

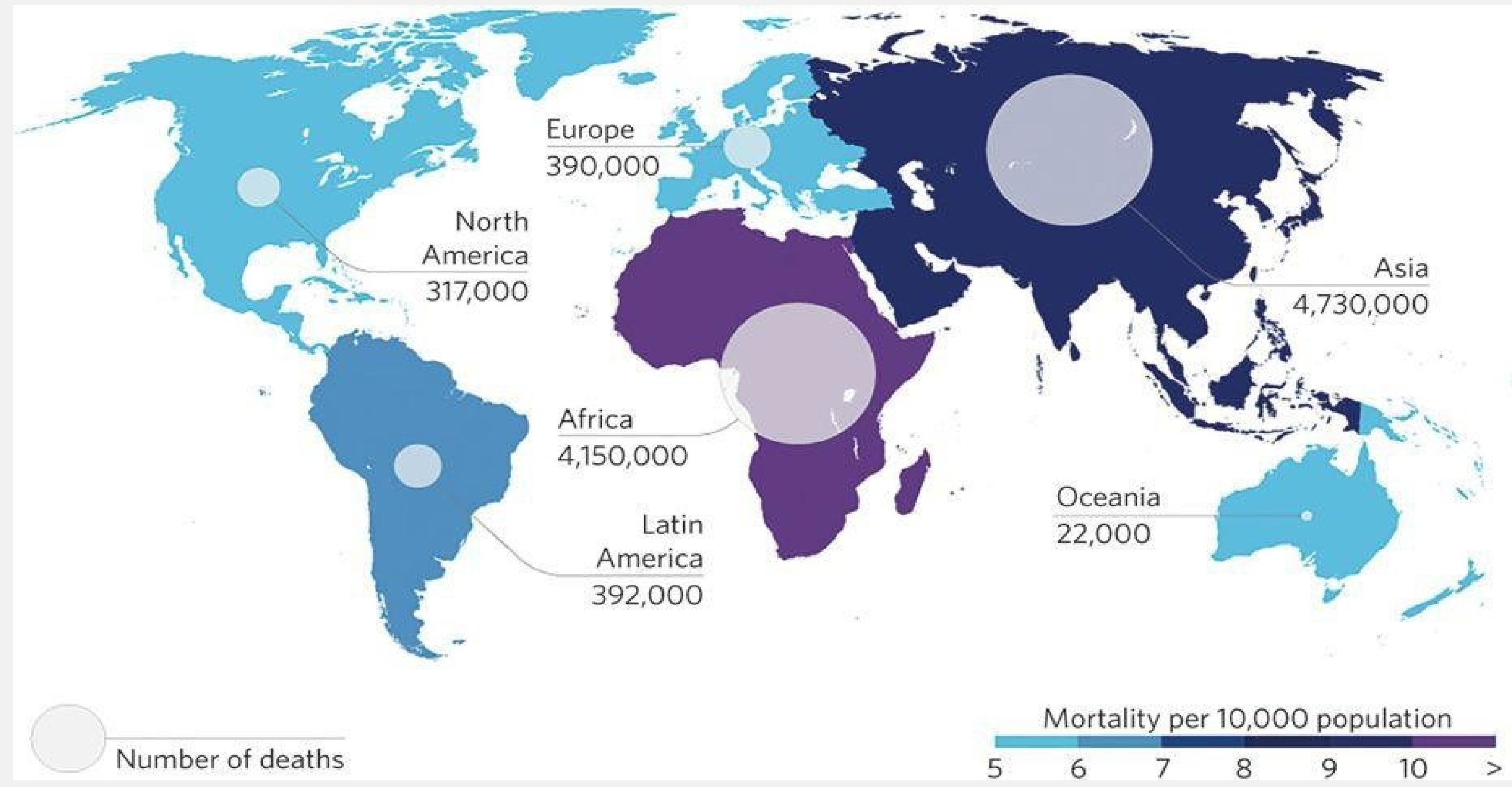
Antimicrobial Resistance As Ecological Public Goods: Mobility and Risk Assessment Via Genomic Analysis of >66000 Replicons

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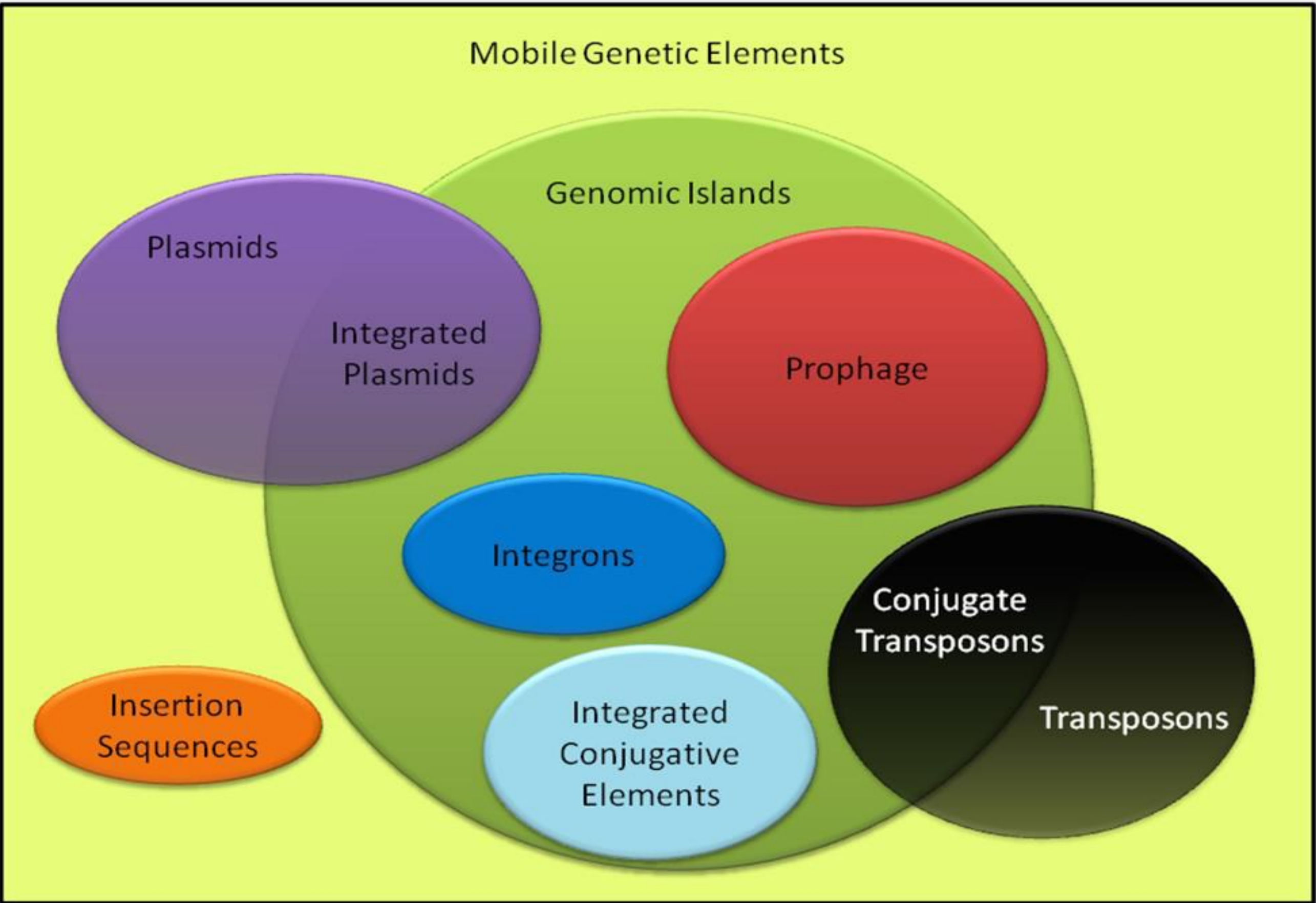
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INTRODUCTION

- Antimicrobial resistance (AMR) and emergence of pan resistant superbugs –over 10 million deaths by 2050¹



- 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



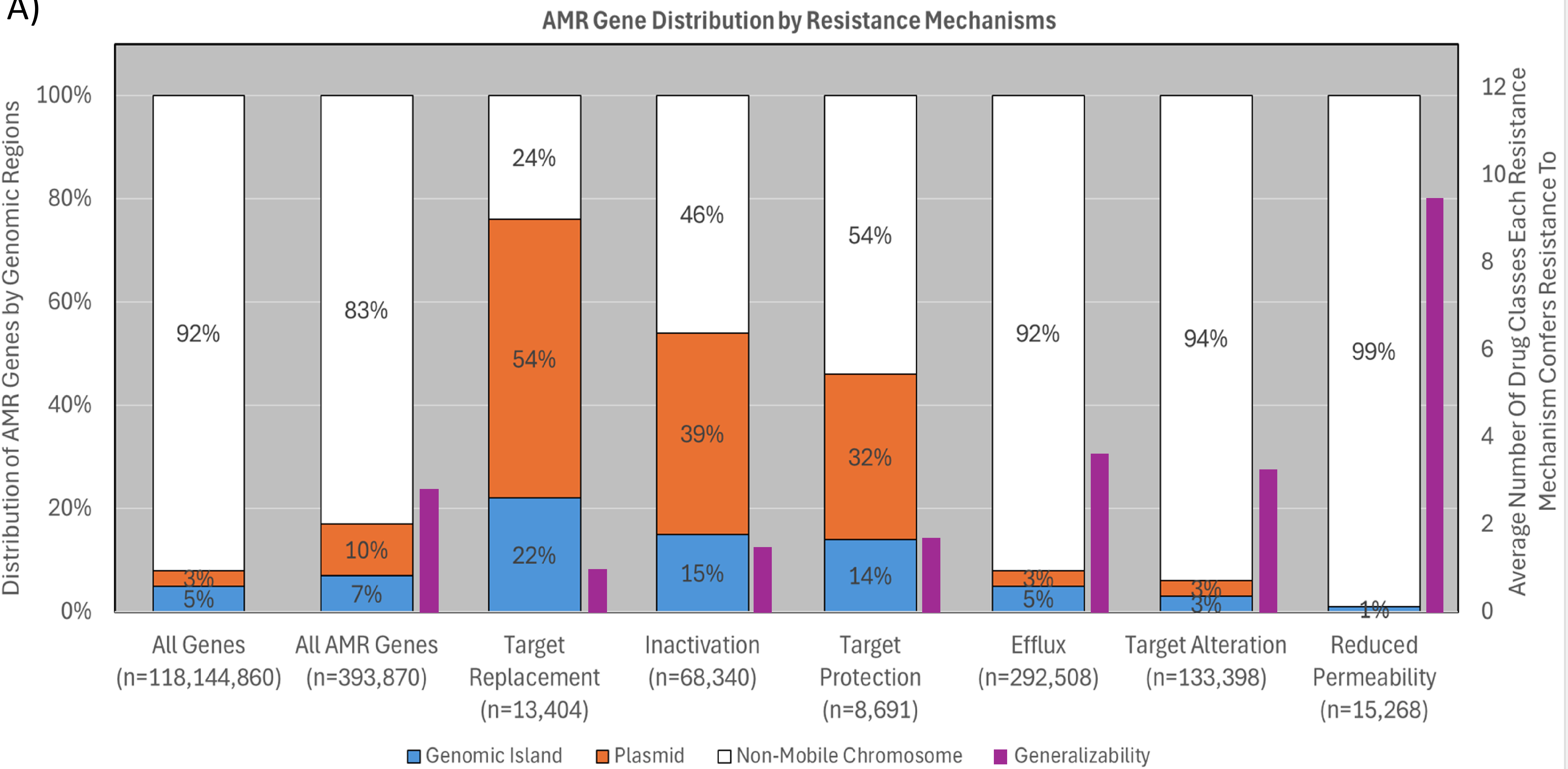
- Virulence factors are disproportionately associated with mobile elements, including plasmids and genomic islands²** –evolutionary advantage to remain mobile

Hypothesis:

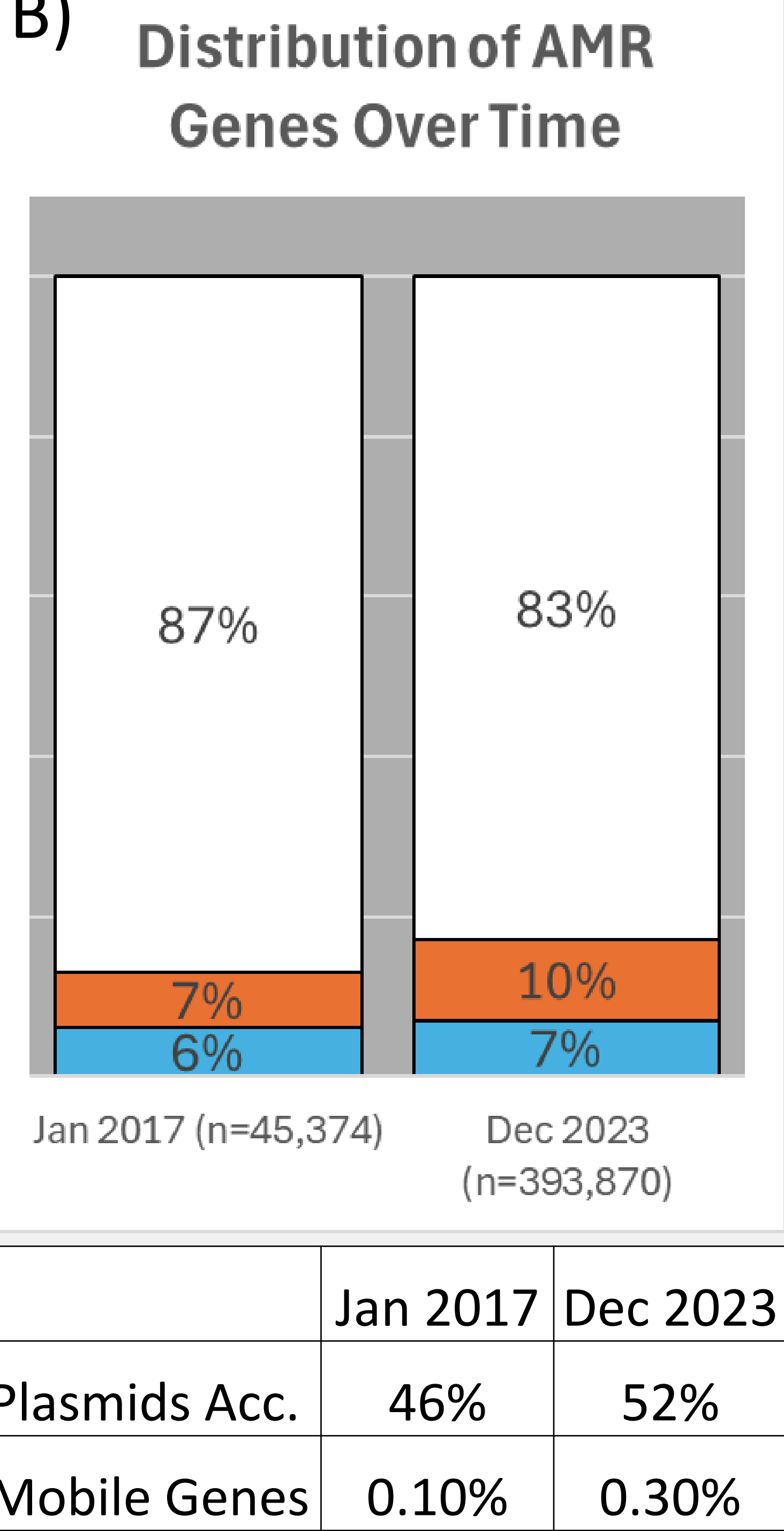
Similarly to VFs, AMR genes are disproportionately associated with mobile sequences but differences should exist for certain AMR gene classes.

RESULTS

A)



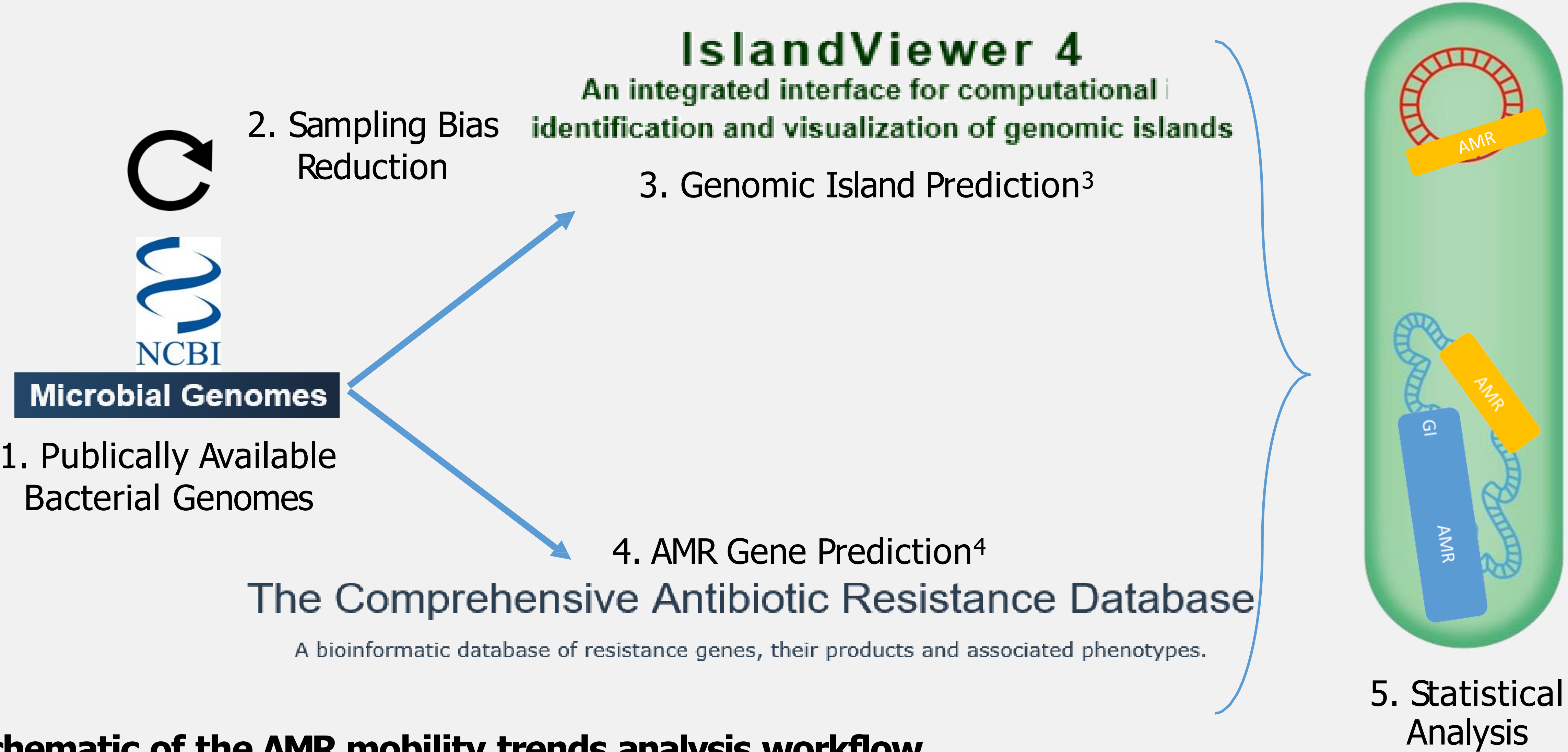
B)



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

- A) AMR gene distribution varies based on resistance mechanism, and resistance generalizability (# of drug classes it confer resistance to).
B) There's an increase in the number of genes (including AMR genes) on mobile elements over time in RefSeq.

METHOD



Schematic of the AMR mobility trends analysis workflow

Summary

- Overall, AMR genes are disproportionately associated with mobile sequences. However, a strong predictor of mobility is how specific the resistance is.
- Ecological "Public Goods":
 - An 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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