

Figure S1. Screening of 161 samples in the GSE54236 dataset of the Gene Expression Omnibus database. Screening showed that the samples were evenly distributed without exclusions. After discrete analysis of samples, it was demonstrated that there was no sample with a large degree of dispersion in the population. The red line indicates the screening range.

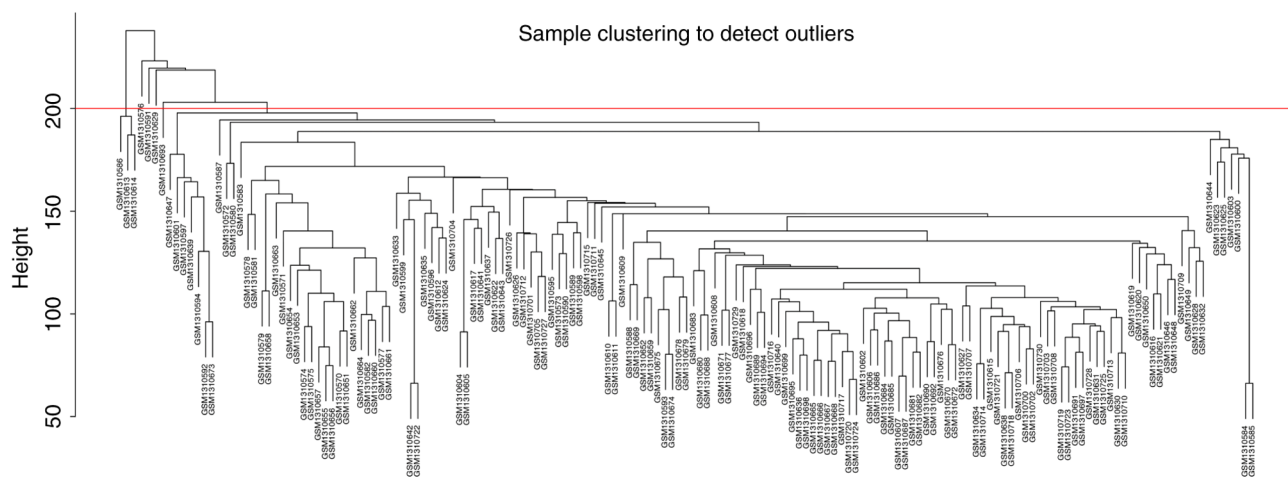


Figure S3. Determination of soft-thresholding power in the weighted gene co-expression network analysis. (A) In the sub-co-expression network of lncRNAs and miRNAs, R was used to analyze the scale-free fit index for various soft-thresholding powers (β). (B) In the sub-co-expression network of miRNAs and mRNAs, R was used to analyze the scale-free fit index for various soft-thresholding powers (β).

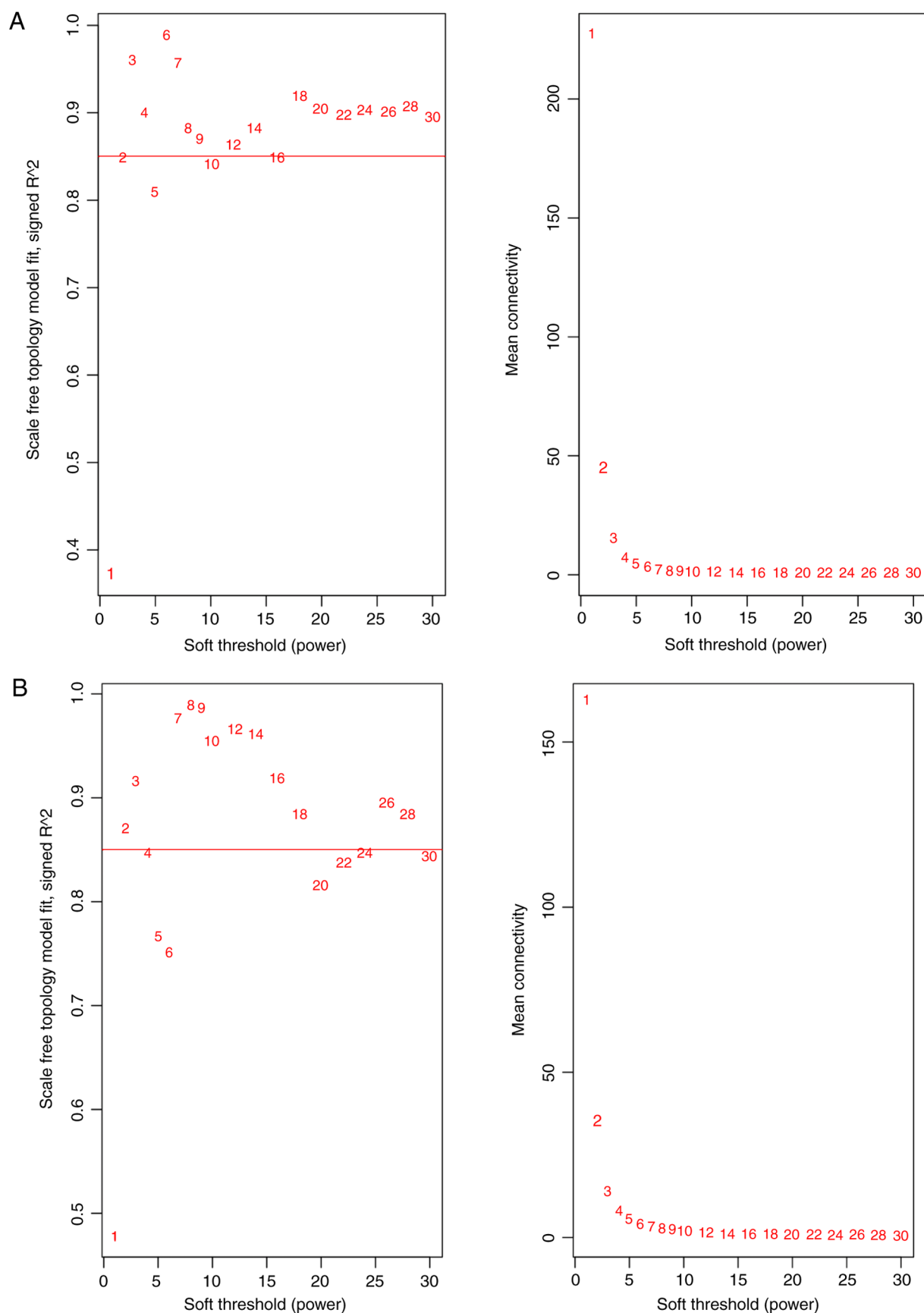


Figure S4. Spatial structure of ROR1-AS1 and its transcript information in the NONCODE database. Two-dimensional stem-loop structure of long noncoding RNA ROR1-AS1 and its composition sequence. ROR1-AS1, tyrosine protein kinase transmembrane receptor 1 antisense RNA.

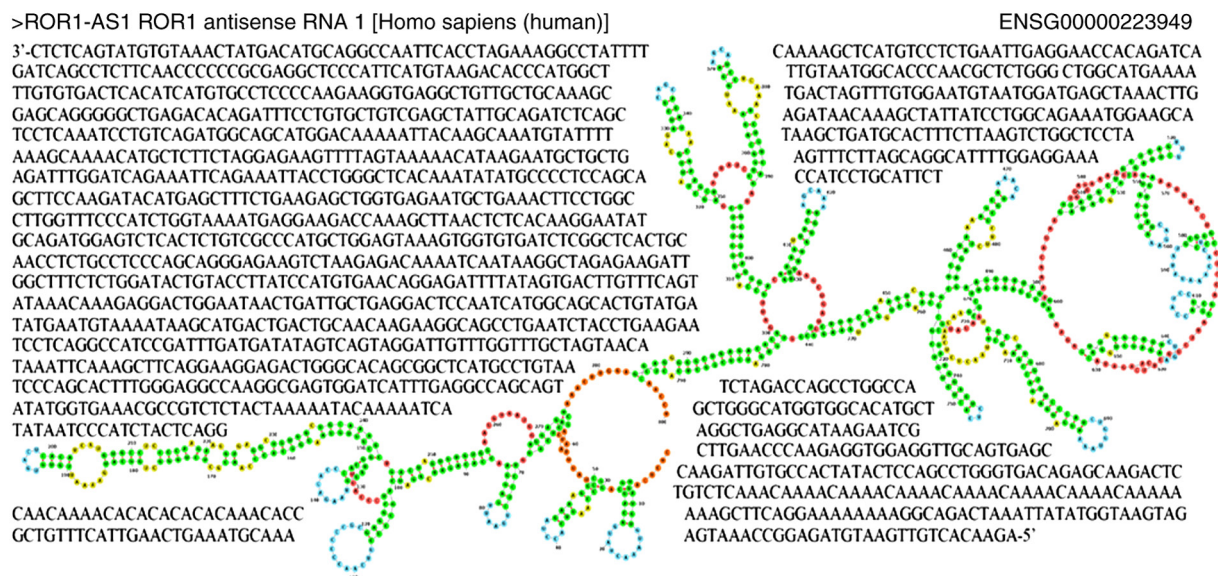


Figure S5. VENN of three databases. Excluding genes with $R < 0.5$, only 12 genes with $R > 0.5$ were retained and verified in the three databases. GEO, Gene Expression Omnibus; MEM, Multi Experiment Matrix; TCGA, The Cancer Genome Atlas.

