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Characterization of miRNA-mRNA-Pathway Network Predicts Significant Biomarkers for Renal Injury in Kidney Biopsies from Patients with Lupus Nephritis

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ABSTRACT In this study, a miRNA-mRNA-pathway network (MMPN) was proposed to identify the predictive biomarkers for response to immune-suppression drugs in the treatment of lupus nephritis (LN). The steps were: detecting differentially expressed genes and differential pathways, predicting miRNAs by computing targetScores, MMPN construction and topological properties for MMPN. Overall, 43 and 37 differential pathways were respectively identified in 3 months (experiment 1 group) and 6 months (experiment 2 group). The most significant common pathway was ribosome. In the MMPN for experiment 1 group, ribosome pathway was regulated by hsa-miRNA-34c. In the MMPN for experiment 2 group, ribosome pathway was regulated by hsa-miRNA-23b, hsa-miRNA-9-3p, hsa-miRNA-530f, and hsa-miRNA-449b. Based on the degree > 30, 6 nodes were extracted as hubs in experiment 1 and 2 groups, including hsa-let-7f, hsa-miRNA-147, hsa-miRNA-34c, hsa-miRNA-146b, ribosome pathway, and hsa-miR-530f. Ribosome, hsa-miRNA-34c, hsa-miRNA-530f, might serve as prognostic biomarkers of LN outcomes and treatment response.