

Watchmaker mRNA Library Prep Kit

Product Description

The Watchmaker mRNA Library Prep Kit is designed for the highly streamlined preparation of stranded mRNA sequencing libraries from 2.5 ng to 1000 ng intact total eukaryotic RNA with high library complexity and low coverage bias.

The Watchmaker mRNA Library Prep Kit enriches for mature, polyadenylated mRNAs and converts those mRNAs to adapter-ligated, double-stranded cDNA fragments through a small number of chemical and enzymatic manipulations:

- Highly specific capture of full-length polyadenylated (poly(A)) RNA transcripts such as eukaryotic mRNA and some non-coding RNAs
- RNA fragmentation and priming for 1st strand cDNA synthesis
- 1st strand cDNA synthesis leveraging a specifically engineered reverse transcriptase
- Combined 2nd strand cDNA synthesis and A-tailing, during which dUTP is incorporated to maintain strand information
- Adapter ligation, where truncated, full-length, or custom adapters utilizing a 3' T overhang are ligated to fragments
- Library amplification with Equinox™ Amplification Master Mix (2X) for high-fidelity and high-efficiency PCR

Kit Contents

| Bundled kit | Kit | Kit code | Description | Component Volume | | |
|---|------------------------------------|--|---------------------------------------|---------------------|------------|---------|
| | | | | 24 rxn kit | 96 rxn kit | |
| Watchmaker mRNA Library Prep Kit 7BK0001-024 (24 rxn) 7BK0001-096 (96 rxn) | Watchmaker mRNA Capture Kit | 7K0105-024 (24 rxn) 7K0105-096 (96 rxn) | mRNA Capture Beads | 270 µL | 1.2 mL | |
| | | | Bead Prep Buffer | 2.8 mL | 12 mL | |
| | | | Capture Buffer | 9.5 mL | 37 mL | |
| | | | | Final Wash Buffer | 6.8 mL | 27 mL |
| | | | | Frag & Prime Buffer | 290 µL | 1.3 mL |
| | | | | 1st Strand Buffer | 240 µL | 1.08 mL |
| | | | | 1st Strand Enzyme | 30 µL | 120 µL |
| | | | | 2nd Strand Buffer | 370 µL | 1.68 mL |
| | | | | 2nd Strand Enzyme | 30 µL | 120 µL |
| | Watchmaker RNA Library Prep Kit | 7K0078-024 (24 rxn) 7K0078-096 (96 rxn) | Ligation Buffer | 1.06 mL | 4.8 mL | |
| | | | Ligation Enzyme | 140 µL | 600 µL | |
| | | | Equinox Amplification Master Mix (2X) | 690 µL | 3 mL | |
| | | | P5/P7 Primer Mix (10X) | 144 µL | 600 µL | |
| | | | FFPE Treatment Buffer ¹ | 140 µL | 600 µL | |

¹The FFPE Treatment Buffer is not required or recommended for mRNA library preparation. When used on its own or in conjunction with the Polaris™ Depletion Kit, the Watchmaker RNA Library Prep Kit is compatible with the FFPE samples.

For custom formats, contact the **Sales Team** at sales@watchmakergenomics.com.

Table of Contents

| | |
|---|----|
| Product Description | 1 |
| Kit Contents | 1 |
| Product Applications | 2 |
| Storage and Handling | 2 |
| Workflow Overview | 2 |
| Required Materials not Included | 3 |
| Prior to Starting | 3 |
| Library Construction Protocol | 5 |
| Appendix A: Amplification with Paramagnetic Purification Beads | 12 |
| Revision History | 12 |

Product Applications

This workflow was developed to address the highly specific needs of mRNA sequencing and the associated areas of variant calling, isoform and gene fusion identification, and gene expression analysis. These applications require high library complexity, low bias, uniform coverage, and minimal experimental variability in order to support robust sensitivity, specificity, and reproducibility.

This library preparation kit is ideally suited for:

- Gene expression analysis
- Isoform/splice variant/gene fusion identification
- Single nucleotide variant detection
- Novel transcript discovery
- Workflows that employ unique molecular identifiers (UMIs) for improved sensitivity

Storage and Handling

The Watchmaker mRNA Library Prep Kits are shipped on cold packs. **Upon receipt, store the Watchmaker mRNA Capture Kit (K0105) at 4°C and the Watchmaker RNA Library Prep Kit (K0078) at -20 ± 5°C.**

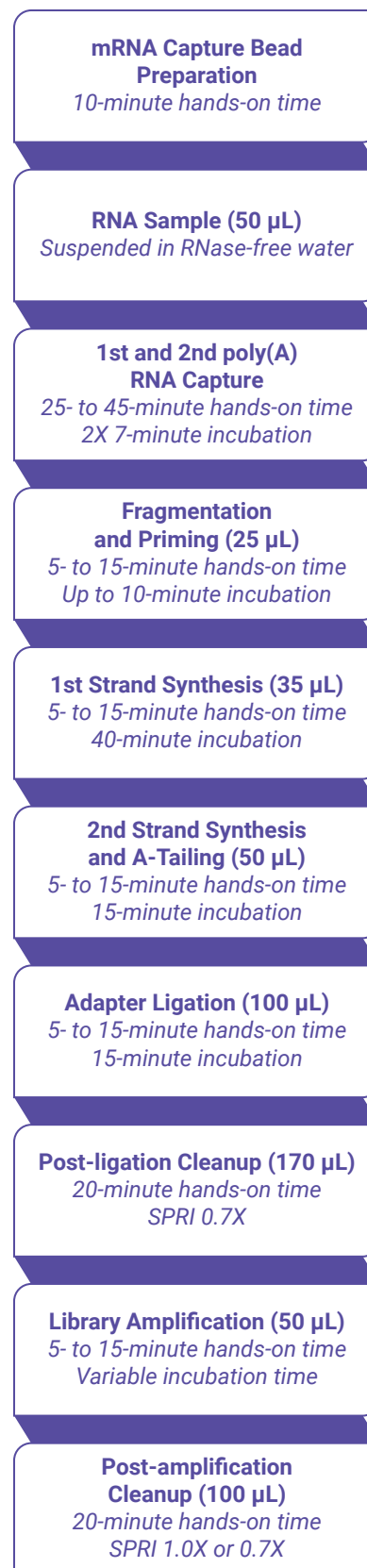
Some components are viscous; therefore, take care to homogenize solutions thoroughly before use and during reaction setup. SPRI beads should be handled as per the manufacturer's guidelines.

Buffers in the Watchmaker mRNA Capture Kit should be mixed by inverting the tubes and NOT by vortexing to prevent foaming. All buffers in the Watchmaker RNA Library Prep Kit should be vortexed for at least 5 sec before use.

Enzymes and the Equinox Amplification Master Mix (2X) should be inverted ten times prior to use. The 1st Strand Buffer is photosensitive. Keep it in the kit box until thawing is required. Take care to protect it from direct sunlight while thawing and in use.

All master mixes (buffer and enzyme combined) prepared in the protocol should be stored at 4°C unless stated otherwise. The master mixes should be stable for up to 24 hours at 4°C.

Workflow Overview



Required Materials not Included

- Adapters (see **Prior to Starting**)
- Adapter diluent (e.g., 10 mM Tris-HCl, pH 8.0, 10 mM NaCl)
- Magnetic rack compatible with 0.2 mL PCR tubes and/or 96-well plate
- Magnetic rack compatible with 1.5 – 2 mL microtubes
- Ampure® XP Beads (Beckman Coulter, Inc. #A63881) or equivalent
- 80% Ethanol
- 200 µL thin-wall PCR tubes compatible with thermocycler, or 96-well 0.2 mL PCR Plates and Plate-Seal
- 1 mL, 2 mL, 5 mL microtubes (RNase-free)
- RNase-free water
- 10 mM Tris-HCl, pH 8.0
- Thermocycler
- Vortex mixer and/or plate vortexer
- Plate centrifuge and/or benchtop picofuge
- Fragment Analyzer™, Bioanalyzer®, TapeStation (Agilent Technologies, Inc.), or similar instrument and consumables

These protocols are designed for use with the specified labware, consumables, and calibrated equipment.

Prior to Starting

Input RNA Quality and Quantity

This kit is compatible with intact (RIN >7) total RNA samples suspended in 50 µL of RNase-free water.

High-quality total RNA ranging from 2.5 – 1000 ng has been tested and shown to produce high-performing libraries.

RNA should be accurately quantified by Qubit® Fluorometer or similar prior to starting.

Assess total RNA quality via an electrophoretic method, such as Agilent BioAnalyzer or TapeStation.

ERCC RNA Spike-In Controls are not recommended for use with the Watchmaker mRNA Library Prep Kit due to their short poly(A) tails (20 – 26 nt long), which do not imitate typical polyadenylated RNA transcripts. If ERCC RNA Spike-In Controls are included, a lower number of reads mapping to ERCCs is expected due to lower efficiency hybridization to the oligo dT.

Input RNA Purity

RNA inputs should be free from contaminating DNA. If the total RNA contains DNA, remove the contamination by incubating with DNase I (not supplied with kit). Residual DNase I may interfere with library preparation, so it is important to ensure no residual enzyme remains in the sample.

RNA should be suspended in RNase-free water and be free of salts (e.g., Mg²⁺, or guanidinium salts), chelating agents (e.g., EDTA or EGTA), and organics (e.g., phenol or ethanol).

RNA Handling

To avoid RNase contamination, work in a laminar flow hood, if available, and keep all sample and reagent tubes closed unless in use. Wear gloves when handling reagents and preparing libraries. Change gloves and pipette tips if they come into contact with non-sterile surfaces.

To avoid RNA degradation, store RNA in an RNase-free diluent and limit the number of sample freeze-thaw cycles.

Insert Size

The standard protocol targets ~200 bp inserts.¹ When targeting ~300 bp inserts, add 2 extra cycles of PCR amplification (**Step 10**) and make use of a 0.7X post-amplification SPRI cleanup (**Step 11.2**).

Mixing Considerations

The Watchmaker mRNA Library Prep Kit has been developed to provide robust and reproducible data when employing either vortex or pipette mixing.

¹As assessed by Illumina NovaSeq (Picard mean insert size)

It is recommended to make use of vortexing (2,000 rpm on an appropriate vortex mixer) where possible as it provides uniform and reproducible mixing of samples. Tubes and/or plates should be sealed prior to vortexing and briefly centrifuged after vortexing. Extreme care should be taken to ensure that no residual droplets remain on the side or at the top of tubes and/or plates after centrifuging.

For automation, or if access to an appropriate vortex mixer is not available, use pipette mixing. Samples should be pipetted carefully to minimize foaming and tubes/plates briefly centrifuged after mixing.

Adapters

This kit is compatible with adapters that have a 3' overhanging T to facilitate adapter orientation during dscDNA ligation. Note that adapter quality impacts overall library preparation efficiency. Ensure that adapters are adequately duplexed and at the appropriate concentration prior to use.

When using 'stubby', adapters where sample indexes are added during subsequent library amplification, user-supplied, uniquely indexed PCR primers will be required for the amplification of each library to be sequenced on the same flow cell.

Stubby adapters provide improved library prep efficiency due to the ability to include them at increased concentrations in the ligation reaction. We strongly recommend the use of stubby adapters for maximum performance.

This workflow is also compatible with full-length adapters where sample indexes are added during ligation. When using full-length adapters, a unique sample index is required for all samples to be sequenced on the same flow cell. Refer to the technical documentation provided by the adapter vendor for recommendations on optimal pooling.

Contact support@watchmakergenomics.com for more details and our Adapter Recommendations Guide.

P5/P7 Amplification Primers

The P5/P7 Primer Mix (10X) is supplied at a concentration of 20 μ M of each primer and is appropriate for the amplification of full-length adapter-ligated libraries.

P5: AATGATACGGCGACCACCGA

P7: CAAGCAGAAGACGGCATAACGAGAT

User-supplied Amplification Primers

When using truncated, or 'stubby', adapters in multiplexed

sequencing workflows, a uniquely barcoded primer mix will be required (and must be added individually) for each library to be sequenced on the same flow cell.

Primers should always use equimolar concentrations of the forward and reverse primers. A primer pre-mix containing 20 μ M of each primer (resulting in a final concentration of 2 μ M each in the amplification reaction) is recommended.

Primers may also incorporate chemical modifications (e.g., one or more 3'-phosphorothioate bonds) to improve specificity.

Use a buffered solution, such as 10 mM Tris-HCl, pH 8.0, to store and dilute primers. Limit the number of freeze-thaw cycles.

Library Amplification Optimization

Annealing Temperature

For the truncated adapter scheme detailed in Glenn, et al. 2019,² use an annealing temperature of 55°C. For other primers, an annealing temperature gradient (55°C to 70°C) may be performed to determine the optimal condition for amplification.

Extension Time

Longer extension times may be employed to ensure efficient amplification of longer-insert libraries. A 30-sec extension is sufficient for libraries with a mode fragment size up to 500 bp; a 45-sec extension time is recommended for libraries with mode fragment sizes >500 bp. The optimal condition for each application may have to be determined empirically.

Cycle Number

This protocol provides a starting point for PCR cycle number optimization based on RNA input into library preparation and insert size. Adapter-ligated libraries may be quantified by qPCR or estimated by other means or methods to determine the optimal number of amplification cycles for the desired library yield.

SPRI Purification Beads

The protocol outlined below assumes the use of AMPure XP (Beckman Coulter) reagent for bead purification steps.

Other SPRI bead brands may be used, assuming they are nuclease-free and deliver equivalent sizing performance at the given bead ratios. Otherwise, bead purification ratios will need to be optimized for the bead brand used.

Ensure beads are equilibrated to room temperature and thoroughly resuspended via vortexing prior to use.

²Glenn TC, Nilsen RA, Kieran TJ, et al. Adapterama I: universal stubs and primers for 384 unique dual-indexed or 147,456 combinatorially-indexed Illumina libraries (iTru & iNext). *PeerJ*. 2019;7:e7755. Published 2019 Oct 11. doi:10.7717/peerj.7755]

Library Construction Protocol

Recommendations

- All mRNA Capture components should be equilibrated to room temperature for 20 minutes and inverted several times before use.

NOTE: Do NOT vortex Watchmaker mRNA Capture Kit buffers.

- Ensure all Watchmaker RNA Library Prep Kit buffers are fully thawed on ice before use. Once thawed, invert the tubes several times, and vortex for at least 5 sec to ensure the reagent is fully mixed.
- The Fragmentation & Priming Master mix (**Step 4.1**) may be prepared ahead of time and stored on ice before use.
- Place enzymes and the Equinox Amplification Master Mix (2X) on ice before use. Invert the tubes 10 times to mix.
- Vortexing is recommended for reaction mixing throughout. Where possible, centrifuge briefly to remove any excess liquid from the tubes and collect all liquid in the tube lids prior to opening them—see **Prior to Starting: Mixing Considerations**.
- We recommend making master mixes for each enzymatic reaction step with a 10% excess to account for loss during pipetting.
- Ensure SPRI purification beads are fully equilibrated to room temperature and thoroughly resuspended by vortexing prior to use.

1. RNA and mRNA Capture Bead Preparation

- After thawing on ice, dilute the total RNA sample to a final volume of 50 μL with RNase-free water.
- Vortex mRNA Capture Beads until all beads are well resuspended (5 – 10 secs).
- Prepare the mRNA Capture Beads in bulk by aliquoting 10.5 μL of beads (10 μL + 5% excess) per reaction into a microtube.

NOTE: A recommended maximum of 28 or 36 reactions can be prepared in a 1.5 mL and 2 mL tube, respectively. Multiple tubes, or larger microtubes, may be required depending on the number of reactions.

- Place the tube on the magnetic rack at room temperature for 2 min or until the solution is clear.
- Remove and discard all of the storage buffer from the tube. Take care not to disturb the beads.
- Remove the tube from the magnetic rack and keep at room temperature.
- Wash the beads by adding 52.5 μL of Bead Prep Buffer per reaction to the bulk beads from **Step 1.6**. Pipette mix at the highest feasible volume ≥ 10 times to fully resuspend the beads. Take care to avoid foaming.
- Place the tube on the magnetic rack at room temperature for 2 min or until the solution is clear.
- Remove and discard all of the Bead Prep Buffer from the tube. Take care not to disturb the beads.
- Remove the tube from the magnetic rack and keep at room temperature.
- Add 52.5 μL of Bead Prep Buffer per reaction to the bulk beads from **Step 1.10**. Pipette at the highest feasible volume ≥ 10 times to fully resuspend the beads. Take care to avoid foaming.
- Store the washed mRNA Capture Beads at room temperature and proceed to **1st Poly(A) RNA Capture**.

NOTE: Washed beads from **Step 1.11** can be stored in the Bead Prep Buffer for up to 1 week at 4°C. Ensure beads are fully resuspended after storage before continuing.

2. 1st Poly(A) RNA Capture

- Program a thermocycler as indicated below and initiate the run to heat the block:

NOTE: This thermocycler program is used again in **Step 3.1**.

| Step | Temperature | Time |
|-----------------|-------------|-------|
| Lid temperature | 80°C | N/A |
| HOLD | 25°C | HOLD |
| Denaturation | 75°C | 2 min |
| Hybridization | 25°C | 5 min |
| HOLD | 25°C | HOLD |

2.2 To each tube, add the following:

| Component | Volume (μL) |
|---|-------------|
| RNA sample | 50 |
| Washed mRNA Capture Beads (from Step 1.12) | 50 |

2.3 Mix on an appropriate vortex mixer (2,000 rpm) for 5 sec. Briefly centrifuge to collect all liquid in the bottom of the tubes.

WORKFLOW: If pipette mixing, mix the reaction 10 times with a pipette set to 80 μL. Briefly centrifuge if possible. See **Prior to Starting: Mixing Considerations**.

2.4 Place the tubes into the preheated thermocycler (programmed and initiated in **Step 2.1**). Advance the thermocycler from the initial 25°C hold.

2.5 Upon completion of thermocycling, place the tubes on the magnetic rack at room temperature for 2 min, or until the beads have collected on the side of the tubes.

2.6 While on the magnet, remove and discard all of the supernatant from each tube. Avoid disturbing the beads.

2.7 While on the magnet, and without disturbing the beads, gently add 180 μL Capture Buffer to the tubes. If using a 0.3 mL tube, then use 250 μL to fill tube capacity. **This is to remove any remaining uncaptured RNA adsorbed to the tubes.**

2.8 While still on the magnet, remove and discard all of the supernatant from each tube. Avoid disturbing the beads.

2.9 Remove the tubes from the magnetic rack and add 100 μL of Capture Buffer to each tube.

2.10 Mix on an appropriate vortex mixer (2,000 rpm) for 5 sec to resuspend the beads. Briefly centrifuge to collect all liquid in the bottom of the tubes.

WORKFLOW: If pipette mixing, mix the reaction 10 times with a pipette set to 80 μL to fully resuspend the beads in the Capture Buffer and to avoid excessive foaming. Briefly centrifuge if possible. See **Prior to Starting: Mixing Considerations**.

2.11 Proceed immediately to **2nd Poly(A) RNA Capture**.

3. 2nd Poly(A) RNA Capture

3.1 Program a thermocycler as indicated below and initiate the run to heat the block:

| Step | Temperature | Time |
|-----------------|-------------|-------|
| Lid temperature | 80°C | N/A |
| HOLD | 25°C | HOLD |
| Denaturation | 75°C | 2 min |
| Hybridization | 25°C | 5 min |
| HOLD | 25°C | HOLD |

3.2 Place the tubes into the preheated thermocycler (programmed and initiated in **Step 3.1**). Advance the thermocycler from the initial 25°C hold.

3.3 Upon completion of thermocycling, place the tubes on the magnetic rack at room temperature for 2 min.

3.4 Remove and discard all of the supernatant from each tube. Avoid disturbing the beads.

3.5 While on the magnet, and without disturbing the beads, gently add 180 μL Final Wash Buffer to the tubes. If using a 0.3 mL tube, then use 250 μL to fill tube capacity. **This is to remove any remaining uncaptured RNA adsorbed to the tubes.**

3.6 While on the magnet, remove and discard all of the supernatant from the tubes. Avoid disturbing the beads.

NOTE: Any remaining Final Wash Buffer in the tubes will dilute the poly(A) RNA proceeding into Library Preparation, but will not negatively impact the Library Preparation chemistry.

3.7 Remove the tubes from the magnetic rack and proceed immediately with **Fragmentation and Priming**.

4. Fragmentation and Priming

4.1 Prepare the Frag & Prime Master Mix as follows for each reaction:

| Component | Volume (μL) |
|---------------------|-------------|
| Frag & Prime Buffer | 10.8 |
| RNase-free water | 16.2 |

- 4.2 Mix on a touch vortex mixer (2,000 to 3,000 rpm) for 4 sec. Briefly centrifuge to collect all liquid in the bottom of the tube.
- 4.3 Add 27 μ L of the Frag & Prime Master Mix to the beads from **Step 3.7**.
- 4.4 Mix on an appropriate vortex mixer (2,000 to 3,000 rpm) for 4 sec to resuspend the beads. Briefly centrifuge to collect all liquid in the bottom of the tubes.

WORKFLOW: If pipette mixing, mix the reaction 10 times with a pipette set to 25 μ L to resuspend the beads in the Frag & Prime Master Mix. Briefly centrifuge if possible. See **Prior to Starting: Mixing Considerations**.

- 4.5 Program a thermocycler as indicated below, and initiate the run to hold at 4°C:

NOTE: Insert size is adjusted through modulating the Post-amplification SPRI ratio (**Step 11.2**) and amplification cycles (**Step 10**). Irrespective of insert size required, the RNA Fragmentation conditions remain the same. See **Prior to Starting: Insert Size** for more details.

| Step | Temperature | Time |
|-------------------|-------------|--------|
| Lid temperature | 105°C | N/A |
| Pre-cooling | 4°C | HOLD |
| RNA Fragmentation | 85°C | 10 min |
| HOLD (Priming) | 12°C | HOLD |

- 4.6 Place the tubes into the preheated thermocycler. Advance the thermocycler from the initial 4°C hold to start the RNA Fragmentation incubation.
- 4.7 After the program has finished and the samples have returned to 12°C, place the tubes on a magnet for at least 2 min, or until all beads have been collected on the tube walls and the solution is clear.
- 4.8 Carefully remove 25 μ L of the supernatant, transfer to fresh, labeled tubes, and proceed immediately to **1st Strand Synthesis**.

NOTE: Take care not to disturb the beads, as bead carryover can interfere with 1st Strand Synthesis.



Safe stopping point. Samples can be frozen at -20°C for <24 hours.

5. 1st Strand Synthesis

NOTE: The 1st Strand Buffer is photosensitive. Keep it in the kit box until thawing is required. Take care to protect it from direct sunlight while thawing and in use.

- 5.1 Program a thermocycler as indicated below and initiate the run to cool the block:

| Step | Temperature | Time |
|-----------------|-------------|--------|
| Lid temperature | 105°C | N/A |
| Pre-cooling | 4°C | HOLD |
| cDNA synthesis | 25°C | 10 min |
| | 42°C | 15 min |
| RT inactivation | 70°C | 15 min |
| HOLD | 4°C | HOLD |

- 5.2 For each reaction, prepare the 1st Strand Master Mix as follows on ice:

| Component | Volume (μ L) |
|-------------------|-------------------|
| 1st Strand Buffer | 9 |
| 1st Strand Enzyme | 1 |

- 5.3 Mix on a touch vortexer (2,000 to 3,000 rpm) for 4 sec. Briefly centrifuge to collect all liquid in the bottom of the tubes.
- 5.4 To each tube, add the 1st Strand Master Mix as specified below on ice:

| Component | Volume (μ L) |
|--|-------------------|
| Fragmented RNA (from Step 4.8) | 25 |
| 1st Strand Master Mix | 10 |

- 5.5 Mix on an appropriate vortex mixer (2,000 to 3,000 rpm) for 4 sec. Briefly centrifuge to collect all liquid in the bottom of the tubes.
- 5.6 Place reactions in the chilled thermocycler (programmed and initiated in **Step 5.1**). Advance the thermocycler from the initial 4°C hold to start the 25°C incubation.
- 5.7 Once the 1st Strand Synthesis reaction has completed, place the tubes on ice or leave in the thermocycler at 4°C. Proceed immediately to **2nd Strand Synthesis and A-Tailing**.

6. 2nd Strand Synthesis and A-Tailing

- 6.1 Program a thermocycler as indicated below and initiate the run to cool the block:

| Step | Temperature | Time |
|----------------------|-------------|--------|
| Lid temperature | 80°C | N/A |
| Pre-cooling | 4°C | HOLD |
| 2nd Strand Synthesis | 42°C | 5 min |
| A-Tailing | 62°C | 10 min |
| HOLD | 4°C | HOLD |

- 6.2 For each reaction, prepare the 2nd Strand Master Mix as follows on ice:

| Component | Volume (μL) |
|-------------------|-------------|
| 2nd Strand Buffer | 14 |
| 2nd Strand Enzyme | 1 |

- 6.3 Mix on a touch vortexer (2,000 to 3,000 rpm) for 4 sec. Briefly centrifuge to collect all liquid in the bottom of the tubes.
- 6.4 To each tube, add the 2nd Strand Master Mix as specified below on ice:

| Component | Volume (μL) |
|------------------------------|-------------|
| 1st Strand Synthesis product | 35 |
| 2nd Strand Master Mix | 15 |

- 6.5 Mix on an appropriate vortex mixer (2,000 to 3,000 rpm) for 4 sec. Briefly centrifuge to collect all liquid in the bottom of the tubes.
- 6.6 Place reactions in the chilled thermocycler (programmed and initiated in **Step 6.1**). Advance the thermocycler from the initial 4°C hold to start the 42°C incubation.
- 6.7 Proceed to adapter ligation after the program has finished and the samples have returned to 4°C. Proceed immediately to **Adapter Ligation**.

7. Adapter Ligation

NOTE: See **Prior to Starting** for considerations in adapter selection and design.

- 7.1 Program a thermocycler as indicated below:

| Step | Temperature | Time |
|-----------------|-------------|-------------------|
| Lid temperature | OFF | N/A |
| Pre-cooling | 4°C | HOLD |
| Ligation | 20°C | 15 min |
| HOLD | 4°C | HOLD ¹ |

¹Maintain samples on ice following ligation to reduce adapter-dimer formation prior to **Post-ligation Cleanup**.

- 7.2 Vortex the thawed Ligation Buffer for 20 sec to fully homogenize the solution before centrifuging to collect all of the solution at the bottom of the tubes and placing it on ice.
- 7.3 Using an appropriate diluent (e.g., 10 mM Tris-HCl, pH 8.0, 10 mM NaCl), prepare the required volume of each adapter at the concentration specified in either **Table 1** or **Table 2** based on adapter design. 5 μL of adapter at the appropriate concentration is required per ligation reaction.

NOTE: Storing adapter solutions at concentrations <10 μM for extended periods of time is not recommended.

Table 1. Full-length adapter concentration by RNA input into library prep

| RNA input (ng) | Adapter concentration (μM) |
|------------------|----------------------------|
| ≤50 ¹ | 0.3 |
| 51 – 150 | 1 |
| 151 – 1000 | 4 |

¹A second post-ligation cleanup (**Step 9**) is recommended for inputs of 50 ng and lower when using full-length adapters.

Table 2. Truncated ('stubby') adapter concentration by RNA input into library prep

| RNA input (ng) | Adapter concentration (μM) |
|------------------|----------------------------|
| ≤10 ¹ | 1 |
| 11 – 250 | 4 |
| 251 – 1000 | 10 |

¹A second post-ligation cleanup (**Step 9**) is recommended for inputs of 10 ng and lower when using 'stubby' adapters.

- 7.4 Add 5 μL of appropriately diluted adapter to each tube (**Step 6.7**).

7.5 Prepare the Ligation Master Mix as follows:

| Component | Volume (μL) |
|-----------------|-------------|
| Ligation Buffer | 40 |
| Ligation Enzyme | 5 |

7.6 Mix on a touch vortexer (2,000 or 3,000 rpm) for 4 sec. Briefly centrifuge to collect all liquid in the bottom of the tubes.

7.7 To each tube, add the Ligation Master Mix as specified below on ice:

| Component | Volume (μL) |
|--|-------------|
| 2nd Strand Synthesis product and adapter | 55 |
| Ligation Master Mix | 45 |

7.8 The Ligation Master Mix is viscous. Carefully pipette a minimum volume of 80 μL up and down a minimum of 10 times. Briefly centrifuge if needed to collect all liquid in the bottom of the tubes.

7.9 Place the tubes in the thermocycler and initiate the program (programmed in **Step 7.1**).

7.10 Once the program has completed, proceed immediately to **Post-ligation Cleanup**.

8. Post-ligation Cleanup

8.1 Freshly prepare at least 0.4 mL of an 80% ethanol solution for each reaction.

8.2 Vortex **room temperature** SPRI beads to thoroughly mix. Add 70 μL (0.7X) of room temperature resuspended beads to each ligation reaction.

8.3 Mix on an appropriate vortex mixer (2,000 or 3,000 rpm) for 4 sec. Briefly centrifuge to collect all liquid in the bottom of the tubes.

8.4 Incubate the library-bead mixtures at room temperature for at least 5 min to maximize library recovery.

8.5 Place tubes on a magnet for at least 5 min, or until all beads have been collected on the tube walls and the solution is clear.

8.6 Carefully remove and discard the supernatant from each tube.

8.7 Add 200 μL of freshly prepared 80% ethanol to each tube, taking care to not disturb the bead pellet on the tube walls.

8.8 Incubate tubes at room temperature for at least 30 sec without removing them from the magnet or disturbing the bead pellet. Carefully remove and discard the ethanol.

8.9 Repeat **Steps 8.7 – 8.8**, for a total of two washes.

OPTIONAL: Tubes can be briefly centrifuged to pull down excess ethanol prior to removal with a P10 pipette.

8.10 Allow remaining ethanol to evaporate by allowing the pellets to air dry for 3 – 5 min.

NOTE: Beads have been sufficiently dried when cracks appear in the surface of the bead pellet and no liquid is visible in the tubes. Residual trace ethanol in the library amplification reaction may decrease performance.

8.11 Remove tubes from the magnet and carefully resuspend each bead pellet in 22 μL of 10 mM Tris-HCl, pH 8.0.

8.12 Incubate tubes at room temperature for at least 2 mins before placing back on the magnet.

8.13 Leave tubes on the magnet for at least 2 min, or until all beads have collected on the tube walls and the solution is clear.

8.14 Carefully transfer 20 μL of each library-containing supernatant to a new, labeled tube.



Safe stopping point. Samples can be stored at 4°C for <24 hours or frozen at -20°C for up to 4 weeks.

9. 2nd Post-ligation Cleanup (Optional)

NOTE: This is an optional step and only recommended when working with:

- Full-length adapters and equal to or lower than 50 ng of RNA.
- Truncated ('stubby') adapters and equal to or lower than 10 ng of RNA.

9.1 Freshly prepare at least 0.4 mL of an 80% ethanol solution for each reaction.

9.2 Vortex room temperature SPRI beads to thoroughly mix. Add 20 μL (1X) of room temperature resuspended beads to each eluted library from **Step 8.14**.

9.3 Mix on an appropriate vortex mixer (2,000 to 3,000 rpm) for 4 sec. Briefly centrifuge to collect all liquid in the bottom of the tubes.

- 9.4 Incubate the library-bead mixtures at room temperature for at least 5 min to maximize library recovery.
- 9.5 Place tubes on a magnet for at least 5 min, or until all beads have been collected on the tube walls and the solution is clear.
- 9.6 Carefully remove and discard the supernatant from each tube.
- 9.7 Add 200 μ L of freshly prepared 80% ethanol to each tube, taking care to not disturb the bead pellet on the tube walls.
- 9.8 Incubate tubes at room temperature for at least 30 sec without removing the tubes from the magnet or disturbing the bead pellet. Carefully remove and discard the ethanol.
- 9.9 Repeat **Steps 9.7 – 9.8** for a total of two washes.
OPTIONAL: Tubes can be briefly centrifuged to pull down excess ethanol prior to removing with a p10 pipette.
- 9.10 Allow remaining ethanol to evaporate by allowing the pellets to air dry for 3 – 5 min.
NOTE: Beads have been sufficiently dried when cracks appear in the surface of the bead pellet and no liquid is visible in the tubes. Residual trace ethanol in the library amplification reaction may decrease performance.
- 9.11 Remove tubes from the magnet and carefully resuspend each bead pellet in 22 μ L of 10 mM Tris-HCl, pH 8.0.
- 9.12 Incubate tubes at room temperature for at least 2 min before placing back on the magnet.
- 9.13 Leave tubes on the magnet for at least 2 min, or until all beads have collected on the tube walls and the solution is clear.
- 9.14 Carefully transfer 20 μ L of each library-containing supernatant to a new, labeled tube.



Safe stopping point. Samples can be stored at 4°C for <24 hours or frozen at -20°C for up to 4 weeks.

10. Library Amplification and Strand Selection

- Library amplification is required for strand-specific sequencing regardless of adapter configuration used.
- If your workflow requires library amplification in the presence of paramagnetic beads, refer to **Appendix A** for bead compatibility.

10.1 Thaw and equilibrate the Equinox Amplification Master Mix (2X) on ice. Once thawed, invert several times or swirl vigorously to mix (**DO NOT VORTEX**).

10.2 Program a thermocycler as indicated below:

| Step ¹ | Temperature | Time | Cycles |
|----------------------|--|-------------|--------------------|
| Initial denaturation | 98°C | 45 sec | 1 |
| Denaturation | 98°C | 15 sec | |
| Annealing | P5/P7 primers: 60°C ² Indexed primers: 55°C ³ | 30 sec | See Table 3 |
| Extension | 72°C | 30 – 45 sec | |
| Final extension | 72°C | 60 sec | 1 |
| – | 12°C | HOLD | 1 |

¹For additional details on optimizing amplification, see **Prior to Starting**.

²Appropriate temperature for P5/P7 Primer Mix (10X).

³For the truncated adapter scheme detailed in Glenn et. al. 2019, use 55°C. Optimization may be required for other adapter/primer configurations, see **Prior to Starting**.

Table 3. Recommended PCR cycle numbers by RNA amount input into library prep

| RNA input into Library Preparation (ng) | PCR cycles to generate 10 – 50 nM library ¹ |
|---|--|
| 251 – 1000 | 8 – 9 |
| 101 – 250 | 10 – 12 |
| 51 – 100 | 12 – 13 |
| 11 – 50 | 13 – 15 |
| 2.5 – 10 | 16 – 18 |

¹**INSERT SIZE NOTE:** An extra 2 PCR cycles are required when targeting 290 to 310 bp inserts using a 0.7X post-amplification cleanup (Step 11.2).

NOTE: An extra 2 PCR cycles are required when targeting 290 to 310 bp inserts using a 0.7X post-amplification cleanup (**Step 11.2**).

- 10.3 Assemble each amplification reaction in the order specified below:

| Component | Volume (μL) |
|--|-------------|
| Adapter-ligated library | 20 |
| P5/P7 Primer Mix (10X) or User-supplied primers ¹ | 5 |
| Equinox Amplification Master Mix (2X) | 25 |

¹See **Prior to Starting** for more information on user-supplied primers.

- 10.4 Mix on an appropriate vortex mixer (2,000 to 3,000 rpm) for 4 sec. Briefly centrifuge to collect all liquid in the bottom of the tubes.
- 10.5 Place tubes in the thermocycler (programmed in **Step 10.2**) and initiate the program.
- 10.6 Once the program has completed, proceed immediately to **Post-amplification Cleanup**.

11. Post-amplification Cleanup

- 11.1 Freshly prepare at least 0.4 mL of an 80% ethanol solution for each reaction.
- 11.2 Vortex **room temperature** SPRI beads to thoroughly mix. Add 50 μL (1X) of room temperature resuspended beads to each ligation reaction.
- INSERT SIZE NOTE:** When targeting 290 – 310 bp inserts, add 35 μL (a 0.7X ratio) of room temperature resuspended beads to each ligation reaction.
- 11.3 Mix on an appropriate vortex mixer (2,000 to 3,000 rpm) for 4 sec. Briefly centrifuge to collect all liquid in the bottom of the tubes.
- 11.4 Incubate the library-bead mixtures at room temperature for at least 5 min to maximize library recovery.
- 11.5 Place tubes on a magnet for at least 5 min, or until all beads have been collected on the tube walls and the solution is clear.
- 11.6 Carefully remove and discard the supernatant from each tube.

- 11.7 Add 200 μL of freshly prepared 80% ethanol to each tube, taking care to not disturb the bead pellet on the tube wall.

- 11.8 Incubate tubes at room temperature for at least 30 sec without removing them from the magnet or disturbing the bead pellet. Carefully remove and discard the ethanol.

- 11.9 Repeat **Steps 11.7 – 11.8** for a total of two washes.

OPTIONAL: Tubes can be briefly centrifuged to pull down excess ethanol prior to removing with a P10 pipette.

- 11.10 Allow remaining ethanol to evaporate by allowing the pellets to air dry for 3 – 5 min.

NOTE: Beads have been sufficiently dried when cracks appear in the surface of the bead pellet and no liquid is visible in the tubes. Residual trace ethanol in the library amplification reaction may decrease performance.

- 11.11 Remove tubes from the magnet and carefully resuspend each bead pellet in 22 μL of 10 mM Tris-HCl, pH 8.0.

- 11.12 Incubate tubes at room temperature for at least 2 min before placing back on the magnet.

- 11.13 Leave tubes on the magnet for at least 2 min, or until all beads have collected on the tube wall and the solution is clear.

- 11.14 Carefully transfer 20 μL of each library-containing supernatant to a new, labeled tube.

- 11.15 At this point, libraries are ready for quantification, normalization, pooling, hybrid capture, and/or sequencing.

NOTE: We recommend quantifying libraries using qPCR and analyzing quality and sizing using capillary electrophoresis prior to preparing the libraries for sequencing.

Appendix A: Amplification with Paramagnetic Purification Beads

For some library preparation workflows, it may be preferred or advantageous to perform PCR in the presence of paramagnetic purification beads. For example, in hybrid capture workflows, post-capture amplification may be performed by adding PCR mix directly to the capture beads with bound library, eliminating an elution step. Alternatively, libraries may be eluted directly from SPRI beads in the PCR reaction mixture.

We have found paramagnetic purification beads to fall into three categories of compatibility with PCR

and sequencing based on their surface chemistry: Group I—fully compatible, Group II—potentially inhibitory, and Group III—incompatible. While Group II beads are inhibitory to non-optimized PCR systems, Equinox Amplification Master Mix (2X) has been optimized to allow amplification in the presence of both Group I and Group II beads, with no observable loss in performance (e.g., efficiency, uniformity, or fidelity). Equinox Amplification Master Mix (2X) and other library amplification systems are not compatible with the extreme inhibition characterized by Group III beads. Table A details the various paramagnetic bead types evaluated.

Table A. Paramagnetic purification bead types

| Bead type | Vendor | Catalog number | Compatibility/ amount tested* |
|---|--------------------------------|----------------|-------------------------------|
| Group I (Tosyl-activated beads) | | | |
| Dynabeads™ M280 Streptavidin | Thermo Fisher | 11205D | 500 µg |
| Dynabeads MyOne™ Streptavidin T1 | Thermo Fisher | 65601 | 500 µg |
| Group II (Carboxylic acid-activated beads) | | | |
| Dynabeads M270 Streptavidin** | Thermo Fisher | 65305 | 500 µg |
| SPRI | Various, incl. Beckman Coulter | A63882 | 100 µL |
| Dynabeads MyOne Streptavidin C1 | Thermo Fisher | 65001 | 500 µg |
| Group III (Not compatible with PCR) | | | |
| Dynabeads M270 Carboxylic Acid | Thermo Fisher | 14305D | 500 µg |

*Volume of slurry or mass of beads per 50 µL amplification reaction.

**Used in xGen Hybridization and Wash Kit (Integrated DNA Technologies).

Revision History

| Version | Description | Date |
|---------|---|---------|
| 1.0 | • First protocol release | 08/2023 |
| 1.1 | • Typographical error corrected in Step 2.7 to Capture Buffer instead of Final Wash Buffer. | 08/2023 |



5744 Central Avenue, Suite 100
Boulder, CO 80301

www.watchmakergenomics.com

For Research Use Only. Not for use in diagnostic procedures.

This content is covered by patents, trademarks, and/or copyrights owned or controlled by Watchmaker Genomics, Inc.

All other trademarks are the property of their respective owners.

For more information, please visit watchmakergenomics.com/licenses. The use of these products may require you to obtain additional third party intellectual property rights for certain applications.