

Table S1. Comparison of ORFs encoded by the pHN1122-1 with pFRIK2000, pSH146_65, pCHi7122-3, R721 and R64 backbones.

Gene name ^a	Nucleotide position	Function encoded	Percentage amino acid identity (query coverage) ^b				
			pFRIK2000	pSH146_65	pCHi7122-3	R721	R64
<i>hyp</i>	413-54	hypothetical protein	–	–	95.8(119)	–	–
<i>repA</i>	508-1524	replication initiation protein	97.04(338)	99.7(338)	97.34(338)	99.7(338)	74.17(333)
<i>hyp</i>	2002-1622	hypothetical protein	–	95.83(72)	89.72(107)	–	–
<i>yaeA (mok)</i>	2798-3085	modulator of post-segregation killing protein	97.18(71)	95.77(71)	83.16(95)	95.77(71)	–
<i>yaeB (hok)</i>	2928-3089	post-segregation killing protein	11(53)	98.1(53)	83.0(53)	98.11(53)	39.13(46)
<i>yaeC (finO)</i>	3262-3834	conjugal transfer fertility inhibition protein	99.47(190)	100(190)	100(190)	100(190)	35.42(192)
<i>yafA</i>	4136-3852	stability/ partitioning determinant	100(94)	100(94)	100(94)	100(94)	–
<i>yafB (parA)</i>	4875-4210	plasmid partition protein	99.55(221)	99.1(221)	99.1(221)	99.1(221)	24.53(212)
<i>yagA</i>	5461-5790	hypothetical protein	98.17(109)	100(109)	98.17(109)	98.17(109)	–
<i>dnaJ</i>	6322-6708	DnaJ-class molecular chaperone	100(128)	99.22(128)	–	–	–
<i>hyp</i>	6812-7354	hypothetical protein	100(180)	99.36(156)	–	–	–
<i>hyp</i>	11843-12217	hypothetical protein	99.19(124)	–	–	–	–
<i>yceB</i>	13390-12947	hypothetical protein	100(147)	97.28(147)	70.75(147)	70.75(147)	–
<i>ycfA</i>	13687-13869	hypothetical protein	100(60)	100(60)	100(60)	100(60)	–
<i>ycfB</i>	13894-14331	hypothetical protein	100(145)	100(145)	100(145)	100(145)	–
<i>hyp</i>	14782-14462	hypothetical protein	100(106)	98.11(106)	96.3(108)	93.18(44)	62.07(58)
<i>hyp</i>	15294-14779	hypothetical protein	100(171)	97.66(171)	–	–	–

<i>ycgB</i>	16015-15596	hypothetical protein	97.12(139)	89.62(106)	90.91(44)	90.38(104)	–
<i>hyp</i>	16742-16035	hypothetical protein	100(235)	98.56(139)	67.15(137)	67.15(137)	–
<i>traL</i>	17496-16744	conjugal transfer protein	100(250)	100(250)	–	–	–
<i>hyp</i>	17915-17514	hypothetical protein	100(133)	98.04(102)	–	–	–
<i>nikA</i>	18284-18625	relaxosome component	100(113)	100(113)	90.27(113)	100(113)	–
<i>nikB</i>	18622-22827	relaxase	97.53(1419)	99.01(809)	90.48(809), 84.32(338)	82.61(345), 47.81(297)	–
<i>nikC</i>	19601-19900	relaxosome accessory protein	100(99)	99.0(99)	100(99)	100(99)	–
<i>yddA</i>	23310-22870	hypothetical protein	98.63(146)	96.58(146)	95.21(146)	93.15(146)	–
<i>hyp</i>	23986-23555	hypothetical protein	99.3(143)	–	–	–	–
<i>ydfA</i>	24338-24132	transcriptional regulator	100(68)	97.06(68)	86.67(30)	97.06(68)	–
<i>ydfB</i>	24777-24457	hypothetical protein	–	80.17(116)	–	80.17(116)	–
<i>ydfC</i>	25026-24802	hypothetical protein	–	100(74)	–	100(74)	–
<i>ydgA</i>	27408-25252	DNA topoisomerase III, may play a role in DNA segregation	100(718)	95.4(718)	95.51(713)	99.72(718)	–
<i>hyp</i>	28007-27420	hypothetical protein	–	–	97.18(195)	–	–
<i>hyp</i>	28775-28371	hypothetical protein	–	–	99.25(134)	–	–
<i>yeaA</i>	29309-28791	hypothetical protein	98.25(171)	97.66(171)	92.96(71)	96.49(171)	–
<i>yebA</i>	30009-29356	hypothetical protein	98.16(217)	99.08(217)	98.62(217)	98.16(217)	–
<i>rci</i>	31145-30021	shufflon-specific recombinase	DNA 99.47(374)	99.2(374)	99.47(374)	99.47(374)	76.14(373)
<i>hyp</i>	31656-32138	hypothetical protein	–	–	100(117)	–	82.91(117)
<i>pilV</i>	33379-32135	plasmid conjugative transfer pilus-tip adhesin protein	100(341)	95.89(365)	96.16(365)	99.71(347)	50.68(367)

<i>pilU</i>	34027-33392	prepilin peptidase	100(211)	98.1(211)	100(211)	100(211)	27.06(170)
<i>pilT</i>	34513-34031	type IV secretion system pilus Lytic transglycosylase	100(160)	100(160)	100(160)	100(160)	59.4(133)
<i>pilS</i>	35047-34580	type IV leader peptidase family protein	100(155)	92.26(155)	90.32(155)	92.26(155)	29.3(157)
<i>pilR</i>	35047-34580	type IV pilus transmembrane protein	100(369)	99.19(369)	98.92(369)	99.19(369)	25.63(359)
<i>pilQ</i>	37820-36282	plasmid conjugative transfer ATPase	99.61(512)	99.8(512)	99.8(512)	98.26(517)	41.62(507)
<i>pilP</i>	38339-37845	type IV pilus biogenesis periplasmic protein precursor	100(164)	98.78(164)	98.78(164)	98.17(164)	30.33(122)
<i>pilO</i>	39633-38323	type IV pilus biogenesis outer membrane protein	99.77(436)	99.54(436)	99.54(436)	99.31(436)	22.47(365)
<i>pilN</i>	41327-39684	type IV pilus outer membrane secretin lipoprotein	99.82(547)	99.63(547)	99.63(547)	99.63(547)	39.42(553)
<i>yfdA</i>	41838-41320	hypothetical protein	84.09(176)	90.91(176)		94.77(172)	
<i>traK (virD4)</i>	43843-41885	conjugal transfer protein	100(652)	98.16(652)	98.37(613)	99.85(652)	
<i>traJ (virB11)</i>	44914-43859	conjugal transfer protein	100(326)	100(351)	100(351)	100(351)	32.31(130)
<i>traI (virB10)</i>	46072-44933	conjugal transfer protein	99.47(379)	99.21(379)	99.21(379)	99.47(379)	–
<i>traH (virB9)</i>	46832-46062	conjugal transfer outer membrane protein precursor	99.61(256)	99.57(233)	99.22(256)	99.61(256)	–
<i>traG (virB8)</i>	47563-46829	conjugal transfer protein	99.59(244)	100(244)	99.59(244)	99.59(244)	–
<i>traE (virB4)</i>	50084-47727	conjugal transfer protein	99.75(785)	99.49(785)	97.2(785)	99.45(785)	–

<i>traD</i> (<i>virB3</i>)	50410-50090	conjugal transfer protein	99.06(106)	99.06(106)	99.06(106)	95.28(106)	–
<i>traC</i> (<i>virB2</i>)	50771-50481	conjugal transfer prepropilin	100(96)	100(96)	96.88(96)	96.88(96)	–
<i>traB</i> (<i>virB1</i>)	51355-50771	conjugal transfer protein	97.93(193)	98.45(194)	97.93(193)	98.45(193)	–
<i>ygeA</i>	51774-51376	hypothetical protein	99.24(132)	98.48(132)	99.24(132)	99.24(132)	–
<i>pilM</i>	52551-52114	type IV pilus biogenesis protein	97.24(145)	95.17(145)	95.17(145)	95.17(145)	27.03(148)
<i>pilL</i>	53792-52557	type IV pilus biogenesis outer membrane protein precursor	97.08(411)	97.08(411)	97.57(411)	97.08(411)	29.61(233)
<i>yggA</i>	54094-53795	hypothetical protein	100(99)	98.99(99)	97.89(95)	93.94(99)	–
<i>yggB</i>	54793-54161	hypothetical protein	98.58(211)	98.1(211)	98.58(211)	97.63(211)	–
<i>ygiA</i>	54841-55650	possible DNA primas	98.14(269)	91.23(114)	–	99.26(269)	–
<i>ygiB</i>	55933-55697	hypothetical protein	51.67(60)	100(78)	80.26(76)	39.71(68)	–
<i>trbJ</i> (<i>virB5</i>)	56584-55937	conjugal transfer protein	90.16(193)	99.53(215)	87.68(203)	84.04(213)	–
<i>trbL</i> (<i>virB6</i>)	57576-56590	plasmid conjugal transfer protein	67.76(335)	98.78(328)	68.06(335)	68.66(335)	–
<i>yhaB</i>	58136-57834	hypothetical protein	99(100)	100(100)	100(100)	95.35(86)	–
<i>yhbB</i>	59213-58551	hypothetical protein	99.09(220)	52.27(88)	53.41(88)	95.45(220)	–
<i>yhcA</i>	59841-59398	hypothetical protein	100(147)	94.56(147)	96.6(147)	91.84(147)	–
<i>yhdA</i>	60891-59914	hypothetical protein	100(325)	99.69(325)	99.69(325)	97.85(325)	–
<i>yheC</i>	61552-61100	putative protease	98.08(104)	98.08(104)	99.33(150)	99.33(150)	–

^a Genes and proteins in the pHN1122-1 backbone were annotated by reference to R721 (GenBank accession no. AP002527) and by BLASTp searches, hyp presents genes encoding putative proteins. Genes used for phylogenetic analysis are shaded.

^b Amino acid identify was measured for each ORF of pHN1122-1 versus the respective ORFs of pFRIK2000 (NZ_ACXO01000104), pSH146_65 (JN983044), pChi7122-3 (FR851304), R721 (AP002527) and R64 (AP005147).

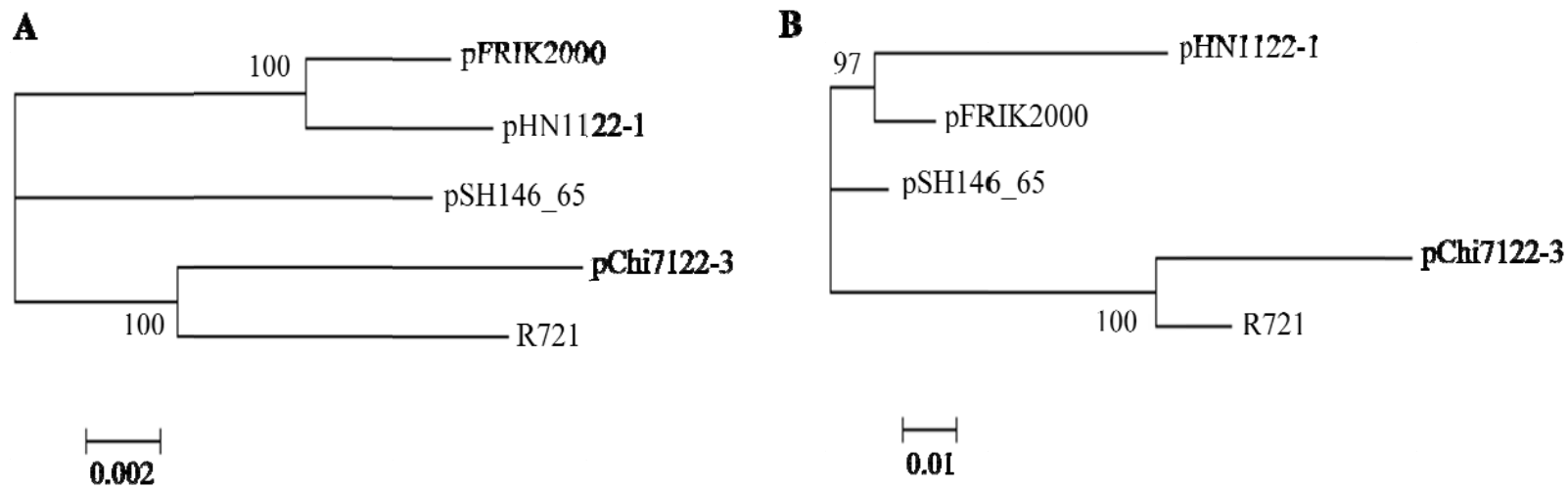


Figure S1. Phylogenetic alignment of 5 IncI2 plasmids. (A) The phylogeny was constructed in MEGA5 using the Neighbor-joining method from concatenated sequences of genes shared by all five IncI2 plasmids (Table S1). Bootstrap consensus trees were inferred using 500 replicates, with numbers at nodes representing percent correspondence. The scale bars represent the number of base substitutions per site. Sequences were obtained from the following GenBank accession nos.: R721, AP002527; pSH146_65, JN983044; pChi7122-3, FR851304; pFRIK2000, NZ_ACXO01000104; pHN1122-1, JN797501). (B) The phylogeny was constructed in MEGA5 using the Maximum Likelihood method from the entire sequences of the five IncI2 plasmids after removing any mobile elements. Bootstrap consensus trees were inferred using 500 replicates.