

Technical Note

NimbleGen Hybridization System Outperforms Rotating Hybridization Wheel

A NimbleGen Hybridization System outperforms a rotating hybridization wheel for hybridizing microarrays as determined by the brightness and uniformity of the original image and high signal:noise ratio of the resulting data.

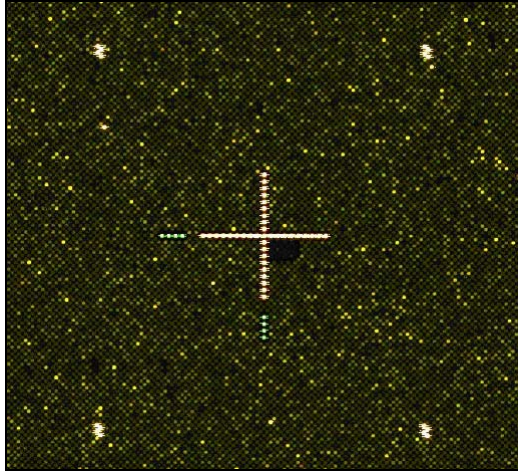
Experimental Summary

1. Test and reference genomic DNA samples were identically labeled and co-hybridized overnight to two CGH arrays (385K probes, human whole-genome, 6kb median probe spacing). One array was hybridized using a NimbleGen Hybridization System and the other using a rotating hybridization wheel.
2. Both arrays were washed using the same protocol.
3. Both arrays were scanned using identical PMT settings on the scanner.
4. Both array images were visualized and analyzed using identical settings in Roche NimbleGen NimbleScan software.

Array Image Comparison

The scan of the array hybridized using a NimbleGen Hybridization System (Figure 1A) produced a brighter image, showing better contrast and uniformity than the scan of the array hybridized using a rotating hybridization wheel (Figure 1B). Fiducial controls are shown in the images for size and zoom comparisons.

A. NimbleGen Hybridization System



B. Rotating Hybridization Wheel

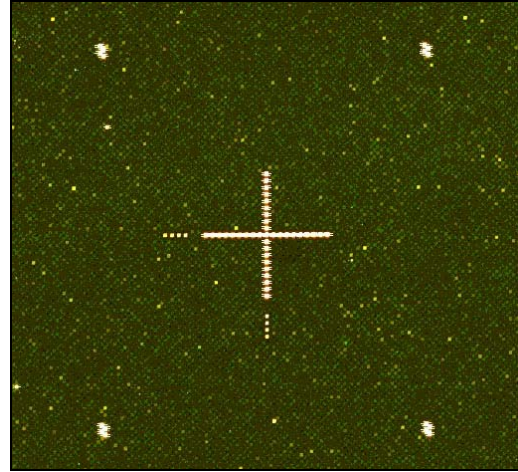


Figure 1. Example Array Images for a NimbleGen Hybridization System and Rotating Hybridization Wheel
The array image for the CGH experiment using a NimbleGen Hybridization System (A) is brighter and shows better contrast and uniformity than when using a rotating hybridization wheel (B).

Data Visualization Comparison

We compared chromosome 6 CGH data extracted from array images for a rotating hybridization wheel and NimbleGen Hybridization System using Roche NimbleGen SignalMap software (Figure 2). There is substantially higher signal:noise ratio in the data for a NimbleGen Hybridization System (bottom track), and the observed shifts are much higher in magnitude relative to the data for a rotating hybridization wheel (top track). When analyzed with NimbleScan software, two duplications are detected in the data for a NimbleGen Hybridization System but are not detected in the data for a rotating hybridization wheel.

We also compared chromosome 8 CGH data extracted from the array images for the rotating hybridization wheel and NimbleGen Hybridization System using SignalMap software (Figure 3). Again, there is substantially higher signal:noise ratio for the NimbleGen Hybridization System (bottom track), and the observed shifts are much higher in magnitude relative to the data for the rotating hybridization wheel (top track). NimbleScan software is able to detect the changes in the data for a NimbleGen Hybridization System but is unable to detect them in the data for a rotating hybridization wheel.

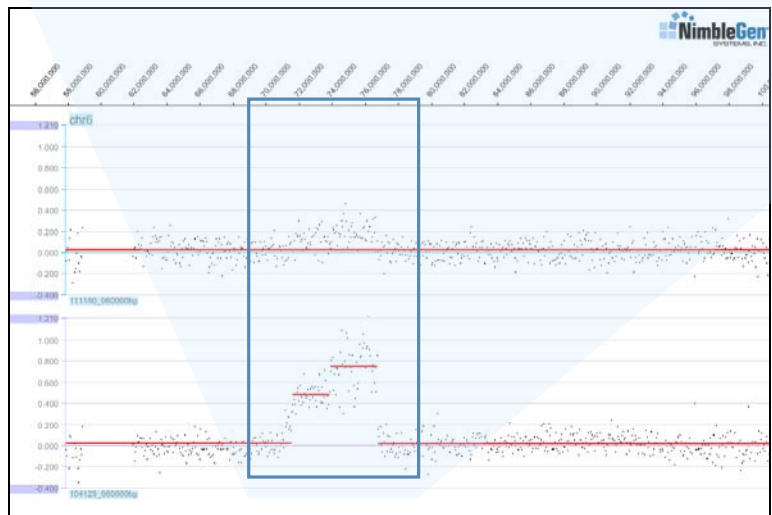
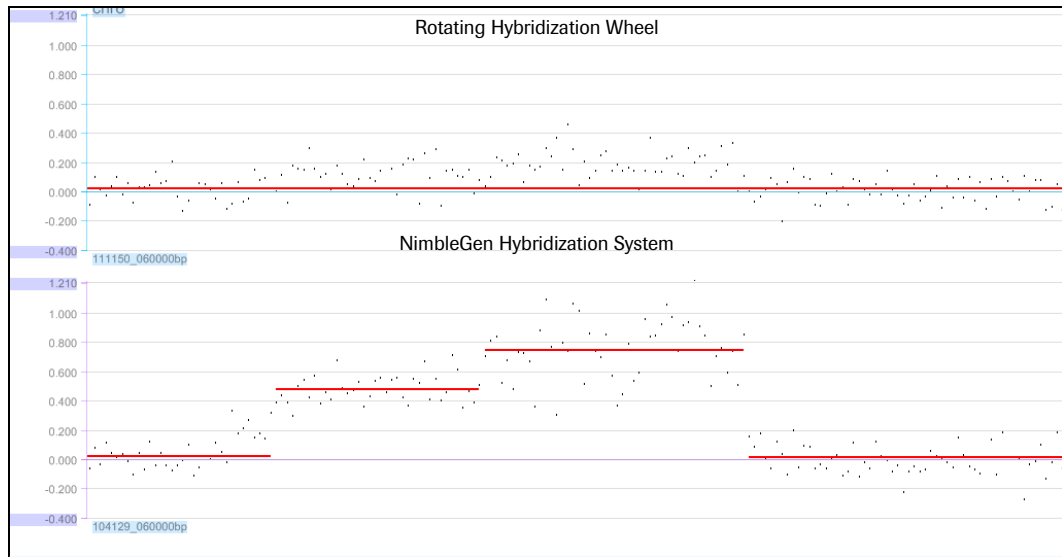


Figure 2. Comparison of Chromosome 6 CGH Data. In addition to higher signal:noise ratio, the observed shifts are higher in magnitude in the data extracted from array images for a NimbleGen Hybridization System (bottom track) relative to the data for a rotating hybridization wheel (top track). A zoom view of a region (indicated by the blue box) of chromosome 6 CGH data shows that two duplications were detected in the data for a NimbleGen Hybridization System but were not detected in the data for a rotating hybridization wheel.

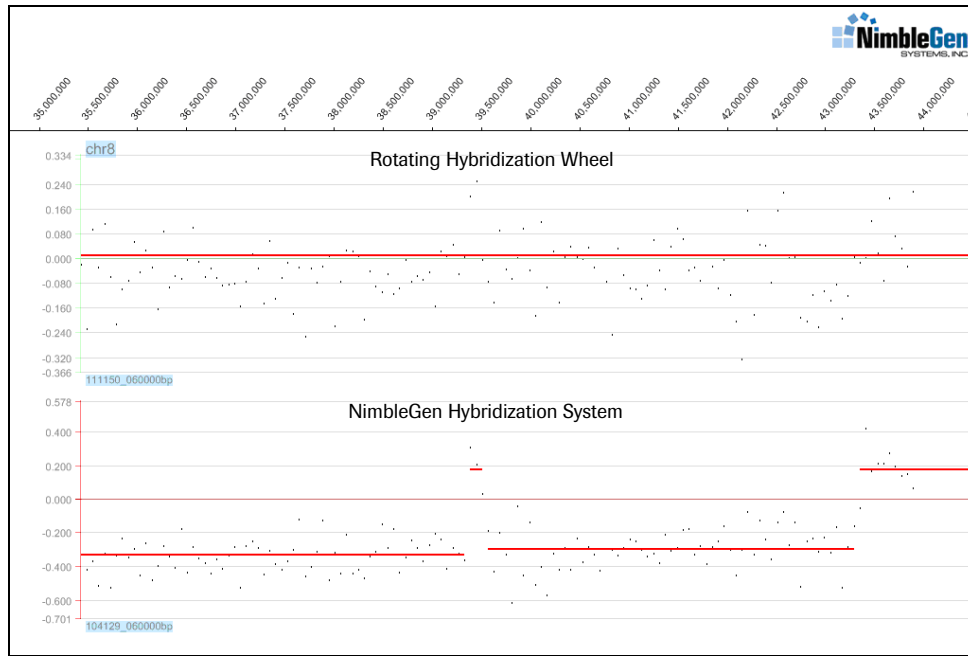


Figure 3. Comparison of Chromosome 8 CGH Data. Higher signal:noise ratio and observed shifts that were higher in magnitude enabled NimbleScan software to detect changes in chromosome 8 CGH data from a NimbleGen Hybridization System (bottom track) but not in the data from a rotating hybridization wheel (top track).

For More Information

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