(coverage+identity)	pKPN-c22	pKPSH11	p6234- 198.371kb	pKPN3- 307_TypeC	pKPN3- 307_typeA	pA1705- qnrS	p911021- tetA	p1642-tetA
pKPN-c22		(99%+99%)	(99%+100%)	(82%+99%)	(81%+99%)	(70%+99%)	(70%+97%)	(70%+99%)
pKPSH11	(92%+99%)		(99%+99%)	(77%+99%)	(82%+99%)	(71%+96%)	(68%+96%)	(68%+96%)
p6234-198.371kb	(92%+100%)	(99%+99%)		(77%+99%)	(82%+98%)	(72%+99%)	(67%+99%)	(67%+99%)
pKPN3-307_TypeC	(68%+99%)	(69%+99%)	(69%+99%)		(97%+99%)	(79%+99%)	(70%+99%)	(70%+98%)
pKPN3-307_typeA	(64%+99%)	(70%+99%)	(71%+99%)	(93%+99%)		(80%+97%)	(68%+97%)	(68%+97%)
pA1705-qnrS	(47%+99%)	(52%+96%)	(53%+99%)	(65%+99%)	(68%+97%)		(88%+99%)	(87%+99%)
p911021-tetA	(51%+99%)	(54%+96%)	(55%+99%)	(63%+99%)	(64%+97%)	(97%+99%)		(99%+99%)
p1642-tetA	(51%+99%)	(55%+96%)	(55%+99%)	(63%+98%)	(64%+97%)	(97%+99%)	(99%+99%)	

Supplementary Table S1 Comparison of plasmids sequences using BLASTN

(coverage+identity)	pKPN-c22	pKPSH11	p6234- 198.371kb	pKPN3- 307_TypeC	pKPN3- 307_typeA	pA1705- qnrS	p911021- tetA	p1642-tetA
pKPN-c22		(99%+99%)	(99%+99%)	(80%+99%)	(81%+99%)	(78%+97%)	(78%+97%)	(78%+97%)
pKPSH11	(98%+99%)		(98%+99%)	(79%+99%)	(80%+98%)	(77%+97%)	(77%+97%)	(77%+96%)
p6234-198.371kb	(99%+99%)	(99%+99%)		(80%+99%)	(81%+98%)	(78%+97%)	(78%+97%)	(78%+96%)
pKPN3-307_TypeC	(98%+99%)	(98%+99%)	(98%+99%)		(98%+99%)	(94%+99%)	(94%+99%)	(94%+99%)
pKPN3-307_typeA	(98%+99%)	(98%+98%)	(98%+98%)	(97%+99%)		(95%+98%)	(95%+98%)	(95%+97%)
pA1705-qnrS	(96%+97%)	(96%+97%)	(96%+97%)	(95%+99%)	(97%+98%)		(100%+99%)	(100%+99%)
p911021-tetA	(96%+97%)	(96%+97%)	(96%+97%)	(95%+99%)	(97%+98%)	(100%+99%)		(100%+99%)
p1642-tetA	(96%+97%)	(96%+96%)	(96%+96%)	(95%+99%)	(97%+97%)	(100%+99%)	(100%+99%)	

Supplementary table S2 Pairwise comparison of plasmids backbone sequences using BLASTN

Supplementary Table S3 Accessory modules of the MDR region from pKPN-c22, pKPSH11, p6234-198.371kb, pKPN3-307_TypeC, _____and pKPN13-307_typeA and the MDR-1 region from pA1705-qnrS

pKPN-c22 MDR region	pKPSH11 MDR region	p6234-198.371kb MDR region	pKPN3- 307_TypeC MDR region	pKPN3-307_typeA MDR region	pA1705-qnrS First MDR region
IS26	ΔIS26–ΔIS26	ISKpn28	Tn3 Family transposon remnant	Tn3 Family transposon remnant	Truncated IS26–sul2–strA– strB–IS26 Transposition unit
In37 residual	∆IS <i>5075</i>	IS26	IS26	IS26	Tn2
IS26	IS26–sul2–strA strB–IS26 Transposition unit residual	∆IS <i>Pa38</i>	In37 residual	∆IS <i>Pa3</i> 8	IS26– <i>sul</i> 2– <i>strA–</i> <i>strB</i> –IS26 Transposition unit residual
Tn1721 residual	Tn2-3'	IS5075	ΔIS26	IS5075	IS5075
Tn <i>5403</i>	IS <i>Ecp1–bla</i> _{CTX-M-15} – Δorf477 Transposition unit	IS26–sul2–strA– strB–IS26 Transposition unit residual	Tn <i>1721 residual</i>	IS26–sul2–strA– strB–IS26 Transposon remnant	∆IS26
Truncated IS <i>3000–qnrB1–</i> IS26 Transposition unit	Tn2-5'	Tn2-3'	ΔTn <i>540</i> 3	ΔTn2	IS26– <i>tetA</i> (D)– <i>tetR</i> (D)–IS26 Transposition unit derivative
In191	IS26 residual	IS <i>Ecp1–bla</i> _{CTX-M-15} – Δorf477 Transposition unit	Truncated IS <i>3000–qnrB1–</i> IS26 Transposition unit	IS <i>Ecp1-bla</i> ctx-M-15- Δorf477 Transposition unit	IS26
ecoRII–ecoRIImet	IS26– <i>cld</i> –IS26 Transposition unit residual	Tn2-5'	In191	Tn2 residual	orf447
IS1X2 residual	•Tn6415 residual	ΔIS26	ecoRII–ecoRIImet	Tn <i>6415</i>	Δ IS <i>K</i> pn38

ΔIS26	ΔIS26	Truncated IS26– <i>cld</i> –IS26	IS1X2 residual	In37 residual	-
		Transposition unit			
ΔTn2	In37 residual	ΔTn2	IS26	IS26	-
IS26-cld-IS26	ΔIS26	ΔTn <i>6415</i>	-	Tn <i>17</i> 21 residual	-
Transposition unit					
∆IS26–IS26	Tn <i>17</i> 21 residual	In37 residual	-	Tn <i>5403</i>	-
-	Tn <i>5403</i>	IS26	-	Truncated	-
				IS26	
				Transposition unit	
-	IS3000–qnrB1– IS26	Tn <i>17</i> 21 residual	-	In191	-
	Transposition unit residual				
-	ΔIS26	Tn <i>54</i> 03-3'	-	ecoRII–ecoRIImet	-
-	In191	IS26	-	IS1X2 residual	-
-	ecoRII–ecoRIImet	Tn <i>54</i> 03-5'	-	IS26	-
-	IS1X2 residual	Truncated IS3000– qnrB1–IS26	-	-	-
		Transposition unit			
-	ΔΙS26–ΔΙS26– ΔΙS26	In191	-	-	-
-		ecoRII–ecoRIImet	-	-	-
-	-	IS26	-	-	-

Supplementary Table S4 Accessory modules of the MDR region from p1642-tetA and p911021-tetA, and the MDR-2 region from pA1705-qnrS

p1642-tetA	p911021-tetA	pA1705-qnrS	
ΔTn <i>17</i> 21	ISEcp1-bla _{CTX-M-14} -IS903D	ΔTn <i>1721</i>	
In363	orf273	In363	
IS26-mph(A)–mrx–mphR(A)–IS6100	orf219	IS26–mph(A)–mrx–mphR(A)– IS6100	
IS26– <i>bla</i> shv-12–IS26	IS26	orf267	
Tn <i>1721</i>	orf762	orf537	
orf627	IS26bla _{SHV-12} IS26	IS26	
IS26–bla _{LAP-2} –qnrS–IS26	IS26	Tn <i>1721</i>	
aacC2–tmrB	ΔIS Vsa5	orf627	
ΔIS <i>Vsa5</i>	aacC2–tmrB	IS26–bla _{LAP-2} –qnrS–IS26	
IS26	IS26-blaLAP-2-qnrS-IS26	aacC2–tmrB	
IS26– <i>bla</i> _{SHV-12} –IS26	orf627	ΔIS <i>Vsa5</i>	
orf219	Tn <i>1721</i>	IS26	
orf273	Tn <i>4352</i>	IS26-bla _{SHV-12} -IS26	
IS <i>Ecp1–bla</i> cTX-M-14–IS903D	IS26-mph(A)–mrx–mphR(A)– IS6100	orf762	
-	In363	IS26	
-	ΔTn <i>17</i> 21	orf219	
-	-	orf273	
-	-	ISEcp1-blactx-m-14-IS903D	