

Genome-wide associations of structural variants with human traits through imputation from long-read assemblies

Corresponding Author: Professor Jian Yang

This manuscript has been previously reviewed at another journal. This document only contains information relating to versions considered at Nature Genetics.

Version 0:

Reviewer comments:

Reviewer #2

(Remarks to the Author)

Thank you for the revised manuscript. All my remaining comments have been addressed, and the inclusion of further details on the de novo assemblies, along with the expanded comparison of structural variants (SVs) using both lenient and more stringent Truvari settings, have strengthened the work. Congratulations to the authors on an excellent and thorough study! I have no further comments.

(Remarks on code availability)

Compared to the first revision, the authors have added the 29 1000 Genomes EUR assemblies as well as the corresponding code repositories for de novo assembly and assembly evaluation. That looks good to me.

credit to the original author(s) and the source, provide a link to the Creative Commons license, and indicate if changes were made.

In cases where reviewers are anonymous, credit should be given to 'Anonymous Referee' and the source.

The images or other third party material in this Peer Review File are included in the article's Creative Commons license, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons license and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder.

To view a copy of this license, visit <https://creativecommons.org/licenses/by/4.0/>

Responses to reviewers' comments

We greatly appreciate the reviewers' thoughtful feedback throughout the review process, which has helped improve the clarity and rigor of our study.

Referee #2:

Remarks to the Author:

Thank you for the revised manuscript. All my remaining comments have been addressed, and the inclusion of further details on the *de novo* assemblies, along with the expanded comparison of structural variants (SVs) using both lenient and more stringent Truvari settings, have strengthened the work. Congratulations to the authors on an excellent and thorough study! I have no further comments.

Re: We thank the reviewer for their positive feedback and for recognizing the value of the expanded Truvari comparisons and the additional details on the *de novo* assemblies.

Remarks on code availability:

Compared to the first revision, the authors have added the 29 1000 Genomes EUR assemblies as well as the corresponding code repositories for *de novo* assembly and assembly evaluation. That looks good to me.

Re: We appreciate the reviewer's confirmation regarding our data and code availability.