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Dear Dr. Cho,

Thank you for the opportunity to revise our manuscript. We also want to thank the reviewers for their insightful comments. We have taken to heart the reviewers' suggestions and made significant revisions to our manuscript in order to address them. In particular, they made suggestions on some of the technical aspects of our study. Thus, we have performed a major overhaul of the pipeline and revamped its statistical underpinnings. We re-implemented it on all 382 individuals from the 1000 Genomes Project and their corresponding 1,280 ChIP-seq and RNA-seq datasets to call allele-specific variants. We then rebuild the AlleleDB database and re-performed all the corresponding downstream analyses. We also included new analyses and prepared new figures and supplementary exhibits to better showcase the utility of our resource, especially as a [genome annotation of allele-specific behavior for the 1000 Genomes Project variant catalog](#). Already, our methodology has been utilized in some of the analyses performed in the [1000 Genomes Structural Variation paper, which is under consideration at \*Nature\*](#). The data used by our paper is not the embargoed part of the 1000 Genomes dataset, so the publication schedule of our paper is not tied to that of the main paper. [As the co-chair of the 1000 Genomes Project Functional Interpretation Group and also a member of the consortium's Structural Variation Group](#), we think that the manuscript is now in good shape and would fit as a companion to the 1000 Genomes papers targeted for publication in *Nature*.

Yours sincerely,

Mark Gerstein

[Co-chair of 1000 Genomes Project Consortium Functional Interpretation Group and Member of the 1000 Genomes Project Consortium Structural Variation Group](#)

Albert L. Williams Professor of Biomedical Informatics,  
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and Computer Science,

Co-director of the Yale Program in Computational Biology and Bioinformatics

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