

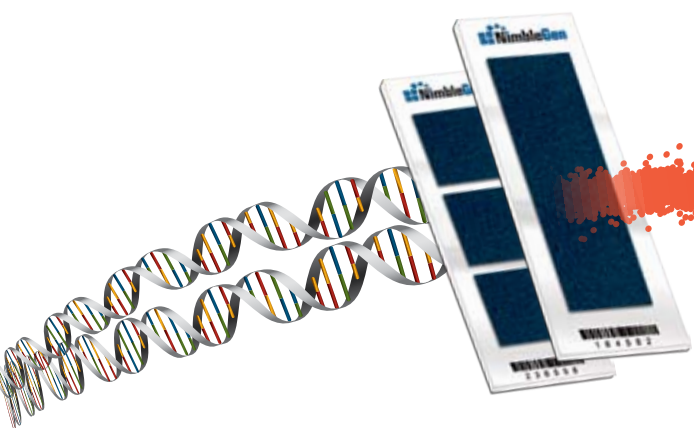
NimbleGen Copy Number Variation (CNV) Arrays

Advance your disease association research

High-Resolution CNV Analysis Enables Disease Research

Recent advances in high-resolution CGH array technology have revealed DNA copy number variants (CNVs) as a significant source of genome variation. Research studies have implicated CNVs in a broad range of common and complex diseases, including autism, schizophrenia, autoimmune disease, and susceptibility to HIV.

With the emergence of high-resolution maps of CNVs, their impact on disease phenotypes has become a key research focus. Life science researchers are rapidly adopting the use of CNV arrays for large-scale genome-wide association studies. To facilitate this effort, Roche NimbleGen has developed Human CNV arrays in 2.1M and 3x720K array formats for comprehensive and high-resolution analysis of genome-wide CNVs.



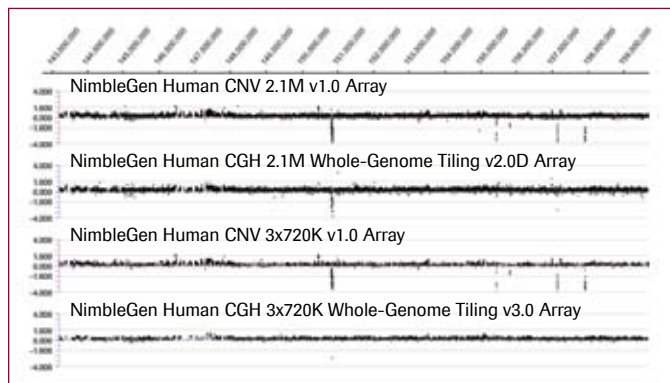
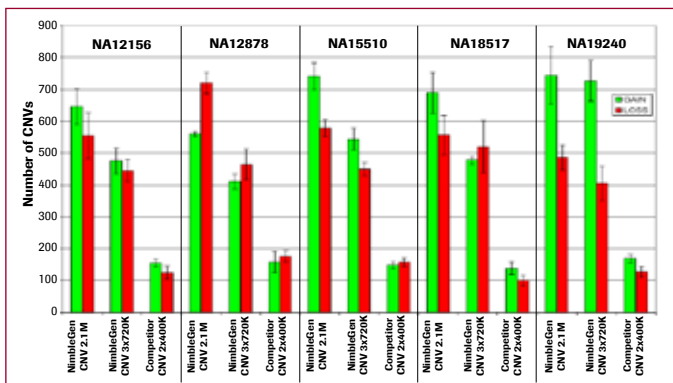
Advantages

- **Comprehensive CNV Detection:**
Targeted regions include:
 - The Database of Genomic Variants
 - 42M High-Resolution CNV Discovery Project
 - Asian Populations
- **Greater Probe Coverage for Confident Results:**
95% of CNVs are represented by at least 5 probes (84% by at least 10 probes).
- **High-Resolution:** Backbone coverage of the entire human genome enables detection of novel CNVs down to ~5-kb resolution.

Performance Data

With the addition of Human CNV Arrays to the NimbleGen portfolio, researchers can now choose from a variety of CGH and CNV arrays to meet their specific needs. With the high probe densities and higher signal-to-noise ratios, NimbleGen CNV arrays detect at least 4-fold more CNVs than the

competitor CNV array (Figure 1). Figure 2 shows sensitive CNV detection using NimbleGen CNV and whole-genome tiling CGH arrays, with more CNVs identified using the CNV arrays.



▲ Figure 1: Lower Noise from Empirically Optimized Probes on NimbleGen CNV Arrays Allows More Sensitive CNV Detection. CNVs in each of 5 samples were detected using the NimbleGen 2.1M CNV array, NimbleGen 3x720K CNV array, and Competitor 2x400K CNV array. Data were analyzed using NimbleScan v2.6. The total number of CNVs detected with each array for each sample are displayed as green bars (copy number gains) or red bars (copy number losses); error bars are SD for N = 4, reference is NA10851.

▲ Figure 2: Cross-platform analysis of CNV regions. CNV regions were analyzed from HapMap research sample NA15510 using the NimbleGen Human CNV 2.1M v1.0, NimbleGen Human CGH 2.1M Whole-Genome Tiling v2.0D, NimbleGen Human CNV 3x720K v1.0, and NimbleGen Human CGH 3x720K Whole-Genome Tiling v3.0 arrays, as indicated. A zoom-in region of Chromosome 1 is displayed in SignalMap software, available from Roche NimbleGen.

Array Specifications	2.1M Array	3x720K Array
Number of DGV (ver. 7) Regions	29,866	29,859
Percentage of DGV (ver. 7) Regions	89%	89%
Number of 42M CNV Regions	8,599	8,599
Percentage of 42M CNV Regions	100%	100%
Number of Asian CNV Regions	2,680	2,680
Total # CNV Regions Covered	41,145	41,138
Percentage of CNV Regions with ≥ 10 probes	84%	82%
Percentage of CNV Regions with ≥ 5 probes	95%	95%
Whole-Genome Backbone (median probe spacing)	1,239 bp	4,750 bp

Ordering Information:

Available Designs	 Delivery Cat. No.	Pack Size
NimbleGen Human CNV 2.1M Array	05 913 152 001	1 slide
	05 913 179 001	5 slides
NimbleGen Human CNV 3x720K Array	05 913 209 001	1 slide
	05 913 217 001	5 slides

Roche Microarray Technical Support:
www.nimblegen.com/arrayssupport

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