

Supplemental Material

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Supplemental tables

Table S1 General features of three *E. coli* genomes

Organization and characterization of the genomes	Strains		
	E15004	E15015	E15017
General features			
Sequenced size (bp)	4,834,707	5,135,345	5,176,582
Assembled size (bp)	4,643,275	4,637,424	4,780,540
GC content (%)	50.49	50.38	50.42
Total number of contigs	59	142	63
Total number of unordered contigs	10	59	18
Function category			
Total number of SNPs	65495	67563	113999
Total number of complete CDS	2593	2607	2502
Total Number of altered CDS	1726	1712	1817
Percent bases missed in reference	9.52%	9.70%	10.93%
Percent bases extra in unordered contigs	10.69%	9.88%	16.74%

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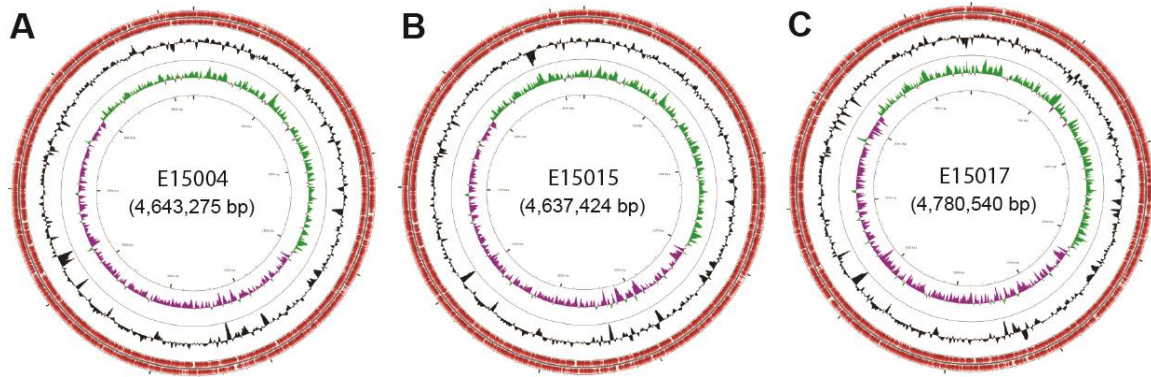
Table S2 List of drug resistance genes identified in the *mcr-1*-positive strain E15015

Resistance genes	Length (bp)	Contigs	Functions/phenotypes
<i>aadA5</i>	789	Contig_102	Aminoglycoside adenylyl-transferase AadA5, Aminoglycoside resistance
<i>strA</i>	804	Contig_84	Aminoglycoside resistance, <i>aph(3'')</i> -Ib
<i>strB</i>	837	Contig_84	Aminoglycoside resistance, <i>aph(6)</i> -Id
<i>blaTEM-1A</i>	861	Contig_84	β -lactam resistance
<i>oqxB</i>	2450	Contig_124	Quinolone resistance
<i>qnrS1</i>	657	Contig_139	Quinolone resistance
<i>floR</i>	1215	Contig_62	Phenicol resistance
<i>sul2</i>	816	Contig_84	Sulphonamide resistance
<i>tet(A)</i>	1172	Contig_84	Tetracycline resistance
<i>dfrA17</i>	474	Contig_102	dihydrofolate reductase DfrA17, Trimethoprim resistance

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11 **Supplemental figures**

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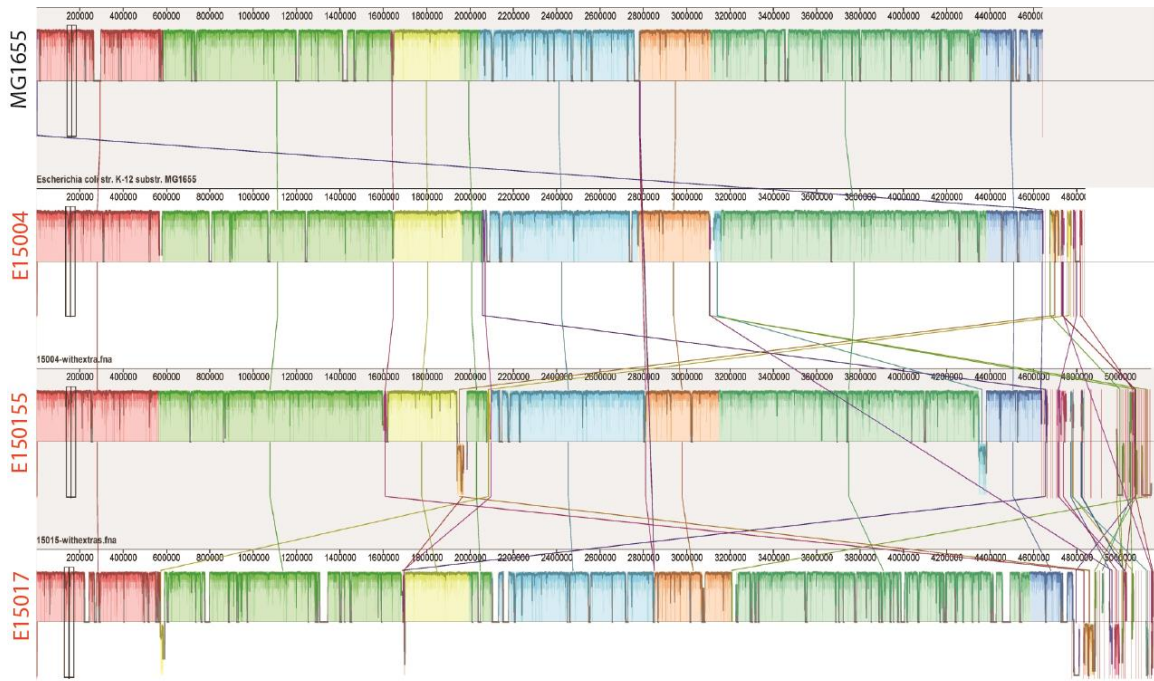
15 **Figure S1** Circular representation of the three assembled genomes (E15004,
16 E15015 and E15017)

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18 The genome maps of E15004 (**A**), E15015 (**B**) and E15017 (**C**) were generated
19 with CGViewer (http://stothard.afns.ualberta.ca/cgview_server/).

20 Individual rings ranging from 1 (inner ring) to 3 (outer ring) separately denote GC
21 Skew (Green: GC skew+; Magenta: GC skew-), GC contents, and putative ORF.

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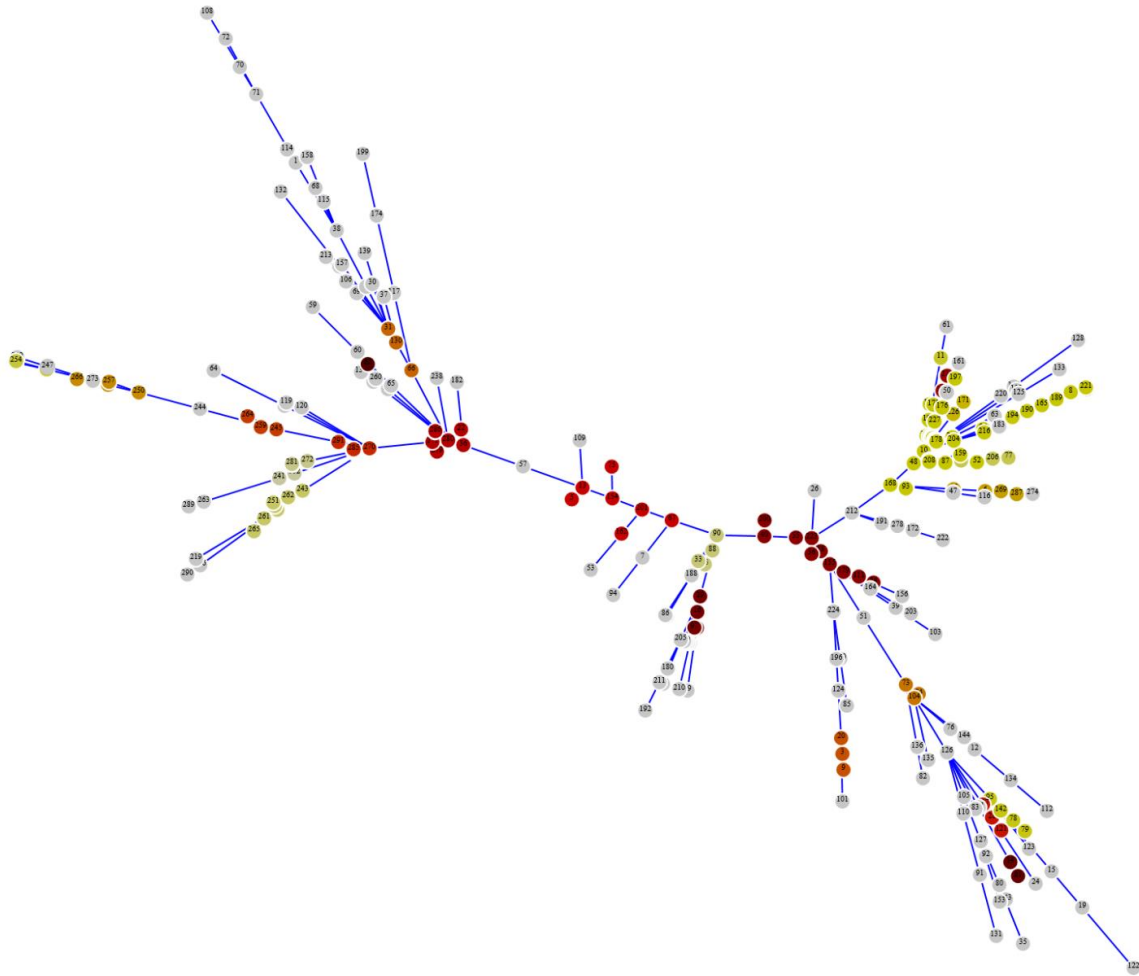
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25 **Figure S2** Linear genomic comparison of the three *micr-1*-positive *E. coli* isolates
 26 (E15004, E15015 and E15017) to the reference strain MG1655

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28 The colored blocks represent Locally Collinear Blocks (LCBs) which share
 29 homology between strains. Lines connecting individual LCBs show their location
 30 in the other genomes. Line plot inside each LCB shows local conservation in
 31 reference strain. Additional unordered contigs of sequenced genomes appear at
 32 right edge.

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36 **Figure S3** A diagram of sequence typing for the three *mcr-1*-positive *E. coli*
37 isolates (E15004, E15015 and E15017) using the MLST server

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39 The three strains (E15004, E15015 and E15017) were assigned to ST40, ST642,
40 and ST648, respectively.