My sincere apology for the late response as I have been spending too much time on my new born. I thank much the efforts of the authors in revising the manuscript. While my view will probably not affect the editor’s/recommender’s decision I feel that further comments may be **helpful for improving the study**, so I hereby provide two more.

A close-up of a text

Description automatically generatedThis is incorrect. As I suggested before, heterotachy is not about across-site difference. It would be good to look at the wiki where it’s indicated in the first sentence “Heterotachy refers to variations in lineage-specific evolutionary rates over time”, and the cited literature there.

Also, the authors have carefully revised the ms regarding the weakness of using single genes in dating. I however still encourage the authors to strengthen and to expand related discussion a bit more, which would make the results and conclusion more stringent, in my view. Places where such discussion might be about could be “*To start with, calibrating only one node is insufficient, but this is precisely the purpose of our analysis, since we study gene trees for which nodes lack calibrations*”. Certainly, it’s the authors’ liberty to take it or not.