

Automating Low-Throughput Library Prep Workflows for Core Facilities

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Even core facilities have some low throughput workflows, for example resequencing of dropouts. Constructing these libraries manually consumes staffs' time and can introduce error, negatively impacting the quality of sequencing data. This can result in higher costs, longer turnaround times, greater number of experimental re-runs, and loss of valuable samples.

The efficiency of a lab can be maximized by minimizing the potential sources of human error and increasing walk-away time by automating NGS library construction with a reliable liquid handler and automation scripts which have been standardized and tested. However, traditional automation has been developed to address the needs of labs running batches of 48 samples or more at the time. These workstations are not always practical for the specific requirements of low throughput workflows.

The BioQule™ NGS System supports the needs of labs with low throughput library preparation workflows by decreasing their hands-on time by 80% and minimizing errors. As is illustrated by the >99% pass rate this system reduces delays and additional costs by increasing the reliability of sequencing data and reducing the need for experiments reruns.

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