

## SUPPLEMENTAL MATERIAL

### **Table S1**

Minimal inhibitory concentration ( $\mu\text{g/ml}$ ) for the 14 antibiotics tested. R, resistant; WT, wild type;

### **Table S2**

**Chromosomal assembly and in-silico analyses of the colistin resistant *E. coli* isolates.** Genomes obtained by de novo assembled with nanopore long reads and polished with Illumina short reads. Phylotype, serotype and MLST were determined with ClermonTyping, and with SerotypeFinder and MLST from CGE-DTU. CDS were annotated with PROKKA and PGAP. BUSCO completeness with a total of 440 genes. Data from NCBI references for phylotyper Be and A correspond to NC\_018658.1 and NC\_000913.3 respectively. Abbreviations: C, BUSCO completeness (%); Ctgs, contigs;

### **Table S3**

Antibiotic Resistance Genes (ARGs) and Virulence Factors (VFs) described by Abricate and CARD database. The legend is on the right side of the table. Chr., chromosome.

### **Table S4**

IncF-family plasmids harboring virulence factors (VF) and antibiotic resistance genes (ARGs). Abbreviations: T4SS, type 4 secretion system.

### **Figure S1**

Prokaryotic Genome Annotation Pipeline (PGAP) annotation of the IncX4 plasmid from the Farmer visualized with SnapGene Viewer.

### **Figure S2**

Prokaryotic Genome Annotation Pipeline (PGAP) annotation of the IncX4 plasmid from P2\_2 visualized with SnapGene Viewer.

***File S1***

GBK file with the annotation of the IncI2 plasmid harbouring *mcr-1* gene from 15A\_1.

***File S2***

GBK file with the annotation of the IncHI2 plasmid harbouring *mcr-1* gene from 15B\_22.