The blood miRNA-sequencing data are deposited in the NCBI Sequence Read Archive database under the accession number SRX9254510-SRX9254519.

In this study, the number of biological replicates of the miRNA-sequencing was shown in line 113 and 133. However, just like any other studies (Jie et al., 2021; Slota et al., 2019), it is failure to present the sequencing depth. Because the read levels of each miRNA were different, and the sequencing depth of current sequencing platforms exceeds that is necessary to quantify miRNAs (Vigneault et al., 2012). Besides, the raw reads and clean reads of each FMD blood sample were shown in Table S4 (> 23 million reads were sequenced for each sample).

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Vigneault F, Ter-Ovanesyan D, Alon S, Eminaga S, C Christodoulou D, Seidman JG, et al. 2012. High-throughput multiplex sequencing of miRNA. *Curr Protoc Hum Genet*. 11:1-10. DOI:10.1002/0471142905.hg1112s73.