



# Module function and two-way clustering analysis of Epstein-Barr virus-related nasopharyngeal cancer

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**ABSTRACT.** This study sought to identify and characterize the function of genes as diagnostic markers for Epstein-Barr virus (EBV)-related nasopharyngeal cancer (NPC). The gene expression profile of GSE13597 was downloaded from the Gene Expression Omnibus database, which included 28 EBV-related NPC gene expression profile data sets, 25 disease samples, and 3 control samples. Data were pre-processed, and differentially expressed genes were screened using the R language. The co-expression coefficient was calculated to construct a co-expression network using Cytoscape. ClusterONE was used to perform module analysis to find enriched gene families. The BiCAT software was used to perform a two-way clustering analysis of differentially expressed gene expression profiles based on the co-expression networks and to verify the enriched gene families, followed by functional enrichment analysis of these gene families. The MCM

gene family was found to be enriched in EBV-related NPC. This gene family is essential for eukaryotic DNA replication. Functional analysis of differentially expressed genes in the co-expression network revealed that the enriched biological processes and pathways were mainly involved in the cell cycle. EBV-related NPC is likely associated mainly with the process of cell reproduction, providing a strong basis for the prevention, diagnosis, and treatment of EBV-related NPC and a direction for targeted chemotherapy.

**Key words:** Nasopharyngeal carcinoma; Co-expression networks; BiCAT; Two-way clustering