

Figure 1 - source data 2



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 CTV1 to CTV5 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 CTV5 haplotype; thus the tree for this clade was created separately and does not have a scale bar.