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Comparative Transcriptomic Profiling of Circular RNAs and Differential Interferon Responses in Porcine Alveolar Macrophages

Porcine reproductive and respiratory syndrome virus (PRRSV) is a globally devastating pathogen with profound impacts on the swine industry. This study employs a whole-transcriptome approach to characterize small RNA transcriptomes (sRNA-Seq) and analyze gene expression and circular RNA (circRNA) dynamics under varying experimental conditions in porcine alveolar macrophages of the viral infection and different antiviral treatments. After stringent quality control, over 98% of reads met high-quality standards, enabling the identification of more than 1,000 differentially expressed circRNAs. Notably, wild-type PRRSV and vaccine strains induced distinct patterns of circRNA regulation. Enrichment analyses of source genes highlighted the regulatory roles of these circRNAs and their potential as biomarkers. These findings enhance our understanding of porcine RNA dynamics and provide a foundation for investigating functional interactions among circRNAs, long non-coding RNAs (lncRNAs), and microRNAs (miRNAs) in PRRSV pathogenesis and host responses.