(a)

(b) Pruning of N gene dataset

(c)

Key:
Lineage 1
Lineage 2
Lineage 3
Lineage 4

S4 Fig. Tree pruning to give a simpler dataset of N gene sequences. The maximum likelihood tree was calculated for the unique N gene sequences and then pruned to give a simpler but equally informative dataset: (a) Full N gene sequence tree (split); (b) plot showing relationship between tree length and degree of pruning; (c) Maximum likelihood tree based on pruned list of 60 sequences. (a), (c): Lineage 1, Lineage 2, Lineage 3, Lineage 4