Dear editors of Genome Research and reviewers,

Thank you very much for reviewing our manuscript once again and for providing final important suggestions and criticism. Please find the new version of the manuscript with changes and improvements that address them.

We enhanced the telomere mapping approach to incorporate the suggestions by Reviewer 2, which allowed us to unambiguously assign telomeric reads to specific chromosomal arms. To that end, we (1) refined the construction of the extended reference genome by masking subtelomere-telomere boundaries that were previously identified as inexact and (2) incorporated a step of the pipeline that filters out ambiguous candidates.

We are glad to report that these actions, in fact, improved the analysis without affecting the conclusions of the paper. While the identities and the amount of the candidate reads changed due to the disambiguation step, the overall results remained the same: motif variants and spectra of haplotypes are still captured, and the measure of interpopulation similarity has even grown slightly larger.

Moreover, several of the concerns we previously raised in the Discussion about incorrect annotation of the human reference genome were addressed at the early stage of the extended reference construction. Importantly, these changes also allowed us to capture a set of well-supported *p*arm telomeric reads and tobe able to analyze and describe haplotypic variation on *p*arms, which provides additional results.

The supplemental files containing the refined extended genome have been updated, and all numerical and qualitative results that were affected by these changes (e.g., exact values of sequence percentage explained by specific motifs), along with the figures, have been updated in the main text and in the supplemental materials as well.

We also addressed all suggestions regarding the formatting of the manuscript and the availability of code: (1) modified the capitalization of terms (10x, Chromosome), (2) re-formatted all citations and references to adhere to the journal’s format, (3) re-rendered figures to be more legible upon reduction, (4) supplied Python scripts as Supplemental File S3, and (5) adjusted the flow of the narrative as much as possible to include the updated results and methods in the appropriate sections of the manuscript.

We hope that addressing your comments, suggestions, and criticism with these changes is satisfactory to the reviewers and the editors.