

Figure 1 - source data 2

A



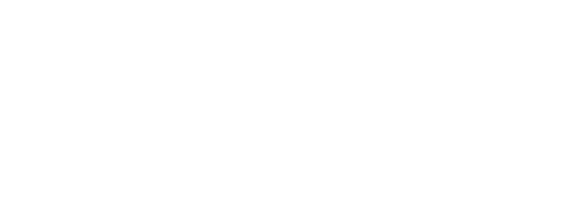
Clade 1

B



Clade 2

C



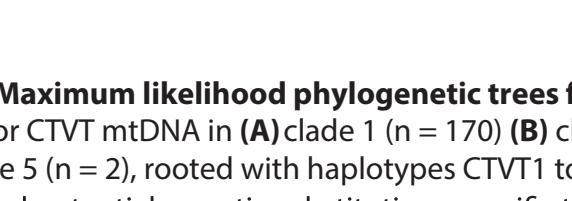
Clade 3

D



Clade 4

E



Clade 5

Figure 1 - source data 2. Maximum likelihood phylogenetic trees for CTVT clades 1 to 5. Maximum likelihood phylogenetic trees for CTVT mtDNA in (A) clade 1 ($n = 170$) (B) clade 2 ($n = 252$) (C) clade 3 ($n = 22$) (D) clade 4 ($n = 3$) and (E) clade 5 ($n = 2$), rooted with haplotypes CTVT1 to CTVT5 respectively, which contain clade-defining germline and potential somatic substitutions specific to each clade (Figure 1-figure supplement 4). Bootstrap values were calculated from 100 bootstrap replicates and are shown where bootstrap values ≥ 60 . Scale bars indicate base substitutions per site. Clade 5 contains only two tumours, which are identical both to each other and to the CTVT5 haplotype; thus the tree for this clade was created separately and does not have a scale bar.