

H553R Rif^R mutant strain

1 GTGTATATGAGCTATTCGTT TACCAGAGAAAAACGTATCC GTAAGAGTTTTGCAAAAGCGG GAAAATGTTTTGGAAGTTCC TTTCTTGCTAGCAACCCAAA TTGATTCTTATGCGAAGTTT
M S Y S F T E K K R I R K S F A K R E N V L E V P F L L A T Q I D S Y A K F
121 TTGCAGCTGGAAAATCGTTT TGACAAAGTACCGATGACG GTCTGCAGGCAGCATTTAAT TCTATTTTCCCGATTGTGAG CCATAACGGTTATGCGCGAT TGGAGTTTGTGATTACACA
L Q L E N A F D K R T D D G L Q A A F N S I F P I V S H N G Y A R L E D S Y A K F
241 TTGGGCGAGCCTTTCTGCGA TAITCCCGAATGTCAGTTGC GGGAACTACTTATGCGAGCC CCCTTCCGCGCGGTATCCG TTTGGTATTTTGGATAAGS AACACTCTAAACCCAGCGTA
L G E P L F D I P E C Q L R G I T Y A A P L E A R I R L V I L D K E A S K P T V
361 AAAGAAGTTCGTGAAAACGA AGTGTATATGGCGAAATTC CGTTGATGACCCCGAGCGGT TCTTTTGTGATTAACGGCAC AGAGCGGTGTGATTGTCTCCC AGTTGCACCCGTTCCGCCGCG
K E V R E N E Y M G E I I F L M T P S G S F V I N G T E R V I V S Q L H R S P G
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V F F E H D K G K T H S S G K L L F S A R I I P Y R G S W L D F E F D P K D L L
601 TATTCCGATATCGACCGCCG CGTGTATATGGCGAAATTC TTTTGTGAAGCTTTGGGG TACAACAATGAGCAAACTCTT GGATATTTTCTACGACAAAG AAACGTTCTATTGTCTTCA
Y F R I D R R R K M P V T I L L K A L G Y N N E Q I L D I F Y D K E T F Y L S S
721 AACGGTGTCAAACCGATTG GTTCGCGAGCGCTGAAAG GCGAACTGCCAAGGTGCGAT ATCTTGGATAAAGAAGGCAA TGTATTGGTTGCCAAAGGTA AGCGTATTACTCGGAAAAT
N G V Q T D L V A G R L K G E T A K V D I L D K E G N I L D K E G N V L V A K G K R I T A K N
841 ATCCGATATTACCAATGCG AGGCCTGACCCGTTGGATG TAGAACCGGAAAGCCTGCTG GGCACCAATGGCTCCCGA TCTGATTGATTCGAAACCG CCGAGGATTGGCTTCTGCC
I R D I T N A A G L T R L D V E P E S L L G K A L A A D L I D S E T G E V L A S A
961 AATGATGAAATACAGAAAGA GTTGTGGCCAAATTTGATA TCAACCGCTAAAAGAAATTC ACGACCTTTACATCAATGA GTTGGATCAGGTGCTTATA TCTCCAATACCTCGCCAGC
N D E I T E E L L A K F D I N G V K E I T T L Y I N E L D Q G A Y I S N T L R T
1081 GATGAGACTGCCCGCGCGCA GCGCGCGGTGTCGCAATTC ACCGTATGATGCGTCCGGG GAAACCGCCACCCGAAGAGGC AGTCGAGCAATGTTTAAAC GCTTGTCTCAGTGAAGAC
D E T A G R G A A R V A I Y R M M R P G E P P T E E A V E Q L F N R L F P S E D
1201 AGCTACGATTTGCCCGCT AGGTGCTATGAAATTTAATA CCGGCACATACGACAAAAA CTGTCCGAAGCCCAACAAA TCTTGTGACGCGCGCTCG TGAACGAAACGTTGCGCGT
S Y D L S R V G R M K F N T R T Y E Q K L S E A Q Q N S W Y G R L L N E T F A G
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A A E K G G Y V L S V E D I V A S I A T L V E L R N G H G E V D D I D H L G N R
1441 GATGAGACTGCCCGCGCGCA GCTGCTGAAACCAATTC CAGCGGTGTCGCGCGTGG GAACCGCTGTAAGAAGACG TTTGAATCAGCGGAACTG AAGCTCAGTGGGCAACGAT
R V R S V G E L T E N Q F R S G L A R V E R A V K E R L N Q A E S E N L M P H D
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L I N A K P V S A A I K E F F G S S Q L C S Q F M D Q T N P L S E V T K R R V S
1681 GATGAGACTGCCCGCGCGCA GCTGCTGAAACCAATTC CAGCGGTGTCGCGCGTGG GAACCGCTGTAAGAAGACG TTTGAATCAGCGGAACTG AAGCTCAGTGGGCAACGAT
A L G P G G L T R E R A G F E V R D V H P T H Y G R V C P I E T P E G P N I G L
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I N S L S V Y A R T N D Y G F L E T P Y R R V I D G K V V T E I D Y A C A A I E
1921 GCGCCCTATGATTGCGACA GCGGCAACCAATGATTC GTTCTTGGAAAGCACTTAC CCGCCGCTTATCGACGGCAA R R V I D G K V V T E I D Y A C A A I E
G R V I A Q A N A D L D S D G N L I G D A T L V T C T R E K G E T I M A T P D R V Q
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Y M D V A T G S A T V A G V S T I P F L E H D D A N R A L M G A N P A L M G A N P
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C L R P E K P M V G T G I E R S V A V D TCTGTACTGCAATCGTTGC S A T A I V A R R G G V V E A G T A T G C A T G C C A C C G T
2281 GTTGTGATTCGTTCATGA V V I R V H D D E A T A G E V G V D I Y V L K F T R S N Q S T N I N K S P A V
2401 AAAGCCGCGATGTTTGGCA ACGCCGCGATTGGTGGCCG ATGGCCGCTCCACCGATTGG GCGCAATGGCTTTGGTCA A A A T T G A C C A T C G C C T T C A T G C C G A A C G G T T A C A A C
K A G D V L Q R G D L V A D G A S T D L G E L A L G Q N M T I A F M P W N G Y N
2521 TACGAAGACTCGATTCTGAT TTCCGAAAAGTGGCTGCGG ATGATCGTTACACTTCGATT CACATTGAGGAATTAATGT CCGTCCCGGATACCAACG TGGGTGCGGAAACATTACC
Y E D S I L I S E K V A A D D R Y T S I H I E E L N V V A R D T K L G A E D I T
2641 CGCGATATCCGAACCTGTC CGAGCTGCAAAAACCGCT TGGACGATCCGCTATCGTT D E S G I V TACATCGTGCAGAAGTAGA AGCCGCGATGTGTTGGTAG GCAAAAGTACCGCTAAGGC
R D I P N L S E R M Q N R L D E S G I V Y I G A E V E A G D V L V G K V T P K G
2761 GAAACCAACTGACCGCGGA AGAAAACTGTGCGCGCA TCTTCCGCAAAAAGCGTCT TCGGCAAAAAGCGTCT CAGCTAAAAGATACTCACT D V K D T S L R M P T G M S G C G T V I D V
E T Q L T P E E K L L R A I F G E K A S D A G A A A G A T A C T C A C T D V K D T S L R M P T G M S G C G T V I D V
2881 CAAGTCTTCACTCGTGAAG TATTCAACGCAAAACCGC CCCAATCCATTATCGATTCC GAGTTGAAAACGCTACCGTTT GAGTTTGAACGACCAATTCG GTATTTCGACACAGCGCA
Q V F T R E G I Q R D K R A Q S I I D S E L K R Y R L D L N D Q L R I F D N D A
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F D R I E R M I V G Q K A N G G P M K L A K G S E I T T E Y L A G D K M A G R H W P S R H D W
3121 TTGCATATCCGTCTGACCGA TGAAGATTTGGCCAAGCT TGGAACTGATTAAGTGA C T G C A A C A A A A C C G C A A G A A G C G G A C A G A G T T A T A C G A A A
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3241 CAAGCGACGAATGCAACC CGCGTCAAAAATGGTGA AAGTTTTATCCCATCAA CCGCTCTCAAGCCGCGGA CAAATGGCGGGCCCGCAG CAAATGGCGGGCCCGCAG CAAATGGCGGGCCCGCAG CAAATGGCGGGCCCGCAG
Q D E L Q P G V Q K M V Q V F I A I K R R L Q A G D K M A G R H G K M A G R H G
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R I L P V D M P V M A D G R P V D I V L N P L G V P C T T G A C A G A C T C T A C A C G C T T G A C A C G A G A T T G
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L D S L T D E I I E L T E N L R K G A C A A T C A C C G T G A T G A C G G C A A A T C A C C G T G A T G A C G G Q I T L Y D G R S G E A F D R K V T V G
3721 TTGGCTTACCAAGCGAAGA TCCTGAGTTGAGAACTGG CTTCAACGACAGTAAACT G I T L Y D G G T C C A T A C A G T C T G G T T A C C C A A C A G C C T T T G G C G G T A A G C T C A G T T C G G T G C C A A
L A Y P S E D F E V E K L G F N D S K T GGTCCATACAGTCTGGTTAC G P Y S L V T G A G A T G C T G A C T G T G A A G T C Q Q P L G G K A Q F G G Q
3841 GTGATGCACTATCTGAAACT GCACCATTGGTTGACGAAA AAATGCACGCGCTTCTACC GATCCATACAGTCTGGTTAC G A Y T L Q A A Y T L Q A E M L T V K S E M L T V K S E M L T V K S
V M H Y L K L H H L V D E K M H A R S T GAGATGCTGACTGTGAAGTC D D V N G R T K M Y E N I
3961 CGTTCCGTTGAGATGAGGT TTGGCATTGGAAGCATACG GTGCGCATACACCGTCAA A A Y T L Q A A Y T L Q A G A G A T T C G T T C A C T G G C C T D D V N G R T K M Y E N I
R F A G E M E V W A L E A Y G C G A T G C G G T A T G C C G A G T C C T T C A C G T A T T G G T T A A A E M L T V K S E M L T V K S
4081 GTCAAGGCGAACACAAAAT V K G E H K I D A G M P E S F N V L V K E I R S L G L D I D L E R Y *

S549F Rif^R mutant strain

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1 GTGTATATGAGCTATTCGTT TACCGAGAAAAACGTATCC GTAAGAGTTTTGCAAGCGG GAAATGTTTTGGAAGTTCC TTTCTTGCTAGCAACCCAAA TTGATTCTTATGCGAAGTTT
M S Y S F T E K K R I R K S F A K R E N V L E V P F L L A T Q I D S Y A K F
121 TTGCAGCTGGAAATGCTTT TGACAAAGTACCGATGACG GTCTGCAGGCAGCATTTAAT TCTATTTTCCCGATTGTGAG CCATAACGGTTATGCGCGAT TGGAGTTTGTGATTACACA
L Q L E N A F D K R T D D G L Q A A F N S I F P I V S H N G Y A R L E F V H Y T
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L G E P L F D I P E C Q L R G I T Y A A P L E A R I R L V I L D K E A S K P T V
361 AAAGAAGTTCGTGAAAACGA AGTGTATATGGCGAAATTC CGTTGATGACCCCGAGCGST TCTTTTGTGATTAACGGCAC AGAGCGGTGTGATTGCTCCC AGTTGCACCCGTTCCGCCGCGC
K E V R E N E Y V M G E I I F L M T P S G S F V I N G T E R V I V S Q I L H R S P G
481 GTATTCTCGAGCATGACAA AGTAAGACGCACTCTTCGC GCAAATGTTATTCTCCGCGC GCATCATTCCCTACCGTGG TTCATGGTTGGATTTTGAAT TTGATCCGAAAGATTGTCTG
V F F E H D K G K T H S S G K L L F S A R I I P Y R G S W L D F E F D P K D L L
601 TATTCCGATATCGACCGCCG AGTGTATATGGCGAAATTC CGTTGATGACCCCGAGCGST TCTTTTGTGATTAACGGCAC AGAGCGGTGTGATTGCTCCC AGTTGCACCCGTTCCGCCGCGC
Y F R I D R R R K M P V T I L L K A L G Y N N E Q I L D I F Y D K E T F Y L S S
721 AACGAGTGTCAAACCGATTG GTTCGCGAGCGCTGAAAG GCGAAACTGCCAAGGTCGAT ATCTTTGGATAAAGAAGGCAA TGTATTGGTTGCCAAAGGTA AGCGTATTACTCGGAAAAAT
N G V Q T D L V A G R L K G E T A K V D I L D K E G N I L D K E G N V L V A K G K R I T A K N
841 ATCCGTGATTTACCAATGC AGGCCTGACCCGTTGGATG TAGAACCGGAAAGCCTGCTG GGCAAAGCATTGGCTCCCGA TCTGATTGATTGCGAAACCG CCGAGGATTGGCTTCTGCC
I R D I T N A A G L T R L D V E P E S L L G K A L A A D L I D S E T G E V L A S A
961 AATGGATAATACAGAAGA GTTGTGGCCAAATTTGATA TCAAACCGCTAAAAGAAATT ACGCATCTTACATCAATGA GTTGGATCAGGTGCTTATA TCTCCAATACCTGCCACAG
N D E I T E E L L A K F D I N G V K E I T T L Y I N E L D Q G A Y I S N T L R T
1081 GTTCCGATGCGCGCGCGCA GCGCGCGGCTGTTCGCAATT ACCTGATGATGCGTCCGGGC GAACCGCCACCCGAAGAGGC AGTCGAGCAATTGTTAACCC GCTTGTCTTCACTGAGAAC
D E T A G R G A A R V A I Y R M M R P G E P P T E E A V E Q L F N R L F P S E D
1201 AGCTACGATTTGCCCGCT AGGTCTGATGAAATTTAATA CGCGCACATACGAACAAAAA CTGTCCGAAGCCCAACAAAA TCTTGTGACGCGCGCTGCG TGAACGAAACGTTTGGCGGT
S Y D L S R V G R M K F N T R T Y E Q K L S E A Q Q N S W Y G R L L N E T F A G
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A A E K G G Y V L S V E D I V A S I A T L V E L R N G H G E V D D I D H L G N R
1441 CAGTACGTTGAGGCGGA GCTGACTGAAACCAATTC CGACGCGTTGGCCCGGTG GAACCGCACTGAAAGAACCG TTTGAATCAGCGGAACTG AAGCTTGTGCGGCTG
R V R S V G E L T E N Q F R S G L A R V E R A V K E R L N O A E S E N L M P H D
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L I N A K P V S A A I K E F F G S S Q L C S Q F M D Q T N P L E E V T H K R R V S
1681 CATTTGGTTCGGGCGTTT GACCTGGAACTGCGCGCT TCGAGGTACGGGAGCTGAT TCGAGGTACGGGAGCTGAT CAGCCCTTATCGACGGCAA R R V I D G K V V T E I D Y A A G G P N I G L
A L G P G G L T R E R A G F E V R D V H P T H Y G R V C P I E T P E G P N I G L
1801 ATCACTCATTTCCGTTTGA TCCGACCAATGATTACG GTTTCTGGAADCCCTTAC CCGCCGCTTATCGACGGCAA R R V I D G K V V T E I D Y A A G G P N I G L
I N S L S V Y A R T N D Y G F L E T P Y R R V I D G K V V T E I D Y A A G G P N I G L
1921 GCGCCCTATGTTCCGTTA GCGCAATGCGGATTTGGAT CAGATGCAATCGATTGGC D G N L I G D A T T V T C T R E K G E T I M A T P D R V Q
G R V T I A Q A N A D L D S C A T C C T G A T T C C G T T C T G A A C A T G A T G C G C G A A C C G C G A T T G A T T G G T G C C A A C A
2041 TATATGACGTGCAACCGG CCAGGTGATTCGTTGCGG Q V I V S V A G S L I P F L E H D D A N R A L M G A N M Q R Q A V P
Y M D V A T G S A T V A G A T G T T C G G T A C C G G T A T C R S V A V D T C T G A T A C T C G A A T C G T T G C S A T A I V A R R G G V E Y V D A N R
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K A G D V L Q R G D L V A D G A S T D L G E L A L G Q N M T I A F M P W N G Y N
2521 TACGAAGACTCGATTCTGAT TTCCGAAAAAGTGGCTGCGG ATGATCGTTACACTTCGATT C A C A T T G A G A A T T G A A T G T C A C A T T G A G A A T T G A A T G T H I E E L N V V A R D T K L G A E D I T
Y E D S I L I S E K V A A D D R Y T S I T A C A T C G G T G C A G A A G T A G A A G C G C G A T G T G T G T A G A G D V L V G A G D V L V G
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R D I P N L S E R M Q N R L D E S G I V Y I G A E V E A G D V L V G K V T P K G
2761 GAAACCAACTGACCGCGGA AGAAAACTGTGCGCGCA TCTTGGCGAAAAAGCGTCT T C G G E K A S G A C G T A A A G A T A C T C A C T D V K D T S L R M P T G M S G C G T V I D V
E T Q L T P E E K L L R A I F G E K A S G A C G T A A A G A T A C T C A C T D V K D T S L R M P T G M S G C G T V I D V
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3001 TTCCAGCTATCGAACGTA TATTGTTGGTCAAAAAGCCA ATGGTGGTCCGATAGCACTG G T A A G G C A G C G A A A T T A C T A C K S E I T T E Y L A G L P S R H D W
F D R I E R A N I V G Q K A N G G P M K L A K G S E I T T E Y L A G L P S R H D W
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F D I R L T Q D E D L A K Q L E L I K V S L Q Q K R E E A D E L Y E I K K K L T
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G D E L Q P G V Q K M V Q V F I A I K R R L Q A G D K M A G R H G K M A G R H G
3361 CGCATTCTGCCAGTGAAGA CATGCCTTACATGGCGGACG GCGTCCGTTAGACATCGTA CTGAACCCATTGGCGGTACC TTCCCGTATGAACATCGGCT S R M N I G Q I L E V H L
R I L P V E D R P V M A D G R P V D I V L N P L G V P C T T G A C A G A C T C A C A C G C T T G A C A C G C T T G A C A C G
3481 GGTGGCAGCAAAAGGTAT CGCGAGCGTATCGACCGTA TGCTGAAAGAGCAACGCAAA GCAGCCGAGTTGCCCGAGTT CTTGAACAGACTTACACAGC C G A C G A G A T T G A A G A G A T
G W A A K G I G E R I D R M L K E O R K A G E L R E F L N R L Y N G S G K K Y D
3601 TTGACAGCCTGACAGATGA AGAAATCTGCAATTTGCGTT CCAACTGCTTAAAGGTGCA TCTTTCGCTTCTCCTGTATT S F A S P V F D G A K E S E I R E H L N
L D S L T D E I I E L T E S N L R K G A C A A T C A C C G T G A T G A C G Q I T L Y D G R S G E A F D R K V T V G
3721 TTGGCTTACCAACGCAAGA TCCTGAGTTGAGAACTGG CTTCAACGACAGTAAACT G F N D S K T G G T C C A T A C A G T C T G G T T A C
L A Y P S E D F E V E K L G A A A T G C A C G C C G T T C A C C G P Y S L V T G A G A T G C T G A C T G T G A A G T C
3841 GTGATGCACTATCTGAAACT GCACCACCTTGGTTGACGAAA AATGACGCGCCGTTCTACC G A T C C A T A C A G T C T G G T T A C
V M H Y L K L H H L V D E K M H A R S T G A G A T G C T G A C T G T G A A G T C
3961 CGTTTCGTTGAGATGAGGT TTGGCATTGGAAGCATACG GTGCGGCATACACCGCTCAA A A Y T L Q A E M L T V K S
R F A G E M E V W A L E A Y G A A Y T L Q A E M L T V K S
4081 GTCAAAGCGCAACAAAAT CGATCCGCTATGCCGAGT CCTTCAACGATTTGGTTAAA GAGATTCTGTTCACTGGGCTT E I R S L G L D I D L E R Y
V K G E H K I D A G M P E S F N V L V K E I R S L G L D I D L E R Y

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FILE S1. Nucleotide and deduced amino acid sequences of the *rpoB* gene from wild type strain 93/4286 and derivative Rif^R mutant strains. Point mutations and corresponding amino acidic substitutions are represented in boldface and corresponding codons are underlined.

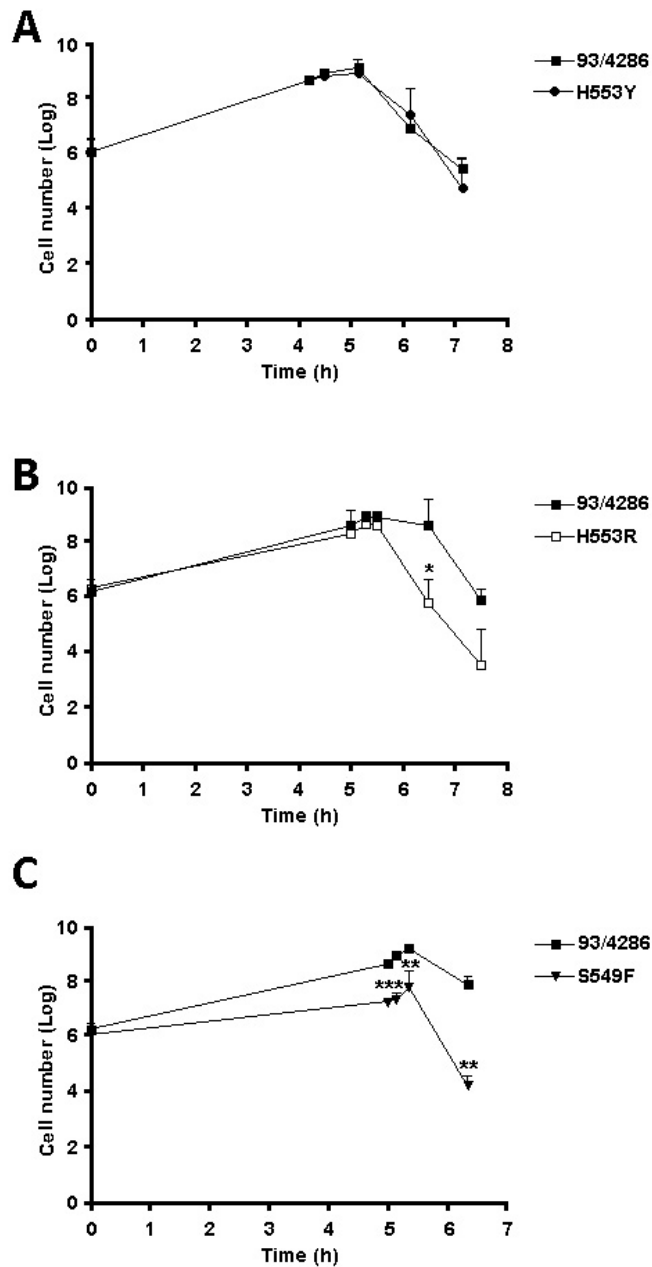


FIG. S1. Evaluation of rifampicin resistant mutants fitness in competition assay. (A-C) Survival curves of rifampicin-susceptible and rifampicin-resistant strains in competition growth in antibiotic-free GC broth at 37°C. The experiments were performed five times with five independent cultures, statistical significance was examined by the Student's t-test. Results are indicated as means \pm SD. Asterisks indicate statistical significance (*, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$).