

Supplementary Material

Microarray Profiling of TGF- β 1-Induced Long Non-Coding RNA Expression Patterns in Human Lung Bronchial Epithelial BEAS-2B Cells

Wentao Hu^{a,b,e} Weiwei Pei^{a,b,e} Lin Zhu^{a,b} Jing Nie^{a,b} Hailong Pei^{a,b}
Jian Zhang^{a,b} Bingyan Li^c Tom K. Hei^d Guangming Zhou^{a,b}

^aSchool of Radiation Medicine and Protection, Medical College of Soochow University, Suzhou, ^bCollaborative Innovation Center of Radiological Medicine of Jiangsu Higher Education Institutions, Suzhou, ^cMedical College of Soochow University, Suzhou, China, ^dCenter for Radiological Research, College of Physician and Surgeons, Columbia University, New York, USA

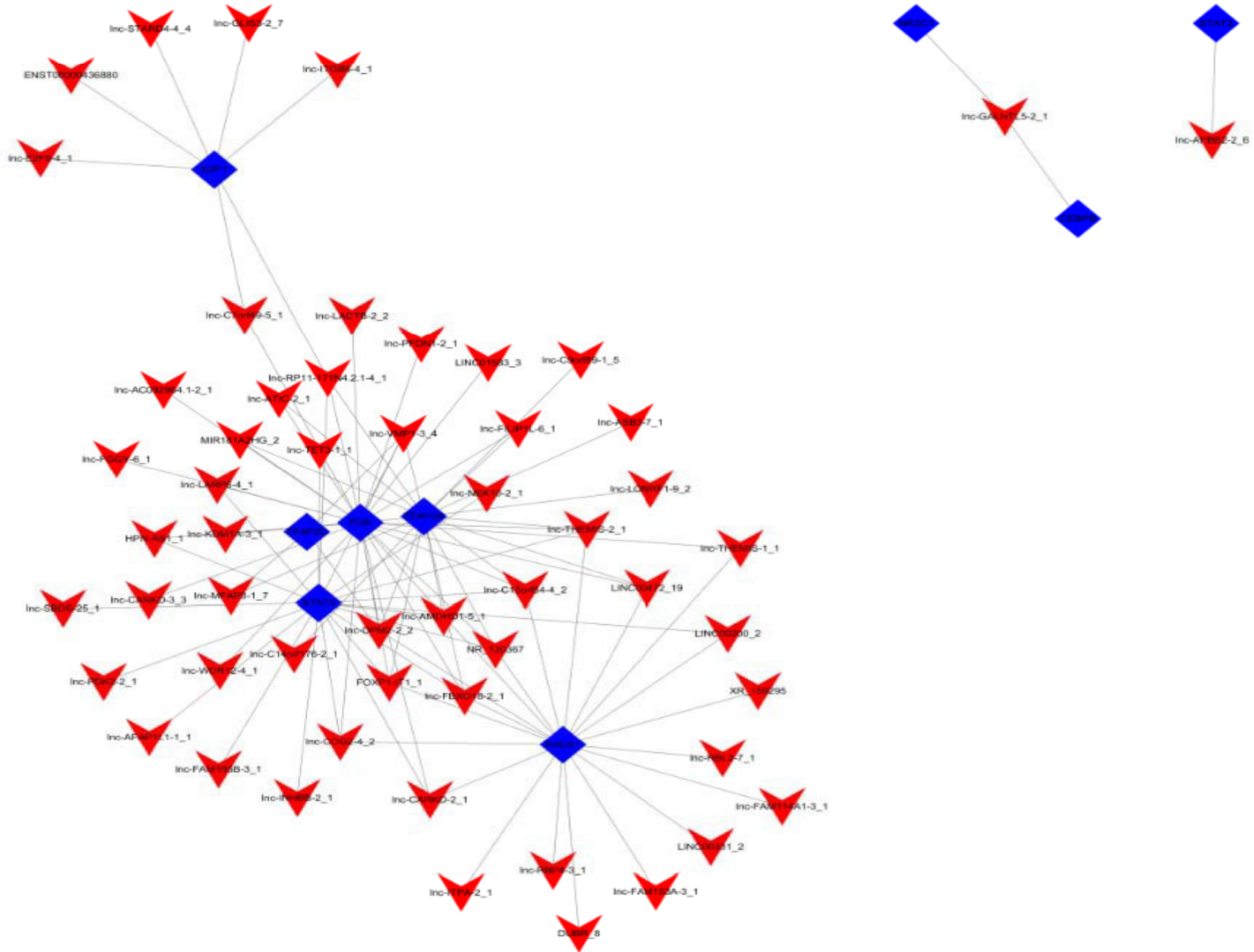


Figure S1. IncRNA-TF core network consisting of the top 100 pairs of lncRNA and TF with the highest credibility. The blue rectangles represent TFs, while red triangles represent lncRNAs.

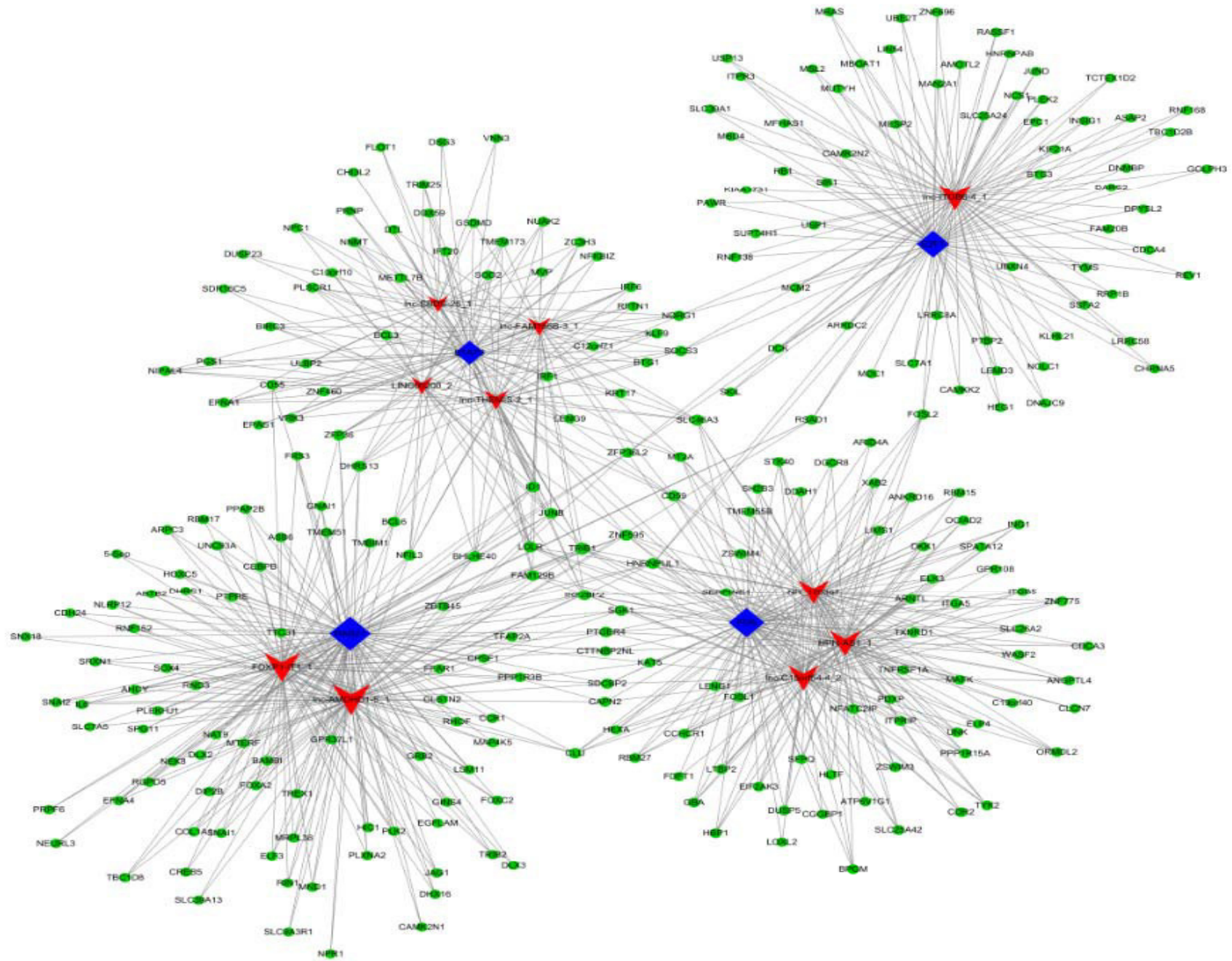


Figure S2. lncRNA-TF-mRNA core network based on the top 10 pairs of lncRNA and TF with the highest credibility. The red arrows represent lncRNAs, blue rectangles represent TFs, while green circles represent mRNAs.