

Table S1. Antimicrobial susceptibility testing of strains EC-ML559 and EC-ML621.

Antimicrobial agent	MIC (mg/L)	
	EC-ML559	EC-ML621
Cefotaxime	≥ 64 (R)	≥ 64 (R)
Ceftazidime	≥ 64 (R)	≥ 64 (R)
Ceftriaxone	≥ 64 (R)	≥ 64 (R)
Cefepime	≥ 64 (R)	≥ 64 (R)
Ertapenem	≥ 8 (R)	≥ 8 (R)
Imipenem	≥ 16 (R)	8 (R)
Meropenem	≥ 16 (R)	≥ 16 (R)
Aztreonam	2 (R)	≥ 64 (R)
Amoxicillin/Clavulanic acid	≥ 32 (R)	≥ 32 (R)
Ticarcillin/Clavulanic acid	≥ 128 (R)	≥ 128 (R)
Piperacillin/Tazobactam	≥ 128 (R)	≥ 128 (R)
Ciprofloxacin	≥ 4 (R)	≥ 4 (R)
Ofloxacin	≥ 8 (R)	≥ 8 (R)
Tetracycline	≥ 16 (R)	≥ 16 (R)
Trimethoprim/Sulfamethoxazole	≥ 320 (R)	≥ 320 (R)
Amikacin	16 (S)	≥ 64 (R)
Gentamicin	≤ 1 (S)	≥ 16 (R)
Tobramycin	≥ 16 (R)	≥ 16 (R)
Colistin	≤ 0.5 (S)	≤ 0.5 (S)
Tigecycline	2 (S)	1 (S)

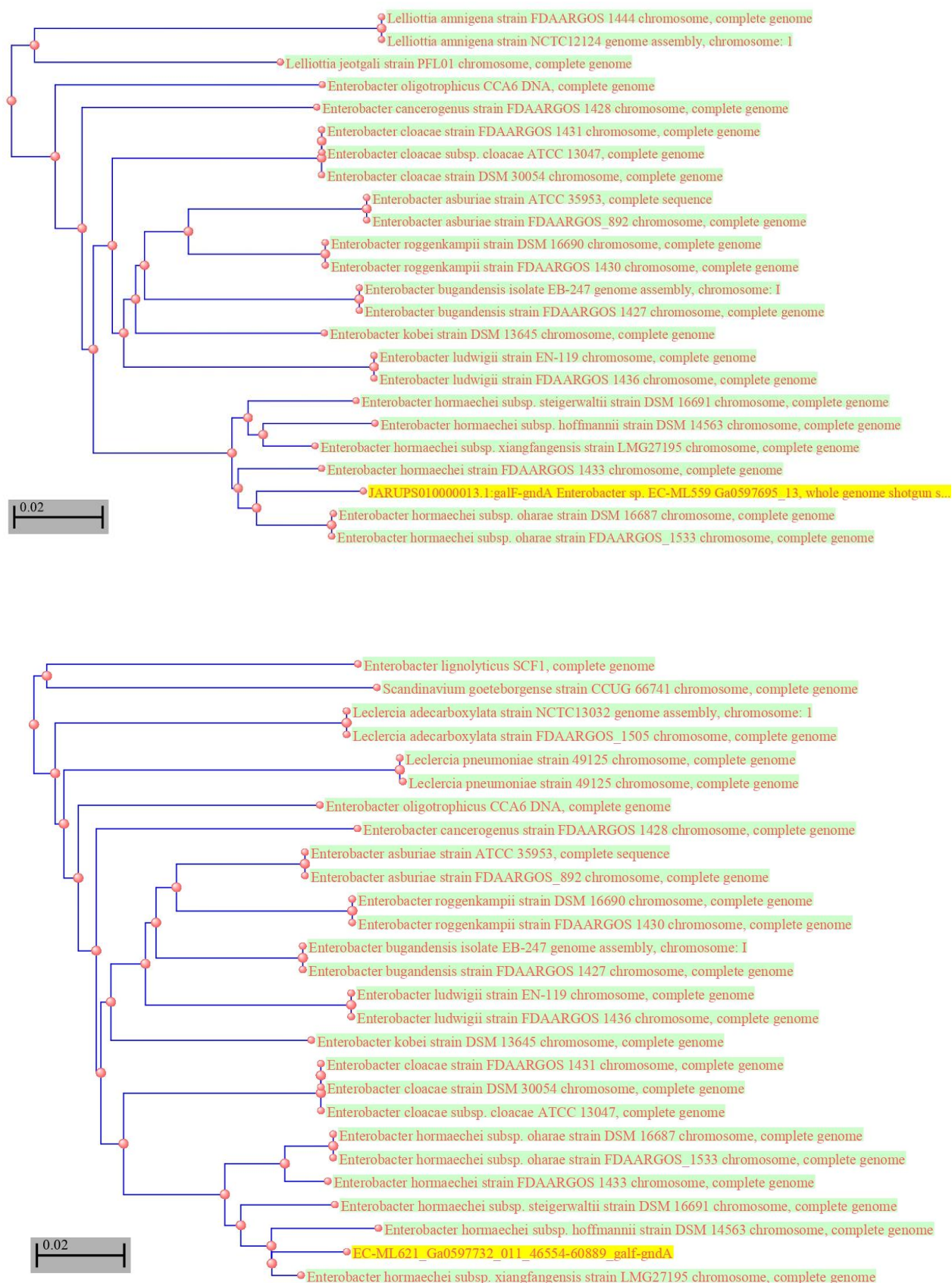
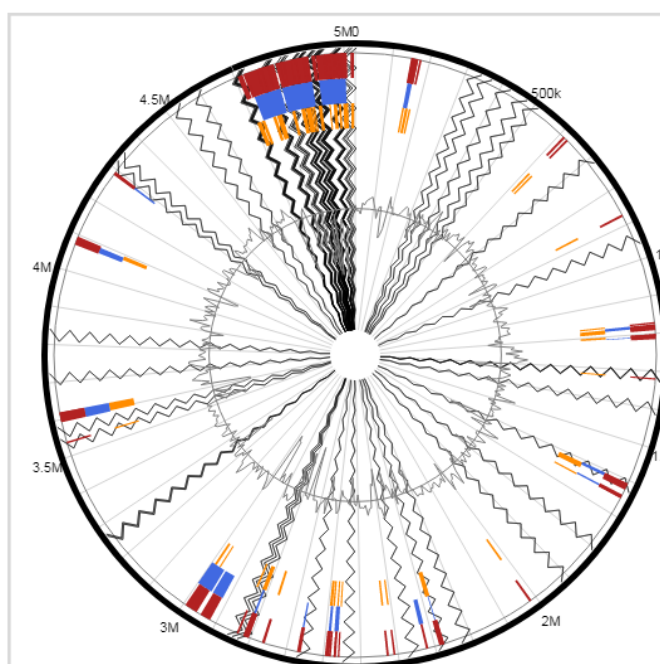


Figure S2. Phylogenetic analysis of the O-antigen clusters of strains EC-ML559 and EC-ML621 compared with other *Enterobacter cloacae* complex type strains.

EC-ML559

Aligned against reference genome *Enterobacter xiangfangensis* strain LMG27195, complete genome



EC-ML621

Aligned against reference genome *Enterobacter xiangfangensis* strain LMG27195, complete genome

Legend

Prediction Methods

- ☒ Integrated
- ☒ IslandPath-DIMOB
- ☒ SIGI-HMM
- ☐ IslandPick (No results found - unavailable for draft genomes)
- ☐ Islander (Not available)

Contigs & Alignment

- ☒ Contig Boundary
- ☒ Alignment

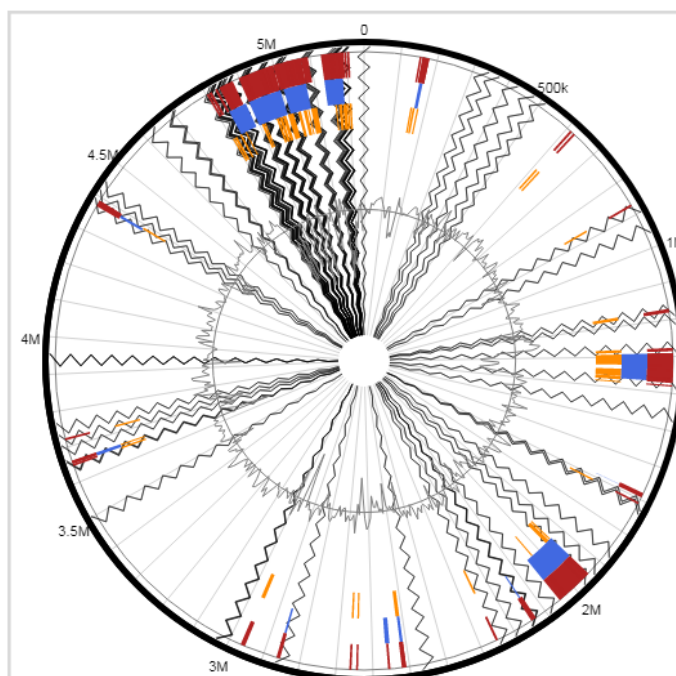


Figure S3. Predicted genomic islands and virulence/resistance gene annotations (when available) are colored within the images based on the legend. Gaps are indicated as grey bars in the circular plot, and any unaligned contigs are displayed at the end of the genome plot (indicated in grey on the circular alignment plot).

