



**S5 Fig. Tree pruning to give a simpler sets of F gene sequences.** The maximum likelihood tree was calculated for the “NoDups” set of F gene sequences and then pruned to give a simpler but almost equally informative dataset: (a) Full F gene sequence tree; (b) plot showing how relative tree length decreases during pruning; (c) pruned tree without lineage conservation; (c) pruned tree with lineage conservation. Note that in (d) the two vaccine strains were deliberately retained by assigning them to their own “lineage”. (a), (d), (d): **Lineage 1**, **Lineage 2**, **Lineage 3**, **Lineage 4**