NimbleGen Sequence Capture 2.1M Human Exome Array

Capture the human exome on a single array

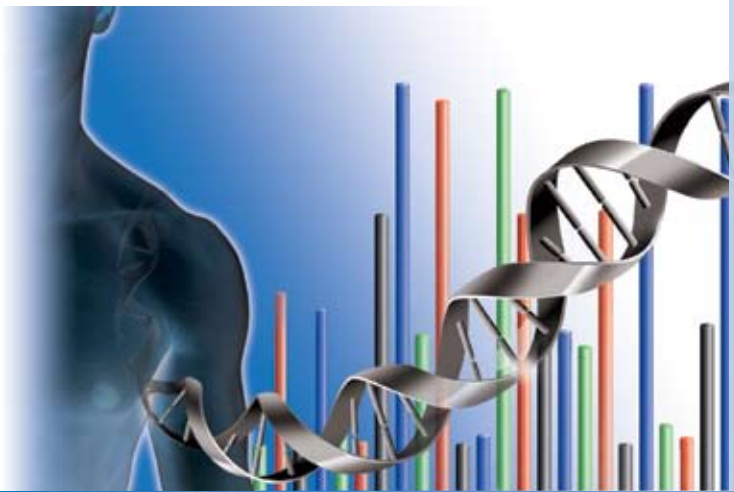
Whole Human Exome Capture

Revolutionizing genetic disease research

Human exome sequencing is considered by many researchers to be the next-generation process for resequencing that will lead to significant biomedical breakthroughs. Exons are the most functionally relevant portion of the genome and are comprised of short segments of DNA that provide the genetic blueprint for proteins. As such, exome sequencing enables the discovery of much of the functional variation that is responsible for many common and rare diseases (e.g. cancer, diabetes, and Alzheimer's disease).

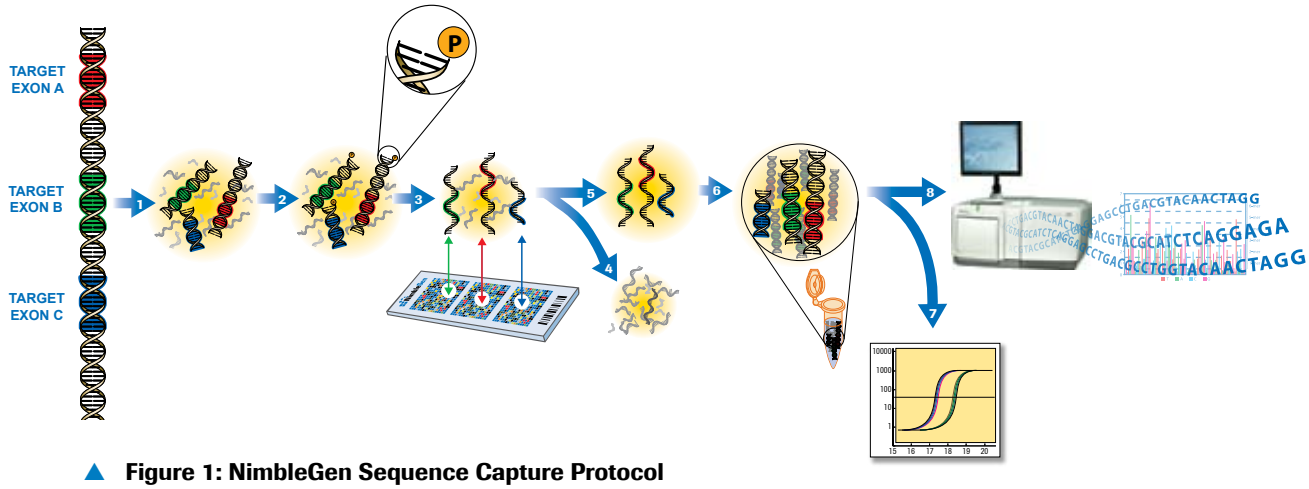
Seize the exome

NimbleGen Sequence Capture arrays enable you to produce targeted, sequencing-ready samples in your lab. Utilizing high-density, long-oligonucleotide NimbleGen 2.1M arrays and an optimized design algorithm, the entire human exome can be captured on a single array. This revolutionary product now allows you to design and perform experiments not technically or economically feasible with PCR-based methods.



Advantages

- **Capture the Human Exome:** Use only one 2.1M array to capture ~180,000 coding exons and 551 miRNA exons in your own lab.
- **Reduce Cost:** Save time and cost compared to PCR-based methods for the preparation of all human coding exons for next-generation sequencing to identify variants and small insertions and deletions.
- **Rely on Design Expertise:** Ensure a high level of human exome capture specificity and sensitivity with an empirically tested and proven capture design algorithm.
- **Learn the Protocol:** Let our certified Sequence Capture trainers guide you through the protocol (Figure 1) on-site, using functionally tested training kits and practice arrays.
- **Generate Data with Confidence:** Utilize built-in control probes to ensure optimal system performance.



▲ **Figure 1: NimbleGen Sequence Capture Protocol**

1. Genomic DNA fragmentation
2. Linker ligation
3. Hybridization
4. Array washing
5. Target fragment elution
6. Amplification
7. Enrichment QC
8. Sequencing

Performance Data: Exome Resequencing of Human Disease Case	
Total size of target region	34Mb
Percentage of 454 unique sequencing reads mapping to exon targets	80%
Percentage of bases with 1x coverage	91%
Median fold coverage	8

▲ **Table 1.** NimbleGen Sequence Capture 2.1M Human Exome v1.0 arrays were used to capture ~180,000 coding exons and 551 miRNA exons from a research study using a human disease case sample. Two PicoTiterPlate kits were used to generate ~1Gb of raw sequence on the captured sample using GS FLX Titanium kits (400bp reads; 1,000,000 reads per plate) and the Genome Sequencer FLX Instrument (454 Life Sciences). Note the high specificity (80%) and percentage of bases with at least one sequencing read (91%) at a median fold coverage (50% of bases) of 8-fold.

Array Specifications	
Array design[1]	Targets ~180,000 human coding exons[2] and 551 miRNA exons
Probes	2.1 million empirically optimized long oligonucleotides
Exome database	Search for your gene of interest and view capture statistics for the 2.1M Human Exome array at *www.nimblegen.com/seqcap*

1 Uses an optimized design algorithm. Repetitive regions were removed using proprietary repeat-masking method.
2 Source of design is from the CCDS database at *www.ncbi.nlm.nih.gov/projects/CCDS*

References and Publications

For a list of recently published research on Roche NimbleGen technologies, go to *www.nimblegen.com/seqcap*

Ordering Information:

Catalog number	**Array Delivery**	05451957001
	Exome Capture Service	05463327001
Catalog description	Seq Cap Human Exome 2.1M Array	

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