Wild type strain 93/4286

```
   1 GTGTATATGAGCTATTCGTT TACCGAGAAAAAACGTATCC GTAAGAGTTTTGCAAAGCGG 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 TTGCAGCTGGAAAATGCTTT TGACAAACGTACCGATGACG GTCTGCAGGCAGCATTTAAT TCTATTTTCCCGATTGTGAG CCATAACGGTTATGCGCGAT TGGAGTTTGTGCATTACACA
     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
 241 TTGGGCGAGCCTTTGTTCGA TATTCCCGAATGTCAGTTGC GCGGAATCACTTATGCAGCC CCCTTGCGCGCGCGTATCCG TTTGGTGATTTTGGATAAGG AAGCATCTAAACCGACGGTA
     L  G  E  P  L  F  D   I  P  E  C  Q  L  R   G  I  T  Y  A  A   P  L  R  A  R  I  R   L  V  I  L  D  K  E   A  S  K  P  T  V
 361 AAAGAAGTTCGTGAAAACGA AGTGTATATGGGCGAAATTC CGTTGATGACCCCGAGCGGT TCTTTTGTGATTAACGGCAC AGAGCGTGTGATTGTCTCCC AGTTGCACCGTTCGCCCGGC
     K  E  V  R  E  N  E   V  Y  M  G  E  I  P   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
 481 GTATTCTTCGAGCATGACAA AGGTAAGACGCACTCTTCCG GCAAATTGTTATTCTCCGCC CGCATCATTCCCTACCGTGG TTCATGGTTGGATTTTGAAT TTGATCCGAAAGATTTGCTG
     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 TATTTCCGTATCGACCGCCG CCGTAAAATGCCGGTAACGA TTTTGTTGAAGGCTTTGGGC TACAACAATGAGCAAATCTT GGATATTTTCTACGACAAAG AAACGTTCTATTTGTCTTCA
     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 AACGGTGTTCAAACCGATTT GGTCGCAGGCCGTCTGAAAG GCGAAACTGCCAAGGTCGAT ATCTTGGATAAAGAAGGCAA TGTATTGGTTGCCAAAGGTA AGCGTATTACTGCGAAAAAT
     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   V  L  V  A  K  G  K   R  I  T  A  K  N
 841 ATCCGTGATATTACCAATGC AGGCCTGACCCGTTTGGATG TAGAACCGGAAAGCCTGCTG GGCAAAGCATTGGCTGCCGA TCTGATTGATTCGGAAACCG GCGAGGTATTGGCTTCTGCC
     I  R  D  I  T  N  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 AATGATGAAATTACAGAAGA GTTGTTGGCCAAATTTGATA TCAACGGCGTAAAAGAAATT ACGACCCTTTACATCAATGA GTTGGATCAGGGTGCTTATA TCTCCAATACCTTGCGCACG
     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 GATGAGACTGCCGGCCGGCA GGCGGCGCGTGTTGCGATTT ACCGTATGATGCGTCCGGGC GAACCGCCCACCGAAGAGGC AGTCGAGCAATTGTTTAACC GCTTGTTCTTCAGTGAAGAC
     D  E  T  A  G  R  Q   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  F  S  E  D
1201 AGCTACGATTTGTCCCGCGT AGGTCGTATGAAATTTAATA CGCGCACATACGAACAAAAA CTGTCCGAAGCCCAACAAAA CTCTTGGTACGGCCGCCTGC TGAACGAAACGTTTGCCGGT
     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
1321 GCTGCCGAAAAAGGCGGTTA TGTCCTGAGCGTCGAAGATA TTGTCGCCTCGATTGCGACT TTGGTCGAGTTGCGTAACGG CCATGGTGAAGTTGACGATA TCGATCACTTGGGCAACCGC
     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 CGAGTACGTTCGGTAGGCGA GCTGACTGAAAACCAATTCC GCAGCGGTTTGGCCCGTGTG GAACGTGCTGTAAAAGAACG TTTGAATCAGGCGGAATCAG AAAACTTGATGCCGCACGAT
     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
1561 TTGATTAATGCAAAACCTGT TTCTGCCGCTATTAAAGAAT TCTTCGGCTCCAGCCAATTG AGTCAGTTTATGGATCAGAC CAACCCCTTGTCTGAAGTAA CCCATAAACGCCGCGTATCT
     L  I  N  A  K  P  V   S  A  A  I  K  E  F   F  G  S  S  Q  L   S  Q  F  M  D  Q  T   N  P  L  S  E  V  T   H  K  R  R  V  S
1681 GCATTGGGTCCGGGCGGTTT GACCCGCGAACGTGCCGGCT TCGAGGTACGGGACGTGCAT CCGACCCACTACGGCCGCGT ATGTCCGATTGAAACGCCTG AAGGTCCGAACATCGGTTTG
     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 ATCAACTCATTGTCCGTTTA TGCGCGCACCAATGATTACG GTTTCTTGGAAACGCCTTAC CGCCGCGTTATCGACGGCAA AGTAACCGAGGAAATCGATT ACTTGTCTGCCATCGAAGAA
     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  T  E  E  I  D  Y   L  S  A  I  E  E
1921 GGCCGCTATGTGATTGCACA GGCGAATGCCGATTTGGATT CAGATGGCAATCTGATTGGC GATTTGGTTACCTGTCGTGA AAAAGGCGAAACCATTATGG CAACGCCCGACCGCGTCCAA
     G  R  Y  V  I  A  Q   A  N  A  D  L  D  S   D  G  N  L  I  G   D  L  V  T  C  R  E   K  G  E  T  I  M  A   T  P  D  R  V  Q
2041 TATATGGACGTGGCAACCGG CCAGGTGGTATCCGTTGCGG CATCCCTGATTCCGTTCTTG GAACATGATGACGCGAACCG CGCATTGATGGGTGCCAACA TGCAACGTCAGGCAGTGCCT
     Y  M  D  V  A  T  G   Q  V  V  S  V  A  A   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
2161 TGCTTGCGTCCTGAAAAACC GATGGTCGGTACCGGTATCG AGCGTTCCGTTGCCGTTGAC TCTGCTACTGCAATCGTTGC CCGCCGAGGCGGCGTGGTCG AGTATGTCGATGCCAACCGT
     C  L  R  P  E  K  P   M  V  G  T  G  I  E   R  S  V  A  V  D   S  A  T  A  I  V  A   R  R  G  G  V  V  E   Y  V  D  A  N  R
2281 GTTGTGATTCGTGTCCATGA CGACGAAGCGACTGCCGGCG AAGTGGGTGTCGATATTTAC AACTTGGTTAAATTTACCCG TTCCAACCAGTCTACCAATA TCAATCAGCGTCCTGCCGTC
     V  V  I  R  V  H  D   D  E  A  T  A  G  E   V  G  V  D  I  Y   N  L  V  K  F  T  R   S  N  Q  S  T  N  I   N  Q  R  P  A  V
2401 AAAGCCGGCGATGTTTTGCA ACGCGGCGATTTGGTGGCCG ATGGCGCGTCCACCGATTTG GGCGAATTGGCTTTGGGTCA AAATATGACCATCGCCTTCA TGCCGTGGAACGGTTACAAC
     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 CACATTGAGGAATTGAATGT CGTTGCCCGCGATACCAAGC TGGGTGCGGAAGACATTACC
     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 CGCGATATTCCGAACTTGTC CGAGCGTATGCAAAACCGCT TGGACGAATCCGGTATCGTT TACATCGGTGCAGAAGTAGA AGCCGGCGATGTGTTGGTAG GCAAAGTAACGCCTAAAGGC
     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 GAAACCCAACTGACGCCGGA AGAAAAACTGTTGCGCGCCA TCTTCGGCGAAAAAGCGTCT GACGTAAAAGATACTTCACT GCGTATGCCTACCGGTATGA GCGGTACGGTTATCGACGTT
     E  T  Q  L  T  P  E   E  K  L  L  R  A  I   F  G  E  K  A  S   D  V  K  D  T  S  L   R  M  P  T  G  M  S   G  T  V  I  D  V
2881 CAAGTCTTCACTCGTGAAGG TATTCAACGCGACAAACGCG CCCAATCCATTATCGATTCC GAGTTGAAACGCTACCGTTT GGATTTGAACGACCAATTGC GTATTTTCGACAACGACGCA
     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
3001 TTCGACCGTATCGAACGTAT GATTGTGGGTCAAAAAGCCA ATGGTGGTCCGATGAAGCTG GCTAAAGGCAGCGAAATTAC TACCGAATATTTGGCGGGTC TGCCGAGCAGGCACGATTGG
     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  L   P  S  R  H  D  W
3121 TTCGATATCCGTCTGACCGA TGAAGATTTGGCCAAGCAGT TGGAACTGATTAAAGTGAGC CTGCAACAAAAACGCGAAGA AGCGGACGAGTTATACGAAA TCAAGAAGAAAAAACTGACC
     F  D  I  R  L  T  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  K  L  T
3241 CAAGGCGACGAATTGCAACC CGGCGTACAAAAAATGGTGA AAGTTTTTATCGCCATCAAA CGCCGTCTGCAAGCCGGCGA CAAAATGGCGGGCCGCCACG GTAACAAAGGCGTGGTATCG
     Q  G  D  E  L  Q  P   G  V  Q  K  M  V  K   V  F  I  A  I  K   R  R  L  Q  A  G  D   K  M  A  G  R  H  G   N  K  G  V  V  S
3361 CGCATTCTGCCAGTGGAAGA CATGCCTTACATGGCGGACG GCCGTCCGGTAGACATCGTA CTGAACCCATTGGGCGTACC TTCCCGTATGAACATCGGTC AGATTTTGGAAGTTCACTTG
     R  I  L  P  V  E  D   M  P  Y  M  A  D  G   R  P  V  D  I  V   L  N  P  L  G  V  P   S  R  M  N  I  G  Q   I  L  E  V  H  L
3481 GGTTGGGCAGCAAAAGGTAT CGGCGAGCGTATCGACCGTA TGCTGAAAGAGCAACGCAAA GCAGGCGAGTTGCGCGAGTT CTTGAACAGACTCTACAACG GCAGCGGTAAGAAAGAAGAT
     G  W  A  A  K  G  I   G  E  R  I  D  R  M   L  K  E  Q  R  K   A  G  E  L  R  E  F   L  N  R  L  Y  N  G   S  G  K  K  E  D
3601 TTGGACAGCCTGACAGATGA AGAAATCATCGAATTGGCTT CCAACCTGCGTAAAGGTGCA TCTTTCGCTTCTCCTGTATT CGACGGTGCGAAAGAGTCTG AAATCCGCGAAATGTTGAAC
     L  D  S  L  T  D  E   E  I  I  E  L  A  S   N  L  R  K  G  A   S  F  A  S  P  V  F   D  G  A  K  E  S  E   I  R  E  M  L  N
3721 TTGGCTTACCCAAGCGAAGA TCCTGAGGTTGAGAAACTGG GCTTCAACGACAGTAAAACT CAAATCACGCTGTATGACGG CCGTTCAGGCGAAGCATTTG ATCGCAAGGTTACAGTCGGT
     L  A  Y  P  S  E  D   P  E  V  E  K  L  G   F  N  D  S  K  T   Q  I  T  L  Y  D  G   R  S  G  E  A  F  D   R  K  V  T  V  G
3841 GTGATGCACTATCTGAAACT GCACCACTTGGTTGACGAAA AAATGCACGCCCGTTCTACC GGTCCATACAGTCTGGTTAC CCAACAGCCTTTGGGCGGTA AAGCTCAGTTCGGTGGCCAA
     V  M  H  Y  L  K  L   H  H  L  V  D  E  K   M  H  A  R  S  T   G  P  Y  S  L  V  T   Q  Q  P  L  G  G  K   A  Q  F  G  G  Q
3961 CGTTTCGGTGAGATGGAGGT TTGGGCATTGGAAGCATACG GTGCGGCATACACGCTGCAA GAGATGCTGACTGTGAAGTC TGATGACGTGAACGGCCGTA CCAAAATGTACGAGAACATC
     R  F  G  E  M  E  V   W  A  L  E  A  Y  G   A  A  Y  T  L  Q   E  M  L  T  V  K  S   D  D  V  N  G  R  T   K  M  Y  E  N  I
4081 GTCAAAGGCGAACACAAAAT CGATGCCGGTATGCCCGAGT CCTTCAACGTATTGGTTAAA GAGATTCGTTCACTGGGCTT GGATATCGATTTGGAACGCT ACTAA
     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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H553Y Rif^R mutant strain

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   1 GTGTATATGAGCTATTCGTT TACCGAGAAAAAACGTATCC GTAAGAGTTTTGCAAAGCGG 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 TTGCAGCTGGAAAATGCTTT TGACAAACGTACCGATGACG GTCTGCAGGCAGCATTTAAT TCTATTTTCCCGATTGTGAG CCATAACGGTTATGCGCGAT TGGAGTTTGTGCATTACACA
     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
 241 TTGGGCGAGCCTTTGTTCGA TATTCCCGAATGTCAGTTGC GCGGAATCACTTATGCAGCC CCCTTGCGCGCGCGTATCCG TTTGGTGATTTTGGATAAGG AAGCATCTAAACCGACGGTA
     L  G  E  P  L  F  D   I  P  E  C  Q  L  R   G  I  T  Y  A  A   P  L  R  A  R  I  R   L  V  I  L  D  K  E   A  S  K  P  T  V
 361 AAAGAAGTTCGTGAAAACGA AGTGTATATGGGCGAAATTC CGTTGATGACCCCGAGCGGT TCTTTTGTGATTAACGGCAC AGAGCGTGTGATTGTCTCCC AGTTGCACCGTTCGCCCGGC
     K  E  V  R  E  N  E   V  Y  M  G  E  I  P   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
 481 GTATTCTTCGAGCATGACAA AGGTAAGACGCACTCTTCCG GCAAATTGTTATTCTCCGCC CGCATCATTCCCTACCGTGG TTCATGGTTGGATTTTGAAT TTGATCCGAAAGATTTGCTG
     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 TATTTCCGTATCGACCGCCG CCGTAAAATGCCGGTAACGA TTTTGTTGAAGGCTTTGGGC TACAACAATGAGCAAATCTT GGATATTTTCTACGACAAAG AAACGTTCTATTTGTCTTCA
     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 AACGGTGTTCAAACCGATTT GGTCGCAGGCCGTCTGAAAG GCGAAACTGCCAAGGTCGAT ATCTTGGATAAAGAAGGCAA TGTATTGGTTGCCAAAGGTA AGCGTATTACTGCGAAAAAT
     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   V  L  V  A  K  G  K   R  I  T  A  K  N
 841 ATCCGTGATATTACCAATGC AGGCCTGACCCGTTTGGATG TAGAACCGGAAAGCCTGCTG GGCAAAGCATTGGCTGCCGA TCTGATTGATTCGGAAACCG GCGAGGTATTGGCTTCTGCC
     I  R  D  I  T  N  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 AATGATGAAATTACAGAAGA GTTGTTGGCCAAATTTGATA TCAACGGCGTAAAAGAAATT ACGACCCTTTACATCAATGA GTTGGATCAGGGTGCTTATA TCTCCAATACCTTGCGCACG
     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 GATGAGACTGCCGGCCGGCA GGCGGCGCGTGTTGCGATTT ACCGTATGATGCGTCCGGGC GAACCGCCCACCGAAGAGGC AGTCGAGCAATTGTTTAACC GCTTGTTCTTCAGTGAAGAC
     D  E  T  A  G  R  Q   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  F  S  E  D
1201 AGCTACGATTTGTCCCGCGT AGGTCGTATGAAATTTAATA CGCGCACATACGAACAAAAA CTGTCCGAAGCCCAACAAAA CTCTTGGTACGGCCGCCTGC TGAACGAAACGTTTGCCGGT
     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
1321 GCTGCCGAAAAAGGCGGTTA TGTCCTGAGCGTCGAAGATA TTGTCGCCTCGATTGCGACT TTGGTCGAGTTGCGTAACGG CCATGGTGAAGTTGACGATA TCGATCACTTGGGCAACCGC
     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 CGAGTACGTTCGGTAGGCGA GCTGACTGAAAACCAATTCC GCAGCGGTTTGGCCCGTGTG GAACGTGCTGTAAAAGAACG TTTGAATCAGGCGGAATCAG AAAACTTGATGCCGCACGAT
     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
1561 TTGATTAATGCAAAACCTGT TTCTGCCGCTATTAAAGAAT TCTTCGGCTCCAGCCAATTG AGTCAGTTTATGGATCAGAC CAACCCCTTGTCTGAAGTAA CCTATAAACGCCGCGTATCT
     L  I  N  A  K  P  V   S  A  A  I  K  E  F   F  G  S  S  Q  L   S  Q  F  M  D  Q  T   N  P  L  S  E  V  T   Y  K  R  R  V  S
1681 GCATTGGGTCCGGGCGGTTT GACCCGCGAACGTGCCGGCT TCGAGGTACGGGACGTGCAT CCGACCCACTACGGCCGCGT ATGTCCGATTGAAACGCCTG AAGGTCCGAACATCGGTTTG
     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 ATCAACTCATTGTCCGTTTA TGCGCGCACCAATGATTACG GTTTCTTGGAAACGCCTTAC CGCCGCGTTATCGACGGCAA AGTAACCGAGGAAATCGATT ACTTGTCTGCCATCGAAGAA
     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  T  E  E  I  D  Y   L  S  A  I  E  E
1921 GGCCGCTATGTGATTGCACA GGCGAATGCCGATTTGGATT CAGATGGCAATCTGATTGGC GATTTGGTTACCTGTCGTGA AAAAGGCGAAACCATTATGG CAACGCCCGACCGCGTCCAA
     G  R  Y  V  I  A  Q   A  N  A  D  L  D  S   D  G  N  L  I  G   D  L  V  T  C  R  E   K  G  E  T  I  M  A   T  P  D  R  V  Q
2041 TATATGGACGTGGCAACCGG CCAGGTGGTATCCGTTGCGG CATCCCTGATTCCGTTCTTG GAACATGATGACGCGAACCG CGCATTGATGGGTGCCAACA TGCAACGTCAGGCAGTGCCT
     Y  M  D  V  A  T  G   Q  V  V  S  V  A  A   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
2161 TGCTTGCGTCCTGAAAAACC GATGGTCGGTACCGGTATCG AGCGTTCCGTTGCCGTTGAC TCTGCTACTGCAATCGTTGC CCGCCGAGGCGGCGTGGTCG AGTATGTCGATGCCAACCGT
     C  L  R  P  E  K  P   M  V  G  T  G  I  E   R  S  V  A  V  D   S  A  T  A  I  V  A   R  R  G  G  V  V  E   Y  V  D  A  N  R
2281 GTTGTGATTCGTGTCCATGA CGACGAAGCGACTGCCGGCG AAGTGGGTGTCGATATTTAC AACTTGGTTAAATTTACCCG TTCCAACCAGTCTACCAATA TCAATCAGCGTCCTGCCGTC
     V  V  I  R  V  H  D   D  E  A  T  A  G  E   V  G  V  D  I  Y   N  L  V  K  F  T  R   S  N  Q  S  T  N  I   N  Q  R  P  A  V
2401 AAAGCCGGCGATGTTTTGCA ACGCGGCGATTTGGTGGCCG ATGGCGCGTCCACCGATTTG GGCGAATTGGCTTTGGGTCA AAATATGACCATCGCCTTCA TGCCGTGGAACGGTTACAAC
     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 CACATTGAGGAATTGAATGT CGTTGCCCGCGATACCAAGC TGGGTGCGGAAGACATTACC
     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 CGCGATATTCCGAACTTGTC CGAGCGTATGCAAAACCGCT TGGACGAATCCGGTATCGTT TACATCGGTGCAGAAGTAGA AGCCGGCGATGTGTTGGTAG GCAAAGTAACGCCTAAAGGC
     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 GAAACCCAACTGACGCCGGA AGAAAAACTGTTGCGCGCCA TCTTCGGCGAAAAAGCGTCT GACGTAAAAGATACTTCACT GCGTATGCCTACCGGTATGA GCGGTACGGTTATCGACGTT
     E  T  Q  L  T  P  E   E  K  L  L  R  A  I   F  G  E  K  A  S   D  V  K  D  T  S  L   R  M  P  T  G  M  S   G  T  V  I  D  V
2881 CAAGTCTTCACTCGTGAAGG TATTCAACGCGACAAACGCG CCCAATCCATTATCGATTCC GAGTTGAAACGCTACCGTTT GGATTTGAACGACCAATTGC GTATTTTCGACAACGACGCA
     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
3001 TTCGACCGTATCGAACGTAT GATTGTGGGTCAAAAAGCCA ATGGTGGTCCGATGAAGCTG GCTAAAGGCAGCGAAATTAC TACCGAATATTTGGCGGGTC TGCCGAGCAGGCACGATTGG
     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  L   P  S  R  H  D  W
3121 TTCGATATCCGTCTGACCGA TGAAGATTTGGCCAAGCAGT TGGAACTGATTAAAGTGAGC CTGCAACAAAAACGCGAAGA AGCGGACGAGTTATACGAAA TCAAGAAGAAAAAACTGACC
     F  D  I  R  L  T  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  K  L  T
3241 CAAGGCGACGAATTGCAACC CGGCGTACAAAAAATGGTGA AAGTTTTTATCGCCATCAAA CGCCGTCTGCAAGCCGGCGA CAAAATGGCGGGCCGCCACG GTAACAAAGGCGTGGTATCG
     Q  G  D  E  L  Q  P   G  V  Q  K  M  V  K   V  F  I  A  I  K   R  R  L  Q  A  G  D   K  M  A  G  R  H  G   N  K  G  V  V  S
3361 CGCATTCTGCCAGTGGAAGA CATGCCTTACATGGCGGACG GCCGTCCGGTAGACATCGTA CTGAACCCATTGGGCGTACC TTCCCGTATGAACATCGGTC AGATTTTGGAAGTTCACTTG
     R  I  L  P  V  E  D   M  P  Y  M  A  D  G   R  P  V  D  I  V   L  N  P  L  G  V  P   S  R  M  N  I  G  Q   I  L  E  V  H  L
3481 GGTTGGGCAGCAAAAGGTAT CGGCGAGCGTATCGACCGTA TGCTGAAAGAGCAACGCAAA GCAGGCGAGTTGCGCGAGTT CTTGAACAGACTCTACAACG GCAGCGGTAAGAAAGAAGAT
     G  W  A  A  K  G  I   G  E  R  I  D  R  M   L  K  E  Q  R  K   A  G  E  L  R  E  F   L  N  R  L  Y  N  G   S  G  K  K  E  D
3601 TTGGACAGCCTGACAGATGA AGAAATCATCGAATTGGCTT CCAACCTGCGTAAAGGTGCA TCTTTCGCTTCTCCTGTATT CGACGGTGCGAAAGAGTCTG AAATCCGCGAAATGTTGAAC
     L  D  S  L  T  D  E   E  I  I  E  L  A  S   N  L  R  K  G  A   S  F  A  S  P  V  F   D  G  A  K  E  S  E   I  R  E  M  L  N
3721 TTGGCTTACCCAAGCGAAGA TCCTGAGGTTGAGAAACTGG GCTTCAACGACAGTAAAACT CAAATCACGCTGTATGACGG CCGTTCAGGCGAAGCATTTG ATCGCAAGGTTACAGTCGGT
     L  A  Y  P  S  E  D   P  E  V  E  K  L  G   F  N  D  S  K  T   Q  I  T  L  Y  D  G   R  S  G  E  A  F  D   R  K  V  T  V  G
3841 GTGATGCACTATCTGAAACT GCACCACTTGGTTGACGAAA AAATGCACGCCCGTTCTACC GGTCCATACAGTCTGGTTAC CCAACAGCCTTTGGGCGGTA AAGCTCAGTTCGGTGGCCAA
     V  M  H  Y  L  K  L   H  H  L  V  D  E  K   M  H  A  R  S  T   G  P  Y  S  L  V  T   Q  Q  P  L  G  G  K   A  Q  F  G  G  Q
3961 CGTTTCGGTGAGATGGAGGT TTGGGCATTGGAAGCATACG GTGCGGCATACACGCTGCAA GAGATGCTGACTGTGAAGTC TGATGACGTGAACGGCCGTA CCAAAATGTACGAGAACATC
     R  F  G  E  M  E  V   W  A  L  E  A  Y  G   A  A  Y  T  L  Q   E  M  L  T  V  K  S   D  D  V  N  G  R  T   K  M  Y  E  N  I
4081 GTCAAAGGCGAACACAAAAT CGATGCCGGTATGCCCGAGT CCTTCAACGTATTGGTTAAA GAGATTCGTTCACTGGGCTT GGATATCGATTTGGAACGCT ACTAA
     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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H553R Rif^{R} mutant strain

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    1 GTGTATATGAGCTATTCGTT TACCGAGAAAAAACGTATCC GTAAGAGTTTTGCAAAGCGG 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 TTGCAGCTGGAAAATGCTTT TGACAAACGTACCGATGACG GTCTGCAGGCAGCATTTAAT TCTATTTTCCCGATTGTGAG CCATAACGGTTATGCGCGAT TGGAGTTTGTGCATTACACA
      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
  241 TTGGGCGAGCCTTTGTTCGA TATTCCCGAATGTCAGTTGC GCGGAATCACTTATGCAGCC CCCTTGCGCGCGCGTATCCG TTTGGTGATTTTGGATAAGG AAGCATCTAAACCGACGGTA
      L  G  E  P  L  F  D   I  P  E  C  Q  L  R   G  I  T  Y  A  A   P  L  R  A  R  I  R   L  V  I  L  D  K  E   A  S  K  P  T  V
  361 AAAGAAGTTCGTGAAAACGA AGTGTATATGGGCGAAATTC CGTTGATGACCCCGAGCGGT TCTTTTGTGATTAACGGCAC AGAGCGTGTGATTGTCTCCC AGTTGCACCGTTCGCCCGGC
      K  E  V  R  E  N  E   V  Y  M  G  E  I  P   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
  481 GTATTCTTCGAGCATGACAA AGGTAAGACGCACTCTTCCG GCAAATTGTTATTCTCCGCC CGCATCATTCCCTACCGTGG TTCATGGTTGGATTTTGAAT TTGATCCGAAAGATTTGCTG
      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 TATTTCCGTATCGACCGCCG CCGTAAAATGCCGGTAACGA TTTTGTTGAAGGCTTTGGGC TACAACAATGAGCAAATCTT GGATATTTTCTACGACAAAG AAACGTTCTATTTGTCTTCA
      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 AACGGTGTTCAAACCGATTT GGTCGCAGGCCGTCTGAAAG GCGAAACTGCCAAGGTCGAT ATCTTGGATAAAGAAGGCAA TGTATTGGTTGCCAAAGGTA AGCGTATTACTGCGAAAAAT
      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   V  L  V  A  K  G  K   R  I  T  A  K  N
  841 ATCCGTGATATTACCAATGC AGGCCTGACCCGTTTGGATG TAGAACCGGAAAGCCTGCTG GGCAAAGCATTGGCTGCCGA TCTGATTGATTCGGAAACCG GCGAGGTATTGGCTTCTGCC
      I  R  D  I  T  N  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 AATGATGAAATTACAGAAGA GTTGTTGGCCAAATTTGATA TCAACGGCGTAAAAGAAATT ACGACCCTTTACATCAATGA GTTGGATCAGGGTGCTTATA TCTCCAATACCTTGCGCACG
      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 GATGAGACTGCCGGCCGGCA GGCGGCGCGTGTTGCGATTT ACCGTATGATGCGTCCGGGC GAACCGCCCACCGAAGAGGC AGTCGAGCAATTGTTTAACC GCTTGTTCTTCAGTGAAGAC
      D  E  T  A  G  R  Q   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  F  S  E  D
 1201 AGCTACGATTTGTCCCGCGT AGGTCGTATGAAATTTAATA CGCGCACATACGAACAAAAA CTGTCCGAAGCCCAACAAAA CTCTTGGTACGGCCGCCTGC TGAACGAAACGTTTGCCGGT
      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
 1321 GCTGCCGAAAAAGGCGGTTA TGTCCTGAGCGTCGAAGATA TTGTCGCCTCGATTGCGACT TTGGTCGAGTTGCGTAACGG CCATGGTGAAGTTGACGATA TCGATCACTTGGGCAACCGC
      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 CGAGTACGTTCGGTAGGCGA GCTGACTGAAAACCAATTCC GCAGCGGTTTGGCCCGTGTG GAACGTGCTGTAAAAGAACG TTTGAATCAGGCGGAATCAG AAAACTTGATGCCGCACGAT
      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
 1561 TTGATTAATGCAAAACCTGT TTCTGCCGCTATTAAAGAAT TCTTCGGCTCCAGCCAATTG AGTCAGTTTATGGATCAGAC CAACCCCTTGTCTGAAGTAA CCCGTAAACGCCGCGTATCT
      L  I  N  A  K  P  V   S  A  A  I  K  E  F   F  G  S  S  Q  L   S  Q  F  M  D  Q  T   N  P  L  S  E  V  T   R  K  R  R  V  S
 1681 GCATTGGGTCCGGGCGGTTT GACCCGCGAACGTGCCGGCT TCGAGGTACGGGACGTGCAT CCGACCCACTACGGCCGCGT ATGTCCGATTGAAACGCCTG AAGGTCCGAACATCGGTTTG
      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 ATCAACTCATTGTCCGTTTA TGCGCGCACCAATGATTACG GTTTCTTGGAAACGCCTTAC CGCCGCGTTATCGACGGCAA AGTAACCGAGGAAATCGATT ACTTGTCTGCCATCGAAGAA
      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  T  E  E  I  D  Y   L  S  A  I  E  E
 1921 GGCCGCTATGTGATTGCACA GGCGAATGCCGATTTGGATT CAGATGGCAATCTGATTGGC GATTTGGTTACCTGTCGTGA AAAAGGCGAAACCATTATGG CAACGCCCGACCGCGTCCAA
      G  R  Y  V  I  A  Q   A  N  A  D  L  D  S   D  G  N  L  I  G   D  L  V  T  C  R  E   K  G  E  T  I  M  A   T  P  D  R  V  Q
 2041 TATATGGACGTGGCAACCGG CCAGGTGGTATCCGTTGCGG CATCCCTGATTCCGTTCTTG GAACATGATGACGCGAACCG CGCATTGATGGGTGCCAACA TGCAACGTCAGGCAGTGCCT
      Y  M  D  V  A  T  G   Q  V  V  S  V  A  A   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
 2161 TGCTTGCGTCCTGAAAAACC GATGGTCGGTACCGGTATCG AGCGTTCCGTTGCCGTTGAC TCTGCTACTGCAATCGTTGC CCGCCGAGGCGGCGTGGTCG AGTATGTCGATGCCAACCGT
      C  L  R  P  E  K  P   M  V  G  T  G  I  E   R  S  V  A  V  D   S  A  T  A  I  V  A   R  R  G  G  V  V  E   Y  V  D  A  N  R
 2281 GTTGTGATTCGTGTCCATGA CGACGAAGCGACTGCCGGCG AAGTGGGTGTCGATATTTAC AACTTGGTTAAATTTACCCG TTCCAACCAGTCTACCAATA TCAATCAGCGTCCTGCCGTC
      V  V  I  R  V  H  D   D  E  A  T  A  G  E   V  G  V  D  I  Y   N  L  V  K  F  T  R   S  N  Q  S  T  N  I   N  Q  R  P  A  V
 2401 AAAGCCGGCGATGTTTTGCA ACGCGGCGATTTGGTGGCCG ATGGCGCGTCCACCGATTTG GGCGAATTGGCTTTGGGTCA AAATATGACCATCGCCTTCA TGCCGTGGAACGGTTACAAC
      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 CACATTGAGGAATTGAATGT CGTTGCCCGCGATACCAAGC TGGGTGCGGAAGACATTACC
      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 CGCGATATTCCGAACTTGTC CGAGCGTATGCAAAACCGCT TGGACGAATCCGGTATCGTT TACATCGGTGCAGAAGTAGA AGCCGGCGATGTGTTGGTAG GCAAAGTAACGCCTAAAGGC
      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 GAAACCCAACTGACGCCGGA AGAAAAACTGTTGCGCGCCA TCTTCGGCGAAAAAGCGTCT GACGTAAAAGATACTTCACT GCGTATGCCTACCGGTATGA GCGGTACGGTTATCGACGTT
      E  T  Q  L  T  P  E   E  K  L  L  R  A  I   F  G  E  K  A  S   D  V  K  D  T  S  L   R  M  P  T  G  M  S   G  T  V  I  D  V
 2881 CAAGTCTTCACTCGTGAAGG TATTCAACGCGACAAACGCG CCCAATCCATTATCGATTCC GAGTTGAAACGCTACCGTTT GGATTTGAACGACCAATTGC GTATTTTCGACAACGACGCA
      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
 3001 TTCGACCGTATCGAACGTAT GATTGTGGGTCAAAAAGCCA ATGGTGGTCCGATGAAGCTG GCTAAAGGCAGCGAAATTAC TACCGAATATTTGGCGGGTC TGCCGAGCAGGCACGATTGG
      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  L   P  S  R  H  D  W
 3121 TTCGATATCCGTCTGACCGA TGAAGATTTGGCCAAGCAGT TGGAACTGATTAAAGTGAGC CTGCAACAAAAACGCGAAGA AGCGGACGAGTTATACGAAA TCAAGAAGAAAAAACTGACC
      F  D  I  R  L  T  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  K  L  T
 3241 CAAGGCGACGAATTGCAACC CGGCGTACAAAAAATGGTGA AAGTTTTTATCGCCATCAAA CGCCGTCTGCAAGCCGGCGA CAAAATGGCGGGCCGCCACG GTAACAAAGGCGTGGTATCG
      Q  G  D  E  L  Q  P   G  V  Q  K  M  V  K   V  F  I  A  I  K   R  R  L  Q  A  G  D   K  M  A  G  R  H  G   N  K  G  V  V  S
 3361 CGCATTCTGCCAGTGGAAGA CATGCCTTACATGGCGGACG GCCGTCCGGTAGACATCGTA CTGAACCCATTGGGCGTACC TTCCCGTATGAACATCGGTC AGATTTTGGAAGTTCACTTG
      R  I  L  P  V  E  D   M  P  Y  M  A  D  G   R  P  V  D  I  V   L  N  P  L  G  V  P   S  R  M  N  I  G  Q   I  L  E  V  H  L
 3481 GGTTGGGCAGCAAAAGGTAT CGGCGAGCGTATCGACCGTA TGCTGAAAGAGCAACGCAAA GCAGGCGAGTTGCGCGAGTT CTTGAACAGACTCTACAACG GCAGCGGTAAGAAAGAAGAT
      G  W  A  A  K  G  I   G  E  R  I  D  R  M   L  K  E  Q  R  K   A  G  E  L  R  E  F   L  N  R  L  Y  N  G   S  G  K  K  E  D
 3601 TTGGACAGCCTGACAGATGA AGAAATCATCGAATTGGCTT CCAACCTGCGTAAAGGTGCA TCTTTCGCTTCTCCTGTATT CGACGGTGCGAAAGAGTCTG AAATCCGCGAAATGTTGAAC
      L  D  S  L  T  D  E   E  I  I  E  L  A  S   N  L  R  K  G  A   S  F  A  S  P  V  F   D  G  A  K  E  S  E   I  R  E  M  L  N
 3721 TTGGCTTACCCAAGCGAAGA TCCTGAGGTTGAGAAACTGG GCTTCAACGACAGTAAAACT CAAATCACGCTGTATGACGG CCGTTCAGGCGAAGCATTTG ATCGCAAGGTTACAGTCGGT
      L  A  Y  P  S  E  D   P  E  V  E  K  L  G   F  N  D  S  K  T   Q  I  T  L  Y  D  G   R  S  G  E  A  F  D   R  K  V  T  V  G
 3841 GTGATGCACTATCTGAAACT GCACCACTTGGTTGACGAAA AAATGCACGCCCGTTCTACC GGTCCATACAGTCTGGTTAC CCAACAGCCTTTGGGCGGTA AAGCTCAGTTCGGTGGCCAA
      V  M  H  Y  L  K  L   H  H  L  V  D  E  K   M  H  A  R  S  T   G  P  Y  S  L  V  T   Q  Q  P  L  G  G  K   A  Q  F  G  G  Q
 3961 CGTTTCGGTGAGATGGAGGT TTGGGCATTGGAAGCATACG GTGCGGCATACACGCTGCAA GAGATGCTGACTGTGAAGTC TGATGACGTGAACGGCCGTA CCAAAATGTACGAGAACATC
      R  F  G  E  M  E  V   W  A  L  E  A  Y  G   A  A  Y  T  L  Q   E  M  L  T  V  K  S   D  D  V  N  G  R  T   K  M  Y  E  N  I
 4081 GTCAAAGGCGAACACAAAAT CGATGCCGGTATGCCCGAGT CCTTCAACGTATTGGTTAAA GAGATTCGTTCACTGGGCTT GGATATCGATTTGGAACGCT ACTAA
      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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S549F Rif^R mutant strain

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   1 GTGTATATGAGCTATTCGTT TACCGAGAAAAAACGTATCC GTAAGAGTTTTGCAAAGCGG 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 TTGCAGCTGGAAAATGCTTT TGACAAACGTACCGATGACG GTCTGCAGGCAGCATTTAAT TCTATTTTCCCGATTGTGAG CCATAACGGTTATGCGCGAT TGGAGTTTGTGCATTACACA
     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
 241 TTGGGCGAGCCTTTGTTCGA TATTCCCGAATGTCAGTTGC GCGGAATCACTTATGCAGCC CCCTTGCGCGCGCGTATCCG TTTGGTGATTTTGGATAAGG AAGCATCTAAACCGACGGTA
     L  G  E  P  L  F  D   I  P  E  C  Q  L  R   G  I  T  Y  A  A   P  L  R  A  R  I  R   L  V  I  L  D  K  E   A  S  K  P  T  V
 361 AAAGAAGTTCGTGAAAACGA AGTGTATATGGGCGAAATTC CGTTGATGACCCCGAGCGGT TCTTTTGTGATTAACGGCAC AGAGCGTGTGATTGTCTCCC AGTTGCACCGTTCGCCCGGC
     K  E  V  R  E  N  E   V  Y  M  G  E  I  P   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
 481 GTATTCTTCGAGCATGACAA AGGTAAGACGCACTCTTCCG GCAAATTGTTATTCTCCGCC CGCATCATTCCCTACCGTGG TTCATGGTTGGATTTTGAAT TTGATCCGAAAGATTTGCTG
     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 TATTTCCGTATCGACCGCCG CCGTAAAATGCCGGTAACGA TTTTGTTGAAGGCTTTGGGC TACAACAATGAGCAAATCTT GGATATTTTCTACGACAAAG AAACGTTCTATTTGTCTTCA
     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 AACGGTGTTCAAACCGATTT GGTCGCAGGCCGTCTGAAAG GCGAAACTGCCAAGGTCGAT ATCTTGGATAAAGAAGGCAA TGTATTGGTTGCCAAAGGTA AGCGTATTACTGCGAAAAAT
     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   V  L  V  A  K  G  K   R  I  T  A  K  N
 841 ATCCGTGATATTACCAATGC AGGCCTGACCCGTTTGGATG TAGAACCGGAAAGCCTGCTG GGCAAAGCATTGGCTGCCGA TCTGATTGATTCGGAAACCG GCGAGGTATTGGCTTCTGCC
     I  R  D  I  T  N  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 AATGATGAAATTACAGAAGA GTTGTTGGCCAAATTTGATA TCAACGGCGTAAAAGAAATT ACGACCCTTTACATCAATGA GTTGGATCAGGGTGCTTATA TCTCCAATACCTTGCGCACG
     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 GATGAGACTGCCGGCCGGCA GGCGGCGCGTGTTGCGATTT ACCGTATGATGCGTCCGGGC GAACCGCCCACCGAAGAGGC AGTCGAGCAATTGTTTAACC GCTTGTTCTTCAGTGAAGAC
     D  E  T  A  G  R  Q   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  F  S  E  D
1201 AGCTACGATTTGTCCCGCGT AGGTCGTATGAAATTTAATA CGCGCACATACGAACAAAAA CTGTCCGAAGCCCAACAAAA CTCTTGGTACGGCCGCCTGC TGAACGAAACGTTTGCCGGT
     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
1321 GCTGCCGAAAAAGGCGGTTA TGTCCTGAGCGTCGAAGATA TTGTCGCCTCGATTGCGACT TTGGTCGAGTTGCGTAACGG CCATGGTGAAGTTGACGATA TCGATCACTTGGGCAACCGC
     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 CGAGTACGTTCGGTAGGCGA GCTGACTGAAAACCAATTCC GCAGCGGTTTGGCCCGTGTG GAACGTGCTGTAAAAGAACG TTTGAATCAGGCGGAATCAG AAAACTTGATGCCGCACGAT
     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
1561 TTGATTAATGCAAAACCTGT TTCTGCCGCTATTAAAGAAT TCTTCGGCTCCAGCCAATTG AGTCAGTTTATGGATCAGAC CAACCCCTTGTTTGAAGTAA CCCATAAACGCCGCGTATCT
     L  I  N  A  K  P  V   S  A  A  I  K  E  F   F  G  S  S  Q  L   S  Q  F  M  D  Q  T   N  P  L  F  E  V  T   H  K  R  R  V  S
1681 GCATTGGGTCCGGGCGGTTT GACCCGCGAACGTGCCGGCT TCGAGGTACGGGACGTGCAT CCGACCCACTACGGCCGCGT ATGTCCGATTGAAACGCCTG AAGGTCCGAACATCGGTTTG
     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 ATCAACTCATTGTCCGTTTA TGCGCGCACCAATGATTACG GTTTCTTGGAAACGCCTTAC CGCCGCGTTATCGACGGCAA AGTAACCGAGGAAATCGATT ACTTGTCTGCCATCGAAGAA
     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  T  E  E  I  D  Y   L  S  A  I  E  E
1921 GGCCGCTATGTGATTGCACA GGCGAATGCCGATTTGGATT CAGATGGCAATCTGATTGGC GATTTGGTTACCTGTCGTGA AAAAGGCGAAACCATTATGG CAACGCCCGACCGCGTCCAA
     G  R  Y  V  I  A  Q   A  N  A  D  L  D  S   D  G  N  L  I  G   D  L  V  T  C  R  E   K  G  E  T  I  M  A   T  P  D  R  V  Q
2041 TATATGGACGTGGCAACCGG CCAGGTGGTATCCGTTGCGG CATCCCTGATTCCGTTCTTG GAACATGATGACGCGAACCG CGCATTGATGGGTGCCAACA TGCAACGTCAGGCAGTGCCT
     Y  M  D  V  A  T  G   Q  V  V  S  V  A  A   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
2161 TGCTTGCGTCCTGAAAAACC GATGGTCGGTACCGGTATCG AGCGTTCCGTTGCCGTTGAC TCTGCTACTGCAATCGTTGC CCGCCGAGGCGGCGTGGTCG AGTATGTCGATGCCAACCGT
     C  L  R  P  E  K  P   M  V  G  T  G  I  E   R  S  V  A  V  D   S  A  T  A  I  V  A   R  R  G  G  V  V  E   Y  V  D  A  N  R
2281 GTTGTGATTCGTGTCCATGA CGACGAAGCGACTGCCGGCG AAGTGGGTGTCGATATTTAC AACTTGGTTAAATTTACCCG TTCCAACCAGTCTACCAATA TCAATCAGCGTCCTGCCGTC
     V  V  I  R  V  H  D   D  E  A  T  A  G  E   V  G  V  D  I  Y   N  L  V  K  F  T  R   S  N  Q  S  T  N  I   N  Q  R  P  A  V
2401 AAAGCCGGCGATGTTTTGCA ACGCGGCGATTTGGTGGCCG ATGGCGCGTCCACCGATTTG GGCGAATTGGCTTTGGGTCA AAATATGACCATCGCCTTCA TGCCGTGGAACGGTTACAAC
     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 CACATTGAGGAATTGAATGT CGTTGCCCGCGATACCAAGC TGGGTGCGGAAGACATTACC
     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 CGCGATATTCCGAACTTGTC CGAGCGTATGCAAAACCGCT TGGACGAATCCGGTATCGTT TACATCGGTGCAGAAGTAGA AGCCGGCGATGTGTTGGTAG GCAAAGTAACGCCTAAAGGC
     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 GAAACCCAACTGACGCCGGA AGAAAAACTGTTGCGCGCCA TCTTCGGCGAAAAAGCGTCT GACGTAAAAGATACTTCACT GCGTATGCCTACCGGTATGA GCGGTACGGTTATCGACGTT
     E  T  Q  L  T  P  E   E  K  L  L  R  A  I   F  G  E  K  A  S   D  V  K  D  T  S  L   R  M  P  T  G  M  S   G  T  V  I  D  V
2881 CAAGTCTTCACTCGTGAAGG TATTCAACGCGACAAACGCG CCCAATCCATTATCGATTCC GAGTTGAAACGCTACCGTTT GGATTTGAACGACCAATTGC GTATTTTCGACAACGACGCA
     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
3001 TTCGACCGTATCGAACGTAT GATTGTGGGTCAAAAAGCCA ATGGTGGTCCGATGAAGCTG GCTAAAGGCAGCGAAATTAC TACCGAATATTTGGCGGGTC TGCCGAGCAGGCACGATTGG
     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  L   P  S  R  H  D  W
3121 TTCGATATCCGTCTGACCGA TGAAGATTTGGCCAAGCAGT TGGAACTGATTAAAGTGAGC CTGCAACAAAAACGCGAAGA AGCGGACGAGTTATACGAAA TCAAGAAGAAAAAACTGACC
     F  D  I  R  L  T  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  K  L  T
3241 CAAGGCGACGAATTGCAACC CGGCGTACAAAAAATGGTGA AAGTTTTTATCGCCATCAAA CGCCGTCTGCAAGCCGGCGA CAAAATGGCGGGCCGCCACG GTAACAAAGGCGTGGTATCG
     Q  G  D  E  L  Q  P   G  V  Q  K  M  V  K   V  F  I  A  I  K   R  R  L  Q  A  G  D   K  M  A  G  R  H  G   N  K  G  V  V  S
3361 CGCATTCTGCCAGTGGAAGA CATGCCTTACATGGCGGACG GCCGTCCGGTAGACATCGTA CTGAACCCATTGGGCGTACC TTCCCGTATGAACATCGGTC AGATTTTGGAAGTTCACTTG
     R  I  L  P  V  E  D   M  P  Y  M  A  D  G   R  P  V  D  I  V   L  N  P  L  G  V  P   S  R  M  N  I  G  Q   I  L  E  V  H  L
3481 GGTTGGGCAGCAAAAGGTAT CGGCGAGCGTATCGACCGTA TGCTGAAAGAGCAACGCAAA GCAGGCGAGTTGCGCGAGTT CTTGAACAGACTCTACAACG GCAGCGGTAAGAAAGAAGAT
     G  W  A  A  K  G  I   G  E  R  I  D  R  M   L  K  E  Q  R  K   A  G  E  L  R  E  F   L  N  R  L  Y  N  G   S  G  K  K  E  D
3601 TTGGACAGCCTGACAGATGA AGAAATCATCGAATTGGCTT CCAACCTGCGTAAAGGTGCA TCTTTCGCTTCTCCTGTATT CGACGGTGCGAAAGAGTCTG AAATCCGCGAAATGTTGAAC
     L  D  S  L  T  D  E   E  I  I  E  L  A  S   N  L  R  K  G  A   S  F  A  S  P  V  F   D  G  A  K  E  S  E   I  R  E  M  L  N
3721 TTGGCTTACCCAAGCGAAGA TCCTGAGGTTGAGAAACTGG GCTTCAACGACAGTAAAACT CAAATCACGCTGTATGACGG CCGTTCAGGCGAAGCATTTG ATCGCAAGGTTACAGTCGGT
     L  A  Y  P  S  E  D   P  E  V  E  K  L  G   F  N  D  S  K  T   Q  I  T  L  Y  D  G   R  S  G  E  A  F  D   R  K  V  T  V  G
3841 GTGATGCACTATCTGAAACT GCACCACTTGGTTGACGAAA AAATGCACGCCCGTTCTACC GGTCCATACAGTCTGGTTAC CCAACAGCCTTTGGGCGGTA AAGCTCAGTTCGGTGGCCAA
     V  M  H  Y  L  K  L   H  H  L  V  D  E  K   M  H  A  R  S  T   G  P  Y  S  L  V  T   Q  Q  P  L  G  G  K   A  Q  F  G  G  Q
3961 CGTTTCGGTGAGATGGAGGT TTGGGCATTGGAAGCATACG GTGCGGCATACACGCTGCAA GAGATGCTGACTGTGAAGTC TGATGACGTGAACGGCCGTA CCAAAATGTACGAGAACATC
     R  F  G  E  M  E  V   W  A  L  E  A  Y  G   A  A  Y  T  L  Q   E  M  L  T  V  K  S   D  D  V  N  G  R  T   K  M  Y  E  N  I
4081 GTCAAAGGCGAACACAAAAT CGATGCCGGTATGCCCGAGT CCTTCAACGTATTGGTTAAA GAGATTCGTTCACTGGGCTT GGATATCGATTTGGAACGCT ACTAA
     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.

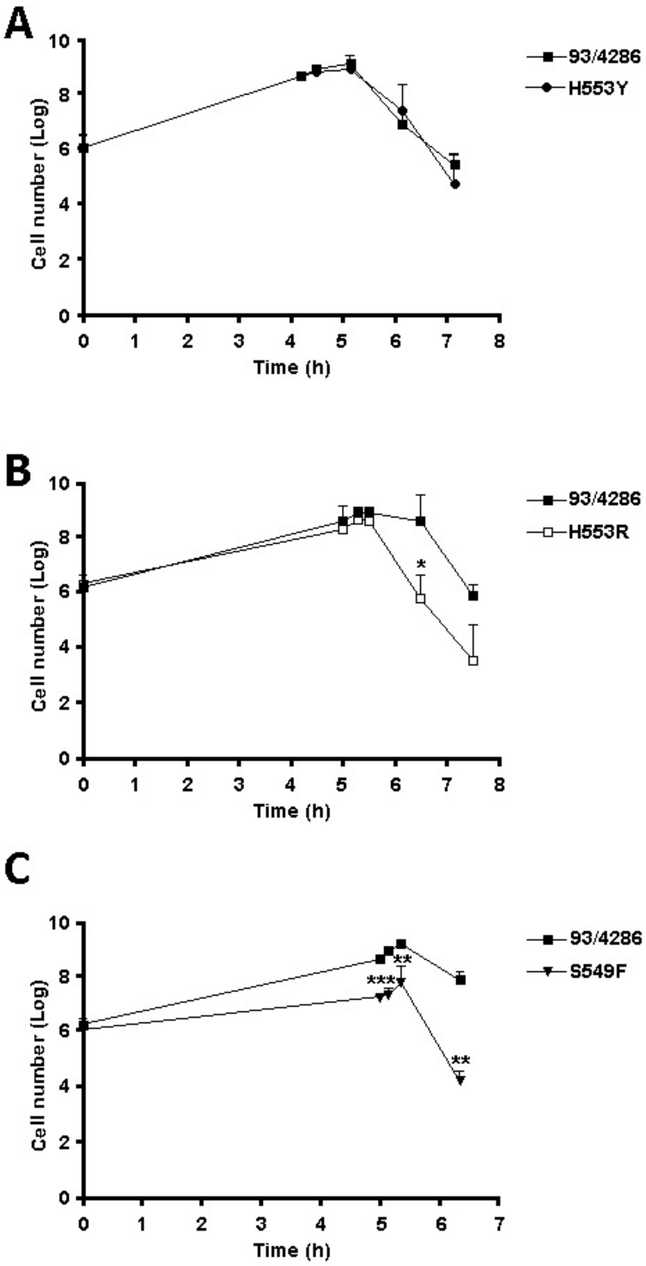

FIG. S1. Evaluation of rifampicin resistant mutants fitness in competition assay. **(A-C)** Survival curves of rifampicin-susceptible and rifampicin-resistant strains in competition growth in antibiotic-free GC broth at 37°C. The experiments were performed five times with five independent cultures, statistical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