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Automated Solution for the Illumina[®] Stranded mRNA Prep, Ligation Kit

RNA library preparation on the epMotion[®] 5075t NGS Solution*



Ligation-based RNA library preparation is a labour intensive process with several sub methods that requires technical know-how, precision and accuracy to generate high-quality libraries. Simplify your RNA library prep with pre-qualified and ready-to-run methods for the Illumina Stranded mRNA Prep kit on the epMotion[®] 5075t NGS Solution.

Product features

- > Calibrated 1-channel and 8-channel dispensing tools for precise liquid handling from 0.2 μL to 1 mL
- Integrated Eppendorf ThermoMixer[®] and thermal module for efficient mixing and reliable temperature control
- > High-quality NGS-specific consumables and space saving accessories are included
- > Intuitive and easy-to-use epBlue software
- > Email notification option and integrated status lighting keeps you informed about the status of your library prep run

Your advantages

- > Better results: Eliminate manual pipetting errors to generate high-quality libraries
- > Increased throughput: Up to 96 samples can be processed without compromising data quality
- > Improved productivity: Automatic dispensing tool exchange allows uninterrupted library prep
- > Greater flexibility: Supports different tube and plate formats
- > Enhanced safety: Fully autoclavable dispensing tools and easy to disinfect worktable minimizes cross contamination while the optional UV lamp and air filter provides clean air conditions
- > Walkaway automation: Ligation and incubation steps as well as upstream nucleic acid purification can be performed on-deck

Request your demo today!

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Workflow Overview



Figure 1: Automated workflow for the Ilumina® Stranded mRNA Prep kit on the epMotion® 5075t NGS Solution. Steps highlighted in dark brown can be automated on the epMotion[®] liquid handler.

Protocol Overview Worktable Configuration epMotion[®] 5075t NGS Solution B0 Liquid B4 B5 (5(2) C4(2 Tip Consumption Capture mRNA Figure 3: Worktable layout for processing Method 1 on the 50µL: 120 epMotion[®] 5075t NGS Solution. 300µL: 592 Elute Run Time: 125 min Application Data Clean-up Figure 4: Analysis Fragment of 1 µL final enriched library **Tip Consumption** using the Agilent Synthesize cDNA 50µL: 304 2100 Bioanalyzer 300µL: 400 and DNA 1000 Run Time: Clean-up cDNA 175 min kit.1 Tip Consumption Adenylate 3' ends 50µL: 488 300µL: 0 15 50 100 Ligate anchors Run Time: 95 min Figure 5: QC æ Θ C [bp] Ж 8 Ľ 업 results of final U Ξ 5 ₹ Tip Consumption 100nq SOng 100nq 100nq Ladder 25nq 25nq SOng 50ng 50ng 100nq 25nq 25nq libraries from 50uL: 192 25ng of input Clean-up fragments 멼 ĿЯ 55 S14 S16 ផ ß 6J S17 S19 8 Я 300µL: 400 using the Run Time: Bioanalyzer.¹ 66 min Key 1500 1000 700 Amplify library Tip Consumption On-deck setup 50uL: 208 500 -Off-deck setup 300µL: 400 400 Run Time: 300 Sub method 100 min 200 150 Indicates safe Clean-up library stopping point 100 -50 — i Figure 2: Overview of the sub-methods for the Illumina® Stranded mRNA Prep kit on the epMotion[®] 5075t NGS Solution.

References

[1] Eppendorf Application Technologies, March 2021, NGS Libraries preparation on epMotion®: Illumina® Stranded mRNA Prep Ligation *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:

www.eppendorf.com/automation

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