

# Agilent Oligonucleotide Array-Based CGH for Genomic DNA Analysis

**Bravo Automated Liquid  
Handling Platform with  
Enzymatic and ULS Labeling**

**Protocol**

**Version 2.3, August 2015**

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

Before you begin, view hands-on  
videos of SurePrint procedures at  
<http://www.agilent.com/genomics/protocolvideos>.



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### CAUTION

A **CAUTION** notice denotes a hazard. It calls attention to an operating procedure, practice, or the like that, if not correctly performed or adhered to, could result in damage to the product or loss of important data. Do not proceed beyond a **CAUTION** notice until the indicated conditions are fully understood and met.

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## In This Guide...

This guide describes the recommended operational procedures to analyze DNA copy number variations using Agilent 60-mer oligonucleotide microarrays for array-based comparative genomic hybridization (aCGH) analysis. This protocol is specifically developed and optimized to use the Bravo Automated Liquid Handling Platform for the labeling (ULS and enzymatic), purification and pre-hybridization steps.

### **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 DNA Isolation**

This chapter describes the method to isolate genomic DNA (gDNA) from blood, cells, frozen tissues, or FFPE samples prior to labeling.

### **3 Sample Preparation for Bravo Platform**

This chapter describes how to prepare the samples to be used on the Bravo Automated Liquid Handling Platform.

### **4 Sample Labeling on the Bravo Platform**

This chapter describes the fragmentation, labeling (ULS and enzymatic), clean-up and preparation of labeled gDNA for hybridization done on the Bravo platform.

### **5 Microarray Processing**

This chapter describes the steps to hybridize, wash and scan Agilent CGH and CGH+SNP microarrays and to extract data using the Agilent Feature Extraction Software. It also tells you how to get the Agilent Reference Genotype Files (Male and Female) for use in Agilent CytoGenomics and Agilent Genomic Workbench.

## 7 Troubleshooting

This chapter contains possible causes for above-threshold DLRSD (Derivative Log Ratio Standard Deviation). A poor DLRSD score reflects high probe-to-probe log ratio noise.

## 8 Reference

This chapter contains reference information related to the labeling kits and the protocol.

## What's new in 2.3

- Added reference to compatibility matrix for non-Agilent scanners.
- Updated product labeling statement.

## What's new in 2.2

- Added note to calibrate hybridization oven on a regular basis for accuracy of the collected data.
- Removed support for obsolete Genomic DNA Enzymatic Labeling Kit.
- For Enzymatic Labeling, changed denaturation temperature to 98°C for primer annealing during labeling and for preparation for hybridization.
- For Enzymatic Labeling, changed hybridization temperature to 67°C.

## What's new in 2.1

- Guidelines for adjusting heat fragmentation times are expanded.
- Support for new SurePrint G3 Human CGH Bundles.

# Content

|          |  |           |
|----------|--|-----------|
| <b>1</b> | <b>Before You Begin</b>                        | <b>9</b>  |
|          | Procedural Notes                               | 10        |
|          | Safety Notes                                   | 11        |
|          | Agilent Oligo CGH Microarray Kit Contents      | 12        |
|          | Required Equipment                             | 19        |
|          | Required Reagents                              | 23        |
|          | Required Bravo Platform Protocols              | 26        |
|          | Required Hardware and Software                 | 26        |
| <b>2</b> | <b>DNA Isolation</b>                           | <b>27</b> |
|          | Blood, Cells or Frozen Tissues                 | 30        |
|          | Step 1. gDNA Extraction                        | 31        |
|          | Step 2. gDNA Quantitation and Quality Analysis | 34        |
|          | FFPE Tissues                                   | 38        |
|          | Step 1. Paraffin Removal                       | 39        |
|          | Step 2. Proteinase K Treatment                 | 40        |
|          | Step 3. gDNA Extraction                        | 41        |
| <b>3</b> | <b>Sample Preparation for Bravo Platform</b>   | <b>43</b> |
|          | Step 1. gDNA Dilution                          | 45        |
|          | Step 2. gDNA Placement in a 96-Well Plate      | 47        |
| <b>4</b> | <b>Sample Labeling on the Bravo Platform</b>   | <b>49</b> |
|          | Setting up the VWorks Software                 | 53        |
|          | Step 1. Log in to the VWorks software          | 53        |
|          | Step 2. Open and start a protocol              | 53        |
|          | ULS Labeling                                   | 55        |
|          | Step 1. ULS Labeling                           | 55        |
|          | Step 2. Purification after ULS labeling        | 61        |

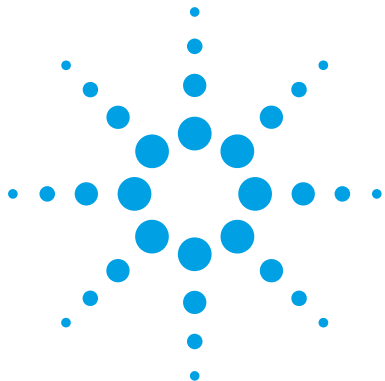
## Contents

|   |            |
|---|------------|
| To determine yield, degree of labeling or specific activity               | 63         |
| Step 3. Preparation of ULS Labeled gDNA for Hybridization                 | 64         |
| Enzymatic Labeling for CGH  | 70         |
| Step 1. Enzymatic Labeling  | 70         |
| Step 2. Purification after Enzymatic Labeling                             | 75         |
| To determine yield, degree of labeling or specific activity               | 77         |
| Step 3. Preparation of Enzymatic Labeled gDNA for Hybridization           | 79         |
| Enzymatic Labeling for CGH+SNP  | 84         |
| Step 1. Enzymatic Labeling  | 84         |
| Step 2. Purification after Enzymatic Labeling                             | 92         |
| To determine yield, degree of labeling or specific activity               | 95         |
| Step 3. Preparation of Enzymatic Labeled gDNA for Hybridization           | 97         |
| <b>5 Microarray Processing</b>  | <b>103</b> |
| Hybridization   | 104        |
| Step 1. Prepare the hybridization assembly                                | 105        |
| Step 2. Hybridize   | 106        |
| Microarray Wash   | 107        |
| Step 1. Prewarm Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 2 (overnight) | 108        |
| Step 2. Wash with Milli-Q ultrapure water                                 | 108        |
| Step 3. Clean with Acetonitrile (Wash Procedure B Only)                   | 109        |
| Step 4. Prewarm Stabilization and Drying Solution (Wash Procedure B Only) | 109        |
| Step 5. Wash microarrays  | 111        |
| Step 6. Put slides in a slide holder                                      | 116        |
| Microarray Scanning and Analysis  | 118        |
| Step 1. Scan the microarray slides  | 118        |
| Step 2. Analyze microarray image  | 120        |
| Step 3. Download Agilent Reference Genotype File                          | 124        |

|          |  |            |
|----------|--|------------|
| <b>7</b> | <b>Troubleshooting</b>   | <b>125</b> |
|          | If you have a low OD260/230 or OD260/280 value   | 126        |
|          | If you have poor sample quality due to residual RNA                                    | 126        |
|          | If you get poor sample quality due to degradation                                      | 127        |
|          | If the estimated concentration is too high or low                                      | 128        |
|          | If you have low specific activity or degree of labeling not due to poor sample quality | 129        |
|          | If you have low yield not due to poor sample quality                                   | 129        |
|          | If you have post-labeling signal loss  | 130        |
|          | If you have high BGNoise values  | 131        |
|          | If you have poor reproducibility   | 131        |
| <b>8</b> | <b>Reference</b>   | <b>133</b> |
|          | Reagent Kit Components   | 134        |
|          | Microarray Handling Tips   | 137        |
|          | Agilent Microarray Layout and Orientation  | 138        |
|          | Array/Sample tracking on microarray slides   | 141        |

## Contents





# 1 Before You Begin

|   |    |
|---|----|
| Procedural Notes                          | 10 |
| Safety Notes                              | 11 |
| Agilent Oligo CGH Microarray Kit Contents | 12 |
| Required Equipment                        | 19 |
| Required Reagents                         | 23 |
| Required Bravo Platform Protocols         | 26 |
| Required Hardware and Software            | 26 |

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



## Procedural Notes

- Follow the procedure described in this document to isolate gDNA from blood, cells, frozen tissues or FFPE samples.
- If the DNA isolation procedure described in this document cannot be followed, make sure that the DNA is free of RNA and protein contamination. For ULS labeling, also make sure the DNA is in one of the following buffers compatible with ULS labeling:
  - TE-buffer (10 mM Tris-HCl, 1 mM EDTA, pH 7.5 or pH 8)
  - 10 mM LiCl
  - 10 to 100 mM Na acetate
  - 10 mM NaCl
- 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 or enzymes on a vortex mixer. Instead, mix the solutions and reactions by gently tapping the tube with your finger.
- Avoid repeated freeze-thaw cycles of solutions containing gDNA or enzymes.
- When preparing frozen reagent stock solutions for use:
  - 1 Thaw the aliquot as quickly as possible without heating above room temperature.
  - 2 Mix briefly on a vortex mixer, and then spin in a microcentrifuge for 5 to 10 seconds to drive the contents off the 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

### CAUTION

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

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### WARNING

- **Cyanine reagents are considered hazardous by the OSHA Hazard Communication Standard (29 CFR 1910.1200). Contains material that causes damage to the following organs: kidneys, liver, cardiovascular system, respiratory tract, skin, eye lens or cornea, stomach. May be harmful if swallowed. Avoid contact with eyes, skin and clothing.**
  - **Agilent-CGHblock may be harmful if swallowed. Avoid contact with eyes, skin and clothing.**
  - **2× HI-RPM Hybridization Buffer is considered hazardous by the OSHA Hazard Communication Standard (29 CFR 1910.1200). Contains material that causes damage to the following organs: skin, central nervous system. May be harmful if swallowed. Avoid contact with eyes, skin and clothing.**
  - **Triton is harmful if swallowed. Risk of serious damage to eyes. Wear suitable PPE. Triton is a component of the Agilent 2× HI-RPM Hybridization Buffer.**
  - **Stabilization and Drying Solution is considered hazardous by the OSHA Hazard Communication Standard (29 CFR 1910.1200). Flammable liquid and vapor. Keep away from heat, sparks and flame. Keep container closed. Use only with adequate ventilation. This solution contains material which causes damage to the following organs: kidneys, liver, cardiovascular system, upper respiratory tract, skin, central nervous system (CNS), eye, lens or cornea.**
-

## Agilent Oligo CGH Microarray Kit Contents

Store microarray kit at room temperature. After the microarray foil pouch is opened, store the microarray slides at room temperature (in the dark) under a vacuum desiccator or N<sub>2</sub> purge box. Do not store microarray slides in open air after breaking foil.

### SurePrint G3 CGH Bundle

- 1-inch × 3-inch microarray slides in quantities of:
  - 50 for 1-pack
  - 25 for 2-pack
  - 12 for 4-pack
  - 6 for 8-pack
- Sufficient reagents and consumables to process 50 (1-pack and 2-pack bundle) or 48 (4-pack and 8-pack bundle) samples:
  - [SureTag Complete DNA Labeling Kit](#)
  - [Oligo aCGH/ChIP-on-chip Hybridization Kit](#)
  - [Hybridization gasket slides](#)
  - [Human Cot-1 DNA](#)
  - [Oligo aCGH/ChIP-on-chip Wash Buffer 1](#) and [Oligo aCGH/ChIP-on-chip Wash Buffer 2](#)
  - [Agilent CytoGenomics Software License](#)

**Table 1** SurePrint G3 CGH and CGH+SNP Bundles

| Part Number      | Description                              |
|------------------|--|
| G5920A, Option 1 | SurePrint G3 Human CGH Bundle, 1×1M      |
| G5921A, Option 1 | SurePrint G3 Human CGH Bundle, 2×400K    |
| G5921A, Option 2 | SurePrint G3 CGH+SNP Bundle, 2×400K      |
| G5922A, Option 1 | SurePrint G3 Human CGH Bundle, 4×180K    |
| G5922A, Option 2 | SurePrint G3 ISCA CGH+SNP Bundle, 4×180K |
| G5923A, Option 1 | SurePrint G3 Human CGH Bundle, 8×60K     |

**Catalog SurePrint HD and G3 CGH Microarray Kits**

- Five 1-inch × 3-inch, 1-pack and 2-pack microarray slides
- Three 1-inch × 3-inch, 4-pack and 8-pack microarray slides

Design files can be downloaded from  
<http://www.agilent.com/genomics/suredesign>.

See the tables that follow for available designs. For more information on CGH designs, go to <http://www.genomics.agilent.com>. Under **Products**, click **CGH & CGH+SNP Microarrays**.

**Table 2** Catalog SurePrint Microarray Kits - Human

| Part Number | Description   |
|-------------|---|
| G4842A*     | SurePrint G3 Human CGH+SNP Microarray Kit 2×400K        |
| G4890A*     | SurePrint G3 Human ISCA CGH+SNP Microarray Kit 4×180K   |
| G4869A*     | SurePrint G3 Human Cancer CGH+SNP Microarray Kit 4×180K |

\* These arrays can only be processed using the enzymatic labeling protocol.

**1 Before You Begin**  
**Agilent Oligo CGH Microarray Kit Contents**

**Table 3** Catalog CGH Microarray Kits - Human

| <b>Part Number</b> | <b>Description</b>   |
|--------------------|--|
| G4447A             | SurePrint G3 Human CGH Microarray Kit 1×1M (5 slides)          |
| G4824A-021529      | SurePrint G3 Human CGH Microarray Slide 1×1M                   |
| G4448A             | SurePrint G3 Human CGH Microarray Kit 2×400K (5 slides)        |
| G4825A-021850      | SurePrint G3 Human CGH Microarray Slide 2×400K                 |
| G4449A             | SurePrint G3 Human CGH Microarray Kit 4×180K (5 slides)        |
| G4826A-022060      | SurePrint G3 Human CGH Microarray Slide 4×180K                 |
| G4450A             | SurePrint G3 Human CGH Microarray Kit 8×60K (5 slides)         |
| G4827A-021924      | SurePrint G3 Human CGH Microarray Slide 8×60K                  |
| G4423B-016266      | SurePrint G3 Human CGH 244A Supplemental Slide 1×244K          |
| G5955A             | SurePrint G3 Human CGH ISCA v2 Microarray Kit 8×60K (3 slides) |
| G4411B             | Human Genome CGH 244A Microarray Kit 1×244K (5 slides)         |
| G4423B-014693      | Human Genome CGH 244A Microarray Slide 1×244K                  |
| G4412A             | Human Genome CGH 105A Microarray Kit 2×105K                    |
| G4425B-014698      | Human Genome CGH 105A Microarray Slide 2×105K                  |
| G4413A             | Human Genome CGH Microarray Kit 4×44K (3 slides)               |
| G4426B-014950      | Human Genome CGH Microarray Slide 4×44K                        |

**Table 4** Catalog CNV Microarray Kits - Human

| Part Number   | Description   |
|---------------|---|
| G4506A        | SurePrint G3 Human CNV Microarray Kit 1×1M (5 slides)         |
| G4824A-023642 | SurePrint G3 Human CNV Microarray Slide 1×1M                  |
| G4507A        | SurePrint G3 Human CNV Microarray Kit 2×400K (5 slides)       |
| G4825A-021365 | SurePrint G3 Human CNV Microarray Slide 2×400K                |
| G4423B-018897 | SurePrint G3 Human CNV Microarray Slide, Slide 1 of 2, 1×244K |
| G4423B-018898 | SurePrint G3 Human CNV Microarray Slide, Slide 2 of 2, 1×244K |
| G4417A        | Human CNV Association Microarray Kit 2×105K (5 slides)        |
| G4425B-022837 | Human CNV Association Microarray Slide 2×105K                 |

**Table 5** Catalog CGH Microarrays- Mouse

| Part Number   | Description   |
|---------------|---|
| G4838A        | SurePrint G3 Mouse CGH Microarray Kit 1×1M (5 slides)   |
| G4824A-027414 | SurePrint G3 Mouse CGH Microarray Slide 1×1M            |
| G4839A        | SurePrint G3 Mouse CGH Microarray Kit 4×180K (3 slides) |
| G4826A-027411 | SurePrint G3 Mouse CGH Microarray Kit 4×180K            |
| G4415A        | Mouse Genome CGH Microarray Kit 1×244K (5 slides)       |
| G4423B-014695 | Mouse Genome CGH Microarray Slide 1×244K                |
| G4416A        | Mouse Genome CGH Microarray Kit 2×105K (5 slides)       |
| G4425B-014699 | Mouse Genome CGH Microarray Slide 2×105K                |

## 1 Before You Begin

### Agilent Oligo CGH Microarray Kit Contents

**Table 6** Catalog CGH Microarrays - Rat

| Part Number   | Description   |
|---------------|---|
| G4840A        | SurePrint G3 Rat CGH Microarray Kit 1×1M (5 slides)   |
| G4824A-027065 | SurePrint G3 Rat CGH Microarray Slide 1×1M            |
| G4841A        | SurePrint G3 Rat CGH Microarray Kit 4×180K (3 slides) |
| G4826A-027064 | SurePrint G3 Rat CGH Microarray Slide 4×180K          |
| G4435A        | Rat Genome CGH Microarray Kit 1×244K (5 slides)       |
| G4423B-015223 | Rat Genome CGH Microarray Slide 1×244K                |
| G4436A        | Rat Genome CGH Microarray Kit 2×105K (5 slides)       |
| G4425B-015235 | Rat Genome CGH Microarray Slide 2×105K                |

**Table 7** Catalog CGH Microarrays - Model Organism/Non-Human

| Part Number   | Description  |
|---------------|--|
| G4826A-024419 | SurePrint G3 Rhesus Macaque CGH Microarray Kit 4×180K (5 slides) |
| G4826A-024422 | SurePrint G3 Chimpanzee CGH Microarray Kit 4×180K (5 slides)     |
| G4826A-025242 | SurePrint G3 Bovine CGH Microarray Kit 4×180K (5 slides)         |
| G4826A-025522 | SurePrint G3 Canine CGH Microarray Kit 4×180K (5 slides)         |
| G4826A-025843 | SurePrint G3 Rice CGH Microarray Slide 4×180K                    |
| G4423B-019553 | Chicken Genome CGH Microarray, 1×244K                            |

### Unrestricted SurePrint HD and G3 CGH Microarrays

- One, two, four or eight microarrays printed on each 1-inch × 3-inch glass slide
- Number of microarray slides vary per kit and per order

Design files can be downloaded from <http://www.agilent.com/genomics/suredesign>.

See the tables that follow for available designs.



**Table 8** Unrestricted CGH Microarrays - Human

| Part Number           | Description  |
|-----------------------|--|
| G4826A, AMADID 031748 | Unrestricted SurePrint G3 CGH ISCA v2 Microarray, 4×180K |
| G4827A, AMADID 031746 | Unrestricted SurePrint G3 CGH ISCA v2 Microarray, 8×60K  |
| G4425B, AMADID 031750 | Unrestricted HD CGH ISCA v2 Microarray, 2×105K           |
| G4426B, AMADID 031747 | Unrestricted HD CGH ISCA v2 Microarray, 4×44K            |

### Custom SurePrint HD and G3 Microarrays

- One, two, four or eight microarray(s) printed on each 1-inch × 3-inch glass slide
- Number of microarrays varies per kit and per order

See the tables that follow for available formats.

**Table 9** Custom SurePrint G3 CGH and CGH+SNP Microarrays

| Part Number | Description                                    |
|-------------|--|
| G4882A*     | SurePrint G3 Custom CGH+SNP Microarray, 1×1M   |
| G4883A*     | SurePrint G3 Custom CGH+SNP Microarray, 2×400K |
| G4884A*     | SurePrint G3 Custom CGH+SNP Microarray, 4×180K |
| G4885A*     | SurePrint G3 Custom CGH+SNP Microarray, 8×60K  |
| G4123A      | SurePrint G3 Custom CGH Microarray, 1×1M       |
| G4124A      | SurePrint G3 Custom CGH Microarray, 2×400K     |
| G4125A      | SurePrint G3 Custom CGH Microarray, 4×180K     |
| G4126A      | SurePrint G3 Custom CGH Microarray, 8×60K      |

\* These arrays can only be processed using the enzymatic labeling protocol.

## 1 Before You Begin

### Agilent Oligo CGH Microarray Kit Contents

**Table 10** Custom SurePrint HD CGH Microarrays

| Part Number | Description                      |
|-------------|----------------------------------|
| G4423A      | Custom HD-CGH Microarray, 1×244K |
| G4425A      | Custom HD-CGH Microarray, 2×105K |
| G4426A      | Custom HD-CGH Microarray, 4×44K  |
| G4427A      | Custom HD-CGH Microarray, 8×15K  |

## Required Equipment

**Table 11** Required equipment

| Description  | Vendor and part number  |
|--|---|
| For Enzymatic Labeling:<br>Bravo Automated Liquid Handling Platform with 96 Channel Disposable LT Pipetting Head, Riser and 2 CPAC Ultraflat heated/cooled Deck Pads   | Agilent p/n G5409A Option 002   |
| For ULS labeling:<br>Bravo Automated Liquid Handling Platform with 96 Channel Disposable LT Pipetting Head   | Agilent p/n G5409A Option 003   |
| Robotic Pipetting Tips (250 µL)  | Agilent p/n 19477-002   |
| Agilent Microarray Scanner Bundle<br>for 1×244K, 2×105K, 4×44K or 8×15K, <i>or</i><br>for 1×1M, 2×400K, 4×180K or 8×60K  | Agilent p/n G4900DA, G2565CA or G2565BA<br>Agilent p/n G4900DA or G2565CA   |
| Hybridization Chamber, stainless   | Agilent p/n G2534A  |
| Hybridization gasket slides, 5-pack<br>(20 and 100 packaging sizes are available)*<br>for 1-pack microarrays <i>or</i><br>for 2-pack microarrays <i>or</i><br>for 4-pack microarrays <i>or</i><br>for 8-pack microarrays | Agilent p/n G2534-60003<br>Agilent p/n G2534-60002<br>Agilent p/n G2534-60011<br>Agilent p/n G2534-60014                    |
| Hybridization oven; temperature set at 65°C for ULS and 67°C for Enzymatic Labeling  | Agilent p/n G2545A  |
| Hybridization oven rotator for Agilent Microarray Hybridization Chambers   | Agilent p/n G2530-60029   |
| Ozone-barrier slide covers (box of 20) <sup>†</sup>  | Agilent p/n G2505-60550   |
| PlateLoc Thermal Microplate Sealer <i>and</i><br>Peelable Aluminum Seal<br><br><i>or</i><br>Heat Sealer<br>Peel-it-lite Foil (removable)   | Agilent p/n G5402A <i>and</i><br>Agilent p/n 24210-001<br><br>Eppendorf p/n 951023078 <i>and</i><br>Eppendorf p/n 951023205 |
| UV-Transilluminator with SYBR photographic filter  | Alpha Innotech p/n Alphamager 2000 or equivalent  |

## 1 Before You Begin

### Required Equipment

**Table 11** Required equipment (continued)

| Description  | Vendor and part number                                      |
|--|---|
| 1.5 mL RNase-free Microfuge Tube<br>(sustainable at 98°C)                                  | Ambion p/n AM12400 or equivalent                            |
| Magnetic stir plate (×1 or ×3) <sup>††</sup>   | Corning p/n 6795-410 or equivalent                          |
| Magnetic stir plate with heating element   | Corning p/n 6795-420 or equivalent                          |
| Thermal cycler with heated lid   | Eppendorf p/n 950000015 or equivalent                       |
| Full skirted 96-well PCR plate<br>(compatible with Bravo platform and thermal<br>cycler)   | Eppendorf p/n 951020401 or equivalent                       |
| Microcentrifuge  | Eppendorf p/n 5430 or equivalent                            |
| Centrifuge (for 96-well plate)   | Eppendorf p/n 5810 or equivalent                            |
| 384-Well Deep Well Microplates   | Greiner Bio-One p/n 781270                                  |
| E-Gel Opener <sup>†</sup>  | Life Technologies p/n G5300-01                              |
| E-Gel PowerBase v.4 <sup>†</sup>   | Life Technologies p/n G6200-04                              |
| Qubit Fluorometer <sup>**</sup>  | Life Technologies p/n Q32857                                |
| Thin wall, clear 0.5 mL PCR tubes <sup>**</sup>  | Life Technologies p/n Q32856 <i>or</i><br>VWR p/n 10011-830 |
| Sterile storage bottle   | Nalgene 455-1000 or equivalent                              |
| UV-VIS spectrophotometer   | NanoDrop 8000 or 2000, or equivalent                        |
| P10, P20, P200 and P1000 pipettes  | Pipetman P10, P20, P200, P1000 or<br>equivalent             |
| 1.5 L glass dish   | Pyrex p/n 213-R or equivalent                               |
| Deep reservoir, 12 column partitions, V bottom,<br>natural polypropylene                   | V&P Scientific p/n VP 572DC                                 |
| Magnetic stir bar, 7.9 × 38.1 mm (×2 or ×4) <sup>††</sup>                                  | VWR p/n 58948-150 or equivalent                             |
| 250 mL capacity slide-staining dish, with slide rack<br>(×3 or ×5) <sup>††</sup>           | Wheaton p/n 900200 <i>or</i><br>Thermo Shandon p/n 121      |
| Circulating water baths or heat blocks set to 37°C,<br>56°C, and 90°C (for DNA extraction) |   |
| Ice bucket   |   |

**Table 11** Required equipment (continued)

| Description   | Vendor and part number |
|---|------------------------|
| Clean forceps   |                        |
| Powder-free gloves  |                        |
| Sterile, nuclease-free aerosol barrier pipette tips             |                        |
| Timer   |                        |
| Vacuum desiccator or N <sub>2</sub> purge box for slide storage |                        |
| Vortex mixer  |                        |

\* Included in the [SurePrint G3 CGH Bundle](#).

† Optional. Recommended when processing arrays with a G2565CA or G2565BA scanner in environments in which ozone levels are 5 ppb or higher.

‡ For use with Life Technologies E-gels.

\*\* Optional.

†† The number varies depending on if wash procedure A or B is selected.

**Table 12** Required equipment for hybridization preparation for 1-pack microarrays.

| Description   | Vendor and part number                                 |
|---|--|
| Deep-well plate   | ABgene p/n AB-0859                                     |
| Eppendorf ThermoStat <i>or</i><br>BioShake iQ Thermomixer | Eppendorf p/n 022670204<br>Q.Instruments p/n 1808-0506 |
| Eppendorf Deep-Well Plate Block                           | Eppendorf p/n 022670565                                |
| Adapter for Deep-Well Plates                              | Q.Instruments p/n 1808-1141                            |

**Table 13** Required equipment for hybridization preparation for 2-pack microarrays.

| Description            | Vendor and part number |
|------------------------|------------------------|
| Tall Chimney PCR plate | ABgene p/n AB-1184     |

## 1 Before You Begin

### Required Equipment

**Table 14** Required equipment for 4-pack and 8-pack microarrays.

| Description         | Vendor and part number   |
|---------------------|--|
| Vacuum Concentrator | Thermo Scientific Savant SpeedVac p/n DNA120-115 or equivalent |

**Table 15** Optional equipment for DNA extraction from tissue or FFPE samples.

| Description    | Vendor and part number                            |
|----------------|---|
| Thermal shaker | Eppendorf Thermomixer p/n 022670000 or equivalent |

## Required Reagents

**Table 16** Required reagents for gDNA isolation

| Description  | Vendor and part number          |
|--|---------------------------------|
| Phosphate Buffered Saline pH 7.4 (PBS)   | Amresco p/n E504-500ML          |
| Clear E-Gel (1.2% agarose, no stain), 18-pack  | Life Technologies p/n G5518-01  |
| SYBR Gold Nucleic Acid Gel Stain   | Life Technologies p/n S11494    |
| SYBR photographic filter   | Life Technologies p/n S7569     |
| TrackIt 1 Kb DNA Ladder  | Life Technologies p/n 10488-072 |
| DNase/RNase-free distilled water   | Life Technologies p/n 10977-015 |
| Qubit dsDNA BR Assay Kit, for use with the Qubit fluorometer (100 assays) <sup>†</sup> | Life Technologies p/n Q32850    |
| RNase A (100 mg/mL)  | Qiagen p/n 19101                |
| DNeasy Blood & Tissue Kit  | Qiagen p/n 69504                |
| Proteinase K (>600 mAU/mL, solution)   | Qiagen p/n 19131                |
| Sodium thiocyanate (NaSCN) <sup>†</sup>  | Sigma-Aldrich 467871-50G        |
| Ethanol (95% to 100% molecular biology grade)  | Sigma-Aldrich p/n E7023-6×500ML |
| Tween 20 <sup>†</sup>  | Sigma-Aldrich p/n P9416-50ML    |

\* Optional.

† Optional components if isolating DNA from FFPE samples.

## 1 Before You Begin

### Required Reagents

**Table 17** Required reagents for enzymatic sample prep and labeling with the SureTag Complete DNA Labeling Kit (for Human Samples)

| Description                                    | Vendor and part number       |
|--|------------------------------|
| SureTag Complete DNA Labeling Kit <sup>†</sup> | Agilent p/n 5190-4240        |
| AutoScreen A, 96-well plates                   | GE Healthcare p/n 25-9005-98 |
| 1×TE (pH 8.0), Molecular grade                 | Promega p/n V6231            |

\* Kit content is listed in “Reagent Kit Components” on page 134.

† Included in the SurePrint G3 CGH Bundle.

**Table 18** Required reagents for enzymatic sample prep and labeling with the SureTag DNA Labeling Kit (or when Human reference DNA is provided separately)

| Description   | Vendor and part number  |
|---|---|
| SureTag DNA Labeling Kit <sup>*</sup>   | Agilent p/n 5190-3400   |
| AutoScreen A, 96-well plate   | GE Healthcare p/n 25-9005-98  |
| For possible use as a reference sample:   |   |
| <ul style="list-style-type: none"> <li>• Human Genomic DNA <i>or</i></li> <li>• Mouse Genomic DNA <i>or</i></li> <li>• Rat Genomic DNA</li> </ul> | <ul style="list-style-type: none"> <li>• For CGH microarrays: Promega p/n G1521 (female) or p/n G1471 (male)</li> <li>• For CGH+SNP microarrays: Coriell p/n NA18507, NA18517, NA12891, NA12878, or NA18579</li> <li>• Jackson Labs p/n 000664 (female and male)</li> <li>• Harlan Sprague Dawley (custom)</li> </ul> |
| 1×TE (pH 8.0), Molecular grade  | Promega p/n V6231   |

\* Kit content is listed in “Reagent Kit Components” on page 134.



**Table 19** Required reagents for ULS sample prep and labeling\*

| Description   | Vendor and part number  |
|---|---|
| Genomic DNA High-Throughput ULS Labeling Kit  | Agilent p/n 5190-0450   |
| Genomic DNA 96-well Purification Module   | Agilent p/n 5190-0451   |
| Oligo aCGH Labeling Kit   | Agilent p/n 5190-0420   |
| DNase/RNase-free distilled water  | Life Technologies p/n 10977-015   |
| For possible use as a reference sample:   |   |
| <ul style="list-style-type: none"> <li>• Human Genomic DNA <i>or</i></li> <li>• Mouse Genomic DNA <i>or</i></li> <li>• Rat Genomic DNA</li> </ul> | <ul style="list-style-type: none"> <li>• Promega p/n G1521 (female) or p/n G1471 (male)</li> <li>• Jackson Labs p/n 000664 (female and male)</li> <li>• Harlan Sprague Dawley (custom)</li> </ul> |

\* ULS is not supported for CGH+SNP.

**Table 20** Required reagents for hybridization and wash

| Description  | Vendor and part number   |
|--|--|
| Oligo aCGH/ChIP-on-chip Wash Buffer Kit <i>or</i>  | Agilent p/n 5188-5226  |
| Oligo aCGH/ChIP-on-chip Wash Buffer 1 <i>and</i>   | Agilent p/n 5188-5221  |
| Oligo aCGH/ChIP-on-chip Wash Buffer 2  | Agilent p/n 5188-5222  |
| Stabilization and Drying Solution*   | Agilent p/n 5185-5979  |
| Oligo aCGH/ChIP-on-chip Hybridization Kit  | Agilent p/n 5188-5220 (25) or p/n 5188-5380 (100)  |
| Cot-1 DNA (1.0 mg/mL)  |  |
| <ul style="list-style-type: none"> <li>• Human Cot-1 DNA <i>or</i></li> <li>• Mouse Cot-1 DNA <i>or</i></li> <li>• Rat Hybloc</li> </ul> | <ul style="list-style-type: none"> <li>Agilent p/n 5190-3393</li> <li>Life Technologies p/n 18440-016</li> <li>Applied Genetics p/n RHB</li> </ul> |
| DNase/RNase-free distilled water   | Life Technologies p/n 10977-015  |
| Milli-Q ultrapure water  | Millipore  |
| Acetonitrile*  | Sigma-Aldrich p/n 271004-1L  |

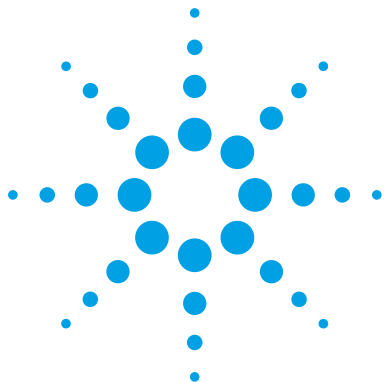
\* Optional components recommended if wash procedure B is selected.

## Required Bravo Platform Protocols

- The Agilent Oligo aCGH Bravo Platform protocols are on the CD that came with your Bravo platform or may be obtained by contacting your local Agilent product specialist.

## Required Hardware and Software

- Refer to the *Bravo Platform User Guide* and the *VWorks Automation Control User Guide* for minimum and recommended computer requirements. See <http://www.genomics.agilent.com>.
- Refer to the Agilent Scanner manual and Agilent CytoGenomics or Feature Extraction manuals for minimum memory requirements and other specifications. Go to <http://www.genomics.agilent.com>.



## 2 DNA Isolation

|  |    |
|--|----|
| Blood, Cells or Frozen Tissues                 | 30 |
| Step 1. gDNA Extraction                        | 31 |
| Step 2. gDNA Quantitation and Quality Analysis | 34 |
| FFPE Tissues                                   | 38 |
| Step 1. Paraffin Removal                       | 39 |
| Step 2. Proteinase K Treatment                 | 40 |
| Step 3. gDNA Extraction                        | 41 |

### NOTE

Agilent cannot guarantee microarray performance and does not provide technical support to those who use non-Agilent protocols in processing Agilent microarrays.

The Agilent array-based Comparative Genomic Hybridization (aCGH) application uses a “two-color” process to measure DNA copy number changes (CNC), and copy-neutral Loss of Heterozygosity or Uniparental Disomy if CGH+SNP microarrays are used, in an experimental sample relative to a reference sample. The type of sample used as a reference is a matter of experimental choice; however, many experimenters use normal commercial gDNA as a reference sample, such as the [Human Reference DNA \(Male and Female\)](#) that is included in the [SureTag Complete DNA Labeling Kit](#).

This chapter describes the Agilent recommended procedure for isolating gDNA from blood, cells, frozen or FFPE tissues using the [DNeasy Blood & Tissue Kit](#). Minor differences exist in the DNA extraction procedure between the ULS and Enzymatic processing method that you will choose in Chapter 4.

FFPE samples are not supported when you process SurePrint G3 CGH+SNP microarrays.



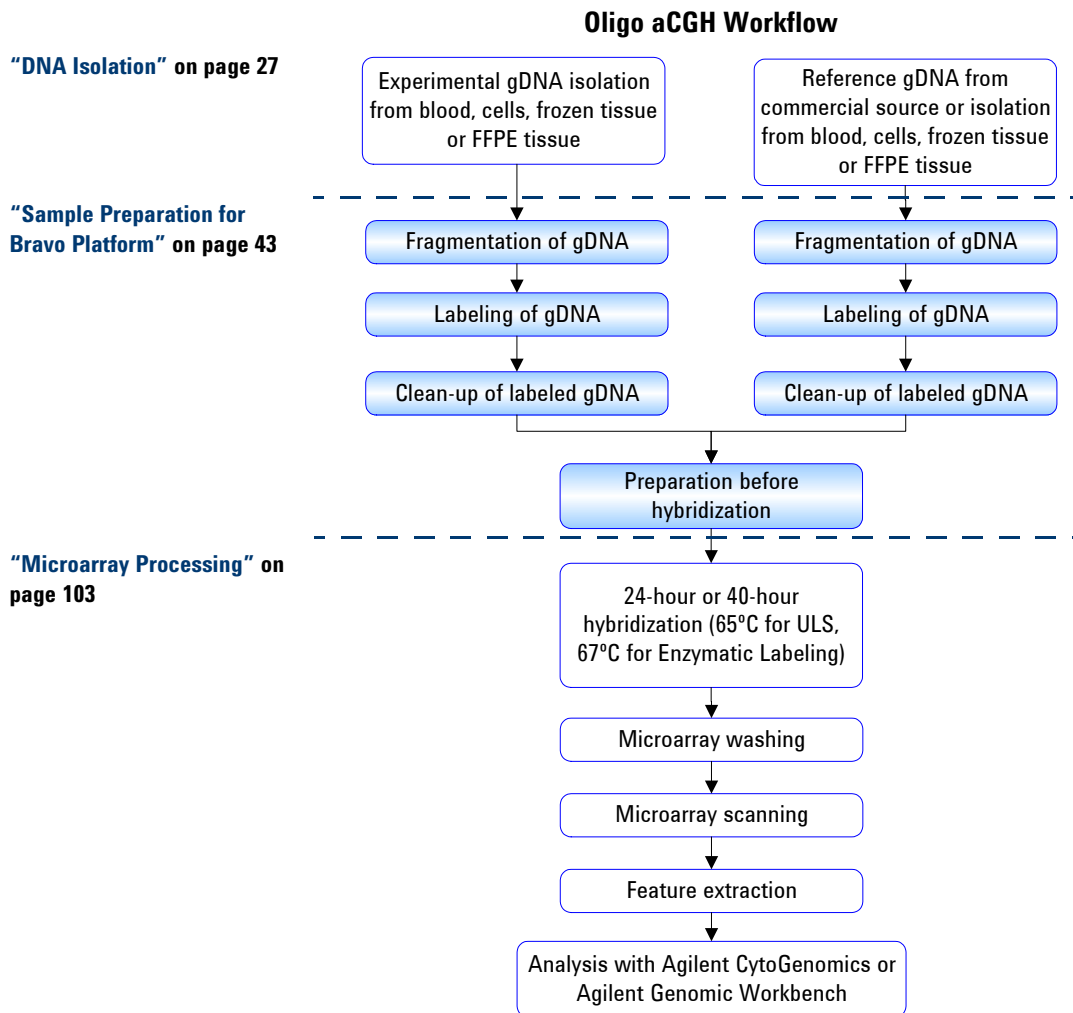
For DNA isolated from FFPE tissues, ULS processing is the only option. Follow the instructions in “[FFPE Tissues](#)” on page 38.

### **CGH+SNP Microarrays**

When you process SurePrint G3 CGH+SNP microarrays, the reference needs to be DNA isolated from a single genotyped individual. You can use one of the following DNA samples as reference:

- 1** Human Reference DNA Male or Female, components of the [SureTag Complete DNA Labeling Kit](#).
- 2** One of five supported HapMap samples: NA18507 (Yoruban Male), NA18517 (Yoruban Female), NA12891 (European Male), NA12878 (European Female), or NA18579 (Chinese Female). The HapMap samples can be ordered from the Coriell Institute for Medical Research.
- 3** You can genotype your own reference DNA isolated from a single individual by hybridizing it against all 5 supported HapMap samples on the Agilent CGH+SNP microarrays. This experiment only needs to be done once.

The input amount of DNA for the experimental sample labeling reaction must be the same as for the reference sample labeling reaction. Inaccurate DNA quantitation can lead to different DNA inputs into the experimental and reference labeling reactions, which increases assay noise (DLRSD). Different DNA isolation methods can also create quantitation artifacts. To minimize assay noise, Agilent recommends to use a fluorometric method (such as Qubit) highly selective for double-stranded DNA. A Nanodrop spectrophotometer can be used to assess gDNA purity. There is no need to re-determine the concentration of the Agilent Human Reference DNA Male and Female, its concentration is 200 ng/ $\mu$ L as measured by both spectrophotometer and fluorometer.



**Figure 1** Workflow diagram for sample preparation and microarray processing. Steps that are in blue use the Bravo Automated Liquid Handling Platform.

## Blood, Cells or Frozen Tissues

This section describes the recommended procedure to isolate gDNA from blood, cells or frozen tissues using the *DNeasy Blood & Tissue Kit*.

**Table 21** Required gDNA amount from blood, cells or frozen tissues

| Microarray format | ULS gDNA input amount requirement (ng) <sup>*</sup> | Enzymatic gDNA input amount requirement (ng) for CGH <sup>*</sup> | Enzymatic gDNA input amount requirement (ng) for CGH+SNP <sup>*</sup> |
|-------------------|---|---|---|
| 1-pack            | 1500  | 500   | 1000  |
| 2-pack            | 1000  | 500   | 1000  |
| 4-pack            | 500   | 500   | 1000  |
| 8-pack            | 250   | 200   | 500   |

\* You can use more gDNA, but the gDNA needs to be at a higher concentration. See [Table 24](#), [Table 25](#) and [Table 26](#) on page 46 for required concentrations.

## Step 1. gDNA Extraction

Use reagents from the DNeasy Blood & Tissue Kit.

- 1 Equilibrate a thermomixer and heat block or water bath to 56°C.
- 2 For blood with nonnucleated erythrocytes (mammals):
  - a Put 20 µL of Proteinase K into the bottom of a 1.5 mL RNase-free Microfuge Tube.
  - b Add 50 to 100 µL of anticoagulated blood.
  - c Add enough Phosphate Buffered Saline pH 7.4 (PBS) to make a total volume of 220 µL.
  - d Go to step 7.
- 3 For blood with nucleated erythrocytes (such as chicken):
  - a Put 20 µL of Proteinase K into the bottom of a 1.5 mL RNase-free Microfuge Tube.
  - b Add 5 to 10 µL of anticoagulant blood.
  - c Add enough Phosphate Buffered Saline pH 7.4 (PBS) to make a total volume of 220 µL.
  - d Go to step 7.
- 4 For cells:
  - a Spin a maximum of  $5 \times 10^6$  cells in a centrifuge for 5 minutes at  $300 \times g$ . Resuspend the pellet in 200 µL of Phosphate Buffered Saline pH 7.4 (PBS).
  - b Add 20 µL of Proteinase K.
  - c Go to step 7.
- 5 For frozen tissue:
  - a Cut up to 25 mg frozen tissue (up to 10 mg for spleen tissue) into small pieces and put into a 1.5 mL RNase-free Microfuge Tube.
  - b Add 180 µL of Buffer ATL.
  - c Add 20 µL of Proteinase K.
  - d Mix well on a vortex mixer.
  - e Incubate in a thermomixer at 56°C shaking at 450 rpm until the tissue is completely lysed.

## 2 DNA Isolation

### Step 1. gDNA Extraction

Lysis time varies depending on the type of tissue processed. Usually lysis is complete in 1 to 3 hours. If it is more convenient, samples can be lysed overnight.

- f** Let the sample cool to room temperature and spin in a microcentrifuge for 30 seconds at  $6,000 \times g$  to drive the contents off the walls and lid.
- g** Go to step 7.
- 6** For further purification of extracted DNA:
  - a** Take a maximum 25  $\mu\text{g}$  of DNA.
  - b** Add enough Phosphate Buffered Saline pH 7.4 (PBS) to make a total volume of 220  $\mu\text{L}$ .
  - c** Add 20  $\mu\text{L}$  of Proteinase K.
- 7** Add 4  $\mu\text{L}$  of RNase A (100 mg/mL), mix on a vortex mixer, and incubate for 2 minutes at room temperature. Spin in a microcentrifuge for 30 seconds at  $6,000 \times g$  to drive the contents off the walls and lid.
- 8** Add 200  $\mu\text{L}$  of Buffer AL to each sample, mix thoroughly on a vortex mixer, and incubate at  $56^\circ\text{C}$  for 10 minutes in a heat block or water bath. Spin in a microcentrifuge for 30 seconds at  $6,000 \times g$  to drive the contents off the walls and lid.
- 9** Add 200  $\mu\text{L}$  of 100% Ethanol to each sample, and mix thoroughly on a vortex mixer. Spin in a microcentrifuge for 30 seconds at  $6,000 \times g$  to drive the contents off the walls and lid.
- 10** Transfer the sample mixture onto a DNeasy Mini Spin Column in a 2 mL Collection Tube. Spin in a centrifuge at  $6,000 \times g$  for 1 minute. Discard the flow-through and collection tube. Put the DNeasy Mini Spin Column in a new 2 mL Collection Tube.
- 11** Before using for the first time, prepare Buffer AW1 by adding 100% Ethanol to the Buffer AW1 bottle (see bottle label for volume). Mark the appropriate check box to indicate that ethanol was added to the bottle.
- 12** Add 500  $\mu\text{L}$  Buffer AW1 onto the column, and spin in a microcentrifuge for 1 minute at  $6,000 \times g$ . Discard the flow-through and collection tube. Put the DNeasy Mini Spin Column in a new 2 mL Collection Tube.
- 13** For Enzymatic labeling: Before using for the first time, prepare Buffer AW2 by adding 100% Ethanol to the Buffer AW2 bottle (see bottle label for volume). Mark the appropriate check box to indicate that ethanol was added to the bottle.



**14** For ULS labeling: Prepare a fresh 80% Ethanol solution by adding 40 mL 100% Ethanol to 10 mL of DNase/RNase-free distilled water.

**CAUTION**

For ULS labeling: Do *not* use Buffer AW2 supplied with the DNeasy Blood & Tissue Kit for the subsequent step because salt from Buffer AW2 will interfere with the subsequent labeling reaction. This is especially important if you need to do a concentration step before labeling.

---

**15** Add the amount below onto the column, and spin in a centrifuge for 3 minutes at  $20,000 \times g$  to dry the DNeasy membrane. Discard the flow-through and collection tube.

- For ULS labeling: 500  $\mu$ L 80% Ethanol
- For Enzymatic labeling: 500  $\mu$ L Buffer AW2

**16** Put the DNeasy Mini Spin Column in a clean 1.5 mL RNase-free Microfuge Tube, and pipette the amount below directly onto the center of the DNeasy column membrane.

- For ULS labeling: 200  $\mu$ L of DNase/RNase-free distilled water
- For Enzymatic labeling: 200  $\mu$ L of Buffer AE

**17** Incubate at room temperature for 1 minute, and then spin in a microcentrifuge for 1 minute at  $6,000 \times g$  to elute the DNA.

**18** Repeat elution with DNase/RNase-free distilled water (for ULS labeling) or Buffer AE (for Enzymatic labeling) once as described in step 16 and step 17. Combine the duplicate samples in one microcentrifuge tube for a final volume of 400  $\mu$ L.

**NOTE**

For ULS labeling: If long term storage is needed, store DNA that was eluted in water at  $-20^{\circ}\text{C}$ . Make small aliquots before you freeze the DNA so as to avoid repeated freeze-thaw cycles.

---

## Step 2. gDNA Quantitation and Quality Analysis

Accurate assessment of gDNA quantity and quality are crucial to the success of an Agilent Oligo aCGH experiment. High quality gDNA should be free of contaminants such as carbohydrates, proteins, and traces of organic solvents, and should also be intact with minimal degradation. gDNA isolated from FFPE samples typically exhibits varying degrees of degradation depending on the age of the tissue and the paraffin embedding protocol used. See “[FFPE Tissues](#)” on page 38 for details on how to isolate gDNA from FFPE tissues.

FFPE samples are not supported when you process SurePrint G3 CGH+SNP microarrays.

Use Quant-iT dsDNA Broad-Range Assay Kit to measure the concentration of double-strand DNA by fluorometry. Use the NanoDrop 2000 UV-VIS Spectrophotometer (or equivalent) to assess gDNA concentration and purity. Use agarose gel electrophoresis to assess gDNA intactness and the average molecular weight for each sample.

### NOTE

Agilent recommends the use of a fluorometric quantitation method for the highest quality data.

### Fluorometry

Use the [Qubit dsDNA BR Assay Kit](#) at room temperature (22°C to 28°C). Temperature fluctuations can affect the accuracy of the assay.

- 1 Set up [Thin wall, clear 0.5 mL PCR tubes](#) for the two standards plus the number of samples you are processing.
- 2 Make a [Qubit working solution](#).

For each standard and sample to be quantified, mix the components in [Table 22](#) together on a vortex mixer for 2 to 3 seconds.

**Table 22** Qubit working solution

| Component              | Amount |
|------------------------|--------|
| Qubit dsDNA BR reagent | 1 µL   |
| Qubit dsDNA BR buffer  | 199 µL |

- 3 Load 190  $\mu\text{L}$  of Qubit working solution into the two Thin wall, clear 0.5 mL PCR tubes labeled for the standards.
- 4 Load 180 to 199  $\mu\text{L}$  of Qubit working solution into the tubes labeled for your samples.
- 5 Add 10  $\mu\text{L}$  of Qubit dsDNA BR standard #1 or Qubit dsDNA BR standard #2 to the appropriate tube.
- 6 Add 1 to 20  $\mu\text{L}$  of your DNA sample to the appropriate tubes.
- 7 Mix the content of all the tubes on a vortex mixer for 2 to 3 seconds. Be careful not to create bubbles.
- 8 Incubate the tubes at room temperature for 2 minutes.
  - To calibrate the Qubit:
    - a On the home screen of the Qubit 1.0, use the up or down arrow to select **dsDNA Broad Range Assay** as assay type, and then press **GO**. The standard screen is automatically displayed.
    - b Select **Run new calibration**, and then press **GO**.
    - c Insert the tube with the first standard into the Qubit Fluorometer, close the lid and press **GO**. After the reading is done, remove the standard.
    - d Insert the tube with the second standard into the Qubit Fluorometer, close the lid, and press **GO**. After the reading is done remove the standard.

The calibration is complete after the second standard has been read.
  - To measure sample concentration:
    - a After the calibration is complete, insert a sample and press **GO**.
    - b When the measurement is complete (approximately 5 seconds later), make a note of the reading.
    - c The result is displayed on the screen. The number displayed is the concentration of the nucleic acid in the assay tube.
    - d Remove the sample from the instrument, insert the next sample, and press **GO**.
    - e Repeat sample readings until all samples have been read.
    - f Calculate the concentration of your original sample.

## 2 DNA Isolation

### Step 2. gDNA Quantitation and Quality Analysis

The Qubit Fluorometer gives a value for the Qubit dsDNA BR assay in  $\mu\text{g/mL}$ . This value corresponds to the concentration after your samples were diluted into the assay tube. To calculate the concentration of your sample, use this equation:

$$\text{Sample concentration} = QF \text{ value} \times (200/y)$$

where

*QF value* = the value given by the Qubit Fluorometer

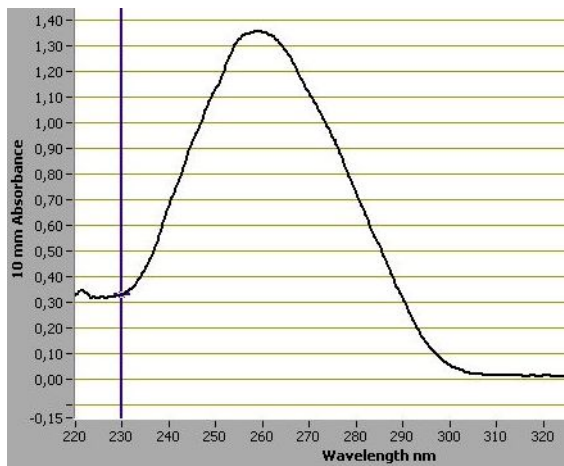
*y* = the volume of sample you added to the assay tube.

### UV-VIS Spectrophotometry

- 1 In the Nanodrop program menu, select **Nucleic Acid Measurement**, and then select **Sample Type** to be **DNA-50**.
- 2 Use 1.5  $\mu\text{L}$  of **DNase/RNase-free distilled water** (for ULS labeling) or **Buffer AE** (for Enzymatic labeling) to blank the instrument.
- 3 Use 1.5  $\mu\text{L}$  of each gDNA sample to measure DNA concentration. Record the gDNA concentration ( $\text{ng}/\mu\text{L}$ ) for each sample. Calculate the yield as

$$\text{Yield } (\mu\text{g}) = \frac{\text{DNA Concentration } (\text{ng}/\mu\text{L}) \times \text{Sample Volume } (\mu\text{L})}{1000 \text{ ng}/\mu\text{g}}$$

- 4 Record the  $A_{260}/A_{280}$  and  $A_{260}/A_{230}$  ratios. High-quality gDNA samples have an  $A_{260}/A_{280}$  ratio of 1.8 to 2.0, which indicates the absence of contaminating proteins. Scanning the absorbance from 220-320 nm will show whether contaminants exist that affect absorbance at 260 nm. Check the absorbance scans for a peak at 260 nm and an overall smooth shape as shown in **Figure 2**. The ideal 260/230 ratio for pure DNA is  $>1.0$ .



**Figure 2** Typical spectrum of pure DNA

### Agarose Gel Electrophoresis

- 1** Load 20 ng of gDNA for each sample in 10  $\mu$ L of DNase/RNase-free distilled water in the well of a single-comb Clear E-Gel (1.2% agarose, no stain). (You do not need to add loading buffer in this system).
- 2** As a control, load 20 ng of Human Reference DNA (Male and Female) or commercial Human Genomic DNA in 10  $\mu$ L of DNase/RNase-free distilled water in one of the wells of the E-Gel.
- 3** Mix 5  $\mu$ L of TrackIt 1 Kb DNA Ladder with 95  $\mu$ L of deionized water and load 10  $\mu$ L of the diluted ladder in one of the wells of the E-Gel.
- 4** Run the gel for 30 minutes as described in Invitrogen's instructions.
- 5** Open the gel cassette with E-Gel Opener as described in Invitrogen's instructions.
- 6** Stain the gel with SYBR Gold Nucleic Acid Gel Stain (diluted 1:10,000 by adding 10  $\mu$ L of SYBR Gold Nucleic Acid Gel Stain to 100 mL of DNase/RNase-free distilled water) in a plastic tray for 15 minutes.
- 7** Visualize the gel on the UV-transilluminator using a SYBR photographic filter.

## FFPE Tissues

This section describes the recommended procedure to isolate gDNA from formalin-fixed paraffin-embedded (FFPE) samples and is based on the method described by van Beers et al. (Br J Cancer. 2006 Jan 30; 94(2):333-7) using the DNeasy Blood & Tissue Kit. Determine the number of FFPE sections needed for your experiment based on the estimates summarized in Table 23. One 20 micron FFPE section containing 1 cm<sup>2</sup> of tissue is estimated to generate a minimal yield of 500 ng of gDNA.

For more information about CGH experiments on FFPE samples, please refer to the application note “Copy Number Analysis of Archival FFPE Tumor Samples by Oligo Array CGH” (p/n 5989-7120EN) available from the Agilent Web site at [www.agilent.com/chem/dnaapplications](http://www.agilent.com/chem/dnaapplications). Note that the CGH+SNP platform does not support FFPE samples.

**Table 23** Estimated number of 20 micron FFPE sections needed per microarray

| Microarray format | gDNA input amount requirement (ng) | Estimated number of 20 micron FFPE sections |
|-------------------|------------------------------------|---|
| 1-pack            | 2000                               | 4 to 5                                      |
| 2-pack            | 1000                               | 3   |
| 4-pack            | 500                                | 2   |
| 8-pack            | 250                                | 1   |

## Step 1. Paraffin Removal

- 1 Equilibrate a heat block or water bath to 90°C and a thermomixer to 37°C.
- 2 Put up to 5 20-micron FFPE sections into a 1.5 mL RNase-free Microfuge Tube.
- 3 Prepare 10% Tween 20, by adding 100 µL Tween 20 to 900 µL of DNase/RNase-free distilled water. The solution can be prepared in advance and stored up to 6 months at room temperature.
- 4 Add 480 µL Phosphate Buffered Saline pH 7.4 (PBS) and 20 µL 10% Tween 20 to the FFPE sections in the 1.5 mL RNase-free Microfuge Tube.
- 5 Transfer the sample tube to a circulating water bath or heat block at 90°C. Incubate at 90°C for 10 minutes.
- 6 Spin immediately for 15 minutes at 10,000 × g in a microcentrifuge.
- 7 Put the sample tube on ice for 2 minutes.
- 8 Remove the resulting wax disc with a pipette tip or tweezers. Remove and discard the supernatant without disturbing the pellet.
- 9 Add 1 mL of 100% Ethanol to the pellet and vortex briefly.
- 10 Spin for 5 minutes at 10,000 × g in a microcentrifuge.
- 11 Remove Ethanol without disturbing the pellet and let the sample tube sit at room temperature with the lid open until residual ethanol has completely evaporated.
- 12 Prepare a 1M NaSCN solution by adding 10 g of Sodium thiocyanate (NaSCN) to 123 mL of DNase/RNase-free distilled water. The solution can be prepared in advance and stored up to 1 month at room temperature.
- 13 Add 400 µL 1M Sodium thiocyanate (NaSCN) to the dry pellet and briefly mix on a vortex mixer.
- 14 Transfer the sample tube to a thermomixer at 37°C. Incubate overnight at 37°C while shaking at 450 rpm.

## Step 2. Proteinase K Treatment

Use reagents from the DNeasy Blood & Tissue Kit.

- 1** Equilibrate a thermomixer to 56°C.
- 2** Transfer the sample tube to a microcentrifuge. Spin for 20 minutes at 10,000 × g.
- 3** Remove and discard the supernatant without disturbing the pellet.
- 4** Add 400 µL Phosphate Buffered Saline pH 7.4 (PBS) to the pellet and vortex briefly.
- 5** Spin again for 20 minutes at 10,000 × g in a microcentrifuge.
- 6** Remove and discard the supernatant without disturbing the pellet.
- 7** Add 360 µL of Buffer ATL.
- 8** Add 40 µL Proteinase K, mix well on a vortex mixer, and incubate overnight in a thermomixer at 56°C shaking at 450 rpm.
- 9** Transfer the sample tube to a microcentrifuge. Spin for 30 seconds at 6,000 × g to drive the contents off the walls and lid.
- 10** Add 40 µL Proteinase K, mix well on a vortex mixer, and incubate in a thermomixer for approximately 6 to 8 hours at 56°C shaking at 450 rpm.
- 11** At the end of the day, transfer the sample tube to a microcentrifuge and spin for 30 seconds at 6,000 × g to drive the contents off the walls and lid.
- 12** Add 40 µL Proteinase K, mix well on a vortex mixer and incubate overnight in a thermomixer at 56°C shaking at 450 rpm.



### Step 3. gDNA Extraction

- 1 Equilibrate a heat block or water bath to 56°C.
- 2 Let samples cool to room temperature and spin in a microcentrifuge for 30 seconds at 6,000 × g to drive the contents off the walls and lid.
- 3 Add 8 µL of RNase A (100 mg/mL), mix on a vortex mixer, and incubate for 2 minutes at room temperature. Transfer the sample tube to a microcentrifuge and spin for 30 seconds at 6,000 × g to drive the contents off the walls and lid.
- 4 Add 400 µL Buffer AL, mix thoroughly on a vortex mixer, and incubate in a circulating water bath or heat block at 56°C for 10 minutes. Transfer the sample tube to a microcentrifuge and spin for 30 seconds at 6,000 × g to drive the contents off the walls and lid.
- 5 Add 440 µL 100% Ethanol, and mix thoroughly on a vortex mixer. Transfer the sample tube to a microcentrifuge and spin for 30 seconds at 6,000 × g to drive the contents off the walls and lid.
- 6 Put two DNeasy Mini Spin Column in two clean 2 mL Collection Tube. Split the entire sample mixture onto two DNeasy Mini Spin Column (i.e. 660 µL each).

**NOTE**

Use two DNeasy Mini Spin Column per sample to prevent clogging.

- 7 Spin in a microcentrifuge for 1 minute at 6,000 × g. Discard the flow-through and collection tube. Put the DNeasy Mini Spin Column in fresh 2 mL Collection Tube.
- 8 Before using for the first time, prepare Buffer AW1 by adding 100% Ethanol to the Buffer AW1 bottle (supplied; see bottle label for volume). Mark the appropriate check box to indicate that ethanol was added to the bottle.
- 9 Add 500 µL Buffer AW1 onto each spin column, and spin in a centrifuge for 1 minute at 6,000 × g. Discard the flow-through and collection tube. Put the DNeasy Mini Spin Column in fresh 2 mL Collection Tube.

## 2 DNA Isolation

### Step 3. gDNA Extraction

**10** Prepare a fresh 80% ethanol solution by adding 40 mL 100% Ethanol to 10 mL of DNase/RNase-free distilled water.

#### CAUTION

Do not use Buffer AW2 supplied with the DNeasy Blood & Tissue Kit for the subsequent step because salt from Buffer AW2 will interfere with the subsequent labeling reaction. This is especially important if you need to do a concentration step before labeling.

**11** Add 500  $\mu$ L of 80% Ethanol onto each column, and spin in a microcentrifuge for 3 minutes at  $20,000 \times g$  to dry the column membrane. Discard the flow-through and collection tube.

**12** Put the DNeasy Mini Spin Column in a clean 1.5 mL RNase-free Microfuge Tube, and add 50  $\mu$ L of DNase/RNase-free distilled water directly to the center of each spin column.

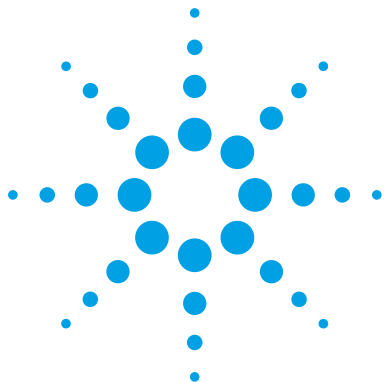
**13** Let stand at room temperature for 1 minute, and then spin in a microcentrifuge for 1 minute at  $6,000 \times g$  to elute the DNA.

**14** Combine the purified DNA from the same sample in one microcentrifuge tube for a final total volume of 100  $\mu$ L.

Measure gDNA concentration and purity, and analyze on an agarose gel as described in “Step 2. gDNA Quantitation and Quality Analysis” on page 34.

#### NOTE

If long term storage is needed, store DNA that was eluted in water at  $-20^{\circ}\text{C}$ . Make small aliquots before you freeze the DNA so as to avoid repeated freeze-thaw cycles.



### 3 Sample Preparation for Bravo Platform

Step 1. gDNA Dilution 45

Step 2. gDNA Placement in a 96-Well Plate 47

This chapter describes how to prepare the samples to be used on the Bravo Automated Liquid Handling Platform.

There is no need to re-determine the concentration of the [Human Reference DNA \(Male and Female\)](#), its concentration is 200 ng/ $\mu$ L as measured by both spectrophotometer and fluorometer.



#### CAUTION

Use equal amounts of gDNA for both the experimental and reference samples. The required gDNA input amount and concentration depends on the microarray format, labeling method and DNA source used (see [Table 21](#) and [Table 23](#)).

Follow the DNA isolation procedure described in [Chapter 2](#), “DNA Isolation”. Failure to clean samples thoroughly will result in unsatisfactory microarray results.

If the DNA isolation procedure described in this document cannot be followed, make sure that the DNA is free of RNA and protein contamination. For ULS labeling, also make sure the DNA is in one of the following buffers compatible with ULS labeling:

- TE-buffer (10 mM Tris-HCl, 1 mM EDTA, pH 7.5 or pH 8)
- 10 mM LiCl
- 10 to 100 mM Na acetate
- 10 mM NaCl

If needed, repurify already isolated DNA. Start from [step 6](#) on [page 32](#) in the previous chapter.

Make sure that the gDNA is completely in solution by pipetting up and down. If needed, incubate at 37°C for 30 minutes. If the gDNA concentration is > 350 ng/μL, dilute 1:2 in [DNase/RNase-free distilled water](#) (if proceeding with ULS labeling), [Buffer AE](#) or [1×TE \(pH 8.0\)](#) (if following the enzymatic labeling) and quantitate again to make sure dilution is accurate.

---

## Step 1. gDNA Dilution

- Dilute the gDNA with nuclease-free water to the concentration listed in Table 24 through Table 26.

Make sure that the volume is higher than the minimum volume requirement for the Bravo platform (μL).

If the gDNA concentration is less than those listed in Table 24 through Table 26, concentrate the sample using a concentrator (such as Speed Vac) to dryness and resuspend in DNase/RNase-free distilled water to the final concentration in those tables.

### CAUTION

Do not excessively dry the gDNA as the pellets will become difficult to resuspend.

**Table 24** gDNA concentration and input amount required per microarray for ULS labeling

| Microarray format         | Concentration requirement (ng/μL)* | Minimum volume requirement for Bravo platform (μL) | Volume that Bravo platform will use |
|---------------------------|------------------------------------|--|-------------------------------------|
| 1-pack (non-FFPE samples) | 100                                | 17   | 15                                  |
| 1-pack (FFPE samples)     | 133.5                              | 17   | 15                                  |
| 2-pack                    | 100                                | 12   | 10                                  |
| 4-pack                    | 100                                | 7  | 5                                   |
| 8-pack                    | 50                                 | 7  | 5                                   |

\* If you want to use more gDNA than what is listed in Table 21 on page 30, use gDNA that is at a higher concentration than is listed in this table.

### 3 Sample Preparation for Bravo Platform

#### Step 1. gDNA Dilution

**Table 25** For CGH: gDNA concentration and input amount required per microarray for Enzymatic labeling

| Microarray format  | Concentration requirement (ng/ $\mu$ L) <sup>*</sup> | Minimum volume requirement for Bravo platform ( $\mu$ L) | Volume that Bravo platform will use |
|--------------------|--|--|-------------------------------------|
| 1-, 2-, and 4-pack | 100  | 7  | 5                                   |
| 8-pack             | 50   | 6  | 4                                   |

\* If you want to use more gDNA than what is listed in [Table 21](#) on page 30, use gDNA that is at a higher concentration than is listed in this table.

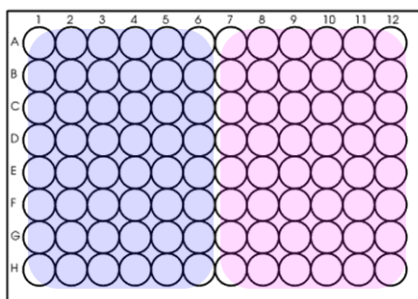
**Table 26** For CGH+SNP: gDNA concentration and input amount required per microarray for Enzymatic labeling

| Microarray format  | Concentration requirement (ng/ $\mu$ L) <sup>*</sup> | Minimum volume requirement for Bravo platform ( $\mu$ L) | Volume that Bravo platform will use |
|--------------------|--|--|-------------------------------------|
| 1-, 2-, and 4-pack | 50   | 22   | 20                                  |
| 8-pack             | 71.4   | 9  | 7                                   |

\* If you want to use more gDNA than what is listed in [Table 21](#) on page 30, use gDNA that is at a higher concentration than is listed in this table.

## Step 2. gDNA Placement in a 96-Well Plate

- 1 In a Full skirted 96-well PCR plate, put the experimental gDNA samples in columns 1 through 6 of the 96-well plate as indicated in Figure 3.
- 2 Put the reference gDNA in columns 7 through 12 as indicated in Figure 3.  
Make sure that the experimental and reference gDNA samples meet the minimum volume requirements indicated in Table 24 on page 45, or Table 25 or Table 26 on page 46.
- 3 Make sure that no air bubbles are stuck at the bottom of the well. If needed, spin the plate in a centrifuge for 30 seconds at  $6,000 \times g$  to drive the contents off the walls.



**Figure 3** 96-well plate layout of gDNA before labeling. Columns 1 through 6 contain 48 experimental gDNA samples (blue). Columns 7 through 12 contain 48 reference gDNA samples (pink).

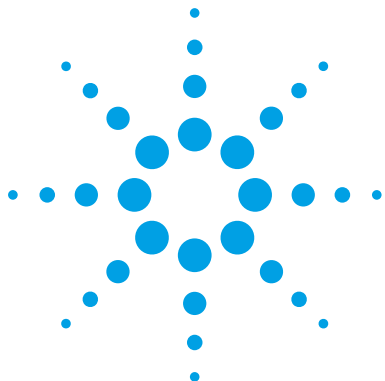
You can process between 1 and 48 experimental samples, but to minimize reagent waste, choose 8, 16, 24, 32, 40 or 48 samples. If you process fewer than 48 samples, add gDNA to the wells column-wise. Fill columns 1 and 7 before you continue to columns 2 and 8.

### CAUTION

The Agilent Oligo aCGH Bravo platform protocols are based on the plate configuration in Figure 3. Therefore, the first 6 columns are always experimental samples and the last 6 columns are always references. The reference sample for A1 is in A7, the reference sample for B1 is in B7, and so on. The pattern for reference DNAs must match the sample pattern. If this configuration is not followed, the samples will not process correctly.

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## 4 Sample Labeling on the Bravo Platform

|   |    |
|---|----|
| Setting up the VWorks Software                                  | 53 |
| Step 1. Log in to the VWorks software                           | 53 |
| Step 2. Open and start a protocol                               | 53 |
| ULS Labeling  | 55 |
| Step 1. ULS Labeling  | 55 |
| Step 2. Purification after ULS labeling                         | 61 |
| To determine yield, degree of labeling or specific activity     | 63 |
| Step 3. Preparation of ULS Labeled gDNA for Hybridization       | 64 |
| Enzymatic Labeling for CGH                                      | 70 |
| Step 1. Enzymatic Labeling                                      | 70 |
| Step 2. Purification after Enzymatic Labeling                   | 75 |
| To determine yield, degree of labeling or specific activity     | 77 |
| Step 3. Preparation of Enzymatic Labeled gDNA for Hybridization | 79 |
| Enzymatic Labeling for CGH+SNP                                  | 84 |
| Step 1. Enzymatic Labeling                                      | 84 |
| Step 2. Purification after Enzymatic Labeling                   | 92 |
| To determine yield, degree of labeling or specific activity     | 95 |
| Step 3. Preparation of Enzymatic Labeled gDNA for Hybridization | 97 |

This chapter describes the fragmentation, labeling, clean-up and preparation of labeled gDNA for hybridization done on the Bravo platform.

The Agilent Oligo aCGH Bravo Platform protocols are on the CD that came with your Bravo platform or may be obtained by contacting your local Agilent product specialist. Nine protocols are available, three each for ULS processing, Enzymatic processing for CGH, and Enzymatic processing for CGH+SNP.



For ULS processing

- FragmentationLabelingProtocol\_ULS (contains both the Fragmentation and Labeling protocol)
- PurificationProtocol\_ULS
- HybridizationPrepProtocol\_ULS

For Enzymatic CGH processing

- FragmentationLabelingProtocol\_Enz (contains both the Fragmentation and Labeling protocol)
- PurificationProtocol\_Enz
- HybridizationPrepProtocol\_Enz

For Enzymatic CGH+SNP processing

- CGH+SNP\_RestrictionDigestionLabelingProtocol\_Enz (contains both the Restriction Digestion and Labeling protocol)
- CGH+SNP\_PurificationProtocol\_Enz
- CGH+SNP\_HybridizationPrepProtocol\_Enz

For DNA isolated from blood, cells or frozen tissue choose either ULS or Enzymatic processing methods. For DNA isolated from FFPE tissues choose the ULS processing method.

### ULS Labeling

The [Genomic DNA High-Throughput ULS Labeling Kit](#) uses a non-enzymatic procedure to differentially label gDNA samples with fluorescent dyes. The kit contains two-color labeling reaction reagents sufficient for:

- 16 1-pack arrays (blood, cells, tissue samples)
- 12 1-pack arrays (FFPE samples) *or*
- 24 2-pack arrays *or*
- 48 4-pack arrays *or*
- 96 8-pack arrays

You also need to order the [Genomic DNA 96-well Purification Module](#) to purify the labeled DNA.

### Enzymatic Labeling for CGH or CGH+SNP

If you choose the Enzymatic processing method for the CGH or CGH+SNP microarrays, you need a Bravo Automated Liquid Handling Platform with 96 Channel Disposable LT Pipetting Head, Riser and 2 CPAC Ultraflat heated/cooled Deck Pads.

The processing of CGH+SNP microarrays requires the restriction digestion of the gDNA with *Alu I* and *Rsa I* (included in the SureTag Complete DNA Labeling Kit and the SureTag DNA Labeling Kit) prior to labeling, to enable the genotyping of SNPs located in the enzymes' recognition sites for the detection of copy-neutral LOH/UPD.

The SureTag Complete DNA Labeling Kit and SureTag DNA Labeling Kit uses random primers and the exo-Klenow fragment to differentially label gDNA samples with fluorescent-labeled nucleotides. The kit contains sufficient two-color labeling reaction reagents for:

- 25 1-pack, 2-pack and 4-pack arrays *or*
- 50 8-pack arrays

You also need to order the AutoScreen A, 96-well plate to purify the labeled DNA.

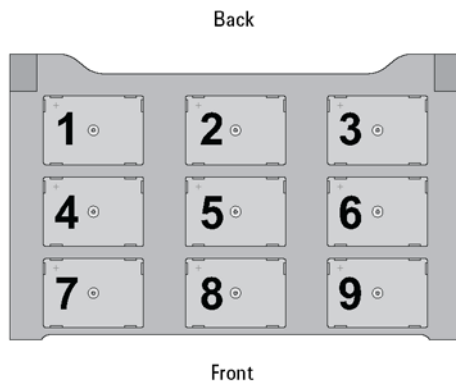
For Agilent's Oligo aCGH application (including CGH+SNP microarrays), the experimental sample is labeled with one dye (Cy5), while the reference sample is labeled with the other dye (Cy3). The Agilent Oligo aCGH protocols available for the Bravo platform will label the experimental samples and reference samples with their respective dye.

### About the Bravo Platform

The Bravo platform is a versatile liquid handler with a nine plate-location platform deck, suitable for handling 96-well, 384-well, and 1536-well plates. The Bravo platform is controlled by the VWorks Automation Control software. Fitted with a choice of seven interchangeable fixed-tip or disposable-tip pipette heads, it accurately dispenses fluids from 0.1  $\mu$ L to 250  $\mu$ L.

Use [Figure 4](#) to familiarize yourself with the location numbering convention on the Bravo platform deck.

## 4 Sample Labeling on the Bravo Platform



**Figure 4** Bravo platform deck

### CAUTION

Before you begin, make sure that you have read and understand operating, maintenance and safety instructions for using your Bravo platform. Refer to the *Bravo Platform User Guide* (G5409-90004) and the *VWorks Software User Guide* (G5415-90002).

---

## Setting up the VWorks Software

To communicate with and to control the robot and integrated devices, the VWorks software uses a device file. You need to create a device file and link the protocols to that device file. See the VWorks User Guide for instructions.

### Step 1. Log in to the VWorks software

- 1 Double-click the VWorks icon on the Windows desktop to start the software.
- 2 In the VWorks window, click **Log in** on the toolbar. The User Authentication dialog box opens.
- 3 Type your VWorks user name and password, and click **OK**. (If no user account is set up, contact the administrator.)

### Step 2. Open and start a protocol

- 1 Click **File > Open**. The Open dialog box opens.
- 2 Locate and select the protocol (.pro) file that you want to open, and click **Open**.
- 3 Click **Simulation is on** in the VWorks toolbar to turn off the simulation mode.  
The button changes to “Simulation is off”.
- 4 Click **Start** on the toolbar.  
The Run Configuration Wizard dialog box opens.

## 4 Sample Labeling on the Bravo Platform

### Step 2. Open and start a protocol

- 5 For each prompt, respond as follows. Click **Next** between each response:

|   |   |
|---|---|
| <b>Run protocol this many times</b>           | 1   |
| <b>Determine when the protocol will start</b> | As soon as possible   |
| <b>Current state of the tip boxes</b>         | <i>Select tip box location and click the icon on the right. Make sure that the state of the tip boxes matches that in the prompt. For example, tip box at location 1 is empty and tip box at location 2 appears full in the prompt.</i> |
| <b>Add notes about the protocol</b>           | <i>Optional.</i>  |

- 6 Click **Finish**.

The Confirm Labware Placement dialog box opens.

- 7 Confirm that the labware on the Bravo platform deck matches the diagram in the software and click **Continue**.

The working plate location appears empty in the VWorks program.

- 8 In the Array format dialog box, type the number that corresponds to the microarray format, and then click **Continue**.

|                              |   |
|------------------------------|---|
| 1×1M or 1×244K microarrays   | 1 |
| 2×400K or 2×105K microarrays | 2 |
| 4×180K or 4×44K microarrays  | 4 |
| 8×60K or 8×15K microarrays   | 8 |

The Select columns dialog box opens.

- 9 Type the number of experimental samples you will process in the run. *Do not count the number of reference samples.*

You can process between 1 and 48 samples. To optimize reagent use, select 8, 16, 24, 32, 40 or 48 samples.

## ULS Labeling

Follow these steps if you are using ULS Labeling. Otherwise, continue to “Enzymatic Labeling for CGH” on page 70 or “Enzymatic Labeling for CGH+SNP” on page 84.

### Step 1. ULS Labeling

In this step, the Bravo platform transfers the correct amount of gDNA from the 96-well plate that was prepared in [Chapter 3](#), “Sample Preparation for Bravo Platform”, to the working plate. You fragment the gDNA in a thermal cycler, the Bravo platform adds the Labeling Master Mix to the fragmented gDNA, then the reactions occur in a thermal cycler.

#### NOTE

Do not fragment gDNA isolated from FFPE tissues. Adjust the fragmentation time of the intact reference gDNA so that the average molecular weight is the same as that of the gDNA isolated from FFPE tissues. This recommendation is based on the method described by Craig JM *et al.* “DNA Fragmentation Simulation Method (FSM) and Fragment Size Matching Improve aCGH Performance of FFPE Tissues,” PLoS One 7(6): e38881.

---

**Bravo Platform Protocol**    FragmentationLabelingProtocol\_ULS

## 4 Sample Labeling on the Bravo Platform

### Step 1. ULS Labeling

#### Initial Deck Layout

| Location | Content  |
|----------|--|
| 1 and 7  | Empty tip box  |
| 2 and 8  | Full tip box   |
| 6        | 384 deep well plate:<br><ul style="list-style-type: none"> <li>• Cy5 Labeling Master Mix in quadrant 1</li> <li>• Cy3 Labeling Master Mix in quadrant 3</li> </ul> |
| 4        | Empty Full skirted 96-well PCR plate   |
| 5        | Sample plate containing the gDNA (prepared in Chapter 3)   |

- 1 Based on your microarray format and sample type, prepare one Cy3 and one Cy5 Labeling Master Mix by mixing the respective components in Table 27 through Table 31.

**Table 27** Multiplier to calculate the volume of Labeling Master Mix (for 1-pack microarrays using non-FFPE samples)\*

| Components                                 | Per reaction (µL) | Total volume needed   | Volume to add per well of 384 deep well plate                       |
|--|-------------------|---|---|
| DNase/RNase-free distilled water           | 1.5               | $(1.5 \mu\text{L} \times N) + 9.6 \mu\text{L}$                |   |
| ULS-Cy 3 Reagent or ULS-Cy 5 Reagent       | 1.5               | $(1.5 \mu\text{L} \times N) + 9.6 \mu\text{L}$                |   |
| 10× Labeling Solution                      | 2                 | $(2 \mu\text{L} \times N) + 12.8 \mu\text{L}$                 |   |
| <b>Final volume of Labeling Master Mix</b> | <b>5</b>          | <b><math>(5 \mu\text{L} \times N) + 32 \mu\text{L}</math></b> | <b><math>((5 \mu\text{L} \times N) + 24 \mu\text{L}) / 8</math></b> |

\* N is the number of experimental samples (8, 16, 24, 32, 40 or 48). Do not count reference samples.



**Table 28** Multiplier to calculate the volume of Labeling Master Mix (for 1-pack microarrays using FFPE samples)\*

| Components                                 | Per reaction (μL) | Total volume needed   | Volume to add per well of 384 deep well plate                       |
|--|-------------------|---|---|
| DNase/RNase-free distilled water           | 1                 | $(1 \mu\text{L} \times N) + 6.4 \mu\text{L}$                  |   |
| ULS-Cy 3 Reagent or ULS-Cy 5 Reagent       | 2                 | $(2 \mu\text{L} \times N) + 12.8 \mu\text{L}$                 |   |
| 10× Labeling Solution                      | 2                 | $(2 \mu\text{L} \times N) + 12.8 \mu\text{L}$                 |   |
| <b>Final volume of Labeling Master Mix</b> | <b>5</b>          | <b><math>(5 \mu\text{L} \times N) + 32 \mu\text{L}</math></b> | <b><math>((5 \mu\text{L} \times N) + 24 \mu\text{L}) / 8</math></b> |

\* N is the number of experimental samples (8, 16, 24, 32, 40 or 48). Do not count reference samples.

**Table 29** Multiplier to calculate the volume of Labeling Master Mix (for 2-pack microarrays using non-FFPE and FFPE samples)\*

| Components                                 | Per reaction (μL) | Total volume needed  | Volume to add per well of 384 deep well plate                        |
|--|-------------------|--|--|
| DNase/RNase-free distilled water           | 7                 | $(7 \mu\text{L} \times N) + 22.4 \mu\text{L}$                  |  |
| ULS-Cy 3 Reagent or ULS-Cy 5 Reagent       | 1                 | $(1 \mu\text{L} \times N) + 3.2 \mu\text{L}$                   |  |
| 10× Labeling Solution                      | 2                 | $(2 \mu\text{L} \times N) + 6.4 \mu\text{L}$                   |  |
| <b>Final volume of Labeling Master Mix</b> | <b>10</b>         | <b><math>(10 \mu\text{L} \times N) + 32 \mu\text{L}</math></b> | <b><math>((10 \mu\text{L} \times N) + 24 \mu\text{L}) / 8</math></b> |

\* N is the number of experimental samples (8, 16, 24, 32, 40 or 48). Do not count reference samples.

## 4 Sample Labeling on the Bravo Platform

### Step 1. ULS Labeling

**Table 30** Multiplier to calculate the volume of Labeling Master Mix (for 4-pack microarrays using non-FFPE and FFPE samples)\*

| Components                                 | Per reaction (μL) | Total volume needed   | Volume to add per well of 384 deep well plate                       |
|--|-------------------|---|---|
| DNase/RNase-free distilled water           | 3.5               | $(3.5 \mu\text{L} \times N) + 22.4 \mu\text{L}$               |   |
| ULS-Cy 3 Reagent or ULS-Cy 5 Reagent       | 0.5               | $(0.5 \mu\text{L} \times N) + 3.2 \mu\text{L}$                |   |
| 10× Labeling Solution                      | 1                 | $(1 \mu\text{L} \times N) + 6.4 \mu\text{L}$                  |   |
| <b>Final volume of Labeling Master Mix</b> | <b>5</b>          | <b><math>(5 \mu\text{L} \times N) + 32 \mu\text{L}</math></b> | <b><math>((5 \mu\text{L} \times N) + 24 \mu\text{L}) / 8</math></b> |

\* N is the number of experimental samples (8, 16, 24, 32, 40 or 48). Do not count reference samples.

**Table 31** Multiplier to calculate the volume of Labeling Master Mix (for 8-pack microarrays using non-FFPE and FFPE samples)\*

| Components                                 | Per reaction (μL) | Total volume needed   | Volume to add per well of 384 deep well plate                       |
|--|-------------------|---|---|
| DNase/RNase-free distilled water           | 3.75              | $(3.75 \mu\text{L} \times N) + 24 \mu\text{L}$                |   |
| ULS-Cy 3 Reagent or ULS-Cy 5 Reagent       | 0.25              | $(0.25 \mu\text{L} \times N) + 1.6 \mu\text{L}$               |   |
| 10× Labeling Solution                      | 1                 | $(1 \mu\text{L} \times N) + 6.4 \mu\text{L}$                  |   |
| <b>Final volume of Labeling Master Mix</b> | <b>5</b>          | <b><math>(5 \mu\text{L} \times N) + 32 \mu\text{L}</math></b> | <b><math>((5 \mu\text{L} \times N) + 24 \mu\text{L}) / 8</math></b> |

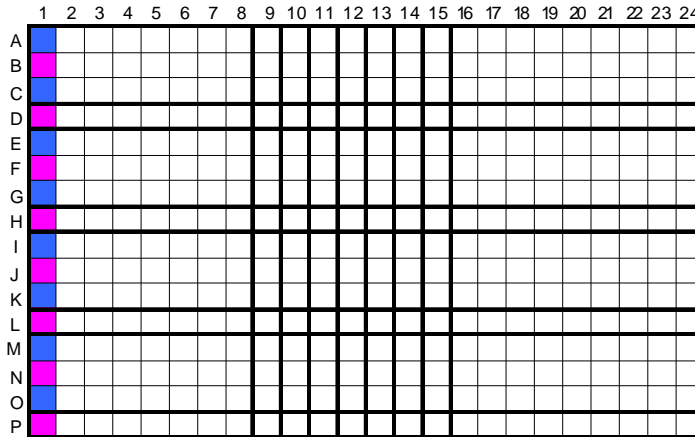
\* N is the number of experimental samples (8, 16, 24, 32, 40 or 48). Do not count reference samples.

#### 2 In a 384 deep well plate:

- Refer to [Table 27](#) through [Table 31](#) for volumes.
- Add the Cy5 Labeling Master Mix to 8 wells in quadrant 1 (location A1, C1, E1, G1, I1, K1, M1, and O1).
- Add the Cy3 Labeling Master Mix to 8 wells in quadrant 3 (location B1, D1, F1, H1, J1, L1, N1, and P1).

See Figure 5.

Make sure that no air bubbles are stuck at the bottom of the well. If needed, spin the plate in a centrifuge for 30 seconds at  $6,000 \times g$  to drive the contents off the walls.



**Figure 5** 384 deep well plate for ULS labeling. Well plate contains Cy5 Labeling Master Mix (blue) in quadrant 1 and Cy3 Labeling Master Mix (pink) in quadrant 3.

- 3** Put the 384 deep well plate at location 6 on the Bravo platform deck.
- 4** Start the FragmentationLabelingProtocol\_ULS protocol run.  
The Bravo platform transfers the correct amount of gDNA from the 96-well plate that was prepared in [Chapter 3](#), “Sample Preparation for Bravo Platform” to the working plate.
- 5** When the Bravo platform pauses at the Protocol User Message task:
  - a** Remove the gDNA sample plate from location 5. If needed, store the leftover gDNA at  $4^{\circ}\text{C}$  for short term storage or at  $-20^{\circ}\text{C}$  for long term storage.
  - b** Remove the working plate from location 4.
  - c** Seal the plate and spin in a centrifuge for 30 seconds at  $6,000 \times g$  to drive the contents off the walls and lid.
  - d** Transfer the working plate to a thermal cycler.
  - e** Program the thermal cycler according to [Table 32](#) and run the program.

## 4 Sample Labeling on the Bravo Platform

### Step 1. ULS Labeling

**Table 32** DNA fragmentation using a thermal cycler

| Step   | Temperature | Time       |
|--------|-------------|------------|
| Step 1 | 95°C        | 10 minutes |
| Step 2 | 4°C         | Hold       |

- 6 Spin the plate in a centrifuge for 30 seconds at  $6,000 \times g$  to drive the contents off the walls and lid.
- 7 Remove the seal and transfer the working plate back to location 4 on the Bravo platform deck.
- 8 Click **Continue** in the VWorks software.  
The Bravo platform adds the Labeling Master Mix to the fragmented gDNA.
- 9 When the protocol run is finished:
  - a Remove the working plate from location 4.
  - b Seal the plate and spin in a centrifuge for 30 seconds at  $6,000 \times g$  to drive the contents off the walls and lid.
  - c Transfer the working plate to a thermal cycler.
  - d Program the thermal cycler according to [Table 33](#) and run the program.

**Table 33** DNA labeling using a thermal cycler

| Step   | Temperature | Time       |
|--------|-------------|------------|
| Step 1 | 85°C        | 30 minutes |
| Step 2 | 4°C         | Hold       |

- 10 Spin the plate in a centrifuge for 30 seconds at  $6,000 \times g$  to drive the contents off the walls and lid.
- 11 Keep the plate at 4°C in the dark until ready to do “[Step 2. Purification after ULS labeling](#)” on page 61.

## Step 2. Purification after ULS labeling

In this step, the Bravo platform prepares the **Genomic DNA 96-well Purification Module**, transfers the labeled DNA to the purification plate, then you collect the labeled, purified DNA by centrifugation.

**Bravo Platform Protocol Used**

PurificationProtocol\_ULS

**Initial Deck Layout**

| Location | Content   |
|----------|---|
| 1        | Full tip box  |
| 4        | Agilent reservoir containing DNase/RNase-free distilled water |
| 7        | When prompted: 96-well plate that contains the labeled gDNA   |
| 8        | After step 4: Pre-spun purification plate/wash plate sandwich |

Use the same centrifuge speed and length for all three spinning steps (step 3, step 6 and step 10). If you spin only one plate, make sure that you counterbalance the plate.

- Carefully remove the top and bottom seals of the purification plate. Once the bottom seal is removed, keep the plate on top of a wash plate. Do not allow the bottom surface to come in contact with laboratory bench top liners, wipes, or other materials.
- Put the purification plate in a re-usable deep well wash plate (supplied).
- Pre-spin the purification plate/wash plate sandwich in a centrifuge for 3 minutes at 3,000 × g.
- Discard the flow-through from the wash plate, and put the purification plate back on the same wash plate. Transfer the purification plate/wash plate sandwich to location 8 on the Bravo platform.
- Start the PurificationProtocol\_ULS protocol run.  
 The Bravo platform adds water to the purification plate/wash plate sandwich.
- When the Bravo platform pauses at the Protocol User Message task, remove the purification plate/wash plate sandwich from location 8 and spin again in a centrifuge for 3 minutes at 3000 × g.

## 4 Sample Labeling on the Bravo Platform

### Step 2. Purification after ULS labeling

- 7 Discard the flow-through.
- 8 Transfer the purification plate to a sample collection plate (supplied) and transfer the purification plate/sample collection plate sandwich to location 8 on the Bravo platform. Put the 96-well plate containing the labeled gDNA on location 7.
- 9 Click **Continue** in the VWorks software.  
For 4-pack and 8-pack microarrays only, the Bravo platform adds water to the labeled DNA. The Bravo platform transfers the labeled DNA to the purification plate/sample collection plate sandwich.
- 10 When the Bravo protocol run is finished, remove the purification plate/sample collection plate sandwich from location 8 and spin in a centrifuge for 3 minutes at  $3,000 \times g$  to collect the purified labeled gDNA. For 1-pack and 2-pack microarrays the volume per sample will be approximately 19  $\mu\text{L}$ . For 4-pack and 8-pack microarrays the volume per sample will be approximately 12.5  $\mu\text{L}$ .
- 11 Take 1.5  $\mu\text{L}$  of each sample to determine the yield and degree of labeling. See “To determine yield, degree of labeling or specific activity” on page 63.
- 12 For 8-pack microarrays only, use a vacuum concentrator to concentrate the labeled samples to 4.5  $\mu\text{L}$ . If needed, you can concentrate the labeled samples to dryness and resuspend in 4.5  $\mu\text{L}$  water.

#### CAUTION

Do not excessively dry the samples as the pellets will become difficult to resuspend.

- 
- 13 Keep the plate at  $4^\circ\text{C}$  in the dark until ready for “Step 3. Preparation of ULS Labeled gDNA for Hybridization” on page 64.

## To determine yield, degree of labeling or specific activity

Use the 8-channel NanoDrop 8000 or single channel NanoDrop 2000 UV-VIS Spectrophotometer to measure the yield, degree of labeling or specific activity.

- 1 From the main menu, select **MicroArray Measurement**, and then select **Sample Type** to be **DNA-50**.
- 2 Use 1.5  $\mu\text{L}$  of 1 $\times$  labeling solution (dilute 10 $\times$  labeling solution 1:10) to blank the instrument.
- 3 Mix the samples.  
You mix the samples before you measure to get a more accurate quantitation.
- 4 Use 1.5  $\mu\text{L}$  of each labeled gDNA sample for quantitation. Measure the absorbance at  $A_{260}$  nm (DNA),  $A_{550}$  nm (cyanine 3), and  $A_{650}$  nm (cyanine 5).
- 5 Calculate the Degree of Labeling or Specific Activity of the labeled gDNA:

$$\text{Degree of Labeling} = \frac{340 \times \text{pmol per } \mu\text{L dye}}{\text{ng per } \mu\text{L gDNA} \times 1000} \times 100\%$$

$$\text{Specific Activity}^* = \frac{\text{pmol per } \mu\text{L dye}}{\mu\text{g per } \mu\text{L gDNA}}$$

\*pmol dyes per  $\mu\text{g}$  gDNA

Note that the Specific Activity is Degree of Labeling divided by 0.034.

- 6 Record the gDNA concentration ( $\text{ng}/\mu\text{L}$ ) for each sample. Calculate the yield as

$$\text{Yield } (\mu\text{g}) = \frac{\text{DNA concentration } (\text{ng}/\mu\text{L}) \times \text{Sample Volume } (\mu\text{L})}{1000 \text{ ng}/\mu\text{g}}$$

As a general guideline, an optimal Cy5 degree of labeling lies between 0.75% and 2.5% and an optimal Cy3 degree of labeling lies between 1.75% and 3.5%, with a Cy3 minus Cy5 range between 1% and 2%. Because the ULS-labeling does not copy or amplify the input DNA, the yield after the labeling should be the same as the input amount of DNA.

**4 Sample Labeling on the Bravo Platform**  
**Step 3. Preparation of ULS Labeled gDNA for Hybridization**

### Step 3. Preparation of ULS Labeled gDNA for Hybridization

In this step, the Bravo platform combines the Cy3 and Cy5 samples and adds the Hybridization Master Mix to the labeled purified DNA samples. You then incubate the sample in a thermal cycler, and the Bravo platform adds the Agilent-CGHblock.

**Bravo Platform Protocol Used**  
 HybridizationPrepProtocol\_ULS

**Initial Deck Layout**

| Location | 1-pack microarray   | 2-pack microarray   | 4-pack and 8-pack microarray  |
|----------|---|---|---|
| 1        | Empty tip box   | Empty tip box   | Empty tip box   |
| 2        | Full tip box  | Full tip box  | Full tip box  |
| 4        | V&P Scientific Reservoir:<br><ul style="list-style-type: none"> <li>column 1: Hybridization Master Mix</li> <li>column 2: Agilent-CGHblock</li> </ul> | V&P Scientific Reservoir:<br><ul style="list-style-type: none"> <li>column 1: Hybridization Master Mix</li> <li>column 2: Agilent-CGHblock</li> </ul> | V&P Scientific Reservoir:<br><ul style="list-style-type: none"> <li>column 1: Hybridization Master Mix</li> <li>column 2: Agilent-CGHblock</li> </ul> |
| 5        |   | Tall Chimney PCR plate placed in Full skirted 96-well PCR plate)  |   |
| 7        | Deep-well plate   |   |   |
| 8        | When you are prompted: Working plate containing the labeled, purified DNA.  | When you are prompted: Working plate containing the labeled, purified DNA.  | Working plate containing the labeled, purified DNA.   |



## Step 3. Preparation of ULS Labeled gDNA for Hybridization

- 1 Prepare the 100× aCGH Blocking Agent:
  - a Add 135  $\mu\text{L}$  of DNase/RNase-free distilled water to the vial containing lyophilized 10× aCGH Blocking Agent (included in the Oligo aCGH/ChIP-on-chip Hybridization Kit).
  - b Mix briefly on a vortex mixer and leave at room temperature for 60 minutes to reconstitute the 10× aCGH Blocking Agent before use or storage.
  - c On the vial of lyophilized 10× aCGH Blocking Agent, cross out “10×” and write “100×”. For ULS labeled samples, you will make and use 100× of the blocking agent.

The 100× aCGH Blocking Agent can be prepared in advance and stored at  $-20^{\circ}\text{C}$ .

- 2 Prepare the Hybridization Master Mix by mixing the components in the tables below according to the microarray format used.

**Table 34** Multiplier to calculate the volume of Hybridization Master Mix for 1-pack microarrays, non-FFPE and FFPE samples \*

| Components                                      | Per reaction ( $\mu\text{L}$ ) | Total volume needed   |
|---|--------------------------------|---|
| DNase/RNase-free distilled water                | 39.8                           | $(39.8 \mu\text{L} \times N) + 157 \mu\text{L}$                   |
| Cot-1 DNA (1.0 mg/mL) <sup>†</sup>              | 50                             | $(50 \mu\text{L} \times N) + 197.2 \mu\text{L}$                   |
| 100× aCGH Blocking Agent <sup>‡</sup>           | 5.2                            | $(5.2 \mu\text{L} \times N) + 20.5 \mu\text{L}$                   |
| 2× HI-RPM Hybridization Buffer <sup>‡</sup>     | 260                            | $(260 \mu\text{L} \times N) + 1025.4 \mu\text{L}$                 |
| <b>Final Volume of Hybridization Master Mix</b> | <b>355</b>                     | <b><math>(355 \mu\text{L} \times N) + 1400 \mu\text{L}</math></b> |

\* N is the number of experimental samples (8, 16, 24, 32, 40 or 48). Do not count reference samples.

† Use Cot-1 DNA (1.0 mg/mL) from the appropriate species.

‡ Included in the Oligo aCGH/ChIP-on-chip Hybridization Kit

## 4 Sample Labeling on the Bravo Platform

### Step 3. Preparation of ULS Labeled gDNA for Hybridization

**Table 35** Multiplier to calculate the volume of Hybridization Master Mix for 2-pack microarrays, non-FFPE and FFPE samples\*

| Components                                      | Per reaction | Total volume needed   |
|---|--------------|---|
| DNase/RNase-free distilled water                | 2.4          | $(2.4 \mu\text{L} \times N) + 21 \mu\text{L}$                     |
| Cot-1 DNA (1.0 mg/mL) <sup>†</sup>              | 25           | $(25 \mu\text{L} \times N) + 218.8 \mu\text{L}$                   |
| 100× aCGH Blocking Agent <sup>‡</sup>           | 2.6          | $(2.6 \mu\text{L} \times N) + 22.8 \mu\text{L}$                   |
| 2× HI-RPM Hybridization Buffer <sup>‡</sup>     | 130          | $(130 \mu\text{L} \times N) + 1137.5 \mu\text{L}$                 |
| <b>Final Volume of Hybridization Master Mix</b> | <b>160</b>   | <b><math>(160 \mu\text{L} \times N) + 1400 \mu\text{L}</math></b> |

\* N is the number of experimental samples (8, 16, 24, 32, 40 or 48). Do not count reference samples.

† Use Cot-1 DNA (1.0 mg/mL) from the appropriate species.

‡ Included in the Oligo aCGH/ChIP-on-chip Hybridization Kit

**Table 36** Multiplier to calculate the volume of Hybridization Master Mix for 4-pack microarrays, non-FFPE and FFPE samples\*

| Components                                      | Per reaction (μL) | Total volume needed  |
|---|-------------------|--|
| Cot-1 DNA (1.0 mg/mL) <sup>†</sup>              | 5                 | $(5 \mu\text{L} \times N) + 114.7 \mu\text{L}$                   |
| 100× aCGH Blocking Agent <sup>‡</sup>           | 1                 | $(1 \mu\text{L} \times N) + 23.0 \mu\text{L}$                    |
| 2× HI-RPM Hybridization Buffer <sup>‡</sup>     | 55                | $(55 \mu\text{L} \times N) + 1262.3 \mu\text{L}$                 |
| <b>Final Volume of Hybridization Master Mix</b> | <b>61</b>         | <b><math>(61 \mu\text{L} \times N) + 1400 \mu\text{L}</math></b> |

\* N is the number of experimental samples (8, 16, 24, 32, 40 or 48). Do not count reference samples.

† Use Cot-1 DNA (1.0 mg/mL) from the appropriate species.

‡ Included in the Oligo aCGH/ChIP-on-chip Hybridization Kit

## Step 3. Preparation of ULS Labeled gDNA for Hybridization

**Table 37** Multiplier to calculate the volume of Hybridization Master Mix for 8-pack microarrays, non-FFPE and FFPE samples\*

| Components                                      | Per reaction (μL) | Total volume needed          |
|---|-------------------|------------------------------|
| Cot-1 DNA (1.0 mg/mL) <sup>†</sup>              | 2                 | (2 μL × N) + 112 μL          |
| 100× aCGH Blocking Agent <sup>‡</sup>           | 0.5               | (0.5 μL × N) + 28 μL         |
| 2× HI-RPM Hybridization Buffer <sup>‡</sup>     | 22.5              | (22.5 μL × N) + 1260 μL      |
| <b>Final Volume of Hybridization Master Mix</b> | <b>25</b>         | <b>(25 μL × N) + 1400 μL</b> |

\* N is the number of experimental samples (8, 16, 24, 32, 40 or 48). Do not count reference samples.

† Use Cot-1 DNA (1.0 mg/mL) from the appropriate species.

‡ Included in the Oligo aCGH/ChIP-on-chip Hybridization Kit

- 3 Add hybridization mix to column 1 of the reservoir in location 4. Be careful not to generate bubbles.
- 4 Use Table 38 to calculate how much Agilent-CGHblock (included in the Genomic DNA High-Throughput ULS Labeling Kit) to use.

**Table 38** Multiplier to calculate volume of Agilent-CGHblock\*

| Format | Total volume needed    |
|--------|------------------------|
| 1-pack | (130 μL × N) + 1400 μL |
| 2-pack | (65 μL × N) + 1400 μL  |
| 4-pack | (27 μL × N) + 1400 μL  |
| 8-pack | (11 μL × N) + 1400 μL  |

\* N is the number of experimental samples (8, 16, 24, 32, 40 or 48). Do not count reference samples.

- 5 Bring the Agilent-CGHblock to room temperature.

## 4 Sample Labeling on the Bravo Platform

### Step 3. Preparation of ULS Labeled gDNA for Hybridization

- 6 Add the [Agilent-CGHblock](#) to the 2nd column of the reservoir in location 4. The addition of [Agilent-CGHblock](#) to the hybridization is needed to eliminate background noise on the microarray. The [Agilent-CGHblock](#) contains components that cannot be heated to 95°C.
- 7 Start the `HybridizationPrepProtocol_ULS` protocol run.

For 1-pack and 2-pack microarrays, the Bravo platform transfers the hybridization master mix to the empty deep-well or tall-chimney plates. Continue at [step 8](#).

For 4-pack and 8-pack microarrays, the Bravo platform combines the Cy5 and Cy3 labeled, purified samples and adds the hybridization master mix. Continue at [step 9](#).
- 8 For 1-pack and 2-pack microarrays:
  - a When the Bravo platform pauses at the Protocol User Message task, put the working plate that contains the labeled, purified DNA at location 8.
  - b Click **Continue** in the VWorks software.

The Bravo platform adds the Cy3 and Cy5 labeled, purified gDNA to the hybridization master mix.

#### NOTE

When the number of samples is greater than 40, the Bravo platform runs out of tips before the end of the protocol run.

If you see the error message **Error in automatic tip operation**, put more tips into the Bravo platform. Go to **Tools > Tip State Editor**, and update the status of the tip boxes.

- 9 When the Bravo platform pauses at the Protocol User Message task:
  - a Remove, seal and transfer the deep-well plate from location 7, tall-chimney plate from location 5, or the PCR plate from location 8 to a thermal cycler.
  - b Program the thermal cycler according to [Table 39](#) and run the program.

For the 1-pack microarray deep-well plates, use an incubator that is compatible with deep-well plates, such as the Eppendorf ThermoStat (Eppendorf p/n 022670204 with deep-well plate block p/n 022670565) or BioShake iQ (Q.Instruments p/n 1808-0506).

## Step 3. Preparation of ULS Labeled gDNA for Hybridization

**Table 39** DNA preparation before hybridization

| Step   | Temperature | Time       |
|--------|-------------|------------|
| Step 1 | 95°C        | 3 minutes  |
| Step 2 | 37°C        | 30 minutes |

**10** Spin the plate in a centrifuge for 30 seconds at  $6,000 \times g$  to drive the contents off the walls and lid.

**11** Remove the seal and transfer the deep-well plate back to location 7, tall-chimney plate back to location 5, or the PCR plate back to location 8 on the Bravo platform deck.

**12** Click **Continue** in the VWorks software.

The Bravo platform adds the [Agilent-CGHblock](#) to the samples.

The samples are ready for the Hybridization step. Continue at [Chapter 4](#), “Microarray Processing and Feature Extraction.”

## Enzymatic Labeling for CGH

Follow the procedure in this section if you are using Enzymatic labeling for CGH with the [SureTag Complete DNA Labeling Kit](#) or [SureTag DNA Labeling Kit](#).

### Step 1. Enzymatic Labeling

In this step, the Bravo platform transfers the correct amount of gDNA from the 96-well plate that was prepared in [Chapter 3](#), “Sample Preparation for Bravo Platform” to the working plate. You denature and fragment the gDNA in the presence of random primers in a thermal cycler, the Bravo platform adds the Labeling Master Mix to the fragmented gDNA, and the labeling reactions are done in a thermal cycler.

**Bravo Platform Protocol**

FragmentationLabelingProtocol\_Enz

**Initial Deck Layout**

| Location   | Content   |
|------------|---|
| 1 and 7    | Empty tip box   |
| 2 and 8    | Full tip box  |
| 5          | Sample plate containing the gDNA (prepared in <a href="#">Chapter 3</a> )   |
| 4 (cooled) | Empty <a href="#">Full skirted 96-well PCR plate</a>  |
| 6 (cooled) | 384 deep well plate: <ul style="list-style-type: none"> <li>• Random primers in quadrant 1</li> <li>• Cy5 Labeling Master Mix in quadrant 2</li> <li>• Cy3 Labeling Master Mix in quadrant 4</li> </ul> |

- 1 Turn on the Bravo Platform CPAC Ultraflat heated/cooled Deck Pads on Positions 4 and 6, set to 4°C.
- 2 Use [Table 40](#) to calculate how much [Random Primer](#) to use.

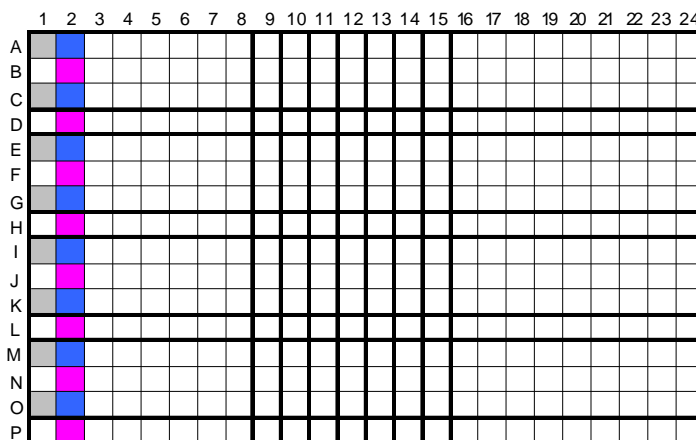
**Table 40** Multiplier to calculate volume of Random Primer \*

| Format                   | Total volume needed                                    | Volume to add per well of 384 deep well plate              |
|--------------------------|--|--|
| 1-pack, 2-pack or 4-pack | $(5 \mu\text{L} \times N \times 2) + 32 \mu\text{L}$   | $((5 \mu\text{L} \times N \times 2) + 24 \mu\text{L})/8$   |
| 8-pack                   | $(2.5 \mu\text{L} \times N \times 2) + 32 \mu\text{L}$ | $((2.5 \mu\text{L} \times N \times 2) + 24 \mu\text{L})/8$ |

\* N is the number of experimental samples (8, 16, 24, 32, 40 or 48). Do not count reference samples.

**3** Refer to **Table 40** for volumes. Add **Random Primer** to 8 wells in quadrant 1 (location A1, C1, E1, G1, I1, K1, M1, and O1). See **Figure 6**.

Make sure that no air bubbles are stuck at the bottom of the well. If needed, spin the plate in a centrifuge for 30 seconds at  $6,000 \times g$  to drive the contents off the walls.



**Figure 6** 384 deep well plate for Enzymatic labeling containing **Random Primer** (gray) in quadrant 1, **Cy5 Labeling Master Mix** (blue) in quadrant 2 and **Cy3 Labeling Master Mix** (pink) in quadrant 4

**4** Prepare one **Cy3** and one **Cy5 Labeling Master Mix** by mixing the components in **Table 41** and **Table 42**, based on your microarray format.

## 4 Sample Labeling on the Bravo Platform

### Step 1. Enzymatic Labeling

5 In a 384 deep well plate:

- Refer to [Table 41](#) and [Table 42](#) for volumes.
- Add the Cy5 Labeling Master Mix to 8 wells in quadrant 2 (location A2, C2, E2, G2, I2, K2, M2, and O2).
- Add the Cy3 Labeling Master Mix to 8 wells in quadrant 4 (location B2, D2, F2, H2, J2, L2, N2, and P2).

See [Figure 6](#).

6 Spin the plate in a centrifuge for 30 seconds at  $6,000 \times g$  to drive the contents off the walls.

Make sure that no air bubbles are stuck at the bottom of the well.

7 Put the 384 deep well plate at location 6 on the Bravo platform deck.

**Table 41** Multiplier to calculate the volume of Labeling Master Mix (for 1-, 2-, or 4-pack microarrays)\*

| Component                                  | Per reaction (µL) | Total volumes needed   | Volume to add per well of 384 deep well plate                      |
|--|-------------------|--|--|
| Nuclease-Free Water                        | 1                 | $(1 \mu\text{L} \times N) + 2.1 \mu\text{L}$                   |  |
| 5× Reaction Buffer                         | 5                 | $(5 \mu\text{L} \times N) + 10.7 \mu\text{L}$                  |  |
| 10× dNTPs <sup>†</sup>                     | 5                 | $(5 \mu\text{L} \times N) + 10.7 \mu\text{L}$                  |  |
| Cyanine 3-dUTP <i>or</i><br>Cyanine 5-dUTP | 3                 | $(3 \mu\text{L} \times N) + 6.4 \mu\text{L}$                   |  |
| Exo (-) Klenow                             | 1                 | $(1 \mu\text{L} \times N) + 2.1 \mu\text{L}$                   |  |
| <b>Final volume of Labeling Master Mix</b> | <b>15</b>         | <b><math>(15 \mu\text{L} \times N) + 32 \mu\text{L}</math></b> | <b><math>((15 \mu\text{L} \times N) + 24 \mu\text{L})/8</math></b> |

\* N is the number of experimental samples (8, 16, 24, 32, 40 or 48). Do not count reference samples.

† used as a 5× dNTP mix



**Table 42** Multiplier to calculate the volume of Labeling Master Mix (for 8-pack microarrays)

| Component                                  | Per reaction (µL) | Total volumes needed   | Volume to add per well of 384 deep well plate                        |
|--|-------------------|--|--|
| Nuclease-Free Water                        | 9                 | $(9 \mu\text{L} \times N) + 15.6 \mu\text{L}$                    |  |
| 5× Reaction Buffer                         | 5                 | $(5 \mu\text{L} \times N) + 8.6 \mu\text{L}$                     |  |
| 10× dNTPs                                  | 2.5               | $(2.5 \mu\text{L} \times N) + 4.3 \mu\text{L}$                   |  |
| Cyanine 3-dUTP <i>or</i><br>Cyanine 5-dUTP | 1.5               | $(1.5 \mu\text{L} \times N) + 2.6 \mu\text{L}$                   |  |
| Exo (-) Klenow                             | 0.5               | $(0.5 \mu\text{L} \times N) + 0.9 \mu\text{L}$                   |  |
| <b>Final volume of Labeling Master Mix</b> | <b>18.5</b>       | <b><math>(18.5 \mu\text{L} \times N) + 32 \mu\text{L}</math></b> | <b><math>((18.5 \mu\text{L} \times N) + 24 \mu\text{L})/8</math></b> |

**8** Start the FragmentationLabelingProtocol\_Enz protocol run.

The Bravo platform adds **Random Primer** to the empty working plate. The Bravo platform transfers the correct amount of gDNA from the 96-well plate that was prepared in **Chapter 3**, “Sample Preparation for Bravo Platform” to the working plate.

**9** When the Bravo platform pauses at the Protocol User Message task:

- a** Remove the gDNA sample plate from location 5. If needed, store the leftover gDNA at 4°C for short term storage or at -20°C for long term storage.
- b** Remove the working plate from location 4.
- c** Seal the plate and spin in a centrifuge for 30 seconds at 6,000 × g to drive the contents off the walls and lid.
- d** Transfer the working plate to a thermal cycler.
- e** Program the thermal cycler according to **Table 43** and run the program.

**Table 43** DNA fragmentation using a thermal cycler

| Step   | Temperature | Time       |
|--------|-------------|------------|
| Step 1 | 98°C        | 10 minutes |
| Step 2 | 4°C         | Hold       |

## 4 Sample Labeling on the Bravo Platform

### Step 1. Enzymatic Labeling

**10** Spin the plate in a centrifuge for 30 seconds at  $6,000 \times g$  to drive the contents off the walls and lid.

**11** Remove the seal and transfer the working plate back to location 4 on the Bravo platform deck.

**12** Click **Continue** in the VWorks software.

The Bravo platform adds the Labeling Master Mix to the fragmented gDNA.

#### NOTE

When the number of samples is greater than 40, the Bravo platform runs out of tips before the end of the protocol run.

If you see the error message **Error in automatic tip operation**, put more tips into the Bravo platform. Go to **Tools > Tip State Editor**, and update the status of the tip boxes.

**13** When the protocol run is finished:

- a** Remove the working plate from location 4.
- b** Seal the plate and spin in a centrifuge for 30 seconds at  $6,000 \times g$  to drive the contents off the walls and lid.
- c** Transfer the working plate to a thermal cycler.
- d** Program the thermal cycler according to [Table 44](#) and run the program.

**Table 44** DNA labeling using a thermal cycler

| Step   | Temperature | Time       |
|--------|-------------|------------|
| Step 1 | 37°C        | 2 hours    |
| Step 2 | 65°C        | 10 minutes |
| Step 3 | 4°C         | Hold       |

**14** Turn off the Bravo Platform CPAC Ultraflat heated/cooled Deck Pads on Positions 4 and 6.

**15** Spin the plate in a centrifuge for 30 seconds at  $6,000 \times g$  to drive the contents off the walls and lid.

**16** Keep the plate at 4°C in the dark until ready to do “[Step 2. Purification after Enzymatic Labeling](#)” on page 75.

## Step 2. Purification after Enzymatic Labeling

In this step, the Bravo platform prepares the AutoScreen-96A Well plates, transfers the labeled DNA to the purification plate, then you collect the labeled purified DNA by centrifugation.

**Bravo Platform Protocol Used**

PurificationProtocol\_Enz

**Initial Deck Layout**

| Location | Content  |
|----------|--|
| 1        | Full tip box   |
| 4        | Agilent reservoir containing DNase/RNase-free distilled water                  |
| 7        | When prompted: 96-well plate containing the labeled gDNA                       |
| 8        | After <a href="#">step 6</a> : Pre-spun purification plate/wash plate sandwich |

Use the same centrifuge speed and length for all three spinning steps ([step 5](#), [step 8](#) and [step 12](#)). If you spin only one plate, make sure that you counterbalance.

- 1** Get a [Full skirted 96-well PCR plate](#) to use as a wash plate, and label it as “Wash Plate”.  
 The wash plate can be reused.
- 2** Get another 96-well PCR plate to use as a collection plate, and label it as “Collection Plate”.
- 3** Carefully remove the top and bottom seals of the purification plate. Once the bottom seal is removed, keep the plate on top of a wash plate. Do not allow the bottom surface to come in contact with laboratory bench top liners, wipes, or other materials.
- 4** Put the purification plate in a reusable wash plate.
- 5** Pre-spin the purification plate/wash plate sandwich in a centrifuge for 5 minutes at 910 × g.
- 6** Discard the flow-through from the wash plate and put the purification plate back on the same wash plate. Transfer the purification plate/wash plate sandwich to location 8 on the Bravo platform.
- 7** Start the PurificationProtocol\_Enz protocol run.

## 4 Sample Labeling on the Bravo Platform

### Step 2. Purification after Enzymatic Labeling

The Bravo platform adds water to the purification plate/wash plate sandwich.

- 8 When the Bravo platform pauses at the Protocol User Message task, remove the purification plate/wash plate sandwich from location 8 and spin again in a centrifuge for 5 minutes at  $910 \times g$ .
- 9 Discard the flow-through.
- 10 Transfer the purification plate to a sample collection plate and transfer the purification plate/sample collection plate sandwich to location 8 on the Bravo platform. Put the 96-well plate containing the labeled gDNA on location 7.
- 11 Click **Continue** in the VWorks software.

The Bravo platform transfers the labeled DNA to the purification plate/sample collection plate sandwich.
- 12 When the protocol run is finished, remove the purification plate/sample collection plate sandwich from location 8 and spin in a centrifuge for 5 minutes at  $910 \times g$  to collect the purified labeled gDNA in the sample collection plate. The volume per sample will be  $\sim 19 \mu\text{L}$ .
- 13 Take  $1.5 \mu\text{L}$  of each sample to determine the yield and degree of labeling or specific activity. See “[To determine yield, degree of labeling or specific activity](#)” on page 77.
- 14 For 8-pack microarrays only, use a vacuum concentrator to concentrate the labeled samples to  $8 \mu\text{L}$ . If needed, you can concentrate the labeled samples to dryness and resuspend in  $8 \mu\text{L}$   $1\times\text{TE}$  (pH 8.0).

#### CAUTION

Do not excessively dry the samples, or the pellets will become difficult to resuspend.

- 
- 15 Keep the plate at  $4^\circ\text{C}$  in the dark until ready for “[Step 3. Preparation of Enzymatic Labeled gDNA for Hybridization](#)” on page 79.

## To determine yield, degree of labeling or specific activity

Use the 8-channel NanoDrop 8000 or single channel NanoDrop 2000 UV-VIS Spectrophotometer to measure yield, degree of labeling or specific activity.

- 1 From the main menu, select **MicroArray Measurement**, and then select **Sample Type** to be **DNA-50**.
- 2 Use 1.5  $\mu\text{L}$  of TE to blank the instrument.
- 3 Mix the samples.  
You mix the samples before you measure to get a more accurate quantitation.
- 4 Use 1.5  $\mu\text{L}$  of each labeled gDNA sample for quantitation. Measure the absorbance at  $A_{260}$  nm (DNA),  $A_{550}$  nm (cyanine 3), and  $A_{650}$  nm (cyanine 5).
- 5 Calculate the Degree of Labeling or Specific Activity of the labeled gDNA:

$$\text{Degree of Labeling} = \frac{340 \times \text{pmol per } \mu\text{L dye}}{\text{ng per } \mu\text{L gDNA} \times 1000} \times 100\%$$

$$\text{Specific Activity}^* = \frac{\text{pmol per } \mu\text{L dye}}{\mu\text{g per } \mu\text{L gDNA}}$$

\*pmol dyes per  $\mu\text{g}$  gDNA

Note that the Specific Activity is Degree of Labeling divided by 0.034.

- 6 Record the gDNA concentration ( $\text{ng}/\mu\text{L}$ ) for each sample. Calculate the yield as

$$\text{Yield } (\mu\text{g}) = \frac{\text{DNA concentration } (\text{ng}/\mu\text{L}) \times \text{Sample Volume } (\mu\text{L})}{1000 \text{ ng}/\mu\text{g}}$$

#### 4 Sample Labeling on the Bravo Platform

To determine yield, degree of labeling or specific activity

Refer to Table 45 for expected yield of labeled gDNA and specific activity after labeling and clean-up, when starting with high quality gDNA.

**Table 45** Expected Yield and Specific Activity after Labeling and Clean-up with the SureTag Complete DNA Labeling Kit or SureTag DNA Labeling Kit

| Input gDNA ( $\mu\text{g}$ ) | Yield ( $\mu\text{g}$ ) | Specific Activity of Cyanine-3 Labeled Sample ( $\text{pmol}/\mu\text{g}$ ) | Specific Activity of Cyanine-5 Labeled Sample ( $\text{pmol}/\mu\text{g}$ ) |
|------------------------------|-------------------------|---|---|
| 0.5                          | 11 to 14                | 22 to 29  | 18 to 25  |
| 0.2*                         | 5 to 7                  | 18 to 27  | 16 to 24  |

\* Half labeling reaction (half the amount of random primers, dye, enzyme and dNTPs)

Check that the Cy3 and Cy5 yield after labeling are the same. If not, refer to “Troubleshooting” on page 125.

## Step 3. Preparation of Enzymatic Labeled gDNA for Hybridization

In this step, the Bravo platform combines the Cy3 and Cy5 samples, adds the Hybridization Master Mix to the labeled purified DNA samples, and you incubate the sample in a thermal cycler.

### Bravo Platform Protocol Used

HybridizationPrepProtocol\_Enz

### Initial Deck Layout

| Location | 1-pack microarray   | 2-pack microarray   | 4-pack and 8-pack microarray  |
|----------|---|---|---|
| 1        | Empty tip box   | Empty tip box   | Empty tip box   |
| 2        | Full tip box  | Full tip box  | Full tip box  |
| 4        | V&P Scientific Reservoir:<br><ul style="list-style-type: none"> <li>column 1: Hybridization Master Mix</li> <li>If number of samples &gt; 32, column 2: Hybridization Master Mix</li> </ul> | V&P Scientific Reservoir:<br><ul style="list-style-type: none"> <li>column 1: Hybridization Master Mix</li> </ul> | V&P Scientific Reservoir:<br><ul style="list-style-type: none"> <li>column 1: Hybridization Master Mix</li> </ul> |
| 5        |   | Tall Chimney PCR plate placed in a Full skirted 96-well PCR plate   |   |
| 7        | Deep-well plate   |   |   |
| 8        | When you are prompted: Working plate containing the labeled, purified DNA.  | When you are prompted: Working plate containing the labeled, purified DNA.  | Working plate containing the labeled, purified DNA.   |

### 1 Prepare the 10× aCGH Blocking Agent:

- a Add 1350 µL of DNase/RNase-free distilled water to the vial containing lyophilized 10× aCGH Blocking Agent (included in the Oligo aCGH/ChIP-on-chip Hybridization Kit).

## 4 Sample Labeling on the Bravo Platform

### Step 3. Preparation of Enzymatic Labeled gDNA for Hybridization

- b** Mix briefly on a vortex mixer and leave at room temperature for 60 minutes to reconstitute the Blocking Agent before use or storage.

The 10× aCGH Blocking Agent can be prepared in advance and stored at -20°C.

- 2** Prepare the Hybridization Master Mix by mixing the components in the tables below according to the microarray format used.

**Table 46** Multiplier to calculate the volume of Hybridization Master Mix for 1-pack microarrays \*

| Component                                       | Per reaction (μL) | Total volume needed in column 1 if N ≤ 32                         | Additional volume needed in column 2 if N > 32                         |
|---|-------------------|---|--|
| 1×TE (pH 8.0)                                   | 123               | $(123 \mu\text{L} \times N) + 355.1 \mu\text{L}$                  | $(123 \mu\text{L} \times (N-32)) + 355.1 \mu\text{L}$                  |
| Cot-1 DNA (1.0 mg/mL) <sup>†</sup>              | 50                | $(50 \mu\text{L} \times N) + 144.3 \mu\text{L}$                   | $(50 \mu\text{L} \times (N-32)) + 144.3 \mu\text{L}$                   |
| 10× aCGH Blocking Agent <sup>‡</sup>            | 52                | $(52 \mu\text{L} \times N) + 150.1 \mu\text{L}$                   | $(52 \mu\text{L} \times (N-32)) + 150.1 \mu\text{L}$                   |
| 2× HI-RPM Hybridization Buffer <sup>‡</sup>     | 260               | $(260 \mu\text{L} \times N) + 750.5 \mu\text{L}$                  | $(260 \mu\text{L} \times (N-32)) + 750.5 \mu\text{L}$                  |
| <b>Final Volume of Hybridization Master Mix</b> | <b>485</b>        | <b><math>(485 \mu\text{L} \times N) + 1400 \mu\text{L}</math></b> | <b><math>(485 \mu\text{L} \times (N-32)) + 1400 \mu\text{L}</math></b> |

\* N is the number of experimental samples (8, 16, 24, 32, 40 or 48). Do not count reference samples.

† Use Cot-1 DNA (1.0 mg/mL) from the appropriate species.

‡ Included in Oligo aCGH/ChIP-on-chip Hybridization Kit



## Step 3. Preparation of Enzymatic Labeled gDNA for Hybridization

**Table 47** Multiplier to calculate the volume of Hybridization Master Mix for 2-pack microarrays

| Component                                       | Per reaction (μL) | Total volume needed   |
|---|-------------------|---|
| 1×TE (pH 8.0)                                   | 44                | $(44 \mu\text{L} \times N) + 273.8 \mu\text{L}$                   |
| Cot-1 DNA (1.0 mg/mL)*                          | 25                | $(25 \mu\text{L} \times N) + 155.6 \mu\text{L}$                   |
| 10× aCGH Blocking Agent†                        | 26                | $(26 \mu\text{L} \times N) + 161.8 \mu\text{L}$                   |
| 2× HI-RPM Hybridization Buffer†                 | 130               | $(130 \mu\text{L} \times N) + 808.9 \mu\text{L}$                  |
| <b>Final Volume of Hybridization Master Mix</b> | <b>225</b>        | <b><math>(225 \mu\text{L} \times N) + 1400 \mu\text{L}</math></b> |

\* Use Cot-1 DNA (1.0 mg/mL) from the appropriate species.

† Included in Oligo aCGH/ChIP-on-chip Hybridization Kit

**Table 48** Multiplier to calculate the volume of Hybridization Master Mix for 4-pack microarrays

| Component                                       | Per reaction (μL) | Total volume needed  |
|---|-------------------|--|
| 1×TE (pH 8.0)                                   | 4                 | $(4 \mu\text{L} \times N) + 74.7 \mu\text{L}$                    |
| Cot-1 DNA (1.0 mg/mL)*                          | 5                 | $(5 \mu\text{L} \times N) + 93.3 \mu\text{L}$                    |
| 10× aCGH Blocking Agent†                        | 11                | $(11 \mu\text{L} \times N) + 205.3 \mu\text{L}$                  |
| 2× HI-RPM Hybridization Buffer†                 | 55                | $(55 \mu\text{L} \times N) + 1026.7 \mu\text{L}$                 |
| <b>Final Volume of Hybridization Master Mix</b> | <b>75</b>         | <b><math>(75 \mu\text{L} \times N) + 1400 \mu\text{L}</math></b> |

\* Use Cot-1 DNA (1.0 mg/mL) from the appropriate species.

† Included in Oligo aCGH/ChIP-on-chip Hybridization Kit

## 4 Sample Labeling on the Bravo Platform

### Step 3. Preparation of Enzymatic Labeled gDNA for Hybridization

**Table 49** Multiplier to calculate the volume of Hybridization Master Mix for 8-pack microarrays

| Component                                       | Per reaction (μL) | Total volume needed          |
|---|-------------------|------------------------------|
| Cot-1 DNA (1.0 mg/mL) <sup>*</sup>              | 2                 | (2 μL × N) + 96.6 μL         |
| 10× aCGH Blocking Agent <sup>†</sup>            | 4.5               | (4.5 μL × N) + 217.2 μL      |
| 2× HI-RPM Hybridization Buffer <sup>†</sup>     | 22.5              | (22.5 μL × N) + 1086.2 μL    |
| <b>Final Volume of Hybridization Master Mix</b> | <b>29</b>         | <b>(29 μL × N) + 1400 μL</b> |

\* Use Cot-1 DNA (1.0 mg/mL) from the appropriate species.

† Included in Oligo aCGH/ChIP-on-chip Hybridization Kit

- 3** Add hybridization master mix to the reservoir in location 4. Be careful not to generate bubbles.
  - For 1-pack and ≤ 32 samples, 2-pack, 4-pack and 8-pack: add to column 1.
  - For 1-pack and > 32 samples: add to column 1 and 2.
- 4** Start the HybridizationPrepProtocol\_Enz protocol run.

For 1-pack and 2-pack microarrays, the Bravo platform transfers the hybridization master mix to the empty deep-well or tall-chimney plates. Continue at [step 5](#).

For 4-pack and 8-pack microarrays, the Bravo platform combines the Cy5 and Cy3 labeled, purified samples and adds the hybridization master mix. Continue at [step 6](#).
- 5** For 1-pack and 2-pack microarrays:
  - a** When the Bravo platform pauses at the Protocol User Message task, put the working plate that contains the labeled, purified DNA at location 8.
  - b** Click **Continue** in the VWorks software.

The Bravo platform adds the Cy3 and Cy5 labeled, purified gDNA to the hybridization master mix.

#### NOTE

When the number of samples is greater than 40, the Bravo platform runs out of tips before the end of the protocol run.

If you see the error message **Error in automatic tip operation**, put more tips into the Bravo platform. Go to **Tools > Tip State Editor**, and update the status of the tip boxes.

## Step 3. Preparation of Enzymatic Labeled gDNA for Hybridization

- 6** When the protocol run is finished, remove, seal, spin, and transfer the deep-well plate from location 7, tall-chimney plate from location 5, or the PCR plate from location 8 to a thermal cycler. Program the thermal cycler according to [Table 50](#) and run the program.

For the 1-pack microarray deep-well plates, use an incubator that is compatible with deep-well plates, such as the Eppendorf ThermoStat (Eppendorf p/n 022670204 with deep-well plate block p/n 022670565) or BioShake iQ (Q.Instruments p/n 1808-0506).

**Table 50** DNA preparation before hybridization

| Step   | Temperature | Time       |
|--------|-------------|------------|
| Step 1 | 98°C        | 3 minutes  |
| Step 2 | 37°C        | 30 minutes |

- 7** Spin the plate in a centrifuge for 30 seconds at  $6,000 \times g$  to drive the contents off the walls and lid.

The samples are ready for the Hybridization step.

## Enzymatic Labeling for CGH+SNP

Follow the procedure in this section if you are using Enzymatic labeling for CGH+SNP with the [SureTag Complete DNA Labeling Kit](#) or [SureTag DNA Labeling Kit](#).

### Step 1. Enzymatic Labeling

In this step, the Bravo platform combines the correct amount of gDNA from the 96-well plate that was prepared in [Chapter 3](#), “Sample Preparation for Bravo Platform” with the Restriction Digestion Master Mix in the working plate. The digested gDNA is denatured in the presence of random primers in a thermal cycler, the Bravo platform adds the Labeling Master Mix to the digested gDNA, and the labeling reactions are done in a thermal cycler.

**Bravo Platform Protocol**

CGH+SNP\_RestrictionDigestionLabelingProtocol\_Enz

**Initial Deck Layout**

| Location   | Content   |
|------------|---|
| 1 and 7    | Empty tip box   |
| 2 and 8    | Full tip box  |
| 5          | Sample plate containing the gDNA (prepared in Chapter 3)  |
| 4 (cooled) | Empty <a href="#">Full skirted 96-well PCR plate</a>  |
| 6 (cooled) | 384 deep well plate: <ul style="list-style-type: none"> <li>• Restriction Digestion Master Mix in quadrant 3</li> <li>• Only when prompted: Random Primers and Labeling Master Mix               <ul style="list-style-type: none"> <li>Random Primers in quadrant 1</li> <li>Cy5 Labeling Master Mix in quadrant 2</li> <li>Cy3 Labeling Master Mix in quadrant 4</li> </ul> </li> </ul> |

- 1 Turn on the Bravo Platform CPAC Ultraflat heated/cooled Deck Pads on Positions 4 and 6, set to 4°C.
- 2 Prepare the Restriction Digestion Master Mix by mixing the components in [Table 51](#) through [Table 52](#), based on your microarray format.

**Table 51** Multiplier to calculate the volume of Restriction Digestion Master Mix (for 1-, 2-, and 4-pack microarrays)

| Components  | Per reaction (μL) | Total Volumes Needed*                                      | Volume to add per well of 384 deep well plate                              |
|---|-------------------|--|--|
| Nuclease-Free Water†                                    | 2.2               | $(2.2 \mu\text{L} \times N \times 2) + 11.7$               |  |
| 10× Restriction Enzyme Buffer†                          | 2.6               | $(2.6 \mu\text{L} \times N \times 2) + 13.9$               |  |
| BSA†  | 0.2               | $(0.2 \mu\text{L} \times N \times 2) + 1.1$                |  |
| Alu I†  | 0.5               | $(0.5 \mu\text{L} \times N \times 2) + 2.7$                |  |
| Rsa I†  | 0.5               | $(0.5 \mu\text{L} \times N \times 2) + 2.7$                |  |
| <b>Final volume of Restriction Digestion Master Mix</b> | <b>6</b>          | <b><math>(6 \mu\text{L} \times N \times 2) + 32</math></b> | <b><math>((6 \mu\text{L} \times N \times 2) + 24 \mu\text{L})/8</math></b> |

\* N is the number of experimental samples (8, 16, 24, 32, 40 or 48). Do not count reference samples.

† Included in the SureTag Complete DNA Labeling Kit and SureTag DNA Labeling Kit

**Table 52** Multiplier to calculate the volume of Restriction Digestion Master Mix (for 8-pack microarrays)

| Components  | Per reaction (μL) | Total Volumes Needed*                                      | Volume to add per well of 384 deep well plate                              |
|---|-------------------|--|--|
| Nuclease-Free Water†                                    | 4.1               | $(4.1 \mu\text{L} \times N \times 2) + 21.9$               |  |
| 10× Restriction Enzyme Buffer†                          | 1.3               | $(1.3 \mu\text{L} \times N \times 2) + 6.9$                |  |
| BSA†  | 0.1               | $(0.1 \mu\text{L} \times N \times 2) + 0.5$                |  |
| Alu I†  | 0.25              | $(0.25 \mu\text{L} \times N \times 2) + 1.3$               |  |
| Rsa I†  | 0.25              | $(0.25 \mu\text{L} \times N \times 2) + 1.3$               |  |
| <b>Final volume of Restriction Digestion Master Mix</b> | <b>6</b>          | <b><math>(6 \mu\text{L} \times N \times 2) + 32</math></b> | <b><math>((6 \mu\text{L} \times N \times 2) + 24 \mu\text{L})/8</math></b> |

\* N is the number of experimental samples (8, 16, 24, 32, 40 or 48). Do not count reference samples.

† Included in the SureTag Complete DNA Labeling Kit and SureTag DNA Labeling Kit

## 4 Sample Labeling on the Bravo Platform

### Step 1. Enzymatic Labeling

- 3 In a 384 deep well plate, add Restriction Digestion Master Mix to 8 wells in quadrant 3 (location B1, D1, F1, H1, J1, L1, N1, and P1). See [Figure 7](#).

|   | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 |
|---|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|
| A |   |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |
| B |   |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |
| C |   |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |
| D |   |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |
| E |   |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |
| F |   |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |
| G |   |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |
| H |   |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |
| I |   |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |
| J |   |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |
| K |   |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |
| L |   |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |
| M |   |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |
| N |   |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |
| O |   |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |
| P |   |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |

**Figure 7** 384 deep well plate for CGH+SNP Enzymatic Labeling containing Restriction Digestion Master Mix in quadrant 3

- 4 Spin the plate in a centrifuge for 30 seconds at  $6,000 \times g$  to drive the contents off the walls and to remove any bubbles that are stuck at the bottom of the well.
- 5 Put the 384 deep well plate at location 6 on the Bravo platform deck.
- 6 Start the `CGH+SNP_RestrictionDigestionLabelingProtocol_Enz` protocol run.

The Bravo platform adds the Restriction Digestion Master Mix to the empty working plate. The Bravo platform transfers the correct amount of gDNA from the 96-well plate that was prepared in [Chapter 3](#), “Sample Preparation for Bravo Platform” to the working plate.

- 7** When the Bravo platform pauses at the Protocol User Message task:
  - a** Remove the gDNA sample plate from location 5. If needed, store the leftover gDNA at 4°C for short term storage, or at -20°C for long term storage.
  - b** Remove the working plate from location 4.
  - c** Seal the plate and spin in a centrifuge for 30 seconds at 6,000 × g to drive the contents off the walls and lid.
  - d** Transfer the working plate to a thermal cycler.
  - e** Program the thermal cycler according to [Table 53](#) and run the program.

**Table 53** DNA restriction digestion using a thermal cycler

| Step   | Temperature | Time       |
|--------|-------------|------------|
| Step 1 | 37°C        | 2 hours    |
| Step 2 | 65°C        | 20 minutes |
| Step 3 | 4°C         | Hold       |

- 8** When the incubation is finished, remove the plate from the thermal cycler and spin the plate in a centrifuge for 30 seconds at 6,000 × g to drive the contents off the walls and lids.

Keep the plate at 4°C until ready to continue to the addition of [Random Primer](#) and Labeling Master Mix.

- 9** Use [Table 54](#) to calculate how much [Random Primer](#) to use.

**Table 54** Multiplier to calculate volume of [Random Primer](#) \*

| Format             | Total volume needed                                    | Volume to add per well of 384 deep well plate              |
|--------------------|--|--|
| 1-, 2-, and 4-pack | $(5 \mu\text{L} \times N \times 2) + 32 \mu\text{L}$   | $((5 \mu\text{L} \times N \times 2) + 24 \mu\text{L})/8$   |
| 8-pack             | $(2.5 \mu\text{L} \times N \times 2) + 32 \mu\text{L}$ | $((2.5 \mu\text{L} \times N \times 2) + 24 \mu\text{L})/8$ |

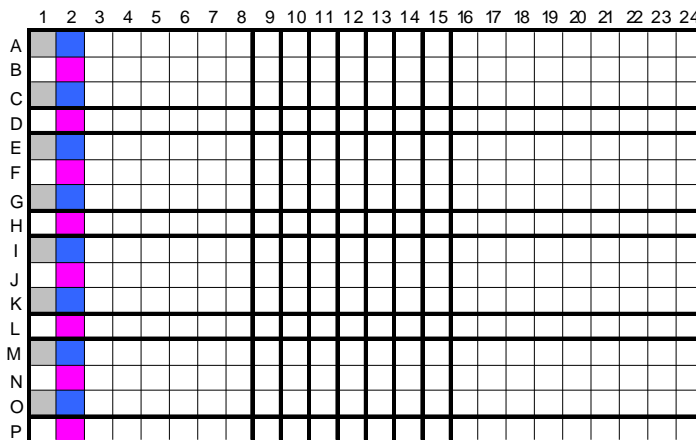
\* N is the number of experimental samples (8, 16, 24, 32, 40 or 48). Do not count reference samples.

- 10** Refer to [Table 54](#) for volumes. Add the [Random Primer](#) to 8 wells in quadrant 1 (location A1, C1, E1, G1, I1, K1, M1, and O1). See [Figure 8](#).

## 4 Sample Labeling on the Bravo Platform

### Step 1. Enzymatic Labeling

Make sure that no air bubbles are stuck at the bottom of the well. If needed, spin the plate in a centrifuge for 30 seconds at  $6,000 \times g$  to drive the contents off the walls.



**Figure 8** 384 deep well plate for Enzymatic labeling containing Random Primer (gray) in quadrant 1, Cy5 Labeling Master Mix (blue) in quadrant 2 and Cy3 Labeling Master Mix (pink) in quadrant 4

**11** Prepare one Cy3 and one Cy5 Labeling Master Mix by mixing the components in [Table 55](#) and [Table 56](#), based on your microarray format.

**12** In the 384 deep well plate:

- Refer to [Table 55](#) and [Table 56](#) for volumes.
- Add the Cy5 Labeling Master Mix to 8 wells in quadrant 2 (location A2, C2, E2, G2, I2, K2, M2, and O2).
- Add the Cy3 Labeling Master Mix to 8 wells in quadrant 4 (location B2, D2, F2, H2, J2, L2, N2, and P2).

See [Figure 8](#).

**13** Spin the plate in a centrifuge for 30 seconds at  $6,000 \times g$  to drive the contents off the walls.

Make sure that no air bubbles are stuck at the bottom of the well.

**14** Put the 384 deep well plate at location 6 on the Bravo platform deck.



**Table 55** Multiplier to calculate the volume of Labeling Master Mix (for 1-, 2-, and 4-pack microarrays)\*

| Component                                  | Per reaction (µL) | Total volumes needed   | Volume to add per well of 384 deep well plate                      |
|--|-------------------|--|--|
| 5× Reaction Buffer                         | 10                | $(10 \mu\text{L} \times N) + 16.8 \mu\text{L}$                 |  |
| 10× dNTPs <sup>†</sup>                     | 5                 | $(5 \mu\text{L} \times N) + 8.4 \mu\text{L}$                   |  |
| Cyanine 3-dUTP <i>or</i><br>Cyanine 5-dUTP | 3                 | $(3 \mu\text{L} \times N) + 5.1 \mu\text{L}$                   |  |
| Exo (-) Klenow                             | 1                 | $(1 \mu\text{L} \times N) + 1.7 \mu\text{L}$                   |  |
| <b>Final volume of Labeling Master Mix</b> | <b>19</b>         | <b><math>(19 \mu\text{L} \times N) + 32 \mu\text{L}</math></b> | <b><math>((19 \mu\text{L} \times N) + 24 \mu\text{L})/8</math></b> |

\* N is the number of experimental samples (8, 16, 24, 32, 40 or 48). Do not count reference samples.

† used as a 5× dNTP mix

**Table 56** Multiplier to calculate the volume of Labeling Master Mix (for 8-pack microarrays)

| Component                                  | Per reaction (µL) | Total volumes needed  | Volume to add per well of 384 deep well plate                       |
|--|-------------------|---|---|
| 5× Reaction Buffer                         | 5                 | $(5 \mu\text{L} \times N) + 16.8 \mu\text{L}$                   |   |
| 10× dNTPs                                  | 2.5               | $(2.5 \mu\text{L} \times N) + 8.4 \mu\text{L}$                  |   |
| Cyanine 3-dUTP <i>or</i><br>Cyanine 5-dUTP | 1.5               | $(1.5 \mu\text{L} \times N) + 5.1 \mu\text{L}$                  |   |
| Exo (-) Klenow                             | 0.5               | $(0.5 \mu\text{L} \times N) + 1.7 \mu\text{L}$                  |   |
| <b>Final volume of Labeling Master Mix</b> | <b>9.5</b>        | <b><math>(9.5 \mu\text{L} \times N) + 32 \mu\text{L}</math></b> | <b><math>((9.5 \mu\text{L} \times N) + 24 \mu\text{L})/8</math></b> |

**15** Remove the seal and transfer the working plate back to location 4 on the Bravo platform deck.

**16** Press the **Go** button to continue the **CGH+SNP\_RestrictionDigestionLabelingProtocol\_Enz** protocol run.

## 4 Sample Labeling on the Bravo Platform

### Step 1. Enzymatic Labeling

The Bravo platform adds the **Random Primer** to the working plate that contains the digested gDNA.

- 17** When the Bravo platform pauses at the Protocol User Message task:
- Remove the working plate from location 4.
  - Seal the plate and spin in a centrifuge for 30 seconds at  $6,000 \times g$  to drive the contents off the walls and lid.
  - Transfer the working plate to a thermal cycler.
  - Program the thermal cycler according to [Table 57](#) and run the program.

**Table 57** DNA denaturation using a thermal cycler

| Step   | Temperature | Time      |
|--------|-------------|-----------|
| Step 1 | 98°C        | 3 minutes |
| Step 2 | 4°C         | Hold      |

**18** Spin the plate in a centrifuge for 30 seconds at  $6,000 \times g$  to drive the contents off the walls and lid.

**19** Remove the seal and transfer the working plate back to location 4 on the Bravo platform deck.

**20** Click **Continue** in the VWorks software.

The Bravo platform adds the Labeling Master Mix to the digested gDNA.

#### NOTE

When the number of samples is 24 or greater, the Bravo platform runs out of tips before the end of the protocol run.

If you see the error message **Error in automatic tip operation**, put more tips into the Bravo platform. Go to **Tools > Tip State Editor**, and update the status of the tip boxes.

**21** When the protocol run is finished:

- Remove the working plate from location 4.
- Seal the plate and spin in a centrifuge for 30 seconds at  $6,000 \times g$  to drive the contents off the walls and lid.
- Transfer the working plate to a thermal cycler.
- Program the thermal cycler according to [Table 58](#) and run the program.

**Table 58** DNA labeling using a thermal cycler

| Step   | Temperature | Time       |
|--------|-------------|------------|
| Step 1 | 37°C        | 2 hours    |
| Step 2 | 65°C        | 10 minutes |
| Step 3 | 4°C         | Hold       |

**22** Turn off the Bravo Platform CPAC Ultraflat heated/cooled Deck Pads on Positions 4 and 6.

**23** Spin the plate in a centrifuge for 30 seconds at 6,000 × g to drive the contents off the walls and lid.

**24** Keep the plate at 4°C in the dark until ready to do “Step 2. Purification after Enzymatic Labeling” on page 92.

## Step 2. Purification after Enzymatic Labeling

In this step, the Bravo platform prepares the AutoScreen-96A Well plates, transfers the labeled DNA to the purification plate, then you collect the labeled purified DNA by centrifugation.

**Bravo Platform Protocol Used** CGH+SNP\_PurificationProtocol\_Enz

**Initial Deck Layout**

| Location | Content   |
|----------|---|
| 1        | Full tip box  |
| 4        | Agilent reservoir containing DNase/RNase-free distilled water |
| 7        | When prompted: 96-well plate containing the labeled gDNA      |
| 8        | After step 6: Pre-spun purification plate/wash plate sandwich |

Use the same centrifuge speed and length for all spinning steps (step 5, step 8, step 12 and step 14). If you spin only one plate, make sure that you counterbalance.

- 1 Get a **Full skirted 96-well PCR plate** to use as a wash plate, and label it as “Wash Plate”.  
The wash plate can be reused.
- 2 Get another 96-well PCR plate to use as a collection plate, and label it as “Collection Plate”.
- 3 Carefully remove the top and bottom seals of the purification plate. Once the bottom seal is removed, keep the plate on top of a wash plate. Do not allow the bottom surface to come in contact with laboratory bench top liners, wipes, or other materials.
- 4 Put the purification plate in a reusable wash plate.
- 5 Pre-spin the purification plate/wash plate sandwich in a centrifuge for 5 minutes at 910 × g.
- 6 Discard the flow-through from the wash plate and put the purification plate back on the same wash plate. Transfer the purification plate/wash plate sandwich to location 8 on the Bravo platform.

- 7** Start the CGH+SNP\_PurificationProtocol\_Enz protocol run. You are prompted to choose the microarray format.  
The Bravo platform adds water to the purification plate/wash plate sandwich.
- 8** When the Bravo platform pauses at the Protocol User Message task, remove the purification plate/wash plate sandwich from location 8 and spin again in a centrifuge for 5 minutes at  $910 \times g$ .
- 9** Discard the flow-through.
- 10** Transfer the purification plate to a sample collection plate and transfer the purification plate/sample collection plate sandwich to location 8 on the Bravo platform. Put the 96-well plate containing the labeled gDNA on location 7.
- 11** Click **Continue** in the VWorks software.  
The Bravo platform transfers 25  $\mu\text{L}$  of the labeled DNA to the purification plate/sample collection plate sandwich.
- 12** Remove the purification plate/sample collection plate sandwich from location 8 and spin in a centrifuge for 5 minutes at  $910 \times g$  to collect the purified labeled gDNA in the sample collection plate. The volume per sample will be  $\sim 19 \mu\text{L}$ .  
For 1-, 2-, and 4-pack microarray formats, return the purification plate/sample collection plate sandwich to location 8.

**CAUTION**

Make sure the plate is positioned in the deck in the same orientation as in the step before. Otherwise, the Cy5-labeled and Cy3-labeled samples will get mixed.

- 13** Click **Continue** in the VWorks software.  
The Bravo platform transfers the remaining 25  $\mu\text{L}$  of labeled DNA to the same purification plate/sample collection plate sandwich.
- 14** When the protocol run is finished, remove the purification plate/sample collection plate sandwich from location 8 and spin in a centrifuge for 5 minutes at  $910 \times g$  to collect the purified labeled gDNA in the sample collection plate.  
The recovered volume per sample will be approximately 19  $\mu\text{L}$ . The total recovered volume per sample will be approximately 38  $\mu\text{L}$ .

## 4 Sample Labeling on the Bravo Platform

### Step 2. Purification after Enzymatic Labeling

**15** Take 1.5  $\mu\text{L}$  of each sample to determine the yield and degree of labeling or specific activity. See “To determine yield, degree of labeling or specific activity” on page 95.

**16** For 4-pack and 8-pack microarrays, use a vacuum concentrator to concentrate the labeled samples:

- For 8-pack microarrays, concentrate to 8  $\mu\text{L}$ . If needed, concentrate the labeled samples to dryness and resuspend in 8  $\mu\text{L}$  of 1 $\times$ TE (pH 8.0).
- For 4-pack microarrays, concentrate to 24.5  $\mu\text{L}$ . If needed, concentrate the labeled samples to dryness and resuspend in 24.5  $\mu\text{L}$  of 1 $\times$ TE (pH 8.0).

As an alternative, transfer 24.5  $\mu\text{L}$  of each experimental and reference labeled DNA to a new plate that will be used for Hybridization preparation. In this case, not all labeled DNA will be hybridized, and consequently the signals will be lower.

#### CAUTION

Do not excessively dry the samples, or the pellets will become difficult to resuspend.

---

**17** Keep the plate at 4°C in the dark until ready for “Step 3. Preparation of Enzymatic Labeled gDNA for Hybridization” on page 97.

## To determine yield, degree of labeling or specific activity

Use the 8-channel NanoDrop 8000 or single channel NanoDrop 2000 UV-VIS Spectrophotometer to measure yield, degree of labeling or specific activity.

**1** From the main menu, select **MicroArray Measurement**, and then select **Sample Type** to be **DNA-50**.

**2** Use 1.5  $\mu\text{L}$  of TE to blank the instrument.

**3** Mix the samples.

You mix the samples before you measure to get a more accurate quantitation.

**4** Use 1.5  $\mu\text{L}$  of each labeled gDNA sample for quantitation. Measure the absorbance at  $A_{260}$  nm (DNA),  $A_{550}$  nm (cyanine 3), and  $A_{650}$  nm (cyanine 5).

**5** Calculate the Degree of Labeling or Specific Activity of the labeled gDNA:

$$\text{Degree of Labeling} = \frac{340 \times \text{pmol per } \mu\text{L dye}}{\text{ng per } \mu\text{L gDNA} \times 1000} \times 100\%$$

$$\text{Specific Activity}^* = \frac{\text{pmol per } \mu\text{L dye}}{\mu\text{g per } \mu\text{L gDNA}}$$

\*pmol dyes per  $\mu\text{g}$  gDNA

Note that the Specific Activity is Degree of Labeling divided by 0.034.

**6** Record the gDNA concentration ( $\text{ng}/\mu\text{L}$ ) for each sample. Calculate the yield as

$$\text{Yield } (\mu\text{g}) = \frac{\text{DNA concentration } (\text{ng}/\mu\text{L}) \times \text{Sample Volume } (\mu\text{L})}{1000 \text{ ng}/\mu\text{g}}$$

#### 4 Sample Labeling on the Bravo Platform

To determine yield, degree of labeling or specific activity

Refer to Table 59 for expected yield of labeled gDNA and specific activity after labeling and clean-up, when starting with high quality gDNA.

**Table 59** Expected Yield and Specific Activity after Labeling and Clean-up with the SureTag Complete DNA Labeling Kit or SureTag DNA Labeling Kit

| Input gDNA ( $\mu\text{g}$ ) | Yield ( $\mu\text{g}$ ) | Specific Activity of Cyanine-3 Labeled Sample ( $\text{pmol}/\mu\text{g}$ ) | Specific Activity of Cyanine-5 Labeled Sample ( $\text{pmol}/\mu\text{g}$ ) |
|------------------------------|-------------------------|---|---|
| 0.5 to 1                     | 12 to 16                | 19 to 30  | 15 to 25  |

Check that the Cy3 and Cy5 yield after labeling are the same. If not, refer to “Troubleshooting” on page 125.



## Step 3. Preparation of Enzymatic Labeled gDNA for Hybridization

In this step, the Bravo platform combines the Cy3 and Cy5 samples, adds the Hybridization Master Mix to the labeled purified DNA samples, and you incubate the sample in a thermal cycler.

### Bravo Platform Protocol Used

CGH+SNP\_HybridizationPrepProtocol\_Enz

### Initial Deck Layout

| Location | 1-pack microarray   | 2-pack microarray   | 4-pack and 8-pack microarray  |
|----------|---|---|---|
| 1        | Empty tip box   | Empty tip box   | Empty tip box   |
| 2        | Full tip box  | Full tip box  | Full tip box  |
| 4        | V&P Scientific Reservoir:<br><ul style="list-style-type: none"> <li>column 1: Hybridization Master Mix</li> <li>If number of samples &gt; 32, column 2: Hybridization Master Mix</li> </ul> | V&P Scientific Reservoir:<br><ul style="list-style-type: none"> <li>column 1: Hybridization Master Mix</li> </ul> | V&P Scientific Reservoir:<br><ul style="list-style-type: none"> <li>column 1: Hybridization Master Mix</li> </ul> |
| 5        |   | Tall Chimney PCR plate placed in a Full skirted 96-well PCR plate   |   |
| 7        | Deep-well plate   |   |   |
| 8        | When you are prompted: Working plate containing the labeled, purified DNA.  | When you are prompted: Working plate containing the labeled, purified DNA.  | Working plate containing the labeled, purified DNA.   |

### 1 Prepare the 100× aCGH Blocking Agent:

- a Add 135 µL of DNase/RNase-free distilled water to the vial containing lyophilized 10× aCGH Blocking Agent (included in the Oligo aCGH/ChIP-on-chip Hybridization Kit).

## 4 Sample Labeling on the Bravo Platform

### Step 3. Preparation of Enzymatic Labeled gDNA for Hybridization

- b** Mix briefly on a vortex mixer and leave at room temperature for 60 minutes to reconstitute the sample before use or storage.
- c** On the vial of lyophilized blocking agent, cross out “10×” and write “100×”. For labeled samples that will hybridize to CGH+SNP arrays, you make and use 100× of the blocking agent.

The 100× aCGH Blocking Agent can be prepared in advance and stored at -20°C.

- 2** Prepare the Hybridization Master Mix by mixing the components in the tables below according to the microarray format used.

**Table 60** Multiplier to calculate the volume of Hybridization Master Mix for 1-pack microarrays\*

| Component                                       | Per reaction (μL) | Total volume needed in column 1 if N ≤ 32                         | Additional volume needed in column 2 if N > 32                         |
|---|-------------------|---|--|
| 1×TE (pH 8.0)                                   | 131.8             | $(131.8 \mu\text{L} \times N) + 412.8 \mu\text{L}$                | $(131.8 \mu\text{L} \times (N-32)) + 412.8 \mu\text{L}$                |
| Human Cot-1 DNA                                 | 50                | $(50 \mu\text{L} \times N) + 156.6 \mu\text{L}$                   | $(50 \mu\text{L} \times (N-32)) + 156.6 \mu\text{L}$                   |
| 100× aCGH Blocking Agent†                       | 5.2               | $(5.2 \mu\text{L} \times N) + 16.3 \mu\text{L}$                   | $(5.2 \mu\text{L} \times (N-32)) + 16.3 \mu\text{L}$                   |
| 2× HI-RPM Hybridization Buffer†                 | 260               | $(260 \mu\text{L} \times N) + 814.3 \mu\text{L}$                  | $(260 \mu\text{L} \times (N-32)) + 814.3 \mu\text{L}$                  |
| <b>Final Volume of Hybridization Master Mix</b> | <b>447</b>        | <b><math>(447 \mu\text{L} \times N) + 1400 \mu\text{L}</math></b> | <b><math>(447 \mu\text{L} \times (N-32)) + 1400 \mu\text{L}</math></b> |

\* N is the number of experimental samples (8, 16, 24, 32, 40 or 48). Do not count reference samples.

† Included in the *Oligo aCGH/ChIP-on-chip Hybridization Kit*

## Step 3. Preparation of Enzymatic Labeled gDNA for Hybridization

**Table 61** Multiplier to calculate the volume of Hybridization Master Mix for 2-pack microarrays\*

| Component                                       | Per reaction (µL) | Total volume needed   |
|---|-------------------|---|
| 1×TE (pH 8.0)                                   | 29.4              | $(29.4 \mu\text{L} \times N) + 220.1 \mu\text{L}$                 |
| Human Cot-1 DNA                                 | 25                | $(25 \mu\text{L} \times N) + 187.2 \mu\text{L}$                   |
| 100× aCGH Blocking Agent†                       | 2.6               | $(2.6 \mu\text{L} \times N) + 19.5 \mu\text{L}$                   |
| 2× HI-RPM Hybridization Buffer†                 | 130               | $(130 \mu\text{L} \times N) + 973.3 \mu\text{L}$                  |
| <b>Final Volume of Hybridization Master Mix</b> | <b>187</b>        | <b><math>(187 \mu\text{L} \times N) + 1400 \mu\text{L}</math></b> |

\* N is the number of experimental samples (8, 16, 24, 32, 40 or 48). Do not count reference samples.

† Included in the Oligo aCGH/ChIP-on-chip Hybridization Kit

**Table 62** Multiplier to calculate the volume of Hybridization Master Mix for 4-pack microarrays\*

| Component                                       | Per reaction (µL) | Total volume needed  |
|---|-------------------|--|
| Human Cot-1 DNA                                 | 5                 | $(5 \mu\text{L} \times N) + 114.6 \mu\text{L}$                     |
| 100× aCGH Blocking Agent†                       | 1.1               | $(1.1 \mu\text{L} \times N) + 25.2 \mu\text{L}$                    |
| 2× HI-RPM Hybridization Buffer†                 | 55                | $(55 \mu\text{L} \times N) + 1260.2 \mu\text{L}$                   |
| <b>Final Volume of Hybridization Master Mix</b> | <b>61.1</b>       | <b><math>(61.1 \mu\text{L} \times N) + 1400 \mu\text{L}</math></b> |

\* N is the number of experimental samples (8, 16, 24, 32, 40 or 48). Do not count reference samples.

† Included in the Oligo aCGH/ChIP-on-chip Hybridization Kit

## 4 Sample Labeling on the Bravo Platform

### Step 3. Preparation of Enzymatic Labeled gDNA for Hybridization

**Table 63** Multiplier to calculate the volume of Hybridization Master Mix for 8-pack microarrays\*

| Component                                       | Per reaction (µL) | Total volume needed  |
|---|-------------------|--|
| 1×TE (pH 8.0)                                   | 4.05              | $(4.05 \mu\text{L} \times N) + 195.5 \mu\text{L}$                |
| Human Cot-1 DNA                                 | 2                 | $(2 \mu\text{L} \times N) + 96.6 \mu\text{L}$                    |
| 100× aCGH Blocking Agent†                       | 0.45              | $(0.45 \mu\text{L} \times N) + 21.7 \mu\text{L}$                 |
| 2× HI-RPM Hybridization Buffer†                 | 22.5              | $(22.5 \mu\text{L} \times N) + 1086.2 \mu\text{L}$               |
| <b>Final Volume of Hybridization Master Mix</b> | <b>29</b>         | <b><math>(29 \mu\text{L} \times N) + 1400 \mu\text{L}</math></b> |

\* N is the number of experimental samples (8, 16, 24, 32, 40 or 48). Do not count reference samples.

† Included in the [Oligo aCGH/ChIP-on-chip Hybridization Kit](#)

- 3 Add hybridization mix to the reservoir in location 4. Be careful not to generate bubbles.
  - For 1-pack and  $\leq 32$  samples, 2-pack, 4-pack and 8-pack: add to column 1.
  - For 1-pack and  $> 32$  samples: add to column 1 and 2.
- 4 Start the **CGH+SNP\_HybridizationPrepProtocol\_Enz** protocol run.

For 1-pack and 2-pack microarrays, the Bravo platform transfers the hybridization master mix to the empty deep-well or tall-chimney plates. Continue at [step 5](#).

For 4-pack and 8-pack microarrays, the Bravo platform combines the Cy5 and Cy3 labeled, purified samples and adds the hybridization master mix. Continue at [step 6](#).
- 5 For 1-pack and 2-pack microarrays:
  - a When the Bravo platform pauses at the Protocol User Message task, put the working plate that contains the labeled, purified DNA at location 8.
  - b Click **Continue** in the VWorks software.

The Bravo platform adds the Cy3 and Cy5 labeled, purified gDNA to the hybridization master mix.

## Step 3. Preparation of Enzymatic Labeled gDNA for Hybridization

**NOTE**

When the number of samples is greater than 40, the Bravo platform runs out of tips before the end of the protocol run.

If you see the error message **Error in automatic tip operation**, put more tips into the Bravo platform. Go to **Tools > Tip State Editor**, and update the status of the tip boxes.

- 6** When the protocol run is finished, remove, seal, spin, and transfer the deep-well plate from location 7, tall-chimney plate from location 5, or the PCR plate from location 8 to a thermal cycler. Program the thermal cycler according to [Table 64](#) and run the program.

For the 1-pack microarray deep-well plates, use an incubator that is compatible with deep-well plates, such as the Eppendorf ThermoStat (Eppendorf p/n 022670204 with deep-well plate block p/n 022670565) or BioShake iQ (Q.Instruments p/n 1808-0506).

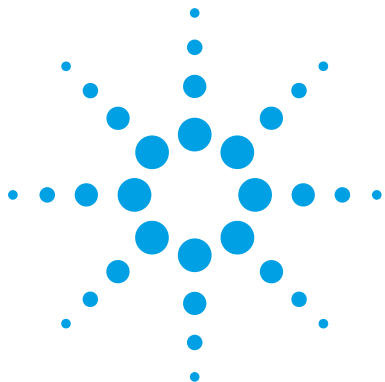
**Table 64** DNA preparation before hybridization

| Step   | Temperature | Time       |
|--------|-------------|------------|
| Step 1 | 98°C        | 3 minutes  |
| Step 2 | 37°C        | 30 minutes |

- 7** Spin the plate in a centrifuge for 30 seconds at  $6,000 \times g$  to drive the contents off the walls and lid.

The samples are ready for the Hybridization step.

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## 5 Microarray Processing

Hybridization 104

Microarray Wash 107

Microarray Scanning and Analysis 118

Microarray processing consists of hybridization, washing, and scanning.



## Hybridization

Familiarize yourself with the assembly and disassembly instructions for use with the Agilent microarray hybridization chamber and gasket slides. Please refer to the Agilent Microarray Hybridization Chamber User Guide (G2534-90001) for in-depth instructions on how to load samples, assemble and disassemble chambers, as well as other helpful tips. This user guide can be downloaded from the Agilent Web site at [www.agilent.com/chem/dnamanuals-protocols](http://www.agilent.com/chem/dnamanuals-protocols).

Before you begin, make sure you read and understand “Microarray Handling Tips” on page 137.



## Step 1. Prepare the hybridization assembly

- 1 Load a clean gasket slide into the Agilent SureHyb chamber base with the gasket label facing up and aligned with the rectangular section of the chamber base. Ensure that the gasket slide is flush with the chamber base and is not ajar.
- 2 Slowly dispense hybridization sample mixture onto the gasket well in a “drag and dispense” manner:
  - 490  $\mu\text{L}$  (for 1-pack microarray)
  - 245  $\mu\text{L}$  (for 2-pack microarray)
  - 100  $\mu\text{L}$  (for 4-pack microarray)
  - 40  $\mu\text{L}$  (for 8-pack microarray)

For multi-pack microarray formats (2-pack, 4-pack or 8-pack microarray), load all gasket wells before you load the microarray slide. For multi-pack formats, refer to “[Agilent Microarray Layout and Orientation](#)” on page 138.

### CAUTION

Keep the temperature of hybridization sample mixtures as close to 37°C as possible. To do this, process them in small batches and/or put them on a heat block, thermal cycler or in an oven.

- 3 Put a microarray slide “active side” down onto the gasket slide, so the numeric barcode side is facing up and the “Agilent”-labeled barcode is facing down. Assess that the sandwich-pair is properly aligned.
- 4 Put the SureHyb chamber cover onto the sandwiched slides and slide the clamp assembly onto both pieces.
- 5 Hand-tighten the clamp firmly onto the chamber.
- 6 Vertically rotate the assembled chamber to wet the slides and assess the mobility of the bubbles. Tap the assembly on a hard surface if necessary to move stationary bubbles.

## Step 2. Hybridize

- 1 Load each assembled chamber into the oven rotator rack. Start from the center of the rack (position 3 or 4 when counting from the left). Set your hybridization rotator to rotate at 20 rpm.
- 2 Hybridize at 65°C for ULS and 67°C for Enzymatic Labeling for:
  - 24 hours for blood, cell and tissue samples (4-pack and 8-pack microarrays)
  - 40 hours for blood, cell and tissue samples (1-pack and 2-pack microarrays)
  - 40 hours for FFPE samples (1-pack, 2-pack, 4-pack and 8-pack microarrays)

### CAUTION

If you are not loading all the available positions on the hybridization rotator rack, be sure to *balance* the loaded hybridization chambers on the rack similar to a centrifuge to prevent unnecessary strain on the oven motor.

---

### CAUTION

You must calibrate the hybridization oven regularly for accuracy of the collected data. Refer to *Agilent G2545A Hybridization Calibration Procedure* (p/n G2545-90002) for more information.

---

For more information on the effects of hybridization temperature and time, as well as the rotation speed on the final microarray results, please refer to the application note titled “60-mer Oligo-Based Comparative Genomic Hybridization” (publication 5989-4848EN) from the Agilent Web site at [www.agilent.com/chem/dnaapplications](http://www.agilent.com/chem/dnaapplications).

### NOTE

The [Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 2](#) that is used in the microarray wash procedure needs to be warmed overnight. While you are waiting for the microarray slides to hybridize, do the steps in “[Step 1. Prewarm Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 2 \(overnight\)](#)” on page 108.

---

## Microarray Wash

### NOTE

The microarray wash procedure must be done in environments where ozone levels are 5 ppb or less. For Scanner C and Scanner B, if ozone levels are between 5 to 10 in your laboratory, use the Agilent Ozone Barrier Slide Cover. SureScan microarray scanner uses a slide holder with a built-in ozone barrier. If ozone levels exceed 10 ppb, use the [Stabilization and Drying Solution](#) together with the ozone barrier.

You can also use Carbon Loaded Non-woven Filters to remove ozone from the air. These filters can be installed in either your HVAC system, or as part of small Ozone Controlled Enclosures. These free-standing enclosures can be installed either on a lab bench or as a walk-in room within your lab. These products are available through filter suppliers listed in Agilent Technical Note 5989-0875EN.

Before you begin, determine which wash procedure to use:

**Table 65** Wash procedure to follow

| Ozone level in your lab | Wash Procedure   | Ozone-Barrier Slide Cover |
|-------------------------|--|---------------------------|
| < 5 ppb                 | "Wash Procedure A (without Stabilization and Drying Solution)" on page 111 | No                        |
| > 5 ppb < 10 ppb        | "Wash Procedure A (without Stabilization and Drying Solution)" on page 111 | Yes                       |
| > 10 ppb                | "Wash Procedure B (with Stabilization and Drying Solution)" on page 113    | Yes                       |

### CAUTION

Do not use detergent to wash the staining dishes as some detergents may leave fluorescent residue on the dishes. If you do, you must ensure that all traces are removed by thoroughly rinsing with [Milli-Q ultrapure water](#).

- Always use clean equipment when conducting the wash procedures.
- Use only dishes that are designated and dedicated for use in Agilent oligo aCGH experiments.

## **Step 1. Prewarm Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 2 (overnight)**

The temperature of Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 2 must be at 37°C for optimal performance.

- 1 Add the volume of buffer required to a **Sterile storage bottle** and warm overnight in an incubator or circulating water bath set to 37°C.
- 2 Put a slide-staining dish with a lid, a **1.5 L glass dish**, and one to two liters of **Milli-Q ultrapure water** in an incubator or water bath set at 37°C to warm overnight.

## **Step 2. Wash with Milli-Q ultrapure water**

Rinse slide-staining dishes, slide racks and stir bars thoroughly with high-quality **Milli-Q ultrapure water** before use and in between washing groups.

- 1 Run copious amounts of **Milli-Q ultrapure water** through the slide-staining dishes, slide racks and stir bars.
- 2 Empty out the water collected in the dishes at least five times.
- 3 Repeat **step 1** and **step 2** until all traces of contaminating material are removed.

### Step 3. Clean with Acetonitrile (Wash Procedure B Only)

Acetonitrile wash removes any remaining residue of [Stabilization and Drying Solution](#) from slide-staining dishes, slide racks and stir bars that were used in previous experiments with “[Wash Procedure B \(with Stabilization and Drying Solution\)](#)” on page 113.

**WARNING**

Do **Acetonitrile** washes in a vented fume hood. **Acetonitrile** is highly flammable and toxic.

- 1 Add the slide rack and stir bar to the slide-staining dish, and transfer to a magnetic stir plate.
- 2 Fill the slide-staining dish with 100% [Acetonitrile](#).
- 3 Turn on the magnetic stir plate and adjust the speed to a setting of 4 (medium speed).
- 4 Wash for 5 minutes at room temperature.
- 5 Discard the [Acetonitrile](#) as is appropriate for your site.
- 6 Repeat [step 1](#) through [step 5](#).
- 7 Air dry everything in the vented fume hood.
- 8 Continue with the [Milli-Q ultrapure water](#) wash as previously instructed.

### Step 4. Prewarm Stabilization and Drying Solution (Wash Procedure B Only)

The [Stabilization and Drying Solution](#) contains an ozone scavenging compound dissolved in [Acetonitrile](#). The compound in solution is present in saturating amounts and may precipitate from the solution under normal storage conditions. If the solution shows visible precipitation, warming of the solution will be necessary to redissolve the compound. Washing slides using [Stabilization and Drying Solution](#) showing visible precipitation will have profound adverse affects on microarray performance.

## 6 Microarray Processing

### Step 4. Prewarm Stabilization and Drying Solution (Wash Procedure B Only)

#### WARNING

The **Stabilization and Drying Solution** is a flammable liquid. Warming the solution will increase the generation of ignitable vapors. Use gloves and eye/face protection in every step of the warming procedures.

---

#### WARNING

Do not use a hot plate, oven, an open flame or a microwave. Do not increase temperature rapidly. Warm and mix the material away from ignition sources.

---

#### WARNING

Failure to follow the outlined process will increase the potential for fire, explosion, and possible personal injury.

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- 1 Put a clean magnetic stir bar into the **Stabilization and Drying Solution** bottle and recap.
- 2 Partially fill a plastic bucket with hot water at approximately 40°C to 45°C (for example from a hot water tap).
- 3 Put the **Stabilization and Drying Solution** bottle into the hot water in the plastic bucket.
- 4 Put the plastic bucket on a magnetic stirrer (*not a hot-plate*) and stir.
- 5 The hot water cools to room temperature. If the precipitate has not all dissolved replenish the cold water with hot water.
- 6 Repeat [step 5](#) until the solution is clear.
- 7 After the precipitate is completely dissolved, allow the solution to equilibrate to room temperature prior to use.

#### CAUTION

Do not filter the **Stabilization and Drying Solution**, or the concentration of the ozone scavenger may vary.

---

## Step 5. Wash microarrays

### Wash Procedure A (*without Stabilization and Drying Solution*)

Always use fresh Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 1 and Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 2 for each wash group (up to five slides).

Table 66 lists the wash conditions for the Wash Procedure A without Stabilization and Drying Solution.

**Table 66** Wash conditions

|             | Dish | Wash buffer                                   | Temperature      | Time      |
|-------------|------|---|------------------|-----------|
| Disassembly | #1   | Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 1 | Room temperature |           |
| 1st wash    | #2   | Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 1 | Room temperature | 5 minutes |
| 2nd wash    | #3   | Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 2 | 37°C             | 1 minute  |

- 1 Completely fill slide-staining dish #1 with Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 1 at room temperature.
- 2 Prepare dish #2:
  - a Put a slide rack into slide-staining dish #2.
  - b Add a magnetic stir bar. Fill slide-staining dish #2 with enough Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 1 at room temperature to cover the slide rack.
  - c Put this dish on a magnetic stir plate.

## 6 Microarray Processing

### Step 5. Wash microarrays

- 3 Prepare dish #3:
  - a Put the prewarmed 1.5 L glass dish on a magnetic stir plate with heating element.
  - b Put the slide-staining dish #3 into the 1.5 L glass dish.
  - c Fill the 1.5 L glass dish with pre-warmed Milli-Q ultrapure water.
  - d Fill the slide-staining dish #3 approximately three-fourths full with Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 2 (warmed to 37°C).
  - e Add a magnetic stir bar.
  - f Turn on the heating element and maintain temperature of Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 2 at 37°C. Monitor with a thermometer.
- 4 Remove one hybridization chamber from the incubator and resume rotation of the others. Record whether bubbles formed during hybridization and if all bubbles are rotating freely.
- 5 Prepare the hybridization chamber disassembly.
  - a Put the hybridization chamber assembly on a flat surface and loosen the thumbscrew, turning counter-clockwise.
  - b Slide off the clamp assembly and remove the chamber cover.
  - c With gloved fingers, remove the microarray-gasket sandwich from the chamber base by lifting one end and then grasping in the middle of the long sides. Keep the microarray slide numeric barcode facing up as you quickly transfer the sandwich to slide-staining dish #1.
  - d Without letting go of the slides, submerge the microarray-gasket sandwich into slide-staining dish #1 containing Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 1.
- 6 With the sandwich completely submerged in Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 1, pry the sandwich open from the barcode end only:
  - a Slip one of the blunt ends of the forceps between the slides.
  - b Gently twist the forceps to separate the slides.
  - c Let the gasket slide drop to the bottom of the staining dish.
  - d Remove the microarray slide, grasp it from the upper corners with thumb and forefinger, and quickly put into slide rack in the slide-staining dish #2 containing Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 1 at room temperature. Minimize exposure of the slide to air. *Touch only the barcode portion of the microarray slide or its edges!*



- 7 Repeat [step 4](#) through [step 6](#) for up to four additional slides in the group. A maximum of five disassembly procedures yielding five microarray slides is advised at one time in order to facilitate uniform washing.
- 8 When all slides in the group are put into the slide rack in slide-staining dish #2, stir at 350 rpm for 5 minutes. Adjust the setting to get good but not vigorous mixing.
- 9 Wash the slides in [Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 2](#):
  - a Transfer slide rack to slide-staining dish #3, which contains [Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 2](#) at 37°C:
  - a Activate the magnetic stirrer.
  - b Wash microarray slides for at least 1 minute and no more than 2 minutes. Adjust the setting to get thorough mixing without disturbing the microarray slides.
- 10 Slowly remove the slide rack trying to minimize droplets on the slides. It should take 5 to 10 seconds to remove the slide rack.
- 11 Discard used [Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 1](#) and [Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 2](#).
- 12 Repeat [step 1](#) through [step 11](#) for the next group of five slides using fresh [Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 1](#) and [Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 2](#) warmed to 37°C.
- 13 Scan slides immediately to minimize the impact of environmental oxidants on signal intensities. If necessary, store slides in orange slide boxes in a N<sub>2</sub> purge box, in the dark.

### **Wash Procedure B (*with Stabilization and Drying Solution*)**

Cyanine reagents are susceptible to degradation by ozone. Use this wash procedure if the ozone level exceeds 10 ppb in your laboratory.

Always use fresh [Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 1](#) and [Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 2](#) for each wash group (up to five slides).

The [Acetonitrile](#) (dish #4) and [Stabilization and Drying Solution](#) (dish #5) below may be reused for washing up to 4 batches of 5 slides (total 20 slides) in one experiment. Do not pour the [Stabilization and Drying Solution](#) back in the bottle.

**WARNING**

**The Stabilization and Drying Solution must be set-up in a fume hood. Put the Wash Buffer 1 and Wash Buffer 2 set-up areas close to, or preferably in, the same fume hood. Use gloves and eye/face protection in every step of the washing procedure.**

Table 67 lists the wash conditions for the Wash Procedure B with **Stabilization and Drying Solution**.

**Table 67** Wash conditions

|                   | Dish | Wash Buffer                                   | Temperature      | Time       |
|-------------------|------|---|------------------|------------|
| Disassembly       | #1   | Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 1 | Room temperature |            |
| 1st wash          | #2   | Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 1 | Room temperature | 5 minutes  |
| 2nd wash          | #3   | Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 2 | 37°C             | 1 minute   |
| Acetonitrile wash | #4   | Acetonitrile                                  | Room temperature | 10 seconds |
| 3rd wash          | #5   | Stabilization and Drying Solution             | Room temperature | 30 seconds |

- 1 In the fume hood, fill slide-staining dish #4 approximately three-fourths full with **Acetonitrile**. Add a magnetic stir bar and put this dish on a magnetic stir plate.
- 2 In the fume hood, fill slide-staining dish #5 approximately three-fourths full with **Stabilization and Drying Solution**. Add a magnetic stir bar and put this dish on a magnetic stir plate.
- 3 Do step 1 through step 9 in “Wash Procedure A (without Stabilization and Drying Solution)” on page 111.
- 4 Remove the slide rack from **Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 2** and tilt the rack slightly to minimize wash buffer carry-over. Quickly transfer the slide rack to slide-staining dish #4 containing **Acetonitrile**, and stir at 350 rpm for 10 seconds.
- 5 Transfer slide rack to slide-staining dish #5 filled with **Stabilization and Drying Solution**, and stir at 350 rpm for 30 seconds.

- 6 Slowly remove the slide rack trying to minimize droplets on the slides. It should take 5 to 10 seconds to remove the slide rack.
- 7 Discard used Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 1 and Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 2.

**NOTE**

The Acetonitrile and the Stabilization and Drying Solution may be reused for washing of up to four batches of five slides (that is, total 20 microarray slides) in one experiment. Pour the Stabilization and Drying Solution to a different marked bottle, and protect from light with other flammables. After each use, rinse the slide rack and the slide-staining dish that were in contact with the Stabilization and Drying Solution with Acetonitrile followed by a rinse in Milli-Q ultrapure water.

---

- 8 Repeat step 1 through step 7 for the next group of five slides using fresh Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 1 and Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 2 prewarmed to 37°C.
- 9 Dispose of Acetonitrile and Stabilization and Drying Solution as flammable solvents.

## Step 6. Put slides in a slide holder

Scan slides immediately to minimize impact of environmental oxidants on signal intensities. If necessary, store slides in the original slide boxes in a N<sub>2</sub> purge box, in the dark.

### For SureScan microarray scanner

- 1 Carefully place the end of the slide without the barcode label onto the slide ledge.
- 2 Gently lower the microarray slide into the slide holder. Make sure that the active microarray surface (with “Agilent”-labeled barcode) faces up, toward the slide cover.
- 3 Close the plastic slide cover, pushing on the tab end until you hear it click.

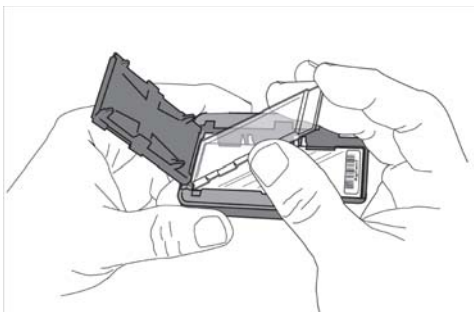
For more detailed instruction, refer to the *Agilent G4900DA SureScan Microarray Scanner System User Guide*.



**Figure 9** Slide in slide holder for SureScan microarray scanner

### For Agilent Scanner B or C

- In environments in which the ozone level exceeds 5 ppb, immediately put the slides with active microarray surface (“Agilent”-labeled barcode) facing up in a slide holder. Make sure that the slide is not caught up on any corner. Put an ozone-barrier slide cover on top of the array as shown in [Figure 10](#). Refer to the *Agilent Ozone-Barrier Slide Cover User Guide* (p/n G2505-90550), included with the slide cover, for more information.



**Figure 10** Inserting the ozone-barrier slide cover

- In environments in which the ozone level is below 5 ppb, put the slides with Agilent barcode facing up in a slide holder.

## Microarray Scanning and Analysis

### Step 1. Scan the microarray slides

A SureScan or Agilent C microarray scanner is required for G3 microarrays.

Agilent provides support for Agilent microarrays scanned on select non-Agilent scanners. Please see “Feature Extraction Compatibility Matrix for Non Agilent scanners” for scanner compatibility and settings ([http://www.chem.agilent.com/Library/usermanuals/Public/G1662-90043\\_ScannerCompatibilityMatrix.pdf](http://www.chem.agilent.com/Library/usermanuals/Public/G1662-90043_ScannerCompatibilityMatrix.pdf)).

*However, Agilent can guarantee the quality of data only if the data comes from Agilent microarrays scanned on Agilent scanners.*

#### Agilent SureScan Microarray Scanner

- 1 Put assembled slide holders into the scanner cassette.
- 2 Select **Protocol AgilentG3\_CGH** for G3 microarrays. Select **Protocol AgilentHD\_CGH** for HD microarrays.
- 3 Verify that the Scanner status in the main window says Scanner Ready.
- 4 Click **Start Scan**.

#### Agilent C Scanner Settings

- 1 Put assembled slide holders with or without the ozone-barrier slide cover into scanner carousel.
- 2 Select Start Slot *m* End Slot *n* where the letter *m* represents the Start slot where the first slide is located and the letter *n* represents the End slot where the last slide is located.
- 3 Select **Profile AgilentG3\_CGH** for G3 microarrays. Select **Profile AgilentHD\_CGH** for HD microarrays.
- 4 Verify scan settings. See [Table 68](#).

**Table 68** C Scanner Scan Settings

|                                | For HD Microarray Formats    | For G3 Microarray Formats    |
|--------------------------------|------------------------------|------------------------------|
| <b>Dye channel</b>             | R+G ( <i>red and green</i> ) | R+G ( <i>red and green</i> ) |
| <b>Scan region</b>             | Agilent HD (61 x 21.6 mm)    | Agilent HD (61 x 21.6 mm)    |
| <b>Scan resolution</b>         | 5 µm                         | 3 µm                         |
| <b>Tiff file dynamic range</b> | 16 bit                       | 16 bit                       |
| <b>Red PMT gain</b>            | 100%                         | 100%                         |
| <b>Green PMT gain</b>          | 100%                         | 100%                         |
| <b>XDR</b>                     | <No XDR>                     | <No XDR>                     |

- 5** Check that **Output Path Browse** is set for desired location.
- 6** Verify that the Scanner status in the main window says Scanner Ready.
- 7** Click **Scan Slot *m-n*** on the Scan Control main window where the letter *m* represents the Start slot where the first slide is located and the letter *n* represents the End slot where the last slide is located.

### Agilent B Scanner Settings

Agilent Scanner Control software v7.0.03 is recommended for 5 µm scans of HD format microarrays.

- 1** Put assembled slide holders, with or without the ozone-barrier slide cover, into scanner carousel.
- 2** Verify Default Scan Settings (click **Settings > Modify Default Settings**).

**Table 69** B Scanner Scan Settings

|                        | For HD Microarray Formats |
|------------------------|---------------------------|
| Scan region            | Scan Area (61 x 21.6 mm)  |
| Scan resolution (µm)   | 5                         |
| eXtended Dynamic range | (cleared)                 |
| Dye channel            | Red&Green                 |
| Red PMT                | 100%                      |
| Green PMT              | 100%                      |

## 6 Microarray Processing

### Step 2. Analyze microarray image

- 3 Select settings for the automatic file naming.
  - **Prefix1** is set to **Instrument Serial Number**.
  - **Prefix2** is set to **Array Barcode**.
- 4 Verify that the Scanner status in the main window says **Scanner Ready**.
- 5 Click **Scan Slot *m-n*** on the Scan Control main window where the letter *m* represents the Start slot where the first slide is located and the letter *n* represents the End slot where the last slide is located.

## Step 2. Analyze microarray image

- After scanning is completed, extract features and analyze.

Feature extraction is the process by which data is extracted from the scanned microarray image (.tif) and translated into log ratios, allowing researchers to identify aberrations in their samples.

Agilent provides Feature Extraction software as a standalone program and as an integral part of CytoGenomics software (Windows version only).

- Use the Windows version of Agilent CytoGenomics for automated and streamlined analysis of human samples. During the extraction and analysis process, Agilent CytoGenomics generates feature extraction files, QC and aberration reports.
- To use Agilent CytoGenomics on a Mac computer, first use Feature Extraction on a computer that is running Windows to extract features. Feature Extraction does not run on Mac computers.
- For non-human samples, use Feature Extraction (available for Windows only) to extract features, and then use Agilent Genomic Workbench to run an analysis workflow on the extracted features.

### Microarray QC Metrics

These metrics are only appropriate for samples analyzed with Agilent CGH microarrays by following the standard operational procedures provided in this user guide. These metrics are reported in the Feature Extraction QC report generated by Feature Extraction (standalone or as included in the Agilent CytoGenomics software). They can be used to assess the relative data quality from a set of microarrays in an experiment. In some cases, they can indicate potential processing errors that have occurred or suggest that the data from



particular microarrays might be compromised. Many factors can influence the range of these metrics, including the microarray format (1-pack, 2-pack, 4-pack or 8-pack), biological sample source, quality of starting gDNA, experimental processing, scanner sensitivity, and image processing. The value guidelines presented below represent the thresholds that Agilent has observed when analyzing samples using this protocol.

To achieve a high SNP call rate and accuracy when processing SurePrint G3 CGH+SNP microarrays, make sure the DLRSD is <0.2.

**Table 70** QC metric thresholds for ULS labeling

|                  | <b>Blood and Cell Samples</b> | <b>Tissue Samples</b> | <b>FFPE Samples</b> |
|------------------|-------------------------------|-----------------------|---------------------|
| BGNoise          | <15                           | <15                   | <15                 |
| Signal Intensity | >90                           | >90                   | >90                 |
| Signal to Noise  | >20                           | >20                   | >10                 |
| Reproducibility  | <0.2                          | <0.2                  | <0.2                |
| DLRSD            | <0.2                          | <0.3                  | <0.4                |

**Table 71** QC metric thresholds for Enzymatic labeling

| <b>Metric</b>    | <b>Excellent</b> | <b>Good</b> | <b>Evaluate</b> |
|------------------|------------------|-------------|-----------------|
| BGNoise          | < 10             | 10 to 20    | > 20            |
| Signal Intensity | > 150            | 50 to 150   | < 50            |
| Signal to Noise  | > 100            | 30 to 100   | < 30            |
| Reproducibility  | < 0.05           | 0.05 to 0.2 | > 0.2           |
| DLRSD            | < 0.2            | 0.2 to 0.3  | > 0.3           |

## 6 Microarray Processing

### Step 2. Analyze microarray image



**Figure 11** Feature Extraction QC Report, page 1

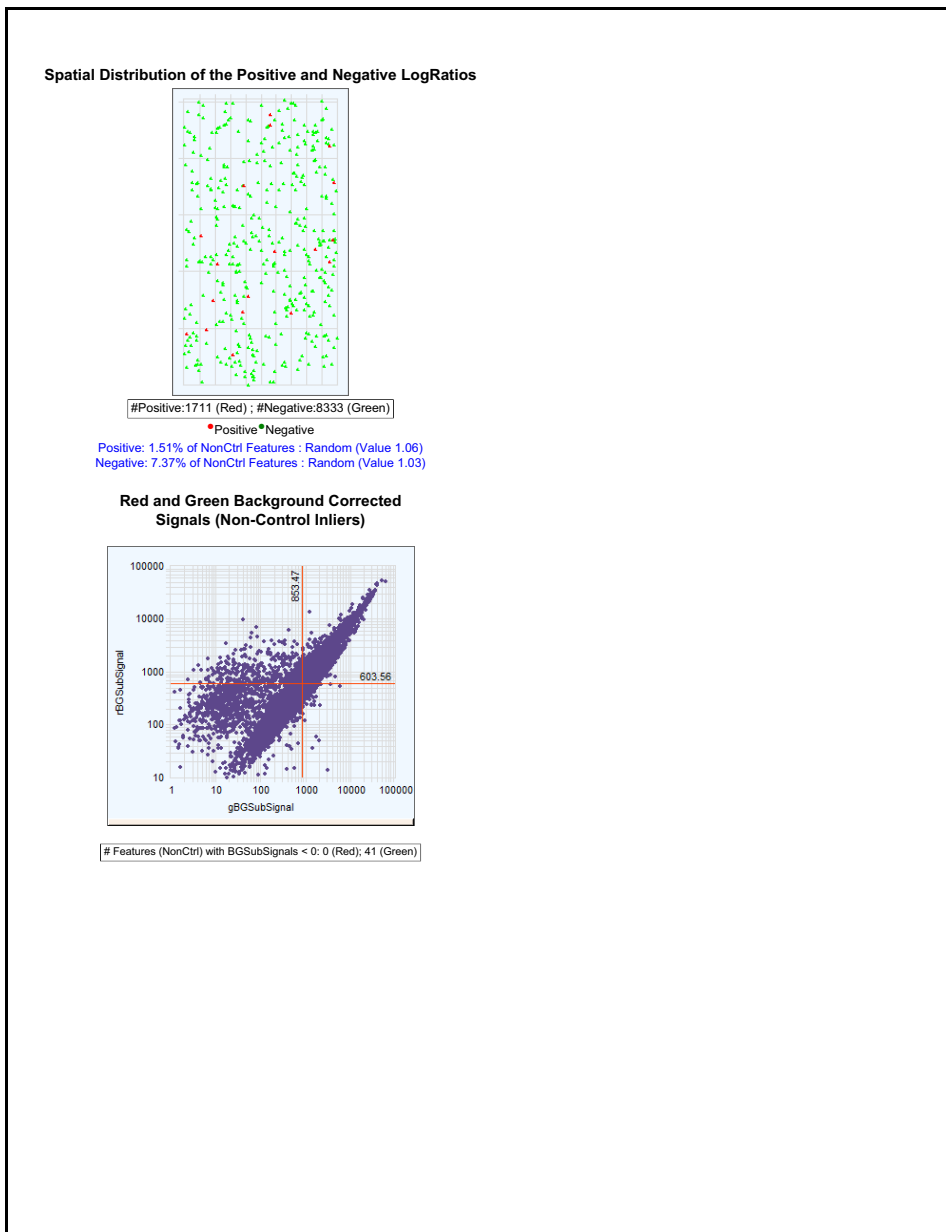


Figure 12 Feature Extraction QC Report, page 2

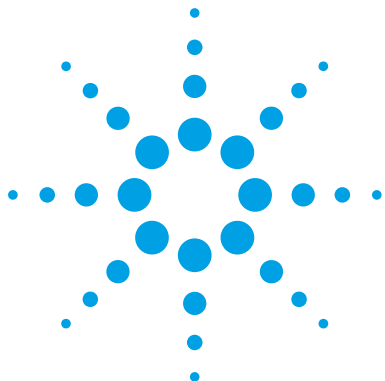
### Step 3. Download Agilent Reference Genotype File

To analyze your data when you have used the [Human Reference DNA \(Male and Female\)](#) and CGH+SNP microarrays with Agilent CytoGenomics 2.0 or Genomic Workbench 6.5 or higher, you need to get the Agilent Reference Genotype File (Male and Female) from Agilent.

The Reference Genotype File is included with Agilent CytoGenomics 2.7.

- 1 Go to <http://www.genomics.agilent.com/article.jsp?pageId=3299>.
- 2 Click the **Download** link for **Agilent Reference Genotype Files (Male and Female)**.
- 3 Click **Save** to save the files.

To load the Agilent Reference Genotype Files (Male and Female), refer to the user guide for Agilent CytoGenomics or Agilent Genomic Workbench.



## 7 Troubleshooting

- If you have a low OD260/230 or OD260/280 value 126
- If you have poor sample quality due to residual RNA 126
- If you get poor sample quality due to degradation 127
- If the estimated concentration is too high or low 128
- If you have low specific activity or degree of labeling not due to poor sample quality 129
- If you have low yield not due to poor sample quality 129
- If you have post-labeling signal loss 130
- If you have high BGNoise values 131
- If you have poor reproducibility 131

This chapter contains potential causes for above-threshold DLRSD (Derivative Log Ratio Standard Deviation). A poor DLRSD score reflects high probe-to-probe log ratio noise.

For troubleshooting information for the Bravo platform, refer to the *Bravo Platform User Guide* (G5409-90004) and the *VWorks Software User Guide* (G5415-90002).



#### If you have a low OD260/230 or OD260/280 value

A low OD260/230 value can indicate contaminants, such as residual salt or organic solvents (which would inhibit enzyme). A low OD260/280 value indicates residual protein. Either condition can result in low specific activity (pmol dye/ $\mu$ g DNA) or Degree of Labeling. See “To determine yield, degree of labeling or specific activity” on page 63, page 77 or page 95.

- ✓ Repurify the DNA using the Qiagen DNeasy protocol. See “DNA Isolation” on page 27. This procedure includes a proteinase K treatment.
- ✓ If you must do a phenol/chloroform DNA extraction, do not get too close to the interface.  

Phenol has an absorbance maximum of 270–275 nm, which is close to that of DNA. Phenol contamination mimics both higher purity and higher yields, because of an upward shift in the OD260 value.
- ✓ Make sure to calibrate the spectrophotometer with the appropriate buffer.
- ✓ The ULS labeling is very sensitive to salt contamination. Use 80% EtOH instead of AW2 in the DNA extraction step and elute in water.
- ✓ The ULS Labeling also labels proteins and RNA that compete for dye. Make sure that the DNA is free of proteins and RNA. See “DNA Isolation” on page 27.

#### If you have poor sample quality due to residual RNA

The input amount of DNA for the experimental sample must be the same as for the reference sample. RNA absorbs at the same wavelength as DNA. Therefore, RNA-contaminated sample can result in a DNA overestimation.

- ✓ Repurify the DNA using the Qiagen DNeasy protocol. See “DNA Isolation” on page 27. This procedure includes a RNase A treatment.
- ✓ The ULS labeling also labels RNA that will hybridize to the probe.

## If you get poor sample quality due to degradation

For non-FFPE samples: On a 1 to 1.5% agarose gel, intact gDNA should appear as a compact, high-molecular weight band with no lower molecular weight smears. Degraded DNA results in biased labeling.

- ✓ Check DNA on a 1 to 1.5% agarose gel. If DNA that was isolated from cells, blood or frozen tissue is degraded, then repurify the DNA using the Qiagen DNeasy protocol. See “DNA Isolation” on page 27.
- ✓ Make sure that the DNA is not over-fragmented prior to labeling. Possible causes are incorrect temperature or length of incubation at 95°C for ULS or 98°C for Enzymatic Labeling, or evaporation (use a thermal cycler with heated lid). Make sure most of the heat fragmented products are between 1000 and 3000 bases in length.

## 7 Troubleshooting

### If the estimated concentration is too high or low

#### If the estimated concentration is too high or low

The input amount of DNA for the experimental sample must be the same as for the reference sample. Precipitated DNA or DNA that is at a very high concentration cannot be quantitated accurately.

Contaminants such as organic solvents and RNA also absorb at 260 nm, which results in an inaccurate DNA quantitation.

- ✓ Make sure that the gDNA is completely in solution by pipetting up and down. If needed, incubate at 37°C for 30 minutes. If the gDNA concentration is > 350 ng/μL, dilute 1:2 in water (or any of the recommended buffers) for ULS labeling, or [Buffer AE](#) or [1×TE \(pH 8.0\)](#) for Enzymatic labeling. Quantitate again to make sure quantitation is accurate.
- ✓ Different DNA isolation methods can create different quantitation artifacts, the risk of assay noise is higher when the experimental and reference DNA samples are isolated from different sources. If you used a spectrophotometer (such as the Nanodrop) for the initial measurement, also use a double-stranded DNA-based fluorometer (such as the Qubit) to verify.
- ✓ If needed, repurify the DNA using the Qiagen DNeasy protocol. See “[DNA Isolation](#)” on page 27.



If you have low specific activity or degree of labeling not due to poor sample quality

## If you have low specific activity or degree of labeling not due to poor sample quality

Low specific activity or degree of labeling can result from sub-optimal labeling conditions such as Cyanine dUTP with too many freeze thaws, enzyme degradation due to being left warm for too long, wrong temperatures or times, volume mistakes, or too much exposure to light or air.

- ✓ Store Cyanine dUTP at -20°C. Keep enzymes on ice and return to -20°C as quickly as possible.
- ✓ Double check incubation times and temperatures (use a calibrated thermometer), and use a thermal cycler with heated lid.
- ✓ Evaporation can be a problem when you process samples at high temperatures. Make sure that sample tubes are well closed or use a plate [Heat Sealer](#) to avoid evaporation.
- ✓ Make sure that the pipettors are not out of calibration.
- ✓ Make sure that the gDNA, reagents, and master mixes are well mixed. Tap the tube with your finger or use a pipette to move the entire volume up and down. Then spin in a microcentrifuge for 5 to 10 seconds to drive the contents off the walls and lid. Do not mix the stock solutions and reactions that contain gDNA or enzymes on a vortex mixer.

## If you have low yield not due to poor sample quality

Possible sample loss during clean-up after labeling.

- ✓ See “[Step 2. Purification after ULS labeling](#)” on page 61 or “[Step 2. Purification after Enzymatic Labeling](#)” on page 75 or page 92 to remove unreacted dye. Many other columns result in the loss of shorter fragments.

## If you have post-labeling signal loss

Signal loss can be due to wash or hybridization conditions that are too stringent, or degradation of the Cyanine 5 signal.

Cyanine 5 signal degradation can be caused by ozone or NO<sub>x</sub> compounds coming from pollution and/or compressors and centrifuges. Cyanine 5 signal degradation can result in less red signal around the edges of the features, a visible gradient of significant Cy5/Cy3 positive ratios and more significant Cy5/Cy3 negative ratios – especially on the left side of the slide and on slides scanned later in a batch.

- ✓ Check that the oven temperature is 65°C for ULS and 67°C for Enzymatic Labeling. If needed, recalibrate the hybridization oven. Follow the steps in *Agilent G2545A Hybridization Calibration Procedure* (p/n G2545-90002).
- ✓ Check that the temperature of Wash 2 is 37°C.
- ✓ Check that Wash 2 was not accidentally used instead of Wash 1.
- ✓ Wash and scan slides in an ozone controlled environment (<5 ppb), such as an ozone tent.
- ✓ Use small batches that can be washed and scanned in about 40 minutes to minimize exposure to air.
- ✓ For Agilent Scanner C or B, use the Agilent Ozone-Barrier Slide Cover (p/n G2505-60550). The SureScan scanner has built-in ozone protection.
- ✓ Use the [Stabilization and Drying Solution](#) as described in “Wash Procedure B (with Stabilization and Drying Solution)” on page 113.

## If you have high BGNoise values

High BGNoise can cause lower signal-to-noise values (see [Table 70](#) or [Table 71](#) for thresholds) and higher DLRSD values. BGNoise is defined as the standard deviation of the signals on the negative controls. If the BGNoise is high, examine the microarray image for visible non-uniformities. High BGNoise is often introduced during hybridization steps or washes.

- ✓ Make sure that the oven is calibrated. Follow the steps in *Agilent G2545A Hybridization Calibration Procedure* (p/n G2545-90002).  
Sample hybridization at incorrect temperatures affects the stringency of the hybridization.

- ✓ Make sure that wash dishes, racks and stir bars are clean. Do not use tap water or detergents to clean wash equipment. If needed, rinse wash equipment with acetonitrile followed by rinses with MilliQ water.

- ✓ If needed, wash the slides with acetonitrile:

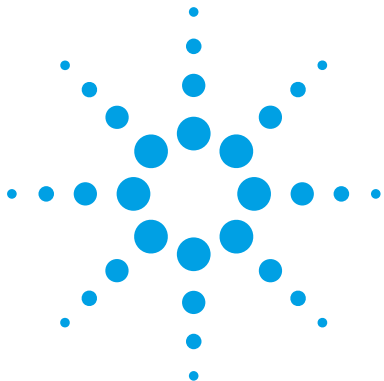
- 1 In the fume hood, fill a slide-staining dish approximately three-fourths full with acetonitrile.
- 2 Add a magnetic stir bar and put this dish on a magnetic stir plate.
- 3 Put the slides in a slide rack and transfer the slide rack to the slide-staining dish containing acetonitrile, and stir at 350 rpm for 1 minute.
- 4 Slowly remove the slide rack and scan the slides immediately.

## If you have poor reproducibility

Poor reproducibility (see [Table 70](#) or [Table 71](#) for thresholds), defined as high CVs of signals of replicated probes may indicate that the hybridization volume was too low or that the oven stopped rotating during the hybridization. Only very high scores on this metric will affect the DLRSD.

- ✓ When setting up the gasket-slide hybridization sandwich dispense the hybridization sample mixture slowly in a “drag and dispense” manner to prevent spills.
- ✓ Check that the oven is rotating.

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## 8 Reference

|  |     |
|--|-----|
| Reagent Kit Components                     | 134 |
| Microarray Handling Tips                   | 137 |
| Agilent Microarray Layout and Orientation  | 138 |
| Array/Sample tracking on microarray slides | 141 |

This chapter contains reference information that pertains to this protocol.

Refer also to:

- Bravo Automated Liquid Handling Platform User Guide (p/n G5409-90004)
- VWorks Automation Control Setup Guide (p/n G5415-90003)
- VWorks Automation Control User Guide (p/n G5415-90002)
- VWorks Software Quick Start (p/n G5415-90004)



## Reagent Kit Components

The contents of the reagent kits used in this protocol are listed here.

**Table 72** DNeasy Blood & Tissue Kit

| Component               |
|-------------------------|
| DNeasy Mini Spin Column |
| 2 mL Collection Tube    |
| Buffer ATL              |
| Buffer AL               |
| Buffer AW1              |
| Buffer AW2              |
| Buffer AE               |
| Proteinase K            |

**Table 73** Qubit dsDNA BR Assay Kit

| Component                  |
|----------------------------|
| Qubit dsDNA BR reagent     |
| Qubit dsDNA BR buffer      |
| Qubit dsDNA BR standard #1 |
| Qubit dsDNA BR standard #2 |

**Table 74** SureTag Complete DNA Labeling Kit and SureTag DNA Labeling Kit

| Component                              |
|--|
| Human Reference DNA (Male and Female)* |
| 10× Restriction Enzyme Buffer          |
| BSA                                    |
| Alu I                                  |
| Rsa I                                  |
| Purification Column†                   |
| Nuclease-Free Water                    |
| Exo (-) Klenow                         |
| 5× Reaction Buffer                     |
| Cyanine 5-dUTP                         |
| Cyanine 3-dUTP                         |
| 10× dNTPs                              |
| Random Primer                          |

\* Included in the SureTag Complete DNA Labeling Kit only.

† Not used in this protocol.

**Table 75** Genomic DNA High-Throughput ULS Labeling Kit

| Component             |
|-----------------------|
| Agilent-CGHblock      |
| 10× Labeling Solution |
| ULS-Cy 5 Reagent      |
| ULS-Cy 3 Reagent      |

**8 Reference**  
**Reagent Kit Components**

**Table 76** Genomic DNA 96-well Purification Module

| Component                                   |
|---|
| 96-well Agilent-KREApure purification plate |
| 96-well collection plate                    |
| 96-well wash plate                          |

**Table 77** Oligo aCGH/ChIP-on-chip Hybridization Kit

| Component                      |
|--------------------------------|
| 2× HI-RPM Hybridization Buffer |
| 10× aCGH Blocking Agent        |

**Table 78** Oligo aCGH/ChIP-on-chip Wash Buffer Kit

| Component                                     |
|---|
| Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 1 |
| Agilent Oligo aCGH/ChIP-on-Chip Wash Buffer 2 |



## Microarray Handling Tips

Each microarray is printed on the side of the glass slide containing the “Agilent”-labeled barcode. This side is called the “active” side. The numeric barcode is on the inactive side of the slide.

### CAUTION

You must familiarize yourself with the assembly and disassembly instructions for use with the Agilent Microarray Hybridization Chamber (G2534A) and gasket slides. Practice slide kits are available.

---

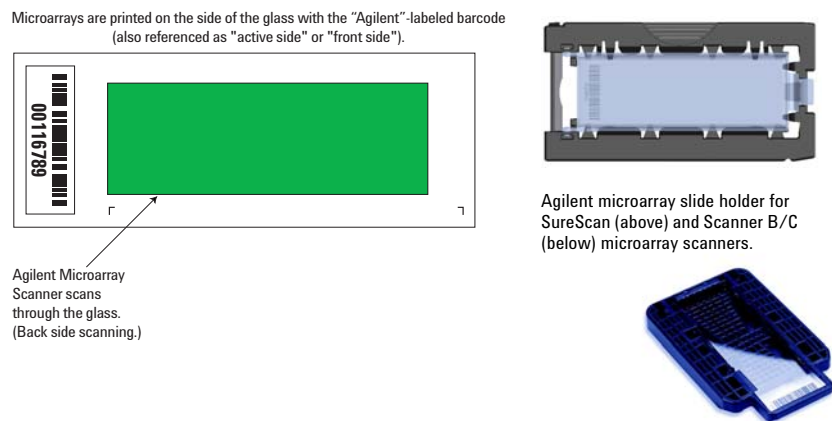
In this “processing and hybridization” procedure, the hybridization mixture is applied directly to the gasket slide, and not to the active side of the oligo microarray. Instead, the active side of the oligo microarray is placed on top of the gasket slide to form a “sandwich slide” pair.

To avoid damaging the microarray, always handle glass slides carefully by their edges. Wear powder-free gloves. Never touch the surfaces of the slides. If you do, you may cause irreparable damage to the microarray.

Never allow the microarray surface to dry out during the hybridization process and washing steps.

## Agilent Microarray Layout and Orientation

### Agilent oligo microarray (1 microarray/slide format) as imaged on the Agilent microarray scanner



**Figure 13** Agilent microarray slide and slide holder

Agilent oligo microarrays formats and the resulting "microarray design files" are based on how the Agilent microarray scanner images 1-inch x 3-inch glass slides. Agilent designed its microarray scanner to scan through the glass slide (back side scanning). The glass slide is securely placed in an Agilent microarray slide holder with the "Agilent" labeled barcode facing the opening of the slide holder (on SureScan Microarray Scanner) or facing the inside of the slide holder (Scanner C or Scanner B). In this orientation, the "active side" containing the microarrays is protected from potential damage by fingerprints and other elements. Once securely placed, the numeric barcode, non-active side of the slide, is visible from the outside of the slide holder.

Figure 13 depicts how the Agilent microarray scanner reads the microarrays and how this relates to the "microarray design files" that Agilent generates during the manufacturing process of its *in situ*-synthesized oligonucleotide microarrays. Thus, if you have a scanner that reads microarrays from the "front side" of the glass slide, the collection of microarray data points will be different in relation to the "microarray design files". Therefore, please take a

moment to become familiar with the microarray layouts for each of the Agilent oligo microarrays and the layout information as it pertains to scanning using a “front side” scanner.

### **Non-Agilent Front Side Microarray Scanners**

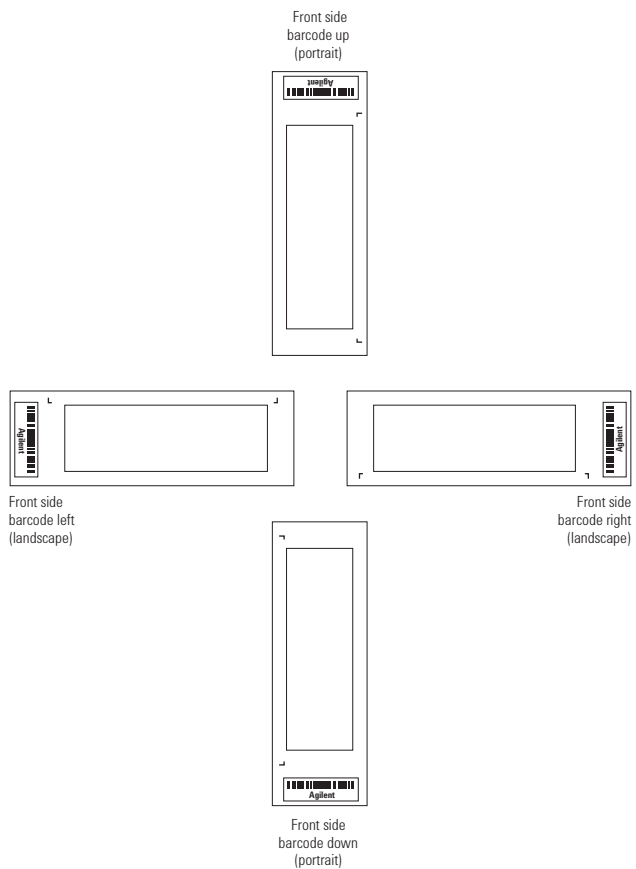
When scanning Agilent oligo microarray slides, the user must determine:

- If the scanner images the microarrays by reading them on the “front side” of the glass slide (“Agilent”-labeled barcode side of the slide) and
- If the microarray image produced by the non-Agilent scanner is oriented in a “portrait” or “landscape” mode, and “Agilent”-labeled barcode is on the left-side, right-side, up or down, as viewed as an image in the imaging software (see [Figure 14](#)).

This changes the feature numbering and location as it relates to the “microarray design files”.

## 8 Reference

### Agilent Microarray Layout and Orientation



**Figure 14** Microarray slide orientation

## Array/Sample tracking on microarray slides

Use the forms below to make notes to track your samples on microarray slides.

Position the gasket slide in the SureHyb chamber base with the label to the left and load the samples: top row, left to right, then lower row, left to right. The array suffix assignments from Feature Extraction will then occur in the order shown.

### Arrays

Array 1\_1

Array 1\_2

|                                 |         |         |
|---------------------------------|---------|---------|
| B<br>A<br>R<br>C<br>O<br>D<br>E | Sample: | Sample: |
|                                 |         |         |
|                                 |         |         |
|                                 |         |         |

Barcode Number \_\_\_\_\_

**Figure 15** 2-pack microarray slides

**8 Reference**

Array/Sample tracking on microarray slides

**Arrays**

|  | Array 1_1 | Array 1_2 | Array 1_3 | Array 1_4 |
|--|-----------|-----------|-----------|-----------|
| <b>B<br/>A<br/>R<br/>C<br/>O<br/>D<br/>E</b> | Sample:   | Sample:   | Sample:   | Sample:   |
|  |           |           |           |           |
|  |           |           |           |           |
|  |           |           |           |           |

**Barcode Number** \_\_\_\_\_

**Figure 16** 4-pack microarray slides

**Arrays**

|  | Array 1_1      | Array 1_2      | Array 1_3      | Array 1_4      |
|--|----------------|----------------|----------------|----------------|
| <b>B<br/>A<br/>R<br/>C<br/>O<br/>D<br/>E</b> | <b>Sample:</b> | <b>Sample:</b> | <b>Sample:</b> | <b>Sample:</b> |
|  |                |                |                |                |
|  |                |                |                |                |
|  |                |                |                |                |
|  | <b>Sample:</b> | <b>Sample:</b> | <b>Sample:</b> | <b>Sample:</b> |
|  |                |                |                |                |
|  |                |                |                |                |
|  |                |                |                |                |
|  | Array 2_1      | Array 2_2      | Array 2_3      | Array 2_4      |

**Barcode Number** \_\_\_\_\_

**Figure 17** 8-pack microarray slide

[www.agilent.com](http://www.agilent.com)

## In This Book

This guide contains information to run the Oligonucleotide Array-Based CGH for Genomic DNA Analysis - Bravo Automated Liquid Handling Platform with Enzymatic and ULS Labeling protocol.

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