TABLE SI	**Primers used to construct *virB10* mutations**
Ala-Cys Insertions	5’ - 3’ primer
05	5’-CATGTGCCGCTTGCTG**GCATGC**ACTATCGTTATTC-3’
10	5’-GATGCATCAACCTC**GCATGC**ATGTGCCGCTTG-3’
15	5’-CGGAGACCAGGGATCC**GCATGC**AGATGCATCAA-3’
20	5’-CGGCGATGTTTGTC**GCATGC**GGAGACCAGGGATC-3’
25	5’-GACCCCGAAAGACG**GCATGC**CCGGCGATGTTTG-3’
30	5’-GATCAATTTCTG**GCATGC**AGACCCCGAAAG-3’
35	5’-CGAGAACGACACCTCC**GCATGC**GACGATCAATTTC-3’
40	5’-CTTAACGATAACGC**GCATGC**GAGAACGACACC-3’
45	5’-CCTAGCCAAATGAG**GCATGC**GCTTAACGATAAC-3’
50	5’-CTTTTGACGCCC**GCATGC**ACCTAGCCAAAT-3’
Cys Substitutions	
S61C	5’-AGTTGACGG**GCATGC**GTTGTC-3’
N69C	5’-GAAATGGCTTAGT**GCATGC**TGCGAT-3’
P77C	5’-GCACCTCAAT**GCATGC**TGGAT-3’
V87C	5’-GAACAGCCTCTTG**GCATGC**TGGAGT-3’
P99C	5’-CGGCTCGCCC**CTGCAG**GGTTGAGGAAC-3’
Y118C	5’-CGCCACTGCT**GCATGC**AAAAATC-3’
S130C	5’**-**GCCCATGTCGCCCTG**GCATGC**GCGCTTG-3’
T173C	5’-GTGCGGCAAGAG**GCATGC**CCTGCTG-3’
N218C	5’-CAAGAAGCA**GCATGC**AGTTCGTTGTTC-3’
G230C	5’-ACCGTTGTT**TGC**GAAATACAGCGTG-3’
V243C	5’-AGGGAGATGAG**GCATGC**TTTGTGTTGTGG-3’
D278C	5’-GGCTCGGT**CTGCAG**CCACTTCTGG-3’
Q295C	5’-TTGAGTGCTGTT**TGC**GGCGCCTTCCAGGCA-3’
G306C	5’-AGCACCTAC**GCATGC**AGCTCGGGTGGC-3’

TABLE SI	Continued
C190S	5’-ACAATAATTCCGAGCATCCTGCAAACCG-3’
C206S	5’-AGGCTATGTAAAGAGTGTCTTGCCTCATTAT-3’
RDLDF-R**K**LDF	5’-TTCGTGGCACGGAAGCTCGATTTCTTTGGTG-3’ 5’-CACCAAAGAAATCGAGCTTCCGTGCCACGAAA-3’
RDLDF-RDL**C**F	5’-CTGGCACGGGACCTC**TGC**TTCTTTGGTGTTTACCA-3’ 5’-GTAAACACCAAAGAAGCAGAGGTCCCG-3’
RDLDF-QNALM	5’-TTTCCATTTTCGTGGCACAGAACGCCCTTATGTTTGGTGTTTACCAG-3’ 5’-GTAAACACCAAACATAAGGGCGTTCGTGCCACGAAAATGG-3’
Deletions	
ΔN18	5’-CGAGCTAAGGAGATAACATATGGTCTCCGACAAACATCGCCGGCGTC-3’ 5’-GACGCCGGCGATGTTTGTCGGAGACCATATGTTATCTCCTTAGCTCG-3’
ΔN46	5’-CTGGTCTCCGASAAACATCGCCGGCGTCATATGATTTGGCTAGGTGGGCGTCAAAAGAAG -3’ 5’-GTCATTCACCTTCTTTTGACGCCCACCTAGCCAAATCATATGACGGCGGCGATGTTTGTCGGA-3’
Δ181-377	5’-CCCGATTTTTAAAGTAACGCAAGGGAC-3’ 5’-TTGCGTTACTTAAAAATCGGGGTG-3’
Δ72-92	5’-GATCGCAGCAAACACTAGCCTACTGTTCCTCAACCGCCAAGGG-3’ 5’-CCCTTGGCGGTTGAGGAACAGTAGGCTTAGTGTTTGCTGCGATC-3’
Δ70-114	5’-TCAACTTTGATCGCAGCAAATATTTTTGCATATAGCAGTGGCGATCAAGG-3’ 5’-CCTTGATCGCCACTGCTATATGCAAAAATATTTGCTGCGATCAAAGTTGA-3’
Δ93-114	5’-TCAAGAGGCTGTTCAGATTTTTGCATATAGCAGTGGCGATCAAGG-3’ 5’-CCTTGATCGCCACTGCTATATGCAAAAATCTGAACAGCCTCTTGA-3’
Δα1(268-287)	5’-GTTAACTAGTCCAAGCGCGGACGAAGCCATGCTCTTGAGTGCTGTTCAAGGCG -3’ 5-CGCCTTGAACAGCACTCAAGAGCATGGCTTCGTCCGCGCTTGGACTAGTTAAC-3’
ΔAC(308-337)	5’-AGGCAGCTAGCACCTACGCTGGATCCACCCTGAAGAAGAATCAGGGTGAGGGTGACACGGTTTC-3 5’-GAAACCGTGTCACCCTGATTCTTCTTCAGGGTGGATCCAGCGTAGCTGCTAGCTGCCTGG-3’
Δα2(308-320)	5’-CAGCTAGCACCTACGCTGGATCCGGTGAACAAACAACTGAGACAGCCC-3’ 5’-GGGCTGTCTCAGTTGTTTGTTCACCGGATCCAGCGTAGGTGCTAGCTG-3’
Δα3(323-337)	5’-GCTTTCAAAATAACGGTGAAACCCTGAAGAAGAATCAGGGTGACACGG-3’ 5’-CCGTGTCACCCTGATTCTTCTTCAGGGTTTCACCGTTATTTTGAAAGC-3’

a. Bases in bold identify *Sph*I (**GCATGC**) and *Pst*I (**CTGCAG**) restriction sites.

b. **TGC** in bold expresses the cysteine residue.