Bioinformatics-Based Functional Exploration of Meiosis-Related Genes in Cervical Cancer

Haoqian Zhang
Department of Obstetrics and Gynecology, The third Affliated Hospital of Zhengzhou University, Zhengzhou, China
Zhengzhou Key Laboratory of Cervical Disease, The third Affliated Hospital of Zhengzhou University, Zhengzhou, China
National Clinical Research Center for Obstetrics and Gynecology, Henan Branch, The third Affliated Hospital of Zhengzhou University, Zhengzhou, China

Yuanhang Zhu
Zhengzhou Key Laboratory of Cervical Disease, The third Affliated Hospital of Zhengzhou University, Zhengzhou, China
National Clinical Research Center for Obstetrics and Gynecology, Henan Branch, The third Affliated Hospital of Zhengzhou University, Zhengzhou, China

Chenchen Ren
Department of Obstetrics and Gynecology, The third Affliated Hospital of Zhengzhou University, Zhengzhou, China
Zhengzhou Key Laboratory of Cervical Disease, The third Affliated Hospital of Zhengzhou University, Zhengzhou, China
National Clinical Research Center for Obstetrics and Gynecology, Henan Branch, The third Affliated Hospital of Zhengzhou University, Zhengzhou, China

Abstract:

Objective: Meiosis-related genes (MRGs) associated with cervical cancer were systematically identified through bioinformatics approaches, and their clinical implications were comprehensively evaluated.

Methods: Differentially expressed genes (DEGs) between cervical cancer tissues and normal tissues were identified through data mining of the TCGA database. Gene Set Enrichment Analysis (GSEA) was employed to screen meiosis-related gene sets with complete datasets and high data integrity. Transcriptomic sequencing data from the GEO database, encompassing varying histopathological grades, HPV infection statuses, and responses to chemoradiotherapy, were systematically curated and subjected to secondary statistical analyses.

Results: Differential expression analysis of 119 meiosis-related genes (MRGs) in cervical carcinogenesis revealed 14 upregulated and 5 downregulated candidates. SYCE2, BLM, RBBP8, and RPA2 emerged