AN EVALUATION OF CURRENT ANTIMICROBIAL RESISTANCE DATABASES

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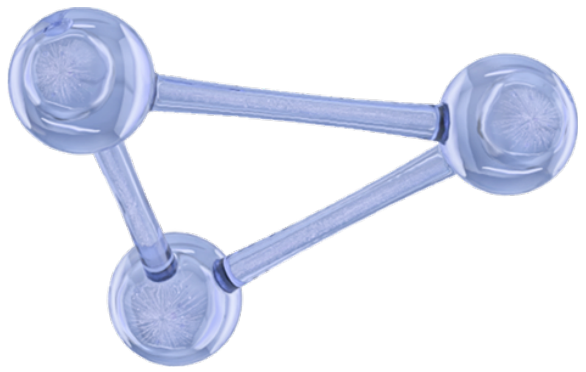
Why AMR Matters

- AMR is a major global health threat
- Drug-resistant infections may cause 10M deaths/year by 2050
- Resistance genes spread rapidly between bacteria
- Many key antibiotics are becoming ineffective
- Resistome tracking remains difficult
- AMR gene cataloguing supports treatment and policy

Objectives

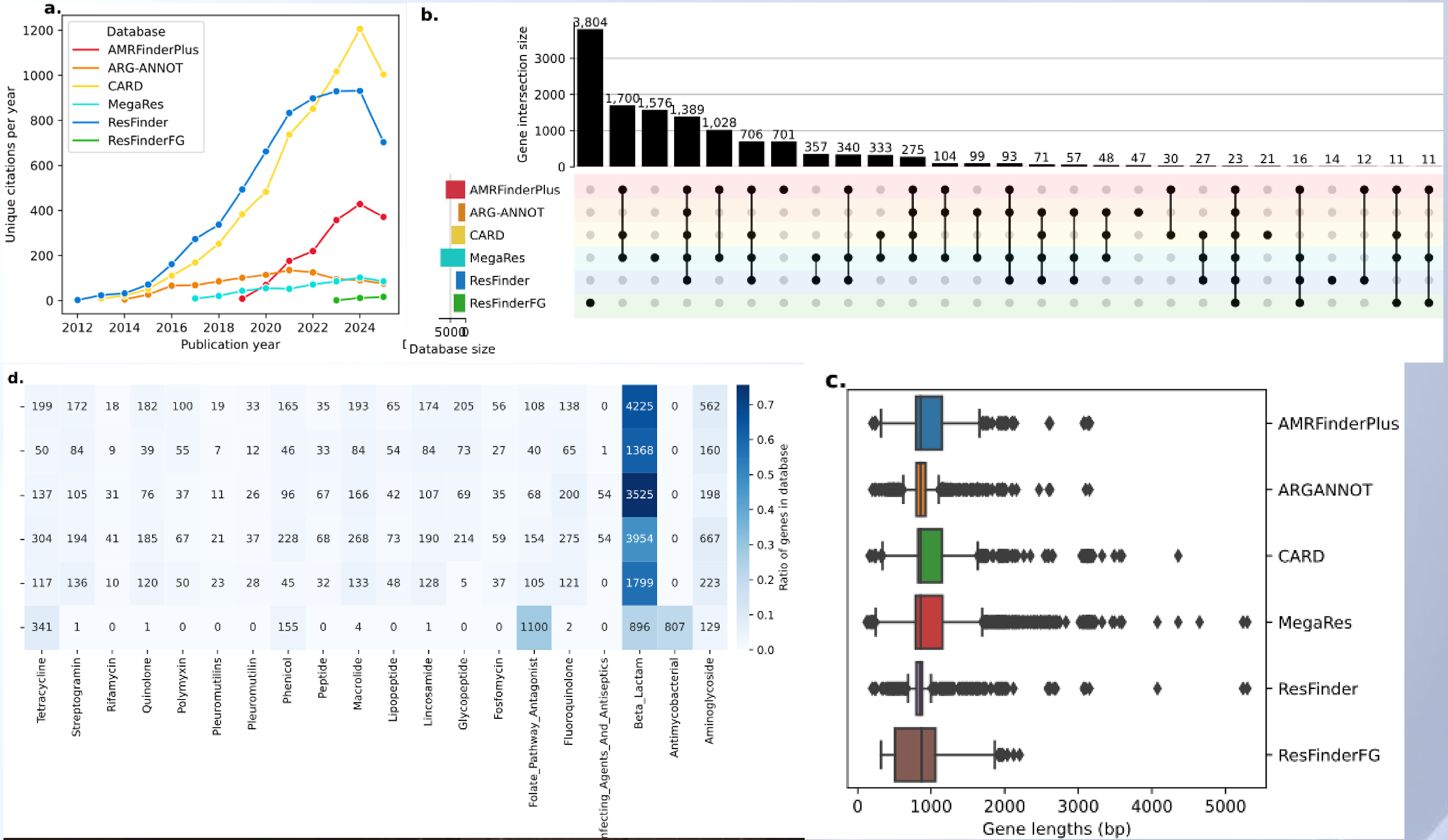


01. Assess how ARG database choice affects resistome profiling across metagenomic datasets from sewage, human-associated samples, agricultural soils, rhizosphere samples, and environmental soils.

02. Compare database-dependent resistome patterns using bacterial-normalised ARG abundance (FPKM), AMR class composition, PCA ordination, Procrustes analysis, and distance-decay relationships.

03. Evaluate clinical relevance using WGS isolate data by comparing PanRes database-based resistance predictions with phenotypic MIC results to assess concordance, overprediction, missed resistance, and ARG overlap.

The databases



The Metagenomic Datasets

Dataset	Samples	Design
Global sewage	1,240	Urban sewage from 351 cities across 111 countries
Faecal cohort	547	ALADDIN birth cohort; 56 mother–child dyads; infants sampled from 3–6 days to 60 months; mothers sampled during pregnancy and postpartum
Cropland soil	819	US soil samples classified as control/wet or dry; 74 samples linked with metadata
Grassland soil	257	US soil samples classified as wet or dry

nature communications

Article https://doi.org/10.1038/s41467-025-66070-7

Geographics and bacterial networks differently shape the acquired and latent global sewage resistomes

nature communications

Article https://doi.org/10.1038/s41467-025-63401-6

Temporal dynamics and microbial interactions shaping the gut resistome in early infancy

nature microbiology

Article https://doi.org/10.1038/s41564-026-02274-x

Drought drives elevated antibiotic resistance across soils

Global Sewage

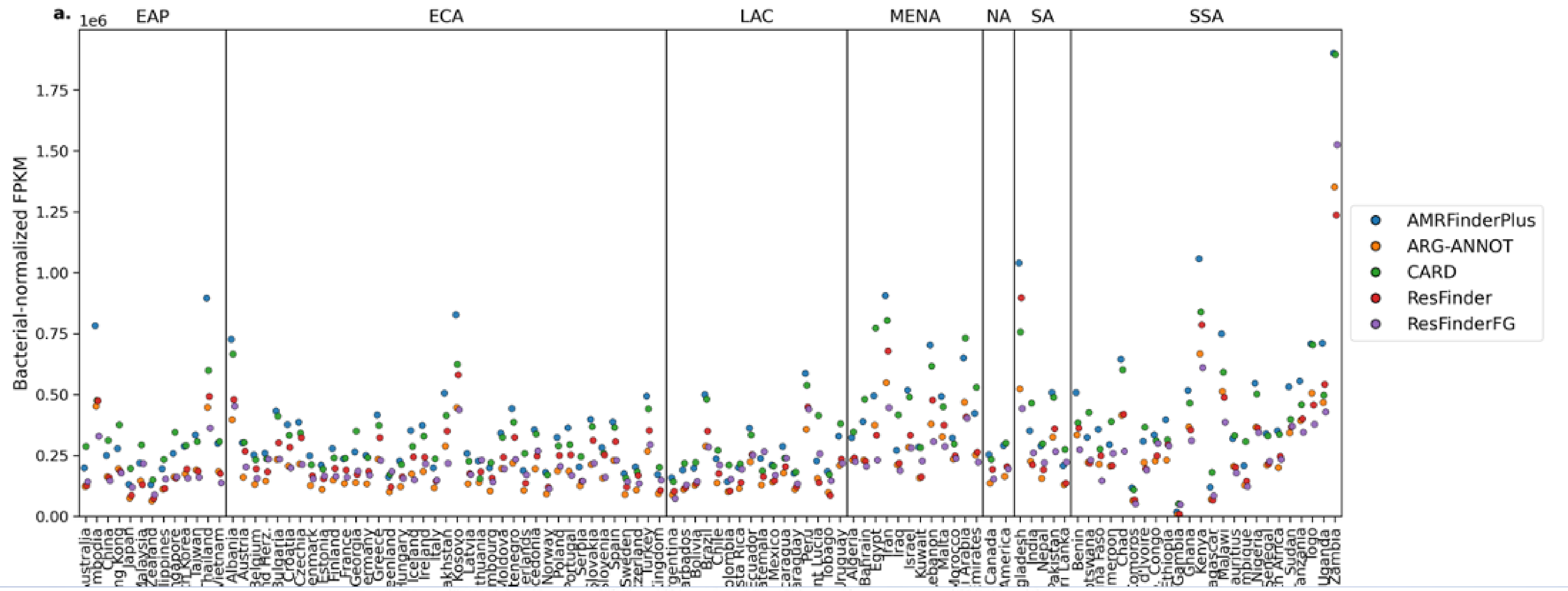
• Database choice strongly affected ARG abundance scale, especially MEGARes.

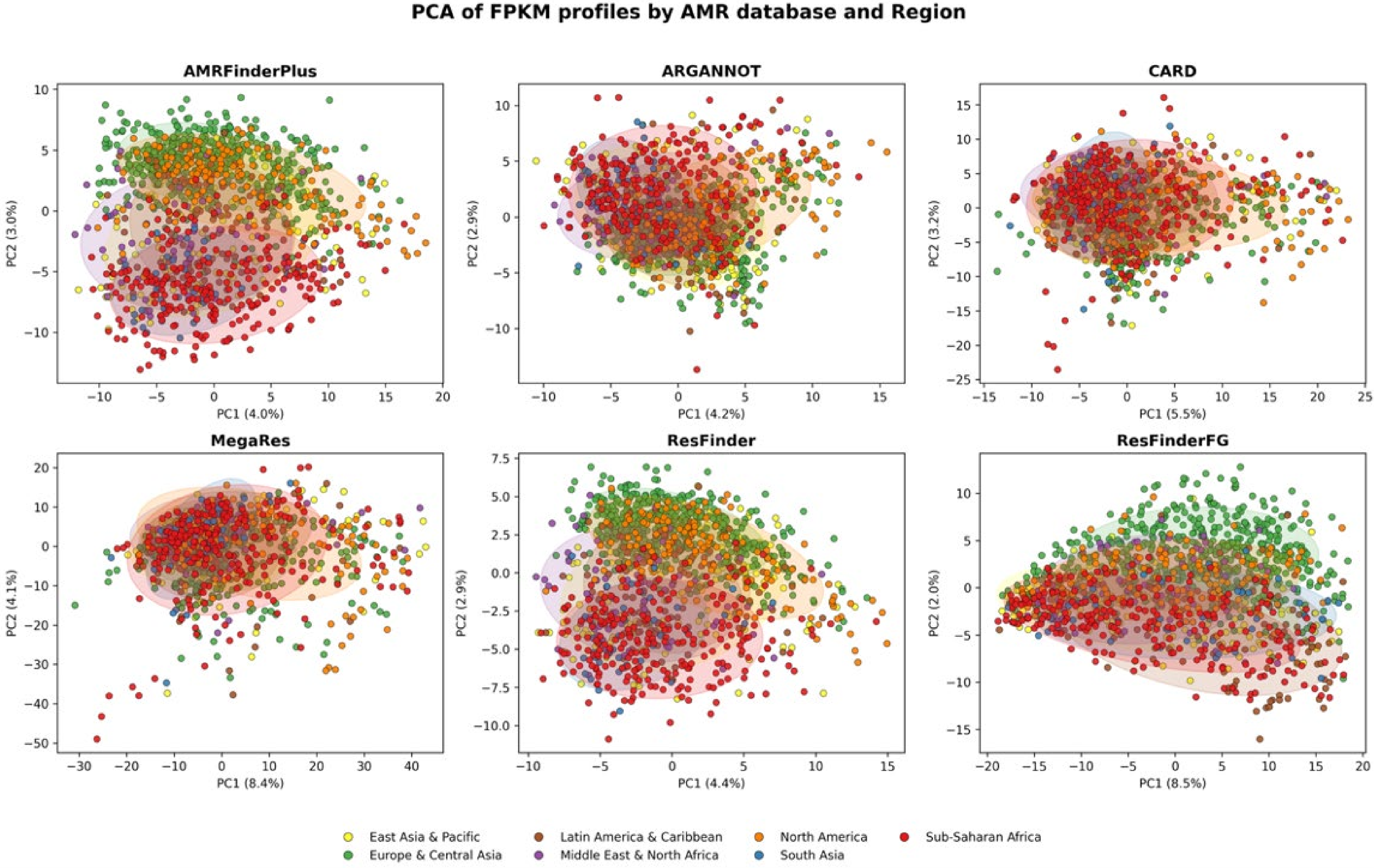
• Broad geographic abundance trends were visible

• PCA suggested partial, not complete, regional separation of sewage resistomes.

• Regional separation was visible across databases, but clearer in some than others.

• Geography influenced sewage resistome profiles, but the strength of this signal depended on the database.





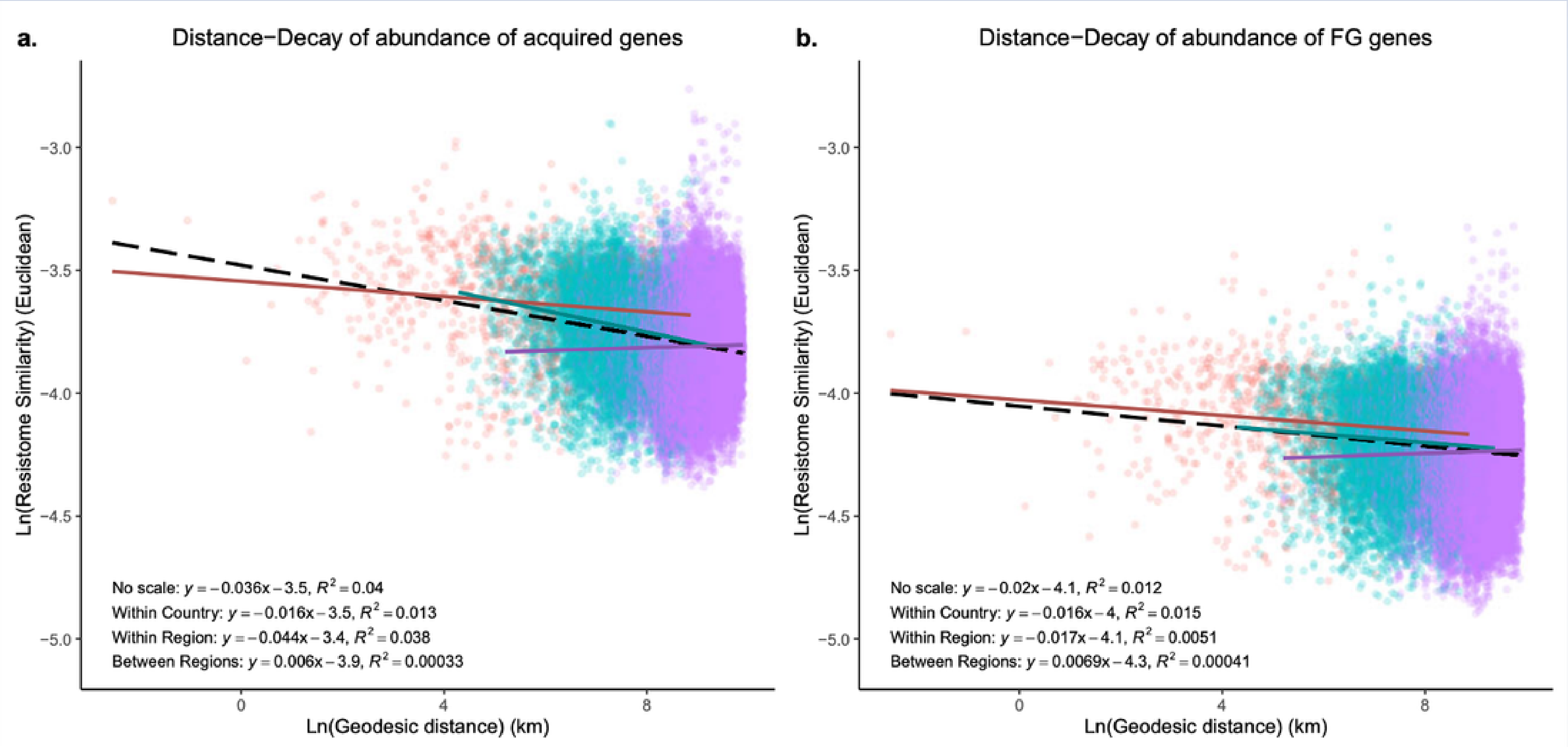
Distance -Decays

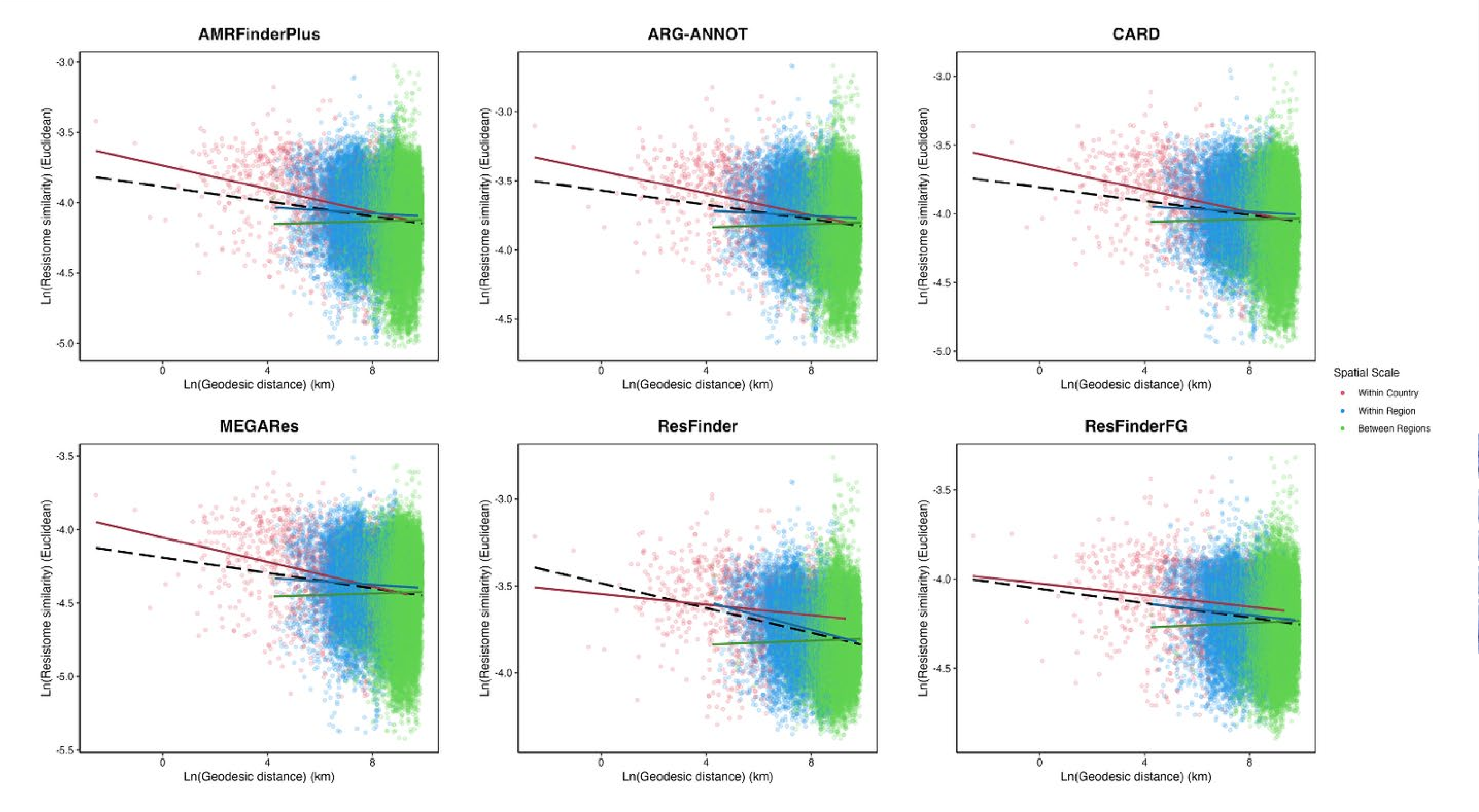
- Tests whether cities farther apart have more different sewage resistomes.

- All database subsets showed the same overall distance-decay trend.

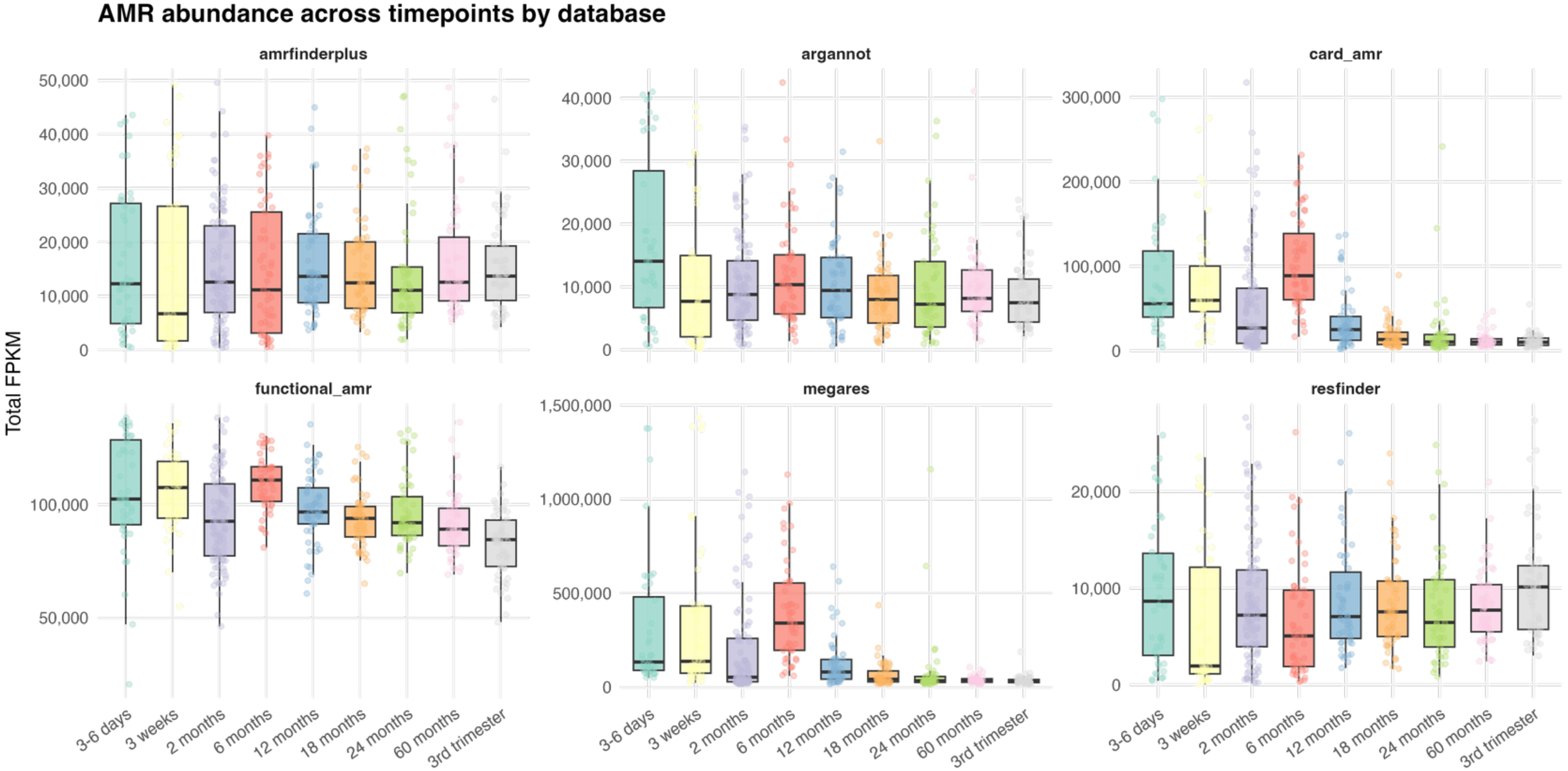
- Overall similarity decreased with distance; the trend was strongest for between-region comparisons, while within-country and within-region trends were flatter or more variable.

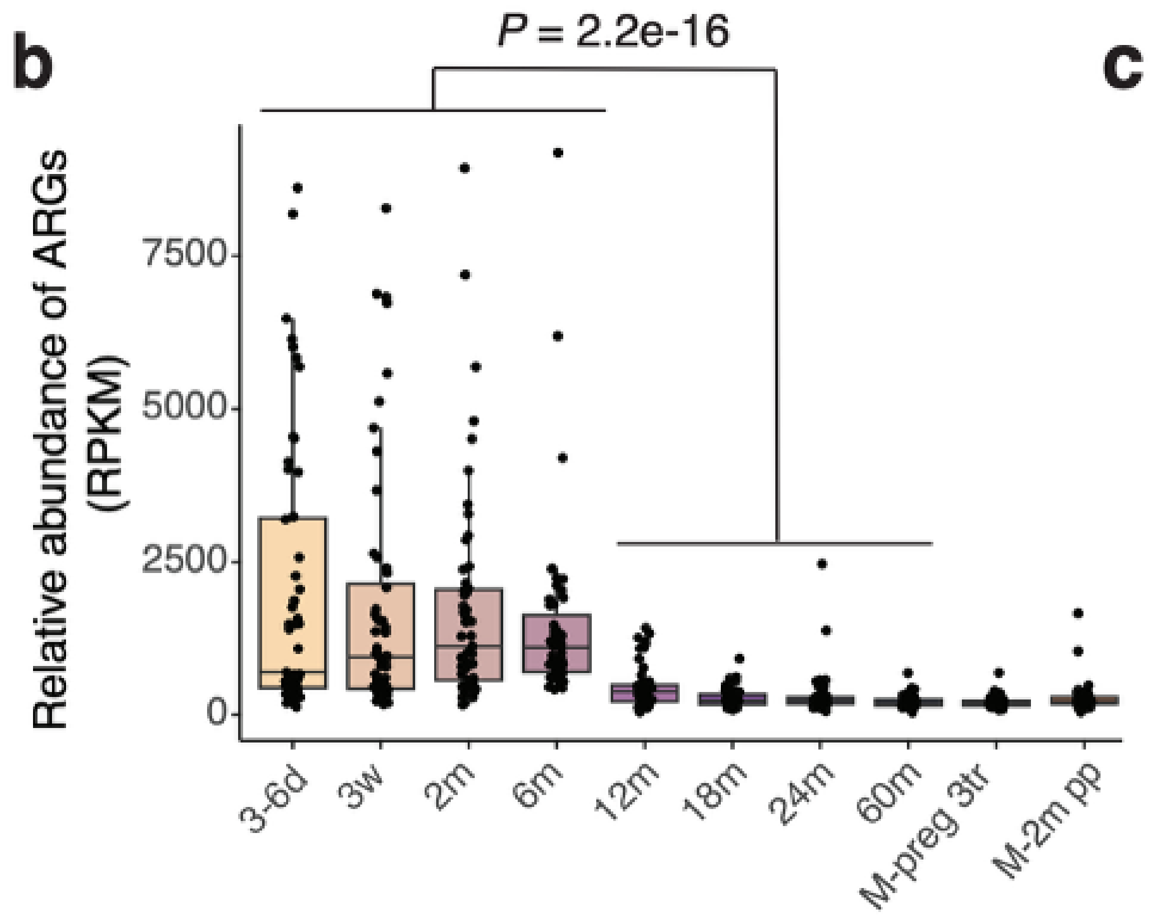
- ResFinder and ResFinderFG matched the acquired/functional ARG patterns reported in the original study.





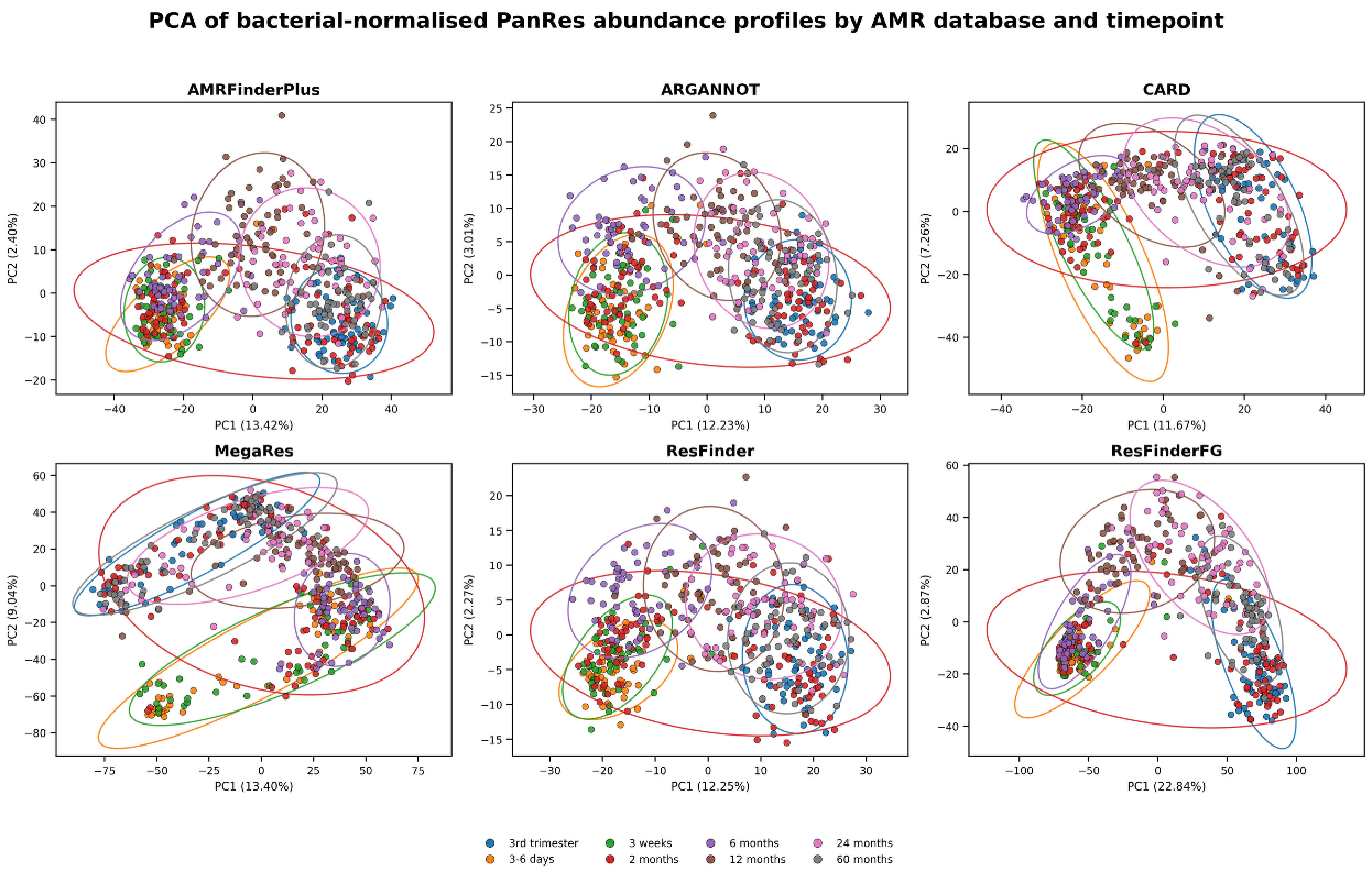
Faecal Dataset





- CARD-based abundance trend resembles the original analysis by Chatzigiannidou et al.
- ARG abundance peaks around early infancy, especially near 6 months, then declines or stabilises at later time points.
- The overall age-related trend is similar across databases, although absolute FPKM values differ.

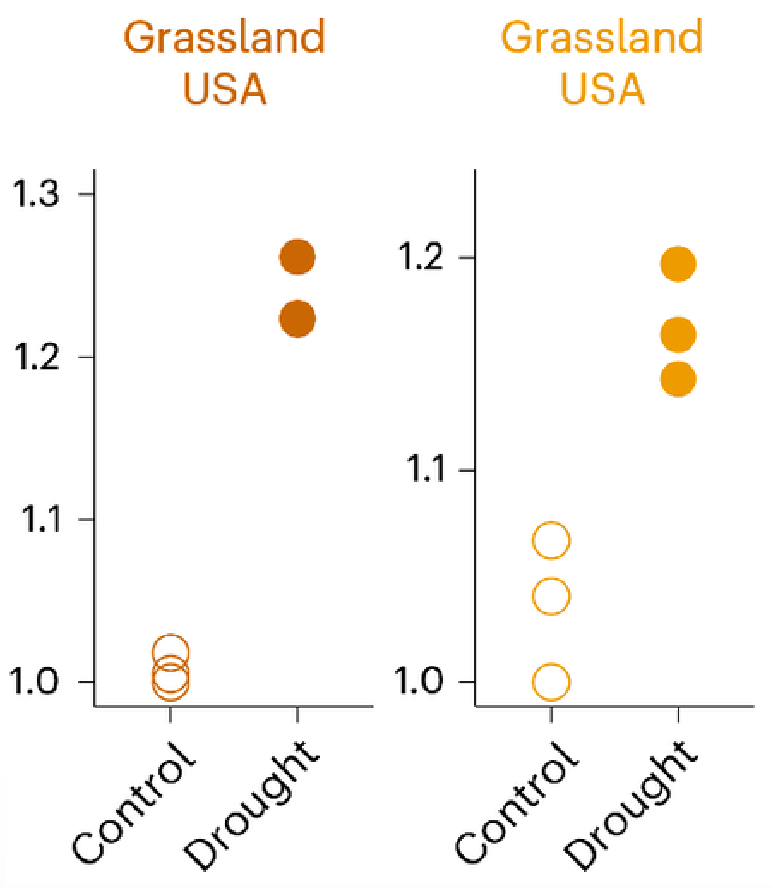
Faecal PCA

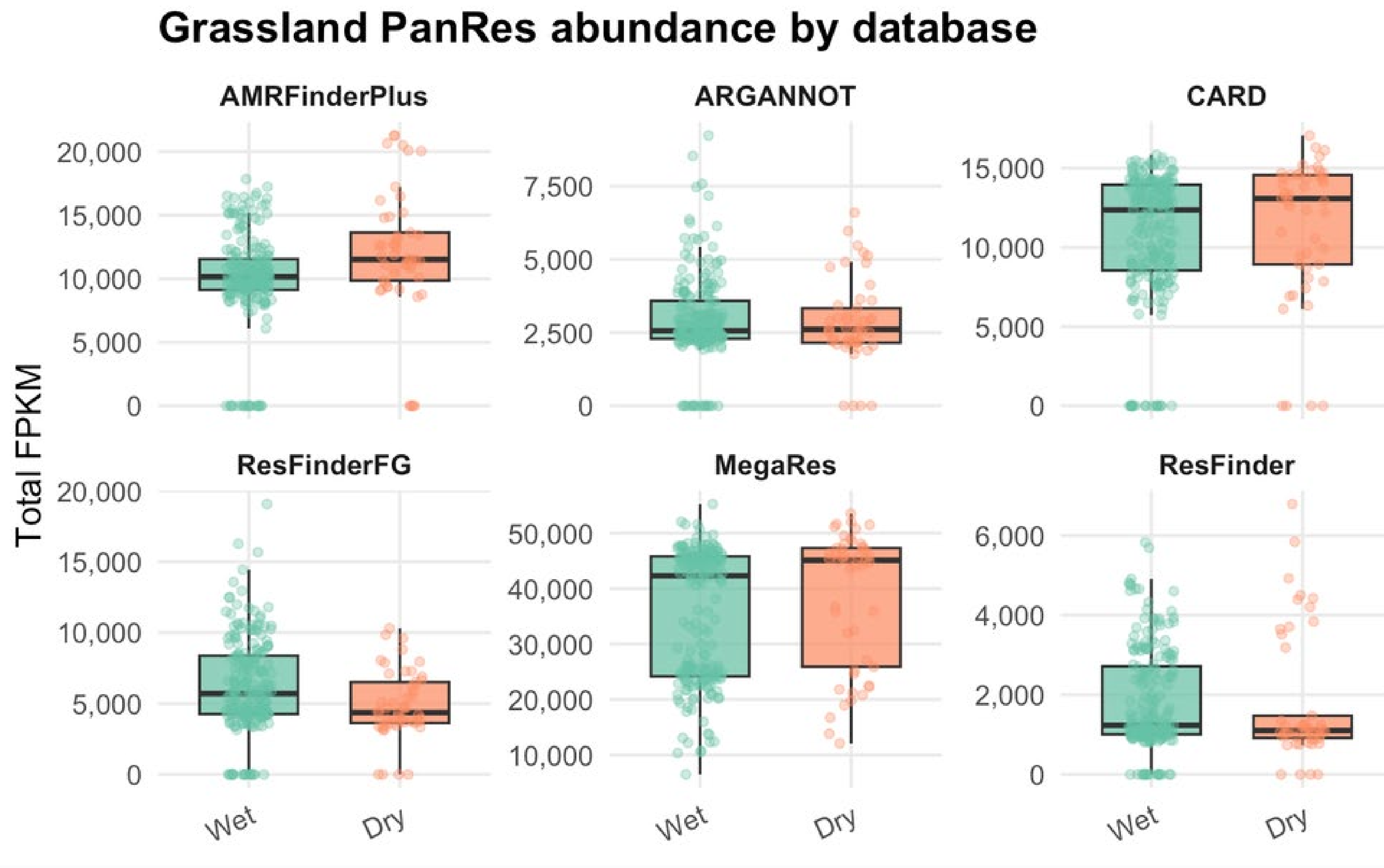


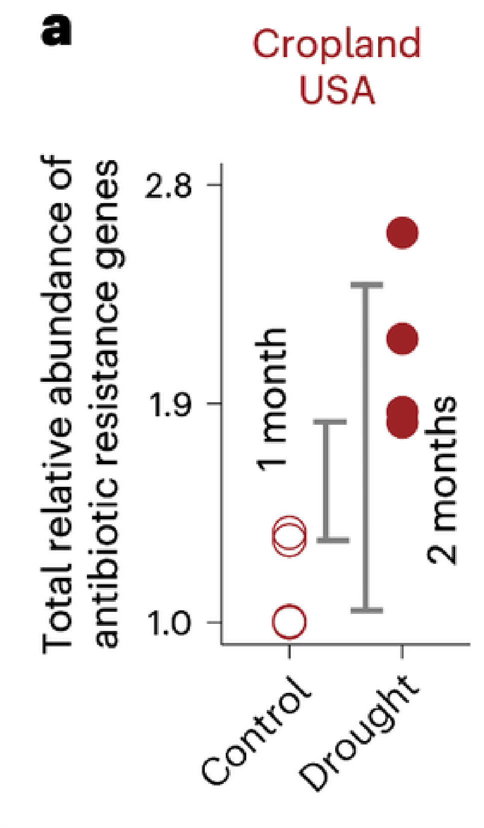
PCA of bacterial-normalised PanRes abundance profiles by AMR database and timepoint
AMRFinderPlus
ARGANNOT
CARD
MegaRes
ResFinder
ResFinderFG
PC1 (13.42%)
PC2 (2.40%)
PC1 (12.23%)
PC2 (3.01%)
PC1 (11.67%)
PC2 (7.26%)
PC1 (13.40%)
PC2 (9.04%)
PC1 (12.25%)
PC2 (2.27%)
PC1 (22.84%)
PC2 (2.87%)
3rd trimester
3-6 days
3 weeks
2 months
6 months
12 months
24 months
60 months

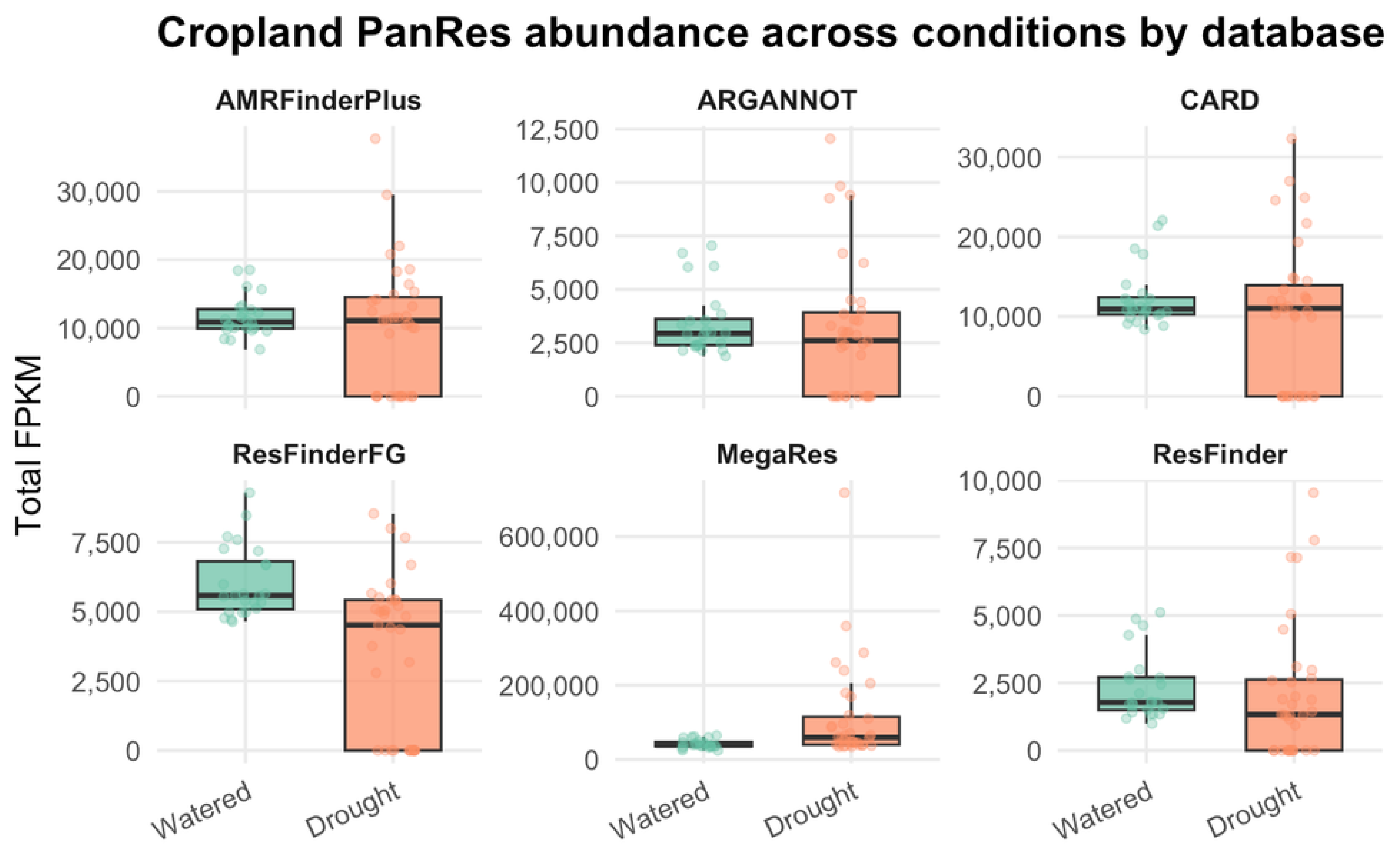
Soil Datasets

- ARG abundance patterns were broadly similar across databases, but did not reproduce the strong drought-enrichment reported previously.
- Difference likely reflects workflow: selected CARD/DIAMOND comparisons with 25 marker-gene normalisation vs broader PanRes/KMA analysis with mOTU-normalised FPKM.

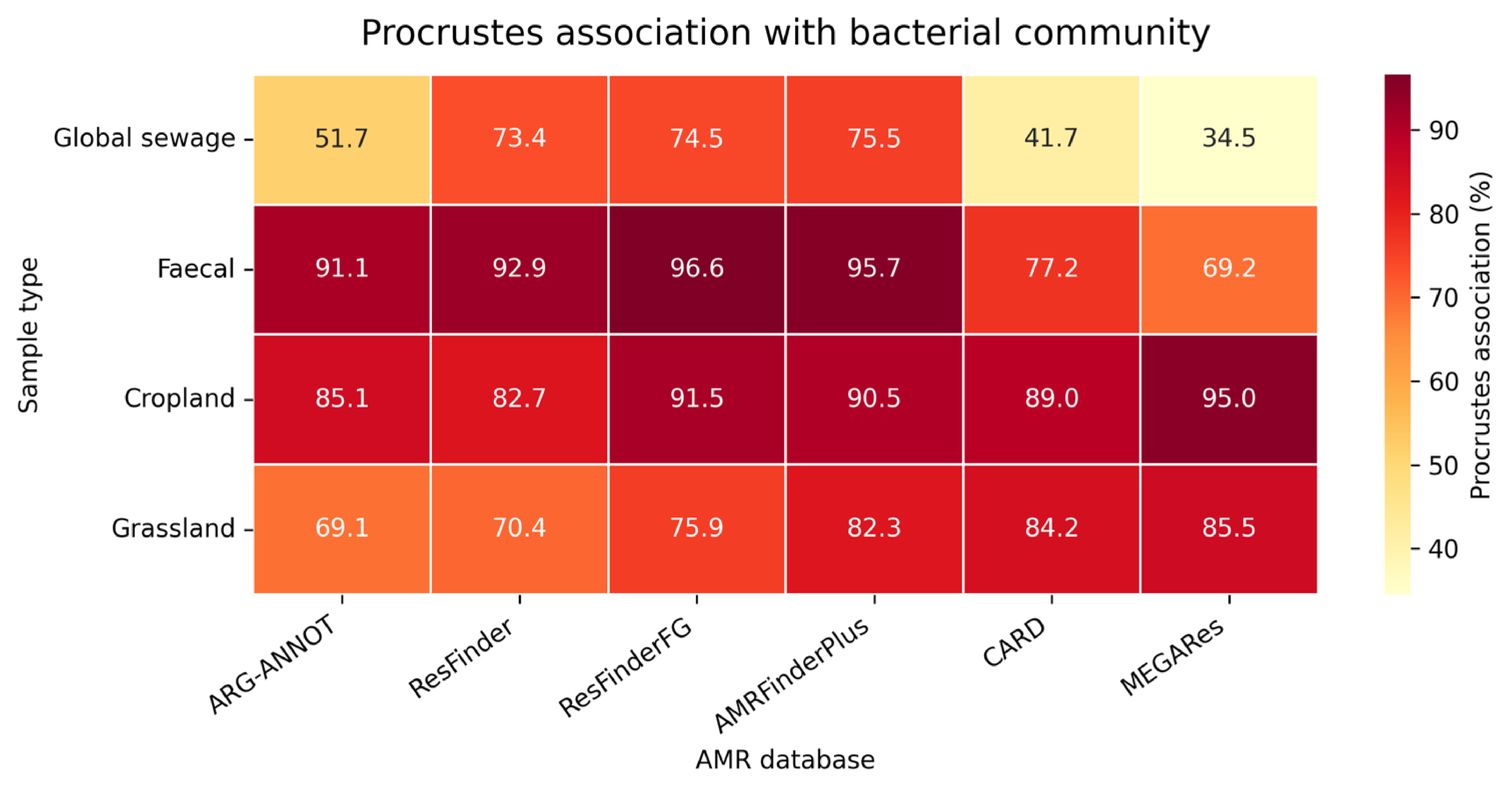








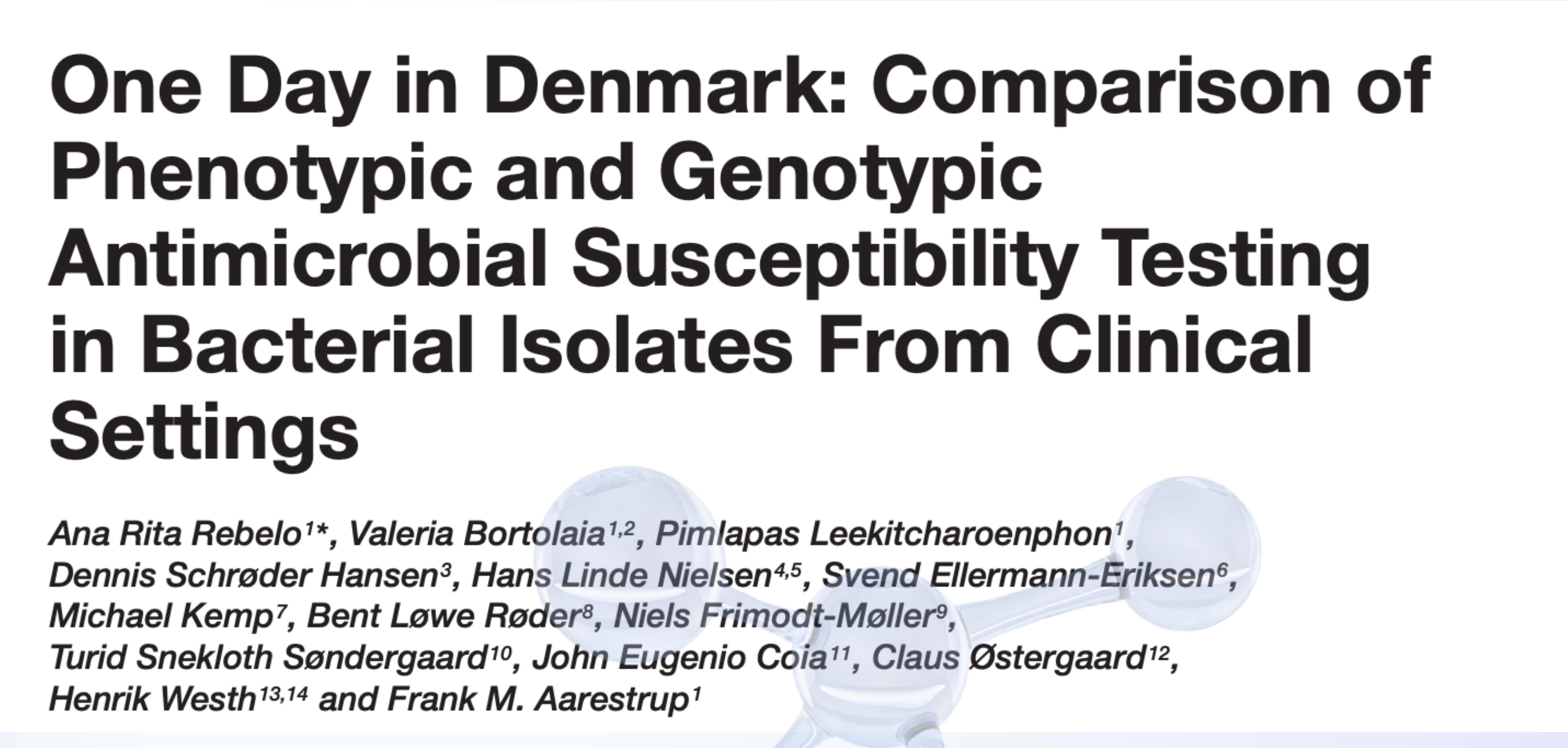
Bacterial Association / Procrustes



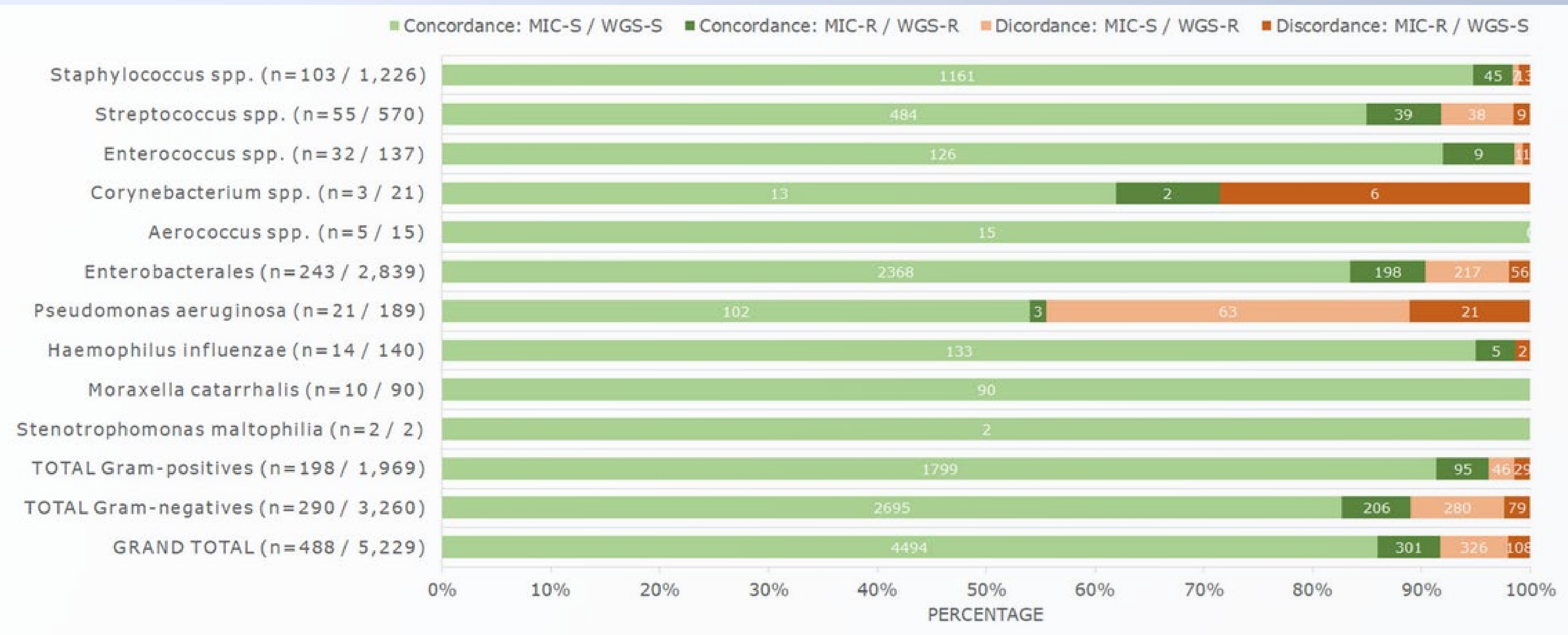
- **Global sewage**
  - Top Procrustes: AMRFinderPlus 75.5%
  - Regional clustering strongest: ResFinderFG / AMRFinderPlus
- **Faecal**
  - Top Procrustes: ResFinderFG 96.6%
  - Age clustering strongest: ResFinderFG
- **Cropland soil**
  - Top Procrustes: MEGARes 95.0%
  - Strong ARG–bacteria coupling
- **Grassland soil**
  - Top Procrustes: MEGARes 85.5%
  - Strong ARG–bacteria coupling

Whole Genome Sequencing Dataset:

One Day in Denmark


One Day in Denmark: Comparison of Phenotypic and Genotypic Antimicrobial Susceptibility Testing in Bacterial Isolates From Clinical Settings

Ana Rita Rebelo[1]*, Valeria Bortolaia[1,2], Pimlapas Leekitcharoenphon[1], Dennis Schrøder Hansen[3], Hans Linde Nielsen[4,5], Svend Ellermann-Eriksen[6], Michael Kemp[7], Bent Løwe Røder[8], Niels Frimodt-Møller[9], Turid Snekloth Søndergaard[10], John Eugenio Coia[11], Claus Østergaard[12], Henrik Westh[13,14] and Frank M. Aarestrup[1]

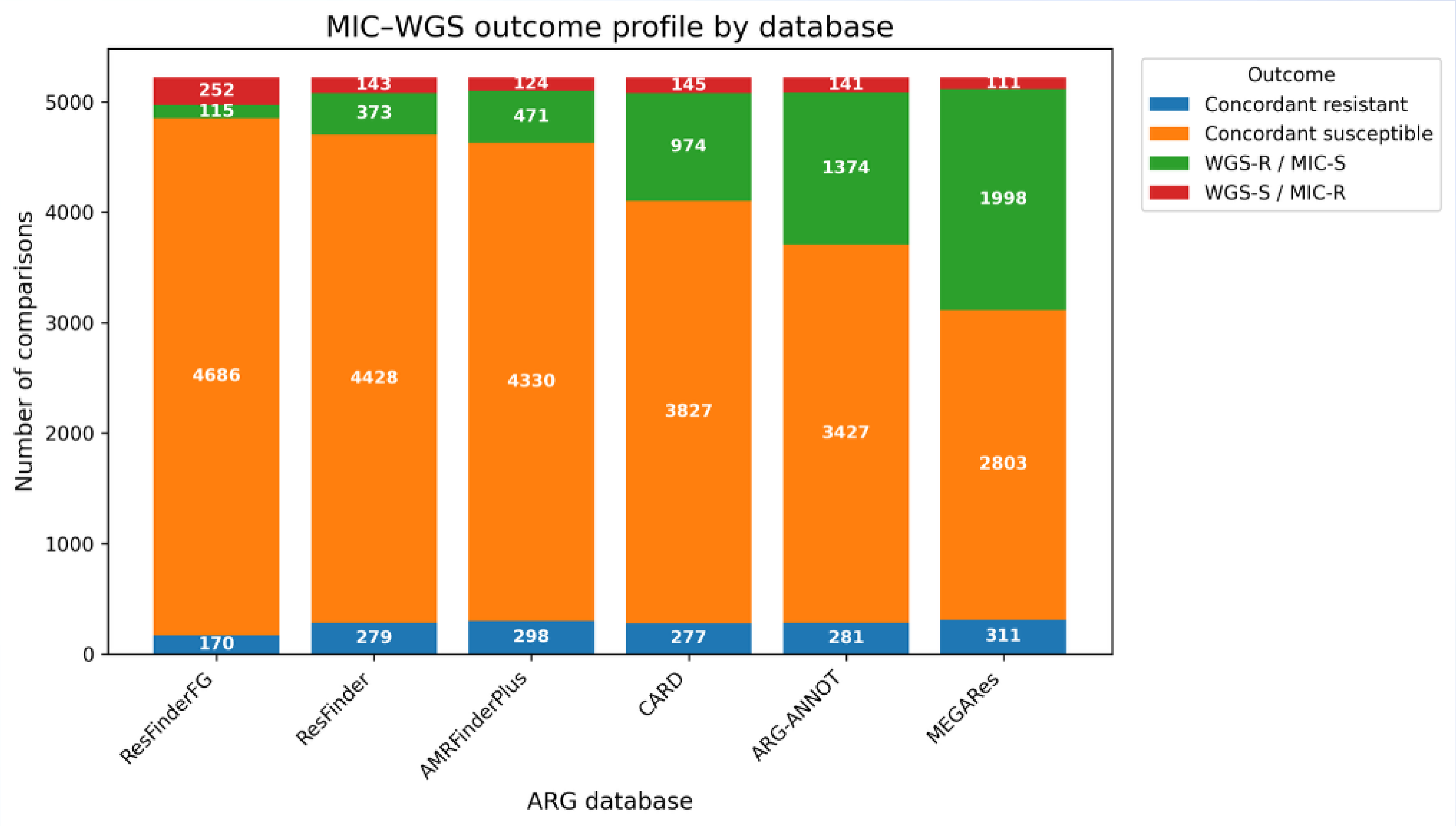


Workflow

- **Setup**
  - 2,006 isolates → BLASTn against each database
  - AST results for 488 samples (random-500 set)
  - Hits cleaned for overlaps (identity ≥ 90%, coverage ≥ 60%)

- **Genotype → phenotype pipeline**
  - Group samples by species; parse MIC tables
  - Breakpoints → MIC-S / MIC-R
  - ARG hits → WGS-S / WGS-R per database
  - Compare genotype vs phenotype → concordance
- **Final Concordances**
  - Gene-specific — WGS-R only for relevant mechanisms (β-lactams: penicillinases, ESBL/AmpC, carbapenemases, mec; dfr→trimethoprim, tet→tetracyclines, van→glycopeptides, mcr→colistin, cfr/optrA/poxtA→linezolid)

Results



Rank	Database	Final Concordance
1	ResFinderFG	92.97%
2	ResFinder	90.12%
3	AMRFinderPlus	88.61%
4	CARD	78.58%
5	ARG-ANNOT	70.99%
6	MEGARes	59.62%

- WGS paper mapped to ResFinder and achieved a final concordance of 91.7%
- Out of 557 unique ARG clusters, only 27 were shared between all 6 databases.
- ARG databases are not interchangeable, they define different versions of the resistome

References

- Chatzigiannidou, I. et al. (2025). Temporal dynamics and microbial interactions shaping the gut resistome in early infancy.*Nature Communications, 16, 8139. https://doi.org/10.1038/s41467-025-63401-6*

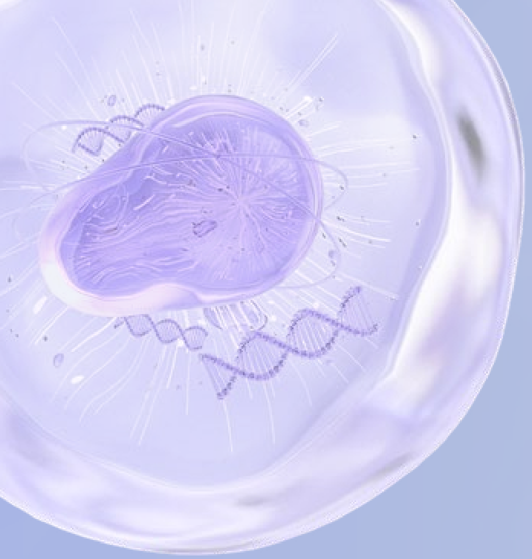
- *Martiny, H. M. et al. (2023). PanRes Collection of antimicrobial resistance genes (Version 1.0.1). Zenodo. https://doi.org/105281/zenodo.10091602*

- *Rebelo, A. R. et al. (2022). One Day in Denmark: Comparison of phenotypic and genotypic antimicrobial susceptibility testingin bacterial isolates from clinical settings. Frontiers in Microbiology, 13, 804627. https://doi.org/10.3389/fmicb.2022.804627*

- *Ferrer Florensa, A. et al. (2022). ResFinder: An open online resource for identification of antimicrobial resistance genes innext-generation sequencing data and prediction of phenotypes from genotypes. Microbial Genomics, 8(1), 000748. https://doi.org/10.1099/mgen.0.000748*

- *SILVA Project. (2024). SILVA 138.2 SSURef NR99 database. https://www.arb-silva.de/ File used: SILVA_138.2_SSURef_NR99_tax_silva_trunc.fasta.gz. Accessed 2026-04-27.*

- *Martiny, H. M. et al. (2024). ARGprofiler: A pipeline for large-scale analysis of antimicrobial resistance genes and their flanking regions in metagenomic datasets. Bioinformatics, 40(3), btae086. https://doi.org/10.1093/bioinformatics/btae086*



THANK YOU

Questions? | An Evaluation of Current Antimicrobial Resistance Databases for Resistome Analyses