Dear editor, dear reviewers,

thank you for the positive assessment and the opportunity to submit a revised version of the manuscript. Following the comments and suggestions of the reviewers, we revised the manuscript, particularly by better explaining traits and the biome concept, and by revising selected sections of the methods.

We are looking forward to your decision.

Yours sincerely,

Simon Scheiter and co-authors

Dear authors:
Thank you for your contribution to Biogeosciences.
Your revised manuscript has been evaluated by two anonymous referees. They judged that it is of good scientific significance and quality and has been improved from the previous manuscript. They recommended that minor amendments be made before it is accepted for publication. Please carefully consider the recommendations of the referees and provide your responses to them.

Thank you for the positive feedback. We considered all reviewer recommendations in our revision. Our responses are provided below.

Review 1

I appreciate the detailed responses given by the authors on my previous comments. These responses in combination with the changes made in the manuscript convincingly deal with most of the comments made. Two points remain to my point of view, but I leave it to the authors to decide whether and how they would like to resolve these points.

Thanks for this positive feedback.

I am still not convinced by the added value of the map created. As I indicated in my original review, and that did not change by the reply provided: I don't see the added values of this analysis and product given the aims of the paper and to me it does not seem to fit the story line, while it adds to the overall complexity of the paper (see my second point). Moreover, 50% of the map is based on extrapolation. While that is common to many other maps too, other maps always include a validation step to evaluate the extrapolation. No such validation was included here. There is thus no way to test the validity of the map.

We agree that the global map adds to the complexity of the manuscript. Nonetheless, we think that it is an important outcome of our study, as it shows that we cannot only reproduce biomes for areas where trait data is available, but that we can also extrapolate to the global scale. We therefore prefer to keep the analysis in the manuscript.

Regarding the validation, we compared the extrapolated biome map to the observation-based biome map used to create the SDM using kappa statistics and TSS as well as by creating a confusing matrix (Table 2). We reworded the methods in section 2.6 and the results in section 3.4 to make this clearer.

Also, while figure 1 helps to better maintain the overview of the design and steps taken in the paper, it is still quite complicated and a lot of concentration of the reader is needed to keep track of all terminology and steps. This cannot be solved easily, but is a point of attention.

We checked the figure. Yet, as we decided to keep the global extrapolation in the manuscript (see previous points) we did not find ways for simplification.

Review 2

1. The introduction can be better structured. The ecological importance of the concept of biomes is not properly introduced, if not neglected. Adding a few sentences at the beginning would greatly help clarify the motivation for your study and draw readers' attention. Similarly, another key concept used throughout the paper, 'trait,' is not introduced. Audiences other than scientists who work in ecology might have difficulty understanding this term at first glance. Additionally, the connection between the previous works cited in the introduction is not very clear. In my opinion, there is still much room for improvement in the introduction.

Following the suggestions of the reviewer, we added (1) statements to highlight the importance of biomes and the biome concept, and (2) a definition of traits in the introduction. We also checked the cited literature and strengthened the connection.

2. A similar issue exists in the 'Data' section. It would be clearer if the author first introduced what is contained in the TRY database, for example.

We revised the 'Data' section 2.1 and added information on the TRY and GBIF databases.

3. The selection of subset traits in Section 2.4 can be better explained. Why is a certain number of subsets selected from the 33 candidates? I recommend incorporating your responses to Reviewer #1 into the manuscript to better explain the connection.

As suggested by the reviewer, we revised section 2.4 to better explain why we selected subsets from the 33 available traits. This revision was based on the points from our previous responses to reviewer #1.