

NimbleGen DNA Methylation 4x72K Array Delivery

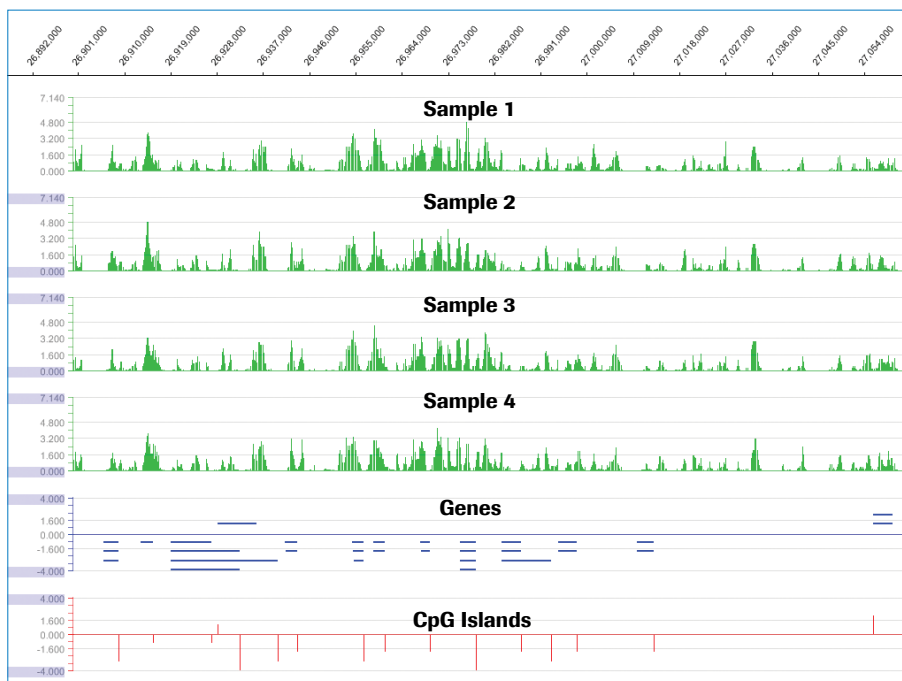
Flexible, cost-effective multiplex platform for targeted DNA Methylation profiling

NimbleGen DNA Methylation 4x72K arrays enable you to reliably detect promoter and genic DNA methylation events, as well as compare differential methylation patterns between cells, tissues, and tumor samples. Each multiplex array permits the simultaneous analysis of four samples at 72,000 probes per sample providing high resolution and sensitivity.

These 4x72K arrays are available for delivery for use in your laboratory or core facility. This platform offers a higher throughput, lower-cost solution for testing four independent samples on a single slide for targeted DNA methylation analysis before scaling up to larger studies. Take advantage of the highly reproducible Human ENCODE design (Figure 1) or customize the array content to target the genomic regions of interest for discovery and validation.

Advantages

- **Cost-Effective, Multiplex Platform for High-Resolution Mapping**
 - Accurately analyze four samples simultaneously on a single slide.
 - Utilize 72,000 probes on each array for high-resolution tiling of biologically significant ENCODE regions or customize the array content to precisely identify methylated regions.
- **High Sensitivity and Specificity for Unparalleled Results**
 - Achieve high sensitivity and specificity with NimbleGen's long, oligo probes (50 - 75mer) in combination with our stringent hybridization protocol.
 - Reliably detect as few as two methyl CpGs per 500bp fragment.
 - Eliminate interarray variation with our 2-color protocol for simultaneous analysis of enriched and control sample on a single array.



◀ **Figure 1: NimbleGen DNA Methylation 4x72K Array Performance.** The same enriched (MeDIP) and control (input) samples (genomic DNA) were labeled with Cy5 and Cy3, respectively, and co-hybridized to the four subarrays according to the protocol. As visualized in SignalMap software, the figure demonstrates the high level of reproducibility of the 4x72K platform by comparing side-by-side the p-value enrichment data from all four subarrays illustrating the methylation landscape of the HoxA cluster.

NimbleGen Human DNA Methylation 4x72K ENCODE Array

Table 1: Design and Ordering Information

Catalog No.	Design No.	Organism	Build	Slides	Number of Arrays per Slide	Resolution (Mean/Median Probe Spacing)
05224381001	570601	Human	hg17	1	4	100bp/105bp

Comments: Each array covers selected biologically significant ENCODE* pilot regions including HoxA, β -globin, Apo, and others. The design includes 277 CpGs on each array.

* The ENCODE region consists of ~30Mb (1%) of the human genome: half of which are random and half of which are manually selected (biologically significant).

NimbleGen DNA Methylation 4x72K Microarray Specifications

Total probes	4 x 72,000
Probe length	50 - 70mer
Probe spacing	Varies depending on design
Feature size	16 μ m x 16 μ m
Array size	7.8mm x 5.7mm
Slide size	1" x 3" (25mm x 76mm) glass
Sequence source	UCSC Genome browser, NCBI



Contact: Roche NimbleGen, Inc.

Toll-free in US: (877) NimbleGen / (877) 646-2534
 (608) 218-7600
 ngsales@nimblegen.com
 www.nimblegen.com



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Roche NimbleGen, Inc.
 504 S. Rosa Road
 Madison, WI 53719 USA