

Automation of the Illumina® COVIDseq™ Test on the epMotion® Liquid Handler*

Rapid and Flexible Library Preparation for SARS-CoV-2 Research



Viral sequencing has become an important and powerful tool in identifying SARS-CoV-2 mutations and studying sources of infection.

At Eppendorf, we have developed pre-qualified methods for the Illumina® COVIDseq™ Test (RUO version) on the epMotion® 5075t NGS Solution* to help you easily automate your library preparation for viral genome analysis.

Product features

- > Up to 15 ANSI/SLAS worktable positions
- > Automatic exchange of 4 dispensing tools
- > Maximum pipetting accuracy from 0.2 to 1,000 µL
- > Optical sensor for detecting labware, liquids, tips
- > Integrated Eppendorf ThermoMixer®^[1] and up to 2 thermal modules for mixing and temperature control
- > UV lamp and air filter system option for decontamination and clean air conditions
- > Email notification and integrated LED lights for visual feedback on system status

Your advantages

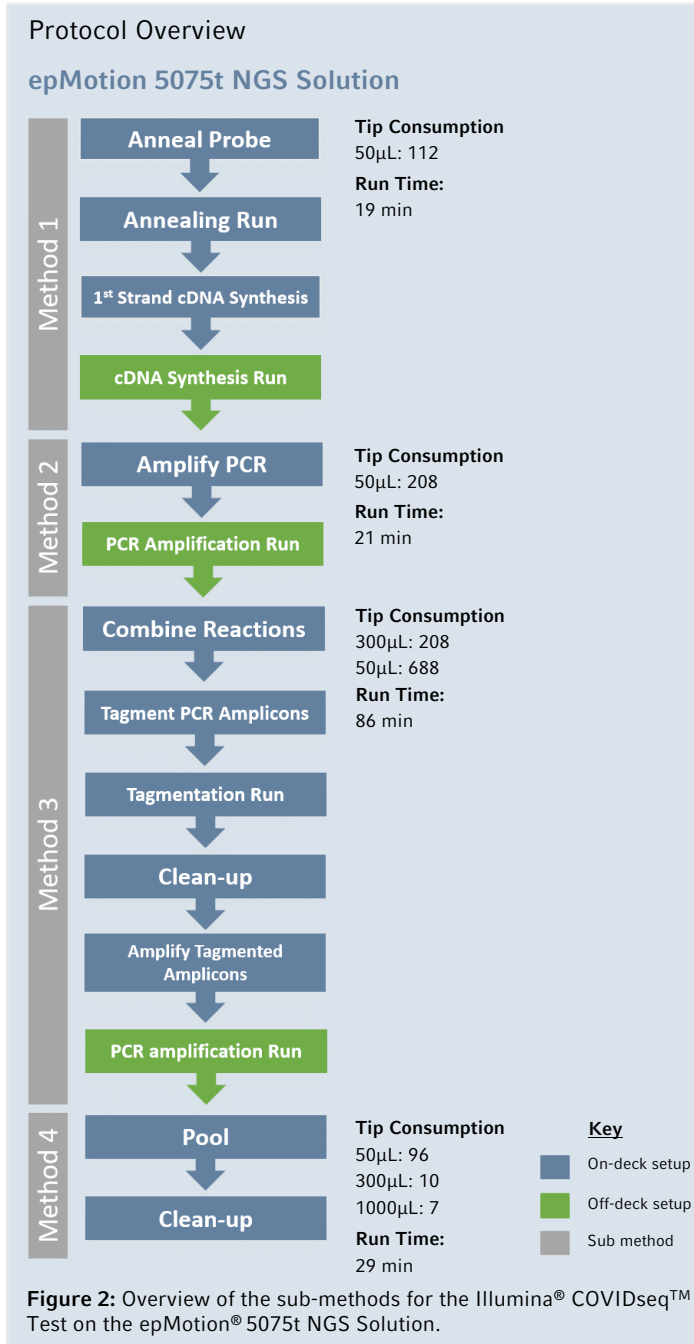
- > **Scalable:** Configurable for batch sizes from 1 – 96 samples to meet your throughput needs
- > **Accurate:** Generate high-quality and reliable libraries with proper size distribution
- > **Highly flexible:** Large worktable supports a variety of tube and plate formats
- > **Reliable:** Optical sensor checks reagents and consumables prior to each run for error-free set up
- > **Cost-effective:** Automatic liquid level detection reduces any dead volume to save on reagent costs
- > **Dynamic:** Runs can be started at any step to automate specific time-consuming and error-prone liquid handling steps
- > **Efficient:** Interrupted runs can be restored from the point where they stopped to improve productivity
- > **Safe:** Fully autoclavable dispensing tools, optional UV lamp and air filter minimize cross-contamination

^[1]For research use only

Workflow Overview



Figure 1: Automated workflow for the Illumina® COVIDseq™ Test on the epMotion® 5075t NGS Solution. Steps shown in brown can be automated on the epMotion® liquid handler.



Worktable Configuration

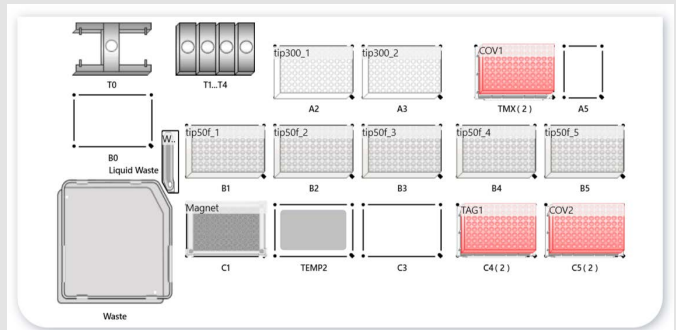


Figure 3: Worktable layout for processing Method 3 on the epMotion® 5075t NGS Solution.

Application Data

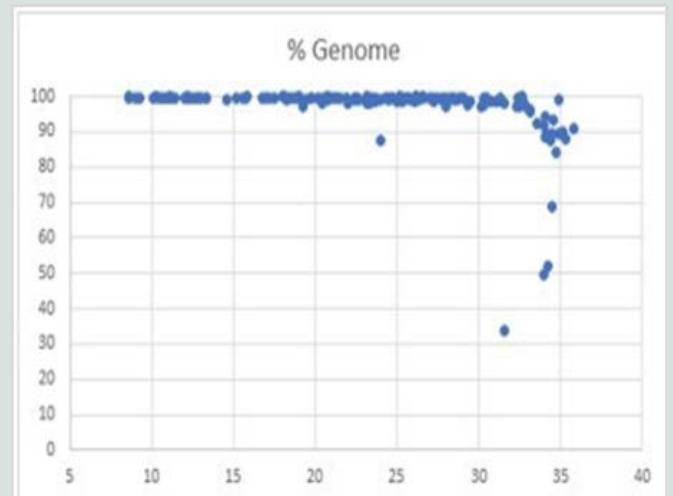


Figure 4: Concentration of the final pooled library analyzed using the Qubit. Plot shows the relationship between sample Ct value and coverage.

The concentration of pooled libraries prepared on the epMotion was determined with the 1X dsDNA High Sensitivity kit on the Qubit 4 Fluorometer. On average the concentration of the final pooled library is approximately 50 ng/µL. This concentration can vary depending on sample quality and viral RNA load. Pooled libraries were sequenced on the Illumina NovaSeq (paired-end 150), with at least 1 million reads/sample. Plot shows the relationship between sample Ct value and coverage. The relation between Ct value and coverage is dependent on various factors including the sample quality, COVIDseq primers, sequencing depth, etc.^[2]

Acknowledgment

^[2] Yale SARS-CoV-2 Genomic Surveillance Initiative.

*Developed on a predecessor model, but thanks to the migration feature, this method can easily be transferred to the newest generation of epMotion®

Contact your sales specialist for more information:

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