

Illumina library construction Protocol

SARAH SIU TZE MAK, SHYAM GOPALAKRISHNAN, CHRISTIAN CAROE, CHUNYU GENG, SHANLIN LIU, MIKKEL-HOLGER S SINDING, LUKAS F K KUDERNA, WENWEI ZHANG, SHUJIN FU, FILIPE G VIEIRA, MIETJE GERMONPRÉ, HERVÉ BOCHERENS, SERGEY FEDOROV, BENT PETERSEN, THOMAS SICHERITZ-PONTEN, TOMAS MARQUES-BONET, GUOJIE ZHANG, HUI JIANG, M THOMAS P GILBERT

Abstract

This single-tube library construction protocol is for degraded DNA using adapters for the Illumina platform.

Citation: SARAH SIU TZE MAK, SHYAM GOPALAKRISHNAN, CHRISTIAN CAROE, CHUNYU GENG, SHANLIN LIU, MIKKEL-HOLGER S SINDING, LUKAS F K KUDERNA, WENWEI ZHANG, SHUJIN FU, FILIPE G VIEIRA, MIETJE GERMONPRÉ, HERVÉ BOCHERENS, SERGEY FEDOROV, BENT PETERSEN, THOMAS SICHERITZ-PONTEN, TOMAS MARQUES-BONET, GUOJIE ZHANG, HUI JIANG, M THOMAS P GILBERT Illumina library construction Protocol. **protocols.io**


dx.doi.org/10.17504/protocols.io.iajcacn


Published: 14 Jun 2017

Before start

Calculate the DNA input and prepare the library adapters.

Materials

- ✓ Bovine Serum Albumin by Contributed by users
- ✓ 25% Poly-Ethylene Glycol by Contributed by users
- ✓ NaCl by Contributed by users
- PB binding buffer [19066](#) by [Qiagen](#)
-  Monarch DNA Cleanup Columns (5ug) - 100 columns [T1034L](#) by [New England Biolabs](#)
- Buffer PE [19065](#) by [Qiagen](#)
- Buffer EB [19086](#) by [Qiagen](#)
- 0.2 mM dNTPs [AM8200](#) by [Thermo Fisher Scientific](#)
- AmpliTaq Gold DNA polymerase by [Applied Biosystems](#)
- MgCl₂ by [Applied Biosystems](#)
- GeneAmp® 10X PCR Buffer II [View](#) by [Applied Biosystems](#)
- SYBR Green by [Thermo Fisher Scientific](#)
- ✓ IS7 and IS8 primers following Meyer and Kircher 2010 by Contributed by users
- AccuGene molecular biology water [51200](#) by [Lonza](#)

 BSA-Molecular Biology Grade - 12 mg [B9000S](#) by [New England Biolabs](#)

✓ Illumina InPE 1.0 forward by Contributed by users

✓ custom made reverse primers by Contributed by users

Protocol

End-repair

Step 1.

End-repair step following Carøe et al. 2017 with the addition of 1 µl "Reaction enhancer" consisting of 25% Poly-Ethylene Glycol (PEG4000); 2 µg/µL Bovine Serum Albumin (BSA) and 400 mM NaCl.

NOTES

GigaScience Database 02 Jun 2017

Carøe C, Gopalakrishnan S, Vinner L, Mak SST, Sindin MHS, Samaniego JA, et al. Single-tube library preparation for degraded DNA. *Methods in ecology and evolution*; 2017; in press.

Ligation

Step 2.

Ligation step following Carøe et al. 2017 with addition of 1 µl 10 µM adapters suited for the Illumina platform.

NOTES

GigaScience Database 02 Jun 2017

Carøe C, Gopalakrishnan S, Vinner L, Mak SST, Sindin MHS, Samaniego JA, et al. Single-tube library preparation for degraded DNA. *Methods in ecology and evolution*; 2017; in press.

Adpater Fill-in & library purification

Step 3.

Fill-in step of the adapter to complete library building and purification using 1:5 volume of PB binding buffer (Qiagen) and using Monarch DNA Cleanup Columns (New England Biolabs, Massachusetts, USA).

NOTES

GigaScience Database 02 Jun 2017

Carøe C, Gopalakrishnan S, Vinner L, Mak SST, Sindin MHS, Samaniego JA, et al. Single-tube library preparation for degraded DNA. *Methods in ecology and evolution*; 2017; in press.

Adpater Fill-in & library purification

Step 4.

Wash with 750 µl buffer PE (Qiagen).

Adpater Fill-in & library purification

Step 5.

Incubate for 5 minutes at 37 °C.

 DURATION

00:05:00

Adpater Fill-in & library purification

Step 6.

Elute in 40 µl buffer EB (Qiagen).

Quantitative real-time PCR (qPCR)

Step 7.

To determine the number of cycles used in index PCR, perform a qPCR in a 20 µl reaction volume using 1:20 dilution of:

- purified library template
- 0.2 mM dNTPs (Invitrogen)
- 0.04 U/µl AmpliTaq Gold DNA polymerase (Applied Biosystems, Foster City, California, USA)
- 2.5 mM MgCl₂ (Applied Biosystems)
- 1X GeneAmp® 10X PCR Buffer II (Applied Biosystems)
- 1 µl SYBR Green (Invitrogen, Carlsbad, California, USA)
- 0.2 µM forward and reverse primers mixture (IS7 and IS8 primers following Meyer and Kircher 2010)
- 13.48 µl AccuGene molecular biology water (Lonza)

Quantitative real-time PCR (qPCR)

Step 8.

qPCR cycling conditions:

cycles temprature time		
1	95 °C	10 min
	95 °C	30 sec
40	60 °C	60 sec
	72 °C	60 sec

(using the Agilent MX3005 qPCR machine)

PCR amplification

Step 9.

100 µl PCR reactions containing:

- 20 µl of purified library
- 0.2 mM dNTPs (Invitrogen)
- 0.1 U/µl AmpliTaq Gold DNA polymerase (Applied Biosystems)
- 2.5 mM MgCl₂ (Applied Biosystems)
- 1X GeneAmp® 10X PCR Buffer II (Applied Biosystems)
- 0.4 mg/ml BSA (New England Biolabs Inc)
- 0.2 µM of each forward (Illumina InPE 1.0 forward)
- custom made reverse primers
- 51.2 µl AccuGene molecular biology water (Lonza, Basel, CH)

PCR amplification

Step 10.

PCR cycling conditions:

cycles	temperature time	
	temperature	time
initial denaturation	95 °C	12 min
	95 °C	30 sec
13-21	60 °C	30 sec
	72 °C	40 sec
elongation step	72 °C	5 min

PCR amplification

Step 11.

Post-PCR, purify libraries with QiaQuick columns (Qiagen).

PCR amplification

Step 12.

Incubate libraries for 10 min at 37 °C.

 DURATION

00:01:00

PCR amplification

Step 13.

Elute libraries with 30 µl buffer EB (Qiagen).

Bead purification

Step 14.

Use small amounts of aliquots after purification for concentration quantification and fragment size estimation with the High-Sensitivity DNA Assay kit 2100 expert High Sensitivity DNA Assay in

Bioanalyzer 2100 (Agilent).

Bead purification

Step 15.

Final purification using the AMPure XP system (Agentcourt, Beckman Counter, Indianapolis, USA) with 1.8X beads:library ratio, in order to remove any persisting primer dimers or other molecules with a fragment size of <100 bp.

Quantification

Step 16.

Prior to sequencing submission, use small amounts of aliquots after purification concentration quantification and fragment size estimation with the High-Sensitivity DNA Assay kit 2100 expert High Sensitivity DNA Assay in Bioanalyzer 2100 (Agilent).

Quantification

Step 17.

Pool libraries in equimolar concentrations for sequencing.

NOTES

GigaScience Database 02 Jun 2017

Meyer M, Kircher M. Illumina sequencing library preparation for highly multiplexed target capture and sequencing. Cold Spring Harb. Protoc. 2010;2010: db.prot5448.