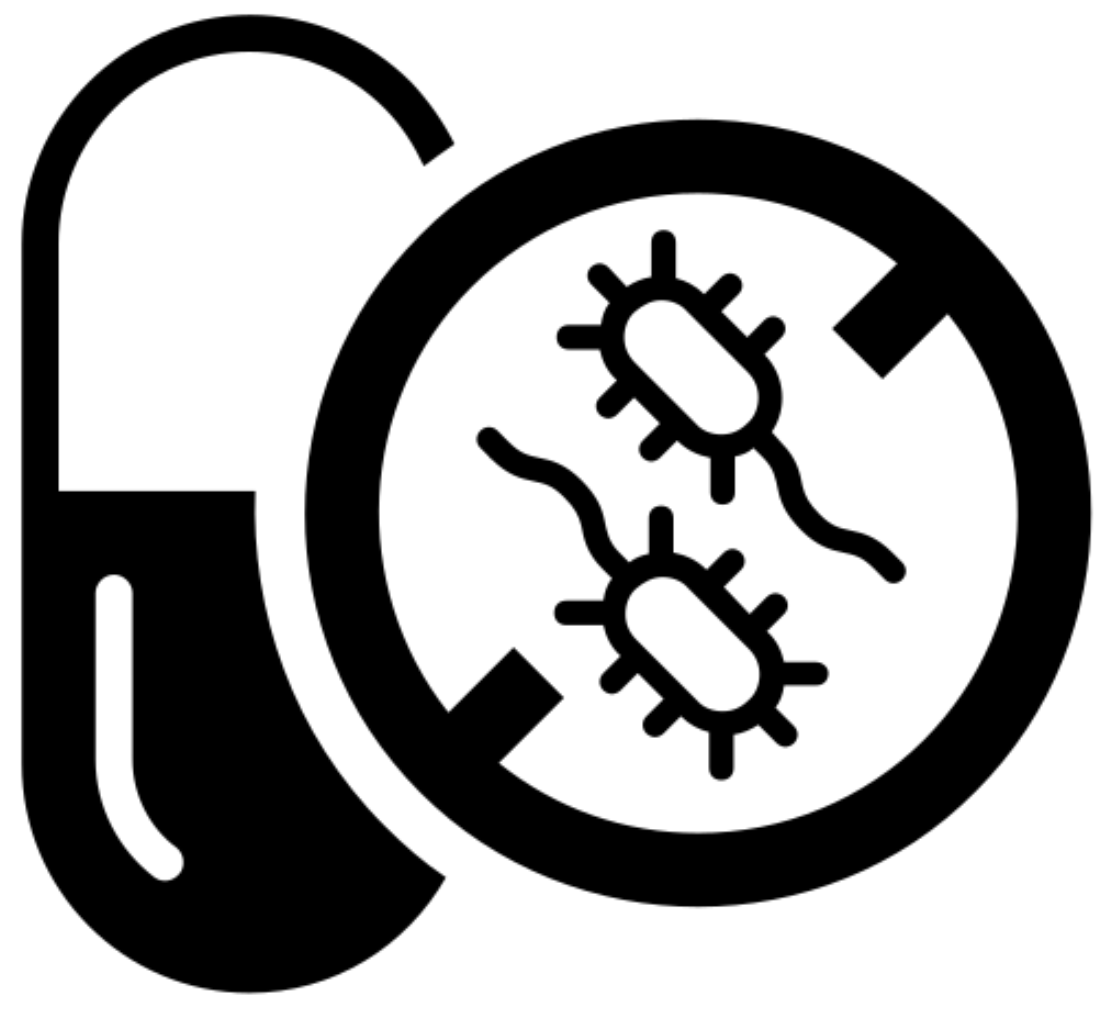


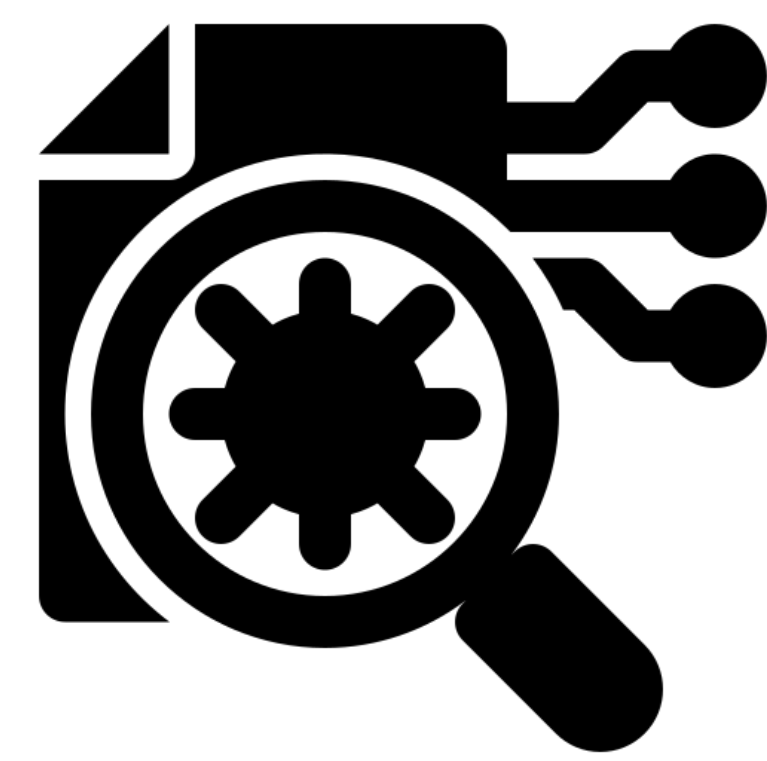
DART: Detection of Antimicrobial Resistance Toolbox

Danielle Wrenn and Devin M. Drown Department of Biology & Wildlife, Institute of Arctic Biology, University of Alaska Fairbanks, Alaska, USA



Antimicrobial Resistance is an Ongoing Public Health Threat

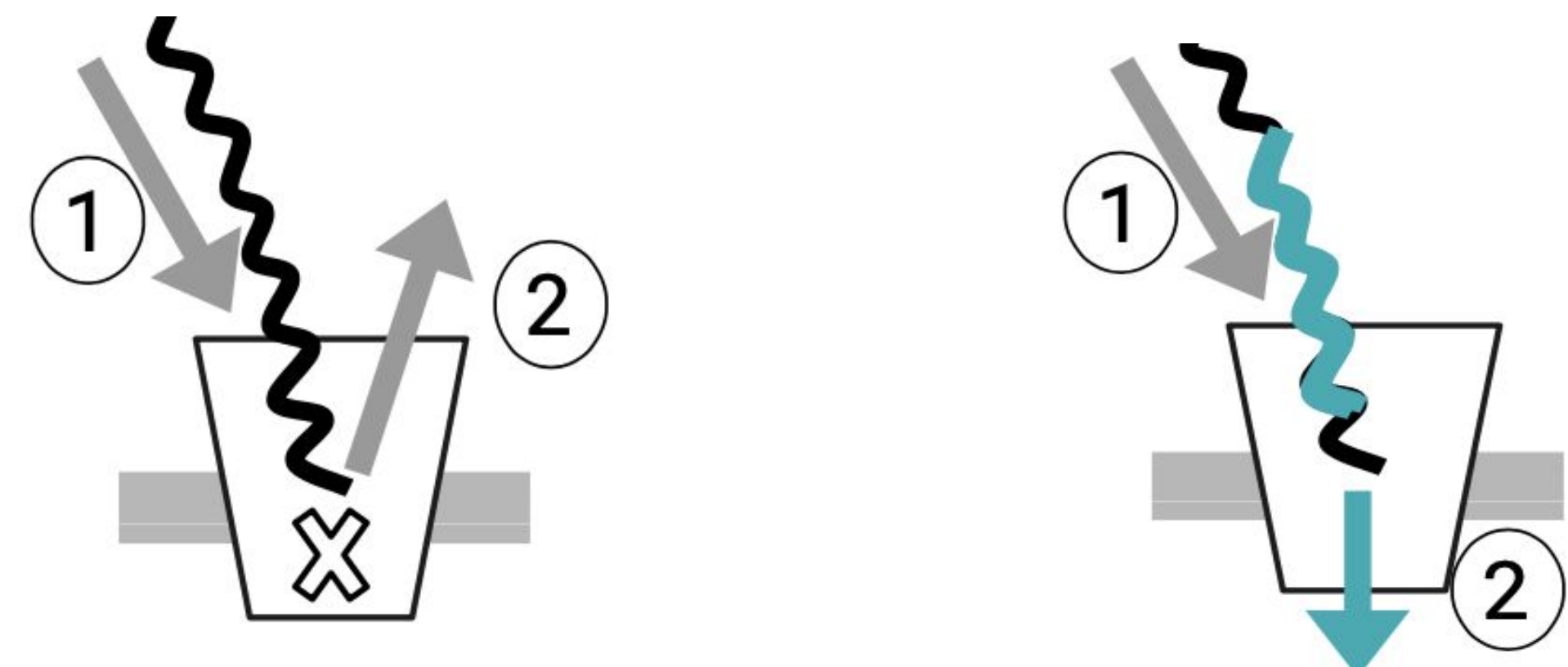
- Over 35,000 Americans die annually from antimicrobial resistant infections (CDC)
- Clinically relevant pathogens can acquire antimicrobial resistance (AMR) genes from environmental organisms (Poirel, et al., 2012)
- Soils serve as environmental reservoirs with high microbial diversity and favorable conditions for horizontal gene transfer (Nesme & Simonet, 2015)
- Environmental surveillance of AMR is a vital tool for understanding and addressing the threat of antimicrobial resistance



DART: Detection of Antimicrobial Resistance Toolbox

- A protocol for the rapid detection of antimicrobial resistance genes in environmental microbial communities
- Utilizes the Oxford Nanopore MinION and its ability to enrich in real time, during sequencing, for a target gene panel

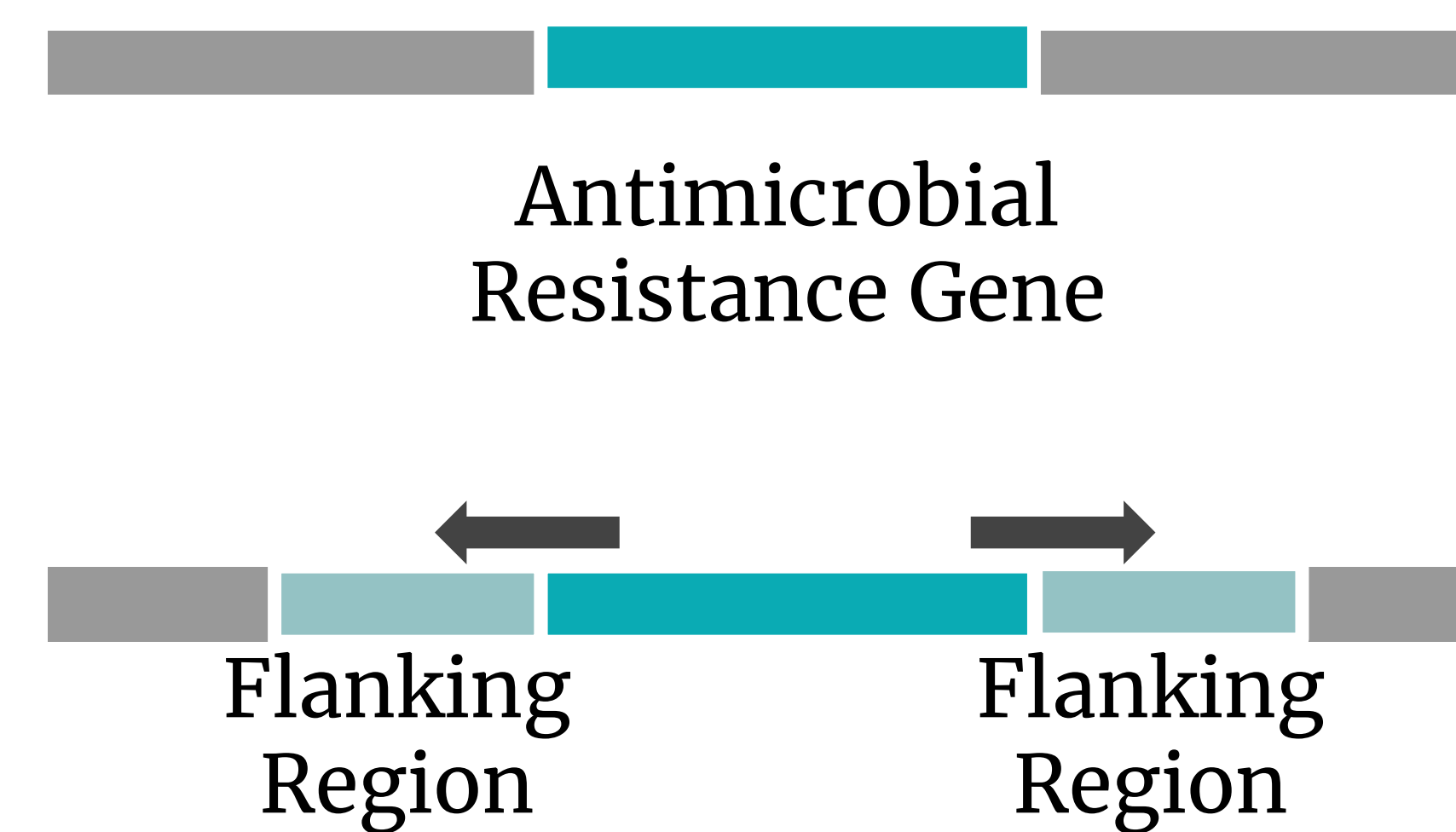
How does the MinION enrich for a target? Adaptive Sampling



- ① Target not detected
- ② Template rejected
- ① Target detected
- ② Template sequenced

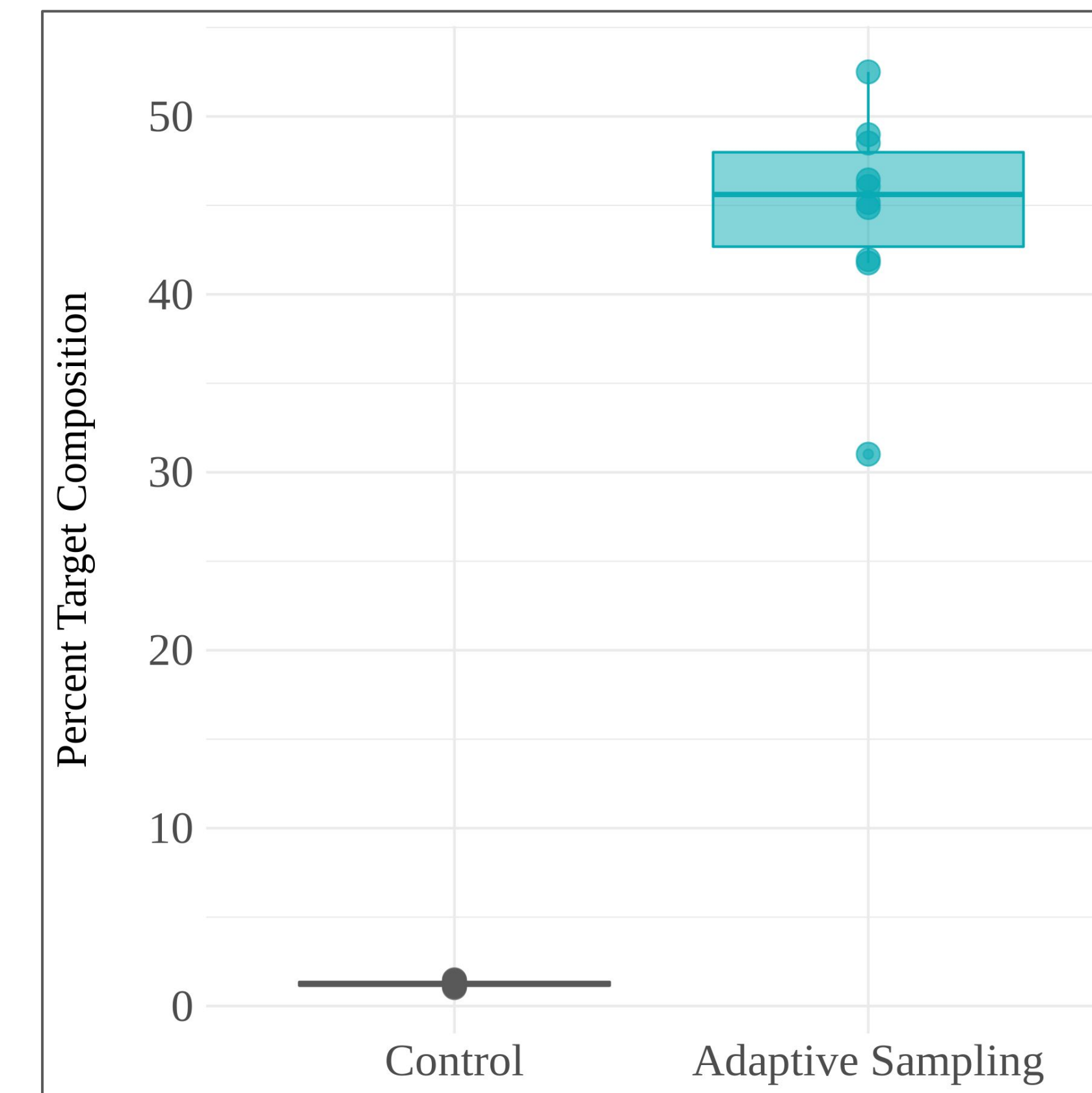
How can we increase target yield? Expand the target region

(Viehweger et al., 2021 and Martin et al., 2022)

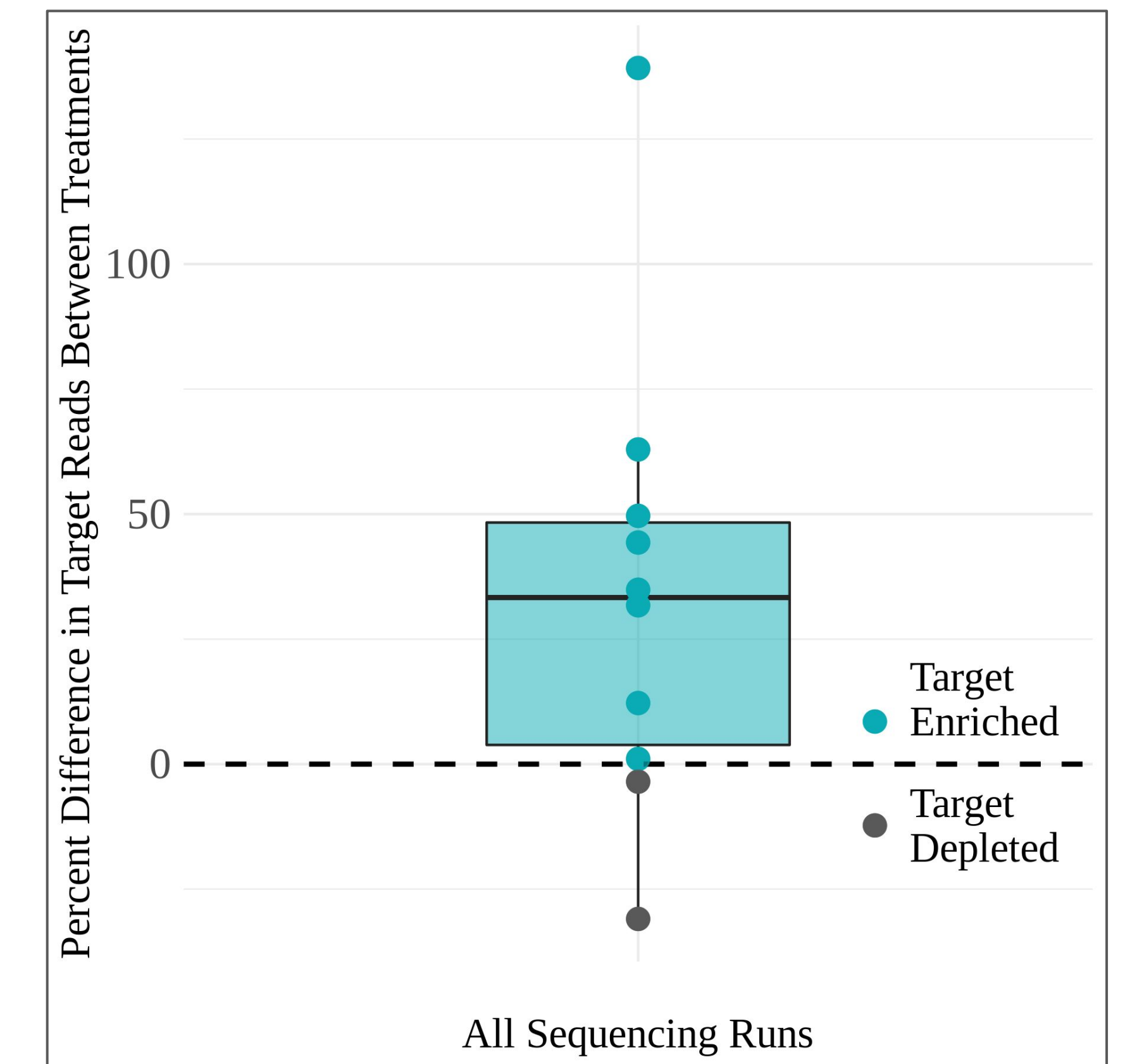


Can Adaptive Sampling Enrich for Antimicrobial Resistance Genes?

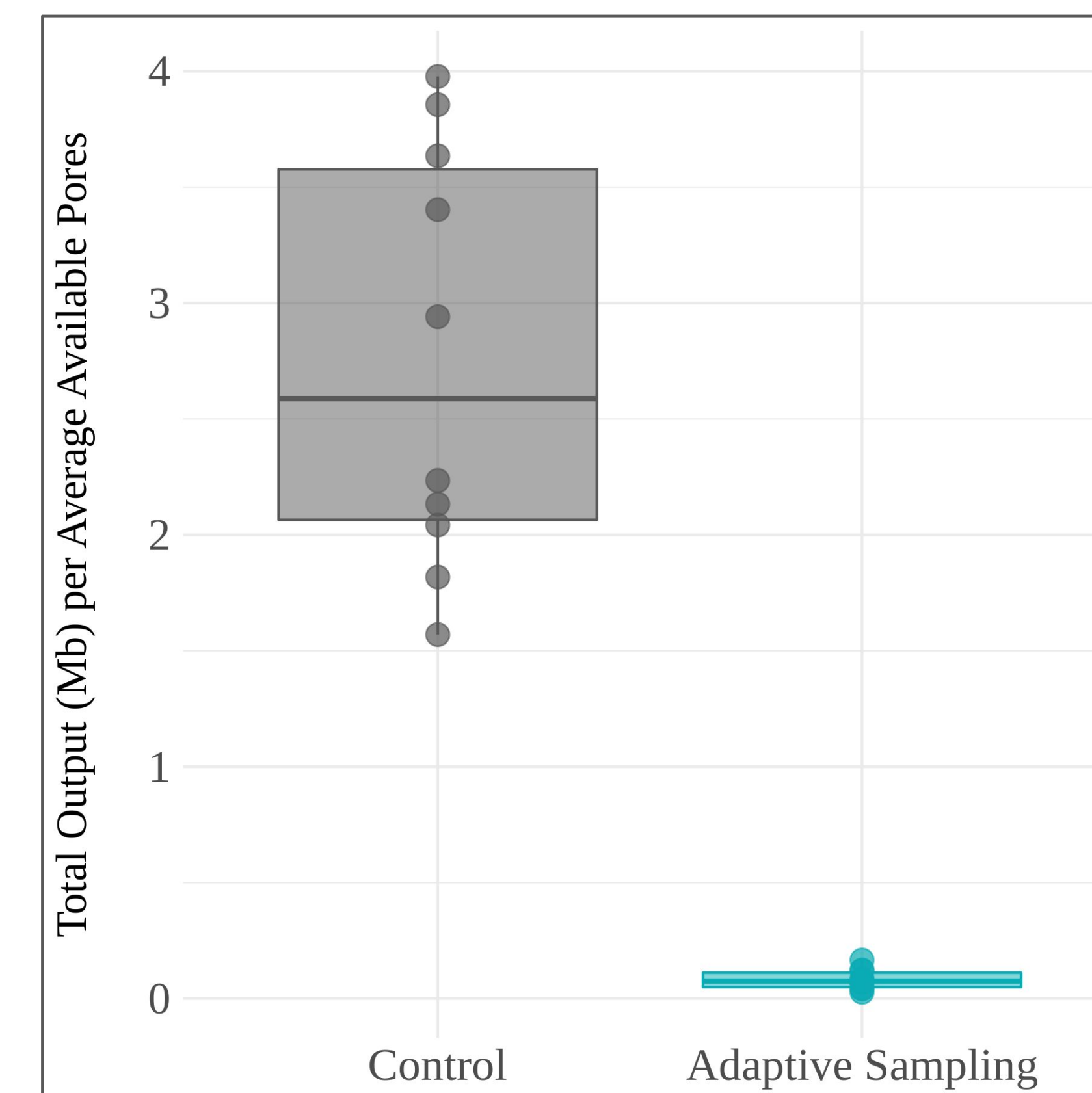
Adaptive Sampling Increases AMR Composition



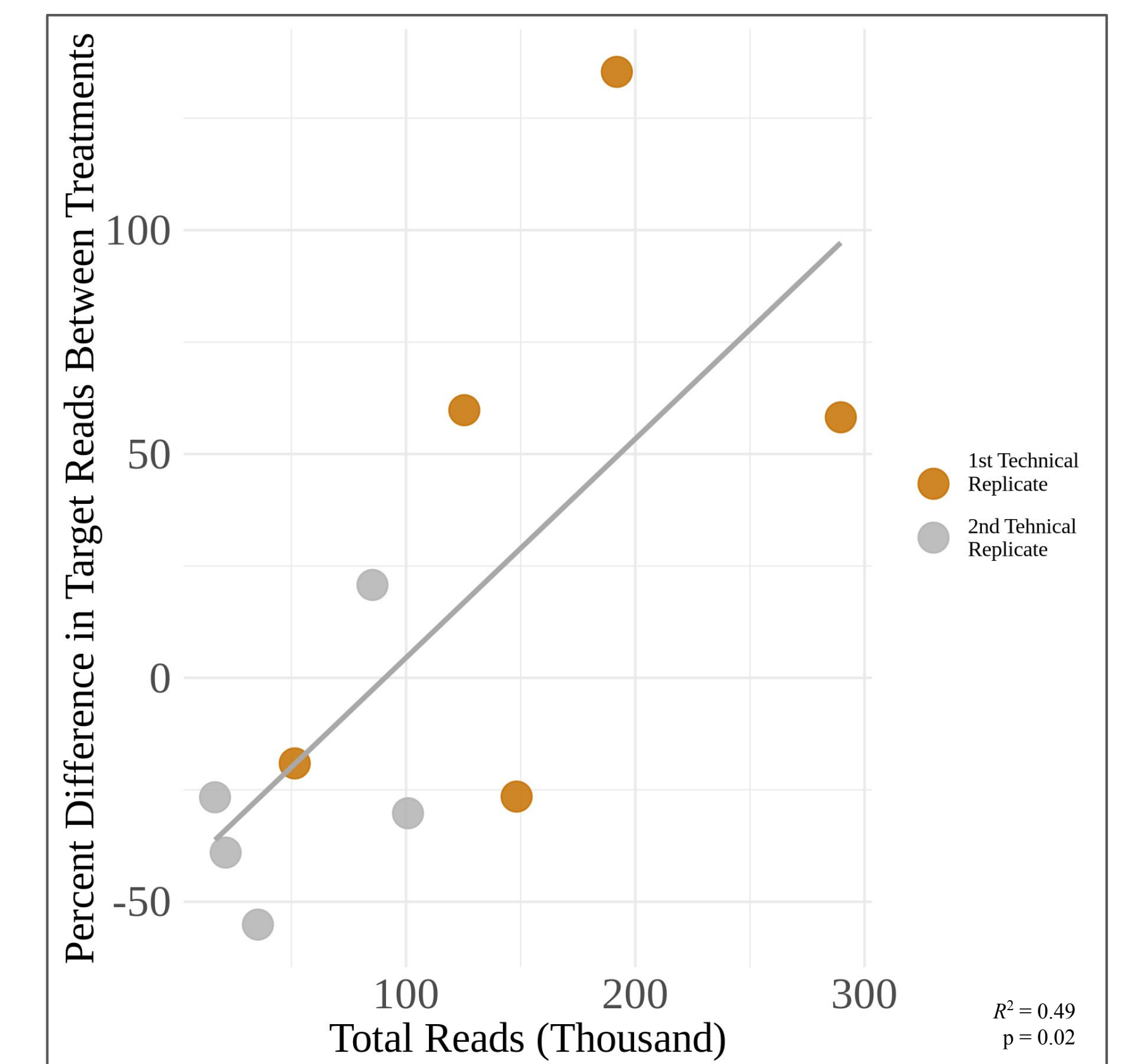
Adaptive Sampling Can Increase AMR Reads



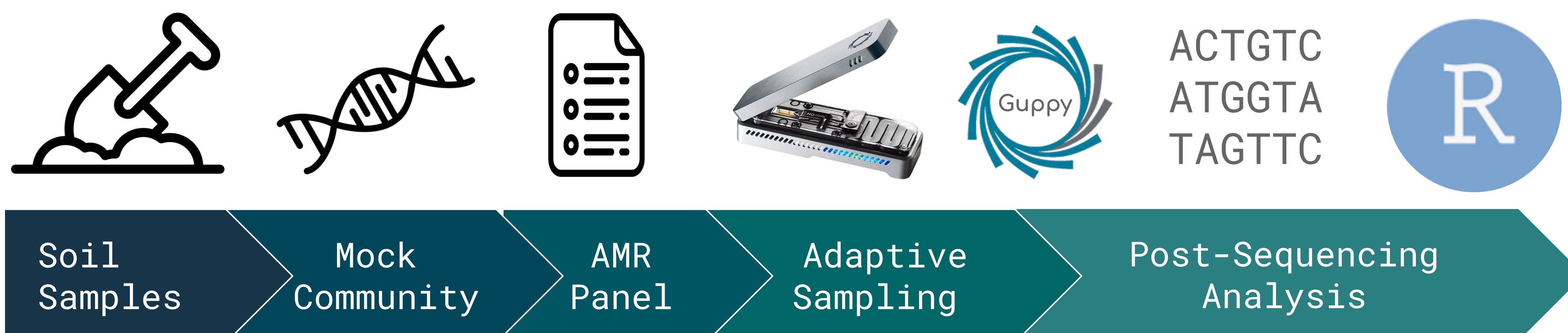
Adaptive Sampling Decreases Total Output



Difference in AMR Yield is Associated with Total Output



Pipeline



Next Steps

- Refinement of DART to increase both total output and AMR yield (Viehweger et al., 2021 and Martin et al., 2022)
- Expansion of the AMR panel to increase its applicability to a broad range of microbial communities
- Testing DART's performance in a real world scenario using environmental samples

Literature Cited: CDC. Antimicrobial resistance threats in the United States. (2019). DOI: 10.1562/cdc.82532. Martin, S., Heavens, D., Lan, Y., Horsfield, S., Clark, M. D., & Leggett, R. M. (2022). Nanopore adaptive sampling: A tool for enrichment of low abundance species in metagenomic samples. *Genome Biology*, 23(1). DOI: 10.1186/s13059-021-02582-x. Nesme, J., & Simonet, P. (2014). The soil resistome: A critical review on antimicrobial resistance origins, ecology and dissemination potential in telluric bacteria. *Environmental Microbiology*, 17(4), 913–930. DOI: 10.1111/1462-2920.12631. Poirel, L., Cattoir, V., & Nordmann, P. (2012). Plasmid-mediated quinolone resistance; interactions between human, animal, and environmental ecologies. *Frontiers in Microbiology*, 3. DOI: 10.3389/fmicb.2012.00024. Viehweger, A., Marquet, M., Hölzer, M., Dietze, N., Pletz, M. W., & Brandt, C. (2021). Adaptive Nanopore sequencing on miniature flow cell detects extensive antimicrobial resistance. <https://doi.org/10.1101/2021.08.29.458107>



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