Dear Editors,

We would like to submit for publication in Oxford Academic Bioinformatics (Section: Application Notes) the enclosed manuscript, “MetaMutationalSigs: Comparison of mutational signature refitting results made easy”. Mutational signature analysis has become very common in cancer genetics and many tools have been developed that use different methods and produce different results. In this manuscript, we describe our tool MetaMutationalSigs which makes mutational signature analysis and comparison across different mutation signature analysis tools user friendly. Our major contributions and insights are as follows:

\* We created a user-friendly wrapper for frequently signature refitting packages using Docker <https://hub.docker.com/r/pp535/metamutationalsigs>. Our tool lets the users bypass the arduous process of handling dependencies for several tools and focus on the research questions instead.

\* We enable easy comparison between different signature refitting tools through our standardized figures. We also provide the users with result data so that they can visualize it as they see fit.

\* We have made our code on GitHub (<https://github.com/PalashPandey/MetaMutationalSigs>).

We sincerely believe that our tool will be of great interest to your readers.

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We confirm that this manuscript has not been published elsewhere and is not under consideration by another journal. All authors have approved the manuscript and agree with its submission to Oxford Academic Bioinformatics. And the authors declare that they have no competing interests.

We thank you very much for your time and consideration in reviewing our manuscript.

Sincerely,

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