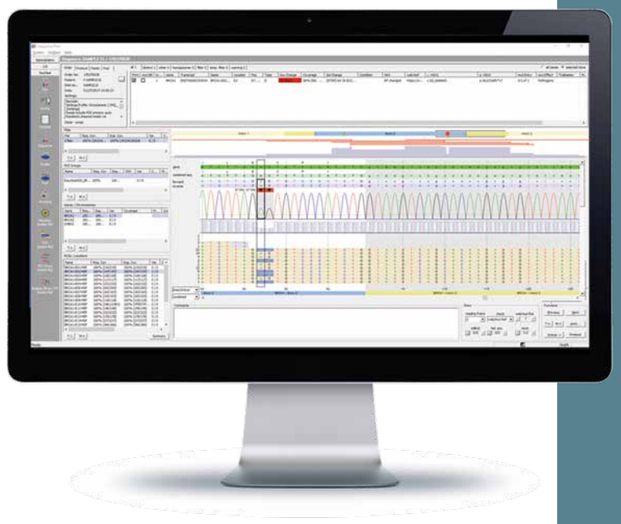


SEQUENCE PILOT: software for genetic analysis

With **SeqNext JSI medical systems** offers a powerful all-in-one solution for robust high-throughput variant detection and interpretation of your NGS data. Development and optimization in close cooperation with our customers guarantees user-friendliness, efficiency and optimal integration into your workflow:

- Ready to use system with an easy import of predefined and validated NimaGen analysis settings
- Benefit from the various advantages of molecular tags (smMIPs)
- Detection (high sensitivity) of base changes, deletions and insertions
- Parallel powerful CNV detection
- Customisable reduction (high specificity) of sequencing artefacts
- Powerful algorithms (mapping / alignment) to ensure high coverage
- Definition of pseudo gene / homology sequences for background reduction
- Compatible with all common sequencing platforms
- Export of FASTQ-, BAM- and VCF-files
- Detection of gene fusions and chromosomal rearrangements
- Analysis of FFPE samples
- Use **varSEAK** for a powerful filtering and interpretation of your variants
- Detailed and customisable patient reports

For more information please visit:
www.jsi-medisys.de
www.varSEAK.bio

JSI medical systems

Ordering information		
ESI-HBOC10-024	EasySeq™ NGS Targeted Capture Kit for HBOC 10 gene panel	24 sample kit
ESI-HBOC10-096	EasySeq™ NGS Targeted Capture Kit for HBOC 10 gene panel	96 sample kit

- For research use only -

Product and Company Information

Product name EasySeq™ NGS Targeted Capture Kit for Hereditary Breast and Ovarian Cancer (HBOC) Gene Panel
Product use For Research Use Only
Company NimaGen BV
Lagelandseweg 56
6545 CG Nijmegen
The Netherlands

In collaboration with Radboud university medical center, dpt. Human Genetics, Nijmegen, The Netherlands

Telephone +31 (0)24 820 02 41
Email info@nimagen.com
Website www.nimagen.com

EasySeq™ NGS Targeted Capture Kit

Hereditary Breast and Ovarian Cancer (HBOC) Gene Panel

NIMAGEN®
a Biologio company

1 tube
10 genes
100% coverage

BRCA1 *RAD51D*
BRCA2 *CDH1*
PALB2 *TP53*
CHEK2 *ATM*
RAD51C *BRIP1*

> smMIP based DNA capturing

- Coding regions 100% covered including intron-exon boundaries in one single tube assay
- Based on Molecular Inversion Probe capturing with single molecule tags (smMIPs)
- Brand new design, containing >1300 smMIPs v2.0 probes with novel backbone
- Simple and robust workflow, extremely low hands-on time: < 1 hour
- Intrinsic refSNPs for sample ID and quality control
- Single Click Analysis with JSI SeqNext Software
- Compatible with all Illumina® Sequencing Platforms

Technology

Using sequence capturing with single molecule Molecular Inversion Probes (smMIP)[1], followed by a barcoding amplification step, the system enables sequencing of the targeted regions in a very simple, fast and robust workflow, resulting in coverage with double probe tiling[2] and independent reading of both strands. The kits contain all reagents for a straightforward, one-step capturing and subsequently sample tagging for NGS sequencing. The resulting libraries are compatible with Illumina sequencing platforms.

Easy, robust and straightforward workflow (figure EasySeq™ workflow)

All EasySeq™ kits consist of a very limited number of hands-on steps:

1. Thaw the capture strips (purple) for the required number of samples, and just add DNA and enzymes. Run the capturing program in a thermal cycler
2. Add the Exo MasterMix and run the exonuclease program in a thermal cycler.
3 Thaw an equal number (as in step 1) of barcoding strips (blue) and transfer a fixed aliquot from the capture strips to the same positions of the barcoding strips. Every well of the Barcoding PCR strips contain unique sample ID barcodes. Run the barcoding PCR program
4. Combine all wells in one tube, purify this single tube with SPRI beads: **Ready for Sequencing**.
5. Import the fastq files into JSI SeqNext software, load the predefined analysis- and ROI settings and simply press the analysis button

Data Analysis

For downstream data analysis, NimaGen recommends **SeqNext** from **JSI medical systems**. Analysis settings templates for the EasySeq™ generated sequence data will be available through JSI (www.JSI-medisys.de).

[1] Hiatt JB, Pritchard CC, Salipante SJ, O'Roak BJ, Shendure, J., Single molecule molecular inversion probes for targeted, high-accuracy detection of low-frequency variation. Genome Res 2013;23:843–54.

[2] Kornelia Neveling et al., BRCA Testing by Single-Molecule Molecular Inversion Probes. Clinical Chemistry 2016; 63:2.

Features

The revolutionary smMIP based enrichment method, in combination with the straightforward, kit design provides a number of unique features:

All probes are manufactured by **Biolegio** and contain NimaGen's novel proprietary smMIP backbone design

- Reduced amplification bias
- Simplified protocol: no need for custom primers
- Compatible with all Illumina platforms, including the new iSeq instrument

No need for DNA fragmentation

The targeted DNA sequences are captured by a pre-aliquoted MasterMix containing a balanced smMIP pool, in one single well per sample: Just add the DNA and start capturing.

Single Molecule analysis

Due to the unique single molecule tags, the system generates consensuses of original molecular captures. This enables ultra-high sensitivity in detecting low mutation rates and ruling out sequencing errors and features intrinsic CNV detection for germline analysis on DNA derived from blood.

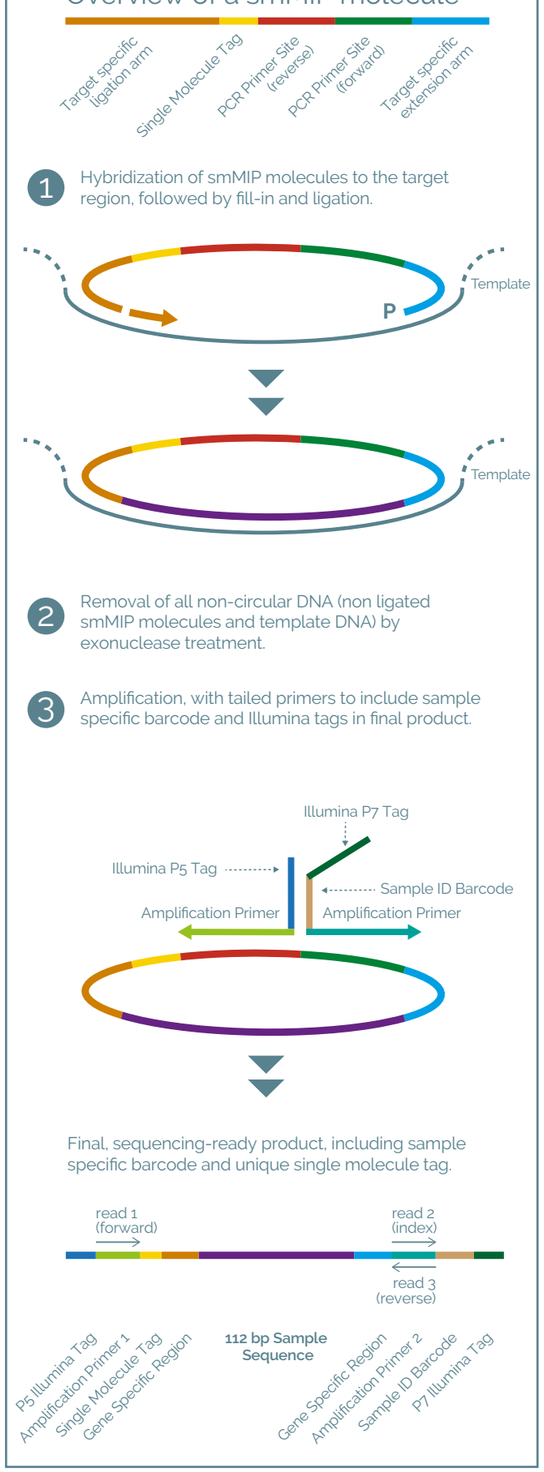
Sample Identification by SNP-smMIPs

Besides the probe pool for capturing the targeted hotspot regions, the assay contains additional identification smMIPs, targeting a set of high variable, genome-wide Single Nucleotide polymorphysms, for additional quality control (sample tracking), error detection (mixed DNA detection), and heritance checking.

Double Tiling

Most of the targeted regions are covered by at least two independent smMIP reads on both strands, enabling identification of formalin induced sequence errors in FFPE samples.

Figure smMIP overview and schematic workflow



EasySeq™ workflow