

**High prevalence of multiple antibiotic resistance in clinical *E. coli* isolates from Bangladesh and prediction of molecular resistance determinants using WGS of an XDR isolate**

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Table S1: Numbers of specialty genes in L16, K-12 substr. MG1655 and O157:H7 str. Sakai.

<b>Property</b>	<b>Source</b>	<b>K-12 substr. MG1655</b>	<b>O157:H7 str. Sakai</b>	<b>L16</b>
Antibiotic Resistance	CARD	75	77	84
	NDARO	1	1	6
	PATRIC	74	80	65
Drug Target	DrugBank	387	385	388
	TTD	58	60	59
Transporter	TCDB	892	909	874
Virulence Factor	PATRIC_VF	215	283	214
	VFDB	60	128	95
	Victors	230	297	229

Table S2: Unique genes in L16 compared to other 46 *E. coli* assemblies from Bangladesh

<b>Annotation</b>	<b>Number of Genes</b>	<b>Genes</b>
CP4-57 prophage; predicted antirestriction protein	2	<i>YffX_3, yffX_4</i>
DLP12 prophage; DNA packaging protein	1	<i>nohB_1</i>
DLP12 prophage; predicted murein endopeptidase	1	<i>rzpD_2</i>
DsdC DNA-binding transcriptional dual regulator	1	<i>dsdC_1</i>
Hypothetical protein	17	-
InsAB' transposase	1	<i>insAB-1</i>
IS1 protein InSA	1	<i>insA-1</i>
Protein SopB	2	<i>SopB_1, sopB_2</i>

Table S3: Eight public genomes closely related to L16.

<b>Genome Name</b>	<b>GenBank Accessions</b>	<b>Collection Date</b>	<b>Isolation Country</b>	<b>Host Name</b>
<i>Escherichia coli</i> strain Ecol_656	CP018979	2012	USA	Human
<i>Escherichia coli</i> strain Ecol_AZ146	CP018991	2012	Italy	Human
<i>Escherichia coli</i> strain 4/0	CP023849	2009	Sweden	Human
<i>Escherichia coli</i> strain S65EC	CP036245	2009	Australia	Human
<i>Escherichia coli</i> str. TO217	LS992192		Germany	-
<i>Escherichia coli</i> strain p11A	CP049077	2015	USA	Human
<i>Escherichia coli</i> strain p4A	CP049085	2015	USA	Human
<i>Escherichia coli</i> strain THO-003	AP022525	2018	Japan	Human



Figure S1: Mean quality values (Phred scores) of sequence reads. Green, forward reads; orange, reverse reads.

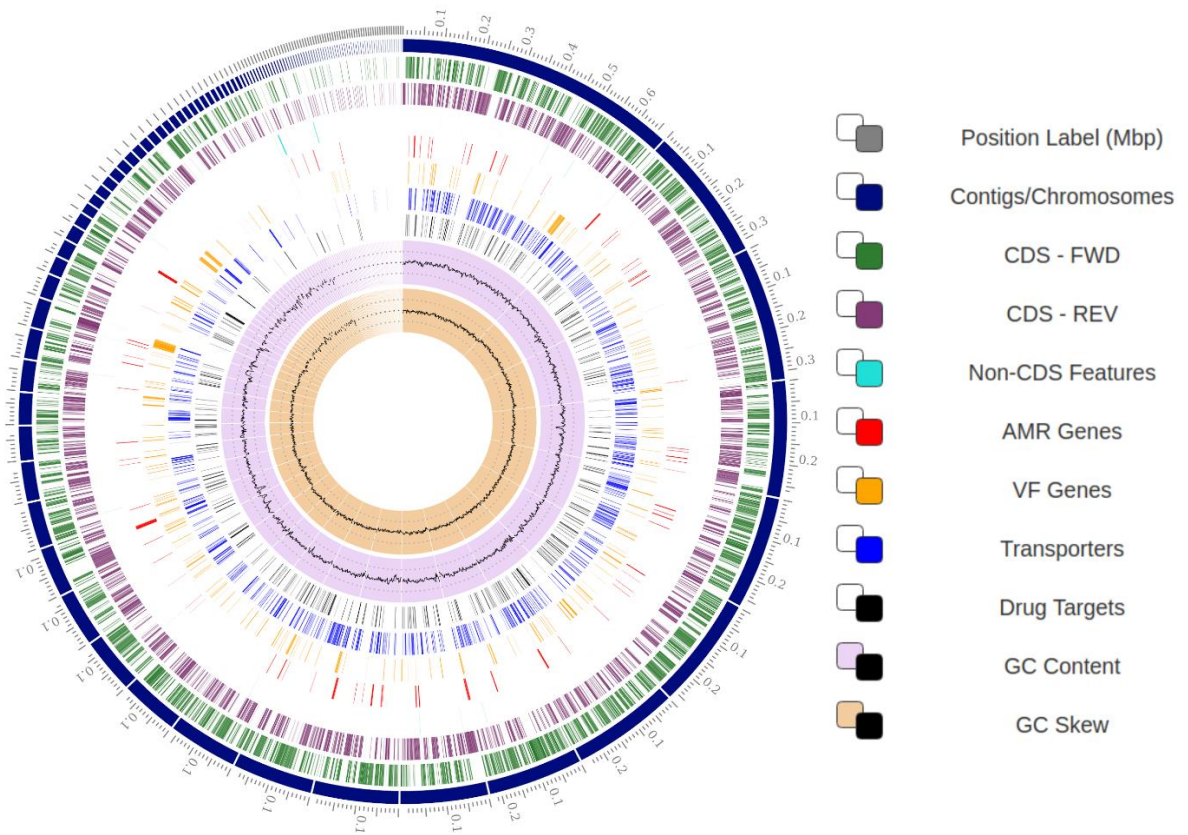


Figure S2: Circular view of the L16 genome.

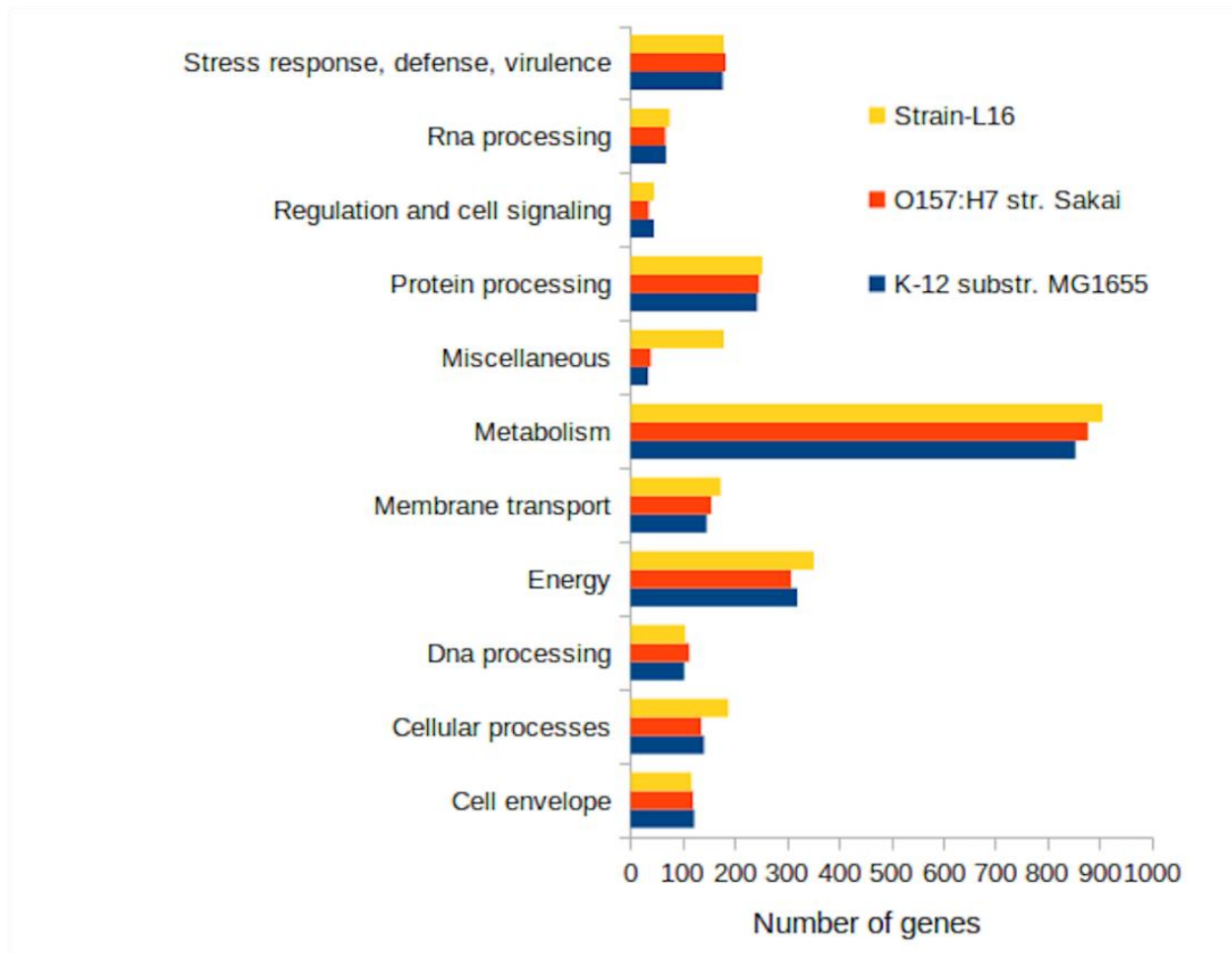


Figure S3: Comparison of the protein subsystems of L16 with two *E. coli* reference genomes, K-12 substr. MG1655 and O157:H7 str. Sakai.

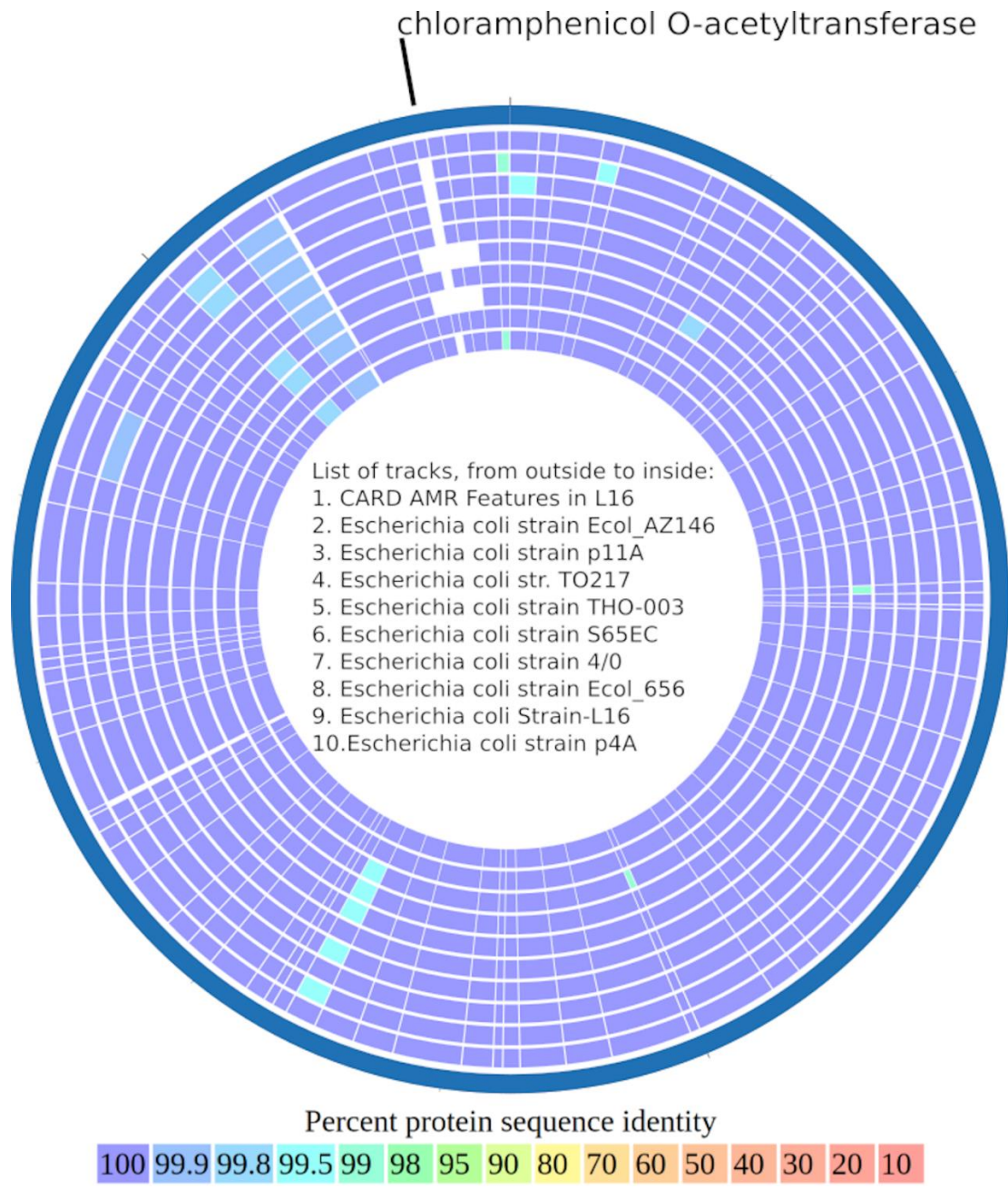


Figure S4: PATRIC alignment of the AMR protein features of L16 to the eight closely related genomes.