Description of Additional Supplementary Files

Supplemental Data 1.  Summary de novo assembly statistics of individual samples.
Supplementary Data 2. Regions of the reference genome that are inaccessible with genome mapping.
Supplementary Data 3. Coordinates and annotation of regions with complex structural variations.
Supplementary Data 4. Large insertions and deletions found in individual samples.
Supplementary Data 5. The list of inversions found in samples.
Supplementary Data 6. The list of multiple indels found in samples.
Supplementary Data 7. The list of translocation breakends.
Supplementary Data 8. The list of duplications and other structural variations.
Supplementary Data 9. The list of indels with statistically significant size differences among super-populations.
Supplementary Data 10. List of copy number variations analyzed by the multiple alignment approach.
Supplementary Data 11. Reference gaps closed with 10X data.

**Response to requests**
(Requests in *italics*, our response in blue)

EDITORIAL REQUESTS:
*We would specifically ask that you include a more thoughtful consideration of how the newly released data can be used by the community, as per Reviewer #3's request.*
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*At the same time we ask that you edit your manuscript to comply with our format and style requirements and to maximise the accessibility and therefore the impact of your work.*
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No human subjects involved. All samples are from the NIH collection in a public repository maintained by the Coriell Institute.

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*"Large structural variants (SV) are understudied in human genetics research because of the difficulty to detect them in the routinely generated short-read sequencing data. Here, the authors generate optical genome maps of 154 individuals from 26 populations that allow comprehensive examination of large SVs."*
The summary reads well and to the point. Approved.

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