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Phenotypic and Genotypic Characterization of Antimicrobial Resistance (AMR) Strains from the ATCC® Collection

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Background

Antimicrobial resistance (AMR) is a global health emergency; to counter this growing threat, researchers need access to authenticated, well-characterized strains to use as standards during the development of diagnostic assays, therapeutics, or other applications.

Here, we describe the phenotypic and genotypic characterization of **one hundred** AMR strains available in the ATCC® collection. To develop and provide this highly curated collection of AMR strains, each strain went through additional testing to establish its phenotypic and genotypic profile.

- **Susceptibility testing:** Strains were tested against a variety of critical drug classes and are provided with the minimal inhibitory concentration (MIC) values and susceptibility profile.
- **Genomic analyses:** Strains were analyzed via whole-genome sequencing (WGS) on two different instruments to ensure the highest-level of accuracy, coverage, and depth. The corresponding assembled and annotated genomes are available on the ATCC® Genome Portal (genomes.atcc.org).
- **Methylation profiles:** Most strains are provided with methylation data accessible through the ATCC® Genome Portal (genomes.atcc.org).

Methods

Susceptibility Testing

To establish the MIC profile, antibiotic susceptibility was generally obtained using VITEK 2 AST cards. We typically selected one or two cards based on the organism, aiming to cover the broadest possible range of antibiotics. MIC ranges for resistant, intermediate, and susceptible are based on criteria within the Clinical and Laboratory Standards Institute (CLSI) Performance Standards for Antimicrobial Susceptibility Testing, 27th Edition. For *Neisseria gonorrhoeae*, antibiotic susceptibility was obtained using bioMérieux ETEST strips and MIC interpretations are based on CLSI M100-Ed35.

Genomic Analyses

For genomic analyses, we used our ISO 9001-compliant standardized sequencing, assembly, and annotation pipelines for each strain. We extracted high-quality DNA and sequenced the DNA on both the Illumina (Illumina) and Oxford Nanopore Technologies (ONT; Oxford Nanopore Technologies) instruments. The data were analyzed for quality and then both data sets were combined to produce a complete *de novo* hybrid assembly. All *de novo* assemblies were then annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) and further curated for AMR-related genes using NCBI AMRFinderPlus, the Comprehensive Antibiotic Resistance Database through the Resistance Gene Identifier software (RGI-CARD; McMaster University), and ResFinder (Technical University of Denmark). The whole-genome sequences are available on the ATCC® Genome Portal.

Methylation Profiles

Methylation profiles were generated with ONT data using the Dorado basecaller version 0.8.0+acec121 (ONT). The methylation profile for many strains are available to customers through the ATCC® Genome Portal.

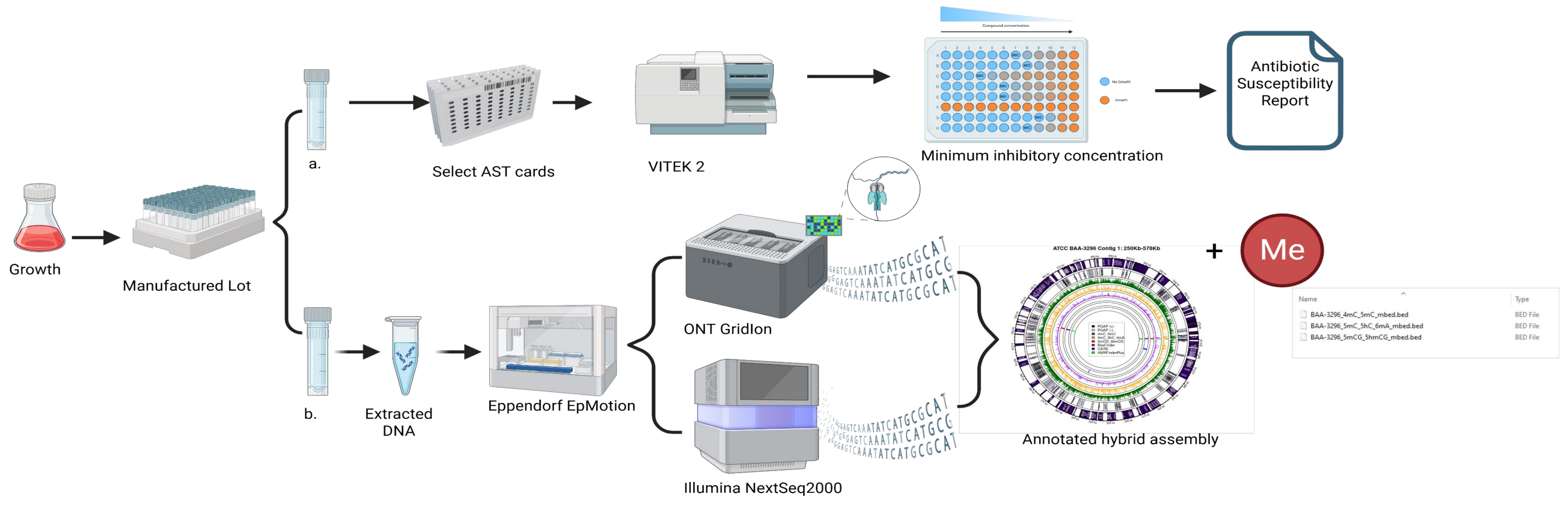
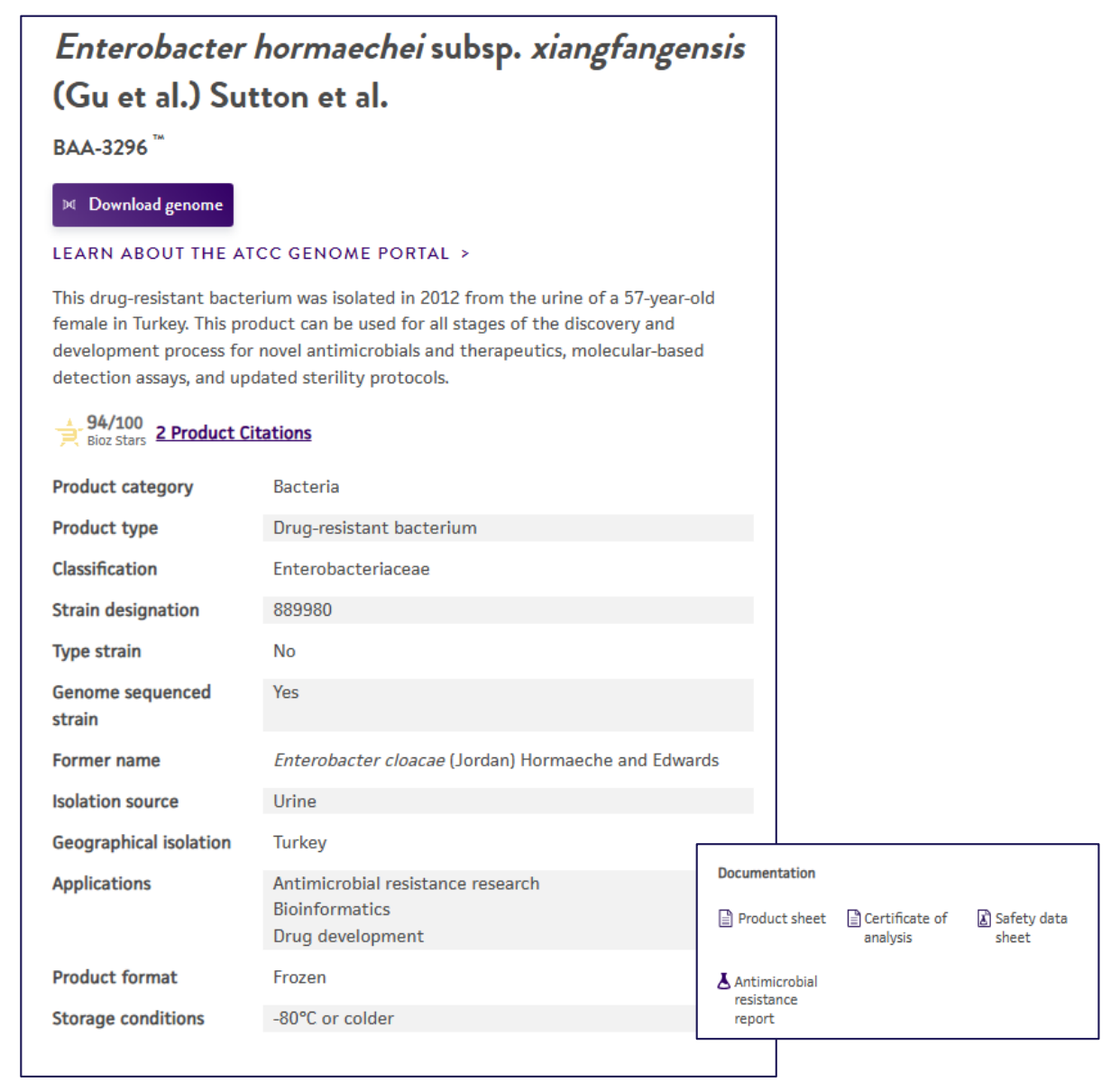


Figure 1: Bacterial strains are grown, vialed, and QC'd according to ATCC® parameters. (A) The appropriate VITEK 2 AST cards (bioMérieux) are selected and loaded on to the VITEK 2 instrument to produce the MIC profile. Note: for *Neisseria gonorrhoeae*, antibiotic susceptibility was obtained using ETEST strips (bioMérieux). (B) DNA is extracted using a method best suited for organism type and next-generation sequencing (NGS) libraries are produced and loaded on the NextSeq 2000 (Illumina) and GridIon (Oxford Nanopore Technologies) instruments. Data from both platforms were QC'd and a subsequent hybrid genome assembly was produced and annotated. ONT base called data was further analyzed for the presence of methylated nucleotides. Image created using BioRender.com

Results

Table 1: Species diversity of antimicrobial-resistant strains

Species	Strains	VITEK 2 Card(s) or ETEST strips	Gram stain
Acinetobacter baumannii	13	AST-XN09 and AST-GN69	Negative
Citrobacter braakii	1	AST-XN09 and AST-GN69	Negative
Citrobacter freundii	4	AST-XN09 and AST-GN69	Negative
Enterobacter asburiae	1	AST-XN09 and AST-GN69	Negative
Enterobacter cloacae	3	AST-XN09 and AST-GN69	Negative
Enterobacter hormaechei	2	AST-XN09 and AST-GN69	Negative
Escherichia coli	17	AST-XN09 and AST-GN69	Negative
Klebsiella oxytoca	1	AST-XN09 and AST-GN69	Negative
Klebsiella pneumoniae	14	AST-XN09 and AST-GN69	Negative
Klebsiella quasipneumoniae	2	AST-XN09 and AST-GN69	Negative
Neisseria gonorrhoeae	5	BioMerieux Etest strips	Negative
Proteus mirabilis	3	AST-XN09 and AST-GN69	Negative
Pseudomonas aeruginosa	15	AST-GN69 and AST-XN06	Negative
Pseudomonas paraeruginosa	1	AST-GN69 and AST-XN06	Negative
Serratia surfactantfaciens	1	AST-GN69 and AST-XN06	Negative
Staphylococcus aureus	2	AST-GP72 and AST-GP75	Positive
Streptococcus pneumoniae	15	AST-ST02	Positive


Enterobacter hormaechei subsp. *xiangfangensis* (Gu et al.) Sutton et al.
BAA-3296™

This drug-resistant bacterium was isolated in 2012 from the urine of a 57-year-old female in Turkey. This product can be used for all stages of the discovery and development process for novel antimicrobials and therapeutics, molecular-based detection assays, and updated sterility protocols.

Product category	Bacteria
Product type	Drug-resistant bacterium
Classification	Enterobacteriaceae
Strain designation	889980
Type strain	No
Genome sequenced strain	Yes
Former name	*Enterobacter cloacae* (Jordan) Hormaeche and Edwards
Isolation source	Urine
Geographical isolation	Turkey
Applications	Antimicrobial resistance research Bioinformatics Drug development
Product format	Frozen
Storage conditions	-80°C or colder

Figure 2: **Example of product page with metadata and available documentation.**

Table 2: MIC values and interpretations of 16 *Klebsiella* spp.

	ATCC® Catalog Number →	BAA-3267™	BAA-3272™	BAA-3258™	BAA-3266™	BAA-3256™	BAA-3264™	BAA-3268™	BAA-3265™	BAA-3269™	BAA-3273™	BAA-3318™	BAA-3297™	BAA-3298™	BAA-3319™	BAA-3309™	BAA-3308™
Antibiotics	**Antibiotic class**								***Klebsiella* spp.**								
Amikacin	Aminoglycosides	≥64 (R)	≥64 (R)	32 (I)	≥64 (R)	≥64 (R)	≥64 (R)	16 (S)	≥64 (R)	≤2 (S)	≤2 (S)	≤2 (S)	≤2 (S)	8 (S)	≥64 (R)	16 (S)	≤2 (S)
Gentamicin	Aminoglycosides	4 (S)	2 (S)	≤1 (S)	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	≤1 (S)	8 (I)	≤1 (S)	≥16 (R)	≥16 (R)	4 (S)	≥16 (R)	≥16 (R)
Tobramycin	Aminoglycosides	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	8 (I)	8 (I)	8 (I)	≥16 (R)	≤16 (R)	≥16 (R)	≥16 (R)	≤0.5 (S)
Ertapenem	Carbapenems	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	4 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≤0.5 (S)	≤0.5 (S)	≥8 (R)	≤0.5 (S)	4 (R)
Imipenem	Carbapenems	8 (I)	≥16 (R)	≥16 (R)	8 (I)	≥16 (R)	≥16 (R)	0.5 (S)	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	1 (S)	≤0.25 (S)	≤0.25 (S)	≤0.25 (S)	≥16 (R)
Meropenem	Carbapenems	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	1 (S)	≤0.25 (S)	8 (I)	≤0.25 (S)	≥16 (R)
Cefalotin	Cephalosporin	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)
Cefazolin	Cephalosporin	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)
Cefepime	Cephalosporin	8 (S)	≥64 (R)	8 (S)	16 (I)	8 (S)	8 (S)	2 (S)	≥64 (R)	≥64 (R)	≥64 (R)	4 (S)	4 (R)	≥8 (R)	32 (R)	≤1 (S)	2 (S)
Cefotaxime	Cephalosporin	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	32 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	16 (R)	≥64 (R)
Cefotetan	Cephalosporin	16 (S)	≥64 (R)	8 (S)	32 (I)	32 (I)	16 (S)	≤4 (S)	≥64 (R)	≥64 (R)	≥64 (R)	4 (S)	≤4 (S)	≤4 (S)	≤4 (S)	≤4 (S)	≥64 (R)
Cefoxitin	Cephalosporin	32 (R)	≥64 (R)	32 (R)	≥64 (R)	≥64 (R)	32 (R)	32 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≤64 (R)	16 (I)	≤4 (S)	32 (R)	≥64 (R)	≥64 (R)
Cefpodoxime	Cephalosporin	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)
Ceftazidime	Cephalosporin	≥64 (R)	32 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	16 (R)	≤64 (R)	≥64 (R)	16 (I)	≥64 (R)
Ceftazidime/Avibactam	Cephalosporin	≤0.12 (S)	≥16 (R)	0.5 (S)	≤0.12 (S)	0.5 (S)	0.5 (S)	≤0.12 (S)	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	0.5 (S)	1 (S)	0.5 (S)	0.25 (S)	0.5 (S)
Ceftriaxone	Cephalosporin	≥64 (R)	≥64 (R)	32 (I)	≥64 (R)	≥64 (R)	≥64 (R)	16 (I)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	32 (I)	8 (S)	≥64 (R)
Cefuroxime	Cephalosporin	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥32 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)
Cefuroxime Axetil	Cephalosporin	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)
Ceftolozane/Tazobactam	Cephalosporin	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32(R)	≥32 (R)	≥32 (R)	≤0.25 (S)	≥32 (R)
Trimethoprim-sulfamethoxazole	Diaminopyrimidines	40 (S)	≤20 (S)	≤20 (S)	≥320 (R)	≥320 (R)	≥320 (R)	80 (R)	≥320 (R)	≥320 (R)	80 (R)	≥320 (R)	≥320 (R)	≥320 (R)	≥320 (R)	≥320 (R)	≤20 (S)
Ciprofloxacin	Fluoroquinolones	≥4 (R)	≥4 (R)	≥4 (R)	≥4 (R)	≥4 (R)	≥4 (R)	≥4 (R)	≥4 (R)	2 (I)	≥4 (R)	≤0.25 (S)	≥4 (R)	≥4 (R)	≥4 (R)	2 (I)	2 (I)
Levofloxacin	Fluoroquinolones	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	1 (S)	≥8 (R)	≤0.12 (S)	4 (I)	≥8 (R)	≥8 (R)	2 (S)	≥8 (R)
Moxifloxacin	Fluoroquinolones	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	2 (S)	≥8 (R)	≤0.25 (S)	≥8 (R)	≥8 (R)	≥8 (R)	2 (S)	≥8 (R)
Tigecycline	Glycylcyclines	1 (S)	4 (I)	2 (S)	≥8 (R)	1 (S)	1 (S)	≥8 (R)	≤0.5 (S)	2(S)	4 (I)	≤0.5 (S)	4 (I)	≤0.5 (S)	2 (S)	≤0.5 (S)	≥16 (R)
Aztreonam	Monobactam	≥64 (R)	≤1 (S)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	16 (I)	≥64 (R)	≥64 (R)	≥64 (R)	32 (R)	≥64 (R)
Nitrofurantoin	Nitrofuran	256 (R)	256 (R)	256 (R)	256 (R)	256 (R)	256 (R)	256 (R)	256 (R)	≤16 (S)	256 (R)	64 (I)	64 (I)	256 (R)	256 (R)	64 (I)	128 (R)
Amoxicillin/Clavulanic Acid	Penicillin	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	16 (I)
Ampicilin/Sultbactam	Penicillin	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)
Ampicillin	Penicillin	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)
Piperacillin/Tazaobactam	Penicillin	≥128 (R)	≥128 (R)	≥128 (R)	≥128 (R)	≥128 (R)	≥128(R)	≥128 (R)	≥128 (R)	≥128 (R)	≥128 (R)	≥128 (R)	≥128 (R)	≥128 (R)	≥128 (R)	16 (S)	≥128 (R)
Nalidixic Acid	Quinolone	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	8 (R)	≥32 (R)	≤2 (S)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)	≥32 (R)
Tetracycline	Tetracyclines	4 (S)	8 (I)	4 (S)	≥16 (R)	4 (S)	4 (S)	8 (I)	2 (S)	≥16 (R)	≥16 (R)	≤1 (S)	≥16 (R)	≥16 (R)	4 (S)	≤1 (S)	≥16 (R)
Metadata	Isolation country	United States	United States	United States	United States	United States	United States	United States	Greece	Thailand	Russia	Italy	Brazil	Belgium	Argentina	France	Japan
	Year of isolation	2012	2010	2010	2010	2012	2011	2010	2012	2013	2014	2013	2013	2012	2014	2014	2013
	Source of isolation	Wound	Deep wound	Deep wound	Unknown	Blood	Urine	Urine	Furuncle	Respiratory sputum	Urine	Urine	Abscess	Endotracheal aspirate	Human endotracheal aspirate	Urine	Urine
	Patient Gender	Unknown	Unknown	Unknown	Unknown	Unknown	Unknown	Unknown	Male	Male	Female	Male	Female	Female	Male	Female	Male
	Patient Age	Unknown	Unknown	Unknown	Unknown	Unknown	Unknown	Unknown	39 years	74 years	83 years	57 years	48 years	40 years	63 years	63 years	79 years

(R) resistant, (I) Intermediate, and (S) susceptible. A report outlining the MIC values and interpretation of susceptibility accompanies each strain. (Supplemental handout available).

Table 3: MIC values and interpretations of 15 *Streptococcus pneumoniae* strains.

	ATCC® Catalog Number →	BAA-3313™	BAA-3321™	BAA-3322™	BAA-3323™	BAA-3324™	BAA-3325™	BAA-3326™	BAA-3327™	BAA-3328™	BAA-3332™	BAA-3329™	BAA-3330™	BAA-3331™	BAA-3334™	BAA-3335™
Antibiotics	**Antibiotic class**								***Streptococcus pneumoniae***							
Cefotaxime (Meningitis)	Cephalosporin	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	4 (R)	≥8 (R)	4 (R)	≥8 (R)	≥8 (R)	2 (R)	4 (R)	4 (R)	4 (R)	4 (R)
Cefotaxime (Other)	Cephalosporin	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	4 (R)	≥8 (R)	4 (R)	≥8 (R)	≥8 (R)	2 (I)	4 (R)	4 (R)	4 (R)	4 (R)
Ceftriaxone (Meningitis)	Cephalosporin	4 (R)	≥8 (R)	4 (R)	4 (R)	4 (R)	4 (R)	≥8 (R)	4 (R)	4 (R)	4 (R)	2 (R)	4 (R)	4 (R)	4 (R)	4 (R)
Ceftriaxone (Other)	Cephalosporin	4 (R)	≥8 (R)	4 (R)	4 (R)	4 (R)	4 (R)	≥8 (R)	4 (R)	4 (R)	4 (R)	2 (I)	4 (R)	4 (R)	4 (R)	4 (R)
Trimethoprim-sulfamethoxazole	Diaminopyrimidines	≥320 (R)	160 (R)	160 (R)	160 (R)	160 (R)	160 (R)	80 (R)	160 (R)	160 (R)	160 (R)	160 (R)	160 (R)	160 (R)	≥320 (R)	160 (R)
Levofloxacin	Fluoroquinolones	≤0.5 (S)	1 (S)	0.5 (S)	0.5 (S)	0.5 (S)	0.5 (S)	0.5 (S)	0.5 (S)	0.5 (S)	1 (S)	0.5 (S)	0.5 (S)	0.5 (S)	0.5 (S)	≤0.25 (S)
Moxifloxacin	Fluoroquinolones	0.12 (S)	0.12 (S)	0.12 (S)	0.12 (S)	0.12 (S)	0.12 (S)	0.12 (S)	0.12 (S)	0.12 (S)	0.12 (S)	0.12 (S)	0.12 (S)	0.12 (S)	0.12 (S)	0.12 (S)
Vancomycin	Glycopeptide	≤0.12 (S)	≤0.12 (S)	0.5 (S)	0.5 (S)	≤0.12 (S)	≤0.12 (S)	0.5 (S)	0.5 (S)	≤0.12 (S)	0.5 (S)	0.5 (S)	0.5 (S)	0.5 (S)	0.5 (S)	0.5 (S)
Tigecycline	Glycylcyclines	≤0.06 (S)	≤0.06 (S)	≤0.06 (S)	≤0.06 (S)	≤0.06 (S)	≤0.06 (S)	≤0.06 (S)	≤0.06 (S)	≤0.06 (S)	≤0.06 (S)	≤0.06 (S)	≤0.06 (S)	≤0.06 (S)	≤0.06 (S)	≤0.06 (S)
Clindamycin	Lincosamides	≥1 (R)	≤0.25 (S)	≥1 (R)	≥1 (R)	≥1 (R)	≥1 (R)	≤0.25 (S)	≥1 (R)	≥1 (R)	≤0.25 (S)	≥1 (R)	≥1 (R)	≤0.25 (S)	≥1 (R)	≥1 (R)
Erythromycin	Macrolides	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	2 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	4 (R)	≥8 (R)	≥8 (R)
Linezolid	Oxazolidinones	≤2 (S)	≤2 (S)	≤2 (S)	≤2 (S)	≤2 (S)	≤2 (S)	≤2 (S)	≤2 (S)	≤2 (S)	≤2 (S)	≤2 (S)	≤2 (S)	≤2 (S)	≤2 (S)	≤2 (S)
Benzylpenicillin (Meningitis)	Penicillin	4 (R)	≥8 (R)	2 (R)	4 (R)	≥8 (R)	4 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	4 (I)	≥8 (R)	4 (R)	4 (R)	≥8 (R)
Benzylpenicillin (Oral)	Penicillin	4 (R)	≥8 (R)	2 (R)	4 (R)	≥8 (R)	4 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	4 (R)	≥8 (R)	4 (R)	4 (R)	≥8 (R)
Benzylpenicillin (Other)	Penicillin	4 N/A	≥8 N/A	2 N/A	4 N/A	≥8 (R)	4 N/A	≥8 N/A	≥8 (R)	≥8N/A	≥8N/A	4 (R)	≥8N/A	4N/A	4N/A	≥8N/A
Benzylpenicillin (Pneumonia)	Penicillin	4 (I)	≥8 (R)	2 (S)	4 (I)	≥8 N/A	4 (I)	≥8 (R)	≥8 N/A	≥8 (R)	≥8 (R)	4N/A	≥8 (R)	4 (I)	4 (I)	≥8 (R)
Tetracycline	Tetracyclines	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	≤0.25 (S)	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)
Metadata	Isolation country	South Korea	Russia	Germany	Hong Kong	South Africa	Austria	United States	United States	Turkey	Israel	China	Italy	Spain	Australia	Kuwait
	Year of isolation	2014	2014	2014	2014	2014	2014	2014	2014	2014	2014	2013	2013	2013	2014	2014
	Source of isolation	Respiratory sputum	Respiratory sputum	Respiratory sputum	Respiratory sputum	Respiratory sputum	Respiratory endotracheal aspirate	Respiratory sputum	Respiratory sputum	Respiratory sputum	Blood	Respiratory sputum	Respiratory bronchoalveolar lavage	Respiratory sputum	Abscess	Respiratory sputum
	Patient Gender	Male	Female	Male	Female	Male	Male	Female	Female	Female	Female	Female	Male	Male	Male	Female
	Patient Age	69 years	54 years	14 years	10 years	4 years	1 year	2 years	49 years	12 years	67 years	75 years	22 years	46 years	1 year	30 years

(R) resistant, (I) Intermediate, and (S) susceptible. A report outlining the MIC values and interpretation of susceptibility accompanies each strain. (Supplemental handout available).

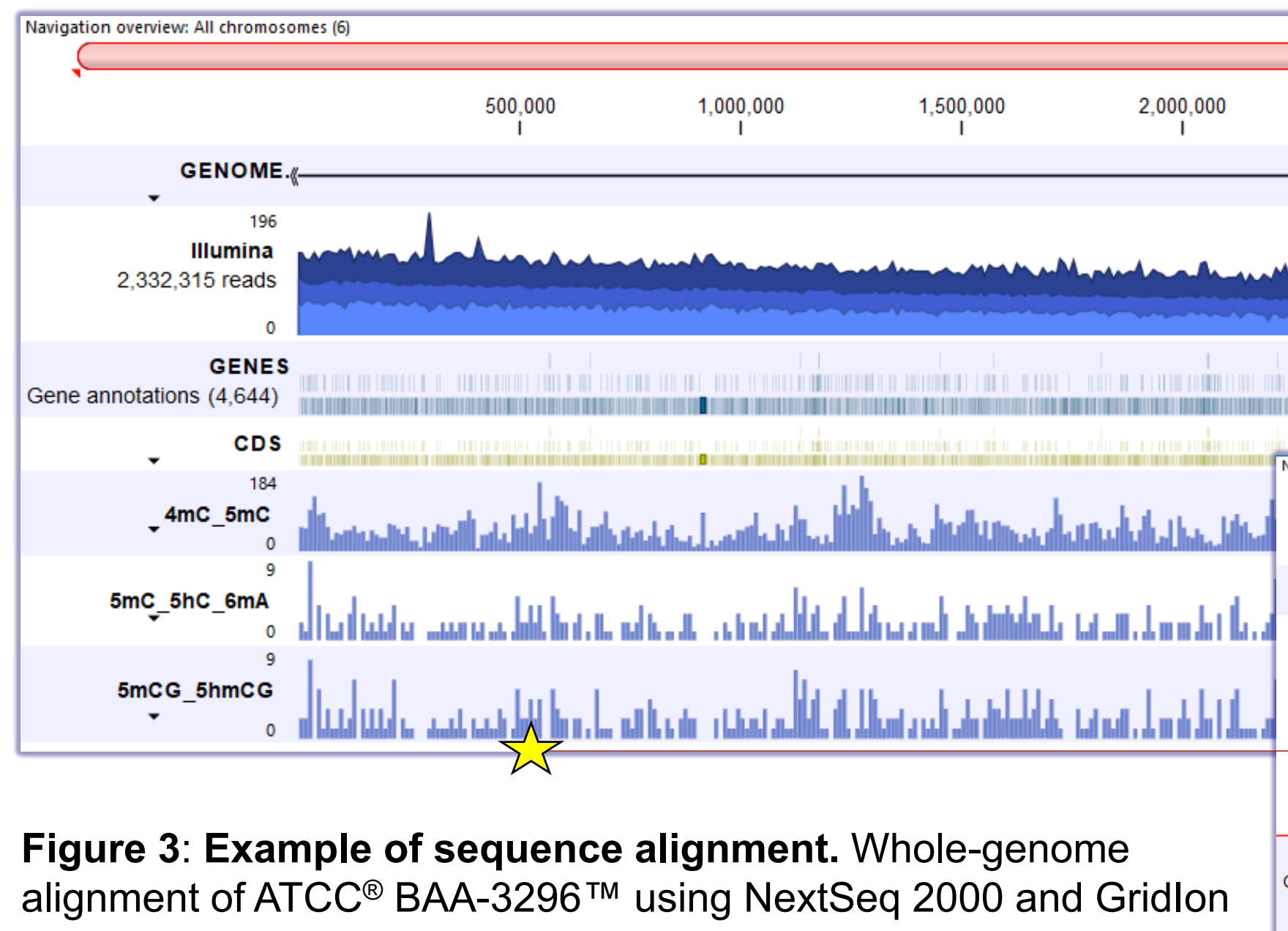


Figure 3: **Example of sequence alignment.** Whole-genome alignment of ATCC® BAA-3296™ using NextSeq 2000 and GridIon data with corresponding methylation data; 4mC_5mC, 5mC_5hC_6mA, and 5mCG_5hmCG calls >50%. CLC Genomics Workbench 25, QIAGEN.

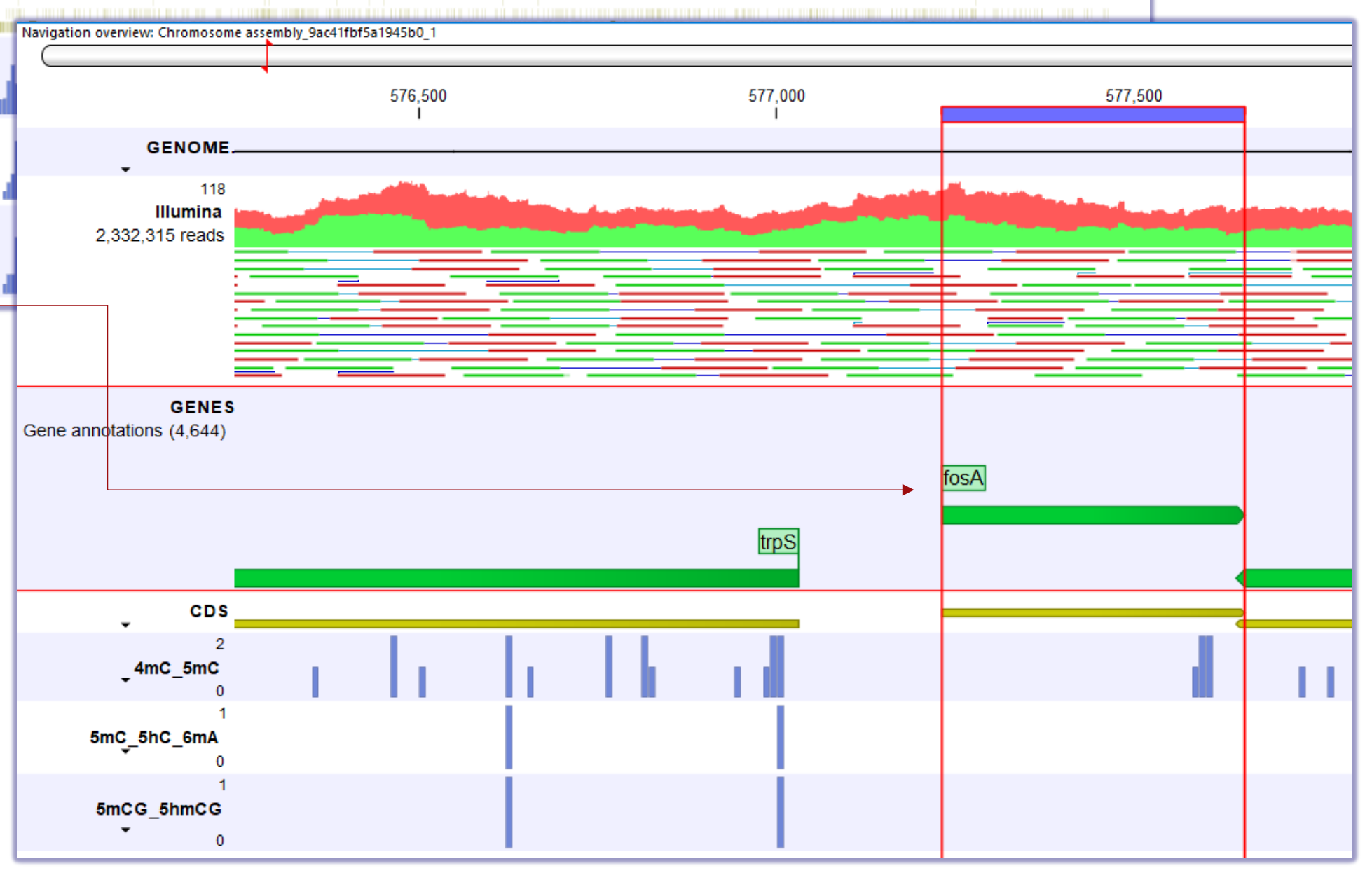


Figure 4: **Focus in on the *fosA* region of *Enterobacter hormaechei* (ATCC® BAA-3296™; Deposited as *Enterobacter cloacae*).** *fosA* (FosA/FosA2 family fosfomycin resistance glutathione transferase) is a gene associated with AMR.

Conclusion

Here, we highlight one hundred clinically relevant and extensively characterized antimicrobial-resistant isolates that are available to the research community. Each strain comes with:

- **Source information** – Geography, collection date, patient age and gender, and collection site
- **Susceptibility data** – MIC values and susceptibility profiles for targeted drugs. The susceptibility profile of each strain is available on atcc.org
- **Genetic data** – The complete and assembled genome sequence, annotated with antibiotic resistance genes and methylation data. Data is available on genomes.atcc.org

Overall, this diverse collection of highly characterized AMR strains provides a valuable resource for diagnostics and therapeutic development.

Explore our AMR clinical isolates at www.atcc.org/AMR

Find the whole-genome sequences on the ATCC Genome Portal at genomes.atcc.org

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