Review of Comparison of Ataxia Telangiectasia Mutated's nucleotide sequence in different model organism

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This project is concerned with the study of phologenetic analysis of ATM nucleotide sequences in different model organisms with the aim of finding the closest model organisms to humans for some experiments that cannot be performed on humans for ethical reasons. I think the purpose of this topic is clear and the process is comprehensive. The report is well formatted, and I love the in-depth analysis of the tree results in the discussion section, which is also closely related to the laboratory research.

I have some minor questions for the author (or maybe it is just my problem), perhaps she could have added a few sentences of explanation for the purpose of clarity. The first question I would like to ask is what criteria were used to select the 10 species in the experimental material? The second question is what is meant by "with reproducibility of 1" in the Maximum likelihood result part? Does it mean that this is the only tree that was the best-scoring/achieved the highest log likelihood?

If there is anything that can continue to be studied in depth – the author mentioned in the discussion that "The best tree showed that the ATM protein's sequence in humans was the most closely related to that of *Bos Taurus* as the branch length. . . . . . . Interestingly, the next closest leaf of the tree was *Mus musculus*. . . 0.138868." I think such a conclusion is also well suited to be validated by setting the assumed two taxa in a group as a constraint for hypothesis testing.