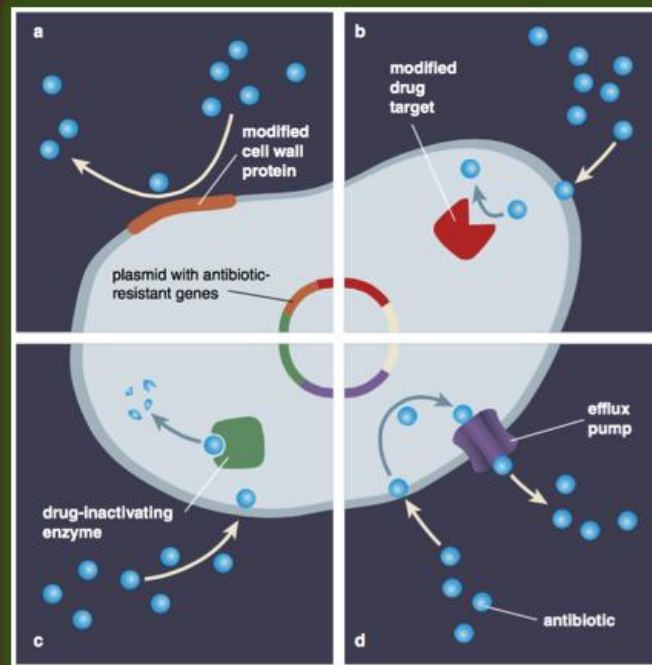


REVEALING ANTIMICROBIAL RESISTANCE GENE MOBILITY TRENDS USING >15000 REPLICONS

BAOFENG (JUSTIN) JIA

BRINKMAN LAB

SIMON FRASER UNIVERSITY, METRO VANCOUVER



ANTIMICROBIAL RESISTANCE (AMR) IS ON THE RISE

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Government pledges more than £30m to fight superbugs

'Game-changing' antibiotic can kill off superbugs

By [Ana Sandoiu](#) | Published Tuesday 27 March 2018

Fact checked by [Jasmin Collier](#)

A new study, published in the *Journal of Medicinal Chemistry*, offers the first proof that a new synthetic form of the antibiotic teixobactin can neutralize drug-resistant bacteria.



Drug resistant E. coli bacteria are already a significant problem in Europe

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Antibiotic resistance is a growing problem around the world

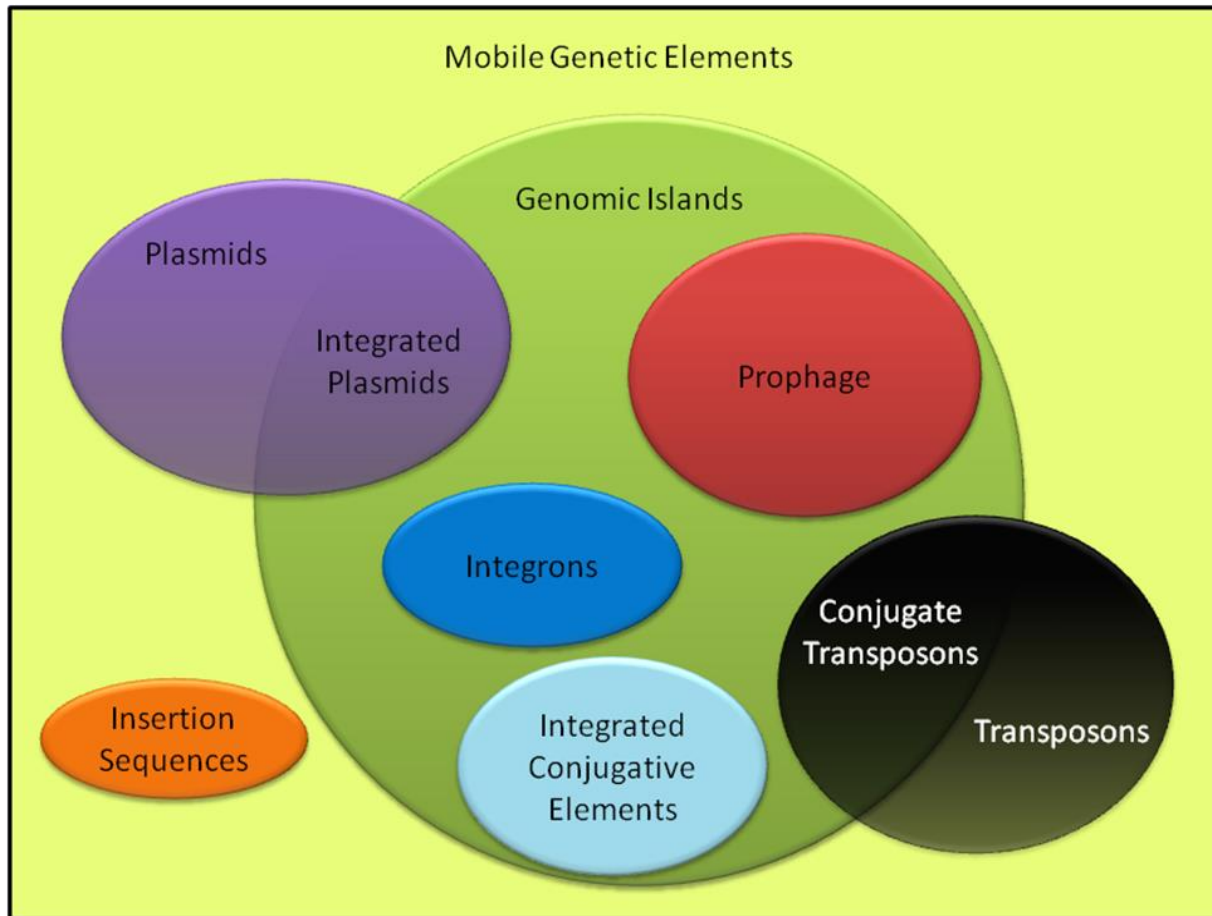
By **Anne Gulland**, GLOBAL HEALTH SECURITY CORRESPONDENT
22 MAY 2018 • 11:30AM

The UK government has given the fight against deadly superbugs a boost with a pledge of £31m for the development of new drugs and diagnostics.



Need for research in understanding AMR mobility trends to improve public health AMR risk assessment and prevention

VIRULENCE FACTORS ARE DISPROPORTIONATELY ASSOCIATED WITH GENOMIC ISLANDS (GI)



There is selective pressure for VFs to be associated with mobile sequences

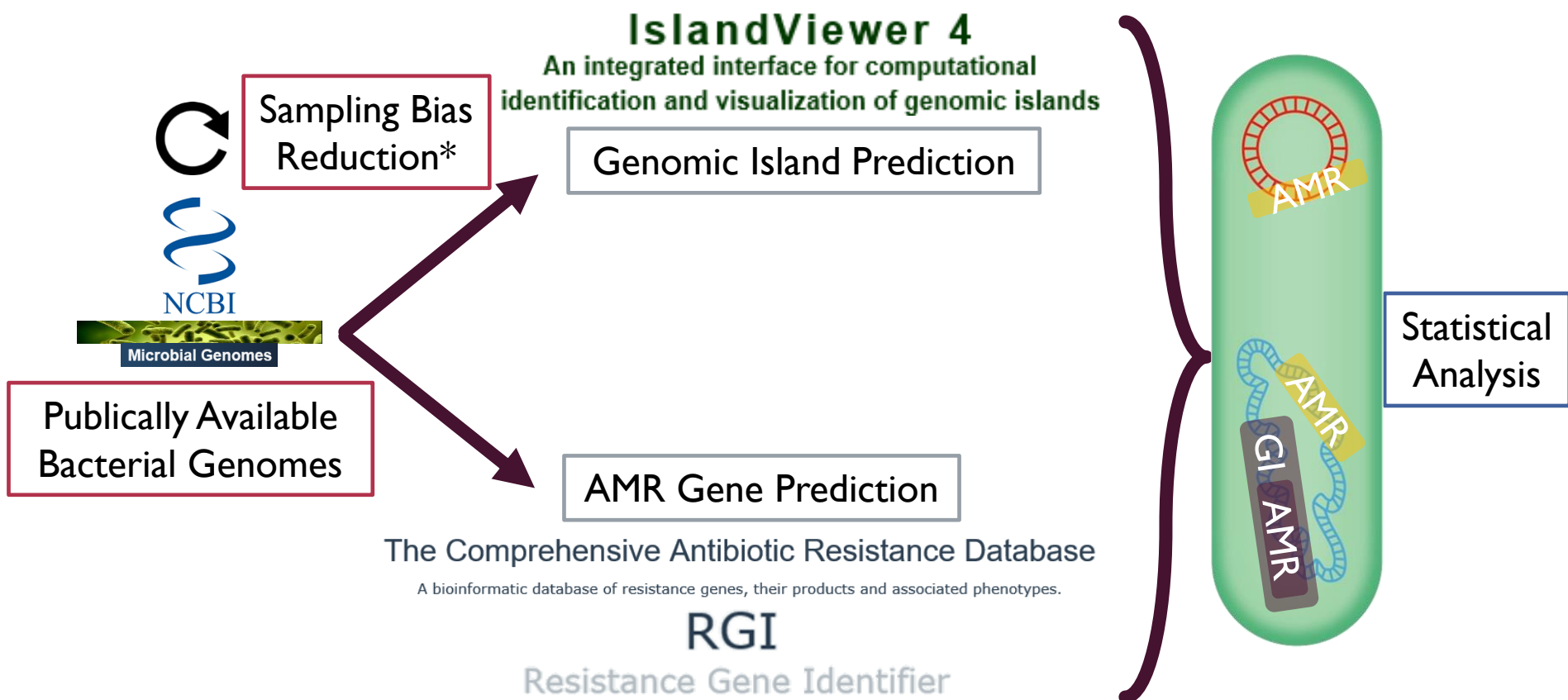
ARE THERE ANY AMR ASSOCIATIONS?

With increasing amount of genomic data, could we gain a more comprehensive understanding of AMR mobility trends that would be useful for public health AMR risk assessments?

Hypothesis:

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

Methodology: Understanding AMR Association



*Analysis was done with and without dataset reduction

(Bertelli, C. et al. 2017, PMID:28472413)
(Jia, B. et al. 2017, PMID:27789705) 5

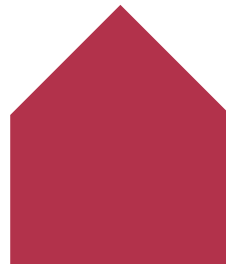
**COLLECTIVELY, AMR GENES ARE
DISPROPORTIONALLY FOUND IN MOBILE
SEQUENCES, PARTICULARLY PLASMIDS**

0.17%



Non-mobile
chromosome

0.18%



Genomic
islands

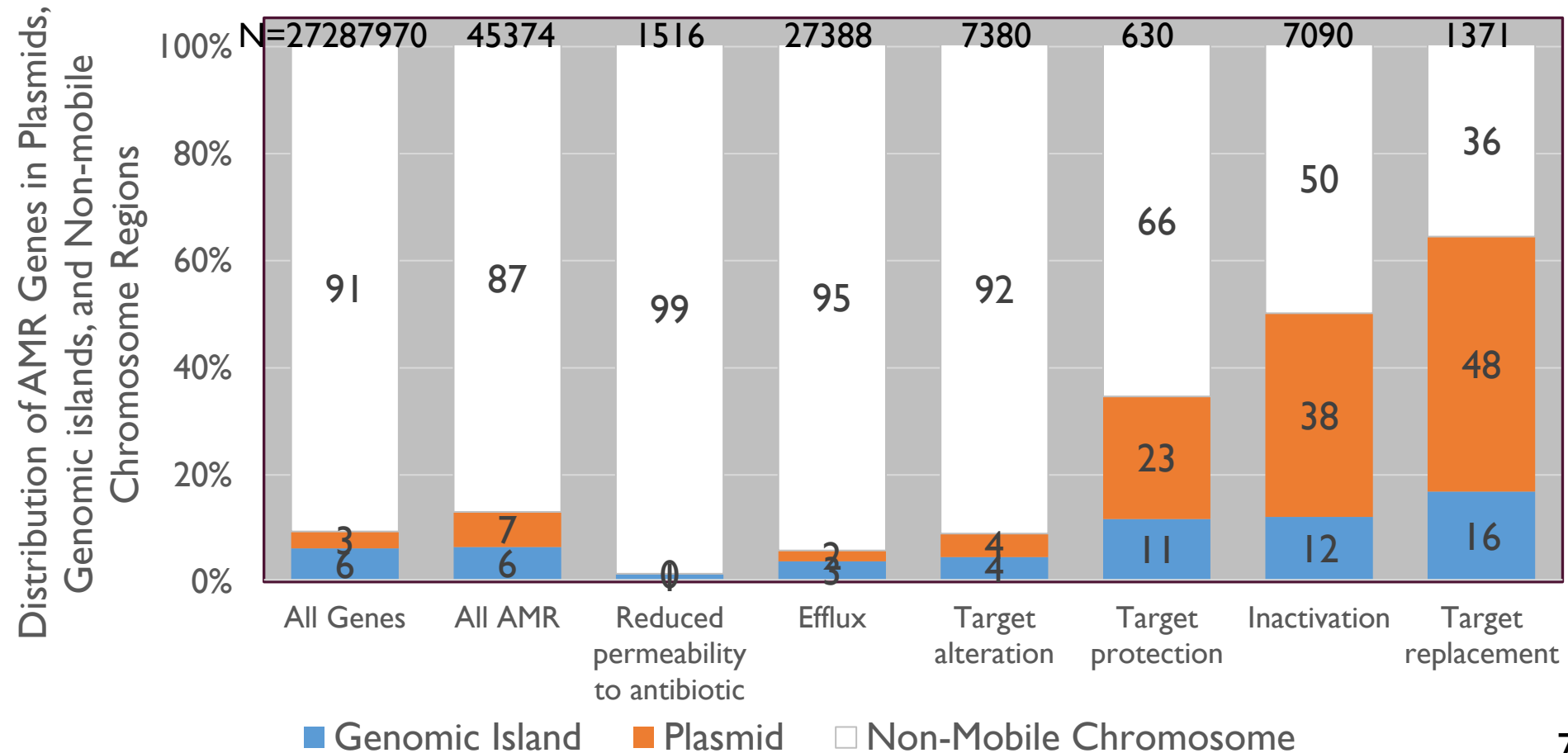
0.46%



Plasmids

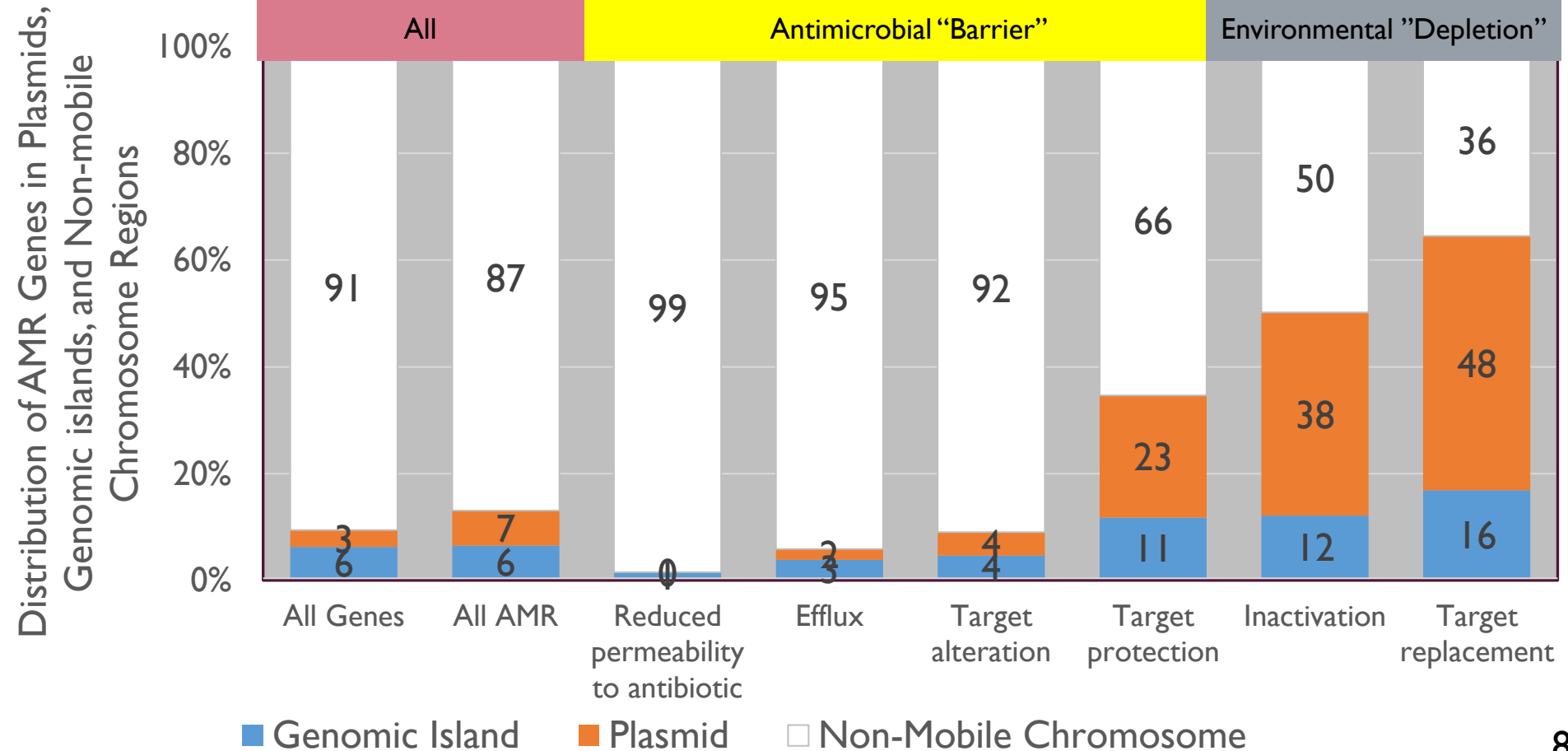
HOWEVER... ASSOCIATIONS DEPEND ON THE AMR MECHANISM

Relative AMR Gene Distribution By Resistance Mechanism



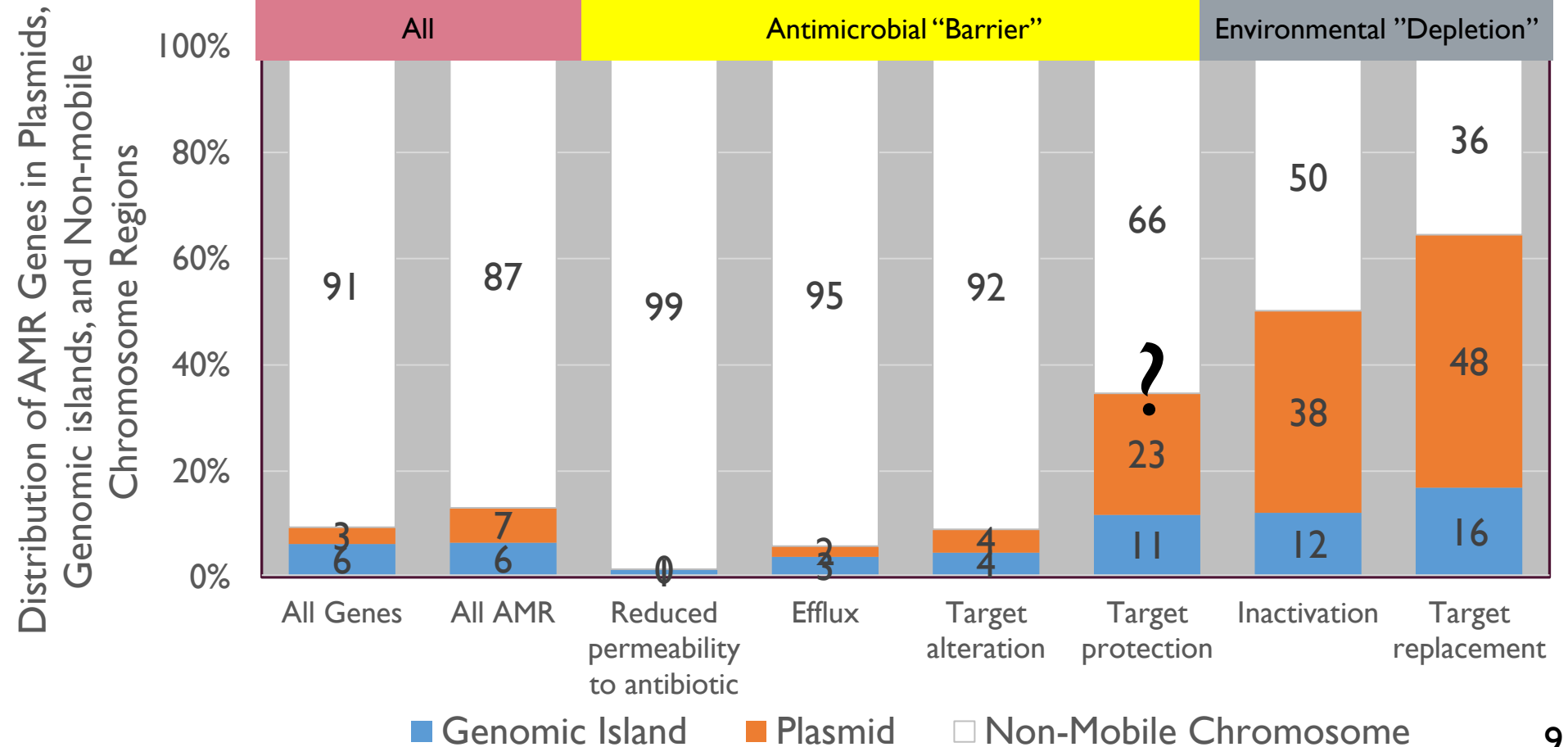
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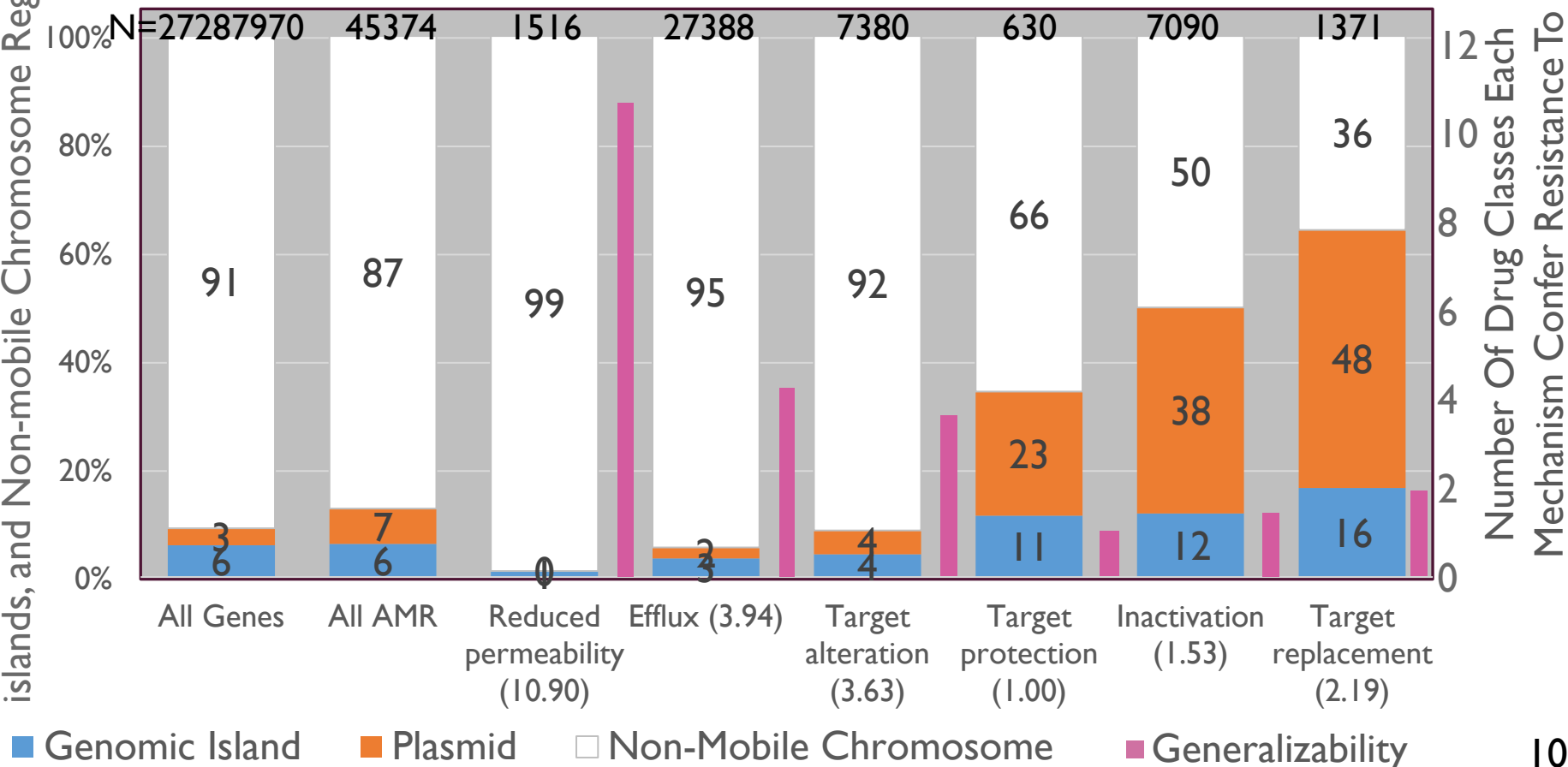
HOWEVER... ASSOCIATIONS DEPEND ON THE AMR MECHANISM

Relative AMR Gene Distribution By Resistance Mechanism



AMR GENES WITH SPECIALIZED FUNCTIONS ARE ASSOCIATED WITH MOBILE ELEMENTS

AMR Gene Distribution By Resistance Mechanisms



SUMMARY & SIGNIFICANCE

- Overall, AMR genes are disproportionately associated with mobile sequences but different trends exist when we break it down
- Ecological “Public Goods”
 - Specialized AMR genes are disproportionately found on mobile elements
 - 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, we could potentially produce a model for AMR gene transmission and exploit this knowledge for future AMR surveillance and public health risk assessment

THANK YOU!

ACKNOWLEDGEMENTS



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