

**Table S1.** Detection of *E. coli* T3SS effector genes in *E. albertii*.

Gene	Strain/pathotype	#Locus tag	Clinical Strains									Chicken strain	Wild bird strains									
			05-3106	07-3866	54-2045	2010C-3449	2011C-4180	2012EL-1823B	2013C-4143	2014C-4015	2014EL-1348	2014C-4356	RM9973	RM9974	RM9976	RM10507	RM10705	RM15112	RM15113	RM15114	RM15115	RM15116
<i>cif</i>	<i>E. coli</i> O127:H6 str. E2348/69 (EPEC)	E2348C_RS03860	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>espB</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z5105	1	1	1*	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
<i>espC</i>	<i>E. coli</i> O127:H6 str. E2348/69 (EPEC)	E2348C_RS15645	1*	1	1	1	1	1	1*	1	1	1	1	1	1	1	1	1	1	1	1	1
<i>espF</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z5100	1	1	1	1	1	1*	1	1*	1*	1	1	1	1	1	1*	1*	1*	1*	1*	1*
<i>espG</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z5142	1	1	1	1	1	1	1	1*	1	1	1	1	1	1	1	1	1	1	1	1
<i>espH</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z5115	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
<i>espJ</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z3071	1	1	1	1	2+1*	1	1	1	1	1	1	1*	1	1*	1*	1	1	1	1*	1
<i>espK</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z1829	1*	1*	2	2	0	1+1*	1	1	1	1*	1	1	1	1*	1	1	1	1	1	1
<i>espL1</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z2749	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1*	0	0	0
<i>espL2</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z4326	0	1*	0	1	0	0	0	1	1	0	0	0	0	0	1	1	1*	1*	1*	1*
<i>espL4</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z5608	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>espM1</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z2565	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
<i>espM2</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z3918	1*	1	1	1*	2	3	1*	2	2	1	0	1	2	3	3	2	2	2	2	2
<i>espN</i>	<i>E. coli</i> O157:H7 str. Sakai (EHEC)	ECs_1561	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>espO1-1</i>	<i>E. coli</i> O157:H7 str. Sakai (EHEC)	ECs_1567	1	0	1	1	0	1	2	1	2	0	1	1	1	1	0	2	2	2	2	2
<i>espO1-2</i>	<i>E. coli</i> O157:H7 str. Sakai (EHEC)	ECs_1821	0	1	0	1	0	1	0	1	1	0	1	1	1	1	0	1	1	1	1	1
<i>espR1</i>	<i>E. coli</i> O157:H7 str. Sakai (EHEC)	ECs_2073	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>espR3</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z3023	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>espR4</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z3026	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>espW</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z3920	1*	1	1	1	0	1	0	1	1	1	1*	1	1	1	0	1	1	1	1	1
<i>espX1</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z0025	0	0	1*	0	1*	1*	1*	1*	1*	0	0	1	0	0	1*	1*	1	0	1*	1*
<i>espX2</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z1019	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>espX4</i>	<i>E. coli</i> O157:H7 str. EC4115 (EHEC)	ECH74115_RS27410	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>espX5</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z5665	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>espX6</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z5935	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
<i>espX7/nleL</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z1822	0	1	0	1	0	1	0	1	1	1	0	0	1	1	1	1	1	1	1	1
<i>espY1</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z0065	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>espY2</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z0078	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>espY3</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z0521	1	1	0	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1
<i>espY4</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z5211	0	0	0	0	0	1	0	0	0	0	0	1	0	0	1*	1*	1*	0	0	0
<i>espY5</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z5214	0	0	0	0	0	1	0	1	3*	0	0	0	0	1*	1*	1	1*	1*	1*	1
<i>espZ</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z5122	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
<i>map</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z5113	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
<i>nleA</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z6024	1*	1	0	1	1*	1	0	1	1	1	1	1	1	1	1*	1	1	1	1	1
<i>nleB1</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z4328	0	1	0	2	0	1	0	1	1	1	1	1	0	1*	1	1	1	1	1	1*
<i>nleB2</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z0985	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>nleB2-2</i>	<i>E. coli</i> O55:H7 str. CB9615 (EPEC)	G2583_RS01765	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0

<i>nleC</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z0986	0	1	0	0	1*	1	0	1	1	1+1*	0	1	1	1	1	1	1	1	1	1
<i>nleD</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z0990	0	0	0	0	1	1	0	1	1	0	0	0	1	0	0	1*	1*	1*	1*	1*
<i>nleE</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z4329	0	1	0	1	0	1	0	1	1	1	1	1	0	1	1	1	1*	1	1	1
<i>nleE-2</i>	<i>E. coli</i> O127:H6 str. E2348/69 (EPEC)	E2348C_ RS05730	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>nleF</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z6020	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
<i>nleG2-2</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z2339	0	1	0	1	2*	1	0	1	1	0	1	2	1	2	1	1	1	1	1	1
<i>nleG2-4</i>	<i>E. coli</i> O55:H7 str. CB9615 (EPEC)	G2583_ RS09785	1	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
<i>nleG5-1</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z2337	1*	3	1	1+1*	0	3+1*	1	2	2+1*	3	2	4+1*	3+1*	4	1+1*	2+1*	2+1*	2+1*	2+1*	2+1*
<i>nleG6-1</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z2338	0	3	0	1	2	3	0	1+1*	1	4	3	4	1	3	2	1+2*	1+1*	1+1*	1+1*	1+1*
<i>nleG6-3</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z3921	0	0	1	1	0	0	0	0	1*	0	0	0	1	0	0	0	0	0	0	0
<i>nleG7</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z2077	0	0	1	1	0	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0
<i>nleG8-2</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z3919	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>nleG-1</i>	<i>E. coli</i> O55:H7 str. CB9615 (EPEC)	G2583_ RS01745	2	2	2	0	1	3	2+1*	3	3	2	1	2	2	4	4	3	3	3	3	3
<i>nleG-2</i>	<i>E. coli</i> O55:H7 str. CB9615 (EPEC)	G2583_ RS01740	0	0	0	0	0	1	0	1	1	0	1	2	1	1	1	0	1	1	1	1
<i>nleH1</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z0989	1	1	1*	1*	2	3	2*	2+1*	2	0	1	2	2	1	2	1+2*	2	2+1*	1+2*	2
<i>nleH2</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z6021	0	0	1*	0	0	0	1*	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>tccP/espF(U)</i>	<i>E. coli</i> O103:H2 str. 12009 (EHEC)	ECO103_ RS12465	1	1	1	1*	1	1	1	1*	1	1	0	1	0	1	1	0	1	1*	1*	1
<i>tir</i>	<i>E. coli</i> O157:H7 str. EDL933 (EHEC)	Z5112	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1*	1*	1	1	1*	1

\*: pseudo gene; presence of mutations

0: Not detected

Numbers equal to or great than 1: the number of the homologs

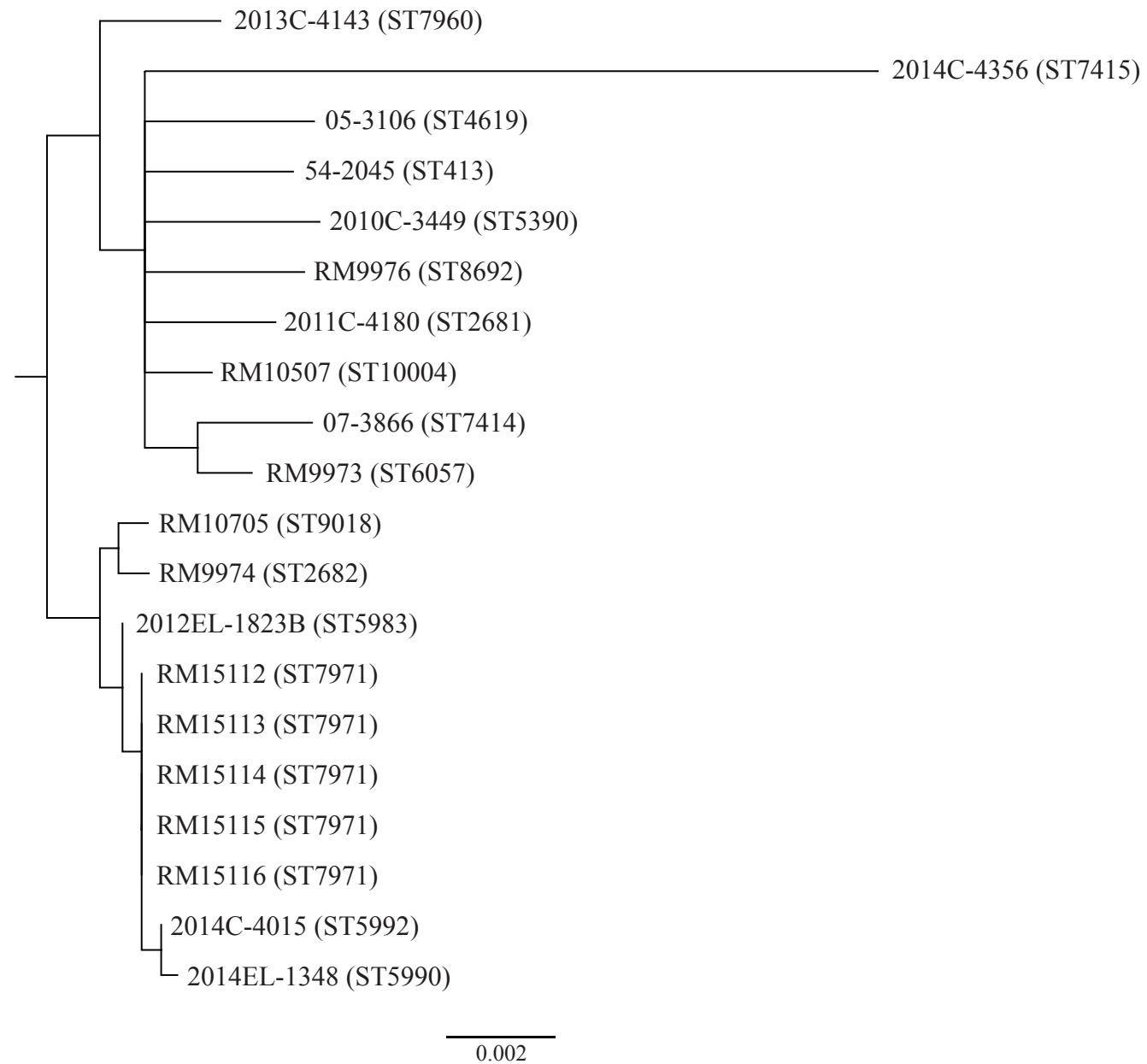
Table S2. Detection of toxin-related genes in *E. albertii*.

<i>Gene</i>	Function	Clinical Strains									Chick strain	Wild bird strains									
		05-3106	07-3866	54-2045	2010C-3449	2011C-4180	2012EL-1823B	2013C-4143	2014C-4015	2014EL-1348	2014C-4356	RM9973	RM9974	RM9976	RM10507	RM10705	RM15112	RM15113	RM15114	RM15115	RM15116
<i>eatA</i>	Serine protease autotransporter toxin EatA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>espC</i>	Serine protease autotransporter toxin EspC	1	0	1*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>espI</i>	Serine protease autotransporter EspI	0	0	1	1	1*	0	1*	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>espP</i>	Serine protease autotransporter EspP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>pet</i>	Serine protease autotransporter toxin Pet	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>pic</i>	Serine protease autotransporter toxin Pic	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>sat</i>	Serine protease autotransporter toxin Sat	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>sigA</i>	Serine protease autotransporter toxin SigA	0	0	0	0	0	0	1*	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>tsh</i>	Temperature-sensitive protease autotransporter hemagglutinin Tsh	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>vat</i>	Vacuolating autotransporter toxin Vat	0	1	0	1	0	2	0	2	2	2	1	1	1	1 + 1*	1 + 1*	2	1 + 1*	2	1 + 1*	1 + 1*
<i>cdiA</i>	Contact-dependent inhibition effector tRNA nuclease	0	1	0	1*	0	0	0	0	0	1	1	0	1*	1	0	0	0	0	0	0
<i>cdiB</i>	ShIB/FhaC/HecB family hemolysin secretion/activation protein	0	1	0	1	0	0	0	0	0	1	1	0	1	1	0	0	0	0	0	0
<i>cdtA</i>	Cytotolethal distending toxin type IV subunit CdtA	1	1	1	1	2	3	1	2	2	1	2	2	2	2	2	2	2	2	2	2
<i>cdtB</i>	Cytotolethal distending toxin type IV nuclease subunit CdtB	1	1	1*	1	1+1*	2+1*	1	2	2	1	2	2	2	2	2	2	2	2	2	2
<i>cdtC</i>	Cytotolethal distending toxin type IV subunit CdtC	1	1	0	1	2	3	1	2	2	1	2	2	2	2	2	2	2	1+1*	2	2
<i>cnf1</i>	Cytotoxic necrotizing factor CNF1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>eltA</i>	Heat-labile enterotoxin LT subunit A	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>eltB</i>	Heat-labile enterotoxin LT subunit B	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>stx1</i>	Heat-stable enterotoxin ST-I group a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>hlyA</i>	Enterohemolysin EhxA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>hlyB</i>	Enterohemolysin T1SS ABC transporter permease/ATPase EhxB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>hlyC</i>	Enterohemolysin-activating lysine-acyltransferase EhxC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>hlyD</i>	Enterohemolysin T1SS ABC transporter subunit EhxD	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>hlyE</i>	Hemolysin HlyE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>efal</i>	lymphostatin Efa1/LifA	0	0	0	1	0	1*	0	1*	1*	0	0	0	0	0	0	0	0	0	0	0
<i>senB</i>	Enterotoxin production-related protein TieB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>toxB</i>	Toxin B	1	1*	0	0	1*	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1*
<i>stx1</i>	Shiga toxin 1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>stx2</i>	Shiga toxin 2	0	0	0	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	1	1
<i>eae</i>	Intimin	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1

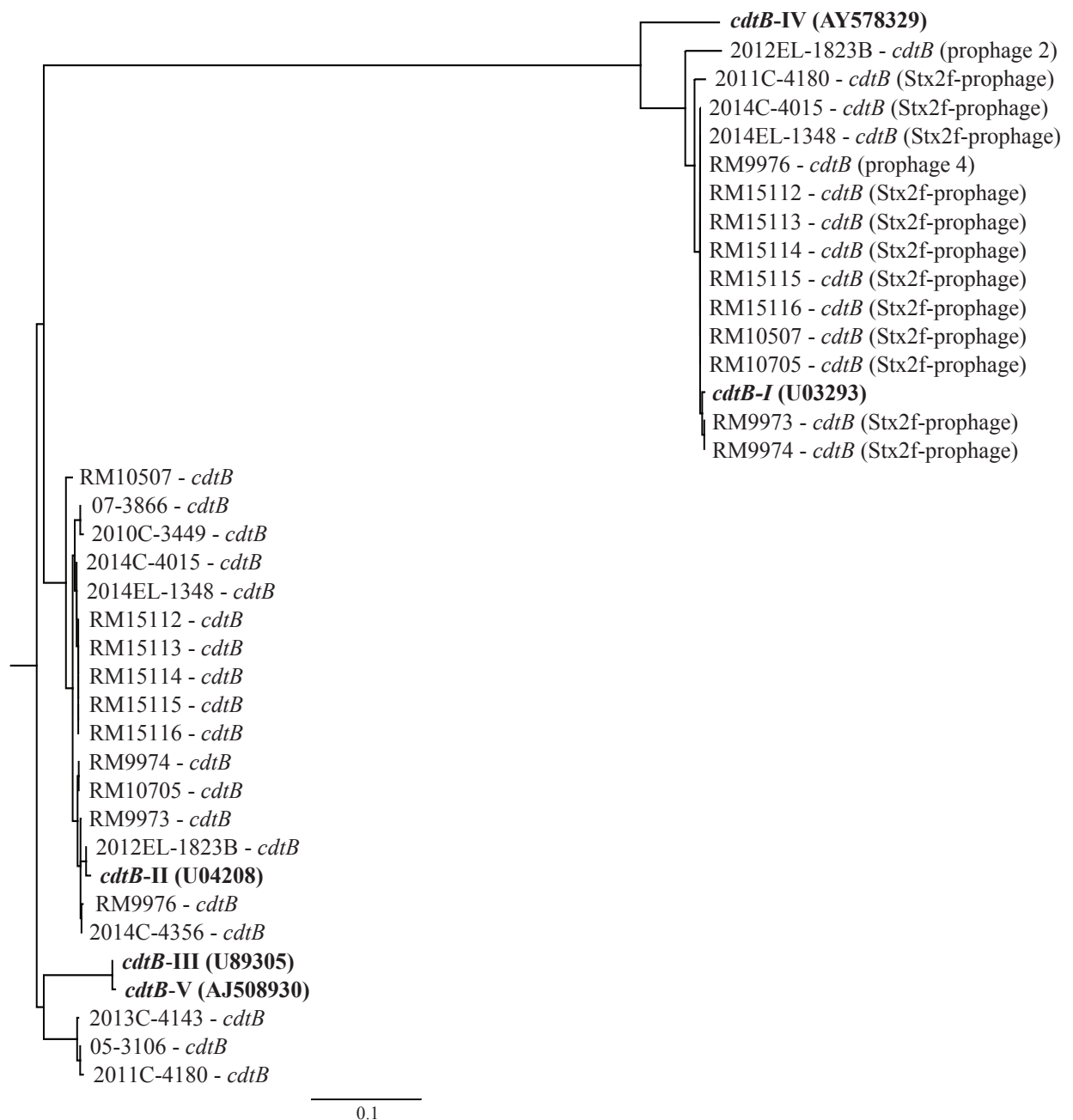
\*: pseudo gene; presence of mutations

0: Not detected

Numbers equal to or great than 1: the number of the homologs



**Figure S1.** Phylogeny of *E. albertii* strains based on sequences of the MLST loci. The concatenated sequences of the seven loci (*adk*, *fumC*, *gyrB*, *icd*, *mdh*, *purA*, and *recA*) were aligned using Clustal Omega and the consensus sequence was used to construct phylogeny tree in Geneious Prime® as detailed in Materials and Methods. The sequence type (ST) was determined using MLST 2.0 service at the Center for Genomic Epidemiology with the *Escherichia coli* #1 configuration.



**Figure S2. Phylogeny of *E. albertii* *cdtB*.** Boldface indicates reference genes for five subtypes. The GenBank accession numbers are shown in parentheses. The *cdtB* gene located on the Stx2f-prophage in strain 2012EL-1823 was not included in the analyses due to an large insertional mutation in the *cdtB* gene (Loucs tag, AYN53\_RS14910).