Supplementary Figure S1. Proportion of detected Nextera and TruSeq adapters along base positions in mate-pair reads.
The plots produced by running FastQC v0.11 on Read1 of raw fastq files are shown for Library 1 (1–6 kb), which was prepared according to the standard protocol, as well as Library 2 (1–6 kb) and Library 3 (11–18 kb), which were prepared according to our modified protocol. Library 4, shown as an unsuccessful example, was also prepared according to our modified protocol and showed an unfavorably high proportion of TruSeq adapter (gray circle) because of insufficient removal of small molecules. The dotted black line in the adapter proportion plot for Library 1 shows the point at which the proportion is plotted for 101-bp-long reads. The peaks in insert size distribution for Libraries 1–4 are located at 869 bp, 545 bp, 501 bp, and 380 bp, respectively. This comparison shows that our modified protocol (Libraries 2 and 3) facilitates the detection of a higher proportion of Nextera adapter in mate-pair reads (green circles), promising larger numbers of mate-pair reads to be used for genome scaffolding.

Figure is shown on Page 2.