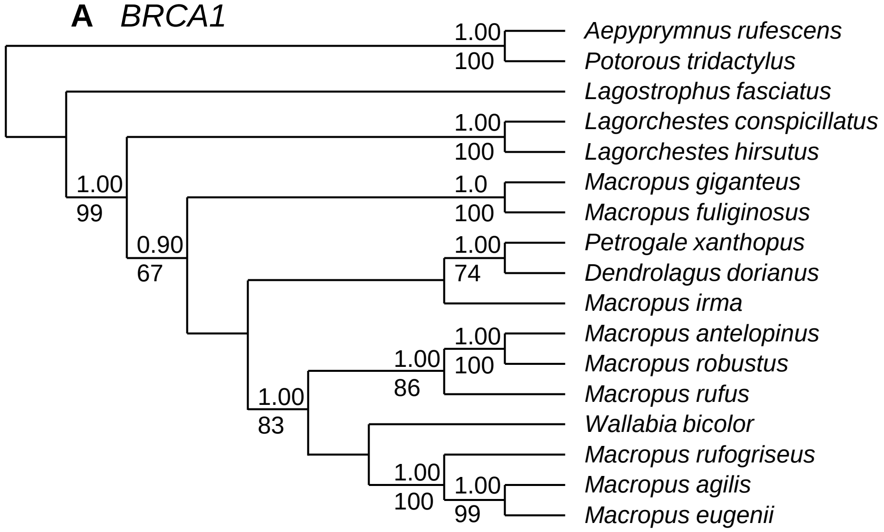
A *BRCA1*



B *IRBP*

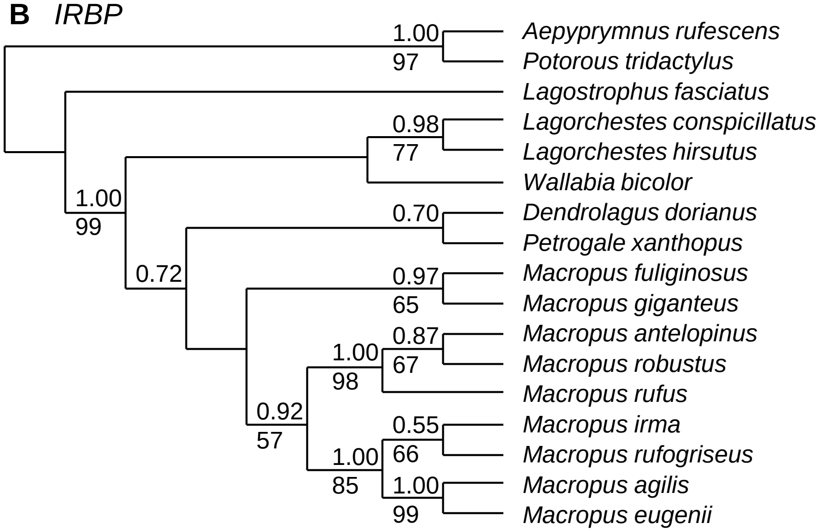
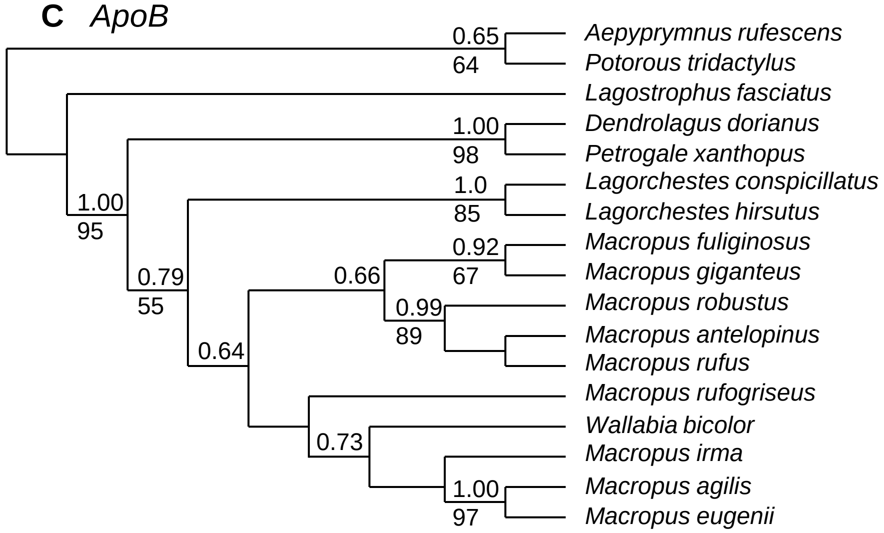


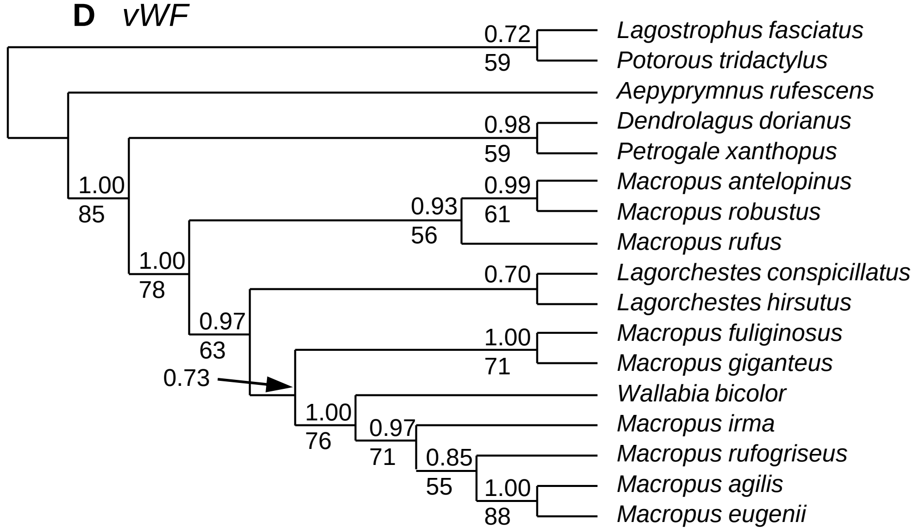
Figure S1. **Individual nuclear gene phylogenies**. (A) *BRCA1*, (B*) IRBP*, (C) *ApoB*, (D) *vWF* and (E) *RAG1*. MrBayes 3.2 Bayesian posterior probabilities (above 0.5) and PAUP* 4.0b10 maximum likelihood bootstrap percentages (>50) are shown above and below branches respectively. Analyses were carried out as per the primary analysis for Nuc_{17}, with substitution models shown in Table 2.

Figure S1 - continued

C *ApoB*



D *vWF*



E *RAG1*