applied biosystems® by life technologies™

5500 Series Genetic Analysis Systems

Pay-Per-Lane Sequencing for every researcher

Key benefits

Sequencing right here, right now
Sequence when you need it, without the wait or any exorbitant reagent penalties for unused lanes

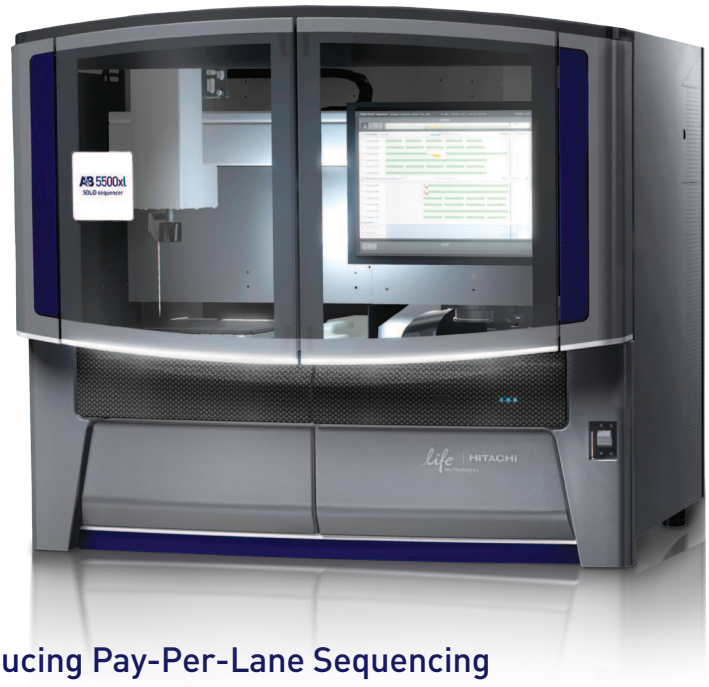
Cost-effective sequencing runs with individually configurable lanes
Run a variety of sequencing applications simultaneously while meeting your budget

Superior low-frequency variant detection for whole exome sequencing or targeted resequencing
Leverage industry-leading accuracy of up to 99.99% for detection of low-frequency variants in disease research

Reproducibility, reliability, and quality for your RNA applications
Trust Ambion® products, protocols, and unrivaled accuracy

Confidence and uniformity in multiplexing with up to 96 barcodes
Utilize robust protocols and well-balanced barcodes for cost-effective multiplexing that works

Optimal analysis solutions for streamlined productivity and freedom to operate
Rely on a comprehensive data analysis solution to advance your research discoveries



Introducing Pay-Per-Lane Sequencing

The 5500 Series Genetic Analysis Systems maximize efficiency and productivity like never before with Pay-Per-Lane Sequencing (PPL-Seq™). Whether you are using two FlowChips with the 5500xl System or one FlowChip with the 5500 System, each FlowChip has six independently addressable and configurable lanes that allow you to sequence your samples when you need to. With the 5500 Series Genetic Analysis Systems, you can run one or a few lanes immediately without the costly reagent penalty for unused lanes. Independent lanes also allow you to run genome, exome, transcriptome, and many more experiments in parallel within the same run. Combining industry-leading accuracy with the new Exact Call Chemistry (ECC) module, the 5500 Series Genetic Analysis Systems are designed to generate superior data quality for variant detection, which is particularly critical for targeted resequencing studies. Reliable protocols for RNA sequencing and a robust, well-balanced barcoding system for cost-effective multiplexing in DNA and RNA applications are unmatched by any platform. The 5500 Series Genetic Analysis Systems are the only next-generation sequencing platforms to integrate Pay-Per-Lane Sequencing (PPL-Seq™) with unrivaled data quality, providing the utmost in flexibility and accuracy for every researcher.

No waiting in line, no reagent penalty

When your research requires a fast turnaround time for a small experiment, the new 5500 Series Genetic Analysis Systems provide optimal efficiency with one or two FlowChips, each equipped with 6 modular lanes built for independent reagent consumption. It is the only next-generation sequencing platform enabling research labs to run just one, a few, or all lanes while paying only for the reagents used for those active lanes. You no longer have to choose between paying a high reagent penalty for unused lanes or delaying your results until the FlowChip is full. The transformative 5500 Series Genetic Analysis Systems bring tailor-made sequencing to truly fit your research demands at any project scale—when you want it.

Configure read length and chemistry of *each lane* for maximum efficiency and freedom to operate

Researchers strive to use their budgets in the most cost-effective manner, while simultaneously accommodating a variety of sequencing applications that can differ in read length and run type (e.g., fragment, paired-end, and mate-paired). From whole genome sequencing to small RNA analysis, the individual, configurable lanes of the 5500 Series Genetic Analysis Systems enable you to run different applications concurrently. This is designed to ensure efficient usage of each lane while specifying the preferred read lengths and run types for each application, giving you unmatched flexibility to address the dynamic needs of your projects most economically. You now are free from the restrictions of applying a single read length and run type across all lanes, which can lead to unnecessary reagent costs when more than one application is required. When your research calls for running genome, exome, transcriptome, and other experiments all at the same time, you have the power to meet those diverse research demands simultaneously and cost-effectively with the 5500 Series Genetic Analysis Systems.

Superior low-frequency variant detection for whole exome sequencing or targeted resequencing

Accuracy is essential, especially when examining heterogeneous samples for the discovery of low-frequency variants in the whole exome or smaller targeted regions. The 5500 Series Genetic Analysis Systems build on the industry-leading accuracy of two-base encoding with the new Exact Call Chemistry Module. ECC provides an orthogonal proofreading strategy by using a different set of encoding probes to interrogate the same sequence again, which means bases are read three times with only minimal additional cost. This unique chemistry approach results in up to 99.99% system accuracy, and enables the detection of even lower-frequency genetic variants. While some claim that higher sequence coverage compensates for less accurate data, this approach often increases the noise, maintaining the same signal-to-noise ratio while significantly escalating the cost of sequencing. The 5500 Series Genetic Analysis Systems allow you to detect low-frequency variants with its superior accuracy without costly over-sequencing, making it an ideal platform for exome resequencing and other targeted resequencing applications.

Reproducibility, reliability, and quality for your RNA applications

Whether performing fragment sequencing for small RNA analysis or paired-end sequencing for whole transcriptome analysis, RNA sequencing demands reproducibility and reliability. The 5500 Series Genetic Analysis Systems offer a superior solution for RNA applications with their inherent accuracy and the robust, innovative protocols offered by Ambion® products. With the accuracy of the 5500 Series Genetic Analysis Systems and the unique method for preserving strand information during RNA library construction, it is possible for researchers to map reads to the genomic DNA strand of origin, which is essential for interpreting results and analysis of reverse strand expression patterns. Additionally, well-developed and proven Ambion® product protocols are critical for generating more reliable results and higher concordance of transcripts relative to the reference sequence databases. As Life Technologies continues to innovate with new protocols for challenging sample types, including clinical research samples with low amounts of starting material and formalin-fixed, paraffin-embedded (FFPE) samples, you can count on 5500 Series Genetic Analysis Systems to be the most reliable and reproducible choice for RNA sequencing.

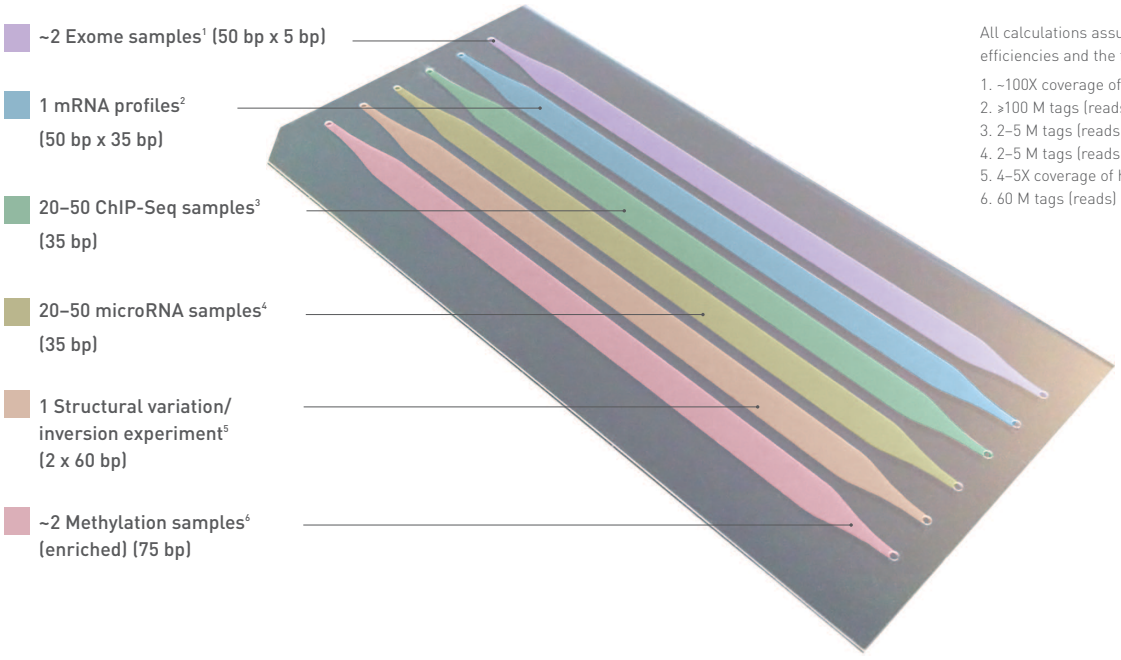
Confidence and uniformity in multiplexing with up to 96 barcodes

With high-throughput sequencing platforms, multiplexing is integral to completing your experiments economically as the required throughput per sample is much less than the available throughput per lane. While a whole exome experiment may require 5 to 10 Gb of sequence data per sample, RNA experiments may only require 2 to 50 million reads per sample. Whether running targeted resequencing or RNA sequencing experiments, the 5500 Series Genetic Analysis Systems can run up to 96 barcodes per lane, providing the ability to multiplex more than a thousand samples in a single sequencing run. Additionally, the robust 5500 barcoding protocols result in more uniform representation of each barcode, which is critical for sample discrimination when multiplexing. Unlike other platforms, the 5500 Series Genetic Analysis Systems provide well-balanced indexing with protocols that distinguish each barcode precisely, thus enabling researchers to combine samples in one lane instead of paying the reagent penalty for using single lanes. With both inferior accuracy and unbalanced barcode representation, there is no cost benefit associated with super-high throughput systems when costs of over-sequencing are properly considered. Whether you are multiplexing tens of exomes or hundreds of small RNA samples, you can rely on the accuracy and robustness of barcoding on the 5500 Series Genetic Analysis Systems,which provides you with premium-quality data in a cost-effective manner.

Optimal analysis solutions for streamlined productivity

Simplifying data analysis of next-generation sequencing data is crucial to accelerating your research. With the 5500 Series Systems, you have access to the best-in-class tools to expedite your research from sample preparation to publishable results. The easy-to-use graphical user interface of the instrument control software is directly integrated with sample preparation and the sequencing chemistry, easily facilitating run setup and run monitoring. Additionally, the optimized algorithms and analysis pipelines of LifeScope™ Genomic Analysis Solutions enable faster translation of next-generation sequencing data to biologically meaningful results, with visualization tools, reports, and annotations to streamline your analysis. Whether you are running large-scale genomic experiments or small- to medium-sized projects, a variety of LifeScope™ Genomic Analysis Solutions are available to enable you to meet your research requirements within any budget. You can choose from installing LifeScope™ Server Software on your own hardware, using a cloud computing option, or using preinstalled, preconfigured LifeScope™ hardware to simply plug into your pipelines for immediate analysis. With the 5500 Series Genetic Analysis Systems, you can count on Life Technologies to provide you with a complete and seamless data analysis solution to move your research forward.

Figure 1. Multiple applications on a single FlowChip with different read lengths and chemistries.



All calculations assume optimal running efficiencies and the following coverage:

1. ~100X coverage of human exome
2. ≥100 M tags (reads) per sample
3. 2–5 M tags (reads) per sample
4. 2–5 M tags (reads) per sample
5. 4–5X coverage of human genome
6. 60 M tags (reads) per sample

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Table 1. 5500 Series Genetic Analysis Systems specifications.

System and features	5500 System (1.0 µm microbeads)	5500xl System (1.0 µm microbeads)	5500xl System (0.75 µm nanobeads available 2nd Half 2011[1])
Pay-Per-Lane Sequencing (PPL-Seq™)	Reagent consumption engineered independently for each lane; users pay only for reagent consumables in the active lanes when performing a partial run.		
Application-Per-Lane Sequencing	Independent FlowChip lanes allow you to configure read length of chemistry for each lane enabling multiple applications in a single run.		
System Accuracy with Exact Call Chemistry (ECC) Module[2]	Up to 99.99%		
Multiplexing	96 barcodes for both RNA and DNA applications		
Independent lanes	1–6 (1 FlowChip)	1–12 (2 FlowChips)	1–12 (2 FlowChips)
Throughput[3,4]	7–9 Gb/day	10–15 Gb/day	>20 Gb/day
Exomes/run[5]	Up to 8 exomes	Up to 16 exomes	Up to 24 exomes
Transcriptomes/run[6]	Up to 8 transcriptomes	Up to 16 transcriptomes	Coming in 2nd Half 2011
Human genome/run[7]	Up to 1 genome (30X average coverage)	Up to 2 genomes (30X average coverage)	Coming in 2nd Half 2011
Maximum read lengths	Mate-paired: 2 x 60 bp Paired-end: 75 bp x 35 bp Fragment: 75 bp	Mate-paired: 2 x 60 bp Paired-end: 75 bp x 35 bp Fragment: 75 bp	Fragment: 50 bp
Sequencing run type	Yield and run times for 1 lane		
PE 50 bp x 5 bp[5,8]	1 exome, 2 days		
PE 50 bp x 35 bp[6,8]	1 transcriptome, 3.5 days		
MP 60 bp x 60 bp[8,]	1 human genome (4–5X average coverage), 7 days		

1. Specifications subject to change.
2. Accuracy is based on sequencing control synthetic beads, and reference-free data analysis.
3. For microbeads, throughput is estimated using fragment forward type runs on control beads deposited at a density of 230–250 K/panel, ~80% passing filter, and 25 bp fragment reads. For nanobeads, throughput estimated using fragment forward type runs on control beads deposited at a density of ~400K/panel, >~80% passing filter, and 25 bp fragment reads. Actual throughput will depend on sample(s) being run.
4. Throughput uses the quality reads from the instrument that pass the primary analysis filter.
5. ~50 Mb exome, 100X average coverage using paired-end (PE) chemistry; 50 bp x 5 bp, reverse 5 bp used for removal of duplicate reads (i.e., de-duplication).
6. ≥100 M reads/sample using PE chemistry, 50 bp x 35 bp.
7. Mate-paired (MP) chemistry, 2 x 60 bp.
8. Run times are approximate and will depend on actual sample(s) being run and do not include use of the ECC module or run setup time.

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