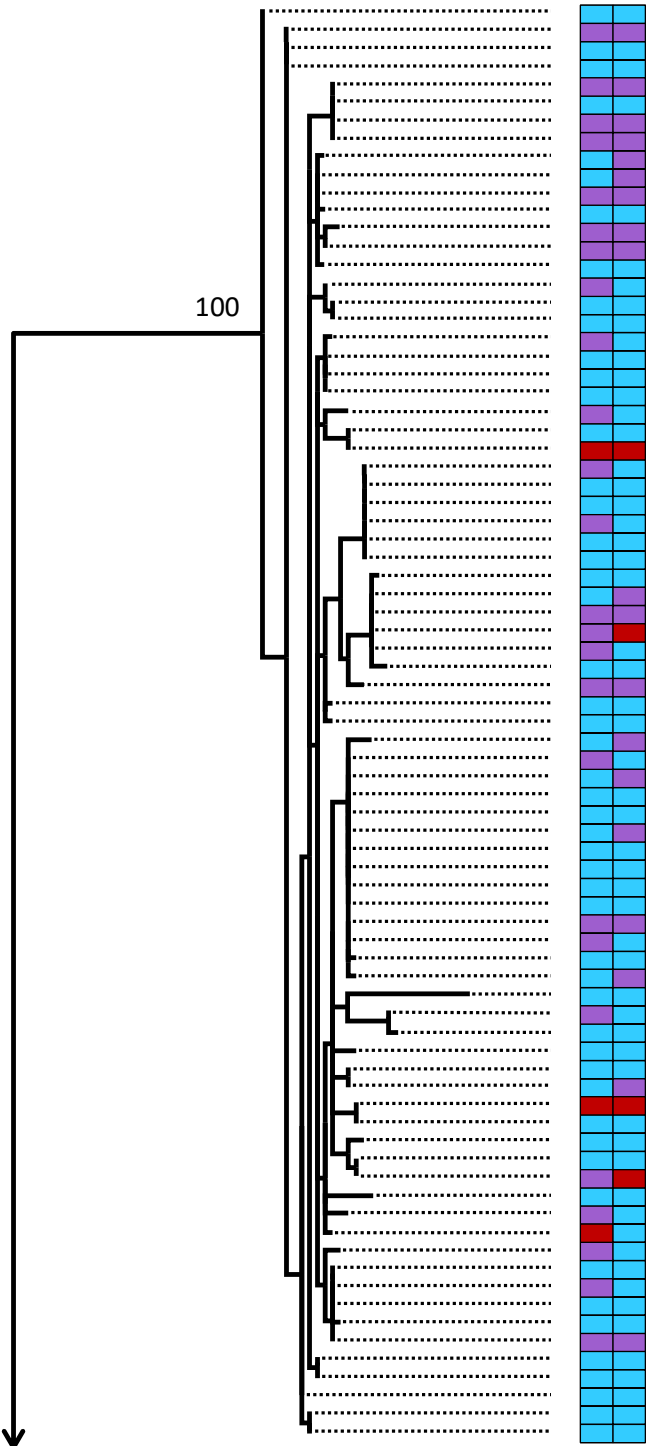
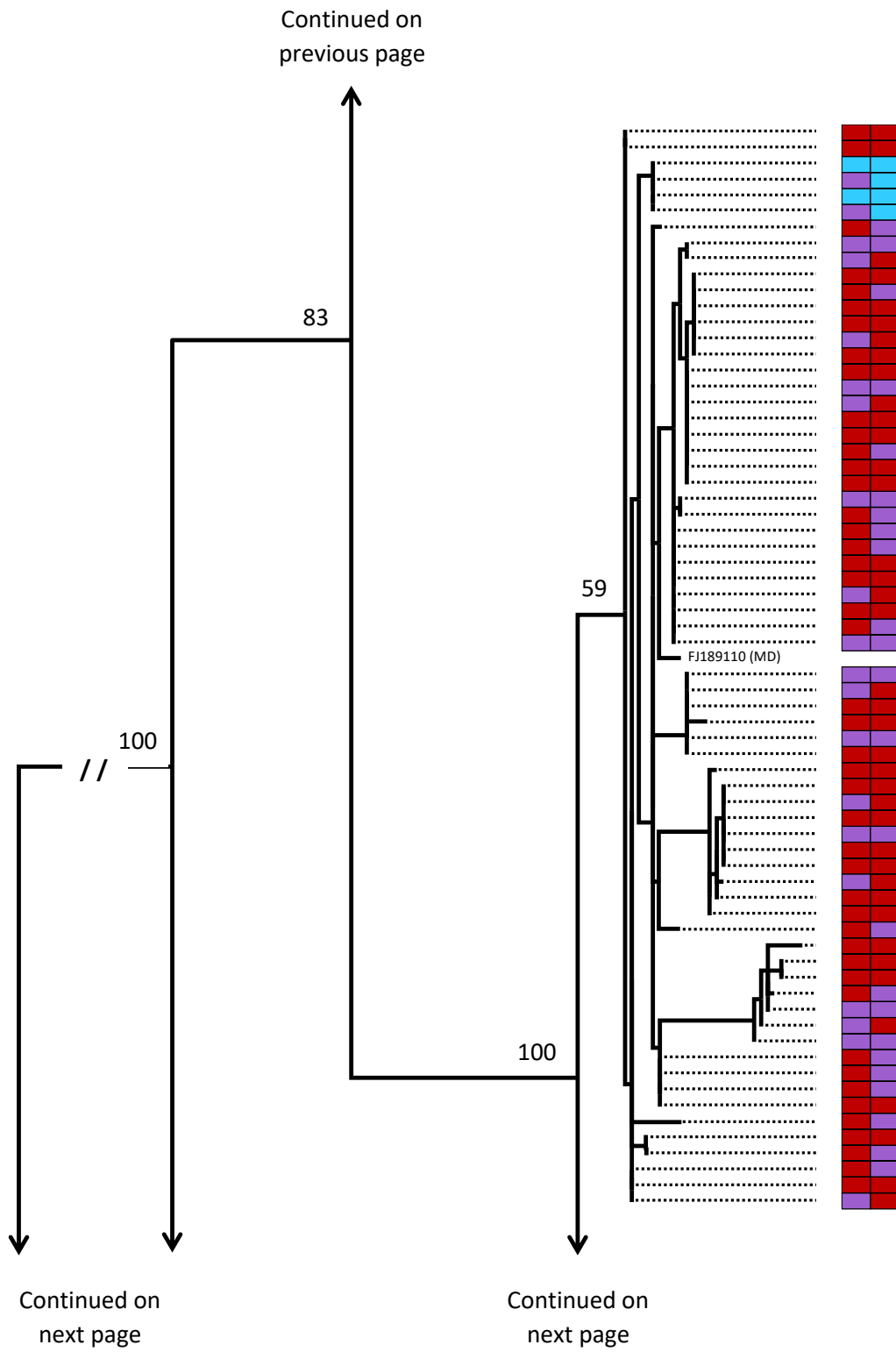


Fig S1 Maximum likelihood tree based on mitochondrial DNA control region haplotypes. Bootstrap values > 0.70 are provided next to internal nodes. The bar chart indicates the assignment of each individual as a black-tailed deer (blue), hybrid (purple), or mule deer (red) based on data from microsatellites (column 1) and SNPs (column 2). Outgroups and mule deer samples collected outside the hybrid zone are designated by GenBank numbers. MD = *Odocoileus hemionus hemionus*; WTD = *Odocoileus virginianus*



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