

# Library Preparation for Chromatin-Immunoprecipitation-based Sequencing (ChIP-Seq)

Note: For safety and biohazard guidelines, *Applied Biosystems SOLiD™ System 2.0 User Guide* preface and "Safety" appendix. For all chemicals in **bold red** type, read the MSDS and follow the handling instructions. Wear appropriate protective eyewear, clothing, and gloves.

DNA derived from ChIP procedure for SOLiD<sup>™</sup> sequencing can range from 100 bp to 2 kb in size with typical yield in the nanogram range. Therefore, the starting point of sample preparation for SOLiD<sup>™</sup> System sequencing varies depending on the input DNA size range. Guidelines are provided in the following table:

ChIP Input DNA Size Range	Starting Point
<200 bp	Start from "Repair DNA Ends and Purify Sample"
≥200 bp	Start from "Shear and Purify the DNA" <sup>1</sup>

## Shear and Purify the DNA

1. Dilute DNA to 5% w/w 2-µm borosilicate glass dry spheres:

Component	Volume (µL)
2-μm glass dry spheres	25 mg
20 ng to 2 μg DNA	X
1 M Tris, pH 8.0	5
Nuclease-free water	Variable
Total	500

- 2. Shear DNA using Covaris<sup>™</sup> S2 System and transfer sheared DNA into a 1.5-mL LoBind tube
- 3. Separate DNA from glass spheres by centrifuging the tube at  $\geq 10,000 \times g$  (13,000 rpm) for 5 minutes and transfer the supernatant to a 15-mL conical propylene tube.
- 4. Purify sheared DNA with Qiagen MinElute<sup>®</sup> Reaction Cleanup Kit ( $\leq 5 \mu g/column$ ).
  - a. Add 3 volumes Buffer ERC to sheared DNA.
  - b. Apply 700 µL sheared DNA solution to a MinElute® column and let stand for 2 minutes at room temperature.
  - c. Centrifuge at  $\geq 10,000 \times g$  (13,000 rpm) for 1 minute and discard flow-through.
  - d. Repeat steps b-c until the entire sample has been loaded onto the column.
  - e. Add 750 µL Buffer PE.
  - f. Centrifuge at  $\geq 10,000 \times g$  (13,000 rpm) for 2 minutes. Discard flow-through. Repeat this step to remove residual wash buffer.
  - g. Air-dry the column for 2 minutes and transfer the column to a clean 1.5-mL LoBind tube.
  - h. Add 20  $\mu$ L Buffer EB to the column and let stand for 2 minutes.
  - i. Centrifuge at  $\geq 10,000 \times g$  (13,000 rpm) for 1 minute.
  - j. Repeat steps h and i.
- 5. Quantitate DNA on the NanoDrop<sup>™</sup> ND-1000 Spectrophotometer if starting DNA > 500 ng. Otherwise assume 70% recovery rate and continue.

<sup>&</sup>lt;sup>1</sup> Starting point at "Repair DNA Ends and Purify Sample" is also possible for fragments  $\geq$  200 bp.

# **Repair DNA Ends and Purify Sample**

1. Mix the following components in a LoBind tube:

Component	Volume (µL)
Sheared DNA	38 or 40
End-Repair 10X Buffer	10
(Epicentre® End-It™)	
ATP (10 mM) (Epicentre®	10
End-It™)	
dNTPs (2.5 mM each)	10
(Epicentre® End-It™)	
End-Repair Enzyme Mix	2
(Epicentre® End-It™)	
Nuclease-free water	Variable
Total	100

- 2. Incubate the tube at room temperature for 30 minutes.
- 3. Purify sheared DNA with Qiagen MinElute® Reaction Cleanup Kit (≤5 μg/column). Elute with 20 μL Buffer EB twice (40 μL total). (Refer to step 4 of "Shear and Purify the DNA" for procedure.)
- 4. Quantitate DNA on the NanoDrop ND-1000 Spectrophotometer if starting DNA > 500 ng. Otherwise, assume 70% recovery rate and continue.

## Ligate P1(ds) and P2(ds) Adaptors to End-Repaired DNA

- Calculate the amount of adaptor needed for the reaction: (# μL adaptor needed) = (# μg DNA) × (10<sup>6</sup> pg/μg) × (1/660 pmol/pg DNA) × (1/insert size) × 30 ÷ (50 pmol/μL adaptor)
- 2. Mix the components below. Adjust volumes as necessary.

Component	Volume (μL)
P1 (ds) Adaptor (50 pmol/µL)	As determined in Step 1
P2 (ds) Adaptor (50 pmol/µL)	As determined in Step 1
2X Quick Ligase Buffer (NEB)	100
Quick Ligase Enzyme (NEB)	5.0
DNA	38-40
Nuclease-free water	Variable
Total	200

- 3. Add 1 µL of Quick Ligase per 40 µL reaction volume and incubate at room temperature for 10 minutes.
- 4. Purify the DNA using the Agencourt® AMPure® Kit.
  - a. Add 1.8 volumes Agencourt® AMPure® beads to the sample. Incubate for 10-15 minutes at room temperature on a rotator.
  - b. Place the tube of sample in the magnetic rack. After the solution clears, remove the supernatant and discard.
  - c. Dispense 200  $\mu$ L freshly prepared 70% ethanol, vortex the tube, and incubate for 30 seconds at room temperature.
  - d. If needed, pool beads from both tubes into one 1.5-mL LoBind tube.
  - e. Place the tube of sample in the magnetic rack. After the solution clears, aspirate out ethanol and discard.
  - f. Repeat steps c-e 2 more times.
  - g. Place the tube of sample in the magnetic rack and remove the supernatant. Pulse-spin to remove the residual ethanol. Repeat this step 2 to 3 more times to remove residual ethanol and then dry the beads at room temperature for 5 minutes.
  - h. Add 22 µL 10 mM Tris pH 8 to the sample and vortex for 10 seconds. Pipette the solution up and down several times to ensure homogeneity.
  - i. Place the tube of sample in the magnetic rack. After the solution clears, transfer the eluted sample (supernatant) into a new 1.5-mL LoBind tube. Repeat this step twice.
- 5. (Optional) Save 2 μL purified ligated library DNA, in case a library QC needs to be run for troubleshooting purposes.

#### Size-Selection of the DNA

- 1. Set up a 6% DNA retardation PAGE gel (Invitrogen<sup>™</sup>) with **1X TBE buffer**.
- 2. Add 6 µL Gel Loading Solution to the sample.
- 3. Load 2 µL TrackIt<sup>™</sup> 25 bp ladder. Load the dye-mixed sample (500 ng to 1 µg per well).
- 4. Run the gel at 160 V for approximately 30 minutes or until the marker is close to the edge of the gel.
- 5. Stain the gel with **Ethidium Bromide** for 5 minutes.
- 6. Destain with nuclease-free water for 2 minutes.
- 7. Excise the band at desired size range using a clean razor blade.
- 8. Make a hole in the bottom of a 0.5-mL tube using a 21 gauge needle and, place the gel piece in this tube.
- 9. Place the 0.5-mL tube with the gel in a 1.5-mL LoBind tube and centrifuge at  $\geq 10,000 \times g$  (13,000 rpm) for 3 minutes. Repeat with a new tube if gel remains in the 0.5-mL tube. Afterwards, pool the tubes.



Figure 1. Excision of ChIP sample cut at desired size range invisible on PAGE gel.

#### Nick Translation and Library Amplification

1. Resuspend gel pieces in 100 µL Invitrogen<sup>™</sup> SuperMix. Transfer the gel solution as follows:

If starting input DNA is	Then
>100 ng	Distribute as 25-µL aliquots in 4 PCR reaction tubes. Add
	75 μL SuperMix to each aliquot.
≤100 ng	Distribute as 33-µL aliquots in 3 PCR reaction tubes. Add
	67 μL SuperMix to each aliquot.

- 2. Add 1.5 µL Library PCR Primer 1 and 1.5 µL Library PCR Primer 2 to each tube of gel mixture.
- 3. Add 0.2 µL AmpliTaq® and 0.25 µL Pfu polymerase.
- 4. Run the PCR cycling program:

Temp (°C)	Time	Condition/note
72	20 min	Nick translation
95	5 min	Hold
95	15 sec	×8-16 cycles
62	15 sec	(see table on
70	1 min	right)
70	5 min	Hold
4	Forever	Hold

Starting Amount of DNA	Number of PCR Cycles	
20 ng to 100 ng	13-16	
100 ng to 1 µg	10-12	
1 µg to 2 µg	8-10	

5. Load and run 4  $\mu$ L of sample on a 2.2% Lonza FlashGel® for 6 minutes at 275 V.

6. If robust amplification products are visible, proceed to step 9. Otherwise, run the PCR cycling program:

Temp (ºC)	Time	Condition
95	5 min	Hold
95	15 sec	
62	15 sec	×2-3 cycles
70	1 min	
70	5 min	Hold
4	Forever	Hold

- 7. Add 1 μL 5X FlashGel® Loading Dye to 4 μL of sample. Load and run the loading dye-sample mixture on a 2.2% Lonza FlashGel® for 6 minutes at 275 V.
- 8. If necessary, repeat steps 6 and 7 until robust library amplification products are observed.
- 9. Pool all PCR samples (including shredded gel pieces) into a 0.45-µm filter Nanosep® spin column with a 1.5-mL LoBind collection tube. Centrifuge at  $\geq 10,000 \times g$  (13,000 rpm) for 5 minutes.
- 10. Purify the DNA using the Agencourt® AMPure® Kit. Elute the DNA with 20 μL 10 mM Tris pH 8 solution. (Refer to step 4 of "Ligate P1(ds) and P2(ds) Adaptors to End-Repaired DNA" for procedure.)
- 11. If there is overamplification, proceed with gel purification and DNA elution. Otherwise, skip to library purity quality control and quantitation.

#### **Library Gel Purification**

- 1. Prepare a 3% or 4% agarose gel in **1X TAE Buffer**.
- 2. Add 2 µL **10X Gel Loading Solution** to the 20 µL fragment library.
- 3. Load 2 µL TrackIt<sup>™</sup> 25 bp ladder. Load DNA sample in the remaining wells.
- 4. Run the gel at 120 V until the dye in the marker is close to the bottom of the gel.
- 5. If needed, stain the gel with **Ethidium Bromide** for 5 minutes.
- 6. Destain with nuclease-free water for 2 minutes.
- 7. Excise the band between 150-200 bp using a clean razor blade and weigh the gel slice in a 15-mL polypropylene conical colorless tube.
- 8. Add 6 volumes Buffer QG to one volume of gel.
- 9. Dissolve the gel slide by vortexing at room temperature for until the gel slice has dissolved completely.
- 10. Add one gel volume of isopropyl alcohol to the sample and mix by inverting the tube several times.
- 11. Apply the sample to MinElute® column(s) (up to 400 mg gel per column) and let the column(s) stand for 2 minutes at room temperature.
- 12. Centrifuge the column(s) at  $\geq 10,000 \times g$  (13,000 rpm) for 1 minute and discard flow-through. Repeat this step until the entire sample is loaded onto the column(s)
- 13. Add 500 µL Buffer QG to each column. Centrifuge at  $\geq 10,000 \times g$  (13,000 rpm) for 1 minute and discard flow-through.
- 14. Add 750 µL Buffer PE to each column. Centrifuge at  $\geq 10,000 \times g$  (13,000 rpm) for 2 minutes and discard flow-through. Repeat centrifugation at  $\geq 10,000 \times g$  (13,000 rpm) for 2 minutes and discard flow-through.
- 15. Air-dry the column(s) for 2 minutes and transfer the samples to clean 1.5-mL LoBind tube(s).
- 16. Add 10  $\mu$ L Buffer EB to each column. Let the column(s) stand for 2 minutes at room temperature and then centrifuge at  $\geq$ 10,000 × g (13,000 rpm) for 1 minute. Repeat this step.
- 17. If necessary, pool the eluted samples and store in a 1.5-mL LoBind tube.

## Library Purity Quality Control (QC) and Quantitation

- 1. Run 1  $\mu$ L of library DNA on a Bioanalyzer.
- 2. On a 2.2% Lonza FlashGel<sup>®</sup>, load 5 μL FlashGel<sup>®</sup> QuantLadder and 5 μL of 2 different amounts of library sample (5 to 20 ng total DNA per sample, in 5 μL total volume).
- 3. Run the gel at 275 V for 6 minutes.
- 4. Quantitate the DNA amount using the FlashGel® QuantLadder as a reference.

 $^{\odot}$  Copyright 2008, Life Technologies Corporation. All rights reserved.

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

NOTICE TO PURCHASER: PLEASE REFER TO THE APPLIED BIOSYSTEMS SOLID™ SYSTEM 2.0 USER GUIDE FOR LIMITED LABEL LICENSE OR DISCLAIMER INFORMATION.

Applied Biosystems, AB (Design) are registered trademarks and SOLiD is a trademark of Life Technologies Corporation or its subsidiaries in the US and/or certain other countries.

AmpliTaq is a registered tradmark of Roche Molecular Systems, Inc.

All other trademarks are the sole property of their respective owners.

12/2008 Part Number 4415141 Rev. A