



# Identification of hub genes and pathways associated with retinoblastoma based on co-expression network analysis

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**ABSTRACT.** The objective of this paper was to identify hub genes and pathways associated with retinoblastoma using centrality analysis of the co-expression network and pathway-enrichment analysis. The co-expression network of retinoblastoma was constructed by weighted gene co-expression network analysis (WGCNA) based on differentially expressed (DE) genes, and clusters were obtained through the molecular complex detection (MCODE) algorithm. Degree centrality analysis of the co-expression network was performed to explore hub genes present in retinoblastoma. Pathway-enrichment analysis was performed using the Kyoto Encyclopedia of Genes and Genomes (KEGG) database. Validation of hub gene expression in retinoblastoma was performed by reverse transcription-polymerase chain reaction (RT-PCR) analysis. The co-expression network based on 221 DE genes between retinoblastoma and normal controls consisted of 210 nodes and 3965 edges, and 5 clusters of the network were evaluated. By assessing the centrality analysis of the co-

expression network, 21 hub genes were identified, such as SNORD115-41, RASSF2, and SNORD115-44. According to RT-PCR analysis, 16 of the 21 hub genes were differently expressed, including RASSF2 and CDCA7, and 5 were not differently expressed in retinoblastoma compared to normal controls. Pathway analysis showed that genes in 2 clusters were enriched in 3 pathways: purine metabolism, p53 signaling pathway, and melanogenesis. In this study, we successfully identified 16 hub genes and 3 pathways associated with retinoblastoma, which may be potential biomarkers for early detection and therapy for retinoblastoma.

**Key words:** Retinoblastoma; Co-expression network; Hub gene; Pathway; Reverse transcription-polymerase chain reaction