

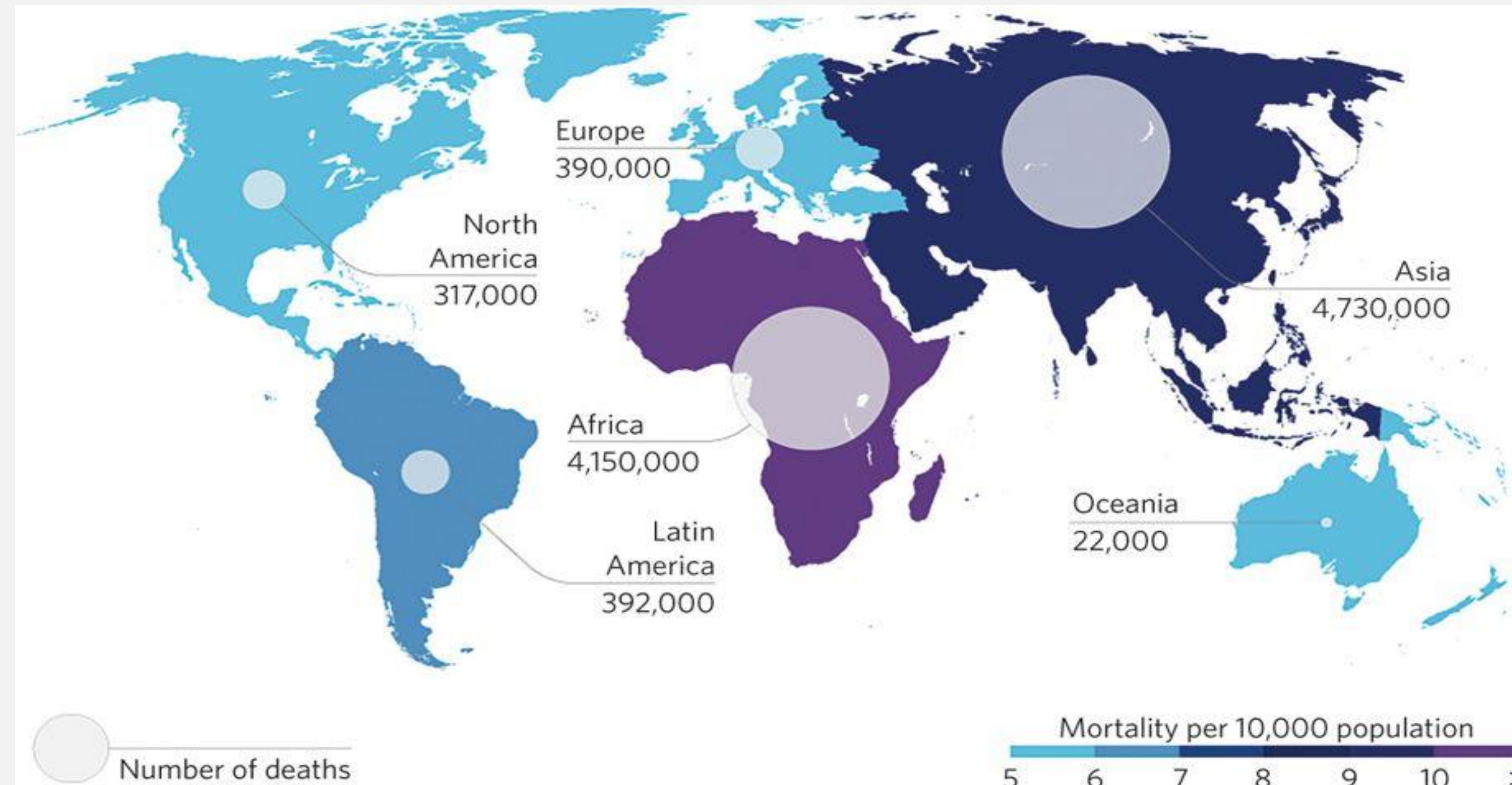
# Revealing Antimicrobial Resistance Gene Mobility Trends Using >15000 Replicons

Baofeng Jia<sup>1</sup>, Claire Bertelli<sup>1,2</sup>, Jason Spence<sup>1</sup>, Fiona .S.L. Brinkman<sup>1</sup>

1. Simon Fraser University. 2. University Hospital Center of Lausanne, Lausanne, Switzerland

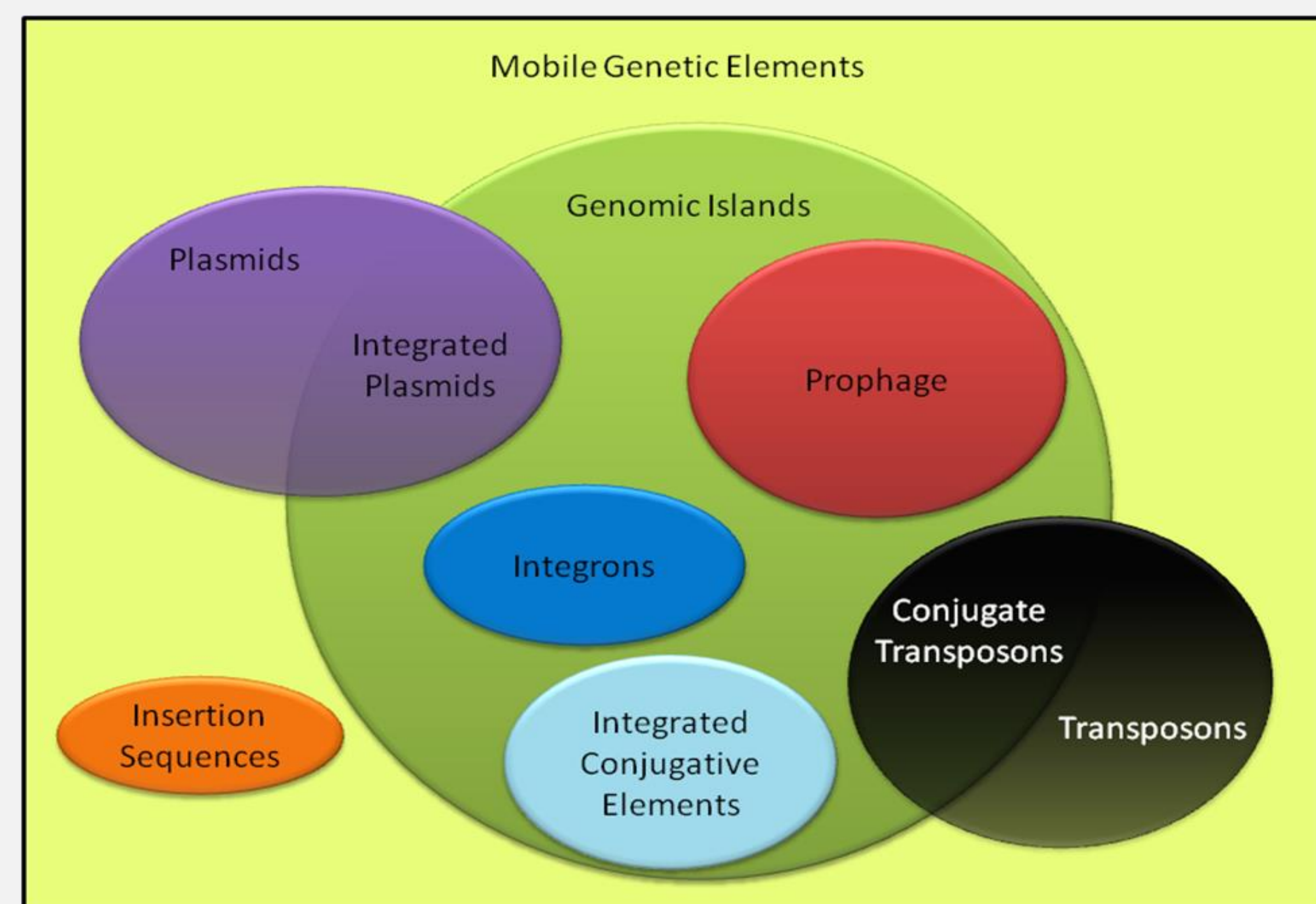
## INTRODUCTION

- Antimicrobial resistance (AMR) and emergence of pan resistant superbugs - over 10 million deaths by 2050<sup>1</sup>



- Need for research in understanding AMR mobility - Improving public health AMR risk assessment and prevention

- Genomic islands - clusters of genes of probable horizontal origin >8kb in length



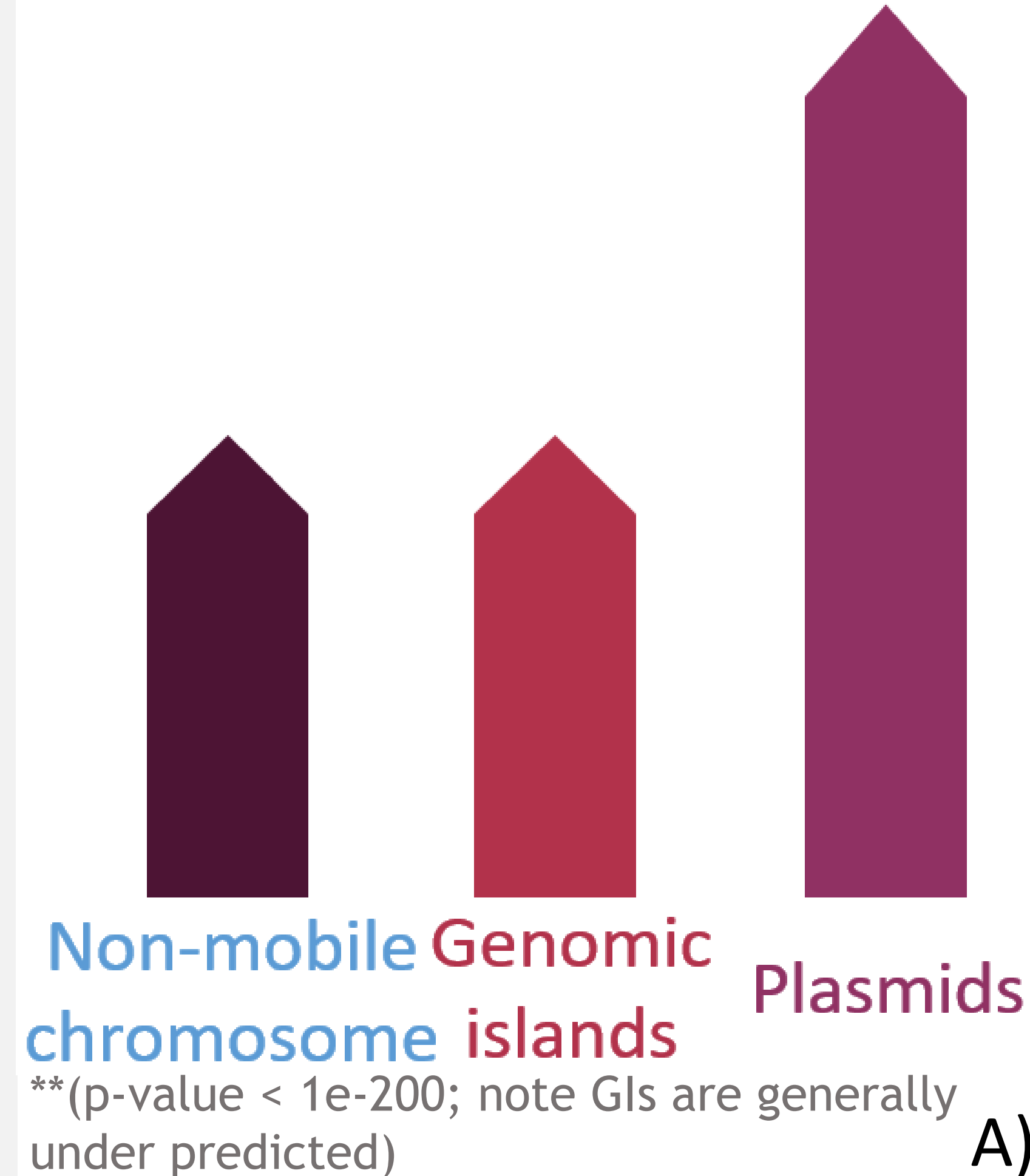
- Virulence factors are disproportionately associated with mobile elements, including plasmids and genomic islands<sup>2</sup> - evolutionary advantage to remain mobile

### Hypothesis:

Similarly to VFs, AMR genes are disproportionately associated with mobile sequences but differences should exist for certain AMR gene classes.

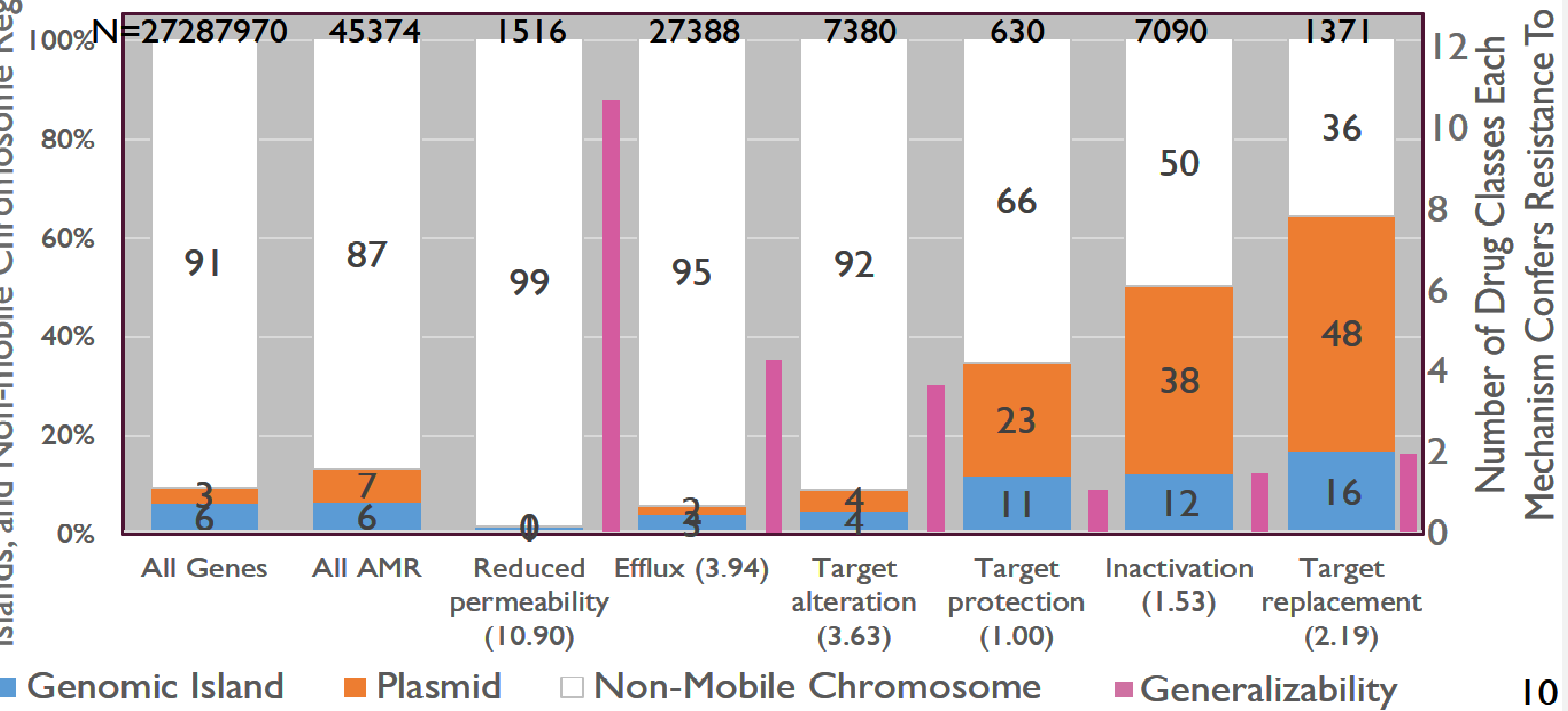
## RESULTS

0.17% 0.18% 0.46%



Distribution of AMR Genes in Plasmids, Genomic islands, and Non-mobile Chromosome Regions

### AMR Gene Distribution By Resistance Mechanism

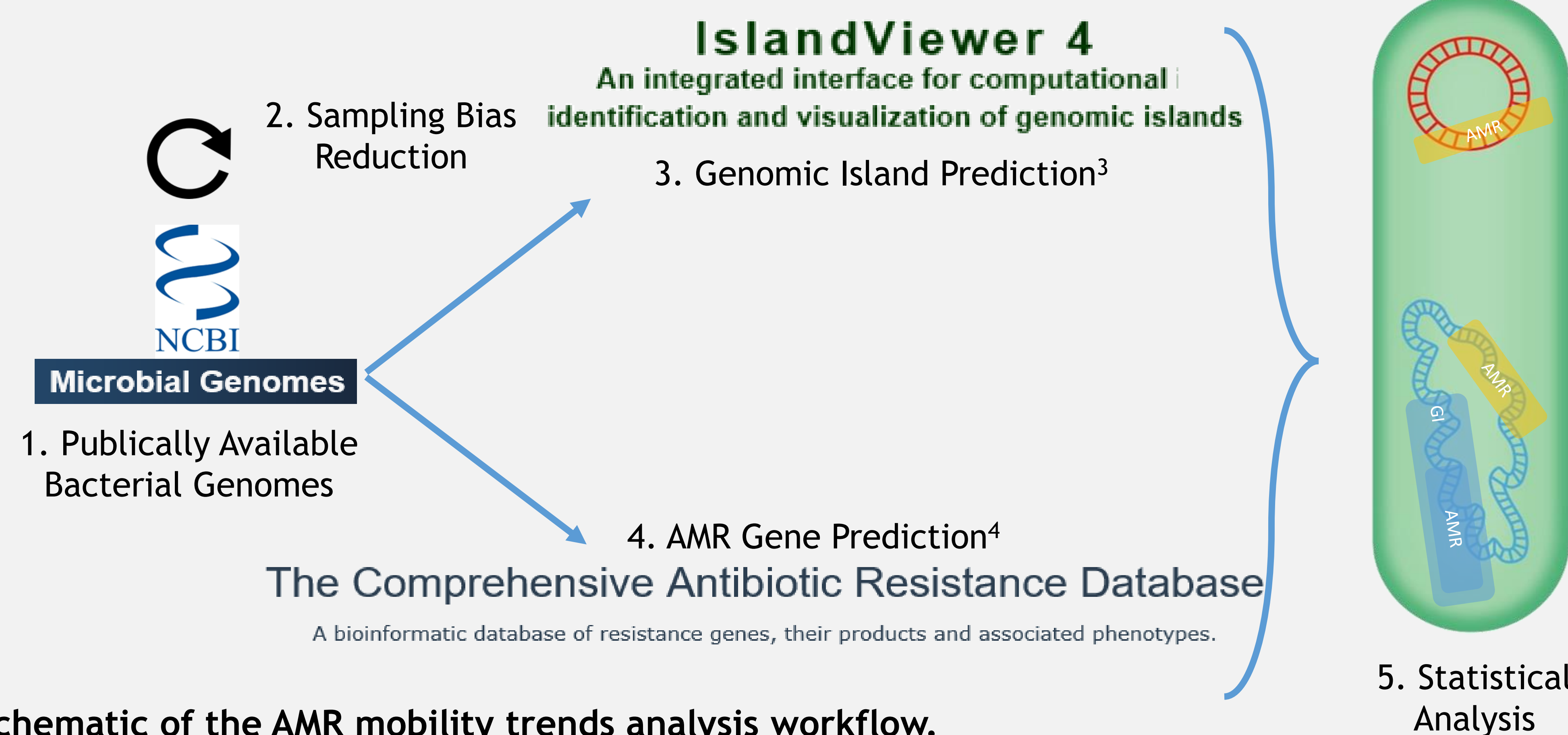


### Distribution of AMR genes amongst the three regions of the bacterial genome

A) Collectively, AMR genes are disproportionately found on mobile sequences, particularly plasmids.

B) AMR genes distribution varies based on resistance mechanism, temporal associations, and resistance generalizability (# of drug classes).

## METHOD



Schematic of the AMR mobility trends analysis workflow.

## Summary

- Overall, AMR genes are disproportionately associated with mobile sequences. However marked differences exist between resistance mechanisms.
- Ecological “Public Goods”:
  - AMR gene does not need to be present in all individuals in order to benefit all members of a community.

**AMR Mobility:**  
{Fitness Cost + Time Since Acquisition + Ecological Public Goods + ???}

With better prediction and ecological sampling, an improved model for AMR gene transmission may be produced and exploited for future AMR surveillance and public health risk assessment.

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