

Takara Bio USA, Inc.

SMART-Seq® mRNA Single Cell LP User Manual

Cat. Nos. 634786, 634787 & 634788
(022223)

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I. Introduction

SMART-Seq mRNA Single Cell LP (Cat. Nos. 634786, 634787 & 634788) is designed to generate high-quality, Illumina® sequencing-ready libraries directly from single cells, especially those with low RNA content. The cDNA synthesis protocol can be completed within one day, and the library can be generated in an easy, two-step protocol within two hours. (Figure 1).

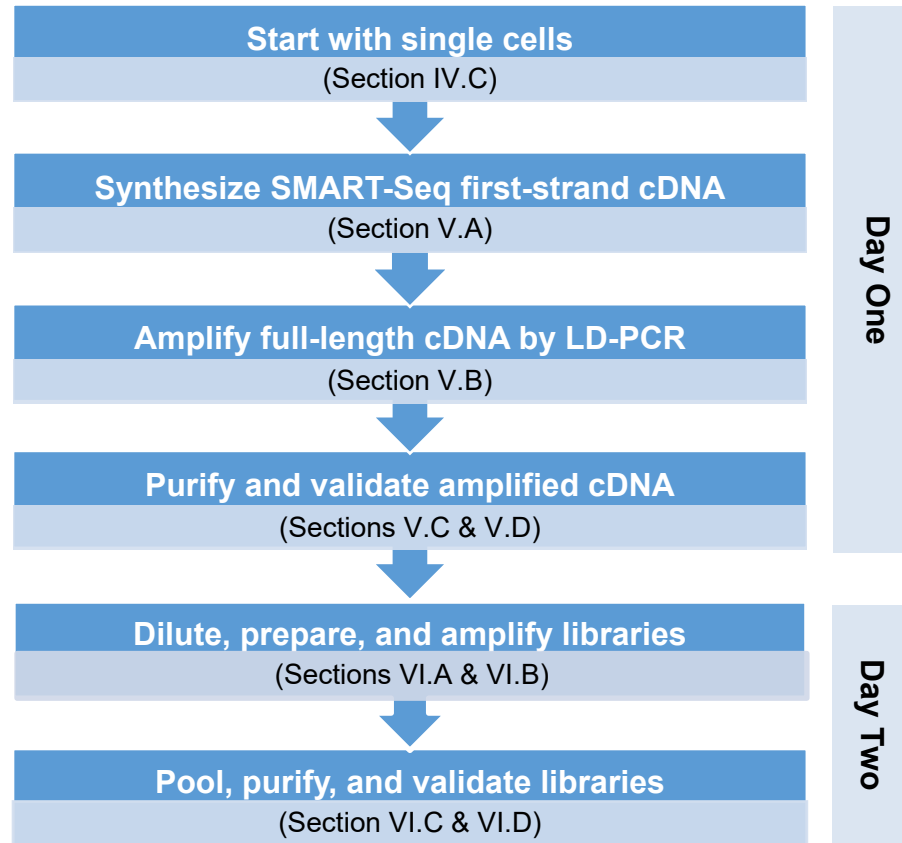


Figure 1. SMART-Seq mRNA Single Cell LP protocol overview.

SMART-Seq mRNA Single Cell LP has been specifically created for single-cell applications and to generate mRNA-seq libraries that clearly outperform previously published protocols (including Smart-seq2 [Picelli et al. 2013]) and existing commercial kits. SMART-Seq mRNA Single Cell LP has been optimized to provide improved performance for cells with very low RNA content, such as PBMCs. Each lot of the kit has been validated with 2 pg of mouse brain total RNA as input.

SMART-Seq mRNA Single Cell LP incorporates our proprietary SMART® (Switching Mechanism at 5' end of RNA Template) technology (Figure 2). This technology relies on the template-switching activity of reverse transcriptase to enrich for full-length cDNAs and to add defined PCR adapters directly to both ends of the first-strand cDNA (Chenchik et al. 1998). This ensures that the final cDNA libraries contain the 5' end of the mRNA and maintain a true representation of the original mRNA transcripts; these factors are critical for transcriptome sequencing and gene expression analysis. SMART technology offers unparalleled sensitivity and unbiased amplification of cDNA transcripts, and it allows direct cDNA synthesis from intact cells.

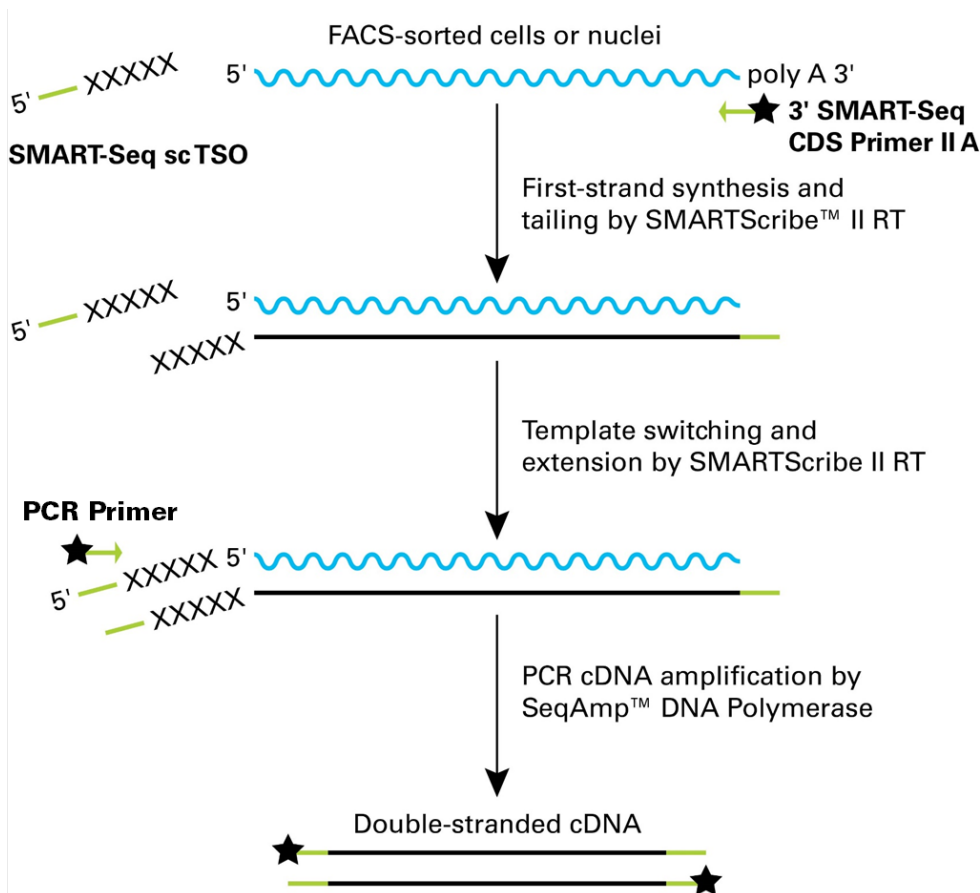


Figure 2. Schematic of the cDNA synthesis technology in the SMART-Seq mRNA Single Cell LP. SMART technology is used in a ligation-free workflow to generate full-length cDNA. Nontemplated nucleotides (indicated by Xs) added by the SMARTScribe II Reverse Transcriptase (RT) hybridize to the SMART-Seq single-cell template-switching oligonucleotide (SMART-Seq sc TSO), which provides a new template for the RT. The SMART adapters used for amplification during PCR—added by the oligo(dT) primer (3' SMART-Seq CDS Primer II A) and TSO—are indicated in green. Chemical modifications to block ligation (if using a ligation-based library preparation method) are present on some primers (indicated by black stars).

Once full-length cDNA is synthesized, libraries are prepared through an enzymatic fragmentation method, followed by ligation of stem-loop adapters and nick extension to create primer binding sites for indexed Illumina adapters. The option of four 96-well unique dual index products (Takara Bio, Cat. Nos. 634752– 634756) tested with the kit allows for multiplexing of up to 384 samples using unique dual indexes (UDIs, Figure 3).

Sequencing library preparation from full-length cDNA incorporates Takara Bio’s patented library preparation chemistry. Unlike other sequencing library preparation kits, which are based on ligation of Y-adapters, our technology uses stem-loop adapters to construct high-quality libraries. The workflow (fragmentation, repair, ligation, amplification, and indexing) takes place in a single tube in about 2 hours. No intermediate purification steps or sample transfers are necessary, which minimizes handling errors (such as sample mix up) and sample loss.

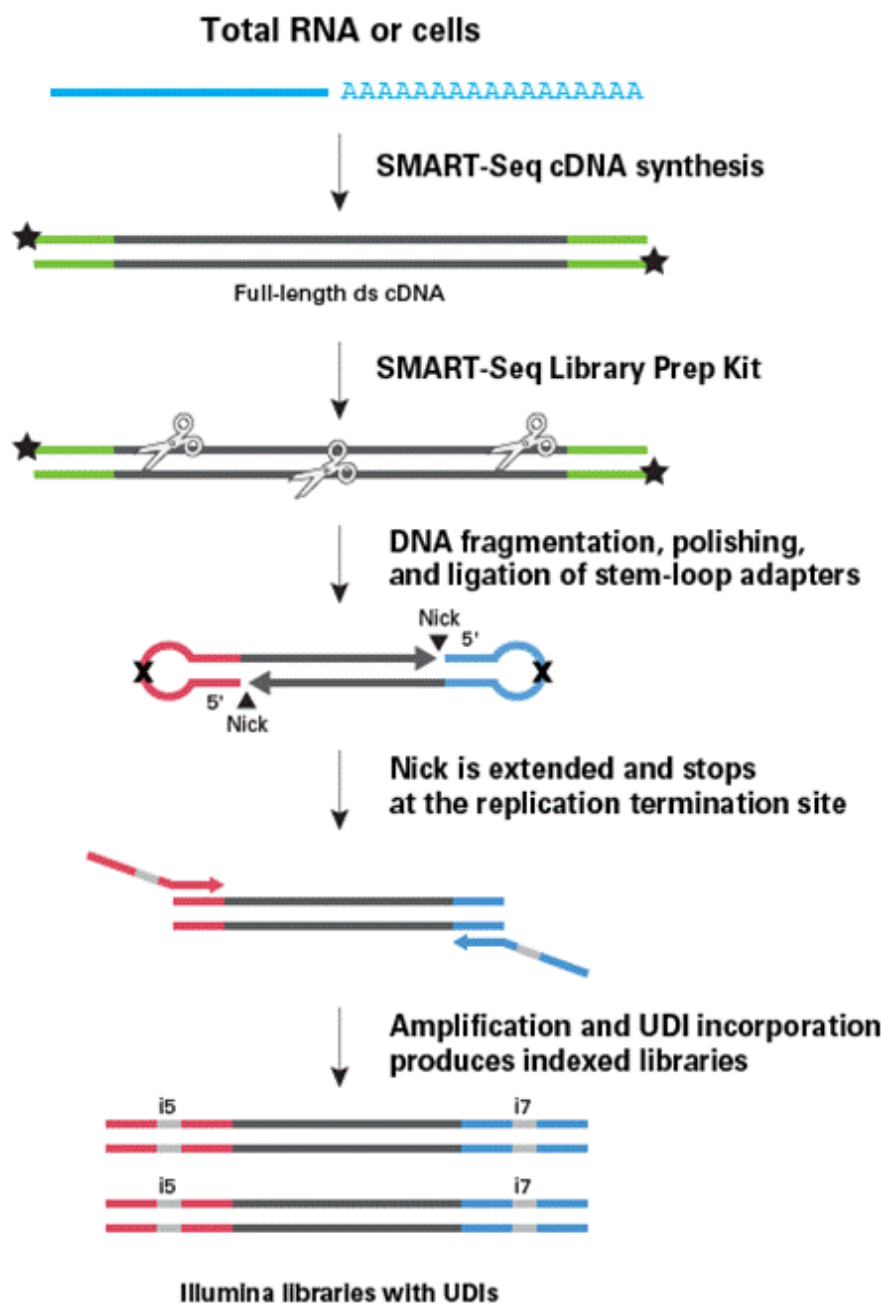


Figure 3. Schematic of the SMART-Seq mRNA Single Cell LP library preparation workflow. Double-stranded cDNA generated using SMART-Seq mRNA Single Cell chemistry is enzymatically fragmented and stem-loop adapters ligated, all in a single step. Libraries are then amplified and indexed, generating Illumina-compatible libraries with UDIs (light gray).

Once purified and quantified, the resulting libraries are ready for Illumina NGS instruments using standard Illumina sequencing reagents and protocols. Sequencing output from Illumina sequencers can be analyzed by our free to use [Cogent™ NGS Analysis Pipeline](#) (CogentAP) and [Cogent NGS Discovery Software](#) (CogentDS).

II. List of Components

SMART-Seq mRNA Single Cell LP contains sufficient reagents to prepare up to 24, 96, or 384 reactions. Freeze-thaw of reagents should be limited to ≤ 6 times. The components in the SMART-Seq mRNA Single Cell LP have been specifically designed to work together and are optimized for this protocol. Please do not make any substitutions. The substitution of reagents in the kit and/or modification of the protocol may lead to unexpected results.

NOTE: Indexing primers are not included in the kit and need to be purchased separately ([Unique Dual Index Kits](#), Takara Bio, Cat. Nos. 634752–634756).

Table 1. SMART-Seq mRNA Single Cell LP components

SMART-Seq mRNA Single Cell LP	Cap Color	634786 (24 rxns)	634787 (96 rxns)	634788 (384 rxns)
SMART-Seq mRNA Single Cell		634789*	634790*	4 x 634790*
Box 1 (Store at -70°C)				
Control Total RNA [†] (1 $\mu\text{g}/\mu\text{l}$)		5 μl	5 μl	4 x 5 μl
Box 2 (Store at -20°C)				
10X Lysis Buffer ^{‡§}	Clear	500 μl	1.85 ml	4 x 1.85 ml
RNase Inhibitor (40 U/ μl)	Orange	60 μl	240 μl	4 x 240 μl
Nuclease-Free Water [§]	Clear	1.7 ml	6.8 ml	4 x 6.8 ml
SMART-Seq sc TSO	White	25 μl	100 μl	4 x 100 μl
3' SMART-Seq CDS Primer II A	White	50 μl	200 μl	4 x 200 μl
SMARTScribe II Reverse Transcriptase	White	50 μl	200 μl	4 x 200 μl
SMART-Seq sc First Strand Buffer (5X)	White	100 μl	400 μl	4 x 400 μl
SeqAmp DNA Polymerase	White	75 μl	250 μl	4 x 250 μl
SeqAmp CB PCR Buffer (2X) [§]	White	1.25 ml	5 ml	4 x 5 ml
PCR Primer	White	25 μl	100 μl	4 x 100 μl
Elution Buffer (10 mM Tris-Cl, pH 8.5)**	–	1.7 ml	2 x 1.7 ml	8 x 1.7 ml
SMART-Seq Library Prep Kit (Store at -20°C)		634764^{††}	R400747^{††}	4 x R400747^{††}
10X FE		24 μl	60 μl	4 x 60 μl
FE Dilution Buffer		250 μl	1 ml	4 x 1 ml
Lib Prep Buffer		120 μl	480 μl	4 x 480 μl
Lib Prep Enzyme		70 μl	280 μl	4 x 280 μl
Rxn Enhancer		100 μl	400 μl	4 x 400 μl
Stem-Loop Adapters		120 μl	480 μl	4 x 480 μl
Amplification Buffer		600 μl	2 x 1.2 ml	8 x 1.2 ml
PrimeSTAR [®] HS DNA Polymerase (5 U/ μl)		30 μl	120 μl	4 x 120 μl
Nuclease-Free Water		1 ml	4 x 1 ml	16 x 1 ml

*Also sold separately.

[†]The Control Total RNA is from mouse brain.

[‡]Store 10X Lysis Buffer at -20°C . Once thawed, the buffer can be stored at 4°C .

[§]Depending on the product size, these components may be packaged in a 1.5 ml tube with the indicated cap color, an 8 ml bottle (10X Lysis Buffer and SeqAmp CB PCR Buffer in Cat. No. 634790), or a 15 ml bottle (Nuclease-Free Water in Cat. No. 634790).

**Store Elution Buffer at -20°C . Once thawed, the buffer can be stored at room temperature.

^{††}Not sold separately.

III. Additional Materials Required

The following reagents and materials are required but not supplied. The specified brands have been validated to work with this protocol.

- Single-channel pipette: 10 μ l, 20 μ l, 200 μ l, and 1,000 μ l
- Eight-channel or 12-channel pipette (recommended): 20 μ l and 200 μ l
- Filter pipette tips: 2 μ l, 20 μ l, 200 μ l, and 1,000 μ l
- Minicentrifuge for 1.5 ml tubes
- Minicentrifuge for 0.2 ml tubes or strips
- 96-well PCR chiller rack, such as IsoFreeze PCR Rack (MIDSCI, Cat. No. 5640-T4) or 96-Well Aluminum Block (Light Labs, Cat. No. A-7079)

For Sample Preparation

- 8-tube strips (Thermo Fisher Scientific, Cat. No. AB0264) or other nuclease-free, PCR-grade tube strips secured in a PCR rack, or 96-well plates that have been validated to work with your FACS instrument (e.g., Bio-Rad iQ 96-Well PCR Plates, Cat. No. 2239441)
- Microplate film (USA Scientific, Cat. No. 2920-0010) for sealing tube strips/plates before sorting
- Aluminum single tab foil seal (USA Scientific, Cat. No. 2938-4100) or cap strips (Thermo Fisher Scientific, Cat. No. AB0784/AB0850) for sealing tubes/plates after sorting
- Low-speed benchtop centrifuge for 96-well plates or tube strips
- Dry ice in a suitable container for flash freezing cells
- **(Optional)** BD FACS Pre-Sort Buffer (BD Biosciences, Cat. No. 563503)
- **(Optional)** SMART-Seq HT Kit Lysis Components (Takara Bio, Cat. No. 634439) or 10X Lysis Buffer (Takara Bio, Cat. No. 635013) for sorting additional plates

For cDNA Synthesis & Amplification

- Two thermal cyclers with heated lids
 - One thermal cycler used only for first-strand cDNA synthesis (Section V.A)
 - One thermal cycler used only for double-stranded cDNA amplification by PCR (Section V.B) and library amplification (Section VI.B)

NOTE: The thermal cycler should always be used with the heated lid option turned on. If prompted to input a specific temperature, use 105°C. Most thermal cyclers with heated lids will automatically adjust the lid temperature just above the highest block temperature within a cycling program. However, if your thermal cycler does not make this automatic adjustment, you may want to follow the manufacturer's instructions to choose a lower lid temperature for the reverse transcription step.

- Thermo Scientific Adhesive PCR Plate Seals (Thermo Fisher, Cat. No. AB0558) for 96-well plates or cap strips (Thermo Fisher, Cat. No. AB0784/AB0850) for 8-tube strips

For Bead Purification

- NucleoMag NGS Clean-up and Size Select (Takara Bio, Cat. Nos. 744970.5, 744970.50 or 744970.500). If the NucleoMag product is not available, the AMPure XP PCR purification kit (Beckman Coulter, Cat. Nos. A63880 or A63881) is an appropriate substitute

NOTES:

- The kit has been specifically validated with the beads listed above. Please do not make any substitutions as it may lead to unexpected results.
 - We strongly recommend aliquoting the beads into 1.5 ml tubes upon receipt and then refrigerating the aliquots. Individual tubes can be removed for each experiment and decreases the chances of bead contamination.
 - Magnetic beads should only be used at room temperature. Individual aliquoted tubes can be removed 30 minutes before an experiment to bring the beads to room temperature.
- 80% ethanol: freshly made for each experiment from molecular-biology-grade 100% ethanol
 - Strong magnetic separation device and centrifuge appropriate for your sample tubes or plates, such as:
 - For 12–24 samples:
 - SMARTer-Seq® Magnetic Separator - PCR Strip (Takara Bio, Cat. No. 635011); accommodates two 8-tube or 12-tube strips
 - Minicentrifuge for 0.2 ml tubes or strips
 - For 24–96 or more samples:
 - Magnetic Stand-96 (Thermo Fisher Scientific, Cat. No. AM10027); accommodates 96 samples in 96-well V-bottom plates (500 µl; VWR, Cat. No. 47743-996) sealed with adhesive PCR Plate Seals (Thermo Fisher Scientific, Cat. No. AB0558)
 - Low-speed benchtop centrifuge for a 96-well plate
 - For 1.5 ml tubes (for pooling sequencing libraries):
 - Magnetic Stand (Takara Bio, Cat. No. 631964)
 - 8-tube strips (Thermo Fisher Scientific, Cat. No. AB0264) or other nuclease-free, PCR-grade tube strips secured in a PCR rack, or 96-well plates (e.g., Bio-Rad iQ 96-Well PCR Plates, Cat. No. 2239441)

For cDNA and Illumina Library Quantification (As Required)

- High Sensitivity DNA Kit (Agilent, Cat. No. 5067-4626) for Bioanalyzer or equivalent high-sensitivity electrophoresis method (may be used in Sections V.D and VI.D)
- Quant-iT PicoGreen dsDNA Assay Kit (Thermo Fisher Scientific, Cat. No. P11496) or Qubit dsDNA HS Assay Kit (Thermo Fisher Scientific, Cat. No. Q32854) (may be used in Sections V.D and VI.D)
- Library Quantification Kit (Takara Bio, Cat. No. 638324) (may be used in Section VI.D)
- Nuclease-free, PCR-grade, thin-wall PCR strips (0.2 ml PCR 8-tube strip; Thermo Fisher Scientific, Cat. No. AB0264) or similar nuclease-free, PCR-grade, thin-wall PCR tubes, strips, or 96-well plates
- Nuclease-free, low-adhesion 1.5 ml tubes (USA Scientific, Cat. No. 1415-2600), DNA LoBind tubes (Eppendorf, Cat. No. 022431021), or similar nucleic acid low-binding tubes

For Illumina Library Preparation

- Nuclease-free, PCR grade, thin-wall PCR strips (0.2 ml PCR 8-tube strip; Thermo Fisher Scientific, Cat. No. AB0264), or similar nuclease-free, PCR-grade thin-wall PCR tubes, strips, or 96-well plates

- Nuclease-free low-adhesion 1.5 ml tubes (USA Scientific, Item No. 1415-2600), DNA LoBind tubes (Eppendorf, Cat. No. 022431021), or similar nucleic acid low-binding tubes
- Benchtop cooler, such as VWR CryoCoolers (VWR, Cat. No. 414004-286)

IV. General Considerations

A. Requirements for Preventing Contamination

Before you set up the experiment, **make sure you have two physically separated workstations:**

- **A PCR clean workstation** for all pre-PCR experiments that require cleanroom conditions, i.e., sample preparation, first-strand cDNA synthesis, and setup prior to amplification (Sections V.A & B).

NOTE: The PCR clean workstation should be in a clean room with positive air flow, as contamination may occur very easily. Once contamination occurs it can be difficult to remove. Strictly obey cleanroom operation rules.

- **A second workstation located in the general laboratory** where you perform cDNA amplification (Section V.B, Step 4), cDNA purification (Section V.C); measure cDNA concentration (Section V.D); and prepare the sequencing libraries (Section VI).

B. General Requirements

- The assay is very sensitive to variations in pipetting volume. Please make sure all your pipettes are calibrated for reliable delivery.
- All lab supplies related to the cDNA synthesis reaction need to be stored in a nucleic-acid-free and nuclease-free closed cabinet.
- Add enzymes to reaction mixtures last and thoroughly incorporate them by gently pipetting the reaction mixture up and down.
- Do not change the amount or concentration of any reaction component. The amounts and concentrations have been carefully optimized for the cDNA synthesis reagents and protocol.
- If you are using this protocol for the first time, we strongly recommend that you perform negative and positive control reactions to verify that the kit components are working properly.

C. Sample Recommendations and Requirements

SMART-Seq mRNA Single Cell LP works best with single cells. This protocol is not suitable for processing large pools of cells or >100 pg of purified RNA. If you wish to use this kit for higher inputs, consult our Technical Support for recommendations.

- We recommend processing no less than 12 reactions to ensure sufficient reagent quantities for all the intended reactions within the kit format.
- This protocol has been validated to generate cDNA starting from intact cells sorted by fluorescence-activated cell sorting (FACS) into 96-well plates or PCR strips. **It cannot be used with cells that have undergone fixation.**
- For the removal of media prior to dilution or FACS, bulk cell suspensions should be washed and resuspended in Mg²⁺- and Ca²⁺-free PBS, as the presence of media can interfere with the first-strand synthesis. It is best to perform at least two washes. If necessary, test the effect of your media or FACS buffer on cDNA synthesis by performing a reaction with control RNA and the estimated amount of media that you expect to accompany your cell. (See Appendix A.)

- Following appropriate washes, cells can be diluted in BD FACS Pre-Sort Buffer (BD Biosciences, Cat. No. 563503) to maintain cells in a single-cell suspension before FACS.
- **Cells should be sorted into 12.5 μl of our recommended sorting buffer (see Appendix A, Section A). If you do not wish to include the CDS IIA oligo in the lysis buffer or if cells are aliquoted in a different buffer, please follow the recommendations in Appendix A, Sections B and C, respectively.**

D. Diluting the Control RNA

Positive control reactions are invaluable to ensure the kit performs as expected and essential for troubleshooting experiments. The best positive control has a similar RNA input mass to your experimental samples. For example, 2 pg of RNA is a good starting point for a single immune cell, while 10–15 pg per cell may be more appropriate for many cell lines (e.g., K-562, HEK293, etc.). Serial dilution is essential to ensure an accurate concentration of the final dilution. Follow the guidelines below to reach a concentration of 1 pg/ μl . When used with 19 cycles of PCR, 2 pg of the Control Total RNA included in the kit should generate a cDNA yield of at least 500 pg/ μl .

NOTE: Make fresh dilutions before each use. If desired, make single-use aliquots of the 50 ng/ μl dilution generated in Step 2 (below) and store at -80°C . When needed, thaw an aliquot, further dilute (Steps 3–6), and throw away any leftover. Make sure to change pipette tips for each dilution step described below. Use low nucleic acid binding tubes for all dilutions.

1. Prepare RNase Inhibitor Water (RI Water) by combining 396 μl of Nuclease-Free Water with 4 μl of RNase Inhibitor. Mix by vortexing and keep on ice until the next step.
2. Dilute Control Total RNA (mouse brain) to 50 ng/ μl by mixing 38 μl of RI Water with 2 μl of Control Total RNA (1 $\mu\text{g}/\mu\text{l}$) in a sterile microcentrifuge tube.
3. Further dilute Control Total RNA to 5 ng/ μl by mixing 45 μl of RI Water with 5 μl of 50 ng/ μl Control Total RNA in a sterile microcentrifuge tube.
4. Further dilute Control Total RNA to 0.25 ng/ μl by mixing 95 μl of RI Water with 5 μl of 5 ng/ μl Control Total RNA in a sterile microcentrifuge tube.
5. Further dilute Control Total RNA to 10 pg/ μl by mixing 120 μl of RI Water with 5 μl of 0.25 ng/ μl Control Total RNA in a sterile microcentrifuge tube.
6. Further dilute Control Total RNA to 1 pg/ μl by mixing 45 μl of RI Water with 5 μl of 10 pg/ μl Control Total RNA in a sterile microcentrifuge tube.
7. Use 1–2 μl of the 10 pg/ μl (from Step 5) or 1 pg/ μl (from Step 6) Control Total RNA as a positive control for the kit and process along with the other samples.

V. cDNA Synthesis

NOTE: Please read the entire set of protocols before starting. The protocols in this user manual have been optimized for cDNA synthesis from single intact cells and subsequent sequencing library preparation. Due to the sensitivity of these protocols, cells should be collected under cleanroom conditions to avoid contamination. The whole process of cDNA synthesis should be carried out in a PCR clean workstation under cleanroom conditions.

A. Protocol: First-Strand cDNA Synthesis

First-strand cDNA synthesis is primed by the 3' SMART-Seq CDS Primer II A and uses the SMART-Seq sc TSO for template switching at the 5' end of the transcript.

IMPORTANT: To avoid introducing contaminants into your samples, the first part of the cDNA synthesis protocol requires the use of a PCR clean workstation, ideally in a clean room.

1. At room temperature, thaw the SMART-Seq sc First Strand Buffer. On ice, thaw all the remaining reagents (except the enzyme) needed for first-strand cDNA synthesis: 10X Lysis Buffer, RNase Inhibitor, Nuclease-Free Water, SMART-Seq sc TSO, and 3' SMART-Seq CDS Primer II A (if needed; see Table 2, below). Gently vortex each reagent to mix and spin down briefly. Store all reagents on ice except the SMART-Seq sc First Strand Buffer.

NOTE: The SMART-Seq sc First Strand Buffer forms precipitates. Keep this buffer at room temperature until ready to use. Make sure to vortex before using to ensure all components are completely in solution.

2. Prepare a stock solution of 10X Reaction Buffer (scale up as needed for use in Step 3, plus 10% of the total reaction mix volume):

19 μ l	10X Lysis Buffer
1 μ l	RNase Inhibitor

20 μ l Total volume

Mix the 10X Reaction Buffer briefly, and then spin down.

NOTE: Lysis Buffer contains a detergent, so it is critical to avoid bubbles when mixing.

3. See Table 2 below for guidelines on setting up your positive and negative controls alongside your cell samples. Prepare each sample (12.5 μ l total volume) in 8-well strips or a 96-well plate.

Table 2. Sample preparation guidelines

Components	Negative control	Positive control	Cells in CSS*	Cells in PSS†	Cells in other buffer‡
10X Reaction Buffer (Step 2)	1 μ l	1 μ l	–	–	1 μ l
Nuclease-Free Water	10.5 μ l	8.5 μ l	–	–	Up to 9.5 μ l
Diluted Control Total RNA§	–	2 μ l	–	–	–
Cell sample	–	–	12.5 μ l	11.5 μ l	1–9.5 μ l
3' SMART-Seq CDS Primer II A	1 μ l	1 μ l	–	1 μ l	1 μ l
Total volume	12.5 μ l	12.5 μ l	12.5 μ l	12.5 μ l	12.5 μ l

*CDS Sorting Solution (CSS) is described in Appendix A, Section A. This buffer already contains the 3' SMART-Seq CDS Primer II A and 10X Reaction Buffer.

†Plain Sorting Solution (PSS) is described in Appendix A, Section B. PSS does not contain the 3' SMART-Seq CDS Primer II A, so it must be added here.

‡Other buffers will not generate optimal results and are not recommended. See Appendix A, Section C, for guidance if you must use a nonvalidated buffer.

§The Control Total RNA is supplied at a concentration of 1 μ g/ μ l. It should be diluted to match the concentration of your test sample using serial dilutions as described in Section IV.D. To minimize pipetting errors, use 2 μ l of the diluted control RNA. For example, dilute to 1 pg/ μ l and use 2 μ l.

4. When ready to start, remove the samples (plate or PCR strips containing the sorted cells) from the freezer and briefly spin to collect the contents at the bottom of the tubes.
5. **(Optional)** If cells were not sorted in CSS, place the samples on ice and add any necessary remaining reagents, including 1 μ l of 3' SMART-Seq CDS Primer II A. Mix well by gently vortexing and then spin the tube(s) briefly to collect the contents at the bottom of the tube.

NOTE: If more than one reagent needs to be added (i.e., the 10X Reaction Buffer, the 3' SMART-Seq CDS Primer II A, and extra Nuclease-Free Water), they can be pooled in a master mix and incorporated into each sample as a single addition.

6. Immediately incubate the tubes at 72°C in a preheated, hot-lid thermal cycler for 3 min.

NOTE: Prepare the RT Master Mix (Step 7) while your tubes are incubating. The SMARTScribe II Reverse Transcriptase will be added just before use (Step 10). Steps 11 & 12 below are critical for first-strand cDNA synthesis and should not be delayed after completing Step 10.

7. Prepare enough RT Premix for all the reactions, plus 10% of the total reaction mix volume, by combining the following reagents in the order shown at room temperature:

RT Premix:

4 μ l	SMART-Seq sc First Strand Buffer
1 μ l	SMART-Seq sc TSO
0.5 μ l	RNase Inhibitor (40 U/ μ l)

5.5 μ l Total volume

8. Immediately after the 3-min incubation at 72°C, place the samples on ice for at least 2 min (but no more than 10 min).
9. Preheat the thermal cycler to 42°C.
10. Add the SMARTScribe II Reverse Transcriptase to the RT Master Mix, plus 10% of the total reaction mix volume.

RT Master Mix:

5.5 μ l	RT Premix (from Step 7)
2 μ l	SMARTScribe II Reverse Transcriptase

7.5 μ l Total volume per reaction

Mix well by gently vortexing and then spin the tube briefly in a minicentrifuge to collect the contents at the bottom of the tube.

11. Add 7.5 μ l of the RT Master Mix to each sample. Mix the contents of the tubes by gently vortexing and spin briefly to collect the contents at the bottom of the tubes.
12. Place the tubes in a thermal cycler with a heated lid, preheated to 42°C. Run the following program:

42°C	180 min
70°C	10 min
4°C	forever

SAFE STOPPING POINT: The tubes can be stored at 4°C overnight.

B. Protocol: cDNA Amplification by LD-PCR

In this step, the PCR Primer amplifies the cDNA by priming to the sequences introduced by the 3' SMART-Seq CDS Primer II A and the SMART-Seq sc TSO.

IMPORTANT: Table 3 provides guidelines for the number of PCR cycles appropriate for the cell type used for the first-strand cDNA synthesis. When using good-quality control RNA such as the Control Total RNA from the kit (mouse brain total RNA), 2 pg should generate ~500–1,500 pg/μl if using 19 cycles. It is best to choose a number of cycles that will yield <1,500 pg/μl. Optimal parameters may vary for different templates, different cell types, and different thermal cyclers. To determine the optimal number of cycles for your sample and conditions, we strongly recommend that you perform a range of cycles. See Appendix B for PCR optimization suggestions.

Table 3. Cycling guidelines based on cell type

Cell type	Approximate RNA equivalent (per cell)	Typical number of PCR cycles
K-562 or HEK293 cells	10–15 pg	17
PBMCs	1–5 pg	20
Jurkat cells	5 pg	17
Lymphoblastoid cells	2–15 pg	17–19

1. Thaw SeqAmp CB PCR Buffer and PCR Primer on ice. Do not thaw SeqAmp DNA Polymerase. Gently vortex each reagent tube to mix and spin down briefly. Store on ice.
2. Prepare enough PCR Master Mix for all the reactions, plus an additional 10% of the total reaction mix volume. Combine the following reagents in the order shown:

PCR Master Mix:

25 μl	SeqAmp CB PCR Buffer (2X)
1 μl	PCR Primer
1 μl	SeqAmp DNA Polymerase
3 μl	Nuclease-Free Water

30 μl Total volume per reaction

NOTE: Remove the SeqAmp DNA Polymerase from the freezer, gently mix the tube without vortexing, and add to the PCR Master Mix just before use. Mix the PCR Master Mix well by vortexing gently and spin the tube briefly to collect the contents at the bottom of the tube.

3. Add 30 μl of PCR Master Mix to each tube containing 20 μl of first-strand cDNA product from Section V.A. Mix well by gently vortexing, and briefly spin to collect the contents at the bottom of the tube.

IMPORTANT: Transfer the samples from the PCR clean workstation to the general lab. All downstream processes should be performed in the general lab.

4. Place the tubes in a preheated thermal cycler with a heated lid and run the following program:

95°C	1 min	
X cycles*:		
98°C	10 sec	}
65°C	30 sec	
68°C	3 min	
72°C	10 min	
4°C	forever	

*Please consult Table 3 for the recommended number of PCR cycles.

SAFE STOPPING POINT: The tubes may be stored at 4°C overnight.

C. Protocol: Purification of Amplified cDNA

In this step, PCR-amplified cDNA is purified by immobilization on NucleoMag NGS Clean-up and Size Select (available from Takara Bio, Cat. No. 744970) beads. The beads are then washed with 80% ethanol, and cDNA is eluted with Elution Buffer.

IMPORTANT: Do not pool the samples at the cDNA purification step. If pooling is desired, it can be performed during library preparation (Section VI).

NOTES:

- Before each use, bring a 1.5 ml aliquot of NucleoMag NGS Clean-up and Size Select beads and the Elution Buffer to room temperature for at least 30 min and mix well by vortexing.
 - Bead:sample ratio is 0.8:1.
 - Prepare fresh 80% ethanol for each experiment. You will need 400 µl per sample.
 - Use a magnetic separation device for 0.2 ml tubes, strip tubes, or a 96-well plate.
1. If purification is performed directly in the PCR tubes or strips using the Takara Bio SMARTer-Seq Magnetic Separator - PCR Strip, add 40 µl of beads to each sample. Mix thoroughly by vortexing for 3–5 sec or pipetting the entire volume up and down at least 10 times. Proceed to Step 2.
(Optional) If you are performing purification with the Thermo Fisher Magnetic Stand-96 (recommended if processing 48–96 samples), cDNA samples need to be transferred to a 96-well V-bottom plate. Distribute 40 µl of beads to each well of the 96-well V-bottom plate, and then use a multichannel pipette to transfer the cDNA. Pipette the entire volume up and down at least 10 times to mix thoroughly. Proceed to Step 2.
 2. Incubate at room temperature for 8 min to let the cDNA bind to the beads.
 3. Briefly spin the samples to collect the liquid from the side of the tubes or plate wells. (Centrifugation is generally not necessary if using a 96-well V-bottom plate as described in Step 1.)
 4. Place the samples on the magnetic separation device for ~5 min or longer, until the liquid appears completely clear and there are no beads left in the supernatant.
 5. While the samples are on the magnetic separation device, remove and discard the supernatant. Take care not to disturb the beads.
 6. Keep the samples on the magnetic separation device. Add 200 µl of freshly made 80% ethanol to each sample without disturbing the beads. Incubate for 30 sec. Then, carefully remove and discard the supernatant, taking care not to disturb the beads. The cDNA remains bound to the beads during the washing process.
 7. Repeat the ethanol wash (Step 6) once more.
 8. Briefly centrifuge the samples to collect the liquid from the side of the tubes or plate wells. Place the samples on the magnetic separation device for 30 sec, then remove any residual ethanol with a pipette.

9. Incubate the samples at room temperature for ~2–2.5 min, until the pellet is no longer shiny, but before cracks appear.

NOTE: Check the pellet frequently during this time and continue to Step 10 when it is dry enough. Please refer to our visual guide for pellet dry-down on our website if you would like additional assistance with this determination.

<https://www.takarabio.com/learning-centers/next-generation-sequencing/faqs-and-tips/rna-seq-tips>

If the beads are overdried, there will be cracks in the pellet. If this occurs, the DNA may not elute well from the beads and recovery may be reduced.

10. Once the beads are dry, remove the samples from the magnetic separation device and add 17 μ l of Elution Buffer to cover the bead pellet. Mix thoroughly by pipetting or gently vortexing to resuspend the beads.
11. Incubate at room temperature for at least 2 min to rehydrate.
12. Briefly spin the samples to collect the liquid from the side of the tubes or plate wells. Place the samples back on the magnetic separation device for 1 min or longer, until the solution is completely clear.
13. Transfer clear supernatant (~15 μ l) containing purified cDNA from each tube/well to a new tube/plate. Do not pool samples at this point. Take care not to carry over any beads with your sample.
14. Proceed to validation immediately or store at -20°C .

D. Protocol: Determination of cDNA Quality and Quantity

Determine cDNA Quality

It is recommended to evaluate the profile of the cDNA using the Agilent 2100 Bioanalyzer and Agilent's High Sensitivity DNA Kit (Agilent, Cat. No. 5067-4626), or the Fragment Analyzer and High Sensitivity Large Fragment Analysis Kit (Agilent, Cat. No. DNF-464). The cDNA profile obtained on an Agilent TapeStation Automated Electrophoresis Systems using a High Sensitivity D5000 ScreenTape (Agilent, Cat. No. 5067-5592) is not as informative as the other two options, but can still deliver usable information, including cDNA yield (see Appendix C for more details). The cDNA profile obtained on a LabChip (PerkinElmer) instrument is typically unsatisfactory and difficult to interpret due to the lack of sensitivity. Evaluation of the cDNA profile is particularly important when performing initial optimization.

When evaluating cDNA quality, use 1 μ l of each amplified cDNA for validation using the Agilent 2100 Bioanalyzer and Agilent's High Sensitivity DNA Kit (see the Agilent High Sensitivity DNA Kit User Manual for instructions). Successful cDNA synthesis and amplification should yield a distinct peak spanning 300–10,000 bp, with a peak around 2,000 bp for the positive control RNA sample (Figure 4, Panel A). Profiles obtained from cells or purified total RNA of lower quality than the control RNA provided in the kit may yield profiles that are more variable, sometimes with a slightly smaller peak. In any case, the negative control should be almost flat with little or no product visible (Figure 4, Panel B). **For quantification, perform smear analysis using a 200–9,000 bp range.**

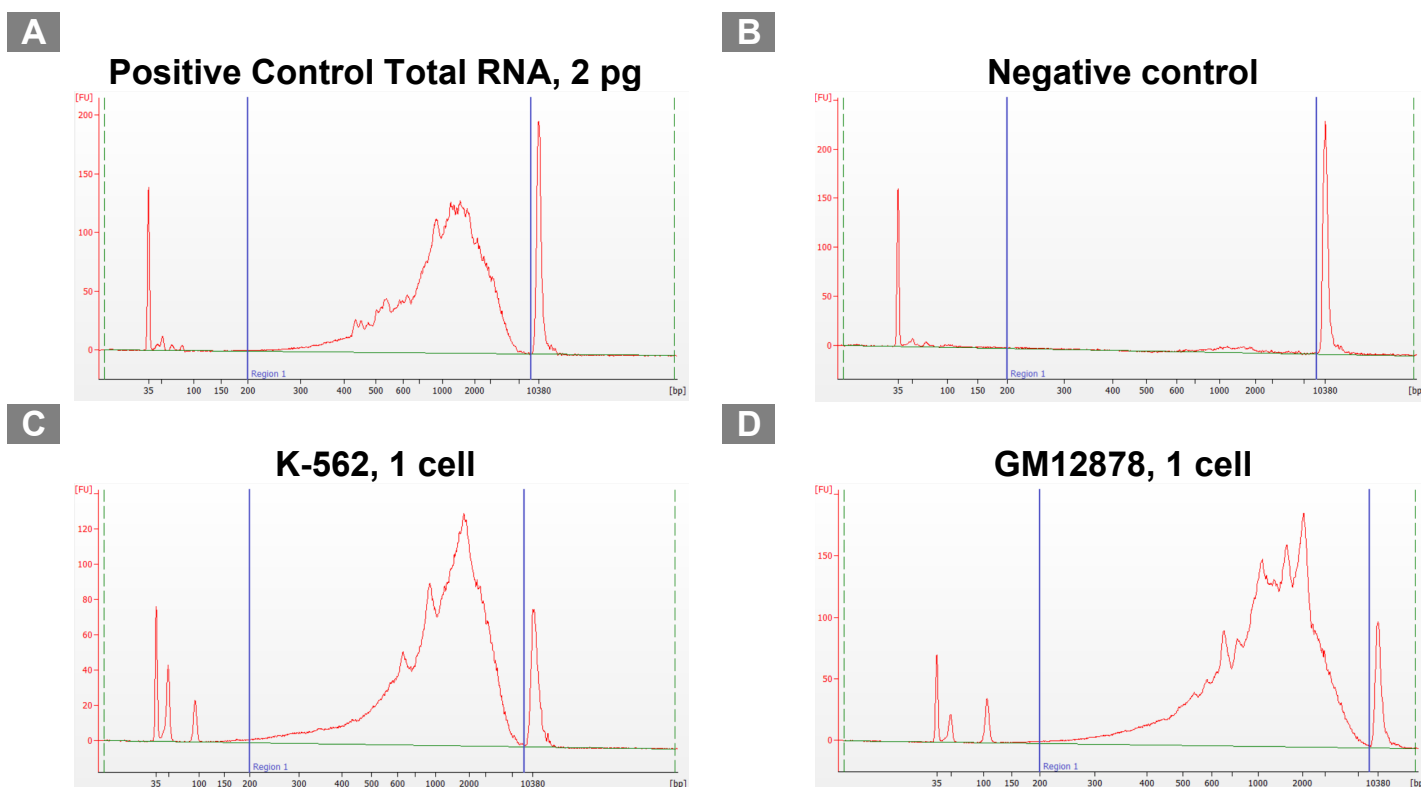


Figure 4. Example electropherogram results from Agilent 2100 Bioanalyzer. All samples were subjected to cDNA synthesis and amplification, as described in the protocol. **Panel A** shows a clean product ($\sim 1,050$ pg/ μ l) following cDNA synthesis and amplification with 19 PCR cycles. The spiky profile with the Control Total RNA is normal. The sharpness of the peak will vary depending on the cell or RNA origin. **Panel B** shows almost no product in the negative control following cDNA synthesis and amplification with 20 PCR cycles. A very small amount of background (~ 25 pg/ μ l) may be present when using 20 cycles, as shown in this example. **Panel C** shows a representative cDNA profile obtained from a single K-562 cell (17 PCR cycles; 1,600 pg/ μ l), and **Panel D** shows a representative cDNA profile obtained from a single GM12878 cell (19 PCR cycles; 2,300 pg/ μ l).

Determine cDNA Quantity

cDNA concentrations obtained with SMART-Seq mRNA Single Cell LP may vary between different cell types and treatments. To minimize library prep variation and to achieve a high sequencing library quality, the concentration of the amplified cDNAs must be carefully determined. Several options are available for quantification. We recommend using the Agilent Bioanalyzer for reliable double-stranded (ds) cDNA quantification. Select the region encompassing 400–9,000 bp to estimate the concentration of ds cDNA.

For processing 96 or more samples, the Quant-iT PicoGreen dsDNA Assay Kit (PicoGreen) is a very sensitive tool is fast and convenient (see below). Alternatively, the Qubit dsDNA HS Assay (Qubit) may be used. However, if using either of these methods, we suggest also performing cDNA quantitation for a subset of the samples on the Bioanalyzer for more accurate results. Refer to the manufacturer's instructions for information on how to use the PicoGreen or Qubit assay reagents.

When using the Qubit or PicoGreen assay for quantification, the negative control may generate an apparent yield up to 200 pg/ μ l (for 20 cycles of PCR), even if the same sample run on the Bioanalyzer appears flat, because low molecular weight primers or primer dimers are detected. A higher number of cycles generates a higher background. For this reason, it is critical to include negative controls that can be used to subtract the background and get a more accurate quantification of the cDNA yield.

1. If using PicoGreen or Qubit assay reagents for quantification, refer to the manufacturer's instructions for information. Remember that it is critical to subtract the value of the negative control to obtain accurate quantification.

2. If cDNA quality was measured, compare the results for your samples and controls (see Figure 3, above) to verify whether the sample is suitable for further processing.
3. Proceed to Library Preparation for Illumina Sequencing (Section VI).

VI. Library Preparation for Illumina Sequencing

Components from the SMART-Seq Library Prep Kit are used in Sections VI.A & B, and the Unique Dual Index Kits (Cat. Nos. 634752–634756) are used in Section VI.B. Before starting, please read the:

- entire set of protocols in Section VI, below,
- [Unique Dual Index Kits Protocol-at-a-Glance](#), that includes the instructions for UDI use, and
- Unique Dual Index Kit Indexes and Plate Map specific for the UDI plate product you are using. This XLSX file includes a plate map and barcode sequences for the UDIs included on the plate and can be accessed either on our website or through hyperlinks in the UDI Kit protocol document, above.

NOTE: If all samples are correctly quantified and normalized to a uniform input amount before library preparation (Section VI.A, Step 4), sequencing libraries can be pooled after amplification and before cleanup (in Section VI.C), and a relatively uniform amount of sequencing reads will be obtained.

A. Protocol: cDNA Dilution and Library Preparation

- If performing library preparation (Section VI.A) and amplification (Section IV.B) on the same day, thaw the following items on ice:
 - Unique Dual Index Kits (Cat. Nos. 634752–634756)
 - SMART-Seq Library Prep Kit components: FE Dilution Buffer, Lib Prep Buffer, Rxn Enhancer, Stem-Loop Adapters, and Amplification Buffer
 - SMART-Seq mRNA Single Cell: Elution Buffer
- Keep 10X FE, Library Prep Enzyme, and PrimeSTAR HS DNA Polymerase (5 U/μl) in the –20°C freezer until used. Use a benchtop cooler to keep the enzymes cold while working with them at the bench.
- We recommend using 8 μl of Elution Buffer as the negative control. Alternatively, you can use the negative control produced during cDNA synthesis (Section V). Negative controls should be used without dilution.

NOTE: If stopping at the end of Section VI.A, keep the Unique Dual Index Kit, Amplification Buffer, and PrimeSTAR HS DNA Polymerase (5 U/μl) in the –20°C freezer until ready to begin Section VI.B.

1. Mix all components by gentle vortexing, and then spin down the tubes briefly to collect the contents at the bottom of the tubes. Keep on ice.
2. On ice, add 4 μl of Stem-Loop Adapters to each tube/well of PCR tubes, 8-tube PCR strips, or a 96-well PCR plate, according to the number of reactions to be performed.
3. Calculate the amounts of cDNA and Elution Buffer needed for each sample to achieve a fixed concentration (one value between 0.125 ng/μl and 1.25 ng/μl) in an 8 μl per sample. Use the notes on the next page as guidelines.

NOTES:

- Only use Elution Buffer to dilute the cDNA; do not use deionized water
- Always use a minimum of 2 µl of cDNA to perform dilution; the total volume of cDNA plus Elution Buffer should be 8 µl
- Samples containing less than 100 pg/µl can still be used without dilution, but you may get fewer reads than for other samples if you pool for cleanup (Section VI.C).
- We recommend using 8 µl of Elution Buffer as the negative control. Alternatively, you can use the negative control produced during cDNA synthesis (Section V). Negative controls should be used without dilution.
- The number of PCR cycles performed during library amplification (Section IV.B, Step 4) depends on the input cDNA amount. Refer to [Table 4](#) for guidelines that may inform cDNA dilution in the current step.

4. Add the freshly diluted cDNA sample or negative control to a tube/well containing the 4 µl of Stem-Loop Adapters (Step 2), for a total reaction volume of 12 µl.
5. On ice, prepare 1X FE by diluting the 10X FE in cold FE Dilution Buffer (~4°C) in a 1:9 ratio (1 part 10X FE to 9 parts FE Dilution Buffer). Prepare enough material to accommodate the Library Prep Master Mix in Step 6, plus 10% of the total reaction mix volume.

NOTE: To allow for greater accuracy pipetting the 10X FE, a minimum of 40 µl of 1X FE Preparation should be prepared, which is enough for 36 rxns.

1X FE Preparation

	1 rxn	1–36 rxns*
FE Dilution Buffer	0.9 µl	36.0 µl
10X FE	0.1 µl	4.0 µl
Total volume	1.0 µl	40.0 µl

*Volumes include ~10% extra for overage.

Mix gently by pipetting up and down 10 times. Spin down and keep on ice. Immediately proceed with assembling the Library Prep Master Mix in Step 6.

6. On ice, prepare the Library Prep Master Mix for all reactions, plus 10% of the total reaction mix volume. Combine the following reagents in the order shown below.

Library Prep Master Mix

- 4 µl Library Prep Buffer
- 3.5 µl Rxn Enhancer
- 2 µl Library Prep Enzyme
- 1 µl 1X FE

10.5 µl Total volume per reaction

NOTES:

- **Library Prep Master Mix is very viscous.** Ensure adequate mixing by vortexing for 5 sec, and then spin the tubes briefly to collect the contents at the bottom of the tubes/plate. If necessary, vortex for an additional 5 sec and spin down again. Keep on ice.
- Discard leftover 1X FE. Do not reuse.

- On ice, assemble the library preparation reaction.

To each tube/well containing 12 μ l cDNA/Stem-Loop Adapters mix or negative control/Stem-Loop Adapters mix from Step 4, add 10.5 μ l of the Library Prep Master Mix prepared in Step 6. Mix by vortexing for 5 sec, and then spin the tubes briefly to collect the contents at the bottom of the tubes/wells.

NOTES:

- During this step, keep the samples cold (4°C) until placed in the thermal cycler.
- Do not create a master mix with the Stem-Loop Adapters and the Library Prep Master Mix.

- Perform the library preparation reaction by placing the tubes/plate in a precooled thermal cycler and running the following program:

20°C 40 min
85°C 10 min
4°C Hold

Proceed to library amplification, Section VI.B.

SAFE STOPPING POINT: The samples can be stored in the thermal cycler at 4°C overnight, or they can be transferred to –20°C for up to a week.

B. Protocol: Library Amplification

- If the samples were stored at –20°C, thaw the samples and the following items on ice:

- The Unique Dual Index Kit being used
- Amplification Buffer from the SMART-Seq Library Prep Kit

NOTE: Keep the PrimeSTAR HS DNA Polymerase (5 U/ μ l) in the –20°C freezer until used. Use a benchtop cooler to keep the enzyme cold while working with it at the bench.

- On ice, prepare the Library Amplification Master Mix for all reactions, plus 10% of the total reaction mix volume.

Library Amplification Master Mix

21.5 μ l	Amplification Buffer
1 μ l	PrimeSTAR HS DNA Polymerase (5 U/ μ l)
3 μ l	Deionized water

25.5 μ l Total volume per reaction

BEFORE PROCEEDING: Please refer to the [Unique Dual Index Kits Protocol-at-a-Glance](#), which contains more information about the use of the Unique Dual Index Kit.

- Add 25.5 μ l of the Library Amplification Master Mix to each reaction from Section VI.A, Step 8.
- Add 2 μ l of a different index from the Unique Dual Index Kit to each reaction. Mix by vortexing for 5 sec, and then spin the tubes briefly to collect the contents at the bottom of the tubes/plate.

- Place the tubes in a thermal cycler with a heated lid (105°C) and perform PCR amplification using the following program:

72°C	3 min
85°C	2 min
98°C	2 min
<u>12–16 cycles:*</u>	
98°C	20 sec
60°C	75 sec
68°C	5 min
4°C	Hold

*Please consult Table 4 for the recommended number of PCR cycles based on cDNA input amount.

Table 4. General recommendations for the number of PCR cycles for library amplification

Input amount of cDNA	Recommended PCR cycles
1 ng*	15–16
2 ng	14–15
5 ng	13–14
10 ng	12–13

*Contact [Technical Support](#) if cDNA input is lower than 1 ng.

SAFE STOPPING POINT: The samples can be stored in the thermal cycler at 4°C overnight, or they can be transferred to –20°C for up to a week.

C. Protocol: Pooling and Purification of Amplified Libraries

PCR-amplified libraries can be purified individually or, optionally, the libraries can be pooled if the input cDNA was quantified and normalized to a uniform input amount before library preparation (Section VI.A, Step 4). Purify the libraries again by immobilization on NucleoMag NGS Clean-up and Size Select beads. The beads are then washed with 80% ethanol, and then the library is eluted with Nuclease-Free Water.

NOTES:

- Before each use, bring bead aliquots to room temperature for at least 30 min and mix well by vortexing. Use room-temperature Nuclease-Free Water for this protocol.
- Bead:sample ratio is 0.8:1.
- Prepare fresh 80% ethanol for each experiment. You need ~400 µl per sample.
- You will need a magnetic separation device for 0.2 ml tubes, 1.5 ml tubes, strip tubes, or a 96-well plate.

- Determine the number of libraries to be pooled based on the desired sequencing depth and sequencer throughput. If preferred, clean up libraries individually before pooling.

NOTE: Please refer to the [Unique Dual Index Kits Protocol-at-a-Glance](#), which contains more information about pooling strategies.

- Pool the libraries by pipetting a fixed volume from each sample into a 1.5 ml tube or PCR tube. Volumes between 2 and 8 μ l are appropriate. See examples in the table below. Do not use less than 2 μ l per sample to ensure greater accuracy.

Table 5. Example volumes of pooled libraries and beads

Number of libraries to be pooled	Volume per library	Total pool volume	Bead volume*
8	8 μ l	64 μ l	52 μ l
12	4 μ l	48 μ l	39 μ l
16	4 μ l	64 μ l	52 μ l
24	2 μ l	48 μ l	39 μ l
32	2 μ l	64 μ l	52 μ l
48	2 μ l	96 μ l	77 μ l
96	2 μ l	192 μ l	154 μ l

*The bead volume is approximately 80% of the total pool volume.

NOTES:

- Do not use less than 2 μ l per sample to ensure greater accuracy.
- If pooling 96 samples, make sure to use a 1.5 ml tube.

- Add a volume of beads representing 80% of the volume of the pooled libraries. See Table 5 for guidance.

NOTE: If cleaning up libraries individually, add 40 μ l of beads to each 50 μ l of sample.

- Mix well by vortexing or pipetting the entire mixture up and down 10 times.

NOTE: The beads are viscous; pipette the entire volume and push it out slowly.

- Incubate at room temperature for 5 min to let the library bind to the beads.
- Briefly spin the sample to collect the liquid from the side of the tube. Place the tube on a magnetic stand for ~2 min or until the liquid appears completely clear, and there are no beads left in the supernatant.
- While the samples are on the magnetic separation device, remove and discard the supernatant. Take care not to disturb the beads.
- Keep the samples on the magnetic separation device. Add 200 μ l of fresh 80% ethanol to each sample without disturbing the beads. Incubate for 30 sec, and then remove and discard the supernatant, taking care not to disturb the beads. The library remains bound to the beads during washing.
- Repeat the ethanol wash (Step 8) once more.
- Briefly centrifuge the samples to collect the liquid from the side of the tube or plate well. Place the samples on the magnetic separation device for 30 sec, then remove any residual ethanol with a pipette.

11. Incubate the samples at room temperature for ~5–15 min, until the pellet is no longer shiny, but before cracks appear.

NOTE: Check the pellet frequently during this time and continue to Step 10 when it is dry enough. Please refer to our visual guide for pellet dry-down on our website if you'd like additional assistance with this determination.

<https://www.takarabio.com/learning-centers/next-generation-sequencing/faqs-and-tips/rna-seq-tips>

If the beads are overdried, there will be cracks in the pellet. If this occurs, the DNA may not elute well from the beads and recovery may be reduced.

12. Once the beads are dry, elute the pooled, purified libraries by adding the required volume of Nuclease-Free Water (provided), based on the number of samples pooled, according to Table 6.

Table 6. Example volumes of Nuclease-Free Water to resuspend libraries

Number of libraries pooled	Nuclease-Free Water*
8	32 µl
12	24 µl
16	32 µl
24	24 µl
32	32 µl
48	48 µl
96	96 µl

*Nuclease-Free Water volume is 50% of the original pool volume (Column 3, Table 5).

NOTE: If cleaning up libraries individually, elute in 25 µl of Nuclease Free Water.

13. Remove from the magnetic separation device and vortex the tube for 3 sec to mix thoroughly. Incubate at room temperature for ~5 min to rehydrate the beads.
14. Briefly spin to collect the liquid from the side of the tube. Place the tube back on the magnetic separation device for ~2 min or longer until the solution is completely clear.
15. Transfer the clear supernatant containing purified libraries to a nuclease-free, low-adhesion tube. Label each tube with sample information. The purified libraries can be stored at –20°C.

D. Protocol: Determination of Amplified Library Quality and Quantity

Library quantification can be performed using fluorescence-detection-based methods, such as the Qubit dsDNA HS Assay or Quant-iT PicoGreen dsDNA Assay Kit. A qPCR assay like the Library Quantification Kit (Takara Bio, Cat. No. 638324) is also recommended for the quantification of the sequencing libraries.

A fragment analyzer, such as the Agilent 2100 Bioanalyzer or TapeStation system (see Figure 5 for expected Bioanalyzer or TapeStation profiles), can be used to assess the quality of the libraries. We recommend diluting an aliquot of each library in TE buffer to ~3 ng/µl. Use 1 µl of this diluted sample for validation using the Agilent 2100 Bioanalyzer and Agilent’s High Sensitivity DNA Kit (see the Agilent High Sensitivity DNA Kit User Manual for instructions).

For loading on Illumina NGS platforms, follow the “Denature and Dilute Libraries Guide” specific to your system.

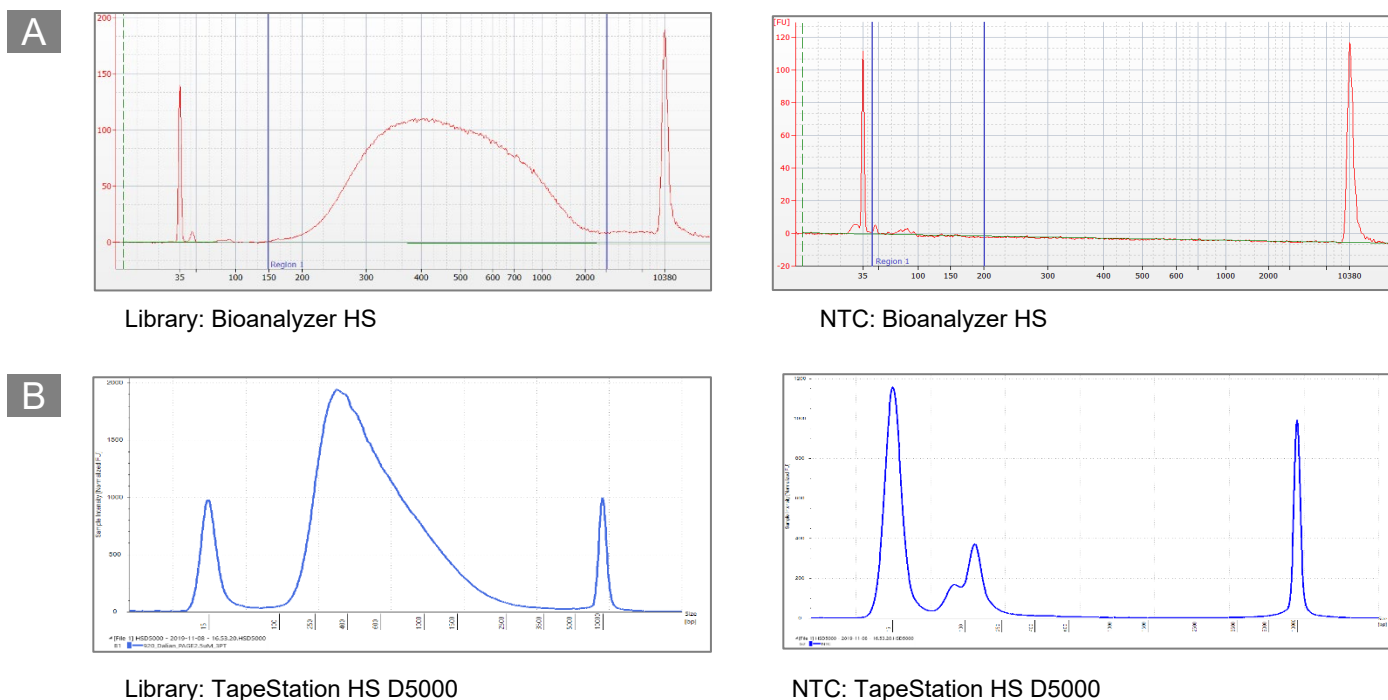


Figure 5. Example electropherogram analysis of SMART-Seq Library Prep Kit. 3 ng of libraries or 1 μ l of NTC control were analyzed using Agilent's High Sensitivity DNA Kit and an Agilent 2100 Bioanalyzer (Bioanalyzer HS) or the TapeStation 4200 and Agilent High Sensitivity D5000 ScreenTape System (TapeStation HS D5000). Shown are examples of successful library profiles from Bioanalyzer HS (Panel A, left) and TapeStation HS D5000 (Panel B, left). The NTC control showed little or no amplification when run on the Bioanalyzer (Panel A, right). Adapter dimers are observed below 200 bp when the NTC was run on the TapeStation (Panel B, right).

VII. References

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Appendix A: FACS Sorting Recommendations

When sorting the cells, we strongly recommend including the oligo required for priming the reverse transcription (3' SMART-Seq CDS Primer II A) in the sorting buffer (see CDS Sorting Solution described in Section A, below). This eliminates a pipetting step when setting up the reverse transcription. However, this is not an absolute requirement for successful cDNA synthesis. For recommendations on sorting in a buffer not containing the 3' SMART-Seq CDS Primer II A, proceed to Section B, below. Alternatively, you can sort cells in a maximum volume of 5 μ l PBS. For recommendations on how to proceed after sorting into ≤ 5 μ l of PBS, see Section C, below.

NOTE: PBS is **NOT** an optimal sorting buffer, as it interferes with the efficiency of cDNA synthesis and PCR amplification.

A. FACS Sorting into a Buffer Containing the CDS II A Oligo

In this protocol, cells are sorted into 12.5 μ l of buffer.

1. Prepare enough sorting buffer to prefill the 96-well plate or PCR strips, as indicated below.

In this protocol, we are assuming that FACS sorting of the cells will not change the volume of liquid in the plate wells. If your sorter dispenses a non-negligible amount of sheath fluid, adjust the volume of the CSS mix by reducing the amount of Nuclease-Free Water to maintain a total volume of 12.5 μ l per well.

- Due to small pipetting volumes, prepare no less than 250 μ l of sorting buffer, which is enough for 18 wells
- Scale up as needed for all reactions; include an additional 10% of the total reaction mix volume for overage
- Be sure to include negative control reactions in the count for the number of wells to prepare

Table 7. CDS Sorting Solution recipe

CDS Sorting Solution (CSS; with 3' SMART-Seq CDS Primer II A):

	Per well	1–18 wells*
10X Lysis Buffer	0.95 μ l	19 μ l
RNase Inhibitor	0.05 μ l	1 μ l
3' SMART-Seq CDS Primer II A	1 μ l	20 μ l
Nuclease-Free Water	10.5 μ l	210 μ l
Total volume	12.5 μl	250 μl

*Volumes include ~10% extra for overage.

Mix briefly, and then spin down.

NOTES:

- The 10X Lysis Buffer contains a detergent; it is critical to avoid bubbles when mixing.
- The 3' SMART-Seq CDS Primer II A provided with each kit is sufficient to collect the same number of cells as the number of reactions in the kit (e.g., a 96-reaction kit contains enough to prepare a 96-well plate). However, if you need to sort large numbers of cells compared to the number of cDNA reactions you plan to prepare, we recommend that you purchase the SMART-Seq HT Lysis Components (Takara Bio, Cat. No. 634439) separately.

2. Aliquot 12.5 μ l of CSS from Step 1 into the appropriate number of wells of PCR tube strips or a 96-well plate.

NOTE: To minimize bubble formation, set single- or multi-channel pipettes to 12.6 μ l and pipette only to the first stop when aliquoting. Changing tips often also minimizes bubble formation.

3. Seal the plate/tube strips with microplate film and briefly spin to collect the sorting buffer at the bottom of the wells.
4. Store the plate/tube strips at -20°C for 10 min at a minimum and up to 24 hr. As the volume of sorting buffer is small, the tubes/plate should be kept at -20°C until just before sorting.

When ready to sort:

5. Unseal the prepared plate/tube strips and sort cells into the sorting solution according to the FACS system manual and desired parameters.
6. Seal the plate/tube strips with an aluminum foil seal or PCR strip caps. Ensure the plate/tube strips are sealed firmly to minimize any evaporation.

NOTE: When using PCR strips, strip caps can be used instead of an aluminum foil seal but are not practical when sorting a large number of samples.

7. Immediately after sorting the cells and sealing the plate, spin briefly to collect the cells at the bottom of each well in the CSS.
8. Place the plate on dry ice to flash-freeze the sorted cells.

NOTE: If using PCR strips, leave them secured on the PCR rack for freezing.

9. Store sorted samples at -80°C until ready to proceed with cDNA synthesis.

NOTES:

- To use PCR strips sealed with an aluminum foil seal, use a clean razor blade to separate the individual strips, then push up slightly on the tubes from under the PCR rack to loosen them before taking out the desired number of strips.
- Long-term storage at -80°C may impact the efficiency of cDNA synthesis; however, it is safe to store the cells for several weeks prior to cDNA synthesis.

B. FACS Sorting into a Buffer Not Containing the CDS IIA Oligo

In this protocol, cells are sorted in 11.5 μl of buffer.

1. Prepare enough sorting buffer to prefill the 96-well plate or PCR strips, as indicated below.

In this protocol, we are assuming that FACS sorting of the cells will not change the volume of liquid in the plate wells. If your sorter dispenses a non-negligible amount of sheath fluid, adjust the volume of the PSS mix by reducing the amount of Nuclease-Free Water to maintain a total volume of 11.5 μl per well.

- Due to small pipetting volumes, prepare no less than 230 μl of sorting buffer, which is enough for 18 wells
- Scale up as needed for all reactions; include an additional 10% of the total reaction mix volume for overage
- Be sure to include negative control reactions in the count for the number of wells to prepare

Table 8. Plain Sorting Solution recipe

Plain Sorting Solution (PSS; without 3' SMART-Seq CDS Primer II A):

	Per well	1–18 wells*
10X Lysis Buffer	0.95 μl	19 μl
RNase Inhibitor	0.05 μl	1 μl
Nuclease-Free Water	10.5 μl	210 μl
Total volume	11.5 μl	230 μl

*Volumes include ~10% extra for overage and are based on use of 2 μl of 3' SMART Seq CDS Primer II A and 9.5 μl Nuclease-Free Water.

- Briefly mix gently, then spin down.

NOTES:

- The 10X Lysis Buffer contains a detergent; it is critical to avoid bubbles when mixing.
- If you need to sort large numbers of cells compared to the number of cDNA reactions you plan to prepare, you have the option to purchase the 10X Lysis Buffer (Takara Bio, Cat. No. 635013) separately.

- Aliquot 11.5 µl of PSS from Step 1 into the appropriate number of wells of PCR tube strips or a 96-well plate.

NOTE: To minimize bubble formation, set single- or multi-channel pipettes to 11.6 µl and pipette only to the first stop when aliquoting. Changing tips often also minimizes bubble formation.

- Seal the plate/tube strips and briefly spin to ensure the sorting buffer collects at the bottom of the wells.
- Store the plate/tube strips at –20°C for 10 min at a minimum and up to 24 hr. As the volume of sorting buffer is small, the tubes/plate should be kept at –20°C until just before sorting.

When ready to sort:

- Unseal the prepared plate/tube strips and sort cells into the sorting solution according to the FACS system manual and desired parameters.
- Seal the plate/tube strips with an aluminum foil seal or PCR strip caps. Ensure the plate/tube strips are sealed firmly to minimize any evaporation.

NOTE: When using PCR strips, strip caps can be used instead of aluminum foil, but are not practical when sorting a large number of samples.

- Immediately after sorting the cells and sealing the plate, spin briefly to collect the cells at the bottom of each well in the PSS.
- Place the plate on dry ice to flash-freeze the sorted cells.

NOTE: If using PCR strips, leave them secured on the PCR rack for freezing.

- Store sorted samples at –80°C until ready to proceed with cDNA synthesis.

NOTES:

- To use PCR strips sealed with an aluminum foil seal, use a clean razor blade to separate the individual strips, then push up slightly on the tubes from under the PCR rack to loosen them before taking out the desired number of strips.
- Long-term storage at –80°C may impact the efficiency of cDNA synthesis; however, it is safe to store the cells for several weeks prior to cDNA synthesis.

IMPORTANT: Since the PSS does not include the 3' SMART-Seq CDS Primer II A, you need to add it when you thaw your samples—see Section V.A, Step 5.

C. FACS Sorting into Nonvalidated Buffers

Sorting into CSS (CDS Sorting Solution) or PSS (Plain Sorting Solution) delivers the best performance from cells isolated with FACS or other single-cell isolation methods. However, it may not always be possible to use these buffers. In such cases, we recommend minimizing the volume of the buffer being carried into the cDNA synthesis reaction. The maximum volume of buffer that can be added to a cDNA synthesis reaction is 10.5 µl.

If using an alternative buffer, we recommend performing a pilot experiment using Control Total RNA and the estimated amount of buffer that you expect to accompany your cell(s) to determine its impact on cDNA synthesis. Sorting cells in 1 μl of 1X PBS is acceptable and will not interfere with kit performance. If it is desired to sort cells in >1 μl of 1X PBS, it is critical to keep the PBS volume below 5 μl . PBS is not an optimal sorting buffer as it interferes with the efficiency of cDNA synthesis and PCR amplification; thus, kit performance (cDNA yield and sensitivity) will be impacted (when using >1 μl of PBS). If you must use 2–5 μl of PBS, the cDNA yield will be lower, and you should consider adding one to three extra PCR cycles to the recommended number of cycles in [Table 3](#) (Section V.B). In addition, you must use PBS without Ca^{2+} and Mg^{2+} (e.g., Sigma, Cat. No. D8537). The addition of RNase Inhibitor in a ratio similar to what is recommended for CDS and PSS may be helpful, although not essential.

When your samples are not in a recommended FACS sorting buffer, we still recommend flash freezing samples on dry ice as quickly as possible after collection and storing them at -80°C until processing. Follow the instructions outlined in Section V.A. for preparing a 10X Reaction Buffer, setting up control reactions, and adding 3' SMART-Seq CDS Primer II A.

Appendix B: PCR Optimization

If you have a sufficient amount of starting material (>1 ng total RNA), we recommend optimizing the PCR cycling parameters for your experiment. If you have a very limited amount of material or your sample is unique, use a similar source of RNA or cells to perform PCR cycle optimization prior to using your actual sample. Choosing the optimal number of PCR cycles ensures that the amplification will remain in the exponential phase. When the yield of PCR products stops increasing with more cycles, the reaction has reached its plateau. Overcycled cDNA can result in a less representative cDNA library. Undercycling, on the other hand, results in a lower cDNA yield. The optimal number of cycles for your experiment is one cycle fewer than is needed to reach the plateau. Be conservative; when in doubt, it is better to use too few cycles than too many.

To perform PCR cycle optimization, prepare several tubes containing an amount of RNA equal to your sample amount. Subject each tube to a different range of PCR cycles. For example, if you have 1 ng of RNA, subject one tube to the recommended a number of cycles. Subject the other two tubes to 2–3 cycles fewer or more than the first tube (e.g., 12, 10, and 8 cycles, N) for a 1 ng sample.

1. Use the following program for thermal cycling:

95°C	1 min	
N cycles:		
98°C	10 sec	}
65°C	30 sec	
68°C	3 min	
72°C	10 min	
4°C	forever	

2. Perform **Purification of Amplified cDNA** ([Section V.C](#)).
3. Run the samples on an Agilent High Sensitivity DNA Chip using the Agilent 2100 Bioanalyzer to evaluate DNA output (Section V.D). See the user manual for the Agilent High Sensitivity DNA Kit for instructions.
4. Determine the optimal number of PCR cycles required for each experimental and control sample. We recommend using the lowest PCR cycle number that generates enough material for library construction.

Appendix C: Expected Results When Analyzing cDNA with TapeStation

The Agilent 2100 Bioanalyzer used with the Agilent High Sensitivity DNA Kit (Agilent, Cat. No. 5067-4626) offers the best option for visualization of cDNA profiles generated with SMART-Seq mRNA Single Cell LP. Another good option, particularly for processing a large number of samples, is the Fragment Analyzer and High Sensitivity Large Fragment Analysis Kit (Agilent, Cat. No. DNF-464).

If these instruments are not available, an Agilent TapeStation system can be used with a High Sensitivity D5000 ScreenTape (Agilent, Cat. No. 5067-5592). Because the scale is very different—as shown in Figure 6—the cDNA profile on the TapeStation may look quite different than the profile on the Bioanalyzer, particularly for yields below 500 pg/μl. However, if the ScreenTape shows a broad smear going from ~600–2,500 bp, the cDNA synthesis can be considered successful, particularly if the negative control, performed with the same number of PCR cycles, shows a relatively flat profile. SMART-Seq mRNA Single Cell LP should generate cDNA yields higher than 500 pg/μl, and the cDNA profile should be detected relatively easily.

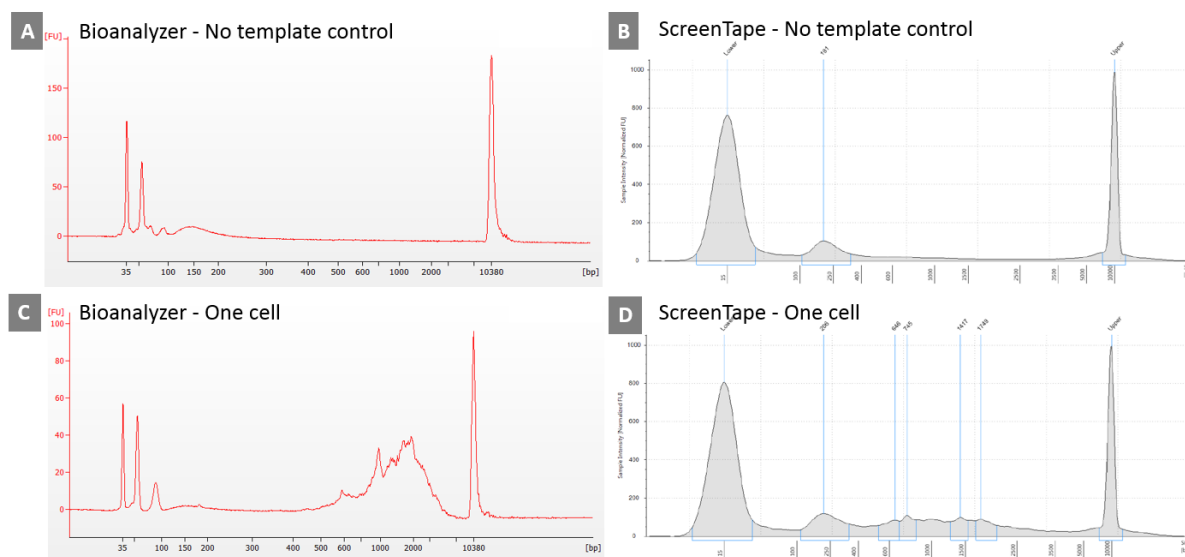


Figure 6. Comparison of electropherogram results from Agilent 2100 Bioanalyzer and Agilent TapeStation system. All samples were subjected to one-step RT-PCR as described in the SMART-Seq HT Kit (Takara Bio, Cat. No. 634437) protocol, using 18 PCR cycles. (cDNA was not generated with the SMART-Seq mRNA Single Cell LP, but rather the SMART-Seq HT Kit, which features a similar technology compatible with cDNA synthesis from single cells and generates a cDNA profile similar to the SMART-Seq mRNA Single Cell LP.) After bead purification, 1 μl of the sample was analyzed using Agilent’s Bioanalyzer High Sensitivity DNA Kit (**Panels A and C**) or the High Sensitivity D5000 ScreenTape (**Panels B and D**). The cDNA generated with the SMART-Seq HT Kit may show a small amount of PCR product between 100 and 200 bp, as shown in the example here, but cDNA generated with the SMART-Seq mRNA Single Cell LP should be relatively flat in this region.

Appendix D: Troubleshooting Guide for Final Libraries

A. Broad peak(s) in Bioanalyzer traces

Description of problem	Possible explanation	Solution
After purification of the amplified library, the Bioanalyzer traces show broad peak(s) extending from <1,000 bp to >10,000 bp.	The library was overamplified.	Perform fewer PCR cycles during the library amplification reaction.
	The Bioanalyzer chip was overloaded.	This is a common problem for high-sensitivity chips. Load ~1–5 ng/μl, and then repeat Bioanalyzer run.

B. High quantity of small molecules in Bioanalyzer traces

Description of problem	Possible explanation	Solution
After purification of the amplified library, the Bioanalyzer trace shows a high quantity of small molecules between 35 and 200 bp.	Bead:sample ratio was higher than the suggested 0.8:1.	Perform an additional bead purification using a ratio of 0.8:1 or 0.7:1.

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