SUPPLEMENTARY DATA 1-3

Supplementary data 1.1: **Primer sequences used for detecting carbapenemase genes in PCR assays of *K. pneumoniae* isolates**

Target	*Gene*	*Primer (5' to 3')*	*Amplicon size (bp)*	*Reference*
IMP	bla$_{IMP}$*(F)*	*GGAATAGAGTGGCTTAAYTCTC*	*232*	*Poirel* et al.*, 2011*
	bla$_{IMP}$*(R)*	*GGTTTAAYAAAACAACCACC*		
KPC	bla$_{KPC}$*(F)*	*TGTCACTGTATCGCCGTC* *CTCAGTGCTCTACAGAAAACC*	*900*	*Doyle* et al.*, 2012*
	bla$_{KPC}$*(R)*	*TTGTCATCCTTGTTAGGCG*		
VIM	bla$_{VIM}$*(F)*	*GATGGTGTTTGGTCGCATA*	*390*	Poirel *et al.*, 2011
	bla$_{VIM}$*(R)*	*CGAATGCGCAGCACCAG*		
OXA	bla$_{OXA-48}$*(F)*	*GCGTGGTTAAGGATGAACAC*	*438*	
	bla$_{OXA-48}$*(R)*	*CATCAAGTTCAACCCAACCG*		
NDM	bla$_{NDM-1}$*(F)*	*GGTTTGGCGATCTGGTTTTC*	*782*	
	bla$_{NDM-1}$*(R)*	*CGGAATGGCTCATCACGATC*		
GES	bla$_{GES}$	*AGTCGGCTAGACCGGAAAG*	*399*	*Dallenne* et al.*, 2010*
	bla$_{GES}$	*TTTGTCCGTGCTCAGGAT*		

F, sense primer, R, antisense primer

Supplementary data 1.2: **Primer sequences used for detecting replicons in CRKP isolates using the PBRT assay**

PCR type	*Target*	*Primer (5' to 3')*	*Amplicon size*	*Reference*
M1	*I1-αγ(F)*	*cgaaagccggacggcagaa*	*139*	*Carattoli* et al., *2005*
	I1-αγ(R)	*tcgtcgttccgccaagttcgt*		
	HI1(F)	*ggagcgatggattacttcagtac*	*471*	
	HI1(R)	*tgccgtttcacctcgtgagta*		
	HI2(F)	*tttctcctgagtcacctgttaacac*	*644*	
	HI2(R)	*ggctcactaccgttgtcatcct*		
	X(R)	*tgagagtcaatttttatctcatgttttagc*		
M2	*M(F)*	*ggatgaaaactatcagcatctgaag*	*738*	*Carattoli* et al., *2015*
	M(R)	*gaactccggcgaaagaccttc*		
	N(F)	*gtctaacgagcttaccgaag*	*559*	
	N(R)	*gtttcaactctgccaagttc*		
	L(F)	*cggaaccgacatgtgcctact*	*854*	
	L(R)	*gaactccggcgaaagaccttc*		
M3	*W(F)*	*cctaagaacaacaaagcccccg*	*242*	*Carattoli* et al., *2005; Villa* et al., *2010*
	W(R)	*ggtgcgcggcatagaaccgt*		
	FIA(F)	*ccatgctggttctagagaaggtg*	*462*	
	FIA(R)	*gtatatccttactggcttccgcag*		
	FIB(F)	*ggagttctgacacacgattttctg*	*683*	
	FIB(R)	*tctgtttattcttttactgtccac*		
M4	*FIC(F)*	*gtgaactggcagatgaggaagg*	*262*	*Carattoli* et al., *2005*
	FIC(R)	*ttctcctcgtcgccaaactagat*		
	P(F)	*ctatggccctgcaaacgcgccagaaa*	*534*	
	P(R)	*tcacgcgccagggcgcagcc*		
	Y(F)	*aattcaaacaacactgtgcagcctg*	*765*	
	Y(R)	*gcgagaatggacgattacaaaacttt*		
M5	*FIIA$_S$(F)*	*ctgtcgtaagctgatggc*	*270*	*Carattoli* et al., *2005*
	FIIA$_S$(R)	*ctctgccacaaacttcagc*		
	A/C(F)	*gagaaccaaagacaaagacctgga*	*465*	
	A/C(R)	*acgacaaacctgaattgcctcctt*		
	T(F)	*ttggcctgtttgtgcctaaaccat*	*750*	
	T(R)	*cgttgattacacttagctttggac*		
S1	*B/O(F)*	*gcggtccggaaagccagaaaac*	*159*	

	B/O(R)	*tctgcgttccgccaagttcga*		
S2	*K(F)*	*gcggtccggaaagccagaaaac*	*160*	*Carattoli* et al., *2005*
	K(R)	*tctttcacgagcccgccaaa*		
S3	*F(F)*	*tgatcgtttaaggaattttg*	*270*	
	F(R)	*gaagatcagtcacaccatcc*		
S4	*FII(F)*	*ctgatcgtttaaggaatttt*	*258-262*	
	FII(R)	*cacaccatcctgcactta*		*Villa* et al., *2010*
S5	*FII_k(F)*	*tcttcttcaatcttggcgga*	*142-148*	
	FII_k(R)	*gcttatgttgcacrgaagga*		

F, sense primer, R, antisense primer

Supplementary data 2.1: **Resistance determinants of the carbapenem-resistant *K. pneumoniae* isolates**

Isolate	*Resistance mechanisms*								*Sequence type*	*Plasmid (Inc) types*
	B-lactams	***Tetracycline***	***Phenicol***	***Fosfomycin***	***Aminoglycosides***	***Quinolone***	***Sulphonamide***	***Trimethoprim***		
Kp8	***OXA-181***, *OXA-1*, *CTX-M-15*, *SHV-28*, *TEM-1B*	tet(A)	catB3	fosA	aac(3)-lla, aac(6')-lb-cr, aph(3'')-lb, aph(6)-ld	aac(6')-lb-cr, oqxA, oqxB, qnrB1, qnrS1	sul2	dfrA14	*307*	*ColKP3*, *IncX3*, *IncFIB(k)*, *IncFII(k)*
Kp10	***NDM-1***, *OXA-1*, *CTX-M-15*, *SHV-11*, *TEM-1B*	tet(A)	catB3	fosA	aac(6')-lb-cr, aph(3'')-lb, aph(6)-ld, rmtC	aac(6')-lb-cr, oqxA, oqxB, qnrB1	sul1, sul2	dfrA14	*39*	*IncFIB(k)*, *IncFII(k)*, *IncFII(yp)*
Kp15	***OXA-181***, *CTX-M-15*, *SHV-1*, *TEM-1B*	tet(A)	catA2	fosA	aac(3)-lla, aac(6')-lb-c*r*, *aac(6')-lb3*, aadA16, aph(3')-lb, aph(6)-ld,	aac(6')-lb-cr, oqxA, oqxB, qnrB6, qnrS1	sul1, sul2	dfrA27	*607*	*ColKP3*, *IncA/C2*, *IncFIA(HI1)*, *IncFIB(k)*, *IncFII(k)*, *IncR*, *IncU*
Kp29	***NDM-7***, *CTX-M-15*, *SCO-1*, *SHV-1*, *TEM-1B*	-	catA2	fosA	aac(3)-lla, aac(6')-lb-cr, aadA16, aph(3')-lb, aph(6)-ld	aac(6')-lb-cr, oqxA, oqxB	sul1, sul2	dfrA27	*17*	*IncFIA(HI1)*, *IncFIB(k)*, *IncFII(k)*, *IncR*, *IncX3*
Kp32	***OXA-48***, *OXA-1*, *CTX-M-15*, *SHV-11*,	tet(A)	catB3	fosA, fosA7	aac(3)-lla, aac(6')-lb-cr, aph(3')-lb, aph(6)-ld	aac(6')-lb-cr, oqxA, oqxB, qnrB1	sul2	dfrA14	*3559*	*IncFIB(k)*, *IncFII(k)*,

	TEM-1B									*IncL/M*
Kp33	***NDM-1***, *OXA-1*, *CTX-M-15*, *SHV-11*, *TEM-1B*	tet(A)	catB3	fosA	aac(6')-lb-cr, aph(3')-lb, aph(6)-ld, rmtC	*aac(6')-lb-cr*, *oqxA*, *oqxB*, *qnrB1*	sul1, sul2	dfrA14	*39*	*IncFIB(k)*, *IncFII(k)*, *IncFII(yp)*

Supplementary data 2.2. ARGs, ompK36 porin, and colistin- and fluoroquinolone-resistance-conferring mutations found on chromosomes of the Klebsiella pneumoniae strains

Strain (MLST)	*Contig (genomic context)*	*Synteny of resistance genes (position on contig)*	*Colistin resistance-conferring mutations* (***mgrB, crrB, kpnEF, phoPQ, and pmrAB*)*	*Fluoroquinolone resistance-conferring mutations* (***gyrA, gyrB parC** and **parE*)*	*ompK36 porin**
KP8 (ST307)	*1 (chromosome)* *5 (chromosome)*	bla*SHV-28(145206-146063)* OqxB19*(3195309-3198461)*:OqxA*(3198485-3199657)* …fosA*(1288555-1288974)*:LysR	crrB *(D189E; V237I)*, pmr*B (L213M)*, pmr*A (A41T)*	par*C (S104I)* gyr*A (S83I)*	*First 22aa were all mutated; no mutation from aa 23-372 (found on contig 5)*
KP10 (ST39)	*1 (chromosome)* *3 (chromosome)* *6 (chromosome)*	bla*SHV-11(45566-46423)* OqxB19*(745718-748870)*:OqxA*(748894-750066)* fosA*(1347213- 1347620)*:LysR	crrB *(gene absent)*, pmr*A (M66I)*	*No mutation*	*First 22aa were all mutated; Del TS (183-184), P185A, A192W, L193S, Y209W, N224T, G225D, D226E, R229S, L230V, D231P, K232A,* *Ins L (232-233), T256S, Del FSGNGE (267-272), S273A, D274G, I276L, Del S (277), I312L, Ins R (313-314), L320I, E349D, D351S, R355N. (found on contig 3)*
KP15 (ST607)	*3 (chromosome)* *5 (chromosome)* *8 (chromosome)*	OqxB19*(1205099-1208251)*:OqxA*(1208275-1209447)* fosA*(1444779-1445186)*:LysR bla*SHV-1(280230-281087)*	crrB *(gene absent)*	*No mutation*	*First 22aa were all mutated; Q54**, Del TS (183-184), P185A, A192W, L193S, Y209W, N224T, G225D, D226E, R229S, L230V, D231P, K232A,* *Ins L (232-233), T256S, Del FSGNGE (267-272), S273A, D274G, I276L, Del S (277), I312L, Ins R (313-314), L320I, E349D, D351S, R355N. (found on contig 2)*
KP29 (ST17)	*6 (chromosome)* *9 (chromosome)*	fosA*(984001-984408)*:LysR… OqxB19*(2832714-2835866)*:OqxA(2835890-2837062) bla*SHV-1(30422-31279)*	crrB *(D189E; V237I)*, kpn*E (K112Q)*, pmr*A (E57G)*	*No mutation*	*First 22aa were all mutated; T86V, S88G, S89T, S90D, D91K, A93S, Del GT (182-183),* *S184D, P185M, L193Q, L204V, Y209W, N224T, G225D, R229N, D231V, K232L, N237D, T256S, Del FSGNGE (267-272), S273A, D274G, I276L, Del S (277),*

					I312L, Ins R (313-314), L320I, E349D, D351S, R355N. (found on contig 6)
KP32 (ST3559)	*1 (chromosome)*	blaSHV-11*(45566-6423)*…fosA*(1599312-1599719)*:LysR…OqxB19*(3483431-3486583)*:OqxA*(3486607-3487779)*	crrB *(gene absent)*, mgrB *(F44L; I45V)*, kpn*E (I88M; K107R)*	*No mutation*	*First 22aa were all mutated; T183A, G191T, F200Y, Ins L (183-184), H220N, N224L, Ins S (228-229), R229K, D231A, K232L, Del FSGNGE (267-272), S273A, D274G, I276L, Del S (277),I312L, Ins R (313-314), L320I, E349D, D351S, R355N. (found on contig 1)*
KP33 (ST39)	*1 (chromosome)*	bla*SHV-11(45566-46423)*	crrB *(gene absent)*, pmr*A (M66I)*	*No mutation*	*First 22aa were all mutated; Del TS (183-184), P185A, A192W, L193S, Y209W, N224T, G225D, D226E, R229S, L230V, D231P, K232A,*
	3 (chromosome)	OqxB19*(745718-748870)*:OqxA*(748894-750066)*			*Ins L (232-233), T256S, Del FSGNGE (267-272), S273A, D274G, I276L, Del S (277), I312L, Ins R (313-314), L320I, E349D, D351S, R355N. (found on contig 3)*
	6 (chromosome)	fosA*(1347213-1347620)*:LysR			

*Genes without mutations are not shown. Reference *K. pneumoniae* genome used was *K. pneumoniae* ATCC 13883 (PRJNA244567)

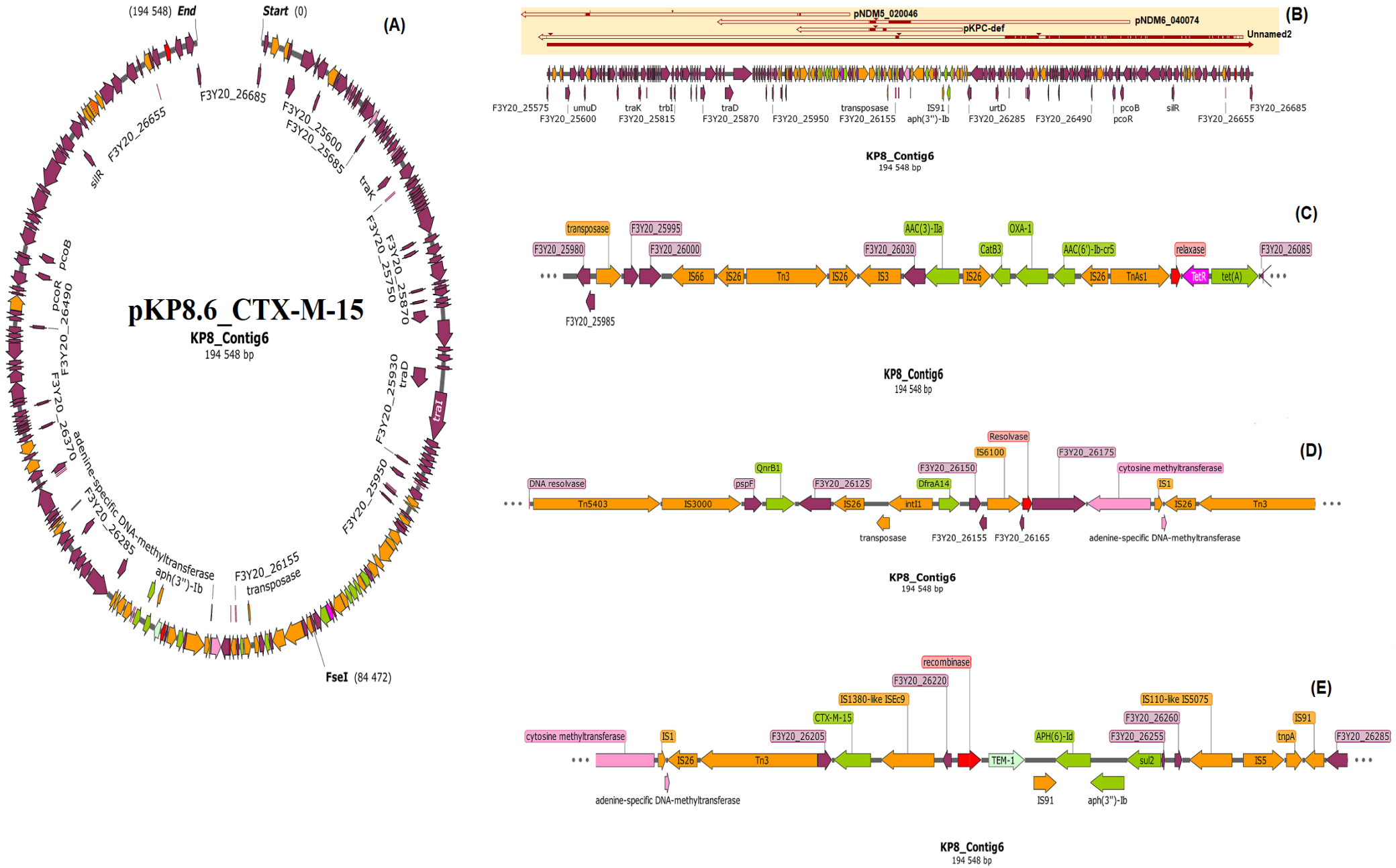
Supplementary data 2.3. Comparison of closely related* K. pneumoniae *strains on the phylogeny tree reported in different countries

Strain	***Country***	***Year***	***Sequence Type (ST)***	***Resistance determinants***	***Plasmids replicons***
KP33_1	*Thailand*	*2015*	*ST14*	***NDM-1***, *CTX-M-15*, aadA2, armA, aph(3')-VlA, msr*(E)*, mph*(E)*, sul1, dfrA12, dfrA1, dfrA14, aac(6')-Ib, aac(6')-Ib-cr, cat, qnrB1, tet(D).	*IncHI1B*
KP64	*Thailand*	*2015*	*ST14*	***NDM-1***, *CTX-M-15*, *OXA-1*, *SHV-28*, *TEM-1B*, aadA2, armA, aph(3')-Vla, msr*(E)*, mph*(E)*, sul1, dfrA12, dfrA1, cat, aac(6')-Ib-cr, aac(6')-Ib, fosA, oqxAB,	*IncR*
CR-HvKP1	*China*	*2016*	*ST11*	***KPC-2***, *CTX-M-65*, *TEM-1B*, rmtB, catA2, fosA14	*IncFII/R*, *Incl1*
CRKP-1215	*South Korea*	*2014*	*ST147*	***NDM-5***, ***OXA-181***, *CTX-M-15*, *TEM-1B*, *SHV-11*, *OXA-1*, aadA3, aac(6')-Ib-cr, aacA4, dfrA23, sul1, mph*(A)*, rmt*(B)*, erm(*B*), fosA, oqxAB	*IncFII*
CN1	*United States*	*2013*	*ST392*	***KPC-2***, *CTX-M-15*, *OXA-1*, *TEM-1B*	-
G702R3B2	*South Africa*	*2016*	*ST152*	*CTX-M-15*, *OXA-1*, *TEM-1B*, aadA16, aac(6')-lb-cr, aac(3'')ll-a, aph(6)-ld, aph(3')-lb, sul1, sul2, tetA, tetB, tetD, dfrA14, dfrA27, oqxA, oqxB, catA1, catB4, fosA, arr-3, gyrA, parC	*IncFIB*, *IncFII*, *IncFII(k)*, *IncN*, *IncQ1*, *ColpVC*, *ColRNAI*
KP33 (This study)	*South Africa*	*2018*	*ST39*	***NDM-1***, *OXA-1*, *CTX-M-15*, *SHV-40*, *SHV-56*, *SHV-79*, *SHV-85*, *SHV-89*, *TEM-1B*, aac(6')-lb-cr, aph(3')-lb, aph(6)-ld, rmtC, aac(6')-lb-cr, oqxA, oqxB, qnrB1, tet(A), fosA, catB3, dfrA14, sul1, sul2	*IncFIB (k)*, *IncFII (k)*, *IncFII (yp)*

Supplementary data 3: **Intact phages identified in carbapenem-resistant *K. pneumoniae* clinical isolates**

Phage identified	***GC%***	***No CDS***	***Length (kb)***	***Isolates***
PHAGE_Salmon_SEN5_NC_028701(21)	*54.79*	*49*	*37.7*	*Kp8, Kp15, Kp29*
PHAGE_Salmon_Fels_2_NC_010463(33)	*51.82*	*42*	*41.5*	*Kp8, Kp32*
PHAGE_Cronob_ENT47670_NC_019927(12)	*53.15*	*71*	*49.1*	*Kp8*
PHAGE_Salmon_SPN3UB_NC_019545(12)	*52.02*	*68*	*55.6*	*Kp8*
PHAGE_Salmon_118970_sal3_NC_031940(11)	*50.44*	*44*	*39.8*	*Kp8, Kp15*
PHAGE_Salmon_SJ46_NC_031129(4)	*52.78*	*27*	*40.5*	*Kp8*
PHAGE_Klebsi_phiKO2_NC_005857(43)	*51.45*	*70*	*54.7*	*Kp8*
PHAGE_Entero_mEp237_NC_019704(10)	*52.26*	*67*	*56.4*	*Kp33, Kp10, Kp29*
PHAGE_Edward_GF_2_NC_026611(21)	*52.58*	*70*	*46.2*	*Kp33, Kp10*
PHAGE_Entero_P1_NC_005856(3)	*54.30*	*31*	*16.5*	*Kp33, Kp10*
PHAGE_Escher_RCS47_NC_042128(3)	*53.61*	*24*	*35.2*	*Kp15*
PHAGE_Escher_RCS47_NC_042128(5)	*53.99*	*34*	*27.1*	*Kp15, Kp29*
PHAGE_Escher_phiV10_NC_007804(33)	*50.84*	*59*	*59.9*	*Kp15*
PHAGE_Salmon_RE_2010_NC_019488(32)	*53.71*	*45*	*37.4*	*Kp29*
PHAGE_Pectob_ZF40_NC_019522(14)	*50.21*	*56*	*48.1*	*Kp29*
PHAGE_Phage_Gifsy_1_NC_010392(11)	*52.09*	*78*	*55.7*	*Kp32*
PHAGE_Salmon_SEN34_NC_028699(25)	*54.27*	*70*	*60.2*	*Kp32*
PHAGE_Staphy_SPbeta_like_NC_029119(3)	*54.40*	*29*	*25.5*	*Kp32*

SUPPLEMENTARY FIGURES 1-14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traD
traI
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(B)
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IS26
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CTX-M-15
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IS1
IS26
Tn3
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IS5
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IS91
aph(3'')-Ib
KP8_Contig6
194 548 bp

Figure S1.1

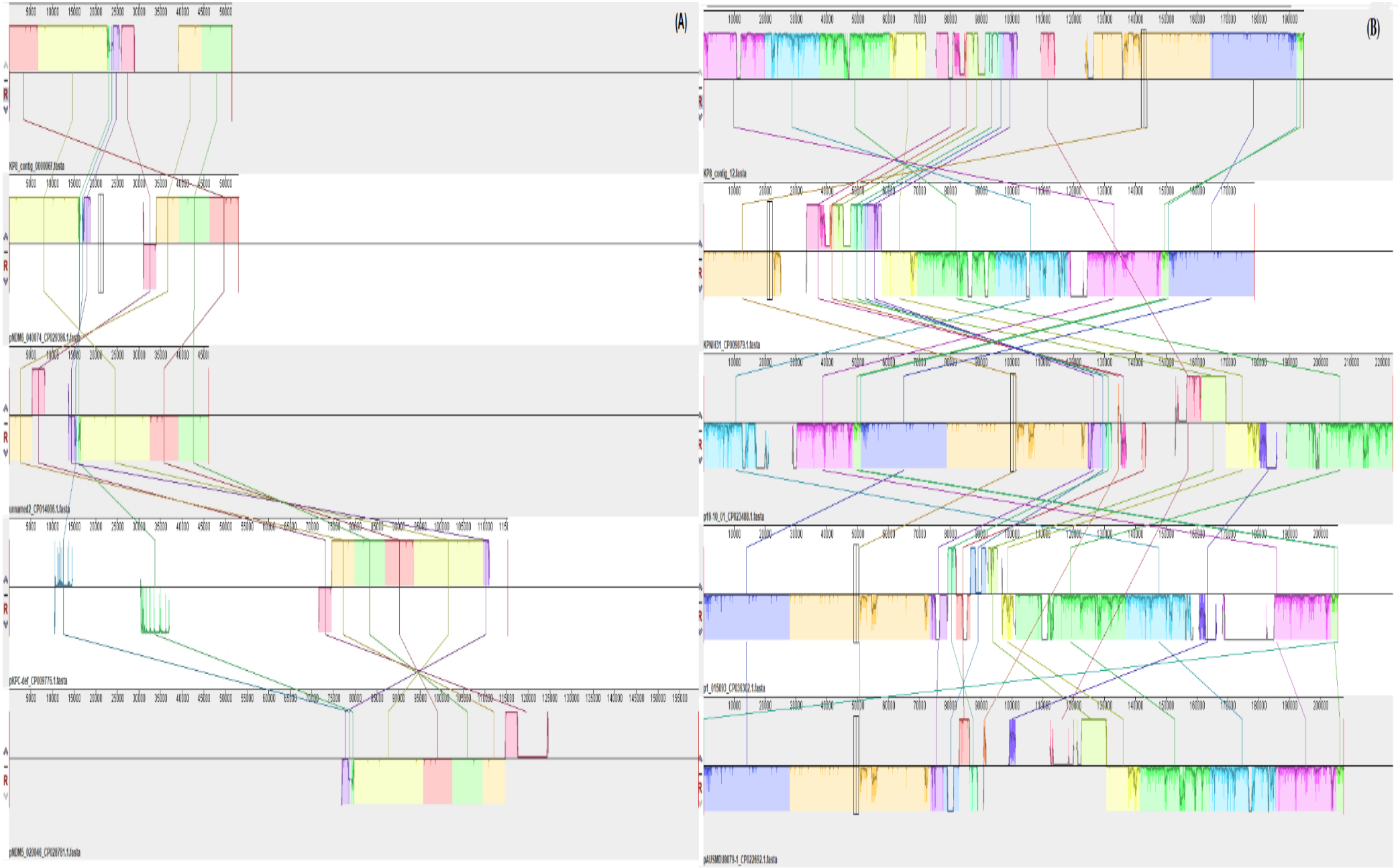
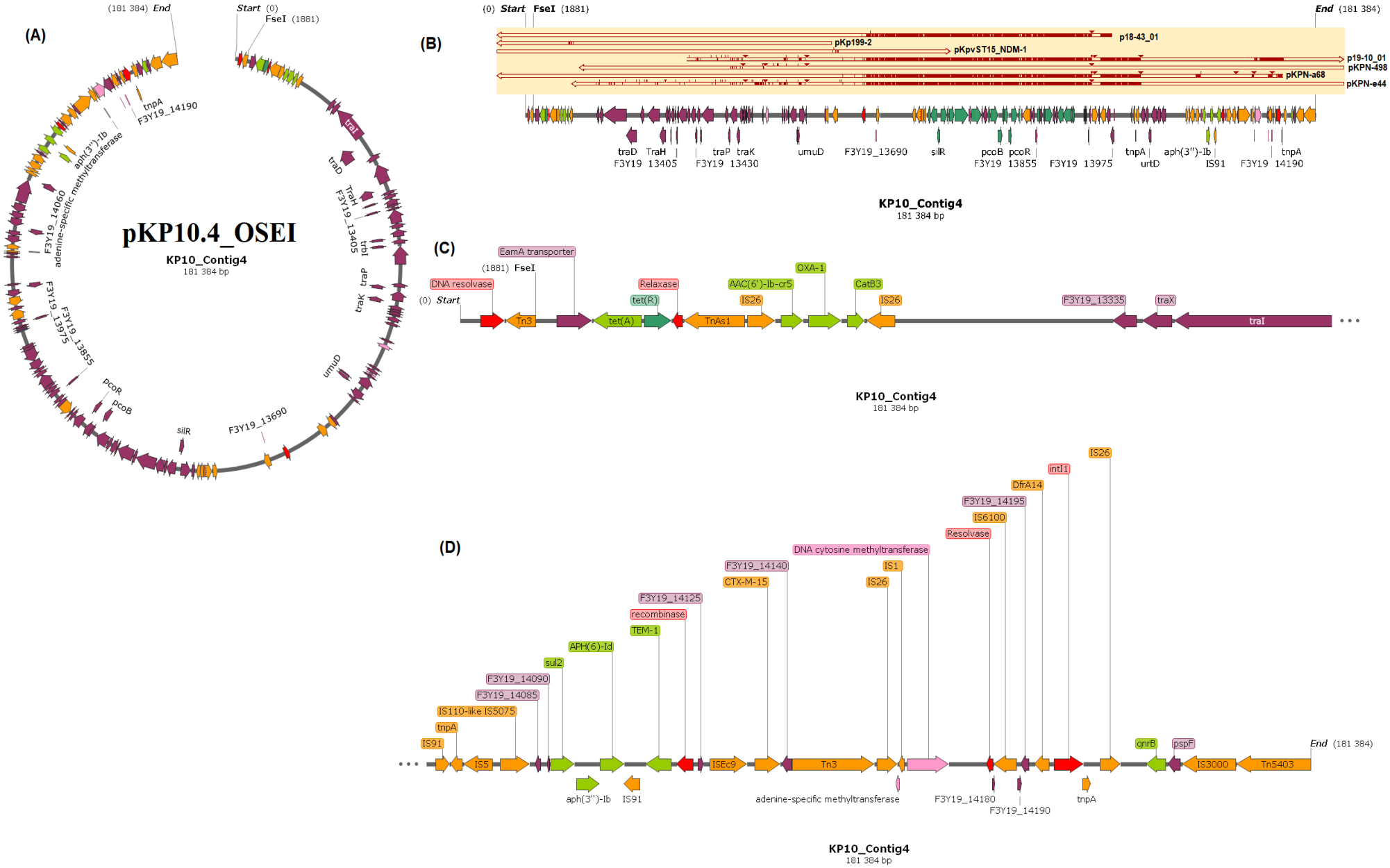


Figure S1.2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F3Y19_13855
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pcoB
silR
F3Y19_13690
umuD
traK
traP
traI
traH F3Y19_13405
traD
(B)
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pKPN-498
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pKPN-e44
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TraH F3Y19 13430
traP traK
umuD
F3Y19_13690
silR
pcoB pcoR F3Y19 13855
F3Y19 13975
tnpA urtD
aph(3'')-Ib IS91
tnpA F3Y19 14190
KP10_Contig4
181 384 bp
(C)
EamA transporter
(1881) FseI
DNA resolvase
Relaxase
AAC(6')-Ib-cr5
OXA-1
CatB3
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tet(R)
IS26
IS26
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Tn3
tet(A)
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traI
KP10_Contig4
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DfrA14
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Resolvase
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CTX-M-15
IS26
F3Y19_14125
recombinase
TEM-1
APH(6)-Id
sul2
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F3Y19_14085
IS110-like IS5075
tnpA
IS91
qnrB
pspF
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Figure S2.1

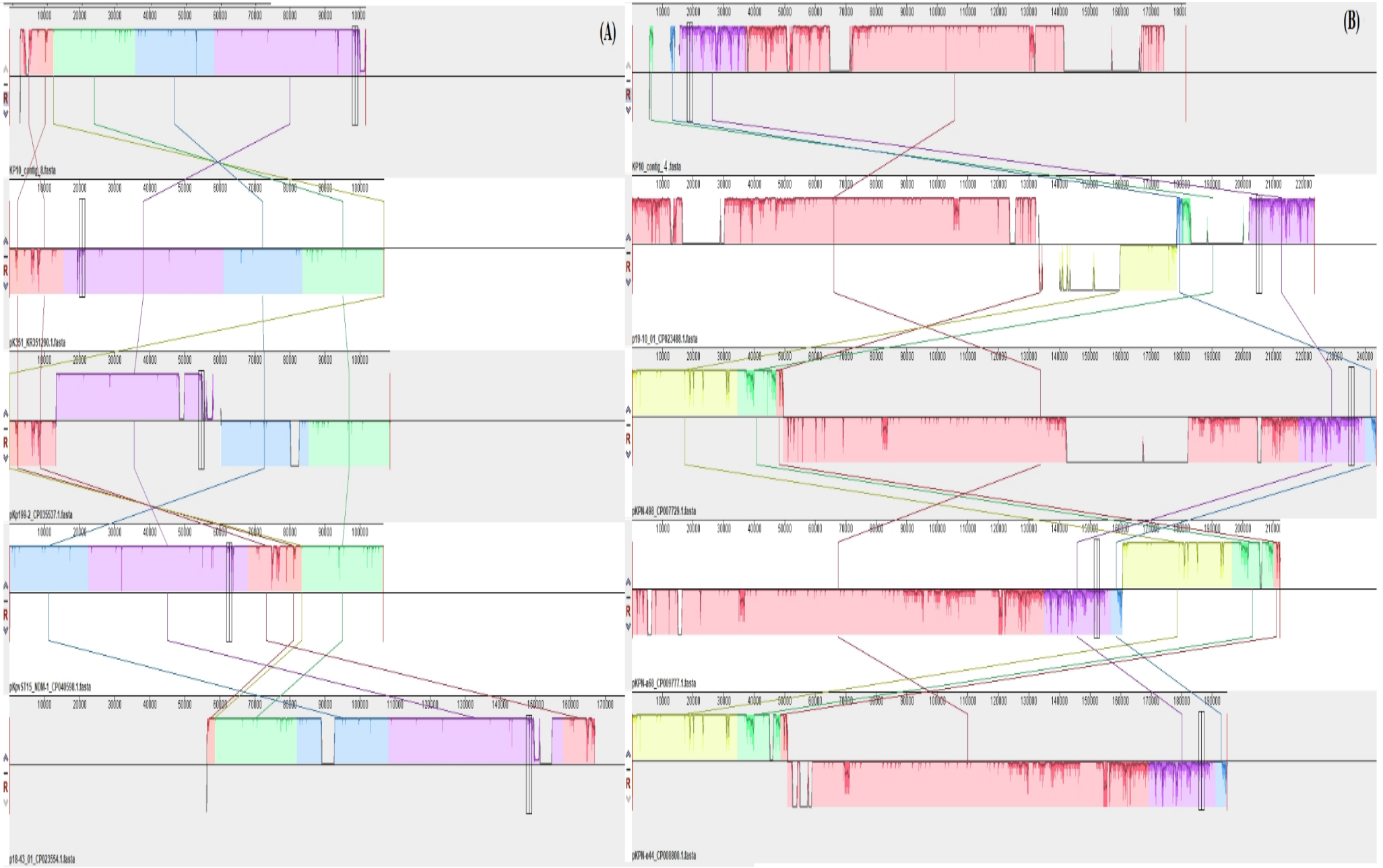


Figure S2.2

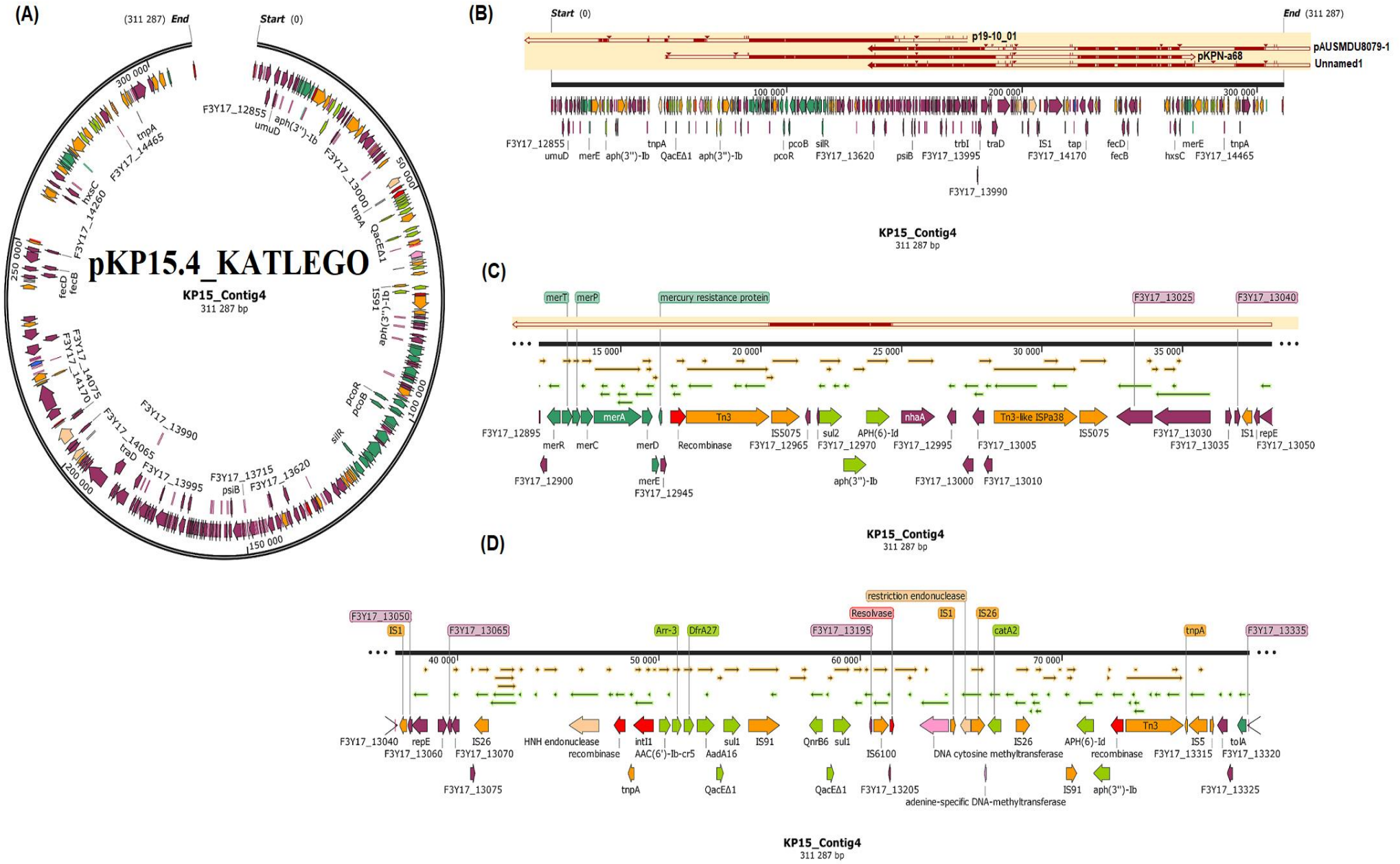

(A)
pKP15.4_KATLEGO
KP15_Contig4
311 287 bp
(B)
p19-10_01
pKPN-a68
pAUSMDU8079-1
Unnamed1
KP15_Contig4
311 287 bp
(C)
KP15_Contig4
311 287 bp
(D)
KP15_Contig4
311 287 bp

Figure S3.1

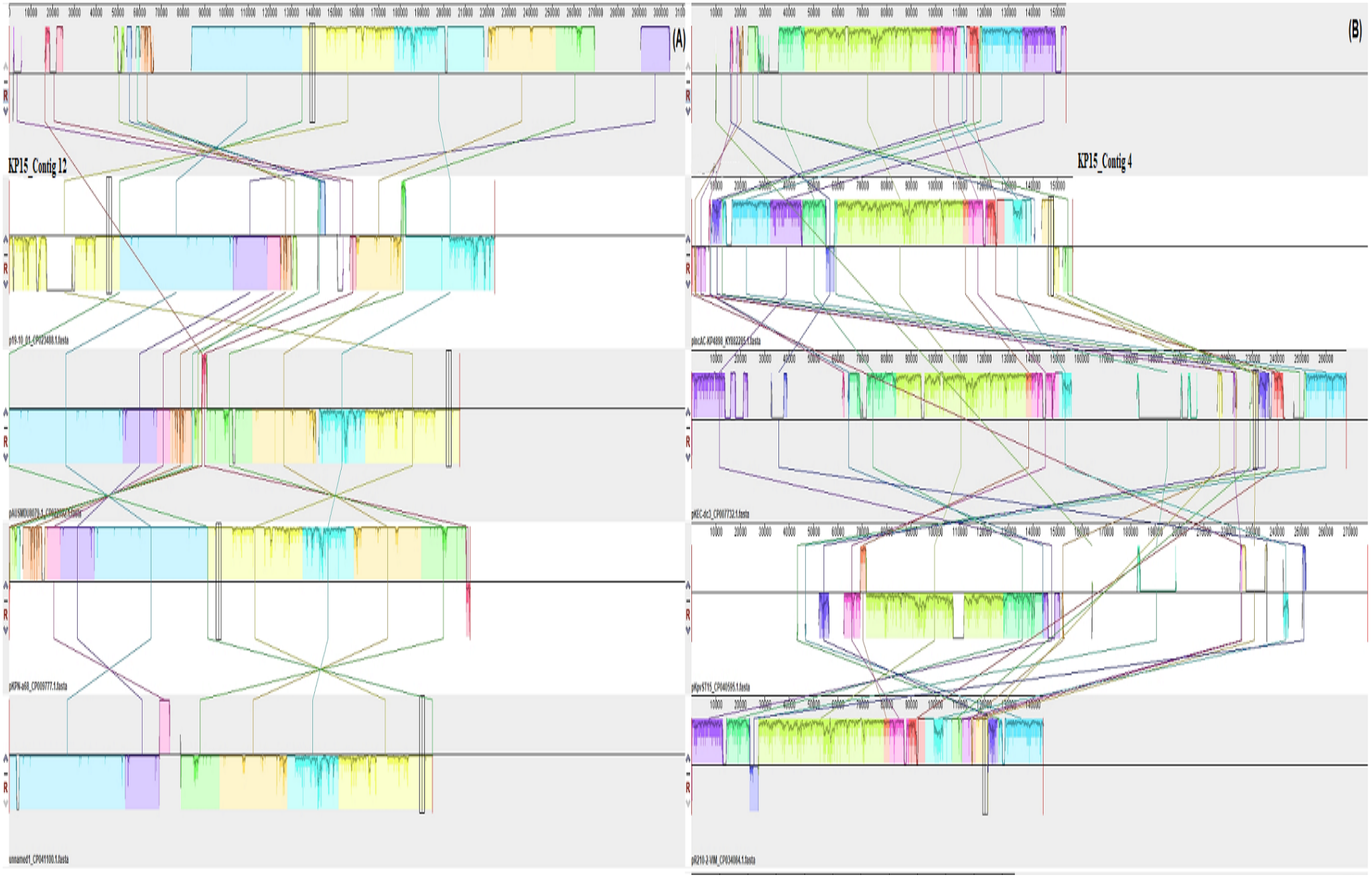


Figure S3.2

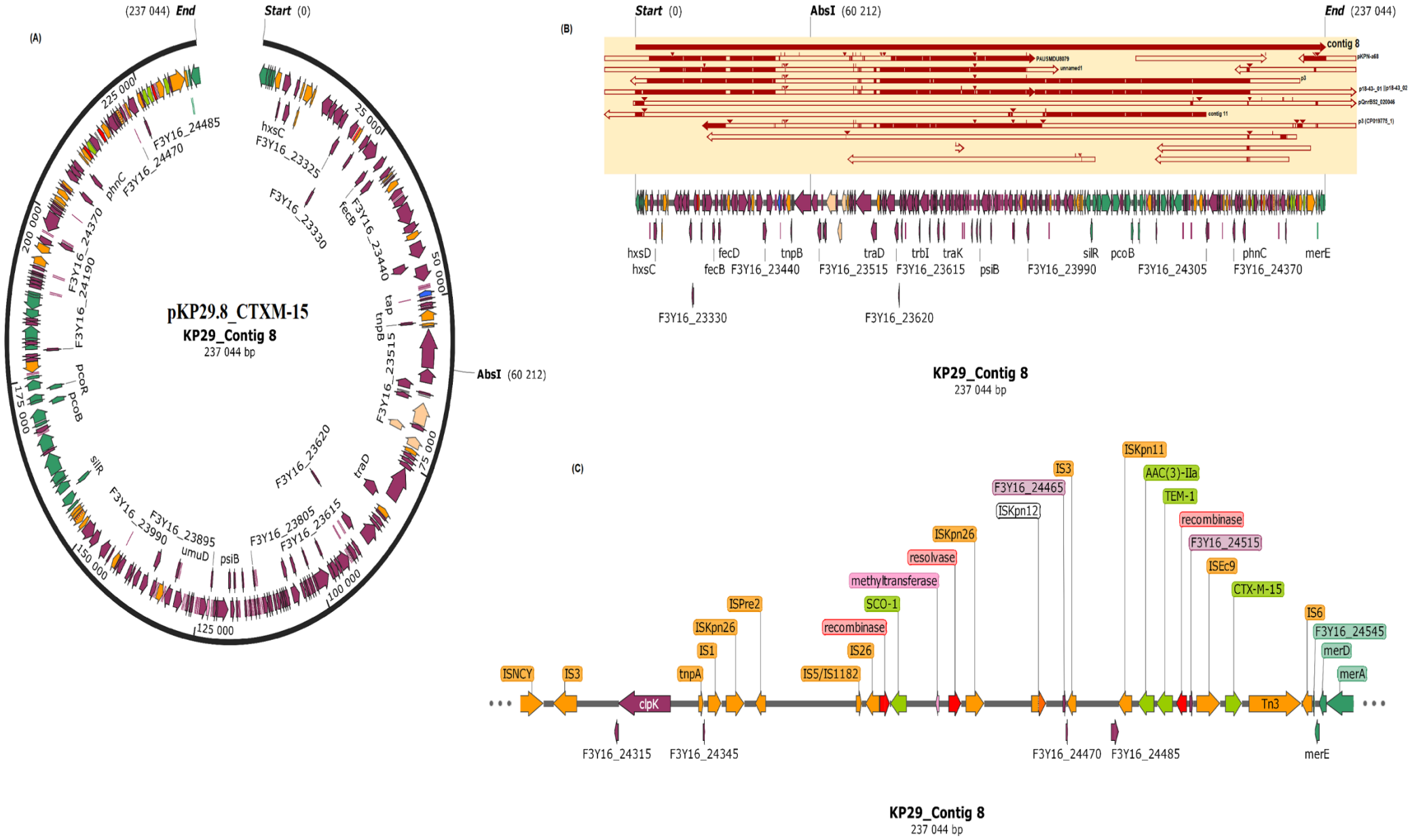

(A)
(237 044) End
Start (0)
AbsI (60 212)
pKP29.8_CTXM-15
KP29_Contig 8
237 044 bp
25 000
50 000
75 000
100 000
125 000
150 000
175 000
200 000
225 000
hxsC
F3Y16_23325
F3Y16_23330
fecB
F3Y16_23440
tap
tnpB
F3Y16_23515
F3Y16_23620
traD
F3Y16_23805
F3Y16_23615
F3Y16_23895
umuD
psiB
F3Y16_23990
silR
pcoB
pcoR
F3Y16_24190
F3Y16_24370
phnC
F3Y16_24470
F3Y16_24485
(B)
Start (0)
AbsI (60 212)
End (237 044)
contig 8
hxsD
hxsC
fecD
fecB
tnpB
F3Y16_23440
traD
F3Y16_23515
trbI
F3Y16_23615
traK
psiB
silR
F3Y16_23990
pcoB
F3Y16_24305
phnC
F3Y16_24370
merE
F3Y16_23330
F3Y16_23620
KP29_Contig 8
237 044 bp
(C)
ISKpn11
AAC(3)-IIa
IS3
F3Y16_24465
TEM-1
ISKpn12
recombinase
ISKpn26
F3Y16_24515
resolvase
ISEc9
methyltransferase
CTX-M-15
ISPre2
SCO-1
IS6
ISKpn26
recombinase
F3Y16_24545
IS1
IS26
merD
ISNCY
IS3
tnpA
IS5/IS1182
merA
clpK
Tn3
F3Y16_24315
F3Y16_24345
F3Y16_24470
F3Y16_24485
merE
KP29_Contig 8
237 044 bp

Figure S4.1

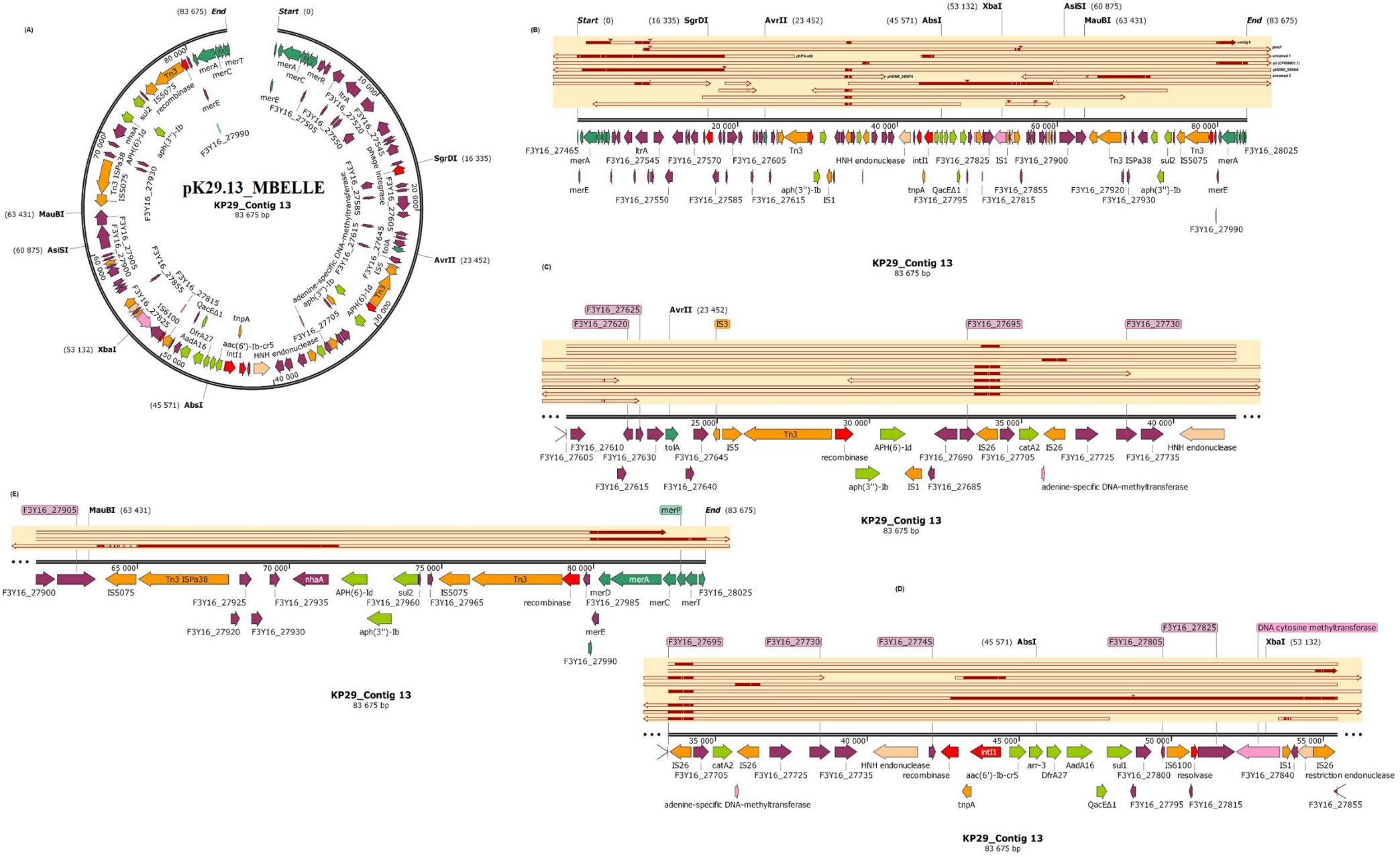

(A)
pK29.13_MBELLE
KP29_Contig 13
83 675 bp
(B)
KP29_Contig 13
83 675 bp
(C)
KP29_Contig 13
83 675 bp
(D)
KP29_Contig 13
83 675 bp
(E)
KP29_Contig 13
83 675 bp

Figure S4.2

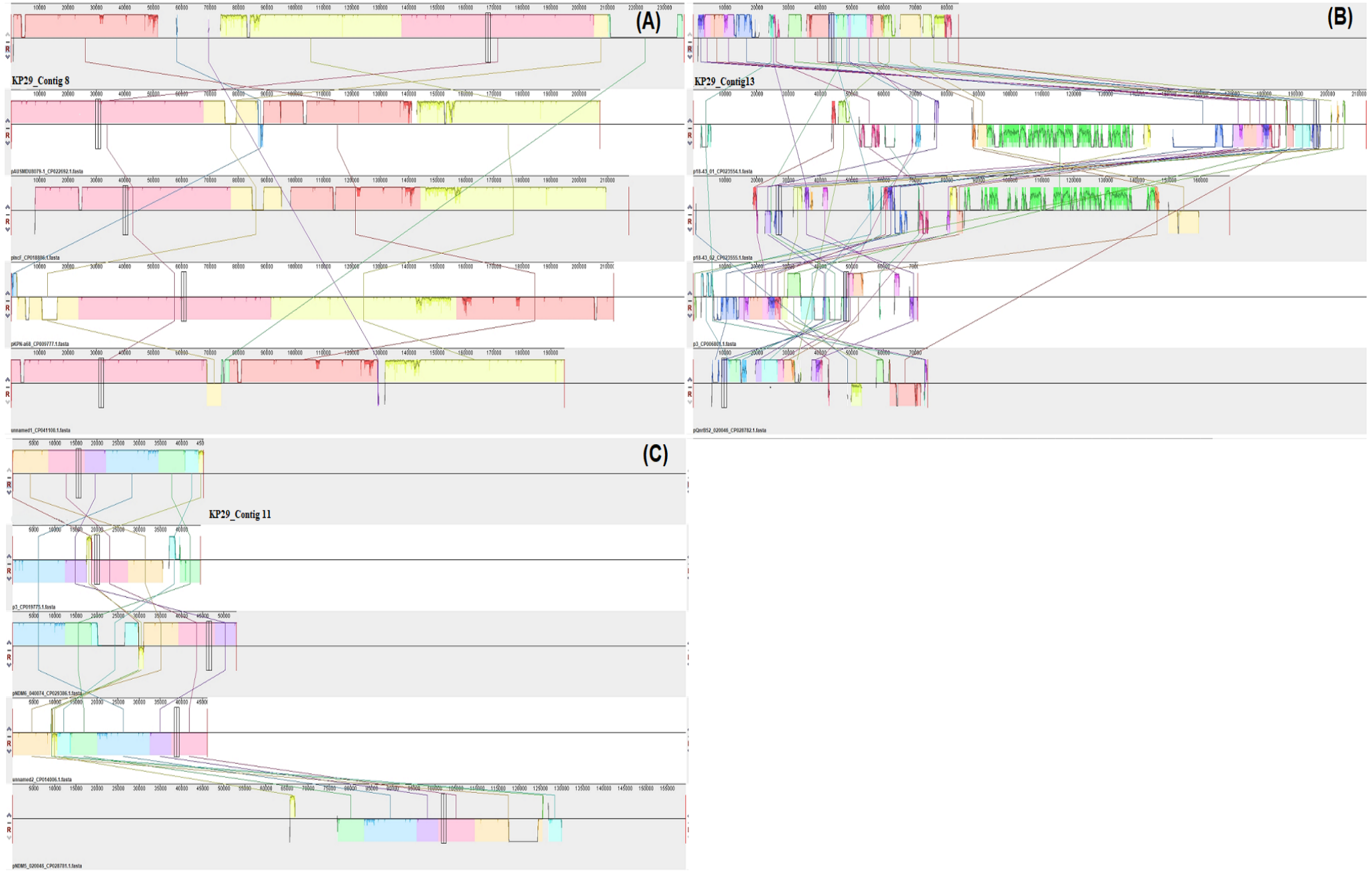


Figure S4.3

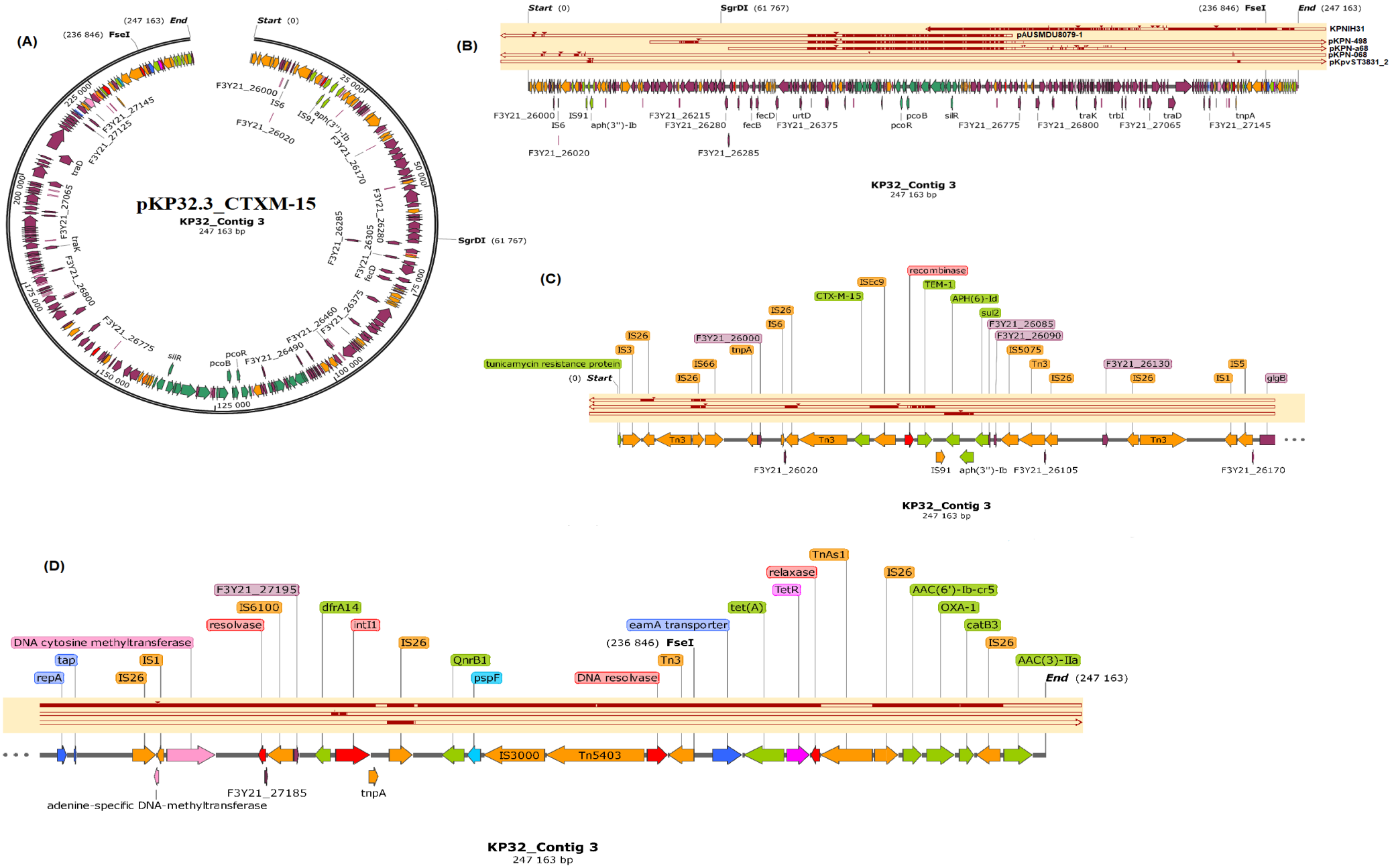

(A)
pKP32.3_CTXM-15
KP32_Contig 3
247 163 bp
(247 163) End
(236 846) FseI
Start (0)
SgrDI (61 767)
(B)
Start (0)
SgrDI (61 767)
(236 846) FseI
End (247 163)
pAUSMDU8079-1
KPNIH31
pKPN-498
pKPN-a68
pKPN-068
pKPvST3831_2
KP32_Contig 3
247 163 bp
(C)
recombinase
ISEc9
TEM-1
CTX-M-15
APH(6)-Id
sul2
F3Y21_26085
F3Y21_26090
IS5075
Tn3
F3Y21_26130
IS5
IS1
glgB
IS26
IS6
IS3
F3Y21_26000
tnpA
IS66
tunicamycin resistance protein
(0) Start
F3Y21_26020
IS91
aph(3'')-Ib
F3Y21_26105
F3Y21_26170
KP32_Contig 3
247 163 bp
(D)
TnAs1
relaxase
TetR
IS26
AAC(6')-Ib-cr5
OXA-1
catB3
AAC(3)-IIa
F3Y21_27195
IS6100
dfrA14
resolvase
intI1
tet(A)
eamA transporter
DNA cytosine methyltransferase
tap
IS1
repA
QnrB1
pspF
DNA resolvase
(236 846) FseI
End (247 163)
IS3000
Tn5403
F3Y21_27185
tnpA
adenine-specific DNA-methyltransferase
KP32_Contig 3
247 163 bp

Figure S5.1

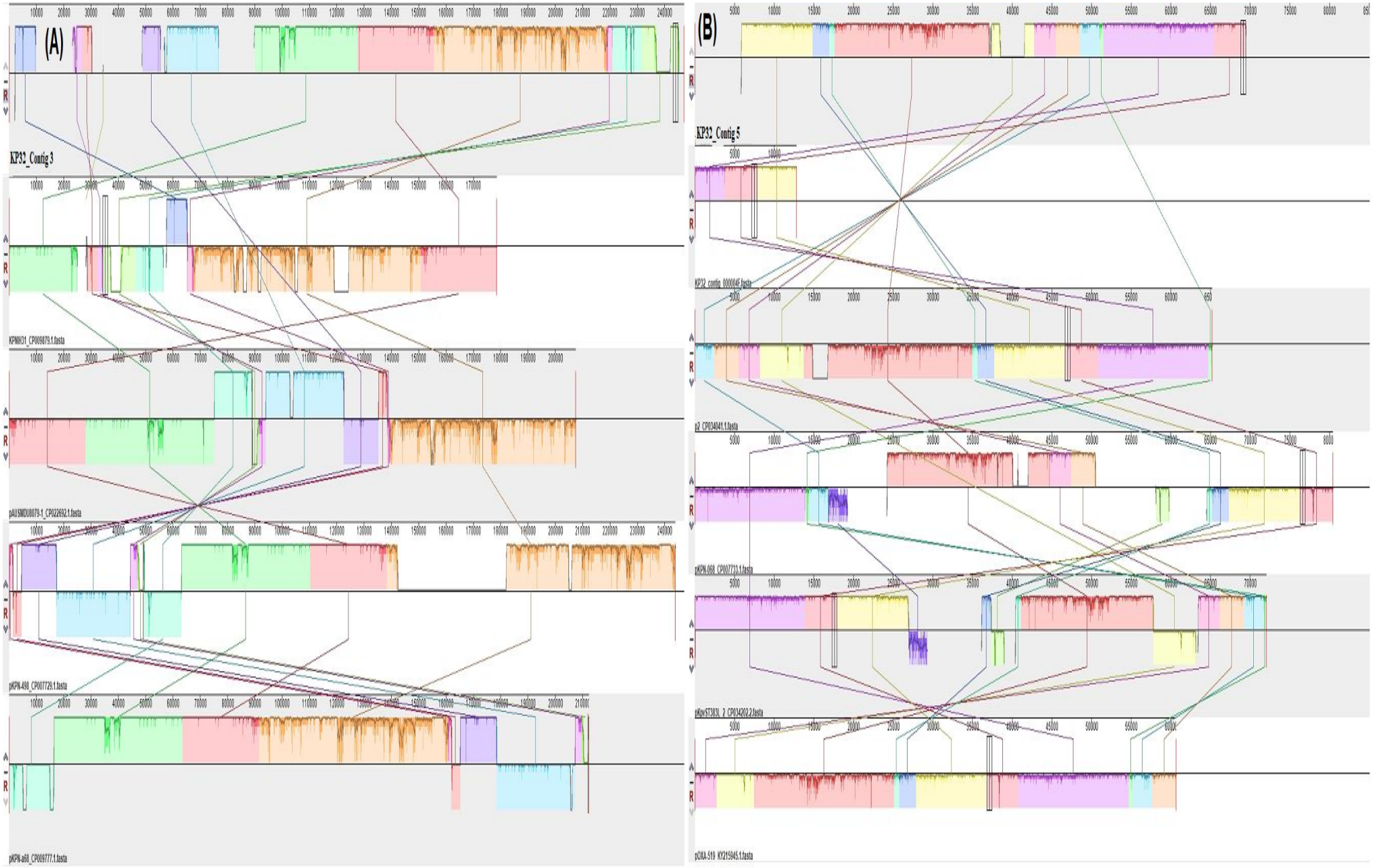

(A)
KP32_Contig 3
KPNIH31_CP009879.1.fasta
pAUSMDU8079-1_CP022692.1.fasta
pKPN-498_CP007726.1.fasta
pKPN-a68_CP009777.1.fasta
(B)
KP32_Contig 5
KP32_contig_000004F.fasta
p2_CP034041.1.fasta
pKPN-868_CP007733.1.fasta
pKpvST383L_2_CP034202.2.fasta
pOXA-519_KY215945.1.fasta

Figure S5.2

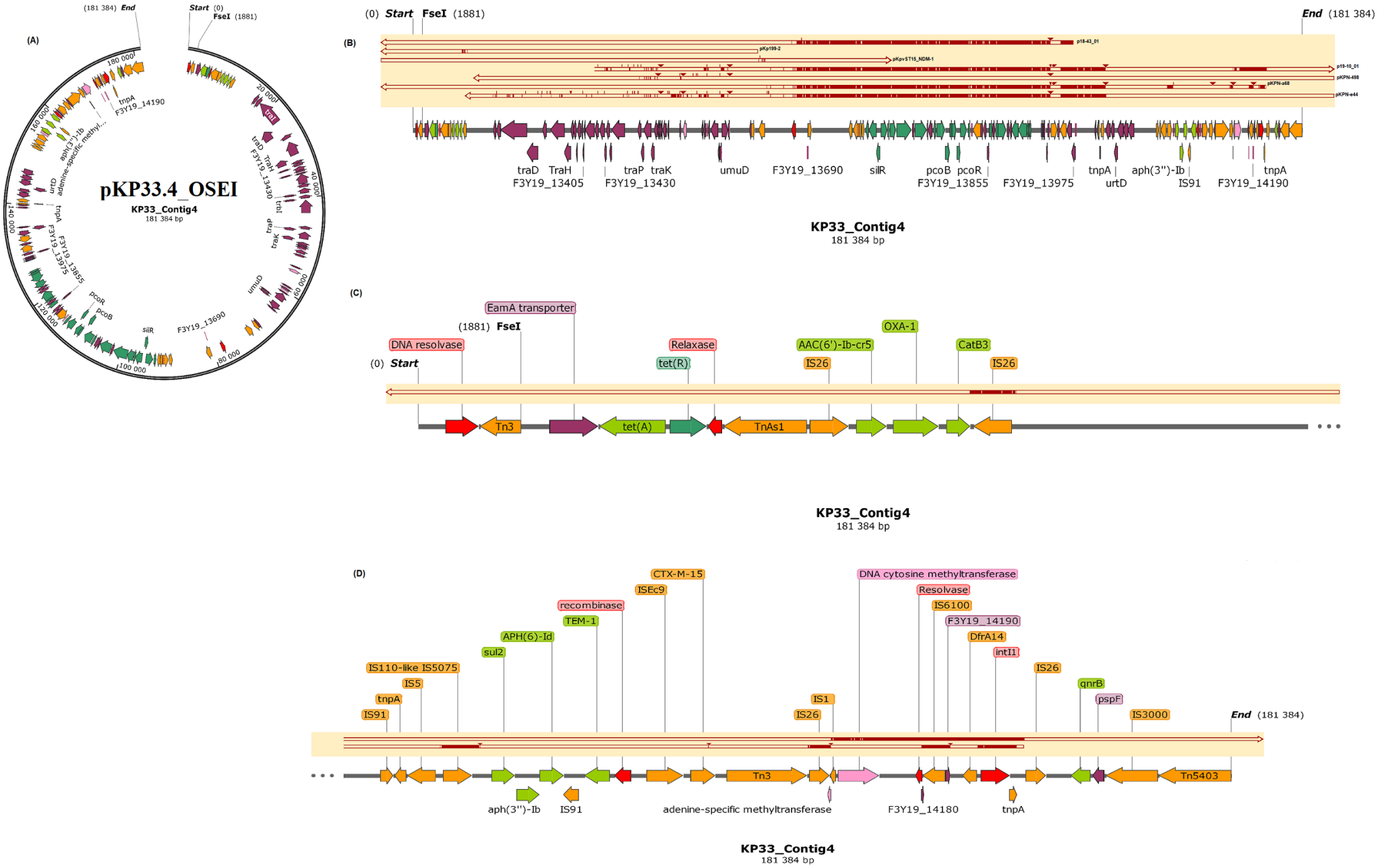

(A)
pKP33.4_OSEI
KP33_Contig4
181 384 bp
(181 384) End
Start (0)
FseI (1881)
(B)
(0) Start FseI (1881)
End (181 384)
traD TraH traP traK umuD F3Y19_13690 silR pcoB pcoR tnpA aph(3'')-Ib tnpA
F3Y19_13405 F3Y19_13430 F3Y19_13855 F3Y19_13975 urtD IS91 F3Y19_14190
KP33_Contig4
181 384 bp
(C)
EamA transporter
(1881) FseI
DNA resolvase
Relaxase
tet(R)
(0) Start
AAC(6')-Ib-cr5
IS26
OXA-1
CatB3
IS26
Tn3
tet(A)
TnAs1
KP33_Contig4
181 384 bp
(D)
CTX-M-15
ISEc9
recombinase
TEM-1
APH(6)-Id
sul2
IS110-like IS5075
IS5
tnpA
IS91
DNA cytosine methyltransferase
Resolvase
IS6100
F3Y19_14190
DfrA14
intI1
IS26
qnrB
pspF
IS3000
End (181 384)
IS1
IS26
Tn3
Tn5403
aph(3'')-Ib
IS91
adenine-specific methyltransferase
F3Y19_14180
tnpA
KP33_Contig4
181 384 bp

Figure S6.1

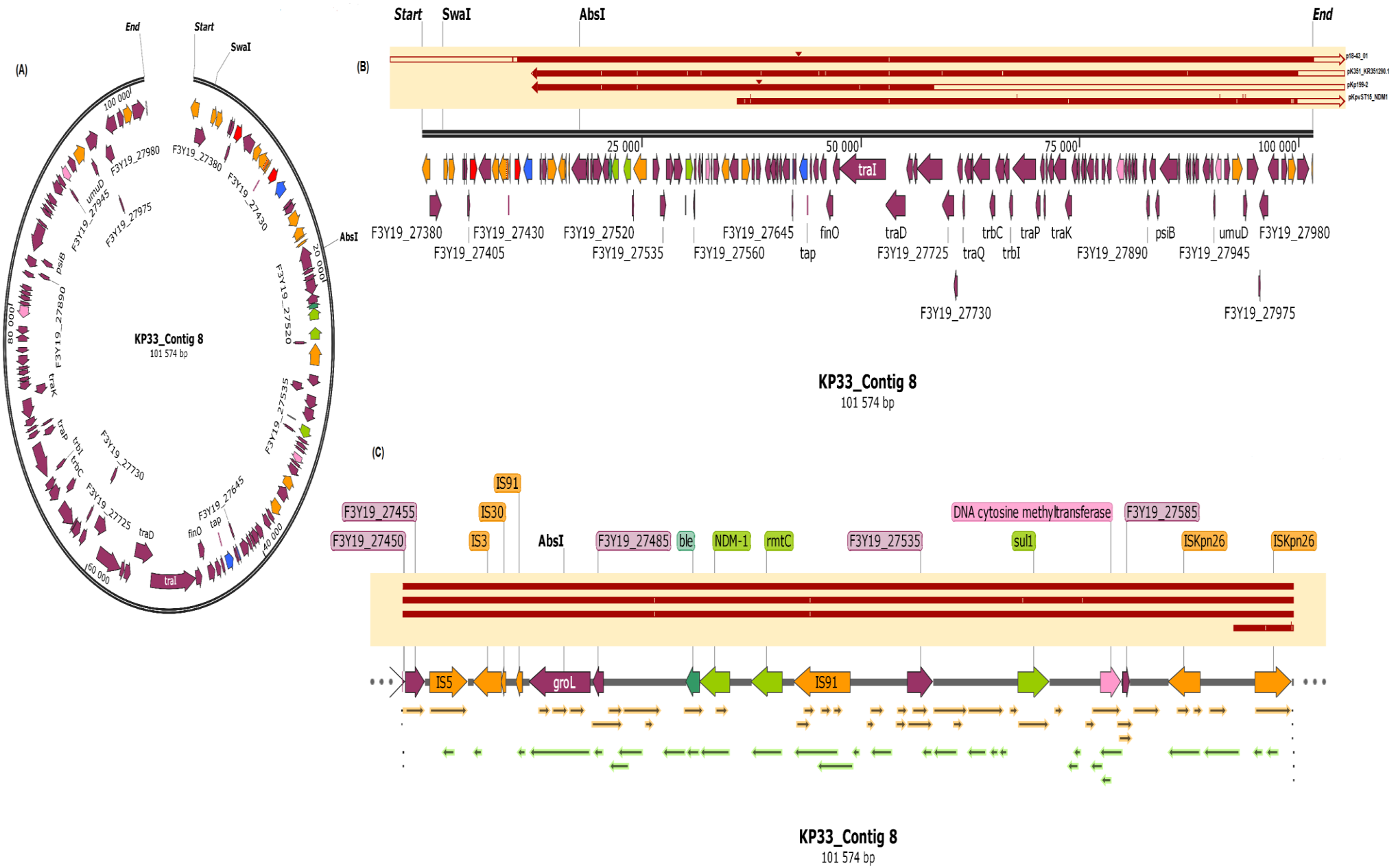

(A)
End
Start
SwaI
AbsI
100 000
20 000
40 000
60 000
80 000
F3Y19_27980
F3Y19_27380
F3Y19_27430
F3Y19_27520
F3Y19_27535
F3Y19_27645
F3Y19_27725
F3Y19_27730
F3Y19_27890
F3Y19_27945
F3Y19_27975
umuD
psiB
traK
trap
tbl
trbC
traD
finO
tap
traI
KP33_Contig 8
101 574 bp
(B)
Start
SwaI
AbsI
End
25 000
50 000
75 000
100 000
traI
F3Y19_27380
F3Y19_27405
F3Y19_27430
F3Y19_27520
F3Y19_27535
F3Y19_27560
F3Y19_27645
tap
finO
traD
F3Y19_27725
F3Y19_27730
traQ
trbC
trbI
traP
traK
F3Y19_27890
psiB
F3Y19_27945
umuD
F3Y19_27980
F3Y19_27975
KP33_Contig 8
101 574 bp
(C)
IS91
F3Y19_27455
F3Y19_27450
IS30
IS3
AbsI
F3Y19_27485
ble
NDM-1
rmtC
F3Y19_27535
DNA cytosine methyltransferase
sul1
F3Y19_27585
ISKpn26
ISKpn26
IS5
groL
IS91
KP33_Contig 8
101 574 bp

Figure S6.2

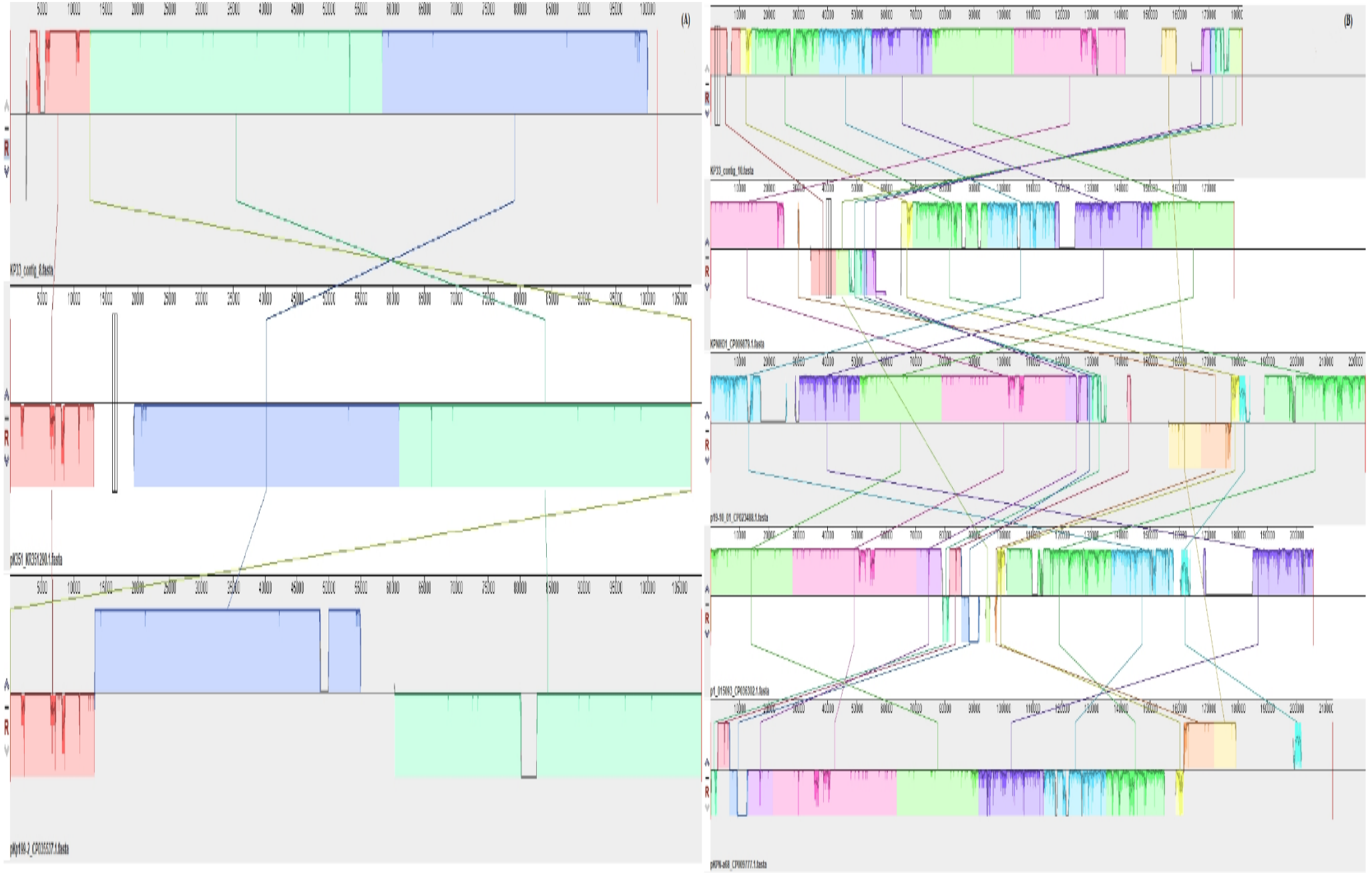


Figure S6.3

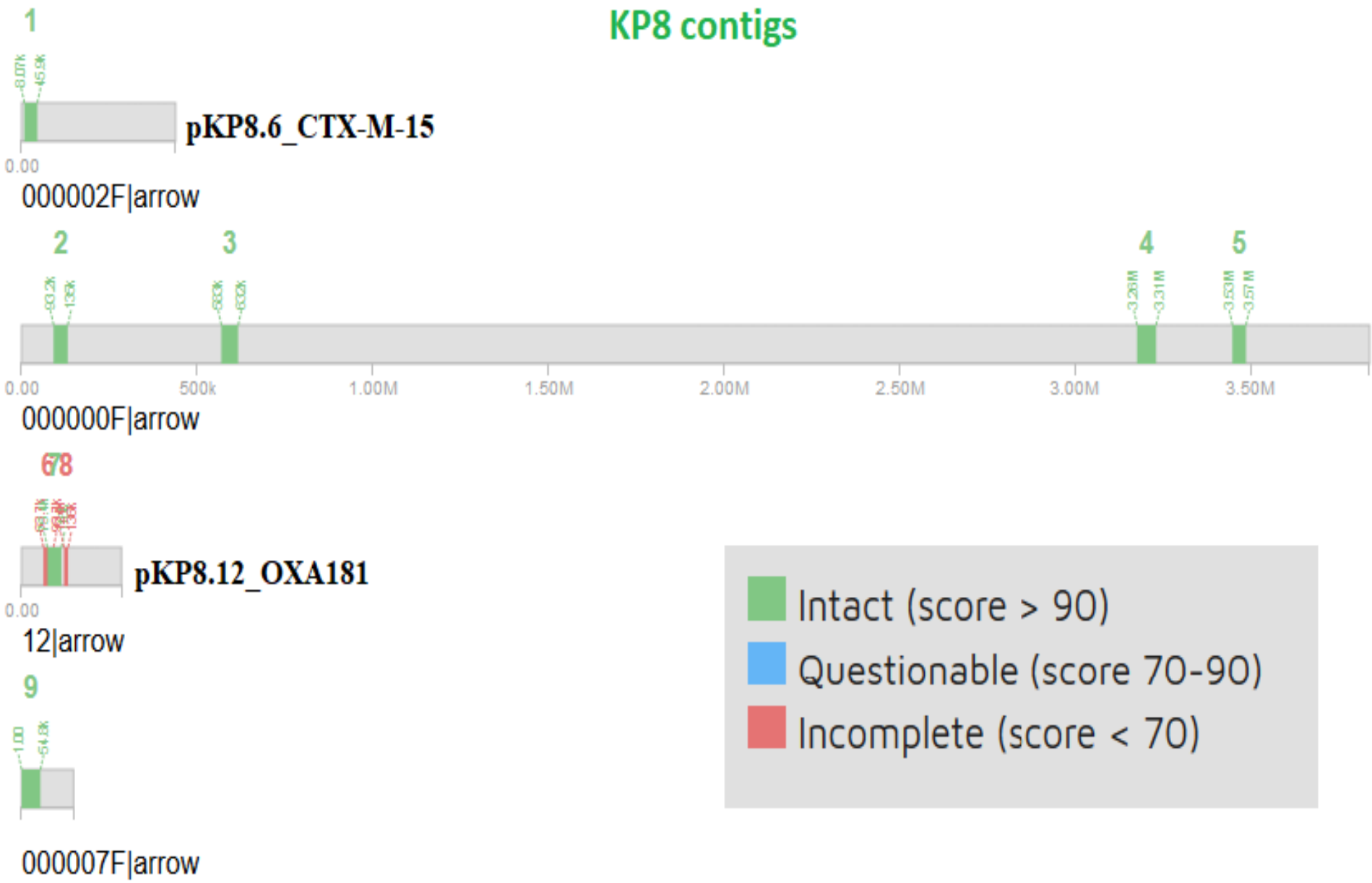

KP8 contigs
1
pKP8.6_CTX-M-15
0.00
000002F|arrow
2
3
4
5
0.00
500k
1.00M
1.50M
2.00M
2.50M
3.00M
3.50M
000000F|arrow
6
7
8
pKP8.12_OXA181
0.00
12|arrow
9
000007F|arrow
Intact (score > 90)
Questionable (score 70-90)
Incomplete (score < 70)

Figure S7.1


Region 1
Region 2
Region 3
Region 4
Region 5
Region 6
Region 7
Region 8
Region 9
Lysis
Terminase
Portal Protein
Protease
Coat Protein
Tail Shaft
Attachment Site
Integrase
Phage-like Protein
Hypotheical Protein
Other
Transposase
Fiber Protein
Plate Protein
tRNA

Figure S7.2

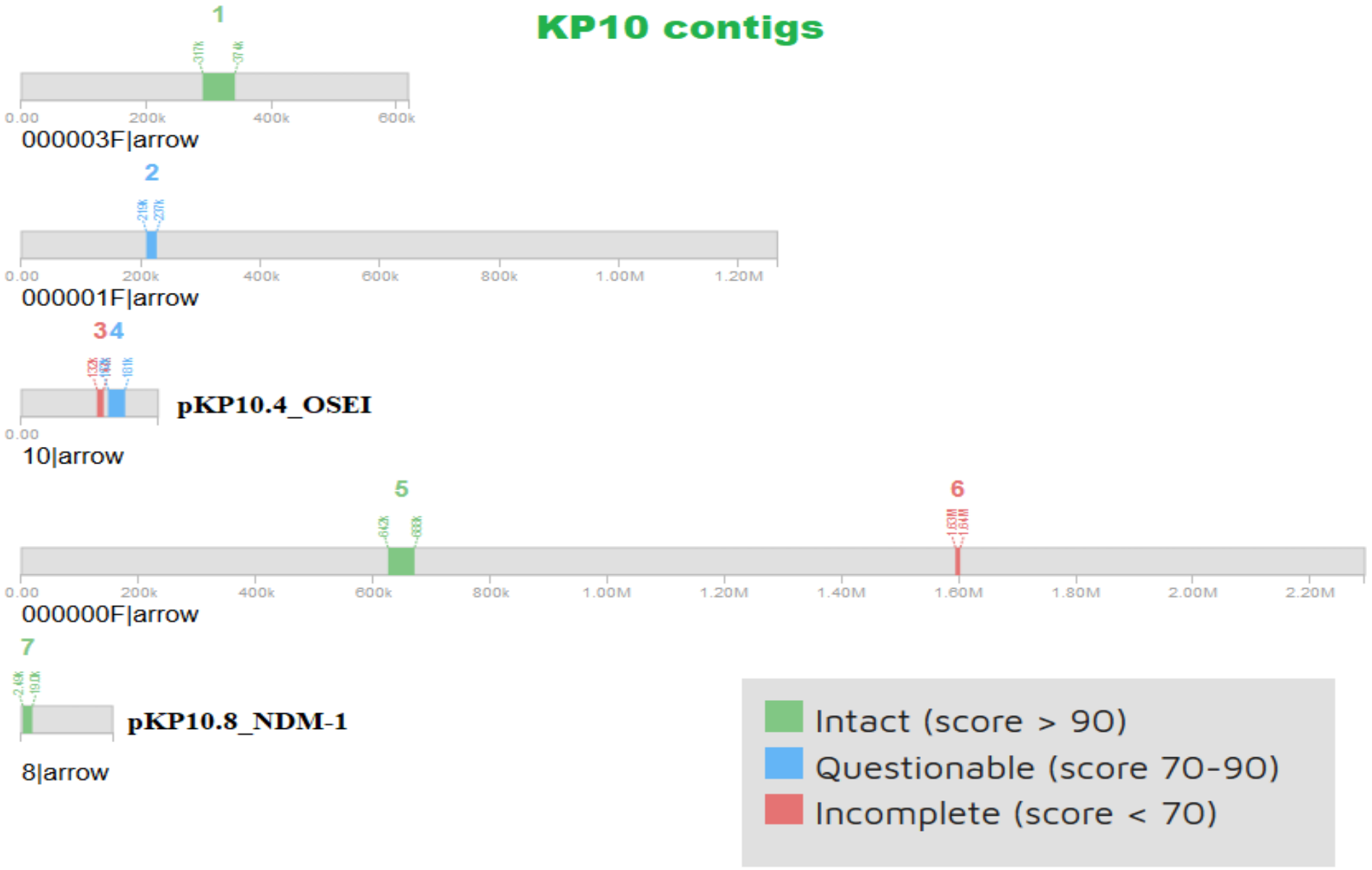

KP10 contigs
1
317k
374k
0.00
200k
400k
600k
000003F|arrow
2
219k
237k
0.00
200k
400k
600k
800k
1.00M
1.20M
000001F|arrow
34
132k
181k
pKP10.4_OSEI
0.00
10|arrow
5
642k
683k
6
1.63M
1.64M
0.00
200k
400k
600k
800k
1.00M
1.20M
1.40M
1.60M
1.80M
2.00M
2.20M
000000F|arrow
7
2.40k
19.0k
pKP10.8_NDM-1
8|arrow
Intact (score > 90)
Questionable (score 70-90)
Incomplete (score < 70)

Figure S8.1

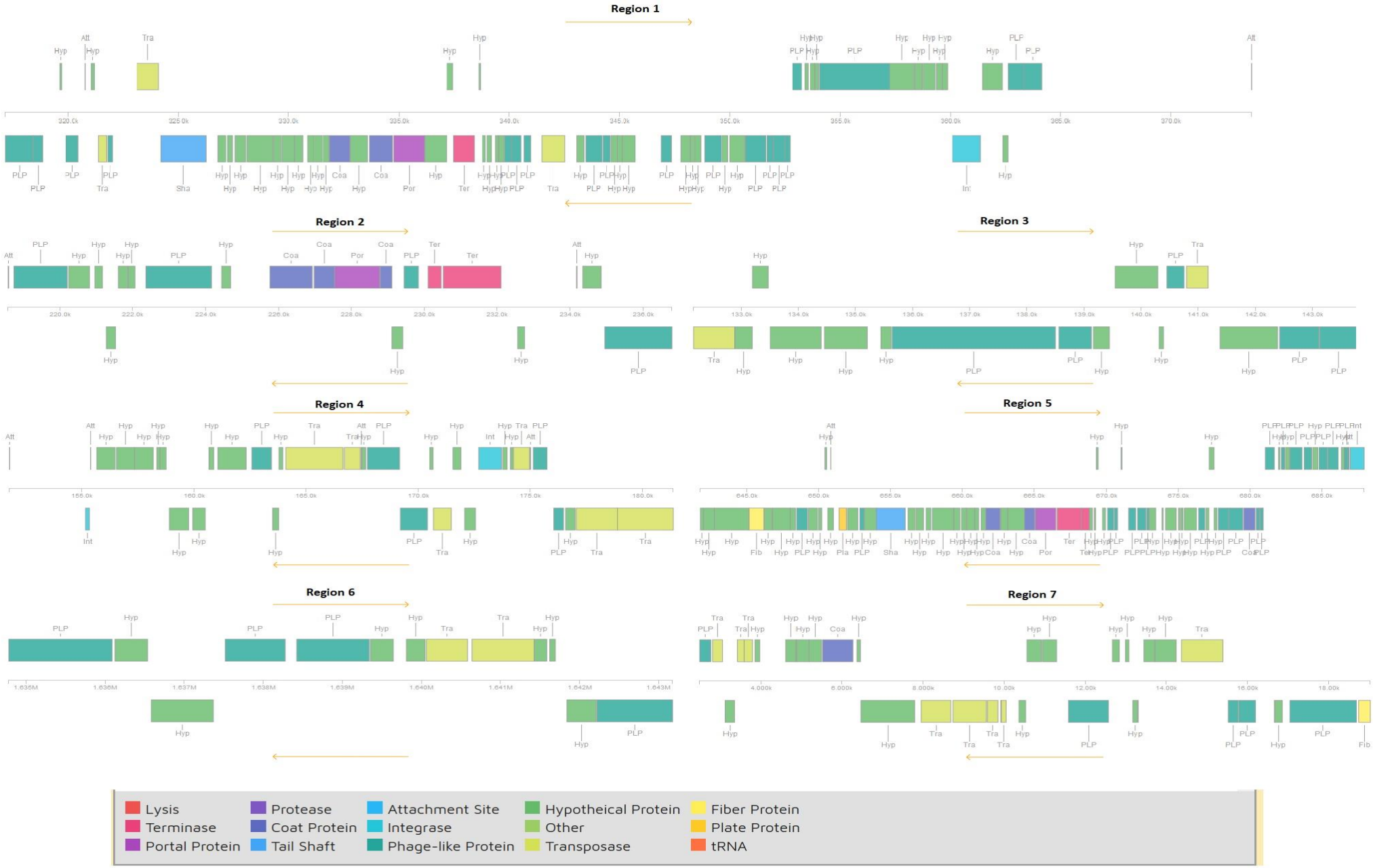

Region 1
Region 2
Region 3
Region 4
Region 5
Region 6
Region 7
Lysis
Terminase
Portal Protein
Protease
Coat Protein
Tail Shaft
Attachment Site
Integrase
Phage-like Protein
Hypotheical Protein
Other
Transposase
Fiber Protein
Plate Protein
tRNA

Figure S8.2

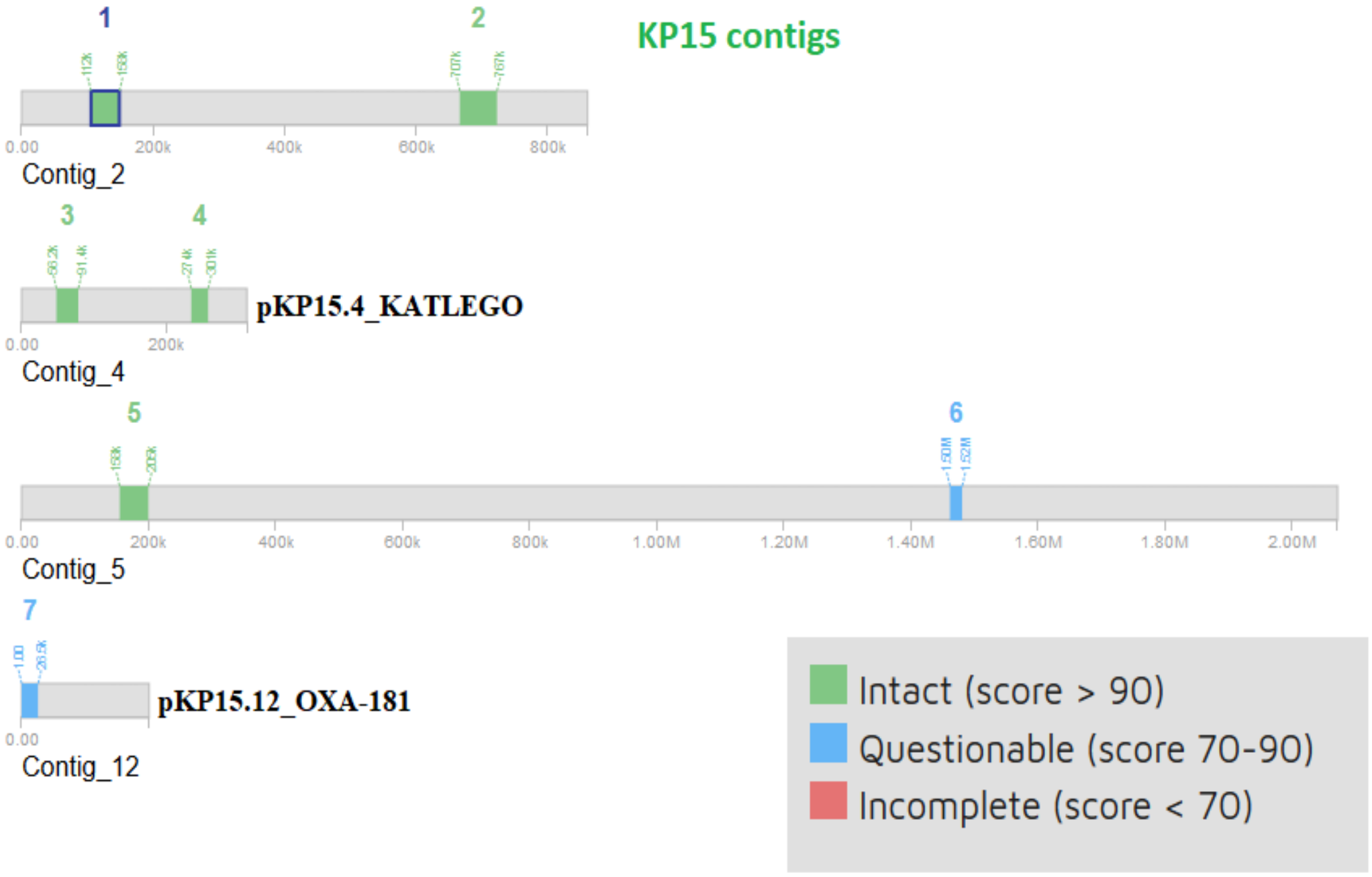

KP15 contigs
1
2
0.00
200k
400k
600k
800k
Contig_2
3
4
pKP15.4_KATLEGO
0.00
200k
Contig_4
5
6
0.00
200k
400k
600k
800k
1.00M
1.20M
1.40M
1.60M
1.80M
2.00M
Contig_5
7
pKP15.12_OXA-181
0.00
Contig_12
Intact (score > 90)
Questionable (score 70-90)
Incomplete (score < 70)

Figure S9.1

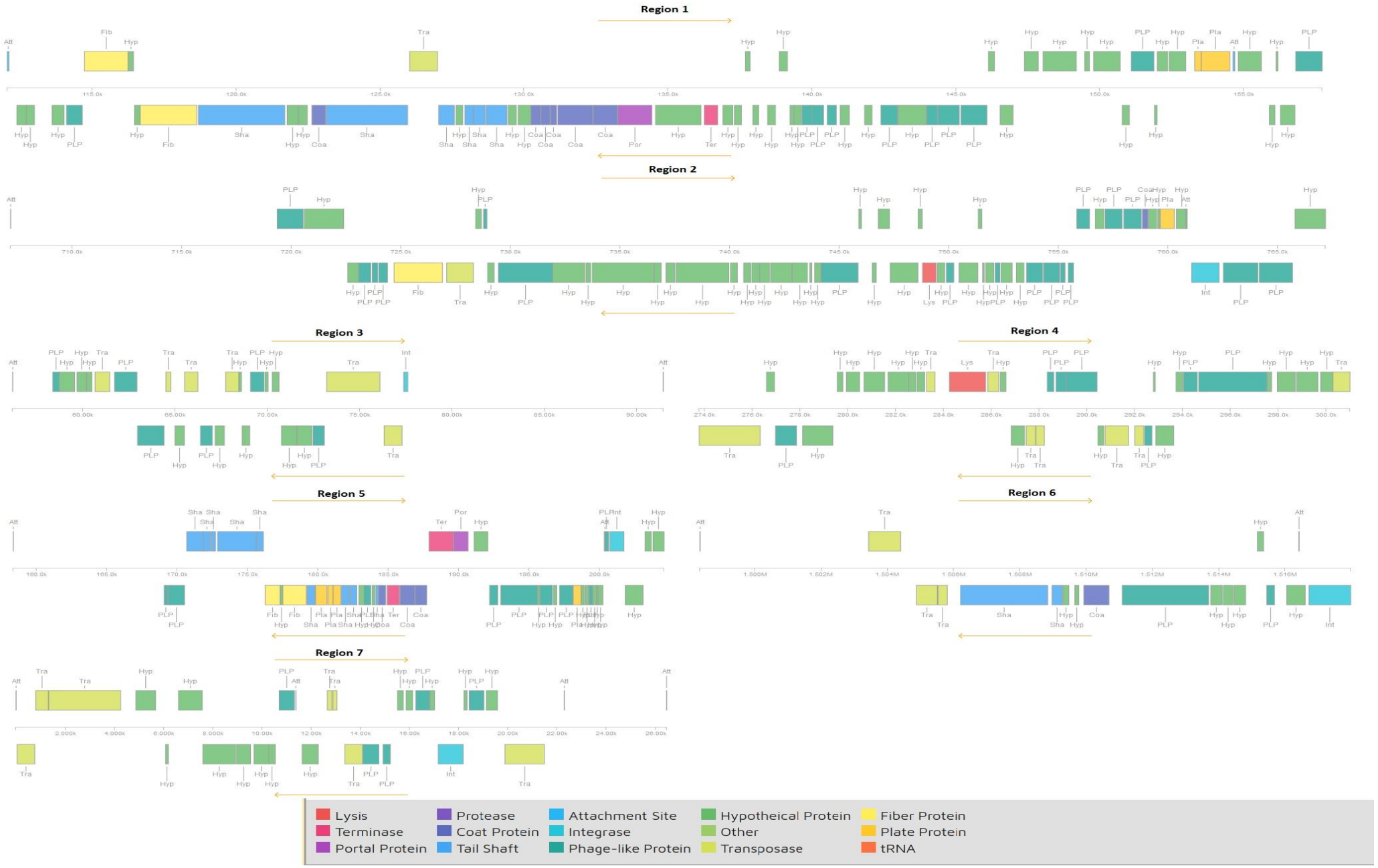

Region 1
Region 2
Region 3
Region 4
Region 5
Region 6
Region 7
Lysis
Terminase
Portal Protein
Protease
Coat Protein
Tail Shaft
Attachment Site
Integrase
Phage-like Protein
Hypotheical Protein
Other
Transposase
Fiber Protein
Plate Protein
tRNA

Figure S9.2

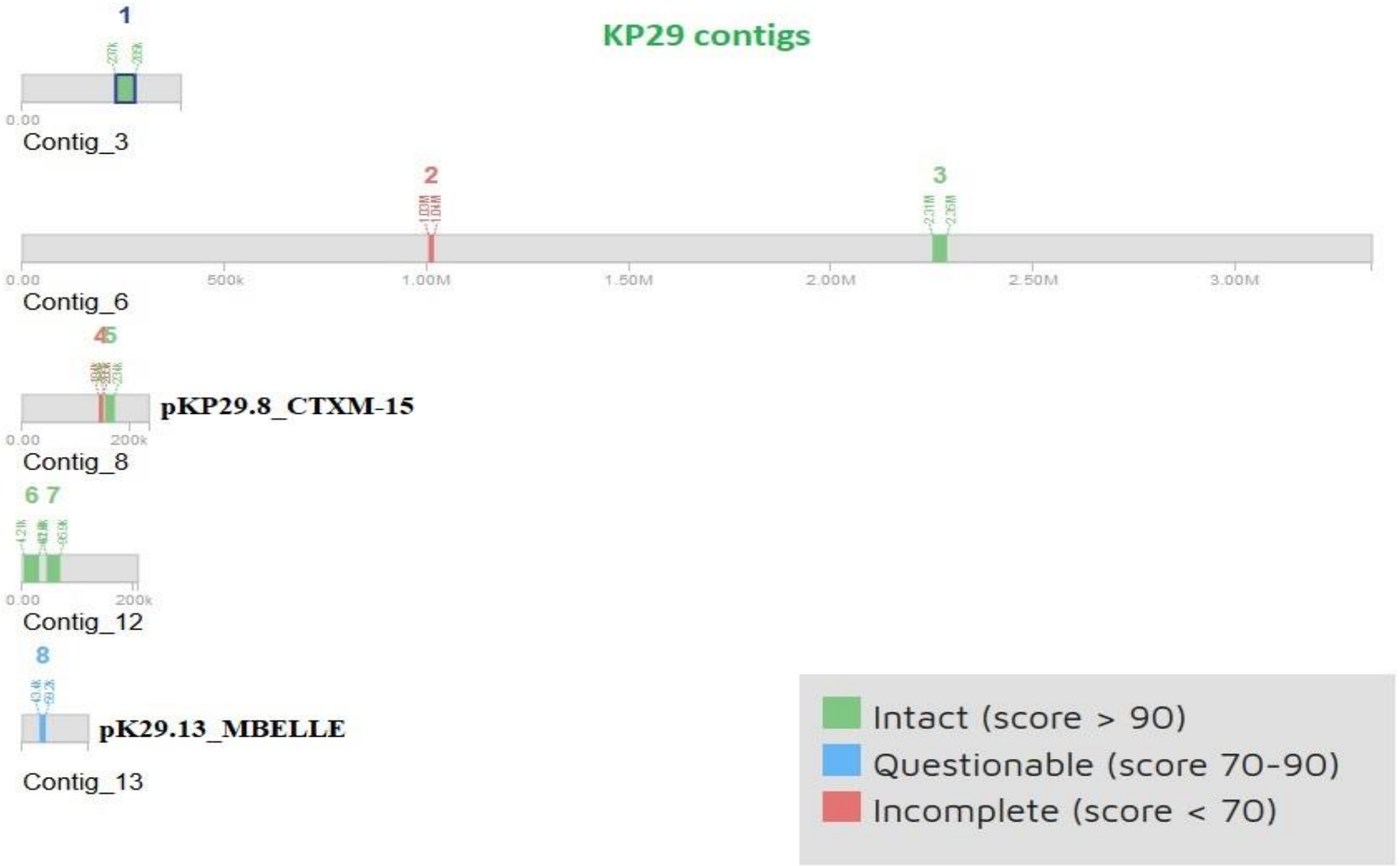

KP29 contigs
1
0.00
Contig_3
2
3
0.00
500k
1.00M
1.50M
2.00M
2.50M
3.00M
Contig_6
4 5
pKP29.8_CTXM-15
0.00
200k
Contig_8
6 7
0.00
200k
Contig_12
8
pK29.13_MBELLE
Contig_13
Intact (score > 90)
Questionable (score 70-90)
Incomplete (score < 70)

Figure S10.1

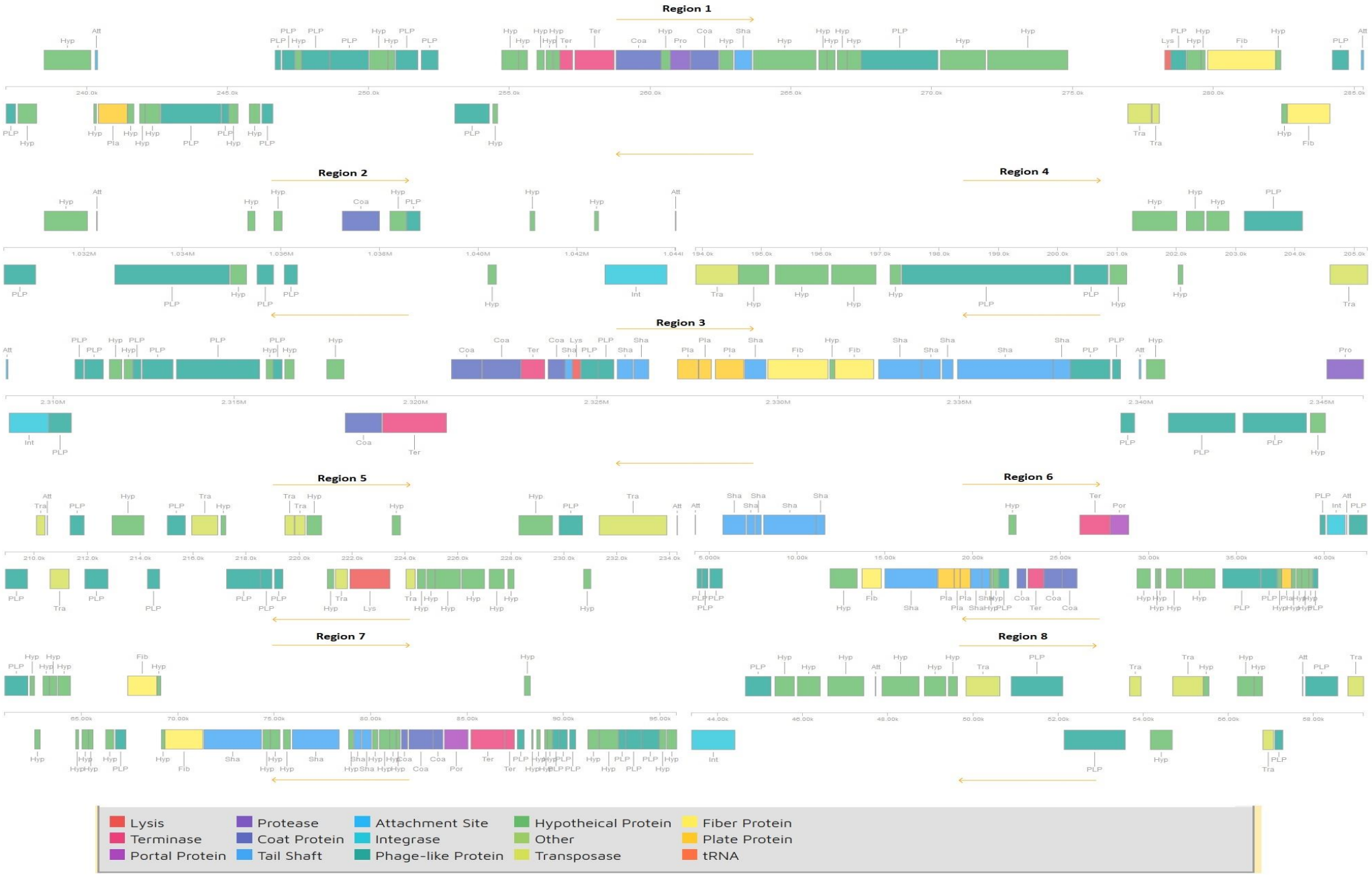

Region 1
Region 2
Region 3
Region 4
Region 5
Region 6
Region 7
Region 8
Lysis
Terminase
Portal Protein
Protease
Coat Protein
Tail Shaft
Attachment Site
Integrase
Phage-like Protein
Hypotheical Protein
Other
Transposase
Fiber Protein
Plate Protein
tRNA

Figure S10.2

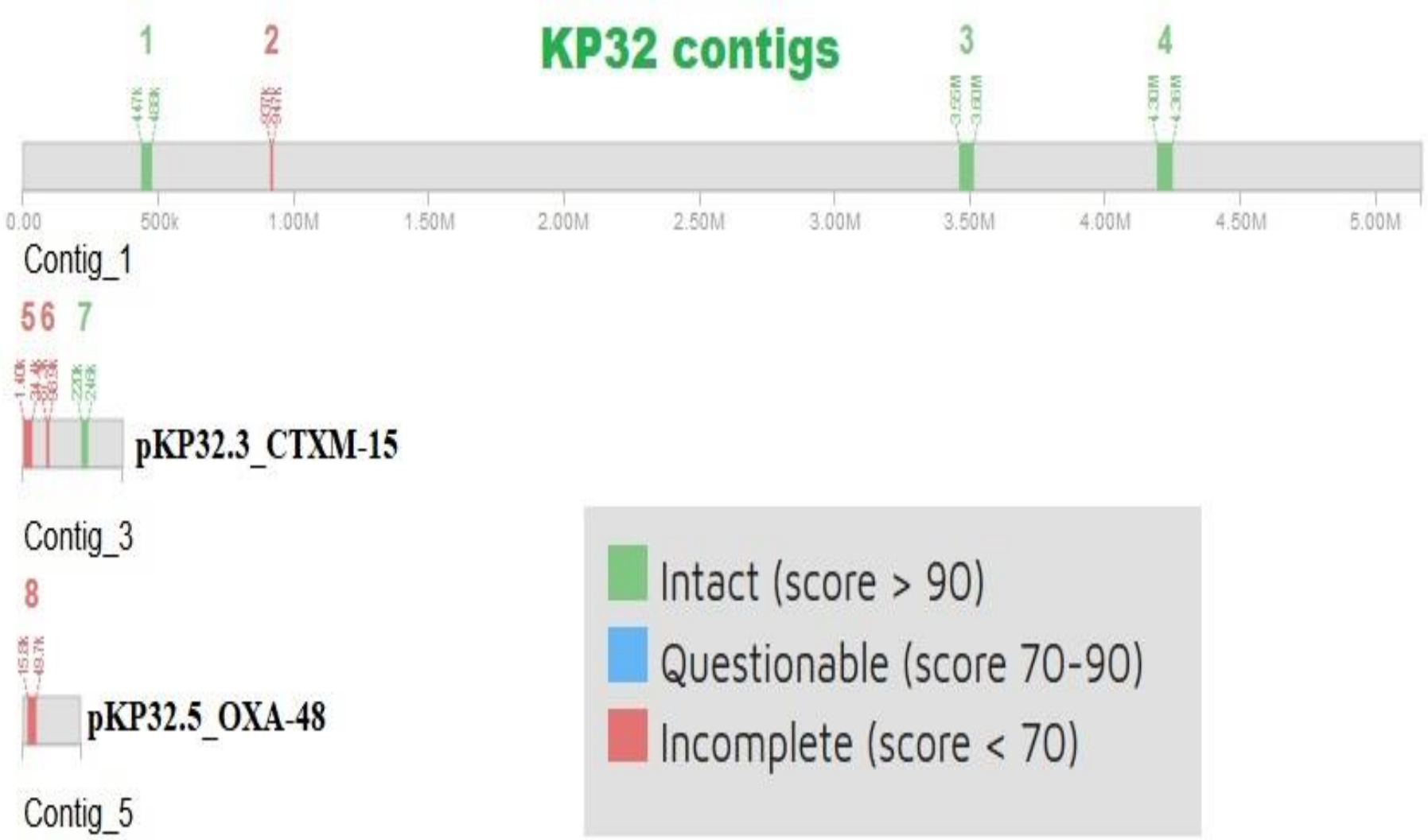

KP32 contigs
1
2
3
4
0.00
500k
1.00M
1.50M
2.00M
2.50M
3.00M
3.50M
4.00M
4.50M
5.00M
Contig_1
56
7
pKP32.3_CTXM-15
Contig_3
8
pKP32.5_OXA-48
Contig_5
Intact (score > 90)
Questionable (score 70-90)
Incomplete (score < 70)

Figure S11.1

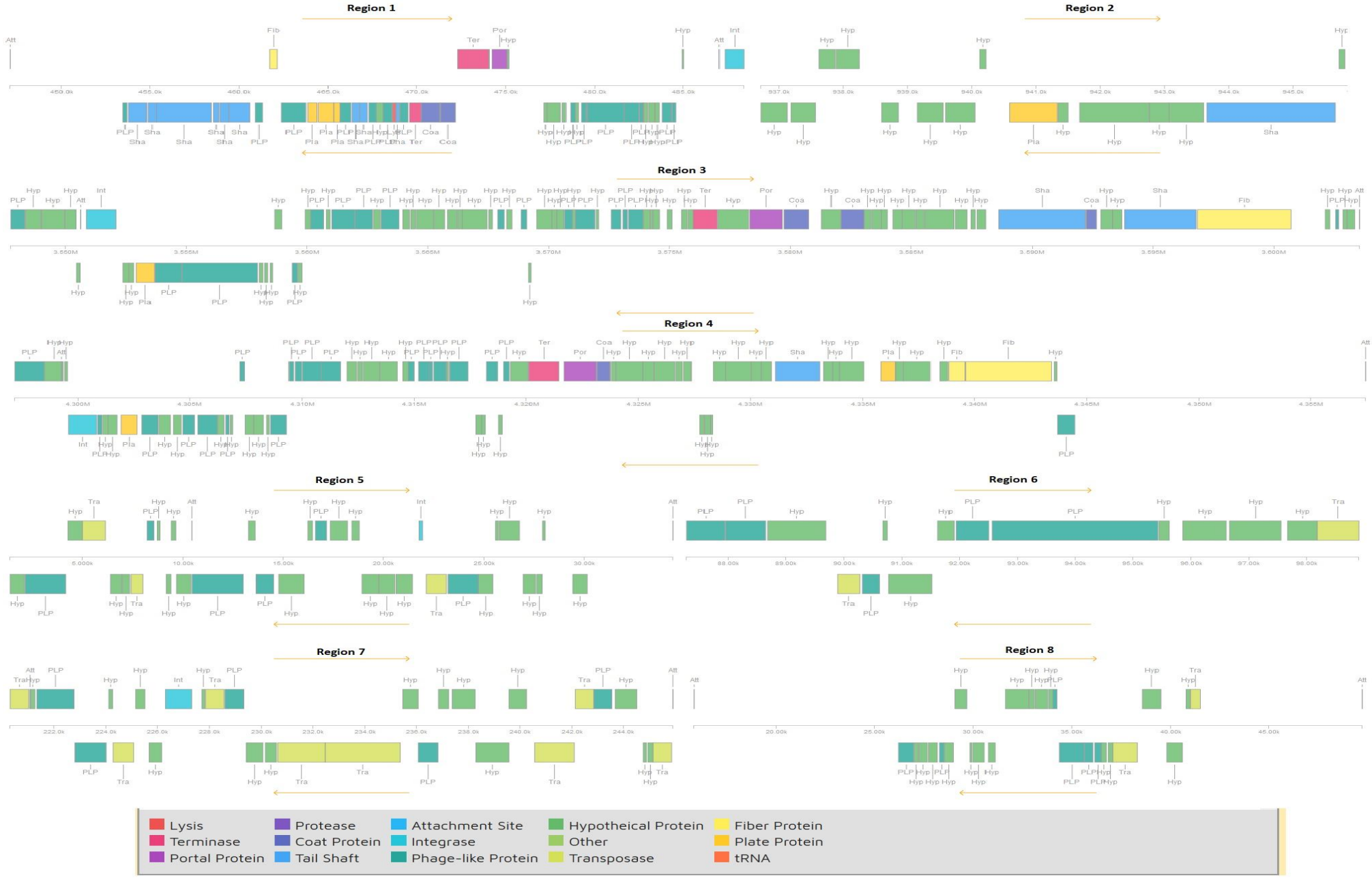

Region 1
Region 2
Region 3
Region 4
Region 5
Region 6
Region 7
Region 8
Lysis
Terminase
Portal Protein
Protease
Coat Protein
Tail Shaft
Attachment Site
Integrase
Phage-like Protein
Hypotheical Protein
Other
Transposase
Fiber Protein
Plate Protein
tRNA

Figure S11.2

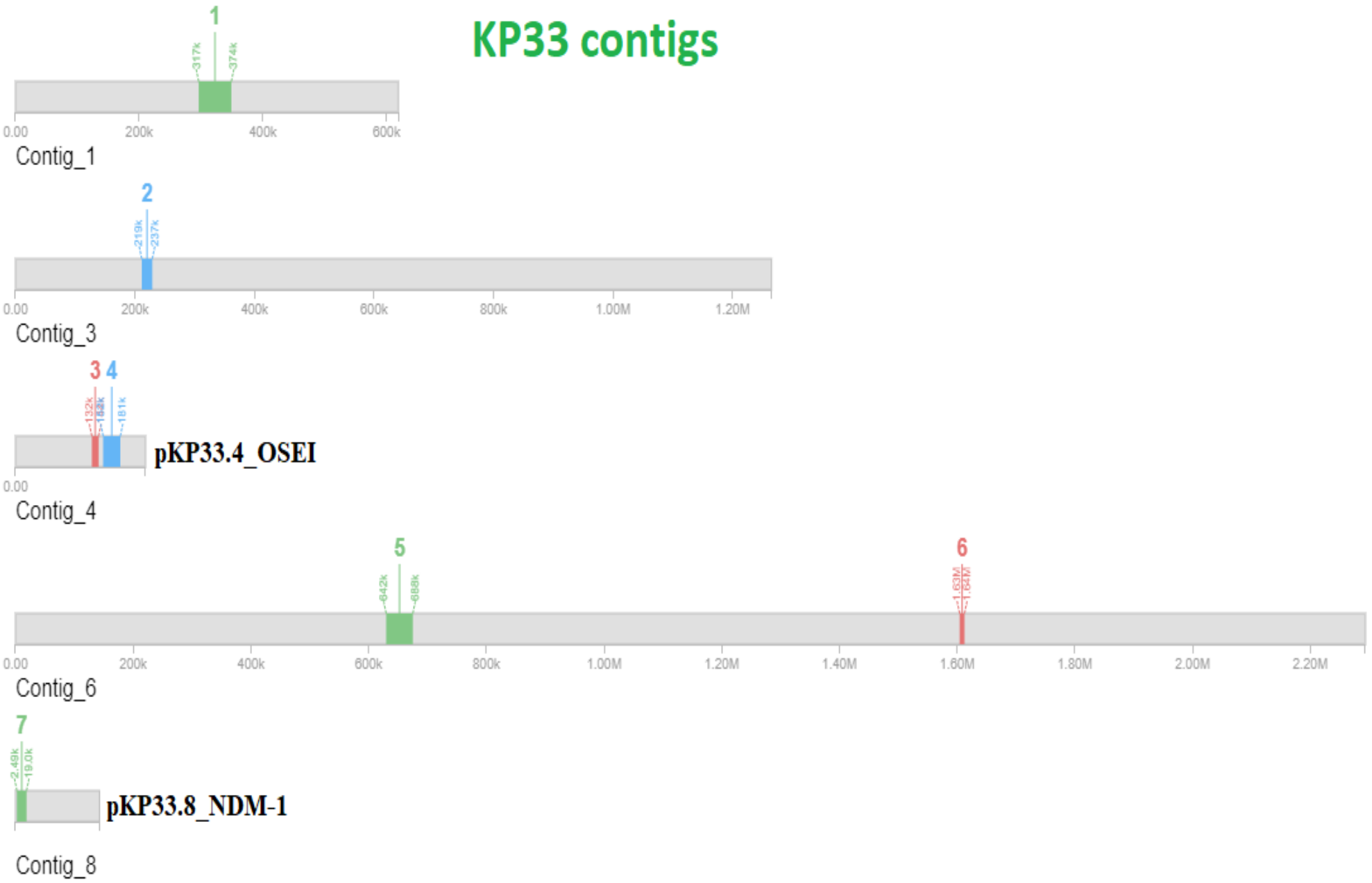

KP33 contigs
1
317k
374k
0.00
200k
400k
600k
Contig_1
2
219k
237k
0.00
200k
400k
600k
800k
1.00M
1.20M
Contig_3
3
4
132k
181k
pKP33.4_OSEI
0.00
Contig_4
5
642k
688k
6
1.63M
1.64M
0.00
200k
400k
600k
800k
1.00M
1.20M
1.40M
1.60M
1.80M
2.00M
2.20M
Contig_6
7
2.49k
19.0k
pKP33.8_NDM-1
Contig_8

Figure S12.1

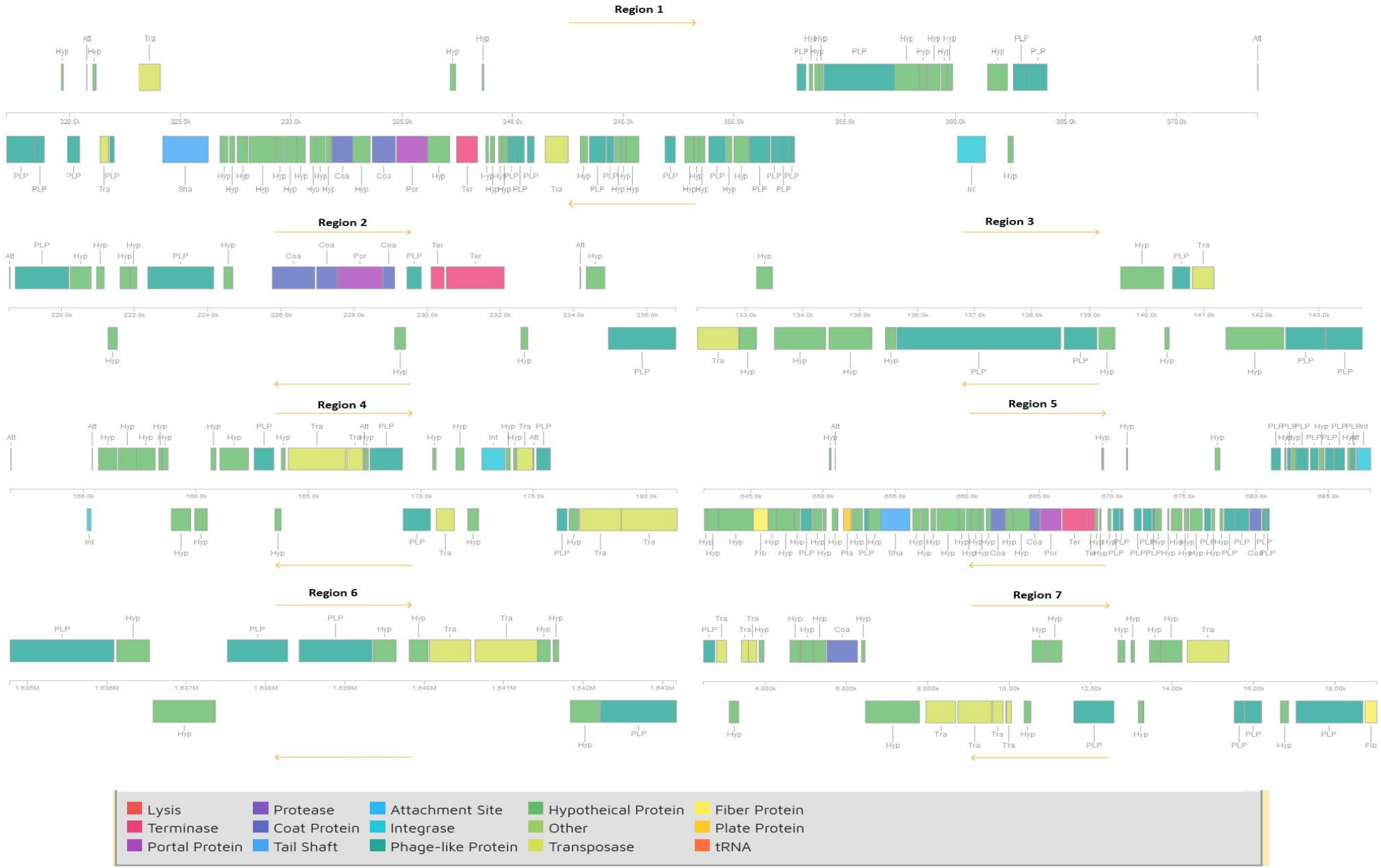

Region 1
Region 2
Region 3
Region 4
Region 5
Region 6
Region 7
Lysis
Terminase
Portal Protein
Protease
Coat Protein
Tail Shaft
Attachment Site
Integrase
Phage-like Protein
Hypotheical Protein
Other
Transposase
Fiber Protein
Plate Protein
tRNA

Figure S12.2

13.1

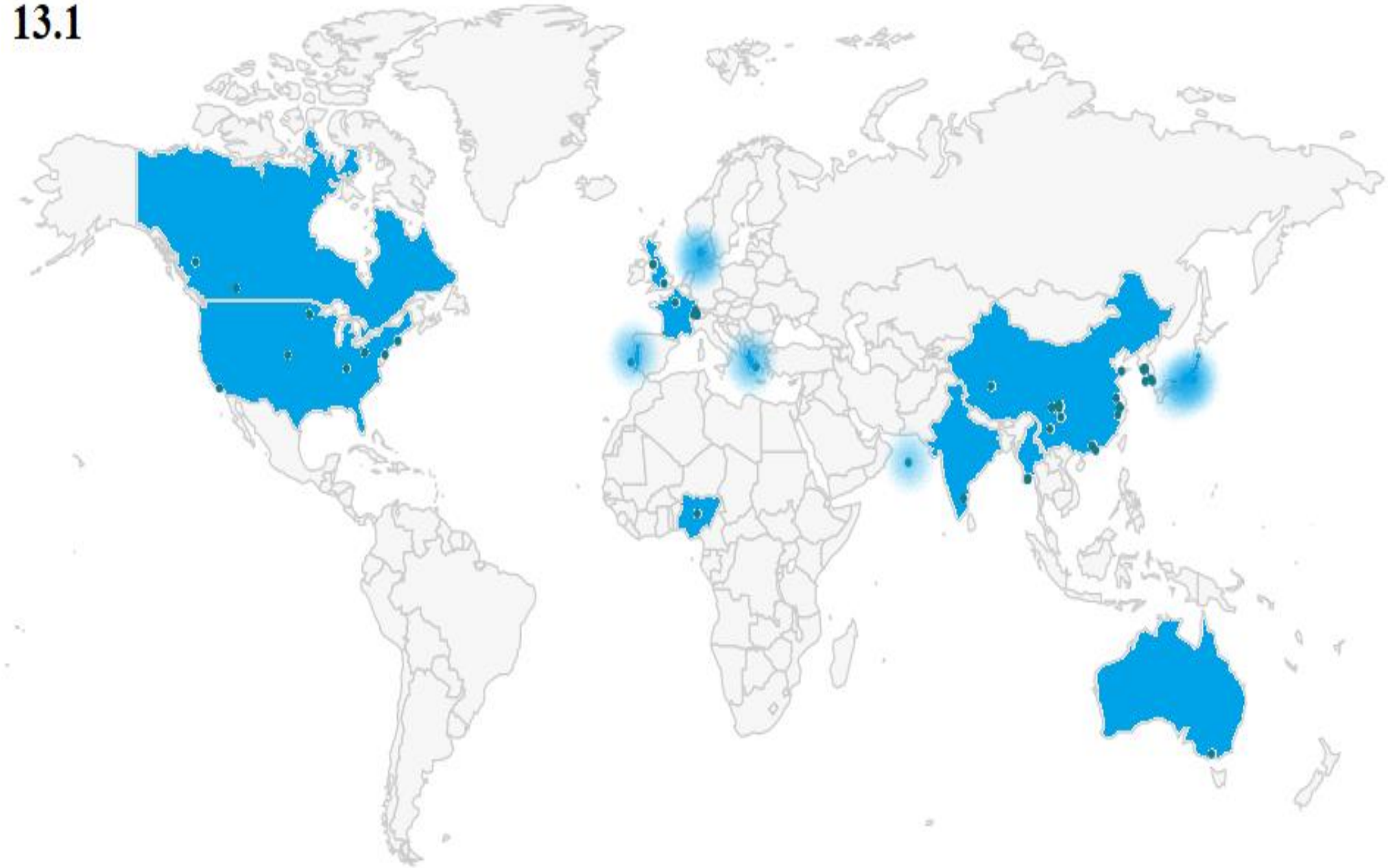


Figure S13.1

13.2

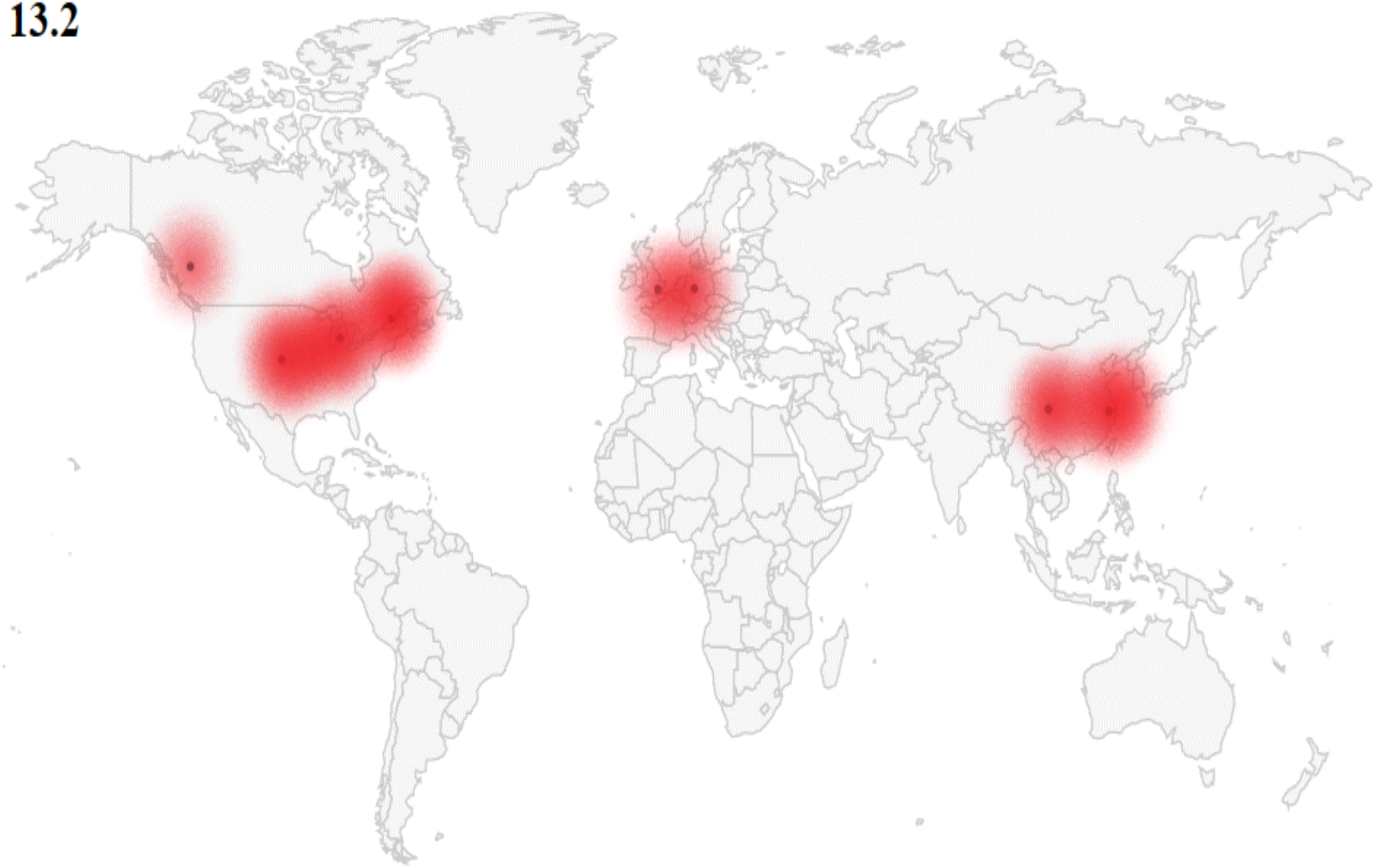


Figure S13.2

13.3

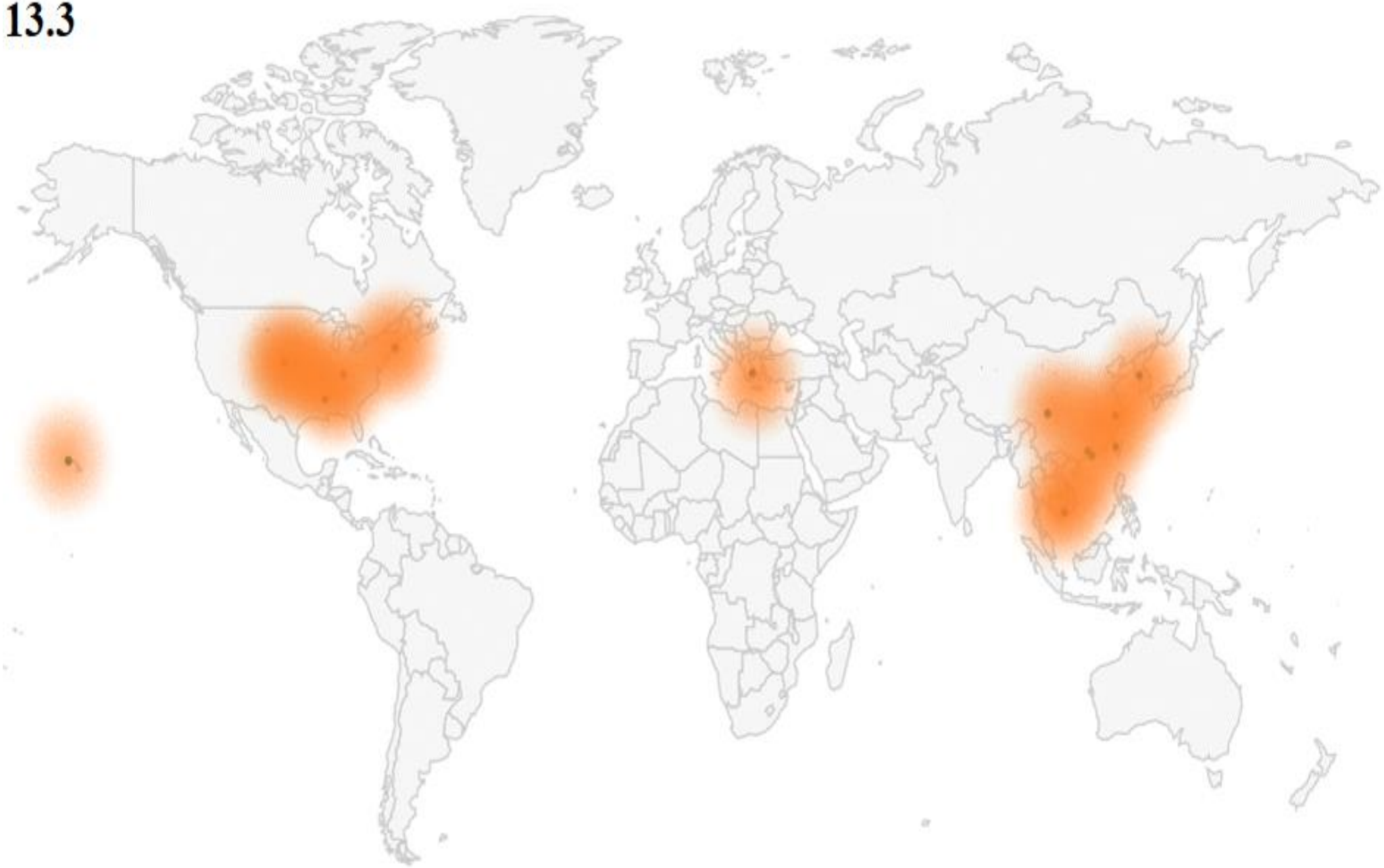


Figure S13.3

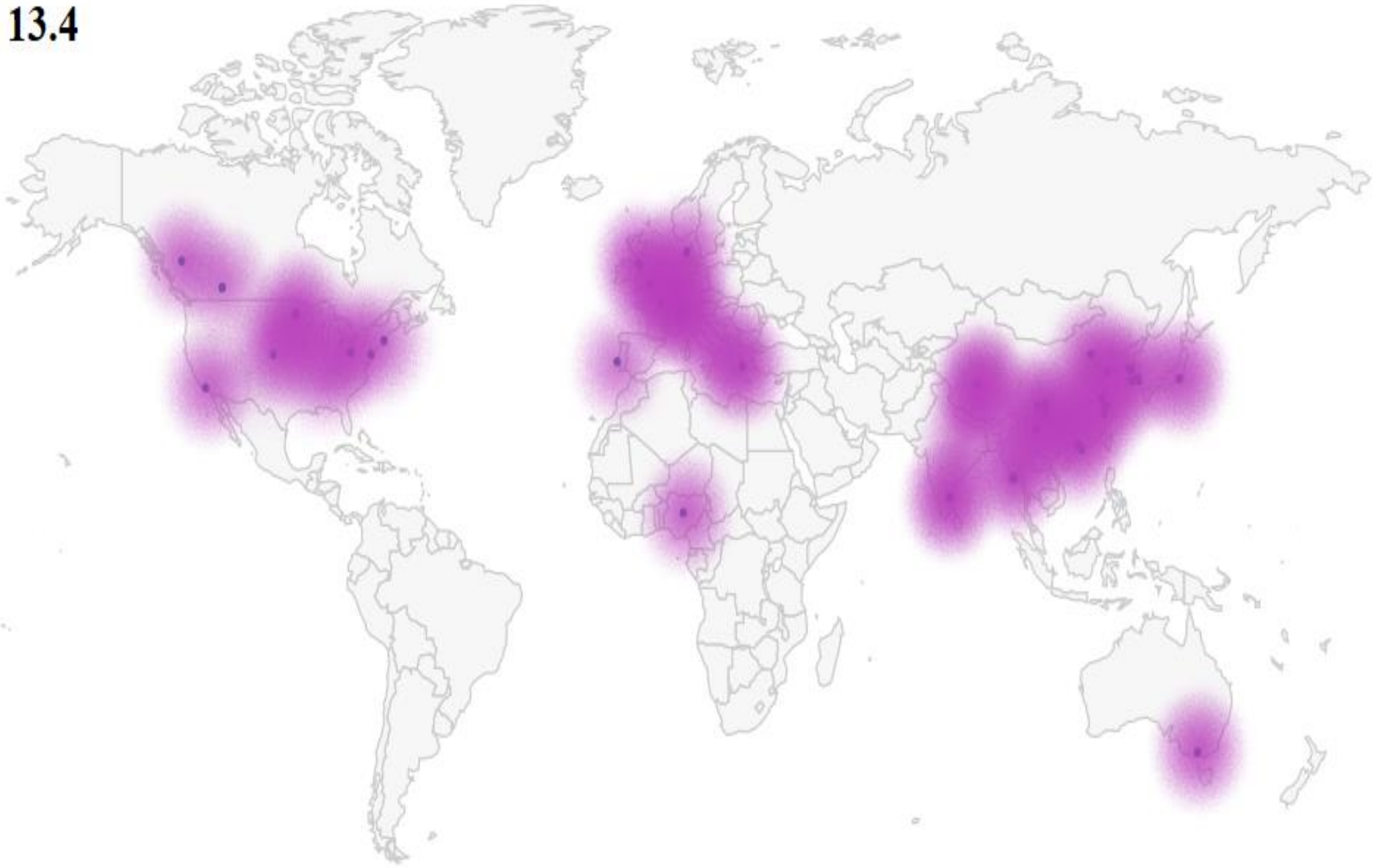


Figure S13.4

13.5

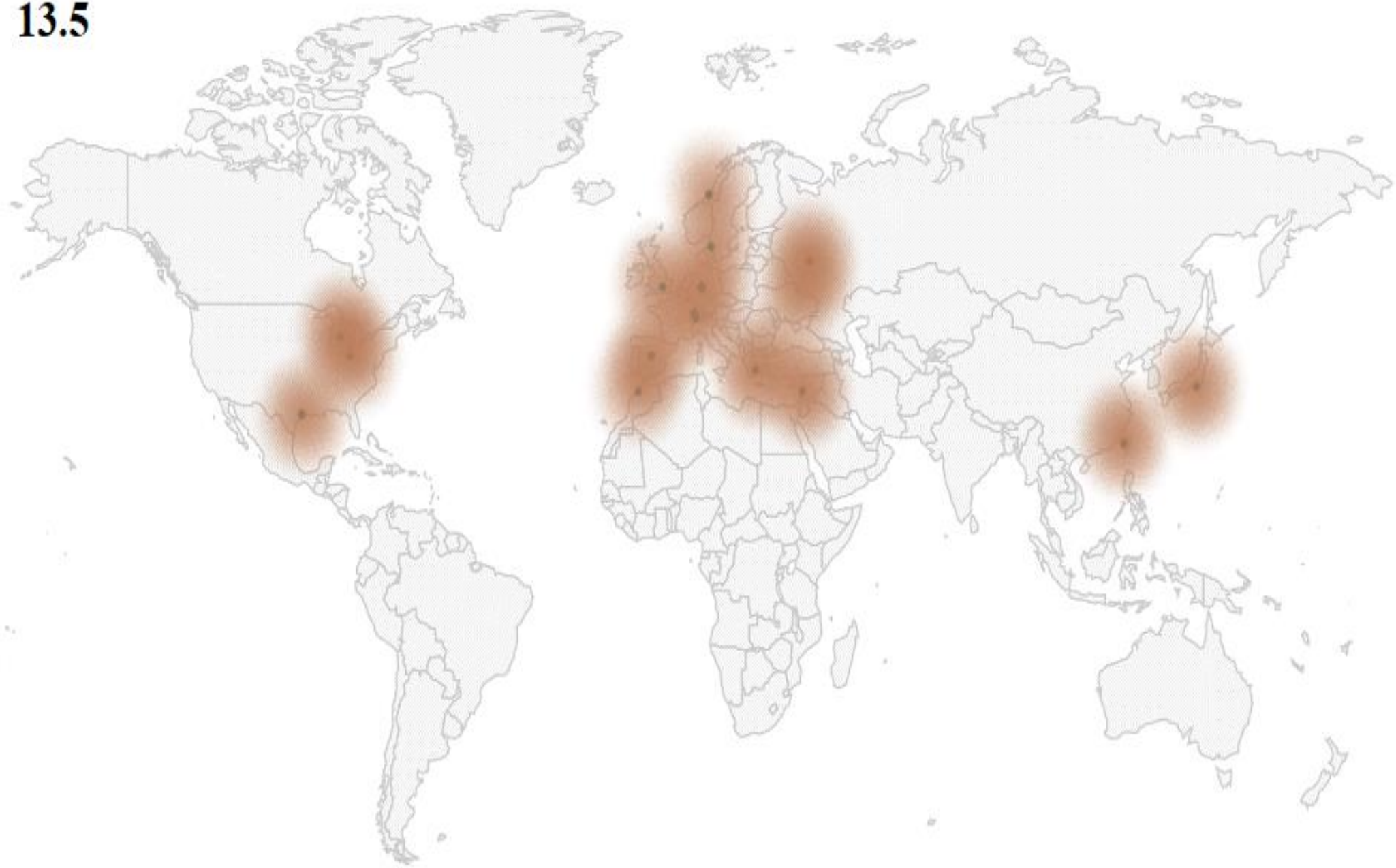


Figure S13.5

13.6

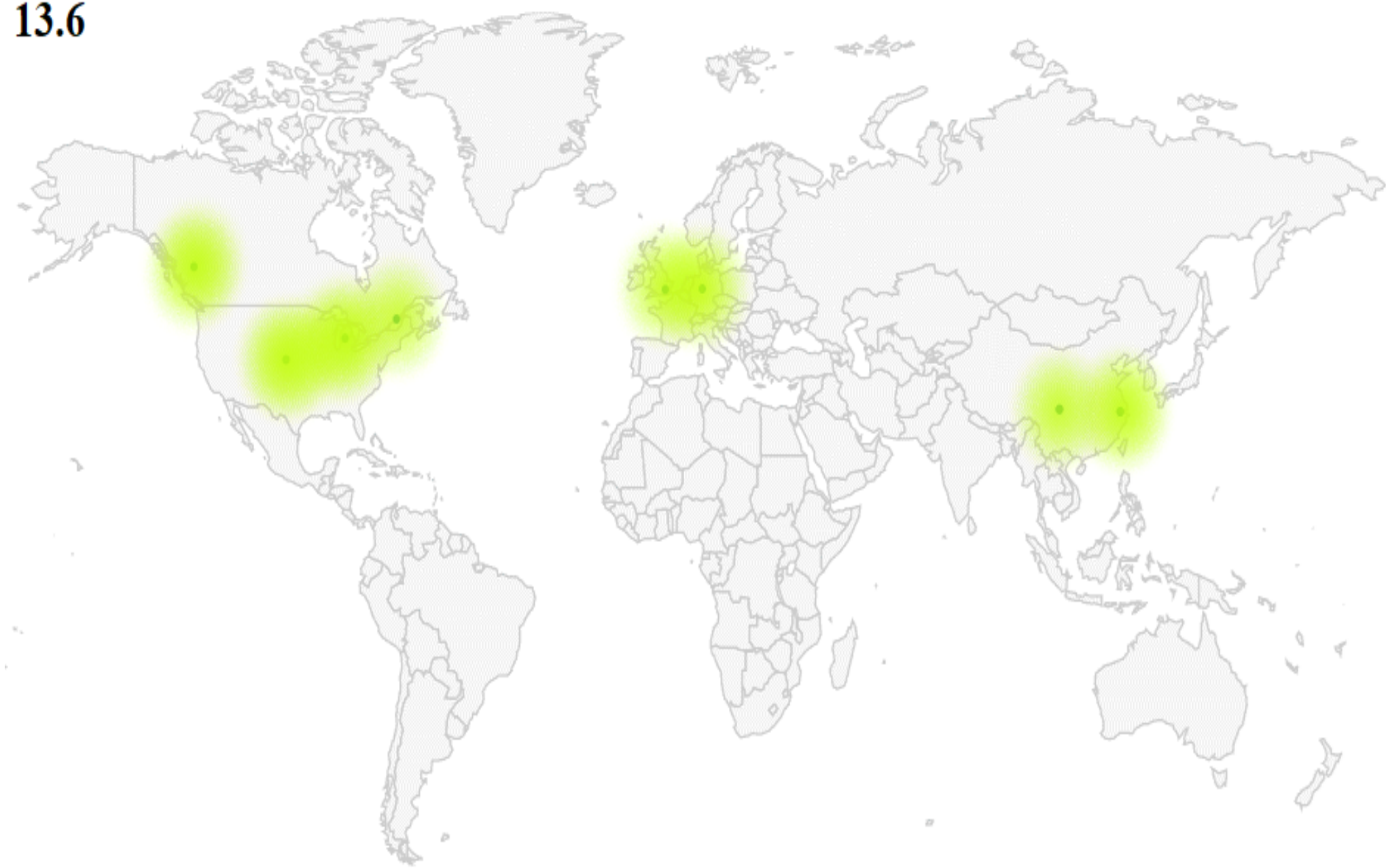


Figure S13.6

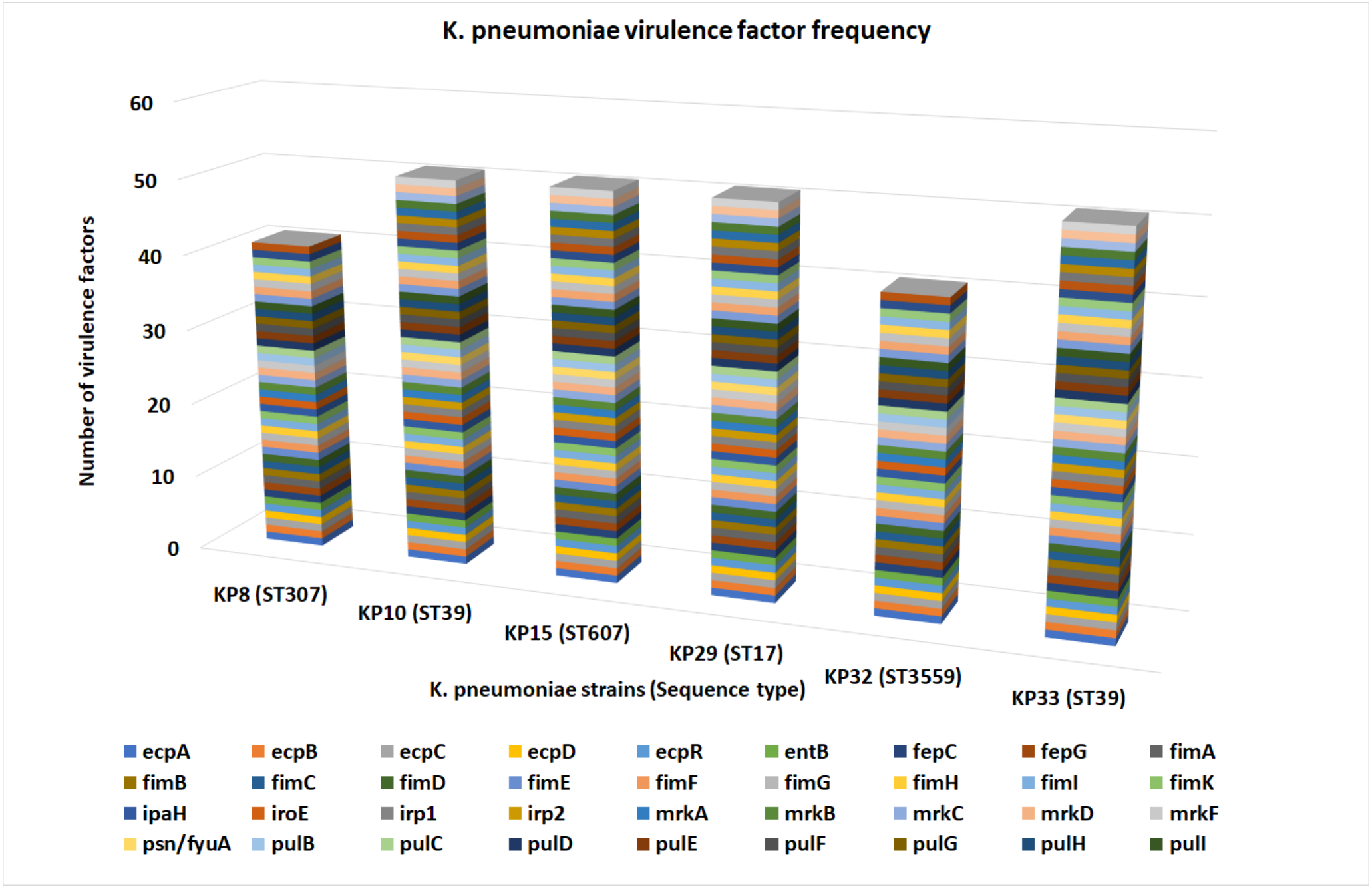

K. pneumoniae virulence factor frequency
Number of virulence factors
60
50
40
30
20
10
0
KP8 (ST307)
KP10 (ST39)
KP15 (ST607)
KP29 (ST17)
KP32 (ST3559)
KP33 (ST39)
K. pneumoniae strains (Sequence type)
ecpA
ecpB
ecpC
ecpD
ecpR
entB
fepC
fepG
fimA
fimB
fimC
fimD
fimE
fimF
fimG
fimH
fimI
fimK
ipaH
iroE
irp1
irp2
mrkA
mrkB
mrkC
mrkD
mrkF
psn/fyuA
pulB
pulC
pulD
pulE
pulF
pulG
pulH
pulI

Figure S14.1

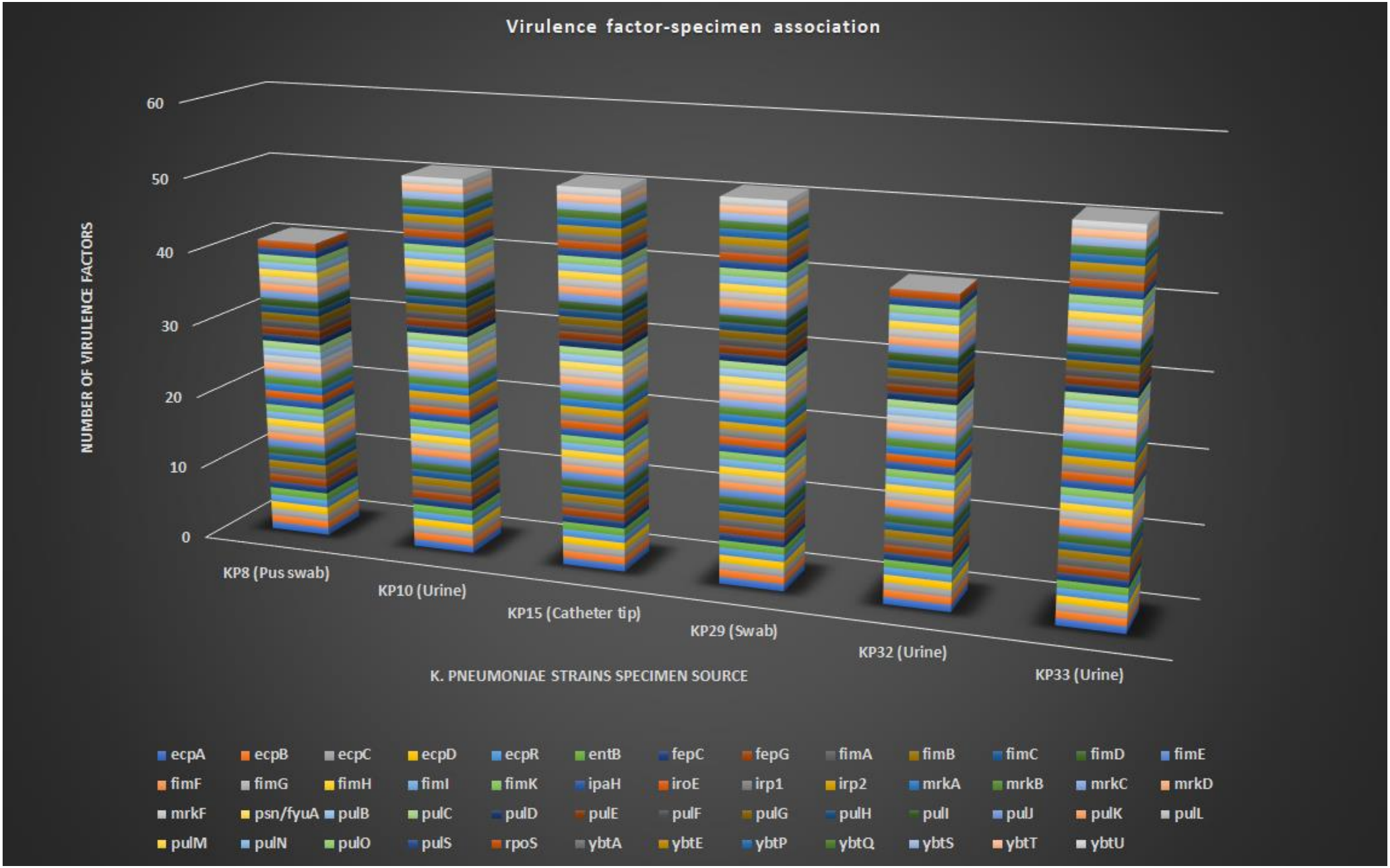
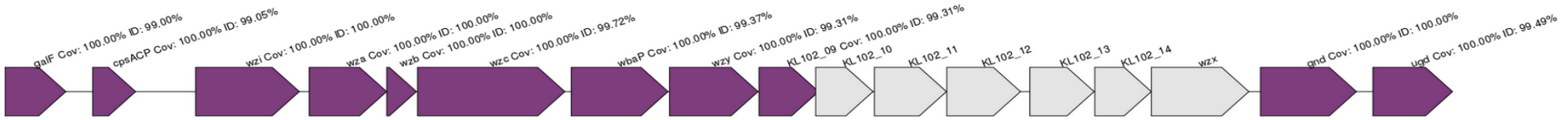

Virulence factor-specimen association
NUMBER OF VIRULENCE FACTORS
60
50
40
30
20
10
0
KP8 (Pus swab)
KP10 (Urine)
KP15 (Catheter tip)
KP29 (Swab)
KP32 (Urine)
KP33 (Urine)
K. PNEUMONIAE STRAINS SPECIMEN SOURCE
ecpA ecpB ecpC ecpD ecpR entB fepC fepG fimA fimB fimC fimD fimE
fimF fimG fimH fimI fimK ipaH iroE irp1 irp2 mrkA mrkB mrkC mrkD
mrkF psn/fyuA pulB pulC pulD pulE pulF pulG pulH pulI pulJ pulK pulL
pulM pulN pulO pulS rpoS ybtA ybtE ybtP ybtQ ybtS ybtT ybtU

Figure S14.2

KP8 **Best locus:** KL102 **Match confidence ℹ :** None **Cov ℹ :** 77.30% **ID ℹ :** 99.11% **Genes:** 11 / 17

KL102 reference ℹ :



Other genes found in locus ℹ : 0 **Other genes found outside locus ℹ :** 2

Allelic type ℹ : wzc: 939 wzi: 173

Assembly pieces ℹ : Download as FASTA

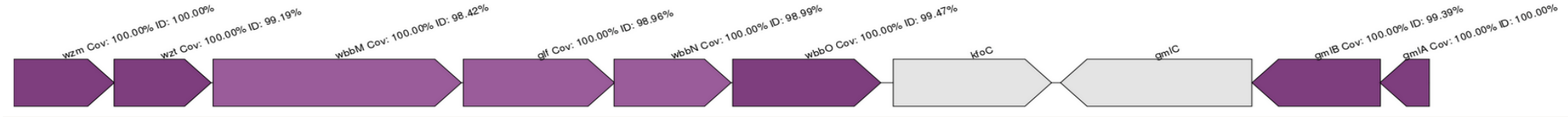
KL102 reference size ℹ : 21217

Length discrepancy ℹ : n/a

Contig name	Start position	End position	Length
Contig_5	3825862	3838302	12441
Contig_11	2	3891	3890

KP8 **Best locus:** O2v2 **Match confidence ℹ :** Low **Cov ℹ :** 93.58% **ID ℹ :** 98.43% **Genes:** 8 / 10

O2v2 reference ℹ :



Other genes found in locus ℹ : 0 **Other genes found outside locus ℹ :** 0

Assembly pieces ℹ : Download as FASTA

O2v2 reference size ℹ : 10812

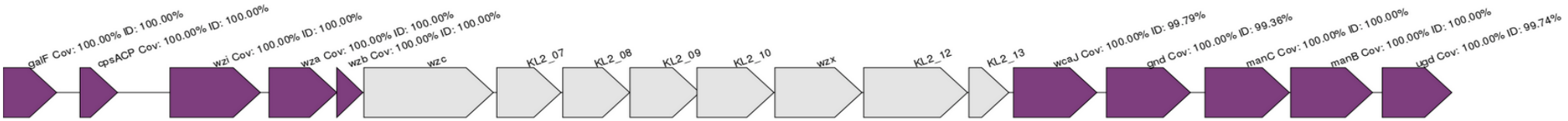
Length discrepancy ℹ : n/a

Contig name	Start position	End position	Length
Contig_11	6927	14325	7399
Contig_3	1	2650	2650

Figure S14.3

KP10 **Best locus:** KL2 **Match confidence ℹ :** None **Cov ℹ :** 61.11% **ID ℹ :** 99.67% **Genes:** 10 / 18

KL2 reference ℹ :



Other genes found in locus ℹ : 0 **Other genes found outside locus ℹ :** 2

Allelic type ℹ : wzc: Not found wzi: 2

Assembly pieces ℹ : Download as FASTA

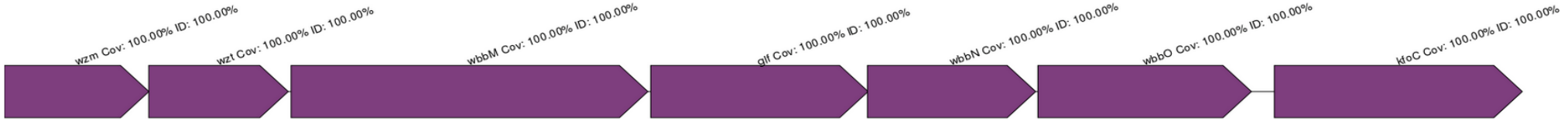
KL2 reference size ℹ : 24287

Length discrepancy ℹ : n/a

Contig name	Start position	End position	Length
Contig_2	774608	782598	7991
Contig_3	1258500	1265243	6744

KP10 **Best locus:** O1v1 **Match confidence ℹ :** Very high **Cov ℹ :** 100.00% **ID ℹ :** 99.99% **Genes:** 7 / 7

O1v1 reference ℹ :



Other genes found in locus ℹ : 0 **Other genes found outside locus ℹ :** 4

Assembly pieces ℹ : Download as FASTA

O1v1 reference size ℹ : 8064

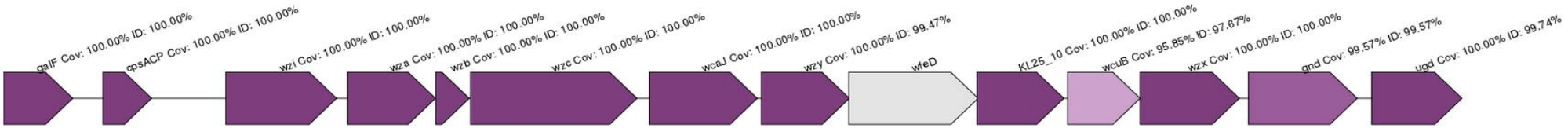
Length discrepancy ℹ : 0 bp

Contig name	Start position	End position	Length
Contig_2	763548	771611	8064

Figure S14.4

KP15 **Best locus:** KL25 **Match confidence :** High **Cov :** 100.00% **ID :** 98.52% **Genes:** 13 / 14

KL25 reference :



Other genes found in locus : 0 **Other genes found outside locus :** 2

Allelic type : wzc: 26 wzi: 133

Assembly pieces : Download as FASTA

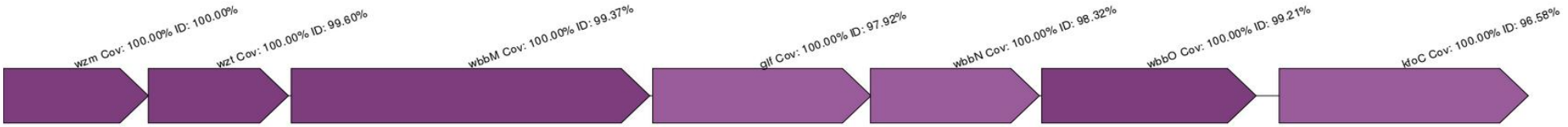
KL25 reference size : 18881

Length discrepancy : +3 bp

Contig name	Start position	End position	Length
Contig_2	288170	307053	18884

KP15 **Best locus:** O1v1 **Match confidence :** Very high **Cov :** 100.00% **ID :** 98.02% **Genes:** 7 / 7

O1v1 reference :



Other genes found in locus : 0 **Other genes found outside locus :** 2

Assembly pieces : Download as FASTA

O1v1 reference size : 8064

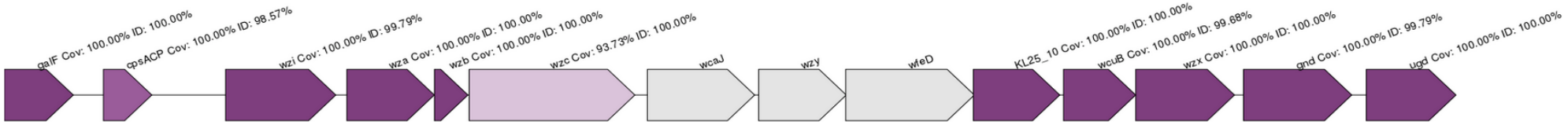
Length discrepancy : -2 bp

Contig name	Start position	End position	Length
Contig_2	275960	284021	8062

Figure S14.5

KP29 **Best locus:** KL25 **Match confidence ⓘ :** None **Cov ⓘ :** 82.98% **ID ⓘ :** 99.02% **Genes:** 11 / 14

KL25 reference ⓘ :



Other genes found in locus ⓘ : 0 ▼ **Other genes found outside locus ⓘ :** 3 ▼

Allelic type ⓘ : wzc: 26 wzi: 141

Assembly pieces ⓘ : Download as FASTA

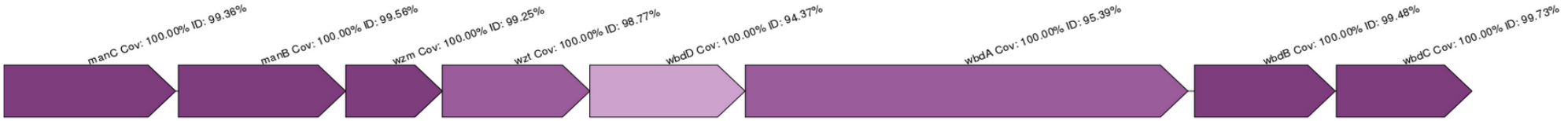
KL25 reference size ⓘ : 18881

Length discrepancy ⓘ : n/a

Contig name	Start position	End position	Length
Contig_4	497504	505058	7555
Contig_6	3332025	3340094	8070

KP29 **Best locus:** O5 **Match confidence ⓘ :** High **Cov ⓘ :** 100.00% **ID ⓘ :** 94.21% **Genes:** 8 / 8

O5 reference ⓘ :



Other genes found in locus ⓘ : 0 ▼ **Other genes found outside locus ⓘ :** 0 ▼

Assembly pieces ⓘ : Download as FASTA

O5 reference size ⓘ : 12084

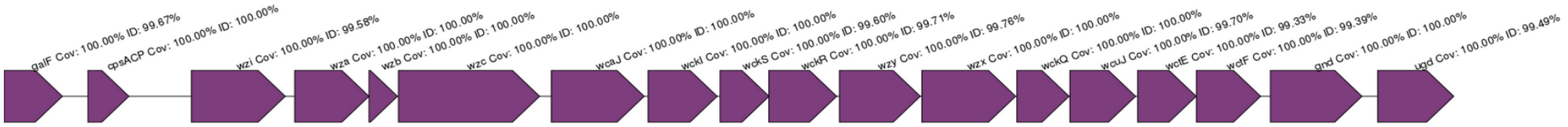
Length discrepancy ⓘ : 0 bp

Contig name	Start position	End position	Length
Contig_4	482391	494474	12084

Figure S14.6

KP32 **Best locus:** KL27 **Match confidence :** Very high **Cov :** 100.00% **ID :** 99.27% **Genes:** 18 / 18

KL27 reference :



Other genes found in locus : 0 **Other genes found outside locus :** 1

Allelic type : wzc: 28 wzi: 187

Assembly pieces : Download as FASTA

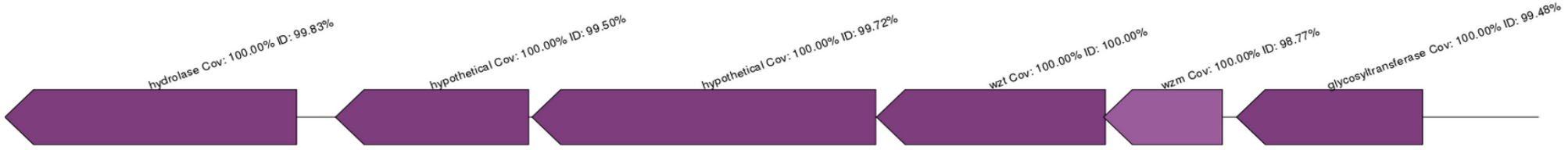
KL27 reference size : 22251

Length discrepancy : -1 bp

Contig name	Start position	End position	Length
Contig_1	4038684	4060933	22250

KP32 **Best locus:** O4 **Match confidence :** Very high **Cov :** 100.00% **ID :** 99.71% **Genes:** 6 / 6

O4 reference :



Other genes found in locus : 0 **Other genes found outside locus :** 0

Assembly pieces : Download as FASTA

O4 reference size : 9449

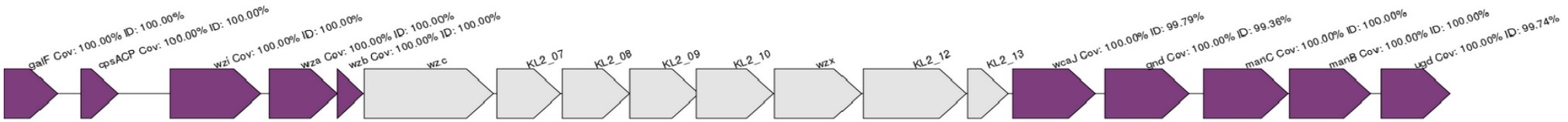
Length discrepancy : +1 bp

Contig name	Start position	End position	Length
Contig_1	4063220	4072669	9450

Figure S14.7

KP33 **Best locus:** KL2 **Match confidence ℹ :** None **Cov ℹ :** 61.11% **ID ℹ :** 99.67% **Genes:** 10 / 18

KL2 reference ℹ :



Other genes found in locus ℹ : 0 **Other genes found outside locus ℹ :** 2

Allelic type ℹ : wzc: Not found wzi: 2

Assembly pieces ℹ : Download as FASTA

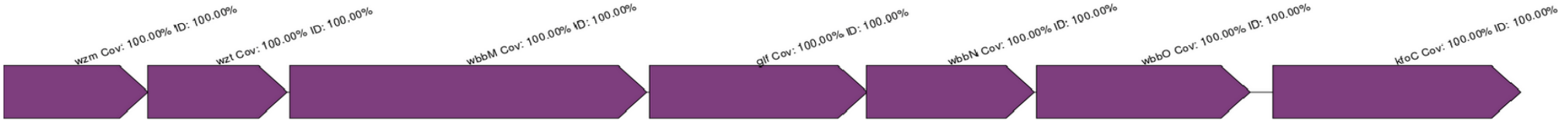
KL2 reference size ℹ : 24287

Length discrepancy ℹ : n/a

Contig name	Start position	End position	Length
Contig_2	774608	782598	7991
Contig_3	1258500	1265243	6744

KP33 **Best locus:** O1v1 **Match confidence ℹ :** Very high **Cov ℹ :** 100.00% **ID ℹ :** 99.99% **Genes:** 7 / 7

O1v1 reference ℹ :



Other genes found in locus ℹ : 0 **Other genes found outside locus ℹ :** 4

Assembly pieces ℹ : Download as FASTA

O1v1 reference size ℹ : 8064

Length discrepancy ℹ : 0 bp

Contig name	Start position	End position	Length
Contig_2	763548	771611	8064

Figure S14.8