

BioQule™ NGS System

English Version

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personalizada, cotizaciones y todo
lo que necesitas para tomar la mejor
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BioQule™ NGS System

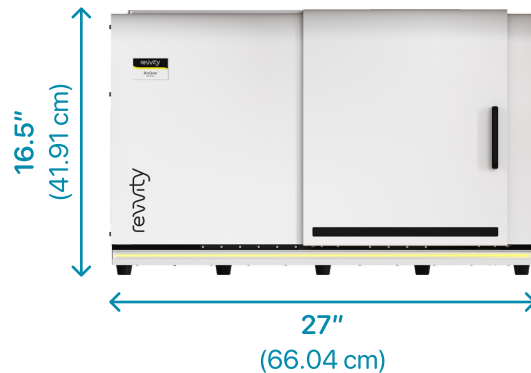
Biología Molecular

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Easy to use, compact solution for automating low throughput library prep

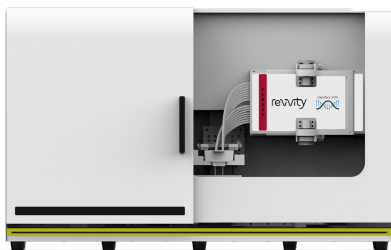
Reimagine low-throughput library prep with the BioQule™ NGS System and simplify your nucleic acid analysis, library prep and quantitation with walk-away automation. This low-cost, open, benchtop instrument delivers libraries ready to load into your sequencer in as little as 15 minutes of hands-on time (HOT), allowing you to focus on what really matters.

- Full walkaway automation (Up to 80% reduction in HOT)
- Easy to use (only 4 touch points)
- Minimize human error (>99% success rate)
- Open system able to automate different applications




Electrical requirements:
100-240VCA a 50-60 Hz


Weight:
45 lbs



Easy NGS library preparation

The BioQule NGS System has been specifically designed so no automation experience is required to generate NGS libraries. Simply pipette your samples, beads, and reagents into the plate, place the cartridge and plate in the instrument, close the door and walk-away. The BioQule NGS System will construct AND quantitate up to 8 libraries while you to focus on what really matters.

Library preparation and quality control in the same system

The BioQule NGS System is equipped with automated fluorescence-based optical quantitation to measure the concentration of each library. You will no longer need to move your samples from one instrument to another to perform concentration analysis on your libraries.

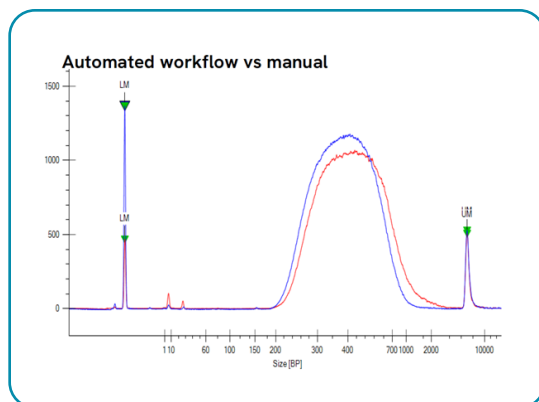


Figure 1: Comparison of electropherogram traces from BioQule DNA-seq libraries prepared using the BioQule NGS system (red) or Manual workflow (blue).



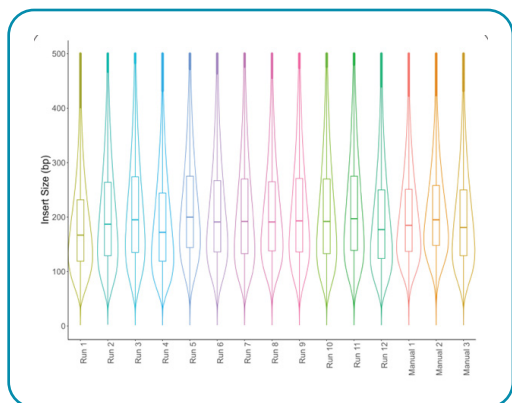


Figure 2: Insert sizes for 12 DNA-seq libraries prepared on the BioQule NGS System and 3 libraries prepared manually, grouped by run. Data shows consistent distribution of insert sizes, with BioQule libraries comparable to manual runs.

The BioQule NGS System constructs libraries with size distributions that are equivalent to those prepared manually.

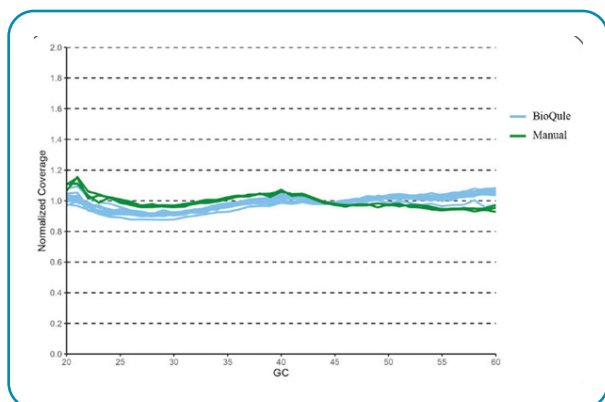


Figure 3: Analysis of GC bias from 15 DNA-seq libraries prepared with the BioQule NGS System (blue) vs manual workflow (green). The results show minimal variability in normalized coverage across 20-60% GC (~95% of the human genome).

