

# SureSelect Target Enrichment for Illumina Paired-End Sequencing Library

SureSelect Target Enrichment Kit

## **Protocol**

Version 1.1.1, November 2010

SureSelect platform manufactured with Agilent SurePrint Technology

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#### Acknowledgement

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#### In this Guide...

This guide describes Agilent's recommended operational procedures to capture genomic regions of interest using Agilent's SureSelect Paired-End Target Enrichment System Kit and sample preparation kits for next-generation sequencing. This protocol is specifically developed and optimized to use Biotinylated RNA oligomer libraries, or Bait, to enrich targeted regions of the genome from repetitive sequences and sequences unrelated to the research focus.

This guide uses the Illumina paired-end sequencing platform for library preparation.

#### 1 Before You Begin

This chapter contains information (such as procedural notes, safety information, required reagents and equipment) that you should read and understand before you start an experiment.

#### 2 Sample Preparation

This chapter describes the steps to prepare the DNA sample for target enrichment.

#### 3 Hybridization

This chapter describes the steps to prepare and hybridize samples.

#### 4 Post-Hybridization Amplification

This chapter describes the steps to amplify, purify, and assess quality of the sample library.

#### What's New in Version 1.1

- Dynabeads MyOne Streptavidin T1 replaces Dynabeads M-280 Streptavidin beads.
- Use of Qubit dsDNA BR Assay to determine concentration of gDNA before shearing.
- New instructions for multiple libraries to mix reagents in large volume, rather than in individual aliquots.
- Addition of a post-hybridization cluster amplification step.

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Alternative Capture Equipment Combinations



Make sure you read and understand the information in this chapter and have the necessary equipment and reagents listed before you start an experiment.

NOTE

Agilent cannot guarantee the SureSelect Target Enrichment kits and cannot provide technical support for the use of non-Agilent protocols to process samples for enrichment.

#### **Procedural Notes**

- To prevent contamination of reagents by nucleases, always wear powder-free laboratory gloves and use dedicated solutions and pipettors with nuclease-free aerosol-resistant tips.
- · Maintain a clean work area.
- Do not mix stock solutions and reactions containing gDNA on a vortex mixer. Instead, gently tap the tube with your finger to mix the sample.
- Avoid repeated freeze-thaw cycles of stock and diluted gDNA solutions.
- When preparing frozen reagent stock solutions for use:
  - 1 Thaw the aliquot as rapidly as possible without heating above room temperature.
  - **2** Mix briefly on a vortex mixer, then spin in a centrifuge for 5 to 10 seconds to drive the contents off of walls and lid.
  - **3** Store on ice or in a cold block until use.
- In general, follow Biosafety Level 1 (BL1) safety rules.

## **Safety Notes**



 Wear appropriate personal protective equipment (PPE) when working in the laboratory.

## **Required Reagents**

 Table 1
 Required Reagents for Library Prep and Post-Hybridization Amplification

Description	Vendor and part number
Agilent DNA 1000 Kit	Agilent p/n 5067-1504
Agilent High Sensitivity DNA Kit	Agilent p/n 5067-4626
Herculase II Fusion DNA Polymerase (includes dNTP mix and 5x Buffer)	Agilent
200 reactions	p/n 600677
400 reactions	p/n 600679
Nuclease-free Water (not DEPC-treated)	Ambion Cat #AM9930
1X Low TE Buffer (10 mM Tris-HCl, pH 8.0, 0.1 mM EDTA)	Applied Biosystems p/n 4389764
Illumina Paired-End Genomic DNA Sample Prep Kit	Illumina Cat # PE-102-1001
Illumina Paired-End Cluster Generation Kit (v4)	Illumina Cat # PE-203-4001
Sybr-Gold	Invitrogen p/n S-11494
Trackit Cyan/Orange Loading Dye (50 mM Tris pH 8.0, 40 mM EDTA, 40% (w/v) sucrose)	Invitrogen p/n 10482-028
Trackit 50 BP DNA ladder	Invitrogen p/n 10488-043

#### 1 Before You Begin

**Required Reagents** 

 Table 1
 Required Reagents for Library Prep and Post-Hybridization Amplification

Description	Vendor and part number
Quant-iT dsDNA BR Assay Kit, for use with the Qubit fluorometer	
100 assays, 2-1000 ng 500 assays, 2-1000 ng	Invitrogen p/n Q32850 Invitrogen p/n Q32853
Qubit assay tubes	Invitrogen p/n Q32856
NuSeive GTG Agarose	Lonza p/n 50080
QIAquick PCR Purification Kit	Qiagen p/n 28104
QIAquick Gel Extraction Kit	Qiagen p/n 28704
MinElute PCR Purification Kit	Qiagen p/n 28004
100% Ethanol, molecular biology grade	Sigma-Aldrich p/n E7023
Isopropanol	Sigma-Aldrich p/n 19516
50x TAE buffer	
Distilled water	

 Table 2
 SureSelect Target Enrichment System Kits

Description	Vendor and part number	
SureSelect Target Enrichment System Kit, Paired-End		
10 reactions	Agilent p/n G3360A*	
25 reactions	Agilent p/n G3360B*	
50 reactions	Agilent p/n G3360C*	
100 reactions	Agilent p/n G3360D*	
250 reactions	Agilent p/n G3360E*	
500 reactions	Agilent p/n G3360F*	
1000 reactions	Agilent p/n G3360G*	
2000 reactions	Agilent p/n G3360H*	
5000 reactions	Agilent p/n G3360J*	

<sup>\*</sup> Order options 001 and 011.

 Table 3
 Required Reagents for Hybridization

Description	Vendor and part number
Nuclease-free Water (not DEPC-treated)	Ambion Cat #AM9930
Dynabeads MyOne Streptavidin T1	Invitrogen
2 mL	Cat #656-01
10 mL	Cat #656-02
100 mL	Cat #656-03
MinElute PCR Purification Kit (50)	Qiagen p∕n 28004
MinElute PCR Purification Kit (250)	Qiagen p/n 28006

## **Optional Reagents**

 Table 4
 Optional Reagents

Description	Vendor and part number
SureSelect Target Enrichment, Demo	Agilent p/n G4459A*

<sup>\*</sup> Order option 001 and 011.

#### 1 Before You Begin

**Required Equipment** 

## **Required Equipment**

 Table 5
 Required Equipment for Library Prep and Post-Hybridization Amplification

Description	Vendor and part number
Agilent 2100 Bioanalyzer	Agilent p/n G2938C
Nuclease-free 1.5 mL microfuge tubes (sustainable at 95°C)	Ambion p/n AM12400 or equivalent
Dark Reader transilluminator	Clare Chemical Research, Inc. p/n DR45M
Thermal cycler	BioRad (MJ Research) DNA Engine PTC-200, Applied Biosystems Veriti Thermal Cycler, or equivalent
Covaris S-series Single Tube Sample Preparation System, Model S2	Covaris
Covaris microTUBE with AFA fiber and snap cap	Covaris p/n 520045
Nuclease-free 0.2 mL PCR tubes, thin-walled	Eppendorf p/n 951010006 or equivalent
Microcentrifuge	Eppendorf Microcentrifuge Model 5417C or equivalent
Qubit Fluorometer	Invitrogen p/n Q32857
P10, P20, P200 and P1000 pipettes	Pipetman P10, P20, P200, P1000 or equivalent
Vacuum concentrator	Savant SpeedVac or equivalent
Disposable scalpels or razor blades	
Electrophoresis unit	
Electrophoresis power supply	
Gel trays and tank	
Ice bucket	

 Table 5
 Required Equipment for Library Prep and Post-Hybridization Amplification

Description	Vendor and part number
Powder-free gloves	
Sterile, nuclease-free aerosol barrier pipette tips	
Timer	
Vortex mixer	
Heat block at 37°C	

 Table 6
 Required Equipment for Hybridization

Description	Vendor and part number
Mx3000P/Mx3005P 96-well tube plates	Agilent p/n 410088 or equivalent
Mx3000P/Mx3005P optical strip caps	Agilent p/n 401425 or equivalent
MicroAmp Clear Adhesive Film	Applied Biosystems p/n 4306311 or equivalent
BD Clay Adams Nutator Mixer	BD Diagnostics p/n 421105 or equivalent
Dynal DynaMag-2 magnetic stand	Invitrogen p/n 123-21D or equivalent
P10, P20, P200 and P1000 pipettes	Pipetman P10, P20, P200, P1000 or equivalent
Pipet-Light Multichannel Pipette, 12 channels	Rainin p/n L12-20 or equivalent
Sterile, nuclease-free aerosol barrier pipette tips	
Thermal cycler	BioRad (MJ Research) DNA Engine PTC-200, Applied Biosystems Veriti Thermal Cycler, or equivalent
Timer	
Vortex mixer	
Water bath or heat block set to 65°C	

#### 1 Before You Begin

**Optional Equipment** 

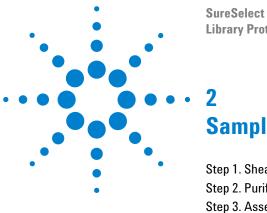
## **Optional Equipment**

 Table 7
 Optional Equipment for Hybridization

Description	Vendor and part number
Tube-strip capping tool	Agilent p/n 410099
Qubit Quantitation Starter Kit	Invitrogen p/n Q32860

 Table 8
 Optional Equipment for Library Prep and Post-Hybridization Amplification

Description	Vendor and part number
Agilent 2100 Bioanalyzer	Agilent p/n G2938C



SureSelect Target Enrichment for Illumina Paired-End Sequencing **Library Protocol** 

# Sample Preparation

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This section contains instructions for prepped library production specific to the Illumina paired-read sequencing platform. It is intended for use with the Illumina Paired-End Genomic DNA Sample Prep Kit (p/n PE-102-1001).

The steps in this section differ from the Illumina protocol in the shear size, the use of the Covaris sample preparation system for gDNA shearing, and the gel purification. Other methods of gDNA shearing have not been validated.

Refer to the Illumina protocol Preparing Samples for Paired-End Sequencing (p/n 1005063 Rev. A) for more information.

NOTE

Make sure genomic DNA samples are of high quality with an OD 260/280 ratio ranging from 1.8 to 2.0. Use the Qubit system to quantify genomic DNA before library preparation.



#### 2 Sample Preparation

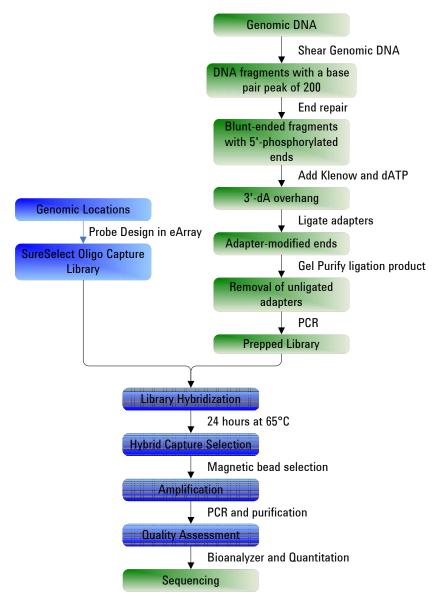


Figure 1 Overall sequencing sample preparation workflow.

 Table 9
 Overview and time requirements

Step	Time
Illumina Prepped library Production	2 days
Library Hybridization	25 hours (optional 72 hours)
Bead preparation	30 minutes
Capture Selection and Washing	2 hours
DNA purification	30 minutes
Post-Hybridization Amplification	1 hour
PCR purification	30 minutes
Bioanalyzer QC	1 hour

#### Step 1. Shear DNA

1 Use the Qubit dsDNA BR Assay to determine the concentration of your gDNA sample. Make sure the gDNA is of high quality (non-degraded,  $A_{260}/A_{280}$  is 1.8 to 2.0).

Follow the instructions for the instrument.

- 2 Dilute 3 μg of high-quality gDNA with 1X Low TE Buffer (or EB buffer) in a 1.5-mL LoBind tube to a total volume of 120 μL.
- **3** Set up the Covaris instrument.
  - **a** Check that the water in the Covaris tank is filled with fresh deionized water to fill line level 12 on the graduated fill line label.
  - **b** Check that the water covers the visible glass part of the tube.
  - **c** Set the chiller temperature to between 2°C to 5°C to ensure that the temperature reading in the water bath displays 5°C.
  - **d** *Optional*. Supplement the circulated water chiller with ethylene glycol to 20% volume to prevent freezing.
  - **e** On the instrument control panel, push the Degas button. Degas the instrument for least 30 minutes before use.

Refer to the Covaris instrument user guide.

- **4** Put a Covaris microTube into the loading and unloading station. Keep the cap on the tube.
- 5 Use a tapered pipette tip to slowly transfer the 120  $\mu L$  DNA sample through the pre-split septa.
  - Be careful not to introduce a bubble into the bottom of the tube.
- **6** Secure the microTube in the tube holder and shear the DNA with the settings in Table 10. The target peak for base pair size is 200 bp.

 Table 10
 Covaris shear settings

Setting	Value
Duty Cycle	10%
Intensity	5
Cycles per Burst	200
Time	180 seconds (or 3 cyles of 60 seconds each)
Set Mode	Frequency sweeping
Temperature	4° to 7° C

- 7 Put the Covaris microTube back into the loading and unloading station.
- **8** While keeping the snap-cap on, insert a pipette tip through the pre-split septa, then slowly remove the sheared DNA.
- **9** Transfer the sheared DNA into a new 1.5-mL LoBind tube.

# Step 2. Purify the sample with the QIAquick PCR Purification Kit

- 1 If you haven't already done so, add the pH indicator to the Buffer PB.
- **2** Add 500 μL of PB per sample and mix well by pipetting.
- 3 Check for the yellow color to make sure buffer PB pH is correct. For more information on how to check buffer pH, refer to the Qiagen QIAquick Handbook. If needed, use 5 μL of the 3M Sodium Acetate (included in the kit) to adjust the pH to the proper range.
- 4 Put a QIAquick spin column in a 2 mL collection tube.
- 5 Transfer the 600  $\mu$ L sample to the QIAquick column. Spin the sample in a centrifuge for 60 seconds at 17,900 x g (13,000 rpm). Discard the flow-through.
- 6 Add 750  $\mu$ L of buffer PE to the column. Spin the sample in a centrifuge for 60 seconds at 17,900 x g (13,000 rpm). Discard the flow-through.
- 7 Put the QIAquick column back in the 2 mL collection tube and spin in a centrifuge for 60 seconds at 17,900 x g (13,000 rpm).
- **8** Transfer the QIAquick column to a new 1.5-mL collection tube to elute the cleaned sample.
- **9** Let sit for 2 minutes to completely evaporate residual ethanol. All traces of ethanol must be removed.
- 10 Add 30 µL of buffer EB (10 mM Tris·Cl, pH 8.5) directly onto the QIAquick filter membrane.
- 11 Wait 60 seconds, then centrifuge for 60 seconds at 17,900 x g (13,000 rpm).
- 12 Collect the eluate.

**Stopping Point** If you do not continue to the next step, store the samples at -20°C.

## Step 3. Assess quality with the Agilent 2100 Bioanalyzer

Use a Bioanalyzer DNA 1000 chip and reagent kit. See the *Agilent DNA 1000 Kit Guide*, at http://www.chem.agilent.com/en-US/Search/Library/\_layouts/Agilent/PublicationSummary.aspx?whid=46764.

- 1 Check that the 2100 Bioanalyzer electrodes have been cleaned as instructed in the reagent kit guide.
- **2** Open the Agilent 2100 Expert Software (version B.02.02 or higher), turn on the 2100 Bioanalyzer and check communication.
- **3** Prepare the chip, samples and ladder as instructed in the reagent kit guide.
- **4** Load the prepared chip into the 2100 Bioanalyzer and start the run within five minutes after preparation.
- **5** Within the instrument context, choose the appropriate assay from the drop down list.
- **6** Start the run. Enter sample names and comments in the Data and Assay context.
- **7** Verify the results.

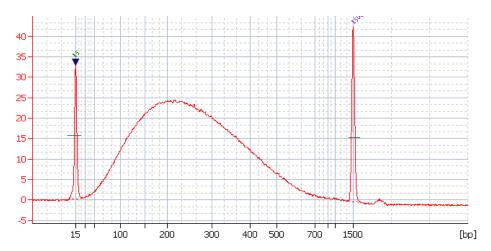


Figure 2 Analysis of sheared DNA using a DNA 1000 Bioanalyzer assay. The electropherogram shows a distribution with a peak size of 200 nucleotides.

#### 2 Sample Preparation

Step 4. Repair the ends

#### Step 4. Repair the ends

To process multiple samples, prepare master mixes with overage at each step, without the DNA sample. Master mixes for preparation of 12 samples (including excess) are shown in each table as an example.

Prepare the master mix on ice.

- 1 If T4 DNA ligase buffer with 10 mM ATP shows a visible precipitate after thawing, warm up to 37°C for 5 minutes and thoroughly mix on a vortex mixer.
- **2** For 1 library (prepare on ice):
  - In a PCR tube, strip tube, or plate, prepare the reaction mix in Table 11. Use the Illumina Paired-End Genomic DNA Sample Prep Kit (p/n PE-102-1001). Mix well by gently pipetting up and down.
- **3** For multiple libraries (prepare on ice):
  - **a** Prepare the reaction mix in Table 11. Use the Illumina Paired-End Genomic DNA Sample Prep Kit (p/n PE-102-1001). Mix well on a vortex mixer.
  - **b** Add 71 µL of the reaction mix to each well or tube.
  - c Add 29 µL of each DNA sample to each well or tube. Mix by pipetting. Change pipette tips between samples.
- 4 Incubate in a thermal cycler for 30 minutes at 20°C. Do not use a heated lid.

Table 11 End Repair Mix\*

Reagent	Volume for 1 Library	Volume for 12 Libraries (includes excess)
DNA sample	~29 µL	
Nuclease-free water	46 μL	575 μL
T4 DNA ligase buffer with 10mM ATP	10 μL	125 μL
10 mM dNTP mix	4 μL	50 μL
T4 DNA polymerase	5 μL	62.5 μL
Klenow DNA polymerase	1 μL	12.5 μL
T4 PNK	5 μL	62.5 μL
Total Volume	100 μL	888 μL (71 μL/sample)

 $<sup>^{*}</sup>$  These reagents are included in the Illumina Paired-End Genomic DNA Sample Prep Kit (p/n PE-102-1001).

# Step 5. Purify the repaired DNA with the QIAquick PCR Purification Kit

- 1 If you haven't already done so, add the pH indicator to the Buffer PB.
- 2 Add 500 μL of PB per sample and mix well by pipetting.
- 3 Check for the yellow color to make sure buffer PB pH is correct. For more information on how to check buffer pH, refer to the Qiagen QIAquick Handbook. If needed, use 5  $\mu$ L of the 3M Sodium Acetate (included in the kit) to adjust the pH to the proper range.
- **4** Put a QIAquick spin column in a 2 mL collection tube.
- 5 Transfer the 600  $\mu$ L sample to the QIAquick column Spin the sample in a centrifuge for 60 seconds at 17,900 x g (13,000 rpm). Discard the flow-through.
- 6 Add 750  $\mu$ L of buffer PE to the column. Spin the sample in a centrifuge for 60 seconds at 17,900 x g (13,000 rpm). Discard the flow-through.
- 7 Put the QIAquick column back in the 2 mL collection tube and spin in a centrifuge for 60 seconds at 17,900 x g (13,000 rpm).
- **8** Transfer the QIAquick column to a new 1.5-mL collection tube to elute the cleaned sample.
- **9** Let sit for 2 minutes to completely evaporate residual ethanol. All traces of ethanol must be removed.
- **10** Add 32 μL of buffer EB directly onto the QIAquick filter membrane. Wait 60 seconds, then spin in a centrifuge for 60 seconds at 17,900 x g (13,000 rpm).
- 11 Collect the eluate.

**Stopping Point** If you do not continue to the next step, store the samples at -20°C.

#### Step 6. Add 'A' Bases to the 3' end of the DNA fragments

- **1** For 1 library (prepare on ice):
  - In a PCR tube, strip tube, or plate, prepare the reaction mix in Table 12. Use the Illumina Paired-End Genomic DNA Sample Prep Kit (p/n PE-102-1001). Mix well by gently pipetting up and down.
- **2** For multiple libraries (prepare on ice):
  - **a** Prepare the reaction mix in Table 12. Use the Illumina Paired-End Genomic DNA Sample Prep Kit (p/n PE-102-1001). Mix well on a vortex mixer.
  - **b** Add 18  $\mu$ L of the reaction mix to each well or tube.
  - c Add 32  $\mu L$  of each DNA sample to each well or tube. Mix by pipetting. Change pipette tips between samples.

Table 12 Adding "A" Bases\*

Reagent	Volume for 1 Library	Volume for 12 Libraries (includes excess)
DNA sample	~32 µL	
10x Klenow buffer	5 μL	62.5 μL
1 mM dATP	10 μL	125 µL
Klenow Fragment (3' to 5' exo minus)	3 μL	37.5 μL
Total Volume	50 μL	225 μL (18 μL/sample)

These reagents are included in the Illumina Paired-End Genomic DNA Sample Prep Kit (p/n PE-102-1001).

3 Incubate in a thermal cycler for 30 minutes at 37°C.

If you use a heated lid, make sure that the lid temperature does not exceed 50°C.

# Step 7. Purify the sample with a Qiagen MinElute PCR Purification Column

- 1 Allow the MinElute columns (stored at 4°C) to come to room temperature.
- 2 If you haven't already done so, add the pH indicator to the Buffer PB.
- 3 Add 250 µL of PB per sample and mix well by pipetting.
- 4 Check for the yellow color to make sure buffer PB pH is correct.
  For more information on how to check buffer pH, refer to the Qiagen MinElute Handbook. If needed, use 5 μL of the 3M Sodium Acetate (included in the kit) to adjust the pH to the proper range.
- **5** Put a MinElute spin column in a 2 mL collection tube.
- **6** Transfer the 300  $\mu$ L sample to the MinElute column. Spin the sample in a centrifuge for 60 seconds at 17,900 x g (13,000 rpm). Discard the flow-through.
- 7 Add 750 μL of buffer PE to the column. Spin the sample in a centrifuge for 60 seconds at 17,900 x g (13,000 rpm). Discard the flow-through.
- **8** Put the MinElute column back in the 2 mL collection tube and spin in a centrifuge for 60 seconds at 17,900 x g (13,000 rpm).
- **9** Transfer the MinElute column to a new 1.5-mL collection tube to elute the cleaned sample.
- **10** Let sit for 2 minutes to completely evaporate residual ethanol. All traces of ethanol must be removed.
- 11 Add 10 µL buffer EB directly onto the MinElute filter membrane. Wait 60 seconds, then spin in a centrifuge for 60 seconds at 17,900 x g (13,000 rpm).
- **12** Collect the eluate, which can be stored at 4°C.

#### Step 8. Ligate the paired-end adapter

This step uses a 10:1 molar ratio of adapter to genomic DNA insert, based on a starting quantity of 3 µg of DNA before fragmentation.

- **1** For 1 library (prepare on ice):
  - In a PCR tube, strip tube, or plate, prepare the reaction mix in Table 13. Use the Illumina Paired-End Genomic DNA Sample Prep Kit (p/n PE-102-1001). Mix well by gently pipetting up and down.
- **2** For multiple libraries (prepare on ice):
  - **a** Prepare the reaction mix in Table 13. Use the Illumina Paired-End Genomic DNA Sample Prep Kit (p/n PE-102-1001). Mix well on a vortex mixer.
  - **b** Add 40  $\mu$ L of the reaction mix to each well or tube.
  - c Add 10  $\mu$ L of each DNA sample to each well or tube. Mix by pipetting. Change pipette tips between samples.

 Table 13
 Ligation master mix\*

Reagent	Volume for 1 Library	Volume for 12 Libraries (includes excess)
DNA sample	10 μL	
Nuclease-free water	4 μL	50 μL
2X DNA ligase buffer	25 μL	313 μL
Paired-End Adapter oligo mix	6 μL	75 μL
DNA ligase	5 μL	62.5 μL
Total Volume	50 μL	500 μL (40 μL/sample)

<sup>\*</sup> These reagents are included in the Illumina Paired-End Genomic DNA Sample Prep Kit (p/n PE-102-1001).

**3** Incubate for 15 minutes at 20°C on a thermal cycler. Do not use a heated lid.

# Step 9. Purify the sample with the QIAquick PCR Purification Kit

- 1 If you haven't already done so, add the pH indicator to the Buffer PB.
- 2 Add 250 μL of PB per sample and mix well by pipetting.
- 3 Check for the yellow color to make sure buffer PB pH is correct.

  For more information on how to check buffer pH, refer to the Qiagen MinElute Handbook. If needed, use 5 μL of the 3M Sodium Acetate (included in the kit) to adjust the pH to the proper range.
- 4 Put a QIAquick spin column in a 2 mL collection tube.
- **5** Transfer the 300  $\mu$ L sample to the QIAquick column. Spin the sample in a centrifuge for 60 seconds at 17,900 x g (13,000 rpm). Discard the flow-through.
- 6 Add 750  $\mu$ L of buffer PE to the column. Spin the sample in a centrifuge for 60 seconds at 17,900 x g (13,000 rpm). Discard the flow-through.
- 7 Put the QIAquick column back in the 2 mL collection tube and spin in a centrifuge for 60 seconds at 17,900 x g (13,000 rpm).
- **8** Transfer the QIAquick column to a new 1.5-mL collection tube to elute the cleaned sample.
- **9** Let sit for 2 minutes to completely evaporate residual ethanol. All traces of ethanol must be removed.
- **10** Add 30 μL of buffer EB directly onto the QIAquick filter membrane. Wait 60 seconds, then centrifuge for 60 seconds at 17,900 x g (13,000 rpm).
- 11 Collect the eluate.

**Stopping Point** If you do not continue to the next step, store the samples at -20°C.

#### Step 10. Select size using a gel

#### WARNING

Prolonged exposure to UV light can damage your DNA.

Excise as narrow a band as possible from the gel during gel purification.

#### **CAUTION**

Do not purify multiple samples on a single gel. Cross-contamination between libraries can occur.

- 1 Prepare a 4% NuSeive agarose gel with distilled water and TAE. Final concentration of TAE should be 1X. Use a large well comb to prevent overloading.
  - Typical gel dimensions are 12 cm x 14 cm, using 100 mL gel volume.
- 2 Add 10 µL of Trackit 50 BP ladder to two lanes on opposite sides of the gel.
- 3 Add 5  $\mu$ L Trackit Loading Buffer to 30  $\mu$ L of the DNA from the purified ligation reaction. Mix on a vortex mixer.
- **4** Load the entire sample in another lane of the gel, leaving at least a gap of one empty lane between the ladders and sample.
- **5** Run the gel at 25 V for 17 hours.
- **6** Incubate the gel in SYBR Gold solution for 60 minutes.
- 7 View the gel on a Dark Reader transilluminator, which is a safer alternative to a UV transilluminator.
- **8** Put a clean ruler across the gel at the 300 bp marker. Use a fresh scalpel or razor blade to excise a 2 mm slice of the sample DNA even with the 300 bp marker.

#### Step 11. Purify the gel

Use a Qiagen Gel Extraction Kit (Qiagen, p/n 28704) to purify the DNA from the agarose slices.

- **1** Weigh the gel slice.
- 2 Add 6 volumes of Buffer QG to 1 volume of gel (100 mg = 100  $\mu$ L). You may need to do this in a 15 mL conical tube or in two tubes.
- **3** Incubate at room temperature for 10 minutes (or until the gel slice has completely dissolved). To help dissolve gel, mix the tube in a vortex mixer every 2 to 3 minutes during the incubation.
- **4** After the gel slice has dissolved completely, check that the color of the mixture is yellow (similar to Buffer QG without dissolved agarose).
- 5 Add 1 gel volume of isopropanol to the sample and mix. For example, if the agarose gel slice is 100 mg, add 100  $\mu L$  isopropanol. Do not spin the sample in a centrifuge at this time.
- **6** Put a QIAquick spin column in a provided 2 mL collection tube.
- 7 To bind DNA, apply the sample to the QIAquick column, and spin in a centrifuge for 1 minute at 17,900 x g (13,000 rpm).
  - The maximum volume of the column reservoir is 800  $\mu L.$  For sample volumes of more than 800  $\mu L,$  simply load and spin again.
- **8** Discard flow-through and put the QIAquick column back in the same collection tube.
- **9** To wash, add 750  $\mu$ L of Buffer PE to QIAquick column and spin in a centrifuge for 2 minutes at 17,900 x g (13,000 rpm).
- 10 Discard the flow-through and spin the QIAquick column in a centrifuge for an additional 1 minute at  $17,900 \times g$  (13,000 rpm).
- **11** Put the QIAquick column into a clean 1.5-mL microcentrifuge tube.
- **12** Let sit for 2 minutes to completely evaporate residual ethanol. All traces of ethanol must be removed.
- 13 To elute DNA, add 30  $\mu$ L of Buffer EB to the center of the QIAquick membrane. Wait 60 seconds, then spin the column in a centrifuge for 1 minute.

#### Step 12. Amplify prepped library

This step uses PCR to selectively enrich those DNA fragments that have adapter molecules on both ends, and to amplify the amount of DNA in the library. The PCR is done with two primers that anneal to the ends of the adapters. Six to eight cycles of PCR are used.

#### **CAUTION**

This protocol was optimized to minimize PCR-based bias in the library preparation. While most library preparations yield enough DNA (500 ng) for at least a single hybridization, poor quality DNA samples or other factors can affect yield.

If yield is consistently below 500 ng, you can hybridize with less library. Do not add less than 250 ng of DNA to the hybridization, or sequencing results can be affected.

To determine the number of cycles needed, do a trial amplification with 6 cycles. If you do not get enough yield, repeat with 8 cycles.

- **1** For 1 library (prepare on ice):
  - In a PCR tube, strip tube, or plate, prepare the reaction mix in Table 14. Use the Illumina Paired-End Genomic DNA Sample Prep Kit (p/n PE-102-1001). Mix well by gently pipetting up and down.
- **2** For multiple libraries (prepare on ice):
  - **a** Prepare the reaction mix in Table 14. Use the Illumina Paired-End Genomic DNA Sample Prep Kit (p/n PE-102-1001). Mix well on a vortex mixer.
  - **b** Add 27 µL of the reaction mix to each well or tube.
  - c Add 23  $\mu L$  of each DNA sample to each well or tube. Mix by pipetting. Change pipette tips between samples.

#### 2 Sample Preparation

**Step 12. Amplify prepped library** 

Table 14 PCR Components\*

Reagent	Volume for 1 Library	Volume for 12 Libraries
DNA	23 μL	
PCR primer PE 1.0	1 μL	12.5 μL
PCR primer PE 2.0	1 μL	12.5 μL
PCR Polymerase (p/n 1000524 from Illumina Kit)	25 μL	312.5 μL
Total Volume	50 μL	337.5 μL (27 μL/reaction)

<sup>\*</sup> These reagents are included in the Illumina Paired-End Genomic DNA Sample Prep Kit (p/n PE-102-1001)

#### **3** Amplify using the following PCR program:

Table 15 PCR protocol

Step	Temperature	Time
Step 1	98°C	30 seconds
Step 2	98°C	10 seconds
Step 3	65°C	30 seconds
Step 4	72°C	30 seconds
Step 5		Repeat Step 2 through Step 4 for a total of 6 to 8 times.
Step 6	72°C	5 minutes
Step 7	4°C	Hold

# Step 13. Purify the sample with the QIAquick PCR Purification Kit

- 1 If you haven't already done so, add the pH indicator to the Buffer PB.
- **2** Add 250 μL of PB per sample and mix well by pipetting.
- 3 Check for the yellow color to make sure buffer PB pH is correct.

  For more information on how to check buffer pH, refer to the Qiagen MinElute Handbook. If needed, use 2 to 3 μL of the 3M Sodium Acetate (included in the kit) to adjust the pH to the proper range.
- **4** Put a QIAquick spin column in a 2 mL collection tub.
- 5 Transfer the 300  $\mu$ L sample to the QIAquick column. Spin the sample in a centrifuge for 60 seconds at 17,900 x g (13,000 rpm). Discard the flow-through.
- 6 Add 750  $\mu$ L of buffer PE to the column. Spin the sample in a centrifuge for 60 seconds at 17,900 x g (13,000 rpm). Discard the flow-through.
- 7 Put the QIAquick column back in the 2 mL collection tube and spin in a centrifuge for 60 seconds at 17,900 x g (13,000 rpm).
- **8** Transfer the QIAquick column to a new 1.5-mL collection tube to elute the cleaned sample.
- **9** Let sit for 2 minutes to completely evaporate residual ethanol. All traces of ethanol must be removed.
- **10** Add 50 μL of buffer EB directly onto the QIAquick filter membrane. Wait 60 seconds, then spin in a centrifuge for 60 seconds at 17,900 x g (13,000 rpm).
- **11** Collect the eluate, which can be stored at 4°C.

# Step 14. Assess quality and quantity with Agilent 2100 Bioanalyzer

Use the Bioanalyzer DNA 1000 to assess the quantity, quality and size distribution of the PCR products.

- 1 Check that the 2100 Bioanalyzer electrodes have been cleaned as instructed in the reagent kit guide.
- **2** Open the Agilent 2100 Expert Software (version B.02.02 or higher), turn on the 2100 Bioanalyzer and check communication.
- **3** Prepare the chip, samples and ladder as instructed in the reagent kit guide.
- **4** Load the prepared chip into the 2100 Bioanalyzer and start the run within five minutes after preparation.
- **5** Within the instrument context, choose the appropriate assay from the drop down list.
- **6** Start the run. Enter sample names and comments in the Data and Assay context.
- 7 Verify the results. Use the manual integration function to determine the library concentration under the 350 bp peak. Measure the concentration of the library by integrating under the peak.

NOTE

A minimum of 500 ng of library is required for hybridization.

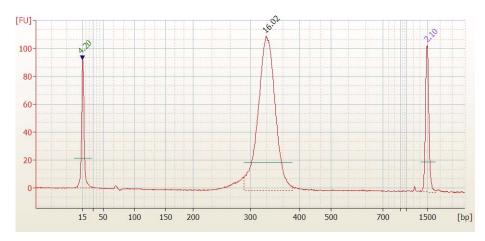


Figure 3 Analysis of amplified prepped library DNA using a Bioanalyzer DNA 1000 assay. The electropherogram shows a single peak in the size range of approximately  $350bp \pm 10\%$ .

#### 2 Sample Preparation

Step 14. Assess quality and quantity with Agilent 2100 Bioanalyzer

SureSelect Target Enrichment for Illumina Paired-End Sequencing Library Protocol

3
Hybridization

Step 1. Hybridize the library 41
Step 2. Prepare magnetic beads 46
Step 3. Select hybrid capture with SureSelect 47
Step 4. Desalt the capture solution with a Qiagen MinElute PCR purification column 49

This chapter describes the steps to combine the prepped library with the blocking agents and the SureSelect capture library.

CAUTION

The ratio of SureSelect capture library to prepped library is critical for successful capture.



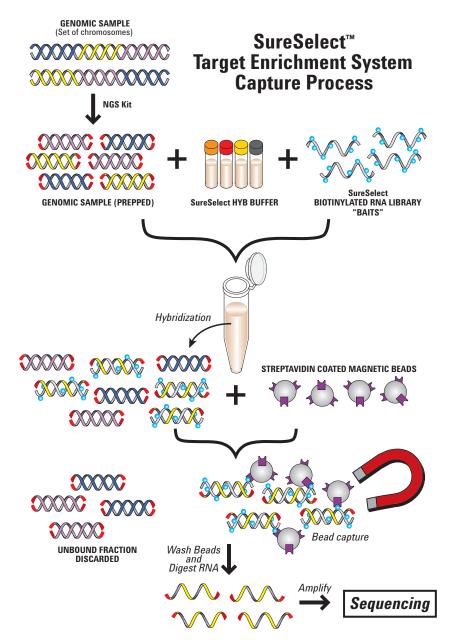


Figure 4 SureSelect Target Enrichment System Capture Process

 Table 16
 SureSelect Reagent Kit Components

Kit Component	250 RXN Kit	50 RXN Kit	Storage
SureSelect Hyb # 1	bottle	tube with orange cap	Room Temperature
SureSelect Hyb # 2	tube with red cap	tube with red cap	Room Temperature
SureSelect Hyb # 4	bottle	tube with black cap	Room Temperature
3M Sodium Acetate	tube with clear cap	tube with clear cap	Room Temperature
SureSelect Binding Buffer	bottle	bottle	Room Temperature
SureSelect Wash Buffer #1	bottle	bottle	Room Temperature
SureSelect Wash Buffer #2	bottle	bottle	Room Temperature
SureSelect Elution Buffer	bottle	bottle	Room Temperature
SureSelect Neutralization Buffer	bottle	bottle	Room Temperature
SureSelect Hyb # 3	tube with yellow cap	tube with yellow cap	-20°C
SureSelect Block #1	tube with green cap	tube with green cap	-20°C
SureSelect Block #2	tube with blue cap	tube with blue cap	-20°C
SureSelect PE Block #3	tube with brown cap	tube with brown cap	-20°C
SureSelect RNase Block	tube with purple cap	tube with purple cap	-20°C
SureSelect GA PCR Primers	tube with clear cap	tube with clear cap	-20°C
SureSelect Oligo Capture Library	tube with red cap	tube with red cap	-80°C

The SureSelect reagents are packaged in separate kits. See Table 17.

 Table 17
 Part number for reagent kits

Reagent Kit	50 reactions	250 reactions
Room temperature reagents	5190-1953	5190-1959
Cold reagents, -20°C	5190-1997	5190-1998

## CAUTION

You must avoid evaporation from the small volumes of the capture during the 24 hour or greater incubation.

If you want to use a different combination of thermal cycler, lid temperature, plates or strips, and sealing method (strip caps or sealing tape), first test the conditions. Incubate 27  $\mu$ L of SureSelect Hybridization Buffer (without DNA) at 65°C for 24 hours (or longer, if applicable) as a test. Include buffer in each well that you might use, including those in the center and those on the edges. Check that you do not get extensive evaporation. Evaporation should not exceed 3 to 4  $\mu$ L.

For a partial list of tested options showing minimal evaporation, refer to "Alternative Capture Equipment Combinations" on page 60.

# Step 1. Hybridize the library

- 1 If the prepped library concentration is below 147 ng/ $\mu$ L, use a vacuum concentrator to concentrate the sample at  $\leq 45$ °C.
  - a Add the entire 50 µL of prepped library to an Eppendorf tube. Poke one or more holes in the lid with a narrow gauge needle.
    - You can also break off the cap, cover with parafilm, and poke a hole in the parafilm.
  - **b** Completely lyophilize. Use a vacuum concentrator on low heat (less than  $45\,^{\circ}\mathrm{C}$ ) to dehydrate.
  - **c** Reconstitute with nuclease-free water to bring the final concentration to  $147 \text{ ng/}\mu\text{L}$  (or greater if sample recovery is of concern). Pipette up and down along the sides of the tube for optimal recovery.
  - **d** Mix well on a vortex mixer and spin in a microfuge for 1 minute.
- 2 Optional. To test recovery after lyophilization, reconstitute the sample to greater than 147 ng/ $\mu$ L and check the concentration on an Agilent Bioanalyzer DNA 1000 chip. See "Step 14. Assess quality and quantity with Agilent 2100 Bioanalyzer" on page 34. After quantitation, adjust the sample to 147 ng/ $\mu$ L.
  - Alternatively, concentrate a 500 ng aliquot at  $\leq 45^{\circ}\mathrm{C}$  down to 3.4  $\mu L$ . If the sample dries up completely, resuspend in 3.4  $\mu L$  of water and mix on a vortex mixer. If processing multiple samples, adjust to equivalent volumes before concentrating.
- **3** Mix the components in Table 18 at room temperature to prepare the hybridization buffer.

Table 18 Hybridization Buffer

Reagent	Volume for 1 capture (µL), includes excess	Volume for 6 captures (µL), includes excess	Volume for 12 captures (µL), includes excess
SureSelect Hyb # 1	25	125	250
SureSelect Hyb # 2 (red cap)	1	5	10
SureSelect Hyb # 3 (yellow cap)	10	50	100
SureSelect Hyb # 4	13	65	130
Total	49	245	490 (40 μL/sample)

Step 1. Hybridize the library

- **4** If precipitate forms, warm the hybridization buffer at 65°C for 5 minutes.
- **5** In a PCR plate, strip tubes, or tubes, prepare the SureSelect capture library mix for target enrichment:
  - a Keep tubes on ice until step 10.
  - **b** For each sample, add 5 µL of SureSelect capture library.
  - c For 1 library, combine 1  $\mu$ L RNase Block (purple cap) with 2  $\mu$ L nuclease-free water. For multiple libraries, use 1 part RNase Block to 2 parts nuclease-free water to make enough mix for 2  $\mu$ L per capture library, plus excess.
  - $\boldsymbol{d}$   $\,$  Add 2  $\mu L$  of diluted RNase Block to each capture library, and mix by pipetting.
- 6 Mix the contents in Table 19 to make the correct amount of SureSelect Block mix for the number of samples used.

Table 19 SureSelect Block Mix

Reagent	Volume for 1 reaction	Volume for 12 reactions (includes excess)
SureSelect Block #1 (green cap)	2.5 μL	31.25 μL
SureSelect Block #2 (blue cap)	2.5 μL	31.25 μL
SureSelect PE Block #3 (brown cap)	0.6 μL	7.5 µL
Total	5.6 μL	70 μL

- 7 In a separate PCR plate, prepare the prepped library for target enrichment.
  - a Add 3.4  $\mu$ L of 147 ng/ $\mu$ L prepped library to the "B" row in the PCR plate. Put each sample into a separate well.
  - **b** Add  $5.6~\mu L$  of the SureSelect Block Mix to each well in row B.
  - **c** Mix by pipetting up and down.
  - **d** Seal the wells of row "B" with caps and put the PCR plate in the thermal cycler. Do not heat the Hybridization Buffer or capture library yet, only the prepped library with blockers.
  - e Run the following thermal cycler program in Table 20.

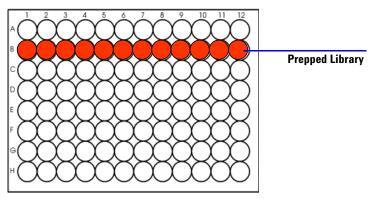


Figure 5 Prepped library shown in red

Table 20 PCR program

Step	Temperature	Time
Step 1	95°C	5 minutes
Step 2	65°C	Hold

**8** Use a heated lid on the thermal cycler at 105°C to hold the temperature of the plate on the thermal cycler at 65°C.

## CAUTION

The lid of the thermal cycler is hot and can cause burns. Use caution when working near the lid.

**9** Maintain the plate at  $65^{\circ}$ C while you load  $40~\mu$ L of hybridization buffer per well into the "A" row of the PCR plate. The number of wells filled in Row A is the number of libraries prepared.

The example in Figure 6 is for 12 captures.

Step 1. Hybridize the library

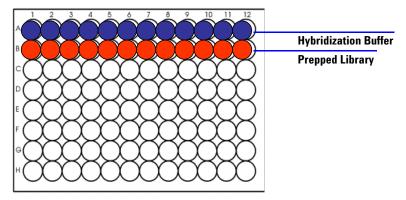


Figure 6 Hybridization buffer shown in blue

Make sure that the plate is at 65°C for a minimum of 5 minutes before you go to step 10.

**10** Add the capture library mix from step 5 to the PCR plate:

- a Add the capture library mix (7  $\mu$ L) to the "C" row in the PCR plate. For multiple samples, use a multi-channel pipette to load the capture library mix into the "C" row in the PCR plate. Keep the plate at 65°C during this time.
- **b** Seal the wells with strip caps. Use a capping tool to make sure the fit is tight.
- **c** Incubate the samples at 65°C for 2 minutes.
- 11 Maintain the plate at  $65^{\circ}$ C while you use a multi-channel pipette to take 13  $\mu$ L of Hybridization Buffer from the "A" row and add it to the SureSelect capture library mix contained in row "C" of the PCR plate for each sample. (See Figure 7.)

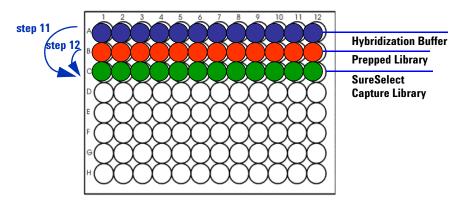


Figure 7 SureSelect Capture Library, or "Baits", shown in Green

- **12** Maintain the plate at 65°C while you use a multi-channel pipette to transfer the entire contents of each prepped library mix in row "B" to the hybridization solution in row "C". (See Figure 7.) Mix well by slowly pipetting up and down 8 to 10 times.
  - The hybridization mixture is now 27 to 29  $\mu L$  , depending on degree of evaporation during the preincubations.
- **13** Seal the wells with strip caps or double adhesive film. Make sure all wells are completely sealed.
  - If you use strip tubes, test for evaporation before you do the first experiment to make sure the tube/capping method is appropriate for the thermal cycler. Check that no more than 3 to 4  $\mu$ L is lost to evaporation.
- **14** Incubate the hybridization mixture for 24 hours at  $65^{\circ}$ C with a heated lid at  $105^{\circ}$ C.
  - Samples may be hybridized for up to 72 hours, but when you hybridize at longer periods, check that there is no extensive evaporation.

Step 2. Prepare magnetic beads

## Step 2. Prepare magnetic beads

- 1 Prewarm SureSelect Wash Buffer #2 at 65°C in a circulating water bath for use in "Step 3. Select hybrid capture with SureSelect".
- **2** Vigorously resuspend the Dynal MyOne Streptavidin T1 (Invitrogen) magnetic beads on a vortex mixer. Dynal beads settle during storage.
- 3 For each hybridization, add 50  $\mu L$  Dynal magnetic beads to a 1.5-mL microfuge tube.
- **4** Wash the beads:
  - a Add 200 µL of SureSelect Binding buffer.
  - **b** Mix the beads on a vortex mixer for 5 seconds.
  - **c** Put the tubes into a magnetic device, such as the Dynal magnetic separator (Invitrogen).
  - **d** Remove and discard the supernatant.
  - **e** Repeat step a through step d for a total of 3 washes.
- 5 Resuspend the beads in 200 μL of SureSelect Binding buffer.

# Step 3. Select hybrid capture with SureSelect

- 1 Estimate and record the volume of hybridization that remained after 24 hour incubation.
- **2** Add the hybridization mixture directly from the thermal cycler to the bead solution, and invert the tube to mix 3 to 5 times.
  - Excessive evaporation, such as when less than 20  $\mu L$  remains after hybridization, can indicate suboptimal capture performance. See Table 23 on page 61 for tips to minimize evaporation.
- **3** Incubate the hybrid-capture/bead solution on a Nutator or equivalent for 30 minutes at room temperature.
  - Make sure the sample is properly mixing in the tube.
- **4** Briefly spin in a centrifuge.
- **5** Separate the beads and buffer on a Dynal magnetic separator and remove the supernatant.
- 6 Resuspend the beads in 500 μL of SureSelect Wash Buffer #1 by mixing on a vortex mixer for 5 seconds.
- 7 Incubate the samples for 15 minutes at room temperature.
- **8** Separate the beads and buffer on a Dynal magnetic separator and remove the supernatant.
- **9** Wash the beads:
  - a Resuspend the beads in 500  $\mu L$  of 65°C prewarmed SureSelect Wash Buffer #2 and mix on a vortex mixer for 5 seconds to resuspend the beads.
  - **b** Incubate the samples for 10 minutes at 65°C in a recirculating water bath, heat block or equivalent.
    - Do not use a tissue incubator. It cannot properly maintain temperature.
  - **c** Invert the tube to mix. The beads may have settled.
  - **d** Separate the beads and buffer on a Dynal magnetic separator and remove the supernatant.
  - **e** Repeat step a through step d for a total of 3 washes. Make sure all of the wash buffer has been removed.
- 10 Mix the beads in 50  $\mu$ L of SureSelect Elution Buffer on a vortex mixer for 5 seconds to resuspend the beads.
- 11 Incubate the samples for 10 minutes at room temperature.

Step 3. Select hybrid capture with SureSelect

- 12 Separate the beads and buffer on a Dynal magnetic separator.
- **13** Use a pipette to transfer the supernatant to a new 1.5-mL microfuge tube. The supernatant contains the captured DNA. The beads can now be discarded.
- 14 Add 50  $\mu L$  of SureSelect Neutralization Buffer to the captured DNA.

# Step 4. Desalt the capture solution with a Qiagen MinElute PCR purification column

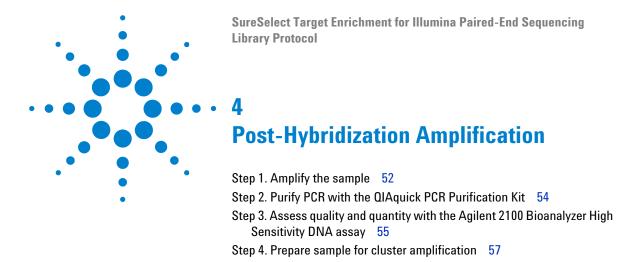
- 1 Allow the MinElute columns (stored at 4°C) to come to room temperature.
- 2 Add 500 μL of PB to the sample and mix well by pipetting.
- 3 Check for the yellow color to make sure buffer PB pH is correct.

  For more information on how to check buffer pH, refer to the Qiagen MinElute Handbook. If needed, use 5 μL of the 3M Sodium Acetate (included in the kit) to adjust the pH to the proper range.
- **4** Put a MinElute spin column in a 2 mL collection tube.
- 5 Transfer the 600 μL sample to the MinElute column. Spin the sample in a centrifuge for 60 seconds at 17,900 x g. Discard the flow-through.
- 6 Add 750 μL of buffer PE to the column. Spin the sample in a centrifuge for 60 seconds at 17,900 x g. Discard the flow-through.
- 7 Put the MinElute column back in the 2 mL collection tube and spin in a centrifuge for 60 seconds at 17,900 x g.
- **8** Air-dry the column for 2 minutes to completely evaporate residual ethanol. All traces of ethanol must be removed.
- **9** Transfer the MinElute column to a new 1.5-mL collection tube to elute the cleaned sample.
- **10** Add 15 μL buffer EB directly onto the MinElute filter membrane. Wait 60 seconds, then spin in a centrifuge for 60 seconds at 17,900 x g (13,000 rpm).

#### **Stopping Point**

If you do not continue to the next step, store the purified DNA in Elution Buffer (EB) at -20  $^{\circ}\mathrm{C}.$ 

Step 4. Desalt the capture solution with a Qiagen MinElute PCR purification column



This chapter describes the steps to amplify, purify, and assess quality of the sample library, and dilute the sample appropriately for cluster amplification.

#### 4 Post-Hybridization Amplification

Step 1. Amplify the sample

# Step 1. Amplify the sample

## **CAUTION**

Do not use amplification enzymes other than Herculase II Fusion DNA Polymerase. Other enzymes have not been validated.

#### **CAUTION**

This protocol was optimized to minimize PCR-based bias in the library preparation.

To determine the number of cycles needed, do a trial amplification with 12 cycles. If you do not get enough yield for Illumina sequencing, repeat with 14 cycles.

#### **CAUTION**

To avoid cross-contaminating libraries, set up PCR reactions (all components except the library DNA) in a dedicated clean area or PCR hood with UV sterilization and positive air flow.

Prepare 1 amplification reaction for each hybrid capture.

- **1** For 1 library:
  - In a PCR tube, strip tube, or plate, prepare the reaction mix in Table 21, on ice. Mix well by gently pipetting up and down.
- **2** For multiple libraries:
  - a Prepare the reaction mix in Table 21, on ice. Mix well on a vortex mixer.
  - **b** Add 43 µL of the reaction mix to each well or tube.
  - ${f c}$  Use a pipette to add 7  $\mu L$  of each DNA sample to each well or tube. Mix by pipetting. Change pipette tips between samples to avoid cross-contamination.

Table 21 Herculase II Master Mix

Reagent	Volume for 1 reaction (includes excess)	Volume for 10 reactions (includes excess)	Volume for 24 reactions (includes excess)
Captured DNA	7 μL	N/A	N/A
Nuclease-free water	30.5 μL	335.5 μL	762.5 μL
5X Herculase II Reaction Buffer*	10 μL	110 µL	250 μL
dNTP mix (25 mM each) <sup>*</sup>	0.5 μL	5.5 μL	12.5 µL
SureSelect GA PCR Primers	1.0 μL	11 μL	25 μL
Herculase II Fusion DNA Polymerase	1.0 μL	11 μL	25 μL
Total	50 μL	473 μL	1,075 μL

<sup>\*</sup> Included with the Herculase II Fusion DNA Polymerase. Do not use the buffer or dNTP mix from any other kit.

 ${f 3}$  Put the tubes in a thermal cycler and run the program in Table 22.

 Table 22
 PCR program

Step	Temperature	Time
Step 1	98°C	30 seconds
Step 2	98°C	10 seconds
Step 3	57°C	30 seconds
Step 4	72°C	30 seconds
Step 5		Repeat Step 2 through Step 4 for a total of 12 to 14 times.
Step 6	72°C	7 minutes
Step 7	4°C	Hold

#### 4 Post-Hybridization Amplification

Step 2. Purify PCR with the QIAquick PCR Purification Kit

# Step 2. Purify PCR with the QIAquick PCR Purification Kit

- 1 If you haven't already done so, add the pH indicator to the Buffer PB.
- 2 Add 250 µL of PB to the sample and mix well by pipetting.
- 3 Check for the yellow color to make sure buffer PB pH is correct.

  For more information on how to check buffer pH, refer to the Qiagen MinElute Handbook. If needed, use 5 μL of the 3M Sodium Acetate (included in the kit) to adjust the pH to the proper range.
- 4 Put a QIAquick spin column in a 2 mL collection tube.
- **5** Transfer the 300  $\mu$ L sample to the QIAquick column. Spin the sample in a centrifuge for 60 seconds at 17,900 x g (13,000 rpm). Discard the flow-through.
- **6** Add 750 μL of buffer PE to the column. Spin the sample in a centrifuge for 60 seconds at 17,900 x g (13,000 rpm). Discard the flow-through.
- 7 Put the QIAquick column back in the 2 mL collection tube and spin in a centrifuge for 60 seconds at 17,900 x g (13,000 rpm).
- **8** Transfer the QIAquick column to a new 1.5-mL collection tube to elute the cleaned sample.
- **9** Let sit for 2 minutes to completely evaporate residual ethanol. All traces of ethanol must be removed.
- 10 Add 30  $\mu$ L of buffer EB directly onto the QIAquick filter membrane. Wait 60 seconds, then spin in a centrifuge for 60 seconds at 17,900 x g (13,000 rpm).
- 11 Collect the eluate, which can be stored at -20°C.

# Step 3. Assess quality and quantity with the Agilent 2100 Bioanalyzer High Sensitivity DNA assay

Use a Bioanalyzer High Sensitivity DNA Assay to assess the quality and size range. Note that the concentration of each sample loaded on the chip must be within the linear range of the assay to accurately quantify (5 pg to 500 pg). You may need to dilute your sample accordingly. Refer to the *Agilent High Sensitivity DNA Kit Guide* at http://www.chem.agilent.com/en-US/Search/Library/\_layouts/Agilent/PublicationSummary.aspx?whid=59504.

- 1 Check that the 2100 Bioanalyzer electrodes have been cleaned as instructed in the reagent kit guide.
- **2** Open the Agilent 2100 Expert Software (version B.02.07 or higher required to run the High Sensitivity Kit), turn on the 2100 Bioanalyzer and check communication.
- **3** Prepare the chip, samples and ladder as instructed in the reagent kit guide.
- **4** Load the prepared chip into the 2100 Bioanalyzer and start the run within five minutes after preparation.
- **5** Within the instrument context, choose the appropriate assay from the drop down list.
- **6** Start the run. Enter sample names and comments in the Data and Assay context.
- **7** Verify the results.

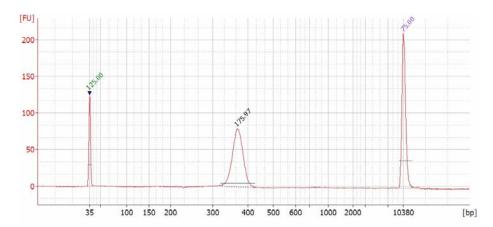
You can use the High Sensitivity Kit to quantify the amount of sample to be used for Illumina sequencing.

The linear range of the High Sensitivity kit is 5 pg to 500 pg. If the reading far exceeds 500 pg, dilute and run the Bioanalyzer chip again. If the yield is too low or non-specific peaks are observed in the electropherogram, repeat the PCR with more or fewer cycles. The goal is to minimize cycles, while you produce enough library for the quantification needed for application to the flow cell.

**8** Continue to sequencing.

#### 4 Post-Hybridization Amplification

Step 3. Assess quality and quantity with the Agilent 2100 Bioanalyzer High Sensitivity DNA assay



**Figure 8** Analysis of Amplified Capture DNA using the High Sensitivity DNA Kit. The electropherogram shows a single peak in the size range of approximately 350 nucleotides.

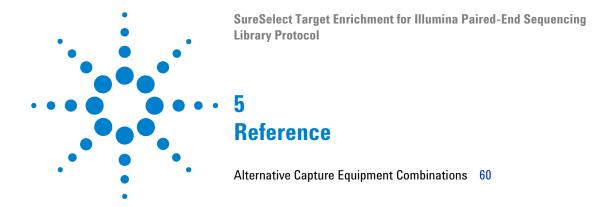
# Step 4. Prepare sample for cluster amplification

In this step you set up cluster amplification with the HP3 and HT1 buffers that are included in the Illumina Paired-End Cluster Generation Kit. Conditions are optimized to provide 500K to 700K clusters/mm2 (SCS v2.6/RTA 1.6) or 700K to 900K clusters/mm2 (SCS v2.8/RTA 1.8), using v4 sequencing chemistry.

- 1 Prepare 10 nM (10 fmol/μL) dilutions of the amplified capture, based on the Bioanalyzer quantitation.
- 2 Dilute 30 fmol (3  $\mu$ L) of amplified capture with 16  $\mu$ L of EB buffer for a total volume of 19  $\mu$ L.
- **3** Add 1 μL of HP3 buffer (2 N NaOH).
- 4 Mix the sample briefly on a vortex mixer
- 5 Incubate for 5 minutes at room temperature to denature the DNA.
- **6** Place the sample on ice until you are ready to proceed to final dilution.
- 7 Dilute 8  $\mu$ L of denatured DNA with 992  $\mu$ L of pre-chilled HT1 buffer for a final concentration of 12 pM.
- **8** Mix the sample briefly on a vortex mixer.
- **9** Continue with cluster generation using the appropriate Illumina Paired-End sequencing protocol.

### 4 Post-Hybridization Amplification

Step 4. Prepare sample for cluster amplification



This chapter contains reference information.

#### 5 Reference

**Alternative Capture Equipment Combinations** 

# **Alternative Capture Equipment Combinations**

Table 23 lists combinations of thermal cycler, lid temperature, plates or strips, and sealing method (strip caps or sealing tape) other than those used in this protocol that have shown minimal evaporation.

Refer to this list for additional of equipment combination options for hybridization. Note that minimal evaporation is needed to ensure good capture results.

 Table 23
 Tested options that show minimal evaporation

PCR Machine	Plate/Strips	Cover	Comments
Stratagene Mx3005P QPCR	Mx3000P Strip Tubes (401428)	MX3000P Optical Strip Caps (401425)	Heated Lid
Stratagene Mx3005P QPCR	MicroAmp Optical 96-well reaction plate (N801-0560)	MicroAmp Clear Adhesive Film (4306311)	Heated Lid; ABI compression pad (4312639)
			Use two layers of film.
ABI GeneAmp 9700	MicroAmp Optical 96-well Reaction Plate (N801-0560)	MicroAmp Caps (8caps/strip) (N801-0535)	Heated Lid
ABI Veriti (4375786)	MicroAmp Optical 96-well Reaction Plate (N801-0560)	MicroAmp Clear Adhesive Film (4306311)	Heated Lid; ABI compression pad (4312639)
			Use two layers of film.
Eppendorf Mastercycler	Eppendorf 8-Tube PCR Tubes	Attached lids	Lid heating set to 75°C
ABI Veriti (4375786)	Stratagene strip tubes 410022 (Mx4000)	Stratagene Strip cap domed 410096 (Robocycler)	Heated Lid
ABI Veriti (4375786)	Stratagene strip tubes 410022 (Mx4000)	Stratagene Optical cap 401425 (Mx3000/3005)	Heated Lid
BioRad (MJ Research) PTC-200	Stratagene strip tubes 410022 (Mx4000)	Stratagene Optical cap 410024 (Mx4000)	Heated Lid
BioRad (MJ Research) PTC-200	Stratagene strip tubes 410022 (Mx4000)	Stratagene Optical cap 401425 (Mx3000/3005)	Heated Lid
BioRad (MJ Research) PTC-200	Stratagene 96-well Plate 410088 (Mx3000/3005)	Stratagene Optical cap 401425 (Mx3000/3005)	Heated Lid

### 5 Reference

**Alternative Capture Equipment Combinations** 

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## In This Book

This guide contains information to run the SureSelect Target Enrichment for Illumina Paired-End Sequencing Library protocol with the SureSelect Target Enrichment Kit.

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