



Predicting Potential Targets of miR-130a in Venous Thromboembolism Based on a Target Score Method

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ABSTRACT This paper proposed to predict potential targets of miR-130a in venous thromboembolism (VTE) utilizing a TargetScore method, and to further uncover the functions of miR-130a in VTE. miRNA-overexpression data were collected and log Fold Change (logFC) value was computed for every gene in the dataset. Subsequently, sequence scores were calculated based on Variational Bayesian-Gaussian Mixture Model and Variational Bayesian Expectation-Maximization algorithm. Ultimately, the target score between miR-130a and each gene was counted by integrating the logFC and sequence scores, to investigate potential targets for miR-130a. Based on the targets, pathway enrichment analysis was conducted to explore significant gene sets in VTE patients. 225 potential targets in VTE were predicted for miR-130a, and 16 significant pathways with $P < 0.05$ were identified for VTE patients after enrichment analysis. MiR-130a was critical for the development of VTE, partially through regulating expressions of potential targets and their gene sets.