Quick-Start Protocol August 2023

QIAseq® FastSelect™ -5S/16S/23S Kit with the Bio-Rad SEQuoia™ Complete Stranded RNA Library Prep Kit

The QIAseq FastSelect -5S/16S/23S Kit (cat. nos. 335925, 335927, 335929) can be used for bacterial 5S/16S/23S rRNA removal with the SEQuoia Complete Stranded RNA Library Prep Kit (cat. nos. 17005726, 17005710). Upon receipt, the FastSelect 5S/16S/23S tube should be immediately stored at –30°C to –15°C in a constant-temperature freezer. All remaining components should immediately be stored in a refrigerator at 2–8°C.

Further information

- *QIAseq FastSelect –5S/16S/23S Handbook:* **www.qiagen.com/HB-2695**
- Safety Data Sheets: **www.qiagen.com/safety**
- Technical assistance: **support.qiagen.com**

Notes before starting

- The BioRad SEQuoia Complete Stranded RNA Library Prep Kit is required for use with this protocol.
- With this protocol, you can also add QIAseq FastSelect –rRNA HMR, QIAseq FastSelect –Globin, QIAseq FastSelect –rRNA Plant, and/or QIAseq FastSelect –rRNA Yeast. Any or all FastSelect products can be combined.
- Prewarm the QIAseq Beads and Bead Binding Buffer to room temperature (15–25°C) prior to use. Ensure that the QIAseq Beads are thoroughly mixed at all times: work quickly and resuspend the beads immediately before use. If a delay in the protocol occurs, simply vortex the beads.

Procedure

1. Thaw the template RNA on ice. Gently mix, briefly centrifuge to collect residual liquid from the sides of the tubes, and then return to ice.

2. Prepare the reagents required for the RNA fragmentation and QIAseq FastSelect rRNA removal:
   2a. Bring the FastSelect 5S/16S/23S, FastSelect FH Buffer, and nuclease-free water to room temperature.
   2b. Only for FastSelect 5S/16S/23S, incubate the tube at 37°C for 5 min, and then vortex to dissolve the precipitate.
   2c. Mix all other reagents vigorously by vortexing, and then briefly centrifuge.
3. On ice, prepare the fragmentation/depletion reaction according to Table 1. Briefly centrifuge, mix by pipetting up and down 10 times, and then centrifuge briefly again.

   Note: If setting up more than one reaction, prepare a volume of master mix that is 10% greater than the required amount for the total number of reactions.

Table 1. Setup of fragmentation/depletion reactions

Component	Volume/reaction
Total RNA	Variable
FastSelect FH Buffer	1.5 µL
FastSelect 5S/16S/23S*	1 µL
Nuclease-free water	Bring total reaction volume to 15 µL
Total volume	**15 µL***

* If needed, add 1 µL QIAseq FastSelect –rRNA HMR, 1 µL QIAseq FastSelect –Globin, 1 µL QIAseq FastSelect –rRNA Plant, and/or 1 µL QIAseq FastSelect –Yeast. To keep the total volume at 15 µL, correspondingly reduce the nuclease-free water by the volume of additional FastSelect products that have been added.

4. Incubate as described in Table 2.

   Important: Regardless of the time and temperature chosen in step 1, steps 2–9 must be performed.
5. Add 19.5 µL QIAseq Beads (prewarmed to room temperature and mixed by vortexing) to the 15 µL reaction. Mix thoroughly by vortexing, and then incubate for 5 min at room temperature.
6. Centrifuge in a table-top centrifuge until the beads are completely pelleted (~2 min).
7. Place the tubes/plate on a magnetic rack for 2 min. Once the solution has cleared, with the beads still on the magnetic stand, carefully remove and discard the supernatant.

Important: Do not discard the beads because they contain the RNA of interest.

8. Add 15 µL of nuclease-free water and 19.5 µL of QIAseq Bead Binding Buffer (prewarmed to room temperature and mixed by vortexing). Mix vigorously by vortexing, and then incubate for 5 min at room temperature.

Table 2. Combined QIAseq fragmentation and FastSelect hybridization protocol

Note	Step	Mean insert size
RNA fragmentation	1*	8 min at 89°C*†
Steps 2–9 are performed regardless of input RNA quality. They need to be performed whether the RNA is high quality, moderate quality, FFPE, or degraded.	2	2 min at 75°C
	3	2 min at 70°C
	4	2 min at 65°C
	5	2 min at 60°C
	6	2 min at 55°C
	7	2 min at 37°C
	8	2 min at 25°C
	9	Hold at 4°C

* For high-quality RNA (RIN ≥8), 8 min at 89°C is the basic recommendation. Alternatively, 4 min at 89°C provides an average insert size of ~325–375 bp, and 12 min at 89°C provides an average insert size of ~125–175 bp.

† If working with RNA with RIN values <8, please refer to Table 1 of *QIAseq FastSelect –5S/16S/23S Handbook* for fragmentation recommendations.

9. Centrifuge in a table-top centrifuge until the beads are completely pelleted (~2 min).
10. Place the tubes/plate on a magnetic rack for 2 min. Once the solution has cleared, with the beads still on the magnetic stand, carefully remove and discard the supernatant.
    Note: You can completely avoid transferring beads by pipetting very slowly.
    Important: Do not discard the beads because they contain the RNA of interest.
11. With the beads still on the magnetic stand, add 200 µL of 80% ethanol. Wait for 30 s. Carefully remove and discard the wash.
12. Repeat the ethanol wash.

    Important: Completely remove all traces of ethanol after this second wash. Remove the ethanol with a 200 µL pipette tip first, and then use a 10 µL pipette to remove any residual ethanol that will settle.

13. With the beads still on the magnetic stand, air-dry at room temperature for 6–10 min until all liquid has evaporated but without overdrying the beads.

    Note: Visually inspect the pellet to confirm that it is completely dry.

14. Remove the beads from the magnetic stand, and elute the RNA from the beads by adding 18 µL Nuclease-free water. Mix well by pipetting or vortexing, and then allow the tubes to sit at room temperature for 2 min to appropriately hydrate the beads.

15. Return the tubes/plate to the magnetic rack until the solution has cleared.

16. Transfer 16 µL of the supernatant to clean tubes/plate. Alternatively, the samples can be stored at –80°C in a constant-temperature freezer.

17. Refer to the *SEQuoia Complete Stranded RNA Library Prep Kit* instruction manual and:

    17a. Add 2 µL of Reagent A Fragmentation Mix to each sample.

    17b. Proceed to "End Repair Step".

    Note 1: The Fragmentation Mix is added, because it likely contains a critical reaction buffer.

    Note 2: Fragmentation is performed during the FastSelect portion of the workflow, so omit the SEQuoia fragmentation step.

    17c. Follow the *SEQuoia Complete Stranded RNA Library Prep Kit* instruction manual to perform all remaining library construction steps.

Document Revision History

Date	Changes
03/2023	Initial release

Scan QR code for handbook.

For up-to-date licensing information and product-specific disclaimers, see the respective QIAGEN kit handbook or user manual.