

Additional File 5 – Bayesian phylogenetic analysis of the 50 largest subfamilies.

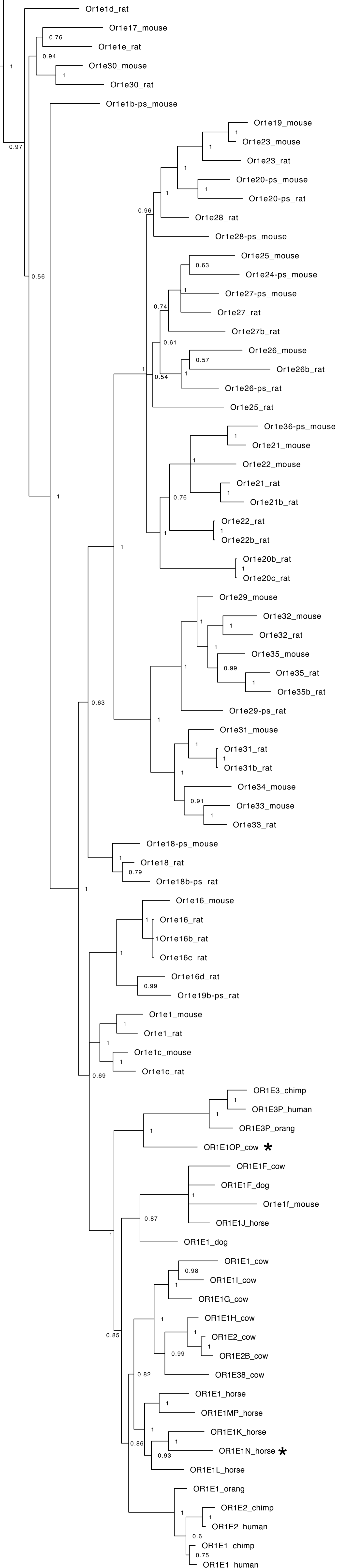
Bayesian phylogenies were generated for the 50 largest OR subfamilies. For each subfamily, Bayesian phylogenetic analysis was performed on the conceptual translation of all members of the subfamily from the mammalian OR repertoires classified in this study (OR pseudogenes with more than two frame disruptions were excluded). Human OR51E1 was used as the outgroup for Class II OR subfamilies, and human OR1E2 was used as the outgroup for Class I OR subfamilies. Alignments were trimmed as described in the methods. Trees were inferred using MrBayes v3.2 {Ronquist, 2012 #65}, with amino acid model prior set to mixed, number of generations = 1,000,000, and burn-in set to 25%. Bayesian trees are displayed with posterior probabilities on the branch nodes. ORs that were renamed manually are annotated with an asterisk (*). Scale bar represents the number of amino acid changes per site.

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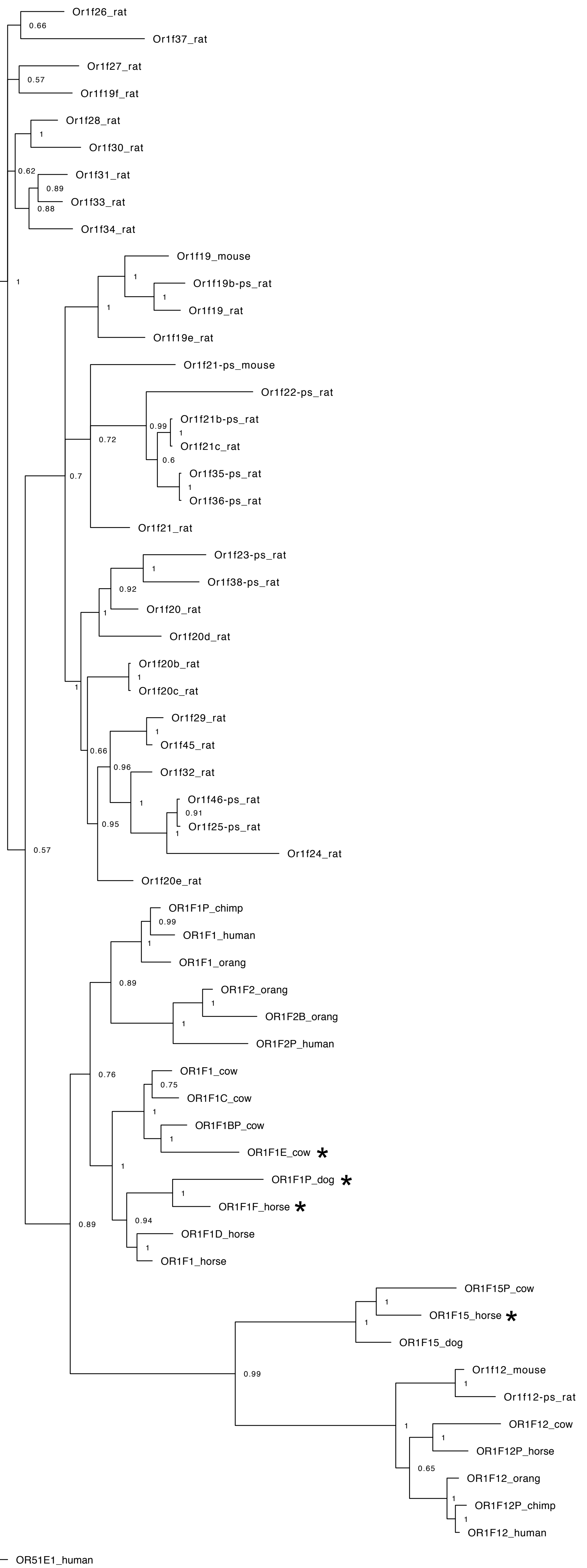
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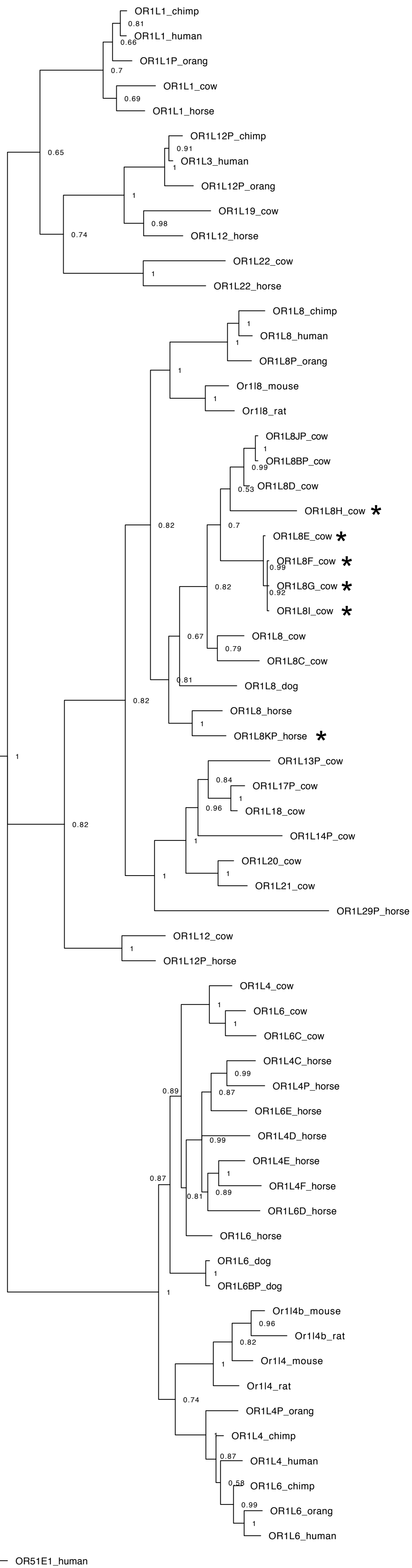
Or1e1d-ps_mouse

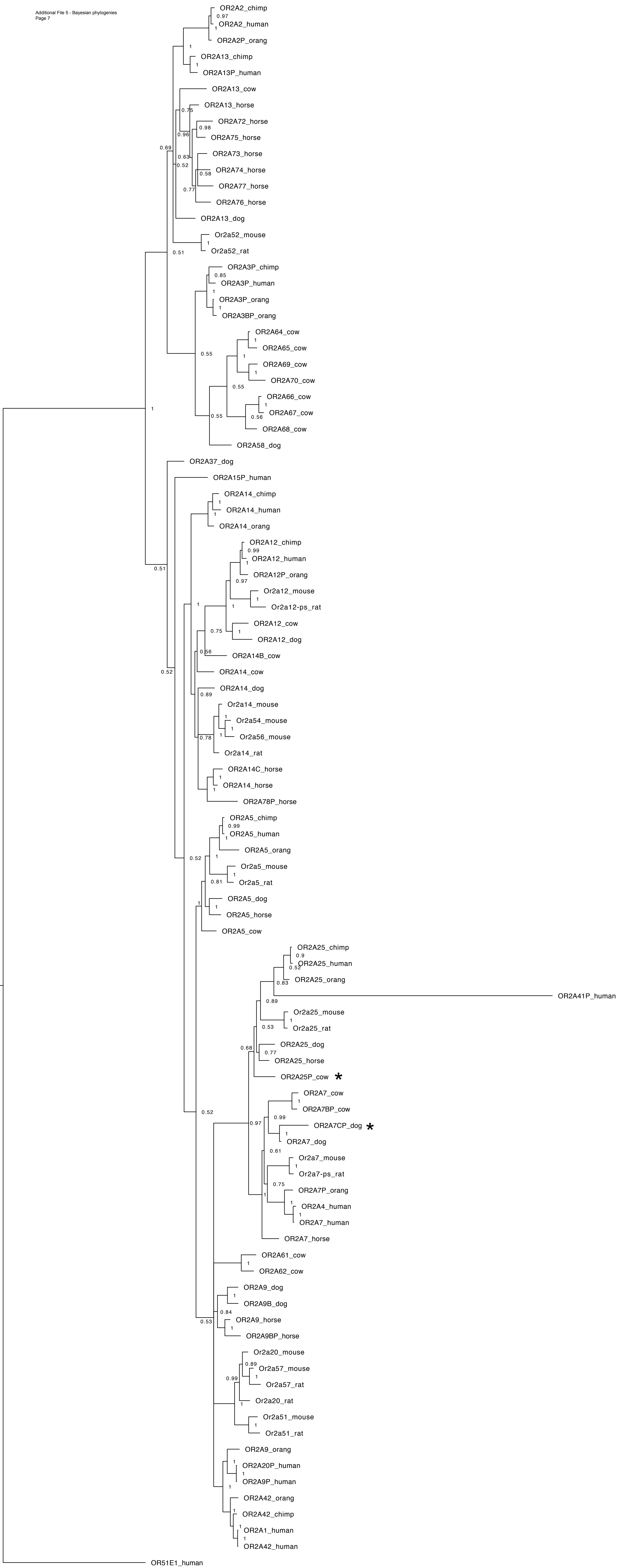


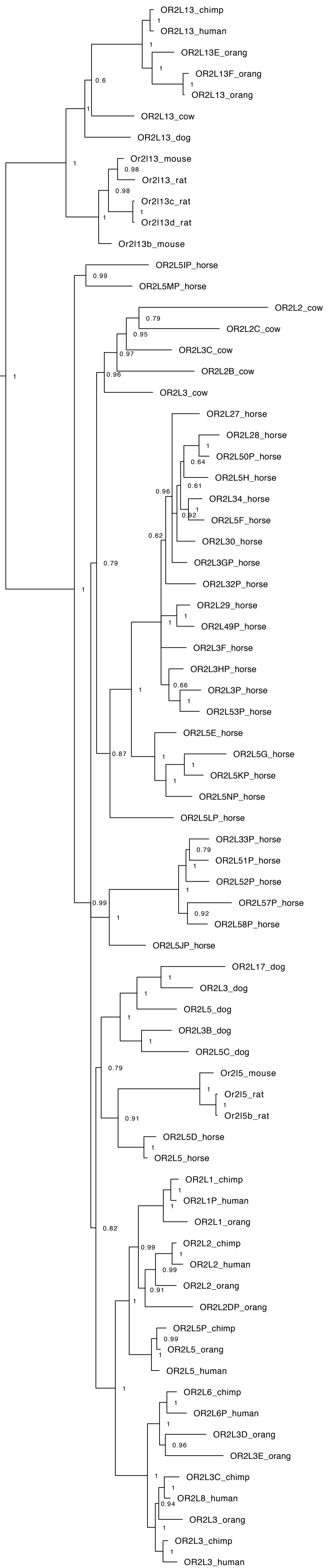
OR51E1_human

0.2

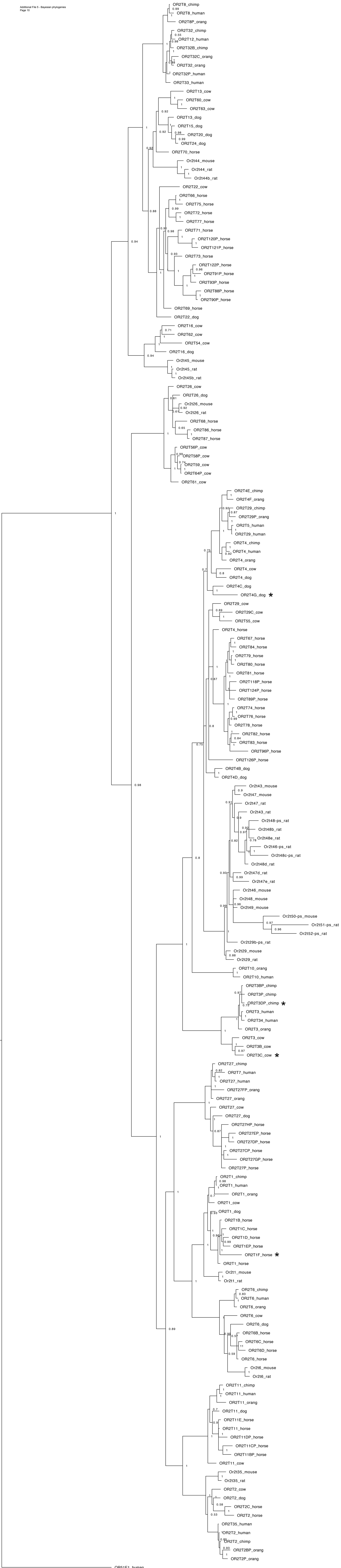


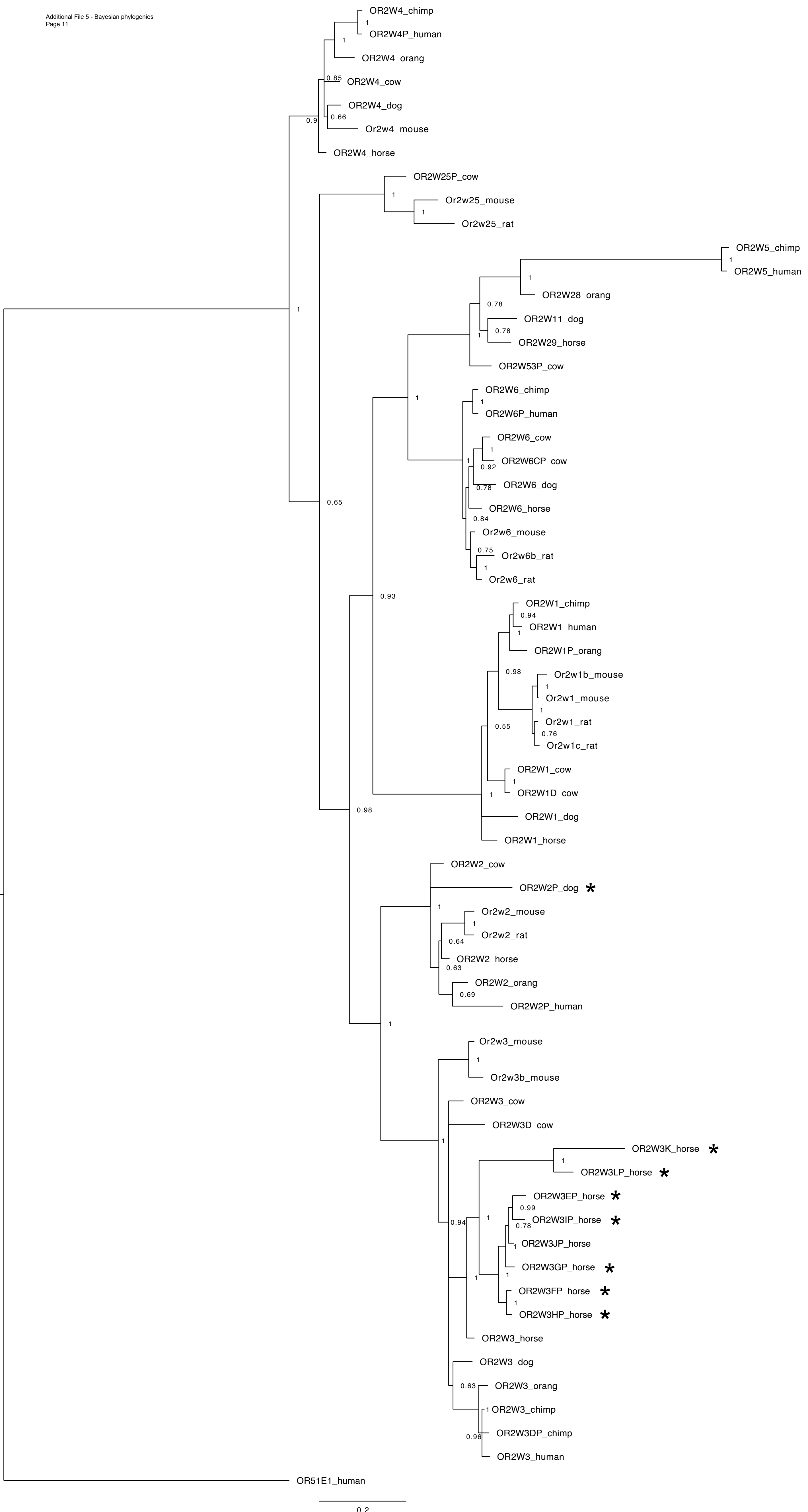


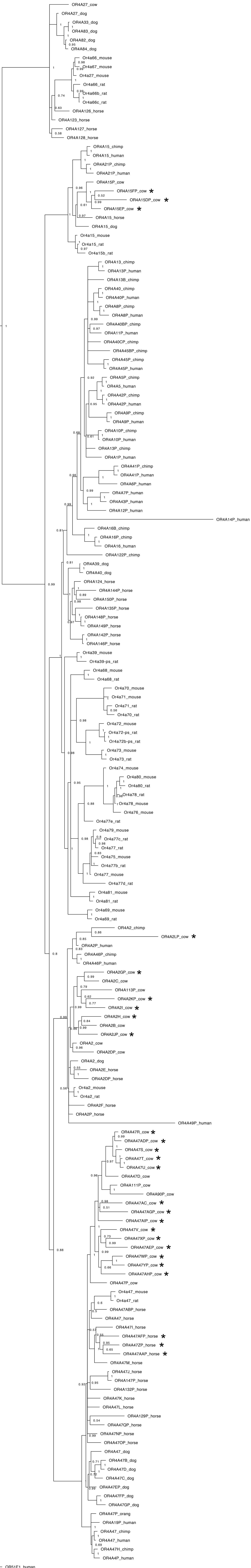




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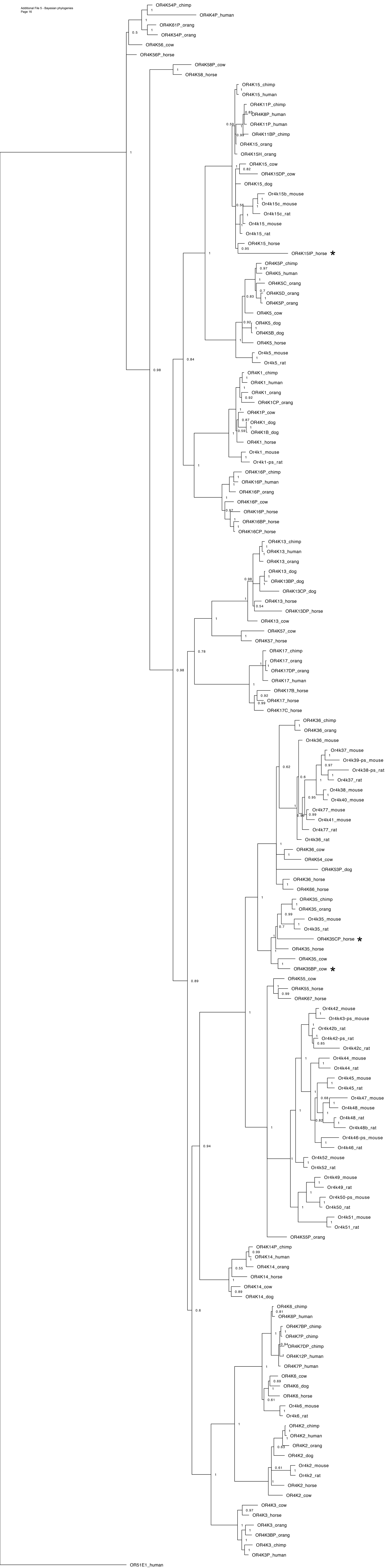


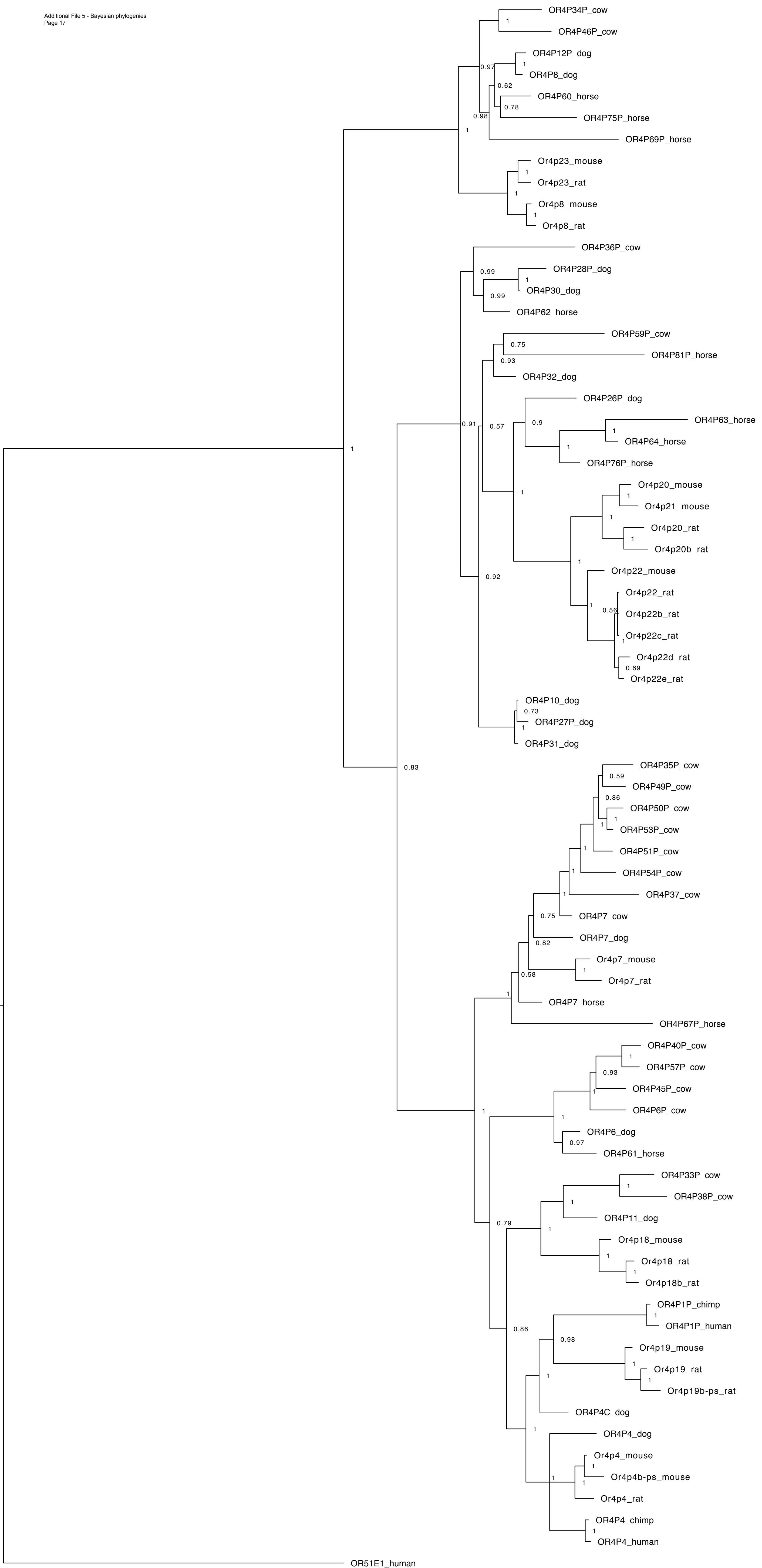


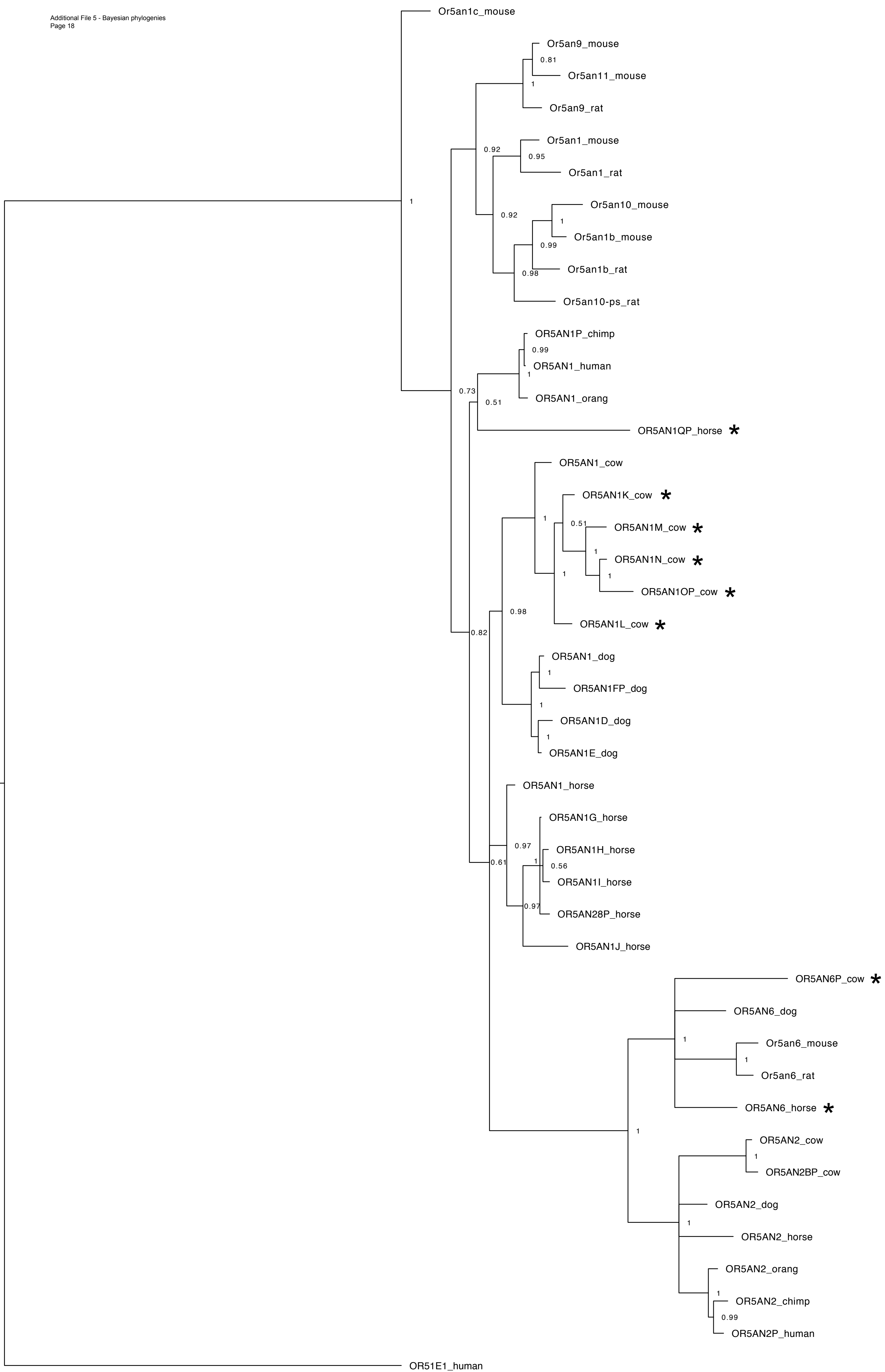


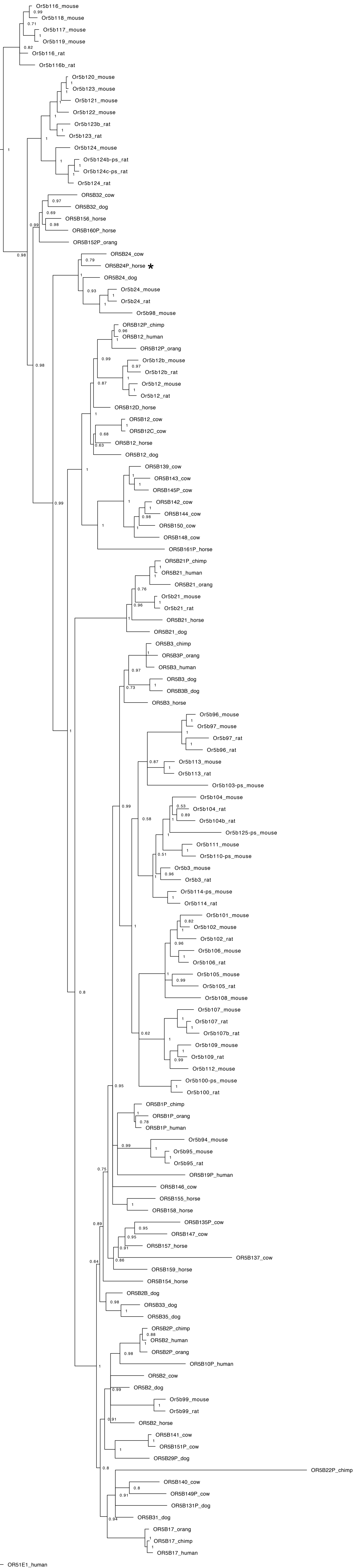
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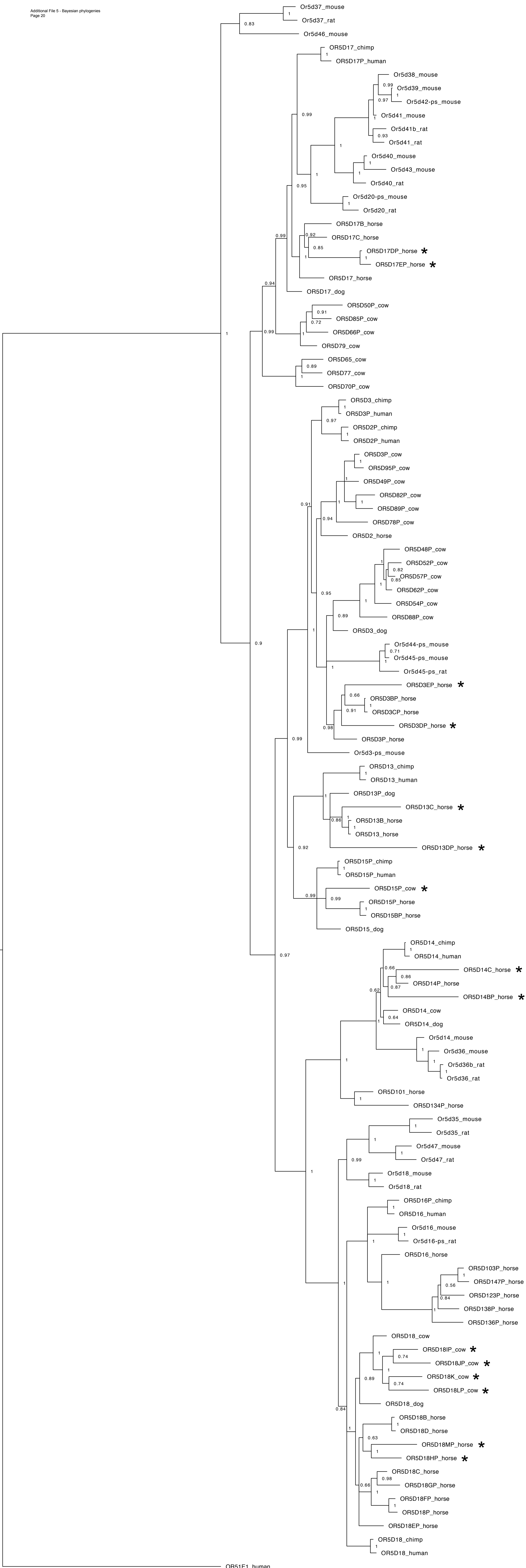


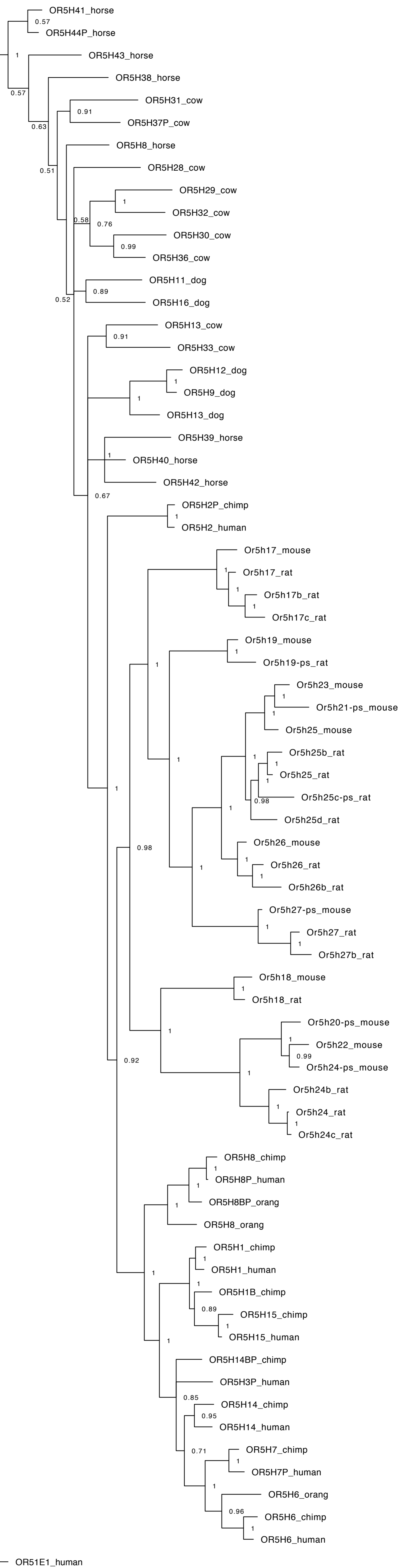






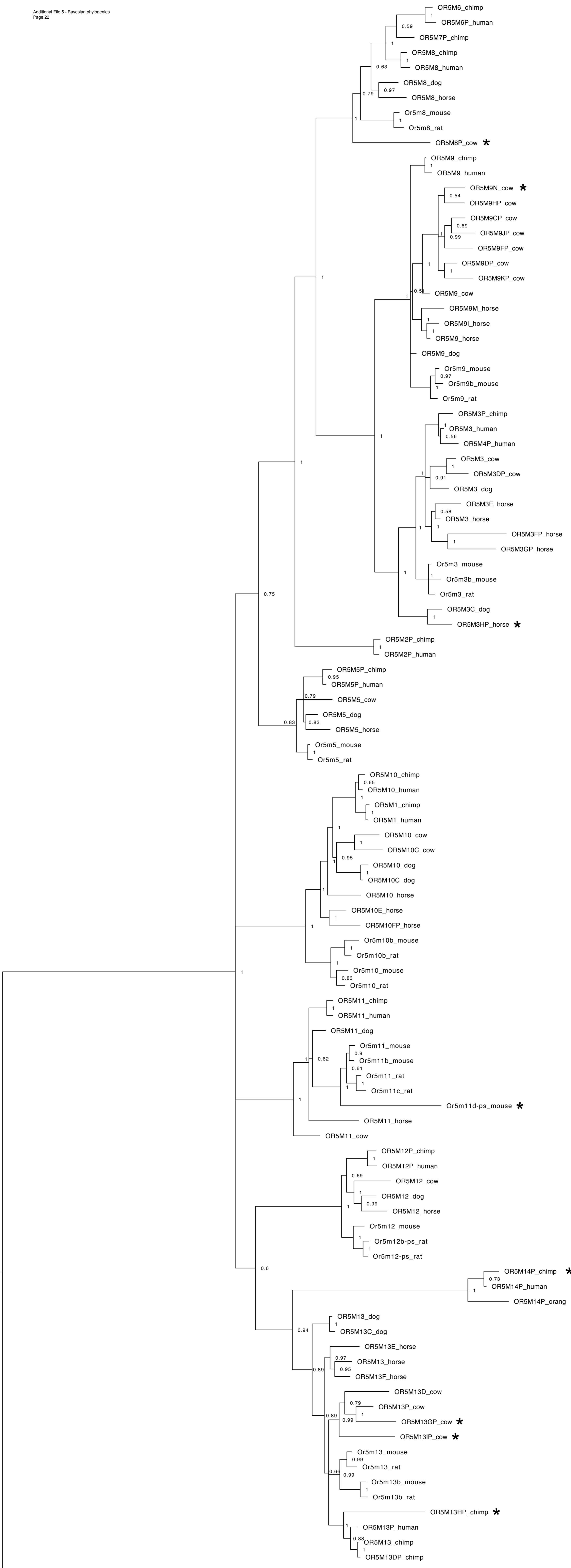


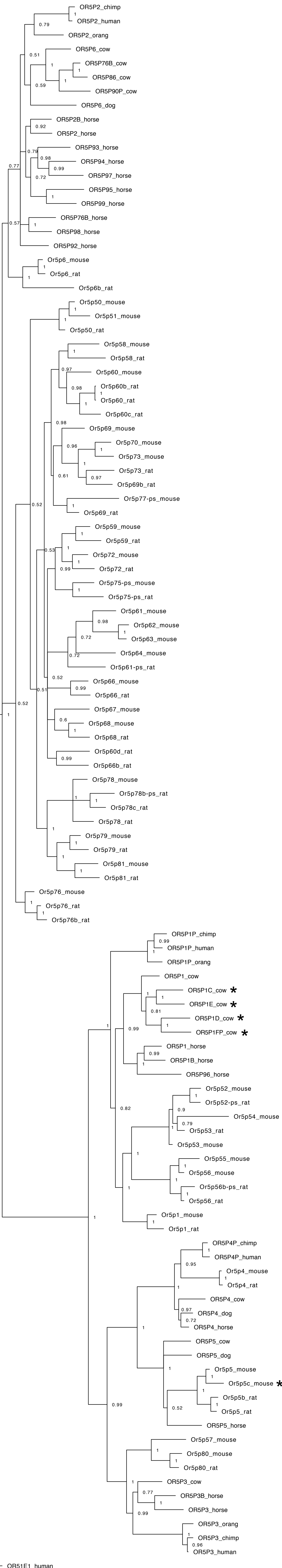


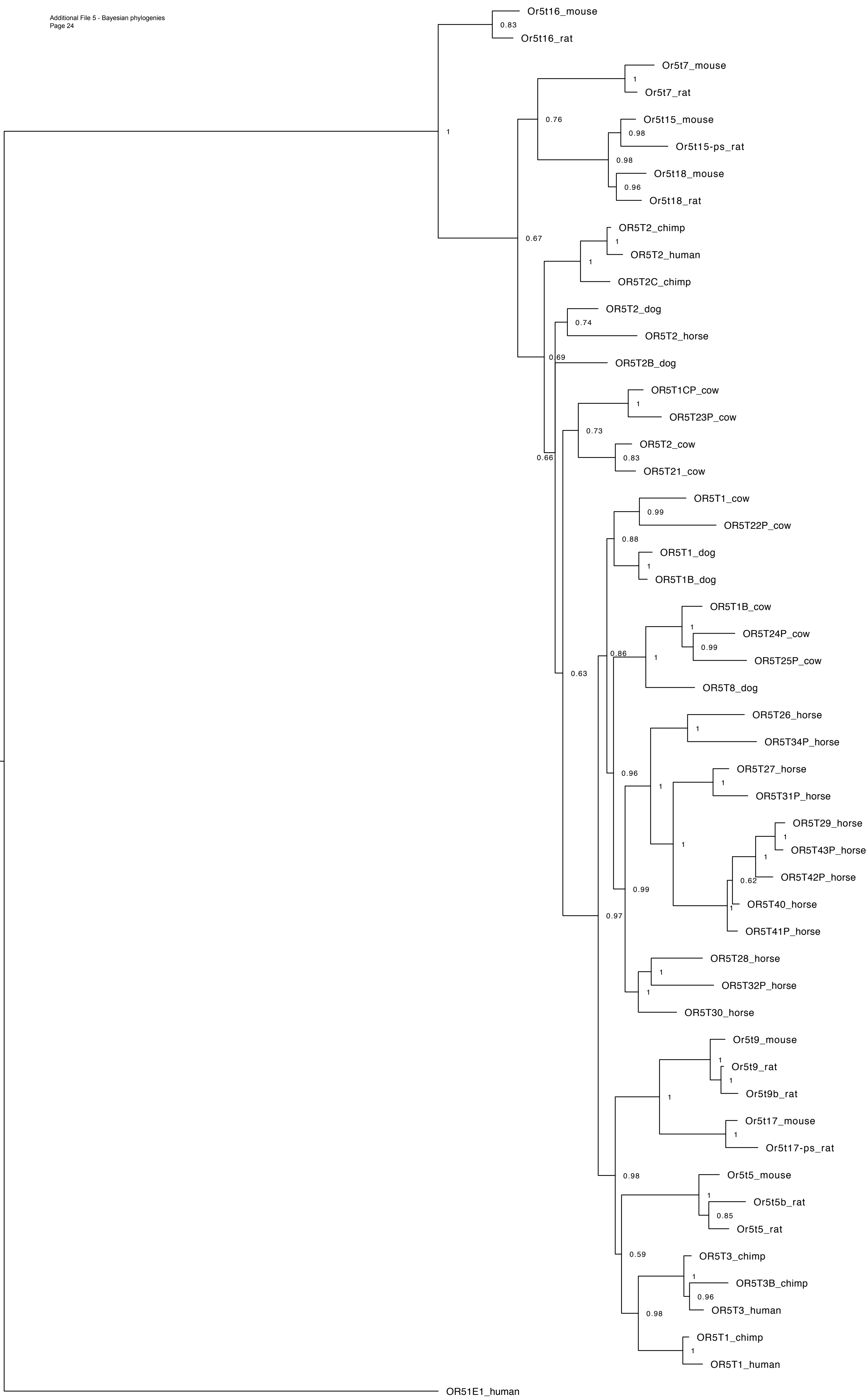


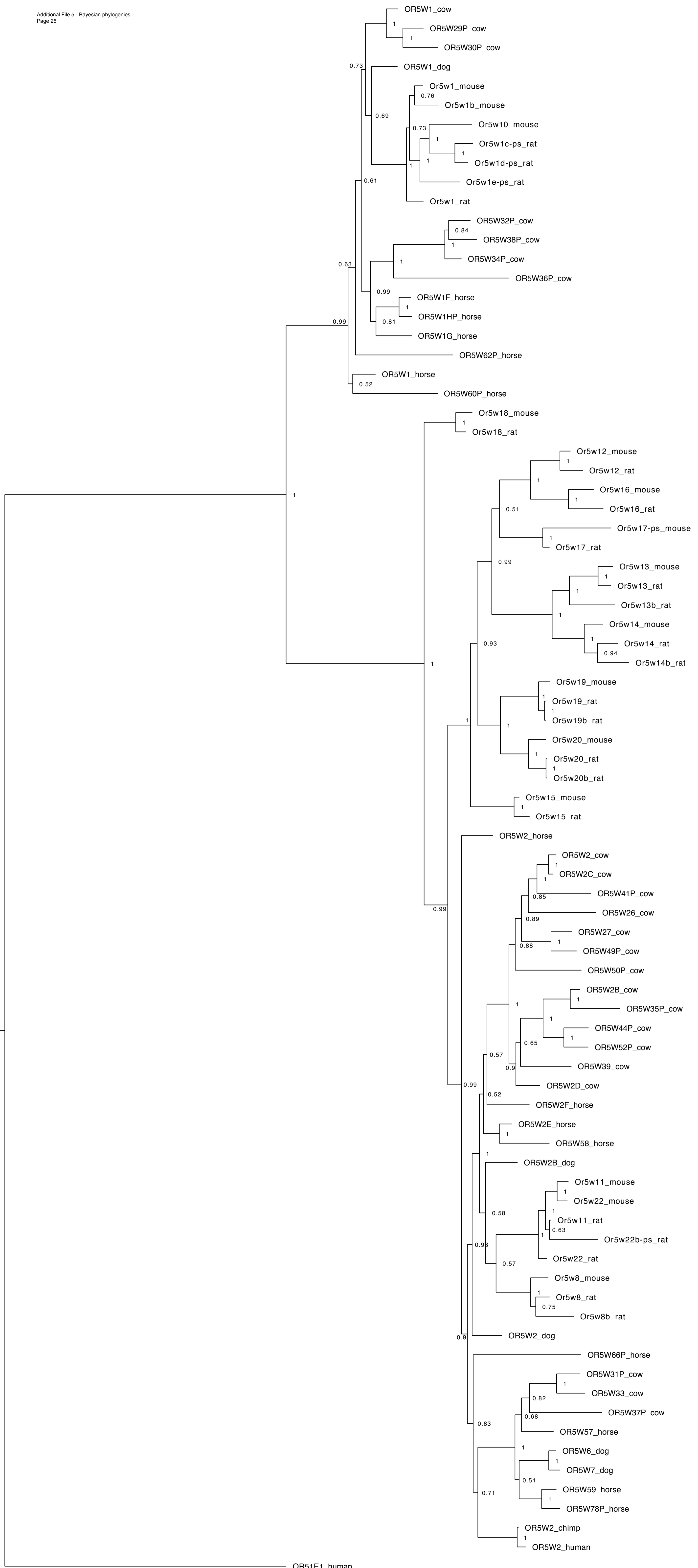
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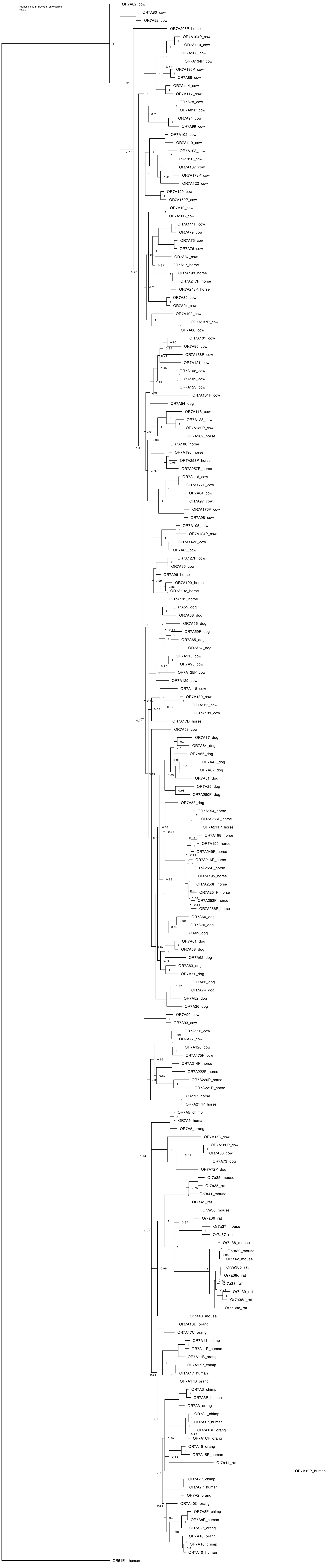
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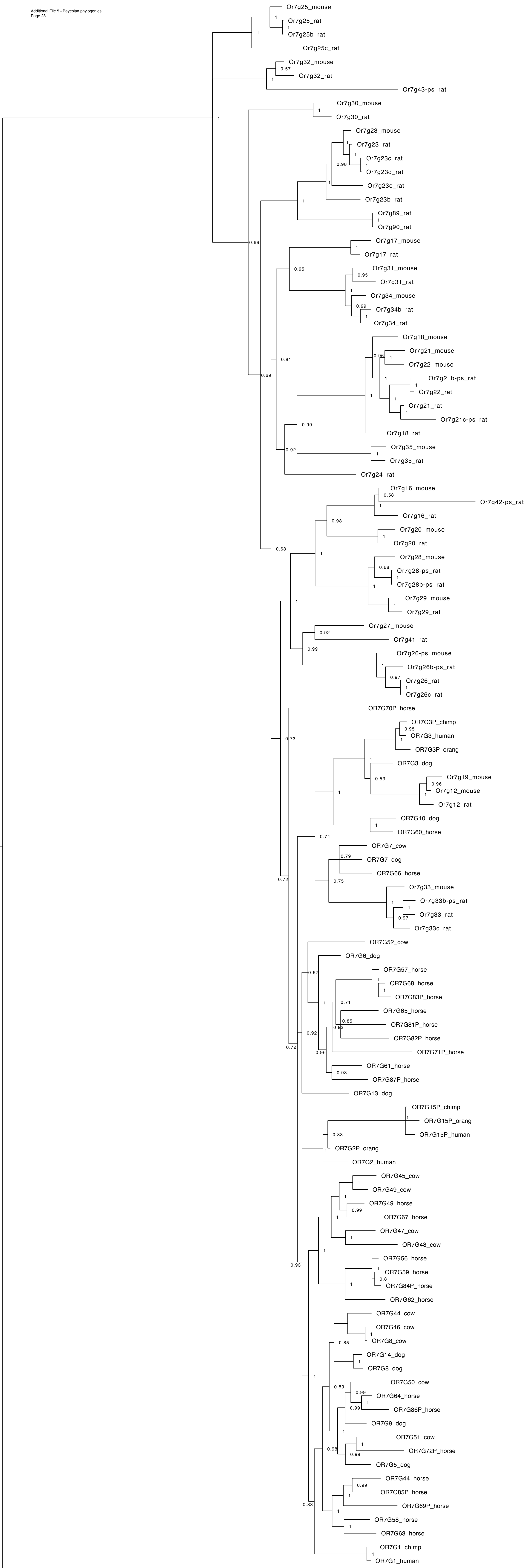






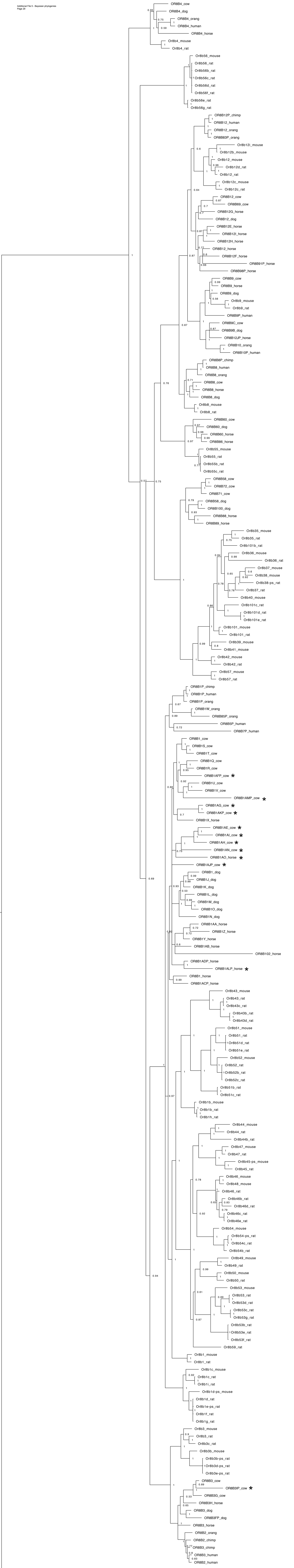






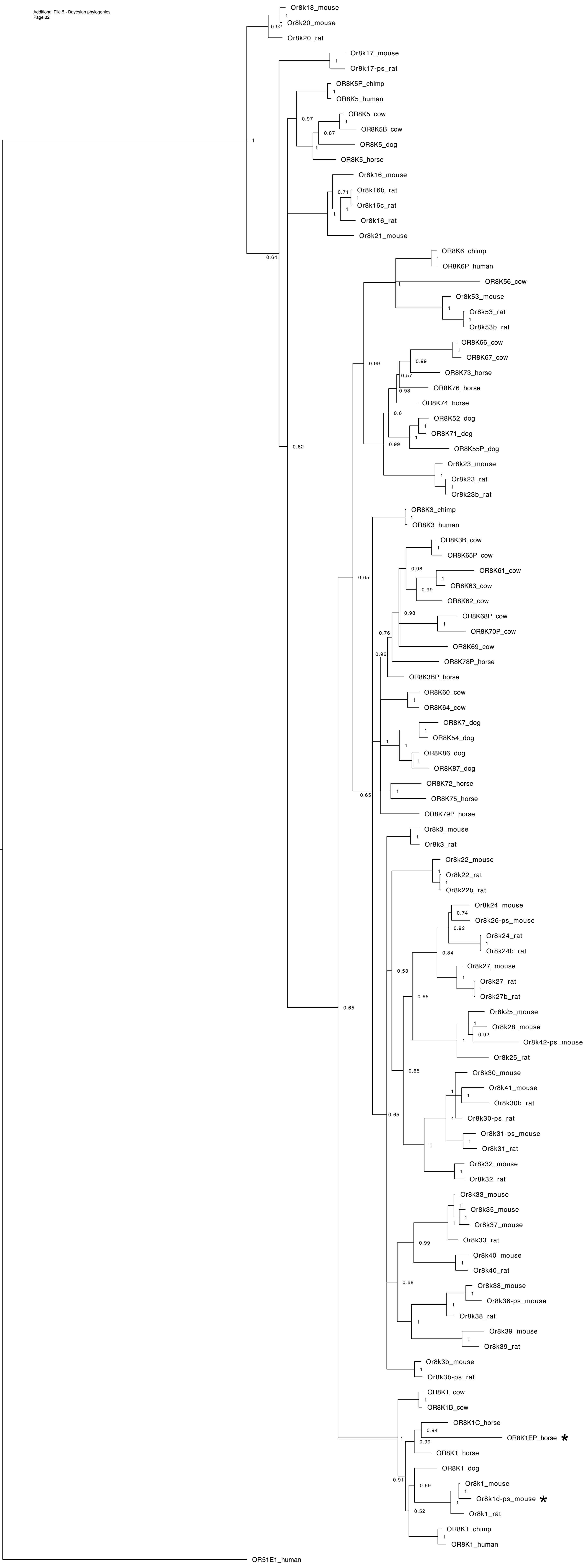
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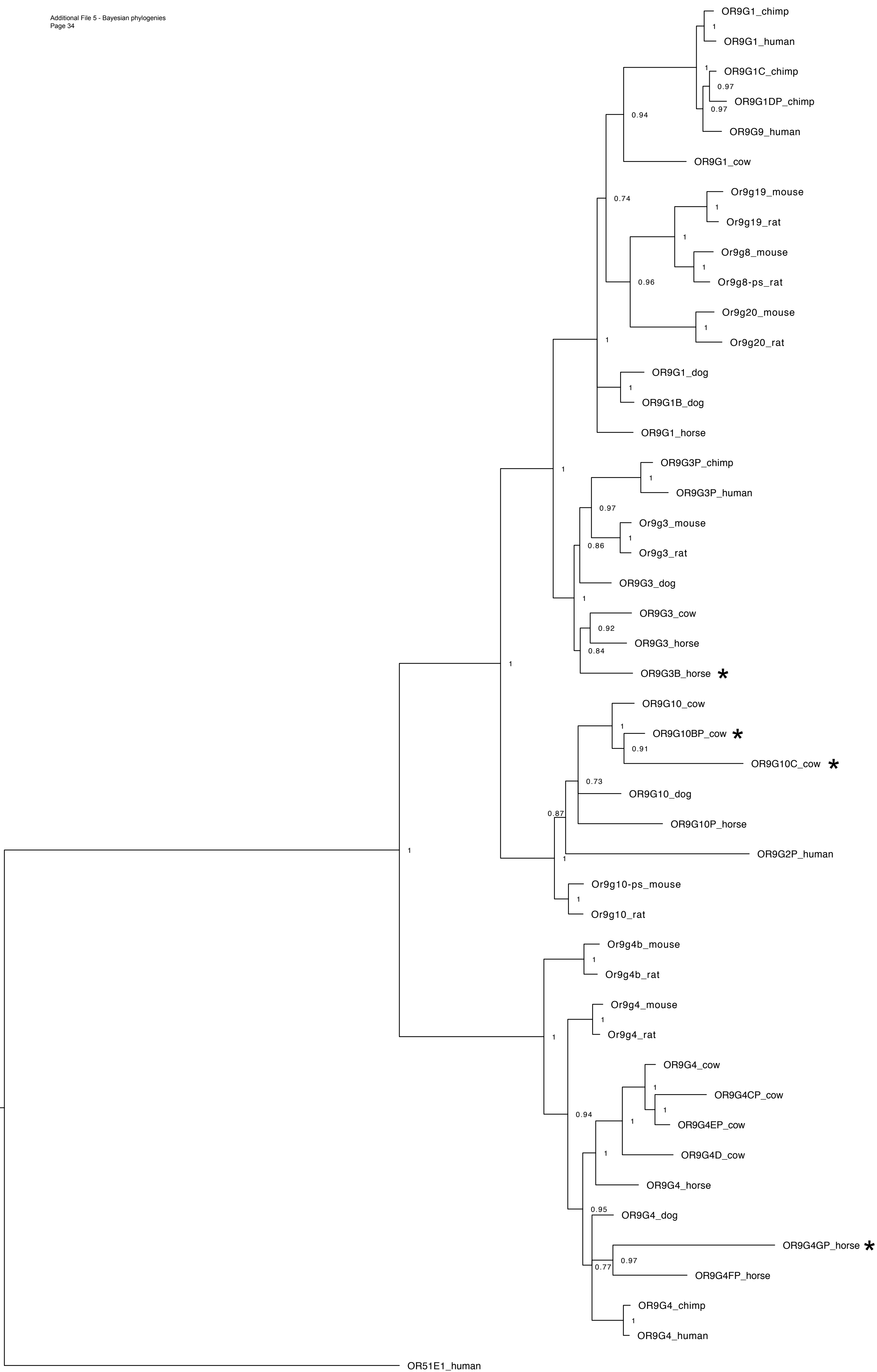


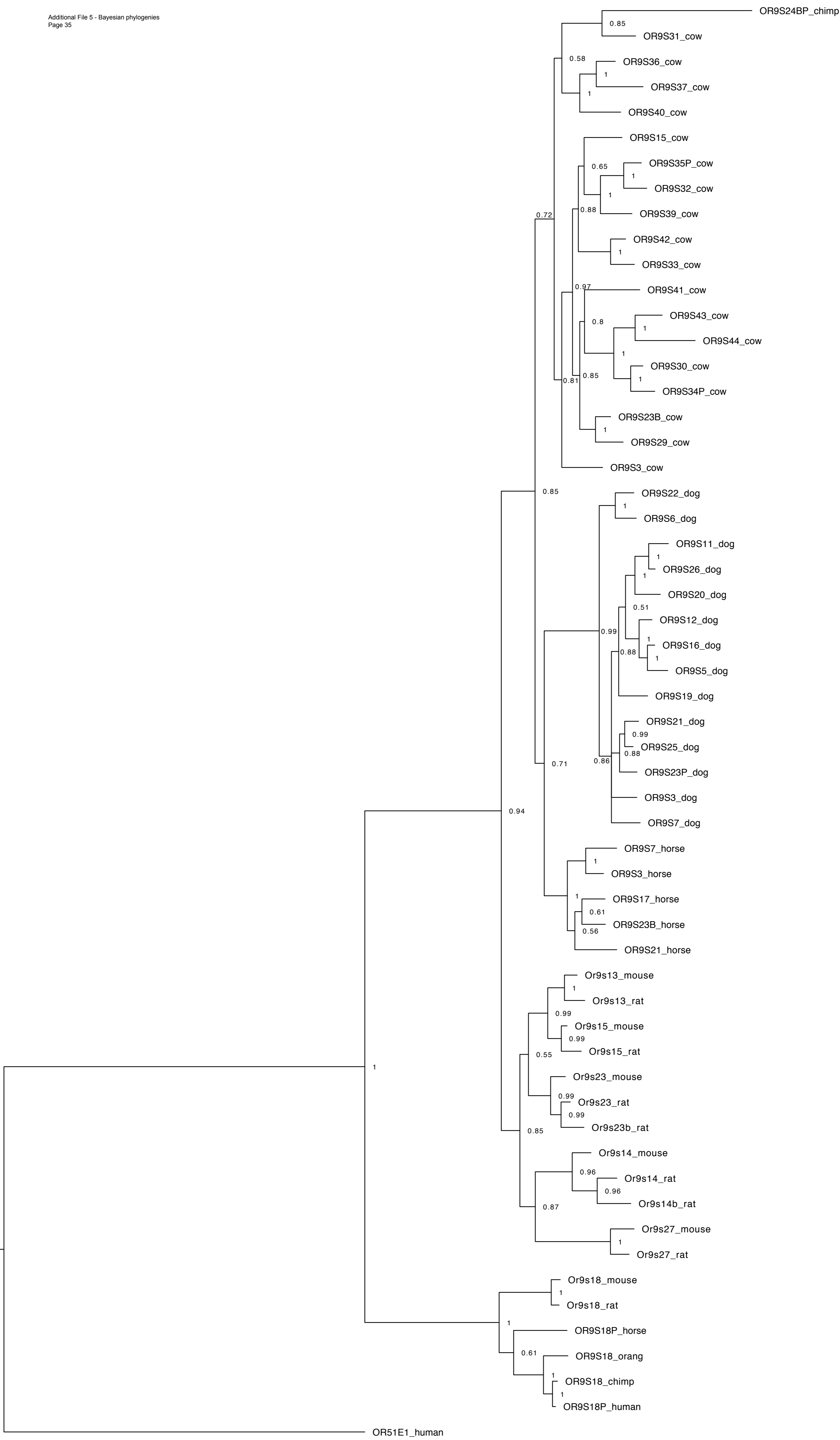
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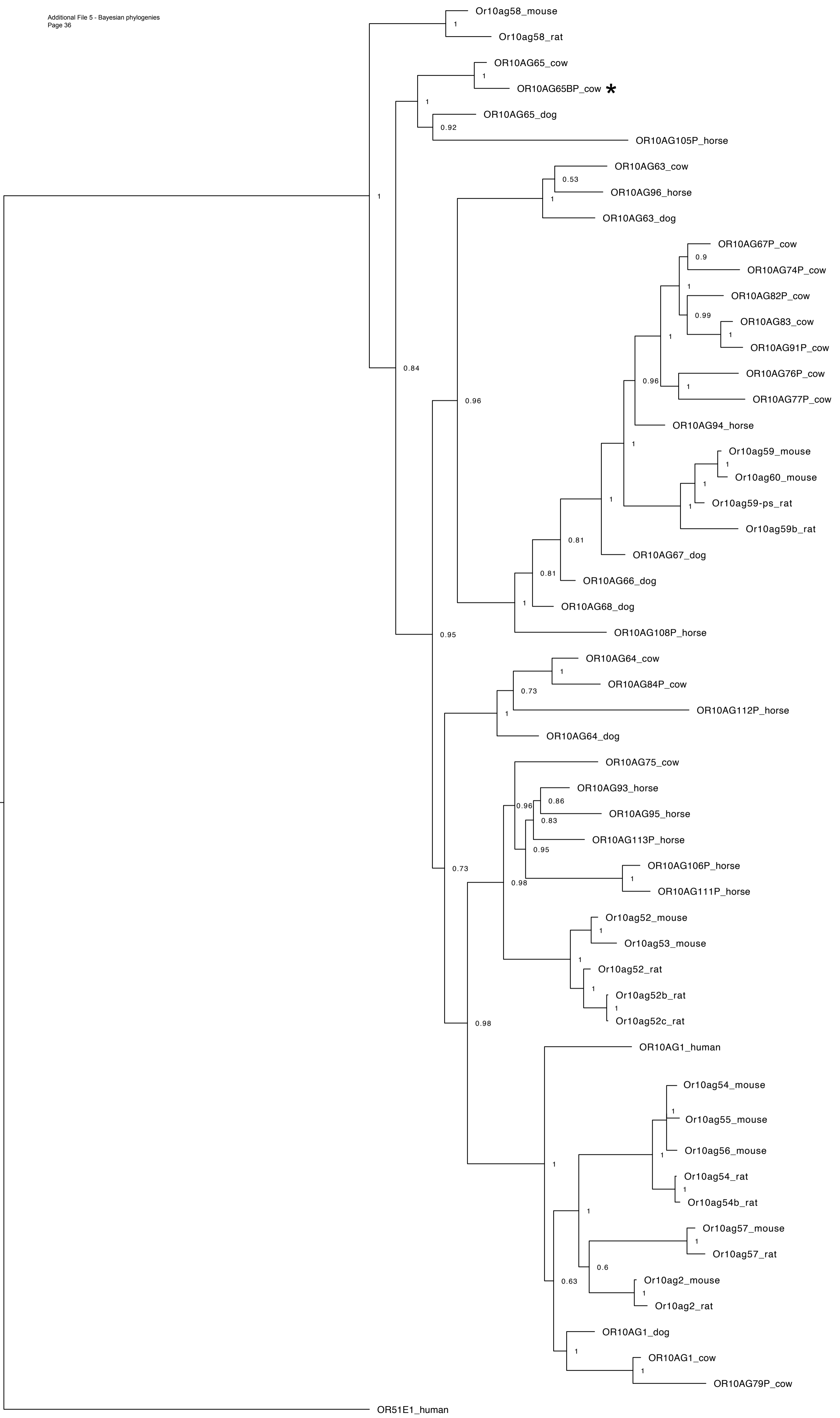




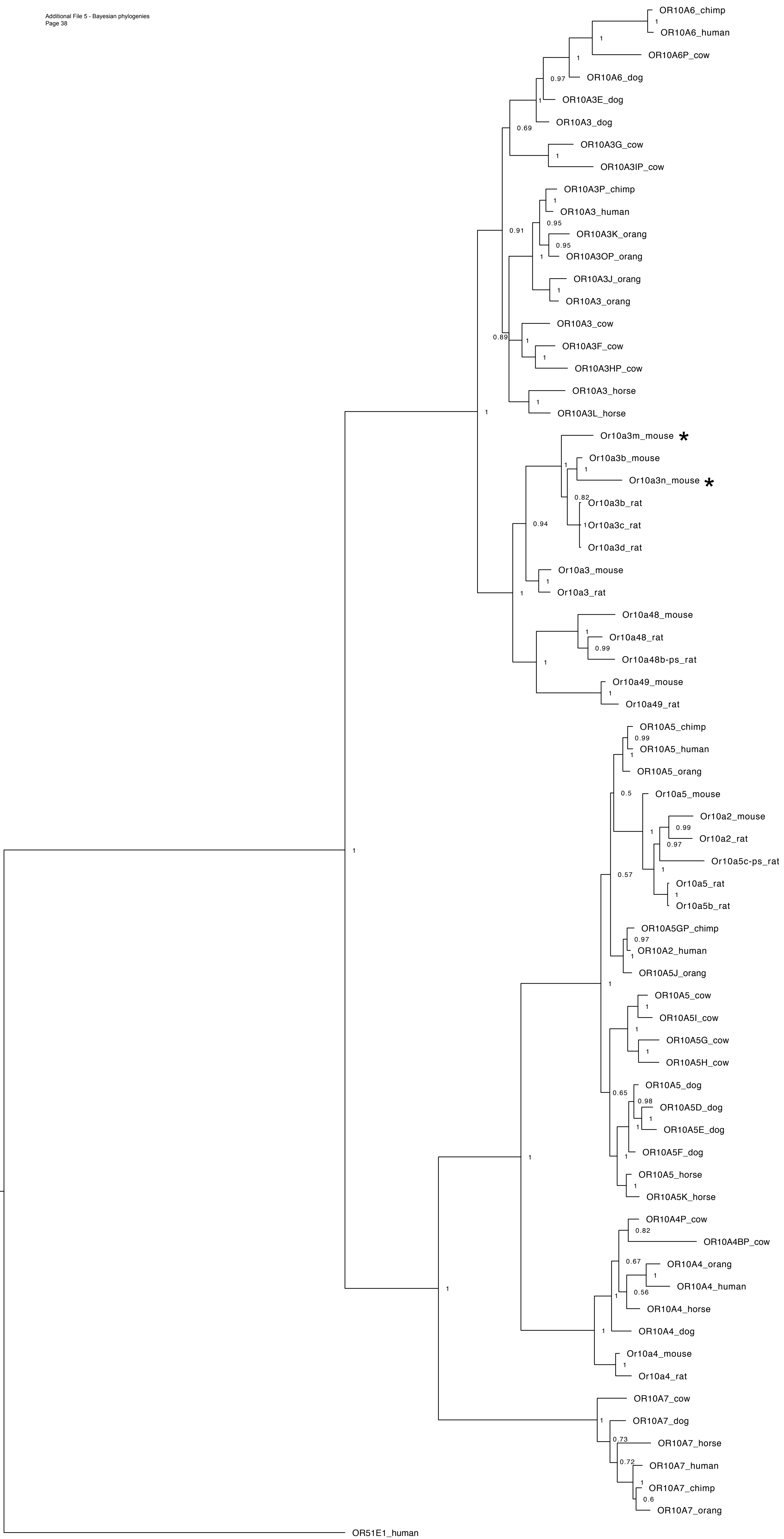


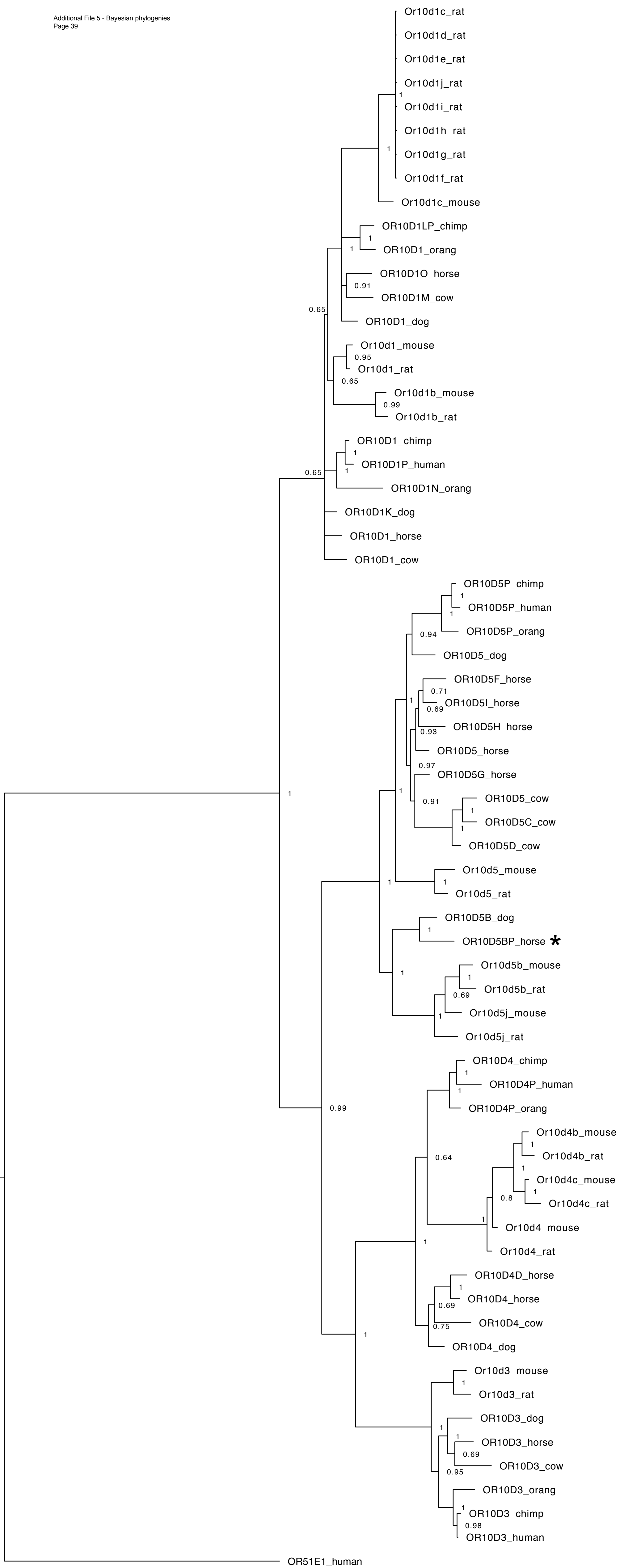


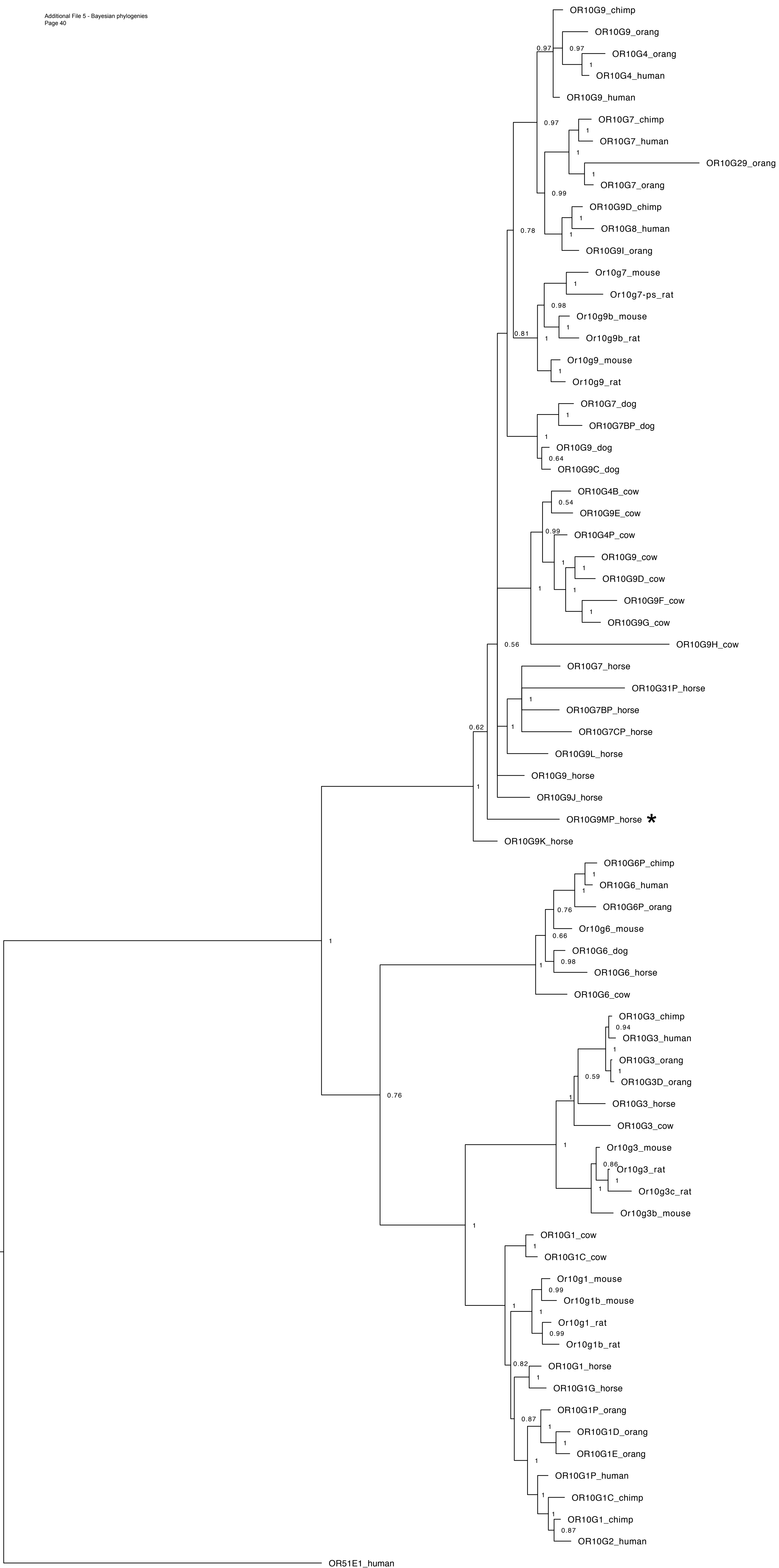


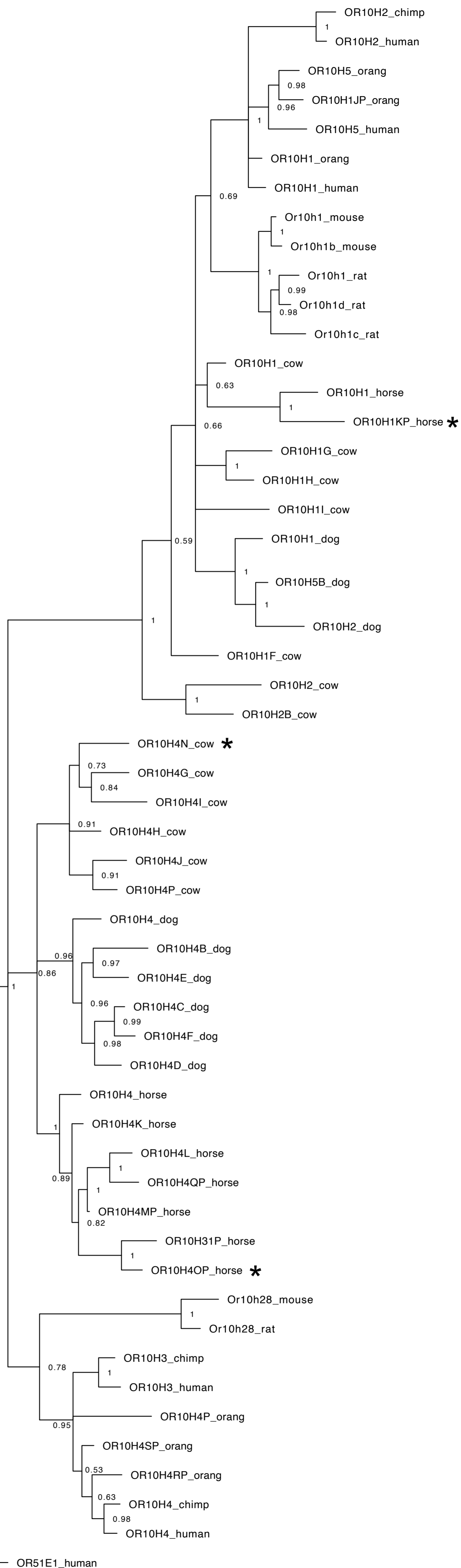


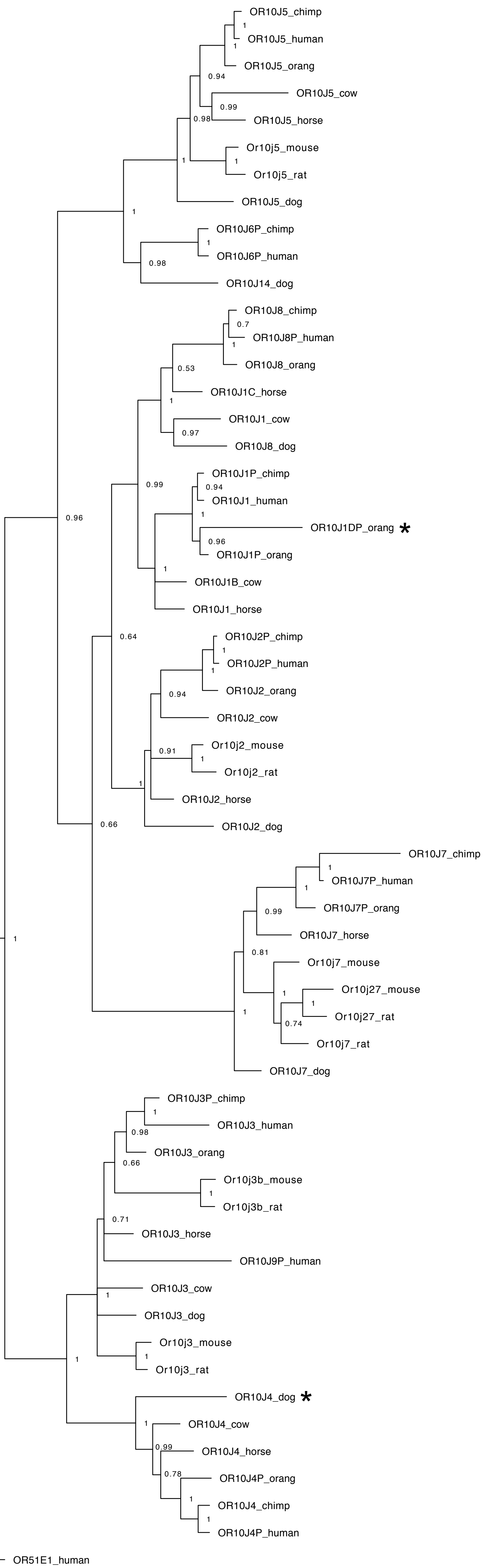


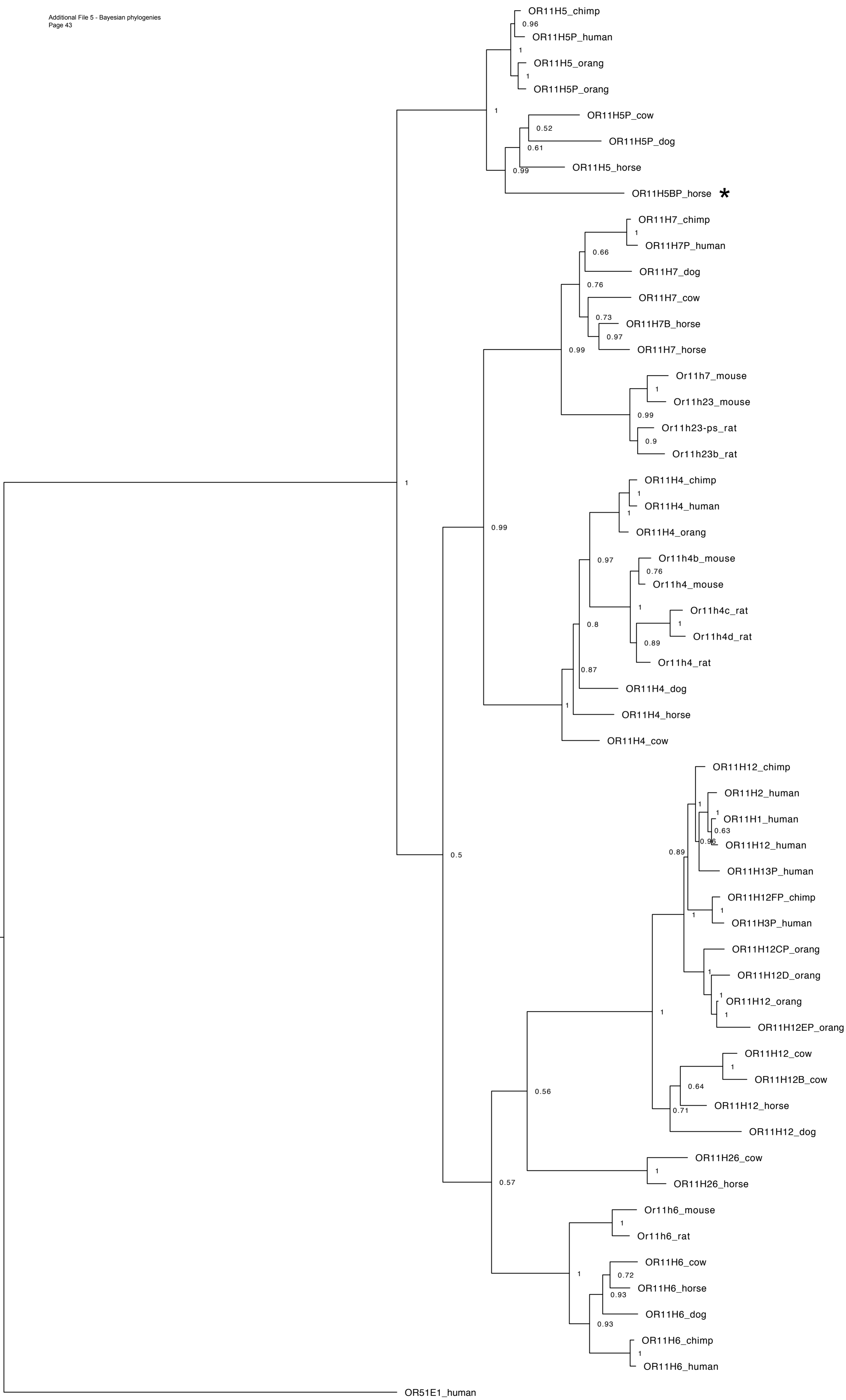


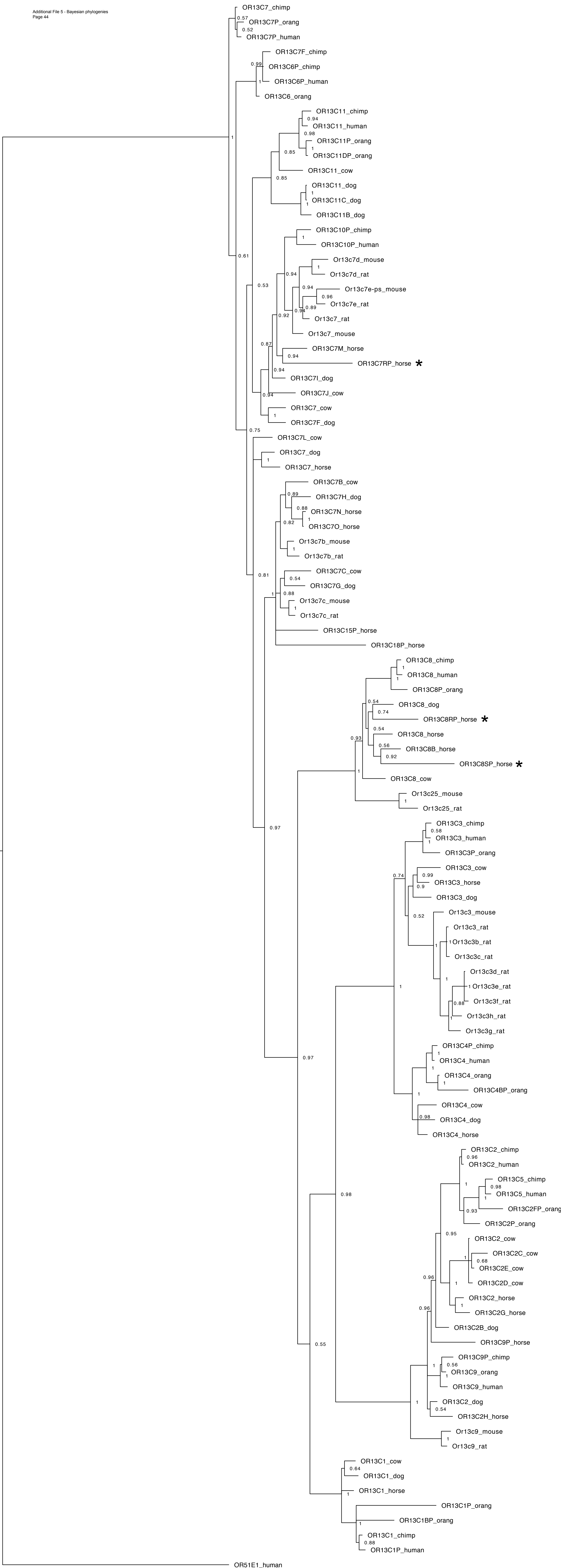


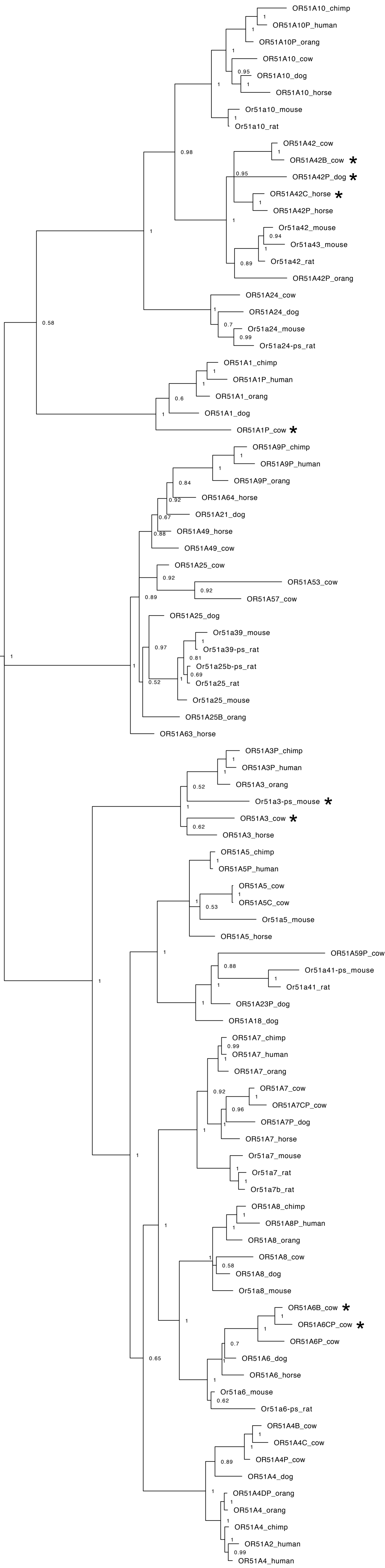












OR1E2_human

0.2

