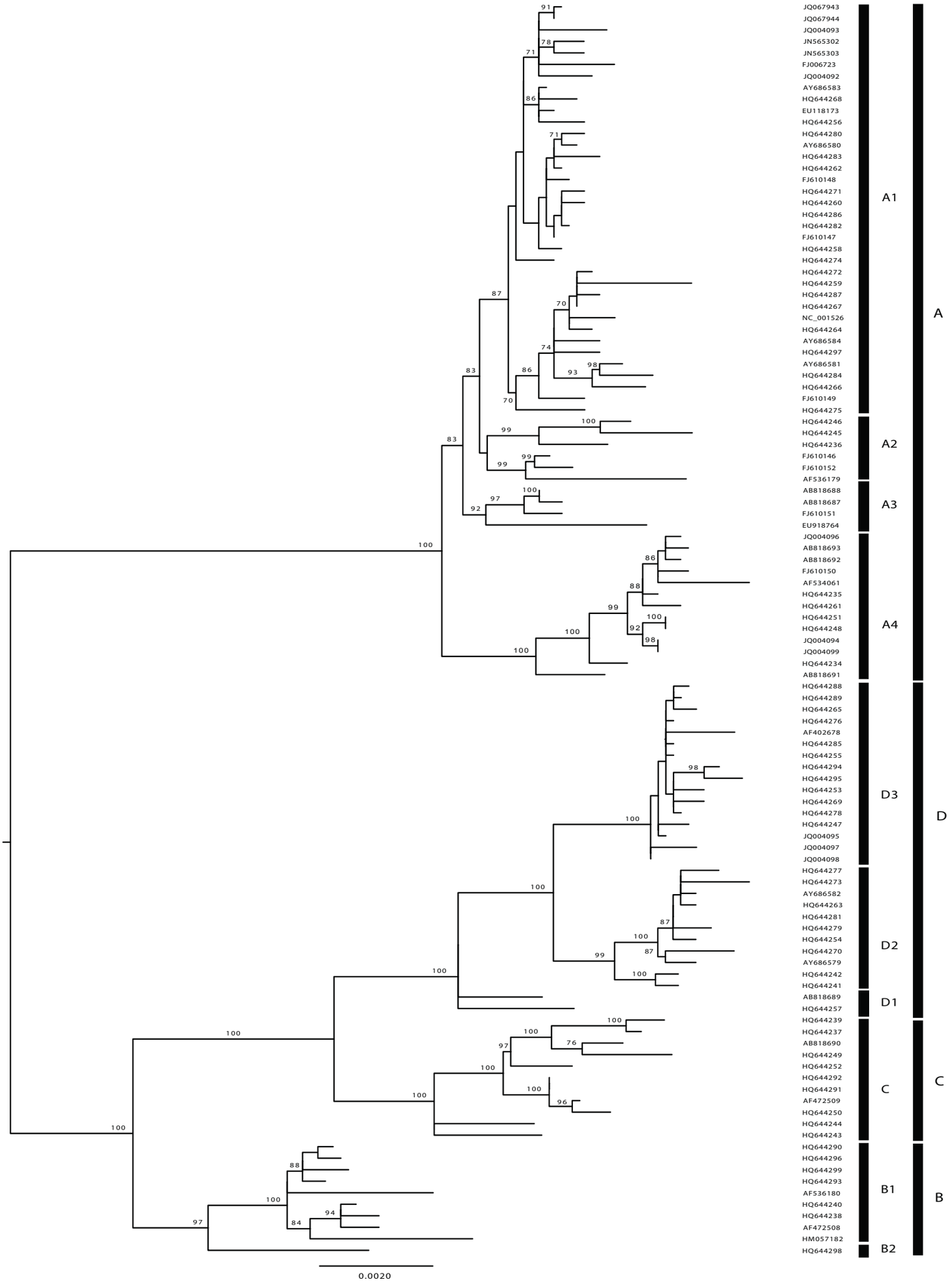

Figure S2: Mid-point rooted HPV16 Best-known maximum likelihood phylogenetic tree, constructed using 109 unique full length genome sequences. HPV16 lineages are classified into four variants: A, B, C and D. Boostrap values above 70 are displayed closed to the corresponding node. GenBank accession numbers are given for all entries.