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Sensitive CGH made simple

Sensitive array-based comparative genomic hybridization (CGH) starts with a robust labeling system. The BioPrime® Array CGH Genomic Labeling System is a fast, efficient labeling kit that allows you to generate high yields of labeled genomic samples with strong signal intensities, improving the sensitivity of your CGH experiments.

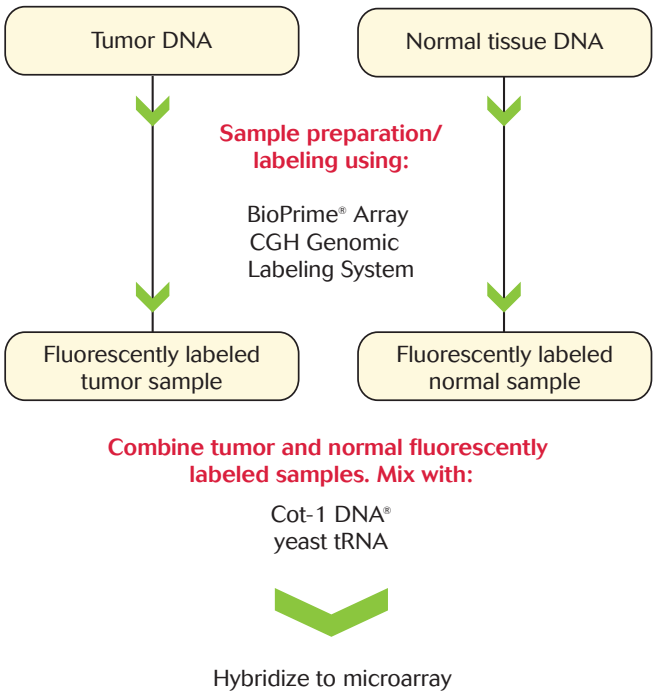
Genomic Profiling with the BioPrime® Array CGH Genomic Labeling System

The recent emergence of array-based CGH enables researchers to perform genome-wide studies of chromosomal aberrations that lead to a variety of diseases. By differentially labeling normal and tumor DNA samples prior to hybridization to a BAC or cDNA array (Figure 1), you can detect variations in gene copy number that underlie diseases such as cancer (1,2). The ability to detect variations in gene copy number depends largely upon the sensitivity of the labeling system used. The BioPrime® Array CGH Genomic Labeling System is optimized for use in array CGH. Using this system, you can expect:

- High yields of labeled genomic DNA
- Strong signal intensities
- Reproducible results

With robust yields and strong signal intensities, you'll obtain the sensitivity you need to perform accurate genomic profiling experiments. And with an optimized kit, you'll make sure you obtain consistent performance.

Figure 1 - Array CGH sample preparation overview



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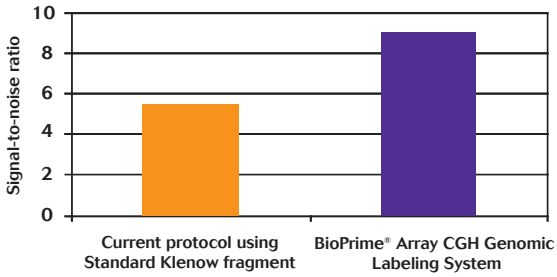
Brighter signals

The exo-Klenow polymerase in the BioPrime® Array CGH Genomic Labeling System incorporates fluorescently modified nucleotides more effectively than standard Klenow, enabling you to obtain stronger signal intensities (Figure 2).

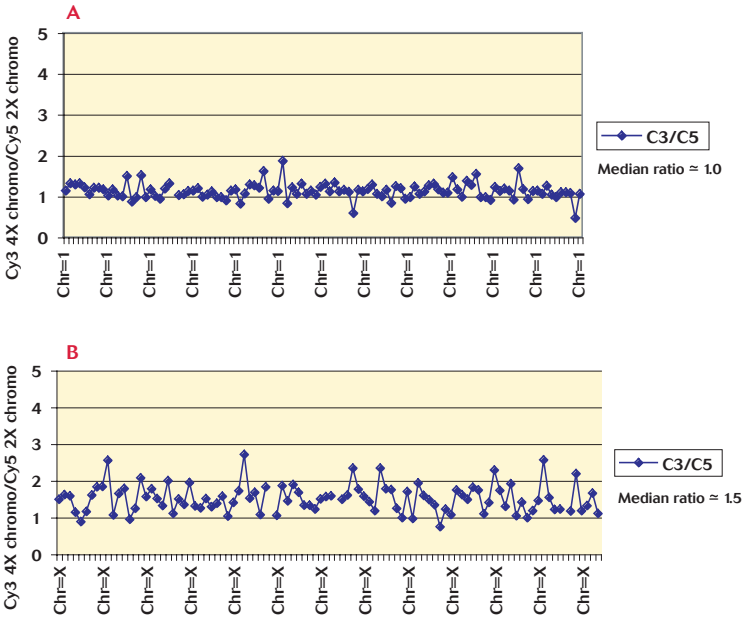
Figure 2 - Increased signal-to-noise ratios using the BioPrime® Array CGH Genomic Labeling System



Comparison of signal to noise ratios of hybridizations to BAC arrays using 1 µg of genomic DNA labeled using current methods with standard Klenow compared to the BioPrime® Array CGH Genomic Labeling System.

With strong signal intensities, you'll obtain the sensitivity you need to detect variations in gene copy number reliably. Figures 3a and 3b show the resulting ratios when genomic DNA from a tumor cell line with four copies of the X chromosome and genomic DNA from a normal female tissue are labeled using the BioPrime® Array CGH Genomic Labeling System and co-hybridized to a BAC array. The fluorescent ratio of the 4X and 2X samples for chromosome 1 is approximately 1.0 (expected), indicating equivalent copy numbers of chromosome 1 in tumor and normal female genomic DNA (Figure 3a). The median ratio of the samples for the X chromosome is 1.5, indicating an increase in copy number between the tumor cell line and normal genomic DNA (Figure 3b).

Figure 3 - The BioPrime® Array CGH Genomic Labeling System provides sensitive detection for reproducible array CGH studies

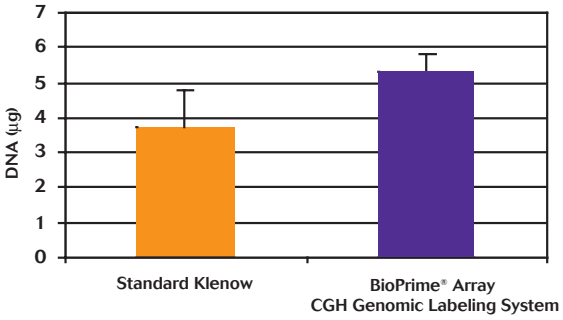


Determination of differential gene copy number with a tumor cell line DNA on BAC arrays. Analysis of the fluorescent ratios of normal female genomic DNA and cell line with four copies of the X chromosome on BAC arrays using the BioPrime® Array CGH Genomic Labeling System.

Improved yields

Current labeling methods for array CGH use a high concentration of the large fragment (Klenow) of DNA polymerase I, which lacks 5'-3' exonuclease activity (3,4). This enzyme incorporates fluorescent nucleotides while replicating the genomic DNA sample, providing a simple and efficient means to label genomic targets prior to hybridization. The BioPrime® Array CGH Genomic Labeling System uses a high concentration of exo- Klenow, lacking both 5'-3' and 3'-5' exonuclease activity. Using exo- Klenow enables you to obtain higher yields of labeled sample than possible with standard Klenow (Figure 4), increasing the sensitivity of your genomic profiling experiments.

Figure 4 - Higher yields of labeled sample using BioPrime® Array CGH Genomic Labeling System

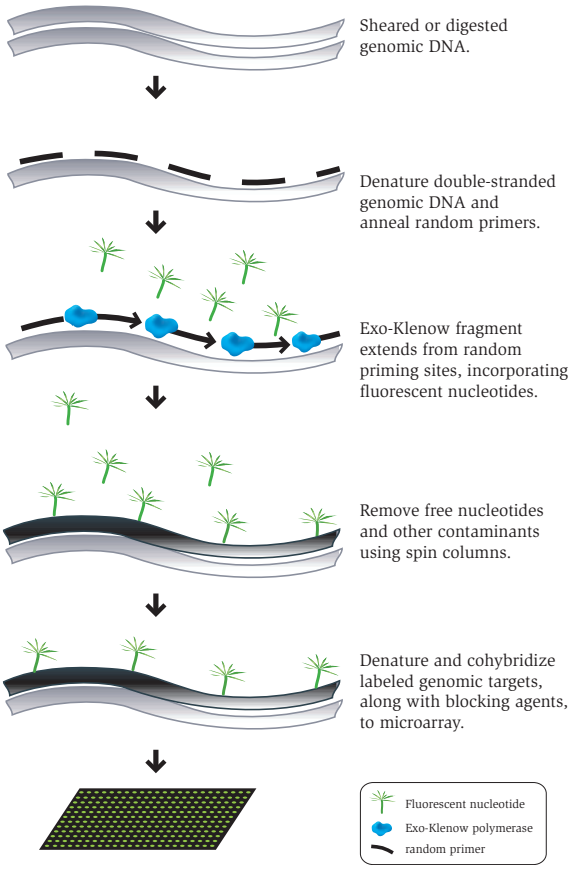


Average total DNA recovered after labeling 2 µg of digested genomic DNA using current protocol (standard Klenow) and the BioPrime® Array CGH Genomic Labeling System. Duplicate reactions were incubated at 37° C for 2 hours.

Simple protocol

The BioPrime® Array CGH Genomic Labeling System is based on a simple random priming protocol and takes less than three hours to complete, requiring minimal "hands on" time. Briefly, sheared or digested genomic DNA is denatured and random octamers annealed to the template strands. The exo-Klenow fragment then extends from the random priming sites, incorporating fluorescent nucleotides during polymerization. The labeled samples are purified on spin columns to remove free nucleotides. The fluorescently labeled material is then heat denatured briefly before hybridization to a microarray (Figure 5).

Figure 5 - Overview of BioPrime® Array CGH Genomic Labeling System protocol



Complete labeling solution

The BioPrime® Array CGH Genomic Labeling System contains all the major reagents (except fluorescent nucleotides) necessary for fast and efficient labeling of genomic DNA samples (Table 1). All reagents are functionally tested so you'll obtain quality performance with every labeling reaction.

Table 1 - BioPrime® Array CGH Genomic Labeling System components

Exo-Klenow Fragment (40 U/µl)	Purification Buffers (A and B)
2.5X Random Primer Solution	Purification Columns
Control DNA (Salmon Sperm)	Stop Buffer
10X dCTP Nucleotide Mix	Distilled Water
10X dUTP Nucleotide Mix	Collection Tubes

Sensitivity made simple

Genomic target preparation is an integral part of obtaining accurate results during genomic profiling experiments. Using the BioPrime® Array CGH Genomic Labeling System, you'll get the sensitivity you need for successful array CGH studies. Call and order today.

Description	Quantity	Cat. no.
BioPrime® Array CGH Genomic Labeling System	30 rxns	18095-011
Human Cot-1 DNA®	500 µg	15279-011
Mouse Cot-1 DNA®	500 µg	18440-016
Yeast tRNA	50 mg	15401-011

References:

1. Pinkel D., *et. al.* (1998) *Nature Genetics* **20:** 207-211.
2. Pollack J.R., *et. al.* (1999) *Nature Genetics* **23:** 41-46.
3. **http://cmgm.stanford.edu/pbrown/protocols/4_genomic.html** (Stanford)
4. **http://www.sanger.ac.uk/HGP/methods/cytogenetics/Labelling.shtml** (Sanger Institute)

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