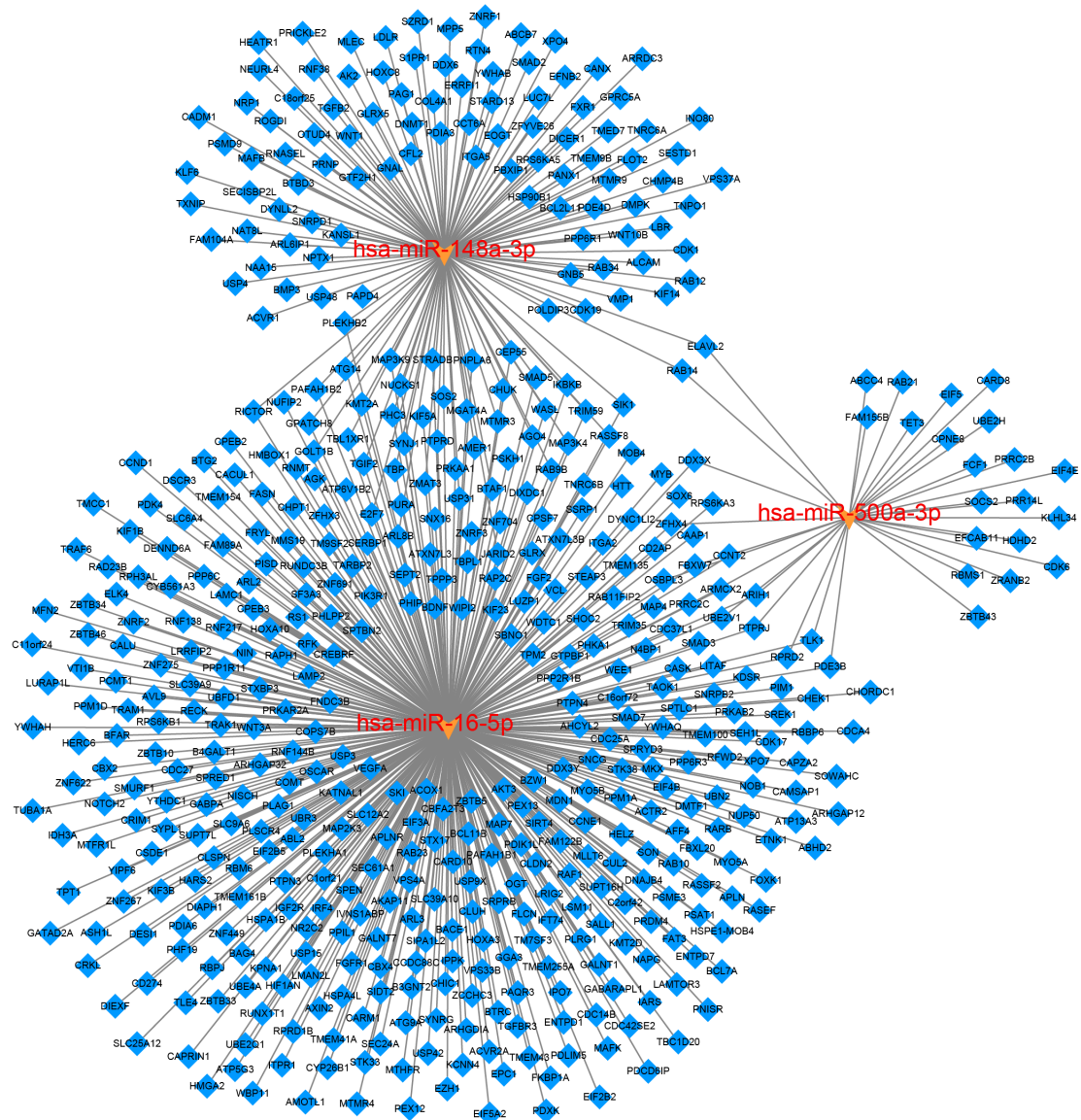
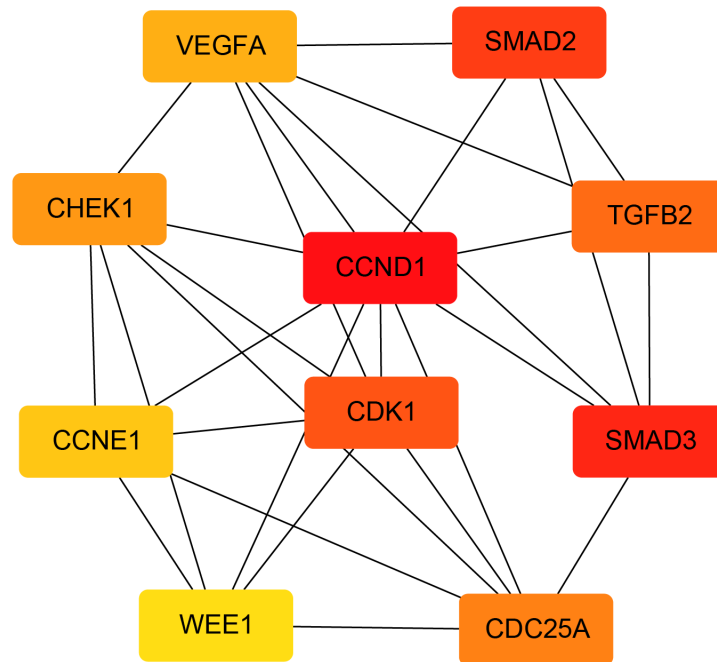


Supplementary Figure 1 The heatmap of 8 differently expressed miRNAs. As a result of comparing the 13 miRNA expression levels of cancer samples and non-cancer samples, 8 miRNAs were found to differ in expression.

Abbreviations: N, non-cancer samples; T, cancer samples.

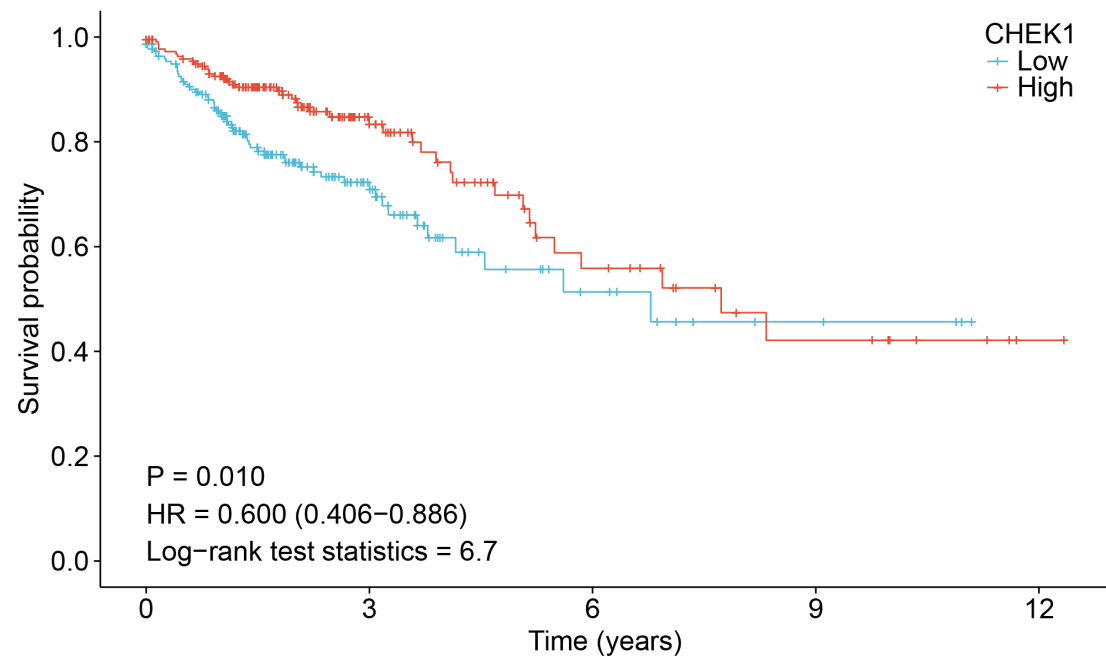


Supplementary Figure 2 Network of miRNA-target gene interaction. The network consists of 542 nodes and 591 edges, of which hsa-miR-16-5p, hsa-miR-148a-3p and hsa-miR-500a-3p correspond to 421, 137 and 33 target genes, respectively. The orange inverted triangle represents the miRNA, the blue diamond represents the target.



Supplementary Figure 3 Network of ten hub genes. We obtained ten hub genes from the PPI network using the cytohubba. The closer the colour of the target to red, the higher its score, indicating that it is a more critical target.

Abbreviations: CCND1, cyclin D1; CCNE1, cyclin E1; CDC25A, cell division cycle 25A; CDK1, cyclin dependent kinase 1; CHEK1, checkpoint kinase 1; SMAD2, SMAD family member 2; SMAD3, SMAD family member 3; TGFB2, transforming growth factor beta 2; VEGFA, vascular endothelial growth factor A; WEE1, WEE1 G2 checkpoint kinase.



Supplementary Figure 4 Overall survival analysis of CHEK1. The higher the expression of CHEK1, the better the prognosis of colon cancer.

Abbreviations: HR, hazard ratio.