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GIGA-D-17-00028**"Alignment of 1000 Genomes Project Reads to Reference Assembly GRCh38"****Original Submission****Liquo Wang (Reviewer 1)**

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Comments to Editor:**Comments to Author:**

The authors described in details how they re-aligned 1000 genome reads to the most recent human reference genome—GRCh38. This is not a trivial job given the large data volume. Although the workflow is similar to that used to map reads to GRCh37, it took immense computing resources to generate the resulting CRAM alignment files, and these CRAM files have great reuse potential.

Some minor concerns:

- 1) In Table 1, the authors should include "Total aligned bases (Gbp)" from GRCh37 for comparison.
- 2) In page 9, line53, the authors used PAR abbreviation without explanation.
- 3) Why Mitochondria chromosome was not included in Figure 2?
- 4) In each panel of Figure 2, it would be helpful to include another line calculated from GRCh37 for side-by-side comparison.
- 5) In Figure 2C, using the median read depth (on Y-axis) across samples would be more informative and less biased by the respective sequences of the Y-chromosome.
- 6) It would be helpful to other users (and the authors themselves when newer reference genome becomes available) if they could automate the whole process described in Figure 1 and make the code public available.

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