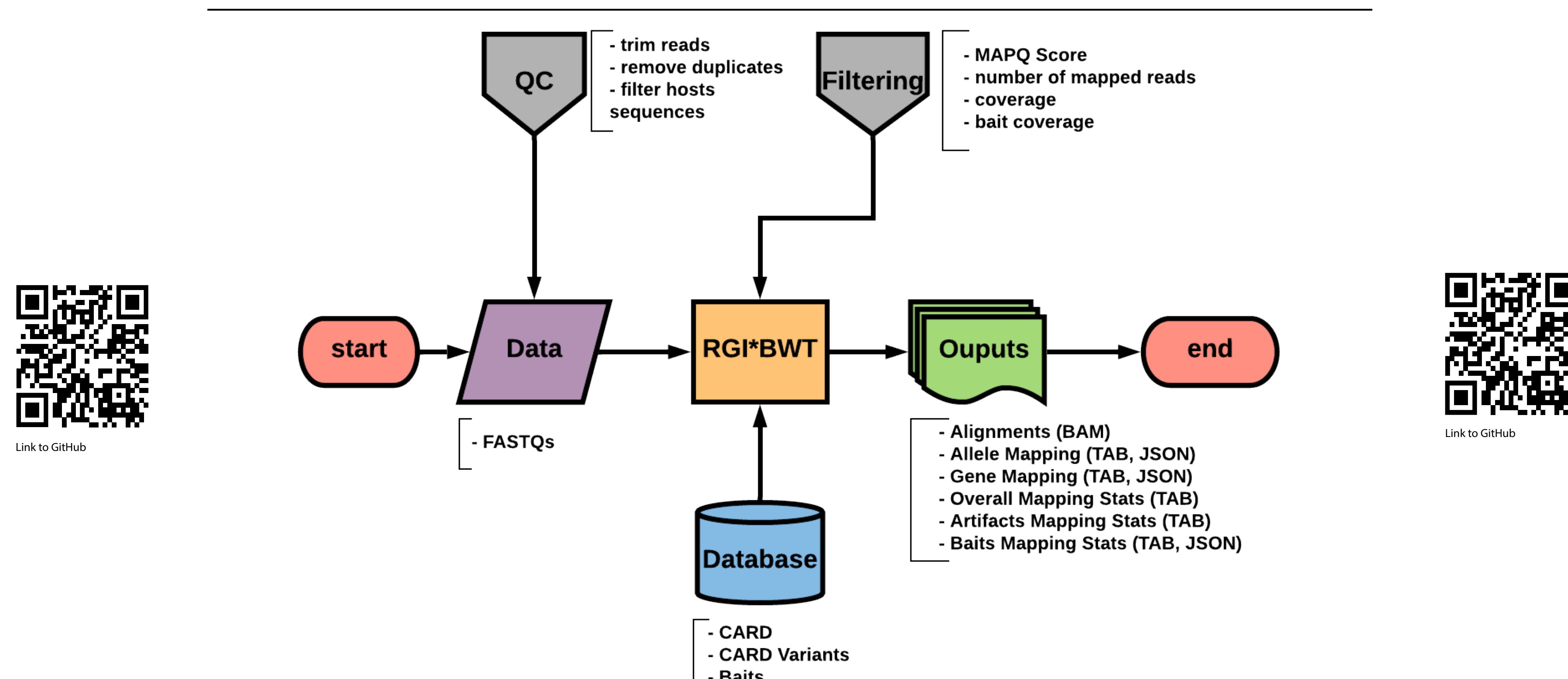


## RGI\*BWT read mapping pipeline using CARD datasets



## Clinical dataset results

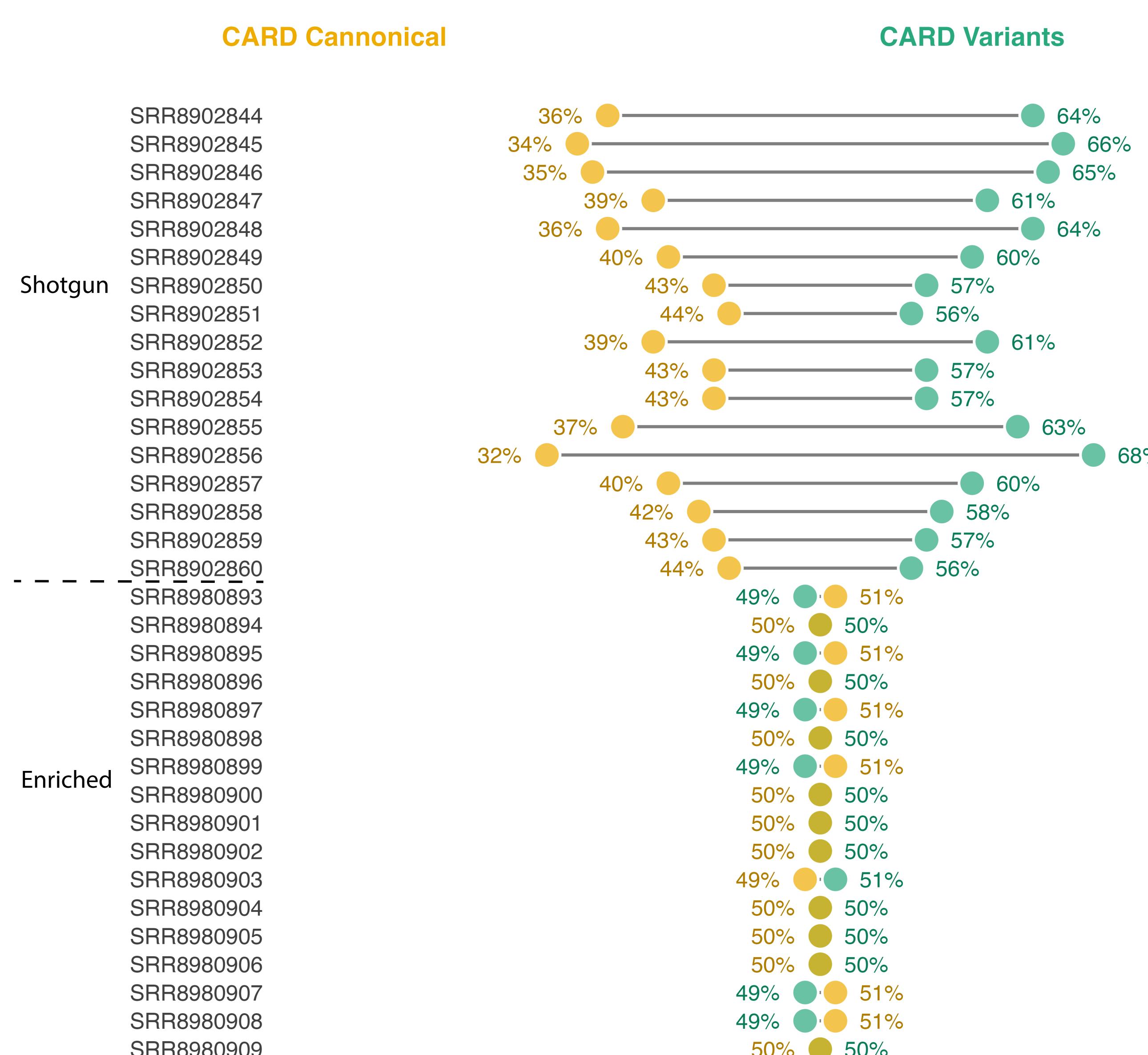


Figure 1. The plot shows percentage reads mapped for both targeted capture isolates and whole-genome sequencing (WGS). More CARD *in silico* variants are needed to map reads for WGS as compared to targeted capture.

## Data Description

- The clinical data was obtained from genome sequencing of clinical pathogens in Hamilton, Ontario, Canada, and sequenced using shotgun and targeted bait capture
- Two wastewater samples sourced from the city of Hamilton Wastewater treatment plant from November 2022 and March 2023 were bait captured using CARD baits, Arbor-synthesized, and shotgun

## Conclusion

Using capture methods and CARD *in silico* variants helps recover more AMR-related reads.

## Wastewater dataset results

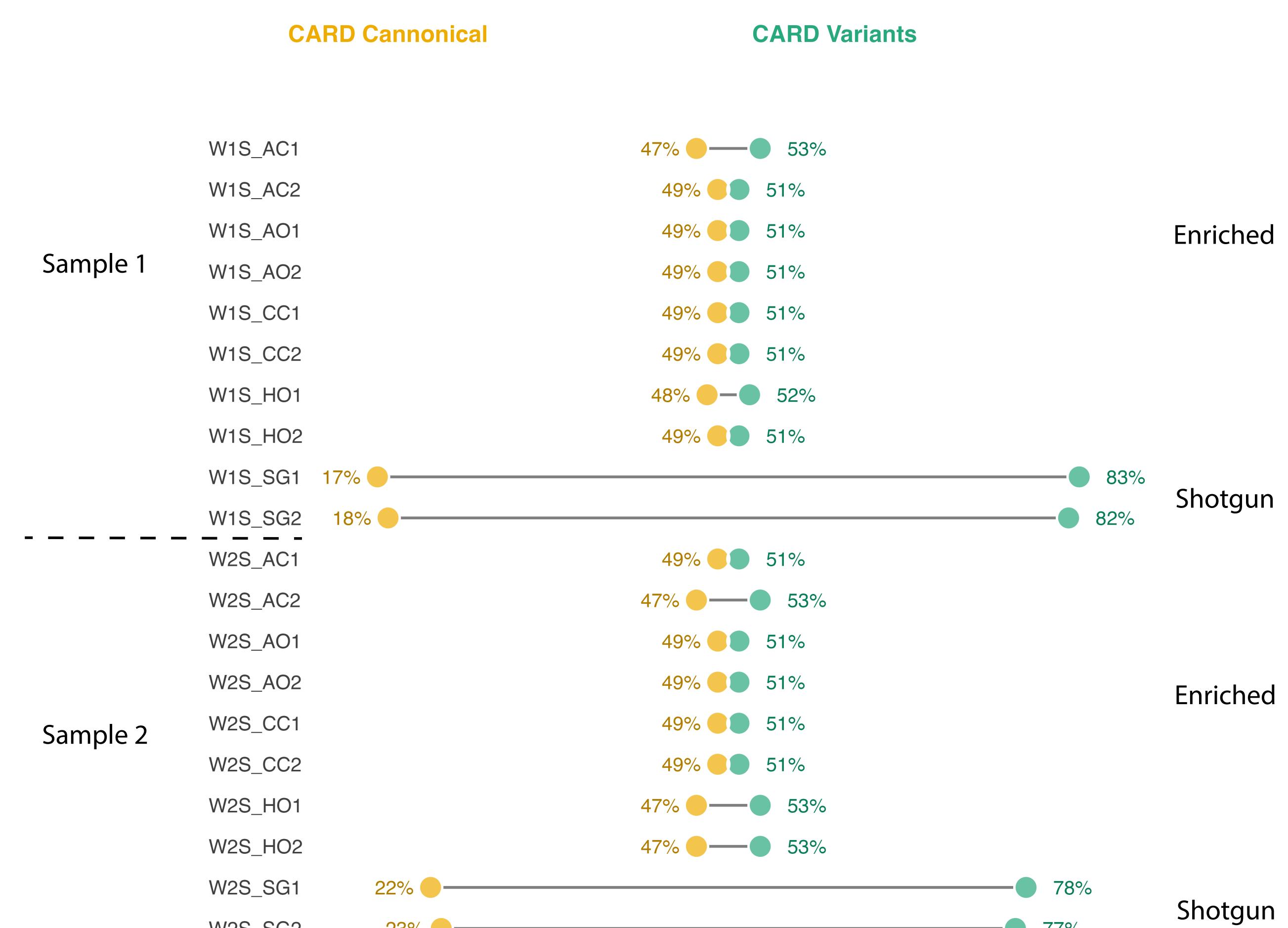


Figure 2. The wastewater samples were mapped to CARD canonical and CARD *in silico* variants. The suffixes are AC (enriched with allCARD), CC (enriched with clinicalCARD), AO (enriched with Arbor-synthesized CARD v1 baits), HO (Enriched with in-house-synthesized CARD v1 baits), and SG - (Shotgun). Each sample has a replicate denoted by 1 and 2.

## References

- Alcock BP, Huynh W, Chalil R, Smith K, and Raphenya A.R et al. CARD 2023: expanded curation, support for machine learning, and resistome prediction at the comprehensive antibiotic resistance database. *Nucleic Acids Res.*, 51(D1):D690–D699, January 2023.
- Guitar and Raphenya A.R et al. Capturing the resistome: A targeted capture method to reveal antibiotic resistance determinants in metagenomes. *Antimicrob. Agents Chemother.*, 64(1), December 2019.