

# Molecular Phylogenetic Analysis of The AIG Family in Vertebrates

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## Supplementary Figures

**Figures S1–S3.** Phylogenetic analysis of the AIG protein (S1) and CDS (S2 and S3) sequences in representative species using ML (S1 and S2) and Bayesian methods (S3). The bootstrap values (S1 and S2) and Bayesian posterior probabilities (S3) are shown for each node. All phylogenetic trees, except for the position of *Peteromyzon marinus* AIG-Ls in S3, show a similar topology with three major clades present in vertebrates. ADTRP, AIG1 and AIG-L are highlighted in blue, black, and red, respectively. Invertebrate AIG-L, which is in red, was used to generate an outgroup.

Figure S1

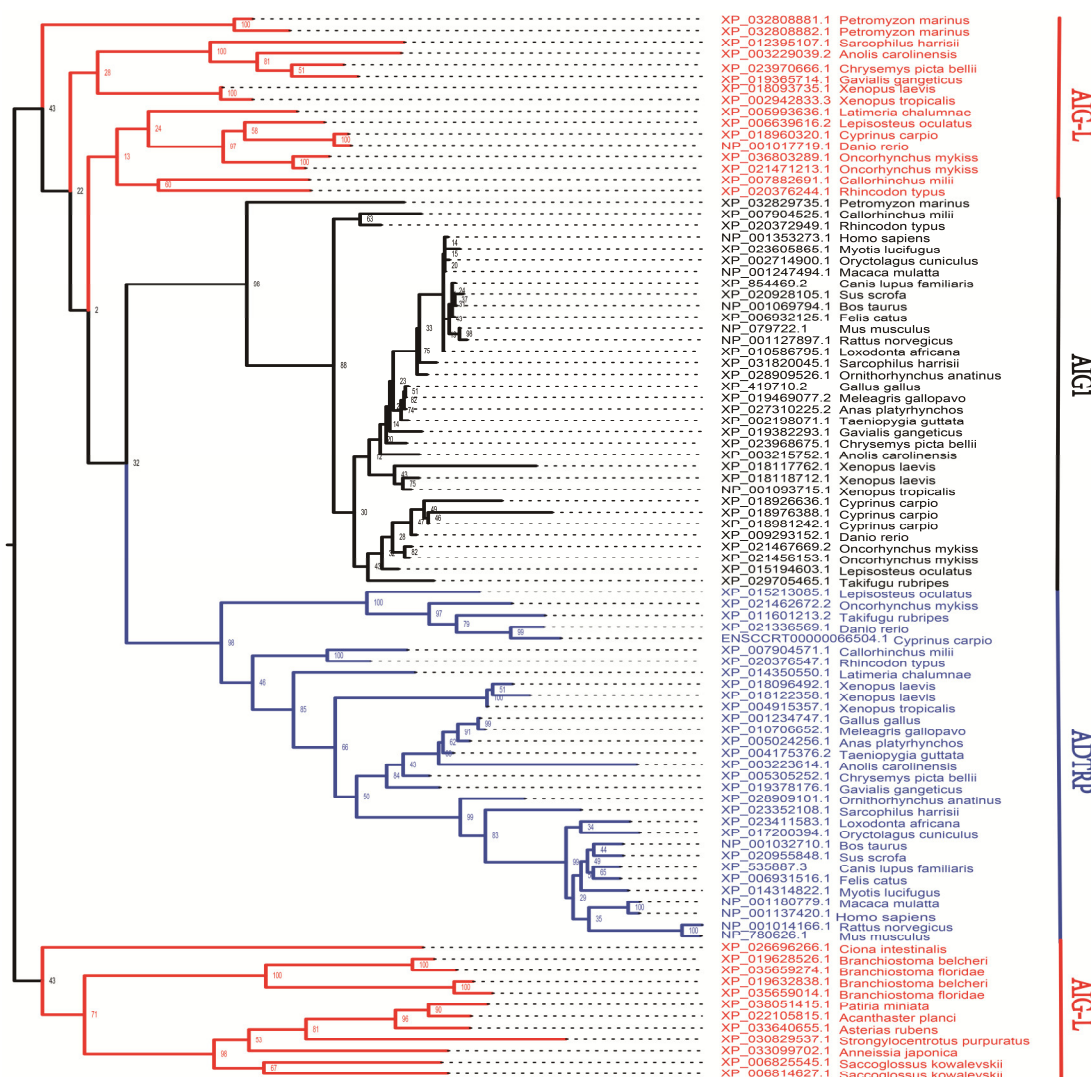


Figure S2

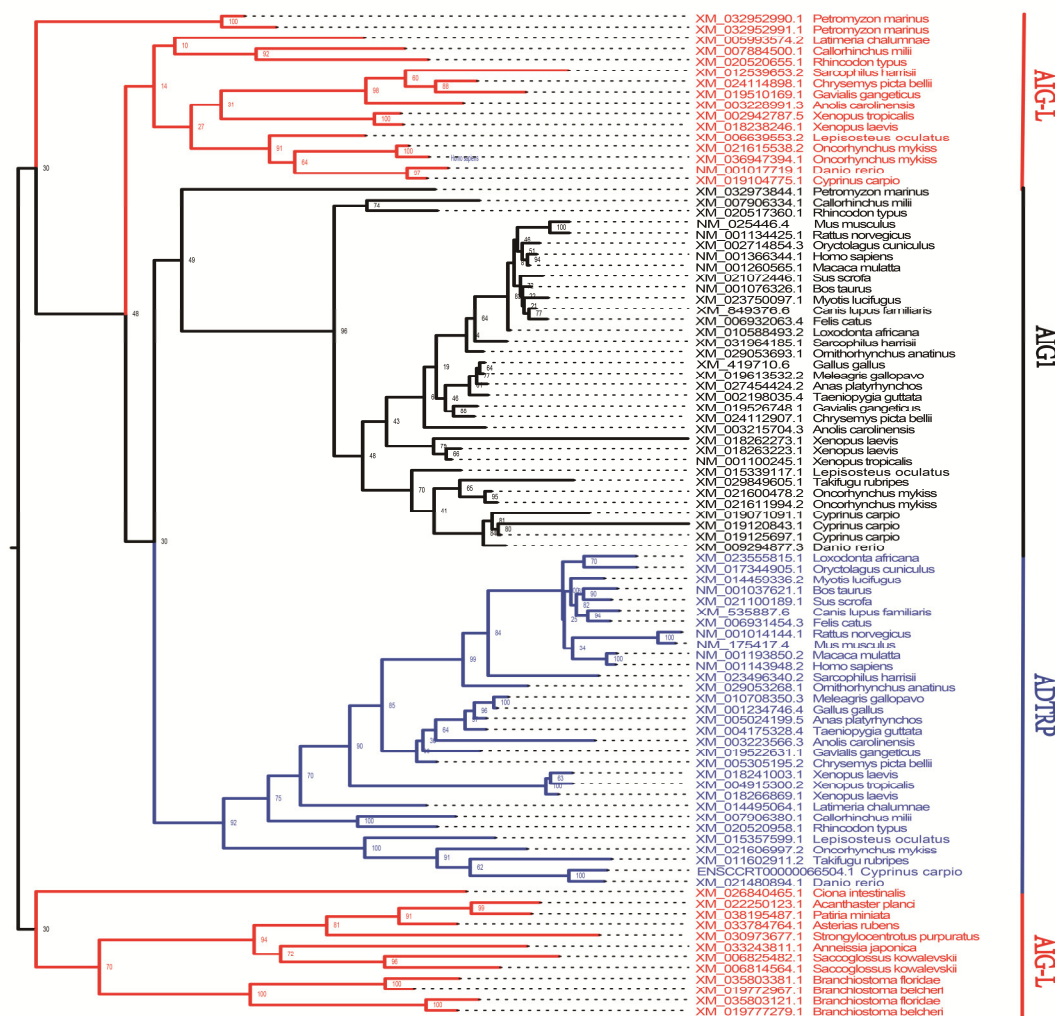
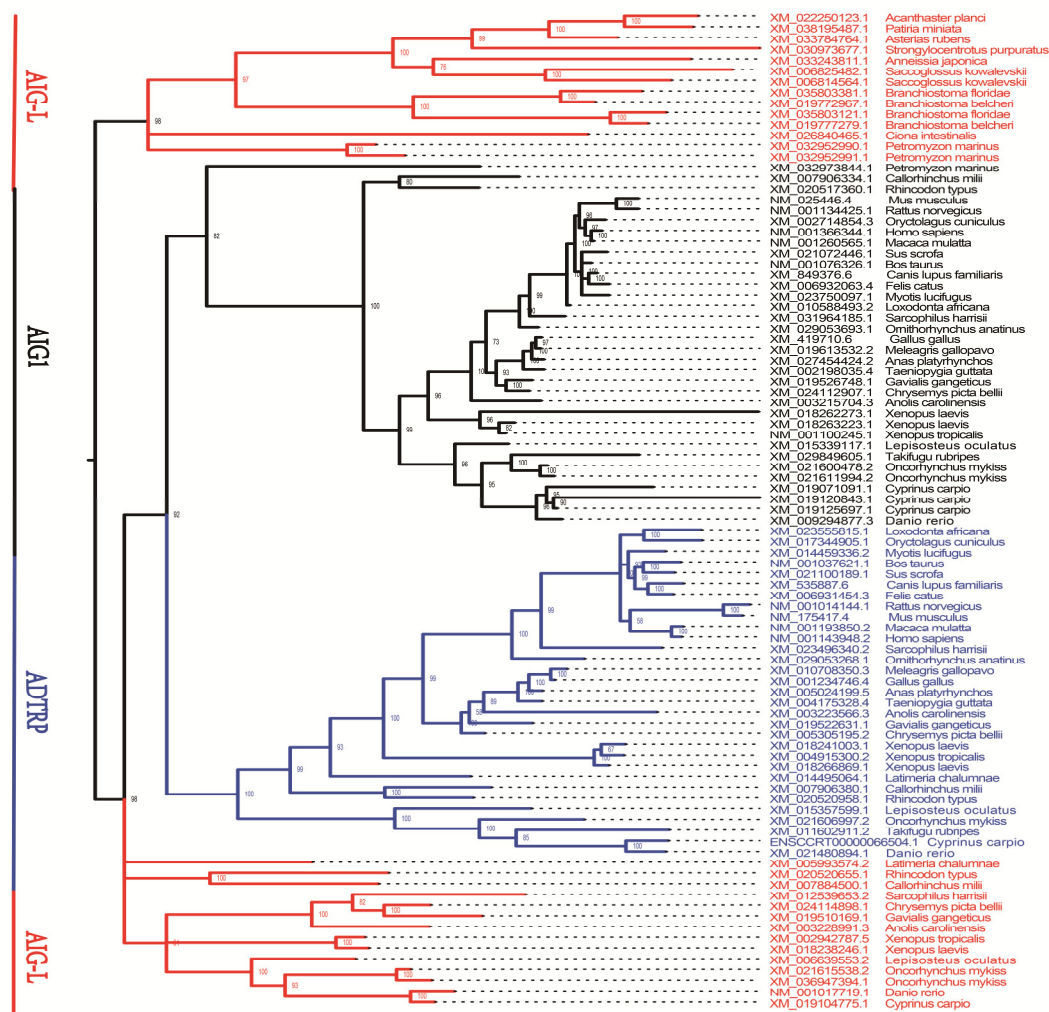
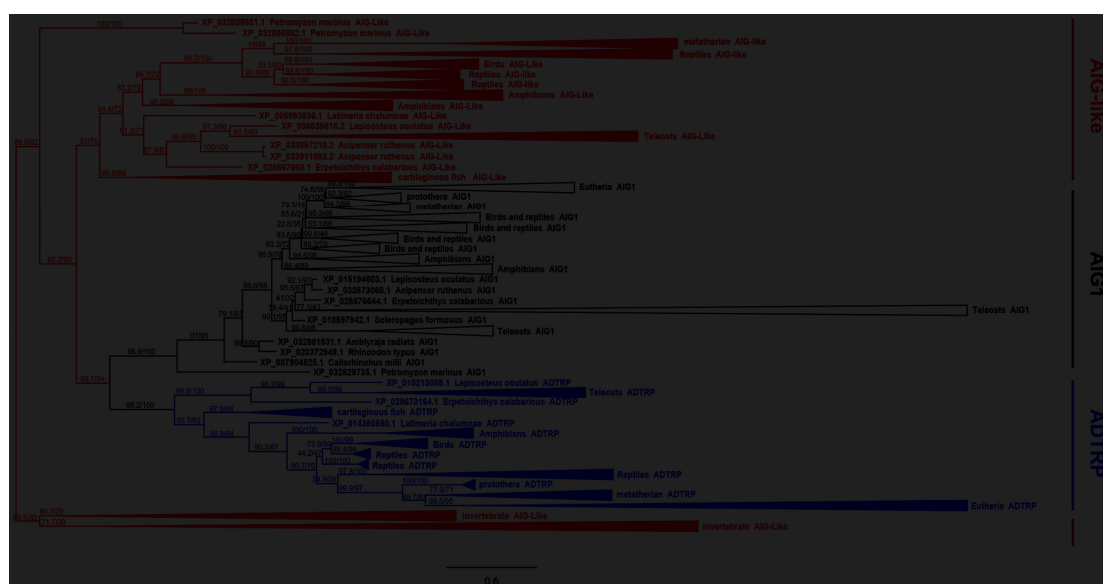
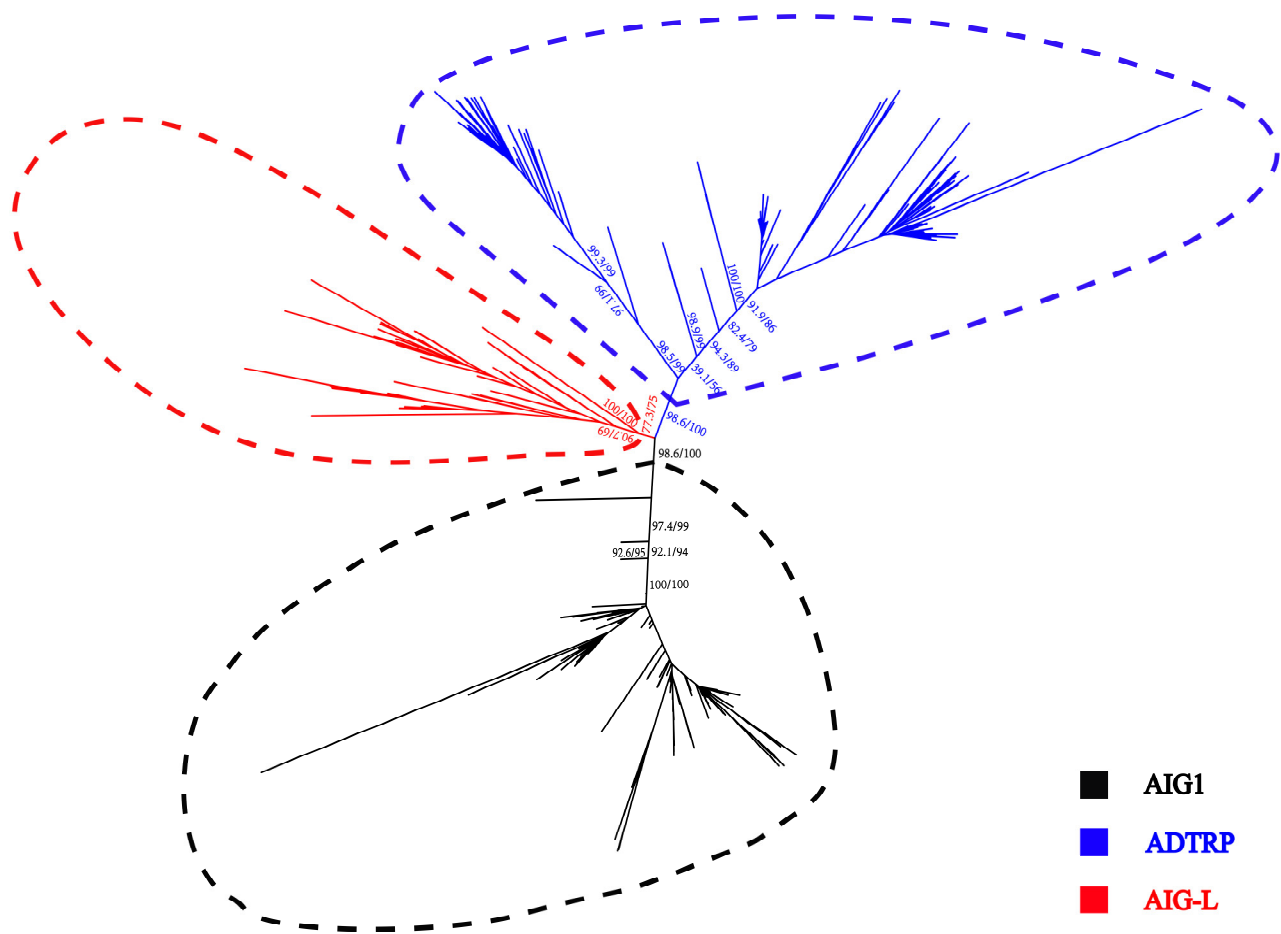


Figure S3





**Figure S4.** Phylogenetic representation of AIG protein sequences in all available species using the ML approach. The rooted tree shows the classification of the AIGs, which was supported by high aLRT (numerators) and bootstrap values (denominators). The values for ADTRP, AIG1, and AIG-L are 98.2/100, 98.9/100, and 89.1/94, respectively. Closely related species were grouped together in collapsed triangles. The invertebrate AIGs were used as outgroup.



**Figure S5.** Phylogenetic representation of AIG protein sequences in all available vertebrates using the ML approach. The radial tree generated was supported by high aLRT (numerators) and bootstrap values (denominators). The values for ADTRP, AIG1, and AIG-L are 98.6/100, 98.6/100, and 77.3/75, respectively.



**Figure S6–S9.** Phylogenetic trees generated by ML approach for mammals (S6), birds (S7), reptiles (S8), and amphibians (S9). ADTRP, AIG1, and AIG-L are labeled by blue, black, and red, respectively. The AIG-L from *Ciona intestinalis* was used as the outgroup.

**Figure S6**

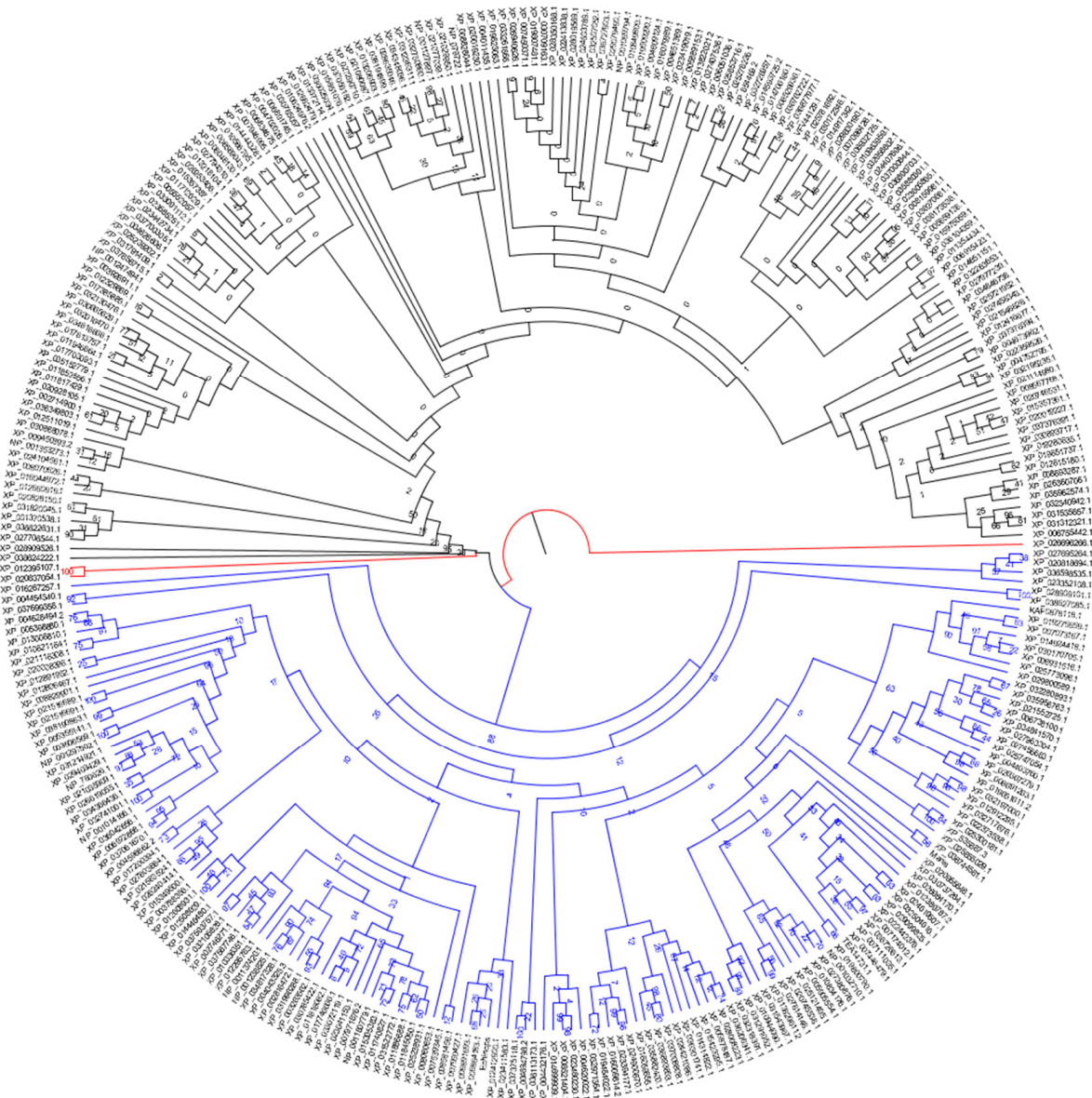
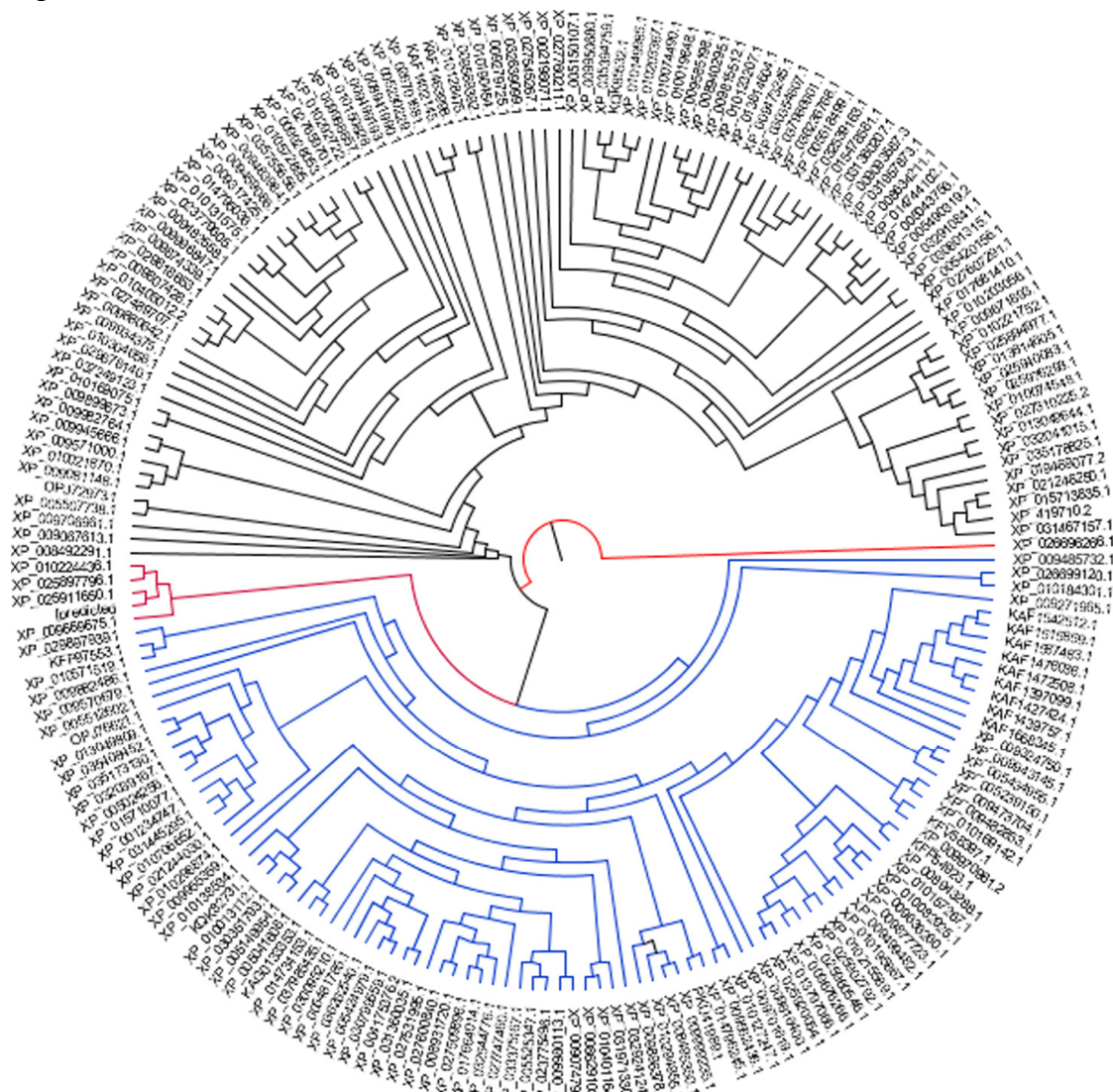


Figure S7



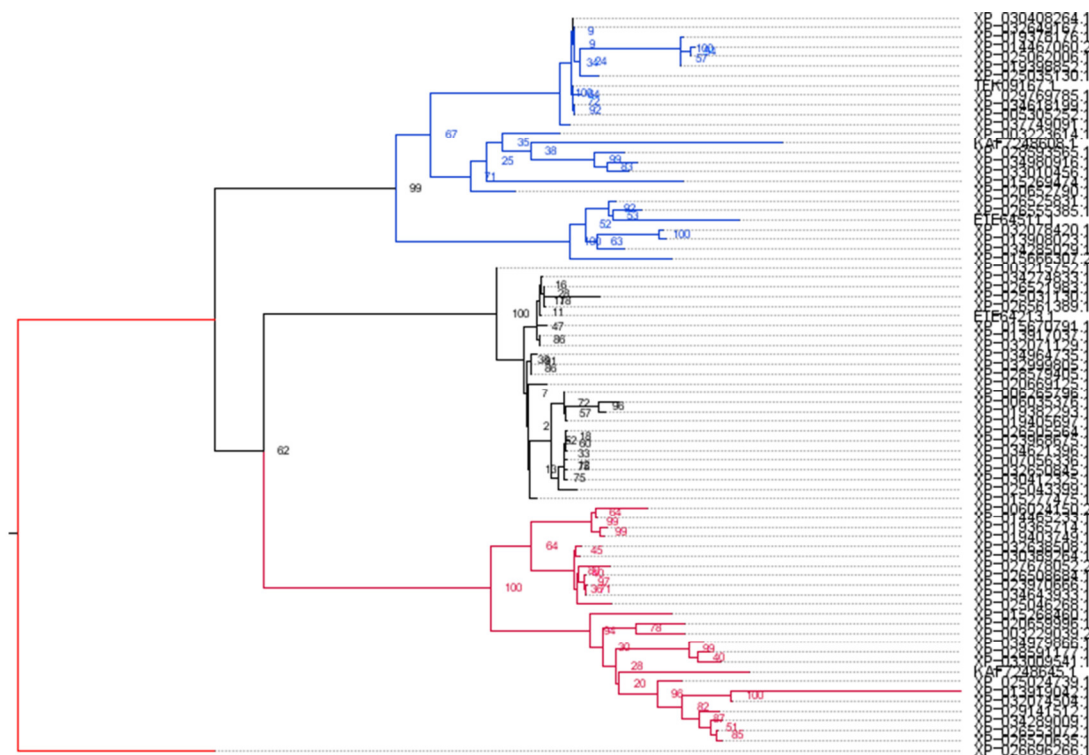
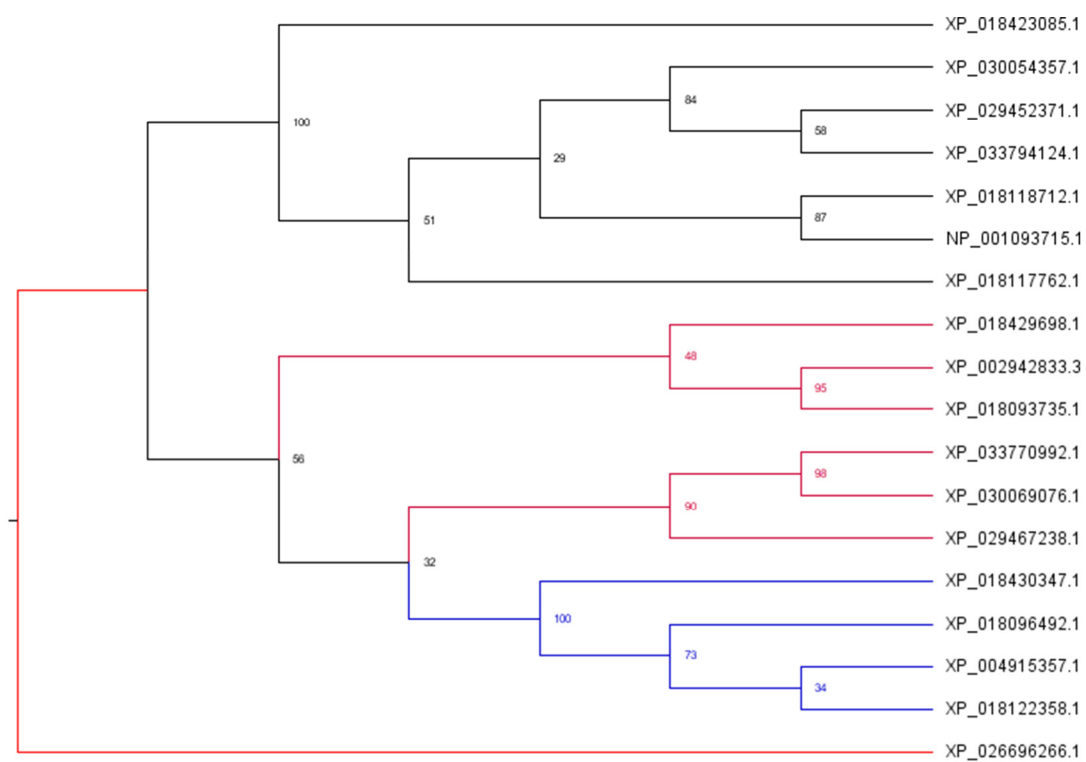




Figure S9



**Figure S10.** Graphical representation of the conserved amino acid sites across all available AIG protein sequences.