

ERRATUM

Erratum to: A reference human genome dataset of the BGISEQ-500 sequencer

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We found several inaccurate descriptions in our recently published paper, “A reference human genome dataset of the BGISEQ-500 sequencer” [1], thus we would like to make the following corrections.

In the Background section, the full name of cPAS should be “combinatorial probe-anchor synthesis” [2] rather than “combined primer anchor synthesis”. So the following sentence should be modified:

1. Sentence “... sequencing library construction and combined primer anchor synthesis (cPAS) for sequencing.” should be changed to “... sequencing library construction and combinatorial probe-anchor synthesis (cPAS) for sequencing.”.

In the Background-Sequencing section, the mentioned sequencing technology should be “rolling circle amplification (RCA)” [2] instead of “PCR amplification”. The RCA step is one of Complete Genomics™ core technologies, which is different from PCR amplification. The key advantage of the DNB technology is that every replicated copy is produced from the original genomic fragment, instead of PCR-utilizing sequencing technologies, in which one amplifies from the already amplified template. Thus two sentences should be modified accordingly:

2. Sentence “... single-strand circular DNA library was first PCR-amplified for 10 minutes...” should be changed to “...

single-strand circular DNA library was first subjected to rolling circle amplification (RCA) for 10 minutes...”.

3. Sentence “After the PCR reaction, 20 μ l DNBs stopping buffer was added to terminate the PCR reaction” should be changed to “After the RCA reaction, 20 μ l DNBs stopping buffer was added to terminate the RCA reaction”.

For clarity we have uploaded detailed and corrected protocols of the sequencing library preparation [3] and sequencing [4] steps to protocols.io.

References

1. Huang J, Liang X, Xuan Y et al. A reference human genome dataset of the BGISEQ-500 sequencer. *Gigascience*. 2017;6(5):1–9. doi: 10.1093/gigascience/gix024.
2. Drmanac R, Sparks AB, Callow MJ et al. Human genome sequencing using unchained base reads on self-assembling DNA nanoarrays. *Science* 2010;327(5961):78–81. doi: 10.1126/science.1181498.
3. Huang J, Liang X, Xuan Y et al. BGISEQ-500 Sequencing. [protocols.io](http://dx.doi.org/10.17504/protocols.io.pq7dmzn). 2018 <http://dx.doi.org/10.17504/protocols.io.pq7dmzn>
4. Huang J, Liang X, Xuan Y et al. BGISEQ-500 WGS library construction. [protocols.io](http://dx.doi.org/10.17504/protocols.io.ps5dng6). 2018 <http://dx.doi.org/10.17504/protocols.io.ps5dng6>