

# Nextera XT DNA Library Prep

## Reference Guide



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## Revision History

Document	Date	Description of Change
Document # 15031942 v05	May 2019	<p>Added information on IDT® for Illumina®–Nextera™ UD Indexes sets A, B, C, and D, including kit contents, preparation procedures, and additional resources.</p> <p>Removed plate layout information.</p> <p>Removed the Pool Libraries section and moved the Check Library Quality section before the Normalize Libraries section.</p> <p>Revised Additional Resources to provide more clarity on the resources available.</p> <p>Revised language throughout document to provide consistency across other Nextera library preparation reference guides.</p> <p>Added protocol for diluting libraries to the starting concentration.</p> <p>Removed obsolesced Nextera XT Index Kit (96 Indexes, 384 Samples) (# FC-131-1002) from Kit Contents.</p>
Document # 15031942 v04	January 2019	<p>Added information on reviewing sequencing workflows to ensure compatibility with library prep methods.</p>
Document # 15031942 v03	February 2018	<p>Updated the normalize libraries procedure to indicate that shaking samples after the five-minute elution is necessary only if samples are not resuspended.</p> <p>Reorganized kit contents information, including renaming some sections to match kit labeling and identify storage temperature.</p> <p>Corrected the diagram that shows how the Nextera XT assay works to clarify each transposome dimer has two of the same adapter color.</p>

Document	Date	Description of Change
Document # 15031942 v02	April 2017	<p>Added the following information:</p> <ul style="list-style-type: none"> <li>• Supported genome size of &lt; 5 Mb.</li> <li>• The ratio of absorbance that indicates contaminants.</li> <li>• Recommendations for PCR amplicons.</li> <li>• AMPure XP bead recommendations for runs <math>\geq 2 \times 250</math> cycles.</li> <li>• Reagent and library volumes in the PCR plate after the tagmentation and amplification steps.</li> <li>• Beckman Coulter Genomics item # A63880 for Agencourt AMPure XP, 5 ml.</li> <li>• Illumina catalog # PE-121-1003 and # FC-121-1003 for the TruSeq Dual Index Sequencing Primer Box.</li> </ul> <p>Added the following technical notes to the list of additional resources:</p> <ul style="list-style-type: none"> <li>• <i>Best Practices for Standard and Bead-Based Normalization in Nextera XT DNA Library Preparation Kits (Pub. No. 470-2016-007)</i></li> <li>• <i>Nextera XT Library Prep: Tips and Troubleshooting (Pub. No. 770-2015-015)</i></li> </ul> <p>Consolidated steps in the pool libraries procedure.</p> <p>Identified the NaOH consumable as molecular biology grade.</p> <p>Specified the use of molecular-grade water or 10 mM Tris-HCl, pH 7.5–8.5 to dilute starting material for DNA quality assessment.</p> <p>Specified proceeding immediately when tagmentation is complete so that neutralization occurs while the transposome is active.</p> <p>Specified a thaw time of 20 minutes for NPM (Nextera PCR Master Mix).</p> <p>Updated the normalize libraries procedure to apply to various sample numbers, not only 96.</p> <p>Updated TCY plate to Hard-Shell 96-well PCR plate, skirted.</p> <p>Updated magnetic stand supplier to Thermo Fisher Scientific.</p> <p>Corrected the catalog numbers for Nextera kits provided in the introduction.</p> <p>Corrected the illustration showing how the Nextera assay works.</p>
Document # 15031942 v01	January 2016	<p>Updated design of workflow diagram.</p> <p>Renamed and combined some procedures as needed to improve continuity.</p> <p>Simplified consumables information at the beginning of each section.</p> <p>Revised step-by-step instructions to be more succinct.</p> <p>Removed reference to obsolete Experienced User Cards and added reference to the Custom Protocol Selector.</p> <p>Clarified AMPure XP bead recommendation for nonamplicon applications. See Clean Up Libraries.</p> <p>Added information about normalizing low yield libraries. See Normalize Libraries.</p> <p>Corrected index adapter labels on the assay diagram.</p>
15031942 Rev. E	January 2015	<p>Corrected kit contents for Nextera XT DNA Library Preparation Index Kit v2 Set A (FC-131-2001) to include index N715.</p>

Document	Date	Description of Change
15031942 Rev. D	September 2014	<p>Added info for new index kits that enable preparation of up to 384 indexed paired-end libraries.</p> <p>Updated DNA Input Recommendations for diluting starting material and the potential results of incomplete tagmentation.</p> <p>Added new Nextera XT Quality Metrics with new information on how to troubleshoot fluctuations in cluster density.</p> <p>Removed Dual Indexing Principle and Low Plexity Pooling Guidelines sections. This information can be found in the Nextera Low-Plex Pooling Guidelines Tech Note on the Nextera XT DNA Library Prep support page.</p> <p>References to read lengths on the MiSeq were updated for v3 chemistry.</p> <p>Added instructions for alternate tip if processing fewer than 24 samples while transferring LNB1 beads in Library Normalization.</p> <p>Added NaOH 1N pH &gt; 12.5 to the Consumables and Equipment list as a user-supplied consumable.</p> <p>Removed Tween 20 from Consumables and Equipment list.</p> <p>Consumable not used in protocol.</p>
15031942 Rev. C	October 2012	<p>Modifications were added in <i>PCR Clean-Up</i> for 2x300 runs on the MiSeq.</p> <p>New section for clustering samples on the HiSeq, HiScanSQ, and GAllx. See Clustering Samples for HiSeq, HiScanSQ, and GAllx.</p> <p>The <i>Dual Indexing Principle</i> section listed incorrect catalog numbers for the Nextera XT Index kits. The correct catalog numbers are now listed.</p> <p>Emphasized making sure the NT (Neutralize Tagment Buffer) and LNS1 (Library Normalization Storage Buffer 1) reagents are at room temperature before use in the protocol.</p> <p>Removed reference to Tris-Cl 10 mM, pH8.5 with 0.1% Tween 20 from the User-Supplied Consumables table because it is not used in this library preparation.</p>
15031942 Rev. B	July 2012	<p>Emphasized making sure the NT (Neutralize Tagment Buffer) and LNS1 (Library Normalization Storage Buffer 1) reagents are at room temperature before use in the protocol.</p> <p>Removed reference to Tris-Cl 10 mM, pH8.5 with 0.1% Tween 20 from the User-Supplied Consumables table because it is not used in this library preparation.</p>
15031942 Rev. A	May 2012	Initial release.

# Table of Contents

<b>Chapter 1 Overview</b> .....	<b>1</b>
Introduction .....	1
DNA Input Recommendations .....	1
PCR Amplicons .....	2
Additional Resources .....	2
<b>Chapter 2 Protocol</b> .....	<b>4</b>
Introduction .....	4
Tips and Techniques .....	4
Library Prep Workflow .....	6
Tagment Genomic DNA .....	7
Amplify Libraries .....	8
Clean Up Libraries .....	9
Check Library Quality .....	10
Normalize Libraries .....	11
Dilute Libraries to the Starting Concentration .....	14
<b>Appendix A Supporting Information</b> .....	<b>15</b>
Introduction .....	15
How the Nextera XT Assay Works .....	15
Nextera XT Quality Metrics .....	16
Kit Contents .....	17
Consumables and Equipment .....	19
Acronyms .....	21
<b>Technical Assistance</b> .....	<b>22</b>

# Chapter 1 Overview

Introduction .....	1
DNA Input Recommendations .....	1
PCR Amplicons .....	2
Additional Resources .....	2

## Introduction

This guide explains how to prepare up to 384 dual-indexed paired-end libraries from DNA using Nextera™ XT Library Prep workflow.

The Nextera XT DNA Library Prep protocol:

- ▶ Uses tagmentation, an enzymatic reaction, to fragment DNA and add partial adapter sequences in only 5 minutes.
- ▶ Master mixed reagents reduce reagent containers, pipetting, and hands-on time.
- ▶ Requires only 1 ng input DNA.
- ▶ Supports genomes that are less than 5 Mb.

**Table 1 Example Applications for Nextera Kits**

Nextera XT (FC-131-1024, FC-131-1096)	Nextera DNA Flex (20018704, 20018705)
Small genomes, amplicons, plasmids	Human genomes, large or complex genomes
PCR amplicons (> 300 bp)*	Small genomes, microbial, plasmids, PCR amplicons (> 150 bp)
Plasmids	Nonhuman mammalian genomes (eg, mouse, rat, bovine)
Microbial genomes (eg, Prokaryotes, archaea)	Plant genomes (eg, Arabidopsis, maize, rice)
Concatenated amplicons	Invertebrate genomes (eg, Drosophila)
Double-stranded cDNA	–
Single-cell RNA-Seq	–

\* Using > 300 bp amplicon size ensures even coverage across the length of the DNA fragment. For more information, see *PCR Amplicons* on page 2.

## DNA Input Recommendations

The Nextera XT protocol is optimized for 1 ng of input DNA. Quantify the starting material before preparing libraries.

Assess DNA purity to ensure that the initial DNA sample does not contain > 1 mM EDTA and is free of organic contaminants, such as phenol and ethanol. These substances can interfere with the Nextera tagmentation reaction and result in assay failure.

## Input DNA Quantification

The enzymatic DNA fragmentation used for this protocol is more sensitive to DNA input compared to mechanical fragmentation. Success depends on accurate quantification of input DNA.

Use a fluorometric-based method to quantify input DNA. For example, if you use the Qubit dsDNA BR Assay system, use 2 µl of each DNA sample with 198 µl of the Qubit working solution. Avoid methods that measure total nucleic acid, such as NanoDrop or other UV absorbance methods.

## Assess DNA Purity

UV absorbance is a common method used for assessing the purity of a DNA sample. The ratio of absorbance at 260 nm to absorbance at 280 nm provides an indication of sample purity. This protocol is optimized for DNA with 260/280 absorbance ratio values of 1.8–2.0, which indicates a pure DNA sample.

For a secondary indication of sample purity, use the ratio of absorbance at 260 nm to absorbance at 230 nm. Target a 260/230 ratio of 2.0–2.2. Values outside this range indicate the presence of contaminants. For a complete list of contaminants, including sources, avoidance, and effects on the library preparation, see the *Nextera XT Troubleshooting Technical Note*.

Dilute the starting material in 10 mM Tris-HCl, pH 7.5–8.5. Incomplete tagmentation caused by contaminants can cause library preparation failure, poor clustering, or low quality sequencing results.

## PCR Amplicons

When starting with PCR amplicons, the PCR amplicon must be > 300 bp. The standard clean up protocol depletes libraries < 500 bp. Therefore, Illumina recommends that amplicons < 500 bp undergo a 1.8 x sample purification bead volume ratio to supernatant during *Clean Up Libraries on page 1*. Shorter amplicons can otherwise be lost during the library cleanup step.

Tagmentation cannot add an adapter directly to the distal end of a fragment, so a drop in sequencing coverage of ~50 bp from each distal end is expected. To ensure sufficient coverage of the amplicon target region, design primers to extend beyond the target region by 50 bp per end.

## Additional Resources

The following resources provide instructions and guidelines for using the Nextera XT DNA Library Prep kit to prepare libraries. Visit the [Nextera XT DNA Library Prep support pages](#) for additional information:

- ▶ Compatible products and requirements for recording sample information, sequencing libraries, and analyzing data.
- ▶ Questions and answers about using the kit.
- ▶ Training videos about the kit and courses for related products and subjects.
- ▶ The latest versions of the kit documentation.

Resource	Description
<a href="#">Custom Protocol Selector</a>	A tool for generating end-to-end instructions tailored to your library prep method, run parameters, and analysis method, with options to refine the level of detail.
<i>Nextera XT DNA Library Prep Kit Checklist (document # 100000006566)</i>	Provides a checklist of the protocol steps intended for experienced users.
<i>Nextera XT Library Prep Kit Consumables and Equipment List (document # 100000006567)</i>	Provides an interactive checklist of user-supplied consumables and equipment.
<i>Nextera XT with RNA Probes (document #1000000070581)</i>	Provides the protocol to use Nextera XT with third-party, RNA-based probes.
<i>Index Adapters Pooling Guide (document # 1000000041074)</i>	Provides pooling guidelines and dual-index strategies for using the 10 base pair IDT for Illumina Nextera DNA UD Indexes or 8 base pair Nextera XT and Nextera XT v2 Indexes with the Nextera XT DNA Library Prep kit.

Resource	Description
<i>Illumina Adapter Sequences</i> (document # 1000000002694)	Provides the nucleotide sequences that comprise Illumina oligonucleotides used in Illumina sequencing technologies.
<i>Illumina Free Adapter Blocking Reagent</i> (document # 1000000047585)	Provides the protocol to block excess free adapter, minimize index hopping, and enhance data quality.
<a href="#">IDT for Illumina Nextera DNA UD Indexes support page</a>	Provides information about IDT for Illumina Nextera DNA Unique Dual (UD) indexes.

# Chapter 2 Protocol

Introduction .....	4
Tips and Techniques .....	4
Library Prep Workflow .....	6
Tagment Genomic DNA .....	7
Amplify Libraries .....	8
Clean Up Libraries .....	9
Check Library Quality .....	10
Normalize Libraries .....	11
Dilute Libraries to the Starting Concentration .....	14

## Introduction

This chapter describes the Nextera XT DNA protocol.

- ▶ Review the planned complete sequencing workflow, from sample through analysis, to ensure compatibility of products and experiment parameters.
- ▶ Before proceeding, confirm kit contents and make sure that you have the required components, equipment, and consumables. This protocol requires library prep reagents and index adapters. Index adapters are sold separately. See [Supporting Information on page 15](#).
- ▶ Follow the protocols in the order shown, using the specified volumes and incubation parameters.

## Prepare for Pooling

If you plan to pool libraries, record information about your samples before starting library prep using Illumina Experiment Manager (IEM), Local Run Manager, or BaseSpace Sequence Hub. For information on the tools compatible with your sequencing system, visit the [Nextera XT DNA Library Prep Product Compatibility page](#).

- ▶ For low-plexity pooling strategies (2-plex to 12-plex), see the *Index Adapters Pooling Guide (document # 1000000041074)*.
- ▶ For index adapter sequences and information about recording the sequences, see *Illumina Adapter Sequences (document # 1000000041074)*.

## Tips and Techniques

Unless a safe stopping point is specified in the protocol, proceed immediately to the next step.

### Avoiding Cross-Contamination

- ▶ When adding or transferring samples or reagent master mixes, change tips between **each sample**.
- ▶ When adding index adapters with a multichannel pipette, change tips between **each row** or **each column**. If using a single channel pipette, change tips between each sample.
- ▶ [Tubes] Open only one index adapter tube at a time to prevent misplacing caps. Remove unused index adapter tubes from the working area.

### Sealing the Plate

- ▶ Always seal the 96-well plate with the adhesive seal using a rubber roller to cover the plate before the following steps in the protocol:
  - ▶ Shaking steps
  - ▶ Thermal cycling steps

- ▶ Centrifuge steps
- ▶ Microseal 'A' adhesive film is used for thermal cycling steps to prevent evaporation.
- ▶ Microseal 'B' adhesive seals are effective at -40°C to 110°C, and suitable for skirted or semiskirted PCR plates. Use microseal 'B' seals for thermal cycling or short-term storage.
- ▶ Microseal 'F' foil seals are effective at temperatures down to -70°C and are suitable for storing the 96-well plates containing the final libraries long-term.

### Handling Agencourt AMPure XP beads (AMPure XP beads)

- ▶ Store the AMPure XP beads stock tube upright in the refrigerator so that the beads are always submerged in the buffer.
- ▶ Vortex the AMPure XP beads stock tube thoroughly until the beads are resuspended. To avoid resettling the beads, centrifugation before pipetting is not recommended.
- ▶ If beads are adhered to the side or top of a 96-well plate, centrifuge at 280 × g for 3 seconds, and then pipette to resuspend.
- ▶ When washing beads:
  - ▶ Use the appropriate magnetic stand for the plate.
  - ▶ Keep the plate on the magnetic stand until the instructions specify to remove it.
  - ▶ Do not agitate the plate while it is on the magnetic stand.
  - ▶ Do not disturb the bead pellet.
  - ▶ If beads are aspirated into pipette tips, dispense back into the plate on the magnetic stand and wait until the liquid is clear (~2 minutes).
  - ▶ If liquid becomes adhered to the side or top of the tube or well, centrifuge at 280 × g for 3 seconds to pull volume into liquid.

### Preparing IDT for Illumina Nextera DNA Unique Dual (UD) Indexes Plate

- ▶ Each index plate is for single use only.
- ▶ IDT® for Illumina® Nextera™ DNA UD Indexes use 10 base pair index codes that differ from Nextera XT and Nextera XT v2 indexes, which use 8 base pair index codes. Confirm your sequencing system is configured for 10 base pair index codes.

Prepare IDT for Illumina Nextera DNA UD Indexes as follows.

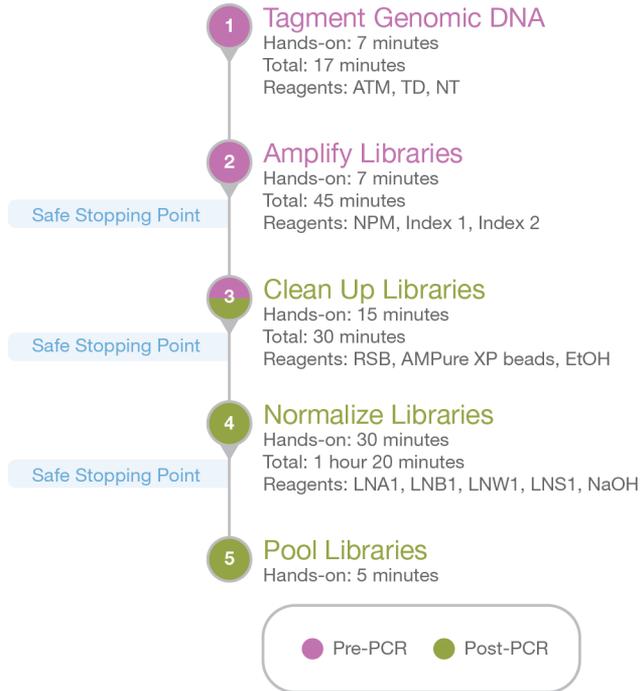
- ▶ Centrifuge at 1000 × g for 1 minute to settle liquid away from the seal.
- ▶ [< 96 samples] Pierce the foil seal on the index adapter plate using a new pipette tip for each well for only the number of samples being processed.
- ▶ [96 samples] Align a new Eppendorf 96-well PCR plate above the index adapter plate and press down to puncture the foil seal on all 96 wells. Press down slowly to avoid tipping the volume over.
- ▶ Discard the empty Eppendorf plate used to puncture the foil seal.

## Library Prep Workflow

The following diagram illustrates the Nextera XT DNA Library Prep workflow. Safe stopping points are marked between steps.

Time estimates are based on processing 8 samples.

**Figure 1** Nextera XT DNA Library Prep Workflow



## Tagment Genomic DNA

This step uses the Nextera transposome to tagment gDNA, which is a process that fragments and tags DNA with adapter sequences.

### Consumables

- ▶ Amplicon Tagment Mix (ATM)
- ▶ Tagment DNA Buffer (TD)
- ▶ Neutralize Tagment Buffer (NT)
- ▶ 96-well PCR plate
- ▶ Microseal 'B' adhesive seals

### Preparation

- 1 Prepare the following consumables:

Item	Storage	Instructions
ATM	-25°C to -15°C	Thaw on ice. Invert the thawed tubes 3–5 times, and then centrifuge briefly.
TD	-25°C to -15°C	Thaw on ice. Invert the thawed tubes 3–5 times, and then centrifuge briefly.
NT	15°C to 30°C	Check for precipitates. If present, vortex until all particulates are resuspended.

- 2 Save the following TAG program on the thermal cycler:
  - ▶ Choose the preheat lid option and set to 100°C
  - ▶ Set the reaction volume to 50 µl
  - ▶ 55°C for 5 minutes
  - ▶ Hold at 10°C

### Procedure

- 1 Add the following volumes *in the order listed* to each well of a new 96-well PCR plate.
  - ▶ TD (10 µl)
  - ▶ 1 ng DNA (5 µl)
- 2 Pipette to mix.
- 3 Add 5 µl ATM to each well.
- 4 Pipette 10 times to mix, and then seal the plate.
- 5 Centrifuge at 280 × g at 20°C for 1 minute.
- 6 Place on the preprogrammed thermal cycler and run the TAG program. When the program reaches 10°C, *immediately* proceed to step 7 because the transposome is still active.
- 7 Add 5 µl NT to each well.
- 8 Pipette 10 times to mix, and then seal the plate.
- 9 Centrifuge at 280 × g at 20°C for 1 minute.
- 10 Incubate at room temperature for 5 minutes.

## Amplify Libraries

This step amplifies the tagmented DNA using a limited-cycle PCR program. The PCR step adds the Index 1 (i7) adapters, Index 2 (i5) adapters, and sequences required for sequencing cluster generation. To confirm indexes selected for low plexity pooling have the appropriate color balance, see the *Index Adapters Pooling Guide* (document #1000000041074).

Index adapter tubes or plates are ordered separately from the library prep components. For a list of compatible index adapters for use with this protocol, see *Kit Contents* on page 17.

### Consumables

- ▶ Nextera PCR Master Mix (NPM)
- ▶ Index adapters (tubes or plates)
- ▶ Microseal 'A' adhesive film

### About Reagents

- ▶ Index adapter plates
  - ▶ A well may contain >10  $\mu$ l of index adapters.
  - ▶ Do not add samples to the index adapter plate.
  - ▶ Each well of the index plate is single use only.
- ▶ Index adapter tubes
  - ▶ Open only one index adapter tube at a time to prevent misplacing caps. Alternatively, use fresh caps after opening each tube.

## Preparation

- 1 Prepare the following consumables:

Item	Storage	Instructions
Index adapters	-25°C to -15°C	Thaw at room temperature . [Tubes] Vortex to mix, and then centrifuge briefly. [Plates] Spin briefly before use.
NPM	-25°C to -15°C	Thaw on ice for 20 minutes.

- 2 Save the following NXT PCR program on a thermal cycler:

- ▶ Choose the preheat lid option and set to 100°C
- ▶ Set the reaction volume to 50  $\mu$ l
- ▶ 72°C for 3 minutes
- ▶ 95°C for 30 seconds
- ▶ 12 cycles of:
  - ▶ 95°C for 10 seconds
  - ▶ 55°C for 30 seconds
  - ▶ 72°C for 30 seconds
- ▶ 72°C for 5 minutes
- ▶ Hold at 10°C

## Procedure

- 1 Add the following index adapter volumes per sample according to your index adapter kit type.

Index Adapter Kit Type	Volume of Index Adapter per Sample
Index Adapter Tubes	5 µl i7 adapter 5 µl i5 adapter
Index Adapter Plate	10 µl pre-paired i7 and i5 index adapters

- Add 15 µl NPM to each well.
- Pipette 10 times to mix, and then seal the plate.
- Centrifuge at 280 × g at 20°C for 1 minute.
- Place on the preprogrammed thermal cycler and run the NXT PCR program.

### SAFE STOPPING POINT

If you are stopping, store at 2°C to 8°C for up to 2 days. Alternatively, leave on the thermal cycler for up to 24 hours.

## Clean Up Libraries

This step uses single-sided bead purification to purify amplified libraries.

### Consumables

- ▶ Agencourt AMPure XP beads (AMPure XP beads)
- ▶ Freshly prepared 80% ethanol (EtOH)
- ▶ Resuspension Buffer (RSB)
- ▶ 96-well 0.8 ml polypropylene deepwell storage plate (midi plate) (2)
- ▶ 96-well PCR plate
- ▶ Microseal 'B' adhesive seal
- ▶ Microseal 'F' foil seals
- ▶ Nuclease-free water

### About Reagents

- ▶ Agencourt AMPure XP beads
  - ▶ Must be at room temperature before use.
  - ▶ Vortex before each use.
  - ▶ Vortex frequently to make sure that beads are evenly distributed.
  - ▶ Aspirate and dispense slowly due to the viscosity of the solution.

## Preparation

- Prepare the following consumables:

Item	Storage	Instructions
AMPure XP beads	2°C to 8°C	Let stand on the benchtop for 30 minutes to bring to room temperature. Vortex and invert to mix.
RSB	-25°C to -15°C	Thaw and bring to room temperature. Vortex to mix. RSB can be stored at 2°C to 8°C after the initial thaw.

- Prepare fresh 80% EtOH from absolute ethanol.

## Procedure

- 1 Centrifuge at 280 x g at 20°C for 1 minute to collect contents at the bottom of the well.
- 2 Transfer 50 µl supernatant from each well of the PCR plate to corresponding wells of a new midi plate.



### NOTE

The ratio of supernatant to volume of AMPure XP beads is 3:2. If you transfer less than 50 µl supernatant, adjust the volume of AMPure XP beads accordingly.

- 3 If you are using standard DNA input, add 30 µl AMPure XP beads to each well containing supernatant.
- 4 If you are using small PCR amplicon sample input, add the AMPure XP beads volume according to your input size in the table below.

Input Size (bp)	AMPure XP Recommendation	AMPure XP Volume (µl)
300–500	1.8x AMPure XP	90
> 500	0.6x AMPure XP (0.5x AMPure XP for ≥ 2 x 250 cycles)	30 (25 µl for ≥ 2 x 250 cycles)

- 5 Seal the plate, and then use a plate shaker at 1800 rpm for 2 minutes.
- 6 Incubate at room temperature for 5 minutes.
- 7 Place on the magnetic stand and wait until the liquid is clear (~2 minutes).
- 8 Without disturbing the beads, remove and discard all supernatant.
- 9 Wash two times as follows.
  - a With the plate on the magnetic stand, add 200 µl fresh 80% EtOH without mixing.
  - b Incubate for 30 seconds.
  - c Without disturbing the beads, remove and discard all supernatant.
- 10 Use a 20 µl pipette to remove and discard residual EtOH.
- 11 Air-dry on the magnetic stand for 15 minutes.
- 12 Remove from the magnetic stand.
- 13 Add 52.5 µl RSB to the beads.
- 14 Seal the plate, and then use a plate shaker at 1800 rpm for 2 minutes.
- 15 Incubate at room temperature for 2 minutes.
- 16 Place on the magnetic stand and wait until the liquid is clear (~2 minutes).
- 17 Transfer 50 µl supernatant to a new 96-well PCR plate.

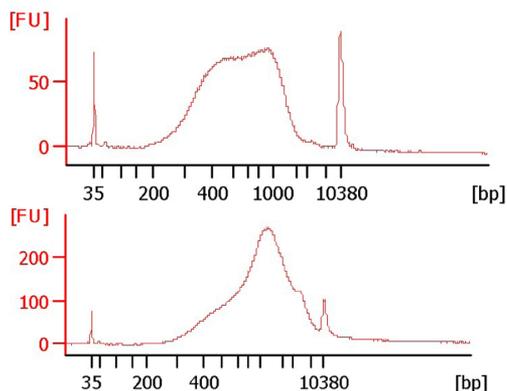
### SAFE STOPPING POINT

If you are stopping, seal the plate with Microseal 'B' adhesive seal or Microseal 'F' foil seal and store at -25°C to -15°C for up to 7 days.

## Check Library Quality

- 1 Run 1 µl undiluted library on an Agilent Technology 2100 Bioanalyzer using a High Sensitivity DNA kit. Typical libraries show a broad size distribution of ~250–1000 bp, as shown in the top panel. Various libraries can be sequenced with average fragment sizes as small as 250 bp or as large as 1500 bp.

Figure 2 Example Bioanalyzer Trace



## Normalize Libraries

This process normalizes the quantity of each library made with Nextera XT Index v2 or Nextera XT Index Kits to ensure more equal library representation in the pooled library.

Do not follow the normalization protocol below and instead manually normalize libraries:

- ▶ If you are using IDT for Illumina Nextera UD Indexes.
- ▶ If the final library yield is < 10 nM.
- ▶ If your sequencing system uses onboard denaturation.

## Consumables

- ▶ Library Normalization Additives 1 (LNA1)
- ▶ Library Normalization Beads 1 (LNB1)
- ▶ Library Normalization Wash 1 (LNW1)
- ▶ Library Normalization Storage Buffer 1 (LNS1)
- ▶ 0.1 N NaOH (fewer than 7 days old) (3 ml per 96 samples)
- ▶ 96-well 0.8 ml polypropylene deep-well storage plate (midi plate)
- ▶ 96-well PCR plate
- ▶ 15 ml conical tube
- ▶ Microseal 'B' adhesive seals

## About Reagents

- ▶ Vortex LNA1 vigorously to make sure that all precipitates have dissolved. Inspect in front of a light.
- ▶ Vortex LNB1 vigorously, with intermittent inversion (at least 1 minute). Repeat until all beads are resuspended and no beads are present at the bottom of the tube when it is inverted.
- ▶ Always use a wide-bore pipette tip for LNA1.
- ▶ Mix only the required amounts of LNA1 and LNB1 for the current experiment. Store the remaining LNA1 and LNB1 separately at the recommended temperatures.
- ▶ Aspirate and dispense beads slowly due to the viscosity of the solution.

### WARNING



This set of reagents contains potentially hazardous chemicals. Personal injury can occur through inhalation, ingestion, skin contact, and eye contact. Wear protective equipment, including eye protection, gloves, and laboratory coat appropriate for risk of exposure. Handle used reagents as chemical waste and discard in accordance with applicable regional, national, and local laws and regulations. For additional environmental, health, and safety information, see the SDS at [support.illumina.com/sds.html](http://support.illumina.com/sds.html).

## Preparation

- 1 Prepare the following consumables:

Item	Storage	Instructions
LNA1	-25°C to -15°C	Prepare under a fume hood. Bring to room temperature. Use a 20°C to 25°C water bath as needed.
LNB1	2°C to 8°C	Bring to room temperature. Use a 20°C to 25°C water bath as needed.
LNW1	2°C to 8°C	Bring to room temperature. Use a 20°C to 25°C water bath as needed.
LNS1	Room temperature	Bring to room temperature.

## Procedure

- 1 Transfer 20  $\mu$ l supernatant from each well of the PCR plate to the corresponding well of a new midi plate.
- 2 Combine the following volumes in a 15 mL conical tube to prepare the LN master mix. Multiply each volume by the number of samples being processed.
  - ▶ LNA1 (46  $\mu$ l)
  - ▶ LNA2 (8  $\mu$ l)
 Reagent overage is included in the volume to ensure accurate pipetting.
- 3 Pipette 10 times to mix.
- 4 Pour the LN master mix into a trough.
- 5 Use a 200  $\mu$ l multichannel pipette to transfer 45  $\mu$ l LN master mix to each well.
- 6 Seal the plate, and then use a plate shaker at 1800 rpm for 30 minutes.
- 7 Place on the magnetic stand and wait until the liquid is clear (~2 minutes).
- 8 Without disturbing the beads, remove and discard all supernatant.
- 9 Wash two times as follows.
  - a Add 45  $\mu$ l LNW1 to each well.
  - b Seal the plate, and then use a plate shaker at 1800 rpm for 5 minutes.
  - c Place on the magnetic stand and wait until the liquid is clear (~2 minutes).
  - d Without disturbing the beads, remove and discard all supernatant.
- 10 Add 30  $\mu$ l 0.1 N NaOH to each well.
- 11 Seal the plate, and then use a plate shaker at 1800 rpm for 5 minutes.
- 12 Add 30  $\mu$ l LNS1 to each well of a new 96-well PCR plate labeled SGP.
- 13 After the 5 minute elution completes, make sure that all samples in the midi plate are resuspended. If they are not, resuspend as follows.
  - a Pipette 10 times to mix or lightly tap the sample plate on the bench.
  - b Seal the plate, and then use a plate shaker at 1800 rpm for 5 minutes.

- 14 Place on a magnetic stand and wait until the liquid is clear (~2 minutes).
- 15 Transfer 30  $\mu$ l supernatant from each well of the midi plate to the corresponding well of the SGP plate.
- 16 Seal the sample plate, and then centrifuge at 1000  $\times$  g for 1 minute.



**NOTE**

At this point, the libraries are single-stranded DNA, which resolves poorly on an agarose gel or Bioanalyzer chip. For quality control, use the double-stranded DNA saved from step 17 of the cleanup procedure.

**SAFE STOPPING POINT**

If you are stopping, store at -25°C to -15°C for up to 7 days.

## Dilute Libraries to the Starting Concentration

This step dilutes libraries to the starting concentration for your sequencing system and is the first step in a serial dilution. After diluting to the starting concentration, libraries are ready to be denatured and diluted to the final loading concentration.

For sequencing, Illumina recommends the read lengths indicated in the table below. If you would like additional overlapped reads, raw coverage, or adjusted the AMPure XP beads recommendations for  $\geq 2 \times 250$  cycles, you can sequence up to  $2 \times 250$  or  $2 \times 300$ , but it is not required.

**Table 2 Recommended Read Length on Illumina Systems**

Sequencing System	Read Length
NovaSeq 6000, HiSeq X*, HiSeq 3000 and HiSeq 4000, NextSeq 500 and NextSeq 550, MiSeq, MiniSeq, iSeq 100	2 x 151
HiSeq 2000, HiSeq 2500 (high output)	2 x 126
HiSeq 2500 (rapid run)	2 x 251

\*Not compatible with IDT for Illumina Nextera DNA UD Indexes (10bp)

IDT for Illumina Nextera DNA UD Indexes uses 10 base pair index codes that differ from the Nextera XT and Nextera XT v2, which use 8 base pair index codes. This change in base pair index codes can require adjustments to your sequencing run set up.

- Calculate the molarity value of the library or pooled libraries using the following formula.
  - For libraries qualified on a Bioanalyzer, use the average size obtained for the library.
  - For all other qualification methods, use 600 bp as the average library size.
$$\frac{\text{ng} / \mu\text{l} \times 10^6}{660 \frac{\text{g}}{\text{mol}} \times \text{average library size (bp)}} = \text{Molarity (nM)}$$
- Using the molarity value, calculate the volumes of RSB and library needed to dilute libraries to the starting concentration for your system.
- Dilute libraries using RSB:
  - Libraries quantified as a multiplexed library pool**—Dilute the pool to the starting concentration for your system.
  - Libraries quantified individually**—Dilute each library to the starting concentration for your system. Add 10  $\mu\text{l}$  each diluted library to a tube to create a multiplexed library pool.
- Follow the denature and dilute instructions for your system to dilute to the final loading concentration.
  - For the iSeq 100 System, see the system guide for dilution instructions (libraries are automatically denatured).
  - For the NovaSeq 6000 System, see the system guide for pool and denature instructions.
  - For the HiSeq 4000 and HiSeq 3000 Systems, see the cBot 2 or cBot system guide for reagent preparation instructions.
  - For all other systems, see the denature and dilute libraries guide.

Optimize concentrations for your workflow and quantification method over subsequent sequencing runs or by flow cell titration.

# Supporting Information

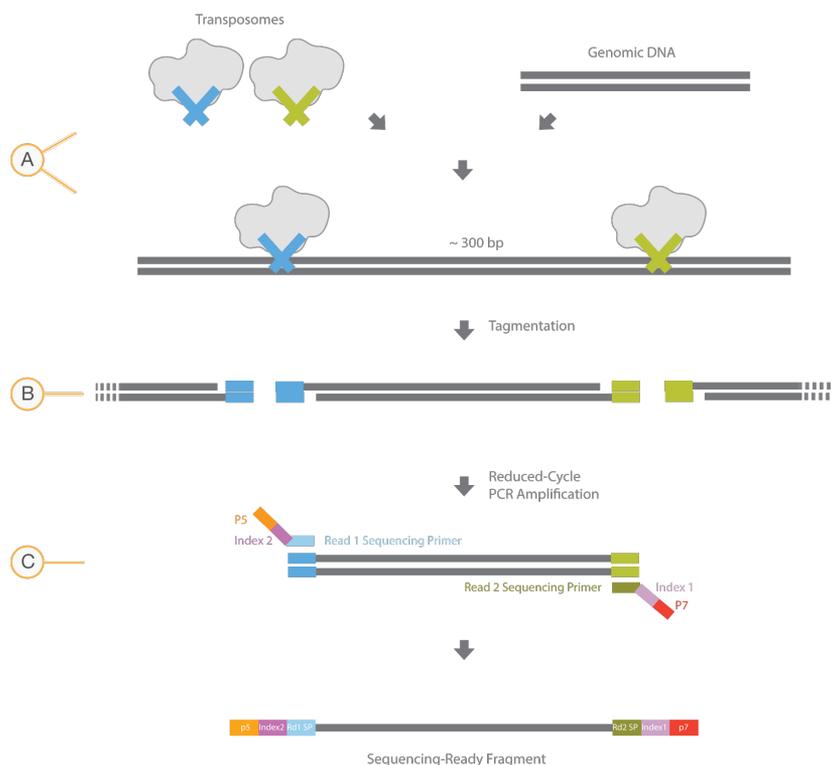
Introduction .....	15
How the Nextera XT Assay Works .....	15
Nextera XT Quality Metrics .....	16
Kit Contents .....	17
Consumables and Equipment .....	19
Acronyms .....	21

## Introduction

The protocol described in this guide assumes that you have reviewed the contents of this section, confirmed workflow contents, and obtained all required consumables and equipment.

## How the Nextera XT Assay Works

The Nextera XT DNA Library Prep uses an engineered transposome to tagment genomic DNA, which is a process that fragments DNA and then tags the DNA with adapter sequences in one step. Limited-cycle PCR uses the adapters to amplify the insert DNA. The PCR step also adds index adapter sequences on both ends of the DNA, which enables dual-indexed sequencing of pooled libraries on Illumina sequencing platforms.



- A Nextera XT transposome with adapters combined with template DNA
- B Tagmentation to fragment and add adapters
- C Limited-cycle PCR to add index adapter sequences

## Nextera XT Quality Metrics

Two factors can cause cluster density fluctuations in libraries prepared with the Nextera XT DNA Library Prep:

- ▶ An average sample size that is too large or too small after tagmentation.
- ▶ A final sample concentration that is too low due to a low yield when starting the bead-based normalization step.

To troubleshoot fluctuations in cluster density, consider checking library size and library concentration. For more information, see *Nextera XT Library Prep: Tips and Troubleshooting (Pub. No. 770-2015-015)*.

### Check Library Size

Larger molecules cluster less efficiently than smaller molecules. If the fragment size after tagmentation is larger than expected, low cluster numbers are possible. The inverse is also true. The average expected library size after tagmentation is between 400 bp and 1.2 kb.

Check the library size with a high sensitivity Bioanalyzer trace after the PCR cleanup step. Look for a long low plateau. Alternatively, PCR-amplify the library with qPCR primers and run the product on an agarose gel. The sequence for these primers is available in the *Sequencing Library qPCR Quantification Guide (document # 11322363)*.

- ▶ **Short libraries indicate too little input DNA**—Requantify the input DNA with a fluorometric method. Start with 10%–25% more input DNA. If the library peak is below 400 bp and you want to continue with this library, dilute the library further.
- ▶ **Long libraries indicate too much input DNA or the presence of inhibitors**—Start with less input DNA, make sure that the input DNA is free from inhibitors, and repeat the quantification step.

For more information on library dilution, see the denature and dilute libraries guide for your sequencing system.

### Check Library Concentration

Bead-based normalization is most efficient when the library yield after amplification is 10–15 nM, or higher. Measure library concentration using high sensitivity dsDNA Qubit after library cleanup, and measure library size with a Bioanalyzer to calculate molarity.

If you are starting with high-quality DNA and see low yield after library cleanup, there are possible issues with AMPure cleanup or the amplification step. If results show either condition, confirm proper storage of the PCR master mix at -25°C to -15°C in a no-frost freezer. Confirm minimal freeze-thaw cycles.

## Kit Contents

Completing the Nextera XT protocol requires library prep reagents and index adapters.

Component	Kit Options	Catalog #	
Library prep reagents	Nextera XT DNA Library Prep (24 Samples)	FC-131-1024	
	Nextera XT DNA Library Prep (96 Samples)	FC-131-1096	
Index adapters	IDT for Illumina Nextera UD Indexes Set A (96 Indexes, 96 Samples)	20027213	
	IDT for Illumina Nextera UD Indexes Set B (96 Indexes, 96 Samples)	20027215	
	IDT for Illumina Nextera UD Indexes Set C (96 Indexes, 96 Samples)	20027215	
	IDT for Illumina Nextera UD Indexes Set D (96 Indexes, 96 Samples)	20027216	
	IDT for Illumina Nextera UD Indexes Set A, B, C, D (384 Indexes, 384 Samples)	20027217	
	Nextera XT Index Kit (24 Indexes, 96 Samples)	FC-131-1001	
	Nextera XT Index Kit v2 Set A (96 Indexes, 384 Samples)	FC-131-2001	
	Nextera XT Index Kit v2 Set B (96 Indexes, 384 Samples)	FC-131-2002	
	Nextera XT Index Kit v2 Set C (96 Indexes, 384 Samples)	FC-131-2003	
	Nextera XT Index Kit v2 Set D (96 Indexes, 384 Samples)	FC-131-2004	
	<b>[Optional]</b> Additional Accessories for Nextera XT Index Kit	Bag of 48 Index Adapter replacement caps, orange	15026585
		Bag of 32 Index Adapter replacement caps, white	15026586
TruSeq Index Plate Fixture Kit		FC-130-1005	

Sequencing primers provided in TruSeq v3 reagent kits are not compatible with Nextera XT libraries. Sequencing Nextera XT libraries on a HiSeq 2500 using TruSeq v3 reagents requires the sequencing primers provided in the Illumina TruSeq Dual Index Sequencing Primer Box. This box is provided in a paired-end (PE-121-1003) and single-read (FC-121-1003) version. One box is needed for each run.

## Nextera XT Library Prep Contents

### Nextera XT Sample Prep Kit– Box 1 of 2

These reagents are shipped at -25°C to -15°C. Promptly store reagents at the indicated tube temperature to ensure proper performance.

Tube Quantity		Acronym	Reagent Name	Storage Temperature
24 Samples	96 Samples			
1	1	ATM	Amplicon Tagment Mix	-25°C to -15°C
1	2	TD	Tagment DNA Buffer	-25°C to -15°C
1	1	HT1	Hybridization Buffer	-25°C to -15°C
1	1	NPM	Nextera PCR Master Mix	-25°C to -15°C
1	4	RSB	Resuspension Buffer	-25°C to -15°C
1	1	LNA1	Library Normalization Additives 1	-25°C to -15°C
1	2	LNW1	Library Normalization Wash 1	2°C to 8°C

## Nextera XT Sample Prep Kit– Box 2 of 2

These reagents are shipped at -25°C to -15°C. Promptly store reagents at the indicated tube temperature to ensure proper performance.

Tube Quantity		Acronym	Reagent Name	Storage Temperature
24 Samples	96 Samples			
1	1	NT	Neutralize Tagment Buffer	Room temperature
1	1	LNB1	Library Normalization Beads 1	2°C to 8°C
1	1	LNS1	Library Normalization Storage Buffer 1	Room temperature

## Index Kit Contents

For index adapter sequences, see *Illumina Adapter Sequences (document # 1000000002694)*.

IDT for Illumina Nextera DNA UD Indexes (96 Indexes, 96 Samples) Plate Format, Store at -25°C to -15°C

Quantity	Description
1	96 Dual Adapter Index Plate

## Nextera XT Index Kit v2 (96 indexes, 384 Samples)

Index Adapters, Store at -25°C to -15°C

Set	Quantity	Description
A	8 tubes	Index Primers, S502, S503, S505–S508, S510, and S511
	12 tubes	Index Primers, N701–N707, N710–N712, N714, and N715

Set	Quantity	Description
B	8 tubes	Index Adapters: S502, S503, S505–S508, S510, and S511
	12 tubes	Index Adapters: N716, N718–N724, and N726–N729
C	8 tubes	Index Adapters: S513, S515–S518, and S520–S522
	12 tubes	Index Adapters: N701–N707, N710–N712, N714, and N715
D	8 tubes	Index Adapters: S513, S515–S518, and S520–S522
	12 tubes	Index Adapters: N716, N718–N724, and N726–N729

### Index Adapter Replacement Caps, Store at 15°C to 30°C

Quantity	Description
1 bag	i7 Index Tube Caps, Orange
1 bag	i5 Index Tube Caps, White

## Nextera XT Index Kit (24 Indexes, 96 Samples)

### Index Adapters, Store at -25°C to -15°C

Quantity	Description
4 tubes	Index Adapters: S502–S504 and S517
6 tubes	Index Adapters: N701–N706

### Index Adapter Replacement Caps, Store at 15°C to 30°C

Quantity	Description
1 bag	i7 Index Tube Caps, Orange
1 bag	i5 Index Tube Caps, White

## TruSeq Index Plate Fixture Kit, Store at Room Temperature (Optional)

Each TruSeq Index Plate Fixture Kit contains two fixtures to help arrange index primers before dispensing to a 96-well plate during library amplification. The fixture pairs with both the 24-sample kit and 96-sample kit.

Quantity	Description
2	TruSeq Index Plate Fixture

## Consumables and Equipment

Confirm that all required user-supplied consumables and equipment are present and available before starting the protocol.

The protocol has been optimized and validated using the items listed. Comparable performance is not guaranteed when using alternate consumables and equipment.

## Consumables

Consumable	Supplier
10 µl pipette tips	General lab supplier
10 µl multichannel pipettes	General lab supplier
10 µl single channel pipettes	General lab supplier
1000 µl pipette tips	General lab supplier
1000 µl multichannel pipettes	General lab supplier
1000 µl single channel pipettes	General lab supplier
200 µl pipette tips	General lab supplier
200 µl multichannel pipettes	General lab supplier
200 µl single channel pipettes	General lab supplier
96-well storage plates, round well, 0.8 ml (midi plate)	Fisher Scientific, catalog # AB-0859
Agencourt AMPure XP, 60 ml kit or 5 ml kit	Beckman Coulter Genomics, item # A63881 (60 ml) Beckman Coulter Genomics, item # A63880 (5 ml)
Distilled water	General lab supplier
Ethanol 200 proof (absolute) for molecular biology (500 ml)	Sigma-Aldrich, product # E7023
Microseal 'A' film	Bio-Rad, catalog # MSA-5001
Microseal 'B' adhesive seals	Bio-Rad, catalog # MSB-1001
Microseal 'F' foil seals	Bio-Rad, catalog # MSF-1001
NaOH 1 N, pH > 12.5, molecular biology grade	General lab supplier
RNase/DNase-free multichannel reagent reservoirs, disposable	VWR, catalog # 89094-658
Ultrapure water	General lab supplier
Hard-Shell 96-well PCR plates	Bio-Rad, catalog # HSP-9601

## Equipment

Equipment	Supplier
High-Speed microplate shaker	VWR, catalog # 13500-890 (110 V/120 V) VWR, catalog # 14216-214 (230 V)
Magnetic stand-96	Thermo Fisher Scientific, catalog # AM10027
Microplate centrifuge	General lab supplier
Vortexer	General lab supplier

## Thermal Cyclers

Use the following recommended settings for selected thermal cycler models. Before performing library prep, validate any thermal cyclers not listed.

Thermal Cycler	Temp Mode	Lid Temp	Vessel Type
Bio-Rad DNA Engine Tetrad 2	Calculated	Heated, Constant at 100°C	Polypropylene plates and tubes
MJ Research DNA Engine Tetrad	Calculated	Heated	Plate
Eppendorf Mastercycler Pro S	Gradient S, Simulated Tube	Heated	Plate

## Acronyms

Acronym	Definition
ATM	Amplicon Tagment Mix
HT1	Hybridization Buffer
LNA1	Library Normalization Additives 1
LNB1	Library Normalization Beads 1
LNS1	Library Normalization Storage Buffer 1
LNW1	Library Normalization Wash 1
NT	Neutralize Tagment Buffer
NPM	Nextera PCR Master Mix
RSB	Resuspension Buffer
SGP	Storage Plate
TD	Tagment DNA Buffer
UD	Unique Dual Index

# Technical Assistance

For technical assistance, contact Illumina Technical Support.

Website: [www.illumina.com](http://www.illumina.com)  
Email: [techsupport@illumina.com](mailto:techsupport@illumina.com)

## Illumina Customer Support Telephone Numbers

Region	Toll Free	Regional
North America	+1.800.809.4566	
Australia	+1.800.775.688	
Austria	+43 800006249	+43 19286540
Belgium	+32 80077160	+32 34002973
China	400.066.5835	
Denmark	+45 80820183	+45 89871156
Finland	+358 800918363	+358 974790110
France	+33 805102193	+33 170770446
Germany	+49 8001014940	+49 8938035677
Hong Kong	800960230	
Ireland	+353 1800936608	+353 016950506
Italy	+39 800985513	+39 236003759
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New Zealand	0800.451.650	
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Singapore	+1.800.579.2745	
South Korea	+82 80 234 5300	
Spain	+34 911899417	+34 800300143
Sweden	+46 850619671	+46 200883979
Switzerland	+41 565800000	+41 800200442
Taiwan	00806651752	
United Kingdom	+44 8000126019	+44 2073057197
Other countries	+44.1799.534000	

**Safety data sheets (SDSs)**—Available on the Illumina website at [support.illumina.com/sds.html](http://support.illumina.com/sds.html).

**Product documentation**—Available for download in PDF from the Illumina website. Go to [support.illumina.com](http://support.illumina.com), select a product, then select **Documentation & Literature**.



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