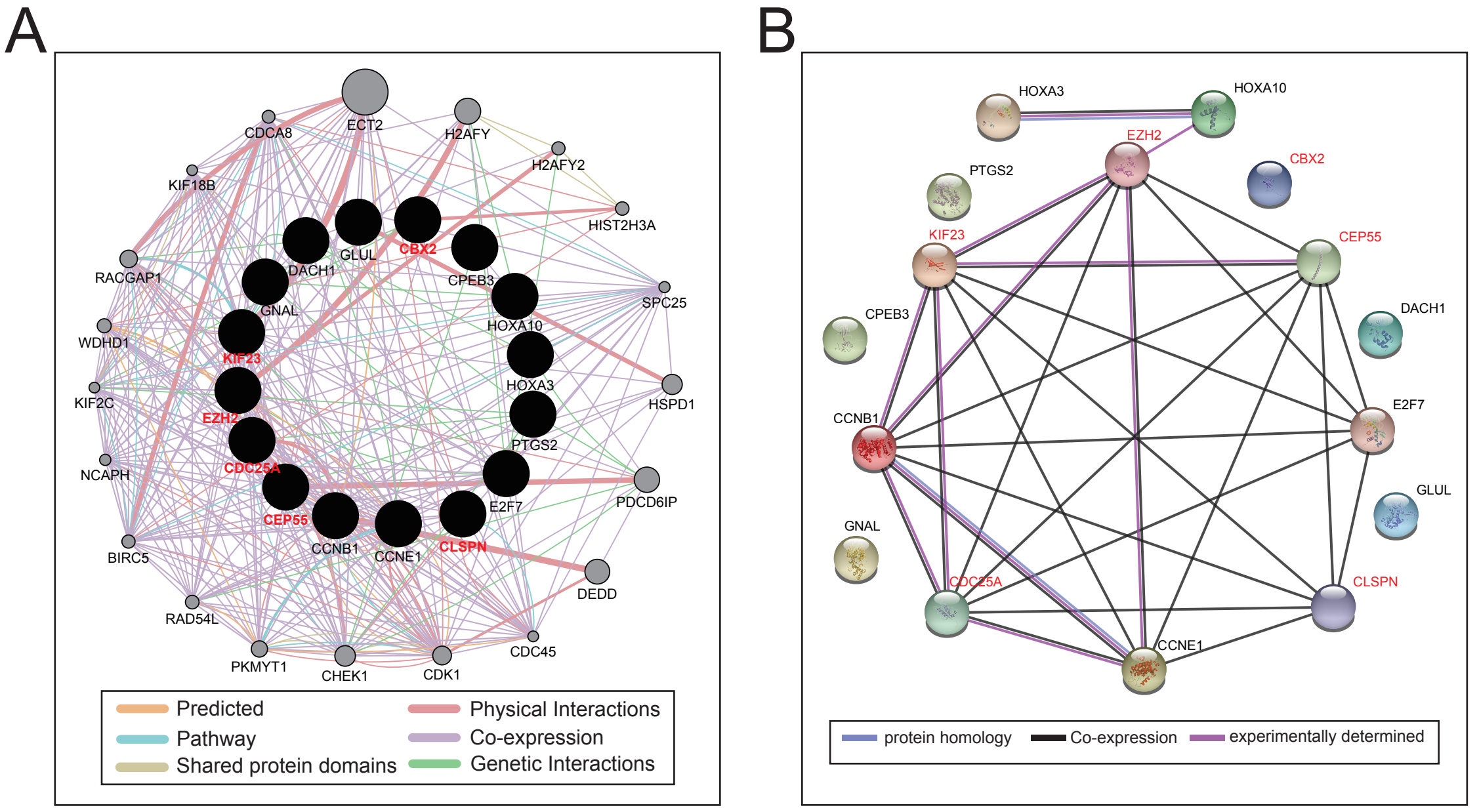

hsa-mir-9-3
hsa-mir-9-1
hsa-mir-9-2
hsa-mir-424
hsa-mir-452
hsa-mir-224
hsa-mir-196b
hsa-mir-1269a
hsa-mir-216a
hsa-mir-216b
hsa-mir-182
hsa-mir-183
hsa-mir-10b
hsa-mir-217
hsa-mir-1269b
hsa-mir-767
hsa-mir-105-2
hsa-mir-105-1
hsa-mir-125b
hsa-mir-490
hsa-mir-196a-2
hsa-mir-196a-1
hsa-mir-1251
hsa-mir-190b
hsa-mir-3662
hsa-mir-3144
hsa-mir-466
hsa-mir-137
hsa-mir-615
hsa-mir-549a
hsa-mir-1254-2
hsa-mir-3189
hsa-mir-520f
hsa-mir-520c
hsa-mir-520h
hsa-mir-4652
hsa-mir-548y
hsa-mir-548k

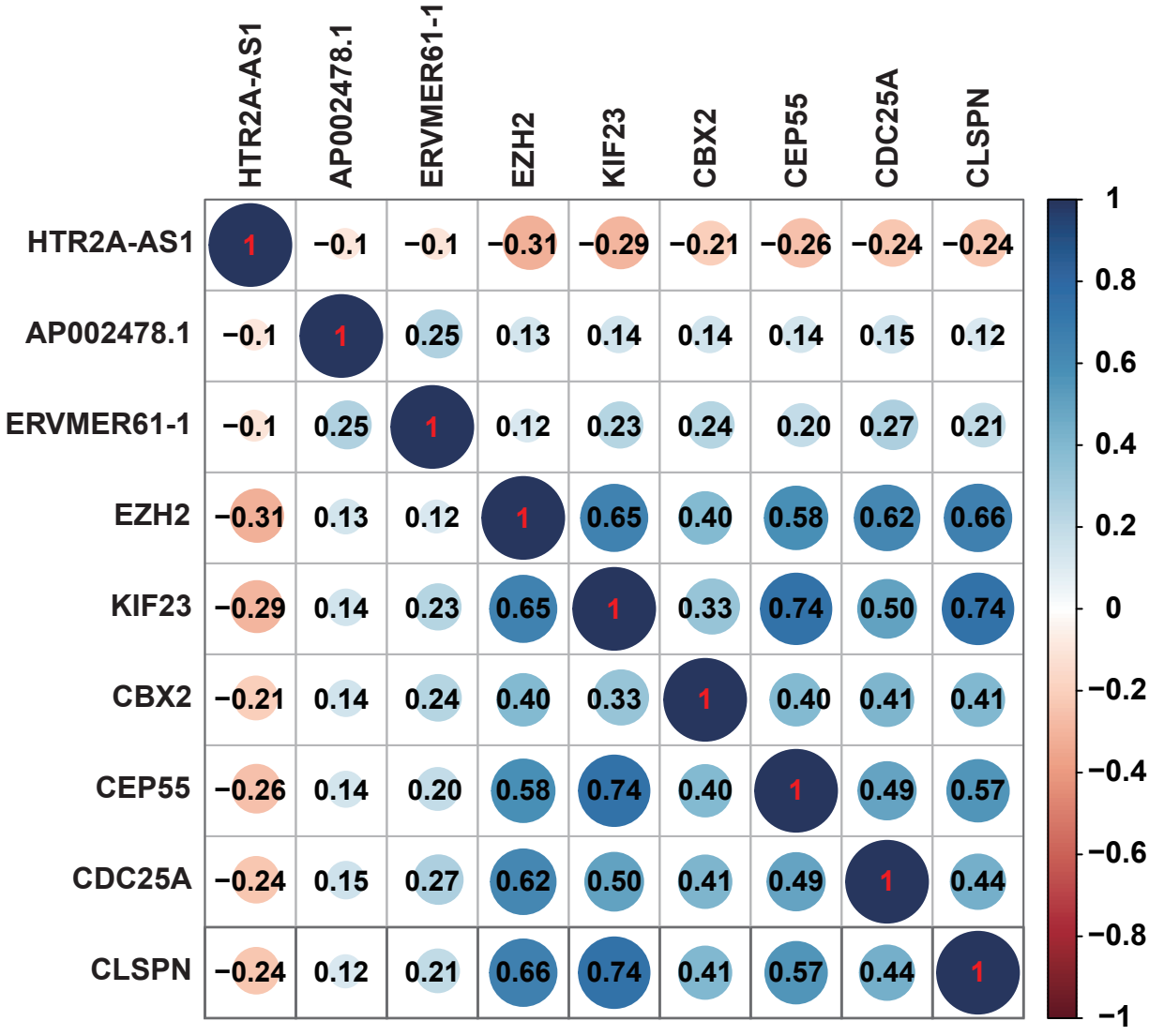

Color Key
and Histogram
Count
Value






5.00E-2
<5.00E-7


A
ECT2
CDCA8
H2AFY
H2AFY2
KIF18B
HIST2H3A
GLUL
CBX2
DACH1
CPEB3
RACGAP1
GNAL
SPC25
HOXA10
WDHD1
KIF23
HOXA3
KIF2C
HSPD1
EZH2
PTGS2
NCAPH
CDC25A
PDCD6IP
E2F7
CEP55
CCNB1
CCNE1
CLSPN
BIRC5
DEDD
RAD54L
CDC45
PKMYT1
CHEK1
CDK1
Predicted
Physical Interactions
Pathway
Co-expression
Shared protein domains
Genetic Interactions
B
HOXA3
HOXA10
EZH2
CBX2
PTGS2
KIF23
CEP55
CPEB3
DACH1
CCNB1
E2F7
GLUL
GNAL
CDC25A
CLSPN
CCNE1
protein homology
Co-expression
experimentally determined


HTR2A-AS1
AP002478.1
ERVMER61-1
EZH2
KIF23
CBX2
CEP55
CDC25A
CLSPN
HTR2A-AS1 1 −0.1 −0.1 −0.31 −0.29 −0.21 −0.26 −0.24 −0.24
AP002478.1 −0.1 1 0.25 0.13 0.14 0.14 0.14 0.15 0.12
ERVMER61-1 −0.1 0.25 1 0.12 0.23 0.24 0.20 0.27 0.21
EZH2 −0.31 0.13 0.12 1 0.65 0.40 0.58 0.62 0.66
KIF23 −0.29 0.14 0.23 0.65 1 0.33 0.74 0.50 0.74
CBX2 −0.21 0.14 0.24 0.40 0.33 1 0.40 0.41 0.41
CEP55 −0.26 0.14 0.20 0.58 0.74 0.40 1 0.49 0.57
CDC25A −0.24 0.15 0.27 0.62 0.50 0.41 0.49 1 0.44
CLSPN −0.24 0.12 0.21 0.66 0.74 0.41 0.57 0.44 1
1
0.8
0.6
0.4
0.2
0
−0.2
−0.4
−0.6
−0.8
−1