Establishing a novel inflammatory bowel disease prediction model based on gene markers identified from single nucleotide variants of the intestinal microbiota

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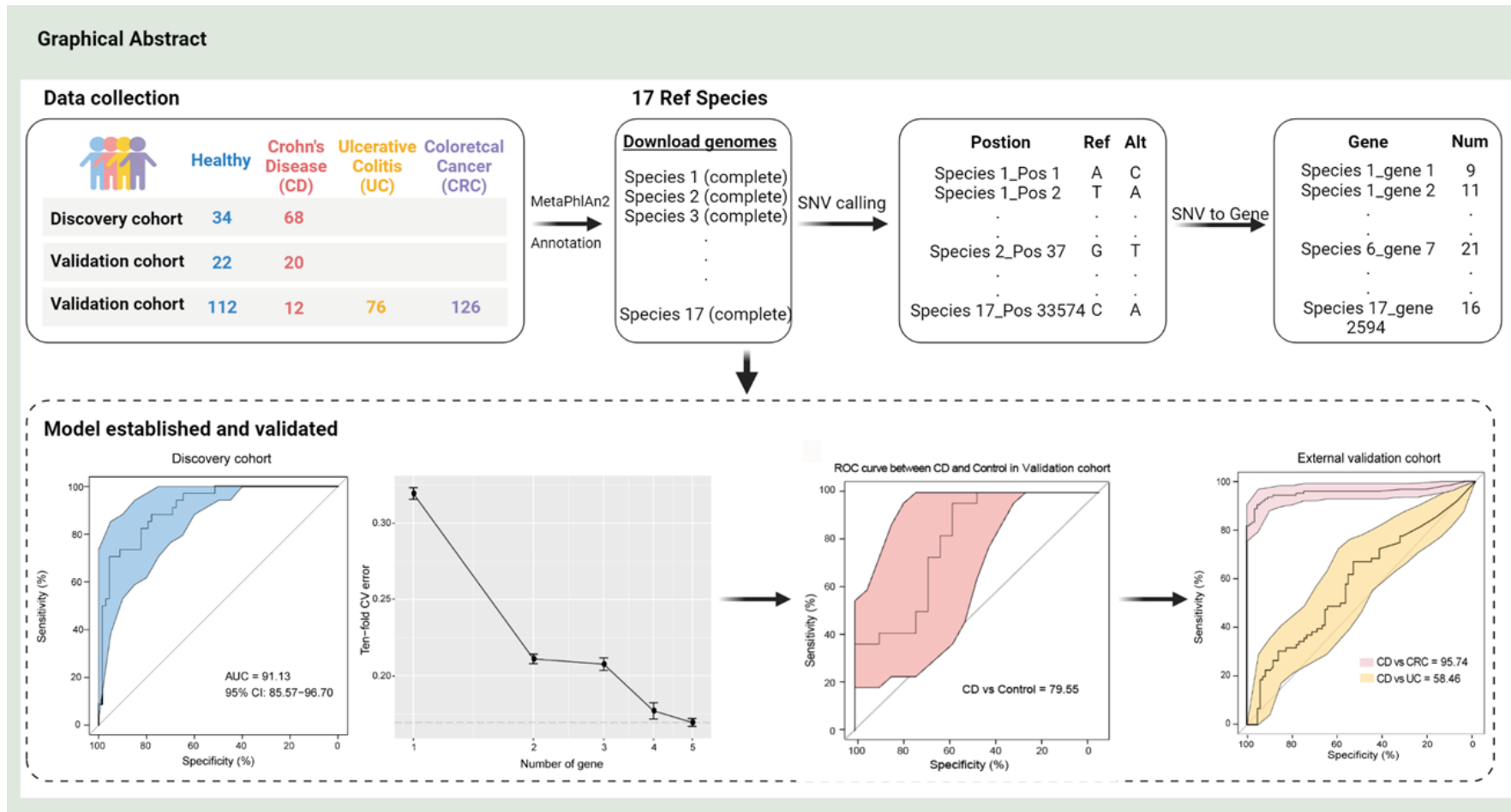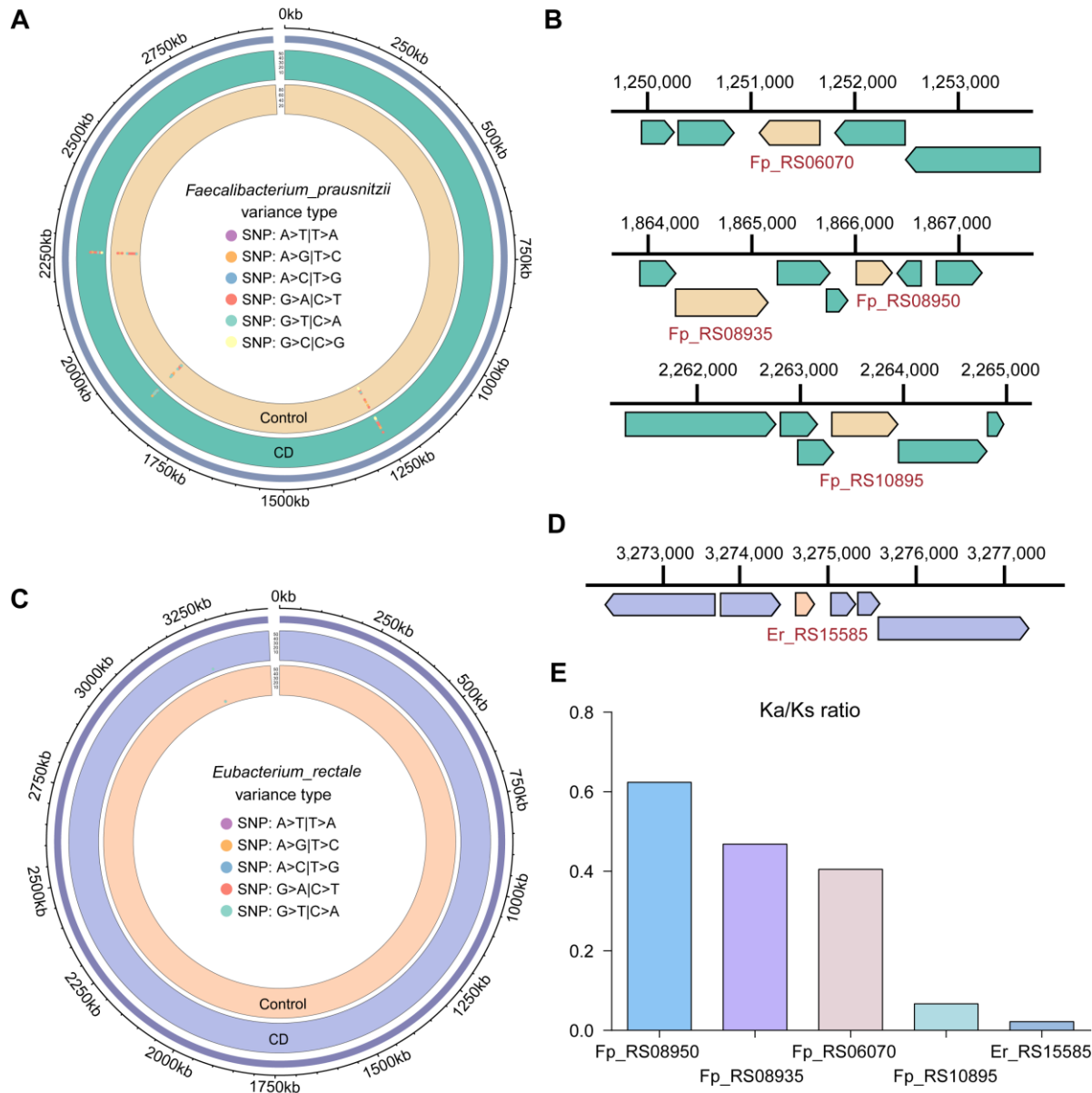
Background

- SNVs are ubiquitous in the genome of microbiota.
- External intervention has an effect on the SNVs of host microbiota.

➡️ **Are the SNVs disease-specific? Can SNVs be used as the biomarker for disease diagnosis?**

> **Mutation-based functional annotation of five gene markers。**

(A, B) The mutation types and locations of the SNVs in *Faecalibacterium prausnitzii*;

(C, D) The mutation types and the locations of the SNVs in *Eubacterium rectale*;

(E) Ka/Ks is the ratio of the nonsynonymous substitution rate (Ka) to the synonymous substitution rate (Ks).

Summary

- Specific gene characteristics based on single nucleotide variants were identified in intestinal microbiome of inflammatory bowel disease (IBD) patients.

- A novel and accurate diagnostic method for predicting IBD was established.

- *Faecalibacterium prausnitzii* showed a decreased abundance in different diseases and carried disease-specific mutation sites within genes.

Shuaiming Jiang, Denghui Chen, Chenchen Ma, Huanwei Liu, Shi Huang, and Jiachao Zhang. 2022. "Establishing a Novel Inflammatory Bowel Disease Prediction Model Based on Gene Markers Identified from Single Nucleotide Variants of the Intestinal Microbiota." *iMeta* e40. https://doi.org/10.1002/imt2.40

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Society: http://www.imeta.science
Publisher: https://onlinelibrary.wiley.com/journal/2770596x

Submission: https://mc.manuscriptcentral.com/imeta

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