

Supplementary Information

Table S1. Gene Information for Development of Plasmid DNA Reference Materials.

gene	name	accession number	sequence (5'–3')	product size (bp)	amino acid mutation
<i>aac(6')-Ib</i>	<i>aac(6')-Ib</i>	MN045292	TTGCGATGCTCTATGAGTGGCTAAATCGATCTCATATCGTCGAGTGGTGGGGCGGAGA AGAAGCACGCCCCGACACTTGCTGACGTACAGGAACAGTACTTGCCAAGCGTTTATAGC GCAAGAGTCCGTCCTACTCCATACATTGCAATGCTGAATGGAGAGCCGATTGGGTATGCC CAGTCGTACGTTGCTCTTGGAAGCGGGGACGGATGGTGGGAAGAAGAAACCGATCCA GGAGTACGCGGAATAGACCAGTTACTGGCGAATGCATCACAACCTGGGCAAAGGCTTG GGAACCAAGCTGGTTCGAGCTCTGGTTGAGTTGCTGTTCAATGATCCCGAGGTCACCA AGATCCAAACGGACCCGTCGCCGAGCAACTTGCGAGCGATCCGATGCTACGAGAAAG CGGGGTTTGAGAGGCAAGGTACCGTAACCAACCCAGATGGTCCAGCCGTGTACATGG TTCAAACACGCCAGGCATTTCGAG	482	–
<i>qnrA</i>	<i>qnrA</i>	MN045282	AGAGGATTTCTCACGCCAGGATTTGAGTGACAGCCGTTTTTCGCCGCTGCCGCTTTTATC AGTGTGACTTCAGCCACTGTCAGCTGCAGGATGCCAGTTTCGAGGATTGCAGTTTCAT TGAAAGCGGCGCCGTTGAAGGGTGTCCTTCAGCTATGCCGATCTGCGCGATGCCAGT TTCAAGGCCTGCCGTCTGTCTTTGGCCAACTTCAGCGGTGCCAACTGCTTTGGCATAG AGTTCAGGGAGTGCGATCTCAAGGGCGCCAACTTTTCCCGGGCCCGCTTCTACAATCA AGTCAGCCATAAGATGTACTTCTGCTCGGCTTATATCTCAGGTTGCAACCTGGCCTATA CCAACTTGAGTGGCCAATGCCTGGAAAAATGCGAGCTGTTTGAACAACCTGGAGCA ATGCCAATCTCAGCGGCGCTTCCTTGATGGGCTCAGATCTCAGCCGCGGCACCTTCTC CCGCGACTGTTGGCAACAGGTCAATCTGCGGGGCTGTGGCCTAACCTTTGCCGATCTG GATGGGCTCGACCCCAGACGGGTCAACCTCGAAGGAGTCAAGATCTGTGCCTGGCA	579	–
<i>qnrB</i>	<i>qnrB</i>	MN045281	GGCATTGAAATTCGCCACTGCCGCGCACAAGGCGCAGATTTCCGCGGTGCAAGCTTTA TGAATATGATCACCACGCGCACCTGGTTTTGCAGCGCATATATCACTAATACTAATCTAA	263	–

			GCTACGCCAATTTTTCGAAAGTCGTGTTGGAAAAGTGTGAGCTGTGGGAAAACCGCT GGATGGGGACTCAGGTAAGTGGGTGCGACGTTTCAGTGGTTCAGATCTCTCCGGCGGCG AGTTTTCGACTTTTCGACTGGCGAGCAGCAA		
<i>qnrS</i>	<i>qnrS</i>	MN045280	GCAAGTTCATTGAACAGGGTGATATTCGTGCTGCCACTTTGATGTCGCAGATCTTCGT GATGCAAGTTTCCAACAATGCCAACTTGCGATGGCAAACCTTCAGTAATGCCAATTGCT ACGGTATAGAGTTCCGTGCGTGTGATTTAAAAGGTGCCAACTTTTCCCGAACAACTT TGCCCATCAAGTGAGTAATCGTATGTACTTTTGCTCAGCATTTATTTCTGGATGTAATCT TTCCTATGCCAATATGGAGAGGGTTTGTTTAGAAAAATGTGAGTTGTTTGAAAATCGCT GGATAGGAACGAACCTAGCGGGTGCATCACTGAAAGAGTCAGACTTAAGTCGAGGTG TTTTTTCCGAAGATGTCTGGGGGCAATTTAGCCTACAGGGGGCCAATTTATGCCACGCC GAACTCGACGGTTTAGA	427	—
<i>oqx4</i>	<i>oqx4</i>	MN045291	GACAGCGTCGCACAGAATGCTGCGCCTCCCGCCCCGACGGTCAGCGCCGCTAAGGTG CTGGTGAAGTCGATCAGTCAGTGGGATAGTTTTAACGGTCGCATTGAAGCGGTGGAGA GCGTTTCAGCTTCGCCCTCGCGTCTCGGGATACATTGATAAAGTGAATTACACTGACGG CCAGGAGGTGAAAAAGGGCCAGGTGCTGTTACGATAGATGACAGAACCTATCGCGC CGCGCTGGAGCAGGCGCAGGCGGCGTTGGCAAGAGCCAAAACGCAGGCCAGCCTCG CGCAAAGCGAGGCGAACCGCACCGATAAATTAGTCCATACCAACCTCGTCTCC	339	—
<i>parC</i>	<i>parC</i>	MN045289	CTATGCGATGTCAGAGCTGGGGCTGAACGCCACCGCTAAATTTAAAAAATCCGCCCCGT ACCGTTGGTGACGTACTGGGTAAAGTATCACCCGCATGGCGACCGCGCCTGCTATGAAG CCATGGTGCTGATGGCGCAGCCGTTCTCTTACCGTTACCCGCTGGTCGATGGCCAGGG GAACTGGGGCGCGCCGGATGATCCGAAGTCATTGCGGGCGATGCGTTATACCGAATCC CGCCTGTCCAAATACGCCGAGCTGCTGTTA	262	Ser80Arg
<i>gyrA</i>	<i>gyrA1</i>	MN045284	CGTTGGTGACGTAATCGGTAAATACCATCCCCACGGCGATTCCGCAGTGTATAACACCA TCGTTTCGATGGCGCAGCCATTCTCGCTGCGTTACATGCTGGTGGATGGTCAGGGTAAC TTCGGTTCTATTGACGGCGACTCCGCGGCGGCAATGCGTTATACGGAGATCCGTCTGG	251	Asp87Asn

		CGAAAATCGCCACGAACTGATGGCCGATCTCGAAAAAGAGACGGTGGATTTCGTGG ATAACTATGACGGTACGG		
		CGTTGGTGACGTAATCGGTAAATACCATCCCCACGGCGATTACGCAGTGTATGACACCA TCGTTTCGTATGGCGCAGCCATTCTCGCTGCGTTACATGCTGGTGGATGGTCAGGGTAAC		
<i>gyrA2</i>	MN045285	TTCGGTTCTATTGACGGCGACTCCGCGGCGGCAATGCGTTATACGGAGATCCGTCTGG CGAAAATCGCCACGAACTGATGGCCGATCTCGAAAAAGAGACGGTGGATTTCGTGG ATAACTATGACGGTACGG	251	Ser83Tyr
		CGTTGGTGACGTAATCGGTAAATACCATCCCCACGGCGATTTCGCAGTGTATGACACC ATCGTTTCGTATGGCGCAGCCATTCTCGCTGCGTTACATGCTGGTGGATGGTCAGGGTAA		
<i>gyrA3</i>	MN045286	CTTCGGTTCTATTGACGGCGACTCCGCGGCGGCAATGCGTTATACGGAGATCCGTCTG GCGAAAATCGCCACGAACTGATGGCCGATCTCGAAAAAGAGACGGTGGATTTCGTG GATAACTATGACGGTACGG	251	Ser83Phe
		CGTTGGTGACGTAATCGGTAAATACCATCCCCACGGCGATTTCGCAGTGTATGGCACCA TCGTTTCGTATGGCGCAGCCATTCTCGCTGCGTTACATGCTGGTGGATGGTCAGGGTAAC		
<i>gyrA4</i>	MN045287	TTCGGTTCTATTGACGGCGACTCCGCGGCGGCAATGCGTTATACGGAGATCCGTCTGG CGAAAATCGCCACGAACTGATGGCCGATCTCGAAAAAGAGACGGTGGATTTCGTGG ATAACTATGACGGTACGG	251	Ser83Phe Asp87Gly
		CGTTGGTGACGTAATCGGTAAATACCATCCCCACGGCGATTTCGCAGTGTATGCCACCA TCGTTTCGTATGGCGCAGCCATTCTCGCTGCGTTACATGCTGGTGGATGGTCAGGGTAAC		
<i>gyrA5</i>	MN045288	TTCGGTTCTATTGACGGCGACTCCGCGGCGGCAATGCGTTATACGGAGATCCGTCTGG CGAAAATCGCCACGAACTGATGGCCGATCTCGAAAAAGAGACGGTGGATTTCGTGG ATAACTATGACGGTACGG	251	Ser83Phe Asp87Ala

Note: “—” means no artificial mutation.

Figure S1. Genetic stability of *aac(6')-Ib*.

Alignment: *aac(6')-Ib*

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original      10 20 30 40 50 60 70 80 90 100 110
3th aac(6')-Ib  --TTGGCAT- GCTCTATGAG TGGCTAAATC GATCTCATAT COTCGACTGG TGGGGCGGAG AAGAAGCAGC CCGGACACTT GCTGACGTAC AGGAACAGTA CTTGCCAAGC
6th aac(6')-Ib  TTTTGGCATT GCCTTATGAG TGGCTAAATC GATCTCATAT COTCGACTGG TGGGGCGGAG AAGAAGCAGC CCGGACACTT GCTGACGTAC AGGAACAGTA CTTGCCAAGC
9th aac(6')-Ib  TTTTGGCATT GCCTTATGAG TGGCTAAATC GATCTCATAT COTCGACTGG TGGGGCGGAG AAGAAGCAGC CCGGACACTT GCTGACGTAC AGGAACAGTA CTTGCCAAGC
12th aac(6')-Ib -TTTGGCAT- GCCTTATGAG TGGCTAAATC GATCTCATAT COTCGACTGG TGGGGCGGAG AAGAAGCAGC CCGGACACTT GCTGACGTAC AGGAACAGTA CTTGCCAAGC
15th aac(6')-Ib -TTTGGCAT- GCCTTATGAG TGGCTAAATC GATCTCATAT COTCGACTGG TGGGGCGGAG AAGAAGCAGC CCGGACACTT GCTGACGTAC AGGAACAGTA CTTGCCAAGC
Clustal Consensus ***** * *****

original      120 130 140 150 160 170 180 190 200 210 220
3th aac(6')-Ib  GTTTTAGCCG AAGAGTCCGT CACTCCATAC ATTGCAATGC TGAATGGAGA GCGCATTTGG TATGCCCACT CTTACGTTGC TCTTGGAAAG GGGACCGAT GCTGGGAAGA
6th aac(6')-Ib  GTTTTAGCCG AAGAGTCCGT CACTCCATAC ATTGCAATGC TGAATGGAGA GCGCATTTGG TATGCCCACT CTTACGTTGC TCTTGGAAAG GGGACCGAT GCTGGGAAGA
9th aac(6')-Ib  GTTTTAGCCG AAGAGTCCGT CACTCCATAC ATTGCAATGC TGAATGGAGA GCGCATTTGG TATGCCCACT CTTACGTTGC TCTTGGAAAG GGGACCGAT GCTGGGAAGA
12th aac(6')-Ib GTTTTAGCCG AAGAGTCCGT CACTCCATAC ATTGCAATGC TGAATGGAGA GCGCATTTGG TATGCCCACT CTTACGTTGC TCTTGGAAAG GGGACCGAT GCTGGGAAGA
15th aac(6')-Ib GTTTTAGCCG AAGAGTCCGT CACTCCATAC ATTGCAATGC TGAATGGAGA GCGCATTTGG TATGCCCACT CTTACGTTGC TCTTGGAAAG GGGACCGAT GCTGGGAAGA
Clustal Consensus *****

original      230 240 250 260 270 280 290 300 310 320 330
3th aac(6')-Ib  AGAAGCCGAT CCAGGACTAC GCGGAATAGA CCAGTTACTG CCGAATGCAT CACAACCTGG CAAAGCCTTG GGAACCAAGC TGGTTCGAGC TCTGTTGAG TTGCTGTTCA
6th aac(6')-Ib  AGAAGCCGAT CCAGGACTAC GCGGAATAGA CCAGTTACTG CCGAATGCAT CACAACCTGG CAAAGCCTTG GGAACCAAGC TGGTTCGAGC TCTGTTGAG TTGCTGTTCA
9th aac(6')-Ib  AGAAGCCGAT CCAGGACTAC GCGGAATAGA CCAGTTACTG CCGAATGCAT CACAACCTGG CAAAGCCTTG GGAACCAAGC TGGTTCGAGC TCTGTTGAG TTGCTGTTCA
12th aac(6')-Ib AGAAGCCGAT CCAGGACTAC GCGGAATAGA CCAGTTACTG CCGAATGCAT CACAACCTGG CAAAGCCTTG GGAACCAAGC TGGTTCGAGC TCTGTTGAG TTGCTGTTCA
15th aac(6')-Ib AGAAGCCGAT CCAGGACTAC GCGGAATAGA CCAGTTACTG CCGAATGCAT CACAACCTGG CAAAGCCTTG GGAACCAAGC TGGTTCGAGC TCTGTTGAG TTGCTGTTCA
Clustal Consensus *****

original      340 350 360 370 380 390 400 410 420 430 440
3th aac(6')-Ib  ATGATCCCGA GGTCAACCAAG ATCCAAACGG ACCCGTCGCC GAGCAACTTG CGAGCGATCC GATGCTACGA GAAAGCGGGG TTTGAGAGGC AAGGTACCGT AACCACCCCA
6th aac(6')-Ib  ATGATCCCGA GGTCAACCAAG ATCCAAACGG ACCCGTCGCC GAGCAACTTG CGAGCGATCC GATGCTACGA GAAAGCGGGG TTTGAGAGGC AAGGTACCGT AACCACCCCA
9th aac(6')-Ib  ATGATCCCGA GGTCAACCAAG ATCCAAACGG ACCCGTCGCC GAGCAACTTG CGAGCGATCC GATGCTACGA GAAAGCGGGG TTTGAGAGGC AAGGTACCGT AACCACCCCA
12th aac(6')-Ib ATGATCCCGA GGTCAACCAAG ATCCAAACGG ACCCGTCGCC GAGCAACTTG CGAGCGATCC GATGCTACGA GAAAGCGGGG TTTGAGAGGC AAGGTACCGT AACCACCCCA
15th aac(6')-Ib ATGATCCCGA GGTCAACCAAG ATCCAAACGG ACCCGTCGCC GAGCAACTTG CGAGCGATCC GATGCTACGA GAAAGCGGGG TTTGAGAGGC AAGGTACCGT AACCACCCCA
Clustal Consensus *****

original      450 460 470 480
3th aac(6')-Ib  GATGCTCCAG CCGTGTACAT GTTTCAAACA CCGCAGGCA- TT-CGAG--
6th aac(6')-Ib  GATGCTCCAG CCGTGTACAT GTTTCAAACA CCGCAGGCAA TTTGAGAA
9th aac(6')-Ib  GATGCTCCAG CCGTGTACAT GTTTCAAACA CCGCAGGCAA -TTGAGAA-
12th aac(6')-Ib GATGCTCCAG CCGTGTACAT GTTTCAAACA CCGCAGGCA- TTTGAGAA
15th aac(6')-Ib GATGCTCCAG CCGTGTACAT GTTTCAAACA CCGCAGGCA- TT-CGAGAA-
Clustal Consensus *****

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Note: “*” means no difference in nucleotide. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 20 nucleotides.

Figure S2. Genetic stability of *parC*.

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Alignment: parC
      .....| .....| .....| .....| .....| .....| .....| .....| .....| ..
      10      20      30      40      50      60      70      80      90
original -YAMSELGLN ATAKFIKKSAR TVGDVLGKTH FHGDRACYEA MVLMAQPPFSY RYPLVDGQGN WGAPDDPKSF AMRYTESRL SKYAEILL-- --
3th parC -YAMSELGLN ATAKFIKKSAR TVGDVLGKTH FHGDRACYEA MVLMAQPPFSY RYPLVDGQGN WGAPDDPKSF AMRYTESRL SKYAEILL-- --
6th parC -LCDVWKLGLN ATAKFIKKSAR TVGDVLGKTH FHGDRACYEA MVLMAQPPFSY RYPLVDGQGN WGAPDDPKSF AMRYTESRL SKYAGLLL-- --
9th parC -LCDVWKLGLN ATAKFIKKSAR TVGDVLGKTH FHGDRACYEA MVLMAQPPFSY RYPLVDGQGN WGAPDDPKSF AMRYTESRL SKYAGLLL-- --
12th parC FYAMSELGLN ATAKFIKKSAR TVGDVLGKTH FHGDRACYEA MVLMAQPPFSY RYPLVDGQGN WGAPDDPKSF AMRYTESRL SKYAEILLNS KI
15th parC -YAMSELGLN ATAKFIKKSAR TVGDVLGKTH FHGDRACYEA MVLMAQPPFSY RYPLVDGQGN WGAPDDPKSF AMRYTESRL SKYAEPAVKQ --
Clustal Consensus . :**** ***** ***** ***** ***** ***** ***** ***** ***** **** :

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Note: “*” means no difference in amino acid. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 10 amino acids.

Figure S3. Genetic stability of *qnrS*.

Alignment: *qnrS*

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-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
      10      20      30      40      50      60      70      80      90     100     110
original  -CCAAGTT-C ATTGAACAGG GTGATATTGG TCGCTGCCAC TTGATCTGCG CAGATCTTGG TGATGCCAAGT TTCCAACAAT GCCAACTTGC GATGCCAAAC TTCAGTAATG
3th qnrS  TCCAAGTTCC CATGAACAGG GTGATATTGG TCGCTGCCAC TTGATCTGCG CAGATCTTGG TGATGCCAAGT TTCCAACAAT GCCAACTTGC GATGCCAAAC TTCAGTAATG
6th qnrS  TCCAAGTTTC ATTGAACAGG GTGATATTGG TCGCTGCCAC TTGATCTGCG CAGATCTTGG TGATGCCAAGT TTCCAACAAT GCCAACTTGC GATGCCAAAC TTCAGTAATG
9th qnrS  TCCAAGTTCC AATGAACAGG GTGATATTGG TCGCTGCCAC TTGATCTGCG CAGATCTTGG TGATGCCAAGT TTCCAACAAT GCCAACTTGC GATGCCAAAC TTCAGTAATG
12th qnrS TCCAAGTTTC CCAGAACAGG GTGATATTGG TCGCTGCCAC TTGATCTGCG CAGATCTTGG TGATGCCAAGT TTCCAACAAT GCCAACTTGC GATGCCAAAC TTCAGTAATG
15th qnrS TCCAAGTTTC CCTGAACAGG GTGATATTGG TCGCTGCCAC TTGATCTGCG CAGATCTTGG TGATGCCAAGT TTCCAACAAT GCCAACTTGC GATGCCAAAC TTCAGTAATG
Clustal Consensus ***** * ***** ***** ***** ***** ***** ***** ***** ***** *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
      120     130     140     150     160     170     180     190     200     210     220
original  CCAATTGCTA CGGTATAGAG TTCCCTGCGT GTGATTTAAA AGCTGCCAAC TTTCGCCGAA CAAACTTTGC CCATCAAGTC AGTAATCGTA TGTACTTTTG CTCAGCATTG
3th qnrS  CCAATTGCTA CGGTATAGAG TTCCCTGCGT GTGATTTAAA AGCTGCCAAC TTTCGCCGAA CAAACTTTGC CCATCAAGTC AGTAATCGTA TGTACTTTTG CTCAGCATTG
6th qnrS  CCAATTGCTA CGGTATAGAG TTCCCTGCGT GTGATTTAAA AGCTGCCAAC TTTCGCCGAA CAAACTTTGC CCATCAAGTC AGTAATCGTA TGTACTTTTG CTCAGCATTG
9th qnrS  CCAATTGCTA CGGTATAGAG TTCCCTGCGT GTGATTTAAA AGCTGCCAAC TTTCGCCGAA CAAACTTTGC CCATCAAGTC AGTAATCGTA TGTACTTTTG CTCAGCATTG
12th qnrS CCAATTGCTA CGGTATAGAG TTCCCTGCGT GTGATTTAAA AGCTGCCAAC TTTCGCCGAA CAAACTTTGC CCATCAAGTC AGTAATCGTA TGTACTTTTG CTCAGCATTG
15th qnrS CCAATTGCTA CGGTATAGAG TTCCCTGCGT GTGATTTAAA AGCTGCCAAC TTTCGCCGAA CAAACTTTGC CCATCAAGTC AGTAATCGTA TGTACTTTTG CTCAGCATTG
Clustal Consensus ***** ***** ***** ***** ***** ***** ***** ***** ***** ***** *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
      230     240     250     260     270     280     290     300     310     320     330
original  ATTTCTGGAT GTAATCTTTT CTATGCCAAT ATGGAGAGGG TTGTTTGA AUAATGTGAG TTGTTTGAAA ATCCCTGGAT AGGAACGAACT CTAGCGGGTG CATCACTGAA
3th qnrS  ATTTCTGGAT GTAATCTTTT CTATGCCAAT ATGGAGAGGG TTGTTTGA AUAATGTGAG TTGTTTGAAA ATCCCTGGAT AGGAACGAACT CTAGCGGGTG CATCACTGAA
6th qnrS  ATTTCTGGAT GTAATCTTTT CTATGCCAAT ATGGAGAGGG TTGTTTGA AUAATGTGAG TTGTTTGAAA ATCCCTGGAT AGGAACGAACT CTAGCGGGTG CATCACTGAA
9th qnrS  ATTTCTGGAT GTAATCTTTT CTATGCCAAT ATGGAGAGGG TTGTTTGA AUAATGTGAG TTGTTTGAAA ATCCCTGGAT AGGAACGAACT CTAGCGGGTG CATCACTGAA
12th qnrS ATTTCTGGAT GTAATCTTTT CTATGCCAAT ATGGAGAGGG TTGTTTGA AUAATGTGAG TTGTTTGAAA ATCCCTGGAT AGGAACGAACT CTAGCGGGTG CATCACTGAA
15th qnrS ATTTCTGGAT GTAATCTTTT CTATGCCAAT ATGGAGAGGG TTGTTTGA AUAATGTGAG TTGTTTGAAA ATCCCTGGAT AGGAACGAACT CTAGCGGGTG CATCACTGAA
Clustal Consensus ***** ***** ***** ***** ***** ***** ***** ***** ***** ***** *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
      340     350     360     370     380     390     400     410     420     430
original  AGAGTCAGAC TTAAGTCGAG GTGTTTTTTC CGAAGATGTC TGGGGGCAAT TTAGCCTACA GGGGGCCAAT TTATGCCACG CCGAACTCGA CGG-TTTAGA -
3th qnrS  AGAGTCAGAC TTAAGTCGAG GTGTTTTTTC CGAAGATGTC TGGGGGCAAT TTAGCCTACA GGGGGCCAAT TTATGCCACG CCGAACTCGC -GTGTTTGA A
6th qnrS  AGAGTCAGAC TTAAGTCGAG GTGTTTTTTC CGAAGATGTC TGGGGGCAAT TTAGCCTACA GGGGGCCAAT TTATGCCACG CCGAACTCGA CGGGTTTGA A
9th qnrS  AGAGTCAGAC TTAAGTCGAG GTGTTTTTTC CGAAGATGTC TGGGGGCAAT TTAGCCTACA GGGGGCCAAT TTATGCCACG CCGAACTCGC CGGGTTTGA A
12th qnrS AGAGTCAGAC TTAAGTCGAG GTGTTTTTTC CGAAGATGTC TGGGGGCAAT TTAGCCTACA GGGGGCCAAT TTATGCCACG CCGAACTCGA CGGGTTTGA A
15th qnrS AGAGTCAGAC TTAAGTCGAG GTGTTTTTTC CGAAGATGTC TGGGGGCAAT TTAGCCTACA GGGGGCCAAT TTATGCCACG CCGAACTCGA CGGGTTTGA A
Clustal Consensus ***** ***** ***** ***** ***** ***** ***** ***** ***** * *****

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Note: “*” means no difference in nucleotide. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 20 nucleotides.

Figure S4. Genetic stability of *oqx4*.

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Alignment: oqx4
      10      20      30      40      50      60      70      80      90      100     110
original  ---GACAGC GTCCACAGA ATGCTGGCC TCCCGCCCG ACCTCAGCG CCGCTAAGCT GCTGGTGAAG TCGATCAGTC AGTGGGATAG TTTTAAACGGT CGCATTGAAG
3th oqx4  ---TGACAGC GTTCCACAGA ATGCTGGCC TCCCGCCCG ACCTCAGCG CCGCTAAGCT GCTGGTGAAG TCGATCAGTC AGTGGGATAG TTTTAAACGGT CGCATTGAAG
6th oqx4  ---TGACAGC GTTCCACAGA ATGCTGGCC TCCCGCCCG ACCTCAGCG CCGCTAAGCT GCTGGTGAAG TCGATCAGTC AGTGGGATAG TTTTAAACGGT CGCATTGAAG
9th oqx4  ---TGACAGC GTTCCACAGA ATGCTGGCC TCCCGCCCG ACCTCAGCG CCGCTAAGCT GCTGGTGAAG TCGATCAGTC AGTGGGATAG TTTTAAACGGT CGCATTGAAG
12th oqx4 ---TGACAGC GTTCCACAGA ATGCTGGCC TCCCGCCCG ACCTCAGCG CCGCTAAGCT GCTGGTGAAG TCGATCAGTC AGTGGGATAG TTTTAAACGGT CGCATTGAAG
15th oqx4 GTTTGACAGC GTCCACAGA ATGCTGGCC TCCCGCCCG ACCTCAGCG CCGCTAAGCT GCTGGTGAAG TCGATCAGTC AGTGGGATAG TTTTAAACGGT CGCATTGAAG
Clustal Consensus ***** * * **** ***** ***** ***** ***** ***** *****

      120     130     140     150     160     170     180     190     200     210     220
original  CGGTGCAGAG CATTACAGTT CCGCTCGCG TCTCGGGATA CATTGATAAA GTGAATTACA CTGACGCCCA GGAGGTGAAA AAGGGCCAGG TGTCTGTTTAC GATAGATGAC
3th oqx4  CGGTGCAGAG CATTACAGTT CCGCTCGCG TCTCGGGATA CATTGATAAA GTGAATTACA CTGACGCCCA GGAGGTGAAA AAGGGCCAGG TGTCTGTTTAC GATAGATGAC
6th oqx4  CGGTGCAGAG CATTACAGTT CCGCTCGCG TCTCGGGATA CATTGATAAA GTGAATTACA CTGACGCCCA GGAGGTGAAA AAGGGCCAGG TGTCTGTTTAC GATAGATGAC
9th oqx4  CGGTGCAGAG CATTACAGTT CCGCTCGCG TCTCGGGATA CATTGATAAA GTGAATTACA CTGACGCCCA GGAGGTGAAA AAGGGCCAGG TGTCTGTTTAC GATAGATGAC
12th oqx4 CGGTGCAGAG CATTACAGTT CCGCTCGCG TCTCGGGATA CATTGATAAA GTGAATTACA CTGACGCCCA GGAGGTGAAA AAGGGCCAGG TGTCTGTTTAC GATAGATGAC
15th oqx4 CGGTGCAGAG CATTACAGTT CCGCTCGCG TCTCGGGATA CATTGATAAA GTGAATTACA CTGACGCCCA GGAGGTGAAA AAGGGCCAGG TGTCTGTTTAC GATAGATGAC
Clustal Consensus ***** ***** ***** ***** ***** ***** ***** ***** ***** ***** *****

      230     240     250     260     270     280     290     300     310     320     330
original  AGAACCTATC GCGCCCGCGT GGAGCAGGCG CAGCCCGCGT TGGCAAGAGC CAAAACCCAG CCCAGCCTCG CCGAAAGCGA GCGGAACCGC ACCGATAAAT TACTGCATAC
3th oqx4  AGAACCTATC GCGCCCGCGT GGAGCAGGCG CAGCCCGCGT TGGCAAGAGC CAAAACCCAG CCCAGCCTCG CCGAAAGCGA GCGGAACCGC ACCGATAAAT TACTGCATAC
6th oqx4  AGAACCTATC GCGCCCGCGT GGAGCAGGCG CAGCCCGCGT TGGCAAGAGC CAAAACCCAG CCCAGCCTCG CCGAAAGCGA GCGGAACCGC ACCGATAAAT TACTGCATAC
9th oqx4  AGAACCTATC GCGCCCGCGT GGAGCAGGCG CAGCCCGCGT TGGCAAGAGC CAAAACCCAG CCCAGCCTCG CCGAAAGCGA GCGGAACCGC ACCGATAAAT TACTGCATAC
12th oqx4 AGAACCTATC GCGCCCGCGT GGAGCAGGCG CAGCCCGCGT TGGCAAGAGC CAAAACCCAG CCCAGCCTCG CCGAAAGCGA GCGGAACCGC ACCGATAAAT TACTGCATAC
15th oqx4 AGAACCTATC GCGCCCGCGT GGAGCAGGCG CAGCCCGCGT TGGCAAGAGC CAAAACCCAG CCCAGCCTCG CCGAAAGCGA GCGGAACCGC ACCGATAAAT TACTGCATAC
Clustal Consensus ***** ***** ***** ***** ***** ***** ***** ***** ***** ***** *****

      340     350
original  CAACCC--TCG TCTCC-----
3th oqx4  CACCCC--TCG TCTCC-----
6th oqx4  CACCCC--TCG TCTCCCT---
9th oqx4  CACCCC--TCG TCTCCCT---
12th oqx4 CACCCC--TCG TCTCCCT---
15th oqx4 CAACCCCTCG TCTCCAAAC AGCAC
Clustal Consensus ** * * * *****

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Note: “*” means no difference in nucleotide. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 20 nucleotides.

Figure S5. Genetic stability of *qnrB*.

Alignment: *qnrB*

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original      -GGCATTGAA ATTGCCCACT GCGCGGCACA AGGCCGAGAT TTCCGCGGTG CAAGCTTTAT GAATATGATC ACCACGGCGA CCTGGTTTTG CAGCGCATAT ATCACTAATA
3th qnrB      TGGCATTGAA ATTGCCCACT GCGCGGCACA AGGCCGAGAT TTCCGCGGTG CAAGCTTTAT GAATATGATC ACCACGGCGA CCTGGTTTTG CAGCGCATAT ATCACTAATA
6th qnrB      TGGCATTGAA ATTGCCCACT GCGCGGCACA AGGCCGAGAT TTCCGCGGTG CAAGCTTTAT GAATATGATC ACCACGGCGA CCTGGTTTTG CAGCGCATAT ATCACTAATA
9th qnrB      TGGCATTGAA ATTGCCCACT GCGCGGCACA AGGCCGAGAT TTCCGCGGTG CAAGCTTTAT GAATATGATC ACCACGGCGA CCTGGTTTTG CAGCGCATAT ATCACTAATA
12th qnrB     TGGCATTGAA ATTGCCCACT GCGCGGCACA AGGCCGAGAT TTCCGCGGTG CAAGCTTTAT GAATATGATC ACCACGGCGA CCTGGTTTTG CAGCGCATAT ATCACTAATA
15th qnrB     TGGCATTGAA ATTGCCCACT GCGCGGCACA AGGCCGAGAT TTCCGCGGTG CAAGCTTTAT GAATATGATC ACCACGGCGA CCTGGTTTTG CAGCGCATAT ATCACTAATA
Clustal Consensus *****

original      CTAATCTAAG CTACGCCAAT TTTTGAAG TCCTCTTGA AAAGTGTGAG CTCTGGGAAA ACCGCTGCAT GGGGACTCAG CTACTGGGTC CGAGCTTCAG TGGTTTCAGAT
3th qnrB      CTAATCTAAG CTACGCCAAT TTTTGAAG TCCTCTTGA AAAGTGTGAG CTCTGGGAAA ACCGCTGCAT GGGGACTCAG CTACTGGGTC CGAGCTTCAG TGGTTTCAGAT
6th qnrB      CTAATCTAAG CTACGCCAAT TTTTGAAG TCCTCTTGA AAAGTGTGAG CTCTGGGAAA ACCGCTGCAT GGGGACTCAG CTACTGGGTC CGAGCTTCAG TGGTTTCAGAT
9th qnrB      CTAATCTAAG CTACGCCAAT TTTTGAAG TCCTCTTGA AAAGTGTGAG CTCTGGGAAA ACCGCTGCAT GGGGACTCAG CTACTGGGTC CGAGCTTCAG TGGTTTCAGAT
12th qnrB     CTAATCTAAG CTACGCCAAT TTTTGAAG TCCTCTTGA AAAGTGTGAG CTCTGGGAAA ACCGCTGCAT GGGGACTCAG CTACTGGGTC CGAGCTTCAG TGGTTTCAGAT
15th qnrB     CTAATCTAAG CTACGCCAAT TTTTGAAG TCCTCTTGA AAAGTGTGAG CTCTGGGAAA ACCGCTGCAT GGGGACTCAG CTACTGGGTC CGAGCTTCAG TGGTTTCAGAT
Clustal Consensus *****

original      CTCCTCGGCG GCGAGTTTT GACTTTGAC TGGCGAGCAG CAAA-
3th qnrB      CTCCTCGGCG GCGAGTTTT GACTTTGAC TGGCGAACAG CAAAA
6th qnrB      CTCCTCGGCG GCGAGTTTT GACTTTGAC TGGCGAACAG CAAAA
9th qnrB      CTCCTCGGCG GCGAGTTTT GACTTTGAC TGGCGAACAG CAAAA
12th qnrB     CTCCTCGGCG GCGAGTTTT GACTTTGAC TGGCGAACAG CAAAA
15th qnrB     CTCCTCGGCG GCGAGTTTT GACTTTGAC TGGCGAACAG CAAAA
Clustal Consensus *****

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Note: “*” means no difference in nucleotide. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 20 nucleotides.

Figure S6. Genetic stability of *qnrA*.

Alignment: qnrA

```

      10      20      30      40      50      60      70      80      90     100     110
original  -AGAGGATTG CT-CACGCCA GGATTTGAGT GACAGCCGGT TTGCGCGCTG CCGCTTTTAT CAGTGTGACT TCAGGCTGAG TCAGCTGCAG GATGCCAGTT TCGAGGATTG
3th qnrA  --AGGATTG  TTCCAGGCCA GATTTTGAGT GACAGCCGGT TTGCGCGCTG CCGCTTTTAT CAGTGTGACT TCAGGCTGAG TCAGCTGCAG GATGCCAGTT TCGAGGATTG
6th qnrA  --AGGATTG  TTCCAGGCCA GATTTTGAGT GACAGCCGGT TTGCGCGCTG CCGCTTTTAT CAGTGTGACT TCAGGCTGAG TCAGCTGCAG GATGCCAGTT TCGAGGATTG
9th qnrA  AGCGGGAGTT TTTTTCGCCA GGATTTGAGT GACAGCCGGT TTGCGCGCTG CCGCTTTTAT CAGTGTGACT TCAGGCTGAG TCAGCTGCAG GATGCCAGTT TCGAGGATTG
12th qnrA AGAGCGGAGT TTTTCAGGCC GATTTTGAGT GACAGCCGGT TTGCGCGCTG CCGCTTTTAT CAGTGTGACT TCAGGCTGAG TCAGCTGCAG GATGCCAGTT TCGAGGATTG
15th qnrA -AGAGGATTG TTTTCAGGCC GATTTTGAGT GACAGCCGGT TTGCGCGCTG CCGCTTTTAT CAGTGTGACT TCAGGCTGAG TCAGCTGCAG GATGCCAGTT TCGAGGATTG
Clustal Consensus  ***  *  *****
      120     130     140     150     160     170     180     190     200     210     220
original  CAGTTTCATT GAAAGCGGGG CCGTTGAAGG GTGTCACTTC AGCTATGCCG ATCTCGGGGA TGCCAGTTTC AAGGCGTCGC GTCTGCTTTT GGCCAATCTC AGCGGTGCCA
3th qnrA  CAGTTTCATT GAAAGCGGGG CCGTTGAAGG GTGTCACTTC AGCTATGCCG ATCTCGGGGA TGCCAGTTTC AAGGCGTCGC GTCTGCTTTT GGCCAATCTC AGCGGTGCCA
6th qnrA  CAGTTTCATT GAAAGCGGGG CCGTTGAAGG GTGTCACTTC AGCTATGCCG ATCTCGGGGA TGCCAGTTTC AAGGCGTCGC GTCTGCTTTT GGCCAATCTC AGCGGTGCCA
9th qnrA  CAGTTTCATT GAAAGCGGGG CCGTTGAAGG GTGTCACTTC AGCTATGCCG ATCTCGGGGA TGCCAGTTTC AAGGCGTCGC GTCTGCTTTT GGCCAATCTC AGCGGTGCCA
12th qnrA CAGTTTCATT GAAAGCGGGG CCGTTGAAGG GTGTCACTTC AGCTATGCCG ATCTCGGGGA TGCCAGTTTC AAGGCGTCGC GTCTGCTTTT GGCCAATCTC AGCGGTGCCA
15th qnrA CAGTTTCATT GAAAGCGGGG CCGTTGAAGG GTGTCACTTC AGCTATGCCG ATCTCGGGGA TGCCAGTTTC AAGGCGTCGC GTCTGCTTTT GGCCAATCTC AGCGGTGCCA
Clustal Consensus  *****
      230     240     250     260     270     280     290     300     310     320     330
original  ACTGCTTTTG CATAGAGTTC AGGAGCATGC ATCTCAAGGG CGCCAACTTT TCCGCGGGCC GCTTCTACAA TCAAGTCAGC CATAAGATGT ACTTCTGCTC GCGTTATATC
3th qnrA  ACTGCTTTTG CATAGAGTTC AGGAGCATGC ATCTCAAGGG CGCCAACTTT TCCGCGGGCC GCTTCTACAA TCAAGTCAGC CATAAGATGT ACTTCTGCTC GCGTTATATC
6th qnrA  ACTGCTTTTG CATAGAGTTC AGGAGCATGC ATCTCAAGGG CGCCAACTTT TCCGCGGGCC GCTTCTACAA TCAAGTCAGC CATAAGATGT ACTTCTGCTC GCGTTATATC
9th qnrA  ACTGCTTTTG CATAGAGTTC AGGAGCATGC ATCTCAAGGG CGCCAACTTT TCCGCGGGCC GCTTCTACAA TCAAGTCAGC CATAAGATGT ACTTCTGCTC GCGTTATATC
12th qnrA ACTGCTTTTG CATAGAGTTC AGGAGCATGC ATCTCAAGGG CGCCAACTTT TCCGCGGGCC GCTTCTACAA TCAAGTCAGC CATAAGATGT ACTTCTGCTC GCGTTATATC
15th qnrA ACTGCTTTTG CATAGAGTTC AGGAGCATGC ATCTCAAGGG CGCCAACTTT TCCGCGGGCC GCTTCTACAA TCAAGTCAGC CATAAGATGT ACTTCTGCTC GCGTTATATC
Clustal Consensus  *****
      340     350     360     370     380     390     400     410     420     430     440
original  TCAGGTTGCA ACCTGGGCTA TACCAACTGT AGTGGCCAA TCGCTGGAAA ATGCGGAGCT TTTGAAUACA ACTGGAGACA TCCCAATCTC AGCGGCGGCT CTTTGATGGG
3th qnrA  TCAGGTTGCA ACCTGGGCTA TACCAACTGT AGTGGCCAA TCGCTGGAAA ATGCGGAGCT TTTGAAUACA ACTGGAGACA TCCCAATCTC AGCGGCGGCT CTTTGATGGG
6th qnrA  TCAGGTTGCA ACCTGGGCTA TACCAACTGT AGTGGCCAA TCGCTGGAAA ATGCGGAGCT TTTGAAUACA ACTGGAGACA TCCCAATCTC AGCGGCGGCT CTTTGATGGG
9th qnrA  TCAGGTTGCA ACCTGGGCTA TACCAACTGT AGTGGCCAA TCGCTGGAAA ATGCGGAGCT TTTGAAUACA ACTGGAGACA TCCCAATCTC AGCGGCGGCT CTTTGATGGG
12th qnrA TCAGGTTGCA ACCTGGGCTA TACCAACTGT AGTGGCCAA TCGCTGGAAA ATGCGGAGCT TTTGAAUACA ACTGGAGACA TCCCAATCTC AGCGGCGGCT CTTTGATGGG
15th qnrA TCAGGTTGCA ACCTGGGCTA TACCAACTGT AGTGGCCAA TCGCTGGAAA ATGCGGAGCT TTTGAAUACA ACTGGAGACA TCCCAATCTC AGCGGCGGCT CTTTGATGGG
Clustal Consensus  *****
      450     460     470     480     490     500     510     520     530     540     550
original  CTCAGATCTC AGGCGCGGCA CTTCTTCCCG CGACTGTGCG CAACAGGTCA ATCTCGGGGG CTGTGGGCTA ACCTTTGGCG ATCTGGATGG GCTCGAGGCC AGACGGGTCA
3th qnrA  CTCAGATCTC AGGCGCGGCA CTTCTTCCCG CGACTGTGCG CAACAGGTCA ATCTCGGGGG CTGTGGGCTA ACCTTTGGCG ATCTGGATGG GCTCGAGGCC AGACGGGTCA
6th qnrA  CTCAGATCTC AGGCGCGGCA CTTCTTCCCG CGACTGTGCG CAACAGGTCA ATCTCGGGGG CTGTGGGCTA ACCTTTGGCG ATCTGGATGG GCTCGAGGCC AGACGGGTCA
9th qnrA  CTCAGATCTC AGGCGCGGCA CTTCTTCCCG CGACTGTGCG CAACAGGTCA ATCTCGGGGG CTGTGGGCTA ACCTTTGGCG ATCTGGATGG GCTCGAGGCC AGACGGGTCA
12th qnrA CTCAGATCTC AGGCGCGGCA CTTCTTCCCG CGACTGTGCG CAACAGGTCA ATCTCGGGGG CTGTGGGCTA ACCTTTGGCG ATCTGGATGG GCTCGAGGCC AGACGGGTCA
15th qnrA CTCAGATCTC AGGCGCGGCA CTTCTTCCCG CGACTGTGCG CAACAGGTCA ATCTCGGGGG CTGTGGGCTA ACCTTTGGCG ATCTGGATGG GCTCGAGGCC AGACGGGTCA
Clustal Consensus  *****
      560     570     580     590
original  ACCTCGAAGG AGTCAAGATC TGTGGC-TGG CA-----
3th qnrA  ACCTCGAAGG AGTCAAGATC TGGGCGCTGG CAAA-----
6th qnrA  ACCTCGAAGG AGTCAAGATC TGGGCGCTGG CAAA-----
9th qnrA  ACCTCGAAGG AGTCAAGCTC TGTGGCCTGG CAAAGTTGAGT TTTT-
12th qnrA ACCTCGAAGG AGTCAAGATC TGTGGCCTGG CAAAGTTGAGT TTTT-
15th qnrA ACCTCGAAGG AGTCAAGATC TGGGCGCTGG CAAAGTACTT TTTT-
Clustal Consensus  *****

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Note: “*” means no difference in nucleotide. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 20 nucleotides.

Figure S7. Genetic stability of *gyrA*.

Alignment: *gyrA1*

```

      |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----|
      10      20      30      40      50      60      70      80
original -VGDVIGKYH PHGDSAVYNT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT-
3th gyrA1 FVGDVIGKYH PHGDSAVYNT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT-
6th gyrA1 -VGDVIGKYH PHGDSAVYNT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT-
9th gyrA1 FVGDVIGKYH PHGDSAVYNT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT-
12th gyrA1 FVGDVIGKYH PHGDSAVYNT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT-
15th gyrA1 -VGDVIGKYH PHGDSAVYNT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT-
Clustal Consensus *****

```

Alignment: *gyrA2*

```

      |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----|
      10      20      30      40      50      60      70      80
original -VGDVIGKYH PHGDYAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT-
3th gyrA2 -VGDVIGKYH PHGDYAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT-
6th gyrA2 -VGDVIGKYH PHGDYAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT-
9th gyrA2 -VGDVIGKYH PHGDYAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT-
12th gyrA2 -VGDVIGKYH PHGDYAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT-
15th gyrA2 IVGDVIGKYH PHGDYAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT-
Clustal Consensus *****

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Alignment: *gyrA3*

```

      |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----|
      10      20      30      40      50      60      70      80
original -VGDVIGKYH PHGDFAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT-
3th gyrA3 SLVTIVIGKYH PHGDFAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT-
6th gyrA3 SLVTIVIGKYH PHGDFAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YERYG
9th gyrA3 -VGDVIGKYH PHGDFAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT-
12th gyrA3 -VGDVIGKYH PHGDFAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT-
15th gyrA3 SLVSVIGKYH PHGDFAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT-
Clustal Consensus : *****

```

Alignment: *gyrA4*

```

      |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----|
      10      20      30      40      50      60      70      80
original -VGDVIGKYH PHGDFAVYGT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT-
3th gyrA4 LVGDVIGKYH PHGDFAVYGT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT-
6th gyrA4 -VGDVIGKYH PHGDFAVYGT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT-
9th gyrA4 -VGDVIGKYH PHGDFAVYGT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT-
12th gyrA4 IVGDVIGKYH PHGDFAVYGT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT-
15th gyrA4 LVGDVIGKYH PHGDFAVYGT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT-
Clustal Consensus *****

```

Alignment: *gyrA5*

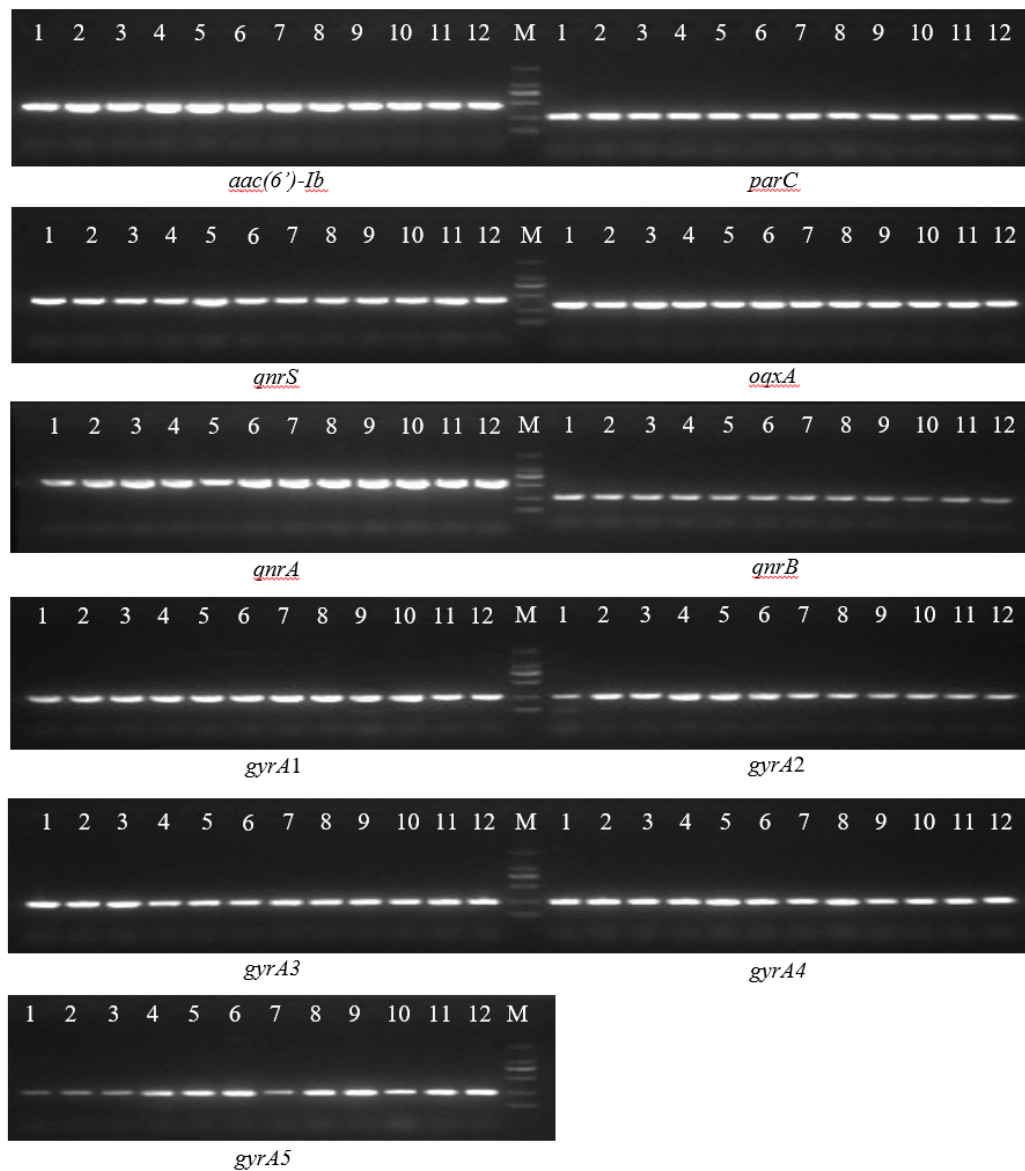
```

      |-----| |-----| |-----| |-----| |-----| |-----| |-----| |-----|
      10      20      30      40      50      60      70      80
original -VGDVIGKYH PHGDFAVYAT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT-
3th gyrA5 SLVTIVIGKYH PHGDFAVYAT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT-
6th gyrA5 SLVTIVIGKYH PHGDFAVYAT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT-
9th gyrA5 -VGDRIGKYH PHGDFAVYAT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YARYG
12th gyrA5 -VGDLIGKYH PHGDFAVYAT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YGRYG
15th gyrA5 -VGDVIGKYH PHGDFAVYAT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YGRYG
Clustal Consensus : *****

```

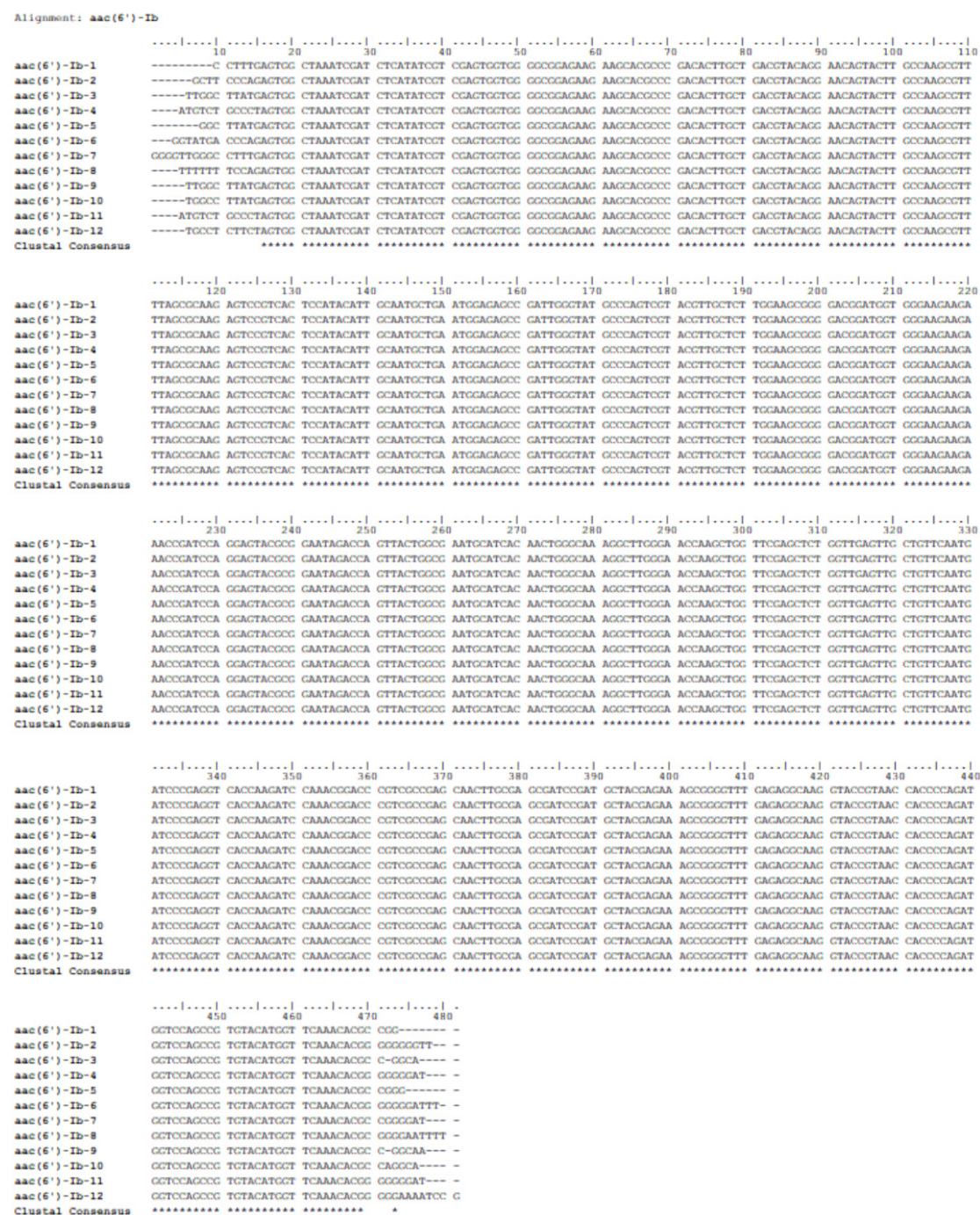
Note: “*” means no difference in amino acid. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 10 amino acids.

Figure S8. PCR results for homogeneity of plasmid DNA reference materials.



Note: Lane M is DL 2000 DNA marker, lanes 1–12 are PCR bands of each reference material in 12 tubes.

Figure S9. Homogeneity of *aac(6')-Ib* in plasmid DNA reference materials.

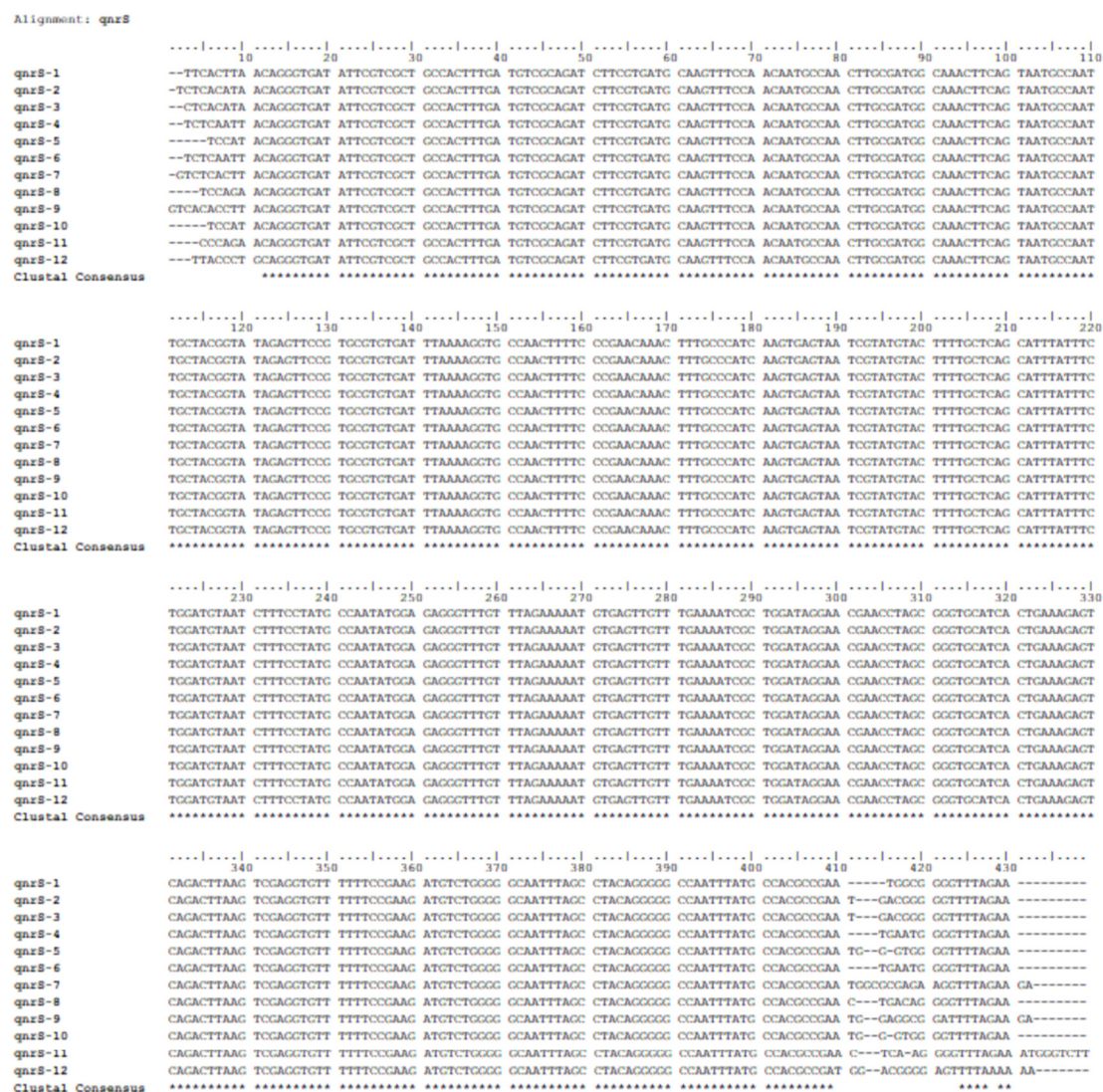


Note: “*” means no difference in nucleotide. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 20 nucleotides.

Alignment: parC

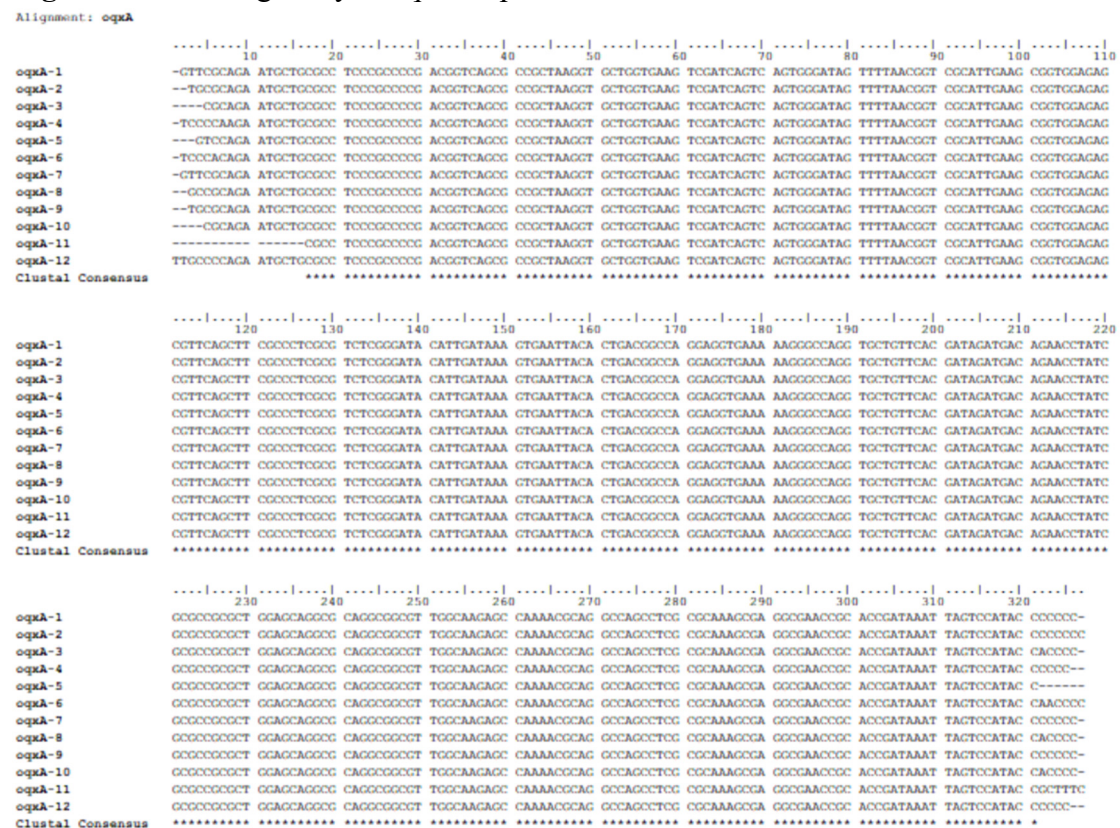
Note: “*” means no difference in amino acid. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 10 amino acids.

Figure S11. Homogeneity of *qnrS* in plasmid DNA reference materials.



Note: “*” means no difference in nucleotide. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 20 nucleotides.

Figure S12. Homogeneity of *oqxA* in plasmid DNA reference materials.



Note: “*” means no difference in nucleotide. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 20 nucleotides.

Figure S13. Homogeneity of *qnrA* in plasmid DNA reference materials.

[illegible]

Note: “*” means no difference in nucleotide. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 20 nucleotides.

Alignment: qnrB

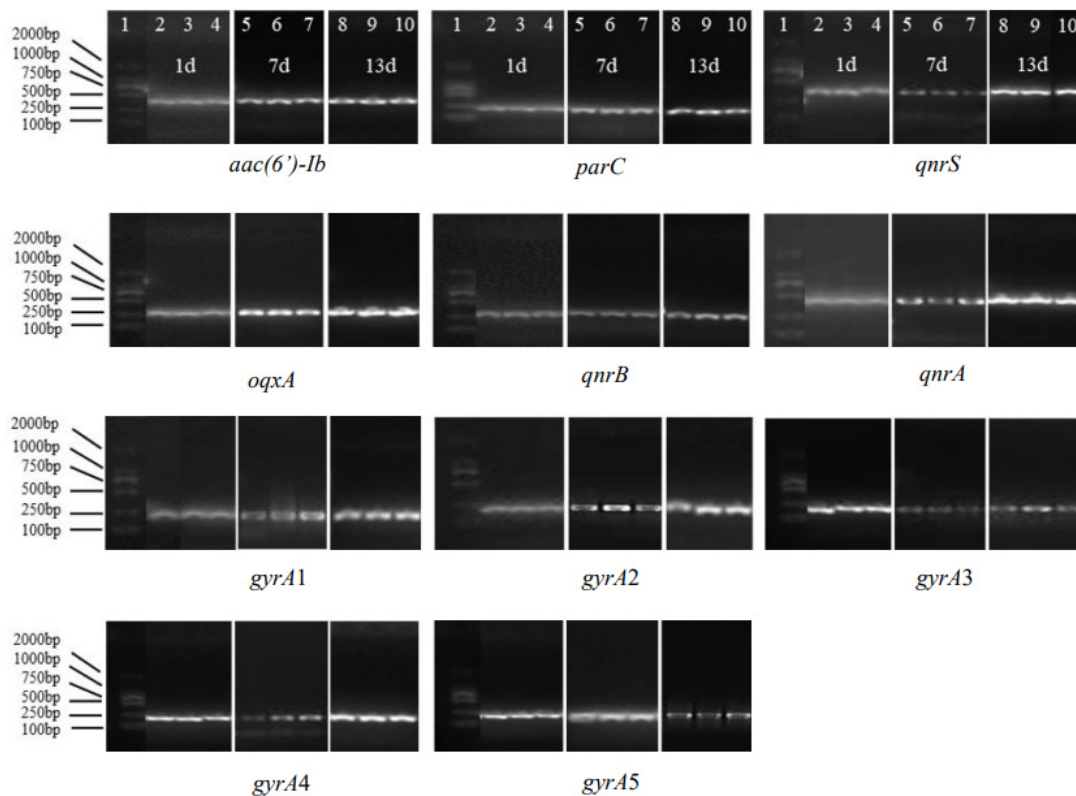
Note: “*” means no difference in nucleotide. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 20 nucleotides.

Figure S15. Homogeneity of *gyrA* in plasmid DNA reference materials.

Alignment: gyrA1											
	10	20	30	40	50	60	70	80			
gyrA1-1	SLVTFFGKYH	PHGDSAVYNT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDT	LTVR-		
gyrA1-2	-RWSRIGKYH	PHGDSAVYNT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	WNGT-		
gyrA1-3	-RWSRIGKYH	PHGDSAVYNT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	WNGT-		
gyrA1-4	-VGDVIGKYH	PHGDSAVYNT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	YDGT-		
gyrA1-5	SLATRIGKYH	PHGDSAVYNT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDK	TERY-		
gyrA1-6	LLVNLPGKYH	PHGDSAVYNT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDK	RERYG		
gyrA1-7	LLVNLPGKYH	PHGDSAVYNT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDK	RERYG		
gyrA1-8	-VGERPGKYH	PHGDSAVYNT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDK	CERYG		
gyrA1-9	SLVSVIGKYH	PHGDSAVYNT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	YDGT-		
gyrA1-10	-RWSRIGKYH	PHGDSAVYNT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	WNGT-		
gyrA1-11	LLVNLPGKYH	PHGDSAVYNT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDK	RERYG		
gyrA1-12	-VGDPIGKYH	PHGDSAVYNT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	WQRY-		
Clustal Consensus	:**** *****										
Alignment: gyrA2											
	10	20	30	40	50	60	70	80			
gyrA2-1	-VGDGPGKYH	PHGDYAVYDT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDK	WERYG		
gyrA2-2	-VADRPGKYH	PHGDYAVYDT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	NDGT-		
gyrA2-3	SLVNGIGKYH	PHGDYAVYDT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	WDGT-		
gyrA2-4	-VGDGIGKYH	PHGDYAVYDT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	WERY-		
gyrA2-5	-VGDVIGKYH	PHGDYAVYDT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	YDGTG		
gyrA2-6	-VHGIGKYH	PHGDYAVYDT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	LARY-		
gyrA2-7	-VADRPGKYH	PHGDYAVYDT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	NDGT-		
gyrA2-8	RWSSAFKYH	PHGDYAVYDT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDK	SNGT-		
gyrA2-9	SLVTIVGKYH	PHGDYAVYDT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	YDGT-		
gyrA2-10	SLVNGIGKYH	PHGDYAVYDT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	WDGT-		
gyrA2-11	-RW-SVIGKYH	PHGDYAVYDT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDK	LQTVR		
gyrA2-12	-VHGIGKYH	PHGDYAVYDT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	LARY-		
Clustal Consensus	:**** *****										
Alignment: gyrA3											
	10	20	30	40	50	60	70	80			
gyrA3-1	SVGARVGKYH	PHGDFAVYDT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDK	M-TVR		
gyrA3-2	HW-FRPGKYH	PHGDFAVYDT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	WERY-		
gyrA3-3	-VGEPIGKYH	PHGDFAVYDT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	-QTVR		
gyrA3-4	SLVVGPGKYH	PHGDFAVYDT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDK	SNGT-		
gyrA3-5	-LVTRPGKYH	PHGDFAVYDT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDK	MGRYG		
gyrA3-6	SLVSVIGKYH	PHGDFAVYDT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	YDGT-		
gyrA3-7	-LVTRPGKYH	PHGDFAVYDT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDK	MGRYG		
gyrA3-8	-VGEAPGKYH	PHGDFAVYDT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	CASVR		
gyrA3-9	FVGDVIGKYH	PHGDFAVYDT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	YDGT-		
gyrA3-10	-VGEPIGKYH	PHGDFAVYDT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	-QTVR		
gyrA3-11	SLVTIVGKYH	PHGDFAVYDT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	YERYG		
gyrA3-12	-VGDGPGKYH	PHGDFAVYDT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	MDGT-		
Clustal Consensus	:**** *****										
Alignment: gyrA4											
	10	20	30	40	50	60	70	80			
gyrA4-1	-VGERIGKYH	PHGDFAVYGT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	LARYG		
gyrA4-2	SLVTRIGKYH	PHGDFAVYGT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	FKRY-		
gyrA4-3	-W-FVIGKYH	PHGDFAVYGT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDK	WERYG		
gyrA4-4	-VHGIGKYH	PHGDFAVYGT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	WNGT-		
gyrA4-5	LVGDRPGKYH	PHGDFAVYGT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDK	CARYG		
gyrA4-6	-CW-PIGKYH	PHGDFAVYGT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	SNGTG		
gyrA4-7	-CW-PIGKYH	PHGDFAVYGT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	SNGTG		
gyrA4-8	-CW-PIGKYH	PHGDFAVYGT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	SNGTG		
gyrA4-9	-VGERPGKYH	PHGDFAVYGT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDK	LNSTG		
gyrA4-10	SLVRPGKYH	PHGDFAVYGT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDK	WNGT-		
gyrA4-11	IVGDVIGKYH	PHGDFAVYGT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	VURYG		
gyrA4-12	-VHGIGKYH	PHGDFAVYGT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	WNGT-		
Clustal Consensus	:**** *****										
Alignment: gyrA5											
	10	20	30	40	50	60	70	80			
gyrA5-1	-VGDPIGKYH	PHGDFAVYAT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	LGRYG		
gyrA5-2	-LVHRIGKYH	PHGDFAVYAT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	WNGT-		
gyrA5-3	SLVVGPGKYH	PHGDFAVYAT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	C-RY-		
gyrA5-4	SLVVGPGKYH	PHGDFAVYAT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDK	LDGT-		
gyrA5-5	-VGEFGKYH	PHGDFAVYAT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	MSRYG		
gyrA5-6	SLVVGPGKYH	PHGDFAVYAT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDK	LDGT-		
gyrA5-7	-VGEFGKYH	PHGDFAVYAT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	MSRYG		
gyrA5-8	-LVHRIGKYH	PHGDFAVYAT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	WNGT-		
gyrA5-9	-VGDRIKGYH	PHGDFAVYAT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	WPTVR		
gyrA5-10	-VGDVIGKYH	PHGDFAVYAT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	K-RY-		
gyrA5-11	CW-FVIGKYH	PHGDFAVYAT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDK	RNGT-		
gyrA5-12	RW-AGIGKYH	PHGDFAVYAT	IVRMAQPFSL	RYMLVDGQGN	PGSIDGDSAA	AMRYTEIRLA	KIAHELMADL	EKETVDFVDN	LDGT-		
Clustal Consensus	:**** *****										

Note: “*” means no difference in amino acid. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 10 amino acids.

Figure S16. PCR results for storage stability of plasmid DNA references materials stored at 37°C.



Note: Lane 1 is DL 2000 DNA marker; lane 2–4, 5–7, and 8–10 are PCR bands of the target gene sampled on the 1st, 7th, and 13th days of storage, respectively. Considering the different sampling timepoints, the gene images were intercepted and spliced using Microsoft Word, and the original images are available upon request.

Figure S17. Sequencing results of *aac(6')-Ib* for stability of plasmid DNA references materials stored at 37°C.

```

Alignment: aac(6')-Ib
      10      20      30      40      50      60      70      80      90     100     110
37-1d  TTGGATGCT ---CTATCA GTGGCTAAAT CGATCTCATA TCCTGAGTGT GTGGGGCGGA GAAGAAGCAC GCGCGACACT TGCTGACGTA CAGGAACAGT ACTTGCCAAG
37-7d  TTGGCGTTT GTTCCGAGA GTGGCTAAAT CGATCTCATA TCCTGAGTGT GTGGGGCGGA GAAGAAGCAC GCGCGACACT TGCTGACGTA CAGGAACAGT ACTTGCCAAG
37-13d TTGGCATTT TCC-CCGAGA GTGGCTAAAT CGATCTCATA TCCTGAGTGT GTGGGGCGGA GAAGAAGCAC GCGCGACACT TGCTGACGTA CAGGAACAGT ACTTGCCAAG
Clustal Consensus ***** * * * * *****

      120     130     140     150     160     170     180     190     200     210     220
37-1d  CTTTTAGCG CAAGAGTCCG TCACTCCATA CATTCCAATG CTGAATGGAG AGCGGATTGG GTATGCCCGAG TCCTACCTTG CTCTTGAAG CCGGACCGGA TGCTGGGAAG
37-7d  CTTTTAGCG CAAGAGTCCG TCACTCCATA CATTCCAATG CTGAATGGAG AGCGGATTGG GTATGCCCGAG TCCTACCTTG CTCTTGAAG CCGGACCGGA TGCTGGGAAG
37-13d CTTTTAGCG CAAGAGTCCG TCACTCCATA CATTCCAATG CTGAATGGAG AGCGGATTGG GTATGCCCGAG TCCTACCTTG CTCTTGAAG CCGGACCGGA TGCTGGGAAG
Clustal Consensus *****

      230     240     250     260     270     280     290     300     310     320     330
37-1d  AAGAAACCGA TCCAGGAGTA CCGCGAATAG ACCAGTTACT GCGCAATGCA TCACAACCTGG CCAAAGGCTT GCGAACCAG CTGCTTCGAG CTCTGTTGA GTTGTGTTTC
37-7d  AAGAAACCGA TCCAGGAGTA CCGCGAATAG ACCAGTTACT GCGCAATGCA TCACAACCTGG CCAAAGGCTT GCGAACCAG CTGCTTCGAG CTCTGTTGA GTTGTGTTTC
37-13d AAGAAACCGA TCCAGGAGTA CCGCGAATAG ACCAGTTACT GCGCAATGCA TCACAACCTGG CCAAAGGCTT GCGAACCAG CTGCTTCGAG CTCTGTTGA GTTGTGTTTC
Clustal Consensus *****

      340     350     360     370     380     390     400     410     420     430     440
37-1d  AATGATCCCG AGGTCAACAA GATCCAAACG GACCGGTGCG CGAGCAACTT GCGAGCGGATC CGATGCTACG AGAAAGCGGG GTTTGAGAGG CAAGGTACCG TAACCAACCC
37-7d  AATGATCCCG AGGTCAACAA GATCCAAACG GACCGGTGCG CGAGCAACTT GCGAGCGGATC CGATGCTACG AGAAAGCGGG GTTTGAGAGG CAAGGTACCG TAACCAACCC
37-13d AATGATCCCG AGGTCAACAA GATCCAAACG GACCGGTGCG CGAGCAACTT GCGAGCGGATC CGATGCTACG AGAAAGCGGG GTTTGAGAGG CAAGGTACCG TAACCAACCC
Clustal Consensus *****

      450     460     470     480     490
37-1d  AGATGCTCCA GCGCTGTACA TGGTTCAAAC ACGGCGAGCA TTC---GAG ---
37-7d  AGATGCTCCA GCGCTGTACA TGGTTCAAAC ACGGCGAGCA TTTTCTGAG GAA
37-13d AGATGCTCCA GCGCTGTACA TGGTTCAAAC ACGGCGTGA TTTT-CGAG AT-
Clustal Consensus ***** * * *

```

Note: “*” means no difference in nucleotide. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 20 nucleotides

Figure S18. Sequencing results of *parC* for stability of plasmid DNA references materials stored at 37°C.

```

Alignment: parC
          |-----|-----|-----|-----|-----|-----|-----|-----|-----|
          10      20      30      40      50      60      70      80
37-1d    -YAMSELGLN ATAKFKKSAR TVGDVLGKYH PHGDRACYEA M/LMAQPFSY RYPLVDGQGN WGAPDDPKSF AAMRYTESRL SKYAEILL-
37-7d    SMRFVKLGLN ATAKFKKSAR TVGDVLGKYH PHGDRACYEA M/LMAQPFSY RYPLVDGQGN WGAPDDPKSF AAMRYTESRL SKYAGLLL-
37-13d   SMRFVELGLN ATAKFKKSAR TVGDVLGKYH PHGDRACYEA M/LMAQPFSY RYPLVDGQGN WGAPDDPKSF AAMRYTESRL SKYAGFAV-
Clustal Consensus : :**** ***** ***** ***** ***** ***** ***** ***** ***** :

```

Note: “*” means no difference in amino acid. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 10 amino acids.

Figure S19. Sequencing results of *qnrS* for stability of plasmid DNA references materials stored at 37°C.

```

Alignment: qnrS
      10      20      30      40      50      60      70      80      90     100     110
37-1d  --GCAAGTTC ATTGAACAGG GTGATATTGC TCGCTGCCAC TTGATGTCGC CAGATCTTCG TGATGCAAGT TTCCAACAAT GCCAACTTCG GATGGCAAAAC TTCAGTAATG
37-7d  TCGAAGTTTT TCGATACAGG GTGATATTGC TCGCTGCCAC TTGATGTCGC CAGATCTTCG TGATGCAAGT TTCCAACAAT GCCAACTTCG GATGGCAAAAC TTCAGTAATG
37-13d -----ACAGG GTGATATTGC TCGCTGCCAC TTGATGTCGC CAGATCTTCG TGATGCAAGT TTCCAACAAT GCCAACTTCG GATGGCAAAAC TTCAGTAATG
Clustal Consensus *****

      120     130     140     150     160     170     180     190     200     210     220
37-1d  CCAATTGCTA CGGTATAGAG TTCGGTGGGT GTGATTTAAA AGGTGCCAAC TTTTCCCGAA CAAACTTTGC CCATCAAGTG AGTAATGCTA TGTACTTTTG CTCAGCATTG
37-7d  CCAATTGCTA CGGTATAGAG TTCGGTGGGT GTGATTTAAA AGGTGCCAAC TTTTCCCGAA CAAACTTTGC CCATCAAGTG AGTAATGCTA TGTACTTTTG CTCAGCATTG
37-13d CCAATTGCTA CGGTATAGAG TTCGGTGGGT GTGATTTAAA AGGTGCCAAC TTTTCCCGAA CAAACTTTGC CCATCAAGTG AGTAATGCTA TGTACTTTTG CTCAGCATTG
Clustal Consensus *****

      230     240     250     260     270     280     290     300     310     320     330
37-1d  ATTTCTGGAT GTAATCTTTC CTATGCCAAT ATGGAGAGGG TTGTTTGAAG AAAATGTGAG TTGTTTGAAA ATCGCTGGAT AGGAACGAAC CTAGCGGGTG CATCACTGAA
37-7d  ATTTCTGGAT GTAATCTTTC CTATGCCAAT ATGGAGAGGG TTGTTTGAAG AAAATGTGAG TTGTTTGAAA ATCGCTGGAT AGGAACGAAC CTAGCGGGTG CATCACTGAA
37-13d ATTTCTGGAT GTAATCTTTC CTATGCCAAT ATGGAGAGGG TTGTTTGAAG AAAATGTGAG TTGTTTGAAA ATCGCTGGAT AGGAACGAAC CTAGCGGGTG CATCACTGAA
Clustal Consensus *****

      340     350     360     370     380     390     400     410     420     430
37-1d  AGAGTCAGAC TTAAGTCGAG GTGTTTTTTC CGAAGATGTC TGGGGGCAAT TTAGCCTACA GGGGGCCAAT TTATGCCACG CGGAATCGA CGGTTTGA- ---
37-7d  AGAGTCAGAC TTAAGTCGAG GTGTTTTTTC CGAAGATGTC TGGGGGCAAT TTAGCCTACA GGGGGCCAAT TTATGCCACG CGGA-TGGG TGGGTTTTA GAA
37-13d AGAGTCAGAC TTAAGTCGAG GTGTTTTTTC CGAAGATGTC TGGGGGCAAT TTAGCCTACA GGGGGCCAAT TTATGCCACG CGGA-TGGA -GAGGTT- ---
Clustal Consensus *****

```

Note: “*” means no difference in nucleotide. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 20 nucleotides.

Figure S20. Sequencing results of *oqx1* for stability of plasmid DNA references materials stored at 37°C.

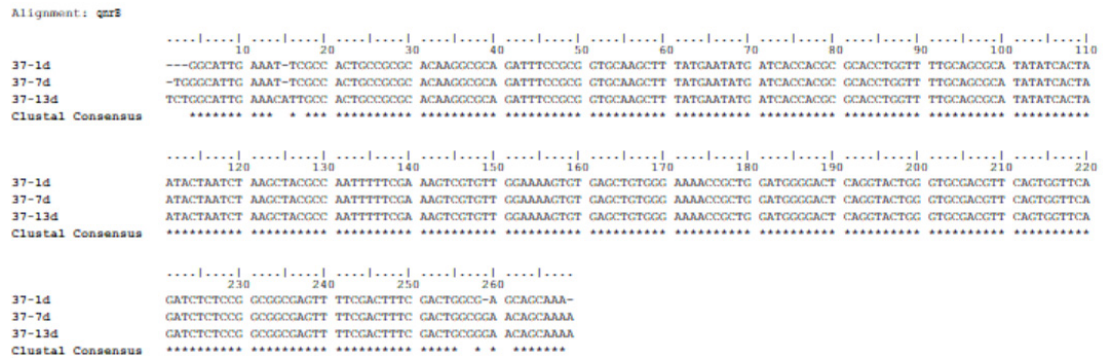
```

Alignment: oqx1
      .....| .....| .....| .....| .....| .....| .....| .....| .....| .....| .....| .....|
      10      20      30      40      50      60      70      80      90     100     110
37-1d  GACAGGCTCG CACAGAATGC TCGCGCTCCG GCGCCGACGG TCAGCGCGCG TAAGGTGCTG GTGAAGTCGA TCAGTCAGTG GCATAGTTTT AACGGTCGCA TTGAAGCGGT
37-7d  -----GGCT CACAGAATGC TCGCGCTCCG GCGCCGACGG TCAGCGCGCG TAAGGTGCTG GTGAAGTCGA TCAGTCAGTG GCATAGTTTT AACGGTCGCA TTGAAGCGGT
37-13d -----TCGCA CACAGAATGC TCGCGCTCCG GCGCCGACGG TCAGCGCGCG TAAGGTGCTG GTGAAGTCGA TCAGTCAGTG GCATAGTTTT AACGGTCGCA TTGAAGCGGT
Clustal Consensus  * *****
      .....| .....| .....| .....| .....| .....| .....| .....| .....| .....| .....| .....|
      120     130     140     150     160     170     180     190     200     210     220
37-1d  GGAGAGCGTT CAGCTTCGCC CTCGGCTCTC GGGATACATT GATAAACTGA ATTACACTGA CGGCCAGGAG CTCGAAAAGG GCCAGGTGCT GTTCACGATA GATGACAGAA
37-7d  GGAGAGCGTT CAGCTTCGCC CTCGGCTCTC GGGATACATT GATAAACTGA ATTACACTGA CGGCCAGGAG CTCGAAAAGG GCCAGGTGCT GTTCACGATA GATGACAGAA
37-13d GGAGAGCGTT CAGCTTCGCC CTCGGCTCTC GGGATACATT GATAAACTGA ATTACACTGA CGGCCAGGAG CTCGAAAAGG GCCAGGTGCT GTTCACGATA GATGACAGAA
Clustal Consensus  *****
      .....| .....| .....| .....| .....| .....| .....| .....| .....| .....| .....| .....|
      230     240     250     260     270     280     290     300     310     320     330
37-1d  CCTATCGGCC CGGCTGGAG CAGCGCCAGG CGGCGTTGCC AAGAGCCAAA ACCCAGGCCA GCGTCGCCCA AAGCGAGGCG AACCGCACCG ATAAATTAGT CCATACCGAC
37-7d  CCTATCGGCC CGGCTGGAG CAGCGCCAGG CGGCGTTGCC AAGAGCCAAA ACCCAGGCCA GCGTCGCCCA AAGCGAGGCG AACCGCACCG ATAAATTAGT CCATACCGCC
37-13d CCTATCGGCC CGGCTGGAG CAGCGCCAGG CGGCGTTGCC AAGAGCCAAA ACCCAGGCCA GCGTCGCCCA AAGCGAGGCG AACCGCACCG ATAAATTAGT CCATACCGCT
Clustal Consensus  *****
      .....| ..
      340
37-1d  CTGCTCTCC- --
37-7d  CTGCTCTCTC CC
37-13d TTC----- --
Clustal Consensus

```

Note: “*” means no difference in nucleotide. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 20 nucleotides.

Figure S21. Sequencing results of *qnrB* for stability of plasmid DNA references materials stored at 37°C.



Note: “*” means no difference in nucleotide. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 20 nucleotides.

Figure S22. Sequencing results of *qnrA* for stability of plasmid DNA references materials stored at 37°C.

```

Alignment: qnrA

      10      20      30      40      50      60      70      80      90     100     110
37-1d  --AGAGGATT TCTCAGCCA GGATTTCAGT GACAGCCGTT TTCCGCGCTG CC-GCTTTTA TCAGTGTGAC TTCAGCCACT GTCAGTGCA GGATGCCAGT TTCGAGGATT
37-7d  -GGAGGTTT TTTTCCGCCA GGATTTCAGT GACAGCCGTT TTCCGCGCTG CC-GCTTTTA TCAGTGTGAC TTCAGCCACT GTCAGTGCA GGATGCCAGT TTCGAGGATT
37-13d AGAGAGGGGT TTTTATCCA GGATTTCAGT GACAGCCGTT TTCCGCGCTG CCGGCTTTTA TCAGTGTGAC TTCAGCCACT GTCAGTGCA GGATGCCAGT TTCGAGGATT
Clustal Consensus *****

      120     130     140     150     160     170     180     190     200     210     220
37-1d  GCAGTTTCAT TGAAGCGGC GCGCTTGAAG GGTGTCACTT CAGCTATGCC GATCTGGGGC ATGCCAGTTT CAAGGCCGTC GCTCTGTCTT TGGCCAACTT CAGCGGTGCC
37-7d  GCAGTTTCAT TGAAGCGGC GCGCTTGAAG GGTGTCACTT CAGCTATGCC GATCTGGGGC ATGCCAGTTT CAAGGCCGTC GCTCTGTCTT TGGCCAACTT CAGCGGTGCC
37-13d GCAGTTTCAT TGAAGCGGC GCGCTTGAAG GGTGTCACTT CAGCTATGCC GATCTGGGGC ATGCCAGTTT CAAGGCCGTC GCTCTGTCTT TGGCCAACTT CAGCGGTGCC
Clustal Consensus *****

      230     240     250     260     270     280     290     300     310     320     330
37-1d  AACTGCTTTG GCATAGAGTT CAGGAGTGC GATCTCAAGG GGGCCAACTT TTCCGGGGCC CGCTTCTACA ATCAAGTCAG CCATAAGATG TACTTCTGCT CGGCTTATAT
37-7d  AACTGCTTTG GCATAGAGTT CAGGAGTGC GATCTCAAGG GGGCCAACTT TTCCGGGGCC CGCTTCTACA ATCAAGTCAG CCATAAGATG TACTTCTGCT CGGCTTATAT
37-13d AACTGCTTTG GCATAGAGTT CAGGAGTGC GATCTCAAGG GGGCCAACTT TTCCGGGGCC CGCTTCTACA ATCAAGTCAG CCATAAGATG TACTTCTGCT CGGCTTATAT
Clustal Consensus *****

      340     350     360     370     380     390     400     410     420     430     440
37-1d  CTCAGGTTCG AACCTGGCCT ATACCAACTT GAGTGGCCAA TGCTGGGAAA AATCGGAGCT GTTTGAAATC AACTGGAGCA ATGCCAATCT CAGCGGCGCT TCCTTGATGG
37-7d  CTCAGGTTCG AACCTGGCCT ATACCAACTT GAGTGGCCAA TGCTGGGAAA AATCGGAGCT GTTTGAAATC AACTGGAGCA ATGCCAATCT CAGCGGCGCT TCCTTGATGG
37-13d CTCAGGTTCG AACCTGGCCT ATACCAACTT GAGTGGCCAA TGCTGGGAAA AATCGGAGCT GTTTGAAATC AACTGGAGCA ATGCCAATCT CAGCGGCGCT TCCTTGATGG
Clustal Consensus *****

      450     460     470     480     490     500     510     520     530     540     550
37-1d  GCTCAGATCT CAGCGCGGCG ACCTTCTGCC GCGACTGTTG GCAACAGGTC AATCTGGGGG GCTGTGGCCT AACCTTTGCC GATCTGGATG GCGTCGACCC CAGACGGGTC
37-7d  GCTCAGATCT CAGCGCGGCG ACCTTCTGCC GCGACTGTTG GCAACAGGTC AATCTGGGGG GCTGTGGCCT AACCTTTGCC GATCTGGATG GCGTCGACCC CAGACGGGTC
37-13d GCTCAGATCT CAGCGCGGCG ACCTTCTGCC GCGACTGTTG GCAACAGGTC AATCTGGGGG GCTGTGGCCT AACCTTTGCC GATCTGGATG GCGTCGACCC CAGACGGGTC
Clustal Consensus *****

      560     570     580
37-1d  AACCTCGAAG GAGTCAAGAT CTGTGCGTGG CA
37-7d  AACCTCGAAG GAGTCAAG-T GGGGGCGGCG CG
37-13d AACCTCGAAG GAGTCATGAT GCTCGCGGCG AA
Clustal Consensus *****

```

Note: “*” means no difference in nucleotide. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 20 nucleotides.

Figure S23. Sequencing results of *gyrA* for stability of plasmid DNA references materials stored at 37°C.

```

Alignment: gyrA1
      10      20      30      40      50      60      70      80
37-1d  VGDVIGKYHP HGDSAVYNTI VRMAQPFSLR YMLVDGQGNF GSIDGDSAAA MRYTEIRLAK IAHELMADLE KETVDFVDNY DGT
37-7d  VGDVIGKYHP HGDSAVYNTI VRMAQPFSLR YMLVDGQGNF GSIDGDSAAA MRYTEIRLAK IAHELMADLE KETVDFVDNY DGT
37-13d VGDVIGKYHP HGDSAVYNTI VRMAQPFSLR YMLVDGQGNF GSIDGDSAAA MRYTEIRLAK IAHELMADLE KETVDFVDNY DGT
Clustal Consensus *****

Alignment: gyrA2
      10      20      30      40      50      60      70      80
37-1d  VGDVIGKYHP HGDIYAVYDTI VRMAQPFSLR YMLVDGQGNF GSIDGDSAAA MRYTEIRLAK IAHELMADLE KETVDFVDNY DGT
37-7d  VADRFPGKYHP HGDIYAVYDTI VRMAQPFSLR YMLVDGQGNF GSIDGDSAAA MRYTEIRLAK IAHELMADLE KETVDFVDNN DGT
37-13d VGDGIGKYHP HGDIYAVYDTI VRMAQPFSLR YMLVDGQGNF GSIDGDSAAA MRYTEIRLAK IAHELMADLE KETVDFVDNW ERY
Clustal Consensus *.A :*****

Alignment: gyrA3
      10      20      30      40      50      60      70      80
37-1d  VGDVIGKYHP HGDFAVYDTI VRMAQPFSLR YMLVDGQGNF GSIDGDSAAA MRYTEIRLAK IAHELMADLE KETVDFVDNY DGT
37-7d  VGDVIGKYHP HGDFAVYDTI VRMAQPFSLR YMLVDGQGNF GSIDGDSAAA MRYTEIRLAK IAHELMADLE KETVDFVDNY DGT
37-13d VGDGPGKYHP HGDFAVYDTI VRMAQPFSLR YMLVDGQGNF GSIDGDSAAA MRYTEIRLAK IAHELMADLE KETVDFVDNM DGT
Clustal Consensus *** :*****

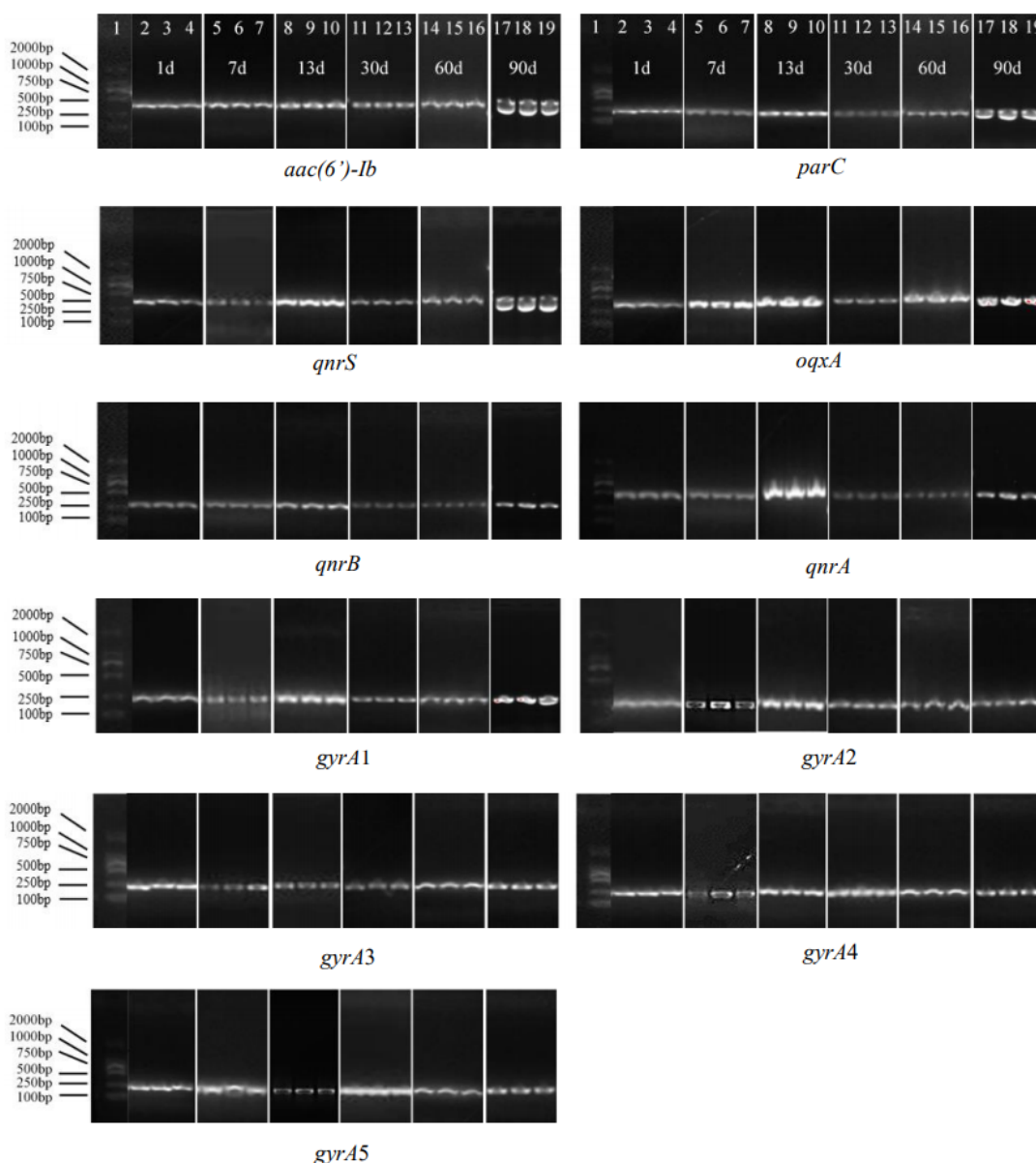
Alignment: gyrA4
      10      20      30      40      50      60      70      80
37-1d  -VGDVIGKYH PHGDFAVYGT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL ENETVDFVDN YDGT-
37-7d  LVGDRPGKYH PHGDFAVYGT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL ENETVDFVDK CARYG
37-13d -W-FVIGKYH PHGDFAVYGT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL ENETVDFVDK WERYG
Clustal Consensus :****

Alignment: gyrA5
      10      20      30      40      50      60      70      80
37-1d  -VGDVIGKYH PHGDFAVYAT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL ENETVDFVDN YDGT
37-7d  SLVNGPGKYH PHGDFAVYAT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL ENETVDFVDK LDGT
37-13d -VGDVIGKYH PHGDFAVYAT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL ENETVDFVDN K-RY
Clustal Consensus : : ****

```

Note: “*” means no difference in amino acid. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 10 amino acids.

Figure S24. PCR results for storage stability of plasmid DNA references materials stored at 4°C.



Note: Lane 1 is DL 2000 DNA marker; lane 2–4, 5–7, 8–10, 11–13, 14–16, and 17–19 are PCR bands of the target gene sampled on the 1st, 7th, 13th, 30th, 60th, and 90th days of storage, respectively. Considering the different sampling timepoints, the gene images were intercepted and spliced using Microsoft Word, and the original images are available upon request.

Figure S25. Sequencing results of *aac(6')-Ib* for stability of plasmid DNA references materials stored at 4°C.

Alignment: *aac(6')-Ib*

```

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
10      20      30      40      50      60      70      80      90      100     110
4-1d    ---TTGGGAT GCT-CTATGA CTGGCTAAAT CGATCTCATA TCGTCGAGTG CTGGGGGGGA GAAGAAGCAC GCGGCACACT TCGTGACGTA CAGGAACAGT ACTTGCCAAAG
4-7d    TCTTTTTCAT CTCTGCCCTA CTGGCTAAAT CGATCTCATA TCGTCGAGTG CTGGGGGGGA GAAGAAGCAC GCGGCACACT TCGTGACGTA CAGGAACAGT ACTTGCCAAAG
4-13d   ATTTTTCGAT TTCATCCAGA CTGGCTAAAT CGATCTCATA TCGTCGAGTG CTGGGGGGGA GAAGAAGCAC GCGGCACACT TCGTGACGTA CAGGAACAGT ACTTGCCAAAG
4-30d   --TTTGGGCT GCTTCCACGA CTGGCTAAAT CGATCTCATA TCGTCGAGTG CTGGGGGGGA GAAGAAGCAC GCGGCACACT TCGTGACGTA CAGGAACAGT ACTTGCCAAAG
4-60d   -CTTTTCGAT ACTTCTCTCA CTGGCTAAAT CGATCTCATA TCGTCGAGTG CTGGGGGGGA GAAGAAGCAC GCGGCACACT TCGTGACGTA CAGGAACAGT ACTTGCCAAAG
4-90d   TTTTGGGAT  TCTGCCAGA CTGGCTAAAT CGATCTCATA TCGTCGAGTG CTGGGGGGGA GAAGAAGCAC GCGGCACACT TCGTGACGTA CAGGAACAGT ACTTGCCAAAG
Clustal Consensus  *  *  *  *  *****  *****  *****  *****  *****  *****  *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
120     130     140     150     160     170     180     190     200     210     220
4-1d    CGTTTTCAGG CAAGAGTCGG TCACTCCATA CATTGCAATG CTGAATGGAG AGCCGATTGG GTATGCCGAG TCGTACGTTG CTCTTGGAGG CGGGGACGGA TCGTGGGAAG
4-7d    CGTTTTCAGG CAAGAGTCGG TCACTCCATA CATTGCAATG CTGAATGGAG AGCCGATTGG GTATGCCGAG TCGTACGTTG CTCTTGGAGG CGGGGACGGA TCGTGGGAAG
4-13d   CGTTTTCAGG CAAGAGTCGG TCACTCCATA CATTGCAATG CTGAATGGAG AGCCGATTGG GTATGCCGAG TCGTACGTTG CTCTTGGAGG CGGGGACGGA TCGTGGGAAG
4-30d   CGTTTTCAGG CAAGAGTCGG TCACTCCATA CATTGCAATG CTGAATGGAG AGCCGATTGG GTATGCCGAG TCGTACGTTG CTCTTGGAGG CGGGGACGGA TCGTGGGAAG
4-60d   CGTTTTCAGG CAAGAGTCGG TCACTCCATA CATTGCAATG CTGAATGGAG AGCCGATTGG GTATGCCGAG TCGTACGTTG CTCTTGGAGG CGGGGACGGA TCGTGGGAAG
4-90d   CGTTTTCAGG CAAGAGTCGG TCACTCCATA CATTGCAATG CTGAATGGAG AGCCGATTGG GTATGCCGAG TCGTACGTTG CTCTTGGAGG CGGGGACGGA TCGTGGGAAG
Clustal Consensus  *****  *****  *****  *****  *****  *****  *****  *****  *****  *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
230     240     250     260     270     280     290     300     310     320     330
4-1d    AAGAAACCGA TCCAGGAGTA CCGCGAATAG ACCAGTTACT GCGCAATGCA TCACAACCTGG GCAAAGGCTT GGGAAACCAAG CTGCTTCGAG CTCTGCTTGA GTTGCTGTTT
4-7d    AAGAAACCGA TCCAGGAGTA CCGCGAATAG ACCAGTTACT GCGCAATGCA TCACAACCTGG GCAAAGGCTT GGGAAACCAAG CTGCTTCGAG CTCTGCTTGA GTTGCTGTTT
4-13d   AAGAAACCGA TCCAGGAGTA CCGCGAATAG ACCAGTTACT GCGCAATGCA TCACAACCTGG GCAAAGGCTT GGGAAACCAAG CTGCTTCGAG CTCTGCTTGA GTTGCTGTTT
4-30d   AAGAAACCGA TCCAGGAGTA CCGCGAATAG ACCAGTTACT GCGCAATGCA TCACAACCTGG GCAAAGGCTT GGGAAACCAAG CTGCTTCGAG CTCTGCTTGA GTTGCTGTTT
4-60d   AAGAAACCGA TCCAGGAGTA CCGCGAATAG ACCAGTTACT GCGCAATGCA TCACAACCTGG GCAAAGGCTT GGGAAACCAAG CTGCTTCGAG CTCTGCTTGA GTTGCTGTTT
4-90d   AAGAAACCGA TCCAGGAGTA CCGCGAATAG ACCAGTTACT GCGCAATGCA TCACAACCTGG GCAAAGGCTT GGGAAACCAAG CTGCTTCGAG CTCTGCTTGA GTTGCTGTTT
Clustal Consensus  *****  *****  *****  *****  *****  *****  *****  *****  *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
340     350     360     370     380     390     400     410     420     430     440
4-1d    AATGATCCCG AGGTCACCAA GATCCAAACG GACCCGTCGC CGAGCAACTT GCGAGCGATC CGATGCTACG AGAAAGCGGG GTTTGAGAGC CAAGGTACCG TAACCAACCC
4-7d    AATGATCCCG AGGTCACCAA GATCCAAACG GACCCGTCGC CGAGCAACTT GCGAGCGATC CGATGCTACG AGAAAGCGGG GTTTGAGAGC CAAGGTACCG TAACCAACCC
4-13d   AATGATCCCG AGGTCACCAA GATCCAAACG GACCCGTCGC CGAGCAACTT GCGAGCGATC CGATGCTACG AGAAAGCGGG GTTTGAGAGC CAAGGTACCG TAACCAACCC
4-30d   AATGATCCCG AGGTCACCAA GATCCAAACG GACCCGTCGC CGAGCAACTT GCGAGCGATC CGATGCTACG AGAAAGCGGG GTTTGAGAGC CAAGGTACCG TAACCAACCC
4-60d   AATGATCCCG AGGTCACCAA GATCCAAACG GACCCGTCGC CGAGCAACTT GCGAGCGATC CGATGCTACG AGAAAGCGGG GTTTGAGAGC CAAGGTACCG TAACCAACCC
4-90d   AATGATCCCG AGGTCACCAA GATCCAAACG GACCCGTCGC CGAGCAACTT GCGAGCGATC CGATGCTACG AGAAAGCGGG GTTTGAGAGC CAAGGTACCG TAACCAACCC
Clustal Consensus  *****  *****  *****  *****  *****  *****  *****  *****  *****

-----|-----|-----|-----|-----|-----|
450     460     470     480
4-1d    AGATGCTCCA GCGGTGTACA TGGTTCAAAC ACGCCA--GG CATTGCGAG-
4-7d    AGATGCTCCA GCGGTGTACA TGGTTCAAAC ACGGGGGGGA TTTTCGGG-
4-13d   AGATGCTCCA GCGGTGTACA TGGTTCAAAC ACGGGGGGGA TATTTTCG-
4-30d   AGATGCTCCA GCGGTGTACA TGGTTCAAAC ACGGGGGGCG TTTTTCG-
4-60d   AGATGCTCCA GCGGTGTACA TGGTTCAAAC ACGGGGATTT TATTGCGG-
4-90d   AGATGCTCCA GCGGTGTACA TGGTTCAAAC ACGGGG--AA TATTGCGG-
Clustal Consensus  *****  *****  *****  ***  **

```

Note: “*” means no difference in nucleotide. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 20 nucleotides.

[illegible]

29

Figure S27. Sequencing results of *qnrS* for stability of plasmid DNA references materials stored at 4°C.

```

Alignment: qnrS
      10      20      30      40      50      60      70      80      90      100     110
4-1d  --GCAACTT CATTGAACAG GGTGATATTC GTCCCTGCCA CTTTGATGTC GCAGATCTTC GTGATGCAAG TTTCACACAA TGCCAACTTG CGATGGCAAA CTTCAGTAAT
4-7d  GATGCAACTT TCTCAACAG GGTGATATTC GTCCCTGCCA CTTTGATGTC GCAGATCTTC GTGATGCAAG TTTCACACAA TGCCAACTTG CGATGGCAAA CTTCAGTAAT
4-13d -GTCCCACTT TCTTTTCAG GGTGATATTC GTCCCTGCCA CTTTGATGTC GCAGATCTTC GTGATGCAAG TTTCACACAA TGCCAACTTG CGATGGCAAA CTTCAGTAAT
4-30d --TGCAACTT T-TTCCACAG GGTGATATTC GTCCCTGCCA CTTTGATGTC GCAGATCTTC GTGATGCAAG TTTCACACAA TGCCAACTTG CGATGGCAAA CTTCAGTAAT
4-60d TGTCAAATT T-TCCCTCAG GGTGATATTC GTCCCTGCCA CTTTGATGTC GCAGATCTTC GTGATGCAAG TTTCACACAA TGCCAACTTG CGATGGCAAA CTTCAGTAAT
4-90d -CTGCAACAG TCTCACACAG GGTGATATTC GTCCCTGCCA CTTTGATGTC GCAGATCTTC GTGATGCAAG TTTCACACAA TGCCAACTTG CGATGGCAAA CTTCAGTAAT
Clustal Consensus  **      *      ***      *****      *****      *****      *****      *****      *****      *****

      120     130     140     150     160     170     180     190     200     210     220
4-1d  GCCAATTGCT ACGGTATAGA GTTCCCTGGC TGTGATTAA AAGGTGCCAA CTTTTCGCCA ACAAACTTTC CCCATCAAGT GAGTAATGCT ATGTACTTTT GCTCAGCATT
4-7d  GCCAATTGCT ACGGTATAGA GTTCCCTGGC TGTGATTAA AAGGTGCCAA CTTTTCGCCA ACAAACTTTC CCCATCAAGT GAGTAATGCT ATGTACTTTT GCTCAGCATT
4-13d GCCAATTGCT ACGGTATAGA GTTCCCTGGC TGTGATTAA AAGGTGCCAA CTTTTCGCCA ACAAACTTTC CCCATCAAGT GAGTAATGCT ATGTACTTTT GCTCAGCATT
4-30d GCCAATTGCT ACGGTATAGA GTTCCCTGGC TGTGATTAA AAGGTGCCAA CTTTTCGCCA ACAAACTTTC CCCATCAAGT GAGTAATGCT ATGTACTTTT GCTCAGCATT
4-60d GCCAATTGCT ACGGTATAGA GTTCCCTGGC TGTGATTAA AAGGTGCCAA CTTTTCGCCA ACAAACTTTC CCCATCAAGT GAGTAATGCT ATGTACTTTT GCTCAGCATT
4-90d GCCAATTGCT ACGGTATAGA GTTCCCTGGC TGTGATTAA AAGGTGCCAA CTTTTCGCCA ACAAACTTTC CCCATCAAGT GAGTAATGCT ATGTACTTTT GCTCAGCATT
Clustal Consensus  *****      *****      *****      *****      *****      *****      *****      *****      *****      *****

      230     240     250     260     270     280     290     300     310     320     330
4-1d  TATTTCTGGA TGTAACTTTT CCTATGCCAA TATGGAGAGG GTTTGTTTAG AAAAATGTGA GTTGTTTGAA AATCGCTGGA TAGGAACGAA CCTAGCGGGT GCATCACTGA
4-7d  TATTTCTGGA TGTAACTTTT CCTATGCCAA TATGGAGAGG GTTTGTTTAG AAAAATGTGA GTTGTTTGAA AATCGCTGGA TAGGAACGAA CCTAGCGGGT GCATCACTGA
4-13d TATTTCTGGA TGTAACTTTT CCTATGCCAA TATGGAGAGG GTTTGTTTAG AAAAATGTGA GTTGTTTGAA AATCGCTGGA TAGGAACGAA CCTAGCGGGT GCATCACTGA
4-30d TATTTCTGGA TGTAACTTTT CCTATGCCAA TATGGAGAGG GTTTGTTTAG AAAAATGTGA GTTGTTTGAA AATCGCTGGA TAGGAACGAA CCTAGCGGGT GCATCACTGA
4-60d TATTTCTGGA TGTAACTTTT CCTATGCCAA TATGGAGAGG GTTTGTTTAG AAAAATGTGA GTTGTTTGAA AATCGCTGGA TAGGAACGAA CCTAGCGGGT GCATCACTGA
4-90d TATTTCTGGA TGTAACTTTT CCTATGCCAA TATGGAGAGG GTTTGTTTAG AAAAATGTGA GTTGTTTGAA AATCGCTGGA TAGGAACGAA CCTAGCGGGT GCATCACTGA
Clustal Consensus  *****      *****      *****      *****      *****      *****      *****      *****      *****      *****

      340     350     360     370     380     390     400     410     420     430
4-1d  AAGAGTCAGA CTTAAGTCGA GGTCTTTTTT CGCAAGATGT CTGGGGGCCA TTAGCCTAC AGGGGGCCAA TTATGCCAC GCGCAACT-- -TGGCGTTT AGA--
4-7d  AAGAGTCAGA CTTAAGTCGA GGTCTTTTTT CGCAAGATGT CTGGGGGCCA TTAGCCTAC AGGGGGCCAA TTATGCCAC GCGCAATGAA --TGGCGTTT AGA--
4-13d AAGAGTCAGA CTTAAGTCGA GGTCTTTTTT CGCAAGATGT CTGGGGGCCA TTAGCCTAC AGGGGGCCAA TTATGCCAC GCGCAATGGA GCGAGACTTT TAAAA--
4-30d AAGAGTCAGA CTTAAGTCGA GGTCTTTTTT CGCAAGATGT CTGGGGGCCA TTAGCCTAC AGGGGGCCAA TTATGCCAC GCGCAATGGG -TGGCGTTT AGA--
4-60d AAGAGTCAGA CTTAAGTCGA GGTCTTTTTT CGCAAGATGT CTGGGGGCCA TTAGCCTAC AGGGGGCCAA TTATGCCAC GCGCAATGGA CCGGAGTTTT AAAAA
4-90d AAGAGTCAGA CTTAAGTCGA GGTCTTTTTT CGCAAGATGT CTGGGGGCCA TTAGCCTAC AGGGGGCCAA TTATGCCAC GCGCAATGGA GCGGAGTTTT AGAAGA
Clustal Consensus  *****      *****      *****      *****      *****      *****      *****      *****      *****      *

```

Note: “*” means no difference in nucleotide. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 20 nucleotides.

Figure S28. Sequencing results of *oqx4* for stability of plasmid DNA references materials stored at 4°C.

```

Alignment: oqx4
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
4-1d      ---GACAGCG -TCCACAGA ATGCTGCGCC TCCCGCCCGC ACGGTCAGCG CCGCTAAGCT GCTGCTGAAG TCGATCAGTC AGTGGGATAG TTTTAACGGT CCGATTGAAG
4-7d      CCAGACAGCT GTCCCAAGA ATGCTGCGCC TCCCGCCCGC ACGGTCAGCG CCGCTAAGCT GCTGCTGAAG TCGATCAGTC AGTGGGATAG TTTTAACGGT CCGATTGAAG
4-13d     -CAGACAGCG -TTGTCCAGA ATGCTGCGCC TCCCGCCCGC ACGGTCAGCG CCGCTAAGCT GCTGCTGAAG TCGATCAGTC AGTGGGATAG TTTTAACGGT CCGATTGAAG
4-30d     -----T CCGACCCAGA ATGCTGCGCC TCCCGCCCGC ACGGTCAGCG CCGCTAAGCT GCTGCTGAAG TCGATCAGTC AGTGGGATAG TTTTAACGGT CCGATTGAAG
4-60d     -AGAACAGCG CTTGCCCAA ATGCTGCGCC TCCCGCCCGC ACGGTCAGCG CCGCTAAGCT GCTGCTGAAG TCGATCAGTC AGTGGGATAG TTTTAACGGT CCGATTGAAG
4-90d     -TGACAGCG TTTGGCCAGA ATGCTGCGCC TCCCGCCCGC ACGGTCAGCG CCGCTAAGCT GCTGCTGAAG TCGATCAGTC AGTGGGATAG TTTTAACGGT CCGATTGAAG
Clustal Consensus
*****
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
4-1d      CGGTGGAGAG CTTTCAGCTT CCGCCTCGCG TCTCGGGATA CATTGATAAA GTGAATTACA CTGACGGCCA GGAGCTGAAA AAGGCCCAGG TGCTGTTTAC GATAGATGAC
4-7d      CGGTGGAGAG CTTTCAGCTT CCGCCTCGCG TCTCGGGATA CATTGATAAA GTGAATTACA CTGACGGCCA GGAGCTGAAA AAGGCCCAGG TGCTGTTTAC GATAGATGAC
4-13d     CGGTGGAGAG CTTTCAGCTT CCGCCTCGCG TCTCGGGATA CATTGATAAA GTGAATTACA CTGACGGCCA GGAGCTGAAA AAGGCCCAGG TGCTGTTTAC GATAGATGAC
4-30d     CGGTGGAGAG CTTTCAGCTT CCGCCTCGCG TCTCGGGATA CATTGATAAA GTGAATTACA CTGACGGCCA GGAGCTGAAA AAGGCCCAGG TGCTGTTTAC GATAGATGAC
4-60d     CGGTGGAGAG CTTTCAGCTT CCGCCTCGCG TCTCGGGATA CATTGATAAA GTGAATTACA CTGACGGCCA GGAGCTGAAA AAGGCCCAGG TGCTGTTTAC GATAGATGAC
4-90d     CGGTGGAGAG CTTTCAGCTT CCGCCTCGCG TCTCGGGATA CATTGATAAA GTGAATTACA CTGACGGCCA GGAGCTGAAA AAGGCCCAGG TGCTGTTTAC GATAGATGAC
Clustal Consensus
*****
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
4-1d      AGAAGCTATC GCGCGCGGCT GGAGCAGGCG CAGCGCGGCT TGGCAAGAGC CAAAGCCAG GCGAGGCTCG GCGAAGCCA GCGCAACCGC ACCGATAAAT TAGTCCATAC
4-7d      AGAAGCTATC GCGCGCGGCT GGAGCAGGCG CAGCGCGGCT TGGCAAGAGC CAAAGCCAG GCGAGGCTCG GCGAAGCCA GCGCAACCGC ACCGATAAAT TAGTCCATAC
4-13d     AGAAGCTATC GCGCGCGGCT GGAGCAGGCG CAGCGCGGCT TGGCAAGAGC CAAAGCCAG GCGAGGCTCG GCGAAGCCA GCGCAACCGC ACCGATAAAT TAGTCCATAC
4-30d     AGAAGCTATC GCGCGCGGCT GGAGCAGGCG CAGCGCGGCT TGGCAAGAGC CAAAGCCAG GCGAGGCTCG GCGAAGCCA GCGCAACCGC ACCGATAAAT TAGTCCATAC
4-60d     AGAAGCTATC GCGCGCGGCT GGAGCAGGCG CAGCGCGGCT TGGCAAGAGC CAAAGCCAG GCGAGGCTCG GCGAAGCCA GCGCAACCGC ACCGATAAAT TAGTCCATAC
4-90d     AGAAGCTATC GCGCGCGGCT GGAGCAGGCG CAGCGCGGCT TGGCAAGAGC CAAAGCCAG GCGAGGCTCG GCGAAGCCA GCGCAACCGC ACCGATAAAT TAGTCCATAC
Clustal Consensus
*****
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
4-1d      CAAAGCTC--- GTCTCC---
4-7d      CCCCC-TCTC GTCTCTGA
4-13d     C-----
4-30d     CCGTT-TC-----
4-60d     CCCCCGTCCC GTCTCAAAA
4-90d     CCCCCCTCC- GTCTCAC--
Clustal Consensus
*

```

Note: “*” means no difference in nucleotide. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 20 nucleotides.

Figure S29. Sequencing results of *qnrB* for stability of plasmid DNA references materials stored at 4°C.

```

Alignment: qnrB
      10      20      30      40      50      60      70      80      90     100     110
4-1d  ---GGCATTG AAA-TTGGC ACTGCGGGG ACAAGGGCA GATTTCGGG GTGCAAGCTT TATGAATATG ATCACCACGC GCACCTGGTT TTGCAGCGCA TATATCACTA
4-7d  AGAGGCATTG AAA-ATGGC ACTGCGGGG ACAAGGGCA GATTTCGGG GTGCAAGCTT TATGAATATG ATCACCACGC GCACCTGGTT TTGCAGCGCA TATATCACTA
4-13d --AGGCATTG AAAATATGGC ACTGCGGGG ACAAGGGCA GATTTCGGG GTGCAAGCTT TATGAATATG ATCACCACGC GCACCTGGTT TTGCAGCGCA TATATCACTA
4-30d -TGGGCATTG AAA-TTGGC ACTGCGGGG ACAAGGGCA GATTTCGGG GTGCAAGCTT TATGAATATG ATCACCACGC GCACCTGGTT TTGCAGCGCA TATATCACTA
4-60d -TAGGCATTG AAAATTGGC ACTGCGGGG ACAAGGGCA GATTTCGGG GTGCAAGCTT TATGAATATG ATCACCACGC GCACCTGGTT TTGCAGCGCA TATATCACTA
4-90d --GGGCATTG AAAAATGGC ACTGCGGGG ACAAGGGCA GATTTCGGG GTGCAAGCTT TATGAATATG ATCACCACGC GCACCTGGTT TTGCAGCGCA TATATCACTA
Clustal Consensus *****

      120     130     140     150     160     170     180     190     200     210     220
4-1d  ATACTAATCT AAGCTACGCC AATTTTTCGA AACTCTGTGT GGAAGAGTGT GAGCTGTGGG AAAACCGCTG GATGGGGACT CAGCTACTGG GTCCGACGTT CAGTGGTTCA
4-7d  ATACTAATCT AAGCTACGCC AATTTTTCGA AACTCTGTGT GGAAGAGTGT GAGCTGTGGG AAAACCGCTG GATGGGGACT CAGCTACTGG GTCCGACGTT CAGTGGTTCA
4-13d ATACTAATCT AAGCTACGCC AATTTTTCGA AACTCTGTGT GGAAGAGTGT GAGCTGTGGG AAAACCGCTG GATGGGGACT CAGCTACTGG GTCCGACGTT CAGTGGTTCA
4-30d ATACTAATCT AAGCTACGCC AATTTTTCGA AACTCTGTGT GGAAGAGTGT GAGCTGTGGG AAAACCGCTG GATGGGGACT CAGCTACTGG GTCCGACGTT CAGTGGTTCA
4-60d ATACTAATCT AAGCTACGCC AATTTTTCGA AACTCTGTGT GGAAGAGTGT GAGCTGTGGG AAAACCGCTG GATGGGGACT CAGCTACTGG GTCCGACGTT CAGTGGTTCA
4-90d ATACTAATCT AAGCTACGCC AATTTTTCGA AACTCTGTGT GGAAGAGTGT GAGCTGTGGG AAAACCGCTG GATGGGGACT CAGCTACTGG GTCCGACGTT CAGTGGTTCA
Clustal Consensus *****

      230     240     250     260     270
4-1d  GATCTCTCCG GCGGCGAGTT TTGGACTTTC GACTGGCG-A GCAGCAAA--
4-7d  GATCTCTCCG GCGGCGAGTT TTGGACTTTC GACTGGCG-A GCAGCAAA--
4-13d GATCTCTCCG GCGGCGAGTT TTGGACTTTC GA-TGGCGGA ACAGCAAAA--
4-30d GATCTCTCCG GCGGCGAGTT TTGGACTTTC GACTGGCGGA ACAGCAAAA--
4-60d GATCTCTCCG GCGGCGAGTT TTGGACTTTC GA-TGGCGGA ACAGCAAAA--
4-90d GATCTCTCCG GCGGCGAGTT TTGGACTTTC GACTGGCGGA ACAGCAAAAT A
Clustal Consensus *****

```

Note: “*” means no difference in nucleotide. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 20 nucleotides.

Figure S30. Sequencing results of *qnrA* for stability of plasmid DNA references materials stored at 4°C.

```

Alignment: qnrA
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
10      20      30      40      50      60      70      80      90      100     110
4-1d    --ACAGGATT TCTACGCCA GCAATTGACT CACAGCCGTT TTGCGCGCTG CCGCTTTTAT CAGCTGTGACT TCAGCCACTG TCAGCTGCAG CATGCCAGTT TCGAGGATTG
4-7d    --GCGAGCTTT TTTTGGCCA GCAATTGACT CACAGCCGTT TTGCGCGCTG CCGCTTTTAT CAGCTGTGACT TCAGCCACTG TCAGCTGCAG CATGCCAGTT TCGAGGATTG
4-13d   --GCAGGATT TTTTACCCA GCAATTGACT CACAGCCGTT TTGCGCGCTG CCGCTTTTAT CAGCTGTGACT TCAGCCACTG TCAGCTGCAG CATGCCAGTT TCGAGGATTG
4-30d   AGGGGGAGTT TTTTGGCCA GCAATTGACT CACAGCCGTT TTGCGCGCTG CCGCTTTTAT CAGCTGTGACT TCAGCCACTG TCAGCTGCAG CATGCCAGTT TCGAGGATTG
4-60d   -AAGGGGCTT TTTTGGCCA GCAATTGACT CACAGCCGTT TTGCGCGCTG CCGCTTTTAT CAGCTGTGACT TCAGCCACTG TCAGCTGCAG CATGCCAGTT TCGAGGATTG
4-90d   --AGGGGCTT TTTTACCCA GCAATTGACT CACAGCCGTT TTGCGCGCTG CCGCTTTTAT CAGCTGTGACT TCAGCCACTG TCAGCTGCAG CATGCCAGTT TCGAGGATTG
Clustal Consensus  * * * * *

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
120     130     140     150     160     170     180     190     200     210     220
4-1d    CAGTTTCATT CAAAGCGCGC CCGTTGAAGG GTGTCACCTT AGCTATGCCG ATCTGCGCGA TGCCAGTTTC AAGGCGTGCC GTCTGTCTTT GCGCACTTC AGCGGTGCCA
4-7d    CAGTTTCATT CAAAGCGCGC CCGTTGAAGG GTGTCACCTT AGCTATGCCG ATCTGCGCGA TGCCAGTTTC AAGGCGTGCC GTCTGTCTTT GCGCACTTC AGCGGTGCCA
4-13d   CAGTTTCATT CAAAGCGCGC CCGTTGAAGG GTGTCACCTT AGCTATGCCG ATCTGCGCGA TGCCAGTTTC AAGGCGTGCC GTCTGTCTTT GCGCACTTC AGCGGTGCCA
4-30d   CAGTTTCATT CAAAGCGCGC CCGTTGAAGG GTGTCACCTT AGCTATGCCG ATCTGCGCGA TGCCAGTTTC AAGGCGTGCC GTCTGTCTTT GCGCACTTC AGCGGTGCCA
4-60d   CAGTTTCATT CAAAGCGCGC CCGTTGAAGG GTGTCACCTT AGCTATGCCG ATCTGCGCGA TGCCAGTTTC AAGGCGTGCC GTCTGTCTTT GCGCACTTC AGCGGTGCCA
4-90d   CAGTTTCATT CAAAGCGCGC CCGTTGAAGG GTGTCACCTT AGCTATGCCG ATCTGCGCGA TGCCAGTTTC AAGGCGTGCC GTCTGTCTTT GCGCACTTC AGCGGTGCCA
Clustal Consensus  *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
230     240     250     260     270     280     290     300     310     320     330
4-1d    ACTGCTTTGG CATAGACTTC AGGAGTGGC ATCTCAAGGG CGCCAACTTT TCGCGGGGCC GCTTCTACAA TCAAGTCAGC CATAAGATGT ACTTCTGCTC GCCTTATATC
4-7d    ACTGCTTTGG CATAGACTTC AGGAGTGGC ATCTCAAGGG CGCCAACTTT TCGCGGGGCC GCTTCTACAA TCAAGTCAGC CATAAGATGT ACTTCTGCTC GCCTTATATC
4-13d   ACTGCTTTGG CATAGACTTC AGGAGTGGC ATCTCAAGGG CGCCAACTTT TCGCGGGGCC GCTTCTACAA TCAAGTCAGC CATAAGATGT ACTTCTGCTC GCCTTATATC
4-30d   ACTGCTTTGG CATAGACTTC AGGAGTGGC ATCTCAAGGG CGCCAACTTT TCGCGGGGCC GCTTCTACAA TCAAGTCAGC CATAAGATGT ACTTCTGCTC GCCTTATATC
4-60d   ACTGCTTTGG CATAGACTTC AGGAGTGGC ATCTCAAGGG CGCCAACTTT TCGCGGGGCC GCTTCTACAA TCAAGTCAGC CATAAGATGT ACTTCTGCTC GCCTTATATC
4-90d   ACTGCTTTGG CATAGACTTC AGGAGTGGC ATCTCAAGGG CGCCAACTTT TCGCGGGGCC GCTTCTACAA TCAAGTCAGC CATAAGATGT ACTTCTGCTC GCCTTATATC
Clustal Consensus  *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
340     350     360     370     380     390     400     410     420     430     440
4-1d    TCAGGTTGCA ACCTGGGCTA TACCAACTTG AGTGGCCAAT GCCTGGAJAA ATGCGAGCTG TTTGAAJACA ACTGGAGCAA TGCCAAATCTC AGCGGCGCTT CTTTGATGGG
4-7d    TCAGGTTGCA ACCTGGGCTA TACCAACTTG AGTGGCCAAT GCCTGGAJAA ATGCGAGCTG TTTGAAJACA ACTGGAGCAA TGCCAAATCTC AGCGGCGCTT CTTTGATGGG
4-13d   TCAGGTTGCA ACCTGGGCTA TACCAACTTG AGTGGCCAAT GCCTGGAJAA ATGCGAGCTG TTTGAAJACA ACTGGAGCAA TGCCAAATCTC AGCGGCGCTT CTTTGATGGG
4-30d   TCAGGTTGCA ACCTGGGCTA TACCAACTTG AGTGGCCAAT GCCTGGAJAA ATGCGAGCTG TTTGAAJACA ACTGGAGCAA TGCCAAATCTC AGCGGCGCTT CTTTGATGGG
4-60d   TCAGGTTGCA ACCTGGGCTA TACCAACTTG AGTGGCCAAT GCCTGGAJAA ATGCGAGCTG TTTGAAJACA ACTGGAGCAA TGCCAAATCTC AGCGGCGCTT CTTTGATGGG
4-90d   TCAGGTTGCA ACCTGGGCTA TACCAACTTG AGTGGCCAAT GCCTGGAJAA ATGCGAGCTG TTTGAAJACA ACTGGAGCAA TGCCAAATCTC AGCGGCGCTT CTTTGATGGG
Clustal Consensus  *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
450     460     470     480     490     500     510     520     530     540     550
4-1d    CTCAGATCTC AGCGCGGCGA CTTTCTCCCG CGACTGTTGG CAACAGGTCA ATCTGCGGGG CTGTGGGCTA ACCTTTGCGG ATCTGGATGG GCTCGACCCC AGACGGGTCA
4-7d    CTCAGATCTC AGCGCGGCGA CTTTCTCCCG CGACTGTTGG CAACAGGTCA ATCTGCGGGG CTGTGGGCTA ACCTTTGCGG ATCTGGATGG GCTCGACCCC AGACGGGTCA
4-13d   CTCAGATCTC AGCGCGGCGA CTTTCTCCCG CGACTGTTGG CAACAGGTCA ATCTGCGGGG CTGTGGGCTA ACCTTTGCGG ATCTGGATGG GCTCGACCCC AGACGGGTCA
4-30d   CTCAGATCTC AGCGCGGCGA CTTTCTCCCG CGACTGTTGG CAACAGGTCA ATCTGCGGGG CTGTGGGCTA ACCTTTGCGG ATCTGGATGG GCTCGACCCC AGACGGGTCA
4-60d   CTCAGATCTC AGCGCGGCGA CTTTCTCCCG CGACTGTTGG CAACAGGTCA ATCTGCGGGG CTGTGGGCTA ACCTTTGCGG ATCTGGATGG GCTCGACCCC AGACGGGTCA
4-90d   CTCAGATCTC AGCGCGGCGA CTTTCTCCCG CGACTGTTGG CAACAGGTCA ATCTGCGGGG CTGTGGGCTA ACCTTTGCGG ATCTGGATGG GCTCGACCCC AGACGGGTCA
Clustal Consensus  *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
560     570     580
4-1d    ACCTCGAAGG ACTCAAGATC TGTGCGCTGC A-----
4-7d    ACCTCGAAGG ACTCAAGATC -GGGCGCGCC CTGGA--
4-13d   ACCTCGAAGG ACTCAAGATC -GGGCGCGCC GGGAAA-
4-30d   ACCTCGAAGG ACTCAAGATC -GGGCGCGCTT GG-----
4-60d   ACCTCGAAGG ACTCAG--TC -GGGCGCGCC GGGGGAC
4-90d   ACCTCGAAGG ACTCAAGCTG -GGACCGGCG CCTGGAC
Clustal Consensus  ***** * *

```

Note: “*” means no difference in nucleotide. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 20 nucleotides.

Figure S31. Sequencing results of *gyrA* for stability of plasmid DNA references materials stored at 4°C.

```

Alignment: gyrA1

      .....| .....| .....| .....| .....| .....| .....| .....| .....| .....|
      10      20      30      40      50      60      70      80
4-1d  -VG-DVIGKY HPHGDSAVTN TIVRMAQPFSL RYMLVDGQG NFGSIDGDSA AMRYTEIRL AKIAHELMAD LEKETVDFVD NYDGT-
4-7d  LLV-NLPGKY HPHGDSAVTN TIVRMAQPFSL RYMLVDGQG NFGSIDGDSA AMRYTEIRL AKIAHELMAD LEKETVDFVD KERYG
4-13d -VG-AGPGKY HPHGDSAVTN TIVRMAQPFSL RYMLVDGQG NFGSIDGDSA AMRYTEIRL AKIAHELMAD LEKETVDFVD KSTVR-
4-30d -VG-ERPGKY HPHGDSAVTN TIVRMAQPFSL RYMLVDGQG NFGSIDGDSA AMRYTEIRL AKIAHELMAD LEKETVDFVD KERYG
4-60d -RW-FRPGKY HPHGDSAVTN TIVRMAQPFSL RYMLVDGQG NFGSIDGDSA AMRYTEIRL AKIAHELMAD LEKETVDFVD TLTVR-
4-90d -VG-DPIGKY HPHGDSAVTN TIVRMAQPFSL RYMLVDGQG NFGSIDGDSA AMRYTEIRL AKIAHELMAD LEKETVDFVD NWQRY-
Clustal Consensus : *** *****

Alignment: gyrA2

      .....| .....| .....| .....| .....| .....| .....| .....| .....| .....|
      10      20      30      40      50      60      70      80
4-1d  VGDVIGKYTH HGDYAVYDTI VRMAQPFSL RYMLVDGQGNF GSIDGDSAAA MRYTEIRLAK IAHELMADLE KETVDFVDNY DGT-
4-7d  VADRPGKYTH HGDYAVYDTI VRMAQPFSL RYMLVDGQGNF GSIDGDSAAA MRYTEIRLAK IAHELMADLE KETVDFVDNN DGT-
4-13d VGDGPGKYTH HGDYAVYDTI VRMAQPFSL RYMLVDGQGNF GSIDGDSAAA MRYTEIRLAK IAHELMADLE KETVDFVDNW ERYG
4-30d VADRPGKYTH HGDYAVYDTI VRMAQPFSL RYMLVDGQGNF GSIDGDSAAA MRYTEIRLAK IAHELMADLE KETVDFVDNN DGT-
4-60d RW-SVPGKYTH HGDYAVYDTI VRMAQPFSL RYMLVDGQGNF GSIDGDSAAA MRYTEIRLAK IAHELMADLE KETVDFVDKL QTVR
4-90d VGHGIGKYTH HGDYAVYDTI VRMAQPFSL RYMLVDGQGNF GSIDGDSAAA MRYTEIRLAK IAHELMADLE KETVDFVDNL ARY-
Clustal Consensus : *****

Alignment: gyrA3

      .....| .....| .....| .....| .....| .....| .....| .....| .....| .....|
      10      20      30      40      50      60      70      80
4-1d  -VGDVIGKYH PHGDFAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT-
4-7d  -LVTRPGKYH PHGDFAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK MGRYG
4-13d -VGHGPGKYH PHGDFAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK SETVR
4-30d -VGDVIGKYH PHGDFAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT-
4-60d SVGARVPGKYH PHGDFAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK M-TVR
4-90d -VGEAPGKYH PHGDFAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN CASVR
Clustal Consensus : : *****

Alignment: gyrA4

      .....| .....| .....| .....| .....| .....| .....| .....| .....| .....|
      10      20      30      40      50      60      70      80
4-1d  -VGDVIGKYH PHGDFAVYGT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN --YDGT-
4-7d  -VGERPGKYH PHGDFAVYGT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK --LNGT-
4-13d SLVTRIGKYH PHGDFAVYGT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN --FGRY-
4-30d LVGDRPGKYH PHGDFAVYGT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK --CARYG
4-60d LLVIGIGKYH PHGDFAVYGT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK -VTVR--
4-90d -VGHGIGKYH PHGDFAVYGT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN --WNGT-
Clustal Consensus : : *****

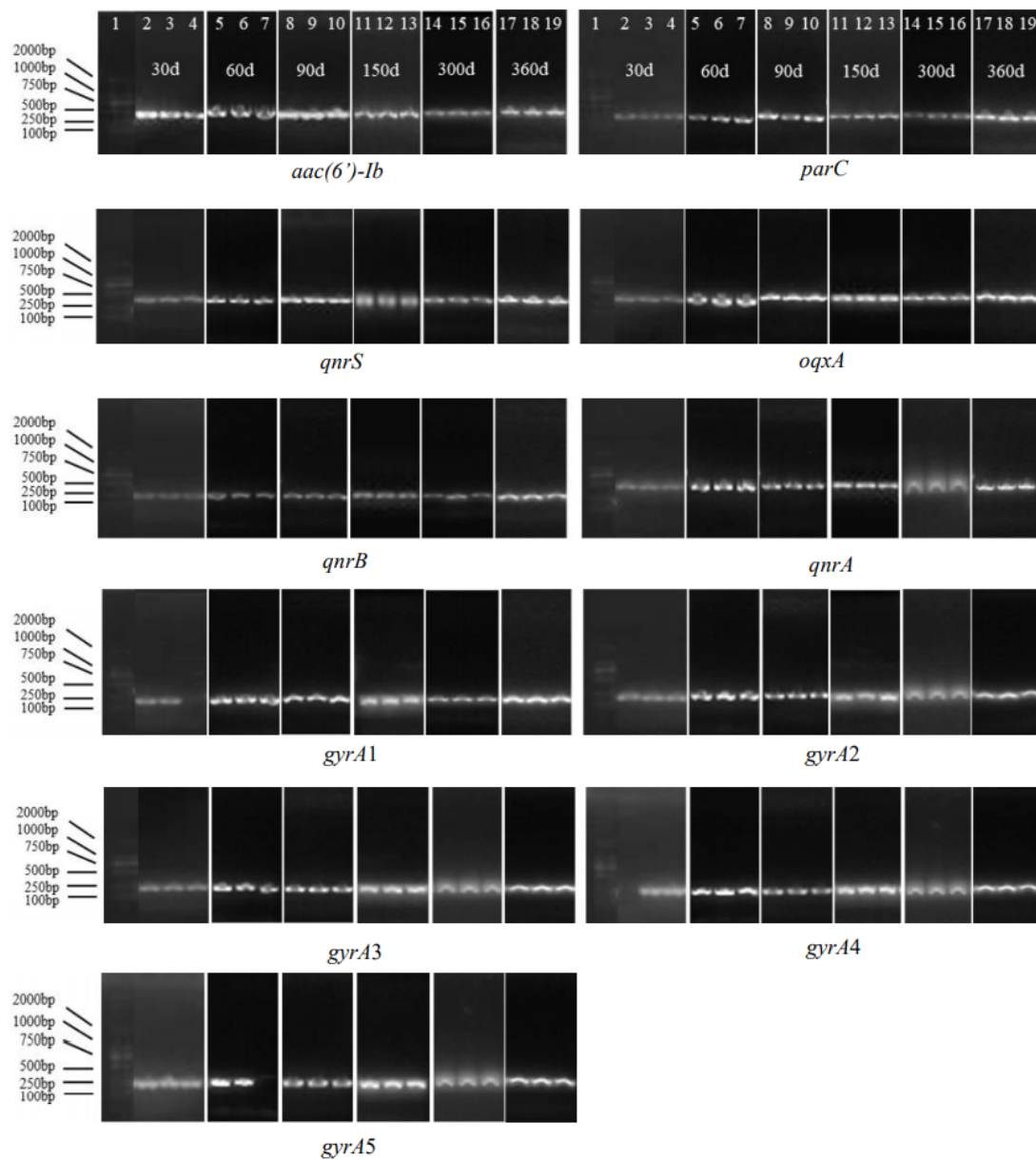
Alignment: gyrA5

      .....| .....| .....| .....| .....| .....| .....| .....| .....| .....|
      10      20      30      40      50      60      70      80
4-1d  -VGDVIGKYH PHGDFAVYAT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT-
4-7d  -VGEFPGKYH PHGDFAVYAT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN MSRYG
4-13d CW-FVIGKYH PHGDFAVYAT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK RNGT-
4-30d SLVNGPGKYH PHGDFAVYAT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK LDGT-
4-60d -VGDPFGKYH PHGDFAVYAT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN LGRYG
4-90d -VGDRIGKYH PHGDFAVYAT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN WPTVR
Clustal Consensus : *****

```

Note: “*” means no difference in amino acid. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 10 amino acids.

Figure S32. PCR results for storage stability of plasmid DNA references materials stored at -20°C .



Note: Lane 1 is DL 2000 DNA marker; lane 2–4, 5–7, 8–10, 11–13, 14–16, and 17–19 are PCR bands of the target gene sampled on the 30th, 60th, 90th, 150th, 300th, and 360th days of storage, respectively. Considering the different sampling timepoints, the gene images were intercepted and spliced using Microsoft Word, and the original images are available upon request.

Figure S33. Sequencing results of *aac(6')-Ib* for stability of plasmid DNA references materials stored at -20°C .

```

Alignment: aac(6')-Ib
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d      TTTGATCTCT GCGTAGAGT GCGTAAATCG ATCTCATATC GTCCAGTGGT GGGGCGGAGA AGAAGCACCG CCGACACTTG CTGACCTACA GGAACAGTAC TTGCCAAGCG
-20 - 60d      TTTGAGGCTC GTTTCOCAGT GCGTAAATCG ATCTCATATC GTCCAGTGGT GGGGCGGAGA AGAAGCACCG CCGACACTTG CTGACCTACA GGAACAGTAC TTGCCAAGCG
-20 - 90d      TTTGCGGTAT GAGCCAGAGT GCGTAAATCG ATCTCATATC GTCCAGTGGT GGGGCGGAGA AGAAGCACCG CCGACACTTG CTGACCTACA GGAACAGTAC TTGCCAAGCG
-20 - 150d     TTTTGGATAA TCTCCAGAGT GCGTAAATCG ATCTCATATC GTCCAGTGGT GGGGCGGAGA AGAAGCACCG CCGACACTTG CTGACCTACA GGAACAGTAC TTGCCAAGCG
-20 - 300d     TTGGAATTTT TTTCCAGAGT GCGTAAATCG ATCTCATATC GTCCAGTGGT GGGGCGGAGA AGAAGCACCG CCGACACTTG CTGACCTACA GGAACAGTAC TTGCCAAGCG
-20 - 360d     TTTGCGGTGC CTCTTCTAGT GCGTAAATCG ATCTCATATC GTCCAGTGGT GGGGCGGAGA AGAAGCACCG CCGACACTTG CTGACCTACA GGAACAGTAC TTGCCAAGCG
Clustal Consensus **          *** *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d      TTTTAGCCCA AGACTCCGTC ACTCCATACA TTCCAATGCT GAATGGAGAG CCGATTGGGT ATGCCCACTC GTACGTTGCT CTTGGAAGCG GGCACGGATG GTGGGAAGAA
-20 - 60d      TTTTAGCCCA AGACTCCGTC ACTCCATACA TTCCAATGCT GAATGGAGAG CCGATTGGGT ATGCCCACTC GTACGTTGCT CTTGGAAGCG GGCACGGATG GTGGGAAGAA
-20 - 90d      TTTTAGCCCA AGACTCCGTC ACTCCATACA TTCCAATGCT GAATGGAGAG CCGATTGGGT ATGCCCACTC GTACGTTGCT CTTGGAAGCG GGCACGGATG GTGGGAAGAA
-20 - 150d     TTTTAGCCCA AGACTCCGTC ACTCCATACA TTCCAATGCT GAATGGAGAG CCGATTGGGT ATGCCCACTC GTACGTTGCT CTTGGAAGCG GGCACGGATG GTGGGAAGAA
-20 - 300d     TTTTAGCCCA AGACTCCGTC ACTCCATACA TTCCAATGCT GAATGGAGAG CCGATTGGGT ATGCCCACTC GTACGTTGCT CTTGGAAGCG GGCACGGATG GTGGGAAGAA
-20 - 360d     TTTTAGCCCA AGACTCCGTC ACTCCATACA TTCCAATGCT GAATGGAGAG CCGATTGGGT ATGCCCACTC GTACGTTGCT CTTGGAAGCG GGCACGGATG GTGGGAAGAA
Clustal Consensus *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d      GAAACCCATC CAGCACTAGC CGGAATAGAC CAGTTACTGC CGAATGCATC ACAACTGGGC AAAGGCTTGC GAACCAAGCT GGTTCGAGCT CTGGTTGAGT TGCTGTTCAA
-20 - 60d      GAAACCCATC CAGCACTAGC CGGAATAGAC CAGTTACTGC CGAATGCATC ACAACTGGGC AAAGGCTTGC GAACCAAGCT GGTTCGAGCT CTGGTTGAGT TGCTGTTCAA
-20 - 90d      GAAACCCATC CAGCACTAGC CGGAATAGAC CAGTTACTGC CGAATGCATC ACAACTGGGC AAAGGCTTGC GAACCAAGCT GGTTCGAGCT CTGGTTGAGT TGCTGTTCAA
-20 - 150d     GAAACCCATC CAGCACTAGC CGGAATAGAC CAGTTACTGC CGAATGCATC ACAACTGGGC AAAGGCTTGC GAACCAAGCT GGTTCGAGCT CTGGTTGAGT TGCTGTTCAA
-20 - 300d     GAAACCCATC CAGCACTAGC CGGAATAGAC CAGTTACTGC CGAATGCATC ACAACTGGGC AAAGGCTTGC GAACCAAGCT GGTTCGAGCT CTGGTTGAGT TGCTGTTCAA
-20 - 360d     GAAACCCATC CAGCACTAGC CGGAATAGAC CAGTTACTGC CGAATGCATC ACAACTGGGC AAAGGCTTGC GAACCAAGCT GGTTCGAGCT CTGGTTGAGT TGCTGTTCAA
Clustal Consensus *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d      TGATCCCGAG GTCACCAAGA TCCAAACCGA CCGCTCGCCG AGCAACTTGC GAGCGATCCG ATGCTACGAG AAAGCGGGGT TTGAGAGCCA AGTACCCGTA ACCACCCCG
-20 - 60d      TGATCCCGAG GTCACCAAGA TCCAAACCGA CCGCTCGCCG AGCAACTTGC GAGCGATCCG ATGCTACGAG AAAGCGGGGT TTGAGAGCCA AGTACCCGTA ACCACCCCG
-20 - 90d      TGATCCCGAG GTCACCAAGA TCCAAACCGA CCGCTCGCCG AGCAACTTGC GAGCGATCCG ATGCTACGAG AAAGCGGGGT TTGAGAGCCA AGTACCCGTA ACCACCCCG
-20 - 150d     TGATCCCGAG GTCACCAAGA TCCAAACCGA CCGCTCGCCG AGCAACTTGC GAGCGATCCG ATGCTACGAG AAAGCGGGGT TTGAGAGCCA AGTACCCGTA ACCACCCCG
-20 - 300d     TGATCCCGAG GTCACCAAGA TCCAAACCGA CCGCTCGCCG AGCAACTTGC GAGCGATCCG ATGCTACGAG AAAGCGGGGT TTGAGAGCCA AGTACCCGTA ACCACCCCG
-20 - 360d     TGATCCCGAG GTCACCAAGA TCCAAACCGA CCGCTCGCCG AGCAACTTGC GAGCGATCCG ATGCTACGAG AAAGCGGGGT TTGAGAGCCA AGTACCCGTA ACCACCCCG
Clustal Consensus *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d      ATGCTCCAGC CCGTACATG GTTCAAAAC GGGGGGATT TTCCG-GAGA --
-20 - 60d      ATGCTCCAGC CCGTACATG GTTCAAAAC GGGGAATATT TCGAGAGAA- --
-20 - 90d      ATGCTCCAGC CCGTACATG GTTCAAAAC GGGGGGATT TTTTCCGAGA --
-20 - 150d     ATGCTCCAGC CCGTACATG GTTCAAAAC GGGGGAATT TTCCGGAA- --
-20 - 300d     ATGCTCCAGC CCGTACATG GTTCAAAAC GGGGGAATT TTTCCGAGAA TA
-20 - 360d     ATGCTCCAGC CCGTACATG GTTCAAAAC GGGGGAATT CCGAGAA- --
Clustal Consensus *****

```

Note: “*” means no difference in nucleotide. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 20 nucleotides.

Figure S34. Sequencing results of *parC* for stability of plasmid DNA references materials stored at -20°C .

```

Alignment: parC
      .....| .....| .....| .....| .....| .....| .....| .....| .....|
      10      20      30      40      50      60      70      80
-20 - 30d  -YAICELGLN ATAKPIKKSAR TVGDVLGKHY PHGDRACYEA MVLMAQPFSY RYPLVDGQGN WGAPDDPKSF AAMRYTESRL SKYAGCCS
-20 - 60d  SMRLKLGLN ATAKPIKKSAR TVGDVLGKHY PHGDRACYEA MVLMAQPFSY RYPLVDGQGN WGAPDDPKSF AAMRYTESRL SKYGGLLF
-20 - 90d  SMRLVELGLN ATAKPIKKSAR TVGDVLGKHY PHGDRACYEA MVLMAQPFSY RYPLVDGQGN WGAPDDPKSF AAMRYTESRL SKYAGPAV
-20 - 150d -YAICKLGLN ATAKPIKKSAR TVGDVLGKHY PHGDRACYEA MVLMAQPFSY RYPLVDGQGN WGAPDDPKSF AAMRYTESRL SKYAGLLL
-20 - 300d SMRLSELGLN ATAKPIKKSAR TVGDVLGKHY PHGDRACYEA MVLMAQPFSY RYPLVDGQGN WGAPDDPKSF AAMRYTESRL SKYAGPAV
-20 - 360d SMR-FELGLN ATAKPIKKSAR TVGDVLGKHY PHGDRACYEA MVLMAQPFSY RYPLVDGQGN WGAPDDPKSF AAMRYTESRL SKYAKSAV
Clustal Consensus :**** *****

```

Note: “*” means no difference in amino acid. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 10 amino acids.

Figure S35. Sequencing results of *qnrS* for stability of plasmid DNA references materials stored at -20°C .

```

Alignment: qnrS
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
      10      20      30      40      50      60      70      80      90     100     110
-20 - 30d  AAGTT--TCT CAATTA-CAG GGTGATATTC GTGGCTGCCA CTTTGATGTC GCAGATCTTC GTGATGCAAG TTTCACAACAA TGCCAACTTG CGATGGCAAA CTTCAGTAAT
-20 - 60d  -AAAT--TTT ACCCTG-CAG GGTGATATTC GTGGCTGCCA CTTTGATGTC GCAGATCTTC GTGATGCAAG TTTCACAACAA TGCCAACTTG CGATGGCAAA CTTCAGTAAT
-20 - 90d  -GTGT--TCT CACATAACAG GGTGATATTC GTGGCTGCCA CTTTGATGTC GCAGATCTTC GTGATGCAAG TTTCACAACAA TGCCAACTTG CGATGGCAAA CTTCAGTAAT
-20 - 150d -AATTGCTCT CACTTA-CAG GGTGATATTC GTGGCTGCCA CTTTGATGTC GCAGATCTTC GTGATGCAAG TTTCACAACAA TGCCAACTTG CGATGGCAAA CTTCAGTAAT
-20 - 300d AAGTT--CTT CACTTAACAG GGTGATATTC GTGGCTGCCA CTTTGATGTC GCAGATCTTC GTGATGCAAG TTTCACAACAA TGCCAACTTG CGATGGCAAA CTTCAGTAAT
-20 - 360d CAATT--TTC CTCTA-CAG GGTGATATTC GTGGCTGCCA CTTTGATGTC GCAGATCTTC GTGATGCAAG TTTCACAACAA TGCCAACTTG CGATGGCAAA CTTCAGTAAT
Clustal Consensus  *      *  *** *****

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
      120     130     140     150     160     170     180     190     200     210     220
-20 - 30d  GCCAATTGCT ACGGTATAGA GTTCGGTGGC TGTGATTAA AAGGTGCCAA CTTTCCCGA ACAAACTTG CCCATCAAGT GAGTAATCGT ATGTACTTTT GCTCAGCATT
-20 - 60d  GCCAATTGCT ACGGTATAGA GTTCGGTGGC TGTGATTAA AAGGTGCCAA CTTTCCCGA ACAAACTTG CCCATCAAGT GAGTAATCGT ATGTACTTTT GCTCAGCATT
-20 - 90d  GCCAATTGCT ACGGTATAGA GTTCGGTGGC TGTGATTAA AAGGTGCCAA CTTTCCCGA ACAAACTTG CCCATCAAGT GAGTAATCGT ATGTACTTTT GCTCAGCATT
-20 - 150d GCCAATTGCT ACGGTATAGA GTTCGGTGGC TGTGATTAA AAGGTGCCAA CTTTCCCGA ACAAACTTG CCCATCAAGT GAGTAATCGT ATGTACTTTT GCTCAGCATT
-20 - 300d GCCAATTGCT ACGGTATAGA GTTCGGTGGC TGTGATTAA AAGGTGCCAA CTTTCCCGA ACAAACTTG CCCATCAAGT GAGTAATCGT ATGTACTTTT GCTCAGCATT
-20 - 360d GCCAATTGCT ACGGTATAGA GTTCGGTGGC TGTGATTAA AAGGTGCCAA CTTTCCCGA ACAAACTTG CCCATCAAGT GAGTAATCGT ATGTACTTTT GCTCAGCATT
Clustal Consensus  *****

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
      230     240     250     260     270     280     290     300     310     320     330
-20 - 30d  TATTTCGGA TCTAATCTTT CCTATGCCAA TATGGAGAGG GTTTCGTTAG AAAAAATGTA GTTGTTCGAA AATCGCTGGA TAGGAACGAA CCTAGCGGGT GCATCACTGA
-20 - 60d  TATTTCGGA TCTAATCTTT CCTATGCCAA TATGGAGAGG GTTTCGTTAG AAAAAATGTA GTTGTTCGAA AATCGCTGGA TAGGAACGAA CCTAGCGGGT GCATCACTGA
-20 - 90d  TATTTCGGA TCTAATCTTT CCTATGCCAA TATGGAGAGG GTTTCGTTAG AAAAAATGTA GTTGTTCGAA AATCGCTGGA TAGGAACGAA CCTAGCGGGT GCATCACTGA
-20 - 150d TATTTCGGA TCTAATCTTT CCTATGCCAA TATGGAGAGG GTTTCGTTAG AAAAAATGTA GTTGTTCGAA AATCGCTGGA TAGGAACGAA CCTAGCGGGT GCATCACTGA
-20 - 300d TATTTCGGA TCTAATCTTT CCTATGCCAA TATGGAGAGG GTTTCGTTAG AAAAAATGTA GTTGTTCGAA AATCGCTGGA TAGGAACGAA CCTAGCGGGT GCATCACTGA
-20 - 360d TATTTCGGA TCTAATCTTT CCTATGCCAA TATGGAGAGG GTTTCGTTAG AAAAAATGTA GTTGTTCGAA AATCGCTGGA TAGGAACGAA CCTAGCGGGT GCATCACTGA
Clustal Consensus  *****

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
      340     350     360     370     380     390     400     410     420     430
-20 - 30d  AAGAGTCAGA CTTAAGTCGA GGTCTTTTTT CCGAAGATGT CTGGGGGCCAA TTAGCCTAC AGGGGGCCAA TTTATGCCAC GCGGAATGCA --ATGGGGTT T-AGAA--
-20 - 60d  AAGAGTCAGA CTTAAGTCGA GGTCTTTTTT CCGAAGATGT CTGGGGGCCAA TTAGCCTAC AGGGGGCCAA TTTATGCCAC GCGGAATGCA --GGGGACTT TTAAAAAA
-20 - 90d  AAGAGTCAGA CTTAAGTCGA GGTCTTTTTT CCGAAGATGT CTGGGGGCCAA TTAGCCTAC AGGGGGCCAA TTTATGCCAC GCGGAATGCA --CGGGGGTT TTAGAAA--
-20 - 150d AAGAGTCAGA CTTAAGTCGA GGTCTTTTTT CCGAAGATGT CTGGGGGCCAA TTAGCCTAC AGGGGGCCAA TTTATGCCAC GCGGAATGGC GCGAGAAGGT TTAGAAGA
-20 - 300d AAGAGTCAGA CTTAAGTCGA GGTCTTTTTT CCGAAGATGT CTGGGGGCCAA TTAGCCTAC AGGGGGCCAA TTTATGCCAC GCGGAATGGC --CGGGGTT T-AGAA--
-20 - 360d AAGAGTCAGA CTTAAGTCGA GGTCTTTTTT CCGAAGATGT CTGGGGGCCAA TTAGCCTAC AGGGGGCCAA TTTATGCCAC GCGGAATGGC --AGGGGGTT TAAAAA--
Clustal Consensus  *****

```

Note: “*” means no difference in nucleotide. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 20 nucleotides.

Figure S36. Sequencing results of *oqx4* for stability of plasmid DNA references materials stored at -20°C .

```

Alignment: oqx4
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d  --CAGC-TGT  CCCCAGAAT  GCTGCGCTC  CCGCCCCGAC  GGTGAGGCC  GCTAAGGTGC  TGGTGAAGTC  GATCAGTCAG  TGGGATAGTT  TTAACGGTCG  CATTGAAGCG
-20 - 60d  ACCAGGGTAT  GATC-CGAAT  GCTGCGCTC  CCGCCCCGAC  GGTGAGGCC  GCTAAGGTGC  TGGTGAAGTC  GATCAGTCAG  TGGGATAGTT  TTAACGGTCG  CATTGAAGCG
-20 - 90d  -ACAGCGGTG  TTGCGAGAAT  GCTGCGCTC  CCGCCCCGAC  GGTGAGGCC  GCTAAGGTGC  TGGTGAAGTC  GATCAGTCAG  TGGGATAGTT  TTAACGGTCG  CATTGAAGCG
-20 - 150d  GACAGCGTTT  TCCC-AGAAT  GCTGCGCTC  CCGCCCCGAC  GGTGAGGCC  GCTAAGGTGC  TGGTGAAGTC  GATCAGTCAG  TGGGATAGTT  TTAACGGTCG  CATTGAAGCG
-20 - 300d  GACAGCGTTT  TCCC-AGAAT  GCTGCGCTC  CCGCCCCGAC  GGTGAGGCC  GCTAAGGTGC  TGGTGAAGTC  GATCAGTCAG  TGGGATAGTT  TTAACGGTCG  CATTGAAGCG
-20 - 360d  GACAGCGTTT  CCCCCAGAAT  GCTGCGCTC  CCGCCCCGAC  GGTGAGGCC  GCTAAGGTGC  TGGTGAAGTC  GATCAGTCAG  TGGGATAGTT  TTAACGGTCG  CATTGAAGCG
Clustal Consensus  ***          **** ***** ***** ***** ***** ***** ***** ***** ***** *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d  GTGGAGAGCG  TTCAGCTTCG  CCTTCCGCTC  TCGGATACA  TTGATAAAGT  GAATTACACT  GACGGCCAGG  AGGTGAAAAA  GGCCGAGGTG  CTGTTACAGG  TAGATGACAG
-20 - 60d  GTGGAGAGCG  TTCAGCTTCG  CCTTCCGCTC  TCGGATACA  TTGATAAAGT  GAATTACACT  GACGGCCAGG  AGGTGAAAAA  GGCCGAGGTG  CTGTTACAGG  TAGATGACAG
-20 - 90d  GTGGAGAGCG  TTCAGCTTCG  CCTTCCGCTC  TCGGATACA  TTGATAAAGT  GAATTACACT  GACGGCCAGG  AGGTGAAAAA  GGCCGAGGTG  CTGTTACAGG  TAGATGACAG
-20 - 150d  GTGGAGAGCG  TTCAGCTTCG  CCTTCCGCTC  TCGGATACA  TTGATAAAGT  GAATTACACT  GACGGCCAGG  AGGTGAAAAA  GGCCGAGGTG  CTGTTACAGG  TAGATGACAG
-20 - 300d  GTGGAGAGCG  TTCAGCTTCG  CCTTCCGCTC  TCGGATACA  TTGATAAAGT  GAATTACACT  GACGGCCAGG  AGGTGAAAAA  GGCCGAGGTG  CTGTTACAGG  TAGATGACAG
-20 - 360d  GTGGAGAGCG  TTCAGCTTCG  CCTTCCGCTC  TCGGATACA  TTGATAAAGT  GAATTACACT  GACGGCCAGG  AGGTGAAAAA  GGCCGAGGTG  CTGTTACAGG  TAGATGACAG
Clustal Consensus  ***** ***** ***** ***** ***** ***** ***** ***** ***** ***** *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d  AACCTATCGC  GCGCGCTCG  AGCAGGCCA  GCGCGCTTG  GCAAGGCCA  AAACCCAGG  CAGCTTCGCG  CAAAGCCAGG  CGAACCCGAC  CGATAAATTA  GTCCATACCC-
-20 - 60d  AACCTATCGC  GCGCGCTCG  AGCAGGCCA  GCGCGCTTG  GCAAGGCCA  AAACCCAGG  CAGCTTCGCG  CAAAGCCAGG  CGAACCCGAC  CGATAAATTA  GTCCATATCC
-20 - 90d  AACCTATCGC  GCGCGCTCG  AGCAGGCCA  GCGCGCTTG  GCAAGGCCA  AAACCCAGG  CAGCTTCGCG  CAAAGCCAGG  CGAACCCGAC  CGATAAATTA  GTCCATATCC
-20 - 150d  AACCTATCGC  GCGCGCTCG  AGCAGGCCA  GCGCGCTTG  GCAAGGCCA  AAACCCAGG  CAGCTTCGCG  CAAAGCCAGG  CGAACCCGAC  CGATAAATTA  GTCCATAGAA
-20 - 300d  AACCTATCGC  GCGCGCTCG  AGCAGGCCA  GCGCGCTTG  GCAAGGCCA  AAACCCAGG  CAGCTTCGCG  CAAAGCCAGG  CGAACCCGAC  CGATAAATTA  GTCCATAC--
-20 - 360d  AACCTATCGC  GCGCGCTCG  AGCAGGCCA  GCGCGCTTG  GCAAGGCCA  AAACCCAGG  CAGCTTCGCG  CAAAGCCAGG  CGAACCCGAC  CGATAAATTA  GTCCATACCC-
Clustal Consensus  ***** ***** ***** ***** ***** ***** ***** ***** ***** ***** *****

-----|-----|-----|
-20 - 30d  CCGCTCTCGT  CTCCTGA--
-20 - 60d  CCGCTCTCGT  CTCATAAA-
-20 - 90d  CCGCTCTCGT  CTCCT---
-20 - 150d  CCATTTTGGT  CTCCTATGA
-20 - 300d  CCGCTCTCGT  CTCCTAGC-
-20 - 360d  CCGCTC--GT  CTCCT---
Clustal Consensus  **          ***

```

Note: “*” means no difference in nucleotide. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 20 nucleotides.

Figure S37. Sequencing results of *qnrB* for stability of plasmid DNA references materials stored at -20°C .

```

Alignment: qnrB
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
      10      20      30      40      50      60      70      80      90     100     110
-20 - 30d  -ACAGGCATT GAAATC-GC CACTGCCGCG CACAAGGCGC AGATTTCGCG GGTGCAAGCT TTATGAATAT GATCACCACG CGCACTGCT TTTGCAGCG ATATATCACT
-20 - 60d  -TCAGGCATT GAAAGAATTC CACTGCCGCG CACAAGGCGC AGATTTCGCG GGTGCAAGCT TTATGAATAT GATCACCACG CGCACTGCT TTTGCAGCG ATATATCACT
-20 - 90d  -ATGGGCATT GAAAAAT-GC CACTGCCGCG CACAAGGCGC AGATTTCGCG GGTGCAAGCT TTATGAATAT GATCACCACG CGCACTGCT TTTGCAGCG ATATATCACT
-20 - 150d CAGGGGCATT GAAAAAT-GC CACTGCCGCG CACAAGGCGC AGATTTCGCG GGTGCAAGCT TTATGAATAT GATCACCACG CGCACTGCT TTTGCAGCG ATATATCACT
-20 - 300d --TGGGCATT GAAATC-GC CACTGCCGCG CACAAGGCGC AGATTTCGCG GGTGCAAGCT TTATGAATAT GATCACCACG CGCACTGCT TTTGCAGCG ATATATCACT
-20 - 360d --TAGGCATT GAAACTTCGC CACTGCCGCG CACAAGGCGC AGATTTCGCG GGTGCAAGCT TTATGAATAT GATCACCACG CGCACTGCT TTTGCAGCG ATATATCACT
Clustal Consensus ***** *

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
      120     130     140     150     160     170     180     190     200     210     220
-20 - 30d  AATACTAATC TAAGCTACGC CAATTTTTCG AAAGTCGCTG TCGAAAAAGTc TGAGCTGTGG GAAAAACCGCT GGATGGGGAC TCAGGTACTG GCTCCGACGT TCAGTGGTTC
-20 - 60d  AATACTAATC TAAGCTACGC CAATTTTTCG AAAGTCGCTG TCGAAAAAGTc TGAGCTGTGG GAAAAACCGCT GGATGGGGAC TCAGGTACTG GCTCCGACGT TCAGTGGTTC
-20 - 90d  AATACTAATC TAAGCTACGC CAATTTTTCG AAAGTCGCTG TCGAAAAAGTc TGAGCTGTGG GAAAAACCGCT GGATGGGGAC TCAGGTACTG GCTCCGACGT TCAGTGGTTC
-20 - 150d AATACTAATC TAAGCTACGC CAATTTTTCG AAAGTCGCTG TCGAAAAAGTc TGAGCTGTGG GAAAAACCGCT GGATGGGGAC TCAGGTACTG GCTCCGACGT TCAGTGGTTC
-20 - 300d AATACTAATC TAAGCTACGC CAATTTTTCG AAAGTCGCTG TCGAAAAAGTc TGAGCTGTGG GAAAAACCGCT GGATGGGGAC TCAGGTACTG GCTCCGACGT TCAGTGGTTC
-20 - 360d AATACTAATC TAAGCTACGC CAATTTTTCG AAAGTCGCTG TCGAAAAAGTc TGAGCTGTGG GAAAAACCGCT GGATGGGGAC TCAGGTACTG GCTCCGACGT TCAGTGGTTC
Clustal Consensus *****

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
      230     240     250     260     270
-20 - 30d  AGATCTCTCC GCGCGCCAGT TTTGCACTTT CGACTGGC-G AGCAGCAAAA -
-20 - 60d  AGATCTCTCC GCGCGCCAGT TTTGCACTTT CGATGGCG-T AACAGCAAAA -
-20 - 90d  AGATCTCTCC GCGCGCCAGT TTTGCACTTT CGACTGGC-A AACAGCAAAA A
-20 - 150d AGATCTCTCC GCGCGCCAGT TTTGCACTTT CGACTGGCGA AACAGCAAAA -
-20 - 300d AGATCTCTCC GCGCGCCAGT TTTGCACTTT CGACTGGC-A A-CAGCAAAA A
-20 - 360d AGATCTCTCC GCGCGCCAGT TTTGCACTTT CGACTGGC-G AACAGCAAAA -
Clustal Consensus *****

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Note: “*” means no difference in nucleotide. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 20 nucleotides.

Figure S38. Sequencing results of *qnrA* for stability of plasmid DNA references materials stored at -20°C .

```

Alignment: qnrA
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d      GGTITTTTTT CCCCAGGATT TGACTGACAG CCGTTTTTCG CCGTGGCGCT TTTATCAGTG TGACTTCAGC CACTGTCAGC TCCAGGATGC CAGTTTCGAG GATTGCAGTT
-20 - 60d      -GGITTTTTT TCCCAGGATT TGACTGACAG CCGTTTTTCG CCGTGGCGCT TTTATCAGTG TGACTTCAGC CACTGTCAGC TCCAGGATGC CAGTTTCGAG GATTGCAGTT
-20 - 90d      -GGITTTTTT TCCCAGGATT TGACTGACAG CCGTTTTTCG CCGTGGCGCT TTTATCAGTG TGACTTCAGC CACTGTCAGC TCCAGGATGC CAGTTTCGAG GATTGCAGTT
-20 - 150d     -GGITTTTTT TCCCAGGATT TGACTGACAG CCGTTTTTCG CCGTGGCGCT TTTATCAGTG TGACTTCAGC CACTGTCAGC TCCAGGATGC CAGTTTCGAG GATTGCAGTT
-20 - 300d     -GGITTTTTT CCCCAGGATT TGACTGACAG CCGTTTTTCG CCGTGGCGCT TTTATCAGTG TGACTTCAGC CACTGTCAGC TCCAGGATGC CAGTTTCGAG GATTGCAGTT
-20 - 360d     AGTITTTTTT CCCCAGGATT TGACTGACAG CCGTTTTTCG CCGTGGCGCT TTTATCAGTG TGACTTCAGC CACTGTCAGC TCCAGGATGC CAGTTTCGAG GATTGCAGTT
Clustal Consensus *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d      TCATTGAAG CCGCCCGCTT GAAGGGTCTC ACTTCAGCTA TCCCGATCTG CCGGATGCCA GTTTCAGGCC CTGCGGCTCTG TCTTTGGCCA ACTTCAGCGG TCCCAACTGC
-20 - 60d      TCATTGAAG CCGCCCGCTT GAAGGGTCTC ACTTCAGCTA TCCCGATCTG CCGGATGCCA GTTTCAGGCC CTGCGGCTCTG TCTTTGGCCA ACTTCAGCGG TCCCAACTGC
-20 - 90d      TCATTGAAG CCGCCCGCTT GAAGGGTCTC ACTTCAGCTA TCCCGATCTG CCGGATGCCA GTTTCAGGCC CTGCGGCTCTG TCTTTGGCCA ACTTCAGCGG TCCCAACTGC
-20 - 150d     TCATTGAAG CCGCCCGCTT GAAGGGTCTC ACTTCAGCTA TCCCGATCTG CCGGATGCCA GTTTCAGGCC CTGCGGCTCTG TCTTTGGCCA ACTTCAGCGG TCCCAACTGC
-20 - 300d     TCATTGAAG CCGCCCGCTT GAAGGGTCTC ACTTCAGCTA TCCCGATCTG CCGGATGCCA GTTTCAGGCC CTGCGGCTCTG TCTTTGGCCA ACTTCAGCGG TCCCAACTGC
-20 - 360d     TCATTGAAG CCGCCCGCTT GAAGGGTCTC ACTTCAGCTA TCCCGATCTG CCGGATGCCA GTTTCAGGCC CTGCGGCTCTG TCTTTGGCCA ACTTCAGCGG TCCCAACTGC
Clustal Consensus *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d      TTTGGCATAG AGTTCAGGGA GTCCGATCTC AAGGGGCGCA ACTTTTCGCG GCGCCGCTTC TACAATCAAG TCAGCCATAA GATGTACTTC TGTTCGGCTT ATATCTCAGG
-20 - 60d      TTTGGCATAG AGTTCAGGGA GTCCGATCTC AAGGGGCGCA ACTTTTCGCG GCGCCGCTTC TACAATCAAG TCAGCCATAA GATGTACTTC TGTTCGGCTT ATATCTCAGG
-20 - 90d      TTTGGCATAG AGTTCAGGGA GTCCGATCTC AAGGGGCGCA ACTTTTCGCG GCGCCGCTTC TACAATCAAG TCAGCCATAA GATGTACTTC TGTTCGGCTT ATATCTCAGG
-20 - 150d     TTTGGCATAG AGTTCAGGGA GTCCGATCTC AAGGGGCGCA ACTTTTCGCG GCGCCGCTTC TACAATCAAG TCAGCCATAA GATGTACTTC TGTTCGGCTT ATATCTCAGG
-20 - 300d     TTTGGCATAG AGTTCAGGGA GTCCGATCTC AAGGGGCGCA ACTTTTCGCG GCGCCGCTTC TACAATCAAG TCAGCCATAA GATGTACTTC TGTTCGGCTT ATATCTCAGG
-20 - 360d     TTTGGCATAG AGTTCAGGGA GTCCGATCTC AAGGGGCGCA ACTTTTCGCG GCGCCGCTTC TACAATCAAG TCAGCCATAA GATGTACTTC TGTTCGGCTT ATATCTCAGG
Clustal Consensus *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d      TTGCAACCTG GCTTATACCA ACTTGAGTGG CCAATGCTTG GAAAAATGCG AGCTGTTTGA AAACAACCTG AGCAATGCCA ATCTCAGCGG CGCTTCCTTG ATGGGCTCAG
-20 - 60d      TTGCAACCTG GCTTATACCA ACTTGAGTGG CCAATGCTTG GAAAAATGCG AGCTGTTTGA AAACAACCTG AGCAATGCCA ATCTCAGCGG CGCTTCCTTG ATGGGCTCAG
-20 - 90d      TTGCAACCTG GCTTATACCA ACTTGAGTGG CCAATGCTTG GAAAAATGCG AGCTGTTTGA AAACAACCTG AGCAATGCCA ATCTCAGCGG CGCTTCCTTG ATGGGCTCAG
-20 - 150d     TTGCAACCTG GCTTATACCA ACTTGAGTGG CCAATGCTTG GAAAAATGCG AGCTGTTTGA AAACAACCTG AGCAATGCCA ATCTCAGCGG CGCTTCCTTG ATGGGCTCAG
-20 - 300d     TTGCAACCTG GCTTATACCA ACTTGAGTGG CCAATGCTTG GAAAAATGCG AGCTGTTTGA AAACAACCTG AGCAATGCCA ATCTCAGCGG CGCTTCCTTG ATGGGCTCAG
-20 - 360d     TTGCAACCTG GCTTATACCA ACTTGAGTGG CCAATGCTTG GAAAAATGCG AGCTGTTTGA AAACAACCTG AGCAATGCCA ATCTCAGCGG CGCTTCCTTG ATGGGCTCAG
Clustal Consensus *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d      ATCTCAGCGG CCGCACCTTC TCCCGCGACT GTTGGCAACA GGTCAATCTG CCGGGCTGTG GCGTAACTTT TGCCGATCTG GATGGGCTCG ACCCCAGAGG GGTCAACCTC
-20 - 60d      ATCTCAGCGG CCGCACCTTC TCCCGCGACT GTTGGCAACA GGTCAATCTG CCGGGCTGTG GCGTAACTTT TGCCGATCTG GATGGGCTCG ACCCCAGAGG GGTCAACCTC
-20 - 90d      ATCTCAGCGG CCGCACCTTC TCCCGCGACT GTTGGCAACA GGTCAATCTG CCGGGCTGTG GCGTAACTTT TGCCGATCTG GATGGGCTCG ACCCCAGAGG GGTCAACCTC
-20 - 150d     ATCTCAGCGG CCGCACCTTC TCCCGCGACT GTTGGCAACA GGTCAATCTG CCGGGCTGTG GCGTAACTTT TGCCGATCTG GATGGGCTCG ACCCCAGAGG GGTCAACCTC
-20 - 300d     ATCTCAGCGG CCGCACCTTC TCCCGCGACT GTTGGCAACA GGTCAATCTG CCGGGCTGTG GCGTAACTTT TGCCGATCTG GATGGGCTCG ACCCCAGAGG GGTCAACCTC
-20 - 360d     ATCTCAGCGG CCGCACCTTC TCCCGCGACT GTTGGCAACA GGTCAATCTG CCGGGCTGTG GCGTAACTTT TGCCGATCTG GATGGGCTCG ACCCCAGAGG GGTCAACCTC
Clustal Consensus *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d      GAAGGAGTCA AGTGGGGGCG CCGCGTGGAC AA--
-20 - 60d      GAAGGAGTCA CG--GGGGCG TCGCGGGGAG ----
-20 - 90d      GAAGGAGTCA AA--GGAGCG CTGGGGGGCA AAA-
-20 - 150d     GAAGGAGTCA TG--GGAG-- -CGCGGGCAA AAAT
-20 - 300d     GAAGGAGTCA AAGGGGGGCG CCGCGGGGAA AA--
-20 - 360d     GAAGGAGTCA AGTGGGGGCG CCGTGGCAA- ----
Clustal Consensus ***** ** *

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Note: “*” means no difference in nucleotide. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 20 nucleotides.

Figure S39. Sequencing results of *gyrA* for stability of plasmid DNA references materials stored at -20°C .

```

Alignment: gyrA1

      .....| .....| .....| .....| .....| .....| .....| .....| .....| .....|
      10      20      30      40      50      60      70      80
-20 - 30d  -LLVNLPGKY HPHGDSAVYN TIVMAQPFSL RYMLVDGQG NFGSIDGDSA AMRYTEIRL AKIAHELMAD LEKETVDFVD KERYG
-20 - 60d  --RW-GPGKY HPHGDSAVYN TIVMAQPFSL RYMLVDGQG NFGSIDGDSA AMRYTEIRL AKIAHELMAD LEKETVDFVD KMTVR
-20 - 90d  -RW-SRIGKY HPHGDSAVYN TIVMAQPFSL RYMLVDGQG NFGSIDGDSA AMRYTEIRL AKIAHELMAD LEKETVDFVD NWNGT-
-20 - 150d -SLATRIGKY HPHGDSAVYN TIVMAQPFSL RYMLVDGQG NFGSIDGDSA AMRYTEIRL AKIAHELMAD LEKETVDFVD KTERY-
-20 - 300d -RW-PRPGKY HPHGDSAVYN TIVMAQPFSL RYMLVDGQG NFGSIDGDSA AMRYTEIRL AKIAHELMAD LEKETVDFVD TLTVR-
-20 - 360d LVG-DRPGKY HPHGDSAVYN TIVMAQPFSL RYMLVDGQG NFGSIDGDSA AMRYTEIRL AKIAHELMAD LEKETVDFVD KIDGT-
Clustal Consensus  :*** *****

Alignment: gyrA2

      .....| .....| .....| .....| .....| .....| .....| .....| .....| .....|
      10      20      30      40      50      60      70      80
-20 - 30d  -VADRFGKYH PHGDYAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN NDGT-
-20 - 60d  RW--SVGKYH PHGDYAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK LQTVR
-20 - 90d  SLVNGIGKYH PHGDYAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN WDGT-
-20 - 150d RWSAPFGKYH PHGDYAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK SNGT-
-20 - 300d -VADRFGKYH PHGDYAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN NDGT-
-20 - 360d -VGDGFGKYH PHGDYAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK SDGT-
Clustal Consensus  :**** *****; :

Alignment: gyrA3

      .....| .....| .....| .....| .....| .....| .....| .....| .....| .....|
      10      20      30      40      50      60      70      80
-20 - 30d  -LVTRFGKYH PHGDFAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK MGRYG
-20 - 60d  HW--FRPGKYH PHGDFAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK WERY-
-20 - 90d  -VGEPIGKYH PHGDFAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN -QTVR
-20 - 150d SLVVGFGKYH PHGDFAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK SNGT-
-20 - 300d SVGARVGKYH PHGDFAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK M-TV
-20 - 360d -VGDGFGKYH PHGDFAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK IDGT-
Clustal Consensus  :**** *****

Alignment: gyrA4

      .....| .....| .....| .....| .....| .....| .....| .....| .....| .....|
      10      20      30      40      50      60      70      80
-20 - 30d  -VGERFGKYH PHGDFAVYGT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK LNMT--
-20 - 60d  -VGERFGKYH PHGDFAVYGT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK METVR-
-20 - 90d  -CW-PIGKYH PHGDFAVYGT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN -SNGTD
-20 - 150d SLVVGFGKYH PHGDFAVYGT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK -MNGT-
-20 - 300d -VGERIGKYH PHGDFAVYGT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN LARYG-
-20 - 360d LLVIGIGKYH PHGDFAVYGT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK -VTVR-
Clustal Consensus  :**** *****

Alignment: gyrA5

      .....| .....| .....| .....| .....| .....| .....| .....| .....| .....|
      10      20      30      40      50      60      70      80
-20 - 30d  -VGEFGKYH PHGDFAVYAT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN MSRYG
-20 - 60d  SLVIGYGYH PHGDFAVYAT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK ANGT-
-20 - 90d  -LVHRIKYH PHGDFAVYAT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN WNGT-
-20 - 150d SLVVGFGKYH PHGDFAVYAT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN C-RY-
-20 - 300d RW-AGIGKYH PHGDFAVYAT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN LDGT-
-20 - 360d -VGDRIKYH PHGDFAVYAT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN WPTVR
Clustal Consensus  :**** *****

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Note: “*” means no difference in amino acid. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 10 amino acids.