**Introduction**: Atrial fibrillation (AF) is the most frequent arrhythmogenic disease, and radiofrequency ablation plays a key role in the treatment of AF. However, the recurrence rate of atrial fibrillation after ablation is an important issue. Therefore, developing new and reliable biomarkers for predicting the recurrence of AF after ablation and screening AF patients who respond well to ablation therapy is an important subject.

**Methods**: RNA-seq was used to compare the difference of plasma circRNAs expression between atrial fibrillation and normal subjects. We applied RT-PCR to detect the content of target circRNA in large sample population. Then we followed up patients after AF ablation for 12 months and drew ROC curve to evaluate the predictive significance of different factors for recurrence of atrial fibrillation.

**Result**: The results of RNA-seq of plasma from five patients with isolated persistent atrial fibrillation and five healthy controls showed significant differences in circRNA expression between the two groups. After GO and pathway analysis, we selected circRNAs related to the recurrence of AF for validation in a large sample including 70 samples from isolated atrial fibrillation patients and 80 non-atrial fibrillation individuals. All patients were followed up for 12 months. After ablation, we found 6 recurrent patients. The ROC curves showed that AUC was 0.826 for the plasma level of hsa_circ_0032931 as a single predictor. However, the AUC was increased to 0.933 for the combination of hsa_circ_0032931 and AF duration.

**Conclusion**: Hsa_circ_0032931 plus AF duration can better predict the recurrence of AF. This finding is of clinical significance when managing AF patients.