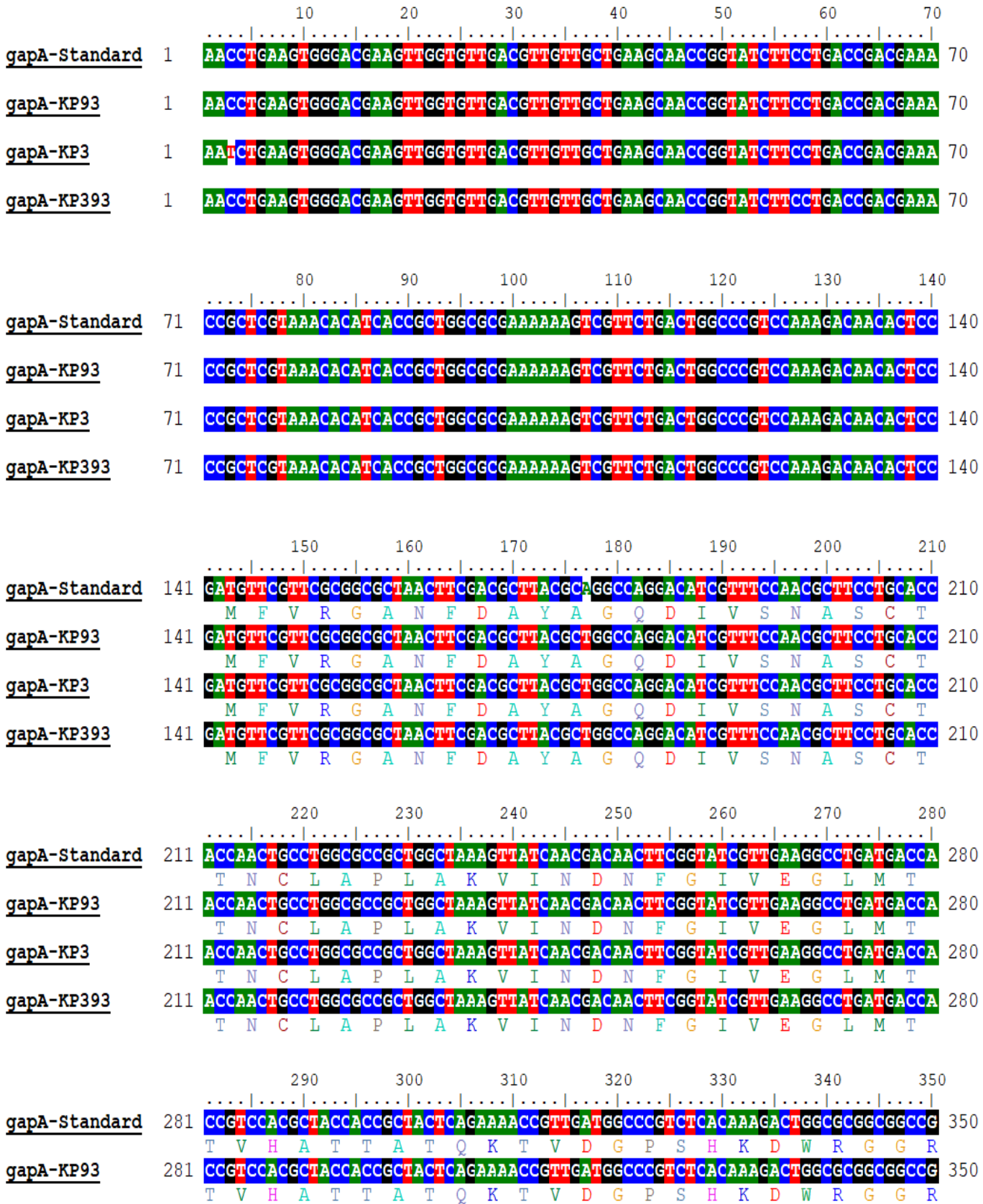


GapA alignment and mutations



GapA alignment and mutations

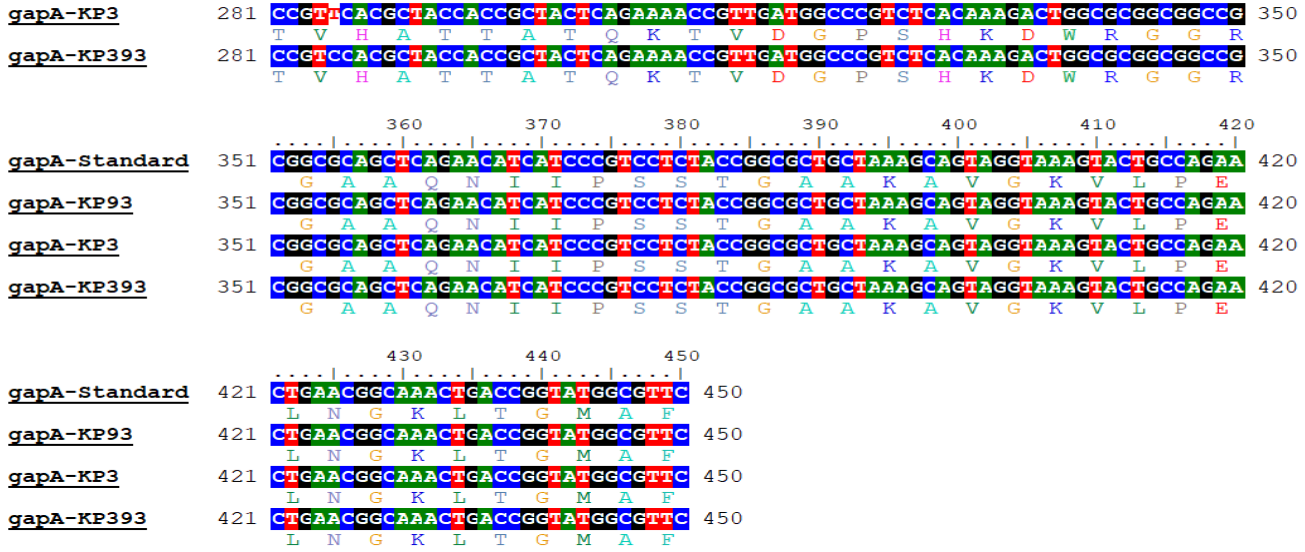


Figure S1A. The multiple sequence alignment of nucleotides and translated nucleotides of *gapA* genes of the three isolates.

infB alignment and mutations

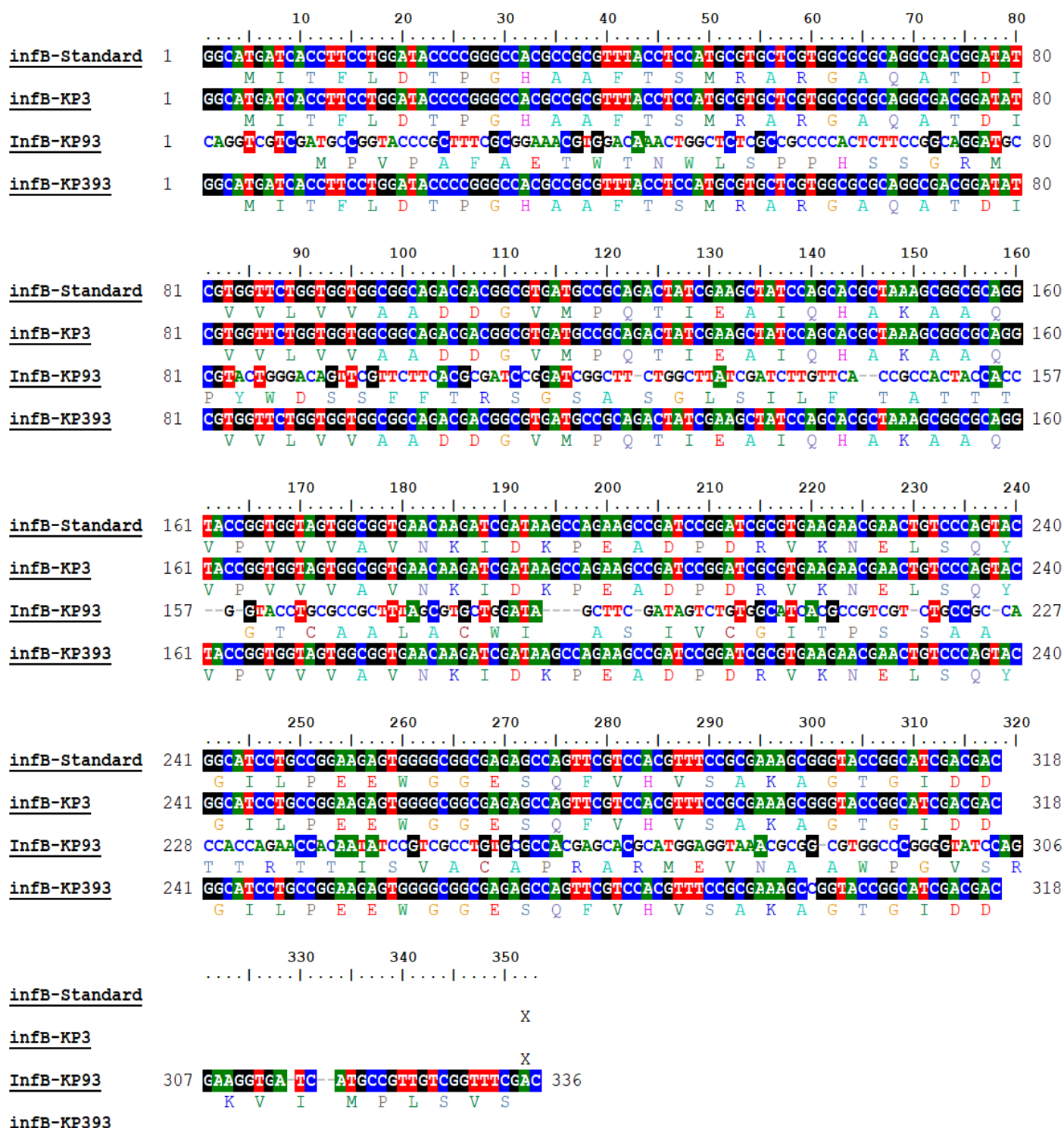


Figure S1B. Multiple sequence alignment of nucleotides and translated nucleotides of *infB* genes of the three isolates.

mdh alignment and mutation

| | | 10 | 20 | 30 | 40 | 50 | 60 | 70 | |
|--------------|-----|---|-----|-----|-----|-----|-----|-----|-----|
| mdh-standard | 1 | GGCGCGGATGTAGTGCTGATCTCCGCGGGCGTGGCGCGTAAGCCCGGCATGGATCGTTCCGACCTGTTTA | | | | | | | 70 |
| | | G A D V V L I S A G V A R K P G M D R S D L F | | | | | | | |
| mdh-KP3 | 1 | GGCGCGGATGTAGTGCTGATCTCCGCGGGCGTGGCGCGTAAGCCCGGCATGGATCGTTCCGACCTGTTTA | | | | | | | 70 |
| | | G A D V V L I S A G V A R K P G M D R S D L F | | | | | | | |
| mdh-KP93 | 1 | GGCGCGGATGTAGTGCTGATCTCCGCGGGCGTGGCGCGTAAGCCCGGCATGGATCGTTCCGACCTGTTTA | | | | | | | 70 |
| | | G A D V V L I S A G V A R K P G M D R S D L F | | | | | | | |
| mdh-KP393 | 1 | AACGCGCA--TAGTGSCCG--TCGCCTTCCACGTAG--GCGC--ACTCCACCACGCCTTTTTTCC--CCCTG--- | | | | | | | 61 |
| | | N A H S G R R L P R R R T P P R L F P P | | | | | | | |
| | | 80 | 90 | 100 | 110 | 120 | 130 | 140 | |
| mdh-standard | 71 | ATGTGAATGCGGGTATCGTGAAGAACCTCGTGCAGCAGATTGCCAAAACCTGCCCGCAGGCCTGCATCGG | | | | | | | 140 |
| | | N V N A G I V K N L V Q Q I A K T C P Q A C I G | | | | | | | |
| mdh-KP3 | 71 | ATGTGAATGCGGGTATCGTGAAGAACCTCGTGCAGCAGATTGCCAAAACCTGCCCGCAGGCCTGCATCGG | | | | | | | 140 |
| | | N V N A G I V K N L V Q Q I A K T C P Q A C I G | | | | | | | |
| mdh-KP93 | 71 | ATGTGAATGCGGGTATCGTGAAGAACCTCGTGCAGCAGATTGCCAAAACCTGCCCGCAGGCCTGCATCGG | | | | | | | 140 |
| | | N V N A G I V K N L V Q Q I A K T C P Q A C I G | | | | | | | |
| mdh-KP393 | 62 | CA--TG--GCGCGAACCAAGAGAGACC--AAAA--CGSG--AGCCGCCTGGCCCATCGACAAGGTCGCGGACC | | | | | | | 126 |
| | | A W R E P E R D Q N G Q P P G P S T R S P T | | | | | | | |
| | | 150 | 160 | 170 | 180 | 190 | 200 | 210 | |
| mdh-standard | 141 | CATTATACCAACCCGGTGAATACCACCGTGGCTATCGCCGCCGAAGTACTGAAAAAGCCGGCGTGTAC | | | | | | | 210 |
| | | I I T N P V N T T V A I A A E V L K K A G V Y | | | | | | | |
| mdh-KP3 | 141 | CATTATACCAACCCGGTGAATACCACCGTGGCTATCGCCGCCGAAGTACTGAAAAAGCCGGCGTGTAC | | | | | | | 210 |
| | | I I T N P V N T T V A I A A E V L K K A G V Y | | | | | | | |
| mdh-KP93 | 141 | CATTATACCAACCCGGTGAATACCACCGTGGCTATCGCCGCCGAAGTACTGAAAAAGCCGGCGTGTAC | | | | | | | 210 |
| | | I I T N P V N T T V A I A A E V L K K A G V Y | | | | | | | |
| mdh-KP393 | 127 | CGC--CGCCGCTTTTCCGCTTCCACGACTTCCGTTACCAGCGTTCCTGAAT---A--CGT--TTAGTCAGGTCGG | | | | | | | 189 |
| | | R R P L S L P R L R Y R R S E Y V * S G R | | | | | | | |
| | | 220 | 230 | 240 | 250 | 260 | 270 | 280 | |
| mdh-standard | 211 | GATAAAAACAAACTGTTCCGGCGTTACCACGCTGGACATCATCCGTTCCAATACCTTTGTGGCGGAGCTGA | | | | | | | 280 |
| | | D K N K L F G V T T L D I I R S N T F V A E L | | | | | | | |
| mdh-KP3 | 211 | GATAAAAACAAACTGTTCCGGCGTTACCACGCTGGACATCATCCGTTCCAATACCTTTGTGGCGGAGCTGA | | | | | | | 280 |
| | | D K N K L F G V T T L D I I R S N T F V A E L | | | | | | | |
| mdh-KP93 | 211 | GATAAAAACAAACTGTTCCGGCGTTACCACGCTGGACATCATCCGTTCCAATACCTTTGTGGCGGAGCTGA | | | | | | | 280 |
| | | D K N K L F G V T T L D I I R S N T F V A E L | | | | | | | |
| mdh-KP393 | 190 | CAATTTCCCTGATTCGCTAAAGCTGACCGCCGSSGATCTGCCACAGTAAAGGCAGAA--TGGTGACCCCGAGTG | | | | | | | 259 |
| | | Q F P D R * S * R R G S A T V K A E W * P R S | | | | | | | |
| | | 290 | 300 | 310 | 320 | 330 | 340 | 350 | |
| mdh-standard | 281 | AAGGTAAATCGGCAACCGAGGTGGAAGTCCCGGTCATTGGTGGTCACTCCGGGGTCACCATTTCTGCCTTT | | | | | | | 350 |
| | | K G K S A T E V E V P V I G G H S G V T I L P L | | | | | | | |
| mdh-KP3 | 281 | AAGGTAAATCGGCAACCGAGGTGGAAGTCCCGGTCATTGGTGGTCACTCCGGGGTCACCATTTCTGCCTTT | | | | | | | 350 |
| | | K G K S A T E V E V P V I G G H S G V T I L P L | | | | | | | |

mdh alignment and mutation

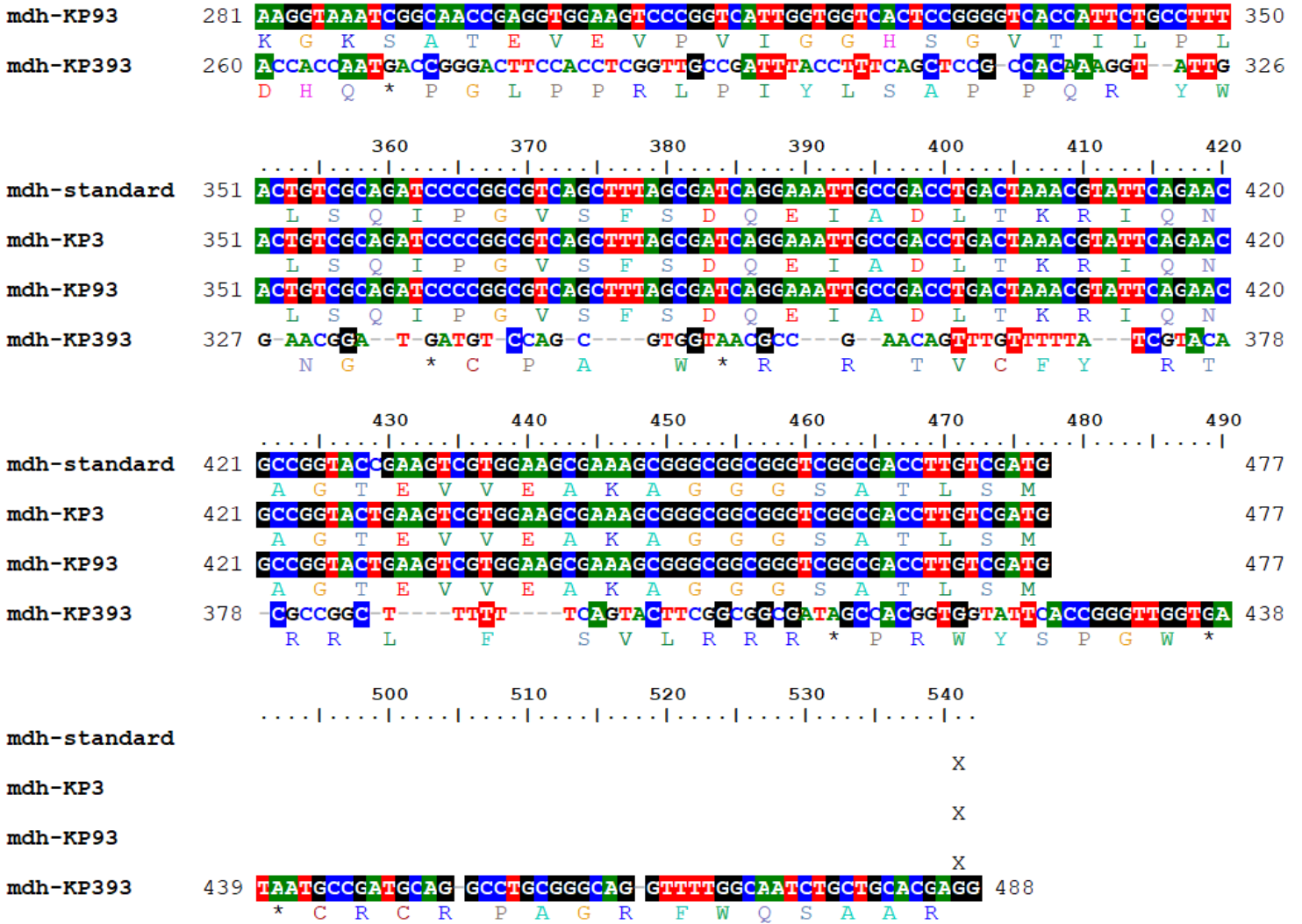


Figure S1C. Multiple sequence alignment of nucleotides and translated nucleotides of *mdh* genes of the three isolates

10 20 30 40 50 60 70
pgi-Standard 1 GAGTCCAACGGTAAGTATGTTGACCGTAACGGCCACGGGTAGACTACCAGACTGGCCCAATCATCTGGG 70
E S N G K Y V D R N G H A V D Y Q T G P I I W
pgi-KP3 1 GAGTCCAACGGTAAGTATGTTGACCGTAACGGCCACGGGTAGACTACCAGACTGGCCCAATCATCTGGG 70
E S N G K Y V D R N G H A V D Y Q T G P I I W
pgi-KP93 1 GAGTCCAACGGTAAGTATGTTGACCGTAACGGCCACGGGTAGACTACCAGACTGGCCCAATCATCTGGG 70
E S N G K Y V D R N G H A V D Y Q T G P I I W
pgi- KP393 1 GAGTCCAACGGTAAGTATGTTGACCGTAACGGCCACGGGTAGACTACCAGACTGGCCCAATCATCTGGG 70
E S N G K Y V D R N G H A V D Y Q T G P I I W

80 90 100 110 120 130 140
pgi-Standard 71 GTGAGCCGGGCACCAACGGTCAGCACGCGTTCTACCAGCTGATCCACCAGGGCACCAAAATGGTACCGTG 140
G E P G T N G Q H A F Y Q L I H Q G T K M V P C
pgi-KP3 71 GTGAGCCGGGCACCAACGGTCAGCACGCGTTCTACCAGCTGATCCACCAGGGCACCAAAATGGTACCGTG 140
G E P G T N G Q H A F Y Q L I H Q G T K M V P C
pgi-KP93 71 GTGAGCCGGGCACCAACGGTCAGCACGCGTTCTACCAGCTGATCCACCAGGGCACCAAAATGGTACCGTG 140
G E P G T N G Q H A F Y Q L I H Q G T K M V P C
pgi- KP393 71 GTGAGCCGGGCACCAACGGTCAGCACGCGTTCTACCAGCTGATCCACCAGGGCACCAAAATGGTACCGTG 140
G E P G T N G Q H A F Y Q L I H Q G T K M V P C

150 160 170 180 190 200 210
pgi-Standard 141 CGATTTTCATCGCTCCGGCTATCACCACAAACCCGCTGTCTGACCACCATCAGAAACTGCTGTCTAACTTC 210
D F I A P A I T H N P L S D H H Q K L L S N F
pgi-KP3 141 CGATTTTCATCGCTCCGGCTATCACCACAAACCCGCTGTCTGACCACCATCAGAAACTGCTGTCTAACTTC 210
D F I A P A I T H N P L S D H H Q K L L S N F
pgi-KP93 141 CGATTTTCATCGCTCCGGCTATCACCACAAACCCGCTGTCTGACCACCATCAGAAACTGCTGTCTAACTTC 210
D F I A P A I T H N P L S D H H Q K L L S N F
pgi- KP393 141 CGATTTTCATCGCTCCGGCTATCACCACAAACCCGCTGTCTGACCACCATCAGAAACTGCTGTCTAACTTC 210
D F I A P A I T H N P L S D H H Q K L L S N F

220 230 240 250 260 270 280
pgi-Standard 211 TTCGCCAGACCGAGGCCCTGGCCTTTGGTAAATCCCGCGAAGTGGTTGAGCAGGAATATCGCGATCAGG 280
F A Q T E A L A F G K S R E V V E Q E Y R D Q
pgi-KP3 211 TTCGCCAGACCGAGGCCCTGGCCTTTGGTAAATCCCGCGAAGTGGTTGAGCAGGAATATCGCGATCAGG 280
F A Q T E A L A F G K S R E V V E Q E Y R D Q
pgi-KP93 211 TTCGCCAGACCGAGGCCCTGGCCTTTGGTAAATCCCGCGAAGTGGTTGAGCAGGAATATCGCGATCAGG 280
F A Q T E A L A F G K S R E V V E Q E Y R D Q
pgi- KP393 211 TTCGCCAGACCGAGGCCCTGGCCTTTGGTAAATCCCGCGAAGTGGTTGAGCAGGAATATCGCGATCAGG 280
F A Q T E A L A F G K S R E V V E Q E Y R D Q

290 300 310 320 330 340 350
pgi-Standard 281 GTAAAGACCCGGCGACCCCTGGAGCACGTGGTGCCGTTCAAAGTGTTCGAAGGTAACCGCCCGACTAACTC 350
G K D P A T L E H V V P F K V F E G N R P T N S
pgi-KP3 281 GTAAAGACCCGGCGACCCCTGGAGCACGTGGTGCCGTTCAAAGTGTTCGAAGGTAACCGCCCGACTAACTC 350
G K D P A T L E H V V P F K V F E G N R P T N S
pgi-KP93 281 GTAAAGACCCGGCGACCCCTGGAGCACGTGGTGCCGTTCAAAGTGTTCGAAGGTAACCGCCCGACTAACTC 350
G K D P A T L E H V V P F K V F E G N R P T N S
pgi- KP393 281 GTAAAGACCCGGCGACCCCTGGAGCACGTGGTGCCGTTCAAAGTGTTCGAAGGTAACCGCCCGACTAACTC 350
G K D P A T L E H V V P F K V F E G N R P T N S

360 370 380 390 400 410 420
.....

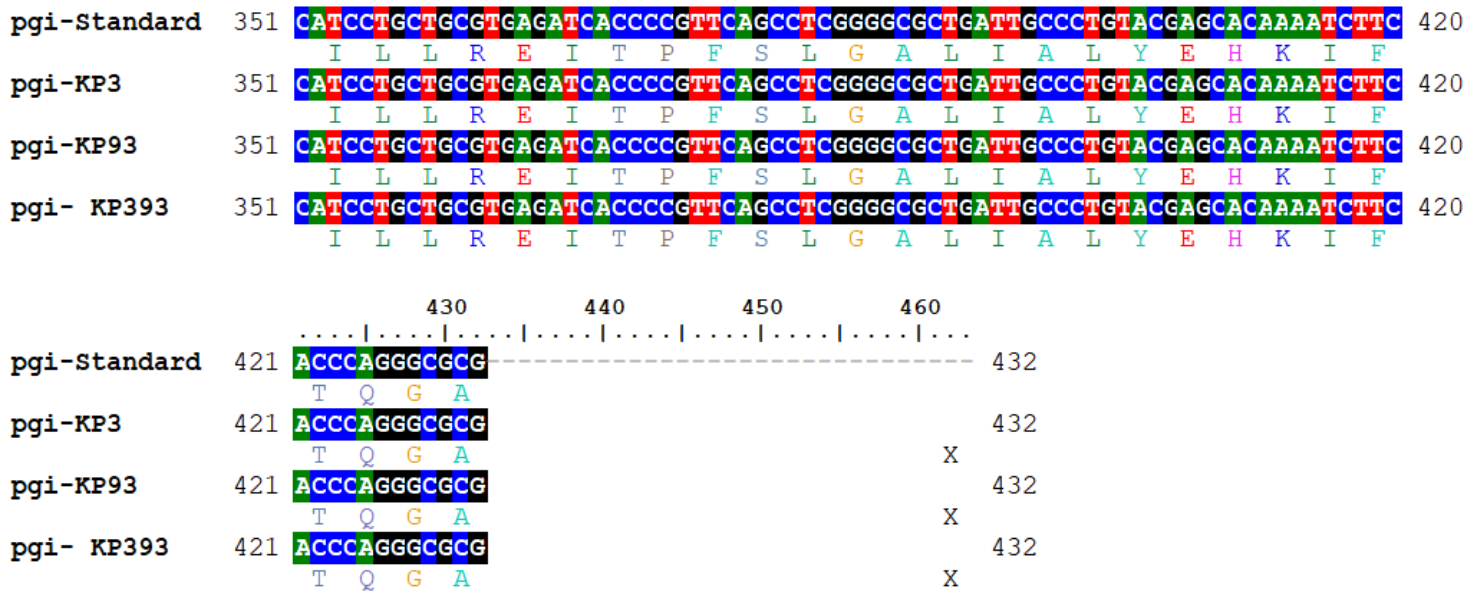
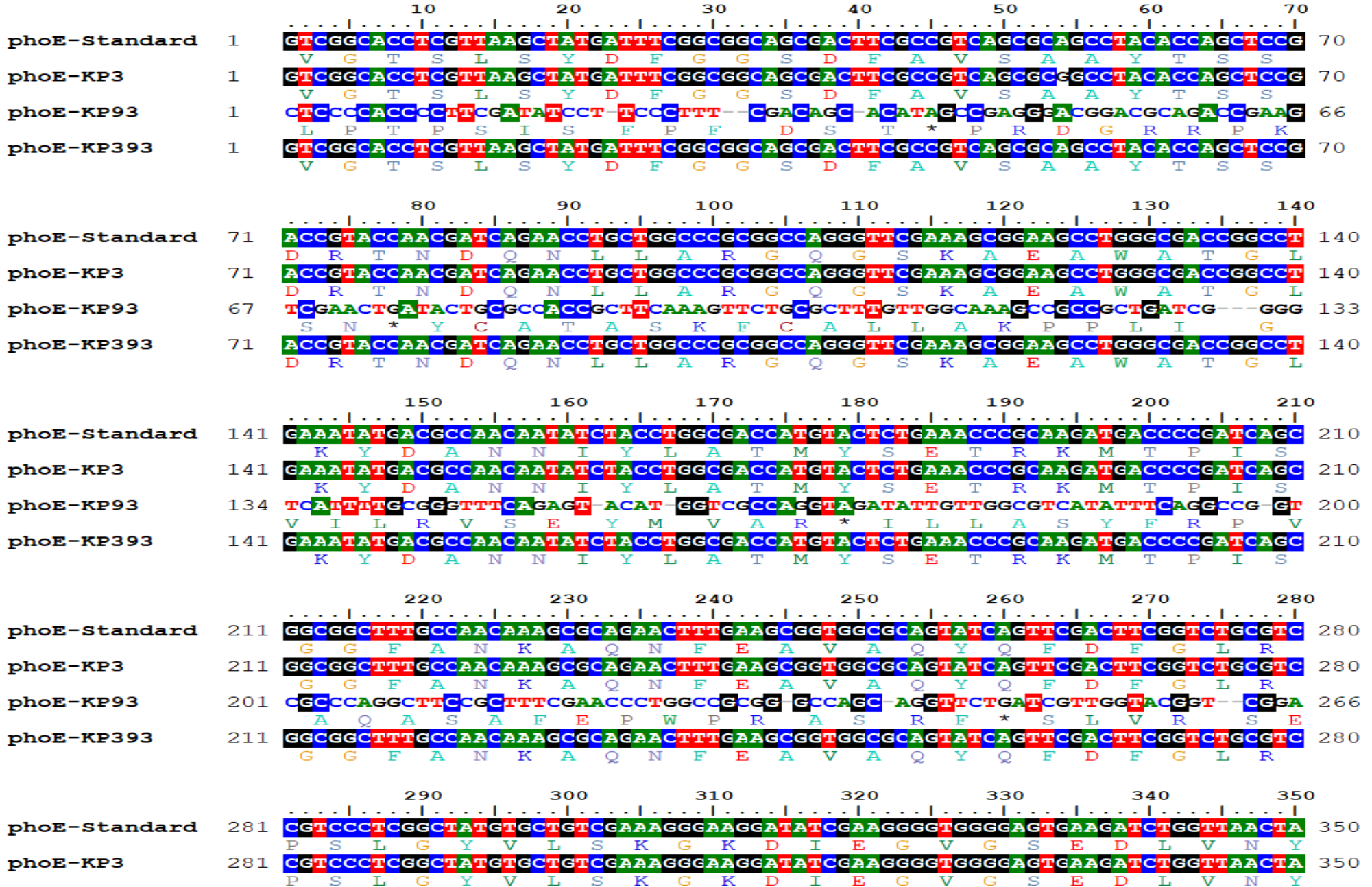


Figure S1D. Multiple sequence alignment of nucleotides and translated nucleotides of *pgi* genes of the three isolates

phoE mutations and alignment



phoE mutations and alignment

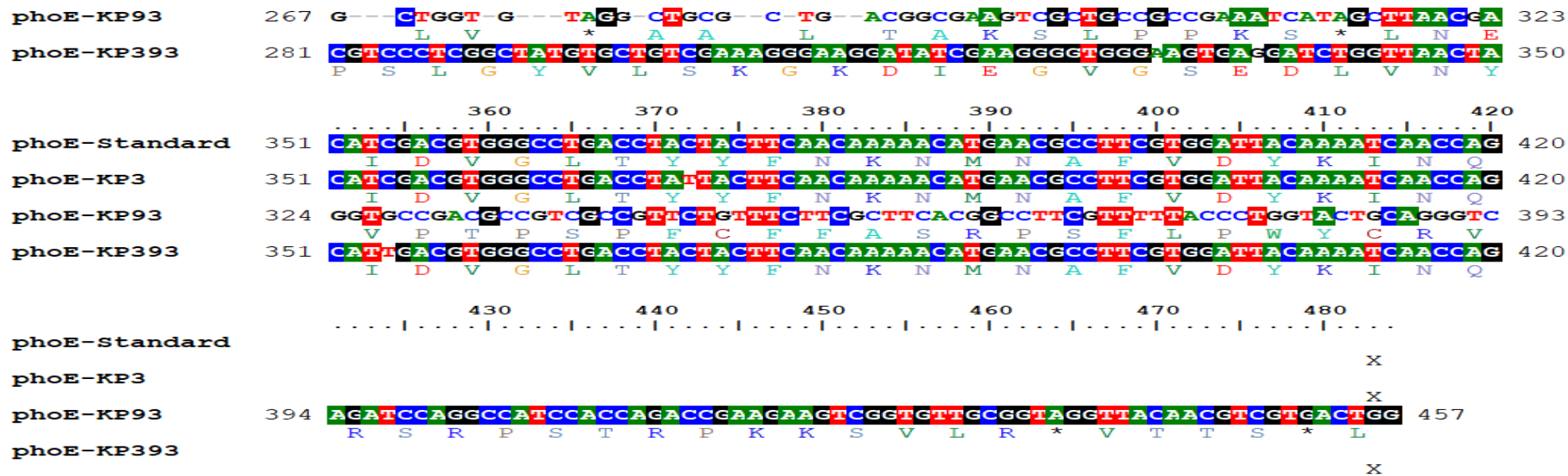
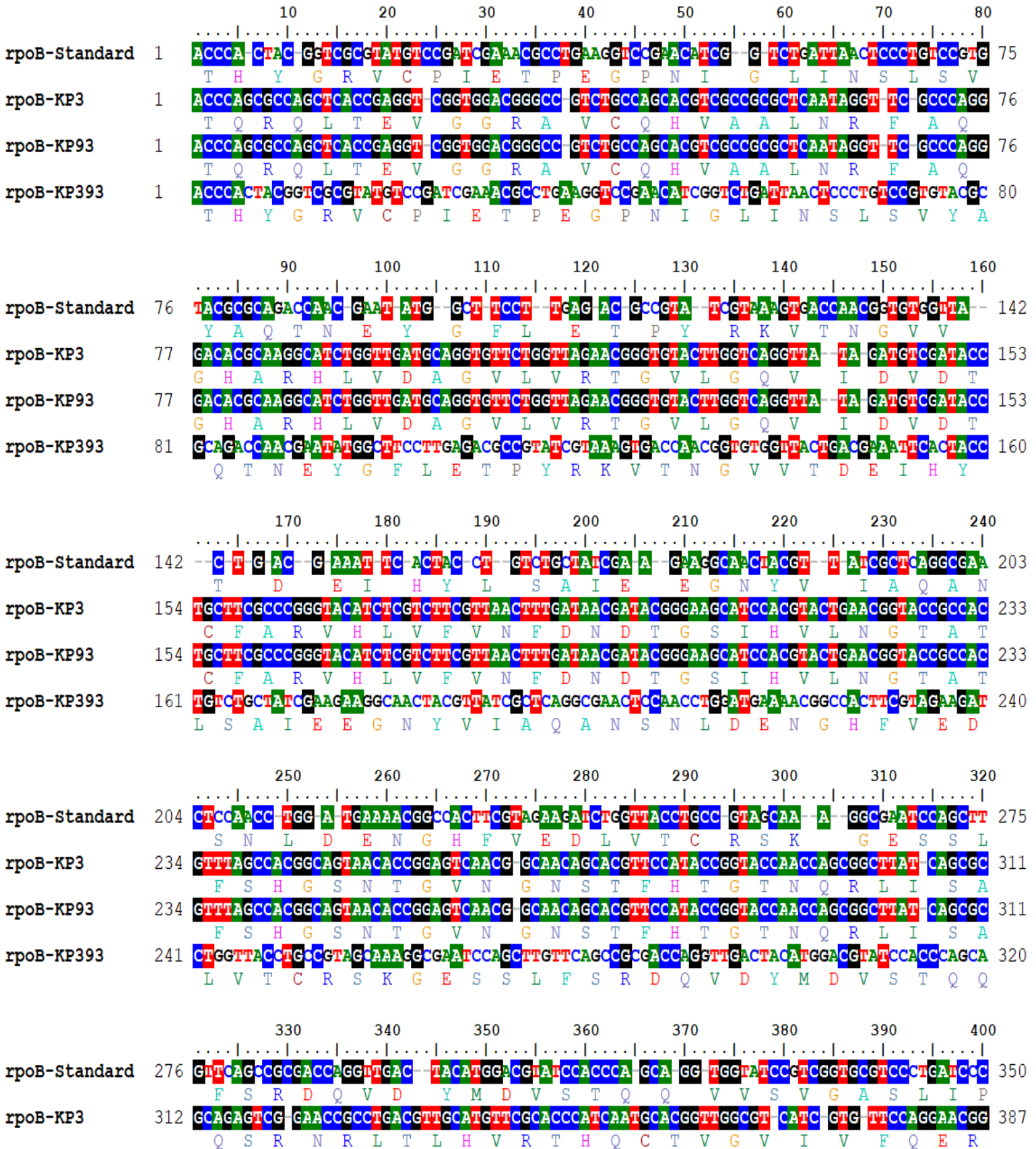


Figure S1E. Multiple sequence alignment of nucleotides and translated nucleotides of *phoE* genes of the three isolates

rpoB mutations & alignment



rpoB mutations & alignment

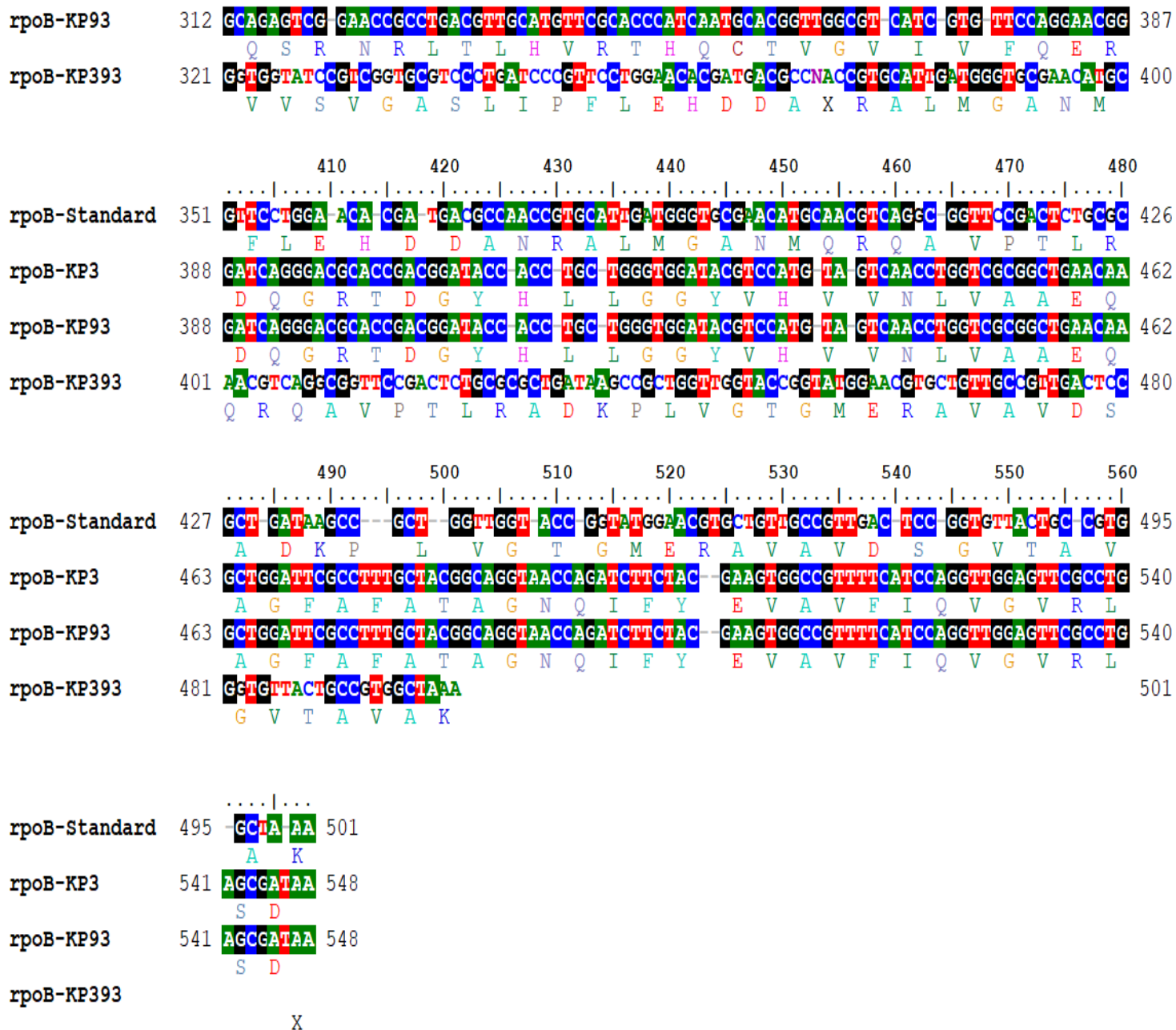
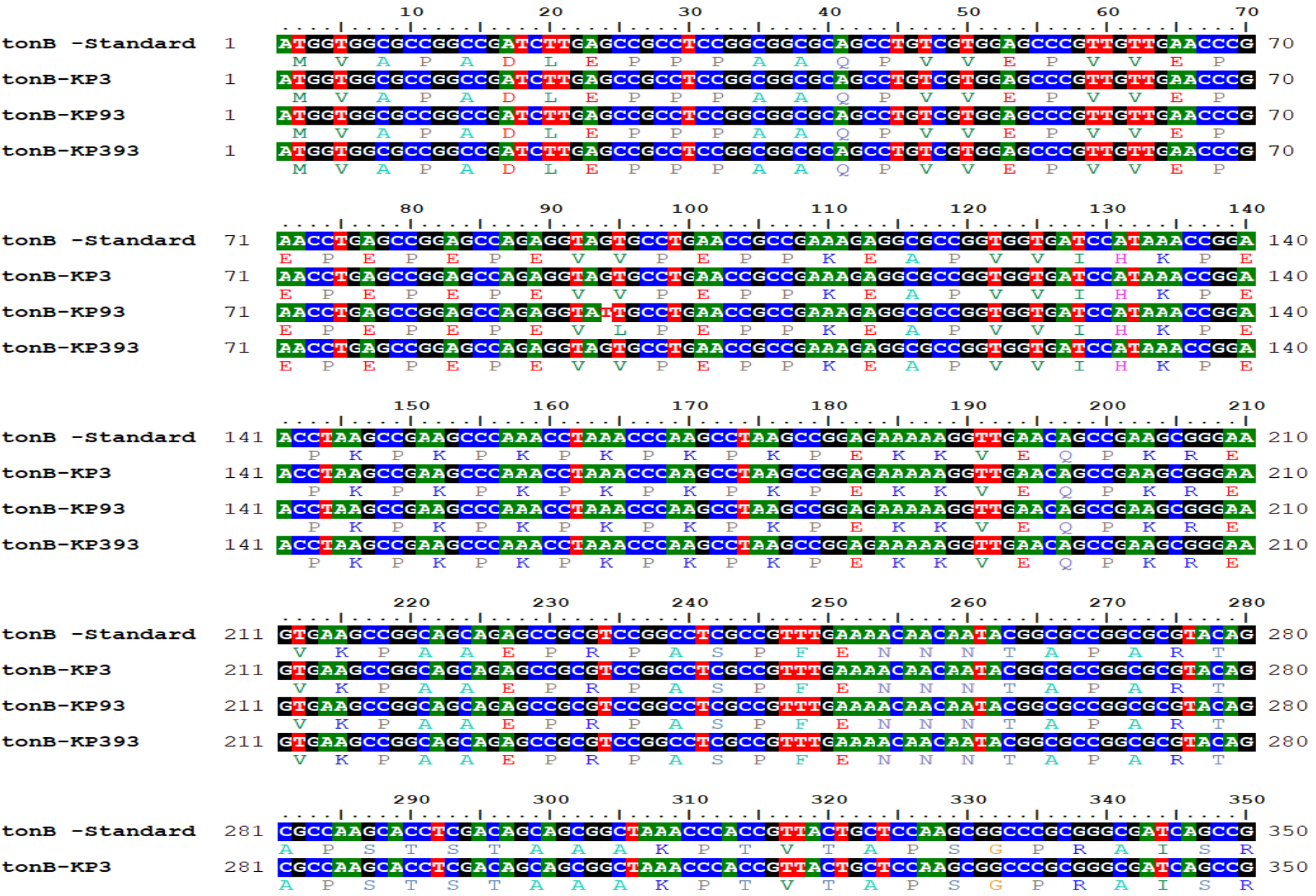


Figure S1F. Multiple sequence alignment of nucleotides and translated nucleotides of *rpoB* genes of the three isolate

tonB alignment and mutations



tonB alignment and mutations

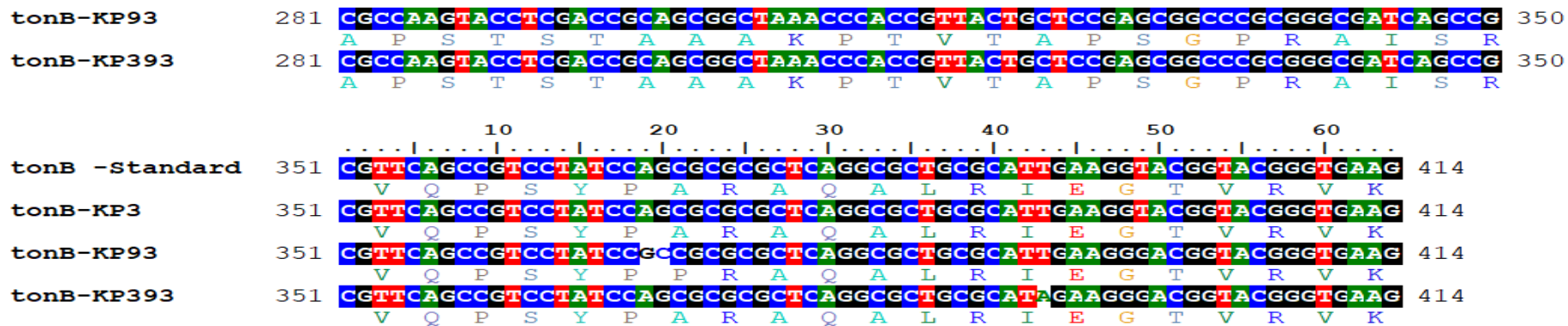


Figure S1G. Multiple sequence alignment of nucleotides and translated nucleotides of *tonB* genes of the three isolate