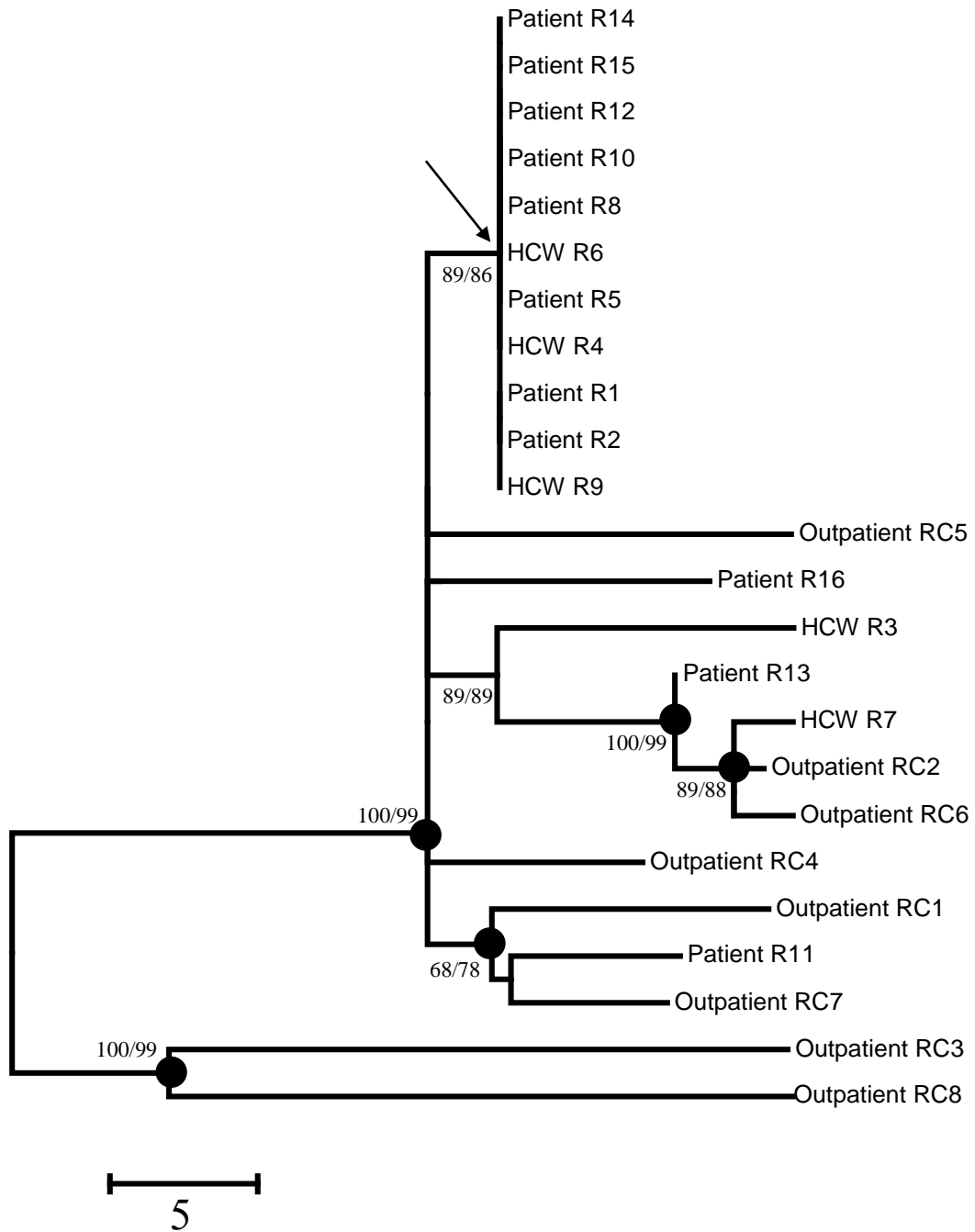


Figure 1. Phylogenetic tree reflecting the relationships of strains based on whole genome re-sequencing and analysis.



The tree topology was obtained from a boot-strapped neighbor-joining analysis. Nodes for which bootstrap values equaled or exceed 70 % are indicated by a numerical value. The bootstrap values derived from maximum likelihood analysis is also indicated (NJ/ML). Polytomies indicate branching points that were not consistently supported by bootstrap analyses. Nodes supported by Bayesian analysis, with posterior probability values greater than 95 %, are indicated with black circles. The node indicated by the arrow represents 11 identical genomes based on mapping to the reference genome (GenBank AF013254.1).