

Table S1 Information on *gshB*-bearing plasmids

Plasmid	Accession No	Size (bp)	Country	Species	Specimen	Incompatibility type	Multi-IS locus of <i>gshB</i>
pYD786-4*	KU254581.1	25,678	U.S.	<i>E. coli</i>	urine	IncX2	IS26-ΔIS1294- <i>gshB</i> -ΔISSba14
pSJ_255	CP011062.1	255,368	China	<i>E. coli</i>	pheasant duodenum	IncHI2, IncN	IS26-ΔIS1294- <i>gshB</i> -ΔISSba14
pSLK172-1**	CP017632.1	369,298	China	<i>E. coli</i>	human feces	IncHI2, IncN, IncY	IS26-ΔIS1294- <i>gshB</i> -ΔISSba14
pHNFP460-1**	KJ020575.1	99,868	China	<i>E. coli</i>	pig feces	IncN, IncFII	IS26-ΔIS1294- <i>gshB</i> -ΔISSba14
pE80**	KU321583.1	138,718	China	<i>E. coli</i>	chicken meat	IncFII, IncN	IS26-ΔIS1294- <i>gshB</i> -ΔISSba14
pHSHLJ1-MCR1	KX856066.1	238,539	China	<i>Salmonella</i> Typhimurium	human feces	IncHI2, IncN	IS26-ΔIS1294- <i>gshB</i> -ΔISSba14
pMCR_WCHEC16 13**	CP019214.1	289,255	China	<i>E. coli</i>	sewage	IncHI2, IncN	IS26-ΔIS1294- <i>gshB</i> -ΔISSba14
PCN061p6	CP006642.1	145,722	China	<i>E. coli</i>	lung of a pig	IncX1, IncN, IncFIB	IS26-ΔIS1294- <i>gshB</i> -ΔISSba14
plasmid B (EC D9)	CP010154.1	78,557	China	<i>E. coli</i>	dog	IncY	IS26-ΔIS1294- <i>gshB</i> -ΔISSba14
EC D4 chromosome	CP010143.1	4,821,305	China	<i>E. coli</i>	dog	IncX1, IncY	IS26-ΔIS1294- <i>gshB</i> -ΔISSba14
pSLK172-2**	CP017633.1	120,528	China	<i>E. coli</i>	human feces	IncX1, IncN, IncFII	ΔIS26-ΔIS1294- <i>gshB</i> -ΔISSba14
plasmid B** (EC S30)	CP010233.1	136,060	China	<i>E. coli</i>	forest soil	IncI1	IS26-Δorf- <i>gshB</i> -ΔISSba14
pMR0516mcr*	KX276657.1	225,069	U.S.	<i>E. coli</i>	urine	IncF	IS26-Δ <i>gshB</i> -ΔISSba14
pC629**	CP015725.1	210,106	China	<i>Salmonella</i> Indiana	chicken carcass	IncHI2, IncN	IS26-Δ <i>gshB</i> -ΔISSba14

* plasmids coexisting with *fosA6* or *fosA3*** plasmids carrying *fosA3*

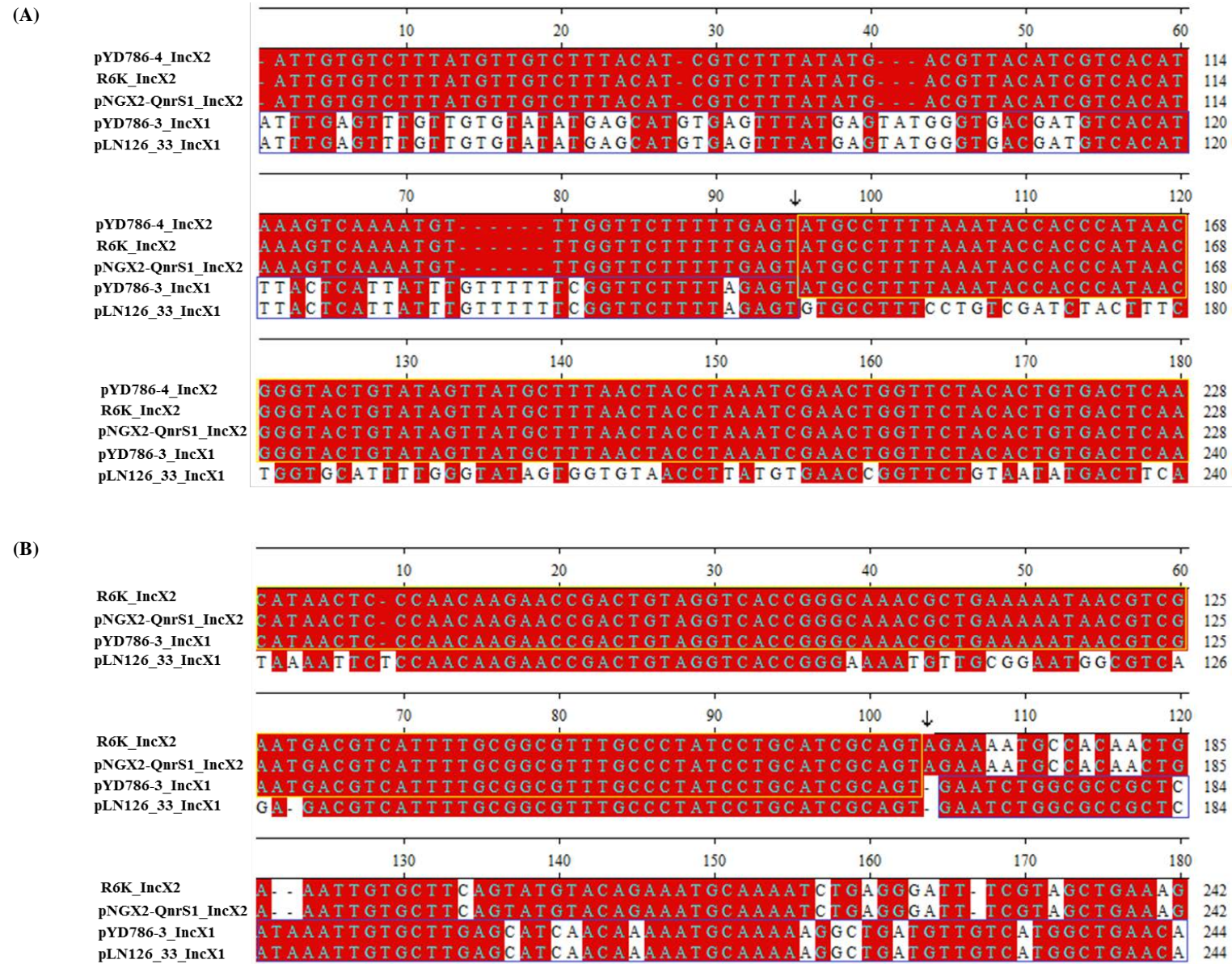
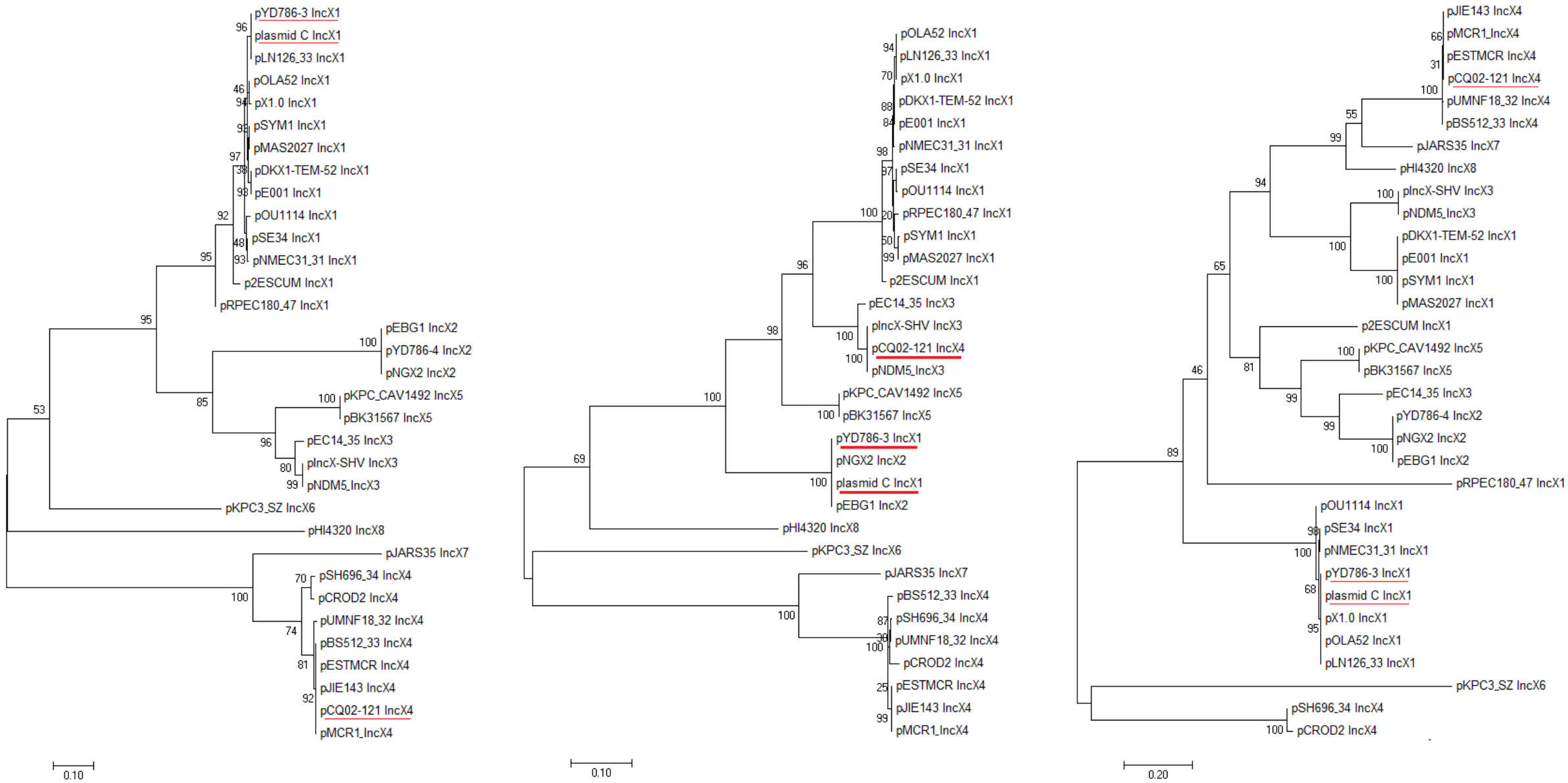


Figure S1. Sequence alignments of representative IncX1 and IncX2 plasmids surrounding recombination breakpoints (A) Sequences between *parA* and *tnpR*_{R6K}. R6K, nt 7567-7735; pLN126_33, nt 30181-30002. (B) Sequences in α -LIR. R6K, nt 329-425; pLN126_33, nt 6009-5833. Putative recombination junction sites are denoted by black arrows at position 30121 and 21749 of pYD786-3.



(A) *bis* of IncX

(B) *taxC* of IncX

(C) *pir* of IncX

Figure S2. Phylogenetic relationships of three conserved backbone genes from IncX plasmids, (A) *bis* of IncX. (B) *taxC* of IncX. (C) *pir* of IncX. Maximum-likelihood trees are constructed using Mega7. Hybrid plasmids are indicated using red underlines.