



Supplementary Material

Identification and Verification of Hub mRNA-miRNA-lncRNA Network on Psoriasis by Integrated Bioinformatics Analysis

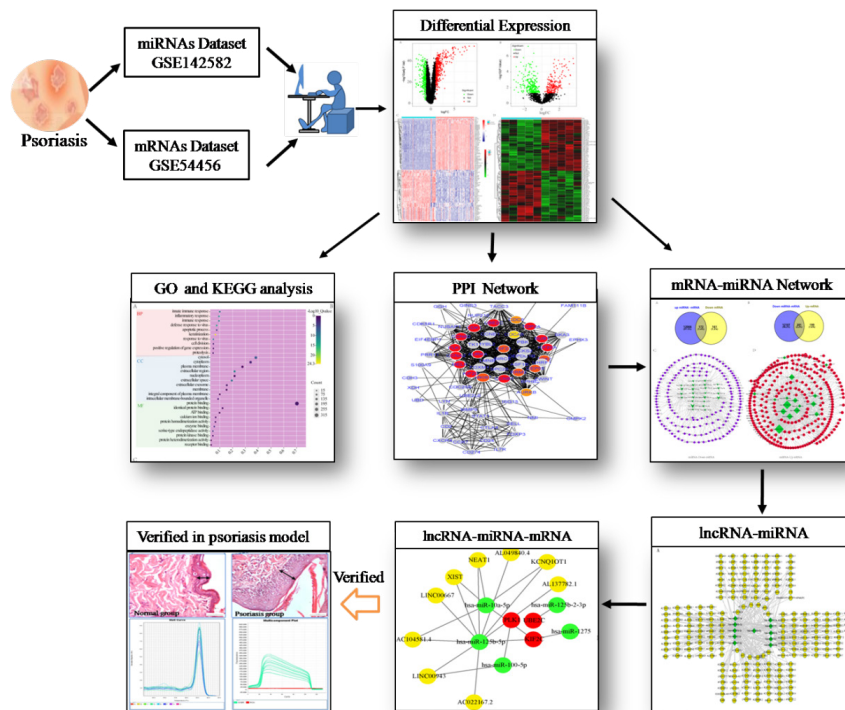
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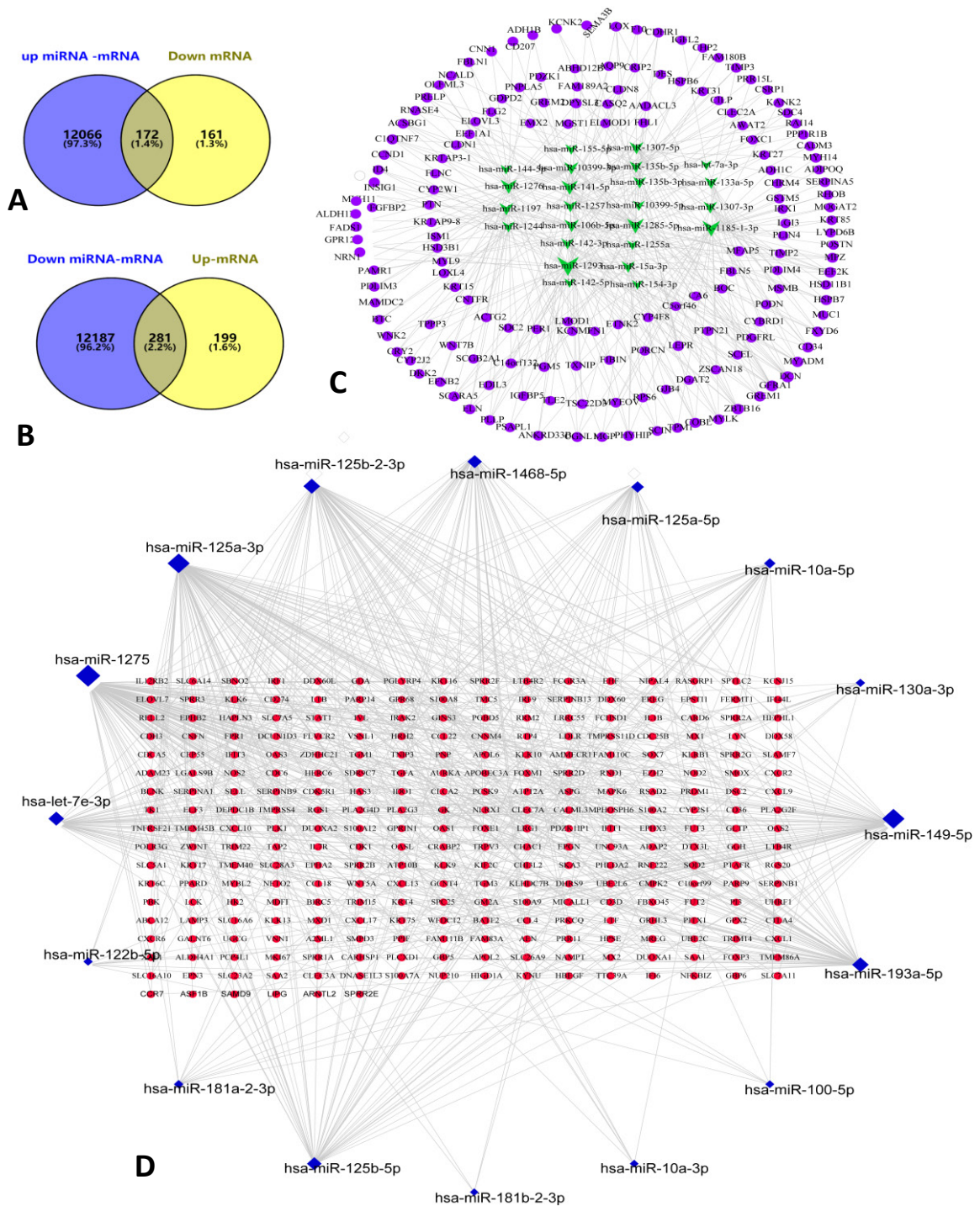
Supplementary Fig. S1. Workflow of bioinformatics analysis to research psoriasis pathogenesis.

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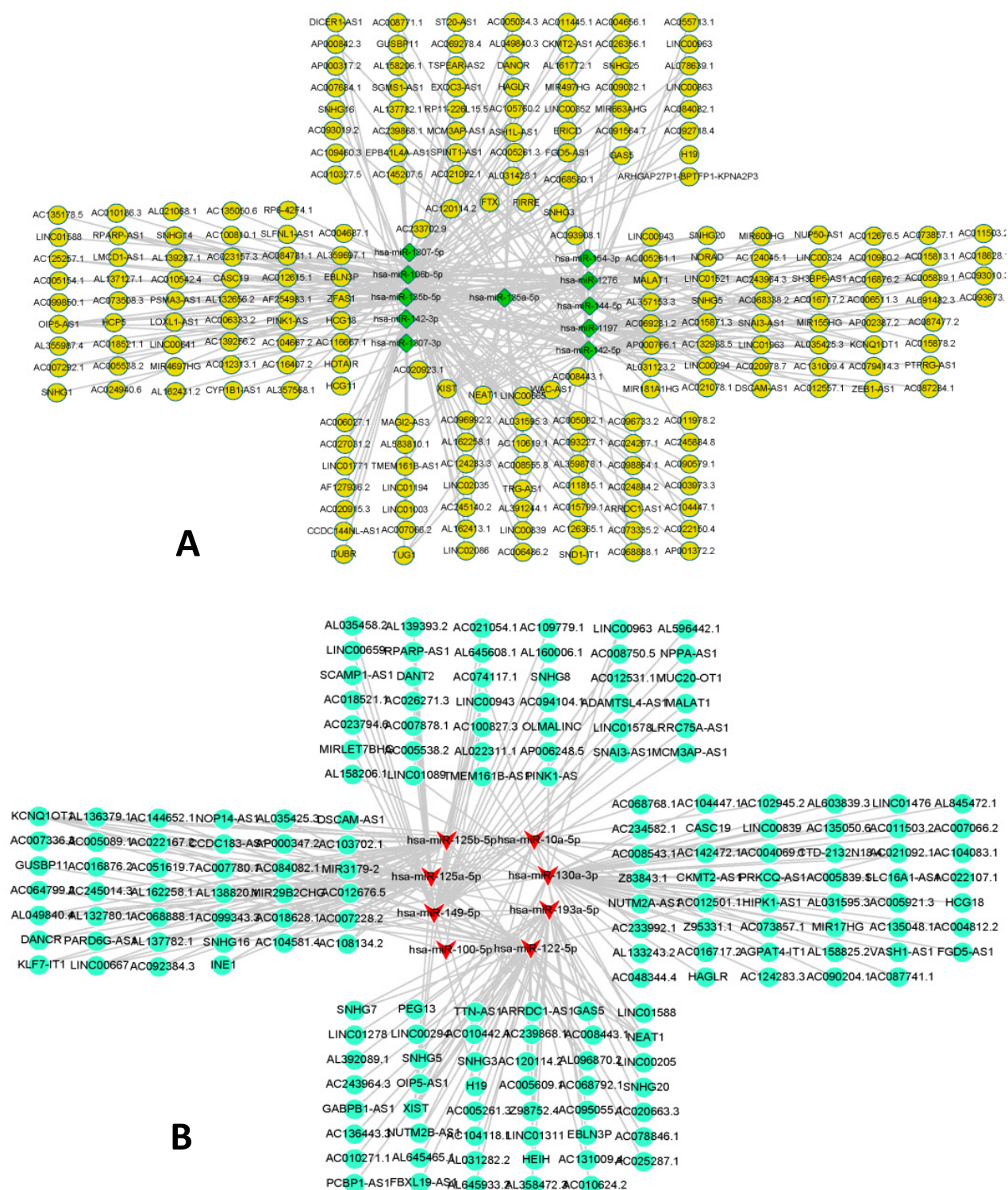


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Supplementary Fig. S2. (A) Venn diagram comparison of the up regulated DEMiRNAs predicted target mRNAs and the down regulated DEMRNAs. (B) Venn diagram comparison of down regulated DEMiRNAs predicted target mRNAs and the up regulated DEMRNAs. (C) The network of up-regulated DEMiRNAs predict target mRNA and the down-regulated DEMRNAs. Green nodes represent up-regulated DEMiRNAs and purple circles represent mRNA. (D) The network of down-regulated DEMiRNAs predict target mRNA and the up-regulated DEMRNAs. Blue diamonds represent down-regulated DEMiRNAs and red circles represents mRNA.



Supplementary Fig. S3. The lncRNA-miRNA regulatory network. (A) The network of up-regulated DE miRNAs and predicted target lncRNAs. Yellow nodes represent lncRNA, while green nodes represent miRNA. (B) The network of down-regulated DE miRNAs and the predicted target lncRNAs. Blue nodes represent lncRNA, while red nodes represent miRNAs. Interactions between DE miRNA and lncRNA were expressed as the grey lines.

Supplementary Table SI. The reaction system and process of cDNA synthase.

Components	Volume (μL)
Total RNA	≤ 9
gDNA eraser	1
RNase free H ₂ O	Up to 10
42 °C for 5 min	
2× SPARKscript II RT plus master mix	10
50 °C for 15 min and 85 °C for 5 min	