

Majority	TTATACCTCCACGCGCTTGCCCGATCTCAAGCTATCACTAGTAGTCTCTGTTTCACGAAATTCGACTGTCTATCTTTCTATCACCAATCGTTAATAATTAATCAAAACTTAGGATCCAGGACGCAGCAAGCCAACAGGCCAACCAAGTCC																		
	310	320	330	340	350	360	370	380	390	400	410	420	430	440	450				
Tw1T.....T.....															450			
Tw2I.....T.....T.....															450			
Tw3T.....T.....															450			
Tw4	CCC.....														450			
Tw5T.....G.....T.....A															450			
Tw6	CCC.....C.....														450			
Tw7	CCC.....														450			
Vacc-N	TC	A	TG.C.A.....A.CG.....AGC.A.....G.....AT.....T.....G.....												450			
Vacc-PA.....A.....G.....I.....															450			
Vacc-Q	TC	A	TG.C.A.....C.....AGC.A.....G.....AT.....T.....G.....												450			
Majority	ACCAATCCGAGGCCGGGCAGGAACCCCCACAACAGACAAGCCCCATGCACAACAAAATTCGCAAAAAATCCAAACCTTGCACACACCCGACAAGATCCCCTCCAACAACACAGCACCAGATCCGCCGAGACCAAGACCTCCCAAGGA																		
	460	470	480	490	500	510	520	530	540	550	560	570	580	590	600				
Tw1G.....G.....															600			
Tw2C.....															600			
Tw3G.....															600			
Tw4T.....															600			
Tw5G.....T.....A.A.....															600			
Tw6T.....															600			
Tw7T.....															600			
Vacc-N	GC.A.G	AC.G.....GGG.C.....GC.....AAA.T.....A.....C.G.C.C.....C.....GA.C.AA.....G.....G.C.....												600				
Vacc-P	G.A.	GT.....C.....G.....A.AAA.....A.....C.T.C.C.....A.....G.....G.C.....												600				
Vacc-Q	GC.A.G	AC.G.....GGG.C.....GC.....A.AAA.....T.....A.....C.G.C.C.....C.....GA.C.AA.....G.....G.C.....												600				
Majority	CGACACAGCATAACATCGGCTCAGAGATCCACGCACCATGGTCCCTCGAACATCGGACAGGTCGGTCCACTACATAATGAACAGGACCAAGTCTTGCAAGCAAATAGCCACAGATCGGATAACATCCCGCCTCAGAGACCACGAGGGT																		
	610	620	630	640	650	660	670	680	690	700	710	720	730	740	750				
Tw1	..T.T.....T.....															750			
Tw2	..T.T.....A.T.....															750			
Tw3	..T.T.....T.....															750			
Tw4	..C.....C.....C.....															750			
Tw5	..T.T.....T.....C.....A.....															750			
Tw6	..C.....C.....C.....															750			
Tw7	..C.....C.....C.....															750			
Vacc-NA.....C.....TC.A.....G.AC.....TC.....CC.....T.....CC.....T.A.G.....GT.....G.A.....C.....															750			
Vacc-PC.....C.....A.....C.....G.....G.C.T.....G.....G.....G.....															750			
Vacc-QA.....C.....T.A.....AC.....TC.....CC.....T.....CC.....T.A.G.....AGT.....G.A.....C.....															750			

Phylogenetic tree and sequence alignment of the Fsp gene. The tree shows relationships between various isolates, with a scale bar indicating 10, 30, and 40 substitutions per site. The alignment shows the ATG start codon and the TGC stop codon for most isolates, with some variations in the stop codon (AAA, GAA, CAA, ACA).

Isolate	Sequence
TW1	ATG.....TGC.....
TW2	ATG.....CGC.....
TW-KS2	ATG.....TGC.....
TW-TP1	ATG.....TGC.....
TW-KL1	ATG.....TGC.....
HeB-07	ATG.....TGC.....
JL-07	ATG.....TGC.....
NM	ATG.....TGC.....
ZD01	ATG.....TGC.....
BS0610	ATG.....TGC.....
Asia-2 007Lm	ATG.....AAA.....
5047/91	ATG.....AAA.....
R252/72	ATG.....AAA.....
Rockborn	ATG.....AAA.....
X65509	ATG.....AAA.....
A75/17	ATG.....GAA.....
01-2689	ATG.....GAA.....
5804	ATG.....CAA.....
5804P	ATG.....CAA.....
00-2601	ATG.....GAA.....
Vacc-P	ATG.....AAA.....
Vaccine X	ATG.....AAA.....
Vacc-Q	ATG.....AAA.....
Onderstepoort	ATG.....AAA.....
Snyder Hill	ATG.....ACA.....