

# Molecular Epidemiology of ESBL E. coli Over a 2 Year Period in Worcester Massachusetts USA

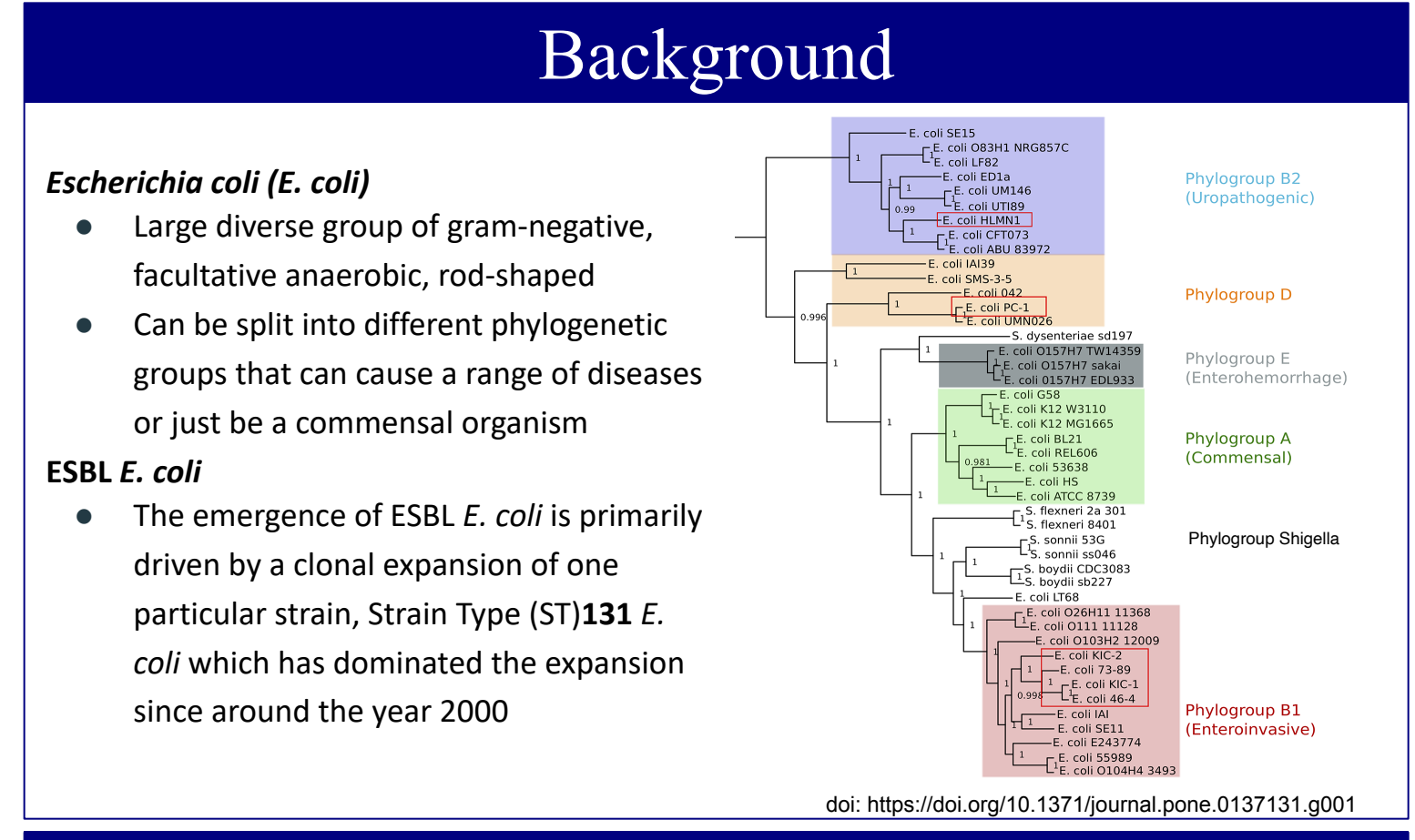


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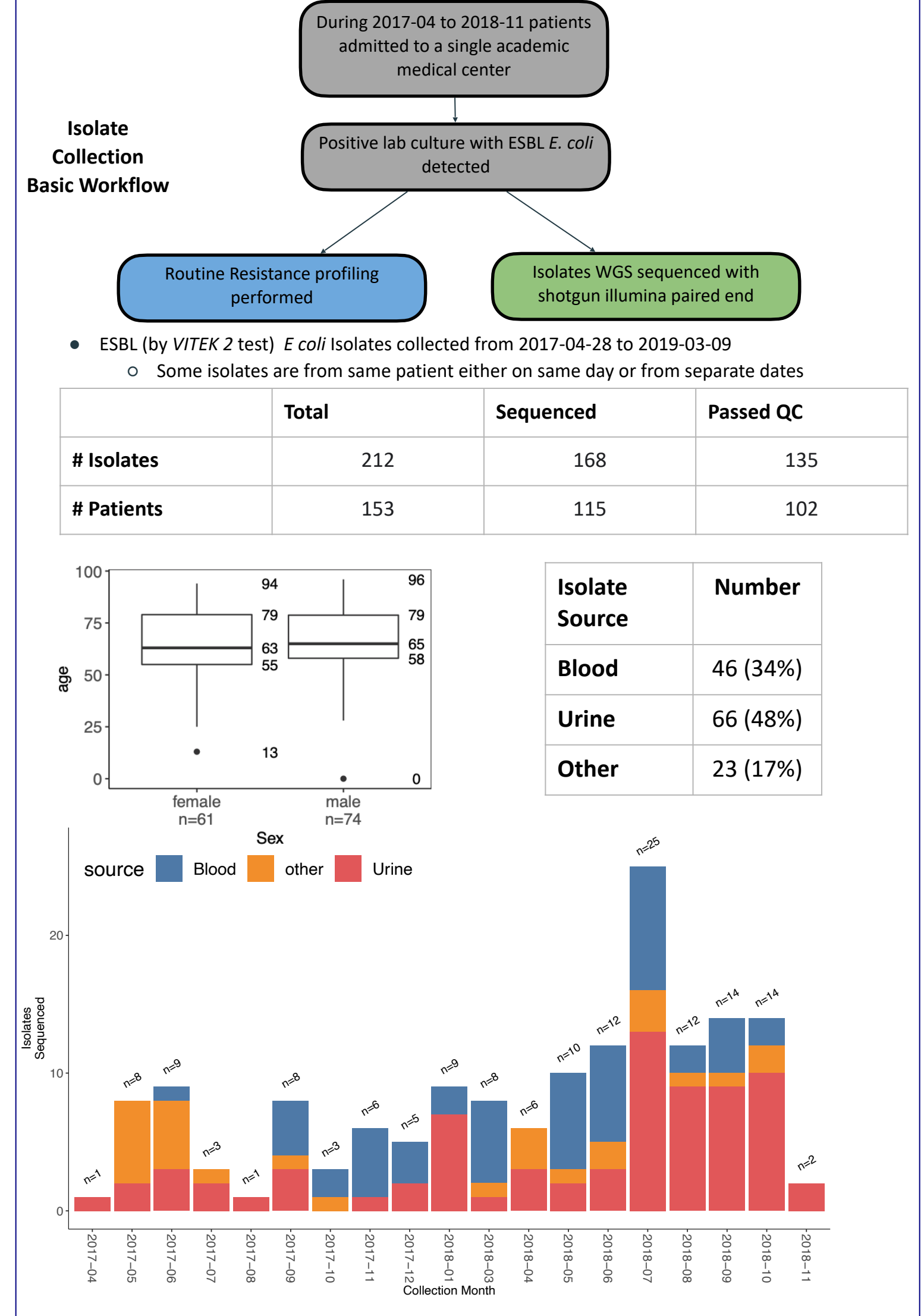


### Abstract

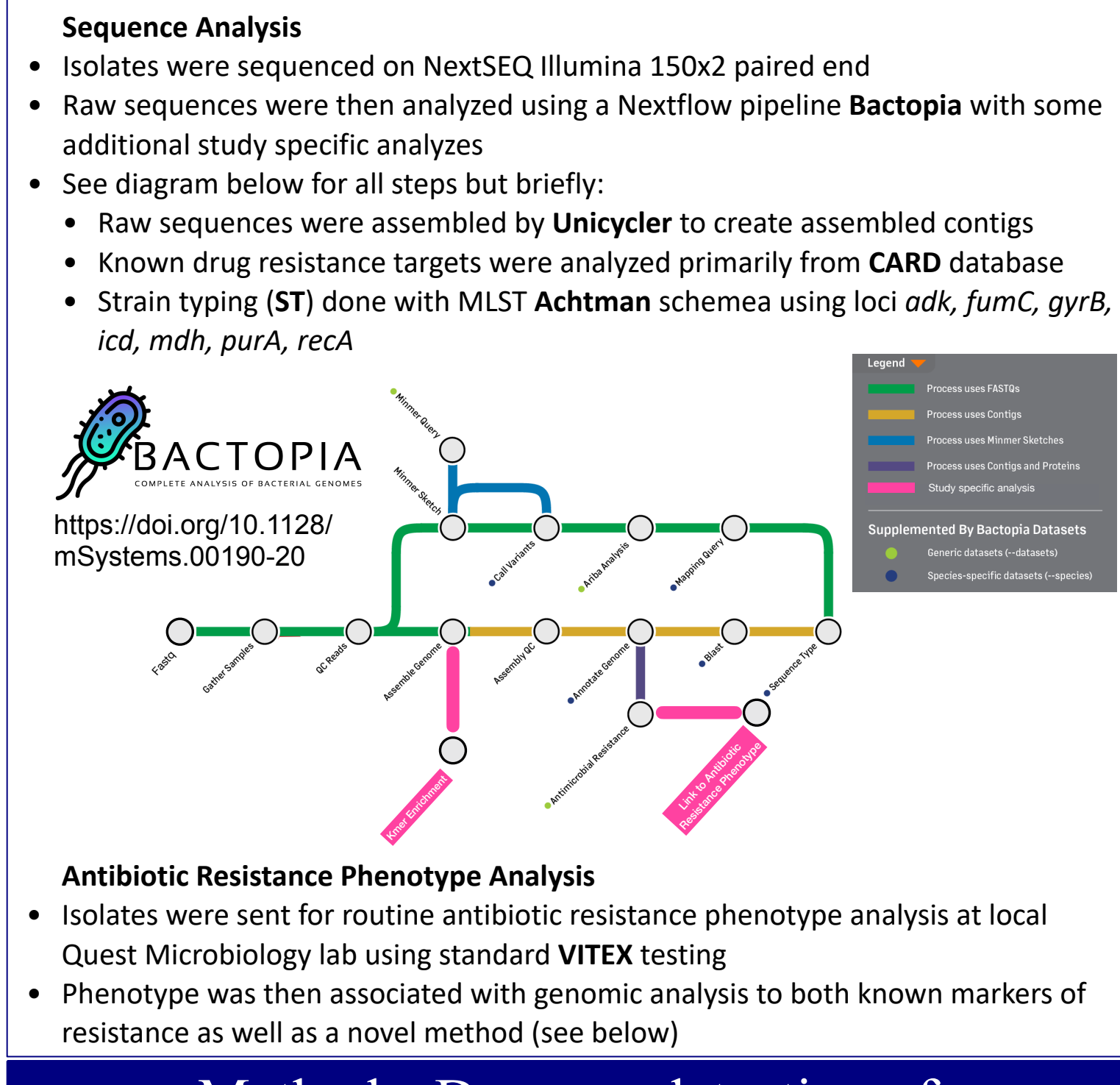
To better understand the population genomics of extended-spectrum beta-lactamase (ESBL) producing *Escherichia coli* and their associated antibiotic resistance phenotypes, 129 phenotypically identified ESBL isolates collected between 2017-04 to 2018-11 from a single academic medical center underwent whole genome sequencing (WGS) with the presence of antibiotic resistance genes identified by screening against the CARD database. The odds of phenotypic resistance to beta-lactam agents were calculated for each known resistance gene. A novel approach based on k-mer-enrichment among antibiotic resistance phenotypic groups was developed to detect genomic markers associated with phenotypic resistance. The presence of known beta-lactamase CTX-M-15 appears to increase the odds of resistance to key beta-lactam agents. A novel k-mer-enrichment approach identified a novel marker of piperacillin-tazobactam resistance



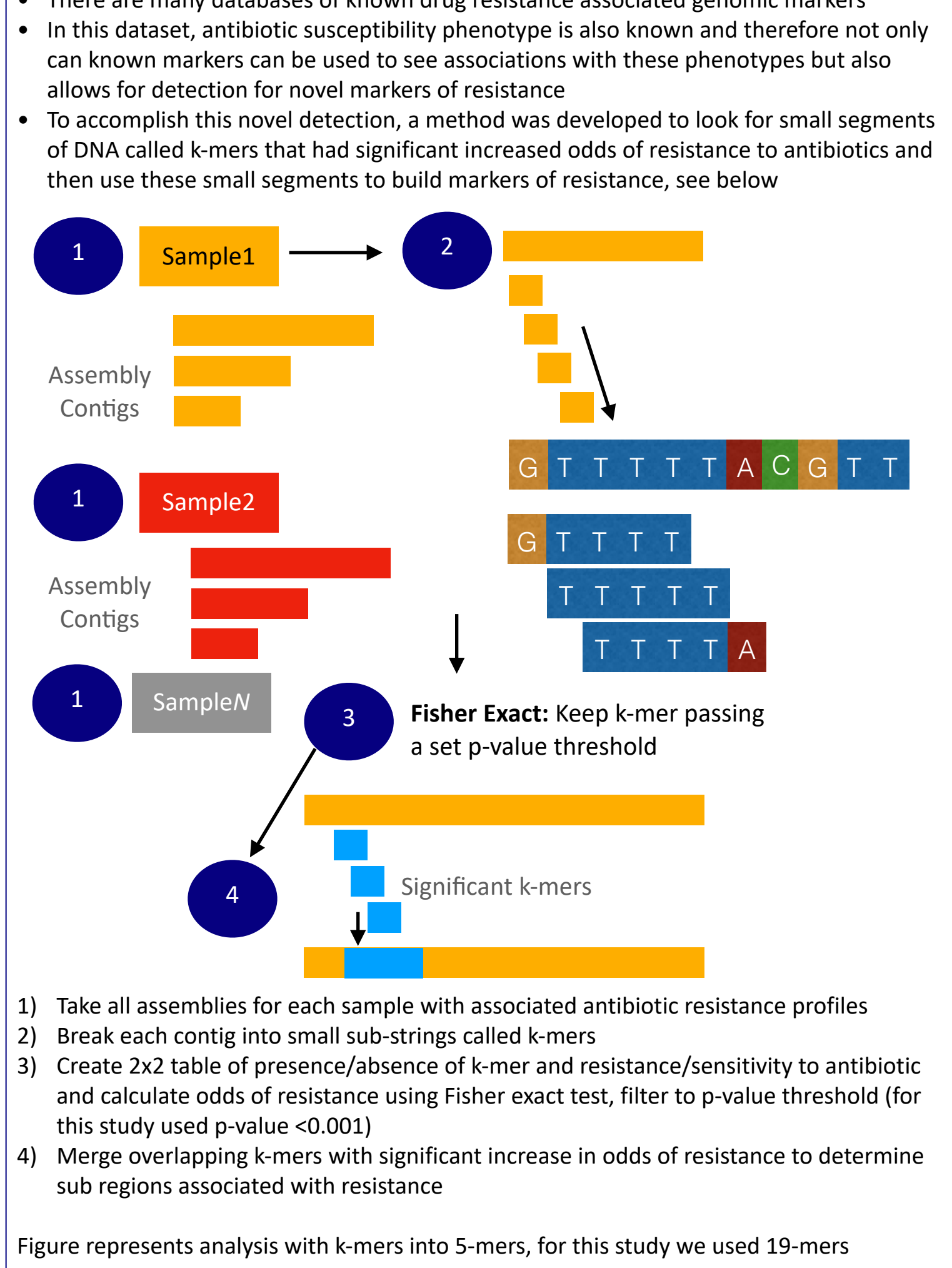
### Methods: Isolate Collection



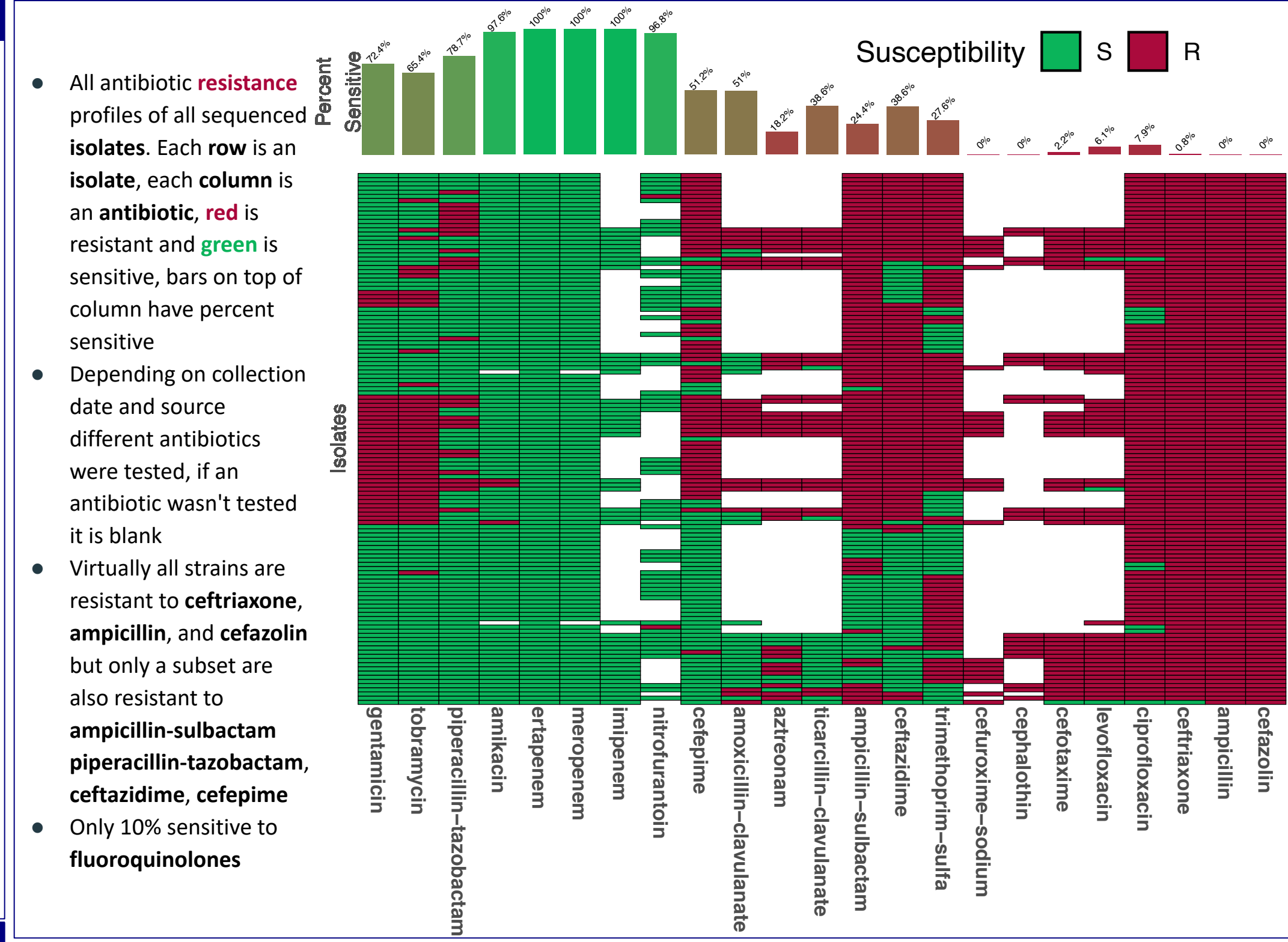
### Methods: Genomic Analysis Antibiotic Resistance Phenotype



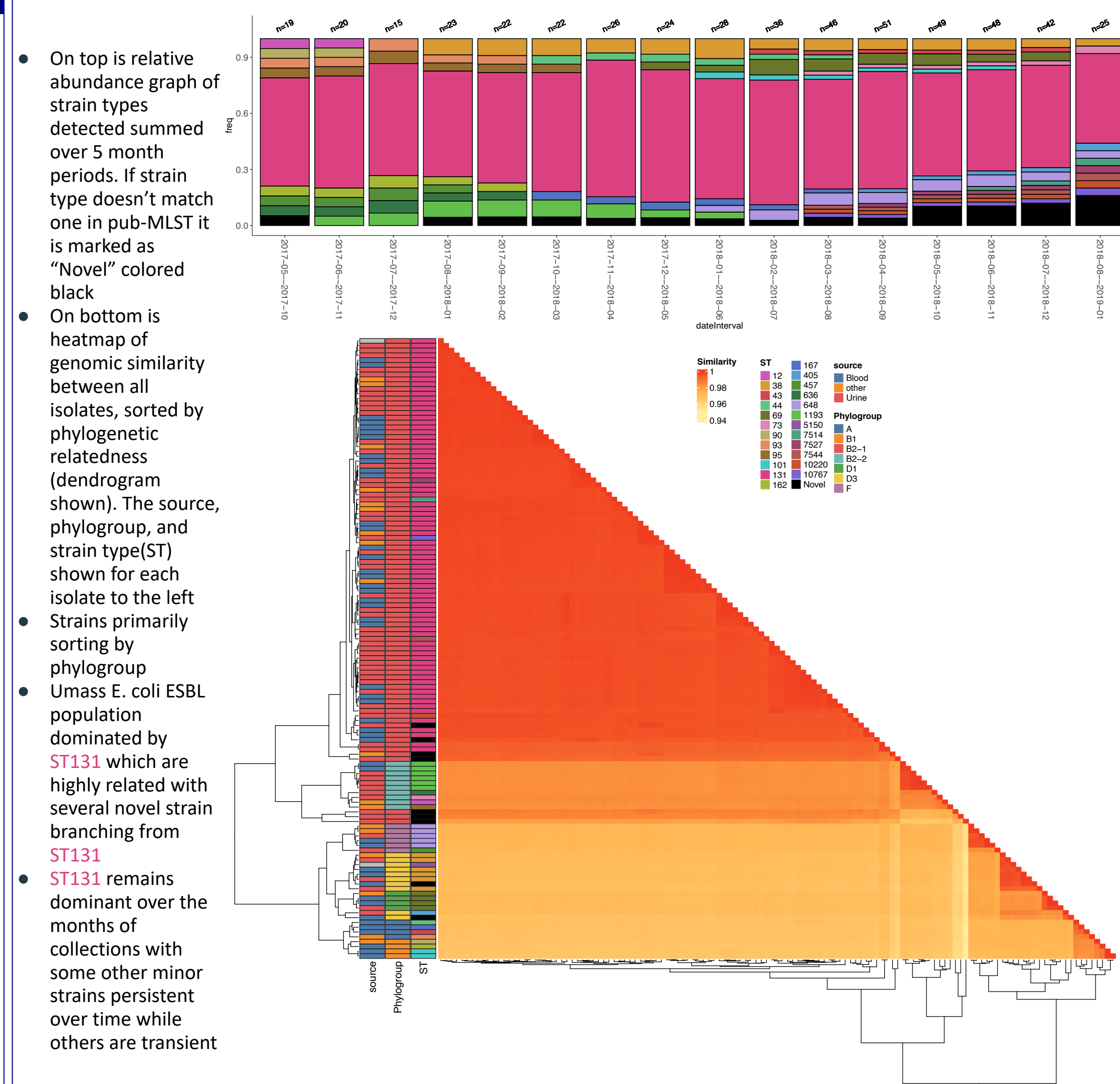
### Methods: De-novo detection of markers of antibiotic resistance



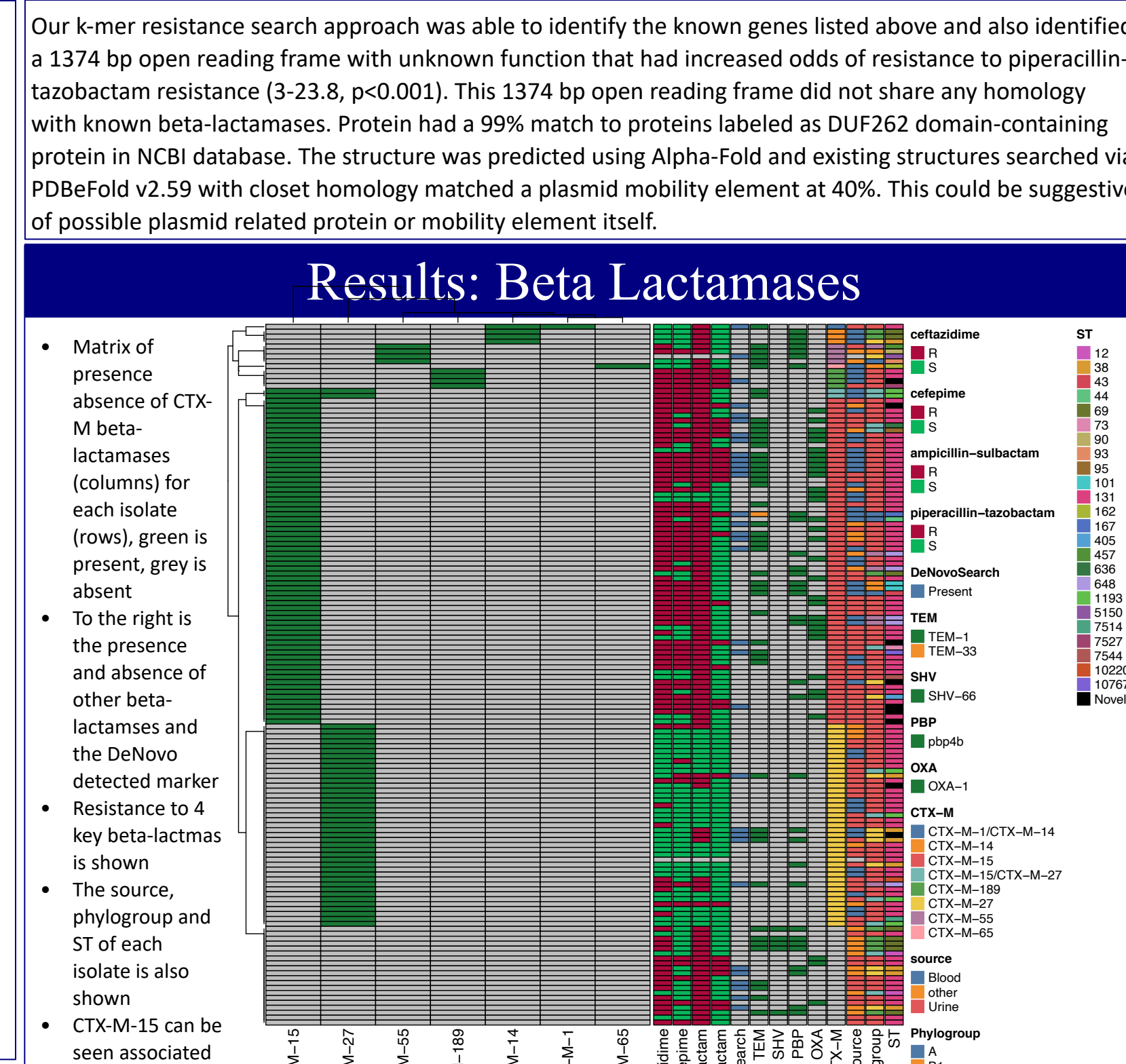
### Results: Antibiotics Profiles



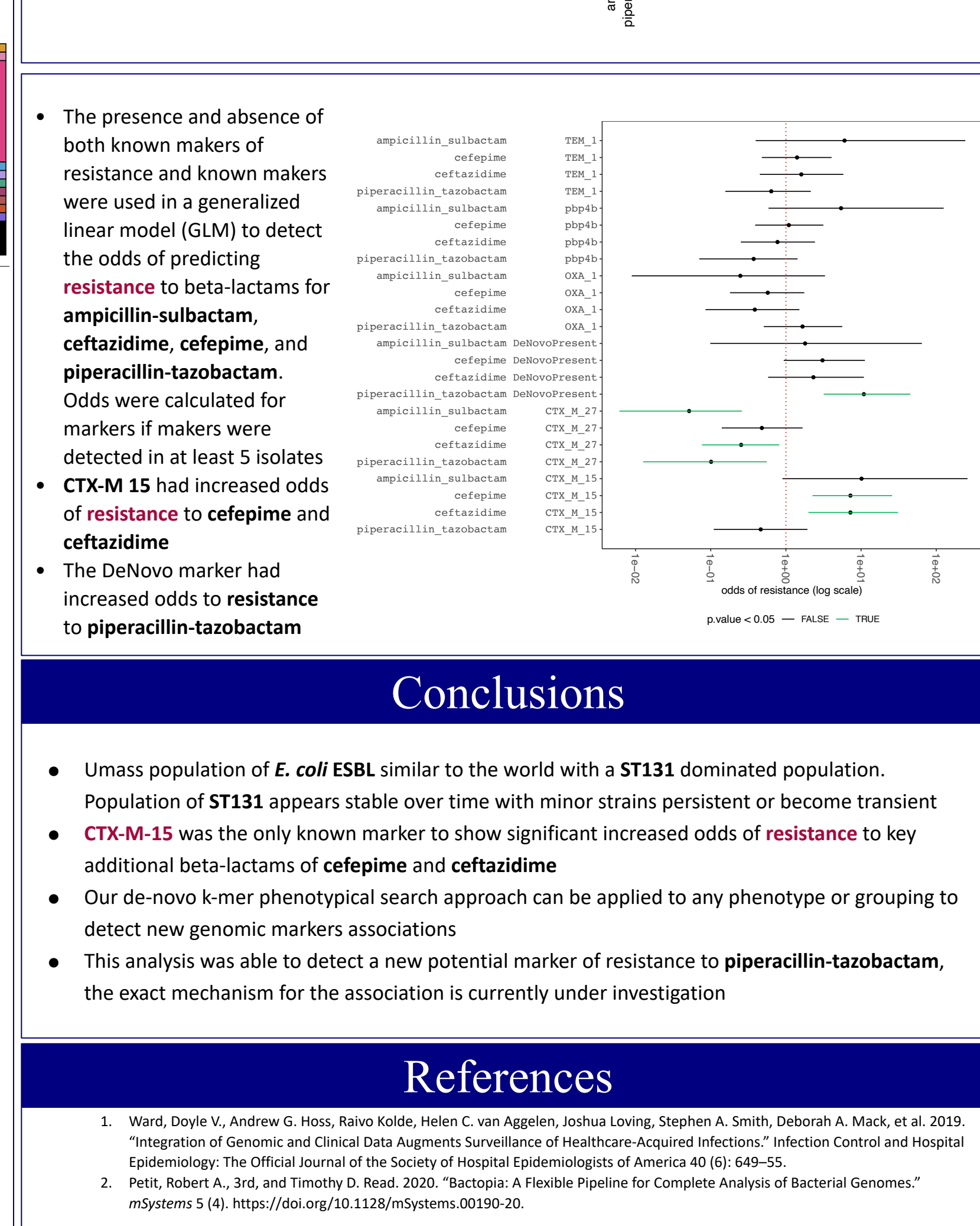
### Results: Population Structure



### Results Novel Markers Detection



### Results: Population Structure



### Conclusions

- Umass population of *E. coli* ESBL similar to the world with a **ST131** dominated population. Population of **ST131** appears stable over time with minor strains persistent or become transient
- CTX-M-15** was the only known marker to show significant increased odds of **resistance** to key additional beta-lactams of **cefepime** and **ceftazidime**
- Our de-novo k-mer phenotypic search approach can be applied to any phenotype or grouping to detect new genomic markers associations
- This analysis was able to detect a new potential marker of resistance to **piperacillin-tazobactam**, the exact mechanism for the association is currently under investigation

### References

- Ward, Doyle V., Andrew G. Hoss, Raivo Kolde, Helen C. van Aggelen, Joshua Loving, Stephen A. Smith, Deborah A. Mack, et al. 2019. "Integration of Genomic and Clinical Data Augments Surveillance of Healthcare-Acquired Infections." *Infection Control and Hospital Epidemiology: The Official Journal of the Society of Hospital Epidemiologists of America* 40 (6): 649-55.
- Petit, Robert A., 3rd, and Timothy D. Read. 2020. "Bactopia: A Flexible Pipeline for Complete Analysis of Bacterial Genomes." *mSystems* 5 (4). <https://doi.org/10.1128/mSystems.00190-20>.