

## Supplementary Figure Legends

**Figure S1.** For patients with (A) UC and (B) CD, hematoxylin and eosin staining of intestinal tissue and colonoscopy images were obtained at three different time points: baseline, after treatment improvement, and following disease recurrence. Scale bar: 1 mm. UC, ulcerative colitis; CD, Crohn's disease.

**Figure S2. Analysis of gut microbiota at baseline revealed no significant differences between patients with Crohn's disease and those with ulcerative colitis.** (A) Alpha diversity indices of gut microbiota at baseline in patients with Crohn's disease and ulcerative colitis. (B) Beta diversity indices of gut microbiota at baseline in patients with Crohn's disease and ulcerative colitis. UC, ulcerative colitis; CD, Crohn's disease. NS, not significant.

**Figure S3. Correlation analysis between differential bacterial genera at baseline and baseline clinical indicators in IBD patients with and without relapse post-treatment.** (A) Dot plot showing the correlation analysis of baseline clinical indicators in patients with (R) and without (NR) relapse. The x-axis represents various baseline clinical indicators (e.g., BMI, Age, ALB, dNLR, etc.), and the y-axis represents the correlation coefficient values. (B) Heatmap showing the correlation analysis between baseline clinical indicators and differential bacterial genera in patients with and without relapse. The x-axis lists the baseline clinical indicators, while the y-axis lists the differential bacterial genera. The color gradient represents the strength and direction of the correlations, with red indicating positive correlations and blue indicating negative correlations. NS, not significant; \*P < 0.05; \*\*P < 0.01; \*\*\*P < 0.001.

**Figure S4. Prediction of relapse risk based on differential bacterial genera at**

**baseline in IBD patients with and without relapse.** (A) Lefse analysis of discriminative intestinal bacterial genera at baseline in IBD patients with and without relapse. (B) Random forest model to predict IBD relapse post-treatment based on differential bacterial genera at baseline.

**Figure S5. Prediction of relapse risk based on clinical indicators at baseline in patients with and without relapse.** (A) Lasso analysis of differential clinical indicators. (B) Clinical indicators used for discrimination at baseline in patients with and without relapse. (C) Random forest model to predict IBD relapse post-treatment based on clinical indicators selected by lasso analysis at baseline.

**Figure S6. Prediction of relapse risk based on clinical indicators after treatment in patients with and without relapse.** (A) Lasso analysis of clinical indicators. (B) Gini index of clinical indicators for differentiation between patients with and without relapse after treatment. (C) Random forest model to predict IBD relapse after treatment based on clinical indicators selected by Lasso analysis.

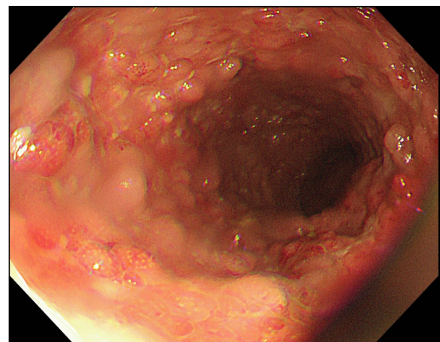
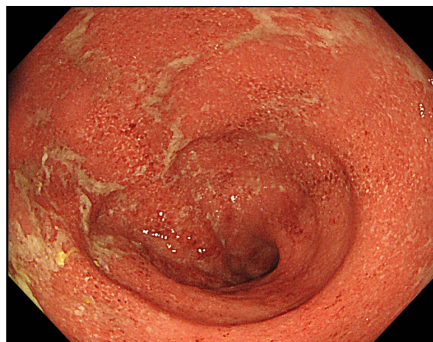
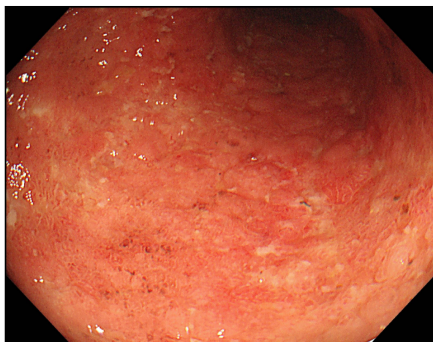
**Figure S7. Prediction of relapse risk in IBD patients based on differential bacterial taxa and clinical indicators post-treatment.** (A) Gini index of differential taxa identified by LEfSe analysis and clinical indicators selected by lasso analysis. (B) Random forest model for predicting IBD relapse post-treatment using differential bacterial taxa and clinical indicators.

Figure S1

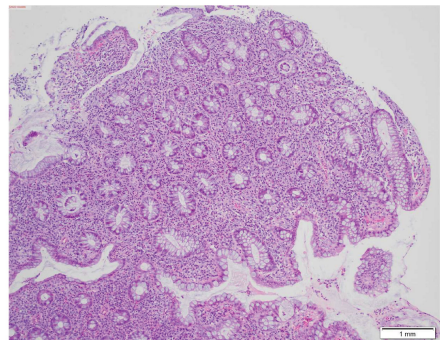
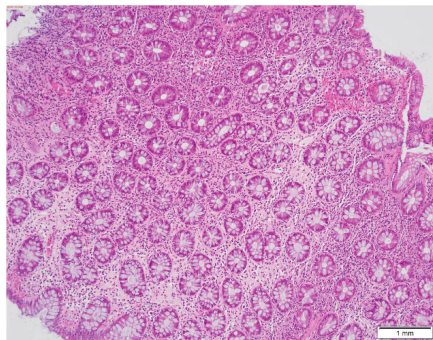
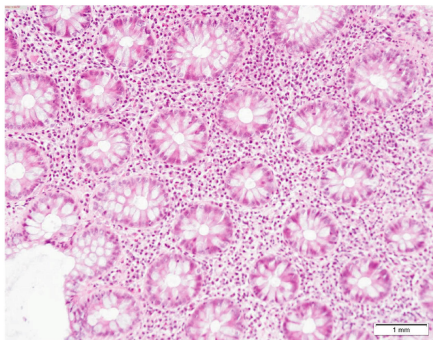
A

Ulcerative colitis

Colonoscopy



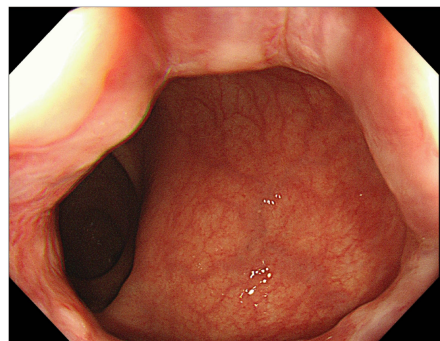
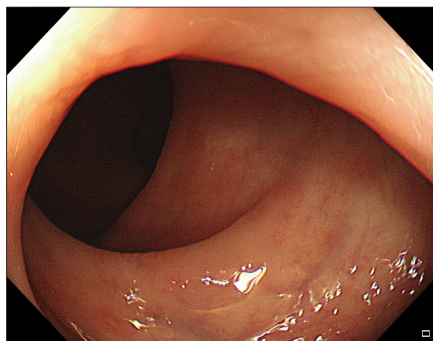
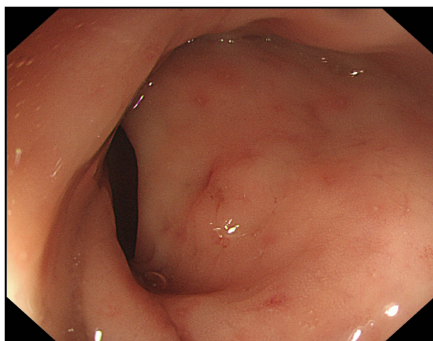
H&E



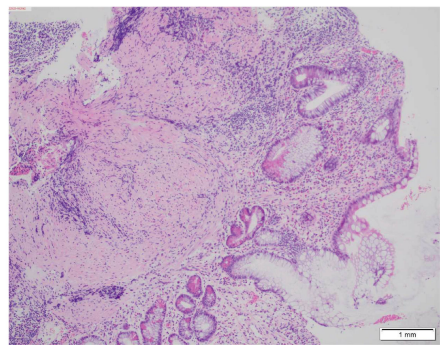
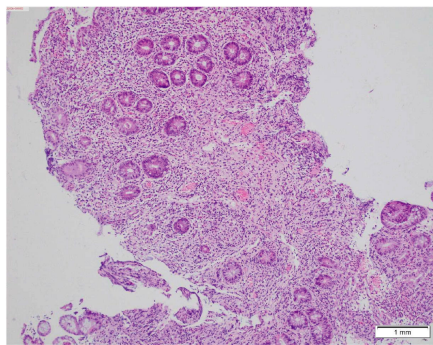
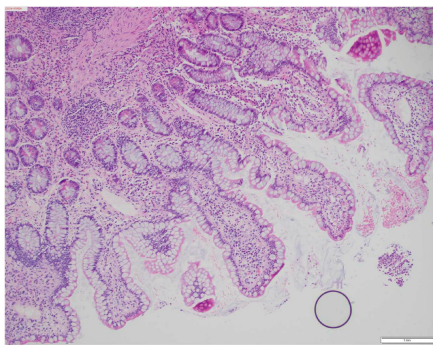
B

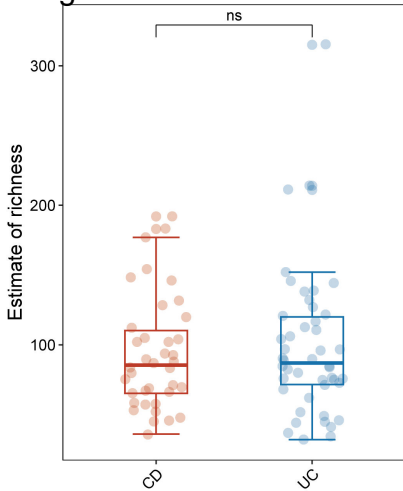
Crohn's disease

Colonoscopy

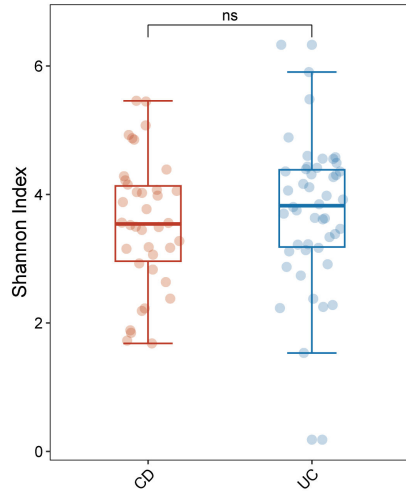


H&E

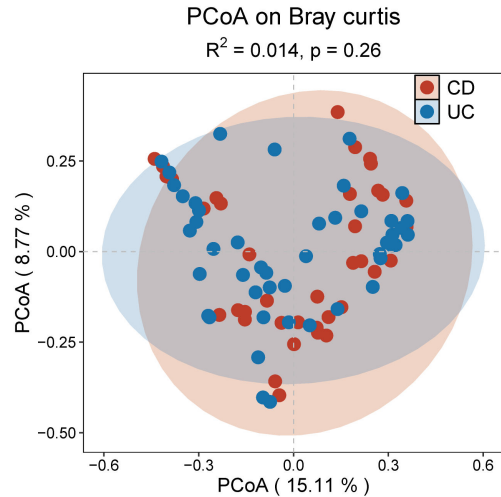


**A Figure S2**

CD  
UC

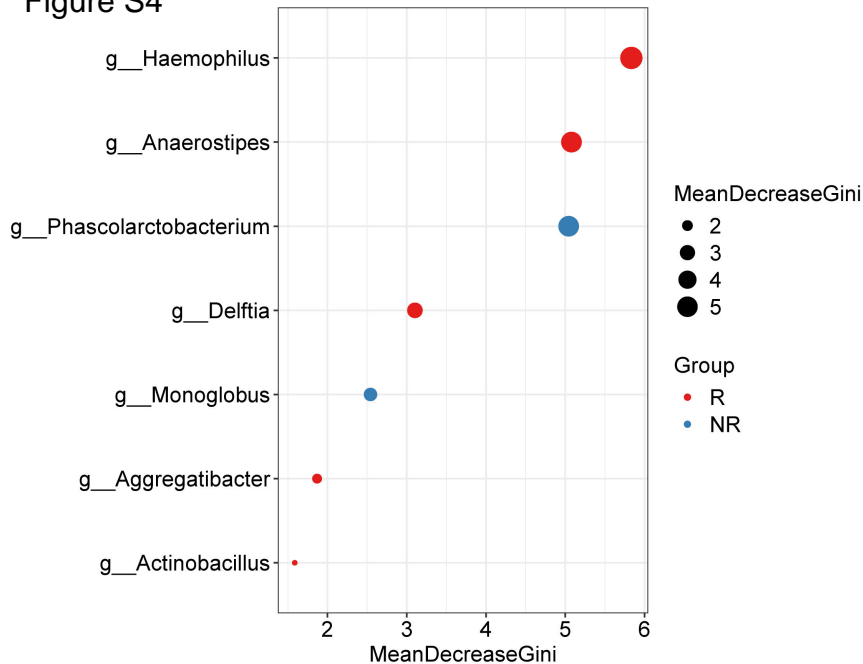


CD  
UC

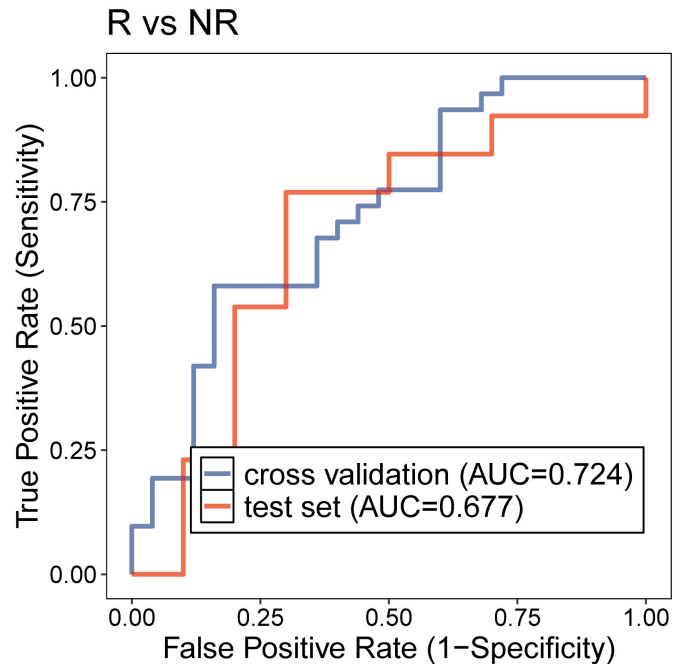
**B**



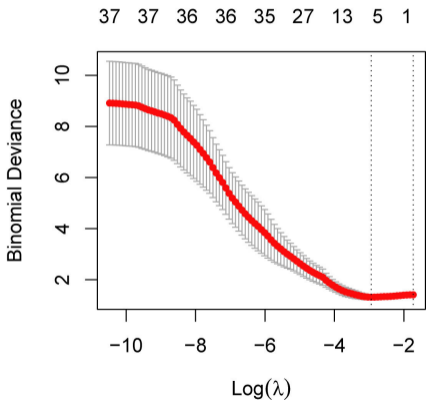
A Figure S4



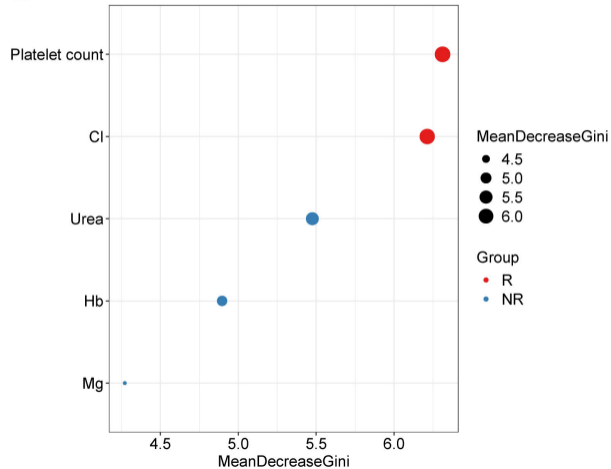
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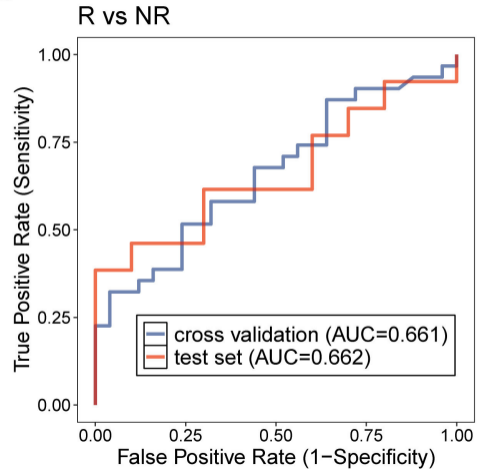
**A** Figure S5

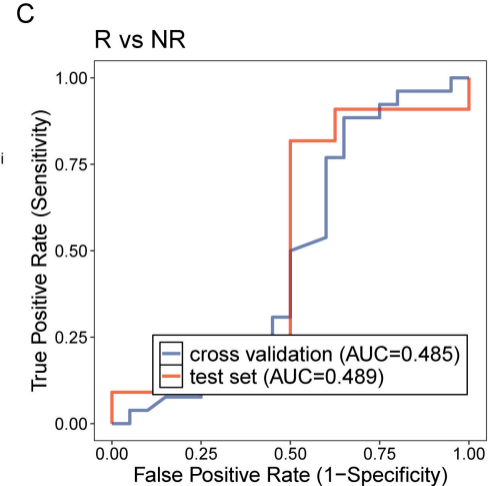
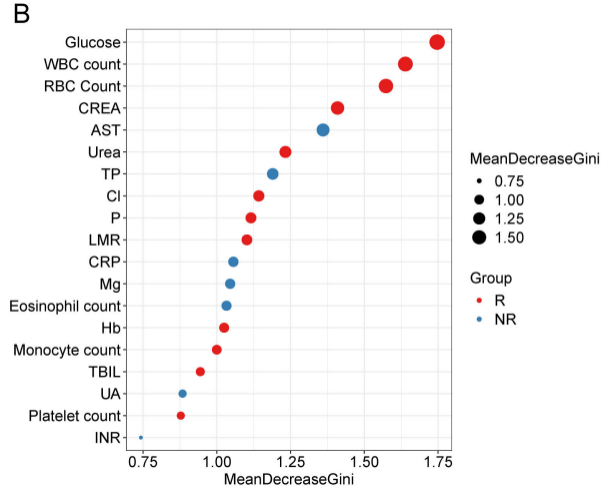
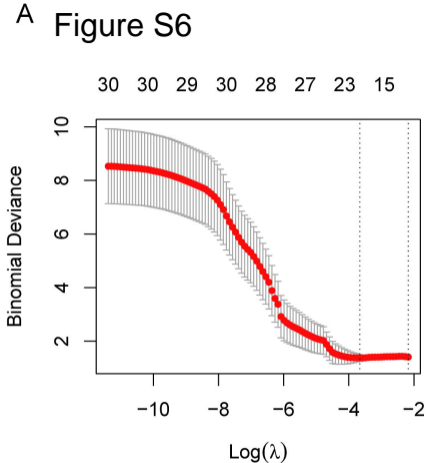


**B**

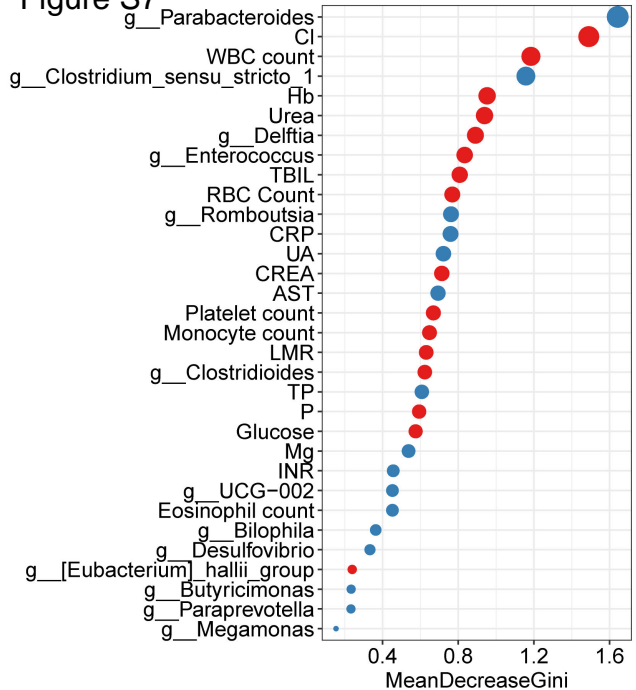


**C**





A Figure S7



B

