invitrogen

SuperScript™ IV Single Cell/Low-Input cDNA PreAmp Kit

USER GUIDE

Catalog Numbers 11752048, 11752096, 11752192, 11752384, and 11752480

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The information in this guide is subject to change without notice.

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Revision	Date	Description
A.0	11 October 2021	New manual for introduction of the SuperScript™ IV Single Cell/Low-Input cDNA PreAmp Kit.

Contents

1 Product information

IMPORTANT! Before using this product, read and understand the information in the "Safety" appendix in this document.

Product description

The Invitrogen™ SuperScript™ IV Single Cell/Low-Input cDNA PreAmp Kit is designed for efficient cDNA synthesis and amplification directly from intact single cells (1–1000 cells/sample), or low amounts of total RNA (2 pg to 10 ng). The kit contains all required components to perform cell lysis, reverse transcription (RT), and PCR amplification in a convenient premixed format. A combination of superior enzymes (SuperScript™ IV Reverse Transcriptase and Platinum™ SuperFi™ U DNA Polymerase) enables high yields, sensitivity, and accuracy.

Key features of the kit:

- **Superior sensitivity**—easy detection of low abundant targets from as low as single cell or 2 pg of total RNA.
- **High quality cDNA**—full-length transcript information with uniform coverage.
- **Streamlined workflow**—simple one-tube protocol.
- **Time saving**—short lysis and reverse transcription times.
- **Universal**—global preamplification compatible with downstream analysis by NGS or real-time PCR.

Procedure overview

The SuperScript™ IV Single Cell/Low-Input cDNA PreAmp Kit leverages the terminal deoxynucleotidyl transferase (TdT) activity of SuperScript™ IV Reverse Transcriptase. A Capturing Oligonucleotide containing oligo(dT) and adapter sequences is used as a primer for selective first strand cDNA synthesis from poly(A)-containing RNAs. When the reverse transcriptase reaches the 5‘ end of the RNA template, TdT activity adds 1–3 extra nucleotides to the cDNA end, enabling template switching and ligation-free incorporation of the adapter sequence at the 3‘ end of the resulting cDNA. Adapter sequences incorporated at both ends of the cDNA serve as primer-binding sites in the subsequent PCR amplification step, allowing global preamplification of full-length templates. Due to the short reaction times and minimal hands-on time, this simple one-tube preamplification protocol can be completed in about two hours. The high quality global cDNA obtained can be used for next-generation sequencing (NGS) applications or for gene expression analysis by real-time PCR.

Contents and storage

Table 1 SuperScript™ IV Single Cell/Low-Input cDNA PreAmp Kit (Cat. No. 11752048, 48 reactions)

Contents	Amount	Storage [1]
10X Lysis Buffer	48 µL	–20°C ± 5°C
Capturing Oligonucleotide	48 µL	
4X SuperScript™ cDNA Synthesis Master Mix	240 µL	
Template Switching Oligonucleotide	48 µL	
2X Platinum™ SuperFi™ U Preamplification Master Mix	2 × 1.2 mL	
Preamplification Primer	48 µL	
Nuclease-free water	2 × 1.25 mL	
RNase Inhibitor	19 µL	

[1] See the expiration date on the label.

Table 2 Additional kit formats

	Cat. No. 11752096 (96 reactions)	Cat. No. 11752192 (192 reactions)	Cat. No. 11752384 (384 reactions)	Cat. No. 11752480 (480 reactions)
SuperScript™ IV Single Cell/Low-Input cDNA PreAmp Kit (Cat. No. 11752048)	2 boxes	4 boxes	8 boxes	10 boxes

Required materials not supplied

Unless otherwise indicated, all materials are available through **thermofisher.com**. "MLS" indicates that the material is available from **fisherscientific.com** or another major laboratory supplier.

Catalog numbers that appear as links open the web pages for those products.

Required materials for cDNA synthesis and preamplification

Item	Source
Equipment	
Thermal cycler with heated lid, one of the following (or equivalent): • Veriti™ 96-Well Thermal Cycler • ProFlex™ 96-well PCR System • ProFlex™ 3 × 32-well PCR system	 4375786 4484075 4484073
Benchtop microcentrifuge	**MLS**
Vortex mixer	**MLS**
Heat block and/or thermal mixer	**MLS**
Cooling rack for 0.2-mL PCR tubes or plates	**MLS**
Calibrated single-channel or multichannel pipettes (1 µL–1,000 µL)	**MLS**
Tubes, plates, and other consumables	
0.2-mL thin-walled PCR tubes or plates	**thermofisher.com/plastics**
Nuclease-free pipette tips	**MLS**
Disposable gloves	**MLS**

Additional optional materials for cDNA purification

Item	Source
Tris buffers for elution, one of the following: • 10 mM Tris-HCl buffer, pH 7.5–8.5 • TE buffer (10 mM Tris-HCl, pH 8.0, 1 mM EDTA) • Low TE buffer (10 mM Tris-HCl, pH 8.0, 0.1 mM EDTA) [1]	**MLS**
Magnetic rack, one of the following (or equivalent): • Invitrogen™ DynaMag™-2 Magnet (for 1.5-mL tubes) • Invitrogen™ DynaMag™–96 Side Magnet (for PCR strips or 96-well 0.2-mL plates)	12321D 12331D
Agencourt™ AMPure™ XP beads	Beckman Coulter™ A63880
Eppendorf™ 1.5-mL DNA LoBind microcentrifuge tubes, or equivalent 1.5-mL nuclease-free tubes	022431021
Ethanol, 96–100% (molecular biology grade)	**MLS**

[1] For use with library preparation kits that are not compatible with EDTA-containing elution buffers.

Workflow

Workflow

5 min

Prepare RT reaction mix

Keep the prepared RT reaction mix at room temperature until use.

5 min

Perform the lysis/hybridization reaction

1. Prepare the lysis/hybridization reactions.
2. Incubate for 1 minute at 72°C.

40 min

Perform the RT reaction

1. Immediately add RT reaction mix to each sample.
2. Set up the thermal cycling conditions, then start the RT reaction.

STOPPING POINT Synthesized cDNA can be stored at –70°C for up to 1 week.

~1 h

Preamplify the cDNA

1. Prepare the preamplification reaction mix.
2. Perform the preamplification reaction.
3. Proceed to the next step according to your application.
   - For qPCR—Use samples immediately.
   - For NGS—Proceed to purify the samples.

Preamplified cDNA samples can be stored at -20°C for up to 7 days. Purification is recommended prior to long-term storage.

[~40] m

Purify the preamplified cDNA

- For NGS applications—Purification is required to remove excess preamplification primers and enzymes that can impact library preparation.
- For qPCR applications—Purification is not required, however, it can be used to concentrate samples for detection of low-expression targets.

Use the cDNA samples for qPCR or NGS

See "Guidelines for downstream applications" on page 17.

2 Methods

Procedural guidelines

- Carefully read the entire contents of this user guide before starting the procedure.
- Keep all reagents, reaction mixes, and samples on ice, unless otherwise indicated.
- To prevent cross-contamination, carefully pipet reagents and samples to avoid splashing.
- Pipet viscous reagents slowly. Gently vortex or pipet up and down several times to ensure complete mixing.
- Prepare reactions in 0.2-mL PCR tubes (or plates) on ice or a benchtop tube cooler.
- For multiple reactions, prepare a single reaction mix, then dispense the appropriate volume to each reaction tube to minimize pipetting error. Scale common components proportionally based on the volumes indicated per sample, then add 5–10% overage.
- To prevent nuclease contamination:
  - Wear laboratory gloves during the procedures. Gloves protect you from the reagents, and they protect the nucleic acid from nucleases that are present on skin.
  - Use nucleic acid-free pipette tips to handle the reagents, and avoid putting used tips into the reagent containers.
  - Decontaminate lab benches and pipettes before you begin.
- Room temperature is 20–25°C unless otherwise indicated.
- Follow “Good laboratory practices for PCR and RT-PCR” on page 20.

Guidelines for RNA samples

- The kit is designed for use with intact cells or purified total RNA. Because only poly(A)-containing RNA is amplified, rRNA depletion or mRNA enrichment is not required.
- For optimal results, use high-quality poly(A) RNA and total RNA.
- Use intact mammalian cells only.
- Purification of total RNA is required for cDNA preamplification of RNA isolated from plant, fungi, or other cell wall-containing organisms.
- Ensure that input RNA is free of contaminants, such as residual traces of proteins, organic solvents, and salts that can degrade the RNA or decrease the activity and sensitivity of enzymes.
- Ensure that purified RNA is suspended in nuclease-free water or low-salt storage or elution buffer.
- RNA quantity in cells can vary by cell type, cell cycle, and cell health. Optimization of the PCR cycle number may be needed to reach desired yields.
- For cell suspension and sorting, we recommend using balanced salt solutions, such as PBS, HBSS, EBSS, or other common PBS-based cell-sorting buffers.

Before you begin

- Thaw reagents at room temperature for 5 minutes, then mix thoroughly. Centrifuge the tubes and store on ice until use.
- Preheat a thermal cycler or thermal shaker to 72°C.
- Centrifuge all reagent tubes before opening to collect the contents.

Prepare RT reaction mix

1. Prepare the RT reaction.

Component	Volume per reaction [1]
Nuclease-free water	4 µL
4X SuperScript™ cDNA Synthesis Master Mix	5 µL
Template Switching Oligonucleotide	1 µL
Total volume per reaction	**10 µL**

[1] Include 5–10% excess volume to compensate for pipetting error when preparing a master mix for multiple reactions.

2. Keep RT reaction mix at room temperature until the “Perform the RT reaction” step.

Perform the lysis/hybridization reaction

1. Prepare the lysis/hybridization reaction—Combine the following components.

Component	Volume per reaction
10X Lysis Buffer	1 µL
Capturing Oligonucleotide	1 µL
(Optional) RNase Inhibitor [1]	0.4 µL
Sample (cells or small quantity of RNA)	Variable
Nuclease-free water	to final volume of 10 µL
Total volume per reaction	**10 µL**

[1] Recommended for samples that can contain RNases, such as cells or other non-purified samples.

2. Pipet up and down 5–8 times to mix, then briefly centrifuge to collect the contents.
3. Incubate for 1 minute at 72°C, then briefly centrifuge to collect the contents.

Immediately proceed to perform the RT reaction.

Perform the RT reaction

1. Add 10 µL of RT reaction mix to each reaction well or tube containing the lysed sample, then briefly centrifuge.
2. Set up the thermal cycling conditions for the reverse transcription reaction.

Step	Temperature	Heated lid temperature	Time
RT and template-switching	50°C	105°C	30 minutes [1]
Enzyme inactivation	85°C		5 minutes
Hold	4°C		∞

[1] For cell samples, the incubation time can be increased up to 90 minutes to improve sensitivity. Specificity, however, may be lowered due to increased yields of intronic or other non-mRNA poly(A)-containing RNA.

3. Load the plate or tubes into the thermal cycler, then start the run.
4. At the end of the run, briefly centrifuge the samples, then store on ice until ready to use.

STOPPING POINT Store synthesized cDNA at -70°C for up to 1 week.

Preamplify the cDNA

1. If frozen, thaw the cDNA samples. Vortex gently, then centrifuge briefly to collect the contents. Place the plate or tube on ice.

2. Prepare preamplification reaction mix—Combine the following components for the required number of samples.

Component	Volume per sample [1]
Nuclease-free water	29 µL
2X Platinum™ SuperFi™ U Preamplification Master Mix	50 µL
Preamplification Primer	1 µL
Total volume per sample	**80 µL**

[1] Include 5–10% excess volume to compensate for pipetting error when preparing the master mix for multiple reactions.

3. Add 80 µL of the preamplification reaction mix to each cDNA sample for a final reaction volume of 100 µL.

4. Pipet up and down or gently vortex to mix, then briefly centrifuge to collect the contents.

5. Set up the thermal cycling conditions for the preamplification reaction.

Step	Temperature	Time	Cycles
Initial denaturation	98°C	30 seconds	1
Denaturation	98°C	10 seconds	• 21 cycles for 2 pg of total RNA • 18 cycles for 10 pg of total RNA, or single cells • 15 cycles for 100 pg of total RNA, or up to 10 cells • 11 cycles for 1–10 ng of total RNA, or 100–1,000 cells **Note:** An additional 2–3 cycles are required for smaller cells, such as Jurkat, Daudi, or peripheral blood mononuclear cells (PBMC).
Annealing	65°C	10 seconds	
Extension	67°C	3 minutes [1]	
Final extension	67°C	5 minutes[1]	1
Hold	4°C	∞	

[1] For amplification of >10 kb RNA targets, such as poly(A)-containing viral genomic RNA, we recommend increasing the extension and final extension times to 6 minutes.

6. Load the plate or tubes into the thermal cycler, then start the run.

7. At the end of the run, briefly centrifuge the samples, then place on ice.

8. Determine whether cDNA purification is needed, then proceed as indicated.

Application	cDNA purification	Action
qPCR	Not required	Use samples immediately. See "Guidelines for downstream applications" on page 17. **Note:** If needed, purification can be used to concentrate samples for detection of low-expression targets (see "Purify the preamplified cDNA" on page 14).
NGS	Required	Proceed to purify the samples (see "Purify the preamplified cDNA").

Note: Purification is also recommended prior to long-term storage. See "Purify the preamplified cDNA" on page 14.

Store preamplified cDNA samples at -20°C for up to 7 days.

Purify the preamplified cDNA

Note: Purification reagents are not supplied with the kit. See "Additional optional materials for cDNA purification" on page 8.

1. Gently vortex the Agencourt™ AMPure™ XP beads tube to resuspend the magnetic beads completely.
2. Bind the preamplified cDNA to the beads.
   a. Add 70 µL of the bead suspension to a 1.5-mL low-bind tube.
   b. Transfer 100 µL of each preamplified cDNA sample to a bead-containing tube.
   c. Thoroughly vortex or pipet up and down several times to mix the cDNA with the bead suspension. Briefly centrifuge to collect droplets that may have formed on the walls of the tube.
   d. Incubate for 5 minutes at room temperature.
3. Remove the supernatant from the beads:
   a. Place the tube in a magnetic rack for at least 2 minutes to separate the beads from the solution. Wait for the solution to clear before proceeding to the next step.
   b. With the tube in the magnetic rack, use a pipette to carefully aspirate, then discard the supernatant.

      IMPORTANT! Do not disturb the magnetic beads. Remove all of the supernatant from each tube.
4. Leave the tube in the magnetic rack.
   a. Add 200 µL of 80% ethanol to each sample.

b. Incubate for 30 seconds at room temperature.

IMPORTANT! Do not resuspend the magnetic beads in the ethanol.

c. With the tube in the magnetic rack, use a pipette to carefully aspirate, then discard the supernatant.

5. Repeat step 4.

6. Elute the cDNA from the beads:
   a. Remove the tube from the magnetic rack.
   b. Add 50 µL of nuclease-free water to each sample, then thoroughly vortex or pipet up and down several times to mix.
   c. Incubate for 1 minute at room temperature, then briefly centrifuge.
   d. Place the tube in the magnetic rack for at least 2 minutes to separate the beads from the solution. Wait for the solution to clear before proceeding to the next step.
   e. With the tube in the magnetic rack, collect 48 µL of the eluate, then transfer to a new low-bind tube.

IMPORTANT! Do not disturb the magnetic beads.

7. Bind the eluted cDNA to new beads.
   a. Gently vortex the Agencourt™ AMPure™ XP beads tube to resuspend the magnetic beads completely.
   b. Add 40 µL of the bead suspension to the eluate collected in step 6.
   c. Thoroughly vortex or pipet up and down several times to mix the cDNA with the bead suspension. Briefly centrifuge to collect droplets that may have formed on the walls of the tube.
   d. Incubate for 5 minutes at room temperature.

8. Remove the supernatant from the beads:
   a. Place the tube in a magnetic rack for at least 2 minutes to separate the beads from the solution. Wait for the solution to clear before proceeding to the next step.
   b. With the tube in the magnetic rack, use a pipette to carefully aspirate, then discard the supernatant.

IMPORTANT! Do not disturb the magnetic beads. Remove all of the supernatant from each tube.

9. Leave the tube in the magnetic rack.
   a. Add 200 µL of 80% ethanol to each sample.

b. Incubate for 30 seconds at room temperature.

IMPORTANT! Do not resuspend the magnetic beads in the ethanol.

c. With the tube in the magnetic rack, use a pipette to carefully aspirate, then discard the supernatant.

10. Repeat step 9.

11. With the tube in the magnetic rack, air-dry the beads for 2 minutes at room temperature, or until all traces of ethanol are removed.

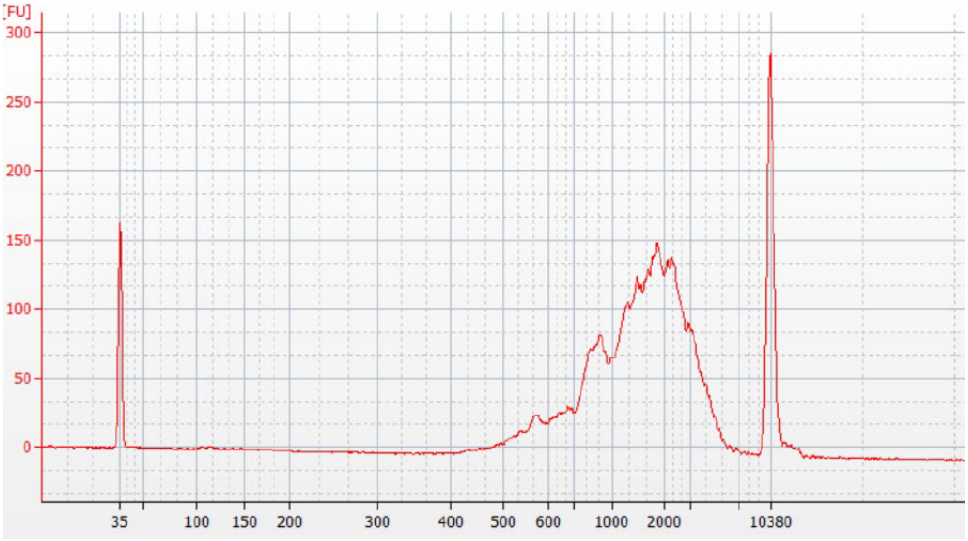
12. Remove the tube from the magnetic rack.
    a. Add 17 µL of Tris buffer (see "Additional optional materials for cDNA purification" on page 8) directly to the pellet to resuspend the beads.
    b. Thoroughly vortex or pipet up and down several times to mix the suspension.
    c. Incubate for 1 minute at room temperature, then briefly centrifuge.

13. Elute the cDNA from the beads.
    a. Place the tube in the magnetic rack for at least 2 minutes to separate the beads from the solution. Wait for the solution to clear before proceeding to the next step.
    b. With the tube in the magnetic rack, collect 15 µL of the eluate, then transfer to a new low-bind tube for storage or later use.

IMPORTANT! Do not disturb the magnetic beads.

14. Store the purified cDNA sample at -20°C or proceed directly to qPCR or NGS. See "Guidelines for downstream applications" on page 17.

Guidelines for downstream applications

Application	Guidelines
qPCR	• Purification of preamplified cDNA is not required, but can be used to concentrate samples for detection of low-expression targets. • For purified cDNA samples—Proceed directly to qPCR with undiluted samples. • For unpurified cDNA samples—Dilute samples 1:10 to 1:100. The sample input volume should not exceed 20% of the final reaction volume. • We recommend the use of TaqMan™ Fast Advanced Master Mix (Cat. No. 4444556) for all TaqMan™-based detection methods. • We recommend the use of PowerTrack™ SYBR™ Green Master Mix (Cat. No. A46012) for all SYBR GREEN™-based detection methods. • Do not exceed the sample input volume recommended by the manufacturer of the qPCR reagent.
NGS	• Purification of preamplified cDNA is required to remove excess preamplification primers and enzymes that can impact library preparation. • Both ligation- and transposase-based methods can be used for library preparation. Because the final preamplified product is dsDNA, use DNA library preparation kits for library preparation (e.g., Collibri™ ES DNA Library Prep Kits or Illumina® Nextera® XT DNA Library Preparation Kit). • See the appropriate library preparation kit user guide for DNA input requirements and library preparation conditions. • We recommend the Agilent™ 2100 Bioanalyzer™ Instrument for library quantification. To quantify the yield of amplified DNA, use size range 300–9,000 bp. Final preamplification reaction products should have a peak at approximately 2 kb (see Figure 1).  **Figure 1 Example results from the Agilent™ 2100 Bioanalyzer™ Instrument** Amplification products from 2 pg of Universal Human Reference RNA.

Troubleshooting

Troubleshooting: qPCR

Observation	Possible cause	Recommended action
Low amplified product yield	The quality of RNA input was poor.	Use high-quality RNA with intact poly(A) sequences at the 3' ends.
	The number of amplification cycles was insufficient.	The quantity of RNA in cells and other biological samples can vary significantly. Perform screening experiments to estimate the amount of RNA input, then adjust the number of amplification cycles accordingly.
Low-expression targets are not detected	The sample DNA concentration was too low.	Perform the purification procedure to concentrate the cDNA sample, then proceed directly to qPCR with undiluted sample. See “Purify the preamplified cDNA” on page 14.
Amplification curve shows no amplification for synthetic RNA spikes (positive control)	The RNA spikes did not have poly(A) tails.	Use RNA spikes that contain high-quality poly(A) tails.
High base fluorescence signal	Excess preamplification primers in the PCR.	Purify the cDNA sample. See “Purify the preamplified cDNA” on page 14.
		Increase the sample dilution before qPCR.
Non-uniform amplification	The quality of RNA input was poor. Degraded 5' ends of RNA resulted in a bias towards amplification at the 3' end.	Use high-quality RNA with intact poly(A) sequences at the 3' ends.
	The RNA input was too high.	Do not use more than 10 ng of total RNA.
	Too many amplification cycles were used.	Do not use more cycles than recommended.

Troubleshooting: NGS

Observation	Possible cause	Recommended action
High primer-dimer content in sequencing results	The purification procedure was not performed or was performed incorrectly.	Perform capillary electrophoresis to determine the primer concentration.
High primer-dimer content in the purified, amplified product	The purification procedure was not performed or was performed incorrectly.	Bring the volume of the sample up to 48 µL with nuclease-free water, then repeat the second stage of the purification procedure. See “Purify the preamplified cDNA” on page 14 (step 7).
Low amplified product yield	The quality of RNA input was poor.	Use high-quality RNA with intact poly(A) sequences at the 3' ends.
	The number of amplification cycles was insufficient.	The quantity of RNA in cells and other biological samples can vary significantly. Perform screening experiments to estimate the amount of RNA input, then adjust the number of amplification cycles accordingly.
Extra peak(s) (>300 bp) are present in capillary electrophoresis data	The concentration of internal control spikes, such as ERCC RNA, was too high.	Reduce the concentration of internal control spikes. Optimization experiments may be needed to determine the appropriate concentration for each input amount and/or type.
	The amount of amplified rRNA products was too high.	Reduce the RT reaction step to 30 minutes.
Extra peak(s) (<300 bp) are present in capillary electrophoresis data	The purification procedure was performed incorrectly.	Bring the volume of the sample up to 48 µL with nuclease-free water, then repeat the second stage of the purification procedure. See “Purify the preamplified cDNA” on page 14 (step 7).

B

Supplemental information

Good laboratory practices for PCR and RT-PCR

- Wear clean gloves and a clean lab coat.
  - Do not wear the same gloves and lab coat that you have previously used when handling amplified products or preparing samples.
- Change gloves if you suspect that they are contaminated.
- Maintain separate areas and dedicated equipment and supplies for:
  - Sample preparation and reaction setup.
  - Amplification and analysis of products.
- Do not bring amplified products into the reaction setup area.
- Open and close all sample tubes carefully. Avoid splashing or spraying samples.
- Keep reactions and components capped as much as possible.
- Use a positive-displacement pipettor or aerosol-resistant barrier pipette tips.
- Clean lab benches and equipment periodically with 10% bleach solution or DNA decontamination solution.

C

Safety

WARNING! GENERAL SAFETY. Using this product in a manner not specified in the user documentation may result in personal injury or damage to the instrument or device. Ensure that anyone using this product has received instructions in general safety practices for laboratories and the safety information provided in this document.

- Before using an instrument or device, read and understand the safety information provided in the user documentation provided by the manufacturer of the instrument or device.
- Before handling chemicals, read and understand all applicable Safety Data Sheets (SDSs) and use appropriate personal protective equipment (gloves, gowns, eye protection, and so on). To obtain SDSs, see the “Documentation and Support” section in this document.

Chemical safety

WARNING! GENERAL CHEMICAL HANDLING. To minimize hazards, ensure laboratory personnel read and practice the general safety guidelines for chemical usage, storage, and waste provided below. Consult the relevant SDS for specific precautions and instructions:

- Read and understand the Safety Data Sheets (SDSs) provided by the chemical manufacturer before you store, handle, or work with any chemicals or hazardous materials. To obtain SDSs, see the "Documentation and Support" section in this document.
- Minimize contact with chemicals. Wear appropriate personal protective equipment when handling chemicals (for example, safety glasses, gloves, or protective clothing).
- Minimize the inhalation of chemicals. Do not leave chemical containers open. Use only with sufficient ventilation (for example, fume hood).
- Check regularly for chemical leaks or spills. If a leak or spill occurs, follow the manufacturer cleanup procedures as recommended in the SDS.
- Handle chemical wastes in a fume hood.
- Ensure use of primary and secondary waste containers. (A primary waste container holds the immediate waste. A secondary container contains spills or leaks from the primary container. Both containers must be compatible with the waste material and meet federal, state, and local requirements for container storage.)
- After emptying a waste container, seal it with the cap provided.
- Characterize (by analysis if needed) the waste generated by the particular applications, reagents, and substrates used in your laboratory.
- Ensure that the waste is stored, transferred, transported, and disposed of according to all local, state/provincial, and/or national regulations.
- **IMPORTANT!** Radioactive or biohazardous materials may require special handling, and disposal limitations may apply.

Biological hazard safety

WARNING! BIOHAZARD. Biological samples such as tissues, body fluids, infectious agents, and blood of humans and other animals have the potential to transmit infectious diseases. Conduct all work in properly equipped facilities with the appropriate safety equipment (for example, physical containment devices). Safety equipment can also include items for personal protection, such as gloves, coats, gowns, shoe covers, boots, respirators, face shields, safety glasses, or goggles. Individuals should be trained according to applicable regulatory and company/ institution requirements before working with potentially biohazardous materials. Follow all applicable local, state/provincial, and/or national regulations. The following references provide general guidelines when handling biological samples in laboratory environment.

- U.S. Department of Health and Human Services, *Biosafety in Microbiological and Biomedical Laboratories (BMBL)*, 6th Edition, HHS Publication No. (CDC) 300859, Revised June 2020
  https://www.cdc.gov/labs/pdf/CDC-BiosafetymicrobiologicalBiomedicalLaboratories-2020-P.pdf
- Laboratory biosafety manual, fourth edition. Geneva: World Health Organization; 2020 (Laboratory biosafety manual, fourth edition and associated monographs)
  www.who.int/publications/i/item/9789240011311

D Documentation and support

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  - Safety Data Sheets (SDSs; also known as MSDSs)

  Note: For SDSs for reagents and chemicals from other manufacturers, contact the manufacturer.

Limited product warranty

Life Technologies Corporation and/or its affiliate(s) warrant their products as set forth in the Life Technologies' General Terms and Conditions of Sale at **www.thermofisher.com/us/en/home/global/terms-and-conditions.html**. If you have any questions, please contact Life Technologies at **www.thermofisher.com/support**.