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GIGA-D-17-00028

"Alignment of 1000 Genomes Project Reads to Reference Assembly

Original Submission

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View Individual Reviewer Comments added to Publons, you can then choose whether or not to claim your Publons credit. I understand this statement. **Comments to Editor:** The manuscript is very helpful to users who wish to use GRCh38 for human reference genome. The manuscript is acceptable after a few minor revisions described above is solved. **Comments to Author:** The manuscript describes the data not for remapping of 1000 Genome Project reads to GRCh38. Remapping to the newest reference genome is very useful for users who wish to use the resource for their own research project. Thus, the resource described in the manuscript is very precious for research community. Reviewer checked the URLs described in the manuscript and confirmed that all the URLs are alive now. Improvements (GRCh37 -> GRCh38) of mapping are successfully summarized in Table 1 and readers can easily grasp the difference. Reviewer cannot find any information about the advantage of CRAM. Although reviewer thinks that the compression by CRAM is superior to other generic compression methods (gzip and bzip2), some real data in data size about the comparison of compression by CRAM to that by gzip and/or bzip2 might be of help to readers who wish to switch to use CRAM for the compression of their own data. It would be much more helpful if the CPU time for compression by CRAM is compared to those by gzip and/or bzip. Minor point: Term 'HLA' is not explained in the main text while it is in the 'List of abbreviations'.

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