Robust, Streamlined, Express DNA Library Preparation Methods Meet Requirements of High-throughput Library Construction

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As next generation sequencing technologies improve and capacities expand, library construction has increasingly become the bottleneck for fast data turnaround and overall cost. There is a growing need for faster, easier, and automatable protocols that perform reliably and do not compromise the quality of the libraries produced. We have developed two new "DNA sample in, library out" workflows with mechanical or enzymatical shearing approaches, allowing for a single tube, standardized protocol for fast library preparation. The streamlined, user-friendly workflows reduce hands-on time by combining reaction steps, removing clean-ups, and simplifying the protocols by using a single adaptor concentration and one PCR cycling condition. They allow many DNA samples of varying sources and input amount (10 ng to 200 ng) to be processed in one setting without normalization or adjusting reaction conditions. We have applied these two robust workflows to generate high quality sequencing data. We expect these library preparation methods will serve in a myriad of NGS applications, including clinical and diagnostic settings.