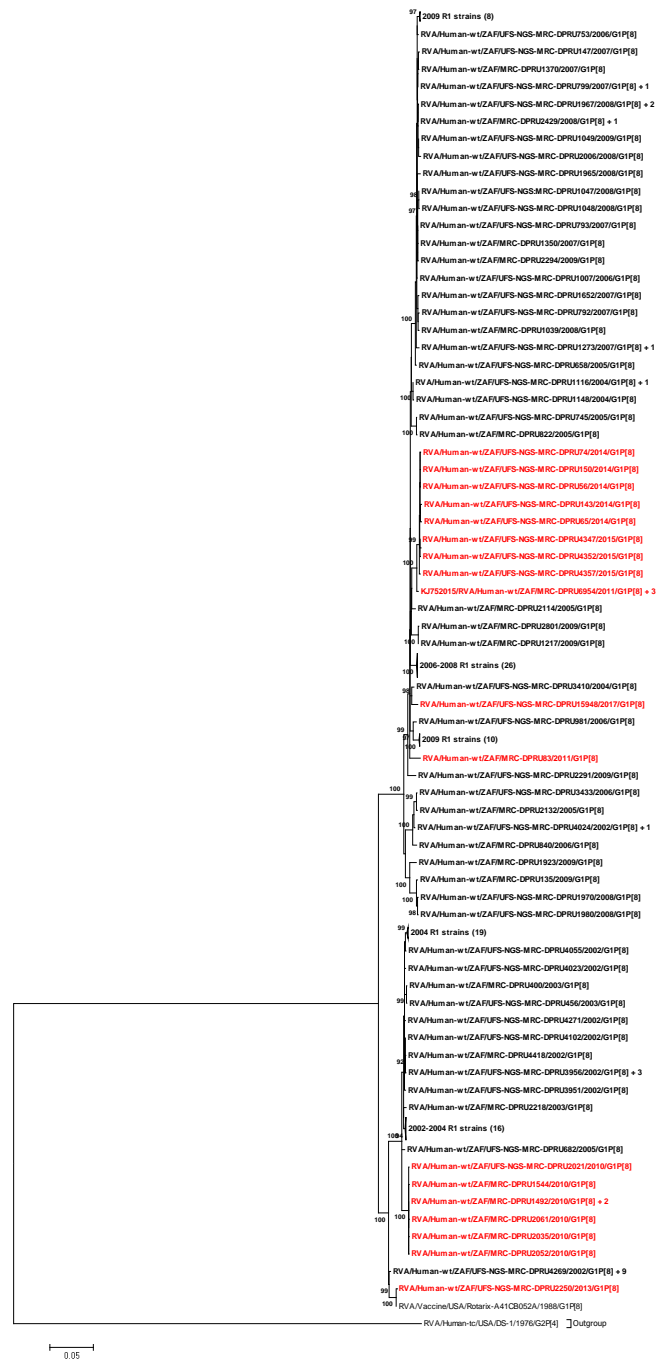
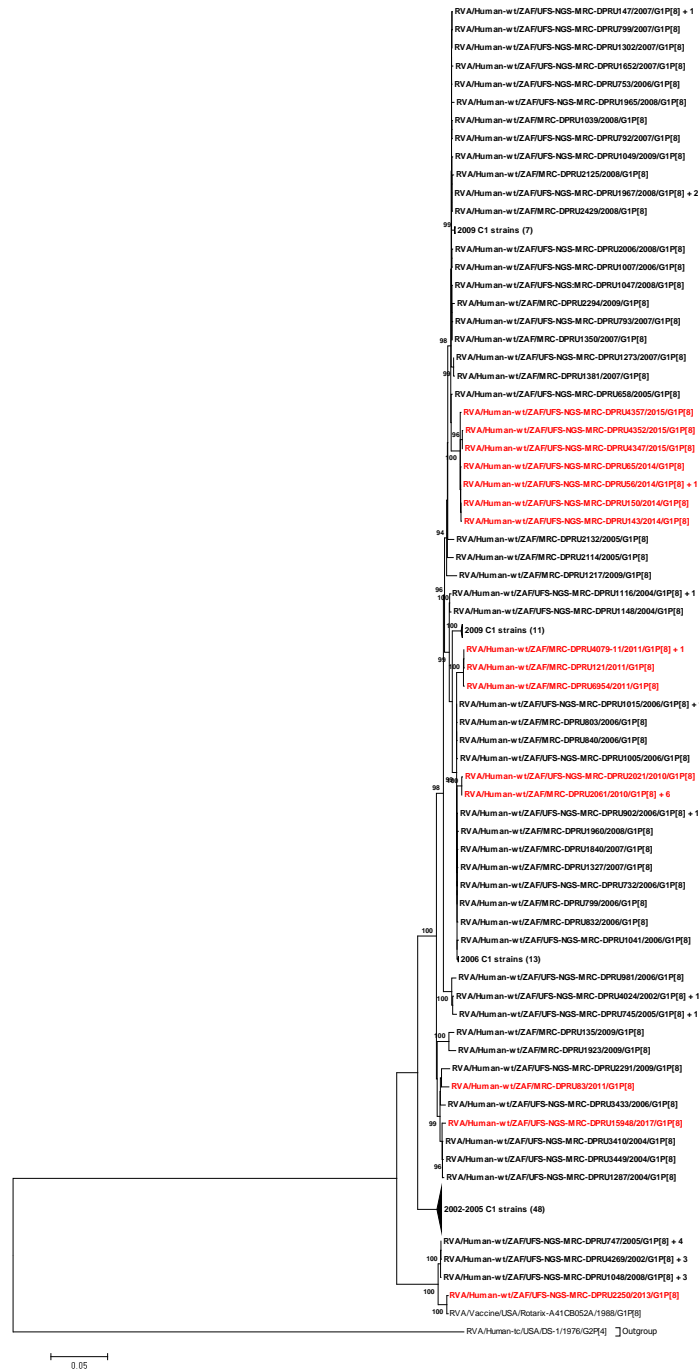


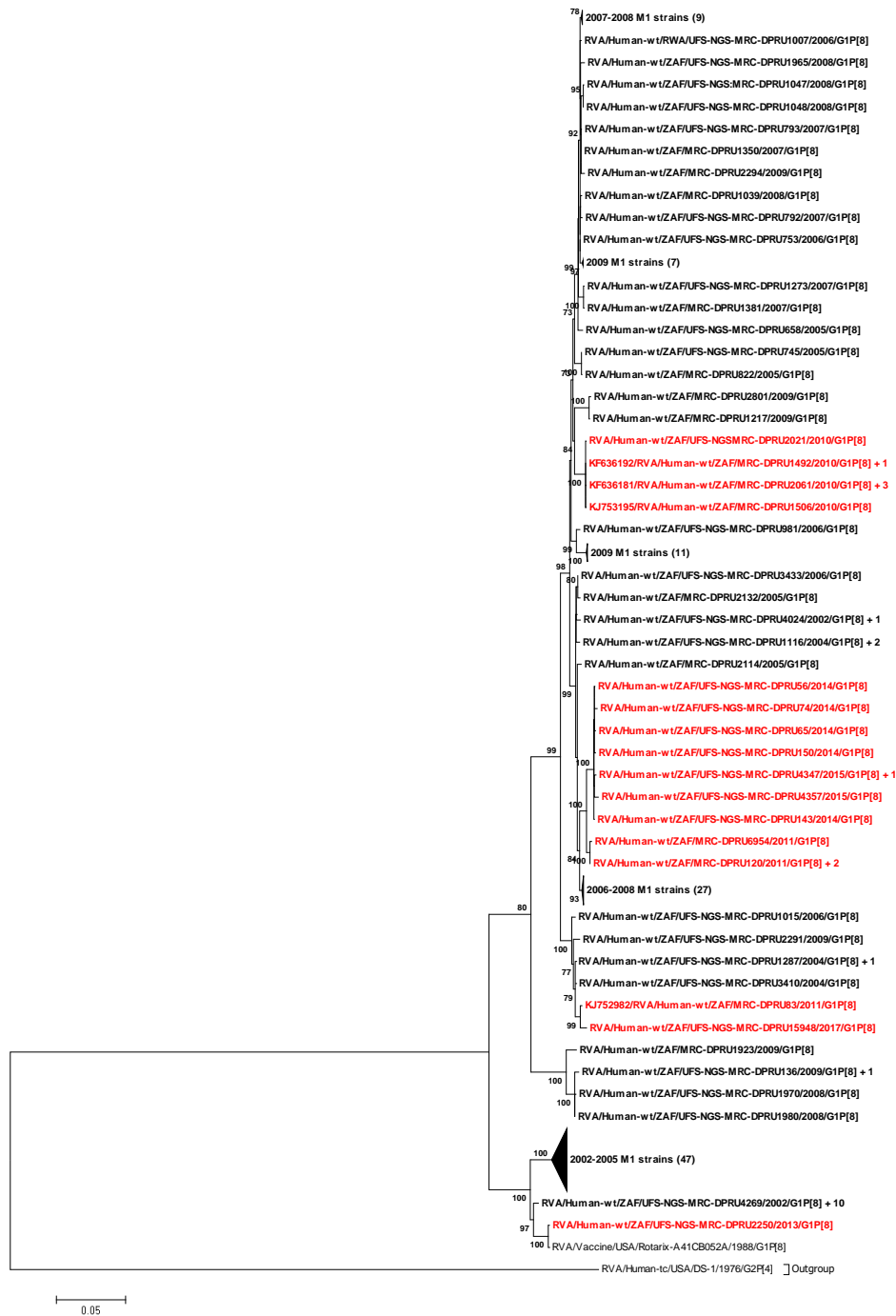
## Supplementary data 4: Additional phylograms



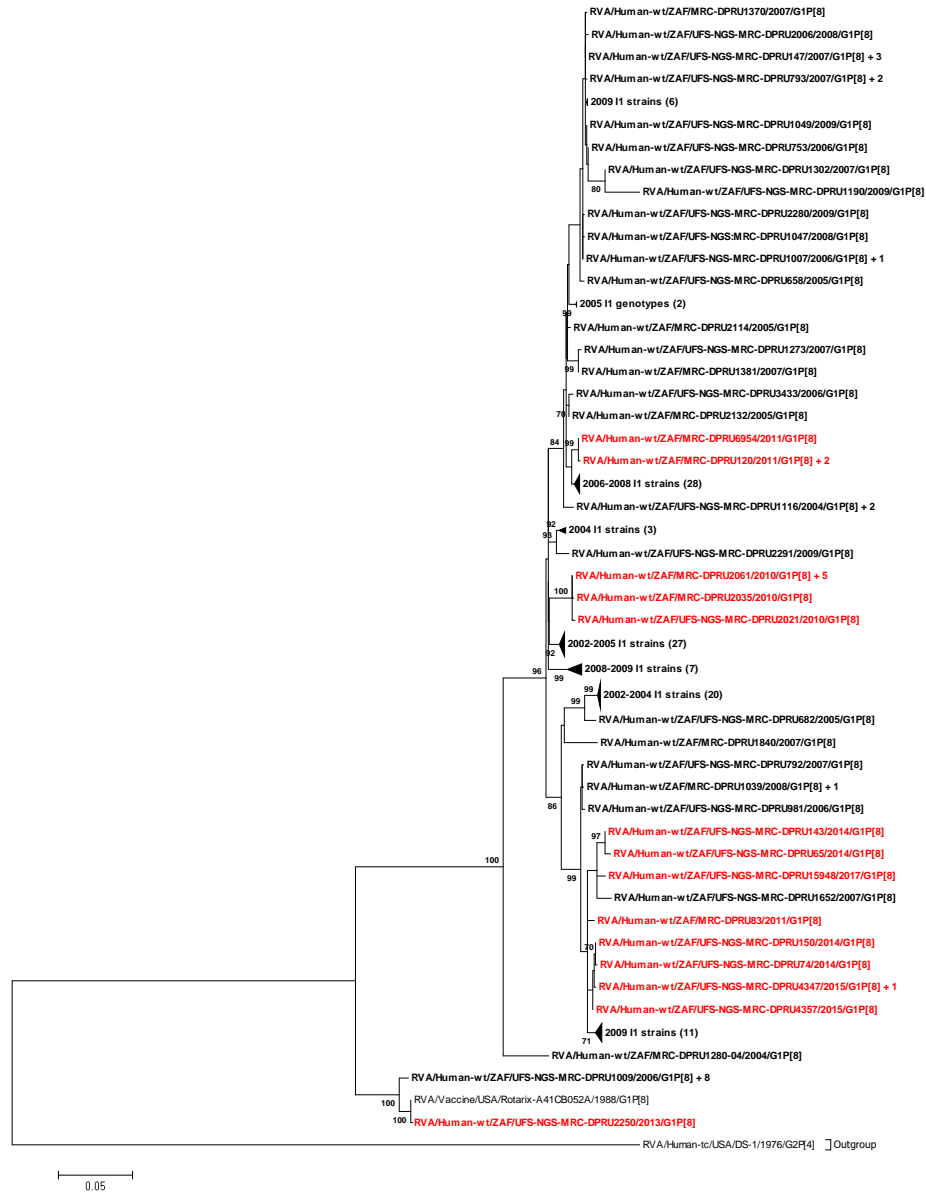
**Figure S1:** Maximum likelihood phylogenetic tree based on the full-length nucleotide sequences of the genome segment 1 encoding VP1 protein. The T92+G+I evolutionary model was used for phylogenetic inference. South African pre-vaccine R1 strains are highlighted in bold-face while post-vaccine strains are highlighted in bold-red. Adjacent to some sequences is indicated a plus (+) sign followed by the number of identical sequences (S3). The number in brackets denotes the number of compressed strains. Only bootstrap values  $\geq 70\%$  are shown adjacent to each branch node. Scale bar indicates the number of nucleotide substitutions per site.



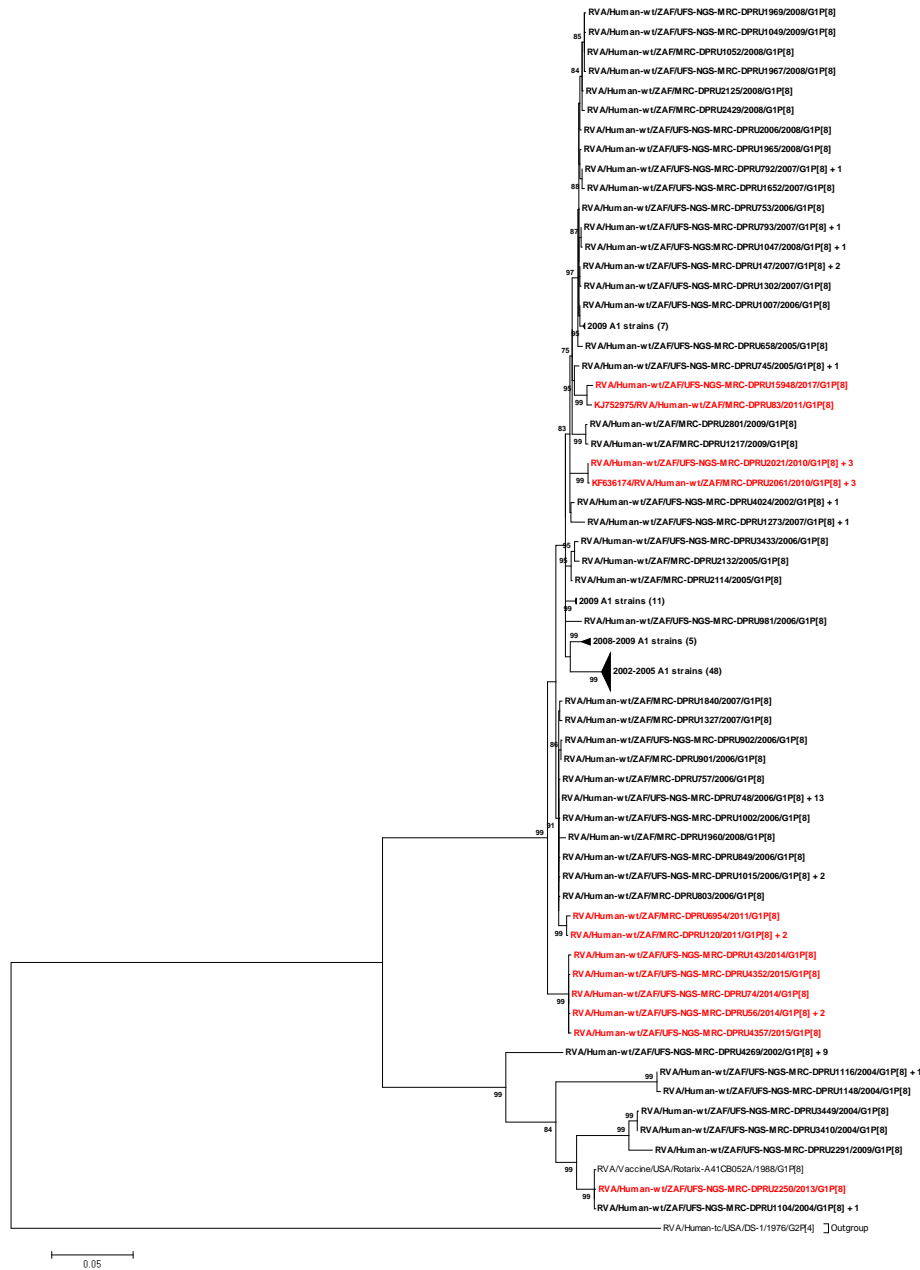
**Figure S2:** Maximum likelihood phylogenetic tree based on the full-length nucleotide sequences of the genome segment 2 encoding VP2 protein. The T92+G+I evolutionary model was used for phylogenetic inference. South African pre-vaccine C1 strains are highlighted in bold-face while post-vaccine strains are highlighted in bold-red. Adjacent to some sequences is indicated a plus (+) sign followed by the number of identical sequences (S3). The number in brackets denotes the number of compressed strains. Only bootstrap values  $\geq 70\%$  are shown adjacent to each branch node. Scale bar indicates the number of nucleotide substitutions per site.



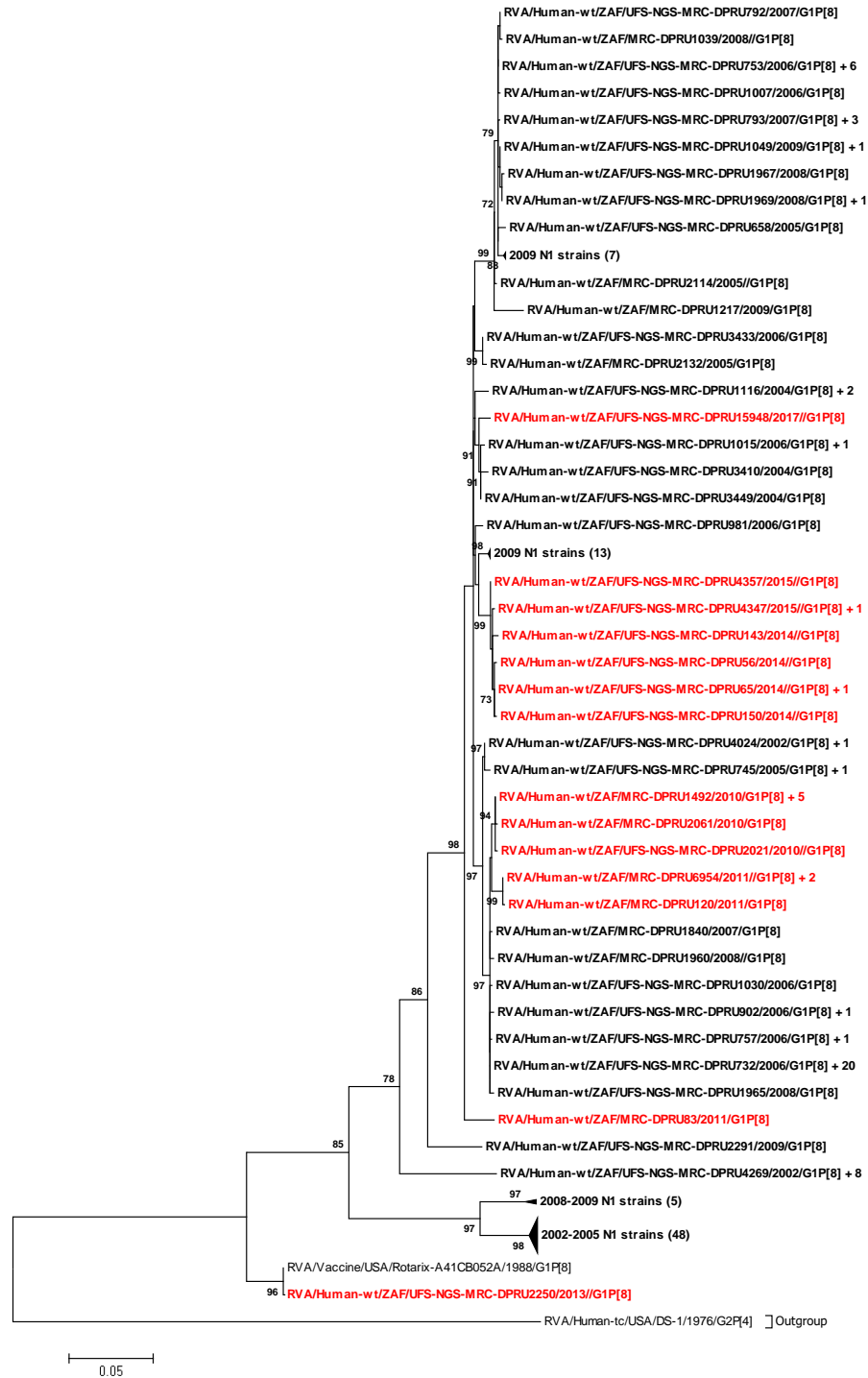
**Figure S3:** Maximum likelihood phylogenetic tree based on the full-length nucleotide sequences of the genome segment 3 encoding VP3 protein. The GTR+ G evolutionary model was used for phylogenetic inference. South African pre-vaccine M1 strains are highlighted in bold-face while post-vaccine strains are highlighted in bold-red. Adjacent to some sequences is indicated a plus (+) sign followed by the number of identical sequences (S3). The number in brackets denotes the number of compressed strains. Only bootstrap values  $\geq 70\%$  are shown adjacent to each branch node. Scale bar indicates the number of nucleotide substitutions per site.



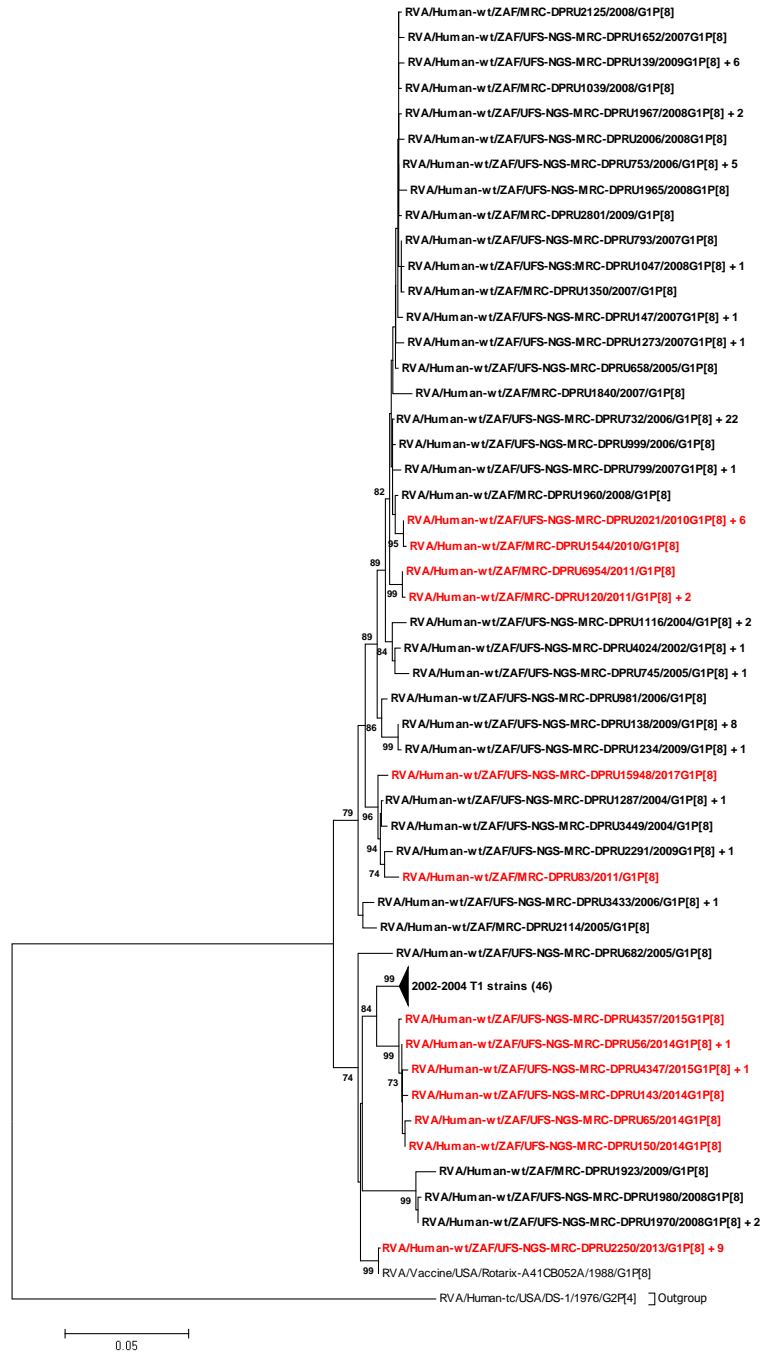
**Figure S4:** Maximum likelihood phylogenetic tree based on the full-length nucleotide sequences of the genome segment 6 encoding VP6 protein. The T92+G+I evolutionary model was used for phylogenetic inference. South African pre-vaccine I1 strains are highlighted in bold-face while post-vaccine strains are highlighted in bold-red. Adjacent to some sequences is indicated a plus (+) sign followed by the number of identical sequences (S3). The number in brackets denotes the number of compressed strains. Only bootstrap values  $\geq 70\%$  are shown adjacent to each branch node. Scale bar indicates the number of nucleotide substitutions per site.



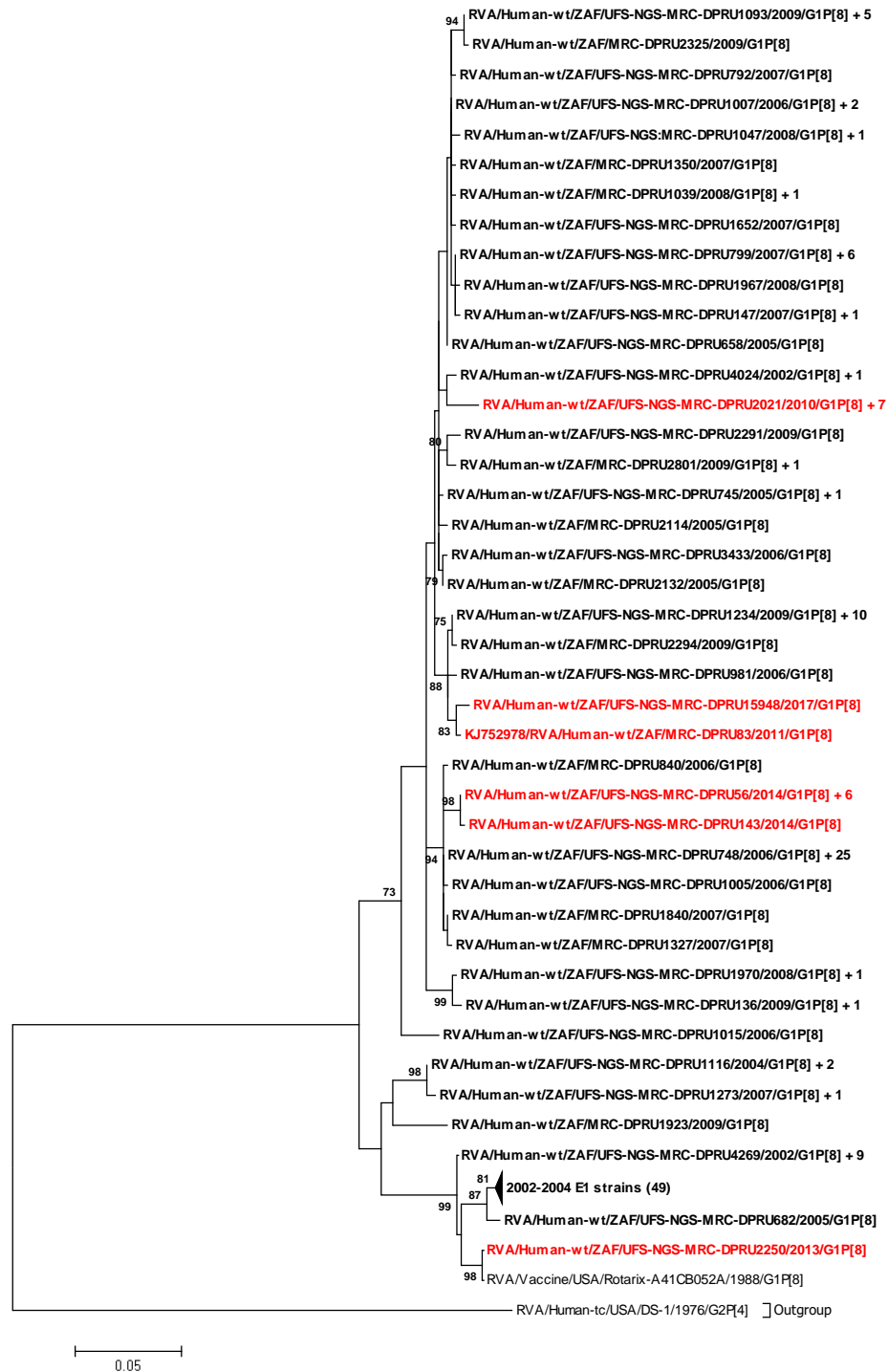
**Figure S5:** Maximum likelihood phylogenetic tree based on the full-length nucleotide sequences of the genome segment 5 encoding NSP1 protein. The T92 + I evolutionary model was used for phylogenetic inference. South African pre-vaccine A1 strains are highlighted in bold-face while post-vaccine strains are highlighted in bold-red. Adjacent to some sequences is indicated a plus (+) sign followed by the number of identical sequences (S3). The number in brackets denotes the number of compressed strains. Only bootstrap values  $\geq 70\%$  are shown adjacent to each branch node. Scale bar indicates the number of nucleotide substitutions per site.



**Figure S6:** Maximum likelihood phylogenetic tree based on the full-length nucleotide sequences of the genome segment 8 encoding NSP2 protein. The T92 + G evolutionary model was used for phylogenetic inference. South African pre-vaccine N1 strains are highlighted in bold-face while post-vaccine strains are highlighted in bold-red. Adjacent to some sequences is indicated a plus (+) sign followed by the number of identical sequences (S3). The number in brackets denotes the number of compressed strains. Only bootstrap values  $\geq 70\%$  are shown adjacent to each branch node. Scale bar indicates the number of nucleotide substitutions per site.

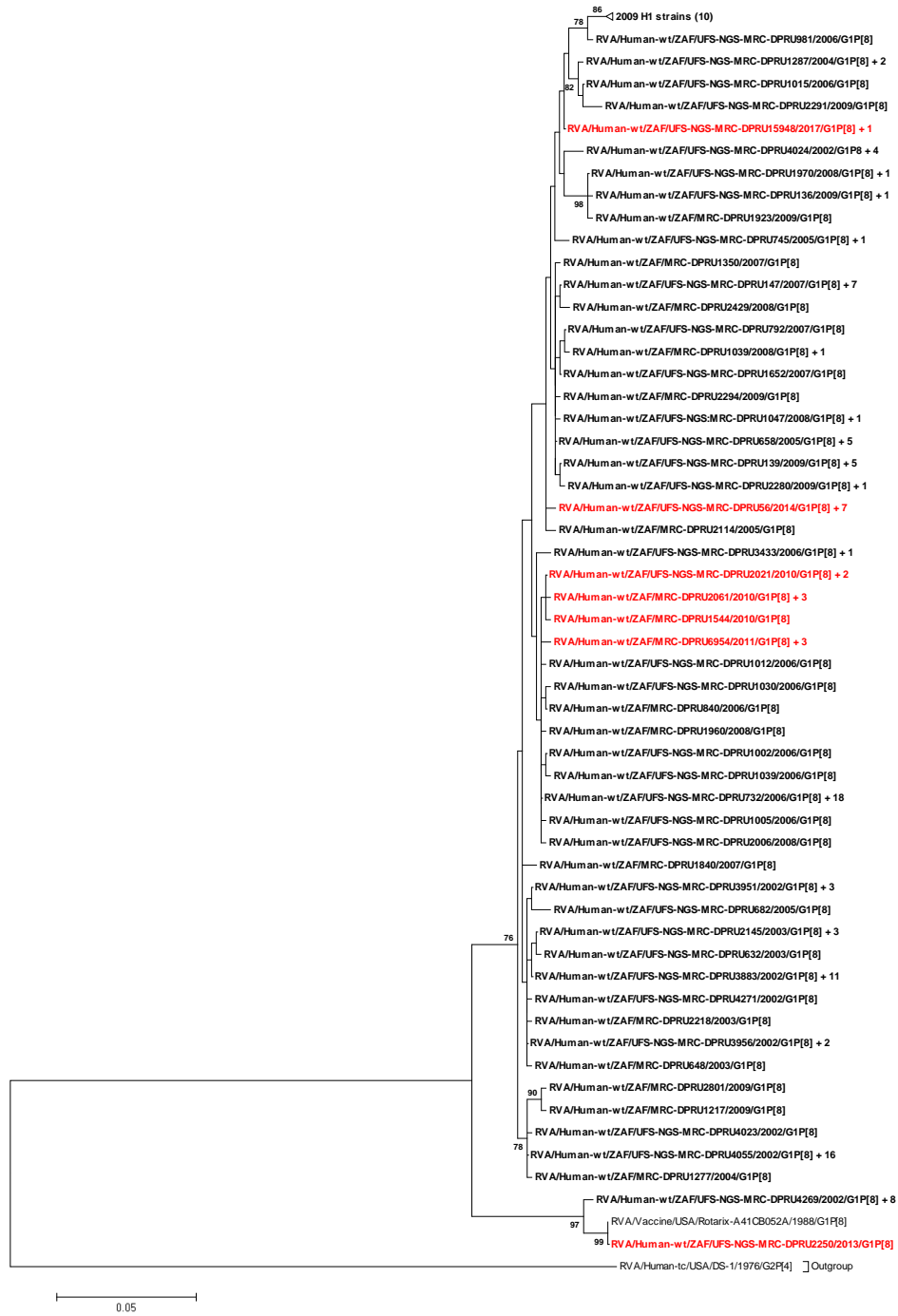


**Figure S7:** Maximum likelihood phylogenetic tree based on the full-length nucleotide sequences of the genome segment 7 encoding NSP3 protein. The TN93 + I evolutionary model was used for phylogenetic inference. South African pre-vaccine T1 strains are highlighted in bold-face while post-vaccine strains are highlighted in bold-red. Adjacent to some sequences is indicated a plus (+) sign followed by the number of identical sequences (S3). The number in brackets denotes the number of compressed strains. Only bootstrap values  $\geq 70\%$  are shown adjacent to each branch node. Scale bar indicates the number of nucleotide substitutions per site.



**Figure S8:** Maximum likelihood phylogenetic tree based on the full-length nucleotide sequences of the genome segment 10 encoding NSP4 protein. The T92 +G evolutionary model was used for phylogenetic inference. South African pre-vaccine E1 strains are highlighted in bold-face while post-vaccine strains are highlighted in bold-red. Adjacent to some sequences is indicated a plus (+) sign followed by the number of identical sequences (S3). The number in brackets denotes the number of compressed strains. Only bootstrap values  $\geq 70\%$  are shown adjacent to each branch node. Scale bar indicates the number of nucleotide substitutions per site.





**Figure S9:** Maximum likelihood phylogenetic tree based on the full-length nucleotide sequences of the genome segment 11 encoding NSP5 protein. The T92 + I evolutionary model was used for phylogenetic inference. South African pre-vaccine H1 strains are highlighted in bold-face while post-vaccine strains are highlighted in bold-red. Adjacent to some sequences is indicated a plus (+) sign followed by the number of identical sequences (S3). The number in brackets denotes the number of compressed strains. Only bootstrap values  $\geq 70\%$  are shown adjacent to each branch node. Scale bar indicates the number of nucleotide substitutions per site.