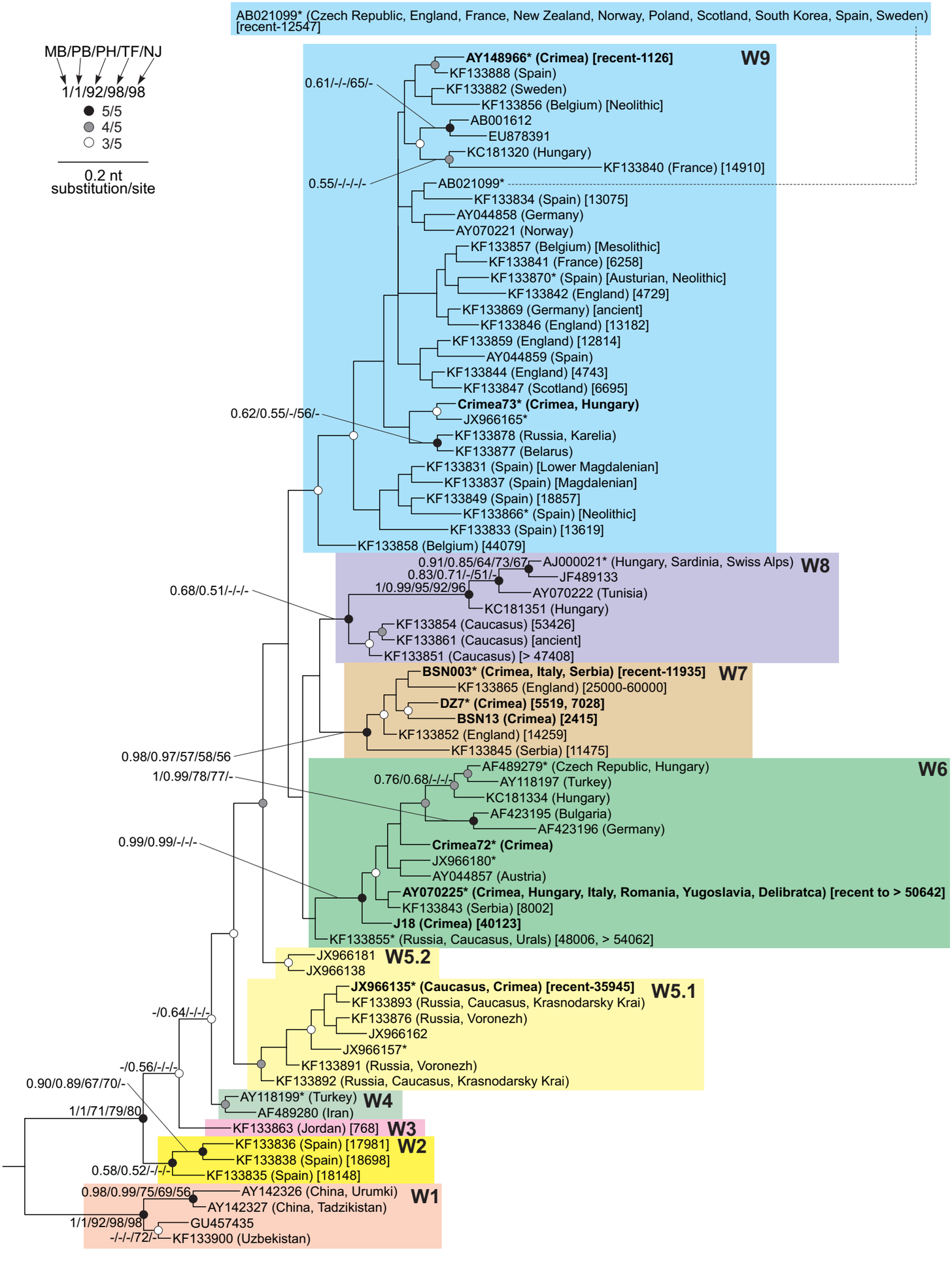Fig. S5. MrBayes tree based on the shorter alignment for the Western lineage of red deer. Sequences newly obtained in this study from Crimea specimens are **bolded**. The asterisk indicates that a given sequence is represented by more than one accession number. The shading of circles at nodes corresponds to the number of methods (out of five) which recovered the given node. A probable age or calibrated dates are shown in square brackets. Numbers at nodes, in the order shown, correspond to: posterior probabilities estimated in MrBayes (MB) and PhyloBayes (PB), bootstrap values obtained in PhyML (PH), TreeFinder (TF) and PAUP by neighbor joining methods (NJ). Values of the posterior probabilities and bootstrap percentages ≤ 0.50 and 50%, respectively, were omitted or indicated by a dash "-".