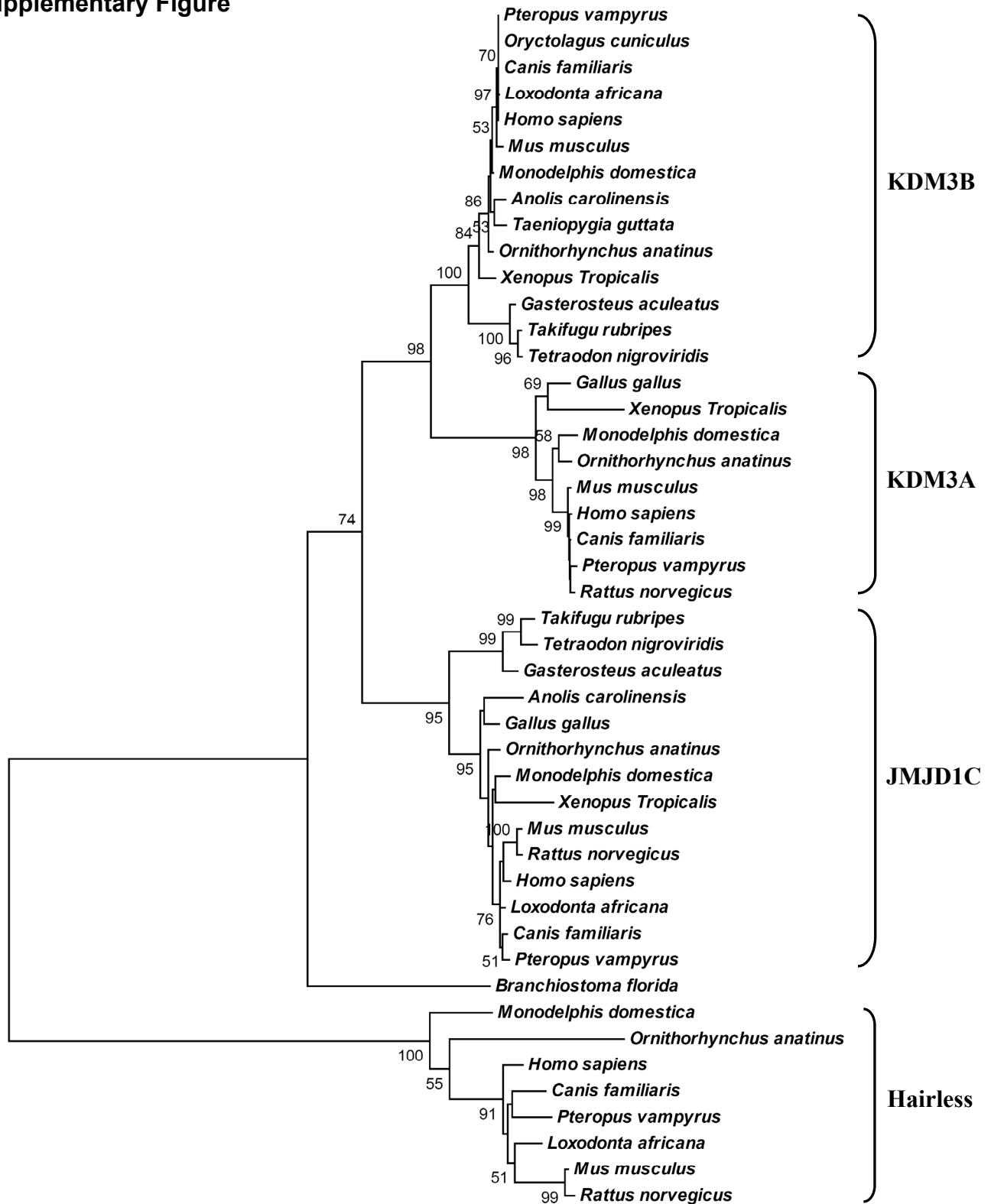# Molecular evolution of *HR*, a gene that regulates the postnatal cycle of the hair follicle

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Supplementary Figure

Supplementary Figure. Molecular Phylogenetic analysis by Maximum Likelihood method

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-11085.6583) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values ≥ 50% are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.6609). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 46 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 391 positions in the final dataset.