

The GenapSys™ Sequencing Platform

Sequencing Without Compromise

Exceptional Accuracy

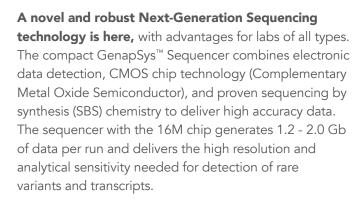
Highly accurate data validated by numerous applications in experienced third party labs

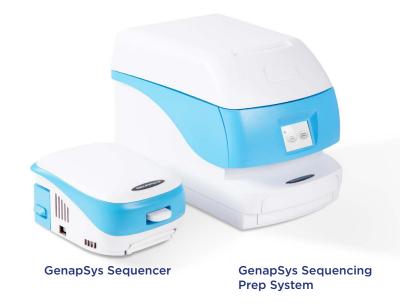
Unrivaled Scalability

A range of outputs tuned to your sample throughput needs

Amazing Affordability

Modest run and instrument pricing enable operational flexibility





- Fast, cost-effective runs that match your sample throughput needs and applications
- Perform runs on your own schedule, without having to wait for additional sample batching
- Control the sequencing process from beginning to end for higher confidence in sample integrity and data analysis results
- Affordable list price puts sequencing within the reach of virtually any lab

Streamlined 4-step workflow using the GenapSys Platform



Step 1: Library preparation



Step 2: Clonal Amplification



Step 3: Sequencing



Step 4: Data Analysis

Library Preparation

The sequencer is compatible with a broad range of library preparation methodologies. Performance has been demonstrated across multiple kits.

Clonal Amplification

Addition of pooled libraries and run consumables is followed by a simple run setup process. Once in operation, the GenapSys Sequencing Prep System automates the clonal amplification procedure in an unattended 4-hour run. The final amplified product is then ready for sequencing.

Sequencing

Amplified material is loaded into a sequencing chip. The user-friendly system interface walks the user through consumables loading and the run setup procedure. The system uses our proprietary high accuracy SBS chemistry to deliver high-quality data.

Data Analysis

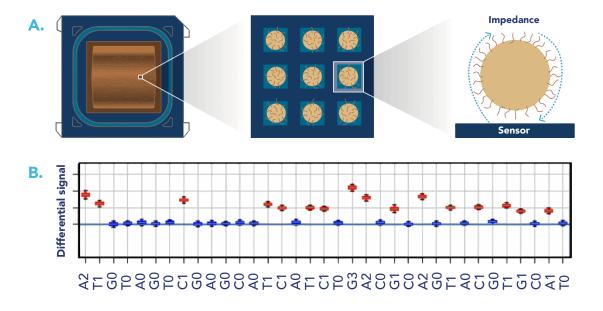
The sequencing run output is a standard FASTQ file. This allows for existing secondary analysis tools to be utilized for analysis of GenapSys data. For highest quality results, we recommend customers to use GenHub, our proprietary cloud hosted solution, to run secondary analyses with empirically derived, optimized parameters for GenapSys data. This obviates the need for expensive additional localized servers. Additionally GenHub provides customers real time monitoring of the status of the sequencing run as well as accessing FASTQ and VCF files of all runs.

Novel Base Detection Technology

The CMOS sequencing chip contains millions of individual sensors, which are each loaded with a clonally amplified bead. The electrodes in each sensor measure minute changes in impedance when nucleotides are incorporated opposite the bead-bound templates.

When a nucleotide is incorporated, the measured impedance value of that sensor will jump creating a graph that resembles a staircase. Information on how the signal has changed can be summarized as differential signal. The magnitude of the differential signal correlates with the number of incorporated nucleotides.

The plot contains a representative example of acquired data showing the distribution of measured differential signal across multiple nucleotide flows for a single template sequence. Flows that are expected to have nucleotide incorporations are highlighted in red. Non-incorporating flows are shown in blue and do not deviate significantly from the baseline. The inferred sequence, including the number of nucleotides in each incorporation is shown at right.



Scalable output supports a wide range of applications

16M Chip Output Specifications

| Average Read Length | Reads | Output (Gb) | Accuracy | Run Time (Hours) |
|---------------------|--------|-------------|-----------------|-----------------------------|
| >150 bp | 10-13M | 1.2 - 2.0 | >80% bases >Q30 | ~24 (read length dependent) |

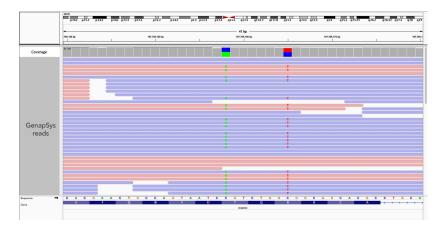
The 16M Chip with an initial output of 1.2 - 2.0 Gb per run enables the following applications:

- Targeted resequencing
 - Amplicon based
 - Hybridization capture based
 - Long-range PCR
- Small genome sequencing
- Gene editing validation
- 16S rRNA-sequencing
- Targeted mRNA sequencing
- Small RNA sequencing
- Targeted single cell assay sequencing

Applications that can be run on a cluster of sequencers using 16M Chips or on the 144M Chip (available 2020):

- Highly multiplexed targeted panels
- Exomes
- Transcriptomes
- Single cell gene expression

Key data demonstrate sequencer performance and accuracy.



 $\textbf{Fig. 1} \ \mathsf{IGV} \ \mathsf{visualization} \ \mathsf{of} \ \mathsf{two} \ \mathsf{heterozygous} \ \mathsf{SNPs} \ \mathsf{in} \ \mathsf{the} \ \mathsf{RUBCN} \ \mathsf{gene}.$

The GenapSys platfrom has been validated against market leading systems over various genomic samples in third party expert labs with >80% bases >Q30. The platform with the 16M chip is capable of generating 1.2 - 2.0 Gb of high-quality sequence data in a single run and delivers the high resolution and analytical sensitivity needed for detection of rare variants and transcripts. Routine performance exceeds 99% accuracy with an average read length of >150 bp.

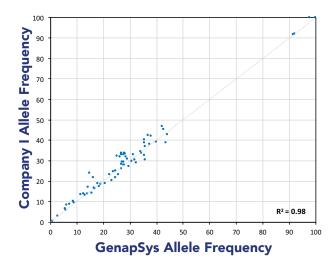


Fig. 2 Correlation of allele frequencies measured from sequencing data generated by GenapSys and an established sequencing platform. Sequenced libraries were generated from the Oncospan Reference DNA standard enriched using a pan cancer hybrid capture panel.

System specifications and ordering information

| Parameter | GenapSys Sequencer (P/N 1001500) | GenapSys Sequencing Prep System (P/N 1000712) |
|---|--|---|
| Dimensions (WxDxH) | 19 cm x 30 cm x 14 cm (7.5 in. x 11.75 in. x 5.5 in.) | 28.5 cm x 41.1 cm x 32.8 cm (11.2 in. x 16.2 in. x 12.9 in.) |
| Weight | 4.3 kg (9.5 lbs.) | 14.6 kg (32.1 lbs.) |
| Instrument control computer (external)*† | Operating System: Windows 10 PRO | NA |
| | Processor: x64-based with 2.0 GHz clock or faster | |
| | RAM: At least 8 GB | |
| | Hard Drive: At least 200 GB | |
| | Graphics Card: Compatible with DirectX 9 or later with WDDM 1.0 driver | |
| | Display: At least 1600 x 900 | |
| | Compatible Browser: Google Chrome | |
| Operating environment | Temperature: 19°C to 25°C (22°C ±3°C) | Temperature: 19°C to 25°C (22°C ±3°C) |
| | Humidity: Noncondensing 30-75% relative humidity | Humidity: Noncondensing 30-75% relative humidity |
| | Altitude: Less than 2000m (6500 ft) | Altitude: Less than 2000m (6500 ft) |
| | Air Quality: Pollution degree rating of II | Air Quality: Pollution degree rating of II |
| | Heat Output: 852 BTU/hr @ 250W | Heat Output: 852 BTU/hr @ 250W |
| | For Indoor Use Only | For Indoor Use Only |
| Power requirements | 100 - 240 VAC, 50-60 Hz, 250W | 100 - 240 VAC, 50-60 Hz, 250W |
| Instrument configuration | RFID tracking for consumables | RFID tracking for consumables |
| Radio frequency identifier (RFID) | Frequency 13.56 MHz | Frequency 13.56 MHz |
| | Power: Supply current 120 mA | Power: Supply current 120 mA |
| Product safety and | NRTL certified IEC | NRTL certified IEC |
| compliance | FCC/IC Approved | FCC/IC Approved |

^{*} Laptop or PC is customer supplied

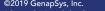
To learn more about the Genapsys Sequencing Platform, visit GenapSys.com

See the following application notes for specific applications and workflows:

- GenapSys Sequencing Platform: Variant Calling
- GenapSys Sequencing Platform: Small Genome Sequencing
- GenapSys Sequencing Platform: Oncology Research Applications

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 $^{^{\}scriptscriptstyle\dagger}$ One computer should be able to control up to 8 Sequencers