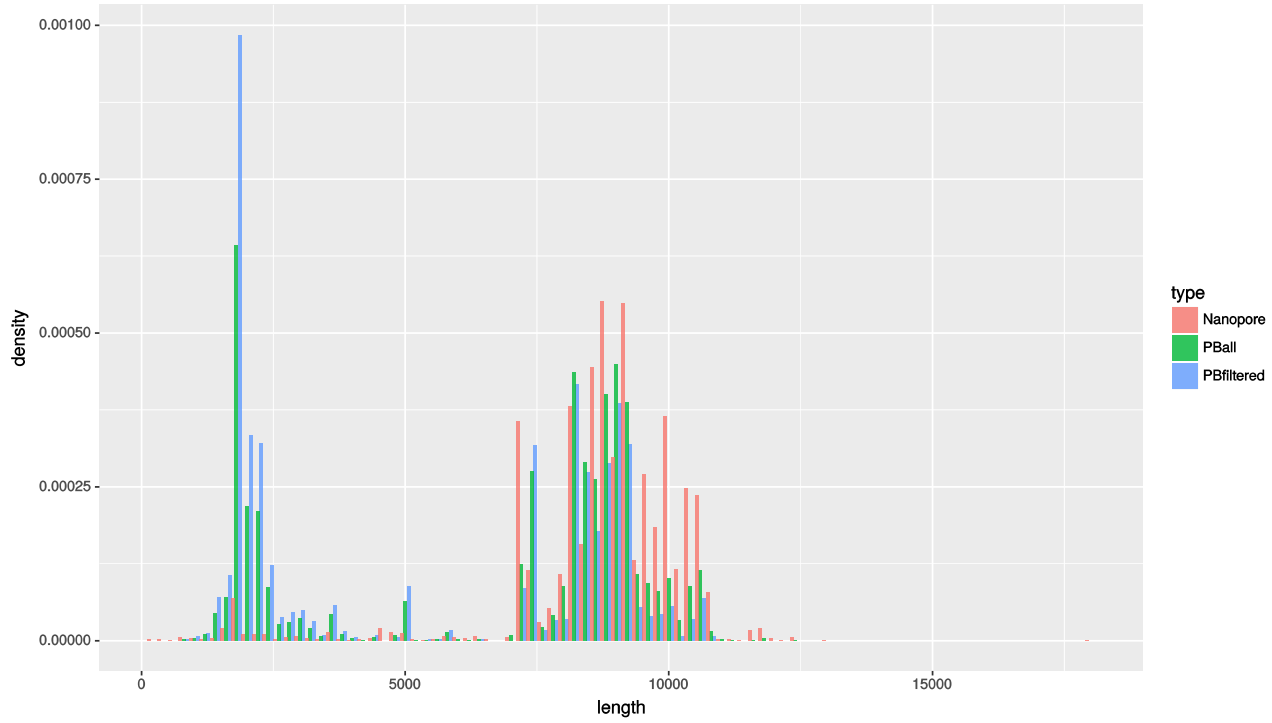
Supplemental Material S4

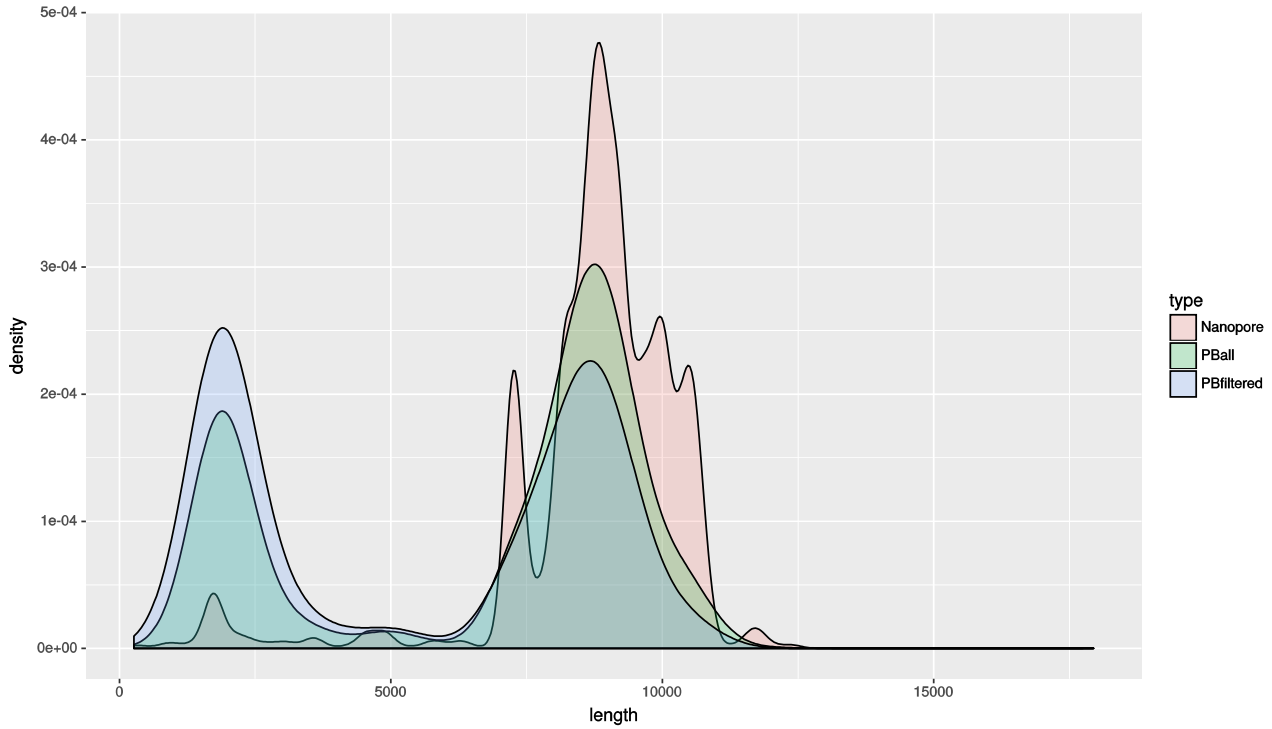
In general, our PCR products were usually clean but occasionally we observed secondary smaller sized bands with a weak intensity. Due to the circular sequencing, PacBio superimposes short fragments, which is why the manufacturer recommends to remove these secondary bands by using additional steps (e.g., by using a PippinPrep instrument). Since we didn't employ this step, it was thus not surprising, that our weak small bands were problematic for PacBio, which resulted in decreased yields for our very long TR amplicons. Nanopore's output on the other hand resembled more or less the pictures that we have seen in the agarose gels after the TR-PCR (Figure S4.1). In summary, we basically can maintain the methods for Nanopore sequencing that we already use for Sanger sequencing, without necessarily implementing additional steps, as we may need for PacBio sequencing.

Figure S4.1 A & B. (A) Comparison of TR sequencing output in terms of sequence length on the PacBio RSII instrument (reads of insert, ROS) and on the Oxford Nanopore MinION instrument of the identical DNA pool. The PBall mark all PacBio ROS sequences, and the PBfiltered represents ROS that are filtered with a maximum error rate of 0.02 identical to our data processing steps (around 60% of the sequences are retained after quality filtering). **(B)** The data is also plotted as density to normalize the variability in absolute counts: Nanopore, PBall, and PBfilterd consisted in total of 8016, 5654, and 3373 sequences, respectively.

A.



B.


5e-04
4e-04
3e-04
2e-04
1e-04
0e+00
density
0
5000
10000
15000
length
type
Nanopore
PBall
PBfiltered