

## 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 AGAAGCACGCCCACACTTGCTGACGTACAGGAACAGTACTTGCCAAGCGTTTTAGC GCAAGAGTCCGTCCTACTCCATACATTGCAATGCTGAATGGAGAGCCGATTGGGTATGCC CAGTCGTACGTTGCTCTTGGAAGCGGGACGGATGGTGGGAAGAAGAAACCGATCCA GGAGTACGCGGAATAGACCAGTTACTGGCGAATGCATCACAACCTGGGCAAAGGCTTG GGAACCAAGCTGGTTCGAGCTCTGGTTGAGTTGCTGTTCAATGATCCCGAGGTCACCA AGATCCAAACGGACCCGTCGCCGAGCAACTTGCGAGCGATCCGATGCTACGAGAAAG CGGGGTTTGAGAGGCAAGGTACCGTAACCAACCCAGATGGTCCAGCCGTGTACATGG TTCAAACACGCCAGGCATTTCGAG	482	–
<i>qnrA</i>	<i>qnrA</i>	MN045282	AGAGGATTTCTCACGCCAGGATTTGAGTGACAGCCGTTTTTCGCCGCTGCCGCTTTTATC AGTGTGACTTCAGCCACTGTCAGCTGCAGGATGCCAGTTTCGAGGATTGCAGTTTCAT TGAAAGCGGCGCCGTTGAAGGGTGTCACTTCAGCTATGCCGATCTGCGCGATGCCAGT TTCAAGGCCTGCCGTCTGTCTTTGGCCAACCTTCAGCGGTGCCAACTGCTTTGGCATAG AGTTCAGGGAGTGCATCTCAAGGGCGCCAACTTTTCCCGGGCCCGCTTCTACAATCA AGTCAGCCATAAGATGTACTTCTGCTCGGCTTATATCTCAGGTTGCAACCTGGCCTATA CCAACTTGAGTGGCCAATGCCTGGAAAAATGCGAGCTGTTTGAAAACAACCTGGAGCA ATGCCAATCTCAGCGGCGCTTCCTTGATGGGCTCAGATCTCAGCCGCGGCACCTTCTC CCGCGACTGTTGGCAACAGGTCAATCTGCGGGGCTGTGGCCTAACCTTTGCCGATCTG GATGGGCTCGACCCAGACGGGTCAACCTCGAAGGAGTCAAGATCTGTGCCTGGCA	579	–
<i>qnrB</i>	<i>qnrB</i>	MN045281	GGCATTGAAATTCGCCACTGCCGCGCACAAGGCGCAGATTTCCGCGGTGCAAGCTTTA TGAATATGATCACCACGCGCACCTGGTTTTGCAGCGCATATATCACTAATACTAATCTAA	263	–

			GCTACGCCAATTTTTTCGAAAGTCGTGTTGGAAAAGTGTGAGCTGTGGGAAAACCGCT GGATGGGGACTCAGGTA CTGGGTGCGACGTT CAGTGGTTCAGATCTCTCCGGCGGCG AGTTTTCGACTTTCGACTGGCGAGCAGCAA		
<i>qnrS</i>	<i>qnrS</i>	MN045280	GCAAGTTCATTGAACAGGGTGATATTCGTGCTGCCACTTTGATGTCGCAGATCTTCGT GATGCAAGTTTCCAACAATGCCAACTTGCGATGGCAA ACTTCAGTAATGCCAATTGCT ACGGTATAGAGTTCCGTGCGTGTGATTTAAAAGGTGCCAACTTTCCCGAACAACTT TGCCCATCAAGTGAGTAATCGTATGTA CTTTTGCTCAGCATTATTTCTGGATGTAATCT TTCTATGCCAATATGGAGAGGGTTTGT TTAGAAAAATGTGAGTTGTTTGAAAATCGCT GGATAGGAACGAACCTAGCGGGTGCATCACTGAAAGAGTCAGACTTAAGTCGAGGTG TTTTTTCCGAAGATGTCTGGGGGCAATTAGCCTACAGGGGGCCAATTTATGCCACGCC GAACTCGACGGTTTAGA	427	–
<i>oqxA</i>	<i>oqxA</i>	MN045291	GACAGCGTCGCACAGAATGCTGCGCCTCCCGCCCCGACGGTCAGCGCCGCTAAGGTG CTGGTGAAGTCGATCAGTCAGTGGGATAGTTTTAACGGTTCGCATTGAAGCGGTGGAGA GCGTTCAGCTTCGCCCTCGCGTCTCGGGATACATTGATAAAGTGAATTACACTGACGG CCAGGAGGTGAAAAAGGGCCAGGTGCTGTTACGATAGATGACAGAACCTATCGCGC CGCGCTGGAGCAGGCGCAGGCGGCGTTGGCAAGAGCCAAAACGCAGGCCAGCCTCG CGCAAAGCGAGGCGAACCGCACCGATAAATTAGTCCATAACCAACCTCGTCTCC	339	–
<i>parC</i>	<i>parC</i>	MN045289	CTATGCGATGTCAGAGCTGGGGCTGAACGCCACCGCTAAATTTAAAAAATCCGCCCCT ACCGTTGGTGACGTA CTGGGTAAGTATCACCCGCATGGCGACCGCGCCTGCTATGAAG CCATGGTGCTGATGGCGCAGCCGTTCTCTTACCGTTACCCGCTGGTCGATGGCCAGGG GAACTGGGGCGCGCCGGATGATCCGAAGTCATTTCGCGGCGATGCGTTATACCGAATCC CGCCTGTCCAAATACGCCGAGCTGCTGTTA	262	Ser80Arg
<i>gyrA</i>	<i>gyrA1</i>	MN045284	CGTTGGTGACGTAATCGGTAAATACCATCCCCACGGCGATTCCGCAGTGTATAACACCA TCGTTTCGATGGCGCAGCCATTCTCGCTGCGTTACATGCTGGTGGATGGTCAGGGTAAC TTCGGTTCTATTGACGGCGACTCCGCGGCGGCAATGCGTTATACGGAGATCCGTCTGG	251	Asp87Asn

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

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Note: “-” means no artificial mutation.



**Figure S2.** Genetic stability of *parC*.

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Alignment: parC
      .....| .....| .....| .....| .....| .....| .....| .....| .....| .....| ..
      10      20      30      40      50      60      70      80      90
original  -YAMSELGLN ATAKFIGKSAR TVGDVLGKYH FHGDRACYEA MVLMAQPPFSY RYPLVDGQGN WGAPDDPKSF AMRYTESRL SKYAELL-- --
3th parC  -YAMSELGLN ATAKFIGKSAR TVGDVLGKYH FHGDRACYEA MVLMAQPPFSY RYPLVDGQGN WGAPDDPKSF AMRYTESRL SKYAELL-- --
6th parC  -LCDVWKLGLN ATAKFIGKSAR TVGDVLGKYH FHGDRACYEA MVLMAQPPFSY RYPLVDGQGN WGAPDDPKSF AMRYTESRL SKYAGLLL-- --
9th parC  -LCDVWKLGLN ATAKFIGKSAR TVGDVLGKYH FHGDRACYEA MVLMAQPPFSY RYPLVDGQGN WGAPDDPKSF AMRYTESRL SKYAGLLL-- --
12th parC FYAMSELGLN ATAKFIGKSAR TVGDVLGKYH FHGDRACYEA MVLMAQPPFSY RYPLVDGQGN WGAPDDPKSF AMRYTESRL SKYAELLNS KI
15th parC -YAMSELGLN ATAKFIGKSAR TVGDVLGKYH FHGDRACYEA MVLMAQPPFSY RYPLVDGQGN WGAPDDPKSF AMRYTESRL SKYAEPAVWQ --
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*.**



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 *oqxA*.

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Alignment: oqxA
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
original  ---GACAGC GTCCACAGCA ATGCTGGCCG TCCCGCCCGC ACGGTCAGCG CCGCTAAGGT GCTGGTGAAG TCGATCAGTC AGTGGGATAG TTTTAAACGGT CGCATTGAAG
3th oqxA  ---TGACAGC GTTCCACAGA ATGCTGGCCG TCCCGCCCGC ACGGTCAGCG CCGCTAAGGT GCTGGTGAAG TCGATCAGTC AGTGGGATAG TTTTAAACGGT CGCATTGAAG
6th oqxA  ---TGACAGC GTTCCACAGA ATGCTGGCCG TCCCGCCCGC ACGGTCAGCG CCGCTAAGGT GCTGGTGAAG TCGATCAGTC AGTGGGATAG TTTTAAACGGT CGCATTGAAG
9th oqxA  ---TGACAGC GTTCCACAGA ATGCTGGCCG TCCCGCCCGC ACGGTCAGCG CCGCTAAGGT GCTGGTGAAG TCGATCAGTC AGTGGGATAG TTTTAAACGGT CGCATTGAAG
12th oqxA ---TGACAGC GTTCCACAGA ATGCTGGCCG TCCCGCCCGC ACGGTCAGCG CCGCTAAGGT GCTGGTGAAG TCGATCAGTC AGTGGGATAG TTTTAAACGGT CGCATTGAAG
15th oqxA GTTTGACAGC GTCCACAGCA ATGCTGGCCG TCCCGCCCGC ACGGTCAGCG CCGCTAAGGT GCTGGTGAAG TCGATCAGTC AGTGGGATAG TTTTAAACGGT CGCATTGAAG
Clustal Consensus ***** * * * * * *****

original  CGGTGCAGAG CTTTCAGCTT CCGCCTCGCG TCTCCGGATA CATTGATAAA GTGAATTACA CTGACGCCCA GGAGGTGAAA AAGGGCCAGG TGTCTTTCAC GATAGATGAC
3th oqxA  CGGTGCAGAG CTTTCAGCTT CCGCCTCGCG TCTCCGGATA CATTGATAAA GTGAATTACA CTGACGCCCA GGAGGTGAAA AAGGGCCAGG TGTCTTTCAC GATAGATGAC
6th oqxA  CGGTGCAGAG CTTTCAGCTT CCGCCTCGCG TCTCCGGATA CATTGATAAA GTGAATTACA CTGACGCCCA GGAGGTGAAA AAGGGCCAGG TGTCTTTCAC GATAGATGAC
9th oqxA  CGGTGCAGAG CTTTCAGCTT CCGCCTCGCG TCTCCGGATA CATTGATAAA GTGAATTACA CTGACGCCCA GGAGGTGAAA AAGGGCCAGG TGTCTTTCAC GATAGATGAC
12th oqxA CGGTGCAGAG CTTTCAGCTT CCGCCTCGCG TCTCCGGATA CATTGATAAA GTGAATTACA CTGACGCCCA GGAGGTGAAA AAGGGCCAGG TGTCTTTCAC GATAGATGAC
15th oqxA CGGTGCAGAG CTTTCAGCTT CCGCCTCGCG TCTCCGGATA CATTGATAAA GTGAATTACA CTGACGCCCA GGAGGTGAAA AAGGGCCAGG TGTCTTTCAC GATAGATGAC
Clustal Consensus *****

original  AGAACCTATC CCGCCCGCGT GGAGCAGGGC CAGCCCGCGT TGGCAAGAGC CAAAACCCAG CCCAGCCTCG CCGAAAGCGA GCGGAACCGC ACCGATAAAT TACTCCATAC
3th oqxA  AGAACCTATC CCGCCCGCGT GGAGCAGGGC CAGCCCGCGT TGGCAAGAGC CAAAACCCAG CCCAGCCTCG CCGAAAGCGA GCGGAACCGC ACCGATAAAT TACTCCATAC
6th oqxA  AGAACCTATC CCGCCCGCGT GGAGCAGGGC CAGCCCGCGT TGGCAAGAGC CAAAACCCAG CCCAGCCTCG CCGAAAGCGA GCGGAACCGC ACCGATAAAT TACTCCATAC
9th oqxA  AGAACCTATC CCGCCCGCGT GGAGCAGGGC CAGCCCGCGT TGGCAAGAGC CAAAACCCAG CCCAGCCTCG CCGAAAGCGA GCGGAACCGC ACCGATAAAT TACTCCATAC
12th oqxA AGAACCTATC CCGCCCGCGT GGAGCAGGGC CAGCCCGCGT TGGCAAGAGC CAAAACCCAG CCCAGCCTCG CCGAAAGCGA GCGGAACCGC ACCGATAAAT TACTCCATAC
15th oqxA AGAACCTATC CCGCCCGCGT GGAGCAGGGC CAGCCCGCGT TGGCAAGAGC CAAAACCCAG CCCAGCCTCG CCGAAAGCGA GCGGAACCGC ACCGATAAAT TACTCCATAC
Clustal Consensus *****

original  CAACC--TCG TCTCC-----
3th oqxA  CACCCC--TCG TCTCC-----
6th oqxA  CACCCC--TCG TCTCCCT---
9th oqxA  CACCCC--TCG TCTCCCT---
12th oqxA CACCCC--TCG TCTCCCT---
15th oqxA 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*.

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Alignment: qnrB
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
original      -GGCATTGAA ATTGCCACT GCGCGGCACA AGGCCAGAT TTCCGGGTG CAAGCTTTAT GAATATGATC ACCACGGCGA CCTGGTTTTG CAGCCCATAT ATCACTAATA
3th qnrB      TGGCATTGAA ATTGCCACT GCGCGGCACA AGGCCAGAT TTCCGGGTG CAAGCTTTAT GAATATGATC ACCACGGCGA CCTGGTTTTG CAGCCCATAT ATCACTAATA
6th qnrB      TGGCATTGAA ATTGCCACT GCGCGGCACA AGGCCAGAT TTCCGGGTG CAAGCTTTAT GAATATGATC ACCACGGCGA CCTGGTTTTG CAGCCCATAT ATCACTAATA
9th qnrB      TGGCATTGAA ATTGCCACT GCGCGGCACA AGGCCAGAT TTCCGGGTG CAAGCTTTAT GAATATGATC ACCACGGCGA CCTGGTTTTG CAGCCCATAT ATCACTAATA
12th qnrB     TGGCATTGAA ATTGCCACT GCGCGGCACA AGGCCAGAT TTCCGGGTG CAAGCTTTAT GAATATGATC ACCACGGCGA CCTGGTTTTG CAGCCCATAT ATCACTAATA
15th qnrB     TGGCATTGAA ATTGCCACT GCGCGGCACA AGGCCAGAT TTCCGGGTG CAAGCTTTAT GAATATGATC ACCACGGCGA CCTGGTTTTG CAGCCCATAT ATCACTAATA
Clustal Consensus *****

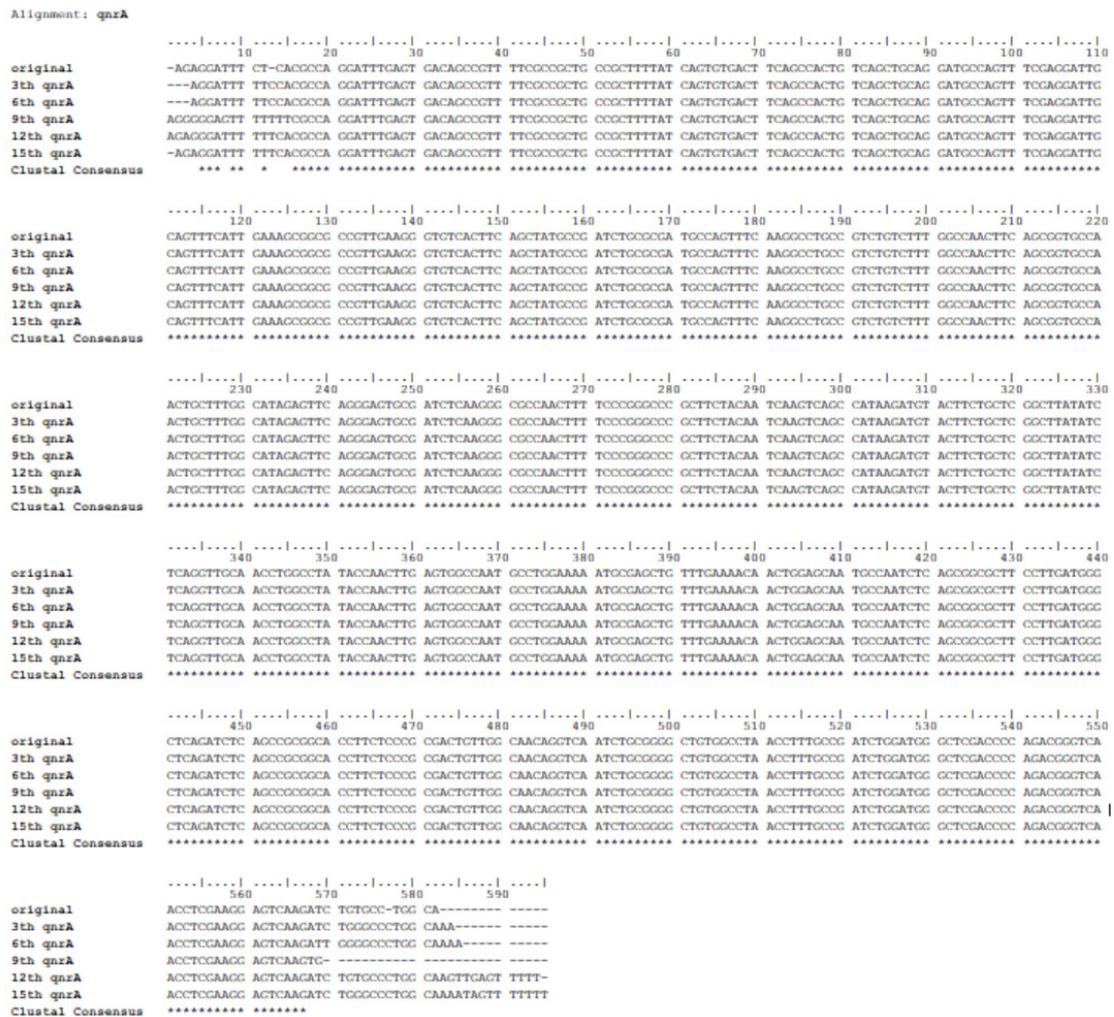
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
original      CTAATCTAAG CTACGCCAAT TTTTCGAAG TCCTCTTGG AAAGTGTGAG CTCCTGGAAA ACCCGTGGAT GGGGACTCAG CTAAGTGGTC CGAGCTTCAG TGGTTCAGAT
3th qnrB      CTAATCTAAG CTACGCCAAT TTTTCGAAG TCCTCTTGG AAAGTGTGAG CTCCTGGAAA ACCCGTGGAT GGGGACTCAG CTAAGTGGTC CGAGCTTCAG TGGTTCAGAT
6th qnrB      CTAATCTAAG CTACGCCAAT TTTTCGAAG TCCTCTTGG AAAGTGTGAG CTCCTGGAAA ACCCGTGGAT GGGGACTCAG CTAAGTGGTC CGAGCTTCAG TGGTTCAGAT
9th qnrB      CTAATCTAAG CTACGCCAAT TTTTCGAAG TCCTCTTGG AAAGTGTGAG CTCCTGGAAA ACCCGTGGAT GGGGACTCAG CTAAGTGGTC CGAGCTTCAG TGGTTCAGAT
12th qnrB     CTAATCTAAG CTACGCCAAT TTTTCGAAG TCCTCTTGG AAAGTGTGAG CTCCTGGAAA ACCCGTGGAT GGGGACTCAG CTAAGTGGTC CGAGCTTCAG TGGTTCAGAT
15th qnrB     CTAATCTAAG CTACGCCAAT TTTTCGAAG TCCTCTTGG AAAGTGTGAG CTCCTGGAAA ACCCGTGGAT GGGGACTCAG CTAAGTGGTC CGAGCTTCAG TGGTTCAGAT
Clustal Consensus *****

-----|-----|-----|-----|
original      CTCCTCCGGCG CCGAGTTTTG GACTTTTCGAC TGGCGAACG CAAAA
3th qnrB      CTCCTCCGGCG CCGAGTTTTG GACTTTTCGAC TGGCGAACG CAAAA
6th qnrB      CTCCTCCGGCG CCGAGTTTTG GACTTTTCGAC TGGCGAACG CAAAA
9th qnrB      CTCCTCCGGCG CCGAGTTTTG GACTTTTCGAC TGGCGAACG CAAAA
12th qnrB     CTCCTCCGGCG CCGAGTTTTG GACTTTTCGAC TGGCGAACG CAAAA
15th qnrB     CTCCTCCGGCG CCGAGTTTTG GACTTTTCGAC TGGCGAACG 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*.



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*.

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

Alignment: gyrA2
      .....| .....| .....| .....| .....| .....| .....| .....| .....| .....|
      10      20      30      40      50      60      70      80
original  -VGDVIGKYH PHGDYAVYDT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVFN YDGT-
3th gyrA2  -VGDVIGKYH PHGDYAVYDT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVFN YDGT-
6th gyrA2  -VGDVIGKYH PHGDYAVYDT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVFN YDGT-
9th gyrA2  -VGDVIGKYH PHGDYAVYDT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVFN YDGT-
12th gyrA2 -VGDVIGKYH PHGDYAVYDT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVFN YDGTG
15th gyrA2 IVGDVIGKYH PHGDYAVYDT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVFN YDGTG
Clustal Consensus  *****

Alignment: gyrA3
      .....| .....| .....| .....| .....| .....| .....| .....| .....| .....|
      10      20      30      40      50      60      70      80
original  -VGDVIGKYH PHGDFAVYDT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVFN YDGT-
3th gyrA3  SLVTVIGKYH PHGDFAVYDT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVFN YDGT-
6th gyrA3  SLVIVIGKYH PHGDFAVYDT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVFN YERYG
9th gyrA3  -VGDVIGKYH PHGDFAVYDT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVFN YDGT-
12th gyrA3 -VGDVIGKYH PHGDFAVYDT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVFN YDGT-
15th gyrA3 SLVSVIGKYH PHGDFAVYDT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVFN YDGT-
Clustal Consensus  : ***** A;

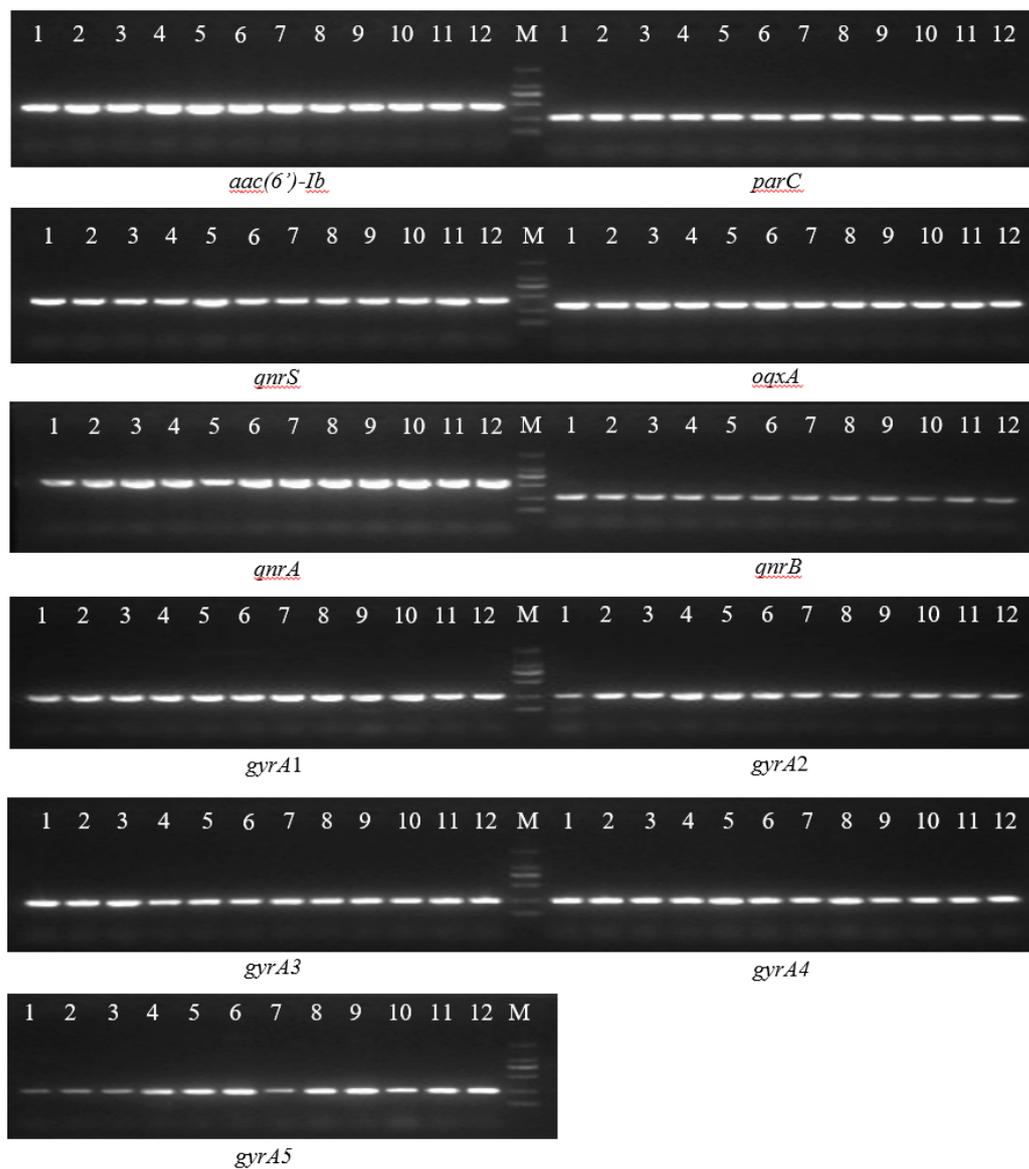
Alignment: gyrA4
      .....| .....| .....| .....| .....| .....| .....| .....| .....| .....|
      10      20      30      40      50      60      70      80
original  -VGDVIGKYH PHGDFAVYGT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVFN YDGT-
3th gyrA4  LVGDVIGKYH PHGDFAVYGT IVRMAQPPSL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

Alignment: gyrA5
      .....| .....| .....| .....| .....| .....| .....| .....| .....| .....|
      10      20      30      40      50      60      70      80
original  -VGDVIGKYH PHGDFAVYAT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVFN YDGT-
3th gyrA5  SLVTVIGKYH PHGDFAVYAT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVFN YDGT-
6th gyrA5  SLVTVIGKYH PHGDFAVYAT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVFN YDGT-
9th gyrA5  -VGDVIGKYH PHGDFAVYAT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVFN YARYG
12th gyrA5 -VGDVIGKYH PHGDFAVYAT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVFN YGRYG
15th gyrA5 -VGDVIGKYH PHGDFAVYAT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVFN YGRYG
Clustal Consensus  : *****

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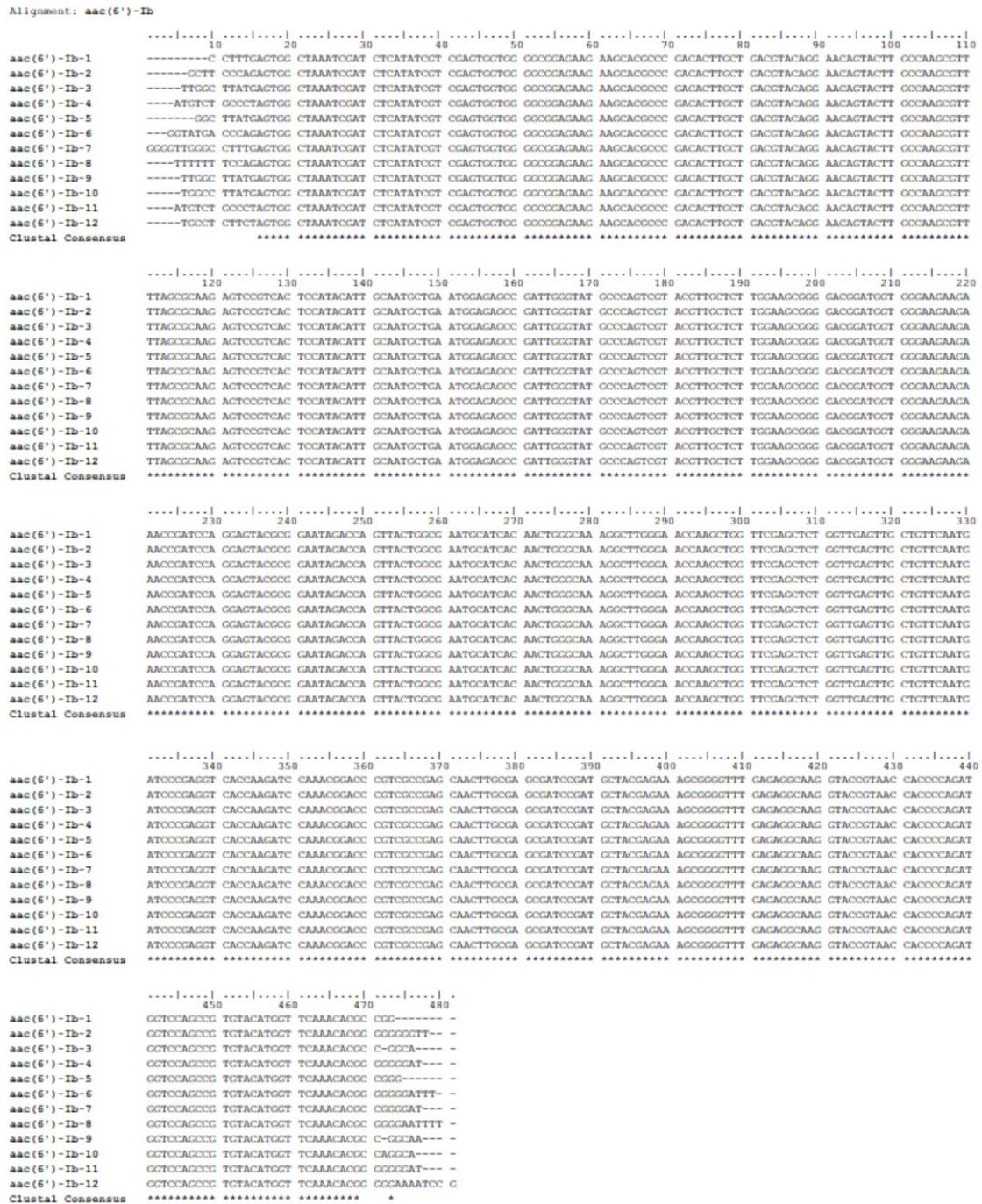
Note: “\*” means no difference in amino acid. Due to the instability of Sanger sequencing, it is common that there are differences in the first and last 10 amino acids.

**Figure 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.

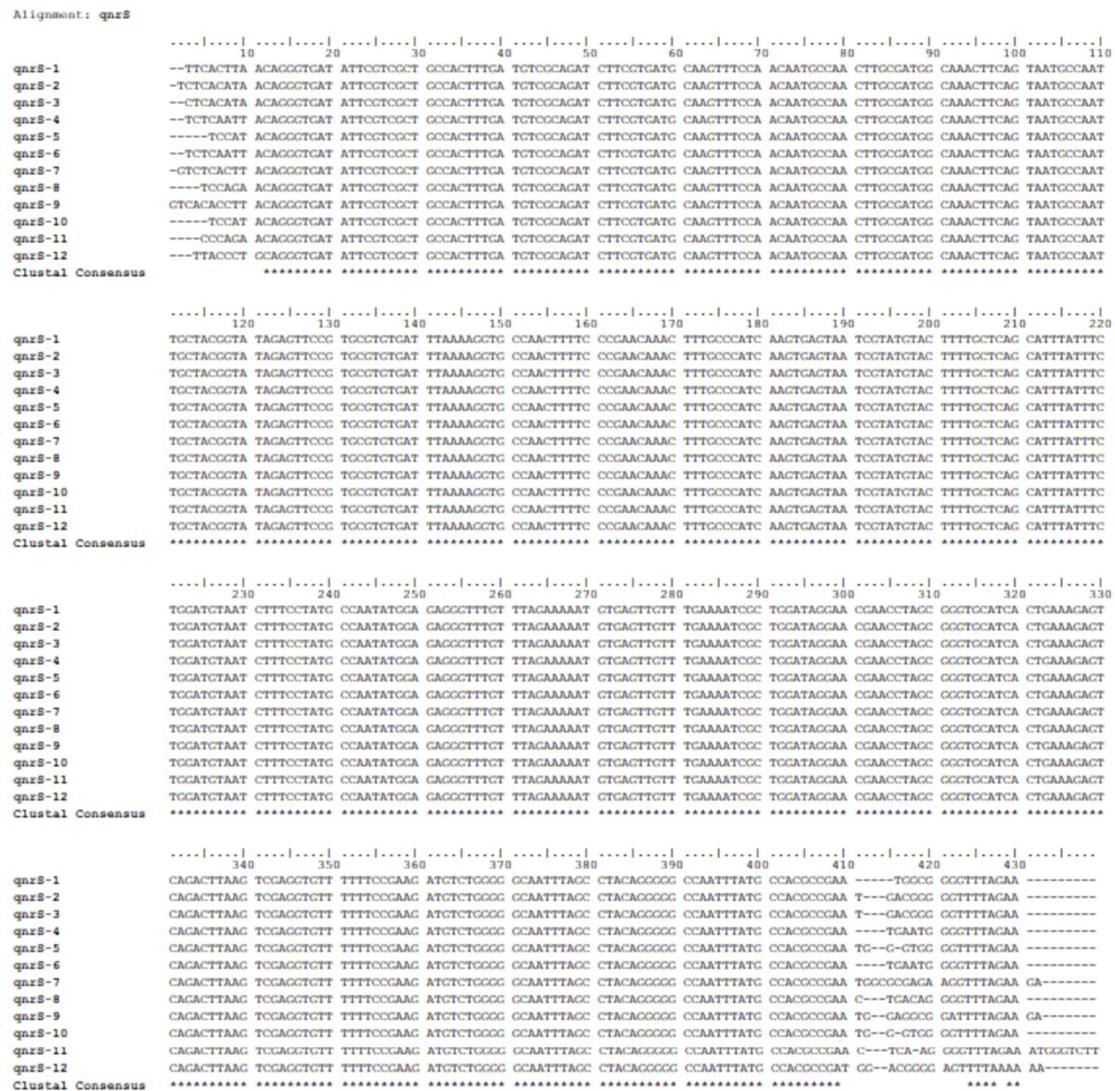
**Figure S10.** Homogeneity of *parC* in plasmid DNA reference materials.

```

Alignment: parC
      .....| .....| .....| .....| .....| .....| .....| .....| .....|
      10      20      30      40      50      60      70      80
parC-1  -YAMSELGLN ATAKFKKSAR TVGDVLGKYH FHGDRACYEA MVLMAQPFYSY RYPLVDGQGN WGAPDDPKSF AAMRYTESRL SKYAEALL-
parC-2  SMR-FELGLN ATAKFKKSAR TVGDVLGKYH FHGDRACYEA MVLMAQPFYSY RYPLVDGQGN WGAPDDPKSF AAMRYTESRL SKYAKSAV-
parC-3  SMRFVKLGLN ATAKFKKSAR TVGDVLGKYH FHGDRACYEA MVLMAQPFYSY RYPLVDGQGN WGAPDDPKSF AAMRYTESRL SKYAGLL-
parC-4  -YAMSELGLN ATAKFKKSAR TVGDVLGKYH FHGDRACYEA MVLMAQPFYSY RYPLVDGQGN WGAPDDPKSF AAMRYTESRL SKYAEAAV-
parC-5  SMRFVKLGLN ATAKFKKSAR TVGDVLGKYH FHGDRACYEA MVLMAQPFYSY RYPLVDGQGN WGAPDDPKSF AAMRYTESRL SKYAGLL-
parC-6  -YAMSELGLN ATAKFKKSAR TVGDVLGKYH FHGDRACYEA MVLMAQPFYSY RYPLVDGQGN WGAPDDPKSF AAMRYTESRL SKYAEPAV-
parC-7  SMRLKVLGLN ATAKFKKSAR TVGDVLGKYH FHGDRACYEA MVLMAQPFYSY RYPLVDGQGN WGAPDDPKSF AAMRYTESRL SKYGGLLF-
parC-8  FYAMVELGLN ATAKFKKSAR TVGDVLGKYH FHGDRACYEA MVLMAQPFYSY RYPLVDGQGN WGAPDDPKSF AAMRYTESRL SKYAGVCC-
parC-9  SMRFVKLGLN ATAKFKKSAR TVGDVLGKYH FHGDRACYEA MVLMAQPFYSY RYPLVDGQGN WGAPDDPKSF AAMRYTESRL SKYAGLL-
parC-10 SMRLVELGLN ATAKFKKSAR TVGDVLGKYH FHGDRACYEA MVLMAQPFYSY RYPLVDGQGN WGAPDDPKSF AAMRYTESRL SKYAGPAV-
parC-11 -YAMSELGLN ATAKFKKSAR TVGDVLGKYH FHGDRACYEA MVLMAQPFYSY RYPLVDGQGN WGAPDDPKSF AAMRYTESRL SKYAEALL-
parC-12 SMRFVKLGLN ATAKFKKSAR TVGDVLGKYH FHGDRACYEA MVLMAQPFYSY RYPLVDGQGN WGAPDDPKSF AAMRYTESRL SKYAGLL-
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 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.

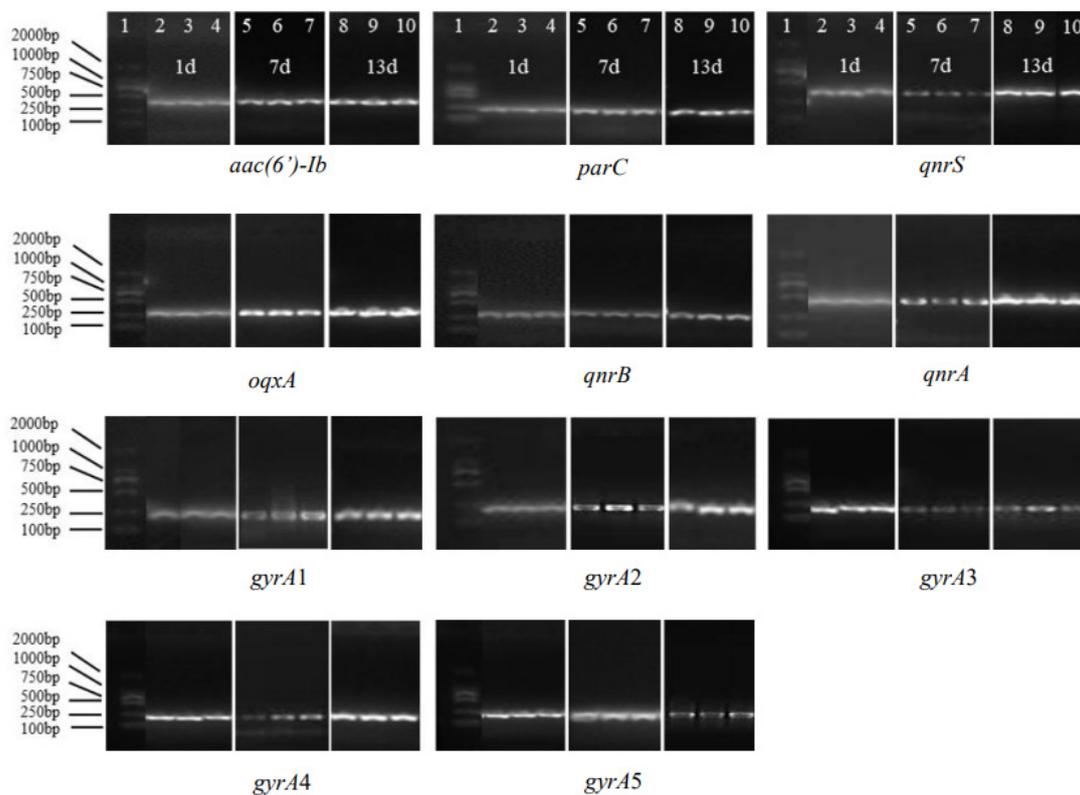








**Figure S16.** PCR results for storage stability of plasmid DNA references materials stored at 37°C.



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 1<sup>st</sup>, 7<sup>th</sup>, and 13<sup>th</sup> 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 TCCTCGAGTG GTGGGGCGGA GAAGAAGCAC GCCCGACACT TGCTGACGTA CAGGAACACT ACTTGGCAAG
37-7d  TTGGCGTTT GCTTCCGAGA GTGGCTAAAT CGATCTCATA TCCTCGAGTG GTGGGGCGGA GAAGAAGCAC GCCCGACACT TGCTGACGTA CAGGAACACT ACTTGGCAAG
37-13d TTGGGATTT TCC-CCCAGA GTGGCTAAAT CGATCTCATA TCCTCGAGTG GTGGGGCGGA GAAGAAGCAC GCCCGACACT TGCTGACGTA CAGGAACACT ACTTGGCAAG
Clustal Consensus ***** * * * * *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
      120     130     140     150     160     170     180     190     200     210     220
37-1d  COTTTTAGCG CAAGAGTCCG TCACCTCCATA CATTGCAATG CTGAATGGAG AGCCGATTGG GTATGCCCCAG TCGTACGTTG CTCTTGGGAG CCGGGACCGA TGGTGGGAG
37-7d  COTTTTAGCG CAAGAGTCCG TCACCTCCATA CATTGCAATG CTGAATGGAG AGCCGATTGG GTATGCCCCAG TCGTACGTTG CTCTTGGGAG CCGGGACCGA TGGTGGGAG
37-13d COTTTTAGCG CAAGAGTCCG TCACCTCCATA CATTGCAATG CTGAATGGAG AGCCGATTGG GTATGCCCCAG TCGTACGTTG CTCTTGGGAG CCGGGACCGA TGGTGGGAG
Clustal Consensus *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
      230     240     250     260     270     280     290     300     310     320     330
37-1d  AGAAACCGA TCCAGGACTA CCGCGAATAG ACCAGTTACT GCGCAATGCA TCACAACCTGG CCAAAGGCTT GCGAACCAG CTGCTTCGAG CTCTGCTTGA GTTCTGTTC
37-7d  AGAAACCGA TCCAGGACTA CCGCGAATAG ACCAGTTACT GCGCAATGCA TCACAACCTGG CCAAAGGCTT GCGAACCAG CTGCTTCGAG CTCTGCTTGA GTTCTGTTC
37-13d AGAAACCGA TCCAGGACTA CCGCGAATAG ACCAGTTACT GCGCAATGCA TCACAACCTGG CCAAAGGCTT GCGAACCAG CTGCTTCGAG CTCTGCTTGA GTTCTGTTC
Clustal Consensus *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
      340     350     360     370     380     390     400     410     420     430     440
37-1d  AATGATCCCG AGGTCACCAA GATCCAAACG GACCCGTCGG CGAGCAACTT GCGAGCGGATC CGATGCTACC AGAAAGCGGG GTTTGAGAGG CAAGGTACCG TAACCACCCC
37-7d  AATGATCCCG AGGTCACCAA GATCCAAACG GACCCGTCGG CGAGCAACTT GCGAGCGGATC CGATGCTACC AGAAAGCGGG GTTTGAGAGG CAAGGTACCG TAACCACCCC
37-13d AATGATCCCG AGGTCACCAA GATCCAAACG GACCCGTCGG CGAGCAACTT GCGAGCGGATC CGATGCTACC AGAAAGCGGG GTTTGAGAGG CAAGGTACCG TAACCACCCC
Clustal Consensus *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
      450     460     470     480     490
37-1d  AGATGCTCCA GCCCTGTACA TGGTTCAAAC ACGGGGCGCA TTC---GAG ---
37-7d  AGATGCTCCA GCCCTGTACA TGGTTCAAAC ACGGGGCGGG TTTTCTGAG GAA
37-13d AGATGCTCCA GCCCTGTACA TGGTTCAAAC ACGGGGTGAA TTTT-CGGAG 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 ATAKFKGSAR TVGDVLGKYH FHGDRACYEA M/MLAQPFPSY RYPLVDGQGN WGAPDDPKSF AAMRYTESRL SKYAELL-
37-7d    SMRFVKLGLN ATAKFKGSAR TVGDVLGKYH FHGDRACYEA M/MLAQPFPSY RYPLVDGQGN WGAPDDPKSF AAMRYTESRL SKYAGLL-
37-13d   SMRFVELGLN ATAKFKGSAR TVGDVLGKYH FHGDRACYEA M/MLAQPFPSY 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 CTGATATTGC TCGCTGCCAC TTTGATGTCG CAGATCTTCG TGATGCCAAGT TTCCAAACAAT GCCAACTTGC GATGGCAAAC TTCAGTAATG
37-7d  TCGAAGTTTT TCCATACAGG CTGATATTGC TCGCTGCCAC TTTGATGTCG CAGATCTTCG TGATGCCAAGT TTCCAAACAAT GCCAACTTGC GATGGCAAAC TTCAGTAATG
37-13d -----ACAGG CTGATATTGC TCGCTGCCAC TTTGATGTCG CAGATCTTCG TGATGCCAAGT TTCCAAACAAT GCCAACTTGC GATGGCAAAC TTCAGTAATG
Clustal Consensus
      *****

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
      120     130     140     150     160     170     180     190     200     210     220
37-1d  CCAATTGCTA CGGTATAGAG TTCCTGCGGT GTGATTTAAA AGTGCACAAC TTTTCCCGAA CAAACTTTGC CCATCAAGTG AGTAATCGTA TGTACTTTTG CTCAGCATTT
37-7d  CCAATTGCTA CGGTATAGAG TTCCTGCGGT GTGATTTAAA AGTGCACAAC TTTTCCCGAA CAAACTTTGC CCATCAAGTG AGTAATCGTA TGTACTTTTG CTCAGCATTT
37-13d CCAATTGCTA CGGTATAGAG TTCCTGCGGT GTGATTTAAA AGTGCACAAC TTTTCCCGAA CAAACTTTGC CCATCAAGTG AGTAATCGTA TGTACTTTTG CTCAGCATTT
Clustal Consensus
      *****

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
      230     240     250     260     270     280     290     300     310     320     330
37-1d  ATTTCTGGAT CTAATCTTTC CTATGCCAAT ATGGAGAGGC TTTGTTTAGA AAAATCTGAG TTGTTTGAAA ATGCTCGGAT AGGAACGAAC CTAGCGGCTG CATCACTGAA
37-7d  ATTTCTGGAT CTAATCTTTC CTATGCCAAT ATGGAGAGGC TTTGTTTAGA AAAATCTGAG TTGTTTGAAA ATGCTCGGAT AGGAACGAAC CTAGCGGCTG CATCACTGAA
37-13d ATTTCTGGAT CTAATCTTTC CTATGCCAAT ATGGAGAGGC TTTGTTTAGA AAAATCTGAG TTGTTTGAAA ATGCTCGGAT AGGAACGAAC CTAGCGGCTG CATCACTGAA
Clustal Consensus
      *****

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
      340     350     360     370     380     390     400     410     420     430
37-1d  AGAGTCAGAC TTAAGTCGAG GTGTTTTTTC CGAAGATGTC TGGGGCCAAT TTAGCCTACA GGGGGCCAAT TTATGCCACG CCGAACTCGA CGGTTTACA ---
37-7d  AGAGTCAGAC TTAAGTCGAG GTGTTTTTTC CGAAGATGTC TGGGGCCAAT TTAGCCTACA GGGGGCCAAT TTATGCCACG CCGAA-TGGG TGGGGTTTTA GAA
37-13d AGAGTCAGAC TTAAGTCGAG GTGTTTTTTC CGAAGATGTC TGGGGCCAAT TTAGCCTACA GGGGGCCAAT TTATGCCACG CCGAA-TGGA -GACGTT---
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.

```

Alignment: qnrB
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
37-1d   10 20 30 40 50 60 70 80 90 100 110
37-7d   --GGCATTC AAAT-TGGCC ACTGCCGGC ACAAGCGCGA GATTTCCGGC CTCGAAGCTT TATCAATATC ATCACCAGCC GCACCTGGTT TTGCAGCGCA TATATCACTA
37-13d  TCGGCATTC AAAT-TGGCC ACTGCCGGC ACAAGCGCGA GATTTCCGGC CTCGAAGCTT TATCAATATC ATCACCAGCC GCACCTGGTT TTGCAGCGCA TATATCACTA
Clustal Consensus ***** * * * * *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
37-1d   120 130 140 150 160 170 180 190 200 210 220
37-7d   ATACTAATCT AAGCTAGCC AATTTTTCGA AACTCGTGT GGAAAAGTCT GAGCTGTGG AAAACCGCTG GATGGGGACT CAGCTACTGG CTCGCACGTT CAGTGGTTCA
37-13d  ATACTAATCT AAGCTAGCC AATTTTTCGA AACTCGTGT GGAAAAGTCT GAGCTGTGG AAAACCGCTG GATGGGGACT CAGCTACTGG CTCGCACGTT CAGTGGTTCA
Clustal Consensus *****

-----|-----|-----|-----|-----|
37-1d   230 240 250 260
37-7d   GATCTCTCC GCGCGAGTT TTCGACTTC GACTGCC-A GCAGCAAA-
37-13d  GATCTCTCC GCGCGAGTT TTCGACTTC GACTGCCGA ACAGCAAAA
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 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 TCTCAGCCCA GGATTTGACT GACAGCCGTT TTCCGCGCTG CC-GCTTTTA TCAGTGTGAC TTCAGCCACT GTCAGTCCA GGATGCCACT TTCGAGGATT
37-7d  -GGAGGTTT TTTTCCCCA GGATTTGACT GACAGCCGTT TTCCGCGCTG CC-GCTTTTA TCAGTGTGAC TTCAGCCACT GTCAGTCCA GGATGCCACT TTCGAGGATT
37-13d AGAGAGGGT TTTTATCCA GGATTTGACT GACAGCCGTT TTCCGCGCTG CCGCTTTTA TCAGTGTGAC TTCAGCCACT GTCAGTCCA GGATGCCACT TTCGAGGATT
Clustal Consensus ***** * * * * * *****

      |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
      120     130     140     150     160     170     180     190     200     210     220
37-1d  GCAGTTTCAT TCAAAGCGGC GCGCTTGAAG GGTGTCACTT CAGCTATGCC GATCTGGCGG ATGCCAGTTT CAAGGCCCTG CCTCTGTCTT TGGCCAACCT CAGCGGTGCC
37-7d  GCAGTTTCAT TCAAAGCGGC GCGCTTGAAG GGTGTCACTT CAGCTATGCC GATCTGGCGG ATGCCAGTTT CAAGGCCCTG CCTCTGTCTT TGGCCAACCT CAGCGGTGCC
37-13d GCAGTTTCAT TCAAAGCGGC GCGCTTGAAG GGTGTCACTT CAGCTATGCC GATCTGGCGG ATGCCAGTTT CAAGGCCCTG CCTCTGTCTT TGGCCAACCT CAGCGGTGCC
Clustal Consensus ***** ***** ***** ***** ***** ***** ***** ***** ***** *****

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

      |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
      340     350     360     370     380     390     400     410     420     430     440
37-1d  CTCAGGTTGC AACCTGGCCT ATACCAACTT GAGTGGCCAA TGCTGGAAA AATCCGAGCT GTTTGAAAC AACCTGGAGCA ATGCCAATCT CAGCGGCCTC TCCTTGATGG
37-7d  CTCAGGTTGC AACCTGGCCT ATACCAACTT GAGTGGCCAA TGCTGGAAA AATCCGAGCT GTTTGAAAC AACCTGGAGCA ATGCCAATCT CAGCGGCCTC TCCTTGATGG
37-13d CTCAGGTTGC AACCTGGCCT ATACCAACTT GAGTGGCCAA TGCTGGAAA AATCCGAGCT GTTTGAAAC AACCTGGAGCA ATGCCAATCT CAGCGGCCTC TCCTTGATGG
Clustal Consensus ***** ***** ***** ***** ***** ***** ***** ***** ***** *****

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

      |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
      560     570     580
37-1d  AACCTCGAAG GAGTCAAGAT CTGTGCGTGG CA
37-7d  AACCTCGAAG GAGTCAAG-T GGGGGCGGCC CG
37-13d AACCTCGAAG GAGTCATGAT GCTGCGCGCC 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.

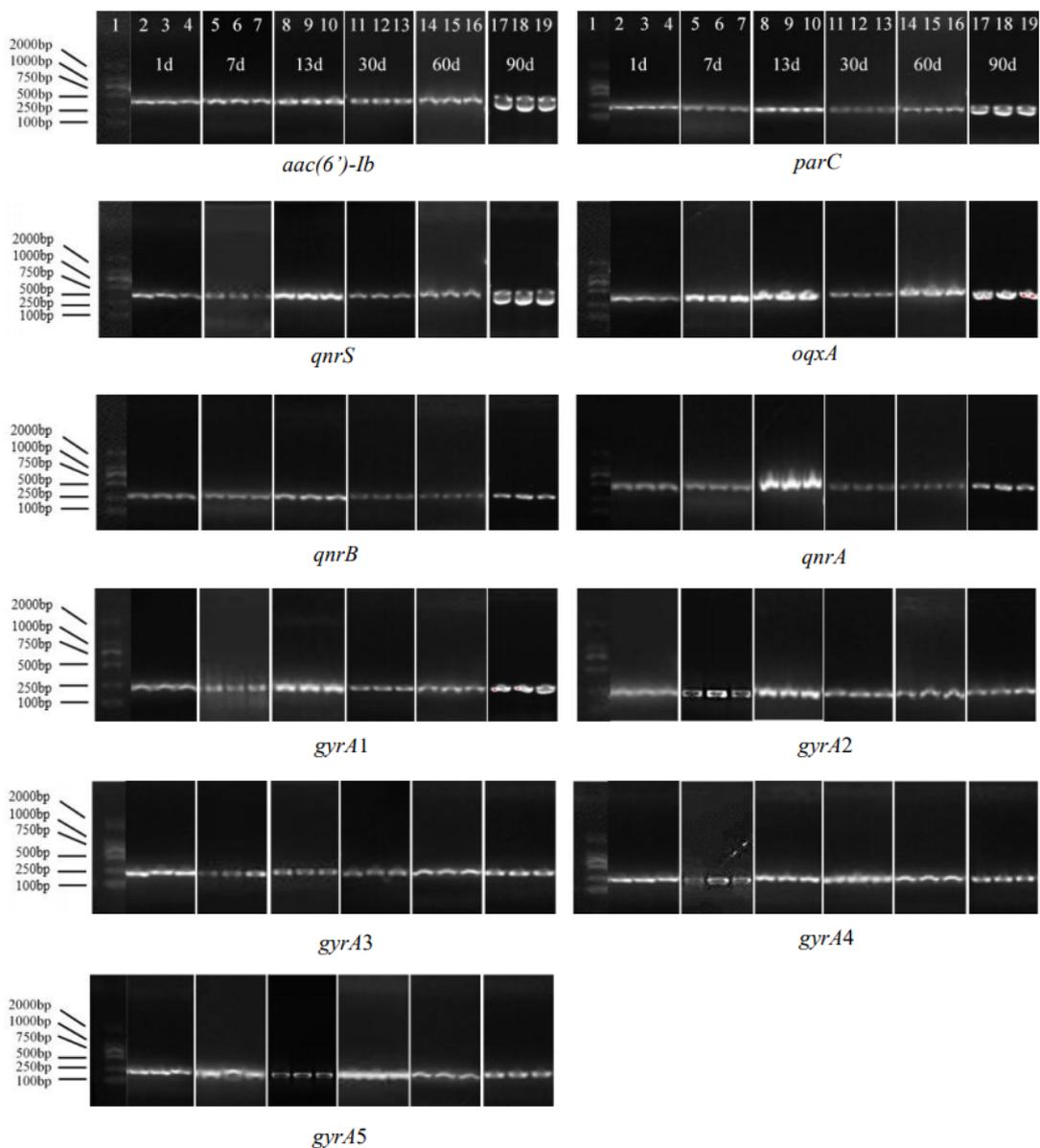
```

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 HGDYAVYDTI VRMAQPFSLR YMLVDGQGNF GSIDGDSAAA MRYTEIRLAK IAHELMADLE KETVDFVDNY DGT
37-7d  VADRFPGKYHP HGDYAVYDTI VRMAQPFSLR YMLVDGQGNF GSIDGDSAAA MRYTEIRLAK IAHELMADLE KETVDFVDNW DGT
37-13d VGDGIGKYHP HGDYAVYDTI 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 EKETVDFVDN YDGT-
37-7d  LVGDRPGKYH PHGDFAVYGT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK CARYG
37-13d -W-FVIGKYH PHGDFAVYGT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK WERYG
Clustal Consensus :****
Alignment: gyrA5
      .....| .....| .....| .....| .....| .....| .....| .....| .....| .....| .....
      10      20      30      40      50      60      70      80
37-1d  -VGDVIGKYH PHGDFAVYAT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT
37-7d  SLVNGPGKYH PHGDFAVYAT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK LDGT
37-13d -VGDVIGKYH PHGDFAVYAT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN 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 1<sup>st</sup>, 7<sup>th</sup>, 13<sup>th</sup>, 30<sup>th</sup>, 60<sup>th</sup>, and 90<sup>th</sup> 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 S26.** Sequencing results of *parC* for stability of plasmid DNA references materials stored at 4°C.

```

Alignment: parC
      .....| .....| .....| .....| .....| .....| .....| .....| .....| .....| .....| .....|
      10      20      30      40      50      60      70      80
4-1d  -YAMSELGLN ATAKFKKSAR TVGDVLGKYH PHGDRACYEA MVLMAQPPSY RYPLVDGQGN WGAPDDPKSF AAMRYTESRL SKYAELLL-
4-7d  -YAICELGLN ATAKFKKSAR TVGDVLGKYH PHGDRACYEA MVLMAQPPSY RYPLVDGQGN WGAPDDPKSF AAMRYTESRL SKYAGCCS-
4-13d SMRFVELGLN ATAKFKKSAR TVGDVLGKYH PHGDRACYEA MVLMAQPPSY RYPLVDGQGN WGAPDDPKSF AAMRYTESRL SKYAVICCL
4-30d SMRFVELGLN ATAKFKKSAR TVGDVLGKYH PHGDRACYEA MVLMAQPPSY RYPLVDGQGN WGAPDDPKSF AAMRYTESRL SKYAGLLL-
4-60d FYAMVELGLN ATAKFKKSAR TVGDVLGKYH PHGDRACYEA MVLMAQPPSY RYPLVDGQGN WGAPDDPKSF AAMRYTESRL SKYAGVCCL
4-90d SMRFVELGLN ATAKFKKSAR TVGDVLGKYH PHGDRACYEA MVLMAQPPSY RYPLVDGQGN WGAPDDPKSF AAMRYTESRL SKYAGLLL-
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 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  --GCAAGT  CATTGAACAG  GGTGATATTC  GTCGCTGCCA  CTTTGATGTC  GCAGATCTTC  GTGATGCAAG  TTTCACACAA  TGCCAACTTG  CGATGGCAAA  CTTCAGTAAT
4-7d  GATGCAAGT  TCTCAACAG  GGTGATATTC  GTCGCTGCCA  CTTTGATGTC  GCAGATCTTC  GTGATGCAAG  TTTCACACAA  TGCCAACTTG  CGATGGCAAA  CTTCAGTAAT
4-13d -GTGCGACT  TGTTTGCAG  GGTGATATTC  GTCGCTGCCA  CTTTGATGTC  GCAGATCTTC  GTGATGCAAG  TTTCACACAA  TGCCAACTTG  CGATGGCAAA  CTTCAGTAAT
4-30d --TGCAAGT  T-TCCACAG  GGTGATATTC  GTCGCTGCCA  CTTTGATGTC  GCAGATCTTC  GTGATGCAAG  TTTCACACAA  TGCCAACTTG  CGATGGCAAA  CTTCAGTAAT
4-60d TGTCAAAT  T-TCCCTCAG  GGTGATATTC  GTCGCTGCCA  CTTTGATGTC  GCAGATCTTC  GTGATGCAAG  TTTCACACAA  TGCCAACTTG  CGATGGCAAA  CTTCAGTAAT
4-90d -CTGCAAG  TCTCACACAG  GGTGATATTC  GTCGCTGCCA  CTTTGATGTC  GCAGATCTTC  GTGATGCAAG  TTTCACACAA  TGCCAACTTG  CGATGGCAAA  CTTCAGTAAT
Clustal Consensus  **      *      ***      *****      *****      *****      *****      *****      *****      *****      *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
      120     130     140     150     160     170     180     190     200     210     220
4-1d  GCGAATGCT  ACGGTATAGA  GTTCCCTGGC  TGTGATTAA  AAGGTGCCAA  CTTTTCCCGA  ACAAACCTTG  CCCATCAAGT  GAGTAATCGT  ATGTACTTTT  GCTCAGCATT
4-7d  GCGAATGCT  ACGGTATAGA  GTTCCCTGGC  TGTGATTAA  AAGGTGCCAA  CTTTTCCCGA  ACAAACCTTG  CCCATCAAGT  GAGTAATCGT  ATGTACTTTT  GCTCAGCATT
4-13d GCGAATGCT  ACGGTATAGA  GTTCCCTGGC  TGTGATTAA  AAGGTGCCAA  CTTTTCCCGA  ACAAACCTTG  CCCATCAAGT  GAGTAATCGT  ATGTACTTTT  GCTCAGCATT
4-30d GCGAATGCT  ACGGTATAGA  GTTCCCTGGC  TGTGATTAA  AAGGTGCCAA  CTTTTCCCGA  ACAAACCTTG  CCCATCAAGT  GAGTAATCGT  ATGTACTTTT  GCTCAGCATT
4-60d GCGAATGCT  ACGGTATAGA  GTTCCCTGGC  TGTGATTAA  AAGGTGCCAA  CTTTTCCCGA  ACAAACCTTG  CCCATCAAGT  GAGTAATCGT  ATGTACTTTT  GCTCAGCATT
4-90d GCGAATGCT  ACGGTATAGA  GTTCCCTGGC  TGTGATTAA  AAGGTGCCAA  CTTTTCCCGA  ACAAACCTTG  CCCATCAAGT  GAGTAATCGT  ATGTACTTTT  GCTCAGCATT
Clustal Consensus  *****      *****      *****      *****      *****      *****      *****      *****      *****      *****      *****

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

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
      340     350     360     370     380     390     400     410     420     430
4-1d  AAGACTCAGA  CTTAAGTCGA  GGTCTTTTTT  CCGAAGATGT  CTGGGGCCAA  TTTAGCCTAC  AGGGGGCCAA  TTTATGCCAC  GCGCAATGGA  --TGGGTTTT  AGAA--
4-7d  AAGACTCAGA  CTTAAGTCGA  GGTCTTTTTT  CCGAAGATGT  CTGGGGCCAA  TTTAGCCTAC  AGGGGGCCAA  TTTATGCCAC  GCGCAATGGA  --TGGGTTTT  AGAA--
4-13d AAGACTCAGA  CTTAAGTCGA  GGTCTTTTTT  CCGAAGATGT  CTGGGGCCAA  TTTAGCCTAC  AGGGGGCCAA  TTTATGCCAC  GCGCAATGGA  --TGGGTTTT  AGAA--
4-30d AAGACTCAGA  CTTAAGTCGA  GGTCTTTTTT  CCGAAGATGT  CTGGGGCCAA  TTTAGCCTAC  AGGGGGCCAA  TTTATGCCAC  GCGCAATGGA  --TGGGTTTT  AGAA--
4-60d AAGACTCAGA  CTTAAGTCGA  GGTCTTTTTT  CCGAAGATGT  CTGGGGCCAA  TTTAGCCTAC  AGGGGGCCAA  TTTATGCCAC  GCGCAATGGA  --TGGGTTTT  AGAA--
4-90d AAGACTCAGA  CTTAAGTCGA  GGTCTTTTTT  CCGAAGATGT  CTGGGGCCAA  TTTAGCCTAC  AGGGGGCCAA  TTTATGCCAC  GCGCAATGGA  --TGGGTTTT  AGAA--
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 *oqxA* for stability of plasmid DNA references materials stored at 4°C.

```

Alignment: oqxA
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
      10      20      30      40      50      60      70      80      90     100     110
4-1d  ---GACAGCG -TCCACAGA ATGCTGGCC TCCCGCCCG ACGGTCAGCG CCGCTAAGCT GCTGGTGAAG TCGATCAGTC AGTGGGATAG TTTTAACGCT CGCATTGAAG
4-7d  CCAGACAGCT GTCCCCAGA ATGCTGGCC TCCCGCCCG ACGGTCAGCG CCGCTAAGCT GCTGGTGAAG TCGATCAGTC AGTGGGATAG TTTTAACGCT CGCATTGAAG
4-13d -CAGACAGCG -TTGTCCAGA ATGCTGGCC TCCCGCCCG ACGGTCAGCG CCGCTAAGCT GCTGGTGAAG TCGATCAGTC AGTGGGATAG TTTTAACGCT CGCATTGAAG
4-30d -----T CGCACCCCAA ATGCTGGCC TCCCGCCCG ACGGTCAGCG CCGCTAAGCT GCTGGTGAAG TCGATCAGTC AGTGGGATAG TTTTAACGCT CGCATTGAAG
4-60d -AGAACAGCG CTTGCCCCAA ATGCTGGCC TCCCGCCCG ACGGTCAGCG CCGCTAAGCT GCTGGTGAAG TCGATCAGTC AGTGGGATAG TTTTAACGCT CGCATTGAAG
4-90d -TGACAGCG  TTTGGCCACA ATGCTGGCC TCCCGCCCG ACGGTCAGCG CCGCTAAGCT GCTGGTGAAG TCGATCAGTC AGTGGGATAG TTTTAACGCT CGCATTGAAG
Clustal Consensus
          * *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
      120     130     140     150     160     170     180     190     200     210     220
4-1d  CGGTGGAGAG CTTTCAGCTT CGCCCTCGCG TCTCGGGATA CATTGATAAA GTGAATTACA CTGACGGCCA GGAGCTGAAA AAGGCCAGG TGCTGTTTAC GATAGATGAC
4-7d  CGGTGGAGAG CTTTCAGCTT CGCCCTCGCG TCTCGGGATA CATTGATAAA GTGAATTACA CTGACGGCCA GGAGCTGAAA AAGGCCAGG TGCTGTTTAC GATAGATGAC
4-13d CGGTGGAGAG CTTTCAGCTT CGCCCTCGCG TCTCGGGATA CATTGATAAA GTGAATTACA CTGACGGCCA GGAGCTGAAA AAGGCCAGG TGCTGTTTAC GATAGATGAC
4-30d CGGTGGAGAG CTTTCAGCTT CGCCCTCGCG TCTCGGGATA CATTGATAAA GTGAATTACA CTGACGGCCA GGAGCTGAAA AAGGCCAGG TGCTGTTTAC GATAGATGAC
4-60d CGGTGGAGAG CTTTCAGCTT CGCCCTCGCG TCTCGGGATA CATTGATAAA GTGAATTACA CTGACGGCCA GGAGCTGAAA AAGGCCAGG TGCTGTTTAC GATAGATGAC
4-90d CGGTGGAGAG CTTTCAGCTT CGCCCTCGCG TCTCGGGATA CATTGATAAA GTGAATTACA CTGACGGCCA GGAGCTGAAA AAGGCCAGG TGCTGTTTAC GATAGATGAC
Clustal Consensus
          *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
      230     240     250     260     270     280     290     300     310     320     330
4-1d  AGAACCTATC CCCCCCGCT GGAGCAGCG CAGCCCGCT TGGCAAGAG CAAACCCAG GCCAGCTCG GCCAAAGCCA GCGCAACCG ACCGATAAAT TAGTCCATAC
4-7d  AGAACCTATC CCCCCCGCT GGAGCAGCG CAGCCCGCT TGGCAAGAG CAAACCCAG GCCAGCTCG GCCAAAGCCA GCGCAACCG ACCGATAAAT TAGTCCATAC
4-13d AGAACCTATC CCCCCCGCT GGAGCAGCG CAGCCCGCT TGGCAAGAG CAAACCCAG GCCAGCTCG GCCAAAGCCA GCGCAACCG ACCGATAAAT TAGTCCATAC
4-30d AGAACCTATC CCCCCCGCT GGAGCAGCG CAGCCCGCT TGGCAAGAG CAAACCCAG GCCAGCTCG GCCAAAGCCA GCGCAACCG ACCGATAAAT TAGTCCATAC
4-60d AGAACCTATC CCCCCCGCT GGAGCAGCG CAGCCCGCT TGGCAAGAG CAAACCCAG GCCAGCTCG GCCAAAGCCA GCGCAACCG ACCGATAAAT TAGTCCATAC
4-90d AGAACCTATC CCCCCCGCT GGAGCAGCG CAGCCCGCT TGGCAAGAG CAAACCCAG GCCAGCTCG GCCAAAGCCA GCGCAACCG ACCGATAAAT TAGTCCATAC
Clustal Consensus
          *****

-----|-----|
      340
4-1d  CAACTC--- GTCTCC--
4-7d  CCCC-TCTC GTCTCTGA
4-13d C-----
4-30d CGCT-TC--
4-60d CCCCCCTCC GTCTCAAA
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-TTCGGC ACTGCGCGGC ACAAGGGCGA GATTTCCGGG CTGCAAGCTT TATGAATATC ATCACCACGC GCACCTGGTT TTGCAGCGCA TATATCACTA
4-7d   AGAGGCATTG AAA-ATCGGC ACTGCGCGGC ACAAGGGCGA GATTTCCGGG CTGCAAGCTT TATGAATATC ATCACCACGC GCACCTGGTT TTGCAGCGCA TATATCACTA
4-13d  --AGGCATTG AAAATATCGGC ACTGCGCGGC ACAAGGGCGA GATTTCCGGG CTGCAAGCTT TATGAATATC ATCACCACGC GCACCTGGTT TTGCAGCGCA TATATCACTA
4-30d  -TGGCATTG AAA-TTCGGC ACTGCGCGGC ACAAGGGCGA GATTTCCGGG CTGCAAGCTT TATGAATATC ATCACCACGC GCACCTGGTT TTGCAGCGCA TATATCACTA
4-60d  -TAGGCATTG AAAAATTCGGC ACTGCGCGGC ACAAGGGCGA GATTTCCGGG CTGCAAGCTT TATGAATATC ATCACCACGC GCACCTGGTT TTGCAGCGCA TATATCACTA
4-90d  --GGCATTG AAAAATTCGGC ACTGCGCGGC ACAAGGGCGA GATTTCCGGG CTGCAAGCTT TATGAATATC ATCACCACGC GCACCTGGTT TTGCAGCGCA TATATCACTA
Clustal Consensus ***** ** * ***** ***** ***** ***** ***** ***** ***** ***** *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
      120     130     140     150     160     170     180     190     200     210     220
4-1d   ATACTAATCT AAGCTACGCC AATTTTTCGA AACTCTCTGT GGAAAAGTGT GAGCTGTGG AAAACCGCTG GATGGGGACT CAGTACTGG GTCCGACCTT CAGTGGTTCA
4-7d   ATACTAATCT AAGCTACGCC AATTTTTCGA AACTCTCTGT GGAAAAGTGT GAGCTGTGG AAAACCGCTG GATGGGGACT CAGTACTGG GTCCGACCTT CAGTGGTTCA
4-13d  ATACTAATCT AAGCTACGCC AATTTTTCGA AACTCTCTGT GGAAAAGTGT GAGCTGTGG AAAACCGCTG GATGGGGACT CAGTACTGG GTCCGACCTT CAGTGGTTCA
4-30d  ATACTAATCT AAGCTACGCC AATTTTTCGA AACTCTCTGT GGAAAAGTGT GAGCTGTGG AAAACCGCTG GATGGGGACT CAGTACTGG GTCCGACCTT CAGTGGTTCA
4-60d  ATACTAATCT AAGCTACGCC AATTTTTCGA AACTCTCTGT GGAAAAGTGT GAGCTGTGG AAAACCGCTG GATGGGGACT CAGTACTGG GTCCGACCTT CAGTGGTTCA
4-90d  ATACTAATCT AAGCTACGCC AATTTTTCGA AACTCTCTGT GGAAAAGTGT GAGCTGTGG AAAACCGCTG GATGGGGACT CAGTACTGG GTCCGACCTT CAGTGGTTCA
Clustal Consensus ***** ***** ***** ***** ***** ***** ***** ***** ***** ***** *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
      230     240     250     260     270
4-1d   GATCTCTCCG GCGGGCAGTT TTGCAGTTTC GACTGGCG-A GCAGCAAAA-
4-7d   GATCTCTCCG GCGGGCAGTT TTGCAGTTTC GACTGGCG-A GCAGCAAAA-
4-13d  GATCTCTCCG GCGGGCAGTT TTGCAGTTTC GA-TGGCGGA ACAGCAAAA-
4-30d  GATCTCTCCG GCGGGCAGTT TTGCAGTTTC GACTGGCGGA ACAGCAAAA-
4-60d  GATCTCTCCG GCGGGCAGTT TTGCAGTTTC GA-TGGCGGA ACAGCAAAA-
4-90d  GATCTCTCCG GCGGGCAGTT TTGCAGTTTC GACTGGCGGA ACAGCAAAA 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 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 HPHGDSAVIN TIVRMAQPPS LRYMLVDGQG NFGSIDGDSA AAMRYTEIRL AKIAHELMAD LEKETVDFVD NYDGT-
4-7d  -LLV-NLPGKY HPHGDSAVIN TIVRMAQPPS LRYMLVDGQG NFGSIDGDSA AAMRYTEIRL AKIAHELMAD LEKETVDFVD KRERYG
4-13d -VG-AGPGKY HPHGDSAVIN TIVRMAQPPS LRYMLVDGQG NFGSIDGDSA AAMRYTEIRL AKIAHELMAD LEKETVDFVD KSTVR-
4-30d -VG-ERPGKY HPHGDSAVIN TIVRMAQPPS LRYMLVDGQG NFGSIDGDSA AAMRYTEIRL AKIAHELMAD LEKETVDFVD KCERYG
4-60d -RW-FRPGKY HPHGDSAVIN TIVRMAQPPS LRYMLVDGQG NFGSIDGDSA AAMRYTEIRL AKIAHELMAD LEKETVDFVD TLTVR-
4-90d -VG-DPIGKY HPHGDSAVIN TIVRMAQPPS LRYMLVDGQG NFGSIDGDSA AAMRYTEIRL AKIAHELMAD LEKETVDFVD NWQRY-
Clustal Consensus : .*** *****

```

```

Alignment: gyrA2
      .....| .....| .....| .....| .....| .....| .....| .....| .....| .....|
      10      20      30      40      50      60      70      80
4-1d  VGDVIGKYH HGDYAVYDTI VRMAQPPSLR YMLVDGQGNF GSIDGDSAAA MRYTEIRLAK IAHELMADLE KETVDFVDNY DGT-
4-7d  VADRFGKYH HGDYAVYDTI VRMAQPPSLR YMLVDGQGNF GSIDGDSAAA MRYTEIRLAK IAHELMADLE KETVDFVDNN DGT-
4-13d VGDGFGKYH HGDYAVYDTI VRMAQPPSLR YMLVDGQGNF GSIDGDSAAA MRYTEIRLAK IAHELMADLE KETVDFVDNW ERYG
4-30d VADRFGKYH HGDYAVYDTI VRMAQPPSLR YMLVDGQGNF GSIDGDSAAA MRYTEIRLAK IAHELMADLE KETVDFVDNN DGT-
4-60d RW-SVFGKYH HGDYAVYDTI VRMAQPPSLR YMLVDGQGNF GSIDGDSAAA MRYTEIRLAK IAHELMADLE KETVDFVDKL QTVR
4-90d VGHGIGKYH HGDYAVYDTI VRMAQPPSLR YMLVDGQGNF GSIDGDSAAA MRYTEIRLAK IAHELMADLE KETVDFVDNL ARY-
Clustal Consensus : .**** *****

```

```

Alignment: gyrA3
      .....| .....| .....| .....| .....| .....| .....| .....| .....| .....|
      10      20      30      40      50      60      70      80
4-1d  -VGDVIGKYH PHGDFAVYDT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT-
4-7d  -LVTRFGKYH PHGDFAVYDT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK MGRYK
4-13d -VGHGFGKYH PHGDFAVYDT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK SETVR
4-30d -VGDVIGKYH PHGDFAVYDT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT-
4-60d SVGARVGYH PHGDFAVYDT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK M-TVR
4-90d -VGEAFGKYH PHGDFAVYDT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN CASVR
Clustal Consensus : .**** *****

```

```

Alignment: gyrA4
      .....| .....| .....| .....| .....| .....| .....| .....| .....| .....|
      10      20      30      40      50      60      70      80
4-1d  -VGDVIGKYH PHGDFAVYGT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN --YDGT-
4-7d  -VGERFGKYH PHGDFAVYGT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK --LNGT-
4-13d SLVTRIGKYH PHGDFAVYGT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN --FGRY-
4-30d LVGDRFGKYH PHGDFAVYGT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK --CARYG
4-60d LLVIGIGKYH PHGDFAVYGT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK -VTVR--
4-90d -VGHGIGKYH PHGDFAVYGT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN --WNGT-
Clustal Consensus : .**** *****

```

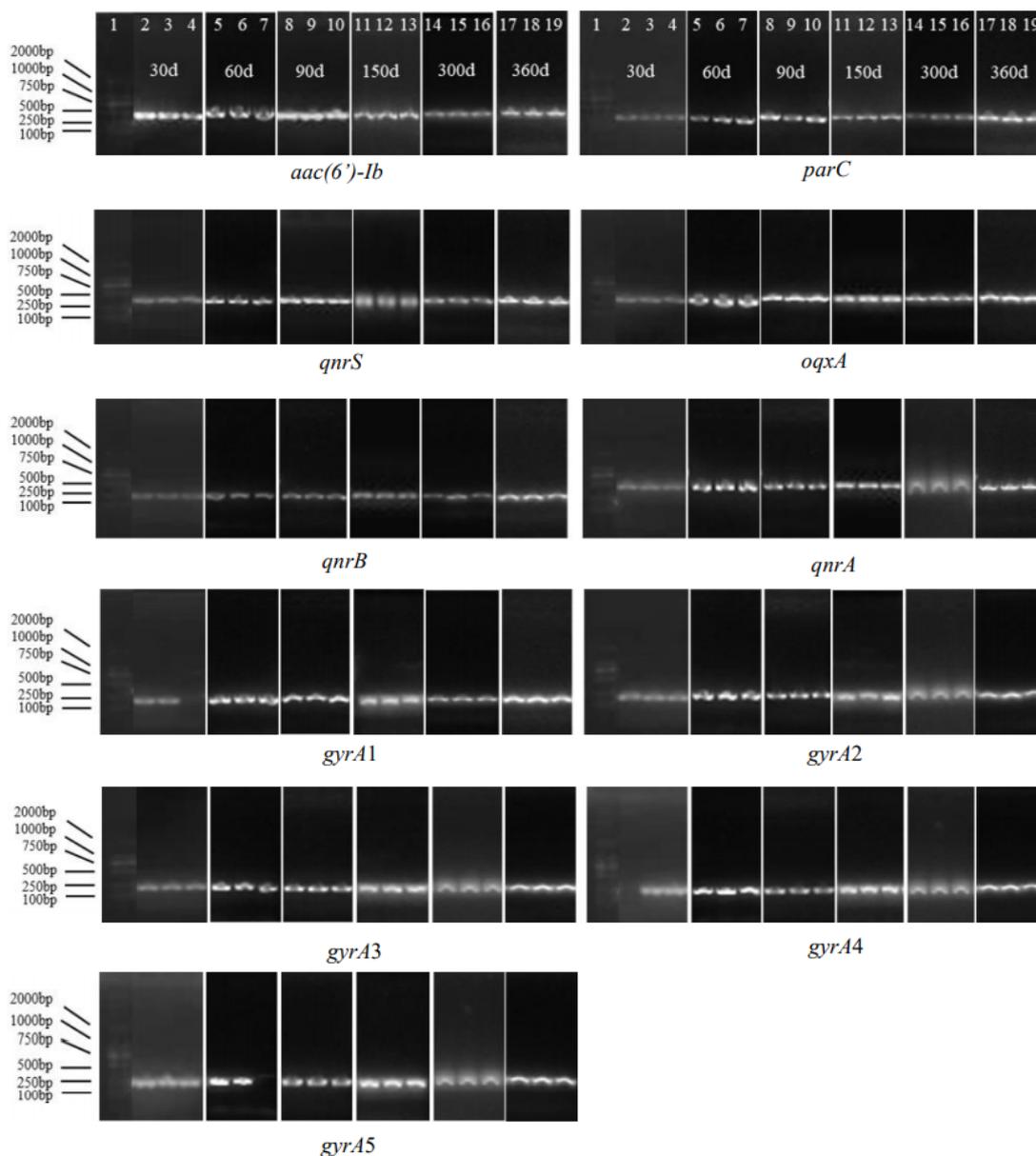
```

Alignment: gyrA5
      .....| .....| .....| .....| .....| .....| .....| .....| .....| .....|
      10      20      30      40      50      60      70      80
4-1d  -VGDVIGKYH PHGDFAVYAT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN YDGT-
4-7d  -VGEFGKYH PHGDFAVYAT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN MSRYG
4-13d CW-FVIGKYH PHGDFAVYAT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK RNGT-
4-30d SLVNGFGKYH PHGDFAVYAT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK LDGT-
4-60d -VGDPPGKYH PHGDFAVYAT IVRMAQPPSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDN LGRYK
4-90d -VGDRIKYH PHGDFAVYAT IVRMAQPPSL 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  $-20^{\circ}\text{C}$ .



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 30<sup>th</sup>, 60<sup>th</sup>, 90<sup>th</sup>, 150<sup>th</sup>, 300<sup>th</sup>, and 360<sup>th</sup> 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  $-20^{\circ}\text{C}$ .

```

Alignment: aac(6')-Ib
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d  TTTGATGCT GCGTAGACT GCGTAAATCG ATCTCATATC CTCGAGTGT GGGCCGGAGA AGAAGCACGC CCGACACTTG CTGACCTACA GGAACAGTAC TTGCCAAGCG
-20 - 60d  TTTGAGGCTC GTTTCAGACT GCGTAAATCG ATCTCATATC CTCGAGTGT GGGCCGGAGA AGAAGCACGC CCGACACTTG CTGACCTACA GGAACAGTAC TTGCCAAGCG
-20 - 90d  TTTGGGTAT GAGCCAGACT GCGTAAATCG ATCTCATATC CTCGAGTGT GGGCCGGAGA AGAAGCACGC CCGACACTTG CTGACCTACA GGAACAGTAC TTGCCAAGCG
-20 - 150d  TTTTGATAA TCTCCAGACT GCGTAAATCG ATCTCATATC CTCGAGTGT GGGCCGGAGA AGAAGCACGC CCGACACTTG CTGACCTACA GGAACAGTAC TTGCCAAGCG
-20 - 300d  TTGGAATTT TTTCCAGACT GCGTAAATCG ATCTCATATC CTCGAGTGT GGGCCGGAGA AGAAGCACGC CCGACACTTG CTGACCTACA GGAACAGTAC TTGCCAAGCG
-20 - 360d  TTTGGGCTGC CTCCTTACT GCGTAAATCG ATCTCATATC CTCGAGTGT GGGCCGGAGA AGAAGCACGC CCGACACTTG CTGACCTACA GGAACAGTAC TTGCCAAGCG
Clustal Consensus  **          *** *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d  TTTTAGCCCA AGAGTCCGTC ACTCCATACA TTGCAATGCT GAATGGAGAG CCGATTGGGT ATGCCCACTC GTACCTTGCT CTTGGAAGCC GGGACGGATC CTGGGAAGAA
-20 - 60d  TTTTAGCCCA AGAGTCCGTC ACTCCATACA TTGCAATGCT GAATGGAGAG CCGATTGGGT ATGCCCACTC GTACCTTGCT CTTGGAAGCC GGGACGGATC CTGGGAAGAA
-20 - 90d  TTTTAGCCCA AGAGTCCGTC ACTCCATACA TTGCAATGCT GAATGGAGAG CCGATTGGGT ATGCCCACTC GTACCTTGCT CTTGGAAGCC GGGACGGATC CTGGGAAGAA
-20 - 150d  TTTTAGCCCA AGAGTCCGTC ACTCCATACA TTGCAATGCT GAATGGAGAG CCGATTGGGT ATGCCCACTC GTACCTTGCT CTTGGAAGCC GGGACGGATC CTGGGAAGAA
-20 - 300d  TTTTAGCCCA AGAGTCCGTC ACTCCATACA TTGCAATGCT GAATGGAGAG CCGATTGGGT ATGCCCACTC GTACCTTGCT CTTGGAAGCC GGGACGGATC CTGGGAAGAA
-20 - 360d  TTTTAGCCCA AGAGTCCGTC ACTCCATACA TTGCAATGCT GAATGGAGAG CCGATTGGGT ATGCCCACTC GTACCTTGCT CTTGGAAGCC GGGACGGATC CTGGGAAGAA
Clustal Consensus  *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d  GAAACCCATC CAGGACTAGC CGGAATAGAC CAGTTACTGC CGAATGCATC ACAACTGGCC AAAGGCTTGC GAACCAAGCT GCTTCGAGCT CTGGTTGAGT TGCTGTTCAA
-20 - 60d  GAAACCCATC CAGGACTAGC CGGAATAGAC CAGTTACTGC CGAATGCATC ACAACTGGCC AAAGGCTTGC GAACCAAGCT GCTTCGAGCT CTGGTTGAGT TGCTGTTCAA
-20 - 90d  GAAACCCATC CAGGACTAGC CGGAATAGAC CAGTTACTGC CGAATGCATC ACAACTGGCC AAAGGCTTGC GAACCAAGCT GCTTCGAGCT CTGGTTGAGT TGCTGTTCAA
-20 - 150d  GAAACCCATC CAGGACTAGC CGGAATAGAC CAGTTACTGC CGAATGCATC ACAACTGGCC AAAGGCTTGC GAACCAAGCT GCTTCGAGCT CTGGTTGAGT TGCTGTTCAA
-20 - 300d  GAAACCCATC CAGGACTAGC CGGAATAGAC CAGTTACTGC CGAATGCATC ACAACTGGCC AAAGGCTTGC GAACCAAGCT GCTTCGAGCT CTGGTTGAGT TGCTGTTCAA
-20 - 360d  GAAACCCATC CAGGACTAGC CGGAATAGAC CAGTTACTGC CGAATGCATC ACAACTGGCC AAAGGCTTGC GAACCAAGCT GCTTCGAGCT CTGGTTGAGT TGCTGTTCAA
Clustal Consensus  *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d  TGATCCCGAG CTCACCAAGA TCCAAACCGA CCGCTCGCCG AGCAACTTGC GAGCGATCCG ATGCTACGAG AAAGCGGGGT TTGAGAGCCA AGGTACCCTA ACCACCCGAG
-20 - 60d  TGATCCCGAG CTCACCAAGA TCCAAACCGA CCGCTCGCCG AGCAACTTGC GAGCGATCCG ATGCTACGAG AAAGCGGGGT TTGAGAGCCA AGGTACCCTA ACCACCCGAG
-20 - 90d  TGATCCCGAG CTCACCAAGA TCCAAACCGA CCGCTCGCCG AGCAACTTGC GAGCGATCCG ATGCTACGAG AAAGCGGGGT TTGAGAGCCA AGGTACCCTA ACCACCCGAG
-20 - 150d  TGATCCCGAG CTCACCAAGA TCCAAACCGA CCGCTCGCCG AGCAACTTGC GAGCGATCCG ATGCTACGAG AAAGCGGGGT TTGAGAGCCA AGGTACCCTA ACCACCCGAG
-20 - 300d  TGATCCCGAG CTCACCAAGA TCCAAACCGA CCGCTCGCCG AGCAACTTGC GAGCGATCCG ATGCTACGAG AAAGCGGGGT TTGAGAGCCA AGGTACCCTA ACCACCCGAG
-20 - 360d  TGATCCCGAG CTCACCAAGA TCCAAACCGA CCGCTCGCCG AGCAACTTGC GAGCGATCCG ATGCTACGAG AAAGCGGGGT TTGAGAGCCA AGGTACCCTA ACCACCCGAG
Clustal Consensus  *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d  ATGCTCCAGC CCGTACATG GTTCAAACAC GGGGGGATT TTCCG-GAGA --
-20 - 60d  ATGCTCCAGC CCGTACATG GTTCAAACAC GGGGAATATT TCGAGAGAA --
-20 - 90d  ATGCTCCAGC CCGTACATG GTTCAAACAC GGGGGGATT TTTTCCGAGA --
-20 - 150d  ATGCTCCAGC CCGTACATG GTTCAAACAC GGGGGAATT TTCCGGAA --
-20 - 300d  ATGCTCCAGC CCGTACATG GTTCAAACAC GGGGGGATT TTTCCAGAAA TA
-20 - 360d  ATGCTCCAGC CCGTACATG GTTCAAACAC GGGGGAATT CCGAGAAAC --
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 S35.** Sequencing results of *qnrS* for stability of plasmid DNA references materials stored at  $-20^{\circ}\text{C}$ .

```

Alignment: qnrS
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d  AAGTT--TCT CAATTA-CAG GGTGATATTC GTGGTGCCA CTTTGATGTC GCAGATCTTC GTGATGCAAG TTTCACAACAA TGCCAACTTC CGATGGCAAA CTTCAGTAAT
-20 - 60d  -AAAT--TTT ACCCTG-CAG GGTGATATTC GTGGTGCCA CTTTGATGTC GCAGATCTTC GTGATGCAAG TTTCACAACAA TGCCAACTTC CGATGGCAAA CTTCAGTAAT
-20 - 90d  -GTCT--TCT CACATAACAG GGTGATATTC GTGGTGCCA CTTTGATGTC GCAGATCTTC GTGATGCAAG TTTCACAACAA TGCCAACTTC CGATGGCAAA CTTCAGTAAT
-20 - 150d -AATTGGTCT CACTTA-CAG GGTGATATTC GTGGTGCCA CTTTGATGTC GCAGATCTTC GTGATGCAAG TTTCACAACAA TGCCAACTTC CGATGGCAAA CTTCAGTAAT
-20 - 300d AAGTT--CTT CACTTAACAG GGTGATATTC GTGGTGCCA CTTTGATGTC GCAGATCTTC GTGATGCAAG TTTCACAACAA TGCCAACTTC CGATGGCAAA CTTCAGTAAT
-20 - 360d CAATT--TTC CTCTA-CAG GGTGATATTC GTGGTGCCA CTTTGATGTC GCAGATCTTC GTGATGCAAG TTTCACAACAA TGCCAACTTC CGATGGCAAA CTTCAGTAAT
Clustal Consensus * * * * *
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d  GCCAATGCT ACGGTATAGA GTTCCGTGGC TGTGATTTAA AAGGTGCCAA CTTTCCCGCA ACAAACTTTG CCCATCAAGT GAGTAATCGT ATGACTTTTT GCTCAGCATT
-20 - 60d  GCCAATGCT ACGGTATAGA GTTCCGTGGC TGTGATTTAA AAGGTGCCAA CTTTCCCGCA ACAAACTTTG CCCATCAAGT GAGTAATCGT ATGACTTTTT GCTCAGCATT
-20 - 90d  GCCAATGCT ACGGTATAGA GTTCCGTGGC TGTGATTTAA AAGGTGCCAA CTTTCCCGCA ACAAACTTTG CCCATCAAGT GAGTAATCGT ATGACTTTTT GCTCAGCATT
-20 - 150d GCCAATGCT ACGGTATAGA GTTCCGTGGC TGTGATTTAA AAGGTGCCAA CTTTCCCGCA ACAAACTTTG CCCATCAAGT GAGTAATCGT ATGACTTTTT GCTCAGCATT
-20 - 300d GCCAATGCT ACGGTATAGA GTTCCGTGGC TGTGATTTAA AAGGTGCCAA CTTTCCCGCA ACAAACTTTG CCCATCAAGT GAGTAATCGT ATGACTTTTT GCTCAGCATT
-20 - 360d GCCAATGCT ACGGTATAGA GTTCCGTGGC TGTGATTTAA AAGGTGCCAA CTTTCCCGCA ACAAACTTTG CCCATCAAGT GAGTAATCGT ATGACTTTTT GCTCAGCATT
Clustal Consensus *****
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d  TATTTCTGGA TCTAATCTTT CCTATGCCAA TATGGAGAGG GTTGTGTTAG AAAAATCTGA GTTGTGTTGAA AATCGCTGGA TAGGAACGAA CCTAGCGGGT GCATCACTGA
-20 - 60d  TATTTCTGGA TCTAATCTTT CCTATGCCAA TATGGAGAGG GTTGTGTTAG AAAAATCTGA GTTGTGTTGAA AATCGCTGGA TAGGAACGAA CCTAGCGGGT GCATCACTGA
-20 - 90d  TATTTCTGGA TCTAATCTTT CCTATGCCAA TATGGAGAGG GTTGTGTTAG AAAAATCTGA GTTGTGTTGAA AATCGCTGGA TAGGAACGAA CCTAGCGGGT GCATCACTGA
-20 - 150d TATTTCTGGA TCTAATCTTT CCTATGCCAA TATGGAGAGG GTTGTGTTAG AAAAATCTGA GTTGTGTTGAA AATCGCTGGA TAGGAACGAA CCTAGCGGGT GCATCACTGA
-20 - 300d TATTTCTGGA TCTAATCTTT CCTATGCCAA TATGGAGAGG GTTGTGTTAG AAAAATCTGA GTTGTGTTGAA AATCGCTGGA TAGGAACGAA CCTAGCGGGT GCATCACTGA
-20 - 360d TATTTCTGGA TCTAATCTTT CCTATGCCAA TATGGAGAGG GTTGTGTTAG AAAAATCTGA GTTGTGTTGAA AATCGCTGGA TAGGAACGAA CCTAGCGGGT GCATCACTGA
Clustal Consensus *****
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d  AAGAGTCAGA CTTAAGTCGA GGTGTTTTTT CCGAAGATGT CTGGGGGCCAA TTTAGCCTAC AGGGGGCCAA TTTATGCCAC GCCGAATGCA --ATGGGGTT T-AGAA--
-20 - 60d  AAGAGTCAGA CTTAAGTCGA GGTGTTTTTT CCGAAGATGT CTGGGGGCCAA TTTAGCCTAC AGGGGGCCAA TTTATGCCAC GCCGAATGCA --GGGGACTT TTAAAAAA
-20 - 90d  AAGAGTCAGA CTTAAGTCGA GGTGTTTTTT CCGAAGATGT CTGGGGGCCAA TTTAGCCTAC AGGGGGCCAA TTTATGCCAC GCCGAATGCA --CGGGGTTT TTAGAAA--
-20 - 150d AAGAGTCAGA CTTAAGTCGA GGTGTTTTTT CCGAAGATGT CTGGGGGCCAA TTTAGCCTAC AGGGGGCCAA TTTATGCCAC GCCGAATGCA --CGGGGACTT TTAGAAA--
-20 - 300d AAGAGTCAGA CTTAAGTCGA GGTGTTTTTT CCGAAGATGT CTGGGGGCCAA TTTAGCCTAC AGGGGGCCAA TTTATGCCAC GCCGAATGCA --CGGGGTT T-AGAA--
-20 - 360d AAGAGTCAGA CTTAAGTCGA GGTGTTTTTT CCGAAGATGT CTGGGGGCCAA TTTAGCCTAC AGGGGGCCAA TTTATGCCAC GCCGAATGCA --AGGGGTTT 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 *oqxA* for stability of plasmid DNA references materials stored at  $-20^{\circ}\text{C}$ .

```

Alignment: oqxA
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d  --CAGC-TGT  CCCCAGAAT  GCTGGCCCTC  CCGCCCCGAC  GGTGAGGCC  GCTAAGGTCG  TGGTGAAGTC  GATCAGTCAG  TGGGATAGTT  TTAACGGTCG  CATTGAAGCC
-20 - 60d  ACCAGGGTAT  GATC-CGAAT  GCTGGCCCTC  CCGCCCCGAC  GGTGAGGCC  GCTAAGGTCG  TGGTGAAGTC  GATCAGTCAG  TGGGATAGTT  TTAACGGTCG  CATTGAAGCC
-20 - 90d  -ACAGGCGTG  TTGGCAGAAT  GCTGGCCCTC  CCGCCCCGAC  GGTGAGGCC  GCTAAGGTCG  TGGTGAAGTC  GATCAGTCAG  TGGGATAGTT  TTAACGGTCG  CATTGAAGCC
-20 - 150d  GACAGCCTTT  TCCC-AGAAAT  GCTGGCCCTC  CCGCCCCGAC  GGTGAGGCC  GCTAAGGTCG  TGGTGAAGTC  GATCAGTCAG  TGGGATAGTT  TTAACGGTCG  CATTGAAGCC
-20 - 300d  GACAGCCTTT  TCCC-AGAAAT  GCTGGCCCTC  CCGCCCCGAC  GGTGAGGCC  GCTAAGGTCG  TGGTGAAGTC  GATCAGTCAG  TGGGATAGTT  TTAACGGTCG  CATTGAAGCC
-20 - 360d  GACAGCCTTT  GCCCCAGAAT  GCTGGCCCTC  CCGCCCCGAC  GGTGAGGCC  GCTAAGGTCG  TGGTGAAGTC  GATCAGTCAG  TGGGATAGTT  TTAACGGTCG  CATTGAAGCC
Clustal Consensus  ***          **** *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d  CTGGAGAGCC  TTCAGCTTCG  CCTTCGCCCTC  TCGGATACAG  TTGATAAAGT  GAATTACACT  GACGGCCAGG  AGGTGAAAAA  GGCCCGAGTG  CTCTTCACGA  TAGATGACAG
-20 - 60d  CTGGAGAGCC  TTCAGCTTCG  CCTTCGCCCTC  TCGGATACAG  TTGATAAAGT  GAATTACACT  GACGGCCAGG  AGGTGAAAAA  GGCCCGAGTG  CTCTTCACGA  TAGATGACAG
-20 - 90d  CTGGAGAGCC  TTCAGCTTCG  CCTTCGCCCTC  TCGGATACAG  TTGATAAAGT  GAATTACACT  GACGGCCAGG  AGGTGAAAAA  GGCCCGAGTG  CTCTTCACGA  TAGATGACAG
-20 - 150d  CTGGAGAGCC  TTCAGCTTCG  CCTTCGCCCTC  TCGGATACAG  TTGATAAAGT  GAATTACACT  GACGGCCAGG  AGGTGAAAAA  GGCCCGAGTG  CTCTTCACGA  TAGATGACAG
-20 - 300d  CTGGAGAGCC  TTCAGCTTCG  CCTTCGCCCTC  TCGGATACAG  TTGATAAAGT  GAATTACACT  GACGGCCAGG  AGGTGAAAAA  GGCCCGAGTG  CTCTTCACGA  TAGATGACAG
-20 - 360d  CTGGAGAGCC  TTCAGCTTCG  CCTTCGCCCTC  TCGGATACAG  TTGATAAAGT  GAATTACACT  GACGGCCAGG  AGGTGAAAAA  GGCCCGAGTG  CTCTTCACGA  TAGATGACAG
Clustal Consensus  *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d  AACCTATCCG  GCGCGGCTCG  AGCAGGCCCA  GCGCGGCTTC  GCAGAGCCCA  AAACCCAGGC  CAGCCTCCGC  CAAAGCCAGC  CGAACCCGAC  CGATAAATTA  GTCCATACC-
-20 - 60d  AACCTATCCG  GCGCGGCTCG  AGCAGGCCCA  GCGCGGCTTC  GCAGAGCCCA  AAACCCAGGC  CAGCCTCCGC  CAAAGCCAGC  CGAACCCGAC  CGATAAATTA  GTCCATATCC
-20 - 90d  AACCTATCCG  GCGCGGCTCG  AGCAGGCCCA  GCGCGGCTTC  GCAGAGCCCA  AAACCCAGGC  CAGCCTCCGC  CAAAGCCAGC  CGAACCCGAC  CGATAAATTA  GTCCATATCC
-20 - 150d  AACCTATCCG  GCGCGGCTCG  AGCAGGCCCA  GCGCGGCTTC  GCAGAGCCCA  AAACCCAGGC  CAGCCTCCGC  CAAAGCCAGC  CGAACCCGAC  CGATAAATTA  GTCCATAGAA
-20 - 300d  AACCTATCCG  GCGCGGCTCG  AGCAGGCCCA  GCGCGGCTTC  GCAGAGCCCA  AAACCCAGGC  CAGCCTCCGC  CAAAGCCAGC  CGAACCCGAC  CGATAAATTA  GTCCATACC-
-20 - 360d  AACCTATCCG  GCGCGGCTCG  AGCAGGCCCA  GCGCGGCTTC  GCAGAGCCCA  AAACCCAGGC  CAGCCTCCGC  CAAAGCCAGC  CGAACCCGAC  CGATAAATTA  GTCCATACC-
Clustal Consensus  *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d  CCCCCTCTGCT  CTCCTGA--
-20 - 60d  CCCCCCGCTC  CTCATAAA-
-20 - 90d  CCCCCTCCGT  CTC---
-20 - 150d  CCATTTTGGT  CTC---
-20 - 300d  CCCCCTCTGCT  CTC---
-20 - 360d  CCCCCTCTGCT  CTC---
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  $-20^{\circ}\text{C}$ .

```

Alignment: qnrB
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d  10      20      30      40      50      60      70      80      90     100    110
-AGAGGCATT GAAAAATC-GC CACTGCCCGC CACAAGGGCC AGATTTCGGC GGTGCAAGCT TTATGAATAT GATCACCACG CGCACTGCT TTTGCAGCC ATATATCACT
-20 - 60d  -TCAGGCATT GAAAGAATTC CACTGCCCGC CACAAGGGCC AGATTTCGGC GGTGCAAGCT TTATGAATAT GATCACCACG CGCACTGCT TTTGCAGCC ATATATCACT
-20 - 90d  -ATGGGCATT GAAAAAT-GC CACTGCCCGC CACAAGGGCC AGATTTCGGC GGTGCAAGCT TTATGAATAT GATCACCACG CGCACTGCT TTTGCAGCC ATATATCACT
-20 - 150d CAGGGGCATT GAAAAAT-GC CACTGCCCGC CACAAGGGCC AGATTTCGGC GGTGCAAGCT TTATGAATAT GATCACCACG CGCACTGCT TTTGCAGCC ATATATCACT
-20 - 300d --TGGGCATT GAAAAATC-GC CACTGCCCGC CACAAGGGCC AGATTTCGGC GGTGCAAGCT TTATGAATAT GATCACCACG CGCACTGCT TTTGCAGCC ATATATCACT
-20 - 360d --TAGGCATT GAAACTTCGC CACTGCCCGC CACAAGGGCC AGATTTCGGC GGTGCAAGCT TTATGAATAT GATCACCACG CGCACTGCT TTTGCAGCC ATATATCACT
Clustal Consensus ***** * * *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d  120     130     140     150     160     170     180     190     200     210     220
AATACTAATC TAAGCTACGC CAATTTTTCG AAAGTCCTGT TGGAAAAGTC TGAGCTCTGG GAAAACCCCT GGATGGGGAC TCAGCTACTG GCTCCGACTC TCAGTCGTTT
-20 - 60d  AATACTAATC TAAGCTACGC CAATTTTTCG AAAGTCCTGT TGGAAAAGTC TGAGCTCTGG GAAAACCCCT GGATGGGGAC TCAGCTACTG GCTCCGACTC TCAGTCGTTT
-20 - 90d  AATACTAATC TAAGCTACGC CAATTTTTCG AAAGTCCTGT TGGAAAAGTC TGAGCTCTGG GAAAACCCCT GGATGGGGAC TCAGCTACTG GCTCCGACTC TCAGTCGTTT
-20 - 150d AATACTAATC TAAGCTACGC CAATTTTTCG AAAGTCCTGT TGGAAAAGTC TGAGCTCTGG GAAAACCCCT GGATGGGGAC TCAGCTACTG GCTCCGACTC TCAGTCGTTT
-20 - 300d AATACTAATC TAAGCTACGC CAATTTTTCG AAAGTCCTGT TGGAAAAGTC TGAGCTCTGG GAAAACCCCT GGATGGGGAC TCAGCTACTG GCTCCGACTC TCAGTCGTTT
-20 - 360d AATACTAATC TAAGCTACGC CAATTTTTCG AAAGTCCTGT TGGAAAAGTC TGAGCTCTGG GAAAACCCCT GGATGGGGAC TCAGCTACTG GCTCCGACTC TCAGTCGTTT
Clustal Consensus *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d  230     240     250     260     270
AGATCTCTCC GCGCGCCAGT TTTGCACTTT CCACTGGC-G AGCAGCAAAA -
-20 - 60d  AGATCTCTCC GCGCGCCAGT TTTGCACTTT CCACTGGC-T AACAGCAAAA -
-20 - 90d  AGATCTCTCC GCGCGCCAGT TTTGCACTTT CCACTGGC-A AACAGCAAAA A
-20 - 150d AGATCTCTCC GCGCGCCAGT TTTGCACTTT CCACTGGGA AACAGCAAAA -
-20 - 300d AGATCTCTCC GCGCGCCAGT TTTGCACTTT CCACTGGC-A A-CAGCAAAA A
-20 - 360d AGATCTCTCC GCGCGCCAGT TTTGCACTTT CCACTGGC-G AACAGCAAAA -
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 S38.** Sequencing results of *qnrA* for stability of plasmid DNA references materials stored at  $-20^{\circ}\text{C}$ .

```

Alignment: qnrA
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d  GCTTTTTC CCCCAGGATT TGAGTGACAG CCGTTTTCCG CCGTGCOCCT TTTATCAGTG TGACTTCAGC CACTGTCAGC TGCAGGATGC CAGTTTCGAG GATTGCGATT
-20 - 60d  -CGTTTTTTC TCCAGGATT TGAGTGACAG CCGTTTTCCG CCGTGCOCCT TTTATCAGTG TGACTTCAGC CACTGTCAGC TGCAGGATGC CAGTTTCGAG GATTGCGATT
-20 - 90d  -CGTTTTTTC TCCAGGATT TGAGTGACAG CCGTTTTCCG CCGTGCOCCT TTTATCAGTG TGACTTCAGC CACTGTCAGC TGCAGGATGC CAGTTTCGAG GATTGCGATT
-20 - 150d -CGTTTTTTC TCCAGGATT TGAGTGACAG CCGTTTTCCG CCGTGCOCCT TTTATCAGTG TGACTTCAGC CACTGTCAGC TGCAGGATGC CAGTTTCGAG GATTGCGATT
-20 - 300d -CGTTTTTTC CCCCAGGATT TGAGTGACAG CCGTTTTCCG CCGTGCOCCT TTTATCAGTG TGACTTCAGC CACTGTCAGC TGCAGGATGC CAGTTTCGAG GATTGCGATT
-20 - 360d AGTTTTTTC CCCCAGGATT TGAGTGACAG CCGTTTTCCG CCGTGCOCCT TTTATCAGTG TGACTTCAGC CACTGTCAGC TGCAGGATGC CAGTTTCGAG GATTGCGATT
Clustal Consensus * * * * *

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d  TCATTGAAG CCGCCGCCCT GAAGGGTCTC ACTTCAGCTA TCCCGATCTG CCGGATGCCA GTTTCAGGCC CTGCCGCTCG TCTTTGGCCA ACTTCAGCGG TGCCAACTGC
-20 - 60d  TCATTGAAG CCGCCGCCCT GAAGGGTCTC ACTTCAGCTA TCCCGATCTG CCGGATGCCA GTTTCAGGCC CTGCCGCTCG TCTTTGGCCA ACTTCAGCGG TGCCAACTGC
-20 - 90d  TCATTGAAG CCGCCGCCCT GAAGGGTCTC ACTTCAGCTA TCCCGATCTG CCGGATGCCA GTTTCAGGCC CTGCCGCTCG TCTTTGGCCA ACTTCAGCGG TGCCAACTGC
-20 - 150d TCATTGAAG CCGCCGCCCT GAAGGGTCTC ACTTCAGCTA TCCCGATCTG CCGGATGCCA GTTTCAGGCC CTGCCGCTCG TCTTTGGCCA ACTTCAGCGG TGCCAACTGC
-20 - 300d TCATTGAAG CCGCCGCCCT GAAGGGTCTC ACTTCAGCTA TCCCGATCTG CCGGATGCCA GTTTCAGGCC CTGCCGCTCG TCTTTGGCCA ACTTCAGCGG TGCCAACTGC
-20 - 360d TCATTGAAG CCGCCGCCCT GAAGGGTCTC ACTTCAGCTA TCCCGATCTG CCGGATGCCA GTTTCAGGCC CTGCCGCTCG TCTTTGGCCA ACTTCAGCGG TGCCAACTGC
Clustal Consensus *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d  TTTGGCATAG AGTTCAGGGA GTCCGATCTC AAGGGCGCCA ACTTTTCOCG GGGCCGCTTC TACAATCAAG TCAGCCATAA GATGTACTTC TGCTGGCTT ATATCTCAGG
-20 - 60d  TTTGGCATAG AGTTCAGGGA GTCCGATCTC AAGGGCGCCA ACTTTTCOCG GGGCCGCTTC TACAATCAAG TCAGCCATAA GATGTACTTC TGCTGGCTT ATATCTCAGG
-20 - 90d  TTTGGCATAG AGTTCAGGGA GTCCGATCTC AAGGGCGCCA ACTTTTCOCG GGGCCGCTTC TACAATCAAG TCAGCCATAA GATGTACTTC TGCTGGCTT ATATCTCAGG
-20 - 150d TTTGGCATAG AGTTCAGGGA GTCCGATCTC AAGGGCGCCA ACTTTTCOCG GGGCCGCTTC TACAATCAAG TCAGCCATAA GATGTACTTC TGCTGGCTT ATATCTCAGG
-20 - 300d TTTGGCATAG AGTTCAGGGA GTCCGATCTC AAGGGCGCCA ACTTTTCOCG GGGCCGCTTC TACAATCAAG TCAGCCATAA GATGTACTTC TGCTGGCTT ATATCTCAGG
-20 - 360d TTTGGCATAG AGTTCAGGGA GTCCGATCTC AAGGGCGCCA ACTTTTCOCG GGGCCGCTTC TACAATCAAG TCAGCCATAA GATGTACTTC TGCTGGCTT ATATCTCAGG
Clustal Consensus *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d  TTGCAACCTG GCCTATACCA ACTTGAGTGG CCAATGCCTG GAAAATGCC AGCTGTTTGA AAACAACCTG AGCAATGCCA ATCTCAGCGG CGCTTCCTTG ATGGGCTCAG
-20 - 60d  TTGCAACCTG GCCTATACCA ACTTGAGTGG CCAATGCCTG GAAAATGCC AGCTGTTTGA AAACAACCTG AGCAATGCCA ATCTCAGCGG CGCTTCCTTG ATGGGCTCAG
-20 - 90d  TTGCAACCTG GCCTATACCA ACTTGAGTGG CCAATGCCTG GAAAATGCC AGCTGTTTGA AAACAACCTG AGCAATGCCA ATCTCAGCGG CGCTTCCTTG ATGGGCTCAG
-20 - 150d TTGCAACCTG GCCTATACCA ACTTGAGTGG CCAATGCCTG GAAAATGCC AGCTGTTTGA AAACAACCTG AGCAATGCCA ATCTCAGCGG CGCTTCCTTG ATGGGCTCAG
-20 - 300d TTGCAACCTG GCCTATACCA ACTTGAGTGG CCAATGCCTG GAAAATGCC AGCTGTTTGA AAACAACCTG AGCAATGCCA ATCTCAGCGG CGCTTCCTTG ATGGGCTCAG
-20 - 360d TTGCAACCTG GCCTATACCA ACTTGAGTGG CCAATGCCTG GAAAATGCC AGCTGTTTGA AAACAACCTG AGCAATGCCA ATCTCAGCGG CGCTTCCTTG ATGGGCTCAG
Clustal Consensus *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d  ATCTCAGCCG CCGCACCTTC TCCCGCGACT GTTGGCAACA GGTCAATCTG CCGGGCTCTG GCCTAACCTT TCCCGATCTG GATGGGCTCG ACCCCAGAGG GGTCAACCTC
-20 - 60d  ATCTCAGCCG CCGCACCTTC TCCCGCGACT GTTGGCAACA GGTCAATCTG CCGGGCTCTG GCCTAACCTT TCCCGATCTG GATGGGCTCG ACCCCAGAGG GGTCAACCTC
-20 - 90d  ATCTCAGCCG CCGCACCTTC TCCCGCGACT GTTGGCAACA GGTCAATCTG CCGGGCTCTG GCCTAACCTT TCCCGATCTG GATGGGCTCG ACCCCAGAGG GGTCAACCTC
-20 - 150d ATCTCAGCCG CCGCACCTTC TCCCGCGACT GTTGGCAACA GGTCAATCTG CCGGGCTCTG GCCTAACCTT TCCCGATCTG GATGGGCTCG ACCCCAGAGG GGTCAACCTC
-20 - 300d ATCTCAGCCG CCGCACCTTC TCCCGCGACT GTTGGCAACA GGTCAATCTG CCGGGCTCTG GCCTAACCTT TCCCGATCTG GATGGGCTCG ACCCCAGAGG GGTCAACCTC
-20 - 360d ATCTCAGCCG CCGCACCTTC TCCCGCGACT GTTGGCAACA GGTCAATCTG CCGGGCTCTG GCCTAACCTT TCCCGATCTG GATGGGCTCG ACCCCAGAGG GGTCAACCTC
Clustal Consensus *****

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
-20 - 30d  GAAGGACTCA AGTGGGGCC CCCCCTGGAC AA--
-20 - 60d  GAAGGACTCA GG--GGGGCC TCCGGGGCAG ----
-20 - 90d  GAAGGACTCA AA--GGAGCC CTGGGGGGAA AAA-
-20 - 150d GAAGGACTCA TG--GGAG-- -CCCCGGCAA AAAT
-20 - 300d GAAGGACTCA AAGGGGGCC CCCCGGGGAA AA--
-20 - 360d GAAGGACTCA AGTGGGGCC CCCCCTGGAA----
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 S39.** Sequencing results of *gyrA* for stability of plasmid DNA references materials stored at  $-20^{\circ}\text{C}$ .

```

Alignment: gyrA1
      .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
      10      20      30      40      50      60      70      80
-20 - 30d  -LLVNLPGKY HPHGDSAVYN TIVRMAQPFS LYMLVDGQG NFGSIDGDSA AMRYTEIRL AKIAHELMAD LEKETVDFVD KGRERYG
-20 - 60d  --RW-GPGKY HPHGDSAVYN TIVRMAQPFS LYMLVDGQG NFGSIDGDSA AMRYTEIRL AKIAHELMAD LEKETVDFVD KMGTVR
-20 - 90d  -RW-SRIGKY HPHGDSAVYN TIVRMAQPFS LYMLVDGQG NFGSIDGDSA AMRYTEIRL AKIAHELMAD LEKETVDFVD NWNGT-
-20 - 150d -SLATRIGKY HPHGDSAVYN TIVRMAQPFS LYMLVDGQG NFGSIDGDSA AMRYTEIRL AKIAHELMAD LEKETVDFVD KTERY-
-20 - 300d -RW-PRFGKY HPHGDSAVYN TIVRMAQPFS LYMLVDGQG NFGSIDGDSA AMRYTEIRL AKIAHELMAD LEKETVDFVD TLTVR-
-20 - 360d  LVG-DRFGKY HPHGDSAVYN TIVRMAQPFS LYMLVDGQG 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 EKETVDFVDK NDGT-
-20 - 60d  RW--SVGKYH PHGDYAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK LQTVR
-20 - 90d  SLVNGIGKYH PHGDYAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK WDGT-
-20 - 150d  RWSAFPGRKYH PHGDYAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK SNGT-
-20 - 300d  -VADRFGKYH PHGDYAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK NDGT-
-20 - 360d  -VGDGFGKYH PHGDYAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK SDGT-
Clustal Consensus  :**** *****

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Alignment: gyrA3
      .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
      10      20      30      40      50      60      70      80
-20 - 30d  -LVTRFGKYH PHGDFAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK MGRYG
-20 - 60d  HW-FRFGKYH PHGDFAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK WERY-
-20 - 90d  -VGEPIGKYH PHGDFAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK -QTVR
-20 - 150d  SLVVGFGKYH PHGDFAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK SNGT-
-20 - 300d  SVGARVGRKYH PHGDFAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK M-TVV
-20 - 360d  -VGDGFGKYH PHGDFAVYDT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK IDGT-
Clustal Consensus  :**** *****

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Alignment: gyrA4
      .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
      10      20      30      40      50      60      70      80
-20 - 30d  -VGERFGKYH PHGDFAVYGT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK LMGT--
-20 - 60d  -VGERFGKYH PHGDFAVYGT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK METVR-
-20 - 90d  -CW-PIGKYH PHGDFAVYGT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK -SNGTD
-20 - 150d  SLVVGFGKYH PHGDFAVYGT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK -MNGT-
-20 - 300d  -VGERIGKYH PHGDFAVYGT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK LARYG-
-20 - 360d  LLVIGIGKYH PHGDFAVYGT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK -VTVR-
Clustal Consensus  :**** *****

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Alignment: gyrA5
      .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
      10      20      30      40      50      60      70      80
-20 - 30d  -VGEFGGKYH PHGDFAVYAT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK MSRYG
-20 - 60d  SLVIGYGRKYH PHGDFAVYAT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK ANGT-
-20 - 90d  -LVHRIGKYH PHGDFAVYAT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK WNGT-
-20 - 150d  SLVVGFGKYH PHGDFAVYAT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK C-RY-
-20 - 300d  RW-AGIGKYH PHGDFAVYAT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK LDGT-
-20 - 360d  -VGDGIGKYH PHGDFAVYAT IVRMAQPFSL RYMLVDGQGN FGSIDGDSAA AMRYTEIRLA KIAHELMADL EKETVDFVDK 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.