

# Metagenome Assembled Genome Binning Methods With Short Reads Disproportionately Fail For Plasmids and Genomic Islands

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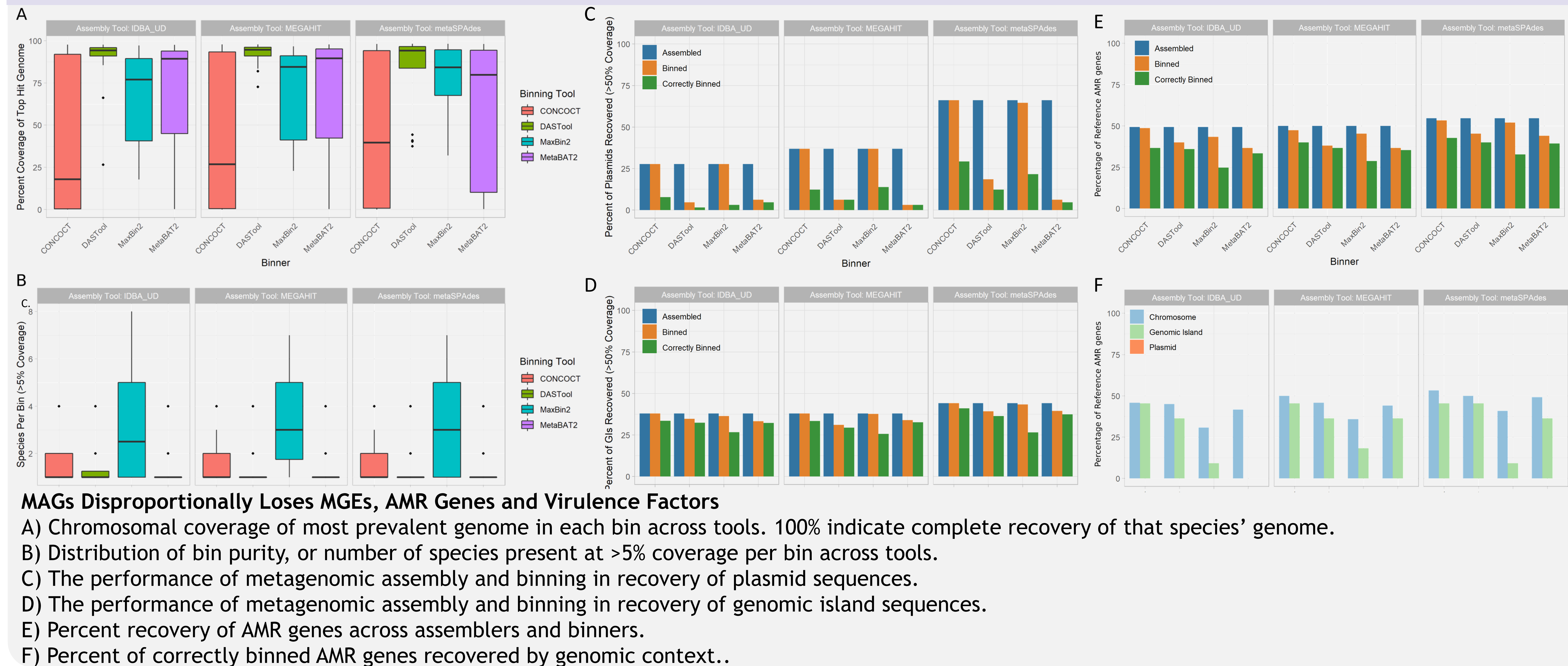
## INTRODUCTION

- Metagenomic methods enable the simultaneous characterization of microbial communities without time-consuming and bias-inducing culturing.
- Metagenome-assembled genome (MAG) binning methods aim to reassemble individual genomes from this data.
- Recovery of mobile genetic elements (MGEs), such as plasmids and genomic islands (GIs), by binning has not been well characterized.
- GIs and plasmids have proven particularly difficult to assemble from short-read sequencing data<sup>1</sup>.
- Given the association of antimicrobial resistance (AMR) genes and virulence factor (VF) genes with MGEs, studying their transmission is a public-health priority<sup>2,3</sup>.

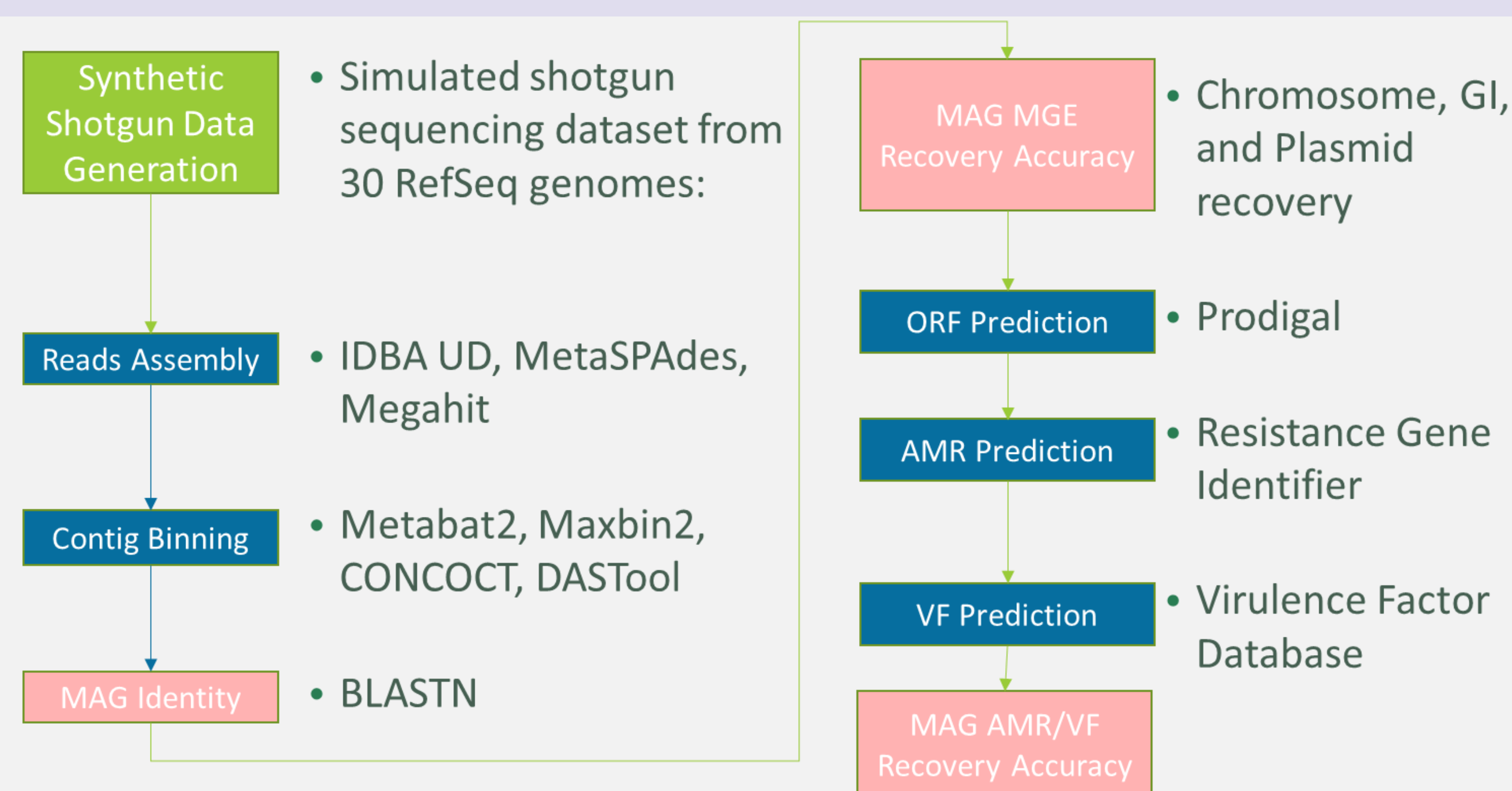
### Hypothesis:

The variable copy number and sequence composition of MGEs makes them problematic for MAG binning methods and thus will not be correctly recovered.

## RESULTS – MAGs Disproportionally Lose MGEs, AMR Genes and Virulence Factors<sup>4</sup>



## METHOD

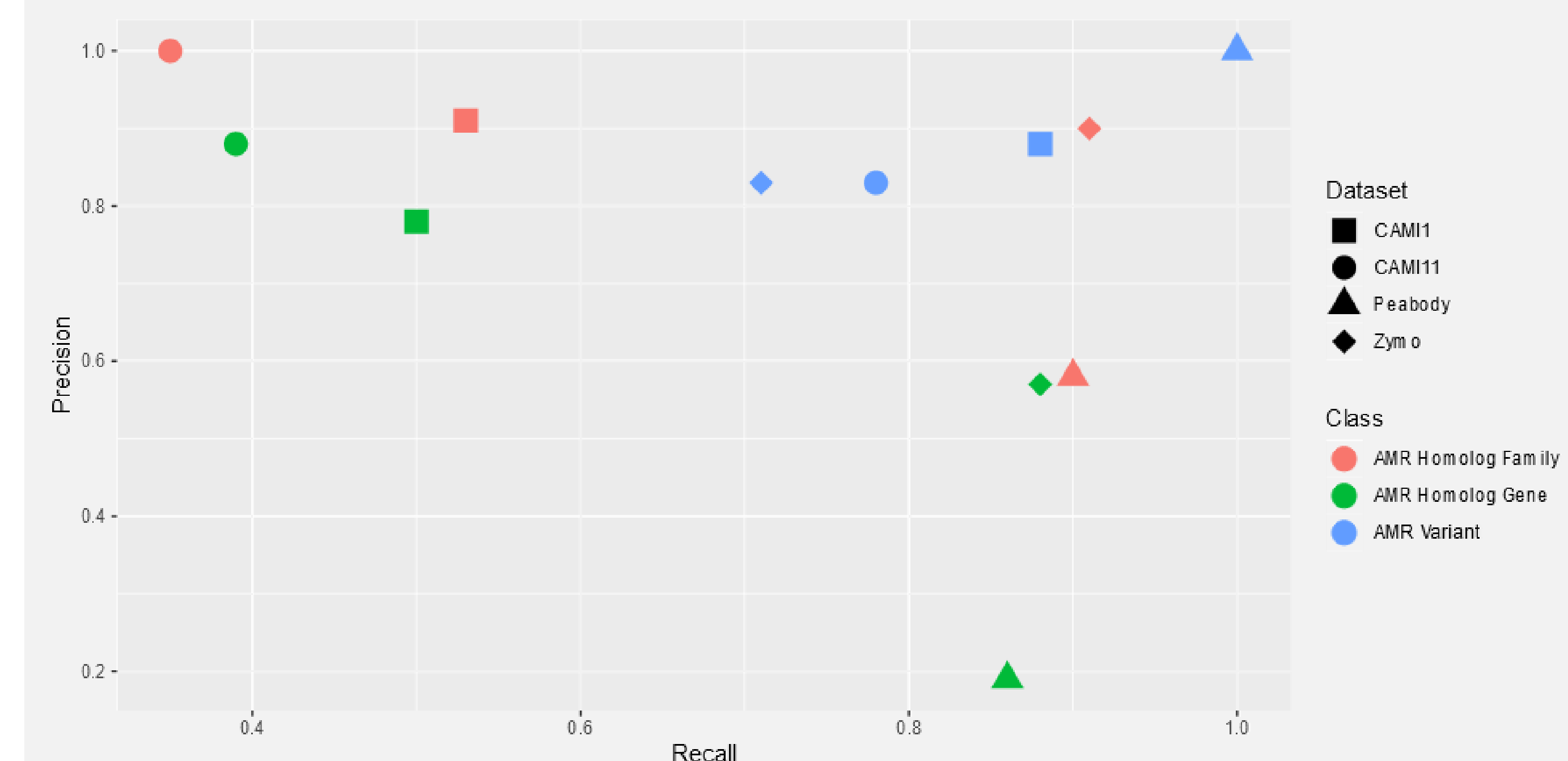


Schematic of the Evaluation of Metagenome Assembled Genome Binning Methods

## SUMMARY & FUTURE DIRECTIONS

- Short-read MAG-binning approaches provide a useful tool to study a bacterial species' core chromosomal elements. However, they have severe limitations in the recovery of MGEs.
- The majority of these MGEs will either fail to be assembled or be incorrectly binned.
- There is a disproportionate loss of key MGE-associated VF and AMR genes in clinically relevant pathogens.
- It is vital we utilize MAGs in conjunction with other methods (e.g. long-read sequencing, read-based sequence homology) before drawing most biological or epidemiological conclusions.

## AMRTime: Read-Based AMR Gene Predictor



Recovery Accuracy of AMRTime for Detecting AMR genes in Metagenomic Datasets with Ground Truth Resistomes.

## Funding & Acknowledgements

SFU

CIHR IRSC  
Canadian Institutes of Health Research  
Instituts de recherche en santé du Canada

NSERC  
CRSNG

GenomeCanada

GenomeAtlantic

Genome  
BritishColumbia

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