



ECCFP: a consecutive full pass based bioinformatic analysis for eccDNA identification from long-read sequencing data

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Wang Li, Biyuan Miao, Jun Zhang, Qingsong Zeng, Tangxuan Zhang, Zetong Wu, Yusheng Song, et al. 2026.
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iMetaOmics 2: e70080. <https://doi.org/10.1002/imo2.70080>



Introduction

◆ Extrachromosomal Circular DNA (eccDNA)

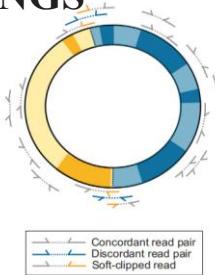
eccDNA is a circular DNA molecule that exists independently of chromosomes

◆ Functions of eccDNA

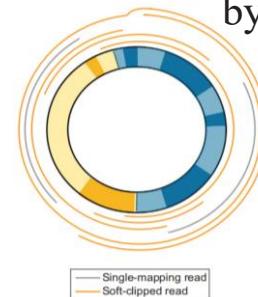
- Drives copy-number variation and gene rearrangements
- Functioning as mobile regulatory elements that involves gene expression regulation
- Plays roles in precision medicine, crop improvement, aging assessment, immunomodulation, and prenatal screening

◆ eccDNA has the potential to be a biomarker for liquid biopsy and monitoring

eccDNA detection by **NGS**



eccDNA detection by **long-read sequencing**



Noer et al. trends in cancer 2022

◆ Current eccDNA identification primarily relies on **high-throughput sequencing technologies**

NGS-Based Detection Technology

Main approach: Relies on indirect inference using split reads and discordant reads spanning junction sites
Key bottleneck: Difficulty in accurately identifying eccDNA derived from repetitive sequences or with chimeric structures due to short read lengths.

TGS-Based Detection Technology

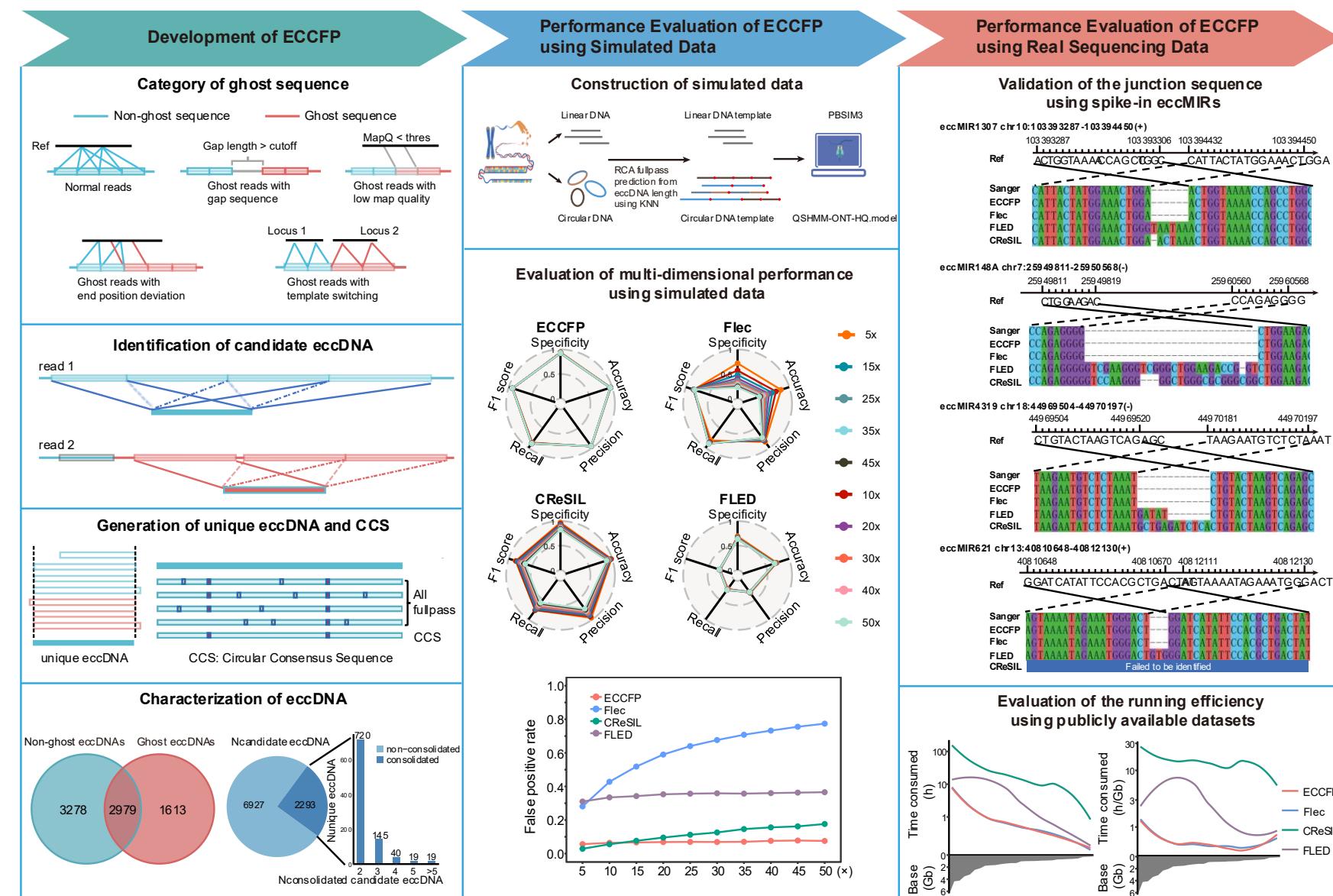
Technical advantage: Long reads enable direct resolution of the complete molecular structure of eccDNA

Current challenge: Existing TGS-based bioinformatics tools still have significant shortcomings in detection sensitivity, false-positive control, and result accuracy



Highlights

ECCFP: a consecutive full pass based bioinformatic analysis for eccDNA identification from long-read sequencing data



- ECCFP is an innovative tool that utilizes all consecutive full passes from individual read and the Boyer-Moore voting algorithm to improve the eccDNA detection
- ECCFP exhibits advantages in overall performance, sensitivity, and accuracy with high runtime efficiency, compared to other pipelines.
- ECCFP is an open-source project available at <https://github.com/WSG-Lab/ECCFP>, featuring easy installation and comprehensive usage tutorials.



Workflow of ECCFP

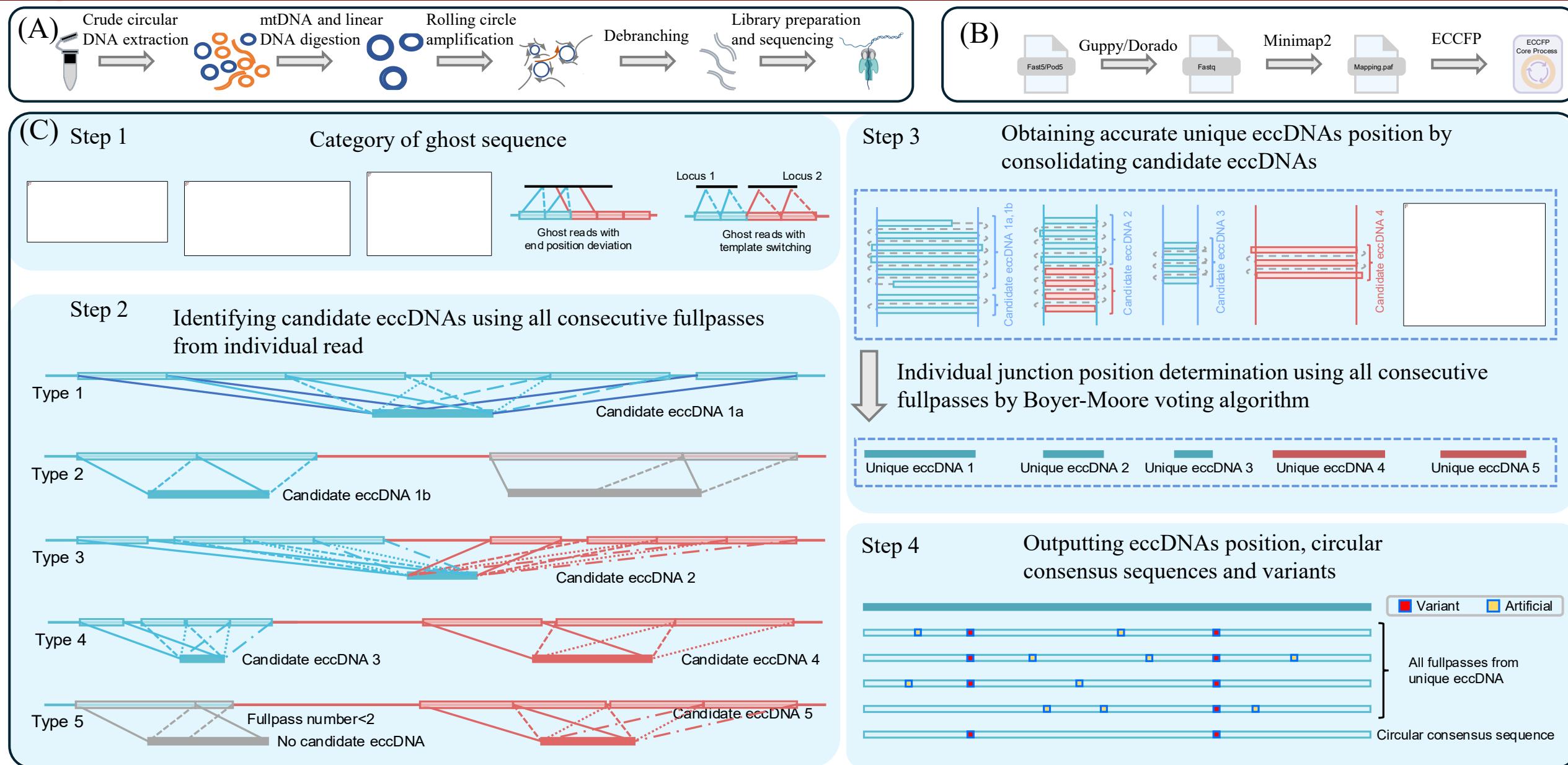


Figure 1. The workflow of eccDNA identification by ECCFP



ECCFP increases the number of eccDNA detection by including ghost sequences

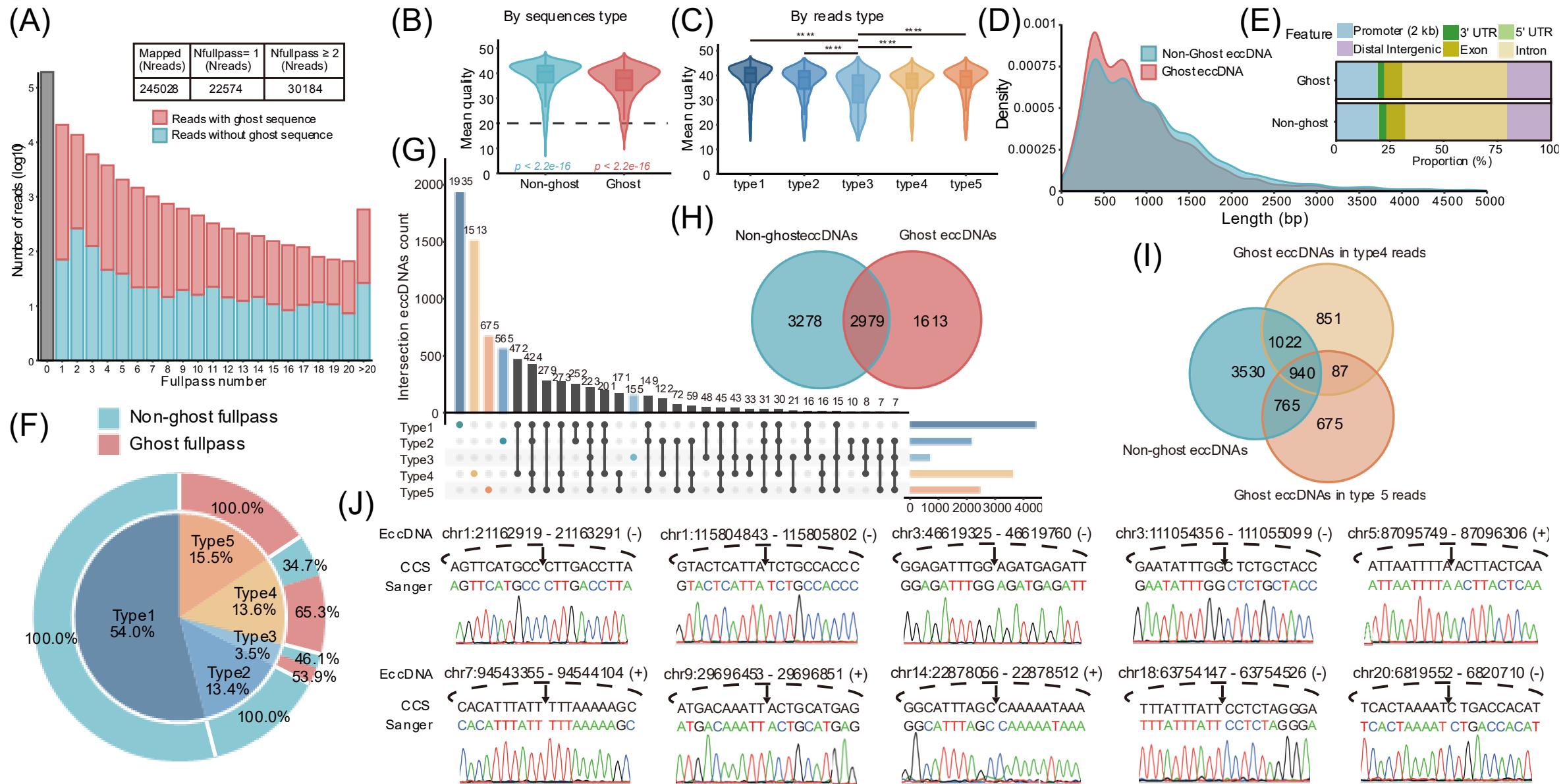


Figure 2. The number of eccDNA detection by ECCFP



ECCFP improves the position of eccDNA detection by Boyer-Moore voting algorithm

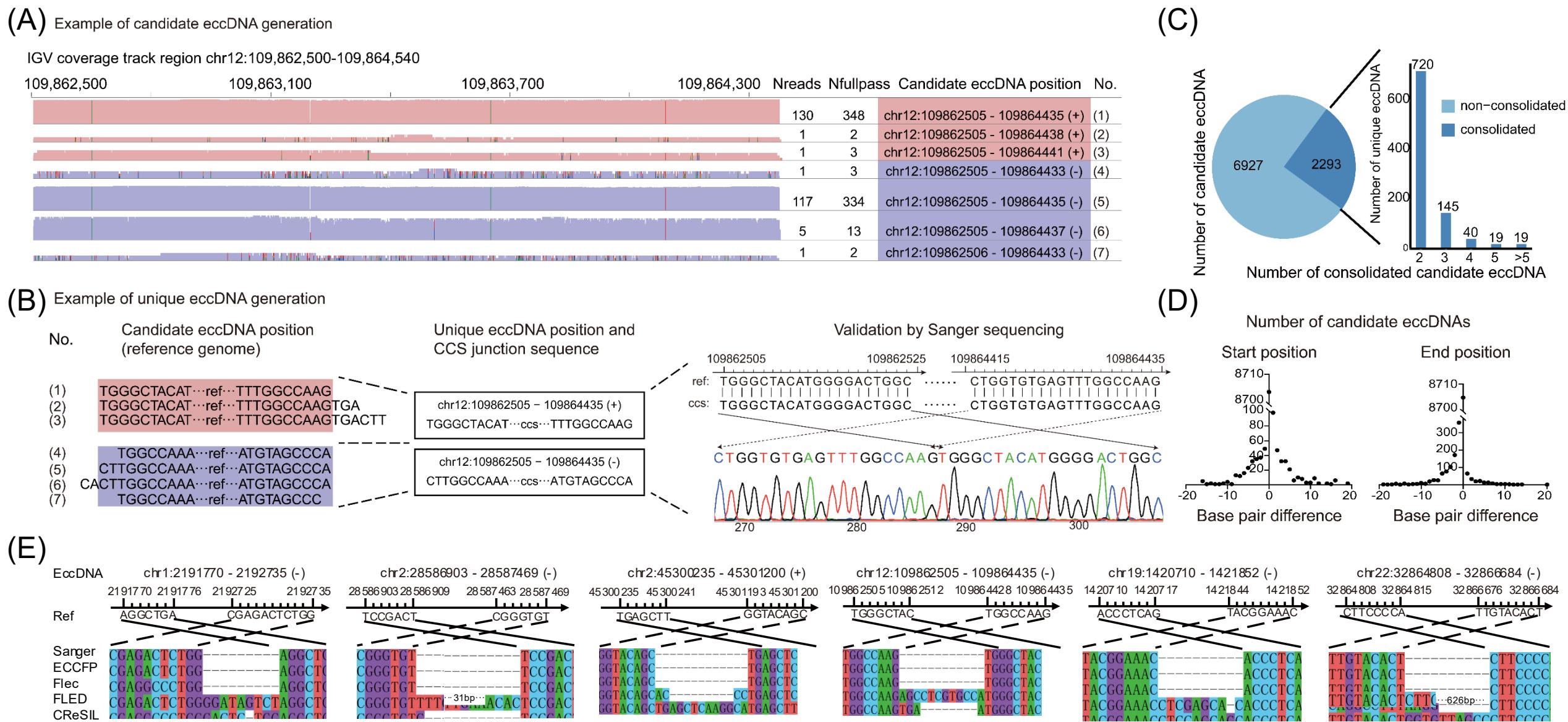
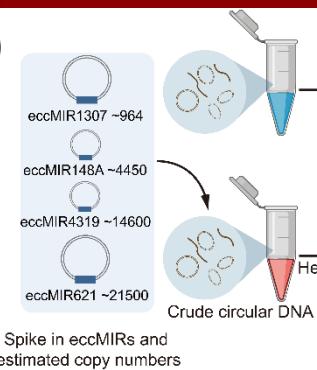


Figure 3. The position of eccDNA characterization by ECCFP

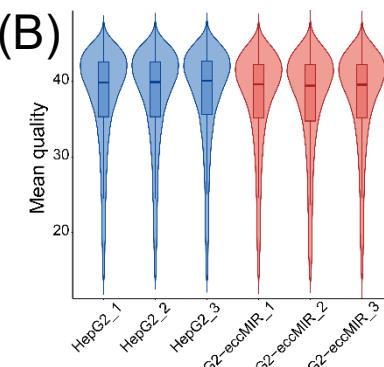


Performance evaluation using spike-in synthetic circular DNA

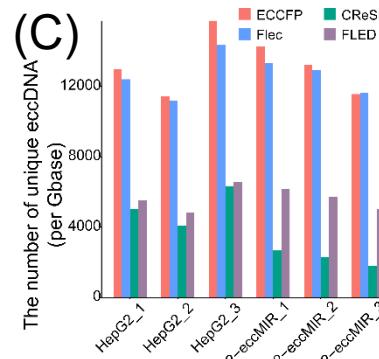
(A)



(B)



(C)



(H)

eccMIR1307 chr10:103393287-103394450(+)

Ref 103393287 103393306 103394432 103394450
ACTGGTAAACCCAGCTGGC CATTACTATGGAAACTGGG

Sanger CATTACTATGGAAACTGGG CATTGGTAAACCCAGCTGGC
ECCFP CATTACTATGGAAACTGGG CATTGGTAAACCCAGCTGGC
Flec CATTACTATGGAAACTGGG CATTGGTAAACCCAGCTGGC
FLED CATTACTATGGAAACTGGG CATTGGTAAACCCAGCTGGC
CReSIL CATTACTATGGAAACTGGG CATTGGTAAACCCAGCTGGC

eccMIR148A chr7:25949811-25950568(-)

Ref 25949811 25949819 25960560 25960568
CTGGAAAGAC CCAGAGGGGG

Sanger CCAGAGGGGG CTCAGAGAC
ECCFP CCAGAGGGGG CTCAGAGAC
Flec CCAGAGGGGG CTCAGAGAC
FLED CCAGAGGGGG CTCAGAGAC
CReSIL CCAGAGGGGG CTCAGAGAC

eccMIR4319 chr18:44969504-44970197(-)

Ref 44969504 44969520 44970181 44970197
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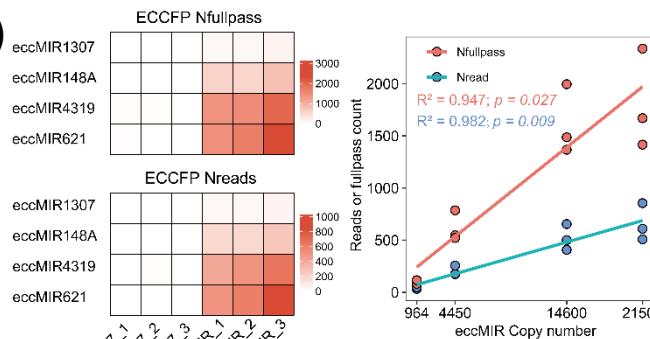
Sanger TAAGAATGTCTCTAAAT CTGTAAGTCAGAGC
ECCFP TAAGAATGTCTCTAAAT CTGTAAGTCAGAGC
Flec TAAGAATGTCTCTAAAT CTGTAAGTCAGAGC
FLED TAAGAATGTCTCTAAAT CTGTAAGTCAGAGC
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eccMIR621 chr13:40810648-40812130(+)

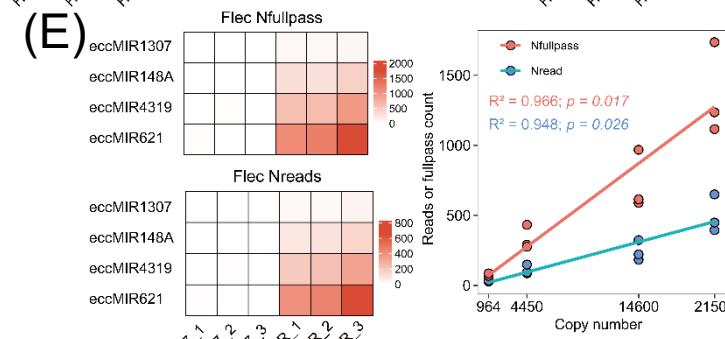
Ref 40810648 40810670 40812111 40812130
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Sanger AGTAAAATAGAAATGGGACT GGATCATATTCCACGCTGACTAT
ECCFP AGTAAAATAGAAATGGGACT GGATCATATTCCACGCTGACTAT
Flec AGTAAAATAGAAATGGGACT GGATCATATTCCACGCTGACTAT
FLED AGTAAAATAGAAATGGGACT GGATCATATTCCACGCTGACTAT
CReSIL AGTAAAATAGAAATGGGACT GGATCATATTCCACGCTGACTAT
Failed to be identified

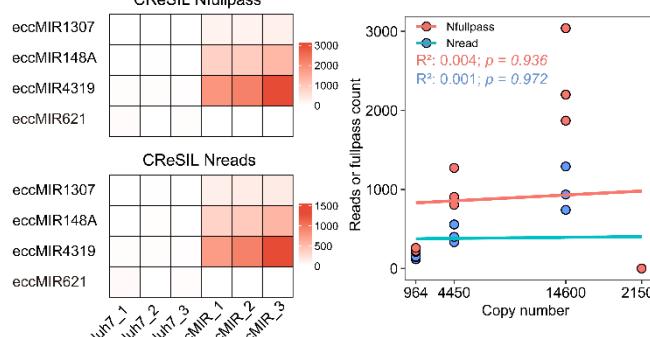
(D)



(E)



(F)



(G)

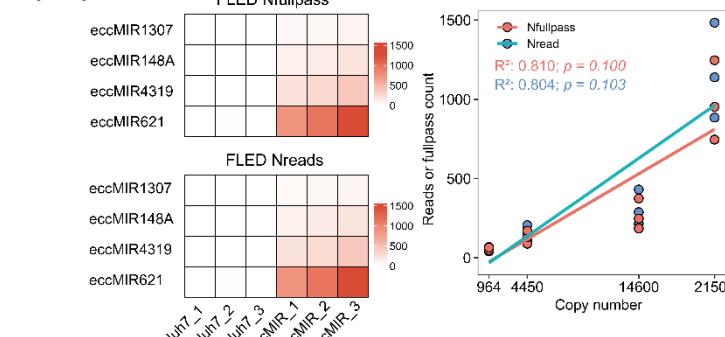


Figure 4. Evaluation of eccDNA detection by ECCFP using spiking in artificially synthesized circular DNA



Performance evaluation using simulated datasets

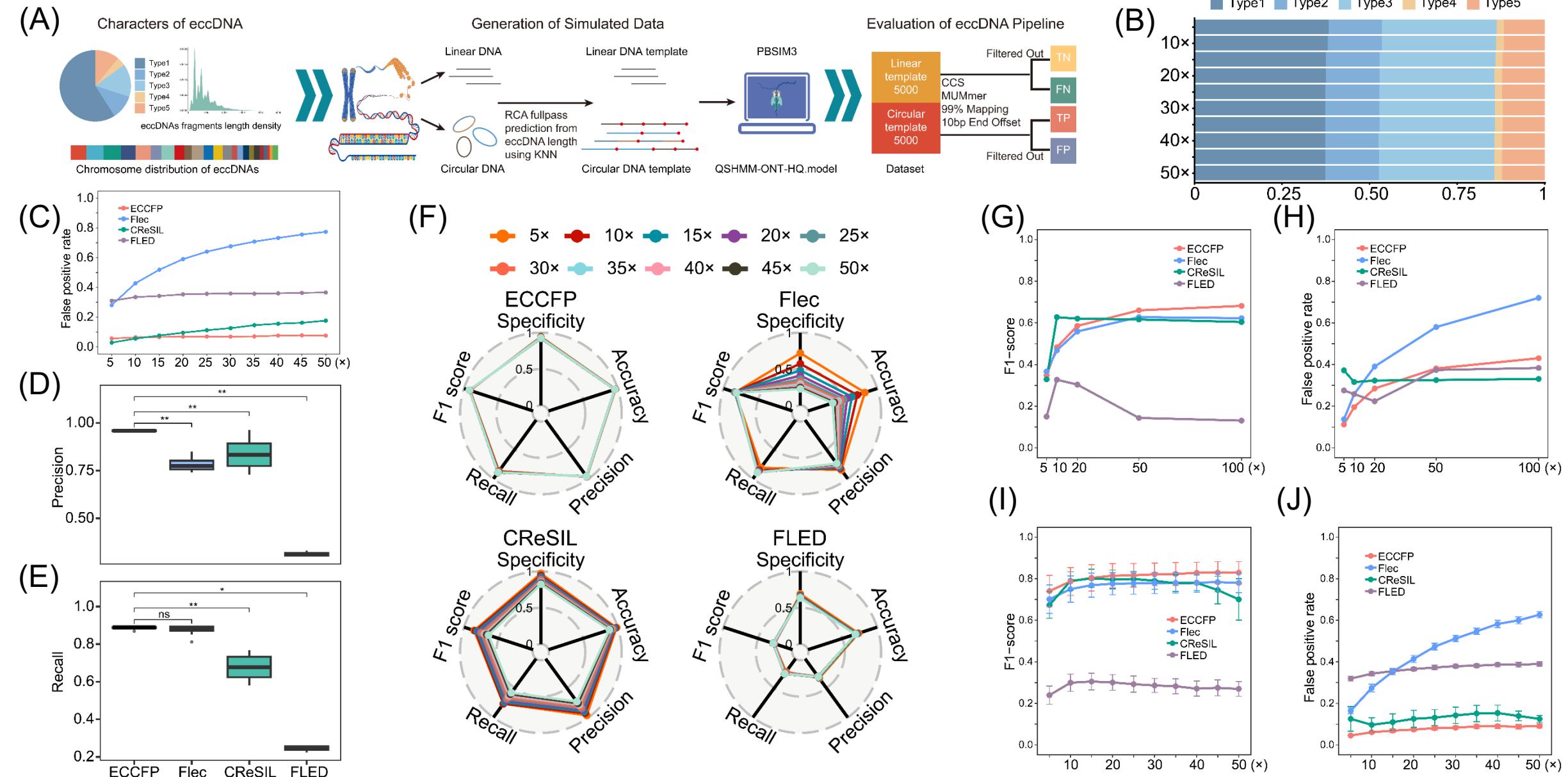
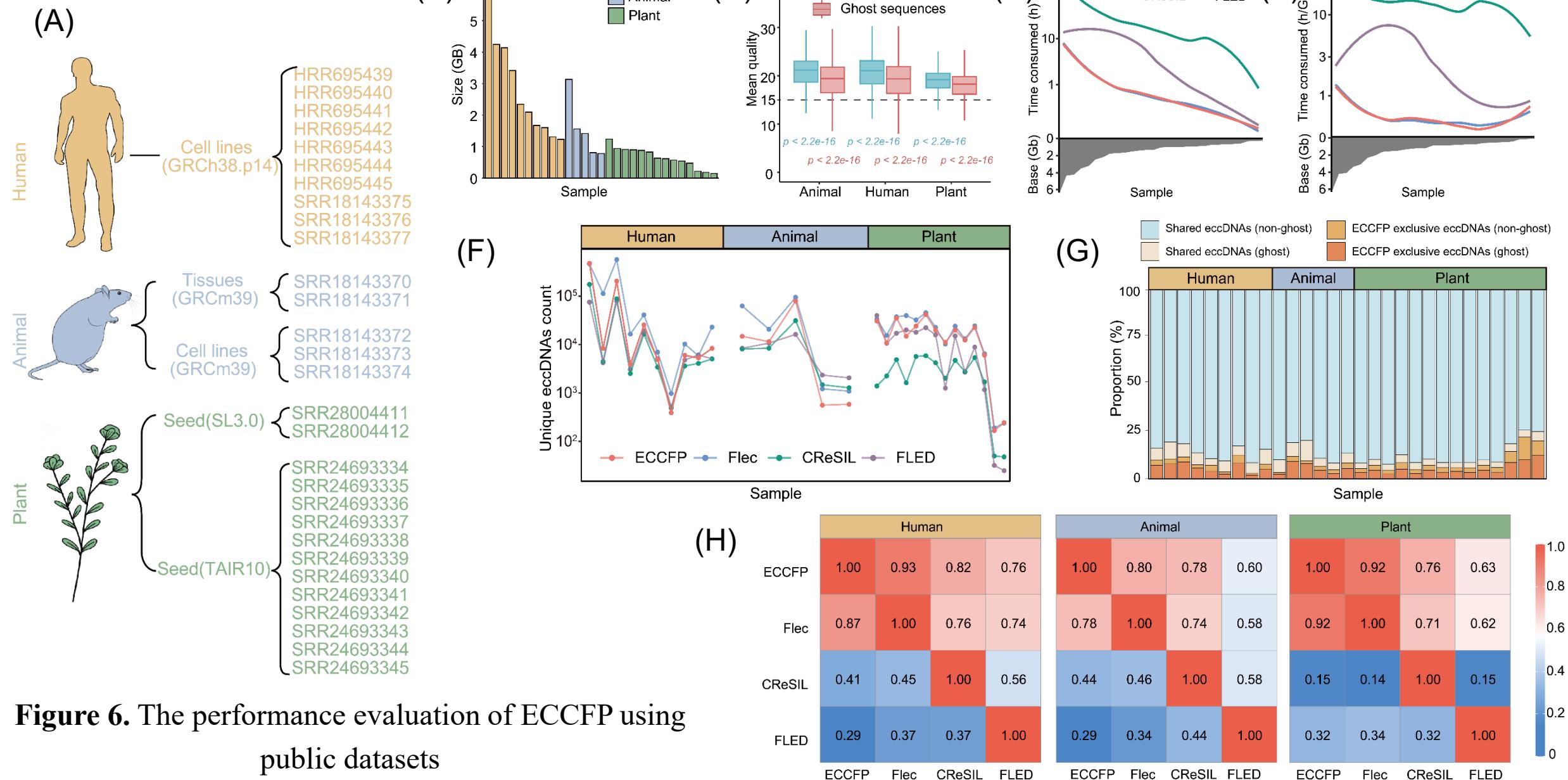


Figure 5. The performance evaluation of ECCFP using simulated data



Performance evaluation using public sequencing datasets





Summary

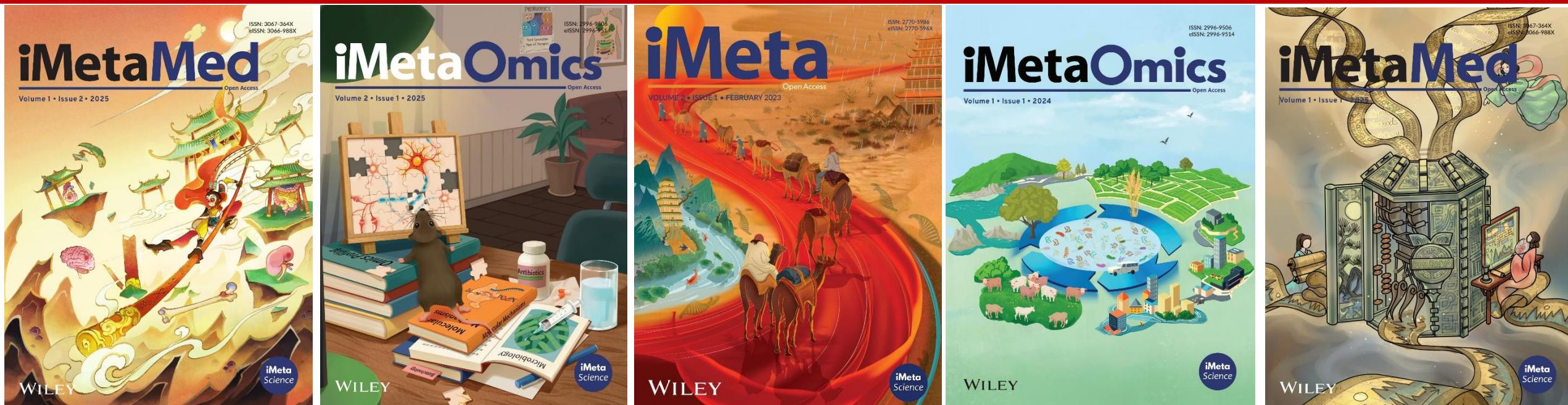
- This study presents **ECCFP**, a novel TGS-based method for eccDNA detection.
- ECCFP employs a **voting algorithm** to integrate support from multiple reads, achieving **precise localization of eccDNA junction sites** and effectively reducing false positives **without significantly increasing algorithmic complexity**.
- Evaluations on **simulated datasets, spike-in experimental datasets, and multi-species public datasets** demonstrate that ECCFP holds **clear advantages in sensitivity, accuracy, and runtime efficiency**.
- ECCFP is an **open-source and user-friendly** bioinformatics pipeline, poised to advance research on eccDNA as a clinical biomarker.

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