		10 20 30 40 50 60 70
gapA-Standard	1	AACCTGAAGTGGGACGAAGTTGGTTGTTGCTGAAGCAACCGGTATCTTCCTGACCGAAAA 70
gapA-KP93	1	AACCTGAAGTGGGACGAAGTTGGTTGACGTTGTTGCTGAAGCAACCGGTATCTTCCTGACCGACGAAA 70
gapA-KP3	1	AA <mark>ICTGAAGTGGGACGAAGTTGGTGTTGACGTTGTTGCTGAAGCAACCGGTATCTTCCT</mark> GACCGACGAAA 70
gapA-KP393	1	AACCTGAAGTGGGACGAAGTTGGTGTTGACGTTGTTGCTGAAGCAACCGGTATCTTCCTGACCGACGAAA 70
		80 90 100 110 120 130 140
gapA-Standard	71	CCGCTCGTAAACACATCACCGCTGGCGCGAAAAAAGTCGTTCTGACTGGCCCGTCCAAAGACAACACTCC 140
gapA-KP93	71	CCGCTCGTAAACACATCACCGCTGGCGGAAAAAAGTCGTTCTGACTGGCCCGTCCAAAGACAACACTCC 140
gapA-KP3	71	CCGCTCGTAAACACATCACCGCTGGCGCGAAAAAAGTCGTTCTGACTGGCCCGTCCAAAGACAACACTCC 140
gapA-KP393	71	CCGCTCGTAAACACATCACCGCTGGCGCGAAAAAAGTCGTTCTGACTGGCCCGTCCAAAGACACACTCC 140
		150 160 170 180 190 200 210
gapA-Standard	141	GATGTTCGTTCGCGGCGCTAACTTCGACGCTTACGCAGGCCAGGACATCGTTTCCAACGCTTCCTGCACC 210 M F V R G A N F D A Y A G Q D I V S N A S C T
gapA-KP93	141	GATGTTCGTTCGCGGCGCTAACTTCGACGCTTACGCTGGCCAGGACATCGTTTCCAACGCTTCCTGCACC 210
gapA-KP3	141	M F V R G A N F D A Y A G Q D I V S N A S C T GATGTTCGTTCGCGGCGCTAACTTCGACGCTTACGCTGGCCCAGGACATCGTTTCCAACGCTTCCTGCACC 210
gapA-KP393	141	M F V R G A N F D A Y A G Q D I V S N A S C T GATGTTCGTTCGCGGCGCTAACTTCGACGCTTACGCTGGCCAGGACATCGTTTCCAACGCTTCCTGCACC 210
		M F V R G A N F D A Y A G Q D I V S N A S C T
		220 230 240 250 260 270 280
gapA-Standard	211	ACCAACTGCCTGGCGCTGGCTAAAGTTATCAACGACAACTTCGGTATCGTTGAAGGCCTGATGACCA 280 T N C L A P L A K V I N D N F G I V E G L M T
gapA-KP93	211	ACCAACTGCCTGGCGCCGCTGGCTAAAGTTATCAACGACAACTTCGGTATCGTTGAAGGCCTGATGACCA 280
gapA-KP3	211	T N C L A P L A K V I N D N F G I V E G L M T ACCAACTGCCTGGCGCTGGCTAAAGTTATCAACGACAACTTCGGTATCGTTGAAGGCCTGATGACCA 280
gapA-KP393	211	T N C L A P L A K V I N D N F G I V E G L M T ACCAACTGCCTGGCGCTGGCTAAAGTTATCAACGACAACTTCGGTATCGTTGAAGGCCTGATGACCA 280
		T N C L A P L A K V I N D N F G I V E G L M T
		290 300 310 320 330 340 350
gapA-Standard	281	CCGTCCACGCTACCACCGCTACTCAGAAAACCGTTGATGGCCCGTCTCACAAAGACTGGCGGCGGCCGGC
дарА-КР93	281	T V H A T T A T Q K T V D G P S H K D W R G G R CCGTCCACGCTACCACCGCTACTCAGAAAACCGTTGATGGCCCGTCTCACAAAGACTGGCGGGGGGCGGCCG 350
		T V H A T T A T Q K T V D G P S H K D W R G G R

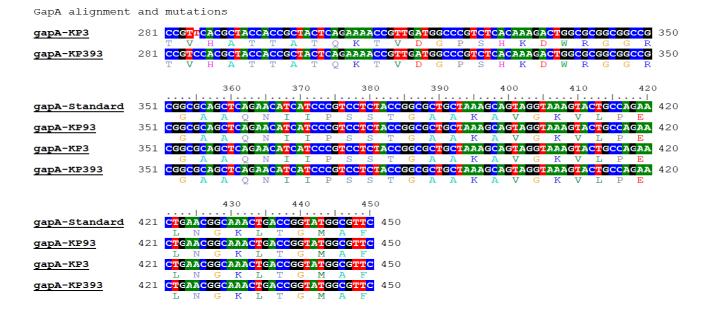


Figure S1A. The multiple sequence alignment of nucleotides and translated nucleotides of gapA genes of the three isolates.

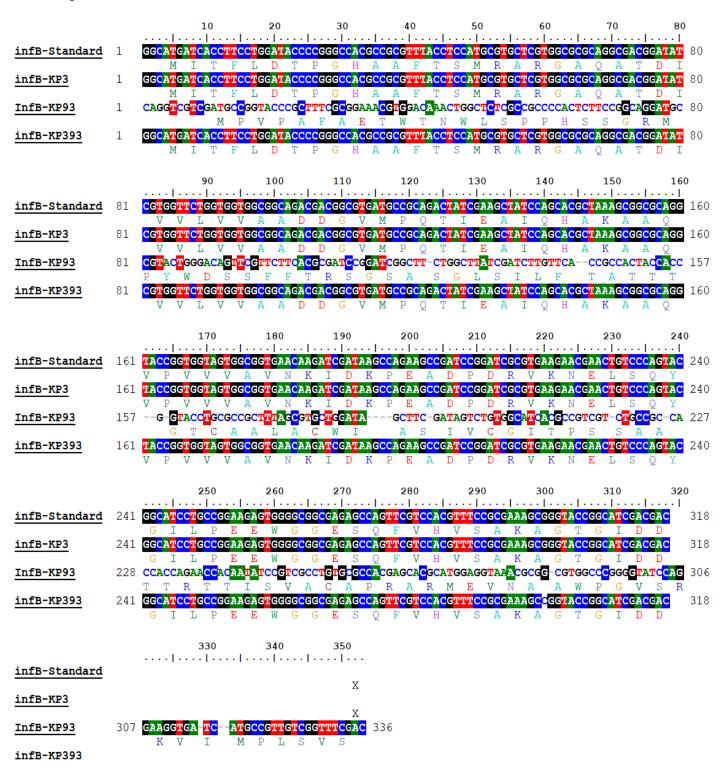


Figure S1B. Multiple sequence alignment of nucleotides and translated nucleotides of *infB* genes of the three isolates.

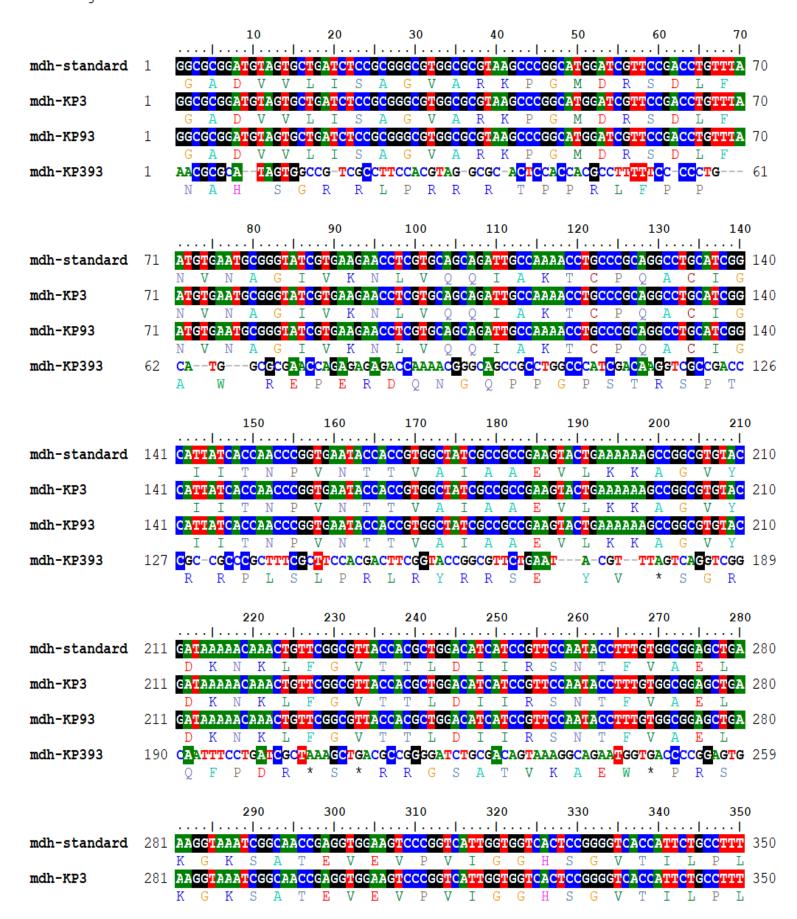
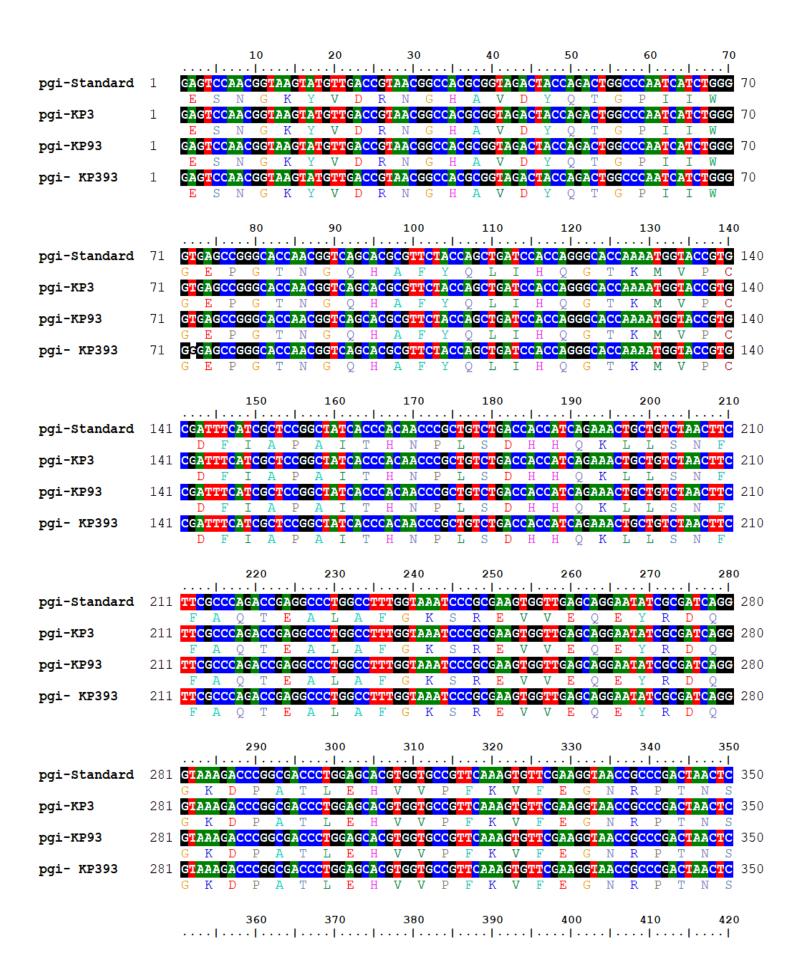


Figure S1C. Multiple sequence alignment of nucleotides and translated nucleotides of *mdh* genes of the three isolates



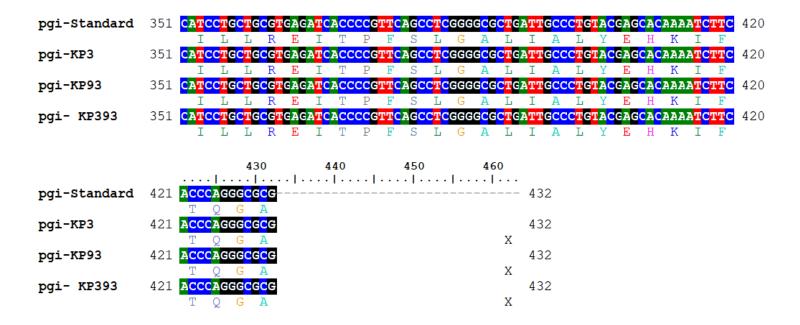


Figure S1D. Multiple sequence alignment of nucleotides and translated nucleotides of pgi genes of the three isolates

		10 20 30 40 50 60 70
phoE-Standard	1	GTCGGCACCTCGTTAAGCTATGATTTCGGCGGCAGCGACTTCGCCGTCAGCGCAGCCTACACCAGCTCCG 70
phoE-KP3	1	V G T S L S Y D F G G S D F A V S A A Y T S S GTCGGCACCTCGTTAAGCTATCGCCGGCAGCGACCTTCGCCGTCAGCGCGCCTACACCAGCTCCG 70
phoE-KP93	1	V G T S L S Y D F G G S D F A V S A A Y T S S CTCCCCACCCTTCCATATCCT-TCCCTTTCGACAGC-ACATAGCCGAGGCACGCAGACCGAAG 66
phoE-KP393	1	L P T P S I S F P F D S T * P R D G R R P K GTCGGCACCTCGTTAAGCTATGATTTCGGCGGCAGCGACCTCGCCGTCAGCGCAGCCTACACCAGCTCCG 70
-		V G T S L S Y D F G G S D F A V S A A Y T S S
		80 90 100 110 120 130 140
phoE-Standard	71	ACCGTACCAACGATCAGAACCTGCTGGCCCGCGGCCAGGGTTCGAAAGCGGAAGCCTGGGCGACCGGCCT 140
phoE-KP3	71	D R T N D Q N L L A R G Q G S K A E A W A T G L
phoE-KP93	67	DRTNDQNLLARGQGSKAEAWATGL TCGAACTGATACTGCGCTTCAAAGTTCTGCGCTTTGTTGGCAAAGCCGCCGCTGATCGGGG 133
phoE-KP393	71	S N * Y C A T A S K F C A L L A K P P L I G ACCGTACCAACGATCAGAACCTGCTGGCCCGCGCCAGGGTTCGAAAGCGGAAGCCTGGCCGCCCT 140
-		D R T N D Q N L L A R G Q G S K A E A W A T G L
		150 160 170 180 190 200 210
phoE-Standard	141	GAAATATGACGCCAACAATATCTACCTGGCGACCATGTACTCTGAAACCCGCAAGATGACCCCGATCAGC 210
phoE-KP3	141	K Y D A N N I Y L A T M Y S E T R K M T P I S GAAA <mark>TAT</mark> GACG <mark>CCAACAATATCT</mark> ACC <mark>TGGCGACCAT</mark> GTACTCTGAAACCCGCAAGA <mark>T</mark> GACCCCGA <mark>T</mark> CAGC 210
phoE-KP93	134	K Y D A N N I Y L A T M Y S E T R K M T P I S TOAT <mark>TTTGCGGCTTTCAGAGT-ACAT-GGTCGCCAGGTAGATATTGTTGGCGTCATATTTCAGGCCG-GT</mark> 200
phoE-KP393	141	V I L R V S E Y M V A R * I L L A S Y F R P V GAAATATGACGCCAACAATATCTACCTGGCGACCATGTACTCTGAAACCCGCAAGATGACCCCGATCAGC 210
_		K Y D A N N I Y L A T M Y S E T R K M T P I S
		220 230 240 250 260 270 280
phoE-Standard	211	GGCGGCTTTGCCAACAAAGCGCAGAACTTTGAAGCGGTGGCGCAGTATCAGTTCGACTTCGGTCTGCGTC 280
phoE-KP3	211	GGCGGCTTTGCCAACAAAGCGCAGAACTTTGAAGCGGTGGCGCAGTATCAGTTCGACTTCGGTCTGCGTC 280
phoE-KP93	201	G G F A N K A Q N F E A V A Q Y Q F D F G L R C <mark>GCCCAGGCTTCCGCTTTCGAACCCTGGCCG</mark> CGG-GCCAGC-AGGTCTGATCGTTGGTACGT-CGGA 266
phoE-KP393	211	A Q A S A F E P W P R A S R F * S L V R S E GGCGGCTTTGCCAACAAAGCGCAGAACTTTGAAGCGGTGGCGCAGTATCAGTTCGACTTCGGTCTGCGTC 280
		G G F A N K A Q N F E A V A Q Y Q F D F G L R
		290 300 310 320 330 340 350
phoE-Standard	281	CGTCCCTCGGCTATGTGCTCGAAAGGGAAGGATATCGAAGGGGTGGGGAGTGAAGATCTGGTTAACTA 350
phoE-KP3	281	CGTCCCTCGGCTATGTGCTGTCGAAAGGGAAGGATATCGAAGGGGTGGGGAGTGAAGATCTGGTTAACTA 350
		PSLGYVLSKGKDIEGVGSEDLVNY

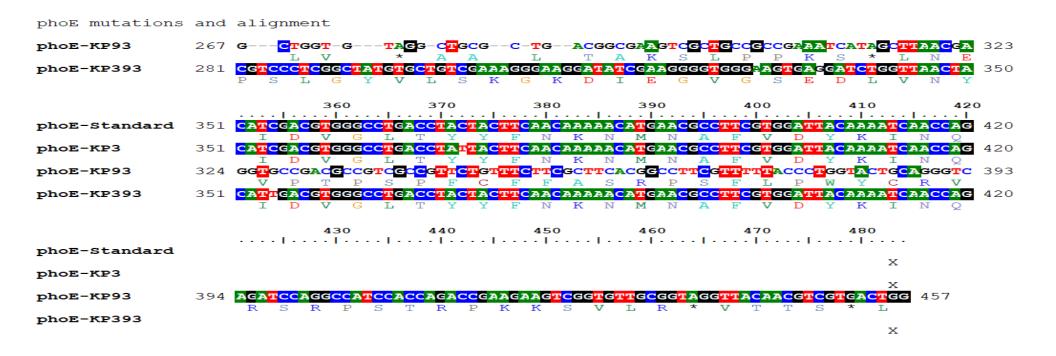


Figure S1E. Multiple sequence alignment of nucleotides and translated nucleotides of phoE genes of the three isolates

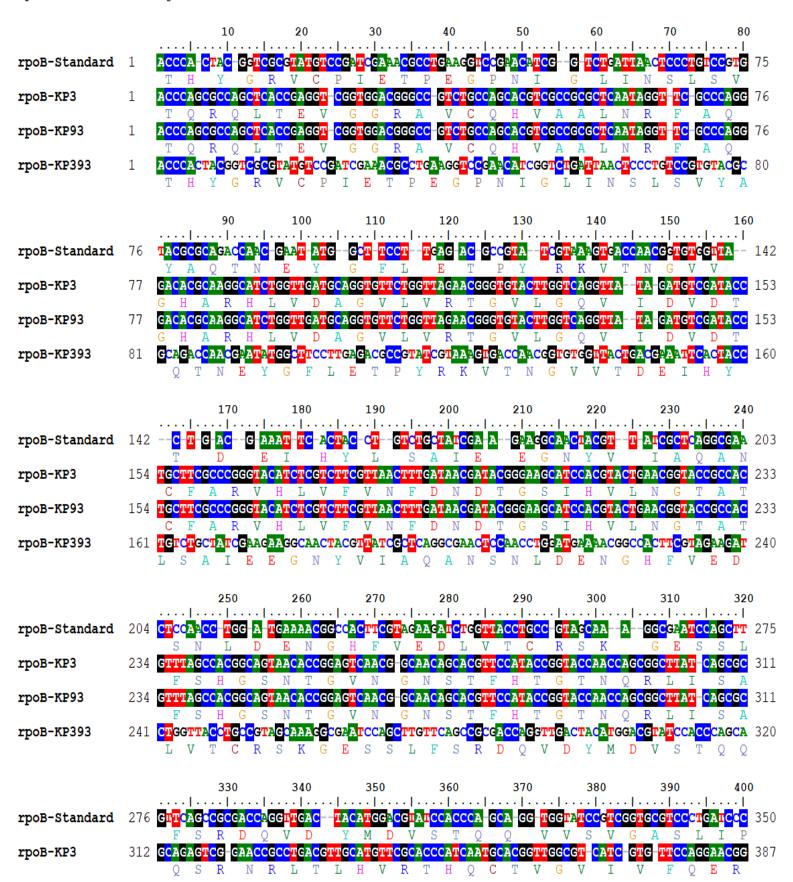


Figure S1F. Multiple sequence alignment of nucleotides and translated nucleotides of *rpoB* genes of the three isolate

X

		10 20 30 40 50	60 70	
tonB -Standard	1	ATGGTGGCGCCGGCCGATCTTGAGCCGCCTCCGGCGCGCAGCCTGTCGTGGAGCCC		
		M V A P A D L E P P P A A Q P V V E P	V V E P	
tonB-KP3	1	ATGGTGGCGCCGATCTTGAGCCGCCTCCGGCGGCAGCCTGTCGTGGAGCCC		
tonB-KP93	1	M V A P A D L E P P P A A Q P V V E P ATGGTGGCGCCGCCGCTCCGGCGCGCGCAGCCTGTCGTGGAGCCCG	V V E P	
	_		V V E P	
tonB-KP393	1	ATGGTGGCGCCGATCTTGAGCCGCCTCCGGCGGCAGCCTGTCGTGGAGCCC		
		M V A P A D L E P P P A A Q P V V E P	V V E P	
		80 90 100 110 120	130 140	
tonB -Standard	71	AACCTGAGCCGGAGCCAGAGGTAGTGCCTGAACCGCCGAAAGAGGCGCCGGTGGTGA		0
tons -standard	/1	E P E P E V V P E P P K E A P V V		J
tonB-KP3	71	AACCTGAGCCGGAGCCAGAGGTAGTGCCTGAACCGCCGAAAGAGGCGCCGGTGGTGA		0
tonB-KP93	71	E P E P E P E V V P E P P K E A P V V D AACCTGAGCCGGAGCCAGAGGTATTGCCTGAACCGCCGAAAGAGGCGCCGGTGGTGAT		0
COMB RE93	/ 1	E P E P E P E V L P E P P K E A P V V		0
tonB-KP393	71	AACCTGAGCCGGAGCCAGAGGTAGTGCCTGAACCGCCGAAAGAGGCGCCGGTGGTGAT		0
		E P E P E V V P E P P K E A P V V I	I H K P E	
		150 160 170 180 190	200 210	
			[[]	
tonB -Standard	141	ACCTAAGCCGAAGCCCAAACCCAAGCCTAAGCCGGAGAAAAAGGTTGAACAC		O
tonB-KP3	141	ACCTAAGCCGAAGCCCAAACCTAAACCCAAGCCTAAGCCGGAGAAAAAGGTTGAACAG		0
		PKPKPKPKPKPEKKVEQ	P K R E	
tonB-KP93	141	ACCTAAGCCGAAGCCCAAACCTAAACCCAAGCCTAAGCCGGAGAAAAAGGTTGAACA		0
tonB-KP393	141	PKPKPKPKPKPKPEKKVEQ ACCTAAGCCGAAGCCTAAACCCAAGCCTAAGCCGGAGAAAAAGGTTGAACA	P K R E G <mark>CCGAAGCGGGAA</mark> 210	0
		P K P K P K P K P E K K V E Q		
		220 230 240 250 260	270 280	
tonB -Standard	211	GTGAAGCCGGCAGCAGAGCCGCGTCCGGCCTCGCCGTTTGAAAACAACAATACGGCG	CCGGCGCGTACAG 280	O
t	211	V K P A A E P R P A S P F E N N N T A		_
tonB-KP3	211	GTGAAGCCGGCAGCAGAGCCGCGTCCGGCCGTTTGAAAACAACAATACGGCGGCGCV K P A A E P R P A S P F E N N N T A		J
tonB-KP93	211	G <mark>TGAAGCCGGCAGCAGAGCCGCGTCCGGCCT</mark> CGCCG <mark>TTT</mark> GAAAACAACAA <mark>T</mark> ACGGCG	CCGGCGCGTACAG 280	0
+ WD202	211	V K P A A E P R P A S P F E N N N T A GTGAAGCCGGCAGCAGCCGCGTCCGCCGTTTGAAAACAATACGGCG		_
tonB-KP393	211	V K P A A E P R P A S P F E N N N T A		J
		290 300 310 320 330	340 350	
tonB -Standard	281	CGCCAAGCACCTCGACAGCAGCGGCTAAACCCACCGTTACTGCTCCAAGCGGCCCGC		0
	201	A P S T S T A A A K P T V T A P S G P I	R A I S R	
tonB-KP3	281	CGCCAAGCACC <mark>T</mark> CGACAGCAGCGGC <mark>T</mark> AAACCCACCG <mark>TT</mark> AC <mark>T</mark> CCAAGCGGCCCGC		0
		A P S T S T A A A K P T V T A P S G P I	RAISR	

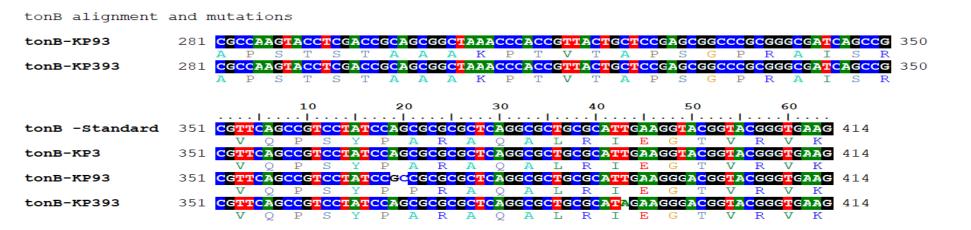


Figure S1G. Multiple sequence alignment of nucleotides and translated nucleotides of tonB genes of the three isolate