

Whole-Genome Sequencing for Risk Assessment of Long-term Shiga Toxin-producing *Escherichia coli*

Technical Appendix

Technical Appendix Table. Presence of marker genes in 2 independent clinical strains and the patient strain in a whole-genome sequencing assessment of the risk of long-term Shiga toxin-producing *Escherichia coli* infection*

Strain	eae (Z5110)	ent/expl2 (Z4326)	nlxB (Z4328)	nlxE (Z4329)	nlxG2-3 (Z2149)	nlxG6 (Z2150)	nlxG5-2 (Z2151)	nlxB2 (Z0985)	nlxC (Z0986)	nlxH1-1 (Z0989)	nlxD (Z0990)	nlxG (Z6010)	nlxF (Z6020)	nlxH1-2 (Z6021)	nlxA (Z6024)	nlxG2-1 (Z6025)	nlxG9 (Z2560)	Z2098	Z2099	Z2121	ureD (Z1142)	espV (Z1387)	espK (Z1829)	espN (Z1824)	espM1 (Z2565)
O26:H11	+	+	+	+	+	+	+	-	+	+	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+
O146:H21	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
O91:H14	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

*Marker designation and locus tags in the annotated genome of enterohemorrhagic *E. coli* O157:H7 strain EDL933 (GenBank accession no. AE005174.1) are shown. Gray shading indicates the patient strain. +, detection of the respective sequences in the contigs of de novo assembled whole-genome sequencing procedures.