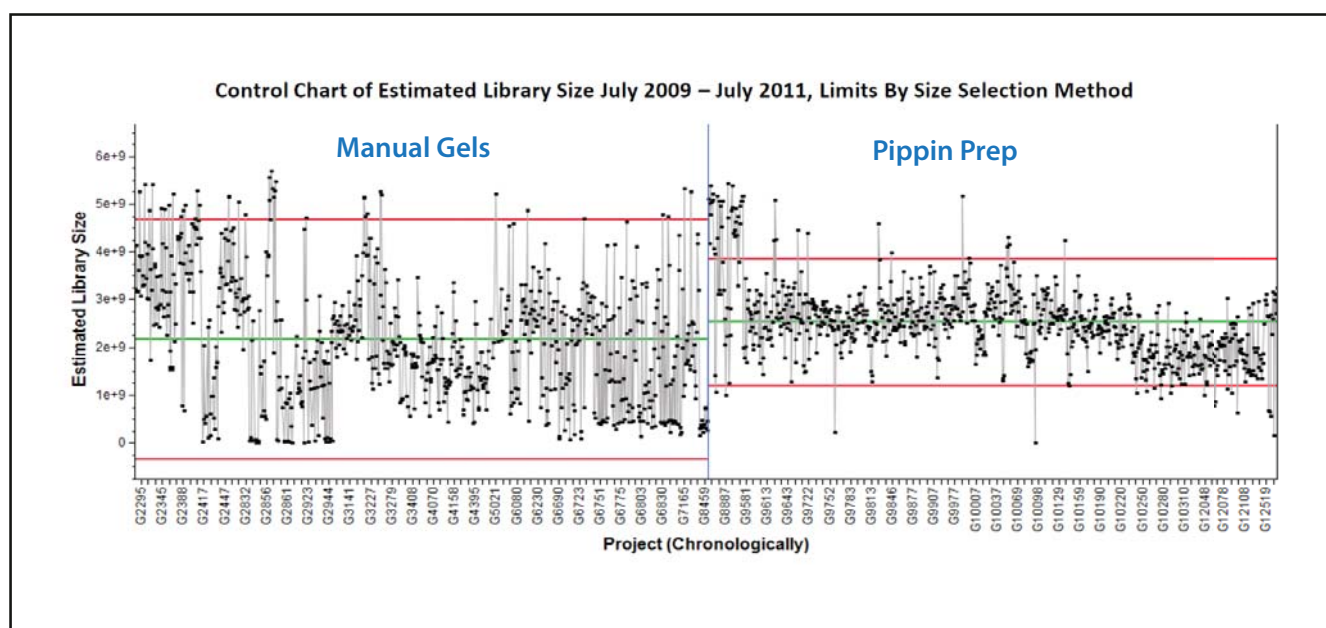


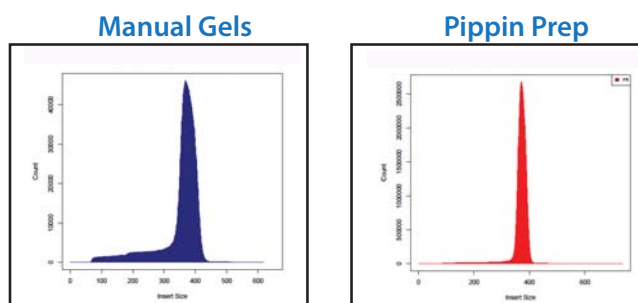


Paired-End Library Construction

In 2010, the Broad Institute integrated Pippin size selection into their pair-end sequencing line, replacing manual gel purification step in the library construction process. The library sizes were estimated and recorded after each run. The chart below shows the chronological record for 1 year before Pippin was implemented, and for 1 year after, showing a marked improvement in library consistency.



Pippin size selections offer several benefits to paired-end sequencing. The images below compare typical insert size distributions from manual gels versus Pippin. With the Pippin, a more narrow distribution can be collected. This provides more aligned reads during assembly which facilitates identification of structural variants. Absence of low molecular weight fragments reduces wasted reads and also improves the identification of variants. Comparatively higher recoveries can reduce the number of amplification cycles required, which produce libraries with greater genetic diversity.



Fragments like you like them.